GENE PRECURSOR-SEQUENCE P-SEQID GENE-SEQ G-SEQID FOLDED PRECURSOR
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GAM25 GAGGCAGGAGAATTGCTTGA 1 CACGCCACTG 2 G AA GAA-- AG GCTT A - A
ACCCAGGAAGTGGAGGCTTC CACTCCAGTC GAGGCAG AG TTGCTT CCCAGGA TGGAG
CAGTG GC TG G
AGTGAGCTGAGAACACGCCA CT ||||||| || |||||| ||||||| ||||| ||||| || ||
CTGCACTCCAGTCCTGGGCA CTCTGTC TC AACGAG GGGTCCT ACCTC GTCAC
CG AC A
ACAGAGCAAGACTCTGTCTC - AG ACAAC G- AC-- - C A

GAM27 TTCCATTTGTTTGTGTCATC 511 GTCATCTCTG 2187 TTG CTCT TTTCTTTG AT-- TT
TCCTT GTCC
TCTGATTTCTTTGAATAATG ATTTCTTTGA TGTCAT GA AATA GG TATAGTTA
GAAAAG C
GTTTATAGTTATCCTTGAAA ATAA |||||| || |||| || ||||||||| ||||||
AGGTCCTTCACTTTTCTTGT ACGGTG CT TTAT CC ATGTCGAT CTTTTC /
TAGCTGTATTCCTAGATATT TTA TT-- TCTCATA- AGAT TT TGTT- ACTT
ATACTCTTCTTGTGGCAATT
GTGAATGGGA

GAM28 TGGTGCCCGGGCAATTTGAT 1 TGTAGGTTTT 1674 - AATTT---- TT A - GG CAG CCGA
A AGA
TACCAACTGCGTGAGGTCCC CTACGGTATG GC GA ACC AC TGCGTGA TCC CGG
GTGGAA TAC C
AGCGGCCGAGTGGAAATACA GCAT || || ||| || ||||||| ||| ||| |||||| |||
GACCTAGTGTTCCACGCTAT CG CT TGG TG ACGCACT AGG GCT CACCTT
GTG /
CGATTGGAGTCACGCATGTA A GTATGGCAT TT A T G- TTA ATCG - ATC
GGTTTTCTACGGTATGGCAT
CGGACACACTA

GAM29 GCAGTCAAGATGTAATGGAT 2 AGTCAAGATG 1675 GA-- AA A AA CATC A
AGCAAAGCCATCGGGAAGAC TAATGGATAG GCAGTCAA TGT TGG TAGCA GC GGG A
CCTTGCTGCTACCGGGACAG CAAA |||||||| ||| ||| ||||| || |||
GATTTGACTGT TGTCAGTT ACA GCC ATCGT CG CCC G
TAGG GG - -- TT-- A

GAM30 GCTCCAAAGAACCAAGAGTG 3 CATTTCACTT 1676 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC

GAM31 GTAAACTCCAACCCAGAATG 4 TTGGAGCAGG 1677 AACCC - - TA AA T CA TCT
AC- CT

GGGAAGAATACTGAATTAGC TTTCATTCTC AGAAT GGGGAA GAA CTG TTAGC GAG CAT GGAC AATT G
TGAGCACATTCTGGACACAA CAAT ||||| |||||| ||| ||| ||||| ||| ||| |||| ||||
TTCTGACCAATTTCAGTCTC TCTTA CCTCTT CTT GAC GGTTG CTC GTA TCTG TTAA A
ATGATCTCTGTTGGAGCAGG TTTTC A A TG GA T TA C-- ACT CC
TTTCATTCTCCAATTCTCTT
TTACAGAAC

GAM32 CTCTTGAGCATGCTGACCAG 5 GACCAGTGCT 1678 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM33 GAGTCAGTCTTTTTTCTCAC 6 TCAGTCTTTT 1679 TC CTT CTTTA- A AG
CTTTATCTGGACAAGGAAGT TTCTCACCTT GAG AGT TTTTCTCAC TCTGG CA G
GGCTAGGATTATTGTGGGAG TATC ||| ||| ||||||||| ||||| ||
AAACTAGCTC CTC TCA AAGAGGGTG GGATC GT A
GA --- TTATTA G GA

GAM34 ACCTTGTAGTGTTCCCTCTC 7 TGTAGTGTTC 1680 TT--- CC TCT CT TTG
TAGGGCTGTTTGTTTCATTT CCTCTCTAGG ACC GTAGTGTTC TC AGGG GT T
CCCTCTGAATGAATGCTGCC GCTG ||| ||||||||| || |||| ||
ACACGGT TGG CGTCGTAAG AG TCCC TA /
CACAC TA TC- TT CTT

GAM35 ACAGTTTATCATCTGAGCCG 8 GAGCAAGATG 1681 --- - AG GAATG TAGC AG CCTGAA G GAGG
AATGGGTAATAGCCGAAGTG ATGGAGAGCT ATCATCT G CC GGTAA CGA TGC GAT ATTATG A
CCCTGAAGATGATTATGGAG GT ||||||| | || ||||| ||| ||| ||| ||||||
GAATTACATGATGTTGATAA TAGTAGA C GG CCGTT GCT ACG TTG TAGTAC /
AGCAATCGAATTTGCCAAGG AGG A GA AA--- TAA- A- AAATAG - ATTA
AGCAAGATGATGGAGAGCTG
T

GAM36 AGCCCGCTCTCCCAGTCATC 9 CATCAGAGTC 1682 C TCT GTCATCA TC --- TGATA G
AGAGTCTGGTTTCTTGATAT TGGTTTCTTG AGCC GC CCCA GAG TGGTT TCT TCC A
CCGAAGGGAAGATTCGGCCA ATAT |||| || |||| ||| ||||| ||| |||
CCTCGTTGGGTTCGCAGGCT TCGG CG GGGT CTC ACCGG AGA AGG A
A CTT TG----- C- CTT ----- G

GAM37 CTCTTGAGCATGCTGACCAG 10 GACCAGTGCT 1683 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||

CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM38 GCTTTTGCTCCAGATGGTTC 11 CCAGTGCCTT 1684 TT TCC T ATACTTT T - AA TC ACA
ATACTTTGCTTGGTCACAAG CAGAACTTTC GCT TGC AGA GGTTC GCT GG TCAC GGACA GC G
GACATCGCACAGTAAAGCTT TCTT ||| ||| ||| ||||| ||| || |||| ||||| ||
GTTCCGTGGTCCCAGTGCCT CGG ACG TCT TCAAG TGA CC GGTG CTTGT CG T
TCAGAACTTTCTCTTGCATG T- TTC T ACTTCCG C T C- T- AAA
GC

GAM39 CTCTTGAGCATGCTGACCAG 12 GACCAGTGCT 1685 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM40 GAGGCGGCTCAGTGTGAAGA 13 AGGCGGCTCA 1686 C C AAGAACTAC CTG
ACTACGGGTTTCCTGATGTT GTGTGAAGAA GAGG GG TCAGTGTG GGGTTTC A
GAAGCTCAGAATTAGCCACA CTAC |||| || |||||||| |||||||
CTGACCTTCTC CTCT CC AGTCACAC CTCGAAG T
T - CGATTAAGA TTG

GAM41 GCTGAAGATTGTGGGCGTGA 14 TCTACACGTG 1687 GA TG ----- - C- GA- A
CCACGGAAGATGACGGCATC CATCGCTGTC GCTGAA T TG GGC GTGA CACG AGATG C
TACACGTGCATCGCTGTCAA AATG |||||| | || ||| |||| |||| |||||
TGACATGGGTTCAGC CGACTT G AC CTG CGCT GTGC TCTAC G
G- GT AGTAA T AC ACA G

GAM42 AGCCATATCTTGTGGTATGT 15 AACAGTATCT 1688 A -- TA-- A ATTTC
TTATAACGTATTTCTTTCAC ACTAAAGATG AGCC TATCTT GTGG TGTTT TAACGT T
ATGTTAAAACAGTATCTACT GGCT |||| |||||| |||| ||||| ||||||
AAAGATGGGCT TCGG GTAGAA CATC ACAAA ATTGTA /
- AT TATG - CACTT

GAM43 CGGCCTATATCGAGATCGCG 16 GGCAAGATCT 1689 G GC GTACA
CCGGTGTACAGCTATCAACT GGTGTAGGCT CGGCCTATATC AGATC GCCGGT G
GGCAAGATCTGGTGTAGGCT G |||||||||| ||||| ||||||
G GTCGGATGTGG TCTAG CGGTCA C
- AA ACTAT

GAM44 TATTGTGTAGGCCAGGCGTG 17 TGAGGTCAGG 1690 TG A G GG CCCC TAT CACTT GA GA

GTGGCTCACCCCCCTGTATT AGTTTGAGAC TGT GGCCAGGC TGGT CTCA CCTG TCTCAG TGG GGCC G
CTCAGCACTTTGGGAGGCCG TAGC ||| |||||||| |||| |||| |||| |||||| ||| ||||
AGGCAGGTTGATCACCTGAG ACG CCGGTCCG ATCA GAGT GGAC GGAGTC ACT TTGG G
GTCAGGAGTTTGAGACTAGC GT A - -- TTGA T-- C---- AG AC
CTGGCCAGCATGGTG

GAM45 GAGGCGGCTCAGTGTGAAGA 18 AGGCGGCTCA 1691 C C AAGAACTAC CTG
ACTACGGGTTTCCTGATGTT GTGTGAAGAA GAGG GG TCAGTGTG GGGTTTC A
GAAGCTCAGAATTAGCCACA CTAC |||| || |||||||| |||||||
CTGACCTTCTC CTCT CC AGTCACAC CTCGAAG T
T - CGATTAAGA TTG

GAM46 GTGCTGAAAGGAATCACTTT 19 TTGCAGTGGC 1692 TG A- - CTT - - - T TG
ATACCCACGCTGGGTGTATT GTAATGTTCT G CTGAA GGAAT CA TAT AC CCAC GC GGG T
CTTGCAGTGGCGTAATGTTC GAAT | ||||| ||||| || ||| || |||| || |||
TGAATTCCACTTTAGTGC C GATTT CCTTA GT GTA TG GGTG CG TCT /
GT CA A CTT A C A T TA

GAM47 TCCAACTTTGTGGAATGGTA 20 GTAAGGATTT 1693 T-- GAATG- AGG AGGG GG
AGGATTTTTAGGGTTGTTTG TTAGGGTTGT TCCAACT TGTG GTA ATTTTT TTGTTT C
GCCAGAACAAGAGAAATAAC TT ||||||| |||| ||| |||||| ||||||
TGCAGAAAACACATATGGTT AGGTTGG ACAC CGT TAAAGA AACAAG /
GGA TAT AAAAGA CAA G--- AC

GAM48 GCTCCAAAGAACCAAGAGTG 21 CATTTCACTT 1694 T - ---------- CAC AGATAG TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCTG GGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| |||||| ||||
TCTAAGACCACGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGGC CCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM49 GCTTGACCAATGACTGGGAA 22 AAGCATCCAC 1695 A--- AA - AGA- T
GATCACTTGGCAGTGAAGCA AGTTGAAGGA GCTTG CC TGACTG GGA TCACT G
TCCACAGTTGAAGGACAGTA CAGT ||||| || |||||| ||| |||||
GGC CGGAT GG GTTGAC CCT AGTGA G
GACA AA A ACGA C

GAM50 GTGGCAGAAGGGTACTCAAG 23 TGACAGAGAC 1696 C - C- AG - TC-- GCA G G
GGACAATCGTGGCATCGGTC ACAGTTTTGC GTGG AGAAGG GTA TCA GGA CAA GTG TC GTCAAG C
AAGGCAGCTTGACAGAGACA TCTG |||| |||||| ||| ||| ||| ||| ||| || ||||||

CAGTTTTGCTCTGGTGAATT CATC TCTTCT CAT AGT TCT GTT CAC AG CAGTTC A
ACATCTTCTCTAC - A TA GG C TTGA AG- A G

GAM51 AAATCAGACCCGGGTTCATT 24 TCAGACCCGG 1697 - C A CTG-- A
CCACTGGCCAGAGGCAGTCT GTTCATTCCA AAATCAGA C CGGGTTC TTCCA GCC G
TGGGAGGATTTGTGTTCTGG CTGG |||||||| | ||||||| ||||| |||
TTT TTTGGTCT G GTTTAGG AGGGT CGG /
T T - TCTGA A

GAM52 AGGGGGGCAAAGTCTATCAG 25 GGGGCAAAGT 1698 G GT A TG TTGAAA TG- AG
G GAT
GTGTTTGAAAGTGTGGCTAA CTATCAGGTG AGGG GGCAAA CT TCAGG T GTG GCTAAGA
TAT ATGT G
GAAGTATGATGTGATGAATG TTTG |||| |||||| || ||||| | ||| ||||||| ||| ||||
ATATGATGAGTCTTGGTATC TCTC TCGTTT GA GGTTT G TAC TGGTTCT GTA
TATA A
CATCGTGTTTGGAAGGATTT G AG A GT C----- CTA GA G GTA
GCTGCTCT

GAM53 CTTTCAGTCTTTATTTGCAG 27 CTTTCAGTCT 1703 T TTT A AA ACCA TATAT --- TT
C CAC
CAAACTACCACTTTATATGG TTATTTGCAG GTCT TA GC GCA CT CTT GGC AGG
TGTGTGT TGTA G
CAGGTTTGTGTGTCTGTACA CAAA |||| || || ||| || ||| ||| ||| ||||||| ||||
CGCACATACACACACATATC CAGA AT CG CGT GA GAG TCG TCC ATACACA
ACAT C
CTTAAGCTCGAGACAGGGTG C TT- G GG CA-- C---- AAT T- C ACA
CGGCTTTACAGACCAAAAAG
TATGGAAG
GAM54 TGGCACCTGGTGAAGAAGAG 28 TGGAATTTGA 1704 - - A AGA TT GA A AT GA T
G G
AATTTGGAATTTGAAGAAGA AGAAGATGAA CCT GGTGA GAAG AT GGAATTT AG AG
GAAGAA GGG GGT CTG A
TGAAGAAGAGGGTGGTGCTG GAAG ||| ||||| |||| || ||||||| || || |||||| ||| ||| |||
GAGCAGGGTCTCCTGATTCT GGA CCATT TTTC TG CCTTGAG TC TC TTTCTT TCC
CTG GAC /
TTTCCTGCTAGAGTTCCCGG T A A A-- GC A- G CT AG T G G
TACTTTATTACCAAGGTTGC
CA
GAM55 ATTATTGCCTAGTCATCAAA 29 TTGCCTAGTC 1705 GTCAT A - ACTC GT CA TC-- T
TTTCT CAC
ATGGAAACTCAAGGTTCCCA ATCAAAATGG CAAA TG GAA AAG TCC GGAA AGCAG
TAT GGC A
GGAATCAGCAGTTATTTTCT AAAC |||| || ||| ||| ||| |||| ||||| ||| |||
GGCCACAAGCTGCCTTTTGT GTTT AC CTT TTC AGG CCTT TTGTT ATG CCG
A
ACTTGTTTACCTTCCAGGAG TTC-- C T A--- TG A- CCAT C TTTT- TCG
TCTTATTCTCACTTTGCTTT

TGGCATCAGAT

GAM56 ACAGTATTTTGGAAAGACAT 30 TGGAAAGACA 1706 T A A TA A TTC TTC

AGGGTAGTTTCCTTCCTTCT TAGGGTAGTT ACAG ATTTTGG AAG CA GGGT GT CTTCC T

CAATGGAAGACACTTGCTGA TCCT |||| ||||||| ||| || |||| || |||||

CTTATCGGAATCCTGT TGTC TAAGGCT TTC GT TTCA CA GAAGG C

C A A CG - --- TAA

GAM57 TGTACTTGAATCAATCATGG 31 TTGAATCAAT 1707 A AA A T TT AC C

TTTACACTCTCCAGAGAGAA CATGGTTTAC TGT CTTG TCA TCA GG TAC TCTC A

AGTATCCTTTGATGAAATAA ACTC ||| |||| ||| ||| || ||| ||||

GGACA ACA GAAT AGT AGT TC ATG AGAG G

G AA - T CT AA A

GAM58 GACAGATAAATAAGGTTGCA 32 TCGGTCTTTT 1708 A TA TA TTGCAT G A A G

TGATGGATATTAGGGGGGAA TCTCTTTCTT GAC GA AA AGG GAT GAT TTAGGGGGG ACA

G

CAGGCCTGTACCCCCCTAAA CGTC ||| || || ||| ||| ||| ||||||||| |||

ATCGGTCTTTTTCTCTTTCT CTG CT TT TCT CTG CTA AATCCCCCC TGT C

TCGTC - TC TC TTTT-- G A A C

GAM59 TGTCCCTCTTCAAGTAATCT 33 TTCAAGTAAT 1709 CCT AAG T AGAATGTG CTT

GAA

AGGAAGAATGTGGATACTCT CTAGGAAGAA TGTC CTTC TAA CTAGGA GATACT

AGGCGT T

TAGGCGTGAATGTAAATGCC TGTG |||| |||| ||| |||||| |||||| ||||||

TTAAGTATTGAAGGTCCTGG ATAG GAAG ATT GGTCCT TTATGA TCCGTA G

TTAGAAGCATGATA TAC --- - GGAAG--- AT- AAT

GAM60 CAGAAGGACGATGCTGAGCC 34 CCTCACAGGC 1710 A A T- G AT--- A GC AA G

CTG

ATGGATCGCGGAAGGCGTCC TGAGTTCTTG CAG AGG CGA GCT AGCC GG TC GG GGC

TCCT G

TCTGGCCTCAGGAGCCACCC CCTC ||| ||| ||| ||| |||| || || || ||| ||||

AGAGCCTCACAGGCTGAGTT GTC TCC GTT TGA TCGG CC AG CC CCG AGGA C

CTTGCCTCTG - - CT G ACACT G A- CA - CTC

GAM61 GCTGTGCTTACTGCAGTGCA 35 ACTGCAGTGC 1711 ACTG AGA CTAA --- -

GAA

GAGGCCTTCTAAGCGCTGCT AGAGGCCTTC GCTGTGCTT CAGTGC GGCCTT GCGCTGCT

CA CGATGCCA T

CACGATGCCAGAATGCAGTG TAAG ||||||||| |||||| |||||| |||||||| || ||||||||

GTATTGCTGCCAGGCAGTGC CGGTACGAA GTCACG CTGGAA CGTGACGG GT

GTTATGGT G

AAGGTCAAGCACTGGGAAAA AAGG AA- ---- ACC C GAC

GCATGGC

GAM62 GCTCCAAAGAACCAAGAGTG 36 CATTTCACTT 1712 T - ---------- CAC GAGATA TC

CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T

TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||

TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /

GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA

ACTCGATTTGCTTCCGGACC

TTTTCCAGAGC

GAM63 TCCTTTTGACAAGAAATGTG 37 TGACAAGAAA 1713 T - AAATGT C AA-- CTGTT T

GTCGTGAAAATTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA TTGGA GC T

GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||

ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T

GA C G GTT--- - GGTA ----- T

GAM64 GCTCCAAAGAACCAAGAGTG 38 CATTTCACTT 1714 T - ---------- CAC GAGATA TC

CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T

TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||

TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /

GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA

ACTCGATTTGCTTCCGGACC

TTTTCCAGAGC

GAM65 GCAGTGGGTTTCCCTATGGC 39 AGTGGGTTTC 1715 - G TCC CT-- TC TT AT

TTGGATCCAGATTAGAATTG CCTATGGCTT GCA GT GGTT CTATGG TGGA CAGA AGA T

ATCTTCTGTCTTCACTTTCC GGAT ||| || |||| |||||| |||| |||| |||

ATAGCTTAACTAACATGC CGT CA TCAA GATACC ACTT GTCT TCT /

A A TTC TTTC CT -- AG

GAM66 TGCTGGTAAAATCACTGGCA 40 TCATATGCTC 1716 TAAAA ACT T TT A- T

TGTTGTTGGAGATTGATAAT GAGTCTCCAG TGCTGG TC GGCATGT G GGAG TTGA A

TCAGAACTTCTTCATATGCT TA |||||| || ||||||| | |||| ||||

CGAGTCTCCAGTA ATGACC AG TCGTATA C CTTC GACT A

TCTG- C-- - TT AA T

GAM67 GCCATTGCTGAGGCCTGGGC 41 TCGCCTGGAC 1717 ---- GGA A- AG GA TG AT -- - TG

TCGCCTGGACCACAAGTTTG CACAAGTTTG GGCCT GGGCTCGCCT CC CA TTT CC ATGT GCCA AACG C

ACCTGATGTATGCCAAACGT ACCT ||||| |||||||||| || || ||| || |||| |||| ||||

GCCTTTGTTCACTGGTACGT CCGGA TTTGAGTGGA GG GT GGG GG TGCA TGGT TTGT C

TGGGGAGGGGATGGAGGAAG GACT A-- AG AG AG GT -- CAC TT
GTGAGTTTTCAGAGGCCCGT
GAGACATGGC
GAM68 AGCCATATCTTGTGGTATGT 42 AACAGTATCT 1718 A -- TA-- A ATTTC
TTATAACGTATTTCTTTCAC ACTAAAGATG AGCC TATCTT GTGG TGTTT TAACGT T
ATGTTAAAACAGTATCTACT GGCT |||| |||||| |||| ||||| ||||||
AAAGATGGGCT TCGG GTAGAA CATC ACAAA ATTGTA /
- AT TATG - CACTT

GAM69 TGAGGCTCCAGGATGATGCT 43 TGAGGCTCCA 1719 CCAGG AT TACAA - C ACC
ACAAAAAGCATTGGCATAAA GGATGATGCT TGAGGCT ATG GC AAAGCAT TGG ATAAA T
ACCTTGCTTTGTCCCAGGTG ACAA ||||||| ||| || ||||||| ||| |||||
CTTTCCCTTGCCACATGACA ACTCCGA TAC CG TTTCGTG ACC TGTTT /
AGCCTCA ACAG- AC TTCCC G C CGT

GAM70 TGCTGTAGGCTGTATGCTGT 44 TAATGCTAAT 1720 ---- T-- C A T- C
TAATGCTAATCGTGATAGGG CGTGATAGGG TGCTG TAGGC GTATGCTGTTAATGCTAAT
GTG TAGGGGTT TTG C
GTTTTTGCCTCCAACTGACT GTTT ||||| ||||| |||||||||||||||||| ||| |||||||| |||
CCTACATATTAGCATTAACA ACGAT GTCCG TATGTGACAATTACGATTA TAC
ATCCTCAG AAC T
GTGTATGATGCCTGTTACTA CATT TAG - - TC C
GCA

GAM71 TGTCAATGTCCATGTCCTGG 45 TGTCCTGGTA 1721 TC T GT TG- CC A T - AG
TAGGCCTTCTTCATGCTTTG GGCCTTCTTC TG AATG CCAT CC GTAGG TTCTTC TGCT TGG
GC C
GGCAGCAAGCTCCATGGTAC ATGC || |||| |||| || ||||| |||||| |||| ||| ||
GAAGGACTTCTGCATTGGTA AC TTAC GGTG GG CGTCT AGGAAG ATGG ACC CG /
GTGGCATTCTCA TC - AT TTA TC C T T AA

GAM72 ACAGTGAAAGTGATGAATGG 46 CTCAATGCCA 1722 AAA AA A GAA CTT C
ACAGAAGACTTGCCAATGCT GGTATTACCA ACAGTG GTGATG TGG CA GA GC A
CAATGCCAGGTATTACCACT CTGT |||||| |||||| ||| || || ||
GT TGTCAC CATTAT ACC GT CT CG A
--- GG - AA- --- T

GAM73 GGTACAGAGAGCTGTGTGCC 47 TCGCCTGGAC 1723 ----- A-- - TG T T AACA- A C
ATGCTGAGCAACACCACAGC CACAAGTTTG GGTA CAG GAGCT GTG CCA GC GAGC CC
CAGC A
CATTGCTGAGGCCTGGGCTC ACCT |||| ||| ||||| ||| ||| || |||| || ||||
GCCTGGACCACAAGTTTGAC CCGT GTC TTTGA CAC GGT CG CTCG GG GTCG T
CTGATGTATGCC ATGTA CAG A CA C - GGTCC A T

GAM74 TGCGCAACTTGGCATGGACA 48 TATCACTGCC 1724 AC A A A-- TC

AATGACTGTGTCTCGCACGG AGCTAGTGTG TGCGCA TTGGC TGG CA ATGACTGTG T
TTATCACTGCCAGCTAGTGT CA |||||| ||||| ||| || |||||||||
GCA ACGTGT GATCG ACC GT TATTGGCAC /
-- - - CAC GC

GAM76 GAAGACGACAGAAGGGAGTG 49 CGACAGAAGG 1725 C-- A - T C- AGGT G
AGCCCAAAGGTTCGAAAGGT GAGTGAGCCC GAAGA GAC GAAGG GAG GAGC CAA TC A
GTTGCAGCTTCTTCGCCTTC AAAG ||||| ||| ||||| ||| |||| ||| ||
GTCAAATCTTC CTTCT CTG CTTCC CTT TTCG GTT GG A
AAA - G C AC GT-- A

GAM77 CCGGTGATTGTGGAAAAGGT 50 ATCACTGTGG 1726 - --- AAA T GTTC- TGTT C
TG CAG G
CTCAGGTTCTCAGATTGTTG CTCAGTTCAT CC GGTGATT GTGGA GGTC CAG TCAGAT
GA AT A GC G
ACATTGACAGGCGGAAGTAC GTGG || ||||||| ||||| |||| ||| |||||| || || | ||
TTGGTTCCATCTGATATCAC GG CTACTAG TACTT TCGG GTC AGTCTA CT TG T
TG A
TGTGGCTCAGTTCATGTGGA A GTG GAC T ACTAT C--- - GT CA- A
TCATCAGG

GAM78 GAAGGGGGACCGGGAGAAAC 51 TTCCCTGTGG 1727 AG GG G AAACG AT G TG CT- -
- TC
GAGATGGGGGTGAAGCTGGA CTATGTTCTG GA GG ACC GGAG AG G GGG AAG GG
AGAT ATT G
GATATTTCGGATGATAATCT GGTT || || ||| |||| || | ||| ||| || |||| |||
ACCTCACTTTCCCTGTGGCT CT CC TGG TCTT TC T TCC TTC CC TCTA TAG G
ATGTTCTGGGTTTCCAATC AA TT G GTA-- GG G CT ACT A A TA

GAM79 CCTACTCCAAAATACTCACA 52 TCTACAGTGT 1728 A - A TC-- -- GA
CTGGACTGAATGAAGTCTAC CAATGTGTCT CCT CTC CAA ATAC ACACTG GACT A
AGTGTCAATGTGTCTTGAGA TGAG ||| ||| ||| |||| |||||| ||||
GAGG GGA GAG GTT TGTG TGTGAC CTGA T
- A C TAAC AT AG

GAM80 GAGTGCAAATCAGTCCATTT 53 CATTTCACTT 1729 T - ---------- CAC GAGATA
TC
CACTTTCACTGTCTGAGATA TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT
TGTCT GGGTC T
GGGTCTCTAAGACCCAGGAT AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
ACAAGGGTGGAATGTAGCTA CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
TATGGACTCGATTTGCTTC - C TATCGATGTA AC- A----- AA

GAM81 TGAAGACTTCCTAAATTTGC 54 TTTGCACATT 1730 AC A TTGCA TTGCC ACCAT

ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM82 CACCCTCGCTTGGAACGGCC 55 TCAGATCCTT 1731 GA G -- G- - G GTG- TA-
ATAGC
TTCAGATCCTTTGGGCTTGG TGGGCTTGGC CTTG AC GCCT TCA ATCC TTTGGGCTTG CT
GGC ATGCC T
CTGTGGGCTAATGCCATAGC TGTG |||| || |||| ||| |||| |||||||||| || ||| |||||
TGGTGAAGGCATATTGCCAC GGAT TG CGGA AGT TGGG GGACCCGGAC GG CCG
TACGG G
TGGGGCAGGCCCAGGTGGGT AA G CG AG T G GTCA TTA AAGTG
GATGAGCAGGCGGTAATAGG
CAGTAAAGGTG
GAM83 AAAGATGATAAAATTCCTGC 56 AAGGAGCTTA 1732 A AT- CT - CTTACA C --
AGA G
TCTCAAGGAGCTTACAGTCT CAGTCTAGTC AAAGATG TAAA TC GCT CTCAAGGAG
GTCTAGT AG GT CA A
AGTCAGGTAGACAGACATGC AGGT ||||||| |||| || ||| ||||||||| ||||||| || || ||
AGACAACTAACTAGATTTCT TTTCTGT GTTT AG CGA GGGTTTCTT TAGATCA TC
CA GT C
TTGGGTAGCCAGACTCTTTG A CTC AC T ------ A AA GAC A
ATGTCTTT

GAM84 GCAGCGCATCTTCTTTGCTC 57 GTGAGCAAAC 1733 - CTTC-- AGA- CTT AA
ACAGAAAGCTCCTTGGACAA CTTCAATGTG GCAG CGCAT TTTGCTCAC AAGCTC
GGACA C
ACTGTGTCTCGAGCTTCCAA TCTG |||| ||||| ||||||||| |||||| |||||
GTGAGCAAACCTTCAATGTG CGTC GTGTA AAACGAGTG TTCGAG TCTGT /
TCTGC T ACTTCC AACC C-- GT

GAM85 CCCTCATAGCAGCCGCATCT 58 GTGAGCAAAC 1734 TA-- C CTTCTTTG- AGAA
CTT A
TCTTTGGCTCACAGAAAGCT CTTCAATGTG CCCTCA GCAG CGCAT GCTCAC AGCTC
GGACA A
CCTTGGACAAATGTGTCTCG TCTG |||||| |||| ||||| |||||| ||||| |||||
AGTTCAAGTGAGCAAACCTT GGGGGT CGTC GTGTA CGAGTG TTGAG TCTGT
T
CAATGTGTCTGCCATTTGGG TTAC T ACTTCCAAA AAC- C-- G
GG

GAM86 TGTGCAGAAGGAGTATTCAG 59 TGATGGAACC 1735 G- A ----- G TATG
TAGGTTATGTAACTGCCTGA GTTGCTCCAT TGT CAGA GGAGTA TTCA TAGGT T
TGGAACCGTTGCTCCATCTG CTGA ||| |||| |||||| |||| |||||
AAGCA ACG GTCT CCTCGT AGGT GTCCG /
AA A TGCCA A TCAA

GAM87 CATGTTGGTCAGGCTGGTCT 60 TGAAGTCAGT 1736 TG C C --- C A GTAAT CCG AC
TGAGCTCCTGACCTCATGAT AGTTTGAGAC AGGCTGGTCT AGCT CTGAC TCA TGATCTG TC TACCT CC C T
CTGCTCATACCTGTAATCCC TAGC |||||||||| |||| ||||| ||| ||||||| || ||||| || |
CGCACTTTGAGAGGCTGAGG TCCGATCAGA TTGA GACTG AGT ATTAGAC AG GTGGA GG G /
TGGACAGATTAACTTGAAGT GT T A TCA - - GTC-- AGA TT
CAGTAGTTTGAGACTAGCCT
GGCCAGCATG
GAM88 CACAAATCAAGACTTCTGTA 61 CATCCAGTGT 1737 CA TC TTCT CC CT A TT
CACTCCATGCCTTGATGATT GCTGTCTTTT CA AA AAGAC GTACACT ATGC TG TGA T
TCTTCAGCAGCATCCAGTGT TTAA || || ||||| ||||||| |||| || |||
GCTGTCTTTTTTAATG GT TT TTCTG CGTGTGA TACG AC ACT /
AA TT T--- CC -- G TC

GAM89 GCTGTCTCAGGCTTTACAAG 62 TTGTTGCTTG 1738 - T - ------ CA
CGATGAGAGACTCATCATAG ATGCAGCTTG GCTG TCTCAGGCT TA CAAGCGATG AGAGACT T
TCTCTGGCACTTGTTGCTTG AGAG |||| ||||||||| || ||||||||| |||||||
ATGCAGCTTGAGAGCAGC CGAC AGAGTTCGA GT GTTCGTTGT TCTCTGA C
G C A TCACGG TA

GAM90 CAGGTTTCCCAAAGACCTGA 63 TCCCAAAGAC 1739 - C-- A A TGT TT
TGTGTGAGGCTTCTTTGCCT CTGATGTGTG CAGG TTT CCAA GACCTG TG GAGGC C
TTTCATAGGTCTTGGCTCAA AGGC |||| ||| |||| |||||| || |||||
ATCCTG GTCC AAA GGTT CTGGAT AC TTCCG T
T CTC - - TT- TT

GAM91 CAGCTACATTGTTGAGTTAG 64 TACTAGAACA 1740 C T-------- GATGATGTT A GA--- TA
TGATGATGTTGTATATGCTG GCTAGCTCAT G TACATTG TGAGTTAGT GTAT TGCT TGGTCT A
ATGGTCTTAACTGGATTACA CGTT | ||||||| |||||||| |||| |||| ||||||
AAAAGCAAATACTAGAACAG T ATGTAAC ACTCGATCG CATA ACGA ATTAGG /
CTAGCTCATCGTTCACCCAA C CCACTTGCT ACAAGAT-- A AAAAC TC
TGTACTTG

GAM92 GCTCCAAAGAACCAAGAGTG 65 CATTTCACTT 1741 T - ---------- CAC GAGATA TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /

GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM93 TGAAGACTTCCTAAATTTGC 66 TTTGCACATT 1742 AC A TTGCA TTGCC ACCAT
ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM94 GTACGCTACTCCTGCTGCTG 67 TTGGCTTCTT 1743 C A C - A C----- TG CAC- A CA
GGAAATG
ACTGGCAAGCTGACACCGAC CAACCAGCAG A GCT CTC TGC TGCTG CTGG AAGC A CG
CC TGG A
CCATGGGGAAATGAGAAAGA TATG | ||| ||| ||| ||||| |||| |||| | || || |||
ACCACCGGCTGAAAATTGGC T CGA GAG ACG ATGAC GACC TTCG T GT GG ACC
/
TTCTTCAACCAGCAGTATGC - C - T - AACTTC GT AAAA C CC AAGAAAG
AGAGCAGCTGC

GAM95 AGGCTTACCAGGAAGCATTT 68 AGACAAGAAA 1744 AG A T CAT--- - ACA- CA A A
ATT
GACATTAGTAAGACAAGAAA TTGCAGCTAC AGGA C TT GA TAGTAA G AGAAATTG GCT
CA GACCCAA C
TTGCAGCTACAAGACCCAAA AAGA |||| | || || |||||| | |||||||| ||| || |||||||
TTCGACTTGGGTCTGGGCAC TCTT G AA CT ATCATT C TCTTTAAT CGG GT
CTGGGTT /
TAATTTCTCAGGCTTTACTA CT - T TAGAGT T GGAC CA - - CAG
TGAGATTCTAAGTCTTCTGA
AAGGCCT
GAM96 GCCTCCAGTCTCAAATAATC 69 TCAAATAATC 1745 CA- ATAA GATA AAA T
CAGGATATCCTAAACCTGAG CAGGATATCC GCCTC GTCTCAA TCCAG TCCT CC G
GAAGGAATACTGGACAGTTG TAAA ||||| ||||||| ||||| |||| ||
GGATGTCGGGGT TGGGG TAGGGTT AGGTC AGGA GG /
CTG GAC- ATA- A-- A

GAM97 GTACGCTACTCCTGCTGCTG 70 TTGGCTTCTT 1746 C A C - A C----- TG CAC- A CA
GGAAATG
ACTGGCAAGCTGACACCGAC CAACCAGCAG A GCT CTC TGC TGCTG CTGG AAGC A CG
CC TGG A
CCATGGGGAAATGAGAAAGA TATG | ||| ||| ||| ||||| |||| |||| | || || |||
ACCACCGGCTGAAAATTGGC T CGA GAG ACG ATGAC GACC TTCG T GT GG ACC
/
TTCTTCAACCAGCAGTATGC - C - T - AACTTC GT AAAA C CC AAGAAAG
AGAGCAGCTGC

GAM98 TGAAGACTTCCTAAATTTGC 71 TTTGCACATT 1747 AC A TTGCA TTGCC ACCAT
ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC
T

AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM99 GTCCAGTGCGTGTACTGTAC 72 TGTACACATC 1748 C G TA TACACATCC A - - CT TC G
ACATCCACACTCATTCTCAC CACACTCATT GTC AGTGC TG CTG AC CTCA TTCT CA CAGGGT CCG A
TCAGGGTTCCCGGACCGGCT CTCA ||| ||||| || ||| || |||| |||| || |||||| |||
GTCCTGCCTGCGGAACTGAG CAG TCATG AC GAT TG GAGT AAGG GT GTCCTG GGC /
GTAAACTAGCTCAGGTACTG - G TC CAAA----- - C C CC TC C
AC

GAM100 GGAGCAGGAAAATGTCATGG 73 TGTCATGGGC 1749 GAAAA A- GC- - TTCACAA GC
GCTGGCTTCTTCACAAGGCA TGGCTTCTTC GGAGCAG TGTC TGG TGG CTTC GGCATT T
TTGCTGCTGATGCTCCGGAG ACAA ||||||| |||| ||| ||| |||| ||||||
TCCAACACCACGGGCAAATT CCTCGTT ACGG ACC ACC GAGG TCGTAG G
GCTCC AA--- GC ACA T CC----- TC

GAM101 CAAGTGTGATCAGTGTCCCA 74 CATGACAGTG 1750 - GA- G CCAA TTAA AA CCAAT
AGGCATTTAACTGGAAGTCC GAAAGCACTA CA AGTGT TCA TGTC GGCAT CTGG GT T
AATTTAATTCGCCACCAGAT TG || ||||| ||| |||| ||||| |||| ||
GTCACATGACAGTGGAAAGC GT TCACG GGT ACAG CTGTA GACC CG T
ACTATG A AAA G TACA ---- AC CTTAA

GAM102 AGATAAATGGATCATGGGAG 75 TGAGTTCTCG 1751 A -- AGT CT TTTAAC- TCC
CAGTTTCTCATGGTTTAACA TGAGATCTAG AGATAA TGGA TCATGGGAGC TT CATGG ACCA C
CCATCCCCCTTGGTACTTCT TTGT |||||| |||| |||||||||| || ||||| ||||
GTCATGGTAGTGAGTTCTCG TCTGTT ATCT AGTGCTCTTG GA GTACT TGGT /
TGAGATCTAGTTGTCT G AG AGT TG GTCTTCA TCC

GAM103 GAAGAAGAGGACCAGAAGCT 76 TCAAAACCTC 1752 AG A CA- AG ----- TG - CT AT
GGTGAGTGCATCACTGGAGC AGACTCAGTG GA AAG GGAC GA CTGG TGAG CA TCA GGAGCCC A
CCATAGGAGGGCTCCTGACT TCCA || ||| |||| || |||| |||| || ||| |||||||
GTCCTCAAAACCTCAGACTC CT TTC CCTG CT GACT ACTC GT AGT CCTCGGG G
AGTGTCCACTTTCTC CT A TGA CA CCAAA CT C -- AG

GAM104 TCCTTCCACCCAATGTAGTG 77 TGTAGTGATT 1753 CCAC TAG--- -- CTTTT-- AC C

ATTCCTCTTTTGAGGCAACC CCTCTTTTGA TCCTT CCAATG TGAT TCCT GAGGCA CGGA C
GGACCCATCTGTGTGTCTCT GGCA ||||| |||||| |||| |||| |||||| |||| TTTGTTAGGACTGTCAGATC AGGAA GGTTAC ACTG AGGA CTCTGT GTCT C CCCATTGGCAAGGA C--- CCCTAG TC TTGTTTT GT A

GAM105 GGCAGAATGCTTGTGAGATT 78 TCGTGACCTG 1754 - CTT-- AT TAAT GG GTT-ATGC
ATAAGCCTAATGGTGGTGAG GTGGTTTGTG GGCA GAATG GTGAG TATAAGCC GGT TGAG TTG C
GTTTTGATGCCGCTTACAAT CCCT |||| ||||| ||||| |||||||| ||| |||| ||| TCACTCGTGACCTGGTGGTT CCGT CTTAC CACTC GTGTTTGG CCA GCTC AAC G
TGTGCCCTCACTGTAACATT A AATGT CC TGGT GT ACTT ATTC CATGCC

GAM106 GTCAGGAGAGAAACACTTGG 79 CATGACGGCT 1755 - A -- G AA- A- G C
GGAGGGGAAAGGACGGCGTG CTGAGTTCTT GTCA GGAGAGA ACA CTT GGGAGGGG AGG CG CGTGGG T
GGCTACCCATGACGGCTCTG CCTG |||| ||||||| ||| ||| |||||||| ||| || |||||| AGTTCTTCCTGGGGCTTGTG CGGT CCTTTCT TGT GGG TCCTTCTT TCT GC GTACCC /
TCTTTCCTTGGC T G TC G GAG CG A A

GAM107 ATGAGAGTCTCCTCCCCGTG 80 TCACCAGGTC 1756 CC GG ACCAG G CTA GAAT AAAA GTAGC
GGTGTCACCAGGTCGTACAT GTACATCGCT CT CCGT GTGTC GTC TACATCG GTA CC ATCACA A
CGCTAGTAGAATCCAAAAAT AGTA || |||| ||||| ||| ||||||| ||| || |||||| CACAGTAGCAGAGGGATGTG GA GGCG TACAG CAG ATGTGGT CGT GG TAGTGT G
ATCGAGGTAGTGCATGGTGT T- -- GAG-- A A-- GAT- AGC- AGGGA AAGACGAGGACATGCGGTAG CTGATTAAAT
GAM108 GCTCCAAAGAACCAAGAGTG 81 CATTTCACTT 1757 T - ---------- ----- A - -- A
CAAATCAGTCCATTTCACTT TCACTGTCTG AG GCAAATC AGTCCAT TTCACTT TC CTG TCT GAGAT G
TCACTGTCTGAGATAGGGTC AGAT || ||||||| ||||||| ||||||| || ||| ||| ||||| TCTAAGACCAGCGATACAAG TT CGTTTAG TCAGGTA AGGTGGG AG GAC AGA CTCTG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AACAT C C AT G ACTCGATTTGCTTCCGGACC TTTTCCAGAGC
GAM109 CAAAGGTGTAAGATATTTTG 82 TGCACATTTA 1758 A-- ATTT C - TC--------- T-AAACCAAG
GATGACCTGGTTATTGTCTG ATATTCAGTA GAT TGGATGA CT GGTTATTG TGC TATTC C
CTTATTCAAACCAAGCTACA ACTG ||| ||||||| || |||||||| ||| |||||

TTTTAGGATATTGCACATTT CTA GCTTACT GA TCAATGAC ACG ATAGG T
AATATTCAGTAACTGAGATC TGA GT-- A G TTATAATTTAC TT ATTTTACA
ATTCGTGATCAGTAGCTTTC
TTTG

GAM110 TTCTGCTTTTTTCCTAATGT 83 CGGAATGTAA 1759 CTTT AA-- C- A ATT ACT AGCA
CATAATCCATTTGACTCCTA ACAAGTAAGG TTCTG TTTCCT TGT ATA TCC TG CCTA T
AGCATGTAAGTAGGTACCAC AAAC ||||| |||||| ||| ||| ||| || ||||
GGAATGTAAACAAGTAAGGA AAGAC AAAGGA ACA TGT AGG AC GGAT G
AACAGAA ---- ATGA AA A C-- CAT GAAT

GAM111 CGATCTGTCCCCTGATGAAC 84 TCCCAATGTT 1760 A T -- GATG-- C CA AC
CTTCAGAAGCACTCGGCTTC AGACGAAGGC CG TC GTCC CCT AAC TT GAAGC T
CCAATGTTAGACGAAGGCAG AGGA || || |||| ||| ||| || |||||
GACGACG GC AG CAGG GGA TTG AA CTTCG /
- - AC AGCAGA T CC GC

GAM112 GTATCTGATGGGAATGGGCA 85 TTTTCACGGC 1761 CTGA A- - AA TAG- TTAC
ATGAAATAGACTTACACACT CATAGCTTCC GTAT TGGGA TG GGC TGAAA AC A
GTACATTTTCACGGCCATAG AATA |||| ||||| || ||| ||||| ||
CTTCCAATAC CATA ACCTT AT CCG ACTTT TG /
---- CG A GC TACA TCAC

GAM113 GCTCGTCAGGCTCGGCGCCC 86 TCGAGCACTC 1762 C C-- CCTG- T T
TGTTCAGTCTGTTGCAGCTG TGAGCTTGGC GCT GTCAGGCTCGG GC TTCAG CTG T
AAATCGAGCACTCTGAGCTT TGGC ||| |||||||||| || ||||| |||
GGCTGGC CGG CGGTTCGAGTC CG AAGTC GAC /
T TCA AGCTA - G

GAM114 GGAAGCCAGGTAGGTAGTCT 87 TAGAAGTAGT 1763 TAGGTAGT- AG A T CA
CCTCCT G
GAGTCAGGATTGGATCAACA AGTTTGATTC GGAAGCCAGG CTG TC GGAT GGAT ACAG
CTCTTGGG A
GCCTCCTCTCTTGGGGACTC TGGT |||||||||| ||| || |||| |||| |||| ||||||||
TCAAGAGCCTGTGTTCATCT CCTTTGGTCT GAT AG TCTA CTTG TGTC
GAGAACTC C
AGAAGTAGTAGTTTGATTCT TAGTTTGAT GA A - -- C----- T
GGTTTCC

GAM115 CTCTGAGTCCCACTACTCTA 88 TCACTGAGCA 1764 TCC -- T--- -- TCA TATT
AGTACCTCATACAATATTTG TAGTGTCCTC CTCTGAG CACTA CTC AAGTA CC TACAA T
TCCTTTGTGACTGGCTTACT AGGG ||||||| ||||| ||| ||||| || |||||
TCACTGAGCATAGTGTCCTC GGGACTC GTGAT GAG TTCAT GG GTGTT G
AGGG CT- AC TCAC TC TCA TCCT

GAM116 GTTTTTTGCGATTTCATTCC 89 TGAGGGAGAT 1765 --- - TCCA G AAAGCT C - TT-
GG

ATTCTTGACCAAAGCTTCTC ATGTAAATTG GCGATTT CAT TTCTT ACC TCT TTTAAGT AGT ATTAT A
TTTAAGTAGTTTATTATGGA TCCA ||||||| ||| ||||| ||| ||| ||||||| ||| |||||
AAATGGTCACACTAACTTAA TGTTAAA GTA AGGGA TGG AGA AAATTCA TCA TGGTA /
AAGACAGGGTGAGGGAGATA ACC T TAG- G GAC--- - A CAC AA
TGTAAATTGTCCACTAGAAA
AT
GAM117 TTGTCTGGAGAAAGGACTAG 90 GGACTAGAGA 1766 A A A----- ---- - ATGTA - C AA
AGAGAAATCCAGCTCAGATG GAAATCCAGC CT GAGAGAA TCCAG CTC AG TTGCTC ATTCCT TTCAG G
TATTGCTCATTCCTCTTCAG TCAG || ||||||| ||||| ||| || |||||| |||||| |||||
AAGGACTGGGTGGGAATGGA GA TTTTCTT AGGTC GAG TC GACGAG TAAGGG GGGTC /
GCAGGGGCTAGAGGAATCTG - - AATCGA TAAG A GGG-- G T AG
GAAGCTAATTCTTTTAGGCT
TTTTCCAACAG
GAM118 ATTCAACAAGTCTTTATTGA 91 TTCAACAAGT 1767 AACAAG TAT A CTCT- C
GCACCTACTCTGTGCCCAGC CTTTATTGAG ATTC TCTT TG GCACCTA GTGC C
ACTGCACTAGGTGCCATGAG CACC |||| |||| || ||||||| ||||
AATACAAGAGT TGAG AGAG AC CGTGGAT CACG /
AACATA T-- - CACGT A

GAM119 GAAGACTTCCTAAATTTGCA 92 TTTGCACATT 1768 AC A TTGCA TTGCC ACCAT
CATTAGCTAGATTGCCATTA AGCTAGATTG GAAG TTCCT AAT CATTAGCTAGA ATTAGC T
GCACCATTAGAGAGTTGATC CCAT |||| ||||| ||| |||||||||||| ||||||
TTTGGCTAATGATTATTCAG CTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GAAAATTTC AA C TTA-- C---- AGAGA

GAM120 GGGGTGGCTTTGGAGTTGCA 93 GTGGCTTTGG 1769 GG T GA C GA GATA TG G GA G A C
GTTGATGTGTGATAGTTGAA AGTTGCAGTT GGGT CTT G GTTG AGTT TGTGT GT AAG TT TT CTGT CTTG T
GGTTGATTGCTGTACTTGCT GATG |||| ||| | |||| |||| ||||| || ||| || || |||| ||||
TGTAAGCATGGGGAGGGGGT CCCA GAG C CAAT TCGG ACACA TA TTT GG AG GGTA GAAT T
TTTGATGTGGACACAGGCTA AA - A- A -- GGTG GT G GG G C G
TAACACGAGAAACCCT

GAM121 ATGGATGGCATAGGTCACAA 94 TGGCATAGGT 1770 GG ACAAAT--- AC CT CCAATATCA - G TG
ATGGGAGACTGGCAGCTAAG CACAAATGGG TA TC GGGAG TGGCAG AAG AAAC CCA TGGAA A
CCAATATCAAAACCCAGTGG AGAC || || ||||| |||||| ||| |||| ||| |||||
AATGACACTTCTATGGAGTT GT AG CCCTT ATCGTC TTC TTTG GGT ATCTT C

TACTTTTCTTTCTGCTATCT AA GCACCCTAT CT T- TTTTCA--- A - CA
TCCCTATCCCACGGAAATGT
CTGTCACCAT
GAM122 AGGATCTTGAATGAGTGCAT 95 GTGCATTGAT 1771 CTT A CAT--- GT- ACT--- ---
TT
TGATTAGTTGAACTGCATAT TAGTTGAACT AGGAT GAATG GTG TGATTA TGA GCAT
ATC G
CTTGTTGATTCTGTGCCACC GCAT ||||| ||||| ||| |||||| ||| |||| |||
CCTTATTGTGATCATTCTCT TTCTA CTTAC CGC ACTAGT ATT CGTG TAG /
CGCCATTCTTATCTT TT- - TCTCTT GTT CCCCAC TCT TT

GAM123 TGTTTGGGATCTGGTCTGAG 96 GGAAGTTGCT 1772 TC T G C GGCA TG TA A - T C
---- AT
GGGGCGGACGGCACTGATAT GGCTTCAGCT TGG CTGAG GGG GGAC C A TCA C GCTG
GGCC GC TCTC G
CAACGCTGTGGCCCGCTCTC GATG ||| ||||| ||| |||| | | ||| | |||| |||| || ||||
ATGATGGGAAGTTGCTGGCT ATC GATTT TCC CTTG G T AGT G CGAC TCGG CG
AGGG /
TCAGCTGATGACTTTGGCAA -- - G A AAAC GT TC A T T T TTGA TA
AGTTCACCTGTTTAGCTACC
CCTGCTGTCAG
GAM124 CATGCCGTTTTAGTTCACGA 97 TTGATCATCG 1773 G TAG A GC CTA-- G CA
AGGCCAAGCTAATGCTGGGC TGAAAGCAGA CAT CCGTTT TTCACGA G CAAG ATGCT GG
C
ACTACTGGGCATATATTTTT TGGA ||| |||||| ||||||| | |||| ||||| ||
GATCATCGTGAAAGCAGATG GTA GGTAGA AAGTGCT C GTTT TACGG TC /
GATG - CGA A TA TTATA G AT

GAM125 GTGTATATTTTAAAGCACAT 98 TAAAGCACAT 1774 T AA A ---- G C
CATGGCTTTAAGTACCATGT CATGGCTTTA GTGTATA TTTA GCAC TCATGG CTTTAA TAC A
GTTAAGGATTCTCATGAAGT AGTA ||||||| |||| |||| |||||| |||||| |||
GCCATAGACTGTACAT TACATGT AGAT CGTG AGTACT GGAATT GTG /
C AC A CTTA - T

GAM126 TGTTTGGGATCTGGTCTGAG 99 GGAAGTTGCT 1775 TC T G C GGCA TG TA A - T C
---- AT
GGGGCGGACGGCACTGATAT GGCTTCAGCT TGG CTGAG GGG GGAC C A TCA C GCTG
GGCC GC TCTC G
CAACGCTGTGGCCCGCTCTC GATG ||| ||||| ||| |||| | | ||| | |||| |||| || ||||
ATGATGGGAAGTTGCTGGCT ATC GATTT TCC CTTG G T AGT G CGAC TCGG CG
AGGG /
TCAGCTGATGACTTTGGCAA -- - G A AAAC GT TC A T T T TTGA TA
AGTTCACCTGTTTAGCTACC
CCTGCTGTCAG
GAM127 CTCCCTCCCTGGACCACAAG 100 TCCCTGGACC 1776 C GGA- AA -- CCT T C
TTTGACCTGATGTATGCCAA ACAAGTTTGA CTCC TCCCT CCAC GTT TGA GA GTATGC A
GCGTGCCTTTGTTCACTGAT CCTG |||| ||||| |||| ||| ||| || ||||||

ACGTGGGTGAGGGGATGGAG GAGG AGGGG GGTG TAG ACT TT CGTGCG /
T AGTG CA TC TGT C A

GAM128 CTCTTGAGCATGCTGACCAG 101 GACCAGTGCT 1777 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM129 TTTTTTCAAGCCCAGATATT 102 TAATGTAACT 1778 TC CC TATTTT - A A T A C--
GG TCT
TTTATTTAATCAATCTAGAT CTAGCTTTCA TTTT AAGC AGA TATT TAATCA TCT GA GGA
GCT AG A G
GGAAGCTCAGGGATCTGTAA GAAA |||| |||| ||| |||| |||||| ||| || ||| ||| || |
TTTTCTAAAAGCTCCTCAGG AAGA TTCG TCT GTAA GTTGGT GGA CT CCT CGA TC
T T
TGGTTGTAATGTAACTCTAG CT A- CAAT-- T - - - - AAA TT TAA
CTTTCAGAAA

GAM130 TCACAGAAGACAAGGAACGA 103 GGAACGACAG 1779 -- ACAA AACGAC GTAGA T
C CGAA
CAGTGGGTAGATGATTTTCC TGGGTAGATG TCAC AGAAG GG AGTGG TGA TTTCCT
TCAC G
TCTCACCGAAGCGCCTGTGA ATTT |||| ||||| || ||||| ||| |||||| ||||
AGGAGATTCAGAATTACTAA AGTG TCTTC CC TCATT ACT AGAGGA AGTG C
GCCGCTTCTCAGTGA AC G--- GAA--- AAG-- T - TCCG

GAM131 TGAAGACTTCCTAAATTTGC 104 TTTGCACATT 1780 AC A TTGCA TTGCC
ACCAT
ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM132 TGAAGACTTCCTAAATTTGC 105 TTTGCACATT 1781 AC A TTGCA TTGCC
ACCAT
ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM133 CCTACTCCAAAATACTCACA 106 TCTACAGTGT 1782 A - A TC-- -- GA
CTGGACTGAATGAAGTCTAC CAATGTGTCT CCT CTC CAA ATAC ACACTG GACT A

AGTGTCAATGTGTCTTGAGA TGAG ||| ||| ||| |||| |||||| ||||
GAGG GGA GAG GTT TGTG TGTGAC CTGA T
- A C TAAC AT AG

GAM134 GTTTGTGCTGACAGAACGAG 107 TGACAGAACG 1783 TG GA GA AGAG- T GAAG---
A
AGGGTGCTCTGAAGTATTTC AGAGGGTGCT GTTTG CT CA ACG GG GCTCT TATTTC A
AACAGAAATGATGCCAAGGA CTGA ||||| || || ||| || ||||| ||||||
GCCCAAGGCCGTGATGAAGA CGAGC GA GT TGC CC CGAGG GTAAAG C
TCGAGC TA A- AG CGGAA - AACCGTA A

GAM135 GCTTTTGCTCCAGATGGTTC 108 CCAGTGCCTT 1784 TT TCC T ATACTTT T - AA TC
ACA
ATACTTTGCTTGGTCACAAG CAGAACTTTC GCT TGC AGA GGTTC GCT GG TCAC
GGACA GC G
GACATCGCACAGTAAAGCTT TCTT ||| ||| ||| ||||| ||| || |||| ||||| ||
GTTCCGTGGTCCCAGTGCCT CGG ACG TCT TCAAG TGA CC GGTG CTTGT CG T
TCAGAACTTTCTCTTGCATG T- TTC T ACTTCCG C T C- T- AAA
GC

GAM136 TCCTTTTGACAAGAAATGTG 109 TGACAAGAAA 1785 T - AAATGT C AA-- CTGTT T
GTCGTGAAAATTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA TTGGA GC
T
GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||
ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T
GA C G GTT--- - GGTA ----- T

GAM137 GACTGCAGTGAGGGGTCACT 110 ACTGCAGTGA 1786 C - GT CAAA
GTAGCCTCAAACTCCCGGGT GGGGTCACTG GACTG AGTGAG GGGTCACT AGCCT C
TCAAGTGATCCTCTTACTTC TAGC ||||| |||||| |||||||| |||||
AGTT TTGAC TCATTC CCTAGTGA TTGGG /
T T AC CCCT

GAM138 AGGAGTTGCCGCATATCATA 111 TATCATATCA 1787 TT C TATCATATC CTT- A
TCAGACTGCTTTGAGAAATC GACTGCTTTG AGGAG GC GCA AGACTG TGAG A
TCATCCCTAGTCTATTGCAG AG ||||| || ||| |||||| ||||
TTGTTTCT TCTTT TG CGT TCTGAT ACTC A
GT A TA------- CCCT T

GAM139 CTGCTGCTGACTGGCAAGCT 112 TTGGCTTCTT 1788 - A C----- TG CAC- A CA
GGAAATG
GACACCGACCCATGGGGAAA CAACCAGCAG CTGC TGCTG CTGG AAGC A CG CC TGG
A
TGAGAAAGAACCACCGGCTG TATG |||| ||||| |||| |||| | || || |||
AAAATTGGCTTCTTCAACCA GACG ATGAC GACC TTCG T GT GG ACC /

GCAGTATGCAG T - AACTTC GT AAAA C CC AAGAAAG

GAM140 CACAAATCCAGCACTTCCTC 113 AGCAACACAT 1789 T GCACTTC-- T T- G
TCCATTTACTCTGTCAGGCT ATGGCTTTGT CACAAA CCA CTCTCCAT TAC CT T
GTATATGGGGAGCAACACAT G |||||| ||| |||||||| ||| ||
ATGGCTTTGTG GTGTTT GGT GAGGGGTA ATG GG C
C ATACACAAC T TC A

GAM141 GAATGTTGCAGAGTACAGAG 114 TTGCAGAGTA 1790 T GCA ACA AAG C- T TCA
AAGTGAGCTTAGGGTGATCA CAGAGAAGTG GAA GTT GAGT GAG TGAG TTAGGG GA T
TTTATTTTCTCTAATATTCA AGCT ||| ||| |||| ||| |||| |||||| ||
AACCTCAACTCAAAACCTTT TTT CAA CTCA CTC ACTT AATCTC TT T
C AA- A-- CAA AT T TAT

GAM142 GCTCCAAAGAACCAAGAGTG 115 CATTTCACTT 1791 AA AA T - TTC--- - GTCT
AATA TT
CAAATCAGTCCATTTCACTT TCACTGTCTG CC GAG GCAAATC AGTCCAT AC TTTCACT
GA GGGTC T
TCACTGTCTGAAATAGGGTC AAAT || ||| ||||||| ||||||| || ||||||| || |||||
TTTAAGACCCAGGATCCAAG GG CTT CGTTTAG TCAGGTA TG AAGGTGG CT
CCCAG /
GGTGGAATGTAGCTATATGG CA C- - C TATCGA T GAAC AGGA AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM143 GACATTTCAATAATACAGGG 116 TTCAATAATA 1792 AT - AG A--- ACA
TAAGTTCATAGCTACAAAGC CAGGGTAAGT GACATTTCA AATACA GGGTA TTCAT GCT A
AAGCCAACATGAGTGCTCAT TCAT ||||||||| |||||| ||||| ||||| |||
GTATTCTGAGATGTC CTGTAGAGT TTATGT CTCGT GAGTA CGA A
C- A -- CAAC ACG

GAM144 TGACCAATCACGTATTTAGA 117 TGGGTATTTC 1793 C C T ---- G
TCCATGTGACATGTGGGTAT TCAGTACTGG TGAC AATCA GTATT AGA TCCATGT A
TTCTCAGTACTGGTTTGTTA TTTG |||| ||||| ||||| ||| |||||||
ATTG TTGGT CATGA TCT GGGTGTA /
T - C TTAT C

GAM145 GTTAGGTTGTTTCCAACATG 118 CAACATGAGT 1794 C- AGT AAGC A TGAA C T
TT G
AGTGTGAGAAGCTAAGTTGA GTGAGAAGCT TTCCAA ATG GTGAG TA GT TGTTGCA
GGGG AAAG TGCAGT C
ATGTTGCACGGGGTAAAGTT AAGT |||||| ||| ||||| || || ||||||| |||| |||| ||||||
TGCAGTGCTAATTGTGTCCT AAGGTT TAC CACTC AT CA GCGACGT CCTC TTTC
GTGTTA T
TTTCTCCTGCAGCGCCTACA TA --- CAA- A TCC- - T CT A
TAAACCTCACCATATTTGGA

AGATTCCTAC
GAM146 GGCGTAATCTTGGCTCACCG 119 CAGGAGCTCA 1795 T- CGCAA CCGC C C C CA CTC
CAACCTCCGCCTCCCGGGTT AGGCTATTGT C TGGCTCAC CCT CTCC GGGTT AAGCGATTCTCCCG CT GC C
CAAGCGATTCTCCCGCCTCA GAGC | |||||||| ||| |||| ||||| |||||||||||||| || ||
GCCTCCCAAGCAGTTGGGAG G ACCGAGTG GGA GAGG CCCGA TTCGTTAAGAGGGT GA CG /
AATTGCTTAAGCCCAGGAGC TT TTATC ACTC A A T -- AAC
TCAAGGCTATTGTGAGCCAT
TGATCGCACC
GAM147 CCTGACACGACACTGGTACA 120 ATGAAGCAGG 1796 GA GA C T A T G---- CAAA TG C
CCATGAAGCAGGGTACCAAA GTACCAAAAC CCT CAC CA TGG AC CCA GAA CAGGGTAC ACTGA CTC A
ACTGATGCTCCAGGGAGATT TGAT ||| ||| || ||| || ||| ||| |||||||| ||||| |||
CGGTAGTACTCTGACCAATT GGA GTG GT ACT TG GGT CTT GTCTCATG TGGCT GAG G
CTGGGTTCAATGAAGTGGAG G- AA A - - - AACCA A--- TA G
G

GAM148 GGACGCATGGAATGCCCTTG 121 GGAAGCTGCC 1797 GA AA- CT --- G
GCAGCCTGCCAAGGAAGCTG AGGCAGAACT G CGCATGG TGCC TGGCAGC CT C
CCAGGCAGAACTATGTGGAC ATGT | ||||||| |||| ||||||| ||
C GTGTATC ACGG ACCGTCG GA C
AG AAG -- AAG A

GAM149 GCTAGTCAGTTCAGCAGGAG 122 TAGTCAGTTC 1798 A TT G AGGA GAGAC ---- CG G- TG
CAGAGACCAGGTTAGCACGC AGCAGGAGCA GCT GTCAG CA C GCA CAGGT TAGCACG GATG GG T
GGATGGGGTGTAATTCAGTG GAGA ||| ||||| || | ||| ||||| ||||||| |||| ||
TTTTTGTGTTGTACAGCCTG CGA CAGTC GT G CGT GTCCG GTTGTGT TTGT CT A
AGAAATGCCAGTGGCCTGAC - CG - AC-- AAAGA ACAT TT GA TA
AGC

GAM150 GAAGGAGTTTTTACTTTCGG 123 TACAGCTAGA 1799 - T - C T AGACC
TTATCTAGCTTTATGAAGAC TAACCAAAGA GAAG GAGTT TTA CTTT GGTTATCTAGCT TATGA A
CAATACACTCATACAGCTAG TAAC |||| ||||| ||| |||| |||||||||||| |||||
ATAACCAAAGATAACAACTC CTTC CTCAA AAT GAAA CCAATAGATCGA ATACT A
GCTTC G C A - C CACAT

GAM151 TCCCACTGTGGTGCCTGGTG 124 TCGCCTGGAC 1800 CC - G T G A - AA CAGAGA - CA T
GAGACCTGGCCAAGGTACAG CACAAGTTTG ACT GTGGT CC GGTG AG CCT GGCC GGTA GCTGTG TG TGC G

AGAGCTGTGTGCATGCTGAG A ||| ||||| || |||| || ||| |||| |||| |||||| || |||
CAACACCACAGCCATTGCTG TGA CACCA GG CCGC TC GGG CCGG TCGT
CGACAC AC ACG /
AGGCCTGGGCTCGCCTGGAC TT A - T - - T AG TAC--- C A- A
CACAAGTTTGA

GAM152 AGCAGAGTCTGATTCTCCAG 125 TGAACTCAGG 1801 AGT-- TTCT A G TG TAGGA
AGTTGAGTGTGGTAGGACAC CTTCAGTCCC AGCAG CTGA CC GAGTT AGTG G C
AGTTTGCACTGAACTCAGGC CCTG ||||| |||| || ||||| |||| |
TTCAGTCCCCCTGCT TCGTC GACT GG CTCAA TCAC T /
CCCCT TC-- A G GT TGACA

GAM153 CGGTGAATGCTGCCGCGATC 126 GTCAGCCTTG 1802 AAT C-- - G TCATGTCT AC
GCCTGGCATCATGTCTCAGG TAGTTGCATC CGGTG GCTGC GC GATC CCTGGCA
CAGGG T
GACTTTTTCTGTGCCAGGGG G ||||| ||||| || |||| ||||||| |||||
GTCAGCCTTGTAGTTGCATC GCTAC TGATG CG CTGG GGACCGT GTCTT /
G GT- TTC A G -------- TT

GAM154 AATCCAAATGTATCATCTTT 127 AGAAATGGAG 1803 AA- T - CATA CCA TA
TCCATATCCCCATCTGTAAA AGAAGTATGT AATCCA TGTA CAT CTTTTC TCC TCTG A
TCAGAAATGGAGAGAAGTAT ACGC |||||| |||| ||| |||||| ||| ||||
GTACGCTGTGGGTT TTGGGT GCAT GTA GAAGAG AGG AGAC /
GTC - T ---- TAA TA

GAM155 GAGTTTCACTCTTTTCACCC 128 TGACAGAATG 1804 C ------ CCA A - G A
AGGCTGGAGTGCAATGGTGT AAGAATGAGA GAGTTTCA TCTTT TCAC GGCTGGAGTGCA
TG GT TG T
GATCTAGGCTCACTGCATTC CTC |||||||| ||||| |||| |||||||||||| || || ||
CAGCCAGAGTGACAGAATGA CTCAGAGT AGAAG AGTG CCGACCTTACGT AC CG
AT /
AGAATGAGACTC A TAAGAC AGA C T G C

GAM156 TGAAGACTTCCTAAATTTGC 129 TTTGCACATT 1805 AC A TTGCA TTGCC
ACCAT
ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM157 TCTTGATTCACCAGGTCTAA 130 TCACCAGGTC 1806 - A AGG AA C TC
ACTGCAGTAATCCATTTACT TAAACTGCAG TCTTGAT TC CC TCTA CTG AGTAA C
CAGCTGGAGAGGAGACATCA TAA ||||||| || || |||| ||| |||||
AGA AGAACTA AG GG AGGT GAC TCATT /

C A AG- C- - TA

GAM158 TCCTTTTGACAAGAAATGTG 131 TGACAAGAAA 1807 T - AAATGT C AA-- CTGTT T
GTCGTGAAAATTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA TTGGA GC
T
GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||
ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T
GA C G GTT--- - GGTA ----- T

GAM159 CTGCTGACGCAGGCTGAAGT 132 TGGACAAGCA 1808 C A AG GAAG - T AAC
TGTTTTCTCACTGGCTAACC GGGCAAGTGA CTG TG CGC GCT TTGTTT TC CACTGGCT C
ACTAAGCCAGTGGACAAGCA TACA ||| || ||| ||| |||||| || ||||||||
GGGCAAGTGATACAG GAC AT GTG CGG GACGAA AG GTGACCGA A
- A AA ---- C - ATC

GAM160 CTCCAAAGAACCAAGAGTGC 133 CATTTCACTT 1809 T - ---------- CAC GAGATA
TC
AAATCAGTCCATTTCACTTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
CACTGTCTGAGATAGGGTCT AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
CTAAGACCCAGGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- GA---- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAG
GAM161 GGCTGAGCCGCAGTAGTTCT 134 AAGCTGCCAG 1810 T CC - A T CCTG
TCAGTGGCAAGCTTTATGTC TTGAAGAACT GGC GAG GCAGTAGTTCTTCAG TGGCA GCTTTA
GT A
CTGACCCAGCTAAAGCTGCC GTTG ||| ||| |||||||||||||| ||||| |||||| ||
AGTTGAAGAACTGTTGCCCT CCG CTC CGTTGTCAAGAAGTT ACCGT CGAAAT CG /
CTGCC T C- G - - ACCC

GAM162 AGTGCCCCACAGAGTCACAG 135 CATTGGACAT 1811 C ------ A A GT TG AC
TGTGTCTGGACAGCCTGGAC TGCTAAGTTG AGTG CCCA CAG GTC CA GTGTC G A
ATTGGACATTGCTAAGTTGG GGTC |||| |||| ||| ||| || ||||| |
GTCACT TCAC GGGT GTT CAG GT TACAG C /
T TGAATC A - -- GT CG

GAM163 GCTCCAAAGAACCAAGAGTG 136 CATTTCACTT 1812 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /

GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM164 CTCTTGAGCATGCTGACCAG 137 GACCAGTGCT 1813 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGGA GAGGG TCG ACG GGTCAC ACC CG TT A
G G G TC- - TC--- GT CCTAT

GAM165 TGATGTGGCTCTGGAAGGCG 138 TGGATGGACG 1814 CGT CA T AA---- CG---- A
G AGG
TGAGCCACGTTCTTCCGCGA CGCTCTCTTC GGAAGG GAGC CGTTC TCCGCG TGGC
AGGAGA GC CG G
ATGGCCGAGGAGAAGCGCGA CAGG |||||| |||| ||||| |||||| |||| |||||| || ||
GGGCTACGAGCGTCTCCTGA CCTTCT CTCG GCAGG AGGTGC ACCG TCCTCT
CG GC /
AGATGCCAAACCAGCGTGGA --- C- T GACCAA TAGAAG G A ATC
TGGACGCGCTCTCTTCCAGG
ACATCA
GAM166 GCTCAATCACTCCCTGCTTA 139 CCCCTGGACC 1815 AT-- CCC TTACCA T CCATC -
- C-- CA
CCACAGTGGGCTGGGACCAT TGCAAGTGTT TCA CACT TGC CAG GGGCTGGGA
AGGT C GT CAC C
CAGGTCGTCCACCACGTTGT ACTG ||| |||| ||| ||| ||||||||| |||| | || |||
GCCCACAGAACCTCTCCCAG AGT GTGA ACG GTC CCCGACCCT TCCA G CA
GTG G
CCCCTGGACCTGCAAGTGTT CATT --- TCCAG- - C---- A A CCC TT
ACTGAGT

GAM167 TAGGTTGTTTCCAACATGAG 140 CAACATGAGT 1816 C- AGT AAGC A TGAA C T
TT G
TGTGAGAAGCTAAGTTGAAT GTGAGAAGCT TTCCAA ATG GTGAG TA GT TGTTGCA
GGGG AAAG TGCAGT C
GTTGCACGGGGTAAAGTTTG AAGT |||||| ||| ||||| || || ||||||| |||| |||| ||||||
CAGTGCTAATTGTGTCCTTT AAGGTT TAC CACTC AT CA GCGACGT CCTC TTTC
GTGTTA T
TCTCCTGCAGCGCCTACATA TA --- CAA- A TCC- - T CT A
AACCTCACCATATTTGGAAG
ATTCCTA
GAM168 TATTATCACAGTGTTATTCT 141 TATCACAGTG 1817 A A - AT TC ---- GG
TCTTCATATCTGTGGCATGA TTATTCTTCT TATT TCAC GT GTT TCT TTCA TATCTGT C
CAGGTGTATCTGAAAGAGAA TCAT |||| |||| || ||| ||| |||| |||||||
ACGACCGTGAAATA ATAA AGTG CA CAA AGA AAGT GTGGACA A
- C G -- GA CTAT GT

GAM169 TATTAGTCGTCACAGCTGTG 142 TACAGCTATA 1818 -- AC- AATTT ACA C TATA
T
ACAATTTTTGGTACAGGTCG GATGTAACTA TATTAGT CGTC AGCTGTGAC TTGGT GGT
GGTA AGG C

GTATATAAGGTCATTCTCTG GTA ||||||| |||| |||||||||| ||||| ||| |||| |||
CCATTACAGCCAGTAGGTTA ATGATCA GTAG TCGACATTG GACCG TTA CCGT
TCT A
CAGCTATAGATGTAACTAGT AT ATA GAT-- ACA - C--- T
A

GAM170 CTTGCCCTCTGTCATCCTAG 143 AGCAGTGTGG 1819 GC TG-- CC C G GA - - T CT
CAGTGTGGATGGTTGGTTGG ATGGTTGGTT CTT CCTC TCAT TAG AGT TG TG GTTG G
TGGGAT T
GATCTTCGTGTCCCGTCTCA GGGA ||| |||| |||| ||| ||| || || |||| | ||||||
GCACACTCGAGCTCTGAAGT GGA GGAG AGTG GTC TCG GC AC CGAC C GCCCTG
C
GAAAGTGAGGAAGG A- TGAA AA - A TC A T T TG

GAM171 CAGGCATAAGCATCACACCC 144 CATCACACCC 1820 - CACACC CCT A TCT A
AGCCTTGAGGATTTTCTTAT AGCCTTGAGG CAGGCAT AAGCAT CAG TG GGATTT TAT C
ACTGTGTTTGAATCCACATG ATTT ||||||| |||||| ||| || |||||| |||
ACTGATAATATGCTTAATGT GTTTGTA TTCGTA GTC AC CCTAAG GTG /
TTG A TAATA- AGT A TTT T

GAM172 TATGGAGTATGGCTTTGGAG 145 TAGTCTATTC 1821 - T CAT TTG---- -
ACAG
CACATGGGTAGTTGGGTCTG CTCTGCTCCT TATGGAGTATG GCTT GGAGCA GGGTAG
GGTCTGTT TCTT G
TTTCTTACAGGATACAGGAT AGGC |||||||||||| |||| |||||| |||||| |||||||| ||||
AATAGATCATTTAGTCTATT GTATCTCGTAT CGGA CCTCGT CTTATC CTAGATAA
AGGA /
CCTCTGCTCCTAGGCATATG A T CTC TGATTTA T CATA
CTCTATG

GAM173 GAAGGAGTTTTTACTTTCGG 146 TACAGCTAGA 1822 - T - C T AGACC
TTATCTAGCTTTATGAAGAC TAACCAAAGA GAAG GAGTT TTA CTTT GGTTATCTAGCT TATGA
A
CAATACACTCATACAGCTAG TAAC |||| ||||| ||| |||| |||||||||||| |||||
ATAACCAAAGATAACAACTC CTTC CTCAA AAT GAAA CCAATAGATCGA ATACT A
GCTTC G C A - C CACAT

GAM174 CTCTTGAGCATGCTGACCAG 147 GACCAGTGCT 1823 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM175 TCTCTGTCAGTCTGCTGTTT 148 CTGTCAGTCT 1824 C T CT - TG GC-- TTGCT ATC
GCAGGCGTCATTGCTGCTAG GCTGTTTGCA TCT TG CAGT GCTGT T CAG GTCA
GCTAGA G

AATCGGTCTTTGGTCCTTTG GGCG ||| || |||| |||||| | ||| |||| ||||||
ATTTAACTGTGACACAGTTG AGA AC GTCG TGACA A GTC TAGT TGGTTT /
CTGCAAGA - - T- C GT AATT TTCC- CTG

GAM176 GCCACCACAAACTCTGCCTT 149 TATTGCACGT 1825 CAAA T -- TTTAA- CA A ------ TT T
TCTTTTAAATAACCCAGCAT GGTCCGGCCT CA CTC GC CTTTCT ATAACC GC TGGA GCAGT GGT T
GGAGCAGTTTGGTTTCCACC GGTT || ||| || |||||| |||||| || |||| ||||| |||
CTATTGCACGTGGTCCGGCC GT GAG CG GGAGGA TATTGG CG GCCT CGTTA CCA C
TGGTTATGAAATCAGGAGGC CA-- T TC CTAAAG TC - GGTGCA TC C
TGCTGAGACTGGGGT

GAM177 GAGGGAGAGCAGCTCTTCAG 150 TTCAGCAGTG 1826 GG CT- TG AGAG A TGA G ATG
CAGTGGCCAGAGTGCCACGT GCCAGAGTGC GAG AGAGCAG CTTCAGCAG GCC TGCC CG CTCT CAG A
GACTCTGCAGATGACCCCTG CACG ||| ||||||| ||||||||| ||| |||| || |||| |||
GGAGCCGGGTGATGGGCACC TTC TTTTGTT GGGGTCGTC CGG GTGG GC GAGG GTC /
TGCTGGGGCTTTTGTTTTTT TT TTC CA GTA- - C-- - CCC
CTT

GAM178 TGAAGACTTCCTAAATTTGC 151 TTTGCACATT 1827 AC A TTGCA TTGCC ACCAT
ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC T
AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM179 TTCATGATTAAGAGATTTAC 152 TGCTATGGAA 1828 A AGATTTACT AAA - AAGAAGTATG A
TGCAAATCCTGCTATGGAAA AGAAGTATGG TTCATG TTAAG GC TCCT GCTATGGA GGCC A
GAAGTATGGGCCAAAAGGCT GCC |||||| ||||| || |||| |||||||| ||||
ACAGTTTATGGCCAGGGCGC AGGTAC AATTC CG GGGA CGGTATTT TCGG A
TGGCATACTTAACATGGA - ATACGGT-- C-- C GACA------ A

GAM180 GCATGCTGGACCAGTGCTGG 153 GACCAGTGCT 1829 A T A C CATAA TG ACTCA
CATAAGCTGAAACTCAAATA GGCATAAGCT GC TGC GG CCAGTG TGG GC AA A
TCCTTTGGCCTCCACACTGG GAA || ||| || |||||| ||| || ||
CTGCAGGC CG ACG TC GGTCAC ACC CG TT A
G - - - TC--- GT CCTAT

GAM181 TTGGCATGCAGTGGTGGTAG 154 TGCTGCCTCC 1830 AT- T T GGC G ATG-
GGAGA T
TGGCGGTGGCAGCATGATGG CTGTTTGGCC TTGGC GCAG GG GGTAGT GGT GCAGCATG
GGC GTC G
GCGGAGAGTCTGCTGACAAG AA ||||| |||| || |||||| ||| |||||||| ||| |||
GCCACTGCGTGCTGCAGCCT AACCG TGTC CC CCGTCG CCG CGTCGTGC CCG
CAG C
GCTGCCTCCCTGTTTGGCCA GTT - T T-- A GTCA GAA-- T
A

GAM182 GCTCCAAAGAACCAAGAGTG 155 CATTTCACTT 1831 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM183 GCCAGTAGGGGTGAGACCGG 156 TCAAATGCCT 1832 C G GA CC ----- ---- A -
TAT
CATGGTGATTTCTTTATGGG CAGCACCTGC GC AGTAGG GT GA GGCAT GGTGA
TTTCTTT TG GGAGGG A
AGGGTATAAGAGTCCTTTGC TGC || |||||| || || ||||| ||||| ||||||| || ||||||
GAAGAGAAACATTTCACTTT CG TCGTCC CG CT CCGTA TCACT AAAGAGA GC
TTTCCT A
CAAATGCCTCAGCACCTGCT - A A- -- AACTT TTAC A G GAG
GC

GAM184 GCCATTGCTGAGGCCTGGGC 157 TCGCCTGGAC 1833 ---- GGA A- AG GA TG AT
--- TG
TCGCCTGGACCACAAGTTTG CACAAGTTTG GGCCT GGGCTCGCCT CC CA TTT CC ATGT
GCCA AACG C
ACCTGATGTATGCCAAACGT ACCT ||||| |||||||||| || || ||| || |||| |||| ||||
GCCTTTGTTCACTGGTACGT CCGGA TTTGAGTGGA GG GT GGG GG TGCA TGGT
TTGT C
TGGGGAGGGGATGGAGGAAG GACT A-- AG AG AG GT -- CAC TT
GTGAGTTTTCAGAGGCCCGT
GAGGACATGGC
GAM185 AGTGCCCCACAGAGTCACAG 158 CATTGGACAT 1834 C ------ A A GT TG AC
TGTGTCTGGACAGCCTGGAC TGCTAAGTTG AGTG CCCA CAG GTC CA GTGTC G A
ATTGGACATTGCTAAGTTGG GGTC |||| |||| ||| ||| || ||||| |
GTCACT TCAC GGGT GTT CAG GT TACAG C /
T TGAATC A - -- GT CG

GAM186 GCTCCAAAGAACCAAGAGTG 159 CATTTCACTT 1835 T - ---------- CAC AGATAG
TC

CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT
TGTCTG GGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| |||||| ||||
TCTAAGACCACGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGGC
CCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM187 GGGAAAGACATAAAGGAGAA 160 CATAAAGGAG 1836 AA CATA GAA---- T GATA
ATA
AGCCCTGATCGATATGTATA AAAGCCCTGA GGG AGA AAGGA AGCCC GATC TGTAT
G
TAGAAGGTATAGCAGATTTG TCGA ||| ||| ||||| ||||| |||| |||||
GGCTGACATGATCCTTCTTC CCC TCT TTCCT TCGGG TTAG ATATG /
TGCCC G- TC-- AGTACAG T ACG- GAA

GAM188 CTGCACGAAGTGGCTGATGG 161 TGACTAGAAA 1837 C- GAAG T ACCA A ACA GT
GAACCATTTCAAGACAGATG ATCCTTCAGC CTG AC TGGCTGA GGGA TTTC AG GAT G
TGAAGATTGACTAGAAAATC TAAA ||| || ||||||| |||| |||| || |||
CTTCAGCTAAAGTAACAG GAC TG ATCGACT TCCT AAAG TC TTA A
AA AA-- - A--- A AG- GA

GAM189 CTACTGGAAAGAAGGCTTTA 162 ACCATGTAAG 1838 - AA- --- - AGA CAGG
TGGAGATCCCAGGAACCAAG CCTGAATTTG CTAC TGG AGA AGGCTT TATGG TCC A
GACCATGTAAGCCTGAATTT TGCC |||| ||| ||| |||||| ||||| |||
GTGCCATGTGG GGTG ACC TTT TCCGAA GTACC AGG A
T GTG AAG T --- AACC

GAM190 TTGTGGCCTGAACTGTGGGT 163 GATCAGAGTC 1839 ACTGT- G - ---- TT G AGA
GG GT
GGCTGAGGGGATCGTTAATT TGGTTCTTGA GGGTG CTGAGGGG ATC GTTAA GAAT
GGGC CTGA CTT G
GAATGGGGCAGACTGAGGCT CATG ||||| |||||||| ||| ||||| |||| |||| |||| |||
TGTGAGGAAGATCAGAGTCT TCTAC GACTTCCC TAG CAGTT CTTG TCTG GACT
GAA A
GGTTCTTGACATGAGATGCC CACTTC A G AGTA -- G A-- A- GG
CTTCAGACATCTCTTCACTC
AGGTCCAA
GAM191 CTCTTGAGCATGCTGACCAG 164 GACCAGTGCT 1840 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM192 AAATGAGTTGTTTTATAGAA 165 TGCCTGCTCC 1841 TA AATACCGC AC----- A T-- T
ATAT

TACCGCAAGATGACATTGAG CAGTATGGAC TTT TAG AAGATG ATTG GAGT TAA
GCCAATTGT A
AGTTTAATGCCAATTGTATA ACAT ||| ||| |||||| |||| |||| ||| |||||||||
TACACCGACGGTTGGTCTTG AGG ATC TTCTAC TGAC CTCG GTT
TGGTTGGCA C
CCTGCTCCCAGTATGGACAC GA CAGAAGAT ACAGGTA C TCC C GCCA
ATCTTTAGAAGACCTAAGGG
ATTATTTATTT
GAM193 TAGGTTGTTTCCAACATGAG 166 CAACATGAGT 1842 C- AGT AAGC A TGAA C T
TT G
TGTGAGAAGCTAAGTTGAAT GTGAGAAGCT TTCCAA ATG GTGAG TA GT TGTTGCA
GGGG AAAG TGCAGT C
GTTGCACGGGGTAAAGTTTG AAGT |||||| ||| ||||| || || ||||||| |||| |||| ||||||
CAGTGCTAATTGTGTCCTTT AAGGTT TAC CACTC AT CA GCGACGT CCTC TTTC
GTGTTA T
TCTCCTGCAGCGCCTACATA TA --- CAA- A TCC- - T CT A
AACCTCACCATATTTGGAAG
ATTCCTA
GAM194 ACATCCGGGAATTGCCTGTG 167 TCAGTGCAAG 1843 A---- - T TT AA TAA
TTTTTAATCCTAATGATGGG ACAGTCTTGG ACATCCGGGA TTGC CTG GT TT TCC T
CCAGTTGCTCAGTGCAAGAC ATGT |||||||||| |||| ||| || || |||
AGTCTTGGATGT TGTAGGTTCT AACG GAC CG GA GGG /
GACAG T T TT CC TAG

GAM195 GCAGTCTATTTATCCTCTCC 168 TAGAAAAGTA 1844 - C T ----- TT GAA AAAA
AGAG GT
ATGATGTCTTCGTTAGAAAA AAATGTGAAG TAT CCT TCCA GA TGTCTTCG A AAGT
TGTGA CCCAA T
GTAAAATGTGAAGAGCCCAA AGCC ||| ||| |||| || |||||||| | |||| ||||| |||||
GTTGAATTGGGAAAGTCATG GTA GGA AGGT CT ACGGAAGT T TTCG GTACT
GGGTT G
GAGCTTCATGGTGAAGGCAG C A T TGATG GG AC- AG-- GAAA AA
TAGTTCTTGGAAAGGCATGG
GGGACGAGGAC
GAM196 TCTCTGTCAGTCTGCTGTTT 169 CTGTCAGTCT 1845 C T CT - TG GC-- TTGCT ATC
GCAGGCGTCATTGCTGCTAG GCTGTTTGCA TCT TG CAGT GCTGT T CAG GTCA
GCTAGA G
AATCGGTCTTTGGTCCTTTG GGCG ||| || |||| ||||| | ||| |||| ||||||
ATTTAACTGTGACACAGTTG AGA AC GTCG TGACA A GTC TAGT TGGTTT /
CTGCAAGA - - T- C GT AATT TTCC- CTG

GAM197 CAGCCTCCCACTGTGGTGCC 170 TCGCCTGGAC 1846 CC - G T G A - AA CAGAGA
- CA T
TGGTGGAGACCTGGCCAAGG CACAAGTTTG ACT GTGGT CC GGTG AG CCT GGCC GGTA
GCTGTG TG TGC G
TACAGAGAGCTGTGTGCATG ACCT ||| ||||| || |||| || ||| |||| |||| |||||| || |||
CTGAGCAACACCACAGCCAT TGA CACCA GG CCGC TC GGG CCGG TCGT
CGACAC AC ACG /

TGCTGAGGCCTGGGCTCGCC TT A - T - - T AG TAC--- C A- A
TGGACCACAAGTTTGACCTG

GAM198 GGATTAGACTCCTCGAGGTA 171 TCACTTGGCA 1847 TA TC C TATCCCTT CCTAC
ATTT TT
TCCCTTCTAAGTGGAATCCT TAGTGTCTTC GGAT GAC CT GAGG CTAAGTGGAAT AGT
GCC T
ACAGTATTTGCCTTTTGTGG AAGT |||| ||| || |||| |||||||||| ||| |||
CTGGCTAATTTCACTTGGCA CCTA CTG GA CTTC GGTTCACTTTA TCG CGG T
TAGTGTCTTCAAGTGTCATC -- T- A TGTGATAC A---- GT-- TG
C

GAM199 GCTCCAAAGAACCAAGAGTG 172 CATTTCACTT 1848 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM200 GCAGCCCTGAGATCTCAAGA 173 GCCCTGAGAT 1849 CC GA T TGACATTT G CCA
GTGACATTTGTGAGACCAGC CTCAAGAGTG GCAG CTGA TC CAAGAG GT AGA G
TAATTTGATTAAAATTCTCT ACAT |||| |||| || |||||| || |||
TGGAATCAGCTTTGC CGTT GACT AG GTTCTC TA TTT C
TC A- - TTAAAAT- G AAT

GAM201 GGGAGATGTGTGCAAGCTCA 174 GCTGGTCCTG 1850 A TGT- A- T AC- ATATG
GCCACTCTGAATATGGAAAA CTCTTCACTC GGGAG TG GCA GC CAGCC TCTGA G
GGTCAGGCCGGGCTGGTCCT CC ||||| || ||| || ||||| |||||
GCTCTTCACTCCC CCCTC AC CGT TG GTCGG GGACT A
- TTCT CC - GCC GGAAA

GAM202 CCAAAAGTGCAAATCAGTCC 175 CATTTCACTT 1851 AAGT - ---------- CAC GAAATA
CTT
ATTTCACTTTCACTGTCTGA TCACTGTCTG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGT T
AATAGGGTCTTTAAAACCCA AAAT ||||||| ||||||| |||||||| ||||| ||||
GGATACAAGGGTGGAATGTA CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCA /
GCTATATGGACTCGATTTGC TT-- C TATCGATGTA AC- A----- AAA
TTCCGG

GAM203 GGGCCTTGGTTTGGCAGCCA 176 CAAACCTTTA 1852 TT TG-- AG A- GGA - AA
TTTA-- A G
TGGGAACTGCACGTCAAGAT TCAGGATGAT GGGCC GGTT GC CC TG ACTGCA CGTC
GATG TG TTT C

GTTTATGATTTGCTAAAAAC GCAG ||||| |||| || || || |||||| |||| |||| || |||
AAACCTTTATCAGGATGATG CCCGG CCGG CG GG AC TGACGT GTAG CTAT AC AAA T
CAGTAACAGGGGAAGCAGCT T- TCGA AA GG AA- A GA TTCCAA A A
GGCCTGGCCC

GAM204 GCTGTGTTGCAGTGCATTGT 177 GTGCATTGTG 1853 GCA A TG G TG GGA TG GA CCT TG
GTTGCAGGATTGGGAAGGGC TTGCAGGATT GCTGTGTT GTGC T T T CA T G AGGGCA GTGC G
ACCTGTGCTGGTTGCACTTG GGGA |||||||| |||| | | | || | | |||||| ||||
CTTTGATTGAATGTGGAATG TGACGTAG CATG A A G GT A T TTTCGT CACG /
AAGTACGAAGATGCAGT AAG A GT A GT A-- GT AG T-- TT

GAM205 AGGGAATTCTGGTTTTAGTC 178 AACACCACAG 1854 TT - TT- - ATTG A-- - A G
CATTGGTAGCATTGTGTGTA ACAGCTGCAG AGGGAA C TGG TT AGTCC GTAGC TTGTG TGT TGAG A
TGAGGAGATTCAACACCACA GACT |||||| | ||| || ||||| ||||| ||||| ||| ||||
GACAGCTGCAGGACTCGATA TTTCTT G ACC AG TCAGG CGTCG GACAC ACA ACTT G
TCCATGGCTTCTTT CG T TAT C A--- ACA C - A

GAM206 GCTCCAAAGAACCAAGAGTG 179 CATTTCACTT 1855 T - ---------- CAC GAGATA TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM207 AAGGGTTGTTTTGTTGTTAG 180 TGAAGCTAGA 1856 T TGTTGT AA A-- GTCCATT
GTAAATAGATATTAGGCAGT TACCTAAAGC AAGGGT GTTT TAGGTA TAG TATTAGGCA T
CCATTTCTAAAATATGCCTG TACC |||||| |||| |||||| ||| |||||||||
ATGAAGCTAGATACCTAAAG TTCCCA CGAA ATCCAT ATC GTAGTCCGT C
CTACCCTT T ------ AG GAA ATAAAAT

GAM208 AACTGAGGTGCACAAGCAGT 181 TGCACAAGCA 1857 - AA- - C-- ACT GT ATGAA AT
GCACGTCCACTGCCGAGGTC GTGCACGTCC AACTG AGGTGCAC GCAG TGCA GTCC GCCGAG CTGGAC C G
TGGACATGAACATGCTGGTG ACTG ||||| |||||||| |||| |||| |||| |||||| |||||| |
GTCTAGTTTGGTCTGGGGCC TTGGC TTCACGTG CGTC ACGT CGGG TGGTTT GATCTG G /
TATGCACCTGCATCGTGCAC A CTA C ATC GTC -- GTG-- TC

TTACGGTT

GAM209 TTAAATTTCTGTATCTGTCG 182 TAAGCTAGGG 1858 TT T TC G GATT--- G
CCCTGAGCTGATTTTGAAAG GTTAGTATAG TTAAAT CTGTA CTG GCCCT AGCT TT A
ATGGTATAAGCTAGGGGTTA TTGT |||||| ||||| ||| ||||| |||| ||
GTATAGTTGTTTAA AATTTG GATAT GAT TGGGG TCGA AG A
TT - -- A ATATGGT A

GAM210 ACTAGGGATGCTTTTCAGTA 183 TCAGTACTAG 1859 T TT - AG T- TT TC - ACTA
T
TTAGGGATGCTTTTTTCAGT GGATGTACTA GC T C AGTATT GGA GC TTT AGTACT
AGGGATGT GGGAGTAC G
ACTAGGGATGTACTAGGGAG GGGA || | | |||||| ||| || ||| |||||| |||||||| ||||||||
TACTGAGTACTCCTGAAGAT CG A G TTGTGA TTT CG AGG TCATGA TTTTTGTA
TCCTCATG /
GTTTTTCAGTACTAGGGATG T GG A CT TT T- GA C GAAG A
CTTTTTTCAGTGTTAGGGAT
GCTTTTCAGT
GAM211 GTGGGGAGAACAGCGTCTTT 184 TCCTCCAGTG 1860 A GT TTTACC - CC -- G A
CC T
TACCTGTCACCGAAGCCAGG GCGTTCTTTT GTGGGGAGAAC GC CT TGT CA GAAGC CA
GA GC CGTT G
AAGCCCCGTTTGTAAGCGTG TAC |||||||||| || || ||| || ||||| || || || ||||
TGTTGTGGTGCTTTATTGTA CATTTTTCTTG CG GA ACA GT TTTCG GT TT TG
GCGA T
CATCCTCCAGTGGCGTTCTT - GT CCTCCT T TA TG G G T- A
TTTAC

GAM212 AAAGTGGCAGGATGATGGCA 185 GGCAGGATGA 1861 TG - T T- AAGT G T AGTT
AGT GA
TAAGTGGGAAGAACCTTGAG TGGCATAAGT AAAG GCAG GA GA GGCAT GG AAGAACCT G
TAAT CT A
TTTAATAGTCTGAAAAAGTG GGGA |||| |||| || || ||||| || |||||||| | |||| ||
GTTACAGGTTCTTGCTATGC TTTT TGTC CT CT TCGTA TC TTCTTGGA C ATTG GA
/
TTTTCCTCTCTGTGGTTTT GG T C TT ---- G - ---- GT- AA

GAM213 TCAATGTGAATGCACTGCCC 186 TCAGAGCAGA 1862 CA-- CCAATCA G - A ---- TG T --
- T AG
AATCAGAGCAGACAGCGACT CAGCGACTTG CTGC GA CAG AC GCGA CT GCGACC
CG AGG GGG A
TGGCGACCTCGAGGTGGGAG GCGA |||| || ||| || |||| || |||||| || ||| |||
AGCTCCTCCTGAATGTGGTC GACG CT GTC TG TGCT GA CGCTGG GT TCC
CCT /
GCTGAGGCCCTCGTGGTACT TTCG CGACTAA G A G CCCG GT T AAG T CG
GGTCAATCAGCGCAGGCTTC
GTTCCAATCCA
GAM214 AAGGAGGAGCAGGCCACGTG 187 AGGAGGAGCA 1863 CACGT - A GTCGTT TG A A A- A
C- G TG C AC

CCCCAATTGTCGTTGTGAGA GGCCACGTGC GGC GCCC CA TT G AG TC GT AG GC TCT C C GGA C

TCAGTAAGAGCCTCTGCTGC CCCA ||| |||| || || | || || || || || ||| | | |||

CGGAACCTGTCCGTGGAGAA CCG TGGG GT AG C TC AG CG TC CG AGA G G CCT /

AGCCCTGAGCGAGCTTGCTT TCT-- T G ATTT-- GT G - AG C AA - GT - GT

TAGAGTGTGGGTTCTGCCTG

TGCCCAATTT

GAM215 CTTTTTGTTAAATGGATCCC 188 TCCCAAATAT 1864 TG TAAATGG - - ACAAA T AA

AAATATTTACAAAGCCATCA TTACAAAGCC CTTTT T ATCC CAA ATATTT GCCA CAG C

GAACCACCTGTGGCAAATGT ATCA ||||| | |||| ||| |||||| |||| |||

ATTGTGGATATTGTGAAAAG GAAAA G TAGG GTT TGTAAA CGGT GTC C

GT TTA---- T A ----- - CA

GAM216 CTTGCCCCTCTCTGTCTTCT 189 TGGAAAGACA 1865 -- CT T - GG G G --- CTTTAT A

CTTTCTGGTTCTTGCCTTGT TGGGGAGGTG CTCTCT GTCTT C TT CT TTCTT CCTT TCTCTGTGT GG GC C

CTCTGTGTGGCTTTATGCAC GTAA |||||| ||||| | || || ||||| |||| ||||||||| || ||

ATGCTTTACACCCATGCACA GAGGGG CAGAA G GA GA AAGAG GGAA AGGGACACG CC CG A

GGGAAAAGGGGAGAAGGAGC TA AG T C GG G A TAC ACATTT T

AGTGGAAAGACATGGGGAGG

TGGTAAG

GAM217 TGAAACGTGAAGTCCTGTTT 190 TGAGAGAAGT 1866 A - TGTT ATGCCA-- AC AC-- G

TGAATGCCAAACCCACCATT CAGTTTGGGC TGA AC GTGAAGTCC TTGA AACCC CATTC TGGT C

CACTGGTGCTGACTACATAG TTCA ||| || ||||||||| |||| ||||| ||||| ||||

AATGGGGTTGAGAGAAGTCA ACT TG CACTTCGGG GACT TTGGG GTAAG ATCA T

GTTTGGGCTTCACAGTGTCA G A TTT- GAAGAGAG -- ATAC G

GAM218 TCCTGTGGTATGTAGGTTTC 191 TGTGGTATGT 1867 G TAT A TT TC CAC

TGCTTCCTCACCAACCAGTG AGGTTTCTGC TCCT TGG GT GGT CTGCT CT C

GGCAGTCACCAACCCGAAGG TTCC |||| ||| || ||| ||||| ||

A AGGA GCC CA CCA GACGG GA A

A --- A CT GT CCA

GAM219 GGCTCCTGAGGTGGCTGATC 192 GTAGAGCAAA 1868 C GT GC A GA C G G GT

GAATTGGGGACTATGTCCAG TGTTTCAGGA GG TCCTGAG G TG TC ATTGGGGA TAT TCCA T C

TGTCATGGTGGGGTATCCCT TCC || ||||||| | || || |||||||| ||| |||| |

AGTAGAGCAAATGTTTCAGG CC AGGACTT T AC AG TGATCCCT ATG GGGT G /

ATCC T TG AA G A- - - G TA

GAM220 GAGCTCATTATCCAGTCTGT 193 TCCAGTCTGT 1869 - T- GT-- -- GA- - G
GCCAACTGAAGTAGGAGACT GCCAACTGAA GAGC TCATTATCCAG CT GCCA ACT AGT AG
A
GACTGTGAGTGCTGGCTAAA GTAG |||| |||||||||| || |||| ||| ||| ||
AGCCCTGGGTGGTGAGGCTC CTCG AGTGGTGGGTC GA CGGT TGA TCA TC G
G CC AAAT CG GTG G A

GAM221 TGCTCTATATTGAGTTTTGT 194 AAAGTGTGGT 1870 CTATA ------- - --- GC
ATGATTCATGCCTTTGGCAA CATGCAGGCA TGCT TTGAGTT TTGTATGATT CA
TGCCTTTG A
TCAAGGGCAAAGTGTGGTCA GGAC |||| ||||||| |||||||||| || ||||||||
TGCAGGCAGGACAATTCAAG ACGA AACTTAA GACGTACTGG GT ACGGGAAC /
ACAGCA CAG-- CAGGACG T GAA TA

GAM222 TCCTCTGATTCCCAACCCAG 195 TGAGAGAAGG 1871 --- A CAGG - GG --- C GAATG
A G
GCCTTGCCCCTGGCCTCCCA AGAGGGAGCA T TCCCA CC CCTTGC CCCT CC TC CAC
GTT ATATATAT T
CGAATGGTTAATATATATGT GGGA | ||||| || |||||| |||| || || ||| ||| ||||||||
AGATATATATGAACACGGTG A AGGGT GG GGGACG GGGA GG AG GTG CAA
TATATATA A
AGAGAAGGAGAGGGAGCAGG CGG - ATA- A GA AAG A GCA-- G G
GATAGGTGGGAGGCATCAGA
GGA
GAM223 CTTTTCCACTTGCCCCACGT 196 TGGGAGGCAG 1872 T CAC ------ T TT
CTCTGCCTCTGGACTTACTG GGCACGTGGG CTTTTCCAC TGCCC GTCTCT GCC CTGGAC
A
TTCAGGGCCAGGTGGGAGGC AAAG ||||||||| ||||| |||||| ||| ||||||
AGGGCACGTGGGAAAG GAAAGGGTG ACGGG CGGAGG CGG GACTTG /
C A-- GTGGAC - TC

GAM224 CTCCAAAGAACCAAGAGTGC 197 CATTTCACTT 1873 T - ---------- CAC GAGATA
TC
AAATCAGTCCATTTCACTTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
CACTGTCTGAGATAGGGTCT AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
CTAAGACCCAGGATACAAGG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GTGGAATGTAGCTATATGGA - C TATCGATGTA AC- A----- AA
CTCGATTTGCTTCCGGACCT
TTTCCAGAG
GAM225 TTGGTTTTTTGGCGATTTCA 198 TGAGGGAGAT 1874 - - - TCCA G AAAGCT C -
TTAT TGG
TTCCATTCTTGACCAAAGCT ATGTAAATTG TGG CGATTT CAT TTCTT ACC TCT TTTAAGT
AGT TA A
TCTCTTTAAGTAGTTTATTA TCCA ||| |||||| ||| ||||| ||| ||| ||||||| ||| ||
TGGAAAATTGTCACACTAAC ACC GTTAAA GTA AGGGA TGG AGA AAATTCA TCA
GT A

TTAAAAGACAGGGTGAGGGA C T T TAG- G GAC--- - A CACT TAA
GATATGTAAATTGTCCACTA
GAAAATTAAA
GAM226 CCTTCTCCATCTGCTGGTCT 199 TTAGTCTTTC 1875 - CT CT TC CC CT- -
ATACAAG A
GAGCTGGGAGCTGGAGTCAG TCTCTCTCTC GCT GGTCTGAG GGGAG GGAG AGGC AGT
CC GGGAC CCC C
GCCCAGTCTCCGGGACATAC TCAG ||| |||||||| ||||| |||| |||| ||| || ||||| |||
AAGCCCACATGGGAGTCCCA CGA TCGGACTC CTCTC TCTC TCTG TCG GG CCCTG
GGG A
GGCACGCTTAGTCTTTCTCT G T- -- TT AT CAC A A------ T
CTCTCTCTCAGGCTGAGCTG
GGTGCAGTTGG
GAM227 CAGTGCGTGTACTGTACACA 200 TGTACACATC 1876 G TA - AC A CACTCA T CT TC
G
TCCACACTCATTCTCACTCA CACACTCATT CAGTGC TG CT GT AC TCCA TTC CA
CAGGGT CCG A
GGGTTCCCGGACCGGCTGTC CTCA |||||| || || || || |||| ||| || |||||| |||
CTGCCTGCGGAACTGGAGGT GTCATG AC GA CA TG AGGT AGG GT GTCCTG GGC
/
AAACTAGCTCAGGTACTG G TC T AA G CA---- C CC TC C

GAM228 ATGGAGATGTTGAGGTAAAG 201 TGAGGTAAAG 1877 GAT GA ------- TGA A- G
TAGTTTGAGTTGTCACTGAC TAGTTTGAGT ATGGA GTT GGTA AAGTAGTT GTTGTC CT
A
CAGCAGGCAATAATTGCTTT TGTC ||||| ||| |||| |||||||| |||||| ||
TATAGGTGCCAAAATTCCAT TACCT TAA CCGT TTCGTTAA TAACGG GA C
--- AA GGATATT --- AC C

GAM229 GCACGAGGCATGCACATGCA 202 TGGTGGCCGG 1878 ATG AT A GA-- C - C T
GAA
CGCCGGGATTCCTCTGCTGC TGGTTTTGTG GCACGAGGC CAC GC CGCCGG TTCCT TGC
TGC AT TGAATTA G
CATTTGAATTAGAAGAAAAT C ||||||||| ||| || |||||| ||||| ||| ||| || |||||||
AATTTATATGCATGCACAGG CGTGTTTTG GTG CG GTGGTT AAGGA ACG ACG TA
ATTTAAT A
AAGATATTGGTGGCCGGTGG --- GC - ATAG C T - T AAA
TTTTGTGC

GAM230 CTGACACAGGACGTGGAAAT 203 TCGTATCAGT 1879 C--- C TACTAATAT T - CCTTT
T- T AGC
ACTAATATGGCTGCTGGGAC GCTCAGTGTC AGGA GTGGAAA GGC GCTGGG ACT
CG GTA TTC A
TCCTTTCGTGTATTTCAGCA TCTC |||| ||||||| ||| |||||| ||| || ||| |||
AGAGAATTATTTCGTATCAG TCCT TACCTTT CTG TGACTC TGA GC TAT AAG
/
TGCTCAGTGTCTCTCCAACT AATC T TCAACCTCT - G CTAT- TT T AGA
TTTCCATTTCCTCTAAGGTC

AG
GAM231 GCTCCAAAGAACCAAGAGTG 204 CATTTCACTT 1880 A AA T - TTC--- - GT GAG AG- TC
CAAATCAGTCCATTTCACTT TCACTGTCTG CC GAG GCAAATC AGTCCAT AC TTTCACT CT AT GGTC T
TCACTGTCTGAGATAGGGTC AGAT || ||| ||||||| ||||||| || ||||||| || || ||||
TCTAAGACCAGGATACAAGG GG CTT CGTTTAG TCAGGTA TG AAGGTGG GA TA CCAG /
GTGGAATGTAGCTATATGGA A C- - C TATCGA T -- ACA GGA AA
CTCGATTTGCTTCCGGACCT
TTTCCAGAGC
GAM233 TGCATGCGCTGCTGGCCATT 205 GGGACAAGAT 1881 T TGGCCA C CGA- A - T GTATTGA TA
GCCCTCACGATGTACCCCAT GTTGCGCATG TGCATGCGC GC TTG CCTCA TGT CCC CA GC TGA G
GCGTATTGATGATAGCATTC CA ||||||||| || ||| ||||| ||| ||| || || ||| |||
ACCTCCAGCTGCGGGACAAA ACGTACGCG TG AAC GGGGT ACA GGG GT CG ACT C
TATGGGGACAAGATGTTGCG T TAG--- A ATAA - C - ACCTCC- TA
CATGCA

GAM234 TAGGTTGTTTCCAACATGAG 206 CAACATGAGT 1882 C- AGT AAGC A TGAA C T TT G
TGTGAGAAGCTAAGTTGAAT GTGAGAAGCT TTCCAA ATG GTGAG TA GT TGTTGCA GGGG AAAG TGCAGT C
GTTGCACGGGGTAAAGTTTG AAGT |||||| ||| ||||| || || ||||||| |||| |||| |||||| |||
CAGTGCTAATTGTGTCCTTT AAGGTT TAC CACTC AT CA GCGACGT CCTC TTTC GTGTTA T
TCTCCTGCAGCGCCTACATA TA --- CAA- A TCC- - T CT A
AACCTCACCATATTTGGAAG
ATTCCTA
GAM235 GTCAAGATTTTAACAAACAT 207 TGAGGTAGGT 1883 A TTTT ACAT AT-- ACA
CTTAATCCTCACAACAACCC AAGTCATTGT GTCA GA AACAA CTTA CCTCACA A
TGTGAGGTAGGTAAGTCATT TTCA |||| || ||||| |||| |||||||
GTTTCATGAT TAGT CT TTGTT GAAT GGAGTGT /
A ---- ACT- GGAT CCC

GAM236 TCAGTGCTCTAAAGAACTTT 208 TCAGTGCTCT 1884 - A- ---- GTA G GT TCT
GTATTTGGGCAGCTGTGCTC AAAGAACTTT TCAGTG CTCT AAG AACTTT TTT GGCAGCT GC G
TGTCATGTCAGGCTGCTGGG GTAT |||||| |||| ||| |||||| ||| ||||||| ||
ACAGGAGTTGATGCTTACGG AGTCGC GGGG TTC TTGAGG AGG TCGTCGG TG T
GGCCGCTGA C CA GTAG AC- G AC TAC

GAM237 GTCCAGTGCGTGTACTGTAC 209 TGTACACATC 1885 C G TA TACACATCC A - - CT TC G
ACATCCACACTCATTCTCAC CACACTCATT GTC AGTGC TG CTG AC CTCA TTCT CA CAGGGT CCG A

TCAGGGTTCCCGGACCGGCT CTCA ||| ||||| || ||| || |||| |||| || |||||| |||
GTCCTGCCTGCGGAACTGAG CAG TCATG AC GAT TG GAGT AAGG GT GTCCTG
GGC /
GTAAACTAGCTCAGGTACTG - G TC CAAA----- - C C CC TC C
AC

GAM238 CCAGCCCAGTCGGGTTAACA 210 CAGTCGGGTT 1886 G A T TTAACATCC -- G GA
TCCAAAGGACTGAGCTCTGA AACATCCAAA CCA CCC G CGGG AAAGG ACT AGCTCT A
ACAAAGAGTTAAGTTACCTT GGAC ||| ||| | |||| ||||| ||| ||||||
TTAAGCATTTCGCGGGGTGG GGT GGG C GCTT TTTCC TGA TTGAGA C
G - - TACGAAT-- AT A AA

GAM239 AGAGAAACCTGACATGTGGG 211 TGAAGCTGCC 1887 AAC ATGTG TACC T TC AAT
A GC
CATACCTCAGTGATCCTTAA AGTCAGATCT AGAGA CTGAC GGCA TCAG GA CTT AG
ATG C
TAGAATGGCCCCCGTGCTTC CT ||||| ||||| |||| |||| || ||| || |||
CAAGTGTCCTGAAGCTGCCA TCTCT GACTG CCGT AGTC CT GAA TC TGC /
GTCAGATCTCT A-- A---- CGA- - GT CCT G CC

GAM240 GAAGCTTGACATTTTAGTTT 212 TCAGGAGTAG 1888 C TG T- CATTA TT -- A
GCCATTATGTTAAAAACATC ATTGTTAGTG GAAG T ACATT TAGTTTGC TG AAA AACATCT
A
TAAATAGGTGTTAGTTTCTC TTGA |||| | ||||| |||||||| || ||| |||||||
AGGAGTAGATTGTTAGTGTT TTTC A TGTGA GTTAGATG AC TTT TTGTGGA A
GACTTT - GT TT AGG-- TC GA T

GAM241 GAGTGCAAATCAGTCCATTT 213 CATTTCACTT 1889 T - ---------- CAC AGATAG
TC
CACTTTCACTGTCTGAGATA TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT
TGTCTG GGTC T
GGGTCTCTAAGACCACGGAT AGAT ||| ||||||| ||||||| |||||||| |||||| ||||
ACAAGGGTGGAATGTAGCTA CTT CGTTTAG TCAGGTA AGGTGGGA ATAGGC
CCAG /
TATGGACTCGATTTGCTTC - C TATCGATGTA AC- A----- AA

GAM242 GCTCCAAAGAACCAAGAGTG 214 CATTTCACTT 1890 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC

GAM243 TGAAGCTGCCAGGTGCATTT 215 TGAAGCTGCC 1891 AT G- ATAAA AG TA--- C--
GT T
AAGTGGTGGTCTATAAAGCA AGGTGCATTT C TTAAGTGGT GTCT GC TGGCTTTC
GCTGGG GCG GGC C
GTGGCTTTCTAGCTGGGCGC AAGT | ||||||||| |||| || |||||||| |||||| ||| |||
GGTGGCTCATGCCTGCAATC G AGTTCGCTA CAGA CG GCCGGAGG CGACCC
CGT CCG A
CCAGCACTTTGGAGGCCGAG -- GA ----- GA TTTCA TAA -- T
GCAGACAGATCGCTTGAGCA
CAGGAGTTCG
GAM244 TTGGTAAAATGTCACTGCCT 216 AGAGCAAGAT 1892 A AC------- - A-- C ACG AC
TCAGGACACACTACGGGTCA GTTGGGATAT TTGGTAAA TGTC TGC CTTC GGACA ACT
GGTC A
CACTGATCAAGTTGTTCAAA TTAC |||||||| |||| ||| |||| ||||| ||| ||||
GAAGAGCAAGATGTTGGGAT AACCATTT ATAG ACG GAAG CTTGT TGA CTAG /
ATTTACCAA - GGTTGTAGA A AAA - A-- TC

GAM245 AGGAGAGGGGAGCGGTAGTT 217 GCGGTAGTTA 1893 G G ---- AC ATA AA-- C C
ACGTTGCATAGTGGTCAAAG CGTTGCATAG AGGA AGGGGA CGGT AGTT GTTGC GTGGTC
AG TGC G
CTGCCGAGGTACTCCAGGGC TGGT |||| |||||| |||| |||| ||||| |||||| || |||
CGCACGGTAGCACAGCTTGA TTCT TCTCCT GTCA TCGA CGATG CGCCGG TC
ATG A
TACTGGTCCTCTGTCTT G G TAGT CA GCA GACC - G

GAM246 ATGAGTATTGATCTGTCCCA 218 TATTGATCTG 1894 AT TCT GC C AGG G
GCCTGTGCATTGCTCCGAGG TCCCAGCCTG ATGAGT TGA GTCCCA CTGTGCATTG TCCG
CA T
CAGTTCTGAGTGGATGATGT TGCA |||||| ||| |||||| |||||||||| |||| ||
ACAGATGGGATTCCTCAGCT TACTCG ACT TAGGGT GACATGTAGT AGGT GT T
CAT -- CCT A- - GA- C

GAM247 CTTCTTTGGTCCATAAATCT 219 ACTGGTTTTA 1895 TTG- ---- TC GAA-- TT
CAGGAATGTTTTAGGCAGAA CCCTGTGGAT CTTCT GTCCATA AA TCAG TGT T
AACTGGTTTTACCCTGTGGA AATC ||||| ||||||| || |||| |||
TAATCAGAAG GAAGA TAGGTGT TT GGTC ACG /
CTAA CCCA TT AAAAG GA

GAM248 GCACTGGGCATGCTGGCAGG 220 TGGCAGGAGC 1896 T- ----- AG- GG T ATA
TAACGG
AGCAGGCACGGGCATGGCCT AGGCACGGGC GCATGC GG CAGGAGC GCACG CA
GGCCT GGGTCTCTA G
ATAGGGTCTCTATAACGGGG ATGG |||||| || ||||||| ||||| || ||||| |||||||||
TCTACTAGGGGCCTCAAGGT CGTGTG CC GTCTTCG CGTGT GT CTGGA
TCCGGGGAT /
CTTGATGTGCATAGCTTCTG TT CAATA ATA A- T AC- CATCTG

ATAACCCTTGTGTGCACTAC
TATGATTTGC
GAM249 GCCTGCCTGAACCCTGGGTC 221 CATGACGGCT 1897 A GG--- - A -- G AA- A- G
C
AGGAGAGAAACACTTGGGGA CTGAGTTCTT CCCT GTCA GGAGAGA ACA CTT GGGAGGGG
AGG CG CGTGGG T
GGGGAAAGGACGGCGTGGGC CCTG |||| |||| ||||||| ||| ||| |||||||| ||| || ||||||
TACCCATGACGGCTCTGAGT GGGA CGGT CCTTTCT TGT GGG TCCTTCTT TCT GC
GTACCC /
TCTTCCTGGGGCTTGTGTCT C GAAGA T G TC G GAG CG A A
TTCCTTGGCAGAAGAGGGCA
CAGCCAAGGC
GAM250 GCTTTTGCTCCAGATGGTTC 222 CCAGTGCCTT 1898 TT TCC T ATACTTT T - AA TC
ACA
ATACTTTGCTTGGTCACAAG CAGAACTTTC GCT TGC AGA GGTTC GCT GG TCAC
GGACA GC G
GACATCGCACAGTAAAGCTT TCTT ||| ||| ||| ||||| ||| || |||| ||||| ||
GTTCCGTGGTCCCAGTGCCT CGG ACG TCT TCAAG TGA CC GGTG CTTGT CG T
TCAGAACTTTCTCTTGCATG T- TTC T ACTTCCG C T C- T- AAA
GC

GAM251 TCCTTTTGACAAGAAATGTG 223 TGACAAGAAA 1899 T - AAATGT C AA-- CTGTT T
GTCGTGAAAATTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA TTGGA GC
T
GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||
ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T
GA C G GTT--- - GGTA ----- T

GAM252 GGATGTTGGCCTAGTTCTGT 224 TGGAAGACTA 1900 ATGT A T A A T -- A
GTGGAAGACTAGTGATTTTG GTGATTTTGT GG TGGCCT GT CTGTGTGG AGACT GTGATTT
GTTGTT TTTAG T
TTGTTTTTAGATAACTAAAT TGTT || |||||| || |||||||| ||||| ||||||| |||||| |||||
CGACAACAAATCACAGTCTG CC ACCGGA CA GGTATACC TCTGA CACTAAA CAACAG
AAATC A
CCATATGGCACAGGCCATGC GT-- - C G - - CT A
C

GAM253 ACAGTTTATCTTCTGAGCCG 225 GAGCAAGATG 1901 --- T - AG GAATG TAGC AG
CCTGAA G GAGG
AATGGGTAATAGCCGAAGTG ATGGAGAGCT ATC TCT G CC GGTAA CGA TGC GAT
ATTATG A
CCCTGAAGATGATTATGGAG GT ||| ||| | || ||||| ||| ||| ||| ||||||
GAATTACATGATGTTGATAA TAG AGA C GG CCGTT GCT ACG TTG TAGTAC /
AGCAATCGAATTTGCCAAGG AGG T A GA AA--- TAA- A- AAATAG - ATTA
AGCAAGATGATGGAGAGCTG
T
GAM254 TGAAGACTTCCTAAATTTGC 226 TTTGCACATT 1902 AC A TTGCA TTGCC
ACCAT
ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC
T

AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM255 GTCTCTCCCAACTGTTAAGT 227 AACCAAGATG 1903 C TC- TGTTAA - ---- TA
TCTAGGTATTGTACTTCCAA TTGGCATGAA GT TC CCAAC GTTCT AGGT ATTG C
TTTTAACTTCAGAACCAAGA C || || ||||| ||||| |||| ||||
TGTTGGCATGAAC CA AG GGTTG CAAGA TTCA TAAC T
- TAC TAGAAC C ATTT CT

GAM256 CCCAGCTCTTCATGTGACCT 228 GAGATCATTA 1904 A--- T-- C GT- A
CCGTCTGGAGACCGGCAAGG TTGAAGAGCG CCC GCTCTTCA GTGA CTCC CTGG G
AGATCATTATTGAAGAGCGA ACCG ||| |||||||| |||| |||| ||||
CCGGG GGG CGAGAAGT TACT GAGG GGCC /
CCAG TAT A AAC A

GAM257 CACAAATCCAGCACTTCCTC 229 AGCAACACAT 1905 T GCACTTC-- T T- G
TCCATTTACTCTGTCAGGCT ATGGCTTTGT CACAAA CCA CTCTCCAT TAC CT T
GTATATGGGGAGCAACACAT G |||||| ||| |||||||| ||| ||
ATGGCTTTGTG GTGTTT GGT GAGGGGTA ATG GG C
C ATACACAAC T TC A

GAM258 TGAAGACTTCCTAAATTTGC 230 TTTGCACATT 1906 AC A TTGCA TTGCC
ACCAT
ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM259 GCCTATGAACAACAGCCCTG 231 TACTTCTCAG 1907 G -- CCCATAC GG TCCT
AC- GA
AGGCCCATACAGTGGAGGCA ATGGATGTTG AACA CC CTGAGG AGTGGA CACCTTC
GAG TATCTGTGA T
CCTTCTCCTGAGACTATCTG AATT |||| || |||||| |||||| ||||||| ||| |||||||||
TGAGATGATCACAGATGTAC TTGT GG GACTCT TCATCT GTGGGAG CTC
GTAGACACT /
CTCCTGAGGGTGAGTCTACT A TA ------- GA TC-- CAT AG
TCTCAGATGGATGTTGAATT
GGT
GAM260 AGTCTCTGAAGTATTCCATG 232 GGGCATTGTA 1908 A TC TGCCTTTTG TTTCCTC TA
TGTCAA G CAA
CCTTTTGGACCCTTTCCTCG TGTTGCTTCT GA GTAT CA GACCC GCAAC AC CT
TTGAT A
CAACTAACTGTCAACTGTTG GTGG || |||| || ||||| ||||| || || |||||

ATCAAAAAAGTCAAGGGCAT TT CGTA GT TTGGG CGTTG TG GG AACTG /
TGTATGTTGCTTCTGTGGGT - GT CTTATTA-- TGTCTT- TA TTAC-- G AAA
TATTATTCTGTGATGCTTAG
GACT

GAM261 GCTCCAAAGAACCAAGAGTG 233 CATTTCACTT 1909 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC

GAM262 GCTGTGTTGCAGTGCATTGT 234 GTGCATTGTG 1910 GCA A TG G TG GGA TG GA
CCT TG
GTTGCAGGATTGGGAAGGGC TTGCAGGATT GCTGTGTT GTGC T T T CA T G AGGGCA
GTGC G
ACCTGTGCTGGTTGCACTTG GGGA |||||||| |||| | | | || | | |||||| ||||
CTTTGATTGAATGTGGAATG TGACGTAG CATG A A G GT A T TTTCGT CACG /
AAGTACGAAGATGCAGT AAG A GT A GT A-- GT AG T-- TT

GAM263 TACTCAAGGGAAAATTGTGG 235 TGACAGAGAC 1911 T AG G GA G G
ATTGGTCAAGGAGCTTGACA ACAGTTTTGC TAC CA G AAAATTGTG TT GTCAAG A
GAGACACAGTTTTGCTCTGG TCTG ||| || | ||||||||| || ||||||
TG GTG GT C TTTTGACAC AG CAGTTC /
- CT G AG A G

GAM264 ACAGTGAGCAAAAGCTTTTA 236 TGAGCAAAAG 1912 T - AAAA --- CCT
GGTGTCCTCAGTACATTTTA CTTTTAGGTG ACAG GA GC GCTTTT AGGTGT C
AGAGAGTGCAAGCGTCCTGT T |||| || || |||||| ||||||
TGTC CT CG TGAGAG TTTACA /
- G AACG AAT TGA

GAM265 TCACTTCAATCTTATTTCTC 237 TCAATCTTAT 1913 AATC -- A A- TC CATC AA
TTACTATCTATGTCTGGACA TTCTCTTACT TCACTTC TTATTTCT CTTACT TCT TG TGGA
ACGA A
TCACGAAAACACTTGTCTCC ATCT ||||||| |||||||| |||||| ||| || |||| ||||
AATCAACGGACAGTGGGGAG AGTGGGG AATAAAGG GGGTGA AGG AC ACCT
TGTT C
GAAATAATTCAGGGGTGA ACTT AG C CA TA C--- CA

GAM266 GAAGCTTGACATTTTAGTTT 238 TCAGGAGTAG 1914 C TG T- CATTA TT -- A
GCCATTATGTTAAAAACATC ATTGTTAGTG GAAG T ACATT TAGTTTGC TG AAA AACATCT
A
TAAATAGGTGTTAGTTTCTC TTGA |||| | ||||| |||||||| || ||| |||||||

AGGAGTAGATTGTTAGTGTT TTTC A TGTGA GTTAGATG AC TTT TTGTGGA A
GACTTT - GT TT AGG-- TC GA T

GAM267 TTTTTCCCTTTAACTTCTCA 239 TTCTCAGTGG 1915 CT TC A GAAT T CC ATT
GG
GTGGACTGAATTCTGTTTCC ACTGAATTCT TTTTTCC TTAACTTC AGTGG CT TCTGTT CCA
GG TTT A
ACCGGATTTTTGGACTAAAA GTTT ||||||| |||||||| ||||| || |||||| ||| || |||
TAGCTTATGGCAACAGAGGC AAAAAGG AATTGGGG TCATC GG AGACAA GGT TC
AAA C
TACTCTGGGGTTAAGGAAAA -- TC - ---- C AT GAT AT
A

GAM268 GTATCATCTGGGAAATCTGT 240 TCATCTGGGA 1916 A AAATC- C--- G-- GCC
CTCAAGATCTGGCCTCCCAC AATCTGTCTC GTATC TCTGGG TGT TCAA ATCTG T
GGATATGTTGAAGTAACAAG AAGA ||||| |||||| ||| |||| |||||
CTTGCCTAGAGATGC CGTAG AGATCC ACA AGTT TAGGC C
- GTTCGA ATGA GTA ACC

GAM269 TGAGGCAGGAGAATCGCTTG 241 AGAGGTAGAG 1917 AGAA GA-- A GGTA GT
A- CAA
AGCCCAAGAGGTAGAGGTTG GTTGCAGTGA TGAGGCAGG TCGCTT GCCCA GA GAG
TGCAGTG GC G
CAGTGAGCCAAGATCGCGCC GC ||||||||| |||||| ||||| || ||| ||||||| ||
ACTGCACTCCAGTCTGGGCA ACTCTGTCC AGTGAG CGGGT CT CTC ACGTCAC
CG /
ACAGAGTGAGACCCTGTCTC CAG- ACAA - GAC- -- CG CTA
A

GAM270 TGTCTGGAGAAAGGACTAGA 242 GGACTAGAGA 1918 GA A ATCCAG- ------- A- - C
AA
GAGAAATCCAGCTCAGATGT GAAATCCAGC CT GAGAGAA CTCAGAT GT TTGCTC
ATTCCT TTCAG G
ATTGCTCATTCCTCTTCAGA TCAG || ||||||| ||||||| || |||||| |||||| |||||
AGGACTGGGTGGGAATGGAG GA TTTTCTT GGGTCTA CG GACGAG TAAGGG
GGGTC /
CAGGGGCTAGAGGAATCTGG GG - AATCGAA AGGAGAT GG G T AG
GAAGCTAATTCTTTTAGGGC
TTTTTCCAACA
GAM271 GCTCCAAAGAACCAAGAGTG 243 CATTTCACTT 1919 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC

TTTTCCAGAGC
GAM272 TTCGGATGTTGCCTGCACTG 244 CCTGCACTGA 1920 GCACTGAA GTAAT TG GAA G G GA - G C
AAGGCATTTGTAATCATGAT AGGCATTTGT CCT GGCATTT CA AT CAC GT AT CTCTT GT TTCAT A
GAACACGGTGATGACTCTTG AATC ||| ||||||| || || ||| || || ||||| || ||||| TGTTCATCACTGTGAAGACA GGG TTGTAAG GT TG GTG TA TA GAGAA CA AAGTG C
AAGAGGATGATGGTGATAGT -------- TT--- GT ATA G G G- A G T TGTGTTGAATGTTGGGCAAA TTCTGAA
GAM273 AATCCAAATGTATCATCTTT 245 AGAAATGGAG 1921 AA- T - CATA CCA TA TCCATATCCCCATCTGTAAA AGAAGTATGT AATCCA TGTA CAT CTTTTC TCC TCTG A TCAGAAATGGAGAGAAGTAT ACGC |||||| |||| ||| |||||| ||| |||| GTACGCTGTGGGTT TTGGGT GCAT GTA GAAGAG AGG AGAC / GTC - T ---- TAA TA

GAM274 GTCTTGGAGGTGGGAGCGGA 246 TTCACAGTGC 1922 TTG - GATAA G- ------- C TAAGCAGGTCTCTCAGGAGA GCCATGTTCT GTC GAGGTGG GAGCG GCA GT CTCT A GGAAATTCACAGTGCGCCAT CCAC ||| ||||||| ||||| ||| || |||| GTTCTCCACTTCAATGAT TAG CTTCACC CTTGT CGT CA GAGA G TAA T ACCG- GA CTTAAAG G

GAM275 ATTGACGCACAGCAGTGGGG 247 TCCTCCAGTG 1923 C A GT TTTACC - CC -- G A CC T
AGAACAGCGTCTTTTACCTG GCGTTCTTTT AG AGTGGGGAGAAC GC CT TGT CA GAAGC CA GA GC CGTT G
TCACCGAAGCCAGGAAGCCC TACT || |||||||||||| || || ||| || ||||| || || || |||| CGTTTGTAAGCGTGTGTTGT TC TCATTTTTCTTG CG GA ACA GT TTTCG GT TT TG GCGA T
GGTGCTTTATTGTACATCCT - - GT CCTCCT T TA TG G G T- A CCAGTGGCGTTCTTTTTACT CTAATGTTCTT
GAM276 ACCGGTTATGGTGCTGCTGT 248 TGGAGCCTGG 1924 GG T - AC GTTGGAGC G TT T T
GAACACTGCCAAGTTGGAGC CTCTGTTTGT CGGTTAT TGC GCT GTGA ACTGCCAA CTGGCTCT T G GCCG C
CTGGCTCTGTTTGTGCCGTC GCCG ||||||| ||| ||| |||| |||||||| |||||||| | | |||| TTTGGTCTGGGAGGAGTCGG GTCGGTG ATG CGG TACT TGACGGTT GGCTGAGG G T TGGT T
ATTGGCAGTTATCATGGGCT AA T G AT A------- A GG C T GTAAAGTGGCTGGT

GAM277 TTTGGTGATGTCACTGCTGG 249 TCACAGTCTG 1925 TG GATG T- G - CTATC T- A A
GAGGTGGCTATCCTGTGGAC TGAAAAACTG TT GT TCAC GCTG GAG GTGG CTG GG CC C
CACCTGGCCTCCAGACCCAC AA || || |||| |||| ||| |||| ||| || || ACTCACAGTCTGTGAAAAAC AA CA AGTG TGAC CTC CACC GAC CC GG C

TGAA GT AAA- TC A A CA--- CT - T

GAM278 TATTAGAACAGTGCTTGAGT 250 CTATTATTAC 1926 G GA-- ---- AACAAACGT T---
TATT T
GAGTCAGCTCTCAACAAACG TTTTGCTACC A TGCTT GTGAGTCAGCT CTC TAGC
GTGAT GT A
TTAGCTGTGATTATTGTTAT ATCT | ||||| |||||||||| ||| |||| ||||| ||
TACTATTATTACTTTTGCTA T ACGAG TATTTAGTCGA GAG ATCG CATTA CA
T
CCATCTAAGAGCTCCAGCTG - ACGG CCTC AATCTACC- TTTT TTAT T
ATTTATGGCAGAGCATGTTC
TGATG
GAM279 TTTGGTGATGTCACTGCTGG 251 TCACAGTCTG 1927 TG GATG T- G - CTATC T- A A
GAGGTGGCTATCCTGTGGAC TGAAAAACTG TT GT TCAC GCTG GAG GTGG CTG GG CC
C
CACCTGGCCTCCAGACCCAC AA || || |||| |||| ||| |||| ||| || ||
ACTCACAGTCTGTGAAAAAC AA CA AGTG TGAC CTC CACC GAC CC GG C
TGAA GT AAA- TC A A CA--- CT - T

GAM280 GTGGCACAATTTGAATTCAG 252 TGGCACAATT 1928 A AT ATTCA--- AAC- GACT
ATT-- G G
TAAAACAGGGGAGACTGGAG TGAATTCAGT GGC CA TTGA GTAA AGGGGA GGAGGG
GGGA TTT G
GGATTGGGAGTTTGGAGAGG AAAA ||| || |||| |||| |||||| |||||| |||| |||
TCCCTTTCACCCTCCTCCTT CCG GT AACT CATT TTTCCT CCTCCC CCCT
GAG /
TAAAATTACAGTAACTCTCA - C- CTCAATGA AAAA ---- ACTTT G A
ACTGGCCAT

GAM281 TCCTTTTGACAAGAAATGTG 253 TGACAAGAAA 1929 T - AAATGT C AA-- CTGTT T
GTCGTGAAAATTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA TTGGA GC
T
GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||
ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T
GA C G GTT--- - GGTA ----- T

GAM282 ATAAGCTGCTCTAATTGCCA 254 TCTGCTGTGA 1930 C C A TG CA- T TG TTGT G
ACT G
AGAATTCACATGTGGTTGTA TGGACACTTG ATAAG TG TCTA T C AGAAT CACATG G
ATGCA CTTT GG A
TGCAGCTTTACTGGGAGACT T ||||| || |||| | | ||||| |||||| | ||||| |||| ||
GAAGTGTATCTGCATGTGAT TGTTC AC AGGT A G TCTTA GTGTAC C TATGT GAAG
TC G
TCTGCTGTGATGGACACTTG - - - GT TCG - GT ---- - --- A
T

GAM283 GCCTGCCTGAACCCTGGGTC 255 CATGACGGCT 1931 A GG--- - A -- G AA- A- G
C

AGGAGAGAAACACTTGGGGA CTGAGTTCTT CCCT GTCA GGAGAGA ACA CTT GGGAGGGG AGG CG CGTGGG T

GGGGAAAGGACGGCGTGGGC CCTG |||| |||| ||||||| ||| ||| |||||||| ||| || ||||||

TACCCATGACGGCTCTGAGT GGGA CGGT CCTTTCT TGT GGG TCCTTCTT TCT GC GTACCC /

TCTTCCTGGGGCTTGTGTCT C GAAGA T G TC G GAG CG A A

TTCCTTGGCAGAAGAGGGCA

CAGCACAGGC

GAM284 CAGCCTCCCACTGTGGTGCC 256 TCGCCTGGAC 1932 C - G T G A - AA- CAGAGA - CA T

TGGTGGAGACCTGGCCAAGG CACAAGTTTG ACT GTGGT CC GGTG AG CCT GGCC GGTA GCTGTG TG TGC G

TACAGAGAGCTGTGTGCATG ACCT ||| ||||| || |||| || ||| |||| |||| |||||| || |||

CTGAGCAACACCACAGCCAT TGA CACCA GG CCGC TC GGG CCGG TCGT CGACAC AC ACG /

TGCTGAGGGCCTGGGCTCGC T A - T - - T GAG TAC--- C A- A

CTGGACCACAAGTTTGACCT

G

GAM285 GCATCAGAGCTTCACAGTGG 257 TTCACAGTGG 1933 CAG T AC- C - CCC ACAAATA CCA G G

CCAGAGTACCCCTACAAATA CCAGAGTACC GCAT AGC TC AGTGGC AGA GTA CT GAG GT CTGA C

GAGCCAGTGCTGAGCAATCA CCTA |||| ||| || |||||| ||| ||| || ||| || ||||

GACGTATTCAGATGCATTTA CGTA TCG AG TCACCG TTT CGT GA CTT CA GACT A

GCCACTTTAGATGCTATGC --- T ATT A A A-- ------- ATG - A

GAM286 GTGGGGAGAACAGCGTCTTT 258 TCCTCCAGTG 1934 A GT TTTACC - CC -- G A CC T

TACCTGTCACCGAAGCCAGG GCGTTCTTTT GTGGGGAGAAC GC CT TGT CA GAAGC CA GA GC CGTT G

AAGCCCCGTTTGTAAGCGTG TAC |||||||||| || || ||| || ||||| || || || ||||

TGTTGTGGTGCTTTATTGTA CATTTTTCTTG CG GA ACA GT TTTCG GT TT TG GCGA T

CATCCTCCAGTGGCGTTCTT - GT CCTCCT T TA TG G G T- A

TTTAC

GAM287 GTATTTGCAGGTGATATGGG 259 CAGGAAGCAG 1935 - GG G GA A- AA AC- AATGA

TGAATGAGAAATGACCCTGT GTTGGCATAG GTAT TTGCA TGATAT GGT ATG GA TG CCTGT C

AATGACGAAGGACAGGAAGC CCAG |||| ||||| |||||| ||| ||| || || |||||

AGGTTGGCATAGCCAGTATC CGTA AGCGT GCTATG CCG TAC TT AC GGACA /

GATGCGACATGC C A- A A- GG GG GAA GGAAG

GAM288 GGCTGTCCTCAGGGTTCAGC 260 TATAACAGCC 1936 CTC TCA ATG --- - GC TTA CT

TATGATAGAGACTCAGCTGG ACCTTGACAG GGCTGTC AGGGT GCT ATAGA GACT CA TGGC GG T

CTTAGGCTTCATCCACTGCC TC ||||||| ||||| ||| ||||| |||| || |||| ||
AATGAAGTCAAATTTATAAC CTGACAG TTCCA CGA TATTT CTGA GT ACCG CC C
AGCCACCTTGACAGTC --- C-- CAA AAA A A- TCA TA

GAM289 TGCTTTTCCAAACCAAAGCC 261 AAGCTGAGTT 1937 TT A-- CAA CACA A - -- A
ACAGCACGGTGGCTGCTTTC GAAGGAATTG TGC TTCC AAC AGC GC CG GTGGCTGCT
TTCA A
AAATATGAACAGGCAGCCAC TG ||| |||| ||| ||| || || |||||||| ||||
GCGAGTAAGCTGAGTTGAAG GTG AAGG TTG TCG TG GC CACCGACGG AAGT T
GAATTGTG TT AAG AG- AA-- A G AC A

GAM290 GGAACAGCTCTTTGTTAAGG 262 TAAGGTGCCT 1938 G TG A TGCCTTT AG GA AT
TGCCTTTGAGCAGATAGATG TTGAGCAGAT GGAACA CTCTT TT AGG GAGC ATA TG G
ATGAACACGTGTAGGCTCCC AGAT |||||| ||||| || ||| |||| ||| ||
TGGATGAAGAGTGTTCC CCTTGT GAGAA AG TCC CTCG TGT AC /
- GT G ------- GA GC AA

GAM291 ATGAAGTCAACTGGTATCTG 263 TTTTCACGGC 1939 G AA - ATC A A- - AA TAG-
TTAC
ATGGGAATGGGCAATGAAAT CATAGCTTCC ATGAA TC CTG GT TG TGGGA TG GGC TGAAA
AC A
AGACTTACACACTGTACATT AATA ||||| || ||| || || ||||| || ||| ||||| ||
TTCACGGCCATAGCTTCCAA TATTT AG GAC CG AT ACCTT AT CCG ACTTT TG /
TACAAGCACAGGGGAGTTTA G GG A AAC A CG A GC TACA TCAC
T

GAM292 GAGGCAGAGGAATTGCTTGA 264 AGAAGGTAGA 1940 A GAA GA-- GAA A- GT -
C A
ACCCAGAAGGTAGAGGTTGC GGTTGCAGTG GAGGC GAG TTGCTT ACCCA GGT GAG
TGCAGTG TG TG G
AGTGTGCTGAGATCACACCA TGCT ||||| ||| |||||| ||||| ||| ||| ||||||| || ||
CTGCACTCCAGCCTGGGTGA CTCTG CTC AACGAG TGGGT CCG CTC ACGTCAC
AC AC A
CAGAGCAAGACTCCGTCTC C AG- ACAG --- AC -- C - T

GAM293 GGCTTCAAGATGTAATGTAA 265 TCATTGCACA 1941 GAT A- GGA- G
ATGAGGACGTGACAATGGGT TTGCTAATTG GGCTTCAA GTAATGT AATGA CGT A
GTCATTGCACATTGCTAATT AAGT |||||||| ||||||| ||||| |||
GAAGTC CTGAAGTT CGTTACA TTACT GTA C
AAT CG GTGG A

GAM294 TACTCAAGGGAAAATGTGGA 266 TGACAGAGAC 1942 CA G A GA G G
TTTGGTCAAGGAGCTTGACA ACAGTTTTGC TACT AG GAAA TGTG TTTG TCAAG A
GAGACACAGTTTTGCTCTGG TCTG |||| || |||| |||| |||| |||||
TG GTGG TC TTTT ACAC AGAC AGTTC /

TC G G AG - G

GAM295 CCAGTATTGGGGGCTAACAG 267 TTCACAGTGG 1943 - AACA TG -- C
TTGCTGTGGCCCACGGCTTC CATGGAGTCC CCAGTAT TGGGGGCT GT CTGTG GCC A
ACAGTGGCATGGAGTCCCCA CCAC ||||||| |||||||| || ||||| |||
CGTGCTGG GGTCGTG ACCCCTGA CG GACAC CGG /
C GGTA GT TT C

GAM296 ATCACCCCATGTAGGTGTAC 268 CACAGCAGTG 1944 A C-- G ------ GACAAA-
ATCTGAC G
ATTGTGACAAAGTGCATCTG TTAAAATGGG CCC ATGTAGGT T ACATTGT GTGC
CACTAAGGG C
ACCACTAAGGGGCCCCCTTG CCTG ||| |||||||| | ||||||| |||| |||||||||
GTGACCCCAGCACATTCACA GGG TACGTCCG G TGTGACG CACG
GTGGTTCCC /
GCAGTGTTAAAATGGGCCTG A TTT G TAAAAT ACACTTA ACCCCA- C
CATTTTGGGAGAT

GAM297 GCTCCAAAGAACCAAGAGTG 269 CATTTCACTT 1945 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM298 TGGAGAAGGGTACTCAAGGG 270 TGACAGAGAC 1946 - C- -- - GA G G
AAAATTGTGGATTTGGTCAA ACAGTTTTGC TGGAGAAGG GTA TCA AGGG AAAATTGTG TTTG
TCAAG A
GGAGCTTGACAGAGACACAG TCTG ||||||||| ||| ||| |||| ||||||||| |||| |||||
TTTTGCTCTGGTGAATTACA ATTTCTTCT CAT AGT TCTC TTTTGACAC AGAC AGTTC /
TCTTCTTTA A TA GG G AG - G

GAM299 CATCTTGGAGGCCTGATCTT 271 TGGAGGCCTG 1947 - A CTG ---- A
TGTGGCCAGAAGGCGATTCA ATCTTTGTGG CATCTTG G GGC ATCTTTGTG GCC G
CAAAGATGCCCCTCAAGATG CC ||||||| | ||| ||||||||| |||
GTAGAAC C CCG TAGAAACAC CGG A
T C --- TTAG A

GAM300 AAAGTAATTTAGAATACTGG 272 TTCTTGTGGC 1948 GAATA---- - T-- - C TCAAACA-
- TC
CAAGGGGCTTTGAAGCCATG CATAGCTGTC A CTGGCAAGG GGCT TGA AGC
ATGGTTAC TTAG T
GTTACTCAAACATTAGTCTG ATGT | ||||||||| |||| ||| ||| |||||||| ||||

TCTAAATTTTTCTTGTGGCC T GATTGTTCT CCGA ACT TCG TACCGGTG AATC
/
ATAGCTGTCATGTAGCCATC ATAAAAGTC A TGT G A TTCTTTTTA TG
TTGTTAGCTGAAAATATAAA
TTAATTT
GAM301 GGGTTGACAGAAGGAGAGTA 273 TGACAGAAGG 1949 ACAGA AGA CA TTA-- A AAA
A TCA
AACATTTTAACCATTAAAAC AGAGTAAACA GGGTTG AGG GTAAA TT ACC TT ACTG TC
A
TGATCTCAAATCGACGGTGG TTTT |||||| ||| ||||| || ||| || |||| ||
AAAGGTGTCATAAGATTTAC CCCAAC TCC CATTT AA TGG AA TGGC AG /
CCCTACCAACCC CA--- C-- AG TACTG A GG- - CTA

GAM302 GTCTGTGGAGTGGCTGGAGG 274 CAAGGTCATC 1950 - A G GAGG ACACTAT A A
AGGATGAACACTATGATTAC TTATGCAGAT GTC TGTGG GTG CTG AGGATGA GATT CC C
CACCAGGAGATTGCAAGGTC ATGC ||| ||||| ||| ||| ||||||| |||| ||
ATCTTATGCAGATATGCTAC CAG ACATC TAT GAC TTCTACT TTAG GG C
ATGAC T G A GTA- GGAACG- A A

GAM303 GCTCCAAAGAACCAAGAGTG 275 CATTTCACTT 1951 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM304 AAGGATATGGGAATTCAGTG 276 TGAAAGAACA 1952 A AA T AA- GGG G- -- AT- -
TTC
AAAGAACATGGGTTGTGGAG TGGGTTGTGG TGGG TTCAG GAAAG CAT TTGT GAGT CAG
TAATGT GGA A
TCAGATTAATGTGGATTCAA AGTC |||| ||||| ||||| ||| |||| |||| ||| |||||| |||
ATTCCTGCATTACTGCTGCA ACCC GAGTC TTTTC GTA AACG TTTA GTC ATTACG
CCT /
ATTTGGGCAAATAATGGAGC G -- - GAG ATA GG AC GTC T TAA
TTTTCTGAGCCCAGTTCCTT

GAM305 CCCAATGCCAGGCTGCGCAG 277 CAGGCTGCGC 1953 A---- CAGG-- - TG AGA-- A
GTAG
TTGAAGAACAATGAGTAGGC AGTTGAAGAA CCCA TGC CTG CGCAGT A ACA TGA G
AGGTCATGTGCACGTTGGCT CAAT |||| ||| ||| |||||| | ||| |||
GTGTTAGATAAATGTAAAAA GGGT ATG GAT GTGTCG T TGT ACT /
CTGGG CAAAA TAAATA T GT GCACG - GGAC

GAM306 TGGCGTGAGGTGGAGTGAGG 278 TGGCGAAGCG 1954 G AG- G GA GGCGAA GGCA
G

TGGCGAAGCGAGGGCACTTG AGGGCACTTG TG CGTG GTG AGT GGT GCGAG
CTTGAAAT C
AAATGCGGTTTCAAGCTCGT AAAT || |||| ||| ||| ||| ||||| ||||||||
GGACAGCCCGACTGCACAAA AC GCAC CAC TCA CCG TGCTC GAACTTTG /
CACGGCA G AAA G GC ACAGG- ---- G

GAM307 CAAGGAGACACTGTTGCACA 279 CAGGACACGA 1955 AG ACT C A- A C T AC TG
G
GGACACGATTACGGTGTGAC TTACGGTGTG CAAGG AC GTTGCA AGG CACG TTA GG GTG
GCG AGA C
GCGTGAGAGCGATCTTGCGC ACGC ||||| || |||||| ||| |||| ||| || ||| ||| |||
AGTACTCCTTAAGTGTGAGT GTTCC TG CAATGT TCT GTGT AAT CC CAT CGC TCT
G
CTTGTAACCGTAACCTTG AA C-- - GA G T T GA GT A

GAM308 GTGTATGGAGAACACTGTGT 280 AACACTGTGT 1956 TG---- GA---- A GA ATCA
GTGTG GTAT
GTGTTAAGATGTAACAGATG GTGTTAAGAT CTGTG TGTTAA TGT ACA TG TGAGTGT
GGTC A
ATCATGAGTGTGTGTGGGTC GTAA ||||| |||||| ||| ||| || ||||||| ||||
GTATAACACAGACCGAATGC GACAC GCAGTT ACA TGT AC ACTCGTA CCAG
A
TCACAGATGTAACAGAACGA CTTAAA AGCAAG A AG ---- AG--- ACAC
TTGACGAAATTCCACAGGTC
AACTAGATGC
GAM309 TAGTCTGCAGGTAGTAGATG 281 TGCAGGTAGT 1957 CA--- T TA - TG T AT
ATGGTTCCATCTCGGCATTG AGATGATGGT TAGTCTG GG AG GAT GA GT CC C
TCTATCCTCTCCATATTCAG TCC ||||||| || || ||| || || ||
ACTG GTCAGAC CC TC CTA CT TA GG /
TTATA - TC T GT C CT

GAM310 AAGAGCTTCGCATCTGCGCA 282 TGAGGTATGT 1958 CT ATC ------ T CC -- C- A
CATTCCCCCATCTGCTCCAA ATATTTGTGC AAGAG TCGC TGCGC ACAT CC CA TCTG
TCC A
GGGACACAGAAATGAGGTAT ACCG ||||| |||| ||||| |||| || || |||| |||
GTATATTTGTGCACCGTGAC TTCTT AGTG ACGTG TGTA GG GT AGAC AGG /
TTTCTT TC CC- TTTATA T A- AA AC G

GAM311 TGTTTGGGATCTGGTCTGAG 283 GGAAGTTGCT 1959 TC T G C GGCA TG TA A - T C
---- AT
GGGGCGGACGGCACTGATAT GGCTTCAGCT TGG CTGAG GGG GGAC C A TCA C GCTG
GGCC GC TCTC G
CAACGCTGTGGCCCGCTCTC GATG ||| ||||| ||| |||| | | ||| | |||| |||| || ||||
ATGATGGGAAGTTGCTGGCT ATC GATTT TCC CTTG G T AGT G CGAC TCGG CG
AGGG /
TCAGCTGATGACTTTGGCAA -- - G A AAAC GT TC A T T T TTGA TA

AGTTCACCTGTTTAGCTACC
CCTGCTGTCAG
GAM312 GGAGAGAAACACTTGGGGAG 284 CATGACGGCT 1960 A --- TG GA A- G C
GGGATAGGACGGCGTGGGCT CTGAGTTCTT GGAGAGA ACA CT GGGAGGG TAGG CG
CGTGGG T
ACCCATGACGGCTCTGAGTT CCTG ||||||| ||| || ||||||| |||| || ||||||
CTTCCTGGGGCTTGTGTCTT CCTTTCT TGT GG CCTTCTT GTCT GC GTACCC /
TCC G TCG GT GA CG A A

GAM313 TATTAAGAGGCAGAAAATTG 285 GTGCAGTTCT 1961 A - A--- ATATTGA TTT
CACAATATTGAACTTTTTTC AGTTTGCATT TATTA GAG GCAGA AATTGCACA ACTTT C
CACTGAAGTAGTGTGCAGTT CCTG ||||| ||| ||||| ||||||||| |||||
CTAGTTTGCATTCCTGATA ATAGT CTT CGTTT TTGACGTGT TGAAG C
C A GATC GA----- TCA

GAM314 CGTTAAGTTGGGGTGACACC 286 TCCCTGCAAT 1962 GACAC TG --- -- TCG-- - A--
GA ACTGTC
AGGTGAGCCACGGTCCTCGG CCGAATTTGT CAGG AGC CACGGT CC GCAC CAG
TGAG ACC T
CACCAGATGAGGAACCACTG GTG |||| ||| |||||| || |||| ||| |||| |||
TCTCAATAAGGTCTCAGTGC GTCC TCG GTGCCA GG TGTG GTC ACTC TGG
/
TGTGTGTGTAATGGTTACCG AC--- CT AGA TT TAATG T GTG -- AATAAC
TGAGAGCTTCCCTGCAATCC
GAATTTGTGTG
GAM315 ATAAATGTCTCTCAGAAGAG 287 TTCATTGCAT 1963 AT- - AA---- GAA A G ACAT GA
GGATT
GAAGTACAGGCAGTACATGA GACGAACTTG GTCTCT CAG GAG GT CA GCAGT GAATC
AAAGGT C
ATCGAAAAGGTGGATTCAAC AAGT |||||| ||| ||| || || ||||| ||||| ||||||
AGACCTTTGGATTTCATTGC CAGGGA GTT TTC CA GT CGTTA TTTAG TTTCCA
/
ATGACGAACTTGAAGTGTTG AGT A GTGAAG AAG - A C--- G- GACAA
AAGGGACTGATTAT

GAM316 GCTCCAAAGAACCAAGAGTG 288 CATTTCACTT 1964 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM317 GTTTGTGCTGACAGAACGAG 289 TGACAGAACG 1965 TG GA GA AGAG- T GAAG---
A
AGGGTGCTCTGAAGTATTTC AGAGGGTGCT GTTTG CT CA ACG GG GCTCT TATTTC A

AACAGAAATGATGCCAAGGA CTGA ||||| || || ||| || ||||| ||||||
GCCCAAGGCCGTGATGAAGA CGAGC GA GT TGC CC CGAGG GTAAAG C
TCGAGC TA A- AG CGGAA - AACCGTA A

GAM318 ATGAAGTGGCTCCTCCTGAG 290 TGAGTACCAT 1966 TG GCTCCTCCT TA T GA C T
G
TACCATCGGAAAGCTGTGTG CGGAAAGCTG A AAGTG GAG CCA CG AAG TG GTGAGAG
C
AGAGGCACTCTCACTCACTT TGTG | ||||| ||| ||| || ||| || |||||||
ATGTTGGATCTCCGTAAACA T TTTAC CTC GGT GT TTC AC CACTCTC /
CATTTTGT GT ACAAATGC- TA T A- - T A

GAM319 GGAAGATGTGGCAGGCTTCT 291 TATTGAACAT 1967 G- GCTTC GTAATAA TT
TGCCAA A- GT
GAGGAGTGGTAATAATGTTA TTACTACGTT GCAG TGAGGAGTG TG ATGT TAAAT
TCAATGAA G
TGTTGCCAATAAATATCAAT CCAG |||| ||||||||| || |||| ||||| ||||||||
GAAGTGCAATTTATTGAACA TGTC ACTTTTCAC AC TGCA ATTTA AGTTATTT
C
TTTACTACGTTCCAGGCACT AA AA--- GG----- CT TC---- CA AA
TTTCAAACTGTAAGTGTCTT
TC
GAM320 GGATAGAATGTGGTGGTACT 292 TACTGCAGTG 1968 TAGAA TG GTA TG G--- A CC
GCAGTGAGAGGCATGGTTCC AGAGGCATGG GGA TG GTG C CAGTGAGA GC TGGTT T
TTAGACCAGGCAACATTTCA TT ||| || ||| | |||||||| || |||||
TTGTGGCATTCCAGTTTCC CCT AC TAC G GTTACTTT CG ACCAG /
TTG-- CT --- GT ACAA G AT

GAM321 TGGAGAAGGGTACTCAAGGG 293 TGACAGAGAC 1969 - C- ---- G GA G G
AAACTGTGGATTGGTCAAGG ACAGTTTTGC TGGAGAAGG GTA TCA AG GAAACTGTG TT
GTCAAG A
AGCTTGACAGAGACACAGTT TCTG ||||||||| ||| ||| || ||||||||| || ||||||
TTGCTCTGGTGAATTACATC ATTTCTTCT CAT AGT TC TTTTGACAC AG CAGTTC /
TTCTTTA A TA GGTC G AG A G

GAM322 GAAGGGTACTCAAGGGAACA 294 TGACAGAGAC 1970 -- C- AG A C- GA G G
CATTGTGGATTGGTCAAGGA ACAGTTTTGC GAAG GGTA TCA GGA CA ATTGTG TT
GTCAAG A
GCTTGACAGAGACACAGTTT TCTG |||| |||| ||| ||| || |||||| || ||||||
TGCTCTGGTGAATTACCATC CTTC CCAT AGT TCT GT TGACAC AG CAGTTC /
TTC TA TA GG C TT AG A G

GAM323 GCCACAGGAGCTGCCAGTTT 295 GAGCTGCCAG 1971 ACA-- G - --- GA A - AAT
GACGAATCTGGGCAATTCTA TTTGACGAAT GCC GGA CTGC CA GTTT CGA TCTGG GC T
AGTACCAGAATCGGAGAACC CTGG ||| ||| |||| || |||| ||| ||||| ||

AATGAGCAGTCTGATCGGGC CGG TCT GACG GT CAAG GCT AGACC TG C
GCTAG - A AAC AG A A AAT

GAM324 GGATCGCGGAAGGCGTCCTC 296 CCTCACAGGC 1972 T A TC-- T CA GA CAC
TGGCCTCAGGAGCCACCCAG TGAGTTCTTG GGA CGCGGA GGCG CTC GGCCT G GC C
AGCCTCACAGGCTGAGTTCT CCTC ||| |||||| |||| ||| ||||| | ||
TGCCTCTGTGTCC CCT GTGTCT CCGT GAG TCGGA C CG C
- - TCTT - CA TC AGA

GAM325 GCTCCAAAGAACCAAGAGTG 297 CATTTCACTT 1973 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM326 TGGAGAAGGGTACTCAAGGG 298 TGACAGAGAC 1974 - C- -- A- GA G CG
AAAATTGTGGATTGGTCAAC ACAGTTTAGC TGGAGAAGG GTA TCA AGGG AAATTGTG TT
GTCAA A
GAGCTTGACAGAGACACAGT TCTG ||||||||| ||| ||| |||| |||||||| || |||||
TTAGCTCTGGTGAATTACAT ATTTCTTCT CAT AGT TCTC TTTGACAC AG CAGTT /
CTTCTTTA A TA GG GA AG A CG

GAM327 TGCTTCTTTGCAAGGTATTA 299 AAGGTATTAG 1975 T A ---- T GTATG T
GGTTGTCATTGTATGGATTA GTTGTCATTG TGCTTCTT GCA GGTATT AGGT GTCATT GAT
A
TAATCAAAATGACACTTCAC TATG |||||||| ||| |||||| |||| |||||| |||
AAATACCTGTTGAGGAGTA ATGAGGAG TGT CCATAA TTCA CAGTAA CTA T
T - ACAC - AA--- A

GAM328 AGGGGGGCAAAGTCTATCAG 300 GGGGCAAAGT 1976 G GT A TG TTGAAA TG-
AG G GAT
GTGTTTGAAAGTGTGGCTAA CTATCAGGTG AGGG GGCAAA CT TCAGG T GTG GCTAAGA
TAT ATGT G
GAAGTATGATGTGATGAATG TTTG |||| |||||| || ||||| | ||| ||||||| ||| ||||
ATATGATGAGTCTTGGTATC TCTC TCGTTT GA GGTTT G TAC TGGTTCT GTA
TATA A
CATCGTGTTTGGAAGGATTT G AG A GT C----- CTA GA G GTA
GCTGCTCT

GAM329 TGAGAGGAGAATGAAGGGAA 301 TTAAAGGTCC 1977 AG - -- AACAGT A ATC
CAGTACCTTATGGCTATCTT AGCCAGCTTC TG AGGAGAA TGAAG GG ACCTT TGGCT T
CAGGTTAAAGGTCCAGCCAG AGTT || ||||||| ||||| || ||||| |||||

CTTCAGTTCTTCTGCCA AC TCTTCTT ACTTC CC TGGAA ATTGG /
CG G GA GACC-- - ACT

GAM330 CTCTTGAGCATGCTGACCAG 302 GACCAGTGCT 1978 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM331 GGTTCCTCGTGGAGAAACAG 303 TCGGGCTCGT 1979 TC A A- C TT A- ----- --
AAG
CACACGTTAGCAGGCTTGGA GTCTGTCCTC GGTTCC GTGG GA ACAG ACACG AGC GGCT
TGGA GAAC G
GAACAAGGCCTAGTTCTGTC CCAT |||||| |||| || |||| ||||| ||| |||| |||| ||||
CATGAGTAGTCGGGCTCGTG CCAGGG TACC CT TGTC TGTGC TCG CTGA ACCT
CTTG C
TCTGTCCTCCCATCTGGGAC TC - CC - -- GG TGAGT GT ATC
C

GAM332 TTCTGCTTTTTTCCTAATGT 304 CGGAATGTAA 1980 CTTT AA-- C- A ATT ACT AGCA
CATAATCCATTTGACTCCTA ACAAGTAAGG TTCTG TTTCCT TGT ATA TCC TG CCTA T
AGCATGTAAGTAGGTACCAC AAAC ||||| |||||| ||| ||| ||| || ||||
GGAATGTAAACAAGTAAGGA AAGAC AAAGGA ACA TGT AGG AC GGAT G
AACAGAA ---- ATGA AA A C-- CAT GAAT

GAM333 GCTCCAAAATGATCTCCTTT 305 TGACTCCGTG 1981 ATGATC TTT- G- CA C GGT
GACTCCGTGTCTTCACATCC TCTTCACATC GCTCCAAA TCC GACTCCGT TCTT CATC AG
C
AGGGTCACACTGATGGCAAG CAG |||||||| ||| |||||||| |||| |||| ||
AGGATGGGGTTCCCTGGGTT CGGGGTTT GGG TTGGGGTA AGAA GTAG TC /
TGGGGC ------ TCCC GG CG - ACA

GAM334 GCTCCAAAGAACCAAGAGTG 306 CATTTCACTT 1982 T - ---------- CAC AGATAG
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT
TGTCTG GGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| |||||| ||||
TCTAAGACCACGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGGC
CCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM335 GGAAGTTATGTGCTGACAGA 307 TGACAGAACG 1983 AAG T - ---- GA AGAG-- T
GAAG--- A
ACGAGAGGGTGCTCTGAAGT AGAGGGTGCT GG TTA GTGCT GA CA ACG GG GCTCT
TATTTC A

ATTTCAACAGAAATGATGCC CTGA || ||| ||||| || || ||| || ||||| ||||||
AAGGAGCCCAAGGACCGTGA CC AGT CACGA CT GT TGC CC CGAGG
GTAAAG C
TGAAGATCGAGCACCTGAAC GCA C G AGAA AG CAGGAA - AACCGTA A
GCC

GAM336 AGACACTGAATTGGACATTG 308 TGCAAGTCTG 1984 T -- A ATTTC CT C
ATTTCCTTTTCTCTGCGTCA TGATTTTGTG AGACAC GAATT GGAC TTG CTTTTCT GCGT A
AAATGTCAAGGAAAGTTGCA TTT |||||| ||||| |||| ||| ||||||| ||||
AGTCTGTGATTTTGTGTTT TTTGTG TTTAG TCTG AAC GAAAGGA TGTA A
T TG - GTT-- AC A

GAM337 TGGGAAGAATTGGAAGTTAC 309 TGGGAAGAAT 1985 G- GA ------ A T G
ATGCTGTATATGCAATGTCC TGGAAGTTAC TGG AAGAATTG AGTT AC TGCTG ATAT C
AGCAGTCTGATAAACTGACG ATGC ||| |||||||| |||| || ||||| ||||
ATTCTTAATCA ACT TTCTTAGC TCAA TG ACGAC TGTA /
AA AG ATAGTC - C A

GAM338 GGGCTCCTCATGACACCTTG 310 TACACAGCCA 1986 TC ACACC TACAC AACT G
GA T
CTACACAGCCAACTTTGTGG ACTTTGTGGC GGGCTCC ATG TTGC AGCC TTGTGGC
CCT GGTGC G
CGCCTGAGGTGCTGAAGCGC GCCT ||||||| ||| |||| |||| ||||||| ||| |||||
CAGGGCTACGATGAAGGCTG TCCGAGG TAC AGCG TCGG AGCATCG GGA
CCGCG A
CGACATCTGGAGCCT TC ----- ----- AAGT - -- A

GAM339 ACAATTTTGGCCGGTTGTCT 311 ATAACAGCTA 1987 T CG CTG- ATA A
GGTTAATAAATTAACAATTG GCCAACATTG ACAAT TTGGC GTTGT GTTA AATT A
GTAATGATAACAGCTAGCCA T ||||| ||||| ||||| |||| ||||
ACATTGT TGTTA AACCG CGACA TAAT TTAA /
C AT ATAG GG- C

GAM340 CAGCCTCCCACTGTGGTGCC 312 TCGCCTGGAC 1988 C - G T G A - AA ACA G ---
- ATG
TGGCGGAGACCTGGCCAAGG CACAAGTTTG ACT GTGGT CC GGCG AG CCT GGCC GGT
GA AGCTGTG TGC C
TACAGAGAGCTGTGTGCATG ACCT ||| ||||| || |||| || ||| |||| ||| || ||||||| |||
CTGAGCAATACCACAGCTGT TGA CACCA GG CCGC TC GGG CCGG CCG TT
TCGACAC ACG /
TGCCGAGGCCTGGGCTCGCC T A - T - - T AG --- G CATA AGT
TGGACCACAAGTTTGACCTG

GAM341 TAAGGGTTGTTTTGTTGCTA 313 TGAAGCTAGA 1989 T TGTTGC AA A--
GTCCATT
GGTAAATAGATATTAGGCAG TACCTAAAGC TAAGGGT GTTT TAGGTA TAG TATTAGGCA
T

TCCATTTCTAAAATATGCCT TACC ||||||| |||| |||||| ||| |||||||||
GATGAAGCTAGATACCTAAA ATTCCCA CGAA ATCCAT ATC GTAGTCCGT C
GCTACCCTTA T ------ AG GAA ATAAAAT

GAM342 GGGATCTGGTCTGAGGGGGC 314 GGAAGTTGCT 1990 TC TC G C GGCA TG TA A - C ---- AT
GGACGGCACTGATATCAACG GGCTACAGCT TGG TGAG GGG GGAC C A TCA C GCTGTGGCC GC TCTC G
CTGTGGCCCGCTCTCATGAT GATG ||| |||| ||| |||| | | ||| | ||||||||| || ||||
GGGAAGTTGCTGGCTACAGC ATC ATTT TCC CTTG G T AGT G CGACATCGG CG AGGG /
TGATGACTTTGGCAAAGTTC C- T- G A AAAC GT TC A T T TTGA TA
ACCTGTTTATCTACTCCT

GAM343 ATGATAATCTACCTCACTTT 315 TTCCCTGTGG 1991 A TA CTTT - G A TTC G
CCCTGTGGCTATGTTCTGGG CTATGTTCTG ATGATA TC CCTCA CC CT TGGCT TG TGG T
TTTCCAATCAGGCCGAGTGG G |||||| || ||||| || || ||||| || |||
TTTGAGGACGATGTCAT TACTGT AG GGAGT GG GA GCCGG AC ACC T
- CA TT-- T - - TA- T

GAM344 GAAGGTGTCCACAGTGAGGC 316 GTCCCTGAGA 1992 TCCACAG GCA TG - G GG -- TC
GCAACTGGTGGAGTCTGGGG CTCTCATGTG GAAGGTG TGAGGC AC GTG GAGTCT GGGGA CCT GG A
GAGGCCTGGTCAAGCCTGGG AAGC ||||||| |||||| || ||| |||||| ||||| ||| ||
GGGTCCCTGAGACTCTCATG CTTCCAT GCTCCG TG TAC CTCAGA TCCCT GGG CC /
TGAAGCCTCGAAATTTACCT TTAAA-- AAG -- T G GG GT GA
TC

GAM345 GAGGGCCTCTTTCCCAGGCT 317 TCCCAGGCTC 1993 TT GC-- AT-- GCGC
CCTGTATGCCGAGCGCCCCA CTGTATGCCG GAGGGCCTC TCCCAG TCCTGT GCCGA C
AATTGGTCCCCATAGGACAG A ||||||||| |||||| |||||| |||||
ACTGGGACTGGGGTCCTC CTCCTGGGG AGGGTC AGGATA TGGTT C
TC AGAC CCCC AAAC

GAM346 AGTGGGACTGCTTCACAGAA 318 TGAAAGACAT 1994 A CT GAAGAAAA - CATAAA TGCCT T TA
GAAAAGCCTGGTTCATAAAA GGGTTGTGAT GTGGG CTG TCACA GCCTG GTT ACTTG GA GTTC G
CTTGTGCCTGATGTTCTAGC GGCC ||||| ||| ||||| ||||| ||| ||||| || ||||
AGAACCTTTATCAAGTGAAA CACCC GGT AGTGT TGGGT CAG TGAAC TT CAAG /
GACATGGGTTGTGATGGCCC - -- -------- A AAAG-- TAT-- C AC
ACT

GAM347 GCAATGATGATTATTACTTT 319 GATTATTACT 1995 TGA AT- TTT CT --- TT TAT

TGTACTCTGAAGATTATTTA TTTGTACTCT GCAA TGATT TAC TGTA CTG AAGATTA TA C
TATCAGGTTACTTAGTCTTT GAAG |||| ||||| ||| |||| ||| ||||||| ||
CCCGGGATACATCTGTGTTG CGTT ACTGA GTG ACAT GGC TTCTGAT AT A
AGTCACTTTGC TC- GTT TCT AG CCT TC TGG

GAM348 GAGAACTCCAAGTGTTGGCA 320 TCAAAGACAT 1996 A-- - A ------ AG--- A
GTCTCCTAAACATTGGGAGG TGGGCAGTAG GAG ACT CC AGTGTT GGC TCTCCTAA C
AATGAGCTTTCAAAGACATT ACTC ||| ||| || |||||| ||| ||||||||
GGGCAGTAGACTC CTC TGA GG TTACAG TCG GGAGGGTT /
AGA C G AAACTT AGTAA A

GAM349 GACTGCACATTCTAAGTTGA 321 GACTGCACAT 1997 G AAG GA GA GGGC T AT
CCTGATTGGGCTATTTGTGG TCTAAGTTGA GACT CACATTCT TT CCT TT TATTTG GGG A
GATATTTTCCCAAATAAGGA CCTG |||| |||||||| || ||| || |||||| |||
AGGGGAAGGGGGATGTGAGT TTGA GTGTAGGG AA GGA GA ATAAAC CCT T
T - GG- GG AG ---- - TT

GAM350 CCTTTTGTTTGCCAGGCACT 322 TAACGTGCCT 1998 TT C--- T TTA CATT TTTC
GTTTTAAGTGTTTTGCATTT TAGTGCAGAC CCT TGTTTGC AGGCAC GTT AGTGTTTTG
TATTC A
ATTCTTTCATTATGGATATT ACAG ||| ||||||| |||||| ||| ||||||||| |||||
AAGACATTATAACGTGCCTT GGA ACAGACG TCCGTG CAA TTACAGAAT ATAGG /
AGTGCAGACACAGG C- TGAT - TA- T--- TATT

GAM351 GACAACTTGTTGGGTACATA 323 TGATGGAGGA 1999 TT TATC CG TAATAT CTG
CCA TAT
TCAGTATACGACATTAATAT GATTGTATGT TG GGGTACA AGTATA ACAT ATCTCC TCC
ATTAGGT C
ATCTCCCTGTCCCCAATTAG TATA || ||||||| |||||| |||| |||||| ||| |||||||
GTTATCAGTCACTTGATGGA AC CTTATGT TTATAT TGTA TAGAGG AGG
TAGTTCA A
GGAGATTGTATGTTATATAT TT TTCA AT TGT--- --- --- CTG
TACTTTGTATTCTTCACAGT
GTC
GAM352 TGATAGTTATCCTTGTTAGC 324 TAGTTATCCT 2000 T A- - TAG--- T TGTAT AG
TTCGGTCTCTTCATGTATGC TGTTAGCTTC TGA AGTT TCC TTGT CTTCGGTC CTTCA
GCCAAA G
CAAAAGGATATTTGGCTTTT GGTC ||| |||| ||| |||| |||||||| ||||| ||||||
GGAGGATTGAGGAGAATCAC ACT TCAA AGG AACA GGAGTTAG GAGGT CGGTTT
A
AATGGAGGAACTTCA - GG T CTAAGA - TTT-- AT

GAM353 TGGAGAAGGGTACTCAAGGG 325 TGACAGAGAC 2001 - C- -- - - GA G G
AAAATGTGGATTGGTCAAGG ACAGTTTTGC TGGAGAAGG GTA TCA AGGG AAAA TGTG TT
GTCAAG A

AGCTTGACAGAGACACAGTT TCTG |||||||||| ||| ||| |||| |||| |||| || ||||||
TTGCTCTGGTGAATTACATC ATTTCTTCT CAT AGT TCTC TTTT ACAC AG CAGTTC /
TTCTTTA A TA GG G G AG A G

GAM354 TGTTTGGGATCTGGTCTGAG 326 GGAAGTTGCT 2002 TC T G C GGCA TG TA A - T C
---- AT
GGGGCGGACGGCACTGATAT GGCTTCAGCT TGG CTGAG GGG GGAC C A TCA C GCTG
GGCC GC TCTC G
CAACGCTGTGGCCCGCTCTC GATG ||| ||||| ||| |||| | | ||| | |||| |||| || ||||
ATGATGGGAAGTTGCTGGCT ATC GATTT TCC CTTG G T AGT G CGAC TCGG CG
AGGG /
TCAGCTGATGACTTTGGCAA -- - G A AAAC GT TC A T T T TTGA TA
AGTTCACCTGTTTAGCTACC
CCTGCTGTCAG
GAM355 CAAAACATATCGGATACTGC 327 ATACTGCAGT 2003 - CA---- AACTGTGT GG AC G
C-- C
AGTGGAAGAACTGTGTTTTG GGAAGAACTG TACTG GTGGAAG TTTGAAT ATG
TCCTCT ATA TTG T
AATGGATGACTCCTCTGATA TGTT ||||| ||||||| ||||||| ||| |||||| ||| |||
CTTGCTTTCAATCCTGTGAG ATGAT TACTTTC AAACTTA TAT AGGAGA TGT
AAC T
AGGAACTATAATTCAAACTT G TTTTAG -------- A- CA G CCT T
TCATGATTTTTAGTAGAAAG
AAATGTATG
GAM356 CAAAACATATCGGATACTGC 328 ATACTGCAGT 2004 - CA---- AACTGTGT GG AC G
C-- C
AGTGGAAGAACTGTGTTTTG GGAAGAACTG TACTG GTGGAAG TTTGAAT ATG
TCCTCT ATA TTG T
AATGGATGACTCCTCTGATA TGTT ||||| ||||||| ||||||| ||| |||||| ||| |||
CTTGCTTTCAATCCTGTGAG ATGAT TACTTTC AAACTTA TAT AGGAGA TGT
AAC T
AGGAACTATAATTCAAACTT G TTTTAG -------- A- CA G CCT T
TCATGATTTTTAGTAGAAAG
AAATGTATG
GAM357 CAGGAGTGGGACATAAAGCT 329 ATAAAGCTAT 2005 GA C A CTA CAAGA- CA CTT
ATGACAAGATAGATCAGGTC GACAAGATAG CAG GTGGGA AT AAG TGA TAGAT GGTC
G
CTTGCCTTGACTGAGTCTGA ATCA ||| |||||| || ||| ||| ||||| ||||
ATACATCACCTTCATTTCCA GTC CACCTT TA TTC ACT GTCTG TCAG C
CCTCTG TC - C C-- ACATAA AG TTC

GAM358 AGTTCAGGTACTCCATGTGA 330 AAGCTGCCAT 2006 CA- TG ATATGG -- AA CGTG C
A- C A
TATATGGTTCCACAATCCTC TGAAGATCTG TC TG AT TTC CAC TCCTCAG TTAA TG
AGC TTGTTG G
AGCGTGTTAACTGAAGCCTT GGGA || || || ||| ||| ||||||| |||| || ||| ||||||
GTTGAGTTTAACAAAGCTGC AG AC TG AAG GTG AGGGGTC AGTT AC TCG
AACAAT T

CATTGAAGATCTGGGGAAAG ACA GT ------ AA AA TAGA - CG A T
TGAAGAAGTTGCAACAGAGT
TTTGGGCT
GAM359 GCTGTGTTGCAGTGCATTGT 331 GTGCATTGTG 2007 GCA A G TG GGA TG GA CCT TG
GTTGCAGGATTGGGAAGGGC TTGCAGGATT GCTGTGTT GTGC TTGT T CA T G AGGGCA GTGC G
ACCTGTGCTGGTTGCACTTG GGGA ||||||||| |||| |||| | || | | |||||| ||||
CTTTGATTGAATGTGGAATG TGACGTAG CATG AGTA G GT A T TTTCGT CACG /
AAGTACGAAGATGCAGT AAG A A GT A-- GT AG T-- TT

GAM360 GTATCTGATGGGAATGGGCA 332 TTTTCACGGC 2008 CTGA A- - AA C AG TTAC
ATGAACATAGACTTACACAC CATAGCTTCC GTAT TGGGA TG GGC TGAA AT AC A
TGTACATTTTCACGGCCATA AATA |||| ||||| || ||| |||| || ||
GCTTCCAATAC CATA ACCTT AT CCG ACTT TA TG /
---- CG A GC T CA TCAC

GAM361 TACAGTTTGGATGGTGGCTC 333 CACCTGTAGA 2009 TTT- CTCATCACC AAC CT CC- TG T AA
ATCACCTGTAGAACCTGACT ACCTGACTTG TACAG GGATGGTGG TGTAG CTGA TGG G GC GG T
TGGCCGTGGCTGGAATCCAC GCCG ||||| ||||||||| ||||| |||| ||| | || ||
TCGTTGCCTTCCACTTCAGT GTGTC CCTACCACT ACATT GACT ACC C TG TC C
TACACCTCACTCACCATCCT CTCT CACTCC--- --- TC TTC GT C AC
CTCCTGTG

GAM362 CTGCCAAGAGTGAGCGGGTG 334 TCCCAGGAAC 2010 G GAACGA T CT----- -- - CCGCG CT C
AACGACTGTGGCTGACCGTA CCGTCTATTT CGGGT CTG GG GACCGTA ATC CTGGA CTG TAAG C
ATCCTGGACCGCGCTGCTTA TTGT ||||| ||| || ||||||| ||| ||||| ||| ||||
AGCCATCTTGGACAGACCTC GCCCA GAC CC TTGGTAT TGG GACCT GAC GTTC A
CAGTGGTTCTATGGTTTCCT T AG---- - TTTTCCT CT T CCA-- AG T
TTTCCCAGGAACCCGTCTAT
TTTTGTTGTG
GAM363 GCCTGATGTGACAAGCATGC 335 TGACAAGCAT 2011 TGAT ---- A T A
GGTGAGTGAACATTACTTCT GCGGTGAGTG GCC GTGACAA GC TGCGG GAGTGA C
TGCAAGTGACTTTGTCATGG A ||| ||||||| || ||||| ||||||
C CGG TACTGTT TG ACGTT TTCATT /
---- TCAG A C A

GAM364 GAGGATGAGGTCCTTGCTGA 336 GCTGAGCTGA 2012 - G - -- G C AA
GCTTCGCAAACGGCAGGCTG AGGCACTTAG GA GGAT AGGT CCTT GCT AGCTT GC A
AGCTGAAGGCACTTAGTCCA TCCA || |||| |||| |||| ||| ||||| ||
TC CT CCTG TTCA GGAA CGA TCGGA CG /

A A C GT G - GC

GAM365 GAAGGGTACTCAAGCGACCA 337 TGACAGAGAC 2013 - C- ---- CC GA GGC G
CTGTGGACTCGGCCAAGGAG ACAGTTTTGC GAAG GGTA TCA AGCGA ACTGTG CTC
CAAG A
CTTGACAGAGACACAGTTTT TCTG |||| |||| ||| ||||| |||||| ||| ||||
GCTCTGGTGACTTACCTCTT CTTC CCAT AGT TCGTT TGACAC GAG GTTC /
C T TC GGTC T- A- ACA G

GAM366 TGGAGAAGGGTACTCAAGGG 338 TGACAGAGAC 2014 - C- -- - GATAAG G
AAAATTGTGGATAAGGTCAA ACAGTTTTGC TGGAGAAGG GTA TCA AGGG AAAATTGTG
GTCAAG A
GGAGCTTGACAGAGACACAG TCTG ||||||||| ||| ||| |||| ||||||||| ||||||
TTTTGCTCTGGTGAATTACA ATTTCTTCT CAT AGT TCTC TTTTGACAC CAGTTC /
TCTTCTTTA A TA GG G AGAGA- G

GAM367 TACTCAAGGGAAAACTGTGG 339 TGACAGAGAC 2015 T AG G GA G G
ATTGGTCAAGGAGCTTGACA ACAGTTTTGC TAC CA G AAAACTGTG TT GTCAAG A
GAGACACAGTTTTGCTCTGG TCTG ||| || | ||||||||| || ||||||
TG GTG GT C TTTTGACAC AG CAGTTC /
- CT G AG A G

GAM368 TTAAATTTCTGTATCTGTCG 340 TAAGCTAGGG 2016 TT T TC G GATT--- G
CCCTGAGCTGATTTTGAAAG GTTAGTATAG TTAAAT CTGTA CTG GCCCT AGCT TT A
ATGGTATAAGCTAGGGGTTA TTGT |||||| ||||| ||| ||||| |||| ||
GTATAGTTGTTTAA AATTTG GATAT GAT TGGGG TCGA AG A
TT - -- A ATATGGT A

GAM369 ATACTTTACGTTCTTCTAAT 341 TGACTAAGTT 2017 AA CATTTTTCCATC CAC
CACTTT - A
TCTTGTCATTTTTCCATCCT CACAGGAAAA TTCT TTCTTGT CTTG TAAATG TTGCT
GATATTA T
TGCACTAAATGCACTTTTTG GGGA |||| ||||||| |||| |||||| ||||| |||||||
CTGATATTAATGTTAATGTC AGGG AAGGACA GAAT GTTTAC GACGG
CTGTAAT G
TGGCAGCTCCATTTGACTAA AA CTT--------- CA- CTC--- T T
GTTCACAGGAAAAGGGATGG
CGCTGACTGT
GAM370 CCAAGAGTGCAAATCAGTCC 342 CATTTCACTT 2018 -- G A C C- CAC GAGATA
TC
ATTTCACTTTCACTGTCTGA TCACTGTCTG CCAA GAGT CA AT AGT CATTTCACTTT TGTCT
GGGTC T
GATAGGGTCTCTAAGACCCA AGAT |||| |||| || || ||| |||||||||| ||||| |||||
GGATACAAGGGTGGAATGTA GGTT CTCA GT TA TCG GTAAGGTGGGA ATAGG
CCCAG /

GCTATATGGACTCGATTGG AG G A - AT AC- A----- AA

GAM371 CCCGTGTGTTTCAGCTCTTG 343 TCAGCTCTTG 2019 TG-- CTCTT TCTCTT A CCT --- AC
TTTCTCTTCCAATGCCCTTC TTTCTCTTCC CCCGTG TTTCAG GTT CCA TGC TCA GAGGA C
AGAGGAACCAATCCTTTCTT AATG |||||| |||||| ||| ||| ||| ||| |||||
GACAGCAATGGTGCATGACT GGGTAC AGAGTC CAG GGT ACG AGT TTCCT /
TATCCTGAGAAGATCATGGG TAGA CTATT TACGT- A AC- TCT AA

GAM372 ATGAGTATTGATCTGTCCCA 344 TATTGATCTG 2020 AT TCT GC C AGG G
GCCTGTGCATTGCTCCGAGG TCCCAGCCTG ATGAGT TGA GTCCCA CTGTGCATTG TCCG CA T
CAGTTCTGAGTGGATGATGT TGCA |||||| ||| |||||| |||||||||| |||| ||
ACAGATGGGATTCCTCAGCT TACTCG ACT TAGGGT GACATGTAGT AGGT GT T
CAT -- CCT A- - GA- C

GAM373 TCAAGGGAACACTTGTGGAC 345 TGACAGAGAC 2021 AG A C-- GA G G
TTGGTCAAGGAGCTTGACAG ACAGTTTTGC TCA GGA CA TTGTG CTT GTCAAG A
AGACACAGTTTTGCTCTGGT TCTG ||| ||| || ||||| ||| ||||||
GA AGT TCT GT GACAC GAG CAGTTC /
GG C TTT A- A G

GAM374 TACTCAAGGGAACACATGTG 346 TGACAGAGAC 2022 AG G C A GA G G
GATTCGGTCAAGGAGCTTGA ACAGTTTTGC TACTCA G AA AC TGTG TTC GTCAAG A
CAGAGACACAGTTTTGCTCT TCTG |||||| | || || |||| ||| ||||||
GGGTG GTGGGT C TT TG ACAC GAG CAGTTC /
CT G T - A- A G

GAM375 TGGAGAAGGGTACTCAAGGG 347 TGACAGAGAC 2023 - C- -- - GA G G
AAAATTGTGGATTGGTCAAG ACAGTTTTGC TGGAGAAGG GTA TCA AGGG AAAATTGTG TT GTCAA A
AGCTTGACAGAGACACAGTT TCTG ||||||||| ||| ||| |||| ||||||||| || |||||
TTGCTCTGGTGAATTACATC ATTTCTTCT CAT AGT TCTC TTTTGACAC AG CAGTT G
TTCTTTA A TA GG G AG A C

GAM376 AGCAGTGGGGAGAACAGCGT 348 TCCTCCAGTG 2024 C A GT TTTACC - CC -- G A CC T
CTTTTACCTGTCACCGAAGC GCGTTCTTTT AG AGTGGGGAGAAC GC CT TGT CA GAAGC CA GA GC CGTT G
CAGGAAGCCCCGTTTGTAAG TACT || |||||||||| || || ||| || ||||| || || || ||||
CGTGTGTTGTGGTGCTTTAT TC TCATTTTTCTTG CG GA ACA GT TTTCG GT TT TG GCGA T
TGTACATCCTCCAGTGGCGT - - GT CCTCCT T TA TG G G T- A

TCTTTTTACTCT

GAM377 ACTACCAGCCTCCCACTGTG 349 TCGCCTGGAC 2025 CC - G T G A - AA- CAGAGA - CA T
GTGCCTGGTGGAGACCTGGC CACAAGTTTG ACT GTGGT CC GGTG AG CCT GGC GGTA GCTGTG TG TGC G
AAGGTACAGAGAGCTGTGTG ACCT ||| ||||| || |||| || ||| ||| |||| |||||| || |||
CATGCTGAGCAACACCACAG TGA CACCA GG CCGC TC GGG CCG TCGT CGACAC AC ACG /
CCATTGCTGAGGCCTGGGCT TT A - T - - T GAG TAC--- C A- A
CGCCTGGACCACAAGTTTGA
CCTGATGT
GAM378 GTGGTTTAATCTGGAAGGAG 350 ACCCGTGTTC 2026 AG---- A A AGTCCAAA G TC TCCT TGC
CAGAAGCTGTGGAGTCCAAA CTATCCTTGT GA GAGC GA GCTGTGG GGACCC TGT CTA TGTTG C
GGACCCGTGTTCCTATCCTT TG || |||| || ||||||| |||||| ||| ||| |||||
GTTGTGCCACTTGACACGTT CT CTTG TT TGACACC CCTGGG ACA GAT ACAGT /
TAGCACAAGGGTCCCCACAG CTGCCA A G -------- A C- TTGC TCA
TGTTAGTTCACCGTCTCCAG
CAATCAC
GAM379 TATGAGGAGATTCAACACCA 351 AACACCACAG 2027 CA CAGCTGC - TAT - CTTC-- C ACA
CAGACAGCTGCAGGACTCGA ACAGCTGCAG ACACCACAGA AGGACTC GA CCA TGG TTTCC ATTC A
TATCCATGGCTTCTTTCCCA GACT |||||||||| ||||||| || ||| ||| ||||| ||||
TTCACAAAACGGGTAGGAAA TGTGGTGTCT TCTTGGG CT GGT ACT AAAGG TGGG /
CACATTTCACTGGCTTCAGG -- AAA---- A TC- C TTACAC A CAA
GTTCTAAATCTGTGGTGTTC
TCCTTATG
GAM380 TCAGCTGGGGTTTGAGGGTG 352 GGGAGGACCA 2028 TG TTT AAAT AA ACTTT AACT -- T CT
AAATTCAATGACTTTCGTGA GGGCATGTGC GGG GAGGGTG TC TG CGTG CCTTGG CTCCTA GTG C
ACTCCTTGGCTCCTATGTGC AGGG ||| ||||||| || || |||| |||||| |||||| |||
TCTTCACCTGGGAGGACCAG CCC CTTCCAC AG AC GTAC GGGACC GAGGGT CAC /
GGCATGTGCAGGGATGACCA GT T-- CAGT GG GT--- ---- AG C TT
CCTTCTCCCTGGGACCTGA

GAM381 CAGCCTCCCACTGTGGTGCC 353 TCGCCTGGAC 2029 CC - G T G A - AA CAGAGA - CA T
TGGTGGAGACCTGGCCAAGG CACAAGTTTG AC TGTGGT CC GGT GAG CCT GGCC GGTA GCTGTG TG TGC G
TACAGAGAGCTGTGTGCATG ACCT || |||||| || ||| ||| ||| |||| |||| |||||| || |||
CTGAGCAACACCACAGCCAT TG ACACCA GG CCG CTC GGG CCGG TCGT CGACAC AC ACG /
TGCTGAGGCCTGGGCTCGCC TT A - T - - T AG TAC--- C A- A

TGGACCACAAGTTTGACCTG

GAM382 GACCTGCTGCCTGACTACCT 354 TGCCTGACTA 2030 C T CT TA T - ------- - C AC-
T
GGCTGCCATAGATGAGGCCC CCTGGCTGCC TACC GG GCCA GA GAGGCCC TGGC AGC
CTTGCA GTG GC C
TGGCAGCCTTGCACGTGACG ATAG |||| || |||| || ||||||| |||| ||| |||||| ||| ||
CTCCAGTTCCCACTGCAAGA GTGG CC TGGT CT CTTCGGG ACCG TTG GAACGT
CAC TG C
GTTCATCCTGGCCATGGGCT - T -- C- T T GTCCTAC A - CCT A
TCTTCCTGGTCCTGGTGATG
GAGCAGATC
GAM383 TCATATATGATAGATGTGGC 355 TCCCATATGT 2031 -- AGAT CG G CATCTT-
CCTTT
CGTCTTGTATATCATCTTGG AGAAGAAGCC TCATATA TGAT GTGGC TCTT TATAT
GGTTAG T
TTAGCCTTTTTCCTTCCTAA ATTA ||||||| |||| ||||| |||| ||||| ||||||
CTTTCCCATATGTAGAAGAA AGTGTAT GTTA TACCG AGAA ATGTA TCAATC T
GCCATTACGATTGCTTATGT TC GCAT A- G TACCCTT CTTCC
GA

GAM384 CCTCAGCACCATGTGACAAT 356 TCAGCACCAT 2032 - C T AT AT AAGA
CATGCCGAAGACTTTGTGGT GTGACAATCA CCT CAGCAC ATG GACA C GCCG C
GGGGCTGTCCTGTGTGTTGT TGCC ||| |||||| ||| |||| | ||||
AGG GGA GTTGTG TGT CTGT G TGGT /
T - C CG GG GTTT

GAM385 CCAGTCCCAGAGGTGTATGT 357 AGAGGTGTAT 2033 GT - AGA ATG GT T
TGCCACAGTGTTTGAAAACT GTTGCCACAG CCA C CC GGTGT TTGCCACA GTT G
ATGTGGCAGATATCGAGGTG TGTT ||| | || ||||| |||||||| |||
GATGG GGT G GG CTATA GACGGTGT CAA A
AG T AG- --- AT A

GAM386 GCTTTTGCTCCAGATGGTTC 358 CCAGTGCCTT 2034 TT TCC T ATACTTT T - AA TC
ACA
ATACTTTGCTTGGTCACAAG CAGAACTTTC GCT TGC AGA GGTTC GCT GG TCAC
GGACA GC G
GACATCGCACAGTAAAGCTT TCTT ||| ||| ||| ||||| ||| || |||| ||||| ||
GTTCCGTGGTCCCAGTGCCT CGG ACG TCT TCAAG TGA CC GGTG CTTGT CG T
TCAGAACTTTCTCTTGCATG T- TTC T ACTTCCG C T C- T- AAA
GC

GAM387 GTCACCTCAATGGGACTGCT 359 TGAAAGACAT 2035 A A CT AGAAAAGC G - ATAAA
TGCCT T TA
TCACAGAAGAAAAGCCTGGT GAGTTTGTGA TGGG CTG TCACAGA CT GT TC ACTTG
GA GTTC G
TCATAAAACTTGTGCCTGAT TGGC |||| ||| ||||||| || || || ||||| || ||||
GTTCTAGCAGAACCTTTATC ACCC GGT AGTGTTT GA TA AG TGAAC TT CAAG
/

AAGTGAAAGACATGAGTTTG A - -- -------- G C AAAG- TAT-- C AC
TGATGGCCCAACTATGTGAC

GAM388 TCTGATTTTATTACAGGTCT 360 TATTACAGGT 2036 T-- - TC- CA- TA CA
GTTCATTTTATGGCATTCTC CTGTTCATTT TCTGA TTTAT TACAGG TGTT TTT TGG T
AAGGAAGAAAACATGTCCTG TATG ||||| ||||| |||||| |||| ||| |||
TAGGTAAATATTTAGA AGATT AAATG ATGTCC ACAA AAG ACT /
TAT G TGT AAG GA CT

GAM389 CTACTGGAAAGAAGGCTTTA 361 ACCATGTAAG 2037 - AA- --- - AGA CAGG
TGGAGATCCCAGGAACCAAG CCTGAATTTG CTAC TGG AGA AGGCTT TATGG TCC A
GACCATGTAAGCCTGAATTT TGCC |||| ||| ||| |||||| ||||| |||
GTGCCATGTGG GGTG ACC TTT TCCGAA GTACC AGG A
T GTG AAG T --- AACC

GAM390 GCTTGAACCTGGGAGGTAGA 362 GAGGTAGAGG 2038 GA-- AGGTA GT G A - A
GGTTGCAGTGAGTCAAGATT TTGCAGTGAG GCTT ACCTGGG GAG TGCA TG GT CA G
GTACCAGTGCACTCCAGCCC TCA |||| ||||||| ||| |||| || || ||
AGGTAACAGAGC CGAG TGGACCC CTC ACGT AC CA GT A
ACAA GAC-- -- G - T T

GAM391 ACAGTGAAAGTGATGAATGG 363 CTCAATGCCA 2039 AAA AA A GAA TTG
ACAGAAGGTTTGCCAATGCT GGTATTACCA ACAGTG GTGATG TGG CA GGT C
CAATGCCAGGTATTACCACT CTGT |||||| |||||| ||| || |||
GT TGTCAC CATTAT ACC GT TCG C
--- GG - AAC TAA

GAM392 AAGTGAAAGACATGAGTTGT 364 TGAAAGACAT 2040 AG ATG ATGTGA AA- C TGA
T CC
GATGGCACATATGTGACTGA GAGTTGTGAT ATG TTGTG GCACAT CTG TTCAGG TAA
TTGCACTGT GA A
ATTCAGGCTAATGATTGCAC GGCA ||| ||||| |||||| ||| |||||| ||| |||||||| ||
TGTTGACCAGAATCACAGTG TAC AACAT CGTGTG GAC AAGTTC ATT
AGCGTGACA CT G
CGAACTTACTTGAAGTGCAG A- A-- AGATGA GTG - CA- - AA
AGTAGAGTGTGCATACAAAC
ATGTCAGAATT
GAM393 GGAAGTTGCTCTGGGTGAGG 365 TGAGGCAGTG 2041 C-- G A GATTGTT---- AA TG ---
C --- T
CAGTGATTGTTTAGTGAATG ATTGTTTAGT TG GTG GGCAGT TAGTG TG AGG GC
GAGGA CA T
TGAGGGCCGAGGACATTATT GAAT || ||| |||||| ||||| || ||| || ||||| ||
GCACTCTTCTGTAAACTTTG AT TAC CCGTCG GTCAC AT TTC TG CTTCT GT
A
TAAACACTGTGGTACCTTAA TTT G - AATTCCATGGT AA GT AAA T CAC T
GCTGCCCATGTATTTTAAAA

TTTCC
GAM394 TGGATGTTGGCCTAGTTCTG 366 TGGAAGACTA 2042 T - A T A A T -- TG
TGTGGAAGACTAGTGATTTT GTGATTTTGT TGGA GT TGGCCT GT CTGTGTGG AGACT
GTGATTT GTTGTT TTTA A
GTTGTTTTTATGATACTAAA TGTT |||| || |||||| || |||||||| ||||| ||||||| |||||| ||||
TCGACAACAAATCACAGTCT ATCT CG ACCGGA CA GGTATACC TCTGA CACTAAA
CAACAG AAAT T
GCCATATGGCACAGGCCATG C T - C G - - CT CA
CCTCTA

GAM395 AGACTTGAACAAGATAAATC 367 ATGGCTGCTC 2043 AACA T-- C A AA GAG T -- T AT-
--- AAAC
CCAGACCAAAGAGAGTCTAC AGTTGAAGAT G AGA AAAT CCAG CC AGA TC AC AGTA GC
TAG C
AGTATGCATTAGAAACCTTG CTAG | ||| |||| |||| || ||| || || |||| || |||
ACTATGAATGGCTGCTCAGT C TCT TTTA GGTC GG TCT AG TG TCGT CG ATC
/
TGAAGATCTAGGACTGGATT CG-- CAC - A A- AGA T AC - GTAAGT AGTT
TCACTCTGCCAGGTTT

GAM396 TTCTCGTGGGCGGCAGTTGC 368 AGCAATTGAT 2044 - A GCT TCC - TG TGTTGT A
CAT TGA
TTTTGTTGTTCCCCAGCAAT GTTGTCATAG CG GC GTT TTTGTTGT CCA GCAAT A CAT
GCAGC AG G
TGATGTTGTCATAGCAGCCA CAGC || || ||| |||||||| ||| ||||| | ||| ||||| ||
TAGTGAGTATCTTGTTGCGG GC CG TAA AAGCAGCA GGT TGTTA T GTG CGTTG
TC /
TGTCTTGATTGTGTGGTGTA T A AT- TGT G GT CT---- G T-- TAT
CGACGAATAAATAGCTCGCT
TTTTTGAGAA
GAM397 GCCTGACAGTGTAGCTGCAA 369 AAGGAGCTCT 2045 - TG T-- AG - CT-- G-- C
ACTCTGCTCCTGATCCATGG CAGCTTTGCA GC C ACAG GT CTGCAAA CT GCTCCT ATC
A
GTAAAAGGAGCTCTCAGCTT GAAG || | |||| || ||||||| || |||||| |||
TGCAGAAGCCTTCTGTTGGT CG G TGTC CG GACGTTT GA CGAGGA TGG T
GC T GT TTC AA C CTCT AAA G

GAM398 GACCTGCTGCCTGACTACCT 370 TGCCTGACTA 2046 C T CT TA T - ------ - C AC-
T
GGCTGCCATAGATGAGGCCC CCTGGCTGCC TACC GG GCCA GA GAGGCCC TGGTCAG C
CTTGCA GTG GC C
TGGTCAGCCTTGCACGTGAC ATAG |||| || |||| || ||||||| ||||||| | |||||| ||| ||
GCTCCAGTTCCCACTGCAAG GTGG CC TGGT CT CTTCGGG ACCGGTC G GAACGT
CAC TG C
AGTTCATCCTGGCCATGGGC - T -- C- T T CTACTT A - CCT A
TTCTTCCTGGTCCTGGTGAT
GGAGCAGATC
GAM399 ATTGACGCACAGCAGTGGGG 371 TCCTCCAGTG 2047 C A GT TTTACC - CC -- G
A CC T

AGAACAGCGTCTTTTACCTG GCGTTCTTTT AG AGTGGGGAGAAC GC CT TGT CA GAAGC CA GA GC CGTT G
TCACCGAAGCCAGGAAGCCC TACT || |||||||||||| || || ||| || ||||| || || || ||||
CGTTTGTAAGCGTGTGTTGT TC TCATTTTTCTTG CG GA ACA GT TTTCG GT TT TG GCGA T
GGTGCTTTATTGTACATCCT - - GT CCTCCT T TA TG G G T- A
CCAGTGGCGTTCTTTTTACT
CTAATGTTCTT
GAM400 CAGCCTCCCACTGTGGTGCC 372 TCGCCTGGAC 2048 C - G T G A - AA ACA G --- - ATG
TGGCGGAGACCTGGCCAAGG CACAAGTTTG ACT GTGGT CC GGCG AG CCT GGCC GGT GA AGCTGTG TGC C
TACAGAGAGCTGTGTGCATG ACCT ||| ||||| || |||| || ||| |||| ||| || ||||||| |||
CTGAGCAATACCACAGCTGT TGA CACCA GG CCGC TC GGG CCGG CCG TT TCGACAC ACG /
TGCCGAGGCCTGGGCTCGCC T A - T - - T AG --- G CATA AGT
TGGACCACAAGTTTGACCTG

GAM401 GCTCCAAAGAACCAAGAGTG 373 CATTTCACTT 2049 T - ---------- CAC GAGATA TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM402 GCAGCAGAGAGGCCCCTTTC 374 ACTCAGTGAA 2050 A GC CT AGGT GGG
AAGGTGTTCGGGTAAAGAAC GGAACTCCTG GCAGCAG GAG CC TTCA GTTC T
TCAGTGAAGGAACTCCTGTT TTGC ||||||| ||| || |||| ||||
GC CGTTGTC CTC GG AAGT CAAG /
- AA -- GACT AAA

GAM403 TGGAGAAGGGTACTCAAGGG 375 TGACAGAGAC 2051 - C- -- - C GA G G
AAAATCGTGGATTTGGTCAA ACAGTTTTGC TGGAGAAGG GTA TCA AGGG AAAAT GTG TTTG TCAAG A
GGAGCTTGACAGAGACACAG TCTG ||||||||| ||| ||| |||| ||||| ||| |||| |||||
TTTTGCTCTGGTGAATTACA ATTTCTTCT CAT AGT TCTC TTTTG CAC AGAC AGTTC /
TCTTCTTTA A TA GG G A AG - G

GAM404 CAACTTTTTCCCTGGGCAAA 376 TCCCTGGGCA 2052 TTTT TG G AA A AAA AA--- C A G G T
GTATTCCCAAATTTAACAGC AAGTATTCCC C TCCC G CA GT TTCCC TTT CAG GTGT GTTT TT GCTT C
GTGTAGTTTGTTGGCTTTCA AAAT | |||| | || || ||||| ||| ||| |||| |||| || ||||
CAAGTGGGGAAGCGATACAC G AGGG C GT CA AGGGG AAG GTC CATA CGAA GG TGAA A

TGGCAACGAAGACGGGGAAC C--- GT - CC - CAG CAACG A G G G C
CCTGCTGGGGACGTTG

GAM405 TCTCCACCGCAGTTGGACTG 377 ATCAAAGACA 2053 AC C GAC- CA GCA
ACAGGCAGCAAGTGGTGCTC GCTCTGAGGA TCTCC CG AGTTG TGA GGCA A
ATCAAAGACAGCTCTGAGGA GG ||||| || ||||| ||| ||||
GG GGAGG GT TCGAC ACT TCGT G
A- C AGAA AC GGT

GAM406 TGTTTGGGATCTGGTCTGAG 378 GGAAGTTGCT 2054 TC T G C GGCA TG TA A - T C
---- AT
GGGGCGGACGGCACTGATAT GGCTTCAGCT TGG CTGAG GGG GGAC C A TCA C GCTG
GGCC GC TCTC G
CAACGCTGTGGCCCGCTCTC GATG ||| ||||| ||| |||| | | ||| | |||| |||| || ||||
ATGATGGGAAGTTGCTGGCT ATC GATTT TCC CTTG G T AGT G CGAC TCGG CG
AGGG /
TCAGCTGATGACTTTGGCAA -- - G A AAAC GT TC A T T T TTGA TA
AGTTCACCTGTTTAGCTACC
CCTGCTGTCAG
GAM407 GTAGCGTCCAAGATTTACCA 379 TACCACCACA 2055 A AAG TT ACCA TTA TG
ACC- T
CCACATCATGATTACAGATG TCATGATTAC GT GCGTCC AT ACC CATCATGA CAGA GTC
AAC T
GTCACCAACTTATGTTTTAG AGAT || |||||| || ||| |||||||| |||| ||| |||
GATTTTTTGACTTTATGATG CG CGTAGG TA TGG GTAGTATT GTTT TAG TTG A
GGTTTATAGGGATGCAGC A GA- TT ---- TCA TT GATT T

GAM408 TCGAGATACAGCTGCATGGA 380 TTGGTCCCCT 2056 G AGCT- T- --- GA T A T C
CTGTAGGCAGAATTGTGAGC GCTACAAGTG TC AGATAC GCA GGACT GTAGGCA AT GTG
GC GCTT C
TGCTTCCTGAAGCTGCCATC TCTG || |||||| ||| ||||| ||||||| || ||| || ||||
ATGATGTCTACTTTGGTCCC AG TCTGTG CGT CCTGG CATCTGT TA TAC CG CGAA
T
CTGCTACAAGTGTCTGA - AACAT CC TTT AG C - T G

GAM409 GCTTTTGCTCCAGATGGTTC 381 CCAGTGCCTT 2057 TT TCC T ATACTTT T - AA TC
ACA
ATACTTTGCTTGGTCACAAG CAGAACTTTC GCT TGC AGA GGTTC GCT GG TCAC
GGACA GC G
GACATCGCACAGTAAAGCTT TCTT ||| ||| ||| ||||| ||| || |||| ||||| ||
GTTCCGTGGTCCCAGTGCCT CGG ACG TCT TCAAG TGA CC GGTG CTTGT CG T
TCAGAACTTTCTCTTGCATG T- TTC T ACTTCCG C T C- T- AAA
GC

GAM410 CCAAGAGTGCAAATCAGTCC 382 CATTTCACTT 2058 T - ---------- CAC GAGATA
TC
ATTTCACTTTCACTGTCTGA TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T

GATAGGGTCTCTAAGACCCA AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
GGATACAAGGGTGGAATGTA CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GCTATATGGACTCGATTTGC - C TATCGATGTA AC- A----- AA
TTCCGG

GAM411 GACCCCCTACTTTGATGCTG 383 GAGCTGCCAC 2059 CCCTA GATGC C CAC- - GG
GCGCCTCATGCACTGAGCAG CTTGGAAGAA GACC CTTT TGGCG CTCATG TGAG CA A
GAAATGCCTCGATACCATGA CGGT |||| |||| ||||| |||||| |||| ||
GCTGCCACCTTGGAAGAACG CTGG GAAG ACCGT GAGTAC GCTC GT /
GTC CAA-- GTTCC C CATA C AA

GAM412 TTACCCTAAGGAATGCTTTG 384 TAAGGAATGC 2060 - AAG A TT ATAA-- A T
CCATAACCACATTTAATGGG TTTGCCATAA TTAC CCT GA TGCT GCC CC CAT T
GAAAACGGCAGTATCACAGG CCAC |||| ||| || |||| ||| || |||
TGTAA AATG GGA CT ATGA CGG GG GTA /
T CA- - -- CAAAAG - A

GAM413 ATCTGCACTTGTCCTCATGA 385 TCATGAGCCG 2061 ---- --- CCA- CAG--- A CC--
TG- A
GCCGCGTCCAATGTCCAGCC CGTCCAATGT TCA TGA GCCGCGT ATGTC CCCAC
GCTG CC GCC G
CACAGCTGCCCCTGGCCAGA CCAG ||| ||| ||||||| ||||| ||||| |||| || |||
AGGTGATGGAGAATAGCAGT AGT ACT CGGCGCA TACAG GGGTG CGAT GG
TGG A
GGGACACCCGACATCTTAAC TAAC TCA ATTC CCCACA A AAGA TAG A
GCGGCACTTCACAATTGATG
ACTTTGAGAT
GAM414 GCACCAACAGAAGGTTTCTG 386 GGAGCAAAGT 2062 CA AAGGTT G GAGA TTTA
C
CAAGGCTGAGAGCTCCTTTT TTGCAGGCTG GCAC ACAG TCTGCAAG CT GCTCCT CC A
ACCCATGGGACCAGGAGCAA TGTG |||| |||| |||||||| || |||||| ||
AGTTTGCAGGCTGTGTGC CGTG TGTC GGACGTTT GA CGAGGA GG T
-- ------ - AA-- CCA- G

GAM415 TTCTCCATGATGACAAGGAA 387 TGCTGGGCTC 2063 --- AGTC- CCATCC CACAG
CTCCCT GA- G A
GTCTCTGCCATCCTGGCCAC CCTGCATGAC AAGGA TCTG TGGC TGCTGGG
GCAT CA TG A
AGTGCTGGGCTCCCTGCATG AGTG ||||| |||| |||| ||||||| |||| || ||
ACAGTGAAAACAGTGACAAT TTCTT AGAC ACCG ACGACCT TGTA GT AC A
GTTCCAGCAAAGCCACCAGA GAA GAAAC C----- AA--- ------ ACA G A
CAAAGTTCTTAAGGTCACAG
GAGAG
GAM416 TATTATGGTAAATGCTCTAA 388 TAAATGCTCT 2064 A AAAT AGA CC- --- TT
GACTCCTGAGCCAACTTTTA AAGACTCCTG TATT TGGT GCTCTA CT TGAGCCA AC T
TGTAACTGGCTTACCTAGGC AGCC |||| |||| |||||| || ||||||| ||

TGGGGCTTGAACTAAGTA ATGA ATCA CGGGGT GA ATTCGGT TG T
- AGTT CG- TCC CAA TA

GAM417 TGAAGACTTCCTAAATTTGC 389 TTTGCACATT 2065 AC A TTGCA TTGCC
ACCAT
ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM418 GTGGCAACGTTTTAAACTGG 390 CAGTGCTATG 2066 TG GT - TAACA- TAAAATAT
CTAACAGACCTTAAAATATC TTTAAAGTTG G GCAAC TTTAAAC TGGC GACCT C
CCCCTACCTGGGTCCTCAGT CTGC | ||||| ||||||| |||| |||||
GCTATGTTTAAAGTTGCTGC C CGTTG AAATTTG ATCG CTGGG C
GT -- T TGACTC TCCATCCC

GAM419 GGTGGTATCACCATTTGATA 391 TATCACCATT 2067 T C- - G C- A AAAT
TCTACTTGATGGAAATTTGA TGATATCTAC GG GGTATCA CAT TT ATAT TACTTG TGG T
GACCAGTAAGTACTATGTGA TTGA || ||||||| ||| || |||| |||||| |||
ATATGATTGATGCCCC CC CCGTAGT GTA AA TGTA ATGAAT ACC T
- TA T G TC G AGAG

GAM420 ATCTACCTCACTTTCCCTGT 392 TTCCCTGTGG 2068 TA CTTT - G A TTC G
GGCTATGTTCTGGGTTTCCA CTATGTTCTG ATC CCTCA CC CT TGGCT TG TGG T
ATCAGGCCGAGTGGTTTGAG G ||| ||||| || || ||||| || |||
GACGAT TAG GGAGT GG GA GCCGG AC ACC T
CA TT-- T - - TA- T

GAM421 CCTGTTCCTCTCACGCCCTC 393 AAGCTGCCAG 2069 TCAC CTCACCT T CC - A
T CCTG
ACCTGGCTGAGCCGCAGTAG TTGAAGAACT GCC GGC GAG GCAGTAGTTCTTCAG
TGGCA GCTTTA GT A
TTCTTCAGTGGCAAGCTTTA GTTG ||| ||| ||| |||||||||||||| ||||| |||||| ||
TGTCCTGACCCAGCTAAAGC CGG CCG CTC CGTTGTCAAGAAGTT ACCGT
CGAAAT CG /
TGCCAGTTGAAGAACTGTTG CTT- TCC---- T C- G - - ACCC
CCCTCTGCCCCTGGCTTCGA
GGAGGAGG
GAM422 AAGGGTTGTTTTGTTGTTAG 394 TGAAGCTAGA 2070 T TGTTGT AA A-- GTCCATT
GTAAATAGATATTAGGCAGT TACCTAAAGC AAGGGT GTTT TAGGTA TAG TATTAGGCA
T
CCATTTCTAAAATATGCCTG TACC |||||| |||| |||||| ||| |||||||||
ATGAAGCTAGATACCTAAAG TTCCCA CGAA ATCCAT ATC GTAGTCCGT C
CTACCCTT T ------ AG GAA ATAAAAT

GAM423 AGTTCCTCAGCCCATGTTTT 395 TGGAGAAGCA 2071 CTCAG TC TCCT C TT- ATA-
-- AG
CCCTCCTTCCTTCAGTTTGA TGGGACCTGA AGTTC CCCATGTTT CC TCCTT AGT GACA
GGGGTGG C
CAATAGGGGTGGAGCAACCA ACT ||||| ||||||||| || ||||| ||| |||| |||||||
CTTTGCAGGATGTCTCTGCT TCAAG GGGTACGAA GG GGGGA TCG CTGT
TTTCACC /
TAGGGGCTATGGAGAAGCAT TCCA- GA TATC T TCT AGGACG AA
GGGACCTGAACT

GAM424 AGAATGGGGAAGAATACTGA 396 TTGGAGCAGG 2072 - - TA AA T CA TCT AC-
CT
ATTAGCTGAGCACATTCTGG TTTCATTCTC AGAAT GGGGAA GAA CTG TTAGC GAG CAT
GGAC AATT G
ACACAATTCTGACCAATTTC CAAT ||||| |||||| ||| ||| ||||| ||| ||| |||| ||||
AGTCTCATGATCTCTGTTGG TCTTA CCTCTT CTT GAC GGTTG CTC GTA TCTG
TTAA A
AGCAGGTTTCATTCTCCAAT A A TG GA T TA C-- ACT CC
TCT

GAM425 GCTCCAAAGAACCAAGAGTG 397 CATTTCACTT 2073 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM426 CACAAATCCAGCACTTCCTC 398 AGCAACACAT 2074 T GCACTTC-- T T- G
TCCATTTACTCTGTCAGGCT ATGGCTTTGT CACAAA CCA CTCTCCAT TAC CT T
GTATATGGGGAGCAACACAT G |||||| ||| |||||||| ||| ||
ATGGCTTTGTG GTGTTT GGT GAGGGGTA ATG GG C
C ATACACAAC T TC A

GAM427 TGGCGGATTAGAAACCCGTA 399 AACCCGTAGA 2075 GGA - G AT C-- TT
GATCAGTTCTAGGTTAGCCC TCAGTTCTAG TGGC TTAGAAAC CC TAG CAGTT TAGG A
TGATTAACTGCCCTGGGTGT G |||| |||||||| || ||| ||||| ||||
TTCTGGGCCA ACCG GGTCTTTG GG GTC GTCAA GTCC /
--- T - CC TTA CG

GAM428 GACTTAGGGTTGTAGATCTC 400 AGGCTCCACG 2076 AGG ATCTCT C T - GGT TG
G C
TCTCTTCTTGGGCCGGTTTG AGCAGCTGCA GACTT GTTGTAG CT TTC TGG GCC T
GAGT AA A

GAGTGAACAGTTGACTTTGG ACAG ||||| ||||||| || ||| ||| ||| | |||| ||
CAAGGCTCCACGAGCAGCTG CTGGA CAACGTC GA GAG ACC CGG G TTCA TT /
CAACAGGTC --- ------ C C T AAC GT G G

GAM429 CCCCAGAATCTAGCCATGCA 401 AATCACTGGC 2077 AGAA- T------ TC GAAT
GTCCTCTGAATTCATTAAGA TGGGAAAGAG CCCC TCTAGCCA GCAG CTCT T
GCTGTTAATCACTGGCTGGG GGG |||| |||||||| |||| ||||
AAAGAGGGG GGGG GGGTCGGT TGTC GAGA C
AGAAA CACTAAT -- ATTA

GAM430 GAGATATGAAGTACTCAAGT 402 CAACGGCTTG 2078 - A TAC AC - ACCACG
CACTTGTGGGTACCACGCCC ACATCTACAT GAGA TATG AG TCAAGTC TTGTG GGT C
ATCCAACCGCGCAACGGCTT GTTC |||| |||| || ||||||| ||||| |||
GACATCTACATGTTCTC CTCT GTAC TC AGTTCGG AACGC CCA C
T A TAC C- G ACCTAC

GAM431 ACTACCAGGGTGAAACTAGC 403 TACCAGGGTG 2079 ACC- T - AGCA - CT--------- C
A
ATTGGGCCATACTCTACTCG AAACTAGCAT ACT AGGG GAA ACT TTGGGC CATA
CTACT GC C
CACAGCTAGTAGTCTTTGTC TGGG ||| |||| ||| ||| |||||| |||| ||||| ||
ATCTATGCGCCTAGATTGGG TGA TCCC CTT TGG GATCCG GTAT GATGA CG /
TATTCCCCCTCTCAAGT ACTC C A GTTA C CTACTGTTTCT T A

GAM432 ATCCCAAGTGTTGACACAGC 404 TCCCAAGTGT 2080 AAGT GA CA - CCCA CT A
CATCTTGTCCCATCCCTGGA TGACACAGCC ATCCC GTT CACAGC TCT TGT TCC GGA G
AGCCTCTTTGGAAACCACAT ATCT ||||| ||| |||||| ||| ||| ||| |||
AGAGCTGTGCTGGCTCACGG TAGGG CGG GTGTCG AGA ACA AGG TCT C
GAT CACT TC -- T CCAA TT C

GAM433 GCAGGAGATGCAAGTTTCAG 405 GAGATGCAAG 2081 G T ------- - CT
GATGTTCCCCACTGAGCTGG TTTCAGGATG GCAGGAGAT CAAGT TCA GGATGTTCC CCA
G
AGGAATATCTACAGCAGTGA TTCC ||||||||| ||||| ||| ||||||||| |||
TGCTTGAATTTTTTGT TGTTTTTTA GTTCG AGT TCTATAAGG GGT A
A T GACGACA A CG

GAM434 TAGTATGTGTTTCTTAAACA 406 GTGAGCTAGG 2082 - TAAA AGCGTAT T TATAG--
AGGG A AG
TCATTTAGCGTATCCTATCT TTTCAAGTGA CT CATCATTT CCTA CTTAC TTTTGCT
AA GTT A
TACTATAGTTTTGCTAGGGA TGAG || ||||||| |||| ||||| ||||||| || |||
AAGTTAGAGAAGGCATTAAA GA GTAGTGAA GGAT GAGTG GAAACGA TT
CGG G

GCAAAGATGACATGTGAGCT T ---- CTTT--- C TACAGTA AA-- A AA
AGGTTTCAAGTGATGAGTTG
GCATTTACTA
GAM435 GCTCCAAAGAACCAAGAGTG 407 CATTTCACTT 2083 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM436 TTCCGGTGATTGTGGAAAAG 408 ATCACTGTGG 2084 - --- AAA T GCTC- TGTT C
TG CAA G
GTCTCAGGCTCTCAGATTGT CTCAGTTCAT CC GGTGATT GTGGA GGTC CAG TCAGAT
GA AT A AC G
TGACATTGACAAACGGAAGT GTGG || ||||||| ||||| |||| ||| |||||| || || | ||
ACTTGGTTCCATCTGATATC GG CTACTAG TACTT TCGG GTC AGTCTA CT TG T
TG A
ACTGTGGCTCAGTTCATGTG A GTG GAC T ACTAT C--- - GT CA- A
GATCATCAGGAA

GAM437 GGGATGGTGGCTCATCACCT 409 CACCTGTAGA 2085 CATCACC AAC CT CC- TG T
AA
GTAGAACCTGACTTGGCCGT ACCTGACTTG GGGATGGTGGCT TGTAG CTGA TGG G
GC GG T
GGCTGGAATCCACTCGTTGC GCCG |||||||||||| ||||| |||| ||| | || ||
CTTCCACTTCAGTTACACCT TCCTACCACTGA ACATT GACT ACC C TG TC C
CAGTCACCATCCT CTCC--- --- TC TTC GT C AC

GAM438 ATGGTCCAACTTTGTGGAAT 410 GTAAGGATTT 2086 -- T-- GAATG- AGG AGGG
GG
GGTAAGGATTTTTAGGGTTG TTAGGGTTGT ATGG TCCAACT TGTG GTA ATTTTT
TTGTTT C
TTTGGCCAGAACAAGAGAAA TT |||| ||||||| |||| ||| |||||| ||||||
TAACTGCAGAAAACACATAT TACC AGGTTGG ACAC CGT TAAAGA AACAAG /
GGTTGGAAACCAT AA TAT AAAAGA CAA G--- AC

GAM439 GGGCTCCTCATGACACCTTG 411 TACACAGCCA 2087 TC ACACC TACAC AACT G
GA T
CTACACAGCCAACTTTGTGG ACTTTGTGGC GGGCTCC ATG TTGC AGCC TTGTGGC
CCT GGTGC G
CGCCTGAGGTGCTGAAGCGC GCCT ||||||| ||| |||| |||| ||||||| ||| |||||
CAGGGCTACGATGAAGGCTG TCCGAGG TAC AGCG TCGG AGCATCG GGA
CCGCG A
CGACATCTGGAGCCT TC ----- ----- AAGT - -- A

GAM440 GTGAGATCAAACTGAAGTCC 412 CCAATTAACC 2088 - A ACT A CCAATTAA GA AG CA

AATTAACCTCTGGATCCAGC TCTGGATCCA GTG AG TCAA GA GT CCTCTG TCC CTGC A

TGCCAATTTGCAGGGAATAG GCTG ||| || |||| || || |||||| ||| ||||

AGGAGAGAAGCATCTGTTGA CAC TC AGTT CT CG GGAGAT AGG GACG T

ACTGCAC G A GT- A AAGAGA-- A- -- TT

GAM441 ACCGGTTATGGTGCTGCTGT 413 TGGAGCCTGG 2089 GG T - AC GTTGGAGC G TT T T

GAACACTGCCAAGTTGGAGC CTCTGTTTGT CGGTTAT TGC GCT GTGA ACTGCCAA CTGGCTCT T G GCCG C

CTGGCTCTGTTTGTGCCGTC GCCG ||||||| ||| ||| |||| |||||||| |||||||| | | ||||

TTTGGTCTGGGAGGAGTCGG GTCGGTG ATG CGG TACT TGACGGTT GGCTGAGG G T TGGT T

ATTGGCAGTTATCATGGGCT AA T G AT A------- A GG C T

GTAAAGTGGCTGGT

GAM442 ATGTATGTTGACAGTCGCTA 414 TTGACAGTCG 2090 ATG- A C AAGTT ---- - AGC

AGTTTCCACATGCACAAGCA CTAAGTTTCC ATGT TTG CAGT GCT TCCA CATG CACA A

TCGTGTGCCATGCTTCTGGA ACAT |||| ||| |||| ||| |||| |||| ||||

CGAACAGCACTGCAAAGCCA TACA AAC GTCA CGA AGGT GTAC GTGT /

CAT CCGA - - CAAGC CTTC C GCT

GAM443 CTGCTGCTGACTGGCAAGCT 415 TTGGCTTCTT 2091 - A C----- TG CAC- A CA GGAAATG

GACACCGACCCATGGGGAAA CAACCAGCAG CTGC TGCTG CTGG AAGC A CG CC TGG A

TGAGAAAGAACCACCGGCTG TATG |||| ||||| |||| |||| | || || |||

AAAATTGGCTTCTTCAACCA GACG ATGAC GACC TTCG T GT GG ACC /

GCAGTATGCAG T - AACTTC GT AAAA C CC AAGAAAG

GAM444 ATGCATGCGCTGCTGGCCAT 416 GGGACAAGAT 2092 T TGGCCA C CG ACC AT-- A A

TGCCCTCACGATGTACCCCA GTTGCGCATG ATGCATGCGC GC TTG CCTCA ATGT CCATGCAGT CG TGAG G

TGCAGTATCGATGAGAGCAT CAT |||||||||| || ||| ||||| |||| ||||||||| || ||||

TCACCGTCCAGCTGCGTGGA TACGTACGCG TG AAC GGGGT TACA GGTGCGTCG GC ACTT C

GAACATATGGGGACAAGATG T TAG--- A A- AGA ACCT C A

TTGCGCATGCAT

GAM445 GGACTTATGATAAAGGTTCA 417 ATGCCCCTTC 2093 C A AAA TT CC----- -- CTG

GCTCCAGGGGTAGTACCTGA AGACCAGCTG GGA TT TGAT GG CAGCT AGGGGTA GTAC A

GTGTGTGCCATGCCCCTTCA TTCC ||| || |||| || ||||| ||||||| ||||

GACCAGCTGTTCCATCAGAA CCT AA ACTA CC GTCGA TCCCCGT CGTG G
TTCC T G --- TT CCAGACT AC TGT

GAM446 GAAGACTTCCTAAATTTGCA 418 TTTGCACATT 2094 AC A TTGCA TTGCC ACCAT
CATTAGCTAGATTGCCATTA AGCTAGATTG GAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
GCACCATTAGAGAGTTGATC CCAT |||| ||||| ||| ||||||||||| ||||||
TTTGGCTAATGATTATTCAG CTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GAAAATTTC AA C TTA-- C---- AGAGA

GAM447 TCCCACTGTGGTGCCTGGTG 419 TCGCCTGGAC 2095 CC - G T G A - AA CAGAGA
- CA T
GAGACCTGGCCAAGGTACAG CACAAGTTTG ACT GTGGT CC GGTG AG CCT GGCC GGTA
GCTGTG TG TGC G
AGAGCTGTGTGCATGCTGAG A ||| ||||| || |||| || ||| |||| |||| |||||| || |||
CAACACCACAGCCATTGCTG TGA CACCA GG CCGC TC GGG CCGG TCGT
CGACAC AC ACG /
AGGCCTGGGCTCGCCTGGAC TT A - T - - T AG TAC--- C A- A
CACAAGTTTGA

GAM448 GCCTGCCTGAACCCTGGGTC 420 CATGACGGCT 2096 A GG--- - A -- G AA- A- G
C
AGGAGAGAAACACTTGGGGA CTGAGTTCTT CCCT GTCA GGAGAGA ACA CTT GGGAGGGG
AGG CG CGTGGG T
GGGGAAAGGACGGCGTGGGC CCTG |||| |||| ||||||| ||| ||| |||||||| ||| || ||||||
TACCCATGACGGCTCTGAGT GGGA CGGT CCTTTCT TGT GGG TCCTTCTT TCT GC
GTACCC /
TCTTCCTGGGGCTTGTGTCT C GAAGA T G TC G GAG CG A A
TTCCTTGGCAGAAGAGGGCA
CAGCCAAGGC
GAM449 TAAGGGTTGTTTTGTTGTTA 421 TGAAGCTAGA 2097 T TGTTGT AA A-- GTCCATT
GGTAAATAGATATTAGGCAG TACCTAAAGC TAAGGGT GTTT TAGGTA TAG TATTAGGCA
T
TCCATTTCTAAAATATGCCT TACC ||||||| |||| |||||| ||| |||||||||
GATGAAGCTAGATACCTAAA ATTCCCA CGAA ATCCAT ATC GTAGTCCGT C
GCTACCCTTA T ------ AG GAA ATAAAAT

GAM450 GTCCCTCTTTGTCAGGCAGG 422 TAGCTGAGAC 2098 A- AG -- T AG AAA-- CAC C
TAACATT
CTGGAGTGCAGTGGGGTGAA CACAGGTGTG C GGC GCT GGAG GC TGGGGTG ATGGCT
TG AGCCT A
AATGGCTCACTGCAGCCTTA AC | ||| ||| |||| || ||||||| |||||| || |||||
ACATTAACATCTTGGGTTCA G TCG TGA CCTC CG ACTCCAC TACCGA AC TTGGG
/
AGCCATCCTCCCACCTCAGC AG A- AC - -- CCTCC --- - TTCTACA
CTCCCAAGTAGCTGAGACCA
CAGGTGTGAC

GAM451 CTCGCCTGGACCACAAGTTT 423 TCGCCTGGAC 2099 GGA A- AG GA TG AT --- TG
GACCTGATGTATGCCAAACG CACAAGTTTG CTCGCCT CC CA TTT CC ATGT GCCA AACG
C
TGCCTTTGTTCACTGGTACG ACCT ||||||| || || ||| || |||| |||| ||||
TTGGGGAGGGGATGGAGGAA GAGTGGA GG GT GGG GG TGCA TGGT TTGT C
GGTGAG A-- AG AG AG GT -- CAC TT

GAM452 GAGTGCAAATCAGTCCATTT 424 CATTTCACTT 2100 T - ---------- CAC GAGATA
CTT
CACTTTCACTGTCTGAGATA TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT
TGTCT GGGT T
GGGTCTTTAAAACCCAGGAT AGAT ||| ||||||| ||||||| |||||||| ||||| ||||
ACAAGGGTGGAATGTAGCTA CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCA /
TATGGACTCGATTTGCTTC - C TATCGATGTA AC- A----- AAA

GAM453 TGAAGCGCACTCAAAAGCAT 425 TCTGCAGTGC 2101 GCA AA- T -- - AGACT G-
G
TACGTCGTGGTCGAGACTGA ACCGTGTCAT TGAAGC CTCAA GCAT ACGT CGTGGT CG
GACG CTG T
CGGCTGGTGACAGAACGTCT GTGT |||||| ||||| |||| |||| |||||| || |||| |||
GCAGTGCACCGTGTCATGTG ACTTCG GAGTT TGTG TGTA GTGCCA GT CTGC
GAC G
TGTCACTTGAGCTAGCTTCA ATC CAC - CT C GACGT AA A

GAM454 CGGTTTATTTTCAATGTAGT 426 TAGTACTTTT 2102 TT- A CTTTT AATCA GTA
ACTTTTGAAATCAGTTTGGT GAAATCAGTT CGGTTTAT TCA TGTAGTA GA GTTTG C
ACAGAATAAACAGTCTCTAC TG |||||||| ||| ||||||| || |||||
TACAATGATATGTAAGCTG GTCGAATG AGT ACATCAT CT CAAAT A
TAT A CT--- GA--- AAG

GAM455 AGCCACTCGCAAAGCATTCT 427 TGAGGTGCAG 2103 ----- CAA ----- C A ATGACA C
CCACCACAATGACATAGGCA AAATTTGTGC AGCCAC TCG AGCAT TCT CACC CA
TAGG A
TACTTAGCTGAGGTGCAGAA TGTC |||||| ||| ||||| ||| |||| || ||||
ATTTGTGCTGTCGATAGCTG TCGGTG AGC TCGTG AGA GTGG GT ATTC T
TGGCT TCGAT TG- TTTAA C A CG---- A

GAM456 GTTGACTGTAATCTTCAAAT 428 TAGCACCATT 2104 TGTAAT------ AA-- T GG CAG
GGAAAGTCTCCTGGAGGTTC TGAAGTTCTC GTTGAC CTTCAAATGG AG CTCCT
AGGTT A
AGAACCAGATTTGAAGGAGT TTCT |||||| |||||||||| || ||||| |||||
CTAGCACCATTTGAAGTTCT CAACTG GAAGTTTACC TC GAGGA TTTAG A
CTTCTTTCGTCAAC CTTTCTTCTCTT ACGA T AG ACC

GAM457 CTGGAGCTTACATGAAGCCC 429 TTAGGACAGG 2105 G AC-- CA-- C A T
ACTCAGAAATCATTTCCTTA CTTCATTCCC CTGGA CTT ATGAAGCC CT AG AA C
GGACAGGCTTCATTCCCAAG AAGG ||||| ||| |||||||| || || ||
GTCCAG GACCT GAA TACTTCGG GA TC TT A
G CCCT ACAG T C T

GAM458 GGCCAGGTAAAATCATCTTT 430 TCGAAGTTTA 2106 - AAAAT--- T T------ TGAAGA
GTATAGAGCTGAAGAATAAG TCAGGATGTT GG CCAGGT CATCTT GTA AGAGC A
ACTGCTCTCGAAGTTTATCA CACA || |||||| |||||| ||| |||||
GGATGTTCACATGACCTGGA CC GGTCCA GTAGGA TAT TCTCG T
CC A GTACACTT C TTGAAGC TCAGAA

GAM459 CCCGTGGGGCCTCTGTGCAG 431 TCCGTGGGAC 2107 GC TGTGCAG T- G TTT AT- - C
- C G
CTGGTGTTTGGCTTTGAGTA CTCCAGAGTG CTC CTGG GTTT GC GAGT GC CAT CT
GATGA GATGGT C
TGCCATCCTGATGACGATGG AGAA ||| |||| |||| || |||| || ||| || ||||| ||||||
TGCTCACCATCTTCATCAAG GAG GACC CAGG TG CTCA CG GTA GA CTACT
CTACCA T
TATGTGCTGCACTCCGTGGG AA TGA---- TC G C-- CGT T T A T C
ACCTCCAGAGTGAGAACCCC
TGGG
GAM460 GAAGCTTGACATTTTAGTTT 432 TCAGGAGTAG 2108 C TG T- CATTA TT -- A
GCCATTATGTTAAAAACATC ATTGTTAGTG GAAG T ACATT TAGTTTGC TG AAA AACATCT
A
TAAATAGGTGTTAGTTTCTC TTGA |||| | ||||| |||||||| || ||| |||||||
AGGAGTAGATTGTTAGTGTT TTTC A TGTGA GTTAGATG AC TTT TTGTGGA A
GACTTT - GT TT AGG-- TC GA T

GAM461 TATCTATCATGGTGATCAAT 433 GTTGCTATTG 2109 TCAT GATCAATG GTGAT TT TT
AA CTT G
GACCAGTGATTTTTGATGTT TAATTGCTTT TCTA GGT ACCA TTTTGATG GCTA GT
TTG TGG A
GCTATTGTAATTGCTTTGGG GG |||| ||| |||| |||||||| |||| || ||| |||
ATACCACAAATTCTGGCCCA AGGT CCA TGGT AAAATTAC CGGT TA AAC
ACC T
TTAAAAGATGGTAAACCTAG TGAT AA------ AG--- C- CT -- --- A
TTGGATA

GAM462 GCCTATTGTTTTCCCTTCAC 434 GTGTGCAAAG 2110 - T - TAA TTATTT A TCTAT CA--
--- C C
CTATTAATAAATTATTTCTT TTTTTAGGTG CCCT CAC CTAT TAAA CTTT GC TGAT
AAG TGC C
TAGCTCTATTGATCAAAGCT TGGA |||| ||| |||| |||| |||| || |||| ||| |||
GCCCAGGCATTTTAACTAAC GGGG GTG GGTG ATTT GAAA CG ACTA TTT
ACG A

ATCACGTGTGCAAAGTTTTT T T A TGG TT---- - TGTGC CAATCAA T G
AGGTGTGGAGTGTGGGGTTT
AGCAGGAGGC
GAM463 GCTCCAAAGAACCAAGAGTG 435 CATTTCACTT 2111 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM464 CTAAGCTCTCTGCTCCATGA 436 TCAGAAGACT 2112 G TCTCT CCA G-- CC
GGTCTGAGGCCTCACCTCAG CAAAAGTTCC CTAA C GCT TGAG TCTGAGG T
AAGACTCAAAAGTTCCATGT ATGT |||| | ||| |||| |||||||
TAG GATT G TGA ACTC AGACTCC /
- TACCT AA- AGA AC

GAM465 CTTGGTGGTTTATTGCCTAC 437 GGGTACATAA 2113 TTATT - AAAA CAT- ---
T
CAAAAATACATACTTCTTTA AGAAGTATGT TTGGTGGT GCCTAC CA TACATACTTCTTTA
TCCATA GCAT G
CATTCCATAGCATTGTATGT ACTC |||||||| |||||| || |||||||||||||| |||||| ||||
TCATATGGGTACATAAAGAA AATCATTA TGGATG GT ATGTATGAAGAAAT GGGTAT
TGTA /
GTATGTACTCTGAGTAGGTA ----- A CTC- ACAT ACT T
TTACTAAG

GAM466 GTGTATTTTAAAGCTAATGG 438 TTAAAGCTAA 2114 A AAA GG A GGCTTG G
TGGAGGGGCTTGGTGGAAAC TGGTGGAGGG GTGT TTTT GCTAAT TGG GG GTG A
ACAACCACTGGGATTAGCCG GCTT |||| |||| |||||| ||| || |||
AGACACAC CACA AGAG CGATTA GTC CC CAC A
C C-- GG A AA---- A

GAM467 AAGGGTTGTTTTGTTGTTAG 439 TGAAGCTAGA 2115 T TGTTGT AA A-- GTCCATT
GTAAATAGATATTAGGCAGT TACCTAAAGC AAGGGT GTTT TAGGTA TAG TATTAGGCA
T
CCATTTCTAAAATATGCCTG TACC |||||| |||| |||||| ||| |||||||||
ATGAAGCTAGATACCTAAAG TTCCCA CGAA ATCCAT ATC GTAGTCCGT C
CTACCCTT T ------ AG GAA ATAAAAT

GAM468 GCAATAGGAACTACTGGTTT 440 TGGCAACATC 2116 A GAACTA TTTGA GTAAA TGA
TC
GAATGTGTAAATGGGTGATC CAGCAAAACT GCA TAG CTGG ATGT TGGG TC T
TCTCTGAGTCCTGGCAACAT ACTG ||| ||| |||| |||| |||| ||
CCAGCAAAACTACTGC CGT ATC GACC TACA GTCC AG /

C AAAAC- ----- ACG-- TG- TC

GAM469 CTTCCTTGATGCATCTCGAC 441 GACTGGAGAG 2117 TTGA A- GA CA --- AG
ACATCCTTGAAGCACCTCAA AAGGCACTTG CTTCC TGC TCTC CA TCC TTGA C
CATGGACTGGAGAGAAGGCA GAAG ||||| ||| |||| || ||| ||||
CTTGGAAG GAAGG ACG AGAG GT AGG AACT A
TTC- GA AG C- TAC CC

GAM470 TACTTGCTCTCGTCCTGTGA 442 TGTAGTGGAA 2118 T - CG - GT A TT TT A
ATTTTCTTTCATGAGGGAGT AGAAGCATGT TAC TGC TCT TC CT G ATT CT C T
CAATATGTAGTGGAAAGAAG A ||| ||| ||| || || | ||| || |
CATGTA ATG ACG AGA GG GA T TAA GA G G
T A AA T TG A CT GG A

GAM471 GCTCCAAAGAACCAAGAGTG 443 CATTTCACTT 2119 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM472 TGTTGCGGGAGCAGGCCGAG 444 TAAATGCTGC 2120 G - - - A AT - T - CG A C--------
TC
GAATGGCAGTTGGAGTACGT CTGCTGATCT G AG C AGGC CG GGA GG CAGT GG AGTA
TGGG CA GCC A
GGGACACGCCTCATGGGCAG ATCC | || | |||| || ||| || |||| || |||| |||| || |||
ACCTCCTTGCCTAAATGCTG C TC G TCCG GT CCT CT GTCG CC TCGT ATCC GT
CGG /
CCTGCTGATCTATCCATGAG A A T A A AT A T G AA - TCCTCCAGA GT
CCTTGACTACCTCACA

GAM473 AGGCAGGGTTTCCATCGTGC 445 TCAAGTTGCT 2121 C TCCATC GC AA-- T - -- T
TTATAAAACTTAGCACTTCT CAGTCTCCTG AGG AGGGTT GT TTATA ACT AGCA CTT
CTTC G
TCTGATGAAGTCAAGTTGCT TAAA ||| |||||| || ||||| ||| |||| ||| ||||
CAGTCTCCTGTAAAACATCT TCC TCTCAG CA AATGT TGA TCGT GAA GAAG A
GACTCTCCT - TCTA-- A- CCTC C T CT T

GAM474 CGCCCAGCGTGTCGCTCACT 446 GGAGATCATG 2122 T CTT GTG CG AATGAAGA-----
- CA A
TCCGTGCACCCGGATTTAAT GTGAAGGCCA GTCGCTCA CC CACC GATTT TTCTC
GGTGA TCA C
GAAGATTCTCGGTGACATCA TGAG |||||||| || |||| ||||| ||||| |||||| |||

ACAGTGACTTTACCAGAGGG TAGTGAGT GG GTGG CTAGA GGGAG CCATT
AGT A
GATGAAGATGAGGAGATCAT - ACC AA- TA GGAGTAGAAGTAG A TC G
GGTGAAGGCCATGAGTGATT
ACTGGGTG
GAM475 CAGAGTTCACCACCTGATAA 447 TATCACAGCC 2123 - --- CT AA CG A - T- C
GCTCGGATGAGGTTGCTGCT ATCTAGTGGA CAG AGTTCA CCAC GAT GCT GATG GGT TGC
GCTG T
GCTCCCGGCCTGCATGCCCT GCTG ||| |||||| |||| ||| ||| |||| ||| ||| ||||
ATCACAGCCATCTAGTGGAG GTC TCAAGT GGTG CTA CGA CTAT CCG ACG CGGC
C
CTGAACTGCTG G CGA AT C- CA C T TC C

GAM476 TCTGCAAGTGCTGTCTGTCA 448 AACACTGACT 2124 A T- CAATG A AACACT TTAG
G
ATGAAGAGAAACACTGACTG GGTTAGGATT TCTGCA GTGCTG CTGT AAG GA GACTGG
GATTGTT A
GTTAGGATTGTTGACAACGA GTT |||||| |||||| |||| ||| || |||||| |||||||
TTCCAGTCTTGTCCTTGCGG AGACGT CATGAC GGCG TTC CT CTGACC
TTAGCAA /
CTCAGTACATGCAGA A TC ----- - GTT--- ---- C

GAM477 GGTTATGGTGCTGCTGTGAA 449 TGGAGCCTGG 2125 GG T - AC GTTGGAGC G
TT T T
CACTGCCAAGTTGGAGCCTG CTCTGTTTGT GGTTAT TGC GCT GTGA ACTGCCAA
CTGGCTCT T G GCCG C
GCTCTGTTTGTGCCGTCTTT GCCG |||||| ||| ||| |||| |||||||| |||||||| | | ||||
GGTCTGGGAGGAGTCGGATT TCGGTG ATG CGG TACT TGACGGTT GGCTGAGG G
T TGGT T
GGCAGTTATCATGGGCTGTA AA T G AT A------- A GG C T
AAGTGGCT

GAM478 ACGAATCCAGCAAGGCTATG 450 GGGCGAGATG 2126 G T AAG A G GA ATAC
CGACTGTGGACTATACATAC TGTGGCAAAG AC AA CCAGC GCTATGCG CT TG CT A
AAGGGGCGAGATGTGTGGCA CTGG || || ||||| |||||||| || || ||
AAGCTGGCTTGGT TG TT GGTCG CGGTGTGT GA GC GG T
G C AAA A - GG AACA

GAM479 GCTCCAAAGAACCAAGAGTG 451 CATTTCACTT 2127 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC

TTTTCCAGAGC
GAM480 CACAAATCCAGCACTTCCTC 452 AGCAACACAT 2128 T GCACTTC-- T T- G
TCCATTTACTCTGTCAGGCT ATGGCTTTGT CACAAA CCA CTCTCCAT TAC CT T
GTATATGGGGAGCAACACAT G ||||||| ||| |||||||| ||| ||
ATGGCTTTGTG GTGTTT GGT GAGGGGTA ATG GG C
C ATACACAAC T TC A

GAM481 TGAAGACTTCCTAAATTTGC 453 TTTGCACATT 2129 AC A TTGCA TTGCC
ACCAT
ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM482 CTACTGGAAAGAAGGCTTTA 454 ACCATGTAAG 2130 - AA- --- - AGA CAGG
TGGAGATCCCAGGAACCAAG CCTGAATTTG CTAC TGG AGA AGGCTT TATGG TCC A
GACCATGTAAGCCTGAATTT TGCC |||| ||| ||| |||||| ||||| |||
GTGCCATGTGG GGTG ACC TTT TCCGAA GTACC AGG A
T GTG AAG T --- AACC

GAM483 TTTGAATACAATCTGGATTT 455 TGGAGACTTG 2131 - ------- T AACCTGT - --
TCTGA T
CTTGCTATTTCTTGTGCAAC GTTGTTTGGC TTTCTTGCTA TTTCTTG GC ACG CCA
TTTCC ACT G
CTGTACGCCATTTCCTCTGA CAAG |||||||||| ||||||| || ||| ||| ||||| |||
ACTTGCTAGTGCTCTGGAGA GGAGGACGAT AAGGAAC CG TGT GGT AGAGG
TGA C
CTTGGTTGTTTGGCCAAGGA G CCCCTAT - GTT---- T TC TCTCG T
ATATCCCCTAGCAGGAGGGC
TCACTAAGGA
GAM484 GCGCGTTAGCTCTCGAGTTG 456 TGAGATGATG 2132 TT A GCTA GT- A- T
CTAGTCGTTGAGGATTGGAA TGAGAGCTTG GCGCG AGCTCTCG GTT GTC TG GGAT G
TCCACCATGAGATGATGTGA TGTG ||||| |||||||| ||| ||| || ||||
GAGCTTGTGTGC CGTGT TCGAGAGT TAG TAG AC CCTA G
GT G ---- AGT CA A

GAM485 GGCATGGCAGCAGAGAGTAC 457 ACTCAGTGAA 2133 C - A ACC AGGT A GGG
CCTTTCAAGGTGTACAGGGT GGAACTCCTG GG ATG GCAGCAG GAGT CTTTCA GT CA T
AAATGAACTCAGTGAAGGAA TTGC || ||| ||||||| |||| |||||| || ||
CTCCTGTTGCACATCC CC TAC CGTTGTC CTCA GGAAGT CA GT /
- A - A-- GACT A AAA

GAM486 GCCTGAACTTGCATTATGGC 458 TGAAAGAGAT 2134 GA T - GG ---- - GG
TATGGTGGACAAACTGATTG GGTGGCAGTG GCCT ACT GC ATTAT CT AT GGT A

AAAGAGATGGTGGCAGTGAA AAGG |||| ||| || ||||| || || |||
GGC CGGA TGA CG TGGTA GA TA TCA C
AG - G GA AAGT G AA

GAM487 CGTTTGAACCTGGGAGGTAG 459 GGAGGTAGAG 2135 TGAA TG AGGTAGA T- A CAAG
AGGTTGCAGTAGCCAAGATC GTTGCAGTAG CGTT CC GG GG TGCAGT GC A
ACGCCACTGCATTCCAGCCT C |||| || || || |||||| ||
GGGCAACG GCAA GG CC CC ACGTCA CG /
C--- GT GA----- TT C CACT

GAM488 TTTAGATGGGTTGTCTGCAT 460 TAAGCTTTTT 2136 T- A- TG - TTCCTCTC C CCTT GAA T
GGTGGTAAAATAAGCTTTTT CCTCTCGCCT TC GC TGG GTAA AATAAGCTTT GCCTA GT TG GATC C
CCTCTCGCCTACGTCCTTTG ACGT || || ||| |||| |||||||||| ||||| || || ||||
GAAGATCTCCTGATCATACA GG CG GCC CGTT TTATTCGGGA TGGAT CA AC CTAG C
TAACTAGGTAGGGCTTATTC TT AG GT C -------- - AT-- ATA T
TTGCTGCCGGAGCTTGGCAC
CCAGCTCTAGA
GAM489 CCACATGCCTCCCAAAATGA 461 TCCCAAAATG 2137 CTCCCAAAA AAG A G TT GAG
AAGACAAACAGGATTGTTTC AAAGACAAAC CCACATGC TGA ACA ACAG ATTG TCT A
TGAGACCAAGATCAGTCTGT AGGA |||||||| ||| ||| |||| |||| |||
CTGTGATCAGCCTGTGTGTG GGTGTGTG ACT TGT TGTC TGAC AGA /
G TCCG----- AG- C - T- ACC

GAM490 CACTTAGGCACTCTGTCAAA 462 GTGGCATTTC 2138 TAGG CTC ATCCTCC- C- TG G TG ACTCCTGT
TCCTCCCCACCTATGTAGTA AGTTGACATT CACT CA TGTCAA CCAC TA TA TA AGCGG A
TGAGCGGACTCCTGTAACTA GGAT |||| || |||||| |||| || || || |||||
TATGCCTGCTTGTGATGTGT GTGA GT ACAGTT GGTG AT GT GT TCGTC A
ACCGTGGCATTTCAGTTGAC TAG- T-- GACTTTAC CC GT A GT CGTATATC
ATTGGATAGTG

GAM491 GTGTAGGGTTAACTCAAGGA 463 TCAGCAGGTA 2139 AGGG T- - AAG --- AGCA TATTGA TT
AGCTTAATTGATCAGCAGGT TTTATTGAAC GT TTAAC CAA GG CTTA ATTGATC GGTATT ACAC A
ATTTATTGAACACTTACTGT AC || ||||| ||| || |||| ||||||| |||||| ||||
GTGTCTAATGCTCAGATTAG CA AATTG GTT CC GAAT TGATTAG TCGTAA TGTG /
TATGTAAGAGCCATTGCTGT GAGG TC A GA- GTA AC-- TCTG-- TC
TAAGGAGACAT

GAM492 TAAGCATCACACCCAGCCTT 464 CATCACACCC 2140 CACACC CCT A TCT A

GAGGATTTTCTTATACTGTG AGCCTTGAGG TAAGCAT CAG TG GGATTT TAT C
TTTGAATCCACATGACTGAT ATTT ||||||| ||| || |||||| |||
AATATGCTTA ATTCGTA GTC AC CCTAAG GTG /
TAATA- AGT A TTT T

GAM493 CCACATGCCTCCCAAAATGA 465 TCCCAAAATG 2141 CTCCCAAAA AAG A G TT
GAG
AAGACAAACAGGATTGTTTC AAAGACAAAC CCACATGC TGA ACA ACAG ATTG TCT A
TGAGACCAAGATCAGTCTGT AGGA |||||||| ||| ||| |||| |||| |||
CTGTGATCAGCCTGTGTGTG GGTGTGTG ACT TGT TGTC TGAC AGA /
G TCCG----- AG- C - T- ACC

GAM494 TGAAGACTTCCTAAATTTGC 466 TTTGCACATT 2142 AC A TTGCA TTGCC
ACCAT
ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM495 GTGATGGTCCAACTTTGTGG 467 GTAAGGATTT 2143 - --- --- GAATG- AGG AGGG
GG
AATGGTAAGGATTTTTAGGG TTAGGGTTGT GTG ATGGT CCAACTT TGTG GTA ATTTTT
TTGTTT G
TTGTTTGGGCCAGAACAAGA TT ||| ||||| ||||||| |||| ||| |||||| ||||||
GAAATAACTGCAGAAAACAC CGC TACCA GGTTGGG ACAC CGT TAAAGA
AACAAG C
ATATGGGTTGGGAAACCATG G AAG TAT AAAAGA CAA G--- AC
CGC

GAM496 TAAGGGTTGTTTTGTTGTTA 468 TGAAGCTAGA 2144 T TGTTGT AA A-- GTCCATT
GGTAAATAGATATTAGGCAG TACCTAAAGC TAAGGGT GTTT TAGGTA TAG TATTAGGCA
T
TCCATTTCTAAAATATGCCT TACC ||||||| |||| |||||| ||| |||||||||
GATGAAGCTAGATACCTAAA ATTCCCA CGAA ATCCAT ATC GTAGTCCGT C
GCTACCCTTA T ------ AG GAA ATAAAAT

GAM497 AGGACCCGCACCCACGTGGC 469 TTCACAGGTG 2145 -- CAC CT T AT AG C-- C
T GA
TCTGTGCATCCGCAGCAACT CCTGAAATTC GCACC GTGG CTG GC CCGC CAA
TTGGTCTTT TTCCTT GCT G
TGGTCTTTCTTCCTTTGCTG CT ||||| |||| ||| || |||| ||| ||||||||| |||||| |||
AGTTTGGTTAAGGGAAAGGG CGTGG CACT GAC CG GGTG GTT AGCCGGGAA
AGGGAA TGG T
CCGATTATTGAGTGGGCTCA TC A-- T- T -- A- ATT - T TT
GTTCACAGGTGCCTGAAATT

CCT
GAM498 GTCAAGATTTTAACAAACAT 470 TGAGGTAGGT 2146 A TTTT ACAT AT-- ACA
CTTAATCCTCACAACAACCC AAGTCATTGT GTCA GA AACAA CTTA CCTCACA A
TGTGAGGTAGGTAAGTCATT TTCA |||| || ||||| |||| |||||||
GTTTCATGAT TAGT CT TTGTT GAAT GGAGTGT /
A ---- ACT- GGAT CCC

GAM499 GCTCCAAAGAACCAAGAGTG 471 CATTTCACTT 2147 A AA T - TTC--- - GT GAG AG- TC
CAAATCAGTCCATTTCACTT TCACTGTCTG CC GAG GCAAATC AGTCCAT AC TTTCACT CT AT GGTC T
TCACTGTCTGAGATAGGGTC AGAT || ||| ||||||| ||||||| || ||||||| || || ||||
TCTAAGACCAGGATACAAGG GG CTT CGTTTAG TCAGGTA TG AAGGTGG GA TA CCAG /
GTGGAATGTAGCTATATGGA A C- - C TATCGA T -- ACA GGA AA
CTCGATTTGCTTCCGGACCT
TTTCCAGAGC
GAM500 TCAATATTAAAGGGTCTGGA 472 AAGAGTGTGT 2148 GG AAATAG GTGTTGG A TGTACC - TG TT
AAATAGAAGAGTGTGTTGGG TGGGCAGGTA G TCTGGA AAGAGT GCAGGT GTT ATTT A AAGG T
CAGGTAGTTTGTACCATTTA GTTT | |||||| |||||| |||||| ||| |||| | ||||
TGAAGGTTTGTTCCTTTGTT T AGACCT TTTTCG TGTCCG CGA TAAA T TTCC G
AAATTTAGCAGCCTGTACTA GA AAAG-- ATCA--- A TT---- T GT TT
GCTTTTGAAATCCAGAAGTT
TTAACTTCCA
GAM501 TCATCAGACCTGTAATGCAG 473 TGTAATGCAG 2149 CA CT- AT AGAGAA AA GA- - CC C
GCTCTTCTTCACATTATAAG GCTCTTCTTC TGTAATG GG CTTCTTCAC TATA ACAGA AT TGA TTAC A
AGAAACAGAAAATGATGACC ACAT ||||||| || ||||||||| |||| ||||| || ||| ||||
TTACCAATGTAATTCAGAAA ACGTTAT TC GAAGAAGTG ATAT TGTCT TA ACT AATG A
ATGATCTGTGAATATAGTGA CC ATT -- AAG--- AG AAAG T- T
AGAAGTTACTCCTATTGCAG
TAGAAATGA
GAM502 GGTCAAGGCCACCCCTGACA 474 CAGCTCAAGG 2150 T C C C CAC AGTT ---- - AG
CGTTGGCAGTTGGGACACGG ATGACCTTGC GG CAAGG CA CC TGA GTTGGC GGGA CAC GGAA C
AAAGCCCTTCCAGTGAACTT CC || ||||| || || ||| |||||| |||| ||| ||||
CCCGTCAGCTCAAGGATGAC CC GTTCC GT GG ACT CGACTG CCCT GTG CCTT /
CTTGCCC C A A A --- ---- TCAA A CC

GAM503 GGGAAGGCAGTAGGTTGTAT 475 AAGGCAGTAG 2151 GA C ATA A TTCCGA ACA
AGTTATCTTCCGAGGGGCAA GTTGTATAGT GG AGG AGTAGGTTGT GTT TC GGGGCA T
CATCACTGCCCTGAAACCAC TATC || ||| |||||||||| ||| || ||||||

ACAACCTACTACCTCACC CC TCC TCATCCAACA CAA AG TCCCGT /
AC A CAC - ------ CAC

GAM504 ATGCTGATCAAGTTACTTGC 476 TGATCAAGTT 2152 AT- TT----- G TGCAA TA G
TGTGCAATGAGTAATAAAGA ACTTGCTGTG ATGCTG CAAG ACTT CTG TGAG ATAAA A
CCTTTGTCTCTTACCCAGAA CAAT |||||| |||| |||| ||| |||| |||||
GTTTCATGTCTTGTGGCAGC TACGAC GTTC TGAA GAC ATTC TGTTT C
AT GGT TGTACTT - CC--- TC C

GAM505 ACGTCTCCACCAGAGGGACT 477 TCCCAATCCT 2153 TC--- A ----- C T- C
GGTGCTTCTCGGAGCTCCCA CAGACTCCGG ACGTC CACC GAG GGA TGG GCTT T
ATCCTCAGACTCCGGTGAAA TGAA ||||| |||| ||| ||| ||| ||||
GTGACGT TGCAG GTGG CTC CCT ACC CGAG C
TGAAA C AGACT A CT G

GAM506 CGGATGCTCACAGTCTCTGG 478 TGCATGCTCC 2154 AT- TCT-- GA TT AC
ATGAGGA G GC
CAGAACTTGGAGACTGCAAT CTGTAATGCC CGG GCTCACAGTC GGCA AC GGAG TGCA
TCTG CA A
GAGGATCTGGCAGCACGGTG CCAT ||| |||||||||| |||| || |||| |||| |||| ||
GCAGAAGTGCATGCTCCCTG GCC CGAGTGTCAG CCGT TG CCTC ACGT AGAC
GT C
TAATGCCCCATTGACTGTGA ACT TTACC AA TC GT GA----- G GG
GCTCACCG

GAM507 CAGCTGCTAGTGGAAGGACT 479 AGCTGCTAGT 2155 CT- TG ------- - TT GC- C
GTGTTGTGCAGCTGCACATA GGAAGGACTG CAG GCTAG GAAG GACT GTG GT AGCTG
A
GCTATAATTTTATAAGTCTG TGTT ||| ||||| |||| |||| ||| || |||||
CTTTACTTTTGCTAGCTCCC GTC CGATC TTTC CTGA TAT TA TCGAT C
TG CCT GT ATTTCGT A TT ATA A

GAM508 TCTGGATCCGTCTTCACTTC 480 TCTGGATCCG 2156 GATC TC CA TGTT CC - ACCAA
CTGTTGGCCTGAGCAGTACC TCTTCACTTC TCTG CG TT CTTCC GG TGAGC AGT T
AATAACACACTGGTTCACCT CTGT |||| || || ||||| || ||||| |||
TGGAAGGCAAAGCGTAGA AGAT GC AA GAAGG CC ACTTG TCA /
---- GA CG TT-- -- G CACAA

GAM509 GCTCCAAAGAACCAAGAGTG 481 CATTTCACTT 2157 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /

GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM510 GCTCCAAAGAACCAAGAGTG 482 CATTTCACTT 2158 A AA T - TTC--- - GT GAG
AG- TC
CAAATCAGTCCATTTCACTT TCACTGTCTG CC GAG GCAAATC AGTCCAT AC TTTCACT CT
AT GGTC T
TCACTGTCTGAGATAGGGTC AGAT || ||| ||||||| ||||||| || ||||||| || || ||||
TCTAAGACCAGGATACAAGG GG CTT CGTTTAG TCAGGTA TG AAGGTGG GA TA
CCAG /
GTGGAATGTAGCTATATGGA A C- - C TATCGA T -- ACA GGA AA
CTCGATTTGCTTCCGGACCT
TTTCCAGAGC
GAM511 CACAAGTGATGGTCCAACTT 483 GTAAGGATTT 2159 - -- T-- GAATG- AGG AGGG
GG
TGTGGAATGGTAAGGATTTT TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
TAGGGTTGTTTGGCCAGAAC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
AAGAGAAATAACTGCAGAAA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /
ACACATATGGTTGGAAACCA G AA TAT AAAAGA CAA G--- AC
TGCGCTTGTG

GAM512 TTTTAAAGCATAGATCAACA 484 TAAAGCATAG 2160 CAT AACAA A A AC
AAGTAGCTATCAGCACCAGG ATCAACAAAG TTTTAAAG AGATC AGT GCT TCAGC C
TTGGAGCAGCTAAGGTCTCT TAGC |||||||| ||||| ||| ||| |||||
TTTAGGA AGGATTTT TCTGG TCG CGA GGTTG /
C-- AA--- A - GA

GAM513 GCTTGCACGGCTTTCTTTCC 485 CGGAGGGCTG 2161 CG T T AG- -- G TT T- G
T TCCT
TCGGAGGGCTGACTGTTTGT ACTGTTTGTG GCTTGCA GCTT CTTTCC CGG GG CT ACTG
TG GCT CTG GG G
GCTGCTGTGGTCCTGCATGT CTGC ||||||| |||| |||||| ||| || || |||| || ||| ||| ||
TCCAGGAGCTTCACCCAGTG CGGACGT CGGA GAGAGG GTC CC GA TGAC AC CGA
GAC CT C
AGGACCAGGCTGGGAGAGAG -- - - GGA AG G CC TT G - TGTA
GCTGCAGGC

GAM514 CCACATCTGCAAAAGTGTGT 486 TGACTCTACA 2162 A TGCAAA T -------- GAAT
TG AT
GTGGATTCTGCGAATTATTT CACATTCAAC CCAC TC AGTGTGTGTGGA TC TGC
TATTTA GAT A
ATGGATATACAAGTTTCTGA TGAG |||| || |||||||||||| || ||| |||||| |||
ATGCAAGCACTGAATGTGAC GGTG AG TTACACACATCT AG ACG GTAAGT
TTG C
TCTACACACATTCAACTGAG - TCAAC- C TGTAAGTC AAC- CT AA
TGG

GAM515 GGACGCTCAGGCCGACAACA 487 TGGCATCAGC 2163 G G - CAA --- CACA AATG
A G
AGTTCTCCACAGGTTGGAAT CACAAGAGTG GGAC CTCA GC CGA CAAGTT CTC GGTTGG
GCCA TGT C
GGCCAATGTGCAATAATGGC AAAC |||| |||| || ||| |||||| ||| |||||| |||| |||
ATCAGCCACAAGAGTGAAAC TCTG GAGT CG GCT GTTCAA GAG CCGACT CGGT
ATA /
TTGAATCGTGCATGAGGGTC G A T AA- AGT AACA A--- A A
T

GAM516 GTTTGTGCTGACAGAACGAG 488 TGACAGAACG 2164 TG GA GA AGAG- T GAAG---
A
AGGGTGCTCTGAAGTATTTC AGAGGGTGCT GTTTG CT CA ACG GG GCTCT TATTTC A
AACAGAAATGATGCCAAGGA CTGA ||||| || || ||| || ||||| ||||||
GCCCAAGGCCGTGATGAAGA CGAGC GA GT TGC CC CGAGG GTAAAG C
TCGAGC TA A- AG CGGAA - AACCGTA A

GAM517 GTCCAATCCTAACAGCTGCT 489 GTGAGCAATG 2165 --- GC CCT G
CCCTTGGGCCTTCATGTGAG TTATCAGGGT GTCCAATCCT AACA TGCTC TGG C
CAATGTTATCAGGGTTGGAT TGGA |||||||||| |||| ||||| |||
TAGGTTGGGA TTGT ACGAG ACT C
CTA A- TGT T

GAM518 GCTCCAAAGAACCAAGAGTG 490 CATTTCACTT 2166 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM519 CATCATCTGGCAAATTCAGT 491 TGAATCATTA 2167 - GC -- GTAAT GTACTT - T
TGTA-- G
AATTGGAGAGTACTTGCTTC TCAGCATGAT CATCAT CTG AA ATTCA TGGAGA GCT TC
GTT TCT A
TGTTTGTATCTGAGAGGAAT G |||||| ||| || ||||| |||||| ||| || ||| |||
TTTTAACTGACGGCTTCTGT GTAGTA GAC TT TAAGT ACCTCT CGG AG CAA
AGG G
CTCCATGAATCATTATCAGC C TA AC ----- GTCTT- C T TTTTTA A
ATGATG

GAM520 CCGGCCAACATCAAGTGACT 492 TGGTATGTGG 2168 G- A- - AG GA - TG AG
TTATAGCTGCAAGAAATGTG AGAAGTCTGT CCG CC ACAT CA T CTTTATA GC CA A
GTATGTGGAGAAGTCTGTAT ATGT ||| || |||| || | ||||||| || ||
GTGAGGAACGG GGC GG TGTA GT G GAGGTGT TG GT /
AA AG T CT AA A GT AA

GAM521 CACAAGTGATGGTCCAACTT 493 GTAAGGATTT 2169 A - -- T-- GAATG- AGG
AGGG GG
TGTGGAATGGTAAGGATTTT TTAGGGTTGT ACA GTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
TAGGGTTGTTTGGCCAGAAC TT ||| ||| |||| ||||||| |||| ||| |||||| |||||||
AAGAGAAATAACTGCAGAAA TGT CGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /
ACACATATGGTTGGAAACCA C G AA TAT AAAAGA CAA G--- AC
TGCGCCTGTG

GAM522 AGTGGGGAGAACAGCGTCTT 494 TCCTCCAGTG 2170 A GT TTTACC - CC -- G A
CC T
TTACCTGTCACCGAAGCCAG GCGTTCTTTT AGTGGGGAGAAC GC CT TGT CA GAAGC CA
GA GC CGTT G
GAAGCCCCGTTTGTAAGCGT TACT |||||||||||| || || ||| || ||||| || || || ||||
GTGTTGTGGTGCTTTATTGT TCATTTTTCTTG CG GA ACA GT TTTCG GT TT TG
GCGA T
ACATCCTCCAGTGGCGTTCT - GT CCTCCT T TA TG G G T- A
TTTTACT

GAM523 GGGTGCACAAGTGATGGTCC 495 GTAAGGATTT 2171 - -- T-- GAATG- AGG
AGGG GG
AACTTTGTGGAATGGTAAGG TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
ATTTTTAGGGTTGTTTGGCC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
AGAACAAGAGAAATAACTGC TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /
AGAAAACACATATGGTTGGA G AA TAT AAAAGA CAA G--- AC
AACCATGCGCTTGTGACTT

GAM524 GAAATGTGGAGAATTAAAAA 496 TGGAGAATTA 2172 T ATTAA -- T CATTTATAGA
TGTA
GGGTAGTGAGGCTGGCATTT AAAAGGGTAG G GGAGA AAAGGGT AG GAGGCTGG
ATCTGGCTTTCT T
ATAGAATCTGGCTTTCTTGT TGAG | ||||| ||||||| || |||||||| ||||||||||
ATTGGGTGGAAAGCTAGATG C CCTCT TTTTCCG TC CTTTGACC
TAGATCGAAAGG T
AAACCAGTTTCTCTCAGCCT T C---- AC T AAAG------ TGGG
TTTCTCTCCTCAGGTC

GAM525 GACAGACTCTCTCCACATGG 497 ACCATGTAAG 2173 C - AGA CAGG
CACAAATTCAGGCTTTATGG CCTGAATTTG GA AGACTCTCTCCACATGGCACAAATTCAGGCTT
TATGG TCC A
AGATCCCAGGAACCAAGGAC TGCC || |||||||||||||||||||||||||||||||| ||||| |||
CATGTAAGCCTGAATTTGTG CT TTTGAGAGAGGTGTACCGTGTTTAAGTCCGAA GTACC
AGG A
CCATGTGGAGAGAGTTTCTC C T --- AACC

GAM526 GAAGCCATTTGGAGATTGCA 498 GTGCAGTTGG 2174 GCA TGCA AATTAG T GCA GA A TG G
AAGTGCAGTTGGAATTAGCA AATTAGCATT TTGGAGATT AAG GTTGG CA TGGTTTTT CT CCAT T A G
TTGGTTTTTGCACTGACCAT GGTT |||||||||| ||| ||||| || |||||||| || |||| | |
ATTGAGGTATTGAATGGGGA AATTTCTAA TTC CGACC GT ACTAAAGA GA GGTA A T T
GAGAAATCATTGGCCAGCAT ACA TA-- G----- T --- GG - GT A
CTTACAAATCTTTAATAATA
GCTTT
GAM527 CTCTACTCAGGCAGTCGACC 499 TCCCACCAGG 2175 - ACCCG ------ - AA-- CC AGA G AAC
CGCCACGATGAGAAGTGGGA CTTCATTCAC GCAG TCG CCAC GATGA G GTGGGA AGC GGGC CC T
CCAGCAGAGGGCGCCAACTT CCAG |||| ||| |||| ||||| | |||||| ||| |||| ||
CAGGAGTCCGCTTTCCCACC TGTC AGT GGTG TTACT C CACCCT TCG CCTG GG /
AGGCTTCATTCACCCAGTGG A CCA-- ACCCAC T GGAC T- --- A ACT
ACCTGAACTGTTTGGTAGAG

GAM528 AGTCAGTCTCCAGTATAGAT 500 TCCAGTATAG 2176 T TC AT-- T T TAC ATAAT TC
GAGTAGCTATGGGAAAATAC ATGAGTAGCT AG CAG TCCAGT AGATGAG AGCTA GGGAAAA TAGGA CC C
TAGGAATAATCCTCCCAGGC ATGG || ||| |||||| ||||||| ||||| ||||||| ||||| ||
CCTCTTATTTTTTTCCTGGT TC GTT AGGTCA TTTATTC TTGGT CCTTTTT ATTCT GG /
TTCTTATTTCTTAACTGGAT T -- ATTC T - TT- CCC-- AC
TGTCT

GAM529 GGAGCTGAAGGTCTGCGTCA 501 TCACGGTGAA 2177 CT T C----- T TC T-- TTAC- - CA
CGGTGAAAATTCGGGATGTT AATTCGGGAT G GAAGG CTGCGT ACGG GAAAAT GGGA GT AGAG CAT C
TACAGAGCATCACAAATGCC GTTT | ||||| |||||| |||| |||||| |||| || |||| |||
TCTCTCTCGCCGCTCTCTCA C CTTCC GACGTA TGTT CTTTTA CTCT CG TCTC GTA /
TTTTCTTTGTATAACTATGC C- - TCAATA T CT CGC CTCTC C AA
AGCCTTCCCTCT

GAM530 GCTCCAAAGAACCAAGAGTG 502 CATTTCACTT 2178 T - ---------- CAC GAGATA TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC

TTTTCCAGAGC
GAM531 GGTGCACAAGTGATGGTCCA 503 GTAAGGATTT 2179 - -- T-- GAATG- AGG
AGGG GG
ACTTTGTGGAATGGTAAGGA TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
TTTTTAGGGTTGTTTGGCCA TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
GAACAAGAGAAATAACTGCA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /
GAAAACACATATGGTTGGAA G AA TAT AAAAGA CAA G--- AC
ACCATGCGCTTGTGACT

GAM532 TATGATAGGCATTTGCAAAT 504 TTGCAAATTC 2180 A- T--- - CCAA T A-- A
TCACCAAGAGTGACAGATAG ACCAAGAGTG TATGAT GGCAT TGCAAATT CA GAG GACAG
TAGTGCC C
TGCCACGGGCACTGCCACTG ACAG |||||| ||||| |||||||| || ||| ||||| |||||||
TCTCTTCCAATGCAATTTGT ATACTA CCGTA ATGTTTAA GT TTC CTGTC GTCACGG
/
ACATTATGCCGAATCATA AG TTAC C AACC T ACC G

GAM533 TCTCCCAGTCATCACAGTCT 505 CATCACAGTC 2181 - A C CT- T-- T TC A ATTC
CC
GGTGTCTTGATATCCTGAAT TGGTGTCTTG CT CCCAGTC TCA AGT GG GTCT GATA CTGA
TGAAG GGACA T
GAAGATTCGGACACCTCGTT ATAT || ||||||| ||| ||| || |||| |||| |||| ||||| |||||
GTTCTGCACTTCATCAGTTA GA GGGTTAG AGT TCA CC TAGA CTAT GACT ACTTC
CTTGT C
TCAGATGTTCCTATACTATG A - A TAT TTG - T- - ACGT TG
AGATTGGGAAGA

GAM534 GCCTGCCTGAACCCTGGGTC 506 CATGACGGCT 2182 A GG--- - A -- G AA- A- G
C
AGGAGAGAAACACTTGGGGA CTGAGTTCTT CCCT GTCA GGAGAGA ACA CTT GGGAGGGG
AGG CG CGTGGG T
GGGGAAAGGACGGCGTGGGC CCTG |||| |||| ||||||| ||| ||| |||||||| ||| || ||||||
TACCCATGACGGCTCTGAGT GGGA CGGT CCTTTCT TGT GGG TCCTTCTT TCT GC
GTACCC /
TCTTCCTGGGGCTTGTGTCT C GAAGA T G TC G GAG CG A A
TTCCTTGGCAGAAGAGGGCA
CAGCCAAGGC
GAM535 AGAAGTGGAATTGTGAACCA 507 GTGAACCAAA 2183 ATT CCA TTTTA GCAT TTT
AAGTTTTAGGTGCATTGTAA GTTTTAGGTG AGAAGTGGA GTGAA AAG GGT TGTAA T
TTTTGATTTATAACCAATCT CATT ||||||||| ||||| ||| ||| |||||
TTTCACTGATCTACTTCT TCTTCATCT CACTT TTC CCA ATATT /
AGT --- TAA-- ---- TAG

GAM536 CAGTGTGGTTTAATCTGGAA 508 ACCCGTGTTC 2184 T T CT - GAAGCTG A A
GGAGCAGAAGCTGTGGAGTC CTATCCTTGT CAG GTGGT TAAT GGA AGGAGCA TGG
GTCC A

CAAAGGACCCGTGTTCCTAT TGTG ||| ||||| |||| ||| ||||||| ||| ||||
CCTTGTTGTGCCACTTG GTT CACCG GTTG CCT TCCTTGT GCC CAGG /
- T TT A ------- - A

GAM537 CAGTGGTTCTCTCAGCAACA 509 TCAAAGCTGC 2185 TC - AACA-- - A- A TA TGAC T CC
GACATGTCCAGTGGACCGTA AGATTGCCTG GT TCT CAGC GACATGT CC GTGG CCG GTGTTG GG CGC A
GTGTTGTGACGGTCGCCCAT TG || ||| |||| ||||||| || |||| ||| |||||| || |||
CTGCGCCCAGTACCTCGGAT CG AGA GTCG TTGTACA GG TACT GGC CATGAC CC GCG T
CATGCGGAACATGTTGTCAA TT C AAACTG A CG A TC ---- - TC
AGCTGCAGATTGCCTGTG

GAM538 GAAGACTTCCTAAATTTGCA 510 TTTGCACATT 2186 AC A TTGCA TTGCC ACCAT
CATTAGCTAGATTGCCATTA AGCTAGATTG GAAG TTCCT AAT CATTAGCTAGA ATTAGC T
GCACCATTAGAGAGTTGATC CCAT |||| ||||| ||| |||||||||| ||||||
TTTGGCTAATGATTATTCAG CTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GAAAATTTC AA C TTA-- C---- AGAGA

GAM539 CACAAATCCAGCACTTCCTC 512 AGCAACACAT 2188 T GCACTTC-- T T- G
TCCATTTACTCTGTCAGGCT ATGGCTTTGT CACAAA CCA CTCTCCAT TAC CT T
GTATATGGGGAGCAACACAT G |||||| ||| |||||||| ||| ||
ATGGCTTTGTG GTGTTT GGT GAGGGGTA ATG GG C
C ATACACAAC T TC A

GAM540 AGAATGGGGAAGAATACTGA 513 TTGGAGCAGG 2189 - - TA AA T CA TCT AC- CT
ATTAGCTGAGCACATTCTGG TTTCATTCTC AGAAT GGGGAA GAA CTG TTAGC GAG CAT GGAC AATT G
ACACAATTCTGACCAATTTC CAAT ||||| |||||| ||| ||| ||||| ||| ||| |||| ||||
AGTCTCATGATCTCTGTTGG TCTTA CCTCTT CTT GAC GGTTG CTC GTA TCTG TTAA A
AGCAGGTTTCATTCTCCAAT A A TG GA T TA C-- ACT CC
TCT

GAM541 CTGCTGACGCAGGCTGAAGT 514 TGGACAAGCA 2190 C A AG GAAG - T AAC
TGTTTTCTCACTGGCTAACC GGGCAAGTGA CTG TG CGC GCT TTGTTT TC CACTGGCT C
ACTAAGCCAGTGGACAAGCA TACA ||| || ||| ||| |||||| || ||||||||
GGGCAAGTGATACAG GAC AT GTG CGG GACGAA AG GTGACCGA A
- A AA ---- C - ATC

GAM542 AGAAAATTTTGACAGGTAAC 515 TGACAGGTAA 2191 A T C AACT TACA-- C CA ACAA
TGGCTTACAGGCCAATGCAG CTGGCTTACA AGAA ATT TGA AGGT GGCT GGC AATG GCAG T

CAGACAATAAAATTGCCATT GGCC |||| ||| ||| |||| |||| ||| |||| ||||
CGCCACCATCAGTCTCAAAC TCTT TGA ACT TTCA CTGA CCG TTAC CGTT /
TTTCACAGTATTCT A C - AACT CTACCA C -- AAAA

GAM543 CAGATGATGGGACCAGCCCA 516 CAGCCCATTT 2192 A A GG CC CATTT AA GG CTG
TTTAGAAATCAGTGGATATG AGAAATCAGT CAG TG TG A AGCC AGA TCAGT ATATG T
CTGTCGATATGTAAACTGAA GGAT ||| || || | |||| ||| ||||| |||||
ATCTTGCAGGCTTTTCAACA GTC AC AC T TCGG TCT AGTCA TGTAT /
CTG - A TT -- ACGT- AA AA AGC

GAM544 TTGCCTGCTCGTCCGGGAAG 517 AAGGCTGCCA 2193 ----- - GATG AAATCT C G --
GA T ACC
GCGATGTCGAAAATCTCCCG GGTCGAAGAA C CGGGAAGG C TCGA CC GGTAGT TTC
CAC AG GC T
GTAGTGTTCCACGAAGTGCA GTCC | |||||||| | |||| || |||||| ||| ||| || ||
CCTCCAGGCCCTCGGTGATG G GTTCTTCC G AGCT GG CCGTCG AAG GTG TC
CG C
AAGGCTGCCAGGTCGAAGAA CTCTT T AAGA ------ A G TA GC C GAC
GTCCTTCTTGTTCTCGGCTG
GCAGGACGA
GAM545 TTTTCCAGGAATTTATCGAT 518 TGTAGGGTTT 2194 TT T TC- CTCCTG TTT GT
G
CTCCTGTAGGGTTTCTAGTT CTAGTTTATG TT CCAGGAAT TA GAT TAGGG CTA
TTATGGATGT A
TATGGATGTGAAGATGTTCA GATG || |||||||| || ||| ||||| ||| ||||||||||
TAGTAGTCTTGAATAATCTT AG GGTCTTTA GT CTA GTTCT GAT GATACTTGTA A
TTGTATTTCTGGGGGA GG T TTT ATAA-- --- -- G

GAM546 AAGATGCTGCCAGATAAGGA 519 ATGCTGCCAG 2195 - AAGGA GTCG A C A ATG-
AC
CTGTCGCTATGCCCTCTATG ATAAGGACTG AAGATGC TGCCAGAT CT CT TGC CTCT TG
CA C
ATGCAACCTATGAGACCAAG TCGC ||||||| |||||||| || || ||| |||| || ||
GAGAGCAAGAAGGAGGATCT TTCTATG GTGGTCTA GG GA ACG GAGG AC GT /
GGTGTGTATCTT T GGA-- AA-- - A A CAGA AT

GAM547 GGTGGGGACCCCGGGCCGCA 520 GACAAGATGC 2196 C G---- - C -- G AAT- A
GCCTA
TCCTGGCGCTCGTGCGGAAT TGGAGCAGCT GGA CCCGG CC GCATC TG GCGCTCGT CGG
AGG GCTTCA A
AGGAGCTTCAGCCTAAAGAA GGGC ||| ||||| || ||||| || |||||||| ||| ||| ||||||
TGTGAAGCACTTTGTGCTGG CCT GGGTC GG CGTAG AC TGTGAGCA GTC TTC
CGAAGT A
ACGAGTGTGACAAGATGCTG C GACGA T A AG G GTGT A GTAAG
GAGCAGCTGGGCTCCCCTCC

GAM548 GGGGAGCTGTCTTGTCATCT 521 TCTATAAACC 2197 A C T CTTT--- A
TTTAGAGTAAACTATTCTAT TATGCAAACA GGGG GCTGT TTG CAT TAGAGTA A
AAACCTATGCAAACAGCCCC GCCC |||| ||||| ||| ||| ||||||| |||||||
T TCCC CGACA AAC GTA ATCTTAT /
- - - TCCAAAT C

GAM549 ACCGGTTATGGTGCTGCTGT 522 TGGAGCCTGG 2198 GG T - AC GTTGGAGC
G TT T T
GAACACTGCCAAGTTGGAGC CTCTGTTTGT CGGTTAT TGC GCT GTGA ACTGCCAA
CTGGCTCT T G GCCG C
CTGGCTCTGTTTGTGCCGTC GCCG ||||||| ||| ||| |||| |||||||| |||||||| | | ||||
TTTGGTCTGGGAGGAGTCGG GTCGGTG ATG CGG TACT TGACGGTT GGCTGAGG
G T TGGT T
ATTGGCAGTTATCATGGGCT AA T G AT A------- A GG C T
GTAAAGTGGCTGGT

GAM550 GAAGAGTCTCCTGAGCCTTT 523 TGTCACAGTG 2199 TCTCCT- - T - GA ACC
GAATGTGATCACCTCAAGAA CTTTTCTTTT GAAGAG GAGC CT TGA ATGT TC T
ACATGTCACAGTGCTTTTCT CTTT |||||| |||| || ||| |||| ||
TTTCTTTTC CTTTTC TTCG GA ACT TACA AG /
TTTTCTT T C G A- AAC

GAM551 AGGTCATGAATCATTGCATG 524 GGGAAGATGG 2200 TC A- A CA-- G T C A --
ATA
GGAAGATGGTGGCTATACTG TGGCTATACT AGG ATG ATC TTG TGGGAA ATGG GG TAT
CTGA AC G
AACATAGATACGTACTCAGG GAAC ||| ||| ||| ||| |||||| |||| || ||| |||| ||
TGACTTTCATATTCCCACAC TCC TAC TAG AAC ACCCTT TACT TC GTG GACT TG A
ACAAGATAGCATATCCT TA GA - ACAC A T A - CA CAT

GAM552 TAGCACCAGTATAAATAGTG 525 TAGCACCAGT 2201 C- TAAAT C-- AA- GA
ATTTCATTAATCATTGAATC ATAAATAGTG TAGCAC AGTA AGTGATTT ATT TCATT A
AGATGAAGCAGTTATAAATC ATTT |||||| |||| |||||||| ||| |||||
ACTTTTTACTTTGTGCTA ATCGTG TCAT TCACTAAA TGA AGTAG T
TT TTT-- TAT CGA AC

GAM553 GGGTGGGCAGAAACAGGCAG 526 CAGGGTACAT 2202 --- ACAG- GT TAAAA C
AGA T
GGTACATTTTAAAAGGGCTC TTTAAAAGGG GGGTG GGCAGAA GCAGG ACATTT GGG
TCAGC GT G
AGCAGAGTTGAAACAAAGCT CTCA ||||| ||||||| ||||| |||||| ||| ||||| ||
GAACTCAACCAGATGTCCTG CTTAT CCGTTTT CGTCC TGTAGA CTC AGTCG CA
A
CAGCGATTTTGCCAGGTATT GGA AGCGA -- CCAA- A AAA A
C

GAM554 CACAAATCCAGCACTTCCTC 527 AGCAACACAT 2203 T GCACTTC-- T T- G
TCCATTTACTCTGTCAGGCT ATGGCTTTGT CACAAA CCA CTCTCCAT TAC CT T
GTATATGGGGAGCAACACAT G |||||| ||| |||||||| ||| ||
ATGGCTTTGTG GTGTTT GGT GAGGGGTA ATG GG C
C ATACACAAC T TC A

GAM555 AAAGGTTTTTGGAGCTGCAC 528 GCTGCACTGA 2204 GG CTGAA TC T TAGTA
TCA
TGAAGGCATCTTATTTCTAT AGGCATCTTA AAAGGTTTTT AGCTGCA GGCA TTA TTCTA
TA A
AGTATATCAACCTTTAGTTT TTTC |||||||||| ||||||| |||| ||| ||||| ||
TTAGAATTGACCTGCCAATG TTTCCAGAAG TCGATGT CCGT AGT AAGAT AT C
TAGCTGAAGACCTTT -- AA--- CC T TTTTG TTC

GAM556 ATTGACGCACAGCAGTGGGG 529 TCCTCCAGTG 2205 C A GT TTTACC - CC -- G
A CC T
AGAACAGCGTCTTTTACCTG GCGTTCTTTT AG AGTGGGGAGAAC GC CT TGT CA GAAGC
CA GA GC CGTT G
TCACCGAAGCCAGGAAGCCC TACT || |||||||||||| || || ||| || ||||| || || || ||||
CGTTTGTAAGCGTGTGTTGT TC TCATTTTTCTTG CG GA ACA GT TTTCG GT TT TG
GCGA T
GGTGCTTTATTGTACATCCT - - GT CCTCCT T TA TG G G T- A
CCAGTGGCGTTCTTTTTACT
CTAATGTTCTT
GAM557 ATCTTGACAGTTTTGAGGTA 530 TGAGGTAGTC 2206 TT T CA A A ATATT T- GTTT-
GTTTT
GTCAGGTATTTGTAGAATAT AGGTATTTGT GAGG AGT GGT TTTGT GA CTTCAAC TGG
GTCTGAT T
TCTTCAACTTGGGTTTGTCT AGAA |||| ||| ||| ||||| || ||||||| ||| |||||||
GATGTTTTTCTCATGGTTAG TTCC TCA TCA AGATA CT GAAGTTG ACT CAGATTG
C
ACTATTGTCATTGTTGAAGT CT - -- - - ----- TT GTTAT GTACT
CATAGAACTACTCCTTTCAA
CTACTCTTGT
GAM558 GCAAATCAGTCCATTTCACT 531 CATTTCACTT 2207 - ---------- CAC GAGATA TC
TTCACTGTCTGAGATAGGGT TCACTGTCTG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
CTCTAAGACCCAGGATACAA AGAT ||||||| ||||||| |||||||| ||||| |||||
GGGTGGAATGTAGCTATATG CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GACTCGATTTGC C TATCGATGTA AC- A----- AA

GAM559 ATGGTCCAACTTTGTGGAAT 532 GTAAGGATTT 2208 -- T-- GAATG- AGG AGGG
GG
GGTAAGGATTTTTAGGGTTG TTAGGGTTGT ATGG TCCAACT TGTG GTA ATTTTT
TTGTTT C
TTTGGCCAGAACAAGAGAAA TT |||| ||||||| |||| ||| |||||| ||||||

TAACTGCAGAAAACACATAT TACC AGGTTGG ACAC CGT TAAAGA AACAAG /
GGTTGGAAACCAT AA TAT AAAAGA CAA G--- AC

GAM560 TGGCGGATTAGAAACCCGTA 533 AACCCGTAGA 2209 GGA - G AT C-- TT
GATCAGTTCTAGGTTAGCCC TCAGTTCTAG TGGC TTAGAAAC CC TAG CAGTT TAGG A
TGATTAACTGCCCTGGGTGT G |||| |||||||| || ||| ||||| ||||
TTCTGGGCCA ACCG GGTCTTTG GG GTC GTCAA GTCC /
--- T - CC TTA CG

GAM561 CACACCTGGCTAATTTTTTT 534 AAAGTGCTGT 2210 TTTTTA TT-- A - T TC CA
CTGCCA T TTC
AATTTTTTGATAGAGCTGGG GATTGCAGGT TT ATTTT GAT GAG C GGGG TCAC TG
AGGCT GT A
GTCTCACCATGCTGCCAAGG GTG || ||||| ||| ||| | |||| |||| || ||||| ||
CTTGTTTCAAACTACTGGCC AG TGAAA CTG CTC G CCTC AGTG AC TCCGG
CA A
TCAAGTGATCCTCCTGCCTC TGTCG- CCCT A C T CT A- ------ T TCA
AGTCTCCCAAAGTGCTGTGA
TTGCAGGTGTG
GAM562 GGAGGTGCTGCACTTCCAGT 535 AAGAGCCGCG 2211 G - CA CCAT T -- T
CCATGTGCTCGTGCCTGTGG AGAAGCTGCA GGAG TGCTGCA CTTC GT G GCTC GTGCC G
TACAAGAGCCGCGAGAAGCT GTAC |||| ||||||| |||| || | |||| |||||
GCAGTACTCC CCTC ATGACGT GAAG CG C CGAG CATGG /
- C AG ---- - AA T

GAM563 TCATCTAGACCATTCCGCTG 536 TTAGGGTGGT 2212 C AGCATCTGT - GT-- - G G
CTCTC
GAAGCATCTGTCAGACCAGA AGTTGTGTGC C GCTGGA CAGA CCAGAGTA GC ATCA
TCTAAA TCAG T
GTAGTGCATCAGTCTAAAGT TTTG | |||||| |||| |||||||| || |||| |||||| ||||
CAGCTCTCTCTTCTCTGGTT G CGATTT GTCT GGTTTCGT TG TGGT GGATTT
GGTC /
TAGGGTGGTAGTTGTGTGCT T --------- T GTGT A G - TCTTC
TTGGTTCTGTTTAGCTGAGT
GGGTGAATGA
GAM564 GCTCCAAAGAACCAAGAGTG 537 CATTTCACTT 2213 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM565 AAAGGAAACACTGATGGGAA 538 AACACTGATG 2214 A C T GAA- AT A-- AA
TTATCTATGA AA

AGTATGGGGACAGACTCCAA GGAAAGTATG GGAA CA TGA GG AGT GGGGACAG CTCC
GC CCTG G
GCTTATCTATGACCTGAAGG GGGA |||| || ||| || ||| |||||||| |||| || ||||
ACCAGGGCGGGGAGCTCCTG CCTT GT ACT CC TCG TCCCTGTC GAGG CG
GGAC G
TCCCTTCGCTATGACCTCAC - C - AGTA CT CTC GG ---------- CA
TGTTCCTTT

GAM566 GCTCCAAAGAACCAAGAGTG 539 CATTTCACTT 2215 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM567 TCAGCCAGGATAGGAAGTTG 540 GTGATCAATG 2216 TA -- G A A ACC GA C--- AA
C
GGAATACATAGAACCCACAG TGGTTGCATT GGAAGT TG GA TACAT GA CACAG AGTC
TTCCT GGGGAGTC C
GAAGTCCTTCCTAAGGGGAG GCTT |||||| || || ||||| || ||||| |||| ||||| ||||||||
TCCCTGACTCCTCAGAGGAG TCTTCG AC TT GTGTA CT GTGTC TCAG GAGGA
CTCCTCAG /
AATTGACTCTGTGATCAATG CG TT G G A A-- -- TTAA GA T
TGGTTGCATTGCTTCTGCTC
TGGGCTGG
GAM568 GTCTTTGTGGCACAATTTGA 541 TGGCACAATT 2217 A AT TTCA--- AAC- GACT
ATT-- G G
ATTCAGTAAAACAGGGGAGA TGAATTCAGT GGC CA TTGAA GTAA AGGGGA GGAGGG
GGGA TTT G
CTGGAGGGATTGGGAGTTTG AAAA ||| || ||||| |||| |||||| |||||| |||| |||
GAGAGGTCCCCTTCACCCTC CCG GT AACTT CATT TTTCCT CCTCCC CCCT
GAG /
CTCCTTTAAAATTACAGTAA - C- TCAATGA AAAA ---- ACTTC G A
CTTTCAACTGGCCATAATGC

GAM569 GAGTGATTCAGACTGAGAGT 542 AGAAGGATTT 2218 --- GAGA- - A --------- TTT- A
TAA
GGCTAAATCTAGAAGGATTT TTGGATGCAT CT GTGG CTA ATCTA GAAGGAT
TGGATGC TTA C
TTGGATGCATTATAACCTTT TA || |||| ||| ||||| ||||||| ||||||| |||
TAGGTATTCATCTTATCCTT GA TACC GGT TAGAT TTTCCTA ACTTATG GAT
C
TAGCTAAGAATAGATCTGGA CCC ACAAG A C AAGAATCGA TTCT - TTT
CCATGAACAAGCCCTTCTGA
AATCATCCTC
GAM570 CAAAGATAGTAAGTGGCATA 543 AAAGATAGTA 2219 A A GGCAT --- A
GTCAGGATTTGAACACAGGG AGTGGCATAG CAAAGAT GTA GT AGTCAGGA TTTG A

CTTCCTGACTCTAAAGCCTA TCAG ||||||| ||| || |||||||| ||||
CAATCTTTG GTTTCTA CAT CG TCAGTCCT GGAC C
A C AAATC TCG A

GAM571 CTCTTGAGCATGCTGACCAG 544 GACCAGTGCT 2220 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM572 GTTGATGTCAAATCTCTAGA 545 TCAAATCTCT 2221 - TCA C T TCT-- ---- CTCAG
CTCCTCTGCTGGGCTCAGAC AGACTCCTCT GTT GATG AAT TCTAGAC CC GC TGGG A
CCATACCCATATTGCCATCT GCTG ||| |||| ||| ||||||| || || ||||
GGTGTTTGGACATTCTCATC CGG CTAC TTA AGGTTTG GG CG ACCC C
TGGC T TC- C T TCTAC TTAT ATACC

GAM573 ATCCTGCCACAATATTTTTA 546 CAGTCTTTTG 2222 A A TTAATTACGT---- AT ACAT CC
ACCCATTT
ATTACGTACAAAGATCTGAC TCTCTCTCTT C CA TATTT ACAAAG CTG GTCA
CAGGG C
ATGTCACCCAGGGACCCATT CAAG | || ||||| |||||| ||| |||| |||||
TCACCCACTGCTCTGTTTGG G GT GTAAA TGTTTT GAC CGGT GTCTC /
CCGCCAGTCTTTTGTCTCTC A G CGAACTTCTCTCTC CT CGC- TT
GTCACCCA
TCTTCAAGCAAATGGTGAGG
CGGAT
GAM574 CTCTTGAGCATGCTGACCAG 547 GACCAGTGCT 2223 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM575 TCCGAGATCTGTGCCAATGT 548 TATTGCAACT 2224 AG --- -- CA A ATTGCA
GA
TATTGCAACTTCACTAATTG TCACTAATTG TCCG ATCTGTGC CAATGT TATTG ACTTC CTA
TGCCA T
CATGCCAGATCCGTGGCAGG CATG |||| |||||||| |||||| ||||| ||||| ||| |||||
ACCGTGGGAGGTACGATACA AGGT TAGACGCG GTTACA ATAGC TGGAG GGT
ACGGT C
ACATTGAATGCGCAGATGAT AG TAA AC A- - GCCAGG GC
GGA

GAM576 TGTTTGGGATCTGGTCTGAG 549 GGAAGTTGCT 2225 TC T G C GGCA TG TA A - T C
---- AT
GGGGCGGACGGCACTGATAT GGCTTCAGCT TGG CTGAG GGG GGAC C A TCA C GCTG
GGCC GC TCTC G

CAACGCTGTGGCCCGCTCTC GATG ||| ||||| ||| |||| | | ||| | |||| |||| || ||||
ATGATGGGAAGTTGCTGGCT ATC GATTT TCC CTTG G T AGT G CGAC TCGG CG
AGGG /
TCAGCTGATGACTTTGGCAA -- - G A AAAC GT TC A T T T TTGA TA
AGTTCACCTGTTTAGCTACC
CCTGCTGTCAG
GAM577 ATGCACATCTTAAAAATACA 550 ATACAGTAGA 2226 A AAAAA AGTA ACAACCA AG T
GTAGAACAACCATTGACATA ACAACCATTG ATGC CATCTT TAC GA TTGACAT TG T
GTGTTTACAGCATGTTAAGT ACAT |||| |||||| ||| || ||||||| ||
GTCGTAAGTAATCTGGGGAT TGCG GTAGGG ATG CT AATTGTA AC T
GGCGT - GTCTA AATG GTG---- CG A

GAM578 TCCTTTTGACAAGAAATGTG 551 TGACAAGAAA 2227 T - AAATGT C AA-- CTGTT T
GTCGTGAAAACTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA CTGGA GC
T
GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||
ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T
GA C G GTT--- - GGTA ----- T

GAM579 AGAACCAGTCTTTGTACTCT 552 CCAGTCTTTG 2228 T T T TCTC- AAC AG
CCCTAAACAGCAGCAGGCTT TACTCTCCCT AGAACCAG CTT G AC CCTA AGC C
AGGATTTTGTCAGGCCTGGT AAAC |||||||| ||| | || |||| |||
TCT TCTTGGTC GGA C TG GGAT TCG /
C - - TTTTA --- GA

GAM580 TGACCTGCGTATTTGTGAGT 553 GTGAGTAAGA 2229 A CGT T AGA TT - AGT -- A-
AA
AAGAGTTTCCGGAGTACACT GTTTCCGGAG TG CCTG ATTTG GAGTA GT CC GG ACACTA
CT GTTTGCAA G
ACTAGTTTGCAAAAGCATTG TACA || |||| ||||| ||||| || || || |||||| || ||||||||
TAAGCAAAGCATGGTGTTAG AC GGAC TGAGC CTCGT CA GG CC TGTGGT GA
CGAATGTT /
CCAGGGGACGTGCTCCGAGT - CTT - G-- GG A GAT AC AA AC
TTCCAGGCA

GAM581 CTTTTGCTCCAGATGGTTCA 554 CCAGTGCCTT 2230 TT TCC T ATACTTT T - AA TC
ACA
TACTTTGCTTGGTCACAAGG CAGAACTTTC CT TGC AGA GGTTC GCT GG TCAC GGACA
GC G
ACATCGCACAGTAAAGCTTG TCTT || ||| ||| ||||| ||| || |||| ||||| ||
TTCCGTGGTCCCAGTGCCTT GG ACG TCT TCAAG TGA CC GGTG CTTGT CG T
CAGAACTTTCTCTTGCATGG T- TTC T ACTTCCG C T C- T- AAA

GAM582 TCATAATGGAGGCGGTTACC 555 TAATGATTTT 2231 TA- A C TTA- C CT TCGT A--
TG
CCCATGCTAATCTCGTGATA ATAGGGGCTT TCA ATGG GG GG CCCC ATG AATC GAT
GTGAG A

GTGAGTGAGTTCTCACAAAA TCCC ||| |||| || || |||| ||| |||| ||| |||||
TCTAATGATTTTATAGGGGC GGT TGCC CC CC GGGG TAT TTAG CTA CACTC G
TTTCCCCACCGTGTTTGG TTG A - TTTC A T- TAAT AAA TT

GAM583 TTAAATAACCCGGCATGGAG 556 TATTGCACGT 2232 AA C A ------ TT T
CAGTTTGGTTTCCACCCTAT GGTCCGGCCT TT ATAACC GGC TGGA GCAGT GGT T
TGCACGTGGTCCGGCCTGGT GGTT || |||||| ||| |||| ||||| |||
TATGAAA AA TATTGG CCG GCCT CGTTA CCA C
AG T - GGTGCA TC C

GAM584 TGCACAAATCAAGACTTCTG 557 CATCCAGTGT 2233 A- -- TC TTCT CC CT A TT
TACACTCCATGCCTTGATGA GCTGTCTTTT TGC CA AA AAGAC GTACACT ATGC TG TGA
T
TTTCTTCAGCAGCATCCAGT TTAA ||| || || ||||| ||||||| |||| || |||
GTGCTGTCTTTTTTAATGAA ACG GT TT TTCTG CGTGTGA TACG AC ACT /
GCA AA AA TT T--- CC -- G TC

GAM585 CTTTGTGGGAATGGCTCTAC 558 ACGCACCAGT 2234 TG A TCT----- C CGCAC T A
GA T C C
TTCGTAACGCACCAGTTGAA TGAAATCAGA G GG ATGGC ACTT GTAA CAGT GAA TCA
TAC GT TTC A
ATCAGATACTGTCTTCCAAT TACT | || ||||| |||| |||| |||| ||| ||| ||| || |||
GAAAACGTAAATGATTCACT C CC TACCG TGAA TATT GTCA CTT AGT ATG CA
AAG A
GAAATTATAAGTTATTCAAT CT C TAACTTAT - AAA-- - - AA - A T
GCCATCCCTCCAAAG

GAM586 GCTGGAGGCACCCATAAGGT 559 CACCCATAAG 2235 --- C ATAA - CCTTCTTCAC
TCT CT
TCTGCTGAGAGCCTTCTTCA GTTCTGCTGA G GAGG ACCC GGTTCTGCTGA GAG
TCATATG GGCA G
CTCATATGTCTGGCACTGTG GAGC | |||| |||| |||||||||| ||| ||||||| ||||
TTGCTTTCTATGTGGCCTCT T CTCT TGGG CCAAGACGACT CTC GGTGTAT
TCGT T
CTCTTCAGCAGAACCCACCG TCA T CCAC T TCTCC----- CTT TG
GGTTTCTCACTTAGC

GAM587 GCCTGCCTGAACCCTGGGTC 560 CATGACGGCT 2236 A GG--- - A -- G AA- A- G
C
AGGAGAGAAACACTTGGGGA CTGAGTTCTT CCCT GTCA GGAGAGA ACA CTT GGGAGGGG
AGG CG CGTGGG T
GGGGAAAGGACGGCGTGGGC CCTG |||| |||| ||||||| ||| ||| |||||||| ||| || ||||||
TACCCATGACGGCTCTGAGT GGGA CGGT CCTTTCT TGT GGG TCCTTCTT TCT GC
GTACCC /
TCTTCCTGGGGCTTGTGTCT C GAAGA T G TC G GAG CG A A
TTCCTTGGCAGAAGAGGGCA
CAGCCAAGGC

GAM588 ATATAGCCATTAATATCTAT 561 TATTCATCTT 2237 ATTA TCT GTA-- GA
GGAGTATGTCTGAGGAAAGA GTCCCGGCTG ATATAGCC ATA ATGGA TGTCT G
TAGAATATTCATCTTGTCCC TGT |||||||| ||| ||||| |||||
GGCTGTGT TGTGTCGG TGT TACTT ATAGA G
CCC- TC- ATAAG AA

GAM589 CATGCCGTTTTAGTTCACGA 562 TTGATCATCG 2238 G TAG A GC CTA-- G CA
AGGCCAAGCTAATGCTGGGC TGAAAGCAGA CAT CCGTTT TTCACGA G CAAG ATGCT GG
C
ACTACTGGGCATATATTTTT TGGA ||| |||||| ||||||| | |||| ||||| ||
GATCATCGTGAAAGCAGATG GTA GGTAGA AAGTGCT C GTTT TACGG TC /
GATG - CGA A TA TTATA G AT

GAM590 TCAAATCATCGGTTTTCAGT 563 CACCTGTAGA 2239 AAA T T-- - GGAT C
TTGGATGGTGGCTCATCACC ACCTGACTTG TC TCA CGGTT TCAG TTT GGTGG T
TGTAGAACCTGACTTGGCCG GCCG || ||| ||||| |||| ||| |||||
TGGCTGGA AG GGT GCCGG AGTC AAG CCACT C
GTC - TTC C ATGT A

GAM591 CTGAGAATCCACAATACAGT 564 TACAGTAGTG 2240 - ATCC- TA----- T TAAC- GAA
AGTGTGGATAACTTTCAAGA TGGATAACTT CTG AGA ACAA CAG AGTGTGGA TTTCAA
G
AGCCATTGGAAACATCTCCA TCAA ||| ||| |||| ||| |||||||| ||||||
CATTCTGGGATGACTTGTAA GAC TCT TGTT GTC TTACACCT AAGGTT /
ATGTCTACAG A GTAAA CAGTAGG - CTACA ACC

GAM592 TTGTCTGGAGAAAGGACTAG 565 GGACTAGAGA 2241 A A A----- ---- - ATGTA - C
AA
AGAGAAATCCAGCTCAGATG GAAATCCAGC CT GAGAGAA TCCAG CTC AG TTGCTC
ATTCCT TTCAG G
TATTGCTCATTCCTCTTCAG TCAG || ||||||| ||||| ||| || |||||| |||||| |||||
AAGGACTGGGTGGGAATGGA GA TTTTCTT AGGTC GAG TC GACGAG TAAGGG
GGGTC /
GCAGGGGCTAGAGGAATCTG - - AATCGA TAAG A GGG-- G T AG
GAAGCTAATTCTTTTAGGCT
TTTTCCAACAG
GAM593 TGTTTGGGATCTGGTCTGAG 566 GGAAGTTGCT 2242 TC T G C GGCA TG TA A - T C
---- AT
GGGGCGGACGGCACTGATAT GGCTTCAGCT TGG CTGAG GGG GGAC C A TCA C GCTG
GGCC GC TCTC G
CAACGCTGTGGCCCGCTCTC GATG ||| ||||| ||| |||| | | ||| | |||| |||| || ||||
ATGATGGGAAGTTGCTGGCT ATC GATTT TCC CTTG G T AGT G CGAC TCGG CG
AGGG /
TCAGCTGATGACTTTGGCAA -- - G A AAAC GT TC A T T T TTGA TA
AGTTCACCTGTTTAGCTACC
CCTGCTGTCAG

GAM594 TCAGGCACTGAGTTCATTTC 567 TATTGCACTG 2243 CA- A TTTC C - CCT--- C---
CTAG
ACTGACACGGGCCCTGGACT TCTCAGTTTG TCAGG CTG GTTCA ACTGA ACGG GC
GGACT CCAC A
CCCACCTAGAACATGTGGAT AACC ||||| ||| ||||| ||||| |||| || ||||| ||||
TTAGTTCTCTATTGCACTGT AGTTC GAC CAAGT TGACT TGTC CG CTTGA GGTG
/
CTCAGTTTGAACCAGATACT ATA - T--- C A TTATCT TTTA TACA
TGA

GAM595 GCCTGCCTGAACCCTGGGTC 568 CATGACGGCT 2244 A GG--- - A -- G AA- A- G
C
AGGAGAGAAACACTTGGGGA CTGAGTTCTT CCCT GTCA GGAGAGA ACA CTT GGGAGGGG
AGG CG CGTGGG T
GGGGAAAGGACGGCGTGGGC CCTG |||| |||| ||||||| ||| ||| |||||||| ||| || ||||||
TACCCATGACGGCTCTGAGT GGGA CGGT CCTTTCT TGT GGG TCCTTCTT TCT GC
GTACCC /
TCTTCCTGGGGCTTGTGTCT C GAAGA T G TC G GAG CG A A
TTCCTTGGCAGAAGAGGGCA
CAGCCAAGGC
GAM596 GCTCCAAAGAACCAAGAGTG 569 CATTTCACTT 2245 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM597 GTCGTCGGGAAGGAACAAGA 570 CAGAGCAATT 2246 - AA ACA -- CA - AGAATA T
GGAAATTA
GGCTCCAGTTGGAGTGCTCA TTAACAGAGG GG GGA AGAGG CTC GTTGGAGT GCTC
CTCC CGA C
GAATACTCCTCGAGGAAATT CCCT || ||| ||||| ||| |||||||| |||| |||| |||
ACAATGAAAGTCGTGGAGGC CC CCT TCTCC GAG CAATTTTA CGAG GAGG GCT
/
CAGAGCAATTTTAACAGAGG A A- --- CG A- A ACCG-- T GAAAGTAA
CCCTCTTCCACCATTACGAC

GAM598 CTGGAGGAACTTGCTTTGTA 571 TGACAGAGGA 2247 A T A AGA------- AGC - AG
CCAGATCCAGCTGCTGAAGG CAAAGTCAGC CTGGAGGA CT GCTTTGT CC TCC TG
CTGA G
ACCTCAGACATACGGAGAAT TCCT |||||||| || ||||||| || ||| || ||||
GACAGAGGACAAAGTCAGCT GACCTCCT GA TGAAACA GG AGG AC GACT A
CCTCCAG C C - AGACAGTAAG CAT A CC

GAM599 AAGGGTTGTTTTGTTGTTAG 572 TGAAGCTAGA 2248 T TGTTGT AA A-- GTCCATT
GTAAATAGATATTAGGCAGT TACCTAAAGC AAGGGT GTTT TAGGTA TAG TATTAGGCA
T

CCATTTCTAAAATATGCCTG TACC |||||| |||| |||||| ||| |||||||||
ATGAAGCTAGATACCTAAAG TTCCCA CGAA ATCCAT ATC GTAGTCCGT C
CTACCCTT T ------ AG GAA ATAAAAT

GAM600 TCCTTTTGACAAGAAATGTG 573 TGACAAGAAA 2249 T - AAATGT C AA-- CTGTT T
GTCGTGAAAATTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA TTGGA GC
T
GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||
ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T
GA C G GTT--- - GGTA ----- T

GAM601 TTCCTTCCTCCAGGCAGCTC 574 TCGTTAACCT 2250 CC C TCACAGAC - --- C T
AGAGT
ACAGACATGACCTCATTCCC CTGCTTCCTA TTCCTTCCT AGG AGC ATGA CCTCAT TCC
TC CCC C
TCTCCCAGAGTCCCATAGGG GGGA ||||||||| ||| ||| |||| |||||| ||| || |||
GTGAAGGACAGGTGGGGATC AAGGAGGGA TCC TCG TGCT GGGGTG AGG AG
GGG C
GTTAACCTCTGCTTCCTAGG -- T TCTCCAAT A GAC A T GATAC
GAGGAA

GAM602 AGAATGGGGAAGAATACTGA 575 TTGGAGCAGG 2251 - - TA AA T CA TCT AC-
CT
ATTAGCTGAGCACATTCTGG TTTCATTCTC AGAAT GGGGAA GAA CTG TTAGC GAG CAT
GGAC AATT G
ACACAATTCTGACCAATTTC CAAT ||||| |||||| ||| ||| ||||| ||| ||| |||| ||||
AGTCTCATGATCTCTGTTGG TCTTA CCTCTT CTT GAC GGTTG CTC GTA TCTG
TTAA A
AGCAGGTTTCATTCTCCAAT A A TG GA T TA C-- ACT CC
TCT

GAM603 GCAGCAGAGAGGCCCCTTTC 576 ACTCAGTGAA 2252 A GC CT AGGT GGG
AAGGTGTTCGGGTAAAGAAC GGAACTCCTG GCAGCAG GAG CC TTCA GTTC T
TCAGTGAAGGAACTCCTGTT TTGC ||||||| ||| || |||| ||||
GC CGTTGTC CTC GG AAGT CAAG /
- AA -- GACT AAA

GAM604 CAGCCTCCCACTGTGGTGCC 577 TCGCCTGGAC 2253 CC - G T G A - AA CAGAGA
- CA T
TGGTGGAGACCTGGCCAAGG CACAAGTTTG ACT GTGGT CC GGTG AG CCT GGCC GGTA
GCTGTG TG TGC G
TACAGAGAGCTGTGTGCATG ACCT ||| ||||| || |||| || ||| |||| |||| |||||| || |||
CTGAGCAACACCACAGCCAT TGA CACCA GG CCGC TC GGG CCGG TCGT
CGACAC AC ACG /
TGCTGAGGCCTGGGCTCGCC TT A - T - - T AG TAC--- C A- A
TGGACCACAAGTTTGACCTG

GAM605 TGTTGGGTACTAGACATGTT 578 TTGGGTACTA 2254 G CT-- C CTAGC TCTACCCA
T
TGCTAGCTGACCATCTACCC GACATGTTTG TGTT GGTA AGA ATGTTTG TGACCA AC G
AACTGAAGTATGCCTTTGGT CTAG |||| |||| ||| ||||||| |||||| ||
CATAAGCATTTCTTATCTAC ACAA CCAT TCT TACGAAT ACTGGT TG A
CGAACA G CTAT T ----- TTCCGTA- A

GAM606 TGGATACAAGCCTAAGCTTC 579 TGTGGGGCCT 2255 C TAA TTTTAA AA
ATTTTTAATGAAAAAGTCTT GGTTTTTGTT TGGATA AAGCC GCTTCAT TGAA A
CAGTTGTGTGGGGCCTGGTT CA |||||| ||||| ||||||| ||||
TTTGTTCA ACTTGT TTTGG CGGGGTG ACTT G
T TC- TGTTG- CT

GAM607 GCTCCTCCGGCCTCAGCCTC 580 TACCTGGGAC 2256 C-- CA TCT---- TA GGA
TGTG TTTG
TCGAGTACCTGGGACTACAA TACAAGTGTG CTCCGGCCT GCC CGAG CCTG CTACAAG
AGCCAG G
GTGTGAGCCAGTTTGGTAAT AGCC ||||||||| ||| |||| |||| ||||||| ||||||
TTTGGCTAATTTTTGTAGAA GAGGTCGGA CGG GCTC GGGC GATGTTT
TCGGTT T
ACGGGGTCTCGCCATGTTGG CGT C- TTGTACC TG AAA TTAA TTAA
CCAGGCTGGAGTGCAGC

GAM608 CTGGCTCCTGAGGTGGCTGA 581 GTAGAGCAAA 2257 C- GT GC A GA C G G GT
TCGAATTGGGGACTATGTCC TGTTTCAGGA CTGG TCCTGAG G TG TC ATTGGGGA TAT
TCCA T C
AGTGTCATGGTGGGGTATCC TCCC |||| ||||||| | || || |||||||| ||| |||| |
CTAGTAGAGCAAATGTTTCA GACC AGGACTT T AC AG TGATCCCT ATG GGGT G /
GGATCCCAG CT TG AA G A- - - G TA

GAM609 TCCTTTTGACAAGAAATGTG 582 TGACAAGAAA 2258 T - AAATGT C AA-- CTGTT T
GTCGTGAAAATTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA TTGGA GC
T
GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||
ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T
GA C G GTT--- - GGTA ----- T

GAM610 TCTGGACAAAGTAGGTGGTC 583 TGCATGGAAA 2259 CAA G G AG C TC
AGTTTCCATCCATGTTCCAT GAGTATGTAT TCTGGA AGTA GTG TC TTTCCAT CATGT C
ATATGCATGGAAAGAGTATG TCTT |||||| |||| ||| || ||||||| |||||
TATTCTTTTCAGA AGACTT TTAT TAT AG AAAGGTA GTATA /
TTC G G -- C TA

GAM611 CACACCTGGCTAATTTATCC 584 AAAGTGCTGT 2260 TATC TAT- CAA- T TC CA
CTGCCA T TTC

ACTTTTATGATCAAGCTGGG GATTGCAGGT ATT CACTTT GAT GC GGGG TCAC TG
AGGCT GT A
GTCTCACCATGCTGCCAAGG GTG ||| |||||| ||| || |||| |||| || ||||| ||
CTTGTTTCAAACTACTGGCC TAG GTGAAA CTG CG CCTC AGTG AC TCCGG
CA A
TCAAGTGATCCTCCTGCCTC TGTC CCCT ACTC T CT A- ------ T TCA
AGTCTCCCAAAGTGCTGTGA
TTGCAGGTGTG
GAM612 ACTATGGGGACAAGATGTTG 585 GGGACAAGAT 2261 - A TG CGCAT AAA CCAC
- A
CGCATGCAGAAAGGTGACCC GTTGCGCATG ACTATGGG GACA GA TTG GCAG GGTGAC
AAGT CT T
ACAAGTCTATGAAGAACTTT CAGA |||||||| |||| || ||| |||| |||||| |||| ||
TCAGTTACTCCTGCCCCAAG TGATGTCC CTGT CT AAC CGTC TCATTG TTCA GA
G
TTCCTGTCGCCTGTAGT G C TG CC--- C-- ACTT A A

GAM613 CTCCAAAGAACCAAGAGTGC 586 CATTTCACTT 2262 T - ---------- CAC AGATA
TC
AAATCAGTCCATTTCACTTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT
TGTCTG GGGTC T
CACTGTCTGAGATAGGGTCT AGAT ||| ||||||| ||||||| |||||||| |||||| |||||
CTAAGACCCACGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGGC
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A---- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAG
GAM614 CAGAAGGGGTTTTTATCAAA 587 AGAAGTAGTA 2263 AG- TTTA GTAG---- - AA
AG AA
AATATGTAGATTCTACTACA GTAGCAGTAG AGA GGGTT TCAAAAATAT ATT CTACTAC
TATTTT CT A
ATATTTTAGCTAAAGAAGAA TAGT ||| ||||| |||||||||| ||| ||||||| |||||| ||
GAAGTAGTAGTAGCAGTAGT TCT CCCAG AGTTTTTATG TGA GATGATG
ATGAAG GA /
AGTCAGTATTTTTGACCCTG CAA TCCC ACTGATGA C -- AA AG
ACCCAACTCTG

GAM615 CTTCCTTGATGCATCTCGAC 588 GACTGGAGAG 2264 TTGA A- GA CA --- AG
ACATCCTTGAAGCACCTCAA AAGGCACTTG CTTCC TGC TCTC CA TCC TTGA C
CATGGACTGGAGAGAAGGCA GAAG ||||| ||| |||| || ||| ||||
CTTGGAAG GAAGG ACG AGAG GT AGG AACT A
TTC- GA AG C- TAC CC

GAM616 GCTCCAAAGAACCAAGAGTG 589 CATTTCACTT 2265 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||

TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM617 TCAGGAATACAAGAATCAAC 590 TAGAATGTAA 2266 A GA AAC -------- - CATA
TCCA TC
TGCTGGTTCCATAGCTTCTG CAGATGTTGT AGGA TACAA ATC TGC TG GTTC
GCTTCTGGA GTG C
GATCCAGTGTCCCTTTACCT AATC |||| ||||| ||| ||| || |||| |||||||||| |||
TCAGAAGCCTGAACACACTT TTCT ATGTT TAG ATG AC CAAG CGAAGACTT
CAT C
AGAATGTAACAGATGTTGTA A G- ACA TAAGATTC A TC-- C--- TT
ATCTTGA

GAM618 TGAAGACTTCCTAAATTTGC 591 TTTGCACATT 2267 AC A TTGCA TTGCC
ACCAT
ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM619 GCCTTGGTCGTGTCGTCCTG 592 CTTGGTCGTG 2268 T--- T- A--- AG -- ACTG
CC
CACGCAGTTGGTGCACTGGG TCGTCCTGCA GCCTTGGTCGTG CG CCTGC CGC TTGG
TGC GGCGC A
CGCCCACCAGCGCCACTAGC CGCA |||||||||||| || ||||| ||| |||| ||| ||||||
ATCCCGAAGGCGGTCAGCAG CGGGATTAGCAC GT GGACG GCG AGCC ACG
CCGCG C
GTTTGTCACCACGATTAGGG CACT TT ACTG GA CT ATCA AC
C

GAM620 GCTCCAAAGAACCAAGAGTG 593 CATTTCACTT 2269 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM621 AGAATCCGTGTGTAGTGTGT 594 ATTGGTGGTA 2270 C T T - CACA TAC
CCTGCCT AGA
TCTACATAAGCACATACTTA CCTTATGGTA C GTGTGTAGTG GT CTAC ATAAG TACT TTTTG
AGATGC C
CTTTTGCCTGCCTAGATGCA GACT | |||||||||| || |||| ||||| |||| ||||| ||||||
GACACAGGTATCTTATACTT G TATACGTTAT CA GATG TATTC GTGG AAAAC
TCTATG A

CAAAATTGGTGGTACCTTAT C - - G CATG TT- TTCATAT GAC
GGTAGACTATTGCATATCGA
TTCT
GAM622 TCCTTTTGACAAGAAATGTG 595 TGACAAGAAA 2271 T - AAATGT C AA-- CTGTT T
GTCGTGAAAATTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA TTGGA GC
T
GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||
ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T
GA C G GTT--- - GGTA ----- T

GAM623 ACTTCGACACCTACGACGAT 596 GGCCATGGTT 2272 GACAC AC- - TA GA- T C
TG GC
CGGGCCTACAGCAGACTTCG CCCTGTAGCC ACTTC CTACG GATCG GGCC CAGCA CT
CGG GGC T A
GCGGCTGTGCAGAGTGGTCC AGAA ||||| ||||| ||||| |||| ||||| || ||| ||| |
CGCGGCAGTGCTGGTGGCCA TGAAG GATGT TTGGT CCGG GTCGT GG GCC CTG
G /
TGGTTCCCTGTAGCCAGAAG ACC-- CCC A TG GAC C - GT AG
T

GAM624 TGAAGACTTCCTAAATTTGC 597 TTTGCACATT 2273 AC A TTGCA TTGCC
ACCAT
ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM625 CGAGCGGGCCCTGCCGCCAG 598 TGTGCAAATC 2274 - C C GAGGGTTG TCT A
G
AGAGGGTTGGGCATGTCTAT CATGCTTCTG CGA GCGGGCC TGCCG CAGA GGCATG
ATTTG GCGAG T
TTGAGCGAGGTCATTTGTGC ATGG ||| ||||||| ||||| |||| |||||| ||||| |||||
AAATCCATGCTTCTGATGGT GCT TGCCCGG ATGGT GTCT TCGTAC TAAAC TGTTT
C
AGGCCCGTATCG A - A -------- C-- G A

GAM626 ACTGCATTGAGAGGGAGTTG 599 ACTGCATTGA 2275 GCATT- A- G AAAT A ATGA
TGGGAAATAAGAAGAATGAA GAGGGAGTTG ACT GAG GGGA TTGTGGG AAGA GA A
AGCCTCTCTTTCTGTCCGCA TGGG ||| ||| |||| ||||||| |||| ||
GATCCTGACTTTTCCAAAGT TGA TTC TCCT GACGCCT TTCT CT /
AACCTT AG A GTCT - CCGA

GAM627 GTCCAGTGCGTGTACTGTAC 600 TGTACACATC 2276 C G TA TACACATCC A - - CT
TC G
ACATCCACACTCATTCTCAC CACACTCATT GTC AGTGC TG CTG AC CTCA TTCT CA
CAGGGT CCG A

TCAGGGTTCCCGGACCGGCT CTCA ||| ||||| || ||| || |||| |||| || |||||| |||
GTCCTGCCTGCGGAACTGAG CAG TCATG AC GAT TG GAGT AAGG GT GTCCTG
GGC /
GTAAACTAGCTCAGGTACTG - G TC CAAA----- - C C CC TC C
AC

GAM628 CTCTTGAGCATGCTGACCAG 601 GACCAGTGCT 2277 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM629 ACCGGTTATGGTGCTGCTGT 602 TGGAGCCTGG 2278 GG T - AC GTTGGAGC
G TT T T
GAACACTGCCAAGTTGGAGC CTCTGTTTGT CGGTTAT TGC GCT GTGA ACTGCCAA
CTGGCTCT T G GCCG C
CTGGCTCTGTTTGTGCCGTC GCCG ||||||| ||| ||| |||| |||||||| |||||||| | | ||||
TTTGGTCTGGGAGGAGTCGG GTCGGTG ATG CGG TACT TGACGGTT GGCTGAGG
G T TGGT T
ATTGGCAGTTATCATGGGCT AA T G AT A------- A GG C T
GTAAAGTGGCTGGT

GAM630 TGCTTCTTTGCAAGGTATTA 603 AAGGTATTAG 2279 T A ---- T GTATG T
GGTTGTCATTGTATGGATTA GTTGTCATTG TGCTTCTT GCA GGTATT AGGT GTCATT GAT
A
TAATCAAAATGACACTTCAC TATG |||||||| ||| |||||| |||| |||||| |||
AAATACCTGTTGAGGAGTA ATGAGGAG TGT CCATAA TTCA CAGTAA CTA T
T - ACAC - AA--- A

GAM631 CCGGGCCGCATCCTGGCGCT 604 GACAAGATGC 2280 G---- - C -- G AAT- A
GCCTA
CGTGCGGAATAGGAGCTTCA TGGAGCAGCT CCGG CC GCATC TG GCGCTCGT CGG AGG
GCTTCA A
GCCTAAAGAATGTGAAGCAC GG |||| || ||||| || |||||||| ||| ||| ||||||
TTTGTGCTGGACGAGTGTGA GGTC GG CGTAG AC TGTGAGCA GTC TTC CGAAGT
A
CAAGATGCTGGAGCAGCTGG GACGA T A AG G GTGT A GTAAG

GAM632 GCTCCAAAGAACCAAGAGTG 605 CATTTCACTT 2281 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC

TTTTCCAGAGC
GAM633 GCCTGCCTGAACCCTGGGTC 606 CATGACGGCT 2282 A GG--- - A -- G AA- A- G
C
AGGAGAGAAACACTTGGGGA CTGAGTTCTT CCCT GTCA GGAGAGA ACA CTT GGGAGGGG
AGG CG CGTGGG T
GGGGAAAGGACGGCGTGGGC CCTG |||| |||| ||||||| ||| ||| |||||||| ||| || ||||||
TACCCATGACGGCTCTGAGT GGGA CGGT CCTTTCT TGT GGG TCCTTCTT TCT GC
GTACCC /
TCTTCCTGGGGCTTGTGTCT C GAAGA T G TC G GAG CG A A
TTCCTTGGCAGAAGAGGGCA
CAGCCAAGGC
GAM634 GCCTGCCTGAACCCTGGGTC 607 CATGACGGCT 2283 A GG--- - A -- G AA- A- G
C
AGGAGAGAAACACTTGGGGA CTGAGTTCTT CCCT GTCA GGAGAGA ACA CTT GGGAGGGG
AGG CG CGTGGG T
GGGGAAAGGACGGCGTGGGC CCTG |||| |||| ||||||| ||| ||| |||||||| ||| || ||||||
TACCCATGACGGCTCTGAGT GGGA CGGT CCTTTCT TGT GGG TCCTTCTT TCT GC
GTACCC /
TCTTCCTGGGGCTTGTGTCT C GAAGA T G TC G GAG CG A A
TTCCTTGGCAGAAGAGGGCA
CAGCCAAGGC
GAM635 AGCCATATCTTGTGGTATGT 608 AACAGTATCT 2284 A -- TA-- A ATTTC
TTATAACGTATTTCTTTCAC ACTAAAGATG AGCC TATCTT GTGG TGTTT TAACGT T
ATGTTAAAACAGTATCTACT GGCT |||| |||||| |||| ||||| ||||||
AAAGATGGGCT TCGG GTAGAA CATC ACAAA ATTGTA /
- AT TATG - CACTT

GAM636 GGATTAGAAACCCGTAGATC 609 AACCCGTAGA 2285 A CG- AT C-- TT
AGTTCTAGGTTAGCCCCTGA TCAGTTCTAG GG TTAGAAACC TAG CAGTT TAGG A
TTAACTGCCCTGGGTGGTTT G || ||||||||| ||| ||||| ||||
CTGGGCC CC GGTCTTTGG GTC GTCAA GTCC G
G TGG CC TTA CC

GAM637 GCCTGAGAAATGAAGGTGTG 610 TGAAGGTGTG 2286 AA-- G ----- TC GCTCC-- A
AGTTCTGTGCTCCTGGGATC AGTTCTGTGC GCCTGAG AT AAGGT GTGAGT TGT
TGGG T
ATCCACTCCTGAACAACTCA TCCT ||||||| || ||||| |||||| ||| ||||
TTGAAAACCTTGGTGCCATT TGGACTT TG TTCCA TACTCA ACA ACCT C
CAGGT ACCG G AAAGT -- AGTCCTC A

GAM638 AGTGGGTGCACAAGTGATGG 611 GTAAGGATTT 2287 - -- T-- GAATG- AGG
AGGG GG
TCCAACTTTGTGGAATGGTA TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
AGGATTTTTAGGGTTGTTTG TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
GCCAGAACAAGAGAAATAAC TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /

TGCAGAAAACACATATGGTT G AA TAT AAAAGA CAA G--- AC
GGAAACCATGCGCTTGTGAC
TTTTCT
GAM639 GAAGACTTCCTAAATTTGCA 612 TTTGCACATT 2288 AC A TTGCA TTGCC ACCAT
CATTAGCTAGATTGCCATTA AGCTAGATTG GAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
GCACCATTAGAGAGTTGATC CCAT |||| ||||| ||| |||||||||| ||||||
TTTGGCTAATGATTATTCAG CTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GAAAATTTC AA C TTA-- C---- AGAGA

GAM640 TTTATGTGTTGTCGTGCAGG 613 TATGTGTTGT 2289 A TG GTG AGA G G
TAGAGGGCAAGTAATTGGTT CGTGCAGGTA TTT TGTGT TC CAGGT GG CAA T
GAGGCCTGAAGGATGACATA GAGG ||| ||||| || ||||| || |||
CAAG GAA ATACA AG GTCCG TT GTT A
C GT GAA GAG G A

GAM641 TCAGTGTTTGCTTCAGAGTT 614 TGAGGAAGAT 2290 TG TGC AGT AA-- TG - AA
TGAGGAAGATGTTGGATTGT GTTGGATTGT TCAG TT TTCAG TTGAGG GA TTGGA TTGTT
A
TAAATAAAGCAGCTCCAGTT T |||| || ||||| |||||| || ||||| |||||
TCAGGACCTCGACTGGATTT AGTC AG AGGTC AGCTCC CT GACCT GACGA T
GATCCTGA CT TTT --- AGGA TT C AA

GAM642 AGGGGGGCAAAGTCTATCAG 615 GGGGCAAAGT 2291 G GT A TG TTGAAA TG-
AG G GAT
GTGTTTGAAAGTGTGGCTAA CTATCAGGTG AGGG GGCAAA CT TCAGG T GTG GCTAAGA
TAT ATGT G
GAAGTATGATGTGATGAATG TTTG |||| |||||| || ||||| | ||| ||||||| ||| ||||
ATATGATGAGTCTTGGTATC TCTC TCGTTT GA GGTTT G TAC TGGTTCT GTA
TATA A
CATCGTGTTTGGAAGGATTT G AG A GT C----- CTA GA G GTA
GCTGCTCT

GAM643 CTCCGTGATCTCACTTATAT 616 TCACAGAAGC 2292 G A - ATA--- G AAA
GTGGAATCTAAAAATGATAG AGAGTGTAGA CTCC TG TCT CACTT TGTG AATCTA A
ATTCACAGAAGCAGAGTGTA CAGG |||| || ||| ||||| |||| ||||||
GACAGGAG GAGG AC AGA GTGAG ACAC TTAGAT /
- - T ACGAAG - AGT

GAM644 ATTCCATGTTTGTGGCTCAA 617 TTCACAGTGC 2293 CT ATG CACTTAAATT C TG TCAA
TCT - A CC
TGTCTTACACTTAAATTTCA CTCAAGATTC TGG CA TCTTA TCA AG CC GAT CA GG
GGGCA C
CAGTGCCTCAAGATTCTCAG TCAG ||| || ||||| ||| || || ||| || || |||||
GAGGGCACCCACATGTTCCC ACC GT GGAAT AGT TC GG CTA GT CC CTTGT
A

ATGCGTATCCGGTGCTTTGA TT AA- AC-------- T GT C--- TGC A - AC
CATAAGGAATGTTCCATATC
CATGGCCGAT
GAM645 GTGCTGCAGGAGGCGGCTCA 618 AGGCGGCTCA 2294 - CAG C C AAGAACTAC
CTG
GTGTGAAGAACTACGGGTTT GTGTGAAGAA GTGC TG GAGG GG TCAGTGTG GGGTTTC
A
CCTGATGTTGAAGCTCAGAA CTAC |||| || |||| || |||||||| |||||||
TTAGCCACACTGACCTTCTC TACG AC CTCT CC AGTCACAC CTCGAAG T
AGTCATGCAT T TGA T - CGATTAAGA TTG

GAM646 ACAGTGAGCAAAAGCTTTTA 619 TGAGCAAAAG 2295 T - AAAA --- CCT
GGTGTCCTCAGTACATTTTA CTTTTAGGTG ACAG GA GC GCTTTT AGGTGT C
AGAGAGTGCAAGCGTCCTGT T |||| || || |||||| ||||||
TGTC CT CG TGAGAG TTTACA /
- G AACG AAT TGA

GAM647 CCTTGTGACAAGAAATGTGG 620 TGACAAGAAA 2296 - AAATGT C AA-- CTGTT T
TCGTGAAAATTGGACTGTTG TGTGGTCGTG CCTTGTGAC AAG GGT GTGAA TTGGA GC
T
CTTCTGCTCCAGATGGTTCA AAAA ||||||||| ||| ||| ||||| ||||| ||
TACTTTGCTTGGTCACAAGG GGAACACTG TTC TCA TACTT GACCT CG C
G GTT--- - GGTA ----- T

GAM648 ACCTTGGAAGAGAAAGAAGT 621 TGGAAGAGAA 2297 TT A AGA G ---- ATA
TTGTAGGTTGGAATACACAT AGAAGTTTGT ACC GGA GAGAA AGTTT TAGGTT GGA C
CTGGAGAATTTGGAAACTAT AGGT ||| ||| ||||| ||||| |||||| |||
TCTCTCTTGGT TGG TCT CTCTT TCAAA GTTTAA TCT /
T- - A-- G GAGG ACA

GAM649 TTTGGCAGAGAATGACTCTG 622 TTAGGGCTAG 2298 GA CT AG TA ------ T TC TT
A AAA
CAGTTAAGCTAAGGGCGTGT TCGTTTGTGC CA GAATGACT GC TTAAGC AG GGCG GT
AGA GTGG GG A
TCAGATTGTGGAGGAAAAGT TAAG || |||||||| || |||||| || |||| || ||| |||| ||
GGCCGCCATTTTAGACTTGC GT TTTGCTGA CG GATTCG TC CCGT CA TTT TACC
CC G
CGCATAACTCGGCTTAGGGC G- T- G- GC AATACG T GA -- G GGT
TAGTCGTTTGTGCTAAG

GAM650 GTGCCAACCTGAGGGGCGCG 623 AGCTGCCGGT 2299 AA- - G CG---- CA--- -- AC
GA G
ATGGTTGCAGCCAGATCGGG TGAAGTGCTG CCT GAGGG CG ATGGTTGCAGC
GATCGG GC CCA GTC G
CACCCAGAGTCGGTGATAGT TAGC ||| ||||| || |||||||||| |||||| || ||| |||
GGAGCTGCCGGTTGAAGTGC GGA CTCCT GT TACCGATGTCG TTGGCC CG
GGT TAG /

TGTAGCCATAATACATGGTC AGA A G ACATAA TGAAG GT A- GA T
CTCAAGGAGATGCGC

GAM651 GGACAGAAGATATAGTGAGG 624 TTGCATCTAG 2300 -- G GG --- AG G - G C-- GC
CTCCAC
GTTGTGCATGAGAGGGATCT CACAAAACTG ATAGT AG TTGTGC ATG AGG AT CT CCA
AGACAT CT T
GCCACAGACATGCCTCTCCA ATTA ||||| || |||||| ||| ||| || || ||| |||||| ||
CTCCCAACAGAAATGTCTTT TATTA TC AACACG TAC TCC TA GA GGT TCTGTA GA
/
CTGGAAGAATGCCTTGCATC GT G AA ATC GT G A A CTT AA CAACCC
TAGCACAAAACTGATTATTG
CCCCTCTGTCC
GAM652 ACTACCAGCCTCCCACTGTG 625 TCGCCTGGAC 2301 CC - G T G A - AA CAGAGA
- CA T
GTGCCTGGTGGAGACCTGGC CACAAGTTTG ACT GTGGT CC GGTG AG CCT GGCC GGTA
GCTGTG TG TGC G
CAAGGTACAGAGAGCTGTGT ACCT ||| ||||| || |||| || ||| |||| |||| |||||| || |||
GCATGCTGAGCAACACCACA TGA CACCA GG CCGC TC GGG CCGG TCGT
CGACAC AC ACG /
GCCATTGCTGAGGCCTGGGC TT A - T - - T AG TAC--- C A- A
TCGCCTGGACCACAAGTTTG
ACCTGATGT
GAM653 TGCACAAATCAAGACTTCTG 626 CATCCAGTGT 2302 A- -- TC TTCT CC CT A TT
TACACTCCATGCCTTGATGA GCTGTCTTTT TGC CA AA AAGAC GTACACT ATGC TG TGA
T
TTTCTTCAGCAGCATCCAGT TTAA ||| || || ||||| ||||||| |||| || |||
GTGCTGTCTTTTTTAATGAA ACG GT TT TTCTG CGTGTGA TACG AC ACT /
GCA AA AA TT T--- CC -- G TC

GAM654 CAGGACTTTATGTGGATCCG 627 TGGATCCGTA 2303 TATG CC TG- TT AT - GA----
ATA- AGA
TATGAGTTGGCTTCATTACG TGAGTTGGCT T TGGAT GTA AG GGCTTC TA CGAGA
GAAAC AC G
AGAGAGAAACATAACAGAGG TCAT | ||||| ||| || |||||| || ||||| ||||| ||
CAGTGATGGTTTCAGAAAAT G ACCTG TAT TC CCGGAG AT GTTTT CTTTG TG
/
TTTGATATAGAGGCCCCTAA GA-- TT CAA C- AT A AAAAGA GTAG ACG
CTATTTGTCCAAGGAGTCTG

GAM655 CACAAGTGATGGTCCAACTT 628 GTAAGGATTT 2304 - -- T-- GAATG- AGG AGGG
GG
TGTGGAATGGTAAGGATTTT TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
TAGGGTTGTTTGGCCAGAAC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
AAGAGAAATAACTGCAGAAA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /
ACACATATGGTTGGAAACCA G AA TAT AAAAGA CAA G--- AC
TGCGCTTGTG

GAM656 TCTCCAAAATTAGTTTTTAA 629 TTTAATACAT 2305 --- - T TAG ATACAAAGA G- A TG T

TACATTCAGGTAGGTTATAC TCAGGTAGGT TTTTT AATAC AT CAGG GTT GTTG TCCCG GGCC GGC G

AAAGAGTTGGTCCCGAGGCC TATA ||||| ||||| || |||| ||| |||| ||||| |||| |||

TGGGCTGAGGCCTGGGCCCT AGAAA TTGTG TG GTCC CGA CAGT AGGGT CCGG CCG A

GGGAAGTGACAGCAGCCCTG CTT A T CGA --------- GA C GT G

TGTAGTGTTTTCAAAGATCA

GGCGTGGGGA

GAM657 ATCCACGGGCTGCAGAATGG 630 CATCTCTGTC 2306 C G A TAT T C GC AAC

ATATTGTATTAGCAGGCATG TGAGTTCTTG ATCCA GGGCT CAGA TGGA TGTAT AG AG ATGAA A

AAAACAACATTCATCTCCTT GGT ||||| ||||| |||| |||| ||||| || || |||||

GTGCATCTCTGTCTGAGTTC TGGGT CTTGA GTCT GTCT ACGTG TC TC TACTT /

TTGGGT T - - CT- T C -- ACA

GAM658 GCAAGAGAGGCCCAATCTCA 631 GAGAGTCACA 2307 A---- CCAA-- A- TA T

ACTGTAGACTGTGTCCCAGT GCTTCAGGTG GCAAG GAGGC TCTC ACTG GAC G

AAGAGAGTCACAGCTTCAGG TTTG ||||| ||||| |||| |||| |||

TGTTTGC CGTTT CTTCG AGAG TGAC CTG /

GTGGA ACACTG AA C- T

GAM659 GCTCCAAAGAACCAAGAGTG 632 CATTTCACTT 2308 T - ---------- CAC GAGATA TC

CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T

TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||

TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /

GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA

ACTCGATTTGCTTCCGGACC

TTTTCCAGAGC

GAM660 TTCTCCATGATGACAAGGAA 633 TGCTGGGCTC 2309 --- AGTC- CCATCC CACAG CTCCCT GA- G A

GTCTCTGCCATCCTGGCCAC CCTGCATGAC AAGGA TCTG TGGC TGCTGGG GCAT CA TG A

AGTGCTGGGCTCCCTGCATG AGTG ||||| |||| |||| ||||||| |||| || ||

ACAGTGAAAACAGTGACAAT TTCTT AGAC ACCG ACGACCT TGTA GT AC A

GTTCCAGCAAAGCCACCAGA GAA GAAAC C----- AA--- ------ ACA G A

CAAAGTTCTTAAGGTCACAG

GAGAG

GAM661 CTTTGGGGGAATGGCTCTAC 634 ACGCACCAGT 2310 A TCT----- C CGCAC T A GA T C C

TTCGTAACGCACCAGTTGAA TGAAATCAGA GGGGG ATGGC ACTT GTAA CAGT GAA TCA TAC GT TTC A

ATCAGATACTGTCTTCCAAT TACT ||||| ||||| |||| |||| |||| ||| ||| ||| || |||

GAAAACGTAAATGATTCACT CCTCC TACCG TGAA TATT GTCA CTT AGT ATG CA AAG A
GAAATTATAAGTTATTCAAT C TAACTTAT - AAA-- - - AA - A T
GCCATCCCTCCAAAG

GAM662 CTACTGGAAAGAAGGCTTTA 635 ACCATGTAAG 2311 - AA- --- - AGA CAGG
TGGAGATCCCAGGAACCAAG CCTGAATTTG CTAC TGG AGA AGGCTT TATGG TCC A
GACCATGTAAGCCTGAATTT TGCC |||| ||| ||| |||||| ||||| |||
GTGCCATGTGG GGTG ACC TTT TCCGAA GTACC AGG A
T GTG AAG T --- AACC

GAM663 ACACAAGATGAGCATCAATA 636 ATGCAGATGG 2312 A AT TCAATA AACAC T ATGTTATAT
TACAACACCTATCTTTATAA AAGGTACTTG AC CAAG GAGCA TAC CTATCT TATAA T
ATGTTATATTCAAGAGTTAT TTCC || |||| ||||| ||| |||||| |||||
TATGCAGATGGAAGGTACTT TG GTTC CTTGT ATG GGTAGA GTATT /
GTTCCTTGCGT C -- TC---- GAA-- C ATTGAGAAC

GAM664 CACAAGTGATGGTCCAACTT 637 GTAAGGATTT 2313 - -- T-- GAATG- AGG AGGG GG
TGTGGAATGGTAAGGATTTT TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA ATTTTT TTGTTT C
TAGGGTTGTTTGGCCAGAAC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
AAGAGAAATAACTGCAGAAA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA AACAAG /
ACACATATGGTTGGAAACCA G AA TAT AAAAGA CAA G--- AC
TGCGCTTGTG

GAM665 GCCTTTAAAGCTGCCAACGG 638 TTAAAGCTGC 2314 AAA T CA - - A- GCAG------ AC
CTCCCTGCGAGCGCTGCAGG CAACGGCTCC GCCTTT GC GC ACG GCTCC CTGCG GCGCT GCC A
CCACAGTCGGCAATTCCTAC CTGC |||||| || || ||| ||||| ||||| ||||| |||
AAGTGCAACGCGGAGGAGCA CGGAAG TG TG TGC CGAGG GGCGC CGTGA CGG G
CGTCCGTGTCACGAAGGC CAC - CC A A AA ACATCCTTAA CT

GAM666 GTCCAGTGCGTGTACTGTAC 639 TGTACACATC 2315 C G TA TACACATCC A - - CT TC G
ACATCCACACTCATTCTCAC CACACTCATT GTC AGTGC TG CTG AC CTCA TTCT CA CAGGGT CCG A
TCAGGGTTCCCGGACCGGCT CTCA ||| ||||| || ||| || |||| |||| || |||||| |||
GTCCTGCCTGCGGAACTGAG CAG TCATG AC GAT TG GAGT AAGG GT GTCCTG GGC /
GTAAACTAGCTCAGGTACTG - G TC CAAA----- - C C CC TC C
AC

GAM667 GCCTGCCTGAACCCTGGGTC 640 CATGACGGCT 2316 A GG--- - A -- G AA- A- G C
AGGAAAGAAACACTTGGGGA CTGAGTTCTT CCCT GTCA GGAAAGA ACA CTT GGGAGGGG AGG CG CGTGGG T
GGGGAAAGGACGGCGTGGGC CCTG |||| |||| ||||||| ||| ||| |||||||| ||| || ||||||
TACCCATGACGGCTCTGAGT GGGA CGGT CCTTTCT TGT GGG TCCTTCTT TCT GC GTACCC /
TCTTCCTGGGGCTTGTGTCT C GAAAA T G TC G GAG CG A A
TTCCTTGGCAAAAGAGGGCA
CAGCCAAGGC
GAM668 GTCCAGTGCGTGTACTGTAC 641 TGTACACATC 2317 C G TA TACACATCC A - - CT TC G
ACATCCACACTCATTCTCAC CACACTCATT GTC AGTGC TG CTG AC CTCA TTCT CA CAGGGT CCG A
TCAGGGTTCCCGGACCGGCT CTCA ||| ||||| || ||| || |||| |||| || |||||| |||
GTCCTGCCTGCGGAACTGAG CAG TCATG AC GAT TG GAGT AAGG GT GTCCTG GGC /
GTAAACTAGCTCAGGTACTG - G TC CAAA----- - C C CC TC C
AC

GAM669 GGCCAGGCACAGTGGCTCAC 642 TGAGGTCAGG 2318 A GG C CTGTAA CA A --- GAG GA
ACCTGTAATCCCAGCACTCT AGTTTGAGAC GGCCAGGC CAGT CTCA AC TCC GC CTC TGA GCC G
GAGAGGCCGAGGTAGGCGGA TGGT |||||||| |||| |||| || ||| || ||| ||| |||
TCACTTGAGGTCAGGAGTTT CCGGTCTG GTCA GAGT TG AGG TG GAG ACT CGG G
GAGACTGGTCTGGCC - -- T ------ AC - TTC AGG AT

GAM670 GCTCCAAAGAACCAAGAGTG 643 CATTTCACTT 2319 T - ---------- CAC GAGATA TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM671 TGACCGATTTCTCCTGGTGT 644 TAGCACCATT 2320 TCC --- TC
TCAGAGTCTGTTTTTGTCTA TGAAATCGGT TGACCGATTTC TGGTGTT CAGAG T
GCACCATTTGAAATCGGTTA TA |||||||||| ||||||| |||||
ATTGGCTAAAG ACCACGA GTTTT /
TTT TCT TG

GAM672 GCTCCAAAGAACCAAGAGTG 645 CATTTCACTT 2321 T - ---------- CAC GAGATA TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T

TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM673 CACAGTGGCTTCCCTTAGAA 646 CCAGTCTTTG 2322 T TTCCCTT T T TCTC--- AAC
AG
CCAGTCTTTGTACTCTCCCT TACTCTCCCT CACAG GGC AGAACCAGTCTT G AC CCTA
AGC C
AAACAGCAGCAGGCTTAGGA AAAC ||||| ||| |||||||||||| | || |||| |||
ATTCTTGTCCAGGGCTGGTT GTGTC TCG TCTTGGTCGGGA C TG GGAT TCG /
CTTGCGTGCTCTGTG - TGCGT-- - C TTCTTAA --- GA

GAM674 GTGGCACAATTTGAATTCAG 647 TGGCACAATT 2323 A AT TTCA--- AAC- GACT
ATT-- G G
TAAAACAGGGGAGACTGGAG TGAATTCAGT GGC CA TTGAA GTAA AGGGGA GGAGGG
GGGA TTT G
GGATTGGGAGTTTGGAGAGG AAAA ||| || ||||| |||| |||||| |||||| |||| |||
TCCCTTTCACCCTCCTCCTT CCG GT AACTT CATT TTTCCT CCTCCC CCCT
GAG /
TAAAATTACAGTAACTTTCA - C- TCAATGA AAAA ---- ACTTT G A
ACTGGCCAT

GAM675 GCTGCTGAGTTCTGGACACA 648 TGGCTCAGTC 2324 GC TT AC ATT TCCC
GCATTTCTTTCCCAGAATGA CAGCTTGAAA GCT TGAG CTGGAC AGC TCTT A
GACTGGCTCAGTCCAGCTTG GC ||| |||| |||||| ||| ||||
AAAGC CGA GTTC GACCTG TCG AGAG /
AA -- AC GTC TAAG

GAM676 GTTTAGATACACTTATATAC 649 TACTATATAG 2325 CACAAATA TA- A- TT ACA
ATT AG
ACAAATACTTACCATTGTGT GTGTGTACTA CTTATATA CT CC TTGTGTTACAA GCCT GT
TAGTAC T
TACAATTGCCTACAGTATTT GGC |||||||| || || |||||||||| |||| || ||||||
AGTACAGTCACGTGCTGCAC GGATATAT GA GG GACACGATGTT TGGA CA
GTCGTG C
AGGTTTGTAGCACAGGAGGA CATATCG- TAA AG -- --- C-- CA
ATAGGCTATACTATATAGGT
GTGTACTAGGC
GAM677 GCTCCAAAGAACCAAGAGTG 650 CATTTCACTT 2326 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA

ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM678 TATCTGCCGTGCCTCTCTTC 651 TGTAGAGACT 2327 TGC CTCT C CCA A G TC AAC
CCTACCCAAAAGTGATGAGT TGGGTATGTG TATC CGTGCCT TC CTAC AA GTGAT AGT TG A
TCTGAACAAGACAAGACTGT ATA |||| ||||||| || |||| || ||||| ||| ||
CATATTGTAGAGACTTGGGT ATAG GTATGGG AG GATG TT TACTG TCA AC /
ATGTGATA T-- TTC- A --- A - GA AGA

GAM679 GTAGGGGTGAGACCGGCATG 652 TCAAATGCCT 2328 - AGACC ----- ---- AGG- TAT
GTGATTTCTTTAGGGGAGGG CAGCACCTGC GTAG GGGTG GGCAT GGTGA TTTCTTT GGAGGG A
TATAAGAGTCCTTTGCGAAG TGC |||| ||||| ||||| ||||| ||||||| ||||||
AGAAACATTTCACTTTCAAA CGTC TCCAC CCGTA TCACT AAAGAGA TTTCCT A
TGCCTCAGCACCTGCTGC G GACT- AACTT TTAC AGCG GAG

GAM680 TCCTTTTGACAAGAAATGTG 653 TGACAAGAAA 2329 T - AAATGT C AA-- CTGTT T
GTCGTGAAAATTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA TTGGA GC T
GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||
ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T
GA C G GTT--- - GGTA ----- T

GAM681 GGAGGTGGAGAGCTTTCAGT 654 TACAGGTGCA 2330 GTG A TCA T - G AG- - CA TTTT G AG
TCATATGGACCAGACATCAC TCGTGCACAT GAG GCTT GT CAT ATG ACC AC ATCAC AGCT TGCT TG T
CAAGCTTTTTTGCTGTGAGT AAGC ||| |||| || ||| ||| ||| || ||||| |||| |||| ||
CCCGGAGCGTGCAGTTCAGT CTC CGAA CA GTG TAC TGG TG TAGTG TTGA GCGA GC /
GATCGTACAGGTGCATCGTG TTG - TA- C C G ACA C AC CGT- G CC
CACATAAGCCTCGTTATCC

GAM682 GGGTGCACAAGTGATGGTCC 655 GTAAGGATTT 2331 - -- T-- GAATG- AGG AGGG GG
AACTTTGTGGAATGGTAAGG TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA ATTTTT TTGTTT C
ATTTTTAGGGTTGTTTGGCC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
AGAACAAGAGAAATAACTGC TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA AACAAG /
AGAAAACACATATGGTTGGA G AA TAT AAAAGA CAA G--- AC
AACCATGCGCTTGTGACTT

GAM683 TTCTCCATGATGACAAGGAA 656 TGCTGGGCTC 2332 --- AGTC- CCATCC CACAG CTCCCT GA- G A

GTCTCTGCCATCCTGGCCAC CCTGCATGAC AAGGA TCTG TGGC TGCTGGG
GCAT CA TG A
AGTGCTGGGCTCCCTGCATG AGTG ||||| |||| |||| ||||||| |||| || ||
ACAGTGAAAACAGTGACAAT TTCTT AGAC ACCG ACGACCT TGTA GT AC A
GTTCCAGCAAAGCCACCAGA GAA GAAAC C----- AA--- ------ ACA G A
CAAAGTTCTTAAGGTCACAG
GAGAG
GAM684 GCTTTTGCTCCAGATGGTTC 657 CCAGTGCCTT 2333 TT TCC T ATACTTT T - AA TC
ACA
ATACTTTGCTTGGTCACAAG CAGAACTTTC GCT TGC AGA GGTTC GCT GG TCAC
GGACA GC G
GACATCGCACAGTAAAGCTT TCTT ||| ||| ||| ||||| ||| || |||| ||||| ||
GTTCCGTGGTCCCAGTGCCT CGG ACG TCT TCAAG TGA CC GGTG CTTGT CG T
TCAGAACTTTCTCTTGCATG T- TTC T ACTTCCG C T C- T- AAA
GC

GAM685 CTACTGGAAAGAAGGCTTTA 658 ACCATGTAAG 2334 - AA- --- - AGA CAGG
TGGAGATCCCAGGAACCAAG CCTGAATTTG CTAC TGG AGA AGGCTT TATGG TCC A
GACCATGTAAGCCTGAATTT TGCC |||| ||| ||| |||||| ||||| |||
GTGCCATGTGG GGTG ACC TTT TCCGAA GTACC AGG A
T GTG AAG T --- AACC

GAM686 GCTGTGGCGCACTGCAAACG 659 TGATTGAGCC 2335 CAC AAAC -- G ATCAA
GAAC
CGGCAATGGTCTCATCAAGG GCGCACGCTA GCTGTGGCG TGC GCGGC AAT GTCTC
GGT G
TGAACGGGCGGCCCCTGGAG CAGT ||||||||| ||| ||||| ||| ||||| |||
ATGATTGAGCCGCGCACGCT TGACATCGC ACG CGCCG TTA TAGAG CCG /
ACAGT --- ---- AG G GTCC- GCGG

GAM687 TGGTCATGCCTATAATCCTG 660 TGAGGTCAGG 2336 ---- ATAA- A TGAG GCG
GCACTTTGAGAGGCAATGCG AGTTTGAGAC TGGTCATGC CT TCCTGGC CTT AGGCAAT
G
GTCAGATTGCTTGAGGTCAG TAGC ||||||||| || ||||||| ||| |||||||
GAGTTTGAGACTAGCGTGGC ACCGGTGCG GA AGGACTG GAG TTCGTTA T
CA ATCA GTTTG - ---- GAC

GAM688 CAGCCTCCCACTGTGGTGCC 661 TCCCCTGGAC 2337 CC - G T T A - AA CAGAGA
- CA T
TGGTGGAGACCTGGCCAAGG CACAAGTTTG ACT GTGGT CC GG GGAG CCT GGCC GGTA
GCTGTG TG TGC G
TACAGAGAGCTGTGTGCATG ACCT ||| ||||| || || |||| ||| |||| |||| |||||| || |||
CTGAGCAACACCACAGCCAT TGA CACCA GG CC CCTC GGG CCGG TCGT
CGACAC AC ACG /
TGCTGAGGCCTGGGCTCCCC TT A - T - - T AG TAC--- C A- A
TGGACCACAAGTTTGACCTG

GAM689 AACCCAGAATGGGGAAGAAT 662 TTGGAGCAGG 2338 CCC - - TA AA T CA TCT AC- CT
ACTGAATTAGCTGAGCACAT TTTCATTCTC AA AGAAT GGGGAA GAA CTG TTAGC GAG CAT GGAC AATT G
TCTGGACACAATTCTGACCA CAAT || ||||| |||||| ||| ||| ||||| ||| ||| |||| ||||
ATTTCAGTCTCATGATCTCT TT TCTTA CCTCTT CTT GAC GGTTG CTC GTA TCTG TTAA A
GTTGGAGCAGGTTTCATTCT TC- A A TG GA T TA C-- ACT CC
CCAATTCTCTTT

GAM690 TGTCTCTCGCAAAATGTGGA 663 TCGCAAAATG 2339 TCGCAAA G - CTTA T
CAAGGCACTTATTGTCTTCA TGGACAAGGC TGTCTC AT TGG ACAAGGCA TTG C
ACTCATGCTTTGTACCGGGT ACTT |||||| || ||| |||||||| |||
GAGACA ACAGAG TG GCC TGTTTCGT AAC T
------- G A ACTC T

GAM691 AGGTCACACAGTTGGTAAAT 664 CACACAGTTG 2340 TCACA T AAAT T AG ACT
GATGGAGCTAGGACTAGAAC GTAAATGATG AGG CAGT GGT GA GG CTAGG A
CTAGGCCTTCTGACTTGCTG GAGC ||| |||| ||| || || |||||
CCTCCCT TCC GTCG TCA CT CC GATCC /
CTCC- T GT-- T G- AAG

GAM692 AGAGACCACCAATGCCCTTG 665 AGAGGTAGTG 2341 A- AA- - T CA- C AA
GACACACAGAATCCCCTTGA GGTGGCATTC AGAG CCACC TGCC CT GGA CA AG T
TTTCCCAGAGGTAGTGGGTG T |||| ||||| |||| || ||| || ||
GCATTCT TCTT GGTGG ATGG GA CCT GT TC C
AC GTG A C TTA - CC

GAM693 CTGGAGTGCAGTGGTGCGAT 666 TACAGTAGCT 2342 -------- TG C C C C -- CCC-- ATT
CTTGGCTCACTGCAACCTCC GGGATTACAG TGC GATCT GCT ACTG AA CTC GC CT GGTTGAGGCA C
GCCTCCCGGTTGAGGCAATT ACAT ||| ||||| ||| |||| || ||| || || ||||||||||
CTCCTGCCTCAGCCTCCCAA GCG TTAGG CGA TGAC TT GAG CG GA CCGACTCCGT /
GTAGCTGAGATTACAGTAGC TACAGACA GT - A A T AT ACCCT CCT
TGGGATTACAGACATGCGCC
ACCATGTCCAG
GAM694 GGAGTAGCTGGGACTACAGG 667 ACTACAGGTG 2343 -- G T GGT CGT C-- TT
TGCACGTGATCATACCTAAA CACGTGATCA GGAG TAGCT GGAC ACA GCA GATCATA CTAAA T
TTTTTTTTTAGAGATGTGGT TACC |||| ||||| |||| ||| ||| ||||||| |||||
CTTGCTGTGTTGTCCAGGCT CCTC GTCGG CCTG TGT CGT CTGGTGT GATTT T
GGTCTCC TG A T GT- T-- AGA TT

GAM695 TAGGAAGAAATGTTGGTATC 668 TGGCATAGGT 2344 T TC TTA T A G AGG AAA A--- C-- AG

CTCCATTATAGATGGATGGC CACAAATGGG GGTA CTCCA TAGA GG TG CAT TCAC TGGG
GA TGGC C
ATAGGTCACAAATGGGAGAC AGAC |||| ||||| |||| || || ||| |||| |||| || ||||
TGGCAGCTAAGCCAATATCA TCAT GAGGT ATCT TC AC GTA GGTG ACCC CT
ACCG T
AAACCCAGTGGAATGACACT - TT --- - - A A-- --- AAAA ATA AA
TCTATGGAGTTTACTTTTCT
TCCTG
GAM696 ATTCTCATCGTGGAGATCTT 669 TTCCTCAGAC 2345 TC CG A TT CA-- - AT CT
TGGCAGCGCATTGGCCTCTT CTCCAGAGTG AT TCAT TGGAG TCT GG GCG C TGGCCT T
TGGGGTCATCGTCGCAATTC AAGA || |||| ||||| ||| || ||| | ||||||
CTCAGACCTCCAGAGTGAAG TA AGTG ACCTC AGA CC CGC G ACTGGG /
AT GA AG C CT TTAA T CT GT

GAM697 CTCTTGAGCATGCTGACCAG 670 GACCAGTGCT 2346 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM698 TCATGCCTGTAACCCCAGTG 671 GTGCATTGTG 2347 CCC A- T CACATT CTC
CT C
CATTGTGAGGTCACATTGGG AGGTCACATT GTAA CAGTGC TTG GAGGT GGGAGGAT
TTGAGGCCAGG GTT T
AGGATCTCTTGAGGCCAGGC GGGA |||| |||||| ||| ||||| |||||||| |||||||||| |||
TGTTCTCAAACTCCTGGCCT CATT GTTGCG AGC CTCCG TCCTTCTG
AACTCCGGTCC CAA C
CAATCAGTCTTCCTGCCTCA AGA AA - ACTCCG ACT T- A
GCCTCCGAAAGCGTTGAGAT
TACAGGCGTGA
GAM699 GGATTAGAAACCCGTAGATC 672 AACCCGTAGA 2348 A - G AT C-- TT
AGTTCTAGGTTAGCCCTGAT TCAGTTCTAG GG TTAGAAAC CC TAG CAGTT TAGG A
TAACTGCCCTGGGTGTTTCT G || |||||||| || ||| ||||| ||||
GGGCC CC GGTCTTTG GG GTC GTCAA GTCC /
G T - CC TTA CG

GAM700 CAGTGTTTGCTTCAGAGTTT 673 TGAGGAAGAT 2349 TGCT ---- AA-- TG - AA
GAGGAAGATGTTGGATTGTT GTTGGATTGT CAGTGTT TCAGAGTT TGAGG GA TTGGA
TTGTT A
AAATAAAGCAGCTCCAGTTT T ||||||| |||||||| ||||| || ||||| |||||
CGGGACCTCGACTGGATTTT GTTACAG AGTTTTAG GCTCC CT GACCT GACGA T
GATCCTGACATTG TCCT GTCA AGGG TT C AA

GAM701 CTAGTTCTCCTGTGAAGCTG 674 TGAAGCTGTC 2350 - CT GA T GC- TG TCTCA C CT
GAA
TCAGCCTGATCTCATGCCAC AGCCTGATCT CTAGT TCTC GT AGC GTCA C A TG CACA
GT A

ACTGTGAAATGAACTATGTG CATG ||||| |||| || ||| |||| | | || |||| ||
CCAGTTTGGAAATGATTGCT GGTCG AGAG CA TCG TAGT G T AC GTGT CA /
GACCTGAGATGCTGG T TC G- T AAA GT TG--- C AT AGT

GAM702 TAAGGGTTGTTTTGTTGTTA 675 TGAAGCTAGA 2351 T TGTTGT AA A-- GTCCATT
GGTAAATAGATATTAGGCAG TACCTAAAGC TAAGGGT GTTT TAGGTA TAG TATTAGGCA
T
TCCATTTCTAAAATATGCCT TACC ||||||| |||| |||||| ||| |||||||||
GATGAAGCTAGATACCTAAA ATTCCCA CGAA ATCCAT ATC GTAGTCCGT C
GCTACCCTTA T ------ AG GAA ATAAAAT

GAM703 TTCCTGTAACCACTGTGAAA 676 TAACCACTGT 2352 A AC --- ------ CAC
AATGAGAA
TCGGTTAACCTTAGACAAAG GAAATCGGTT TGAA TCGGTTA CTTAGA CAAAG TGAGAA
TTCTGCT G
TGAGAACACTTCTGCTAATG AACC |||| ||||||| |||||| ||||| |||||| |||||||
AGAAGGAGGTGGAGGCAGAA ATTT GGTCAGT GAATTT GTTTC ACTCTT
AAGACGG /
TTTCTCAGATTATCTTTGGG - GT AGG TATTAG T-- AGGTGGAG
ATTTAAGTGTGACTGGTTTA
CCTTGGAGAA
GAM704 GGGAGAAGATGAGGCAGCCA 677 TGAAGCTGCC 2353 A AGA - GCCA TG AG G CC
TGGTGGAGTCAGTAGGCCTG AGATGTCCTT GGG GA TGAGG CA TGG G TCA TAGG T
GCCCTAGTGAAGCTGCCAGA AATC ||| || ||||| || ||| | ||| ||||
TGTCCTTAATCGCCT TCC CT ATTCC GT ACC C AGT ATCC G
G A-- T AG-- GT GA G CG

GAM705 TGCCCAGTCTTATATTACTT 678 GCCACAAATA 2354 CCA T A---- G- CTT AACCAT
CC A
GTGATCTTGAAATGGAAACC TAGATAAAGC TGC GTCT ATATT CTT TGAT GAAATGGA
GT TGTT T
ATGTCCTGTTATTGAACAAG A ||| |||| ||||| ||| |||| |||||||| || ||||
CTCTTCTCTATTTTTTCATC ACG TAGA TATAA GAA ACTA TTTTATCT CG ACAA
T
AGAAAGCCACAAATATAGAT AAA - ACACC AG CTT CTTCT- A- G
AAAGCA

GAM706 ATTCATGTGTTCTCTTGAAA 679 CACCGGGAGA 2355 A G- AA-- A A- TG
GGAAAGGGAGAGCTGTAAGC AAAGCAGGAA ATTC TGT TTCTCTTG AGGA AGGG GAGC T
TTCACTCTGTCCTACACCGG T |||| ||| |||||||| |||| |||| ||||
GAGAAAAGCAGGAAT TAAG ACG AAGAGGGC TCCT TCTC TTCG /
G AA CACA G AC AA

GAM707 AATAACCCGGCATGGAGCAG 680 TATTGCACGT 2356 C A ------ TT T
TTTGGTTTCCACCCTATTGC GGTCCGGCCT AATAACC GGC TGGA GCAGT GGT T
ACGTGGTCCGGCCTGGTTAT GGTT ||||||| ||| |||| ||||| |||

T TTATTGG CCG GCCT CGTTA CCA C
T - GGTGCA TC C

GAM708 GCTGGAGGCTGTGCAGAAGG 681 ATGAGCACAG 2357 AG- T AGAA - GCA CA AAC-
A-- T
TATCCTGCAGACCATGAACT TTGTAAGGTG GCTGG GCTG GC GGTAT CCT GAC TG
TGAGC CTGG T
GAGCACTGGTTCCCAGACCG TGCC ||||| |||| || ||||| ||| ||| || ||||| ||||
TTCATGAGCACAGTTGTAAG CGACC CGAC CG CCGTG GGA TTG AC ACTTG
GACC /
GTGTGCCGAGAGCCAGCACG GCA - AGAG T ATG AC GAGT CCA C
CCAGC

GAM709 TGAGTAGGTAGTGTGGCCAA 682 GTCACAGAGG 2358 CC T ACAAC CA T -- T G
- GA
GAGATCAGCACAACCTTTGC CTGTTCTTTT GTGG AAGAGA CAGC CTTTG GGCTGACT GC
TAAG CT ACA GT C
AGGCTGACTTGCTAAGTCTG TCAC |||| |||||| |||| ||||| |||||||| || |||| || ||| ||
ACAGTGACAAACTTGTGAGC CACT TTTTCT GTCG GAGAC CTGACTGA CG ATTC GA
TGT CA /
TTACTGCAGTCAGTCACAGA -- T ----- A- - TC - G T AA
GGCTGTTCTTTTTCACACAC
CCCTTCA
GAM710 GGGTCAATGGAGGCCTCTCT 683 GTCAATGGAG 2359 CA CC T CGT- A
TCTGTCGTGCCCAAGTCTGG GCCTCTCTTC GGGT ATGGAGG TCTCT CTGT GCCCA G
GCCTCTGCAGAGAGACCTCC TGTC |||| ||||||| ||||| |||| |||||
ATGCCC CCCG TACCTCC AGAGA GACG CGGGT T
-- -- - TCTC C

GAM711 CAGATGTCTCTGGGGCAGAT 684 TGGAGAAATG 2360 --- CC- CTG CTA G GC AG --
AGCT
CCCCACTGTCCTACCAGTTG GCAAGTCTAG CTGGGGC AGAT CCA TC CCA TT CCT
CCCA GACTCTG G
CCCTAGCCCAGACTCTGAGC AGTC ||||||| |||| ||| || ||| || ||| |||| |||||||
TGCTCACCGGAGTCATTGGG GACTCTG TCTG GGT AG GGT AA GGA GGGT
CTGAGGC C
AAGGAAAAGTGGAGAAATGG AGA AAC AA- A-- G AA A- TA CACT
CAAGTCTAGAGTCTCAGAAA
CTCCCCTG
GAM712 CCGGTTACGCCTGAGTGCCC 685 TGAGTGCCCT 2361 GT T G - - TT TG TT CA
TGGTTGTTGTGCTTGACAAT GGTTGTTGTG CCG TACGCC GA TGC CCT GGTTG G C GA A
TTCTGTGTCGACTGAGGCGC CTTG ||| |||||| || ||| ||| ||||| | | ||
AGTCGGCGTACACGG GGC ATGCGG CT ACG GGA TCAGC T G CT /
AC - G C G -- GT T- TT

GAM713 GGTAGGTAGTGTGGCCAAGA 686 GTCACAGAGG 2362 CC T ACAAC CA T -- T
G - GA

GATCAGCACAACCTTTGCAG CTGTTCTTTT GTGG AAGAGA CAGC CTTTG GGCTGACT GC
TAAG CT ACA GT C
GCTGACTTGCTAAGTCTGAC TCAC |||| |||||| |||| ||||| |||||||| || |||| || ||| ||
AGTGACAAACTTGTGAGCTT CACT TTTTCT GTCG GAGAC CTGACTGA CG ATTC GA
TGT CA /
ACTGCAGTCAGTCACAGAGG -- T ----- A- - TC - G T AA
CTGTTCTTTTTCACACACCC
CTTCATGCC
GAM714 CAGAAGGGGTTTTTATCAAA 687 AGAAGTAGTA 2363 AG- TTTA GTAG---- - AA
AG AA
AATATGTAGATTCTACTACA GTAGCAGTAG AGA GGGTT TCAAAAATAT ATT CTACTAC
TATTTT CT A
ATATTTTAGCTAAAGAAGAA TAGT ||| ||||| |||||||||| ||| ||||||| |||||| ||
GAAGTAGTAGTAGCAGTAGT TCT CCCAG AGTTTTTATG TGA GATGATG
ATGAAG GA /
AGTCAGTATTTTTGACCCTG CAA TCCC ACTGATGA C -- AA AG
ACCCAACTCTG

GAM715 TAAGGGTTGTTTTGTTGTTA 688 TGAAGCTAGA 2364 T TGTTGT AA A-- GTCCATT
GGTAAATAGATATTAGGCAG TACCTAAAGC TAAGGGT GTTT TAGGTA TAG TATTAGGCA
T
TCCATTTCTAAAATATGCCT TACC ||||||| |||| |||||| ||| |||||||||
GATGAAGCTAGATACCTAAA ATTCCCA CGAA ATCCAT ATC GTAGTCCGT C
GCTACCCTTA T ------ AG GAA ATAAAAT

GAM716 GAGTGCAAATCAGTCCATTT 689 CATTTCACTT 2365 G A C C- CAC GAGATA TC
CACTTTCACTGTCTGAGATA TCACTGTCTG GAGT CA AT AGT CATTTCACTTT TGTCT
GGGTC T
GGGTCTCTAAGACCCAGGAT AGAT |||| || || ||| |||||||||| ||||| |||||
ACAAGGGTGGAATGTAGCTA CTCA GT TA TCG GTAAGGTGGGA ATAGG CCCAG /
TATGGACTC G A - AT AC- A----- AA

GAM717 ACCGGTTATGGTGCTGCTGT 690 TGGAGCCTGG 2366 GG T - AC GTTGGAGC
G TT T T
GAACACTGCCAAGTTGGAGC CTCTGTTTGT CGGTTAT TGC GCT GTGA ACTGCCAA
CTGGCTCT T G GCCG C
CTGGCTCTGTTTGTGCCGTC GCCG ||||||| ||| ||| |||| |||||||| |||||||| | | ||||
TTTGGTCTGGGAGGAGTCGG GTCGGTG ATG CGG TACT TGACGGTT GGCTGAGG
G T TGGT T
ATTGGCAGTTATCATGGGCT AA T G AT A------- A GG C T
GTAAAGTGGCTGGT

GAM718 GGTCGCTAGGCAACTATTTC 691 TAACGGCTCT 2367 A A ATTTCCAG- - -- A- GC
CAGCTGACTGAGCATTGCAA GAGTGCAGAT GGTCGCT GGC ACT CTG ACT GAGC
TTGCAA T
GCTCATTGTAACGGCTCTGA ATCT ||||||| ||| ||| ||| ||| |||| ||||||
GTGCAGATATCTTACAGTGG TCAGCGG CCG TGA GAC TGA CTCG AATGTT /
CCAGGCGACT A G CATTCTATA G GT GC AC

GAM719 GATTATTATATACAAGATGT 692 TTTGGCATGA 2368 T A- - G GAA AGTA AA C AG

AGCTTAAGTGTTCTGGAAAT CAGGAACTTG TACAAGA GT GCTT AAGT TTCTG ATG AAAGTG TCTTATGT TC A

GAGTAAAAGTGAATCTTATG GAGT ||||||| || |||| |||| ||||| ||| |||||| |||||||| ||

TCTCAGATAGAATGTAGGAG GTGTTCT TA TGAG TTCA AGGAC TAC TTTCAT AGGATGTA AG /

TACTTTGGCATGACAGGAAC T GG G - AG- GG-- G- - AT

TTGGAGTGGATTTCTTGTGT

CAATATAATT

GAM720 CTCTTGAGCATGCTGACCAG 693 GACCAGTGCT 2369 G A TGA C CATAA TG ACTCA

TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A

CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||

CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A

- G TC- - TC--- GT CCTAT

GAM721 CTGGCTTAGGCTTCATCCAC 694 TATAACAGCC 2370 A - TCCA-- CCA GT

TGCCAATGAAGTCAAATTTA ACCTTGACAG CTGGCTT GGCT TCA CTG ATGAA C

TAACAGCCACCTTGACAGTC TCGA ||||||| |||| ||| ||| |||||

GAAGCTAG GATCGAA CTGA AGT GAC TATTT A

G C TCCACC AA- AA

GAM722 CAGTGCCACAATGGGTCAGC 695 CCTACAGTGA 2371 T ---- A G- G ACC AACACCAT AG A

TGTACCAGGAACACCATGAA CGACAGTGTC CAG GCC ACA TG GTCA CTGT AGG GA AAG C

GAAGACTTCTTTCTCTACAT TACG ||| ||| ||| || |||| |||| ||| || |||

TGCCTACAGTGACGACAGTG GTC CGG TGT AC CAGT GACA TCC CT TTC T

TCTACGGCCTG - CATC G AG - --- GTTACAT- CT T

GAM723 GCTTTGAAGGCAGCAGCATT 696 AGCAGCATTG 2372 A- CA G AGGT C

GTACAGGTGCTTCTCAAAGC TACAGGTGCT GCTTTGAAGGC GCAG TT TAC GCTT T

GTGGAACCTTGCAGGCCTTC T |||||||||| |||| || ||| ||||

AGGGC CGGGACTTCCG CGTT AA GTG CGAA C

GA CC G ---- A

GAM724 GAAGACTTCCTAAATTTGCA 697 TTTGCACATT 2373 AC A TTGCA TTGCC ACCAT

CATTAGCTAGATTGCCATTA AGCTAGATTG GAAG TTCCT AAT CATTAGCTAGA ATTAGC T

GCACCATTAGAGAGTTGATC CCAT |||| ||||| ||| |||||||||| ||||||

TTTGGCTAATGATTATTCAG CTTT AAGGA TTA GTAATCGGTTT TAGTTG /

GAAAATTTC AA C TTA-- C---- AGAGA

GAM725 GCCTGCCTGAACCCTGGGTC 698 CATGACGGCT 2374 A GG--- - A -- G GAA A- G C

AGGAGAGAAACACTTGGGGA CTGAGTTCTT CCCT GTCA GGAGAGA ACA CTT GGGAGGGG AGG CG CGTGGG T

GGGGGAAAGGACGGCGTGGG CCTG |||| |||| ||||||| ||| ||| |||||||| ||| || ||||||

CTACCCATGACGGCTCTGAG GGGA CGGT CCTTTCT TGT GGG TCCTTCTT TCT GC GTACCC /

TTCTTCCTGGGGCTTGTGTC C GAAGA T G TC G GAG CG A A

TTTCCTTGGCAGAAGAGGGC

ACAGCCAAGGC

GAM726 ACCTGTGTGCAGGCGCCGGT 699 ACGGAACGCT 2375 G ---- C- G T - G

GGTCTTTCAGGTGGGTACTC TTGCCACAGT ACCTGTGT CAGGC GC GGTG TCT TCAG GT G

TGACGGAACGCTTTGCCACA CTGG |||||||| ||||| || |||| ||| |||| ||

GTCTGGACATGGGT TGGGTACA GTCTG CG TCGC AGG AGTC CA G

G ACAC TT A C T T

GAM727 CACAAGTGATGGTCCAACTT 700 GTAAGGATTT 2376 - -- T-- GAATG- AGG AGGG GG

TGTGGAATGGTAAGGATTTT TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA ATTTTT TTGTTT C

TAGGGTTGTTTGGCCAGAAC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||

AAGAGAAATAACTGCAGAAA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA AACAAG /

ACACATATGGTTGGAAACCA G AA TAT AAAAGA CAA G--- AC

TGCGCTTGTG

GAM728 GAGAACGTAGACGTCTGGAT 701 TAGACGTCTG 2377 ACG A AACT- AAA CCAC--- TTT

AACTGAAGTAAAGTATCCAC GATAACTGAA GAGA TAG CGTCTGGAT GAAGT GTAT AGGGTTTTAT A

AGGGTTTTATTTTAGCTTGT GTAA |||| ||| |||||||| ||||| |||| ||||||||||

AGAACTCTTAGAGCTATGCA CTTT GTC GTAGACCTA CTTCA CGTA TCTCAAGATG G

AACTTCCCAAGATCCAGATG AA- A GAACC AA- TCGAGAT TTC

ACTGAATTTC

GAM729 TCACCCAGTGGTTCTCTCAG 702 TCAAAGCTGC 2378 TC - AACA-- - A- A TA TGAC T CC

CAACAGACATGTCCAGTGGA AGATTGCCTG GT TCT CAGC GACATGT CC GTGG CCG GTGTTG GG CGC A

CCGTAGTGTTGTGACGGTCG TGA || ||| |||| ||||||| || |||| ||| |||||| || |||

CCCATCTGCGCCCAGTACCT CG AGA GTCG TTGTACA GG TACT GGC CATGAC CC GCG T

CGGATCATGCGGAACATGTT TT C AAACTG A CG A TC ---- - TC

GTCAAAGCTGCAGATTGCCT

GTGA

GAM730 GCTCCAAAGAACCAAGAGTG 703 CATTTCACTT 2379 T - ---------- CAC GAGATA TC

CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T

TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM731 TCTCCTTTGGCAGCTCCTTT 704 GCAGCTCCTT 2380 C --- G TT- T TC TG
TCTTCTCCTAGCTGAGTGTT TTCTTCTCCT TCTC TTTGGC A CTCCT TCT C CTAGC A
AGTGGTGGGTGTAGGAGGTG AGC |||| |||||| | ||||| ||| | |||||
GAGCTAGAGAGA AGAG AGATCG T GAGGA GGG G GATTG /
- AGG G TGT T GT TG

GAM732 GCCTCACTGGACTCGTCTGC 705 TCGAAGACCA 2381 C ------ C C AAGAG GG C
AG T
ACAAGAGTGGGGTTCCGGAG AAGTGTATGC GC TCACT GGACT GT TGCAC TGG TTC
GGAGT CCC C
TAGCCCTCGTGGGAAGCTCT AGTC || ||||| ||||| || ||||| ||| ||| ||||| |||
CGAAGACCAAAGTGTATGCA TG AGTGG CCTGA CG ATGTG ACC AAG TCTCG
GGG G
GTCCCTTCGTGGTGACGT C TGCTTC - T AA--- AG C AA T

GAM733 TATTTTGCGTAGGCAGAAAC 706 TTGCGTAGGC 2382 C A- CAGTGA - A A
CAAATA
AGTGAGGAGTACAAAGCAAA AGAAACAGTG TATTTTG GT GGCAGAAA GGA GTACA AGCA
AGCTA C
GCTACAAATACCACCAATGG AGGA ||||||| || |||||||| ||| ||||| |||| |||||
TTCTGCTATGTGCATCCGAT ATAAAGT TA CCGTTTTT CCT CGTGT TCGT TTGGT /
ATTTTTTGCCCGATCTGAAA C GC TATAG- A A C AACCAC
TA

GAM734 GAAGACTTCCTAAATTTGCA 707 TTTGCACATT 2383 AC A TTGCA TTGCC ACCAT
CATTAGCTAGATTGCCATTA AGCTAGATTG GAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
GCACCATTAGAGAGTTGATC CCAT |||| ||||| ||| |||||||||| ||||||
TTTGGCTAATGATTATTCAG CTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GAAAATTTC AA C TTA-- C---- AGAGA

GAM735 TAGGAAGATAAGTTACCCTG 708 TGGGGCTAGT 2384 AGATA A T -- GA-- TT C C
A
CAGAATAATGAAGTTTCACA AATTGTTTGT TAGGA AGTT CCC GCA GAATAAT AGT CA
AAC TCAGC C
ACCTCAGCACTGTTGGTGTT TGTG ||||| |||| ||| ||| ||||||| ||| || ||| |||||
TGGGGCTAGTAATTGTTTGT GTCCT TCAG GGG TGT TTTGTTA TCG GT TTG
GGTTG /
TGTGGGAGACTGTCCTG G---- A - TG ATGA GG - T T

GAM736 AATCTTGAAACCTAGTGAAG 709 TGGTGGATCC 2385 C- AGGAA GA-- C G GT TT A---- G
GAACTTGAGTCACTAGTGAC ATTTGGTTGT C TAGTGA CTT GTCA TAGT ACA CGG GTGGG TAGCTT T
AGTCGGTTGTGGGATAGCTT AGCT | |||||| ||| |||| |||| ||| ||| ||||| ||||||
GTGAAGGCTGGTGGATCCAT G ATTATT GAA CGGT ATCG TGT GTT TACCT GTCGGA G
TTGGTTGTAGCTAATGGCGT AA AA--- AGTG A A TG -- AGGTG A
GAAAGAATTATTAAAGTTTT
AAGGTT
GAM737 CTTTTTGTTAAATGGATCCC 710 TCCCAAATAT 2386 TG TAAATGG AATATT AA- T AA
AAATATTTACAAAGCCATCA TTACAAAGCC CTTTT T ATCCCA TACA GCCA CAG C
GAACCACCTGTGGCAAATGT ATCA ||||| | |||||| |||| |||| |||
ATTGTGGGATATTGTGAAAA GAAAA G TAGGGT ATGT CGGT GTC C
G GT TTA---- GTT--- AAA - CA

GAM738 GCCTGCCTGAACCCTGGGTC 711 CATGACGGCT 2387 A GG--- - A -- G AA- A- G C
AGGAGAGAAACACTTGGGGA CTGAGTTCTT CCCT GTCA GGAGAGA ACA CTT GGGAGGGG AGG CG CGTGGG T
GGGGAAAGGACGGCGTGGGC CCTG |||| |||| ||||||| ||| ||| |||||||| ||| || ||||||
TACCCATGACGGCTCTGAGT GGGA CGGT CCTTTCT TGT GGG TCCTTCTT TCT GC GTACCC /
TCTTCCTGGGGCTTGTGTCT C GAAGA T G TC G GAG CG A A
TTCCTTGGCAGAAGAGGGCA
CAGCCAAGGC
GAM739 CACAAATCCAGCACTTCCTC 712 AGCAACACAT 2388 T GCACTTC-- T T- G
TCCATTTACTCTGTCAGGCT ATGGCTTTGT CACAAA CCA CTCTCCAT TAC CT T
GTATATGGGGAGCAACACAT G |||||| ||| |||||||| ||| ||
ATGGCTTTGTG GTGTTT GGT GAGGGGTA ATG GG C
C ATACACAAC T TC A

GAM740 AGGTAGTCAAGATTTTAACA 713 TGAGGTAGGT 2389 GTA A TTTT ACAT AT-- ACA
AACATCTTAATCCTCACAAC AAGTCATTGT AG GTCA GA AACAA CTTA CCTCACA A
AACCCTGTGAGGTAGGTAAG TTCA || |||| || ||||| |||| |||||||
TCATTGTTTCATGATAAACT TC TAGT CT TTGTT GAAT GGAGTGT /
AAA A ---- ACT- GGAT CCC

GAM741 TCCACGCTTAAACGAATGAC 714 TGCTATGTAT 2390 G TA - - ACTTT TG AG
TTTTATAGTGCAGCATGTGC TCTGCTTCCA TCCAC CT AA C GAATG TATAG C C
TATGTATTCTGCTTCCAGGT GGTG ||||| || || | ||||| ||||| |
GGA AGGTG GA TT G CTTAT GTATC G /
- CC C T ----- GT TA

GAM742 CTTCAGGTGGACGAAGAGGA 715 GAGGAAGTGC 2391 AG CGA- A A C C T AAA
AGTGCTGGCATTGCTGGAAA TGGCATTGCT CTTC GTGGA AG GGA GTG TGG ATTGC GG A

AGGTGCTGCAGTCCCACATG GG |||| ||||| || ||| ||| ||| ||||| ||
TCCCTGCCATCCACTCGAGG GGAG CACCT TC CCT TAC ACC TGACG TC G
CT ACCG - G - C - GTG

GAM743 CCTTCCTGTGGTTAGTAGGT 716 TGTGGTTAGT 2392 CT T AGTA TT TC CAC
TTCTGCTTCCTCACCAACCA AGGTTTCTGC CCTTC G GGTT GGT CTGCT CT C
GTGGGCAGTCACCAACCCGA TTCC ||||| | |||| ||| ||||| ||
AGG GGAAG C CCAA CCA GACGG GA A
-- - ---- CT GT CCA

GAM744 TCTTTATGTACTGTCAGGTG 717 AGTCTCAGCC 2393 T ACTG GG AG ----- AA-
CCAGAA CCC
GGACGCAGCTCAGGAAAGAC AGCTTTGGGA TCTTTA GT TCAGGT GACGC CTCA GG
AGAC ATC C
CCAGAAATCCCCCTCATGAT GGTG |||||| || |||||| ||||| |||| || |||| |||
CACAGAGTCTCAGCCAGCTT AGAAGT CA GGTCCG CTGTG GGGT CC TCTG
TAG T
TGGGAGGTGTCAGCCTGGAC C CA-- A- GA TTCGA GAC AGACAC TAC
ACCTGAAGA

GAM745 GCTGATAGGCCAGGTCAGCC 718 TGTCATAGGC 2394 T CC A - - C GTG
TGTGCTCGGCGGGTGTTGAC GGCCTTCTTC GCTGA AGG AGGTC GCCTGTG C TCGG GG T
CTCGATGTCATAGGCGGCCT AGT ||||| ||| ||||| ||||||| | |||| ||
TCTTCAGT TGACT TCT TCCGG CGGATAC G AGCT CC /
- -- - T T - AGT

GAM746 ACTACCAGCCTCCCACTGTG 719 TCGCCTGGAC 2395 CC - G T G A - AA CAGAGA
- CA T
GTGCCTGGTGGAGACCTGGC CACAAGTTTG ACT GTGGT CC GGTG AG CCT GGCC GGTA
GCTGTG TG TGC G
CAAGGTACAGAGAGCTGTGT ACCT ||| ||||| || |||| || ||| |||| |||| |||||| || |||
GCATGCTGAGCAACACCACA TGA CACCA GG CCGC TC GGG CCGG TCGT
CGACAC AC ACG /
GCCATTGCTGAGGCCTGGGC TT A - T - - T AG TAC--- C A- A
TCGCCTGGACCACAAGTTTG
ACCTGATGT
GAM747 CACAAGTGATGGTCCAACTT 720 GTAAGGATTT 2396 - G-- T-- GAATG- AGG
AGGG GG
TGTGGAATGGTAAGGATTTT TTAGGGTTGT ACAAGTG ATG TCCAACT TGTG GTA
ATTTTT TTGTTT C
TAGGGTTGTTTGGCCAGAAC TT ||||||| ||| ||||||| |||| ||| |||||| ||||||
AAGAGAAATAACTGCAGAAA TGTTCGC TAC GGGTTGG ACAC CGT TAAAGA
AACAAG /
ACACATATGGTTGGGAAACA G AAA TAT AAAAGA CAA G--- AC
TGCGCTTGTG

GAM748 GTCAAGATTTTAACAAACAT 721 TGAGGTAGGT 2397 A TTTT ACAT AT-- ACA

CTTAATCCTCACAACAACCC AAGTCATTGT GTCA GA AACAA CTTA CCTCACA A
TGTGAGGTAGGTAAGTCATT TTCA |||| || ||||| |||| |||||||
GTTTCATGAT TAGT CT TTGTT GAAT GGAGTGT /
A ---- ACT- GGAT CCC

GAM749 GCTTTTGCTCCAGATGGTTC 722 CCAGTGCCTT 2398 TT TCC T ATACTTT T - AA TC ACA
ATACTTTGCTTGGTCACAAG CAGAACTTTC GCT TGC AGA GGTTC GCT GG TCAC GGACA GC G
GACATCGCACAGTAAAGCTT TCTT ||| ||| ||| ||||| ||| || |||| ||||| ||
GTTCCGTGGTCCCAGTGCCT CGG ACG TCT TCAAG TGA CC GGTG CTTGT CG T
TCAGAACTTTCTCTTGCATG T- TTC T ACTTCCG C T C- T- AAA
GC

GAM750 TCCTTTTGACAAGAAATGTG 723 TGACAAGAAA 2399 T - AAATGT C AA-- CTGTT T
GTCGTGAAAATTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA TTGGA GC T
GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||
ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T
GA C G GTT--- - GGTA ----- T

GAM751 GCTATTTTAGAAGGTGTCCA 724 TCCCTGAGAC 2400 TTA -- GTGT GCA T T G GG -- TA
GTGTGAGGTGCAGCTGGTGG TCTCCTGTGT GAAGGTG TCCA GAGGT GC GG GGAGTCT GGGGA TTT GG C
AGTCTGGGGGAGGTTTGGTA AGCC ||||||| |||| ||||| || || ||||||| ||||| ||| ||
CAGCCTGGAGGGTCCCTGAG TTTCCAC AGGT CTCCG TG CC TCTCAGA TCCCT GAG CC /
ACTCTCCTGTGTAGCCTCTG --- TT ---- ATG T - G GG GT GA
GATTCACCTTTAGTAGT

GAM752 GGAAGGTCATTCACCCAATG 725 TCACCCAATG 2401 CATTCA T AA AA TT
CAAACAAAGCATTTTCTGCA CAAACAAAGC GGAAGGT CCCAA GC ACA GCA T
ATGTCAGCTTGGGAAACTTT A ||||||| ||||| || ||| |||
CC CCTTTCA GGGTT CG TGT CGT /
AA---- - AC AA CT

GAM753 GCTCCAAAGAACCAAGAGTG 726 CATTTCACTT 2402 T - ---------- CAC GAGATA TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC

GAM754 GCTCCAAAGAACCAAGAGTG 727 CATTTCACTT 2403 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM755 ACTGCACGTCAAGATGTTTA 728 CAAACCTTTA 2404 - AA TTTA-- A G
TGATTTTGCTAAAAACAAAC TCAGGATGAT ACTGCA CGTC GATG TG TTTT C
CTTTATCAGGATGATGCAGT GCAG |||||| |||| |||| || ||||
TGACGT GTAG CTAT AC AAAA T
A GA TTCCAA - A

GAM756 GCATGACTGCCATGGAGAGG 729 GGCGTAGATG 2405 G CC GGA -- T GC CAT - T
AT AT
GCGTAGATGCTGGCATAGTA CTGGCATAGT GCAT ACTG AT GAGGG CG AGAT TGG AGT
AC GCAT GAGG T
CTGCATATGAGGATTGTCCT ACTG |||| |||| || ||||| || |||| ||| ||| || |||| ||||
TCATGCTGTCACTCACCGAG CGTG TGAC TG CTCCC GC TCTG GCC TCA TG CGTA
TTCC /
GTCTCGTTCCCTCGAGTCAC G AC AG- TT - GA AC- C T C- TG
AGTGGTGC

GAM757 AGATGATTGAGCCGCGCACG 730 TGATTGAGCC 2406 CA-- AG-- AGCT - ------- TC--
CG
CTACAGTACAAGCTGCTGGA GCGCACGCTA GCG CGCTAC TACA GC TGGA GCCAGT
TGCTTCT G
GCCAGTTCTGCTTCTCGGCA CAGT ||| |||||| |||| || |||| |||||| |||||||
AGGAGCGATTTGCTGGTGTA TGC GTGGTG ATGT TG GCCT TGGTCG
GCGAGGA /
GACATCCGTGTCCGTGTAAA ACTG GGAA GCC- T ACAGATG TTTA AC
GGGTGGTGGTCACGTGGCCC
AATTTATGCT
GAM758 CTTTGTGGGAATGGCTCTAC 731 ACGCACCAGT 2407 TG A TCT----- C CGCAC T A
GA T C C
TTCGTAACGCACCAGTTGAA TGAAATCAGA G GG ATGGC ACTT GTAA CAGT GAA TCA
TAC GT TTC A
ATCAGATACTGTCTTCCAAT TACT | || ||||| |||| |||| |||| ||| ||| ||| || |||
GAAAACGTAAATGATTCACT C CC TACCG TGAA TATT GTCA CTT AGT ATG CA
AAG A
GAAATTATAAGTTATTCAAT CT C TAACTTAT - AAA-- - - AA - A T
GCCATCCCTCCAAAG

GAM759 ACTACCAGCCTCCCACTGTG 732 TCGCCTGGAC 2408 CC - G T G A - AA CAGAGA
- CA T
GTGCCTGGTGGAGACCTGGC CACAAGTTTG ACT GTGGT CC GGTG AG CCT GGCC GGTA
GCTGTG TG TGC G

CAAGGTACAGAGAGCTGTGT ACCT ||| ||||| || |||| || ||| |||| |||| ||||||| || |||
GCATGCTGAGCAACACCACA TGA CACCA GG CCGC TC GGG CCGG TCGT
CGACAC AC ACG /
GCCATTGCTGAGGCCTGGGC TT A - T - - T AG TAC--- C A- A
TCGCCTGGACCACAAGTTTG
ACCTGATGT
GAM760 CCGATGAACTGCTCCTTCCA 733 TTCCACATCT 2409 G -- CCT A AGACAC C- CA
CATCTAGACACAAGCAGACA AGACACAAGC CC ATGA ACTGCT TCC CATCT AAG AGA T
TTTTCTCACTTTCCACAGGT AGA || |||| |||||| ||| ||||| ||| |||
GGGATGTGGCAGTCCTCATG GG TACT TGACGG AGG GTGGA TTC TCT /
G - CC TGT - CACCT- AC TT

GAM761 GTGGAAGCAGGCTGGCTGCT 734 GGCAAGAAGC 2410 A A- TG GCTGGG A----- AT
GGGGCTTCAGGGATTTCCCC TGGTTGAGCT GTGG AGC GGC GCT GCTTC GGG T
ATATACGAGGCAAGAAGCTG GCCA |||| ||| ||| ||| ||||| |||
GTTGAGCTGCCAT TACC TCG TTG CGA CGGAG CCC /
G AG GT AGAA-- CATATA CT

GAM762 GCAAATCAGTCCATTTCACT 735 CATTTCACTT 2411 - ---------- CAC GAGATA TC
TTCACTGTCTGAGATAGGGT TCACTGTCTG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
CTCTAAGACCCAGGATACAA AGAT ||||||| ||||||| |||||||| ||||| |||||
GGGTGGAATGTAGCTATATG CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GACTCGATTTGC C TATCGATGTA AC- A----- AA

GAM763 TCCCTGCCATTGACAAGCTG 736 TCAGTTTTTT 2412 C-- ACA C TAT CG AAGG TTT
TATGACGTTGAGGAAGGCAA CATCTCTACA TCC TGCCATTG AG TG GA TTGAGG CAA T
TTTTCTTTTTGAGCCTCAGT ATGG ||| |||||||| || || || |||||| |||
TTTTTCATCTCTACAATGGC AGG ACGGTAAC TC AC TT GACTCC GTT C
AACAGGA ACA ATC T TT- TT GA-- TTT

GAM764 CTCTTGAGCATGCTGACCAG 737 GACCAGTGCT 2413 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM765 GTCTTCAGTTCCCTTTGCAG 738 TGCAGGAAGA 2414 CA C A GA T AG----- A C
GAAGAGTCGTGAGCACCATC GTCGTGAGCA GTCTT GTTC CTTTGC G AGAG CGTG CACC
TCAGGCCC A
AGGCCCCACAGGGTTTGAGG CCAT ||||| |||| |||||| | |||| |||| |||| ||||||||
GTGGGGCAGACGCGCCTCTC CAGGG CAAG GGAACG C TCTC GCGC GTGG
AGTTTGGG C
TCGGCAAGGTGAACCGGGAC C- T G TC C AGACGGG G A

GAM766 CAGGGCCTCGAACTCGTCGA 739 TCTTGTACTT 2415 TC A TC - T TT TTG CT
TGCGCTGCTTGGTGTTGCCC GTCCCGGCCT CAGGGCC GA C GT CGA GCGCTGC GGTG
CC G
TGCCGGATCTGCCGCAGCGT TG ||||||| || | || ||| ||||||| |||| ||
CTTGTACTTGTCCCGGCCTT GTTCCGG CT G CA GTT TGCGACG CCGT GG /
G CC - TT T C -- CTA CC

GAM767 GCCTGCCTGAACCCTGGGTC 740 CATGACGGCT 2416 A GG--- - A -- G AA- A- G
C
AGGAGAGAAACACTTGGGGA CTGAGTTCTT CCCT GTCA GGAGAGA ACA CTT GGGAGGGG
AGG CG CGTGGG T
GGGGAAAGGACGGCGTGGGC CCTG |||| |||| ||||||| ||| ||| |||||||| ||| || ||||||
TACCCATGACGGCTCTGAGT GGGA CGGT CCTTTCT TGT GGG TCCTTCTT TCT GC
GTACCC /
TCTTCCTGGGGCTTGTGTCT C GAAGA T G TC G GAG CG A A
TTCCTTGGCAGAAGAGGGCA
CAGCAAAGGC
GAM768 GCTTTTATCTTAGAGGCAGC 741 CAGCTGCAGT 2417 A TTAGAG A G GA -- A
AAATG
AGAAGGTTTGGAGCCAAGGA GTGAAAGGGG GCTTTT TC GCAGC GAAG TTTG GCC
AAGGA TG A
ATGAAATGATGAGGCGTCCT C |||||| || ||||| |||| |||| ||| ||||| ||
TCAGGTAATGAACTTCAGCT CGGGGA AG CGTCG CTTC AAGT TGG TTCCT GC /
GCAGTGTGAAAGGGGC A TGTGA- A - AA AC - GGAGT

GAM769 CTCTTGAGCATGCTGACCAG 742 GACCAGTGCT 2418 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM770 GGTGAGCAAGCCCAGGAGAA 743 AAGCCCAGGA 2419 G- A AGG --- TG A TGGG TG
TTTTATT
TGCTGCAATCTTGGGGGTGG GAATGCTGCA GGT AGC AGCCC AGAATG C CA TCT GG G
T
TTTTATTTATTTCTTTTTGC ATCT ||| ||| ||||| |||||| | || ||| || |
CAAATAGAGTGTGGATTCAT CCG TCG TCGGG TTTTAC G GT AGA CC T A
TTTAGGGGCTAGCTAAGCC AA A GA- TTA GT G TAAA GT TTTCTTT

GAM771 GGCCTGGGCGAGTCAGGCTT 744 CTGGGCGAGT 2420 CT A GGCTTG A T GT
GCGTCAGTATTCTCCAGTGC CAGGCTTGCG GGC GGGCG GTCA CGTC GTATTC CCA G
AATGGGAGTATAGACGATGA TCAG ||| ||||| |||| |||| |||||| |||
TGCGCCCCGCC CCG CCCGC TAGT GCAG TATGAG GGT C
C- G A----- A - AA

GAM772 GTCAGTGCATAACCTGCGTT 745 TCAAGCTGCC 2421 AC--- T CC---- AA GAAG T TG
A CG
CATCCGTTAAATCAGAAGCC ACATGATTGT TA CTGCG TCAT GTT ATCA CCATT G CTG
GCTTTGT A
ATTTGTGCTGAGCTTTGTCG AGCA || ||||| |||| ||| |||| |||||| | ||| |||||||
AGAAATAAAGCATAGTGTAG GT GATGT AGTA CGA TAGT GGTGA T GAT
CGAAATA G
TGGAGATGATCAAGCTGCCA GACAC T CACCGT AC AGA- - GT A AA
CATGATTGTAGCACAGTGTG
TTAAATGAC
GAM773 GCTCCAAAGAACCAAGAGTG 746 CATTTCACTT 2422 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM774 GCTTTGAAGGCAGCAGCATT 747 AGCAGCATTG 2423 A- CA G AGGT C
GTACAGGTGCTTCTCAAAGC TACAGGTGCT GCTTTGAAGGC GCAG TT TAC GCTT T
GTGGAACCTTGCAGGCCTTC T |||||||||| |||| || ||| ||||
AGGGC CGGGACTTCCG CGTT AA GTG CGAA C
GA CC G ---- A

GAM775 CCGCTCATTTTTTTTCTCTC 748 CTCATTTTTT 2424 TT TT C ----- T T GCC
TCTACCTTGTTTGGTTATGG TTCTCTCTCT CCGCTCA TT TTCTCT TCT ACC TGTT
GGTTATG A
CCACTTACATAGCCAGCATG ACCT ||||||| || |||||| ||| ||| |||| |||||||
GTGATGTGGAAAGAGAACTG GGTGAGT GG AAGAGA AGG TGG ACGA CCGATAC C
GTCTGAGTGG CT TC A TGTAG T - ATT

GAM776 GGGGTGCACAAGTGGATGGG 749 GTAAGGATTT 2425 G G- T-- GAATG- AGG
AGGG GG
TCCAACTTTGTGGAATGGTA TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
AGGATTTTTAGGGTTGTTTG TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
GCCAGAACAAGAGAAATAAC TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /
TGCAGAAAACACATATGGTT G AA TAT AAAAGA CAA G--- AC
GGAAACCATGCGCTTGTGAC
TTT
GAM777 AGGCTGCAGAACATGGAGGT 750 TTCCTGCCTC 2426 -- ACAT T CC CT
CACCGATGCTTGAACATTCC CCTATTTGCC AGGCT GCAGA GGAGG CA GATG T
TGCCTCCCTATTTGCCAGGC AGGC ||||| ||||| ||||| || ||||

TT TTCGG CGTTT CCTCC GT TTAC G
AC ATC- - CC AA

GAM778 CCTACTCCAAAATACTCACA 751 TCTACAGTGT 2427 A - A TC-- -- GA
CTGGACTGAATGAAGTCTAC CAATGTGTCT CCT CTC CAA ATAC ACACTG GACT A
AGTGTCAATGTGTCTTGAGA TGAG ||| ||| ||| |||| |||||| ||||
GAGG GGA GAG GTT TGTG TGTGAC CTGA T
- A C TAAC AT AG

GAM779 TTCTCCATGATGACAAGGAA 752 TGCTGGGCTC 2428 --- AGTC- CCATCC CACAG
CTCCCT GA- G A
GTCTCTGCCATCCTGGCCAC CCTGCATGAC AAGGA TCTG TGGC TGCTGGG
GCAT CA TG A
AGTGCTGGGCTCCCTGCATG AGTG ||||| |||| |||| ||||||| |||| || ||
ACAGTGAAAACAGTGACAAT TTCTT AGAC ACCG ACGACCT TGTA GT AC A
GTTCCAGCAAAGCCACCAGA GAA GAAAC C----- AA--- ------ ACA G A
CAAAGTTCTTAAGGTCACAG
GAGAG
GAM780 GGTGAACTTTTAGCTCCTGC 753 TGACAAGAAA 2429 - CA ---- T - AAATGT C AA--
CTGTT T
AGCTCCTTTTGACAAGAAAT TGTGGTCGTG CTG GC TCCTT TGAC AAG GGT GTGAA
TTGGA GC T
GTGGTCGTGAAAATTGGACT AAAA ||| || ||||| |||| ||| ||| ||||| ||||| ||
GTTGCTTTTGCTCCAGATGG GAC CG AGGAA ACTG TTC TCA TACTT GACCT
CG T
TTCATACTTTGCTTGGTCAC T A- CTAC C G GTT--- - GGTA ----- T
AAGGACATCGCACAGTAAAG
CTTGTTCCC
GAM781 TGAAGACTTCCTAAATTTGC 754 TTTGCACATT 2430 AC A TTGCA TTGCC
ACCAT
ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM782 CTCCCCTCTCACCAAGCATT 755 ACTGCAGGTA 2431 A CATTGT AG-- T A AAC
CAAG T- TT
GTGTGCAGACCTGTTAGAGA AAGGCATCTT CCAAG GTGC ACCTGT AG GA TGTCCGT
GGCT CCTG T
AACTGTCCGTCAAGGGCTTC GGGC ||||| |||| |||||| || || ||||||| |||| ||||
CTGTTTCTTCAGGCCAGTCA GGTTC TACG TGGACG TC CT ACGGGTA CTGA
GGAC C
GTCATGGGCATGTCACTGCA G ------ GAAA - A GT- CTGA CC TT
GGTAAAGGCATCTTGGGCCA
TAATTAG
GAM783 TGAAGACTTCCTAAATTTGC 756 TTTGCACATT 2432 AC A TTGCA TTGCC
ACCAT

ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM784 TGAGACGTCACCTAGACAAC 757 TTCCTGCCTC 2433 CG C---- CAACC- -- AAT C
CT
CGGCTGCAGAAATGGAGGTA CCTATTTGCC TGAGA TCA CTAGA GGCT GCAGA
GGAGGTAG GATG T
GCGATGCTTGAACATTCCTG AGGC ||||| ||| ||||| |||| ||||| |||||||| ||||
CCTCCCTATTTGCCAGGCTT ACTCT AGT GGTCT TCGG CGTTT CCTCCGTC
TTAC G
ACATTTCTGGTCTGCTGAGA AG CGTCT TTACAT AC ATC C AA
TCTCA

GAM785 GGAAGCCAGGTAGGTAGTCT 758 TAGAAGTAGT 2434 TAGGTAGT- AG A T CA
CCTCCT G
GAGTCAGGATTGGATCAACA AGTTTGATTC GGAAGCCAGG CTG TC GGAT GGAT ACAG
CTCTTGGG A
GCCTCCTCTCTTGGGGACTC TGGT |||||||||| ||| || |||| |||| |||| ||||||||
TCAAGAGCCTGTGTTCATCT CCTTTGGTCT GAT AG TCTA CTTG TGTC
GAGAACTC C
AGAAGTAGTAGTTTGATTCT TAGTTTGAT GA A - -- C----- T
GGTTTCC

GAM786 CCATGCAGTGATTGTCCTTG 759 TTCCTGGGAC 2435 GTCC-- TC-- CTTTTC A TCT---
TA AT
TTTCTCACATTCTTTTCCCA TTCAAATGTG T TTGTT TCACATT CC CAGGAGAT GAA
AACAT T
CAGGAGATTCTGAATAAACA ATTG | ||||| ||||||| || |||||||| ||| |||||
TATTAAGATGTTCTTCCTTT G AACAA AGTGTAA GG GTCCTTTA CTT TTGTA
A
GCATTTCCTGGGACTTCAAA TCTCAT TGTT ACTTCA - CGTTTC C- GA
TGTGATTGTAACAATACTCT
GATCAAGGTG
GAM787 GGGTGCACAAGTGATGGTCC 760 GTAAGGATTT 2436 - -- T-- GAATGG AGG
AGGG GG
AACTTTGTGGAATGGGTAAG TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
GATTTTTAGGGTTGTTTGGC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
CAGAACAAGAGAAATAACTG TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /
CAGAAAACACATATGGTTGG G AA TAT AAAAGA CAA G--- AC
AAACCATGCGCTTGTGACTT

GAM788 GTGTAATAGTCAAGGAAAAG 761 TCATTGGCAA 2437 AG- AA AAAA ACA- AT- GA A
ACACT
GGCAACAGTATTGGATCATT AGTGTCTCCC GTGTAAT TC GG GGGCA GT TG TC
TTCCTTAG A

CCTTAGACACTAATCAGCTG AAGA ||||||| || || ||||| || || || ||||||||
GGGAAAGAGTCATTGGCAAA CACATTG AG CC TCTGT CG AC AG AAGGGGTC
/
GTGTCTCCCAAGAATGGTTA GTA AA C--- GAAA GTT TG A GACTA
CAC

GAM789 GTGTTGCCAGGCTGGTCTCA 762 TCCTCAGCCC 2438 C C- AA- CCT C ATC
AATTCCTGGGCTCAGGAGAT TCAAGTGTGG GTGTTGC AGGCTGGT TC ATT GGGCT
AGGAG T
CTTCCCTCCTCAGCCCTCAA ATTA ||||||| |||||||| || ||| ||||| |||||
GTGTGGATTACCGGCCTAGC CGTAACG TCCGGCCA AG TGA CCCGA TCCTC /
AATGC A TT GTG ACT C CCT

GAM790 GGTGAGCAGCAGGCGAGTGA 763 AGTGAGCAAA 2439 - AG -- CAA TCAT------- A
GCAAAGCTTCATCTGTATTT GCTTCATCTG GGTG AGC CAGGCG AGTGAG AGCT
CTGT T
ACAGTCCCTCCCCATGGCTC T |||| ||| |||||| |||||| |||| ||||
TCATTACCGCCTGAGCTCCA CCAC TCG GTCCGC TTACTC TCGG GACA T
CC C A- CA --- TACCCCTCCCT T

GAM791 TTCAACAGGTATTTATCTGA 764 TTCAACAGGT 2440 --- C AAGT - ACA CC TTTTG
AGT
AGTACTGGGTACAGGCCAGT ATTTATCTGA TCAACAG GTATTTAT TG ACTG GGT GG
AGTTT TATAA A
TTTTTTGTATAAAGTAGTTA AGTA ||||||| |||||||| || |||| ||| || ||||| |||||
TTGTGTTTTGAACTACCACC AGTTGTC TATAAGTA AC TGAC CCA CC TCAAG
GTGTT G
ACAGTCATGCAAATGAATAT GAG A GTAC A --- A- TTTT- ATT
GAGCTGTTGAG

GAM792 GAGCTGCATCTTGGATTTCG 765 TGAAGAAGCA 2441 - T- A C T TC GCCGAGG CG
AT GG
CTTCCTCTTCTTTCTCAGCC GAGCAAGTGG CA CTTGG TTTCGCTT CTCT CTT TCA TTA
GTG TAGCAA G
GAGGTTACGGTGATTAGCAA AAAC || ||||| |||||||| |||| ||| ||| ||| ||| ||||||
GGGCAGTTGCTACCACTATA GT GAACC AAGGTGAA GAGA GAA AGT AAT CAC
ATCGTT C
AAGATACATGAAGAAGCAGA A TC A C C GA ACATAGA AT C- GA
GCAAGTGGAAACCAAGCTTG
ATCATGGCTT
GAM793 GCCTGGTTCATAAAACTTGT 766 TGAAAGACAT 2442 TGGT A TG ------- ---- TA
GCCTGATGTTCTAGCAGAAC GAGTTGTGTG GCC TCATA AACT TG CCTGAT GTTC G
CTTTATCAGGTGAAAGACAT ATGG ||| ||||| |||| || |||||| ||||
GAGTTGTGTGATGGC CGG AGTGT TTGA AC GGACTA CAAG /
T--- G GT AGAAAGT TTTC AC

GAM794 GGGCATAATTAGTCAGTGCA 767 TCAGTGCACT 2443 - TA T A ACAA - TTCAAACTT
TTT

CTAACAATTATGTACATTCA AACAATTATG GGGC ATAAT G CAGTGC CTA TTAT GTACA
GATTAT A
AACTTGATTATTTTAAATAT TACA |||| ||||| | |||||| ||| |||| ||||| ||||||
GATCTTCAGCTGTACTGTAA TCTG TGTTA C GTCATG GAT AATG CATGT CTAGTA
/
ATAGAGTACTGCATTGTAGT A -- - A A--- T CGACTT--- TAA
CT

GAM795 CATCCATGGCCATGAGTATT 768 TATTGATCTG 2444 T GCC AT TCT GC C
AGG G
GATCTGTCCCAGCCTGTGCA TCCCAGCCTG CA CCATG ATGAGT TGA GTCCCA
CTGTGCATTG TCCG CA T
TTGCTCCGAGGCAGTTCTGA TGCA || ||||| |||||| ||| |||||| |||||||||| |||| ||
GTGGATGATGTACAGATGGG GT GGTGC TACTCG ACT TAGGGT GACATGTAGT
AGGT GT T
ATTCCTCAGCTCATTTGCGT T GTT -- CCT A- - GA- C
GGTTG

GAM796 CAAAATACCAAACGTAGTAC 769 TACCAAACGT 2445 A C T G CA-- GATCTA
AAAGGTCC GC
ACAGCAAATTTATGTCTCAG AGTACACAGC TAC CAG AAATT AT TCT GCTACAT CAAGTT
CAGGA C
CTACATGATCTACAAGTTAA AAAT ||| ||| ||||| || ||| ||||||| |||||| |||||
AGGTCCCAGGAGCCCCATCC ATG GTC TTTGA TG AGA CGATGTG GTTCAA
GTCCT C
TGAACTTGGAAAGTGTAGCC - - - G CTTC AAAG-- -------- AC
TTCAGAGGTAGTTTCTGGTA
CATCGTTTTG
GAM797 GCTCCAAAGAACCAAGAGTG 770 CATTTCACTT 2446 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM798 ATGGAGAGTGTTTGATGTCC 771 CACCGAATTG 2447 AG T-- ATAAT---- - AAGAC
AGATAATGCCCGAAGACTTA GACATCTACA ATGGAG TGTT GATGTCCAG GCC CG T
GACATGCGGCTTCACCGAAT GCAA |||||| |||| |||||||||| ||| ||
TGGACATCTACAGCAAGTTC TGCCTT ACGA CTACAGGTT CGG GT T
CGT GA CAT AAGCCACTT C ACAGA

GAM799 CTGTCACCCTGGTCTATCCA 772 TGACAGTAAG 2448 G CC G A---- C A ATT
CATCTCCTATTCCTGAGGAG AGCAGTGAGA CT TCAC TG TCT TC AC TCTCCT C
AGTTGACAGTAAGAGCAGTG G || |||| || ||| || || ||||||
AGAG GA AGTG AC AGA AG TG AGAGGA /
G -- G ATGAC T - GTC

GAM800 CCCTAGAAGAAACTTTTTTC 773 TGGAAGGCAG 2449 AA A TTTTCCC---- AG GGCT T AT
CCAGAAAATGAGGCCTGGCT TGTTTTCTTG CCCTAG GAA CTT AGAAAATG GCCT GG GCTC C
GGTGCTCATCCTGAGTTCCT TAAC |||||| ||| ||| |||||||| |||| || |||| GGAAGGCAGTGTTTTCTTGT GGGGTC CTT GAG TCTTTTGT CGGA CC TGAG / AACCATCTGAGATTCCTGGG -- A TCTACCAATGT GA AGGT T TC G

GAM801 TGTTGGGGAGCAATGGGATG 774 TCACAGGGAG 2450 AA AT CTC AAA- - GT C A TG TGTGG
AAGGCTCACAGGGAGAAAAG AAAAGACTAG TGGG GAAGG ACAGGGAG AGA CTA CTCT GGT TGG GC T
ACTAGTCTCTCGGTATGGTG TCTC |||| ||||| |||||||| ||| ||| |||| ||| ||| || GCTGTGGTGGTATGCTGTTA ACCC CTTCT TGTTTCTT TCT GAT GGGA TCG ATT CG /
AGCTAGGGTGTAGCTCTCAG -- -- T-- GGAC C GT - A GT TATGG GTTCTTTGTTTCTTCCCCAG ACCAAAGGCA
GAM802 CCACTTGCAATTATTTGAGG 775 TGCCGTGGAG 2451 A AT AACT- G T TA A--- GACCC
AACTCCGCCGCTGGCGCCCA GCCTCCCTTC CC CTTGCA TATTTGAGG CC CCGC GGCGCCCAT CC GC C
TTACCAGCGACCCCACAGAA AAGT || |||||| ||||||||| || |||| ||||||||| || || GCCACCGGCGTGGGTGCCGT GG GAACGT GTGAACTTC GG GGTG CCGTGGGTG GG CG A
GGAGGCCTCCCTTCAAGTGC - C- CCTCC A - C- CCAC AAGAC TGCAAGGG

GAM803 AGTCAGTAGCGCCACATCTG 776 TAGCGCCACA 2452 CA TT ATA T --- GG --- C G T AT
GTTTATAAGTAAGAGATCCC TCTGGTTTAT CA TCTGG T AG AAGAGATC CC GC GA AAT CTATTTTG GT G
GGGCGACAATGCTATTTTGT AAGT || ||||| | || |||||||| || || || ||| |||||||| ||
GTATGCCAACCTAAGATGGG GT AGATT G TC TTCTTTAG GG CG TT TTA GGTAGAAT CA C
ATTATTAAGGCAGGACTGAT A- GG AG- - TCA A- GAA A G C AC TTCTTCTGAGGGTTAGAATG GCTAAGCGACT
GAM804 GTTATGTGGGATATGGAGTT 777 TCATACAACT 2453 - TAC CC -- T A AA- A- G
ACTCTTTCCAGGGCTTACAG TCAGCATCCA TATGGAGT TCTTT AGGGCTTACA GG TGCTGAA GT ATGGT CCT T
GTTGCTGAAAGTAAATGGTA GTGT |||||||| ||||| |||||||||| || ||||||| || ||||| ||| CCTGTTAAGGAAATCATACA ATGTCTTA AGAAA TTTTGGGTGT CC ACGACTT CA TACTA GGA T
ACTTCAGCATCCAGTGTGGG C --- -- GA T - ACA AA A TTTTAAAGAATTCTGTACTT

CCATTTATAAT
GAM805 GACAGAAATGAAAGGCATTA 778 AAGGAACTCA 2454 A ATTATT - AA AA- C G AGT --
- GAAAAC
TTCTTGCCTTCAAGGAACTC CAGTCTAGTG GGC CTTG CCTTC GG CT ACA TCT
GGGCTG TCA T
ACAGTCTAGTGGGCTGTCAG GGCT ||| |||| ||||| || || ||| ||| |||||| |||
AAAACTAAGCAAATGATTCC CCG GAAC GGGAG CC GA TGT AGA CCTGAC AGT
A
AGTCCAGAGTGTTAGGTGCC - GT---- A A- GTG T G --- CTT AAACGA
AGAGGGACAAGTGGCCAGCT
GTCTGTC
GAM806 GCTCCAAAGAACCAAGAGTG 779 CATTTCACTT 2455 A AA T - TTC--- - GT GAG
AG- TC
CAAATCAGTCCATTTCACTT TCACTGTCTG CC GAG GCAAATC AGTCCAT AC TTTCACT CT
AT GGTC T
TCACTGTCTGAGATAGGGTC AGAT || ||| ||||||| ||||||| || ||||||| || || ||||
TCTAAGACCAGGATACAAGG GG CTT CGTTTAG TCAGGTA TG AAGGTGG GA TA
CCAG /
GTGGAATGTAGCTATATGGA A C- - C TATCGA T -- ACA GGA AA
CTCGATTTGCTTCCGGACCT
TTTCCAGAGC
GAM807 CCGAGGTCGTGCCACTGCAG 780 TCTGTGGTAT 2456 --- AG GCCA AGCA C
TCTAA- T
TCCACCTGGCCAACACAGCA GACAGAACTG TGCCAC TGC TCCACCTG ACAC GGCCT TC
AATAATAAT A
GGCCTCTCTCTAAAATAATA GG |||||| ||| |||||||| |||| ||||| || |||||||||
ATTATTATTATTGTTATTCT ATGGTG ACG GGGTGGAC TGTG CCGGA AG
TTGTTATTA T
TGACAGGCCAGTGTAGAACA TCT -- AAGA A--- C TTCTTA T
GGTGGGGCATCTGTGGTATG
ACAGAACTGGG
GAM808 GCTCCAAAGAACCAAGAGTG 781 CATTTCACTT 2457 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM809 AGAATGGGGAAGAATACTGA 782 TTGGAGCAGG 2458 - - TA AA T CA TCT AC-
CT
ATTAGCTGAGCACATTCTGG TTTCATTCTC AGAAT GGGGAA GAA CTG TTAGC GAG CAT
GGAC AATT G
ACACAATTCTGACCAATTTC CAAT ||||| |||||| ||| ||| ||||| ||| ||| |||| ||||
AGTCTCATGATCTCTGTTGG TCTTA CCTCTT CTT GAC GGTTG CTC GTA TCTG
TTAA A
AGCAGGTTTCATTCTCCAAT A A TG GA T TA C-- ACT CC
TCT

GAM810 GTGTATGTGTGTGTGTTACT 783 TGTAAACATC 2459 T T- - T AGTG A
GGCATCTAGTGGGTAGGGGC CTACCATGCA GTGTATG GTG GTGTT AC GGCATCT GGT G
CAGGGATGCTGTAAACATCC C ||||||| ||| ||||| || ||||||| |||
TACCATGCAC CACGTAC CAT TACAA TG TCGTAGG CCG G
- CC A - GA-- G

GAM811 GGTTTTTCGGTACTTCGAAT 784 GCCTGTAAAG 2460 ---- CGA TTT
AGGCCATTTTCTCCTGGCCT TTTCTGCTGA GGTTTTTCGGT ACTT ATAGGCCA T
GTAAAGTTTCTGCTGAGAAA GAAA |||||||||||| |||| ||||||||
TC CTAAAGAGTCG TGAA TGTCCGGT C
TCTT A-- CCT

GAM812 GGGTGCACAAGTGATGGTCC 785 GTAAGGATTT 2461 - -- T-- GAATG- AGG
AGGG GG
AACTTTGTGGAATGGTAAGG TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
ATTTTTAGGGTTGTTTGGCC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
AGAACAAGAGAAATAACTGC TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /
AGAAAACACATATGGTTGGA G AA TAT AAAAGA CAA G--- AC
AACCATGCGCTTGTGACTT

GAM813 TCCCAGTCATCACAGTCTGG 786 CATCACAGTC 2462 AGT GG GA CT AA A TACT CTC
T TT- TAGC
TTTCTTGATATCCTGAAAGA TGGTTTCTTG CT TTTCTT TATC G AG AGA GGGCAC GT
GG CTG T
AGATACTGGGCACCTCGTTG ATAT || |||||| |||| | || ||| |||||| || || |||
GTTCTGTAGCTTCATCAGTT GA AAAGGG ATAG T TC TCT CCCGTG CA TC GAC
/
TCTCACAATGTGCCCTCTCC --- AA TG AG AC C ---- TAA C TTT TACT
TCATGAGATAGTGGGAAAAA
AGTATTTGGGA
GAM814 GTTTCCCACTTTTCTCCCAT 787 TCTGTCATTT 2463 CTC A TCA T
CCATAAAAAGC G
CTGTCATTTTTCTCTTTCCA TTCTCTTTCC GTTTCCCACTTTT CC TCTG TTTTTC CTTT
TAATG T
TAAAAAGCTAATGGTGACGT ATAA |||||||||||| || |||| |||||| |||| |||||
TATCAAAGAGTGAAGGAGTC CAAGGGGTGGGAA GG AGAC AGGAAG GAGA
ATTGC G
AGAGGCTAAGGGTGGGGAAC TC- - TG- T AACT------- A

GAM815 GGTGCACAAGTGATGGTCCA 788 GTAAGGATTT 2464 - -- T-- GAATG- AGG
AGGG GG
ACTTTGTGGAATGGTAAGGA TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
TTTTTAGGGTTGTTTGGCCA TT ||||||| |||| ||||||| |||| ||| |||||| ||||||

GAACAAGAGAAATAACTGCA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /
GAAAACACATATGGTTGGAA G AA TAT AAAAGA CAA G--- AC
ACCATGCGCTTGTGACT

GAM816 TGCAGATTCTGATTCAGTAG 789 TGATTCAGTA 2465 AT G- GT TGG TG CCTGA CT-
TCTAACAG C
GTTTGTGGTTGGTCCTGAAG GGTTTGTGGT TCT ATTCA AGGTTTG T GT AGCA GCATT
GCC C
CACTGCATTTCTAACAGGCC TGGT ||| ||||| ||||||| | || |||| ||||| |||
CCCAGGTGATGCTGCTGCTG AGA TGAGT TTCAAAC G CA TCGT CGTAG
TGG C
CTACACTGGACCAAACTTTG CG GG -- CA- GT CATCG CGT -------- A
AGTGGAGAGCCTGCA

GAM817 GCTCCAAAGAACCAAGAGTG 790 CATTTCACTT 2466 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM818 TGCTATCAAAGTGATTTCAC 791 GGCAGGAAGT 2467 G TC - - AGTG A GATAACA
TCTC-- - T
TGCCCTCAGTGGCCACCGTG GGCAGTTCAG AAGT ATT ACTGCC CT C GCC CCGT
GTTGAC GG AT G
ATAACAGTTGACTCTCGGAT TGAT |||| ||| |||||| || | ||| |||| |||||| || ||
TGCTGTACCTCATATGTCAA TTTA TGA TGACGG GA G CGG GGCA CAACTG CC
TG C
CACCGCAGACGGAGGCAGGA G CT T A GA-- A GACGCCA TATACT A T
AGTGGCAGTTCAGTGATTTT
GCTAATTATA
GAM819 CTCTTGAGCATGCTGACCAG 792 GACCAGTGCT 2468 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM820 GCTATGAGGCTGTCCTCAGG 793 TATAACAGCC 2469 ATGA CTC TCA ATG --- - GC
TTA CT
GTTCAGCTATGATAGAGACT ACCTTGACAG CT GGCTGTC AGGGT GCT ATAGA GACT
CA TGGC GG T
CAGCTGGCTTAGGCTTCATC TCGA || ||||||| ||||| ||| ||||| |||| || |||| ||
CACTGCCAATGAAGTCAAAT GA CTGACAG TTCCA CGA TATTT CTGA GT ACCG
CC C
TTATAACAGCCACCTTGACA AG-- --- C-- CAA AAA A A- TCA TA

GTCGAAGC

GAM821 GCTGCTGTGGAATATTGTTG 794 TGCGGTGGTA 2470 G - AT GTT CT TG AAATTG
AG TG GGAA
ATTTCTCACTGTGGCCCGAA GGTTGTAGAT CTGT GGA ATT GATTT CACTG GCCCG
TGG C GCAG G
ATTGTGGAGCTGGCAGGGAA TCTT |||| ||| ||| ||||| ||||| ||||| ||| | ||||
GTGTGTTGTTGGAGTCGAGC GACA CTT TAG TTGGA GTGGC CGGGT GCT G
TGTT /
CTGGGCTGCGGTGGTAGGTT G A CT ATG TG GT CCGA-- GA GT GTGT
GTAGATTCTTCAACAGGGGC

GAM822 GCTCCAAAGAACCAAGAGTG 795 CATTTCACTT 2471 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM823 AAAGGAAACACTGATGGGAA 796 AACACTGATG 2472 A C T GAA- AT AGACTCCA
ATCTA AA
AGTATGGGGAAGACTCCAAG GGAAAGTATG AAAGGAA CA TGA GG AGT GGGGA
AGCTT TGACCTG G
CTTATCTATGACCTGAAGGA GGGA ||||||| || ||| || ||| ||||| ||||| |||||||
CCAGGTCGGGGAGCTCCTGT TTTCCTT GT ACT CC TCG TCCCT TCGAG
GCTGGAC G
CCCTTCGCTATGACCTCACT - C - AGTA CT GTCC---- GG--- CA
GTTCCTTT

GAM824 CTCAAATACTCATCTGATAA 797 TGGCAAGATG 2473 ATAA T GAGAAA TGA GGATG
AAGA GG C CA
AGCTTACGGGAGAAAAGTTC TCGGCGGTCA AGC TACGG AGTTC CCTG GC TGTC
CGGT AGT G
TGACCTGGGATGGCAAGATG GT ||| ||||| ||||| |||| || |||| |||| |||
TCGGCGGTCAGTCAGGATGC TTG GTGCC TCAGG GGAC CG ACAG GTTA
TCG G
TATTGAAGACAGCAGACAGG ---- - AGAG-- CCC AGA-- ---- AA - TA
CCCGGACTGAGACCGTGGTT
GATGACTGGG
GAM825 TTCACAGAGGAACTTAAGAA 798 AGGAACTTAA 2474 CAGA A AAGAA GA-- G G
GTATGGAGTGACGACTTGGG GAAGTATGGA TTCA GGA CTT GTATG GT ACGACTTG G
TTCGAGTTGTGATGCTACAT GTGA |||| ||| ||| ||||| || |||||||
ATGATAAAGCTCCAGTTGAA AAGT CCT GAA TATAC TA TGTTGAGC T
TGA- C ATAG- ATCG G T

GAM826 GAACAGGGTTTATATTCGAA 799 TGAGTGCTAT 2475 ATAT----- A AGA TGA GA

GCACAGACGTTGACCGGACT GACAAACCTG GAACAGGGTTT TCG AGCAC CGT CCG C
TTGGATGAGTGCTATGACAA GAAG |||||||||| ||| ||||| ||| |||
ACCTGGAAGCCCTGTTT TTTGTCCCGAA AGT TCGTG GTA GGT /
GGTCCAAAC A A-- --- TT

GAM827 GGCGGATGATCACTGGGAAC 800 TGGCTGGATC 2476 TC AACA C ---- G C C --- TTC
ATGGCCCTCATCCAGGTGCA CCTGATGGCC A ACTGGG TGGCC TCA TCCAG TG AGGC ACGGT GGTGGGC C
GGCCACGGTGGTGGGCTTCC ACTT | |||||| ||||| ||| ||||| || |||| ||||| |||||||
TGGCGTCCATCGCAGCCGTC T TGACTT ACCGG AGT AGGTC GT TCTG TGCCG CTACCTG T
GTCTTTGGCTGGATCCCTGA TA C--- T CCCT G T C ACG CGG
TGGCCACTTCAGTATTCCGC
ACGCC
GAM828 CGCGTGATTGCAGCATCTGT 801 AGGAGATGGA 2477 GAT- - A G GCG T A CT- A
CCAGCGCTTATTCGAGCTCT AGAAGTATGT CGCGT TGCA GC TCT TCCA CTTAT CG GCT CT A
CTAAGAAGCCTAGCCGTGTA ACAA ||||| |||| || ||| |||| ||||| || ||| ||
GGAGATGGAAGAAGTATGTA GCGCA ATGT TG AGA AGGT GGATG GC CGA GA G
CAAGACGCG GAAC A A - AGA T - TCC A

GAM829 TATAAAAATGGCTTCTGCAT 802 AAGCTGCAGT 2478 AAAAT TT T - TT --- CAC
CTGACCATTGCTGAAGGCAC CGCTGAACTG TATA GGC CTGCA CT GACCA GCT GAAGG C
CCATATCTTCACTGGCCTTG TA |||| ||| ||||| || ||||| ||| |||||
GTTAAGCTGCAGTCGCTGAA ATGT TCG GACGT GA TTGGT CGG CTTCT C
CTGTA CAAG- CT C A TC TCA ATA

GAM830 AAGGGTTGTTTTGTTGTTAG 803 TGAAGCTAGA 2479 T TGTTGT AA A-- GTCCATT
GTAAATAGATATTAGGCAGT TACCTAAAGC AAGGGT GTTT TAGGTA TAG TATTAGGCA T
CCATTTCTAAAATATGCCTG TACC |||||| |||| |||||| ||| |||||||||
ATGAAGCTAGATACCTAAAG TTCCCA CGAA ATCCAT ATC GTAGTCCGT C
CTACCCTT T ------ AG GAA ATAAAAT

GAM831 ATTGACGCACAGCAGTGGGG 804 TCCTCCAGTG 2480 C A GT TTTACC - CC -- G A CC T
AGAACAGCGTCTTTTACCTG GCGTTCTTTT AG AGTGGGGAGAAC GC CT TGT CA GAAGC CA GA GC CGTT G
TCACCGAAGCCAGGAAGCCC TACT || |||||||||||| || || ||| || ||||| || || || ||||
CGTTTGTAAGCGTGTGTTGT TC TCATTTTTCTTG CG GA ACA GT TTTCG GT TT TG GCGA T
GGTGCTTTATTGTACATCCT - - GT CCTCCT T TA TG G G T- A
CCAGTGGCGTTCTTTTTACT
CTAATGTTCTT

GAM832 GTTCACAGAGGAACTTAAGA 805 AGGAACTTAA 2481 AGA A AAGAA G ---- TG
AGTATGGAGTGACGACTTGT GAAGTATGGA GTTCAC GGA CTT GTATG AGTG
ACGACTTG G
GGTTCGAGTTGTGTGATGCT GTGA |||||| ||| ||| ||||| |||| ||||||||
ACATATGATAAAGCTCCAGT CAGGTG CCT GAA TATAC TCGT TGTTGAGC /
GGAC A-- C ATAG- A AGTG TT

GAM833 CTCCGTGATCTCACTTATAT 806 TCACAGAAGC 2482 G A - ATA--- G AAA
GTGGAATCTAAAAATGATAG AGAGTGTAGA CTCC TG TCT CACTT TGTG AATCTA A
ATTCACAGAAGCAGAGTGTA CAGG |||| || ||| ||||| |||| ||||||
GACAGGAG GAGG AC AGA GTGAG ACAC TTAGAT /
- - T ACGAAG - AGT

GAM834 GCTTTACAAGTCAGGTGTAG 807 AGTCAGGTGT 2483 --- A - - ATG T CCTCTAC
GTTGCATGTCTCAGTCCTCT AGGTTGCATG GCTTT ACA GT CAGGTGTAG GTTGC TC CAGT
C
ACCATCCTGCACTGTGAGCA TCTC ||||| ||| || ||||||||| ||||| || ||||
GCACTATACCTGTGCGTGTC CGAAA TGT CG GTCCATATC CGACG AG GTCA /
TGAAAGC GTC G T A --- T CGTCCTA

GAM835 GCTCCAAAGAACCAAGAGTG 808 CATTTCACTT 2484 A AA T - TTC--- - GT GAG
AG- TC
CAAATCAGTCCATTTCACTT TCACTGTCTG CC GAG GCAAATC AGTCCAT AC TTTCACT CT
AT GGTC T
TCACTGTCTGAGATAGGGTC AGAT || ||| ||||||| ||||||| || ||||||| || || ||||
TCTAAGACCAGGATACAAGG GG CTT CGTTTAG TCAGGTA TG AAGGTGG GA TA
CCAG /
GTGGAATGTAGCTATATGGA A C- - C TATCGA T -- ACA GGA AA
CTCGATTTGCTTCCGGACCT
TTTCCAGAGC
GAM836 TCTGGGAACTTTGTCCCAGA 809 TCACTGGGAA 2485 --- TG -- A TGC T AT
GGGGCACCTGCCGTGTATTA AGTATCTCCC TCTGGGA ACTT TCCCA GAGGGGC CC CGTG
ATT G
TGGTGATCACGTGGGCCCCT AGA ||||||| |||| ||||| ||||||| || |||| |||
CACTGGGAAAGTATCTCCCA AGACCCT TGAA AGGGT CTCCCCG GG GCAC TAG /
GA CTA -- CA - T-- - TG

GAM837 TACATTTCACTTTCACTGTC 810 CATTTCACTT 2486 CAC GAGATA TC
TGAGATAGGGTCTCTAAGAC TCACTGTCTG TACATTTCACTTT TGTCT GGGTC T
CCAGGATACAAGGGTGGAAT AGAT |||||||||||| ||||| |||||
GTA ATGTAAGGTGGGA ATAGG CCCAG /
AC- A----- AA

GAM838 ATAGTAAACCAAGATGTGAT 811 TGACTTCCAT 2487 - AG--- G A AAA G C
AGAAAAAAAGGTGACTCGTT CAGGTACTGG ATAGT AAACCA AT TGAT GAA AAG TGA T

GGCTTGACTTCCATCAGGTA TGGT |||||| |||||| || |||| ||| ||| |||
CTGGTGGTTTCACTGT TGTCA TTTGGT TG ACTA CTT TTC GTT C
C GGTCA G C CAG G G

GAM839 TGAAGACTTCCTAAATTTGC 812 TTTGCACATT 2488 AC A TTGCA TTGCC ACCAT
ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC T
AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM840 GGTGGGGACCCCGGGCCGCA 813 GACAAGATGC 2489 C G---- - C -- G AAT- A GCCTA
TCCTGGCGCTCGTGCGGAAT TGGAGCAGCT GGA CCCGG CC GCATC TG GCGCTCGT CGG AGG GCTTCA A
AGGAGCTTCAGCCTAAAGAA GGGC ||| ||||| || ||||| || |||||||| ||| ||| ||||||
TGTGAAGCACTTTGTGCTGG CCT GGGTC GG CGTAG AC TGTGAGCA GTC TTC CGAAGT A
ACGAGTGTGACAAGATGCTG C GACGA T A AG G GTGT A GTAAG
GAGCAGCTGGGCTCCCCTCC

GAM841 TCCCTCACTGGGTAGTAGAG 814 CATAAAGTAG 2490 A G A GAG G AGGACATAAA AA----- CT AT
AAGATCTGAGGACATAAAGT GGAAAGCCCA CT GGT GTA AA ATCTG GTAGGG AGCCCA TC T
AGGGAAAGCCCACTTCATTT CTTC || ||| ||| || ||||| |||||| |||||| ||
TGATCTGGGCTGGGAAGTGC GA CCA TAT TT TAGAC CGTCCC TCGGGT AG /
CCTGCCAGCGACAGATGTTA G A C GA- G AGCGAC---- GTGAAGGG CT TT
GTATCACCAAGGAAGGGA

GAM842 AGGGGAGCGGTAGTTACGTT 815 GCGGTAGTTA 2491 G --- AC ATA AA-- C C
GCATAGTGGTCAAAGCTGCC CGTTGCATAG AGGGGA CGGT AGTT GTTGC GTGGTC AG TGC G
GAGGTACTCCAGGGCCGCAC TGGT |||||| |||| |||| ||||| |||||| || |||
GGTAGCACAGCTGATACTGG TCTCCT GTCA TCGA CGATG CGCCGG TC ATG A
TCCTCT G TAG CA GCA GACC - G

GAM843 ACATGGGAGTCTTTTTCTAT 816 GGAGTCTTTT 2492 - G TT CT AA ATTT CATCCATGC T TT
CTCATAAAATATTTGGGAAC TCTATCTCAT CAT GGGA TCT TTCTAT CAT AAT GGGAA AGGAA AT T
ATCCATGCAGGAATATTTTT AAAA ||| |||| ||| |||||| ||| ||| ||||| ||||| ||
AGTTTTCCTTCTTTCCCTCA GTA TCTT AGG AAGATG GTA TTG CCCTT TCCTT TG /
AGTTGCATGTGTAGAATGGG A G GT T- CG AACT TCT------ T AT

AGTTCTAATGT

GAM844 GCTCCAAAGAACCAAGAGTG 817 CATTTCACTT 2493 T - ---------- CAC AGATAG
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT
TGTCTG GGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| |||||| ||||
TCTAAGACCACGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGGC
CCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM845 TGCCCAGTCTTATATTACTT 818 GCCACAAATA 2494 CCA T A---- G- CTT AACCAT
CC A
GTGATCTTGAAATGGAAACC TAGATAAAGC TGC GTCT ATATT CTT TGAT GAAATGGA
GT TGTT T
ATGTCCTGTTATTGAACAAG A ||| |||| ||||| ||| |||| |||||||| || ||||
CTCTTCTCTATTTTTTCATC ACG TAGA TATAA GAA ACTA TTTTATCT CG ACAA
T
AGAAAGCCACAAATATAGAT AAA - ACACC AG CTT CTTCT- A- G
AAAGCA

GAM846 CTGCTGGCTTAGTGCCTCAG 819 TTAGTGCCTC 2495 CT CCT-- ACTT A G
AACTTTGGTGTATTGGTCTC AGAACTTTGG CTGCTGG TAGTG CAGA TGGTGT TTG T
AGACACCACTTTGCCATCCA TGTA ||||||| ||||| |||| |||||| |||
CTATCCGGCGG GGCGGCC ATCAC GTTT ACCACA GAC C
T- CTACC C--- - T

GAM847 GGGCGCTACAGCTCACTAGA 820 TCACTAGAGA 2496 TACA AG AC G G GAAT G
TCAA TT
GACACGACTCAGTGGAGTGC CACGACTCAG CGC GCTCACTAG ACACG TCA TGGA TGCCA
CC ACAC GG G
CAGAATCCGACACTCAAGGT TGGA ||| ||||||||| ||||| ||| |||| ||||| || |||| ||
TGTTCCGTGTGGGCATGGCA GTG TGAGTGGTC TGTGT AGT GCCT ACGGT GG
TGTG CC /
TCCGTGAATGTGTGCCTGGT ---- CG A- - - AC-- G ---- TT
GAGTGTGTCC

GAM848 GAGGTTAAAAGGCTTGGAAC 821 TTGGTCACCT 2497 A- G T C TT- G TA
AAGTTACTAAGGCTACTATG TCTTCCAGTG GAGGTTA AA GCT GGAA AAG ACTAAG C C
CTTGGTCACCTTCTTCCAGT TTAC ||||||| || ||| |||| ||| |||||| |
GTTACTGACCTC CTCCAGT TT TGA CCTT TTC TGGTTC G T
CA G - C CAC - TA

GAM849 GGTGAATTTCCGGGTGTTTG 822 TTCCTCAGGC 2498 GT C A CTAA-- - TTTCT ATA
TGTTCA AT
CCAAACTCTAACTAGGTTTC TTCAAGTGTG CCGG GTTTG CA ACT CT AGG AGGA ATG
CTCTG T

TAGGAATAATGTGTTCACTC ATAA |||| ||||| || ||| || ||| |||| ||| |||||
TGATTACCAGGGCATGCCTC GGCT TAAAT GT TGA GA TCC TCCT TAC
GGGAC /
CTTTCCTCAGGCTTCAAGTG GC A G ACTTCG C TT--- CCG ------ CA
TGATAAATCGTCGGAATTTG
ACC
GAM850 CTGAGATGAACAGGTATTTA 823 TGAACAGGTA 2499 ATGAA T A- - A TG ATTC-----
GG TT
CTGAGCAGTTGTATTCAGAT TTTACTGAGC CTGAG CAGG ATTT CTG AGC GT T
AGATATG TC C
ATGGGTCTTCATGAATCATG AGTT ||||| |||| |||| ||| ||| || | ||||||| ||
TTTAACAATCAGATGACCGC GACTT GTCC TGAA GAT TCG CA A TTTGTAC AG
/
TATAGGCAAGTTCCTGAGCT CGA-- T CG A C GT GACTAACAA TA TA
TCAG

GAM851 GAAGGTCTGCGTCACGGTGA 824 TCACGGTGAA 2500 T C----- T TC T-- TTAC- -
CA
AAATTCGGGATGTTTACAGA AATTCGGGAT GAAGG CTGCGT ACGG GAAAAT GGGA GT
AGAG CAT C
GCATCACAAATGCCTCTCTC GTTT ||||| |||||| |||| |||||| |||| || |||| |||
TCGCCGCTCTCTCATTTTCT CTTCC GACGTA TGTT CTTTTA CTCT CG TCTC GTA
/
TTGTATAACTATGCAGCCTT - TCAATA T CT CGC CTCTC C AA
C

GAM852 GTCGTTACCATTCATAGAGC 825 TTGGCCGCCT 2501 G A AGA CC- A ---- TG- G
AGAGTTACCTGGACCGCATG TAACCAGCTT GTC TTACCATTC TAGAGC GTTA TGG CCG
CA TG C
TGGCAACAAACTGATATTGG TAGA ||| ||||||||| |||||| |||| ||| ||| || ||
CCGCCTTAACCAGCTTTAGA CGG AATGGTAAG ATTTCG CAAT GCC GGT GT AC A
ATGGTAAGGGC G - AC- TCC - TATA CAA A

GAM853 GTTCTGTGGGCAGTGGCATG 826 GCAGTGGCAT 2502 TG GGG A A A- G T
ACAGATTTGGGTTTCTGAAA GACAGATTTG GTTC T CAGTGGC TG CAG TTT GG T
GATTGCCAGCTACTGGGTGG GG |||| | ||||||| || ||| ||| ||
AGC CGAG G GTCATCG AC GTT AAA TC /
GT G-- - C AG G T

GAM854 GCTTTTGCTCCAGATGGTTC 827 CCAGTGCCTT 2503 TT TCC T ATACTTT T - AA TC
ACA
ATACTTTGCTTGGTCACAAG CAGAACTTTC GCT TGC AGA GGTTC GCT GG TCAC
GGACA GC G
GACATCGCACAGTAAAGCTT TCTT ||| ||| ||| ||||| ||| || |||| ||||| ||
GTTCCGTGGTCCCAGTGCCT CGG ACG TCT TCAAG TGA CC GGTG CTTGT CG T
TCAGAACTTTCTCTTGCATG T- TTC T ACTTCCG C T C- T- AAA
GC

GAM855 TCCTTTTGACAAGAAATGTG 828 TGACAAGAAA 2504 T - AAATGT C AA-- CTGTT T
GTCGTGAAAATTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA TTGGA GC
T
GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||
ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T
GA C G GTT--- - GGTA ----- T

GAM856 AGAGGAACTTAAGAAGTATG 829 AGGAACTTAA 2505 AAC- G GT ACAATAG---- T
AAGCAA
GAGTTACCACAATAGTAAGA GAAGTATGGA AGAGG TTAAGAA TATGGA TACC
TAAGAGTA GTG C
GTATGTGAAGCAACTTATGA GTTA ||||| ||||||| |||||| |||| |||||||| |||
CACTACTCTTGTGGAGAAAG TTTCC AGTTCTT GTACCT ATGG GTTCTCAT CAC
/
AAGGTATCCATGTTCTTGAT GGTT - -- AAGAAAGAGGT - AGTATT
TGGCCTTT

GAM857 CACAAGTGATGGTCCAACTT 830 GTAAGGATTT 2506 - -- T-- GAATG- AGG AGGG
GG
TGTGGAATGGTAAGGATTTT TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
TAGGGTTGTTTGGCCAGAAC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
AAGAGAAATAACTGCAGAAA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /
ACACATATGGTTGGAAACCA G AA TAT AAAAGA CAA G--- AC
TGCGCTTGTG

GAM858 TCTCTTTATTCTCAGTTTTG 831 TTTGCACAGT 2507 TTATTC TT GT T ACTCACA A
TT
CACAGTAATAAGTTGACTCA AATAAGTTGA TCTCT TCAG TTGCACA AATAAG TG CAG C
A
CACAGACTTAAAGCCTGAAA CTCA ||||| |||| ||||||| |||||| || ||| |
ACATCTTATTTGTGCAGTCT GGAGA AGTC GACGTGT TTATTC AC GTC G /
GACTACACAGAGG CACATC T- -- T AAAA--- C AA

GAM859 ATCCCAAGTGTTGACACAGC 832 TCCCAAGTGT 2508 AAGT GA CA - CCCA CT A
CATCTTGTCCCATCCCTGGA TGACACAGCC ATCCC GTT CACAGC TCT TGT TCC GGA G
AGCCTCTTTGGAAACCACAT ATCT ||||| ||| |||||| ||| ||| ||| |||
AGAGCTGTGCTGGCTCACGG TAGGG CGG GTGTCG AGA ACA AGG TCT C
GAT CACT TC -- T CCAA TT C

GAM860 GGCTATTTTAAAAGGTGTCC 833 TCCCTGAGAC 2509 A -- GTG A - G GT G G--
T TA
AGTGTGAAGTGCAGCATGGT TCTCACATGT AAA GGTG TCCA TGA G TGCA CATG
GGAGTCT GGGGA GCT GG C
GGAGTCTGGGGGGAGGCTTGG GCAG ||| |||| |||| ||| | |||| |||| ||||||| ||||| ||| ||
TACAGCCTGGCAGGTCCCTG TTT CCAC AGGT ACT C ACGT GTAC TCTCAGA TCCCT
CGG CC /

AGACTCTCACATGTGCAGCC C TT --- C G - AC G GGA T GA
TCATGGATTCACCCTTTAGA
TGATTATAGCC
GAM861 GCTTCTGGAGCTGAAGGTCT 834 TCACGGTGAA 2510 CT- T C----- T TC T-- TTAC-
- CA
GCGTCACGGTGAAAATTCGG AATTCGGGAT GAAGG CTGCGT ACGG GAAAAT GGGA GT
AGAG CAT C
GATGTTTACAGAGCATCACA GTTT ||||| |||||| |||| |||||| |||| || |||| |||
AATGCCTCTCTCTCGCCGCT CTTCC GACGTA TGTT CTTTTA CTCT CG TCTC
GTA /
CTCTCATTTTCTTTGTATAA TCC - TCAATA T CT CGC CTCTC C AA
CTATGCAGCCTTCCCTCTCT
TTCTGGGATGT
GAM862 GACATTTCAATAATACAGGG 835 TTCAATAATA 2511 AT - AG A--- ACA
TAAGTTCATAGCTACAAAGC CAGGGTAAGT GACATTTCA AATACA GGGTA TTCAT GCT A
AAGCCAACATGAGTGCTCAT TCAT ||||||||| |||||| ||||| ||||| |||
GTATTCTGAGATGTC CTGTAGAGT TTATGT CTCGT GAGTA CGA A
C- A -- CAAC ACG

GAM863 CTCTTCAGCCAGGGATGACA 836 CAGCCAGGGA 2512 C-- CA- ACA TC GCC
TCCCT
TTCCAATCGGAGCCATCTCT TGACATTCCA CTCTT AGC GGGATG TTCCAA GGA ATCTC
T
CCCTTTTGATTGAGATTCCT ATCG ||||| ||| |||||| |||||| ||| |||||
TGGAAGATATCCCATTGCTA GAGGA TCG CCCTAT AAGGTT CCT TAGAG T
TTAGGAG TTA TTA AG- -- --- TTAGT

GAM864 TCTTCATGGAGCTCACATTC 837 ATGGAGCTCA 2513 AG--- CTA GG GAG AACA A
A
TAGTGGGGGAGATAACAGTA CATTCTAGTG TCTTCATGG CTCACATT GTG G AT GTA
GTA A
AGTAAAAATATATACAAGGT GGGG ||||||||| |||||||| ||| | || ||| |||
AATTTCACAGTGTGAGAAGT AGAAGTATC GAGTGTGA CAC T TG CAT TAT A
ACTATGAAGA ATGAA --- TT AA- GAA- A A

GAM865 TCATCTGGATATGCTTCAGG 838 GGCAACAAAT 2514 CT A - CA A AAC GAACC------
T GAGGA
TCAACAGGTAACAGATGAAC GAAAGTCTAC AT GGAT TGCTTCA GGT AC GGT AGAT
GCC CTG A
CGCCTCTGGAGGAACACGTG AGCT || |||| ||||||| ||| || ||| |||| ||| |||
CAGGGCAACAAATGAAAGTC TG CTTA ACGAAGT CCA TG TCG TCTG CGG GAC
C
TACAGCTGGTAAACCATGAA T- A A AA G ACA AAAGTAAACAA - GTGCA
GCAAATTCTGTGG

GAM866 GCTCCAAAGAACCAAGAGTG 839 CATTTCACTT 2515 T - ---------- CAC GAGATA
TC

CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM867 AGTGGGGAGAACAGCGTCTT 840 TCCTCCAGTG 2516 A GT TTTACC - CC -- G A
CC T
TTACCTGTCACCGAAGCCAG GCGTTCTTTT AGTGGGGAGAAC GC CT TGT CA GAAGC CA
GA GC CGTT G
GAAGCCCCGTTTGTAAGCGT TACT |||||||||||| || || ||| || ||||| || || || ||||
GTGTTGTGGTGCTTTATTGT TCATTTTTCTTG CG GA ACA GT TTTCG GT TT TG
GCGA T
ACATCCTCCAGTGGCGTTCT - GT CCTCCT T TA TG G G T- A
TTTTACT

GAM868 TTCCCAAAATATACCAGCTT 841 TGAGGTAGTT 2517 AAAATATACC CAA - --- -
TGT CAT
GTCAATGCACTGTGAGGTAG AGGTTGTGCT CC AGCTTGT TGC ACTG TGAGGTA
GTTAGGT GCTT C
TTAGGTTGTGCTTCATCTCT T || ||||||| ||| |||| ||||||| ||||||| ||||
GAGTGCTTAATGTATCTCAT GG TCGAATA ACG TGGC ACTCTAT TAATTCG
TGAG /
TTCGGTAGCAGAATAAGCTT AT-------- AG- A TTT G --- TCT
AGGGAA

GAM869 TCTCTGTCAGTCTGCTGTTT 842 CTGTCAGTCT 2518 C T CT - TG GC-- TTGCT ATC
GCAGGCGTCATTGCTGCTAG GCTGTTTGCA TCT TG CAGT GCTGT T CAG GTCA
GCTAGA G
AATCGGTCTTTGGTCCTTTG GGCG ||| || |||| ||||| | ||| |||| ||||||
ATTTAACTGTGACACAGTTG AGA AC GTCG TGACA A GTC TAGT TGGTTT /
CTGCAAGA - - T- C GT AATT TTCC- CTG

GAM870 CAGCAGCCAGGTTCAAATGA 843 TCAAATGACA 2519 - A ACACA TC CC G
A
CACAGACATCTGTCCCCTGG CAGACATCTG CCAGGTTCAA TG GACA TGT CCTG
CAGTACCACAGCACCAGGCCTC C
CAGTACCACAGCACCAGGCC TCCC |||||||||| || |||| ||| |||| ||||||||||||||||||||
TCACTGAGGCCTGGTGTTGT GGTCCGAGTT AC TTGT GCA GGAC
GTCATGGTGTTGTGGTCCGGAG /
GGTACTGGCAGGTAACGTTG A G ATTA- T- AT G T
TTATTACAGTTGAGCCTGGA
CTGATG
GAM871 TGTGGTTTAATCTGGAAGGA 844 ACCCGTGTTC 2520 AG---- A A AGTCCAAA G TC
TCCT TGC
GCAGAAGCTGTGGAGTCCAA CTATCCTTGT GA GAGC GA GCTGTGG GGACCC TGT
CTA TGTTG C

AGGACCCGTGTTCCTATCCT TG || |||| || ||||||| |||||| ||| ||| |||||
TGTTGTGCCACTTGACACGT CT CTTG TT TGACACC CCTGGG ACA GAT
ACAGT /
TTAGCACAAGGGTCCCCACA CTGCCA A G -------- A C- TTGC TCA
GTGTTAGTTCACCGTCTCCA
GCAATCACG
GAM872 AGGAGGTGAGGAGGTAGCCT 845 TGGAGGCTGG 2521 GC AC- T TGG GA GA --
GA A- G
GACGGGTGCAGTGGGGAGGA ATGTTGGTGG GGAGGTA CTG GGG GCAG GGAG AGGG
AC ATG CAGCCT GG C
AGGGGAACATGGACAGCCTA CTCT ||||||| ||| ||| |||| |||| |||| || ||| |||||| ||
GGGCAGCTGGAGGCTGGATG TCTCCGT GAT TCC CGTC TCTC TCTC TG TGT
GTCGGA TC A
TTGGTGGCTCTGTCTCTCTG A- GCT - --- TG GG GT AG GG G
CCCTTCGTAGATGCCTCTGT
CACAGCACTT
GAM873 GCTCCAAAGAACCAAGAGTG 846 CATTTCACTT 2522 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM874 TAGTGGGGAGACTGAAAGGC 847 AGGCAATAAT 2523 GA T AA C - CC T CA----
C
AATAATATTGGCCTAGCGTC ATTGGCCTAG TAGTGGG GAC GA GG AATAAT ATTGG TAGCG
CC GGGC G
CCAGGGCCGGGCCCATAGTA CGTC ||||||| ||| || || |||||| ||||| ||||| || ||||
GGTGCTATACTAATGGTTAT GTCACCC TTG CT CC TTATTG TAATC ATCGT GG
CCCG /
TTCCCATCGTTCTCCCACTG TC - AC T G AT - ATGATA G

GAM875 CCATATCCAGAGAACTCAAG 848 TCCAGAGAAC 2524 C GAA- ----- GTGAA GAT G
AA
GTGTGAATACCAGATCCGGT TCAAGGTGTG CCATATC AGA CTC AAGGT TACCA CCG
TTGGAG A
TGGAGAAAGGGTTCCAAGTG AATA ||||||| ||| ||| ||||| ||||| ||| ||||||
GTGGTGACCTTGCGGAGAGA GGTGTAG TTT GAG TTCCA GTGGT GGT AACCTT
G
AGATTTTGATGTGG T AGAA AGGCG ----- --- G GG

GAM876 GCCAGGGTTCACATGTGGCC 849 TTCACATGTG 2525 ----- GG AA AT- T---- A
AAGTTATCATGTCATCCGAC GCCAAGTTAT GCCAGGGT TCACATGT CC GTT CA GTC T
CAAGCTGCAGAACAAGGAGC CATG |||||||| |||||||| || ||| || |||
ATGTGATTGAGGCCCTGGC CGGTCCCG AGTGTACG GG CAA GT CAG C

GAGTT A- AA GAC CGAAC C

GAM877 GCAAATCAGTCCATTTCACT 850 CATTTCACTT 2526 - ---------- CAC GAGATA TC
TTCACTGTCTGAGATAGGGT TCACTGTCTG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
CTCTAAGACCCAGGATACAA AGAT ||||||| ||||||| |||||||| ||||| |||||
GGGTGGAATGTAGCTATATG CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GACTCGATTTGC C TATCGATGTA AC- A----- AA

GAM878 CTCTTGAGCATGCTGACCAG 851 GACCAGTGCT 2527 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM879 TGTCCAGGCCTGCTTTGCTC 852 TTTGCAGATG 2528 CA ------- T T T AGG
GTTTGTCAAAGAGGGATGGC GCTAAGTTTC TGTC GGCCTG CTT GC CGTTTG CAAAG G
TTTGCAGATGGCTAAGTTTC CTTC |||| |||||| ||| || |||||| |||||
CTTCAGGCTCTGACA ACAG TCGGAC GAA CG GTAGAC GTTTC A
TC TTCCTTT T - - GGT

GAM880 TGAGGTTTTGCAATTTTGAA 853 GTGCATTCTA 2529 TTTTGCAAT A ATAC - AA
ATAT
GAGAATACCACAGAAAATGC GTGTGTCATT TGAGG TTTGAAG GA CAC AGA ATGCATC
C
ATCATATCAAGAGGTGCATT TCAA ||||| ||||||| || ||| ||| |||||||
CTAGTGTGTCATTTCAAGTT ATTCC GAACTTT CT GTG TCT TACGTGG /
CCTTA TT------- A GT-- A -- AGAA

GAM881 GGAGTGCAATGGCTGGGAAA 854 GGCCAGATGA 2530 G-- ATG-- - AAA- GA T A TG
AA
TCAGATCTTTTCTGGACTGA GAGTGAGACA GGA TGCA GCTG GG TCA TCTT TCTGG C
A A
AAACATTGGCCAGATGAGAG CCGC ||| |||| |||| || ||| |||| ||||| | |
TGAGACACCGCAGTAAGCGT CCT ACGT TGAC CC AGT AGAG AGACC G T /
GCAGGGTCC GGG GCGAA G ACAG G- T - GT AC

GAM882 GGTACAGAGAGCTGTGTGCA 855 TCGCCTGGAC 2531 ----- A-- - - G T T AACA- A C
TGCTGAGCAACACCACAGCC CACAAGTTTG GGTA CAG GAGCT GTG T CA GC GAGC CC
CAGC A
ATTGCTGAGGCCTGGGCTCG ACCT |||| ||| ||||| ||| | || || |||| || ||||
CCTGGACCACAAGTTTGACC CCGT GTC TTTGA CAC A GT CG CTCG GG GTCG T
TGATGTATGCC ATGTA CAG A C G C - GGTCC A T

GAM883 TCAACACTGCTTTGAACTCT 856 ACACTAGGAC 2532 C-- GCT C-- TAC A---- TAT AC
CCTTACGTAGGTATCCAACT ACAGTTCAGC TCAA ACT TTGAACT TCCT GT GG CCA T
TCATGGCTCCACAAAACACT TAAG |||| ||| ||||||| |||| || || |||
AGGACACAGTTCAGCTAAGT AGTT TGA GACTTGA AGGA CA CC GGT T
TCTTTGA TCT ATC CAC TCA AAACA TC- AC

GAM884 TTTTGGATATAAAGAAGTTA 857 TGGATATAAA 2533 T AG ---- - TC CAC
TGAGGCCTCCTGTCACATTC GAAGTTATGA TTTTGGA ATAA AAGTTAT GAGG CC CTGT A
ACAGCTGGTTCTCCAAAATA GGCC ||||||| |||| ||||||| |||| || ||||
ATTTGGTTGTTTCAAAA AAAACTT TGTT TTTAATA CTCT GG GACA /
- GG AAAC T TC CTT

GAM885 TTGATCTTCGTTGTAACGGA 858 TTCACAGTGG 2534 T TAAC ACTGGG AG G C
G
TAACTGGGTTTTCAGGCGTG GAAAGTATCC TTGATC TCGTTG GGATA TTTTC GC
TGTGAAT ATA T
TGAATCATAGTTGTATAATT ATCA |||||| |||||| ||||| ||||| || ||||||| |||
CACAGTGGGAAAGTATCCAT AACTAG AGTAAC CCTAT GAAAG TG ACACTTA TAT T
CAATGACGATCAA C TA-- ------ GG - A G

GAM886 TGTAAGCCAGCCAGAACCAG 859 CATCAAAGCT 2535 AA- C C -- CCA --- C CTTG
GAAAA
TCCATGATGGGTAGTCACCT GTAGTTCTCG TGT GC AGC AGAAC CAGT TGATGGG TAGT
AC TTCAG C
TGTTCAGGAAAACAGTTACT CTAG ||| || ||| ||||| |||| ||||||| |||| || |||||
GAAATCAGTCACTATGTCCC ACA TG TCG TCTTG GTCG ACTACCC ATCA TG
AAGTC /
ATCAAAGCTGTAGTTCTCGC AGG A C AT AA- TGT C ACTA ATTGA
TAGTGGAACA

GAM887 TGCCATTGACAAGCTGTATG 860 TCAGTTTTTT 2536 ACA C TAT CG AAGG TTT
ACGTTGAGGAAGGCAATTTT CATCTCTACA TGCCATTG AG TG GA TTGAGG CAA T
CTTTTTGAGCCTCAGTTTTT ATGG |||||||| || || || |||||| |||
TCATCTCTACAATGGCA ACGGTAAC TC AC TT GACTCC GTT C
ATC T TT- TT GA-- TTT

GAM888 CTGGAGTGCAGTGGTGCGAT 861 TACAGTAGCT 2537 -------- TG C C C C -- CC--
ATT
CTTGGCTCACTGCAACCTCC GGGATTACAG TGC GATCT GCT ACTG AA CTC GC CTC
GGTTGAGGCA C
GCCTCCCGGTTGAGGCAATT ACAT ||| ||||| ||| |||| || ||| || ||| ||||||||||
CTCCTGCCTCAGCCTCCCGA GCG TTAGG CGA TGAC TT GAG CG GAG
CCGACTCCGT /
GTAGCTGAGATTACAGTAGC TACAGACA GT - A A T AT CCCT CCT

TGGGATTACAGACATGCGCC
ACCATGTCCAG
GAM889 TCTGAGCAGCTTGAAGCACT 862 AAGCACTCAC 2538 -- - T A - AG--- AGAA AA
CACAGAAGCTGAAGAACAAA AGAAGCTGAA TCTGAG CA GCT GAAGC CTCACA GA CTGA
C A
GTGGGGGTCAGAACTATCAT GAAC |||||| || ||| ||||| |||||| || |||| |
GTGGGGGCTTCTAGCATGAA AGATTT GT CGA CTTCG GGGTGT CT GACT G /
TTTAGA AA A T G A ATCAA GGGG TG

GAM890 GGCTCCAGATATTTCTTTTG 863 TCACGGGGAG 2539 CT GATA - TC AA T AA
TCCCAAGTTGCTCTCAACAG AAAAATGGGT GG CCA TTTCTTT TG CC GTTGC CTC C
GGGCGCAATCGGGTTCACGG CC || ||| ||||||| || || ||||| |||
GGAGAAAAATGGGTCC CC GGT AGAGGGG AC GG TAACG GGG /
TG AAAA C TT GC C GA

GAM891 GCAGCCATGGGAACTGCACG 864 CAAACCTTTA 2540 AG A- GGA - AA TCTA-- A G
TCAAGATGTCTATGATTTGC TCAGGATGAT GC CC TG ACTGCA CGTC GATG TG TTT C
TAAAAACAAACCTTTATCAG GCAG || || || |||||| |||| |||| || |||
GATGATGCAGTAACAGGGGA CG GG AC TGACGT GTAG CTAT AC AAA T
AGC AA GG AA- A GA TTCCAA A A

GAM892 GTGATGTCCAGGTACTTGGA 865 TCAGTGCTTG 2541 ATG A G T G AGAGAA GAA
TTATGGAGAAGAGAATTGGA AAGAACCTGG GTG TCCAGGT CTT GA TAT GAGA TTG G
AGAAACAGACATCTCAGTGC AAAC ||| ||||||| ||| || ||| |||| |||
TTGAAGAACCTGGAAACAT TAC AGGTCCA GAA TT GTG CTCT GAC /
AA- A G C A ACA--- AAA

GAM893 GAGTGCAAATCAGTCCATTT 866 CATTTCACTT 2542 T - ---------- CAC GAGATA
TC
CACTTTCACTGTCTGAGATA TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT
TGTCT GGGTC T
GGGTCTCTAAGACCCAGGAT AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
ACAAGGGTGGAATGTAGCTA CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
TATGGACTCGATTTGCTTC - C TATCGATGTA AC- A----- AA

GAM894 GCTGATAGGCCAGGTCAGCC 867 TGTCATAGGC 2543 T CC A - - C GTG
TGTGCTCGGCGGGTGTTGAC GGCCTTCTTC GCTGA AGG AGGTC GCCTGTG C TCGG GG T
CTCGATGTCATAGGCGGCCT AGT ||||| ||| ||||| ||||||| | |||| ||
TCTTCAGT TGACT TCT TCCGG CGGATAC G AGCT CC /
- -- - T T - AGT

GAM895 CCTATAGGAAATAAGACAAA 868 TTAGTGTTTG 2544 TAT AATA GA
CGCTGGGGGAAGAGCCTTAG TCTCTCTCCT CC AGGA AGACAAACGCTGGGG A

TGTTTGTCTCTCTCCTTTTG TTTG || |||| ||||||||||||||| G GG TCCT TCTGTTTGTGATTCC G TTT CTC- GA

GAM896 GTGGGGAGAACAGCGTCTTT 869 TCCTCCAGTG 2545 A GT TTTACC - CC -- G A CC T
TACCTGTCACCGAAGCCAGG GCGTTCTTTT GTGGGGAGAAC GC CT TGT CA GAAGC CA GA GC CGTT G
AAGCCCCGTTTGTAAGCGTG TAC |||||||||| || || ||| || ||||| || || || |||| TGTTGTGGTGCTTTATTGTA CATTTTTCTTG CG GA ACA GT TTTCG GT TT TG GCGA T
CATCCTCCAGTGGCGTTCTT - GT CCTCCT T TA TG G G T- A TTTAC

GAM897 CCTACTCCAAAATACTCACA 870 TCTACAGTGT 2546 A - A TC-- -- GA
CTGGACTGAATGAAGTCTAC CAATGTGTCT CCT CTC CAA ATAC ACACTG GACT A
AGTGTCAATGTGTCTTGAGA TGAG ||| ||| ||| |||| |||||| |||| GAGG GGA GAG GTT TGTG TGTGAC CTGA T
- A C TAAC AT AG

GAM898 GACTTGACTTCGGGGAAGCT 871 CAGCTGGCAG 2547 A-- GGAA ---- - C
GCCAGGGCAGATGATGCCCG TGCTGAAGAA GACTTG CTTCGG GCTGCCAG GGCAGATGAT GC C
GCAATTATTTGTCTCAGCTG CCGA |||||| |||||| |||||||| |||||||||| || GCAGTGCTGAAGAACCGAGT CTGAGC GAAGTC TGACGGTC CTGTTTATTA CG / C CAA G--- GACT A G

GAM899 GCTTAAGGCCGGGTGTTCAA 872 TTCAAAGTGT 2548 TAA- CG CAAA T TT TCTTTG
AGTGTCTTAACTTCTGTCTT CTTAACTTCT GCT GGC GGTGTT GTG CTTAAC CTG A
TGACTTTCCCAGCGTTGAGT G ||| ||| |||||| ||| |||||| ||| CATCAACACTTTGCCAATTA CGA CCG TCACAA TAC GAGTTG GAC / GC TTAA TT C--- T C- CCTTTC

GAM900 GCTCCCGCCTGTAATCTCAG 873 TAATCTCAGC 2549 A A G CA A TG - TG TCTC
CACTTTGAGGAGGGCCAAGG ACTTTGAGGA CTGTAATCTCAGC CTTTG GGAGG C AGGTGGGAGG T CTTGAG C G G
TGGGAGGATTGCTTGAGCTG GGGC |||||||||||| ||||| ||||| | |||||||||| | |||||| | | GTCTCGAACTCCTGGACTTA GACATTAGGGTCG GAAAC CCTCT G TCCGCCCTCC A GAATTC G C A
AGTGAGCCTCCCGCCTCAGT C - - AC G GT A GT CTCA CTCCCAAAGCGCTGGGATTA CAGGCAGGAGC
GAM901 TGGCTATTTTAAAAGGTGTC 874 TCCCTGAGAC 2550 A- -- T- GAAG ACTTGT G G- - T TA
CAGTGTGAAGTGCAACTTGT TCTCTGTGTG AAAGGTG TCCAG GT TGCA GGAGTCT GGGGA GCT GG G

GGAGTCTGGGGGAGGCTTGG CAGC ||||||| ||||| || |||| ||||||| ||||| ||| ||
TAGAGCCTGGCGGGTCCCTG TTTCCAC AGGTC CG ACGT TCTCAGA TCCCT
CGG CC /
AGACTCTCTGTGTGCAGCCT AG TT TC ---- GTGTC- G GGG T GA
CTGGATTCACCTTTGATGAG
TATGCCA
GAM902 GGTGAGCAAGCCCAGGAGAA 875 AAGCCCAGGA 2551 G- A AG --- G TG A TGGG TG
TTTTATTT
TGCTGCAATCTTGGGGGTGG GAATGCTGCA GGT AGC AGCCC GA GAAT C CA TCT GG G
A
TTTTATTTATTTCTTTTTTG ATCT ||| ||| ||||| || |||| | || ||| || |
CCAAATAGAGTGTGGATTCA CCG TCG TCGGG CT CTTA G GT AGA CC T /
TTTCAGGGGCTAGCTAAGCC AA A GA TTA - GT G TAAA GT TTTTCTTT

GAM903 CTGCTGCTGACTGGCAAGCT 876 TTGGCTTCTT 2552 - A C----- TG CAC- A CA
GGAAATG
GACACCGACCCATGGGGAAA CAACCAGCAG CTGC TGCTG CTGG AAGC A CG CC TGG
A
TGAGAAAGAACCACCGGCTG TATG |||| ||||| |||| |||| | || || |||
AAAATTGGCTTCTTCAACCA GACG ATGAC GACC TTCG T GT GG ACC /
GCAGTATGCAG T - AACTTC GT AAAA C CC AAGAAAG

GAM904 GCTCCAAAGAACCAAGAGTG 877 CATTTCACTT 2553 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM905 GCTCCAAAGAACCAAGAGTG 878 CATTTCACTT 2554 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM906 GCAGCCAGAACTGAGCAGCA 879 AGCAGCAGTG 2555 AGAAC AG A - AAG
GTGACAGGACATCAAAGCGT ACAGGACATC GCAGCC TGAGC CAGTGAC GGACA TCA C
GTGGCTGTTCGTCACTGAGC A |||||| ||||| ||||||| ||||| |||
TCACCAGGCTGT TGTCGG ACTCG GTCACTG CTTGT GGT /
ACC-- A- - C GTG

GAM907 AAGGCAGCTCTGGTGTTGAT 880 AGCTCTGGTG 2556 CTCTG TT GAA TCA TTC
GAATTCCCTCAGCTTCTATT TTGATGAATT AAGGCAG GTG GAT TTCCC GC T
TGTCTGGGAAAGTCTTTATC CCCT ||||||| ||| ||| ||||| ||
TGTCTT TTCTGTC TAT CTG AAGGG TG A
----- TT A-- TC- TTT

GAM908 TAATGAGTTTTGAGCTCTGG 881 TGACTGAATG 2557 T A TCT TAAA TTCCCA --- C - T
GT T C
CTAAAGGTTTTCCCACATTC CTTTGCCACA TG GC GGC GGTT CAT TCATTA AC TCA
AAG TTC CA C
ATTACACTCATAAGGTTTCT CTCA || || ||| |||| ||| |||||| || ||| ||| ||| ||
CACCAGTGTGAATTCTTTGA AC CG TCG TCAG GTA AGTAAT TG AGT TTC AAG
GT A
TGTATAATGAGATATGAACT - - TT- TAAG TTTCAA TAG A T - TT T G
TTGACTGAATGCTTTGCCAC
ACTCATTA
GAM909 GAACATCACTGGGTGCAGTG 882 TCACTGGGTG 2558 A A GTG T C A AA----- G A
TGCTCATGCCTGTAATCCCA CAGTGTGCTC GAAC TC CTGG CAG GTG TC TGCCTGT
TCCCA C C
GCACTTGTGGGAGGCCGAAG ATGC |||| || |||| ||| ||| || ||||||| ||||| |
CAGGCAGACCACCTGAGGTC CTTG AG GACT GTC CAC AG ACGGACG AGGGT G T
AGGAGTTC - - GGA - C - AAGCCGG - T

GAM910 GGGTGCACAAGTGATGGTCC 883 GTAAGGATTT 2559 CAAGTGA -- T-- GAATG- AGG
AGGG GG
AACTTTGTGGAATGGTAAGG TTAGGGTTGT CA TGGT CCAACT TGTG GTA ATTTTT
TTGTTT C
ATTTTTAGGGTTGTTTGGCC TT || |||| |||||| |||| ||| |||||| ||||||
AGAACAAGAGAAAATAACTG GT ACCA GGTTGG ACAC CGT TAAAAG
AACAAG /
CAGAAAACACATATGGTTGG ------- AG TAT AAAAGA CAA AG-- AC
GAACCATGCGCCT

GAM911 GCTCCAAAGAACCAAGAGTG 884 CATTTCACTT 2560 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM912 ATCTGTCAGGAGCAAGGACT 885 CATCACTGTT 2561 CAA TACTT CA
ACTTTGGCATTAACCATCAC TGATTTCTTG ATCTGTCAGGAG GGAC TGG T
TGTTTGATTTCTTGACAGGT ACAG |||||||||||| |||| |||
TGGACAGTTCTT TTTG ACC T

TAG TCACT AA

GAM913 TTGAGATTGGATGTCTTTGG 886 CATCACATCT 2562 T CT GAAC C G A ACA G - GGA A GAGG
GAACCATTACTCGGCCCATC GAGTATGTTG GT TTGG CATTA TCG CCC TC TCT AGTA TGTT GTC CC A
ACATCTGAGTATGTTGGAGT GAGT || |||| ||||| ||| ||| || ||| |||| |||| ||| ||
CACCGAGGATCAAGGAGACA CA GACC GTGAT AGC GGG AG AGG TCGT ACGA CAG GG /
GCACTGCTGGAGAGGGCGAT - AG AA-- - - - --- - C --- A AACT
AGTGAACCAGGAACTACAAG
AGTCAG
GAM914 GGACAATGCCATGTAGTGAG 887 AACGCTGCTC 2563 - - A CT-- ACCAGA- GCT GA AT AC
GACAACTGGACACCAGAACG TGGACAGATG TGC CATGTA GTG GGACAA GGAC ACGCT CTG CAG GG T
CTGCTCTGGACAGATGGACT G ||| |||||| ||| |||||| |||| ||||| ||| ||| ||
TTACCCCTGACAGTGAGCGT ATG GTACGT CAC CCTGTT CCTG TGCGA GAC GTC CC T
GGCCGAGGTCCTCTCTTGTC A A A CTCT GAGCCGG GT- A- C- AT
CACACATGCATGAGTATACC
CC
GAM915 TTGATACTTAAGGAAGTGCT 888 TATTGCTAAG 2564 GAAGT - G AGAA AG CG AGA CCA
GGATATTGCTAAGAATTCAG AATTCAGGTA AG GCTGGAT ATT CTA TTCAGGT TCT GGATCTCC GTCT T
GTAGTCTCGGGATCTCCAGA GTCT || ||||||| ||| ||| ||||||| ||| |||||||| ||||
GTCTCCATGCTAGGACAGGA TC TGATCTG TAA GGT AGGTCCA AGA TCTAGAGG CAGG G
GATCTTCAGAACCTGGAGGA GAC-- A A AAGG -- CT A-- ATC
ATGGAAATAGTCTAGTCAGC
TTATTTGTCAA
GAM916 AGAATGGGGAAGAATACTGA 889 TTGGAGCAGG 2565 - - TA AA T CA TCT AC- CT
ATTAGCTGAGCACATTCTGG TTTCATTCTC AGAAT GGGGAA GAA CTG TTAGC GAG CAT GGAC AATT G
ACACAATTCTGACCAATTTC CAAT ||||| |||||| ||| ||| ||||| ||| ||| |||| ||||
AGTCTCATGATCTCTGTTGG TCTTA CCTCTT CTT GAC GGTTG CTC GTA TCTG TTAA A
AGCAGGTTTCATTCTCCAAT A A TG GA T TA C-- ACT CC
TCT

GAM917 TTAATGTTTATTGTGATCAT 890 TGATCAGAAG 2566 TA T-- GA-- CA - TG AG A
CTCATGTTAGTGTGTGAGAC GTGAGTGAGC T ATGT TATTGT TCATCT TG TTAG TGTG ACG T
GATGACGTAACATGTGCTGA AATG | |||| |||||| |||||| || |||| |||| |||
TCAGAAGGTGAGTGAGCAAT A TACG GTAACG AGTGGA AC AGTC GTAC TGC G
GCATGCATCGA GC TAC AGTG AG T GT AA A

GAM918 TTCCCCAAGCAATTGCTCAA 891 AAGCTGGCAG 2567 AATTG-- C CAA CT AG AAAATT -- TT

CTGTCCAAGGAAGCTGGCAG TTGAAAAATT AAGC CTCAA TGTC GGAAG GGC TTGA CATTCA TG T

TTGAAAAATTCATTCATGTT CATT |||| ||||| |||| ||||| ||| |||| |||||| ||

TCACATCTGAATGCGAATAT TTCG GAGTT ATAG TCTTC TCG AATT GTAAGT AC /

TAAAAGCTCTTCTAGATATT GAATAAA T A-- -- AA ATAAGC CT AC

TGAGAAATAAGGCTTGTGGA

G

GAM919 TGATCTCTTCCTTCTGCTTC 892 TTCCCTGTGA 2568 TCT CCCT- TCAAGA TT-- CT TC

CCTGTGACCTCAAGATGAGT CCTCAAGATG TGATC TCCTTCTGCTT GTGACC TGAG TCAA TTTTAA A

TTCAACTTTTTAATCACCTT AGTT ||||| |||||||||||| |||||| |||| |||| |||||| AGAGTCTTGATCTTTTCAGG ATTGG AGGGGGATGGA CGCTGG ACTT AGTT GAGATT /

GTTGGTCGCTTTTAAGGTAG TTT ATTTT TTGGG- TTCT CT CC

GGGGATTTGGTTA

GAM920 GCCCCATCGAGAAGCTGCAG 893 GCCCCATCGA 2569 A - C C CC--- T CC TCTTCCCCT T C

AACCCAATTGTGACCCAGTT GAAGCTGCAG TCGAG AAG TG AGAA CAATTG GA CAGT CTGTGA GCT T

CTTCCCCTCTGTGATGCTCT AACC ||||| ||| || |||| |||||| || |||| |||||| ||| GGGGCTTCACAGTGATACTG AGCTC TTC GC TCTT GTTAGT CT GTCA GACACT CGG G

CCTCTGATTGTCTACTTCTC - C C C CATCT - CC TAGT----- T G

CGCCTTCCTCGAGGC

GAM921 TCAAATGCAATAGACATTGT 894 AGAAAAGATG 2570 ATA GAA TG - TT A A- - - CCT C

GAAAGCTGGCATTTCAGAAG TTGGCATTGC GACATTGT AGC G CA TCAG AGT TAGC TCTTTTC CTA GAA T

TATAGCTCTTTTCCTACCTG TGAT |||||||| ||| | || |||| ||| |||| ||||||| ||| |||

AACTCTTCCCTGGAGAAAAG CTGTAACG TTG T GT AGTC TTA GTTG AGAAAAG GGT CTT /

ATGTTGGCATTGCTGATTGT GAC AA- GT T T- G CG T A CC- C

TTGGTTAAGCAATGTCCAGT

GCTAGGA

GAM922 GCCTACTCTCAGAAATGGCT 895 GGCAAGACCT 2571 T AAATG CC- CCA CCAGA GCA

CCCTCCCATGCCCCAGAGCT GGGCACAGCT GCCTACTC CAG GCTC TC TGCC GCT T

GCATCTAAAGCACATTGGCA GGAG |||||||| ||| |||| || |||| |||

AGACCTGGGCACAGCTGGAG TGGGTGAG GTC CGGG AG ACGG CGA C

TGGGT - GACA- TCC A-- TTACA AAT

GAM923 CACATCATGGAAATCATTCT 896 TGGCCTGGAT 2572 A AAT- T TAAA- ---- - ATC

GGGGTCCTAAAACTGTGATA CCCTGAATGC CACATC TGGA CATTC GGGGTCC ACTG TGATA GAGGGG G

GAGGGGATCGATCCTTCCTC AACT |||||| |||| ||||| ||||||| |||| ||||| |||||| ATGTCATCTTCGGTGGCCTG GTGTGG GTCT GTAAG CCCTAGG TGGC ACTGT CTCCTT A

GATCCCTGAATGCAACTCTG - CAAC T TCCGG TTCT A CCT GGTGTG

GAM924 TGCTTGAACATTCCTGCCTC 897 TTCCTGCCTC 2573 AACA CTCCCTATTT C C-- TGT

CCTATTTGCCAGGCTTTCAT CCTATTTGCC TGCTTG TTCCTGC GC AGGCTTT ATTTC C

TTCTGTCTGCTGAGATCTCA AGGC |||||| ||||||| || ||||||| ||||| GAGCCTGCCCAACAGCAGGG ACGAAC AGGGACG CG TCCGAGA TAGAG T AAGCCAAGCA CGA- ACAACC---- - CTC TCG

GAM925 TCTGGACAAAGTAGGTGGTC 898 TGCATGGAAA 2574 CAA G G AG C TC

AGTTTCCATCCATGTTCCAT GAGTATGTAT TCTGGA AGTA GTG TC TTTCCAT CATGT C

ATATGCATGGAAAGAGTATG TCTT |||||| |||| ||| || ||||||| ||||| TATTCTTTTCAGA AGACTT TTAT TAT AG AAAGGTA GTATA / TTC G G -- C TA

GAM926 CAGACATCACAGGCTGGTTC 899 CATCACAGGC 2575 A - C TCT TA-- T

TTGATATCCTGAAGGAAGAT TGGTTCTTGA CAGAC TCAC AGG TGGT TGA TCC G

TCGGCCACCTCGTGGGTCTG TATC ||||| |||| ||| |||| ||| ||| GTCTG GGTG TCC ACCG GCT AGG A - C - --- TAGA A

GAM927 GAGGGACTCGCTGGCAGCAG 900 AGGCAAGGCT 2576 G CT G G CAA ACCGCTC TG

CCCAAGCCTGACCGCTCGGA GTTGGCAGGG GAG GA C CTG CAGCAGCC GCCTG GGAG T

GTGTACTTTCCTTGACAGGC CTCG ||| || | ||| |||||||| ||||| |||| AAGGCTGTTGGCAGGGCTCG TTC CT G GAC GTTGTCGG CGGAC CCTT A CTT G CG - G AA- AGTT--- TC

GAM928 AGCATTGTGCATCGTGGCTT 901 GTGCATCGTG 2577 ATT GT - AT- CA - C-- T CC

GTCATTGTCAGTGTCACCTA GCTTGTCATT AGC GTGCATC GGCTT GTC TGT GTGT CA CTA GC T

TGCCCTCTGTTTAGACTTGA GTCA ||| ||||||| ||||| ||| ||| |||| || ||| || ACACCCACGCACGACTGGGC TCG CATGTAG TCGGG CAG GCA CACA GT GAT TG /

TGATGTACTCAGCT ACT -- T CAC CC A TCA T TC

GAM929 GTTGAAGCTTTTGACCTTAC 902 TGGCTGGATC 2578 TT TTA CAA- AAT --- AA--- TCCCCA AAA

AACAAATAAATGGGATGTAA TCTGTATGCA GACC CAA ATA GGGAT GT TGACCGAATT AG G
TGACCGAATTTCCCCAAGAA ATTG |||| ||| ||| ||||| || |||||||||| ||
AGAAGCTCCATCAGTTTGGT TTGG GTT TAT CTCTA CG ACTGGTTTGA TC /
CAGCCTGGCTGGATCTCTGT -- TG- AACG GT- GGT GTCCG CTACC- GAA
ATGCAATTGGTGGTTTTGCT
ATGATTCAAC
GAM930 GGCCTCAATGGTGGCAGCAT 903 TACACCGGGT 2579 A G AGCATGA CT C TCCC----
G A AG
GAGCTGTGCTTTCCACTCGT GAACCTACAG TGGT GC GCTGTG TTC ACTCG TGCT
CGTGGCCC CA G
CCCTGCTGCGTGGCCCACAA TCCT |||| || |||||| ||| ||||| |||| |||||||| ||
GGACCTGGGGGCCATGAGCG ACCA CG TGACAT AAG TGGGC GCGA
GTACCGGG GT A
CCTTACACCGGGTGAACCTA - A CCAATCC CC - CACATTCC - G CC
CAGTCCTAACCGCAACCAGA
GTGCC
GAM931 GCTTTCTGTTATCTGCAGTC 904 AGAGGTCATG 2580 TT ------ GT- TGTTGCC
CTCTACTGTTGCCTCTCCTG TAGGTTGCAT GCT CTGTT ATCTGCA CCTCTAC T
TGTAGAGGTCATGTAGGTTG GGAC ||| ||||| ||||||| |||||||
CATGGACAGGGAGC CGA GACAG TGGATGT GGAGATG /
GG GTACGT ACT TGTCCTC

GAM932 GACGGATACTTCGGGTGGAG 905 TGGAGAAGAC 2581 GGA T-- AGAAGACAGG G
ACTC C- A G
AAGACAGGGCACAGTGGTAC AGGGCACAGT GAC TACT CGGGTGG GCACA TGGT
TGGAT CCA G T
TCTGGATCCCAAGGTGACTG GGTA ||| |||| ||||||| ||||| |||| ||||| ||| |
GTTGTTTAATCGTGTGCATA CTG GTGG GCTCACC CGTGT GCTA ATTTG GGT
C G
GAACGAGCCACTCGCTTGGT AA- TTC GAGCAAGATA - ---- TT - A
GAAGTC

GAM933 TCACCCAGTGGTTCTCTCAG 906 TCAAAGCTGC 2582 TC - AACA-- - A- A TA TGAC
T CC
CAACAGACATGTCCAGTGGA AGATTGCCTG GT TCT CAGC GACATGT CC GTGG CCG
GTGTTG GG CGC A
CCGTAGTGTTGTGACGGTCG TGA || ||| |||| ||||||| || |||| ||| |||||| || |||
CCCATCTGCGCCCAGTACCT CG AGA GTCG TTGTACA GG TACT GGC CATGAC
CC GCG T
CGGATCATGCGGAACATGTT TT C AAACTG A CG A TC ---- - TC
GTCAAAGCTGCAGATTGCCT
GTGA
GAM934 GGCATGAGAACACAGCCCTA 907 TCATCTGGGC 2583 AA A-- TAAAAAGTT ATG
AAAAGTTCCTCCTATGGAAA ACAGTGGTTC GGCATGAG CAC GCCC CCTCCT G
GAGGGGGTCATCTGGGCACA ATGC |||||||| ||| |||| ||||||
GTGGTTCATGCC CCGTACTT GTG CGGG GGGGGA A
G- ACA TCTACT--- GAA

GAM935 ACTGTGCATCTACACCGAGC 908 TCTACACCGA 2584 GT- A AC--- G G G TCTC CA
ACGCTGTCTCTCCCCGCCAG GCACGCTGTC ACT GC TCT ACC AGCAC CT TC CCCGC G
TTGCGGGACTGGGAGGTGCT TCTC ||| || ||| ||| ||||| || || |||||
GGTCCTAGGGAAGCTCAAGT TGA CG AGG TGG TCGTG GA GG GGGCG /
ACT A GATCC - - G TCA- TT

GAM936 CACAAGTGATGGTCCAACTT 909 GTAAGGATTT 2585 - -- T-- GAATG- AGG AGGG
GG
TGTGGAATGGTAAGGATTTT TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
TAGGGTTGTTTGGCCAGAAC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
AAGAGAAATAACTGCAGAAA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /
ACACATATGGTTGGAAACCA G AA TAT AAAAGA CAA G--- AC
TGCGCTTGTG

GAM937 CTGGACCTGCCTGGGTCGCC 910 TGCCTGGGTC 2586 --- GG- ATGCCCT GAGTA
TTATGCCCTGGTGAGTAGAA GCCTTATGCC CTGGA CCTGCCT GTCGCCTT GGT G
TATGCCCCTTCGAGGTGGCA CTGG ||||| ||||||| |||||||| |||
CAAGGCAGGACTTCCAG GACCT GGACGGA CGGTGGAG CCG /
TCA ACA CTTCC-- TATAA

GAM938 CTGGACCTGCCTGGGTCGCC 911 TGCCTGGGTC 2587 --- GG- ATGCCCT GAGTA
TTATGCCCTGGTGAGTAGAA GCCTTATGCC CTGGA CCTGCCT GTCGCCTT GGT G
TATGCCCCTTCGAGGTGGCA CTGG ||||| ||||||| |||||||| |||
CAAGGCAGGACTTCCAG GACCT GGACGGA CGGTGGAG CCG /
TCA ACA CTTCC-- TATAA

GAM939 TACATAGAAGTTGCCAGCTG 912 TAGAAGTTGC 2588 TA GTT- C TCT- C- C CC
TTCTAGCCATGCTCGCCATT CAGCTGTTCT TACA GAA GCCAG TGT AGC ATG TCG A
CGAATATCAGTTCTGTACAT AGCC |||| ||| ||||| ||| ||| ||| |||
CTGGCTATATTCCTTGTG GTGT CTT CGGTC ACA TTG TAT AGC /
TC ATAT T TGTC AC A TT

GAM940 CCAGCTCGAGGAGGGGGCCA 913 AGAGGAAGAA 2589 G C GAG CAA G A G GC AGT
A - TC
AGAGGAAGAAGGATGCAGAG GGATGCAGAG CCA CT GAG GGGGC GA GA GAA GAT AG
GGGGC GT ACAG A
TGGGGCAGTACAGTCACCTC TGGG ||| || ||| ||||| || || ||| ||| || ||||| || ||||
TGTCACAGTCCCTGATTATG GGT GG CTC CCCCG CT TT TTT TTG TT CCCTG CA
TGTC C
TTGTTTATTGTCCGAGCCCC A C AG- AGC G A G TA AGT A C TC
GACTCCGGATGG

GAM941 CAGTGCAGTCACCCATAAAG 914 CATAAAGTAG 2590 G C A TAA--- G

TAGAAAGCACTACTAACAGC AAAGCACTAC CAGTGCA TCA CCATAAAGTAG AAGCACTAC CA C
ACTGGAGGGTGTAGTGTTTC TAAC ||||||| ||| |||||||||| ||||||||| ||
CTACTTTATGGATGAGTGTA GTCATGT AGT GGTATTTCATC TTTGTGATG GT A
CTG G A C TGGGAG C

GAM942 TCACAGTGGTACTGGGTCGG 915 TGCCTTGCTC 2591 -- - CT C CCA- G TC TAG
CCAGAGGGGCGGGCAGTCAG CCTGCCTGCT TCAC AG TGGTA GGGT GG GAGG GCGGGCAG AGGTT A
GTTTAGACGTCAGCCTCCTT ACCA |||| || ||||| |||| || |||| |||||||| |||||
GCTTGTGCCTTGCTCCCTGC AGTG TC ACCAT TCCG CC TTCC TGTTCGTT TCCGA C
CTGCTACCAGCTTGGTGA GT G CG T CTCG G CC CTG

GAM943 GGGAGCTGTTCTCCAGGCTT 916 GTGACAAGAG 2592 TTCTCCA AC AGTT- --- TGT--- TCT
GGGTGACAAGAGTTGCAGGC TTGCAGGCTG GGGAGCTG GGCTTGGGTG AAG GCA GGC TGGC A
TGTTGGCTCTAGCTGCCATC TTGG |||||||| |||||||||| ||| ||| ||| |||| /
CCTTGCCCTATGCTCAAGCT CTCTCGGT CCGAACCTAC TTC CGT CCG ACCG
TCCATCCAAGCCCTTGGCTC TC----- C- GAACT ATC TTCCCT TCG
TC

GAM944 AGATCGAGCCGGTACCTCGC 917 CTGTCGTTAG 2593 TC- - TAC- C T ATC
GACGTGTATCCCTAGCTGTC TAGTTTGTGC AGA GAGC CGG CT GCGACG GT C
GTTAGTAGTTTGTGCTCCAT TCCA ||| |||| ||| || |||||| ||
TCT TCT CTCG GTT GA TGCTGT CG /
TAC T TGAT T - ATC

GAM945 CAGAGAGCTGTGTGCATGCT 918 TCGCCTGGAC 2594 A-- - - G T T AACA- A C
GAGCAACACCACAGCCATTG CACAAGTTTG CAG GAGCT GTG T CA GC GAGC CC CAGC A
CTGAGGCCTGGGCTCGCCTG ACCT ||| ||||| ||| | || || |||| || ||||
GACCACAAGTTTGACCTG GTC TTTGA CAC A GT CG CTCG GG GTCG T
CAG A C G C - GGTCC A T

GAM946 AATCCGGCCGGGCTATCAGG 919 GGCAAGATGG 2595 CG--- - T AGG-- AGAA G GT
AGCCATCAGAAGCCGCCACC CTAGCAAGAT AATC GCCG GGC ATC AGCCATC GCC CCACC G
GTGACGGGTGGGGCAAGATG GCTG |||| |||| ||| ||| ||||||| ||| |||||
GCTAGCAAGATGCTGCGGCA TTAG CGGC TCG TAG TCGGTAG CGG GGTGG A
TATAGATT ATATA G - AACGA AA-- - GC

GAM947 GCTCCAAAGAACCAAGAGTG 920 CATTTCACTT 2596 T - ---------- CAC GAGATA TC

CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM948 GCTCCAAAGAACCAAAAGTG 921 CATTTCACTT 2597 AAGT - ---------- CAC GAGATA CTC
CAAATCAGTCCATTTCACTT TCACTGTCTG GCAAATC AGTCCAT TTCACTTT TGTCT GGGT T
TCACTGTCTGAGATAGGGTC AGAT ||||||| ||||||| |||||||| ||||| ||||
TCTAAAACCCAGGATACAAG CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCA /
GGTGGAATGTAGCTATATGG TT-- C TATCGATGTA AC- A----- AAA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM949 CTTGACCTTCATGCACTCAG 922 TCATGCACTC 2598 G C G - A AGC AT
AAGCTTTGGATGATTCCCCA AGAAGCTTTG CTT AC TTCAT CA CTC GA TTTGGATG T
TCCAAAATATTAGAGATGAA GATG ||| || ||||| || ||| || ||||||||
TGAAAGTGAAG GAA TG AAGTA GT GAG TT AAACCTAC C
G A A A A ATA CC

GAM950 ATGTGTGCACTGTGTAGTTT 923 GTGCACTGTG 2599 GTG AGTTT CAAA CAGA- GAAAG TA
CATTACAAAAGATCAGATCA TAGTTTCATT AT TGCACTGTGT CATTA AGAT TCAT GGAG A
TGAAAGGGAGTAACTCTCCG ACAA || |||||||||| ||||| |||| |||| ||||
AGGATGGGAATTATCTTGAT TG ATGTGACGCG GTAGT TCTA GGTA CCTC /
GTGGCGCAGTGTAATAGT ATA GT--- ---- TTAAG GGAG- TC

GAM951 CTTTGAAGGCAGCAGCATTG 924 AGCAGCATTG 2600 A- CA G AGGT C
TACAGGTGCTTCTCAAAGCG TACAGGTGCT CTTTGAAGGC GCAG TT TAC GCTT T
TGGAACCTTGCAGGCCTTCA T |||||||||| |||| || ||| ||||
AGG GGAACTTCCG CGTT AA GTG CGAA C
GA CC G ---- A

GAM952 TGGTGGTTCCACTGTGTGCT 925 AAAGTGTGTT 2601 G CC G AAA G GT GGA - TG- - - A
AAAGTGTGTTCGTGACAGGA CGTGACAGGA TT ACT TGTGCT GTGT TTC GACA TCA AGCG CT TTCCTT T
TCAAGCGTGCTTTCCTTATC TCAA || ||| |||||| |||| ||| |||| ||| |||| || ||||||
GAGGAGCAGAAAATCGTTGT AG TGA ACACGA CACG AAG TTGT AGT TTGC GA GAGGAG /
GAAAGTGTTGAAGGCACAAG A AC G A-- G -- GAA G TAAAA C C
CACAGAGTCAGAAAGCTA

GAM953 GAATGCACTGCCCAATCAGA 926 TCAGAGCAGA 2602 CA- CCAATCA G - A ---- TG T ---
--- T G
GCAGACAGCGACTTGGCGAC CAGCGACTTG CTGC GA CAG AC GCGA CT GCGACC C
GAGG GT A
CTCGAGGTGTGAGAGCTCCT GCGA |||| || ||| || |||| || |||||| | |||| ||
CCTGAATGTGGTCGCTGAGG GACG CT GTC TG TGCT GA CGCTGG G CTCC
CG G
CCCTCGTGGTACTGGTCAAT TCG CGACTAA G A G CCCG GT T TAAGTC T A
CAGCGCAGGCTCGTTC

GAM954 GACCAGAGTAGTGCATCAGT 927 TTAGGGTGGT 2603 GT-- - G G CTCTC
CTAAAGTCAGCTCTCTCTTC AGTTGTGTGC GACCAGAGTA GC ATCA TCTAAA TCAG T
TCTGGTTTAGGGTGGTAGTT TTTG |||||||||| || |||| |||||| ||||
GTGTGCTTTGGTT TTGGTTTCGT TG TGGT GGATTT GGTC /
GTGT A G - TCTTC

GAM955 GATTTCAGGTTATCCGCTTG 928 CAGGTTATCC 2604 A- TC CTT--- - CC
CCTTAGCCTCCCTAAGTGCT GCTTGCCTTA GATTTC GGTTA CGCTTGC AGC CT C
CACATTGCAGGCGTTAGCCG GCCT |||||| ||||| ||||||| ||| ||
CGAAGTC CTGAAG CCGAT GCGGACG TCG GA /
CG T- TTACAC T AT

GAM956 CACTGTTAAGAAGTTGAGCT 929 CAGCTGCAGT 2605 GAAG GA A TTAGAG A G GA -
- A AAATG
TTTATCTTAGAGGCAGCAGA GTGAAAGGGG TT GCTTTT TC GCAGC GAAG TTTG GCC
AAGGA TG A
AGGTTTGGAGCCAAGGAATG CAGG || |||||| || ||||| |||| |||| ||| ||||| ||
AAATGATGAGGCGTCCTTCA AG CGGGGA AG CGTCG CTTC AAGT TGG TTCCT
GC /
GGTAATGAACTTCAGCTGCA AGA- GA A TGTGA- A - AA AC - GGAGT
GTGTGAAAGGGGCAGGAAGA
CTGGCAGCTG
GAM957 CAGTCGCTTTTTGTTAAATG 930 TCCCAAATAT 2606 --- T G AA- TG - - - ACAAA T
AA
GATCCCAAATATTTACAAAG TTACAAAGCC CAGTC GCT TTT TT A G ATCC CAA ATATTT
GCCA CAG C
CCATCAGAACCACCTGTGGC ATCA ||||| ||| ||| || | | |||| ||| |||||| |||| |||
AAATGTATTGTGGATATTGT GTCAG CGG AAA AA T T TAGG GTT TGTAAA CGGT
GTC C
GAAAAGAAATGGCATTGACT TTA T G AAG GT A T A ----- - CA
G

GAM958 CAAACGGGCTTCAGAACTGG 931 CATTCACGGA 2607 ACG T GAA- TG CAGA AG CA--
TG
GACAGAGGAGTGTGACAATC CTGAGTTCTT CAA GGC TCA C GGA GG TGTGA ATCTC
G
TCTGGTGGGGATGCATTCAC GGAG ||| ||| ||| | ||| || ||||| |||||

GGACTGAGTTCTTGGAGGAT GTT CCG AGT G TCT TC GCACT TAGGG /
GATGCCATGTTG GTA T AGGA GT TGAG AG TACG GT

GAM959 CATTCCTTTCTAAGTGTGTT 932 AAGAACTCAC 2608 T T- TAA-- T AT--- AT
TTATGGCATCCTGCCCACAA AGTCTGATTA CAT CCT TC GTG GTTTT GGC C
AGAACTCACAGTCTGATTAG GGAT ||| ||| || ||| ||||| |||
GATG GTA GGA AG CAC CAAGA CCG /
- TT TCTGA T AACAC TC

GAM960 GTTGAGATCGTTCAGTATGA 933 TGAGATCGTT 2609 TTCAGT A C -- CTC C
AGTAGAGCAGAGATGCCCTC CAGTATGAAG GTTGAGATCG ATGAAGT GAG AGAGA TGCC
TCCG A
TCCGCAGCCGGGCGGTAGTT TAGA |||||||||| ||||||| ||| ||||| |||| ||||
CTCTCTCGCTTCGTTGATTT CAATTTTAGT TGCTTCG CTC TCTCT ATGG GGGC G
TAAC ------ - - TG C-- C

GAM961 GCCTGCTCCGAAATATGCTG 934 GAAATATGCT 2610 CC ATATG A-- - - -- - T
GACATAGCTGCTGAATCTGG GGACATAGCT GCCTGCT GAA CTGG CAT AGC TGCT
GAATCTGG GA T
GATTGTTCATTAGGTTCGAA GCTG ||||||| ||| |||| ||| ||| |||| |||||||| ||
GCATGCTCATGAAGCCAGGT CGGACGA CTT GACC GTA TCG ACGA CTTGGATT CT
G
TGTTCAGCAGGC -- GTTG- GAA C T AG A T

GAM962 CAGAGGACCTGCACACATGC 935 AACACTGTTC 2611 - A T - CT TG --- T- T TCCT
TACTGGTCCTGACTGTGTTT TGGCAAGCTG CAGA GG CC GCA CACATG AC GT CC GAC
GTGTTT T
TCCTTCCATAAACACTGTTC GTTT |||| || || ||| |||||| || || || ||| ||||||
TGGCAAGCTGGTTTTATGTG GTTT CC GG CGT GTGTAT TG CG GG TTG CACAAA /
CTGCTGGACCATTTG A A T C TT GT AAC TC T TACC

GAM963 GCCTTTCTTTTAAATAACCC 936 TATTGCACGT 2612 CTTTTAA C A ------ TT T
GGCATGGAGCAGTTTGGTTT GGTCCGGCCT GCCTTT ATAACC GGC TGGA GCAGT
GGT T
CCACCCTATTGCACGTGGTC GGTT |||||| |||||| ||| |||| ||||| |||
CGGCCTGGTTATGAAATCAG CGGAGG TATTGG CCG GCCT CGTTA CCA C
GAGGC ACTAAAG T - GGTGCA TC C

GAM964 TCTCTTGCCCTCTGTCATCC 937 AGCAGTGTGG 2613 T ------ CC C G GA - - T
CT
TAGCAGTGTGGATGGTTGGT ATGGTTGGTT TC CTTGCCCT CTGTCAT TAG AGT TG TG
GTTG G TGGGAT T
TGGGATCTTCGTGTCCCGTC GGGA || |||||||| ||||||| ||| ||| || || |||| | ||||||
TCAGCACACTCGAGCTCTGA AG GGACGGGA GACAGTG GTC TCG GC AC CGAC C
GCCCTG C

AGTGACAGTGAGGAAGGGCA - AGGAGT AA - A TC A T T TG
GGGA

GAM965 ACTACCAGCCTCCCACTGTG 938 TCGCCTGGAC 2614 CC - G T G A - AA CAGAGA
- CA T
GTGCCTGGTGGAGACCTGGC CACAAGTTTG ACT GTGGT CC GGTG AG CCT GGCC GGTA
GCTGTG TG TGC G
CAAGGTACAGAGAGCTGTGT ACCT ||| ||||| || |||| || ||| |||| |||| |||||| || |||
GCATGCTGAGCAACACCACA TGA CACCA GG CCGC TC GGG CCGG TCGT
CGACAC AC ACG /
GCCATTGCTGAGGCCTGGGC TT A - T - - T AG TAC--- C A- A
TCGCCTGGACCACAAGTTTG
ACCTGATGT
GAM966 GGCTAATATTTTAAATTTTT 939 TTCCACAGTG 2615 AAT ------ -- TTTC TCC
CTAGGCT AA
AGTAGAGACAGGGTTTCGCT CTAAGATTAC TTTTAGTA GAGAC AGGG GC ATTGC
GGTCTCA C
CCATTGCCTAGGCTGGTCTC CAGT |||||||| ||||| |||| || ||||| |||||||
AAACTCTGGGACTCAAGCAA AGAATCGT TTCTG TCCC CG TAACG
TCAGGGT /
TCTGCCCCCCTCAGTCTTCC TT- GACACC AC CC-- TC- AAC---- CT
ACAGTGCTAAGATTACCAGT
GTGAGCC
GAM967 GTCTTCCCTCAAGCTGCTCA 940 TCAAGCTGCT 2616 CC --- T - A TTTT A
GCACCCTGTTTTGCAACTAT CAGCACCCTG GTCTT CTCAA GC GC TCAGC CCCTG GCA C
GCTGGGGGCTGATGCGCCTA TTTT ||||| ||||| || || ||||| ||||| |||
TTGAGAAGGGC CGGGA GAGTT CG CG AGTCG GGGGT CGT T
A- ATC - T - ---- A

GAM968 GCTGATCAAGACTGCAGTGA 941 ACTGCAGTGA 2617 G AGA-- CA CA ---- TT AGAA
CAGGCAGCCTTAGTGAGAAT CAGGCAGCCT GCT ATCA CTG GTGA GGC AGCC AGTG
T
GACCCACTTCGGTTTTAAGC TAGT ||| |||| ||| |||| ||| |||| ||||
CTCATCCCAGCAATATGATG CGA TAGT GAC TACT CCG TTGG TCAC /
AGC G ATAAC CC -- AATT CT CCAG

GAM969 GCAGTGCTTTGTAGTTCTCA 942 AGTGCTTTGT 2618 -- TG CT TGT CTTTC CCCT
TTAAT
TTGTAGGGATCTTTCACCTC AGTTCTCATT GCAGTGCT T TAGTT CAT AGGGAT ACCT
GG T
CCTGGTTAATTGTATTCCTA GTAG |||||||| | ||||| ||| |||||| |||| ||
GGTATTTTATTCTTTTGTGG CGTTATGG A GTTAA GTG TTCTTA TGGA CC /
TAATTGTGAATGGTATTGC TA GT TG TT- TTTTA T--- TTATG

GAM970 GCTCCAAAGAACCAAGAGTG 943 CATTTCACTT 2619 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T

TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM971 GTTTCACTGGGGAAAAACTA 944 TCACTGGGGA 2620 A G AA T ATTA C CTA
CCTAAGATTATTTTCACAGC AAAACTACCT GTTTC CTG GGAA ACTACC AAG TTTT ACAG C
TACCAATTTGTCAGAAACTT AAGA ||||| ||| |||| |||||| ||| |||| ||||
TGGTGGTGTTTTGCGGGAGG CGGAG GGC TTTT TGGTGG TTC AAGA TGTT C
C - G G- T A--- C TAA

GAM972 GGATCCCGGACGAGTGCAAT 945 GGCCAGATGA 2621 T GG- AG AA C GGAAA GA T
A TG AA
GGCTGGGAAATCAGATCTTT GAGTGAGACA GGA CCC ACG TGC TGG TG TCA TCTT
TCTGG C A A
TCTGGACTGAAAACATTGGC CCGC ||| ||| ||| ||| ||| || ||| |||| ||||| | |
CAGATGAGAGTGAGACACCG CCT GGG TGC ATG GCC AC AGT AGAG AGACC G T
/
CAGTAAGCGTGCAGGGTTCC T ACG GA AC - AG--- G- T - GT AC

GAM973 GCTCCAAAGAACCAAGAGTG 946 CATTTCACTT 2622 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM974 ATGATAATCTACCTCACTTT 947 TTCCCTGTGG 2623 A TA CTTT - G A TTC G
CCCTGTGGCTATGTTCTGGG CTATGTTCTG ATGATA TC CCTCA CC CT TGGCT TG TGG T
TTTCCAATCAGGCCGAGTGG G |||||| || ||||| || || ||||| || |||
TTTGAGGACGATGTCAT TACTGT AG GGAGT GG GA GCCGG AC ACC T
- CA TT-- T - - TA- T

GAM975 GCGAAGCGGTTCTTAATTAA 948 TTAGTTGTAA 2624 --- AT ------- TC- TT---
GTGA
CTGCCTCCCTCTTATCCTGT GATGTATTGT GCGGT TCTTA TAACT GCC
CCTCTTATCCTG GCCT A
TGCCTGTGAAGAGGGGGTTG TTGG ||||| ||||| ||||| ||| |||||||||||| ||||
AGCCAGGATAGGAGGTTTGG TGTTA AGAAT GTTGA CGG GGAGGATAGGAC
TGGG /
CTTGCTTTAGTTGTAAGATG TGT -- TTTCGTT TTT CGAGT GGAG
TATTGTTTGGC

GAM976 TCAATAGATGGAAAAGATGT 949 TCCATAGCAG 2625 AAAAGA T TA GCA TCTTTC
GA - TAAA
CTCCATAGCAGTGCACGTTT TGCACGTTTC AGATGG TG CTCCA GCAGT CGTT AGG
GCC TTGGC A
CTTTCAGGGAGCCTTGGCTA TTTC |||||| || ||||| ||||| |||| ||| ||| |||||
AAAGAATGTTAGTGGTCACC TCTACC AC GAGGT CGTCG GTAG TCC TGG
GATTG /
TCCTGATGGCTGCTGGAGCC ------ C -- --- TCC--- AC T TAAG
ACCATCTTAGA

GAM977 GAGGGTAAGGAACGATGCTG 950 AAGGAACGAT 2626 - A G TATG C-- - --- - --- C
C
TGGTATGACCTCTGCACACC GCTGTGGTAT GGAA CG TGCT TGG ACCT TG CACA CCA GC
GG TGGCGGGG C
AGCGGCTGGCGGGGCCCTCC GACC |||| || |||| ||| |||| || |||| ||| || || ||||||||
CGTCACCCCCAGCATGGGAA TCTT GT GCGA ACC TGGG AC GTGT GGT CG CC
ACTGCCCT /
TGTGTCATACGGGTAGCCCA C G A CGA- CAT T AAG A ACC C C
AAGCGGTGCTTCTTTTTCTT
C
GAM978 GAAGACTTCCTAAATTTGCA 951 TTTGCACATT 2627 AC A TTGCA TTGCC ACCAT
CATTAGCTAGATTGCCATTA AGCTAGATTG GAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
GCACCATTAGAGAGTTGATC CCAT |||| ||||| ||| |||||||||| ||||||
TTTGGCTAATGATTATTCAG CTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GAAAATTTC AA C TTA-- C---- AGAGA

GAM979 GACCTGCTGCCTGACTACCT 952 TGCCTGACTA 2628 C T CT TA T - ------- - C AC-
T
GGCTGCCATAGATGAGGCCC CCTGGCTGCC TACC GG GCCA GA GAGGCCC TGGC AGC
CTTGCA GTG GC C
TGGCAGCCTTGCACGTGACG ATAG |||| || |||| || ||||||| |||| ||| |||||| ||| ||
CTCCAGTTCCCACTGCAAGA GTGG CC TGGT CT CTTCGGG ACCG TTG GAACGT
CAC TG C
GTTCATCCTGGCCATGGGCT - T -- C- T T GTCCTAC A - CCT A
TCTTCCTGGTCCTGGTGATG
GAGCAGATC
GAM980 GCCAGTCTTTTGTCTCTCTC 953 CAGTCTTTTG 2629 GTCTTTTG CT TC T- AGG
TTCAGCAATGGTGAGGCGGA TCTCTCTCTT GCCA TCTCT CT AGCAA GGTG C
TACCCTTTGCTCGGGGAAGA CAGC |||| ||||| || ||||| ||||
GAAATCCATGGT TGGT AGAGA GG TCGTT CCAT /
ACCTAA-- AG GC TC AGG

GAM981 GCATGGCTCCCCTCAACCAG 954 ATGGCTCCCC 2630 A CCTCAACCAG T CTT C----
TC TT
CTTGTGTGACCTTGGGCCAG TCAACCAGCT GC TGGCTCC CTTG GTGAC GGG CAG
AC G
TCACTTGGTGTCTCTGAAAC TGTG || ||||||| |||| ||||| ||| ||| ||

TCCCGTCACTGAGATCATAC CG ATCGAGG GAGT CACTG CCC GTC TG /
AGGAGCTAGC - ACATACTA-- - --- TCAAA TC TG

GAM982 GCTCCAAAGAACCAAGAGTG 955 CATTTCACTT 2631 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM983 GGTCAGAGCTCATTCGACAG 956 ATTCGACAGT 2632 TT G - G GA
TGAAGGCATTGTTTGACAGA GAAGGCATTG GGTCAGAGCTCA C ACAG T AAGGCATTGTTT C
AACGGTGCTTTGGTCTGTGT TTT |||||||||||| | |||| | ||||||||||||
TGGGCTCTGATT TTAGTCTCGGGT G TGTC G TTTCGTGGCAAA /
T- - T G GA

GAM984 CAGGTTTAAGTGTTCCTTCT 957 AAGCTGCTCA 2633 - TT-- TT ATTT----- AA T
TATTTCAGAATCTAGTGAAG GTTGGAAGAA CA GGT AAGTG CCTTCTT CAG TC A
CTGCTCAGTTGGAAGAAGGT GGTC || ||| ||||| ||||||| ||| ||
CACTTCAGTACCTTG GT CCA TTCAC GGAAGAA GTC AG G
T TGAC T- GGTTGACTC GA T

GAM985 TTCACAGAGGAACTTAAGAA 958 AGGAACTTAA 2634 AGA A AAGAA G GA--- G
GTATGGAGTGACGACTTGGT GAAGTATGGA TTCAC GGA CTT GTATG AGT CGACTTG T
TCGAGTTGGTGATGCTACAT GTGA ||||| ||| ||| ||||| ||| |||||||
ATGATAAAGCTCCAGTGGA AGGTG CCT GAA TATAC TCG GTTGAGC /
A-- C ATAG- A TAGTG T

GAM986 TCTCTGTCAGTCTGCTGTTT 959 CTGTCAGTCT 2635 C T CT - TG GC-- TTGCT ATC
GCAGGCGTCATTGCTGCTAG GCTGTTTGCA TCT TG CAGT GCTGT T CAG GTCA
GCTAGA G
AATCGGTCTTTGGTCCTTTG GGCG ||| || |||| ||||| | ||| |||| ||||||
ATTTAACTGTGACACAGTTG AGA AC GTCG TGACA A GTC TAGT TGGTTT /
CTGCAAGA - - T- C GT AATT TTCC- CTG

GAM987 CATGGTGCTGGGACATGAAG 960 CAGGTGATCG 2636 ----- GAAG C A--- -- AAA- GT G
- AAAGC
CTTCGGGAACAGTCGAAAAA TGTTGCCATC CAT CTT GGGA CAG TCGA A G
GATCATC GGT A
GTGGGATCATCGGTAAAGCA GAGC ||| ||| |||| ||| |||| | | ||||||| |||
CCTAAAACCAGGTGATCGTG GTA GAG CCCT GTC AGCT T T CTAGTGG CCA
C

TTGCCATCGAGCCTGGTGCT AAGTA AAA- C CGTG CG ACCG TG G A AAATC
CCCCGAGAAAATGATGAATT
CTGCAAGATG
GAM988 GGGAGAAATATGGGGACAAG 961 GGGACAAGAT 2637 AGAAA - A TG CGCAT AAA
CCAC - A
ATGTTGCGCATGCAGAAAGG GTTGCGCATG GGG TATGGG GACA GA TTG GCAG
GGTGAC AAGT CT T
TGACCCACAAGTCTATGAAG CAGA ||| |||||| |||| || ||| |||| |||||| |||| ||
AACTTTTCAGTTACTCCTGC CCC ATGTCC CTGT CT AAC CGTC TCATTG TTCA
GA G
CCCAAGTTCCTGTCGCCTGT GTG-- G C TG CC--- C-- ACTT A A
AGTGCCC

GAM989 ATGGTCCAACTTTGTGGAAT 962 GTAAGGATTT 2638 -- T-- GAATG- AGG AGGG
GG
GGTAAGGATTTTTAGGGTGT TTAGGGTGTT ATGG TCCAACT TGTG GTA ATTTTT
TGTTT C
TTGGCCAGAACAAGAGAAAT T |||| ||||||| |||| ||| |||||| |||||
AACTGCAGAAAACACATATG TACC AGGTTGG ACAC CGT TAAAGA ACAAG /
GTTGGAAACCAT AA TAT AAAAGA CAA GA-- AC

GAM990 GAAGCGGGCGTCAGTCTCTT 963 TCAGTCTCTT 2639 C C TTT CTTCCCA -
ACTTCTT CT
TCTCTTCCCACCTGCTGCTG TCTCTTCCCA GAAGCGGG GTCAGT TC CT CCTGCTG CTG
CAGGTTC T
ACTTCTTCAGGTTCCTTAAG CCTG |||||||| |||||| || || ||||||| ||| |||||||
AACCTGCAGCCAGTAGGCAG CTTTGTTC CAGTCA AG GA GGATGAC GAC
GTCCAAG /
TGCAGCTTGAACTGACTCTT T - TTC CGTGAC- C ------- AA
GTTTC

GAM991 GGGTTCCCAAATTCTCCTTG 964 TGGATTAGTA 2640 CCCAA - C T TG ATT
CTGTTCTGCATCATTGTCTA AAGAAGAATG GGGTT ATTCT C TTGCTG TC CATC G
GATGGATTAGTAAAGAAGAA AAAA ||||| ||||| | |||||| || ||||
TGAAAACTC CTCAA TAAGA G AATGAT AG GTAG T
AAG-- A A T -- ATC

GAM992 GATTGCTTGTGCCATAGGAG 965 TGAGAAGTAG 2641 GCTT - G CT TG - G------- --
- A
CTGTTGCAAACCGGGACCTC GTTGTGTGAC ATT GT GCCATA GAG GT CA AACC
GGACCTCGCT GGC T
GCTGGCATTGCCACGAGCGG TTTG ||| || |||||| ||| || || |||| |||||||||| |||
GGTCTGAGAAGTAGGTTGTG TAG CG CGGTGT TTT CA GT TTGG TCTGGGGCGA
CCG /
TGACTTTGTGTGGCTGCTGA AAGT T G -- GT G ATGAAGAG GCA T
AGATC

GAM993 AGATCTTCTGTGTGTTTACC 966 TGGAGAAGCA 2642 TTACC C T CCCCA TA - TA
G---- A

TCTCCCTGTCTCGCACCCCA CGCACAGAGC TGTGT TCTCC TG CTCGCA AGG TTT T
GTGCT TTGAC T
AGGTATTTTTAGTGCTGTTG AGGT ||||| ||||| || |||||| ||| ||| | ||||| |||||
ACATCAGTTAAAAGTAAGCA ACGCA AGAGG AC GAGTGT TCC AGG A CACGA
AATTG C
CCGACGGACGCCTCACTGTG CGA-- T T CAC-- GC C GC ATGAA A
AGTCATGGAGAAGCACGCAC
AGAGCAGGTCT
GAM994 TGAGCCAGGGGCAGCTCCGG 967 TGGTAGTTGC 2643 GC CTCC - ACAG - CCA
A
TGGCGGCCCACAGGACACCA AGGGCACGTC TGA CAGGGGCAG GGTGGCG GCCC GAC
ACCAGCC TCTTGC G
GCCCCATCTTGCAGGTGTAG ATTC ||| |||||||||| ||||||| |||| ||| ||||||| ||||||
GACAGGTTGGTAGTTGCAGG ACT GTCCCTGTT TTACTGC CGGG TTG TGGTTGG
AGGATG G
GCACGTCATTCCATTTGTCC A- TACC A ACG- A AC- T
CTGATCA

GAM995 GCTCCAAAGAACCAAGAGTG 968 CATTTCACTT 2644 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM996 TCTACCCCTTACTAGTAGTC 969 TTGCATAGAC 2645 ATC GAC CCTTAACC TTTC C G
T G- ATA
ATCTAGACTAAGTACCTTAA TACTAAAGTG AGTC TA TAAGTA TCAC CT AGTT TAT
AGG GGTG A
CCTCACTTTCCTCAGTTGTA GTAC |||| || |||||| |||| || |||| ||| ||| ||||
TTAGGGGGTGATAACAGTAC TCAG AT GTTCGT AGTG GA TCGG ATA TCC
CCAT /
CAACCTCATAGGGCTAGTGT --- AC- -------- T--- - G C AA GAC
GATGCTTGCATAGACTACTA
AAGTGGTACA
GAM997 CTACTAAATGTGAGACAATG 970 TACTAAATGT 2646 AAA- - G- TG- TA
CATTGTACACTTAATGATCT GAGACAATGC CTACT TG TGA ACAA CATTG C
TGTAGTTATCAGAAGAGTGG ATTG ||||| || ||| |||| |||||
GGTGA AC ATT TGTT GTAAT A
GAAG T GA CTA TC

GAM998 TGTTTGGGATCTGGTCTGAG 971 GGAAGTTGCT 2647 TC T G C GGCA TG TA A - T C
---- AT
GGGGCGGACGGCACTGATAT GGCTTCAGCT TGG CTGAG GGG GGAC C A TCA C GCTG
GGCC GC TCTC G
CAACGCTGTGGCCCGCTCTC GATG ||| ||||| ||| |||| | | ||| | |||| |||| || ||||

ATGATGGGAAGTTGCTGGCT ATC GATTT TCC CTTG G T AGT G CGAC TCGG CG
AGGG /
TCAGCTGATGACTTTGGCAA -- - G A AAAC GT TC A T T T TTGA TA
AGTTCACCTGTTTAGCTACC
CCTGCTGTCAG
GAM999 GATTACCACAGAGACATGAG 972 CATTATAATC 2648 - CAGAG GTAA TTT T TC
AG C A
TAATGTGTTTTGCTATGATG TTATGGTACC ACCA ACATGA TGTG TGCTATGA
GTTATGATG ACT G AAT G
TTATGATGTCACTAGGCAAT GCAT |||| |||||| |||| |||||||| ||||||||| ||| | |||
AGGAGTTTTTCAGTTCCATT TGGT TGTACT ACGC ATGGTATT TAATATTAC TGA T
TTG G
ATAATCTTATGGTACCGCAT C ATA-- ---- C-- C CT CT T A
CATGTATATGGTCTATC

GAM1000 GGAGGTGACCTGCAGACGGG 973 GGCAGATGCT 2649 - G G GG T GCAGA G A
GCCCT
CAGATGCTGGCAGAGACAGC GGCAGAGACA GGAGGTGA CCT CA ACG CAGA GCTG GACA
CC CAG T
CACAGGCCCTTTATTCACTG GCCA |||||||| ||| || ||| |||| |||| |||| || |||
GGTGTCACAGCCTCTGATGT TCTCCGCT GGA GT TGT GTCT CGAC CTGT GG GTC
T
GTGAGGTTCGCCTCT T - G A- C A---- - - ACTTA

GAM1001 TGGTTTTCTGCCGTGCCTCT 974 TGTAGAGACT 2650 TT TGC CTCT C CCA A G TC
AAC
CTTCCCTACCCAAAAGTGAT TGGGTATGTG TGGT TC CGTGCCT TC CTAC AA GTGAT AGT
TG A
GAGTTCTGAACAAGACAAGA ATAC |||| || ||||||| || |||| || ||||| ||| ||
CTGTCATATTGTAGAGACTT ACCA AG GTATGGG AG GATG TT TACTG TCA AC /
GGGTATGTGATACCA T- T-- TTC- A --- A - GA AGA

GAM1002 CACTAGGGGCCAGCATCTGA 975 TCAAGTGCTT 2651 TAG AGCA AACTT T TA
GAACTTCACTTTAATATCTT CAGAATAGGT CAC GGGCC TCTGAG CACTT AA T
TCAAGTGCTTCAGAATAGGT TCAT ||| ||||| |||||| ||||| ||
TCATCGTG GTG CTTGG AGACTT GTGAA TT /
CTA ATA- C---- C TC

GAM1003 GGACCTGCTTTCCTGCTTTG 976 TGTATGTTTC 2652 CTTTCC TT TGCCT CA C -
G
GGTCTTGCCTGTCAGACAGC CTATTTATAG GGACCTG TGC TGGGTCT GT GA AGCAT
CAT T
ATCATGTATATGTATGTTTC ATTC ||||||| ||| ||||||| || || ||||| |||
CTATTTATAGATTCATCGTA TCTGGAC ATG ACTTAGA TA CT TTGTA GTA A
TGTCAGGTCT TGT--- CT TATT- TC - T T

GAM1004 TCCCACTGTGGTGCCTGGCG 977 TCGCCTGGAC 2653 C - G T G A - AA ACA G -- -- ATG
GAGACCTGGCCAAGGTACAG CACAAGTTTG ACT GTGGT CC GGCG AG CCT GGCC GGT GA AGCTGTG TGC C
AGAGCTGTGTGCATGCTGAG A ||| ||||| || |||| || ||| |||| ||| || ||||||| |||
CAATACCACAGCTGTTGCCG TGA CACCA GG CCGC TC GGG CCGG CCG TT TCGACAC ACG /
AGGCCTGGGCTCGCCTGGAC T A - T - - T AG --- G CATA AGT
CACAAGTTTGA

GAM1005 CGAGGCTGGTGTTGTGAAGA 978 GAGGCTGGTG 2654 --- ---- GAA--- C T A- C
TCCTGGTGTCGCATGGGCCG TTGTGAAGAT CGAGGCT GGTG TTGT GAT CTGGTG CGC TGGGC G
CGCCCGCCGTGTTACCGGTA CCTG ||||||| |||| |||| ||| |||||| ||| |||||
TTGTAAGAACAAGCCGTACC GCTCTGA CCAT AACA TTA GGCCAT GTG GCCCG /
CAAAGTCTCG AAC GCCG AGAATG T T CC C

GAM1006 GCTCCAAAGAACCAAGAGTG 979 CATTTCACTT 2655 T - ---------- CAC GAGATA TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1007 AAATCAGACCCGGGTTCATT 980 TCAGACCCGG 2656 - C A CTG-- A
CCACTGGCCAGAGGCAGTCT GTTCATTCCA AAATCAGA C CGGGTTC TTCCA GCC G
TGGGAGGATTTGTGTTCTGG CTGG |||||||| | ||||||| ||||| |||
TTT TTTGGTCT G GTTTAGG AGGGT CGG /
T T - TCTGA A

GAM1008 GGATCCCGGACGAGTGCAAT 981 GGCCAGATGA 2657 T GG- AG AA C GGAAA GA T A TG AA
GGCTGGGAAATCAGATCTTT GAGTGAGACA GGA CCC ACG TGC TGG TG TCA TCTT TCTGG C A A
TCTGGACTGAAAACATTGGC CCGC ||| ||| ||| ||| ||| || ||| |||| ||||| | |
CAGATGAGAGTGAGACACCG CCT GGG TGC ATG GCC AC AGT AGAG AGACC G T /
CAGTAAGCGTGCAGGGTTCC T ACG GA AC - AG--- G- T - GT AC

GAM1009 CCGGGCCGCATCCTGGCGCT 982 GACAAGATGC 2658 G TC G AATAGGA -- AAAGAA-- GA T
CGTGCGGAATAGGAGCTTCA TGGAGCAGCT CATCCTG CGC GT CGG GCTTCAGC CT TTGT AGCAC T
GCCTAAAGAATTGTGAAGCA GGAC ||||||| ||| || ||| ||||||| || |||| |||||

CTTTGTGCTGGACGAGTGTG GTAGGGC GCG CA GTC CGAGGTCG GA AGCA
TCGTG /
ACAAGATGCTGGAGCAGCTG G TA G GA----- TA ACAGTGTG GG T
GACATGCGGCGGGATGTGCA
GG
GAM1010 GCCTTTAAAGCTGCCAACGG 983 TTAAAGCTGC 2659 AAA T CA - - A- GCAG------
AC
CTCCCTGCGAGCGCTGCAGG CAACGGCTCC GCCTTT GC GC ACG GCTCC CTGCG GCGCT
GCC A
CCACAGTCGGCAATTCCTAC CTGC |||||| || || ||| ||||| ||||| ||||| |||
AAGTGCAACGCGGAGGAGCA CGGAAG TG TG TGC CGAGG GGCGC CGTGA
CGG G
CGTCCGTGTCACGAAGGC CAC - CC A A AA ACATCCTTAA CT

GAM1011 GCCTTTAAAGCTGCCAACGG 984 TTAAAGCTGC 2660 AAA T CA - - A- GCAG------
AC
CTCCCTGCGAGCGCTGCAGG CAACGGCTCC GCCTTT GC GC ACG GCTCC CTGCG GCGCT
GCC A
CCACAGTCGGCAATTCCTAC CTGC |||||| || || ||| ||||| ||||| ||||| |||
AAGTGCAACGCGGAGGAGCA CGGAAG TG TG TGC CGAGG GGCGC CGTGA
CGG G
CGTCCGTGTCACGAAGGC CAC - CC A A AA ACATCCTTAA CT

GAM1012 GCCTTTAAAGCTGCCAACGG 985 TTAAAGCTGC 2661 AAA T CA - - A- GCAG------
AC
CTCCCTGCGAGCGCTGCAGG CAACGGCTCC GCCTTT GC GC ACG GCTCC CTGCG GCGCT
GCC A
CCACAGTCGGCAATTCCTAC CTGC |||||| || || ||| ||||| ||||| ||||| |||
AAGTGCAACGCGGAGGAGCA CGGAAG TG TG TGC CGAGG GGCGC CGTGA
CGG G
CGTCCGTGTCACGAAGGC CAC - CC A A AA ACATCCTTAA CT

GAM1013 CTGTCCTGTTGGCTATGGTG 986 GCCAAGATGC 2662 - -- -- GG ---- G GCA A
TGC
GTGGCTGCTGCGCAGGCATG AGTCATAGCA CTG TCCTGT TGGCT AT TGGT GGCT CTGC
GGC TGGG C
GGTGCCAGGTCCCAGCCACA GGAT ||| |||||| ||||| || |||| |||| |||| ||| ||||
GTAGGGGTCTCGGGCCAAGA GGC AGGACG ACTGA TA ACCG CTGG GATG CCG
ACCC A
TGCAGTCATAGCAGGATCGG T AT CG GA GGCT G ACA - TGG

GAM1014 GGAGAGAAACACTTGGGGAG 987 CATGACGGCT 2663 A -- G AA- A- G C
GGGAAAGGACGGCGTGGGCT CTGAGTTCTT GGAGAGA ACA CTT GGGAGGGG AGG CG
CGTGGG T
ACCCATGACGGCTCTGAGTT CCTG ||||||| ||| ||| |||||||| ||| || ||||||
CTTCCTGGGGCTTGTGTCTT CCTTTCT TGT GGG TCCTTCTT TCT GC GTACCC /

TCC G TC G GAG CG A A

GAM1015 GGTCTGTGTGAAGCATCACT 988 ATCACTTTGC 2664 A ACT GC TAATG G- GC TCT
A- TT
TTGCAGGGATTACTAATGGT AGGGATTACT A GCATC TT AGGGATTAC GTG GGCA AGG
GTGA TTAAG A
GGGGCAGCAGGTCTGTGAAT AATG | ||||| || ||||||||| ||| |||| ||| |||| |||||
TAAGTTATCTCTTGACCTCA T CGTAG AA TCCTTAATG CAC CTGT TCC CACT
AGTTC T
CCCTCATGTCAACACAAATG A AAC A- TAAA- AA AC --- CC TC
TAATTCCTAAACAAGATGCA
TTGCCAGTCT
GAM1016 GTCTGTGGAGTGGCTGGAGG 989 CAAGGTCATC 2665 - A G GAGG ACACTAT A A
AGGATGAACACTATGATTAC TTATGCAGAT GTC TGTGG GTG CTG AGGATGA GATT CC C
CACCAGGAGATTGCAAGGTC ATGC ||| ||||| ||| ||| ||||||| |||| ||
ATCTTATGCAGATATGCTAC CAG ACATC TAT GAC TTCTACT TTAG GG C
ATGAC T G A GTA- GGAACG- A A

GAM1017 GATTGATTTGGAAGATGGAG 990 TGGAAGATGG 2666 ATT AG G GTTCA- TG A AA
GAGTTCAGCTGTAACTAAAC AGGAGTTCAG GATTG TGGA AT GAGGA GC TA CT A
GGGGTGTGGCAAATGGTTCT CTGT ||||| |||| || ||||| || || ||
TGGTGTCTACAGTAATC CTAAT ATCT TG TTCTT CG GT GG /
GAC G- G GGTAAA GT G GC

GAM1018 GGCCTGGCTCCTGAGGTGGC 991 GTAGAGCAAA 2667 C C- GT GC A GA C G G
GT
TGATCGAATTGGGGACTATG TGTTTCAGGA GG CTGG TCCTGAG G TG TC ATTGGGGA TAT
TCCA T C
TCCAGTGTCATGGTGGGGTA TCCC || |||| ||||||| | || || |||||||| ||| |||| |
TCCCTAGTAGAGCAAATGTT TC GACC AGGACTT T AC AG TGATCCCT ATG GGGT G /
TCAGGATCCCAGACT A CT TG AA G A- - - G TA

GAM1019 TGTTTGGGATCTGGTCTGAG 992 GGAAGTTGCT 2668 TC T G C GGCA TG TA A - T
C ---- AT
GGGGCGGACGGCACTGATAT GGCTTCAGCT TGG CTGAG GGG GGAC C A TCA C GCTG
GGCC GC TCTC G
CAACGCTGTGGCCCGCTCTC GATG ||| ||||| ||| |||| | | ||| | |||| |||| || ||||
ATGATGGGAAGTTGCTGGCT ATC GATTT TCC CTTG G T AGT G CGAC TCGG CG
AGGG /
TCAGCTGATGACTTTGGCAA -- - G A AAAC GT TC A T T T TTGA TA
AGTTCACCTGTTTAGCTACC
CCTGCTGTCAG
GAM1020 TATCTCTATATCCCCAAACT 993 TGAATCACGT 2669 A AA TTAT AA--- GCCA ----
ATA
TATTACTTAAGATGCCATTA GAATAGCAAG TCTCT TATCCCC AC TACTT GAT TTATTCA
ATTCAT G

TTCAATTCATATAGAAAATG TCGG ||||| ||||||| || ||||| ||| ||||||| ||||||
AATCACGTGAATAGCAAGTC AGGGA GTGGGGG TG GTGAA CTG GATAAGT
TAAGTA /
GGTTGAAGTGTGTGTGGGGG G G- TGT- GTTGG AAC- GCAC AAA
GTGGAGGGATG

GAM1021 GGGAAGGTGATAACATGGGG 994 TCACCAGGTG 2670 G A--- A - -- TT
AAGAGGTTTTGCTTGTTTTT AAAATCAGCT GGGAAG TGAT AC TGG GGAAGA GG T
CACCAGGTGAAAATCAGCTT TCCT |||||| |||| || ||| |||||| ||
CCT TCCTTC ACTA TG ACC CTTTTT TC /
G AAAG G A GT GT

GAM1022 TCATTTGTCCTTGTACTACA 995 TTACATCATT 2671 T ACA AA AC-- CATA AATC -
CT AGTA
GTGAAAAGATACGGATCATA CACAAAAGTG GTACT GTGAA GAT GGAT TGCA TCAG
CTTAT TCA T
TGCAAATCTCAGCTTATCTT CCAT ||||| ||||| ||| |||| |||| |||| ||||| |||
CAAGTATCAAGGTGATATAA CGTGA CACTT CTA CCTA GCGT AGTC GAATA
AGT C
GTCTGATGCGGAATCCTTAC C AAA A- CATT AG-- ---- T T- GGAA
ATCATTCACAAAAGTGCCAT
TGCGGCTGA
GAM1023 GTATGAGAGCCAATTGAGTG 996 AAGGAGCTGA 2672 GAA- TC ATA
TTACCAATATAATGGAATTT CATTATATTG GTATGAGAGCCAATTGAGTGTTACCAATATAATG
TTT TTTC T
TCTTTCATATGTAGGAAAAG GTAA |||||||||||||||||||||||||||||||| ||| ||||
GAGCTGACATTATATTGGTA CATACTCTCGGTTAACTCACAATGGTTATATTAC GAG
AAAG G
ACACTCAATTGGCTCTCATA AGTC GA GAT
C

GAM1024 GACTTAGGGTTGTAGATCTC 997 AGGCTCCACG 2673 AGG ATCTCT C T - GGT TG
G C
TCTCTTCTTGGGCCGGTTTG AGCAGCTGCA GACTT GTTGTAG CT TTC TGG GCC T
GAGT AA A
GAGTGAACAGTTGACTTTGG ACAG ||||| ||||||| || ||| ||| ||| | |||| ||
CAAGGCTCCACGAGCAGCTG CTGGA CAACGTC GA GAG ACC CGG G TTCA TT /
CAACAGGTC --- ------ C C T AAC GT G G

GAM1025 CTGGTTGATCCGTGATGCCT 998 TGGTTGATCC 2674 - TGAT TAATCCGAAA-- AC--
GG- TCT AC
TGTATTAATCCGAAAGCTTA GTGATGCCTT CG GCCTTGTAT GCTT ATGGGTG
CTGTT GC A
CATGGGTGGGCTGTTTCTGC GTAT || ||||||||| |||| ||||||| ||||| ||
ACATAGCTCTGACAGATATA GT CGGGACGTA CGAG TACTCAT GACAG CG
/
CTCATCAGGGAGCATACCAC A CC-- CTATTCACCATA GGAC ATA TCT AT
TTATCATGCAGGGCCCTGAG

ATCTAGCCAG
GAM1026 CACAGAACTTGAGGCTGCCT 999 GTGACCAGAA 2675 AGA A GC CT TC - A A -- C
CTTTCCCTGCAGGCATGTAC GGTCCAGGTG CAC ACTTG GGCT CT T CCTGCAG GC TGT CTCTGAGC CC T
TCTGAGCCCCTGAGGCAGTT TG ||| ||||| |||| || | ||||||| || ||| |||||||| ||
TAGGGACAGCTCTGTAGGTG GTG TGGAC CTGG GA A GGATGTC CG ACA GGGATTTG GG G
ACCAGAAGGTCCAGGTGTG --- - AA CC GT T - - AC A

GAM1027 GGCTGCTGAGTGAGAAGGCT 1000 AGAAGGCTGC 2676 T ----- --- ---- C A C GA-T T
GCCAGCAAGATCAACGAGAC CAGCAAGATC GC GCTGA GTGAG AAGGCT GCCAG AAG TCAA GA CCA GC G
CATGCTGCGCCTGGGCATTT AACG || ||||| ||||| |||||| ||||| ||| |||| || ||| ||
TTGGCTTCCTGGCCTTTGGC CG CGACT TACTC TTTCGG CGGTC TTC GGTT TT GGT CG /
TTTGTGCTCATTACCTTCAG T TCCAT GTG TTTC C - T ACG C C
CTGCC

GAM1028 GCTCCAAAGAACCAAGAGTG 1001 CATTTCACTT 2677 T - ---------- CAC GAGATA TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1029 AGTGATGGTCCAACTTTGTG 1002 GTAAGGATTT 2678 - -- T-- GAATG- AGG AGGG GG
GAATGGTAAGGATTTTTAGG TTAGGGTTGT AGTG ATGG TCCAACT TGTG GTA ATTTTT TTGTTT C
GTTGTTTGGCCAGAACAAGA TT |||| |||| ||||||| |||| ||| |||||| ||||||
GAAATAACTGCAGAAAACAC TCGC TACC AGGTTGG ACAC CGT TAAAGA AACAAG /
ATATGGTTGGAAACCATGCG G AA TAT AAAAGA CAA G--- AC
CT

GAM1030 CACTGGGGCAGTTAAGAAGA 1003 TCAGTTTTCT 2679 TG C TTA - CAC TTT
CACAGCTGGTTTTCCCCATC CTCTCTCTCC CAC GGG AG AGA AGA AGCTGGT C
AGTTTTCTCTCTCTCTCCTT TTGG ||| ||| || ||| ||| |||||||
GGTG GTG TCC TC TCT TCT TTGACTA /
GT - TC- C T-- CCC

GAM1031 AGCCCTTCCTGTATATATGC 1004 GTGCATTGTG 2680 CT - TATAT GA - - - A AT
GAATAAGCTCCTAAGTACAG GAGTTTCATG AGCC TCC TGTA GC AT AAGCTCC TAA GTACAG CT T

ACTATTTGGGCTGTGCATTG GCCA |||| ||| |||| || || ||||||| ||| |||||| ||
TGGAGTTTCATGGCCAACTA TCGG GGG ACAT CG TA TTTGAGG GTT CGTGTC GG /
CACGGGTAGGCT AT C CAAC- G- C T A - GT

GAM1032 CCCTTCTGCCTGATGGCACA 1005 TGCCTGATGG 2681 GC T AC----- TC GT
TTCAGCTCCTGTAAGAAGCG CACATTCAGC CCCTTCT CTGA GGC ATTCAGC CT A
CTGGATAAAACAAGCCTTAG TCCT ||||||| |||| ||| ||||||| ||
AAGAAGGG GGGAAGA GATT CCG TAGGTCG GA A
A- - AACAAAA C- AG

GAM1033 GAGTGCAAATCAGTCCATTT 1006 CATTTCACTT 2682 T - ---------- CAC GAGATA
TC
CACTTTCACTGTCTGAGATA TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT
TGTCT GGGTC T
GGGTCTCTAAGACCCAGGAT AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
ACAAGGGTGGAATGTAGCTA CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
TATGGACTCGATTTGCTTC - C TATCGATGTA AC- A----- AA

GAM1034 GGCTCTGTAAGGAGAGGTGC 1007 TGCAGCTGCA 2683 T TA AG G CTGC G TCTAC
AG TTT
AGCTGCAGCAGTGTTCTACC GCAGTGTTCT GGC CTG AGGAG GT CAG AGCA TGT CGGA
TG T
GGAAGTGTTTTGATCATCTG ACCG ||| ||| ||||| || ||| |||| ||| |||| ||
TACAGTGCTTTGGATTCTTC CCG GAC TCCTT TA GTT TCGT ACA GTCT AC /
CTCCCAGGCC - CC CT G ---- G T---- -- TAG

GAM1035 TCTCCCAGTCATCACAGTCT 1008 CATCACAGTC 2684 A CAGTCT TTTCTT C AG A-
TC C----- TC
GGTTTCTTGATATCCTGAAG TGGTTTCTTG CAGTC TCA GG GATAT CTGA GA GAT
GGC ACC G
GAAGATTCGGCCACCTCGTT ATAT ||||| ||| || ||||| |||| || ||| ||| |||
GGTTCTGCAGCTTCATCAGT GTTAG AGT CC TTGTA GACT TT CTA TCG TGG
/
TTCTCAGCATGTTCCCTCTC - ACT--- TCTCCC C CT GA CT ACGTCT TT
CTCATGAGATTGGTGAGA

GAM1036 TCTGGATCCGTCTTCACTTC 1009 TCTGGATCCG 2685 GATC T CA TGTT CC - ACCAA
CTGTTGGCCTGAGCAGTACC TCTTCACTTC TCTG CG CTT CTTCC GG TGAGC AGT T
AATAACACACTGGTTCACCT CTGT |||| || ||| ||||| || ||||| |||
TGGAGGCAAAGCGTACAGA AGAC GC GAA GGAGG CC ACTTG TCA /
AT-- - AC TT-- -- G CACAA

GAM1037 GACTCTATCAAAGTGGCTTT 1010 TATCAAAGTG 2686 CTATC CTTTCT T- GATCAC
TTC

CTTGTATGTTTCGATCACGA GCTTTCTTGT GACT AAAGTGG TGTATG TTC GAGC A
GCTTCAAATGCTCTAAGCAG ATGT |||| ||||||| |||||| ||| ||||
AATTTGTATGTGCCCACTTT CTGA TTTCACC GTATGT AAG CTCG /
TGCTTAGTC TTCGT CGT--- TT ACGAAT TAA

GAM1038 GCCTGACCTGGTTAGATGTA 1011 TCATGTGCCT 2687 T- CTG AT CTCC--- AA--
CAAA
CATGGAGGTATCTCCCGAAT GACAGTCTTG GCC GAC GTTAG GTACATGGAGGTAT CG
TCATA A
CATACAAAATTAAATGTGAA GC ||| ||| ||||| |||||||||||||| || |||||
GACCGTTTATGCATACCTTC CGG CTG CAGTC CGTGTACTTCCATA GC AGTGT
T
ATGTGCCTGACAGTCTTGGC TT A-- -- CGTATTT CAGA AAAT

GAM1039 TGTATGGGATCTGGTCTGAG 1012 GGAAGTTGCT 2688 TC T G GGCA TG TA A - T C
---- AT
GGGGTGGACGGCACTGATAT GGCTTCAGCT TGG CTGAG GGGTGGAC C A TCA C GCTG
GGCC GC TCTC G
CAACGCTGTGGCCCGCTCTC GATG ||| ||||| |||||||| | | ||| | |||| |||| || ||||
ATGATGGGAAGTTGCTGGCT ATC GATTT TCCACTTG G T AGT G CGAC TCGG CG
AGGG /
TCAGCTGATGACTTTGGCAA -- - G AAAC GT TC A T T T TTGA TA
AGTTCACCTGTTTAGCTACC
CCTGCTGTCAG
GAM1040 ATCTTGACAAGCCCTCTAAG 1013 TGGAGAAGAC 2689 T CAA CT AA -- - GA T GC
GAT
CCCTCTTCCCATGAGGTGGT AGGGCACAGT ATCT GA GCC CT GCCC TCTTC CCAT GG
GGTA CTG T
AGCCTGGATTCGACGGATAC GGTA |||| || ||| || |||| ||||| |||| || |||| |||
TTCGGGTGGAGAAGACAGGG TAGG CT TGG GA CGGG AGAAG GGTG CT TCAT
GGC /
CACAGTGGTACTCTGGAT T CA- T- CA AC A GG - A- AGC

GAM1041 TTCCGGTGATTGTGGAAAAG 1014 ATCACTGTGG 2690 - --- AAA T GCTC- TGTT C
TG CAA G
GTCTCAGGCTCTCAGATTGT CTCAGTTCAT CC GGTGATT GTGGA GGTC CAG TCAGAT
GA AT A AC G
TGACATTGACAAACGGAAGT GTGG || ||||||| ||||| |||| ||| |||||| || || | ||
ACTTGGTTCCATCTGATATC GG CTACTAG TACTT TCGG GTC AGTCTA CT TG T
TG A
ACTGTGGCTCAGTTCATGTG A GTG GAC T ACTAT C--- - GT CA- A
GATCATCAGGAA

GAM1042 ACTCCGCTCCGAGTCTGTGA 1015 TCAGTCTGTT 2691 C--- TCTGT -------- CT CTCT
CCTT- AA GA
ACCTGACTGCTCTAAACCCT GTCTCCCTCT T CGAG GA AC GACTG AAAC CATGT
GTG G

TCATGTAAGTGGAGTTACAC AATC | |||| || || ||||| |||| ||||| |||
AGCGTGTGCCTGTTTCTTCA A GCTT CT TG CTGAC TTTG GTGCG CAC T
GTCTGTTGTCTCCCTCTAAT ATGT CTAAT CCCTCTGT T- TTC- TCCGT A- AT
CTTCGTGTAAGTGGAGT

GAM1043 TTCAAGGAGTTCACAGTCTA 1016 CAAGGAGTTC 2692 A CAC - AG C T
GAGCTGGGTTTTCCAACTTC ACAGTCTAGA TTCAAGG GTT AGT CT AG TGGG T
AGCACTATTGACACCTTGGA GCTG ||||||| ||| ||| || || ||||
AGGTTCC CAG TCA GA TC ACCT /
A TTA C CT A T

GAM1044 TATATATTGCTTACAGCTTT 1017 TGTGATCGTT 2693 CT A CT TT - CA CATAT
C
TCTCATTTGATATATAGCAT GTGAAAGTAG TATATATTG TAC GCTTTT CA TGAT ATATAG
TTGTA GA A
TGTACATATGACAAGTCTTT TACA ||||||||| ||| |||||| || |||| |||||| ||||| ||
TGCAAAACTGTGTGATCGTT GTATATGAC ATG TGAAAG GT GCTA TGTGTC AACGT
CT A
GTGAAAGTAGTACAGTATAT -- A T- T- G AA TTT-- G
G

GAM1045 CCCCTAACCCCTCTTCCCAT 1018 TGGAGAAGAC 2694 C AA- C- - GA T GC GAT
GAGGTGGTAGCCTGGATTCG AGGGCACAGT CC CT CCC TCTTC CCAT GG GGTA CTG T
ACGGATACTTCGGGTGGAGA GG || || ||| ||||| |||| || |||| |||
AGACAGGGCACAGTGG GG GA GGG AGAAG GGTG CT TCAT GGC /
T CAC AC A GG - A- AGC

GAM1046 TGGGGGAAAGTGAGTGCCAG 1019 AGACGGGGGA 2695 A TG CAGAC AAAA GA
GT- G
ACGGGGGAAAAACTGGAGTT AAAACTGGAG TGGGGGA AGTGAG C GGGGG ACTG GTT
TG G
GTTGGGGACGTGAAACACAG TTGT ||||||| |||||| | ||||| |||| ||| ||
TGGAGCCTTCACGTGCTTAT GCCTCTT TTATTC G CTTCC TGAC CAA GC G
TATTCTCCG A GT CA--- GAGG A- AGT A

GAM1047 CTCAAAGTAACAAGGTTTTG 1020 TGAGGTCAGA 2696 AA G GGACGCA C A TG
AA----- C
GCTGGACGCAGTGGCTCACG AGTTTGAGAC TCAAAGT CAAG TTTTGGCT GTGG TC CGCC
T TCCCAG A
CCTGTAATCCCAGCAATTTG TTTG ||||||| |||| |||||||| |||| || |||| | ||||||
GGAGGCCGAGGTGGGCGGAC GGTTTCA GTTT AAGACTGG CACC AG GCGG G
AGGGTT A
CACCTGAGGTCAGAAGTTTG GA G AGTC--- - - GT GAGCCGG T
AGACTTTGGG

GAM1048 AGGTCATGAATCATTGCATG 1021 GGGAAGATGG 2697 TC A- A CA-- G T C A --
ATA

GGAAGATGGTGGCTATACTG TGGCTATACT AGG ATG ATC TTG TGGGAA ATGG GG TAT CTGA AC G
AACATAGATACGTACTCAGG GAAC ||| ||| ||| ||| |||||| |||| || ||| |||| ||
TGACTTTCATATTCCCACAC TCC TAC TAG AAC ACCCTT TACT TC GTG GACT TG A
ACAAGATAGCATATCCT TA GA - ACAC A T A - CA CAT

GAM1049 CAAAAGGCAAGATTTGGGCC 1022 AGGCAAGATT 2698 AG T G- CA TT A
ATAGTTTGTTGATGCCAGCA TGGGCCATAG CAAA GCAAGA TTG GC TAG TGTTG T
TTAGAGTGACAATTCTTGTT TTTG |||| |||||| ||| || ||| |||||
CTTTG GTTT TGTTCT AAC TG ATT ACGAC G
CT T AG AG -- C

GAM1050 TGCAGCTGGTGGAGTTGGTA 1023 GGAAGCTGCC 2699 ------ TG AG-- T CTCG
CACTCGTAATCTGTTTCAGG AGCAAAATCT TGCA GCTGG G TTGG ACA T
AAGCTGCCAGCAAAATCTGC GCA |||| ||||| | |||| |||
A ACGT CGACC C GACT TGT /
CTAAAA GT GAAG T CTAA

GAM1051 GCTTTTGCTCCAGATGGTTC 1024 CCAGTGCCTT 2700 TT TCC T ATACTTT T - AA TC ACA
ATACTTTGCTTGGTCACAAG CAGAACTTTC GCT TGC AGA GGTTC GCT GG TCAC GGACA GC G
GACATCGCACAGTAAAGCTT TCTT ||| ||| ||| ||||| ||| || |||| ||||| ||
GTTCCGTGGTCCCAGTGCCT CGG ACG TCT TCAAG TGA CC GGTG CTTGT CG T
TCAGAACTTTCTCTTGCATG T- TTC T ACTTCCG C T C- T- AAA
GC

GAM1052 ATGATGGCTAGTGCCTAAAA 1025 TGAGGTAGGA 2701 A AA G C G A - TG ACTC
TGCCAGCACTTTGGCAGGCT GGATTGTTTG CT GTGCCT AAT CCAGCACTTTGG AGGCT AGGT GGA GGAT TTTGA C
GAGGTAGGAGGATTGTTTGA A || |||||| ||| |||||||||||| ||||| |||| ||| |||| |||||
ACTCCTGACCTCAGGTGATC GA TACGGA TTA GGTCGTGGAACC TCCGG TCCG CCT CCTA GGACT T
CATCCGCCTGGGCCTCCCAA G CA A C G - A GT CCAG
GGTGCTGGAATTACAGGCAT
GAGCCACCGT
GAM1053 AAGGGTTGTTTTGTTGTTAG 1026 TGAAGCTAGA 2702 T TGTTGT AA A-- GTCCATT
GTAAATAGATATTAGGCAGT TACCTAAAGC AAGGGT GTTT TAGGTA TAG TATTAGGCA T
CCATTTCTAAAATATGCCTG TACC |||||| |||| |||||| ||| |||||||||
ATGAAGCTAGATACCTAAAG TTCCCA CGAA ATCCAT ATC GTAGTCCGT C
CTACCCTT T ------ AG GAA ATAAAAT

GAM1054 CCCTGGGTCAGGAGAGAAAC 1027 CATGACGGCT 2703 GG--- - A -- G AA- A- G C

ACTTGGGGAGGGGAAAGGAC CTGAGTTCTT CCCT GTCA GGAGAGA ACA CTT GGGAGGGG AGG CG CGTGGG T
GGCGTGGGCTACCCATGACG CCTG |||| |||| ||||||| ||| ||| |||||||| ||| || ||||||
GCTCTGAGTTCTTCCTGGGG GGGA CGGT CCTTTCT TGT GGG TCCTTCTT TCT GC GTACCC /
CTTGTGTCTTTCCTTGGCAG GAAGA T G TC G GAG CG A A
AAGAGGG

GAM1055 GCCCCTTTTCACGTCTGAGT 1028 TCCCAGATGT 2704 C TTTCACG A- CC T T A A AACC CA
CCCAGATGTTAGACAAGGCA TAGACAAGGC GC CCT TCTG GTC AGA GT AG CA GGC CT G
ACCCTCAGACAGCCGGCCTG AACC || ||| |||| ||| ||| || || || ||| ||
CTACTTCTCAGATGACAGAA CG GGA AGAC TAG TCT CA TC GT CCG GA /
CCTAGGCGC C TCCA--- AG AC T - - - GCC- CA

GAM1056 CAAATCAGTCCATTTCACTT 1029 CATTTCACTT 2705 - TTC--- - GT GAG AG- TC
TCACTGTCTGAGATAGGGTC TCACTGTCTG CAAATC AGTCCAT AC TTTCACT CT AT GGTC T
TCTAAGACCAGGATACAAGG AGAT |||||| ||||||| || ||||||| || || ||||
GTGGAATGTAGCTATATGGA GTTTAG TCAGGTA TG AAGGTGG GA TA CCAG /
CTCGATTTG C TATCGA T -- ACA GGA AA

GAM1057 GAGTTATCACTAACAATAAA 1030 ATAAACCTTA 2706 TCACT AT - AC T ATGA
CCTTAGAAACCATTTATTAT GAAACCATTT GAGTTA AACA AAAC CTTAGAA CA TTATT T
GATATGCCAGTGACTGTTCT ATT |||||| |||| |||| ||||||| || |||||
GGGTGTTTTGTGTTTACTGA CTCAGT TTGT TTTG GGGTCTT GT AGTGA A
CTC CAT-- GT T -- C CCGT

GAM1058 CCTGCTTCTTTGCAAGGTAT 1031 AAGGTATTAG 2707 -- T A ---- T GTATG T
TAGGTTGTCATTGTATGGAT GTTGTCATTG CC TGCTTCTT GCA GGTATT AGGT GTCATT GAT A
TATAATCAAAATGACACTTC TATG || |||||||| ||| |||||| |||| |||||| |||
ACAAATACCTGTTGAGGAGT GG ATGAGGAG TGT CCATAA TTCA CAGTAA CTA T
AATGG TA T - ACAC - AA--- A

GAM1059 TCAGGGCATTAGCACCTTTT 1032 TAGCACCTTT 2708 - A CAC TTAAA A A
TAAATTGGTATCACCAGAGA TTAAATTGGT TCAGG GC TTAG CTTT TTGGT TC C
CCAGGTAAAGCCCCTAAGCT ATC ||||| || |||| |||| ||||| ||
CCTGA AGTCC CG AATC GAAA GACCA AG C
T - CCC TG--- G A

GAM1060 CTGTTCCTCTCACGCCCTCA 1033 AAGCTGCCAG 2709 TCAC CTCACCT T CC - A T CCTG
CCTGGCTGAGCCGCAGTAGT TTGAAGAACT GCC GGC GAG GCAGTAGTTCTTCAG TGGCA GCTTTA GT A

TCTTCAGTGGCAAGCTTTAT GTTG ||| ||| ||| |||||||||||||| |||||| |||||| ||
GTCCTGACCCAGCTAAAGCT CGG CCG CTC CGTTGTCAAGAAGTT ACCGT
CGAAAT CG /
GCCAGTTGAAGAACTGTTGC CTT- TCC---- T C- G - - ACCC
CCTCTGCCCCTGGCTTCGAG
GAGGAG
GAM1061 TGCCCCCTGCTCTGGCTGGT 1034 TTGGTCCCCT 2710 C- C CA C A T G C
CAAACGGAACCAAGTCCGTC TCAACCAGCT TGC CCCTGCT TGGCTGGT AA GG ACCAAG CC
TCTT C
TTCCTGAGAGGTTTGGTCCC ACAG ||| ||||||| |||||||| || || |||||| || ||||
CTTCAACCAGCTACAGCAGG ACG GGGACGA ATCGACCA TT CC TGGTTT GG AGAG /
GCTGCA TC C AC C C - - T

GAM1062 CTCTTCTTTTTCTCTCTCCA 1035 TCTTCTTTTT 2711 C TCCAT TT-- TC T TTTTA A--
GTAG
TGGATTACCTCCTCCAGTCT CTCTCTCCAT CT TC GGA ACC CTCCAGTCTA GT TACC
CCTTTAT A
ATGTTTTTATACCACCTTTA GGAT || || ||| ||| |||||||||| || |||| |||||||
TGTAGATGAAGTGAAGGCAG GA AG CCT TGG GGGGTCAGAT CG GTGG
GGAAGTG /
GGTGGTGCTAGACTGGGGTG T TCTTC TAAC GT - TG--- GAC AAGT
GGTCAATTCCCTTCTGATAG
TCTCGGAG
GAM1063 TCGTTTAATAGATCAGTTCC 1036 GTGTCATTGG 2712 T A ---- G TG T -- - AA
AA
GCTGTGTCATTGGTCAGTGC TCAGTGCATT T TAATAG TCAGTTC CGCT TGTCAT G CAGT
GCATTG GA GCAC G
ATTGGAAAGCACAAGAAGTG GGAA | |||||| ||||||| |||| |||||| | |||| |||||| || ||||
TGATCATAATGTGGATTGCA A ATTGTT GGTCAAG GTGA ACAGTG C GTTA TGTAAT
CT TGTG /
GGTGACAAGTGAGATGAACT T A TAGA - GA - GG A AG AA
GGATTGTTATACGA

GAM1064 TGATAATCTACCTCACTTTC 1037 TTCCCTGTGG 2713 A TA CTTT - G A TTC G
CCTGTGGCTATGTTCTGGGT CTATGTTCTG TGATA TC CCTCA CC CT TGGCT TG TGG T
TTCCAATCAGGCCGAGTGGT G ||||| || ||||| || || ||||| || |||
TTGAGGACGATGTCA ACTGT AG GGAGT GG GA GCCGG AC ACC T
- CA TT-- T - - TA- T

GAM1065 TGAGGTCAGGAGTTTGAGCC 1038 TGAGGTCAGG 2714 G ----- A T G -----
TTTTTG
TGACCAACATGGTGAAACGC AGTTTGAGCC TCAGGA TTTGA GCCTG CCAACATGG GAAAC
CTG GCTAA T
TGGCTAATTTTTGTATTTTT TGAC |||||| ||||| ||||| ||||||||| ||||| ||| |||||
TTAGTAAAGACAGGGTTTCT AGTCCT AAGCT CGGAC GGTTGTACC CTTTG GAC
TGATT /
CCATGTTGGCCAGGCTGGTC A CTGGT C T G AGAAA TTTTTA
TCGAAATCCTGACCTTA

GAM1066 TGAGGCAGGAGAATCACTTG 1039 AGGCAAGAGG 2715 GAGAA A GA-- GGG A GT AGC A

AACCTGGGAGGCAAGAGGTT TTGCAGTGAG TGAGGCAG TC CTT ACCT AGGC AGAG TGCAGTG TG G

GCAGTGAGCTGAGATCATAC CTG |||||||| || ||| |||| |||| |||| ||||||| ||

CACTGCACTCTGGCCTGGGT ACTCTGTC AG GAG TGGG TCCG TCTC ACGTCAC AC A

AACAGAGCGAGACTGTCTCA AG--- C ACAA --- G -- CAT T

GAM1067 ATAAAGCTAAAGTCCATCAT 1040 TGAATCATTA 2716 - GC -- GTAAAT GTACTT - T TGTA-- G

CTGGCAAATTCAGTAAATTG TCAGCATGAT ATCAT CTG AA ATTCA TGGAGA GCT TC GTT TCT A

GAGAGTACTTGCTTCTGTTT GAAA ||||| ||| || ||||| |||||| ||| || ||| |||

GTATCTGAGAGGAATTTTTA TAGTA GAC TT TAAGT ACCTCT CGG AG CAA AGG G

ACTGACGGCTTCTGTCTCCA C TA AC ------ GTCTT- C T TTTTTA A

TGAATCATTATCAGCATGAT

GAAAGGTGTGT

GAM1068 GTAGGTGGCACGTGCCTGTA 1041 GGAGGTAGAG 2717 G TGCC------- - G A AGGCTG GA

ATCCTGGCTACTTGGGAGGC GTTGCATGAG GTA GTGGCACG TGTAATC CTG CT CTTGGG AGGCAG G

TGAGGCAGGAGAATTGCTTA TTGA ||| |||||||| ||||||| ||| || |||||| ||||||

AACTCAGGAGGTAGAGGTTG CGT CACCGTGT ACGTTGG GAT GA GGACTC TTCGTT /

CATGAGTTGAGATTGTGCCA G TAGAGTTGAGT A G - AAA--- AA

CGTGC

GAM1069 CTCTCTATGTCCTGTATCAG 1042 GCCAAGATGC 2718 ATCA - CCTG ATGG T G GCA A T C

TGCTGTCCTGTTGGCTATGG AGTCATAGCA CTGT GTG CTGT TTGGCT TGG GGCT CTGC GGC TGGG GC A

TGGTGGCTGCTGCGCAGGCA GGAT |||| ||| |||| |||||| ||| |||| |||| ||| |||| ||

TGGGTGCCAGGGTCCCAGCC GACG TAC GACG AACCGG GCT CTGG GATG CCG ACCC TG G

ACAGTAGGGGTCTCGGGCCA A--- T TAG- ---- - G ACA - - G

AGATGCAGTCATAGCAGGAT

CGGTAGCGGG

GAM1070 TAGATGATTGAGCCGCGCAC 1043 TGATTGAGCC 2719 CA-- AG-- AGCT - ------- TC-- CG

GCTACAGTACAAGCTGCTGG GCGCACGCTA GCG CGCTAC TACA GC TGGA GCCAGT TGCTTCT G

AGCCAGTTCTGCTTCTCGGC CAGT ||| |||||| |||| || |||| |||||| |||||||

AAGGAGCGATTTGCTGGTGT TGC GTGGTG ATGT TG GCCT TGGTCG GCGAGGA /

AGACATCCGTGTCCGTGTAA ACTG GGAA GCC- T ACAGATG TTTA AC

AGGGTGGTGGTCACGTGGCC

CAGATTTATG
GAM1071 CAGCATAGGTGATCTTCAAC 1044 ACTGCATTGA 2720 TA ATC C C- CC TCCACGT
TGCCTCCGAATCCGCTCCAC ATTGCACTTG CAGCA GGTG TTCAA TGC TCCGAAT GC T
GTTCTTCTCCCGCCTATTCG TTG ||||| |||| ||||| ||| ||||||| ||
GACTGCATTGAATTGCACTT GTTGT TCAC AAGTT ACG AGGCTTA CG C
GTTG -- GTT - TC TC CCCTCTT

GAM1072 GCTCCAAAGAACCAAGAGTG 1045 CATTTCACTT 2721 T - ---------- CAC GAGATA
TC
CAGATCAGTCCATTTCACTT TCACTGTCTG GAG GCAGATC AGTCCAT TTCACTTT
TGTCT GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1073 TTGAGGCGTGTCAGTGGCTG 1046 TCAGTGGCTG 2722 TG C CAG GACA-- T T
ACAGGGCTTGGTTTCCAGCC ACAGGGCTTG T AGG GTGT TGGCT GGGCT GG T
TGTAAAAAGCCAATAATGCT G | ||| |||| ||||| ||||| ||
CCTTGG G TCC CGTA ACCGA TCCGA CC /
GT T ATA AAAATG - T

GAM1074 CATCCATGGCCATGAGTATT 1047 TATTGATCTG 2723 T GCC AT TCT GC C
AGG G
GATCTGTCCCAGCCTGTGCA TCCCAGCCTG CA CCATG ATGAGT TGA GTCCCA
CTGTGCATTG TCCG CA T
TTGCTCCGAGGCAGTTCTGA TGCA || ||||| |||||| ||| |||||| |||||||||| |||| ||
GTGGATGATGTACAGATGGG GT GGTGC TACTCG ACT TAGGGT GACATGTAGT
AGGT GT T
ATTCCTCAGCTCATTTGCGT T GTT -- CCT A- - GA- C
GGTTG

GAM1075 GCAGACAGAGAGTGGGACAT 1048 TAAATGCTCA 2724 CATAAATG - CTC T A AGA-
A---- AA
AAATGCTCAGGCTCAGCTGT GGCTCAGCTG AGAGTGGGA CTC AGG AGCTG GA GAT
AGG AATGG A
GAAGATAGAAGGAAATGGAA TGAA ||||||||| ||| ||| ||||| || ||| ||| |||||
AACCCATTCAGCACCTCAAC TCTCATCCT GAG TCT TCGAC CT CTA TCC
TTACC /
ATCTCCAGCTACATCTAGAG CGGTCTTA A ACA - - CAAC ACGAC CA
ATTCTGGCTCCTACTCTACG
GTATTGT
GAM1076 CAGCTACGGAAGACAGGAAG 1049 AGACAGGAAG 2725 TA CA GA ---- T
GAAGGA-- AG
AGAGCGAGCAGCTGGGGAAG AGAGCGAGCA CAGC CGGAAGA GGAAGA GCGAGC AGC
GGG GAGG G
GAGAGGAGGGACCTCGTAAG GCTG |||| ||||||| |||||| |||||| ||| ||| ||||

TTACCTTGCTTCCAGTTCGT GTCG GCCTTCT CCTTCT TGCTTG TCG TCC CTCC
/
CATCTTCCATCTTCCGCTGC TC A- AC ACCT T ATTGAATG AG
TG

GAM1077 GTATGGATGAGATGAGCTTG 1050 TGCTTATCAG 2726 G GA GA T T- C C GA
GCA- T AA
TAGGTAGGTTGGTGTCCACT CATTGAGTTG TAT GAT GAT GCT GTAGGTAGG TGGTGT CA
TG ACTG CA GG G
GGAACTGGCACATGGAAGGC ATGC ||| ||| ||| ||| ||||||||| |||||| || || |||| || ||
CCCTGAAAACAGTCAATGAA GTA TTG TTA CGA TATTCGTCC ACTACA GT AC TGAC
GT CC /
CATCATCCCTGCTTATCAGC G AG -- C CT A A -- AAAA C CG
ATTGAGTTGATGC

GAM1078 CTTAGGATTGACTGGGCGAT 1051 AGAAAGTCAT 2727 G T G- AGG TT TG - A A
AAGG- TT G
GCAGGCTCTTTTTGGGTTCC GGGTAGCTTG T AC GG CGATGC CTCT T GGTT CC TATGA
CTTT TAG TT T
ATATGAACTTTAAGGTAGTT ATGG | || || |||||| |||| | |||| || ||||| |||| ||| ||
TTGTCCAATTCTGTGAAGAA A TG CC GTTACG GGGG A TCGA GG GTACT GAAA
GTC AA C
AGTCATGGGTAGCTTGATGG A T AA GTA T- GT T - - GAAGT TT C
GGATGGCATTGAACCTGTAA
ATTACCTTGG
GAM1079 GCTGTGTTGCAGTGCATTGT 1052 GTGCATTGTG 2728 GCA A TG G TG GGA TG GA
CCT TG
GTTGCAGGATTGGGAAGGGC TTGCAGGATT GCTGTGTT GTGC T T T CA T G AGGGCA
GTGC G
ACCTGTGCTGGTTGCACTTG GGGA |||||||| |||| | | | || | | |||||| ||||
CTTTGATTGAATGTGGAATG TGACGTAG CATG A A G GT A T TTTCGT CACG /
AAGTACGAAGATGCAGT AAG A GT A GT A-- GT AG T-- TT

GAM1080 CCATATCCAGAGAACTCAAG 1053 TCCAGAGAAC 2729 C GAA- ----- GTGAA GAT G
AA
GTGTGAATACCAGATCCGGT TCAAGGTGTG CCATATC AGA CTC AAGGT TACCA CCG
TTGGAG A
TGGAGAAAGGGTTCCAAGTG AATA ||||||| ||| ||| ||||| ||||| ||| ||||||
GTGGTGACCTTGCGGAGAGA GGTGTAG TTT GAG TTCCA GTGGT GGT AACCTT
G
AGATTTTGATGTGG T AGAA AGGCG ----- --- G GG

GAM1081 AATAGAACACCTCTTTTCTT 1054 ACTGCAGTGA 2730 - TT TTG CTC CTCTT ATTT
TTATTGT
CTTGGTCTCTTCACAGCTCT AGACAGATGG CACC TCT TCTTC GT TTCACAG ACACA
TAAATGC A
TACACAATTTTAAATGCTTA TGTC |||| ||| ||||| || ||||||| ||||| |||||||
TTGTATAGCTGTGTGTTTAC GTGG AGA AGAAG CG GAGTGTC TGTGT ATTTGTG
/

TGTGTGTCTCCTCTGTGAGA T C- TGA TCA TCCTC GTC- TGTCGAT
CTGCAGTGAAGACAGATGGT
GTCTATCTTAT
GAM1082 TCTGGAAGTTGGCATCAATG 1055 TCATTCTGGC 2731 -- ATCAAT - TC
AAGATGGGCTCTGCGCCTGT CATAGCTTCC TCTGGAAGT TGGC GAA GATGGGC T
CATTCTGGCCATAGCTTCCA AGG ||||||||| |||| ||| |||||||
GG GGACCTTCG ACCG CTT CTGTCCG /
AT GT---- A CG

GAM1083 ACTTTATTTTGTATTCAACA 1056 TTCAACAAGT 2732 TATTT-- ACA-- TATCGA CT- C
AGTATTTATCGAGCCCCTAC ATTTATCGAG ACTT TGTATTCA AGTATT GCCC AC A
CATGTTCTGGGCCTAGTATT CCCC |||| |||||||| |||||| |||| ||
GGGAGTGAATATATGAAAAT TGAG ATATAAGT TTATGA CGGG TG /
GAGT TAAAAGT GAGGG TC---- TCT T

GAM1084 TGCTCATGCCAGGGTGAGGT 1057 TGAGGTAGTA 2733 - T T --------- AG A
AGTAAGTTGTATTGTTGTGG AGTTGTATTG TGCT CATGCCAGGG GAGGTAGTAAGTTGTAT
GTTG TGGGGT GG T
GGTAGGGATATTAGGCCCCA TTGT |||| |||||||||| |||||||||||||||| |||| |||||| ||
ATTAGAAGATAACTATACAA ACGG GTGTGGTCCC TTTCATCATTCAACATA CAAT
ACCCCG TT /
CTTACTACTTTCCCTGGTGT T - T AGAAGATTA GA A
GTGGCA

GAM1085 GAGTGCAAATCAGTCCATTT 1058 CATTTCACTT 2734 T - ---------- CAC GAGATA
TC
CACTTTCACTGTCTGAGATA TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT
TGTCT GGGTC T
GGGTCTCTAAGACCCAGGAT AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
ACAAGGGTGGAATGTAGCTA CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
TATGGACTCGATTTGCTTC - C TATCGATGTA AC- A----- AA

GAM1086 TCATGACGGCTCTGAGTTCT 1059 CATGACGGCT 2735 GA- GAG - GG T CCTTG
TCCTGGGGCTTGTGTCTTTC CTGAGTTCTT TCAT CGGCTCT TTCTT CCT GGCT GTGTCTTT
G
CTTGGCAGAAGAGGGCACAG CCTG |||| ||||||| ||||| ||| |||| ||||||||
CCAAGGCAAGGAGGGGCTGA AGTG GTCGGGG AGGAA GGA CCGA CACGGGAG /
AGGTGA GAA --- C A- - AAGAC

GAM1087 AGGGTTCCCTAGACTAATAG 1060 CATCACAAGT 2736 T AAT --- - CC- T C- AGGTT
GTA
CTGATGACTTTCCAGGAGTT TTGAGTTTTG AGACT AGCT GATGA CTTT AGGAGT GAG
CTC GATGCT T
GAGCCTCAGGTTGATGCTGT ACCC ||||| |||| ||||| |||| |||||| ||| ||| ||||||
ATTACAGGCGTTTGGAGTTT TTTGA TTGA CTACT GGAG TCTTCA CTT GAG
TTGCGG T

TCTACTTCTTCAGAGGATCA - GT- ACA A ACT T TT GT--- ACA
TCACAAGTTTGAGTTTTGAC
CCT
GAM1088 GAATGAGACTGCTGATCTTG 1061 TGATATCGCC 2737 GACT ---- ACT TG TGCCCA
G
GACTTGATATTGGTGCCCAG AGGATGATCT GAATGA GCTG ATCTTGG TGATAT G GG
A
GGAGACCCCTTGATATCGCC AGCT |||||| |||| ||||||| |||||| | ||
AGGATGATCTAGCTATCGTT CTTGCT CGAT TAGGACC GCTATA T CC G
C AT-- CTAG --- GT CC---- A

GAM1089 TTCACTTGACTTGGTAATTT 1062 TTCTACAGTG 2738 TT CT TTT TAC ACGTGA GAA
TTTCTACAGTGGACGTGATG GACGTGATGC TTCAC GA TGGTAAT TTC AGTGG TGCT T
CTGAATCCAGGCAGTGCCAC T ||||| || ||||||| ||| ||||| ||||
TTCGAATGTTGCTATTTCTG AGGTG CT ATCGTTG AAG TCACC ACGG /
TGGA T- TT T-- CT- GTG--- ACC

GAM1090 TGTGAAACACAGCCAGTTTC 1063 TGAGATCATC 2739 GAAA ---- T ---- - ACGTA T
GA
TTTGATGACTCAAAACGTAC GTTACAAGCA TGT CACAGCCA GTT CTT TGATGA CTCAAA
CTT GT T
TTTGTGATCTTGCCAAGCTT GCAT ||| |||||||| ||| ||| |||||| |||||| ||| ||
TGAGATCATCGTTACAAGCA ACA GTGTTGGT CGA GAA GCTACT GAGTTT GAA
CG C
GCATTTTGGTTGTGAAAAAC AAAA TTTA C CATT A C---- C TT
A

GAM1091 GTACAGTCCTTGATAACCTG 1064 TACAGTCCTT 2740 AG -- A C AG T- C
TCTGCCTTTCT TC
AGGATTTGGCTCTCAGCTTC GATAACCTGA GTAC TCCTT GAT AC TG GAT TGG TCTCAGCT
AGGC T
TGCCTTTCTAGGCTCTATGC GGAT |||| ||||| ||| || || ||| ||| ||||||||
CTTCTTTCTGTGGCTGGGAT CGTG AGGAA CTA TG AC TTG ACC AGGGTCGG
TCCG /
CCACTGTTTCCAAGTAATCC GA AC A A CT TC T TGTCTTTCT-- TA
AAAGGAAGGTGC

GAM1092 TTGTTGGGGGACTTGGAGAG 1065 TGGAGAGGCA 2741 - CAGA GTT A - ------ -----
CG
GCAGAGCACGTTCGACTCTT GAGCACGTTC CTTGGAG AGG GCAC CG CTCT TCA
CTGACC GTCTCG G
CACTGACCGTCTCGCGGTAC GACT ||||||| ||| |||| || |||| ||| |||||| ||||||
GAGACGACCGGGTCAGATTT GGACCTC TCC TGTG GT GGGG AGT GACTGG
CAGAGC /
CTTGATGGGGATGCAGGTGT C TGG- GAC A T TCTTTA GCCAG AT
GGTCCTCCTCCAGGTCCTTC
AAGCAG
GAM1093 GCAGTCTTGTTCTGTCACCT 1066 GCAGTCTTGT 2742 T--- C TC --- T -- TAT TA

AGGCTGGAGTGCAGTGGTAT TCTGTCACCT GCAG CTTGTT TG ACCT AGGC GGAGT
GCAGTGG GC T
GCTATCAGCTCACTGCAAAC AGGC |||| |||||| || |||| |||| ||||| ||||||| ||
TCCGCCTCCCAGGTTCAAGC CGTC GAACGA AC TGGA TCCG CCTCA CGTCACT
CG /
AAGTCTCCTGC CTCT - T- CCC - AA --- AC

GAM1094 GGGGAGAACAGCGTCTTTTA 1067 TCCTCCAGTG 2743 - C TTTTACC-- - CC -- G A
CC T
CCTGTCACCGAAGCCAGGAA GCGTTCTTTT GGG GAGAA AGCGTC TGT CA GAAGC CA
GA GC CGTT G
GCCCCGTTTGTAAGCGTGTG TACT ||| ||||| |||||| ||| || ||||| || || || ||||
TTGTGGTGCTTTATTGTACA CTC TTTTT TTGCGG ACA GT TTTCG GT TT TG
GCGA T
TCCTCCAGTGGCGTTCTTTT A C TGACCTCCT T TA TG G G T- A
TACTC

GAM1095 TCTGGACAAAGTAGGTGGTC 1068 TGCATGGAAA 2744 CAA G G AG C TC
AGTTTCCATCCATGTTCCAT GAGTATGTAT TCTGGA AGTA GTG TC TTTCCAT CATGT C
ATATGCATGGAAAGAGTATG TCTT |||||| |||| ||| || ||||||| |||||
TATTCTTTTCAGA AGACTT TTAT TAT AG AAAGGTA GTATA /
TTC G G -- C TA

GAM1096 GCTCCAAAGAACCAAGAGTG 1069 CATTTCACTT 2745 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1097 CCGGTGAGTGTAGTTTGCAT 1070 TTGCATTGTA 2746 TG TT- TT A ---- TG- TT
TGTAGGTTTCATTTGCATTT GGTTTCATTT CCGGTGAG TAGT GCA GT GGTT TCATT CATT
T
TTCTAGTGACTAATGATGTT GCAT |||||||| |||| ||| || |||| ||||| ||||
GACCATCTTGTCCTGCTGTG GGTTATTC GTCG TGT TA CCAG AGTAA GTGA /
CTTATTGG GT TCC TC - TTGT TCA TC

GAM1098 GGTGCACAAGTGATGGTCCA 1071 GTAAGGATTT 2747 - -- T-- GAATG- AGG
AGGG GG
ACTTTGTGGAATGGTAAGGA TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
TTTTTAGGGTTGTTTGGCCA TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
GAACAAGAGAAATAACTGCA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /

GAAAACACATATGGTTGGAA G AA TAT AAAAGA CAA G--- AC
ACCATGCGCTTGTGACT

GAM1099 CTGTGTTCTGTCACATGCCA 1072 GCCTGGCCTC 2748 GTTCTG - CCA - CC ----- CCCA - ATTATTA
GCCTGGCCTCCCTGTGTCCC CCTGTGTCCC TCAC ATG GCCTG GCCT CTG TGT GAT CGC A
AGATCGCATTATTAAACCCT AGAT |||| ||| ||||| |||| ||| ||| ||| ||| |||
CCAGCGCATTAGAGCAAGCC AGTG TAC CGGAC CGGA GAC ACG TTA GCG A
TCAGTAAGGCGCAGGCCACA AATCA- C AC- G AT TCCGA AGA- C ACCTCCC
TCGTGAACTAAGCAG

GAM1100 GCTCCAAAGAACCAAGAGTG 1073 CATTTCACTT 2749 T - ---------- ----- AC -- A
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTT TC TGTCT GAGAT G
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| ||||||| || ||||| |||||
TCTAAGACACGGATACAAGG CTT CGTTTAG TCAGGTA AGGTGGG AG ACAGA CTCTG /
GTGGAATGTAGCTATATGGA - C TATCGATGTA AACAT GC AT G
CTCGATTTGCTTCCGGACCT
TTTCCAGAGC
GAM1101 ATGATAATCTACCTCACTTT 1074 TTCCCTGTGG 2750 A TA CTTT - G A TTC G
CCCTGTGGCTATGTTCTGGG CTATGTTCTG ATGATA TC CCTCA CC CT TGGCT TG TGG T
TTTCCAATCAGGCCGAGTGG G |||||| || ||||| || || ||||| || |||
TTTGAGGACGATGTCAT TACTGT AG GGAGT GG GA GCCGG AC ACC T
- CA TT-- T - - TA- T

GAM1102 TGCTGGCTTTTGAACTGAAC 1075 CTTTGTCGGA 2751 -- - AA ACTTT- GA T- C CTCTTAT---- G
TTTGTCGGATGTTGGCAAGC TGTTGGCAAG GCTTT TG CTGA GTCG TGT GGCAAG TGC GAC C
TGCCTCTTATGACGCTGTCT CTGC ||||| || |||| |||| ||| |||||| ||| |||
CTTTACTCCTGCATTTGCCC CGAAG GC GGCT CAGC ACA CCGTTT ACG CTG /
CACAAACGACTTACTCTCGG AA T GA CTCATT AA CC - TCCTCATTTCT T
AGCGTGAAGCAACAGTA

GAM1103 CCGAGGTCGTGCCACTGCAG 1076 TCTGTGGTAT 2752 --- AG GCCA AGCA C TCTAA- T
TCCACCTGGCCAACACAGCA GACAGAACTG TGCCAC TGC TCCACCTG ACAC GGCCT TC AATAATAAT A
GGCCTCTCTCTAAAATAATA GG |||||| ||| |||||||| |||| ||||| || ||||||||
ATTATTATTATTGTTATTCT ATGGTG ACG GGGTGGAC TGTG CCGGA AG TTGTTATTA T
TGACAGGCCAGTGTAGAACA TCT -- AAGA A--- C TTCTTA T
GGTGGGGCATCTGTGGTATG
ACAGAACTGGG
GAM1104 CTCCCCTGGTGTACATAGTA 1077 TCGATGGACC 2753 C- T A TA -- AC

TTGATCAGAACAGGCTTTGG TTGCACTCCA CTCC CTGG GT CA GT ATTGATCAGA A
TCGATGGACCTTGCACTCCA GTAG |||| |||| || || || ||||||||||
GTAGGAG GAGG GACC CA GT CA TAGCTGGTTT G
AT T C TC GG CG

GAM1105 ATGATAATCTACCTCACTTT 1078 TTCCCTGTGG 2754 A TA CTTT - G A TTC G
CCCTGTGGCTATGTTCTGGG CTATGTTCTG ATGATA TC CCTCA CC CT TGGCT TG TGG T
TTTCCAATCAGGCCGAGTGG G |||||| || ||||| || || ||||| || |||
TTTGAGGACGATGTCAT TACTGT AG GGAGT GG GA GCCGG AC ACC T
- CA TT-- T - - TA- T

GAM1106 CACAGCTTCTTGGAGGCCTG 1079 TGGAGGCCTG 2755 G - G GGCTTA G GGG T
GAA G AGC
GCTTATGTGTCTGGGAGGTG GCTTATGTGT CA CTTCTT G AGGCCT TGT TCT AGG
GTGGCA GCA TCCC C
TGGCAGAAGCAGTCCCAGCC CTGG || |||||| | |||||| ||| ||| ||| ||| ||||||| ||| ||||
TGAAGGGATGCTGCCATCCT GT GAGGAA T TCTGGA GTA AGA TCC TACCGT CGT
AGGG T
AAAGAGATGAGGTCTGTAAA - A G ------ G AA- - --- - AAG
GGAGTGTG

GAM1107 CTGCAGATGTGTCCTTTCCT 1080 TTCCTGGAGC 2756 CCTTTC - C T --- C- TG
CCCCTT AG
GGAGCCCTCAGTGTGACATC CCTCAGTGTG CTG GAGCC TCAG GT GACAT TCTGCAGA
TGT CTGG C
TCTGCAGATGTGTCCCCTTC ACAT ||| ||||| |||| || ||||| |||||||| ||| ||||
TGGAGCCCTCAGTGTAACAA GAC CTCGG AGTC CA CTGTG AGACGTCT ACA
GACT /
CTCTGCAGATAGTGTCCTTA ATGT-- T - - TTC AT CA ATGT-- CC
CCTGAGGCTCTCAGTGTAAC
ATCGCTGCAG
GAM1108 ATAATTAGCTTATCAAACCT 1081 TAGCTTATCA 2757 ---- ATCAAACCT TA A TTC
GATGTTACCGAAAGTTTCAT AACCTGATGT ATAATT AGCTT GATGT CCGAA GT A
CCCACATTTGGGGATATCTT TACC |||||| ||||| ||||| ||||| ||
CAAAGCTCTTGAATTAT TATTAA TCGAA CTATA GGTTT CA T
GTTC ACTT----- GG A CCC

GAM1109 ACACTCGGGTCTATGTGGCT 1082 ATAAAGCTAG 2758 GT ----- ------ A G TTA
GACAACTGTGGCCTTTATGC TGACCATGGC ACACTCGG CTATG TGGCT GACA CT
TGGCCT T
CCAGGCTGAGATGTCTAATA TGGG |||||||| ||||| ||||| |||| || ||||||
AAGCTAGTGACCATGGCTGG TGTGGGTC GGTAC ATCGA CTGT GA GTCGGA G
GTGT -- CAGTG AATAAT A - CCC

GAM1110 TGAGGCAGAGAATCGCTTGA 1083 AGGCAAGAGG 2759 A AATC GAA--- AGGCA GT
AGC A

ACCCAGGAGGCAAGAGGTTG TTGCAGTGAG TGAGGC GAG GCTT CCCAGG AGAG TGCAGTG CG G

CAGTGAGCCGAGACCGCACC CCG |||||| ||| |||| |||||| |||| ||||||| ||

ATTGCACTCTAGCCTGGGCA ACTCTG CTC CGAG GGGTCC TCTC ACGTTAC GC A

ACAAGAGCAAAACTCCGTCT C AAAA AACAAC GA--- -- CAC C

CA

GAM1111 TGTGGAATATTGTTGATTTC 1084 TGCGGTGGTA 2760 T ATTGT CT TG AAATTG AG TG GGAA

TCACTGTGGCCCGAAATTGT GGTTGTAGAT TG GGAAT TGATTT CACTG GCCCG TGG C GCAG G

GGAGCTGGCAGGGAAGTGTG TCTT || ||||| |||||| ||||| ||||| ||| | ||||

TTGTTGGAGTCGAGCCTGGG AC TCTTA GTTGGA GTGGC CGGGT GCT G TGTT /

CTGCGGTGGTAGGTTGTAGA T GAT-- TG GT CCGA-- GA GT GTGT

TTCTTCA

GAM1112 CTCCCCGTCTCAGTTCACCT 1085 TGAAGTTGCA 2761 CT CACC A- ACTG A- AT ---- AG TAGG

GCAGACCTGCACTGTCTATA GCATAATCTA CAGTT TGCAG CCTGC TCT TA TTAT CAG TCACG A

ATTTATCAGAGTCACGTAGG GAAG ||||| ||||| ||||| ||| || |||| ||| |||||

AGAATTTGTGAAGTTGCAGC GTCAA ACGTC GGACG AGA AT AATA GTT AGTGT G

ATAATCTAGAAGAACAGCAG T- A--- GG ACA- AG CT CGAC GA TTAA

GGGCTGCAAAACTGTGCCAG

GGAG

GAM1113 CCAAAGAGAGTCTACAGTAT 1086 ATGGCTGCTC 2762 A A C- A- GACTATGAA TGCTC T A G

GCATTAGAAACCTTGACTAT AGTTGAAGAT TCT CAGT TG ATT GAAACCTT TGGC AGT GA GATCTA G

GAATGGCTGCTCAGTTGAAG CTA ||| |||| || ||| |||||||| |||| ||| || ||||||

ATCTAGGACTGGATTTCACT AGA GTCA GC TAA CTTTGGGG ACCG TCA CT TTAGGT A

CTGCCAGGGGTTTCGCAATA A A TA CG --------- TC--- - - C

TCGAACTGAAGAAAGGAGGG

GAM1114 GCTCCCGTCTGCAGCTCCCA 1087 TGCAGCTCCC 2763 --- -- C CA CAATCCA A G G CATT

GCAAGATCAATCCAGAAGGC AGCAAGATCA CCC GTCTG CAG TCCCAG AGAT GA G CAGGT ATTTCTG T

AGGTGATTTCTGCATTTCCA ATCC ||| ||||| ||| |||||| |||| || | ||||| |||||||

ACAGAGGTACCTGGCTCATC GGG CAGAT GTC AGGGTT TCTA CT C GTCCA TGGAGAC /

TCATTGGGACTGGTTAGACA TGA TG - AC ------- - G - AACC

GTGGGTGC

GAM1115 GCTTTTATCTTAGAGGCAGC 1088 CAGCTGCAGT 2764 A TTAGAG A G GA -- ATGAA AT

AGAAGGTTTGGAGCCAAGGA GTGAAAGGGG GCTTTT TC GCAGC GAAG TTTG GCC AAGGA C G
ATGAACATGATGAGGCGTCC C |||||| || ||||| |||| |||| ||| ||||| |
TTCAGGTAATGAACTTCAGC CGGGGA AG CGTCG CTTC AAGT TGG TTCCT G /
TGCAGTGTGAAAGGGGC A TGTGA- A - AA AC GCGGA TA

GAM1116 GCCTGAGTAAATGAAGGTGT 1089 TGAAGGTGTG 2765 AA- G ----- TC GCTCC-- A
GAGTTCTGTGCTCCTGGGAT AGTTCTGTGC GCCTGAGT AT AAGGT GTGAGT TGT TGGG T
CATCCACTCCTGAACAACTC TCCT |||||||| || ||||| |||||| ||| ||||
ATTGAAAACCTTGGTGCCAT TGGACTTA TG TTCCA TACTCA ACA ACCT C
TCAGGT CCG G AAAGT -- AGTCCTC A

GAM1117 GTGCAGCTGCTGTGCCTGAT 1090 TCCCAGATGT 2766 C- G CC - G GA G
GTGGGGACAGCCCTGCTCCC AAACAGAGCA GTGCAG TGCT TG TG AT TGGG CA C
AGATGTAAACAGAGCAACCT ACCT |||||| |||| || || || |||| ||
GCAC CACGTC ACGA AC AT TA ACCC GT C
CA G AA G G TC C

GAM1118 GCTCCAAAGAACCAAGAGTG 1091 CATTTCACTT 2767 T - ---------- CAC GAGATA TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1119 GGGTCTGAAGCGCTGGTGTT 1092 AGCGCTGGTG 2768 A- - TGT AAAT ATC
GTAGAAATCCTCATCACAAA TTGTAGAAAT GGGTCTG AGCG CTGG TGTAG CCTC A
GAGGTGACTGCGTTCCAGTT CCTC ||||||| |||| |||| ||||| ||||
GCTGCCAGGCCT TCCGGAC TCGT GACC GCGTC GGAG C
CG T TT- AGT- AAA

GAM1120 TTTAATATGTTTCAAGTGCT 1093 TCAAGTGCTT 2769 T- TCAAG T A- - TCGT
TCAGAATAGGTTCATCGTGT CAGAATAGGT TTTAA ATGTT TGCT CAG ATA GGTTCA G
TCCTGAACCATATCACTGAG TCA ||||| ||||| |||| ||| ||| ||||||
CAAGTCAACATTCTTAAA AAATT TACAA ACGA GTC TAT CCAAGT /
CT CTGA- - AC A CCTT

GAM1121 CTTATGTAGATCAGGCATGT 1094 TGAGGAGTTT 2770 A AGA GCAT G GCTG- GA AATA - GA
AGAGCTGCTGAGGAGTTTGT GTCAATATTT CTT TGT TCAG GTA AGCT AG GTTTGTC TTTA CTAT G

CAATATTTACTATGAGACAA ACTA ||| ||| |||| ||| |||| || ||||||| |||| ||||
TGGATAAAAGAAGACGGGCA GGA ACA GGTC TAT TCGG TC CGGGCAG AAAT
GGTA A
CTAACCAGGCTGTATCTGGA - --- ---- G ACCAA A- AAGA A AC
CAAGG

GAM1122 TTTCTGGTTCGGTGAGAGCA 1095 CATCCATCTG 2771 G - T AT TTCC T GTATG G
GTGAC ATC
TGAGCGATGGATTCCAGTTC AGCTTCTTGC CGGTGA AG CA GAGCG GGA AGTTC GA
GCG ACA TCG C
TGAGTATGGCGGACAGTGAC GCTC |||||| || || ||||| ||| ||||| || ||| ||| |||
TCGATCCTTCCGATGTGTGC GCCACT TT GT CTCGC TCT TCGAG CT CGT TGT
AGC /
ATCCATCTGAGCTTCTTGCG G A T GT ---- T ACCTA G ----- CTT
CTCTTGATTGTCACCGAGGG
CTCCCAGAAG
GAM1123 TGTTCATTACTGTAGATAAC 1096 TTCATTACTG 2772 -- T- TA AGAG GTTCTA
CCAT TC T
TGAGAGTTAGCTGTTCTAGG TAGATAACTG CA TTACTG AGA ACTG TTAGCT
GGAAAAGG GTT AGT A
AAAAGGCCATGTTTCAGTTA AGAG || |||||| ||| |||| |||||| |||||||| ||| |||
GTGCTATGACTTCTTTTTTC GT GATGAT TCT TGAC AGTTGG CTTTTTTC CAG
TCG G
GATTAAGGTTGAAGCAGTGT CC TC TG GA-- AATTAG TT-- TA T
TCTCTTAGTAGCCTGAACA

GAM1124 CTTTGGAAAGATTTTGTAAG 1097 TTCACAGTGC 2773 TAA TG AAATA C GGAAGT CC
- ---- G
GGTGCAAATAAGACTTTAAG CTCAAGATTC TTG GGG C AGA TTTAAG GGACAT AGT
ACAAA GAA A
GGAAGTGGACATCCAGTACA TCAG ||| ||| | ||| |||||| |||||| ||| ||||| |||
AAGAAGAGATTCCATGTTTG AAC TCC G TTT AAATTC TCTGTA TCG TGTTT
CTT G
TGGCTCAATGTCTTACACTT --- GT ACAC- - ACAT-- AC G GTAC A
AAATTTCACAGTGCCTCAAG
ATTCTCAGGAG
GAM1125 TGGGACATATATTGCATATG 1098 TTGCATATGC 2774 A TT AT A AAAG AAT A
CACAAAAGGTTAATTCAGAC ACAAAAGGTT TGGGAC TATA GCAT GC CA GTT TCAG C
ACTGGCCAGGCATGGTGGCT AATT |||||| |||| |||| || || ||| ||||
CATGCCTGTAGTCCCA ACCCTG ATGT CGTA CG GT CGG GGTC /
- C- CT - GGTA ACC A

GAM1126 AAGTAGTTGAATTTCAGATA 1099 TGAAAGACAT 2775 A - ATTT G ACTA--- AAA C A
AA
ATATACTAAGGAAATCCTCA GTTGTGTGTG AAGT GT TGA CA ATAATAT AGG TC TCACT
AGA A
CTAAGAAAACATTTGAGTGA AGTC |||| || ||| || ||||||| ||| || ||||| |||
AGACCTGAAAGACATGTTGT TTCA CG ACT GT TGTTGTA TCC AG AGTGA TTT /
GTGTGAGTCATGCACTT - T GAGT G CAGAAAG --- A G AC

GAM1127 TGAGACAGGAGAATCACTTG 1100 GAGGTAGAGG 2776 AG AA A-- TGA G AGGTA GT
- GA
AACCGGGGAGGTAGAGGTTG TTGCAGTGAG TGAGAC GAG TC CT ACC GGG GAG
TGCAGTGA GTT G
CAGTGAGTTGAGATGGCATC TT |||||| ||| || || ||| ||| ||| |||||||| |||
ACTGCACTCCAGCCTGGGTG ATTCTG CTC AG GA TGG TCC CTC ACGTCACT
CGG /
ATAGAACGAGACTCGGTCTT G- AG CAA TAG G GAC-- -- A TA
A

GAM1128 CAGCAGCCTAGGACTGGGAG 1101 TCTTGCACTT 2777 A --- G ATAG --- GA
AGATAGGAGAAGTAGGACTG GTCCAGGCTG CAGCAGCCT GGAC TG GAGAG GAGAA
GTAG C
CTGCAGGTTCTCATTGTTCT TTG ||||||||| |||| || ||||| ||||| ||||
TGCACTTGTCCAGGCTGTTG GTTGTCGGA CCTG AC TTCTT CTCTT CGTC /
- TTC G GTTA GGA GT

GAM1129 GGCTGGGTGAAAGACCATGG 1102 TGAAAGACCA 2778 G A A ATG ACT - GT
TGTACTGTGATGTCCAATCT TGGTGTACTG GGCT GGTGAA G CC GTGT GT GAT C
ACCACACAGGGCTTCACCAA TGAT |||| |||||| | || |||| || |||
GCC CCGA CCACTT C GG CACA CA CTA /
A - - GA- C-- T AC

GAM1130 AGGCCCATTGCATTGCACTT 1103 CATTGCACTT 2779 ATTGCAT A GT- ----- GGTG
- GTGG
GTCTCCACTGCCCATCGGTG GTCTCCACTG AGGCCC TGC CTT CTCCA CTGCCCATC
CTG CACT G
CTGCACTGTGGGATGTAGGT CCCA |||||| ||| ||| ||||| ||||||||| ||| ||||
GTCGGAAAGGGTGGGTAGCA TCCGGG ACG GAG GAGGT GATGGGTGG GGC
GTGG A
TGCTGGAGTTAGAGAGCAGG ------- A ATT CGTAC GAAA T ATGT
GCCT

GAM1131 CTCTTGAGCATGCTGACCAG 1104 GACCAGTGCT 2780 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM1132 GTCTTCCCCACCACAACTAA 1105 TACAGTCTGA 2781 CC AC CTA GACCT- G A TA---
C
GATGACCTCCGAGAAGTACC TTGTGCAGGT GTCTT CC CACAA AGAT CC AG AG
CCCAGG G
CAGGCGCCCCTGGGGTTCTC AAAG ||||| || ||||| |||| || || || ||||||
TGCTGGGCTTACAGTCTGAT TAGAA GG GTGTT TCTG GG TC TC GGGTCC C

TGTGCAGGTAAAGAT AT AC AG- ACATTC G G TCTTG C

GAM1133 GCTGCTGTGGAATATTGTTG 1106 TGCGGTGGTA 2782 G - AT GTT CT TG AAATTG
AG TG GGAA
ATTTCTCACTGTGGCCCGAA GGTTGTAGAT CTGT GGA ATT GATTT CACTG GCCCG
TGG C GCAG G
ATTGTGGAGCTGGCAGGGAA TCTT |||| ||| ||| ||||| ||||| ||||| ||| | ||||
GTGTGTTGTTGGAGTCGAGC GACA CTT TAG TTGGA GTGGC CGGGT GCT G
TGTT /
CTGGGCTGCGGTGGTAGGTT G A CT ATG TG GT CCGA-- GA GT GTGT
GTAGATTCTTCAACAGGGGC

GAM1134 TCCAACTTTGTGGAATGGTA 1107 GTAAGGATTT 2783 T-- GAATG- AGG AGGG GG
AGGATTTTTAGGGTTGTTTG TTAGGGTTGT TCCAACT TGTG GTA ATTTTT TTGTTT C
GCCAGAACAAGAGAAATAAC TT ||||||| |||| ||| |||||| ||||||
TGCAGAAAACACATATGGTT AGGTTGG ACAC CGT TAAAGA AACAAG /
GGA TAT AAAAGA CAA G--- AC

GAM1135 ATCCAGAGCATTGTCAGGGC 1108 AGAGCATTGT 2784 CA T T G CA- T
TGTGGGCATCATCCCTGGCA CAGGGCTGTG ATC GAGCAT G CAGGGCT TGGG TCA C
TCCCAGAGCCCTGCTGTGTT GGCA ||| |||||| | ||||||| |||| |||
CCCGAT TAG CTTGTG C GTCCCGA ACCC GGT C
CC T - G TAC C

GAM1136 AGCCATATCTTGTGGTATGT 1109 AACAGTATCT 2785 A -- TA-- A ATTTC
TTATAACGTATTTCTTTCAC ACTAAAGATG AGCC TATCTT GTGG TGTTT TAACGT T
ATGTTAAAACAGTATCTACT GGCT |||| |||||| |||| ||||| ||||||
AAAGATGGGCT TCGG GTAGAA CATC ACAAA ATTGTA /
- AT TATG - CACTT

GAM1137 CTGGGCAGAATAGGACAATT 1110 TAGGACAATT 2786 T C-- --- TT-- -
TATT
TAAGAATCAGTATGAACTCG TAAGAATCAG GAATAGGACAATTTAAGAATCAG ATGAA TCGT
GGA CTT TGGT C
TGGATTCTTTGGTTATTCAT TATG |||||||||||||||||||||| ||||| |||| ||| ||| ||||
TGTACTATAAGCCATTCCTG CTTATCCTGTTAAATTCTTAGTT TACTT AGCG CCT
GAA ATCA A
TGCGATTATTCATTTTGATT T ATT TGT TACC T TGTT
CTTAAATTGTCCTATTCTTG
GCCAG
GAM1138 AGGGGGGCAAAGTCTATCAG 1111 GGGGCAAAGT 2787 G GT A TG TTGAAA TG-
AG G GAT
GTGTTTGAAAGTGTGGCTAA CTATCAGGTG AGGG GGCAAA CT TCAGG T GTG GCTAAGA
TAT ATGT G
GAAGTATGATGTGATGAATG TTTG |||| |||||| || ||||| | ||| ||||||| ||| ||||
ATATGATGAGTCTTGGTATC TCTC TCGTTT GA GGTTT G TAC TGGTTCT GTA
TATA A

CATCGTGTTTGGAAGGATTT G AG A GT C----- CTA GA G GTA
GCTGCTCT

GAM1139 GCTCCAAAGAACCAAGAGTG 1112 CATTTCACTT 2788 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1140 TCCTTTTGACAAGAAATGTG 1113 TGACAAGAAA 2789 T - AAATGT C AA-- CTGTT T
GTCGTGAAAATTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA TTGGA GC
T
GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||
ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T
GA C G GTT--- - GGTA ----- T

GAM1141 TTTCATCAGGCTAGAACTGC 1114 TTCATCAGGC 2790 TCAG AGAACT A AAA AC C
CATAGAAAATGACTCCTCTG TAGAACTGCC TTTCA GCT GCC TAGA TG TC T
ATGCATCTGGGCTAAGCACA ATAG ||||| ||| ||| |||| || ||
TTGAAA AAAGT CGA CGG GTCT AC AG C
TACA AT---- - --- GT T

GAM1142 CAGGGGACTGGCCAGGTAAG 1115 TGGCCAGGTA 2791 ACT GG GA C---- C
CCATTAT T
GAGGAACAGACCACGTGGCC AGGAGGAACA CAGGGG GGCCA TAAGGAG ACAGA CA
GTGG GC C
ATTATGCTCTTGCCTTCCCA GACC |||||| ||||| ||||||| ||||| || |||| ||
CCTGAAACTTCTGTCTCCTT GTCCCT TCGGT ATTCCTC TGTCT GT CACC CG T
ATGGCTCTCCCTG C-- -- -- TCAAA C CTTC--- T

GAM1143 TTGTGGCAGCTGCTCTGAAG 1116 GCTGCTCTGA 2792 CAGCT TGAAG A G C
GTCACTTGTTTTACTGTGGC AGGTCACTTG TTGTGG GCTC GTC CTTGTTTTACT TGGC T
CTGGCCAAGTAGAGTAAGGG TTTT |||||| |||| ||| ||||||||||| ||||
ATGGGTCCACAG GACACC TGGG TAG GAATGAGATGA ACCG /
----- ----- G - G

GAM1144 CTCCGGTCCTTGACACCTGC 1117 TCGACAGAAG 2793 -- ---- AC--- - GAT -- CAC
GGGATATGTCCCTGCACAAT CAGTCGAGCA CTCCGG TC CTTGAC CTG CGG ATGTC
CCTG A
ATCAGGATGACATTATCGAC CTGA |||||| || |||||| ||| ||| ||||| ||||
AGAAGCAGTCGAGCACTGAT GAGGCC AG GAGCTG GAC GCT TACAG GGAC A
TCCGGAG TT TCAC ACGAA A AT- TA TAT

GAM1145 CACAAGTGATGGTCCAACTT 1118 GTAAGGATTT 2794 - -- T-- GAATG- AGG AGGG GG
TGTGGAATGGTAAGGATTTT TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA ATTTTT TTGTTT C
TAGGGTTGTTTGGCCAGAAC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
AAGAGAAATAACTGCAGAAA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA AACAAG /
ACACATATGGTTGGAAACCA G AA TAT AAAAGA CAA G--- AC
TGCGCTTGTG

GAM1146 TGGTGGGAGGCCCTGTGTGA 1119 CTGTCGTGTC 2795 GG T TGTGA T - A CGA CA C
ACGTCAGCAGCCTGTCGAGC GGGCCTGACG TGGTG AGGCCC G ACG CAG C GCCTGT GCT TCGG T
TCATCGGCTAGCCGAGGCCA CTG ||||| |||||| | ||| ||| | |||||| ||| ||||
CAGGTAGTCTGTCGTGTCGG GTCGC TCCGGG C TGC GTC G TGGACA CGG AGCC A
GCCTGACGCTG AG - TG--- T T A C-- -- G

GAM1147 GGTTAATTTCTTTACTATAG 1120 TTACTATAGT 2796 TT--- TA- A TCATAAA G - C - AA
TCATAAAAGTGGGACTTCAC CATAAAAGTG TTAAT CTT CT TAG AGT GGACT TCAC TTG TCAGAGAG A
CTTGTCAGAGAGAAAGCCTC GGAC ||||| ||| || ||| ||| ||||| |||| ||| ||||||||
TCTGAGTAAGTGACAGTTCA AATTA GAG GA ATC TCG CTTGA AGTG AAT AGTCTCTC /
GCTGAAATCTAAAGGTTGAG TGGAT TTG A TAAAG-- A C - G CG
TAGGTATTAACT

GAM1148 GTGGCAGACAGCCAGGATGA 1121 CAGCCAGGAT 2797 C C- CA-- ACTT CCAT T
CTTCTCCCATGGCTACTGCT GACTTCTCCC GTGG AGA AGC GGATG CTC GGC A
GAGTTAACGTCCACTCGCTT ATGG |||| ||| ||| ||||| ||| |||
TTCTTCTAC CATC TCT TCG CCTGC GAG TCG C
T TT CTCA AATT ---- T

GAM1149 CAGCAGCAAGAGACGTCACC 1122 TTCCTGCCTC 2798 CA CGTCACCCTA AAC G - ACAT CACC CT
CTAGAAAACAGGCTGCAGAA CCTATTTGCC GCAG AGAGA GAA AG CTG CAGA GGAGGT GATG T
CATGGAGGTCACCGATGCTT AGGC |||| ||||| ||| || ||| |||| |||||| ||||
GAACATTTCCTGCCTCCCTA CGTC TCTTT CTT TC GAC GTTT CCTCCG TTAC G
TTTGCCAGGCTTTCATTTCT TG A--------- --- G C ATC- TCCT AA
GTCTGCTG

GAM1150 GGACCGATGATTGCTCCTTC 1123 AAGCCTGTCA 2799 A ATGA GCT TC CTA AT CC

CAGGCCTAGGTAGTATGCTC GGTAAGGATG GG CCG TT CCT CAGGC GGTAGT GCT A
CACCGGCCACTGCCAAGCCT GCC || ||| || ||| ||||| |||||| |||
GTCAGGTAAGGATGGCC CC GGT GA GGA GTCCG CCGTCA CGG /
- AG-- AT- CT AA- C- CC

GAM1151 TCTGGACAAAGTAGGTGGTC 1124 TGCATGGAAA 2800 CAA G G AG C TC
AGTTTCCATCCATGTTCCAT GAGTATGTAT TCTGGA AGTA GTG TC TTTCCAT CATGT C
ATATGCATGGAAAGAGTATG TCTT |||||| |||| ||| || ||||||| |||||
TATTCTTTTCAGA AGACTT TTAT TAT AG AAAGGTA GTATA /
TTC G G -- C TA

GAM1152 TATCTCCAAAATCAACTATT 1125 TACGTAAAGA 2801 T CC AACTATT - AG T GATT
CATTATCAGTGCTTAGGATT CTGATGTACA TA CT AAAATC CATTA TC TGC TAG C
CAAAACTACGTAAAGACTGA GGGT || || |||||| ||||| || ||| |||
TGTACAGGGTTTTCAAGTTA AT GA TTTTGG GTAGT AG ATG ATC /
T AC GACAT-- C AA C AAAA

GAM1153 GGGAGGCTGAGGTAGGAGGA 1126 TGAGGTAGGA 2802 C-- GTA T-- T AA
TCATAGTTTCAAAGTGTGGC GGATCATAGT GGGAGG TGAG GGAGGATCA AGT TCA G
ACTTACTGGTTCTCCACTCA TTCA |||||| |||| ||||||||| ||| |||
CTCCCTCCT TCCTCC ACTC CCTCTTGGT TCA GGT /
CTC A-- CAT C GT

GAM1154 GGTACTGACTCTGTTCAGCA 1127 TGACTCTGTT 2803 AC A AGCA -- AA CA GTG
GGACAAACAGCAGAACGTGG CAGCAGGACA GGT TG CTCTGTTC GGA CA CAG GAAC G
GAAGTTCGCCTGAATGATTC AACA ||| || |||||||| ||| || ||| ||||
CGGAGGATAGAGACACACC CCA AC GAGATAGG CCT GT GTC CTTG /
C- A AGG- TA AA CG AAG

GAM1155 CAGCAGTTTAGGTTAAACAA 1128 TAAGCTAGGG 2804 G ---- -- ATA GTTAAA TGT
T CGC
ACATTCCTGGATAATGCGTT GTTAGTATAG TTAG TTAAACAA AC ATTCCTGG ATGC
TTTC ATC GT C
AAATTTCTGTATCTGTCGCC TTGT |||| |||||||| || |||||||| |||| |||| ||| ||
CTGAGCTGATTTTGAAAGAT GATT AATTTGTT TG TGGGGATC TATG AAAG TAG
CG C
GGTATAAGCTAGGGGTTAGT G GATA AT GAA GTAG-- TTT T AGT
ATAGTTGTTTAAGTTAGACA
AAACATGCTG
GAM1156 CAGAGTACTGGGATACCTGA 1129 AGAGTACTGG 2805 T- GATACC TAT GTCACAAAT
CT
AGTATGCGTCACAAATCTTG GATACCTGAA CAGAG ACTGG TGAAG GC CTTGA A
ACTATAATCAAGTAAGCTTT GTAT ||||| ||||| ||||| || |||||
TTTCATAACCAGTTTCTTTG GTTTC TGACC ACTTT CG GAACT T
TT AAT--- TTT AAT------ AA

GAM1157 GCTCCAAAGAACCAAGAGTG 1130 CATTTCACTT 2806 A AA T - TTC--- - GT GAG AG- TC
CAAATCAGTCCATTTCACTT TCACTGTCTG CC GAG GCAAATC AGTCCAT AC TTTCACT CT AT GGTC T
TCACTGTCTGAGATAGGGTC AGAT || ||| ||||||| ||||||| || ||||||| || || ||||
TCTAAGACCAGGATACAAGG GG CTT CGTTTAG TCAGGTA TG AAGGTGG GA TA CCAG /
GTGGAATGTAGCTATATGGA A C- - C TATCGA T -- ACA GGA AA
CTCGATTTGCTTCCGGACCT
TTTCCAGAGC
GAM1158 CTATAGTCCCAGCTACTCAG 1131 TGAGCTCAGG 2807 C CT AG GCTGA G GA
GAGGCTGATTGAGGTGGGAG AGTTTGTGGC CTATAGTC CAG ACTC GAG TT AGGTGG G
GATCACCTGAGCTCAGGAGT TATA |||||||| ||| |||| ||| || ||||||
TTGTGGCTATAG GATATCGG GTT TGAG CTC GA TCCACT /
T -- GA ----- G AG

GAM1159 AGTGGTCAAAAGCACAGGCT 1132 TCAAAAGCAC 2808 T AA- - CT- - --- G
CCTGTTGGAGTGGGGCTACC AGGCTCCTGT AG GGTCA AGC ACAGG CC TGTTGGAGT GGG C
TTGAATTCTAACACGGCTAC TGGA || ||||| ||| ||||| || ||||||||| |||
TTGTAGCTATGTGACCCT TC CCAGT TCG TGTTC GG ACAATCTTA TCC T
- GTA A ATC C AGT A

GAM1160 TAAGTACAAGCACATATGGC 1133 TACAAGCACA 2809 CA C--- - TA-- A CT
TTACAGTAAATGAACTGATT TATGGCTTAC TAAGTA AGCA ATATGG CT CAGT AATGAA G
TTTATTAACTGCTTTGGCCC AGTA |||||| |||| |||||| || |||| ||||||
ATATAAAATGCTGATATTTA ATTTAT TCGT TATACC GG GTCA TTATTT A
AG AAAA C TTTC A TT

GAM1161 ACGCCGCTGGGAATGGTGGC 1134 GCTGGAGTGA 2810 -- G AT G AGA- T - GTA TCT
TAGAGCTTCCACAATGGTAC GGAGCACTTG ACGCC GCTG GA GGTG CT GCT CCA CAATG CAGGCTGC G
AGGCTGCTCTGCCGTGCGGC TCGC ||||| |||| || |||| || ||| ||| ||||| ||||||||
CTGCGTTGCTGGAGTGAGGA TGTGG CGAC CT TCAC GA TGA GGT GTTGC GTCCGGCG C
GCACTTGTCGCAGCCAGGTG AC G GT - GGAG - C --- TGC
T

GAM1162 GTCTTGCTAATTGGTGTATC 1135 GTAAGCATTG 2811 C A- GTATC GTG ---- GC T AA TATT
CCTTGTGTCTAAAGCCAGTG TATTTGAATT GTCTTG TA TTGGT CCTT TC TAAA CAGTG CT TACA T
TCTAATACATATTTTTTTTG GAAT |||||| || ||||| |||| || |||| ||||| || ||||
TAAGCATTGTATTTGAATTG CGGGAC AT GACCA GGAA AG GTTT GTTAC GA ATGT /

AATAAAGGAAACCAGGGTAA A GG AA--- ATA TTAA AT - -- TTTT
CAGGGC

GAM1163 GAGACCCTGCCTTTAAAGCT 1136 TTAAAGCTGC 2812 CCC AAA T CA - - A-
GCAG------ AC
GCCAACGGCTCCCTGCGAGC CAACGGCTCC A TGCCTTT GC GC ACG GCTCC CTGCG
GCGCT GCC A
GCTGCAGGCCACAGTCGGCA CTGC | ||||||| || || ||| ||||| ||||| ||||| |||
ATTCCTACAAGTGCAACGCG T GCGGAAG TG TG TGC CGAGG GGCGC CGTGA
CGG G
GAGGAGCACGTCCGTGTCAC T-- CAC - CC A A AA ACATCCTTAA CT
GAAGGCGTTTTC

GAM1164 TAAGGGAAAATTAATGGGTG 1137 TGGGTGTTTC 2813 A GGG T CTTTA- AA-
AA
TTTCCTCCTTTAGGGAGGTA CTCCTTTAGG TAAGGG AAATTAAT TG TTCCTC GGGAGGT
TGCA G
ATGCAAAGAGTGTGGACATC GAGG |||||| |||||||| || |||||| ||||||| ||||
TTCTAATCTTGAGGAACAGT GTTCCC TTTAGTTG AC AAGGAG TCTTCTA GTGT /
AGTTGATTTCCCTTG - ATG - TTCTAA CAG GA

GAM1165 ATATTTTGCAATGTGAGAAG 1138 TTTGGCTCTG 2814 TT - TG GAAG C AA- - A
AA
GACATGAGATTTGGGAAGGA TGTCTCCACC ATATT GCAAT G A GA ATGAGATTTGGG
GGAC CGGGGT GAAT T
CCGGGGTAGAATAATATGGT CAAA ||||| ||||| | | || |||||||||||| |||| |||||| ||||
TTGGCTCTGTGTCTCCACCC TATGA CGTTA T T CT TACTCTAAACCC TCTG
GTCTCG TTTG A
AAATCTCATATCAAATTGTA T- A GT AAA- A ACC T G GT
ATTGCTAGTAT

GAM1166 TGATGTGTTTAACAACAAAT 1139 TGAGAACATG 2815 CAAAT GA- -------- - TATCTTAC
C- AC
TGTGACAGAGCTGAGTGCTC TGAAACTATG TGT CAGAGCTG AGTGCT CC AGGGT
AATGA T
CTATCTTACAGGGTCAATGA TTA ||| |||||||| |||||| || ||||| |||||
ACTACTTATTAAGCCTTACT ACA GTCTTGAC TCACGA GG TTCCG TTATT /
GGTAGCACTGAATTTAGCAG ----- AGA GATTTAAG T TCA----- AA CA
TTCTGAGAACATGTGAAACT
ATGTTA
GAM1167 GGATTACTGAAAATGTGCTG 1140 TGTGCAAAGT 2816 AAAA GC AAG- C TCTC G
TAGAAAGGCCACTCTCCTGT CTGCAAAACG GGATTACTG TGT TGTAGA GC AC CT T
ACAGTTGTGCAAAGTCTGCA ATAG ||||||||| ||| |||||| || || ||
AAACGATAGTGATTC CTTAGTGAT GCA ACGTCT CG TG GA A
A--- AA GAAA - TT-- C

GAM1168 AGGTACAGAGAGCTGTGTGC 1141 TCGCCTGGAC 2817 A GAGC - G T T AACA- A C
ATGCTGAGCAACACCACAGC CACAAGTTTG AGGT CAGA TGTG T CA GC GAGC CC CAGC
A

CATTGCTGAGGCCTGGGCTC ACCT |||| |||| |||| | || || |||| || ||||
GCCTGGACCACAAGTTTGAC TCCA GTTT ACAC A GT CG CTCG GG GTCG T
CT - GA-- C G C - GGTCC A T

GAM1169 AGAGTTCCTTTCAGTCTTTA 1142 CTTTCAGTCT 2818 T TTT A AA ACCA TATAT --- TT C CAC
TTTGCAGCAAACTACCACTT TTATTTGCAG GTCT TA GC GCA CT CTT GGC AGG TGTGTGT TGTA G
TATATGGCAGGTTTGTGTGT CAAA |||| || || ||| || ||| ||| ||| ||||||| |||| CTGTACACGCACATACACAC CAGA AT CG CGT GA GAG TCG TCC ATACACA ACAT C
ACATATCCTTAAGCTCGAGA C TT- G GG CA-- C---- AAT T- C ACA
CAGGGTGCGGCTTTACAGAC
CAAAAAGTAT
GAM1170 GTGGCACAATTTGAATTCAG 1143 TGGCACAATT 2819 A AT TTCA--- AAC- GACT ATT-- G G
TAAAACAGGGGAGACTGGAG TGAATTCAGT GGC CA TTGAA GTAA AGGGGA GGAGGG GGGA TTT G
GGATTGGGAGTTTGGAGAGG AAAA ||| || ||||| |||| |||||| |||||| |||| ||| TCCCTTTCACCCTCCTCCTT CCG GT AACTT CATT TTTCCT CCTCCC CCCT GAG /
TAAAATTACAGTAACTTTCA - C- TCAATGA AAAA ---- ACTTT G A
ACTGGCCAT

GAM1171 GTGGCACAATTTGAATTCAG 1144 TGGCACAATT 2820 A AT ATTCA--- AAC- GACT ATT-- G G
TAAAACAGGGGAGACTGGAG TGAATTCAGT GGC CA TTGA GTAA AGGGGA GGAGGG GGGA TTT G
GGATTGGGAGTTTGGAGAGG AAAA ||| || |||| |||| |||||| |||||| |||| ||| TCCCTTTCACCCTCCTCCTT CCG GT AACT CATT TTTCCT CCTCCC CCCT GAG /
TAAAATTACAGTAACTCTCA - C- CTCAATGA AAAA ---- ACTTT G A
ACTGGCCAT

GAM1172 TGAGGTTTTGCAATTTTGAA 1145 GTGCATTCTA 2821 TTTTGCAAT A ATAC - AA ATAT
GAGAATACCACAGAAAATGC GTGTGTCATT TGAGG TTTGAAG GA CAC AGA ATGCATC C
ATCATATCAAGAGGTGCATT TCAA ||||| ||||||| || ||| ||| ||||||| CTAGTGTGTCATTTCAAGTT ATTCC GAACTTT CT GTG TCT TACGTGG /
CCTTA TT------- A GT-- A -- AGAA

GAM1173 GTCGGTACCGTGATGGAACT 1146 GAGGTAGTAG 2822 T C GAT TC G - T C
CACTAGCTCCAGTCTGTGCG GTTTTCTGAT GTCGG AC GT GGAAC ACTA CTCC AG CTGTG G
GGTGCAGCTAGGAGGTAGTA TGTT ||||| || || ||||| |||| |||| || ||||| GGTTTTCTGATTGTTCTGAC CAGTC TG TA TTTTG TGAT GAGG TC GACGT G
T T GTC GA G A - G

GAM1174 TCCTTTTGACAAGAAATGTG 1147 TGACAAGAAA 2823 T - AAATGT C AA-- CTGTT T
GTCGTGAAAATTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA TTGGA GC
T
GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||
ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T
GA C G GTT--- - GGTA ----- T

GAM1175 CTCTTGAGCATGCTGACCAG 1148 GACCAGTGCT 2824 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM1176 GGCTAGTGTGCAGGTAGTTG 1149 TGCAGGTAGT 2825 A TG GTAGTT - AG G CA
CTTGCTGCTTAGTCTGGAGT TGCTTGCTGC GGCT GTG CAG GCTTGC TGCTT TCTGGA TG
T
GCATCTCAGTTCAGAGAGCA TTAG |||| ||| ||| |||||| ||||| |||||| ||
GGCAAGTCAGACTGTGTATG CTGG TAT GTC TGAACG ACGAG AGACTT AC /
GGTC G GT AGAC-- G -- G TC

GAM1177 GCTCCAAAGAACCAAGAGTG 1150 CATTTCACTT 2826 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1178 GTTCCTCTCACGCCCTCACC 1151 AAGCTGCCAG 2827 C A--- T-- T CC - A T
CCTG
TGGCTGAGCCGCAGTAGTTC TTGAAGAACT CCTC CC GGC GAG GCAGTAGTTCTTCAG
TGGCA GCTTTA GT A
TTCAGTGGCAAGCTTTATGT GTTG |||| || ||| ||| |||||||||||||| ||||| |||||| ||
CCTGACCCAGCTAAAGCTGC GGAG GG CCG CTC CGTTGTCAAGAAGTT ACCGT
CGAAAT CG /
CAGTTGAAGAACTGTTGCCC - CTTC TCC T C- G - - ACCC
TCTGCCCCTGGCTTCGAGGA
GGAGGAGGAGC
GAM1179 CCCCCAGGCGATTGCGGTCA 1152 TATCTTACAG 2828 GCG GGAGC A T G - ---
AG A
GGAGCACTTTATCTTACAGA ACTGAATGTT ATT GTCA ACTTT TCT ACA AC TGAATGTT
GGTTTT GATGAG G
CTGAATGTTGGTTTTAGGAT GGTT ||| |||| ||||| ||| ||| || |||||||| |||||| ||||||

GAGAGGGCTTATCAGAAGCT TGG CGGT TGAAG AGG TGT TG ATTTGTAA TCGAAG CTATTC G
CGGAATGTTTATGTGTGTGG GA- ATT-- - - G T GGC A- G
AGAAGTTTATGGCAGGGTTG
GAAGGAGGG
GAM1180 AACTGTTTGCAGATTTCTTT 1153 TCACTAGAGA 2829 T TATACA A T TCA AATA AC A TAAAGCA
TATACAGATATACATGGGTT ACTTTGCAGC GA TTCTTT GAT TACA GGGT TG TTAC GTC CTTC A
CATGAATATTACACGTCACT TCAG || |||||| ||| |||| |||| || |||| ||| ||||
TCTAAAGCAACCAGAATGAG TT AAGAGA TTA ATGT CCTA AC AATG CAG GGAG /
GGACACGTAAAGCAATCCTG C TCAC-- C - --- GA-- CA - TAAGACC
TACATTCACTAGAGAACTTT
GCAGCTCAGTT
GAM1181 GGTAGCGTCCAAGATTTACC 1154 TACCACCACA 2830 A AAG TT ACCA TTA TG ACC- T
ACCACATCATGATTACAGAT TCATGATTAC GGT GCGTCC AT ACC CATCATGA CAGA GTC AAC T
GGTCACCAACTTATGTTTTA AGAT ||| |||||| || ||| |||||||| |||| ||| |||
GGATTTTTTGACTTTATGAT CCG CGTAGG TA TGG GTAGTATT GTTT TAG TTG A
GGGTTTATAGGGATGCAGCC A GA- TT ---- TCA TT GATT T

GAM1182 ACCGGTTATGGTGCTGCTGT 1155 TGGAGCCTGG 2831 GG T - AC GTTGGAGC G TT T T
GAACACTGCCAAGTTGGAGC CTCTGTTTGT CGGTTAT TGC GCT GTGA ACTGCCAA CTGGCTCT T G GCCG C
CTGGCTCTGTTTGTGCCGTC GCCG ||||||| ||| ||| |||| |||||||| |||||||| | | ||||
TTTGGTCTGGGAGGAGTCGG GTCGGTG ATG CGG TACT TGACGGTT GGCTGAGG G T TGGT T
ATTGGCAGTTATCATGGGCT AA T G AT A------- A GG C T
GTAAAGTGGCTGGT

GAM1183 TTCAGAGCTGCTGGCATGCT 1156 TCGAAAGTTG 2832 AG - ATGC- GGTAC GACG A A GG ACA
AGCTTGGTACAGGACGTCGT AAAAAGCTAG TTC AGCTG CTGGC TAGCTT AG TCGTTAT CA CA TG A
TATACAACAGGTGACAATTC ACAG ||| ||||| ||||| |||||| || ||||||| || || ||
CAGATGATGATAATGAAAGA GAG TCGAC GATCG GTTGAA TC AGTAATA GT GT AC /
CTCTCGAAAGTTGAAAAAGC AA A AAAAA AGCTC AGAA - A AG CTT
TAGACAGCTAAGAG

GAM1184 GGCTGTACAAGTCTCAGTAC 1157 TCCCAAATGA 2833 TA T GTA CAA- CC CTAGC AC
TCAATGCCCTTATCTAGCTT AGTAACAAAG GGCTG CAAG CTCA CT TGC TTAT TTGGGAG A
GGGAGACAGCACTCCCAAAT AAAT ||||| |||| |||| || ||| |||| |||||||
GAAGTAACAAAGAAATGAGC CTGAC GTTC GAGT GA ATG AGTA AACCCTC G

TTGCAGTC -- - AAA AACA A- ----- AC

GAM1185 TGGGGACAAGAGGTGTGGGT 1158 AGAGGTGTGG 2834 TG TT - TG TTCTTTA GC
GTAAGA CAC
TACATGAGTAGGTTCTTTAG GTTACATGAG GAGG TGGG AC A AGTAGG GTG TATTG
TTTGGGTG C
TGGCTATTGGTAAGATTTGG TAGG |||| |||| || | |||||| ||| ||||| ||||||||
GTGCACCCATCACCCAAGCA CTCC ATTT TG T TCATCC CAC ATGAC
GAACCCAC /
GTATACACGGCATCCTACTT CT TC A GT TACGG-- AT ------ TAC
GTAGTCTTTTATCCCTCACT
CCCTCCCCA
GAM1186 CGTGCTGGAGAAGCAGTGGA 1159 TGGAGAAGCA 2835 GC A C AC CT TGAAG C
TC
CGTCCTTCCTGAAGGCGCGG GTGGACGTCC CGT TGGAG AG AGTGG GTC TCC GCG
GGC A
CTCAACTGCTCTGTACCCGG TTCC ||| ||||| || ||||| ||| ||| ||| |||
AGACTCCCATTTCTACTTCA GCA ACTTC TC TTACC CAG AGG TGT TCG A
ACG -- A T CT -- CCCA- C TC

GAM1187 TTTGAACCTGGGAGGTAGAG 1160 GAGGTAGAGG 2836 AA- TG AGGTA GT A - A
GTTGCAGTGAGTTGAGATCA TTGCAGTGAG TTTG CC GG GAG TGCAGTG GT TG G
TGCCACTGCACTCCAGCCTG TTG |||| || || ||| ||||||| || ||
GGCAACAGA AGAC GG CC CTC ACGTCAC CG AC A
AAC GT GAC-- -- - T T

GAM1188 CTGTTTACAGTTGCACTTGT 1161 AAGGAGTCAC 2837 TTA-- T ACT C CAC TG
GGCCCCTCACTGTGGGGATT AGTTATTGGA CTGT CAGT GC TGTGGC CCT TGTGGGGAT
A
GATCATTCTCATGAAGGAGT ATTG |||| |||| || |||||| ||| |||||||||
CACAGTTATTGGAATTGCAG GACG GTTA TG ACACTG GGA GTACTCTTA /
TTAAG T --- A A-- CT

GAM1189 TACTCAAATTCTCTACTGTA 1162 TCAGTGCCAA 2838 T A ACT - A TT
TGAATTATGCTTTAAGTAGA GGAGAACTTG TAC CAA TTCTCT GTA TGAATT TGC T
ATTCAGTGCCAAGGAGAACT GTG ||| ||| |||||| ||| |||||| |||
TGGTG GTG GTT AAGAGG CGT ACTTAA ATG /
- C AAC G G AA

GAM1190 GACTGTTCCCCACTTGCTGG 1163 CTGGTGGAGT 2839 ---- - A GTCA C T CAA AA--
ACGCT
CTGGCACCGTCAACCCCACC GGCGCCAGCG CTTGCT G GCTGGC CC AC CCACCG GTT
GAGG TGTC G
GTGTTCAAGAGGAATGTCAC CAAA |||||| | |||||| || || |||||| ||| |||| ||||
GCTGCCCATCGACAACGGCC GGACGA C CGACCG GG TG GGTGGT CAA CTCC
ACAG C

TCAACCTGGTGGAGTGGCGC GAAA G C ---- A C --- GGCA CTACC
CAGCGCAAAGAGCAGGCTCG
GGGCCAGGTC
GAM1191 TCCCACTGTGGTGCCTGGTG 1164 TCGCCTGGAC 2840 CC - G T G A - AA CAGAGA
- CA T
GAGACCTGGCCAAGGTACAG CACAAGTTTG ACT GTGGT CC GGTG AG CCT GGCC GGTA
GCTGTG TG TGC G
AGAGCTGTGTGCATGCTGAG A ||| ||||| || |||| || ||| |||| |||| |||||| || |||
CAACACCACAGCCATTGCTG TGA CACCA GG CCGC TC GGG CCGG TCGT
CGACAC AC ACG /
AGGCCTGGGCTCGCCTGGAC TT A - T - - T AG TAC--- C A- A
CACAAGTTTGA

GAM1192 CTGGAGTGCAGTGGTGCGAT 1165 TACAGTAGCT 2841 -------- TG C C C C -- CCC--
ATT
CTTGGCTCACTGCAACCTCC GGGATTACAG TGC GATCT GCT ACTG AA CTC GC CT
GGTTGAGGCA C
GCCTCCCGGTTGAGGCAATT ACAT ||| ||||| ||| |||| || ||| || || ||||||||||
CTCCTGCCTCAGCCTCCCAA GCG TTAGG CGA TGAC TT GAG CG GA
CCGACTCCGT /
GTAGCTGAGATTACAGTAGC TACAGACA GT - A A T AT ACCCT CCT
TGGGATTACAGACATGCGCC
ACCATGTCCAG
GAM1193 GTTACTTGACCTTTCTGTGC 1166 TACCTCGTAA 2842 TTGAC- CT G --- TTTT ACC
TTAA GG GAT
CTCAGTTTTCTTACCCGTTA AGTTTCTGTG GTTAC CTTT GT CCT CAG CTT CG GTAG
AT A
AGTAGGGATGATATTAATAA AAGG ||||| |||| || ||| ||| ||| || |||| ||
CTACCTCGTAAAGTTTCTGT CAATG GAAA CA GGA GTC GAA GC CATC TA /
GAAGGACTAAAAGAGATATG TATAGA AT - AGT TTT- AT- TC-- AA ATT
TAAC

GAM1194 GCCTGCCTGAACCCTGGGTC 1167 CATGACGGCT 2843 A GG--- - A -- G AA- A- G
C
AGGAGAGAAACACTTGGGGA CTGAGTTCTT CCCT GTCA GGAGAGA ACA CTT GGGAGGGG
AGG CG CGTGGG T
GGGGAAAGGACGGCGTGGGC CCTG |||| |||| ||||||| ||| ||| |||||||| ||| || ||||||
TACCCATGACGGCTCTGAGT GGGA CGGT CCTTTCT TGT GGG TCCTTCTT TCT GC
GTACCC /
TCTTCCTGGGGCTTGTGTCT C GAAGA T G TC G GAG CG A A
TTCCTTGGCAGAAGAGGGCA
CAGCCAAGGC
GAM1195 GCCATCCTAATAGGTATGAG 1168 TAGGTATGAG 2844 AA G A TTATATT TTTTC - G-
GATAA ATA A
GTTATATTAGTCCGTTTTCA GTTATATTAG TAG TATG GG AGTCCG ATG CT CT AGAT
CCCA G
TGCTGCTGATAAAGATATAC TCCG ||| |||| || |||||| ||| || || |||| ||||
CCAAGACTGGGCAATTTACA GTC GTAC CC TCAGGT TGC GA GA TTTA
GGGT A
AAAGAAAGACGTTTATTGGA -- G A TTGACAC TATT- A AA AAACA AC- C

CTCACAGTTCCACATGGCTG
GGGAGGT
GAM1196 GCTTCGTATTTATAGACTGC 1169 TCTCAGAGTG 2845 GTATT A TG - T--- CC
CTTTCCCCTGAGGATCTCAG GTTAATGTTC GCTTC TAT GAC C CT TCC T
AGTGGTTAATGTTCCAGGAG CAGG ||||| ||| ||| | || |||
C CGAGG GTA TTG G GA AGG /
ACCTT A GT A CTCT AG

GAM1197 TGGTAGTGGTTTGAGGAATG 1170 TGGAAGGTAA 2846 AGTGG TG AA AG GGTAA AA GAG G
AGTGGAAGGTAAAGAAGTGG AGAAGTGGGA TGGT TT AGG TG TGGAA AG GTGGGAG GCTG G
GAGGAGGCTGGGCACGGTGG GGAG |||| || ||| || ||||| || ||||||| ||||
CTCCCGCCTGTAATTCCAGC ACCG GG TTC AC ACCTT TC CGCCCTC TGGC C
ACTTTGGGAGGCCA GA--- GT -- G- AATG- -- GG- A

GAM1198 ATGGATCCCAAATATTTACA 1171 TCCCAAATAT 2847 - - - ACAAA T AA
AAGCCATCAGAACCACCTGT TTACAAAGCC ATGG ATCC CAA ATATTT GCCA CAG C
GGCAAATGTATTGTGGATAT ATCA |||| |||| ||| |||||| |||| |||
CGT TGCT TAGG GTT TGTAAA CGGT GTC C
A T A ----- - CA

GAM1199 GCTCCAAAGAACCAAGAGTG 1172 CATTTCACTT 2848 A AA T - TTC--- - GT GAG AG- TC
CAAATCAGTCCATTTCACTT TCACTGTCTG CC GAG GCAAATC AGTCCAT AC TTTCACT CT AT GGTC T
TCACTGTCTGAGATAGGGTC AGAT || ||| ||||||| ||||||| || ||||||| || || ||||
TCTAAGACCAGGATACAAGG GG CTT CGTTTAG TCAGGTA TG AAGGTGG GA TA CCAG /
GTGGAATGTAGCTATATGGA A C- - C TATCGA T -- ACA GGA AA
CTCGATTTGCTTCCGGACCT
TTTCCAGAGC
GAM1200 CCAACAAGCTTTACATGCTC 1173 TTCACCAGGG 2849 CA- CAT AA- --- TT C
AATGAATTTTCTGCTGCAGG CTAAAGTTCA CCAA AGCTTTA GCTC TGAA TT CTG T
GAACCTTTCACCAGGGCTAA CTTG |||| ||||||| |||| |||| || |||
AGTTCACTTGG GGTT TTGAAAT CGGG ACTT AA GAC /
CAC --- ACC TCC GG G

GAM1201 TGTTTGGGATCTGGTCTGAG 1174 GGAAGTTGCT 2850 TC T G C GGCA TG TA A - T C ---- AT
GGGGCGGACGGCACTGATAT GGCTTCAGCT TGG CTGAG GGG GGAC C A TCA C GCTG GGCC GC TCTC G
CAACGCTGTGGCCCGCTCTC GATG ||| ||||| ||| |||| | | ||| | |||| |||| || ||||
ATGATGGGAAGTTGCTGGCT ATC GATTT TCC CTTG G T AGT G CGAC TCGG CG AGGG /
TCAGCTGATGACTTTGGCAA -- - G A AAAC GT TC A T T T TTGA TA

AGTTCACCTGTTTAGCTACC
CCTGCTGTCAG
GAM1202 TGCTTCTTTGCAAGGTATTA 1175 AAGGTATTAG 2851 T A ---- T GTATG T
GGTTGTCATTGTATGGATTA GTTGTCATTG TGCTTCTT GCA GGTATT AGGT GTCATT GAT
A
TAATCAAAATGACACTTCAC TATG |||||||| ||| |||||| |||| |||||| |||
AAATACCTGTTGAGGAGTA ATGAGGAG TGT CCATAA TTCA CAGTAA CTA T
T - ACAC - AA--- A

GAM1203 GCTCCAAAGAACCAAGAGTG 1176 CATTTCACTT 2852 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1204 CTCAGTTGTCTGTGAAATGA 1177 TTCATAGCCA 2853 C AA- TT AATACTA GCAG
ATCTTGAGAATACTACCAGC CAAATAGCTG CTCAGTTGT TGTG ATGAATC GAG CCA T
AGTCAAAATGGAAACCACCT AG |||||||| |||| ||||||| ||| |||
TGGTTCATAGCCACAAATAG GAGTCGATA ACAC TACTTGG TTC GGT C
CTGAG A CGA -- CACCAAA AAAA

GAM1205 GAGTGCAAATCAGTCCATTT 1178 CATTTCACTT 2854 T - ---------- CAC GAGATA
TC
CACTTTCACTGTCTGAGATA TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT
TGTCT GGGTC T
GGGTCTCTAAGACCCAGGAT AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
ACAAGGGTGGAATGTAGCTA CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
TATGGACTCGATTTGCTTC - C TATCGATGTA AC- A----- AA

GAM1206 CCTTCTGGATCCTGGAGAAA 1179 TGGATCCTGG 2855 - G ---- A T
GCCAGTGCTGTTGCACTGGT AGAAAGCCAG CCTT CT GATC CTGGAG AAGCCAGTGC G
TTCCTTCAGCCATGGTTGAG TGC |||| || |||| |||||| ||||||||||
CAAGG GGAA GA TTGG GACTTC TTTGGTCACG T
C G TACC C T

GAM1207 CCTTGCCTGAACCCTTGGGG 1180 CATGACGGCT 2856 A GGG- A- A -- G AA- A
G- C
TCAGAAGAGAAACACTTGGG CTGAGTTCTT CCCTT GTCAG AGAGA ACA CTT GGGAGGGG
AGGG CG GTGGG T
GAGGGGAAAGGGACGGGTGG CCTG ||||| ||||| ||||| ||| ||| |||||||| |||| || |||||
GCTACCCATGACGGCTCTGA GGGAG CGGTT TTTCT TGT GGG TCCTTCTT TCTC
GC TACCC /

GTTCTTCCTGGGGCTTGTGT C AAGA CC G TC G GAG G AG A
CTTTCCTTGGCAGAAGAGGG
CACAGCCAAGG
GAM1208 CAGCACAGCGTGCAAAGTGT 1181 TGACTGAAAG 2857 C C AA-- T - CC- GA-- G-
G
TTGGGCTTCCCTTCGAAGGG GAGAGTGAGC CAG ACAG GTGC AG GTTTGGG CTT CTTC
AG GCT A
CTGAGGAGTGACTGAAAGGA CCCG ||| |||| |||| || ||||||| ||| |||| || |||
GAGTGAGCCCCGGGCTCTGC GTC TGTC CACG TC CGGGCCC GAG GAGG TC
TGA G
TGGCACCTGTCTG - - GTCG T C TGA AAAG AG G

GAM1209 TCTTGATTCACCAGGTCTAA 1182 TCACCAGGTC 2858 - A AGG AA C TC
ACTGCAGTAATCCATTTACT TAAACTGCAG TCTTGAT TC CC TCTA CTG AGTAA C
CAGCTGGAGAGGAGACATCA TAA ||||||| || || |||| ||| |||||
AGA AGAACTA AG GG AGGT GAC TCATT /
C A AG- C- - TA

GAM1210 TGTCAGGTTATCCACCTCGG 1183 TCGAGCACTC 2859 GTTAT C- CA - A- CC G
GCAGCTCGTCAGGCTGCGGC TGAGCTTGGC TGTCAG CCA CTCGGG GCTCG TC
GGCTGCGGCG CT T
GCCCTGTTCAGTCTGTTGCA TGGC |||||| ||| |||||| ||||| || |||||||||| ||
GCTGAGATCGAGCACTCTGA ACGGTC GGT GAGTCT CGAGC AG TCGACGTTGT GA
T
GCTTGGCTGGCA ----- TC CA T AG CT C

GAM1211 GCTCCAAAGAACCAAGAGTG 1184 CATTTCACTT 2860 T - ---------- CAC AGATAG
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT
TGTCTG GGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| |||||| ||||
TCTAAGACCACGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGGC
CCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1212 GTAAACTCCAACCCAGAATG 1185 TTGGAGCAGG 2861 AACCC - - TA AA T CA TCT
AC- CT
GGGAAGAATACTGAATTAGC TTTCATTCTC AGAAT GGGGAA GAA CTG TTAGC GAG CAT
GGAC AATT G
TGAGCACATTCTGGACACAA CAAT ||||| |||||| ||| ||| ||||| ||| ||| |||| ||||
TTCTGACCAATTTCAGTCTC TCTTA CCTCTT CTT GAC GGTTG CTC GTA TCTG
TTAA A
ATGATCTCTGTTGGAGCAGG TTTTC A A TG GA T TA C-- ACT CC
TTTCATTCTCCAATTCTCTT
TTACAGAAC
GAM1213 GATAACATATATAGGATGTC 1186 GTGATCAGAA 2862 T A ------ - G AA- AAT

ATGGGACAAGCAATTACAGT TGTTTCAGTG GA AACATATAT GGA TG TCAT GGAC GC T
GAAGTCCAGTGATCAGAATG TGTG || ||||||||| ||| || |||| |||| ||
TTTCAGTGTGTGTTTC CT TTGTGTGTG CTT AC AGTG CCTG TG /
- A TGTAAG T A AAG ACA

GAM1214 TGTTTGGGATCTGGTCTGAG 1187 GGAAGTTGCT 2863 TC T G C GGCA TG TA A - T
C ---- AT
GGGGCGGACGGCACTGATAT GGCTTCAGCT TGG CTGAG GGG GGAC C A TCA C GCTG
GGCC GC TCTC G
CAACGCTGTGGCCCGCTCTC GATG ||| ||||| ||| |||| | | ||| | |||| |||| || ||||
ATGATGGGAAGTTGCTGGCT ATC GATTT TCC CTTG G T AGT G CGAC TCGG CG
AGGG /
TCAGCTGATGACTTTGGCAA -- - G A AAAC GT TC A T T T TTGA TA
AGTTCACCTGTTTAGCTACC
CCTGCTGTCAG
GAM1215 GTGATGGTCCAACTTTGTGG 1188 GTAAGGATTT 2864 G -- T-- GAATG- AGG AGGG
GG
AATGGTAAGGATTTTTAGGG TTAGGGTTGT GT ATGG TCCAACT TGTG GTA ATTTTT
TTGTTT C
TTGTTTGGCCAGAACAAGAG TT || |||| ||||||| |||| ||| |||||| ||||||
AAATAACTGCAGAAAACACA CG TACC AGGTTGG ACAC CGT TAAAGA AACAAG
/
TATGGTTGGAAACCATGC - AA TAT AAAAGA CAA G--- AC

GAM1216 GGATGCTTTTTCTTTCTCTT 1189 TGAAAGTAGA 2865 TT - C GC C- - TAG
GCTTAACCAGTCTGGCTAGT GAGTGGGCAT GGATGCT TTCTTT CT TT TTAAC AGT CTGGC
T
ACTGCCAGTACTATGTTGAA CC ||||||| |||||| || || ||||| ||| |||||
TGAAAGTAGAGAGTGGGCAT CCTACGG GAGAGA GA AG AGTTG TCA GACCG /
CC GT T A TA TA T TCA

GAM1217 TGCTTGAACATTCCTGCCTC 1190 TTCCTGCCTC 2866 AACA CTCCCTATTT C C--
TGT
CCTATTTGCCAGGCTTTCAT CCTATTTGCC TGCTTG TTCCTGC GC AGGCTTT ATTTC
C
TTCTGTCTGCTGAGATCTCA AGGC |||||| ||||||| || ||||||| |||||
GAGCCTGCCCAACAGCAGGG ACGAAC AGGGACG CG TCCGAGA TAGAG T
AAGCCAAGCA CGA- ACAACC---- - CTC TCG

GAM1218 GAGGCTTGAAGGGAAGAGAA 1191 TGACCGGGTG 2867 GAAGA CT C CT GTGA GG-
ATA ACG
CTTGCAACCACTTCTTGTGA GGAATAGCTG AGG GAA TGCAA CA TCTT CCG TGGGA
GCTGTCTCCA G
CCGGGTGGGAATAGCTGTCT TCTC ||| ||| ||||| || |||| ||| ||||| ||||||||||
CCAACGGGAATGGGGATAGC TCC TTT ATGTT GT AGAG GGT GTCCT
CGATAGGGGT /

AATCCTGATATGGATAGAGA AGGG- -- A T- ATA- ATA AA- AAG
TTGATTGTATTTGGGACCTA
GACAGGTACGC
GAM1219 TCTGGGCCTTGGTTTGGCAG 1192 CAAACCTTTA 2868 TT TG-- AG A- GGA - AA
TTTA-- A G
CCATGGGAACTGCACGTCAA TCAGGATGAT GGGCC GGTT GC CC TG ACTGCA CGTC
GATG TG TTT C
GATGTTTATGATTTGCTAAA GCAG ||||| |||| || || || |||||| |||| |||| || |||
AACAAACCTTTATCAGGATG TCCGG CCGG CG GG AC TGACGT GTAG CTAT AC
AAA T
ATGCAGTAACAGGGGAAGCA T- TCGA AA GG AA- A GA TTCCAA A A
GCTGGCCTGGCCTAGG

GAM1220 GGGTGCACAAGTGATGGTCC 1193 GTAAGGATTT 2869 - -- T-- GAATG- AGG
AGGG GG
AACTTTGTGGAATGGTAAGG TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
ATTTTTAGGGTTGTTTGGCC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
AGAACAAGAGAAATAACTGC TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /
AGAAAACACATATGGTTGGA G AA TAT AAAAGA CAA G--- AC
AACCATGCGCTTGTGACTT

GAM1221 AGTGTGGGCACAGGAATATT 1194 TAACAGAAGA 2870 G GGAATA GTAT A
CTGTGTATACCAATGGGTTT TGTGTGTGCA AGTGTG GCACA TTCTGT ACC A
AACAGAAGATGTGTGTGCAC CT |||||| ||||| |||||| |||
T TCACGT TGTGT AAGACA TGG T
G AG---- ATT- G

GAM1222 CTGACTAGAGGCAGGTTCTG 1195 TGACTAGAGG 2871 CT CA TTC ACGTT CT CT
CTACGTTGGCCAGGCTGTCT CAGGTTCTGC CTGA AGAGG GG TGCT GGCCAGG GT C
CAAACTCCTGGCTTCAAGCA TACG |||| ||||| || |||| ||||||| ||
ATCCACCTCTCTCGG GGCT TCTCC CC ACGA TCGGTCC CA /
C- A- TA- ACT-- T- AA

GAM1223 GCTCCAAAGAACCAAGAGTG 1196 CATTTCACTT 2872 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1224 TAGGAAGAAATGTTGGTATC 1197 TGGCATAGGT 2873 T C TTA A G AGG AAA A---
C-- AG
CTCCATTATAGATGGATGGC CACAAATGGG GGTAT CTCCA TAGATGG TG CAT TCAC
TGGG GA TGGC C

ATAGGTCACAAATGGGAGAC AGAC ||||| ||||| ||||||| || ||| |||| |||| || ||||
TGGCAGCTAAGCCAATATCA TCATA GAGGT ATCTATC AC GTA GGTG ACCC CT ACCG T
AAACCCAGTGGAATGACACT - T --- - A A-- --- AAAA ATA AA
ATCTATGGAGTATACTTATT
CTTCCTG

GAM1225 CACAAGTGATGGTCCAACTT 1198 GTAAGGATTT 2874 - -- T-- GAATG- AGG AGGG GG
TGTGGAATGGTAAGGATTTT TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA ATTTTT TTGTTT C
TAGGGTTGTTTGGCCAGAAC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
AAGAGAAATAACTGCAGAAA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA AACAAG /
ACACATATGGTTGGAAACCA G AA TAT AAAAGA CAA G--- AC
TGCGCTTGTG

GAM1226 CTCTTGAGCATGCTGACCAG 1199 GACCAGTGCT 2875 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM1227 CAAGTGAACATCCGCAACAA 1200 TGTGTGTTGC 2876 AG- ACAT G C - GAAAATT AAT AA
GGAGCAACAGAAAATTTAAA TACTTTATTG CA TGA CC CAA AAGG AGCAACA TA CAGTT T
TCAGTTAATTTGACTGTGTG GGTT || ||| || ||| |||| ||||||| || |||||
TGTTGCTACTTTATTGGGTT GT ACT GG GTT TTTC TCGTTGT GT GTCAG /
ATCAAAGTG GAA ATT- - A A ------- GT- TT

GAM1228 TGGTTTTAGTCCATTGGTAG 1201 AACACCACAG 2877 TT- - ATTG A-- - A G
CATTGTGTGTATGAGGAGAT ACAGCTGCAG TGG TT AGTCC GTAGC TTGTG TGT TGAG A
TCAACACCACAGACAGCTGC GACT ||| || ||||| ||||| ||||| ||| ||||
AGGACTCGATATCCA ACC AG TCAGG CGTCG GACAC ACA ACTT G
TAT C A--- ACA C - A

GAM1229 CTGTAGTGAGACATCACAAC 1202 TGCACAGTGT 2878 A G C A--- AG-- ATATA
AGACAAGGCACAATATAAGA CAGAAGTTCT CTGT GT AGACATCA AAC GACA GCACA A
CTGTGTGCACAGTGTCAGAA GATG |||| || |||||||| ||| |||| |||||
GTTCTGATGTTTGATAGCAG GACG TA TTTGTAGT TTG CTGT CGTGT /
A G C AAGA GACA GTCAG

GAM1230 TAAAAGGATGTCACTCGTTC 1203 TCACTCGTTC 2879 ACTCGT ACG- G TTATGA ATCGG TC
AGTACGCCAATGTTCGTTAT AGTACGCCAA AGGATGTC TCAGT CCAAT TTCG TCCTTG CACGCT T

GATCCTTGATCGGCACGCTT TGTT |||||||| ||||| ||||| |||| |||||| ||||||
CTCAGGGCGTGATACAAGGG TTCTACGG AGTCG GGTTA AGGC GGGAAC
GTGCGG C
CTCGGAGATTGGATCCGCTG ------ CCTA G TC---- ATA-- GA
AGGCATCTTTTTA

GAM1231 AACCATCTGCCTGTCCCGGC 1204 CATCTGCCTG 2880 ATCT G C--- C C-- CC C -
T-- CTA
CTGTGCGACCTTGCGAGGCT TCCCGGCCTG AACC GCCT TC CGGC TGTG GA TTG
GAGG CTGC TTC C
GCTTTCCTACTCTGAACCCG TGCG |||| |||| || |||| |||| || ||| |||| |||| |||
CAGCCCTCCCAAATCTACCA TTGG CGGA AG GCTG ACAC CT AAC CTCC GACG
AAG /
CAGTCGTTAAGAAAGGCTTT GTTT A AATT - CAT A- C C CCC TCT
GGGTT

GAM1232 TGCAGCCTCCTGGGATCAAG 1205 TTGCTTGAGT 2881 ----- GA TG CCCA CTCG
TGATCCTCCCATCTCAGCCT CCAGAAAGTG TGCAGCCTC CTGG TCAAG ATCCT
TCTCAGC T
CGTAAGTAGCTGAGGCAGGA AGGC ||||||||| |||| ||||| ||||| |||||||
TTGCTTGAGTCCAGAAAGTG ACGTCGGAG GACC AGTTC TAGGA GGAGTCG A
AGGCTGCA TGAAA TG GT C--- ATGA

GAM1233 CTTGCTCACCCTCGAATCCA 1206 CAATGCAATG 2882 T CCTCGAATCCA- T C AGTGG
TG AT
GTTTCCAGCTTTAAGAGTGG TAAAAAGTGG CTTGC CAC GTT CCAG TTTAAG AACAT
CTGAC T
AACATTGCTGACATTAGGTC CAGG ||||| ||| ||| |||| |||||| ||||| |||||
GGTGATGTTAACTTAAATTG GGACG GTG TAA GGTT AAATTC TTGTA GGCTG /
GCAATGCAATGTAAAAAGTG - AAAAATGTAACG C - AA--- GT GA
GCAGG

GAM1234 GAAGACTTCCTAAATTTGCA 1207 TTTGCACATT 2883 AC A TTGCA TTGCC
ACCAT
CATTAGCTAGATTGCCATTA AGCTAGATTG GAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
GCACCATTAGAGAGTTGATC CCAT |||| ||||| ||| |||||||||| ||||||
TTTGGCTAATGATTATTCAG CTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GAAAATTTC AA C TTA-- C---- AGAGA

GAM1235 GGATTTCCTAAAGGTGCTCA 1208 TCAGGAGGAT 2884 T-- TAAAGGT C A TGTGTAG
T AG
GGAGGATGGTTGTGTAGTCA GGTTGTGTAG GGA TTCC GCT AGG GGATGGT TCA GG
G
TGGAGGACCCCTGGATCCTT TCAT ||| |||| ||| ||| ||||||| ||| ||
GCCATTCCCCTCAGCTAATG CCT GAGG CGA TCC CTTACCG GGT CC /
ACGGAGTGCTCC CGT CAGTAAT C C TTCCTA- C CA

GAM1236 GCATGGACTAGGACCCTGGA 1209 TTGGTTGCTG 2885 CA A AC G AGAAA T --
AG GGC
GGCAGAAATAGTTACCGAGG ATGAGCTTTG G TGG CTAGG CCT GAGGC TAGT ACCGA
GGGGA TTACA C
GGAAGTTACAGGCCTGAGTG AGGT | ||| ||||| ||| ||||| |||| ||||| ||||| |||||
TGAGTCCCTGTTTGGTTGCT C ACC GGTTC GGA TTTCG GTCG TGGTT TCCCT
AGTGT T
GATGAGCTTTGAGGTCCTTG AG - CT G AGTA- T TG G- GAG
GCCAGAC

GAM1237 CAGTGCAGGTGTTAAGAAGG 1210 CAGTGCAGGT 2886 -- GTTAAGA GG T--- C
GGCTGTTTGTTAGGACAAGT GTTAAGAAGG CAGT GCAGGT AGG CTGTTTGT AGGA A
CTTCAGCACAAACGGATCCT GGCT |||| |||||| ||| |||||||| ||||
GCTTGCTTACTG GTCA CGTTCG TCC GGCAAACA TTCT A
TT ------- TA CGAC G

GAM1238 GCTATGTGACTCGGATGGTC 1211 TGAGATGGTT 2887 T TGA- GA T T A C CACA C
TTTCACACGGCACATTTGGA TAGACGGGAA GC ATG CTCG TGG CT TC CA GG TTTGGA A
CATTTCCAGAACTACCATGA TTCA || ||| |||| ||| || || || || ||||||
GATGGTTTAGACGGGAATTC CG TAC GGGC ATT GG AG GT CC AGACCT T
ATGC - TTAA AG T T A A ATCA T

GAM1239 GCTGTGCCTTAGTTCTCCCA 1212 TGATAGTAAT 2888 CC TT-- CC GCAAA
TCGGCAAAAGCATCACGATG CTAGCTCACA GCTGTG TTAG CT CATCG A
ATAGTAATCTAGCTCACAGT GT |||||| |||| || |||||
TGACAC GATC GA GTAGC G
TC TAAT TA ACTAC

GAM1240 GATTTGTGAACATTCTGCAC 1213 TGTGAACATT 2889 TT A T C AGCTA AAA T
ACAGCTACGTAAAGATATTT CTGCACACAG GA TGTGA CA TCTGCA AC CGT GA A
CAGCGATGAAGTCTGCAGAC CTAC || ||||| || |||||| || ||| ||
TGCTCATGTTC CT GTACT GT AGACGT TG GCG CT T
T- C C C AAGTA A-- T

GAM1241 CCCTGACCAGTCTGGGTTCT 1214 CTGACCAGTC 2890 GC TGCC AA- CTTTGACCAT
- CT- TTCC
TGCCACTGCCAGGAAAGTTG TGGGTTCTTG GTTCTT CAC AGGA GTTGGT TTTCAAA
CTG GC T
GTCTTTGACCATTTTCAAAC CCAC |||||| ||| |||| |||||| ||||||| ||| ||
TGCTGCTTCCTCTCTGCTTC CAGGGG GTG TCCT CAACCG AAAGTTT GAC CG
/
CAGCTTTGAAAGCCAACACA A- TCC- ACA ---------- C CTT TCTC
TCCTCCTGTGAGGGGACAAG
ACAAGCAGGG
GAM1242 GGTGCACAAGTGATGGTCCA 1215 GTAAGGATTT 2891 - -- T-- GAATG- AGG
AGGG GG

ACTTTGTGGAATGGTAAGGA TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA ATTTTT TTGTTT C

TTTTTAGGGTTGTTTGGCCA TT ||||||| |||| ||||||| |||| ||| |||||| ||||||

GAACAAGAGAAATAACTGCA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA AACAAG /

GAAAACACATATGGTTGGAA G AA TAT AAAAGA CAA G--- AC

ACCATGCGCTTGTGACT

GAM1243 GAGAACTCAGGTAAATGCTG 1216 AAGCAGCCAT 2892 AC--- TAAA- - AC ATAGG CCA

GTGTACACATAGGGTCCCAA CTTGAAACAG GAGA TCAGG TGCT GGTGT AC GTC A

GTTGACGAGTAGCACCAAGC TCTC |||| ||||| |||| ||||| || |||

AGCCATCTTGAAACAGTCTC CTCT AGTTC ACGA CCACG TG CAG /

GACAA TACCG A A- AG--- TTG

GAM1244 GCTCGCCTGGACCACAAGTT 1217 TCGCCTGGAC 2893 GGA- CAAG G G AT A C CT

TGACCTGATGTATGCCAAGC CACAAGTTTG GCTCGCCT CCA TTT ACCT ATGT GCCA G GTGC A

GTGCCTATTGTACACTGGTA ACCT |||||||| ||| ||| |||| |||| |||| | ||||

CGTAGGGTGAGGGGATGGAG TGAGCGGA GGT GGA TGGG TGCA TGGT C CATG /

GAAGGCGAGT AGGA AGG- G A -- - A TT

GAM1245 GAGGAATGAGTGGAAGGTAA 1218 TGGAAGGTAA 2894 AA AG GG AAAAA GAG G

AAAAGTGGGAGGAGGCTGGG AAAAGTGGGA GAGG TG TGGAA TA GTGGGAG GCTG G

CACGGTGGCTCCCGCCTGTA GGAG |||| || ||||| || ||||||| ||||

ATTCCAGCACTTT TTTC AC ACCTT AT CGCCCTC TGGC C

-- G- A- GTC-- GG- A

GAM1246 ATCAGATACGGAAGACTCTT 1219 TGAAAGACAG 2895 G A- -- ATGC CA ACAG C AA - AAGAAG G

ATGCTCAGCACAACAGGTCC TCGGTCAGTA C GA GAC TCTT TCAG CA GTC GCA TC CGG ATGAT G

GCAAATCCGGAAGAAGATGA ACAT | || ||| |||| |||| || ||| ||| || ||| |||||

TGGAAATCATGACCCGAGAG G CT CTG AGAA AGTT GT CAG CGT AG GCC TACTA A

GTGCAGACAAATGACTTGAA A GG AC ---- CA AAA- A GG A CAG--- A

AGACAGTCGGTCAGTAACAT

TGAT

GAM1247 GGATTGACGTGCATGTACCC 1220 AAGCAAGATG 2896 G--- ATG C A-- ------ G GG

ACAATGTTTTGAAAGAGGGA TTGGTGAGAG GGATT ACGTGC TACC ACA TGTTT TGAAA AG A

TGCTGTTTCAGGAAAAAAGC CACG ||||| |||||| |||| ||| ||||| ||||| ||

AAGATGTTGGTGAGAGCACG CCTAG TGCACG GTGG TGT ACGAA ACTTT TC /

TGGTGGATCC GTGG AGA T AGA AAAAGG G GT

GAM1248 GGGACGGCTTTGACCTGGGC 1221 CTGGGCTGAG 2897 C AC - ---- - - GT-- C- T G T GCC

TGAGTCTGCCTGTGCCGAGT TCTGCCTGTG A GGCTTTG CT GGGCT GA GT CTGCCT GC GAG CT CC GT A

CTGCCTGTGCCATCCAACTG CCGA | ||||||| || ||||| || || |||||| || ||| || || ||

GAGTCTCAAGTCCTGAGGCA T CTGGGAC GA CCCGA CT CA GACGGA TG CTC GA GG CA T

GTACGTCCAGAAGCCCCAGT C GT C AGAC G T GTCC AA T - T ACC

GCAGGGTCCTCCT

GAM1249 TACGTAAGTTGCATTGGTGG 1222 TAAGTTGCAT 2898 T AGATA A -------- T- - T AAACCC GC

AGATAGGCCCCAGGGTGTGG TGGTGGAGAT TGGTGG GGCCCC GGGTGT GGCC CC CC TTT AG T

CCTCCCCTTTTAAACCCAGG AGGC |||||| |||||| |||||| |||| || || ||| ||

CTCACTATCAAGACGGCGGT ACTACC CCGGGG CTCACA TCGG GG GG AGA TC /

TGGCTTTTTATGGACACTCG - AAC-- - GGTATTTT TT C C ACTA-- AC

GGGCCCAACCATCACATTAT

GCGTA

GAM1250 CTCCAAGTTTCTGGATGCCA 1223 CCTGCAGCAG 2899 TC --- GA --- - TTCC TG

CCACATTCCCCTTGTCTAGG AAGCCACTTG C CAAGT TTCTG TGC CACCA CA CCT T

TGCTGGTGCCTGCAGCAGAA TGG | ||||| ||||| ||| ||||| || |||

GCCACTTGTGG G GTTCA AAGAC ACG GTGGT GT GGA /

GT CCG G- TCC C ---- TC

GAM1251 GAAAGTTGGAAGGGTTGAGG 1224 TGAGGGGTGA 2900 - GGAA GAGG AAAAA C TG T G

GGTGAAAAATCACTTATTTG AAAATCACTT G AAAGTT GGGTT GGTG TCA TTATT G ACAGT T

GTACAGTGTGTACTGTTTGG ATTT | |||||| ||||| |||| ||| ||||| | |||||

ATGATGAGTACACTAAAAGC C TTTCAG CCCGA TCAC AGT AGTAG T TGTCA G

CCAGACTTTAC A A--- AAA- ATG-- - GT - T

GAM1252 AACACGCCCGCTGTCAGGGA 1225 TGTCAGGGAG 2901 - CG G - AGTTT ATG

GTAGTTTGTGCCATGAAGGA TAGTTTGTGC AACA CGCC CT TCAG GGAGT GTGCC A

GGCATTTGGCTTTATTGAAA C |||| |||| || |||| ||||| |||||

GAGGTGATGTT TTGT GTGG GA AGTT TTTCG TACGG A

A A- A A GTT-- AGG

GAM1253 GGCTGAGCGCAGTAGTTCTT 1226 AAGCTGCCAG 2902 T C - A T CCTG

CAGTGGCAAGCTTTATGTCC TTGAAGAACT GGC GAG GCAGTAGTTCTTCAG TGGCA GCTTTA GT A

TGACCCAGCTAAAGCTGCCA GTTG ||| ||| |||||||||||||| ||||| |||||| ||

GTTGAAGAACTGTTGCCCTC CCG CTC CGTTGTCAAGAAGTT ACCGT CGAAAT CG /

TGCC T C G - - ACCC

GAM1254 TCACGTACTATAGGTGAACT 1227 TGACAAGAAA 2903 T GG--- AACTTTT- CC

TTTAGCTCCTGCAGCTCCTT TGTGGTCGTG TCACG ACTATA TG AGCT T
TTGACAAGAAATGTGGTCGT A ||||| |||||| || ||||
GA AGTGC TGGTGT AC TCGA /
- AAAGA AGTTTTCC CG

GAM1255 TGTAGCTGATCCTATTCAGC 1228 TATTCAGCCA 2904 C C GC- - AC - ATTTT
CAG
CATCTTTGACAGTGTGTTAT TCTTTGACAG TGTAG TGATC TATTCA CAT CTTTG AGT GTGTT
ATAAT A
TTTATAATCAGAAACAATTA TGTG ||||| ||||| |||||| ||| ||||| ||| ||||| |||||
TCAATACTATTCATAAAGAA ACGTT ACTAG GTAGGT GTA GAAAT TTA CATAA
TATTA A
TGTCATGGATGAGATCATTT T A ACT A AC T C---- ACA
GCA

GAM1256 TGGTTTTAGTCCATTGGTAG 1229 AACACCACAG 2905 TT- - ATTG A-- - A G
CATTGTGTGTATGAGGAGAT ACAGCTGCAG TGG TT AGTCC GTAGC TTGTG TGT TGAG A
TCAACACCACAGACAGCTGC GACT ||| || ||||| ||||| ||||| ||| ||||
AGGACTCGATATCCA ACC AG TCAGG CGTCG GACAC ACA ACTT G
TAT C A--- ACA C - A

GAM1257 GTCTAATGATCTCTATGCAG 1230 ATTCATTGCC 2906 AC---- T GG CCT TTG
CATT CC
ACAGTTCTTGGACCCCTGAA AGGCATTGCC TCTCTATGCAG AG TCTT ACC GAATTCA
CCAGG GCCAA C
TTCATTGCCAGGCATTGCCA AA |||||||||| || |||| ||| ||||||| ||||| |||||
ACCCTACTTGGTTCTTGGAC AGGGGTGCGTC TC AGAG TGG CTTGGGT GGTTC
TGGTT T
CTGGGTTCTGGTAGAGACCT GGCCTC C A- T-- CCA T--- CA
CTCCGGCTGCGTGGGGATCA
CAAGGC
GAM1258 CCTTGGAATGTGAAGAGTGA 1231 TGGAATGTGA 2907 GAA AGA G GTA- CA
GGAGACAGTAGCCATCCAGC AGAGTGAGGA CCTTG TGTGA GTGAGGA ACA GC T
CAGATGTGTTTTCGCATTAT GACA ||||| ||||| ||||||| ||| ||
AACAAGG GGAAC ATATT CGCTTTT TGT CG C
A-- A-- G AGAC AC

GAM1259 TAGCACCAGTATAAATAGTG 1232 TAGCACCAGT 2908 C- TAAAT C-- AA- GA
ATTTCATTAATCATTGAATC ATAAATAGTG TAGCAC AGTA AGTGATTT ATT TCATT A
AGATGAAGCAGTTATAAATC ATTT |||||| |||| |||||||| ||| |||||
ACTTTTTACTTTGTGCTA ATCGTG TCAT TCACTAAA TGA AGTAG T
TT TTT-- TAT CGA AC

GAM1260 GTGATGTGTTTATGGTAGCC 1233 ACTGCGGTGA 2909 A A TAG - GGTGAA AA T -
AAG
CACTGCGGTGAAAGAAACTT AAGAAACTTG GTG TGTGTTT TGG CC CACTGC AGA CT
GTA GGC A

GTAGGCAAGATGTAGTCATA TAGG ||| ||||||| ||| || |||||| ||| || ||| |||
CTGGGATCTGTGGTAGTGTG TAC ACACGAA ACC GG GTGATG TCT GG CAT CTG
T
GAGTCCAGAAGCACAACAT A G TGA T GTG--- AG T A ATG

GAM1261 CAGCTACATTGTTGAGTTAG 1234 TACTAGAACA 2910 C T-------- GATGATGTT A GA-
-- TA
TGATGATGTTGTATATGCTG GCTAGCTCAT G TACATTG TGAGTTAGT GTAT TGCT
TGGTCT A
ATGGTCTTAACTGGATTACA CGTT | ||||||| ||||||||| |||| |||| ||||||
AAAAGCAAATACTAGAACAG T ATGTAAC ACTCGATCG CATA ACGA ATTAGG
/
CTAGCTCATCGTTCACCCAA C CCACTTGCT ACAAGAT-- A AAAAC TC
TGTACTTG

GAM1262 GCCATGAATGGTTTTTAGGG 1235 ATGAATGGTT 2911 TGA G TT- - AT AT- TG C
GATTCAATGGGCTTGGACAG TTTAGGGGAT GCCA ATG TT TAGG GG TCA GGGCT
GACAG A
CATCTGTTAGCCCTGGTGAC TCAA |||| ||| || |||| || ||| ||||| |||||
CACCTGCCCAAGTGTGTTGG CGGT TGT AA GTCC CC AGT CCCGA TTGTC /
C TG- G CCC A -- GGT -- T

GAM1263 CTGCAGCTCCTTTTGACAAG 1236 TGACAAGAAA 2912 CA ---- T - AAATGT C AA--
CTGTT T
AAATGTGGTCGTGAAAATTG TGTGGTCGTG CTG GC TCCTT TGAC AAG GGT GTGAA
TTGGA GC T
GACTGTTGCTTTTGCTCCAG AAAA ||| || ||||| |||| ||| ||| ||||| ||||| ||
ATGGTTCATACTTTGCTTGG GAC CG AGGAA ACTG TTC TCA TACTT GACCT
CG T
TCACAAGGACATCGCACAG A- CTAC C G GTT--- - GGTA ----- T

GAM1264 CTCAGACTGTACTCTTCTAG 1237 CTAGCCATCT 2913 - - CTA - GAAATAC A
CCATCTGAAATACGTTTTCT GAAATACGTT CTCA GACTG TACTCTT GCCA TCT GTTTTCT
G
AGGTAGAGAATAGATTGGTG TTCT |||| ||||| ||||||| |||| ||| |||||||
TAAGGGTACCAGTTGTGAG GAGT TTGAC ATGGGAA TGGT AGA TAAGAGA G
G C TG- T ------- T

GAM1265 GCCTGCCTGAACCCTGGGTC 1238 CATGACGGCT 2914 A GG--- - A -- G AA- A- G
C
AGGAGAGAAACACTTGGGGA CTGAGTTCTT CCCT GTCA GGAGAGA ACA CTT GGGAGGGG
AGG CG CGTGGG T
GGGGAAAGGACGGCGTGGGC CCTG |||| |||| ||||||| ||| ||| |||||||| ||| || ||||||
TACCCATGACGGCTCTGAGT GGGA CGGT CCTTTCT TGT GGG TCCTTCTT TCT GC
GTACCC /
TCTTCCTGGGGCTTGTGTCT C GAAGA T G TC G GAG CG A A

TTCCTTGGCAGAAGAGGGCA
CAGCAAGGC
GAM1266 ACCTTTATCAAGTGAAAGAC 1239 TGAAAGACAT 2915 AAGACATG G ATGGCC AT C--
A -- AAT
ATGAGTTTGTGATGGCCCAA GAGTTTGTGA TGA AGTTT TG CAAT GTGAA TTG GTTT
CAGGGT G
TATGTGAACTTGAGTTTCAG TGGC ||| ||||| || |||| ||||| ||| |||| ||||||
GGTAATGATGCACCCTGTTG ATT TCAAA AC GTTG CATTT GAC CAAG
GTCCCA A
AACACAGAAATTTACCAGTT -------- G ------ AC AAA A TT CGT
GCAGAAACTTTACTTTGAAA
GGT
GAM1267 GCTCCAAAGAACCAAGAGTG 1240 CATTTCACTT 2916 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1268 GTGGGAGGAGGACTGGCAAA 1241 ATGAGAGTAG 2917 A C CAA A A A A TG C
AATATGAGAGTAGGAGTTTG GAGTTTGGGC GTGGG GGAGGA TGG AAAT TGAG GT GG GTT
GGCT T
GGCTCTTGAGCTTGGGCCTG T ||||| |||||| ||| |||| |||| || || ||| ||||
GCCTTCAAATTTCCACTCTT CACTC CTTTCT ACC TTTA ACTT CG TC CGG TCGA T
TCACTCAC A C --- A C G - GT G

GAM1269 GCCTAACTTCACAGTCTTGC 1242 TCACTAGGCA 2918 ACTT--- T CG- GC TTT
AA AA
CTCGGAGCAGGAACTGTTTG GACTGTGCTC GCCTA CACAGTCT GCCT GA AGGAACTG
GAGGC C G
AGGCAACAAGATGGAGCCTC AAAC ||||| |||||||| |||| || |||||||| ||||| |
TGGTTTCTTCACTAGGCAGA TGGGT GTGTCAGA CGGA CT TCTTTGGT CTCCG G
/
CTGTGCTCAAACTGGGT CAAACTC - TCA -- --- AG TA

GAM1270 TGGGTTATGGAAAAGATACG 1243 TTAGGAACAA 2919 GA-- AC--- --- - ----- AG G-
CC
TTTCGAGGGCAGCCGCTAGA CACATTTTTG ATG AAAGAT GTTTC GAG GG CAGCCGCT
ATTTG GG C
TTTGGGGCCCGAATCAACAG CAAC ||| |||||| ||||| ||| || |||||||| ||||| ||
GTGAGTGGCTGAATACCCAC TAC TTTTTA CAAGG CTC CC GTCGGTGA TGGAC
CT G
TCTTAGGAACAACACATTTT AACG CACAA ATT A CATAA G- AA AA
TGCAACATGATCCA

GAM1271 AGAATGGGGAAGAATACTGA 1244 TTGGAGCAGG 2920 - - TA AA T CA TCT AC-
CT
ATTAGCTGAGCACATTCTGG TTTCATTCTC AGAAT GGGGAA GAA CTG TTAGC GAG CAT
GGAC AATT G
ACACAATTCTGACCAATTTC CAAT ||||| |||||| ||| ||| ||||| ||| ||| |||| ||||
AGTCTCATGATCTCTGTTGG TCTTA CCTCTT CTT GAC GGTTG CTC GTA TCTG
TTAA A
AGCAGGTTTCATTCTCCAAT A A TG GA T TA C-- ACT CC
TCT

GAM1272 CTGCACAAGGTCACCCAGGA 1245 TGATGTAGTA 2921 CAAG T A TC TCG GA CTT
AC
GCTCCACAGCTTTCGGCAGA AGCTGTGTGC CTGCA G CACCC GGAGC CACAGCTT GCA
TC GG A
TCCTTGGACAGCGCCTTGAT TCCC ||||| | ||||| ||||| |||||||| ||| || ||
GTAGTAAGCTGTGTGCTCCC GATGT C GTGGG CCTCG GTGTCGAA TGT AG CC G
GGGTGCTGTAG ---- - C T- TGA -- TT- GC

GAM1273 GCTCCAAAGAACCAAGAGTG 1246 CATTTCACTT 2922 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1274 TTTACTGAATATTCAAATCG 1247 ATCGCTGTCT 2923 AATA- AATC TAAAG AG
CTAAT CT
CTGTCTGTTAAAGATGTAGT GTTAAAGATG TTTACTG TTCA GCTGTCTGT ATGT TTA
TTATTT A
TACTAATTTATTTCTATAGA TAGT ||||||| |||| ||||||||| |||| ||| ||||||
ATAATACATGAGGCATGCAG AGGTGAC AAGT CGATAGACG TACG AGT
AATAAG /
ATAGCTGAAGACAGCAGTGG GACAG ---- ----- G- ACAT- AT
A

GAM1275 GCTCCAAAGAACCAAGAGTG 1248 CATTTCACTT 2924 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1276 CACAAGTGATGGTCCAACTT 1249 GTAAGGATTT 2925 - -- T-- GAATG- AGG
AGGG GG

TGTGGAATGGTAAGGATTTT TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA ATTTTT TTGTTT C
TAGGGTTGTTTGGCCAGAAC TT |||||||| |||| ||||||| |||| ||| |||||| ||||||
AAGAGAAATAACTGCAGAAA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA AACAAG /
ACACATATGGTTGGAAACCA G AA TAT AAAAGA CAA G--- AC
TGCGCTTGTG

GAM1277 GCTCTGTGGTCCCTATATTC 1250 TCGACGTCGT 2926 T T TATAT C A TAAGCTA A
GACGTCGTATGATAAGCTAG ATGATAAGCT GC CTG GGTCCC TCGACGT GT TGA GGC T
GCATGTGCCGTCGTTCAACC AGGC || ||| |||||| ||||||| || ||| |||
ACGTCGGTGAGTGGGATCCA CG GAC CTAGGG GGCTGCA CA ACT CCG G
GTGC T - TGAGT C - TGCTG-- T

GAM1278 GCACAGCAGTGGGCGAGAAC 1251 TCCTCCAGTG 2927 GT CG CA TTTTACC-- - C- AGGAA- C T
AAGCGTCTTTTACCTGTCAC GCGTTCTTTT GGG AGAA AGCGTC TGT CAC GAAGCA GC CGTTT G
CGAAGCAAGGAAGCCCGTTT TACT ||| |||| |||||| ||| ||| |||||| || |||||
TGTAAGCGTGTGTGTGGTGC CTC TTTT TTGCGG ACA GTG TTTCGT TG GCGAA /
TTTATGTGTACATCCTCCAG -- AT C- TGACCTCCT T TA GGTGTG T T
TGGCGTTCTTTTTACTCTAA
TGTGC
GAM1279 GTAAACTCCAACCCAGAATG 1252 TTGGAGCAGG 2928 AACCC - - TA AA T CA TCT AC- CT
GGGAAGAATACTGAATTAGC TTTCATTCTC AGAAT GGGGAA GAA CTG TTAGC GAG CAT GGAC AATT G
TGAGCACATTCTGGACACAA CAAT ||||| |||||| ||| ||| ||||| ||| ||| |||| ||||
TTCTGACCAATTTCAGTCTC TCTTA CCTCTT CTT GAC GGTTG CTC GTA TCTG TTAA A
ATGATCTCTGTTGGAGCAGG TTTTC A A TG GA T TA C-- ACT CC
TTTCATTCTCCAATTCTCTT
TTACAGAAC
GAM1280 GTACATTTTGCCCTTGTCCA 1253 TTTGCCCTTG 2929 CAT C- GCAT- A
GGCATGTTTAAGGAGCTCCT TCCAGGCATG GTA TTTGC CTTGTCCAG GTTT A
ACTGGACAGGTTGCAGACTA TTT ||| ||||| ||||||||| ||||
C CAT AGACG GGACAGGTC CGAG /
C-- TT ATCCT G

GAM1281 GGTGGAATGTATATAGAAGT 1254 TGGAATGTAT 2930 T AA- T A -- GTG
TGTCCTGTGGTTTGAGGAAG ATAGAAGTTG GG GG TGTA ATAG AGTTGT CCT G
CAGCTACTATTTGCAGAGCC TCCT || || |||| |||| |||||| |||
TCC CC CC ACGT TATC TCGACG GGA T
T GAG T A AA GTT

GAM1282 TGCCCGACGGAGTATGTAAT 1255 CGACGGAGTA 2931 CC T AATATTT TGAA- - T- A

ATTTAGAGGTGAACATAGTG TGTAATATTT TGC GACGGAGTA GT AGAGG CAT AG GC A
CAAGAGCCCCTGATGGTGCC AGAG ||| ||||||||| || ||||| ||| || ||
CCTCTACCTGCTTTGTCATG ACG CTGTTTCGT CA TCTCC GTA TC CG G
CA TA C ------- CCGTG G CC A

GAM1283 GCTCCAAAGAACCAAGAGTG 1256 CATTTCACTT 2932 T - ---------- CAC GAGATA TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1284 ACTGCAGGCAAGCACCACCA 1257 TAACTGGGCA 2933 A-- C A C TG T AACAT
TGCCCAGCTAATTTTTTGTA CGGTGGTCTC AG ACCACC TGCCCAG TAATTTTT TATTTTTTTGTGGAGAC GGGT A
TTTTTTTGTGGAGACTGGGT ACGC || |||||| ||||||| |||||||| |||||||||||||||| ||||
AACATAGCAAGACCCTGTCT TC TGGTGG ACGGGTC ATTAAAAA ATAGAGAAACACCTCTG CCCA /
CCACAAAGAGATAAAAAATT CAC - C A -- T GAACG
AACTGGGCACGGTGGTCTCA
CGCCTGTAAT
GAM1285 CTTCATGAAGCAGAAAGCAC 1258 TCATGAAGCA 2934 C--- AC A GGAGAG AA
TACGAGCTGAAATGGCTGTA GAAAGCACTA CATGAAG AGAAAGCACT GAGCTGAAATGGCTGTAG TTTG CAGG G
GATTTGGGAGAGCAGGAAGG CGAG ||||||| |||||||||| |||||||||||||||||| |||| ||||
ATCTGAACGAAACTACAGCC GTACTTC TCTTTCGTGA CTCGACTTTACCGACATC AAGC GTCT /
ATTTCAGCTCACAGTGCTTT TTCA CA A AA---- AG
CTACTTCTTCATGAAG

GAM1286 TCCCGCTGTAATCTCAGCAC 1259 TAATCTCAGC 2935 A T A A AG A-- A TG T C CTGTC
TTTGAGGAGGGCAAGGTGGG ACTTTGAGGA TC CAGC CTTTG GG GGC AGGTGGGAGG T CT GAG TCCAGGG T
AGGATTGCTTGAGCTCCAGG GGGC || |||| ||||| || ||| |||||||||| | || ||| |||||||
GCTGTCTCGAAACTCCTGGA AG GTCG GGAAC CC CTG TCCGCCCTCC A GA TTC AGGTCCT C
CTTAGTGAGCCTCCCGCCTC - - - - CT GAC G GT - - CAAAG
AGGTCTCCCCAAGGGCTGGA
TACAGGCAGGA
GAM1287 AGGTCATGAATCATTGCATG 1260 GGGAAGATGG 2936 TC A- A CA-- G T C A -- ATA
GGAAGATGGTGGCTATACTG TGGCTATACT AGG ATG ATC TTG TGGGAA ATGG GG TAT CTGA AC G

AACATAGATACGTACTCAGG GAAC ||| ||| ||| ||| |||||| |||| || ||| |||| ||
TGACTTTCATATTCCCACAC TCC TAC TAG AAC ACCCTT TACT TC GTG GACT TG A
ACAAGATAGCATATCCT TA GA - ACAC A T A - CA CAT

GAM1288 TAGTACCAATGTATTGAAGT 1261 TGAAGTAATA 2937 AT T- TAATACG T ATTA T C - AT
AATACGTTTGTGCATTATGC CGTTTGTGCA TAGTACCA GTA TGAAG TT GTGC TGCA GT TC CAG A
ATGTCTCCAGATAGGTTGTG TTAT |||||||| ||| ||||| || |||| |||| || || |||
AACTTGCAGATGGCATTGAA ATCATGGT CGT ACTTC AG TACG ACGT CA AG GTT /
TATCTTCTTCACCTGCCTGG C- CC TTCTATA T GTAG T - T GG
TACTA

GAM1289 AGGGATGATATTAATAACTA 1262 TACCTCGTAA 2938 AACTA C AAAGTT AG TAAA - A TA TT ATA
CCTCGTAAAGTTTCTGTGAA AGTTTCTGTG CCT GT TCTGTGA AC AGAG AT TG ACATGC GAG G
GACTAAAAGAGATATGTAAC AAGA ||| || ||||||| || |||| || || |||||| |||
ATGCTTGAGATAGTGCCTCG GGG CG AGATACT TG TCTC TG AT TGTACG CTC /
CATGTAGTAAGTCCTCTGTG ----- T AAATC- A- TG-- C A GA -- CGT
TATCATAGACTAAAGCTGGG
CTTCATCTTCT
GAM1290 CTACCTCGTAAAGTTTCTGT 1263 TACCTCGTAA 2939 CGTAA TT AG TAAA - A TA TTGAAAT
GAAGACTAAAAGAGATATGT AGTTTCTGTG CTACCT AG TCTGTGA AC AGAG AT TG ACATGT A
AACATGTTTGAAATAGTGCC AAGA |||||| || ||||||| || |||| || || ||||||
TCGCATGTAGTAAGTCCTCT GGTGGA TC AGATATT TG TCTC TG AT TGTACG /
GTGTATTATAGACTAAAGGT AA--- -- A- TG-- C A GA CTCCGTG
GG

GAM1291 GGATTCGACGGATACTTCGG 1264 TGGAGAAGAC 2940 GGA T-- AGAAGACA G TACTCTG -- GT
GTGGAGAAGACAGGGCACAG AGGGCACAGT AC TACT CGGGTGG GGGCACA TGG GATC CCCAG G
TGGTACTCTGGATCCCCAGG GGTA || |||| ||||||| ||||||| ||| |||| |||||
TGGAACTGGGTTGGTTATAA TG GTGG GCTCACC TTCGTGT GCT TTGG GGGTC G
TTCGTGTGCTTAGAACGAGC AA- TTC GAGCAAGA - TAATA-- TT AA
CACTCGCTTGGTGAAGTCAC
AACAGAGTGC
GAM1292 TGGTTTTAGTCCATTGGTAG 1265 AACACCACAG 2941 TT- - ATTG A-- - A G
CATTGTGTGTATGAGGAGAT ACAGCTGCAG TGG TT AGTCC GTAGC TTGTG TGT TGAG A
TCAACACCACAGACAGCTGC GACT ||| || ||||| ||||| ||||| ||| ||||
AGGACTCGATATCCA ACC AG TCAGG CGTCG GACAC ACA ACTT G
TAT C A--- ACA C - A

GAM1293 GCTTTTTGTTACATGGATCC 1266 TCCCAAATAT 2942 - A - - - ACAAA T AA
CAAATATTTACAAAGCCATC TTACAAAGCC GCT TTTTGTT CATGG ATCC CAA ATATTT GCCA CAG C
AGAACCACCTGTGGCAAATG ATCA ||| ||||||| ||||| |||| ||| |||||| |||| |||
TATTGTGGATATCGTGAAAC CGG AAAGCAA GTGCT TAGG GTT TGTAAA CGGT GTC C
GAAATGGC T A A T A ----- - CA

GAM1294 GGGTGCACAAGTGATGGTCC 1267 GTAAGGATTT 2943 - -- T-- GAATG- AGG AGGG GG
AACTTTGTGGAATGGTAAGG TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA ATTTTT TTGTTT C
ATTTTTAGGGTTGTTTGGCC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
AGAACAAGAGAAATAACTGC TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA AACAAG /
AGAAAACACATATGGTTGGA G AA TAT AAAAGA CAA G--- AC
AACCATGCGCTTGTGACTT

GAM1295 TAATGGTCACTTGATGTGCG 1268 AGGAGGAGCA 2944 T C AT TG C GTTTTA A AC AGAT
CTGGCTGTTTTATCCACCTA GGCCACGTGC TAATGG CA TTG G CG TGGCT TCC CCT TAGC G
CTAGCAGATGCCCGGCTGAA CCCA |||||| || ||| | || ||||| ||| ||| ||||
GGAGGAGCAGGCCACGTGCC GTTGCT GT AAC C GC ACCGG AGG GGA GTCG /
CCAATTGTCGTTG - T CC GT - ACG--- A A- GCCC

GAM1296 GGATGGTGGCTCATCACCTG 1269 CACCTGTAGA 2945 CTCATCACC AAC CT CC- TG T AA
TAGAACCTGACTTGGCCGTG ACCTGACTTG GGATGGTGG TGTAG CTGA TGG G GC GG T
GCTGGAATCCACTCGTTGCC GCCG ||||||||| ||||| |||| ||| | || ||
TTCCACTTCAGTTACACCTC CCTACCACT ACATT GACT ACC C TG TC C
ACTCACCATCC CACTCC--- --- TC TTC GT C AC

GAM1297 TGCCGGCTGAGGTCCATATA 1270 TACAAGATAT 2946 --- CCA AGAA GG T
TAGAACTTGGGTTTTTGAAA AATTTCAGTA TGCCG GCTGAGGT TATAT CTTG TTT T
TACAAGATATAATTTCAGTA AATG ||||| |||||||| ||||| |||| |||
AATGGTA ATGGT TGACTTTA ATATA GAAC AAA /
AAA --- ---- AT G

GAM1298 GCAAATCAGTCCATTTCACT 1271 CATTTCACTT 2947 - ---------- CAC GAGATA TC
TTCACTGTCTGAGATAGGGT TCACTGTCTG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T
CTCTAAGACCCAGGATACAA AGAT ||||||| ||||||| |||||||| ||||| |||||

GGGTGGAATGTAGCTATATG CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GACTCGATTTGC C TATCGATGTA AC- A----- AA

GAM1299 GAAGACACATTTGTAAATTT 1272 TGACGGAAGA 2948 --- --- A C C - TAGAG-- AA CA
- CA
TCAAGCAGCCATAGAGCCAA GATTGAGCTA A TTTGT AA TTTT AAG AGC CA CC CAATT
TGC ATCT A
CAATTCATGCATCTCAAACA CTTC | ||||| || |||| ||| ||| || || ||||| ||| ||||
AGGTGGCAGCAGTTGACGGA T AAACA TT AGGA TTC TCG GT GG GTTGA ACG
TGGA A
AGAGATTGAGCTACTTCAGG TCC AAA C C A A TAGAGAA CA CG G AC
ACTTAAAACAAACCTTGTGC
TCTTC
GAM1300 GGGATCTGGTCTGAGGGGGC 1273 GGAAGTTGCT 2949 TC T G C GGCA TG TA A - T
C--- AT
GGACGGCACTGATATCAACG GGCTTCAGCT TGG CTGAG GGG GGAC C A TCA C GCTG
GGCC GCTTCTC G
CTGTGGCCCGCTTCTCATGA GATG ||| ||||| ||| |||| | | ||| | |||| |||| |||||||
TGGGGAAGTTGCTGGCTTCA ATC GATTT TCC CTTG G T AGT G CGAC TCGG
TGAAGGG A
GCTGATGACTTTGGCAAAGT -- - G A AAAC GT TC A T T TCGT GT
TCACCTGTTTAGCTACCCC

GAM1301 TGTCAATGTCCATGTCCTGG 1274 TGTCCTGGTA 2950 TC T GT TG- CC A T - AG
TAGGCCTTCTTCATGCTTTG GGCCTTCTTC TG AATG CCAT CC GTAGG TTCTTC TGCT TGG
GC C
GGCAGCAAGCTCCATGGTAC ATGC || |||| |||| || ||||| |||||| |||| ||| ||
GAAGGACTTCTGCATTGGTA AC TTAC GGTG GG CGTCT AGGAAG ATGG ACC CG /
GTGGCATTCTCA TC - AT TTA TC C T T AA

GAM1302 GGCTGCTGTGGAATATTGTT 1275 TGCGGTGGTA 2951 G - AT GTT CT TG AA G
AG TG GGAA
GATTTCTCACTGTGGCCCGA GGTTGTAGAT CTGT GGA ATT GATTT CACTG GCCCG GTT
TGG C GCAG G
AGTTGTGGAGCTGGCAGGGA TCTT |||| ||| ||| ||||| ||||| ||||| ||| ||| | ||||
AGTGTGTTGTTGGAGTCGAG GACA CTT TAG TTGGA GTGGC CGGGT CGA GCT G
TGTT /
CCTGGGCTGCGGTGGTAGGT G A CT ATG TG GT C- - GA GT GTGT
TGTAGATTCTTCAACAGGGG
CT
GAM1303 GCTCCAAAGAACCAAGAGTG 1276 CATTTCACTT 2952 A AA T - TTC--- - GT GAG
AG- TC
CAAATCAGTCCATTTCACTT TCACTGTCTG CC GAG GCAAATC AGTCCAT AC TTTCACT CT
AT GGTC T
TCACTGTCTGAGATAGGGTC AGAT || ||| ||||||| ||||||| || ||||||| || || ||||
TCTAAGACCAGGATACAAGG GG CTT CGTTTAG TCAGGTA TG AAGGTGG GA TA
CCAG /

GTGGAATGTAACTATATGGA A C- - C TATCAA T -- ACA GGA AA
CTCGATTTGCTTCCGGACCT
TTTCCAGAGC
GAM1304 GGGGAGTTGCCCAGTCCAGA 1277 TTCATCACTG 2953 CCA C- A T AGAA AA A - ATGT G
ATACTCCACATTGAGAACTT GGTAAGTCTC TTGCCCAGT GAATA TCC CA TG CTT TCCGT TC GTG CGCT T
AATCCGTATCGTGATGTCGC C |||||||||| ||||| ||| || || ||| ||||| || ||| ||||
TGTCCAGTGCACTGAACGGG AATGGGTCA CTTAT AGG GT AC GAA GGGCA AG CAC GTGA C
AAGGACCATTGGGATATATT CTA AT - T CAG- -- - T ---- C
CATCACTGGGTAAGTCTCC

GAM1305 TTGTAAGAACATGTGGTATT 1278 ACCTCTAGCT 2954 A T-- TATTT-- TTCTGT -- TT
TGGTTTTCTGTTCCTGCGTT CCTTCCATGT TTGTA GAACATG GG GGTT TCCT GCG A
AGTTTGCTAAGGATAATGAC TCCT ||||| ||||||| || |||| |||| |||
CTCTAGCTCCTTCCATGTTC AATAT CTTGTAC CC CCAG AGGA CGT G
CTATAA C CTT TCGATCT TAAT-- AT TT

GAM1306 TGCACAAATCAAGACTTCTG 1279 CATCCAGTGT 2955 A- -- TC TTCT CC CT A TT
TACACTCCATGCCTTGATGA GCTGTCTTTT TGC CA AA AAGAC GTACACT ATGC TG TGA T
TTTCTTCAGCAGCATCCAGT TTAA ||| || || ||||| ||||||| |||| || |||
GTGCTGTCTTTTTTAATGAA ACG GT TT TTCTG CGTGTGA TACG AC ACT /
GCA AA AA TT T--- CC -- G TC

GAM1307 GCTCCAAAGAACCAAGAGTG 1280 CATTTCACTT 2956 T - ---------- CAC GAGATA TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1308 CTTAGTAGTAGTTACTGGTT 1281 TACGGTTACT 2957 A- T TGAACATTGT T G ATCTT T
GAACATTGTTTGTTGGTGTC GTGATTACGG CTTAGT GTAGTTAC GGT TTGT GGT TCT GTAAT G
TATCTTGTAATTGAAATTGC ACTA |||||| |||||||| ||| |||| ||| ||| |||||
TCGGGGACCTACGGTTACTG GGATCA CATTAGTG TCA GGCA CCA GGG CGTTA A
TGATTACGGACTAGG GG - TT-------- T G CT--- A

GAM1309 CCTCCCGCTGCCGTCCAGTG 1282 TGTACACATC 2958 GCC C TA TACACATCC A - - CT TC G

CCTGTACTGTACACATCCAC CACACTCATT GTC AGTGCCTG CTG AC CTCA TTCT CA
CAGGGT CCG A
ACTCATTCTCACTCAGGGTT CTCA ||| |||||||| ||| || |||| |||| || |||||| |||
CCCGGACCGGCTGTCCTGCC CAG TCATGGAC GAT TG GAGT AAGG GT
GTCCTG GGC /
TGCGGAACTGAGGTAAACTA --- - TC CAAA----- - C C CC TC C
GCTCAGGTACTGACACTAGG
AGG
GAM1310 GCTCCAAAGAACCAAGAGTG 1283 CATTTCACTT 2959 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1311 GTGATGGTGACCGGTCAGAC 1284 TCAGACCCAG 2960 TG--- G--- GA--- A- C
TCTTA TG
CCAGGTTCATTCCCTCTTAC GTTCATTCCC GTGA GTGACCG TCA CCC GGTT ATTCCC
CGC A
GCTGAAGGCGGGGAATAGCC TCTT |||| ||||||| ||| ||| |||| |||||| |||
CAGGGGAAGATGAGAGACGG CACT CACTGGC AGT GGG CCGA TAAGGG
GCG /
TCACAGTTCTCAC CTTGA AGAG AGAAG AC - ----- GA

GAM1312 CTTTCAGTCTTTATTTGCAG 1285 CTTTCAGTCT 2961 CA- T TTT A AA ACCA TATATGAC
TT C CAC
CAAACTACCACTTTATATGA TTATTTGCAG GTCT TA GC GCA CT CTT AGG TGTGTGT
TGTA G
CAGGTTTGTGTGTCTGTACA CAAA |||| || || ||| || ||| ||| ||||||| ||||
CGCACATACACACACATATC CAGA AT CG CGT GA GAG TCC ATACACA ACAT
C
CTTAAGCTCGAGACAGGGTG AAC C TT- G GG CA-- CTCGAAT- T- C ACA
CGGCTTTACAGACCAAAAAG

GAM1313 TAAACAGAAGTGATAATAGC 1286 TGAGGTAATA 2962 GT--- GTAGAAG AGA
A
AGGGTGTAGAAGACAGAGGA ATTCTGTTGT TAAACAGAA GATAATAGCAGGGT AC
GGAAGACAG G
AGACAGAGCTCTGTTTTTTG TGTT ||||||||| |||||||||||||| || |||||||||
AGGTAATAATTCTGTTGTTG GTTTGTCTT TTGTTGTTGTCTTA TG TTTTTTGTC C
TTCGTCGTTCTGTTTG GCTGC ATAA--- GAG T

GAM1314 GCCATTGCTTTGGTTTGTTA 1287 TTCAAGCTAT 2963 TT ------- TT- TC T -- A
TA
GTATCGGTTTTAGGACTTTT CTGGATAGGC GCCA GCTT TGGTTTG AGTA GGTTT
AGGACT TTT CATC T

ACATCTATATTGGTGAAATC TTTG |||| |||| ||||||| |||| ||||| |||||| ||| ||||
AGTCTTCAGACTTTACTTTT TGGT CGGA ATCGAAC TCAT TCAGA TTCTGA AAA
GTGG A
CAAGCTATCTGGATAGGCTT TT TAGGTCT TTT T- C CT - TT
TGGT

GAM1315 TGGGTCTCCATATCTGCATT 1288 TCTGCATTGT 2964 T CATT T - CTT- - - A
GTCCCAGAAGTGACTTTGGC CCCAGAAGTG TGGGTC CCATATCTG G CCCAGA AGTGA
TGG CA CT A
ACTAAAAAGTTGATCATTAA ACTT |||||| |||||||||| | |||||| ||||| ||| || ||
TTACTGTTTGGGCCAGGTGT ACTCGG GGTGTGGAC C GGGTTT TCATT ACT GT GA
A
GGTGGCTCA T ---- - G AATT A T A

GAM1316 AGAATGGGGAAGAATACTGA 1289 TTGGAGCAGG 2965 - - TA AA T CA TCT AC-
CT
ATTAGCTGAGCACATTCTGG TTTCATTCTC AGAAT GGGGAA GAA CTG TTAGC GAG CAT
GGAC AATT G
ACACAATTCTGACCAATTTC CAAT ||||| |||||| ||| ||| ||||| ||| ||| |||| ||||
AGTCTCATGATCTCTGTTGG TCTTA CCTCTT CTT GAC GGTTG CTC GTA TCTG
TTAA A
AGCAGGTTTCATTCTCCAAT A A TG GA T TA C-- ACT CC
TCT

GAM1317 GCTGGGCGTGGTGGCAGGCA 1290 AGAGGCAGAG 2966 - GG G AC CC- A
AGGC G GG
CCTGTAATCCCGCCTACTCA GTTGCAGTAG GCTG GGCGTGGT CAG C CTGTAATC GCCT
CTCAGG TGAG GA G
GGAGGCTGAGGGAGGGAATC CTGA |||| |||||||| ||| | |||||||| |||| |||||| |||| ||
GCTTGAACCTGAGAGGCAGA CGAC CCGTACCA GTC G GACGTTGG CGGA GAGTCC
GTTC CT /
GGTTGCAGTAGCTGAAACCA A AA - AT AGA - AA-- G AA
TGCCACAGC

GAM1318 CTTCATGAAGCAGAAAGCAC 1291 TCATGAAGCA 2967 C--- AC A GGAGAG
AA
TACGAGCTGAAATGGCTGTA GAAAGCACTA CATGAAG AGAAAGCACT
GAGCTGAAATGGCTGTAG TTTG CAGG G
GATTTGGGAGAGCAGGAAGG CGAG ||||||| |||||||||| |||||||||||||||||| |||| ||||
ATCTGAACGAAACTACAGCC GTACTTC TCTTTCGTGA CTCGACTTTACCGACATC
AAGC GTCT /
ATTTCAGCTCACAGTGCTTT TTCA CA A AA---- AG
CTACTTCTTCATGAAG

GAM1319 TCCAACTTTGTGGAATGGTA 1292 GTAAGGATTT 2968 T-- GAATG- AGG AGGG GG
AGGATTTTTAGGGTTGTTTG TTAGGGTTGT TCCAACT TGTG GTA ATTTTT TTGTTT C
GCCAGAACAAGAGAAATAAC TT ||||||| |||| ||| |||||| ||||||
TGCAGAAAACACATATGGTT AGGTTGG ACAC CGT TAAAGA AACAAG /
GGA TAT AAAAGA CAA G--- AC

GAM1320 TTGCCTGCTCATTTGATCAA 1293 TGAAAACTTA 2969 A - AA T - TT CAT--- GAA T T T TCTT
GCCTTCCCATTACTCATGTT AAAAGTTTGG C TT TGATC GCC TC CCA ACT GTTTTCA AG GC GC TG C
TTCAGAAAGTGCTGCTTGTC AGAT | || ||||| ||| || ||| ||| ||||||| || || || ||
TTCTTTTCCATGTGCCCTGT G AG ACTAG CGG AG GGT TGA CAAAAGT TC CG TG AC T
GTGAAAACTTAAAAAGTTTG A C A- T A T- AAAATT GTG C - T CTTT
GAGATGGCAGATCACGAAGA
GCCAGGGTAG
GAM1321 GCTCCAAAGAACCAAGAGTG 1294 CATTTCACTT 2970 T - ---------- CAC GAGATA TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1322 TGGAGCTGGGCAAGCTGCTG 1295 GGCAAGCTGC 2971 T--- CT C -- T G---- AC GAT
GCGGAGATGCTGGTGCAGGC TGGCGGAGAT TGGAGC GGGCAAGCTG GG GGA GATGC GGT CAGGCT GCA G
TACGCAGATGCCATGCAGCC GCTG |||||| |||||||||| || ||| ||||| ||| |||||| |||
TGGACAAGCCCGCATCGTTC ATCTCG CCTGTTCGGC TC CCT CTACG CCG GTCCGA CGT /
CTCTCGGCTTGTCCCCGTGC TGCC -- T TG C AACAG -- ACC
TCTA

GAM1323 GCTCACGCCTGTGGTCCCAG 1296 AGGAGGGCAG 2972 C T G A G - T TCTC
CACTTTGGGAGGCCAAGGAG GTTGTTTGAG C TGTGGTCCCAGCACT TGGGAG CCAAGG GGGCAGGTT TTTGAG CC GG G
GGCAGGTTGTTTGAGCCTGG CCTG | |||||||||||||| |||||| |||||| ||||||||| |||||| || ||
TCTCGAACTCCTGGCCTCAA G ACATTAGGGTCGTGA ATTCTC GGTTTT CCCGTCTAG GAACTC GG CC /
GGGATCTGCCCGTTTTGGAC A C A G G C T TCAA
TCTTACAGTGCTGGGATTAC
AAGCAAGAGC
GAM1324 CATTTCTTGAAGGAGGCACT 1297 AGGCACTGTG 2973 T AA--- G TGTGGT - TC A G TTTAA
GTGGTTATGAGTTGTCGGGG GTTATGAGTT AT TCTTG GGA GCAC TATGAG TTG GGGGAGT GTG CT C
AGTAGTGGCTTTTAACATTT GTCG || ||||| ||| |||| |||||| ||| ||||||| ||| ||
TGGGCACATTTCCTTTCAGT TG GGAAC TCT TGTG GTATTC GAC TCCTTTA CAC GG /
CTTATGTGTGTGTGTCTGTG T GTGTG G TGT--- T TT - G TTTTA

TGCAAGGTGTG

GAM1325 GCTCCAAAGAACCAAGAGTG 1298 CATTTCACTT 2974 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1326 CCCCGCTGCAAATGATCTAG 1299 TGCAAATGAT 2975 T AA CTAGACT GC GACTTG
T AG
ACTCCTGCTGGGGTTGACTT CTAGACTCCT CCCCGC GCA TGAT CCT TGGGGTT
TTTCAA GGG G
GTTTCAATGGGAGGGGCTCC GCTG |||||| ||| |||| ||| ||||||| |||||| |||
TTGAAAAGCCTGGACCCCAA GGGGTG CGT ACTA GGA ACCCCAG AAAGTT CCT
G
AAGGTAATCAAGTGCGTGGG - GA AT----- AA GTCCGA - CG
G

GAM1327 CCTCCATCCCTTTGTTTGCG 1300 TCAAGCTGCT 2976 TGTTT - G C CT T T ACA TG
C T
TCTGTCATAGTCAGGCTCTG CAGTCTACTG TT GC GTCT TCATAGT AGGCT G GC GGC
TGGG CAGGGAC AG G
TGCTGGCACATGGGTGCAGG TGGG || || |||| ||||||| ||||| | || ||| |||| ||||||| ||
GACCAGTGATCTAGTCCCTG AA CG CAGA GGTGTCA TCTGA C CG TCG ACTC
GTCCCTG TC A
TCCTCAAGCTGCTCAGTCTA CT--- A G - -- T - A-- CT A T
CTGTGGGAGACAGCTCAAGG
GACAGG
GAM1328 CAGAAGCTGCCAGGCATGCT 1301 GAAGCTGCCA 2977 ---- - CA A TGA
ATACTGAGAATTGTGGGTGA GGCATGCTAT CAGAAGCT GC CAGG TGCT TAC G
ACTTGAGCAGATGGTTTCTG AC |||||||| || |||| |||| |||
GTCTTTGG CG GTTC GTGG GTG A
TAGA A AA - TTA

GAM1329 AAAGGAAACACTGATGGGAA 1302 AACACTGATG 2978 A C T GAAAG -- TCCA A
ATGA AA
AGTATGGCGAAGACTCCAAG GGAAAGTATG AAGGAA CA TGA GG TATGGCGAA GAC
AGCTT TCT CCTG G
CTTATCTATGACCTGAAGGA GCGA |||||| || ||| || |||||||| ||| ||||| ||| ||||
CCAGGGCGGAGAGCTCCTGT TTCCTT GT ACT CC GTATCGCTT CTG TCGAG AGG
GGAC G
CCCTTCGCTATGACCTCACT - C - A---- CC TCC- - CG-- CA
GTTCCTTT

GAM1330 GACCTGAGGGCTGTCCTGCA 1303 CATGGACAGT 2979 CC -------- - TCC C----- AGC AA
T - TC

CTGCATCCACTCCTTCATAG CAGAGTCTTG T TGCA CT GCA ACTC TTCAT AGCC GG GG CC C
CAGCCAAGGTGGCCTCCGTG CCAG | |||| || ||| |||| ||||| |||| || || ||
GACCCCGGCTTCATGGACAG G ATGT GA CGT TGAG AGGTA TCGG CC CC GG /
TCAGAGTCTTGCCAGAAAAT AC ACATAAAA C TC- ACTGAC CT- -- - A TG
ACATGTACAGCGGCTAAAGG
TT
GAM1331 GGATAAGCAGATTGTACAGT 1304 AGCAGATTGT 2980 G C--- T A C- TGT
GCATTAGTCCCTGTCTCTTG ACAGTGCATT GGATAA CAGATTGTA AG GC TTAGT CC C
GATATTGAGCCTTTTCTGCA AGTC |||||| ||||||||| || || ||||| ||
ATTTGATTGTCC CCTGTT GTTTAACGT TC CG AGTTA GG T
A CTTT - - TA TTC

GAM1332 TCCCACTGTGGTGCCTGGCG 1305 TCGCCTGGAC 2981 C - G T G A - AA ACA G - --- ATG
GAGACCTGGCCAAGGTACAG CACAAGTTTG ACT GTGGT CC GGCG AG CCT GGCC GGT GA AGCTGTG TGC C
AGAGCTGTGTGCATGCTGAG A ||| ||||| || |||| || ||| |||| ||| || ||||||| |||
CAATACCACAGCTGTTGCCG TGA CACCA GG CCGC TC GGG CCGG CCG TT TCGACAC ACG /
AGGCCTGGGCTCGCCTGGAC T A - T - - T AG --- G CATA AGT
CACAAGTTTGA

GAM1333 GGGTGCACAAGTGATGGTCC 1306 GTAAGGATTT 2982 - -- T-- GAATG- AGG AGGG GG
AACTTTGTGGAATGGTAAGG TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA ATTTTT TTGTTT C
ATTTTTAGGGTTGTTTGGCC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
AGAACAAGAGAAATAACTGC TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA AACAAG /
AGAAAACACATATGGTTGGA G AA TAT AAAAGA CAA G--- AC
AACCATGCGCTTGTGACTT

GAM1334 ACTTATGCCCTGGTGCCTCC 1307 AGAGGTGGCA 2983 A -- G CT CTTCA GCAA
TTGGCTCTTCACAGGATGCA GGTTGCAGAG ACTT TGC CCTG TGCCTC TGGCT CAGGAT A
AAAACAAATCCTGCCAGCTA GT |||| ||| |||| |||||| ||||| ||||||
GAGGTGGCAGGTTGCAGAGG TGGA ACG GGAC GTGGAG ATCGA GTCCTA A
T G TT G -- CC--- AACA

GAM1335 GACAATATGTACCACAGTAC 1308 CACAGTACTG 2984 ATATG C T T G A TCTAAC TGG
TGGTGAGTAATGATAGTCTC GTGAGTAATG GACA TACCA AGTAC GGTGAG AAT AT GTC AAGG A
TAACAAGGTGGACCCTCCTT ATAG |||| ||||| ||||| |||||| ||| || ||| ||||
CATGACAGTAGTTCTTACTG TTGT ATGGT TCGTG TCATTC TTG TG CAG TTCC C
TGCTCTGGTAACACTGTT CACA- C - - A A TAC--- TCC

GAM1336 CCATATCCAGAGAACTCAAG 1309 TCCAGAGAAC 2985 C GAA- ----- GTGAA GAT G AA

GTGTGAATACCAGATCCGGT TCAAGGTGTG CCATATC AGA CTC AAGGT TACCA CCG TTGGAG A

TGGAGAAAGGGTTCCAAGTG AATA ||||||| ||| ||| ||||| ||||| ||| |||||| GTGGTGACCTTGCGGAGAGA GGTGTAG TTT GAG TTCCA GTGGT GGT AACCTT G

AGATTTTGATGTGG T AGAA AGGCG ----- --- G GG

GAM1337 TGTTGGGTAGTGAGGTAGTA 1310 TGAGGTAGTA 2986 GTGAG --- TACT AC- A TG AT-- A- CA

GGTACTTTATAGACTTTTAA GGTACTTTAT TA GTAG TAGG TTATAG TTTTA TTT GAA TG TGA T

TTTTGGAAATTGATGACATC AGAC || |||| |||| |||||| ||||| ||| ||| || ||| CCTCAGGCATGTATTCTGGA GT CGTC GTCC AATGTC AAGGT AAG CTT AC ACT C

AATGGAATTCCTGTAACTTC ATGA- TGT TTC- CTT A GT ATGT GG CC CTGTGTCTGCAGTATGCCCT

ACA

GAM1338 AGGCCAAGCACCTGCGCCTG 1311 TGGGTCCGTC 2987 C CT -- TG CC--- A GG

TCCCTGAACGGGCACGGCCA TGTGCTTGAC AGG CAAGCAC GCG CC T CTG ACGGGCAC C

GTGTCCGTACAGCATCTGTG TT ||| ||||||| ||| || | ||| |||||||| GGTCCGTCTGTGCTTGACTT TTC GTTCGTG TGC GG G GAC TGCCTGTG / A TC CT GT TCTAC A AC

GAM1339 ACCCAGCTGAGTGTGGTAGT 1312 TGAGTGTGGT 2988 - TG TGC-------- TC GAAG A GGG A

GTGTGCCTGTAGTTCTGAGA AGTGTGTGCC TG AGTG GTAGTGTG CTGTAGT TGA TTG GGT AAG T

AGTTGAGGTGGGAAGATTGC TGTA || |||| |||||||| ||||||| ||| ||| ||| ||| TTGAGCCCAGGAGATCAAGG AC TCAC CATCGTAC GACGTCG ACT GAC CCG TTC T

CTGCAGTGAGTTGTGATCAT C GT TAGTGTTGAGT GA AGAG - AG- G GCTACTGCACTCCAGCCTGG

GT

GAM1340 GACATTTCAATAATACAGGG 1313 TTCAATAATA 2989 AT - AG A--- ACA

TAAGTTCATAGCTACAAAGC CAGGGTAAGT GACATTTCA AATACA GGGTA TTCAT GCT A

AAGCCAACATGAGTGCTCAT TCAT ||||||||| |||||| ||||| ||||| ||| GTATTCTGAGATGTC CTGTAGAGT TTATGT CTCGT GAGTA CGA A C- A -- CAAC ACG

GAM1341 TGGTGGGAGGCCCTGTGTGA 1314 CTGTCGTGTC 2990 GG T TGTGA T - A CGA CA C

ACGTCAGCAGCCTGTCGAGC GGGCCTGACG TGGTG AGGCCC G ACG CAG C GCCTGT GCT TCGG T

TCATCGGCTAGCCGAGGCCA CTG ||||| |||||| | ||| ||| | |||||| ||| ||||
CAGGTAGTCTGTCGTGTCGG GTCGC TCCGGG C TGC GTC G TGGACA CGG AGCC
A
GCCTGACGCTG AG - TG--- T T A C-- -- G

GAM1342 ACTTTAATGCCTTCCTTAGA 1315 TAAGGAGAGG 2991 TTA - AGAAA --- GAAG
AACCTC
AATTATGTTGTATTGAAGTC AGGTGTATAG ACT ATGC CTTCCTT TTATGT TGTATT TCA
A
AAACCTCAATCACAATGAAC T ||| |||| ||||||| |||||| |||||| |||
AAATATATTTGCATAAGGAG TGA TATG GGAGGAG AATACG ATATAA AGT A
AGGAGGTGTATAGT --- T AGG-- TTT ACA- AACACT

GAM1343 CTTGGCCTCAAAGAGCTCAC 1316 AAAGAGCTCA 2992 G- -- CACA-- GA- AG- C
GGAGAAGA
ATTCTACTAGAGAAGGCACA CATTCTACTA CTTG CCTCAAA GAGCT TTCTACTA GA GCA
ACAT T
CATGGAGAAGATTATAATAC GAGA |||| ||||||| ||||| |||||||| || ||| ||||
AATGTTGTAAATCCAATAGT GAAC GGGGTTT TTTGA GAGATGAT CT TGT TGTA
T
AGAGATAACCAGTTTATTTT GA TA CCAATA AAC AAA - ACATAATA
GGGGAGCAAG

GAM1344 GAAGCTGCTCAGTTGGAGAA 1317 AAGCTGCTCA 2993 TG A- TG A AAGT AA AAA-
A--- GGG
AGTAAGGAAGCAAACATTGT GTTGGAGAAA GAAGC CTC GT G GA AAGG GC CATTGTT
CCGT G
TACCGTGGGGGCAATGGAGA GTAA ||||| ||| || | || |||| || ||||||| ||||
GGACAGTGAGGAGCCCTTTA TTTCG GGG TA C CT TTCC CG GTGACAG GGTA
/
TCCTGATAAGGGTGGCTTT GT AA GT - AT-- -- AGGA GAGA ACG

GAM1345 GGCGAGATTTCCCAGAAGAA 1318 AAGTCGCCAT 2994 TCCC GAA----- GC TT -
TTGCC G
GTCGCCATTGTTGAAGAACT TGTTGAAGAA GGCGAGATT AGAA GTC CATTG GAA
GAACT GCA A
TTGCCGCAGACATGCTGATG CTTT ||||||||| |||| ||| ||||| ||| ||||| |||
GTTCTTTCTCTGATGAGATG CCGTTCTAA TCTT TAG GTAGT CTT CTTGG CGT
C
AACACCATTCTTGATAATCT TAGT ACCACAAG A- CT T TAGT- A
TGCC

GAM1346 AGTCCATACTTAACATACAC 1319 AAAACTGTGA 2995 T A ATA - C--- TTTTC AT
GTCCACTTTTCACCTATGCC GGTTAAGATG AG CCAT CTTAAC CAC GT CAC ACCT G
AGGTACTGTGTAAAACTGTG GCT || |||| |||||| ||| || ||| ||||
AGGTTAAGATGGCT TC GGTA GAATTG GTG CA GTG TGGA /
- - GA- T AAAT TCA-- CC

GAM1347 GCTGTGTTGCAGTGCATTGT 1320 GTGCATTGTG 2996 GCA A TG G TG GGA TG GA CCT TG
GTTGCAGGATTGGGAAGGGC TTGCAGGATT GCTGTGTT GTGC T T T CA T G AGGGCA GTGC G
ACCTGTGCTGGTTGCACTTG GGGA |||||||| |||| | | | || | | |||||| |||| CTTTGATTGAATGTGGAATG TGACGTAG CATG A A G GT A T TTTCGT CACG / AAGTACGAAGATGCAGT AAG A GT A GT A-- GT AG T-- TT

GAM1348 ATGCACATCTTAAAAATACA 1321 ATACAGTAGA 2997 A AAAAA AGTA ACAACCA AG T
GTAGAACAACCATTGACATA ACAACCATTG ATGC CATCTT TAC GA TTGACAT TG T GTGTTTACAGCATGTTAAGT ACAT |||| |||||| ||| || ||||||| || GTCGTAAGTAATCTGGGGAT TGCG GTAGGG ATG CT AATTGTA AC T GGCGT - GTCTA AATG GTG---- CG A

GAM1349 TGTACATTCAACAAGTCTTT 1322 TTCAACAAGT 2998 - AACAAG TAT A CTCT- C ATTGAGCACCTACTCTGTGC CTTTATTGAG TGTAC ATTC TCTT TG GCACCTA GTGC C CCAGCACTGCACTAGGTGCC CACC ||||| |||| |||| || ||||||| |||| ATGAGAATACAAGAGTAGTA ATATG TGAG AGAG AC CGTGGAT CACG / TA A AACATA T-- - CACGT A

GAM1350 GGGCAGCTCGTCAGGCTGCG 1323 TCGACCACTC 2999 A C G CCCTG--- T T GGGCCCTGTTCAGTCTGTTG TGAGCTTGGC GGGC GCT GTCAGGCT CGGGG TTCAG CTG T
CAGCTGAAATCGACCACTCT TGGC |||| ||| |||||||| ||||| ||||| ||| GAGCTTGGCTGGCAGTCC CCTG CGG CGGTTCGA GTCTC AAGTC GAC / A T - ACCAGCTA - G

GAM1351 AAGGGTTGTTTTGTTGTTAG 1324 TGAAGCTAGA 3000 T TGTTGT AA A-- GTCCATT
GTAAATAGATATTAGGCAGT TACCTAAAGC AAGGGT GTTT TAGGTA TAG TATTAGGCA T
CCATTTCTAAAATATGCCTG TACC |||||| |||| |||||| ||| ||||||||| ATGAAGCTAGATACCTAAAG TTCCCA CGAA ATCCAT ATC GTAGTCCGT C CTACCCTT T ------ AG GAA ATAAAAT

GAM1352 GTTTGTGCTGACAGAACGAG 1325 TGACAGAACG 3001 TG GA GA AGAG- T GAAG--- A
AGGGTGCTCTGAAGTATTTC AGAGGGTGCT GTTTG CT CA ACG GG GCTCT TATTTC A AACAGAAATGATGCCAAGGA CTGA ||||| || || ||| || ||||| |||||| GCCCAAGGCCGTGATGAAGA CGAGC GA GT TGC CC CGAGG GTAAAG C TCGAGC TA A- AG CGGAA - AACCGTA A

GAM1353 CTGATTAACTACCATGTTGT 1326 ACTGCAGTGA 3002 G -- A A TG A-- AAA C CC- - CAAAA
AGGTTTTGGAAAAGCTTCGT CAGGCAGCCT ATTAA CT CC TGT T GGTTTTGG AGCTT GTC TTGG AC G
CCCTTGGACCAAAAGCTGAA TAGT ||||| || || ||| | |||||||| ||||| ||| |||| ||
GTATCAAATTGACAAGCTGA TGATT GA GG ACA G TCAGAACT TCGAA CAG AACT TG /
TCAAGACTGCAGTGACAGGC G CC C - GT ACG AG- - TTA A AAGTC
AGCCTTAGTGAG

GAM1354 ATGAAGTCAACTGGTATCTG 1327 TTTTCACGGC 3003 G AA - ATC A A- - AA TAG- TTAC
ATGGGAATGGGCAATGAAAT CATAGCTTCC ATGAA TC CTG GT TG TGGGA TG GGC TGAAA AC A
AGACTTACACACTGTACATT AATA ||||| || ||| || || ||||| || ||| ||||| ||
TTCACGGCCATAGCTTCCAA TATTT AG GAC CG AT ACCTT AT CCG ACTTT TG /
TACAAGCACAGGGGAGTTTA G GG A AAC A CG A GC TACA TCAC
T

GAM1355 TTGAAGGCATGAGGTTGGCT 1328 AGGCATGAGG 3004 TG ----- A AACA GG
ATATCCAACATTGCGTGGGA TTGGCTATAT TTGAAGGCA AGGT TGGCT TATCC TTGCGTG A
CATATGCGAGGATGAGGCCG CCAA ||||||||| |||| ||||| ||||| |||||||
TCGCTGCCTTGCTTTCAG GACTTTCGT TCCG GCCGG GTAGG AGCGTAT /
-- TCGCT A ---- AC

GAM1356 ATGAAGTCAACTGGTATCTG 1329 TTTTCACGGC 3005 G AA - ATC A A- - AA TAG- TTAC
ATGGGAATGGGCAATGAAAT CATAGCTTCC ATGAA TC CTG GT TG TGGGA TG GGC TGAAA AC A
AGACTTACACACTGTACATT AATA ||||| || ||| || || ||||| || ||| ||||| ||
TTCACGGCCATAGCTTCCAA TATTT AG GAC CG AT ACCTT AT CCG ACTTT TG /
TACAAGCACAGGGGAGTTTA G GG A AAC A CG A GC TACA TCAC
T

GAM1357 CATTCTTTCACATGTTGCTA 1330 TTCACATGTT 3006 CT -- TAA---- T
AGTTGTATTTTATAGCCCAG GCTAAGTTGT CATT TTCACAT GTTGC GTTGTA T
AATGCGATCTATGTGGGTAA A |||| ||||||| ||||| ||||||
ATG GTAA GGGTGTA TAGCG CGATAT /
AT TC TAAGACC T

GAM1358 GAATTGTCAACTGTGCTTTG 1331 TGAAGCTGCT 3007 CT--- - TG GCCCAGA TC A- T C T
GGGCCCAGACATTTTTTTCT CATCTTGATC TCAA GT GCTT GG CATTTTTT TATTTT CTA GAG TGTT A
ATTTTACTATGAGCTGTTTA AAAA |||| || |||| || |||||||| |||||| ||| ||| ||||
TTGATATTTCTAGGAGAGAT AGTT CG CGAA CC GTGAGAAA ATAGAG GAT CTT ATAG T

AAAAGAGTGCCAAAACCTGA CTACT T GT AAAACC- -- AG - T T
AGCTGCTCATCTTGATCAAA
ATTC
GAM1359 GCTTTTGCTCCAGATGGTTC 1332 CCAGTGCCTT 3008 TT TCC T ATACTTT T - AA
TC ACA
ATACTTTGCTTGGTCACAAG CAGAACTTTC GCT TGC AGA GGTTC GCT GG TCAC
GGACA GC G
GACATCGCACAGTAAAGCTT TCTT ||| ||| ||| ||||| ||| || |||| ||||| ||
GTTCCGTGGTCCCAGTGCCT CGG ACG TCT TCAAG TGA CC GGTG CTTGT CG T
TCAGAACTTTCTCTTGCATG T- TTC T ACTTCCG C T C- T- AAA
GC

GAM1360 CCCGTGCCACCTAAGACCCG 1333 ACCCGCAGAT 3009 - G -- A CG A--- G TC CC
TA
CAGATCCGTCATCTGTCCGT CCGTCATCTG CC CGT CCA CCTA GACC C GATCC TCA TGT
GTGTT C
GTTTACGTTAGCGCACATGA TCCG || ||| ||| |||| |||| | ||||| ||| ||| |||||
GGGATCATGAGTAGGTCTGG GG GCA GGT GGGT CTGG G CTAGG AGT ACA
CGCGA G
GAATGGACGAGG A - AA - AT AGTA G -- -- TT

GAM1361 TGTTTGGGATCTGGTCTGAG 1334 GGAAGTTGCT 3010 TC T G C GGCA TG TA A - T
C ---- AT
GGGGCGGACGGCACTGATAT GGCTTCAGCT TGG CTGAG GGG GGAC C A TCA C GCTG
GGCC GC TCTC G
CAACGCTGTGGCCCGCTCTC GATG ||| ||||| ||| |||| | | ||| | |||| |||| || ||||
ATGATGGGAAGTTGCTGGCT ATC GATTT TCC CTTG G T AGT G CGAC TCGG CG
AGGG /
TCAGCTGATGACTTTGGCAA -- - G A AAAC GT TC A T T T TTGA TA
AGTTCACCTGTTTAGCTACC
CCTGCTGTCAG
GAM1362 TTCTCCATGATGACAAGGAA 1335 TGCTGGGCTC 3011 --- AGTC- CCATCC CACAG
CTCCCT GA- G A
GTCTCTGCCATCCTGGCCAC CCTGCATGAC AAGGA TCTG TGGC TGCTGGG
GCAT CA TG A
AGTGCTGGGCTCCCTGCATG AGTG ||||| |||| |||| ||||||| |||| || ||
ACAGTGAAAACAGTGACAAT TTCTT AGAC ACCG ACGACCT TGTA GT AC A
GTTCCAGCAAAGCCACCAGA GAA GAAAC C----- AA--- ------ ACA G A
CAAAGTTCTTAAGGTCACAG
GAGAG
GAM1363 GAAGACTTCCTAAATTTGCA 1336 TTTGCACATT 3012 AC A TTGCA TTGCC
ACCAT
CATTAGCTAGATTGCCATTA AGCTAGATTG GAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
GCACCATTAGAGAGTTGATC CCAT |||| ||||| ||| |||||||||| ||||||
TTTGGCTAATGATTATTCAG CTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GAAAATTTC AA C TTA-- C---- AGAGA

GAM1364 CTGGAGTGCAGTGGTGCGAT 1337 TACAGTAGCT 3013 -------- TG C C C C -- CC--
ATT
CTTGGCTCACTGCAACCTCC GGGATTACAG TGC GATCT GCT ACTG AA CTC GC CTC
GGTTGAGGCA C
GCCTCCCGGTTGAGGCAATT ACAT ||| ||||| ||| |||| || ||| || ||| ||||||||||
CTCCTGCCTCAGCCTCCCGA GCG TTAGG CGA TGAC TT GAG CG GAG
CCGACTCCGT /
GTAGCTGAGATTACAGTAGC TACAGACA GT - A A T AT CCCT CCT
TGGGATTACAGACATGCGCC
ACCATGTCCAG
GAM1365 GGGATGCTAATTTGCAATCA 1338 TGACAAATGA 3014 GG AAT - GG ATGAGAA A
CA
GGTGTCATAATGAGAATAAC TTGACAAAGC G ATGCT TTG CAATCA TGTCATA TA CC A
CCAAACTGGATAAATGTGAC ATTT | ||||| ||| |||||| ||||||| || ||
AAATGATTGACAAAGCATTT C TACGA AAC GTTAGT ACAGTGT AT GG A
C TT --- A AA AA----- A TC

GAM1366 GGCTGTCCTCAGGGTTCAGC 1339 TATAACAGCC 3015 CTC TCA ATG --- - GC
TTA CT
TATGATAGAGACTCAGCTGG ACCTTGACAG GGCTGTC AGGGT GCT ATAGA GACT CA
TGGC GG T
CTTAGGCTTCATCCACTGCC TC ||||||| ||||| ||| ||||| |||| || |||| ||
AATGAAGTCAAATTTATAAC CTGACAG TTCCA CGA TATTT CTGA GT ACCG CC C
AGCCACCTTGACAGTC --- C-- CAA AAA A A- TCA TA

GAM1367 GTAAACTCCAACCCAGAATG 1340 TTGGAGCAGG 3016 AACCC - - TA AA T CA TCT
AC- CT
GGGAAGAATACTGAATTAGC TTTCATTCTC AGAAT GGGGAA GAA CTG TTAGC GAG CAT
GGAC AATT G
TGAGCACATTCTGGACACAA CAAT ||||| |||||| ||| ||| ||||| ||| ||| |||| ||||
TTCTGACCAATTTCAGTCTC TCTTA CCTCTT CTT GAC GGTTG CTC GTA TCTG
TTAA A
ATGATCTCTGTTGGAGCAGG TTTTC A A TG GA T TA C-- ACT CC
TTTCATTCTCCAATTCTCTT
TTACAGAAC
GAM1368 TAGATTTTGTTTCAAACTCA 1341 AACTCATTGT 3017 AA- CATT- T AT-- GAGCAG TTA
A - TCTA
TTGTTTGATGATGGAGAGCA TTGATGATGG TTTCA CT GT TGATG GGA CAAA CA
TAG TGGT C
GCAAATTACAATAGTGGTTC AGAG ||||| || || ||||| ||| |||| || ||| ||||
TACAGTTGCCACCTAATGAA AAAGT GA CA ATTAC CCT GTTT GT ATC ACCG
/
TTTTGAAGGATCCTTGGCAT ATA TCTAT T GGTT AGGAA- TAA A C TTGA
TATACTATCTAGATATGAAA
CATATGTTCTA
GAM1369 TTAAATTTCTGTATCTGTCG 1342 TAAGCTAGGG 3018 TT T TC G GATT--- G
CCCTGAGCTGATTTTGAAAG GTTAGTATAG TTAAAT CTGTA CTG GCCCT AGCT TT A
ATGGTATAAGCTAGGGGTTA TTGT |||||| ||||| ||| ||||| |||| ||

GTATAGTTGTTTAA AATTTG GATAT GAT TGGGG TCGA AG A
TT - -- A ATATGGT A

GAM1370 TTTAAAAGACCTTAAGCTGG 1343 AAGCTGGCAT 3019 AAA - A G GAAG- C -----
GTAG CT
CATTGTGAAGGAACACCATG TGTGAAGGAA TTTA GACC TTA GCTG CATTGT GAA ACC
ATG ACT T
GTAGACTCTTTTGGTAACAT CACC |||| |||| ||| |||| |||||| ||| ||| ||| |||
GTATCGGTATTTAAGTGACA AAGT TTGG AAT TGAC GTAACA TTT TGG TAC TGG
/
ATGCAGTATAACGGTTGGTG GG- C A - GTGAA A CTATG AA-- TT
AA

GAM1371 GTCTCCCTCTCTTGTTCCCT 1344 TATCCCAGCA 3020 TCC A T A- AA - T-
ATGAGGC AC T
AGTTCAGTATGCCCAATAAA CTTTGAGGGG TGT CT GT CAGT TGCCC TAAA TGTT GATGA
CAGGC GG G
TGTTTGATGAATGAGGCCAG CAGA ||| || || |||| ||||| |||| |||| ||||| ||||| ||
GCACGGTGGTCCACGCCTGT ACA GA CG GTCG ACGGG GTTT ACGA CTATT
GTCCG CC G
TATCCCAGCACTTTGAGGGG CTA C - AG GA C CC ------- CA T
CAGAGCTGGCCAGATCACAA
GGTCAGGAGAT
GAM1372 CAGGAGGGTTTCACCCCATG 1345 AGGGTTTCAC 3021 AG TT A - G- - GG
GGTAGTTGGGCCAAACTCGC CCCATGGGTA CAGG GG TC CCC CATG GT AGTT G
GACATGAGGGAGGTTCCACT GTT |||| || || ||| |||| || ||||
TG GTTC CC GG GGG GTAC CG TCAA C
A- TT A A AG C AC

GAM1373 TTCCAGTGCACATGTTCCCT 1346 TGTCTCGCTT 3022 A CT GGC AGCAA GAGTT
AG-- CAC GAA
TGGGCTGAAGTAGCAAGGAT CACAGGAACA TGTTCC TG TGAAGT GGATACA GCAC
GTCT TGA G
ACAGAGTTGCACAGGTCTCA GTGT |||||| || |||||| ||||||| |||| |||| |||
CTGAGAAGATATCACAGGAC ACAAGG AC ACTTCG TCTGTGT CGTG CAGG
ACT /
AAGCGTGCTATGTGTCTCGC - -- --- C---- AT--- CGAA AC- ATA
TTCACAGGAACAGTGTGAAG
AG
GAM1374 CCTTGGTGCCCCTCGACCAG 1347 TTGGTGCCCC 3023 TTG - GA-- GC GTG AC- C
CGTCCTTGTGGGTACAGGTT TCGACCAGCG CC GTGC CCCTC CCA GTCCTT GGT
AGGTT A
CAGGACTTAAGGCCAAAGGA TCCT || |||| ||||| ||| |||||| ||| |||||
CATGGGCGTGAGGGTGTACG GG CATG GGGAG GGT CAGGAA CCG TTCAG /
CCGG CCG T TGCG A- A-- GAA G

GAM1375 GATTTGGGGCTGTGCCTTAG 1348 TGATAGTAAT 3024 -- G CC TT-- CC GCAAA

TTCTCCCATCGGCAAAAGCA CTAGCTCACA GATT TG GGCTGTG TTAG CT CATCG A
TCACGATGATAGTAATCTAG GTTG |||| || ||||||| |||| || |||||
CTCACAGTTGTAACGATC CTAG AT TTGACAC GATC GA GTAGC G
CA G TC TAAT TA ACTAC

GAM1376 CTGTGGCCAGGGTTCACATG 1349 TTCACATGTG 3025 GC ---- GG AA TA CCATCCG
TGGCCAAGTTATCATGTCCA GCCAAGTTAT CTGTG CAGGGT TCACATGT CC GT TCATGT A
TCCGACCAAGCTGCATGAAC CATG ||||| |||||| |||||||| || || ||||||
AAGGAGCATGTGATGAGGCC GACGC GTCCCG AGTGTACG GG CA AGTACG /
CTGCGCAG -- GAGT A- AA -- TCGAACC

GAM1377 TCTGTGTGAAGCATCACTTT 1350 ATCACTTTGC 3026 ACT --- TAA - GG GCA CT ATTAA TC
GCAGGGATTACTAATGGTGG AGGGATTACT C TTGC AGGGATTAC TG GT GGCA GGT GTGA GTTTA T
GGCAGCAGGTCTGTGAATTA AATG | |||| ||||||||| || || |||| ||| |||| |||||
AGTTTATCTCTTTGAGCTCA G AGCG TCCTTAATG AC CA CTGT TCG CACT CGAGT C
CCGCTCATGTCAACACAGAT --- AAA TAG A A- AC- C- ----- TT
GTAATTCCTAAAGCGAGATG
CATTTGCCGGG
GAM1378 TCTTTGAGTTTTATACCTTT 1351 GTAGCATTTT 3027 A ---- C GTAG - G G TT T
GTAGCATTTTAGATGACATT AGATGACATT TCTTTG GTT TTATAC TTT CATTT TA AT ACA GTG T
GTGTTTGTACTTTGTGTGTA GTG |||||| ||| |||||| ||| ||||| || || ||| |||
CGAGTGAAGAATGTGTGAAT AGGAAC CAA AGTGTG AAG GTGAG AT TG TGT CAT T
AAAACCCAAGGA C AATA T AA-- C G - TT G

GAM1379 TGCTGGGATCCTCTGACTTG 1352 TGGGATCCTC 3028 - TC C - T - TC ---- G TT- CT
AGCTCTCCTGAAGCCAGCAT TGACTTGAGC TGCTGG GA CT TG AC TG AGC TCCTG AAGCCA CA TCT C
TTCTCTCTCAGATATTGGTG TCTC |||||| || || || || || ||| ||||| |||||| || |||
GCTTGATCCAGGGATGTTAC ACGACC CT GA AC TG AC TTG GGGAC TTCGGT GT AGA /
ATGTGCAAAGTTCTCCAGCA T T- A G T A TA CTAG G TAT CT

GAM1380 AGGCTTTGCACAGTGGCTCA 1353 TTGCACAGTG 3029 TT CT GTCATGC A T
CTCCTGTCATGCCAGCACTT GCTCACTCCT AGGCT GCACAGTGGCTCA CCT CAGC CTT G
TGGGAGGCTGAGGCATGAGC GTCA ||||| |||||||||||| ||| |||| |||
CATTGTGTCTGGCCT TCCGG TGTGTTACCGAGT GGA GTCG GAG /
TC AC ------- - G

GAM1381 TCAACCACAGTGCATTGTAT 1354 GTGCATTGTA 3030 AC---- TG ---- A GT-------- C
AG TA
GTGTGAATTACGTTGTGAGT TGTGTGAATT AACC AG CAT TGT TGT GAATTA
GTTGTG TGG T
GGTATTATTCAGCACGACTT ACGT |||| || ||| ||| ||| |||||| |||||| |||
GATTTTCTCCCTTCAACAAA TTGG TC GTG ACA ACA TTTAGT CAGCAC ACT
T
CAGAATGTGTCCTTAAACCG CCAAAT CT TAAG A ACTTCCCTCT T G- TA
GTTGA

GAM1382 AGATACAGGACTGGTGAAAT 1355 TACAGGACTG 3031 TGG AAGATG GA C -- C T-
T- AC
GAAGATGGCTTATGATGAAA GTGAAATGAA TGAAATG GCTTAT TGAAAC TG CTG CTTCT
AAAA TGCA C
CCTGCTGCCTTCTTAAAATT GATG ||||||| |||||| |||||| || ||| ||||| |||| ||||
GCAACCACTGCACCTTTTCT ACTTTAT TGAATG ACTTTG AC GAC GAAGG TTTT
ACGT /
GGAAGCCAGATCAAGTTTCA AA- AACA-- A- A TA C TC CC CA
AGTAAGTACAATATTTCAAA
CCTCTGTAACT
GAM1383 GGCGAGCAGTGTTTTTTGTT 1356 TGTGCATGCT 3032 G T TTTT TTCT - T--- TTA
TG
CTGTTTGTGCTCATGCTTAA TTGCCACAGA GGCGA CAG GT TG GTTTGTG C CATGC
ATTTGAA T
TTTGAATGTCTTTCAGGTGT CCTC ||||| ||| || || ||||||| | ||||| |||||||
GCATGCTTTGCCACAGACCT CCGCT GTC CA AC CAGACAC G GTACG TGGACTT
/
CACCACTCTGTCGCC - T CC-- TC-- C TTTC TG- TC

GAM1384 GCGCTCCTCGTCAGTCCCTG 1357 TCCCTGAGAC 3033 TC T TC C A A CC
AGACCCTAACTAGTGAGGTT CCTAACTAGT GCGC CTCG CAG CCTGAGA CCTAACT GTG
GGTTTA G
TACCGTTTAAATCCACGGGT GAGG |||| |||| ||| ||||||| ||||||| ||| ||||||
TAGGCTCTCGGGAGCTGCGA CGTG GAGC GTC GGGCTCT GGATTGG CAC CTAAAT /
GTCGTGC CT - GA C G - TT

GAM1385 TCGGGTTATACTTCATCACT 1358 TTCATCACTG 3034 ATA-- TC GGG AA CT
GGGTAAGTCTCCAAGGACTC GGTAAGTCTC TCGGGTT CTTCA ACT TAAGTCTCC GGA C
ATTCTAGGGAGGCTTAGGTT CAAG ||||||| ||||| ||| ||||||||| |||
GAAGCCTAGAACTCGG GGCTCAA GAAGT TGG ATTCGGAGG TCT /
GATCC -- --- GA TA

GAM1386 GGAAGCTTAATTGATCAGCA 1359 TCAGCAGGTA 3035 AAG --- AGCA TATTGA TT
GGTATTTATTGAACACTTAC TTTATTGAAC GG CTTA ATTGATC GGTATT ACAC A
TGTGTGTCTAATGCTCAGAT AC || |||| ||||||| |||||| ||||
TAGTATGTAAGAGCC CC GAAT TGATTAG TCGTAA TGTG /
GA- GTA AC-- TCTG-- TC

GAM1387 AGGCTGCAGAACATGGAGGT 1360 TTCCTGCCTC 3036 -- ACAT T CC CT
CACCGATGCTTGAACATTCC CCTATTTGCC AGGCT GCAGA GGAGG CA GATG T
TGCCTCCCTATTTGCCAGGC AGGC ||||| ||||| ||||| || ||||
TT TTCGG CGTTT CCTCC GT TTAC G
AC ATC- - CC AA

GAM1388 GCTTGATATTCTTTACCTTG 1361 TACACCAAAT 3037 - TT --- AT--- G --- C - TTT
GGTATTCTTGTGAATATTTG ACAATTCAGA CTTG ATATTC TACCTTGG GT TCTT TGAA TATTTG TG AA T
CTGAATTTTCATTTACACCA AGAC |||| |||||| |||||||| || |||| |||| |||||| || ||
AATACAATTCAGAAGACAGA GAAT TGTGAG ATGGAACC CG AGAA ACTT ATAAAC AC TT /
GGCTTTCCAAGGTATGAGTG G T- TTT GAGAC G AAC C A TAC
TGTAAGT

GAM1389 GAGACAGAACCGTTCACTCT 1362 AGACAGAACC 3038 A A ACT - AA-- G
TCCGGAAAGGGGGCTGAAAC GTTCACTCTT GAG CAG ACCGTTC CTTCC GG AG G
CAGGGAGCCGAGTGGTATTG CCGG ||| ||| ||||||| ||||| || ||
CTC CTC GTT TGGTGAG GAGGG CC TC G
- A CC- A AAAG G

GAM1390 GGTCTGTGTGAAGCATCACT 1363 ATCACTTTGC 3039 A ACT GC TAATG G- GC TCT A- TT
TTGCAGGGATTACTAATGGT AGGGATTACT A GCATC TT AGGGATTAC GTG GGCA AGG GTGA TTAAG A
GGGGCAGCAGGTCTGTGAAT AATG | ||||| || ||||||||| ||| |||| ||| |||| |||||
TAAGTTATCTCTTGACCTCA T CGTAG AA TCCTTAATG CAC CTGT TCC CACT AGTTC T
CCCTCATGTCAACACAAATG A AAC A- TAAA- AA AC --- CC TC
TAATTCCTAAACAAGATGCA
TTGCCAGTCT
GAM1391 CTGCTGCCTGACTACCTGGC 1364 TGCCTGACTA 3040 C T CT TA T - ------- - C AC- T
TGCCATAGATGAGGCCCTGG CCTGGCTGCC TACC GG GCCA GA GAGGCCC TGGC AGC CTTGCA GTG GC C
CAGCCTTGCACGTGACGCTC ATAG |||| || |||| || ||||||| |||| ||| |||||| ||| ||
CAGTTCCCACTGCAAGAGTT GTGG CC TGGT CT CTTCGGG ACCG TTG GAACGT CAC TG C
CATCCTGGCCATGGGCTTCT - T -- C- T T GTCCTAC A - CCT A
TCCTGGTCCTGGTGATGGAG
CAG
GAM1392 TCCTCAGCGTGTTAACTGAA 1365 AAGCTGCCAT 3041 C G AAC A- C TGA
GCCTTGTTGAGTTTTACAAA TGGAGATCTG TCCTCAG GT TT TG AGC TTGT G
GCTGCCATTGGAGATCTGGG GGGG ||||||| || || || ||| ||||
GG GGGGGTC TA AG AC TCG AACA T

- G GTT CG A TTT

GAM1393 GCTCCAAAGAACCAAGAGTG 1366 CATTTCACTT 3042 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1394 TTAAATAACCCGGCATGGAG 1367 TATTGCACGT 3043 AA C A ------ TT T
CAGTTTGGTTTCCACCCTAT GGTCCGGCCT TT ATAACC GGC TGGA GCAGT GGT T
TGCACGTGGTCCGGCCTGGT GGTT || |||||| ||| |||| ||||| |||
TATGAAA AA TATTGG CCG GCCT CGTTA CCA C
AG T - GGTGCA TC C

GAM1395 CATGGATCCCAAATATTTAC 1368 TCCCAAATAT 3044 -- CAA TT AA- T AA
AAAGCCATCAGAACCACCTG TTACAAAGCC CATGGA TCC ATA TACA GCCA CAG C
TGGCAAATGTATTGTAGGAT ATCA |||||| ||| ||| |||| |||| |||
ATTCGTG GTGCTT AGG TGT ATGT CGGT GTC C
AT A-- T- AAA - CA

GAM1396 GCCTCCATTATGTACTATAT 1369 TACTGTATGA 3045 TATA- ATGAT GACT G-
TTCTT GT
ATGTACTGTATGATGATGTG TGATGTGACT TGTAC TATGTACTGT GATGT GGAT
AGGATG TGACT T
ACTGGATGAGGATGTTCTTT GGAT ||||| |||||||||| ||||| |||| |||||| |||||
GACTGTTAGAGGTTATGTAT ACATG ATGTATGACA TTACA TCTA TTTTAT
ATTGG A
TTTGAATCTTAGACATTTGC TAAGA CCGT- GAT- AG GT--- AG
CACAGTATGTAAGAATGTAC
AGAGGT
GAM1397 CAGGACTTTATGTGGATCCG 1370 TGGATCCGTA 3046 TATG CC TG- TT AT - GA----
ATA- AGA
TATGAGTTGGCTTCATTACG TGAGTTGGCT T TGGAT GTA AG GGCTTC TA CGAGA
GAAAC AC G
AGAGAGAAACATAACAGAGG TCAT | ||||| ||| || |||||| || ||||| ||||| ||
CAGTGATGGTTTCAGAAAAT G ACCTG TAT TC CCGGAG AT GTTTT CTTTG TG
/
TTTGATATAGAGGCCCCTAA GA-- TT CAA C- AT A AAAAGA GTAG ACG
CTATTTGTCCAAGGAGTCTG

GAM1398 TTTAAGAAATACATTTCATA 1371 TTCATAAGGC 3047 A TACA TAAG A TACA A
ATTT
AGGCTATAGCTTACATAGAT TATAGCTTAC TTT AGAAA TTTCA GCT TAGCT TAGAT GTG
C

AGTGATTTCTGTAACGCATC ATAG ||| ||||| ||||| ||| ||||| ||||| |||
TGGGCTAAGTAAATTGAAAA AAG TCTTT AAAGT TGA ATCGG GTCTA CGC T
CTTTTCTGGAA G TCA- TAAA - ---- - AATG

GAM1399 CACCAGGGTTCCTTATTAAA 1372 TATCACAGCA 3048 A- G TATTA AAACT---- - GC
AGTGCAAACTGGGCTGGGCG CTTTGGGAGG CACC GG TTCCT AAAGTGC GGGC
TGGGC A
CATTGGTTCATGCCTTTTAT CCGA |||| || ||||| ||||||| |||| |||||
CACAGCACTTTGGGAGGCCG GTGG CC GAGGG TTTCACG TCCG ACTTG T
AGGTG AG G ----- ACACTATTT T GT

GAM1400 CACCAGGGTTCCTTATTAAA 1373 TATCACAGCA 3049 A- G TATTA AAACT---- - GC
AGTGCAAACTGGGCTGGGCG CTTTGGGAGG CACC GG TTCCT AAAGTGC GGGC
TGGGC A
CATTGGTTCATGCCTTTTAT CCGA |||| || ||||| ||||||| |||| |||||
CACAGCACTTTGGGAGGCCG GTGG CC GAGGG TTTCACG TCCG ACTTG T
AGGTG AG G ----- ACACTATTT T GT

GAM1401 GGAAGGTTCCAGAGTACAGA 1374 TGAGGCAGTA 3050 A T GGC G CTT TG
TGATC ACCT T
TGAGGCAGTAGGATGATACT GGATGATACT CCAGAGT CAGA GA AGTAG ATGATA GAG AG
TTTGGA GG A
TGAGTGAGTGATCTTTGGAA TGAG ||||||| |||| || ||||| |||||| ||| || |||||| ||
CCTGGTAGACCTGAGTTCAA GGTTTCA GTCT CT TTATT TACTGT CTC TC AAACTT
CC G
ATCTTGCTCCTGTCATTTAT - - GAA - C-- GT T---- GAGT A
TAAGTCTCTGACTTTGGCTA
AGTTCC
GAM1402 GGAAGGTTCCAGAGTACAGA 1375 TGAGGCAGTA 3051 A T GGC G CTT TG
TGATC ACCT T
TGAGGCAGTAGGATGATACT GGATGATACT CCAGAGT CAGA GA AGTAG ATGATA GAG AG
TTTGGA GG A
TGAGTGAGTGATCTTTGGAA TGAG ||||||| |||| || ||||| |||||| ||| || |||||| ||
CCTGGTAGACCTGAGTTCAA GGTTTCA GTCT CT TTATT TACTGT CTC TC AAACTT
CC G
ATCTTGCTCCTGTCATTTAT - - GAA - C-- GT T---- GAGT A
TAAGTCTCTGACTTTGGCTA
AGTTCC
GAM1403 AGATGTTCGCTCGTGCAGTA 1376 TGCAGTACTG 3052 TTC-- C CAG - A A T AT
CTGTGGTTAAATGACAATTT TGGTTAAATG AGATG GCT GTG TACTGTG GTTA ATG CAA TT
G
ATGTGGATTTGCATGTAATA ACAA ||||| ||| ||| ||||||| |||| ||| ||| ||
CACAGTGAGACACAGTAATT TCTAT TGA CAC GTGACAC TAAT TAC GTT AG /
TTATCT TTTAA - AGA A G - T GT

GAM1404 CACAAGTGATGGTCCAACTT 1377 GTAAGGATTT 3053 - -- T-- GAATG- AGG
AGGG GG

TGTGGAATGGTAAGGATTTT TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA ATTTTT TTGTTT C
TAGGGTTGTTTGGCCAGAAC TT |||||||| |||| ||||||| |||| ||| |||||| ||||||
AAGAGAAATAACTGCAGAAA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA AACAAG /
ACACATATGGTTGGAAACCA G AA TAT AAAAGA CAA G--- AC
TGCGCTTGTG

GAM1405 TATTGTCCCTTTTACCTCAA 1378 AGAGGAGTTG 3054 C TT --- - -- AA
GAGGCTGTAAAGAATAGCTA GTTGGAATAG TATTGT CC TTA CCTC AAGA GGCTGT A
GTCTTAGAGGAGTTGGTTGG TG |||||| || ||| |||| |||| ||||||
AATAGTG GTGATA GG GGT GGAG TTCT TCGATA /
A TT TGA A GA AG

GAM1406 CTGGACATTGATTCGCTGGT 1379 AATCACAGTC 3055 ACATT CT TTC T CT
TCTGGCTGTTGGTTCCTGGG ATTTTCCGAG CTGG GATTCG GG TGGCTGT GGTTC G
AGAATCACAGTCATTTTCCG TCCC |||| |||||| || ||||||| |||||
AGTCCCCAG GACC CTGAGC CT ACTGACA CTAAG G
C---- -- TTT - AG

GAM1407 GCCCTGGCAGGCACGATAGA 1380 TCATCAACTC 3056 C- C - T AA AAATACT TT
AGAAAATACTTGTTACACAT TCAGTTCTTG GCC TGGCAGG AC GA AG GA TG A
CCTCATCAACTCTCAGTTCT CCAA ||| ||||||| || || || || ||
TGCCAATGGT TGG ACCGTTC TG CT TC CT AC /
TA T A C AA ACTCCT- AC

GAM1408 GGAGGGAATTATAACAAGAT 1381 GTGCAGAAAA 3057 ATTATAACAA A CC AGAT G G TG AAA C CA
TGGGACCCAACCAGATGGCT GTTTCAAGGT A G TTGGGAC AACC GGCT TT TG CC GCA AGGAA A
GTTGTGTGCCAAAGCACAGG TTGT | | ||||||| |||| |||| || || || ||| |||||
AACAAACTTTTCTATGTGGG T C GGCCCTG TTGG TTGA AA AC GG TGT TCTTT A
TGCAGAAAAGTTTCAAGGTT ---------- - T- AACT A G GT G-- A TC
TGTCCCGGCTCTTTCC

GAM1409 CTTACCTTTTTCTTAGCTTA 1382 TAGCTTATTC 3058 AG GTG TG T G TT AT TTGTC -- TG
TTCGTGTTGCCTTACTGGTT GTGTTGCCTT TT CTTATTC T CCT ACT GT GT TCTGA GTAT TACTTCT A
TGTATTCTGATTGTCGTATT ACTG || ||||||| | ||| ||| || || ||||| |||| |||||||
ACTTCTTGAACAGGAGTAGA AG GGGTAGG G GGA TGA CA CG AGACT CATG ATGAGGA /
GTACTCAGATCGCCACAAGT -- AA- GT - A C- CT ----- AG CA
AGGTGGAAGGATGGGGAGAC
AGTGGGCAAG
GAM1410 CAGAGAGCTGTGTGCATGCT 1383 TCGCCTGGAC 3059 A-- - - G T T AACA- A C

GAGCAACACCACAGCCATTG CACAAGTTTG CAG GAGCT GTG T CA GC GAGC CC CAGC A
CTGAGGCCTGGGCTCGCCTG ACCT ||| ||||| ||| | || || |||| || ||||
GACCACAAGTTTGACCTG GTC TTTGA CAC A GT CG CTCG GG GTCG T
CAG A C G C - GGTCC A T

GAM1411 CAGCCTCCCACTGTGGTGCC 1384 TCGCCTGGAC 3060 CC - G T G A - AA CATAGA
- CA T
TGGTGGAGACCTGGCCAAGG CACAAGTTTG ACT GTGGT CC GGTG AG CCT GGCC GGTA
GCTGTG TG TGC G
TACATAGAGCTGTGTGCATG ACCT ||| ||||| || |||| || ||| |||| |||| |||||| || |||
CTGAGCAACACCACAGCCAT TGA CACCA GG CCGC TC GGG CCGG TCGT
CGACAC AC ACG /
TGCTGAGGCCTGGGCTCGCC TT A - T - - T AG TAC--- C A- A
TGGACCACAAGTTTGACCTG

GAM1412 GCTCCAAAGAACCAAGAGTG 1385 CATTTCACTT 3061 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1413 GGTGCACAAGTGATGGTCCA 1386 GTAAGGATTT 3062 - -- T-- GAATG- AGG
AGGG GG
ACTTTGTGGAATGGTAAGGA TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
TTTTTAGGGTTGTTTGGCCA TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
GAACAAGAGAAATAACTGCA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /
GAAAACACATATGGTTGGAA G AA TAT AAAAGA CAA G--- AC
ACCATGCGCTTGTGACT

GAM1414 GACATTGGATGGGACAGATG 1387 GGACAGATGA 3063 T T AG A GGAG ATT C
ACAGTGGAGCACATTGGTCC CAGTGGAGCA GACAT GGA GGGAC ATG CAGT CAC GGTCC
C
CCTCGGACCCGTGACTGCCG CATT ||||| ||| ||||| ||| |||| ||| |||||
TAGTCCCTCCATGTC CTGTA CCT CCCTG TGC GTCA GTG CCAGG T
- - A- C ---- C-- C

GAM1415 GTGATGGTCCAACTTTGTGG 1388 GTAAGGATTT 3064 G -- T-- GAATG- AGG AGGG
GG
AATGGTAAGGATTTTTAGGG TTAGGGTTGT GT ATGG TCCAACT TGTG GTA ATTTTT
TTGTTT C
TTGTTTGGCCAGAACAAGAG TT || |||| ||||||| |||| ||| |||||| ||||||
AAATAACTGCAGAAAACACA CG TACC AGGTTGG ACAC CGT TAAAGA AACAAG
/

TATGGTTGGAAACCATGC - AA TAT AAAAGA CAA G--- AC

GAM1416 GTGTAGACGGGGCACCAGAC 1389 CAATTTTACT 3065 ACG- A- G C G --------
TCTTCA
GGGGAGTCAAGTGGCCGGGG TTTGGTCACG GTAG GGGCACC GAC GGGAGT AAGT GCC
GGGGTGCT C
TGCTTCTTCACTGCCACCAG GTGC |||| ||||||| ||| |||||| |||| ||| ||||||||
CACTTCCTATTATTGGCAAT TATT CTCGTGG CTG TTTTCA TTTA CGG CTTCACGA
T
TTTACTTTTGGTCACGGTGC GACA CA G T A TTATTATC CCACCG
TCACAGTTATAC

GAM1417 CTTAGCTGCTTGCCTTTGGG 1390 GATAGTTTAG 3066 GG TT C ATT G G
GAAAAAT - AA
GACATTTTGCTGCACATTTT TGATGTACTA CCTTTGG ACATT GCTG AC TTAA AGGACT
GAAA AC AGTT A
AAGAGGACTGGAAAGAAAAA GGGG ||||||| ||||| |||| || |||| |||||| |||| || ||||
TACAGTTAAAACAAACTAGT GGGGATC TGTAG TGAT TG AGTT TCTTGG TTTT TG
TCAA A
CTATTTTAGGTTCTGTTGAT A- -- T AT- G A ATC---- A AC
AGTTTAGTGATGTACTAGGG
GAATGCTGGG
GAM1418 GGCTTAGGGCTAGTCGTTTG 1391 TTAGGGCTAG 3067 T CTA----- T- A TT
TGCTAAGTTAAACTAGGCTT TCGTTTGTGC GGC TAGGG GTCGTTTG GCT AG A
TAAATGACGCAATTCTCCCT TAAG ||| ||||| |||||||| ||| ||
GCGTC CTG GTCCC CAGTAAAT CGG TC /
C TCTTAACG TT A AA

GAM1419 GGGTCGCTCAGTTCATTGGT 1392 CAGTTCATTG 3068 A- ATT AAAACGG A G AG
AAAACGGGCACTGAGCGTAG GTAAAACGGG GGGTCGCTC GTTC GGT GC CT AGCGT C
CCAGCGCTGGGCGCATAGAC CACT ||||||||| |||| ||| || || |||||
CTGGAGCGAGGGCGACTT TTCAGCGGG CGAG CCA CG GG TCGCG /
AG GT- GATA--- C G AC

GAM1420 TTGTGGAAAGGATTAAGGCG 1393 TTGGAACTGG 3069 T A A GCGA TGAGA A CCG
ACCATGAGACCGTAGAGGCC ATTCATTCCC TTG GGAA GGATT AG CCA CCGT GAGG A
GAGCACCTCGCGGAAATTGG CAA ||| |||| ||||| || ||| |||| ||||
AACTGGATTCATTCCCCAA AAC CCTT CTTAG TC GGT GGCG CTCC /
C A G AA-- TAAA- - ACG

GAM1421 GCCTTTCTTTTAAATAACCC 1394 TATTGCACGT 3070 CTTTTAA C A ------ TT T
GGCATGGAGCAGTTTGGTTT GGTCCGGCCT GCCTTT ATAACC GGC TGGA GCAGT
GGT T
CCACCCTATTGCACGTGGTC GGTT |||||| |||||| ||| |||| ||||| |||
CGGCCTGGTTATGAAATCAG CGGAGG TATTGG CCG GCCT CGTTA CCA C
GAGGC ACTAAAG T - GGTGCA TC C

GAM1422 GAGGATTTACAAGTGGACTC 1395 TTTACAAGTG 3071 ATTTACA ACTC- TC TCT CT G
AGTTCCATCTTACAGGGCCT GACTCAGTTC GAGG AGTGG AGT CA TACAGGGC C A
CGAAAGGAGTCCTGTATTGT CATC |||| ||||| ||| || |||||||| |
TATTTTTCGTCACTACCTC CTCC TCACT TTA GT ATGTCCTG G A
A------ GCTTT TT T-- AG A

GAM1423 AGGGAACTGAAGTAAAGGTC 1396 ACTGAAGTAA 3072 AACTGA AG - A TA- TA
ACTAGTATTCTATGCTATTA AGGTCACTAG AGGG AGTAA GTC ACTAGT TTC TGC T
GCAACCGAGACTGGTAGACA TATT |||| ||||| ||| |||||| ||| |||
TTATTGCCCCT TCCC TTATT CAG TGGTCA GAG ACG /
CG---- A- A - CCA AT

GAM1424 GTATTGAAGTAGTACGTTTT 1397 TGAAGTAGTA 3073 - T TACG TT - T T C - AT
TGCATTATGCATGTCTCCAG CGTTTTTGCA GTA TTGAAG AG TT TGC ATTA GCA GT TC CAG
A
ATAGGTTGTGAACTTGCTGA TTAT ||| |||||| || || ||| |||| ||| || || |||
TGGCATTGAATATCTTCTTC CGT GACTTC TC AG ACG TAGT CGT CA AG GTT /
AGCTGC C T TATA TT G - T - T GG

GAM1425 TGGAGCAACACTCCATGAAG 1398 ACTCCATGAA 3074 ---- CCA- -- G CT
CTCTCCTC
GCATCTCTGTTTCTCTCCTC GGCATCTCTG TGGA GCAACACT TGA AG CAT CTGTTT
C
CGCTAAACCAAGCAGTTGTG TTT |||| |||||||| ||| || ||| ||||||
GCTTTTCAGCATAGTGTTGT ACCT TGTTGTGA ACT TC GTG GACGAA /
ATGTTCCA TGTA TACG TT G TT CCAAATCG

GAM1426 CAGCTCGGTCCCCGCGGTAT 1399 TACTGATACT 3075 G CCC TGTC C G
GTCTTACGTGTGAAAATACT GTGATCACAG CAGCTC GT CGCGGTA TTA GTGT A
GATACTGTGATCACAGAGCT AGCT |||||| || ||||||| ||| ||||
G GTCGAG CA GTGTCAT AGT CATA A
A CTA ---- - A

GAM1427 GTGAGAATAAGATGGAGTTT 1400 ACTCCAGTGA 3076 GA- AA TG A GTGGG - AAAC-
A- A GCT
TGTGGGATTGGAGCCAAACC AGGACTTGTC T GAAT GA G GTTTT ATTGGAG CC CCA
AGGGG GAT T
CAAAGGGGAGATGCTTGAGG AGAT | |||| || | ||||| ||||||| || ||| ||||| |||
ATCCTCCTGGTGGAAGTGGG A TTTA CT T CAGGA TGACCTC GG GGT TCCTC
CTA G
ACTCCAGTGAAGGACTTGTC AGG GA GT - AG--- A GTGAA GG - GGA
AGATTTGGAAC

GAM1428 GTATCATCTGGGAAATCTGT 1401 TCATCTGGGA 3077 A AAATC- C--- G-- GCC
CTCAAGATCTGGCCTCCCAC AATCTGTCTC GTATC TCTGGG TGT TCAA ATCTG T
GGATATGTTGAAGTAACAAG AAGA ||||| |||||| ||| |||| |||||
CTTGCCTAGAGATGC CGTAG AGATCC ACA AGTT TAGGC C
- GTTCGA ATGA GTA ACC

GAM1429 TAGACACTGAATTGGACATT 1402 TGCAAGTCTG 3078 T -- A ATTTC CT C
GATTTCCTTTTCTCTGCGTC TGATTTTGTG TAGACAC GAATT GGAC TTG CTTTTCT GCGT G
GAAATGTCAAGGAAAGTTGC TTTG ||||||| ||||| |||| ||| ||||||| ||||
AAGTCTGTGATTTTGTGTTT GTTTGTG TTTAG TCTG AAC GAAAGGA TGTA A
G T TG - GTT-- AC A

GAM1430 GATAATCTACCTCACTTTCC 1403 TTCCCTGTGG 3079 A TA CTTT - G A TTC G
CTGTGGCTATGTTCTGGGTT CTATGTTCTG GATA TC CCTCA CC CT TGGCT TG TGG T
TCCAATCAGGCCGAGTGGTT G |||| || ||||| || || ||||| || |||
TGAGGACGATGTC CTGT AG GGAGT GG GA GCCGG AC ACC T
- CA TT-- T - - TA- T

GAM1431 CTTTCAGTCTTTATTTGCAG 1404 CTTTCAGTCT 3080 CA- T TTT A AA ACCA TATATGAC
TT C CAC
CAAACTACCACTTTATATGA TTATTTGCAG GTCT TA GC GCA CT CTT AGG TGTGTGT
TGTA G
CAGGTTTGTGTGTCTGTACA CAAA |||| || || ||| || ||| ||| ||||||| ||||
CGCACATACACACACATATC CAGA AT CG CGT GA GAG TCC ATACACA ACAT
C
CTTAAGCTCGAGACAGGGTG AAC C TT- G GG CA-- CTCGAAT- T- C ACA
CGGCTTTACAGACCAAAAAG

GAM1432 CCAGTCTGCAGCTCCCAGCG 1405 TGCAGCTCCC 3081 CTG------ CT- - - T TCGAC
ACA
TGATCGACGCAGAAGACAGG AGCGTGATCG CCAGT CAG CC CAG CG GA GCAGAAG
G
TGATTTCTGCATTTCCGACT ACGC ||||| ||| || ||| || || |||||||
GAGGTAACTGATTCATCTCA GGTCA GTC GG GTC GC CT CGTCTTT G
CTGG CTCTACTTA AAT A A - TTA-- AGT

GAM1433 GCTCCAAAGAACCAAGAGTG 1406 CATTTCACTT 3082 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC

GAM1434 GACAGATGGACTAAAAGGAT 1407 AAAGGATTTT 3083 C A GA -- GG CTG
TTTATAGGGGCATGTCTGCT ATAGGGGCAT GACAGATGGA TAA AG TTT TATA GGCATGT C
TCATATGCTGGTATATCAGA GT ||||||||||| ||| || ||| |||| |||||||
GACTGTTATCCATTTGTT TTGTTTACCT ATT TC AGA ATAT TCGTATA /
- G AG CT GG CTT

GAM1435 TCCTTTTGACAAGAAATGTG 1408 TGACAAGAAA 3084 T - AAATGT C AA-- CTGTT T
GTCGTGAAAATTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA TTGGA GC
T
GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||
ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T
GA C G GTT--- - GGTA ----- T

GAM1436 CCTGGAGGCTCCTGTGCTCC 1409 TGTGCTCCGT 3085 T CC TCC CT -- ACC
GTGGTCTTCATCCACCGCCA GGTCTTCATC CC GGAGGCT TGTGC GTGGT TCA TCC G
GGAGCTGATAACCACCCTGT C || ||||||| ||||| ||||| ||| |||
ACATCGGCTTCCTGG GG CCTTCGG ACATG CACCA AGT AGG /
T CT TCC AT CG ACC

GAM1437 GCCATTGACAAGCTGTATGA 1410 TCAGTTTTTT 3086 ACA C TAT CG AAGG TTT
CGTTGAGGAAGGCAATTTTC CATCTCTACA GCCATTG AG TG GA TTGAGG CAA T
TTTTTGAGCCTCAGTTTTTT ATGG ||||||| || || || |||||| |||
CATCTCTACAATGGC CGGTAAC TC AC TT GACTCC GTT C
ATC T TT- TT GA-- TTT

GAM1438 AAAATTCATGGTCTGAAGAG 1411 TCACCAGTGG 3087 TT GT- A ATA--- TCAC- AT
AAAA TA
CATACCACTTCACGTTTCAT AAACCAGCAT AA CATG CTGAAG GC CCACT GTTTC
TTGGA GTTC T
TTGGAAAAAGTTCTATCAGG TTCA || |||| |||||| || ||||| ||||| ||||| ||||
ATTTCAAGGAGCTCACCAGT TT GTAC GACTTT CG GGTGA CGAGG AACTT
TAGG /
GGAAACCAGCATTTCAGTGA TC AGT A ACCAAA CCACT -- ---- AC
CATGCTTTTT

GAM1439 CTCTTCTGCTCTAGAGTTCG 1412 TAGCAGGAAA 3088 GC-- GT GC A G G
ATAGC
TGCCCTGATTGAAGGTAGTT TGGCATCTAG CTCTTCT TCTAGA TCGT CCTG TTGAAG TA
TTT C
TATAGCCATGGGAGAGGTGG AAAA ||||||| |||||| |||| |||| |||||| || |||
CTTTAGCAGGAAATGGCATC GGGAGGG AGATCT GGTA GGAC GATTTC GT GAG A
TAGAAAAAGGGAGGG AAAA AC AA - G G AGGGT

GAM1440 TGGTGAGACGGGCAATGACA 1413 TGAAGCTGTG 3089 GCA ACACG AA A TG - A - G
- TT

CGGCAAGCGGCATCGTGCTG CAGCATGACT CGG ATG GC GCGGC TCG CTG GT CAG AGC TGT GACAGCTC G
GTACAGAGCGTGTGACAGCT GCAT ||| ||| || ||||| ||| ||| || ||| ||| ||| ||||||||
CTTGGCGGGTTGTCTGCAGC GTC TAC CG TGTCG AGT GAC CG GTC TCG ACG CTGTTGGG /
TGCTGGCGCAGAGTGAAGCT AG- GA--- -- A GA G - G - T CG
GTGCAGCATGACTGCATCCC
A
GAM1441 CACAATCCTCAGCGTGTTAA 1414 AAGCTGCCAT 3090 AA- CGTG C A C A
CTGGAAGCCTTGTTGAGTTT TGAAGATCTG CAC TCCTCAG TTAA TGG AGC TTGTTG G
AACAAAGCTGCCATTGAAGA GGGG ||| ||||||| |||| ||| ||| ||||||
TCTGGGGGAAAGTG GTG GGGGGTC AGTT ACC TCG AACAAT T
AAA TAGA - G A T

GAM1442 GGATGGTGGCTCATCACCTG 1415 CACCTGTAGA 3091 CTCATCACC AAC CT C- TG T AA
TAGAACCTGACTTGGCGGTG ACCTGACTTG GGATGGTGG TGTAG CTGA TGG GG GC GGG T
GCTGGGAATCCACTCGTTGC GCGG ||||||||| ||||| |||| ||| || || |||
CTTCCACTTCAGTTACACCT CCTACCACT ACATT GACT ACC CC TG CTC C
CACTCACCATCC CACTCC--- --- TC TT GT - AC

GAM1443 GGTTTCAGTTGGATGGTGGC 1416 CACCTGTAGA 3092 TTTC TT CTCATCACC AAC CT C- TG T AA
TCATCACCTGTAGAACCTGA ACCTGACTTG G AG GGATGGTGG TGTAG CTGA TGG GG GC GGG T
CTTGGCGGTGGCTGGGAATC GCGG | || ||||||||| ||||| |||| ||| || || |||
CACTCGTTGCCTTCCACTTC C TC CCTACCACT ACATT GACT ACC CC TG CTC C
AGTTACACCTCACTCACCAT ---- T- CACTCC--- --- TC TT GT - AC
CCTCTCC

GAM1444 CACAGATGCAATGCAGACAG 1417 TGCAATGCAG 3093 AGATG T -- C TG - G- T
GACTTGGCAGAGTTGCCTGA ACAGGACTTG CAC CAA GC AGACAGGA T G CA AG T
TGACTGATCCTGTCTTGGCT GCAG ||| ||| || |||||||| | | || ||
TTGGGACGTG GTG GTT CG TCTGTCCT A C GT TC G
CAGG- T GT - GT A AG C

GAM1445 TTGTCTGGAGAAAGGACTAG 1418 GGACTAGAGA 3094 A A A----- ---- - ATGTA - C AA
AGAGAAATCCAGCTCAGATG GAAATCCAGC CT GAGAGAA TCCAG CTC AG TTGCTC ATTCCT TTCAG G
TATTGCTCATTCCTCTTCAG TCAG || ||||||| ||||| ||| || |||||| |||||| ||||| |||||
AAGGACTGGGTGGGAATGGA GA TTTTCTT AGGTC GAG TC GACGAG TAAGGG GGGTC /
GCAGGGGCTAGAGGAATCTG - - AATCGA TAAG A GGG-- G T AG
GAAGCTAATTCTTTTAGGCT

TTTTCCAACAG
GAM1446 TGACAGTGTGCACAGGCATG 1419 AGGCATGATG 3095 CACA A ATG GCA CA---
ATG
ATGTTGGCAGTGGCAGAGGG TTGGCAGTGG TGACAGTGTG GGC TG TTG GTGG
GAGGG A
ATGAGAATCTTCGTAGACCA CAGA |||||||||| ||| || ||| |||| |||||
TACAAACCCAGCCCCACATT ATTGTTACAC CCG AC AAC TACC CTTCT /
GTTA C--- - CCA A-- AGATG AAG

GAM1447 CACAAGTGATGGTCCAACTT 1420 GTAAGGATTT 3096 - -- T-- GAATG- AGG
AGGG GG
TGTGGAATGGTAAGGATTTT TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
TAGGGTTGTTTGGCCAGAAC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
AAGAGAAATAACTGCAGAAA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /
ACACATATGGTTGGAAACCA G AA TAT AAAAGA CAA G--- AC
TGCGCTTGTG

GAM1448 TGTAAGTAGGAGAGTGATAT 1421 TAAGGCAAGG 3097 G TATTT C-- G G- TA- A
ACAGAGAGT G GG
TTGATCAGGAGAGCGTGGTT TTACCAAGGC TGA GAT AGGA AGC TGGT CT GC
TCTCCCA TA T
ACTAGCACAGAGAGTTCTCC TTCC ||| ||| |||| ||| |||| || || ||||||| ||
CAGTAGGTTAATAGTGGGGG ACT CTA TCCT TCG ACCA GA CG GGGGGGT
AT T
GTAAGGCAAGGTTACCAAGG A TC--- AAA - GA TTG A GAAT----- G AA
CTTCCTAAAATCCTTCAAAA
ACCTTTTATG
GAM1449 CAGTGTGGTTTAATCTGGAA 1422 ACCCGTGTTC 3098 T T CT - GAAGCTG A A
GGAGCAGAAGCTGTGGAGTC CTATCCTTGT CAG GTGGT TAAT GGA AGGAGCA TGG
GTCC A
CAAAGGACCCGTGTTCCTAT TGTG ||| ||||| |||| ||| ||||||| ||| ||||
CCTTGTTGTGCCACTTG GTT CACCG GTTG CCT TCCTTGT GCC CAGG /
- T TT A ------- - A

GAM1450 CAGTTCTTACTTGGGAAAAC 1423 TCGCCTGGAC 3099 T TT - AAAA TT---- G A- AGA--
- CA T
CTTGCCGAGGTACAGAGAGC CACAAGTTTG TC ACTTG GG CC GCC AGGT CAG
GCTGTG TG TGC G
TGTGTGCATGCTGAGCAACA ACCT || ||||| || || ||| |||| ||| |||||| || |||
CCACAGCCATTGCTGAGGCC AG TGAAC CC GG CGG TCCG GTC CGACAC AC
ACG /
TGGGCTCGCCTGGACCACAA C TT A A--- TCCGCT G GA GTTAC C A- A
GTTTGACCTG

GAM1451 GCTCCAAAGAACCAAGAGTG 1424 CATTTCACTT 3100 T - ---------- CAC GAGATA
TC

CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1452 GCTTCAACTTTGACTTTCTG 1425 TGCCAGAGGA 3101 A- T TG CAGA GTGA ACA
G G
CCAGAGGAGAGTGAGCACAA GAGTGAGCAC GCTTCA CTT GACTTTC C GGAGA GC
ATATCT GG C
TATCTGGGGCACCTAAGATG AATA |||||| ||| ||||||| | ||||| || |||||| ||
TAGCATGTTTCCGAAAGTGG CGGAGT GGA TTGGAGG G CCTTT CG TGTAGA TC
A
GAGGTTTAGGACTGAGGC CA T GT AAAG GTA- A-- A C

GAM1453 GAGTGCAAATCAGTCCATTT 1426 CATTTCACTT 3102 T - ---------- CAC GAGATA
TC
CACTTTCACTGTCTGAGATA TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT
TGTCT GGGTC T
GGGTCTCTAAGACCCAGGAT AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
ACAAGGGTGGAATGTAGCTA CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
TATGGACTCGATTTGCTTC - C TATCGATGTA AC- A----- AA

GAM1454 GTGATTGTTATAGTTAATTC 1427 AAGCTCAGTT 3103 TCT AAA AAGAC ATG
TAACAA A- TGC
TGCTGGAAAAACAAGACCAG TGAAGAACTG TAGTTAAT GCTGGA AC CAGTT CAA
GAGT CAGAA C
TTATGCAATAACAAGAGTAC CATT |||||||| |||||| || ||||| ||| |||| |||||
AGAATGCCCCTTTCTGAAGC ATTAGTTA CGATCT TG GTCAA GTT CTCG
GTCTT /
TCAGTTTGAAGAACTGCATT TT- A-- CTTAC GAA TGA--- AA TCC
CGTATCTAGCTTATTGATTA
TACTCAGTTAT
GAM1455 CTCTTGAGCATGCTGACCAG 1428 GACCAGTGCT 3104 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM1456 GACGGGGGGAGCTGTGTAAC 1429 TTAAGTGCCA 3105 --- T CT-- AT-- GCAT A
CTAC A AC
TGATGATTTGGCAGCATCTT GTATGTATCT CTG GTAA GATG TTGGCA CTTAAG AGA
TA TGGTGG A
AAGAAGACTACTAATGGTGG AAAT ||| |||| |||| |||||| |||||| ||| || ||||||

ACATCACTACCAATGAATTT GAC CATT CTAT GACCGT GAATTT TTT GT
ACCATC T
ATTTAAGTGCCAGTATGTAT AAA C AAAT GTAT ---- A AA-- A AC
CTAAATTACCCAGAAAATAA
CTCCTAGCCTC
GAM1457 CTGAGCTGGTTTAGACGTCG 1430 TTAGACGTCG 3106 - AGACG AAA T- TAC TG
T
TGAAAGGTAGTTTACCTACT TGAAAGGTAG CTGAGCTG GTTT TCGTG GGTAG TTACC
TGA A G
GATGATGTGTTGTTGCATGG TTTA ||||||||| |||| ||||| ||||| ||||| ||| |
TAATCCTGCTCAGTACGAGA GACTTGAC CAAG AGCAT TCGTC AATGG GTT T T
GGAACGCAGTTCAG G GAG-- GAC CT TAC GT G

GAM1458 TACGTCCAATCATTAGGCGC 1431 TCCCTGTAGA 3107 TC A C T T A - TA
CCTCCCTGT TTC ACC
TCAGTGCGTGCACCTTCCCT CCTCCCTGTG ATT GG GCTCAG GCG GC CCT TCCCTG GA
GA TGGC C
GTAGACCTCCCTGTGATTCT ATTC ||| || |||||| ||| || ||| |||||| || || ||||
GGCACCCACAGCCAACTCTT TAA CC TGGGTC CGT CG GGA GGGGAC CT CT
ACCG /
GTATCTTTCCCCAGGGGCAG -- A - - - - C CC TTCTATGTT CA- ACA
GGCTGCCTGGGTCCAAATCC
GACGTG
GAM1459 CTGTTCAAAGGGATAACAGT 1432 ATAAAACAGA 3108 AAA ATAA CAC-- AACAG -------
CTCCT
GGCACCTGTAACAGTGTCTC TCAATCATTG TC GGG CAGTGG CTGT TGTCTCT
CCCCAGC G
TCCCCAGCCTCCTGGAATTG AGCC || ||| |||||| |||| ||||||| |||||||
TTGGGGGATGAAAAGAGATA AG CCC GTTACT GACA ATAGAGA GGGGTTG
/
AAACAGATCAATCATTGAGC A-- GA-- AACTA AA--- AAAGTAG TTAAG
CCAGAGCAG

GAM1460 GATGACCTATCCATTAATCA 1433 TCAGGCCCAG 3109 CTATCCATTAAT CC- TT - -
TCA
GGCCCAGGTTCATTCCTCGT GTTCATTCCT GATGAC CAGGC AGG CATT CCT CGTT
G
TTCAGCTTGATGTAGGAAAT CGTT |||||| ||||| ||| |||| ||| ||||
GCCCCTAACGCTTGTTCTTG CTACTG GTTCG TCC GTAA GGA GTAG /
TCATC TTCTT------- CAA CC A T TTC

GAM1461 CTCTGCAGCACCATATAAAT 1434 CAGCACCATA 3110 TGC - ATAAATTC AAT TC - A
T
TCTGAATCATTTTTCCTTCA TAAATTCTGA CTC AGCA CCAT TG CATTTT CTT CA TAT C
ATATTCGTGTACTGTAAGTG ATCA ||| |||| |||| || |||||| ||| || |||
AAGTGCAATAACACAGTGGA GAG TCGT GGTG AC GTGAAG GAA GT ATG G
TGCTTGAG T-- A ACACAATA --- T- T C T

GAM1462 TCATCGTGGAGATCTTTTGG 1435 TCCTTCAGAC 3111 CG A TTT CA-- CCCAT CT
CAGCGCCCATTGGCCTCTTT CTCCAGAGTG TCAT TGGAG TCT GG GCG TGGCCT T
GGGGTCATCCGTCGCAATTC A |||| ||||| ||| || ||| ||||||
CTTCAGACCTCCAGAGTGA AGTG ACCTC AGA CC CGC ACTGGG /
AG C CTT TTAA TGCCT GT

GAM1463 TTGCGCACCTGGTCTCCTTC 1436 TGCCTGGAGA 3112 CG --- TTCAAAA TCG A C
AAAAGCTCGACTTCACCTCC CCTCAAGGTG TTG CACCT GGTCTCC GC ACTTC CCT C
AAGGGAGGAGTAATGCCTGG AATA ||| ||||| ||||||| || ||||| |||
AGACCTCAAGGTGAATAA AAT GTGGA CCAGAGG CG TGAGG GGG A
AA ACT TC----- TAA A A

GAM1464 TCCTTTTGACAAGAAATGTG 1437 TGACAAGAAA 3113 T - AAATGT C AA-- CTGTT T
GTCGTGAAAATTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA TTGGA GC
T
GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||
ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T
GA C G GTT--- - GGTA ----- T

GAM1465 GCTCCAAAGAACCAAGAGTG 1438 CATTTCACTT 3114 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1466 TGTGAAGCTGCCACACTCAT 1439 TGAAGCTGCC 3115 G CC- T--- CTA
CCATTCTATCGCTGATGGCA ACACTCATCC TGT AAGCTG ACACTCA CCATT T
TTTGGGTGTTTTCAGTTTGG ATT ||| |||||| ||||||| |||||
CA ACG TTTGAC TGTGGGT GGTAG C
G TTT TTAC TCG

GAM1467 GACATTTCAATAATACAGGG 1440 TTCAATAATA 3116 AT - AG A--- ACA
TAAGTTCATAGCTACAAAGC CAGGGTAAGT GACATTTCA AATACA GGGTA TTCAT GCT A
AAGCCAACATGAGTGCTCAT TCAT ||||||||| |||||| ||||| ||||| |||
GTATTCTGAGATGTC CTGTAGAGT TTATGT CTCGT GAGTA CGA A
C- A -- CAAC ACG

GAM1468 GTGTGGCTTTTTGAGGTAAT 1441 TGAGGTAATA 3117 G TTTG TAATA TT G- TGC
AAGTTTATGGTACGAGTGCA AGTTTATGGT GTGTG CTT AGG AG TATGGTAC AG A
CTGTCTAAGTATCATGCTCT ACGA ||||| ||| ||| || |||||||| ||

CCTAAGATACAC CACAT GAA TCC TC GTACTATG TC C
A ---- ----- TC AA TGT

GAM1469 GGACTCTGGCCTGTGTCTAC 1442 TCTGGCCTGT 3118 G- GTG C TGA-- GTAGC
TCTCCTGATGTGTAGCCCAC GTCTACTCTC GGACTCT GCCT TCTACT TCC TGT C
CAACAGTAATGGAAGTAGAG CTGA ||||||| |||| |||||| ||| |||
GGTAGGGGGTTT TTTGGGG TGGG AGATGA AGG ACA /
GA --- - TAATG ACCAC

GAM1470 GGATTCCCAGGCTTTGAACT 1443 GGCAGTGTAG 3119 AT CCAG G TG G A- -
GGTG- AAT
GCTGAGGTATACTATGTGAC CTTAGTGGTT GG TC GCTTT AAC CTGAG TATACT TGT GAC
ATG G
GGTGATGAATGAACACGTGG GGGA || || ||||| ||| ||||| |||||| ||| ||| |||
AAAGTCGACGGCAGTGTAGC CC AG CGAGG TTG GATTC ATGTGA GCA CTG TGC
A
TTAGTGGTTGGGAGCACAGA C- ACA- G GT G CG G AAAGG ACA
CCC

GAM1471 TTCCAGAAAGAGACAAGCAA 1444 CAGAAAGAGA 3120 A - ACAA A CTT TC A
CTACTTTTCTCAGAATATAA CAAGCAACTA TTCC GAAA GAG GCA CTA T TCAGAAT T
TTTTGAAGATCTTAGTGCCT CTTT |||| |||| ||| ||| ||| | |||||||
CATTTCGGAG GAGG CTTT CTC CGT GAT A AGTTTTA /
- A ---- - TCT GA A

GAM1472 GTGGCAGTGACTTCTGTTAG 1445 AGAGATCTTT 3121 C T ------- -- TG TG- CTTTG TG
TT T
GTCTTGTGGCAGTGTCCTTT ATTGAAACCG GA TTC GTT AGGTCTT G GCAG TC T A
CTCTTGGT A
GTTGATTCTCTTGGTTATAA AATC || ||| ||| ||||||| | |||| || | | ||||||||
TCAAGAGTTTTGGACCCTGA CT AAG CAA TCTAGAG T CGTC AG G T
GAGAACTA T
ACTCTGCTGTGAGAGATCTT - C AGTTATT AG GT TCA TCCCA GT TT A
TATTGAAACCGAATCATGAC
CCCAC
GAM1473 CTACTGGAAAGAAGGCTTTA 1446 ACCATGTAAG 3122 - AA- --- - AGA CAGG
TGGAGATCCCAGGAACCAAG CCTGAATTTG CTAC TGG AGA AGGCTT TATGG TCC A
GACCATGTAAGCCTGAATTT TGCC |||| ||| ||| |||||| ||||| |||
GTGCCATGTGG GGTG ACC TTT TCCGAA GTACC AGG A
T GTG AAG T --- AACC

GAM1474 CCCCTGAATTAAGCAGAAAG 1447 TGCCTGTTTC 3123 ----- TAA GAA- TCTT T T T T-
CTGC GT
TCTTCATGGCTTTTCTGGTC CTGATATGCC GAAT GCA AG CA GGC TTTC GGTC TCGG
TCAGG T
TTCGGCTGCTCAGGGTTCAT ATTC |||| ||| || || ||| |||| |||| |||| |||||

CTGACGATTCGACTGACCCG CTTA CGT TC GT CCG AAAG CCAG AGCT AGTCT /
AAATGCCTGTTTCCTGATAT TCGTT C-- ATAG CTTT - T C TC TAGC AC
GCCATTCTTGCTGGGGG

GAM1475 TACGCAGCCTCCCACTGTGG 1448 TCGCCTGGAC 3124 CC - G T G A - AA CAGAGA - CA T
TGCCTGGTGGAGACCTGGCC CACAAGTTTG ACT GTGGT CC GGTG AG CCT GGCC GGTA GCTGTG TG TGC G
AAGGTACAGAGAGCTGTGTG ACCT ||| ||||| || |||| || ||| |||| |||| |||||| || |||
CATGCTGAGCAACACCACAG TGA CACCA GG CCGC TC GGG CCGG TCGT CGACAC AC ACG /
CCATTGCTGAGGCCTGGGCT TT A - T - - T AG TAC--- C A- A
CGCCTGGACCACAAGTTTGA
CCTGATGTA
GAM1476 GGATCTAGAAAATAGTGAGG 1449 TGAAAGAGCA 3125 TC T TGAAAGA TAC A - GGCAGATA
TGAAAGAGCATACAGTAGTG TACAGTAGTG GGA TAGAAAATAG GAGG GCA AGT GTGA GAA A
AGAAGGCAGATAATTAGTAT AGAA ||| |||||||||| |||| ||| ||| |||| |||
ATTCGTCGCGACTTCTGCCC TCT ATTTTTTGTC CTCC CGT TCA CGCT CTT /
TCCTGTTTTTTATCTCT CT - ------- CT- G G ATATGATT

GAM1477 AGAGTTGGTGCAGACTTTTC 1450 TGCAGACTTT 3126 TT AGA TCTC- ------ A CT
TCTCTTCTATGATGTGCTGT TCTCTCTTCT AGAG GGTGC CTTT TCTT CTATG TGTG G
CCACACATGGCCACCAAAGA ATGA |||| ||||| |||| |||| ||||| ||||
CACACAAAGACAGCATCTCT TCTC CTACG GAAA AGAA GGTAC ACAC /
CT T- ACA CACAC ACCACC - CT

GAM1478 GGAGAATCACTTGAACCCGG 1451 AGGCAAGAGG 3127 AA GAA--- AGGCAA GT AGC A
GAGGCAAGAGGTTGCAGTGA TTGCAGTGAG GGAG TCACTT CCCGGG GAG TGCAGTG TG G
GCTGAGATCACACCACTGTA CTG |||| |||||| |||||| ||| ||||||| ||
CTCCAGCCTGGGCCACAAGA CCTC AGTGAG GGGTCC CTC ATGTCAC AC A
GTGAAACTCC AA AACACC GAC--- -- CAC T

GAM1479 TGTCAGGTTATCCACCTCGG 1452 TCGAGCACTC 3128 GTTAT C- CA - A- CC G
GCAGCTCGTCAGGCTGCGGC TGAGCTTGGC TGTCAG CCA CTCGGG GCTCG TC GGCTGCGGCG CT T
GCCCTGTTCAGTCTGTTGCA TGGC |||||| ||| |||||| ||||| || |||||||||| ||
GCTGAGATCGAGCACTCTGA ACGGTC GGT GAGTCT CGAGC AG TCGACGTTGT GA T
GCTTGGCTGGCA ----- TC CA T AG CT C

GAM1480 CACTGAACATTTGCTGAAAC 1453 TCCCAATATG 3129 C AA- TGAAAC T TG TTGTT TTCA AT

TGTGGTGCTTTGTTGCTTCA CAGATGAAGC CA TG CATTTGC TG GG CT GC AGATG
G
AGATGATGCACATCTGCTTT ATTG || || ||||||| || || || || |||||
TAGTGTCCCAATATGCAGAT GT AC GTAGACG AC CT GA CG TCTAC /
GAAGCATTG T GAA TATA-- C GT TTTT- ---- AC

GAM1481 GGCTGTCCTCAGGGTTCAGC 1454 TATAACAGCC 3130 CTC TCA ATG --- - GC
TTA CT
TATGATAGAGACTCAGCTGG ACCTTGACAG GGCTGTC AGGGT GCT ATAGA GACT CA
TGGC GG T
CTTAGGCTTCATCCACTGCC TC ||||||| ||||| ||| ||||| |||| || |||| ||
AATGAAGTCAAATTTATAAC CTGACAG TTCCA CGA TATTT CTGA GT ACCG CC C
AGCCACCTTGACAGTC --- C-- CAA AAA A A- TCA TA

GAM1482 TTCCTTTCAGTCTTTATTTG 1455 CTTTCAGTCT 3131 CA T TTT A AA ACCA TATATGAC
TT C CAC
CAGCAAACTACCACTTTATA TTATTTGCAG T GTCT TA GC GCA CT CTT AGG
TGTGTGT TGTA G
TGACAGGTTTGTGTGTCTGT CAAA | |||| || || ||| || ||| ||| ||||||| ||||
ACACGCACATACACACACAT A CAGA AT CG CGT GA GAG TCC ATACACA ACAT
C
ATCCTTAAGCTCGAGACAGG AC C TT- G GG CA-- CTCGAAT- T- C ACA
GTGCGGCTTTACAGACCAAA
AAGTATGGAA
GAM1483 TGTGGTTTAATCTGGAAGGA 1456 ACCCGTGTTC 3132 AG---- A A AGTCCAAA G TC
TCCT TGC
GCAGAAGCTGTGGAGTCCAA CTATCCTTGT GA GAGC GA GCTGTGG GGACCC TGT
CTA TGTTG C
AGGACCCGTGTTCCTATCCT TG || |||| || ||||||| |||||| ||| ||| |||||
TGTTGTGCCACTTGACACGT CT CTTG TT TGACACC CCTGGG ACA GAT
ACAGT /
TTAGCACAAGGGTCCCCACA CTGCCA A G -------- A C- TTGC TCA
GTGTTAGTTCACCGTCTCCA
GCAATCACG
GAM1484 GTCCAGTGCGTGTACTGTAC 1457 TGTACACATC 3133 C G TA TACACATCC A - - CT
TC G
ACATCCACACTCATTCTCAC CACACTCATT GTC AGTGC TG CTG AC CTCA TTCT CA
CAGGGT CCG A
TCAGGGTTCCCGGACCGGCT CTCA ||| ||||| || ||| || |||| |||| || |||||| |||
GTCCTGCCTGCGGAACTGAG CAG TCATG AC GAT TG GAGT AAGG GT GTCCTG
GGC /
GTAAACTAGCTCAGGTACTG - G TC CAAA----- - C C CC TC C
AC

GAM1485 GAATGCCCTAACCCACGTTC 1458 TGGAGAACCC 3134 C AA AC TA TATGCA ---- C
T A G
TTACCACTATGCACCAGGCA GGGCAGTGCA GAATGC CT CCC GTTCT CCAC CC
AGGCAC CGC AG TA A

CCCGCTAGATAGATCTACCT TTT |||||| || ||| ||||| |||| || |||||| ||| || ||
CGCGAGTGCCTACACGGACT TTTACG GA GGG CAAGA GGTG GG TCCGTG GCG TC AT T
CTGTGGAGAACCCGGGCAGT T C- CC -- TCTCA- CACA A C C C
GCATTT

GAM1486 TAGGATTGCCATTACAACAG 1459 TTACAACAGC 3135 AT AC ACAC GCT ATTAC GAA T TG TC
CATACACTCAGCTATCGATT ATACACTCAG TACA AGCAT TCA ATCG GC TGGCGCC CAC GTCAGT T
ACGCGAATGGCGCCTCACTG CTAT |||| ||||| ||| |||| || ||||||| ||| ||||||
GTCAGTTCTTGGCTGATGTG ATGT TCGTA AGT TGGC CG ACCGTGG GTG TAGTCG /
TGGTGCCAATAGCCTCACGG -- A- ---- AC- ACTC- ATA T -- GT
TCATGAATGCTATGTAGCTG
ATCTTA
GAM1487 GCTAACAAGTTCTGTAAGGG 1460 CTCGGATCCG 3136 TAA TAA GC ATT TG TT
CCCATTATGGTTGATTTGTC TAGAGCTTGG GC CAAGTTCTG GG CC A G G
TCGGATCCGTAGAGCTTGGC C || ||||||||| || || | |
CG GTTCGAGAT CC GG T T /
--- G-- TA CTC GT TA

GAM1488 AAGACTGTTCGATGGGCAGA 1461 GGCAGATGCT 3137 A AT AGA--- G AGCT CGA GA
TGCTGGCATAGCTGCACGAG GGCATAGCTG AAG CTGTTCG GGGC TGCTG CAT GCA GGT T
GTGATGGGCCAATGCTGGTG CACG ||| ||||||| |||| ||||| ||| ||| |||
GCAGCGAGTAAAGCCTTGGA TTC GACAGGT TCCG GCGAC GTG CGT CCG /
CAGACTT A -- AAATGA G GT-- AA- GG

GAM1489 AGGCTGCAGAACATGGAGGT 1462 TTCCTGCCTC 3138 -- ACAT T CC CT
CACCGATGCTTGAACATTCC CCTATTTGCC AGGCT GCAGA GGAGG CA GATG T
TGCCTCCCTATTTGCCAGGC AGGC ||||| ||||| ||||| || ||||
TT TTCGG CGTTT CCTCC GT TTAC G
AC ATC- - CC AA

GAM1490 TCTTGATTCACCAGGTCTAA 1463 TCACCAGGTC 3139 - A AGG AA C TC
ACTGCAGTAATCCATTTACT TAAACTGCAG TCTTGAT TC CC TCTA CTG AGTAA C
CAGCTGGAGAGGAGACATCA TAA ||||||| || || |||| ||| |||||
AGA AGAACTA AG GG AGGT GAC TCATT /
C A AG- C- - TA

GAM1491 TCCAACTTTGTGGAATGGTA 1464 GTAAGGATTT 3140 T-- GAATG- AGG AGGG GG
AGGATTTTTAGGGTTGTTTG TTAGGGTTGT TCCAACT TGTG GTA ATTTTT TTGTTT C
GCCAGAACAAGAGAAATAAC TT ||||||| |||| ||| |||||| ||||||
TGCAGAAAACACATATGGTT AGGTTGG ACAC CGT TAAAGA AACAAG /

GGA TAT AAAAGA CAA G--- AC

GAM1492 ACCAAATGAGGCAGTATTAT 1465 TGAGGCAGTA 3141 AA- A TATT-- A
TATTTTATAGAGATAGGATT TTATTATTTT ACCA TG GGCAGTAT ATTTTAT G
TAGCTATGTTGCCCAGGCTG AT |||| || |||||||| |||||||
GT TGGT AC CCGTTGTA TAGGATA A
CGG - TCGATT G

GAM1493 GCTCATGCCATCCTTGCAAA 1466 AGAGGTAGTA 3142 TC AA CA-- A-- TG - TG GTA-- ACAG
CCTCCAGCAAAATGAGTGTC AGTGGCAGAG TGCCA CTTGC ACCTC GCA AA A G TC TTTCTGTTT A
GTATTTCTGTTTACAGATGA C ||||| ||||| ||||| ||| || | | || |||||||||
GGAAACAGAGAAGTTAGGTG ACGGT GAATG TGGAG CGT TT T C GG AGAGACAAA T
CCTTGTTCAATGCCCTAGAG -- A- ATCC AAC GT C GT ATTGA GGAG
GTAGTAAGTGGCAGAGC

GAM1494 GCTGTGTTGCAGTGCATTGT 1467 GTGCATTGTG 3143 GCA A TG G TG GGA TG GA CCT TG
GTTGCAGGATTGGGAAGGGC TTGCAGGATT GCTGTGTT GTGC T T T CA T G AGGGCA GTGC G
ACCTGTGCTGGTTGCACTTG GGGA |||||||| |||| | | | || | | |||||| ||||
CTTTGATTGAATGTGGAATG TGACGTAG CATG A A G GT A T TTTCGT CACG /
AAGTACGAAGATGCAGT AAG A GT A GT A-- GT AG T-- TT

GAM1495 TGGCACCTGGTGAAGAAGAG 1468 TGGAATTTGA 3144 - - A AGA TT GA A AT GA T G G
AATTTGGAATTTGAAGAAGA AGAAGATGAA CCT GGTGA GAAG AT GGAATTT AG AG GAAGAA GGG GGT CTG A
TGAAGAAGAGGGTGGTGCTG GAAG ||| ||||| |||| || ||||||| || || |||||| ||| ||| |||
GAGCAGGGTCTCCTGATTCT GGA CCATT TTTC TG CCTTGAG TC TC TTTCTT TCC CTG GAC /
TTTCCTGCTAGAGTTCCCGG T A A A-- GC A- G CT AG T G G
TACTTTATTACCAAGGTTGC
CA
GAM1496 CTTATTGTACACTTACTATG 1469 TATTGTACAC 3145 A AC T T G AA GTT
TGCCAGAAATTGTTTTGAAA TTACTATGTG CTT TTGT ACT AC ATGT CCAGA TT T
GCTTTGGGATATGTCAGTCA CCAG ||| |||| ||| || |||| ||||| ||
ACAAAAG GAA AACA TGA TG TATA GGTTT AA /
- AC C - G CG AGT

GAM1497 GCTCCAAAGAACCAAGAGTG 1470 CATTTCACTT 3146 T - ---------- CAC GAGATA TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T

TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1498 CTGTGGGCGGTGTCCAGGTT 1471 TATCACAGCC 3147 GGG - C G CC TA C- A T
T- C
CACCACCTGTAGCTCGGTGA ATCTGGTGGA CTGT CGGT GT CAG TTCACCA TG GCT GGTG
GGT GC GCTG T
GGTTGCTGCTGCTCCCGGCC GCTG |||| |||| || ||| ||||||| || ||| |||| ||| || ||||
TGCTGCCCTATCACAGCCAT GACA GTCG CA GTC AGGTGGT AC CGA CTAT CCG CG
CGGC C
CTGGTGGAGCTGAACTGCTG AA- T A G CT -- CA C T TC C
AAACAG

GAM1499 TGGGCGTGAGGCAGTCAGTT 1472 TGAGGCAGTC 3148 G - G GTTT- ATTTT A-
G
ATATGTTTGGGCATTTTTTC AGTTATATGT TGGGC TGAG GCAGTCA TTATAT GGGC
TTCAGGT GAT G
AGGTAGATGGGTGTTGAGCT TTGG ||||| |||| ||||||| |||||| |||| ||||||| |||
TGAACGCTTTCTTAATATGG ATCCG ATTT CGTCGGT GGTATA TTCG AAGTTCG
TTG G
TGGCTGCTTTTAGGCCTA G T - ATTCT C---- AG T

GAM1500 TATGTTGTGATTCGGTTTGA 1473 TATTTCACAT 3149 T- A TTT T C A A -
CCCAAGT
ATATGCTGAAGTGAGCAATT TTTCTACTTG TATG TGTG TTCGG GAA ATG TGAAGTG GCA
TTAT GATTTG G
ATGATTTGCCCAAGTGCAAT AACA |||| |||| ||||| ||| ||| ||||||| ||| |||| ||||||
ACAACAAATCTATAATGTAT GTAC ACAC AAGTT CTT TAC ACTTTAT TGT AATA
CTAAAC C
ATTTCACATTTTCTACTTGA TT - CAT T - A - T AACATAA
ACACATTCATG

GAM1501 GATCGAACCTGAGCCTTTTG 1474 TCAGTGCATT 3150 --- ----- TT AT TGCTA - CA- -
C G
AGAATTGCCTGCTACGGCCT TCAGAGCTGG ACCTGA GCCTT GAGA TGCC CGGC
CTGG GC CTG CC A
GGCAGCCTGCCCGAGTGGTC GCAT |||||| ||||| |||| |||| |||| |||| || ||| ||
AGTGCATTTCAGAGCTGGGC TGGACT TGGGG TTCT ACGG GTCG GACT CG
GAC GG G
ATCTTTGGGGTCTATGTCAG GAG GTATC T- -- ----- A TTA T T T
GTGAGCCAATC

GAM1502 GCCTTAGATATCAATGAAAG 1475 ATGAAAGCTA 3151 TA T AA T - - TGA---- A
CTACACACCATTGAGATGGG CACACCATTG GCCT GA ATC TGAAAGC ACA CA CCAT
GATGGGCGG C
CGGACTGTTGCCTATTGAGC AGAT |||| || ||| ||||||| ||| || |||| |||||||||

ATTGTGGATGATGTGTTTTC TGGA CT TAG ACTTTTG TGT GT GGTG TTATCCGTT T
AGATTTCCAGGT C- T -- - A A TTACGAG G

GAM1503 TCAGTTTCCCTGGAGCTTCT 1476 AGTCAGAAGA 3152 TT CT CTTC - G- CTTC- A-
AGA
GCTACTGGTTCCTTCCCTGG CAGTGAGCAC TCAG TCC GGAG TGCT ACTG TTC
CCTGGGGT TGGC G
GGTATGGCAGAGGGAGTCGG CTCC |||| ||| |||| |||| |||| ||| |||||||| ||||
CATCTCAGGAGTCAGAAGAC AGTC AGG CCTC ACGA TGAC AAG GGACTCTA
GCTG /
AGTGAGCACCTCCCCGGACT TC CC C--- G AG ACTGA CG AGG
CTGA

GAM1504 CAGTGGTTCTCTCAGCAACA 1477 TCAAAGCTGC 3153 TC - AACA-- - A- A TA
TGAC T CC
GACATGTCCAGTGGACCGTA AGATTGCCTG GT TCT CAGC GACATGT CC GTGG CCG
GTGTTG GG CGC A
GTGTTGTGACGGTCGCCCAT TG || ||| |||| ||||||| || |||| ||| |||||| || |||
CTGCGCCCAGTACCTCGGAT CG AGA GTCG TTGTACA GG TACT GGC CATGAC
CC GCG T
CATGCGGAACATGTTGTCAA TT C AAACTG A CG A TC ---- - TC
AGCTGCAGATTGCCTGTG

GAM1505 TCCATGATGGGGAGGAAGCT 1478 GGCCTGGGTC 3154 GGA T G G T TAT------ GA
- GGG
GCAGGGCCTGGGTCTCCTTA TCCTTATGCC GA AGC GCA GGCCTGG TC CCT GCCACTG
TGGAGTC TG A
TGCCACTGGATGGAGTCTGG ACTG || ||| ||| ||||||| || ||| ||||||| ||||||| ||
GGAGACACAGGGCTTCACAG CT TCG TGT CCGGATT AG GGG CGGTGAC
ACTTCGG AC G
TGGCTGCTTCTGTGGGTGAA GTG - A A T TGTCTTCGT -- G ACA
TTAGGCCATGTGCTGTGTCT
AAGTTGTGGA
GAM1506 AAAGTGGGTGCACAAGTGAT 1479 GTAAGGATTT 3155 - -- TC- GAATG- AGG
AGGG GG
GGTCCAACTTCTGTGGAATG TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
GTAAGGATTTTTAGGGTTGT TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
TTGGCCAGAACAAGAGAAAT TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /
AACTGCAGAAAACACATATG G AA TAT AAAAGA CAA G--- AC
GTTGGAAACCATGCGCTTGT
GACTTTTTCT
GAM1507 CCTCCCTTGCAAGGAAACAC 1480 GAGACCCTCG 3156 --- CTGTA C--- ACT TTCAT-
C- CAGA
TGTATCACTCATGGCACTGC TGAAAGCTAG GGAAACA TCACT ATGGC GCTTTT
GTTTC CCT A
TTTTTTCATGTTTCCCCTCA TCAT ||||||| ||||| ||||| |||||| ||||| |||
GAAGTCCCAGGTCGAGACCC CCTTTGT AGTGA TACTG CGAAAG CAGAG
GGA G

TCGTGAAAGCTAGTCATTCA AAG ----- CACT AT- TGCTCC CT CCCT
CAGTGATGTTTCCGAAAAGG
TAGGCCATGG
GAM1508 GTGACCTACTCTTGCCTCAT 1481 TGGAGAGCAG 3157 - CTAC C A ATTACGA A- T
CCGGAGTTATTACGAAGGAG GGCTCTGTGC GTG AC TCTTGC TC TCCGGAGTT AGG GC
C
CTCCGCAGCCTGACTGAGCT AC ||| || |||||| || ||||||||| ||| ||
CTGGAGAGCAGGGCTCTGTG CAC TG GGGACG AG AGGTCTCGA TCC CG /
CAC G TCTC - - GTCAG-- GA C

GAM1509 GTCGGTGCCCTGGAGGTTGT 1482 GTGAGCAAGT 3158 C - T - CT C
CTTCGCTGCCTTGCTTCGTG TTCCAGGCGC GTCGGTGCC TGGAGG TTG CTT CG GC T
AGCAAGTTTCCAGGCGCTGA TGAC ||||||||| |||||| ||| ||| || ||
C CAGTCGCGG ACCTTT AAC GAG GC CG /
- G - T TT T

GAM1510 AGGGCTGAGAATCCAGAGGA 1483 TGCTAAAGAC 3159 GA GGCGTGA GGAA---- A ---
TG CC TCATA
GGGCGTGAACTGTCCGGAAA AGGGGCAGTG A GGAG ACTGTCC AGCA GGC T GAG
AGACC T
GCAAGGCTTGGAGCCAGACC ATTA | |||| ||||||| |||| ||| | ||| |||||
TCATATGCACTTGGTCTATT T TCTC TGACGGG TCGT CCG G CTT TCTGG
G
CTGGTGCGCCTGCTAAAGAC -- ATTAG-- GACAGAAA - CGT GT A- TTCAC
AGGGGCAGTGATTACTCTTG
GATCGGTCCT
GAM1511 GTGGGGAGAACAGCGTCTTT 1484 TCCTCCAGTG 3160 A GT TTTACC - CC -- G A
CC T
TACCTGTCACCGAAGCCAGG GCGTTCTTTT GTGGGGAGAAC GC CT TGT CA GAAGC CA
GA GC CGTT G
AAGCCCCGTTTGTAAGCGTG TAC |||||||||| || || ||| || ||||| || || || ||||
TGTTGTGGTGCTTTATTGTA CATTTTTCTTG CG GA ACA GT TTTCG GT TT TG
GCGA T
CATCCTCCAGTGGCGTTCTT - GT CCTCCT T TA TG G G T- A
TTTAC

GAM1512 AGAATGGGGAAGAATACTGA 1485 TTGGAGCAGG 3161 - - TA AA T CA TCT AC-
CT
ATTAGCTGAGCACATTCTGG TTTCATTCTC AGAAT GGGGAA GAA CTG TTAGC GAG CAT
GGAC AATT G
ACACAATTCTGACCAATTTC CAAT ||||| |||||| ||| ||| ||||| ||| ||| |||| ||||
AGTCTCATGATCTCTGTTGG TCTTA CCTCTT CTT GAC GGTTG CTC GTA TCTG
TTAA A
AGCAGGTTTCATTCTCCAAT A A TG GA T TA C-- ACT CC
TCT

GAM1513 GTACAACCTGGCCATTGGTT 1486 GGACAGGATG 3162 CCTG - GTT - C - GA
TCACCTGTCCCTGGCTGAAG ACAGTGAGCA GTACAA GC CATTG TCA CCTGTCC TGG CT A

AAGATCATGGACAGGATGAC CACT |||||| || ||||| ||| ||||||| ||| ||
AGTGAGCACACTTGTGC CGTGTT CG GTGAC AGT GGACAGG ACT GA /
CACA A --- A T A AG

GAM1514 TCTCTAACAAGGTGCAGAGC 1487 TTCACAGTGG 3163 AACA ATTG TGAT T
TTAGCTGATTGGTGAACAGT CTAAGTTCTG TCTCT AGGTGCAGAGCTTAGCTG GTGAACAG
TGG T
GATTGGTTTCCGCTTTGTTC CACC ||||| |||||||||||||||||| |||||||| |||
ACAGTGGCTAAGTTCTGCAC AGAGA TCCACGTCTTGAATCGGT CACTTGTT GCC /
CTGAAGAGA AG-- GA-- TC-- T

GAM1515 ATTCAACAAGTCTTTATTGA 1488 TTCAACAAGT 3164 AACAAG TAT A CTCT- C
GCACCTACTCTGTGCCCAGC CTTTATTGAG ATTC TCTT TG GCACCTA GTGC C
ACTGCACTAGGTGCCATGAG CACC |||| |||| || ||||||| ||||
AATACAAGAGT TGAG AGAG AC CGTGGAT CACG /
AACATA T-- - CACGT A

GAM1516 CTCTTGAGCATGCTGACCAG 1489 GACCAGTGCT 3165 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM1517 TCTCCAACAGCTGTTCCAGT 1490 AGGCAGTGGT 3166 CT- TC - T -- C -- A AA-
ATCT GAG
TCCTGCAGGCCACCGCCCAG GTTTGCTGGT GT CAGTT CC GCAG GCCAC GCC CAGGA G
GGG TTGGT T
GAAGAAGGGATCTTTGGTGA GGCT || ||||| || |||| ||||| ||| ||||| | ||| |||||
GTCCCAACCAGTCAGCCCAG CG GTCGG GG CGTT TGGTG CGG GTCCT C CCC
GACCA C
GCTCCTGCAGGCAGTGGTGT CCC TC T T TG A AC - GGA GACT ACC
TTGCTGGTGGCTGCTGCCCC
CTGCCGGACA
GAM1518 ATATTAGGACCATTAGTCAC 1491 GTCACAGTGG 3167 C- TTA A - AAAAGT ATA
AAAG GA
AGTGGCAAAAGTTCTTAGAT CAAAAGTTCT ATATTAGGA CA GTCAC GTGG C TCTTAG
TTGA AA T
ATTGAAAAGAAGATGTGTTA TAGA ||||||||| || ||||| |||| | |||||| |||| ||
GGTCAACTGCTAAGATGGTC TATAGTCCT GT TAGTG CACC G AGAATC AACT TT
G
CACAGTGATCCCTGCCTCCT CC CCC A T GT---- GTC GGA- GT
GATAT

GAM1519 GCTGTCAACGGATATTTATT 1492 TCAACGGATA 3168 - AA A TATT--- G - C
GGGCGTGCTCAACAGCCAGG TTTATTGGGC GCTGT C CGG TATT GGGC TG CT A
CCCTGTTCATGGTACTGAAG GTGC ||||| | ||| |||| |||| || ||

AACAGC CGACA G GTC ATGG CCCG AC GA A
A AA - TACTTGT G C C

GAM1520 GAAGACTTCCTAAATTTGCA 1493 TTTGCACATT 3169 AC A TTGCA TTGCC ACCAT
CATTAGCTAGATTGCCATTA AGCTAGATTG GAAG TTCCT AAT CATTAGCTAGA ATTAGC T
GCACCATTAGAGAGTTGATC CCAT |||| ||||| ||| |||||||||| ||||||
TTTGGCTAATGATTATTCAG CTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GAAAATTTC AA C TTA-- C---- AGAGA

GAM1521 GCTCTCCCAGTCATCACAGT 1494 TCATCACAGT 3170 CT - CATCACA - ATA
CTGGTCTCTTGATATCTGTA CTGGTCTCTT GCT CC CAGT GTCTGGTCT CTTG T
GGAAGATCGGACACACTGTG G ||| || |||| ||||||||| ||||
GTCAGC CGA GG GTCA CAGGCTAGA GGAT /
CT T CA----- A GTC

GAM1522 TGCTGTACTCATCACAGAAT 1495 TCGAAGTTCT 3171 ------- - AC-- GG- ---- - TCAAT T- TT
GGGACAGAGGGCTCTCAATA TCAGGATGAT AC TCATC AGAAT GACAG AGG GCTC AGA CA C
GATCATTCCCTTGTTTCTCC GTCA || ||||| ||||| ||||| ||| |||| ||| ||
CCTGGGCTTCTTGAGCTGTC TG AGTAG TCTTG CTGTC TCT CGGG TCT GT C
GAAGTTCTTCAGGATGATGT AATATAC T GACT AAG GAGT T TCCCC TT TC
CATATAACACAGCA

GAM1523 GGTGCATGTGGGAACACTCT 1496 TTCAGAGTGG 3172 T GGGA- T- CCCC G- CCAACC
GGTGCCCCCCGCTGGAGCTG ACTACATTCT GG GCATGT ACACTC GGTG CCGCT GAGCTGG C
GCCAACCCCGAGAACCAGTT GAGT || |||||| |||||| |||| ||||| |||||||
CAGAGTGGACTACATTCTGA TC CGTGCA TGTGAG TTAC GGTGA CTTGACC /
GTGTGATGAACGTGCCT - AGTAG TC ATCA GA AAGAGC

GAM1524 CTCTTGAGCATGCTGACCAG 1497 GACCAGTGCT 3173 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM1525 GTTGGGAGATGGTGTGGTCC 1498 TGGAATGGAA 3174 - G GTGGT GAA AAA A AA- ATA T A
TGGAATGGAAAAAGCATGAA AAAGCATGAA GTTG GGA ATGGT CCTG TGGA AGC TG GTGA TG CTT A

GTGAATATGTCTTAAGCGAG GTGA |||| ||| ||||| |||| |||| ||| || |||| || |||
CCAGTCATCTGCAAGTTATG CGAC TTT TATCA GGGC GCCT TTG AC TACT AC
GAG G
TCCGCGGGTAACTATGTTTA A G AT--- --- GTA A GTC G-- C C
CAGC

GAM1526 TGGCACCTGGTGAAGAAGAG 1499 TGGAATTTGA 3175 - A AGA TT GA A- AT GA
T G G
AATTTGGAATTTGAAGAAGA AGAAGATGAA CCT GGTGA GAAG AT GGAATTT AG AG
GAAGAA GGG GGT CTG A
TGAAGAAGAGGGTGGTGCTG GAAG ||| ||||| |||| || ||||||| || || |||||| ||| ||| |||
GAGCAGGGTCTCCTGATTCT GGA CCATT TTTC TG CCTTGAG TC TC TTTCTT TCC
CTG GAC /
TTTCCTGGCTAGAGTTCCCG A A A-- GC A- GG CT AG T G G
GTACTTTATTACCAAGGTTG
CCA
GAM1527 GTAACTAGCCATTCTCATGA 1500 TGAAATGACA 3176 CA A ATGAAA CAT T TG --
A AGAAA
TGAAATGACATTGGTATTTG TTGGTATTTG GTAACTAGC TTCTC TG TGA TGG ATT AGAG
GG AC A
AGAGGGAACAGAAAAATCAC AGAG ||||||||| ||||| || ||| ||| ||| |||| || ||
AGTACCTGCTCTTGAGTTCA CATTGATCG AAGGG AC ACT ACT TGA TCTC CC TG
A
TTCACGCTACAGGGAAGAGC AG - ATCGC- T-- - GT GT A ACACT
TAGTTAC

GAM1528 CCCATTTCAATTGTATGGTC 1501 CATTTCAATT 3177 - CATGG AA AA GAATG G
T TA
TGAGACATGGTCTCAATATA GTATGGTCTG GTATG GTCTGAGA TCTC TATATATT TGG
GT GCTT CAATA A
TATTAATGGGAATGGTGGCT AGAC ||||| |||||||| |||| |||||||| ||| || |||| |||||
TTCAATATAAGATTATTGCA CATAC CGGATTTT GGAG GTGTGTAA GCC CA TGGA
GTTAT G
GGTGACGACCGGGAATGTGT A TAA-- -- GG AG--- G C TA
GGAGGAATTTTTAGGCACAT
ACAAGGCCGGG
GAM1529 TTCATGGTGGGCTCTCTTCA 1502 TTCATGGTGG 3178 G TC TCAT- A GA CACT A AT
TATCATAGACACACTGGATC GCTCTCTTCA TTCATG TGGGC TCT ATC TA CA GG TC A
ATATTAGAACCCTGGATACG TATC |||||| ||||| ||| ||| || || || ||
GTTACACGGAAGGTTCACAT AAGTAC ACTTG AGG TGG AT GT CC AG T
GAA - GA CACAT C AG C--- A AT

GAM1530 CAAGTCTTCCATGTTGAAGA 1503 AAGTCTTCCA 3179 - CC AA- C-- A CA
CCAAGGGCATTTCTCCATGC TGTTGAAGAC CAA GTCTT ATGTTG GA CA GGG T
AATCGGGCAACGTCAGGACA CAAG ||| ||||| |||||| || || |||
TTG GTT CAGGA TGCAAC CT GT CCT T
A C- GGG AAC A CT

GAM1531 ATGAAGTCAACTGGTATCTG 1504 TTTTCACGGC 3180 G AAC ATC A-- A- - AA TAG-
TTAC
ATGGGAATGGGCAATGAAAT CATAGCTTCC ATGAA TC TGGT TG TGGGA TG GGC TGAAA
AC A
AGACTTACACACTGTACATT AATA ||||| || |||| || ||||| || ||| ||||| ||
TTCACGGCCATAGCTTCCAA TATTT AG ACCA AC ACCTT AT CCG ACTTT TG /
TACAAGCACCAAGGAGTTTA G GA- CGA ATA CG A GC TACA TCAC
T

GAM1532 GGGGACAAGATGTTGCGCAT 1505 GGGACAAGAT 3181 G A TG CGCAT AAA CCAC -
A
GCAGAAAGGTGACCCACAAG GTTGCGCATG GG GACA GA TTG GCAG GGTGAC AAGT
CT T
TCTATGAAGAACTTTTCAGT CAGA || |||| || ||| |||| |||||| |||| ||
TACTCCTGCCCCAAGTTCCT CC CTGT CT AAC CGTC TCATTG TTCA GA G
GTCGCC G C TG CC--- C-- ACTT A A

GAM1533 TTGTGAGATCAGCGTGACAG 1506 TGAGATCAGC 3182 CA---- T - GA G TG GTG TG
TG G TT
GAGTGTGTGTGTGTGTGTGT GTGACAGGAG T GCG GA CAG GTGT TG TGTGT
TGTTATCTG GG T TGG T
GTTATCTGTGGGTGTGTGGT TGTG | ||| || ||| |||| || ||||| ||||||||| || | |||
TTGGTTGGGTGCTGCCAGGT A CGT CT GTC CATA AT ATACG ACGGTGGAC TC G
GTT /
GGCAAAGGCATATGTAAATA TTTCTA - A TA A GT GAA CG GT G GG
CATCTGATCTGCATCTTTAT
TTCACAG
GAM1534 TTCCTCTCACGCCCTCACCT 1507 AAGCTGCCAG 3183 C A--- T-- T CC G A T
CCTG
GGCTGAGCCGCAGTAGTTCT TTGAAGAACT CCTC CC GGC GAG GCAGTAGTTCTTCAG
TGGCA GCTTTA GT A
TCAGGTGGCAAGCTTTATGT GTTG |||| || ||| ||| |||||||||||||| ||||| |||||| ||
CCTGACCCAGCTAAAGCTGC GGAG GG CCG CTC CGTTGTCAAGAAGTT ACCGT
CGAAAT CG /
CAGTTGAAGAACTGTTGCCC - CTTC TCC T C- G - - ACCC
TCTGCCCCTGGCTTCGAGGA
GGAGGAGGAG
GAM1535 TCCAACTTTGTGGAATGGTA 1508 GTAAGGATTT 3184 T-- GAATG- AGG AGGG GG
AGGATTTTTAGGGTTGTTTG TTAGGGTTGT TCCAACT TGTG GTA ATTTTT TTGTTT C
GCCAGAACAAGAGAAATAAC TT ||||||| |||| ||| |||||| ||||||
TGCAGAAAACACATATGGTT AGGTTGG ACAC CGT TAAAGA AACAAG /
GGA TAT AAAAGA CAA G--- AC

GAM1536 CCCTAGAATGTGGCAACGTA 1509 TGTGGCAACG 3185 A ATGT AACG G C - A
GTTTGTGCTCGCCGAGAACG TAGTTTGTGC CCCT GA GGC TAGTTT TG TCGC CG G
TGTGACCAAAATTGGCCTCA TCGC |||| || ||| |||||| || |||| ||
GGG GGGA CT CCG GTTAAA AC AGTG GC A
- ---- ---- - C T A

GAM1537 AGCAGGACCTTCCCCGTACG 1510 TTCAAAGCGG 3186 CTTCC ------ G A CA
CCAATTATGCATATACATAA CTATAGTTTT AGCAGGAC CCGT AC CCA TTATG T
TGGGGTTTCAAAGCGGCTAT GCT |||||||| |||| || ||| |||||
AGTTTTGCT TCGTTTTG GGCG TG GGT AATAC A
ATATC AAACTT G - AT

GAM1538 CCATATCCAGAGAACTCAAG 1511 TCCAGAGAAC 3187 C GAA- ----- GTGAA GAT G
AA
GTGTGAATACCAGATCCGGT TCAAGGTGTG CCATATC AGA CTC AAGGT TACCA CCG
TTGGAG A
TGGAGAAAGGGTTCCAAGTG AATA ||||||| ||| ||| ||||| ||||| ||| ||||||
GTGGTGACCTTGCGGAGAGA GGTGTAG TTT GAG TTCCA GTGGT GGT AACCTT
G
AGATTTTGATGTGG T AGAA AGGCG ----- --- G GG

GAM1539 CTGTGCCTATAATTCCAGCA 1512 AAGCTGCCAT 3188 ATAA G CAC GA TGT CT G TG
----- ATGT
TGACACCTGACATGTGCCTT GCTGAAGAAC TTCCA CATGA CT CA GC TGG AGCTT A
GCTGAC T
GGGAGCTTTGAGCTGACATG TCAT ||||| ||||| || || || ||| ||||| | ||||||
TTAGAAGTCAGTCTACATTG AGGGT GTACT GA GT CG ACC TCGAA T TGACTG
/
AAGCTGCCATGCTGAAGAAC AG-- - CAA A- --- T- G GT ACATC AAGA
TCATGTGGGAGAACACACAG

GAM1540 GTAAACTCCAACCCAGAATG 1513 TTGGAGCAGG 3189 AACCC - - TA AA T CA TCT
AC- CT
GGGAAGAATACTGAATTAGC TTTCATTCTC AGAAT GGGGAA GAA CTG TTAGC GAG CAT
GGAC AATT G
TGAGCACATTCTGGACACAA CAAT ||||| |||||| ||| ||| ||||| ||| ||| |||| ||||
TTCTGACCAATTTCAGTCTC TCTTA CCTCTT CTT GAC GGTTG CTC GTA TCTG
TTAA A
ATGATCTCTGTTGGAGCAGG TTTTC A A TG GA T TA C-- ACT CC
TTTCATTCTCCAATTCTCTT
TTACAGAAC
GAM1541 CAGTATCAAGTGCTTGGACT 1514 TCAAGTGCTT 3190 CAAG T- CTC TG - G
CCATGTGCTGTTTCCCGGAA GGACTCCATG CAGTAT TGC TGGA CA TGCTGTTTC CC G
GGAGAAGCAGCGTGTGCATC TGCT |||||| ||| |||| || |||||||||| ||
TGTTGCAAGAATGCTG GTCGTA ACG GTCT GT GCGACGAAG GG A
AGA- TT AC- GT A A

GAM1542 TGTTTGGGATCTGGTCTGAG 1515 GGAAGTTGCT 3191 TC T G C GGCA TG TA A - T
C ---- AT
GGGGCGGACGGCACTGATAT GGCTTCAGCT TGG CTGAG GGG GGAC C A TCA C GCTG
GGCC GC TCTC G

CAACGCTGTGGCCCGCTCTC GATG ||| ||||| ||| |||| | | ||| | |||| |||| || |||| ATGATGGGAAGTTGCTGGCT ATC GATTT TCC CTTG G T AGT G CGAC TCGG CG AGGG / TCAGCTGATGACTTTGGCAA -- - G A AAAC GT TC A T T T TTGA TA AGTTCACCTGTTTAGCTACC CCTGCTGTCAG

GAM1543 ATCTGTCAGGAGCAAGGACT 1516 CATCACTGTT 3192 CAA TACTT CA ACTTTGGCATTAACCATCAC TGATTTCTTG ATCTGTCAGGAG GGAC TGG T TGTTTGATTTCTTGACAGGT ACAG |||||||||||| |||| ||| TGGACAGTTCTT TTTG ACC T TAG TCACT AA

GAM1544 TCCTTTTGACAAGAAATGTG 1517 TGACAAGAAA 3193 T AAGAAATGT C AA-- CTGT T GTCGTGAAAATTGGACTGTG TGTGGTCGTG TCCTT TGAC GGT GTGAA TTGGA GC T CTTTTGCTCCAGATGGTTCA AAAA ||||| |||| ||| ||||| ||||| || TACTTTGCTTTGGTCACAAG AGGAA ACTG TCA TACTT GACCT CG T GA C GTTTCGTT- - GGTA ---- T

GAM1545 AGCCATATCTTGTGGTATGT 1518 AACAGTATCT 3194 A -- TA-- A ATTTC TTATAACGTATTTCTTTCAC ACTAAAGATG AGCC TATCTT GTGG TGTTT TAACGT T ATGTTAAAACAGTATCTACT GGCT |||| |||||| |||| ||||| |||||| AAAGATGGGCT TCGG GTAGAA CATC ACAAA ATTGTA / - AT TATG - CACTT

GAM1546 CCTACTCCAAAATACTCACA 1519 TCTACAGTGT 3195 A - A TC-- -- GA CTGGACTGAATGAAGTCTAC CAATGTGTCT CCT CTC CAA ATAC ACACTG GACT A AGTGTCAATGTGTCTTGAGA TGAG ||| ||| ||| |||| |||||| |||| GAGG GGA GAG GTT TGTG TGTGAC CTGA T - A C TAAC AT AG

GAM1547 GCCCTCACCTGGCTGAGCCG 1520 AAGCTGCCAG 3196 CTCACCT T CC - A T CCTG CAGTAGTTCTTCAGTGGCAA TTGAAGAACT GCC GGC GAG GCAGTAGTTCTTCAG TGGCA GCTTTA GT A GCTTTATGTCCTGACCCAGC GTTG ||| ||| ||| |||||||||||||| ||||| |||||| || TAAAGCTGCCAGTTGAAGAA CGG CCG CTC CGTTGTCAAGAAGTT ACCGT CGAAAT CG / CTGTTGCCCTCTGCCCCTGG TCC---- T C- G - - ACCC C

GAM1548 GGATTAGAAACCCGTAGATC 1521 AACCCGTAGA 3197 A - G AT C-- TT AGTTCTAGGTTAGCCCTGAT TCAGTTCTAG GG TTAGAAAC CC TAG CAGTT TAGG A TAACTGCCCTGGGTGTTTCT G || |||||||| || ||| ||||| |||| GGGCC CC GGTCTTTG GG GTC GTCAA GTCC / G T - CC TTA CG

GAM1549 GTGAAGTGGCAGGAATGGGG 1522 TGAAGGCCTG 3198 TG T - G AGAACAA TT AGA
TAGAACAACGCTTTTCAGAC GTTCTTTGTC G AAG GGCAG GAAT GGGT CGCT TC C
TACAGATGGTGAAGGCCTGG TTTT | ||| ||||| |||| |||| |||| || ||
TTCTTTGTCTTTTGC C TTT CTGTT CTTG TCCG GTGG AG T
GT - T G GAA---- T- ACA

GAM1550 GGCGTCACTGCCCTGATGGG 1523 TGAAAAGCCT 3199 ---- TGAT GG- TG A- CA
CGGTTGGGAAGGCAAAACCT TTGGGTAGTG GGC GTCACTGCCC GGGC T GG AGG A
GCCCTGAAAAGCCTTTGGGT ATTC ||| |||||||||| |||| | || |||
AGTGATTCTAGCC CCG TAGTGATGGG TCCG A CC TCC /
ATCT TT-- AAA GT CG AA

GAM1551 GCTCCAAAGAACCAAGAGTG 1524 CATTTCACTT 3200 AA T - TTC--- - GT GAG
AG-- TC
CAAATCAGTCCATTTCACTT TCACTGTCTG CC GAG GCAAATC AGTCCAT AC TTTCACT CT
AT GGTC T
TCACTGTCTGAGATAGGGTC AGAT || ||| ||||||| ||||||| || ||||||| || || ||||
TCTAAGACCATGGATACAAG GG CTT CGTTTAG TCAGGTA TG AAGGTGG GA TA
CCAG /
GGTGGAATGTAGCTATATGG C- - C TATCGA T -- ACA GGTA AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1552 GGAGGTAGAGGTTGCAGTGA 1525 GAGGTAGAGG 3201 AGAG----- AG T ---- G
GTCGAGATGGTGCCATTGCT TTGCAGTGAG GGAGGT GTTGC TGAG CGAGA TG T
CTCGTTTGGGCAACAAGAGT TCGA |||||| ||||| |||| ||||| ||
GAAACCTCT TCTCCA CAACG GTTT GCTCT AC G
AAGTGAGAA G- - CGTT C

GAM1553 GGGTGCACAAGTGATGGTCC 1526 GTAAGGATTT 3202 - -- T-- GAATG- AGG
AGGG GG
AACTTTGTGGAATGGTAAGG TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
ATTTTTAGGGTTGTTTGGCC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
AGAACAAGAGAAATAACTGC TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /
AGAAAACACATATGGTTGGA G AA TAT AAAAGA CAA G--- AC
AACCATGCGCTTGTGACTT

GAM1554 AGAACACAGAAGCTGCCAGG 1527 GAAGCTGCCA 3203 CA GAA G CA A TGA
CATGCTATACTGAGAATTGT GGCATGCTAT AGAA CA GCT CCAGG TGCT TAC G
GGGTGAACTTGGAGCAGATG AC |||| || ||| ||||| |||| |||
GTTTCT TCTT GT CGA GGTTC GTGG GTG A
TG AGA - AA - TTA

GAM1555 TACAGTCGTCGGGAAGGAAC 1528 CAGAGCAATT 3204 GG A AAC -- CA - AGAATA
T GGAAATTA

AAGAGGCTCCAGTTGGAGTG TTAACAGAGG G A GG AAGAGG CTC GTTGGAGT GCTC
CTCC CGA C
CTCAGAATACTCCTCGAGGA CCCT | | || |||||| ||| |||||||| |||| |||| |||
AATTACAATGAAAGTCGTGG C T CC TTCTCC GAG CAATTTTA CGAG GAGG GCT
/
AGGCCAGAGCAATTTTAACA AT A ACC CG A- A ACCG-- T GAAAGTAA
GAGGCCCTCTTCCACCATTA
CGACCCCTTA
GAM1556 TTGGCCCAATTCCAATCTTC 1529 TAGCACCATT 3205 CCC C TCTTC T A
TGCTAACTTTTCCACCTGGA TGAAATTAAC TTGG AATT CAA TGCTAAC TTTCC C
GATGTTAGCACCATTTGAAA CAA |||| |||| ||| ||||||| |||||
TTAACCAA AACC TTAA GTT ACGATTG AGAGG C
AA- A TACC- T T

GAM1557 CTCTTGAGCATGCTGACCAG 1530 GACCAGTGCT 3206 G A TGA C CATAA TG ACTCA
TGCTGGCATAAGCTGAAACT GGCATAAGCT CTCTT AGC TGC CCAGTG TGG GC AA A
CAAATATCCTTTGGCCTCCA GAA ||||| ||| ||| |||||| ||| || ||
CACTGGCTGCAGGCTGGGAG GAGGG TCG ACG GGTCAC ACC CG TT A
- G TC- - TC--- GT CCTAT

GAM1558 TGGCACCTTGGTGAAGAAGA 1531 TGGAATTTGA 3207 - A AGA TT GA A AT GA
T G G
GAATTTGGAATTTGAAGAAG AGAAGATGAA CCTTGGTGA GAAG AT GGAATTT AG AG
GAAGAA GGG GGT CTG A
ATGAAGAAGAGGGTGGTGCT GAAG ||||||||| |||| || ||||||| || || |||||| ||| ||| |||
GGAGCAGGGTCTCCTGATTC GGAACCATT TTTC TG CCTTGAG TC TC TTTCTT TCC
CTG GAC /
TTTTCCTGCTAGAGTTCCCG T A A-- GC A- G CT AG T G G
GTACTTTATTACCAAGGTTG
CCA
GAM1559 TGCCTCCCGAAGGAAGTGGG 1532 CACGCCGAAG 3208 AA G AAC C A----- C AG
G G AA AA
TCAACGCACGCAAGGCCTGC GATGCTGCCG CG GGAA TGGGTC GCA GCA GGC TGC
TCTAGT TCA CC G A
AGTCTAGTGTCAGCCAAGAA ATCC || |||| |||||| ||| ||| ||| ||| |||||| ||| || |
ACTCCAGGATGAACTGGGAG GT CCTT GCCTAG CGT CGT CCG ACG GGGTCA
AGT GG C /
GCACGCCGAAGGATGCTGCC G- A C-- - AGGAAG C GA - A AC TC
GATCCGATTCCGTGGGAAGC
A
GAM1560 AGGGGGGCAAAGTCTATCAG 1533 GGGGCAAAGT 3209 G GT A TG TTGAAA TG-
AG G GAT
GTGTTTGAAAGTGTGGCTAA CTATCAGGTG AGGG GGCAAA CT TCAGG T GTG GCTAAGA
TAT ATGT G
GAAGTATGATGTGATGAATG TTTG |||| |||||| || ||||| | ||| ||||||| ||| ||||
ATATGATGAGTCTTGGTATC TCTC TCGTTT GA GGTTT G TAC TGGTTCT GTA
TATA A
CATCGTGTTTGGAAGGATTT G AG A GT C----- CTA GA G GTA

GCTGCTCT

GAM1561 ACCGGTTATGGTGCTGCTGT 1534 TGGAGCCTGG 3210 GG T - AC GTTGGAGC
G TT T T
GAACACTGCCAAGTTGGAGC CTCTGTTTGT CGGTTAT TGC GCT GTGA ACTGCCAA
CTGGCTCT T G GCCG C
CTGGCTCTGTTTGTGCCGTC GCCG ||||||| ||| ||| |||| |||||||| |||||||| | | ||||
TTTGGTCTGGGAGGAGTCGG GTCGGTG ATG CGG TACT TGACGGTT GGCTGAGG
G T TGGT T
ATTGGCAGTTATCATGGGCT AA T G AT A------- A GG C T
GTAAAGTGGCTGGT

GAM1562 GTCACCCAGGAGCTCCACAG 1535 TGATGTAGTA 3211 T A TC TCG GA CTT AC
CTTTCGGCAGATCCTTGGAC AGCTGTGTGC G CACCC GGAGC CACAGCTT GCA TC GG A
AGCGCCTTGATGTAGTAAGC TCCC | ||||| ||||| |||||||| ||| || ||
TGTGTGCTCCCGGGTGC C GTGGG CCTCG GTGTCGAA TGT AG CC G
- C T- TGA -- TT- GC

GAM1563 GAAGACTTCCTAAATTTGCA 1536 TTTGCACATT 3212 AC A TTGCA TTGCC
ACCAT
CATTAGCTAGATTGCCATTA AGCTAGATTG GAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
GCACCATTAGAGAGTTGATC CCAT |||| ||||| ||| |||||||||| ||||||
TTTGGCTAATGATTATTCAG CTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GAAAATTTC AA C TTA-- C---- AGAGA

GAM1564 GTTACCACACTGGCCTTCTT 1537 TACCACACTG 3213 CAC G T----- T--- TG
TTTGGTGTTGGTCTGCTTGA GCCTTCTTTT GTTAC ACTG CCTTCTTTT GGTGT GGTC C
CCCATCGCACTCTGGTCAGG TGGT ||||| |||| ||||||||| ||||| ||||
GGAAGGGCGGTTGTAAT TAATG TGGC GGAAGGGGA TCACG CCAG /
T-- G CTGGTC CTAC TT

GAM1565 AGCTCCTGCAGCTCCTTTTG 1538 TGACAAGAAA 3214 - CA ---- T - AAATGT C AA--
CTGTT T
ACAAGAAATGTGGTCGTGAA TGTGGTCGTG CTG GC TCCTT TGAC AAG GGT GTGAA
TTGGA GC T
AATTGGACTGTTGCTTTTGC AAAA ||| || ||||| |||| ||| ||| ||||| ||||| ||
TCCAGATGGTTCATACTTTG GAC CG AGGAA ACTG TTC TCA TACTT GACCT
CG T
CTTGGTCACAAGGACATCGC T A- CTAC C G GTT--- - GGTA ----- T
ACAGTAAAGCT

GAM1566 GCTTTTGCTCCAGATGGTTC 1539 CCAGTGCCTT 3215 TT TCC T ATACTTT T - AA
TC ACA
ATACTTTGCTTGGTCACAAG CAGAACTTTC GCT TGC AGA GGTTC GCT GG TCAC
GGACA GC G
GACATCGCACAGTAAAGCTT TCTT ||| ||| ||| ||||| ||| || |||| ||||| ||

GTTCCGTGGTCCCAGTGCCT CGG ACG TCT TCAAG TGA CC GGTG CTTGT CG T
TCAGAACTTTCTCTTGCATG T- TTC T ACTTCCG C T C- T- AAA
GC

GAM1567 TCCTTTTGACAAGAAATGTG 1540 TGACAAGAAA 3216 T - AAATGT C AA-- CTGTT T
GTCGTGAAAATTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA TTGGA GC
T
GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||
ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T
GA C G GTT--- - GGTA ----- T

GAM1568 GGTGCACAAGTGATGGTCCA 1541 GTAAGGATTT 3217 - G- T-- GAATG- AGG
AGGG GG
ACTTTGTGGAATGGTAAGGA TTAGGGTTGT CACAAGTG ATG TCCAACT TGTG GTA
ATTTTT TTGTTT C
TTTTTAGGGTTGTTTGGCCA TT |||||||| ||| ||||||| |||| ||| |||||| ||||||
GAACAAGAGAAATAACTGCA GTGTTCGC TAC AGGTTGG ACAC CGT TAAAGA
AACAAG /
GAAAACACATATGGTTGGAA G AA TAT AAAAGA CAA G--- AC
ACATGCGCTTGTGACT

GAM1569 GTGATGGTCCAACTTTGTGG 1542 GTAAGGATTT 3218 G -- T-- GAATG- AGG AGGG
GG
AATGGTAAGGATTTTTAGGG TTAGGGTTGT GT ATGG TCCAACT TGTG GTA ATTTTT
TTGTTT C
TTGTTTGGCCAGAACAAGAG TT || |||| ||||||| |||| ||| |||||| ||||||
AAATAACTGCAGAAAACACA CG TACC AGGTTGG ACAC CGT TAAAGA AACAAG
/
TATGGTTGGAAACCATGC - AA TAT AAAAGA CAA G--- AC

GAM1570 GGGCTCCTCATGACACCTTG 1543 TACACAGCCA 3219 TC ACACC TACAC AACT G
GA T
CTACACAGCCAACTTTGTGG ACTTTGTGGC GGGCTCC ATG TTGC AGCC TTGTGGC
CCT GGTGC G
CGCCTGAGGTGCTGAAGCGC GCCT ||||||| ||| |||| |||| ||||||| ||| |||||
CAGGGCTACGATGAAGGCTG TCCGAGG TAC AGCG TCGG AGCATCG GGA
CCGCG A
CGACATCTGGAGCCT TC ----- ----- AAGT - -- A

GAM1571 GGTCTCAGTGTATGACAGAT 1544 TCAGTGTATG 3220 G A CAG CG- - AG
CACGGAGGAAGCACATCATT ACAGATCACG GGTCTCA TGT TGA ATCA GAG GA C
TAGCTGATACTTAAACATGA GAGG ||||||| ||| ||| |||| ||| ||
GACC CCAGAGT ACA ATT TAGT TTT CT A
- A CA- CGA A AC

GAM1572 GAGTGCAAATCAGTCCATTT 1545 CATTTCACTT 3221 T - ---------- CAC GAGATA
TC

CACTTTCACTGTCTGAGATA TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT
TGTCT GGGTC T
GGGTCTCTAGGACCCAGGAT AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
ACAAGGGTGGAATGTAGCTA CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
TATGGACTCGATTTGCTTC - C TATCGATGTA AC- A----- GA

GAM1573 TGAAGACTTCCTAAATTTGC 1546 TTTGCACATT 3222 AC A TTGCA TTGCC
ACCAT
ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC
T
AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM1574 TGAGCAAATCAGTCTGAGTA 1547 CAAATCAGTC 3223 AG TCT AAGATAG GAA TG TG
CTCA TAC
AGATAGGTGAGAACTGATGA TGAGTAAGAT TG CAAATCAG GAGT GTGA C A AGG
CAGGAAT T
GGCTCACAGGAATTACTAAT AGGT || |||||||| |||| |||| | | ||| |||||||
TATTTCTGATACCTTGTTGG AC GTTTAGTC TTCG TACT G T TCC GTCTTTA A
GTCATATAATGGCTTTCTGA G- T-- GTAATA- G-- GT GT ATA- TTA
TTTGGCA

GAM1575 CAAATCAGTCTGAGTAAGAT 1548 CAAATCAGTC 3224 TCT AAGATAG GAA G TG
CTCCA TAC
AGGTGAGAACTGATGAGGCT TGAGTAAGAT CAAATCAG GAGT GTGA CT A AGG
GGAAAT T
CCAGGAAATTACTAATTATT AGGT |||||||| |||| |||| || | ||| ||||||
TCTGATACCTTGTGGGTCAT GTTTAGTC TTCG TACT GG T TCC TCTTTA A
ATAATGGCTTTCTGATTTG T-- GTAATA- --- G GT ATAG- TTA

GAM1576 CAGTGGTTCTCTCAGCAACA 1549 TCAAAGCTGC 3225 TC - AACA-- - A- A TA
TGAC T CC
GACATGTCCAGTGGACCGTA AGATTGCCTG GT TCT CAGC GACATGT CC GTGG CCG
GTGTTG GG CGC A
GTGTTGTGACGGTCGCCCAT TG || ||| |||| ||||||| || |||| ||| |||||| || |||
CTGCGCCCAGTACCTCGGAT CG AGA GTCG TTGTACA GG TACT GGC CATGAC
CC GCG T
CATGCGGAACATGTTGTCAA TT C AAACTG A CG A TC ---- - TC
AGCTGCAGATTGCCTGTG

GAM1577 TGGCACCTGGTGAAGAAGAG 1550 TGGAATTTGA 3226 - - A AGA TT GA A AT GA
T G G
AATTTGGAATTTGAAGAAGA AGAAGATGAA CCT GGTGA GAAG AT GGAATTT AG AG
GAAGAA GGG GGT CTG A
TGAAGAAGAGGGTGGTGCTG GAAG ||| ||||| |||| || ||||||| || || |||||| ||| ||| |||

GAGCAGGGTCTCCTGATTCT GGA CCATT TTTC TG CCTTGAG TC TC TTTCTT TCC CTG GAC /
TTTCCTGCTAGAGTTCCCGG T A A A-- GC A- G CT AG T G G
TACTTTATTACCAAGGTTGC
CA
GAM1578 GGCACCTATGACGATTATGT 1551 TGGAAAGAAA 3227 A ATTA GAAGGAC GT
TGAAGGACTTCATGTGTTTG TGGCACCGAC GGCACCTATG CG TGTT TTCATGT T
ACATGGAAAGAAATGGCACC ATGG |||||||||| || |||| |||||||
GACATGGGTGCT TCGTGGGTAC GC ACGG AGGTACA /
A C--- TAAAGAA GT

GAM1579 GGAGGGGACAGGGAGCTTCC 1552 TAACTGATGC 3228 --- GG T CTA CT G
TAGGTCTGTTGATAAACTAA TTTGTCAAGT GGAGGG GACA GAGC TC GGT GTT A
CTGATGCTTTGTCAAGTCTT CTTC |||||| |||| |||| || ||| |||
CC CCTTCT CTGT TTCG AG TCA CAA T
GAA -- T --- AT A

GAM1580 ATTGACGCACGGCAGTGGGG 1553 TCCTCCAGTG 3229 C A GT TTTACC - CC -- G A CC T
AGAACAGCGTCTTTTACCTG GCGTTCTTTT GG AGTGGGGAGAAC GC CT TGT CA GAAGC CA GA GC CGTT G
TCACCGAAGCCAGGAAGCCC TACT || |||||||||||| || || ||| || ||||| || || || ||||
CGTTTGTAAGCGTGTGTTGT TC TCATTTTTCTTG CG GA ACA GT TTTCG GT TT TG GCGA T
GGTGCTTTATTGTACATCCT - - GT CCTCCT T TA TG G G T- A
CCAGTGGCGTTCTTTTTACT
CTAATGTTCTT
GAM1581 TGTTTGGGATCTGGTCTGAG 1554 GGAAGTTGCT 3230 TC T G C GGCA TG TA A - T C ---- AT
GGGGCGGACGGCACTGATAT GGCTTCAGCT TGG CTGAG GGG GGAC C A TCA C GCTG GGCC GC TCTC G
CAACGCTGTGGCCCGCTCTC GATG ||| ||||| ||| |||| | | ||| | |||| |||| || |||| |||
ATGATGGGAAGTTGCTGGCT ATC GATTT TCC CTTG G T AGT G CGAC TCGG CG AGGG /
TCAGCTGATGACTTTGGCAA -- - G A AAAC GT TC A T T T TTGA TA
AGTTCACCTGTTTAGCTACC
CCTGCTGTCAG
GAM1582 TCCTTGCGAATGGCTCCCAT 1555 GGCAGCTTGT 3231 T G CCATTT CA TT- AA C AGATA A
TTGACACATTCCTAAGTCTA ACAGGTCTTG TCC TGC AATGGCTC GA CA CCT GT TAAG CCC C
AGAGATACCCACTAGGGCAG AATC ||| ||| |||||||| || || ||| || |||| |||
CTTGTACAGGTCTTGAATCC AGG ACG TTACCGGG CT GT GGA CA GTTC GGG T
CTGGGCCATTGGCACGGA C G TCC--- AA TCT -- T GAC-- A

GAM1583 CAGTGTGGTTTAATCTGGAA 1556 ACCCGTGTTC 3232 T T CT - GAAGCTG A A
GGAGCAGAAGCTGTGGAGTC CTATCCTTGT CAG GTGGT TAAT GGA AGGAGCA TGG GTCC A

CAAAGGACCCGTGTTCCTAT TGTG ||| ||||| |||| ||| ||||||| ||| ||||
CCTTGTTGTGCCACTTG GTT CACCG GTTG CCT TCCTTGT GCC CAGG /
- T TT A ------- - A

GAM1584 AGCAGTGGGGAGAACAGCGT 1557 TCCTCCAGTG 3233 C A GT TTTACC - CC -- G A CC T
CTTTTACCTGTCACCGAAGC GCGTTCTTTT AG AGTGGGGAGAAC GC CT TGT CA GAAGC CA GA GC CGTT G
CAGGAAGCCCCGTTTGTAAG TACT || |||||||||||| || || ||| || ||||| || || || ||||
CGTGTGTTGTGGTGCTTTAT TC TCATTTTTCTTG CG GA ACA GT TTTCG GT TT TG GCGA T
TGTACATCCTCCAGTGGCGT - - GT CCTCCT T TA TG G G T- A
TCTTTTTACTCT

GAM1585 GAGAAATTATTTGGACAAGA 1558 TGGACAAGAT 3234 AAA A CAAGAT G AT TT
TGTTGGCAAATCACTTTTAC GTTGGCAAAT GAG TT TTTGGA GTTG CAA CACT T
AGGTGCTTGTAACCTCCAGG CACT ||| || |||||| |||| ||| ||||
AGACCTC CTC AG GGACCT CAAT GTT GTGG A
C-- A C----- - C- AC

GAM1586 AGGCGGCTCAGTGTGAAGAA 1559 AGGCGGCTCA 3235 C C AAGAACTAC CTG
CTACGGGTTTCCTGATGTTG GTGTGAAGAA AGG GG TCAGTGTG GGGTTTC A
AAGCTCAGAATTAGCCACAC CTAC ||| || |||||||| |||||||
TGACCTTCT TCT CC AGTCACAC CTCGAAG T
T - CGATTAAGA TTG

GAM1587 CAACCATACGTGGTTTTACC 1560 CGTGGTTTTA 3236 AC T -- CCT --- ATTTAC
TAGGGGTAGGATTTACCAAA CCTAGGGGTA CA CA ACGT GGTTTTA AGGGGT AGG C
ACGCCTTGCACCCCTTGAAA GG || || |||| ||||||| |||||| |||
CCTTGCGTCTGTGTG GT GT TGCG CCAAAGT TCCCCA TCC /
GT C TT --- CGT GCAAAA

GAM1588 AACTCATAGGCTGGCCAGCA 1561 TCAAGTGCTT 3237 CA GG CC TC ACTTCAC
TCTGAGAACTTCACTTTAAT CAGAATAGGT AACT TA CTGG AGCA TGAGA T
ATCTTTCAAGTGCTTCAGAA T |||| || |||| |||| |||||
TAGGTT TTGG AT GACT TCGT ACTTT T
-- AA -- GA CTATAAT

GAM1589 ACCGGTTATGGTGCTGCTGT 1562 TGGAGCCTGG 3238 GG T - AC GTTGGAGC G TT T T
GAACACTGCCAAGTTGGAGC CTCTGTTTGT CGGTTAT TGC GCT GTGA ACTGCCAA CTGGCTCT T G GCCG C
CTGGCTCTGTTTGTGCCGTC GCCG ||||||| ||| ||| |||| |||||||| |||||||| | | ||||
TTTGGTCTGGGAGGAGTCGG GTCGGTG ATG CGG TACT TGACGGTT GGCTGAGG G T TGGT T

ATTGGCAGTTATCATGGGCT AA T G AT A------- A GG C T
GTAAAGTGGCTGGT

GAM1590 CGAACCCAGAGAATAGCAGG 1563 TCAGTTTTTC 3239 - - AAT C T --- A-- TTATG
ATAAACCCTTACCATTATGT TTCTCCTTCT CGAA CCC AGAG AG AGGA AAAC CCTT CCA
T
GAACTTGGGAAAAGGTCAGT AGGG |||| ||| |||| || |||| |||| |||| |||
TTTTCTTCTCCTTCTAGGGT GCTT GGG TCTT TC TTCT TTTG GGAA GGT /
TTCG T A CC- - T ACT AAG TCAAG

GAM1591 TTAAGAACTAAAGCTGAGAT 1564 TATCACAGCA 3240 AG CT -- CT - T T -
TTCCTG
TCTCCTATTCTGTTGTTGAG ATTTGAGAAG TTA AACTAAAG GAGA TTCTC ATT CTGT GT
GAG GGGC C
GGGCTTCCTGCATGCCCGCC TTTT ||| |||||||| |||| ||||| ||| |||| || ||| ||||
CATTTTATCACAGCAATTTG AGT TTGGTTTT CTTT AAGAG TAA GACA TA TTT CCCG
/
AGAAGTTTTCTTTTTGGTTT CT T- TG TT C C T A CCCGTA
CTGA

GAM1592 GCTTTTGCTCCAGATGGTTC 1565 CCAGTGCCTT 3241 TT TCC T ATACTTT T - AA
TC ACA
ATACTTTGCTTGGTCACAAG CAGAACTTTC GCT TGC AGA GGTTC GCT GG TCAC
GGACA GC G
GACATCGCACAGTAAAGCTT TCTT ||| ||| ||| ||||| ||| || |||| ||||| ||
GTTCCGTGGTCCCAGTGCCT CGG ACG TCT TCAAG TGA CC GGTG CTTGT CG T
TCAGAACTTTCTCTTGCATG T- TTC T ACTTCCG C T C- T- AAA
GC

GAM1593 CCCTCTGGTTCTGGTTGACA 1566 TGGTTGACAG 3242 G- TG T --- A T- A T AT
GAAGTATGTATTATCAGATT AAGTATGTAT CCCTCTG TTC GT GACA GA GTA GT TTA CAG
T
CCCTGTGAGGCTTTACATCC TATC ||||||| ||| || |||| || ||| || ||| |||
CATGTTTGCTGGAGAACAGA GGGAGAC GAG CG TTGT CT CAT CG AGT GTC /
GGG AA GT T ACC A TT G - CC

GAM1594 GCTCCAAAGAACCAAGAGTG 1567 CATTTCACTT 3243 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1595 CACAAATCCAGCACTTCCTC 1568 AGCAACACAT 3244 T GCACTTC-- T T- G
TCCATTTACTCTGTCAGGCT ATGGCTTTGT CACAAA CCA CTCTCCAT TAC CT T

GTATATGGGGAGCAACACAT G |||||| ||| |||||||| ||| ||
ATGGCTTTGTG GTGTTT GGT GAGGGGTA ATG GG C
C ATACACAAC T TC A

GAM1596 GACGCTTTATATTTCTGAAG 1569 GAGAGCATAG 3245 - GTTCA- GAA CAT- -- CC T
AACC TA
TTCAGCTGAACACCATGGCT TATTCAGGAG ATATTTCTGAA GCT CAC GGC TGGAG AG
GTC GAG G
GGAGCCAGTGTCAACCGAGT TGTT |||||||||| ||| ||| ||| ||||| || ||| |||
AGTGTCTCCCGGACCTCTTC TGTGAGGACTT CGA GTG CCG ACTTC TC CAG
CTC T
ATTGCCTAAAGTGAGAGCAT T ATGATA GA- AAAT TT -- - GCC- TG
AGTATTCAGGAGTGTTTTTT
AGTT
GAM1597 CATGCCGTTTTAGTTCACGA 1570 TTGATCATCG 3246 G TAG A GC CTA-- G CA
AGGCCAAGCTAATGCTGGGC TGAAAGCAGA CAT CCGTTT TTCACGA G CAAG ATGCT GG
C
ACTACTGGGCATATATTTTT TGGA ||| |||||| ||||||| | |||| ||||| ||
GATCATCGTGAAAGCAGATG GTA GGTAGA AAGTGCT C GTTT TACGG TC /
GATG - CGA A TA TTATA G AT

GAM1598 AAGAGGCTCCAGTTGGAGTG 1571 CAGAGCAATT 3247 -- CA - AGAATA T
GGAAATTA
CTCAGAATACTCCTCGAGGA TTAACAGAGG AAGAGG CTC GTTGGAGT GCTC CTCC CGA
C
AATTACAATGAAAGTCGTGG CCCT |||||| ||| |||||||| |||| |||| |||
AGGCCAGAGCAATTTTAACA TTCTCC GAG CAATTTTA CGAG GAGG GCT /
GAGGCCCTCTT CG A- A ACCG-- T GAAAGTAA

GAM1599 CCTGAAGTGTTATATGCAGG 1572 TGAAGTGTTA 3248 A ATAT A- A AG -- CCA
ATATGATAGCTCTGTTCCAG TATGCAGGAT CCTGA GTGTT GC GG TATGAT CTCT GTT G
ACTCAACTTGGAGGATCATG ATGA ||||| ||||| || || |||||| |||| |||
ACTACGCTCAACATGTTAGG GGATT TACAA CG TC GTACTA GAGG CAA A
G CT-- CA A G- TT CTC

GAM1600 GCTTTTGCTCCAGATGGTTC 1573 CCAGTGCCTT 3249 TT TCC T ATACTTT T A A -
TC ACA
ATACTTTGCTTGGTCACAAG CAGAACTTTC GCT TGC AGA GGTTC GCT GGTC CA GGA
CA GC G
GACATCGCACAGTAAAGCTT TCTT ||| ||| ||| ||||| ||| |||| || ||| || ||
GTTCCGTGGACCCAGTGCCT CGG ACG TCT TCAAG TGA CCAG GT CCT GT CG T
TCAGAACTTTCTCTTGCATG T- TTC T ACTTCCG C - G T T- AAA
GC

GAM1601 ATGATAATCTACCTCACTTT 1574 TTCCCTGTGG 3250 A TA CTTT - G A TTC G
CCCTGTGGCTATGTTCTGGG CTATGTTCTG ATGATA TC CCTCA CC CT TGGCT TG TGG T

TTTCCAATCAGGCCGAGTGG G |||||| || ||||| || || ||||| || |||
TTTGAGGACGATGTCAT TACTGT AG GGAGT GG GA GCCGG AC ACC T
- CA TT-- T - - TA- T

GAM1602 CCTCAGCACCATTGACAATC 1575 TCAGCACCAT 3251 - - TT AT A- - G
AGCCCGAAGACTTTGTGGTG TGACAATCAG CCT CAGCAC CA GACA C GCC CGAA A
GGGCTGTCCTGTGTGTTGTA CCCG ||| |||||| || |||| | ||| ||||
GG GGA GTTGTG GT CTGT G TGG GTTT /
T T C- CG GG T C

GAM1603 CGCTCGTTCGTAACAACAGT 1576 TGACATTACT 3252 TTC ACA - C- AAC
GAGTTACATGAACATTACAT GTGATACTGA CGCTCG GTA ACAGTGA GTTA ATG A
TCTGACATTACTGTGATACT GTG |||||| ||| ||||||| |||| |||
GAGTG GTGAGT CAT TGTCATT CAGT TAC /
--- AG- A CT ATT

GAM1604 GCTCCAAAGAACCAAGAGTG 1577 CATTTCACTT 3253 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1605 CTGGCTCCTGAGGTGGCTGA 1578 GTAGAGCAAA 3254 C- GT GC A GA C G G GT
TCGAATTGGGGACTATGTCC TGTTTCAGGA CTGG TCCTGAG G TG TC ATTGGGGA TAT
TCCA T C
AGTGTCATGGTGGGGTATCC TCCC |||| ||||||| | || || |||||||| ||| |||| |
CTAGTAGAGCAAATGTTTCA GACC AGGACTT T AC AG TGATCCCT ATG GGGT G /
GGATCCCAG CT TG AA G A- - - G TA

GAM1606 GAGGCGGCTCAGTGTGAAGA 1579 AGGCGGCTCA 3255 C C AAGAACTAC CTG
ACTACGGGTTTCCTGATGTT GTGTGAAGAA GAGG GG TCAGTGTG GGGTTTC A
GAAGCTCAGAATTAGCCACA CTAC |||| || |||||||| |||||||
CTGACCTTCTC CTCT CC AGTCACAC CTCGAAG T
T - CGATTAAGA TTG

GAM1607 CTGGAGTGCAGTGGTGCGAT 1580 TACAGTAGCT 3256 -------- TG C C C C -- CCC--
ATT
CTTGGCTCACTGCAACCTCC GGGATTACAG TGC GATCT GCT ACTG AA CTC GC CT
GGTTGAGGCA C
GCCTCCCGGTTGAGGCAATT ACAT ||| ||||| ||| |||| || ||| || || ||||||||||
CTCCTGCCTCAGCCTCCCAA GCG TTAGG CGA TGAC TT GAG CG GA
CCGACTCCGT /

GTAGCTGAGATTACAGTAGC TACAGACA GT - A A T AT ACCCT CCT
TGGGATTACAGACATGCGCC
ACCATGTCCAG
GAM1608 GAGGCGGCTCAGTGTGAAGA 1581 AGGCGGCTCA 3257 C C AAGAACTAC CTG
ACTACGGGTTTCCTGATGTT GTGTGAAGAA GAGG GG TCAGTGTG GGGTTTC A
GAAGCTCAGAATTAGCCACA CTAC |||| || |||||||| |||||||
CTGACCTTCTC CTCT CC AGTCACAC CTCGAAG T
T - CGATTAAGA TTG

GAM1609 AGAATGGGGAAGAATACTGA 1582 TTGGAACAGG 3258 - - TA AA T CA TCT AC-
CT
ATTAGCTGAGCACATTCTGG TTTCATTCTC AGAAT GGGGAA GAA CTG TTAGC GAG CAT
GGAC AATT G
ACACAATTCTGACCAATTTC CAAT ||||| |||||| ||| ||| ||||| ||| ||| |||| ||||
AGTCTCATGATCTCTGTTGG TCTTA CCTCTT CTT GAC GGTTG CTC GTA TCTG
TTAA A
AACAGGTTTCATTCTCCAAT A A TG AA T TA C-- ACT CC
TCT

GAM1610 CCATTTTACAGTATAATGAA 1583 TACAGTATAA 3259 TT AG ATGAAG TC AGA
GCACTACCTCCATGAGAATT TGAAGCACTA CCAT TAC TATA CACTACC CATG A
CACGTGTGGTAGTGGTATAG CCTC |||| ||| |||| ||||||| ||||
GGTGTTATGG GGTA GTG ATAT GTGATGG GTGC T
TT GG G----- T- ACT

GAM1611 GCCTAATTTCTCACCAGGTT 1584 CACCAGGTTG 3260 A ACCA- G ACA CCCAG A
GACTTCCTACAGGTCCCAGG ACTTCCTACA GCCT ATTTCTC GGTT ACTTCCT GGT GC T
CATTTGCACTAAAGGAAGTG GGTC |||| ||||||| |||| ||||||| ||| ||
AGCTCCACAGGGAAATGAGG CGGA TAAAGGG TCGA TGAAGGA TCA CG T
C G ACACC G AA- ----- T

GAM1612 TGTGTAAGAGGTAGTAAAGT 1585 AGAGGTAGTA 3261 G GAA - T ----- AA AA- -
AG C
TGAATAGGAGATGAGGGTAG AAGTTGAATA A TAAAGTT TAG GAGA GAGG GTAGAG
GGTG TGA GAG AGT T
AGAAGGTGAATGAGAGAGAG GGAG | ||||||| ||| |||| |||| |||||| |||| ||| ||| |||
TCTGTGCTTGCTTGTCGGCG T GTTTTAG ATT CTTT CTCC TATCTT CCGC GCT TTC
TCG G
CGCCACTTCTATTAGTACCT A ATG A - ATGAT CA GCG G GT T
CTTTCATTAGTAGATTTTGA
TATATCACACA
GAM1613 AGAGAAACCTGACATGTGGG 1586 TGAAGCTGCC 3262 AAC ATGTG TACC T TC AAT
A GC
CATACCTCAGTGATCCTTAA AGTCAGATCT AGAGA CTGAC GGCA TCAG GA CTT AG
ATG C
TAGAATGGCCCCCGTGCTTC CT ||||| ||||| |||| |||| || ||| || |||
CAAGTGTCCTGAAGCTGCCA TCTCT GACTG CCGT AGTC CT GAA TC TGC /

GTCAGATCTCT A-- A---- CGA- - GT CCT G CC

GAM1614 GAGGCGGCTCAGTGTGAAGA 1587 AGGCGGCTCA 3263 C C AAGAACTAC CTG
ACTACGGGTTTCCTGATGTT GTGTGAAGAA GAGG GG TCAGTGTG GGGTTTC A
GAAGCTCAGAATTAGCCACA CTAC |||| || |||||||| |||||||
CTGACCTTCTC CTCT CC AGTCACAC CTCGAAG T
T - CGATTAAGA TTG

GAM1615 GTGCAGCTGCTGTGCCTGAT 1588 TCCCAGATGT 3264 C- G CC - G GA G
GTGGGGACAGCCCTGCTCCC AAACAGAGCA GTGCAG TGCT TG TG AT TGGG CA C
AGATGTAAACAGAGCAACCT ACCT |||||| |||| || || || |||| ||
GCAC CACGTC ACGA AC AT TA ACCC GT C
CA G AA G G TC C

GAM1616 GCGGCGGGCTGGCTGGGAAG 1589 TGAATCGTAA 3265 C - GG GGAA -- ATC
AAGAATA- GA
GGTTTGAATCGTAAAGAATA AGAATAAGGA GCGG G GGCT CTG GGG TTTGA GTA
AGGAGAG C
AGGAGAGGACTGCTTTCCTG GAG |||| | |||| ||| ||| ||||| ||| |||||||
AAAACACTACTCAGAATCCC CGCC C CCGA GAC CCC AGACT CAT TCCTTTC /
AACAGAAGCCTCTCCGC T T A- AA-- TA --- CACAAAAG GT

GAM1617 TACTCAAATTCTCTACTGTA 1590 TCAGTGCCAA 3266 T A ACT - A TT
TGAATTATGCTTTAAGTAGA GGAGAACTTG TAC CAA TTCTCT GTA TGAATT TGC T
ATTCAGTGCCAAGGAGAACT GTG ||| ||| |||||| ||| |||||| |||
TGGTG GTG GTT AAGAGG CGT ACTTAA ATG /
- C AAC G G AA

GAM1618 AGCTGTGTGAGGCTATATTT 1591 TGAATGTAGA 3267 TGT GG - T A C ------- AAAC
TCTTTAATACTTCAGCCAAA AGCAAGTATG AGCTG GA CT ATATTT CTTT ATA TTCA
GCCA A
ACAACATATGGCAACAGATT AGAA ||||| || || |||||| |||| ||| |||| |||
GAATGTAGAAGCAAGTATGA TCGAC CT GA TATGAA GAAG TGT AAGT CGGT A
GAATCCAGCT --- AA G C A - TAGACAA ATAC

GAM1619 TGTATGCATATTTTAAAAGT 1592 TGCCTGGAGA 3268 TA TATT A CTC - TA TT T AA
TATACA
CTCCTCCAGCTAAACCATTA CACTTTCAGT TGCA TT AAAGT CTCCAG C AACCA AGC TTT
TGGGG T
GCTTTTAATGGGGTATACAT TTTT |||| || ||||| |||||| | ||||| ||| ||| |||||
TTTTCTTTCCAAGGGATGTT ACGT GA TTTCA GAGGTC G TTGGT TTG AGG ACCTT
/
TGGTTATGCCTGGAGACACT CG TTTT C CA- C TA -- T GA TCTTTT
TTCAGTTTTTGCAGCCA

GAM1620 ATGGTCCAACTTTGTGGAAT 1593 GTAAGGATTT 3269 -- T-- GAATG- AGG AGGG
GG
GGTAAGGATTTTTAGGGTTG TTAGGGTTGT ATGG TCCAACT TGTG GTA ATTTTT
TTGTTT C
TTTGGCCAGAACAAGAGAAA TT |||| ||||||| |||| ||| |||||| ||||||
TAACTGCAGAAAACACATAT TACC AGGTTGG ACAC CGT TAAAGA AACAAG /
GGTTGGAAACCAT AA TAT AAAAGA CAA G--- AC

GAM1621 GTTGCCGGTCCAAACTGTCC 1594 TGCAGGTAGT 3270 C TCCAAA G CAAA T-- AGT
TTTTC GT
AAATACTTGCAGGTAGTAGT AGTTTTCCGC GTTGC GG CT TC TACT GCAGGT AG
CGCT G
TTTCCGCTGTGATAAGTGTA T ||||| || || || |||| |||||| || ||||
CCTTCACCTGCTCCAGTGAT CAACG CC GA AG GTGA CGTCCA TC GTGA A
GAGAGCCTCCAGCAAC A TCC--- G TA-- CCT CT- CAT-- AT

GAM1622 GAGGCGGCTCAGTGTGAAGA 1595 AGGCGGCTCA 3271 C C AAGAACTAC CTG
ACTACGGGTTTCCTGATGTT GTGTGAAGAA GAGG GG TCAGTGTG GGGTTTC A
GAAGCTCAGAATTAGCCACG CTAC |||| || |||||||| |||||||
CTGACCTTCTC CTCT CC AGTCGCAC CTCGAAG T
T - CGATTAAGA TTG

GAM1623 CTCTGGTATGAATTAGCCAC 1596 TAGCCACAGA 3272 TA AATTAGC --- CTG CGAT C
TC T
AGACTGATGTTCGATGCCTC CTGATGTTCG CTCTGG TG CAC AGA ATGTT GCCT
GGGCT TGGG C
GGGCTTCTGGGTCCCTCAAG ATGC |||||| || ||| ||| ||||| |||| ||||| ||||
GGCCCAGGTGACATGATCTC GAGATC AC GTG TCT TACAG TGGA CCCGG
ACTC /
CAGTGCAGCCTAGAG CG ------- ACC AG- ---- - GA C

GAM1624 GCTCCAAAGAACCAAGAGTG 1597 CATTTCACTT 3273 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1625 GTGCACTGTTCTCAGAAATT 1598 TCCCAAGTCT 3274 CAC C AGAAA AA CCT TT
TTAGGCAATTGGCCTTCTTG AGAAAAAGAC GTG TGTT TC TTTTAGGC TTGG TC G
CAGATCCCAAGTCTAGAAAA AACA ||| |||| || |||||||| |||| ||
AGACAACAATCAC CAC ACAA AG AAGATCTG AACC AG /

TA- C AAA-- -- CT- AC

GAM1626 CTGGGAAAGACATGGTTAGT 1599 TGGGAAAGAC 3275 CA-- GG CT-- - G
TACTTCCAGGAGACTGAGAT ATGGTTAGTT CTGGGAAAGA T TTAGTTA TC CAG A
ATATAACTAGTTGCTCATTT ACTT |||||||||| | ||||||| || |||
TTTCCAG GACCTTTTTT G GATCAAT AG GTC G
ACTC TT ATAT A A

GAM1627 CCAAATGCTACTTTGACCTT 1600 TAGAAAGAGC 3276 A AC GC C - GA- AG A
GCCATTT TT
TGCGCCTTGGCACACGACAG ATGGGAACTG CTTTG CTTT GCCTTGG ACA C CAGT CCTAT
TTT TGTC C
TAGCCTATATTTGCCATTTT AAGG ||||| |||| ||||||| ||| | |||| ||||| ||| |||| /
GTCTTCTTGACATAGAAAGA GAAAC GAAG TGGAACT TGT G GTCA GGGTA GAG
ACAG /
GCATGGGAACTGAAGGTTGT A A- GT T T GAA A- C AAAGAT- TT
TTCAAGGTTGGAAGACAAAG
ACTTCTATGG
GAM1628 GTCCAGTGCGTGTACTGTAC 1601 TGTACACATC 3277 C G TA TACACATCC A - - CT
TC G
ACATCCACACTCATTCTCAC CACACTCATT GT CAGTGC TG CTG AC CTCA TTCT CA
CAGGGT CCG A
TCAGGGTTCCCGGACCGGCT CTCA || |||||| || ||| || |||| |||| || |||||| ||| /
GTCCTGCCTGCGGAACTGAG CA GTCATG AC GAT TG GAGT AAGG GT GTCCTG
GGC /
GTAAACTAGCTCAGGTACTG - G TC CAAA----- - C C CC TC C
AC

GAM1629 TCTGCAAGTGCTGTCTGTCA 1602 AACACTGACT 3278 A T- CAATG A AACACT
TTAG G
ATGAAGAGAAACACTGACTG GGTTAGGATT TCTGCA GTGCTG CTGT AAG GA GACTGG
GATTGTT A
GTTAGGATTGTTGACAACGA GTT |||||| |||||| |||| ||| || |||||| |||||||
TTCCAGTCTTGTCCTTGCGG AGACGT CATGAC GGCG TTC CT CTGACC
TTAGCAA /
CTCAGTACATGCAGA A TC ----- - GTT--- ---- C

GAM1630 TTAAATAGGTCTGTGTGGGG 1603 AACTGCCAGT 3279 TCTGT TG TG GCC- TTG TTTCA
- G TT
AATGAGCCTTTCAGTTGGGT CTGAGAACTA G G GGGAA A TTTCAG GGT AGTTTCT
TAGTTAT AG T
TTTCAAGTTTCTTAGTTATG TTGT | | ||||| | |||||| ||| ||||||| ||||||| ||
AGTTTTTTTGGTAGCTGTAG C C TCCTT T AGAGTC CCG TCAAAGA GTCGATG
TT /
AAACTGCCAGTCTGAGAACT TCTC- GT GT ATCA TGA ----- T G TT
ATTGTTCCTTGCCTCTCTTG
GATAA

GAM1631 TTAGTGTGGTTTAATCTGGA 1604 ACCCGTGTTC 3280 T T CT - GAAGCTG A A
AGGAGCAGAAGCTGTGGAGT CTATCCTTGT TTAG GTGGT TAAT GGA AGGAGCA TGG
GTCC A
CCAAAGGACCCGTGTTCCTA TGTG |||| ||||| |||| ||| ||||||| ||| ||||
TCCTTGTTGTGCCACTTGA AGTT CACCG GTTG CCT TCCTTGT GCC CAGG /
- T TT A ------- - A

GAM1632 GGCATGGAATAATTGTATTT 1605 AATTATGCAC 3281 T ATAA- AT C GC C ATTCTT
TAT CCT
TGCTGGCAATAGACACATTC AGTTTCTGTT A GGA TTGT TTTG TG AATAGA AC TAT
TTGCAGATT C
TTTATTATTTGCAGATTCCT ATCA | ||| |||| |||| || |||||| || ||| |||||||||
CATCAAATCTGTAATTATGC T CCT AACA AAAT AC TTGTCT TG GTA AATGTCTAA
A
ACAGTTTCTGTTATCAATAA - AAGAA -- A TA T ACAC-- TT- ACT
AACAAAAGAATCCTGTT

GAM1633 AGAAATCGTAAAATACTTAT 1606 TGGGTAGTGC 3282 - AAA- TATA TAG GTGCT-
T G
AACCTATCTTAGAGAAATGA TTGTGCTGGT AGAAATC GTA TACT ACCTATCT AGAAATGA
GGTT GAGA T
GTGCTGGTTTGAGAGTGTTT TTCT ||||||| ||| |||| |||||||| |||||||| |||| ||||
TTTAACTGAAAGATTATTTC TCTTTGG CGT GTGA TGGGTAGA TCTTTATT TCAA
TTTT G
TAGATGGGTAGTGCTTGTGC T GTTC ---- --- AGAAAG T T
TGGTTTCT

GAM1634 GCTCCAAAGAACCAAGAGTG 1607 CATTTCACTT 3283 T - ---------- CAC GAGATA
TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT
GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG
CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1635 AGTCCATTTCACTTTCACTG 1608 CATTTCACTT 3284 C- AC GAGATA TC
TCTGAGATAGGGTCTCTAAG TCACTGTCTG AGT CATTTCACTTTC TGTCT GGGTC T
ACCCAGGATACGAGGGTGGA AGAT ||| |||||||||||| ||||| |||||
ATGTAGCT TCG GTAAGGTGGGAG ATAGG CCCAG /
AT C- A----- AA

GAM1636 GGCAACAGCATGTTCATGGA 1609 CATCCAGTCT 3285 ----- A TC- T TTT TT A
GTTTCT C TC
ACTTCAGTTTCTTTGTAGGA GAGTTCCATC AGC TGT ATGGAACT CAG CT GT GGAGC
AATTT TG T
GCGTTTCTAATTTCTGTCTA CTGC ||| ||| |||||||| ||| || || ||||| ||||| ||

ACAAAAATTTCCCAGTTTCA TCG GCG TACCTTGA GTC GA TA CTTTG TTAAA AC /
TCCAGTCTGAGTTCCATCCT CCTTC - TCC - T-- CC - ACCCT- A AA
GCGGCTCTTCCTGTGCC

GAM1637 CTTACCTTCCTAAACTAAAC 1610 CGTGGTTTTC 3286 TTCCTAAACT A- G CC
CAACAGGGGCCAGATCTGTG CCTTTGGTGA CTTACC AAACCA CA GGG A
CGTGGTTTTCCCTTTGGTGA G |||||| |||||| || |||
G GAGTGG TTTGGT GT TCT /
TTTCCCT--- GC G AG

GAM1638 GTGGAGGAAGAACTGGAGAA 1611 ACTGATCGAG 3287 G A A G GAAA GAA AA AG-- A-- T TAG
AAGGAAGGCTAAAACAGTCA TCGTCCTGCG GTG AGGA GA CT GA AG GGCTA AC TC GGATG TGGCT A
GGATGTTGGCTTAGAAGCAG C ||| |||| || || || || ||||| || || ||||| |||||
CCATCATTTAAAGAAAGCGT CGC TCCT CT GA CT TC TCGAT TG AG TTTAC ACCGA /
AATAGCTCACTGATCGAGTC G G - G AG-- AC- AA CGAA AAA T CGA
GTCCTGCGC

GAM1639 GTGCACCACGCTCATTACTG 1612 TGAATGAGCC 3288 TCA A - A CATCT AG ACGCAAA A C GCT
GACGTACGAAGTACATCTGA ACGCAAATCT TT CTGGACG TACG AGTA GAATG CC TCTC TG AAT G
ATGAGCCACGCAAATCTCAT CATG || ||||||| |||| |||| ||||| || |||| || |||
GCAATGCTGCTAAATTCCAG AA GGCCTGT ATGT TCGT CTTGC GG AGGG AC TTA C
GGACAGGTCCGTTCTATAAT TG- - G C AATAT CT AC----- - C AAT
GCTCTGTAGTGTCCGGAAGT
GCAGGTACAT
GAM1640 GGGCCTTGGTTGGCAGCCAT 1613 CAAACCTTTA 3289 TT TG AG--- A- GGA - AA TTTA-- A G
GGGAACTGCACGTCAAGATG TCAGGATGAT GGGCC GGT GC CC TG ACTGCA CGTC GATG TG TTT C
TTTATGATTTGCTAAAAACA GCAG ||||| ||| || || || |||||| |||| |||| || |||
AACCTTTATCAGGATGATGC CCCGG CCG CG GG AC TGACGT GTAG CTAT AC AAA T
AGTAACAGGGGAAGCAGCTG T- GT ACGAA GG AA- A GA TTCCAA A A
GCCTGGCCC

GAM1641 GCTGTGGCGCACTGCAAACG 1614 TGATTGAGCC 3290 CAC AAAC -- G ATCAA GAAC
CGGCAATGGTCTCATCAAGG GCGCACGCTA GCTGTGGCG TGC GCGGC AAT GTCTC GGT G
TGAACGGGCGGCCCCTGGAG CAGT ||||||||| ||| ||||| ||| ||||| |||
ATGATTGAGCCGCGCACGCT TGACATCGC ACG CGCCG TTA TAGAG CCG /
ACAGT --- ---- AG G GTCC- GCGG

GAM1642 TGAAGACTTCCTAAATTTGC 1615 TTTGCACATT 3291 AC A TTGCA TTGCC ACCAT
ACATTAGCTAGATTGCCATT AGCTAGATTG TGAAG TTCCT AAT CATTAGCTAGA ATTAGC T
AGCACCATTAGAGAGTTGAT CCAT ||||| ||||| ||| |||||||||| ||||||
CTTTGGCTAATGATTATTCA ACTTT AAGGA TTA GTAATCGGTTT TAGTTG /
GGAAAATTTCA AA C TTA-- C---- AGAGA

GAM1643 GTAAACTCCAACCCAGAATG 1616 TTGGAGCAGG 3292 AACCC - - TA AA T CA TCT AC- CT
GGGAAGAATACTGAATTAGC TTTCATTCTC AGAAT GGGGAA GAA CTG TTAGC GAG CAT GGAC AATT G
TGAGCACATTCTGGACACAA CAAT ||||| |||||| ||| ||| ||||| ||| ||| |||| ||||
TTCTGACCAATTTCAGTCTC TCTTA CCTCTT CTT GAC GGTTG CTC GTA TCTG TTAA A
ATGATCTCTGTTGGAGCAGG TTTTC A A TG GA T TA C-- ACT CC
TTTCATTCTCCAATTCTCTT
TTACAGAAC
GAM1644 GCAAGAGCTTTTGCAGAACA 1617 TGCAGAACAG 3293 CA AA TT A CA CT-GGCCC-- AC A
GAATGGTTTGTCATTCATTG AATGGTTTGT TTTTG GAACAG TGGT GTC TT TTGAAA TC TAG TCTAC A
AAACTTCGGCCCTAGACTCT CATT ||||| |||||| |||| ||| || |||||| || ||| |||||
ACAAATGTAGAAGCTGCTTT AAGAC TTTGTT GCCA TAG AG AATTTT AG GTC AGATG A
TCAGACAATTTTAACAGAGA TC AC TT - AC AAC ACTTTTC GA T
TTTACCGCATTGTTTCTCAG
AAGCAAATGT
GAM1645 CACAAATCCAGCACTTCCTC 1618 AGCAACACAT 3294 T GCACTTC-- T T- G
TCCATTTACTCTGTCAGGCT ATGGCTTTGT CACAAA CCA CTCTCCAT TAC CT T
GTATATGGGGAGCAACACAT G |||||| ||| |||||||| ||| ||
ATGGCTTTGTG GTGTTT GGT GAGGGGTA ATG GG C
C ATACACAAC T TC A

GAM1646 AGTCATCGGTTTTCAGTTTG 1619 CACCTGTAGA 3295 T T-- - GGAT C
GATGGTGGCTCATCACCTGT ACCTGACTTG AGTCA CGGTT TCAG TTT GGTGG T
AGAACCTGACTTGGCCGTGG GCCG ||||| ||||| |||| ||| |||||
CT TCGGT GCCGG AGTC AAG CCACT C
- TTC C ATGT A

GAM1647 GCTCCAAAGAACCAAGAGTG 1620 CATTTCACTT 3296 T - ---------- CAC GAGATA TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /

GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1648 GGGTACGAAAAGAACACAGA 1621 AGAAGCTGCC 3297 T AAA-- C AGAAG - AT- A
TGA
AGCTGCCAGGATGCTATACT AGGATGCTAT GGG ACG AGAA AC CTGC CAGG GCT TAC
G
GAGAATTGTGGGTGAACTTG AC ||| ||| |||| || |||| |||| ||| |||
AGCAGATGGTTTCTGAGGAC CCC TGC TCTT TG GACG GTTC TGG GTG A
GTCCC - AGGAG - GTA-- A AAG - TTA

GAM1649 CCTGGCAGATGCCATCAATG 1622 TGACTTCAGA 3298 - A- CATC -- A G
AGTTTGAGGGTGGTATGATG CTCATTCAGC CCTG GCAG TGC AATGAGTTTGAGG GTGGT
TGAT C
CTGGTCAGCCATGACTTCAG AGGT |||| |||| ||| |||||||||||| ||||| ||||
ACTCATTCAGCAGGTTGCAC GGAC CGTT ACG TTACTCAGACTTC TACCG ACTG T
AGG A GG AC-- AG - G

GAM1650 AGTGAAGGATGGAGCAAGGT 1623 AAGTAGCACG 3299 GCAA --- A-- A TG--- A-- -
- GCC
CGTCTGGGCTATGAGCTGTG AGAAGCTCCG GGTCGTCT GGGCT TG GCTG TGGGCC
TGGGTA CAG A
TGGGCCATGGGTACAGGCCA AGGA |||||||| ||||| || |||| |||||| |||||| |||
AGACTGAATACCCAATAGGT TCGGTAGG CTCGA GC CGAT ACCTGG ACCCAT
GTC /
CCAGGAAGTAGCACGAGAAG GAAG AGC AGA A GAAGG ATA AA AGA
CTCCGAGGATGGCTGAAGTC
CAGGCGTCTCT
GAM1651 GTGCTTCAACTGGTATTTAT 1624 TTCAACTGGT 3300 T T ATTTA - AGAG GGACAA
TA
GAGGCCCTAGAGCTCCGGGA ATTTATGAGG GTGCT CAAC GGT TGAGGC CCT CTCCG
TGA A
CAATGATAAGACTCGCTATA CCCT ||||| |||| ||| |||||| ||| ||||| |||
TGGGGAAGGGTGTCTCAAAG CACGA GTTG TCG ACTCTG GGG GGGGT GCT G
GCTGTTGAGCAC - - GAA-- T AA-- ATATC- CA

GAM1652 AAATCAAGACTTCTGTACAC 1625 CATCCAGTGT 3301 TC TTCT CC CT A TT
TCCATGCCTTGATGATTTCT GCTGTCTTTT AAA AAGAC GTACACT ATGC TG TGA T
TCAGCAGCATCCAGTGTGCT TTT ||| ||||| ||||||| |||| || |||
GTCTTTTTTT TTT TTCTG CGTGTGA TACG AC ACT /
TT T--- CC -- G TC

GAM1653 TCCACCTGTGCCTATAATTC 1626 AAGCTGCCAT 3302 CCTATAA G CAC GT- CT G TG
----- ATGT
CAGCATGACACCTGTGCCTT GCTGAAGAAC G TTCCA CATGA CT GC TGG AGCTT A
GCTGAC T

GGGAGCTTTGAGCTGACATG TCAT | ||||| ||||| || || ||| ||||| | ||||||
TTAGAAGTCAGTCTACATTG C AGGGT GTACT GA CG ACC TCGAA T TGACTG
/
AAGCTGCCATGCTGAAGAAC ACAAG-- - CAA AGT T- G GT ACATC AAGA
TCATGTGGGAGAACACACAG
AAATCGAGA
GAM1654 GAGGCGGCTCAGTGTGAAGA 1627 AGGCGGCTCA 3303 C C AAGAACTAC CTG
ACTACGGGTTTCCTGATGTT GTGTGAAGAA GAGG GG TCAGTGTG GGGTTTC A
GAAGCTCAGAATTAGCCACA CTAC |||| || |||||||| |||||||
CTGACCTTCTC CTCT CC AGTCACAC CTCGAAG T
T - CGATTAAGA TTG

GAM1655 GAGGCGGCTCAGTGTGAAGA 1628 AGGCGGCTCA 3304 C C AAGAACTAC CTG
ACTACGGGTTTCCTGATGTT GTGTGAAGAA GAGG GG TCAGTGTG GGGTTTC A
GAAGCTCAGAATTAGCCACA CTAC |||| || |||||||| |||||||
CTGACCTTCTC CTCT CC AGTCACAC CTCGAAG T
T - CGATTAAGA TTG

GAM1656 AGTGGGTGCACAAGTGATGG 1629 GTAAGGATTT 3305 - -- T-- GAATG- AGG
AGGG GG
TCCAACTTTGTGGAATGGTA TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA
ATTTTT TTGTTT C
AGGATTTTTAGGGTTGTTTG TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
GCCAGAACAAGAGAAATAAC TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA
AACAAG /
TGCAGAAAACACATATGGTT G AA TAT AAAAGA CAA G--- AC
GGAAACCATGCGCTTGTGAC
CTTTTCT
GAM1657 GCCTGCCTGAACCCTGGGTC 1630 CATGACGGCT 3306 A GG--- - A -- G AA- A- G
C
AGGAGAGAAACACTTGGGGA CTGAGTTCTT CCCT GTCA GGAGAGA ACA CTT GGGAGGGG
AGG CG CGTGGG T
GGGGAAAGGACGGCGTGGGC CCTG |||| |||| ||||||| ||| ||| |||||||| ||| || ||||||
TACCCATGACGGCTCTGAGT GGGA CGGT CCTTTCT TGT GGG TCCTTCTT TCT GC
GTACCC /
TCTTCCTGGGGCTTGTGTCT C GAAGA T G TC G GAG CG A A
TTCCTTGGCAGAAGAGGGCA
CAGCAAGGC
GAM1658 CTGAGGCAGGAGAAATTGCT 1631 GAGGTAGAGG 3307 G AAA GAA--- AGGTA GT
A T AG
TGAACCCAGGAGGTAGAGGT TTGCAGTGAG CTGAGGCAG AG TTGCTT CCCAGG GAG
TGCAGTG G CA A
TGCAGTGAGTCAAGATCATG TCA ||||||||| || |||||| |||||| ||| ||||||| | ||
CCATTGCACTCCAACCTGGG GACTCTGTC TC AACGAG GGGTCC CTC ACGTTAC
C GT T
CGACAAGAGCAAAACTCTGT - AA- AACAGC AAC-- -- - - AC
CTCAG

GAM1659 CTGAGGCAGGAGAAATTGCT 1632 GAGGTAGAGG 3308 G AAA GAA--- AGGTA GTT
A T AG
TGAACCCAGGAGGTAGAGGT TTGCAGTGAG CTGAGGCAG AG TTGCTT CCCAGG GAG
GCAGTG G CA A
TGCAGTGAGTCAAGATCATG TCA |||||||||| || |||||| |||||| ||| |||||| | ||
CCATTGCCACTCCAACCTGG GACTCTGTC TC AACGAG GGGTCC CTC CGTTAC
C GT T
GCGACAAGAGCAAAACTCTG - AA- AACAGC AAC-- AC- - - AC
TCTCAG

GAM1660 GTAGGCCATTGGATAATCGG 1633 ATAAGGATTT 3309 - A A CGGG AA -- C A--
GAAATATAA
GATAAGGATTTGAGGGGCAT GAGGGGCATT CC TTGG TAAT AT GGATTTGA GGGG
ATTCAT GATG G
TCATAGATGGAAATATAAGT CATA || |||| |||| || |||||||| |||| |||||| ||||
TCAAGAGGCATCAGCATGGA GG AATC ATTA TA TCTAGGCT TCCC TAGGTA CTAC
/
TACCCTATTCGGATCTGGAT A A C AAG- GG TA A CGA GGAGAACTT
GAAATTACCTAAAGGAGAAA
ATGC
GAM1661 TAGAGCTGGATTACTGAAAG 1634 TAGAGCTGGA 3310 A AAAG --- TTT
TCTGAATTTGCGTTTCATAA TTACTGAAAG TAGAGCTGGATT CTG TCT GAA G
GAAAAACAGGATCTAGTTCT TCTG |||||||||||| ||| ||| |||
A ATCTTGATCTAG GAC AGA CTT /
- AAAA ATA TGC

GAM1662 GGAGGGTGAACTTGGATGCA 1635 TCTCCTGGTG 3311 T CC- ---- TA C TC TTT
ACA C A
CTGACCCAGCACCTAGACAA GAAACTCCAG GGATGCAC GAC AG CACC GA AAGA TTGG
CCC GAGG AGG G
GATCTTGGTTTCCCACAGAG TTCG |||||||| ||| || |||| || |||| |||| ||| |||| |||
GCAGGAGTCCTACCTCGGGC CCTACGTG TTG TC GTGG CT TTCT AACC GGG
CTCC TCC /
CAAACTCTTCTCCTGGTGGA C ACC AAAG TC C CA --- --- A T
AACTCCAGTTCGTGCATCCA
GGCACCAGCC
GAM1663 CCGAGCTGAACAGGACCAGT 1636 CAGTGCAATT 3312 A GAAC CCA ATT GTG-- TT-
ATCA A
GCAATTTAAGAGGTGCATGT TAAGAGGTGC CG GCT AGGA GTGCA TAAGAG CATG
TATA AGAAGA G
TTATAATCAAGAAGAAGACT ATGT || ||| |||| ||||| |||||| |||| |||| ||||||
CTTTTATGTACACCATGATA GT TGA TCCT TACGT GTTCTC GTAC ATGT
TTTTCT A
TACTCTTGTCTGCATATCCT G GTC- A-- CT- ATATA CAC A--- C
CTGAGTGTGG

GAM1664 AAAGCCATCACACCAGCCTT 1637 CTGCATTTTT 3313 ATC- C-- CTT - TAC CA
AAAATCAGGATTATTTACAT AGTTGCATTG AAAGCC ACA CAGC AAAAT CAGGATTATT
ATC A

CCAAATTGATCAATGGTTCT TCAG |||||| ||| |||| ||||| |||||||||| |||
GCATTTTTAGTTGCATTGTC TTTTGG TGT GTTG TTTTA GTCTTGGTAA TAG A
AGCGGTTTT CGAC TAC AT- C C-- TT

GAM1665 GCTCCAAAGAACCAAGAGTG 1638 CATTTCACTT 3314 T - ---------- CAC GAGATA TC
CAAATCAGTCCATTTCACTT TCACTGTCTG GAG GCAAATC AGTCCAT TTCACTTT TGTCT GGGTC T
TCACTGTCTGAGATAGGGTC AGAT ||| ||||||| ||||||| |||||||| ||||| |||||
TCTAAGACCCAGGATACAAG CTT CGTTTAG TCAGGTA AGGTGGGA ATAGG CCCAG /
GGTGGAATGTAGCTATATGG - C TATCGATGTA AC- A----- AA
ACTCGATTTGCTTCCGGACC
TTTTCCAGAGC
GAM1666 GTAAACTCCAACCCAGAATG 1639 TTGGAGCAGG 3315 AACCC - - TA AA T CA TCT AC- CT
GGGAAGAATACTGAATTAGC TTTCATTCTC AGAAT GGGGAA GAA CTG TTAGC GAG CAT GGAC AATT G
TGAGCACATTCTGGACACAA CAAT ||||| |||||| ||| ||| ||||| ||| ||| |||| ||||
TTCTGACCAATTTCAGTCTC TCTTA CCTCTT CTT GAC GGTTG CTC GTA TCTG TTAA A
ATGATCTCTGTTGGAGCAGG TTTTC A A TG GA T TA C-- ACT CC
TTTCATTCTCCAATTCTCTT
TTACAGAAC
GAM1667 CCTGGATTCGACGGATACTT 1640 TGGAGAAGAC 3316 - GGA T-- AGAAGACAGG G ACTC C- A G
CGGGTGGAGAAGACAGGGCA AGGGCACAGT GAC TACT CGGGTGG GCACA TGGT TGGAT CCA G T
CAGTGGTACTCTGGATCCCA GGTA ||| |||| ||||||| ||||| |||| ||||| ||| |
AGGTGACTGGTTGTTTAATC CTG GTGG GCTCACC CGTGT GCTA ATTTG GGT C G
GTGTGCATAGAACGAGCCAC A AA- TTC GAGCAAGATA - ---- TT - A
TCGCTTGGTGAAGTCACAAC
AGAGTGCAGG
GAM1668 TGGCAAGGTACAGAGAGCTG 1641 TCGCCTGGAC 3317 ------ A GAGC - G T T AACA- A C
TGTGCATGCTGAGCAACACC CACAAGTTTG TGGCA AGGT CAGA TGTG T CA GC GAGC CC CAGC A
ACAGCCATTGCTGAGGCCTG ACCT ||||| |||| |||| |||| | || || |||| || ||||
GGCTCGCCTGGACCACAAGT ACCGT TCCA GTTT ACAC A GT CG CTCG GG GTCG T
TTGACCTGATGTATGCCA ATGTAG - GA-- C G C - GGTCC A T

GAM1669 TTGTATGTTGTATGTGTTAT 1642 TCATTCTATT 3318 A TATTATCAT A TT AT GTGG GTAG
TATCATTCTATTTCATCTCT TCATCTCTCC TTGTATGTTGT TGTGT TCT T C CTCTCCTTT CT T
CCTTTGTGGCTGTAGTGGAG TTTG |||||||||| ||||| ||| | | |||||||| ||

AAGAAAGAGGAGGGGAGGGG AGCATATAACA GCGCG AGA G G GGGAGGAGA
GA G
AGAGCGCGACAATATACGA - --------- - GG AG AA-- AGAG

GAM1670 TCATCAGACCTGTAATGCAG 1643 TGTAATGCAG 3319 CA CT- AT AGAGAA AA
GA-- CC C
GCTCTTCTTCACATTATAAG GCTCTTCTTC TGTAATG GG CTTCTTCAC TATA ACAGA AT
TGA TTAC A
AGAAACAGAAAATGATGACC ACAT ||||||| || ||||||||| |||| ||||| || ||| ||||
TTACCAATGTAATTCAGAAA ACGTTAT TC GAAGAAGTG ATAT TGTCT TA ACT
AATG A
ATGATCTGTGAATATAGTGA CC ATT -- AAG--- AG AAAG T- T
AGAAGTTACTCCTATTGCAG
TAGAAATGA
GAM1671 GGCTGGCATTCCACCAGTCG 1644 TGCCTGGACC 3320 C TC CA -- ATTCGATG CG
GTATTCGATGAGCTGCGTTA AGTGTATGCC GG TGGCAT CAC GTC GGT AGCTG T
ACAGCTGCCTGGACCAGTGT ATCC || |||||| ||| ||| ||| |||||
ATGCCATCC CC ACCGTA GTG CAG CCG TCGAC T
T T- AC GT -------- AA

GAM1672 GCCATTGACAAGCTGTATGA 1645 TCAGTTTTTT 3321 ACA C TAT CG AAGG TTT
CGTTGAGGAAGGCAATTTTC CATCTCTACA GCCATTG AG TG GA TTGAGG CAA T
TTTTTGAGCCTCAGTTTTTT ATGG ||||||| || || || |||||| |||
CATCTCTACAATGGC CGGTAAC TC AC TT GACTCC GTT C
ATC T TT- TT GA-- TTT

GAM1673 GCTTTTGCTCCAGATGGTTC 1646 CCAGTGCCTT 3322 TT TCC T ATACTTT T - AA
TC ACA
ATACTTTGCTTGGTCACAAG CAGAACTTTC GCT TGC AGA GGTTC GCT GG TCAC
GGACA GC G
GACATCGCACAGTAAAGCTT TCTT ||| ||| ||| ||||| ||| || |||| ||||| ||
GTTCCGTGGTCCCAGTGCCT CGG ACG TCT TCAAG TGA CC GGTG CTTGT CG T
TCAGAACTTTCTCTTGCATG T- TTC T ACTTCCG C T C- T- AAA
GC

GAM1674 TCCTTTTGACAAGAAATGTG 1647 TGACAAGAAA 3323 T - AAATGT C AA-- CTGTT T
GTCGTGAAAATTGGACTGTT TGTGGTCGTG TCCTT TGAC AAG GGT GTGAA TTGGA GC
T
GCTTTTGCTCCAGATGGTTC AAAA ||||| |||| ||| ||| ||||| ||||| ||
ATACTTTGCTTGGTCACAAG AGGAA ACTG TTC TCA TACTT GACCT CG T
GA C G GTT--- - GGTA ----- T

GAM1675 GATTGAGGCGGAGCATGACG 1648 ACGCAACACG 3324 G AGCA --- A A GGAGA G
G- G
CAACACGGAAGCTGGAGAAC GAAGCTGGAG GATT AGGCGG TGA CGCA CACGGA GCT
AC AGG GGCA A

GAGGGGGCAGAAATGCCAGC AACG |||| |||||| ||| |||| |||||| ||| || ||| ||||
CTGTGGCTCTGTGGTGTGCC TTAA TCCGTC ACT GTGT GTGTCT CGG TG TCC CCGT A
TTCACCCCTGCCTGAATT G CCC- TCC G - ----- - GA A

GAM1676 GTGGCAGGGAGAGAAGCCAG 1649 TCAAACTGGT 3325 GAGAGA ATGAT CAACA T AC
ACATGATGTTCAACAATGTG CTGGCTCCTG GTGGCAGG AGCCAGAC GTT ATG GG T
GACTTCCCCTCATCAAACTG TCAC |||||||| |||||||| ||| ||| ||
GTCTGGCTCCTGTCAC CACTGTCC TCGGTCTG CAA TAC CC T
------ GT--- AC--- T CC

GAM1677 AGCCATATCTTGTGGTATGT 1650 AACAGTATCT 3326 A -- TA-- A ATTTC
TTATAACGTATTTCTTTCAC ACTAAAGATG AGCC TATCTT GTGG TGTTT TAACGT T
ATGTTAAAACAGTATCTACT GGCT |||| |||||| |||| ||||| ||||||
AAAGATGGGCT TCGG GTAGAA CATC ACAAA ATTGTA /
- AT TATG - CACTT

GAM1678 TCTTTATTGTCAATCTTGTG 1651 TGGAGCACGC 3327 ATT -- T GG -- A GG TCT CC
CGGGGCGCACCACCGGCCCG AGCGCACGTG TCTTT GTC AATC TGTGCG GC GC CCACC CCCG CGC G
TCTCGCCCGCCGCGCCGGGG ATTA ||||| ||| |||| |||||| || || ||||| |||| |||
AGGTGGAGCACGCAGCGCAC AGAAA CAG TTAG GCACGC CG CG GGTGG GGGC GCG /
GTGATTAGGACCCGAAAGA GCC GA T GA CA A AG C-- CC

GAM1679 CCTGTGTGATATTGTTCTGC 1652 GGCCCAGCTC 3328 CTTA AAG CCC T C -- TG GGAGAGT G
TTAAAGAAGGTGGGCCCAGC AGCAGGGACA TGTTCTG AAG GTGGG AGC CAG AGGGA CAGTT G CC A
TCAGCAGGGACAGTTTGGGG GTTT ||||||| ||| ||||| ||| ||| ||||| ||||| | ||
AGAGTCCGAGAGGCTGGGCT ACAAGGC TTC CACCC TCG GTC TCCCT GTCGG C GG G
GATTCCCTTCTGTGCTCCCA C--- GTA --- T T TA GT ------- A
CATGCTTCCGGAACAGTGAC
AGG
GAM1680 CACAAGTGATGGTCCAACTT 1653 GTAAGGATTT 3329 - -- T-- GAATG- AGG AGGG GG
TGTGGAATGGTAAGGATTTT TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA ATTTTT TTGTTT C
TAGGGTTGTTTGGCCAGAAC TT ||||||| |||| ||||||| |||| ||| |||||| ||||||
AAGAGAAATAACTGCAGAAA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA AACAAG /
ACACATATGGTTGGAAACCA G AA TAT AAAAGA CAA G--- AC
TGCGCTTGTG

GAM1681 CACAAGTGATGGTCCAACTT 1654 GTAAGGATTT 3330 - -- T-- GAATG- AGG AGGG GG
TGTGGAATGGTAAGGATTTT TTAGGGTTGT ACAAGTG ATGG TCCAACT TGTG GTA ATTTTT TTGTTT C
TAGGGTTGTTTGGCCAGAAC TT |||||||| |||| ||||||| |||| ||| |||||| ||||||
AAGAGAAATAACTGCAGAAA TGTTCGC TACC AGGTTGG ACAC CGT TAAAGA AACAAG /
ACACATATGGTTGGAAACCA G AA TAT AAAAGA CAA G--- AC
TGCGCTTGTG

GAM1682 TCCTAACTTTCCCATATGTA 1655 TCCCATATGT 3331 TA T - GAAGAA - A
GAAGAAGCCATTAAGAATGC AGAAGAAGCC TCC AC TTC CCATATGTA GC CATT A
GTTACATGTGGAGAATGTGG ATT ||| || ||| ||||||||| || ||||
A AGG TG AAG GGTGTACAT TG GTAA /
-- T A ------ C G

GAM1683 GTGATGGACTGTATGGGGCT 1656 GGAGGCTGCC 3332 AC - ----- A- TG
GGCAGCCATGTGAAGCGGAG AGGATGATCT GTGATGG TGTA TGGGG CTGGCAGCC TG A
GCTGCCAGGATGATCTCACT CACT ||||||| |||| ||||| ||||||||| ||
ACACATTATTAC CATTATT ACAT ACTCT GACCGTCGG GC /
AC C AGTAG AG GA

GAM1684 CTTTTATGCGCCCGGAACTC 1657 GGCAAGCTGC 3333 ACTC T-- TG A TA --------- - G
CTTTTCTTTGCTGAAAGGTA TGATAAAGCT CCGGA CTTT CTTTGC A AGGTA TAGCT GCT GTTACA A
TATAGCTGCTGTTACAGAAA GCCT ||||| |||| |||||| | ||||| ||||| ||| ||||||
TGTGGCAAGCTGCTGATAAA GGTCT GAAG GAAACG T TCCGT GTCGA CGA CGGTGT A
GCTGCCTGCCTGTTGGCAAA CAAA CTC GT G CC AATAGTCGT A A
GCTCGAAGAAACTCTGGGTG
AAGAGG
GAM1685 TTATGGTGCTGCTGTGAACA 1658 TGGAGCCTGG 3334 G GCT AC GTTGGAGC G TT T T
CTGCCAAGTTGGAGCCTGGC CTCTGTTTGT TTATGGT CT GTGA ACTGCCAA CTGGCTCT T G GCCG C
TCTGTTTGTGCCGTCTTTGG GCCG ||||||| || |||| |||||||| |||||||| | | ||||
TCTGGGAGGAGTCGGATTGG AATGTCG GG TACT TGACGGTT GGCTGAGG G T TGGT T
CAGTTATCATGGGGCTGTAA G --- AT A------- A GG C T

GAM1686 GAAGCTTGACATTTTAGTTT 1659 TCAGGAGTAG 3335 C TG T- CATTA TT -- A
GCCATTATGTTAAAAACATC ATTGTTAGTG GAAG T ACATT TAGTTTGC TG AAA AACATCT A
TAAATAGGTGTTAGTTTCTC TTGA |||| | ||||| |||||||| || ||| |||||||
AGGAGTAGATTGTTAGTGTT TTTC A TGTGA GTTAGATG AC TTT TTGTGGA A

GACTTT - GT TT AGG-- TC GA T

GAM1687 GAAGCTTGACATTTTAGTTT 1660 TCAGGAGTAG 3336 C TG T- CATTA TT -- A
GCCATTATGTTAAAAACATC ATTGTTAGTG GAAG T ACATT TAGTTTGC TG AAA AACATCT
A
TAAATAGGTGTTAGTTTCTC TTGA |||| | ||||| |||||||| || ||| |||||||
AGGAGTAGATTGTTAGTGTT TTTC A TGTGA GTTAGATG AC TTT TTGTGGA A
GACTTT - GT TT AGG-- TC GA T

GAM1688 TCAACGGTATAAGGGACTTT 1661 ATAAGGGACT 3337 GGT A - CTTT TTTT - T
CTA
TAAGGGATTTTAGGTGGCTT TTTAAGGGAT TCAAC AT AG GGA TAAGGGA AGGTG GC
TAGA T
AGACTATATTTCTGTGCTCA TTTA ||||| || || ||| ||||||| ||||| || ||||
CCTTTCTTTATTCACTCATT AGTTG TA TC CTT ATTTCTT TCCAC CG GTCT /
AGTTGA AT- C A ---- ---- T T TTA

GAM1689 GCCCTGTGCCAACGCCGTCC 1662 GGACAGGATG 3338 CCAA G CGA A ACAA A CG
CCA C C - GA
GACAACATACAAGTGCACAT ACAGTGAGCA TG CGCC TC CA CAT GTGC CAT GTT
CCTG CC TGG CT A
CGGTTCCACCTGCCCCTGGC CGCT || |||| || || ||| |||| ||| ||| |||| || ||| ||
TGAAGAAGATCATGGACAGG AT GCGG AG GT GTG CACG GTG CAG GGAC GG
ACT GA /
ATGACAGTGAGCACGCTGGT C--- G AGG C GTCG A A- TA- A T A AG
GCTGGGAGAGGGCGCTACAG
AGGC
GAM1690 GTGGGGGACCAGAGGAGAGA 1663 GGACCAGAGG 3339 ----- AGA A - C G - AGGA A
CCA ACC
GAGCACCGAGAGGGGCAGGA AGAGAGAGCA GGA CC GGAGAG GAG CAC GA AGG GGC
TG AGGA CAG T
TGAAGGACCACAGACCTGCG CCGA ||| || |||||| ||| ||| || ||| ||| || |||| |||
CTGCTTCCTACACAGCCTCC CCT GG CCTCTT CTC GTG CT TCC CCG AC TCCT
GTC /
TGTCGTGACTCATTCTCCAA TAATT AA- A A - G T AC-- A TC- GCG
GGTTAATTCCTCCAC

GAM1691 AGCCTGGCTCTGACAGTGGT 1664 TGAGTATCGT 3340 A G A---- - TG GA ATCACGA
AA TT
ACAACAGCGGTGGTGGACCT GTAGAGCTAG CTCTG CA TGGTAC ACAGCG G GTG CCTG
GGGC GCAG G
GATCACGAGGGCAAGCAGTT TGCT ||||| || |||||| |||||| | ||| |||| |||| ||||
GAGCTGTAGCCCACACGCAG GAGAT GT GCTATG TGTCGC C CAT GGAC CCCG
TGTC /
GAGTACTCCTCGCTGTGCTG - - AGTCG T CT GA GCACA-- A- GA
AGTATCGTGTAGAGCTAGTG
CT

GAM1692 GTGTATATTTTAAAGCACAT 1665 TAAAGCACAT 3341 T AA A ---- GT C
CATGGCTTTAAGTACCATGT CATGGCTTTA GTGTATA TTTA GCAC TCATGG CTTTAA AC A
TGTTAAGGATTCTCATGAAG AGTA ||||||| |||| |||| |||||| |||||| ||
TGCCATAGACTGTACAT TACATGT AGAT CGTG AGTACT GGAATT TG /
C AC A CTTA GT T

GAM1693 ACTCTTTCTGTAGAAATCAT 1666 TACAAGCTGG 3342 A -- A--- - - T TT T
TAACAGA
CTTTACAAGCTGGGTGTTCT GTGTTCTTTT AGA ATCA TCTTT CA AGC TGGG G
CTTTTTGCGCAGA GAC C
TTTTGCGCAGATGACTAACA TGCG ||| |||| ||||| || ||| |||| | ||||||||||||| |||
GACAGGCAGCGTTTTTGTGC TTT TAGT AGGAA GT TCG GCTC C GGAAAACGTGTTT
TTG /
AAAAGGCCTCGTGCTATGAC G CT CCCA A T - -- - CGACGGA
CCAAGGATCTGATGTTTAAC
AGATAAGT
GAM1694 TCAGAGCTGCCAGTTAGAAG 1667 AGAGCTGCCA 3343 A GTT - - --- T -- A--
CTT
ATGGTTCCCTTGAGGGTTGA GTTAGAAGAT CAG GCTGCCA AGAAGATG GTT CC CT
GAGGGT TGAA GAAAT T
AAGAAATCTTTGAAATTTCA GGTT ||| ||||||| |||||||| ||| || || |||||| |||| |||||
CCTTCATGACCTTCCAGTTT GTC CGACGGT TCTTTTAC TAA GG GA CTTCCA ACTT
CTTTA /
GGCAATGCATTTTCTTGTGG A GT- G C TTT C GT CCA AAG
CAGCACTGA

GAM1695 TTCTGCGGGAGGGCAATATA 1668 AGAGGTTGTA 3344 -- ATA- - G GT
TAAATTGGGGGTGAACCGCG CCCTTTTGTA TTCTGCGGGAGGG CAAT TAAAT TG GG G
TGTTTAAGAGGTTGTACCCT GAA |||||||||||||| |||| ||||| || ||
TTTGTAGAA AAGATGTTTTCCC GTTG ATTTG GC CC /
AT GAGA T G AA

GAM1696 AGAGTAGCTTATTGTGTTTA 1669 CAGTGAAGCA 3345 CTTA G AGG C ATA- TCG
GGCGCCGAGACCATAATTCG GAAATCACTA AGAGTAG TT TGTTT CGC GAGACC AT T
TCATATGTCGGGTCTCAGTG CTTT ||||||| || ||||| ||| |||||| ||
AAGCAGAAATCACTACTTT TTTCATC AA ACGAA GTG CTCTGG TA /
ACTA G --- A GCTG TAC

GAM1697 GATTACAGGTGTGAGCCACC 1670 TCAGCTGGGC 3346 CA CCTCAAATCA---
A GT CT
ATGCCCGGCCCTCAAATCAT ACAGTGGCTC GTGTGAGCCAC TGCCCGGC
TCAGACTTTTAAGAAA T CT C
CAGACTTTTAAGAAAATGTC ACGC |||||||||| |||||||| |||||||||||||| | ||
TCTCTCCAGGTATTTCTTGA CGCACTCGGTG ACGGGTCG
GGTTTGAGAGTTCTTT A GA T
GAGTTTGGAAAATCAGCATC AC ACTACGACTAAAA - TG CC
AGCTGGGCACAGTGGCTCAC

GCCTATAATC
GAM1698 TCCCACTGTGGTGCCTGGTG 1671 TCGCCTGGAC 3347 CC - G T G A - AA CAGAGA
- CA T
GAGACCTGGCCAAGGTACAG CACAAGTTTG ACT GTGGT CC GGTG AG CCT GGCC GGTA
GCTGTG TG TGC G
AGAGCTGTGTGCATGCTGAG A ||| ||||| || |||| || ||| |||| |||| |||||| || |||
CAACACCACAGCCATTGCTG TGA CACCA GG CCGC TC GGG CCGG TCGT
CGACAC AC ACG /
AGGCCTGGGCTCGCCTGGAC TT A - T - - T AG TAC--- C A- A
CACAAGTTTGA

GAM1699 TCACGTACTATAGGTGAACT 1672 TGACAAGAAA 3348 T GG--- AACTTTT- CC
TTTAGCTCCTGCAGCTCCTT TGTGGTCGTG TCACG ACTATA TG AGCT T
TTGACAAGAAATGTGGTCGT A ||||| |||||| || ||||
GA AGTGC TGGTGT AC TCGA /
- AAAGA AGTTTTCC CG

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GENE    TARGET    UTR SEQUENCE          SEQID   BINDING-SITE
======== ========= === ==================== ======= ==========================
GAM25   A1BG     3'  CACGCCATTGCACTCCAGCCT  3         C
                         CGCCA TGCACTCCAGTC
                         ||||| ||||||||||||
                         GCGGT ACGTGAGGTCGG
                            A
GAM25   APPL     3'  CACACCACTGCACTCCAGCCT  4
                         CGCCACTGCACTCCAGTC
                         ||||||||||||||||||
                         GTGGTGACGTGAGGTCGG

GAM25   ATP6V1A1 3'  CACGCCATTGCACTCCAGCCT  3         C
                         CGCCA TGCACTCCAGTC
                         ||||| ||||||||||||
                         GCGGT ACGTGAGGTCGG
                            A
GAM25   CASP8    3'  CACGCCACTGCACTCCAGCCT  5
                         CGCCACTGCACTCCAGTC
                         ||||||||||||||||||
                         GCGGTGACGTGAGGTCGG

GAM25   CR1      3'  ACGCCACTGCACTCCAGCCT   7
                         CCACTGCACTCCAGTC
                         ||||||||||||||||
                         GGTGACGTGAGGTCGG

GAM25   CYP2B6   3'  CACGCCACTGCACTCCAGCCT  5
                         CGCCACTGCACTCCAGTC
                         ||||||||||||||||||
                         GCGGTGACGTGAGGTCGG

GAM25   EIF2S3   3'  CACGCCACTGCACTCCAGCCT  5
                         CGCCACTGCACTCCAGTC
                         ||||||||||||||||||
                         GCGGTGACGTGAGGTCGG

GAM25   EVC      3'  CACGCCACTGCACTCCAGCCT  5
                         CGCCACTGCACTCCAGTC
                         ||||||||||||||||||
                         GCGGTGACGTGAGGTCGG

GAM25   F2RL3    3'  CACGCCACTGCACTCCAGCCT  5
                         CGCCACTGCACTCCAGTC
                         ||||||||||||||||||
                         GCGGTGACGTGAGGTCGG

GAM25   FUT1     3'  CACGCCACTGCACTCCAGCCT  5
                         CGCCACTGCACTCCAGTC
                         ||||||||||||||||||
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                                GCGGTGACGTGAGGTCGG

GAM25   LZTS1    3'  CATGCCACTGCACTCCAGCCT  9
                                GCCACTGCACTCCAGTC
                                ||||||||||||||||
                                CGGTGACGTGAGGTCGG

GAM25   PAICS    3'  CACGCCACTGCACTCCAGCCT  5
                                CGCCACTGCACTCCAGTC
                                ||||||||||||||||||
                                GCGGTGACGTGAGGTCGG

GAM25   PPP1R12B 3'  CACACCACTGCACTCCAGCCT  4
                                CGCCACTGCACTCCAGTC
                                ||||||||||||||||||
                                GTGGTGACGTGAGGTCGG

GAM25   PSMB2    3'  ACGCCACAGCACTCCAGCCT  10       T
                                CCAC GCACTCCAGTC
                                |||| ||||||||||
                                GGTG CGTGAGGTCGG
                                  T
GAM25   TERF2    3'  CACGCCACTGCACTCCAGCCT  5
                                CGCCACTGCACTCCAGTC
                                ||||||||||||||||||
                                GCGGTGACGTGAGGTCGG

GAM27   CNTN3    3'  TAGAGGAAAAAATCAGGAATGA 66697      CT    ____
          C                      GTCAT  CTGAT   TTCTTTG
                                |||||  |||||   |||||||
                                CAGTA  GACTA   AGGAGAT
                                   AG    AAAA
GAM27   GSTA3    5'  TCAAAGAAACCAAGAGAC    5949     A   C  A
                                GTC TCT TG TTTCTTTGA
                                ||| ||| || |||||||||
                                CAG AGA AC AAAGAAACT
                                 _  _  C
GAM27   LDLR     3'  TTATTCAAAGACAGAGAAGAC  4993     A     ATT
                                GTC TCTCTG   TCTTTGAATAA
                                ||| ||||||   ||||||||||
                                CAG AGAGAC   AGAAACTTATT
                                  A    ___
GAM27   PCK1     5'  CAAAGAGAAGAAAGGTGAC   59944       CTGA
                                GTCATCT   TTTCTTTG
                                |||||||   ||||||||
                                CAGTGGA   AGAGAAAC
                                    AAGA
GAM27   PMP22    3'  GAGAAATCAGTGAC       4328      TCT
                                GTCA  CTGATTTCTT
                                ||||  ||||||||||
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                                CAGT   GACTAAAGAG
                                  ___
GAM27   PRNP     3'  TTATTCAAAAAAATCCTAGAG  4339      __    C
                                CTCT  GATTT TTTGAATAA
                                ||||  ||||| |||||||||
                                GAGA  CTAAA AAACTTATT
                                  TC    A
GAM27   RSN      3'  TTATTCAAAGAAATATCTGAG  11399     TG__
                                CTC    ATTTCTTTGAATAA
                                |||    ||||||||||||||
                                GAG    TAAAGAAACTTATT
                                  TCTA
GAM27   TLR1     5'  GAAGAAATCAGGATAAC     12314    C   T
                                GT ATC CTGATTTCTTT
                                || ||| ||||||||||
                                CA TAG GACTAAAGAAG
                                 A  _
GAM27   DKFZp434G179 3'  ATTCAAAGAGAACAGTAATGAC 80089      CT   A
                                GTCAT  CTG TTTCTTTGAAT
                                |||||  ||| |||||||||||
                                CAGTA  GAC AGAGAAACTTA
                                   AT   A
GAM27   FLJ10038  3'  TTAAGGAAACTAAAGATGAC   35751       C  A
                                GTCATCT TG TTTCTTTGA
                                ||||||| || |||||||||
                                CAGTAGA AT AAAGGAATT
                                    A  C
GAM27   FLJ11186  3'  TATTCAAAATGGAGGAGGAGAT 37146        GA   __
            GAC                   GTCATCTCT  TTTC  TTTGAATA
                                |||||||||  ||||  ||||||||
                                CAGTAGAGG  GAGG  AAACTTAT
                                     AG    TA
GAM27   FLJ14007  3'  ATTCAAAGATTCAAGTCAGA   45208       ____
                                TCTGATT    TCTTTGAAT
                                |||||||    |||||||||
                                AGACTGA    AGAAACTTA
                                    ACTT
GAM27   KIAA0940  3'  ATTCAAAGAATTGGTAATTGAC 29865     TCT_ TG   T
                                GTCA    C  ATT CTTTGAAT
                                ||||    |  ||| ||||||||
                                CAGT    G  TAA GAAACTTA
                                  TAAT GT   _
GAM27   KIAA1954  3'  ATTCAAAGAATTAGA      77715        T
                                TCTGATT CTTTGAAT
                                ||||||| ||||||||
                                AGATTAA GAAACTTA
                                    _
GAM27   MGC13168  3'  GGAAAAGCCAGAGATGAC    51212          A__
                                GTCATCTCTG   TTTCT
                                ||||||||||   |||||
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                                CAGTAGAGAC   AAAGG
                                     CGA
GAM27   SYNCOILIN 3'  TCACCCAAAATGGAGATGGC   47898         A   CTT
                                GTCATCTCTG TTT   TGA
                                |||||||||| |||   |||
                                CGGTAGAGGT AAA   ACT
                                     A   CCC
GAM27   TCL6    3'  ATTCAGCATCAGAGAGAC    40095    A      TTCT
                                GTC TCTCTGAT    TTGAAT
                                ||| ||||||||    ||||||
                                CAG AGAGACTA    GACTTA
                                  _       C___
GAM27   TCL6    3'  ATTCAGCATCAGAGAGAC    40126    A      TTCT
                                GTC TCTCTGAT    TTGAAT
                                ||| ||||||||    ||||||
                                CAG AGAGACTA    GACTTA
                                  _       C___
GAM27   TIP120B  3'  CAAAGAAATAGGGTGA      72418      T   A
                                TCATC CTG TTTCTTTG
                                ||||| ||| ||||||||
                                AGTGG GAT AAAGAAAC
                                  _  _
GAM27   LOC122402 3'  ATTTTGGAAATCAGAGATTAC  74124    C          TT
                                GT ATCTCTGATTTCT  GAAT
                                || ||||||||||||  ||||
                                CA TAGAGACTAAAGG  TTTA
                                 T           T_
GAM27   LOC145757 3'  AGAAATCAAAGAGAC       77450     A   C
                                GTC TCT TGATTTCT
                                ||| ||| ||||||||
                                CAG AGA ACTAAAGA
                                  _   A
GAM27   LOC147514 3'  ATTCAAAGAAGAAATGAT    67557      C   GATT
                                GTCAT TCT    TCTTTGAAT
                                ||||| |||    |||||||||
                                TAGTA AGA    AGAAACTTA
                                   A  _____
GAM27   LOC158814 3'  TCCTAGAACCAGAGAGGAC   82005     A     AT    TT
                                GTC TCTCTG  TTCT  GA
                                ||| ||||||  ||||  ||
                                CAG AGAGAC  AAGA  CT
                                  G     C_    TC
GAM27   LOC220431 5'  TTATTCACCTCTTCAGAGA   94338        TTTCTT
                                TCTCTGA     TGAATAA
                                |||||||     |||||||
                                AGAGACT     ACTTATT
                                     TCTCC_
GAM27   LOC254610 5'  TATCCAAAGATCAGAGTGAC  96276     T     TT     A
                                GTCA CTCTGA  TCTTTG ATA
                                |||| ||||||  |||||| |||
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                                CAGT GAGACT  AGAAAC TAT
                                  _     __     C
GAM28   C5R1     3'  ACCTAAAAAACCTGCA      8198          C  C
                                TGTAGGTTTT TA GGT
                                |||||||||| || |||
                                ACGTCCAAAA AT CCA
                                     A  _
GAM28   CEPT1    5'  CCAGCCACAAAAAACCTACA    20328          CTAC   A
                                TGTAGGTTTT    GGT TGG
                                ||||||||||    ||| |||
                                ACATCCAAAA    CCG ACC
                                     ACA_  _
GAM28   DDX33    3'  CCACACCACATCTGGGCTTACA 39369          TCTAC_   A
                                TGTAGGTTT     GGT TGG
                                |||||||||     ||| |||
                                ACATTCGGG     CCA ACC
                                     TCTACA   C
GAM28   LOC134266 3'  ACCACAGGAAACCCACA     75161     A       AC
                                TGT GGTTTTCT  GGT
                                ||| ||||||||  |||
                                ACA CCAAAGGA  CCA
                                  C       CA
GAM28   LOC145314 3'  GCCACAGAAAACCACA      77088     A       ACGGTA
                                TGT GGTTTTCT     TGGC
                                ||| ||||||||     ||||
                                ACA CCAAAAGA     ACCG
                                  _       C_____
GAM28   LOC219561 3'  ATGCCACAAACAAGAAAACC   91756          ACGGTA
                                GGTTTTCT     TGGCAT
                                ||||||||     ||||||
                                CCAAAAGA     ACCGTA
                                     ACAAAC
GAM28   LOC221632 3'  GCCACACGCATGGAAAACC    93802          CG_  A
                                GGTTTTCTA   GT TGGC
                                |||||||||   || ||||
                                CCAAAAGGT   CA ACCG
                                     ACG  C
GAM29   ACTN2    3'  TGCTAGCACATCTTGAT      6594           AATGGA
                                GTCAAGATGT     TAGCA
                                ||||||||||     |||||
                                TAGTTCTACA     ATCGT
                                     CG____
GAM29   BCL2     3'  TCACATCTGCATCTTAACT    5304      C       _  _
                                AGT AAGATGTA ATG GA
                                ||| |||||||| ||| ||
                                TCA TTCTACGT TAC CT
                                  A       C   A
GAM29   BMP4     3'  CTAAACATTCACCTTGAC     6830         A  T    GA
                                GTCAAG TG AATG  TAG
                                |||||| || ||||  |||
```

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                                CAGTTC AC TTAC  ATC
                                   C _   AA
GAM29   BMP4    3' CTAAACATTCACCTTGAC   55634      A T   GA
                                GTCAAG TG AATG  TAG
                                |||||| || ||||  |||
                                CAGTTC AC TTAC  ATC
                                   C _   AA
GAM29   BMP4    3' CTAAACATTCACCTTGAC   55638      A T   GA
                                GTCAAG TG AATG  TAG
                                |||||| || ||||  |||
                                CAGTTC AC TTAC  ATC
                                   C _   AA
GAM29   CADPS   3' TTGCTTTTACGTCTCAACT  65208    CA     TGGAT
                                AGT  AGATGTAA   AGCAA
                                |||  ||||||||   |||||
                                TCA  TCTGCATT   TCGTT
                                  AC      T____
GAM29   COL17A1 3' TGCTATCTAGATCTGAACT  4936     CA   GTAA
                                AGT  AGAT   TGGATAGCA
                                |||  ||||   |||||||||
                                TCA  TCTA   ATCTATCGT
                                  AG   G___
GAM29   DCN     5' GTGTAATTACATCTCAGCT   8619     CA      GGATA
                                AGT  AGATGTAAT   GC
                                |||  |||||||||   ||
                                TCG  TCTACATTA   TG
                                  AC       ATG__
GAM29   HIVEP3  5' TCTGACACATCTTGAC     44440        AA
                                GTCAAGATGT  TGGA
                                ||||||||||  ||||
                                CAGTTCTACA  GTCT
                                      CA
GAM29   IRTA2   3' TGATATCCATCACATCTTATCT 48411   TC     A     G
                                AG  AAGATGT ATGGATA CA
                                ||  ||||||| ||||||| ||
                                TC  TTCTACA TACCTAT GT
                                 TA     C      A
GAM29   LZTFL1  3' TTATGTATTACATTTTAAC   39760   C       G
                                GT AAGATGTAATG ATAG
                                || ||||||||||| ||||
                                CA TTTTACATTAT TATT
                                 A         G
GAM29   RBBP9   3' TGCTATTTTGCATC       70144       TG
                                GATGTAA  GATAGCA
                                |||||||  |||||||
                                CTACGTT  TTATCGT
                                         __
GAM29   TGFBR2  3' TTCATTACACTTGACT     12272       A
                                AGTCAAG TGTAATGGA
                                ||||||| |||||||||
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                                TCAGTTC ACATTACTT
                                        _
GAM29   BART1    3'  TGTGATCACATCTTGTCT    23988    T      AATG   A
                                AG CAAGATGT    GAT GCA
                                || ||||||||    ||| |||
                                TC GTTCTACA    CTA TGT
                                 T      _____   G
GAM29   BPESC1   3'  TGCTGTCCCCACATCCTGAT   41478     A    AAT
                                GTCA GATGT   GGATAGCA
                                |||| |||||   ||||||||
                                TAGT CTACA   CCTGTCGT
                                  C    CC_
GAM29   C1orf21  5'  GTGCACACATCTTGAC      47962          AA  G
                                GTCAAGATGT  TG AT
                                ||||||||||  || ||
                                CAGTTCTACA  AC TG
                                      C_  G
GAM29   C6orf37  3'  CTACTACCATCTTGGCT     67477          _  A
                                AGTCAAGATG TA TGG
                                |||||||||| || |||
                                TCGGTTCTAC AT ATC
                                      C  C
GAM29   DKFZp547E052 3'  TGCTATAACACATCTTGC    50101    T      AATGG
                                G CAAGATGT    ATAGCA
                                | ||||||||    ||||||
                                C GTTCTACA    TATCGT
                                _      CAA__
GAM29   DKFZP727M111 3'  CTACCATTACATCCTGAT    31408     A       A
                                GTCA GATGTAATGG TAG
                                |||| |||||||||| |||
                                TAGT CTACATTACC ATC
                                  C       _
GAM29   FLJ10210 5'  TGACAAACCACATCTTGACT   35902          AAT  ATAG_
                                AGTCAAGATGT   GG    CA
                                ||||||||||   ||    ||
                                TCAGTTCTACA   CC    GT
                                      ___  AAACA
GAM29   FLJ13114 3'  TGCTGTTGTTTACATC      44605        TG
                                GATGTAA  GATAGCA
                                |||||||  |||||||
                                CTACATT  TTGTCGT
                                    TG
GAM29   FLJ13984 3'  TTTGAATTTATTACATCT    45455           AG
                                AGATGTAATGGAT  CAAA
                                ||||||||||||  ||||
                                TCTACATTATTTA  GTTT
                                       A_
GAM29   FLJ20808 5'  TGGTGACCTCATCTTGACT   35674          TAAT  A  G
                                AGTCAAGATG    GG TA CA
                                ||||||||||    || || ||
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                                TCAGTTCTAC   CC GT GT
                                     T___  A  G
GAM29   FLJ31709  3'  TGCAAACCCATCTTGAC    58273        TAAT  ATA
                                GTCAAGATG   GG  GCA
                                |||||||||   ||  |||
                                CAGTTCTAC   CC  CGT
                                     ____  AAA
GAM29   GT650     3'  CTGCCATAACATCTTGA    53454        A   A
                                TCAAGATGT ATGG TAG
                                ||||||||| |||| |||
                                AGTTCTACA TACC GTC
                                     A   _
GAM29   H_GS165L15.1 3'  CTATTCATTTTGACT      16925         T
                                AGTCAAGATG AATGG
                                |||||||||| |||||
                                TCAGTTTTAC TTATC

                                     _
GAM29   HCA4      3'  TTTGCTATCCATTTGCA    77598      _
                                TGTAA TGGATAGCAAA
                                ||||| ||||||||||
                                ACGTT ACCTATCGTTT
                                   T
GAM29   KIAA1317  3'  TCAATTACATCCTGACT    86033      A      G
                                AGTCA GATGTAAT GA
                                ||||| |||||||| ||
                                TCAGT CTACATTA CT
                                   C       A
GAM29   SERPING1  3'  GCTATCCACCAAAAGGGCT   3556      AAGA  TAA
                                AGTC   TG   TGGATAGC
                                ||||   ||   ||||||||
                                TCGG   AC   ACCTATCG
                                  GAAA  C__
GAM29   LOC130576 5'  TGCCCATTAATCTTGAC    74954        G     ATA
                                GTCAAGAT TAATGG   GCA
                                |||||||| ||||||   |||
                                CAGTTCTA ATTACC   CGT
                                     _    ____
GAM29   LOC144453 3'  GCTACCTCCATCTTGA     76846        TAAT  A
                                TCAAGATG   GG TAGC
                                ||||||||   || ||||
                                AGTTCTAC   CC ATCG
                                     CT__  _
GAM29   LOC146226 5'  TTTGCTACCAGGAATCTTGAC  83626        GTAA  A
                                GTCAAGAT   TGG TAGCAAA
                                ||||||||   ||| |||||||
                                CAGTTCTA   ACC ATCGTTT
                                     AGG_  _
GAM29   LOC154062 3'  CTTTCCACATTTTGACT    81033         AAT   T
                                AGTCAAGATGT   GGA AG
                                ||||||||||   ||| ||
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                                TCAGTTTTACA   CCT TC
                                      ___   T
GAM29   LOC158656 5'  GCACCAATCTTGACT      73037        GTAA   ATA
                                AGTCAAGAT   TGG   GC
                                |||||||||   |||   ||
                                TCAGTTCTA   ACC   CG
                                     _____  A__
GAM29   LOC221025 5'  CCATTGTCAACATTTTGAC   93175         _____
                                GTCAAGATGT   AATGG
                                ||||||||||   |||||
                                CAGTTTTACA   TTACC
                                      ACTG
GAM29   LOC256364 5'  TTCATCACTCATCTTGACT   94804         TA__
                                AGTCAAGATG   ATGGA
                                ||||||||||   |||||
                                TCAGTTCTAC   TACTT
                                      TCAC
GAM29   LOC93395  5'  GCTATTCACTTGAC       60499       ATGTAA
                                GTCAAG     TGGATAGC
                                ||||||     ||||||||
                                CAGTTC     ACTTATCG
                                     _______
GAM30   ADH1B    3'  CTTAGACATAAAGTAAAAT   72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM30   AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM30   FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                     _
GAM30   JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM30   KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||  ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM30   PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
```

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                                TAAAGTGAAA TGACA
                                     A
GAM30   PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG   A
                                TTTCACTTTCA  TCTG GA
                                ||||||||||  |||| ||
                                AAAGTGAAAGT  GGAC CT
                                      T__   _
GAM30   WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM30   ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017        CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM30   CG012   5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM30   EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM30   FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||         |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM30   FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM30   KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                   A       CT
GAM30   KLHL6   3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                   _  G
GAM30   NIR3    3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
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                                TAA GTGAAAGTGACG
                                  C
GAM30   PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM30   PP35     3' ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM30   PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148         TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__    TT
GAM30   SEP15    3' TCCTACAGTAAGAGTGAAA   14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A     TC
GAM30   SFXN2    3' CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                      AAAGG
GAM30   LOC149703 3' ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC       CTGTCTGAGAT
                                ||||       ||||||||||||
                                AAAG       GACAGACTCTA
                                  GTTTGCC
GAM30   LOC154007 3' ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT      GT TGAGAT
                                |||||||      || ||||||
                                AAAGTGA      CA ACTCTA
                                     TTTCC_  A
GAM30   LOC155004 3' TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM30   LOC222134 5' ACAGTGAAGTGAAATG       94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM31   CLCN5    5' TGAAATACCTAAGCTGCTCCAA 3595          ________
                                TTGGAGCAG      GTTTCA
                                |||||||||      ||||||
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                                AACCTCGTC      TAAAGT
                                     GAATCCA
GAM31   FLRT2    5' ATTGAAAAATGAGGTCTGC   25056     GT     CTC
                                GCAG  TTCATT   CAAT
                                ||||  ||||||   ||||
                                CGTC  GAGTAA   GTTA
                                  TG     AAA
GAM31   IL17     3' TGGGGAAAATGAAACCCTCC  9333      CA      __
                                GGAG  GGTTTCAT  TCTCCA
                                ||||  ||||||||  ||||||
                                CCTC  CCAAAGTA  AGGGGT
                                  __       AA
GAM31   NLGN1    5' TGAAGATGCTGCTCCAA     30026        G__
                                TTGGAGCAG   TTTCA
                                |||||||||   |||||
                                AACCTCGTC   GAAGT
                                     GTA
GAM31   POLG     3' GTGATAAACCTGCTCCAA    10682          __
                                TTGGAGCAGGTT  TCAT
                                ||||||||||||  ||||
                                AACCTCGTCCAA  AGTG
                                      AT
GAM31   TPK1     3' GGAGAACCTGTCCAA       42384       G    TTCAT
                                TTGGA CAGGT    TCTCC
                                ||||| |||||    |||||
                                AACCT GTCCA    AGAGG
                                  _    _____
GAM31   C1orf8   5' GAGAATGAAACCCTC       16832     CA
                                GAG  GGTTTCATTCTC
                                |||  ||||||||||||
                                CTC  CCAAAGTAAGAG
                                  __
GAM31   CLIC6    3' TGGAGAACATGTTCCAA     82536        G  TTCAT
                                TTGGAGCA GT    TCTCCA
                                |||||||| ||    ||||||
                                AACCTTGT CA    AGAGGT
                                     A _____
GAM31   CLIPR-59 3' TGGAGAATTTCAATGCCCCGA 31374     A   GGTTTC
                                TTGG GCA     ATTCTCCA
                                |||| |||     ||||||||
                                AGCC CGT     TAAGAGGT
                                  C   AACTT_
GAM31   DKFZP547L112 3' TGGAGAACTCTTGCTCCA    66532         TTTCA
                                TGGAGCAGG    TTCTCCA
                                |||||||||    |||||||
                                ACCTCGTTC    AAGAGGT
                                     TC___
GAM31   EPS8R3   5' GGACCACCTGCTCCAA      55701          TTCATTC
                                TTGGAGCAGGT     TCC
                                ||||||||||      |||
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                                AACCTCGTCCA      AGG
                                      CC_____
GAM31   EPS8R3   5' GGACCACCTGCTCCAA     57404          TTCATTC
                                TTGGAGCAGGT      TCC
                                ||||||||||       |||
                                AACCTCGTCCA      AGG
                                      CC_____
GAM31   FLJ20552 3' AGAACAAAACTGCTCCAA    35389         G   CA
                                TTGGAGCAG TTT  TTCT
                                ||||||||| |||  ||||
                                AACCTCGTC AAA  AAGA
                                     _  AC
GAM31   FLJ22865 5' TGGAGAAAACTGCTCTAA    47071         GTTTCA
                                TTGGAGCAG     TTCTCCA
                                |||||||||     |||||||
                                AATCTCGTC     AAGAGGT
                                      AA____
GAM31   KIAA0372 5' ATTGAAATTTGTTACCTACTCC 27663       C    TT  TTCTC
            AA                    TTGGAG AGGT  CA    CAAT
                                |||||| ||||  ||    ||||
                                AACCTC TCCA  GT    GTTA
                                   A    TT  TTAAA
GAM31   PRO0132  5' ATGAAACCACTCCAA      26101       CA
                                TTGGAG  GGTTTCAT
                                ||||||  ||||||||
                                AACCTC  CCAAAGTA
                                   A_
GAM31   TEX27    3' AGAGTGGAACCCGCTGCAA   41658     G   A
                                TTG AGC GGTTTCATTCT
                                ||| ||| ||||||||||
                                AAC TCG CCAAGGTGAGA
                                  G   C
GAM31   LOC149373 3' ATTGGGGTGATGATACCCACCC 79312      AGCA   T    _
            CAA                    TTGG    GGT TCATT CTCCAAT
                                ||||    ||| ||||| |||||||
                                AACC    CCA AGTAG GGGGTTA
                                   CCAC   T    T
GAM31   LOC152687 3' TTGGAGAATATTGCTCC     80643        GTTTC
                                GGAGCAG     ATTCTCCAA
                                |||||||     |||||||||
                                CCTCGTT     TAAGAGGTT
                                   A____
GAM31   LOC51202  3' ATTGGAGAATGAAACCTGCTCC 33017
            AA                    TTGGAGCAGGTTTCATTCTCCAAT
                                ||||||||||||||||||||||||
                                AACCTCGTCCAAAGTAAGAGGTTA

GAM32   ADAMTS8   5' TCGGGCCGCCAGCACCTG    22886     _      ATAAG
                                CAG TGCTGGC     CTGA
                                ||| |||||||     ||||
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                                GTC ACGACCG    GGCT
                                  C      CCG__
GAM32   BAP1    3'  TCAGGGACCCAGCACTGG    16219          CATAAG
                                CCAGTGCTGG    CTGA
                                ||||||||||    ||||
                                GGTCACGACC    GACT
                                      CAGG__
GAM32   BF      5'  TTCAGCTTGGACACTG     8140       CTGGCA
                                CAGTG    TAAGCTGAA
                                |||||    |||||||||
                                GTCAC    GTTCGACTT
                                   AG_____
GAM32   C1QB    3'  TTCAACTCTGTGTCCCAGCACT 4923    A        __   _ C
            GGC                    G CCAGTGCTGG  CATA AG TGAA
                                | ||||||||||  |||| || ||||
                                C GGTCACGACC  GTGT TC ACTT
                                _        CT    C  A
GAM32   CHC1    3'  CAGCCCTGAGCACTGTGTC    7020     _     __ CATAA
                                GAC CAGTGCT  GG    GCTG
                                ||| |||||||  ||    ||||
                                CTG GTCACGA  CC    CGAC
                                  T      GT  _____
GAM32   CMRF35  5'  CAGAGCTGTCAGCACCGG    21929    A       TAAG
                                CC GTGCTGGCA    CTG
                                || |||||||||    |||
                                GG CACGACTGT    GAC
                                 C        CGA_
GAM32   EPHB6   3'  TCAGCCCTGGACACTGGTC    15466        _ TG CATAA
                                GACCAGTG C  G    GCTGA
                                ||||||||  |  |    |||||
                                CTGGTCAC G  C    CGACT
                                     A GT C____
GAM32   EVPL    5'  CAGCCTGAGCCAGCACT     8803          A  A
                                AGTGCTGGC TA GCTG
                                ||||||||| || ||||
                                TCACGACCG GT CGAC
                                      A  C
GAM32   GARP    3'  CAGCCCAGCACTGG        18594          CATAA
                                CCAGTGCTGG    GCTG
                                ||||||||||    ||||
                                GGTCACGACC    CGAC
                                      _____
GAM32   GJB5    3'  CAGCTCGACGGCACTGG     17945         GCATA
                                CCAGTGCTG    AGCTG
                                |||||||||    |||||
                                GGTCACGGC    TCGAC
                                      AGC__
GAM32   GPR81   3'  CTTACCAGCATTAGTC     50757     C       CA
                                GAC AGTGCTGG  TAAG
                                ||| ||||||||  ||||
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                                CTG TTACGACC  ATTC
                                  A      __
GAM32   IFI16    5'  AGCAAGCCAGCACTAGTC    71221     C       ATAA
                                GAC AGTGCTGGC    GCT
                                ||| |||||||||    |||
                                CTG TCACGACCG    CGA
                                  A       AA__
GAM32   KRT4     3'  CAGCTGGGCCCAGCACTGGT   9635          _ ATA
                                ACCAGTGCTGG C   AGCTG
                                |||||||||||  |   |||||
                                TGGTCACGACC G   TCGAC
                                      C GG_
GAM32   MAP3K9   3'  TTCAGCTTCCCAAACACCAGT  60709    CA   C_   CAT
                                AC  GTG  TGG   AAGCTGAA
                                ||  |||  |||   ||||||||
                                TG  CAC  ACC   TTCGACTT
                                 AC   AA   C__
GAM32   MGAT5    5'  TCAGCTTACAGTTCCTG     10028     T_   GCA
                                CAG  GCTG   TAAGCTGA
                                |||  ||||   ||||||||
                                GTC  TGAC   ATTCGACT
                                  CT    ____
GAM32   MOCS1    3'  TTCAGCTTAACAGTTGCCCGGT 92037      A_   _   GCA
           C                     GACC  GTG CTG   TAAGCTGAA
                                ||||  ||| |||   |||||||||
                                CTGG  CGT GAC   ATTCGACTT
                                  CC   T   A__
GAM32   P23      3'  TCAGCTTATACCCGGGCT    21719     G    C_
                                AGT CTGG  ATAAGCTGA
                                ||| ||||  |||||||||
                                TCG GGCC  TATTCGACT
                                  _    CA
GAM32   PFKFB4   3'  TCAGCCACATGCAACACTGTGT 15874     _     CTG    AA_
           C                     GAC CAGTG   GCAT   GCTGA
                                ||| |||||   ||||   |||||
                                CTG GTCAC   CGTA   CGACT
                                  T    AA_    CAC
GAM32   PTPRK    3'  TTCAGCCTGTGGCCCAGCACTG 11125           __    A
           GTC                     GACCAGTGCTGG  CATA GCTGAA
                                ||||||||||||  |||| ||||||
                                CTGGTCACGACC  GTGT CGACTT
                                      CG    C
GAM32   RNPEPL1  3'  CGGATGCCAGCACCTG      36676     _       AAG
                                CAG TGCTGGCAT   CTG
                                ||| |||||||||   |||
                                GTC ACGACCGTA   GGC
                                  C       ____
GAM32   UBE2L3   3'  TCAGCCCTGGCACTGGC     12507    A      TG CATAA
                                G CCAGTGC  G    GCTGA
                                | |||||||  |    |||||
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                                C GGTCACG  C    CGACT
                                _      GT C____
GAM32   APXL2    5'  CAGCCTCAGCACTCATC    75185    CC      CATAA
                                GA  AGTGCTGG    GCTG
                                ||  ||||||||    ||||
                                CT  TCACGACT    CGAC
                                 AC       C____
GAM32   ARHGEF9  3'  TTCAGCTTACCAAGCA     30824     _ CA
                                TGCT GG  TAAGCTGAA
                                |||| ||  |||||||||
                                ACGA CC  ATTCGACTT
                                  A  __
GAM32   CEGP1    3'  TTCAGCTTCCTCTAGCCCGG  40589    AGT    CAT
                                CC   GCTGG   AAGCTGAA
                                ||   |||||   ||||||||
                                GG   CGATC   TTCGACTT
                                 CC_    TCC
GAM32   DKFZp547D155 3'  CAGCCCTGAGACCACTGGTC  70435        CTGG  TAA
                                GACCAGTG   CA   GCTG
                                ||||||||   ||   ||||
                                CTGGTCAC   GT   CGAC
                                     CAGA  CC_
GAM32   DKFZP727G051 3'  TTCAGCCCATCAACCAGCATTG 69483          CATAA__
            GTC                  GACCAGTGCTGG      GCTGAA
                                ||||||||||||      ||||||
                                CTGGTTACGACC      CGACTT
                                       AACTACC
GAM32   DUSP14   5'  CACTGTCACCAGCACTGCTC  22834    C       CATA  C
                                GA CAGTGCTGG    AG TG
                                || |||||||||    || ||
                                CT GTCACGACC    TC AC
                                 C       ACTG  _
GAM32   FLJ10206 5'  CAGCTTATGCCAGGAGTC    35898     CAGTG
                                GAC    CTGGCATAAGCTG
                                |||    ||||||||||||||
                                CTG    GACCGTATTCGAC
                                  AG___
GAM32   FLJ20967 5'  GGCGCCCAGCACTGGTT     41962          CATAA
                                GACCAGTGCTGG    GCT
                                ||||||||||||    |||
                                TTGGTCACGACC    CGG
                                       CG___
GAM32   FLJ22569 3'  TTCAGCTTACTAAACTG     43679     GC   CA
                                CAGT  TGG  TAAGCTGAA
                                ||||  |||  |||||||||
                                GTCA  ATC  ATTCGACTT
                                  A_   __
GAM32   FOXN4    3'  TTCAGCTTGGACACACTGG   75574       C  GCA
                                CCAGTG TG   TAAGCTGAA
                                ||||||  ||   |||||||||
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                                GGTCAC AC   GTTCGACTT
                                   _ AG_
GAM32   GW112    3'  TTCAACTGAAGCCAGCACTGGT 21194          ATA  C
           T                    GACCAGTGCTGGC   AG TGAA
                                ||||||||||||   || ||||
                                TTGGTCACGACCG   TC ACTT
                                      AAG  A
GAM32   HOOK2    3'  CAGCTCACATGGCGCCCAGCAC 25256        ____  A__
           TGG                   CCAGTGCTGG   CAT   AGCTG
                                ||||||||||   |||  |||||
                                GGTCACGACC   GTA   TCGAC
                                     CGCG   CAC
GAM32   jdp2     3'  TTCAGCACAGCCAGCAT     55327        ATAA
                                GTGCTGGC   GCTGAA
                                ||||||||   ||||||
                                TACGACCG   CGACTT
                                   ACA_
GAM32   KIAA0767 3'  TCTGCTGCCAGCACAGG     60632    A       TAA  T
                                CC GTGCTGGCA   GC GA
                                || |||||||||   || ||
                                GG CACGACCGT   CG CT
                                 A        ___  T
GAM32   KIAA0923 3'  TCAGCTTGATGCATGGTC    25838      G   TGGCA
                                GACCA TGC    TAAGCTGA
                                ||||| |||    ||||||||
                                CTGGT ACG    GTTCGACT
                                   _  TA___
GAM32   KIAA0982 3'  TTCACTGTTTGCCAGCAC    25852        TA_  C
                                GTGCTGGCA   AG TGAA
                                |||||||||   || ||||
                                CACGACCGT   TC ACTT
                                     TTG  _
GAM32   KIAA1000 3'  TTCAGCTTTGCAAAGTACTGG  65281        G_   T
                                CCAGTGCT  GCA AAGCTGAA
                                ||||||||  ||| ||||||||
                                GGTCATGA  CGT TTCGACTT
                                     AA  _
GAM32   MAP3K3   3'  TCAGCCTGGGCGCTGGTC    9999         GG  TAA
                                GACCAGTGCT  CA   GCTGA
                                ||||||||||  ||   |||||
                                CTGGTCGCGG  GT   CGACT
                                     __  C__
GAM32   MGC16037 5'  CTTGTCCAGCACTAGTC     51821     C       C
                                GAC AGTGCTGG ATAAG
                                ||| |||||||| |||||
                                CTG TCACGACC TGTTC
                                  A       _
GAM32   MIDORI   3'  TCAGCTTATCCTGCAACT    73792     _  T  C
                                AGT GC GG ATAAGCTGA
                                ||| || || |||||||||
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                                TCA CG CC TATTCGACT
                                  A  T  _
GAM32   MtFMT    5'  CAGTGGCGAGCACTGG      57651         G  ATAA
                                CCAGTGCT GC    GCTG
                                |||||||| ||    ||||
                                GGTCACGA CG    TGAC
                                     G  G___
GAM32   PCDH16   5'  TCAGTTCCAACCACTGG     72826       C_   CATA
                                CCAGTG  TGG    AGCTGA
                                ||||||  |||    ||||||
                                GGTCAC  ACC    TTGACT
                                   CA  _____
GAM32   QKI      3'  CAGCTTATCAACTCGTC     65439     C   GCTGGC
                                GAC AGT      ATAAGCTG
                                ||| |||      ||||||||
                                CTG TCA      TATTCGAC
                                  C   AC_____
GAM32   TNRC6    3'  CAACTTTTAGCACTG       70506          CAT   C
                                CAGTGCTGG   AAG TG
                                |||||||||   ||| ||
                                GTCACGATT   TTC AC
                                     ___  A
GAM32   TOB2     3'  CAGCCCAGGCCAGCACTG    95618           ATAA
                                CAGTGCTGGC    GCTG
                                ||||||||||    ||||
                                GTCACGACCG    CGAC
                                      GACC
GAM32   TU12B1-TY 3'  TCAGCCCACAGCACTGTC    33406     C      GCATAA
                                GAC AGTGCTG      GCTGA
                                ||| |||||||      |||||
                                CTG TCACGAC      CGACT
                                  _      ACC___
GAM32   TUSP     3'  TCAGCCTAAGAGCGCAGCACTG 39641          _  A__  A
                                CAGTGCTG GC   TA GCTGA
                                |||||||| ||   || |||||
                                GTCACGAC CG   AT CGACT
                                     G  AGA  C
GAM32   USP19    3'  TCAGCTTATGCATCTGGT    88959       TGCTG
                                ACCAG    GCATAAGCTGA
                                |||||    ||||||||||
                                TGGTC    CGTATTCGACT
                                   TA___
GAM32   ZD52F10  3'  CAGCCTGTGCCAGCCCTGG   52819      T       A
                                CCAG GCTGGCATA GCTG
                                |||| ||||||||| ||||
                                GGTC CGACCGTGT CGAC
                                  C        C
GAM32   LOC145268 3'  TCAGCTTACAAGAGCCACTG   77062       _  GGCA
                                CAGTG CT    TAAGCTGA
                                ||||| ||    ||||||||
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                                GTCAC GA    ATTCGACT
                                   C  GAAC
GAM32   LOC149296 5'  CAGCTTATGGGCAGCA      79256       G_
                                TGCTG  CATAAGCTG
                                |||||  |||||||||
                                ACGAC  GTATTCGAC
                                   GG
GAM32   LOC161877 5'  TCAGGGCAGGCCAGCGCTGG   82326           ATAAG
                                CCAGTGCTGGC    CTGA
                                ||||||||||     ||||
                                GGTCGCGACCG    GACT
                                      GACGG
GAM32   LOC163115 5'  TCAGCCCCTGACAGCACTGG   82413         G  TAA
                                CCAGTGCTG CA   GCTGA
                                ||||||||| ||   |||||
                                GGTCACGAC GT   CGACT
                                     A  CCC
GAM32   LOC196500 3'  TCAGCTCACTCAGTGGTC    87744      AGT    CATA
                                GACC   GCTGG    AGCTGA
                                ||||   |||||    ||||||
                                CTGG   TGACT    TCGACT
                                  ____    CAC_
GAM32   LOC197287 3'  TCAGCTCATGTGTTTTGCACTG 60865       T_     __
                                CAGTGC  GGCATA  AGCTGA
                                ||||||  ||||||  ||||||
                                GTCACG  TTGTGT  TCGACT
                                   TT      AC
GAM32   LOC200470 5'  TCAGCCTGCGGCGCTGG     90069         G  TAA
                                CCAGTGCTG CA   GCTGA
                                ||||||||| ||   |||||
                                GGTCGCGGC GT   CGACT
                                     _  C__
GAM32   LOC221584 3'  CAGCTTATGTGGCAC       93828       G
                                GTGCTG CATAAGCTG
                                |||||| |||||||||
                                CACGGT GTATTCGAC
                                  _
GAM32   LOC51716  3'  CAGCTCATGGCCCTAGCA    32787       ____  A
                                TGCTGG   CAT AGCTG
                                ||||||   ||| |||||
                                ACGATC   GTA TCGAC
                                   CCG   C
GAM32   LOC92196  5'  CAGAGCACCAGCACTGGC    68456   A       CATAAG
                                G CCAGTGCTGG     CTG
                                | ||||||||||     |||
                                C GGTCACGACC     GAC
                                _        ACGA__
GAM33   ABCC11    5'  ATAAAGCAAGAAGACTGA    52505          TCTCAC
                                TCAGTCTTTTT     CTTTAT
                                ||||||||||     ||||||
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                                AGTCAGAAGAA     GAAATA
                                      C_____
GAM33   DCT     5'  TGAAAAGAAAAGACTGA     8625          C_
                                TCAGTCTTTTTT  TCA
                                ||||||||||||  |||
                                AGTCAGAAAAGA  AGT
                                   AA
GAM33   FEZ1    3'  ATAAAGGCCAGAAAAAA     42564        CA
                                TTTTTTCT  CCTTTAT
                                ||||||||  |||||||
                                AAAAAAGA  GGAAATA
                                     CC
GAM33   IGSF6   3'  ATAAAGGTAAACTGAAAAGAC  19576        TCTC_
                                GTCTTTTT    ACCTTTAT
                                ||||||||    ||||||||
                                CAGAAAAG    TGGAAATA
                                     TCAAA
GAM33   MS4A1   3'  GTGAAAAAAGAAGACT      3750          C_
                                AGTCTTTTTT  TCAC
                                ||||||||||  ||||
                                TCAGAAGAAA  AGTG
                                   AA
GAM33   SS18    3'  GATAAAGGTGAGGGGAAGAC   18885       T TT
                                GTCTT T  CTCACCTTTATC
                                ||||| |  ||||||||||||
                                CAGAA G  GAGTGGAAATAG
                                   _ GG
GAM33   TFAP4   3'  GGGGAGAAAAAAAAC       12239    C       A
                                GT TTTTTTCTC CCT
                                || |||||||| |||
                                CA AAAAAAGAG GGG
                                 A       _
GAM33   TYRO3   5'  ATAAAAATAAAAGGACTGA   20843          TCTCACC
                                TCAGTCTTTTT      TTTAT
                                ||||||||||      |||||
                                AGTCAGGAAAA      AAATA
                                   TAA____
GAM33   WISP1   3'  ATAAAGGTTTAAAGCTGA    13939      T   TTTCTC
                                TCAG CTTT     ACCTTTAT
                                ||||  ||||     ||||||||
                                AGTC GAAA     TGGAAATA
                                   _    TT____
GAM33   BLP2    3'  ATAAAGGTAAGATAAATGA   54332    T   T   C
                                TC TTT TCT ACCTTTAT
                                || ||| ||| ||||||||
                                AG AAA AGA TGGAAATA
                                 T   T   A
GAM33   BLP2    3'  ATAAAGGTAAGATAAATGA   47114    T   T   C
                                TC TTT TCT ACCTTTAT
                                || ||| ||| ||||||||
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                                AG AAA AGA TGGAAATA
                                 T   T   A
GAM33   FLJ20045  3'  ATGAAGAGGGGAAACCAGA   34413     TT     AC
                                TCT  TTTCTC  CTTTAT
                                |||  ||||||  ||||||
                                AGA  AAAGGG  GAAGTA
                                  CC     GA
GAM33   GRIN3A    3'  AAAGGTGTGGGGAAGCTGA   55964      CT   TT T
                                TCAGT  TTT  C CACCTTT
                                |||||  |||  | |||||||
                                AGTCG  AAG  G GTGGAAA
                                   __   GG T
GAM33   KIAA1966  5'  GATAAAAATGAGAAAAAGGG   55893          CC
                                TCTTTTTTCTCA  TTTATC
                                ||||||||||||  ||||||
                                GGGAAAAAGAGT  AAATAG
                                      AA
GAM33   KLK7      3'  ATAAAGGTGGGGAAAAAAGTCT 57726      T        _
            GA                    TCAG CTTTTTTCTC ACCTTTAT
                                ||||| |||||||||| ||||||||
                                AGTC GAAAAAAGGG TGGAAATA
                                  T        G
GAM33   KLK7      3'  ATAAAGGTGGGGAAAAAAGTCT 17286      T        _
            GA                    TCAG CTTTTTTCTC ACCTTTAT
                                ||||| |||||||||| ||||||||
                                AGTC GAAAAAAGGG TGGAAATA
                                  T        G
GAM33   PLCL1     3'  ATAAAAGTGAATGAAAGATT   20632         TTC    C
                                AGTCTTTT   TCAC TTTAT
                                ||||||||   |||| |||||
                                TTAGAAAG   AGTG AAATA
                                     TA_    A
GAM33   PRO2289   5'  GTGATAAAAAAGACTGA     37795           C
                                TCAGTCTTTTTT TCAC
                                |||||||||||| ||||
                                AGTCAGAAAAAA AGTG
                                      T
GAM33   ROBO2     3'  TGAAGAAAAAGACTGA      62488           TC
                                TCAGTCTTTTT  TCA
                                ||||||||||  |||
                                AGTCAGAAAAA  AGT
                                      GA
GAM33   SNTG1     3'  AAAGGTGATATTTAAAGAT   38570       TTTC_
                                GTCTTT    TCACCTTT
                                ||||||    ||||||||
                                TAGAAA    AGTGGAAA
                                   TTTAT
GAM33   TM4SF11   3'  ATAAAGATGAGAGAAA      32035         C
                                TTTTTCTCA CTTTAT
                                ||||||||| ||||||
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                                AAAGAGAGT GAAATA
                                     A
GAM33   VEZATIN   3'  ATAAAAATGAGATAGAAGA   34223       T    CC
                                TCTTTT TCTCA  TTTAT
                                |||||| |||||  |||||
                                AGAAGA AGAGT  AAATA
                                   T    AA
GAM33   LOC115098 3'  ATAAAGGTGGCGGCAAGGCT   56592       T TT T
                                AGTCTT T  C CACCTTTAT
                                |||||| |  | |||||||||
                                TCGGAA G  G GTGGAAATA
                                   C GC _
GAM33   LOC146861 3'  TAAAGGCAAAGACTGA      76297        TTTCTCA
                                TCAGTCTTT      CCTTTA
                                |||||||||      ||||||
                                AGTCAGAAA      GGAAAT
                                     C_______
GAM33   LOC147392 3'  TAAAGGCAAAGACTGA      75665        TTTCTCA
                                TCAGTCTTT      CCTTTA
                                |||||||||      ||||||
                                AGTCAGAAA      GGAAAT
                                     C_______
GAM33   LOC158187 3'  ATAAAGGTGCAAGACTGA    86687        TTTTCT
                                TCAGTCTT     CACCTTTAT
                                ||||||||     |||||||||
                                AGTCAGAA     GTGGAAATA
                                     C______
GAM33   LOC197003 3'  ATAAAAGTGAAGGTCAAGAC   87867      TT TC    C
                                GTCTT  T  TCAC TTTAT
                                |||||  |  |||| |||||
                                CAGAA  G  AGTG AAATA
                                   CT GA    A
GAM33   LOC253187 3'  AAAGTTGAGAAAAAAGAT    97107           C
                                GTCTTTTTTCTCA CTTT
                                |||||||||||| ||||
                                TAGAAAAAAGAGT GAAA
                                        T
GAM33   LOC256979 5'  AAAGGCAAGAAGGGCTG     96044          CTCA
                                CAGTCTTTTTT    CCTTT
                                ||||||||||    |||||
                                GTCGGGAAGAA    GGAAA
                                     C___
GAM33   LOC85028  3'  AAAGAAGAATAAAAAGACT   53842        TC  AC
                                AGTCTTTTT  TC  CTTT
                                |||||||||  ||  ||||
                                TCAGAAAAA  AG  GAAA
                                     TA  AA
GAM33   LOC93426  3'  GTGAAAAAAAAAGACT      55407          C_
                                AGTCTTTTTT  TCAC
                                ||||||||||  ||||
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                                TCAGAAAAAA  AGTG
                                      AA
GAM34   ADCY7    3'  TAGAGAGAAAAACACCACA   6645      A    CC_
                                TGT GTGTT   CTCTCTA
                                ||| |||||   |||||||
                                ACA CACAA   GAGAGAT
                                  C     AAA
GAM34   GPRK7    3'  AGGGAAAAGGAACACTCA    57625    T      C__
                                TG AGTGTTCC   TCTCT
                                || ||||||||   |||||
                                AC TCACAAGG   AGGGA
                                  _       AAA
GAM34   MYLK     3'  CAGAATGGTAAATGAGAACACT 97019          CCTCT__   GGG
            ACA                    TGTAGTGTTC      CTA   CTG
                                |||||||||       |||   |||
                                ACATCACAAG      GGT   GAC
                                      AGTAAAT   AA_
GAM34   PKNOX1   3'  CTAGAGAAGAAACAATACA   15882     G   CCC
                                TGTA TGTT   TCTCTAG
                                |||| ||||   |||||||
                                ACAT ACAA   AGAGATC
                                  A    AGA
GAM34   ABCA9    3'  AGGGAGGGGAACACCACA    54408     A      _
                                TGT GTGTTCCC TCTCT
                                ||| |||||||| |||||
                                ACA CACAAGGG AGGGA
                                  C       G
GAM34   C8orf17  5'  CAGCCCTAGAAAGAAGGATGAA 39594    GT_   C  __
            C                    GT   TCC TC  TCTAGGGCTG
                                ||   ||| ||  ||||||||||
                                CA   AGG AG  AGATCCCGAC
                                 AGT   A  AA
GAM34   FKBP5    3'  GCCTAAGAAACACTCA      14653    T     CCCTC   A
                                TG AGTGTT     TCT GGGC
                                || ||||||     ||| ||||
                                AC TCACAA     AGA TCCG
                                 _     ______   A
GAM34   FLJ21918 3'  CCCCAGGCGGAGGAACACTCA  46288    T       _  C   A
                                TG AGTGTTCC CT TCT GGG
                                || |||||||| || ||| |||
                                AC TCACAAGG GG GGA CCC
                                 _       A  C   C
GAM34   KIAA0141 3'  AGCCCTAAAGAGGGAGCCT    28726    T       C
                                AG GTTCCCTCT TAGGGCT
                                || ||||||||| |||||||
                                TC CGAGGGAGA ATCCCGA
                                 _       A
GAM34   MAP4K3   3'  CTAGAAAGAAAGAACACTAC   13240         C__  C
                                GTAGTGTTC   CT TCTAG
                                |||||||||   || |||||
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                                CATCACAAG   GA AGATC
                                     AAA  A
GAM34   MGC4643   3'  AGCCCTGAAAAACACACA    51152     A    CCCTC  T
                                TGT GTGTT    TC AGGGCT
                                ||| |||||    || ||||||
                                ACA CACAA    AG TCCCGA
                                  _    AA___  _
GAM34   POPX1     3'  GGCTATAAAAGGGAATACTACA 29799           CTCTAG
                                TGTAGTGTTCCCT     GGCT
                                ||||||||||||     ||||
                                ACATCATAAGGGA     TCGG
                                       AAATA_
GAM34   RC3       3'  AGTTAAAAGGCACACTACA    30920        TC   CTCTAG
                                TGTAGTGT  CCT     GGCT
                                ||||||||  |||     ||||
                                ACATCACA  GGA     TTGA
                                     C_   AAA___
GAM34   LOC130436 3'  CAGTGATAAGAGGGAACACACA 74935     A         C  GG
                                TGT GTGTTCCCTCT TA  GCTG
                                ||| ||||||||||| ||  ||||
                                ACA CACAAGGGAGA AT  TGAC
                                  _         _ AG
GAM34   LOC147229 5'  AGCCCTAAAGGCACCGCA    78317    TA    TCCCT  C
                                TG  GTGT    CT TAGGGCT
                                ||  ||||    || |||||||
                                AC  CACG    GA ATCCCGA
                                 GC   ______  A
GAM34   LOC149619 3'  CAGCCTGTGAAGAACACTACA  84527          CC  TCTA
                                TGTAGTGTTC  TC    GGGCTG
                                ||||||||||  ||    ||||||
                                ACATCACAAG  AG    TCCGAC
                                      A_  TG__
GAM34   LOC163115 3'  CAGCCCCGTGCACGGAAACACT 82411         _  CTCTCTA
           AC                    GTAGTGTT CC      GGGCTG
                                ||||||||  ||      ||||||
                                CATCACAA GG      CCCGAC
                                     A  CACGTGC
GAM34   LOC202759 3'  CTGGAAAAAAACACTACA    73513         CCCTC
                                TGTAGTGTT     TCTAG
                                |||||||||     |||||
                                ACATCACAA     AGGTC
                                      AAAA_
GAM34   LOC90785  3'  CAGCCCCAGAGAGGGACCCCCA 64012     T___       A
           C                     GTG    TCCCTCTCT GGGCTG
                                |||    ||||||||| ||||||
                                CAC    AGGGAGAGA CCCGAC
                                  CCCC        C
GAM34   LOC91272  3'  AGAGAGAGAAACACTACA     65428          _ C
                                TGTAGTGTT C CTCTCT
                                ||||||||| | ||||||
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                                ACATCACAA G GAGAGA
                                    A A
GAM35   AGRN    3' CAGCTCTGCGTTGCTC     78833      AGATG  G
                                GAGCA    ATG AGAGCTG
                                |||||    ||| |||||||
                                CTCGT    TGC TCTCGAC
                                  _____  G
GAM35   ASNA1   3' CTCTCCCACCTCTTGCTC    62978       TGAT
                                GAGCAAGA   GGAGAG
                                ||||||||   ||||||
                                CTCGTTCT   CCTCTC
                                    CCAC
GAM35   BCLG    3' ACAGATACCATCATCCTGC   56978    A      AGAG
                                GCA GATGATGG   CTGT
                                ||| ||||||||   ||||
                                CGT CTACTACC   GACA
                                  C       ATA_
GAM35   BCLG    3' ACAGATACCATCATCCTGC   47776    A      AGAG
                                GCA GATGATGG   CTGT
                                ||| ||||||||   ||||
                                CGT CTACTACC   GACA
                                  C       ATA_
GAM35   BCLG    3' ACAGATACCATCATCCTGC   56972    A      AGAG
                                GCA GATGATGG   CTGT
                                ||| ||||||||   ||||
                                CGT CTACTACC   GACA
                                  C       ATA_
GAM35   C14orf1 3' CAGCTCTCCTTCTATC     23174    _  T
                                GAT GA GGAGAGCTG
                                ||| || |||||||||
                                CTA CT CCTCTCGAC
                                  T  T
GAM35   CLCN6   3' ACAGCTCTGCGGACCTTG   7073     ATGA  G
                                CAAG   TG AGAGCTGT
                                ||||   || ||||||||
                                GTTC   GC TCTCGACA
                                  CAG_  G
GAM35   CLCN6   3' ACAGCTCTGCGGACCTTG   41395    ATGA  G
                                CAAG   TG AGAGCTGT
                                ||||   || ||||||||
                                GTTC   GC TCTCGACA
                                  CAG_  G
GAM35   CLCN6   3' ACAGCTCTGCGGACCTTG   41380    ATGA  G
                                CAAG   TG AGAGCTGT
                                ||||   || ||||||||
                                GTTC   GC TCTCGACA
                                  CAG_  G
GAM35   DISC1   3' ACAGCTTTTCACCTTACTT  37866    C  ATGA
                                GAG AAG   TGGAGAGCTGT
                                ||| |||   ||||||||||
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                                TTC TTC    ACTTTTCGACA
                                  A   C___
GAM35   DNMT3B   3'  CAGCTCTCCAATACTC      22563     CAAGA  A
                                GAG     TG TGGAGAGCTG
                                |||     || ||||||||||
                                CTC     AT ACCTCTCGAC
                                  _____  A
GAM35   DSP      5'  CAGCTTTCCTCCCGCTC     15339      AAGAT  T
                                GAGC     GA GGAGAGCTG
                                ||||     || |||||||||
                                CTCG     CT CCTTTCGAC
                                  CC___  _
GAM35   FUT6     5'  CAGCTCTGCCTCCTCT      3809      T  T  _
                                AGA GA GG AGAGCTG
                                ||| || || |||||||
                                TCT CT CC TCTCGAC
                                  C  _  G
GAM35   HAGH     5'  ACAGCTCTCCCGGCGCAGCTC  18027      AAGA  AT_
                                GAGC    TG   GGAGAGCTGT
                                ||||    ||   ||||||||||
                                CTCG    GC   CCTCTCGACA
                                  AC__  GGC
GAM35   HUS1     3'  ACAGCCTCTGTCACCCCGCC   91097   A  AAGA       A
                                G GC    TGATGGAG GCTGT
                                | ||    |||||||| |||||
                                C CG    ACTGTCTC CGACA
                                 _  CCCC       _
GAM35   IKBKB    3'  ACAGCCTGTCCTCTCCTGCTC  63201       A  T  T   G  _
                                GAGCA GA GA GGA AG CTGT
                                ||||| || || ||| || ||||
                                CTCGT CT CT CCT TC GACA
                                   C  _  _   G  C
GAM35   IL10RA   3'  GCCCCACCATCTTGCT      59644          A   AGA
                                AGCAAGATG TGG   GC
                                ||||||||| |||   ||
                                TCGTTCTAC ACC   CG
                                     C   C__
GAM35   LIMK1    3'  ACAGCCCCTTCTCTCGCTT   9782       A   T  T  AGA
                                GAGC AGA GA GG   GCTGT
                                |||| ||| || ||   |||||
                                TTCG TCT CT CC   CGACA
                                  C   _  T  C__
GAM35   LIMK1    3'  ACAGCCCCTTCTCTCGCTT   33640      A   T  T  AGA
                                GAGC AGA GA GG   GCTGT
                                |||| ||| || ||   |||||
                                TTCG TCT CT CC   CGACA
                                  C   _  T  C__
GAM35   MATN2    5'  ACAGCCTTGCCCCTCTTGCTC  9930         TGATG   A
                                GAGCAAGA    GAG GCTGT
                                ||||||||    ||| |||||
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                                CTCGTTCT    TTC CGACA
                                    CCCCG  _
GAM35   MAX     3' ACAGCTCTCGTTCTCCTT   9942     AT  TG
                                AAG  GA  GAGAGCTGT
                                |||  ||  |||||||||
                                TTC  CT  CTCTCGACA
                                  CT  TG
GAM35   MAX     3' ACAGCTCTCGTTCTCCTT   59035    AT  TG
                                AAG  GA  GAGAGCTGT
                                |||  ||  |||||||||
                                TTC  CT  CTCTCGACA
                                  CT  TG
GAM35   NT5C2   3' TCCCATCATCTACTC      24241    CA       A
                                GAG  AGATGATGG GA
                                |||  ||||||||| ||
                                CTC  TCTACTACC CT
                                  A_       _
GAM35   PAG     3' ACAGCCATGTCATCTT     37397        GAGA
                                AAGATGATG   GCTGT
                                |||||||||   |||||
                                TTCTACTGT   CGACA
                                    AC__
GAM35   PLCB2   3' AGGTCAGCATCATTTGCTC  15889      A     GA  G
                                GAGCA GATGATG  GA CT
                                ||||| |||||||  || ||
                                CTCGT TTACTAC  CT GA
                                   _      GA  G
GAM35   PNOC    5' ACAGCTCTCAGCACCTGCTT  20640      A A  ATG
                                GAGCA G TG   GAGAGCTGT
                                ||||| | ||   |||||||||
                                TTCGT C AC   CTCTCGACA
                                   _ C  GA_
GAM35   RARG    3' AGCCCACCTTCTTGCTC    6376        TGA   AGA
                                GAGCAAGA   TGG   GCT
                                ||||||||   |||   |||
                                CTCGTTCT   ACC   CGA
                                    TCC   ___
GAM35   SCNN1A  3' AGCCCATCATCCTGCTT    6421       A      AGA
                                GAGCA GATGATGG   GCT
                                ||||| ||||||||   |||
                                TTCGT CTACTACC   CGA
                                   C      ___
GAM35   SF3B3   3' ACAGCTCTTTCCCCTCAGCTC 24855     AAGA   T ___
                                GAGC    TGA GG   AGAGCTGT
                                ||||    ||| ||   ||||||||
                                CTCG    ACT CC   TCTCGACA
                                  ____   C  CTT
GAM35   SHMT1   3' ACAGCTTGTACACACTGC   14789    A A  A  GA_
                                GCA G TG TG   GAGCTGT
                                ||| | || ||   |||||||
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                                CGT C AC AC   TTCGACA
                                  _ _ _ ATG
GAM35   SPAG11   5' CAGCTCTTCCCACGCTC    33258     AAGA AT
                                GAGC   TG GGAGAGCTG
                                ||||   || |||||||||
                                CTCG   AC CTTCTCGAC
                                  C___ C_
GAM35   SPAG11   5' CAGCTCTTCCCACGCTC    54241     AAGA AT
                                GAGC   TG GGAGAGCTG
                                ||||   || |||||||||
                                CTCG   AC CTTCTCGAC
                                  C___ C_
GAM35   SPAG11   5' CAGCTCTTCCCACGCTC    54243     AAGA AT
                                GAGC   TG GGAGAGCTG
                                ||||   || |||||||||
                                CTCG   AC CTTCTCGAC
                                  C___ C_
GAM35   SPAG11   5' CAGCTCTTCCCACGCTC    54247     AAGA AT
                                GAGC   TG GGAGAGCTG
                                ||||   || |||||||||
                                CTCG   AC CTTCTCGAC
                                  C___ C_
GAM35   SPAG11   5' CAGCTCTTCCCACGCTC    54249     AAGA AT
                                GAGC   TG GGAGAGCTG
                                ||||   || |||||||||
                                CTCG   AC CTTCTCGAC
                                  C___ C_
GAM35   TBR1     3' CAGCTCTTCCCCAGCTC    21683     AAGA AT
                                GAGC   TG GGAGAGCTG
                                ||||   || |||||||||
                                CTCG   AC CTTCTCGAC
                                  ____ CC
GAM35   TCFL4    3' TTCCATCACCTTCCTC     63466     C   A
                                GAG AAG TGATGGAG
                                ||| ||| ||||||||
                                CTC TTC ACTACCTT
                                  C   C
GAM35   THBD     3' ACAGCTCTCCGGTCTCTCTC  4490      CA   GA
                                GAG  AGAT  TGGAGAGCTGT
                                |||  ||||  ||||||||||||
                                CTC  TCTG  GCCTCTCGACA
                                  TC   __
GAM35   AQP10    3' ACAGCTCTCCTGCCGCTC    54429     AAGATGAT
                                GAGC      GGAGAGCTGT
                                ||||      ||||||||||
                                CTCG      CCTCTCGACA
                                  CCGT____
GAM35   ATF3     5' ACAGCTCTCTTCTCTCGCC   14430   A A   T T
                                G GC AGA GA GGAGAGCTGT
                                | || ||| || ||||||||||
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                                C CG TCT CT TCTCTCGACA
                                 _ C  _ _
GAM35  BRD2    3'  ACACTTCTTCATCTC      17534   T      C
                                GA GATGGAGAG TGT
                                || ||||||||| |||
                                CT CTACTTCTT ACA
                                 _       C
GAM35  BTN2A1  3'  ACAGCCCCATCTTCATCTGC  54337   A    T  GA__
                                GCA GATGA GGA   GCTGT
                                ||| ||||| |||   |||||
                                CGT CTACT TCT   CGACA
                                  _   _  ACCC
GAM35  C17orf31 5'  ACAGCTTTGACCATCCTC   34117   T    __
                                GA GATGG  AGAGCTGT
                                || |||||  ||||||||
                                CT CTACC  TTTCGACA
                                 C    AG
GAM35  C6orf9  3'  CAGCTCTACCCTTCCTC    42077    C  ATGAT  _
                                GAG AAG    GG AGAGCTG
                                ||| |||    || |||||||
                                CTC TTC    CC TCTCGAC
                                  C  _____  A
GAM35  COLEC10  3'  AGCCTCCATCATCATGCTC  21227     A       A
                                GAGCA GATGATGGAG GCT
                                ||||| |||||||||| |||
                                CTCGT CTACTACCTC CGA
                                   A       _
GAM35  DCOHM   3'  ACAGTCTCACTATCTTGCTC  49590        ATG   G
                                GAGCAAGATG   GAGA CTGT
                                ||||||||||   |||| ||||
                                CTCGTTCTAT   CTCT GACA
                                      CA_   _
GAM35  DKFZP566C243 5'  GGCCCACATCTTGC      31172       A  AGA
                                GCAAGATG TGG   GCT
                                |||||||| |||   |||
                                CGTTCTAC ACC   CGG
                                          _  ___
GAM35  DT1P1A10  3'  ACAGCTCTGTACCCCTGCCC  61563   A  AGATGA  G
                                G GCA     TG AGAGCTGT
                                | |||     || ||||||||
                                C CGT     AT TCTCGACA
                                 C  CCCC__  G
GAM35  DZIP1   5'  ACAGCTCTTGTTCCCGCT   30032    AAGAT  TG
                                AGC    GA  GAGAGCTGT
                                |||    ||  |||||||||
                                TCG    CT  TTCTCGACA
                                  CC___  TG
GAM35  FLJ12221  3'  GCCCCTTCATCTTACTC    62551    C     T  AGA
                                GAG AAGATGA GG   GC
                                ||| ||||||| ||   ||
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                                CTC TTCTACT CC   CG
                                  A      T  C__
GAM35   FLJ12875 3' ACAGCTCTTTTTTTATTGC   44607     GAT  TG
                                GCAA   GA  GAGAGCTGT
                                ||||   ||  |||||||||
                                CGTT   TT  TTCTCGACA
                                  AT_  TT
GAM35   FLJ20152 3' ACAGCTCTATTCTGCCTGCTC 38645      AGAT  TGG
                                GAGCA   GA   AGAGCTGT
                                |||||   ||   ||||||||
                                CTCGT   CT   TCTCGACA
                                   CCGT  TA_
GAM35   FLJ20625 3' CAGCTCTTCTCCTCT      35468     T  T
                                AGA GA GGAGAGCTG
                                ||| || |||||||||
                                TCT CT CTTCTCGAC
                                  C  _
GAM35   FLJ22557 3' ACAGCTCTAAATCTTACTT   45253     C    GATGG
                                GAG AAGAT    AGAGCTGT
                                ||| |||||    ||||||||
                                TTC TTCTA    TCTCGACA
                                  A    AA___
GAM35   FYCO1    3' ACAGCTCTTCGTCCCTTGTTC 44484       AT
                                GAGCAAG  GATGGAGAGCTGT
                                |||||||  ||||||||||||
                                CTTGTTC  CTGCTTCTCGACA
                                    C_
GAM35   GGA2     3' ACAGCTCTGGTTCTTGCC    56867   A    TGATGG
                                G GCAAGA     AGAGCTGT
                                | ||||||     ||||||||
                                C CGTTCT     TCTCGACA
                                 _     TGG___
GAM35   GGA2     3' ACAGCTCTGGTTCTTGCC    30455   A    TGATGG
                                G GCAAGA     AGAGCTGT
                                | ||||||     ||||||||
                                C CGTTCT     TCTCGACA
                                 _     TGG___
GAM35   GREB1    3' CAGTGATCATCTTGTTC     27866         GGAGA
                                GAGCAAGATGAT    GCTG
                                ||||||||||||    ||||
                                CTTGTTCTACTA    TGAC
                                       G____
GAM35   H2AV     3' ACAGCTCTCTATACTC     56842    TG
                                GA  ATGGAGAGCTGT
                                ||  ||||||||||||
                                CT  TATCTCTCGACA
                                  CA
GAM35   KIAA0298 3' ACAGCTCTCCCTGGTCCTGT   76574     A   GAT
                                GCA GAT   GGAGAGCTGT
                                ||| |||   ||||||||||
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                                TGT CTG   CCTCTCGACA
                                  C   GTC
GAM35   KIAA1040 3' ACAGCTCTCCAAGCTTTC    72216    GC   ATGA
                                GA  AAG    TGGAGAGCTGT
                                ||  |||    ||||||||||
                                CT  TTC    ACCTCTCGACA
                                 __   GA__
GAM35   KIAA1203 3' ACAGCCCTACATCTTGC     71633         A   AGA
                                GCAAGATG TGG   GCTGT
                                |||||||| |||   |||||
                                CGTTCTAC ATC   CGACA
                                     _   C__
GAM35   KIAA1237 3' ACAGCTGACAAATCATCTCCTC 80463     CA      GGAG_
                                GAG  AGATGAT    AGCTGT
                                |||  |||||||    ||||||
                                CTC  TCTACTA    TCGACA
                                  C_      AACAG
GAM35   KIAA1388 3' ACAGCCCTCTCCGTCTGCTC   93576      AGAT      __
                                GAGCA    GATGGAGA  GCTGT
                                |||||    ||||||||  |||||
                                CTCGT    CTGCCTCT  CGACA
                                   _____       CC
GAM35   KIAA1691 3' ACAGCTCTCCTTCCTCCCGC   92549    AA  T  T
                                GC  GA GA GGAGAGCTGT
                                ||  || || ||||||||||
                                CG  CT CT CCTCTCGACA
                                 CC  C  T
GAM35   KIAA1737 3' CTCCCATCATCCCACTC     67354     CAA      A
                                GAG   GATGATGG GAG
                                |||   |||||||| |||
                                CTC   CTACTACC CTC
                                  ACC       _
GAM35   KIAA1937 3' ACATATTCATCATCCACTC    73691     CAA       GAGC
                                GAG   GATGATGGA    TGT
                                |||   |||||||||    |||
                                CTC   CTACTACTT    ACA
                                  AC_       AT__
GAM35   KSR      5' ACAGCTTCATCACCCCGC    64041    AAGA    GA
                                GC    TGATG  GAGCTGT
                                ||    |||||  |||||||
                                CG    ACTAC  TTCGACA
                                 CCCC    __
GAM35   LEFTB    5' ACAGCCCCACTCTGCCTCTTGC 40652         TGA    A___
           TC                    GAGCAAGA   TGGAG    GCTGT
                                 ||||||||   |||||    |||||
                                 CTCGTTCT   GTCTC    CGACA
                                      CC_    ACCC
GAM35   MGC1842  3' ACAGCCCTCCAGGTCCTCCAGC 65636      AA  T __    A
           TC                    GAGC  GA GA  TGGAG GCTGT
                                 ||||  || ||  ||||| |||||
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                                CTCG  CT CT  ACCTC CGACA
                                  AC  C  GG    C
GAM35   MGC2615  3'  ACAGGATTTCATCATGTTGC  44084     G       AG
                                GCAA ATGATGGAG  CTGT
                                |||| |||||||||  ||||
                                CGTT TACTACTTT  GACA
                                  G       AG
GAM35   MGC2628  3'  ACAGCTCCCCAAGTGTTC   43965     AGATGA  A
                                GAGCA     TGG GAGCTGT
                                ||||||     ||| |||||||
                                CTTGT     ACC CTCGACA
                                   GA____  C
GAM35   NETO1    3'  TCTCCATCATCTCATC     57315    GCA
                                GA  AGATGATGGAGA
                                ||  ||||||||||||
                                CT  TCTACTACCTCT
                                 AC_
GAM35   NPTXR    3'  CAGCTGCATCTTGCTT     54173         ATGGAG
                                GAGCAAGATG     AGCTG
                                ||||||||||     |||||
                                TTCGTTCTAC     TCGAC
                                     G_____
GAM35   NPTXR    3'  CAGCTGCATCTTGCTT     26637         ATGGAG
                                GAGCAAGATG     AGCTG
                                ||||||||||     |||||
                                TTCGTTCTAC     TCGAC
                                     G_____
GAM35   NR4A3    5'  ACAGCTCTCTAGAAACTCGCTC 22735     A  ATGA
                                GAGC AG   TGGAGAGCTGT
                                |||| ||   ||||||||||||
                                CTCG TC   ATCTCTCGACA
                                  C  AAAG
GAM35   PISD     3'  ACATTCACCTCATCCTGCTC  26769     A    T  A   C
                                GAGCA GATGA GG GAG TGT
                                ||||| ||||| || ||| |||
                                CTCGT CTACT CC CTT ACA
                                   C    _  A   _
GAM35   QKI      3'  CTCCCCCACCATCTTGT     65441        A   A_
                                GCAAGATG TGG  GAG
                                |||||||| |||  |||
                                TGTTCTAC ACC  CTC
                                     C   CC
GAM35   RAB20    3'  ACAACTCTGACATTTCTTGTTC 35153        T   G_   C
                                GAGCAAGA GATG  AGAG TGT
                                |||||||| ||||  |||| |||
                                CTTGTTCT TTAC  TCTC ACA
                                     _   AG   A
GAM35   RDH-E2   3'  ACAGCTCTGGATTTCT     57268     T   GG
                                AGA GAT  AGAGCTGT
                                ||| |||  ||||||||
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                                TCT TTA  TCTCGACA
                                  _  GG
GAM35   Rpo1-2   3' ACAACTCTCCATTTCCCTGGC  49874    A  AT_      C
                                GC AG   GATGGAGAG TGT
                                || ||   ||||||||| |||
                                CG TC   TTACCTCTC ACA
                                 G  CCT       A
GAM35   Rpo1-2   3' ACAACTCTCCATTTCCCTGGC  38696    A  AT_      C
                                GC AG   GATGGAGAG TGT
                                || ||   ||||||||| |||
                                CG TC   TTACCTCTC ACA
                                 G  CCT       A
GAM35   S100Z    5' ACAGCAGGGCCTCTTGCTC   55375       TGAT  AGA_
                                GAGCAAGA   GG   GCTGT
                                ||||||||   ||   |||||
                                CTCGTTCT   CC   CGACA
                                     _____  GGGA
GAM35   SMURF2   3' ACAGCTCCTGTACTTGCTC   42714      ATG   A
                                GAGCAAG   ATGG GAGCTGT
                                |||||||   |||| |||||||
                                CTCGTTC   TGTC CTCGACA
                                    A__   _
GAM35   SP140    3' AGTGTCCATCATCTGACTC   23374    CA       GA
                                GAG  AGATGATGGA  GCT
                                |||  ||||||||||  |||
                                CTC  TCTACTACCT  TGA
                                  AG        G_
GAM35   SP192    5' ACAGCTCTTTCCCCTT     41311    AT  TG
                                AAG  GA  GAGAGCTGT
                                |||  ||  |||||||||
                                TTC  CT  TTCTCGACA
                                  CC  __
GAM35   STAF65(gamma) 3'  ACAGCTCTCTATCTC      29419    T
                                GA GATGGAGAGCTGT
                                || ||||||||||||
                                CT CTATCTCTCGACA
                                 _
GAM35   STX1B2   3' ACAGCAGTCCATCACGC    53513    AAGA     GA
                                GC   TGATGGA  GCTGT
                                ||   |||||||  |||||
                                CG   ACTACCT  CGACA
                                 C___      GA
GAM35   ZNF263   3' ACAGCTCTGGAGTCTTGTTC   19221        GATGG
                                GAGCAAGAT    AGAGCTGT
                                |||||||||    ||||||||
                                CTTGTTCTG    TCTCGACA
                                     AGG__
GAM35   LOC115399 3'  ACAGCTCTGACTTCCTGGC   73421    A  AT  TGG_
                                GC AG  GA    AGAGCTGT
                                || ||  ||    ||||||||
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                                CG TC  CT    TCTCGACA
                                 G  __  TCAG
GAM35   LOC115400 3' CTCTCCATCACCTGCTC     73442       A A
                                GAGCA G TGATGGAGAG
                                ||||| | ||||||||||
                                CTCGT C ACTACCTCTC
                                  _ C
GAM35   LOC143381 5' CTCCACCACCTTGTTC      76546        A  A
                                GAGCAAG TG TGGAG
                                ||||||| || |||||
                                CTTGTTC AC ACCTC
                                    C  C
GAM35   LOC143451 3' ACAGCTCTTCTCTCCTTCTC   76560     C   AT  T
                                GAG AAG  GA GGAGAGCTGT
                                ||| |||  || ||||||||||
                                CTC TTC  CT CTTCTCGACA
                                  _   CT  _
GAM35   LOC144404 5' CTGACCATCATCCTGCTC     76828       A       AG
                                GAGCA GATGATGG  AG
                                ||||| ||||||||  ||
                                CTCGT CTACTACC  TC
                                   C       AG
GAM35   LOC145125 3' ACAGCTCTTCTCTCCTTCTC   77002     C   AT  T
                                GAG AAG  GA GGAGAGCTGT
                                ||| |||  || ||||||||||
                                CTC TTC  CT CTTCTCGACA
                                  _   CT  _
GAM35   LOC145231 5' CAGCTCTTTGCCTGCTC      83281       A ATGA GG
                                GAGCA G    T  AGAGCTG
                                ||||| |    |  |||||||
                                CTCGT C    G  TCTCGAC
                                  _ C___ TT
GAM35   LOC146237 3' ACAGCTCCCCGTCATC       83628         A
                                GATGATGG GAGCTGT
                                |||||||| |||||||
                                CTACTGCC CTCGACA
                                     C
GAM35   LOC146237 3' ACAGCTCTCACATTCCTT     83629     AT   _
                                AAG  GATG GAGAGCTGT
                                |||  |||| |||||||||
                                TTC  TTAC CTCTCGACA
                                  C_   A
GAM35   LOC147160 3' ACAGCCTGGTTTCATCTTTCTC 83954     C      TGG_  A
                                GAG AAGATGA    AG GCTGT
                                ||| |||||||    || |||||
                                CTC TTCTACT    TC CGACA
                                  T      TTGG  _
GAM35   LOC148979 5' CTCCATCATCCGCTC        84320       AA
                                GAGC  GATGATGGAG
                                ||||  ||||||||||
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                                CTCG  CTACTACCTC
                                  C_
GAM35   LOC158308 3' ACAGCTCTGTCTGCCTTGTTC 86740       AT_  GG
                                GAGCAAG  GAT  AGAGCTGT
                                |||||||  |||  ||||||||
                                CTTGTTC  CTG  TCTCGACA
                                   CGT  __
GAM35   LOC159765 5' ACAGCTCAACCGTCATCCTC  82195    CAA     A_
                                GAG  GATGATGG  GAGCTGT
                                |||  ||||||||  |||||||
                                CTC  CTACTGCC  CTCGACA
                                  ___      AA
GAM35   LOC160646 3' CAGCTCTCCAGGTGCT     82224     AGATGA
                                AGCA     TGGAGAGCTG
                                ||||     ||||||||||
                                TCGT     ACCTCTCGAC
                                  GG____
GAM35   LOC166341 3' CAGCCCCACTCTGGCTC     82629     A  TGA  AGA
                                GAGC AGA  TGG  GCTG
                                |||| |||  |||  ||||
                                CTCG TCT  ACC  CGAC
                                  G  C__  C__
GAM35   LOC200609 5' ACAACTCTCCATTCTCTTATC  90093    GC   T      C
                                GA  AAGA GATGGAGAG TGT
                                ||  |||| ||||||||| |||
                                CT  TTCT TTACCTCTC ACA
                                 A_   C       A
GAM35   LOC202908 5' CTCTCCATCACCTGCTC     89234      A A
                                GAGCA G TGATGGAGAG
                                ||||| | ||||||||||
                                CTCGT C ACTACCTCTC
                                  _ C
GAM35   LOC253786 5' ACAGCTCCCTGCCCCTGCTC  97041      AGATGAT  A
                                GAGCA      GG GAGCTGT
                                |||||      || |||||||
                                CTCGT      CC CTCGACA
                                   CCCCGT_  _
GAM35   LOC254428 3' ACAGCTCTAACCTCACCT    95453    A  T  __
                                AG TGA GG  AGAGCTGT
                                || ||| ||  ||||||||
                                TC ACT CC  TCTCGACA
                                 C  _  AA
GAM35   LOC254440 3' ACAGCTCTTCTCTCCTTCTC  97062     C  AT  T
                                GAG AAG  GA GGAGAGCTGT
                                ||| |||  || ||||||||||
                                CTC TTC  CT CTTCTCGACA
                                  _  CT  _
GAM35   LOC255696 5' CAGCTCTTCCTATGC       97498     _  ATGAT
                                GCA AG    GGAGAGCTG
                                ||| ||    |||||||||
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                                CGT TC    CTTCTCGAC
                                  A _____
GAM35   LOC256905 5'  ACAGCTCTGGCTCCTGCTC   96862      A  TGATGG
                                GAGCA GA    AGAGCTGT
                                ||||| ||    ||||||||
                                CTCGT CT    TCTCGACA
                                   C  CGG___
GAM35   LOC91012  3'  ACAGCTGCCAATACCCTGCTC 64638      AGA  A   AG
                                GAGCA   TG TGG  AGCTGT
                                |||||   || |||  ||||||
                                CTCGT   AT ACC  TCGACA
                                   CCC  A   G_
GAM35   LOC92379  3'  CAGCTCTCTCCTTTCTC    69148     C   ATGAT
                                GAG AAG    GGAGAGCTG
                                ||| |||    |||||||||
                                CTC TTC    TCTCTCGAC
                                  T   C____
GAM35   LOC92912  3'  ACAGCCTTTGCATTTTGCTC  70842         A GG  A
                                GAGCAAGATG T  AG GCTGT
                                |||||||||| |  || |||||
                                CTCGTTTTAC G  TC CGACA
                                      _ TT  _
GAM36   FGB       3'  AAACCAGACTCTGTTG     17636     T
                                CA CAGAGTCTGGTTT
                                || ||||||||||||
                                GT GTCTCAGACCAAA
                                 T
GAM36   PREP      3'  CAAGAAACCACTGG       10772     AGTC
                                TCAG   TGGTTTCTTG
                                ||||   ||||||||||
                                GGTC   ACCAAAGAAC
                                  ____
GAM36   FLJ13194  3'  ATATCAAAATAGACTTTGAT  47127         GTTTC
                                ATCAGAGTCTG    TTGATAT
                                ||||||||||    |||||||
                                TAGTTTCAGAT    AACTATA
                                      AA___
GAM36   FLJ22944  3'  ATCAAGAAAGCTCT       47121      CTGG
                                AGAGT   TTTCTTGAT
                                |||||   |||||||||
                                TCTCG   AAAGAACTA
                                  ____
GAM36   KIAA0668  3'  CATCTAACCAGGCCCTGATG  66523      A      TCT
                                CATCAG GTCTGGTT   TG
                                |||||| ||||||||   ||
                                GTAGTC CGGACCAA   AC
                                   C       TCT
GAM36   MAPK6     5'  ATCAAGAAACCATCTTGCTGTG 10833    G   C___
                                CA AGT    TGGTTTCTTGAT
                                || |||    ||||||||||||
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                                GT TCG    ACCAAAGAACTA
                                 G   TTCT
GAM36   PRO0097  5'  GGGAAACCAGCCCCTGAT    26099      AGT
                                ATCAG   CTGGTTTCTT
                                |||||   ||||||||||
                                TAGTC   GACCAAAGGG
                                   CCC
GAM36   SCMH1    5'  TATCAAGAAGCTGCTGAC    24258     T__
                                GTC   GGTTTCTTGATA
                                |||   ||||||||||||
                                CAG   TCGAAGAACTAT
                                  TCG
GAM37   ADAMTS8  5'  TCGGGCCGCCAGCACCTG    22886     _      ATAAG
                                CAG TGCTGGC    CTGA
                                ||| |||||||    ||||
                                GTC ACGACCG    GGCT
                                  C      CCG__
GAM37   BAP1     3'  TCAGGGACCCAGCACTGG    16219          CATAAG
                                CCAGTGCTGG     CTGA
                                ||||||||||     ||||
                                GGTCACGACC     GACT
                                     CAGG__
GAM37   BF       5'  TTCAGCTTGGACACTG      8140       CTGGCA
                                CAGTG     TAAGCTGAA
                                |||||     |||||||||
                                GTCAC     GTTCGACTT
                                   AG_____
GAM37   C1QB     3'  TTCAACTCTGTGTCCCAGCACT 4923     A        __    _ C
            GGC                    G CCAGTGCTGG  CATA AG TGAA
                                | ||||||||||  |||| || ||||
                                C GGTCACGACC  GTGT TC ACTT
                                _        CT    C  A
GAM37   CHC1     3'  CAGCCCTGAGCACTGTGTC    7020      _      __ CATAA
                                GAC CAGTGCT  GG     GCTG
                                ||| |||||||  ||     ||||
                                CTG GTCACGA  CC     CGAC
                                  T      GT  _____
GAM37   CMRF35   5'  CAGAGCTGTCAGCACCGG    21929     A       TAAG
                                CC GTGCTGGCA    CTG
                                || |||||||||    |||
                                GG CACGACTGT    GAC
                                 C        CGA_
GAM37   EPHB6    3'  TCAGCCCTGGACACTGGTC    15466         _ TG CATAA
                                GACCAGTG C  G     GCTGA
                                |||||||| |  |     |||||
                                CTGGTCAC G  C     CGACT
                                     A GT C_____
GAM37   EVPL     5'  CAGCCTGAGCCAGCACT     8803           A  A
                                AGTGCTGGC TA GCTG
                                ||||||||| || ||||
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                                TCACGACCG GT CGAC
                                     A  C
GAM37   GARP    3'  CAGCCCAGCACTGG       18594          CATAA
                                CCAGTGCTGG    GCTG
                                ||||||||||    ||||
                                GGTCACGACC    CGAC
                                      _____
GAM37   GJB5    3'  CAGCTCGACGGCACTGG     17945         GCATA
                                CCAGTGCTG    AGCTG
                                |||||||||    |||||
                                GGTCACGGC    TCGAC
                                     AGC__
GAM37   GPR81   3'  CTTACCAGCATTAGTC     50757     C      CA
                                GAC AGTGCTGG  TAAG
                                ||| ||||||||  ||||
                                CTG TTACGACC  ATTC
                                  A       __
GAM37   IFI16   5'  AGCAAGCCAGCACTAGTC    71221     C       ATAA
                                GAC AGTGCTGGC    GCT
                                ||| |||||||||    |||
                                CTG TCACGACCG    CGA
                                  A        AA__
GAM37   KRT4    3'  CAGCTGGGCCCAGCACTGGT   9635           _ ATA
                                ACCAGTGCTGG C   AGCTG
                                |||||||||||  |   |||||
                                TGGTCACGACC G   TCGAC
                                      C GG_
GAM37   MAP3K9  3'  TTCAGCTTCCCAAACACCAGT  60709    CA   C_   CAT
                                AC  GTG  TGG   AAGCTGAA
                                ||  |||  |||   ||||||||
                                TG  CAC  ACC   TTCGACTT
                                 AC   AA   C__
GAM37   MGAT5   5'  TCAGCTTACAGTTCCTG     10028     T_   GCA
                                CAG  GCTG   TAAGCTGA
                                |||  ||||   ||||||||
                                GTC  TGAC   ATTCGACT
                                  CT    ____
GAM37   MOCS1   3'  TTCAGCTTAACAGTTGCCCGGT 92037      A_   _   GCA
            C                    GACC  GTG CTG   TAAGCTGAA
                                ||||  ||| |||   |||||||||
                                CTGG  CGT GAC   ATTCGACTT
                                   CC   T   A__
GAM37   P23     3'  TCAGCTTATACCCGGGCT    21719     G    C_
                                AGT CTGG  ATAAGCTGA
                                ||| ||||  |||||||||
                                TCG GGCC  TATTCGACT
                                  _    CA
GAM37   PFKFB4  3'  TCAGCCACATGCAACACTGTGT 15874     _     CTG    AA_
            C                    GAC CAGTG   GCAT   GCTGA
                                ||| |||||   ||||   |||||
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                                CTG GTCAC   CGTA   CGACT
                                  T    AA_    CAC
GAM37   PTPRK    3'  TTCAGCCTGTGGCCCAGCACTG 11125          __    A
                GTC                   GACCAGTGCTGG  CATA GCTGAA
                                |||||||||||  |||| ||||||
                                CTGGTCACGACC  GTGT CGACTT
                                      CG    C
GAM37   RNPEPL1  3'  CGGATGCCAGCACCTG     36676    _       AAG
                                CAG TGCTGGCAT   CTG
                                ||| |||||||||   |||
                                GTC ACGACCGTA   GGC
                                  C       ___
GAM37   UBE2L3   3'  TCAGCCCTGGCACTGGC     12507    A      TG CATAA
                                G CCAGTGC  G    GCTGA
                                | |||||||  |    |||||
                                C GGTCACG  C    CGACT
                                _      GT C____
GAM37   APXL2    5'  CAGCCTCAGCACTCATC     75185    CC       CATAA
                                GA  AGTGCTGG    GCTG
                                ||  ||||||||    ||||
                                CT  TCACGACT    CGAC
                                 AC       C____
GAM37   ARHGEF9  3'  TTCAGCTTACCAAGCA      30824     _ CA
                                TGCT GG  TAAGCTGAA
                                |||| ||  |||||||||
                                ACGA CC  ATTCGACTT
                                  A __
GAM37   CEGP1    3'  TTCAGCTTCCTCTAGCCCGG   40589    AGT    CAT
                                CC   GCTGG   AAGCTGAA
                                ||   |||||   ||||||||
                                GG   CGATC   TTCGACTT
                                 CC_    TCC
GAM37   DKFZp547D155 3'  CAGCCCTGAGACCACTGGTC   70435        CTGG  TAA
                                GACCAGTG    CA   GCTG
                                ||||||||    ||   ||||
                                CTGGTCAC    GT   CGAC
                                     CAGA  CC_
GAM37   DKFZP727G051 3'  TTCAGCCCATCAACCAGCATTG 69483           CATAA__
                GTC                   GACCAGTGCTGG      GCTGAA
                                ||||||||||||      ||||||
                                CTGGTTACGACC      CGACTT
                                      AACTACC
GAM37   DUSP14   5'  CACTGTCACCAGCACTGCTC   22834    C       CATA  C
                                GA CAGTGCTGG    AG TG
                                || |||||||||    || ||
                                CT GTCACGACC    TC AC
                                 C       ACTG  _
GAM37   FLJ10206 5'  CAGCTTATGCCAGGAGTC    35898     CAGTG
                                GAC    CTGGCATAAGCTG
                                |||    |||||||||||||
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                                CTG    GACCGTATTCGAC
                                  AG___
GAM37   FLJ20967 5'  GGCGCCCAGCACTGGTT     41962          CATAA
                                GACCAGTGCTGG    GCT
                                ||||||||||||    |||
                                TTGGTCACGACC    CGG
                                      CG___
GAM37   FLJ22569 3'  TTCAGCTTACTAAACTG     43679     GC   CA
                                CAGT  TGG  TAAGCTGAA
                                ||||  |||  |||||||||
                                GTCA  ATC  ATTCGACTT
                                  A_  __
GAM37   FOXN4    3'  TTCAGCTTGGACACACTGG    75574       C  GCA
                                CCAGTG TG   TAAGCTGAA
                                ||||||  ||  |||||||||
                                GGTCAC AC   GTTCGACTT
                                   _  AG_
GAM37   GW112    3'  TTCAACTGAAGCCAGCACTGGT 21194           ATA  C
            T                    GACCAGTGCTGGC   AG TGAA
                                ||||||||||||||  ||  ||||
                                TTGGTCACGACCG   TC ACTT
                                      AAG  A
GAM37   HOOK2    3'  CAGCTCACATGGCGCCCAGCAC 25256          ____  A__
            TGG                   CCAGTGCTGG    CAT   AGCTG
                                ||||||||||    |||   |||||
                                GGTCACGACC    GTA   TCGAC
                                     CGCG   CAC
GAM37   jdp2     3'  TTCAGCACAGCCAGCAT     55327         ATAA
                                GTGCTGGC    GCTGAA
                                ||||||||    ||||||
                                TACGACCG    CGACTT
                                    ACA_
GAM37   KIAA0767 3'  TCTGCTGCCAGCACAGG     60632    A       TAA  T
                                CC GTGCTGGCA   GC GA
                                || |||||||||   || ||
                                GG CACGACCGT   CG CT
                                 A        ___  T
GAM37   KIAA0923 3'  TCAGCTTGATGCATGGTC    25838      G   TGGCA
                                GACCA TGC    TAAGCTGA
                                |||||  |||    ||||||||
                                CTGGT ACG    GTTCGACT
                                   _   TA___
GAM37   KIAA0982 3'  TTCACTGTTTGCCAGCAC    25852         TA_  C
                                GTGCTGGCA   AG TGAA
                                |||||||||   ||  ||||
                                CACGACCGT   TC ACTT
                                     TTG  _
GAM37   KIAA1000 3'  TTCAGCTTTGCAAAGTACTGG  65281         G_   T
                                CCAGTGCT  GCA AAGCTGAA
                                ||||||||  |||  ||||||||
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                                GGTCATGA  CGT TTCGACTT
                                    AA  _
GAM37   MAP3K3   3'  TCAGCCTGGGCGCTGGTC    9999         GG  TAA
                                GACCAGTGCT  CA   GCTGA
                                ||||||||||  ||   |||||
                                CTGGTCGCGG  GT   CGACT
                                    ___  C__
GAM37   MGC16037 5'  CTTGTCCAGCACTAGTC     51821     C       C
                                GAC AGTGCTGG ATAAG
                                ||| |||||||| |||||
                                CTG TCACGACC TGTTC
                                  A       _
GAM37   MIDORI   3'  TCAGCTTATCCTGCAACT    73792     _  T  C
                                AGT GC GG ATAAGCTGA
                                ||| || || |||||||||
                                TCA CG CC TATTCGACT
                                  A  T  _
GAM37   MtFMT    5'  CAGTGGCGAGCACTGG      57651        G  ATAA
                                CCAGTGCT GC    GCTG
                                |||||||| ||    ||||
                                GGTCACGA CG    TGAC
                                    G  G___
GAM37   PCDH16   5'  TCAGTTCCAACCACTGG     72826       C_   CATA
                                CCAGTG  TGG    AGCTGA
                                ||||||  |||    ||||||
                                GGTCAC  ACC    TTGACT
                                   CA  _____
GAM37   QKI      3'  CAGCTTATCAACTCGTC     65439     C   GCTGGC
                                GAC AGT      ATAAGCTG
                                ||| |||      ||||||||
                                CTG TCA      TATTCGAC
                                  C   AC_____
GAM37   TNRC6    3'  CAACTTTTAGCACTG       70506         CAT   C
                                CAGTGCTGG   AAG TG
                                |||||||||   ||| ||
                                GTCACGATT   TTC AC
                                    ___  A
GAM37   TOB2     3'  CAGCCCAGGCCAGCACTG    95618          ATAA
                                CAGTGCTGGC    GCTG
                                ||||||||||    ||||
                                GTCACGACCG    CGAC
                                     GACC
GAM37   TU12B1-TY 3'  TCAGCCCACAGCACTGTC    33406     C      GCATAA
                                GAC AGTGCTG      GCTGA
                                ||| |||||||      |||||
                                CTG TCACGAC      CGACT
                                  _      ACC____
GAM37   TUSP     3'  TCAGCCTAAGAGCGCAGCACTG 39641         _  A__  A
                                CAGTGCTG GC   TA GCTGA
                                |||||||| ||   || |||||
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                                GTCACGAC CG   AT CGACT
                                    G  AGA  C
GAM37   USP19    3'  TCAGCTTATGCATCTGGT    88959      TGCTG
                                ACCAG    GCATAAGCTGA
                                |||||    ||||||||||
                                TGGTC    CGTATTCGACT
                                  TA___
GAM37   ZD52F10  3'  CAGCCTGTGCCAGCCCTGG   52819     T       A
                                CCAG GCTGGCATA GCTG
                                |||| ||||||||| ||||
                                GGTC CGACCGTGT CGAC
                                  C       C
GAM37   LOC145268 3'  TCAGCTTACAAGAGCCACTG   77062      _ GGCA
                                CAGTG CT    TAAGCTGA
                                ||||| ||    ||||||||
                                GTCAC GA    ATTCGACT
                                  C  GAAC
GAM37   LOC149296 5'  CAGCTTATGGGCAGCA      79256      G_
                                TGCTG  CATAAGCTG
                                |||||  |||||||||
                                ACGAC  GTATTCGAC
                                  GG
GAM37   LOC161877 5'  TCAGGGCAGGCCAGCGCTGG   82326          ATAAG
                                CCAGTGCTGGC    CTGA
                                ||||||||||    ||||
                                GGTCGCGACCG    GACT
                                     GACGG
GAM37   LOC163115 5'  TCAGCCCCTGACAGCACTGG   82413        G  TAA
                                CCAGTGCTG CA   GCTGA
                                |||||||||  ||   |||||
                                GGTCACGAC GT   CGACT
                                    A  CCC
GAM37   LOC196500 3'  TCAGCTCACTCAGTGGTC    87744     AGT    CATA
                                GACC   GCTGG    AGCTGA
                                ||||   |||||    ||||||
                                CTGG   TGACT    TCGACT
                                  ___    CAC_
GAM37   LOC197287 3'  TCAGCTCATGTGTTTTGCACTG 60865       T_     __
                                CAGTGC  GGCATA  AGCTGA
                                ||||||  ||||||  ||||||
                                GTCACG  TTGTGT  TCGACT
                                   TT     AC
GAM37   LOC200470 5'  TCAGCCTGCGGCGCTGG     90069        G  TAA
                                CCAGTGCTG CA   GCTGA
                                |||||||||  ||   |||||
                                GGTCGCGGC GT   CGACT
                                     _ C__
GAM37   LOC221584 3'  CAGCTTATGTGGCAC       93828       G
                                GTGCTG CATAAGCTG
                                ||||||  |||||||||
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                                CACGGT GTATTCGAC
                                      _
GAM37   LOC51716 3'  CAGCTCATGGCCCTAGCA    32787       ___   A
                                TGCTGG   CAT AGCTG
                                ||||||   ||| |||||
                                ACGATC   GTA TCGAC
                                   CCG   C
GAM37   LOC92196 5'  CAGAGCACCAGCACTGGC    68456   A       CATAAG
                                G CCAGTGCTGG     CTG
                                | ||||||||||     |||
                                C GGTCACGACC     GAC
                                _        ACGA__
GAM38   ACP2     3'  AGAAAGTTCTAGACTG      7851      GC  TC
                                CAGT  CT  AGAACTTTCT
                                ||||  ||  ||||||||||
                                GTCA  GA  TCTTGAAAGA
                                   __  __
GAM38   APTX     5'  AAGAGAAAGAGATCAGGCA   34655      TCAGAA
                                TGCCT     CTTTCTCTT
                                |||||     |||||||||
                                ACGGA     GAAAGAGAA
                                   CTAGA_
GAM38   BCL7A    3'  AGGCTGTCTCCTTAAGGCACTG 40637         C  A__  TT
                                CAGTGCCTT AG   AC  TCT
                                |||||||| ||   ||  |||
                                GTCACGGAA TC   TG  GGA
                                      T  CTC  TC
GAM38   CLC      3'  AAGAGAAAATACTGAAAGCACA 25105    A   C    AAC
            GG                    CC GTGC TTCAG   TTTCTCTT
                                || |||| |||||   ||||||||
                                GG CACG AAGTC   AAAGAGAA
                                 A   A    ATA
GAM38   CNK      3'  AAGCCCTGAAGGCCTG      14517     T      AA
                                CAG GCCTTCAG  CTT
                                ||| ||||||||  |||
                                GTC CGGAAGTC  GAA
                                  _       CC
GAM38   COL4A3   3'  AAGTGCAGGTTCTGAGGGCACC 48549    A           TCT
            GG                    CC GTGCCTTCAGAACTT   CTT
                                || ||||||||||||||   |||
                                GG CACGGGAGTCTTGGA   GAA
                                 C            CGT
GAM38   CSPG4    3'  AAGAGAGACCTGGAGACAC    8570      C     AAC
                                GTG CTTCAG   TTTCTCTT
                                ||| ||||||   ||||||||
                                CAC GAGGTC   AGAGAGAA
                                  A     C__
GAM38   CYP1B1   3'  AAGAGAAAAGAGAGAAACACTG 3651       CC   AGAAC
                                CAGTG  TTC    TTTCTCTT
                                |||||  |||    ||||||||
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                                GTCAC  AAG    AAAGAGAA
                                  A_   AGAGA
GAM38   DLG3    3'  AAGAGAAAAGAGGAGGACTG  40880     G    AGAAC
                                CAGT CCTTC    TTTCTCTT
                                |||| |||||    ||||||||
                                GTCA GGAGG    AAAGAGAA
                                  _    AGA__
GAM38   DLG5    5'  AGGCAGACTCTGAAGGC    82909        A_  T
                                GCCTTCAGA  CT TCT
                                |||||||||  || |||
                                CGGAAGTCT  GA GGA
                                     CA  C
GAM38   FLT1    3'  AAGAGAAACCGGGAGAAGGCAT 8910        AGAAC_
                                GTGCCTTC    TTTCTCTT
                                ||||||||    ||||||||
                                TACGGAAG    AAAGAGAA
                                    AGGGCC
GAM38   GRB10   3'  AGAGAAAATGGCACCTGG    17971    _   TTCAGAAC
                                CCAG TGCC      TTTCTCT
                                |||| ||||      |||||||
                                GGTC ACGG      AAAGAGA
                                  C   TA_______
GAM38   LFG     3'  AAGAGAAAAGGAGCCAAGAACT 76711      GC   CAGAA   _
          GG                    CCAGT  CTT    CTTT CTCTT
                                ||||| |||    |||| |||||
                                GGTCA  GAA    GAAA GAGAA
                                  A_   CCGAG   A
GAM38   MAN2A2  3'  AAGAGAAAGTTCATTCAC    20391    CCTTCA
                                GTG    GAACTTTCTCTT
                                |||    ||||||||||||
                                CAC    CTTGAAAGAGAA
                                 TTA___
GAM38   NLGN3   3'  AAGAAAAGTTCTTAAAACACT  38596     CC  C      C
                                AGTG  TT AGAACTTT TCTT
                                ||||  || |||||||| ||||
                                TCAC  AA TCTTGAAA AGAA
                                  AA  T      _
GAM38   NPAS1   5'  AAGGTCTCCCGAGGGCACT   59879        A_  _
                                AGTGCCTTC  GA ACTTT
                                |||||||||  || |||||
                                TCACGGGAG  CT TGGAA
                                     CC  C
GAM38   PLAG1   3'  AGTGTGTTCCAAAGGCATT   10605       CA   TTT
                                AGTGCCTT  GAAC   CT
                                ||||||||  ||||   ||
                                TTACGGAA  CTTG   GA
                                     AC    TGT
GAM38   PLXNA1  3'  AGAAAATGAAGGCAGTGG    72309    G      GAAC
                                CCA TGCCTTCA    TTTCT
                                ||| ||||||||    |||||
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                                GGT ACGGAAGT    AAAGA
                                  G       A___
GAM38   PPP4R1   3'  AAGAGAAAGTACAGTAAACACT 17620      CCTTCAGA
                                AGTG       ACTTTCTCTT
                                ||||       ||||||||||
                                TCAC       TGAAAGAGAA
                                  AAATGACA
GAM38   ACYP2    3'  AAGAGAAAAATTGTAACACACT 56612      CC  _   AAC
           G                     CAGTG  TT CAG   TTTCTCTT
                                |||||  || |||   ||||||||
                                GTCAC  AA GTT   AAAGAGAA
                                  AC  T   AA_
GAM38   B3GNT6   3'  AGAAATCAGATGAAGGCAT   22503        GAAC_
                                GTGCCTTCA     TTTCT
                                |||||||||     |||||
                                TACGGAAGT     AAAGA
                                     AGACT
GAM38   BAG5     3'  AAGAGAAGGGATAAAGGAC   16835    G   CAGAA
                                GT CCTT     CTTTCTCTT
                                || ||||     |||||||||
                                CA GGAA     GGAAGAGAA
                                 _   ATAG_
GAM38   BIVM     3'  AAGAGAAAAGACTCAAGAAACT 34665      GC   C  AAC
           G                     CAGT  CTT AG   TTTCTCTT
                                ||||  ||| ||   ||||||||
                                GTCA  GAA TC   AAAGAGAA
                                  AA   C  AGA
GAM38   C15orf5  3'  AGAGAAAAGAAAGCAC      48195      C   AGAAC
                                GTGC TTC     TTTCTCT
                                |||| |||     |||||||
                                CACG AAG     AAAGAGA
                                  A   A_____
GAM38   C20orf80  5'  AAGAGAAGAAGATGAAGAAAC  65282    GC    GAAC
                                GT  CTTCA    TTTCTCTT
                                ||  |||||    ||||||||
                                CA  GAAGT    GAAGAGAA
                                 AA     AGAA
GAM38   CLSTN1   3'  AGTTCTGAGGACACTGG     30103       C
                                CCAGTG CTTCAGAACT
                                |||||| ||||||||||
                                GGTCAC GGAGTCTTGA
                                   A
GAM38   DKFZP434P0111 3'  AAGAGAAAGTTTCTGCAC    67368      CTTCA
                                GTGC     GAACTTTCTCTT
                                ||||     ||||||||||||
                                CACG     TTTGAAAGAGAA
                                  TC___
GAM38   DORFIN   5'  AGAATTCTCTGAAGGAAC    31257    G       ACT
                                GT CCTTCAGA   TTCT
                                || ||||||||   ||||
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                                CA GGAAGTCT   AAGA
                                 A       CTT
GAM38   FLJ10300  5' AAGAGAAAGATGAAGACTCTG  35997     TGC    GAA
                                CAG   CTTCA   CTTTCTCTT
                                |||   |||||   |||||||||
                                GTC   GAAGT   GAAAGAGAA
                                  TCA    A__
GAM38   FLJ20373  3' AAGAGAAGAAGGAAAGGCACAG 35070    A     _ AGAAC
           G                     CC GTGCCTT C     TTTCTCTT
                                || ||||||| |    ||||||||
                                GG CACGGAA G     GAAGAGAA
                                 A      A GAA__
GAM38   FLJ23511  5' AGAGAAAAACAAGGCAT     49956        CAGAAC
                                GTGCCTT     TTTCTCT
                                |||||||     |||||||
                                TACGGAA     AAAGAGA
                                    CAA___
GAM38   FLJ30681  3' AGAGAAGAAAGACCACTGG   91782       CCT  AGAAC
                                CCAGTG   TC    TTTCTCT
                                ||||||   ||    |||||||
                                GGTCAC   AG    GAAGAGA
                                   C__   AAA__
GAM38   HDAC11    3' GAGCTATAGGCACTGG      45717         TC  AACTTT
                                CCAGTGCCT  AG     CTC
                                |||||||||  ||     |||
                                GGTCACGGA  TC     GAG
                                     TA _______
GAM38   IKKE      5' AGTGAGCCCTGAAAGCTCTGG  25745      T  C    AA   T
                                CCAG GC TTCAG  CTT CT
                                ||||  || |||||  ||| ||
                                GGTC CG AAGTC  GAG GA
                                  T  A    CC   T
GAM38   KIAA0680  3' AGAGAAAATTGAAGCAT     28232      C    AAC
                                GTGC TTCAG   TTTCTCT
                                ||||  |||||   |||||||
                                TACG AAGTT   AAAGAGA
                                  _    A__
GAM38   KIAA1228  3' AGGGGGTGATTCTGAGGCACTG 65035         T   ___   TT
                                CAGTGCCT CAGA   ACT  CT
                                |||||||| ||||   |||  ||
                                GTCACGGA GTCT   TGG  GA
                                    _   TAG   GG
GAM38   KIAA1300  5' AGGAACCCTGAAGGCA      62860         AAC
                                TGCCTTCAG   TTTCT
                                |||||||||   |||||
                                ACGGAAGTC   AAGGA
                                     CC_
GAM38   KIAA1805  3' AAGAGAAAGTAGAAGCAGCA   79966     __    AGA
                                TGC  CTTC   ACTTTCTCTT
                                |||  ||||   ||||||||||
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                                ACG  GAAG   TGAAAGAGAA
                                  AC    A__
GAM38   LENG1    5'  AAGAGAAAGCTCTGGGCATCCT 84074     __    TT    A
              G                    CAG  TGCC  CAGA CTTTCTCTT
                                   |||  ||||  |||| |||||||||
                                   GTC  ACGG  GTCT GAAAGAGAA
                                     CT    __    C
GAM38   LHX6     3'  AAGAGAAAACTCTGGGGTCA  26854    C      AC
                                   TG CTTCAGA  TTTCTCTT
                                   ||  |||||||  ||||||||
                                   AC GGGGTCT  AAAGAGAA
                                    T      CA
GAM38   N4BP3    3'  AGCTCCAGAAGGCACTGG    66250          A_  A
                                   CCAGTGCCTTC  GA CT
                                   ||||||||||  ||  ||
                                   GGTCACGGAAG  CT GA
                                          AC  C
GAM38   NASP     3'  AGAGGGTGAAGAAACTG     67966     GC    AGA
                                   CAGT  CTTC   ACTTTCT
                                   ||||  ||||   |||||||
                                   GTCA  GAAG   TGGGAGA
                                     AA   ___
GAM38   SMARCF1  3'  AAAATTCTGAAGGAC       20034    G       C
                                   GT CCTTCAGAA TTT
                                   ||  |||||||| |||
                                   CA GGAAGTCTT AAA
                                    _       A
GAM38   SMARCF1  3'  AAAATTCTGAAGGAC       37430    G       C
                                   GT CCTTCAGAA TTT
                                   ||  |||||||| |||
                                   CA GGAAGTCTT AAA
                                    _       A
GAM38   SMARCF1  3'  AAAATTCTGAAGGAC       57480    G       C
                                   GT CCTTCAGAA TTT
                                   ||  |||||||| |||
                                   CA GGAAGTCTT AAA
                                    _       A
GAM38   TED      3'  AAGAGAAAGTCCAGGGACTGG  31630      G   TCA  A
                                   CCAGT CCT   GA CTTTCTCTT
                                   |||||  |||   ||  |||||||||
                                   GGTCA GGA   CT GAAAGAGAA
                                      G   C__  _
GAM38   TGIF2    3'  AGAAGGGTGCTGAAGGC     41447         AA_
                                   GCCTTCAG   CTTTCT
                                   ||||||||   ||||||
                                   CGGAAGTC   GGAAGA
                                        GTG
GAM38   WBSCR20A 3'  AAGAGAAAGAAGAGACAGCA  35958     CT  AGAA
                                   TGC  TC    CTTTCTCTT
                                   |||  ||    |||||||||
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                                ACG  AG    GAAAGAGAA
                                  AC  AGAA
GAM38   LOC115273 3'  AGAAAGTTCTGATGGCCAGG   73356    AGT   T
                                CC   GCC TCAGAACTTTCT
                                ||   ||| ||||||||||||
                                GG   CGG AGTCTTGAAAGA
                                 AC_   T
GAM38   LOC145761 5'  AAGAGAAAGTGGAAGGCATGG  83472     G      AGA
                                CCA TGCCTTC   ACTTTCTCTT
                                ||| |||||||   ||||||||||
                                GGT ACGGAAG   TGAAAGAGAA
                                  _      G__
GAM38   LOC146179 5'  AGAAAGTTTTGGGCCT      77700    T   TT
                                AG GCC  CAGAACTTTCT
                                || |||  ||||||||||
                                TC CGG  GTTTTGAAAGA
                                 _  __
GAM38   LOC147072 3'  AAGAGAAAGTGAGAAGAAACTG 60407      GC    AGA
                                CAGT  CTTC   ACTTTCTCTT
                                ||||  ||||   ||||||||||
                                GTCA  GAAG   TGAAAGAGAA
                                  AA    AG_
GAM38   LOC148758 5'  AGAAAGTTCTGAGAAAC     78962    GCC
                                GT   TTCAGAACTTTCT
                                ||   ||||||||||||
                                CA   GAGTCTTGAAAGA
                                 AA_
GAM38   LOC148932 3'  AGGAATCTGAAGGCACTGG    79103            AC
                                CCAGTGCCTTCAGA  TTTCT
                                ||||||||||||||  |||||
                                GGTCACGGAAGTCT  AAGGA
                                          __
GAM38   LOC149386 5'  AAGTTTTGAAAGCACT      84400       C
                                AGTGC TTCAGAACTT
                                ||||| ||||||||||
                                TCACG AAGTTTTGAA
                                   A
GAM38   LOC150139 3'  AGAAAATAGAAAAAGGCGCTGG 79583          CAGAAC_
                                CCAGTGCCTT      TTTCT
                                ||||||||||      |||||
                                GGTCGCGGAA      AAAGA
                                      AAAGATA
GAM38   LOC152756 3'  AAGATGCAGTTCTGAAAACCTG 85871     TGCC       TTC
                                CAG    TTCAGAACT   TCTT
                                |||    |||||||||   ||||
                                GTC    AAGTCTTGA   AGAA
                                  CAA_       CGT
GAM38   LOC162333 5'  AAGAGAAAGCGATGACACTG   87114      CCT   GAA
                                CAGTG   TCA   CTTTCTCTT
                                |||||   |||   |||||||||
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                                GTCAC   AGT   GAAAGAGAA
                                  ___   AGC
GAM38   LOC199221 3'  AAGAGAAGCTCGAAAGCATGG  80347     G   C   A A   T
                                CCA TGC TTC GA CTT CTCTT
                                ||| ||| ||| || ||| |||||
                                GGT ACG AAG CT GAA GAGAA
                                  _   A   _  C   _
GAM38   LOC203339 3'  AGAGAAAATTGGGCCTG     90542     T    TCAGAAC
                                CAG GCCT      TTTCTCT
                                ||| ||||      |||||||
                                GTC CGGG      AAAGAGA
                                  _    TTA____
GAM38   LOC255017 3'  AGAAAGAGGAACTGG       94624       G   TCAGAA
                                CCAGT CCT     CTTTCT
                                ||||| |||     ||||||
                                GGTCA GGA     GAAAGA
                                   A  _______
GAM38   LOC256021 3'  AAGAGAAACAAAGACAACACTG 96512       CCT  AGAAC
            G                    CCAGTG   TC    TTTCTCTT
                                ||||||  ||    ||||||||
                                GGTCAC   AG    AAAGAGAA
                                    AAC  AAAC_
GAM38   LOC90139  3'  AGAATCCCGAAGGCAT     55396        A_  ACT
                                GTGCCTTC  GA   TTCT
                                ||||||||  ||   ||||
                                TACGGAAG  CT   AAGA
                                    CC  ___
GAM39   ADAMTS8   5'  TCGGGCCGCCAGCACCTG    22886     _      ATAAG
                                CAG TGCTGGC     CTGA
                                ||| |||||||     ||||
                                GTC ACGACCG     GGCT
                                  C      CCG__
GAM39   BAP1      3'  TCAGGGACCCAGCACTGG     16219          CATAAG
                                CCAGTGCTGG     CTGA
                                ||||||||||     ||||
                                GGTCACGACC     GACT
                                     CAGG__
GAM39   BF        5'  TTCAGCTTGGACACTG      8140        CTGGCA
                                CAGTG     TAAGCTGAA
                                |||||     |||||||||
                                GTCAC     GTTCGACTT
                                   AG_____
GAM39   C1QB      3'  TTCAACTCTGTGTCCCAGCACT 4923     A        __    _ C
            GGC                    G CCAGTGCTGG  CATA AG TGAA
                                | ||||||||||  |||| || ||||
                                C GGTCACGACC  GTGT TC ACTT
                                _         CT    C  A
GAM39   CHC1      3'  CAGCCCTGAGCACTGTGTC    7020      _      __ CATAA
                                GAC CAGTGCT  GG    GCTG
                                ||| |||||||  ||    ||||
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                                CTG GTCACGA  CC    CGAC
                                  T      GT  _____
GAM39   CMRF35   5'  CAGAGCTGTCAGCACCGG    21929    A       TAAG
                                CC GTGCTGGCA   CTG
                                || |||||||||   |||
                                GG CACGACTGT   GAC
                                 C       CGA_
GAM39   EPHB6    3'  TCAGCCCTGGACACTGGTC   15466       _ TG CATAA
                                GACCAGTG C  G    GCTGA
                                |||||||| |  |    |||||
                                CTGGTCAC G  C    CGACT
                                     A GT C____
GAM39   EVPL     5'  CAGCCTGAGCCAGCACT     8803         A  A
                                AGTGCTGGC TA GCTG
                                ||||||||| || ||||
                                TCACGACCG GT CGAC
                                     A  C
GAM39   GARP     3'  CAGCCCAGCACTGG       18594         CATAA
                                CCAGTGCTGG    GCTG
                                ||||||||||    ||||
                                GGTCACGACC    CGAC
                                      _____
GAM39   GJB5     3'  CAGCTCGACGGCACTGG     17945        GCATA
                                CCAGTGCTG    AGCTG
                                |||||||||    |||||
                                GGTCACGGC    TCGAC
                                     AGC__
GAM39   GPR81    3'  CTTACCAGCATTAGTC      50757    C      CA
                                GAC AGTGCTGG  TAAG
                                ||| ||||||||  ||||
                                CTG TTACGACC  ATTC
                                  A       __
GAM39   IFI16    5'  AGCAAGCCAGCACTAGTC    71221    C       ATAA
                                GAC AGTGCTGGC   GCT
                                ||| |||||||||   |||
                                CTG TCACGACCG   CGA
                                  A       AA__
GAM39   KRT4     3'  CAGCTGGGCCCAGCACTGGT  9635         _ ATA
                                ACCAGTGCTGG C   AGCTG
                                |||||||||| |   |||||
                                TGGTCACGACC G   TCGAC
                                      C GG_
GAM39   MAP3K9   3'  TTCAGCTTCCCAAACACCAGT 60709   CA  C_  CAT
                                AC  GTG  TGG   AAGCTGAA
                                ||  |||  |||   ||||||||
                                TG  CAC  ACC   TTCGACTT
                                 AC   AA   C__
GAM39   MGAT5    5'  TCAGCTTACAGTTCCTG     10028    T_   GCA
                                CAG  GCTG   TAAGCTGA
                                |||  ||||   ||||||||
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                                GTC  TGAC   ATTCGACT
                                  CT   ___
GAM39   MOCS1    3'  TTCAGCTTAACAGTTGCCCGGT 92037      A_  _  GCA
              C                    GACC  GTG CTG   TAAGCTGAA
                                   ||||  ||| |||   |||||||||
                                   CTGG  CGT GAC   ATTCGACTT
                                     CC   T   A__
GAM39   P23      3'  TCAGCTTATACCCGGGCT    21719     G   C_
                                   AGT CTGG  ATAAGCTGA
                                   ||| ||||  |||||||||
                                   TCG GGCC  TATTCGACT
                                     _   CA
GAM39   PFKFB4   3'  TCAGCCACATGCAACACTGTGT 15874     _    CTG   AA_
              C                    GAC CAGTG   GCAT   GCTGA
                                   ||| |||||   ||||   |||||
                                   CTG GTCAC   CGTA   CGACT
                                     T    AA_   CAC
GAM39   PTPRK    3'  TTCAGCCTGTGGCCCAGCACTG 11125          __   A
              GTC                    GACCAGTGCTGG  CATA GCTGAA
                                   ||||||||||||  |||| ||||||
                                   CTGGTCACGACC  GTGT CGACTT
                                         CG   C
GAM39   RNPEPL1  3'  CGGATGCCAGCACCTG      36676     _       AAG
                                   CAG TGCTGGCAT   CTG
                                   ||| |||||||||   |||
                                   GTC ACGACCGTA   GGC
                                     C       ___
GAM39   UBE2L3   3'  TCAGCCCTGGCACTGGC     12507    A      TG CATAA
                                   G CCAGTGC  G    GCTGA
                                   | |||||||  |    |||||
                                   C GGTCACG  C    CGACT
                                   _      GT C____
GAM39   APXL2    5'  CAGCCTCAGCACTCATC     75185    CC       CATAA
                                   GA  AGTGCTGG    GCTG
                                   ||  ||||||||    ||||
                                   CT  TCACGACT    CGAC
                                    AC       C____
GAM39   ARHGEF9  3'  TTCAGCTTACCAAGCA      30824     _ CA
                                   TGCT GG  TAAGCTGAA
                                   |||| ||  |||||||||
                                   ACGA CC  ATTCGACTT
                                     A  __
GAM39   CEGP1    3'  TTCAGCTTCCTCTAGCCCGG   40589    AGT    CAT
                                   CC   GCTGG   AAGCTGAA
                                   ||   |||||   ||||||||
                                   GG   CGATC   TTCGACTT
                                    CC_    TCC
GAM39   DKFZp547D155 3'  CAGCCCTGAGACCACTGGTC   70435        CTGG  TAA
                                   GACCAGTG   CA   GCTG
                                   ||||||||   ||   ||||
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                                CTGGTCAC   GT  CGAC
                                    CAGA  CC_
GAM39   DKFZP727G051 3'  TTCAGCCCATCAACCAGCATTG 69483          CATAA__
           GTC                   GACCAGTGCTGG      GCTGAA
                                 ||||||||||||      ||||||
                                 CTGGTTACGACC      CGACTT
                                       AACTACC
GAM39   DUSP14   5'  CACTGTCACCAGCACTGCTC  22834    C       CATA  C
                                 GA CAGTGCTGG   AG TG
                                 || |||||||||   || ||
                                 CT GTCACGACC   TC AC
                                  C       ACTG  _
GAM39   FLJ10206 5'  CAGCTTATGCCAGGAGTC   35898    CAGTG
                                 GAC    CTGGCATAAGCTG
                                 |||    ||||||||||||
                                 CTG    GACCGTATTCGAC
                                   AG___
GAM39   FLJ20967 5'  GGCGCCCAGCACTGGTT    41962          CATAA
                                 GACCAGTGCTGG    GCT
                                 ||||||||||||    |||
                                 TTGGTCACGACC    CGG
                                       CG___
GAM39   FLJ22569 3'  TTCAGCTTACTAAACTG    43679     GC   CA
                                 CAGT  TGG  TAAGCTGAA
                                 ||||  |||  |||||||||
                                 GTCA  ATC  ATTCGACTT
                                   A_  __
GAM39   FOXN4    3'  TTCAGCTTGGACACACTGG   75574       C  GCA
                                 CCAGTG TG   TAAGCTGAA
                                 ||||||  ||  |||||||||
                                 GGTCAC AC   GTTCGACTT
                                    _  AG_
GAM39   GW112    3'  TTCAACTGAAGCCAGCACTGGT 21194           ATA  C
           T                     GACCAGTGCTGGC   AG TGAA
                                 ||||||||||||||  || ||||
                                 TTGGTCACGACCG   TC ACTT
                                       AAG  A
GAM39   HOOK2    3'  CAGCTCACATGGCGCCCAGCAC 25256         _____  A__
           TGG                   CCAGTGCTGG    CAT   AGCTG
                                 ||||||||||    |||   |||||
                                 GGTCACGACC    GTA   TCGAC
                                     CGCG   CAC
GAM39   jdp2     3'  TTCAGCACAGCCAGCAT     55327        ATAA
                                 GTGCTGGC    GCTGAA
                                 ||||||||    ||||||
                                 TACGACCG    CGACTT
                                     ACA_
GAM39   KIAA0767 3'  TCTGCTGCCAGCACAGG     60632    A       TAA  T
                                 CC GTGCTGGCA   GC GA
                                 || |||||||||   || ||
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                                GG CACGACCGT   CG CT
                                 A        ___  T
GAM39   KIAA0923 3' TCAGCTTGATGCATGGTC    25838      G   TGGCA
                                GACCA TGC    TAAGCTGA
                                ||||| |||    ||||||||
                                CTGGT ACG    GTTCGACT
                                   _  TA___
GAM39   KIAA0982 3' TTCACTGTTTGCCAGCAC    25852        TA_  C
                                GTGCTGGCA   AG TGAA
                                |||||||||   || ||||
                                CACGACCGT   TC ACTT
                                     TTG  _
GAM39   KIAA1000 3' TTCAGCTTTGCAAAGTACTGG  65281        G_   T
                                CCAGTGCT  GCA AAGCTGAA
                                ||||||||  ||| ||||||||
                                GGTCATGA  CGT TTCGACTT
                                    AA  _
GAM39   MAP3K3   3' TCAGCCTGGGCGCTGGTC    9999         GG  TAA
                                GACCAGTGCT  CA   GCTGA
                                ||||||||||  ||   |||||
                                CTGGTCGCGG  GT   CGACT
                                     __  C__
GAM39   MGC16037 5' CTTGTCCAGCACTAGTC     51821     C       C
                                GAC AGTGCTGG ATAAG
                                ||| |||||||| |||||
                                CTG TCACGACC TGTTC
                                  A       _
GAM39   MIDORI   3' TCAGCTTATCCTGCAACT    73792     _  T  C
                                AGT GC GG ATAAGCTGA
                                ||| || || |||||||||
                                TCA CG CC TATTCGACT
                                  A  T  _
GAM39   MtFMT    5' CAGTGGCGAGCACTGG      57651        G  ATAA
                                CCAGTGCT GC    GCTG
                                |||||||| ||    ||||
                                GGTCACGA CG    TGAC
                                    G  G___
GAM39   PCDH16   5' TCAGTTCCAACCACTGG     72826       C_   CATA
                                CCAGTG  TGG    AGCTGA
                                ||||||  |||    ||||||
                                GGTCAC  ACC    TTGACT
                                   CA  _____
GAM39   QKI      3' CAGCTTATCAACTCGTC     65439     C   GCTGGC
                                GAC AGT     ATAAGCTG
                                ||| |||     ||||||||
                                CTG TCA     TATTCGAC
                                  C   AC_____
GAM39   TNRC6    3' CAACTTTTAGCACTG       70506         CAT   C
                                CAGTGCTGG   AAG TG
                                |||||||||   ||| ||
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                                GTCACGATT   TTC AC
                                     ___   A
GAM39   TOB2     3'  CAGCCCAGGCCAGCACTG    95618          ATAA
                                CAGTGCTGGC    GCTG
                                ||||||||||    ||||
                                GTCACGACCG    CGAC
                                     GACC
GAM39   TU12B1-TY 3'  TCAGCCCACAGCACTGTC    33406     C      GCATAA
                                GAC AGTGCTG     GCTGA
                                ||| |||||||     |||||
                                CTG TCACGAC     CGACT
                                  _      ACC___
GAM39   TUSP     3'  TCAGCCTAAGAGCGCAGCACTG 39641         _ A__  A
                                CAGTGCTG GC   TA GCTGA
                                |||||||| ||   || |||||
                                GTCACGAC CG   AT CGACT
                                     G  AGA  C
GAM39   USP19    3'  TCAGCTTATGCATCTGGT    88959       TGCTG
                                ACCAG    GCATAAGCTGA
                                |||||    ||||||||||||
                                TGGTC    CGTATTCGACT
                                   TA___
GAM39   ZD52F10   3'  CAGCCTGTGCCAGCCCTGG    52819      T       A
                                CCAG GCTGGCATA GCTG
                                |||| ||||||||| ||||
                                GGTC CGACCGTGT CGAC
                                   C        C
GAM39   LOC145268 3'  TCAGCTTACAAGAGCCACTG   77062       _ GGCA
                                CAGTG CT    TAAGCTGA
                                ||||| ||    ||||||||
                                GTCAC GA    ATTCGACT
                                   C  GAAC
GAM39   LOC149296 5'  CAGCTTATGGGCAGCA      79256       G_
                                TGCTG  CATAAGCTG
                                |||||  |||||||||
                                ACGAC  GTATTCGAC
                                   GG
GAM39   LOC161877 5'  TCAGGGCAGGCCAGCGCTGG   82326          ATAAG
                                CCAGTGCTGGC     CTGA
                                ||||||||||     ||||
                                GGTCGCGACCG    GACT
                                     GACGG
GAM39   LOC163115 5'  TCAGCCCCTGACAGCACTGG   82413         G  TAA
                                CCAGTGCTG CA   GCTGA
                                ||||||||| ||   |||||
                                GGTCACGAC GT   CGACT
                                     A  CCC
GAM39   LOC196500 3'  TCAGCTCACTCAGTGGTC    87744      AGT    CATA
                                GACC   GCTGG    AGCTGA
                                ||||   |||||    ||||||
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                                CTGG   TGACT    TCGACT
                                  ___     CAC_
GAM39   LOC197287 3'  TCAGCTCATGTGTTTTGCACTG 60865       T_     __
                                CAGTGC  GGCATA  AGCTGA
                                ||||||  ||||||  ||||||
                                GTCACG  TTGTGT  TCGACT
                                   TT      AC
GAM39   LOC200470 5'  TCAGCCTGCGGCGCTGG     90069         G  TAA
                                CCAGTGCTG CA   GCTGA
                                |||||||||  ||   |||||
                                GGTCGCGGC GT   CGACT
                                     _  C__
GAM39   LOC221584 3'  CAGCTTATGTGGCAC       93828       G
                                GTGCTG CATAAGCTG
                                |||||| |||||||||
                                CACGGT GTATTCGAC

                                _
GAM39   LOC51716  3'  CAGCTCATGGCCCTAGCA    32787        ___   A
                                TGCTGG   CAT AGCTG
                                ||||||   ||| |||||
                                ACGATC   GTA TCGAC
                                   CCG   C
GAM39   LOC92196  5'  CAGAGCACCAGCACTGGC    68456   A        CATAAG
                                G CCAGTGCTGG     CTG
                                | ||||||||||     |||
                                C GGTCACGACC     GAC
                                _        ACGA__
GAM40   CDH10     3'  TAGTTCTCCCTTAAGCAACCT  22058     CG   CAGTGT  A
                                AGG  GCT     GA GAACTA
                                |||  |||     || ||||||
                                TCC  CGA     CT CTTGAT
                                  AA   ATTCC_  _
GAM40   DACH      3'  TAGTTCTTCCATAACCACCT   54971     C  CTCA   T
                                AGG GG    GTG GAAGAACTA
                                ||| ||    ||| |||||||||
                                TCC CC    TAC CTTCTTGAT
                                  A  AA__   _
GAM40   HPS1      3'  TCTTCCAGAGCTGCCT      3969          AG  T
                                AGGCGGCTC  TG GAAGA
                                |||||||||  || |||||
                                TCCGTCGAG  AC CTTCT
                                     __  _
GAM40   PCTK1     5'  TCTTCAGGCTGCCT        52264         CAGTG
                                AGGCGGCT    TGAAGA
                                ||||||||    ||||||
                                TCCGTCGG    ACTTCT
                                     _____
GAM40   RORB      5'  AGCTCTTCGCCGACCACCT   22606     C  C  AGT      A
                                AGG GG TC   GTGAAGA CT
                                ||| || ||   ||||||| ||
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                                TCC CC AG   CGCTTCT GA
                                  A  _  C__      C
GAM40   SPTBN4   3'  AGTCCCCATGGCCGCCT     47386        CAGT   AA  A
                                AGGCGGCT    GTG  GA CT
                                ||||||||    |||  || ||
                                TCCGCCGG    TAC  CT GA
                                     _____   CC  _
GAM40   ZNF200   3'  GTAGTTCTGAATTCCCAAGCTG 12909        CAGT_  GA
           CCT                    AGGCGGCT    GT  AGAACTAC
                                ||||||||     ||  ||||||||
                                TCCGTCGA     TA  TCTTGATG
                                     ACCCT  AG
GAM40   BTN2A1   3'  GTAATTCTCAGTGTGTGAGCTG 54342          _ TG GA    C
           CCT                    AGGCGGCTCA G  T  AGAA TAC
                                ||||||||||  |  |  |||| |||
                                TCCGTCGAGT T  G  TCTT ATG
                                     G GT AC    A
GAM40   CFP1     3'  TAGCTCCGTCAAGCTGCCT    58771        CAGTG   A_  A
                                AGGCGGCT    TGA  GA CTA
                                ||||||||     |||  || |||
                                TCCGTCGA     ACT  CT GAT
                                     ______  GC  C
GAM40   FENS-1   3'  TGGGAGTCACACAAGCCGCCT  40445        CA     AGAA
                                AGGCGGCT  GTGTGA    CTA
                                ||||||||  ||||||    |||
                                TCCGCCGA  CACACT    GGT
                                     A_     GAG_
GAM40   FLJ14082 3'  AGTTCTTCCTAAGGCACCC    46668    CG   CAG  T
                                GG  GCT   TG GAAGAACT
                                ||  |||   || ||||||||
                                CC  CGG   AT CTTCTTGA
                                  CA   A__  C
GAM40   FLJ20539 5'  TGGGGCCACCTGAGCCGCC    35363          T   AAGAA
                                GGCGGCTCAG GTG     CTA
                                ||||||||||  |||     |||
                                CCGCCGAGTC CAC     GGT
                                     _   CGG__
GAM40   FLJ22301 3'  AGCCCTTCACGTAGCCTCCT   45756     C    CAG      AA
                                AGG GGCT   TGTGAAG  CT
                                |||  ||||   |||||||  ||
                                TCC CCGA   GCACTTC  GA
                                  T    T__      CC
GAM40   HEMGN    5'  TAGAGAAAAAAACTGAGCCACC 37380     C       GTGAAGAA
           T                     AGG GGCTCAGT       CTA
                                |||  ||||||||       |||
                                TCC CCGAGTCA       GAT
                                  A       AAAAAAGA
GAM40   KIAA0379 3'  GTAGTTCTTGCGAATGCCACC  68150    C   TCAG   G
                                GG GGC    TGT AAGAACTAC
                                || |||    ||| |||||||||
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                                CC CCG    GCG TTCTTGATG
                                 A   TAA_  _
GAM40   KIAA0494  3'  TCTCACACTGACCACC      28750    C  C       A
                                GG GG TCAGTGTGA GA
                                || || ||||||||| ||
                                CC CC AGTCACACT CT
                                 A  _       _
GAM40   LACE1     3'  CTTCACATTAAACCACCT    91837     C  CTC
                                AGG GG   AGTGTGAAG
                                ||| ||   |||||||||
                                TCC CC   TTACACTTC
                                  A  AAA
GAM40   NAPG      3'  TAGTTCTTCAGGTAGCACCT  96730     CG   CAG G
                                AGG  GCT   T TGAAGAACTA
                                |||  |||   | ||||||||||
                                TCC  CGA   G ACTTCTTGAT
                                  A_   T__ G
GAM40   PRO2405   5'  AGGAGCACATTAAGCCGCCT  37798        C     AAGAA
                                AGGCGGCT AGTGTG     CT
                                |||||||| ||||||     ||
                                TCCGCCGA TTACAC     GA
                                     A      GAG__
GAM40   LOC121219 5'  AGTCCTCAGCGAAGCCGCCT  74040        CA  G   A  A
                                AGGCGGCT  GT TGA GA CT
                                ||||||||  || ||| || ||
                                TCCGCCGA  CG ACT CT GA
                                     AG  _   C  _
GAM40   LOC146990 3'  CTTCACACCCAGCCGCCT    83886        CA
                                AGGCGGCT  GTGTGAAG
                                ||||||||  ||||||||
                                TCCGCCGA  CACACTTC
                                     CC
GAM40   LOC148371 5'  TTCCACTGAGCCACC       78809     C       T
                                GG GGCTCAGTG GAA
                                || ||||||||| |||
                                CC CCGAGTCAC CTT
                                 A        _
GAM40   LOC152274 3'  AGTCCCTGCAGGAGCAGCCT  80498      G    AG    AA  A
                                AGGC GCTC  TGTG  GA CT
                                |||| ||||  ||||  || ||
                                TCCG CGAG  ACGT  CT GA
                                  A   G_    CC  _
GAM40   LOC200261 3'  AGTTGCTCCACTGAGTCACC   88653     C       T  AG
                                GG GGCTCAGTG GA  AACT
                                || |||||||| ||  ||||
                                CC CTGAGTCAC CT  TTGA
                                 A        _ CG
GAM40   LOC201562 5'  GTAGTCCGGCCCGAGCCGCT   88975        AGT  GAA  A
                                GGCGGCTC   GT   GA CTAC
                                ||||||||   ||   || ||||
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                                TCGCCGAG   CG   CT GATG
                                     CC_  GC_  _
GAM40   LOC202347 3'  TCATGGCAGAGCCGCCT     90349          A  _
                                AGGCGGCTC GT GTGA
                                ||||||||| || ||||
                                TCCGCCGAG CG TACT
                                      A  G
GAM40   LOC220370 3'  TCACCTCACTGAGCCACCT    92834     C       ___
                                AGG GGCTCAGT   GTGA
                                ||| |||||||   ||||
                                TCC CCGAGTCA   CACT
                                  A       CTC
GAM40   LOC221838 5'  TTCCACTGAGCCACC       92546     C        T
                                GG GGCTCAGTG GAA
                                || ||||||||| |||
                                CC CCGAGTCAC CTT
                                 A       _
GAM40   LOC51716  3'  AGTTCCACACTGAGCGCCT    32786       G        AA
                                AGGCG CTCAGTGTG  GAACT
                                ||||| |||||||||  |||||
                                TCCGC GAGTCACAC  CTTGA
                                     _       __
GAM40   LOC89919  3'  CTTCCACTGAGCCACC       60722     C        T
                                GG GGCTCAGTG GAAG
                                || ||||||||| ||||
                                CC CCGAGTCAC CTTC
                                 A       _
GAM40   LOC91947  3'  TAGTTCTTTCATTGTAAGCCGC 67614         __     T
            T                    GGCGGCT  CAGTG GAAGAACTA
                                |||||||  ||||| |||||||||
                                TCGCCGA  GTTAC TTTCTTGAT
                                    AT    _
GAM41   DKFZP434D1335 3'  ATGGCAATACATGTGTAGA    65114          C  C
                                TCTACACGTG AT GCTGT
                                |||||||||| || |||||
                                AGATGTGTAC TA CGGTA
                                      A  A
GAM41   DKFZP762D096 3'  CATTGGTACTGAACACGTACAG 65576     AC     CA   C GT
            A                    TCT  ACGTG  TCG T  CAATG
                                ||| |||||  ||| |  |||||
                                AGA  TGCAC  AGT A  GTTAC
                                  CA    A_   C TG
GAM41   EVI5     3'  CATTGACAGCGAACATTTCATG 18992      CA____
                                CGTG     TCGCTGTCAATG
                                ||||     ||||||||||||
                                GTAC     AGCGACAGTTAC
                                  TTTACA
GAM41   FLJ13114  3'  ACAGGCTGCCATGTGTAGA   44592          _ TCG
                                TCTACACGTG CA   CTGT
                                |||||||||| ||   ||||
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                                AGATGTGTAC GT   GACA
                                      C  CG_
GAM41   H2AFY2   5' ATTGACACGCACAGATAGA   37841     CAC   ATCGC
                                TCTA   GTGC    TGTCAAT
                                ||||   ||||    |||||||
                                AGAT   CACG    ACAGTTA
                                  AGA   C____
GAM41   HTCD37   3' ACTTGTTCTGCATGTGTAGA   67669          TC  T_
                                TCTACACGTGCA  GC  GT
                                ||||||||||||  ||  ||
                                AGATGTGTACGT  TG  CA
                                       CT  TT
GAM41   KIAA0152 3' CATTGACAGCGGCACAGTGAGA 28294     A  _   AT
                                TCT CAC GTGC  CGCTGTCAATG
                                ||| ||| ||||  ||||||||||
                                AGA GTG CACG  GCGACAGTTAC
                                  _  A   __
GAM41   KIAA1190 3' CATTGACAACTGCTCGTGTA   71098       T   TCGC
                                TACACG GCA    TGTCAATG
                                ||||||| |||    ||||||||
                                ATGTGC CGT    ACAGTTAC
                                   T   CA__
GAM41   PRO0132   5' CATTGATGCACGCATAG     26103     CA       C
                                CTA  CGTGCATCG TG
                                |||  |||||||| ||
                                GAT  GCACGTAGT AC
                                  AC        T
GAM41   ZNF263    3' CATTGGCAGATTACACATGTA  19224     C   CATCG
                                TACA GTG     CTGTCAATG
                                |||| |||     |||||||||
                                ATGT CAC     GACGGTTAC
                                  A   ATTA_
GAM41   LOC115648 3' CATTGACAAAGGGCACAATAGA 59296      CAC    A  GC
                                TCTA   GTGC TC  TGTCAATG
                                ||||   |||| ||  ||||||||
                                AGAT   CACG GG  ACAGTTAC
                                  AA_   _  AA
GAM41   LOC145945 5' ATTGACAGCAGTATGT      83571       ATC
                                ACGTGC   GCTGTCAAT
                                ||||||   |||||||||
                                TGTATG   CGACAGTTA
                                   A__
GAM42   B3GNT3    3' CCCACCTGGTACTGTT      26517         TACTAA  A
                                AACAGTATC     AG TGGG
                                |||||||||     || ||||
                                TTGTCATGG     TC ACCC
                                      _______ C
GAM42   CSPG3     3' AGCCCATTGACTTAGAAACTGT 15227       A    CTAAA
           T                     AACAGT TCTA    GATGGGCT
                                ||||||| ||||    ||||||||
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                                TTGTCA AGAT    TTACCCGA
                                   A   TCAG_
GAM42   EVA1    3' AGCCCATCTCTAATGAGGACT 58572    A  AC_ A
                                AGT TCT  TA AGATGGGCT
                                ||| |||  || |||||||||
                                TCA GGA  AT TCTACCCGA
                                  _  GTA  C
GAM42   ID4     3' CTTTAATAGATACTGT     7754         C
                                ACAGTATCTA TAAAG
                                |||||||||| |||||
                                TGTCATAGAT ATTTC
                                      A
GAM42   RAD51C  3' TTTAGAGATACTGTT     54255        A
                                AACAGTATCT CTAAA
                                |||||||||| |||||
                                TTGTCATAGA GATTT
                                      _
GAM42   RHO     3' AGCCCATCTTCAGCAGTTGCT 5018     T  A  A
                                AGTA CT CT AAGATGGGCT
                                |||| || || ||||||||||
                                TCGT GA GA TTCTACCCGA
                                  T  C  C
GAM42   STAR    3' CTCATTAGTAGACATGTT   4445     GTA     AAG
                                AACA  TCTACTA  ATGGG
                                ||||  |||||||  |||||
                                TTGT  AGATGAT  TACTC
                                  AC_     ___
GAM42   CD109   3' AGTGGTCTCAGTAGATACT  56046       AA   GG
                                AGTATCTACT  AGAT  GCT
                                ||||||||||  ||||  |||
                                TCATAGATGA  TCTG  TGA
                                      C_   G_
GAM42   FLJ00024 3' AGCCCATCCCTGGGACCTGC  63747    TCTA  AA
                                GTA   CTA  GATGGGCT
                                |||   |||  ||||||||
                                CGT   GGT  CTACCCGA
                                  CCAG  CC
GAM42   FLJ20666 3' GCTTACCACAGATACTGTT  35510       ACTAAAGA
                                AACAGTATCT     TGGGC
                                ||||||||||     |||||
                                TTGTCATAGA     ATTCG
                                      CACC____
GAM42   FLJ20666 3' GCTTACCACAGATACTGTT  37089       ACTAAAGA
                                AACAGTATCT     TGGGC
                                ||||||||||     |||||
                                TTGTCATAGA     ATTCG
                                      CACC____
GAM42   FLJ22969 3' GGCTCAGCAGATGCTGT    68657       ACTAAAGA
                                ACAGTATCT     TGGGCT
                                |||||||||     ||||||
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                                TGTCGTAGA       ACTCGG
                                     CG_______
GAM42   GGTLA1   5' AGCCCATCTCTGTCCCATTGT  14657       ATCT  TAA
                                ACAGT    AC   AGATGGGCT
                                |||||    ||   |||||||||
                                TGTTA    TG   TCTACCCGA
                                   CCC_  TC_
GAM42   KIAA0240 3' TTTAGTAGATTCTGTT      92443       T
                                AACAG ATCTACTAAA
                                ||||| ||||||||||
                                TTGTC TAGATGATTT
                                   T
GAM42   KIAA1028 3' TTTATTAGATACTGTT      91952           C
                                AACAGTATCTA TAAA
                                |||||||||| ||||
                                TTGTCATAGAT ATTT
                                      T
GAM42   KIAA1332 3' CATCAAAAGATACTGTT     71163          ACTAAA
                                AACAGTATCT     GATG
                                ||||||||||     ||||
                                TTGTCATAGA     CTAC
                                      AAA___
GAM42   KIAA1497 3' ATCTTTAGTAGACACT      67503     A
                                AGT TCTACTAAAGAT
                                ||| ||||||||||||
                                TCA AGATGATTTCTA
                                  C
GAM42   KIAA1858 3' AGCCCATCTCTAGCACACCTTG 67133     TATCTA   A
                                CAG      CTA AGATGGGCT
                                |||      ||| |||||||||
                                GTT      GAT TCTACCCGA
                                  CCACAC   C
GAM42   p25      3' GCCCATCCAGGACACTCC    22851    C   A   ACTAAA
                                A AGT TCT      GATGGGC
                                | ||| |||      |||||||
                                C TCA AGG      CTACCCG
                                 C   C   AC____
GAM42   PME-1    3' AGCCCATCTTTTCTGTGACTGT 32351       ATCTACT
                                ACAGT      AAAGATGGGCT
                                |||||      ||||||||||||
                                TGTCA      TTTCTACCCGA
                                   GTGTCT_
GAM42   PRO0628  3' AGCCCATCTTCTGTACTGCT   26205      TC   TA
                                AGTA  TAC  AAGATGGGCT
                                ||||  |||  ||||||||||
                                TCGT  ATG  TTCTACCCGA
                                  C_   TC
GAM42   LOC122728 3' AGCCCATCTGCTGTATTACTG  74150       TC   TAA
                                CAGTA  TAC   AGATGGGCT
                                |||||  |||   |||||||||
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                                GTCAT  ATG   TCTACCCGA
                                   T_   TCG
GAM42   LOC130507 3'  ATCTCTAGTAAATACTGTT   74948        C    A
                                AACAGTAT TACTA AGAT
                                |||||||| ||||| ||||
                                TTGTCATA ATGAT TCTA
                                     A    C
GAM42   LOC144110 3'  AGCCTGGGGCAGCAGGTACTG  76672        A  AAAGA
                                CAGTATCT CT    TGGGCT
                                |||||||| ||    ||||||
                                GTCATGGA GA    GTCCGA
                                     C  CGGG_
GAM42   LOC145368 3'  AGCCCATCTGCTGTATTACTG  77092      TC   TAA
                                CAGTA  TAC   AGATGGGCT
                                |||||  |||   |||||||||
                                GTCAT  ATG   TCTACCCGA
                                   T_   TCG
GAM42   LOC149830 3'  CCCATCTCTAAGGCAGGATGCT 84724        A__  AA_
           G                     CAGTATCT   CT   AGATGGG
                                |||||||   ||   |||||||
                                GTCGTAGG   GA   TCTACCC
                                     ACG  ATC
GAM42   LOC150236 5'  AGCCCATCCCCCAGTTCACT   79680    ATCT   AAA_
                                AGT    ACT    GATGGGCT
                                |||    |||    ||||||||
                                TCA    TGA    CTACCCGA
                                  CT__   CCCC
GAM42   LOC150279 3'  CCCATGAGGCTCAGATGCTGTT 79667         ACTAAAG
                                AACAGTATCT      ATGGG
                                ||||||||||      |||||
                                TTGTCGTAGA      TACCC
                                     CTCGGAG
GAM42   LOC150423 3'  AGCCCATCTCCTGTATTACTG  79863      TC   TAA
                                CAGTA  TAC   AGATGGGCT
                                |||||  |||   |||||||||
                                GTCAT  ATG   TCTACCCGA
                                   T_   TCC
GAM42   LOC151405 5'  AGATGGGCTTTAGTAAAGACTG 85334      ATC       ATGGG
           T                     ACAGT   TACTAAAG    CT
                                |||||   ||||||||    ||
                                TGTCA   ATGATTTC    GA
                                   GAA       GGGTA
GAM42   LOC151473 3'  AGCCCATCTCTAGACTCTCGT  80250    _ TA    CTAA
                                AC AG  TCTA    AGATGGGCT
                                || ||  ||||    |||||||||
                                TG TC  AGAT    TCTACCCGA
                                 C  TC    C___
GAM42   LOC153196 5'  AGCCCATCCTTGGGACCCTACT 85953      TCTA_    A
                                AGTA    CTAA GATGGGCT
                                ||||    |||| ||||||||
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                                TCAT    GGTT CTACCCGA
                                  CCCAG   C
GAM42   LOC221002 3'  AGCCCATTCAGATAAAACTG  91475     ___   ACTAAA
                                CAGT  ATCT    GATGGGCT
                                ||||  ||||    ||||||||
                                GTCA  TAGA    TTACCCGA
                                  AAA   C_____
GAM42   LOC255290 5'  AGCCCATCTCTGTCCCATTGT  95607     ATCT  TAA
                                ACAGT   AC  AGATGGGCT
                                ||||||  ||  |||||||||
                                TGTTA   TG  TCTACCCGA
                                  CCC_  TC_
GAM42   LOC91907  3'  ATCTTTAGTAGACACT     67493     A
                                AGT TCTACTAAAGAT
                                ||| ||||||||||||
                                TCA AGATGATTTCTA
                                  C
GAM43   ABCD1     3'  CAGCCTACACTGCCAGCC    3461      AAGATCT
                                GGC     GGTGTAGGCTG
                                |||     ||||||||||
                                CCG     TCACATCCGAC
                                 ACCG___
GAM43   AHR       5'  CAGCCTACACCGGGTTCC    7878    A
                                A GATCTGGTGTAGGCTG
                                | ||||||||||||||||
                                C TTGGGCCACATCCGAC
                                 C
GAM43   AKAP1     3'  AGCGTCCAGATCTGCC      57708     A     TGTAG
                                GGCA GATCTGG    GCT
                                |||| |||||||    |||
                                CCGT CTAGACC    CGA
                                  _     TG___
GAM43   ATSV      3'  CTTTCATCAGATCCTGCC    15055     A       T
                                GGCA GATCTGGTG AGG
                                |||| ||||||||| |||
                                CCGT CTAGACTAC TTC
                                  C       T
GAM43   B4GALT3   5'  CAGCTTGAACCTAGATCTCACC 13676    CA    _  G
                                GG  AGATCT GGT TAGGCTG
                                ||  |||||| ||| |||||||
                                CC  TCTAGA CCA GTTCGAC
                                 AC     T  A
GAM43   BTD       3'  GTGGCACCAGATTCC      3553     CAA       AG
                                GG  GATCTGGTGT  GC
                                ||  ||||||||||  ||
                                CC  TTAGACCACG  TG
                                 ___        G_
GAM43   CARKL     3'  CAGCCAGGCAGACTCCTGCC  25185     A _   GTGTA
                                GGCA GA TCTG    GGCTG
                                |||| || ||||    |||||
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                                CCGT CT AGAC    CCGAC
                                  C  C   GGA__
GAM43   CD9     5'  CAGCCTACAGCCGCCTGC   8337     A ATC  _
                                GCA G   TGG TGTAGGCTG
                                ||| |   ||| |||||||||
                                CGT C   GCC ACATCCGAC
                                  _ C__   G
GAM43   DFFB    5'  CAGCTTGCAGAGCTCACC   87379    CA  A   GGT
                                GG  AG TCT   GTAGGCTG
                                ||  || |||   ||||||||
                                CC  TC AGA   CGTTCGAC
                                 AC  G  ___
GAM43   FUS1    3'  TTTGCACCAAATCCTCC    23455    CAA   C
                                GG   GAT TGGTGTAGG
                                ||   ||| |||||||||
                                CC   CTA ACCACGTTT
                                 TC_   A
GAM43   FXYD6   3'  AGCCTGCGGTCCTGCC     41837     A    TGGT
                                GGCA GATC    GTAGGCT
                                |||| ||||    |||||||
                                CCGT CTGG    CGTCCGA
                                  C   _____
GAM43   FZD1    3'  CAGCCTGCGCTTAGATTTTACC 13032    C      _
                                GG AAGATCTG GTGTAGGCTG
                                || |||||||| ||||||||||
                                CC TTTTAGAT CGCGTCCGAC
                                 A       T
GAM43   GASC1   5'  CCGCGCGCCAGACACTGCC   64244     AGA      A_
                                GGCA   TCTGGTGT  GG
                                ||||   ||||||||  ||
                                CCGT   AGACCGCG  CC
                                  CAC       CG
GAM43   GFI1    3'  CAGTCTGCAGATCCTACC    17932    CAA    GGT
                                GG   GATCT   GTAGGCTG
                                ||   |||||   ||||||||
                                CC   CTAGA   CGTCTGAC
                                 ATC    ____
GAM43   HDAC5   3'  CAGCCTACTTCCCCTTCC    57605    C   ATCT  T_
                                GG AAG    GG  GTAGGCTG
                                || |||    ||  ||||||||
                                CC TTC    CC  CATCCGAC
                                 _   C___  TT
GAM43   HSF4    5'  CAGCCCACACCAGGTCGCGC   59775    AA        A
                                GC  GATCTGGTGT GGCTG
                                ||  |||||||||| |||||
                                CG  CTGGACCACA CCGAC
                                 CG         C
GAM43   ITGB3   3'  CCTTCAGATTTGCC        3994       A      TGT
                                GGCA GATCTGG   AGG
                                |||| |||||||   |||
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                                CCGT TTAGACT   TCC
                                  _     ___
GAM43   ITSN2    3'  CAGACCACCAGATGTTACC   38972    C  G      TAGG
                                GG AA ATCTGGTG    CTG
                                || || ||||||||    |||
                                CC TT TAGACCAC    GAC
                                 A  G       CA__
GAM43   KRT8     3'  CAGCCTACCCCTCCTGC     9637      A  TCT  T
                                GCA GA   GG GTAGGCTG
                                ||| ||   || ||||||||
                                CGT CT   CC CATCCGAC
                                  C  C__  _
GAM43   L1CAM    3'  CAGCTTGGGCAGATCTCC    43752    CA      G G
                                GG  AGATCTG T TAGGCTG
                                ||  ||||||| | |||||||
                                CC  TCTAGAC G GTTCGAC
                                 __      _ G
GAM43   L1CAM    3'  CAGCTTGGGCAGATCTCC    4714     CA      G G
                                GG  AGATCTG T TAGGCTG
                                ||  ||||||| | |||||||
                                CC  TCTAGAC G GTTCGAC
                                 __      _ G
GAM43   LGALS3BP 3'  CGGCCACCAGATGTCGCC    69318     AAG      GTA
                                GGC   ATCTGGT   GGCTG
                                |||   |||||||   |||||
                                CCG   TAGACCA   CCGGC
                                  CTG      ___
GAM43   LGS      3'  CAAACTTACCAGATCTTGTC   33360            T  GC
                                GGCAAGATCTGGTG AG  TG
                                |||||||||||||| ||  ||
                                CTGTTCTAGACCAT TC  AC
                                        _  AA
GAM43   MIA      3'  CAGCCTACCGCTGGCCCTGCC  21525      A AT TG  _
                                GGCA G  C  GTG TAGGCTG
                                |||| |  |  ||| |||||||
                                CCGT C  G  CGC ATCCGAC
                                  _ CC GT   C
GAM43   NRAP     3'  CAGCCCATCCCAGATCTTCC   20507    C       TG A
                                GG AAGATCTGG  T GGCTG
                                || |||||||||  | |||||
                                CC TTCTAGACC  A CCGAC
                                 _       CT C
GAM43   PDE1B    3'  CAGCCCCCCACCCCAGATCTTA 6241     _       T  A___
           GC                     GC AAGATCTGG GT    GGCTG
                                || |||||||||  ||    |||||
                                CG TTCTAGACC CA    CCGAC
                                 A        C  CCCC
GAM43   PDGFRB   5'  CTGCACCAGTCCTGCC      65975      A  T
                                GGCA GA CTGGTGTAG
                                |||| || |||||||||
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                                CCGT CT GACCACGTC
                                  C  _
GAM43   PDGFRB   3'  CAGCCTGCAGCCCTTGCC    65970       ATCT  _
                                GGCAAG   GG TGTAGGCTG
                                ||||||   || |||||||||
                                CCGTTC   CC ACGTCCGAC
                                   _____  G
GAM43   PKLR     3'  CAGCCTACCCTTGTACCCC   4314     CAAG  CT  T
                                GG   AT  GG GTAGGCTG
                                ||   ||  || ||||||||
                                CC   TG  CC CATCCGAC
                                 CCA_  TT  _
GAM43   POLK     3'  AGCCAAGATCTTGCC      32563          GGTGTA
                                GGCAAGATCT     GGCT
                                ||||||||||     ||||
                                CCGTTCTAGA     CCGA
                                      A_____
GAM43   PPP1R12B 5'  TCTACACCAGTTCCC      49485    CAA  T
                                GG   GA CTGGTGTAGG
                                ||   || ||||||||||
                                CC   CT GACCACATCT
                                 ___  T
GAM43   PPP1R12B 5'  TCTACACCAGTTCCC      49474    CAA  T
                                GG   GA CTGGTGTAGG
                                ||   || ||||||||||
                                CC   CT GACCACATCT
                                 ___  T
GAM43   PRM2     5'  AGCCACCAGATCTCC       10891    CA       GTA
                                GG  AGATCTGGT   GGCT
                                ||  |||||||||   ||||
                                CC  TCTAGACCA   CCGA
                                 __       ___
GAM43   RAB6A    3'  CAGCCTACTTTATCTCTCC   11192    CA   CTGGT
                                GG  AGAT    GTAGGCTG
                                ||  ||||    ||||||||
                                CC  TCTA    CATCCGAC
                                 TC    TTT__
GAM43   RAMP3    3'  AGCCCCAGCTCCTGCC      19586     A  T   TGTA
                                GGCA GA CTGG    GGCT
                                |||| || ||||    ||||
                                CCGT CT GACC    CCGA
                                  C  C   _____
GAM43   SLA2     3'  CAGCCTACACCAAATCCAGCC  49892     AA   C
                                GGC  GAT TGGTGTAGGCTG
                                |||  ||| ||||||||||||
                                CCG  CTA ACCACATCCGAC
                                  AC   A
GAM43   SLC5A1   3'  CAGCCAGTTGTAAATTTTGCC  4427         C  GT TA
                                GGCAAGAT TG  G  GGCTG
                                |||||||| ||  |  |||||
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                                CCGTTTTA AT  T  CCGAC
                                     A  GT GA
GAM43   TUFT1    3'  CAGCCTACGCTGCCCTGGCC   39253     A  ATC
                                GGC AG   TGGTGTAGGCTG
                                ||| ||   ||||||||||||
                                CCG TC   GTCGCATCCGAC
                                  G  CC_
GAM43   VGF      5'  GCAGCCCACGGGACGCCAGACC 12594    A       A_____    III
           T                     AG TCTGGTGT     GGCTG   C
                                || ||||||||     |||||   |
                                TC AGACCGCA     CCGAC   G
                                 C       GGGCAC    III
GAM43   XPC      3'  CAGCCCTTGTCAGATTCACC   16130    CAA     GT TA
                                GG   GATCTG  G  GGCTG
                                ||   ||||||  |  |||||
                                CC   TTAGAC  T  CCGAC
                                 AC_     TG TC
GAM43   C17orf26  3'  CAGCCTACTCCTTCTT      57542      TCT  T
                                AAGA   GG GTAGGCTG
                                ||||   || ||||||||
                                TTCT   CC CATCCGAC
                                  T__  T
GAM43   CAT56    3'  CAGCCTGTAGAGACTCGCC    47513     A  A_   GTG
                                GGC AG  TCTG   TAGGCTG
                                ||| ||  ||||   |||||||
                                CCG TC  AGAT   GTCCGAC
                                  C  AG   ___
GAM43   CNNM4    3'  CAGCCTATGGGGGATCTGGCC  39478     A     GG
                                GGC AGATCT  TGTAGGCTG
                                ||| ||||||  |||||||||
                                CCG TCTAGG  GTATCCGAC
                                  G     GG
GAM43   DKFZp434F142 3'  CTTACACCAGCTCCTGCC     50025      A  T
                                GGCA GA CTGGTGTAGG
                                |||| || ||||||||||
                                CCGT CT GACCACATTC
                                  C  C
GAM43   DKFZp566D234 3'  CTTGCACCAAATCCTGTC     61864      A   C
                                GGCA GAT TGGTGTAGG
                                |||| ||| |||||||||
                                CTGT CTA ACCACGTTC
                                  C   A
GAM43   DKFZP727M111 5'  CAATCTCCCAGATTTGCC     31406      A      TGT  GC
                                GGCA GATCTGG   AG  TG
                                |||| |||||||   ||  ||
                                CCGT TTAGACC   TC  AC
                                  _      C__  TA
GAM43   FLJ10324  5'  CAGCCCCCGACATCCTGCC    36027      A   CTGG  TA
                                GGCA GAT    TG  GGCTG
                                |||| |||    ||  |||||
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                                CCGT CTA   GC  CCGAC
                                  C   CA__  CC
GAM43   FLJ10704 3' CAGCCTGCAGACCCCGCC   36451    AAGA   GGT
                                GGC   TCT   GTAGGCTG
                                |||   |||   ||||||||
                                CCG   AGA   CGTCCGAC
                                  CCCC  ___
GAM43   FLJ10898 5' CAGCCATTTCAGGTCTCACC  59423   CA      T  A
                                GG  AGATCTGG GT GGCTG
                                ||  |||||||| || |||||
                                CC  TCTGGACT TA CCGAC
                                 AC       T  _
GAM43   FLJ12057 3' CAGCCCCTGCATTCCTGCC   45435     A  TCTG    __
                                GGCA GA   GTGTA  GGCTG
                                |||| ||   |||||  |||||
                                CCGT CT   TACGT  CCGAC
                                  C _____    CC
GAM43   FLJ12681 3' CAGCCTACACGCATCCC    42871    CAA   CTG
                                GG   GAT   GTGTAGGCTG
                                ||   |||   ||||||||||
                                CC   CTA   CACATCCGAC
                                 ___   CG_
GAM43   FLJ12998 3' CAGCCTACGTCACATTTGCC  42836      ATC  GT
                                GGCAAG   TG  GTAGGCTG
                                ||||||   ||  ||||||||
                                CCGTTT   AC  CATCCGAC
                                   AC_  TG
GAM43   FLJ13166 3' CAGGTACCAAATCTGGCC    46564    A   C    TAGG
                                GGC AGAT TGGTG    CTG
                                ||| |||| |||||    |||
                                CCG TCTA ACCAT    GAC
                                  G   A    G___
GAM43   FLJ13769 3' CAGAATCCAGGTCTTACC    46604    C       TGTAGG
                                GG AAGATCTGG     CTG
                                || |||||||||     |||
                                CC TTCTGGACC     GAC
                                 A        TAA___
GAM43   FLJ14840 5' CAGCTCTGCAGACCCTGC    51657    AGA   GGT   _
                                GCA   TCT   GTAG GCTG
                                |||   |||   |||| ||||
                                CGT   AGA   CGTC CGAC
                                  CCC   ___    T
GAM43   FLJ20093 3' CTGTCACCAGATATTGCC    34554      G      _
                                GGCAA ATCTGGTG TAG
                                ||||| |||||||| |||
                                CCGTT TAGACCAC GTC
                                   A       T
GAM43   FLJ20097 3' CAGCCTACACCTCTAACTGCT  34560     AGATCT
                                GGCA     GGTGTAGGCTG
                                ||||     ||||||||||
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                                TCGT     CCACATCCGAC
                                  CAATCT
GAM43   FLJ20507  3'  CAGCCTACACCCAGCC     60211     AAGATCT
                                GGC      GGTGTAGGCTG
                                |||      ||||||||||
                                CCG      CCACATCCGAC
                                  AC_____
GAM43   FLJ20507  3'  CAGCCTACACCCAGCC     35276     AAGATCT
                                GGC      GGTGTAGGCTG
                                |||      ||||||||||
                                CCG      CCACATCCGAC
                                  AC_____
GAM43   FLJ21126  3'  AGTCCCAGTCTTGCC      90326       T   TGTA
                                GGCAAGA CTGG   GGCT
                                ||||||| ||||   ||||
                                CCGTTCT GACC   CTGA
                                  _   _____
GAM43   FLJ21588  3'  CAGCGGCACCAGACTCACC   49833    CA  A      AG
                                GG  AG TCTGGTGT  GCTG
                                ||  || ||||||||  ||||
                                CC  TC AGACCACG  CGAC
                                 AC  _       G_
GAM43   FLJ22362  3'  CAGCTGCCCCACATCTTGCC  43071        C   T   G
                                GGCAAGAT TGG GTAG CTG
                                |||||||| ||| |||| |||
                                CCGTTCTA ACC CGTC GAC
                                     C   C   _
GAM43   FLJ22684  3'  CCTGCAACCTCTGCC      46789     A  TCT   _
                                GGCA GA   GGT GTAGG
                                |||| ||   ||| |||||
                                CCGT CT   CCA CGTCC
                                  _ ____   A
GAM43   FLJ23093  3'  AGCTCCCAGATCTGCC     44976     A      TGTA
                                GGCA GATCTGG    GGCT
                                |||| |||||||    ||||
                                CCGT CTAGACC    TCGA
                                  _      C____
GAM43   FLJ32934  3'  CAGCCTGTCAGCATTCTCACC  58225    CA   TC  G  _
                                GG  AGA  TG TG TAGGCTG
                                ||  |||  || || |||||||
                                CC  TCT  AC AC GTCCGAC
                                 AC   T_  G  T
GAM43   FYCO1     3'  CAGCCCACACCAGACCTCC    44488    CA  A      A
                                GG  AG TCTGGTGT GGCTG
                                ||  || ||||||||| |||||
                                CC  TC AGACCACA CCGAC
                                 __ C       C
GAM43   HYA22     3'  CAGCCCCTTGCTAGATATTACC 19419    C  G       TA_
                                GG AA ATCTGGTG   GGCTG
                                || || ||||||||   |||||
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                                CC TT TAGATCGT   CCGAC
                                 A  A       TCC
GAM43   IKKE     3'  CAGCCTACCTCCCTCCTGGC   25748    G  A  TCT  T_
                                G CA GA   GG  GTAGGCTG
                                | || ||   ||  ||||||||
                                C GT CT   CC  CATCCGAC
                                 G  C  C__  TC
GAM43   IL-17RC  3'  CAGCGGCGCCAGACCCTGC    51199     AGA       AG
                                GCA   TCTGGTGT  GCTG
                                |||   ||||||||  ||||
                                CGT   AGACCGCG  CGAC
                                  CCC       G_
GAM43   KIAA0169 3'  CAGCCTACACTGCACCCTGGC  72815    A  ATCT_
                                GC AG    GGTGTAGGCTG
                                || ||    ||||||||||
                                CG TC    TCACATCCGAC
                                 G  CCACG
GAM43   KIAA0446 5'  CAGCCTAGATTTTCCAATCTTG 68857         C  ____ G
            CC                    GGCAAGAT TGG    T TAGGCTG
                                |||||||| |||    | |||||||
                                CCGTTCTA ACC    A ATCCGAC
                                    _  TTTT G
GAM43   KIAA1054 3'  CAGGGACCCAGATCTTGCT    68430           T  AGG
                                GGCAAGATCTGG GT   CTG
                                |||||||||||| ||   |||
                                TCGTTCTAGACC CA   GAC
                                      _ GG_
GAM43   KIAA1196 3'  CCTCAGCAGCCCTTGCC     61463       AT   G  T
                                GGCAAG  CTG TG AGG
                                ||||||  ||| || |||
                                CCGTTC  GAC AC TCC
                                   CC   G  _
GAM43   KIAA1203 3'  AGCCCTACATCTTGCC      71634        C   TGTA
                                GGCAAGAT TGG    GGCT
                                |||||||| |||    ||||
                                CCGTTCTA ATC    CCGA
                                    C  _____
GAM43   KIAA1219 3'  CAGCCAACAGATCCCTGCC    61366      A_     GTGTA
                                GGCA  GATCTG    GGCTG
                                ||||  ||||||    |||||
                                CCGT  CTAGAC    CCGAC
                                  CC     AA___
GAM43   KIAA1271 3'  CAGCCTCCAGGGATCT      69539       GG  T
                                AGATCT  TG AGGCTG
                                ||||||  || ||||||
                                TCTAGG  AC TCCGAC
                                   G_  C
GAM43   KIAA1322 3'  CAGCCTAGACAATCTCGTC    72733     A   CTG  G
                                GGC AGAT   GT TAGGCTG
                                ||| ||||   || |||||||
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                                CTG TCTA   CA ATCCGAC
                                  C    A__  G
GAM43   KIAA1538 3' CTTTCACCAGATGCC      71544      AGA      T
                                GGCA   TCTGGTG AGG
                                ||||   ||||||| |||
                                CCGT   AGACCAC TTC
                                  ___      T
GAM43   KIAA1577 3' AGCCTTCTATCTTGCC      64470        CT  TGT
                                GGCAAGAT  GG   AGGCT
                                ||||||||  ||   |||||
                                CCGTTCTA  CT   TCCGA
                                    T_  ___
GAM43   KIAA1742 3' CAGCCTCCTGGGTCTCACC   77658    CA    TG TGT
                                GG  AGATC  G   AGGCTG
                                ||  |||||  |   ||||||
                                CC  TCTGG  C   TCCGAC
                                 AC     GT C__
GAM43   KIAA1822 3' CAGGGACTCCGATCTTGCC   67563         T  T  AGG
                                GGCAAGATC GG GT   CTG
                                |||||||||  || ||   |||
                                CCGTTCTAG CC CA   GAC
                                     _  T  GG_
GAM43   KIAA1858 3' CAGCCCACACCCCTGCGCC   67134     A_  ATCT    A
                                GGC  AG    GGTGT GGCTG
                                |||  ||    ||||| |||||
                                CCG  TC    CCACA CCGAC
                                  CG  C___     C
GAM43   KIAA1908 5' CAGCCTCCTGCACCCCTGCC   73395     A ATCT    ___
                                GGCA G    GGTGT   AGGCTG
                                ||||  |   |||||   ||||||
                                CCGT C    CCACG   TCCGAC
                                  _ C___     TCC
GAM43   LGI4     3' CAGCCTACTGGACCTCC     57765    CA  A  TG  GT
                                GG  AG TC  GT  AGGCTG
                                ||  || ||  ||  ||||||
                                CC  TC AG  CA  TCCGAC
                                 __  C  GT  __
GAM43   LMOD1    5' CAGCCTGCTGGGACCCTGTC   24040     AGA   GGT
                                GGCA   TCT   GTAGGCTG
                                ||||   |||   ||||||||
                                CTGT   AGG   CGTCCGAC
                                  CCC   GT_
GAM43   MGC16491 3' CAGCCTGTGGTGATCCC     53637    CAA    T G GT
                                GG   GATC G T  AGGCTG
                                ||   |||| | |  ||||||
                                CC   CTAG T G  TCCGAC
                                 ___    _ G TG
GAM43   MGC3248  3' CAGCCTACCCTGTATTTGCC   50652       ATCT  T
                                GGCAAG    GG GTAGGCTG
                                ||||||    || ||||||||
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                                CCGTTT   CC CATCCGAC
                                   ATGT  _
GAM43   NUP54    5'  CAGCCTACACAAGCTCCTACC  60097    CAA  T  G
                                GG   GA CT GTGTAGGCTG
                                ||   || || ||||||||||
                                CC   CT GA CACATCCGAC
                                 ATC  C  A
GAM43   PELI2    3'  CAGAAAGGCCAGATTTTACC   41180    C        GTAGG
                                GG AAGATCTGGT    CTG
                                || ||||||||||    |||
                                CC TTTTAGACCG    GAC
                                 A        GAAA_
GAM43   PI4KII   3'  AGCCATAGGCCCTGCC      37339      A ATCT   G  _
                                GGCA G    GGT TA GGCT
                                |||| |    ||| || ||||
                                CCGT C    CCG AT CCGA
                                  _ _____  G  A
GAM43   SCYA19   3'  CTGCACCAGACCTGACC     20781    CA  A
                                GG  AG TCTGGTGTAG
                                ||  || ||||||||||
                                CC  TC AGACCACGTC
                                 AG  C
GAM43   SDC3     3'  CAGCCTCACACAGATCTTCC   27742    C       _   T
                                GG AAGATCTG GTG AGGCTG
                                || |||||||| ||| ||||||
                                CC TTCTAGAC CAC TCCGAC
                                  _       A   _
GAM43   SPEC1    3'  CAGCCCAGAAGAAATGCT    39607     AGA   GG  TA
                                GGCA   TCT  TG  GGCTG
                                ||||   |||  ||  |||||
                                TCGT   AGA  AC  CCGAC
                                  AA_   AG  __
GAM43   TSPAN-5  3'  AGCCTGCAGTCTCGCC      19155     A   CTGG
                                GGC AGAT    TGTAGGCT
                                ||| ||||    ||||||||
                                CCG TCTG    ACGTCCGA
                                  C   _____
GAM43   VEZATIN  3'  CAGCTGTCACCAGATTTTACC  34224    C        TA
                                GG AAGATCTGGTG  GGCTG
                                || ||||||||||  |||||
                                CC TTTTAGACCAC  TCGAC
                                 A          TG
GAM43   LOC112868 3'  CAGCCCCTCATGTCTTGCC   72891        C   TGTA
                                GGCAAGAT TGG    GGCTG
                                |||||||| |||    |||||
                                CCGTTCTG ACT    CCGAC
                                     T  CC__
GAM43   LOC121838 5'  CAGAAGAAACCAGCCTTGCC  75996       AT    GTAGG
                                GGCAAG  CTGGT    CTG
                                ||||||  |||||    |||
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                                CCGTTC  GACCA    GAC
                                   C_    AAGAA
GAM43   LOC122792 3' CAGTTAGTCCAGATCTGCC   59143     A     TGTA
                                GGCA GATCTGG   GGCTG
                                |||| |||||||   |||||
                                CCGT CTAGACC   TTGAC
                                  _     TGA_
GAM43   LOC125268 3' CAGCCTACACCACCTC     76071    TC
                                GA  TGGTGTAGGCTG
                                ||  ||||||||||||
                                CT  ACCACATCCGAC
                                 CC
GAM43   LOC132332 3' AGCCTACATCCTAGC      76161    A  ATCT
                                GC AG   GGTGTAGGCT
                                || ||   ||||||||||
                                CG TC   CTACATCCGA
                                 A  ____
GAM43   LOC145082 5' CAGTGAGCCAAGATCTTGCC  83236         _  GTAG
                                GGCAAGATCT GGT   GCTG
                                |||||||||| |||   ||||
                                CCGTTCTAGA CCG   TGAC
                                      A  AG__
GAM43   LOC146268 3' CAGTGTGGCCAGATTT     77803         G  G
                                AGATCTGGT TA GCTG
                                ||||||||| || ||||
                                TTTAGACCG GT TGAC
                                      _ G
GAM43   LOC146669 3' AGCCTGGGACCTTGCT     78050       A  GGTG
                                GGCAAG TCT   TAGGCT
                                |||||| |||   ||||||
                                TCGTTC AGG   GTCCGA
                                   C  ____
GAM43   LOC146795 3' CCTGTGCAGGTCTTGCC    78131         G TG
                                GGCAAGATCT G  TAGG
                                |||||||||| |  ||||
                                CCGTTCTGGA C  GTCC
                                      _ GT
GAM43   LOC148545 3' CAGCCTAAACATTTTGCC    78897        CTG  G
                                GGCAAGAT   GT TAGGCTG
                                ||||||||   || |||||||
                                CCGTTTTA   CA ATCCGAC
                                     ___  A
GAM43   LOC149832 5' CAGCCCCCAGAGGACCTTGCC 84697       A  GG  TA
                                GGCAAG TCT  TG  GGCTG
                                |||||| |||  ||  |||||
                                CCGTTC AGG  AC  CCGAC
                                   C  AG  CC
GAM43   LOC150378 5' CAGCCTACGCTCCCCAGCC   79740    AAGATCT
                                GGC     GGTGTAGGCTG
                                |||     ||||||||||
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                                CCG      TCGCATCCGAC
                                  ACCCC__
GAM43   LOC151632 5'  CAGCCTGCCAACCCTGC     85465     A ATCT  __
                                GCA G    GGT  GTAGGCTG
                                ||| |    |||  ||||||||
                                CGT C    CCA  CGTCCGAC
                                  _ _____   AC
GAM43   LOC152317 5'  CAGTCTGTCACCAGATCTTG   85639           _
                                CAAGATCTGGTG TAGGCTG
                                |||||||||||| |||||||
                                GTTCTAGACCAC GTCTGAC
                                       T
GAM43   LOC153243 3'  CAGCCTACCCCTCCTGC     80793     A  TCT  T
                                GCA GA   GG GTAGGCTG
                                ||| ||   || ||||||||
                                CGT CT   CC CATCCGAC
                                  C  C__  _
GAM43   LOC159036 3'  CAGCCTATGGATAGACCC    86971    CAAG    GGT
                                GG    ATCT   GTAGGCTG
                                ||    ||||   ||||||||
                                CC    TAGG   TATCCGAC
                                 CAGA   ___
GAM43   LOC159184 3'  TCTACACCAGTTCCC       60053    CAA  T
                                GG   GA CTGGTGTAGG
                                ||   || ||||||||||
                                CC   CT GACCACATCT
                                 ___  T
GAM43   LOC162333 5'  CAGCAGTGCCCAAATCTGTACC 87123    CA_   C   T   G_
                                GG   AGAT TGG GTA  GCTG
                                ||   |||| ||| |||  ||||
                                CC   TCTA ACC CGT  CGAC
                                 ATG    A   _   GA
GAM43   LOC166793 5'  CAGCCTGTGAATGACTCTGCC  59226      A  _  TGG GT
                                GGCA GA TC   T  AGGCTG
                                |||| || ||   |  ||||||
                                CCGT CT AG   G  TCCGAC
                                  _  C  TAA TG
GAM43   LOC170132 5'  CTGCACCAGACCCTGACC    82573    CA  A_
                                GG  AG  TCTGGTGTAG
                                ||  ||  ||||||||||
                                CC  TC  AGACCACGTC
                                 AG  CC
GAM43   LOC196743 3'  CAGCCTACTCTGTTCCACC    87506    CAA  TCT  T
                                GG   GA   GG GTAGGCTG
                                ||   ||   || ||||||||
                                CC   CT   TC CATCCGAC
                                 AC_  TG_  T
GAM43   LOC196955 5'  CAGCCTACATCTTTCTCC    77368    CA   TCT
                                GG  AGA   GGTGTAGGCTG
                                ||  |||   ||||||||||
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                                CC  TCT   CTACATCCGAC
                                 __   TT_
GAM43   LOC199796 5'  CAGCCCTGCATCGACCT     74450    A  T       _
                                AG TC GGTGTAGG CTG
                                || || |||||||| |||
                                TC AG CTACGTCC GAC
                                 C  _       C
GAM43   LOC200470 5'  CAGCCTTGGGATCTCAGCC    90058     A_     GGTGT
                                GGC  AGATCT    AGGCTG
                                |||  ||||||    ||||||
                                CCG  TCTAGG    TCCGAC
                                  AC     GT___
GAM43   LOC221876 5'  CAGTGGGCCAGAGCTCGCC    93919     A  A     G AG
                                GGC AG TCTGGT T  GCTG
                                ||| || |||||| |  ||||
                                CCG TC AGACCG G  TGAC
                                  C  G     G __
GAM43   LOC221962 3'  CAGCCTGGGCTACAGATCTTGT 92680           __  G
          C                      GGCAAGATCTG  GT TAGGCTG
                                ||||||||||  || |||||||
                                CTGTTCTAGAC  CG GTCCGAC
                                       AT  G
GAM43   LOC253216 5'  AGCCAGCAGCCCTGCC      94954      A ATCT  _   A
                                GGCA G    GG TGT GGCT
                                |||| |    || ||| ||||
                                CCGT C    CC ACG CCGA
                                  _ _____  G   A
GAM43   LOC254014 5'  AGCCCTCGGATCTGCC      95205      A      TGTA
                                GGCA GATCTGG    GGCT
                                |||| |||||||    ||||
                                CCGT CTAGGCT    CCGA
                                  _      C___
GAM43   LOC254423 3'  CAGCCTACACCATCCATTTGC  97435       ATC_
                                GCAAG    TGGTGTAGGCTG
                                |||||    ||||||||||||
                                CGTTT    ACCACATCCGAC
                                   ACCT
GAM43   LOC255330 5'  GGCTGGTACCAGGTCTCACC   95814    CA        TA
                                GG  AGATCTGGTG  GGCT
                                ||  ||||||||||  ||||
                                CC  TCTGGACCAT  TCGG
                                 AC         GG
GAM43   LOC257449 3'  CAGCCTCCTGGGTCTCACC    62719    CA    TG TGT
                                GG  AGATC  G   AGGCTG
                                ||  |||||  |   ||||||
                                CC  TCTGG  C   TCCGAC
                                 AC    GT C__
GAM43   LOC51312  5'  CAGCCTCCTGCGCCCCGCC    33506     AAGATCT    ___
                                GGC      GGTGT   AGGCTG
                                |||      |||||   ||||||
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                                CCG      CCGCG   TCCGAC
                                  CC_____    TCC
GAM43   LOC90750 3'  CAGTGGTCCAGACTTGCC    63919       A    TGTAG
                                GGCAAG TCTGG    GCTG
                                ||||||| |||||    ||||
                                CCGTTC AGACC    TGAC
                                   _    TGG__
GAM43   LOC91266 5'  CAGTTTTGCCAGATCCAACC   65410    CAA       T
                                GG   GATCTGGTG AGGCTG
                                ||   ||||||||| |||||||
                                CC   CTAGACCGT TTTGAC
                                 AAC       _
GAM44   ADAMTS4   3'  TCTTGAACTCCTGACCTCA   17522            TG
                                TGAGGTCAGGAGTT  AGA
                                |||||||||||||  |||
                                ACTCCAGTCCTCAA  TCT
                                         GT
GAM44   AQP6     3'  GTCTCAAACTCCTGACCT    7959
                                AGGTCAGGAGTTTGAGAC
                                ||||||||||||||||||
                                TCCAGTCCTCAAACTCTG

GAM44   AQP6     3'  GTCTCAAACTCCTGACCT    53939
                                AGGTCAGGAGTTTGAGAC
                                ||||||||||||||||||
                                TCCAGTCCTCAAACTCTG

GAM44   ARSF     5'  GCTGGTCTCGAACTCCCGACCT 64601        A
            CA                    TGAGGTC GGAGTTTGAGACTAGC
                                ||||||| ||||||||||||||||
                                ACTCCAG CCTCAAGCTCTGGTCG
                                     C
GAM44   ATP1B2    3'  GCTGGTCTCGAACTCCCGACCT 8053         A
            CA                    TGAGGTC GGAGTTTGAGACTAGC
                                ||||||| ||||||||||||||||
                                ACTCCAG CCTCAAGCTCTGGTCG
                                     C
GAM44   ATP7A    3'  CTGGTCTTAAACTCCTAACCTC 3522        C
            A                     TGAGGT AGGAGTTTGAGACTAG
                                ||||||| |||||||||||||||
                                ACTCCA TCCTCAAATTCTGGTC
                                   A
GAM44   AXL      3'  GCTGGTCTAAAACTCCTGACCT 41600             G
            CA                    TGAGGTCAGGAGTTT AGACTAGC
                                ||||||||||||||| ||||||||
                                ACTCCAGTCCTCAAA TCTGGTCG
                                         A
GAM44   AXL      3'  GCTGGTCTAAAACTCCTGACCT 8103              G
            CA                    TGAGGTCAGGAGTTT AGACTAGC
                                ||||||||||||||| ||||||||
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                                ACTCCAGTCCTCAAA TCTGGTCG
                                      A
GAM44   C7      3'  GTCTCCAACTCCTGACCTCA  5166            T
                                TGAGGTCAGGAGTT GAGAC
                                |||||||||||||| |||||
                                ACTCCAGTCCTCAA CTCTG
                                      C
GAM44   CBFA2T2  3'  GCTGGTCTCAAACCCCGGACCT 17473       A  A
           CA                     TGAGGTC GG GTTTGAGACTAGC
                                |||||||  || ||||||||||||
                                ACTCCAG CC CAAACTCTGGTCG
                                   G  C
GAM44   CCNF     3'  GCTAGTCTCGAACTCATGACCT 8320         G
           CA                     TGAGGTCA GAGTTTGAGACTAGC
                                |||||||| ||||||||||||||
                                ACTCCAGT CTCAAGCTCTGATCG
                                    A
GAM44   CHRNB4   3'  GCTGATTTCGAACTCCTGACCT 5633               C
           CA                     TGAGGTCAGGAGTTTGAGA TAGC
                                |||||||||||||||||| ||||
                                ACTCCAGTCCTCAAGCTTT GTCG
                                      A
GAM44   CLECSF12 3'  TAGTCCCGAACTCCTGACCTCA 76699            A
                                TGAGGTCAGGAGTTTG GACTA
                                |||||||||||||| |||||
                                ACTCCAGTCCTCAAGC CTGAT
                                      C
GAM44   CORO2B   3'  CTCTAACCTCCTGACCTCA   64571          _  T
                                TGAGGTCAGGAG TT GAG
                                |||||||||||| || |||
                                ACTCCAGTCCTC AA CTC
                                      C  T
GAM44   CYP1A2   3'  CTAGTCTCAAACTCCTGACCTC 69107
           A                     TGAGGTCAGGAGTTTGAGACTAG
                                |||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGATC

GAM44   CYP1A2   3'  GCTTGTCTCGAACTCCTGACCC 69118    A           T
           CA                     TG GGTCAGGAGTTTGAGAC AGC
                                || ||||||||||||||| |||
                                AC CCAGTCCTCAAGCTCTG TCG
                                 C             T
GAM44   CYP1A2   3'  CTAGTCTCAAACTCCTGACCTC 5687
           A                     TGAGGTCAGGAGTTTGAGACTAG
                                |||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGATC

GAM44   CYP1A2   3'  GCTTGTCTCGAACTCCTGACCC 5698     A           T
           CA                     TG GGTCAGGAGTTTGAGAC AGC
                                || ||||||||||||||| |||
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                                AC CCAGTCCTCAAGCTCTG TCG
                                 C             T
GAM44   DFFB    3'  GCTGGTCTCAAACTCCTGACCT 87391
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   DFFB    3'  GCTGTTCTCGAACTCCTGACCT 87392                C
            CA                    TGAGGTCAGGAGTTTGAGA TAGC
                                  |||||||||||||||||| ||||
                                  ACTCCAGTCCTCAAGCTCT GTCG
                                               T
GAM44   DISC1   3'  GTCTCAAACTCCTGACCTCA   37890
                                  TGAGGTCAGGAGTTTGAGAC
                                  ||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTG

GAM44   DSP     3'  TCTCAAACCCCCAACCCA    15342    A   CA  A
                                  TG GGT  GG GTTTGAGA
                                  || |||  || ||||||||
                                  AC CCA  CC CAAACTCT
                                   _   AC  C
GAM44   EPB72   3'  GCTAGTCACGAACTCCTAACCT 14605        C        A
            CA                    TGAGGT AGGAGTTTG GACTAGC
                                  ||||||| ||||||||| |||||||
                                  ACTCCA TCCTCAAGC CTGATCG
                                      A        A
GAM44   EVC     3'  TCTCGAACTCCTGACCTCA    27300
                                  TGAGGTCAGGAGTTTGAGA
                                  ||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCT

GAM44   FCAR    3'  GCTGGTCTCGAACTCCTGACCT 55751
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   FCAR    3'  GCTGGTCTCGAACTCCTGACCT 55762
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   FCAR    3'  GCTGGTCTCGAACTCCTGACCT 55773
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   FCAR    3'  GCTGGTCTCGAACTCCTGACCT 55784
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   FCAR    3'  GCTGGTCTCGAACTCCCGACCT 55802        A
            CA                    TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
                                  ACTCCAG CCTCAAGCTCTGGTCG
                                     C
GAM44   FCAR    3'  GCTGGTCTCGAACTCCTGACCT 8856
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   FZD4    3'  GCTGGTCTCGAACTCCTGACCT 24145
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   G6PC    3'  GCTGGTCTCGAACTCCTGACCT 3830
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   GRAF    3'  GCTGATCTCGAACTCCTGACCT 30565                C
            CA                    TGAGGTCAGGAGTTTGAGA TAGC
                                  |||||||||||||||||| ||||
                                  ACTCCAGTCCTCAAGCTCT GTCG
                                              A
GAM44   HCN4    3'  GCCAGTCCCAGCCTGACCTC   18490          AGT   A   A
                                  GAGGTCAGG   TTG GACT GC
                                  |||||||||   ||| |||| ||
                                  CTCCAGTCC   GAC CTGA CG
                                        ___   C   C
GAM44   HCS     3'  GCTGGTCTCAAACTCCTGAGCT 38477      G
            CA                    TGAG TCAGGAGTTTGAGACTAGC
                                  |||| ||||||||||||||||||
                                  ACTC AGTCCTCAAACTCTGGTCG
                                    G
GAM44   HSPA5   3'  CTAGTCTTCCCTTACCTCA   18081        C   AGTTT
                                  TGAGGT AGG     GAGACTAG
                                  |||||| |||     ||||||||
                                  ACTCCA TCC     TTCTGATC
                                     T   C_____
GAM44   IFNAR2  3'  GCTGGTCTCGAACTCCTGACCT 6044
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   IL11    3'  GCTGGTTTCGAACTCCTGACCT 5329
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTTTGGTCG

GAM44   JAK3    3'  GCTGATCTCGAACTCCTAACCT 4005        C         C
            CA                  TGAGGT AGGAGTTTGAGA TAGC
                                |||||| |||||||||||| ||||
                                ACTCCA TCCTCAAGCTCT GTCG
                                  A         A
GAM44   KMO     3'  GCCAGTCTCAAACTCCTGGCCT 13450                A
            CA                  TGAGGTCAGGAGTTTGAGACT GC
                                |||||||||||||||||||| ||
                                ACTCCGGTCCTCAAACTCTGA CG
                                            C
GAM44   MAK     3'  GCTGGTCTCAAACTCCTGACCT 19763
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM44   MEFV    3'  GCCGGTCTCAAACTCCTGACCT 4139                 TA
            CA                  TGAGGTCAGGAGTTTGAGAC  GC
                                |||||||||||||||||||  ||
                                ACTCCAGTCCTCAAACTCTG  CG
                                            GC
GAM44   MEFV    3'  GCTGGTCTCGAACTCCTGACCT 4148
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   MFI2    3'  GCTGGTCTCAAACCCCCAGCCT 52817       CA  A
            CA                  TGAGGT  GG GTTTGAGACTAGC
                                ||||||  || ||||||||||||
                                ACTCCG  CC CAAACTCTGGTCG
                                  AC  C
GAM44   MICB    3'  GCCCAGTTTCAAACTCCTGACC 19827                A_
            TCA                  TGAGGTCAGGAGTTTGAGACT  GC
                                |||||||||||||||||||  ||
                                ACTCCAGTCCTCAAACTTTGA  CG
                                            CC
GAM44   MLANA   3'  GCTGGTCTCAAACTCCTGACCT 18588
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM44   NCOA6   5'  GCTAGTCTGGAACTCCTGAGCT 25970      G         G
            CA                  TGAG TCAGGAGTTT AGACTAGC
                                |||| |||||||||| ||||||||
                                ACTC AGTCCTCAAG TCTGATCG
                                  G         G
GAM44   NCOA6   5'  GCTGGTCTCAAACTCCTGACCT 25975
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAACTCTGGTCG

GAM44   NDRG3    3'  GCTGGTCTCAAACTCCTGACCT 49301
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   NQO1     3'  GCTGGTCTCAAACTCCTGACCT 6163
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   PDE6B    3'  GCTGGTCTCGAACTCCTGACCT 4287
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   PER2     3'  GCTGGTCTCGAACTCCTGACCT 43038
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   PIK3CD   3'  GCTGGTCTCGAACTCCTGACCT 17248
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   PRKR     3'  GCTGGTCTCAAACTCCTGACCT 10885
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   RAP1GA1  3'  CAGCCTCCTGGCCCCA      11250    A       T
                                  TG GGTCAGGAG TTG
                                  || ||||||||| |||
                                  AC CCGGTCCTC GAC
                                    C       C
GAM44   RGS9     5'  GCTAGCCTCAAACTCCTGGGCT 13834      G          A
            CA                    TGAG TCAGGAGTTTGAG CTAGC
                                  |||| |||||||||||| |||||
                                  ACTC GGTCCTCAAACTC GATCG
                                     G          C
GAM44   RHD      3'  GCTGATCTCAAACTCCTGACCT 32310               C
            CA                    TGAGGTCAGGAGTTTGAGA TAGC
                                  |||||||||||||||||| ||||
                                  ACTCCAGTCCTCAAACTCT GTCG
                                                     A
GAM44   RHD      3'  GCTGATCTCAAACTCCTGACCT 32619               C
            CA                    TGAGGTCAGGAGTTTGAGA TAGC
                                  |||||||||||||||||| ||||
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                                ACTCCAGTCCTCAAACTCT GTCG
                                                    A
GAM44   RP2      3'  GCTGGTCTCGAACTCCTGACCT 22620
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   RPP30    3'  GTCTCAATCTCCTGACCTCA  21170          T
                                  TGAGGTCAGGAG TTGAGAC
                                  |||||||||||| |||||||
                                  ACTCCAGTCCTC AACTCTG
                                         T
GAM44   SAS      3'  GCTGGTCTCGAACTCCTGACCT 19957
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   SCML2    3'  GCTGGTCTCAAACTCCTGACCT 20321
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   SEDL     3'  GCTGGTTTCAAACTCCTGACCT 27350
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTTTGGTCG

GAM44   SFRP1    3'  CAGTCTCAGATGCCCC      11564    TCA  A       A
                                  GG   GG GTTTGAGACT G
                                  ||   || |||||||||| |
                                  CC   CC TAGACTCTGA C
                                   ___  G         C
GAM44   SH3BP2   3'  GCTGGTCTCGAACTCCTGACCT 11607
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   SHOX     3'  GCTGGTCTCGAACTCCTGACCT 22541
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   SIL      3'  GCTGGTCTCAAACTCCCGACCT 11694        A
            CA                    TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
                                  ACTCCAG CCTCAAACTCTGGTCG
                                      C
GAM44   SLA2     3'  GCTGGTGTCGAACTCCTGACCT 49903             G
            CA                    TGAGGTCAGGAGTTTGA ACTAGC
                                  |||||||||||||||| ||||||
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                                ACTCCAGTCCTCAAGCT TGGTCG
                                      G
GAM44   SLC6A12  3'  CAAACCCCTGACTTCA      11731          A
                                TGAGGTCAGG GTTTG
                                |||||||||| |||||
                                ACTTCAGTCC CAAAC
                                      C
GAM44   SNX15    3'  GCTGGTCTCGAACTCCTGACCT 73746
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   SPN      3'  GCTGGTCTCAAACTCCTGACCT 11924
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   SULT2B1  5'  GCTGGTCTCAAACTCCTGACCT 16028
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   TAT      3'  GCTGGTCTCAAACTCCTGACCT 4472
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   TCOF1    3'  AGCTCCCATGACCTCA      4484          __
                                TGAGGTCA  GGAGTT
                                ||||||||  ||||||
                                ACTCCAGT  CCTCGA
                                     AC
GAM44   TES      3'  GCTGGTCTCAAACTCCTGACCT 72009
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   TIM3     3'  GTCTCAAACTCCTGACCTCA   51347
                                TGAGGTCAGGAGTTTGAGAC
                                |||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTG

GAM44   TMPRSS3  3'  GCTGCTCTCAAACCCCTGACCT 50529          A       C
           CA                     TGAGGTCAGG GTTTGAGA TAGC
                                  |||||||||| |||||||| ||||
                                  ACTCCAGTCC CAAACTCT GTCG
                                        C       C
GAM44   TMPRSS3  3'  GCTGCTCTCAAACCCCTGACCT 50508          A       C
           CA                     TGAGGTCAGG GTTTGAGA TAGC
                                  |||||||||| |||||||| ||||
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                                ACTCCAGTCC CAAACTCT GTCG
                                      C       C
GAM44   TMPRSS3   3'  GCTGCTCTCAAACCCCTGACCT 43797          A       C
          CA                    TGAGGTCAGG GTTTGAGA TAGC
                                |||||||||| |||||||| ||||
                                ACTCCAGTCC CAAACTCT GTCG
                                      C       C
GAM44   TNFRSF10B 3'  GCTGGTCTCGAACTCCTGACCT 13874
          CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   TRAF5    3'  GCTGATCTCAAACTCCTGACCT 16083              C
          CA                    TGAGGTCAGGAGTTTGAGA TAGC
                                |||||||||||||||||| ||||
                                ACTCCAGTCCTCAAACTCT GTCG
                                        A
GAM44   TRPM6    3'  GCTGGTCTCAAACTCCTGACCT 34543
          CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM44   TRPV1    3'  GCTGGTCTCGAACTCCTGACCT 38091
          CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   TRPV1    3'  GCTGGTCTCGAACTCCTGACCT 54875
          CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   TRPV1    3'  GCTGGTCTCGAACTCCTGACCT 54809
          CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   TRPV1    3'  GCTGGTCTCGAACTCCTGACCT 54842
          CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   VHL      3'  GCTGGTTTCAAACTCCTGACCT 5075
          CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTTTGGTCG

GAM44   XRCC2    3'  GCTGGTCTCGAACTCCTGACCT 18328
          CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   ZNF157   3'  GCTGGTCTCTAACTCCTGACCT 12879            T
            CA                  TGAGGTCAGGAGTT GAGACTAGC
                                |||||||||||||| |||||||||
                                ACTCCAGTCCTCAA CTCTGGTCG
                                       T
GAM44   AAK1     3'  GCTGGTCTCGAACTCCTGACCT 29851
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   ARHGAP5  5'  GCTGGTGTCGAACTCCCAACCT 77077      CA       G
            CA                  TGAGGT  GGAGTTTGA ACTAGC
                                ||||||  ||||||||| ||||||
                                ACTCCA  CCTCAAGCT TGGTCG
                                   AC       G
GAM44   ATP1B4   3'  GCTGGTCTCGAACTCCTGACCT 23824
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   BA108L7.2 3'  GCTAGTCTCGAACTCCTGACCT 48264
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGATCG

GAM44   C13orf1   3'  GCTGGTCTCAAACTCCTGACCT 39972
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM44   C20orf142 3'  GCTGGTCTCAAACTCCTGACCG 74779    A
            CA                  TG GGTCAGGAGTTTGAGACTAGC
                                || ||||||||||||||||||||
                                AC CCAGTCCTCAAACTCTGGTCG
                                  G
GAM44   C21orf25  3'  GCTGGTCTCGAACTCCTGACCT 63551
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   C9orf9    3'  GTCTCAATCTCCTGACCTCA   38522          T
                                TGAGGTCAGGAG TTGAGAC
                                |||||||||||| |||||||
                                ACTCCAGTCCTC AACTCTG
                                       T
GAM44   CDC14B    3'  GCTGGTCTCGAACTCCTGACCT 52857
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   CHRAC1   3'  GCTTGTCTCAAACTCCTAACCT 33875       C          T
            CA                  TGAGGT AGGAGTTTGAGAC AGC
                                |||||| |||||||||||||| |||
                                ACTCCA TCCTCAAACTCTG TCG
                                   A          T
GAM44   CPSF2    3'  GCTGGCCTCAAACTCCCGACCT 61590        A        A
            CA                  TGAGGTC GGAGTTTGAG CTAGC
                                ||||||| |||||||||| |||||
                                ACTCCAG CCTCAAACTC GGTCG
                                   C        C
GAM44   CPSF2    3'  GCTGGTCTCAAACTCCTGACCT 61594
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM44   CSL4     3'  GCTGTCTCAAACTCCTGGCCTC 32114              T
            A                    TGAGGTCAGGAGTTTGAGAC AGC
                                 |||||||||||||||||||| |||
                                 ACTCCGGTCCTCAAACTCTG TCG
                                                 _
GAM44   DBR1     3'  GTCTCCAACTCCTGACCTCA   32536           T
                                TGAGGTCAGGAGTT GAGAC
                                |||||||||||||| |||||
                                ACTCCAGTCCTCAA CTCTG
                                      C
GAM44   DCOHM    3'  GCTGATCTCAAACTCCTGGCCT 49606              C
            CA                  TGAGGTCAGGAGTTTGAGA TAGC
                                |||||||||||||||||| ||||
                                ACTCCGGTCCTCAAACTCT GTCG
                                      A
GAM44   DKFZp434A2417 3'  GCTGATCTCAAACTCCCAACCT 66105       CA         C
            CA                  TGAGGT  GGAGTTTGAGA TAGC
                                |||||| ||||||||||| ||||
                                ACTCCA  CCTCAAACTCT GTCG
                                   AC         A
GAM44   DKFZP434J037 3'  GCTGGTCTCAAACTCCCGACCT 48217       A
            CA                  TGAGGTC GGAGTTTGAGACTAGC
                                ||||||| ||||||||||||||||
                                ACTCCAG CCTCAAACTCTGGTCG
                                   C
GAM44   DKFZP564O0423 3'  GCTGTTCTCAAACTCCTGGCCT 91695              C
            CA                  TGAGGTCAGGAGTTTGAGA TAGC
                                |||||||||||||||||| ||||
                                ACTCCGGTCCTCAAACTCT GTCG
                                      T
GAM44   DSCR6    3'  TTTGAACTCCTGACCTCA    38555           TG
                                TGAGGTCAGGAGTT  AG
                                |||||||||||||  ||
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                                ACTCCAGTCCTCAA  TT
                                      GT
GAM44   EVI5    3'  GCTGATCTCAAACTTCTGACCT 19002              C
          CA                    TGAGGTCAGGAGTTTGAGA TAGC
                                |||||||||||||||||| ||||
                                ACTCCAGTCTTCAAACTCT GTCG
                                     A
GAM44   EVI5    3'  GCTGGTCTCGAACTCCTAACCT 19004       C
          CA                    TGAGGT AGGAGTTTGAGACTAGC
                                ||||||| ||||||||||||||||
                                ACTCCA TCCTCAAGCTCTGGTCG
                                  A
GAM44   FBP17   3'  GCTGGTCTCAAACTCCTGACCT 72799
          CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM44   FLJ10232 3'  GCTGGTCCCGAACTCCTGACCT 35928             A
          CA                    TGAGGTCAGGAGTTTG GACTAGC
                                |||||||||||||||| |||||||
                                ACTCCAGTCCTCAAGC CTGGTCG
                                      C
GAM44   FLJ10298 3'  GCTGGTCTCAAACTCCTGACCT 35992
                                AGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                TCCAGTCCTCAAACTCTGGTCG

GAM44   FLJ10607 3'  GCCGGTCTCAAACTCCTGAGCT 77116      G          TA
          CA                    TGAG TCAGGAGTTTGAGAC  GC
                                |||| ||||||||||||||  ||
                                ACTC AGTCCTCAAACTCTG  CG
                                  G           GC
GAM44   FLJ10901 3'  GCTGGTCTCGAACTCCTGACCT 36831
          CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   FLJ12363 3'  GCTGGTCTCAAACTCCTGACCT 49687
          CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM44   FLJ12649 3'  GCTAGTCTCGAAATCCTGGCCT 44779          G
          CA                    TGAGGTCAGGA TTTGAGACTAGC
                                |||||||||| ||||||||||
                                ACTCCGGTCCT AAGCTCTGATCG
                                     A
GAM44   FLJ12668 3'  GCTGGTCTCAAACTCCTGACCT 46519
          CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAACTCTGGTCG

GAM44   FLJ12687  3'  GCTGGTCTCAAACTCCTGACCT 46200
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   FLJ12787  3'  GCTGGTCTAAAACTCCTGACCT 49750            G
                CA                TGAGGTCAGGAGTTT AGACTAGC
                                  |||||||||||||| ||||||||
                                  ACTCCAGTCCTCAAA TCTGGTCG
                                            A
GAM44   FLJ12975  3'  TCTCGAACTCCTGACCTCA   69594
                                  TGAGGTCAGGAGTTTGAGA
                                  ||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCT

GAM44   FLJ13072  5'  GCTGGTCTCGAACTCCTGACCT 89819
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   FLJ13102  3'  GCTGGTCTCGAACTCCTGACCT 46014
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   FLJ14351  3'  GCCAGTCTTGAACTCCTGAGCT 45325     G       TG    A
                CA                TGAG TCAGGAGTT  AGACT GC
                                  |||| |||||||||  ||||| ||
                                  ACTC AGTCCTCAA  TCTGA CG
                                    G       GT    C
GAM44   FLJ20034  3'  GCTGGTCTCAAACTCCCGACCT 34376        A
                CA                TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
                                  ACTCCAG CCTCAAACTCTGGTCG
                                      C
GAM44   FLJ20034  3'  GTCTCAAACTCCCGACCTCA   34382        A
                                  TGAGGTC GGAGTTTGAGAC
                                  ||||||| ||||||||||||
                                  ACTCCAG CCTCAAACTCTG
                                      C
GAM44   FLJ20419  3'  CAAACTCCCGCCTCA      35139       CA
                                  TGAGGT  GGAGTTTG
                                  ||||||  ||||||||
                                  ACTCCG  CCTCAAAC
                                     C_
GAM44   FLJ20452  3'  GCTGGTCTCGAACTCCTGACCT 35205
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   FLJ20700  3'  GCTGGTCTCGAACTCCTGACCT 35580
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   FLJ20813  3'  GCTGGTCTCAAACTCCTGACCT 35687
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   FLJ21324  5'  GCTGGTCTCAAACTCCTGACCT 91206
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   FLJ21459  3'  GCTGGTCTCGAACTCCTGACCT 44519
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   FLJ22329  3'  CTGGTCTCGAACTCCTGACCTC 45068
                A                  TGAGGTCAGGAGTTTGAGACTAG
                                   |||||||||||||||||||||||
                                   ACTCCAGTCCTCAAGCTCTGGTC

GAM44   FLJ22529  3'  GCTAGTCTCAAACCCCTGACCT 45572          A
                TA                TGAGGTCAGG GTTTGAGACTAGC
                                  |||||||||| ||||||||||||
                                  ATTCCAGTCC CAAACTCTGATCG
                                        C
GAM44   FLJ22529  3'  GCTGGTCTCGAACTCCTGACCT 45576
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   FLJ22684  3'  CTGGTCTCAAACTCCTGACCTC 46794
                A                  TGAGGTCAGGAGTTTGAGACTAG
                                   |||||||||||||||||||||||
                                   ACTCCAGTCCTCAAACTCTGGTC

GAM44   FLJ23392  3'  GCTGGTCTCAAATTCCTGACCC 45543    A
                CA                TG GGTCAGGAGTTTGAGACTAGC
                                  || ||||||||||||||||||||
                                  AC CCAGTCCTTAAACTCTGGTCG
                                    C
GAM44   FLJ23556  3'  GCTGGTCTCGAACTCCTGACCT 45955
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   FLJ25416 5' GCTGGTCTCAAACTCCCTACCT 58812       CA
            CA                    TGAGGT  GGAGTTTGAGACTAGC
                                  ||||||  ||||||||||||||||
                                  ACTCCA  CCTCAAACTCTGGTCG
                                     TC
GAM44   FLJ30532 3' GTCTCAAGCTCCTGACCTCA  58550
                                  TGAGGTCAGGAGTTTGAGAC
                                  ||||||||||||||||||||
                                  ACTCCAGTCCTCGAACTCTG

GAM44   FLJ32865 3' GCTGGTCTCAAACCCCTGACCT 58179          A
            CA                    TGAGGTCAGG GTTTGAGACTAGC
                                  ||||||||||| ||||||||||||
                                  ACTCCAGTCC CAAACTCTGGTCG
                                        C
GAM44   GGA2    3' GCTGGTCTCGAACTCCTGACCT 56887
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   GGA2    3' GCTGGTCTCGAACTCCTGACCT 30473
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   GNG4    3' GCTGGTCTCAAACTCCTGACCT 15621
            C                      GAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  CTCCAGTCCTCAAACTCTGGTCG

GAM44   GTF2H3  3' GTCTCAAACTCCTGAGCTCA  7707       G
                                  TGAG TCAGGAGTTTGAGAC
                                  |||| ||||||||||||||
                                  ACTC AGTCCTCAAACTCTG
                                     G
GAM44   H2AV    3' CTGGTCTCAAACTCCTGACCTC 56851
            A                      TGAGGTCAGGAGTTTGAGACTAG
                                  |||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTC

GAM44   HSPC065 3' GCTGGTCTCGAACTCCTGACCT 26315
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   HSPC232 3' GCTAGTCTCTAACTCCTGGCCT 33232             T
            CA                    TGAGGTCAGGAGTT GAGACTAGC
                                  |||||||||||||| |||||||||
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                                ACTCCGGTCCTCAA CTCTGATCG
                                        T
GAM44   JAM1     3' GCTGGTCTCAAACTCCTGACCT 33765
            C                   GAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                CTCCAGTCCTCAAACTCTGGTCG

GAM44   JAM1     3' GCTGGTCTCAAACTCCTGACCT 57903
            C                   GAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                CTCCAGTCCTCAAACTCTGGTCG

GAM44   JAM1     3' GCTGGTCTCAAACTCCTGACCT 57932
            C                   GAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                CTCCAGTCCTCAAACTCTGGTCG

GAM44   JAM1     3' GCTGGTCTCAAACTCCTGACCT 57958
            C                   GAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                CTCCAGTCCTCAAACTCTGGTCG

GAM44   KIAA0022 3' GCTGGTCTCAAACTCCTGACCT 29668
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM44   KIAA0063 3' GCTGGTCTCAAACTCCCGACCT 29635       A
            CA                  TGAGGTC GGAGTTTGAGACTAGC
                                ||||||| ||||||||||||||||
                                ACTCCAG CCTCAAACTCTGGTCG
                                    C
GAM44   KIAA0161 3' GCTACTCTCAAACTCCTGACCT 28507              C
            CA                  TGAGGTCAGGAGTTTGAGA TAGC
                                |||||||||||||||||| ||||
                                ACTCCAGTCCTCAAACTCT ATCG
                                          C
GAM44   KIAA0186 3' GCTGGTCTCAAACTCCTGGCCT 40759
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                ACTCCGGTCCTCAAACTCTGGTCG

GAM44   KIAA0186 3' GCTGGTTTCAAACTCCTGACCT 40760
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTTTGGTCG

GAM44   KIAA0186 3' GTTTCAAACTCCTGACCTCA  40763
                                TGAGGTCAGGAGTTTGAGAC
                                ||||||||||||||||||||
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                                ACTCCAGTCCTCAAACTTTG

GAM44   KIAA0205 3' CTCGAACTCCTGACCTCA    29581
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM44   KIAA0391 3' TCTCAAACTCCTGACCTCA    27925
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM44   KIAA0513 3' GCTGGTCTCGAACTCCTGACCT 28365
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   KIAA0515 3' TTTCAAACCCCCATCCTCA    63819       TCA  A
                                TGAGG   GG GTTTGAGA
                                |||||   || ||||||||
                                ACTCC   CC CAAACTTT
                                   TAC  C
GAM44   KIAA0555 3' GCTGGTCTCGAACTCCTGACCT 28886
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   KIAA0561 3' GCTGGTCTCGAACTCCTGACCT 65894
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   KIAA0720 3' GCTGGTCTCGAACTCCTGACCC 62324     A
            CA                    TG GGTCAGGAGTTTGAGACTAGC
                                || ||||||||||||||||||||
                                AC CCAGTCCTCAAGCTCTGGTCG
                                 C
GAM44   KIAA0737 3' GCTGGTCTCGAACTCCTGACCT 29144
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   KIAA0841 3' CTGGTCTCGAACTCCTGACCTC 71384
            A                     TGAGGTCAGGAGTTTGAGACTAG
                                |||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTC

GAM44   KIAA0889 3' GCTGGTCTCGAACTCCCGACCT 31142         A
            CA                    TGAGGTC GGAGTTTGAGACTAGC
                                |||||||  ||||||||||||||||
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                                ACTCCAG CCTCAAGCTCTGGTCG
                                    C
GAM44   KIAA0961  3'  GCTGGTCTCAACTCCTGACCTC 29737            T
            A                    TGAGGTCAGGAGTT GAGACTAGC
                                 ||||||||||||| |||||||||
                                 ACTCCAGTCCTCAA CTCTGGTCG
                                                _
GAM44   KIAA1026  3'  GTCTTCAACTCCTGACCTCA   71203            T
                                 TGAGGTCAGGAGTT GAGAC
                                 ||||||||||||| |||||
                                 ACTCCAGTCCTCAA TTCTG
                                       C
GAM44   KIAA1054  3'  GCTGGTCTCGAACTCCTGACCT 68443
            CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                   ||||||||||||||||||||||||
                                   ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   KIAA1128  3'  GCTGGTCTCGAACTCCTGACCT 68482
            CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                   ||||||||||||||||||||||||
                                   ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   KIAA1143  3'  GTCTCAATCTCCTGACCTCA   68688            T
                                 TGAGGTCAGGAG TTGAGAC
                                 |||||||||||| |||||||
                                 ACTCCAGTCCTC AACTCTG
                                       T
GAM44   KIAA1145  3'  AGTCCCACCCTGATCTCA    65619          A  TT A
                                 TGAGGTCAGG GT  G GACT
                                 |||||||||| ||  | ||||
                                 ACTCTAGTCC CA  C CTGA
                                      _  __ C
GAM44   KIAA1161  5'  GCTAGTCTCAAACTCCTGACCT 81754
                                 AGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||
                                 TCCAGTCCTCAAACTCTGATCG

GAM44   KIAA1170  3'  GCTGACCTCAAACTCCTGACCT 69855                AC
            CA                     TGAGGTCAGGAGTTTGAG  TAGC
                                   ||||||||||||||||  ||||
                                   ACTCCAGTCCTCAAACTC  GTCG
                                         CA
GAM44   KIAA1198  3'  GCTGGTCTCAAACTCCTGACCT 63325
            CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                   ||||||||||||||||||||||||
                                   ACTCCAGTCCTCAAACTCTGGTCG

GAM44   KIAA1200  3'  GCTGGTCTCGAACTCCTGACCT 62379
            CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                   ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   KIAA1257  3'  GCTGGTCTCAAACTCCCGACTT 62750        A
            CA                    TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| |||||||||||||||
                                  ACTTCAG CCTCAAACTCTGGTCG
                                      C
GAM44   KIAA1467  3'  GCTGGTCACGAACTCCTGACCT 71612              A
            CA                    TGAGGTCAGGAGTTTG GACTAGC
                                  |||||||||||||||| |||||||
                                  ACTCCAGTCCTCAAGC CTGGTCG
                                           A
GAM44   KIAA1493  3'  GCTGGTCTCAAACTCCTGACCT 64163
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   KIAA1497  5'  GTCTCGAACTCCTGACCTCA   67515
                                  TGAGGTCAGGAGTTTGAGAC
                                  ||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTG

GAM44   KIAA1615  3'  GTCTCAAACTCCCGACCTCA   68721        A
                                  TGAGGTC GGAGTTTGAGAC
                                  ||||||| ||||||||||||
                                  ACTCCAG CCTCAAACTCTG
                                      C
GAM44   KIAA1617  3'  GCTAGTCTTGAACTCCCAACCT 91428       CA     TG
            CA                    TGAGGT  GGAGTT  AGACTAGC
                                  ||||||  ||||||  ||||||||
                                  ACTCCA  CCTCAA  TCTGATCG
                                     AC     GT
GAM44   KIAA1655  3'  GCTGGTCTCAAACTCCTGACCT 66620
            C                      GAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  CTCCAGTCCTCAAACTCTGGTCG

GAM44   KIAA1712  3'  GCTGGTCTCAAACTCCTGACCT 67540
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   KIAA1737  3'  GCTGGTCTCGAACTCCTGACCT 67359
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   KIAA1862  3'  CAGCCGTTCCTGATCTCA    68924          T__
                                  TGAGGTCAGGAG   TTG
                                  ||||||||||||   |||
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                                ACTCTAGTCCTT   GAC
                                      GCC
GAM44   KIAA1922  5'  GCTGGTCTCGAACTCCTGACCT 73634
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   KIAA1985  3'  CAGACTCTGACCCCA      44713    A     G
                                  TG GGTCAG AGTTTG
                                  || |||||| ||||||
                                  AC CCAGTC TCAGAC
                                   C     _
GAM44   LY117     5'  GCCAGTCCCTGATCCCTGACCT 92352        AG  TGA    A
                                  AGGTCAGG  TT   GACT GC
                                  ||||||||  ||   |||| ||
                                  TCCAGTCC  AG   CTGA CG
                                       CT  TCC    C
GAM44   LY117     5'  GCCAGTCCCTGATCCCTGACCT 97746        AG  TGA    A
                                  AGGTCAGG  TT   GACT GC
                                  ||||||||  ||   |||| ||
                                  TCCAGTCC  AG   CTGA CG
                                       CT  TCC    C
GAM44   LY117     5'  GCCAGTCCCTGATCCCTGACCT 97847        AG  TGA    A
                                  AGGTCAGG  TT   GACT GC
                                  ||||||||  ||   |||| ||
                                  TCCAGTCC  AG   CTGA CG
                                       CT  TCC    C
GAM44   MAP-1     3'  GCTAGTTTCGAACTCCTGACCT 42181
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTTTGATCG

GAM44   MCLC      3'  GCTGGTCTCGAACTCCTGACCT 30689
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   MEF-2     3'  GCTGGTCTCAAACTCCTGACCT 64391
            C                     GAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  CTCCAGTCCTCAAACTCTGGTCG

GAM44   MGC:13379 3'  AGTCCCCTGCTGACCTCA     33244          G  TTTGA
                                  TGAGGTCAG AG     GACT
                                  ||||||||| ||     ||||
                                  ACTCCAGTC TC     CTGA
                                       G  CC___
GAM44   MGC13204  3'  GCTGGTCTCAAAATCCTGACCT 48839           G
            CA                    TGAGGTCAGGA TTTGAGACTAGC
                                  |||||||||| ||||||||||
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                                ACTCCAGTCCT AAACTCTGGTCG
                                      A
GAM44   MGC21738  3'  TCGAACTCCTGACCTCA     58921
                                TGAGGTCAGGAGTTTGA
                                ||||||||||||||||
                                ACTCCAGTCCTCAAGCT

GAM44   MKRN4     3'  GCTGGTCTCGAACTCCTGACCT 47752
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   moblak    3'  GCTGGTCTCAAACTCCTGACTT 55507
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTTCAGTCCTCAAACTCTGGTCG

GAM44   MRPL44    3'  CTAGTCTTGAACTCCTGACCTC 43318             TG
            A                     TGAGGTCAGGAGTT  AGACTAG
                                  ||||||||||||||  |||||||
                                  ACTCCAGTCCTCAA  TCTGATC
                                        GT
GAM44   MRPS27    3'  GCTGGTCTCAACCTCCTGACCT 30640           T
            CA                    TGAGGTCAGGAG TTGAGACTAGC
                                  ||||||||||||| ||||||||||
                                  ACTCCAGTCCTC AACTCTGGTCG
                                        C
GAM44   NAPG      5'  GCTGTTCTCAAACTCCTAAGCT 96727      GTC          C
            CA                    TGAG   AGGAGTTTGAGA TAGC
                                  ||||   |||||||||||| ||||
                                  ACTC   TCCTCAAACTCT GTCG
                                    GAA          T
GAM44   NXN       3'  GCTGGTCTCGAACTCCTGACCT 42421
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   OPN4      3'  CTCAAAACTCCTGCCCCA    52718    A  T       _
                                TG GG CAGGAGTTT GAG
                                || || ||||||||| |||
                                AC CC GTCCTCAAA CTC
                                 C _        A
GAM44   OSBPL2    3'  GCTGGTCTCAAACTCCCGACCT 57868        A
            CA                    TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
                                  ACTCCAG CCTCAAACTCTGGTCG
                                      C
GAM44   OSBPL2    3'  GCTGGTCTCAAACTCCCGACCT 29217        A
            CA                    TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
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                                ACTCCAG CCTCAAACTCTGGTCG
                                    C
GAM44   PELI1    5' GCTGGTCTCAAACTCCCAACCT 40275       CA
           CA                     TGAGGT  GGAGTTTGAGACTAGC
                                  ||||||  ||||||||||||||||
                                  ACTCCA  CCTCAAACTCTGGTCG
                                     AC
GAM44   PIP3-E   3' GCTGGTTTCAAACTCCTGACCT 66808
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTTTGGTCG

GAM44   PRIC285  3' GCCAGCCTGCCTCCTGGCCTCA 61436          TTTG  A  A
                                  TGAGGTCAGGAG    AG CT GC
                                  ||||||||||||    || || ||
                                  ACTCCGGTCCTC    TC GA CG
                                         CG__  C  C
GAM44   PRO0245  5' GCTAGTCTCAAACTCCCGAGCC 26132    A  _  A
           CA                     TG GG TC GGAGTTTGAGACTAGC
                                  || || || ||||||||||||||||
                                  AC CC AG CCTCAAACTCTGATCG
                                   _  G  C
GAM44   PRO0529  5' GCTGGTCTCAAACTCCTGACCT 25995
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   PRO2955  3' GCTGGTCTCAAACTCCTGACCT 37642
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   PSTPIP2  3' GCTGGTCTCAAACTCCTGACCT 44394
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   RAI      5' GCTGGTCTCAAACTCCTGATCT 21885
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCTAGTCCTCAAACTCTGGTCG

GAM44   SC4MOL   3' GCTGGTCTCAAACTTCTGACCT 22159
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCTTCAAACTCTGGTCG

GAM44   SCAMP-4  3' GCTGGTCTCGAACTCCTGACCT 54397
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   SFXN2    3'  CTGGTCTCGAACTCCTGACCTC 73944
            A                    TGAGGTCAGGAGTTTGAGACTAG
                                 ||||||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTCTGGTC

GAM44   SIRPB1   3'  CTAGTCTTGAACTCCCGACCTC 20248        A     TG
            A                    TGAGGTC GGAGTT  AGACTAG
                                 |||||||  ||||||  |||||||
                                 ACTCCAG CCTCAA  TCTGATC
                                    C     GT
GAM44   SLC19A3  3'  GCTGGTCTCAAACTCCTGACTT 47494
            CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                   ||||||||||||||||||||||||
                                   ACTTCAGTCCTCAAACTCTGGTCG

GAM44   STAF65(gamma) 3'  GCTGGTCTCAAAACTCCTGACC 29439                _
            TCA                    TGAGGTCAGGAGTTT GAGACTAGC
                                   |||||||||||||| |||||||||
                                   ACTCCAGTCCTCAAA CTCTGGTCG
                                            A
GAM44   TBCC     3'  TCTCGAACTCCTGACCTCA    12142
                                   TGAGGTCAGGAGTTTGAGA
                                   ||||||||||||||||||
                                   ACTCCAGTCCTCAAGCTCT

GAM44   TCL6     3'  GCTGGTCTCAAACTCCTGAGCT 40108      G
            CA                     TGAG TCAGGAGTTTGAGACTAGC
                                   |||| ||||||||||||||||||
                                   ACTC AGTCCTCAAACTCTGGTCG
                                     G
GAM44   TCL6     3'  GCTGGTCTCAAACTCCTGAGCT 40141      G
            CA                     TGAG TCAGGAGTTTGAGACTAGC
                                   |||| ||||||||||||||||||
                                   ACTC AGTCCTCAAACTCTGGTCG
                                     G
GAM44   THEA     3'  GCTGGTCTCAAACTCCTGACTT 66293
            CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                   ||||||||||||||||||||||||
                                   ACTTCAGTCCTCAAACTCTGGTCG

GAM44   TRIM16   3'  GCAGATCTCAAACTCCTGACCT 21339                _ A
            C                      GAGGTCAGGAGTTTGAGA CT GC
                                   |||||||||||||||| || ||
                                   CTCCAGTCCTCAAACTCT GA CG
                                            A _
GAM44   TU12B1-TY 3'  GCTGGTCTCAAACTCCTAGCCT 33395       TC
            CA                     TGAGG  AGGAGTTTGAGACTAGC
                                   |||||  ||||||||||||||||
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                                ACTCC  TCCTCAAACTCTGGTCG
                                  GA
GAM44   TU12B1-TY 3'  GCTGGTCTCGAACTCCTGACCT 33396
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   UBF-fl   3'  GCTGGTCTCAAACTCCTGACCT 51567
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   USP22    3'  GTCTCAAACTCCTGACCTCA  68020
                                  TGAGGTCAGGAGTTTGAGAC
                                  ||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTG

GAM44   VDU1     3'  GCTAGTCTCAAACTCCTGACCT 30420
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGATCG

GAM44   VPS33A   3'  GCTGGTCTCAAACTCCTGACCT 43341
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   WBSCR23  3'  GCTGGTCTCAAACTCCTGACCT 46766
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   ZNF17    3'  GCTGGTCTCAAACTCCCGACCT 82393        A
            CA                    TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
                                  ACTCCAG CCTCAAACTCTGGTCG
                                     C
GAM44   LOC112687 3'  GCTGGTCCCAAACTCCTGACCT 72864              A
            CA                    TGAGGTCAGGAGTTTG GACTAGC
                                  |||||||||||||||| |||||||
                                  ACTCCAGTCCTCAAAC CTGGTCG
                                           C
GAM44   LOC115219 5'  GCTAGTCTCAAACTCCTGACGT 73309    G
            C                      GA GTCAGGAGTTTGAGACTAGC
                                   || ||||||||||||||||||||
                                   CT CAGTCCTCAAACTCTGATCG
                                    G
GAM44   LOC115648 3'  GCTGGGTCTCGAACTCCTGACC 59302                  _
            TCA                     TGAGGTCAGGAGTTTGAGACT AGC
                                    |||||||||||||||||||| |||
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                                ACTCCAGTCCTCAAGCTCTGG TCG
                                                    G
GAM44   LOC119392 3'  GCTGGTCTCGAACTCCTGACCT 59137
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC120114 3'  GCTGGTCTCAAACTCCTGACCT 75535
            C                     GAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  CTCCAGTCCTCAAACTCTGGTCG

GAM44   LOC120224 5'  GCTTATCTCGAACTCCTGACCT 57103                CT
            CA                    TGAGGTCAGGAGTTTGAGA  AGC
                                  ||||||||||||||||||  |||
                                  ACTCCAGTCCTCAAGCTCT  TCG
                                                    AT
GAM44   LOC124216 3'  GCCAGTCTCAAACTCCTGACCT 74263                 A
            C                     GAGGTCAGGAGTTTGAGACT GC
                                  |||||||||||||||||||  ||
                                  CTCCAGTCCTCAAACTCTGA CG
                                                    C
GAM44   LOC126364 3'  GCTGGTCTCGAACTCCTGACCT 75695
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC126669 3'  GCTGGTCTCAAACTCCTGACCT 75410
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   LOC130639 5'  CTCGAACTCCTGACCTCA     74970
                                  TGAGGTCAGGAGTTTGAG
                                  ||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTC

GAM44   LOC132625 3'  GCTAGTCTCAAACTCCTGACCT 75908
            C                     GAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  CTCCAGTCCTCAAACTCTGATCG

GAM44   LOC135154 3'  GCTGGTCTCGAACTCCTGACCT 75219
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC135293 3'  GCTGGTCTCGAACTCCTGACCT 76187
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC142927 5'  GCTGGTGTCAAACTCCTGGCCT 76428              G
            CA                  TGAGGTCAGGAGTTTGA ACTAGC
                                |||||||||||||||| ||||||
                                ACTCCGGTCCTCAAACT TGGTCG
                                      G
GAM44   LOC143916 3'  GCTGGTCTCAAACTTCTGACCT 76644
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||
                                ACTCCAGTCTTCAAACTCTGGTCG

GAM44   LOC144317 5'  GCTGGTCTCGAACTCCTGACCT 76796
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC144519 3'  GCTAGTCTCGAACTCCTGACCT 76872
                                AGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                TCCAGTCCTCAAGCTCTGATCG

GAM44   LOC144524 5'  GCTGGTCTCAAACTCCTGAACT 83133     G
            CA                  TGAG TCAGGAGTTTGAGACTAGC
                                |||| ||||||||||||||||||
                                ACTC AGTCCTCAAACTCTGGTCG
                                  A
GAM44   LOC145453 5'  CTGGTCTCAAACTCCTGACCTC 77139
            A                    TGAGGTCAGGAGTTTGAGACTAG
                                ||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTC

GAM44   LOC146050 3'  GCTGGTCTCAAACTCCCGACCT 77645       A
            CA                  TGAGGTC GGAGTTTGAGACTAGC
                                ||||||| ||||||||||||||||
                                ACTCCAG CCTCAAACTCTGGTCG
                                    C
GAM44   LOC146229 3'  GCTGGTCTCAAACTCCTGACCT 77762
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM44   LOC146229 3'  GCTGGTCTCAAACTCCTGACCT 77763
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM44   LOC146229 3'  GCTGGTCTCAAACTCCTGACTT 77764
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
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                                ACTTCAGTCCTCAAACTCTGGTCG

GAM44   LOC146901 3'  GCTGGTCTCGAACTCCTGACCT 83844
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC146952 5'  GCTGGTCTCAAACTCCTGACCT 83872
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   LOC147817 3'  GCTGGTCTCAAACTCCTGACCT 78502
                TA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ATTCCAGTCCTCAAACTCTGGTCG

GAM44   LOC148709 3'  GCTAGTCTCAAACTCCCGACCT 78945      A
                TA                TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
                                  ATTCCAG CCTCAAACTCTGATCG
                                     C
GAM44   LOC148918 5'  GCTGGTCTCGAACTCCTGACCT 79075
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC149577 3'  CTGGTCTCGAACTCCTGACCTC 84512
                A                 TGAGGTCAGGAGTTTGAGACTAG
                                  |||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTC

GAM44   LOC149692 3'  GCTGGTCTCGAACTCCTGACCT 84591
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC149692 3'  GTCTCAAAGTCCTGACCTCA   84594          G
                                  TGAGGTCAGGA TTTGAGAC
                                  |||||||||| ||||||||
                                  ACTCCAGTCCT AAACTCTG
                                        G
GAM44   LOC149711 3'  GCTGGTCACAAACTCCTGACCT 84685              A
                CA                TGAGGTCAGGAGTTTG GACTAGC
                                  |||||||||||||||| |||||||
                                  ACTCCAGTCCTCAAAC CTGGTCG
                                           A
GAM44   LOC150225 3'  GCTGGTCTCAAACTCCTGACCT 85001
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAACTCTGGTCG

GAM44   LOC150290 3'  CTGGTCTCAAACTCCTGGCCTC 79774
                A                TGAGGTCAGGAGTTTGAGACTAG
                                 ||||||||||||||||||||||
                                 ACTCCGGTCCTCAAACTCTGGTC

GAM44   LOC150960 3'  GCTGGTCTCAAATTCCTGACCT 80068
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTTAAACTCTGGTCG

GAM44   LOC151475 5'  GCTAGTTTCAAACTCCTGACCT 85408
                TA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ATTCCAGTCCTCAAACTTTGATCG

GAM44   LOC151701 3'  GCTGGTCTCGAACTCCTGACCT 85486
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC151979 5'  GCTAGTGTCGATCTCCTGACCT 80423          T   G
                CA                TGAGGTCAGGAG TTGA ACTAGC
                                  |||||||||||| |||| ||||||
                                  ACTCCAGTCCTC AGCT TGATCG
                                        T   G
GAM44   LOC152137 3'  GCTGGTCTCGAACCCCTGACCT 80482         A
                CA                TGAGGTCAGG GTTTGAGACTAGC
                                  |||||||||| ||||||||||||
                                  ACTCCAGTCC CAAGCTCTGGTCG
                                       C
GAM44   LOC152794 5'  GCTAGTCTTGAACTCCTGACCT 80679           TG
                CA                TGAGGTCAGGAGTT  AGACTAGC
                                  |||||||||||||  ||||||||
                                  ACTCCAGTCCTCAA  TCTGATCG
                                        GT
GAM44   LOC153688 3'  GCTGGTCTCGAACTCCCAACCT 86115       CA
                CA                TGAGGT  GGAGTTTGAGACTAGC
                                  ||||||  ||||||||||||||||
                                  ACTCCA  CCTCAAGCTCTGGTCG
                                     AC
GAM44   LOC153811 3'  GCTAGCCTCAAACTCCTGGGCT 80951     G          A
                C                  GAG TCAGGAGTTTGAG CTAGC
                                   ||| |||||||||||| |||||
                                   CTC GGTCCTCAAACTC GATCG
                                     G          C
GAM44   LOC153811 3'  GCTGGTCTCAAACTCCTGACCT 80954
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAACTCTGGTCG

GAM44   LOC154877 3'  GCTGGTTTCGAACTCCCGACCT 86303        A
                CA                TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
                                  ACTCCAG CCTCAAGCTTTGGTCG
                                     C
GAM44   LOC155372 3'  GTCCCCAACTCCTGACCTCA   81343             TGA
                                  TGAGGTCAGGAGTT   GAC
                                  ||||||||||||||   |||
                                  ACTCCAGTCCTCAA   CTG
                                           CCC
GAM44   LOC157247 5'  GCTGGTCTCGAACTCCTGACCT 81373
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC157858 5'  GCTGGTCTCAAACTCCTGACCT 86596
                C                  GAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  CTCCAGTCCTCAAACTCTGGTCG

GAM44   LOC158014 5'  GCTGGTCTCGAACTCCTGACCT 81652
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC158402 5'  GCTAGTCTCGAGCTCGTGACCT 86807         G
                CA                TGAGGTCA GAGTTTGAGACTAGC
                                  |||||||| ||||||||||||||
                                  ACTCCAGT CTCGAGCTCTGATCG
                                      G
GAM44   LOC158629 5'  GCTAGCCCCAAACTCCTGGGCT 86877      G          AGA
                CA                TGAG TCAGGAGTTTG   CTAGC
                                  |||| ||||||||||   |||||
                                  ACTC GGTCCTCAAAC   GATCG
                                    G          CCC
GAM44   LOC162427 3'  GCTGGTCTCAAACTCCTGACCT 82352
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   LOC169611 3'  GCCAGTCTCAAACTCCTGACCT 82767                A
                CA                TGAGGTCAGGAGTTTGAGACT GC
                                  |||||||||||||||||||| ||
                                  ACTCCAGTCCTCAAACTCTGA CG
                                                C
GAM44   LOC196047 5'  GCTAGTCTCAAACTCCTGACCT 89603
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAACTCTGATCG

GAM44   LOC196955 5'  TAAGCTCCTGCCCCCA      77387     A  T
                                TG GG CAGGAGTTTG
                                || || ||||||||||
                                AC CC GTCCTCGAAT
                                 C  C
GAM44   LOC197358 3'  GCTGGTCTCGAACTCCTGACCT 88044
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC199699 3'  GCTGGTCTCAAACTCCTGGCCT 88311
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCGGTCCTCAAACTCTGGTCG

GAM44   LOC199906 3'  GCTGGTCTCAAACTCCTGACCT 88485
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   LOC200014 3'  GCTGGTCTCGAACTCCTGACCT 88536
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC200314 3'  CTGGTCTCGAACTCCTGACCTC 90010
            A                     TGAGGTCAGGAGTTTGAGACTAG
                                  |||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTC

GAM44   LOC200339 3'  GCTAGTCATGAACTCCTGGCCT 90035              A
            CA                    TGAGGTCAGGAGTTTG GACTAGC
                                  |||||||||||||||| |||||||
                                  ACTCCGGTCCTCAAGT CTGATCG
                                              A
GAM44   LOC200407 3'  GCTGGTCTCAAACTCCTGACCT 90045
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   LOC201164 3'  GCTGGTCTCAAACTCCTGACCT 88120
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   LOC201627 3'  GCTGGTCTCAAACTCCCGACCT 89020        A
            CA                    TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
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                                ACTCCAG CCTCAAACTCTGGTCG
                                    C
GAM44   LOC219529 5'  CTCAAACTCCTGAGCCCA    92970    A  _
                                TG GG TCAGGAGTTTGAG
                                || || ||||||||||||||
                                AC CC AGTCCTCAAACTC
                                 _  G
GAM44   LOC219673 5'  GCTGGTCTCAAACGCCTGACCT 93034          A
            CA                    TGAGGTCAGG GTTTGAGACTAGC
                                ||||||||||| ||||||||||||||
                                ACTCCAGTCC CAAACTCTGGTCG
                                      G
GAM44   LOC220074 3'  GCTGGTCTCAAACTCCTGACCT 59279
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM44   LOC220739 3'  CTGGTCTCCCTGCCCCA     92929    A  T    AGTTT
                                TG GG CAGG    GAGACTAG
                                || || ||||    ||||||||
                                AC CC GTCC    CTCTGGTC
                                 C  _   _____
GAM44   LOC221060 3'  GCTGGTCTCGAACTCCTGACCT 93213
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC221271 3'  GCTGATCTCAAACTCCTGATCT 91865                C
            CA                    TGAGGTCAGGAGTTTGAGA TAGC
                                |||||||||||||||||| ||||
                                ACTCTAGTCCTCAAACTCT GTCG
                                           A
GAM44   LOC221418 3'  CAAACCCTGACCTCA       93635          A
                                TGAGGTCAGG GTTTG
                                |||||||||| |||||
                                ACTCCAGTCC CAAAC
                                      _
GAM44   LOC245771 5'  GCTGGTCTCGAACTCCTGACCT 92896
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC253765 3'  AGTCTCAAAGACCTGA      95028       AG
                                TCAGG  TTTGAGACT
                                |||||  |||||||||
                                AGTCC  AAACTCTGA
                                   AG
GAM44   LOC253805 3'  GCTGGTCTCGAACTCCTGACCT 96432
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC254268 3'  GCTGGTCTCAAACTCCTGACCT 95412
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM44   LOC254532 5'  GTCTCAAACTCCTGACCTCA   96643
                                TGAGGTCAGGAGTTTGAGAC
                                |||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTG

GAM44   LOC254655 3'  GCTGGTCTCGAACTCCTGACCT 95474
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC255065 5'  TCTCAAACTCCTGACCTCA    96585
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM44   LOC255065 5'  TCTCAAACTCCTGACCTCA    96586
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM44   LOC255104 3'  AGCTCTCCCCTGGCCTCA     95394          AGTTT   A
                                TGAGGTCAGG     GAG CT
                                ||||||||||     ||| ||
                                ACTCCGGTCC     CTC GA
                                      CCT__   _
GAM44   LOC255308 3'  CAGTCTCTCCTGACCTCA     94532          GTTT     A
                                TGAGGTCAGGA    GAGACT G
                                ||||||||||    |||||| |
                                ACTCCAGTCCT    CTCTGA C
                                     ____      C
GAM44   LOC255497 3'  GCTGGTCTCGAACTCCTGACCT 97193
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC256364 5'  GCTGGTCACAAACTCCTGGCCT 94802              A
            CA                  TGAGGTCAGGAGTTTG GACTAGC
                                ||||||||||||||| |||||||
                                ACTCCGGTCCTCAAAC CTGGTCG
                                          A
GAM44   LOC51193  3'  GCCAGTCTCAAACTCCTGGACT 32907      GT           A
            CA                  TGAG  CAGGAGTTTGAGACT GC
                                ||||  |||||||||||||| ||
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                                ACTC  GTCCTCAAACTCTGA CG
                                  AG            C
GAM44   LOC51200  3'  GCTGGTCTCAAACTCCCAACCT 33001       CA
           CA                     TGAGGT  GGAGTTTGAGACTAGC
                                  ||||||  ||||||||||||||||
                                  ACTCCA  CCTCAAACTCTGGTCG
                                    AC
GAM44   LOC51219  5'  GCTGGTCTCGAACTCCCGACCT 33124        A
           CA                     TGAGGTC GGAGTTTGAGACTAGC
                                  |||||||  ||||||||||||||||
                                  ACTCCAG CCTCAAGCTCTGGTCG
                                     C
GAM44   LOC57107  3'  GCTAGTCTCGAACTCCTGACCT 39838
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGATCG

GAM44   LOC57146  3'  GCTAGTCTCAAACTCCTGACCT 39922
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGATCG

GAM44   LOC90072  3'  GCTGGTCTCGAACTCCCGACCT 61299        A
           CA                     TGAGGTC GGAGTTTGAGACTAGC
                                  |||||||  ||||||||||||||||
                                  ACTCCAG CCTCAAGCTCTGGTCG
                                     C
GAM44   LOC90591  3'  GTCTCGAACTCCTGACCTCA   63439
                                  TGAGGTCAGGAGTTTGAGAC
                                  ||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTG

GAM44   LOC90918  3'  GCTGGTCTCAAACTCCTGACCT 64359
           TA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ATTCCAGTCCTCAAACTCTGGTCG

GAM44   LOC91115  3'  GTCTCCAACTCCTGACCTCA   64947             T
                                  TGAGGTCAGGAGTT GAGAC
                                  ||||||||||||| |||||
                                  ACTCCAGTCCTCAA CTCTG
                                           C
GAM44   LOC91291  5'  GCTGGTCTCAAACTCCTGAC   65483
                                  GTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||
                                  CAGTCCTCAAACTCTGGTCG

GAM44   LOC91561  5'  GCTGGTCTCGAACTCCTGACCT 66454
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC91963 3'  TCTCAAACTCCTGAGCTCA   67699      G
                                TGAG TCAGGAGTTTGAGA
                                |||| ||||||||||||||
                                ACTC AGTCCTCAAACTCT
                                  G
GAM44   LOC92267 3'  GCTGGTCTCAAACTCCTGACCT 68621
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM44   LOC92697 5'  GCTGGTCTCGAACTCCCAACCT 70277       CA
            CA                    TGAGGT  GGAGTTTGAGACTAGC
                                  ||||||  ||||||||||||||||
                                  ACTCCA  CCTCAAGCTCTGGTCG
                                     AC
GAM44   LOC92841 3'  GCTGGTCACGAACTCCTGACCT 70715              A
            CA                    TGAGGTCAGGAGTTTG GACTAGC
                                  |||||||||||||||| |||||||
                                  ACTCCAGTCCTCAAGC CTGGTCG
                                            A
GAM44   LOC93349 3'  GCTGGTCTCGAACTCCTGACCT 56462
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM44   LOC93408 5'  GCTGGTCTCAAACTCCTGGCCT 56481
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCGGTCCTCAAACTCTGGTCG

GAM45   CDH10    3'  TAGTTCTCCCTTAAGCAACCT  22058     CG   CAGTGT  A
                                AGG  GCT     GA GAACTA
                                |||  |||     || ||||||
                                TCC  CGA     CT CTTGAT
                                  AA   ATTCC_  _
GAM45   DACH     3'  TAGTTCTTCCATAACCACCT   54971     C  CTCA   T
                                AGG GG    GTG GAAGAACTA
                                ||| ||    ||| |||||||||
                                TCC CC    TAC CTTCTTGAT
                                  A  AA__   _
GAM45   HPS1     3'  TCTTCCAGAGCTGCCT      3969          AG  T
                                AGGCGGCTC  TG GAAGA
                                |||||||||  || |||||
                                TCCGTCGAG  AC CTTCT
                                           __  _
GAM45   PCTK1    5'  TCTTCAGGCTGCCT        52264         CAGTG
                                AGGCGGCT    TGAAGA
                                ||||||||    ||||||
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                                TCCGTCGG    ACTTCT
                                   _____
GAM45   RORB    5' AGCTCTTCGCCGACCACCT   22606    C  C  AGT     A
                                AGG GG TC   GTGAAGA CT
                                ||| || ||   ||||||| ||
                                TCC CC AG   CGCTTCT GA
                                  A  _  C__      C
GAM45   SPTBN4   3' AGTCCCCATGGCCGCCT    47386       CAGT   AA  A
                                AGGCGGCT    GTG  GA CT
                                ||||||||    |||  || ||
                                TCCGCCGG    TAC  CT GA
                                     ____   CC  _
GAM45   ZNF200   3' GTAGTTCTGAATTCCCAAGCTG 12909       CAGT_  GA
            CCT                   AGGCGGCT    GT  AGAACTAC
                                ||||||||    ||  ||||||||
                                TCCGTCGA    TA  TCTTGATG
                                     ACCCT  AG
GAM45   BTN2A1   3'  GTAATTCTCAGTGTGTGAGCTG 54342         _ TG GA    C
            CCT                   AGGCGGCTCA G  T  AGAA TAC
                                |||||||||| |  |  |||| |||
                                TCCGTCGAGT T  G  TCTT ATG
                                      G GT AC    A
GAM45   CFP1     3'  TAGCTCCGTCAAGCTGCCT   58771       CAGTG   A_  A
                                AGGCGGCT    TGA  GA CTA
                                ||||||||    |||  || |||
                                TCCGTCGA    ACT  CT GAT
                                     _____  GC  C
GAM45   FENS-1   3'  TGGGAGTCACACAAGCCGCCT  40445       CA     AGAA
                                AGGCGGCT  GTGTGA   CTA
                                ||||||||  ||||||   |||
                                TCCGCCGA  CACACT   GGT
                                     A_     GAG_
GAM45   FLJ14082 3'  AGTTCTTCCTAAGGCACCC   46668    CG   CAG  T
                                GG  GCT   TG GAAGAACT
                                ||  |||   || ||||||||
                                CC  CGG   AT CTTCTTGA
                                  CA   A__  C
GAM45   FLJ20539  5'  TGGGGCCACCTGAGCCGCC   35363         T   AAGAA
                                GGCGGCTCAG GTG    CTA
                                |||||||||| |||    |||
                                CCGCCGAGTC CAC    GGT
                                     _   CGG__
GAM45   FLJ22301  3'  AGCCCTTCACGTAGCCTCCT  45756    C   CAG     AA
                                AGG GGCT   TGTGAAG  CT
                                ||| ||||   |||||||  ||
                                TCC CCGA   GCACTTC  GA
                                  T   T__      CC
GAM45   HEMGN    5'  TAGAGAAAAAAACTGAGCCACC 37380    C      GTGAAGAA
            T                   AGG GGCTCAGT       CTA
                                ||| ||||||||       |||
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                                TCC CCGAGTCA       GAT
                                  A       AAAAAAGA
GAM45   KIAA0379 3' GTAGTTCTTGCGAATGCCACC 68150    C   TCAG   G
                                GG GGC    TGT AAGAACTAC
                                || |||    ||| |||||||||
                                CC CCG    GCG TTCTTGATG
                                 A   TAA_  _
GAM45   KIAA0494 3' TCTCACACTGACCACC      28750    C  C       A
                                GG GG TCAGTGTGA GA
                                || || ||||||||| ||
                                CC CC AGTCACACT CT
                                 A  _       _
GAM45   LACE1    3' CTTCACATTAAACCACCT    91837     C  CTC
                                AGG GG   AGTGTGAAG
                                ||| ||   |||||||||
                                TCC CC   TTACACTTC
                                  A  AAA
GAM45   NAPG     3' TAGTTCTTCAGGTAGCACCT   96730     CG   CAG G
                                AGG  GCT   T TGAAGAACTA
                                |||  |||   | ||||||||||
                                TCC  CGA   G ACTTCTTGAT
                                  A_   T__ G
GAM45   PRO2405   5' AGGAGCACATTAAGCCGCCT   37798        C     AAGAA
                                AGGCGGCT AGTGTG     CT
                                |||||||| ||||||     ||
                                TCCGCCGA TTACAC     GA
                                     A     GAG__
GAM45   LOC121219 5' AGTCCTCAGCGAAGCCGCCT   74040        CA  G   A  A
                                AGGCGGCT  GT TGA GA CT
                                ||||||||  || ||| || ||
                                TCCGCCGA  CG ACT CT GA
                                     AG  _   C  _
GAM45   LOC146990 3' CTTCACACCCAGCCGCCT    83886        CA
                                AGGCGGCT  GTGTGAAG
                                ||||||||  ||||||||
                                TCCGCCGA  CACACTTC
                                     CC
GAM45   LOC148371 5' TTCCACTGAGCCACC       78809    C       T
                                GG GGCTCAGTG GAA
                                || |||||||| |||
                                CC CCGAGTCAC CTT
                                 A       _
GAM45   LOC152274 3' AGTCCCTGCAGGAGCAGCCT   80498     G   AG   AA  A
                                AGGC GCTC  TGTG  GA CT
                                |||| ||||  ||||  || ||
                                TCCG CGAG  ACGT  CT GA
                                  A   G_    CC  _
GAM45   LOC200261 3' AGTTGCTCCACTGAGTCACC   88653    C       T  AG
                                GG GGCTCAGTG GA  AACT
                                || |||||||| ||  ||||
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                                CC CTGAGTCAC CT  TTGA
                                 A       _ CG
GAM45   LOC201562 5'  GTAGTCCGGCCCGAGCCGCT   88975        AGT  GAA  A
                                GGCGGCTC   GT   GA CTAC
                                ||||||||   ||   || ||||
                                TCGCCGAG   CG   CT GATG
                                    CC_  GC_  _
GAM45   LOC202347 3'  TCATGGCAGAGCCGCCT     90349         A  _
                                AGGCGGCTC GT GTGA
                                ||||||||| || ||||
                                TCCGCCGAG CG TACT
                                      A  G
GAM45   LOC220370 3'  TCACCTCACTGAGCCACCT    92834     C       ___
                                AGG GGCTCAGT   GTGA
                                ||| ||||||||   ||||
                                TCC CCGAGTCA   CACT
                                  A       CTC
GAM45   LOC221838 5'  TTCCACTGAGCCACC       92546    C       T
                                GG GGCTCAGTG GAA
                                || |||||||||  |||
                                CC CCGAGTCAC CTT
                                 A       _
GAM45   LOC51716  3'  AGTTCCACACTGAGCGCCT    32786      G       AA
                                AGGCG CTCAGTGTG  GAACT
                                ||||| |||||||||  |||||
                                TCCGC GAGTCACAC  CTTGA
                                   _       __
GAM45   LOC89919  3'  CTTCCACTGAGCCACC      60722    C       T
                                GG GGCTCAGTG GAAG
                                || |||||||||  ||||
                                CC CCGAGTCAC CTTC
                                 A       _
GAM45   LOC91947  3'  TAGTTCTTTCATTGTAAGCCGC 67614        __    T
           T                     GGCGGCT  CAGTG GAAGAACTA
                                |||||||  ||||| |||||||||
                                TCGCCGA  GTTAC TTTCTTGAT
                                    AT    _
GAM46   DGKI     5'  GAGATCACACCACTGCAA    16345         C  A  G
                                TTGCAGTGG GT AT TT
                                ||||||||| || || ||
                                AACGTCACC CA TA AG
                                      A  C  G
GAM46   GTF2F1    3'  GACACCACGCCACTGCA     9151           AA
                                TGCAGTGGCGT  TGTT
                                ||||||||||  ||||
                                ACGTCACCGCA  ACAG
                                       CC
GAM46   HADHB    3'  ATTCAGAATCTAAACACCACTG 3938        C  AAT_
                                CAGTGG GT    GTTCTGAAT
                                |||||| ||    |||||||||
```

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                                GTCACC CA    TAAGACTTA
                                   A  AATC
GAM46   TGFBR1   3' ATTCAGAACATTACATGCC   16047     __
                                GGC  GTAATGTTCTGAAT
                                |||  ||||||||||||||
                                CCG  CATTACAAGACTTA
                                  TA
GAM46   TGFBR3   3' GCATACACCACTGCAA      12274         C   A
                                TTGCAGTGG GTA TGT
                                ||||||||| ||| |||
                                AACGTCACC CAT ACG
                                     A  _
GAM46   APCL     3' TCAAGGTACGCCCACTGCAA  19685         _   ATG TC
                                TTGCAGTGG CGTA   T  TGA
                                ||||||||| ||||   |  |||
                                AACGTCACC GCAT   G  ACT
                                     C    ___ GA
GAM46   FLJ12716 3' TCAGAACACATACACAACAA  41656     CA   GCGTAA
                                TTG  GTG     TGTTCTGA
                                |||  |||     ||||||||
                                AAC  CAC     ACAAGACT
                                  AA   ATAC__
GAM46   FLJ20686 3' GGAGATCACGCCACTGCAA   35535           A  G
                                TTGCAGTGGCGT AT TTC
                                |||||||||||| || |||
                                AACGTCACCGCA TA AGG
                                       C  G
GAM46   MGC12435 3' ATTCAGAACATTTTTCCTG   48688     T  CGT
                                CAG GG   AATGTTCTGAAT
                                ||| ||   ||||||||||||
                                GTC CT   TTACAAGACTTA
                                  _  TT_
GAM46   TRIAD3   3' CAAAACCCGTGCGCCACTGCAG 94501           AT_   C
                                TTGCAGTGGCGTA   GTT TG
                                ||||||||||||   ||| ||
                                GACGTCACCGCGT   CAA AC
                                       GCC   A
GAM46   LOC149296 5' TCAGACCACTGCAA       79261         CGTAATGT
                                TTGCAGTGG       TCTGA
                                |||||||||       |||||
                                AACGTCACC       AGACT
                                                _________
GAM46   LOC152441 5' TCTGCCATCACCCACTGCAA  85735         C  A   TTCT
                                TTGCAGTGG GT ATG    GA
                                ||||||||| || |||    ||
                                AACGTCACC CA TAC    CT
                                     _  C   CGT_
GAM46   LOC162239 3' CAGAACATCCATAGC       82339     A    CGTA
                                GC GTGG    ATGTTCTG
                                || ||||    ||||||||
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                                CG TACC    TACAAGAC
                                 A  _____
GAM46   LOC204119 5'  TCAGAACACCAGATGGTCCAC  90655      __  AA__
                                GTGG  CGT    TGTTCTGA
                                ||||  |||    ||||||||
                                CACC  GTA    ACAAGACT
                                  TG   GACC
GAM46   LOC221688 5'  AGAGATTACACCACTGCAA    93675         C    G
                                TTGCAGTGG GTAAT TTCT
                                ||||||||| ||||| ||||
                                AACGTCACC CATTA GAGA
                                     A    _
GAM46   LOC253263 3'  ATTCAGAAAGAGAGCCACTGCG 97027          GTAATG
            A                    TTGCAGTGGC     TTCTGAAT
                                ||||||||||     ||||||||
                                AGCGTCACCG     AAGACTTA
                                     AGAGA_
GAM47   ARNT2    3'  AAACAACCCGTGCATCCCTGC  29450     A    TTTTA
                                GTA GGAT     GGGTTGTTT
                                ||| ||||     |||||||||
                                CGT CCTA     CCCAACAAA
                                  C    CGTG_
GAM47   LCT      3'  AACCGTAAAAATCCTT      9697           G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
                                TTCCTAAAAAT CCAA
                                     G
GAM47   RPL15    3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM47   FBXO30   3'  AACTAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                 G        AA
GAM47   KIAA0494  3'  AACAACCCTTACTTAC      28736      GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                  AT_____
GAM47   PRO0641   5'  AAACAACCCCAAAACTTG    26210      GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                  ___    C
GAM47   SMT3H2   3'  AACAACATAAAAATCCTTGC   22670           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
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                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM47   LOC120103 3'  AACCTATGAAAAATCCTTGC   74002          A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||  |||||
                                CGTTCCTAAAAA   TCCAA
                                       GTA
GAM47   LOC129831 3'  AAACAACCCCAATGTCC     74889     TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM47   LOC133088 5'  AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                      GTA GGATTTTT    TTGTTT
                                ||| ||||||||    ||||||
                                CGT CCTAAAAA    AACAAA
                                  C       GATAA
GAM47   LOC148089 3'  GGCCCTAAAAATTCCTAC    78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM47   LOC154547 3'  AACAACATAAAAATCCTTGC   76050          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM47   LOC158104 3'  ACAGCCAAAAATCCTTA     60313          AG
                                TAAGGATTTTT  GGTTGT
                                ||||||||||  ||||||
                                ATTCCTAAAAA  CCGACA
                                       __
GAM47   LOC205880 5'  AAACAACCATCATCCTGAC   90709    A    TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM47   LOC221561 3'  AACAACATAAAAATCCTTGC   92130          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM47   LOC257591 3'  AACAACATAAAAATCCTTGC   97840          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM47   LOC51145  3'  AGCTAAAATCCTTAC       32393          TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
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                                CATTCCTAAAA  TCGA
                                     ___
GAM48  ADH1B   3' CTTAGACATAAAGTAAAAT  72644     C    CAC
                                ATTT ACTTT  TGTCTGAG
                                |||| |||||  ||||||||
                                TAAA TGAAA  ACAGATTC
                                  A    T__
GAM48  AHR     3' ATCTCAGATGTTAAAATAAATG 7875      CAC  C  T
                                CATTT  TTT AC GTCTGAGAT
                                |||||  ||| || |||||||||
                                GTAAA  AAA TG TAGACTCTA
                                   TA_  T  _
GAM48  FDFT1   3' TAGGAAAGTGAAATG      15518          A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                     _
GAM48  JTB     3' ATCTCAGACAGTGAAAGTGAAA 21959
          TG                     CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM48  KLF4    3' TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM48  PHYH    3' ACAGTAAAAGTGAAAT     20608         C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM48  PKD2    3' TCCAGGTTGAAAGTGAAA    60096          CTG   A
                                TTTCACTTTCA  TCTG GA
                                ||||||||||  |||| ||
                                AAAGTGAAAGT  GGAC CT
                                      T__   _
GAM48  WRN     3' GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM48  ZNF216  3' ATCTGCACAGCAAAGTGAAA  20017        CA   CTG
                                TTTCACTTT  CTGT  AGAT
                                |||||||||  ||||  ||||
                                AAAGTGAAA  GACA  TCTA
                                     C_   CG_
GAM48  CG012   5' CTCACTCTGAAAGTGAA    83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
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                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM48   EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                |||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM48   FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC       GTCTGAGAT
                                 ||||||       |||||||||
                                 GTAAAG       CAGACTCTA
                                    AAACATTT_
GAM48   FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                    C__
GAM48   KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM48   KLHL6    3'  ATCTCAGAGCAGGAAA      55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM48   NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM48   PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM48   PP35     3'  ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM48   PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148        TCAC   C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM48   SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
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                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM48   SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM48   LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM48   LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM48   LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM48   LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM49   B3GNT3   3'  GTTCCAACTGTGGATGC     26518           AA
                                GCATCCACAGTTG  GGAC
                                ||||||||||||  ||||
                                CGTAGGTGTCAAC  CTTG
                                          __
GAM49   BMP5     5'  TCTTAACAACTGTGGAT     40777          A_
                                ATCCACAGTTG  AGGA
                                ||||||||||  ||||
                                TAGGTGTCAAC  TTCT
                                     AA
GAM49   CACNB1   3'  ACTGTCCTGTCCTTTGTGGCTG 5567     T     TT  _
           C                     GCA CCACAG  GA AGGACAGT
                                |||  ||||||  ||  ||||||||
                                CGT GGTGTT  CT TCCTGTCA
                                  C     TC  G
GAM49   CACNG3   5'  ACTGTCCTCGGCTCCAGAAACT 21538     CA  CAC     A
           T                     AAG  TC   AGTTGA GGACAGT
                                |||  ||   ||||||| |||||||
                                TTC  AG   TCGGCT CCTGTCA
                                  AA  ACC     _
GAM49   CDH18    5'  ACTGTCCTTCCTAAAGATGCT  17031       CAC  TT
                                AGCATC   AG  GAAGGACAGT
                                ||||||   ||  ||||||||||
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                                TCGTAG  TC  CTTCCTGTCA
                                   AAA  __
GAM49   COX11    3'  TTTCAACTGTAGGTGC     15193      C
                                GCATC ACAGTTGAAG
                                ||||| ||||||||||
                                CGTGG TGTCAACTTT
                                   A
GAM49   DYRK1A   3'  ACTGTCAAGCCTGTGGATG   55239        TTGAAG
                                CATCCACAG    GACAGT
                                |||||||||    ||||||
                                GTAGGTGTC    CTGTCA
                                     CGAA__
GAM49   DYRK1A   3'  ACTGTCAAGCCTGTGGATG   55197        TTGAAG
                                CATCCACAG    GACAGT
                                |||||||||    ||||||
                                GTAGGTGTC    CTGTCA
                                     CGAA__
GAM49   DYRK1A   3'  ACTGTCAAGCCTGTGGATG   7348         TTGAAG
                                CATCCACAG    GACAGT
                                |||||||||    ||||||
                                GTAGGTGTC    CTGTCA
                                     CGAA__
GAM49   HMGCS2   3'  ACTGTCCTGGGCTTATGGTGC  18623      CAC   GA
                                GCATC  AGTT  AGGACAGT
                                |||||  ||||  ||||||||
                                CGTGG  TCGG  TCCTGTCA
                                   TAT   G_
GAM49   MYEOV    3'  CTGTCTTTCTGTAGACCCT   57049    CA  C   GTT
                                AG  TC ACA   GAAGGACAG
                                ||  || |||   |||||||||
                                TC  AG TGT   CTTTCTGTC
                                 CC  A  ___
GAM49   RAB36    3'  ACTGTCCTTCTGCCACGGACGC 16946    A   ACA  T
           T                     AGC TCC   GT GAAGGACAGT
                                ||| |||   || ||||||||||
                                TCG AGG   CG CTTCCTGTCA
                                  C   CAC  T
GAM49   RELA     3'  ACTGCCCCCAACTTTGTGGATG 41751        __   AA  A
           T                     GCATCCACA  GTTG  GG CAGT
                                |||||||||  ||||  || ||||
                                TGTAGGTGT  CAAC  CC GTCA
                                     TT   CC  _
GAM49   SLC38A2  3'  CTGTCTTCCGTGGATGTTT   38590        AGTT   G
                                AAGCATCCAC   GAAG ACAG
                                ||||||||||   |||| ||||
                                TTTGTAGGTG   CTTC TGTC
                                     C___   _
GAM49   TBL2     3'  CTGTCCTCATCTGGAGC    52183    A   CAGT   A
                                GC TCCA   TGA GGACAG
                                || ||||   ||| ||||||
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                                CG AGGT    ACT CCTGTC
                                 _    CT__   _
GAM49   TMEPAI    3'  ACTGTCCCTGCAGAGTGGATGC 39439          AG   AA_
            TT                   AAGCATCCAC  TTG   GGACAGT
                                ||||||||||  |||   |||||||
                                TTCGTAGGTG  GAC   CCTGTCA
                                     A_   GTC
GAM49   DKFZP434K1772 5'  CCACCCAGCCTGTGGATGT    67709          _   AA_
                                GCATCCACAG TTG   GG
                                |||||||||| |||   ||
                                TGTAGGTGTC GAC   CC
                                     C   CCA
GAM49   DKFZP564D0462 3'  ACTGTCCTTGCTTTGGAGACTT 70496     CA    C   TG
                                AAG  TCCA AGT  AAGGACAGT
                                |||  |||| |||  |||||||||
                                TTC  AGGT TCG  TTCCTGTCA
                                  AG    T   __
GAM49   DKFZP564F013 3'  CTCCAACTGTGCATGCT     94207       C       A
                                AGCAT CACAGTTG AG
                                ||||| ||||||||  ||
                                TCGTA GTGTCAAC TC
                                   C       C
GAM49   DKFZP564O1664 3'  TTTCAACTGAAAATGCTT     47940        CCA
                                AAGCAT   CAGTTGAAG
                                ||||||   |||||||||
                                TTCGTA   GTCAACTTT
                                   AAA
GAM49   DKFZp762P2111 3'  ACTGCCCTTCTGTGCTGTGGAT 86350    C       T__     A
            CCT                    AG ATCCACAGT   GAAGG CAGT
                                || |||||||||   ||||| ||||
                                TC TAGGTGTCG   CTTCC GTCA
                                 C        TGT    C
GAM49   FLJ13657  3'  TCCTTCCACAATTAGGGATGCT 45721          ACA___  T
            T                    AAGCATCC     GT GAAGGA
                                ||||||||     || ||||||
                                TTCGTAGG     CA CTTCCT
                                     GATTAA  C
GAM49   FLJ20097  3'  CTGTCCTAGTGAATAGCTT    34562      _  C   AGTTGA
                                AAGC AT CAC     AGGACAG
                                |||| || |||     |||||||
                                TTCG TA GTG     TCCTGTC
                                  A  A   A_____
GAM49   FLJ20489  3'  ACTGCCCTTCAACTAGAGCTT  35247      A  CAC        A
                                AAGC TC   AGTTGAAGG CAGT
                                |||| ||   ||||||||| ||||
                                TTCG AG   TCAACTTCC GTCA
                                  _ A__        C
GAM49   FLJ23309  3'  ACTGTCCTGACAAGTGGA    46059       AG   A_
                                TCCAC  TTG  AGGACAGT
                                |||||  |||  ||||||||
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                                AGGTG  AAC  TCCTGTCA
                                  __   AG
GAM49   KIAA0161  3'  CTGCCCTTTAACATGC      28504      CCACA       A
                                GCAT    GTTGAAGG CAG
                                ||||    |||||||| |||
                                CGTA    CAATTTCC GTC
                                  _____       C
GAM49   KIAA0676  3'  CCTCCATCCGTGGATGCTT    30452          AGT  A
                                AAGCATCCAC   TG AGG
                                ||||||||||   || |||
                                TTCGTAGGTG   AC TCC
                                     CCT  C
GAM49   MGC11352  5'  TCTTTCAACTATAGACCCTT   64808     CA  CAC
                                AAG  TC   AGTTGAAGGA
                                |||  ||   ||||||||||
                                TTC  AG   TCAACTTTCT
                                  CC  ATA
GAM49   TEX27     3'  CCTGCAACTGCAAATGTTT    41660       CCA     A
                                AAGCAT   CAGTTG AGG
                                ||||||   |||||| |||
                                TTTGTA   GTCAAC TCC
                                   AAC     G
GAM49   LOC112817 3'  TCTTTCTACTGTGGATGCTT   56519           T
                                AAGCATCCACAGT GAAGGA
                                |||||||||||| ||||||
                                TTCGTAGGTGTCA CTTTCT
                                      T
GAM49   LOC146287 5'  ACTGTTTATAATATGGATGCTT 83649         CA    AA
                                AAGCATCCA  GTTG  GGACAGT
                                |||||||||  ||||  |||||||
                                TTCGTAGGT  TAAT  TTTGTCA
                                     A_    A_
GAM49   LOC149127 3'  ACTGTGTGGATAACTGTGGGT  84342          AAGG_
                                ATCCACAGTTG    ACAGT
                                ||||||||||     |||||
                                TGGGTGTCAAT    TGTCA
                                      AGGTG
GAM49   LOC160777 3'  CTACCCTCATGGATGCT     82240        CAGT   A  AC
                                AGCATCCA    TGA GG  AG
                                ||||||||    ||| ||  ||
                                TCGTAGGT    ACT CC  TC
                                   _____   _  CA
GAM49   LOC197285 3'  ACTGTCCTGTCTGCAGATGCT  87787       CA   TTGA
                                AGCATC  CAG    AGGACAGT
                                ||||||  |||    ||||||||
                                TCGTAG  GTC    TCCTGTCA
                                   AC   TG__
GAM49   LOC203339 3'  TGCCCTTTGATGCTT       90553        CACAGTT    A
                                AAGCATC      GAAGG CA
                                |||||||      ||||| ||
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                                TTCGTAG      TTTCC GT
                                   _______    C
GAM49   LOC219731 5'  CCATAAACTGTGGTTGCTT   93091      T      GAA
                                AAGCA CCACAGTT   GG
                                ||||| ||||||||   ||
                                TTCGT GGTGTCAA   CC
                                   T       ATA
GAM49   LOC93082  3'  ACTATCCTTCTGATGGGGTGCT 56440        A  GTT     C
           T                     AAGCATCC CA   GAAGGA AGT
                                ||||||||  ||   |||||| |||
                                TTCGTGGG GT   CTTCCT TCA
                                   _  AGT     A
GAM50   ARCN1    3'  AGACTGCACTCTCTGTCA    7970          CA_
                                TGACAGAGA   CAGTTT
                                |||||||||   ||||||
                                ACTGTCTCT   GTCAGA
                                      CAC
GAM50   CBFA2T2  3'  GAGCAAAACTCTGTCT     17466      C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                   C
GAM50   CTLA4    3'  CAGAGCTGGGATGTTTCTGTCA 17807          CAGTTTT
                                TGACAGAGACA      GCTCTG
                                ||||||||||       ||||||
                                ACTGTCTTTGT      CGAGAC
                                      AGGGT__
GAM50   ITK      3'  CAGAACAGGAGTGATGTCTCTG 18674        _  G    C
                                CAGAGACA CA TTTTG TCTG
                                |||||||| || ||||| ||||
                                GTCTCTGT GT AGGAC AGAC
                                      A  G    A
GAM50   LAMP2    3'  GGTGAAACCCCATCTCTATCA  25716     C    CACA    TG
                                TGA AGAGA    GTTT  CT
                                ||| |||||    ||||  ||
                                ACT TCTCT    CAAA  GG
                                  A    ACCC    GT
GAM50   MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   40865        A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM50   MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   52960        A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM50   MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   52963        A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
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                                ACTGTCTC  GTG  GAAAC
                                    CCC  G_
GAM50   PDGFRB   5' CAGAGCCTGGAACTGTG    65969        __
                                CACAGTTTT  GCTCTG
                                |||||||||  ||||||
                                GTGTCAAGG  CGAGAC
                                   TC
GAM50   PTPRA    3' AGAGCGGTATCTCTG      55087      C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM50   PTPRA    3' AGAGCGGTATCTCTG      55079      C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM50   PTPRA    3' AGAGCGGTATCTCTG      11088      C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM50   RAD51L3  3' CAAAACTCAGGTATGTCTCTGT 56065       C_____
                                ACAGAGACA     AGTTTTG
                                |||||||||     |||||||
                                TGTCTCTGT     TCAAAAC
                                    ATGGAC
GAM50   TBL2     3' CAGAACTGTGTTCCATCA    52178    CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM50   TBL2     3' CAGAACTGTGTTCCATCA    24924    CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM50   AGTRL2   5' CAGAGCAAGAACTGTTC    17691    C     _
                                GA ACAGTTTT GCTCTG
                                || |||||||| ||||||
                                CT TGTCAAGA CGAGAC
                                 _      A
GAM50   CABP5    3' AGAGCGGTATCTTTGCCA    39079    A    C  AGTTT
                                TG CAGAGA AC    TGCTCT
                                || |||||| ||    ||||||
                                AC GTTTCT TG    GCGAGA
                                 C    A _____
GAM50   CUL4A    5' AGAGCAGCACCTCCATCA    13149    CA  ACACA  T
                                TGA  GAG    GT TTGCTCT
                                |||  |||    || |||||||
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                                ACT  CTC     CA GACGAGA
                                  AC   _____  C
GAM50   DKFZp761O17121 3'  CAGACAGCCCCTGTGTCTCTGT 50136            TT_   C
            C                    GACAGAGACACAG   TTG TCTG
                                 ||||||||||||   ||| ||||
                                 CTGTCTCTGTGTC   GAC AGAC
                                       CCC   _
GAM50   FLJ10375  3'  CAGAGGCCTGTGTCTGTGCCA  36073    A  G       TTTTG
                                 TG CA AGACACAG    CTCTG
                                 || || ||||||||    |||||
                                 AC GT TCTGTGTC    GAGAC
                                  C  G       CG___
GAM50   FLJ10738  5'  CAAAGCCAGCCCTCTGTCA   36527        ACACA
                                 TGACAGAG    GTTTTG
                                 ||||||||    ||||||
                                 ACTGTCTC    CGAAAC
                                      CCGAC
GAM50   FLJ10803  3'  CAAAACAAAACTCTGTCA    36660        ACACA
                                 TGACAGAG    GTTTTG
                                 ||||||||    ||||||
                                 ACTGTCTC    CAAAAC
                                      AAAA_
GAM50   FLJ10842  3'  AAAGTGTGCTCTGTCA      36723        A   G
                                 TGACAGAG CACA TTT
                                 |||||||| |||| |||
                                 ACTGTCTC GTGT AAA
                                      _   G
GAM50   FLJ13153  3'  CAGAGCCCAGCATCCATCTCTG 45555         CACA_   TT
            TCA                    TGACAGAGA    GTT  GCTCTG
                                 |||||||||    |||  ||||||
                                 ACTGTCTCT    CGA  CGAGAC
                                      ACCTA   CC
GAM50   FLJ20035  3'  CAAACCTGCCATGTTCTGTCA  34395        A  ___   T
                                 TGACAGAG CA   CAG TTTG
                                 |||||||| ||   ||| ||||
                                 ACTGTCTT GT   GTC AAAC
                                      _ ACC   C
GAM50   FLJ22195  5'  CAGAGCAGAGGGAAGTCTCTGC 42800    A      ACAG
            CA                     TG CAGAGAC    TTTTGCTCTG
                                 || ||||||||   ||||||||||
                                 AC GTCTCTG    GAGACGAGAC
                                  C      AAGG
GAM50   FLJ32191  5'  GAACTGCACCTCTGTCA     58411        ACA
                                 TGACAGAG   CAGTTT
                                 ||||||||   ||||||
                                 ACTGTCTC   GTCAAG
                                      CAC
GAM50   KIAA1023  3'  CAAAGCTGTATCTGCTATCA   34255     C  _   C
                                 TGA AG AGA ACAGTTTTG
                                 ||| || ||| |||||||||
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                                ACT TC TCT TGTCGAAAC
                                  A G   A
GAM50   KIAA1586 5' AGTGTGATGTGTCTCTG     92326          GTT TG T
                                CAGAGACACA   T  C CT
                                ||||||||||   |  | ||
                                GTCTCTGTGT   A  G GA
                                      ___ GT T
GAM50   KIAA1754 3' GACTAACGTCTCTGTCA     63236          AC_
                                TGACAGAGAC   AGTT
                                ||||||||||   ||||
                                ACTGTCTCTG   TCAG
                                      CAA
GAM50   LANCL2   3' CAGAGTGCACTGCAGCTCTGTC 37995         ACA    TTT
            A                    TGACAGAG   CAGT   GCTCTG
                                ||||||||   ||||   ||||||
                                ACTGTCTC   GTCA   TGAGAC
                                     GAC    CG_
GAM50   LIG-1    3' CAGAGCAGGCCTGTCCATGCCA 63893    A  GAGAC    TT
                                TG CA    ACAG  TTGCTCTG
                                || ||    ||||  ||||||||
                                AC GT    TGTC  GACGAGAC
                                 C  ACC__    CG
GAM50   MGC5242  3' AGAGTACATGTCTCTG      43823         CAGTTT
                                CAGAGACA     TGCTCT
                                ||||||||     ||||||
                                GTCTCTGT     ATGAGA
                                     AC____
GAM50   OSMR     3' CAGAGCTGGCACCCTGTCA    14345       AGACA
                                TGACAG    CAGTTTTG
                                ||||||    ||||||||
                                ACTGTC    GTCGAGAC
                                    CCACG
GAM50   RAB21    3' CAGAACAAAACTGTGGATC    30383    GA        C
                                GA  CACAGTTTTG TCTG
                                ||  |||||||||| ||||
                                CT  GTGTCAAAAC AGAC
                                 AG         A
GAM50   SPTLC2   3' CAGAGCAAAACTGTGTCTC    16799
                                GAGACACAGTTTTGCTCTG
                                |||||||||||||||||||
                                CTCTGTGTCAAAACGAGAC

GAM50   TGIF2    3' GAGTCATGCTCTGTCA      41454         A  CAGTTT  _
                                TGACAGAG CA      TG CTC
                                |||||||| ||      || |||
                                ACTGTCTC GT      AC GAG
                                     _  _______  T
GAM50   WBSCR23  5' GCTGACTGTGTCTCCATCA   46765     CA         TT
                                TGA  GAGACACAGTT  GC
                                |||  ||||||||||  ||
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                                ACT  CTCTGTGTCAG  CG
                                  AC         T_
GAM50   LOC115129 3' GGCAAAACCCCGTCTCT     73235       ACA
                                AGAGAC   GTTTTGCT
                                ||||||   ||||||||
                                TCTCTG   CAAAACGG
                                   CCC
GAM50   LOC129198 3' AGCAAGCTGTGCCTC       76117     A       T
                                GAG CACAGTTT GCT
                                ||| |||||||| |||
                                CTC GTGTCGAA CGA
                                  C       _
GAM50   LOC145231 3' GGTGAAACTATGTCTCT     83293       C    TG
                                AGAGACA AGTTT  CT
                                ||||||| |||||  ||
                                TCTCTGT TCAAA  GG
                                    A    GT
GAM50   LOC145483 3' GAGCAAAACTCTGTCT      77243      C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                   C
GAM50   LOC146713 3' GAGCAAAACTCCGTCT      83726      AC
                                AGAC  AGTTTTGCTC
                                ||||  ||||||||||
                                TCTG  TCAAAACGAG
                                  CC
GAM50   LOC149175 3' CAGGGTGAAACCACGTCTCT  79208       ACA   TG
                                AGAGAC   GTTT  CTCTG
                                ||||||   ||||  |||||
                                TCTCTG   CAAA  GGGAC
                                   CAC   GT
GAM50   LOC150299 3' CAGAACCTGCATCTTTGTCA  84968         CA  _
                                TGACAGAGA  CAG TTTTG
                                |||||||||  ||| |||||
                                ACTGTTTCT  GTC AAGAC
                                     AC   C
GAM50   LOC153277 3' TAAAACTGTGCCTGTGCCA   85990    A  G  A
                                TG CA AG CACAGTTTTG
                                || || || ||||||||||
                                AC GT TC GTGTCAAAAT
                                 C  G  C
GAM50   LOC155179 3' CAAAGCTGTATCTGCTATCA  81312     C  _  C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM50   LOC221074 3' AAAGTGTGTCTCTTTCA     93177     C       G
                                TGA AGAGACACA TTT
                                ||| ||||||||| |||
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                                ACT TCTCTGTGT AAA
                                  T       G
GAM50   LOC221103 5'  AGTTTATGTGTGCTCTGTCA   93244        _    GTTTT
                                TGACAGAG ACACA    GCT
                                |||||||| |||||    |||
                                ACTGTCTC TGTGT    TGA
                                    G    ATT__
GAM50   LOC255988 5'  CAGAGCCCAGCATCCATCTCTG 97608        CACA_  TT
           TCA                   TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                     ACCTA   CC
GAM51   CTSB    3'  CCAGTGGAACAGCGGGAGACCT 64725    A___   G_  TCAT
           G                    CAG   CCCG  GT   TCCACTGG
                                |||   ||||  ||   ||||||||
                                GTC   GGGC  CA   AGGTGACC
                                  CAGA   GA  ____
GAM51   HIVEP3   5'  CCAATAGAATAGCGTGGGCCCT 44432    A_   G   C   CAC
           GA                    TCAG  CCCG GTT ATTC   TGG
                                ||||  |||| ||| ||||   |||
                                AGTC  GGGT CGA TAAG   ACC
                                  CC   G   _   ATA
GAM51   SPAG8    3'  CAGTGAAATGGACCTG     24898         C
                                CGGGTTCATT CACTG
                                |||||||||| |||||
                                GTCCAGGTAA GTGAC
                                     A
GAM51   FLJ13614  3'  CAGTGGAACTCAGAACTGA   57450     ACCC   TCAT
                                TCAG   GGGT   TCCACTG
                                ||||   ||||   |||||||
                                AGTC   CTCA   AGGTGAC
                                  AAGA   ____
GAM51   FLJ32468  5'  CAGTGGAGGTCAAGCCTG    59040      CA__
                                CGGGTT   TTCCACTG
                                ||||||   ||||||||
                                GTCCGA   GAGGTGAC
                                   ACTG
GAM51   JM11     3'  CAGTGGATCTGGACCC     53254       T_
                                GGGTTCA  TCCACTG
                                |||||||  |||||||
                                CCCAGGT  AGGTGAC
                                    CT
GAM51   KIAA0800  3'  AGTGGAATAGTCTGA      28145       CCGGGTTC
                                TCAGAC       ATTCCACT
                                ||||||       ||||||||
                                AGTCTG       TAAGGTGA
                                   A_______
GAM51   KIAA1962  3'  CCAGCAGAATGAAGGGATGGG  81916     GG__     CA
                                CCCG   TTCATTC  CTGG
                                ||||   |||||||  ||||
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                                GGGT   AAGTAAG  GACC
                                  AGGG     AC
GAM51   RASGRP4   3' AATGAGCAGCCCAGGCCTGG  53645     A  C   ___
                                TCAG CC GGGT   TCATT
                                |||| || ||||   |||||
                                GGTC GG CCCG   AGTAA
                                  C  A   ACG
GAM51   SC4MOL    3' CCAGTAAAACCATAGGCCTGA 22153     A  CG_   CATTCC
                                TCAG CC   GGTT    ACTGG
                                |||| ||   ||||    |||||
                                AGTC GG   CCAA    TGACC
                                  C  ATA   AA____
GAM51   ZNF31     5' CAGTGGATCCCTGGCCTGA   64982     A  C   TTCAT
                                TCAG CC GGG    TCCACTG
                                |||| || |||    |||||||
                                AGTC GG CCC    AGGTGAC
                                  C  T   T____
GAM51   LOC118611 5' CAGTGGAACAGAAGCCC     75471      _ A_
                                GGGTT C  TTCCACTG
                                ||||| |  ||||||||
                                CCCGA G  AAGGTGAC
                                   A AC
GAM51   LOC121133 3' CCAGTGGAAGCTCGTGCCTGA  75990     ACC    TCA
                                TCAG   CGGGT   TTCCACTGG
                                ||||   |||||  |||||||||
                                AGTC   GCTCG   AAGGTGACC
                                  CGT    ___
GAM51   LOC127281 3' CCAGTGGGGCTCCCCGCATCTG 74644      CC    TTCA
           A                     TCAGA  CGGG   TTCCACTGG
                                |||||  ||||   |||||||||
                                AGTCT  GCCC   GGGGTGACC
                                  AC   CTC_
GAM51   LOC127687 3' AATGAATACCCAGTCTGA    74687       CC   __
                                TCAGAC  GGGT  TCATT
                                ||||||  ||||  |||||
                                AGTCTG  CCCA  AGTAA
                                   A_   TA
GAM51   LOC146987 3' CCAGTGGAATAAATCT      83898      C
                                GGGTT ATTCCACTGG
                                ||||| ||||||||||
                                TCTAA TAAGGTGACC
                                   A
GAM51   LOC152457 3' CAGTGGAATAGGACCT      80607       _
                                GGGTTC ATTCCACTG
                                |||||| |||||||||
                                TCCAGG TAAGGTGAC
                                   A
GAM51   LOC220980 5' CCAGCAGTGGGCCCAGG     93150    C       CCA
                                CC GGGTTCATT   CTGG
                                || |||||||||   ||||
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                                GG CCCGGGTGA   GACC
                                 A       C__
GAM51   LOC51016 3'  CAGCGGGGCCCGGTTC     63736    C     TCAT   A
                                GA CCGGGT    TCC CTG
                                || ||||||    ||| |||
                                CT GGCCCG    GGG GAC
                                 T     _____   C
GAM51   LOC92095 3'  CAGCAGAGCCCGAGCCCGG   68091        A__   CA
                                CCGGGTTC   TTC  CTG
                                ||||||||   |||  |||
                                GGCCCGAG   GAG  GAC
                                     CCC   AC
GAM51   LOC92096 3'  CAGCAGAGCCCGAGCCCGG   68097        A__   CA
                                CCGGGTTC   TTC  CTG
                                ||||||||   |||  |||
                                GGCCCGAG   GAG  GAC
                                     CCC   AC
GAM51   LOC92710 3'  CCAGTGGAATAGGATAGCTGA  70355     ACCCGG   _
                                TCAG     GTTC ATTCCACTGG
                                ||||     |||| ||||||||||
                                AGTC     TAGG TAAGGTGACC
                                  GA_____   A
GAM52   ACN      5'  AACACCCAAGCGCCCC      30367      AAA T  ATCA
                                GGGGC   G CT    GGTGTT
                                |||||   | ||    ||||||
                                CCCCG   C GA    CCACAA
                                   ____ _  AC__
GAM52   CLCN6    3'  AAACACCTCTCTCTCCCC    41379     CAA  TCTATC
                                GGGG   AG     AGGTGTTT
                                ||||   ||     ||||||||
                                CCCC   TC     TCCACAAA
                                   ___  TCTC__
GAM52   CLCN6    3'  AAACACCTCTCTCTCCCC    41394     CAA  TCTATC
                                GGGG   AG     AGGTGTTT
                                ||||   ||     ||||||||
                                CCCC   TC     TCCACAAA
                                   ___  TCTC__
GAM52   CLCN6    3'  AAACACCTCTCTCTCCCC    7072      CAA  TCTATC
                                GGGG   AG     AGGTGTTT
                                ||||   ||     ||||||||
                                CCCC   TC     TCCACAAA
                                   ___  TCTC__
GAM52   CNTN3    3'  TATCTGATCAGACTTTGCCCC  66698          _
                                GGGGCAAAGTCT ATCAGGTG
                                |||||||||||| ||||||||
                                CCCCGTTTCAGA TAGTCTAT
                                       C
GAM52   CSRP1    3'  CAAACACCTTTCCCTTTGCCCT 14526         TCTATC
                                GGGGCAAAG     AGGTGTTTG
                                |||||||||     |||||||||
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                                TCCCGTTTC     TCCACAAAC
                                     CCTT__
GAM52   MYCL2    3'  TGATAGATTTTGCCCC      18191
                                GGGGCAAAGTCTATCA
                                ||||||||||||||||
                                CCCCGTTTTAGATAGT

GAM52   NTSR1    3'  ACTTCCTGCCAAACTTTGCCCC 10284          CTAT   T_
                                GGGGCAAAGT   CAGG  GT
                                ||||||||||   ||||  ||
                                CCCCGTTTCA   GTCC  CA
                                     AACC   TT
GAM52   RAB26    3'  CAAGTGGACAGACTTTGCC   26822          A  AGG_
                                GGCAAAGTCT TC   TG
                                |||||||||| ||   ||
                                CCGTTTCAGA AG   AC
                                     C  GTGA
GAM52   STK10    3'  CCTGATAGACCTGCCCC     19984       AA
                                GGGGCA  GTCTATCAGG
                                ||||||  ||||||||||
                                CCCCGT  CAGATAGTCC
                                   C_
GAM52   TCTA     3'  CAAACACCCACATACCTGGCCC 42234      AAA  CTATCA
                                GGGC   GT     GGTGTTTG
                                ||||   ||     ||||||||
                                CCCG   CA     CCACAAAC
                                  GTC  TACAC_
GAM52   ELKS     3'  CAAACACTACAAACTTCATCCC 30502      CA    CTATCA
                                GGGG  AAGT     GGTGTTTG
                                ||||  ||||     ||||||||
                                CCCT  TTCA     TCACAAAC
                                  AC    AACA__
GAM52   FLJ23537 3'  CAAACACCTGCCTCTCTTCAAC 46023     GCA   TCTAT
           CC                     GGG   AAG    CAGGTGTTTG
                                |||   |||    ||||||||||
                                CCC   TTC    GTCCACAAAC
                                  AAC   TCTCC
GAM52   KIAA0433 5'  CAAACACCTCACCCCTGCCTC  30835       AAGTCTATC
                                GGGGCA       AGGTGTTTG
                                ||||||       |||||||||
                                CTCCGT       TCCACAAAC
                                   CCCCAC___
GAM52   KIAA0450 3'  CACTGCTGATGACTTTGCCCC  27620          T    __
                                GGGGCAAAGTC ATCAG  GTG
                                |||||||||| |||||  |||
                                CCCCGTTTCAG TAGTC  CAC
                                      _    GT
GAM52   LEAP-2   5'  AAATATAAACTTTGCCCC    53739          CTATCAG
                                GGGGCAAAGT     GTGTTT
                                ||||||||||     ||||||
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                                CCCCGTTTCA      TATAAA
                                     AA_____
GAM52   LOC147077 3'  CACCTCCTAATAGACTTAGCCC 78249      A      C___
            C                    GGGGC AAGTCTAT    AGGTG
                                 ||||| ||||||||    |||||
                                 CCCCG TTCAGATA    TCCAC
                                    A       ATCC
GAM53   AARS    3'  TTGCTGCAGAGAATAAAAG   7833      CAG    TATT
                                 CTTT   TCTT    TGCAGCAA
                                 ||||   ||||    ||||||||
                                 GAAA   AGAG    ACGTCGTT
                                   ATA    ____
GAM53   ADRA2B  3'  TTGCTGCAGGGAGATGAAAG  5466       G     AT
                                 CTTTCA TCTTT  TTGCAGCAA
                                 ||||||| |||||  |||||||||
                                 GAAAGT AGAGG  GACGTCGTT
                                    _    __
GAM53   AGRN    3'  CTGTGAAATAAAGTCTGAAA   78836       T      _
                                 TTTCAG CTTTATTT GCAG
                                 |||||| |||||||| ||||
                                 AAAGTC GAAATAAA TGTC
                                    T       G
GAM53   BECN1   3'  TTTGCTGCAGTCTGAAAACTGA 13650       C    T_
            AA                     TTTCAGT TTTA  TTGCAGCAAA
                                 ||||||| ||||  ||||||||||
                                 AAAGTCA AAGT  GACGTCGTTT
                                     A    CT
GAM53   CLASP1  3'  CTGCAACTGCTAGGACTGAAAG 65302          TAT__
                                 CTTTCAGTCTT     TTGCAG
                                 ||||||||||     ||||||
                                 GAAAGTCAGGA     AACGTC
                                       TCGTC
GAM53   DNMT3L  5'  CTGCAAACCGGCACTGAAGG   25358        _ TTA
                                 CTTTCAGT CT   TTTGCAG
                                 |||||||| ||   |||||||
                                 GGAAGTCA GG   AAACGTC
                                     C  CC_
GAM53   ENC1    3'  TTTGCTGCACAAACATGAAA   13287      GTCTTTATT
                                 TTTCA        TGCAGCAAA
                                 |||||        |||||||||
                                 AAAGT        ACGTCGTTT
                                    ACAAAC___
GAM53   FLRT3   3'  CTGCAAAACACTGGAA      25216        CTTTA
                                 TTTCAGT     TTTGCAG
                                 |||||||     |||||||
                                 AAGGTCA     AAACGTC
                                     CA___
GAM53   FSTL3   3'  AAATAAAGACTCAAAG      19605      C
                                 CTTT AGTCTTTATTT
                                 |||| ||||||||||
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                                GAAA TCAGAAATAAA
                                  C
GAM53   KCNK10   3'  CTGTGCCATAAACAACTGAAAG 40969       C_    TT_
                                CTTTCAGT  TTTAT   GCAG
                                ||||||||  |||||   ||||
                                GAAAGTCA  AAATA   TGTC
                                    AC    CCG
GAM53   KCNK10   3'  CTGTGCCATAAACAACTGAAAG 56338       C_    TT_
                                CTTTCAGT  TTTAT   GCAG
                                ||||||||  |||||   ||||
                                GAAAGTCA  AAATA   TGTC
                                    AC    CCG
GAM53   KCNK10   3'  CTGTGCCATAAACAACTGAAAG 56343       C_    TT_
                                CTTTCAGT  TTTAT   GCAG
                                ||||||||  |||||   ||||
                                GAAAGTCA  AAATA   TGTC
                                    AC    CCG
GAM53   RP2      3'  TTTGATAAAACTAAGACTGAAA 22622         TA   GCAG
                                TTTCAGTCTT  TTT   CAAA
                                ||||||||||  |||   ||||
                                AAAGTCAGAA  AAA   GTTT
                                     TC   ATA_
GAM53   SCA1     5'  TGCTGCAAGGAACTGATAG   4401     T    CTTTA
                                CT TCAGT    TTTGCAGCA
                                || |||||    |||||||||
                                GA AGTCA    GAACGTCGT
                                 T    AG___
GAM53   VSX1     3'  CTGTCAAAGGCTGAAA      27466          ATTT
                                TTTCAGTCTTT   GCAG
                                ||||||||||   ||||
                                AAAGTCGGAAA   TGTC
                                      C___
GAM53   DKFZP586C1324 3'  CTGCATTGGGTGAAGACTAAAA 69797     C       ___
                                TTT AGTCTTTATT   TGCAG
                                ||| ||||||||||   |||||
                                AAA TCAGAAGTGG   ACGTC
                                  A        GTT
GAM53   DNAH7    3'  TGAAATAAATAAAGACTAAAG  38159     C         CAG
                                CTTT AGTCTTTATTTG   CA
                                |||| ||||||||||||   ||
                                GAAA TCAGAAATAAAT   GT
                                  _          AAA
GAM53   EDR1     3'  TGCTGCAGGGACTAAAAG    15385     C    TTAT
                                CTTT AGTCT    TTGCAGCA
                                |||| |||||    ||||||||
                                GAAA TCAGG    GACGTCGT
                                  A    ____
GAM53   FLJ10305 5'  CTGCAGCCAGCACTGAAAG   68359        _  TTAT
                                CTTTCAGT CT    TTGCAG
                                |||||||| ||    ||||||
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                                GAAAGTCA GA    GACGTC
                                    C  CC__
GAM53   FLJ10460  3'  TTTGCTGCTGGTAATACTGAAA 36135        CT    TT
            G                    CTTTCAGT  TTAT  GCAGCAAA
                                 ||||||||  ||||  ||||||||
                                 GAAAGTCA  AATG  CGTCGTTT
                                    T_   GT
GAM53   FLJ20340  3'  TTTGCTACAAAGGGGCTGCAAA 34981      _      TA    C
            G                    CTTT CAGTCTT  TTTG AGCAAA
                                 |||| |||||||  |||| ||||||
                                 GAAA GTCGGGG  AAAC TCGTTT
                                   C      __    A
GAM53   FLJ22557  3'  TGTTGAAAAGACTGAAAG    45256          ATTTG
                                 CTTTCAGTCTTT    CAGCA
                                 ||||||||||||    |||||
                                 GAAAGTCAGAAA    GTTGT
                                       A____
GAM53   FLJ22940  5'  TGCTGCAGACCAGAAAG    44698      A_   TTATTT
                                 CTTTC  GTCT    GCAGCA
                                 |||||  ||||    ||||||
                                 GAAAG  CAGA    CGTCGT
                                   AC   _______
GAM53   GBTS1     3'  TTGCTGTTGCAAGACTGAAGG  59066         TATTT
                                 CTTTCAGTCTT    GCAGCAA
                                 ||||||||||    |||||||
                                 GGAAGTCAGAA    TGTCGTT
                                       CGT__
GAM53   GT650     3'  CTGCTATTCAAAAACTGAGAG  53455       C   ATTT_
                                 CTTTCAGT TTT    GCAG
                                 ||||||||| |||    ||||
                                 GAGAGTCA AAA    CGTC
                                    A   CTTAT
GAM53   KIAA0537  3'  GCTGTGACAACAGACTGAAA   29250        TTAT TG
                                 TTTCAGTCT   T  CAGC
                                 |||||||||   |  ||||
                                 AAAGTCAGA   A  GTCG
                                    CAAC GT
GAM53   KIAA1165  3'  CTGCCTTAAAGATTGAAA    67406          TTT
                                 TTTCAGTCTTTA   GCAG
                                 ||||||||||||   ||||
                                 AAAGTTAGAAAT   CGTC
                                       TC_
GAM53   KIAA1464  3'  TTGCTACAAATAAGGA     68278          C
                                 TCTTTATTTG AGCAA
                                 |||||||||| |||||
                                 AGGAATAAAC TCGTT
                                       A
GAM53   MAP2K4    3'  TGCCACAAACCACCAGGACTGA 11553          TA___    CA
            AAG                    CTTTCAGTCTT    TTTG  GCA
                                 ||||||||||    ||||  |||
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                                GAAAGTCAGGA    AAAC  CGT
                                     CCACC    AC
GAM53   NYD-SP15  3'  GAATAAATACTGAAAG      48110         C
                                CTTTCAGT TTTATTT
                                |||||||| |||||||
                                GAAAGTCA AAATAAG
                                     T
GAM53   PEX11A    3'  TTTGCTGAATGAATAAAAATTG 13890         C      G__
          AAAG                    CTTTCAGT TTTATTT   CAGCAAA
                                |||||||| |||||||   |||||||
                                GAAAGTTA AAATAAG   GTCGTTT
                                     A      TAA
GAM53   PIGM      5'  TGCTGCAAAGAACCGAAGG    59047       A  CTTTA
                                CTTTC GT     TTTGCAGCA
                                ||||| ||     |||||||||
                                GGAAG CA     AAACGTCGT
                                   C  AG___
GAM53   PPIL3     5'  GCTGTAAGACTGAGA       55656         TTATT
                                TTTCAGTCT    TGCAGC
                                |||||||||    ||||||
                                AGAGTCAGA    ATGTCG
                                             _____
GAM53   PPIL3     5'  GCTGTAAGACTGAGA       55658         TTATT
                                TTTCAGTCT    TGCAGC
                                |||||||||    ||||||
                                AGAGTCAGA    ATGTCG
                                             _____
GAM53   PPIL3     5'  GCTGTAAGACTGAGA       50645         TTATT
                                TTTCAGTCT    TGCAGC
                                |||||||||    ||||||
                                AGAGTCAGA    ATGTCG
                                             _____
GAM53   SLC17A6   3'  TTGCTGTAAAAATGAAA      39749       GTCTTTA
                                TTTCA      TTTGCAGCAA
                                |||||      ||||||||||
                                AAAGT      AAATGTCGTT
                                   AA_____
GAM53   TBLR1     3'  CTGCCAATTAAAGACTAGAAG  45101      TC       T  _
                                CTT  AGTCTTTA TTG CAG
                                |||  |||||||| ||| |||
                                GAA  TCAGAAAT AAC GTC
                                  GA       T   C
GAM53   ZNF304    3'  TTGCTAGGAAAGACTGAAA    40319           ATTT
                                TTTCAGTCTTT    GCAG
                                ||||||||||    ||||
                                AAAGTCAGAAA    CGTT
                                     GGAT
GAM53   LOC113115 5'  TGCTGTAAGACAGAAAG      56547       A    TTATT
                                CTTTC GTCT     TGCAGCA
                                ||||| ||||     |||||||
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                                GAAAG CAGA     ATGTCGT
                                  A  _____
GAM53   LOC115004 3'  TGCTGCTCAGACTGAA      73176         TTATTT
                                TTCAGTCT      GCAGCA
                                ||||||||      ||||||
                                AAGTCAGA      CGTCGT
                                    CT____
GAM53   LOC145845 3'  CAGATAAAGACTAAAA      83552      C
                                TTT AGTCTTTATTTG
                                ||| ||||||||||||
                                AAA TCAGAAATAGAC
                                  A
GAM53   LOC160897 3'  GCAGTACCAAGACTGAAA    82246          TAT_
                                TTTCAGTCTT    TTGC
                                ||||||||||    ||||
                                AAAGTCAGAA    GACG
                                      CCAT
GAM53   LOC162333 5'  CTCAGATAAAGACTGAA      87129            C
                                TTCAGTCTTTATTTG AG
                                |||||||||||||| ||
                                AAGTCAGAAATAGAC TC
                                                _
GAM53   LOC223073 5'  TTGCCTGAAGACTGAAA      94381          TTT
                                TTTCAGTCTTTA   GCAG
                                ||||||||||||   ||||
                                AAAGTCAGAAGT   CGTT
                                      C__
GAM53   LOC255177 3'  CTGGGATTACAGAGACTGAAA  96604          AT__  G
                                TTTCAGTCTTT    TT CAG
                                ||||||||||    || |||
                                AAAGTCAGAGA    AG GTC
                                      CATT  G
GAM53   LOC256730 3'  TTGCAGCAAGACTGAAA      95236         TTATT   A
                                TTTCAGTCT     TGC GCAA
                                |||||||||     ||| ||||
                                AAAGTCAGA     ACG CGTT
                                    _____   A
GAM53   LOC257469 3'  CTGCTGGTGAAGACTG       95714          TT
                                CAGTCTTTAT  GCAG
                                ||||||||||  ||||
                                GTCAGAAGTG  CGTC
                                      GT
GAM53   LOC90529  3'  TGCCGCAGACTGAAGG       63165         TTATTT  A
                                CTTTCAGTCT     GC GCA
                                ||||||||||     || |||
                                GGAAGTCAGA     CG CGT
                                    _______  C
GAM54   ABCB11    5'  TCTGGCTTCCTCAAATTC     13618         A    ATGA
                                GAATTTGA GAAG    AGA
                                ||||||||| ||||    |||
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                                CTTAAACT CTTC    TCT
                                     C    GG__
GAM54   APC      3'  CTTCATCTTCTTGTTGCA    3477     G   TTG
                                TG AAT   AAGAAGATGAAG
                                || |||   ||||||||||||
                                AC TTG   TTCTTCTACTTC
                                 G   ___
GAM54   ATP1B2   3'  CTTCCCAGAATATCCTTCAAGT 8049           AA    AA____
            TCCA                   GGAATTTGAAG  GATG     GAAG
                                |||||||||||  ||||     ||||
                                CCTTGAACTTC  CTAT     CTTC
                                       __   AAGACC
GAM54   CA4      3'  TCAGCTCTCCAAGTTCCA    5552          A   AGA
                                TGGAATTTG AGA   TGA
                                |||||||||| |||   |||
                                ACCTTGAAC TCT   ACT
                                     C   CG_
GAM54   CEP1     5'  CTTCCGTTCGTTCTTCAAAACC 22816     AA       _  T__
            CA                   TGG  TTTGAAGAA GA   GAAG
                                |||  |||||||||| ||   ||||
                                ACC  AAACTTCTT CT   CTTC
                                  CA        G  TGC
GAM54   CEP2     3'  CTTCATCTTCTCCTTCAA    23227      ___
                                TTGA   AGAAGATGAAG
                                ||||   ||||||||||||
                                AACT   TCTTCTACTTC
                                  TCC
GAM54   FBLN5    3'  CTTCTTCACCTCTTCCACTCC  20916     ATTT     A A
                                GGA    GAAGA G TGAAGAAG
                                |||    ||||| | ||||||||
                                CCT    CTTCT C ACTTCTTC
                                  CAC_     _ C
GAM54   GAC1     3'  TCCCCATCTTCTCTCTGCCCA  20945     AATTT  _       AA
                                TGG    GA AGAAGATG  GA
                                |||    || ||||||||  ||
                                ACC    CT TCTTCTAC  CT
                                  CGT__  C       CC
GAM54   GATA4    3'  CTTCCCTCCTCAAATTCC    9005          A  AGAT
                                GGAATTTGA GA    GAAG
                                |||||||||  ||    ||||
                                CCTTAAACT CT    CTTC
                                     C  CC__
GAM54   MGA      3'  TTCTTTATCCCAAATCCCA   62812     A    AAGAA
                                TGG ATTTG    GATGAAGAA
                                ||| |||||    |||||||||
                                ACC TAAAC    CTATTTCTT
                                  C    C____
GAM54   PIK3R3   3'  TCGTTTCCTTACAAATTCCA  61064         _  A
                                TGGAATTTG AAG AGATGA
                                |||||||||  ||| ||||||
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                                ACCTTAAAC TTC TTTGCT
                                     A   C
GAM54   POU2F2   3'  TCTTCATCCTCATCCTCC    10692     ATTT  A  A
                                GGA    GA GA GATGAAGA
                                |||    || || ||||||||
                                CCT    CT CT CTACTTCT
                                  C___  A  C
GAM54   PTPRS    3'  TCCTTTCCTTCCAATTCCA   11141       T   A   T
                                TGGAATT GAAG AGA GA
                                ||||||| |||| ||| ||
                                ACCTTAA CTTC TTT CT
                                    C   C   C
GAM54   PTPRS    3'  TCCTTTCCTTCCAATTCCA   55645       T   A   T
                                TGGAATT GAAG AGA GA
                                ||||||| |||| ||| ||
                                ACCTTAA CTTC TTT CT
                                    C   C   C
GAM54   PTPRS    3'  TCCTTTCCTTCCAATTCCA   55648       T   A   T
                                TGGAATT GAAG AGA GA
                                ||||||| |||| ||| ||
                                ACCTTAA CTTC TTT CT
                                    C   C   C
GAM54   PTPRS    3'  TCCTTTCCTTCCAATTCCA   55651       T   A   T
                                TGGAATT GAAG AGA GA
                                ||||||| |||| ||| ||
                                ACCTTAA CTTC TTT CT
                                    C   C   C
GAM54   SELL     3'  TCCCCACCTTCTTCAGCCACC  5393     AAT       A  AA
                                GG   TTGAAGAAG TG  GA
                                ||   ||||||||| ||  ||
                                CC   GACTTCTTC AC  CT
                                  ACC        C  CC
GAM54   TEM7     3'  CTTTTTCTTCCTCAAATTC   39885        A    T
                                GAATTTGA GAAGA GAAG
                                |||||||| ||||| ||||
                                CTTAAACT CTTCT TTTC
                                     C    T
GAM54   WT1      3'  TTCTTCATCCAACTTCCA    44357      T  AAGAA
                                TGGAA TTG    GATGAAGAA
                                ||||| |||    |||||||||
                                ACCTT AAC    CTACTTCTT
                                   C  _____
GAM54   WT1      3'  TTCTTCATCCAACTTCCA    44367      T  AAGAA
                                TGGAA TTG    GATGAAGAA
                                ||||| |||    |||||||||
                                ACCTT AAC    CTACTTCTT
                                   C  _____
GAM54   WT1      3'  TTCTTCATCCAACTTCCA    44377      T  AAGAA
                                TGGAA TTG    GATGAAGAA
                                ||||| |||    |||||||||
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                                ACCTT AAC    CTACTTCTT
                                  C  _____
GAM54   WT1      3'  TTCTTCATCCAACTTCCA    4592       T   AAGAA
                                TGGAA TTG    GATGAAGAA
                                ||||| |||    |||||||||
                                ACCTT AAC    CTACTTCTT
                                  C  _____
GAM54   AD-003   5'  CTTCCCCATCTTCTTC      25931          AA
                                GAAGAAGATG  GAAG
                                ||||||||||  ||||
                                CTTCTTCTAC  CTTC
                                      CC
GAM54   CEACAM7  3'  CTTCTAGCTCCTTCAATCCCA  22557     AAT     A  AT_
                                TGG   TTGAAG AG   GAAG
                                |||   |||||| ||   ||||
                                ACC   AACTTC TC   CTTC
                                  CT_     C  GAT
GAM54   CSMD1    3'  CTTCTTTGTCCTCAATTTCCA  73120      T    AGAA  TG
                                TGGAA TTGA    GA  AAGAAG
                                ||||| ||||    ||  ||||||
                                ACCTT AACT    CT  TTCTTC
                                  T    C___  GT
GAM54   DDX34    3'  CATGTCTCCAGATTCCA     27979         A   AG
                                TGGAATTTG AGA  ATG
                                ||||||||| |||  |||
                                ACCTTAGAC TCT  TAC
                                      C   G_
GAM54   DKFZP434B205 3'  CTTCTTCATCTTCCTGGACGTC 75320    ATTTGAA
                                GA      GAAGATGAAGAAG
                                ||      |||||||||||||
                                CT      CTTCTACTTCTTC
                                 GCAGGTC
GAM54   FENS-1   3'  CTTCCCTTTCCCCCAAATTCC  40439        AA_   AT
                                GGAATTTG   GAAG  GAAG
                                ||||||||   ||||  ||||
                                CCTTAAAC   CTTT  CTTC
                                     CCC    CC
GAM54   FLJ13262  3'  ATCCTCTCCAAATTCC      46155         A   A
                                GGAATTTG AGA GAT
                                |||||||| ||| |||
                                CCTTAAAC TCT CTA
                                     C   C
GAM54   FLJ20170  3'  TCACCTTCTTCAACTCCA    34672      AT       A
                                TGGA  TTGAAGAAG TGA
                                ||||  ||||||||| |||
                                ACCT  AACTTCTTC ACT
                                  C_       C
GAM54   FLJ20375  3'  CTTCTCCCTGCTAAATTCCA   35085         A_  AA  T
                                TGGAATTTG  AG  GA GAAG
                                |||||||||  ||  || ||||
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                                ACCTTAAAT  TC  CT CTTC
                                     CG  C_  _
GAM54   FLJ20802 3' CTTCTTCACCTTTGCATCC   35669    ATT  AA   A
                                GGA   TG  GAAG TGAAGAAG
                                |||   ||  |||| ||||||||
                                CCT   AC  TTTC ACTTCTTC
                                  ___  G_   C
GAM54   FLJ22055 3' CTTCATCTTCTGCTCCA    45496     ATTTGA
                                TGGA     AGAAGATGAAG
                                ||||     ||||||||||
                                ACCT     TCTTCTACTTC
                                  CG____
GAM54   HUMAGCGB 5' CTATGCCTTCCTCAAGTTCCA 25231          A   AT A
                                TGGAATTTGA GAAG  G AG
                                |||||||||| ||||  | ||
                                ACCTTGAACT CTTC  T TC
                                      C   CG A
GAM54   INA     3' CACCTCCTTCAATTCCA    51187       T   A  A
                                TGGAATT GAAG AG TG
                                ||||||| |||| || ||
                                ACCTTAA CTTC TC AC
                                    _   C  C
GAM54   KIAA0451 5' TCATAATTCTCAAATTCCA   29114         AG AG
                                TGGAATTTGA  A  ATGA
                                ||||||||||  |  ||||
                                ACCTTAAACT  T  TACT
                                      CT AA
GAM54   KIAA0972 5' CTTCTTCATCCCCTTGCCCA  30010    AATTTG  AA
                                TGG     AAG  GATGAAGAAG
                                |||     |||  ||||||||||
                                ACC     TTC  CTACTTCTTC
                                  CG____   CC
GAM54   MGC15854 5' TTCCCCATCTTCTCCTCTA   58852     ATTT  A     AA
                                TGGA   GA GAAGATG  GAA
                                ||||   || |||||||  |||
                                ATCT   CT CTTCTAC  CTT
                                  C___  _      CC
GAM54   MGC17998 3' TTCCTCATCTTCTGGTCC    58746    ATTTGA       A
                                GGA     AGAAGATGA GAA
                                |||     ||||||||| |||
                                CCT     TCTTCTACT CTT
                                  GG____        C
GAM54   MIL1    3' TCTTCACCCCCAGGTTCC    31097        AAGAAGA
                                GGAATTTG      TGAAGA
                                ||||||||      ||||||
                                CCTTGGAC      ACTTCT
                                    CCCC___
GAM54   NYD-SP21 3' CTTCAGCTTCCTCAAATTC   50873        A   A
                                GAATTTGA GAAG TGAAG
                                |||||||| |||| |||||
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                                CTTAAACT CTTC ACTTC
                                     C    G
GAM54   PCDH19   3'  TTCTTCATCCAAAATTGCA   63713    G    GAAGAA
                                TG AATTT     GATGAAGAA
                                || |||||     |||||||||
                                AC TTAAA     CTACTTCTT
                                 G    AC____
GAM54   PEG10    3'  CTTCACCGTCTTCAAACTCCA  30525      A       AGA
                                TGGA TTTGAAGA   TGAAG
                                |||| ||||||||   |||||
                                ACCT AAACTTCT   ACTTC
                                  C       GCC
GAM54   TRIM16   3'  TCATCTTCTAGTGCCA     21343     A   TGA
                                TGG ATT   AGAAGATGA
                                ||| |||   |||||||||
                                ACC TGA   TCTTCTACT
                                  G   ___
GAM54   LOC124245 3'  CTCCATCTTCTTCCCTGGCC   58152    AATTT        A
                                GG    GAAGAAGATG AG
                                ||    |||||||||| ||
                                CC    CTTCTTCTAC TC
                                 GGTCC        C
GAM54   LOC144231 5'  ATCTTCCTCAAACTTCA     83011      A    A
                                TGGA TTTGA GAAGAT
                                |||| ||||| ||||||
                                ACTT AAACT CTTCTA
                                  C    C
GAM54   LOC145739 3'  TCATTCTTCAAAGCCCA     77443     AA       AG
                                TGG  TTTGAAGA  ATGA
                                |||  ||||||||  ||||
                                ACC  AAACTTCT  TACT
                                  CG      __
GAM54   LOC146856 3'  CTTCCTTTTTTCTTCTTCAACC 82802      AT        T_   _
            TCCA                   TGGA  TTGAAGAAGA  GAAG AAG
                                |||| ||||||||||  |||| |||
                                ACCT  AACTTCTTCT  TTTC TTC
                                  CC        TT    C
GAM54   LOC147166 3'  TCATCTTCTAGTGCCA     78290     A   TGA
                                TGG ATT   AGAAGATGA
                                ||| |||   |||||||||
                                ACC TGA   TCTTCTACT
                                  G   ___
GAM54   LOC151124 5'  TCTGTTCTTCCCCAAATTCC   85234        AA    TGA
                                GGAATTTG  GAAGA   AGA
                                ||||||||  |||||   |||
                                CCTTAAAC  CTTCT   TCT
                                     CC    TG_
GAM54   LOC151405 5'  CTTCTTCATGACACCAAATCCA 85337      A    AAGAAG
                                TGGA TTTG     ATGAAGAAG
                                |||| ||||     |||||||||
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                                ACCT AAAC     TACTTCTTC
                                  _   CACAG_
GAM54   LOC151438 5' CTTCTGGGACCAAATTCCA   85365        A____
                                TGGAATTTG    AGAAG
                                |||||||||    |||||
                                ACCTTAAAC    TCTTC
                                     CAGGG
GAM54   LOC153469 3' CTTCATCTTCTCCTCA      80841    __
                                TGA  AGAAGATGAAG
                                |||  ||||||||||
                                ACT  TCTTCTACTTC
                                  CC
GAM54   LOC157909 5' CTTCTCAGACTTAAAATTCCA 81627       G   AAGA   A
                                TGGAATTT AAG    TGA GAAG
                                |||||||| |||    ||| ||||
                                ACCTTAAA TTC    ACT CTTC
                                     A   AG__   _
GAM54   LOC165140 5' TCTTCATCTTCTGCATCCA    82467     ATT  A
                                TGGA   TG AGAAGATGAAGA
                                ||||   || ||||||||||||
                                ACCT   AC TCTTCTACTTCT
                                  ___ G
GAM54   LOC169831 5' CTTCTTCATCTTCCCTTC     82783     __
                                GAA  GAAGATGAAGAAG
                                |||  ||||||||||||
                                CTT  CTTCTACTTCTTC
                                  CC
GAM54   LOC197414 3' CTTGGCTTCTTCAAACGCCA   88066     AA        ATG
                                TGG  TTTGAAGAAG   AAG
                                |||  ||||||||||   |||
                                ACC  AAACTTCTTC   TTC
                                  GC         GG_
GAM54   LOC219894 3' CTTCCCAACTTCTTCAAATTC  93281           A  AA
                                GAATTTGAAGAAG TG  GAAG
                                |||||||||||| ||  ||||
                                CTTAAACTTCTTC AC  CTTC
                                       A  C_
GAM54   LOC255040 3' CTTCCTTTTGCTCCAAATTCC  96382        A  _    T
                                GGAATTTG AG AAGA GAAG
                                |||||||| || |||| ||||
                                CCTTAAAC TC TTTT CTTC
                                     C  G    C
GAM54   LOC255041 3' CTTCCTTTTGCTCCAAATTCC  96388        A  _    T
                                GGAATTTG AG AAGA GAAG
                                |||||||| || |||| ||||
                                CCTTAAAC TC TTTT CTTC
                                     C  G    C
GAM54   LOC90371  5' TCTTCATCCTCCTCTACC     62504     AATTT  A  A
                                GG     GA GA GATGAAGA
                                ||     || || ||||||||
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                                CC    CT CT CTACTTCT
                                 AT___  C  C
GAM54   LOC92539 5'  TCCTCTCTTCAAGTCCCA    69643     A       A  T
                                TGG ATTTGAAGA GA GA
                                ||| ||||||||| || ||
                                ACC TGAACTTCT CT CT
                                  C       _  C
GAM55   BCAT1    3'  CCACATTATAACTAGGCAA    66201         C  C  AA
                                TTGCCTAGT AT AA  TGG
                                ||||||||| || ||  |||
                                AACGGATCA TA TT  ACC
                                     A  _  AC
GAM55   CRY1     5'  TCCGCCGACTAGGCAA      14523          ATCAAAA
                                TTGCCTAGTC      TGGA
                                ||||||||||      ||||
                                AACGGATCAG      GCCT
                                     CC_____
GAM55   GPRC5B   3'  GTTTCCATCTGTCCTGAGCAA  32665     C   TCAT  AA
                                TTGC TAG   CA  ATGGAAAC
                                |||| |||   ||  ||||||||
                                AACG GTC   GT  TACCTTTG
                                  A  CT__  C_
GAM55   MXI1     3'  TTCCATTTTCCTACAGGCAG   19904       A  CATC
                                TTGCCT GT   AAAATGGAA
                                |||||| ||   |||||||||
                                GACGGA CA   TTTTACCTT
                                   _  TCC_
GAM55   MXI1     3'  TTCCATTTTCCTACAGGCAG   55265       A  CATC
                                TTGCCT GT   AAAATGGAA
                                |||||| ||   |||||||||
                                GACGGA CA   TTTTACCTT
                                   _  TCC_
GAM55   PIGN     3'  TTCATGTTAATGACTAGG    24674         C  A
                                CCTAGTCAT AA ATGGA
                                ||||||||| || |||||
                                GGATCAGTA TT TACTT
                                     A  G
GAM55   PKHD1    3'  TCCTAGTTCAATGCTAGGCAA  56917         T   CA  AT_
                                TTGCCTAG CAT  AA   GGA
                                |||||||| |||  ||   |||
                                AACGGATC GTA  TT   CCT
                                     _   AC  GAT
GAM55   PPL      3'  TCCAATGACTGGACAA      10706     C       CAAAA
                                TTG CTAGTCAT     TGGA
                                ||| ||||||||     ||||
                                AAC GGTCAGTA     ACCT
                                  A       _____
GAM55   SMARCA1  3'  GTTTCCATTTTAGTCAC     11780    C  C
                                GT AT AAAATGGAAAC
                                || || ||||||||||
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                                CA TG TTTTACCTTTG
                                 C  A
GAM55   SMARCA1   3'  GTTTCCATTTTAGTCAC     57390    C  C
                                GT AT AAAATGGAAAC
                                || || ||||||||||
                                CA TG TTTTACCTTTG
                                 C  A
GAM55   TBXA2R    5'  TTTCCATTTTGTAAAGCA    6507     CTAGTCAT
                                TGC       CAAAATGGAAA
                                |||       ||||||||||
                                ACG       GTTTTACCTTT
                                  AAAT_____
GAM55   DKFZP586F1318 3'  TTTCCATTTGCAAAGTGACTAG 31621        CA___
                                CTAGTCAT    AAATGGAAA
                                ||||||||    |||||||||
                                GATCAGTG    TTTACCTTT
                                     AAACG
GAM55   FLJ10120  3'  TTTCCATTTTAGAAAGTGCAA  35836     _  AG  ATC
                                TTGC CT  TC   AAAATGGAAA
                                |||| ||  ||   ||||||||||
                                AACG GA  AG   TTTTACCTTT
                                  T  A_  A__
GAM55   KIAA0202  3'  GTTTCCATTCTGAAAAATAG   64370    GTCA   A
                                CTA    TCA AATGGAAAC
                                |||    ||| |||||||||
                                GAT    AGT TTACCTTTG
                                  AAAA   C
GAM55   KIAA0471  3'  TTCCATTTAATACAGGCAA   29404       A  CATCA
                                TTGCCT GT    AAATGGAA
                                |||||| ||    ||||||||
                                AACGGA CA    TTTACCTT
                                   _  TAA__
GAM55   MGC2647   3'  GTTTCTCTTTGATGACCAGG   73707     A       AT
                                CCT GTCATCAAA  GGAAAC
                                ||| |||||||||  ||||||
                                GGA CAGTAGTTT  TCTTTG
                                  C        C_
GAM55   MGC4309   3'  CCATTTTGAAGAGATGCAA   44128     CTAG  A
                                TTGC    TC TCAAAATGG
                                ||||    || |||||||||
                                AACG    AG AGTTTTACC
                                  TAG_  A
GAM55   MGC5139   5'  GTTCCCATTTTGGAGGACAGAC 74109     C  A   A_       A
          AA                    TTG CT GTC  TCAAAATGG AAC
                                ||| || |||  ||||||||| |||
                                AAC GA CAG  GGTTTTACC TTG
                                  A  _   GA        C
GAM55   PRO1596   3'  GTTTCCATTTTTGTGC     48386    T   C
                                G CAT AAAATGGAAAC
                                | ||| ||||||||||
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                                C GTG TTTTACCTTTG
                                 _  T
GAM55   LOC130026 3'  TTCTATTTGATTACTAAGCAA  56652     C   C     A
                                TTGC TAGT ATCAAA TGGAA
                                |||| |||| |||||| |||||
                                AACG ATCA TAGTTT ATCTT
                                  A   T    _
GAM55   LOC144699 3'  GTTTCCATTTTAATGG      76915      C
                                TCAT AAAATGGAAAC
                                |||| ||||||||||
                                GGTA TTTTACCTTTG
                                  A
GAM55   LOC146146 3'  GTTTCCATTTTATAGATAAGCA 77677      CTA   ATC
           A                     TTGC   GTC   AAAATGGAAAC
                                |||| |||  ||||||||||
                                AACG   TAG   TTTTACCTTTG
                                  AA_   ATA
GAM55   LOC149706 5'  TTTCCATTTTACAGACAAGG   84646     A   ATC
                                CCT GTC   AAAATGGAAA
                                ||| |||   |||||||||
                                GGA CAG   TTTTACCTTT
                                  A   ACA
GAM55   LOC219855 3'  TCCATTTTGATAAGG       91517     AGTC
                                CCT    ATCAAAATGGA
                                |||    ||||||||||
                                GGA    TAGTTTTACCT
                                  A___
GAM55   LOC221474 5'  TCCATGTGGACTGGACAA    92387     C     ATCAAA
                                TTG CTAGTC     ATGGA
                                ||| ||||||     |||||
                                AAC GGTCAG     TACCT
                                  A     GTG___
GAM55   LOC253187 5'  CCAATGACTGGCAA        97114       T     CAAAA
                                TTGCC AGTCAT     TGG
                                ||||| ||||||    |||
                                AACGG TCAGTA     ACC
                                   _    _____
GAM55   LOC254394 3'  TTCAGGATACTAGGCAA     95984         C   AAAATG
                                TTGCCTAGT ATC      GAA
                                ||||||||| |||      |||
                                AACGGATCA TAG      CTT
                                     _  GA____
GAM55   LOC254778 3'  GTTTCAGGCATGATACTAGGCA 96130         C    AAATG
           A                     TTGCCTAGT ATCA     GAAAC
                                ||||||||| ||||    |||||
                                AACGGATCA TAGT     CTTTG
                                     _   ACGGA
GAM55   LOC255446 5'  GTTTCCATCTCAAAGAAGGCA  97155      AG  ATCAAA
                                TGCCT  TC     ATGGAAAC
                                |||||  ||     ||||||||
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                                ACGGA AG    TACCTTTG
                                  __ AAACTC
GAM56  EVI2A   3' GAATAGGTCCTTTATCTTTCCA 26392       CAT   AGT
                                TGGAAAGA  AGGGT  TTC
                                ||||||||  |||||  |||
                                ACCTTTCT  TCCTG  AAG
                                    ATT   GAT
GAM56  GNB3    3' GAACTGCCCCATCTCCTCC   9077    A_  CATA
                                GGA AGA   GGGTAGTTT
                                ||| |||   |||||||||
                                CCT TCT   CCCGTCAAG
                                 CC  AC__
GAM56  HIS1    3' AAGCTATCCACCTTTCCA    21309       ACATA
                                TGGAAAG   GGGTAGTTT
                                |||||||   |||||||||
                                ACCTTTC   CCTATCGAA
                                    CA___
GAM56  RASGRP1 3' AGAAAACTACCCATATTCCA  19202     AGACATA      C
                                TGGAA     GGGTAGTTT CT
                                |||||     ||||||||| ||
                                ACCTT     CCCATCAAA GA
                                  ATA____       A
GAM56  WNT5A   5' GAAACTGCCTATATCTTGCCA  12665    A   C   G
                                TGG AAGA ATAGG TAGTTTC
                                ||| |||| ||||| |||||||
                                ACC TTCT TATCC GTCAAAG
                                 G   A   _
GAM56  CALN1   3' GAAGCTGCGCCCCACCTTTCCA 48869       ACATA _
                                TGGAAAG   GG GTAGTTTC
                                |||||||   || ||||||||
                                ACCTTTC   CC CGTCGAAG
                                    CACC_ G
GAM56  DKFZP434K1772 3' GAGACTGCCTCTCCA     67712     AAGACATA
                                TGGA      GGGTAGTTTC
                                ||||      ||||||||||
                                ACCT      TCCGTCAGAG
                                  C_______
GAM56  DKFZP564I0422 3' AGGAAACTACTTATATCTTCAC 48713   GA   C   G
           A                     TG  AAGA ATAGG TAGTTTCCT
                                ||  |||| ||||| |||||||||
                                AC  TTCT TATTC ATCAAAGGA
                                 AC   A   _
GAM56  ESDN    3' AGGAAACTACTAATCTTGCCA  55170    A   CATAG
                                TGG AAGA    GGTAGTTTCCT
                                ||| ||||    ||||||||||
                                ACC TTCT    TCATCAAAGGA
                                 G   AA___
GAM56  FLJ10597 3' GAAGCTGCCTATGCGTCC   36315    AAGA    G
                                GGA   CATAGG TAGTTTC
                                |||   |||||| |||||||
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                                CCT   GTATCC GTCGAAG
                                  GC__    _
GAM56   FLJ13456 3' AGGAAATTTTCCACATCTTTC 65932      CATA  T
                                GAAAGA   GGG AGTTTCCT
                                ||||||   ||| ||||||||
                                CTTTCT   CCT TTAAAGGA
                                   ACA_  T
GAM56   KIAA0483 3' GAAACTGTCCCTTTCCA    30790      ACATA GT   C
                                TGGAAAG   GG  AGTTT C
                                |||||||    ||  ||||| |
                                ACCTTTC    CC  TCAAA G
                                   _____ TG   A
GAM56   KIAA0682 3' GAATTCCCACCTATGTCTTTCC 32475          GT__
           A                     TGGAAAGACATAGG   AGTTT
                                ||||||||||||||   |||||
                                ACCTTTCTGTATCC   TTAAG
                                        ACCC
GAM56   KIAA0763 3' GGAAACTCTCCCTCTCCA    29534    AAGACAT   T_
                                TGGA     AGGG  AGTTTCC
                                ||||     ||||  |||||||
                                ACCT     TCCC  TCAAAGG
                                  C_______   TC
GAM56   KIAA1462 3' AGGAAACTTGCCATCCTCTCA 91381   A  CATAG   _
                                A AGA    GGTA GTTTCCT
                                | |||    |||| |||||||
                                A TCT    CCGT CAAAGGA
                                 C  CCTA_   T
GAM56   NR2F1    3' AGGAAACTAATGGACCTTCCA 95948     AGA_  AGGG
                                TGGAA   CAT   TAGTTTCCT
                                |||||   |||   |||||||||
                                ACCTT   GTA   ATCAAAGGA
                                   CCAG  ____
GAM56   RAB33B   3' AGGAAACTACCCCAGAATCT  48486    CATA_
                                AGA    GGGTAGTTTCCT
                                |||    ||||||||||||
                                TCT    CCCATCAAAGGA
                                  AAGAC
GAM56   SEPW1    3' TACCCCATGTCTTCCC     11540    A     A
                                GG AAGACAT GGGTA
                                || ||||||| |||||
                                CC TTCTGTA CCCAT
                                 C      C
GAM56   U5-116KD 3' AGGAAACTGCTGCCTCCCC   14906    AA  A  TAGG
                                GG  AG CA   GTAGTTTCCT
                                ||  || ||   ||||||||||
                                CC  TC GT   CGTCAAAGGA
                                 CC  C  _____
GAM56   LOC143287 3' AAGTACCCTATCCTTCCCA   82926    A   AC      G
                                TGG AAG  ATAGGGTA TT
                                ||| |||  |||||||| ||
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                                ACC TTC  TATCCCAT AA
                                  C  C_      G
GAM56   LOC144058 5'  AAGCTGCCCTCACCCCTCCA  76664     AAGACAT
                                TGGA      AGGGTAGTTT
                                ||||      ||||||||||
                                ACCT      TCCCGTCGAA
                                  CCCCAC_
GAM56   LOC151126 3'  AGAAAACCATTCTCTATTTTTC 80123       CAT    A   C
           CA                     TGGAAAGA   AGGGT GTTT CT
                                ||||||||   ||||| |||| ||
                                ACCTTTTT   TCTTA CAAA GA
                                    ATC    C   A
GAM56   LOC257475 3'  GGAAACTTGCCGTTTCCA    72421     AA   ATAG   _
                                TGGA  GAC    GGTA GTTTCC
                                ||||  |||    |||| ||||||
                                ACCT  TTG    CCGT CAAAGG
                                  __  ____    T
GAM57   CDH2     3'  AAACAGTGACATTTGATTCAA  8374        ___   G
                                TTGAATCAA   TCAT GTTT
                                |||||||||   |||| ||||
                                AACTTAGTT   AGTG CAAA
                                    TAC    A
GAM57   EGLN1    5'  GAGTGTAGTATGACTAATTCA  41895      CAA    GT
                                TGAAT   TCATG  TTACACTC
                                |||||   |||||  ||||||||
                                ACTTA   AGTAT  GATGTGAG
                                  ATC    __
GAM57   MAB21L1   3'  AGTGTAAACTTCTGTTCAA   18760      CAATCAT
                                TTGAAT      GGTTTACACT
                                ||||||      ||||||||||
                                AACTTG      TCAAATGTGA
                                   TCT____
GAM57   NAP1L3   3'  AGACCACATTTGATTCAA    15794        TCA
                                TTGAATCAA   TGGTTT
                                |||||||||   ||||||
                                AACTTAGTT   ACCAGA
                                    TAC
GAM57   PKIB     3'  TGTAAATCAAACATGATTGATT 50643          ____
           TAA                    TTGAATCAATCATG    GTTTACA
                                ||||||||||||||    |||||||
                                AATTTAGTTAGTAC    TAAATGT
                                      AAAC
GAM57   TSG101   3'  AGTGTAAAATATTTTGAATCAA 20838     A    TCATGG
                                TTGA TCAA     TTTACACT
                                ||||  ||||     ||||||||
                                AACT AGTT     AAATGTGA
                                  A   TTATA_
GAM57   FLJ20605  5'  AAGCATATAGATTGGTTCAA   35444         _   _
                                TTGAATCAATC ATG GTTT
                                |||||||||| ||| ||||
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                                AACTTGGTTAG TAT CGAA
                                      A   A
GAM57   KIAA1265  3'  GCCTGATTGATTTAA       70790           T
                                TTGAATCAATCA GGT
                                |||||||||||| |||
                                AATTTAGTTAGT CCG
                                          _
GAM57   LOC143188 5'  GCCAGTTGATTCAA        82899          CA
                                TTGAATCAAT  TGGT
                                ||||||||||  ||||
                                AACTTAGTTG  ACCG
                                          __
GAM57   LOC149684 3'  AACCATGACTGACTTAA     84609      A   A
                                TTGA TCA TCATGGTT
                                |||| ||| ||||||||
                                AATT AGT AGTACCAA
                                  C   C
GAM57   LOC153222 3'  GAGCATAAACCATGATT     80788           CA
                                AATCATGGTTTA  CTC
                                ||||||||||||  |||
                                TTAGTACCAAAT  GAG
                                      AC
GAM57   LOC201895 3'  TAAACATGATTGATCAA     89093      A       G
                                TTGA TCAATCATG TTTA
                                |||| ||||||||| ||||
                                AACT AGTTAGTAC AAAT
                                  _       _
GAM57   LOC203276 3'  AGTGCAAACTGTGCTTGTCCAA 90472     AAT   T      A
                                TTG   CAA CATGGTTT CACT
                                |||   ||| |||||||| ||||
                                AAC   GTT GTGTCAAA GTGA
                                  CT_   C       C
GAM57   LOC203305 3'  AGTGCAAACTGTGCTTGTCCAA 90516     AAT   T      A
                                TTG   CAA CATGGTTT CACT
                                |||   ||| |||||||| ||||
                                AAC   GTT GTGTCAAA GTGA
                                  CT_   C       C
GAM57   LOC254243 3'  AGTGCAAACTGTGCTTGTCCAA 97401     AAT   T      A
                                TTG   CAA CATGGTTT CACT
                                |||   ||| |||||||| ||||
                                AAC   GTT GTGTCAAA GTGA
                                  CT_   C       C
GAM57   LOC56267  3'  GTGCTGATTGATTCA       39012           TGGTTTA
                                TGAATCAATCA      CAC
                                ||||||||||       |||
                                ACTTAGTTAGT      GTG
                                      C_______
GAM57   LOC90038  3'  AGTGCAAACTGTGCTTGTCCAA 61145     AAT   T      A
                                TTG   CAA CATGGTTT CACT
                                |||   ||| |||||||| ||||
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                                AAC   GTT GTGTCAAA GTGA
                                  CT_   C       C
GAM57   LOC90844  3'  GAGTACAAACTGTATGATTCAA 64208         ATC      AC
                                TTGAATCA   ATGGTTT  ACTC
                                ||||||||   |||||||  ||||
                                AACTTAGT   TGTCAAA  TGAG
                                     A__      CA
GAM57   LOC91689  3'  AACTAGAATGATTCAA      52821         A  A
                                TTGAATCA TC TGGTT
                                |||||||| || |||||
                                AACTTAGT AG ATCAA
                                     A  _
GAM58   CEACAM1   3'  AGCAAAGAGAAGAAAACC    8146      C         _
                                GGT TTTTTCTCTTT CT
                                ||| |||||||||| ||
                                CCA AAGAAGAGAAA GA
                                  A          C
GAM58   EDNRA     3'  AAGAGAAAAAGATCGA      64102
                                TCGGTCTTTTTCTCTT
                                ||||||||||||||||
                                AGCTAGAAAAAGAGAA

GAM58   HOXD4     3'  GAAAGGGAAAAAAACC      27523     C
                                GGT TTTTTCTCTTTC
                                ||| ||||||||||||
                                CCA AAAAAGGGAAAG
                                  A
GAM58   PRKG1     3'  GACAAAGAAAGAAAGCCC    20747     T   TTTC       C
                                GG CTT    TCTTTCTT GTC
                                || |||    |||||||| |||
                                CC GAA    AGAAAGAA CAG
                                 C  _____       A
GAM58   CTNNBIP1  3'  GACTTGAAAAGAAAGAAACC   39663     C      C    TTC
                                GGT TTTTTCT TTTC   GTC
                                ||| ||||||| ||||   |||
                                CCA AGAAAGA AAAG   CAG
                                  A      _    TT_
GAM58   FLJ10300  5'  GACAGGGAAAAAGAAAAAGACA 36001    G        C     TC
           GA                     TC GTCTTTTTCT TTTCT  GTC
                                ||| |||||||||| |||||  |||
                                AG CAGAAAAAGA AAAGG  CAG
                                 A         A     GA
GAM58   FLJ14327  3'  GACATTAGAGAAAAAAACTGA  46136       C        TTCT
                                TCGGT TTTTTCTCT    TC
                                ||||| |||||||||    ||
                                AGTCA AAAAAGAGA    AG
                                   A         TTAC
GAM58   FLJ14440  3'  AAAGAGCCAAAAGATC      51356         T_
                                GGTCTTTT  CTCTTT
                                ||||||||  ||||||
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                                CTAGAAAA  GAGAAA
                                    CC
GAM58   KIAA1786 3'  GACAGTTTCGGAAAAAAAGACT 66029          C   TTCTTC
           GA                    TCGGTCTTTTT TCT     GTC
                                 |||||||||| |||     |||
                                 AGTCAGAAAAA AGG     CAG
                                      A   CTTTGA
GAM58   PLP1     5'  GAAAAAGTAAAAGACCGA    5007          T  C
                                 TCGGTCTTTT CT TTTC
                                 |||||||||| || ||||
                                 AGCCAGAAAA GA AAAG
                                      T  A
GAM58   PRO0628  5'  GAAAGAAAAAGAGACC     26206         C
                                 GGTCTTTTT TCTTTC
                                 |||||||| ||||||
                                 CCAGAGAAA AGAAAG
                                      A
GAM58   ROBO2    3'  ACATGAAGAAAAAGACTGA   62483           CTT  TTC
                                 TCGGTCTTTTTCT   TC   GT
                                 ||||||||||||   ||   ||
                                 AGTCAGAAAAAGA   AG   CA
                                       ___  TA_
GAM58   SDC3     3'  GACAGTGGAAAAAAGAGACC  27751         CTC    TC_
                                 GGTCTTTTT   TTTCT   GTC
                                 |||||||||   |||||   |||
                                 CCAGAGAAA   AAAGG   CAG
                                       ___    TGA
GAM58   SLC11A2  3'  ACAAAGAAGGGGAAAAACTGA  5232       CT          C
                                 TCGGT  TTTTCTCTTTCTT GT
                                 |||||  |||||||||||| ||
                                 AGTCA  AAAAGGGGAAGAA CA
                                    __          A
GAM58   TIGD4    5'  GATCCAAAGAGAAAAAGACTGA 89069              CT_
                                 TCGGTCTTTTTCTCTTT   TC
                                 ||||||||||||||||   ||
                                 AGTCAGAAAAAGAGAAA   AG
                                          CCT
GAM58   LOC159199 5'  AAGAAAGAAAGACC       82178       TTTC
                                 GGTCTT    TCTTTCTT
                                 ||||||    ||||||||
                                 CCAGAA    AGAAAGAA
                                      ____
GAM58   LOC197319 3'  GAGAGAAAAAATCCGA     87972      TC
                                 TCGG  TTTTTCTCTT
                                 ||||  ||||||||||
                                 AGCC  AAAAAGAGAG
                                   TA
GAM58   LOC202134 3'  GAAAAAAAAGAAAAAGAC    90320          C   C
                                 GTCTTTTTCT TTT TTC
                                 |||||||||| ||| |||
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                                CAGAAAAAGA AAA AAG
                                      A   A
GAM58   LOC220763 5'  GACGAAGAAAAGCCCAAGATC  73346       TTT  C
                                GGTCTT   CT TTTCTTCGTC
                                ||||||   || ||||||||||
                                CTAGAA   GA AAAGAAGCAG
                                   CCC  _
GAM58   LOC222193 3'  GACAAAGAAAAAGAAAGAGA   94181         C     C
                                TCTTTTTCT TTTCTT GTC
                                ||||||||| |||||| |||
                                AGAGAAAGA AAAGAA CAG
                                      A     A
GAM58   LOC253272 5'  GAAAGAGAAAAAAAGC      95362    C_
                                GT  TTTTTCTCTTTC
                                ||  ||||||||||||
                                CG  AAAAAGAGAAAG
                                 AA
GAM59   CACNG3    3'  CACATTCTTCCCTCCTTGGA   21540       TAATCTA
                                TTCAAG      GGAAGAATGTG
                                ||||||      ||||||||||||
                                AGGTTC      CCTTCTTACAC
                                   CTC_____
GAM59   CLTC      3'  CTTCCCAGATTATTGAA     16781       G     A
                                TTCAA TAATCT GGAAG
                                ||||| |||||| |||||
                                AAGTT ATTAGA CCTTC
                                   _     C
GAM59   MDS1      3'  GTTCCCCAGATTACTTGA     17162           A  AA
                                TCAAGTAATCT GG  GAAT
                                ||||||||||| ||  ||||
                                AGTTCATTAGA CC  CTTG
                                      C  __
GAM59   RPS6KA6   3'  TCTGCTAAATTACTTGAA    27170          C   GA
                                TTCAAGTAAT TAG  AGA
                                |||||||||| |||  |||
                                AAGTTCATTA ATC  TCT
                                      A   G_
GAM59   VASP      5'  CACATTCTCCCCAGGAAGCCGG 12565    AA  AA   A  A
           A                     TC  GT  TCT GG AGAATGTG
                                ||  ||  ||| || ||||||||
                                AG  CG  GGA CC TCTTACAC
                                 GC  AA   C  C
GAM59   DKFZP564D172 3'  CACATTATATTTTAATTACTTG 49386          C    AG_
           AA                     TTCAAGTAAT TAGGA   AATGTG
                                |||||||||| |||||   ||||||
                                AAGTTCATTA ATTTT   TTACAC
                                      _    ATA
GAM59   KIAA1708  3'  CACACTTTCAAATTATTTGAA  67031          CTA    AA
                                TTCAAGTAAT   GGAAG  TGTG
                                ||||||||||   |||||  ||||
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                                AAGTTTATTA  CTTTC  ACAC
                                     AA_    __
GAM59   LRG     3'  TTTCCCAGATCTCTTGAA    53754       TA   A
                                TTCAAG  ATCT GGAAG
                                ||||||  |||| |||||
                                AAGTTC  TAGA CCTTT
                                   TC   C
GAM59   PDZD2   3'  ACACCCTTCTTTATTTGAA   80855        TCTA    AA
                                TTCAAGTAA   GGAAG  TGT
                                |||||||||   |||||  |||
                                AAGTTTATT   TCTTC  ACA
                                     _____   CC
GAM59   LOC143524 3'  CACATTCCTCAGGCTTACTTGA 76592        T  AG  A
                                TCAAGTAA CT  GA GAATGTG
                                |||||||| ||  || |||||||
                                AGTTCATT GG  CT CTTACAC
                                     C  A_  C
GAM59   LOC150568 5'  CACCGATGCCTAAATACTTGAA 85041        ATC    AAGAAT
                                TTCAAGTA   TAGG     GTG
                                ||||||||   ||||     |||
                                AAGTTCAT   ATCC     CAC
                                     AA_    GTAGC_
GAM59   LOC151473 3'  CTTCCCAGATCATTTGAA    80256       A    A
                                TTCAAGT ATCT GGAAG
                                ||||||| |||| |||||
                                AAGTTTA TAGA CCTTC
                                     C    C
GAM59   LOC221296 3'  TTTTTCCTAAATTGCTT     91975       C
                                AAGTAAT TAGGAAGAA
                                ||||||| |||||||||
                                TTCGTTA ATCCTTTTT
                                     A
GAM59   LOC89231  3'  CACAGAGCTCCTAGATCCTTGA 92729       TA       A AA_
            A                    TTCAAG  ATCTAGGA G   TGTG
                                ||||||  |||||||| |   ||||
                                AAGTTC  TAGATCCT C   ACAC
                                   C_       _ GAG
GAM60   ADCY7    3'  GAGACAACTTGGACAACCTGTG 6639         _____ TG   __
            AG                    CTCACAGG   C  AGT  TCTT
                                ||||||||   |  |||  ||||
                                GAGTGTCC   G  TCA  AGAG
                                     AACA GT   AC
GAM60   AES     3'  GAGGCAAGCTAAGGCCTGGAGG 6676      A     GAGTT
                                CCTC CAGGCT    CTTGCCTC
                                |||| ||||||    ||||||||
                                GGAG GTCCGG    GAACGGAG
                                  _     AATC_
GAM60   C21orf2  3'  GGGCCCTCAGCTGTGAGG    17016        G    TTCTT
                                CCTCACAG CTGAG    GCCT
                                |||||||| |||||    ||||
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                                GGAGTGTC GACTC    CGGG
                                   _    C____
GAM60   CASP3    3' GAGCACTCAGCCCGGGAGG   52196     ACA      T
                                CCTC   GGCTGAGT CTT
                                ||||   |||||||| |||
                                GGAG   CCGACTCA GAG
                                  GGC       C
GAM60   CASP3    3' GAGCACTCAGCCCGGGAGG   15102     ACA      T
                                CCTC   GGCTGAGT CTT
                                ||||   |||||||| |||
                                GGAG   CCGACTCA GAG
                                  GGC       C
GAM60   CELSR3   3' GAGGACCCACCTGTGAGG    7400         C  A
                                CCTCACAGG TG GTTCTT
                                ||||||||| || ||||||
                                GGAGTGTCC AC CAGGAG
                                   _ C
GAM60   DMD      5' CAGCCACTCAGCCAGTGA    14394     A      TC
                                TCAC GGCTGAGT  TTG
                                |||| ||||||||  |||
                                AGTG CCGACTCA  GAC
                                  A       CC
GAM60   DMD      5' CAGCCACTCAGCCAGTGA    14417     A      TC
                                TCAC GGCTGAGT  TTG
                                |||| ||||||||  |||
                                AGTG CCGACTCA  GAC
                                  A       CC
GAM60   DMD      5' CAGCCACTCAGCCAGTGA    14424     A      TC
                                TCAC GGCTGAGT  TTG
                                |||| ||||||||  |||
                                AGTG CCGACTCA  GAC
                                  A       CC
GAM60   DYRK2    3' AGGTTCTCTCAGCCTGGGA   13125    A       TTCTT
                                TC CAGGCTGAG    GCCT
                                || |||||||||    ||||
                                AG GTCCGACTC    TGGA
                                 G       TCT__
GAM60   DYRK2    3' AGGTTCTCTCAGCCTGGGA   21389    A       TTCTT
                                TC CAGGCTGAG    GCCT
                                || |||||||||    ||||
                                AG GTCCGACTC    TGGA
                                 G       TCT__
GAM60   FHIT     5' AAGACTTCAACTGTGAGG    8895        GC   T
                                CCTCACAG  TGAG TCTT
                                ||||||||  |||| ||||
                                GGAGTGTC  ACTT AGAA
                                   A_   C
GAM60   GPR56    3' AGCAAGAACTCCTGGAG     19063    A   CTG      C
                                CTC CAGG   AGTTCTTGC T
                                ||| ||||   ||||||||| |
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                                GAG GTCC   TCAAGAACG A
                                  _   ___        A
GAM60   HP      3'  GCAAGATTTCAGCCTGGAAG   17639    CA       T
                                CT  CAGGCTGAG TCTTGC
                                ||  ||||||||| ||||||
                                GA  GTCCGACTT AGAACG
                                 AG        T
GAM60   ITCH    5'  AAGTGACTCAAACTGTGAG    48947       GC     _
                                CTCACAG  TGAGTT CTT
                                |||||||  |||||| |||
                                GAGTGTC  ACTCAG GAA
                                    AA     T
GAM60   LAMC2   3'  AAGATTTTCCCAGTCTGTGA   38145         AGT___
                                TCACAGGCTG     TCTT
                                ||||||||||     ||||
                                AGTGTCTGAC     AGAA
                                      CCTTTT
GAM60   LPP     5'  AGACAAGATCGGCCTG      18743        GT    C
                                CAGGCTGA  TCTTG CT
                                ||||||||  ||||| ||
                                GTCCGGCT  AGAAC GA
                                    __    A
GAM60   MASP1   3'  GCAATCTTTCAGCCTTGA    57472     C       TTC
                                TCA AGGCTGAG   TTGC
                                ||| ||||||||   ||||
                                AGT TCCGACTT   AACG
                                  _       TCT
GAM60   PDGFRB  3'  AGGCAAGAAAACTGCAGGG   65967     CA   GCTGAG
                                CCT  CAG     TTCTTGCCT
                                |||  |||     |||||||||
                                GGG  GTC     AAGAACGGA
                                  AC   AA_____
GAM60   PMP2    3'  AGGCAAGAAAGAACCATGTG   10670     _  CTGAG
                                CACA GG    TTCTTGCCT
                                ||||  ||    |||||||||
                                GTGT CC    AAGAACGGA
                                  A  AAGA_
GAM60   RNMT    3'  GCTTGCTCAGCCATGAG     13722      CA       TCTT
                                CTCA  GGCTGAGT    GC
                                ||||  ||||||||    ||
                                GAGT  CCGACTCG    CG
                                  A_       TT__
GAM60   SULT1A3 5'  GGAACTCAGCCTGTGAG     12053
                                CTCACAGGCTGAGTTCT
                                |||||||||||||||||
                                GAGTGTCCGACTCAAGG

GAM60   TBL1X   3'  AAGATGGCCCAGCCCGTGGGG  18923       A    A  __
                                CCTCAC GGCTG GT  TCTT
                                |||||| ||||| ||  ||||
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                                GGGGTG CCGAC CG  AGAA
                                   C    C  GT
GAM60   TNFAIP2  3'  GTTCCTTCTCAGCCTGAGAGG  20832     A       TTCTT
                                CCTC CAGGCTGAG    GC
                                |||| |||||||||    ||
                                GGAG GTCCGACTC    TG
                                  A       TTCCT
GAM60   TRPM1    5'  GAGACTCAGCCTGAGA     10059    A       T
                                TC CAGGCTGAGT CTT
                                || |||||||||| |||
                                AG GTCCGACTCA GAG
                                 A       _
GAM60   ZNF91    5'  GGCCCAGCCTGTGTGG      12822    T       AGTTCTT
                                CC CACAGGCTG      GCC
                                || |||||||||      |||
                                GG GTGTCCGAC      CGG
                                 T       C_______
GAM60   acmsd    5'  CAGGGCAGCCAGTGA      56355     A    AGT
                                TCAC GGCTG   TCTTG
                                |||| |||||   |||||
                                AGTG CCGAC   GGGAC
                                  A    ____
GAM60   BICD2    5'  GAGGGCCCGGCCTGCGAG    70394     A     A
                                CTC CAGGCTG GTTCTT
                                ||| ||||||| ||||||
                                GAG GTCCGGC CGGGAG
                                  C      C
GAM60   C9orf14  5'  GAGGCAAGATTTTCCTG     86674     CT    T
                                CAGG  GAGT CTTGCCTC
                                ||||  |||| ||||||||
                                GTCC  TTTA GAACGGAG
                                  T_   _
GAM60   CPSF2    3'  GAGGCCTCCCCAGCCTGTGGG  61585          AGTTCTT
                                CTCACAGGCTG      GCCTC
                                ||||||||||       |||||
                                GGGTGTCCGAC      CGGAG
                                       CCCTC__
GAM60   CTCFL    3'  AGGCAAATGTGTACCTGTAAGG 82502     C    C  AG TC
                                CCT ACAGG TG  T  TTGCCT
                                ||| ||||| ||  |  ||||||
                                GGA TGTCC AT  G  AACGGA
                                  A    _  GT TA
GAM60   D2S448   3'  GAGGCAGCATTTCAGCTGTGAG 73523        G    TTC
           G                     CCTCACAG CTGAG   TTGCCTC
                                ||||||||| |||||   |||||||
                                GGAGTGTC GACTT   GACGGAG
                                      _    TAC
GAM60   DDM36    3'  GAGGCCCTTCCCACCCTGTGAG 40572         C  AGTTCTT
           G                     CCTCACAGG TG      GCCTC
                                ||||||||| ||      |||||
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                                GGAGTGTCC AC      CGGAG
                                      C  CCTTCC_
GAM60   DKFZp434G171 5'  AGGCAGGCCAACCTGGAG    79429     A    C  A TT
                                CTC CAGG TG G  CTTGCCT
                                ||| |||| || |  |||||||
                                GAG GTCC AC C  GGACGGA
                                  _    A  _ ___
GAM60   DKFZP434K1772 5'  AGGCCCCACCACCCAGCCTGTG 67708          A  TCTT__
          G                      TCACAGGCTG GT     GCCT
                                ||||||||||  ||     ||||
                                GGTGTCCGAC CA     CGGA
                                      C  CCACCC
GAM60   FLJ10688  3'  GAAGCAAAATAAACTCAGCC   36415         C___    C
                                GGCTGAGTT    TTGC TC
                                |||||||||    |||| ||
                                CCGACTCAA    AACG AG
                                      ATAA    A
GAM60   FLJ12960  3'  AGACAAAAGCTTTAACTGTGAG 44945         GCT    C   C
          G                      CCTCACAG   GAGTT TTG CT
                                ||||||||   ||||| ||| ||
                                GGAGTGTC   TTCGA AAC GA
                                     AAT    A   A
GAM60   FLJ20487  3'  AGGCAAGTCTGCCACGAG    35245     ACA   T  GTT
                                CTC   GGC GA   CTTGCCT
                                |||   ||| ||   |||||||
                                GAG   CCG CT   GAACGGA
                                  CA_   T  ___
GAM60   FLJ20694  3'  GAGACAAGAACTGAGTT     35548      G       C
                                GGCT AGTTCTTG CTC
                                |||| |||||||| |||
                                TTGA TCAAGAAC GAG
                                  G       A
GAM60   FLJ22362  5'  GAGGCCTGACCAACCGCGAGG  43076      ACA  C  A   CTT
                                CCTC   GG TG GTT   GCCTC
                                ||||   || || |||   |||||
                                GGAG   CC AC CAG   CGGAG
                                  CG_  A  _   TC_
GAM60   ICB-1     3'  AAGTTACCAGCCTGTGAG     16756           A  T_
                                CTCACAGGCTG GT  CTT
                                ||||||||||| ||  |||
                                GAGTGTCCGAC CA  GAA
                                      _  TT
GAM60   KIAA0372  3'  GAAGCAAAGAAAAAGCTGTAAG 27664    C    G  GAG    _  C
                                CT ACAG CT   TTCTT GC TC
                                || |||| ||   ||||| || ||
                                GA TGTC GA   AAGAA CG AG
                                 A    _  AA_     A  A
GAM60   KIAA0557  3'  AGGCCGCCAGGCTGCGAGG    77987      A   G   A  TCTT
                                CCTC CAG CTG GT    GCCT
                                |||| ||| ||| ||    ||||
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                                GGAG GTC GAC CG    CGGA
                                  C   G   _ C___
GAM60   KIAA0599 3' GAGACAATTTCCCACTCACCTG 77179         C     TC____   C
            TGAGG                  CTCACAGG TGAGT      TTG CTC
                                |||||||| |||||      ||| |||
                                GAGTGTCC ACTCA      AAC GAG
                                     _    CCCTTT   A
GAM60   KIAA0601 3' GAGGCAAGCAAGTGCTGTGA   62511        _   GAGTT
                                TCACAG GCT     CTTGCCTC
                                |||||| |||    ||||||||
                                AGTGTC TGA     GAACGGAG
                                   G   AC___
GAM60   KIAA0809 5' AGGCAAGAACCTAGCCTCCGAG 80576      AC      A
            G                   CCTC  AGGCTG GTTCTTGCCT
                                ||||  |||||| ||||||||||
                                GGAG  TCCGAT CAAGAACGGA
                                  CC     C
GAM60   KIAA1468 5' AACTCCCCAGCCTGCAGAG    91772     A_     ___
                                CTC  CAGGCT   GAGTT
                                |||  ||||||   |||||
                                GAG  GTCCGA   CTCAA
                                  AC     CCC
GAM60   KIAA1904 3' AGCTCAGCCCTGAGG       73477       CA
                                CCTCA  GGCTGAGTT
                                |||||  |||||||||
                                GGAGT  CCGACTCGA
                                   C_
GAM60   KIAA1956 3' AGGCAAGAACATCCTGGAGG   78430      A    CTGA
                                CCTC CAGG    GTTCTTGCCT
                                |||| ||||    ||||||||||
                                GGAG GTCC    CAAGAACGGA
                                   _    TA__
GAM60   KRTHB2   3' GTTGAACCCAAACTGTGAG    52287        GC  A    TT
                                CTCACAG  TG GTTC  GC
                                |||||||  || ||||  ||
                                GAGTGTC  AC CAAG  TG
                                     AA  C    T_
GAM60   MGC27382 3' GAGATGGACTCAGCTCATGAGG 58453       CA         TTGC
                                CCTCA  GGCTGAGTTC    CTC
                                |||||  ||||||||||    |||
                                GGAGT  TCGACTCAGG    GAG
                                   AC         TA__
GAM60   MOST2    5' AGACAAGAACTCCCTGAGG    39673      CA  CT       C
                                CCTCA  GG  GAGTTCTTG CT
                                |||||  ||  |||||||| ||
                                GGAGT  CC  CTCAAGAAC GA
                                   __  __        A
GAM60   NYD-SP26 5' AGCAAGACCTGTGAG       52420         CTGAGT     C
                                CTCACAGG     TCTTGC T
                                ||||||||     |||||| |
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                                GAGTGTCC     AGAACG A
                                       _______     A
GAM60   PGDS     3'  AGACAGCTACATCAGCCTGCCA 27162    CA       _  TC   C
              G                    CT  CAGGCTGA GT  TTG CT
                                   ||  |||||||| ||  ||| ||
                                   GA  GTCCGACT CA  GAC GA
                                    CC       A  TC   A
GAM60   PHYHIP   3'  GCAAACAGAGAGCCTGTGGG   28610          GAGTTC
                                   CTCACAGGCT     TTGC
                                   ||||||||||     ||||
                                   GGGTGTCCGA     AACG
                                         GAGACA
GAM60   PP3501   3'  GAGACTCAGCCACAAGG     41370     CACA       T
                                   CCT    GGCTGAGT CTT
                                   |||    |||||||| |||
                                   GGA    CCGACTCA GAG
                                     ACA_       _
GAM60   PPP1R1A  3'  GAGGCAAGAGCAGAGCCTGAGA 22147    A     GA
                                   TC CAGGCT  GTTCTTGCCTC
                                   || ||||||  ||||||||||||
                                   AG GTCCGA  CGAGAACGGAG
                                    A     GA
GAM60   PRDM9    3'  AGGCAAGAAGAGTCCAGAAGG  39574     CACA    GAG
                                   CCT    GGCT   TTCTTGCCT
                                   |||    ||||   |||||||||
                                   GGA    CTGA   AAGAACGGA
                                     AGAC    G__
GAM60   RNF8     3'  AAGGGCTCAGCCTGTGA     14212
                                   TCACAGGCTGAGTTCTT
                                   |||||||||||||||||
                                   AGTGTCCGACTCGGGAA

GAM60   SUCLG2   3'  AGGCAAGAATCACTG       65607     GC   G
                                   CAG  TGA TTCTTGCCT
                                   |||  ||| |||||||||
                                   GTC  ACT AAGAACGGA
                                     __   _
GAM60   SV2B     3'  GAACATCAGCCTGCAAG     29297    CA       _
                                   CT  CAGGCTGA GTTC
                                   ||  |||||||| ||||
                                   GA  GTCCGACT CAAG
                                    AC       A
GAM60   TIP120B  3'  AGGCCCCCAGCCCAAGCTGTGA 72416         GC  A   CTT_
              GG                     CCTCACAG  TG GTT    GCCT
                                   ||||||||  || |||    ||||
                                   GGAGTGTC  AC CGA    CGGA
                                        GA  C   CCCC
GAM60   TIX1     3'  AGGCAAGAATGCCCATGTAAGG 61737     C   __   TGA
                                   CCT ACA  GGC   GTTCTTGCCT
                                   ||| |||  |||   ||||||||||
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                                GGA TGT  CCG   TAAGAACGGA
                                  A  AC  ___
GAM60   VPS39    3'  GAGACTCTGCTCAGGCCTGTGA 62845        _   _____
            GG                    CCTCACAGGC TGAGT   TCTT
                                  |||||||||| |||||   ||||
                                  GGAGTGTCCG ACTCG   AGAG
                                       G    TCTC
GAM60   ZNF17    5'  AGGCCCAGCCCTGTGAG    82384       _  AGTTCTT
                                  CTCACAGG CTG     GCCT
                                  |||||||| |||     ||||
                                  GAGTGTCC GAC     CGGA
                                       C  C_____
GAM60   LOC120103 3'  GAGACCACTCAGCCTTGAG   74005     C       __
                                  CTCA AGGCTGAGT  TCTT
                                  |||| |||||||||  ||||
                                  GAGT TCCGACTCA  AGAG
                                    _       CC
GAM60   LOC123096 3'  GAGGCACCATATCAGCCTGCGG 74202    A      GTTCT
            G                     CTC CAGGCTGA    TGCCTC
                                  ||| ||||||||    ||||||
                                  GGG GTCCGACT    ACGGAG
                                    C       ATACC
GAM60   LOC123905 5'  GAGGACGCACTCAGCCTG    74249         TCTTG
                                  CAGGCTGAGT    CCTC
                                  ||||||||||    ||||
                                  GTCCGACTCA    GGAG
                                       CGCA_
GAM60   LOC124989 5'  GAGGCAAGAACTATTGGGC   74385    G___
                                  GCT   AGTTCTTGCCTC
                                  |||   ||||||||||||
                                  CGG   TCAAGAACGGAG
                                    GTTA
GAM60   LOC125704 5'  GAGGCAAGAAGGTGCTGCAGG  74409    CACA  TGAG
                                  CCT   GGC   TTCTTGCCTC
                                  |||   |||   ||||||||||
                                  GGA   TCG   AAGAACGGAG
                                    CG__  TGG_
GAM60   LOC125929 3'  GAGGCTTACTCAGCCTGTGGG  75674          TCTT
                                  CTCACAGGCTGAGT   GCCTC
                                  ||||||||||||||   |||||
                                  GGGTGTCCGACTCA   CGGAG
                                         TT__
GAM60   LOC145864 5'  GAGGCAAGGGAGGCCTGCCAGG 77556    CA    GAGT
                                  CCT  CAGGCT   TCTTGCCTC
                                  |||  ||||||   |||||||||
                                  GGA  GTCCGG   GGAACGGAG
                                    CC    AG__
GAM60   LOC148085 3'  AGACAAAAATGTCAGGCCTGTG 84114         GA__  C  C
            AG                    CTCACAGGCT   GTT TTG CT
                                  |||||||||   ||| ||| ||
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                                GAGTGTCCGG   TAA AAC GA
                                     ACTG  A  A
GAM60   LOC148356 3' AGACAAAAATATGCCTGTGA  74565       TGA  C  C
                                TCACAGGC  GTT TTG CT
                                ||||||||  ||| ||| ||
                                AGTGTCCG  TAA AAC GA
                                    TA_  A  A
GAM60   LOC150279 3' AGGCAAGGAATTGCCCTGAGG  79664     CA  TGAG
                                CCTCA  GGC   TTCTTGCCT
                                |||||  |||   |||||||||
                                GGAGT  CCG   AGGAACGGA
                                  C_  TTA_
GAM60   LOC150299 3' AAGTTTCTCAACCTGTGGG   84964       C   TT_
                                CTCACAGG TGAG  CTT
                                |||||||| ||||  |||
                                GGGTGTCC ACTC  GAA
                                     A   TTT
GAM60   LOC150372 5' GAGAACCAGCCTGTGAGG    79800         A
                                CCTCACAGGCTG GTTCTT
                                |||||||||||| ||||||
                                GGAGTGTCCGAC CAAGAG
                                          _
GAM60   LOC150837 5' AGACAAGGCGAGCCTGTGA   80016       GA  T   C
                                TCACAGGCT  GT CTTG CT
                                |||||||||  || |||| ||
                                AGTGTCCGA  CG GAAC GA
                                     G_ _   A
GAM60   LOC150838 5' AGACAAGGCGAGCCTGTGA   85123       GA  T   C
                                TCACAGGCT  GT CTTG CT
                                |||||||||  || |||| ||
                                AGTGTCCGA  CG GAAC GA
                                     G_ _   A
GAM60   LOC151878 3' GCAAGACTTGTAAGG      80376    C   CTGAGT
                                CCT ACAGG     TCTTGC
                                ||| |||||     ||||||
                                GGA TGTTC     AGAACG
                                  A   _______
GAM60   LOC152271 3' GAGACAGCTTCAGCCTGTGTAG 80519   _       TTC  C
                                CT CACAGGCTGAG  TTG CTC
                                || ||||||||||  ||| |||
                                GA GTGTCCGACTT  GAC GAG
                                 T        C__  A
GAM60   LOC157860 3' GAGATAAACTCAGCCACAAGG  86568    CACA     ___
                                CCT   GGCTGAGT  TCTT
                                |||   ||||||||  ||||
                                GGA   CCGACTCA  AGAG
                                  ACA_      AAT
GAM60   LOC158292 5' AAGCTGTTCAGCCTGGAG    86726    A      TT_
                                CTC CAGGCTGAG  CTT
                                ||| |||||||||  |||
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                                GAG GTCCGACTT   GAA
                                  _       GTC
GAM60   LOC162137 5'  AGGCAAGGCGAGGCCCGCAGAG 87110     ACA_   GA  T
                                CTC   GGCT  GT CTTGCCT
                                |||   ||||  || |||||||
                                GAG   CCGG  CG GAACGGA
                                  ACGC   AG  _
GAM60   LOC197117 3'  GCCCTGAACTCAGCCTGGAGG  89719      A         TT_
                                CCTC CAGGCTGAGTTC   GC
                                |||| ||||||||||||   ||
                                GGAG GTCCGACTCAAG   CG
                                  _         TCC
GAM60   LOC199883 3'  AGACAAGAAAAATCCTGTGAG  89869        CTGAG     C
                                CTCACAGG    TTCTTG CT
                                ||||||||    |||||| ||
                                GAGTGTCC    AAGAAC GA
                                     TAAA_    A
GAM60   LOC200020 3'  AGACAAGAAAAATCCTGTGAG  89927        CTGAG     C
                                CTCACAGG    TTCTTG CT
                                ||||||||    |||||| ||
                                GAGTGTCC    AAGAAC GA
                                     TAAA_    A
GAM60   LOC200862 5'  AGACAGGACCCTCAGCCTCGAG 90179      AC       T_    C
           G                     CCTC  AGGCTGAG  TCTTG CT
                                ||||  ||||||||  ||||| ||
                                GGAG  TCCGACTC  AGGAC GA
                                  C_       CC     A
GAM60   LOC202915 3'  GAGAGCCCACCTGTGAGG    90391         C  A
                                CCTCACAGG TG GTTCTT
                                ||||||||| || ||||||
                                GGAGTGTCC AC CGAGAG
                                     _ C
GAM60   LOC219295 5'  GGCAAACTCGCCTGTGA     92994         T    CT
                                TCACAGGC GAGTT  TGCC
                                |||||||| |||||  ||||
                                AGTGTCCG CTCAA  ACGG
                                     _    __
GAM60   LOC219731 5'  AGACAAGGGAGGAGCCTGTGAG 93088          GAG     C
                                CTCACAGGCT   TTCTTG CT
                                ||||||||||   |||||| ||
                                GAGTGTCCGA   GGGAAC GA
                                     GGA     A
GAM60   LOC221794 5'  AGCTTCAGCCTGTGTAG     93912    _        _
                                CT CACAGGCTGA GTT
                                || ||||||||||| |||
                                GA GTGTCCGACT CGA
                                  T         T
GAM60   LOC256987 3'  GAGGACAGGACTCAGCCTGCAG 95947     CA          TG
           GG                     CCT  CAGGCTGAGTTCT  CCTC
                                ||| ||||||||||||  ||||
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                                GGG  GTCCGACTCAGGA  GGAG
                                  AC           CA
GAM60   LOC257489 3'  AGGCAAGAATCACTG      65611     GC   G
                                CAG  TGA TTCTTGCCT
                                |||  ||| |||||||||
                                GTC  ACT AAGAACGGA
                                  __   _
GAM60   LOC51015  5'  AAGTTCCTCAGCCTGTACGG   32117    TC       TT_
                                CC  ACAGGCTGAG   CTT
                                ||  ||||||||||   |||
                                GG  TGTCCGACTC   GAA
                                 CA        CTT
GAM60   LOC90288  3'  GCAAGAAAATGCGCTTTAAGG  62096     CAC  _  TGAG
                                CCT   AG GC    TTCTTGC
                                |||   || ||    |||||||
                                GGA   TC CG    AAGAACG
                                  ATT  G  TAA_
GAM60   LOC90906  3'  GAGGCAAGACCAAGCC      64299      GA  T
                                GGCT  GT CTTGCCTC
                                ||||  || ||||||||
                                CCGA  CA GAACGGAG
                                  AC  _
GAM60   LOC91355  5'  AGACAAGGGGGACTGTGAGG   65710        G  GAG     C
                                CCTCACAG CT   TTCTTG CT
                                ||||||||  ||   ||||||  ||
                                GGAGTGTC GG   GGGAAC GA
                                     A  ___     A
GAM60   LOC92080  3'  GACTCAGCCCTGAGG       68049      CA
                                CCTCA  GGCTGAGTT
                                |||||  |||||||||
                                GGAGT  CCGACTCAG
                                   C_
GAM61   ATP11A    3'  GCCTCCCGCACTGCAG      77032         A_
                                CTGCAGTGC  GAGGC
                                |||||||||  |||||
                                GACGTCACG  CTCCG
                                     CC
GAM61   DPYSL2    3'  AGAACTGAATAACTGCAGT   7290         GCAGA  CC
                                ACTGCAGT    GG  TTCT
                                ||||||||    ||  ||||
                                TGACGTCA    TC  AAGA
                                     ATAAG  __
GAM61   EGLN2     5'  AGGGGGCTCCACTCCACAGC   34095    A   C  A__
                                GC GTG AG   GGCCTTCT
                                ||  ||| ||   ||||||||
                                CG CAC TC   TCGGGGGA
                                 A   C  ACC
GAM61   JMJ       3'  CTTAGAAAACCTAGATACTGCA 17130         CAG   CC
            GT                    ACTGCAGTG   AGG  TTCTAAG
                                |||||||||   |||  |||||||
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                                TGACGTCAT   TCC  AAGATTC
                                     AGA   AA
GAM61   MAT2A    3'  TAGAAACAACACTGTAGT    19787         CAGAGGCC
                                ACTGCAGTG       TTCTA
                                |||||||||       |||||
                                TGATGTCAC       AAGAT
                                     AACA____
GAM61   MSL3L1   5'  TTAAAAGGCCTCCCCACT    22311      CA      C
                                AGTG  GAGGCCTT TAA
                                ||||  |||||||| |||
                                TCAC  CTCCGGAA ATT
                                  CC       A
GAM61   NRAP     3'  AGAAGGCCCACCAGCTGCAG   20506        GCAGA
                                CTGCAGT    GGCCTTCT
                                |||||||    ||||||||
                                GACGTCG    CCGGAAGA
                                     ACCAC
GAM61   Nrap     3'  CTTAGCATGCCCTTCACTGCAG 43347         C  A   CTT
           T                     ACTGCAGTG AG GGC   CTAAG
                                |||||||| || |||   |||||
                                TGACGTCAC TC CCG   GATTC
                                     T  _   TAC
GAM61   Nrap     3'  CTTAGCATGCCCTTCACTGCAG 57635         C  A   CTT
           T                     ACTGCAGTG AG GGC   CTAAG
                                |||||||| || |||   |||||
                                TGACGTCAC TC CCG   GATTC
                                     T  _   TAC
GAM61   PCDHB9   3'  CTTAGAAGAAAAACCACTGCA  38938        CAGAGGC
                                TGCAGTG      CTTCTAAG
                                |||||||      ||||||||
                                ACGTCAC      GAAGATTC
                                     CAAAAA_
GAM61   PRDM2    3'  CTTGAGGGCCTCCCCACCGCAG 24247      A   CA       T
                                CTGC GTG  GAGGCCTTC AAG
                                |||| |||  ||||||||| |||
                                GACG CAC  CTCCGGGAG TTC
                                  C   CC       _
GAM61   RPL10    3'  AAGGCCTCTGGTTTTTTGTA   20027      TG___
                                TGCAG    CAGAGGCCTT
                                |||||    ||||||||||
                                ATGTT    GTCTCCGGAA
                                   TTTTG
GAM61   SEDL     5'  GGCCTCCCACTGCAGT      27351         CA
                                ACTGCAGTG  GAGGCC
                                |||||||||  ||||||
                                TGACGTCAC  CTCCGG
                                     C_
GAM61   SSA1     5'  AAGGTCTCCACACTGCTGT   11975    T     CA
                                AC GCAGTG  GAGGCCTT
                                || ||||||  ||||||||
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                                TG CGTCAC  CTCTGGAA
                                 T     AC
GAM61   CSR1     3'  AGAAAGCCTCACCTACAG    32674     C  TGCA    C
                                CTG AG    GAGGC TTCT
                                ||| ||    ||||| ||||
                                GAC TC    CTCCG AAGA
                                  A  CA__     A
GAM61   DCNP1    3'  CCTAACCTGCATTGCAG     55620          ___
                                CTGCAGTGCAG   AGG
                                ||||||||||   |||
                                GACGTTACGTC   TCC
                                      CAA
GAM61   DKFZP564L2423 3'  AGAAGGCCCTTCTACTTCAGT  62364      C    C_  A
                                ACTG AGTG  AG GGCCTTCT
                                |||| ||||  || ||||||||
                                TGAC TCAT  TC CCGGAAGA
                                  T    CT  _
GAM61   DKFZP586F1524 3'  CCTCCGCCACTGCAGT      31489         _ A
                                ACTGCAGTG C GAGG
                                ||||||||| | ||||
                                TGACGTCAC G CTCC
                                     C C
GAM61   FLJ22056  3'  AGGCCTCTGCCCTGCAG     42533       T
                                CTGCAG GCAGAGGCCT
                                |||||| ||||||||||
                                GACGTC CGTCTCCGGA
                                   C
GAM61   FLJ22671  3'  AGACTCTGCACTGCA       45862           GC
                                TGCAGTGCAGAG  CT
                                ||||||||||||  ||
                                ACGTCACGTCTC  GA
                                      A_
GAM61   FOXP1    3'  CTTAGAACCCCTCCACACTTCA 51065     C    CA    CC
           G                     CTG AGTG  GAGG  TTCTAAG
                                ||| ||||  ||||  |||||||
                                GAC TCAC  CTCC  AAGATTC
                                  T   AC    CC
GAM61   KIAA1617  3'  CTTAGAAGGATCACTGCAG   91425        CAGAGG
                                CTGCAGTG     CCTTCTAAG
                                ||||||||     |||||||||
                                GACGTCAC     GGAAGATTC
                                     TA_____
GAM61   KIAA1911  3'  AGAAATACTGCACTGAGT    73505     G       AGGCC
                                ACT CAGTGCAG    TTCT
                                ||| ||||||||    ||||
                                TGA GTCACGTC    AAGA
                                  _       ATA__
GAM61   MGC10646  3'  CTTAGTCTGTCTGCTCTGCAG  51107       T    GGCCTT
                                CTGCAG GCAGA     CTAAG
                                |||||| |||||     |||||
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                                GACGTC CGTCT     GATTC
                                   T    GTCT__
GAM61   MGC12679  3' AGAAAATCTACTGCAGT     51202        GC   GGCC
                                ACTGCAGT  AGA    TTCT
                                ||||||||  |||    ||||
                                TGACGTCA  TCT    AAGA
                                    __   AA__
GAM61   MGC14386  5' AGTCGCCTCCCCGCACCGCTGT 53207    T  A    A__    CTT
                                AC GC GTGC   GAGGC   CT
                                || || ||||   |||||   ||
                                TG CG CACG   CTCCG   GA
                                 T  C    CCC    CT_
GAM61   MGC16279  5' AGAAAGCCAAGCCCGCTGCAG  51884        CAGA_   C
                                CTGCAGTG    GGC TTCT
                                ||||||||    ||| ||||
                                GACGTCGC    CCG AAGA
                                    CCGAA   A
GAM61   MGC16279  3' AGAAAGCCAAGCCCGCTGCAG  62874        CAGA_   C
                                CTGCAGTG    GGC TTCT
                                ||||||||    ||| ||||
                                GACGTCGC    CCG AAGA
                                    CCGAA   A
GAM61   PPFIA4    3' GCCTGGTCTGCACTGCA     70325          ___
                                TGCAGTGCAGA   GGC
                                ||||||||||   |||
                                ACGTCACGTCT   CCG
                                      GGT
GAM61   PROL1     3' CTTAGAAGAAATAAACTGCA   41132       GCAGAGGC
                                TGCAGT       CTTCTAAG
                                ||||||       ||||||||
                                ACGTCA       GAAGATTC
                                   AATAAA__
GAM61   RTN4IP1   5' CTTAGAAGAAATGCATGCACTG 51193          GAGGC__
           CGGT                   ACTGCAGTGCA      CTTCTAAG
                                ||||||||||      ||||||||
                                TGGCGTCACGT      GAAGATTC
                                      ACGTAAA
GAM61   SLC6A13   3' GGAGGCCTCCCACTGCA     33517        CA
                                TGCAGTG  GAGGCCTTC
                                |||||||  |||||||||
                                ACGTCAC  CTCCGGAGG
                                   C_
GAM61   LOC121274 5' TAGAACCCACACTGCAGT    74064         CAGA  CC
                                ACTGCAGTG   GG  TTCTA
                                |||||||||   ||  |||||
                                TGACGTCAC   CC  AAGAT
                                     AC__  __
GAM61   LOC130471 3' AGGCTCAGCACTGCAG      74938         A   G
                                CTGCAGTGC GAG CCT
                                ||||||||| ||| |||
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                                GACGTCACG CTC GGA
                                     A  _
GAM61   LOC130643 5'  GGGCCTTTGCACTGCA      74962
                                TGCAGTGCAGAGGCCT
                                ||||||||||||||||
                                ACGTCACGTTTCCGGG

GAM61   LOC145622 5'  AGTCTTCTGCACTAAG      77293    GC        C
                                CT  AGTGCAGAGG CT
                                ||  ||||||||||  ||
                                GA  TCACGTCTTC GA
                                 A_         T
GAM61   LOC149113 3'  AAGGCAGACATTGCAGT     79159         CAGAG
                                ACTGCAGTG    GCCTT
                                |||||||||    |||||
                                TGACGTTAC    CGGAA
                                     AGA__
GAM61   LOC151124 5'  GGGGTGACCTTCGCACTGCAGT 85231          AG  ___
                                ACTGCAGTGC  AGG   CCTT
                                ||||||||||  |||   ||||
                                TGACGTCACG  TCC   GGGG
                                     CT   AGT
GAM61   LOC154403 3'  AAGGCAGACATTGCAGT     81067         CAGAG
                                ACTGCAGTG    GCCTT
                                |||||||||    |||||
                                TGACGTTAC    CGGAA
                                     AGA__
GAM61   LOC154992 3'  AAGGCAGACATTGCAGT     81208         CAGAG
                                ACTGCAGTG    GCCTT
                                |||||||||    |||||
                                TGACGTTAC    CGGAA
                                     AGA__
GAM61   LOC196484 5'  AGAAAGCCAAGCCCGCTGCAG  62871         CAGA_  C
                                CTGCAGTG    GGC TTCT
                                ||||||||    ||| ||||
                                GACGTCGC    CCG AAGA
                                     CCGAA   A
GAM61   LOC200014 3'  CTTAAAAGGCCTTTGTTGTAG  88527       GT        C
                                CTGCA  GCAGAGGCCTT TAAG
                                |||||  |||||||||| ||||
                                GATGT  TGTTTCCGGAA ATTC
                                   __         A
GAM61   LOC201868 3'  AAGGCAGACATTGCAGT     89072         CAGAG
                                ACTGCAGTG    GCCTT
                                |||||||||    |||||
                                TGACGTTAC    CGGAA
                                     AGA__
GAM61   LOC221865 5'  GGGGCCTCCGCCTGCAG     92488       T  A
                                CTGCAG GC GAGGCCTT
                                ||||||  ||  ||||||||
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                                GACGTC CG CTCCGGGG
                                   _ C
GAM61   LOC254528 3'  TTAGAAGGCCTCCTACTGT   95055       CA
                                GCAGTG  GAGGCCTTCTAA
                                ||||||  ||||||||||||
                                TGTCAT  CTCCGGAAGATT
                                   C_
GAM61   LOC257017 5'  CTTAGAAAACCTAATGTGTACT 97373        G___   CC
           GC                    GCAGTGCA   AGG  TTCTAAG
                                ||||||||   |||  |||||||
                                CGTCATGT   TCC  AAGATTC
                                     GTAA   AA
GAM61   LOC91069  3'  AGAAAGCCAAACCTGCTGC   64771    GT   A___   C
                                GCA  GCAG   GGC TTCT
                                |||  ||||   ||| ||||
                                CGT  CGTC   CCG AAGA
                                  __   CAAA   A
GAM62   ABCF1    3'  ATTCAGGCACATGAAGGTGGAG 6566           C_      AT
           TG                    CATTTCACTTTCA  TGTCTGAG
                                ||||||||||||  ||||||||
                                GTGAGGTGGAAGT  ACGGACTT
                                      AC       A
GAM62   ACVRL1   5'  GCGGTGGAGGGGAGGTG     3418        A
                                CATTTC CTTTCACTGT
                                |||||| ||||||||||
                                GTGGAG GGAGGTGGCG
                                   G
GAM62   ADRA1A   3'  TCTTGATGGAAGTGAGG     5448          CTG  T
                                TTTCACTTTCA   TC GAGA
                                ||||||||||   || ||||
                                GGAGTGAAGGT   AG TTCT
                                      ___  _
GAM62   AGT      3'  ATTTTAGAGAATGGGGGTGGGG 3453    TT   TT  CTG
                                T  CACT  CA   TCTGAGAT
                                |  ||||  ||   ||||||||
                                G  GTGG  GT   AGATTTTA
                                 GG   GG  AAG
GAM62   AIM1     3'  ATCTCAGGCTGGAGTGCAGTG  91816     T     CACT
                                CATT CACTTT    GTCTGAGAT
                                |||| ||||||    |||||||||
                                GTGA GTGAGG    CGGACTCTA
                                  C     T___
GAM62   AKAP13   3'  GTTTTGGGCATGGATAAAGTGA 22144        ___   C   TG
           AG                    TTTCACT   TTCA TGTC  AGAT
                                |||||||   |||| ||||  ||||
                                GAAGTGA   AGGT ACGG  TTTG
                                   AAT   _   GT
GAM62   AKAP13   3'  GTTTTGGGCATGGATAAAGTGA 23248        ___   C   TG
           AG                    TTTCACT   TTCA TGTC  AGAT
                                |||||||   |||| ||||  ||||
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                                GAAGTGA  AGGT ACGG  TTTG
                                   AAT   _   GT
GAM62   AKAP13   3'  GTTTTGGGCATGGATAAAGTGA 58580       ___   C   TG
           AG                    TTTCACT  TTCA TGTC  AGAT
                                 |||||||  |||| ||||  ||||
                                GAAGTGA  AGGT ACGG  TTTG
                                   AAT   _   GT
GAM62   ATP11B   3'  ATTTCAGGTGTGGCTGTGGAAT 80315       TT   TGT
           G                     CATTTCAC  TCAC  CTGAGAT
                                 ||||||||  ||||  |||||||
                                GTAAGGTG  GGTG  GACTTTA
                                   TC   TG_
GAM62   B4GALT4  3'  TAGCAGGAGGGTGGAGTG    13674          A   T
                                CATTTCACTTTC CTG CTG
                                ||||||||||| ||| |||
                                GTGAGGTGGGAG GAC GAT
                                      _  _
GAM62   BLAME    3'  ATCTGGGAGTGAGGGTGGAG   39239          TG   G
                                TTTCACTTTCAC  TCT AGAT
                                ||||||||||||  ||| ||||
                                GAGGTGGGAGTG  AGG TCTA
                                   __   G
GAM62   C20orf1  5'  ATTTCAGAAAAGGGGTGAAA   23999         CACTG
                                TTTCACTTT    TCTGAGAT
                                |||||||||    ||||||||
                                AAAGTGGGG    AGACTTTA
                                   AAA__
GAM62   C21orf5  3'  TTTCAGGCTAGGTGCGGTG   17614     TT   __
                                CACT  CACT  GTCTGAGA
                                ||||  ||||  ||||||||
                                GTGG  GTGG  CGGACTTT
                                  C_   AT
GAM62   CAPN10   3'  GTCTCAGAACCGAGTGAGGTG  43604         TCACTG
                                CATTTCACTT     TCTGAGAT
                                ||||||||||     ||||||||
                                GTGGAGTGAG     AGACTCTG
                                   CCA___
GAM62   CARPX    5'  TCGGGTGGGAGTGCGAGTG   39426      _   TT   TGT
                                CATTT CACT  CAC   CTGA
                                ||||| ||||  |||   ||||
                                GTGAG GTGA  GTG   GGCT
                                  C   GG   ___
GAM62   CARPX    3'  ATTTCAGATAGTGTCCTAGGA  39415    A  TT__
                                TC CT   CACTGTCTGAGAT
                                || ||   ||||||||||||
                                AG GA   GTGATAGACTTTA
                                 _ TCCT
GAM62   CASP10   3'  TTTTGGACTGGGTGCGGTG   52111     TT   __   TG
                                CACT  CACT  GTC  AGA
                                ||||  ||||  |||  |||
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                                GTGG  GTGG  CAG  TTT
                                  C_   GT   GT
GAM62   CASP10   3'  TTTTGGACTGGGTGCGGTG   52127     TT   __   TG
                                CACT  CACT  GTC  AGA
                                ||||  ||||  |||  |||
                                GTGG  GTGG  CAG  TTT
                                  C_   GT   GT
GAM62   CCND1    3'  GTGGTGGCAGTGGAGGTGGGGT 53891     TT          TGAGAT
           G                     CAT  CACTTTCACTGTC
                                |||  ||||||||||||
                                GTG  GTGGAGGTGACGG
                                  GG          TGGTG
GAM62   CDK4     5'  GTCACATGGTGAGGGTGGGG   53763   TT         C   GAT
                                T  CACTTTCACTGT TGA
                                |  ||||||||||| |||
                                G  GTGGGAGTGGTA ACT
                                 GG         C   G
GAM62   CDK4     5'  GTCACATGGTGAGGGTGGGG   3573    TT         C   GAT
                                T  CACTTTCACTGT TGA
                                |  ||||||||||| |||
                                G  GTGGGAGTGGTA ACT
                                 GG         C   G
GAM62   CDKN2A   5'  TATCTTGGAGGTCCGGGTGGGA 54230     TT   G_____  TG
           GTGGGG                 ACT  CACT     TC  AGAT   A
                                |||  ||||     ||  ||||  |
                                TGA  GTGG     AG  TCTA   T
                                  GG   GCCTGG  GT
GAM62   CDKN2A   5'  GTCCGGGTGGGAGTGGGGGTGG 54229   TT   TT   G___    A
           GGTG                    T  CACT  CACT    TCTG GAT
                                |  ||||  ||||    |||| |||
                                G  GTGG  GTGA    GGGC CTG
                                 GG   GG   GGGT   _
GAM62   CDKN2B   3'  AGGTGGTGGAGTGGAGTG    54353          T   TG
                                CATTTCACTT CAC  TCT
                                ||||||||| |||  |||
                                GTGAGGTGAG GTG  GGA
                                      _  GT
GAM62   CERD4    3'  ATCTCAGAGCAGAGGAGGTGGG 23849   TT     A  _
           G                     T  CACTTTC CTG TCTGAGAT
                                |  ||||||| ||| ||||||||
                                G  GTGGAGG GAC AGACTCTA
                                 GG      A   G
GAM62   CHRM1    3'  TTTTCCTGGGAGTGGGAGTCAA 94794      C   TT   G  T_   T
           GTG                     CATTT ACT  CACT TC  GAGA
                                |||||  |||  ||||  ||  ||||
                                GTGAA TGA  GTGA GG  CTTT
                                  C   GG   G  TC    TA
GAM62   CLASP1   3'  GGGGGTGGGGTGGGGTG    65305     TT    T   G
                                CAT  CACTT CACT TC
                                |||  ||||| |||| ||
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                                GTG  GTGGG GTGG GG
                                  GG    _   G
GAM62   CMAR     5' ATTTTGGACGGTGCTCTGA   17772     CTTT     TG
                                TCA   CACTGTC  AGAT
                                |||   |||||||  ||||
                                AGT   GTGGCAG  TTTA
                                  CTC_     GT
GAM62   COL1A1   3' ATCTATGTGATGGGTGGGGTG  3601     TT   _   TGTCTG
                                CAT  CACTT TCAC    AGAT
                                |||  ||||| ||||     ||||
                                GTG  GTGGG AGTG    TCTA
                                  GG    T   TA____
GAM62   COL4A4   5' CAGGCGGGGAAGTGGGGTG   3626     TT     A
                                CAT  CACTTTC CTGTCTG
                                |||  ||||||| |||||||
                                GTG  GTGAAGG GGCGGAC
                                  GG     _
GAM62   COL4A6   3' GTCTTAGGCAGGCAAGAGAATT 8473     ___   CA_
            GAAATG                TCA   CTTT   CTGTCTGAGAT
                                |||   ||||   ||||||||||
                                AGT   GAGA   GACGGATTCTG
                                  TAA    ACG
GAM62   CPT1B    3' GCCCAGGTGGTGGAGGTGGGGT 15199    TT       TG    AGAT
                                AT  CACTTTCAC  TCTG
                                ||  |||||||||  ||||
                                TG  GTGGAGGTG  GGAC
                                  GG       GT    CCG
GAM62   D10S170  3' GTTTTGTACTTTGGTAGTGAAG 18367         T   CT  CT
            TG                    CATTTCACT TCA  GT  GAGAT
                                |||||||||| |||  ||  |||||
                                GTGAAGTGA GGT  CA  TTTTG
                                     T   TT  TG
GAM62   DDEF2    3' ATTTTAGGCGGCCAGTGAACTG 13952    T     TTCA
                                CA TTCACT    CTGTCTGAGAT
                                || ||||||    ||||||||||
                                GT AAGTGA    GGCGGATTTTA
                                 C     CC__
GAM62   DES      3' TCTCAGGCTGGTGGGAG     72132    TT   _
                                CT  CACT GTCTGAGA
                                ||  |||| ||||||||
                                GA  GTGG CGGACTCT
                                  GG    T
GAM62   DLEC1    3' TAGAGAGAGTGAGGTG      23706           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTGGAGTGAGAG GAT
                                        A
GAM62   DPYSL3   3' ATCTCAGCTTATATGAAAGTCA 7311      C      C   ___
            AGTG                    TTT ACTTTCA TGT   CTGAGAT
                                ||| ||||||| |||   |||||||
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                                GAA TGAAAGT ATA   GACTCTA
                                  C      _  TTC
GAM62   DRIL1    3'  GTTTTGGACATTCAGAGAGATG 17831       A  TTCAC    TG
                                CATTTC CT    TGTC  AGAT
                                |||||| ||    ||||  ||||
                                GTAGAG GA    ACAG  TTTG
                                   A  CTT__   GT
GAM62   DXS1283E  3'  GTTTTAGATAGTTTTTGATGGA 70836      CTTTC_
            A                    TTTCA     ACTGTCTGAGAT
                                |||||     ||||||||||||
                                AAGGT     TGATAGATTTTG
                                   AGTTTT
GAM62   EHF      3'  GTCTCAGATGGTTAGGACAAAG 24063      __ ___
            TGGA                   CACTT  TC   ACTGTCTGAGAT
                                |||||  ||   ||||||||||||
                                GTGAA  AG   TGGTAGACTCTG
                                   AC  GAT
GAM62   EIF2B1   5'  CTGCGGAAGTGGAGTG      59658       T    G   _
                                CACTT CACT TCTG AG
                                ||||| |||| |||| ||
                                GTGAG GTGA AGGC TC
                                   _   _    G
GAM62   EPHA1    3'  GTTTTAAAAGGGAGGTGGGG   17861    TT      A  GTC
                                T  CACTTTC CT   TGAGAT
                                |  ||||||| ||   ||||||
                                G  GTGGAGG GA   ATTTTG
                                 GG       _  AA_
GAM62   ESRRA    3'  ATCTCAGGGAGGGAAGGGGATG 15479     TT A     A  G
                                CAT  C CTTTC CT TCTGAGAT
                                |||  | ||||| || ||||||||
                                GTA  G GAAGG GA GGACTCTA
                                  GG _    _  G
GAM62   FCAR     3'  GCACTGAGAGTGAAGTG     55798            C
                                CATTTCACTTTCA TGT
                                |||||||||||| |||
                                GTGAAGTGAGAGT ACG
                                        C
GAM62   FCAR     3'  GCACTGAGAGTGAAGTG     55814            C
                                CATTTCACTTTCA TGT
                                |||||||||||| |||
                                GTGAAGTGAGAGT ACG
                                        C
GAM62   FGF2     3'  GTCTCAGATACTTGGGAGGCTG 8873       _    AC__
            AGGTG                   TTCA CTTTC    TGTCTGAGAT
                                |||| |||||   ||||||||||
                                GAGT GGAGG    ATAGACTCTG
                                  C    GTTC
GAM62   FRAT2    3'  GGCTGGTGAAGGTGGGA     23881    TT       _
                                T  CACTTTCACT GTC
                                |  |||||||||| |||
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                                A  GTGGAAGTGG CGG
                                 GG         T
GAM62   GCKR     3'  ATTTCAGAAATAAAATGAAATG 7635         C   CACTG
                                CATTTCA TTT     TCTGAGAT
                                ||||||| |||     ||||||||
                                GTAAAGT AAA     AGACTTTA
                                    A   TAA__
GAM62   GNPI     3'  GTCTTAGGCCTTCATGGAGTGG 18448         CACT__
            A                    TTCACTTT     GTCTGAGAT
                                ||||||||     |||||||||
                                AGGTGAGG     CGGATTCTG
                                     TACTTC
GAM62   GPR61    3'  TGGGCTGGTGGGAGTGGGAT   78914    TT    TT   _
                                AT  CACT  CACT GTCTG
                                ||  ||||  |||| |||||
                                TA  GTGA  GTGG CGGGT
                                 GG    GG    T
GAM62   GUCY1B3  3'  ATCTTGGATTATGGGGTGAAG  5963         T  CT   TG
                                TTTCACTT CA  GTC  AGAT
                                |||||||| ||  |||  ||||
                                GAAGTGGG GT  TAG  TCTA
                                     _ AT   GT
GAM62   GYG2     3'  ATTTCAGGTGAGTCAGGGTTGG 14047      TC     C  _ GT
            ATG                    CATT  ACTTT AC T  CTGAGAT
                                ||||  ||||| || |  |||||||
                                GTAG  TGGGA TG G  GACTTTA
                                  GT     C  A TG
GAM62   HHEX     3'  ATTTCAGGCAGCCTTGGAGT   10784      CA__
                                ACTTT    CTGTCTGAGAT
                                |||||    ||||||||||||
                                TGAGG    GACGGACTTTA
                                   TTCC
GAM62   HMGA2    3'  TCTGGGGTGGGGTGGGGTG    13004     TT    TTCA TG   G
                                CAT  CACT    C  TCT AGA
                                |||  ||||    |  ||| |||
                                GTG  GTGG    G  GGG TCT
                                  GG    ____ GT   G
GAM62   HOXD4    5'  TTTTGGGGTACTAGGGAGTGAG 27534         TT AC_ GT  G   T
            GT                    ATTTCACT  C   T  CT AGA
                                ||||||||  |   |  || |||
                                TGGAGTGA  G   A  GG TTT
                                     GG ATC TG  G   TG
GAM62   HPCAL1   3'  TTATGTATGGTGAAGTGGAGTG 9272          T     CTGAGAT
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTGAGGTGAA GTGGTA
                                      _     TGTATTA
GAM62   HPCAL1   5'  GTGGTGACAGGTGAAATG    56190          _   TG
                                CATTTCACTT TCAC  T
                                |||||||||| ||||  |
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                                GTAAAGTGGA AGTG  G
                                      C    GT
GAM62   HPCAL1   3'  TTATGTATGGTGAAGTGGAGTG 56191          T     CTGAGAT
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTGAGGTGAA GTGGTA
                                      _     TGTATTA
GAM62   IGF1R    3'  TTCTCTCAGTGAAGGTGGGG  6049    TT        TCT    T
                                T  CACTTTCACTG   GAGA
                                |  ||||||||||   ||||
                                G  GTGGAAGTGAC   CTCT
                                 GG         T__    TT
GAM62   IL11     3'  ATTTCAGGAGCAGGGGTGGGA  5324    TT     CA  G
                                T  CACTTT  CT TCTGAGAT
                                |  ||||||  || ||||||||
                                A  GTGGGG  GA GGACTTTA
                                 GG     AC  _
GAM62   IL13RA1  3'  TTAGGGGCAGTGGAGGTAGAAT 7782      TC          GAGAT
             G                   CATT  ACTTTCACTGTCT
                                ||||  ||||||||||||
                                GTAA  TGGAGGTGACGGG
                                   GA           GATTG
GAM62   IL1F5    3'  ATTTCTGTGGGGGTGGGGTG  24377     TT    TT   TGTCT
                                CAT  CACT  CAC    GAGAT
                                |||  ||||  |||    |||||
                                GTG  GTGG  GTG    CTTTA
                                  GG    GG   T____
GAM62   IL1RN    3'  GATGGTGAAAGTAAGTG     5143       C
                                CATTT ACTTTCACTGTC
                                ||||| ||||||||||||
                                GTGAA TGAAAGTGGTAG
                                      _
GAM62   IL24     3'  TTGGGGTGGGGGTAAGGTG   22447      C   TT    GT TG
                                CATTT ACT  CACT  C  A
                                ||||| |||  ||||  |  |
                                GTGGA TGG  GTGG  G  T
                                   A   GG    __ GT
GAM62   IRS1     3'  ATCTTTTTTTTGGATGTGGGAT 18662     TT   T    CTGTCT
             G                   CAT  CAC TTCA     GAGAT
                                |||  ||| ||||     |||||
                                GTA  GTG AGGT     TTCTA
                                  GG   T    TTTTT_
GAM62   IRS2     3'  TCTCAATGGAAGTGAAAT    59723           CTGTC
                                ATTTCACTTTCA    TGAGA
                                ||||||||||||    |||||
                                TAAAGTGAAGGT    ACTCT
                                      A____
GAM62   JTB      3'  CTATCTCAGACAGTGAAAGTGA 21961
             AATG                   CATTTCACTTTCACTGTCTGAGAT
                                ||||||||||||||||||||||||
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                                GTAAAGTGAAAGTGACAGACTCTA
                                                   TCC
GAM62   KCNA7   3'  TCTCAGAGCAGGGGAGTG   49061     TT A  _
                                CACT  C CTG TCTGAGA
                                ||||  | ||| |||||||
                                GTGA  G GAC AGACTCT
                                  GG _  G
GAM62   KCNK6   3'  ATGGAGGAGGTGAGGTG    16690          A
                                CATTTCACTTTC CTGT
                                |||||||||||| ||||
                                GTGGAGTGGAGG GGTA
                                       A
GAM62   KCNK6   3'  TTTCAGGCTGAGTGTGGTG   16699     TT   __
                                CACT  CACT  GTCTGAGA
                                ||||  ||||  ||||||||
                                GTGG  GTGA  CGGACTTT
                                  T_   GT
GAM62   LAMC1   3'  GTCTCAGGCCACAATGGGGTG  9677     TT  CTTTCACT
                                CAT  CA      GTCTGAGAT
                                |||  ||      |||||||||
                                GTG  GT      CGGACTCTG
                                  GG  AACAC___
GAM62   MALT1   3'  ATTTTAGATGCCTGTGAAAT   22291       TTTCACT
                                ATTTCAC     GTCTGAGAT
                                |||||||     |||||||||
                                TAAAGTG     TAGATTTTA
                                    TCCG___
GAM62   MAPK14  3'  TCCTCCATGGTGGAAGGGGGTG 57335     TT A       CT   AT
                                CAT  C CTTTCACTGT  GAG
                                |||  | ||||||||||  |||
                                GTG  G GAAGGTGGTA  CTC
                                  GG _       C_   CTT
GAM62   MAPK14  3'  TCCTCCATGGTGGAAGGGGGTG 7161      TT A       CT   AT
                                CAT  C CTTTCACTGT  GAG
                                |||  | ||||||||||  |||
                                GTG  G GAAGGTGGTA  CTC
                                  GG _       C_   CTT
GAM62   MAPK14  3'  TCCTCCATGGTGGAAGGGGGTG 57346     TT A       CT   AT
                                CAT  C CTTTCACTGT  GAG
                                |||  | ||||||||||  |||
                                GTG  G GAAGGTGGTA  CTC
                                  GG _       C_   CTT
GAM62   MAPRE1  3'  ATTTTTTGGGGAAGTGAGGTG  24661          A  GTCT
                                CATTTCACTTTC CT   GAGAT
                                |||||||||||| ||   |||||
                                GTGGAGTGAAGG GG   TTTTA
                                       _ TT__
GAM62   MBP     5'  TTTTGGAAGGTGGAGTG    89783      T   G  TG
                                CACTT CACT TC  AGA
                                ||||| |||| ||  |||
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                                GTGAG GTGG AG  TTT
                                  _   A  GT
GAM62   MGAT5   5' TGCCTCATGGTGGGAGTGAAA 10030       TT   TC   AT
                                TTTCACT  CACTG  TGAG
                                |||||||  |||||  ||||
                                AAAGTGA  GTGGT  ACTC
                                    GG   __   CGTT
GAM62   MGEA5   3' GTTTCAGAAGTGTCAGGGTGGA 24218         __   G
           GTG                   ATTTCACTTT  CACT TCTGAGAT
                                |||||||||  |||| ||||||||
                                TGAGGTGGGA  GTGA AGACTTTG
                                     CT   _
GAM62   MMP19   3' TCAATGGTGGAGGGAGATG   10086      A       C
                                CATTTC CTTTCACTGT TGA
                                |||||| |||||||||| |||
                                GTAGAG GGAGGTGGTA ACT

                                  _       _
GAM62   MMP19   3' TCAATGGTGGAGGGAGATG   42975      A       C
                                CATTTC CTTTCACTGT TGA
                                |||||| |||||||||| |||
                                GTAGAG GGAGGTGGTA ACT

                                  _       _
GAM62   MMP19   3' TCAATGGTGGAGGGAGATG   42981      A       C
                                CATTTC CTTTCACTGT TGA
                                |||||| |||||||||| |||
                                GTAGAG GGAGGTGGTA ACT

                                  _       _
GAM62   MMP19   3' TCAATGGTGGAGGGAGATG   42985      A       C
                                CATTTC CTTTCACTGT TGA
                                |||||| |||||||||| |||
                                GTAGAG GGAGGTGGTA ACT

                                  _       _
GAM62   MOG     3' TCTTGGCAGGGGTGGAG    10107       TCA  T TG
                                TTTCACTT  CTG C  AGA
                                ||||||||  ||| |  |||
                                GAGGTGGG  GAC G  TCT
                                   ___  _ GT
GAM62   MPP4    5' TATCGGGAGCAGTGAGGTG   52347     T    __   GAT
                                CACTT CACTGT  CTGA
                                |||||  ||||||  ||||
                                GTGGA GTGACG  GGCT
                                  _    AG   ATT
GAM62   MS4A1   3' ATTTTGGGGAGACAAAGGGAAA 3748       A   CA  G  TG
           TG                   CATTTC CTTT  CT TC  AGAT
                                ||||||  ||||  ||  ||  ||||
                                GTAAAG GAAA  GA GG  TTTA
                                   G   CA  G  GT
GAM62   MTNR1A  3' ACAATGAAAGTGGGGTG    19887    TT      C
                                CAT  CACTTTCA TGT
                                |||  |||||||| |||
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                                GTG  GTGAAAGT ACA
                                  GG       A
GAM62   MYOZ1    5'  ATCTCAGGCTCTAGGTGCAATG 41149      T     TCACT
                                CATT CACTT    GTCTGAGAT
                                |||| |||||    |||||||||
                                GTAA GTGGA    CGGACTCTA
                                  C    TCT__
GAM62   NAV2     3'  TTTCATTAGGGGTGGGGTG   60162     TT    TCA   TC
                                CAT  CACTT   CTG  TGAGA
                                |||  |||||   |||  |||||
                                GTG  GTGGG   GAT  ACTTT
                                  GG    ___   T_
GAM62   NDST2    3'  ATCTTGGGAGGTGGGGAGGAAT 13296       AC TT    GT TG
           G                     CATTTC  T  CACT  C  AGAT
                                ||||||  |  ||||  |  ||||
                                GTAAGG  G  GTGG  G  TCTA
                                   A_ GG    AG GT
GAM62   NEBL     3'  TTTTTGTGGTAGGGAAGTGGGA 21126     TT      A  GT _    T
           TG                    CAT  CACTTTC CT  C TGAGA
                                |||  ||||||| ||  | |||||
                                GTA  GTGAAGG GA  G GTTTT
                                  GG      _ TG T     TA
GAM62   NEU1     3'  GTCTTGGGCAGGTCTAGTGAGC 4742     T     TTCA     TG
           TG                    CA TTCACT    CTGTC  AGAT
                                || ||||||    |||||  ||||
                                GT GAGTGA    GACGG  TCTG
                                 C     TCTG    GT
GAM62   NEUROD2  3'  ATTTTGGCGGGAGGGGAAGTG  20478       A    A   T TG
                                CATTTC CTTTC CTG C  AGAT
                                |||||| ||||| ||| |  ||||
                                GTGAAG GGGAG GGC G  TTTA
                                   _    _  _ GT
GAM62   NFE2L1   3'  TGTCTGCCCCAGACAAGTGGGA 12177     TT   _    ____
           GTGAAATG                 ACT  CACT GTCTG    AGAT   G
                                |||  |||| |||||    ||||   |
                                TGA  GTGA CAGAC    TCTG   T
                                  GG   A    CCCG
GAM62   NFRKB    5'  GTCTTAAGGGAAGTGAAAGAGG 20497      A      G_   _
           AGTG                    ATTTC CTTTCACT  TCT GAGAT
                                |||||| ||||||||  ||| |||||
                                TGAGG GAAAGTGA  GGA TTCTG
                                   A       AG   A
GAM62   NGB      3'  GTTTTGGTGGCAGAGGTGGGAT 41188     TT     CA   T TG
           G                     CAT  CACTTT  CTG C  AGAT
                                |||  ||||||  ||| |  ||||
                                GTA  GTGGAG  GGT G  TTTG
                                  GG     AC   _ GT
GAM62   NLGN1    3'  CCTTTTGGTAAGGTGAAGTG   30024          C   GTCT   AT
                                CATTTCACTTT ACT    GAG
                                |||||||||| |||    |||
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                                GTGAAGTGGAA TGG   TTC
                                      _  TT__  CT
GAM62   NPC2    3'  GTCTTAGGTGGTTTCATTAAAT 21223     CACTTTC  TG
            G                  CATTT     AC  TCTGAGAT
                               |||||     ||  ||||||||
                               GTAAA     TG  GGATTCTG
                                  TTACTT_  GT
GAM62   OCRL    3'  GTTTCTTGGTGGGGGTGGGG  4264    TT   TT   GTCT
                               T  CACT  CACT   GAGAT
                               |  ||||  ||||   |||||
                               G  GTGG  GTGG   CTTTG
                                GG   GG   TT__
GAM62   OCRL    3'  GTTTCTTGGTGGGGGTGGGG  7830    TT   TT   GTCT
                               T  CACT  CACT   GAGAT
                               |  ||||  ||||   |||||
                               G  GTGG  GTGG   CTTTG
                                GG   GG   TT__
GAM62   PER2    3'  TTTTTGATGGAGGTGAAAT   43051          CTG  T
                               ATTTCACTTTCA   TC GAGA
                               ||||||||||||   || ||||
                               TAAAGTGGAGGT   AG TTTT
                                     ___  T
GAM62   PGAM1   3'  TTTCATGGCAGTGAAA     76276          _
                               TTTCACTGTC TGAGA
                               |||||||||| |||||
                               AAAGTGACGG ACTTT
                                     T
GAM62   PIGN    5'  GTCTCAGTCCTGTGCAAAGTGA 24672          _  TGT_
            GATG                  ATTTCACTTT CAC   CTGAGAT
                               |||||||||| |||   |||||||
                               TAGAGTGAAA GTG   GACTCTG
                                     C  TCCT
GAM62   PKP4    3'  GAAATGTGAAAGTGAAGTG   13266           TG_
                               CATTTCACTTTCAC   TC
                               ||||||||||||||   ||
                               GTGAAGTGAAAGTG   AG
                                        TAA
GAM62   PRDM2   3'  GTCTCGGAGAAACGGGTGAGCT 24250    T     TCACTG
            G                  CA TTCACTT     TCTGAGAT
                               || |||||||     ||||||||
                               GT GAGTGGG     AGGCTCTG
                                C      CAAAG_
GAM62   PSEN1   5'  ATAGTGGAGGCTGGGATG    23621    TT  _
                               CAT  CA CTTTCACTGT
                               |||  || ||||||||||
                               GTA  GT GGAGGTGATA
                                 GG  C
GAM62   RALB    3'  GTTTTGGAGGAGGGAGTGGAGT 11245        TT A  G  TG
                               ATTTCACT  C CT TC  AGAT
                               ||||||||  | || ||  ||||
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                                TGAGGTGA  G GG AG  TTTG
                                     GG A  _  GT
GAM62   RAMP3    3'  CGGTGAGATGGAGTG       19589        C
                                CATTTCA TTTCACTG
                                ||||||| ||||||||
                                GTGAGGT AGAGTGGC

                                _
GAM62   RANBP7   3'  ATTTTGGGGGTGGGGGGGA   21113     A  TT    G  TG
                                TTC CT  CACT TC  AGAT
                                ||| ||  |||| ||  ||||
                                AGG GG  GTGG GG  TTTA
                                  _ GG    _ GT
GAM62   RGS19IP1 3'  GATGGTGAGGGGAGGTG     62509       A
                                CATTTC CTTTCACTGTC
                                |||||| ||||||||||
                                GTGGAG GGGAGTGGTAG

                                _
GAM62   RNASE1   3'  ATTTTGGGGGTGAAGAGTGGGT 63875    T       _    G  TG
           TG                     CA TTCACTTT CACT TC  AGAT
                                || ||||||||| |||| ||  ||||
                                GT GGGTGAGA GTGG GG  TTTA
                                 T       A    _ GT
GAM62   RNGTT    3'  ATTTTGGACATTGTGAAGGAAA 13729       A   T  __    TG
           TG                     CATTTC CTT CAC  TGTC  AGAT
                                |||||| ||| |||  ||||  ||||
                                GTAAAG GAA GTG  ACAG  TTTA
                                   _  _  TT    GT
GAM62   RXRB     3'  CAGTGGTGGAGGTGGG      41758            T
                                TTCACTTTCACTG CTG
                                |||||||||||||| |||
                                GGGTGGAGGTGGT GAC

                                _
GAM62   SEDL     3'  ATTCTGCAGTTGGGAGTGAAAT 27322          TT  _    CT   AT
           G                     CATTTCACT  CA CTGT  GAG
                                |||||||||  || ||||  |||
                                GTAAAGTGA  GT GACG  CTT
                                     GG  T    T_   A
GAM62   SH3BP4   3'  CAGTAGAGTGAGGTG       27232           C
                                CATTTCACTTT ACTG
                                |||||||||||| ||||
                                GTGGAGTGAGA TGAC

                                _
GAM62   SIGLEC6  3'  ATTTTAAGACTGAAAGTGAAAT 59926           CT   _
                                ATTTCACTTTCA  GTCT GAGAT
                                ||||||||||||  |||| |||||
                                TAAAGTGAAAGT  CAGA TTTTA
                                      __    A
GAM62   SLC17A2  5'  TTTAATGGTGAAGGTAAGTG   19546       C         C
                                CATTT ACTTTCACTGT TGAG
                                ||||| |||||||||| ||||
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                                GTGAA TGGAAGTGGTA ATTT
                                  _       _
GAM62   SLC19A1  5' GTCTCGGGGCCCTGGGGTGAG  11758       T  CT   _
                                TTCACTT CA  GTCT GAGAT
                                ||||||| ||  |||| |||||
                                GAGTGGG GT  CGGG CTCTG
                                    _ CC    G
GAM62   SLC38A2  3' TCTCGGGTTAAGGGAAGTG   38593       A  G__
                                CACTTTC CT   TCTGAGA
                                ||||||| ||   |||||||
                                GTGAAGG GA   GGGCTCT
                                    _ ATT
GAM62   SLC6A4   3' TTTTGGACGTGTGAGGATG   6452     CT    _   TG
                                CA  TTCAC TGTC  AGA
                                ||  ||||| ||||  |||
                                GT  GAGTG GCAG  TTT
                                 AG    T    GT
GAM62   SLC7A8   3' GTCTTGGGGCAGGGTGAAA   24282       TTCA   _ TG
                                TTTCACT    CTGT C  AGAT
                                |||||||    |||| |  ||||
                                AAAGTGG    GACG G  TCTG
                                    _____   G GT
GAM62   SMARCB1  3' TCGGGTGGGGGTGGAGTG    65586        TT   TGT
                                CATTTCACT  CAC   CTGA
                                |||||||||  |||   ||||
                                GTGAGGTGG  GTG   GGCT
                                     GG  ___
GAM62   SNCA     3' TTAATTATTGAAAGTGGGGTG  4433     TT      C  TC
                                CAT  CACTTTCA TG  TGA
                                |||  |||||||| ||  |||
                                GTG  GTGAAAGT AT  ATT
                                  GG       T  TA
GAM62   SRRM2    3' TTTGGGGTGGGAGGGAATG   32918       A  TT   GT TG
                                CATTTC CT  CACT  C  AG
                                |||||| ||  ||||  |  ||
                                GTAAGG GA  GTGG  G  TT
                                    _ GG   __ GT
GAM62   SSPN     3' GTCTTAGAAGAAAGTGGAAT   17445         ACTG
                                ATTTCACTTTC    TCTGAGAT
                                ||||||||||    ||||||||
                                TAAGGTGAAAG    AGATTCTG
                                      A___
GAM62   STAR     3' ATCTCCATCTGGTGACAGTGGG 4443     TT   T    GTCT_
            ATG                   CAT  CACT TCACT    GAGAT
                                |||  |||| |||||    |||||
                                GTA  GTGA AGTGG    CTCTA
                                  GG   C    TCTAC
GAM62   T        3' GTCTCAGGTTAAGAAGGAAATG 12077       A   CACTG
                                CATTTC CTTT    TCTGAGAT
                                |||||| ||||    ||||||||
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                                GTAAAG GAAG    GGACTCTG
                                   _   AATT_
GAM62   TAF1C    3'  TGGTGAGGGTGGAGTG     19060
                                CATTTCACTTTCACTG
                                ||||||||||||||||
                                GTGAGGTGGGAGTGGT

GAM62   TIMP3    3'  GTTTTAGTGTCAAAAGTGAGAT 4517          CACTGT
           G                     CATTTCACTTT     CTGAGAT
                                ||||||||||      |||||||
                                GTAGAGTGAAA     GATTTTG
                                      ACTGT_
GAM62   TMOD4    5'  TACCACACAGTGGGAGGGGGTG 25331     TT A  TT     C  AGAT
                                CAT  C CT  CACTGT TG
                                |||  | ||  |||||| ||
                                GTG  G GA  GTGACA AC
                                  GG _  GG     C  CATG
GAM62   TNFRSF4  3'  ATCTTGGCCAGGGTGGAGTG   12451        TTCA   T TG
                                CATTTCACT    CTG C  AGAT
                                |||||||||    ||| |  ||||
                                GTGAGGTGG    GAC G  TCTA
                                     _____  C GT
GAM62   TRH      3'  CAGCCAGTGAGGGTGGGGTG   23051     TT         T
                                CAT  CACTTTCACTG CTG
                                |||  |||||||||| |||
                                GTG  GTGGGAGTGAC GAC
                                  GG         C
GAM62   TRHDE    3'  TTTTGGGCAATGTGAGAG    25393        __    TG
                                CTTTCAC  TGTC  AGA
                                |||||||  ||||  |||
                                GAGAGTG  ACGG  TTT
                                    TA    GT
GAM62   TRIM9    3'  GTTTCAAATGGGTGGTGGGGTG 53761     TT    TTCA    C
                                CAT  CACT    CTGT TGAGAT
                                |||  ||||    |||| ||||||
                                GTG  GTGG    GGTA ACTTTG
                                  GG   TG__    A
GAM62   TSG      3'  ATTTCCTACTGTGAGTGGAGTG 40231         TT    T  CT
                                CATTTCAC  TCAC GT  GAGAT
                                ||||||||  |||| ||  |||||
                                GTGAGGTG  AGTG CA  CTTTA
                                     __    T  TC
GAM62   TSLP     5'  TTTAGTGTGAAACTGGGGTG   52310     TT  C     TGT
                                CAT  CA TTTCAC   CTGAG
                                |||  || ||||||   |||||
                                GTG  GT AAAGTG   GATTT
                                  GG  C     T__
GAM62   VDAC1    3'  TTTGGGGTGGAGAAGGTGGA   12583         A TG   G   T
                                TTCACTTTC C  TCT AGA
                                |||||||||  |  ||| |||
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                                AGGTGGAAG G  GGG TTT
                                     A GT   G   T
GAM62   VDR     3'  TCTTTGTGAGAGTGAGCTG   4571     T        TGTCT
                                CA TTCACTTTCAC    GAGA
                                || ||||||||||    ||||
                                GT GAGTGAGAGTG    TTCT
                                 C         T____
GAM62   WNT10B  3'  GGGTGGTGGGGGTCAGGTG   12675      C   TT   TG
                                CATTT ACT  CAC  TCT
                                ||||| |||  |||  |||
                                GTGGA TGG  GTG  GGG
                                   C   GG   GT
GAM62   ZNF239  5'  GTCAGGATAATGGTGGGAATGG 19042   TT  C TT    ____   GAT
           GGTG                    CA T  CACTGT   CTGA
                                 || |  ||||||   ||||
                                 GT A  GTGGTA    GACT
                                GG  A GG     ATAG    G
GAM62   AKAP6   5'  GTTTTGGAAAGAAGTGAGGT   14996         CACTG  TG
                                ATTTCACTTT    TC  AGAT
                                ||||||||||    ||  ||||
                                TGGAGTGAAG    AG  TTTG
                                     AA___  GT
GAM62   APXL2   3'  TAGGTGGAGAGGGTGGGGTG   75196     TT      A TG
                                CAT  CACTTTC C  TCTG
                                |||  ||||||| |  ||||
                                GTG  GTGGGAG G  GGAT
                                  GG      A GT
GAM62   ARFGAP3  3'  ATCTCAGGCGGCAGTGAAGT   27385        TTCA
                                ATTTCACT    CTGTCTGAGAT
                                ||||||||    ||||||||||
                                TGAAGTGA    GGCGGACTCTA
                                     C___
GAM62   ARHGEF9  3'  TTTTAGGTACTGTGAAGG    30827        __ GT
                                CTTTCAC  T  CTGAGA
                                |||||||  |  ||||||
                                GGAAGTG  A  GATTTT
                                     TC TG
GAM62   ARHGEF9  3'  TTTTGGGGAAGTGAAAT     30829          ACTGT TG
                                ATTTCACTTTC     C  AGA
                                ||||||||||     |  |||
                                TAAAGTGAAGG     G  TTT
                                      _____ GT
GAM62   BCL2L1   3'  GTCTGTGTGAAGGTGAAA    56807          TGTCTG
                                TTTCACTTTCAC     AGAT
                                ||||||||||||     ||||
                                AAAGTGGAAGTG     TCTG
                                      TG____
GAM62   C19orf7  3'  AGACAGTGAGAGTGAAA     61124
                                TTTCACTTTCACTGTCT
                                |||||||||||||||||
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                                AAAGTGAGAGTGACAGA

GAM62   C1orf17  3'  TTTCAGAGTGGGGAAGTG    68219       A  _
                                CACTTTC CTG TCTGAGA
                                ||||||| ||| |||||||
                                GTGAAGG GGT AGACTTT
                                    _  G
GAM62   C1orf34  3'  GCAGTGAGGGTGAGCTG    60673    T
                                CA TTCACTTTCACTGT
                                || ||||||||||||||
                                GT GAGTGGGAGTGACG
                                 C
GAM62   C20orf151 3'  TCTGGCAGTGAGGGTGGAG   88703             T
                                TTTCACTTTCACTGTC GA
                                |||||||||||||||| ||
                                GAGGTGGGAGTGACGG CT
                                          T
GAM62   C20orf21  3'  TCTCAGGACAAGTGGAAG    35117       _  _
                                CTTTCACT GTC TGAGA
                                |||||||| ||| |||||
                                GAAGGTGA CAG ACTCT
                                     A  G
GAM62   C20orf29  3'  GTCTCAGACTCCCCTGAGGGTG 37129          CT___
            GAG                   TTTCACTTTCA    GTCTGAGAT
                                ||||||||||    |||||||||
                                GAGGTGGGAGT    CAGACTCTG
                                      CCCCT
GAM62   C20orf60  3'  TAGGGGTGGGGGGTGGGATG   53738    TT   TT   G
                                CAT  CACT  CACT TCTG
                                |||  ||||  |||| ||||
                                GTA  GTGG  GTGG GGAT
                                  GG   GG   _
GAM62   C22orf5   5'  GACAGTGAGGGGGGGATG    24342    TT A
                                CAT  C CTTTCACTGTC
                                |||  | ||||||||||
                                GTA  G GGGAGTGACAG
                                  GG _
GAM62   C8orf2    3'  ATAGTGAAAGTAAGATG    23157      C
                                CATTT ACTTTCACTGT
                                ||||| ||||||||||
                                GTAGA TGAAAGTGATA
                                   A
GAM62   CCR5    3'  ATTTCAGACTGAATGGGGGGTGG 5147    TT   TT  CT__
            GG                    T  CACT  CA   GTCTGAGAT
                                |  ||||  ||   |||||||||
                                G  GTGG  GT   CAGACTTTA
                                 GG   GG  AAGT
GAM62   CCR6    3'  TCTCTTCAGGGTGGGGTG    15173    TT   TTCA  TCT
                                CAT  CACT   CTG   GAGA
                                |||  ||||   |||  ||||
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                                GTG  GTGG   GAC   CTCT
                                  GG   ____   TT_
GAM62   CCR6    3'  TCTCTTCAGGGTGGGGTG   48589    TT   TTCA  TCT
                                CAT  CACT   CTG   GAGA
                                |||  ||||   |||   ||||
                                GTG  GTGG   GAC   CTCT
                                  GG   ____   TT_
GAM62   CECR7   5'  ATAGTGGGAATGAAATG    79615       C TT
                                CATTTCA T  CACTGT
                                |||||||  |  ||||||
                                GTAAAGT A  GTGATA
                                    A GG
GAM62   CENTA2  3'  TCTCAGATGGCTGAAATGT   37269    _    _
                                AC TTTCA CTGTCTGAGA
                                || ||||| ||||||||||
                                TG AAAGT GGTAGACTCT
                                 T    C
GAM62   CEP3    3'  ATCTTGGCAAAAAAAGGAAGTG 21247      A   CAC  T TG
                                CATTTC CTTT   TG C  AGAT
                                ||||||  ||||   ||  |  ||||
                                GTGAAG GAAA   AC G  TCTA
                                   _   AAA  _ GT
GAM62   CHSY1   3'  TTGGGGACAAAAGTGAAATG   29905         CAC    GA  T
                                CATTTCACTTT   TGTCT  GA
                                ||||||||||   |||||  ||
                                GTAAAGTGAAA   ACAGG  TT
                                      ___    GG  T
GAM62   CNNM2   3'  GGACAGTGAGGGAGGAATG   34461      A
                                CATTTC CTTTCACTGTCT
                                ||||||  ||||||||||||
                                GTAAGG GGGAGTGACAGG
                                   A
GAM62   COLEC10 3'  TTTCAGACCATGTGGAATG   21230       TTTCACT
                                CATTTCAC      GTCTGAGA
                                ||||||||      ||||||||
                                GTAAGGTG      CAGACTTT
                                     TAC____
GAM62   CRR9    3'  ATTTCAGGTGGTTTTCTAAGTG 47878      TC___  TG
                                CACTT    AC  TCTGAGAT
                                |||||    ||  ||||||||
                                GTGAA    TG  GGACTTTA
                                   TCTTT  GT
GAM62   CYYR1   3'  ATTTTAGGTGGGTGTGAAGTG  53670        TTTCA TG
                                CATTTCAC    C  TCTGAGAT
                                ||||||||    |  ||||||||
                                GTGAAGTG    G  GGATTTTA
                                     TG___ GT
GAM62   DAPK3   3'  GTCGTGGGACGGGGAGGGTGGG 7211     TT     A     GA_
            ATG                   CAT  CACTTTC CTGTCT   GAT
                                |||  ||||||| ||||||   |||
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                                GTA  GTGGGAG GGCAGG   CTG
                                  GG      G     GTG
GAM62   DDX8     3'  GGATGGGAAGGTGGAGTG    17053           A
                                CATTTCACTTTC CTGTCT
                                |||||||||||| ||||||
                                GTGAGGTGGAAG GGTAGG
                                                 _
GAM62   DKFZp434B217 3'  GGGTTTGGGCGGGAGTGGGCTG 70701    T      TCA    TG  AT
                                CA TTCACTT   CTGTC  AG
                                || |||||||   |||||  ||
                                GT GGGTGAG   GGCGG  TT
                                 C       ___     GT  GGGT
GAM62   DKFZP434K028 3'  CTTACAGTGGAGGTAAAGTG   93231       C         CT
                                CATTT ACTTTCACTGT  GAG
                                ||||| ||||||||||  |||
                                GTGAA TGGAGGTGACA  TTC
                                   A          __
GAM62   DKFZp434O0320 3'  GGTGGCAGGTGGAGTG      83696          _
                                CATTTCACTT TCACT
                                |||||||||| |||||
                                GTGAGGTGGA GGTGG
                                      C
GAM62   DKFZP434O047 5'  ATTTTGGACAAGGTGCTGAAGT 31503        CTTT   __  TG
        G                        CATTTCA    CACT  GTC  AGAT
                                |||||||    ||||  |||  ||||
                                GTGAAGT    GTGG  CAG  TTTA
                                    C___    AA   GT
GAM62   DKFZp547F072 5'  TCCATGGGCGGGGGTGGGGTG  50094     TT    TT A  GTC  A  T
                                CAT  CACT  C CT   TG GA
                                |||  ||||  | ||   || ||
                                GTG  GTGG  G GG   AC CT
                                  GG    GG C  GT_  _  T
GAM62   DKFZP564C103 3'  TCTTAGATAAGTAAGGTG    31612       C  _
                                CACTTT ACT GTCTGAGA
                                |||||| ||| ||||||||
                                GTGGAA TGA TAGATTCT
                                   _  A
GAM62   DKFZP564I052 3'  GTTTTGAGAGGGGAGTAGAAGT 66719       _  TT A  G  T
        G                        CATTTC ACT  C CT TC GAGAT
                                |||||| |||  | || || |||||
                                GTGAAG TGA  G GA AG TTTTG
                                   A   GG _  G  _
GAM62   DKFZP564I052 3'  GTTTTAGGTGGTGATCTTAAAT 66718      CACTT    TG
        G                        CATTT    TCAC  TCTGAGAT
                                |||||    ||||  ||||||||
                                GTAAA    AGTG  GGATTTTG
                                   TTCT_   GT
GAM62   DKFZP566G1424 3'  ATTTTGGACTCAGTGAAAGTG  84773          __  TG
                                CACTTTCACT  GTC  AGAT
                                ||||||||||  |||  ||||
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                                GTGAAAGTGA  CAG  TTTA
                                      CT   GT
GAM62   DKFZp761N1114 3'  GTTTCAGAAAGCTGGGTGGTGG 79022      _   _ G
                                TCACT TTCA CT TCTGAGAT
                                ||||| |||| || ||||||||
                                GGTGG GGGT GA AGACTTTG
                                   T   C  A
GAM62   DKFZp762P2111 3'  GTCTCAGGTGTTCTGGGGATG  86361     TT ACTTT   TGT
                                CAT  C    CAC   CTGAGAT
                                |||  |    |||   |||||||
                                GTA  G    GTG   GACTCTG
                                  GG GTCTT  ___
GAM62   DKFZp762P2111 3'  TGAGAAACAGTGGAGTGGAGTG 86365          T     CTGAGAT
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTGAGGTGAG GTGACA
                                      _     AAGAGTA
GAM62   DMRTA2   3'  GTTTTGTTTAGGAGGGTGGG   60660         A   TC
                                TTCACTTTC CTG  TGAGAT
                                ||||||||| |||  ||||||
                                GGGTGGGAG GAT  GTTTTG
                                      _  TT
GAM62   DRIL2    3'  ATCGTGGGGGCGGGGAGGTGGA 21322          A     GA__
           GTG                    ATTTCACTTTC CTGTCT    GAT
                                ||||||||||| ||||||    |||
                                TGAGGTGGAGG GGCGGG    CTA
                                      _     GGTG
GAM62   EAT2     3'  TCAGGTGAAGGTGAGG      79281           TGT
                                TTTCACTTTCAC   CTGA
                                ||||||||||||   ||||
                                GGAGTGGAAGTG   GACT
                                      ____
GAM62   EPS8R1   5'  TAGAACATGAAGGTGGGATG   34803     TT      C  _
                                CAT  CACTTTCA TGT CTG
                                |||  |||||||| ||| |||
                                GTA  GTGGAAGT ACA GAT
                                  GG       _  A
GAM62   FBXL3B   5'  ATCTTCTGTATGTAGGAGGTGG 24070          _  TGTCT_
           AATG                    ATTTCACTTTC AC     GAGAT
                                ||||||||||| ||     |||||
                                TAAGGTGGAGG TG     TTCTA
                                      A  TATGTC
GAM62   FHX      3'  TCAAGGGTGAAAGTGATGATG  37307      _        GTC
                                CATT TCACTTTCACT   TGA
                                |||| ||||||||||   |||
                                GTAG AGTGAAAGTGG   ACT
                                   T         GA_
GAM62   FKSG42   3'  GTCTCAGGGTGGGAAGTGGGA  49335   TT     _   GT
                                T  CACTTTC ACT  CTGAGAT
                                |  ||||||| |||  |||||||
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                                A  GTGAAGG TGG  GACTCTG
                                 GG      G  __
GAM62   FLJ00024  3' GTCTTGGGAGAAGGGTGAGG  63765        CA  G  TG
                                TTTCACTTT  CT TC  AGAT
                                |||||||||  || ||  ||||
                                GGAGTGGGA  GA GG  TCTG
                                     A_  _  GT
GAM62   FLJ10052  3' ATCTCAGGCTCCACAGTGAGG  35771       TTCACT
                                TTTCACT     GTCTGAGAT
                                |||||||     |||||||||
                                GGAGTGA     CGGACTCTA
                                    CACCT_
GAM62   FLJ11506  3' TGGGTGGGGAAGTGAAATG   45115          A TG
                                CATTTCACTTTC C  TCTG
                                ||||||||||||| |  ||||
                                GTAAAGTGAAGG G  GGGT
                                       _ GT
GAM62   FLJ12056  3' TTTGGGGGCAGGGAGGTTGGGT 46258     TC     A     GA  T
           G                     CATT  ACTTTC CTGTCT  GA
                                ||||  |||||| ||||||  ||
                                GTGG  TGGAGG GACGGG  TT
                                  GT     _     GG  TT
GAM62   FLJ12121  3' GTTTTGGACAGTCATTTGGAAT 46458       CTTTC     TG
                                ATTTCA    ACTGTC  AGAT
                                ||||||    ||||||  ||||
                                TAAGGT    TGACAG  TTTG
                                   TTAC_     GT
GAM62   FLJ12547  3' ATCTCAGCCAGAGAGAGTGAAC 46489    T       A   T
           TG                    CA TTCACTTTC CTG CTGAGAT
                                || |||||||| ||| |||||||
                                GT AAGTGAGAG GAC GACTCTA
                                 C        A   C
GAM62   FLJ12581  3' TCTCATGGAGGGTGGAGT    45881          ACTGTC
                                ATTTCACTTTC     TGAGA
                                ||||||||||     |||||
                                TGAGGTGGGAG     ACTCT
                                       GT____
GAM62   FLJ12787  3' TTTCAGGTCAGAGGAA      49756      A  _
                                TTTC CTG TCTGAGA
                                |||| ||| |||||||
                                AAGG GAC GGACTTT
                                  A   T
GAM62   FLJ12891  3' ACTGTGGAGGTGGAGTG     46335           T
                                CATTTCACTTTCAC GT
                                |||||||||||||| ||
                                GTGAGGTGGAGGTG CA
                                          T
GAM62   FLJ13072  5' GACAGTGAGAGTGAAA      89814
                                TTTCACTTTCACTGTC
                                ||||||||||||||||
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                                AAAGTGAGAGTGACAG

GAM62   FLJ13852 3' TGGGCAGTGGTAGGTGGGGTG 43579     TT    _
                                CAT  CACTT TCACTGTCTG
                                |||  ||||| ||||||||||
                                GTG  GTGGA GGTGACGGGT
                                  GG    T
GAM62   FLJ14107 3' GCAGGGGAGGTGAAATG     46693           A
                                CATTTCACTTTC CTGT
                                |||||||||||| ||||
                                GTAAAGTGGAGG GACG
                                       G
GAM62   FLJ14346 3' GGCAGGGAAGTGAGATG     46714           A
                                CATTTCACTTTC CTGTC
                                |||||||||||| |||||
                                GTAGAGTGAAGG GACGG

                                       _
GAM62   FLJ14502 3' GTTTTGGGCTTAATAAATGGGG 62717     TT  C  TCACT   TG
          TG                      CAT  CA TT    GTC  AGAT
                                |||  || ||    |||  ||||
                                GTG  GT AA    CGG  TTTG
                                  GG  A  TAATT   GT
GAM62   FLJ14641 5' CGGGGAAGTGGAATG       51483           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAGGTGAAGG GGC

                                       _
GAM62   FLJ14743 3' GCTCTGGGGTGGGGGTGGGGTG 68064     TT   TT   G  T   AT
                                CAT  CACT  CACT TC GAG
                                |||  ||||  |||| || |||
                                GTG  GTGG  GTGG GG CTC
                                  GG   GG   _ T   GT
GAM62   FLJ20034 3' TTTGTACGTGAGGGTGGA    34392           T  CT
                                TTCACTTTCAC GT  GAG
                                |||||||||| ||  |||
                                AGGTGGGAGTG CA  TTT
                                       _ TG
GAM62   FLJ20043 3' GTTTTGGGAAAGGAGTGGGAT  34406    TT     CACTG  TG
                                AT  CACTTT    TC  AGAT
                                ||  ||||||    ||  ||||
                                TA  GTGAGG    GG  TTTG
                                 GG     AAA__  GT
GAM62   FLJ20306 3' GAAGGTGGAGGTGGAA      34916           G
                                TTTCACTTTCACT TC
                                |||||||||||| ||
                                AAGGTGGAGGTGG AG
                                       A
GAM62   FLJ20340 3' TTGGAGTGGAGTGGGGTG    34980     TT    T  TG  TG
                                CAT  CACTT CAC  TC  A
                                |||  ||||| |||  ||  |
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                                GTG  GTGAG GTG  AG  T
                                  GG    _  __  GT
GAM62   FLJ20400 3' TTCTTGACTGAAGGTGAGATG  66514          CT   T   T
                                CATTTCACTTTCA  GTC GAGA
                                |||||||||||||  ||| ||||
                                GTAGAGTGGAAGT  CAG TTCT
                                       __  _   TT
GAM62   FLJ20729 3' GTCTTGGAGTGCAAGTGGTATG 35649    T    T  TG  TG
                                CAT TCACTT CAC  TC  AGAT
                                ||| |||||| |||  ||  ||||
                                GTA GGTGAA GTG  AG  TCTG
                                  T    C  __ GT
GAM62   FLJ21125 3' GTTTGGATGCAGGAAGGTGGGA 44892    TT     A   __ TG  AT
           TG                     CAT  CACTTTC CTGT  C  AG
                                |||  ||||||| ||||  |  ||
                                GTA  GTGGAAG GACG  G  TT
                                  GG      _   TA GT  G
GAM62   FLJ21162 3' TCTTGGGCTGGGTGCAGTG   45896     TT   __  TG
                                CACT  CACT  GTC  AGA
                                ||||  ||||  |||  |||
                                GTGA  GTGG  CGG  TCT
                                  C_   GT   GT
GAM62   FLJ21324 5' ATCTGCAGGTGGAAGGAGGTG  91189      A     TGT  _
                                CATTTC CTTTCAC   CTG AGAT
                                ||||||| |||||||   ||| ||||
                                GTGGAG GAAGGTG   GAC TCTA
                                   _     ___  G
GAM62   FLJ21736 3' TTTCAGATGGAAGTGAGA    46234          CTG
                                TTTCACTTTCA   TCTGAGA
                                ||||||||||   |||||||
                                AGAGTGAAGGT   AGACTTT
                                      ___
GAM62   FLJ22378 3' GTCTCGGGTCCAGGGAGTGGAG 46905        TT ACTG
                                TTTCACT  C    TCTGAGAT
                                |||||||  |   ||||||||
                                GAGGTGA  G    GGGCTCTG
                                    GG ACCT
GAM62   FLJ22659 5' GTGGTGAAGGTTAAATG     46261      C       TG
                                CATTT ACTTTCAC  T
                                |||||  ||||||||  |
                                GTAAA TGGAAGTG  G
                                   T       GT
GAM62   FLJ23059 3' ATCTCAGAACAGAAGGGTGGGA 49933   TT     CA   _
                                T  CACTTT  CTGT CTGAGAT
                                |  ||||||  |||| |||||||
                                A  GTGGGA  GACA GACTCTA
                                 GG     A_   A
GAM62   FLJ23091 3' ACCTCATGTGGGGGTGGGGTG  46124    TT   TT  TGTC   AT
                                CAT  CACT  CAC    TGAG
                                |||  ||||  |||   ||||
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                                GTG  GTGG  GTG   ACTC
                                  GG   GG  T___   CAA
GAM62   FLJ23185 3' TTTCAGGCAGGTGGAG     46837     CA
                                CTTT  CTGTCTGAGA
                                ||||  ||||||||||
                                GAGG  GACGGACTTT
                                  TG
GAM62   FLJ23309 3' ATCTTGGGTGATGGAGGAAATG 46061      A   T  C GT TG
                                CATTTC CTT CA T  C  AGAT
                                |||||| ||| || |  |  ||||
                                GTAAAG GAG GT G  G  TCTA
                                   _  _  A TG GT
GAM62   FLJ23476 3' GTCTCAGGTGGCTGCGTGTGGT 44962    TT   TTT  _ TG
          G                      CAT  CAC   CA C  TCTGAGAT
                                |||  |||   || |  ||||||||
                                GTG  GTG   GT G  GGACTCTG
                                  GT   C__  C GT
GAM62   FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM62   FLJ23556 3' GTTTTAATAAGGGAGGTGGAA  45956         A  GTC
                                TTTCACTTTC CT   TGAGAT
                                |||||||||| ||   ||||||
                                AAGGTGGAGG GA   ATTTTG
                                      _  ATA
GAM62   FLJ31762 3' TCTTCTGGGGGTGAGATG    58145        TT  CTGTCT
                                CATTTCACT  CA     GAGA
                                |||||||||  ||     ||||
                                GTAGAGTGG  GT     TTCT
                                     GG  C_____
GAM62   FTSJ3    3' GTCTGAAGAACAGTGAGGTGGA 34455         T     _  G_
          GTG                     ATTTCACTT CACTGT CT  AGAT
                                |||||||||| ||||||  ||  ||||
                                TGAGGTGGA GTGACA GA  TCTG
                                     _     A  AG
GAM62   G4       5' ATCTCAGATTGTGGGGGTGTGG 90991       _    TT   T
          ATG                     CATTT CACT  CAC GTCTGAGAT
                                |||||  ||||  |||  |||||||||
                                GTAGG GTGG  GTG TAGACTCTA
                                   T   GG   T
GAM62   GBTS1    3' ATTTTGGGGAGTGGGTGATATG 59050     T    TT    G  TG
                                CAT TCACT  CACT TC  AGAT
                                |||  |||||  ||||  ||  ||||
                                GTA AGTGG  GTGA GG  TTTA
                                  T    __   G  GT
GAM62   GBTS1    3' TTAGTGAGGGAAGGTGAGATG  59064          A  GT_
                                CATTTCACTTTC CT   CTGA
                                ||||||||||||  ||   ||||
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                                GTAGAGTGGAAG GG   GATT
                                      _ AGT
GAM62   GK001    3' TTTCTGGTGGGAGTGGGGTG  39503    TT   TT    TCT   T
                                CAT  CACT  CACTG   GAGA
                                |||  ||||  |||||   ||||
                                GTG  GTGA  GTGGT   CTTT
                                  GG   GG    ___    T
GAM62   GPS2     5' GTCTTTGAGGTGAAAGTGGAA 15671           G  T
                                TTTCACTTTCACT TC GAGAT
                                |||||||||||| || |||||
                                AAGGTGAAAGTGG AG TTCTG
                                      _ T
GAM62   GPT2     3' TTTCAGATCTGGAGAAATG   55962       ACT   CT
                                CATTTC   TTCA  GTCTGAGA
                                ||||||   ||||  ||||||||
                                GTAAAG   AGGT  TAGACTTT
                                   ___    C_
GAM62   GRSF1    3' ATTTTAGAACAAGTAGGGGTG 9139       TC  _ _
                                CACTT  ACT GT CTGAGAT
                                |||||  ||| || |||||||
                                GTGGG  TGA CA GATTTTA
                                   GA   A  A
GAM62   HBXAP    5' CAGTGAAATGAAGTG      33420        C
                                CATTTCA TTTCACTG
                                ||||||| ||||||||
                                GTGAAGT AAAGTGAC
                                      _
GAM62   HIC      5' GTTTCAGGATTGTAGGAGTGGA 67452        TC  TG_
            A                    TTTCACTT  AC   TCTGAGAT
                                ||||||||  ||   ||||||||
                                AAGGTGAG  TG   GGACTTTG
                                     GA  TTA
GAM62   HIF1AN   3' ATCTATTCAGTGGGAGTGGGGT 61968    TT   TT    TCTG
                                AT  CACT  CACTG    AGAT
                                ||  ||||  |||||    ||||
                                TG  GTGA  GTGAC    TCTA
                                 GG   GG    TTA_
GAM62   HSF2     3' TCGGGGGTGGGATGGGATG   15710    TT  C TT   G
                                CAT  CA T  CACT TCTGA
                                |||  || |  |||| |||||
                                GTA  GT A  GTGG GGGCT
                                  GG  _ GG   _
GAM62   HSPC054  3' TTTTACAGCTGTGGAAAGTGAA 26264          _ T T  _   T
            GTG                    ATTTCACTTTC AC G CTG AGA
                                |||||||||| || | ||| |||
                                TGAAGTGAAAG TG C GAC TTT
                                      G  T _   A   TG
GAM62   HXCP2    3' ATCTCAGTTTGGGAAGTGGGAT 50832     TT      ACTGT
            G                    CAT  CACTTTC    CTGAGAT
                                |||  |||||||    |||||||
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                                GTA  GTGAAGG    GACTCTA
                                  GG      GTTT_
GAM62   HYPK     3'  TCTTGGGTCAAGTAGAGTG   33080       C  _ _  TG
                                CACTTT ACT G TC  AGA
                                |||||| ||| | ||  |||
                                GTGAGA TGA C GG  TCT
                                   _  A T  GT
GAM62   IL18BP   3'  TCTTGGGCAGAGGAGGTG    19113       A    TG
                                CACTTTC CTGTC  AGA
                                ||||||| |||||  |||
                                GTGGAGG GACGG  TCT
                                    A    GT
GAM62   IL22R    3'  GTGGTGAAGATGAAATG     41192       C     TG
                                CATTTCA TTTCAC  T
                                ||||||| ||||||  |
                                GTAAAGT GAAGTG  G
                                    A     GT
GAM62   IMAGE3451454 3'  GTTTTAGCCAAAAGTGAAAT   53873          CAC  T
                                ATTTCACTTT   TG CTGAGAT
                                ||||||||||   || |||||||
                                TAAAGTGAAA   AC GATTTTG
                                     ___  C
GAM62   KIAA0092  3'  ATTTTGGAATAAAGTGAGA    27967         CACTG  TG
                                TTTCACTTT    TC  AGAT
                                |||||||||    ||  ||||
                                AGAGTGAAA    AG  TTTA
                                     TA___  GT
GAM62   KIAA0174  5'  ATTTTGGATGGTGAACCCTGAA 78592       CT_       TG
          GT                      ATTTCA   TTCACTGTC  AGAT
                                |||||||  |||||||||  ||||
                                TGAAGT   AAGTGGTAG  TTTA
                                   CCC       GT
GAM62   KIAA0212  3'  GTGAGACCGTGGTGAAAGGGGG 27940   TT A      ___    GAGAT
          ATG                     T  C CTTTCACT   GTCT
                                |  | ||||||||   ||||
                                A  G GAAAGTGG   CAGA
                                 GG G       TGC    GTG
GAM62   KIAA0284  3'  TGGTGGGGGTGGACGTG     63119     _     TT
                                CAT TTCACT  CACTG
                                ||| ||||||  |||||
                                GTG AGGTGG  GTGGT
                                  C     GG
GAM62   KIAA0285  5'  GGCAGTGGAGGTGAGA      29020
                                TTTCACTTTCACTGTC
                                ||||||||||||||||
                                AGAGTGGAGGTGACGG

GAM62   KIAA0419  5'  ATTTCAGATAGTGTGTGA    28187      TTT
                                TCAC   CACTGTCTGAGAT
                                ||||   ||||||||||||
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                                AGTG  GTGATAGACTTTA
                                  T__
GAM62   KIAA0426 3' GTTTTAGATGGTGTTACTGAGA 28261      CTTT
                                TTTCA   CACTGTCTGAGAT
                                |||||   ||||||||||||||
                                AGAGT   GTGGTAGATTTTG
                                   CATT
GAM62   KIAA0453 3' GTCTTGCTGGGGGGTGGTGATG 69049     _    TT ACT  CT
                                CATT TCACT  C   GT  GAGAT
                                |||| |||||  |   ||  |||||
                                GTAG GGTGG  G   CG  TTCTG
                                  T    GG GT_  __
GAM62   KIAA0459 3' ATTTCAGATGGGATGCAGGTG  60983      T  __
                                CACTT CA  CTGTCTGAGAT
                                |||||  ||  ||||||||||||
                                GTGGA GT  GGTAGACTTTA
                                   C  AG
GAM62   KIAA0523 3' ATCTTGGGCTCACAAGTGAGG  67728       TCACT   TG
                                TTTCACTT    GTC  AGAT
                                ||||||||    |||  ||||
                                GGAGTGAA    CGG  TCTA
                                     CACT_   GT
GAM62   KIAA0552 3' GTTTTGGGGGGCAAGGTGGAG  28320        CA  G  TG
                                TTTCACTTT  CT TC  AGAT
                                |||||||||  || ||  ||||
                                GAGGTGGAA  GG GG  TTTG
                                     C_  G  GT
GAM62   KIAA0660 3' GTTTCAGGCAGGAGTGGGGT   24515    TT    TCA
                                AT  CACTT   CTGTCTGAGAT
                                ||  |||||   ||||||||||||
                                TG  GTGAG   GACGGACTTTG
                                 GG    ____
GAM62   KIAA0759 3' GTTTCTGTTTTGAAAGTGAAAT 67329           CTGTCT
           G                     CATTTCACTTTCA     GAGAT
                                ||||||||||||||     |||||
                                GTAAAGTGAAAGT     CTTTG
                                       TTTGT_
GAM62   KIAA0795 3' ATTTCAGGGAAGAGGTGGGAT  46588    TT     CA  GT
                                AT  CACTTT  CT  CTGAGAT
                                ||  ||||||  ||  |||||||
                                TA  GTGGAG  GG  GACTTTA
                                 GG     AA  __
GAM62   KIAA0830 3' ATTTCAGCAGTGTGAAGGTAAA 69694      CA   _    T
           TG                    CATTT  CTTT CACTG CTGAGAT
                                |||||  ||||  |||||  |||||||
                                GTAAA  GAAG GTGAC GACTTTA
                                   TG   T    _
GAM62   KIAA0871 3' ATTTCAGAATAGGAAGTAAATG 30299      C     ACTG
                                CATTT ACTTTC    TCTGAGAT
                                |||||  ||||||    ||||||||
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                                GTAAA TGAAGG    AGACTTTA
                                  _     ATA_
GAM62   KIAA0893 3' GTTTCAGGCTAAAAGGTAAATG 30360      C    CACT
                                CATTT ACTTT    GTCTGAGAT
                                ||||| |||||    |||||||||
                                GTAAA TGGAA    CGGACTTTG
                                  _    AAT_
GAM62   KIAA0918 3' GTTTCAACGTTTAGGGTGAAGT 73134          CAC   C
           G                     CATTTCACTTT   TGT TGAGAT
                                ||||||||||   ||| ||||||
                                GTGAAGTGGGA   GCA ACTTTG
                                      TTT   _
GAM62   KIAA0931 3' ATCTCAGACTAATGGGGTGTGA 67412     _ TT  CT_
                                TCAC T  CA   GTCTGAGAT
                                |||| |  ||   |||||||||
                                AGTG G  GT   CAGACTCTA
                                  T GG  AAT
GAM62   KIAA0934 3' GGCATGGGGGTGAAATG     64223         TT  C
                                CATTTCACT  CA TGTC
                                |||||||||  || ||||
                                GTAAAGTGG  GT ACGG
                                     GG  _
GAM62   KIAA0978 3' CTCGACGTGAGGGTGAAATG   70480           T   T
                                CATTTCACTTTCAC GTC GAG
                                |||||||||||||| ||| |||
                                GTAAAGTGGGAGTG CAG CTC
                                          _   _
GAM62   KIAA1036 3' TGATGGGGGGTGGGGGTGGGGT 29831     TT    TT    G    AGAT
           G                     CAT  CACT  CACT TCTG
                                |||  ||||  |||| ||||
                                GTG  GTGG  GTGG GGGT
                                  GG   GG   G   AGTG
GAM62   KIAA1046 3' ATCTTAGAAGAGGGGTGGG   29990        CACTG
                                TTCACTTT    TCTGAGAT
                                ||||||||    ||||||||
                                GGGTGGGG    AGATTCTA
                                     AGA__
GAM62   KIAA1046 3' TTTCAGATGTTGGAAATG    30002    C    CT
                                CA TTTCA  GTCTGAGA
                                || |||||  ||||||||
                                GT AAGGT  TAGACTTT
                                 A    TG
GAM62   KIAA1237 3' TTTTGGATGAAGTGAGGG    80476        __  TG
                                CTTTCACT  GTC  AGA
                                ||||||||  |||  |||
                                GGGAGTGA  TAG  TTT
                                     AG   GT
GAM62   KIAA1257 3' GTTGGCACGACTGAGAGTGGGA 62755     TT      CT  _ A_
           TG                     CAT  CACTTTCA  GTC TG  GAT
                                |||  ||||||||  ||| ||  |||
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                                GTA  GTGAGAGT  CAG AC  TTG
                                  GG       __   C  GG
GAM62   KIAA1456 3' GTTTTGGAGGAAGGAGGAAATG 67006       A_    A TG  TG
                                CATTTC  CTTTC C  TC  AGAT
                                ||||||  ||||| |  ||  ||||
                                GTAAAG  GGAAG G  AG  TTTG
                                   GA    _ __  GT
GAM62   KIAA1538 3' GTTTTAGACAGGCTCCCTGAA  71556     CTTTCA
                                TTCA     CTGTCTGAGAT
                                ||||     ||||||||||
                                AAGT     GACAGATTTTG
                                  CCCTCG
GAM62   KIAA1559 3' TTGGAGACAGTGAGGGAAGTG  73078       A   T      GAGAT
                                CATTTC CTT CACTGTCT
                                |||||| ||| ||||||||
                                GTGAAG GGA GTGACAGA
                                   _  _       GGTTT
GAM62   KIAA1560 3' TTTGGGAGAGGGAGGGA     64183    A    A  G   G
                                TC CTTTC CT TCT AGA
                                || ||||| || ||| |||
                                AG GGAGG GA AGG TTT
                                 _    _ G   G
GAM62   KIAA1655 5' TCTCACTGAGAGTGAGA     66634          CTGTC
                                TTTCACTTTCA    TGAGA
                                ||||||||||    |||||
                                AGAGTGAGAGT    ACTCT
                                      C_____
GAM62   KIAA1655 5' ATCTCACCTCCAGTGGGAGGGA 66590      A  TT    TC__
           AGTG                   ATTTC CT  CACTG    TGAGAT
                                |||||  ||  |||||    ||||||
                                TGAAG GA  GTGAC    ACTCTA
                                  G  GG    CTCC
GAM62   KIAA1729 3' GTCTTAGGCGATTTGTGGGGTG 89130     TT   TTTCAC
                                CAT  CAC     TGTCTGAGAT
                                |||  |||     ||||||||||
                                GTG  GTG     GCGGATTCTG
                                  GG   TTTA__
GAM62   KIAA1799 5' ATCTTATTTCCGGTGGCGGTGA 74634        T     TC__
           GGTG                   ATTTCACT TCACTG    TGAGAT
                                |||||||| ||||||    ||||||
                                TGGAGTGG GGTGGC    ATTCTA
                                    C     CTTT
GAM62   KIAA1808 5' CATTGAGGGTGAGGTG      85861            C
                                CATTTCACTTTCA TG
                                |||||||||||||| ||
                                GTGGAGTGGGAGT AC
                                       T
GAM62   KIAA1811 3' ATCTCTCTGCGGGGTGGGGTG  64793     TT   TTCA   CT_
                                CAT  CACT   CTGT   GAGAT
                                |||  ||||   ||||  |||||
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                              GTG  GTGG   GGCG   CTCTA
                                GG   ____   TCT
GAM62   KIAA1821  3'  GGGCAGTGAGGGTGAGG     71790
                              TTTCACTTTCACTGTCT
                              ||||||||||||||||
                              GGAGTGGGAGTGACGGG

GAM62   KIAA1893  3'  GTCTCGGGCAGCACGTGAGGT  73217        TTTCA
                              ATTTCAC    CTGTCTGAGAT
                              |||||||    ||||||||||
                              TGGAGTG    GACGGGCTCTG
                                  CAC__
GAM62   KPNA6     3'  GCAGAGGAGGGTGGAGTG    24609          A_
                              CATTTCACTTTC  CTGT
                              ||||||||||||  ||||
                              GTGAGGTGGGAG  GACG
                                     GA
GAM62   LMOD1     3'  ATCTTTGAGGTGAGGGTGGGGT 24038     TT        G  T
            G                  CAT  CACTTTCACT TC GAGAT
                              |||  ||||||||||  || |||||
                              GTG  GTGGGAGTGG AG TTCTA
                                GG         _  T
GAM62   LY6G5B    5'  TTTCAGGCTCAGAGAAGTG    41131       CACT_
                              CACTTT     GTCTGAGA
                              ||||||     ||||||||
                              GTGAAG     CGGACTTT
                                 AGACT
GAM62   MAGE-E1   3'  GATTGGACGGTGGAGCTGGGAT 47945     TT  C        TG GAT
            G                  CAT  CA TTTCACTGTC  A
                              |||  ||  ||||||||||  |
                              GTA  GT GAGGTGGCAG  T
                                GG  C         GT AG
GAM62   MGC10960  3'  ATCTCCCCAGGAGGGTGAGATG 51003           A   TCT
                              CATTTCACTTTC CTG   GAGAT
                              |||||||||||| |||   |||||
                              GTAGAGTGGGAG GAC   CTCTA
                                     _   CC_
GAM62   MGC2628   3'  ATTTCCGGGTTAGGGTGGAATG 43968           C   GT T
                              CATTTCACTTT ACT  C GAGAT
                              |||||||||||  |||  | |||||
                              GTAAGGTGGGA TGG  G CTTTA
                                     T   __ C
GAM62   MGC27044  5'  CTTGGTGTTGAAAGTGAAATG  58673           CTGT TG
                              CATTTCACTTTCA    C  AG
                              ||||||||||||||   |  ||
                              GTAAAGTGAAAGT    G  TC
                                      TGT_ GT
GAM62   MGC35558  3'  TCTCAGGTGGGTGAGGG     58787        _ TG
                              CTTTCA C  TCTGAGA
                              |||||| |  |||||||
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                                GGGAGT G  GGACTCT
                                   G GT
GAM62   MGC4251   3'  GTTGGCCTGGTGGGGGTGGAGT 50460        TT   __  TGAGAT
                                ATTTCACT  CACT  GTC
                                ||||||||  ||||  |||
                                TGAGGTGG  GTGG  CGG
                                     GG   TC   TTG
GAM62   MLLT10    5'  AGGCGGTGGAGGGGAGGTG   16166       A
                                CATTTC CTTTCACTGTCT
                                ||||||| ||||||||||||
                                GTGGAG GGAGGTGGCGGA
                                   G
GAM62   MOCS3     3'  TCTTGGACATGTGAGATGT   27161    _    _   TG
                                AC TTTCAC TGTC  AGA
                                || |||||| ||||  |||
                                TG AGAGTG ACAG  TCT
                                 T     T   GT
GAM62   NR6A1     3'  ATTTTGAGGGAGAGGGTGGGAT 52867     TT     A  G  T
           G                     CAT  CACTTTC CT TC GAGAT
                                |||  ||||||| || || |||||
                                GTA  GTGGGAG GG AG TTTTA
                                  GG      A  G  _
GAM62   NR6A1     3'  ATTTTGAGGGAGAGGGTGGGAT 52879     TT     A  G  T
           G                     CAT  CACTTTC CT TC GAGAT
                                |||  ||||||| || || |||||
                                GTA  GTGGGAG GG AG TTTTA
                                  GG      A  G  _
GAM62   NR6A1     3'  ATTTTGAGGGAGAGGGTGGGAT 7642      TT     A  G  T
           G                     CAT  CACTTTC CT TC GAGAT
                                |||  ||||||| || || |||||
                                GTA  GTGGGAG GG AG TTTTA
                                  GG      A  G  _
GAM62   P450RAI-2 3'  TGGTGGAGATGGAATG      39107        C
                                CATTTCA TTTCACTG
                                ||||||| ||||||||
                                GTAAGGT GAGGTGGT
                                    A
GAM62   PALM      3'  TCTCAGGCAGTTGGGGTGA   10417        TC
                                TCACTT  ACTGTCTGAGA
                                ||||||  ||||||||||
                                AGTGGG  TGACGGACTCT
                                   GT
GAM62   PB1       3'  ATTTTAGTTACTGGGGGTGGGG 36368    TT    TT  C  T
                                T  CACT  CA TG CTGAGAT
                                |  ||||  || || |||||||
                                G  GTGG  GT AT GATTTTA
                                 GG   GG  C  T
GAM62   pcnp      3'  GTTTTGAAATTGGGGTGTGGGG 39789     TT   _ TT  CTG  T
           TG                     CAT  CAC T  CA   TC GAGAT
                                |||  ||| |  ||   || |||||
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                                GTG  GTG G  GT   AG TTTTG
                                  GG   T GG  TAA  _
GAM62   PEF      3'  TCTGTGGAGAGTGGAGTG    24754       T    G   _
                                CACTT CACT TCTG AGA
                                ||||| |||| |||| |||
                                GTGAG GTGA AGGT TCT
                                   _   G    G
GAM62   PGGT1B   3'  ATTTTAGATTGGGAGGGTGGGG 17231    TT      ACT
                                T  CACTTTC   GTCTGAGAT
                                |  |||||||   |||||||||
                                G  GTGGGAG   TAGATTTTA
                                 GG      GGT
GAM62   PINK1    3'  GTCTGTGAATGGTGAGGGTGGG 50543    TT         _ TG
           A                     T  CACTTTCACTGT C  AGAT
                                |  ||||||||||||  |  ||||
                                A  GTGGGAGTGGTA G  TCTG
                                 GG          A TG
GAM62   PP1057   5'  GTTTTGTGGGGGTGGGAGTGGA 48435        TT    G  _
           G                     TTTCACT  CACT TC TGAGAT
                                |||||||  |||| ||  ||||||
                                GAGGTGA  GTGG GG GTTTTG
                                    GG    G  T
GAM62   PRMT3    3'  GTTTTTAATGTGGGGGTAGAGT 65025      TC   TT   TGTCT
           G                     CATT  ACT  CAC     GAGAT
                                ||||  |||  |||    |||||
                                GTGA  TGG  GTG    TTTTG
                                  GA   GG   TAAT_
GAM62   PRMT6    3'  GTTTCGCGGGGGAGTGAGG   36272        TT A    CT
                                TTTCACT  C CTGT  GAGAT
                                |||||||  | ||||  |||||
                                GGAGTGA  G GGCG  CTTTG
                                    GG _   __
GAM62   PRO2900  5'  TTCAACTGAGAGTGAGGTG   37809           CT  C
                                CATTTCACTTTCA  GT TGAG
                                ||||||||||||  ||  ||||
                                GTGGAGTGAGAGT  CA ACTT
                                                __  _
GAM62   PSMF1    3'  GTCTTAGGTGTTCTATGGGAGG 22354    A  TT  C____ GT
           AAGTG                   TC CT  CA     T  CTGAGAT
                                || ||  ||    |  |||||||
                                AG GA  GT    G  GATTCTG
                                 _  GG  ATCTT TG
GAM62   PXR2b    3'  ATTTTTAACTTGGGGGTGAAA  33338        TT  CT  CT
                                TTTCACT  CA  GT  GAGAT
                                |||||||  ||  ||  |||||
                                AAAGTGG  GT  CA  TTTTA
                                    GG  T_  AT
GAM62   RAB6B    3'  GTCTTTAGGAGTAGGGTGGGAT 33414     TT     C   G    _
           G                     CAT  CACTTT ACT TCTGA GAT
                                |||  ||||||  ||| |||||  |||
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                                GTA  GTGGGA TGA GGATT CTG
                                  GG     _  _    T
GAM62   RACGAP1  3'  GTCTCAGGGTGGGAAGTGGGA  25200   TT     _  GT
                                T  CACTTTC ACT  CTGAGAT
                                |  ||||||| |||  |||||||
                                A  GTGAAGG TGG  GACTCTG
                                 GG      G  __
GAM62   RAD51    3'  TTTCAGGCCAGTGTGGTG    56023     TT    _
                                CACT  CACTG TCTGAGA
                                ||||  ||||| |||||||
                                GTGG  GTGAC GGACTTT
                                  T_    C
GAM62   RAD51    3'  TTTCAGGCCAGTGTGGTG    11229     TT    _
                                CACT  CACTG TCTGAGA
                                ||||  ||||| |||||||
                                GTGG  GTGAC GGACTTT
                                  T_    C
GAM62   RASSF2   3'  GTTTCAGGTTGAAGGGAAATG  28443       A     CTG
                                CATTTC CTTTCA   TCTGAGAT
                                |||||| ||||||   ||||||||
                                GTAAAG GGAAGT   GGACTTTG
                                   _     T__
GAM62   RBM7     3'  ATTTTAGACACTTTAGGAGGGG 32235    TT A    CAC__
           GTG                    AT  C CTTT     TGTCTGAGAT
                                ||  | ||||    ||||||||||
                                TG  G GAGG    ACAGATTTTA
                                 GG _    ATTTC
GAM62   RIL      3'  GGGGGTGGTGGTGGGGTG    13488     TT    T    G
                                CAT  CACT TCACT TC
                                |||  |||| ||||| ||
                                GTG  GTGG GGTGG GG
                                  GG   T    G
GAM62   RILP     5'  GTCCCAGTGGAGGGTGGGGTG  48694     TT      ACTGT   A
                                CAT  CACTTTC    CTG GAT
                                |||  |||||||    ||| |||
                                GTG  GTGGGAG    GAC CTG
                                  GG      GT___   C
GAM62   RNO2     5'  ATTTTTTTAGTGGAGATGGGGT 52762     TT  C       TCT
           G                     CAT  CA TTTCACTG   GAGAT
                                |||  || ||||||||   |||||
                                GTG  GT GAGGTGAT   TTTTA
                                  GG  A       TT_
GAM62   RoXaN    3'  ACAGTGGGTGTGAGATG     46627         T
                                CATTTCAC TTCACTGT
                                |||||||| ||||||||
                                GTAGAGTG GGGTGACA
                                     T
GAM62   SAE1     3'  TTTTGGGAGAAAGGAGATG   18537       A    ACTG  TG
                                CATTTC CTTTC    TC  AGA
                                |||||| |||||    ||  |||
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                                GTAGAG GAAAG   GG  TTT
                                   _    A___  GT
GAM62   SDS3    3'  ATTTTTCCATTGAAGGTGGAGT 69223          C  TCT
                                ATTTCACTTTCA TG   GAGAT
                                |||||||||||| ||   |||||
                                TGAGGTGGAAGT AC   TTTTA
                                       T  CT_
GAM62   SEMA4C  3'  ACATATGGAGGTGGGGTG    35052     TT      C_
                                CAT  CACTTTCA  TGT
                                |||  ||||||||  |||
                                GTG  GTGGAGGT  ACA
                                  GG       AT
GAM62   SFXN5   3'  TCTTAGGGTAGGGGAAGTG   58040       A  GT _
                                CACTTTC CT  C TGAGA
                                |||||||  ||  | |||||
                                GTGAAGG GA  G ATTCT
                                     G  TG G
GAM62   SGT1    3'  ATTTCAGACATGGTGAAACTG  21992    C     __
                                CA TTTCACT  GTCTGAGAT
                                || |||||||  |||||||||
                                GT AAAGTGG  CAGACTTTA
                                 C      TA
GAM62   SH3BGRL2 3'  ATCTCAGACAGTGATCAGGA   48883    ACTT
                                TC    TCACTGTCTGAGAT
                                ||    ||||||||||||||
                                AG    AGTGACAGACTCTA
                                 GACT
GAM62   SMC1L1  3'  GTCTTAGGCAGTTACCTGAAA  71960      CTTTC
                                TTTCA     ACTGTCTGAGAT
                                |||||     ||||||||||||
                                AAAGT     TGACGGATTCTG
                                   CCAT_
GAM62   SPTLC2  5'  GTTTCGGGGAGGTGGGTGGGGT 16809     TT    TCA  G
           G                     CAT  CACTT   CT TCTGAGAT
                                |||  |||||   || ||||||||
                                GTG  GTGGG   GA GGGCTTTG
                                  GG    TG_  G
GAM62   STK29   3'  GTCTCAGGCAGTGGGGG     87579    TT
                                CT  CACTGTCTGAGAT
                                ||  ||||||||||||
                                GG  GTGACGGACTCTG
                                 GG
GAM62   TA-PP2C  3'  GTAGACGCGGTGGGGGCGGGGT 57759     TT A  TT   __    AGAT
           G                     CAT  C CT  CACT  GTCTG
                                |||  | ||  ||||  |||||
                                GTG  G GG  GTGG  CAGAT
                                  GG C  GG    CG    G
GAM62   THEA    3'  TTTTAGGCCAGGTGTGGTG   66305     TT   __
                                CACT  CACT  GTCTGAGA
                                ||||  ||||  ||||||||
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                                GTGG  GTGG  CGGATTTT
                                  T_   AC
GAM62   TIAM2    3'  ATCTTGGGCTGTATCAAGGGAG 24931       A   TC_  T   TG
           TG                    CATTTC CTT   AC GTC  AGAT
                                 ||||||  |||   ||  |||  ||||
                                 GTGAGG GAA   TG CGG  TCTA
                                   _   CTA  T   GT
GAM62   TP53TG3  3'  ATCTTGGACATCTTGGAGATG  31102       ACTTTCAC    TG
                                 CATTTC       TGTC  AGAT
                                 ||||||       ||||  ||||
                                 GTAGAG       ACAG  TCTA
                                    GTTCT___    GT
GAM62   TRIP3    3'  GTTTCAGGCAGACTTGGGGT   78220    TT  CTTTCA
                                 AT  CA     CTGTCTGAGAT
                                 ||  ||     ||||||||||
                                 TG  GT     GACGGACTTTG
                                  GG  TCA___
GAM62   VIAAT    3'  GTTTTGGGGGGAGGCGGGGTG  54541     TT A     A  GT TG
                                 CAT  C CTTTC CT  C  AGAT
                                 |||  | ||||| ||  |  ||||
                                 GTG  G GGAGG GG  G  TTTG
                                   GG C     _ __ GT
GAM62   VPS39    3'  GTCTTTGATGGTGGTGAGGGTG 62849           ___   T
           GG                    TTCACTTTCACT   GTC GAGAT
                                 ||||||||||||   ||| |||||
                                 GGGTGGGAGTGG   TAG TTCTG
                                        TGG   T
GAM62   ZAP3     3'  GTTTTGGGGAGGGAGGGAG   77224     A    A  G  TG
                                 TTC CTTTC CT TC  AGAT
                                 ||| ||||| || ||  ||||
                                 GAG GGAGG GA GG  TTTG
                                   _    _  G  GT
GAM62   ZNF297B  3'  ATTTCAGTACTAAGGTGGTGA  25775       T  ACT  _
                                 TCACT TC   GT CTGAGAT
                                 |||||  ||   || |||||||
                                 AGTGG GG   CA GACTTTA
                                    T  AAT  T
GAM62   ZNF323   5'  ATCTTAAGATTGTGAAAGTGGA 48077           T   _
           G                     TTTCACTTTCAC GTCT GAGAT
                                 ||||||||||||  |||| |||||
                                 GAGGTGAAAGTG TAGA TTCTA
                                        T    A
GAM62   ZNF84    3'  TCTTGGACTTCAGGAAATG   12817       A  TTCACT   TG
                                 CATTTC CT     GTC  AGA
                                 ||||||  ||     |||  |||
                                 GTAAAG GA     CAG  TCT
                                    _ CTT___   GT
GAM62   LOC114987 3'  TCTTGAGGGGAGTGGGATG   59124     TT    TT A  GTC
                                 CAT  CACT  C CT   TGAGA
                                 |||  ||||  | ||   |||||
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                                GTA  GTGA  G GA   GTTCT
                                  GG    GG _  ___
GAM62   LOC115219 5'  GGCGGTGGAGGGGAGATG    73312        A
                                CATTTC CTTTCACTGTC
                                ||||||| ||||||||||
                                GTAGAG GGAGGTGGCGG
                                   G
GAM62   LOC115297 3'  ATCTCAGATATCCTACGGTGAG 72884        TTCAC_
          A                      TTTCACT     TGTCTGAGAT
                                |||||||      ||||||||||
                                AGAGTGG     ATAGACTCTA
                                    CATCCT
GAM62   LOC116150 3'  TCTTACTTGAGAGTGAG     56638          CT  CT
                                TTCACTTTCA  GT  GAGA
                                ||||||||||  ||  ||||
                                GAGTGAGAGT  CA  TTCT
                                      T_  __
GAM62   LOC124446 3'  TTTTAGAAAAAGTGAAG     74293          CACTG
                                TTTCACTTT    TCTGAGA
                                |||||||||    |||||||
                                GAAGTGAAA    AGATTTT
                                     A____
GAM62   LOC126964 3'  GTTTTGGTGGGATGGGGGGAGG 74622        A  TT  _  GT TG
          TG                     CATTTC CT  CA CT  C  AGAT
                                |||||| ||  || ||  |  ||||
                                GTGGAG GG  GT GG  G  TTTG
                                   _  GG  A  GT GT
GAM62   LOC128977 3'  GTCTGTGAACAGTGGGGGTGGG 74827    TT    TT     _ TG
          G                      T  CACT  CACTGT C  AGAT
                                |  ||||  |||||| |  ||||
                                G  GTGG  GTGACA G  TCTG
                                 GG    GG     A TG
GAM62   LOC130940 5'  GTCTCGGGCGCGGGAGGGGGTG 57139     TT A  TT AC
                                CAT  C CT  C  TGTCTGAGAT
                                |||  | ||  |  ||||||||||
                                GTG  G GA  G  GCGGGCTCTG
                                  GG _  GG C_
GAM62   LOC131368 3'  ATTTCAGATACTTTAAGTGAAT 75858    T      TCAC
          TG                     CA TTCACTT    TGTCTGAGAT
                                || |||||||    ||||||||||
                                GT AAGTGAA    ATAGACTTTA
                                 T      TTTC
GAM62   LOC134288 3'  TCCACAGAGGTGAGAGTCGGGT 75178      TC       G    AGAT
          G                      CATT  ACTTTCACT TCTG
                                ||||  ||||||||| ||||
                                GTGG  TGAGAGTGG AGAC
                                  GC        _    ACCTT
GAM62   LOC142948 3'  GTCTTGGCAGCATGGAAGTGAG 82891          __   T TG
          A                      TTTCACTTTCA  CTG C  AGAT
                                ||||||||||  ||| |  ||||
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                                AGAGTGAAGGT  GAC G  TCTG
                                      AC   _ GT
GAM62   LOC143279 5'  GTCCTGGTGGTGGAGGTGGGG  76511   TT       TG  TGA
                                T  CACTTTCAC  TC   GAT
                                |  |||||||||  ||   |||
                                G  GTGGAGGTG  GG   CTG
                                 GG        GT  TC_
GAM62   LOC144483 3'  TTTCATGGCAGTGAAA      60179          _
                                TTTCACTGTC TGAGA
                                |||||||||| |||||
                                AAAGTGACGG ACTTT
                                      T
GAM62   LOC144486 3'  TTTTGGTGTGAAGGTGAAAT   83090           TGT TG   T
                                ATTTCACTTTCAC   C  AGA
                                ||||||||||||   |  |||
                                TAAAGTGGAAGTG   G  TTT
                                       T__ GT   T
GAM62   LOC144845 5'  GTGGGGCAAGGTGGGGGTGAAG 56664         TT   __   GAGAT
          TG                     CATTTCACT  CACT  GTCT
                                |||||||||  ||||  ||||
                                GTGAAGTGG  GTGG  CGGG
                                     GG    AA    GTG
GAM62   LOC144845 5'  TCGCTCAGGGAGGTGGAGTG   56665          A   TC
                                CATTTCACTTTC CTG  TGA
                                |||||||||||| |||  |||
                                GTGAGGTGGAGG GAC  GCT
                                      _   TC
GAM62   LOC145828 5'  GTTTTGGAAGGGAGAGGAGGTG 83538       A    A  G  TG
                                CATTTC CTTTC CT TC  AGAT
                                ||||||  |||||  ||  ||  ||||
                                GTGGAG GAGAG GG AG  TTTG
                                   _    _  A  GT
GAM62   LOC146050 3'  ATCTCAGATGATTTAGGAAGTG 77625        ACT___
                                CACTTTC     GTCTGAGAT
                                |||||||     |||||||||
                                GTGAAGG     TAGACTCTA
                                     ATTTAG
GAM62   LOC146229 3'  GTGGTAGAGTGGAATG      77769          C  TG
                                CATTTCACTTT AC  T
                                |||||||||||  ||  |
                                GTAAGGTGAGA TG  G
                                      _  GT
GAM62   LOC146336 3'  GACAGTGAGGCTGAAATG    77832        C
                                CATTTCA TTTCACTGTC
                                |||||||  ||||||||||
                                GTAAAGT GGAGTGACAG
                                     C
GAM62   LOC146728 5'  TCGGAGTGGGGTGGAGTG    83753          T   TG
                                CATTTCACTT CAC  TCTGA
                                |||||||||  |||  |||||
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                                GTGAGGTGGG GTG  AGGCT
                                      _  __
GAM62   LOC146990 5'  ATCTCGGGCGGCTGGAGGGGTG 83884       __   _
            AGG                   TTCACT  TTCA CTGTCTGAGAT
                                  ||||||  |||| ||||||||||
                                  GAGTGG  AGGT GGCGGGCTCTA
                                     GG   C
GAM62   LOC147632 5'  TGGTGGAATGAGATG       56670        C
                                  CATTTCA TTTCACTG
                                  ||||||| ||||||||
                                  GTAGAGT AAGGTGGT
                                      _
GAM62   LOC148413 3'  GCAGTGAGGATGGAGTG     78830        CT
                                  CATTTCA  TTCACTGT
                                  |||||||  ||||||||
                                  GTGAGGT  GAGTGACG
                                       AG
GAM62   LOC148479 3'  GTTCCCTGCAGTGGAGGTGGAC 78879    T          CT_   AT
            TG                     CA TTCACTTTCACTGT   GAG
                                  || ||||||||||||||   |||
                                  GT AGGTGGAGGTGACG   CTT
                                   C           TCC   G
GAM62   LOC148529 5'  TCTTAGGCGAGTGGGAG     84172    TT   _
                                  CT  CACT GTCTGAGA
                                  ||  |||| ||||||||
                                  GA  GTGA CGGATTCT
                                   GG   G
GAM62   LOC149076 3'  ATCTTGGAGGCAGGGAGGTGAG 79148          A     __
            G                      TTTCACTTTC CTGTCT  GAGAT
                                  ||||||||||  ||||||  |||||
                                  GGAGTGGAGG GACGGA  TTCTA
                                        _     GG
GAM62   LOC149182 5'  TCTTGTGCAGGGTGAGATG    84379         TTCA    CT
                                  CATTTCACT    CTGT  GAGA
                                  |||||||||    ||||  ||||
                                  GTAGAGTGG    GACG  TTCT
                                       ____    TG
GAM62   LOC149711 3'  ATTTCACCTGCTTGGAAAGTGA 84673          ACT  C__
            GATG                     ATTTCACTTTC   GT   TGAGAT
                                  ||||||||||   ||   ||||||
                                  TAGAGTGAAAG   CG   ACTTTA
                                        GTT  TCC
GAM62   LOC149837 5'  GTTTTGAGGGTGGAATGAGGTG 84745       C      G  T
                                  CATTTCA TTTCACT TC GAGAT
                                  ||||||| ||||||| || |||||
                                  GTGGAGT AAGGTGG AG TTTTG
                                      _      G  _
GAM62   LOC149844 5'  GGTGGTGGGGGTGGTGGTG   79519     _    TT   TG
                                  CATT TCACT  CAC  TC
                                  |||| |||||  |||  ||
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                                GTGG GGTGG  GTG  GG
                                  T    GG   GT
GAM62   LOC149844 3'  TGGTGAGTGAGATG       79521        TT
                                CATTTCAC  TCACTG
                                ||||||||  ||||||
                                GTAGAGTG  AGTGGT
                                    __
GAM62   LOC150225 3'  GTCTTTTGCAGGTGAAGGTGGG 85009   TT      _   CT
           A                     T  CACTTTCAC TGT  GAGAT
                                |  |||||||||  |||  |||||
                                A  GTGGAAGTG ACG  TTCTG
                                 GG       G   TT
GAM62   LOC150351 5'  TTTTAGATAGTACGAAGT    60249      C_
                                ACTTT  ACTGTCTGAGA
                                |||||  ||||||||||
                                TGAAG  TGATAGATTTT
                                   CA
GAM62   LOC150358 3'  TCTCAGAGAGTGAAGTGA    84928       T   G
                                TCACTT CACT TCTGAGA
                                ||||||| |||| |||||||
                                AGTGAA GTGA AGACTCT
                                   _   G
GAM62   LOC150819 5'  GTTAGGGAGCAGTGAAAGTGAG 85122            ___   GAT
           G                     TTTCACTTTCACTGT   CTGA
                                ||||||||||||||   ||||
                                GGAGTGAAAGTGACG   GATT
                                        AGG   G
GAM62   LOC150933 3'  ATTTCAGTCACAGGAAATGGGG 85156    TT  C   A   __
           TG                    CAT  CA TTTC CTGT  CTGAGAT
                                |||  || |||| ||||  |||||||
                                GTG  GT AAAG GACA  GACTTTA
                                  GG  _   _   CT
GAM62   LOC151056 3'  ATCTTTTTTGGGAGTGAACTG  80106    T     TT  CTGTCT
                                CA TTCACT  CA     GAGAT
                                || ||||||  ||     |||||
                                GT AAGTGA  GT     TTCTA
                                 C     GG  TTT___
GAM62   LOC151176 3'  GTTTTGATAAGGGGGTGATGTG 85263     T    TT AC   T
                                CAT TCACT  C  TGTC GAGAT
                                ||| |||||  |  |||| |||||
                                GTG AGTGG  G  ATAG TTTTG
                                  T    GG A_   _
GAM62   LOC151194 3'  ATTTTAGATGGTGAAATTAGAA 59213      AC_
           GT                    ATTTC   TTTCACTGTCTGAGAT
                                |||||   ||||||||||||||||
                                TGAAG   AAAGTGGTAGATTTTA
                                   ATT
GAM62   LOC151414 3'  ATTTTGGCATATGGGGGTGGAG 80235       TT  C   _ TG
                                TTTCACT  CA TGT C  AGAT
                                |||||||  || ||| |  ||||
```

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                                GAGGTGG  GT ATA G  TTTA
                                    GG  _  C GT
GAM62   LOC151438 5'  TTTTCGGTGTGAAGGTGGGATG 85373    TT      TGT    T
                                CAT  CACTTTCAC   CTGAGA
                                |||  |||||||||   ||||||
                                GTA  GTGGAAGTG   GGCTTT
                                  GG       T__     TT
GAM62   LOC151610 3'  GGATGGTGGGAGTGAAG    80288       TT
                                TTTCACT  CACTGTCT
                                |||||||  ||||||||
                                GAAGTGA  GTGGTAGG
                                    GG
GAM62   LOC151658 5'  GTGGTGGAGTGGAGTG     85481         T   TG
                                CATTTCACTT CAC  T
                                |||||||||| |||  |
                                GTGAGGTGAG GTG  G
                                      _  GT
GAM62   LOC151826 3'  TTTTAGGCTAGTGAAA     80370       _
                                TTTCACT GTCTGAGA
                                ||||||| ||||||||
                                AAAGTGA CGGATTTT
                                    T
GAM62   LOC151904 5'  CCCTGCGTGGTGGAGGGAGGTG 80387       A      TG CTGAGAT
                                CATTTC CTTTCAC  T
                                |||||| |||||||  |
                                GTGGAG GGAGGTG  G
                                    _     GT CGTCCCT
GAM62   LOC152274 3'  TCTTGGATTGGATGAGATG   80509       CT   CT   TG
                                CATTTCA  TTCA  GTC  AGA
                                |||||||  ||||  |||  |||
                                GTAGAGT  AGGT  TAG  TCT
                                    __   __  GT
GAM62   LOC152275 3'  GGGGGGCGACAGGGAGGTGGGAT 85620    TT     A    TGAGAT
          G                      CAT  CACTTTC CTGTC
                                |||  ||||||| |||||
                                GTA  GTGGAGG GACAG
                                  GG     _    CGGGGGT
GAM62   LOC152633 5'  GTCTTGCTGTGCTGGGGGTGGG 85817    TT   TT  CTGTCT_
          GTG                     CAT  CACT  CA     GAGAT
                                |||  ||||  ||     |||||
                                GTG  GTGG  GT     TTCTG
                                  GG   GG  CGTGTCG
GAM62   LOC152805 5'  TCTCAGGATGAGTGAGG     80689       TCACTG
                                TTTCACTT     TCTGAGA
                                ||||||||     |||||||
                                GGAGTGAG     GGACTCT
                                    TA____
GAM62   LOC153196 5'  GTCTTAGAGCTAGAGATGAGGT 85975       C   ACTG
          G                      CATTTCA TTTC    TCTGAGAT
                                ||||||| ||||   ||||||||
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                                GTGGAGT AGAG   AGATTCTG
                                   _   ATCG
GAM62   LOC153222 3' TTTTGGAGGAGTGAAAT    80791         CACTG  TG
                                ATTTCACTTT    TC  AGA
                                ||||||||||    ||  |||
                                TAAAGTGAGG    AG  TTT
                                     _____  GT
GAM62   LOC153339 5' GTTTTGGTGGGGTGGTGGGATG 86012     TT   T  A   T TG
                                CAT  CACT TC CTG C  AGAT
                                |||  |||| || ||| |  ||||
                                GTA  GTGG GG GGT G  TTTG
                                  GG   T _  _ GT
GAM62   LOC153651 3' TTTTAGATGGTGATTGT    80918    TT
                                AC  TCACTGTCTGAGA
                                ||  ||||||||||||
                                TG  AGTGGTAGATTTT
                                 TT
GAM62   LOC153711 3' TCGGGTGGGAGAGGGA     86138     A    A TG
                                TTC CTTTC C  TCTGA
                                ||| ||||| |  |||||
                                AGG GAGAG G  GGGCT
                                  _    _ GT
GAM62   LOC153811 3' GCAGTGGGGGTAAGGTG    80950      C   TT
                                CATTT ACT  CACTGT
                                ||||| |||  ||||||
                                GTGGA TGG  GTGACG
                                   A   GG
GAM62   LOC154386 3' GTTTCAGTTCTGGAAGGTGAAA 81084         ACTGT
                                TTTCACTTTC    CTGAGAT
                                ||||||||||    |||||||
                                AAAGTGGAAG    GACTTTG
                                     GTCTT
GAM62   LOC154792 3' TTTTGGATATGTGAGAG    86250       _   TG
                                CTTTCAC TGTC  AGA
                                ||||||| ||||  |||
                                GAGAGTG ATAG  TTT
                                    T   GT
GAM62   LOC154877 3' GTCTTTACTGAGGGTGGCAGTG 86306     T    G  T___
                                CACT TCACT TC   GAGAT
                                |||| ||||| ||   |||||
                                GTGA GGTGG AG   TTCTG
                                  C    G  TCAT
GAM62   LOC157623 5' CAACGAGGCGGTGTGGGTGGAG 81493        TT      GAGAT
           TG                    CATTTCACT  CACTGTCT
                                 |||||||||  ||||||||
                                 GTGAGGTGG  GTGGCGGA
                                      GT      GCAACT
GAM62   LOC157693 3' TCTTGGACGCAGTGAAGT    81558        TTCAC   TG
                                ATTTCACT    TGTC  AGA
                                ||||||||    ||||  |||
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                                TGAAGTGA    GCAG  TCT
                                    C____   GT
GAM62   LOC157918 3' GTCTTGGGCACAGGTGGGGT  86649   TT   TCAC   TG
                                AT  CACTT   TGTC  AGAT
                                ||  |||||   ||||  ||||
                                TG  GTGGA   ACGG  TCTG
                                 GG    C___   GT
GAM62   LOC157919 3' GTTTCAGACAGTGGAA     81637
                                TTTCACTGTCTGAGAT
                                ||||||||||||||||
                                AAGGTGACAGACTTTG

GAM62   LOC158117 3' GGCGTGGTGGAATGGAATG   81709       C     __
                                CATTTCA TTTCACT  GTC
                                |||||||  |||||||  |||
                                GTAAGGT AAGGTGG  CGG
                                    _      TG
GAM62   LOC158382 5' ACGGGGGAAGTGAGGTG     86782          A
                                CATTTCACTTTC CTGT
                                ||||||||||| ||||
                                GTGGAGTGAAGG GGCA
                                       G
GAM62   LOC158382 5' GTGGTGGAAGATGAAGTG    86789       _     TG
                                CATTTCA CTTTCAC  T
                                |||||||  |||||||  |
                                GTGAAGT GAAGGTG  G
                                    A      GT
GAM62   LOC158954 3' TTTTGGGTGGGGGGGGAAGTG  60437      A  TT   TGT TG
                                CATTTC CT  CAC   C  AGA
                                ||||||  ||  |||   |  |||
                                GTGAAG GG  GTG   G  TTT
                                   G  GG   ___ GT
GAM62   LOC159184 5' TCAATGGTGAAGGTGAAGT   60051            C
                                ATTTCACTTTCACTGT TGA
                                |||||||||||||||  |||
                                TGAAGTGGAAGTGGTA ACT
                                                 _
GAM62   LOC163882 3' ATGCTGGCAGTGAGAGTGAAA  82163            TGAGAT
                                TTTCACTTTCACTGTC
                                ||||||||||||||||
                                AAAGTGAGAGTGACGG
                                       TCGTA
GAM62   LOC166983 5' GTCTGGCCCAAGGGGAGGTGGA 87266         A  ___   T  GAT
           GTG                    TTTCACTTTC CT   GTC GA
                                ||||||||||  ||   |||  ||
                                GAGGTGGAGG GA   CGG CT
                                      G  ACC   T  G
GAM62   LOC169436 5' GGGGTAGATGTGGGGGTGGAAT 82743         TT   T    AGAT
           G                     CATTTCACT  CAC GTCTG
                                |||||||||  |||  |||||
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                                GTAAGGTGG  GTG TAGAT
                                     GG  _    GGGGT
GAM62   LOC196761 3' GTTTTGGGCAGTGGAG     89556         TG
                                TTTCACTGTC  AGAT
                                ||||||||||  ||||
                                GAGGTGACGG  TTTG
                                      GT
GAM62   LOC197379 3' GATGGTGAGGGTGGGGT     89742    TT
                                AT  CACTTTCACTGTC
                                ||  ||||||||||||
                                TG  GTGGGAGTGGTAG
                                 GG
GAM62   LOC197414 3' ATTTTGGGCAGGCGCTGAGTGG 88061   TT    TCA__    TG
           GG                     T  CACTT    CTGTC  AGAT
                                |  |||||    |||||  ||||
                                G  GTGAG    GACGG  TTTA
                                 GG    TCGCG    GT
GAM62   LOC201203 3' ATCTCAGATTGTGAGGTAAATG 88140      C   T   T
                                CATTT ACTT CAC GTCTGAGAT
                                ||||| |||| ||| |||||||||
                                GTAAA TGGA GTG TAGACTCTA
                                   _   _  T
GAM62   LOC201895 3' TCTTAGGCCAGTGCAGTG    89094     TT   _
                                CACT  CACTG TCTGAGA
                                ||||  ||||| |||||||
                                GTGA  GTGAC GGATTCT
                                  C_    C
GAM62   LOC202152 3' ATCTCAGATTTAAAAACGTGGG 89157    TT  _  CACT
           ATG                    CAT  CAC TTT   GTCTGAGAT
                                |||  ||| |||   |||||||||
                                GTA  GTG AAA    TAGACTCTA
                                  GG   C   AATT
GAM62   LOC203275 3' GGCGTGGTGGAATGGAATG   89325       C     __
                                CATTTCA TTTCACT  GTC
                                |||||||  |||||||  |||
                                GTAAGGT AAGGTGG  CGG
                                    _      TG
GAM62   LOC203317 5' GTCTTGCCAATGGAAGTTGGAG 89333       _    C  TC
           TG                     CATTTCA CTTTCA TG  TGAGAT
                                |||||||  ||||||  ||  ||||||
                                GTGAGGT GAAGGT AC  GTTCTG
                                    T     A  C_
GAM62   LOC219333 3' GTCAGGGCAGTGGAAGTGGA  93542             GA
                                TTCACTTTCACTGTCT  GAT
                                ||||||||||||||||  |||
                                AGGTGAAGGTGACGGG  CTG
                                          A_
GAM62   LOC219529 3' GTCTCAGGTGAGTGGAGG    92972       _ GT
                                CTTTCAC T  CTGAGAT
                                |||||||  |  |||||||
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                                GGAGGTG G  GACTCTG
                                    A TG
GAM62   LOC220143 5'  GCGGGAGGGTGAAATG      93589           A
                                CATTTCACTTTC CTGT
                                |||||||||||| ||||
                                GTAAAGTGGGAG GGCG
                                                _
GAM62   LOC220549 5'  GCGGTGAGAGAGAGGTG     92919       A
                                CATTTC CTTTCACTGT
                                |||||| ||||||||||
                                GTGGAG GAGAGTGGCG
                                   A
GAM62   LOC220739 5'  ATTTCCCATGGGAGTGGAGT   92925        TT  C  TCT
                                ATTTCACT  CA TG   GAGAT
                                ||||||||  || ||   |||||
                                TGAGGTGA  GT AC   CTTTA
                                     GG  _  C__
GAM62   LOC221400 3'  GTCTCAGGTTGATGGTGGGGTG 92299     TT    T   CTG
                                CAT  CACT TCA   TCTGAGAT
                                |||  |||| |||   ||||||||
                                GTG  GTGG AGT   GGACTCTG
                                  GG    T   T__
GAM62   LOC221405 3'  TTTTAGATTAGTGGAA      93892         _
                                TTTCACTG TCTGAGA
                                |||||||| |||||||
                                AAGGTGAT AGATTTT
                                     T
GAM62   LOC221415 3'  TTTCCTGGGGGTTGAGGTG   93878       C   G  T_
                                CACTTT ACT TC  GAGA
                                |||||| ||| ||  ||||
                                GTGGAG TGG GG  CTTT
                                   T   G  TC
GAM62   LOC221584 3'  TCTCGAGAGAAAGGGAGTG   93833       A    A  GTC
                                CATTTC CTTTC CT   TGAGA
                                |||||| ||||| ||   |||||
                                GTGAGG GAAAG GA   GCTCT
                                   _    A  ____
GAM62   LOC221683 5'  GTCTTAGGTTTTGGTGTGA   93717     TT   CT
                                TCAC  TCA  GTCTGAGAT
                                ||||  |||  |||||||||
                                AGTG  GGT  TGGATTCTG
                                  T_   TT
GAM62   LOC221865 3'  ATTTTGGGTATATGGGGTGAAA 92486          CAC GT TG
          T                      ATTTCACTTT   T  C  AGAT
                                ||||||||||   |  |  ||||
                                TAAAGTGGGG   A  G  TTTA
                                      TAT TG GT
GAM62   LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
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                                GTAAAGTGAA GTGACA
                                          _
GAM62   LOC245728 5'  TTCAGGCAATGAAGTG      91135       T  C
                                CACTT CA TGTCTGAG
                                ||||| || ||||||||
                                GTGAA GT ACGGACTT
                                  _  A
GAM62   LOC253115 3'  ATTTTTATTGTGGGGTGGGATG 94494     TT    T   TGTCT
                                CAT  CACTT CAC    GAGAT
                                |||  ||||| |||    |||||
                                GTA  GTGGG GTG    TTTTA
                                  GG    _   TTAT_
GAM62   LOC254485 3'  CTGGGAAGTGAGGTG       95013       T   G   G
                                CACTT CACT TCT AG
                                ||||| |||| ||| ||
                                GTGGA GTGA AGG TC
                                  _   _   G
GAM62   LOC254755 3'  GCAGGGAGGTGGGGTG      97369     TT      A
                                CAT  CACTTTC CTGT
                                |||  ||||||| ||||
                                GTG  GTGGAGG GACG
                                  GG      _
GAM62   LOC254756 3'  GCAGGGAGGTGGGGTG      97363     TT      A
                                CAT  CACTTTC CTGT
                                |||  ||||||| ||||
                                GTG  GTGGAGG GACG
                                  GG      _
GAM62   LOC255391 5'  TCTCTGGGGGTGCGGTG     97614      TT    G  T
                                CACT  CACT TC GAGA
                                ||||  |||| || ||||
                                GTGG  GTGG GG CTCT
                                  C_    G  T
GAM62   LOC255394 3'  GTTTCAGACACTGCTTAGGTGC 94886     T     T__  C
          AGTG                    ATT CACTT   CA TGTCTGAGAT
                                ||| |||||   || ||||||||||
                                TGA GTGGA   GT ACAGACTTTG
                                  C     TTC  C
GAM62   LOC255452 5'  GTCTCTATCCGAGAGGGTGGAG 97543             ACTGTCT
          TG                    CATTTCACTTTC      GAGAT
                                ||||||||||||      |||||
                                GTGAGGTGGGAG      CTCTG
                                      AGCCTAT
GAM62   LOC255480 3'  TCTTGAGGAGGTGAAGG     96521         GT  _
                                CTTTCACT  CT GAGA
                                ||||||||  || ||||
                                GGAAGTGG  GA TTCT
                                     AG  G
GAM62   LOC255779 3'  ATTTCCCCATGCAAAGTGGGAT 96013     TT     _  C  TCT
          G                     CAT  CACTTT CA TG   GAGAT
                                |||  |||||| || ||   |||||
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                                GTA  GTGAAA GT AC   CTTTA
                                  GG     C  _  CC_
GAM62   LOC256145 5'  GTCTCGGGCATCGTGGG     96543       __
                                TTCAC  TGTCTGAGAT
                                |||||  ||||||||||
                                GGGTG  ACGGGCTCTG
                                   CT
GAM62   LOC256405 5'  ATCTCAGGACCAGATAGTGGAG 95872          T  ACTG
           TG                     CATTTCACT TC    TCTGAGAT
                                |||||||||  ||    ||||||||
                                GTGAGGTGA AG    GGACTCTA
                                     T  ACCA
GAM62   LOC256639 5'  GTCTTGCTTCAGGAAGGTGAAG 96219           A   TC_
           TG                     CATTTCACTTTC CTG   TGAGAT
                                ||||||||||||  |||   ||||||
                                GTGAAGTGGAAG GAC   GTTCTG
                                      _  TTC
GAM62   LOC257048 3'  TATGTAGGTAGTGGGGGGAAAT 96216       A  TT    GT   AGAT
           G                       CATTTC CT  CACT  CTG
                                ||||||  ||  ||||  |||
                                GTAAAG GG  GTGA  GAT
                                   _  GG    TG   GTATT
GAM62   LOC257554 5'  ATCTCAGATTGTGGGGGTGTGG 97691       _   TT   T
           ATG                      CATTT CACT  CAC GTCTGAGAT
                                |||||  ||||  |||  |||||||||
                                GTAGG GTGG  GTG TAGACTCTA
                                   T   GG   T
GAM62   LOC257556 3'  ATTTTTATTGTGGGGTGGGATG 97707     TT    T   TGTCT
                                CAT  CACTT CAC     GAGAT
                                |||  |||||  |||    |||||
                                GTA  GTGGG GTG     TTTTA
                                  GG     _   TTAT_
GAM62   LOC257617 3'  ATTTTTATTGTGGGGTGGGATG 97813     TT    T   TGTCT
                                CAT  CACTT CAC     GAGAT
                                |||  |||||  |||    |||||
                                GTA  GTGGG GTG     TTTTA
                                  GG     _   TTAT_
GAM62   LOC51107  3'  TTTCTGCTGAGGGTGGAGTG   32064           CT  CT
                                CATTTCACTTTCA  GT  GAGA
                                ||||||||||||  ||  ||||
                                GTGAGGTGGGAGT  CG  CTTT
                                      __  T_
GAM62   LOC51152  3'  GTCTCAAAGGAGAAAGTGAGGT 32454           A  GTC
           G                       CATTTCACTTTC CT   TGAGAT
                                ||||||||||||  ||   ||||||
                                GTGGAGTGAAAG GG   ACTCTG
                                      A  AA_
GAM62   LOC51716  3'  GCAGTGAAGGTGAGGT     32792
                                ATTTCACTTTCACTGT
                                ||||||||||||||||
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                                TGGAGTGGAAGTGACG

GAM62   LOC56912  5' CTCACGAGAGTGGAAG     39336        G _
                                CTTTCACT TC TGAG
                                |||||||| || ||||
                                GAAGGTGA AG ACTC
                                     G  C
GAM62   LOC56959  5' TCTTGACCGGAGGTGGAA    81927          ACT   T
                                TTTCACTTTC   GTC GAGA
                                ||||||||||   ||| ||||
                                AAGGTGGAGG   CAG TTCT
                                      C__   _
GAM62   LOC89135  3' TGGTGAGTGAGATG       60319        TT
                                CATTTCAC  TCACTG
                                ||||||||  ||||||
                                GTAGAGTG  AGTGGT

                                   __
GAM62   LOC90170  5' GGTGGTGAGGGTTAAATG    61710      C       TG
                                CATTT ACTTTCAC  TC
                                ||||| ||||||||  ||
                                GTAAA TGGGAGTG  GG
                                   T       GT
GAM62   LOC90826  5' GTCTTGGGTTTGGAATGTGAAA 64095        _    CTG  TG
           TG                     CATTTCAC TTTCA   TC  AGAT
                                ||||||||| |||||   ||  ||||
                                GTAAAGTG AAGGT   GG  TCTG
                                     T    TT_  GT
GAM62   LOC91363  3' ATCTCAGAACAGAAGGGTGGGA 65776   TT     CA   _
                                T  CACTTT  CTGT CTGAGAT
                                |  ||||||  |||| |||||||
                                A  GTGGGA  GACA GACTCTA
                                 GG     A_    A
GAM62   LOC91450  3' GTTTTGGGCAGAGGAGTGGGG  66076   TT     CA    TG
                                T  CACTTT  CTGTC  AGAT
                                |  ||||||  |||||  ||||
                                G  GTGAGG  GACGG  TTTG
                                 GG     A_    GT
GAM62   LOC91628  3' GCAGTGGATGTGGGATG     66760     TT   T
                                CAT  CAC TTCACTGT
                                |||  ||| ||||||||
                                GTA  GTG AGGTGACG
                                  GG   T
GAM62   LOC92305  3' GTCTCAGACTCCTGGGTAGGGG 56418     TT _   TCACT
           TG                     CAT  C ACTT    GTCTGAGAT
                                |||  | ||||    |||||||||
                                GTG  G TGGG    CAGACTCTG
                                  GG A    TCCT_
GAM62   LOC93349  3' CTTAGGCGGATGGAGG      56457       _
                                CTTTCA CTGTCTGAG
                                |||||| |||||||||
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                                GGAGGT GGCGGATTC
                                   A
GAM62   LOC93587 3'  TAGGAGAAAGTGAGGTG    72648          A_
                                CATTTCACTTTC  CTG
                                ||||||||||||  |||
                                GTGGAGTGAAAG  GAT
                                      AG
GAM63   AQP3    3'  TTCACGATCCACCCTTTC    59593     T_   _
                                GAAA  GTGG TCGTGAA
                                ||||  |||| |||||||
                                CTTT  CACC AGCACTT
                                  CC   T
GAM63   ARSB    3'  TCACGACTCTTGTC       3502        AATGTG
                                GACAAGA    GTCGTGA
                                |||||||    |||||||
                                CTGTTCT    CAGCACT
                                           _______
GAM63   B4GALT5  3'  TTTTCACAAAAATAGTCCTTTG 16519       AAA_  GGTC
            TCA                   TGACAAG   TGT   GTGAAAA
                                |||||||   |||   |||||||
                                ACTGTTT   ATA   CACTTTT
                                    CCTG   AAAA
GAM63   CHRNA3   3'  TCGTTACCCATTTCTT     5610        T   CG
                                AAGAAATG GGT  TGA
                                |||||||| |||  |||
                                TTCTTTAC CCA  GCT
                                    _  TT
GAM63   DRD1    3'  TTACAACCACATTTCTGGCCA  5840    ACA        C
                                TG   AGAAATGTGGT GTGA
                                ||   |||||||||||| ||||
                                AC   TCTTTACACCA CATT
                                 CGG         A
GAM63   FUT1    3'  TCTGATCACATCCCCTGTC   3798     AGAA       T
                                GACA   ATGTGGTCG GA
                                ||||   ||||||||| ||
                                CTGT   TACACTAGT CT
                                  CCCC       _
GAM63   IRF1    3'  GCCACATTTCTGATCA     64345    CA
                                TGA  AGAAATGTGGT
                                |||  ||||||||||
                                ACT  TCTTTACACCG
                                  AG
GAM63   MAP3K8   5'  TCACGACCACCTCATG     17791    A  AAT
                                CA GA   GTGGTCGTGA
                                || ||   ||||||||||
                                GT CT   CACCAGCACT
                                 A  C__
GAM63   NGFR    3'  TTCTGACCACACTTCCTGTC   10231     A   A      T
                                GACA GAA TGTGGTCG GAA
                                |||| ||| |||||||| |||
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                                CTGT CTT ACACCAGT CTT
                                  C  C      _
GAM63   OLR1     3'  TTCACAACAGTTCTTGTTA   10341         ATGTG  C
                                TGACAAGAA    GT GTGAA
                                |||||||||    || |||||
                                ATTGTTCTT    CA CACTT
                                     GA___  A
GAM63   POU4F1   3'  CACTGAAAACATTTTTGTCA  20660         A  GG  _
                                TGACAAGAA TGT  TC GTG
                                ||||||||| |||  || |||
                                ACTGTTTTT ACA  AG CAC
                                     _  AA  T
GAM63   SMP1     3'  TTTCACATGAATAATTTTTGTC 26705         A  GGTC
           A                     TGACAAGAA TGT   GTGAAA
                                |||||||||| |||   ||||||
                                ACTGTTTTT ATA   CACTTT
                                     A  AGTA
GAM63   ZNF264   3'  TTCTATTAACATTTCTTTTCA  12769     C       GGTCGT
                                TGA AAGAAATGT     GAA
                                ||| |||||||||     |||
                                ACT TTCTTTACA     CTT
                                  T       ATTAT_
GAM63   C20orf175 3'  CGAGCTCCACGTTTCCTGCCA  55063    A  A       ___
                                TG CA GAAATGTGG   TCG
                                || || |||||||||   |||
                                AC GT CTTTGCACC   AGC
                                 C  C        TCG
GAM63   CAPNS2   3'  TTTCACAACCCTACATATTTCT 50323     CA      ____  C
           GATCA                   TGA  AGAAATGT    GGT GTGAAA
                                |||  ||||||||   ||| ||||||
                                ACT  TCTTTATA    CCA CACTTT
                                  AG       CATC   A
GAM63   CLDN6    3'  TTTACACTCACATTTTTATCA  41041     CA       _  C
                                TGA  AGAAATGTG GT GTGAA
                                |||  ||||||||| || |||||
                                ACT  TTTTTACAC CA CATTT
                                  A_       T  _
GAM63   DKFZP564L0864 3'  GCACCAATTTCTTGCCA     72555    A      G   C
                                TG CAAGAAAT TGGT GT
                                || |||||||| |||| ||
                                AC GTTCTTTA ACCA CG
                                 C       _   _
GAM63   DKFZP566B183 3'  TTTCCATAAACATTTCTTTTCA 31330     C       GGTCGT
                                TGA AAGAAATGT     GAAA
                                ||| |||||||||     ||||
                                ACT TTCTTTACA     CTTT
                                  T       AATAC_
GAM63   GTF2E1   3'  TACAGACCTCTTGTCA      18616         AATGT   _
                                TGACAAGA    GGTC GTG
                                ||||||||    |||| |||
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                                ACTGTTCT    CCAG CAT
                                      _____   A
GAM63   KIAA0089  3'  TTTTAATTCACATTTCTT    69967          TCG
                                AAGAAATGTGG   TGAAA
                                ||||||||||   |||||
                                TTCTTTACACT   ATTTT
                                      TA_
GAM63   KIAA0373  5'  TTTTCAAAGTAACATTTCTT   28015        GGTCG
                                AAGAAATGT    TGAAAA
                                |||||||||    ||||||
                                TTCTTTACA    ACTTTT
                                     ATGAA
GAM63   KIAA1813  3'  TTTTCACACTGTAAATTTCTTG 70314         __ TG  C
            T                    ACAAGAAAT  G  GT GTGAAAA
                                |||||||||  |  || |||||||
                                TGTTCTTTA  T  CA CACTTTT
                                     AA GT  _
GAM63   KIAA1951  3'  TTCCAGGCTTCTCTTGTCA   73766        AATGT   GT
                                TGACAAGA    GGTC  GAA
                                ||||||||    ||||  |||
                                ACTGTTCT    TCGG  CTT
                                     CT___    AC
GAM63   MGC4170   3'  TTCACCATTTCTTGTC      44227          TGGTC
                                GACAAGAAATG    GTGAA
                                ||||||||||    |||||
                                CTGTTCTTTAC    CACTT
                                      _____
GAM63   NRN1      3'  CACTGCACATTTCTCCTCA   33432     CA       GTC
                                TGA  AGAAATGTG   GTG
                                |||  |||||||||   |||
                                ACT  TCTTTACAC   CAC
                                  CC        GT_
GAM63   PLA2G12   3'  TTTTCACAACCACATTT     48028          C
                                AAATGTGGT GTGAAAA
                                ||||||||| |||||||
                                TTTACACCA CACTTTT
                                     A
GAM63   PPY2      3'  CACTCCACATTCCTGGCCA   40819    ACA  A      TC
                                TG   AG AATGTGG  GTG
                                ||   || |||||||  |||
                                AC   TC TTACACC  CAC
                                  CGG  C      T_
GAM63   ZNF31     3'  TTTGTAGACCACATTTCCTGTT 64992       A         _ TG
              A                   TGACA GAAATGTGGTC G  AA
                                |||||  ||||||||||| |  ||
                                ATTGT CTTTACACCAG T  TT
                                   C          A GT
GAM63   LOC115219 3'  CACGACAACGGGTCCTCA    73295     CAA  AA   G
                                TGA   GA  TGT GTCGTG
                                |||   ||  ||| ||||||
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                                ACT   CT  GCA CAGCAC
                                  C__  GG   A
GAM63   LOC120376 5' TTCAGAGCATTTCTTTCA    75986     C       GG  G
                                TGA AAGAAATGT  TC TGAA
                                ||| |||||||||  || ||||
                                ACT TTCTTTACG  AG ACTT
                                  _       __ _
GAM63   LOC133418 3' TTTCATATACATTTTTTGCCA  75094    A        GTC
                                TG CAAGAAATGTG   GTGAAA
                                || ||||||||||   ||||||
                                AC GTTTTTTACAT   TACTTT
                                  C         A__
GAM63   LOC151199 3' TTAAAACCACAGCTCTTGCCA  80174    A    AA     CG
                                TG CAAGA  TGTGGT  TGA
                                || |||||  ||||||  |||
                                AC GTTCT  ACACCA  ATT
                                  C    CG     AA
GAM63   LOC152317 5' TCACACTGACTTTTGTCA    85649        AATG    C
                                TGACAAGA    TGGT GTGA
                                ||||||||    |||| ||||
                                ACTGTTTT    GTCA CACT
                                     CA__    _
GAM63   LOC152674 3' TTCAACCCACCCTCTTGTCA   85841        AAT    TCG
                                TGACAAGA   GTGG   TGAA
                                ||||||||   ||||   ||||
                                ACTGTTCT   CACC   ACTT
                                     CC_    CA_
GAM63   LOC152845 5' CATGACCACATTTTTCA     60330     CAA
                                TGA   GAAATGTGGTCGTG
                                |||   ||||||||||||||
                                ACT   TTTTACACCAGTAC
                                  ____
GAM63   LOC154743 3' TTTAGTCCACATTGTCTTGTCA 81118         _      TCG
                                TGACAAGA AATGTGG   TGAA
                                |||||||| |||||||   ||||
                                ACTGTTCT TTACACC   ATTT
                                     G      TG_
GAM63   LOC165476 5' TTCACGGCACCTTCT       87201      AT   G
                                AGAA  GTG TCGTGAA
                                ||||  ||| |||||||
                                TCTT  CAC GGCACTT
                                  C_  _
GAM63   LOC254266 5' TTTTCGGTCACACATCTTATCA 97356     C    AA    GT  T
                                TGA AAGA  TGTG  CG GAA
                                ||| ||||  ||||  || |||
                                ACT TTCT  ACAC  GC TTT
                                  A   AC    TG  T
GAM63   LOC255919 3' TTTCATTCTTACATTTCTAATC 95043     CA         TC
           A                     TGA  AGAAATGTGG  GTGAAA
                                ||| ||||||||||  ||||||
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                                ACT  TCTTTACATT  TACTTT
                                  AA         CT
GAM63   LOC51754  5'  CACGGCCACATCTCTGTCA   71027       A  A
                                TGACA GA ATGTGGTCGTG
                                |||||  ||  ||||||||||
                                ACTGT CT TACACCGGCAC
                                   _  C
GAM63   LOC55862  3'  ACCTCATTTCTTGCCA      37485     A        T
                                TG CAAGAAATG GGT
                                ||  |||||||||  |||
                                AC GTTCTTTAC CCA
                                 C         T
GAM63   LOC55954  3'  CACGTGGTCACTTTTCTCATCA 38877      CA     T   GT __
                                TGA  AGAAA GTG  C  GTG
                                |||  |||||  |||  |  |||
                                ACT  TCTTT CAC  G  CAC
                                  AC     T   TG TG
GAM64   ADH1B     3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                ||||  |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                   A     T__
GAM64   AHR       3'  ATCTCAGATGTTAAAATAAATG 7875        CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   |||  ||  |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM64   FDFT1     3'  TAGGAAAGTGAAATG       15518            A
                                CATTTCACTTTC CTG
                                ||||||||||||  |||
                                GTAAAGTGAAAG GAT
                                          _
GAM64   JTB       3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                ||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM64   KLF4      3'  TCCCAGACAGTGGATATG     14891     CT         A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||  ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM64   PHYH      3'  ACAGTAAAAGTGAAAT      20608           C
                                ATTTCACTTT ACTGT
                                ||||||||||  |||||
                                TAAAGTGAAA TGACA
                                      A
GAM64   PKD2      3'  TCCAGGTTGAAAGTGAAA     60096           CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   ||||  ||
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                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM64   WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM64   ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017        CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM64   CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM64   EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM64   FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                 ||||||        |||||||||
                                 GTAAAG        CAGACTCTA
                                    AAACATTT_
GAM64   FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                    C__
GAM64   KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                   A       CT
GAM64   KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                   _  G
GAM64   NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM64   PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598         CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
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                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM64   PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM64   PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                     TA__   TT
GAM64   SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A     TC
GAM64   SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                     AAAGG
GAM64   LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM64   LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM64   LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM64   LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM65   ALOX15   3'  CCAAGCCACAAGCTGACCCCT  6684     T    TCCCTA
                                AG GGGTT     TGGCTTGG
                                || |||||     ||||||||
                                TC CCCAG     ACCGAACC
                                 _    TCGAAC
GAM65   CALD1    3'  ATCCTGTTTCTAAAGAAACCCA 52461         CCTAT_  TT
           T                     GTGGGTTTC     GGC  GGAT
                                |||||||||     |||  ||||
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                                TACCCAAAG     TTG  CCTA
                                     AAATCT   T_
GAM65   CALD1    3'  ATCCTGTTTCTAAAGAAACCCA 52525         CCTAT_   TT
            T                    GTGGGTTTC     GGC  GGAT
                                 |||||||||     |||  ||||
                                 TACCCAAAG     TTG  CCTA
                                      AAATCT   T_
GAM65   CHRNA2   5'  AGCCCCAGGAAAACCCAC    5600         C   AT
                                 GTGGGTTT CCT  GGCT
                                 ||||||||  |||  ||||
                                 CACCCAAA GGA  CCGA
                                      A   CC
GAM65   DAZ      3'  ATCCAAACACTGAAACCTAC   82111         CCTA  GC
                                 GTGGGTTTC    TG  TTGGAT
                                 |||||||||    ||  ||||||
                                 CATCCAAAG    AC  AACCTA
                                      TC__    A_
GAM65   DAZ      3'  ATCCAAACACTGAAACCTAC   82112         CCTA  GC
                                 GTGGGTTTC    TG  TTGGAT
                                 |||||||||    ||  ||||||
                                 CATCCAAAG    AC  AACCTA
                                      TC__    A_
GAM65   DAZ      3'  ATCCAAACACTGAAACCTAC   82113         CCTA  GC
                                 GTGGGTTTC    TG  TTGGAT
                                 |||||||||    ||  ||||||
                                 CATCCAAAG    AC  AACCTA
                                      TC__    A_
GAM65   SLC16A2  3'  TCCCCAAAGGAAAACCCACT   21504         C   A   CTT
                                 AGTGGGTTT CCT TGG   GGA
                                 |||||||||  ||| |||   |||
                                 TCACCCAAA GGA ACC   CCT
                                      A   A   ___
GAM65   EDG1     3'  ATCTGCATAAGGAAGCCCACT  59326          C    G TT
                                 AGTGGGTTTCC TATG C  GGAT
                                 ||||||||||| |||| |  ||||
                                 TCACCCGAAGG ATAC G  TCTA
                                       A    _ __
GAM65   FKSG79   3'  CCAAGCCACAGGGAAGAACTT  50744       __     A
                                 GGGTT  TCCCT TGGCTTGG
                                 |||||  ||||| ||||||||
                                 TTCAA  AGGGA ACCGAACC
                                    GA    C
GAM65   FLJ22160 5'  CCAGGAAAGAAACCCATT    44731         CCTATGG
                                 AGTGGGTTTC      CTTGG
                                 ||||||||||      |||||
                                 TTACCCAAAG      GGACC
                                      AAA_____
GAM65   FYCO1    3'  TCCAAGAGCAAAACCCACT   44497         CC  ATGG
                                 AGTGGGTTT  CT    CTTGGA
                                 |||||||||  ||    ||||||
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                                TCACCCAAA  GA   GAACCT
                                     AC  ____
GAM65   KIAA1032  3'  CCAAGCCACAGGATACCT    66154     TTC   A
                                GGGT   CCT TGGCTTGG
                                ||||   ||| ||||||||
                                TCCA   GGA ACCGAACC
                                  TA_   C
GAM65   MOV10    3'  CCAAGCCATTCCACCCCCT   40582    T   TTCCCT
                                AG GGGT     ATGGCTTGG
                                || ||||     |||||||||
                                TC CCCA     TACCGAACC
                                 C   CCT___
GAM65   ZNF323    5'  ATCTGGGACCAAGAAACCCAC  48076        CCTA  _  TG
                                GTGGGTTTC   TGG CT  GAT
                                |||||||||   ||| ||  |||
                                CACCCAAAG   ACC GG  CTA
                                     A___   A  GT
GAM65   LOC146229 3'  AGCCAGAAAGAAACCCACT   77728         CCTA
                                AGTGGGTTTC   TGGCT
                                ||||||||||   |||||
                                TCACCCAAAG   ACCGA
                                      AAAG
GAM65   LOC203522 5'  ATCCAAACCTCATAAAACCCAC 89370        CCCTAT  C
                                GTGGGTTT     GG TTGGAT
                                ||||||||     || ||||||
                                CACCCAAA     CC AACCTA
                                     ATACT_  A
GAM65   LOC256158 5'  GCCACAGGGAAACCCCCT    97668    T        A
                                AG GGGTTTCCCT TGGC
                                || ||||||||| ||||
                                TC CCCAAAGGGA ACCG
                                 C         C
GAM66   IL18R1    3'  TGGGGACTGAGCATATGA    13908          G
                                TCATATGCTC AGTCTCCA
                                |||||||||| ||||||||
                                AGTATACGAG TCAGGGGT
                                          _
GAM66   IRTA1     3'  ACTGGAGACTCACTTGCATCA  48415   T   TC__
                                A ATGC   GAGTCTCCAGT
                                | ||||   ||||||||||
                                A TACG   CTCAGAGGTCA
                                 C   TTCA
GAM66   MDM4      3'  ACTGGAGCTAACAATGA     9976      A  CTCG  T
                                TCAT TG   AG CTCCAGT
                                |||| ||   || |||||||
                                AGTA AC   TC GAGGTCA
                                  _  AA__  _
GAM66   RBBP9     3'  ACTGGGGAAAGAAAACATGA   70126     ATGC  GAG
                                TCAT   TC   TCTCCAGT
                                ||||   ||   ||||||||
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                                AGTA   AG  AGGGGTCA
                                  CAAA  AA_
GAM66   STAT4    5' GAGACTCGAACACTGA     12005    TA  C
                                TCA  TG TCGAGTCTC
                                |||  || |||||||||
                                AGT  AC AGCTCAGAG
                                  C_  A
GAM66   TERF1    3' TACCAGAGTTAAAGCATATG  33977       CG  T  CA
                                CATATGCT  AG CTC  GTA
                                ||||||||  || |||  |||
                                GTATACGA  TT GAG  CAT
                                     AA  _  AC
GAM66   UGT1A1   3' ACTGAGAACAGCATATGA   4873        CGAG   C
                                TCATATGCT   TCTC AGT
                                |||||||||   |||| |||
                                AGTATACGA   AGAG TCA
                                     CA__   _
GAM66   UGT1A4   3' ACTGAGAACAGCATATGA   23058       CGAG   C
                                TCATATGCT   TCTC AGT
                                |||||||||   |||| |||
                                AGTATACGA   AGAG TCA
                                     CA__   _
GAM66   UGT1A9   3' ACTGAGAACAGCATATGA   40709       CGAG   C
                                TCATATGCT   TCTC AGT
                                |||||||||   |||| |||
                                AGTATACGA   AGAG TCA
                                     CA__   _
GAM66   VENTX2   3' TACTGGAGAATATATAT    27116     CTCGAG
                                ATATG    TCTCCAGTA
                                |||||    |||||||||
                                TATAT    AGAGGTCAT
                                   ATA___
GAM66   ZNF146   3' TACTGAAGAGAAAGACATGCAT 23087       ___ GAG   __
           ATGA                  TCATATGC  TC  TCTC  CAGTA
                                |||||||  ||  ||||  |||||
                                AGTATACG  AG  AGAG  GTCAT
                                     TAC  AA_   AA
GAM66   AGTRL2   5' GGATTCGGCATATGA     17694       T
                                TCATATGC CGAGTCT
                                ||||||| |||||||
                                AGTATACG GCTTAGG
                                        _
GAM66   BAG5     3' TACTGGAGACGGGT      16851     GA
                                GCTC  GTCTCCAGTA
                                ||||  ||||||||||
                                TGGG  CAGAGGTCAT
                                   __
GAM66   BCCIP    3' TACTGGAGAGAGACA     54307   _  GAG
                                TG CTC  TCTCCAGTA
                                || |||  |||||||||
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                                AC GAG   AGAGGTCAT
                                 A  ___
GAM66   C3IP1    3'  ACTGGAGACAGCATA      41280       CGA
                                TATGCT   GTCTCCAGT
                                ||||||   |||||||||
                                ATACGA   CAGAGGTCA
                                   ___
GAM66   ERN1     3'  ACTGGAGACCGGAATTGA    7517      TATG T  A
                                TCA    C CG GTCTCCAGT
                                |||    | || |||||||||
                                AGT    G GC CAGAGGTCA
                                  TAA_ _ _
GAM66   FLJ11457 5'  ACTGGAGAACCAAATGA     45395      A  CTCGAG
                                TCAT TG     TCTCCAGT
                                |||| ||     ||||||||
                                AGTA AC     AGAGGTCA
                                  A  CA_____
GAM66   FLJ20004 5'  ACTGGAGACCCGGAGTGT    95283       _ A
                                ATGCTC G GTCTCCAGT
                                ||||||| | |||||||||
                                TGTGAG C CAGAGGTCA
                                   G C
GAM66   FLJ20070 3'  ACTGGAGAAAGGCCTTATGA   34473      T_   CGAG
                                TCATA  GCT    TCTCCAGT
                                |||||  |||    ||||||||
                                AGTAT  CGG    AGAGGTCA
                                   TC   AA__
GAM66   FLJ20070 3'  ACTGGAGGAAGGCCATATGA   34474       CT GAG
                                TCATATG  C   TCTCCAGT
                                |||||||  |   ||||||||
                                AGTATAC  G   GGAGGTCA
                                    CG AA_
GAM66   FLJ21106 5'  TACTGGAGGCGACGAACA    46999    C   A_
                                TG TCG  GTCTCCAGTA
                                || |||  ||||||||||
                                AC AGC  CGGAGGTCAT
                                 A   AG
GAM66   FLJ22393 5'  TACTGGAGACGAGACCA     47063    C  GA
                                TG TC  GTCTCCAGTA
                                || ||  ||||||||||
                                AC AG  CAGAGGTCAT
                                 C  AG
GAM66   FLJ22615 3'  ACTGGAGACAAGCATG      68514       CGA
                                TATGCT   GTCTCCAGT
                                ||||||   |||||||||
                                GTACGA   CAGAGGTCA
                                   A__
GAM66   H2AV     3'  GAGACCCCGAGCATAT      56852        A_
                                ATATGCTCG  GTCTC
                                |||||||||  |||||
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                                TATACGAGC  CAGAG
                                     CC
GAM66   HSZFP36  3' ACTGGAGACGGACCACATA   63479     C__  GA
                                TATG   TC  GTCTCCAGT
                                ||||   ||  |||||||||
                                ATAC   AG  CAGAGGTCA
                                  ACC  G_
GAM66   HSZFP36  3' ACTGGAGAGAAGCCATATGA  63480       _  CGAG
                                TCATATG CT    TCTCCAGT
                                |||||||  ||    ||||||||
                                AGTATAC GA    AGAGGTCA
                                    C  AG__
GAM66   KIAA0152 3' TACTGGAGAAAAAGCAT    28303      CGAG
                                ATGCT    TCTCCAGTA
                                |||||    |||||||||
                                TACGA    AGAGGTCAT
                                  AAA_
GAM66   KIAA1979 3' ACTGGAGAAGCCATAATGA   88272     _  _  CGAG
                                TCAT ATG CT    TCTCCAGT
                                ||||  |||  ||    ||||||||
                                AGTA TAC GA    AGAGGTCA
                                  A   C  _____
GAM66   MGC13071 5' TACTGGAGAGAAGCCACATGA 51090     AT_   CGAG
                                TCAT   GCT    TCTCCAGTA
                                ||||   |||    |||||||||
                                AGTA   CGA    AGAGGTCAT
                                  CAC   AG__
GAM66   MSTP032  3' ACTGGAGACAAGCAATCTGA  47438    TA_   CGA
                                TCA   TGCT   GTCTCCAGT
                                |||   ||||   |||||||||
                                AGT   ACGA   CAGAGGTCA
                                  CTA    A__
GAM66   PAPOLG   3' TACTGAAAGTCAGTATATGA  43173        C  GTCTC
                                TCATATGCT GA     CAGTA
                                |||||||||  ||    |||||
                                AGTATATGA CT     GTCAT
                                     _  GAAA_
GAM66   PRO0246  5' TACTAAAGAATTAATGAGCATG 26139        AG___   CC
                                TATGCTCG     TCT  AGTA
                                ||||||||     |||  ||||
                                GTACGAGT     AGA  TCAT
                                     AATTA   AA
GAM66   VPS39    3' ACTGGAGAGTTCCATG     62841     CTC  G
                                TATG   GA TCTCCAGT
                                ||||   ||  ||||||||
                                GTAC   TT AGAGGTCA
                                  C__  G
GAM66   ZFD25    3' TACTGGAGAAAAGCCATA    32583     _  CGAG
                                TATG CT    TCTCCAGTA
                                ||||  ||    |||||||||
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                                ATAC GA    AGAGGTCAT
                                  C  AA__
GAM66   ZNF272   5' ACTGGAGAGAAGCCCTATGA  61900      T_  CGAG
                                TCATA  GCT    TCTCCAGT
                                |||||  |||    ||||||||
                                AGTAT  CGA    AGAGGTCA
                                   CC   AG__
GAM66   ZNF302   3' TACTGGAGAAAAGCCATAT   37928      _ CGAG
                                ATATG CT    TCTCCAGTA
                                ||||| ||    |||||||||
                                TATAC GA    AGAGGTCAT
                                  C  AA__
GAM66   ZNF302   3' TACTGGAGAAAAGCCATAT   37419      _ CGAG
                                ATATG CT    TCTCCAGTA
                                ||||| ||    |||||||||
                                TATAC GA    AGAGGTCAT
                                  C  AA__
GAM66   LOC151610 3' ACTAGGTTCTTCCCAGCATATG 80284         C__   TCT  _
            A                    TCATATGCT   GAG   CC AGT
                                |||||||||   |||   || |||
                                AGTATACGA   TTC   GG TCA
                                     CCC   TT_  A
GAM66   LOC155060 3' TACTGGAGATCTCAGC      86333     C  _
                                GCT GAG TCTCCAGTA
                                ||| ||| |||||||||
                                CGA CTC AGAGGTCAT
                                  _  T
GAM66   LOC163255 3' TACTGGAGAGAAACCATATGA  82450       CTCGAG
                                TCATATG     TCTCCAGTA
                                |||||||     |||||||||
                                AGTATAC     AGAGGTCAT
                                    CAAAG_
GAM66   LOC202347 5' ACTGGAAACTAGAAATTTGA   90343     T  GC  G   C
                                TCA AT  TC AGT TCCAGT
                                ||| ||  || ||| ||||||
                                AGT TA  AG TCA AGGTCA
                                  T  A_  A   A
GAM66   LOC256414 3' TACTGGAGAAGATGTCATAGGA 96828     A   _ TCGAG
                                TC TATG C    TCTCCAGTA
                                || |||| |    |||||||||
                                AG ATAC G    AGAGGTCAT
                                 G    T TAGA_
GAM66   LOC90333  3' ACTGGAGAAAAGCCATAGA   62280    A   _ CGAG
                                TC TATG CT    TCTCCAGT
                                || |||| ||    ||||||||
                                AG ATAC GA    AGAGGTCA
                                  _   C  AA__
GAM66   LOC90591  3' ACTGGAGAGAAACAGTATGA   63411       GCTCGAG
                                TCATAT      TCTCCAGT
                                ||||||      ||||||||
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                                AGTATG      AGAGGTCA
                                   ACAAAG_
GAM67   ARHGEF6   3'  CAAACTTGAAGCCAGGC     68197       ACCA
                                GCCTGG    CAAGTTTG
                                ||||||    ||||||||
                                CGGACC    GTTCAAAC
                                   GAA_
GAM67   CNTN2     3'  GTCACAACCCAGGTGA      17411        ACCACAA  _
                                TCGCCTGG      GTT TGAC
                                ||||||||      ||| ||||
                                AGTGGACC      CAA ACTG
                                    ________  C
GAM67   CORO2A    3'  AAACTGTGGTCCAGAGA     12642    GC        A
                                TC  CTGGACCACA GTTT
                                ||  ||||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM67   CORO2A    3'  AAACTGTGGTCCAGAGA     53398    GC        A
                                TC  CTGGACCACA GTTT
                                ||  ||||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM67   GRLF1     3'  AGGTCAGAAAGTGGCCCAGG   78551      A    AAG
                                CCTGG CCAC   TTTGACCT
                                |||||  ||||  ||||||||
                                GGACC GGTG   AGACTGGA
                                   C    AA_
GAM67   LAPTM5    3'  AGGCTTGTGGTCAAGC      22199    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCGGA
                                 AA_
GAM67   POU2AF1   3'  AGATTTACAGTCCAGGC     20647        CAC
                                GCCTGGAC   AAGTTT
                                ||||||||   ||||||
                                CGGACCTG   TTTAGA
                                     ACA
GAM67   PTGS1     3'  GTCTCCTGTCTTATGGTCCAG  54574        C   TTT___
                                CTGGACCA AAG      GAC
                                |||||||| |||      |||
                                GACCTGGT TTC      CTG
                                     A   TGTCCT
GAM67   PTGS1     3'  GTCTCCTGTCTTATGGTCCAG  6355         C   TTT___
                                CTGGACCA AAG      GAC
                                |||||||| |||      |||
                                GACCTGGT TTC      CTG
                                     A   TGTCCT
GAM67   TRIM34    5'  AGGTCAAGTTGAGCCCAG     55224      ACCA   G
                                CTGG    CAA TTTGACCT
                                ||||    ||| ||||||||
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                                GACC    GTT GAACTGGA
                                  CGA_  _
GAM67   TRIM9    5'  AGGCCAGGCAAGTCCAGGC   30749        CACAA    A
                                GCCTGGAC    GTTTG CCT
                                ||||||||    ||||| |||
                                CGGACCTG    CGGAC GGA
                                    AA___    C
GAM67   ABLIM    5'  GATATGTAACCCAGGCGG    22030        ACC   A
                                TCGCCTGG   ACA GTT
                                ||||||||   ||| |||
                                GGCGGACC   TGT TAG
                                    CAA   A
GAM67   AMOT     3'  AGGCATCTTCATGGTCCAGGGA 55716    G       C_   TT  A
                                TC CCTGGACCA  AAG  TG CCT
                                || |||||||||  |||  || |||
                                AG GGACCTGGT  TTC  AC GGA
                                 _       AC   T_ _
GAM67   DKFZp434D177 5'  TTAGACCCAGGCGA       79443        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                              _______
GAM67   DKFZp434D177 5'  TTAGACCCAGGCGA       50056        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                              _______
GAM67   FLJ23420  3'  CAAGTGGGTCCAGGC       46845         A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                              _ __
GAM67   HSA249128 5'  GGCGCGGTCCAGGCGG      34152          ACAA
                                TCGCCTGGACC    GTT
                                ||||||||||    |||
                                GGCGGACCTGG    CGG
                                      CG__
GAM67   MGC15668  5'  AGACCCGGTGGTCCAGACG    51277    C       AA_
                                CG CTGGACCAC   GTTT
                                || |||||||||   ||||
                                GC GACCTGGTG   CAGA
                                 A        GCC
GAM67   MGC22014  3'  AGGTCCCGAGTGTAACCCAGGT 64486        ACC   AGTTT
           GA                     TCGCCTGG   ACA    GACCT
                                ||||||||   |||    |||||
                                AGTGGACC   TGT    CTGGA
                                    CAA   GAGCC
GAM67   SDCCAG10  5'  AGAGTTGTGGTCCAAAGA    19641    GCC        G
                                TC   TGGACCACAA TTT
                                ||   |||||||||| |||
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                                AG   ACCTGGTGTT AGA
                                 AA_         G
GAM67   LOC115442 3'  AGGTCAGGGATGGTCCAG    72676         CAAG
                                CTGGACCA    TTTGACCT
                                ||||||||    ||||||||
                                GACCTGGT    GGACTGGA
                                     AG__
GAM67   LOC129011 5'  AGACCTGCGGTCCAGGC     74862         A  A
                                GCCTGGACC CA GTTT
                                ||||||||| || ||||
                                CGGACCTGG GT CAGA
                                      C  C
GAM67   LOC130536 5'  GCAAAGTCCAGGCG        75746         CACAAG    A
                                CGCCTGGAC     TTTG C
                                |||||||||     |||| |
                                GCGGACCTG     AAAC G
                                     _______   C
GAM67   LOC149108 3'  AGACTTCACTGTGGTCCA    84357         _____
                                TGGACCACA    AGTTT
                                |||||||||    |||||
                                ACCTGGTGT    TCAGA
                                      CACT
GAM67   LOC221688 5'  AGACTCGGGCCCAGACGA    93674     C    A  ACA
                                TCG CTGG CC   AGTTT
                                ||| |||| ||   |||||
                                AGC GACC GG   TCAGA
                                  A   C  GC_
GAM67   LOC256228 5'  AGACTTGTGGTCAAAGC     96233    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCAGA
                                 AAA
GAM67   LOC257441 5'  TTAGACCCAGGCGA        95566         ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                     _______
GAM67   LOC91960  3'  AGGTGCCTCTCGTGGTCCAAGC 67657    C       A  TTTG
                                GC TGGACCAC AG    ACCT
                                || |||||||| ||    ||||
                                CG ACCTGGTG TC    TGGA
                                 A       C  TCCG
GAM67   LOC92840  3'  GTCCCTCGGGTCCAGGC     56435         ACA  TTT
                                GCCTGGACC   AG   GAC
                                |||||||||   ||   |||
                                CGGACCTGG   TC   CTG
                                      GC_  C__
GAM68   B3GNT3    3'  CCCACCTGGTACTGTT      26517         TACTAA  A
                                AACAGTATC     AG TGGG
                                |||||||||     || ||||
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                                TTGTCATGG     TC ACCC
                                       _______ C
GAM68   CSPG3    3'  AGCCCATTGACTTAGAAACTGT 15227       A    CTAAA
              T                  AACAGT TCTA     GATGGGCT
                                 ||||||| ||||    |||||||||
                                 TTGTCA AGAT     TTACCCGA
                                    A    TCAG_
GAM68   EVA1     3'  AGCCCATCTCTAATGAGGACT  58572     A   AC_  A
                                 AGT TCT   TA AGATGGGCT
                                 ||| |||   || |||||||||
                                 TCA GGA   AT TCTACCCGA
                                   _   GTA  C
GAM68   ID4      3'  CTTTAATAGATACTGT      7754           C
                                 ACAGTATCTA TAAAG
                                 |||||||||| |||||
                                 TGTCATAGAT ATTTC
                                       A
GAM68   RAD51C   3'  TTTAGAGATACTGTT      54255          A
                                 AACAGTATCT CTAAA
                                 |||||||||| |||||
                                 TTGTCATAGA GATTT
                                       _
GAM68   RHO      3'  AGCCCATCTTCAGCAGTTGCT  5018       T  A  A
                                 AGTA CT CT AAGATGGGCT
                                 |||| || || ||||||||||
                                 TCGT GA GA TTCTACCCGA
                                   T  C  C
GAM68   STAR     3'  CTCATTAGTAGACATGTT    4445      GTA      AAG
                                 AACA   TCTACTA   ATGGG
                                 ||||   |||||||   |||||
                                 TTGT   AGATGAT   TACTC
                                   AC_      ____
GAM68   CD109    3'  AGTGGTCTCAGTAGATACT   56046         AA    GG
                                 AGTATCTACT  AGAT  GCT
                                 ||||||||||  ||||  |||
                                 TCATAGATGA  TCTG  TGA
                                       C_   G_
GAM68   FLJ00024 3'  AGCCCATCCCTGGGACCTGC  63747     TCTA   AA
                                 GTA   CTA  GATGGGCT
                                 |||   |||  ||||||||
                                 CGT   GGT  CTACCCGA
                                   CCAG   CC
GAM68   FLJ20666 3'  GCTTACCACAGATACTGTT   35510         ACTAAAGA
                                 AACAGTATCT      TGGGC
                                 ||||||||||      |||||
                                 TTGTCATAGA      ATTCG
                                       CACC____
GAM68   FLJ20666 3'  GCTTACCACAGATACTGTT   37089         ACTAAAGA
                                 AACAGTATCT      TGGGC
                                 ||||||||||      |||||
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                                TTGTCATAGA       ATTCG
                                      CACC____
GAM68   FLJ22969  3'  GGCTCAGCAGATGCTGT     68657         ACTAAAGA
                                ACAGTATCT       TGGGCT
                                |||||||||       ||||||
                                TGTCGTAGA       ACTCGG
                                      CG_______
GAM68   GGTLA1    5'  AGCCCATCTCTGTCCCATTGT  14657       ATCT  TAA
                                ACAGT    AC   AGATGGGCT
                                |||||    ||   |||||||||
                                TGTTA    TG   TCTACCCGA
                                   CCC_  TC_
GAM68   KIAA0240  3'  TTTAGTAGATTCTGTT      92443       T
                                AACAG ATCTACTAAA
                                ||||| ||||||||||
                                TTGTC TAGATGATTT
                                   T
GAM68   KIAA1028  3'  TTTATTAGATACTGTT      91952           C
                                AACAGTATCTA TAAA
                                |||||||||||| ||||
                                TTGTCATAGAT ATTT
                                      T
GAM68   KIAA1332  3'  CATCAAAAGATACTGTT     71163          ACTAAA
                                AACAGTATCT     GATG
                                ||||||||||     ||||
                                TTGTCATAGA     CTAC
                                      AAA___
GAM68   KIAA1497  3'  ATCTTTAGTAGACACT      67503     A
                                AGT TCTACTAAAGAT
                                ||| ||||||||||||
                                TCA AGATGATTTCTA
                                  C
GAM68   KIAA1858  3'  AGCCCATCTCTAGCACACCTTG 67133     TATCTA   A
                                CAG      CTA AGATGGGCT
                                |||      ||| |||||||||
                                GTT      GAT TCTACCCGA
                                  CCACAC   C
GAM68   p25       3'  GCCCATCCAGGACACTCC    22851    C   A   ACTAAA
                                A AGT TCT      GATGGGC
                                | ||| |||      |||||||
                                C TCA AGG      CTACCCG
                                 C   C   AC____
GAM68   PME-1     3'  AGCCCATCTTTTCTGTGACTGT 32351       ATCTACT
                                ACAGT       AAAGATGGGCT
                                |||||       ||||||||||||
                                TGTCA       TTTCTACCCGA
                                   GTGTCT_
GAM68   PRO0628   3'  AGCCCATCTTCTGTACTGCT   26205      TC   TA
                                AGTA  TAC  AAGATGGGCT
                                ||||  |||  ||||||||||
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                                TCGT  ATG  TTCTACCCGA
                                  C_   TC
GAM68   LOC122728 3'  AGCCCATCTGCTGTATTACTG  74150      TC   TAA
                                CAGTA  TAC   AGATGGGCT
                                |||||  |||   |||||||||
                                GTCAT  ATG   TCTACCCGA
                                   T_   TCG
GAM68   LOC130507 3'  ATCTCTAGTAAATACTGTT    74948        C    A
                                AACAGTAT TACTA AGAT
                                |||||||| ||||| ||||
                                TTGTCATA ATGAT TCTA
                                     A    C
GAM68   LOC144110 3'  AGCCTGGGGCAGCAGGTACTG  76672        A  AAAGA
                                CAGTATCT CT    TGGGCT
                                |||||||| ||    ||||||
                                GTCATGGA GA    GTCCGA
                                     C  CGGG_
GAM68   LOC145368 3'  AGCCCATCTGCTGTATTACTG  77092      TC   TAA
                                CAGTA  TAC   AGATGGGCT
                                |||||  |||   |||||||||
                                GTCAT  ATG   TCTACCCGA
                                   T_   TCG
GAM68   LOC149830 3'  CCCATCTCTAAGGCAGGATGCT 84724        A__  AA_
           G                     CAGTATCT   CT   AGATGGG
                                |||||||   ||   |||||||
                                GTCGTAGG   GA   TCTACCC
                                     ACG  ATC
GAM68   LOC150236 5'  AGCCCATCCCCCAGTTCACT   79680    ATCT   AAA_
                                AGT    ACT    GATGGGCT
                                |||    |||    |||||||||
                                TCA    TGA    CTACCCGA
                                  CT__   CCCC
GAM68   LOC150279 3'  CCCATGAGGCTCAGATGCTGTT 79667         ACTAAAG
                                AACAGTATCT      ATGGG
                                ||||||||||      |||||
                                TTGTCGTAGA      TACCC
                                     CTCGGAG
GAM68   LOC150423 3'  AGCCCATCTCCTGTATTACTG  79863      TC   TAA
                                CAGTA  TAC   AGATGGGCT
                                |||||  |||   |||||||||
                                GTCAT  ATG   TCTACCCGA
                                   T_   TCC
GAM68   LOC151405 5'  AGATGGGCTTTAGTAAAGACTG 85334      ATC       ATGGG
           T                     ACAGT   TACTAAAG    CT
                                |||||   ||||||||    ||
                                TGTCA   ATGATTTC    GA
                                   GAA       GGGTA
GAM68   LOC151473 3'  AGCCCATCTCTAGACTCTCGT  80250    _  TA    CTAA
                                AC AG  TCTA    AGATGGGCT
                                || ||  ||||    |||||||||
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                                TG TC  AGAT    TCTACCCGA
                                 C  TC    C___
GAM68   LOC153196 5'  AGCCCATCCTTGGGACCCTACT 85953      TCTA_    A
                                AGTA     CTAA GATGGGCT
                                ||||     |||| ||||||||
                                TCAT     GGTT CTACCCGA
                                  CCCAG    C
GAM68   LOC221002 3'  AGCCCATTCAGATAAAACTG   91475      ___    ACTAAA
                                CAGT   ATCT     GATGGGCT
                                ||||   ||||     ||||||||
                                GTCA   TAGA     TTACCCGA
                                  AAA    C_____
GAM68   LOC255290 5'  AGCCCATCTCTGTCCCATTGT  95607      ATCT  TAA
                                ACAGT    AC   AGATGGGCT
                                |||||    ||   |||||||||
                                TGTTA    TG   TCTACCCGA
                                   CCC_  TC_
GAM68   LOC91907  3'  ATCTTTAGTAGACACT      67493     A
                                AGT TCTACTAAAGAT
                                ||| ||||||||||||
                                TCA AGATGATTTCTA
                                  C
GAM69   AF3P21    3'  CATCCATCCTGGAGCCTCA    33194            _
                                TGAGGCTCCAGGATG ATG
                                |||||||||||||| |||
                                ACTCCGAGGTCCTAC TAC
                                      C
GAM69   APLP1     3'  TCTTCCTGGAGCCCCA      17706    A        T
                                TG GGCTCCAGGA GA
                                || ||||||||| ||
                                AC CCGAGGTCCT CT
                                 C         T
GAM69   AQP5      5'  GCAGCGGCCTGGAGCCTC     7935           A  A
                                GAGGCTCCAGG TG TGC
                                |||||||||| || |||
                                CTCCGAGGTCC GC ACG
                                      G  G
GAM69   ASTN      3'  TGTGGCAAATGCTGGAGCCTCA 69340           G  GA
                                TGAGGCTCCAG AT  TGCTACA
                                |||||||||| ||  |||||||
                                ACTCCGAGGTC TA  ACGGTGT
                                      G  A_
GAM69   ATF7      3'  AGCCCCGGAGCCTCA       22463         A  ATGAT
                                TGAGGCTCC GG     GCT
                                ||||||||| ||     |||
                                ACTCCGAGG CC     CGA
                                     C _____
GAM69   BCL7B     3'  TGTAGCATCATCTTCCT      8136      CTCC
                                AGG    AGGATGATGCTACA
                                |||    ||||||||||||||
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                                TCC   TTCTACTACGATGT
                                  ____
GAM69   CCND1    5' GCAAAGTCCTGGAGCCTC    53888          GA
                                GAGGCTCCAGGAT TGC
                                |||||||||||| |||
                                CTCCGAGGTCCTG ACG
                                      AA
GAM69   CDH1     3' TAGCTCACTGTAACCTCA    15150      CTC  GA  T
                                TGAGG  CAG TGA GCTA
                                |||||  ||| ||| ||||
                                ACTCC  GTC ACT CGAT
                                  AAT  __  _
GAM69   CORO2B   5' TGGTGTCATCCAGGAGCCCCA 64577    A    A
                                TG GGCTCC GGATGATGCTA
                                || |||||| ||||||||||
                                AC CCGAGG CCTACTGTGGT
                                 C    A
GAM69   ED1      3' GCAGACCTGGAGCTTCA     7372          ATGA
                                TGAGGCTCCAGG   TGC
                                ||||||||||   |||
                                ACTTCGAGGTCC   ACG
                                      AG__
GAM69   GRAF     3' TTACCTGGAGCTCA       30581     G     A
                                TGAG CTCCAGG TGA
                                |||| ||||||| |||
                                ACTC GAGGTCC ATT
                                  _     _
GAM69   MASP1    3' TCACCCCTGAGCCTCA      8538        C  A_
                                TGAGGCTC AGG  TGA
                                |||||||| |||  |||
                                ACTCCGAG TCC  ACT
                                    _  CC
GAM69   MHC2TA   3' GTATCCCATGAGCCTCA     4184        CA  AT
                                TGAGGCTC  GG  GATGC
                                |||||||  ||  |||||
                                ACTCCGAG  CC  CTATG
                                     TA  __
GAM69   NEURL    3' GTAGCCCCCTGGAGCCCA    14863    A      ATGAT
                                TG GGCTCCAGG    GCTAC
                                || |||||||||    |||||
                                AC CCGAGGTCC    CGATG
                                 _       CC____
GAM69   RPP30    3' AGCTCACTGCAACCTCA     21160      CTC  GA  T
                                TGAGG  CAG  TGA GCT
                                |||||  |||  ||| |||
                                ACTCC  GTC  ACT CGA
                                  AAC  __  _
GAM69   TACC1    3' CACACCAGAGCCTCA       20792        CA  A  A
                                TGAGGCTC  GG TG TG
                                ||||||||  || || ||
```

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                                ACTCCGAG  CC AC AC
                                    A_ _ _
GAM69   TCTA     3'  CATAGCCTGCAGCCTCA     42236       C   ATG
                                TGAGGCT CAGG   ATG
                                ||||||| ||||   |||
                                ACTCCGA GTCC   TAC
                                    C   GA_
GAM69   TLX1     3'  TGGTGTCACCCCAGAGCC    18635      CA  A
                                GGCTC  GG TGATGCTA
                                |||||  || ||||||||
                                CCGAG  CC ACTGTGGT
                                   AC  C
GAM69   TNFRSF5  3'  TCACCCTGGAGCCCA      6977     A       A
                                TG GGCTCCAGG TGA
                                || ||||||||| |||
                                AC CCGAGGTCC ACT
                                 _       C
GAM69   C16orf7  3'  TGAGGACCATCCTGGAGCCTCA 16945           ATG  A
                                TGAGGCTCCAGGATG   CT CA
                                ||||||||||||||   || ||
                                ACTCCGAGGTCCTAC   GG GT
                                         CA_  A
GAM69   CLST11240 5'  GCAGCATAGGAGTCTCA     33169        AGG   A
                                TGAGGCTCC   ATG TGC
                                |||||||||   ||| |||
                                ACTCTGAGG   TAC ACG
                                     A__   G
GAM69   DEFCAP   3'  GCAGACCTCATAGAGCCTCA  29952       C___   ATGA
                                TGAGGCTC    AGG    TGC
                                ||||||||    |||    |||
                                ACTCCGAG    TCC    ACG
                                     ATAC   AG__
GAM69   DEFCAP   3'  GCAGACCTCATAGAGCCTCA  52228       C___   ATGA
                                TGAGGCTC    AGG    TGC
                                ||||||||    |||    |||
                                ACTCCGAG    TCC    ACG
                                     ATAC   AG__
GAM69   DEFCAP   3'  GCAGACCTCATAGAGCCTCA  52232       C___   ATGA
                                TGAGGCTC    AGG    TGC
                                ||||||||    |||    |||
                                ACTCCGAG    TCC    ACG
                                     ATAC   AG__
GAM69   DGKD     3'  AGCATCATCGGATCGCCCA   59397    A   __   AG
                                TG GGC  TCC  GATGATGCT
                                || |||  |||  |||||||||
                                AC CCG  AGG  CTACTACGA
                                 _  CT   __
GAM69   DKFZp434J0226 3'  TGGCACCCATCCTGGGCCCCA  72337    A   T      A_
                                TG GGC CCAGGATG  TGCTA
                                || ||| ||||||||  |||||
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                                AC CCG GGTCCTAC  ACGGT
                                 C  _      CC
GAM69   DKFZP762D096 3' GCAGTCCTGGAACCCA     65577    A  C      GA
                                TG GG TCCAGGAT  TGC
                                || || ||||||||  |||
                                AC CC AGGTCCTG  ACG
                                 _ A      __
GAM69   E2IG4    3' GCAGTTCTGGAGCCTCA     90911           GA
                                TGAGGCTCCAGGAT  TGC
                                ||||||||||||||  |||
                                ACTCCGAGGTCTTG  ACG
                                                __
GAM69   FLJ11029 5' CATCATCCTGGAACTTCA    60974      C
                                TGAGG TCCAGGATGATG
                                ||||| ||||||||||||
                                ACTTC AGGTCCTACTAC
                                   A
GAM69   FLJ20190 5' GCATTGTCCCAAGGCCTCA   34704       CCA   TG
                                TGAGGCT   GGA  ATGC
                                |||||||   |||  ||||
                                ACTCCGG   CCT  TACG
                                    AAC   GT
GAM69   FLJ21438 5' TGTATGCCCTGGAGCC      61527        ATGAT  _
                                GGCTCCAGG    GC TACA
                                |||||||||    || ||||
                                CCGAGGTCC    CG ATGT
                                     _____ T
GAM69   FLJ22378 3' GCAGCCGGCCCCCAGGCCTCA 46899       CCA  A_  A_
                                TGAGGCT   GG  TG  TGC
                                |||||||   ||  ||  |||
                                ACTCCGG   CC  GC  ACG
                                    ACC  CG  CG
GAM69   HSJ1     3' GTAACACTGAGCCTCA      22137        C  GATGA  C
                                TGAGGCTC AG    TG TAC
                                |||||||| ||    || |||
                                ACTCCGAG TC    AC ATG
                                    _ _____  A
GAM69   HSOBRGRP 3' CACAGACCAAGAGCCTCA    34032        CA  A_  A
                                TGAGGCTC  GG  TG TG
                                ||||||||  ||  || ||
                                ACTCCGAG  CC  AC AC
                                    AA  AG  _
GAM69   HTMP10   3' ATCATCCAGAGCCTCA      52606        CA
                                TGAGGCTC  GGATGAT
                                ||||||||  |||||||
                                ACTCCGAG  CCTACTA
                                    A_
GAM69   KCNS1    3' CATCACCCTGAGCCTCA      9574         C   A
                                TGAGGCTC AGG TGATG
                                |||||||| ||| |||||
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                                ACTCCGAG TCC ACTAC
                                     _  C
GAM69   KIAA0514 5' TGTTATCCCACAGCCCCA   28100   A   CCA
                                TG GGCT  GGATGATG
                                || ||||  ||||||||
                                AC CCGA  CCTATTGT
                                 C   CAC
GAM69   KIAA0668 3' GAGCACTGAGCCTCA     66525       C  GATGA   A
                                TGAGGCTC AG    TGCT C
                                |||||||| ||    |||| |
                                ACTCCGAG TC    ACGA G
                                     _ _____   C
GAM69   KIAA1257 3' GTAGCATCAGAACCTC     62753     C  CAGGA
                                GAGG TC    TGATGCTAC
                                |||| ||    |||||||||
                                CTCC AG    ACTACGATG
                                  A _____
GAM69   KIAA1303 3' GCTCCACCCTGGAGCCCA   66003   A      A  AT
                                TG GGCTCCAGG TG  GC
                                || |||||||| ||  ||
                                AC CCGAGGTCC AC  CG
                                 _       C  CT
GAM69   KIAA1340 5' GCAGCTTCCCGGGCCTCA   69183      T  A  TGA
                                TGAGGC CC GGA  TGC
                                |||||| || |||  |||
                                ACTCCG GG CCT  ACG
                                   _ C  TCG
GAM69   KIAA1822 3' GCAGGCCTGGGGCCCCA    67569   A      ATGA
                                TG GGCTCCAGG   TGC
                                || |||||||||   |||
                                AC CCGGGGTCC   ACG
                                 C       GG__
GAM69   KIAA1941 3' TGAGCAGCATCCCGGGCCTCA 74846      T  A   A   A
                                TGAGGC CC GGATG TGCT CA
                                |||||| || ||||| |||| ||
                                ACTCCG GG CCTAC ACGA GT
                                   _ C   G   _
GAM69   MGC11279 3' GCCCCACCCTGGAGCTTCA   44252         A  AT
                                TGAGGCTCCAGG TG  GC
                                |||||||||||| ||  ||
                                ACTTCGAGGTCC AC  CG
                                      C  CC
GAM69   MGC4415  3' TGTAGCATTCCAGAGCTCA   48956    G  CA  TG
                                TGAG CTC  GGA  ATGCTACA
                                |||| |||  |||  ||||||||
                                ACTC GAG  CCT  TACGATGT
                                  _  A_  __
GAM69   MIDORI   3' GCTCTTGATCCTGGGGCCCCA 73789   A       ___ T
                                TG GGCTCCAGGAT  GA GC
                                || ||||||||||  || ||
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                                AC CCGGGGTCCTA  CT CG
                                 C        GTT  _
GAM69   P2RXL1   3' GCCACCTGGAGCCTCA     18382          A  AT
                                TGAGGCTCCAGG TG  GC
                                |||||||||||| ||  ||
                                ACTCCGAGGTCC AC  CG
                                          _  __
GAM69   PP3501   5' CATCTGCCCAGAGCCTCA    41369        CA  AT
                                TGAGGCTC  GG  GATG
                                ||||||||  ||  ||||
                                ACTCCGAG  CC  CTAC
                                     AC  GT
GAM69   RNF24    3' TCTCCTGGAGCCTCA      23321          T
                                TGAGGCTCCAGGA GA
                                |||||||||||| ||
                                ACTCCGAGGTCCT CT
                                          _
GAM69   SETMAR   3' TGGAGCAGTCATCCTAGACCCC 73660    A  C  C     _   A
           A                     TG GG TC AGGATGA TGCT CA
                                || || || ||||||| |||| ||
                                AC CC AG TCCTACT ACGA GT
                                 _ C A     G   G
GAM69   SZF1     5' AGCCAGACACCAGAGCCTCA  32230       CA  A  AT__
                                TGAGGCTC  GG TG   GCT
                                ||||||||  || ||   |||
                                ACTCCGAG  CC AC   CGA
                                     A_  _  AGAC
GAM69   TLK2     3' GTAGCACAAAGGCTCA     22450     G  CCAGGA  A
                                TGAG CT     TG TGCTAC
                                |||| ||     || ||||||
                                ACTC GA     AC ACGATG
                                  G  A_____  _
GAM69   TLK2     3' GTAGCACAAAGGCTCA     78199     G  CCAGGA  A
                                TGAG CT     TG TGCTAC
                                |||| ||     || ||||||
                                ACTC GA     AC ACGATG
                                  G  A_____  _
GAM69   TOLLIP   3' TGTGCCATCTTGGAGCCTCA  38691           AT  T
                                TGAGGCTCCAGGATG  GC ACA
                                ||||||||||||||  || |||
                                ACTCCGAGGTTCTAC  CG TGT
                                          __  _
GAM69   ZF5128   3' TGTCCCTACCTGGAGCCTCA  26809          AT__
                                TGAGGCTCCAGG   GATG
                                ||||||||||||   ||||
                                ACTCCGAGGTCC   CTGT
                                       ATCC
GAM69   LOC116113 3' AGCCCCTCCCGAGCCTCA   92210        CA  TGAT
                                TGAGGCTC  GGA   GCT
                                ||||||||  |||   |||
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                                ACTCCGAG  CCT    CGA
                                    C_   CCC_
GAM69   LOC146227 3' GTGCAGCCTCCTGGAGCCCCA  77713    A        TGA   T
                                TG GGCTCCAGGA   TGC AC
                                || ||||||||||   ||| ||
                                AC CCGAGGTCCT   ACG TG
                                 C         CCG   _
GAM69   LOC146336 3' TAGCTCACTGGAGCCTC     77834          GA   T
                                GAGGCTCCAG  TGA GCTA
                                ||||||||||  ||| ||||
                                CTCCGAGGTC  ACT CGAT
                                      __   _
GAM69   LOC149302 5' TAGAGTCCCGAGCCTCA     79271        CA    GA
                                TGAGGCTC  GGAT  TG
                                ||||||||  ||||  ||
                                ACTCCGAG  CCTG  AT
                                    C_    AG
GAM69   LOC149603 3' GCAACCTGGGCCTCA       70638       T    ATGA
                                TGAGGC CCAGG    TGC
                                ||||||| |||||    |||
                                ACTCCG GGTCC    ACG
                                   _    A___
GAM69   LOC151584 3' GCAGGAGGCCTGGAGCCATCA  85449     _       ATGA_
                                TGA GGCTCCAGG     TGC
                                ||| |||||||||     |||
                                ACT CCGAGGTCC     ACG
                                  A        GGAGG
GAM69   LOC157931 3' TGTGCTTACCCTGGGCCTCA   86667      T    A   T  T
                                TGAGGC CCAGG TGA GC ACA
                                |||||| ||||| ||| || |||
                                ACTCCG GGTCC ATT CG TGT
                                   _    C   _ _
GAM69   LOC158402 3' GCCCTCAATCCTGGGGCCTCA  86806           _ T_
                                TGAGGCTCCAGGAT GA  GC
                                |||||||||||||| ||  ||
                                ACTCCGGGGTCCTA CT  CG
                                       A  CC
GAM69   LOC197342 3' GCCCCACCCTGGGCCTCA    88003       T    A  AT
                                TGAGGC CCAGG TG  GC
                                |||||| ||||| ||  ||
                                ACTCCG GGTCC AC  CG
                                   _    C  CC
GAM69   LOC219743 3' CGTCATCCTGGAGCTTCA    93127
                                TGAGGCTCCAGGATGATG
                                ||||||||||||||||||
                                ACTTCGAGGTCCTACTGC

GAM69   LOC221103 3' CATACATCCCCTGAGCCTCA  93245        CA_    _
                                TGAGGCTC   GGATG ATG
                                ||||||||   ||||| |||
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                                ACTCCGAG   CCTAC TAC
                                     TCC     A
GAM69   LOC253392 5'  CATTTCCTGGGGCCTCA     96449           T
                                TGAGGCTCCAGGA GATG
                                |||||||||||| ||||
                                ACTCCGGGGTCCT TTAC
                                          _
GAM69   LOC253769 5'  AGGATTTCCAGAGCCTCA    97225        CA   T   G
                                TGAGGCTC  GGA GAT CT
                                ||||||||  ||| ||| ||
                                ACTCCGAG  CCT TTA GA
                                     A_   _   G
GAM69   LOC253983 3'  CATCATCCCGAAGCCTT     96624       CCA
                                GAGGCT   GGATGATG
                                ||||||   ||||||||
                                TTCCGA   CCTACTAC
                                   AGC
GAM69   LOC254559 5'  TGTCATCTTGGAGCCCCA    96599    A
                                TG GGCTCCAGGATGATG
                                || ||||||||||||||
                                AC CCGAGGTTCTACTGT
                                 C
GAM69   LOC51157  3'  GCCTTACCCTGGGCCTCA    32490       T    A   T
                                TGAGGC CCAGG TGA GC
                                |||||| ||||| ||| ||
                                ACTCCG GGTCC ATT CG
                                   _    C   C
GAM70   FLJ10980  3'  ACCCCCAGTTAGATTA      64649       G    A_
                                TAATC TGAT  GGGGT
                                ||||| ||||  |||||
                                ATTAG ATTG  CCCCA
                                   _    AC
GAM70   LOC154089 3'  ATCACAATTGGCATTA      81035          C
                                TAATGCTAAT GTGAT
                                |||||||||| |||||
                                ATTACGGTTA CACTA
                                      A
GAM71   EPB41     5'  CATGAAGACTTGACCAAGA    15430    C   _   CCT
                                TC TGGT AGG   TCTTCATG
                                || |||| |||   ||||||||
                                AG ACCA TTC   AGAAGTAC
                                 A   G  ___
GAM71   LILRB5    3'  AAGACCACCAGGACA       22421         A  C
                                TGTCCTGGT GG CTT
                                ||||||||| || |||
                                ACAGGACCA CC GAA
                                      _ A
GAM71   PWP2H     3'  CATGTAGCCCATCAGGACA   17308         A   CTTCTT
                                TGTCCTGGT GGC     CATG
                                ||||||||| |||     ||||
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                                ACAGGACTA CCG      GTAC
                                     C   AT____
GAM71   DKFZP434P211 3'  AAGGCCTTCCAGGACA      27257         T
                                TGTCCTGG AGGCCTT
                                |||||||| |||||||
                                ACAGGACC TCCGGAA
                                     T
GAM71   FLJ20464  3'  GCATGAAGAAAGTTCCCTGGAC 35233       T  TA   C
          A                      TGTCC GG  GGC TTCTTCATGC
                                 ||||| ||  ||| ||||||||||
                                 ACAGG CC  TTG AAGAAGTACG
                                   T  C_   A
GAM71   KIAA1911  5'  GCATTCACGCCTACCAGGACA  73507            CTTCTTC
                                 TGTCCTGGTAGGC      ATGC
                                 ||||||||||||       ||||
                                 ACAGGACCATCCG      TACG
                                        CACT___
GAM71   NY-REN-60 3'  CATAAAGAACTTTCCTCAGGAC 67108        GT   CC__    C
          A                      TGTCCTG  AGG    TTCTT ATG
                                 |||||||  |||    ||||| |||
                                 ACAGGAC  TCC    AAGAA TAC
                                     __   TTTC     A
GAM71   LOC130471 3'  CATGAAGAAACTCAGACA    74940      CT   AGGCC
                                 TGTC  GGT    TTCTTCATG
                                 ||||  |||    |||||||||
                                 ACAG  TCA    AAGAAGTAC
                                   AC  ______
GAM71   LOC144147 3'  AAGACCTACCAGCACA      71728     C       C
                                 TGT CTGGTAGG CTT
                                 ||| |||||||| |||
                                 ACA GACCATCC GAA
                                   C       A
GAM71   LOC147976 5'  CATAAAGAAGAAGCTAGGA    78587        AGGC     C
                                 TCCTGGT    CTTCTT ATG
                                 |||||||    |||||| |||
                                 AGGATCG    GAAGAA TAC
                                      AA__      A
GAM71   LOC164295 5'  GCACTTTGGCCCACCAGAACA  82510     C    A    TTCTTCA
                                 TGT CTGGT GGCC       TGC
                                 ||| ||||| ||||       |||
                                 ACA GACCA CCGG       ACG
                                   A    C    TTTC___
GAM71   LOC200860 3'  AGAAAGCCTCCAGGACA     90158         T    C
                                 TGTCCTGG AGGC TTCT
                                 |||||||| |||| ||||
                                 ACAGGACC TCCG AAGA
                                      _    A
GAM71   LOC201626 5'  CACGAAGAAGGTGACTGAGGAC 88987       _   AG        A
                                 GTCCT GGT  GCCTTCTTC TG
                                 ||||| |||  ||||||||| ||
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                                CAGGA TCA  TGGAAGAAG AC
                                   G   G_        C
GAM71   LOC257464 3'  GTGTTGGCTACCAGGACA    89673          G  TTCTT
                                TGTCCTGGTAG CC     CAT
                                |||||||||||  ||     |||
                                ACAGGACCATC GG     GTG
                                      _  TT___
GAM72   PCDHB7    5'  ACAGTGGTAATAGGAATTGGG  38441       G  AGG
                                CTCAAT CC   TATTACCACTGT
                                ||||||  ||   ||||||||||||
                                GGGTTA GG   ATAATGGTGACA
                                   A  ___
GAM72   PTPN13    3'  GTAATATTGGCATAGA      54773    A      G
                                TC ATGCCAG TATTAC
                                || |||||||  ||||||
                                AG TACGGTT ATAATG
                                 A      _
GAM72   PTPN13    3'  GTAATATTGGCATAGA      20759    A      G
                                TC ATGCCAG TATTAC
                                || |||||||  ||||||
                                AG TACGGTT ATAATG
                                 A      _
GAM72   PTPN13    3'  GTAATATTGGCATAGA      54775    A      G
                                TC ATGCCAG TATTAC
                                || |||||||  ||||||
                                AG TACGGTT ATAATG
                                 A      _
GAM72   PYGB      3'  CAGCAGGCCTGGCACTGGG    11171      A       ATTACCA
                                CTCA TGCCAGGT       CTG
                                ||||  ||||||||       |||
                                GGGT ACGGTCCG       GAC
                                  C       GAC_____
GAM72   FLJ10482  3'  ACAGAATCCACACCTGCATTGA 36159         C    ATTACCA
                                TCAATGC AGGT       CTGT
                                |||||||  ||||       ||||
                                AGTTACG TCCA       GACA
                                     _    CACCTAA
GAM72   FLJ10781  3'  ACAGTAGTAATATTCTATCAT  36628     CC   _     C
                                ATG  AGG TATTAC ACTGT
                                |||  |||  ||||||  |||||
                                TAC  TCT ATAATG TGACA
                                  TA   T     A
GAM72   FLJ23120  3'  ACAATGACATATTTGGCA    85141          TAC  C
                                TGCCAGGTAT   CA TGT
                                ||||||||||   ||  |||
                                ACGGTTTATA   GT ACA
                                      CA_  A
GAM72   KIAA0316  3'  ACAGTGGTTCTAGCATT     69667       C   TATT
                                AATGC AGG    ACCACTGT
                                |||||  |||    ||||||||
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                                TTACG TCT    TGGTGACA
                                  A  _____
GAM72   KIAA0970  3'  ACAGTGGCATTTAGCACTGGCA 29954          _  ATTA__
            TTGAG                  CTCAATGCCAG GT     CCACTGT
                                |||||||||| ||     |||||||
                                GAGTTACGGTC CG     GGTGACA
                                     A  ATTTAC
GAM72   MDS031    3'  ACAGTGGTAATGAAACATT   37468      CCAGG
                                AATG    TATTACCACTGT
                                ||||    ||||||||||||
                                TTAC    GTAATGGTGACA
                                  AAA__
GAM72   SNRK      3'  ACAGTGAGTGTCTGCACTGAG  34763      A   C  GT   AC
                                CTCA TGC AG  ATT  CACTGT
                                |||| ||| ||  |||  ||||||
                                GAGT ACG TC  TGA  GTGACA
                                  C   _  TG   __
GAM72   LOC145225 3'  ACAGCAATAATACCTAGGGAG  83299     AATG  _       CCA
                                CTC    CC AGGTATTA   CTGT
                                |||    || ||||||||   ||||
                                GAG    GG TCCATAAT   GACA
                                  _____  A       AAC
GAM72   LOC145624 5'  AATACCTGGCATAGAG      83403     A
                                CTC ATGCCAGGTATT
                                ||| ||||||||||||
                                GAG TACGGTCCATAA
                                  A
GAM72   LOC150005 3'  ACAGTGGTGGTATCCACCACTG 84814      A  CCA
            AG                    CTCA TG   GGTATTACCACTGT
                                |||| ||   ||||||||||||||
                                GAGT AC   CTATGGTGGTGACA
                                  C  CAC
GAM72   LOC158835 3'  ACAGCCCCATCTCCCGGCATTG 82006         A  TATTACCA
            AG                    CTCAATGCC GG       CTGT
                                |||||||||  ||       ||||
                                GAGTTACGG CC       GACA
                                     C  TCTACCCC
GAM72   LOC197201 3'  ACAGTACCTTACCTGGCTCTGA 87928      AT       TTACC
            G                     CTCA  GCCAGGTA     ACTGT
                                ||||  ||||||||     |||||
                                GAGT  CGGTCCAT     TGACA
                                  CT       TCCA_
GAM72   LOC200078 3'  ACAGTGGGGCATCCGGCACTGA 88569     A    A  TATTA
                                TCA TGCC GG     CCACTGT
                                ||| |||| ||     |||||||
                                AGT ACGG CC     GGTGACA
                                  C    _  TACGG
GAM72   LOC220739 3'  AGTGCCTGGCACTGAG      92923      A
                                CTCA TGCCAGGTATT
                                |||| ||||||||||
```

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                                GAGT ACGGTCCGTGA
                                  C
GAM72   LOC221322 5'  GCAGCAGGTGGCATTG     91930       AGGTATT   A_
                                CAATGCC      ACC  CTGT
                                |||||||      |||  ||||
                                GTTACGG      TGG  GACG
                                   ________  AC
GAM72   LOC91351  3'  ACAATGTAGTCCTGGCATT   65703        T    CAC
                                AATGCCAGG ATTAC   TGT
                                ||||||||| |||||   |||
                                TTACGGTCC TGATG   ACA
                                     _    TA_
GAM73   ARHGEF6   3'  CAAACTTGAAGCCAGGC     68197       ACCA
                                GCCTGG    CAAGTTTG
                                ||||||    ||||||||
                                CGGACC    GTTCAAAC
                                   GAA_
GAM73   CNTN2     3'  GTCACAACCCAGGTGA      17411       ACCACAA  _
                                TCGCCTGG      GTT TGAC
                                ||||||||      ||| ||||
                                AGTGGACC      CAA ACTG
                                   ________  C
GAM73   CORO2A    3'  AAACTGTGGTCCAGAGA     12642    GC        A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM73   CORO2A    3'  AAACTGTGGTCCAGAGA     53398    GC        A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM73   GRLF1     3'  AGGTCAGAAAGTGGCCCAGG   78551      A   AAG
                                CCTGG CCAC   TTTGACCT
                                ||||| ||||   ||||||||
                                GGACC GGTG   AGACTGGA
                                   C    AA_
GAM73   LAPTM5    3'  AGGCTTGTGGTCAAGC      22199    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCGGA
                                 AA_
GAM73   POU2AF1   3'  AGATTTACAGTCCAGGC     20647        CAC
                                GCCTGGAC   AAGTTT
                                ||||||||   ||||||
                                CGGACCTG   TTTAGA
                                     ACA
GAM73   PTGS1     3'  GTCTCCTGTCTTATGGTCCAG 54574        C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
```

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                                GACCTGGT TTC     CTG
                                    A   TGTCCT
GAM73   PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  6355        C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                    A   TGTCCT
GAM73   TRIM34   5'  AGGTCAAGTTGAGCCCAG    55224     ACCA   G
                                CTGG    CAA TTTGACCT
                                ||||    ||| ||||||||
                                GACC    GTT GAACTGGA
                                  CGA_   _
GAM73   TRIM9    5'  AGGCCAGGCAAGTCCAGGC   30749       CACAA    A
                                GCCTGGAC    GTTTG CCT
                                ||||||||    ||||| |||
                                CGGACCTG    CGGAC GGA
                                    AA___    C
GAM73   ABLIM    5'  GATATGTAACCCAGGCGG    22030       ACC   A
                                TCGCCTGG   ACA GTT
                                ||||||||   ||| |||
                                GGCGGACC   TGT TAG
                                    CAA   A
GAM73   AMOT     3'  AGGCATCTTCATGGTCCAGGGA 55716    G       C_   TT  A
                                TC CCTGGACCA  AAG  TG CCT
                                || |||||||||  |||  || |||
                                AG GGACCTGGT  TTC  AC GGA
                                 _       AC   T_ _
GAM73   DKFZp434D177 5'  TTAGACCCAGGCGA       50056       ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                    ________
GAM73   DKFZp434D177 5'  TTAGACCCAGGCGA       79443       ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                    ________
GAM73   FLJ23420  3'  CAAGTGGGTCCAGGC       46845        A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                    _ __
GAM73   HSA249128 5'  GGCGCGGTCCAGGCGG      34152         ACAA
                                TCGCCTGGACC    GTT
                                ||||||||||    |||
                                GGCGGACCTGG    CGG
                                      CG__
GAM73   MGC15668  5'  AGACCCGGTGGTCCAGACG   51277    C       AA_
                                CG CTGGACCAC   GTTT
                                || |||||||||   ||||
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                                GC GACCTGGTG   CAGA
                                 A        GCC
GAM73   MGC22014  3' AGGTCCCGAGTGTAACCCAGGT 64486        ACC   AGTTT
            GA                    TCGCCTGG   ACA    GACCT
                                  ||||||||   |||    |||||
                                  AGTGGACC   TGT    CTGGA
                                       CAA   GAGCC
GAM73   SDCCAG10  5' AGAGTTGTGGTCCAAAGA    19641    GCC        G
                                  TC   TGGACCACAA TTT
                                  ||   |||||||||| |||
                                  AG   ACCTGGTGTT AGA
                                   AA_         G
GAM73   LOC115442 3' AGGTCAGGGATGGTCCAG    72676        CAAG
                                  CTGGACCA    TTTGACCT
                                  ||||||||    ||||||||
                                  GACCTGGT    GGACTGGA
                                       AG__
GAM73   LOC129011 5' AGACCTGCGGTCCAGGC     74862         A  A
                                  GCCTGGACC CA GTTT
                                  ||||||||| || ||||
                                  CGGACCTGG GT CAGA
                                       C  C
GAM73   LOC130536 5' GCAAAGTCCAGGCG        75746         CACAAG    A
                                  CGCCTGGAC     TTTG C
                                  |||||||||     |||| |
                                  GCGGACCTG     AAAC G
                                        _______   C
GAM73   LOC149108 3' AGACTTCACTGTGGTCCA    84357         _____
                                  TGGACCACA    AGTTT
                                  |||||||||    |||||
                                  ACCTGGTGT    TCAGA
                                       CACT
GAM73   LOC221688 5' AGACTCGGGCCCAGACGA    93674     C    A  ACA
                                  TCG CTGG CC   AGTTT
                                  ||| |||| ||   |||||
                                  AGC GACC GG   TCAGA
                                    A    C  GC_
GAM73   LOC256228 5' AGACTTGTGGTCAAAGC     96233    CTG
                                  GC   GACCACAAGTTT
                                  ||   ||||||||||||
                                  CG   CTGGTGTTCAGA
                                   AAA
GAM73   LOC257441 5' TTAGACCCAGGCGA        95566         ACCACAA
                                  TCGCCTGG      GTTTGA
                                  ||||||||      ||||||
                                  AGCGGACC      CAGATT
                                        _______
GAM73   LOC91960  3' AGGTGCCTCTCGTGGTCCAAGC 67657    C       A  TTTG
                                  GC TGGACCAC AG    ACCT
                                  || |||||||| ||    ||||
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                                CG ACCTGGTG TC    TGGA
                                 A       C  TCCG
GAM73   LOC92840 3'  GTCCCTCGGGTCCAGGC     56435         ACA  TTT
                                GCCTGGACC   AG   GAC
                                |||||||||   ||   |||
                                CGGACCTGG   TC   CTG
                                     GC_  C__
GAM74   ADARB1   3'  CACACTAGGTTGTAACAG     6630      C__   _
                                CTG   CAGC TAGTGTG
                                |||   |||| |||||||
                                GAC   GTTG ATCACAC
                                  AAT   G
GAM74   ADARB1   3'  CACACTAGGTTGTAACAG     31720     C__   _
                                CTG   CAGC TAGTGTG
                                |||   |||| |||||||
                                GAC   GTTG ATCACAC
                                  AAT   G
GAM74   APPBP2   3'  TACACAGATGGCAGTG      21080        G  A
                                CACTGCCA CT GTGTG
                                |||||||| || |||||
                                GTGACGGT GA CACAT
                                     A  _
GAM74   CALD1    3'  TGTTAGCTGACAGTGGTA     52530        C     GT
                                TATCACTG CAGCTA  G
                                |||||||| ||||||  |
                                ATGGTGAC GTCGAT  T
                                     A     TG
GAM74   CALD1    3'  TGTTAGCTGACAGTGGTA     52466        C     GT
                                TATCACTG CAGCTA  G
                                |||||||| ||||||  |
                                ATGGTGAC GTCGAT  T
                                     A     TG
GAM74   CD4      3'  TACAAGGCTGGCAGTGA      5229           AG
                                TCACTGCCAGCT  TGTG
                                ||||||||||||  ||||
                                AGTGACGGTCGG  ACAT
                                      A_
GAM74   CLN5     3'  CACATTGAATGGCAGTGATA   21423          GC
                                TATCACTGCCA  TAGTGTG
                                ||||||||||  |||||||
                                ATAGTGACGGT  GTTACAC
                                      AA
GAM74   COX15    3'  TGCAGAGCTGGCAGCAATG    15197     CA       AGTG
                                TAT  CTGCCAGCT   TGCA
                                |||  |||||||||   ||||
                                GTA  GACGGTCGA   ACGT
                                  AC        G___
GAM74   DSG3     5'  TGCAGACGGCTGGCAGGATA   8687      A       A  G
                                TATC CTGCCAGCT GT TGCA
                                |||| ||||||||| || ||||
```

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                                ATAG GACGGTCGG CA ACGT
                                  _       _ G
GAM74   FBXL7    3'  TACAGCTGGCAGAGA      24553    A       A
                                TC CTGCCAGCT GTG
                                || ||||||||| |||
                                AG GACGGTCGA CAT
                                 A       _
GAM74   GOSR1    3'  TGCAAGACTGACAGTGATG   16830       C  _  AGTG
                                TATCACTG CAG CT   TGCA
                                |||||||| ||| ||   ||||
                                GTAGTGAC GTC GA   ACGT
                                     A  A ____
GAM74   HPS4     5'  TGCAGACAGCCACAGTGATA  41988       CCA  A  G
                                TATCACTG  GCT GT TGCA
                                ||||||||  ||| || ||||
                                ATAGTGAC  CGA CA ACGT
                                     AC_  _ G
GAM74   JAG1     3'  TACACTGGCAATGGTA     4001       __
                                TGCCA  GCTAGTGTG
                                |||||  |||||||||
                                ATGGT  CGGTCACAT
                                   AA
GAM74   JRKL     5'  ACAACTGGCAGTGAT      13659         CTAG
                                ATCACTGCCAG   TGT
                                ||||||||||   |||
                                TAGTGACGGTC   ACA
                                      A___
GAM74   KCNK5    3'  TACATACTGGCAACGATG   13613     AC    CTA
                                TATC  TGCCAG  GTGTG
                                ||||  ||||||  |||||
                                GTAG  ACGGTC  TACAT
                                  CA    A__
GAM74   NFRKB    5'  CACCAGGAACTGGCAGTG   20495        ___  A
                                CACTGCCAG  CT GTG
                                |||||||||  || |||
                                GTGACGGTC  GA CAC
                                     AAG  C
GAM74   PSCD4    3'  TGCAAGCACTGGTAGTGATA  25408         CTA  G
                                TATCACTGCCAG  GT TGCA
                                ||||||||||||  || ||||
                                ATAGTGATGGTC  CG ACGT
                                      A__  A
GAM74   PTPN14   3'  TGCAGGTGGCTGGCAG     18254         G G
                                CTGCCAGCTA T TGCA
                                |||||||||| | ||||
                                GACGGTCGGT G ACGT
                                      _ G
GAM74   SCD      3'  TGCTCTCAGCTGGCAGTG   17351         AGTGT
                                CACTGCCAGCT   GCA
                                ||||||||||    |||
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                                GTGACGGTCGA    CGT
                                     CTCT_
GAM74   SLC1A4   3' GCCTGCCAGCAGTGATG    11717        CA  T  TGT
                                TATCACTGC  GC AG   GC
                                |||||||||  || ||   ||
                                GTAGTGACG  CG TC   CG
                                     AC  _  ___
GAM74   UBE2G2   3' CACACTTAGTGACAGTGATG  64850        CCA   _
                                TATCACTG   GCTA GTGTG
                                ||||||||   |||| |||||
                                GTAGTGAC   TGAT CACAC
                                     AG_   T
GAM74   XT3      3' ATATGCTGGCAGCAATA    39520    CA      TA
                                TAT  CTGCCAGC  GTGT
                                |||  ||||||||  ||||
                                ATA  GACGGTCG  TATA
                                  AC       __
GAM74   AKAP6    3' CACACTTCCAGTGATA     14989        CCAGCT
                                TATCACTG    AGTGTG
                                ||||||||    ||||||
                                ATAGTGAC    TCACAC
                                     CT_____
GAM74   AP3M1    3' TGCACATTGTAACAGT     23919     CCA  T
                                ACTG   GC AGTGTGCA
                                ||||   || ||||||||
                                TGAC   TG TTACACGT
                                  AA_  _
GAM74   BET3     3' TGCACATTCAGGAGCGA    26966    A  G  AGCT
                                TC CT CC    AGTGTGCA
                                || || ||    ||||||||
                                AG GA GG    TTACACGT
                                 C  _  AC__
GAM74   C21orf58 3' GCAGCTACTGGCAGT      54194        C    G
                                ACTGCCAG TAGT TGC
                                |||||||| |||| |||
                                TGACGGTC ATCG ACG
                                     _    _
GAM74   CD36L2   3' CACGGCGCTGGCAAGTGATA  18568        _     TA_
                                TATCACT GCCAGC   GTG
                                ||||||| ||||||   |||
                                ATAGTGA CGGTCG   CAC
                                     A      CGG
GAM74   DKFZp434P2235 5' CACACAGGCAGTGGTA     50039          AGCTA
                                TATCACTGCC    GTGTG
                                ||||||||||    |||||
                                ATGGTGACGG    CACAC
                                     A_____
GAM74   DKFZp761H079 3' CACAGCGACCTAACAGTGATG  58731        CCA____   A
                                TATCACTG      GCT GTG
                                ||||||||      ||| |||
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                                GTAGTGAC      CGA CAC
                                    AATCCAG  _
GAM74   FLJ10540  3'  TGCATTTCTCTTGGCAGTGATA 36260          CTAGT
                                TATCACTGCCAG    GTGCA
                                ||||||||||||    |||||
                                ATAGTGACGGTT    TACGT
                                    CTCTT
GAM74   FLJ13964  3'  TGCACATGGGGCAGTGGTA   49795         AGCTA
                                TATCACTGCC    GTGTGCA
                                ||||||||||    |||||||
                                ATGGTGACGG    TACACGT
                                    GG___
GAM74   FLJ20081  3'  TGCACACTAACCTGGGTGA   34510     TG   C_
                                TCAC  CCAG  TAGTGTGCA
                                ||||  ||||  |||||||||
                                AGTG  GGTC  ATCACACGT
                                  __   CA
GAM74   FLJ20871  3'  CGCACTAGCATGTGATA    42027      TGCCA
                                TATCAC    GCTAGTGTG
                                ||||||    |||||||||
                                ATAGTG    CGATCACGC
                                   TA___
GAM74   FLJ20896  3'  TACTACTCGCAGTGATA    44813        C  C
                                TATCACTGC AG TAGTG
                                |||||||||  ||  |||||
                                ATAGTGACG TC ATCAT
                                    C  _
GAM74   FLJ32449  3'  TGCACACTAGGGGCA      58725     AG
                                TGCC  CTAGTGTGCA
                                ||||  ||||||||||
                                ACGG  GATCACACGT
                                  G_
GAM74   GR6       3'  CACACAGCAGGCAGTGG    23727        A   A
                                TCACTGCC GCT GTGTG
                                ||||||||  |||  |||||
                                GGTGACGG CGA CACAC
                                    A   _
GAM74   GT650     5'  TATTAGCTGGCAGAGATA   53457     A
                                TATC CTGCCAGCTAGTG
                                ||||  ||||||||||||
                                ATAG GACGGTCGATTAT
                                  A
GAM74   KIAA0063  5'  GCACTTTGACAGTGGTA    29629        C   CTAGT
                                TATCACTG CAG    GTGC
                                ||||||||  |||    ||||
                                ATGGTGAC GTT    CACG
                                    A   T_____
GAM74   KIAA0451  3'  CACCAGGGGCTGGCAGCAGTA 29103     CA       AGT_
                                TAT  CTGCCAGCT    GTG
                                |||  |||||||||    |||
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                                ATG  GACGGTCGG   CAC
                                  AC       GGAC
GAM74   KIAA1037 3' TGCCCTTTAGCTGGCAG    30436         TGT
                                CTGCCAGCTAG   GCA
                                ||||||||||   |||
                                GACGGTCGATT   CGT
                                      TCC
GAM74   KIAA1399 3' CACGGGTGAGCTGGCAGGGA  70247   A      AG__
                                TC CTGCCAGCT   TGTG
                                || |||||||||   ||||
                                AG GACGGTCGA   GCAC
                                 G       GTGG
GAM74   KIAA1483 3' GCAGCTGCCAGTGATA     69872       C    A
                                TATCACTG CAGCT GT
                                |||||||| ||||| ||
                                ATAGTGAC GTCGA CG
                                     C    _
GAM74   KIAA1617 3' TGCCCTAGCTGGCAG      91435         TGT
                                CTGCCAGCTAG   GCA
                                ||||||||||   |||
                                GACGGTCGATC   CGT
                                      C__
GAM74   KIAA1819 5' TGCACATTTTGAACAGTGA   69681      CCAGCT
                                TCACTG     AGTGTGCA
                                ||||||     ||||||||
                                AGTGAC     TTACACGT
                                   AAGTT_
GAM74   KIAA1950 3' CACGGCGGCAGTGA       92588       A  A
                                TCACTGCC GCT GTG
                                |||||||| ||| |||
                                AGTGACGG CGG CAC
                                      _  _
GAM74   LHX9     3' GCAACCTGGCAGTAATA     84176     C      CTA  G
                                TAT ACTGCCAG   GT TGC
                                ||| ||||||||   || |||
                                ATA TGACGGTC   CA ACG
                                  A       ___  _
GAM74   MGC5508  3' CACAGCTGCAGTGATA      44032       C    A
                                TATCACTGC AGCT GTG
                                ||||||||| |||| |||
                                ATAGTGACG TCGA CAC
                                      _   _
GAM74   NCOA5    5' CGCGCTGGTAGCGATA      40584     A      TA
                                TATC CTGCCAGC  GTG
                                |||| ||||||||  |||
                                ATAG GATGGTCG  CGC
                                  C       __
GAM74   RGPR     3' TGCACATGAGCAGAGTGA    52421      GCCA  A
                                TCACT    GCT GTGTGCA
                                |||||    ||| |||||||
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                                AGTGA   CGA TACACGT
                                  GA__  G
GAM74   RNB6     3'  CGCCTCAGCTGGCGGTGA    32929          _ T
                                TCACTGCCAGCT AG GTG
                                |||||||||||| || |||
                                AGTGGCGGTCGA TC CGC
                                       C  _
GAM74   Rpo1-2   3'  TACACTGGCTATGATA     38710      CTGCC
                                TATCA    AGCTAGTGTG
                                |||||    ||||||||||
                                ATAGT    TCGGTCACAT
                                  A____
GAM74   RYBP     5'  TGCACAGCAGTTGGCAGT    59472         AG
                                ACTGCCAGCT  TGTGCA
                                |||||||||  ||||||
                                TGACGGTTGA  ACACGT
                                     CG
GAM74   TA-KRP   3'  GCACTTAACAGTGATG     50692       CCAGC  T
                                TATCACTG    TAG GTGC
                                ||||||||    ||| ||||
                                GTAGTGAC    ATT CACG
                                    A____  _
GAM74   TRAF4    3'  TGCCCTAAGCTGGCAATGG   62632    C      _ TGT
                                TCA TGCCAGCT AG  GCA
                                ||| |||||||| ||  |||
                                GGT ACGGTCGA TC  CGT
                                  A      A  C__
GAM74   WDR9     3'  TACACAAGTAAACTGGCAGT  38557       ____ A
                                ACTGCCAG   CT GTGTG
                                ||||||||   || |||||
                                TGACGGTC   GA CACAT
                                    AAAT  A
GAM74   LOC121536 3'  CACTTTACTACAGTGATA    74084       CC  CT_
                                TATCACTG  AG  AGTG
                                |||||||  ||  ||||
                                ATAGTGAC  TC  TCAC
                                    A_  ATT
GAM74   LOC143903 3'  TTACCTGGCAGTGATA     76623          C
                                TATCACTGCCAG TAG
                                |||||||||||| |||
                                ATAGTGACGGTC ATT
                                       C
GAM74   LOC146782 5'  CACACAGGCAGTGGTA     76291         AGCTA
                                TATCACTGCC   GTGTG
                                ||||||||||   |||||
                                ATGGTGACGG   CACAC
                                      A____
GAM74   LOC147136 3'  TGCCTGAGCCGGCAGTGATG  78271         A  AGTGT
                                TATCACTGCC GCT   GCA
                                |||||||||| |||   |||
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                                GTAGTGACGG CGA    CGT
                                      C  GTC__
GAM74   LOC148397 5' CGCAGCTGGCAATGG      78815    C      A
                                TCA TGCCAGCT GTG
                                ||| |||||||| |||
                                GGT ACGGTCGA CGC
                                  A      _
GAM74   LOC149566 5' TGCACTCCGTGACAGTGGTA  84495       CCA  TAGT
                                TATCACTG  GC   GTGCA
                                ||||||||  ||   |||||
                                ATGGTGAC  TG   CACGT
                                     AG_  CCT_
GAM74   LOC153339 3' TGCACAAGAAGCAGTGATG   86016       CAG  AG
                                TATCACTGC  CT  TGTGCA
                                |||||||||  ||  ||||||
                                GTAGTGACG  GA  ACACGT
                                      AA_  __
GAM74   LOC157621 5' TGCATGTGCCAGCAGTGAT   86497       CA  TA TG
                                ATCACTGC  GC  G  TGCA
                                ||||||||  ||  |  ||||
                                TAGTGACG  CG  T  ACGT
                                     AC  __ GT
GAM74   LOC157622 5' TGCATGTGCCAGCAGTGAT   86503       CA  TA TG
                                ATCACTGC  GC  G  TGCA
                                ||||||||  ||  |  ||||
                                TAGTGACG  CG  T  ACGT
                                     AC  __ GT
GAM74   LOC157653 5' CACACAGAGTTGGCAG      81523        A_
                                CTGCCAGCT  GTGTG
                                |||||||||  |||||
                                GACGGTTGA  CACAC
                                      GA
GAM74   LOC163882 3' CAGACATGCTGGCAGTGA    82164         TA  G
                                TCACTGCCAGC  GT TG
                                ||||||||||  || ||
                                AGTGACGGTCG  CA AC
                                       TA  G
GAM74   LOC196527 3' CACGGCTGACTTGCAGTGATA 87754         ____    A
                                TATCACTGC   CAGCT GTG
                                |||||||||   ||||| |||
                                ATAGTGACG   GTCGG CAC
                                      TTCA   _
GAM74   LOC196812 5' CACTGGCTAACAGTGAT     89566       CC
                                ATCACTG  AGCTAGTG
                                |||||||  ||||||||
                                TAGTGAC  TCGGTCAC
                                    AA
GAM74   LOC219562 5' CACACAGGCAGTGGTA      90768         AGCTA
                                TATCACTGCC    GTGTG
                                |||||||||    |||||
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                                ATGGTGACGG    CACAC
                                    A____
GAM74   LOC221042 3'  TGCACGGCTCTGGCAGTG    93193        CT  _
                                CACTGCCAG  AGT GTGCA
                                |||||||||  ||| |||||
                                GTGACGGTC  TCG CACGT
                                    __  G
GAM74   LOC221641 3'  TGCACACTAGCCTGGGTGA   93731     TG   _
                                TCAC  CCAG CTAGTGTGCA
                                ||||  |||| ||||||||||
                                AGTG  GGTC GATCACACGT
                                  __   C
GAM74   LOC255798 3'  TACACAAGACAGTGATA     97007        CCAG  A
                                TATCACTG    CT GTGTG
                                ||||||||    || |||||
                                ATAGTGAC    GA CACAT
                                    A___  A
GAM74   LOC257181 5'  CACACAGGCAGTGGTA      94591         AGCTA
                                TATCACTGCC    GTGTG
                                ||||||||||    |||||
                                ATGGTGACGG    CACAC
                                    A____
GAM74   LOC51157  5'  GCACAAAGGGTAACAAGCAGTG 32489        CA___  AG_
           ATA                    TATCACTGC    GCT   TGTGC
                                |||||||||    |||  |||||
                                ATAGTGACG    TGG   ACACG
                                    AACAA   GAA
GAM74   LOC90538  3'  TGCTGTGCTGGCAGTGA     63198         _
                                TCACTGCCAGC TAGTG
                                |||||||||| |||||
                                AGTGACGGTCG GTCGT
                                    T
GAM74   LOC91351  3'  TACACTTCCTGGCAGTGAT   65708         CT
                                ATCACTGCCAG  AGTGTG
                                ||||||||||  ||||||
                                TAGTGACGGTC  TCACAT
                                    CT
GAM74   LOC91813  5'  CGCTGGCTGCAGCGA      67249    A   C
                                TC CTGC AGCTAGTG
                                || |||| ||||||||
                                AG GACG TCGGTCGC
                                 C   _
GAM74   LOC93333  5'  CAAAAGCTGGCAGAGATA    72064     A       AG
                                TATC CTGCCAGCT  TG
                                |||| |||||||||  ||
                                ATAG GACGGTCGA  AC
                                  A       AA
GAM76   ADD2     3'  TTGGGCTCCCTCCTGCCT    33966    AA    T
                                AG  GGGAG GAGCCCAA
                                ||  ||||| ||||||||
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                                TC  TCCTC CTCGGGTT
                                 CG    C
GAM76   ADD2    3'  TTGGGCTCCCTCCTGCCT   33949   AA   T
                                AG  GGGAG GAGCCCAA
                                ||  ||||| ||||||||
                                TC  TCCTC CTCGGGTT
                                 CG    C
GAM76   ADD2    3'  TTGGGCTCCCTCCTGCCT   33938   AA   T
                                AG  GGGAG GAGCCCAA
                                ||  ||||| ||||||||
                                TC  TCCTC CTCGGGTT
                                 CG    C
GAM76   ADD2    3'  TTGGGCTCCCTCCTGCCT   33955   AA   T
                                AG  GGGAG GAGCCCAA
                                ||  ||||| ||||||||
                                TC  TCCTC CTCGGGTT
                                 CG    C
GAM76   ADRB3   3'  TTGAACTTCACTCCTCCCTCA  3440   C  AA      CC_
                                A AG  GGGAGTGAG   CAA
                                | ||  |||||||||   |||
                                A TC  TCCTCACTT   GTT
                                 C  CC       CAA
GAM76   ATP8B2  3'  CTCTGCTCCCTTCTTC     65223   C       _
                                GA AGAAGGGAGT GAG
                                || ||||||||| |||
                                CT TCTTCCCTCG CTC
                                  _       T
GAM76   BLTR2   5'  CTTTGGACTGATCACCCT   39040    A_  G  C
                                AGGG  GT AG CCAAAG
                                ||||  || || ||||||
                                TCCC  TA TC GGTTTC
                                   AC  G  A
GAM76   BRIP1   3'  TGGGCTCACTGCAACCTTC  49402     G___
                                GAAGG   AGTGAGCCCA
                                |||||   ||||||||||
                                CTTCC   TCACTCGGGT
                                   AACG
GAM76   BSN     3'  TGGGCTCCGTTTCCTTC    12930      GT_
                                GAAGGGA  GAGCCCA
                                |||||||  |||||||
                                CTTCCTT  CTCGGGT
                                    TGC
GAM76   C21orf2 3'  GGACTCCCCTTCTGTGG    17013   G      AGT  C
                                C ACAGAAGGG  GAG CC
                                | |||||||||  ||| ||
                                G TGTCTTCCC  CTC GG
                                 G       ___  A
GAM76   CD28    3'  TGGGCTCAGCTGCTCCTGT   20442    AA  G  _
                                ACAG  GG AG TGAGCCCA
                                ||||  || || ||||||||
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                                TGTC  TC TC ACTCGGGT
                                  C_  G  G
GAM76   CYP27A1  3'  TGAGCTTTTGCCACTTCTATC  5774     C    _ AGT   C
                                GA AGAAG GG   GAGC CA
                                || ||||| ||   |||| ||
                                CT TCTTC CC   TTCG GT
                                 A    A  GTT    A
GAM76   DGAT2    3'  GTTTGATCTCCCTTCTG     50790          T__
                                CAGAAGGGAG   GAGC
                                ||||||||||   ||||
                                GTCTTCCCTC   TTTG
                                      TAG
GAM76   DGKG     5'  GGTCCCCCTTCTGTC       7207           AGT  G
                                GACAGAAGGG   GA CC
                                ||||||||||   || ||
                                CTGTCTTCCC   CT GG
                                      C__  _
GAM76   DSC3     3'  TGGGCCCCCTTCTTTCG     8683      C      AGTGA
                                CGA AGAAGGG    GCCCA
                                ||| |||||||    |||||
                                GCT TCTTCCC    CGGGT
                                  T      C____
GAM76   DSC3     3'  TGGGCCCCCTTCTTTCG     44348     C      AGTGA
                                CGA AGAAGGG    GCCCA
                                ||| |||||||    |||||
                                GCT TCTTCCC    CGGGT
                                  T      C____
GAM76   DYSF     3'  TGAGATCACCCCACTTCCATC  13021    CA   _ A   GCC
                                GA  GAAG GG GTGA   CA
                                ||  |||| || ||||   ||
                                CT  CTTC CC CACT   GT
                                 AC    A  C    AGA
GAM76   FOSB     3'  CTCGGTCTCCCTTCCGTC    22103     A      __
                                GAC GAAGGGAG  TGAG
                                ||| ||||||||  ||||
                                CTG CTTCCCTC  GCTC
                                  C       TG
GAM76   GGT2     5'  TGGGCTCGCCTCTTC       73713       A
                                GAAGGG GTGAGCCCA
                                |||||| |||||||||
                                CTTCTC CGCTCGGGT
                                     _
GAM76   GPR56    3'  TGGTCACTCCTCCTG       19077     AA       GC
                                CAG  GGGAGTGA  CCA
                                |||  ||||||||  |||
                                GTC  TCCTCACT  GGT
                                  C_       __
GAM76   JRK      3'  TGGGCCCATTTCCTCTCTCG  86539     C  A      A
                                CGA AGA GGGAGTG GCCCA
                                ||| ||| ||||||| |||||
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                                GCT TCT CCTTTAC CGGGT
                                  C  _     C
GAM76   KMO     3'  CTTTGGACCCATTGGTTTTGTC 13449        GGG   AGC
                G                  CGACAGAA  AGTG  CCAAAG
                                   ||||||||  ||||  ||||||
                                   GCTGTTTT  TTAC  GGTTTC
                                       GG_   CCA
GAM76   LPO     3'  GGCTTCTCCTTTCTGTC     67867          T
                                   GACAGAAGGGAG GAGCC
                                   ||||||||||| |||||
                                   CTGTCTTTCCTC TTCGG
                                             _
GAM76   MME     3'  CTTTGGGCCTCTGCTTCTCTC  6142     C    _   TGA
                                   GA AGAAG GGAG  GCCCAAAG
                                   || ||||| ||||  ||||||||
                                   CT TCTTC TCTC  CGGGTTTC
                                    C    G   ___
GAM76   MME     3'  CTTTGGGCCTCTGCTTCTCTC  23489    C    _   TGA
                                   GA AGAAG GGAG  GCCCAAAG
                                   || ||||| ||||  ||||||||
                                   CT TCTTC TCTC  CGGGTTTC
                                    C    G   ___
GAM76   MME     3'  CTTTGGGCCTCTGCTTCTCTC  23510    C    _   TGA
                                   GA AGAAG GGAG  GCCCAAAG
                                   || ||||| ||||  ||||||||
                                   CT TCTTC TCTC  CGGGTTTC
                                    C    G   ___
GAM76   MME     3'  CTTTGGGCCTCTGCTTCTCTC  23499    C    _   TGA
                                   GA AGAAG GGAG  GCCCAAAG
                                   || ||||| ||||  ||||||||
                                   CT TCTTC TCTC  CGGGTTTC
                                    C    G   ___
GAM76   MMP2    3'  CTTCAGGCTCTTCTCCTTTC  15765        T_    CA
                                   GAAGGGAG  GAGCC  AAG
                                   ||||||||  |||||  |||
                                   CTTTCCTC  CTCGG  TTC
                                       TT    AC
GAM76   NEURL   3'  TGGGAGACCCCTTCTGT    14866         A  GAG
                                   ACAGAAGGG GT   CCCA
                                   |||||||| ||   ||||
                                   TGTCTTCCC CA   GGGT
                                        _ GA_
GAM76   NR0B2   3'  TGGGCCAAGACTCCTGTC   41742       A  GGAG  A
                                   GACAG AG    TG GCCCA
                                   ||||| ||    || |||||
                                   CTGTC TC    AC CGGGT
                                     C  AGA_ _
GAM76   OSR1    3'  GGCACCCCCTTCTTC       17567    C      A  GA
                                   GA AGAAGGG GT  GCC
                                   || ||||||| ||  |||
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                                CT TCTTCCC CA  CGG
                                 _      C  __
GAM76   PIK3C2B  3'  TGGAAAGCATTCCCCATCCATC 10580    CA  A_      AGC_
                                GA  GA  GGGAGTG    CCA
                                ||  ||  |||||||    |||
                                CT  CT  CCCTTAC    GGT
                                 AC  AC      GAAA
GAM76   POLR2C   3'  CTCTAAACCCTTTCTGTC    10684          A  ___
                                GACAGAAGGG GT   GAG
                                |||||||||| ||   |||
                                CTGTCTTTCC CA   CTC
                                      _ AAT
GAM76   PTBP1    3'  GGGCCTTCCCTTCTG       11009          TGA
                                CAGAAGGGAG   GCCC
                                ||||||||||   ||||
                                GTCTTCCCTT   CGGG
                                      C__
GAM76   PTBP1    3'  GGGCCTTCCCTTCTG       49254          TGA
                                CAGAAGGGAG   GCCC
                                ||||||||||   ||||
                                GTCTTCCCTT   CGGG
                                      C__
GAM76   RAB36    3'  CTTCAGGCCTCACTGTCCTTCT 16960         _     _ CA
           G                     CAGAAGGG AGTGAG CC  AAG
                                ||||||||| |||||| ||  |||
                                GTCTTCCT TCACTC GG  TTC
                                     G     C  AC
GAM76   SLC7A6   3'  CTTTGGGCTCAGAAATGTCTGT 14305   G    AGGGAG
           GG                    C ACAGA     TGAGCCCAAAG
                                | |||||      ||||||||||
                                G TGTCT     ACTCGGGTTTC
                                 G    GTAAAG
GAM76   TARBP2   3'  TGGGCTCATGTATCTGCG    14811    A   AGGGA
                                CG CAGA    GTGAGCCCA
                                || ||||    |||||||||
                                GC GTCT    TACTCGGGT
                                 _   ATG__
GAM76   TARBP2   3'  TGGGCTCATGTATCTGCG    56171    A   AGGGA
                                CG CAGA    GTGAGCCCA
                                || ||||    |||||||||
                                GC GTCT    TACTCGGGT
                                 _   ATG__
GAM76   TARBP2   3'  TGGGCTCATGTATCTGCG    56163    A   AGGGA
                                CG CAGA    GTGAGCCCA
                                || ||||    |||||||||
                                GC GTCT    TACTCGGGT
                                 _   ATG__
GAM76   UBE2I    5'  TGGGCTCGAACCCTGCCTG   12495     A_   AG
                                CAG  AGGG  TGAGCCCA
                                |||  ||||  ||||||||
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                                GTC  TCCC  GCTCGGGT
                                  CG   AA
GAM76   VPREB3   3'  TGAGCCTTGCTTCCCCTCTGT  25385      A   _ TG  _ C
                                ACAGA GGGA G  AG C CA
                                ||||| |||| |  || | ||
                                TGTCT CCCT C  TC G GT
                                   C   T GT  C A
GAM76   AP1GBP1  3'  CTTAGATCTCCCTTCCATTG  54519    CA      ___
                                CGA  GAAGGGAG  TGAG
                                |||  ||||||||  ||||
                                GTT  CTTCCCTC  ATTC
                                  AC      TAG
GAM76   AP1GBP1  3'  CTTAGATCTCCCTTCCATTG  23393    CA      ___
                                CGA  GAAGGGAG  TGAG
                                |||  ||||||||  ||||
                                GTT  CTTCCCTC  ATTC
                                  AC      TAG
GAM76   AP1GBP1  3'  CTTAGATCTCCCTTCCATTG  54531    CA      ___
                                CGA  GAAGGGAG  TGAG
                                |||  ||||||||  ||||
                                GTT  CTTCCCTC  ATTC
                                  AC      TAG
GAM76   BRPF3    3'  GCTCACACTCTCTCCCG    92319    AC  A  A
                                CG  AGA GGG GTGAGC
                                ||  ||| ||| ||||||
                                GC  TCT CTC CACTCG
                                 CC  _  A
GAM76   C1orf8   5'  TGGGCTACTTCTTC       16833      G  G
                                GAAGG AGT AGCCCA
                                ||||| ||| ||||||
                                CTTCT TCA TCGGGT
                                   _  _
GAM76   C20orf141 5'  TGAGCTCACCCTTCTGTC    54950        AG    C
                                GACAGAAGGG  TGAGC CA
                                ||||||||||  ||||| ||
                                CTGTCTTCCC  ACTCG GT
                                     __    A
GAM76   CARD14   5'  CTTCAGGCTCTTCCTTCTG   44106       GT    CA
                                CAGAAGGGA  GAGCC  AAG
                                |||||||||  |||||  |||
                                GTCTTCCTT  CTCGG  TTC
                                     __    AC
GAM76   CECR6    3'  TTGTCTTCTACCTTCTGTC   49093       GAGT   CC
                                GACAGAAGG   GAG  CAA
                                |||||||||   |||  |||
                                CTGTCTTCC   CTT  GTT
                                    AT__   CT
GAM76   CECR7    5'  CTTCAGGCCTTCCCTTCT    79621       TGA   CA
                                AGAAGGGAG   GCC  AAG
                                |||||||||   |||  |||
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                                TCTTCCCTT  CGG  TTC
                                     C__  AC
GAM76  COLEC10  3'  TTTGAACCCCTTTCTGT    21231        A  GAGCC
                                ACAGAAGGG GT    CAAA
                                ||||||||| ||    ||||
                                TGTCTTTCC CA    GTTT
                                     C  A____
GAM76  DKFZp434F2322 3'  TTGGTGCACCGCTTCTGTCG  69738        _  AGTGA  _
                                CGACAGAAG GG    GC CCAA
                                ||||||||| ||    || ||||
                                GCTGTCTTC CC    CG GGTT
                                     G  A____  T
GAM76  DKFZP434K028 3'  GCCACCCCCTCCTGTC     93234      A   A   A
                                GACAG AGGG GTG GC
                                ||||| |||| ||| ||
                                CTGTC TCCC CAC CG
                                   C   C  _
GAM76  DKFZP727G051 3'  GGCTCGTTACCCCTGT     69473     AA  _
                                ACAG  GGG AGTGAGCC
                                ||||  ||| ||||||||
                                TGTC  CCC TTGCTCGG
                                   __  A
GAM76  EBNA1BP2  3'  CTTTGATCCCTTCTGTTG    22389          GT_
                                CGACAGAAGGGA  GAG
                                ||||||||||||  |||
                                GTTGTCTTCCCT  TTC
                                      AGT
GAM76  ECE2     3'  GGCTCACTCAGCCTGGCG    28068    A  AAGG
                                CG CAG   GAGTGAGCC
                                || |||   |||||||||
                                GC GTC   CTCACTCGG
                                 G  CGA_
GAM76  FLJ10849  3'  TGAACTCACTGTCTTTTCTC  36758    C     G     CC
                                GA AGAAGG AGTGAG  CA
                                || |||||| ||||||  ||
                                CT TTTTCT TCACTC  GT
                                 C     G     AA
GAM76  FLJ11722  3'  TTGGGCTCCAGCCCTCTG    46402     A  AGT
                                CAGA GGG   GAGCCCAA
                                |||| |||   ||||||||
                                GTCT CCC   CTCGGGTT
                                   _  GAC
GAM76  FLJ12287  3'  CTTTGGACACCAACACTCCCTT 42314          AGC____
          CT                     AGAAGGGAGTG      CCAAAG
                                ||||||||||||      ||||||
                                TCTTCCCTCAC      GGTTTC
                                      AACCACA
GAM76  FLJ12287  3'  TGGGACTCCCTTCT       42321          GAG
                                AGAAGGGAGT   CCCA
                                ||||||||||   ||||
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                                TCTTCCCTCA  GGGT
                                    ___
GAM76   FLJ12443 3' TGGGCTCCGCTCCTCA     45733   A     _
                                A GGGAGTG AGCCCA
                                | ||||||| ||||||
                                A TCCTCGC TCGGGT
                                 C      C
GAM76   FLJ12816 3' TGGGCTCCTTTTCT       41936       AGT
                                AGAAGGG  GAGCCCA
                                |||||||  |||||||
                                TCTTTTC  CTCGGGT
                                   ___
GAM76   FLJ13158 3' CTCAGACCCTCTCTTCCATTG 46110    CA      ____
                                CGA  GAAGGGAG   TGAG
                                |||  ||||||||   ||||
                                GTT  CTTCTCTC   ACTC
                                  AC       CCAG
GAM76   FLJ13204 5' GCTCACCATTTTCTTTCG    45418    C    GA
                                CGA AGAAGG  GTGAGC
                                ||| ||||||  ||||||
                                GCT TCTTTT  CACTCG
                                  T     AC
GAM76   FLJ20208 3' GGGCTCCACACTTCCATCT   34746    A    ___
                                AGA GGGAGT   GAGCCC
                                ||| ||||||   ||||||
                                TCT CCTTCA   CTCGGG
                                  A     CAC
GAM76   FLJ20507 3' TGGGCTCTCTTCCTC      35304    A    T
                                GA GGGAG GAGCCCA
                                || ||||| |||||||
                                CT CCTTC CTCGGGT
                                 _    T
GAM76   FLJ20507 3' TGGGCTCTCTTCCTC      60239    A    T
                                GA GGGAG GAGCCCA
                                || ||||| |||||||
                                CT CCTTC CTCGGGT
                                 _    T
GAM76   GOLGB1   3' TTTGGACCACTCCCTTC    15636         AGC
                                GAAGGGAGTG   CCAAA
                                ||||||||||   |||||
                                CTTCCCTCAC   GGTTT
                                      CA_
GAM76   KIAA0057 3' GGCCACCTCCTGTC       24437      AA   A   A
                                GACAG  GGG GTG GCC
                                |||||  ||| ||| |||
                                CTGTC  CTC CAC CGG
                                   __  _  _
GAM76   KIAA0152 3' CTTTGGGCTTTCTCCTTCTGTG 28299   G      G  T
            G                    C ACAGAAGG AG GAGCCCAAAG
                                | ||||||| || ||||||||||
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                                G TGTCTTCC TC TTCGGGTTTC
                                 G       _ T
GAM76   KIAA0443 5' TGGAGGACCCCCTTCTGTC   28185         A  GAGC
                                GACAGAAGGG GT    CCA
                                |||||||||| ||    |||
                                CTGTCTTCCC CA    GGT
                                      C  GGA_
GAM76   KIAA0444 3' CTTTGGGCCTGGGCCCCCTG  62344     AA   AG GA
                                CAG  GGG  T  GCCCAAAG
                                |||  |||  |  ||||||||
                                GTC  CCC  G  CGGGTTTC
                                  C_   GG TC
GAM76   KIAA0595 3' TTGGGCCCTTCCCTGCT     30500    A     TGA
                                AG AGGGAG   GCCCAA
                                || ||||||   ||||||
                                TC TCCCTT   CGGGTT
                                 G     CC_
GAM76   KIAA0819 3' TTCAAACCCTTTTTGTC     63584          AG_
                                GACAGAAGGG   TGAG
                                ||||||||||   ||||
                                CTGTTTTTCC   ACTT
                                      CAA
GAM76   KIAA1399 3' TGGACCCCTCCTGCTCG     70254     _  A    A  GAGC
                                CGA CAG AGGG GT    CCA
                                ||| ||| |||| ||    |||
                                GCT GTC TCCC CA    GGT
                                  C   C    _ _____
GAM76   KIAA1538 5' TTCAAGTCCCTTCTTC      71561    C       G_
                                GA AGAAGGGA  TGAG
                                || ||||||||  ||||
                                CT TCTTCCCT  ACTT
                                 _       GA
GAM76   KIAA1543 5' GCCACCCGCTTCTGTC      70985         _ A   A
                                GACAGAAG GG GTG GC
                                |||||||| || ||| ||
                                CTGTCTTC CC CAC CG
                                     G  _   _
GAM76   KIAA1602 3' CTTGGTCCCTTCTCTC      64630    C       G
                                GA AGAAGGGA TGAG
                                || |||||||| ||||
                                CT TCTTCCCT GTTC
                                 C       G
GAM76   KIAA1617 3' TGAGCGTCCCTTCTGTC     91434           GTGA  C
                                GACAGAAGGGA    GC CA
                                ||||||||||    || ||
                                CTGTCTTCCCT    CG GT
                                      G___  A
GAM76   KIAA1755 3' TGAACTCAATGTCTTCTGTC  61357         GAG    CC
                                GACAGAAGG   TGAG  CA
                                |||||||||   ||||  ||
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                                CTGTCTTCT  ACTC  GT
                                     GTA   AA
GAM76  LNIR    3'  GGCCTGGCTCCTTCTGTTG  48134       G  G  C
                                CGACAGAAGG AGT AG CC
                                |||||||||| ||| || ||
                                GTTGTCTTCC TCG TC GG
                                      _  G  C
GAM76  LYPLA2  3'  TTTGGGCCCCCTCCTGT    23432    A   AGTGA
                                ACAG AGGG   GCCCAAA
                                |||| ||||   |||||||
                                TGTC TCCC   CGGGTTT
                                  C   C____
GAM76  MAPK11  3'  TTGGGCTCTCTTCTGTC    10850        GTGA
                                GACAGAAGGGA   GCCCAA
                                ||||||||||   ||||||
                                CTGTCTTCTCT   CGGGTT
                                      ____
GAM76  MGC32043 3'  TGGGCTCACTTGCCTGCCT  58058   A_  _
                                AG  AGG GAGTGAGCCCA
                                ||  ||| ||||||||||
                                TC  TCC TTCACTCGGGT
                                 CG   G
GAM76  MGC33367 3'  TTCAGGCTCCTTCTGTC    58147       GAGTG   CA
                                GACAGAAGG   AGCC  AA
                                |||||||||   ||||  ||
                                CTGTCTTCC   TCGG  TT
                                      _____   AC
GAM76  MR      5'  CTTTGGGCTTTGCTGCTGTC  48319     A  G  GTG
                                GACAG AG GA   AGCCCAAAG
                                ||||| || ||   |||||||||
                                CTGTC TC TT   TCGGGTTTC
                                   G  G  ___
GAM76  NYD-SP11 5'  GGCTCATTCCCCTGTGG    49214   G   AA
                                C ACAG  GGGAGTGAGCC
                                | ||||  ||||||||||
                                G TGTC  CCCTTACTCGG
                                 G   __
GAM76  OSBPL7  3'  GGCCATCCCTCCTGTC     34809     A   G  A
                                GACAG AGGGA TG GCC
                                ||||| ||||| || |||
                                CTGTC TCCCT AC CGG
                                   C    _ _
GAM76  PIPPIN  3'  TGGGTGCACCCCCTGCCT   79697   A_   A  A
                                AG  AGGG GTG GCCCA
                                ||  |||| ||| |||||
                                TC  TCCC CAC TGGGT
                                 CG   C  G
GAM76  PRO1866 5'  GGAGCCTCCCTTCTGTC    37551         TGA _
                                GACAGAAGGGAG   GC CC
                                ||||||||||||  || ||
```

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                                CTGTCTTCCCTC  CG GG
                                      ___ A
GAM76   PRO2521  3'  TGGGTTTTCCCTTT      37594       GT
                                GAAGGGA  GAGCCCA
                                |||||||  |||||||
                                TTTCCCT  TTTGGGT
                                   __
GAM76   PTD008   3'  GGCTTACCCCTCCTG      32350    A   A
                                CAG AGGG GTGAGCC
                                ||| |||| |||||||
                                GTC TCCC CATTCGG
                                  C   _
GAM76   SAC2     5'  GGGCGTTCCCTCTGCCG     30057    A   A   GTGA
                                CG CAGA GGGA   GCCC
                                || |||| ||||   ||||
                                GC GTCT CCCT   CGGG
                                 C   _   TG__
GAM76   SES2     3'  CTTTGCCTTCTCTCCCCTGTC  48810      AA    T   CC
                                GACAG  GGGAG GAG  CAAAG
                                |||||  ||||| |||  |||||
                                CTGTC  CCCTC CTT  GTTTC
                                   __    T   CC
GAM76   SRF      3'  TTGGTGTTTCCCTTCCTCG    11954     CA      TGA  _
                                CGA  GAAGGGAG   GC CCAA
                                |||  ||||||||   || ||||
                                GCT  CTTCCCTT   TG GGTT
                                  C_       ___  T
GAM76   SSI-1    5'  GGCTGGCCCCTTCTGT      13629         A  G
                                ACAGAAGGG GT AGCC
                                ||||||||| || ||||
                                TGTCTTCCC CG TCGG
                                      _ G
GAM76   STAF65(gamma) 3'  CTCTAAACCCTTTCTGTC    29434          A ___
                                GACAGAAGGG GT   GAG
                                |||||||||| ||   |||
                                CTGTCTTTCC CA   CTC
                                      _ AAT
GAM76   TFEC     5'  CTTTGGTTGTCCCTTCTG    24292         GTGAGC
                                CAGAAGGGA     CCAAAG
                                |||||||||     ||||||
                                GTCTTCCCT     GGTTTC
                                    GTT___
GAM76   TIGA1    5'  CTTTGGGCTCCTGCCGCTG   53801     AA  G  T
                                CAG  GG AG GAGCCCAAAG
                                |||  || || ||||||||||
                                GTC  CC TC CTCGGGTTTC
                                  G_  G  _
GAM76   TM9SF1   3'  TTTGGGCATTCCTTCCC     21137       T __
                                GGGAG GA  GCCCAAA
                                ||||| ||  |||||||
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                                CCCTT CT  CGGGTTT
                                   C  TA
GAM76   USP22    3' TGGGCATTCCCTCCAGCG    68032    ACA  A     GA
                                CG   GA GGGAGT  GCCCA
                                ||   || ||||||  |||||
                                GC   CT CCCTTA  CGGGT
                                 GAC  _     __
GAM76   LOC115286 3' CTCACCTCCACTTCTGTC    73373         _   _
                                GACAGAAG GGAG TGAG
                                |||||||| |||| ||||
                                CTGTCTTC CCTC ACTC
                                     A    C
GAM76   LOC124470 3' TTGGGCTTTTCTTTCCGTC   75645     A      GT
                                GAC GAAGGGA  GAGCCCAA
                                ||| |||||||  ||||||||
                                CTG CTTTCTT  TTCGGGTT
                                  C      __
GAM76   LOC124930 3' TGGGCTCAGATCTGTCCTGTC  74361       AA_   AG
                                GACAG   GGG  TGAGCCCA
                                |||||   |||  ||||||||
                                CTGTC   TCT  ACTCGGGT
                                   CTG   AG
GAM76   LOC143173 5' TTGACTTACCTTCTGTC     60377         _   G
                                GACAGAAGG GAGT AG
                                ||||||||| |||| ||
                                CTGTCTTCC TTCA TT
                                      A    G
GAM76   LOC147063 3' GTCTCATTCCCCTCCGTC    83928     A  A       _
                                GAC GA GGGAGTGAG C
                                ||| || ||||||||| |
                                CTG CT CCCTTACTC G
                                  C  C        T
GAM76   LOC148137 3' TTGGGCTCCTACCTC       58443    A  G  T
                                GA GG AG GAGCCCAA
                                || || || ||||||||
                                CT CC TC CTCGGGTT
                                 _  A  _
GAM76   LOC148397 3' CTCATGCCCCCTTCTATC    78816    C      A__
                                GA AGAAGGG   GTGAG
                                || |||||||   |||||
                                CT TCTTCCC   TACTC
                                 A      CCG
GAM76   LOC149319 5' TGGGCTCGCCTCTTC       79304       A
                                GAAGGG GTGAGCCCA
                                |||||| |||||||||
                                CTTCTC CGCTCGGGT
                                     _
GAM76   LOC149837 3' CTCTACTGCCTTCTGTC     84731         G  _
                                GACAGAAGG AGT GAG
                                ||||||||| ||| |||
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                                CTGTCTTCC TCA CTC
                                     G   T
GAM76   LOC150319 3' CTCCGCCTCCCTTCTGTGG   79653   G       T__
                                C ACAGAAGGGAG   GAG
                                | ||||||||||   |||
                                G TGTCTTCCCTC   CTC
                                 G         CGC
GAM76   LOC150498 3' CTCATTCCTCCCCTCCTTCG   79905    CA  A    ___
                                CGA  GA GGGAG   TGAG
                                |||  || |||||   ||||
                                GCT  CT CCCTC   ACTC
                                  TC  C    CTT
GAM76   LOC151534 5' TGAGCCCACGCCATCCCGTC   56687    A_  A  GA   A  C
                                GAC  GA GG  GTG GC CA
                                |||  || ||  ||| || ||
                                CTG  CT CC  CAC CG GT
                                  CC  A  G_   C  A
GAM76   LOC152286 3' TTCCCTCCCTCTGTC      85635      A    T
                                GACAGA GGGAG GAG
                                |||||| ||||| |||
                                CTGTCT CCCTC CTT
                                   _    C
GAM76   LOC153328 3' TGGGCTCAGCCACTCCCT    80810       _____
                                AGGGAGT    GAGCCCA
                                |||||||    |||||||
                                TCCCTCA    CTCGGGT
                                    CCGA
GAM76   LOC158267 5' GGGCTCATGGTCCTATC     81836    A   __
                                GA GGGA  GTGAGCCC
                                || ||||  ||||||||
                                CT TCCT  TACTCGGG
                                 A   GG
GAM76   LOC164681 5' TGGACTCAGTGCTTCCTGTC  82549     GAA    ___  C
                                GACA   GGGAGT   GAG CCA
                                ||||   ||||||   ||| |||
                                CTGT   CCTTCG   CTC GGT
                                  ___     TGA   A
GAM76   LOC166341 3' GCTTCTCTTCTGTTG      82632          GTG
                                CGACAGAAGGGA   AGC
                                ||||||||||||   |||
                                GTTGTCTTCTCT   TCG
                                       ___
GAM76   LOC196528 3' TTGAACTCCTTCCACTG     87766     AA    T   CC
                                CAG  GGGAG GAG  CAA
                                |||  ||||| |||  |||
                                GTC  CCTTC CTC  GTT
                                  A_    _   AA
GAM76   LOC199918 5' TGAGGATGGCCCCTTCTGCG  89876    A      A  GAG  _
                                CG CAGAAGGG GT   CC CA
                                || |||||||| ||   || ||
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                                GC GTCTTCCC CG   GG GT
                                 _       _ GTA  A
GAM76   LOC201102 3'  GGCACCCCCTTCTGTGG     88094    G       A  GA
                                C ACAGAAGGG GT  GCC
                                | ||||||||| ||  |||
                                G TGTCTTCCC CA  CGG
                                 G       C  __
GAM76   LOC202860 3'  GCCACTCCCTCCTGTGG     89222    G   A       A
                                C ACAG AGGGAGTG GC
                                | |||| |||||||| ||
                                G TGTC TCCCTCAC CG
                                 G   C       _
GAM76   LOC220018 5'  CTTTGGGCAAGTTCCTTC     93401        G GA
                                GAAGGGA T  GCCCAAAG
                                ||||||| |  ||||||||
                                CTTCCTT G  CGGGTTTC
                                    _ AA
GAM76   LOC220846 3'  TTGAACTTCACTCCTCCCTCA  90822    C  AA       CC_
                                A AG  GGGAGTGAG   CAA
                                | ||  |||||||||   |||
                                A TC  TCCTCACTT   GTT
                                 C  CC        CAA
GAM76   LOC222962 3'  GGGCTTCCCCTTCTGTC     92876          AGT
                                GACAGAAGGG   GAGCCC
                                ||||||||||   ||||||
                                CTGTCTTCCC   TTCGGG
                                      C__
GAM76   LOC51003  5'  TGGGCTTTTGCTCTGTC     32152       A G  GT
                                GACAGA G GA  GAGCCCA
                                |||||| | ||  |||||||
                                CTGTCT C TT  TTCGGGT
                                   _ G  __
GAM76   LOC51027  3'  TGGGCCCCATTCTGTTG     59367         _   AGTGA
                                CGACAGAA GGG    GCCCA
                                |||||||| |||    |||||
                                GTTGTCTT CCC    CGGGT
                                    A  _____
GAM76   LOC90379  5'  TTTGGGCTTCCTCCGCCTG   62539     AAG   TG
                                CAG   GGAG  AGCCCAAA
                                |||   ||||  ||||||||
                                GTC   CCTC  TCGGGTTT
                                  CG_   CT
GAM76   LOC91960  3'  CTTTGCAGCCTCCTCTTCTGTC 67661         _   TGA  C_
                                GACAGAAG GGAG   GC  CAAAG
                                |||||||| ||||   ||  |||||
                                CTGTCTTC CCTC   CG  GTTTC
                                     T   ___  AC
GAM77   BRCA1    3'  CCACAGGTACAAGCCACAGGA  23558    A       CA  TCA
                                TC CTGTGGCT  GT   TGTGG
                                || ||||||||  ||   |||||
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                                AG GACACCGA  CA   ACACC
                                 _       A_  TGG
GAM77   MXI1     3'  CCAAGGTCTGAGCCACAG    55259          TTCATG
                                CTGTGGCTCAG     TGG
                                ||||||||||      |||
                                GACACCGAGTC     ACC
                                      TGGA__
GAM77   MXI1     3'  CCAAGGTCTGAGCCACAG    19898          TTCATG
                                CTGTGGCTCAG     TGG
                                ||||||||||      |||
                                GACACCGAGTC     ACC
                                      TGGA__
GAM77   MYO1C    3'  CAGGCCGGGCCACAG       61202          A   CATG
                                CTGTGGCTC GTT    TG
                                |||||||| |||    ||
                                GACACCGGG CGG    AC
                                     C  _____
GAM77   RBBP2    3'  ACTGAGCCACAGTGAT      17318
                                ATCACTGTGGCTCAGT
                                ||||||||||||||||
                                TAGTGACACCGAGTCA

GAM77   TCF3     3'  CCACACGAACTAGGGCAGTGGT 70731          GG TC     A
                                ATCACTGT  C  AGTTC TGTGG
                                ||||||||  |  ||||| |||||
                                TGGTGACG  G  TCAAG ACACC
                                   __ GA     C
GAM77   C20orf20 3'  CCACCCCCCAGGCCACAGTGAT 36852            CAGTTCAT
                                ATCACTGTGGCT       GTGG
                                ||||||||||||       ||||
                                TAGTGACACCGG       CACC
                                      ACCCCC__
GAM77   FLJ12132 3'  CACCCCAAGCCACAGTGA    46466          CAGTTCAT
                                TCACTGTGGCT       GTG
                                ||||||||||        |||
                                AGTGACACCGA       CAC
                                      ACCC_____
GAM77   MGC2408  3'  CACATGAACCAATACAG     50324       GCTCA
                                CTGTG    GTTCATGTG
                                |||||    |||||||||
                                GACAT    CAAGTACAC
                                   AAC__
GAM77   LOC163231 5' CACACATTCACCACAGTG    82436        CTC   TCA
                                CACTGTGG   AGT   TGTG
                                ||||||||   |||   ||||
                                GTGACACC   TTA   ACAC
                                     AC_   C__
GAM77   LOC201229 3' CCACATGAACCAAGGAGAGAC 88142     GG   A___
                                GT  CTC    GTTCATGTGG
                                ||  |||    ||||||||||
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                                CA  GAG    CAAGTACACC
                                 GA   GAAC
GAM78   AQP6     3'  AACCCAGGAGGGACCCAGG    7936       T  _  ATG
                                CCTG GG CT   TTCTGGGTT
                                |||| || ||   |||||||||
                                GGAC CC GG   AGGACCCAA
                                  _  A  G__
GAM78   AQP6     3'  AACCCAGGAGGGACCCAGG    53905      T  _  ATG
                                CCTG GG CT   TTCTGGGTT
                                |||| || ||   |||||||||
                                GGAC CC GG   AGGACCCAA
                                  _  A  G__
GAM78   FLJ32752  5'  AACCCTCCTATCAGCCACAGGG 58335            ATGTTCT
            AA                    TTCCCTGTGGCT      GGGTT
                                |||||||||||       |||||
                                AAGGGACACCGA      CCCAA
                                      CTATCCT
GAM78   KIAA0161  3'  AACCCAGATAGGGACCACAGAG 28494    C     _  ATGT
            A                     TC CTGTGG CT    TCTGGGTT
                                || |||||| ||    ||||||||
                                AG GACACC GG    AGACCCAA
                                 A     A  GAT_
GAM78   RHOBTB2   3'  ACCCGGCAGCCCAGAGAA    60941     C   T   ATGTT
                                TTC CTG GGCT    CTGGGT
                                ||| ||| ||||    ||||||
                                AAG GAC CCGA    GGCCCA
                                  A  _   C_____
GAM78   LOC148529 5'  AACACAGCCACAGGAGAA    84164     _       A
                                TTC CCTGTGGCT TGTT
                                ||| ||||||||| ||||
                                AAG GGACACCGA ACAA
                                  A       C
GAM78   LOC152457 3'  ACCCACGAGCCCAGAGAA    80606     C   T   ATGTTC
                                TTC CTG GGCT     TGGGT
                                ||| ||| ||||     |||||
                                AAG GAC CCGA     ACCCA
                                  A  _   GC_____
GAM78   LOC152503 5'  CTAGGATCACAGCCACAGG    85769         A  _
                                CCTGTGGCT TG TTCTGG
                                ||||||||| || ||||||
                                GGACACCGA AC AGGATC
                                     C  T
GAM78   LOC158434 3'  AACCCAGAATAAACCACTGGGA 86817       T    CTA
            A                     TTCCC GTGG   TGTTCTGGGTT
                                ||||| ||||   ||||||||||
                                AAGGG CACC   ATAAGACCCAA
                                   T   AA_
GAM78   LOC168391 5'  AACCCAGAACTTCATAAAGAA  82692     CC    CTAT
                                TTC  TGTGG   GTTCTGGGTT
                                |||  |||||   ||||||||||
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                                AAG  ATACT    CAAGACCCAA
                                  AA     T___
GAM79   B4GALT1   3'  CAAGAGTCAGAACTGTAGA   7666          GTCAA  TG
                                TCTACAGT    TG  TCTTG
                                ||||||||    ||  |||||
                                AGATGTCA    AC  AGAAC
                                    AG___  TG
GAM79   DGKA      3'  CAAAACACATACATTG      7201        CA     C
                                CAGTGT  ATGTGT TTG
                                ||||||  |||||| |||
                                GTTACA  TACACA AAC
                                   __      A
GAM79   MTMR6     3'  CTCAAAACACAATTTGCACTGT 93549         C  _   C
          A                      TACAGTGT AAT GTGT TTGAG
                                ||||||||| ||| |||| |||||
                                ATGTCACG TTA CACA AACTC
                                    T   A   A
GAM79   SLC4A4    3'  CTCAAGACACAGACACCCACAG 13635     ACA_    AA
          A                      TCT    GTGTC  TGTGTCTTGAG
                                |||    |||||  ||||||||||
                                AGA    CACAG  ACACAGAACTC
                                  CACC     __
GAM79   CUL4A     3'  CTCAAGACTTCAACCTGCAGA  13153     A   T  CAA  T_
                                TCT CAG GT   TG  GTCTTGAG
                                ||| ||| ||   ||  ||||||||
                                AGA GTC CA   AC  CAGAACTC
                                  C   _ ___  TT
GAM79   FLJ11301  3'  CAAGACACTAGCACTGTAGA   37226          CAAT
                                TCTACAGTGT    GTGTCTTG
                                ||||||||||    ||||||||
                                AGATGTCACG    CACAGAAC
                                     AT__
GAM79   GPR105    3'  GACACACCCACACCGTAGA    29655       A    CAA
                                TCTAC GTGT   TGTGTC
                                ||||| ||||   ||||||
                                AGATG CACA   ACACAG
                                   C    CCC
GAM79   LAP1B     5'  CTCAAGACACACCATGGGC    64584     AA___
                                GTC    TGTGTCTTGAG
                                |||    ||||||||||
                                CGG    ACACAGAACTC
                                  GTACC
GAM79   PRDM10    3'  CTCAAGACACATTGACACTGTA 39578
          GA                     TCTACAGTGTCAATGTGTCTTGAG
                                ||||||||||||||||||||||||
                                AGATGTCACAGTTACACAGAACTC

GAM79   SEMA3C    3'  CTCTTCTACATTGACAC     21061          TCTT
                                GTGTCAATGTG    GAG
                                ||||||||||    |||
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                                CACAGTTACAT   CTC
                                      CTT_
GAM79   LOC255654 3'  GACATCCACACTGTAGA    96887         CAAT
                                TCTACAGTGT   GTGTC
                                ||||||||||   |||||
                                AGATGTCACA   TACAG
                                     CC__
GAM79   LOC96652  3'  CTCAAGACAGGACACTGCGGA  65467   TA     AATG
                                TC  CAGTGTC   TGTCTTGAG
                                ||  |||||||   |||||||||
                                AG  GTCACAG   ACAGAACTC
                                 GC     G___
GAM80   ADH1B     3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM80   AHR       3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM80   FDFT1     3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                                _
GAM80   JTB       3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM80   KLF4      3'  TCCCAGACAGTGGATATG    14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM80   PHYH      3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM80   PKD2      3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM80   WRN       3'  GGGCAGTGAAAATGAAA     5098        C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
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                                AAAGT AAAGTGACGGG
                                   A
GAM80   ZNF216   3' ATCTGCACAGCAAAGTGAAA  20017        CA   CTG
                                TTTCACTTT CTGT  AGAT
                                ||||||||| ||||  ||||
                                AAAGTGAAA GACA  TCTA
                                     C_  CG_
GAM80   CG012    5' CTCACTCTGAAAGTGAA    83218        CT CT
                                TTCACTTTCA GT GAG
                                |||||||||| || |||
                                AAGTGAAAGT CA CTC
                                      CT __
GAM80   EIF2C2   3' ATCTTCTGAGAGTGAAAG   71946        G T_
                                CTTTCACT TC GAGAT
                                |||||||| || |||||
                                GAAAGTGA AG TTCTA
                                     G TC
GAM80   FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC       GTCTGAGAT
                                ||||||       |||||||||
                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM80   FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA  TCACTGTCTGAGAT
                                |||||||  ||||||||||||||
                                GTAAAGT  AGTGACAGACTCTA
                                    C__
GAM80   KIAA0984 3' TTTGTCCAGTGAAAATGAA  65534     C      TC
                                TTCA TTTCACTG TGAG
                                |||| |||||||| ||||
                                AAGT AAAGTGAC GTTT
                                  A      CT
GAM80   KLHL6    3' ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM80   NIR3     3' GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM80   PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598        CA G
                                TTCACTTT CT TCTGAGAT
                                |||||||| || ||||||||
                                AAGTGAAA GG AGACTCTA
                                     CC G
GAM80   PP35     3' ATCTCAGACTGAAA       22814      CT
                                TTTCA GTCTGAGAT
                                ||||| |||||||||
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                                AAAGT  CAGACTCTA
                                  __
GAM80   PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM80   SEP15     3'  TCCTACAGTAAGAGTGAAA   14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM80   SFXN2     3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM80   LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM80   LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM80   LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM80   LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM81   CNGA1     3'  CAACTGATAATGTGCAAA    59507          GC   A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                     A_   _
GAM81   ESRRG     3'  TGGCAGTCTTATGTGCAAA   66396         TAGCT
                                TTTGCACAT    AGATTGCCA
                                |||||||||    |||||||||
                                AAACGTGTA    TCTGACGGT
                                     T_____
GAM81   KCNJ3     3'  GCAATAATGTGCAAA       9525           GCTAGA
                                TTTGCACATTA     TTGC
                                ||||||||||     ||||
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                                AAACGTGTAAT     AACG
                                        ______
GAM81   SDC2     3'  GCAAATTAATGTGTAAA     67132          CTAGA
                                TTTGCACATTAG    TTGC
                                ||||||||||||    ||||
                                AAATGTGTAATT    AACG
                                      A____
GAM81   USP9X    3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
           A                     TTTGCACATTAGC     GCCAT
                                 ||||||||||||||    |||||
                                 AAATGTGTAATCG     CGGTA
                                       TAGTC_
GAM81   AMOTL1   3'  GGCAAGTAATGTGCAAA     73650          G  AGAT
                                TTTGCACATTA CT    TGCC
                                ||||||||||| ||    ||||
                                AAACGTGTAAT GA    ACGG
                                        _ ____
GAM81   BCAR3    3'  AGTAATAATGTGCAAA      13098          __
                                TTTGCACATTA  GCT
                                ||||||||||  |||
                                AAACGTGTAAT  TGA
                                      AA
GAM81   DKFZP434B044 3'  TGACAATTAAATGTGCAGA    48930          AGCTA    C
                                TTTGCACATT    GATTG CA
                                |||||||||     ||||| ||
                                AGACGTGTAA    TTAAC GT
                                      A____    A
GAM81   MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                TTTGCACATTAG  AGA TG CAT
                                ||||||||||||  ||| || |||
                                AGACGTGTAATC  TTT AC GTA
                                       __  T  A
GAM81   PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
           AA                    TTTGCACATTAGCTAGATTGCCAT
                                 ||||||||||||||||||||||||||
                                 AAACGTGTAATCGATCTAACGGTA

GAM82   COL4A3   3'  CAGCCAAACCACTGA      48552     ATCCTT   GC
                                TCAG     TGG  TTGGCTG
                                ||||     |||  |||||||
                                AGTC     ACC  AACCGAC
                                  _______  A_
GAM82   COL4A3   3'  CAGCCAAACCACTGA      48564     ATCCTT   GC
                                TCAG     TGG  TTGGCTG
                                ||||     |||  |||||||
                                AGTC     ACC  AACCGAC
                                  _______  A_
GAM82   CRAT     3'  ACAGCCAAGCCCACCCTGG   5656      ATCCTT
                                TCAG     TGGGCTTGGCTGT
                                ||||     |||||||||||||
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                                GGTC     ACCCGAACCGACA
                                  CC____
GAM82   CRAT     3'  ACAGCCAAGCCCACCCTGG   14348     ATCCTT
                                TCAG     TGGGCTTGGCTGT
                                ||||     ||||||||||||
                                GGTC     ACCCGAACCGACA
                                  CC____
GAM82   MRPL49   3'  ACAGGGGCCAAAGGCCTGA   69562     AT      G  TGG
                                TCAG  CCTTTGG CT   CTGT
                                ||||  ||||||| ||   ||||
                                AGTC  GGAAACC GG   GACA
                                  C_      G  ___
GAM82   NRIP1    5'  ACAGCCAGAAGAACACTGA   59948     ATCCTT  GG  __
                                TCAG     TG  CT  TGGCTGT
                                ||||     ||  ||  |||||||
                                AGTC     AC  GA  ACCGACA
                                  _______  AA  AG
GAM82   RAB11A   3'  CAGGCAGCCCAAAAGATTT   16232      C       T G
                                AGATC TTTGGGCT G CTG
                                ||||| |||||||| | |||
                                TTTAG AAACCCGA C GAC
                                   A       _ G
GAM82   SLC26A3  5'  CACAGCCAACAGAAAAATC   3669     CC   GGGC
                                GAT  TTT    TTGGCTGTG
                                |||  |||    |||||||||
                                CTA  AAG    AACCGACAC
                                  AA   AC__
GAM82   AKR1D1   3'  CACAGCCAAGATAAGATC    19974     CT   GG
                                GATC  TTG  CTTGGCTGTG
                                ||||  |||  ||||||||||
                                CTAG  AAT  GAACCGACAC
                                  __   A_
GAM82   ARHGEF9  3'  CTTAGCCCAAAAGATCTGA   30809       C       T
                                TCAGATC TTTGGGCT GG
                                ||||||| |||||||| ||
                                AGTCTAG AAACCCGA TC
                                    A       T
GAM82   C20orf100 3'  CCAGCCCAAAGAACCTG     51808     ATC       T
                                CAG   CTTTGGGCT GG
                                |||   ||||||||| ||
                                GTC   GAAACCCGA CC
                                  CAA       _
GAM82   FLJ12443 5'  ACAACCAAGTGGAAATC     45725    __  TTTGG     C
                                GA  TCC     GCTTGG TGT
                                ||  |||     |||||| |||
                                CT  AGG     TGAACC ACA
                                 AA  _____     A
GAM82   KIAA0493 5'  CACAGCCAGTGTAAGAAGCCTG 64272      ATC    GG  _
           A                     TCAG   CTTT  GC TTGGCTGTG
                                ||||   ||||  || |||||||||
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                                AGTC   GAAG  TG GACCGACAC
                                  C__    AA  T
GAM82   KIAA1573  5'  CAGCTAGCCAAAAAAATCCGA  62684    A   CC   G    T
                                TC GAT  TTT GGCT GGCTG
                                || |||  ||| |||| |||||
                                AG CTA  AAA CCGA TCGAC
                                 C   AA   A   _
GAM82   KIAA1910  3'  CAACCGAAAGGGCCTGA     73325      AT    G  C
                                TCAG  CCTTT GG TTG
                                ||||  ||||| || |||
                                AGTC  GGAAA CC AAC
                                  CG    G  _
GAM82   MGC20470  3'  CAGCTGAGCCCAAGGGACCTGA 58961      A         TG
                                TCAG TCCTTTGGGCT  GCTG
                                |||| ||||||||||  ||||
                                AGTC AGGGAACCCGA  CGAC
                                  C         GT
GAM82   NRN1     3'  CACAGCCAAAATCGGACCTC   33431    TCC    GC
                                GA   TTTGG  TTGGCTGTG
                                ||   |||||  |||||||||
                                CT   AGGCT  AACCGACAC
                                 CC_    AA
GAM82   SCYB11    3'  CACTGCCCAAAGGAGTC     87441    _        T_
                                GA TCCTTTGGGC  TG
                                || ||||||||||  ||
                                CT AGGAAACCCG  AC
                                 G         TC
GAM82   SLC2A10   3'  CACAGCCATTATAAAAAATT   47816     CC    GGCT
                                GAT  TTTG    TGGCTGTG
                                |||  ||||    ||||||||
                                TTA  AAAT    ACCGACAC
                                  AA    ATT_
GAM82   LOC150372 3'  CACAGCCAATATTGCAGGAACT 79789      A    T   GC
            GA                    TCAG TCCT TGG  TTGGCTGTG
                                |||| |||| |||  |||||||||
                                AGTC AGGA GTT  AACCGACAC
                                  A   C   AT
GAM82   LOC151278 3'  CACAACCAAAGCAGGAGG    80200       GG    _  C
                                CCTTT  GCTT GG TGTG
                                |||||  |||| || ||||
                                GGAGG  CGAA CC ACAC
                                   A_    A  A
GAM82   LOC257086 5'  CACAACCAAGCTTAGGAGCCGA 97510    AGA    TT       C
                                TC   TCCT  GGGCTTGG TGTG
                                ||   ||||  |||||||| ||||
                                AG   AGGA  TTCGAACC ACAC
                                 CCG    __       A
GAM83   ASPA     3'  GCTAGTCTGTAAGCTCCTT    3504             T
                                AAGGAGCTTACAG CTAGT
                                |||||||||||| |||||
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                                TTCCTCGAATGTC GATCG
                                       T
GAM83   CDKN1A   3'  CTAGACTGTAAACCTCT     54298      C_
                                GGAG  TTACAGTCTAG
                                ||||  ||||||||||
                                TCTC  AATGTCAGATC
                                  CA
GAM83   DDX16    3'  CTGACACCAGCTCCTT      91030        TACA  CTA
                                AAGGAGCT    GT   GTCAG
                                ||||||||    ||   |||||
                                TTCCTCGA    CA   CAGTC
                                     C___  ___
GAM83   FGA      3'  GCTAGACTGTAAGTTCCTT    41561
                                AAGGAGCTTACAGTCTAGT
                                ||||||||||||||||||
                                TTCCTTGAATGTCAGATCG

GAM83   LHCGR    3'  CTGTAGACTGTAAACTCCT    4071       C        GT
                                AGGAG TTACAGTCTA  CAG
                                ||||| ||||||||||  |||
                                TCCTC AATGTCAGAT  GTC
                                  A        __
GAM83   MLC1     3'  ACCTGACCAGACTGTGGGTCCC 57583     AG        A
          T                      AGG  CTTACAGTCT GTCAGGT
                                 |||  |||||||||| |||||||
                                 TCC  GGGTGTCAGA CAGTCCA
                                   CT         C
GAM83   MLC1     3'  ACCTGACCAGACTGTGGGTCCC 30772     AG        A
          T                      AGG  CTTACAGTCT GTCAGGT
                                 |||  |||||||||| |||||||
                                 TCC  GGGTGTCAGA CAGTCCA
                                   CT         C
GAM83   PRX      3'  CCTGAAGTGAAGCTCC      40528        A  GTCTAG
                                GGAGCTT CA     TCAGG
                                ||||||| ||     |||||
                                CCTCGAA GT     AGTCC
                                     _  GA____
GAM83   SELL     3'  CCTGACCAACAGTTCCTT    5391         TACA  CTA
                                AAGGAGCT    GT   GTCAGG
                                ||||||||    ||   ||||||
                                TTCCTTGA    CA   CAGTCC
                                     _____  AC_
GAM83   C4.4A    3'  ACTAGACTGTGAGCTCCT    26940
                                AGGAGCTTACAGTCTAGT
                                ||||||||||||||||||
                                TCCTCGAGTGTCAGATCA

GAM83   C7orf13  3'  CTAAACCATGAGCTCCTT    50928          CA  C
                                AAGGAGCTTA  GT TAG
                                ||||||||||  || |||
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                                TTCCTCGAGT  CA ATC
                                      AC  A
GAM83   FLJ21839  5'  CCCGACCAGACTGTGCT     41548     TT      A   A
                                AGC  ACAGTCT GTC GG
                                |||  ||||||| ||| ||
                                TCG  TGTCAGA CAG CC
                                  __      C   C
GAM83   MGC32043  3'  TAGACTGTAAGCTCCTT     58057
                                AAGGAGCTTACAGTCTA
                                |||||||||||||||||
                                TTCCTCGAATGTCAGAT

GAM83   TBX19     3'  ATTAGACTGTAAGCCTCT    17650    GA
                                AG  GCTTACAGTCTAGT
                                ||  ||||||||||||||
                                TC  CGAATGTCAGATTA
                                 TC
GAM83   URG4      3'  AGACTGTGAGCTCCTT      35500
                                AAGGAGCTTACAGTCT
                                ||||||||||||||||
                                TTCCTCGAGTGTCAGA

GAM83   LOC134121 5'  AGACTGTAAGCTTCCT      75148      _
                                AGGA GCTTACAGTCT
                                |||| ||||||||||
                                TCCT CGAATGTCAGA
                                  T
GAM83   LOC144231 3'  GCTAGACTGTAAGCCCTT    83017      A
                                AAGG GCTTACAGTCTAGT
                                |||| ||||||||||||||
                                TTCC CGAATGTCAGATCG
                                  _
GAM83   LOC146268 3'  CTAGACTGTGAGCTCCT     77807
                                AGGAGCTTACAGTCTAG
                                |||||||||||||||||
                                TCCTCGAGTGTCAGATC

GAM83   LOC148183 3'  CCTGTGCTACAAGCTCCTT    84118          ACAGTC   _
                                AAGGAGCTT     TAGT CAGG
                                |||||||||     |||| ||||
                                TTCCTCGAA     ATCG GTCC
                                     C_____    T
GAM83   LOC148823 3'  ACCTATGACCTGTAAGCTCT   59204           TCTA   __
                                GGAGCTTACAG    GTCA  GGT
                                ||||||||||    ||||  |||
                                TCTCGAATGTC    CAGT  CCA
                                      ____    AT
GAM83   LOC163404 3'  ACTAGACTGTGAGCTCCT     82123
                                AGGAGCTTACAGTCTAGT
                                ||||||||||||||||||
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```
                                TCCTCGAGTGTCAGATCA

GAM83   LOC169245 5' ACCTGACTGTCAGCAGCCCC  87281    A  TACAGTC
                                GG GCT      TAGTCAGGT
                                || |||      |||||||||
                                CC CGA      GTCAGTCCA
                                 C  CGACT__
GAM83   LOC196202 5' ACCCATTGGCCAAAAGCTCCTT 89438        ACA T    CA
                                AAGGAGCTT   G CTAGT  GGT
                                |||||||||   | |||||  |||
                                TTCCTCGAA   C GGTTA  CCA
                                     AAC _    C_
GAM83   LOC196957 3' ACCCATGCACCGAAGCTCCT   87812        ACA  C  GTCA
                                AGGAGCTT   GT TA   GGT
                                ||||||||   || ||   |||
                                TCCTCGAA   CA GT   CCA
                                     GC_  C  AC__
GAM83   LOC196961 3' ACCCATGCACCGAAGCTCCT   87833        ACA  C  GTCA
                                AGGAGCTT   GT TA   GGT
                                ||||||||   || ||   |||
                                TCCTCGAA   CA GT   CCA
                                     GC_  C  AC__
GAM83   LOC197138 3' ACCCATGCACCGAAGCTCCT   87906        ACA  C  GTCA
                                AGGAGCTT   GT TA   GGT
                                ||||||||   || ||   |||
                                TCCTCGAA   CA GT   CCA
                                     GC_  C  AC__
GAM83   LOC203197 3' GCTAGACTGTAAACTCCTT    89290       C
                                AAGGAG TTACAGTCTAGT
                                |||||| ||||||||||||
                                TTCCTC AATGTCAGATCG
                                   A
GAM83   LOC245727 3' ACCCATGCACCGAAGCTCCT   91120        ACA  C  GTCA
                                AGGAGCTT   GT TA   GGT
                                ||||||||   || ||   |||
                                TCCTCGAA   CA GT   CCA
                                     GC_  C  AC__
GAM83   LOC257542 3' CTGACACCAGCTCCTT      97706        TACA  CTA
                                AAGGAGCT   GT   GTCAG
                                ||||||||   ||   |||||
                                TTCCTCGA   CA   CAGTC
                                     C___  ___
GAM83   LOC257593 3' CTGACACCAGCTCCTT      97826        TACA  CTA
                                AAGGAGCT   GT   GTCAG
                                ||||||||   ||   |||||
                                TTCCTCGA   CA   CAGTC
                                     C___  ___
GAM83   LOC54516  3' ACCTGACTGGATCAAGCCC   38757    A   ACA
                                GG GCTT   GTCTAGTCAGGT
                                || ||||   ||||||||||||
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                                CC CGAA   TAGGTCAGTCCA
                                 _   C__
GAM84   ART3     5' CATCCTGAAGACTTGCTTAC  6786        AC    AT
                                GTGAGCAA  CTTCA  GTG
                                ||||||||  |||||  |||
                                CATTCGTT  GAAGT  TAC
                                    CA    CC
GAM84   AP1GBP1  3' CACCAGAAGCTTGCTCAC   23390       AC   AAT
                                GTGAGCAA  CTTC   GTG
                                ||||||||  ||||   |||
                                CACTCGTT  GAAG   CAC
                                    C_    AC_
GAM84   AP1GBP1  3' CACCAGAAGCTTGCTCAC   54516       AC   AAT
                                GTGAGCAA  CTTC   GTG
                                ||||||||  ||||   |||
                                CACTCGTT  GAAG   CAC
                                    C_    AC_
GAM84   FLJ10044 3' CAATGAAGGCTTGTTCAC   35765       A    A
                                GTGAGCAA CCTTCA TG
                                |||||||| |||||| ||
                                CACTTGTT GGAAGT AC
                                    C     A
GAM84   FLJ12903 3' TATTGAAGAGCTGCCCAC   42780     A   AAC
                                GTG GCA   CTTCAATG
                                ||| |||   ||||||||
                                CAC CGT   GAAGTTAT
                                  C   CGA
GAM84   FLJ13322 3' CATTGAAGATTCACTTAC   45297      CA  C
                                GTGAG  AA CTTCAATG
                                |||||  || ||||||||
                                CATTC  TT GAAGTTAC
                                   AC  A
GAM84   HT008    3' AGACCAAAAGTTTGCTCA    59801        C  CAA  T
                                TGAGCAAAC TT   TG GTCT
                                ||||||||| ||   || ||||
                                ACTCGTTTG AA   AC CAGA
                                    A  ___  _
GAM84   KIAA0326 3' CAGGGGTCAAAGCATTTGCTCA 64320        C_   CAA  _ G
            C                    GTGAGCAAA  CTT   TG T TCTG
                                ||||||||  |||   || | ||||
                                CACTCGTTT  GAA   AC G GGAC
                                    AC   ___  T G
GAM84   Kv6.3    3' CACCTCGAAGGTTTACTCAC  56037      C      AAT
                                GTGAG AAACCTTC   GTG
                                ||||| ||||||||   |||
                                CACTC TTTGGAAG   CAC
                                   A       CTC
GAM84   MGC5560  3' ATTAAAGGTTTGCCCAT    38785     A       C
                                GTG GCAAACCTT AAT
                                ||| |||||||| |||
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                                TAC CGTTTGGAA TTA
                                  C        A
GAM84   OSBPL2   3'  CAGACACATTGAAAGTGACTGC 57857     A__  C
                                GCA   AC TTCAATGTGTCTG
                                |||   || ||||||||||||
                                CGT   TG AAGTTACACAGAC
                                  CAG  A
GAM84   OSBPL2   3'  CAGACACATTGAAAGTGACTGC 29206     A__  C
                                GCA   AC TTCAATGTGTCTG
                                |||   || ||||||||||||
                                CGT   TG AAGTTACACAGAC
                                  CAG  A
GAM84   PRO2831  5'  CAGACACACATCTGCACTTGCT 37600        ACCTTCAA_
           CA                     TGAGCAA        TGTGTCTG
                                |||||||        ||||||||
                                ACTCGTT        ACACAGAC
                                    CACGTCTAC
GAM84   SMCR5    5'  AGACACGCAGTCTGCTGAC   58589    G    A  CTTCAA
                                GT AGCA AC     TGTGTCT
                                || |||| ||     |||||||
                                CA TCGT TG     GCACAGA
                                 G   C  AC____
GAM84   LOC116150 3' CATGTTAAAATCTTGCTCAC   56631        ACCTTC
                                GTGAGCAA     AATGTG
                                ||||||||     ||||||
                                CACTCGTT     TTGTAC
                                     CTAAAA
GAM84   LOC145317 3' CAGACACAGAGGCCCAGCTCAC 83321       AAA_   CAA
                                GTGAGC   CCTT   TGTGTCTG
                                ||||||   ||||  ||||||||
                                CACTCG   GGAG   ACACAGAC
                                   ACCC   ___
GAM84   LOC145921 5' CAGAATTATATTGAGATCTACT 76015      CAAACC       __
           CAC                    GTGAG     TTCAATGTG  TCTG
                                |||||     |||||||||  ||||
                                CACTC     GAGTTATAT  AGAC
                                   ATCTA_       TA
GAM84   LOC168966 5' AGACACGCAGACCACTCAC   87277      CAAACCT  AA
                                GTGAG      TC  TGTGTCT
                                |||||      ||  |||||||
                                CACTC      AG  GCACAGA
                                   ACC____  AC
GAM84   LOC221715 3' CAGAGAAGGTTTGCTGAC    93751    G        AA
                                GT AGCAAACCTTC  TG
                                || ||||||||||  ||
                                CA TCGTTTGGAAG  AC
                                 G         AG
GAM84   LOC253566 5' CAGAATTATATTGAGATCTACT 94962      CAAACC       __
           CAC                    GTGAG     TTCAATGTG  TCTG
                                |||||     |||||||||  ||||
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                                CACTC     GAGTTATAT  AGAC
                                   ATCTA_       TA
GAM84   LOC255520 3'  CATCAAAGATTTGCTCA     95852        C   CA
                                TGAGCAAA CTT  ATG
                                |||||||| |||  |||
                                ACTCGTTT GAA  TAC
                                     A   AC
GAM84   LOC255779 3'  GGGCTTATTGAAGGCCTGTCAC 96015      G  AA       T
                                GTGA CA  CCTTCAATG GTCT
                                |||| ||  ||||||||| ||||
                                CACT GT  GGAAGTTAT CGGG
                                  _ CC       T
GAM84   LOC84549  3'  CAGACACACCCTCTGCCAC   50699     A  AACCTTCAA
                                GTG GCA       TGTGTCTG
                                ||| |||       ||||||||
                                CAC CGT       ACACAGAC
                                  _  CTCCC_____
GAM84   LOC91056  3'  AGACACACTAGTGCTC     94755      AAC  TCAA
                                GAGCA   CT    TGTGTCT
                                |||||   ||    |||||||
                                CTCGT   GA    ACACAGA
                                   ____ TC__
GAM85   ART3     5'  CATCCTGAAGACTTGCTTAC  6786        AC    AT
                                GTGAGCAA  CTTCA  GTG
                                ||||||||  |||||  |||
                                CATTCGTT  GAAGT  TAC
                                     CA    CC
GAM85   AP1GBP1   3'  CACCAGAAGCTTGCTCAC    23390       AC   AAT
                                GTGAGCAA  CTTC   GTG
                                ||||||||  ||||   |||
                                CACTCGTT  GAAG   CAC
                                     C_    AC_
GAM85   AP1GBP1   3'  CACCAGAAGCTTGCTCAC    54516       AC   AAT
                                GTGAGCAA  CTTC   GTG
                                ||||||||  ||||   |||
                                CACTCGTT  GAAG   CAC
                                     C_    AC_
GAM85   FLJ10044  3'  CAATGAAGGCTTGTTCAC    35765        A    A
                                GTGAGCAA CCTTCA TG
                                |||||||| |||||| ||
                                CACTTGTT GGAAGT AC
                                     C     A
GAM85   FLJ12903  3'  TATTGAAGAGCTGCCCAC    42780     A  AAC
                                GTG GCA   CTTCAATG
                                ||| |||   ||||||||
                                CAC CGT   GAAGTTAT
                                  C   CGA
GAM85   FLJ13322  3'  CATTGAAGATTCACTTAC    45297      CA  C
                                GTGAG  AA CTTCAATG
                                |||||  || ||||||||
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                                CATTC  TT GAAGTTAC
                                   AC  A
GAM85   HT008    3'  AGACCAAAAGTTTGCTCA    59801         C  CAA  T
                                TGAGCAAAC TT   TG GTCT
                                ||||||||| ||   || ||||
                                ACTCGTTTG AA   AC CAGA
                                    A  ___  _
GAM85   KIAA0326 3'  CAGGGGTCAAAGCATTTGCTCA 64320         C_   CAA  _ G
          C                      GTGAGCAAA  CTT   TG T TCTG
                                 |||||||||  |||   || | ||||
                                 CACTCGTTT  GAA   AC G GGAC
                                    AC   ___  T G
GAM85   Kv6.3    3'  CACCTCGAAGGTTTACTCAC   56037       C       AAT
                                GTGAG AAACCTTC   GTG
                                ||||| ||||||||   |||
                                CACTC TTTGGAAG   CAC
                                   A       CTC
GAM85   MGC5560  3'  ATTAAAGGTTTGCCCAT     38785     A       C
                                GTG GCAAACCTT AAT
                                ||| ||||||||| |||
                                TAC CGTTTGGAA TTA
                                  C        A
GAM85   OSBPL2   3'  CAGACACATTGAAAGTGACTGC 29206     A__  C
                                GCA   AC TTCAATGTGTCTG
                                |||   || ||||||||||||||
                                CGT   TG AAGTTACACAGAC
                                  CAG  A
GAM85   OSBPL2   3'  CAGACACATTGAAAGTGACTGC 57857     A__  C
                                GCA   AC TTCAATGTGTCTG
                                |||   || ||||||||||||||
                                CGT   TG AAGTTACACAGAC
                                  CAG  A
GAM85   PRO2831  5'  CAGACACACATCTGCACTTGCT 37600        ACCTTCAA_
          CA                      TGAGCAA        TGTGTCTG
                                  |||||||        ||||||||
                                  ACTCGTT        ACACAGAC
                                     CACGTCTAC
GAM85   SMCR5    5'  AGACACGCAGTCTGCTGAC   58589    G   A  CTTCAA
                                GT AGCA AC      TGTGTCT
                                || |||| ||      |||||||
                                CA TCGT TG      GCACAGA
                                 G   C  AC_____
GAM85   LOC116150 3'  CATGTTAAAATCTTGCTCAC   56631         ACCTTC
                                GTGAGCAA      AATGTG
                                ||||||||      ||||||
                                CACTCGTT      TTGTAC
                                     CTAAAA
GAM85   LOC145317 3'  CAGACACAGAGGCCCAGCTCAC 83321        AAA_    CAA
                                GTGAGC    CCTT   TGTGTCTG
                                ||||||    ||||   ||||||||
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                                CACTCG   GGAG   ACACAGAC
                                   ACCC   ___
GAM85   LOC145921 5'  CAGAATTATATTGAGATCTACT 76015      CAAACC      __
            CAC                   GTGAG     TTCAATGTG  TCTG
                                  |||||     |||||||||  ||||
                                  CACTC     GAGTTATAT  AGAC
                                     ATCTA_       TA
GAM85   LOC168966 5'  AGACACGCAGACCACTCAC   87277      CAAACCT  AA
                                  GTGAG      TC  TGTGTCT
                                  |||||      ||  |||||||
                                  CACTC      AG  GCACAGA
                                     ACC____  AC
GAM85   LOC221715 3'  CAGAGAAGGTTTGCTGAC    93751    G        AA
                                  GT AGCAAACCTTC  TG
                                  || ||||||||||  ||
                                  CA TCGTTTGGAAG  AC
                                    G         AG
GAM85   LOC253566 5'  CAGAATTATATTGAGATCTACT 94962      CAAACC      __
            CAC                   GTGAG     TTCAATGTG  TCTG
                                  |||||     |||||||||  ||||
                                  CACTC     GAGTTATAT  AGAC
                                     ATCTA_       TA
GAM85   LOC255520 3'  CATCAAAGATTTGCTCA     95852        C   CA
                                  TGAGCAAA CTT  ATG
                                  |||||||| |||  |||
                                  ACTCGTTT GAA  TAC
                                       A   AC
GAM85   LOC255779 3'  GGGCTTATTGAAGGCCTGTCAC 96015     G  AA       T
                                  GTGA CA  CCTTCAATG GTCT
                                  |||| ||  ||||||||| ||||
                                  CACT GT  GGAAGTTAT CGGG
                                    _ CC        T
GAM85   LOC84549  3'  CAGACACACCCTCTGCCAC   50699     A  AACCTTCAA
                                  GTG GCA        TGTGTCTG
                                  ||| |||        ||||||||
                                  CAC CGT        ACACAGAC
                                    _  CTCCC____
GAM85   LOC91056  3'  AGACACACTAGTGCTC      94755      AAC  TCAA
                                  GAGCA   CT    TGTGTCT
                                  |||||   ||    |||||||
                                  CTCGT   GA    ACACAGA
                                     ___  TC__
GAM86   CTSK     5'  CAGACAACAGATTTCCATCA   4621         CC__   CTCCA
                                  TGATGGAA   GTTG    TCTG
                                  ||||||||   ||||    ||||
                                  ACTACCTT   CAAC    AGAC
                                       TAGA   _____
GAM86   EFNB2    3'  CAGGCTGTAATTCCATCA    14571        ACC    TCCA
                                  TGATGGA   GTTGC   TCTG
                                  |||||||   |||||   ||||
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                                ACTACCT  TAATG   GGAC
                                   ___    TC__
GAM86  ENAM    3' AGCAACATTTCCATCA     49076       CC
                                TGATGGAA  GTTGCT
                                ||||||||  ||||||
                                ACTACCTT  CAACGA
                                     TA
GAM86  GABRA5  5' TGGACCAACGGCTCCACCA  60193   A   A    C
                                TG TGGA CCGTTG TCCA
                                || |||| |||||| ||||
                                AC ACCT GGCAAC AGGT
                                 C   C    C
GAM86  IKBKB   3' CAGATGGAGCTCTCGCTTCCTC 63203    T   C  TT_
          A                      TGA GGAA CG   GCTCCATCTG
                                ||| |||| ||   ||||||||||
                                ACT CCTT GC   CGAGGTAGAC
                                  _   C  TCT
GAM86  KIAA0523 3' CAGATGGAAGCTTCCTCCA  67729     ACCGTT  _
                                TGGA     GCT CCATCTG
                                ||||     ||| |||||||
                                ACCT     CGA GGTAGAC
                                  CCTT__   A
GAM86  KIAA0939 3' CAGATGGAATGACTCCCATC  62008      AACC   GC
                                GATGG   GTT  TCCATCTG
                                |||||   |||  ||||||||
                                CTACC   CAG  AGGTAGAC
                                  CT__   TA
GAM86  MGC10981  3' CAGATGGACTCAGGAGCCCATC 51014       AA_  GTTGC
          A                      TGATGG   CC    TCCATCTG
                                ||||||  ||    ||||||||
                                ACTACC   GG    AGGTAGAC
                                   CGA  ACTC_
GAM86  MY014    5' CAGATGGAACAACGGTTACAGT 48139     GG_      C
          C                      GAT   AACCGTTG TCCATCTG
                                |||   |||||||| ||||||||
                                CTG   TTGGCAAC AGGTAGAC
                                  ACA       A
GAM86  LOC123722 3' GAATAACAGTTCCACCA     74230    A    C   C
                                TG TGGAAC GTTG TC
                                || |||||| |||| ||
                                AC ACCTTG CAAT AG
                                 C     A   A
GAM86  LOC129831 3' CAGATGTTGTACTTCCATCA  74893        CCGT   TC
                                TGATGGAA   TGC  CATCTG
                                ||||||||   |||  ||||||
                                ACTACCTT   ATG  GTAGAC
                                     C___   TT
GAM86  LOC150848 5' TCAGATGAAATTGTTCCATC  85130        C  GCTC
                                GATGGAAC GTT   CATCTGA
                                |||||||| |||   |||||||
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                                CTACCTTG TAA    GTAGACT
                                    T  A___
GAM86   LOC91149 3'  TCAAATGTTGAACATTTCCATC 65084        CC   GCTC   C
            A                    TGATGGAA  GTT    CAT TGA
                                 |||||||| |||    ||| |||
                                 ACTACCTT  CAA    GTA ACT
                                     TA   GTT_   A
GAM87   ATP7A    3'  CTGGTCTTAAACTCCTAACCTC 3522      A  C  T
            A                    TGA GT AG AGTTTGAGACTAG
                                 ||| || || ||||||||||||
                                 ACT CA TC TCAAATTCTGGTC
                                   C  A  C
GAM87   BCL9     3'  CAAACTACGACCTCA      15065     A   A
                                 TGA GTC GTAGTTTG
                                 ||| ||| ||||||||
                                 ACT CAG CATCAAAC
                                   C  _
GAM87   CCNF     3'  GCTAGTCTCGAACTCATGACCT 8320      A    GT
            CA                   TGA GTCA  AGTTTGAGACTAGC
                                 ||| ||||  ||||||||||||||
                                 ACT CAGT  TCAAGCTCTGATCG
                                   C    AC
GAM87   CYP1A2   3'  CTAGTCTCAAACTCCTGACCTC 5687      A    T
            A                    TGA GTCAG AGTTTGAGACTAG
                                 ||| ||||| ||||||||||||
                                 ACT CAGTC TCAAACTCTGATC
                                   C    C
GAM87   CYP1A2   3'  CTAGTCTCAAACTCCTGACCTC 69107     A    T
            A                    TGA GTCAG AGTTTGAGACTAG
                                 ||| ||||| ||||||||||||
                                 ACT CAGTC TCAAACTCTGATC
                                   C    C
GAM87   DFFB     3'  GCTGGTCTCAAACTCCTGACCT 87391     A    T
            CA                   TGA GTCAG AGTTTGAGACTAGC
                                 ||| ||||| |||||||||||||
                                 ACT CAGTC TCAAACTCTGGTCG
                                   C    C
GAM87   DISC1    3'  GTCTCAAACTCCTGACCTCA   37890     A    T
                                 TGA GTCAG AGTTTGAGAC
                                 ||| ||||| ||||||||||
                                 ACT CAGTC TCAAACTCTG
                                   C    C
GAM87   HMGE     3'  CTAGTTACTAATGACCTCA    72729     A   G    TTGA
                                 TGA GTCA TAGT    GACTAG
                                 ||| |||| ||||    ||||||
                                 ACT CAGT ATCA    TTGATC
                                   C   A   ____
GAM87   KMO      3'  GCCAGTCTCAAACTCCTGGCCT 13450     A    T         A
            CA                   TGA GTCAG AGTTTGAGACT GC
                                 ||| ||||| |||||||||| ||
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                                ACT CGGTC TCAAACTCTGA CG
                                  C    C         C
GAM87   MAK     3'  GCTGGTCTCAAACTCCTGACCT 19763     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   MEFV    3'  GCCGGTCTCAAACTCCTGACCT 4139      A    T        TA
            CA                    TGA GTCAG AGTTTGAGAC  GC
                                  ||| ||||| ||||||||||  ||
                                ACT CAGTC TCAAACTCTG  CG
                                  C    C         GC
GAM87   MICB    3'  GCCCAGTTTCAAACTCCTGACC 19827     A    T        A_
            TCA                    TGA GTCAG AGTTTGAGACT  GC
                                  ||| ||||| ||||||||||  ||
                                ACT CAGTC TCAAACTTTGA  CG
                                  C    C         CC
GAM87   MLANA   3'  GCTGGTCTCAAACTCCTGACCT 18588     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   MMP19   3'  CTAGCCCGAACTGACTTCA   42978          AGT   AGA
                                TGAAGTCAGT   TTG   CTAG
                                ||||||||||   |||   ||||
                                ACTTCAGTCA   AGC   GATC
                                      ____   CC_
GAM87   NCOA6   5'  GCTGGTCTCAAACTCCTGACCT 25975     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   NDRG3   3'  GCTGGTCTCAAACTCCTGACCT 49301     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   NQO1    3'  GCTGGTCTCAAACTCCTGACCT 6163      A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   PRKR    3'  GCTGGTCTCAAACTCCTGACCT 10885     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   RHD     3'  GCTGATCTCAAACTCCTGACCT 32310     A    T       C
            CA                    TGA GTCAG AGTTTGAGA TAGC
                                  ||| ||||| ||||||||| ||||
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                                ACT CAGTC TCAAACTCT GTCG
                                  C    C       A
GAM87   RHD     3' GCTGATCTCAAACTCCTGACCT 32619     A    T       C
           CA                    TGA GTCAG AGTTTGAGA TAGC
                                ||| ||||| ||||||||| ||||
                                ACT CAGTC TCAAACTCT GTCG
                                  C    C       A
GAM87   SCML2   3' GCTGGTCTCAAACTCCTGACCT 20321     A    T
           CA                    TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   SEDL    3' GCTGGTTTCAAACTCCTGACCT 27350     A    T
           CA                    TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTTTGGTCG
                                  C    C
GAM87   SIL     3' GCTGGTCTCAAACTCCCGACCT 11694     A   AGT
           CA                    TGA GTC   AGTTTGAGACTAGC
                                ||| |||   ||||||||||||||
                                ACT CAG   TCAAACTCTGGTCG
                                  C   CCC
GAM87   SLC6A12  3' CAAACCCCTGACTTCA      11731          TA
                                TGAAGTCAG  GTTTG
                                |||||||||  |||||
                                ACTTCAGTC  CAAAC
                                     CC
GAM87   SPN     3' GCTGGTCTCAAACTCCTGACCT 11924     A    T
           CA                    TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   SULT2B1  5' GCTGGTCTCAAACTCCTGACCT 16028     A    T
           CA                    TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   TAT     3' GCTGGTCTCAAACTCCTGACCT 4472      A    T
           CA                    TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   TES     3' GCTGGTCTCAAACTCCTGACCT 72009     A    T
           CA                    TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   TIM3    3' GTCTCAAACTCCTGACCTCA  51347     A    T
                                TGA GTCAG AGTTTGAGAC
                                ||| ||||| ||||||||||
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                                ACT CAGTC TCAAACTCTG
                                  C    C
GAM87   TMPRSS3  3' GCTGCTCTCAAACCCCTGACCT 50508    A    TA      C
           CA                     TGA GTCAG  GTTTGAGA TAGC
                                ||| |||||  |||||||| ||||
                                ACT CAGTC  CAAACTCT GTCG
                                  C    CC       C
GAM87   TMPRSS3  3' GCTGCTCTCAAACCCCTGACCT 50529    A    TA      C
           CA                     TGA GTCAG  GTTTGAGA TAGC
                                ||| |||||  |||||||| ||||
                                ACT CAGTC  CAAACTCT GTCG
                                  C    CC       C
GAM87   TMPRSS3  3' GCTGCTCTCAAACCCCTGACCT 43797    A    TA      C
           CA                     TGA GTCAG  GTTTGAGA TAGC
                                ||| |||||  |||||||| ||||
                                ACT CAGTC  CAAACTCT GTCG
                                  C    CC       C
GAM87   TRAF5    3' GCTGATCTCAAACTCCTGACCT 16083    A    T       C
           CA                     TGA GTCAG AGTTTGAGA TAGC
                                ||| ||||| ||||||||| ||||
                                ACT CAGTC TCAAACTCT GTCG
                                  C    C        A
GAM87   TRPM6    3' GCTGGTCTCAAACTCCTGACCT 34543    A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   VHL      3' GCTGGTTTCAAACTCCTGACCT 5075     A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTTTGGTCG
                                  C    C
GAM87   BA108L7.2 3' GCTAGTCTCGAACTCCTGACCT 48264    A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAGCTCTGATCG
                                  C    C
GAM87   C11orf9  3' GCTAATCTCCCCCTAGCTTCA 25211       CAG   TTT   C
                                TGAAGT   TAG   GAGA TAGC
                                ||||||   |||   |||| ||||
                                ACTTCG   ATC   CTCT ATCG
                                   ___   CCC    A
GAM87   C13orf1  3' GCTGGTCTCAAACTCCTGACCT 39972    A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   CHRAC1   3' GCTTGTCTCAAACTCCTAACCT 33875    A  C  T       T
           CA                     TGA GT AG AGTTTGAGAC AGC
                                ||| || || |||||||||| |||
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                                ACT CA TC TCAAACTCTG TCG
                                  C A C         T
GAM87   CPSF2    3' GCTGGCCTCAAACTCCCGACCT 61590     A   AGT       A
           CA                     TGA GTC   AGTTTGAG CTAGC
                                ||| |||   |||||||| |||||
                                ACT CAG   TCAAACTC GGTCG
                                  C   CCC       C
GAM87   CPSF2    3' GCTGGTCTCAAACTCCTGACCT 61594     A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   DKFZp434A2417 3' GCTGATCTCAAACTCCCAACCT 66105     A  CAGT       C
           CA                     TGA GT    AGTTTGAGA TAGC
                                ||| ||    ||||||||| ||||
                                ACT CA    TCAAACTCT GTCG
                                  C  ACCC        A
GAM87   DKFZP434J037 3' GCTGGTCTCAAACTCCCGACCT 48217     A   AGT
           CA                     TGA GTC   AGTTTGAGACTAGC
                                ||| |||   ||||||||||||||
                                ACT CAG   TCAAACTCTGGTCG
                                  C   CCC
GAM87   EVI5     3' GCTGATCTCAAACTTCTGACCT 19002     A    T       C
           CA                     TGA GTCAG AGTTTGAGA TAGC
                                ||| ||||| ||||||||| ||||
                                ACT CAGTC TCAAACTCT GTCG
                                  C    T       A
GAM87   FBP17    3' GCTGGTCTCAAACTCCTGACCT 72799     A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   FLJ12363  3' GCTGGTCTCAAACTCCTGACCT 49687     A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   FLJ12668  3' GCTGGTCTCAAACTCCTGACCT 46519     A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   FLJ12687  3' GCTGGTCTCAAACTCCTGACCT 46200     A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   FLJ20034  3' GCTGGTCTCAAACTCCCGACCT 34376     A   AGT
           CA                     TGA GTC   AGTTTGAGACTAGC
                                ||| |||   ||||||||||||||
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                                ACT CAG   TCAAACTCTGGTCG
                                  C   CCC
GAM87   FLJ20813  3'  GCTGGTCTCAAACTCCTGACCT 35687     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   FLJ21324  5'  GCTGGTCTCAAACTCCTGACCT 91206     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   FLJ22529  3'  GCTAGTCTCAAACCCCTGACCT 45572     A    TA
            TA                    TGA GTCAG  GTTTGAGACTAGC
                                  ||| |||||  ||||||||||||
                                ATT CAGTC  CAAACTCTGATCG
                                  C    CC
GAM87   FLJ22625  3'  GCTGGTCTCAAACTGCTGACTT 45259
            CA                    TGAAGTCAGTAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                ACTTCAGTCGTCAAACTCTGGTCG

GAM87   FLJ22684  3'  CTGGTCTCAAACTCCTGACCTC 46794     A    T
            A                     TGA GTCAG AGTTTGAGACTAG
                                  ||| ||||| ||||||||||||
                                ACT CAGTC TCAAACTCTGGTC
                                  C    C
GAM87   FLJ32865  3'  GCTGGTCTCAAACCCCTGACCT 58179     A    TA
            CA                    TGA GTCAG  GTTTGAGACTAGC
                                  ||| |||||  ||||||||||||
                                ACT CAGTC  CAAACTCTGGTCG
                                  C    CC
GAM87   H2AV      3'  CTGGTCTCAAACTCCTGACCTC 56851     A    T
            A                     TGA GTCAG AGTTTGAGACTAG
                                  ||| ||||| ||||||||||||
                                ACT CAGTC TCAAACTCTGGTC
                                  C    C
GAM87   IL14      5'  CAAGCCACTGACTTCA      95430          A
                                TGAAGTCAGT GTTTG
                                |||||||||| |||||
                                ACTTCAGTCA CGAAC
                                       C
GAM87   KIAA0022  3'  GCTGGTCTCAAACTCCTGACCT 29668     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   KIAA0063  3'  GCTGGTCTCAAACTCCCGACCT 29635     A   AGT
            CA                    TGA GTC   AGTTTGAGACTAGC
                                  ||| |||   ||||||||||||||
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                                ACT CAG   TCAAACTCTGGTCG
                                  C   CCC
GAM87   KIAA0161 3' GCTACTCTCAAACTCCTGACCT 28507     A    T       C
            CA                    TGA GTCAG AGTTTGAGA TAGC
                                  ||| ||||| ||||||||| ||||
                                  ACT CAGTC TCAAACTCT ATCG
                                    C    C        C
GAM87   KIAA0186 3' GCTGGTTTCAAACTCCTGACCT 40760     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAACTTTGGTCG
                                    C    C
GAM87   KIAA0391 3' TCTCAAACTCCTGACCTCA   27925     A    T
                                  TGA GTCAG AGTTTGAGA
                                  ||| ||||| |||||||||
                                  ACT CAGTC TCAAACTCT
                                    C    C
GAM87   KIAA1161 5' GCTAGTCTCAAACTCCTGAC   81753       T
                                  GTCAG AGTTTGAGACTAGC
                                  ||||| ||||||||||||||
                                  CAGTC TCAAACTCTGATCG
                                     C
GAM87   KIAA1170 3' GCTGACCTCAAACTCCTGACCT 69855     A    T      AC
            CA                    TGA GTCAG AGTTTGAG  TAGC
                                  ||| ||||| ||||||||  ||||
                                  ACT CAGTC TCAAACTC  GTCG
                                    C    C       CA
GAM87   KIAA1198 3' GCTGGTCTCAAACTCCTGACCT 63325     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAACTCTGGTCG
                                    C    C
GAM87   KIAA1257 3' GCTGGTCTCAAACTCCCGACTT 62750        AGT
            CA                    TGAAGTC   AGTTTGAGACTAGC
                                  |||||||   ||||||||||||||
                                  ACTTCAG   TCAAACTCTGGTCG
                                      CCC
GAM87   KIAA1493 3' GCTGGTCTCAAACTCCTGACCT 64163     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAACTCTGGTCG
                                    C    C
GAM87   KIAA1615 3' GTCTCAAACTCCCGACCTCA   68721     A  AGT
                                  TGA GTC   AGTTTGAGAC
                                  ||| |||   ||||||||||
                                  ACT CAG   TCAAACTCTG
                                    C   CCC
GAM87   KIAA1617 3' GCTAGTCTTGAACTCCCAACCT 91428     A  CAGT   TG
            CA                    TGA GT    AGTT  AGACTAGC
                                  ||| ||    ||||  ||||||||
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                                ACT CA    TCAA  TCTGATCG
                                  C  ACCC    GT
GAM87   KIAA1712  3'  GCTGGTCTCAAACTCCTGACCT 67540     A     T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAACTCTGGTCG
                                    C    C
GAM87   LHFPL2    3'  GCTATACAACCCTGACTTCA   69951          TAGT   AGAC
                                  TGAAGTCAG    TTG    TAGC
                                  |||||||||    |||    ||||
                                  ACTTCAGTC    AAC    ATCG
                                       CC__    AT__
GAM87   MAP-1     3'  GCTAGTTTCGAACTCCTGACCT 42181     A     T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAGCTTTGATCG
                                    C    C
GAM87   MGC:13379 3'  AGTCCCCTGCTGACCTCA     33244     A       TTTGA
                                  TGA GTCAGTAG     GACT
                                  ||| ||||||||     ||||
                                  ACT CAGTCGTC     CTGA
                                    C       CC___
GAM87   moblak    3'  GCTGGTCTCAAACTCCTGACTT 55507          T
            CA                    TGAAGTCAG AGTTTGAGACTAGC
                                  ||||||||| ||||||||||||||
                                  ACTTCAGTC TCAAACTCTGGTCG
                                       C
GAM87   MRPL44    3'  CTAGTCTTGAACTCCTGACCTC 43318     A     T    TG
            A                      TGA GTCAG AGTT  AGACTAG
                                  ||| ||||| ||||  |||||||
                                  ACT CAGTC TCAA  TCTGATC
                                    C    C    GT
GAM87   OSBPL2    3'  GCTGGTCTCAAACTCCCGACCT 57868     A   AGT
            CA                    TGA GTC   AGTTTGAGACTAGC
                                  ||| |||   ||||||||||||||
                                  ACT CAG   TCAAACTCTGGTCG
                                    C   CCC
GAM87   OSBPL2    3'  GCTGGTCTCAAACTCCCGACCT 29217     A   AGT
            CA                    TGA GTC   AGTTTGAGACTAGC
                                  ||| |||   ||||||||||||||
                                  ACT CAG   TCAAACTCTGGTCG
                                    C   CCC
GAM87   PELI1     5'  GCTGGTCTCAAACTCCCAACCT 40275     A  CAGT
            CA                    TGA GT    AGTTTGAGACTAGC
                                  ||| ||    ||||||||||||||
                                  ACT CA    TCAAACTCTGGTCG
                                    C  ACCC
GAM87   PIP3-E    3'  GCTGGTTTCAAACTCCTGACCT 66808     A     T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
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                                ACT CAGTC TCAAACTTTGGTCG
                                  C    C
GAM87   PRO0245  5' GCTAGTCTCAAACTCCCGA   26131    AGT
                                TC   AGTTTGAGACTAGC
                                ||   ||||||||||||||
                                AG   TCAAACTCTGATCG
                                 CCC
GAM87   PRO0529  5' GCTGGTCTCAAACTCCTGACCT 25995     A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   PRO2955  3' GCTGGTCTCAAACTCCTGACCT 37642     A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   PSTPIP2  3' GCTGGTCTCAAACTCCTGACCT 44394     A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   SC4MOL   3' GCTGGTCTCAAACTTCTGACCT 22159     A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    T
GAM87   SIRPB1   3' CTAGTCTTGAACTCCCGACCTC 20248     A   AGT   TG
           A                     TGA GTC   AGTT  AGACTAG
                                ||| |||   ||||  |||||||
                                ACT CAG   TCAA  TCTGATC
                                  C  CCC   GT
GAM87   SLC19A3  3' GCTGGTCTCAAACTCCTGACTT 47494          T
           CA                     TGAAGTCAG AGTTTGAGACTAGC
                                |||||||||| ||||||||||||||
                                ACTTCAGTC TCAAACTCTGGTCG
                                      C
GAM87   SRF      3' GCCAGCCTCCTTGCTGACCCCA 11949    AA       TTT   A  A
                                TG  GTCAGTAG   GAG CT GC
                                ||  ||||||||   ||| || ||
                                AC  CAGTCGTT   CTC GA CG
                                 CC       C__   C  C
GAM87   THEA     3' GCTGGTCTCAAACTCCTGACTT 66293          T
           CA                     TGAAGTCAG AGTTTGAGACTAGC
                                |||||||||| ||||||||||||||
                                ACTTCAGTC TCAAACTCTGGTCG
                                      C
GAM87   UBF-fl   3' GCTGGTCTCAAACTCCTGACCT 51567     A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
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                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   USP22    3' GTCTCAAACTCCTGACCTCA  68020     A    T
                                TGA GTCAG AGTTTGAGAC
                                ||| ||||| ||||||||||
                                ACT CAGTC TCAAACTCTG
                                  C    C
GAM87   VDU1     3' GCTAGTCTCAAACTCCTGACCT 30420     A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGATCG
                                  C    C
GAM87   VPS33A   3' GCTGGTCTCAAACTCCTGACCT 43341     A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   WBSCR23  3' GCTGGTCTCAAACTCCTGACCT 46766     A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   ZNF17    3' GCTGGTCTCAAACTCCCGACCT 82393     A   AGT
           CA                     TGA GTC   AGTTTGAGACTAGC
                                ||| |||   ||||||||||||||
                                ACT CAG   TCAAACTCTGGTCG
                                  C   CCC
GAM87   LOC115219 5' CTAGTCTCAAACTCCTGA    73304      T
                                TCAG AGTTTGAGACTAG
                                |||| ||||||||||||
                                AGTC TCAAACTCTGATC
                                  C
GAM87   LOC124216 3' GCCAGTCTCAAACTCCTGACCT 74263    A    T        A
           C                      GA GTCAG AGTTTGAGACT GC
                                || ||||| |||||||||| ||
                                CT CAGTC TCAAACTCTGA CG
                                 C    C         C
GAM87   LOC126669 3' GCTGGTCTCAAACTCCTGACCT 75410    A    T
           CA                     TGA GTCAG AGTTTGAGACTAGC
                                ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   LOC132625 3' GCTAGTCTCAAACTCCTGACCT 75908    A    T
           C                      GA GTCAG AGTTTGAGACTAGC
                                || ||||| ||||||||||||||
                                CT CAGTC TCAAACTCTGATCG
                                 C    C
GAM87   LOC134266 3' CTAATCATTCACTGACTT    75164        AGTT   GAC
                                AAGTCAGT    TGA   TAG
                                ||||||||    |||   |||
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                                TTCAGTCA   ACT   ATC
                                    CTT_   A__
GAM87   LOC143916 3'  GCTGGTCTCAAACTTCTGACCT 76644     A    T
          CA                      TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAACTCTGGTCG
                                    C    T
GAM87   LOC145268 3'  CACAACACTGACTTCA      77053          A  _
                                  TGAAGTCAGT GTT TG
                                  |||||||||| ||| ||
                                  ACTTCAGTCA CAA AC
                                        _  C
GAM87   LOC145453 5'  CTGGTCTCAAACTCCTGACCTC 77139     A    T
          A                       TGA GTCAG AGTTTGAGACTAG
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAACTCTGGTC
                                    C    C
GAM87   LOC145497 5'  GCTACAAGAGAACTACTACCTC 77216    A  TC       GAGAC
          CA                      TG AG  AGTAGTTT     TAGC
                                  || ||  ||||||||     ||||
                                  AC TC  TCATCAAG     ATCG
                                   C  CA       AGAAC
GAM87   LOC146050 3'  GCTGGTCTCAAACTCCCGACCT 77645     A   AGT
          CA                      TGA GTC   AGTTTGAGACTAGC
                                  ||| |||   ||||||||||||||
                                  ACT CAG   TCAAACTCTGGTCG
                                    C   CCC
GAM87   LOC146229 3'  GCTGGTCTCAAACTCCTGACCT 77762     A    T
          CA                      TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAACTCTGGTCG
                                    C    C
GAM87   LOC146229 3'  GCTGGTCTCAAACTCCTGACCT 77763     A    T
          CA                      TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAACTCTGGTCG
                                    C    C
GAM87   LOC146229 3'  GCTGGTCTCAAACTCCTGACTT 77764          T
          CA                      TGAAGTCAG AGTTTGAGACTAGC
                                  |||||||||| ||||||||||||||
                                  ACTTCAGTC TCAAACTCTGGTCG
                                       C
GAM87   LOC146952 5'  GCTGGTCTCAAACTCCTGACCT 83872     A    T
          CA                      TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAACTCTGGTCG
                                    C    C
GAM87   LOC148709 3'  GCTAGTCTCAAACTCCCGACCT 78945     A   AGT
          TA                      TGA GTC   AGTTTGAGACTAGC
                                  ||| |||   ||||||||||||||
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                                ATT CAG   TCAAACTCTGATCG
                                  C   CCC
GAM87   LOC150225 3'  GCTGGTCTCAAACTCCTGACCT 85001     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAACTCTGGTCG
                                    C    C
GAM87   LOC152794 5'  GCTAGTCTTGAACTCCTGACCT 80679     A    T   TG
            CA                    TGA GTCAG AGTT  AGACTAGC
                                  ||| ||||| ||||  ||||||||
                                  ACT CAGTC TCAA  TCTGATCG
                                    C    C   GT
GAM87   LOC153811 3'  GCTGGTCTCAAACTCCTGACCT 80954     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAACTCTGGTCG
                                    C    C
GAM87   LOC158434 3'  TCAAACACTGACCTCA      86825     A    A
                                  TGA GTCAGT GTTTGA
                                  ||| |||||| ||||||
                                  ACT CAGTCA CAAACT
                                    C    _
GAM87   LOC162427 3'  GCTGGTCTCAAACTCCTGACCT 82352     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAACTCTGGTCG
                                    C    C
GAM87   LOC169611 3'  GCCAGTCTCAAACTCCTGACCT 82767     A    T        A
            CA                    TGA GTCAG AGTTTGAGACT GC
                                  ||| ||||| |||||||||||  ||
                                  ACT CAGTC TCAAACTCTGA CG
                                    C    C         C
GAM87   LOC196047 5'  GCTAGTCTCAAACTCCTGACCT 89603     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAACTCTGATCG
                                    C    C
GAM87   LOC199906 3'  GCTGGTCTCAAACTCCTGACCT 88485     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAACTCTGGTCG
                                    C    C
GAM87   LOC200407 3'  GCTGGTCTCAAACTCCTGACCT 90045     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAACTCTGGTCG
                                    C    C
GAM87   LOC201164 3'  GCTGGTCTCAAACTCCTGACCT 88120     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
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                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM87   LOC201627 3'  GCTGGTCTCAAACTCCCGACCT 89020     A   AGT
            CA                    TGA GTC   AGTTTGAGACTAGC
                                  ||| |||   ||||||||||||||
                                  ACT CAG   TCAAACTCTGGTCG
                                    C   CCC
GAM87   LOC220074 3'  GCTGGTCTCAAACTCCTGACCT 59279     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAACTCTGGTCG
                                    C    C
GAM87   LOC221037 5'  GCTAATCCTCAAACTCTGACTT 93156         T       AC_
            CA                    TGAAGTCAG AGTTTGAG   TAGC
                                  |||||||| ||||||||   ||||
                                  ACTTCAGTC TCAAACTC   ATCG
                                       _       CTA
GAM87   LOC254268 3'  GCTGGTCTCAAACTCCTGACCT 95412     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                  ACT CAGTC TCAAACTCTGGTCG
                                    C    C
GAM87   LOC254532 5'  GTCTCAAACTCCTGACCTCA   96643     A    T
                                  TGA GTCAG AGTTTGAGAC
                                  ||| ||||| |||||||||
                                  ACT CAGTC TCAAACTCTG
                                    C    C
GAM87   LOC255065 5'  TCTCAAACTCCTGACCTCA    96585     A    T
                                  TGA GTCAG AGTTTGAGA
                                  ||| ||||| |||||||||
                                  ACT CAGTC TCAAACTCT
                                    C    C
GAM87   LOC256281 3'  GCCAGTCTTGGCCACTCACCCC 94942     AA  C   A T TG    A
            A                      TG  GT AGT G T  AGACT GC
                                  ||  || ||| | |  ||||| ||
                                  AC  CA TCA C G  TCTGA CG
                                   CC  C   C _ GT    C
GAM87   LOC51193  3'  GCCAGTCTCAAACTCCTGGACT 32907     AG   T        A
            CA                    TGA  TCAG AGTTTGAGACT GC
                                  |||  |||| |||||||||||| ||
                                  ACT  GGTC TCAAACTCTGA CG
                                    CA   C         C
GAM87   LOC51200  3'  GCTGGTCTCAAACTCCCAACCT 33001     A  CAGT
            CA                    TGA GT    AGTTTGAGACTAGC
                                  ||| ||    ||||||||||||||
                                  ACT CA    TCAAACTCTGGTCG
                                    C  ACCC
GAM87   LOC57107  3'  GCTAGTCTCGAACTCCTGACCT 39838     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
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                                ACT CAGTC TCAAGCTCTGATCG
                                  C    C
GAM87   LOC57146 3'  GCTAGTCTCAAACTCCTGACCT 39922     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGATCG
                                  C    C
GAM87   LOC92267 3'  GCTGGTCTCAAACTCCTGACCT 68621     A    T
            CA                    TGA GTCAG AGTTTGAGACTAGC
                                  ||| ||||| ||||||||||||||
                                ACT CAGTC TCAAACTCTGGTCG
                                  C    C
GAM88   ATRN    3'  TTAATGGGTGCAGCACAC    57809        C  TT
                                GTGTGCTGT TT  TTAA
                                ||||||||| ||  ||||
                                CACACGACG GG  AATT
                                      T  GT
GAM88   ATRN    3'  TTAATGGGTGCAGCACAC    23833        C  TT
                                GTGTGCTGT TT  TTAA
                                ||||||||| ||  ||||
                                CACACGACG GG  AATT
                                      T  GT
GAM88   BHLHB3   3'  TTAAAAAAGACATAATGGATG  47769       GTGTGC
                                CATCCA     TGTCTTTTTTAA
                                ||||||     ||||||||||||
                                GTAGGT     ACAGAAAAAATT
                                   AAT___
GAM88   MLLT2    3'  TAAAAAAGAAGCACCACGAGAT 19851     CA  _   G
            G                    CATC  GTG TGCT TCTTTTTTA
                                 ||||  ||| |||| |||||||||
                                GTAG  CAC ACGA AGAAAAAAT
                                  AG  C   _
GAM88   MTMR2    3'  AAAGAACACACTGCATG     32379     C      CTG
                                CAT CAGTGTG   TCTTT
                                ||| |||||||   |||||
                                GTA GTCACAC   AGAAA
                                  C      A__
GAM88   SCN3A    3'  AAGGAAACACACTGGAT     22627          CTG
                                ATCCAGTGTG   TCTTT
                                |||||||||   |||||
                                TAGGTCACAC   AGGAA
                                      AA_
GAM88   SOX9     3'  TAAAAAAGACAGCAAACT    4440      G
                                AGT TGCTGTCTTTTTTA
                                ||| ||||||||||||||
                                TCA ACGACAGAAAAAAT
                                  A
GAM88   CNOT7    3'  TAAAAAAGACAAGAAACT    25333     GTG _
                                AGT   CT GTCTTTTTTA
                                |||   || ||||||||||
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                                TCA   GA CAGAAAAAAT
                                  AA_  A
GAM88   DKFZp762K2015 3'  AAAAAAGAAGCCAC       72472     T   G
                                GTG GCT TCTTTTTT
                                ||| ||| ||||||||
                                CAC CGA AGAAAAAA
                                  _  _
GAM88   FUBP3    3'  TTAAAAAAGACAATTGGA    63735       GTGC
                                TCCAGT    TGTCTTTTTTAA
                                ||||||    ||||||||||||
                                AGGTTA    ACAGAAAAAATT
                                    ____
GAM88   GOLPH3   3'  TTAAATTGAAACAGCACA    42116        C  T_
                                TGTGCTGT TT  TTTAA
                                |||||||| ||  |||||
                                ACACGACA AG  AAATT
                                     A  TT
GAM88   KIAA1001  3'  AAAAAAGACTTTGCCTGG    30286     T   CT
                                CCAG GTG  GTCTTTTTT
                                |||| |||  |||||||||
                                GGTC CGT  CAGAAAAAA
                                  _   TT
GAM88   KIAA1466  3'  AAAAAAGACATAGAC       71912     G  C
                                GT TG TGTCTTTTTT
                                || || ||||||||||
                                CA AT ACAGAAAAAA
                                 G  _
GAM88   KIAA1468  3'  TAAAAAAGACATTGGCTG    91776      GTGC
                                CAGT    TGTCTTTTTTA
                                ||||    ||||||||||
                                GTCG    ACAGAAAAAAT
                                  GTT_
GAM88   KIAA1883  3'  TAAAAAAGACAAAAACA     73420     GC_
                                TGT   TGTCTTTTTTA
                                |||   ||||||||||
                                ACA   ACAGAAAAAAT
                                  AAA
GAM88   MEGF10   3'  TTAAAAAAGAAAATCTGGA    50587       TGTGCTG
                                TCCAG      TCTTTTTTAA
                                |||||      ||||||||||
                                AGGTC      AGAAAAAATT
                                   TAAA___
GAM88   MOST2    5'  TAAAAAAGACAGGAGGA     39690     AGTGTG
                                TCC     CTGTCTTTTTTA
                                |||     ||||||||||||
                                AGG     GACAGAAAAAAT
                                  AG____
GAM88   PPP1R16B  3'  TTAAAAAAAACAGTCGCT    61394      T    C
                                AGTG GCTGT TTTTTTAA
                                |||| ||||| ||||||||
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                                TCGC TGACA AAAAAATT
                                  _    A
GAM88   SLC11A2   3'  AAAAGCGCAGACTGGATG    5230        G   T T
                                CATCCAGT TGC G CTTTT
                                |||||||| ||| | |||||
                                GTAGGTCA ACG C GAAAA
                                    G  _ _
GAM88   LOC124783 5'  AAAGAGCACACTGGA      74334         TG
                                TCCAGTGTGC  TCTTT
                                ||||||||||  |||||
                                AGGTCACACG  AGAAA
                                     __
GAM88   LOC144248 5'  TAAAAAAGACAAACA      76743     GC
                                TGT  TGTCTTTTTTA
                                |||  ||||||||||
                                ACA  ACAGAAAAAAT
                                  A_
GAM88   LOC146712 5'  AAGGCCAGCACACAGGA     83712     A      _
                                TCC GTGTGCTG TCTT
                                ||| |||||||| ||||
                                AGG CACACGAC GGAA
                                  A       C
GAM88   LOC146723 3'  AAAAAAGACACTTGTACAC   78081       ___
                                GTGTGC   TGTCTTTTTT
                                ||||||   ||||||||||
                                CACATG   ACAGAAAAAA
                                    TTC
GAM88   LOC151040 3'  TTAATGGGTGCAGCACAC    80105         C  TT
                                GTGTGCTGT TT  TTAA
                                ||||||||| ||  ||||
                                CACACGACG GG  AATT
                                      T  GT
GAM88   LOC153606 5'  TTAAAACAAAACAAACACTGGA 86077         GC   C  _
                                TCCAGTGT  TGT TT TTTTAA
                                ||||||||  ||| || ||||||
                                AGGTCACA  ACA AA AAAATT
                                     A_   A  C
GAM88   LOC157697 5'  GACAGCACACAGATG       81549      CA
                                CATC  GTGTGCTGTC
                                ||||  ||||||||||
                                GTAG  CACACGACAG
                                  A_
GAM88   LOC220906 3'  AAAAAGACCCACACCGGA    91395     A    CT
                                TCC GTGTG  GTCTTTTT
                                ||| |||||  ||||||||
                                AGG CACAC  CAGAAAAA
                                  C    C_
GAM88   LOC222252 3'  TTAATGGGTGCAGCACAC    94310         C  TT
                                GTGTGCTGT TT  TTAA
                                ||||||||| ||  ||||
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                                CACACGACG GG  AATT
                                     T  GT
GAM88   LOC222697 3'  TAAAAAAACACACTGGA     94354         CTGTC
                                TCCAGTGTG    TTTTTTA
                                |||||||||    |||||||
                                AGGTCACAC    AAAAAAT
                                     A____
GAM88   LOC90317  5'  AAAGGAGTCACACTGGA     62248         _  G
                                TCCAGTGTG CT TCTTT
                                ||||||||| || |||||
                                AGGTCACAC GA GGAAA
                                     T  _
GAM88   LOC90829  3'  TTAATGGGTGCAGCACAC    64101         C  TT
                                GTGTGCTGT TT  TTAA
                                ||||||||| ||  ||||
                                CACACGACG GG  AATT
                                     T  GT
GAM88   LOC92876  3'  TTAATGGGTGCAGCACAC    70806         C  TT
                                GTGTGCTGT TT  TTAA
                                ||||||||| ||  ||||
                                CACACGACG GG  AATT
                                     T  GT
GAM89   RTN3      3'  CTCAGTATCAAGCACAA     73899      T      AGCT
                                TTGT GCTTGATGC    TGAG
                                |||| |||||||||    ||||
                                AACA CGAACTATG    ACTC
                                  _       _____
GAM89   SYNGR1    3'  CTCCCCATCAAGCACAA     16316      T      CAGCTT
                                TTGT GCTTGATG     GAG
                                |||| ||||||||     |||
                                AACA CGAACTAC     CTC
                                  _       CC_____
GAM89   FLJ20073  3'  CTCTCAAACTGAGGAGCAACA  34482         GATG   C
                                TGTTGCTT    CAG TTGAGAG
                                ||||||||    ||| |||||||
                                ACAACGAG    GTC AACTCTC
                                     GA__   A
GAM89   LOC152905 3'  CTCAGTATCAAGCACAA     60475      T      AGCT
                                TTGT GCTTGATGC    TGAG
                                |||| |||||||||    ||||
                                AACA CGAACTATG    ACTC
                                  _       _____
GAM89   LOC168448 3'  CTCTCAAGCTGAATGACAA   82698       GCTTGATG
                                TTGTT       CAGCTTGAGAG
                                |||||       ||||||||||||
                                AACAG       GTCGAACTCTC
                                   TAA_____
GAM89   LOC256401 3'  CTCTCAAGCTGAATGACAA   96018       GCTTGATG
                                TTGTT       CAGCTTGAGAG
                                |||||       ||||||||||||
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                                AACAG       GTCGAACTCTC
                                  TAA_____
GAM89   LOC57406 3'  CTCAGGTTCCACACACAAGCAA 40345          A___  C
            CAA                   TTGTTGCTTG    TG AGCTTGAG
                                  ||||||||||    || ||||||||
                                  AACAACGAAC    AC TTGGACTC
                                      ACAC  C
GAM90   BMP1     3'  GCCTCACATTCCAGTCCTTTGA 20423    C    AC   AT
            GA                    TC CAAAG  CTG  GTGTGAGGC
                                  || |||||  |||  |||||||||
                                  AG GTTTC  GAC  TACACTCCG
                                   A    CT   CT
GAM90   CPD      3'  TTCACATAGGCCTCTGGGA   7132       A  A   GAT
                                  TCCCA AG CCT   GTGTGAG
                                  ||||| || |||   |||||||
                                  AGGGT TC GGA   TACACTT
                                    C  C  ___
GAM90   LHX3     3'  GCCTCCTCCATCAGATCCTTTG 27374         AC_     TGT
            GGA                   TCCCAAAG   CTGATG   GAGGC
                                  ||||||||   ||||||   |||||
                                  AGGGTTTC   GACTAC   CTCCG
                                      CTA     CTC
GAM90   MEOX1    3'  CCTCAGCCAGGTCTTCTGGA   25729     CA      AT  G
                                  TCC  AAGACCTG  GT TGAGG
                                  |||  ||||||||  || |||||
                                  AGG  TTCTGGAC  CG ACTCC
                                   TC      __  _
GAM90   MEOX1    3'  CCTCAGCCAGGTCTTCTGGA   15755     CA      AT  G
                                  TCC  AAGACCTG  GT TGAGG
                                  |||  ||||||||  || |||||
                                  AGG  TTCTGGAC  CG ACTCC
                                   TC      __  _
GAM90   MYH11    3'  CTTCTCACGTCAGGCCTTTGAG 10174    C    A       T
            A                     TC CAAAG CCTGATGTG GAGG
                                  || ||||| |||||||||| ||||
                                  AG GTTTC GGACTGCAC CTTC
                                   A    C       T
GAM90   MYH11    3'  CTTCTCACGTCAGGCCTTTGAG 43135    C    A       T
            A                     TC CAAAG CCTGATGTG GAGG
                                  || ||||| |||||||||| ||||
                                  AG GTTTC GGACTGCAC CTTC
                                   A    C       T
GAM90   MYH11    3'  CTTCTCACGTCAGGCCTTTGAG 43148    C    A       T
            A                     TC CAAAG CCTGATGTG GAGG
                                  || ||||| |||||||||| ||||
                                  AG GTTTC GGACTGCAC CTTC
                                   A    C       T
GAM90   NAPB     3'  GCCTGTGAGCTAGGTCTTCAAG 70185    CCA      AT  GTG_
            A                     TC   AAGACCTG  GT   AGGC
                                  ||   ||||||||  ||   ||||
```

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                                AG  TTCTGGAT CG   TCCG
                                 AAC      __ AGTG
GAM90   PFKFB4   3' GCCCAAGGACCATGCCTTTGGG 15870       ACC ATGTG A
           A                    TCCCAAAG  TG    TG GGC
                                |||||||| ||    || |||
                                AGGGTTTC  AC    AC CCG
                                    CGT CAGGA _
GAM90   RBL1    3' GCCTCTAATCCCAGGACTTTGG 11262       A   AT GT
           GA                    TCCCAAAG CCTG GT GAGGC
                                |||||||| |||| || |||||
                                AGGGTTTC GGAC TA CTCCG
                                    A  CC AT
GAM90   REG1A   3' CCTACCCCAGTCTTTGG    88849       C AT GTG
                                CCAAAGAC TG GT  AGG
                                |||||||| ||  ||  |||
                                GGTTTCTG AC CA  TCC
                                    _ CC ___
GAM90   RPP30   3' GCCTACGTAAGGTCTTTG   21166       G  GTG
                                CAAAGACCT ATGT  AGGC
                                ||||||||| ||||  ||||
                                GTTTCTGGA TGCA  TCCG
                                    A  ___
GAM90   RPS6KA1 3' GCCTCACACAGTTGCTTCAAGG 59317    CA_  ACCTGA
           A                    TCC  AAG    TGTGTGAGGC
                                |||  |||    ||||||||||
                                AGG  TTC    ACACACTCCG
                                 AAC  GTTG__
GAM90   SNRPN   5' GCCTTCCCCTAGGTCTTCAGA 43014   CCA     ATGTGT
                                TC  AAGACCTG    GAGGC
                                ||  ||||||||    |||||
                                AG  TTCTGGAT    TTCCG
                                 AC_     CCCC__
GAM90   SNRPN   5' GCCTTCCCCTAGGTCTTCAGA 42999   CCA     ATGTGT
                                TC  AAGACCTG    GAGGC
                                ||  ||||||||    |||||
                                AG  TTCTGGAT    TTCCG
                                 AC_     CCCC__
GAM90   SNRPN   5' GCCTTCCCCTAGGTCTTCAGA 43007   CCA     ATGTGT
                                TC  AAGACCTG    GAGGC
                                ||  ||||||||    |||||
                                AG  TTCTGGAT    TTCCG
                                 AC_     CCCC__
GAM90   SNRPN   5' GCCTTCCCCTAGGTCTTCAGA 42993   CCA     ATGTGT
                                TC  AAGACCTG    GAGGC
                                ||  ||||||||    |||||
                                AG  TTCTGGAT    TTCCG
                                 AC_     CCCC__
GAM90   SYT1    3' GCCTCATGTTCAGTCTTCAGGA 18902   CA   C  T TG
                                TCC AAGAC TGA G  TGAGGC
                                ||| ||||| ||| |  ||||||
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                                AGG  TTCTG ACT T  ACTCCG
                                  AC     _  _ GT
GAM90   TIRAP    3'  ACCATCAGGTTCCAGGA     53562     CAAA        T
                                TCC    GACCTGATG GT
                                |||    ||||||||| ||
                                AGG    TTGGACTAC CA
                                  ACC_        _
GAM90   AAK1     3'  GCCTGTGCTACCAGCTCTTTGG 29847          C   AT_ TG G
           GA                     TCCCAAAGA CTG   G  T AGGC
                                |||||||| |||   |  | ||||
                                AGGGTTTCT GAC   C  G TCCG
                                     C   CAT GT _
GAM90   ARAP3    3'  GCCCCACATATTATCCCTG    42504    AA  CC       A
                                CA  GA  TGATGTGTG GGC
                                ||  ||  ||||||||| |||
                                GT  CT  ATTATACAC CCG
                                 CC  __        C
GAM90   ASB16    5'  GCCTCCACCCAGGTCTCACAGG 69937     CAA_      AT   T
           A                     TCC    AGACCTG  GTG GAGGC
                                |||    |||||||  ||| |||||
                                AGG    TCTGGAC  CAC CTCCG
                                  ACAC      C_  _
GAM90   BMF      3'  CCTCCAGCAGACCTCAGGGA   53154      AA  AC   ATG  T
                                TCCC  AG  CTG   TG GAGG
                                ||||  ||  |||   || ||||
                                AGGG  TC  GAC   AC CTCC
                                  AC  CA   G__  _
GAM90   C20orf106 3'  GCCTGTGGTCCCAGAACTTTGG 55058         AC   ATGTGTG
           GA                     TCCCAAAG  CTG      AGGC
                                ||||||||  |||      ||||
                                AGGGTTTC  GAC      TCCG
                                     AA   CCTGGTG
GAM90   C20orf188 3'  GCCTGCCCCAGGTCTTTGGG   31579           AT  GTG
                                CCCAAAGACCTG  GT   AGGC
                                ||||||||||||  ||   ||||
                                GGGTTTCTGGAC  CG   TCCG
                                       CC  ___
GAM90   DKFZP434J193 3'  CCCAAGGCCCAAGTGCTTTGGG 71004         AC  GAT  G_  A
           A                     TCCCAAAG  CT   GT  TG GG
                                ||||||||  ||   ||  || ||
                                AGGGTTTC  GA   CG  AC CC
                                     GT  ACC  GA  _
GAM90   DKFZP564I1171 5'  CCTCGCCAGGTCTTTG      71586          ATGT
                                CAAAGACCTG    GTGAGG
                                ||||||||||    ||||||
                                GTTTCTGGAC    CGCTCC
                                              _____
GAM90   DKFZP586N2124 5'  CCTCACACTCCCTCTGG     31247     A  ACCT  T
                                CCA AG    GA GTGTGAGG
                                ||| ||    || ||||||||
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                                GGT TC    CT CACACTCC
                                  C  C___  _
GAM90   FLJ12876  3' CCTCACCCAGGTTTT      42783        ATGT
                                AAGACCTG   GTGAGG
                                ||||||||   ||||||
                                TTTTGGAC   CACTCC
                                    C___
GAM90   FLJ22055  3' CCTCACACCTCTCCTGGGA   45494      AA  CCT  T
                                TCCCA  GA   GA GTGTGAGG
                                |||||  ||   || ||||||||
                                AGGGT  CT   CT CACACTCC
                                  C_  ___  C
GAM90   KIAA0700  3' CTTCAGCCAAACCTTTGGGA  72055        ACCTGA  TG
                                TCCCAAAG     TG  TGAGG
                                ||||||||     ||  |||||
                                AGGGTTTC     AC  ACTTC
                                    CAA___  CG
GAM90   KIAA0970  3' CCTCTTCAGGTCTTGAGA    29958    CCA       TGTGT
                                TC   AAGACCTGA    GAGG
                                ||   |||||||||    ||||
                                AG   TTCTGGACT    CTCC
                                 AG_       T____
GAM90   KIAA0982  3' CCTCAGAGACGGGTCTTTGGGA 25847           ATGTG
                                TCCCAAAGACCTG    TGAGG
                                ||||||||||||    |||||
                                AGGGTTTCTGGGC    ACTCC
                                      AGAG_
GAM90   KIAA0984  3' CTTATACAAGTCCTTGGGA   65528       A   CTGA
                                TCCCAA GAC    TGTGTGAG
                                |||||| |||    ||||||||
                                AGGGTT CTG    ACATATTC
                                   C   A___
GAM90   KIAA1001  3' GCCTGTAGTCCCAGAGCTTTGG 30292        AC   ATGTGTG
           GA                    TCCCAAAG  CTG      AGGC
                                ||||||||  |||      ||||
                                AGGGTTTC  GAC      TCCG
                                    GA   CCTGATG
GAM90   KIAA1228  3' CCTCACACATAGGATGTGGGA  65040      AAGA    A
                                TCCCA    CCTG TGTGTGAGG
                                |||||    |||| |||||||||
                                AGGGT    GGAT ACACACTCC
                                  GTA_   _
GAM90   KIAA1511  3' GCCTCACACAGCCTCTTCAGGA 70167     CA    CCTGA
                                TCC  AAGA    TGTGTGAGGC
                                |||  ||||    ||||||||||
                                AGG  TTCT    ACACACTCCG
                                  AC   CCG__
GAM90   KIAA1594  3' CACATCAGGTTTTCAGA     72083    CCA
                                TC   AAGACCTGATGTG
                                ||   |||||||||||||
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                                AG  TTTTGGACTACAC
                                 AC_
GAM90  KIAA1831 3' GCCAACACCAAGTCTTGCAGGA 63783    CA_   C AT   GA
                                TCC  AAGAC TG  GTGT  GGC
                                |||  ||||| ||  ||||  |||
                                AGG  TTCTG AC  CACA  CCG
                                  ACG    A __   A_
GAM90  MFN2    3' GCCTCATGGAAGCCTTTGAGG 29602   _    AC  GATG
                                CC CAAAG  CT   TGTGAGGC
                                || |||||  ||   ||||||||
                                GG GTTTC  GA   GTACTCCG
                                 A    C_  AG__
GAM90  MGC2560  5' CTCAAACCTTTGGGA      48780        ACCTGAT  G
                                TCCCAAAG     GT TGAG
                                ||||||||     || ||||
                                AGGGTTTC     CA ACTC
                                    ________  A
GAM90  MGC2562  3' GCCTTTAGTCCCAGCTCTTTGG 50444        C   ATGTGT
            GA                    TCCCAAAGA CTG     GAGGC
                                |||||||||| |||     |||||
                                AGGGTTTCT GAC     TTCCG
                                     C   CCTGAT
GAM90  MIG     3' GCCTCACACACAATGTGTCT   10038     C___  A
                                AGAC    TG TGTGTGAGGC
                                ||||    || ||||||||||
                                TCTG    AC ACACACTCCG
                                  TGTA  _
GAM90  PIWIL2   3' CCTGTAATCCAAGCACTTTGGG 36054       AC  GAT  GTG
            A                    TCCCAAAG  CT   GT   AGG
                                ||||||||  ||   ||   |||
                                AGGGTTTC  GA   TA   TCC
                                     AC  ACC  ATG
GAM90  PRO1483  3' CCTCACAGGAGTTTTGAGA   37720    C    AC  GATG
                                TC CAAAG  CT   TGTGAGG
                                || |||||  ||   |||||||
                                AG GTTTT  GG   ACACTCC
                                 A    GA  ____
GAM90  SNT-2    3' GCCTCACACTCCTGTC     21842     CT  T
                                GAC  GA GTGTGAGGC
                                |||  || |||||||||
                                CTG  CT CACACTCCG
                                  TC  _
GAM90  SNURF    3' GCCTTCCCCTAGGTCTTCAGA  19053    CCA      ATGTGT
                                TC   AAGACCTG     GAGGC
                                ||   ||||||||     |||||
                                AG   TTCTGGAT     TTCCG
                                 AC_       CCCC__
GAM90  TIMM13   3' CCTCCTTCAGGCCTTTGGGG   24940        A    TGTGT
                                TCCCAAAG CCTGA    GAGG
                                |||||||| |||||    ||||
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                                GGGGTTTC GGACT    CTCC
                                     C    TC___
GAM90   ZFP106   3' GCCACATACCAAGCTTTGGGA 42469       AC  GAT    A
                                TCCCAAAG  CT   GTGTG GGC
                                ||||||||  ||   ||||| |||
                                AGGGTTTC  GA   CATAC CCG
                                     __  AC_    A
GAM90   LOC145739 3' GCTTCATGCAGATCTCTGG   77441    A   CCTGA
                                CCA AGA    TGTGTGAGGC
                                ||| |||    ||||||||||
                                GGT TCT    ACGTACTTCG
                                  C   AG___
GAM90   LOC147859 5' CCTCTCTCTCGGCCTTTGGGA 87174       A  T  TGTGT
                                TCCCAAAG CC GA    GAGG
                                |||||||| || ||    ||||
                                AGGGTTTC GG CT    CTCC
                                     C  _  CTCT_
GAM90   LOC149650 3' GCCCACTCGTATCAGGTCCCGG 79468     AAA       T__   A
           GA                    TCCC   GACCTGATG   GTG GGC
                                ||||   |||||||||   ||| |||
                                AGGG   CTGGACTAT   CAC CCG
                                  CC_       GCT   _
GAM90   LOC150157 5' CCTCACACCCAGGACCTCTGAG 84875    AA   ___    AT
           G                     CC  AGA   CCTG  GTGTGAGG
                                ||  |||   ||||  ||||||||
                                GG  TCT   GGAC  CACACTCC
                                 AG   CCA   C_
GAM90   LOC154860 5' GCCTGGGACAGGTCTTTG    86273         ATGTGTG
                                CAAAGACCTG      AGGC
                                ||||||||||      ||||
                                GTTTCTGGAC      TCCG
                                     AGGG___
GAM90   LOC196872 5' GCCTCACAGCTCTGTCTGTGGG 87797      A   CT  TG
           A                     TCCCA AGAC  GA  TGTGAGGC
                                ||||| ||||  ||  ||||||||
                                AGGGT TCTG  CT  ACACTCCG
                                   G   T_  CG
GAM90   LOC200940 3' GCCTCACATCGCAGCCTC    88954    C_  AT
                                GA  CTG  GTGTGAGGC
                                ||  |||  |||||||||
                                CT  GAC  TACACTCCG
                                 CC   GC
GAM90   LOC221410 3' CCTGTAATCCAAGCACTTTGGG 92058       AC  GAT  GTG
           A                     TCCCAAAG  CT   GT   AGG
                                ||||||||  ||   ||   |||
                                AGGGTTTC  GA   TA   TCC
                                     AC  ACC  ATG
GAM90   LOC222962 3' GTCTGCATCAGCCTCTGGGA   92877      A  AC     GTG
                                TCCCA AG  CTGATGT   AGGC
                                ||||| ||  |||||||   ||||
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                                AGGGT TC  GACTACG   TCTG
                                  C  C_     ___
GAM90   LOC254842 5'  CCTCACCCAGTCACCGGGA   97596     AAA   CTGA  T
                                TCCC   GAC    TG GTGAGG
                                ||||   |||    || ||||||
                                AGGG   CTG    AC CACTCC
                                  CCA   ____  C
GAM90   LOC57147  3'  CCTCAAAAGCAGGCTTTGGGA  39931        A    ATGTG
                                TCCCAAAG CCTG     TGAGG
                                |||||||| ||||     |||||
                                AGGGTTTC GGAC     ACTCC
                                     _   GAAA_
GAM90   LOC92249  5'  GCCTCACACACCACGT      68565    C  A
                                AC TG TGTGTGAGGC
                                || || ||||||||||
                                TG AC ACACACTCCG
                                 C  C
GAM91   AR        5'  GAGCTAGCCGCTCCAGTG    3493       A  ACA
                                TACT GA   GCTAGCTC
                                |||| ||   ||||||||
                                GTGA CT   CGATCGAG
                                  C  CGC
GAM92   ADH1B     3'  CTTAGACATAAAGTAAAAT   72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM92   AHR       3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM92   FDFT1     3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                                _
GAM92   JTB       3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM92   KLF4      3'  TCCCAGACAGTGGATATG     14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM92   PHYH      3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
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                                TAAAGTGAAA TGACA
                                     A
GAM92   PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG   A
                                TTTCACTTTCA  TCTG GA
                                ||||||||||  |||| ||
                                AAAGTGAAAGT  GGAC CT
                                      T__   _
GAM92   WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM92   ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017        CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM92   CG012   5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM92   EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM92   FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM92   FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM92   KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534     C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                   A       CT
GAM92   KLHL6   3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                   _  G
GAM92   NIR3    3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
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                                TAA GTGAAAGTGACG
                                  C
GAM92   PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM92   PP35     3' ATCTCAGACTGAAA      22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM92   PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148        TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM92   SEP15    3' TCCTACAGTAAGAGTGAAA   14934       C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM92   SFXN2    3' CTCAGGGGAAAAAAGTGAAA  73941        CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM92   LOC149703 3' ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM92   LOC154007 3' ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM92   LOC155004 3' TCATTTAAGTGAAAGGAAA   81226     A      GTC_
                                TTTC CTTTCACT   TGA
                                |||| ||||||||   |||
                                AAAG GAAAGTGA   ACT
                                  _      ATTT
GAM92   LOC222134 5' ACAGTGAAGTGAAATG     94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM93   CNGA1    3' CAACTGATAATGTGCAAA    59507         GC  A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
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                                AAACGTGTAAT  GTC AAC
                                      A_  _
GAM93   ESRRG    3'  TGGCAGTCTTATGTGCAAA   66396        TAGCT
                                TTTGCACAT    AGATTGCCA
                                |||||||||    |||||||||
                                AAACGTGTA    TCTGACGGT
                                     T____
GAM93   KCNJ3    3'  GCAATAATGTGCAAA      9525          GCTAGA
                                TTTGCACATTA     TTGC
                                ||||||||||     ||||
                                AAACGTGTAAT     AACG
                                       ______
GAM93   SDC2     3'  GCAAATTAATGTGTAAA     67132          CTAGA
                                TTTGCACATTAG    TTGC
                                ||||||||||||    ||||
                                AAATGTGTAATT    AACG
                                      A____
GAM93   USP9X    3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
           A                     TTTGCACATTAGC     GCCAT
                                ||||||||||||      |||||
                                AAATGTGTAATCG     CGGTA
                                       TAGTC_
GAM93   AMOTL1   3'  GGCAAGTAATGTGCAAA     73650          G  AGAT
                                TTTGCACATTA CT    TGCC
                                |||||||||| ||    ||||
                                AAACGTGTAAT GA    ACGG
                                      _ _____
GAM93   BCAR3    3'  AGTAATAATGTGCAAA      13098          __
                                TTTGCACATTA  GCT
                                ||||||||||  |||
                                AAACGTGTAAT  TGA
                                      AA
GAM93   DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930         AGCTA    C
                                TTTGCACATT     GATTG CA
                                |||||||||     ||||| ||
                                AGACGTGTAA     TTAAC GT
                                     A____     A
GAM93   MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                TTTGCACATTAG  AGA TG CAT
                                ||||||||||||  ||| || |||
                                AGACGTGTAATC  TTT AC GTA
                                      __  T  A
GAM93   PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
           AA                    TTTGCACATTAGCTAGATTGCCAT
                                ||||||||||||||||||||||||||
                                AAACGTGTAATCGATCTAACGGTA

GAM94   ASPH     5'  TGGATTGAAGAAATCAA     39396     GC      _
                                TTG  TTCTTCAA CCA
                                |||  |||||||| |||
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                                AAC  AAGAAGTT GGT
                                  TA       A
GAM94   ASPH    5'  TGGATTGAAGAAATCAA    50626    GC      _
                                TTG  TTCTTCAA CCA
                                |||  |||||||| |||
                                AAC  AAGAAGTT GGT
                                  TA       A
GAM94   ASPH    5'  TGGATTGAAGAAATCAA    50634    GC      _
                                TTG  TTCTTCAA CCA
                                |||  |||||||| |||
                                AAC  AAGAAGTT GGT
                                  TA       A
GAM94   FOS     5'  GCGAGCAACTGAGAAGCCAA  17906        T  ACCA  A_
                                TTGGCTTCT CA    GC  GT
                                |||||||| ||    ||  ||
                                AACCGAAGA GT    CG  CG
                                      _ CAA_  AG
GAM94   FSTL1   3'  ATACTGCTAGTTAACCCAG   23010     C  CTTC   C
                                TTGG TT    AAC AGCAGTAT
                                ||||  ||    ||| ||||||||
                                GACC AA    TTG TCGTCATA
                                  C _____  A
GAM94   NR4A2   3'  TGAGTTGAAGAAGGCAA    20535    G       _
                                TTG CTTCTTCAAC CA
                                ||| |||||||||| ||
                                AAC GAAGAAGTTG GT
                                  G        A
GAM94   NXF5    3'  CTGGCTGACCAAGAAGCCAA  51966        ___  A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
                                AACCGAAGA   AGT GGTC
                                      ACC   C
GAM94   NXF5    3'  CTGGCTGACCAAGAAGCCAA  52508        ___  A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
                                AACCGAAGA   AGT GGTC
                                      ACC   C
GAM94   NXF5    3'  CTGGCTGACCAAGAAGCCAA  52513        ___  A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
                                AACCGAAGA   AGT GGTC
                                      ACC   C
GAM94   NXF5    3'  CTGGCTGACCAAGAAGCCAA  52517        ___  A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
                                AACCGAAGA   AGT GGTC
                                      ACC   C
GAM94   NXF5    3'  CTGGCTGACCAAGAAGCCAA  52521        ___  A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
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                                AACCGAAGA  AGT GGTC
                                     ACC  C
GAM94   POLG     5' GCCAGTAAAAGAAGCCAA   10680        CA  CA
                                TTGGCTTCTT  AC  GC
                                ||||||||||  ||  ||
                                AACCGAAGAA  TG  CG
                                     AA  AC
GAM94   FLJ12377 3' TGTTGGATAAAGAAGCCAA   46487        CAA
                                TTGGCTTCTT  CCAGCA
                                ||||||||||  ||||||
                                AACCGAAGAA  GGTTGT
                                     ATA
GAM94   FLJ13102 3' ACGGCGATTGAGAAGCCAA   46002        T  CCA  A
                                TTGGCTTCT CAA  GC GT
                                |||||||||  |||  || ||
                                AACCGAAGA GTT  CG CA
                                     _  AG_  G
GAM94   FLJ23120 3' CATACTAAATGAAAGAAGCCAG 85145        CAAC  GC_
                                TTGGCTTCTT   CA  AGTATG
                                ||||||||||   ||  ||||||
                                GACCGAAGAA   GT  TCATAC
                                     A___  AAA
GAM94   FREQ     3' GCGGCCAAGAAGCCAA     26582        CAA  A
                                TTGGCTTCTT  CC GC
                                ||||||||||  || ||
                                AACCGAAGAA  GG CG
                                     CC_  _
GAM94   KIAA0232 3' TTGCTAACTGAAGAAGCCAA  72764         ACC
                                TTGGCTTCTTCA  AGCAG
                                ||||||||||||  |||||
                                AACCGAAGAAGT  TCGTT
                                      CAA
GAM94   KIAA0987 3' GCAATTAAAGAGGCCAA    24563        C  CCA
                                TTGGCTTCTT AA  GC
                                |||||||||| ||  ||
                                AACCGGAGAA TT  CG
                                     A  AA_
GAM94   PPFIA2   5' ATTGATCAATTGAAGAAGC   13261        CCAG_
                                GCTTCTTCAA   CAGT
                                ||||||||||   ||||
                                CGAAGAAGTT   GTTA
                                     AACTA
GAM94   SNPH     3' ACAGCTTACTGAAAAAGCCAG  28236       C   ACC  A
                                TTGGCTT TTCA  AGC GT
                                ||||||| ||||  ||| ||
                                GACCGAA AAGT  TCG CA
                                    A   CAT  A
GAM94   LOC134957 3' ACGTGACAGATGAAGAAACCAA 57661     C     ACCAG  _
                                TTGG TTCTTCA   CA GT
                                |||| |||||||   || ||
```

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                                AACC AAGAAGT    GT CA
                                  A      AGACA  G
GAM94   LOC136895 5'  CTGCCAAAGAAGCCAA      57168          CAACCA
                                TTGGCTTCTT     GCAG
                                ||||||||||     ||||
                                AACCGAAGAA     CGTC
                                     AC____
GAM94   LOC162333 5'  ACTAAGCTGAAGAGGCCAA   87115           ACCA __
                                TTGGCTTCTTCA   GC  AGT
                                ||||||||||||   ||  |||
                                AACCGGAGAAGT   CG  TCA
                                      ____  AA
GAM94   LOC253227 5'  ACTACTGGTAAGAAGCCA    97506         CA    C
                                TGGCTTCTT  ACCAG AGT
                                |||||||||  ||||| |||
                                ACCGAAGAA  TGGTC TCA
                                     __    A
GAM94   LOC255452 3'  GCAGCCGAAGAAGCCA      97538          AACCA  A
                                TGGCTTCTTC     GC GT
                                ||||||||||     || ||
                                ACCGAAGAAG     CG CG
                                     C____  A
GAM95   CHN1     3'  TCCTGTAGCTGCATTATTTCT  8433         __        A
                                AGAAAT  TGCAGCTACA GA
                                ||||||  |||||||||| ||
                                TCTTTA  ACGTCGATGT CT
                                   TT         C
GAM95   FLRT2    3'  TTGCAAATTCTTGTCT      25071          A
                                AGACAAGAA TTGCAG
                                ||||||||| ||||||
                                TCTGTTCTT AACGTT
                                     A
GAM95   GPR81    3'  TGGCTGCATTTTCTTATCT    50770     C     T
                                AGA AAGAAA TGCAGCTA
                                ||| |||||| ||||||||
                                TCT TTCTTT ACGTCGGT
                                  A     T
GAM95   ICA1     3'  AGATGCAATCTCTTGTCT     42255         A     G
                                AGACAAGA ATTGCA CT
                                |||||||| |||||| ||
                                TCTGTTCT TAACGT GA
                                     C     A
GAM95   MGP      3'  CTGTATATTCTCTTGTCT     6129          _  _
                                AGACAAGA AAT TGCAG
                                |||||||| ||| |||||
                                TCTGTTCT TTA ATGTC
                                     C   T
GAM95   NR1D1    5'  TGGTTGCAACCTCTCTTC     41365    CA   AA
                                GA  AGA  TTGCAGCTA
                                ||  |||  |||||||||
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                                CT  TCT  AACGTTGGT
                                 TC   CC
GAM95   TLR9     5' TGTAGCTGCTGTCCAGTCT   33852     AA  AATT
                                AGAC  GA   GCAGCTACA
                                ||||  ||   |||||||||
                                TCTG  CT   CGTCGATGT
                                  AC  GT__
GAM95   TNFRSF17  5' TCTTGTAGAGATATTACTTGTC 6820       A   TGCAG
                                GACAAG AAT    CTACAAGA
                                |||||| |||    ||||||||
                                CTGTTC TTA    GATGTTCT
                                   A  TAGA_
GAM95   TPD52L2   3' TGTTACGCAATTTTTTATCT   12369     C       AGCT
                                AGA AAGAAATTGC   ACA
                                ||| ||||||||||   |||
                                TCT TTTTTTAACG   TGT
                                  A        CAT_
GAM95   TSNAX     3' CTGTTTAAATTTCTTGTT    19999          ___
                                GACAAGAAATT   GCAG
                                ||||||||||   ||||
                                TTGTTCTTTAA   TGTC
                                      ATT
GAM95   ARHE      3' TCTTACAAGCACTTTGTCTTGT 17714        AATTGCA   AC_
           CT                    AGACAAGA     GCT   AAGA
                                ||||||||     |||   ||||
                                TCTGTTCT     CGA   TTCT
                                    GTTTCA_   ACA
GAM95   C5orf6    3' TGGTGCCAATTTCTTTTC    33488    C       CA
                                GA AAGAAATTG  GCTA
                                || |||||||||  ||||
                                CT TTCTTTAAC  TGGT
                                 T       CG
GAM95   CDCA7     3' CTGCAGTTTCTTCTCT      49203     C
                                AGA AAGAAATTGCAG
                                ||| ||||||||||||
                                TCT TTCTTTGACGTC
                                  C
GAM95   CLSTN1    3' TGTAGCTGCTCTGTTT      30107      A  AATT
                                AGACA GA    GCAGCTACA
                                ||||| ||    |||||||||
                                TTTGT CT    CGTCGATGT
                                   _ ____
GAM95   DGKD      3' CTGCAGTGGCTTCTTGTC    59405        ___
                                GACAAGAA   ATTGCAG
                                ||||||||   |||||||
                                CTGTTCTT   TGACGTC
                                     CGG
GAM95   DKFZp761G2113 3' TGGGGCTGCAATGCCCTGTCT  69912      AGAA      TA
                                AGACA   ATTGCAGC  CA
                                |||||   ||||||||  ||
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                                TCTGT   TAACGTCG GT
                                  CCCG      GG
GAM95   DRF1     3' AGAAGCAATTTCTATCT    47024    CA       AG
                                AGA AGAAATTGC CT
                                ||| ||||||||| ||
                                TCT TCTTTAACG GA
                                  A_       AA
GAM95   FLJ10656 3' CTTGTGAGAAATCTCTTGTTT 36386        A  GCAGC
                                AGACAAGA ATT    TACAAG
                                |||||||| |||    ||||||
                                TTTGTTCT TAA    GTGTTC
                                    C  AGA__
GAM95   FLJ20813 3' CTGCAGTCTCTTGTCT     35684        A
                                AGACAAGA ATTGCAG
                                |||||||| |||||||
                                TCTGTTCT TGACGTC
                                    C
GAM95   FLJ23306 3' GCTGAGTTTCTTGTC      44560          G
                                GACAAGAAATT CAGC
                                |||||||||||| ||||
                                CTGTTCTTTGA GTCG
                                          _
GAM95   GKAP42   5' AGCGCAATTTCTTTCT     47384    C       A
                                AGA AAGAAATTGC GCT
                                ||| |||||||||| |||
                                TCT TTCTTTAACG CGA
                                  _       _
GAM95   H-L(3)MBT 3'  TCTCTGAGCCTACATCTTCTTG 31309         AT  CA_  A _
            TCT                   AGACAAGAA  TG   GCT CA AGA
                                ||||||||| ||  ||| || |||
                                TCTGTTCTT  AC   CGA GT TCT
                                    CT  ATC  _ C
GAM95   HMGN4    5'  TCTTGTGGAGATCTCCTGTC  20981     A  A   GCAG
                                GACA GA ATT    CTACAAGA
                                |||| || |||    ||||||||
                                CTGT CT TAG    GGTGTTCT
                                  C  C   A___
GAM95   HSPC009  3'  TCTTGTAGTTTGTTTCCTTGTT 25831        _   TGC
            T                    AGACAAG AAAT   AGCTACAAGA
                                ||||||| ||||   ||||||||||
                                TTTGTTC TTTG   TTGATGTTCT
                                    C    T__
GAM95   IGF2AS   3' CTGTCCAATTTCTTGCT     33098    A       __
                                AG CAAGAAATTG  CAG
                                || ||||||||||  |||
                                TC GTTCTTTAAC  GTC
                                  _        CT
GAM95   KIAA0057 3' TTGCAATTTTTCTGTCT     24449      _
                                AGACA AGAAATTGCAG
                                ||||| ||||||||||
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                                TCTGT TTTTTAACGTT
                                   C
GAM95   KIAA0275 3' CTTGTAGCTGTTTTCTTTC   28678    C     TT
                                GA AAGAAA  GCAGCTACAAG
                                || ||||||  ||||||||||
                                CT TTCTTT  TGTCGATGTTC
                                 _     __
GAM95   KIAA0515 3' TGAGCTTCTTGTCT        63816         AATTGC    A
                                AGACAAGA     AGCT CA
                                ||||||||     |||| ||
                                TCTGTTCT     TCGA GT
                                     _______   _
GAM95   KIAA0783 5' GCTGTGCAATTTCTGGTCT   27801      A         __
                                AGAC AGAAATTGCA  GC
                                |||| ||||||||||  ||
                                TCTG TCTTTAACGT  CG
                                   G         GT
GAM95   KIAA1821 3' CTGCAGTTTCTTGCT       71783     A
                                AG CAAGAAATTGCAG
                                || ||||||||||||
                                TC GTTCTTTGACGTC
                                 _
GAM95   LGI3     3' CTGTAGCTGTCGCTTTCT     57743       T _       A
                                AGAAA TG CAGCTACA G
                                ||||| || |||||||| |
                                TCTTT GC GTCGATGT C
                                   C  T       C
GAM95   LRRN3    5' GGCTGCAGCCTCCTGCCT    69439    A  A  AA
                                AG CA GA  TTGCAGCT
                                || || ||  ||||||||
                                TC GT CT  GACGTCGG
                                 C  C  CC
GAM95   MGC27171 3' AGCTGCAGCCTCTTGCCT    58085    A    AA
                                AG CAAGA  TTGCAGCT
                                || |||||  ||||||||
                                TC GTTCT  GACGTCGA
                                 C    CC
GAM95   PGLYRP   3' TCCTGTGTTGCAATTCTCTGTC 53578      _   A      T   A
                                GACA AGAA TTGCAGC ACA GA
                                |||| |||| ||||||| ||| ||
                                CTGT TCTT AACGTTG TGT CT
                                   C   _      _  C
GAM95   PIWIL2   3' TGTAGAATAAGATTTCTTTCT  36060     C       GCAG_
                                AGA AAGAAATT    CTACA
                                ||| ||||||||    |||||
                                TCT TTCTTTAG    GATGT
                                  _       AATAA
GAM95   RNAC     3' TCTCATAGCTGCAGTTC     19314     A       CA
                                GAA TTGCAGCTA  AGA
                                ||| |||||||||  |||
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                                CTT GACGTCGAT  TCT
                                  _       AC
GAM95   TCL6     5'  CTTGTAGAACATTTTCTTGT   40133        T  CAG
                                ACAAGAAA TG   CTACAAG
                                |||||||| ||   |||||||
                                TGTTCTTT AC   GATGTTC
                                    T  AA_
GAM95   TCL6     5'  CTTGTAGAACATTTTCTTGT   40158        T  CAG
                                ACAAGAAA TG   CTACAAG
                                |||||||| ||   |||||||
                                TGTTCTTT AC   GATGTTC
                                    T  AA_
GAM95   LOC121838 5'  CTTGTAGTTCTTTCTGTCT   75999       A    TTGC
                                AGACA GAAA    AGCTACAAG
                                ||||| ||||    |||||||||
                                TCTGT CTTT    TTGATGTTC
                                  _   C___
GAM95   LOC145501 3'  TGGCTGCACTTCCTTGCCT   77257    A    A  T
                                AG CAAG AA TGCAGCTA
                                || |||| || ||||||||
                                TC GTTC TT ACGTCGGT
                                 C    C  C
GAM95   LOC148529 5'  GGTCAGCAATTTCTTGCCT   84169    A         A_
                                AG CAAGAAATTGC  GCT
                                || ||||||||||  |||
                                TC GTTCTTTAACG  TGG
                                 C          AC
GAM95   LOC148894 3'  GCCAATAATTCTTGTCT     84258          __   CA
                                AGACAAGAA  ATTG  GC
                                |||||||||  ||||  ||
                                TCTGTTCTT  TAAC  CG
                                     AA   __
GAM95   LOC150295 3'  CTGCAGTTCCTTTTCT      84961     C   A
                                AGA AAG AATTGCAG
                                ||| ||| ||||||||
                                TCT TTC TTGACGTC
                                  T   C
GAM95   LOC150933 3'  CTTCAAGCTCTGCAGTTTCCTG 85161       A       __  AC
           TCT                    AGACA GAAATTGCA  GCT  AAG
                                |||||| |||||||||  |||  |||
                                TCTGT CTTTGACGT  CGA  TTC
                                   C        CT   AC
GAM95   LOC200563 5'  AGCACAATTTCTCATCT     90092     CA      CA
                                AGA  AGAAATTG  GCT
                                |||  ||||||||  |||
                                TCT  TCTTTAAC  CGA
                                  AC       A_
GAM95   LOC254266 3'  GGCTGCAGTCTCCCGTC     97353     AA  A
                                GAC  GA ATTGCAGCT
                                |||  || |||||||||
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                                CTG  CT TGACGTCGG
                                  CC  C
GAM95   LOC255995 3'  TCTTGTAGAAATTGATTTCCTT 96977     CAA     GCAG_
            CT                    AGA   GAAATT    CTACAAGA
                                  |||   ||||||    ||||||||
                                  TCT   CTTTAG    GATGTTCT
                                    TC_     TTAAA
GAM95   LOC256683 5'  CTGGAGAAACAATCTTCTTGTC 96280         _   CAG  ACA
            T                     AGACAAGAA ATTG   CT   AG
                                  |||||||||| ||||   ||   ||
                                  TCTGTTCTT TAAC   GA   TC
                                       C    AAA  GG_
GAM95   LOC91496  5'  CTGCAGCTTCTTGTCT      66222          A
                                  AGACAAGAA TTGCAG
                                  |||||||||| ||||||
                                  TCTGTTCTT GACGTC
                                       C
GAM96   FUT4     3'  ATAACCTGGATTTTTT      8962      T       A
                                  AAA AATCCAGG TAT
                                  ||| |||||||| |||
                                  TTT TTAGGTCC ATA
                                    T       A
GAM96   GYG      3'  GTTCTGGATATTTGA       14691         A
                                  TCAAATA TCCAGGAT
                                  ||||||| ||||||||
                                  AGTTTAT AGGTCTTG
                                             _
GAM96   MUC3B    3'  TTAGGATACCCCGGGT      94270      A  A
                                  ATCC GG TATCCTAA
                                  |||| || ||||||||
                                  TGGG CC ATAGGATT
                                    C  C
GAM96   ORC2L    3'  TTAGAGATATTCTGAATTTTTT 20550       T   C       _
            GA                    TCAAA AAT CAGGATATC CTAA
                                  ||||| ||| ||||||||| ||||
                                  AGTTT TTA GTCTTATAG GATT
                                     T   A        A
GAM96   PCDHA9   3'  AGGTATCTGATTATTTGA    25756          CA    T
                                  TCAAATAATC  GGATA CCT
                                  ||||||||||  ||||| |||
                                  AGTTTATTAG  TCTAT GGA
                                              __    _
GAM96   PKIB     3'  TTAGGATATTTTTGTCTGA   50644     A   TCCA
                                  TCA ATAA    GGATATCCTAA
                                  ||| ||||    ||||||||||||
                                  AGT TGTT    TTTATAGGATT
                                    C   _____
GAM96   PXF      3'  GATACATTCTGGCTTATTTGA  11151         T     __
                                  TCAAATAA CCAGGA  TATC
                                  |||||||| ||||||  ||||
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                                AGTTTATT GGTCTT  ATAG
                                     C     AC
GAM96   RBBP6    3'  TTAAAATATTGCTGCTTGATTA 73474         ___  _    CC
            TTTGA                   TCAAATAATC   CAG GATAT  TAA
                                    ||||||||||   ||| |||||  |||
                                    AGTTTATTAG   GTC TTATA  ATT
                                         TTC   G    AA
GAM96   RBBP9    3'  TATCCTCCTGATTATTTGA    70140         C__
                                    TCAAATAATC   AGGATA
                                    ||||||||||   ||||||
                                    AGTTTATTAG   TCCTAT
                                         TCC
GAM96   TCF3     3'  AGGAGATCCTGGACTGCCTGA  70728     AA  A      A
                                    TCA  TA TCCAGGAT TCCT
                                    |||  || |||||||| ||||
                                    AGT  GT AGGTCCTA AGGA
                                      CC  C       G
GAM96   C22orf23  3'  TTAGGATTTACTTATTTGA    50785       ATCC  GAT
                                    TCAAATA    AG   ATCCTAA
                                    |||||||    ||   |||||||
                                    AGTTTAT    TC   TAGGATT
                                         ____ ATT
GAM96   FLJ22649  3'  TTTAGGATATGTTTGATTACTG 41638    AAA    C  G
            GA                        TC   TAATC AG ATATCCTAAA
                                    ||   ||||| || ||||||||||
                                    AG   ATTAG TT TATAGGATTT
                                     GTC    T  G
GAM96   H2AV     3'  TATCCTGGATTACCTGG     56857     AA
                                    TCA  TAATCCAGGATA
                                    |||  ||||||||||||
                                    GGT  ATTAGGTCCTAT
                                      CC
GAM96   KIAA0143  3'  ATATCCTGGATTTCTGA     64780     AAT
                                    TCA   AATCCAGGATAT
                                    |||   ||||||||||||
                                    AGT   TTAGGTCCTATA
                                      CT_
GAM96   KIAA0258  3'  AGGATGGATTATTGA       28807      A      GGATA
                                    TCAA TAATCCA     TCCT
                                    |||| |||||||     ||||
                                    AGTT ATTAGGT     AGGA
                                         _      ______
GAM96   KIAA0431  3'  TTTAGGAGATCCTGGATT    30899          A
                                    AATCCAGGAT TCCTAAA
                                    |||||||||| |||||||
                                    TTAGGTCCTA AGGATTT
                                          G
GAM96   KIAA0441  3'  TAGCTATGCCTGAATTATTTGA 28959          C    ATATC
                                    TCAAATAAT CAGG    CTA
                                    |||||||| ||||    |||
```

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                                AGTTTATTA GTCC    GAT
                                     A   GTATC
GAM96   MEGF11   3' ATGCCCTGGATTATATGA   50578    A       A
                                TCA ATAATCCAGG TAT
                                ||| |||||||||| |||
                                AGT TATTAGGTCC GTA
                                  A        C
GAM96   MGC4677  5' AGGTGTATTGTGATTATTTGA 53507        C G   _
                                TCAAATAATC A GATAT CCT
                                |||||||||| | ||||| |||
                                AGTTTATTAG T TTATG GGA
                                      _ G    T
GAM96   P37NB    3' ATATCCTGAGTCATTTGA    19504      A TC
                                TCAAAT A  CAGGATAT
                                |||||| |  ||||||||
                                AGTTTA T  GTCCTATA
                                   C GA
GAM96   RHOBTB3  3' AGGACTGCAAGATTATTTGA  29741        ___  GATA
                                TCAAATAATC  CAG   TCCT
                                ||||||||||  |||   ||||
                                AGTTTATTAG  GTC   AGGA
                                      AAC  ____
GAM96   SMC1L1   3' ATCTCTGGATATTTGA     71958       A   _
                                TCAAATA TCCAG GAT
                                ||||||| ||||| |||
                                AGTTTAT AGGTC CTA
                                    _    T
GAM96   SRP9     3' TTAGAAACTGGAGATTATTTGA 79194       __   GATATC
                                TCAAATAA  TCCAG     CTAA
                                ||||||||  |||||     ||||
                                AGTTTATT  AGGTC     GATT
                                     AG    AAA___
GAM96   ZNF185   3' GGGCATCCTGGATCCCTGA   23117    AATA      AT
                                TCA   ATCCAGGAT  CC
                                |||   |||||||||  ||
                                AGT   TAGGTCCTA  GG
                                  CCC_       CG
GAM96   LOC120526 3' AGGAAATGGATTATTTG    74013         GGATA
                                CAAATAATCCA    TCCT
                                ||||||||||     ||||
                                GTTTATTAGGT    AGGA
                                      AA___
GAM96   LOC144742 5' TGTGCCTGGATTCCTGA    76949    AAT      _
                                TCA   AATCCAGG ATA
                                |||   |||||||| |||
                                AGT   TTAGGTCC TGT
                                  CC_       G
GAM96   LOC146350 5' GGTCCCTGCATTATTTGA   83665        C   ATAT
                                TCAAATAAT CAGG   CC
                                ||||||||| ||||   ||
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                                AGTTTATTA GTCC    GG
                                      C    CT__
GAM96   LOC148946 5'  TAAGATATCCTAAAAGATTTGG 84312       AATCC       C
                                TCAAAT     AGGATATC TA
                                ||||||     |||||||| ||
                                GGTTTA     TCCTATAG AT
                                   GAAAA       A
GAM96   LOC91115  3'  AGGCAGGTGGATTGTCTGA    64922     A       GGATAT
                                TCA ATAATCCA      CCT
                                ||| |||||||||     |||
                                AGT TGTTAGGT      GGA
                                  C       GGAC__
GAM97   ASPH      5'  TGGATTGAAGAAATCAA     50634     GC       _
                                TTG  TTCTTCAA CCA
                                |||  |||||||| |||
                                AAC  AAGAAGTT GGT
                                  TA       A
GAM97   ASPH      5'  TGGATTGAAGAAATCAA     39396     GC       _
                                TTG  TTCTTCAA CCA
                                |||  |||||||| |||
                                AAC  AAGAAGTT GGT
                                  TA       A
GAM97   ASPH      5'  TGGATTGAAGAAATCAA     50626     GC       _
                                TTG  TTCTTCAA CCA
                                |||  |||||||| |||
                                AAC  AAGAAGTT GGT
                                  TA       A
GAM97   FOS       5'  GCGAGCAACTGAGAAGCCAA   17906         T  ACCA  A_
                                TTGGCTTCT CA    GC  GT
                                ||||||||| ||    ||  ||
                                AACCGAAGA GT    CG  CG
                                      _  CAA_  AG
GAM97   FSTL1     3'  ATACTGCTAGTTAACCCAG    23010      C  CTTC   C
                                TTGG TT    AAC AGCAGTAT
                                |||| ||    ||| ||||||||
                                GACC AA    TTG TCGTCATA
                                  C _____   A
GAM97   NR4A2     3'  TGAGTTGAAGAAGGCAA     20535     G        _
                                TTG CTTCTTCAAC CA
                                ||| ||||||||| ||
                                AAC GAAGAAGTTG GT
                                  G         A
GAM97   NXF5      3'  CTGGCTGACCAAGAAGCCAA   51966         ___   A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
                                AACCGAAGA   AGT GGTC
                                      ACC   C
GAM97   NXF5      3'  CTGGCTGACCAAGAAGCCAA   52508         ___   A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
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                                AACCGAAGA  AGT GGTC
                                     ACC  C
GAM97   NXF5    3' CTGGCTGACCAAGAAGCCAA  52513       ___  A
                                TTGGCTTCT  TCA CCAG
                                |||||||||  ||| ||||
                                AACCGAAGA  AGT GGTC
                                     ACC  C
GAM97   NXF5    3' CTGGCTGACCAAGAAGCCAA  52517       ___  A
                                TTGGCTTCT  TCA CCAG
                                |||||||||  ||| ||||
                                AACCGAAGA  AGT GGTC
                                     ACC  C
GAM97   NXF5    3' CTGGCTGACCAAGAAGCCAA  52521       ___  A
                                TTGGCTTCT  TCA CCAG
                                |||||||||  ||| ||||
                                AACCGAAGA  AGT GGTC
                                     ACC  C
GAM97   POLG    5' GCCAGTAAAAGAAGCCAA    10680       CA  CA
                                TTGGCTTCTT  AC  GC
                                ||||||||||  ||  ||
                                AACCGAAGAA  TG  CG
                                     AA  AC
GAM97   FLJ12377 3' TGTTGGATAAAGAAGCCAA  46487       CAA
                                TTGGCTTCTT  CCAGCA
                                ||||||||||  ||||||
                                AACCGAAGAA  GGTTGT
                                     ATA
GAM97   FLJ13102 3' ACGGCGATTGAGAAGCCAA  46002       T  CCA  A
                                TTGGCTTCT CAA  GC GT
                                ||||||||| |||  || ||
                                AACCGAAGA GTT  CG CA
                                     _  AG_  G
GAM97   FLJ23120 3' CATACTAAATGAAAGAAGCCAG 85145       CAAC  GC_
                                TTGGCTTCTT   CA  AGTATG
                                ||||||||||   ||  ||||||
                                GACCGAAGAA   GT  TCATAC
                                     A___  AAA
GAM97   FREQ    3' GCGGCCAAGAAGCCAA    26582       CAA  A
                                TTGGCTTCTT  CC GC
                                ||||||||||  || ||
                                AACCGAAGAA  GG CG
                                     CC_  _
GAM97   KIAA0232 3' TTGCTAACTGAAGAAGCCAA  72764         ACC
                                TTGGCTTCTTCA  AGCAG
                                ||||||||||||  |||||
                                AACCGAAGAAGT  TCGTT
                                      CAA
GAM97   KIAA0987 3' GCAATTAAAGAGGCCAA    24563       C  CCA
                                TTGGCTTCTT AA  GC
                                |||||||||| ||  ||
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                                AACCGGAGAA TT   CG
                                      A  AA_
GAM97   PPFIA2   5'  ATTGATCAATTGAAGAAGC   13261         CCAG_
                                GCTTCTTCAA     CAGT
                                ||||||||||     ||||
                                CGAAGAAGTT     GTTA
                                      AACTA
GAM97   SNPH     3'  ACAGCTTACTGAAAAAGCCAG  28236       C    ACC   A
                                TTGGCTT TTCA   AGC GT
                                ||||||| ||||   ||| ||
                                GACCGAA AAGT   TCG CA
                                     A    CAT   A
GAM97   LOC134957 3'  ACGTGACAGATGAAGAAACCAA 57661      C      ACCAG  _
                                TTGG TTCTTCA     CA GT
                                |||| |||||||     || ||
                                AACC AAGAAGT     GT CA
                                   A      AGACA  G
GAM97   LOC136895 5'  CTGCCAAAGAAGCCAA      57168         CAACCA
                                TTGGCTTCTT     GCAG
                                ||||||||||     ||||
                                AACCGAAGAA     CGTC
                                      AC____
GAM97   LOC162333 5'  ACTAAGCTGAAGAGGCCAA    87115          ACCA  __
                                TTGGCTTCTTCA    GC  AGT
                                ||||||||||||    ||  |||
                                AACCGGAGAAGT    CG  TCA
                                      _____  AA
GAM97   LOC253227 5'  ACTACTGGTAAGAAGCCA     97506         CA     C
                                TGGCTTCTT  ACCAG AGT
                                |||||||||  ||||| |||
                                ACCGAAGAA  TGGTC TCA
                                      __     A
GAM97   LOC255452 3'  GCAGCCGAAGAAGCCA       97538         AACCA  A
                                TGGCTTCTTC     GC GT
                                ||||||||||     || ||
                                ACCGAAGAAG     CG CG
                                      C_____  A
GAM98   CNGA1    3'  CAACTGATAATGTGCAAA    59507          GC   A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                      A_  _
GAM98   ESRRG    3'  TGGCAGTCTTATGTGCAAA   66396         TAGCT
                                TTTGCACAT     AGATTGCCA
                                |||||||||     |||||||||
                                AAACGTGTA     TCTGACGGT
                                      T_____
GAM98   KCNJ3    3'  GCAATAATGTGCAAA       9525           GCTAGA
                                TTTGCACATTA     TTGC
                                ||||||||||     ||||
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                              AAACGTGTAAT     AACG
                                      ______
GAM98   SDC2     3'  GCAAATTAATGTGTAAA     67132          CTAGA
                              TTTGCACATTAG    TTGC
                              ||||||||||||    ||||
                              AAATGTGTAATT    AACG
                                    A____
GAM98   USP9X    3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
            A                  TTTGCACATTAGC     GCCAT
                              ||||||||||||||    |||||
                              AAATGTGTAATCG     CGGTA
                                     TAGTC_
GAM98   AMOTL1   3'  GGCAAGTAATGTGCAAA     73650          G  AGAT
                              TTTGCACATTA CT    TGCC
                              |||||||||||| ||    ||||
                              AAACGTGTAAT GA    ACGG
                                      _ _____
GAM98   BCAR3    3'  AGTAATAATGTGCAAA      13098          __
                              TTTGCACATTA  GCT
                              ||||||||||  |||
                              AAACGTGTAAT  TGA
                                     AA
GAM98   DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930         AGCTA    C
                              TTTGCACATT    GATTG CA
                              |||||||||    ||||| ||
                              AGACGTGTAA    TTAAC GT
                                    A____    A
GAM98   MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                              TTTGCACATTAG  AGA TG CAT
                              ||||||||||||  ||| || |||
                              AGACGTGTAATC  TTT AC GTA
                                     __  T  A
GAM98   PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
            AA                   TTTGCACATTAGCTAGATTGCCAT
                              ||||||||||||||||||||||||||||
                              AAACGTGTAATCGATCTAACGGTA

GAM99   DACH     3'  TGAGAATGTTTGTAAATGTACA 54974       CATCC   CT
                              TGTACA    ACA  CATTCTCA
                              ||||||    |||  ||||||||
                              ACATGT    TGT  GTAAGAGT
                                 AAA__   TT
GAM99   IL11RA   3'  GGAACGTGTGTAATGTGTACA  15712        C_    TCA
                              TGTACACAT  CACAC   TTCT
                              |||||||||  |||||   ||||
                              ACATGTGTA  GTGTG   AAGG
                                    AT    C__
GAM99   LYPLA1   3'  AGAATGAGGTGGTATTACA   20922      CACAT    A
                              TGTA    CCAC CTCATTCT
                              ||||    |||| ||||||||
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                                ACAT    GGTG GAGTAAGA
                                  TAT__   _
GAM99   NAPB    3'  GAGAATGAATGTATGT     70183     CC   C
                                ACAT  ACA TCATTCTC
                                ||||  ||| ||||||||
                                TGTA  TGT AGTAAGAG
                                  __   A
GAM99   NRF1    3'  GAATATATGTATATGTGTACA  60120        CC   CTC
                                TGTACACAT  ACA   ATTC
                                |||||||||  |||   ||||
                                ACATGTGTA  TGT   TAAG
                                     TA   ATA
GAM99   PRKAB1  3'  AGAGGGAATGGACTGTACA   20734      CA   CA   AT
                                TGTACA  TCCA  CTC  TCT
                                ||||||  ||||  |||  |||
                                ACATGT  AGGT  GGG  AGA
                                   C_   AA   __
GAM99   PTGFR   3'  TGAGAGAGATGTGTACA     6319         CACA
                                TGTACACATC    CTCA
                                ||||||||||    ||||
                                ACATGTGTAG    GAGT
                                     AGA_
GAM99   RBBP5   3'  AGATTGGATAGATGTGTACA   17327         CACAC   T
                                TGTACACATC     TCA TCT
                                ||||||||||     ||| |||
                                ACATGTGTAG     GGT AGA
                                     ATA__   T
GAM99   SAT     3'  TGAGTCATTTAAATGTGTACA  11436        CCAC___
                                TGTACACAT      ACTCA
                                |||||||||      |||||
                                ACATGTGTA      TGAGT
                                     AATTTAC
GAM99   TMP21   3'  AATGGTGATGGATGTGACA   22399     A      _   T
                                TGT CACATCCA CAC CATT
                                ||| |||||||| ||| ||||
                                ACA GTGTAGGT GTG GTAA
                                  _      A   _
GAM99   UBE2V1  3'  TGAAATGTGGATGCATAC    41797     CA      C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
                                CAT  GTAGGTGT  AGT
                                  AC       AA
GAM99   UBE2V1  3'  TGAAATGTGGATGCATAC    42374     CA      C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
                                CAT  GTAGGTGT  AGT
                                  AC       AA
GAM99   UBE2V1  3'  TGAAATGTGGATGCATAC    12522     CA      C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
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                                CAT  GTAGGTGT  AGT
                                  AC       AA
GAM99   ZIC1     3'  AGAATGTTCTAGTAAATGTGTA 12720        CC  ACT__
            C                    GTACACAT  AC    CATTCT
                                 ||||||||  ||    ||||||
                                 CATGTGTA  TG    GTAAGA
                                     AA  ATCTT
GAM99   AF038169 5'  TGAAAATGAGTGCTGTAGATG  25255     __ _      C
                                 CATC  CA CACTCATT TCA
                                 ||||  || |||||||| |||
                                 GTAG  GT GTGAGTAA AGT
                                   AT  C       A
GAM99   CDC14A   3'  AGAAGTGGATGTATATA     13391      C       ACTCA
                                 TGTA ACATCCAC     TTCT
                                 |||| ||||||||     ||||
                                 ATAT TGTAGGTG     AAGA
                                   A       _____
GAM99   DKFZP564I052 3'  GATGATCATGTGATGTGTACA  66710          C   C__
                                 TGTACACATC ACA   TCATT
                                 |||||||||| |||   |||||
                                 ACATGTGTAG TGT   AGTAG
                                       _  ACT
GAM99   DKFZP761F241 3'  TGAGAATGAGTGAGGTTTCGTA 48800       ACAT  A
            CA                     TGTAC    CC CACTCATTCTCA
                                   |||||    || ||||||||||||
                                   ACATG    GG GTGAGTAAGAGT
                                      CTTT  A
GAM99   FLJ11101  3'  AGAAGTGTTGAGTGTGTACA   37049        TC  _    CAT
                                 TGTACACA  CA CACT   TCT
                                 ||||||||  || ||||   |||
                                 ACATGTGT  GT GTGA   AGA
                                     GA  T   ____
GAM99   FLJ14642  3'  AGTATGGGTGTGTACA      51492           C
                                 TGTACACATCCA ACT
                                 |||||||||||| |||
                                 ACATGTGTGGGT TGA
                                        A
GAM99   FLJ20399  3'  GGTGGCTGTGGATGCCACA   35125     ACA       CT
                                 TGT   CATCCACA  CATT
                                 |||   ||||||||  ||||
                                 ACA   GTAGGTGT  GTGG
                                   CC_       CG
GAM99   GFPT1     3'  GAAGATGGGATGTGTACA    9022           A  C  A
                                 TGTACACATCC CA TC TTC
                                 |||||||||||| || || |||
                                 ACATGTGTAGG GT AG AAG
                                          _  _  _
GAM99   KIAA0450  3'  GAGGGCAGTGTGGATG      27640          CA
                                 CATCCACACT  TTCTC
                                 ||||||||||  |||||
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                                GTAGGTGTGA  GGGAG
                                      C_
GAM99   KIAA0530 3' GATGGTATGAAAATGTGTACA 70867        C__  C  T
                                TGTACACAT   CA AC CATT
                                |||||||||   || || ||||
                                ACATGTGTA   GT TG GTAG
                                      AAA  A  _
GAM99   KIAA0753 3' GGGGAGTTAAATGTGTACA   28999        CCAC   ATT
                                TGTACACAT   ACTC   CTC
                                |||||||||   ||||  |||
                                ACATGTGTA   TGAG   GGG
                                      AAT_   ___
GAM99   KIAA0788 3' TGAATTAGGAATGTGTACA   71339        _  ACAC
                                TGTACACAT CC    TCA
                                ||||||||| ||    |||
                                ACATGTGTA GG    AGT
                                      A  ATTA
GAM99   KIAA0855 3' AGAATGAGCAGTGTAC     30400       ATCCACA
                                GTACAC      CTCATTCT
                                ||||||      ||||||||
                                CATGTG      GAGTAAGA
                                   AC_____
GAM99   KIAA0865 5' GAGCAAGTGGAATGTGTACA  61250         _   A__
                                TGTACACAT CCAC   CTC
                                ||||||||| ||||   |||
                                ACATGTGTA GGTG   GAG
                                      A    AAC
GAM99   KIAA0992 3' GGAAGTGTGGAGCACACA    32207    ACACA      CAT
                                TGT    TCCACACT   TCT
                                |||    ||||||||   |||
                                ACA    AGGTGTGA   AGG
                                  CACG_      ___
GAM99   MGC16037 5' TGAGGTGTAGATATGTATA   51822      C   C   _
                                TGTACA ATC ACAC TCA
                                |||||| ||| |||| |||
                                ATATGT TAG TGTG AGT
                                   A  A   G
GAM99   OSRF     3' TGAAAATGCACACAAATGTGTA 59525        CCACACT   C
           CA                    TGTACACAT      CATT TCA
                                |||||||||      |||| |||
                                ACATGTGTA      GTAA AGT
                                      AACACAC    A
GAM99   RAB3-GAP150 3' TGAGAATCAGAGATGTGTA   24839        CACA  C
                                TACACATC    CT ATTCTCA
                                ||||||||    || |||||||
                                ATGTGTAG    GA TAAGAGT
                                      A___  C
GAM99   RAP140   3' GATGGGTAAATGTGTACA    30844        CCAC
                                TGTACACAT    ACTCATT
                                |||||||||    |||||||
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                                ACATGTGTA   TGGGTAG
                                     AA__
GAM99   TACTILE   5' GAGTGCATGTGTACA      19471        CCA
                                TGTACACAT   CACTC
                                |||||||||   |||||
                                ACATGTGTA   GTGAG
                                     C__
GAM99   LOC131873 3' GATGTATGCATATGTGTACA   75880        CCA  CT
                                TGTACACAT   CA  CATT
                                |||||||||   ||  ||||
                                ACATGTGTA   GT  GTAG
                                     TAC  AT
GAM99   LOC134145 3' AGCTGTATATGTGTACA     75144        CC   _
                                TGTACACAT  ACA CT
                                |||||||||  ||| ||
                                ACATGTGTA  TGT GA
                                     TA   C
GAM99   LOC145482 3' AATGGTATGATGTGTACA    77226        CAC  T
                                TGTACACATC   AC CATT
                                ||||||||||   || ||||
                                ACATGTGTAG   TG GTAA
                                      TA_  _
GAM99   LOC148195 3' GAAAAGGTGGATGTGTCA    84129    T       A  CA
                                TG ACACATCCAC CT  TTC
                                || ||||||||||  ||  |||
                                AC TGTGTAGGTG GA  AAG
                                 _        _ A_
GAM99   LOC152633 5' TGAGCTGTACATGTAGAGTGTA 85826       A  C   CT__  TT
           CA                     TGTACAC TC ACA    CA  CTCA
                                |||||||  || |||    ||  ||||
                                ACATGTG AG TGT    GT  GAGT
                                    _ A   ACAT  C_
GAM99   LOC153630 5' AATGAGTGTGCGTAC       86079      ACATC
                                GTAC    CACACTCATT
                                ||||    ||||||||||
                                CATG    GTGTGAGTAA
                                  C_____
GAM99   LOC221662 3' AGAATGAGGGGAATGGGCA   92399    TA  CA   ACA
                                TG  CA  TCC   CTCATTCT
                                ||  ||  |||   ||||||||
                                AC  GT  AGG   GAGTAAGA
                                 GG  A_   G__
GAM99   LOC254659 5' GAGAATGGAGATGCTACA    95113     CA   CACAC
                                TGTA  CATC    TCATTCTC
                                ||||  ||||    ||||||||
                                ACAT  GTAG    GGTAAGAG
                                  C_   A_____
GAM99   LOC83693  3' AGGGTGTGTGGATGGCACA   48830     ACA       TC
                                TGT   CATCCACAC  ATTCT
                                |||   |||||||||  |||||
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                                ACA   GTAGGTGTG  TGGGA
                                  CG_       __
GAM99   LOC90981 3'  AATGGTGATGGATGTGACA   64532     A       _  T
                                TGT CACATCCA CAC CATT
                                ||| |||||||| ||| ||||
                                ACA GTGTAGGT GTG GTAA
                                  _       A   _
GAM100  BCL11B   3'  TTGTGAAGAAGCCAACACTCA  43197      C__
                                TGGG   TGGCTTCTTCACAA
                                ||||   ||||||||||||||
                                ACTC   ACCGAAGAAGTGTT
                                  ACA
GAM100  DDX3     3'  TGTGAAGAAAGTGCATGCA   43761    T   G   GGC
                                TG CATG GCT   TTCTTCACA
                                || |||| |||   |||||||||
                                AC GTAC TGA   AAGAAGTGT
                                  _   G  ____
GAM100  DYRK2    3'  TTGTAAAGAAGCCTCATATTAC 21395     C   GGCT      C
              A                  TGT ATG    GGCTTCTT ACAA
                                ||| |||    |||||||| ||||
                                ACA TAT    CCGAAGAA TGTT
                                  T   ACT_       A
GAM100  DYRK2    3'  TTGTAAAGAAGCCTCATATTAC 13131     C   GGCT      C
              A                  TGT ATG    GGCTTCTT ACAA
                                ||| |||    |||||||| ||||
                                ACA TAT    CCGAAGAA TGTT
                                  T   ACT_       A
GAM100  IL1F5    3'  TGAAAAAGTGCTCATGACA    24385          TG    C
                                TGTCATGGGC  GCTT TTCA
                                ||||||||||  |||| ||||
                                ACAGTACTCG  TGAA AAGT
                                      __    A
GAM100  RXRA     3'  GTGCCCAGCCAGCCCGTGACA  11416             TCTT
                                TGTCATGGGCTGGCT    CAC
                                ||||||||||||||    |||
                                ACAGTGCCCGACCGA    GTG
                                          CCC_
GAM100  CD200    3'  AAGAAAATACATGCCCATGAC  57153          _ GC__
                                GTCATGGGC TG    TTCTT
                                |||||||| ||    |||||
                                CAGTACCCG AC    AAGAA
                                      T  ATAA
GAM100  DC-TM4F2 3'  AAGAACCAGCCCACAACA    48169     CA       C
                                TGT  TGGGCTGG TTCTT
                                |||  |||||||| |||||
                                ACA  ACCCGACC AAGAA
                                  AC       _
GAM100  FLJ12604 3'  AAGTCAGCCATGACA       64435         G
                                TGTCATGG CTGGCTT
                                |||||||| |||||||
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                                ACAGTACC GACTGAA
                                       _
GAM100  FLJ22031  3'  GAGCCAACCCATGATA      46889          C
                                TGTCATGGG TGGCTT
                                ||||||||| ||||||
                                ATAGTACCC ACCGAG
                                     A
GAM100  FLJ22405  3'  AGAAGCCAGCCCATGACA    42517
                                TGTCATGGGCTGGCTTCT
                                ||||||||||||||||||
                                ACAGTACCCGACCGAAGA

GAM100  HT002     3'  TGTGATCAAACCATGACA    25950         GC   CTTCT
                                TGTCATGG  TGG    TCACA
                                ||||||||  |||    |||||
                                ACAGTACC  ACT    AGTGT
                                     AA  _____
GAM100  MGC11352  5'  AAGAACCAGCCCACAACA    64799     CA      C
                                TGT  TGGGCTGG TTCTT
                                |||  |||||||| |||||
                                ACA  ACCCGACC AAGAA
                                  AC      _
GAM100  MGC4796   3'  GACGCACAGCCCATGAC     61486          _  T
                                GTCATGGGCTG GC TC
                                |||||||||| || ||
                                CAGTACCCGAC CG AG
                                     A  C
GAM100  PNMA1     3'  TTGTGAAAAACACGCGAACCTA 20075         CTG  ___  C
           TGACA                    TGTCATGGG   GC   TT TTCACAA
                                |||||||||   ||   || |||||||
                                ACAGTATCC   CG   AA AAGTGTT
                                     AAG  CAC  A
GAM100  LOC114987 3'  AAGTCATAGACCATGACA    59118         GC__
                                TGTCATGG    TGGCTT
                                ||||||||    ||||||
                                ACAGTACC    ACTGAA
                                     AGAT
GAM100  LOC127281 3'  GTGATTAAAAACCAGCCCAAAA 74649     CA      CTTCT__
           CA                     TGT  TGGGCTGG      TCAC
                                |||  ||||||||      ||||
                                ACA  ACCCGACC      AGTG
                                  AA       AAAAATT
GAM100  LOC144603 3'  TTGTGAAGAAGCCAGCCCATGA 60370
           CA                     TGTCATGGGCTGGCTTCTTCACAA
                                |||||||||||||||||||||||||
                                ACAGTACCCGACCGAAGAAGTGTT

GAM100  LOC150418 3'  TGTGAAGAAGCTCTATGACA  65510         GCT
                                TGTCATGG   GGCTTCTTCACA
                                ||||||||   ||||||||||||
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                                ACAGTATC   TCGAAGAAGTGT
                                    ___
GAM100  LOC169611 3'  GGAACCAGCCCACAAC     82771    CA      C
                                GT  TGGGCTGG TTCT
                                ||  |||||||| ||||
                                CA  ACCCGACC AAGG
                                 AC       _
GAM100  LOC199957 3'  TGTGAAGAAGCTCTATGACA  88506        GCT
                                TGTCATGG   GGCTTCTTCACA
                                ||||||||   ||||||||||||
                                ACAGTATC   TCGAAGAAGTGT
                                    ___
GAM100  LOC206463 3'  TGTGAAGAAGCTCTATGACA  89540        GCT
                                TGTCATGG   GGCTTCTTCACA
                                ||||||||   ||||||||||||
                                ACAGTATC   TCGAAGAAGTGT
                                    ___
GAM100  LOC221288 3'  TGTGAAGAAGCCACTTGGATA 93622     A   C
                                TGTC TGGG TGGCTTCTTCACA
                                |||| |||| ||||||||||||
                                ATAG GTTC ACCGAAGAAGTGT
                                  _   _
GAM101  CEACAM1   3'  AGGTTTGTCCACTGTCA     8147          _   A
                                TGACAGTGGA AAGC CT
                                |||||||||| |||| ||
                                ACTGTCACCT TTTG GA
                                     G   _
GAM101  COLQ      3'  GCTTCTCCACTGTCAT      19048         _
                                ATGACAGTGGA AAGC
                                |||||||||| ||||
                                TACTGTCACCT TTCG
                                     C
GAM101  COLQ      3'  GCTTCTCCACTGTCAT      54471         _
                                ATGACAGTGGA AAGC
                                |||||||||| ||||
                                TACTGTCACCT TTCG
                                     C
GAM101  COLQ      3'  GCTTCTCCACTGTCAT      54477         _
                                ATGACAGTGGA AAGC
                                |||||||||| ||||
                                TACTGTCACCT TTCG
                                     C
GAM101  COLQ      3'  GCTTCTCCACTGTCAT      54483         _
                                ATGACAGTGGA AAGC
                                |||||||||| ||||
                                TACTGTCACCT TTCG
                                     C
GAM101  COLQ      3'  GCTTCTCCACTGTCAT      54489         _
                                ATGACAGTGGA AAGC
                                |||||||||| ||||
```

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                                TACTGTCACCT TTCG
                                      C
GAM101  COLQ     3'  GCTTCTCCACTGTCAT     54496          _
                                ATGACAGTGGA AAGC
                                |||||||||||  ||||
                                TACTGTCACCT TTCG
                                      C
GAM101  DPYSL2   3'  CATAGTGCTGTGTCAT     7292       GTGGAA
                                ATGACA     AGCACTATG
                                ||||||     |||||||||
                                TACTGT     TCGTGATAC
                                   G_____
GAM101  EPS8     3'  CATAGTGCCTTTTTCAC     15468       __
                                GTGGAAA  GCACTATG
                                |||||||  ||||||||
                                CACTTTT  CGTGATAC
                                     TC
GAM101  FEZ1     3'  CATAGTGCTGGTTTCTGTC   42568      TG AA
                                GACAG  G  AGCACTATG
                                |||||  |  |||||||||
                                CTGTC  T  TCGTGATAC
                                   TT GG
GAM101  FLNB     3'  GCCCCTTCACTGTCATG     62178          AA_
                                CATGACAGTGGA   GC
                                ||||||||||||   ||
                                GTACTGTCACTT   CG
                                      CCC
GAM101  GABRE    3'  CATAAACCAGTCCACTGTTAT  41771          AAGCAC
                                ATGACAGTGGA     TATG
                                ||||||||||      ||||
                                TATTGTCACCT     ATAC
                                      GACCAA
GAM101  GABRE    3'  CATAAACCAGTCCACTGTTAT  41780          AAGCAC
                                ATGACAGTGGA     TATG
                                ||||||||||      ||||
                                TATTGTCACCT     ATAC
                                      GACCAA
GAM101  GABRE    3'  CATAAACCAGTCCACTGTTAT  41800          AAGCAC
                                ATGACAGTGGA     TATG
                                ||||||||||      ||||
                                TATTGTCACCT     ATAC
                                      GACCAA
GAM101  GABRE    3'  CATAAACCAGTCCACTGTTAT  17108          AAGCAC
                                ATGACAGTGGA     TATG
                                ||||||||||      ||||
                                TATTGTCACCT     ATAC
                                      GACCAA
GAM101  HKE4     3'  CATAGTGTTGGGCACTGTC   22730       GAA
                                GACAGTG   AGCACTATG
                                |||||||   |||||||||
```

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                                CTGTCAC  TTGTGATAC
                                   GGG
GAM101  MAGEA12  3' TAGTTTCCACTGCCTC    18112   __     AGC
                                GA CAGTGGAA  ACTA
                                || ||||||||  ||||
                                CT GTCACCTT  TGAT
                                 CC     ___
GAM101  MSH2    3' CATAGTGTTAACTGTCA    4205       GGAAA
                                TGACAGT   GCACTATG
                                |||||||   ||||||||
                                ACTGTCA   TGTGATAC
                                   AT___
GAM101  NEU3    3' CATAGTGCCTGCATGCTTCATG 21847     C   GAAA_
                                CATGA AGTG   GCACTATG
                                ||||| ||||   ||||||||
                                GTACT TCGT   CGTGATAC
                                  _  ACGTC
GAM101  RAG1    3' AGTGCTTTTTACCACTG    4812       ___
                                CAGTGG  AAAGCACT
                                ||||||  ||||||||
                                GTCACC  TTTCGTGA
                                   ATT
GAM101  SET7    3' CATAGTGCTTTTTTCCTATG  47634     ACAGT
                                CATG   GGAAAGCACTATG
                                ||||   ||||||||||||
                                GTAT   TTTTTCGTGATAC
                                  CCT__
GAM101  SLC25A12 3' CATAGTGCTGCTACCACTG  13522      AA__
                                CAGTGG   AGCACTATG
                                ||||||   ||||||||
                                GTCACC   TCGTGATAC
                                   ATCG
GAM101  STAT1   3' AGTGCTTTCCGTGGCA    23616   A  G
                                TG CA TGGAAAGCACT
                                || || ||||||||||
                                AC GT GCCTTTCGTGA
                                 G  _
GAM101  TXNIP   3' CATAGCACTTTGTTCACTGTCC 21348   T      __  CA
           TG                    CA GACAGTGGA  AAG  CTATG
                                || |||||||||  |||  |||||
                                GT CTGTCACTT  TTC  GATAC
                                 C       GT   AC
GAM101  XPR1    3' AGTGCCCATTGTCA       16425        AAA
                                TGACAGTGG   GCACT
                                |||||||||   |||||
                                ACTGTTACC   CGTGA
                                     ___
GAM101  APOARGC  3' CATACTTCACCACTGTCA   44417        A_  CAC
                                TGACAGTGG  AAG   TATG
                                |||||||||  |||   ||||
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                                ACTGTCACC  TTC   ATAC
                                     AC  ___
GAM101  CYLD     3'  ATAGTAGTTACTGTCA     30882         AAAGC
                                TGACAGTGG    ACTAT
                                |||||||||    |||||
                                ACTGTCATT    TGATA
                                     GA___
GAM101  DKFZp547I094 3'  AGTGCTCTTACCACTG     49631       _ _
                                CAGTGG AA AGCACT
                                |||||| || ||||||
                                GTCACC TT TCGTGA
                                   A  C
GAM101  DKFZP564B1162 3'  ATAATGCTACTGTCA      48529        GGAA   C
                                TGACAGT   AGCA TAT
                                |||||||   |||| |||
                                ACTGTCA   TCGT ATA
                                    ____   A
GAM101  FLJ10261  3'  AGGCTCCCCACTGTCA     35952         AA   A
                                TGACAGTGG  AGC CT
                                |||||||||  ||| ||
                                ACTGTCACC  TCG GA
                                     CC  _
GAM101  KIAA0121  3'  CATAGTGCTTTAAACGTGATG  72656     G  A  GG
                                CAT AC GT  AAAGCACTATG
                                ||| || ||  ||||||||||
                                GTA TG CA  TTTCGTGATAC
                                  G  _  AA
GAM101  KIAA0982  3'  CATAGTGCCCAGCTTGCATG   25846     AC  _   AAA
                                CATG  AG TGG   GCACTATG
                                ||||  || |||   ||||||||
                                GTAC  TC ACC   CGTGATAC
                                  GT  G  ___
GAM101  KIAA1554  3'  GTTCTCCTCACTGTCATG    95155          AA  C
                                CATGACAGTGG  AG AC
                                ||||||||||  || ||
                                GTACTGTCACT  TC TG
                                      CC  T
GAM101  KIAA1729  3'  ATAGTGCTTTTTCCTG     89126     TG
                                CAG  GAAAGCACTAT
                                |||  ||||||||||
                                GTC  TTTTCGTGATA
                                  CT
GAM101  KIAA1795  3'  CATAGTACCTTTTTGCGTAATG 72150     G  A TG    C_
                                CAT AC G  GAAAG  ACTATG
                                ||| || |  |||||  ||||||
                                GTA TG C  TTTTC  TGATAC
                                  A  _ GT    CA
GAM101  MGC22014  3'  GTGTCATCCACTGTCA     64497          AA
                                TGACAGTGGA  GCAC
                                ||||||||||  ||||
```

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                                ACTGTCACCT  TGTG
                                      AC
GAM101  NAT5     3'  ATAGTATTCACTGTATG     32251      A      AAGC
                                CATG CAGTGGA    ACTAT
                                |||| |||||||    |||||
                                GTAT GTCACTT    TGATA
                                  _      A___
GAM101  p25      3'  CATAGTGGTCACCACTGTCA   22847          AAAG
                                TGACAGTGG    CACTATG
                                |||||||||    |||||||
                                ACTGTCACC    GTGATAC
                                      ACTG
GAM101  PHCA     3'  TGTTTTCCACCATTAT      37182      CA
                                ATGA  GTGGAAAGCA
                                ||||  ||||||||||
                                TATT  CACCTTTTGT
                                  AC
GAM101  PRO1575  3'  GCATAGTACTCTTCTGTACGCT 26029       _____  _ C     III
           GTCA                    ACAGTG    GAA AG ACTATG   C
                                ||||||    ||| || ||||||   |
                                TGTCGC    CTT TC TGATAC   G
                                   ATGT   C  A     III
GAM101  RANBP6   3'  GCTTCCACTGCATG       61637      A       A
                                CATG CAGTGGAA GC
                                |||| |||||||| ||
                                GTAC GTCACCTT CG
                                  _      _
GAM101  SAP18    5'  CATGGATTTCCACTGTC     19646          GCA
                                GACAGTGGAAA   CTATG
                                ||||||||||   |||||
                                CTGTCACCTTT   GGTAC
                                      A__
GAM101  SCYB10   3'  CATGGACTTCCACTGCCAT   7798      A       AGCA
                                ATG CAGTGGAA    CTATG
                                ||| ||||||||    |||||
                                TAC GTCACCTT    GGTAC
                                  C       CA__
GAM101  LOC128553 3'  AGTACCCTTTTCACTGTCA   74759           C__
                                TGACAGTGGAAAG   ACT
                                ||||||||||||   |||
                                ACTGTCACTTTTC   TGA
                                      CCA
GAM101  LOC135763 3'  CATAGTGCTTACATT       56789      GA
                                AGTG  AAGCACTATG
                                ||||  ||||||||||
                                TTAC  TTCGTGATAC
                                  A_
GAM101  LOC153577 3'  CATACTCTTTCCACTGACATG  86053      A        CAC
                                CATG CAGTGGAAAG   TATG
                                |||| ||||||||||   ||||
```

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                                GTAC GTCACCTTTC   ATAC
                                  A        TC_
GAM101   LOC163231 3'  AGTGGGAAACTGTCCACTGTCA 82434          A _____
                                TGACAGTGGA AG     CACT
                                |||||||||| ||     ||||
                                ACTGTCACCT TC     GTGA
                                     G  AAAGG
GAM101   LOC163882 3'  CATAGAAGTTGCTTTCCGCCAT 82165     CA        ____
           CA                     TGA  GTGGAAAGCA    CTATG
                                |||  ||||||||||   |||||
                                ACT  CGCCTTTCGT    GATAC
                                  AC         TGAA
GAM101   LOC165246 5'  AGTCTTTCCACTACCA      82477    AC       C
                                TG  AGTGGAAAG ACT
                                ||  ||||||||| |||
                                AC  TCACCTTTC TGA
                                 CA       _
GAM101   LOC196477 3'  CATAGATTTTTCCACCATCA   87721     CA       CA
                                TGA  GTGGAAAG  CTATG
                                |||  ||||||||  |||||
                                ACT  CACCTTTT  GATAC
                                  AC       TA
GAM101   LOC196955 5'  AGTGCGCCCCACTGTCATG    77365          AAA
                                CATGACAGTGG   GCACT
                                ||||||||||   |||||
                                GTACTGTCACC   CGTGA
                                      CCG
GAM101   LOC200316 3'  CATAGTGCCCCCCTGCCTCA   88766     __   T  AAA
                                TGA  CAG GG   GCACTATG
                                |||  ||| ||   ||||||||
                                ACT  GTC CC   CGTGATAC
                                  CC   _  CC_
GAM101   LOC221489 5'  CATAGTGCTCCCAGGACTCATG 93639       CAG_   AA
                                CATGA    TGG  AGCACTATG
                                |||||    |||  |||||||||
                                GTACT    ACC  TCGTGATAC
                                   CAGG   C_
GAM101   LOC253525 5'  CATAGTGCCTTGGGTCA     96263      AGT  AAA
                                TGAC   GG   GCACTATG
                                ||||   ||   ||||||||
                                ACTG   TC   CGTGATAC
                                  GGT  ___
GAM102   TCF7     3'  ACAACTAGATCAAGGAGCCCA  12153    A    CGTGA
                                TG GTTCT     GATCTAGTTGT
                                || |||||     ||||||||||
                                AC CGAGG     CTAGATCAACA
                                 C     AA___
GAM102   FLJ14075  3'  ACCAGATCTCCAAGAACTCA   46046         CGT      A
                                TGAGTTCT   GAGATCT GT
                                ||||||||   ||||||| ||
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                                ACTCAAGA   CTCTAGA CA
                                     AC_      C
GAM102   PDE4DIP   3'  GATCTCACAAGCACTCA     27690       T  C
                                TGAGT CT GTGAGATC
                                |||||| || ||||||||
                                ACTCA GA CACTCTAG
                                   C  A
GAM102   SYNCOILIN 3'  ACAACTAGACTTGAAAAGAAAC 47893    AG    CG_    A
            CA                    TG  TTCT   TGAG TCTAGTTGT
                                ||  ||||   |||| |||||||||
                                AC  AAGA   GTTC AGATCAACA
                                 CA    AAA    _
GAM102   LOC138389 3'  ACAGTGGCCTCAAAGAACTCA  76213         CG    AT   G
                                TGAGTTCT  TGAG  CTA TTGT
                                ||||||||  ||||  ||| ||||
                                ACTCAAGA  ACTC  GGT GACA
                                     A_    C_   _
GAM102   LOC150759 3'  CAACTAGAGGGAGAAGCCA    80004    AG    GTGAGA
                                TG  TTCTC     TCTAGTTG
                                ||  |||||     ||||||||
                                AC  AAGAG     AGATCAAC
                                 CG    GG____
GAM102   LOC151323 3'  CAACTAGAGGGAGAAGCCA    80217    AG    GTGAGA
                                TG  TTCTC     TCTAGTTG
                                ||  |||||     ||||||||
                                AC  AAGAG     AGATCAAC
                                 CG    GG____
GAM102   LOC152313 3'  ACAACCAGATCTCCTGAGAACT 85658          T      A
            CA                    TGAGTTCTCG GAGATCT GTTGT
                                |||||||||| ||||||| |||||
                                ACTCAAGAGT CTCTAGA CAACA
                                      C      C
GAM102   LOC152343 3'  ACAACCAGATCTCTCAGGAACT 80555         CGT      A
            CA                    TGAGTTCT   GAGATCT GTTGT
                                ||||||||   ||||||| |||||
                                ACTCAAGG   CTCTAGA CAACA
                                     ACT      C
GAM102   LOC200399 3'  CAACTAGAGGGAGAAGCCA    88808    AG    GTGAGA
                                TG  TTCTC     TCTAGTTG
                                ||  |||||     ||||||||
                                AC  AAGAG     AGATCAAC
                                 CG    GG____
GAM102   LOC56920  3'  AGGTGTCCACAAGAACTCA    39380         C  _ G
                                TGAGTTCT GTG A ATCT
                                |||||||| ||| | ||||
                                ACTCAAGA CAC T TGGA
                                     A   C G
GAM103   APLP2     3'  TGGACACTGTGGAAAGCTTTGA 90904       ACC_  AGACT
                                TCAAA    TC    CAGTGTCCA
                                |||||    ||    |||||||||
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                                AGTTT  AG   GTCACAGGT
                                  CGAA GT___
GAM103  BCL7B   3' GAATTTGAGGTTCTGA     8132     A      C
                                TCA AACCTCAGA TC
                                ||| ||||||||| ||
                                AGT TTGGAGTTT AG
                                  C       A
GAM103  BN51T   3' GGATTGAGTCTGAG       87496        GT
                                CTCAGACTCA GTCC
                                ||||||||||  ||||
                                GAGTCTGAGT TAGG
                                     __
GAM103  BSN     3' CTGAGTTTGAAATTCTGA    12920    A CC
                                TCA AA TCAGACTCAG
                                ||| ||  ||||||||||
                                AGT TT AGTTTGAGTC
                                  C AA
GAM103  CELSR1  3' GACACTGGAGGTTTT      26484       AGACT
                                AAAACCTC   CAGTGTC
                                ||||||||   |||||||
                                TTTTGGAG   GTCACAG
                                     _____
GAM103  ETS2    3' GACATCTGAGGTTTT      17878         CTCAG
                                AAAACCTCAGA   TGTC
                                ||||||||||   ||||
                                TTTTGGAGTCT   ACAG
                                     _____
GAM103  FEN1    3' TGGACACTAAGTCCATTGTT  14646    CTCA   C
                                AAC   GACT AGTGTCCA
                                |||   |||| ||||||||
                                TTG   CTGA TCACAGGT
                                  TTAC   A
GAM103  GNB3    3' GACTTGAGTCTGAGG      9078          T
                                CCTCAGACTCAG GTC
                                |||||||||||| |||
                                GGAGTCTGAGTT CAG
                                     _
GAM103  HIVEP3  3' CGAGGAGTCTGAGGCTGTGA  44434    AAA       AG
                                TCA  CCTCAGACTC TG
                                |||  |||||||||| ||
                                AGT  GGAGTCTGAG GC
                                  GTC       GA
GAM103  KLHL1   5' GACACTGAACTCTGAG     40486      C_
                                CTCAGA TCAGTGTC
                                ||||||  ||||||||
                                GAGTCT AGTCACAG
                                   CA
GAM103  KLK3    3' TGGACACTGTCCATGAAGCACT 7923     AAACC  GACT
           GA                   TCA   TCA   CAGTGTCCA
                                |||   |||   |||||||||
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                                AGT    AGT   GTCACAGGT
                                  CACGA  ACCT
GAM103  NCOA6    5' TGGAGTCTGTCTGAGGT    25981        TC  TG
                                ACCTCAGAC  AG  TCCA
                                |||||||||  ||  ||||
                                TGGAGTCTG  TC  AGGT
                                     __  TG
GAM103  PCDH7    3' ACTAAGTCTGAGATATTGA   50595     AAC      C
                                TCAA  CTCAGACT AGT
                                ||||  |||||||| |||
                                AGTT  GAGTCTGA TCA
                                  ATA      A
GAM103  PMP22    3' GACGGTCTGTCTGAGGCTCTGA 4327     AAA      TCAG
                                TCA  CCTCAGAC   TGTC
                                |||  ||||||||   ||||
                                AGT  GGAGTCTG   GCAG
                                  CTC      TCTG
GAM103  PNOC     3' TTGAACCTGGGGTTTTGA    20642          AC
                                TCAAAACCTCAG  TCAG
                                ||||||||||||  ||||
                                AGTTTTGGGGTC  AGTT
                                      CA
GAM103  PPP1R12B 5' GACACTGAAGGGCTTGA    49470     AA  CAGAC
                                TCAA  CCT    TCAGTGTC
                                ||||  |||    ||||||||
                                AGTT  GGA    AGTCACAG
                                  CG  _____
GAM103  PPP1R12B 5' GACACTGAAGGGCTTGA    49481     AA  CAGAC
                                TCAA  CCT    TCAGTGTC
                                ||||  |||    ||||||||
                                AGTT  GGA    AGTCACAG
                                  CG  _____
GAM103  RANBP2L1 5' TGGACACTGAACTGACTTTGG 50045     ACC  AC
                                TCAAA  TCAG  TCAGTGTCCA
                                |||||  ||||  ||||||||||
                                GGTTT  AGTC  AGTCACAGGT
                                  C__  A_
GAM103  TCF1     3' GAGTCTGAGGTCCTGA     5033     AA
                                TCA  ACCTCAGACTC
                                |||  ||||||||||
                                AGT  TGGAGTCTGAG
                                  CC
GAM103  ZNF255   5' TGAAGTCTGAGATTTT     19322     C     _
                                AAAA CTCAGACT CA
                                |||| |||||||| ||
                                TTTT GAGTCTGA GT
                                  A      A
GAM103  AGTRL2   5' ACACTGAACTCTGGTGTTGA  17688     A  TC  AC
                                TCAA ACC  AG  TCAGTGT
                                |||| |||  ||  |||||||
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                                AGTT TGG  TC  AGTCACA
                                  G   TC  A_
GAM103  C21orf25  3'  GACACTGATGAGAAGTTTT   63548      __   GAC
                                AAAAC  CTCA   TCAGTGTC
                                |||||  ||||   ||||||||
                                TTTTG  GAGT   AGTCACAG
                                  AA   ____
GAM103  C8orf14   5'  TGAAGTCTGAGATTTTGG    54005      C      _
                                TCAAAA CTCAGACT CA
                                ||||||  |||||||| ||
                                GGTTTT GAGTCTGA GT
                                   A       A
GAM103  C8orf17   5'  GATAAGTCTGAGGCTCTGA   39599     AAA       CAG
                                TCA   CCTCAGACT   TGTC
                                |||   |||||||||   ||||
                                AGT   GGAGTCTGA   ATAG
                                  CTC       ____
GAM103  CCR8      3'  GATATTGAAGTTTTGA      17782        CTCAGAC
                                TCAAAAC      TCAGTGTC
                                |||||||      ||||||||
                                AGTTTTG      AGTTATAG
                                   A_______
GAM103  CSL4      3'  TGGAGTGAGACCTGAGGTTCTG 32116    A       A_   GTG
                                CA AACCTCAG  CTCA   TCCA
                                || ||||||||  ||||   ||||
                                GT TTGGAGTC  GAGT   AGGT
                                 C       CA    G__
GAM103  DKFZP434H0820 3'  GGGGAGCCTGAGGTTTT     63851          A   AGTG
                                AAAACCTCAG CTC    TCC
                                ||||||||||  |||    |||
                                TTTTGGAGTC GAG    GGG
                                     C  _____
GAM103  DKFZP564I052 3'  GAAGGAACCTGGGTTTTGA   66708        T   AC  AGTG
                                TCAAAACC CAG  TC    TC
                                ||||||||  |||  ||    ||
                                AGTTTTGG GTC  AG    AG
                                     _   CA  GA__
GAM103  FLJ12899  3'  TGAGTCTGAATTTTGA      44764       CC
                                TCAAAA  TCAGACTCA
                                ||||||  |||||||||
                                AGTTTT  AGTCTGAGT
                                   A_
GAM103  FLJ20783  3'  GATTTAAGCCTGAGAGTTTGA  35662       AC     A  CAGT
                                TCAAA  CTCAG CT    GTC
                                |||||  |||||  ||    |||
                                AGTTT  GAGTC GA    TAG
                                   GA    C  ATT_
GAM103  FLJ21240  3'  GAGTCTACCTGGGTTTTGA   45840         C____
                                TCAAAACCT    AGACTC
                                |||||||||    ||||||
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                                AGTTTTGGG   TCTGAG
                                     TCCA
GAM103  GMFB     3'  CAAAATGTCTGAGTTTTGA   14664       C     TCAG
                                TCAAAAC TCAGAC   TG
                                ||||||| ||||||   ||
                                AGTTTTG AGTCTG   AC
                                    _     TAAA
GAM103  KIAA0435 5'  TGGACACTGTTCTCAAGTTCTG 28988     A   CTC   CT
           A                     TCA AAC   AGA  CAGTGTCCA
                                ||| |||   |||  |||||||||
                                AGT TTG   TCT  GTCACAGGT
                                  C   AAC   T_
GAM103  KIAA0527 3'  GGACACAGTCTAGAAGCTTTGA 95803      ACC  _    CA
                                TCAAA   TC AGACT  GTGTCC
                                |||||   || |||||  ||||||
                                AGTTT   AG TCTGA  CACAGG
                                   CGA  A    __
GAM103  KIAA1086 3'  GGAGGCTGAGTCCGGAGCCTTG 70749      AAC   A_      G
           A                     TCAA   CTC  GACTCAGT TCC
                                ||||   |||  |||||||| |||
                                AGTT   GAG  CTGAGTCG AGG
                                  CC_   GC       G
GAM103  MGC16386 3'  GAGTCTGAGTTTTGA       54734        C
                                TCAAAAC TCAGACTC
                                ||||||| ||||||||
                                AGTTTTG AGTCTGAG
                                    _
GAM103  MGC23280 3'  TGGACACTGACGGGTTTGTGA  58397     _     CAGAC
                                TCA AAACCT    TCAGTGTCCA
                                ||| ||||||    ||||||||||
                                AGT TTTGGG    AGTCACAGGT
                                  G     C____
GAM103  NDP52    3'  TGCTGGGCCCGAGGCCCTGA   19536     AAA    AGA
                                TCA   CCTC   CTCAGTG
                                |||   ||||   |||||||
                                AGT   GGAG   GGGTCGT
                                  CCC    CCC
GAM103  SERPINA10 3'  GATGCTGAATCTGAGGT     32463         C
                                ACCTCAGA TCAGTGTC
                                |||||||| ||||||||
                                TGGAGTCT AGTCGTAG
                                     A
GAM103  STK38L   3'  ACAACTCTGAGGTTTTGG    69170            CTCAG
                                TCAAAACCTCAGA    TGT
                                ||||||||||||    |||
                                GGTTTTGGAGTCT    ACA
                                       CA___
GAM103  SYTL4    3'  GGACCAGTCTGGGTTTT     54942        T     CAGT
                                AAAACC CAGACT    GTCC
                                |||||| ||||||    ||||
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                                TTTTGG GTCTGA   CAGG
                                  _     C___
GAM103  TADA3L   5' GACACTGAACTGGGCTCTTGA 55993     AAC    AC
                                TCAA  CTCAG  TCAGTGTC
                                ||||  |||||  ||||||||
                                AGTT  GGGTC  AGTCACAG
                                  CTC    A_
GAM103  TADA3L   5' GACACTGAACTGGGCTCTTGA 56003     AAC    AC
                                TCAA  CTCAG  TCAGTGTC
                                ||||  |||||  ||||||||
                                AGTT  GGGTC  AGTCACAG
                                  CTC    A_
GAM103  TADA3L   5' GACACTGAACTGGGCTCTTGA 20982     AAC    AC
                                TCAA  CTCAG  TCAGTGTC
                                ||||  |||||  ||||||||
                                AGTT  GGGTC  AGTCACAG
                                  CTC    A_
GAM103  WIT-1    3' TGGAATTCCAGTCTGAGGTT  31830         CAGTG
                                AACCTCAGACT    TCCA
                                ||||||||||    ||||
                                TTGGAGTCTGA    AGGT
                                      CCTTA
GAM103  LOC130031 5' TGGACACACCAACGAGGTACTG 74907     AA    AGACTCA
          A                      TCA  ACCTC      GTGTCCA
                                 |||  |||||      |||||||
                                 AGT  TGGAG      CACAGGT
                                   CA    CAACCA_
GAM103  LOC144571 3' GGACTCTCTGAGGTTTGA    83154      A      CTCA T
                                TCAAA CCTCAGA    G GTCC
                                ||||| |||||||    | ||||
                                AGTTT GGAGTCT    C CAGG
                                  _      _____ T
GAM103  LOC145800 5' GGAGAGTCTGGGGTCCTGA   77501     AA         AGTG
                                TCA  ACCTCAGACTC    TCC
                                |||  ||||||||||    |||
                                AGT  TGGGGTCTGAG    AGG
                                  CC          _____
GAM103  LOC149157 5' TGGACACTTGGGATATTTTGA  79204       CC  AGA  C
                                TCAAAA  TC   CT AGTGTCCA
                                ||||||  ||   || ||||||||
                                AGTTTT  AG   GG TCACAGGT
                                   AT  ___  T
GAM103  LOC150035 3' TGGACACTGATATGGTTTGGA  84812    A    TCAGAC
                                TC AAACC     TCAGTGTCCA
                                || |||||     ||||||||||
                                AG TTTGG     AGTCACAGGT
                                 G    TAT___
GAM103  LOC152890 3' TGGAGGAGTCTGAGG       80720          AGTG
                                CCTCAGACTC    TCCA
                                |||||||||    ||||
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                                GGAGTCTGAG   AGGT
                                     G___
GAM103  LOC153196 5'  TGGAGGATGAGTCTGAAGTTT  85981     C       GTG
                                AAAC TCAGACTCA   TCCA
                                |||| |||||||||   ||||
                                TTTG AGTCTGAGT   AGGT
                                  A        AGG
GAM103  LOC153205 3'  TGGACACTGACTTTGG      85948      C
                                TCAGA TCAGTGTCCA
                                ||||| ||||||||||
                                GGTTT AGTCACAGGT
                                   C
GAM103  LOC154739 3'  CACTTGAGTCCAAGAGTTTGA  86228      AC  CA    _
                                TCAAA  CT  GACTCA GTG
                                |||||  ||  |||||| |||
                                AGTTT  GA  CTGAGT CAC
                                   GA  AC     T
GAM103  LOC154860 5'  TGAAATCCGAGGTTTTGA    86275         A  C_
                                TCAAAACCTC GA  TCA
                                |||||||||| ||  |||
                                AGTTTTGGAG CT  AGT
                                     C  AA
GAM103  LOC159184 3'  GACACTGAAGGGCTTGA     60048      AA   CAGAC
                                TCAA  CCT    TCAGTGTC
                                ||||  |||    ||||||||
                                AGTT  GGA    AGTCACAG
                                  CG  _____
GAM103  LOC196988 5'  GGAGAGTCTGGGGTCCTGA   87855     AA        AGTG
                                TCA  ACCTCAGACTC    TCC
                                |||  ||||||||||    |||
                                AGT  TGGGGTCTGAG    AGG
                                  CC         ____
GAM103  LOC199733 3'  TTGAGCCTGAGAGTTTGA    89852      AC    A
                                TCAAA  CTCAG CTCAG
                                |||||  ||||| |||||
                                AGTTT  GAGTC GAGTT
                                   GA    C
GAM103  LOC201707 5'  GAATGGGAGGCCTGAGGTTCTG 89036     A      A_   AGTG
           A                     TCA AACCTCAG  CTC    TC
                                ||| |||||||  |||    ||
                                AGT TTGGAGTC  GAG    AG
                                  C       CG   GGTA
GAM103  LOC203276 3'  CACTTGAGTCCAAGAGTTTGA  90476      AC  CA    _
                                TCAAA  CT  GACTCA GTG
                                |||||  ||  |||||| |||
                                AGTTT  GA  CTGAGT CAC
                                   GA  AC     T
GAM103  LOC203305 3'  CACTTGAGTCCAAGAGTTTGA  90520      AC  CA    _
                                TCAAA  CT  GACTCA GTG
                                |||||  ||  |||||| |||
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                                AGTTT  GA  CTGAGT CAC
                                   GA  AC     T
GAM103   LOC220549 5'  GAGTCTGAATTTTGA      92918       CC
                                TCAAAA  TCAGACTC
                                ||||||  ||||||||
                                AGTTTT  AGTCTGAG
                                   A_
GAM103   LOC254243 3'  CACTTGAGTCCAAGAGTTTGA  97405      AC  CA     _
                                TCAAA  CT  GACTCA GTG
                                |||||  ||  |||||| |||
                                AGTTT  GA  CTGAGT CAC
                                   GA  AC     T
GAM103   LOC257235 3'  GAGTCTGAGATTTGA      97060       AC
                                TCAAA  CTCAGACTC
                                |||||  |||||||||
                                AGTTT  GAGTCTGAG
                                   A_
GAM103   LOC257249 5'  ACGTTGGTCTGAGGCTTGA   95922      AA       T
                                TCAA  CCTCAGAC CAGTGT
                                ||||  |||||||| ||||||
                                AGTT  GGAGTCTG GTTGCA
                                   C_       _
GAM103   LOC51696  3'  GAGTGTTAATCTGTGGTTTTGA 32546         T   _______
                                TCAAAACC CAGA     CTC
                                |||||||| ||||     |||
                                AGTTTTGG GTCT     GAG
                                     T    AATTGT
GAM103   LOC90038  3'  CACTTGAGTCCAAGAGTTTGA  61149      AC  CA     _
                                TCAAA  CT  GACTCA GTG
                                |||||  ||  |||||| |||
                                AGTTT  GA  CTGAGT CAC
                                   GA  AC     T
GAM103   LOC91548  5'  GACACTGAATCTGCTGG     66414    T_   C
                                CC  CAGA TCAGTGTC
                                ||  |||| ||||||||
                                GG  GTCT AGTCACAG
                                 TC    A
GAM104   DTNA      3'  CCGAAGAGAGGAACCACCACA  52093     A   A        GA
                                TGT GTG TTCCTCTTTT  GG
                                ||| ||| ||||||||||  ||
                                ACA CAC AAGGAGAGAA  CC
                                  C   C         G_
GAM104   DTNA      3'  CCGAAGAGAGGAACCACCACA  52133     A   A        GA
                                TGT GTG TTCCTCTTTT  GG
                                ||| ||| ||||||||||  ||
                                ACA CAC AAGGAGAGAA  CC
                                  C   C         G_
GAM104   FANCF     3'  CTTTGAAAATGAATCACCACA  42673     A      CTC   TG
                                TGT GTGATTC   TTT  AGG
                                ||| |||||||   |||  |||
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                                ACA CACTAAG   AAA  TTC
                                  C      TA_   GT
GAM104  PCDHB9   3'  TAGAAGAAAAACCACTGCA   38946        A  CC
                                TGTAGTG TT  TCTTTTG
                                ||||||| ||  |||||||
                                ACGTCAC AA  AGAAGAT
                                    C  AA
GAM104  PDE4B    3'  TGGTTCAAAAGGAAACACTACA 10485        A    CT     G
                                TGTAGTG TTCCT  TTTGAG CA
                                ||||||| |||||  |||||| ||
                                ACATCAC AAGGA  AAACTT GT
                                    A    __     G
GAM104  ZNF138   3'  CAGGAGAGAAACACCACA    81185     A   A   C
                                TGT GTG TTC TCTTTTG
                                ||| ||| ||| |||||||
                                ACA CAC AAG AGAGGAC
                                  C   A   _
GAM104  ANKRD6   3'  TGCCTTTTTAAAAAAATCACTA 30092         CCTCTTTT
                                TAGTGATT       GAGGCA
                                ||||||||       ||||||
                                ATCACTAA       TTCCGT
                                     AAAAATTT
GAM104  DKFZP762D096 3'  TGCCCCCTGGGGAATCTCCACA 65582     AGT       TTTTGA
                                TGT   GATTCCTC     GGCA
                                |||   ||||||||     ||||
                                ACA   CTAAGGGG     CCGT
                                  CCT       TCCC__
GAM104  FLJ20972 3'  TAGAAGAGAAACCAGTACA   46728      G  A  C
                                TGTA TG TT CTCTTTTG
                                |||| || || ||||||||
                                ACAT AC AA GAGAAGAT
                                  G  C  A
GAM104  FLJ22833 3'  CCTCAAAAGAAGTTGTC     43102     TC  _
                                GAT  CT CTTTTGAGG
                                |||  || |||||||||
                                CTG  GA GAAAACTCC
                                  TT  A
GAM104  KIAA1040 3'  CCTCCAAGAGTCACTACA    72223         TTC     TT
                                TGTAGTGA   CTCTT  GAGG
                                ||||||||   |||||  ||||
                                ACATCACT   GAGAA  CTCC
                                     ____     C_
GAM104  KIAA1056 5'  AAAAGAGGAATCAACACA    29688     AG
                                TGT  TGATTCCTCTTTT
                                |||  |||||||||||||
                                ACA  ACTAAGGAGAAAA
                                  CA
GAM104  KIAA1136 3'  AAAGAAGAATCACTCA      91315     T       C
                                TG AGTGATTC TCTTT
                                || |||||||| |||||
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                                AC TCACTAAG AGAAA
                                 _      A
GAM104  MRPL30    5'  GCCTCTAAAGAGAGCAATCACT 33246          C     __
           ACA                    TGTAGTGATT CTCTTTT  GAGGC
                                  |||||||||| |||||||  |||||
                                  ACATCACTAA GAGAGAA  CTCCG
                                        C      AT
GAM104  SMC4L1    3'  TGCCAGTTGAGACAATCACCAC 18529     A     CC    TTGA
           A                      TGT GTGATT  TCTT    GGCA
                                  ||| ||||||  ||||    ||||
                                  ACA CACTAA  AGAG    CCGT
                                    C     C_    TTGA
GAM104  TEX27     3'  TGCCCCATGTTAGGAAATCACT 41667          _  CTTT  A
           AC                     GTAGTGATT CCT    TG GGCA
                                  |||||||| |||    || ||||
                                  CATCACTAA GGA    AC CCGT
                                       A   TTGT  C
GAM104  THEA      3'  GCCTCAAAAAAAGAAGGCT   66286     GA   CTC
                                  AGT  TTC   TTTTGAGGC
                                  |||  |||   |||||||||
                                  TCG  AAG   AAAACTCCG
                                    G_   AAA
GAM104  X123      3'  CCTCAAAAAAAAGGAGCACT   69922      A    C__
                                  AGTG TTCCT   TTTTGAGG
                                  |||| |||||   ||||||||
                                  TCAC GAGGA   AAAACTCC
                                    _     AAA
GAM104  YME1L1    3'  TGCCTCAAAAAAAAATTA    57782      CCTC
                                  TGATT    TTTTGAGGCA
                                  |||||    ||||||||||
                                  ATTAA    AAAACTCCGT
                                     AAA_
GAM104  YME1L1    3'  TGCCTCAAAAAAAAATTA    26532      CCTC
                                  TGATT    TTTTGAGGCA
                                  |||||    ||||||||||
                                  ATTAA    AAAACTCCGT
                                     AAA_
GAM104  LOC152485 3'  CCTCAAGACCCACTACA     80609       AT  CTCTT
                                  TGTAGTG  TC    TTGAGG
                                  |||||||  ||    ||||||
                                  ACATCAC  AG    AACTCC
                                      CC  _____
GAM104  LOC154930 3'  CAGGAGAGAAACACCACA    81178     A   A   C
                                  TGT GTG TTC TCTTTTG
                                  ||| ||| ||| |||||||
                                  ACA CAC AAG AGAGGAC
                                    C   A   _
GAM104  LOC163404 3'  TTAAAAGAAATCTCTACA    82130      T    CC
                                  TGTAG GATT  TCTTTTGA
                                  ||||| ||||  ||||||||
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                                ACATC CTAA  AGAAAATT
                                  T   __
GAM104  LOC200488 5'  GAAGAGGAATCACACA      90085     A
                                TGT GTGATTCCTCTTT
                                ||| ||||||||||||
                                ACA CACTAAGGAGAAG
                                 _
GAM104  LOC221806 5'  GAAAGAAGATTCACTACA    92536        T  C
                                TGTAGTGA TC TCTTTT
                                |||||||| || ||||||
                                ACATCACT AG AGAAAG
                                    T  A
GAM104  LOC253264 3'  TGCCTTAAAAAAAAAATCCTAC 94691      T   CCTC
          A                      TGTAG GATT    TTTTGAGGCA
                                ||||| ||||    ||||||||||
                                ACATC CTAA    AAAATTCCGT
                                  _   AAAA
GAM105  BAIAP3    3'  GGACACAGTGCAGGCCAG    14125      G_ _    C
                                CTGGT  GT TTGTG CC
                                |||||  || ||||| ||
                                GACCG  CG GACAC GG
                                  GA  T    A
GAM105  NFE2L1    3'  AGAGCACCTCCCCAAACAC    12166     ACC   T  TTT   C
                                GTG   TGG GG   GTGC CT
                                |||   ||| ||   |||| ||
                                CAC   ACC CC   CACG GA
                                 AA_   _  TC_   A
GAM105  PHEX      5'  ACCAGCCACCAAACCACGA    4796       ACC       T
                                TCGTG   TGGTGGTT GT
                                |||||   |||||||| ||
                                AGCAC   ACCACCGA CA
                                  CAA       C
GAM105  POU3F2    3'  AAATCCACCAAACCATGA     18811       ACC     _
                                TCGTG   TGGTGG TTT
                                |||||   |||||| |||
                                AGTAC   ACCACC AAA
                                  CAA     T
GAM105  RPE       3'  AGGAATATTGACTACCAAATCA 62184      CC       T   C_
          C                      GTGA  TGGTGGTT GTG  CCT
                                ||||  |||||||| |||  |||
                                CACT  ACCATCAG TAT  GGA
                                  AA       T   AA
GAM105  SNCAIP    3'  GGACATTCACCAAGCCAC    95920     ACC     TT   G
                                GTG   TGGTGG  TGT CC
                                |||   ||||||  ||| ||
                                CAC   ACCACT  ACA GG
                                 CGA     T_  _
GAM105  SPOCK     5'  AGAGCCTGAGCCACCAAAGCAC 62813     ACC        T  C
                                GTG   TGGTGGTTTG GC CT
                                |||   |||||||||| || ||
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                                CAC   ACCACCGAGT CG GA
                                  GAA         C  A
GAM105  AP3S2    3'  AGGACACAATCCAAATCAT   19517     CCTGG  T    C
                                GTGA    TGG TTGTG CCT
                                ||||    ||| ||||| |||
                                TACT    ACC AACAC GGA
                                  AA___   T    A
GAM105  FLJ11113 5'  GCACAGCTAGCAAATCA    37070    CC  G    T
                                TGA  TG TGGTT GTGC
                                |||  || ||||| ||||
                                ACT  AC ATCGA CACG
                                  AA  G    _
GAM105  FLJ12505 3'  GCACAAGAGGTCACG      45387       GGTGG
                                CGTGACCT    TTTGTGC
                                ||||||||    |||||||
                                GCACTGGA    GAACACG

                                      _____
GAM105  FLJ13162 3'  GGGTCCCCACAGGTCACGA   46561         G   TTTGT
                                TCGTGACCTG TGG    GCCC
                                |||||||||| |||    ||||
                                AGCACTGGAC ACC    TGGG
                                      _  CC___
GAM105  HH114    3'  AGGACACAAACCTGGTC    50684     TGGT      C
                                GACC    GGTTTGTG CCT
                                ||||    |||||||| |||
                                CTGG    CCAAACAC GGA
                                  T___       A
GAM105  OMD      3'  AGACCCACAGGCCACGA    17213      A    GT
                                TCGTG CCTG  GGTTT
                                ||||| ||||  |||||
                                AGCAC GGAC  CCAGA
                                   C    AC
GAM105  PTP4A1   3'  GGCAGTTTTACCAGGCCTCA  12939     __      TTTG
                                TGA  CCTGGTGG   TGCC
                                |||  ||||||||   ||||
                                ACT  GGACCATT   ACGG
                                  CC       TTG_
GAM105  sdolf    3'  AGAGCACCTGACAAGTCACGA  53193       C  GT  TTT   C
                                TCGTGAC TG  GG   GTGC CT
                                |||||||  ||  ||   |||| ||
                                AGCACTG AC  TC   CACG GA
                                    A  AG  ___    A
GAM105  ZNF361   5'  GGCTTCACAAGTCACGA    37662       CTG   TTTGT
                                TCGTGAC   GTGG    GCC
                                |||||||   ||||    |||
                                AGCACTG   CACT    CGG
                                    AA_    T_____
GAM105  LOC145752 5'  GGCACAAACATGATCACG    83479      CCTGGTG
                                CGTGA      GTTTGTGCC
                                |||||      |||||||||
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                                GCACT      CAAACACGG
                                   AGTA___
GAM105  LOC158062 3'  AGGGGGCCCACCAGACCACGG  86678      AC      TTT  G
                                TCGTG  CTGGTGG   GT CCCT
                                |||||  |||||||   || ||||
                                GGCAC  GACCACC   CG GGGA
                                   CA      ___  G
GAM105  LOC166983 5'  GCACGACAGCCACCAAAGCACG 87264      ACC      __
          A                      TCGTG   TGGTGGT  TTGTGC
                                |||||   |||||||  ||||||
                                AGCAC   ACCACCG  AGCACG
                                   GAA      AC
GAM105  LOC197342 3'  AGAGCAGCACCAGGTCAC    87987          GTTTG   C
                                GTGACCTGGTG     TGC CT
                                ||||||||||     ||| ||
                                CACTGGACCAC     ACG GA
                                      G____   A
GAM105  LOC202309 3'  CAAACCCCCAAGTCAC      90336       C   T
                                GTGAC TGG GGTTTG
                                ||||| ||| ||||||
                                CACTG ACC CCAAAC
                                   A   C
GAM105  LOC222159 5'  TGCAACCACCAGACAC      94082     AC        T
                                GTG  CTGGTGGTT GTG
                                |||  ||||||||| |||
                                CAC  GACCACCAA CGT
                                  A_       _
GAM105  LOC256380 5'  CACAACCACCAAGTCAAGA   95986    G   C       T
                                TC TGAC TGGTGGTT GTG
                                || |||| |||||||| |||
                                AG ACTG ACCACCAA CAC
                                 A   A       _
GAM106  ADAM19    3'  CAGGAAGAAGACTGGCCATTAT 52703       C    CTGAG
          G                      CATGA GGCT     TTCTTCCTG
                                |||||  ||||    |||||||||
                                GTATT CCGG     AAGAAGGAC
                                   A    TCAG_
GAM106  FACL5     5'  CAGGAAGAACTCAGAGCCG    64186
                                CGGCTCTGAGTTCTTCCTG
                                ||||||||||||||||||
                                GCCGAGACTCAAGAAGGAC

GAM106  GNAL      5'  CAGGAAAGAGAGGAGCCGTCG  9058          GAG TC
                                TGACGGCTCT   T  TTCCTG
                                ||||||||||   |  ||||||
                                GCTGCCGAGG   A  AAGGAC
                                      AG_ GA
GAM106  KAL1      3'  CAGGAAGAACTTCTGTCA     4013        CTCT
                                TGACGG    GAGTTCTTCCTG
                                ||||||    ||||||||||||
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                                ACTGTC   TTCAAGAAGGAC
                                     ____
GAM106  MYO1E    3' CAGGAGGACAAAACCACCATG 17187     AC  CTC  AGT
                                CATG  GG   TG   TCTTCCTG
                                ||||  ||   ||   ||||||||
                                GTAC  CC   AC   AGGAGGAC
                                  CA  AAA  ___
GAM106  PRKAR2B  3' CAGAAAGAACTCAGATGT    10804    _        C
                                GC TCTGAGTTCTT CTG
                                || ||||||||||| |||
                                TG AGACTCAAGAA GAC
                                 T         A
GAM106  PUM2     3' AGGATCAAAGCTGTCATG    31014         C   GTTCT
                                CATGACGGCT TGA    TCCT
                                |||||||||| |||    ||||
                                GTACTGTCGA ACT    AGGA
                                      A  _____
GAM106  SKI      3' CAGGAAGTGCAGAGCCGCA   11701    A      AGTT
                                TG CGGCTCTG   CTTCCTG
                                || ||||||||   |||||||
                                AC GCCGAGAC   GAAGGAC
                                 _      GT__
GAM106  TEM8     3' AGGAAGATGCAACCCCATG   36326     AC  CTC  AGT
                                CATG  GG   TG   TCTTCCT
                                ||||  ||   ||   |||||||
                                GTAC  CC   AC   AGAAGGA
                                  C_  A__  GT_
GAM106  ARHGEF4  5' AGAAAAAACTCAGGGC      52207         C  C
                                GCTCTGAGTT TT CT
                                |||||||||| || ||
                                CGGGACTCAA AA GA
                                      A  A
GAM106  FLJ31978 3' CAGGAAGGAACAAGCGCC    58348     T  GAG
                                GGC CT   TTCTTCCTG
                                ||| ||   |||||||||
                                CCG GA   AGGAAGGAC
                                  C  ACA
GAM106  HSU24186 5' AGAACTCAAAGCCGTC      25324        C
                                GACGGCT TGAGTTCT
                                ||||||| ||||||||
                                CTGCCGA ACTCAAGA
                                    A
GAM106  KCNT1    3' AGCTCCCAGGGCCGCCA     61825    A     __
                                TG CGGCTCT  GAGTT
                                || |||||||  |||||
                                AC GCCGGGA  CTCGA
                                 C      CC
GAM106  KIAA1867 3' CAGGAAGAACCCAAGAGCTCAT 94822      CG    GA_
                                ATGA  GCTCT   GTTCTTCCTG
                                ||||  |||||   ||||||||||
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                                TACT  CGAGA   CAAGAAGGAC
                                  __    ACC
GAM106  KIAA1878  3'  AATTCAGAGAATCGTCATG   91707        __
                                CATGACGG  CTCTGAGTT
                                ||||||||  |||||||||
                                GTACTGCT  GAGACTTAA
                                     AA
GAM106  MFN1      3'  CAGGAAGAACTCATGA      35541    _
                                TC TGAGTTCTTCCTG
                                || ||||||||||||
                                AG ACTCAAGAAGGAC
                                 T
GAM106  MIDORI    3'  CAGGGCCCTTCCAGAGCCTGTC 73784       _      AGTTCT
            ATG                    CATGAC GGCTCTG     TCCTG
                                |||||| |||||||     |||||
                                GTACTG CCGAGAC     GGGAC
                                    T      CTTCCC
GAM106  MYH7B     3'  CAGGAAGAACCTGGCTCGCATG 70530     A  _   CTGA
                                CATG CG GCT    GTTCTTCCTG
                                |||| || |||    ||||||||||
                                GTAC GC CGG    CAAGAAGGAC
                                  _ T   TC__
GAM106  RNAHP     3'  AGAAAGCAGCAGCCGTCAT    23761         _  AG
                                ATGACGGCT CTG  TTCT
                                |||||||| |||  ||||
                                TACTGCCGA GAC  AAGA
                                     C   GA
GAM106  SLC37A1   3'  AGACGGAGCTCAGACCC     38561    C        TC
                                GG TCTGAGTTCT  CT
                                || ||||||||||  ||
                                CC AGACTCGAGG  GA
                                 C         CA
GAM106  LOC116236 3'  CAGGAAAAGCACAAACCTCAT  73809     C  CTC  A   C
                                ATGA GG   TG GTT TTCCTG
                                |||| ||   || ||| ||||||
                                TACT CC   AC CGA AAGGAC
                                  _ AA_  A   A
GAM106  LOC124801 3'  CAGGAAGAACTCTCTTGCATG  74336     A   CTCT
                                CATG CGG    GAGTTCTTCCTG
                                |||| |||    ||||||||||||
                                GTAC GTT    CTCAAGAAGGAC
                                  _   CT__
GAM106  LOC222160 5'  AGGAAGAACTCACCCC      94117    CTC
                                GG   TGAGTTCTTCCT
                                ||   ||||||||||||
                                CC   ACTCAAGAAGGA
                                 CC_
GAM106  LOC51094  3'  CAGGAAGAATAAAGCC      32045      CTGA
                                GGCT    GTTCTTCCTG
                                ||||    ||||||||||
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                                CCGA    TAAGAAGGAC
                                  AA__
GAM106  LOC92078  3'  CAGGAAGAAGAATCGACCGTC  67977      C  T  G__
                                GACGG TC GA   TTCTTCCTG
                                ||||| || ||   |||||||||
                                CTGCC AG CT   AAGAAGGAC
                                  _ _  AAG
GAM107  MPST      3'  ACCAGCAATGCCTGGCCTGGT  40886        TA   C   A
                                ACCAGGTCG  CAT GCT GT
                                |||||||||  ||| ||| ||
                                TGGTCCGGT  GTA CGA CA
                                     CC   A   C
GAM107  FLJ20294  3'  TACTAACAAAGGAGACCTGGTG 34882         GTACATCGC
          A                      TCACCAGGTC       TAGTA
                                ||||||||||        |||||
                                AGTGGTCCAG       ATCAT
                                     AGGAAACA_
GAM107  FLJ21551  3'  CTGGCCAACCTGGTGA     45627         CGTACATC
                                TCACCAGGT       GCTAG
                                |||||||||       |||||
                                AGTGGTCCA       CGGTC
                                     AC_______
GAM107  TTTY2     5'  TGAGTATACAACCTGGTGA   87009         C   CA_
                                TCACCAGGT GTA   TCG
                                ||||||||| |||   |||
                                AGTGGTCCA CAT   AGT
                                     A   ATG
GAM107  LOC145368 5'  CGATGTACCACCTGATGA    77093     C    C
                                TCA CAGGT GTACATCG
                                ||| ||||| ||||||||
                                AGT GTCCA CATGTAGC
                                  A    C
GAM107  LOC146316 5'  ACCAGCAACCAGGCTCCTGGTG 60867         TC  ACATC_  A
          G                      TCACCAGG  GT     GCT GT
                                |||||||  ||     ||| ||
                                GGTGGTCC  CG     CGA CA
                                     T_  GACCAA   C
GAM107  LOC149649 5'  TGATGTACAACATGGTGA    84554       G  C
                                TCACCA GT GTACATCG
                                |||||| || ||||||||
                                AGTGGT CA CATGTAGT
                                   A  A
GAM107  LOC159148 5'  TGAGTATACAACCTGGTGA   87018         C   CA_
                                TCACCAGGT GTA   TCG
                                ||||||||| |||   |||
                                AGTGGTCCA CAT   AGT
                                     A   ATG
GAM108  ADH1B     3'  CTTAGACATAAAGTAAAAT   72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
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                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM108  AHR     3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM108  FDFT1   3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                        _
GAM108  JTB     3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM108  KLF4    3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM108  PHYH    3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM108  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                       T__    _
GAM108  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM108  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_    CG_
GAM108  CG012   5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM108  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
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                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM108  FLJ23462  3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
            G                     CATTTC        GTCTGAGAT
                                  ||||||        |||||||||
                                  GTAAAG        CAGACTCTA
                                     AAACATTT_
GAM108  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                  CATTTCA   TCACTGTCTGAGAT
                                  |||||||   ||||||||||||||
                                  GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM108  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                  TTCA TTTCACTG  TGAG
                                  |||| ||||||||  ||||
                                  AAGT AAAGTGAC  GTTT
                                    A       CT
GAM108  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                  TTTC CTG TCTGAGAT
                                  |||| ||| ||||||||
                                  AAAG GAC AGACTCTA
                                    _  G
GAM108  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                  ATT CACTTTCACTGT
                                  ||| ||||||||||||
                                  TAA GTGAAAGTGACG
                                   C
GAM108  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                  TTCACTTT  CT TCTGAGAT
                                  ||||||||  || ||||||||
                                  AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM108  PP35      3'  ATCTCAGACTGAAA       22814      CT
                                  TTTCA  GTCTGAGAT
                                  |||||  |||||||||
                                  AAAGT  CAGACTCTA
                                    __
GAM108  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148         TCAC  C_
                                  CATTTCACTT   TGT  TGAG
                                  ||||||||||   |||  ||||
                                  GTAAAGTGAA   ACG  ACTC
                                       TA__   TT
GAM108  SEP15     3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                  TTTCACTTT ACTGT  GA
                                  ||||||||| |||||  ||
                                  AAAGTGAGA TGACA  CT
                                       A    TC
GAM108  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                  TTTCACTTT    TCTGAG
                                  |||||||||    ||||||
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                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM108  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM108  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM108  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM108  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM109  HADHSC    3'  GTTTAATAAATGTGCA      18032          A  TTCAGT
                                TGCACATTTA TA     AAC
                                |||||||||| ||     |||
                                ACGTGTAAAT AT     TTG
                                     A _______
GAM109  MYO7A     3'  TTGAACAACCAAATGTGCA    4229          AATA_
                                TGCACATTT    TTCAG
                                |||||||||    |||||
                                ACGTGTAAA    AAGTT
                                     CCAAC
GAM109  SYT4      3'  CAGTTGAATTATTAAATATGCA 62437      C       TTCAG
                                TGCA ATTTAATA    TAACTG
                                |||| ||||||||    ||||||
                                ACGT TAAATTAT    GTTGAC
                                  A       TAA__
GAM109  FLJ10702  3'  AGTTACTGAACTATGT      36438      TTAATA
                                ACAT     TTCAGTAACT
                                ||||     ||||||||||
                                TGTA     AAGTCATTGA
                                  TC_____
GAM109  KIAA1155  3'  GTTACTAAAATGTGC       62240         AATATTC
                                GCACATTT      AGTAAC
                                ||||||||      ||||||
                                CGTGTAAA      TCATTG
                                     A_______
GAM109  NCOA2     3'  AGTTACTGAACAGATG      21544       AATA
                                CATTT    TTCAGTAACT
                                |||||    ||||||||||
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                                GTAGA    AAGTCATTGA
                                  C___
GAM109  PGRMC1   3'  CAGGTAAAAATCTTAAATGTGC 21893          T   CAG  A
           A                    TGCACATTTAA ATT   TA CTG
                                |||||||||| |||   || |||
                                ACGTGTAAATT TAA   AT GAC
                                      C   AA_  G
GAM109  SSH2     3'  TTGAATATTAAAATGTGCA   62219        _
                                TGCACATTT AATATTCAG
                                ||||||||| |||||||||
                                ACGTGTAAA TTATAAGTT
                                      A
GAM109  LOC151584 3'  AATATATAAATGTGCA      85447         _
                                TGCACATTTA ATATT
                                |||||||||| |||||
                                ACGTGTAAAT TATAA
                                      A
GAM109  LOC155465 3'  ATTGACAAATACTAAATGTGCA 92517         A  ___
                                TGCACATTTA TAT   TCAGT
                                |||||||||| |||   |||||
                                ACGTGTAAAT ATA   AGTTA
                                      C   AAC
GAM109  LOC158191 3'  TGAATATTAAATGCGC      81785    A
                                GC CATTTAATATTCA
                                || ||||||||||||
                                CG GTAAATTATAAGT
                                 C
GAM109  LOC158310 3'  CTGAACACCAAATGTGTA    86752         AATA
                                TGCACATTT    TTCAG
                                |||||||||    |||||
                                ATGTGTAAA    AAGTC
                                      CCAC
GAM109  LOC58504  3'  GCTTTCTTTATTAAATGTGC   41133          TTC__
                                GCACATTTAATA     AGT
                                ||||||||||||     |||
                                CGTGTAAATTAT     TCG
                                       TTCTT
GAM110  ASTN     3'  TCCTACTTACATTC       69337        AACA    A
                                GAATGTA    AGTA GGA
                                |||||||    |||| |||
                                CTTACAT    TCAT CCT
                                     ____    _
GAM110  BCRP2    3'  TCTCACCCTGTTTACATGCC   62407    A       A_  A
                                GG ATGTAAACA  GT AGG
                                || |||||||||  || |||
                                CC TACATTTGT  CA TCT
                                 G        CC  C
GAM110  CLTC     3'  CCTTATTTCACATTCC      16780        AAAC
                                GGAATGT    AAGTAAGG
                                |||||||    ||||||||
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                                CCTTACA   TTTATTCC
                                   C___
GAM110  CYP3A4   3'  GTTTCCCTACACCTCTTGCATT 33925        ACAA_  A
            CC                   GGAATGTAA    GTA GGAAAC
                                 |||||||||    ||| ||||||
                                 CCTTACGTT    CAT CCTTTG
                                     CTCCA  C
GAM110  DFNA5    3'  TCTGTCACTTGCATTCC    15306      TAAA    AA_
                                 GGAATG   CAAGT  GGA
                                 ||||||   |||||  |||
                                 CCTTAC   GTTCA  TCT
                                    ____   CTG
GAM110  ENAM     3'  TCCCCTACTGCTTACATTCC  49079       ACA   A_
                                 GGAATGTAA  AGTA  GGA
                                 |||||||||  ||||  |||
                                 CCTTACATT  TCAT  CCT
                                     CG_   CC
GAM110  EXTL2    3'  TTTTATTGTTTACATCC    7523     A      G
                                 GGA TGTAAACAA TAAGG
                                 ||| ||||||||| |||||
                                 CCT ACATTTGTT ATTTT
                                   _       _
GAM110  GAS2     3'  TTCCGAAAAGTTTACATTC   17913        AAGTAA
                                 GAATGTAAAC    GGAA
                                 ||||||||||    ||||
                                 CTTACATTTG    CCTT
                                     AAAAG_
GAM110  HHEX     3'  TCCAGAGCTGCCTACATTTC  10785       AACA  AA_
                                 GGAATGTA   AGT  GGA
                                 ||||||||   |||  |||
                                 CTTTACAT   TCG  CCT
                                    CCG_  AGA
GAM110  HOXA3    3'  TTCCTTGCTGCTCACATTCTG 47692       AAACA
                                 CGGAATGT   AGTAAGGAA
                                 ||||||||   |||||||||
                                 GTCTTACA   TCGTTCCTT
                                    CTCG_
GAM110  IL1F5    3'  TCCTCGTGTTTACATTCTG   24384         AGTA
                                 CGGAATGTAAACA  AGGA
                                 ||||||||||||   ||||
                                 GTCTTACATTTGT  TCCT
                                     GC__
GAM110  INHBC    3'  CCCAGCTCTGCCTACATTCTG 18653       AA _ AA
                                 CGGAATGTA  CA AGT  GG
                                 |||||||||  || |||  ||
                                 GTCTTACAT  GT TCG  CC
                                     CC  C   AC
GAM110  ITGB4BP  3'  CCTTCTCCACATTCCG     9403       AAACA  T
                                 CGGAATGT   AG AAGG
                                 ||||||||   || ||||
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                                GCCTTACA    TC TTCC
                                    CC___  _
GAM110  MEA     3'  CCTTATATTCCTACATTCC   27544       AACAA
                                GGAATGTA    GTAAGG
                                ||||||||    ||||||
                                CCTTACAT    TATTCC
                                    CCTTA
GAM110  MGAT5   5'  TTTTTGCTGACATTCCG     10031       AAA  A
                                CGGAATGT   CA GTAAGGA
                                ||||||||   || |||||||
                                GCCTTACA   GT CGTTTTT
                                    ___  _
GAM110  PINX1   3'  TTTCCCCCAAGTTACATTCC   35414       ACAAGTAA
                                GGAATGTAA       GGAAA
                                |||||||||       |||||
                                CCTTACATT       CCTTT
                                     GAACCC__
GAM110  PRex1   3'  GTTTCCTTCAACGTCCACATTC 40434       AA  AAGT
            C                    GGAATGT  AC    AAGGAAAC
                                |||||||  ||    ||||||||
                                CCTTACA  TG    TTCCTTTG
                                    CC  CAAC
GAM110  PTPRN   3'  CCTTCTCCTGCCTACATTCC   11129       AA __  T
                                GGAATGTA  CA  AG AAGG
                                ||||||||  ||  || ||||
                                CCTTACAT  GT  TC TTCC
                                    CC  CC  _
GAM110  SFRS1   3'  TCCTAACATCTACATTCC    22641       AACAA  A
                                GGAATGTA    GT AGGA
                                ||||||||    || ||||
                                CCTTACAT    CA TCCT
                                    CTA__  A
GAM110  SHANK2  3'  TTCCTGTAACTTGTTCTACATT 24591        _     A__
            CC                    GGAATGTA AACAAGT   AGGAA
                                |||||||| |||||||  |||||
                                CCTTACAT TTGTTCA   TCCTT
                                    C      ATG
GAM110  SLC38A2 3'  TTACTTGTTTACATCC     38594     A
                                GGA TGTAAACAAGTAA
                                ||| ||||||||||||
                                CCT ACATTTGTTCATT
                                   _
GAM110  SLC9A1  3'  TTTTGTTTGTTCACACTCC   70416     A  A
                                GGA TGT AACAAGTAAGG
                                ||| ||| ||||||||||
                                CCT ACA TTGTTTGTTTT
                                  C  C
GAM110  SOCS5   3'  GTTTCCTTACCTGCTGCTACA  25799     AA__  A
                                TGTA   CA GTAAGGAAAC
                                ||||   || ||||||||||
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                                ACAT   GT CATTCCTTTG
                                  CGTC  C
GAM110  SRR     3'  GTTTCCTTACCTAAAGGTTCC  41688      GTAAACAA
                                GGAAT      GTAAGGAAAC
                                |||||      ||||||||||
                                CCTTG      CATTCCTTTG
                                   GAAATC__
GAM110  TEM8    3'  TCCAAAATTGCCTATATTCC   36332       AA   GTAA
                                GGAATGTA  CAA   GGA
                                ||||||||  |||   |||
                                CCTTATAT  GTT   CCT
                                     CC   AAAA
GAM110  TFDP1   3'  GTTTCCTTTTGGCCTACTCCC  23049    AAT   AA_   GT
                                GG   GTA   CAA  AAGGAAAC
                                ||   |||   |||  ||||||||
                                CC   CAT   GTT  TTCCTTTG
                                 CT_   CCG   __
GAM110  YWHAZ   3'  TTCCTTTGCTTGCATCCC    12710    A     A   GTA
                                GG ATGTAA CAA   AGGAA
                                || ||||||| |||   |||||
                                CC TACGTT GTT   TCCTT
                                 C     C   ___
GAM110  ZNF26   5'  TCTCCTTGTTCACATCCG    72983     A   A     TAA
                                CGGA TGT AACAAG   GGA
                                |||| ||| ||||||   |||
                                GCCT ACA TTGTTC   TCT
                                  _   C     C__
GAM110  ABLIM   3'  TTCCTTACCTGTCAATA     9781      AA   A
                                TGT   ACA GTAAGGAA
                                |||   ||| ||||||||
                                ATA   TGT CATTCCTT
                                  AC   C
GAM110  ABLIM   3'  TTCCTTACCTGTCAATA     22043     AA   A
                                TGT   ACA GTAAGGAA
                                |||   ||| ||||||||
                                ATA   TGT CATTCCTT
                                  AC   C
GAM110  ARHGAP5 3'  TTCCTTATTCACTTACATT   6757        ACA
                                AATGTAA   AGTAAGGAA
                                |||||||   |||||||||
                                TTACATT   TTATTCCTT
                                    CAC
GAM110  ARHGAP5 3'  TTCCTTATTCACTTACATT   77084       ACA
                                AATGTAA   AGTAAGGAA
                                |||||||   |||||||||
                                TTACATT   TTATTCCTT
                                    CAC
GAM110  ATP6V1B2 3' TTCCCTACCCCGTGCATTCC  8088         AACAA   A
                                GGAATGTA    GTA GGAA
                                ||||||||    ||| ||||
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                                CCTTACGT    CAT CCTT
                                     GCCC_  C
GAM110  C1orf10   5' CCACTTGTTTCATCCC     32465    A  T      AA
                                GG ATG AAACAAGT  GG
                                || ||| ||||||||  ||
                                CC TAC TTTGTTCA  CC
                                 C  _      __
GAM110  CTCFL     3' TTGCCCTGGTTACATTCC    82504        A  A_
                                GGAATGTAA CA  GTAA
                                ||||||||| ||  ||||
                                CCTTACATT GT  CGTT
                                      G  CC
GAM110  FLJ10081  5' TTTCCTCACCTGTTTACA    35805        A  A
                                TGTAAACA GT AGGAAA
                                |||||||| || ||||||
                                ACATTTGT CA TCCTTT
                                     C  C
GAM110  FLJ10618  3' CCTTTGTTTAATTCC      36344      G     GTA
                                GGAAT TAAACAA   AGG
                                ||||| |||||||   |||
                                CCTTA ATTTGTT   TCC
                                  _     ___
GAM110  FLJ13072  3' CCTGCTGTTTACACCC     89808    AA      A  A
                                GG  TGTAAACA GTA GG
                                ||  |||||||| ||| ||
                                CC  ACATTTGT CGT CC
                                 C_      _  _
GAM110  FLJ13449  3' TTCTTGATCCACTTGCATTCC  44621         ACAAG_
                                GGAATGTAA     TAAGGA
                                |||||||||     ||||||
                                CCTTACGTT     GTTCTT
                                      CACCTA
GAM110  FLJ13657  3' TTTCATTTACATTCC       45722          CAAGTAA
                                GGAATGTAAA      GGAA
                                ||||||||||      ||||
                                CCTTACATTT      CTTT
                                     A_______
GAM110  FLJ14393  3' GTTTCCTTACCTGCGTATCT   51321    _    AACAA
                                GGA ATGTA    GTAAGGAAAC
                                ||| |||||    ||||||||||
                                TCT TGCGT    CATTCCTTTG
                                  A    C____
GAM110  FLJ21459  5' TTTCTTATTTACATCCC     44522    A    ACAA
                                GG ATGTAA   GTAAGGAA
                                || ||||||   ||||||||
                                CC TACATT   TATTCTTT
                                 C     _____
GAM110  FLJ23189  3' TTTCTACTGCACTTACATTC   46843        ACA_   A
                                GAATGTAA   AGTA GGAA
                                ||||||||   |||| ||||
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                                CTTACATT   TCAT CTTT
                                    CACG   _
GAM110  GAS2L1   3'  CCTCTGTTGTACATTCCG    21361        _   AGTA
                                CGGAATGTA AACA   AGG
                                ||||||||| ||||   |||
                                GCCTTACAT TTGT   TCC
                                    G   C___
GAM110  GMFB     3'  TTCCAGTTTTTACATTCCG   14672         CAAGTAA
                                CGGAATGTAAA     GGAA
                                ||||||||||      ||||
                                GCCTTACATTT     CCTT
                                      TTGA___
GAM110  GPA33    3'  TCCTTTGCTTCATTCC      19459       TAAAC    _
                                GGAATG    AAGTAA GGA
                                ||||||    |||||| |||
                                CCTTAC    TTCGTT CCT
                                  _____     T
GAM110  HRIHFB2436 3'  TTTACTGTTTACACCCC    26799    AA       A
                                GG  TGTAAACA GTAAG
                                ||  |||||||| |||||
                                CC  ACATTTGT CATTT
                                 CC      _
GAM110  HSPC117  3'  GCTCTGTTTACATTCCG     26677           _
                                CGGAATGTAAACA AGT
                                |||||||||||| |||
                                GCCTTACATTTGT TCG
                                      C
GAM110  HYA22    3'  CCTTATTTGACCACACTCC    19424     A   AAA
                                GGA TGT   CAAGTAAGG
                                ||| |||   |||||||||
                                CCT ACA   GTTTATTCC
                                  C   CCA
GAM110  KIAA0087 3'  TCCTTGGCATTTTACTTCC    28705      T    CAAG
                                GGAA GTAAA    TAAGGA
                                |||| |||||    ||||||
                                CCTT CATTT    GTTCCT
                                   _    TACG
GAM110  KIAA0202 3'  TCCTTACTCACTATAGTC    64371    A   AACA
                                GA TGTA    AGTAAGGA
                                || ||||    ||||||||
                                CT ATAT    TCATTCCT
                                 G   CAC_
GAM110  KIAA0493 3'  CCTTCAAAACCTCTTACATTCC 64273         ACAA ____
                                GGAATGTAA   GT   AAGG
                                |||||||||   ||   ||||
                                CCTTACATT   CA   TTCC
                                     CTC_  AAAC
GAM110  KIAA0643 3'  TCCTATGTTTGCATTCC     45602           AGTA
                                GGAATGTAAACA   AGGA
                                ||||||||||||   ||||
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                                CCTTACGTTTGT   TCCT
                                      A___
GAM110  KIAA0895 3' TTCCATTGCTGTTCAGACTCC 92727    ATGTA   A   _
                                GGA    AACA GTAA GGAA
                                |||    |||| |||| ||||
                                CCT    TTGT CGTT CCTT
                                  CAGAC   _   A
GAM110  KIAA0914 3' CTCTACTGTTTACATT     29678        A  AG
                                AATGTAAACA GTA  G
                                |||||||||| |||  |
                                TTACATTTGT CAT  C
                                      _  CT
GAM110  KIAA0970 3' CCTCATATACTGTACATTCC  29956      AA  A  ____
                                GGAATGT  ACA GTA   AGG
                                |||||||  ||| |||   |||
                                CCTTACA  TGT CAT   TCC
                                   __  _  ATAC
GAM110  KIAA0997 3' TTTCCTCCTCTATATTCC   30195       AACA  TA
                                GGAATGTA   AG  AGGAAA
                                ||||||||   ||  ||||||
                                CCTTATAT   TC  TCCTTT
                                    C___  C_
GAM110  KIAA1061 3' TTTTCTTACCCACATTCC   71180       AAACAA
                                GGAATGT    GTAAGGAAA
                                |||||||    |||||||||
                                CCTTACA    CATTCTTTT
                                   CC____
GAM110  KIAA1265 3' CTTTCTGTTTACATCC     70789    A      A T
                                GGA TGTAAACA G AAGG
                                ||| |||||||| | ||||
                                CCT ACATTTGT C TTTC
                                  _      _ _
GAM110  KIAA1416 3' TCCTACTGTTTACACTC    86463    A      A  A
                                GA TGTAAACA GTA GGA
                                || |||||||| ||| |||
                                CT ACATTTGT CAT CCT
                                 C      _  _
GAM110  LANO    3' CCCTGCTTACATTCC       36620       AACA   A
                                GGAATGTA   AGTA GG
                                ||||||||   |||| ||
                                CCTTACAT   TCGT CC
                                     ____   C
GAM110  MGC10526 5' TTTCCTTACTAGATGACATTTC 50969       AAACA
                                GGAATGT    AGTAAGGAAA
                                |||||||    ||||||||||
                                CTTTACA    TCATTCCTTT
                                   GTAGA
GAM110  MGC23937 3' TCCTGGAATTTTACATTCC   58956        CAAGTA
                                GGAATGTAAA    AGGA
                                ||||||||||    ||||
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                                CCTTACATTT     TCCT
                                     TAAGG_
GAM110  MGC5560  3'  TCCCTGCTACATTCC      38787       AAACA   A
                                GGAATGT    AGTA GGA
                                |||||||    |||| |||
                                CCTTACA    TCGT CCT
                                   _____   C
GAM110  MRPL56   3'  TTTTCTTTGTTTCCATTCC   51691       T    GTA
                                GGAATG AAACAA   AGGAAA
                                |||||| ||||||   ||||||
                                CCTTAC TTTGTT   TCTTTT
                                   C    ___
GAM110  NR6A1    3'  GTTTCCTTACCTGGATCTCC   52875     ATGTAAA  A
                                GGA      CA GTAAGGAAAC
                                |||      || ||||||||||
                                CCT      GT CATTCCTTTG
                                  CTAG___  C
GAM110  NR6A1    3'  GTTTCCTTACCTGGATCTCC   52887     ATGTAAA  A
                                GGA      CA GTAAGGAAAC
                                |||      || ||||||||||
                                CCT      GT CATTCCTTTG
                                  CTAG___  C
GAM110  NR6A1    3'  GTTTCCTTACCTGGATCTCC   7650      ATGTAAA  A
                                GGA      CA GTAAGGAAAC
                                |||      || ||||||||||
                                CCT      GT CATTCCTTTG
                                  CTAG___  C
GAM110  NY-REN-25 3'  TTTCTGTGTTTGCATTCC    60638          AGTA
                                GGAATGTAAACA   AGGAA
                                ||||||||||||   |||||
                                CCTTACGTTTGT   TCTTT
                                      G___
GAM110  OS4      5'  TTTCCTCCTCTTGTTTTCACTC 19188     A  T      TA_
            CG                    CGGA TG AAACAAG   AGGAAA
                                |||| || |||||||   ||||||
                                GCCT AC TTTGTTC   TCCTTT
                                  C  T      TCC
GAM110  PP1628   5'  TCCCCAGTAGTTTACATTCC   47308          AAGTAA
                                GGAATGTAAAC     GGA
                                ||||||||||      |||
                                CCTTACATTTG     CCT
                                      ATGACC
GAM110  PRKRIR   3'  TCGTTGCTGTTTACATTCC    16297          A   G
                                GGAATGTAAACA GTAA GA
                                |||||||||||| |||| ||
                                CCTTACATTTGT CGTT CT
                                      _   G
GAM110  SH3BGRL2 3'  TACTTGTTCTCATTCCG     48889        TA
                                CGGAATG  AACAAGTA
                                |||||||  ||||||||
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                                GCCTTAC  TTGTTCAT
                                    TC
GAM110  SLC16A6  3'  TCTTTGGTTCACATTCCG    16276        A   AAG
                                CGGAATGT AAC   TAAGGA
                                |||||||| |||   ||||||
                                GCCTTACA TTG   GTTTCT
                                    C   ___
GAM110  SLC2A11  5'  TCCTACCCGCATTCCG      47966        AAACAA   A
                                CGGAATGT     GTA GGA
                                ||||||||     ||| |||
                                GCCTTACG     CAT CCT
                                    CC____   _
GAM110  SLK      3'  TTCCCAGCTTGCATTCC     28230       TAAA    AA
                                GGAATG   CAAGT  GGAA
                                ||||||   |||||  ||||
                                CCTTAC   GTTCG  CCTT
                                   ____    AC
GAM110  TA-PP2C  3'  GTTTCCTTACAAAACTACCCCG 57760     AAT   AACAA
                                CGG   GTA    GTAAGGAAAC
                                |||   |||    ||||||||||
                                GCC   CAT    CATTCCTTTG
                                  C__   CAAAA
GAM110  TDRKH    3'  TCTTACCTGTTTACAGCCC    22484    AA      A
                                GG  TGTAAACA GTAAGG
                                ||  |||||||| ||||||
                                CC  ACATTTGT CATTCT
                                  CG       C
GAM110  TLE4     3'  TCCTTTTTGTTCACCCCC    67923    AAT  A     T
                                GG   GT AACAAG AAGGA
                                ||   || |||||| |||||
                                CC   CA TTGTTT TTCCT
                                  CC_  C     _
GAM110  LOC143310 5'  TCCTTTGTTTGCACCCC     76541    AA       GTA
                                GG  TGTAAACAA   AGGA
                                ||  |||||||||   ||||
                                CC  ACGTTTGTT   TCCT
                                  CC        ___
GAM110  LOC144308 3'  TTTCCATAGAGTTTACATCC   83054     A      AAG  A
                                GGA TGTAAAC   TA GGAAA
                                |||  |||||||   || |||||
                                CCT ACATTTG   AT CCTTT
                                  _      AG_  A
GAM110  LOC147229 5'  TCCTTACCTGCGTTCTG     78323         AACAA
                                CGGAATGTA    GTAAGGA
                                |||||||||    |||||||
                                GTCTTGCGT    CATTCCT
                                     C____
GAM110  LOC150848 3'  TCTTTACCTCTACATTCC    85131         AACAA
                                GGAATGTA    GTAAGGA
                                ||||||||    |||||||
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                                CCTTACAT    CATTTCT
                                    CTC__
GAM110  LOC157922 3'  CCTTACTTGAAGTTCT     86632      GTAAA
                                GGAAT    CAAGTAAGG
                                |||||    |||||||||
                                TCTTG    GTTCATTCC
                                  AA___
GAM110  LOC168448 3'  TTCCTTGCCCTCATTCCG    82702       TAAACAA
                                CGGAATG     GTAAGGAA
                                |||||||     ||||||||
                                GCCTTAC     CGTTCCTT
                                    TCC____
GAM110  LOC200107 3'  TACCTGTTTACATTCC      88577          A
                                GGAATGTAAACA GTA
                                |||||||||||| |||
                                CCTTACATTTGT CAT
                                       C
GAM110  LOC204161 5'  CCTTTGTTTACTCTCC      90658     AT      GTA
                                GGA  GTAAACAA   AGG
                                |||  ||||||||   |||
                                CCT  CATTTGTT   TCC
                                  CT       ___
GAM110  LOC219855 3'  TCTTGCTTGTTCAGATTCC    91518      GTA
                                GGAAT   AACAAGTAAGG
                                |||||   ||||||||||
                                CCTTA   TTGTTCGTTCT
                                   GAC
GAM110  LOC255147 5'  GTTTCTTTCTGCCTCCATTCC  95702       TAAACA  T
                                GGAATG     AG AAGGAAAC
                                ||||||     || ||||||||
                                CCTTAC     TC TTTCTTTG
                                   CTCCG_  _
GAM110  LOC256401 3'  TTCCTTGCCCTCATTCCG    96021       TAAACAA
                                CGGAATG     GTAAGGAA
                                |||||||     ||||||||
                                GCCTTAC     CGTTCCTT
                                    TCC____
GAM110  LOC90643  3'  TCCTTACTTTCATCC       63692     A  TAAAC
                                GGA TG     AAGTAAGGA
                                ||| ||     |||||||||
                                CCT AC     TTCATTCCT
                                  _  T____
GAM110  LOC90750  3'  TTCCTTACTCGCATCTG     63928      A   AAACA
                                CGGA TGT    AGTAAGGAA
                                |||| |||    |||||||||
                                GTCT ACG    TCATTCCTT
                                  _   C____
GAM110  LOC91818  3'  TCCTTACTTTCATCC       67272     A  TAAAC
                                GGA TG     AAGTAAGGA
                                ||| ||     |||||||||
```

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                              CCT AC    TTCATTCCT
                                _ T____
GAM110  LOC92181  3'  TCCTTATTTACATTC      68408       ACAA
                              GAATGTAA   GTAAGGA
                              ||||||||   |||||||
                              CTTACATT   TATTCCT
                                   ____
GAM111  AQP6    3'  CCTGCCATCATCATTGGGA   53920       TTAGAC  A
                              TCCCAATG    GA GGCAGG
                              ||||||||    || ||||||
                              AGGGTTAC    CT CCGTCC
                                   TA____  A
GAM111  BACH2   3'  TCCTGCCTTCACCCCATTGGGA 41492       TTAGAC
                              TCCCAATG    GAAGGCAGGA
                              ||||||||    ||||||||||
                              AGGGTTAC    CTTCCGTCCT
                                   CCCA__
GAM111  BICD1   5'  TCCTGCCTCCATCCACCGGGG  8154     AA  TTA  CGA
                              TCCC  TG   GA   AGGCAGGA
                              ||||  ||   ||   ||||||||
                              GGGG  AC   CT   TCCGTCCT
                                CC  ___  ACC
GAM111  CD244   3'  TCCTACCCTGTATCTAACATAG 33063    A      CGA   C_
          G                    CC ATGTTAGA   AGG  AGGA
                              || ||||||||   |||  ||||
                              GG TACAATCT   TCC  TCCT
                               A      ATG   CA
GAM111  FBXL7   3'  CCCACCTTTGTTACGTTG    24547      TA      CA
                              CAATGT  GACGAAGG  GG
                              ||||||  ||||||||  ||
                              GTTGCA  TTGTTTCC  CC
                                 __       AC
GAM111  FGD1    5'  CCTGCCCCCGCGGCTGG     15523     AT   AGA  AA
                              CCA  GTT   CG  GGCAGG
                              |||  |||   ||  ||||||
                              GGT  CGG   GC  CCGTCC
                                __   C__  CC
GAM111  G6PT1   3'  TCCTGCCTTCAGACAAACAGGA 7600     CAA_   AGAC
                              TCC    TGTT    GAAGGCAGGA
                              |||    ||||    ||||||||||
                              AGG    ACAG    CTTCCGTCCT
                                ACAA    A___
GAM111  GLRA1   5'  CCCGCCTCCCTTTAACATCTGG 3914     CA      CGA    A
          A                    TCC  ATGTTAGA   AGGC GG
                              |||  ||||||||   |||| ||
                              AGG  TACAATTT   TCCG CC
                                TC       CCC    C
GAM111  KRTHA8  3'  TCCTGCCTCCCTATCTTGG   22262     TGT   AC  A
                              CCAA   TAG  GA GGCAGGA
                              ||||   |||  || |||||||
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                                GGTT  ATC  CT CCGTCCT
                                  CT_  C_ _
GAM111  NORE1   3'  TCCTGCATGTCTCTAACATT  48720        C  AG_
                                AATGTTAGA GA  GCAGGA
                                |||||||||  ||  ||||||
                                TTACAATCT CT  CGTCCT
                                     _ GTA
GAM111  PAX5    3'  TCCTGCCTCCATTTCTCTGGGA 33636     ATGTT  CGA__
                                TCCCA   AGA   AGGCAGGA
                                |||||   |||   ||||||||
                                AGGGT   TCT   TCCGTCCT
                                  C____  TTACC
GAM111  PFKFB3  3'  CCCACCTTCTCTTCAGGA   82873    CAA  TT  C   CA
                                TCC  TG  AGA GAAGG  GG
                                |||  ||  ||| |||||  ||
                                AGG  AC  TCT CTTCC  CC
                                 ___ T_  _   AC
GAM111  PIGN    5'  CCTGCCTTCGCGCTGAGGA   24669    CAATG   A_
                                TCC   TTAG  CGAAGGCAGG
                                |||   ||||  ||||||||||
                                AGG   AGTC  GCTTCCGTCC
                                 _____  GC
GAM111  TDG     5'  CCTGTAATCCAACATTGGGA  12190        A  CGAAG
                                TCCCAATGTT GA   GCAGG
                                ||||||||| ||   |||||
                                AGGGTTACAA CT   TGTCC
                                     C  AA___
GAM111  TEM8    3'  CCTGCCTTCGTATTGA     36328     _
                                TTAG ACGAAGGCAGG
                                |||| ||||||||||
                                AGTT TGCTTCCGTCC
                                  A
GAM111  ZNF7    5'  CCCGCCTTCGGCATTGGGG   12737        TAGA     A
                                TCCCAATGT   CGAAGGC GG
                                |||||||||   ||||||| ||
                                GGGGTTACG   GCTTCCG CC
                                     ____      C
GAM111  CALN1   3'  CCAGACAGAATCTAGCATCGGG 48859     A      CGAAGGCA
           A                     TCCC ATGTTAGA       GG
                                |||| ||||||||       ||
                                AGGG TACGATCT       CC
                                  C       AAGACAGA
GAM111  CRMP5   3'  TCCTGCCTCCGCTGGCTTTGGG 39294       T    A  A
           A                     TCCCAA GTTAG CG AGGCAGGA
                                |||||| ||||| || ||||||||
                                AGGGTT CGGTC GC TCCGTCCT
                                   T    _ C
GAM111  DKFZP434P211 5'  CCTGCCTTCCTTCCTGGGA   27263      ATGTT  AC
                                TCCCA    AG  GAAGGCAGG
                                |||||    ||  |||||||||
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                                AGGGT    TC  CTTCCGTCC
                                   CCT__  __
GAM111  DKFZP586M0122 3'  CCTGCCTTCTGCATGAGA    31248    CCA   TAGAC
                                TC   ATGT    GAAGGCAGG
                                ||   ||||    |||||||||
                                AG   TACG    CTTCCGTCC
                                 AG_    T____
GAM111  DNAJC5    3'  CCTGCCTTGAAACAT      61452      AGA G
                                ATGTT   C AAGGCAGG
                                |||||   | ||||||||
                                TACAA   G TTCCGTCC
                                   A__ _
GAM111  ELOVL1    3'  CCTGCCTTAAAACTTGGGA   43059       T   AGACG
                                TCCCAA GTT    AAGGCAGG
                                |||||| |||    ||||||||
                                AGGGTT CAA    TTCCGTCC
                                   _   AA___
GAM111  EVI5      3'  TCTGTACCACCTAACATTG    19017         ACGAAG
                                CAATGTTAG     GCAGG
                                |||||||||     |||||
                                GTTACAATC     TGTCT
                                     CACCA_
GAM111  FLJ11078  3'  TCCTGCCTTCATCTGCTTTCCG 37033     CAATGT    C
           GA                     TCC     TAGA GAAGGCAGGA
                                |||     |||| ||||||||||
                                AGG     GTCT CTTCCGTCCT
                                 CCTTTC    A
GAM111  FLJ12355  3'  TCCTGCCTCTGGGAACTGGGA  46483      AT   AGA  A
                                TCCCA  GTT   CG AGGCAGGA
                                |||||  |||   || ||||||||
                                AGGGT  CAA   GT TCCGTCCT
                                   __   GG_  C
GAM111  FLJ12899  3'  CCCCAACTGTCTAACTTGG    44761      T       AA_  CA
                                CCAA GTTAGACG   GG  GG
                                |||| ||||||||   ||  ||
                                GGTT CAATCTGT   CC  CC
                                   _       CAA  __
GAM111  FLJ13195  3'  TCCTGCCTCTCCCTAACACAGG 43259    AA     AC  _
                                CC  TGTTAG  GA AGGCAGGA
                                ||  ||||||  || ||||||||
                                GG  ACAATC  CT TCCGTCCT
                                 AC     C_  C
GAM111  FLJ14431  3'  CCCACCTCCAACATTGGGA   51352          A  CGAA  CA
                                TCCCAATGTT GA    GG  GG
                                |||||||||| ||    ||  ||
                                AGGGTTACAA CT    CC  CC
                                     C  _____  AC
GAM111  FLJ22242  3'  TCCTGCCTCCATCACAT     46868      TA  CGA
                                ATGT  GA   AGGCAGGA
                                ||||  ||   ||||||||
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                                TACA  CT   TCCGTCCT
                                  __ ACC
GAM111  GPT2     3' CCTGCCTTCCCCAGTGGGA   55954      A  TTAGAC
                                TCCCA TG     GAAGGCAGG
                                ||||| ||     |||||||||
                                AGGGT AC     CTTCCGTCC
                                   G  CC____
GAM111  HZFW1    3' TCCTGCCTTCTGGCTCTCA   47463    TT  AC_
                                TG  AG   GAAGGCAGGA
                                ||  ||   ||||||||||
                                AC  TC   CTTCCGTCCT
                                 TC  GGT
GAM111  KIAA0748 3' CCCACCTCCAACAATGGGG   28937      A    A  CGAA  CA
                                TCCCA TGTT GA    GG  GG
                                ||||| |||| ||    ||  ||
                                GGGGT ACAA CT    CC  CC
                                   A    C  ____  AC
GAM111  KIAA1332 3' CCTACCCTACACTTTGGGA   71165      T  _   ACGAA  C
                                TCCCAA GT TAG    GG AGG
                                |||||| || |||    || |||
                                AGGGTT CA ATC    CC TCC
                                    T  C  _____  A
GAM111  KIAA1600 3' TCCTGCCTTGTTTACATT    71447      T    G
                                AATGT AGAC AAGGCAGGA
                                ||||| |||| |||||||||
                                TTACA TTTG TTCCGTCCT
                                  _    _
GAM111  LANO     3' CCTGCCTAAAAGCATTGG    36621        AGACGA
                                CCAATGTT     AGGCAGG
                                ||||||||     |||||||
                                GGTTACGA     TCCGTCC
                                     AAA___
GAM111  LANO     3' CCTGCCTAAAAGCATTGG    47188        AGACGA
                                CCAATGTT     AGGCAGG
                                ||||||||     |||||||
                                GGTTACGA     TCCGTCC
                                     AAA___
GAM111  PELI1    5' TCCTGCCTCCGCTTCCCA    40289    TT_  A  A
                                TG   AG CG AGGCAGGA
                                ||   || || ||||||||
                                AC   TC GC TCCGTCCT
                                 CCT  _  C
GAM111  PTK6     3' CCTTCACCTTTGTCGCTGGG   19935     ATGTTA      C__
                                CCCA     GACGAAGG   AGG
                                ||||     ||||||||   |||
                                GGGT     CTGTTTCC   TCC
                                  CG____       ACT
GAM111  SLC21A11 5' TCCTGCTTTTCCAACATCAAGA 64469    CCA    A  CG
                                TC   ATGTT GA  AAGGCAGGA
                                ||   ||||| ||  |||||||||
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                                AG   TACAA CT  TTTCGTCCT
                                 AAC    C __
GAM111  TESK2    5' TCCTGCCTCAGTGTCAAAC   63183    A   A__
                                GTT GACG   AGGCAGGA
                                ||| ||||   ||||||||
                                CAA CTGT   TCCGTCCT
                                  A   GAC
GAM111  URKL1    3' CCTGCCTCCTGACCCAGGA   35342    CAAT    ACGA
                                TCC   GTTAG   AGGCAGG
                                |||   |||||   |||||||
                                AGG   CAGTC   TCCGTCC
                                  ACC_    C___
GAM111  WBSCR23  3' TCCTGCCTCCGCCTCCCA    46772    TT  A  A
                                TG  AG CG AGGCAGGA
                                ||  || || ||||||||
                                AC  TC GC TCCGTCCT
                                 CC  C  C
GAM111  LOC121629 5' CCTGCCTGTCTAAC       75571       GA
                                GTTAGAC  AGGCAGG
                                |||||||  |||||||
                                CAATCTG  TCCGTCC
                                    __
GAM111  LOC139065 5' TCCTGCCTCCATCTCAGCTGG  75816     AT  _  CGA
                                CCA  GTT AGA   AGGCAGGA
                                |||  ||| |||   ||||||||
                                GGT  CGA TCT   TCCGTCCT
                                  __   C   ACC
GAM111  LOC148710 3' CCTGCCTTCGTCTCCATAGG   84193    A   TT
                                CC ATG  AGACGAAGGCAGG
                                || |||  ||||||||||||
                                GG TAC  TCTGCTTCCGTCC
                                 A   C_
GAM111  LOC149606 3' CCTGCCTTCATCCAAGGTGGGA 79448       A G  A  C
                                TCCCA T TT GA GAAGGCAGG
                                ||||| | || || |||||||||
                                AGGGT G AA CT CTTCCGTCC
                                   _ G  C  A
GAM111  LOC150174 5' CCTGCCTTCCTTCCTGGGA   79607      ATGTT  AC
                                TCCCA    AG  GAAGGCAGG
                                |||||    ||  |||||||||
                                AGGGT    TC  CTTCCGTCC
                                   CCT__  __
GAM111  LOC150213 5' CCTGCCTTCCTTCCTGGGA   74854      ATGTT  AC
                                TCCCA    AG  GAAGGCAGG
                                |||||    ||  |||||||||
                                AGGGT    TC  CTTCCGTCC
                                   CCT__  __
GAM111  LOC150236 5' CCTGCCTTCCTTCCTGGGA   79687      ATGTT  AC
                                TCCCA    AG  GAAGGCAGG
                                |||||    ||  |||||||||
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                                AGGGT    TC  CTTCCGTCC
                                  CCT__  __
GAM111  LOC152313 3'  CCCACCTCCAACACTGGGG   85659      A   A  CGAA  CA
                                TCCCA TGTT GA   GG  GG
                                ||||| |||| ||   ||  ||
                                GGGGT ACAA CT   CC  CC
                                  C   C  ____  AC
GAM111  LOC157858 5'  TCCTGCCTCCGCCTCCCG    86604    TT  A  A
                                TG  AG CG AGGCAGGA
                                ||  || || ||||||||
                                GC  TC GC TCCGTCCT
                                 CC  C  C
GAM111  LOC196955 5'  TCCTGCCCTCTAACATCGG    77390    A       CGAA
                                CC ATGTTAGA   GGCAGGA
                                || ||||||||   |||||||
                                GG TACAATCT   CCGTCCT
                                 C       C___
GAM111  LOC219540 5'  TCCTGCCTCTTGATACACTGG  93602     A   TAGA  _
                                CCA TGT   CGA AGGCAGGA
                                ||| |||   ||| ||||||||
                                GGT ACA   GTT TCCGTCCT
                                  C   TA__   C
GAM111  LOC222160 5'  CCCACCTACAACATTGGGG   94123         AGACGA   CA
                                TCCCAATGTT     AGG  GG
                                ||||||||||     |||  ||
                                GGGGTTACAA     TCC  CC
                                      CA____   AC
GAM111  LOC222256 3'  CCTGCCCTCGTTTTAACA    94261        _  A
                                TGTTAGA CGA GGCAGG
                                ||||||| ||| ||||||
                                ACAATTT GCT CCGTCC
                                    T   C
GAM112  ACCN1    3'  TATTAAAAGCTGGTCTTGTGGA 6584         __    TA   CC
          AA                    TTTTCAC  GGCCA  GCTT  AATA
                                ||||||| |||||  ||||  ||||
                                AAAGGTG  CTGGT  CGAA  TTAT
                                    TT    __   AA
GAM112  IRF2     5'  TTGGTAGCGTGAAAA      9358        GGCCATA   T
                                TTTTCAC      GCT CCAA
                                |||||||      ||| ||||
                                AAAAGTG      CGA GGTT
                                    _______  T
GAM112  PABPN1   5'  ATTGGAAGCTGTCCAGGAAAA  16174      AC  CC
                                TTTTC  GG  ATAGCTTCCAAT
                                |||||  ||  ||||||||||||
                                AAAAG  CC  TGTCGAAGGTTA
                                  GA  __
GAM112  TPO      5'  GAGTTACAGCCGTGAAAA    5046          CA
                                TTTTCACGGC  TAGCTT
                                ||||||||||  ||||||
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                                AAAAGTGCCG  ATTGAG
                                      AC
GAM112  ARHU     3'  TATTAGAAGCTATATTAGCTG  41079      C___       C
                                CGGC    ATAGCTTC AATA
                                ||||    |||||||| ||||
                                GTCG    TATCGAAG TTAT
                                  ATTA       A
GAM112  FLJ12998  3'  ATTGGTTTTGCCGTGAAAA   42835          CATAGCTT
                                TTTTCACGGC       CCAAT
                                ||||||||||       |||||
                                AAAAGTGCCG       GGTTA
                                      TTTT____
GAM112  GNB4     3'  AGCCTATAGCTGTGAAAA    41267          C   _
                                TTTTCACGGC ATAG CT
                                |||||||||| |||| ||
                                AAAAGTGTCG TATC GA
                                      A   C
GAM112  LOC150418 3'  GAGTCGGCCGTGAAGA      65509          ATA
                                TTTTCACGGCC   GCTT
                                ||||||||||   ||||
                                AGAAGTGCCGG   TGAG
                                      C__
GAM112  LOC199957 3'  GAGTCGGCCGTGAAGA      88505          ATA
                                TTTTCACGGCC   GCTT
                                ||||||||||   ||||
                                AGAAGTGCCGG   TGAG
                                      C__
GAM112  LOC91431  5'  ATTGGAAATGCAAGGCCGTGGA 56922          ATA  __
            AA                    TTTTCACGGCC   GC  TTCCAAT
                                ||||||||||   ||  |||||||
                                AAAGGTGCCGG   CG  AAGGTTA
                                      AA_  TA
GAM113  B3GAT1   3'  CCAGCCAAGCTGGTGCTC    53973       CTG
                                GAGCACT   AGCTTGGCTGG
                                |||||||   ||||||||||
                                CTCGTGG   TCGAACCGACC
                                     ___
GAM113  B3GAT1   3'  CCAGCCAAGCTGGTGCTC    37828       CTG
                                GAGCACT   AGCTTGGCTGG
                                |||||||   ||||||||||
                                CTCGTGG   TCGAACCGACC
                                     ___
GAM113  COL4A2   3'  GCCAGCCGTGGCCAGAGGCTCG 8468        A    A  _
            A                     TCGAGC CTCTG GCT TGGCTGGC
                                |||||| ||||| ||| ||||||||
                                AGCTCG GAGAC CGG GCCGACCG
                                   _    _  T
GAM113  EVPL     5'  CCAGCCAAGCCCAGCCTG    8804     CT   A
                                CA  CTG GCTTGGCTGG
                                ||  ||| ||||||||||
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                                GT  GAC CGAACCGACC
                                 CC   C
GAM113  OCLN     5'  GCCAGGTCCAGAGCGCCGA   10316     A  A     AG
                                TCG GC CTCTG  CTTGGC
                                ||| || |||||  ||||||
                                AGC CG GAGAC  GGACCG
                                  _ C    CT
GAM113  TBX1     3'  CCAGTGCCAAAGCGCCCGG   54671     A  A  C  A  TTG
                                TCG GC CT TG GC   GCTGG
                                ||| || || || ||   |||||
                                GGC CG GA AC CG   TGACC
                                  C  C  A  _ ___
GAM113  TRIM14   3'  GCCAAGGAAACCCAGAGTGC   28856        AG____
                                GCACTCTG     CTTGGC
                                ||||||||     ||||||
                                CGTGAGAC     GAACCG
                                     CCAAAG
GAM113  USH3A    3'  GCCAGCAGACATCAGAACACAC 53784     AGCAC_    GCTTG
             CGA                   TCG     TCTGA    GCTGGC
                                |||     |||||    ||||||
                                AGC     AGACT    CGACCG
                                  CACACA    ACAGA
GAM113  Apg4B    3'  GCCCAGCTCAGAGTGCCCG   25285    A         T
                                CG GCACTCTGAGCT GGC
                                || ||||||||||| |||
                                GC CGTGAGACTCGA CCG
                                 C          C
GAM113  APPD     3'  CCAGCCAAGCCCTGCCGA    44213     A   CTCTGA
                                TCG GCA     GCTTGGCTGG
                                ||| |||     ||||||||||
                                AGC CGT     CGAACCGACC
                                  _   CC_____
GAM113  ARFGAP1  3'  GCCAGCCATGCATGCGCCCGA  36592     A  ACTCTGA  T
                                TCG GC      GC TGGCTGGC
                                ||| ||      || ||||||||
                                AGC CG      CG ACCGACCG
                                  C  CGTA___  T
GAM113  dJ383J4.3 3'  GCCATTCTCAAAATGCTGA   66944    G   CTC    CT
                                TC AGCA   TGAG  TGGC
                                || ||||   ||||  ||||
                                AG TCGT   ACTC  ACCG
                                 _    AAA    TT
GAM113  FLJ12387  3'  GCCAGTCACCAGAGCGC     43067    A    AGCT
                                GC CTCTG    TGGCTGGC
                                || |||||    ||||||||
                                CG GAGAC    ACTGACCG
                                 C    C___
GAM113  KIAA1453  3'  CCAGCCCAGAGCACTCGG    46972      CA    AGCTT
                                TCGAG  CTCTG    GGCTGG
                                |||||  |||||    ||||||
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                                GGCTC  GAGAC    CCGACC
                                  AC    _____
GAM113  KIAA1854  3'  CAAGCTCAAAGTGCTC      71738        C
                                GAGCACT TGAGCTTG
                                ||||||| ||||||||
                                CTCGTGA ACTCGAAC
                                    A
GAM113  KIAA1948  5'  GCCAGCCATGCAAAGAG     82402      GA  T
                                CTCT  GC TGGCTGGC
                                ||||  || ||||||||
                                GAGA  CG ACCGACCG
                                  AA  T
GAM113  MGC13114  3'  GCCAGCCAACAACAAATGCCTG 50415     A   CTC  AGC
            A                    TCG GCA   TG   TTGGCTGGC
                                ||| |||   ||   |||||||||
                                AGT CGT   AC   AACCGACCG
                                  C   AA_  AAC
GAM113  MYO3B     3'  GCCAAATCAAAGTACTTGA    57307      C   C   GC
                                TCGAG ACT TGA  TTGGC
                                ||||| ||| |||  |||||
                                AGTTC TGA ACT  AACCG
                                  A   A   A_
GAM113  PGLYRPIalpha 3'  CCAGCCAAGCTGGCTC      53579      ACTCTG
                                GAGC     AGCTTGGCTGG
                                ||||     ||||||||||
                                CTCG     TCGAACCGACC
                                  G_____
GAM113  THEA      3'  GCCAGGAACCAGAGTGCTT    66285         AG_
                                GAGCACTCTG   CTTGGC
                                ||||||||||   ||||||
                                TTCGTGAGAC   GGACCG
                                     CAA
GAM113  LOC128259 5'  CCAACCAGCGGGTGCTC     74726        TGA   T  C
                                GAGCACTC   GCT GG TGG
                                ||||||||   ||| || |||
                                CTCGTGGG   CGA CC ACC
                                    ___   _  A
GAM113  LOC144308 3'  GCCAGCCAGAGTGC        83047        A   T
                                GCACTCTG GCT GGC
                                ||||||| ||| |||
                                CGTGAGAC CGA CCG
                                    _   _
GAM113  LOC148029 3'  GCTCGAGCTCAGAAGCCCGA   78620     A  AC        _
                                TCG GC  TCTGAGCTTG GC
                                ||| ||  |||||||||| ||
                                AGC CG  AGACTCGAGC CG
                                  C  A_         T
GAM113  LOC151568 5'  GCCAACCTGCAGAGCACTCG   56695      CA    _  C
                                CGAG  CTCTG AG TTGGC
                                ||||  ||||| || |||||
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                                GCTC  GAGAC TC AACCG
                                  AC     G  C
GAM113  LOC155036 5'  CCAACCAAGCCCAGTCAGC   86338    ACT   A     C
                                GC   CTG GCTTGG TGG
                                ||   ||| |||||| |||
                                CG   GAC CGAACC ACC
                                 ACT   C     A
GAM113  LOC200933 5'  CCCCATTGCTCAGAGCACTGA  90194    G  CA      T_  CT
                                TC AG  CTCTGAGC  TGG  GG
                                || ||  ||||||||  |||  ||
                                AG TC  GAGACTCG  ACC  CC
                                 _ AC       TT  __
GAM113  LOC203601 3'  GCCGTGGTCACTCAAAGTGCTT 90645         C   CT    __
            GA                    TCGAGCACT TGAG  TGGCT  GGC
                                |||||||||  ||||  |||||  |||
                                AGTTCGTGA ACTC  ACTGG  CCG
                                      A   __    TG
GAM114  C5orf5    3'  ACCAAAATCAAACTGAGATTTC 33463       AG        C
                                GAAGT  TAGTTTGATT TGGT
                                |||||  |||||||||| ||||
                                CTTTA  GTCAAACTAA ACCA
                                   GA        A
GAM114  KIAA1210  5'  ACCAGAAACCACTACCCCTC   96323    A TA    TTGA
                                GA G  GTAGT    TTCTGGT
                                || |  |||||    |||||||
                                CT C  CATCA    AAGACCA
                                 _ CC    CCA_
GAM114  PRO0611   3'  CAGACTGACTACTTCTA     26010          _
                                TAGAAGTAGT AGTTTG
                                |||||||||| ||||||
                                ATCTTCATCA TCAGAC
                                      G
GAM114  RAB24     3'  CAAACCCCTACTTCTA      55388          TA
                                TAGAAGTAG  GTTTG
                                |||||||||  |||||
                                ATCTTCATC  CAAAC
                                      CC
GAM114  LOC206012 5'  TCAAACTACTACTACTA     89524     A
                                TAG AGTAGTAGTTTGA
                                ||| ||||||||||||
                                ATC TCATCATCAAACT
                                  A
GAM114  LOC220469 3'  AGTCAAATCACTACTTC     76383         A
                                GAAGTAGT GTTTGATT
                                |||||||| ||||||||
                                CTTCATCA TAAACTGA
                                      C
GAM114  LOC257042 3'  ACCAGAATCAGAGTGC      96896     G
                                GTA TTTGATTCTGGT
                                ||| ||||||||||||
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                                CGT AGACTAAGACCA
                                  G
GAM114  LOC257486 5'  ACCAGAAACCACTACCCCTC  69240    A TA    TTGA
                                GA G  GTAGT    TTCTGGT
                                || |  |||||    |||||||
                                CT C  CATCA    AAGACCA
                                 _ CC     CCA_
GAM115  ACPT     3'  CCCAACATGTATGCTCAGT   52349         _   CCTCA
                                ACTGAGCATA GTGT    GGG
                                |||||||||| ||||    |||
                                TGACTCGTAT TACA    CCC
                                      G   A____
GAM115  ACPT     3'  CCCAACATGTATGCTCAGT   54981         _   CCTCA
                                ACTGAGCATA GTGT    GGG
                                |||||||||| ||||    |||
                                TGACTCGTAT TACA    CCC
                                      G   A____
GAM115  ACPT     3'  CCCAACATGTATGCTCAGT   54987         _   CCTCA
                                ACTGAGCATA GTGT    GGG
                                |||||||||| ||||    |||
                                TGACTCGTAT TACA    CCC
                                      G   A____
GAM115  ACPT     3'  CCCAACATGTATGCTCAGT   54992         _   CCTCA
                                ACTGAGCATA GTGT    GGG
                                |||||||||| ||||    |||
                                TGACTCGTAT TACA    CCC
                                      G   A____
GAM115  ALDH1B1  3'  CCCTGAAAACATCCTTCTCAGT 5492        CATA   CC
           GA                    TCACTGAG   GTGT  TCAGGG
                                |||||||   ||||  ||||||
                                AGTGACTC   TACA  AGTCCC
                                     TTCC   AA
GAM115  C8orf1   3'  CCCAAGGGATATGTATGCTCA  15086        _     CA
                                TGAGCATA GTGTCCT  GGG
                                |||||||| |||||||  |||
                                ACTCGTAT TATAGGG  CCC
                                     G      AA
GAM115  GJB5     5'  CCCTGAGGAGTAGTCACTCAGT 17946       CATAGTG
                                ACTGAG      TCCTCAGGG
                                ||||||      |||||||||
                                TGACTC      AGGAGTCCC
                                   ACTGATG
GAM115  HCFC1    3'  CCCGGCCCACCCTGCTCAGTGA 70991         TA   TC  CA
                                TCACTGAGCA  GTG  CT  GGG
                                ||||||||||  |||  ||  |||
                                AGTGACTCGT  CAC  GG  CCC
                                      CC   CC  __
GAM115  DKFZp761J1523 3'  CCTGAGGGGCACTCAGCCA   50168    A  AT     _
                                TG GC  AGTGTCC TCAGG
                                || ||  ||||||| |||||
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                                AC CG  TCACGGG AGTCC
                                 _ AC      G
GAM115  FLJ20294  3'  CTGCCACCTCAGTGA      34875        CATA   TCCT
                                TCACTGAG   GTG   CAG
                                ||||||||   |||   |||
                                AGTGACTC   CAC   GTC
                                     _____  C___
GAM115  FLJ23604  3'  CCTAAGGACACTGCAGAGA   46858    A   AGCA       C
                                TC CTG   TAGTGTCCT AGG
                                || |||   ||||||||| |||
                                AG GAC   GTCACAGGA TCC
                                 A  _____        A
GAM115  KIAA0459  3'  CCCTGAAAATCAGACTTCAGTG 60986        CATAGTGTCC
            A                    TCACTGAG        TCAGGG
                                ||||||||        ||||||
                                AGTGACTT        AGTCCC
                                     CAGACTAAA_
GAM115  KIAA0766  3'  CCCCATCACCCACCTCAGTGA  29004        CATA   TCCTCA
                                TCACTGAG   GTG     GGG
                                ||||||||   |||     |||
                                AGTGACTC   CAC     CCC
                                     CACC   TAC___
GAM115  KIAA1374  3'  CCTTGAAAACACTATGCTAAGT 61241       G        CC
            GA                    TCACT AGCATAGTGT  TCAGGG
                                ||||| ||||||||||  ||||||
                                AGTGA TCGTATCACA  AGTTCC
                                   A         AA
GAM115  KIAA1908  5'  CCCTGAGGGAGGAAGCCCAGTG 73397       A  ATAGTG
            A                    TCACTG GC     TCCTCAGGG
                                |||||| ||     |||||||||
                                AGTGAC CG     GGGAGTCCC
                                   C  AAGGA_
GAM115  MYO3B    3'  CCCTGAGGACACCATGT     57303      A
                                GCAT GTGTCCTCAGGG
                                |||| ||||||||||||
                                TGTA CACAGGAGTCCC
                                  C
GAM115  NIN283   3'  CCCTGAGGACACCAAATTGGAT 50068     _ TG GCATA
            GA                    TCA C  A    GTGTCCTCAGGG
                                ||| |  |    ||||||||||||
                                AGT G  T    CACAGGAGTCCC
                                  A GT AAAC_
GAM115  OBTP     5'  CCCTGAGGATACCCATGCTCAG 34244    A       A_
            GA                    TC CTGAGCAT  GTGTCCTCAGGG
                                || ||||||||  ||||||||||||
                                AG GACTCGTA  CATAGGAGTCCC
                                 _       CC
GAM115  TOMM70A  3'  CCTAAAGACACTGTCATGA   29079     C   GCA      CTC
                                TCA TGA   TAGTGTC   AGG
                                ||| |||   |||||||   |||
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                                AGT ACT   GTCACAG   TCC
                                  _  ___      AAA
GAM115  WIT-1    3'  CCCGAGAGTCCTCAGTGA    31823        CATAGT TC   A
                                TCACTGAG     G  CTC GG
                                ||||||||     |  ||| ||
                                AGTGACTC     T  GAG CC
                                    C_____ GA   C
GAM115  LOC116113 3'  CCCTGAGGACCCTGGGGCTCAG 92214         A_   T
          TGG                     TCACTGAGC  TAG GTCCTCAGGG
                                |||||||||  ||| ||||||||||
                                GGTGACTCG  GTC CAGGAGTCCC
                                     GG   C
GAM115  LOC125967 3'  CCCTGAGGCCGGCAGCCCAG   74424     A  ATAG  T
                                CTG GC    TG CCTCAGGG
                                ||| ||    || ||||||||
                                GAC CG    GC GGAGTCCC
                                  C  ACG_  C
GAM115  LOC146159 5'  CCCTGTTTTCTGTGCTCAGT   77678          TGTCCT
                                ACTGAGCATAG     CAGGG
                                ||||||||||      |||||
                                TGACTCGTGTC     GTCCC
                                      TTTT__
GAM115  LOC152441 5'  CCCTGAGCCCTCAACTCAATGA 85732     C    CAT  TGTC
                                TCA TGAG   AG    CTCAGGG
                                ||| ||||   ||    |||||||
                                AGT ACTC   TC    GAGTCCC
                                  A    AAC  CC__
GAM115  LOC152674 3'  CCCTGAGGACACAGTGGTGA   85835     TGAG   A
                                TCAC    CAT GTGTCCTCAGGG
                                ||||    ||| ||||||||||||
                                AGTG    GTG CACAGGAGTCCC
                                   _____   A
GAM115  LOC160717 5'  CCTGAGCAAATGCTCAG     82236        AG  TC
                                CTGAGCAT  TG  CTCAGG
                                ||||||||  ||  ||||||
                                GACTCGTA  AC  GAGTCC
                                     A_  __
GAM115  LOC200470 5'  CCCTGGGGCCACACTCAG     90059       CATA   T
                                CTGAG    GTG CCTCAGGG
                                |||||    ||| ||||||||
                                GACTC    CAC GGGGTCCC
                                   A___   C
GAM115  LOC201175 5'  CCCTGAGGCCCGCCCAGCCG   88135    A  ATA   T_
                                TG GC   GTG  CCTCAGGG
                                || ||   |||  ||||||||
                                GC CG   CGC  GGAGTCCC
                                  _ ACC   CC
GAM115  LOC201229 3'  CCCAAGGGCACTCAGCCA    88143    A  AT      CA
                                TG GC  AGTGTCCT  GG
                                || ||  ||||||||  ||
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                                AC CG  TCACGGGA  CC
                                 _ AC       AC
GAM115  LOC253955 5'  CCCTGAGGACTCAGAACTCA   94425      CATAGT
                                TGAG     GTCCTCAGGG
                                ||||     ||||||||||
                                ACTC     CAGGAGTCCC
                                  AAGACT
GAM115  LOC255762 3'  CCCTGAGGCCAAATTCCCAGT  95026      AGCATAG  T
                                ACTG      TG CCTCAGGG
                                ||||      || ||||||||
                                TGAC      AC GGAGTCCC
                                  CCTTAA_  C
GAM115  LOC51112  5'  CCCCGAGGACGCGGCACCCAGT 32085      AGCATA       A
                                ACTG     GTGTCCTC GGG
                                ||||     |||||||| |||
                                TGAC     CGCAGGAG CCC
                                  CCACGG       C
GAM115  LOC51301  5'  CCCCACCTACTACTCTCAGTGA 33439        CA    TCCTCA
                                TCACTGAG  TAGTG     GGG
                                ||||||||  |||||     |||
                                AGTGACTC  ATCAT     CCC
                                     TC    CCAC__
GAM116  FCN2     3'  GACAACTTACATACACTCC    31740      A_      A
                                GGAG  TATGTAA TTGTC
                                ||||  ||||||| |||||
                                CCTC  ATACATT AACAG
                                  AC      C
GAM116  KCNJ10   3'  CAATACACATACCTCCCTTA   9533         A     AA
                                TGAGGGAG TATGT  ATTG
                                |||||||| |||||  ||||
                                ATTCCCTC ATACA  TAAC
                                     C    CA
GAM116  MTMR2    3'  GACAATTCACATGTCT      32384         A     C
                                AGATATGT AATTGT C
                                |||||||| |||||| |
                                TCTGTACA TTAACA G
                                     C     A
GAM116  RDBP     3'  TGGAAGCTTACACATCTCCCTC 11275          A    ATTG
            A                    TGAGGGAGAT TGTAA    TCCA
                                ||||||||||| |||||    ||||
                                ACTCCCTCTA ACATT    AGGT
                                      C    CGA_
GAM116  STIM1    3'  GACAACTCTCTCCCTTA     60149         TAT  AAAT
                                TGAGGGAGA   GT    TGTC
                                |||||||||   ||    ||||
                                ATTCCCTCT   CA    ACAG
                                     CT_  _____
GAM116  TNFSF4   3'  TGGACAAGCTTACATCTTCCTC 12446         TA    A_
            A                    TGAGGGAGA  TGTAA  TTGTCCA
                                |||||||||  |||||  |||||||
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                                ACTCCTTCT  ACATT  AACAGGT
                                     __    CG
GAM116  AD-020   3'  TTACATACCTCCTTCA     39312        A
                                TGAGGGAG TATGTAA
                                |||||||| |||||||
                                ACTTCCTC ATACATT
                                     C
GAM116  AD-020   3'  TTACATACCTCCTTCA     59388        A
                                TGAGGGAG TATGTAA
                                |||||||| |||||||
                                ACTTCCTC ATACATT
                                     C
GAM116  FLJ13063 5'  GACCACATCTCCCTC      71829         A  TAAATT
                                GAGGGAGAT TG     GTC
                                ||||||||| ||     |||
                                CTCCCTCTA AC     CAG
                                     C _______
GAM116  KIAA0202 3'  ACAATTTAAATTTCCATCA   64366     G     ATG
                                TGA GGAGAT   TAAATTGT
                                ||| ||||||   ||||||||
                                ACT CCTTTA   ATTTAACA
                                  A     A__
GAM116  KIAA0285 3'  GGGCTCCCACACCTCCCTCA  29021        ATA   AAATT
                                TGAGGGAG   TGT    GTCC
                                ||||||||   |||    ||||
                                ACTCCCTC   ACA    CGGG
                                     C__   CCCT_
GAM116  NGEF     3'  CAGTATTACACCACCTCCCTCA 69162        ATA_    _
                                TGAGGGAG    TGTAA ATTG
                                ||||||||    ||||| ||||
                                ACTCCCTC    ACATT TGAC
                                     CACC    A
GAM116  TAF2     3'  TGGACAATTTACACACCC    12088     AGATA
                                GGG    TGTAAATTGTCCA
                                |||    ||||||||||||
                                CCC    ACATTTAACAGGT
                                  AC___
GAM116  LOC152274 3'  TGGCTATAAACACCTCCCTCA  80510        ATA   AAATT T
                                TGAGGGAG   TGT    G CCA
                                ||||||||   |||    | |||
                                ACTCCCTC   ACA    C GGT
                                     C__   AATAT _
GAM116  LOC222008 3'  GACAATTTACAACCT      94008     AGATA
                                GGG    TGTAAATTGTC
                                |||    |||||||||||
                                TCC    ACATTTAACAG
                                  A____
GAM116  LOC91149  3'  GAGAATACATATTCCCTCA   65076        A     AA  G
                                TGAGGGAG TATGTA  TT TC
                                |||||||| ||||||  || ||
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                                ACTCCCTT ATACAT  AA AG
                                      _     __ G
GAM117  AMPD3    3' CTGGATTTCCTTATTCC     4897      CTA   A
                                GGA   GAG GAAATCCAG
                                |||   ||| |||||||||
                                CCT   TTC CTTTAGGTC
                                  TA_   _
GAM117  CDK10    3' CTGAGCTGGATCCCTGCTC    13401     _ AA
                                GAG AG  ATCCAGCTCAG
                                ||| ||  ||||||||||
                                CTC TC  TAGGTCGAGTC
                                  G  CC
GAM117  CDK10    3' CTGAGCTGGATCCCTGCTC    53777     _ AA
                                GAG AG  ATCCAGCTCAG
                                ||| ||  ||||||||||
                                CTC TC  TAGGTCGAGTC
                                  G  CC
GAM117  CDK10    3' CTGAGCTGGATCCCTGCTC    53768     _ AA
                                GAG AG  ATCCAGCTCAG
                                ||| ||  ||||||||||
                                CTC TC  TAGGTCGAGTC
                                  G  CC
GAM117  CLTCL1   3' CTGAGCTGGCCATCCTCTACTC 63671     C     A  AAT
          C                      GGA TAGAG GA   CCAGCTCAG
                                ||| ||||| ||   |||||||||
                                CCT ATCTC CT   GGTCGAGTC
                                  C    _ ACC
GAM117  MCL1     3' CTGAACTCTTTCTAGCC     41717    A       AATC
                                GG CTAGAGAGA    CAG
                                || |||||||||    |||
                                CC GATCTTTCT    GTC
                                  _       CAA_
GAM117  MDM1     3' CTGAGCTGACTTCTACCTAGCC 39271    A   AG    ATC
                                GG CTAG  AGAA   CAGCTCAG
                                || ||||  ||||   ||||||||
                                CC GATC  TCTT   GTCGAGTC
                                  _   CA   CA_
GAM117  PML      3' CTGAGCTGCCTCCTCCAGCCC  52661    A  A   A  AATC
                                GG CT GAG GA    CAGCTCAG
                                || || ||| ||    ||||||||
                                CC GA CTC CT    GTCGAGTC
                                  C  C   _ CC__
GAM117  PML      3' CTGAGCTGCCTCCTCCAGCCC  52667    A  A   A  AATC
                                GG CT GAG GA    CAGCTCAG
                                || || ||| ||    ||||||||
                                CC GA CTC CT    GTCGAGTC
                                  C  C   _ CC__
GAM117  PML      3' CTGAGCTGCCTCCTCCAGCCC  52673    A  A   A  AATC
                                GG CT GAG GA    CAGCTCAG
                                || || ||| ||    ||||||||
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                                CC GA CTC CT    GTCGAGTC
                                 C  C   _ CC__
GAM117  SHOX     3'  TGAGCTGAACTGTAGATCC   4839      _   G  AGAAATC
                                GGA CTA AG      CAGCTCA
                                ||| ||| ||      |||||||
                                CCT GAT TC      GTCGAGT
                                  A   G  AA_____
GAM117  TRPM1    5'  CTGAGCTGTGCCCTCTCCATTC 10057     CTA     AAATC
              C                  GGA   GAGAG    CAGCTCAG
                                |||   |||||    ||||||||
                                CCT   CTCTC    GTCGAGTC
                                  TAC    CCGT_
GAM117  ELOVL1   5'  GGACTTCTCTCTGGCC      43062    A        A
                                GG CTAGAGAGAA TCC
                                || |||||||||| |||
                                CC GGTCTCTCTT AGG
                                 _        C
GAM117  FLJ20296 5'  CTGACGCGTTTCTCTCCATTCC 34890     CTA        CCA  _
                                GGA   GAGAGAAAT   GC TCAG
                                |||   |||||||||   || ||||
                                CCT   CTCTCTTTG   CG AGTC
                                  TAC        ___  C
GAM117  FLJ20721 3'  GACTTCTCTCTAGTGC      35609   G        A
                                G ACTAGAGAGAA TC
                                | ||||||||||| ||
                                C TGATCTCTCTT AG
                                 G          C
GAM117  KIAA0265 3'  AGCGACCTCTTCTCTAGTCC   69874          _  AA  CA
                                GGACTAGAGA GA  TC  GCT
                                |||||||||| ||  ||  |||
                                CCTGATCTCT CT  AG  CGA
                                      T  CC  __
GAM117  KIAA0285 3'  GCTAGATGCCCTCTCTAGTCC  29018           AA_   C
                                GGACTAGAGAG   ATC AGC
                                ||||||||||   ||| |||
                                CCTGATCTCTC   TAG TCG
                                       CCG   A
GAM117  KIAA0820 3'  CTGAGCTGAATCTTAAAAAGCC 69023    ACTAGA    AATC
                                GG     GAGA    CAGCTCAG
                                ||     ||||    ||||||||
                                CC     TTCT    GTCGAGTC
                                  GAAAAA    AA__
GAM117  KIAA1274 3'  GGCATCTCTCTCTGTCC     91367      T      A  _
                                GGAC AGAGAGA AT CC
                                |||| ||||||| || ||
                                CCTG TCTCTCT TA GG
                                   _      C  C
GAM117  KIAA1831 3'  CTGAGCTGCTGTGGCTCCCTAG 63782    A    A   AA  C_
              CC                  GG CTAG GAG  AT  CAGCTCAG
                                || |||| |||  ||  ||||||||
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                                CC GATC CTC  TG  GTCGAGTC
                                 _   C   GG  TC
GAM117  MGC2560   5' CTGAGCTGGATTGACATAGCC  48781    A   GAGAGA
                                GG CTA     AATCCAGCTCAG
                                || |||     ||||||||||||
                                CC GAT     TTAGGTCGAGTC
                                 _  ACAG__
GAM117  Rab11-FIP3 3' CTGAGCTGGATTCGGGACTC   28125     AGA__
                                GAG    AATCCAGCTCAG
                                |||    ||||||||||||
                                CTC    TTAGGTCGAGTC
                                  AGGGC
GAM117  UGT2B10   3' CTGAGCTGGAGCCTCCATGCC  6541     ACTAGA   AAA
                                GG     GAG   TCCAGCTCAG
                                ||     |||   ||||||||||
                                CC     CTC   AGGTCGAGTC
                                 GTAC__   CG_
GAM117  LOC145815 5' GGATTTCTCCCTGACCC     83519    AC   A
                                GG  TAG GAGAAATCC
                                ||  ||| |||||||||
                                CC  GTC CTCTTTAGG
                                 CA   C
GAM117  LOC146745 5' TGAGCTGAGGCTGCAGTCC    78091      AG  AGAAATC
                                GGACT  AG      CAGCTCA
                                |||||  ||      |||||||
                                CCTGA  TC      GTCGAGT
                                   CG  GGA____
GAM117  LOC201243 5' TGAGCTGAGGCTGCAGTCC    88163      AG  AGAAATC
                                GGACT  AG      CAGCTCA
                                |||||  ||      |||||||
                                CCTGA  TC      GTCGAGT
                                   CG  GGA____
GAM117  LOC221929 3' CTGAGCTGGACTTCCTCCTCC  92675     CTA   A   A
                                GGA   GAG GAA TCCAGCTCAG
                                |||   ||| ||| ||||||||||
                                CCT   CTC CTT AGGTCGAGTC
                                  C__   _   C
GAM117  LOC51042  5' GAGCGCACTCTCTAGCC     31854    A      AAATCCA
                                GG CTAGAGAG      GCTC
                                || ||||||||      ||||
                                CC GATCTCTC      CGAG
                                 _       ACG____
GAM117  LOC56912  3' TGAGCTGGCCCCTCTGCC    39337    AC    AGAAAT
                                GG  TAGAG     CCAGCTCA
                                ||  |||||     ||||||||
                                CC  GTCTC     GGTCGAGT
                                 __    CCC___
GAM118  AMPD3     3' GGTGCTCAATAAATGCATATTG 4900       CAA  C
            AA                   TTCAA   GT TTTATTGAGCACC
                                |||||   || ||||||||||||
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                                AAGTT  CG AAATAACTCGTGG
                                   ATA  T
GAM118  CHRND   3'  TGCTCAATGGCTCCCCTGAA  5638     ACA_   TTT
                                TTCA   AGTC  ATTGAGCA
                                ||||   ||||  ||||||||
                                AAGT   TCGG  TAACTCGT
                                  CCCC   ___
GAM118  CNTN3   3'  GGTTTTCAAAAAATTGTTGAA  66696       GTC  A   C
                                TTCAACAA  TTT TTGAG ACC
                                ||||||||  ||| ||||| |||
                                AAGTTGTT  AAA AACTT TGG
                                    ___  A   T
GAM118  CRYBA2  3'  CTCAATAAAGGTTCCTGAA   54045     ACA GT
                                TTCA  A  CTTTATTGAG
                                ||||  |  ||||||||||
                                AAGT  T  GAAATAACTC
                                  CC_ TG
GAM118  CRYBA2  3'  CTCAATAAAGGTTCCTGAA   17798     ACA GT
                                TTCA  A  CTTTATTGAG
                                ||||  |  ||||||||||
                                AAGT  T  GAAATAACTC
                                  CC_ TG
GAM118  CRYBA2  3'  CTCAATAAAGGTTCCTGAA   54044     ACA GT
                                TTCA  A  CTTTATTGAG
                                ||||  |  ||||||||||
                                AAGT  T  GAAATAACTC
                                  CC_ TG
GAM118  CYP46   3'  TGCTCAATAAATGTGTGTTGA  21897      AG C
                                TCAACA  T TTTATTGAGCA
                                ||||||  | ||||||||||
                                AGTTGT  G AAATAACTCGT
                                   GT T
GAM118  DLEU1   3'  CTCAATAAATCTTTGATGAA  19694     A   TC
                                TTCA CAAG  TTTATTGAG
                                |||| ||||  |||||||||
                                AAGT GTTT  AAATAACTC
                                  A   CT
GAM118  EIF1A   3'  AATAAAATACTTGTTGAA    88599         C_
                                TTCAACAAGT  TTTATT
                                ||||||||||  ||||||
                                AAGTTGTTCA  AAATAA
                                     TA
GAM118  GABPB1  3'  TTGATAAAGATTGTTGAA    17908        G      TG
                                TTCAACAA TCTTTAT  A
                                |||||||| |||||||  |
                                AAGTTGTT AGAAATA  T
                                    _      GT
GAM118  GCNT1   3'  GTGCTCAGGGACTT       7654        TTA
                                AAGTCT  TTGAGCAC
                                ||||||  ||||||||
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                                TTCAGG   GACTCGTG
                                   ___
GAM118  GNRHR    5'  GTGCTCAACAGTGTGTTTGAA  4642       _  AGT  TTA
                                TTCAA CA   CT   TTGAGCAC
                                ||||| ||   ||   ||||||||
                                AAGTT GT   GA   AACTCGTG
                                   T  GT_  C__
GAM118  GUCY1B3  3'  GCACCCAATAAATATTTGTTGA 5966          C      A__
            A                    TTCAACAAGT TTTATTG   GC
                                ||||||||||  |||||||   ||
                                AAGTTGTTTA AAATAAC   CG
                                      T      CCA
GAM118  MEF2D    3'  GGCACTCAATAAATGCT     96914     C       CA
                                AGT TTTATTGAG  CC
                                |||  |||||||||  ||
                                TCG AAATAACTC  GG
                                  T        AC
GAM118  MEF2D    3'  GGTGCTCAATAAATGAATG    96915    AG  _
                                CA  TC TTTATTGAGCACC
                                ||  ||  ||||||||||||||
                                GT  AG AAATAACTCGTGG
                                 A_  T
GAM118  NFATC1   3'  GCAGACAAAGACTTTTGAA    20486      C       A  GA
                                TTCAA AAGTCTTT TT  GC
                                |||||  ||||||||  ||  ||
                                AAGTT TTCAGAAA AG  CG
                                   _       C  A_
GAM118  PAG      3'  GGTACTTCTAGACTTGTT     37405         TTATT   C
                                AACAAGTCT     GAG ACC
                                |||||||||     |||  |||
                                TTGTTCAGA     TTC TGG
                                      TC___   A
GAM118  PBX3     3'  GGTGCTGCACAGACTTGT     20566         TTAT  _
                                ACAAGTCT    TG AGCACC
                                ||||||||    ||  ||||||
                                TGTTCAGA    AC TCGTGG
                                     C___  G
GAM118  PLA2G2D  3'  GGTGCTCAATTCATGCCTGTGA 24798      A  A  CTTT
            A                    TTCA CA GT    ATTGAGCACC
                                ||||  ||  ||    ||||||||||
                                AAGT GT CG    TAACTCGTGG
                                  _  C  TACT
GAM118  PLA2G4C  3'  GTGCTCAATAAATGCTTGCTGA 73415     A     C
                                TCA CAAGT TTTATTGAGCAC
                                |||  |||||  ||||||||||||
                                AGT GTTCG AAATAACTCGTG
                                  C    T
GAM118  PML      3'  GGCTGCTCAATAAACACTTGTT 52675          C         _
            GAA                    TTCAACAAGT TTTATTGAGCA CC
                                ||||||||||  ||||||||||  ||
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                                AAGTTGTTCA AAATAACTCGT GG
                                     C         C
GAM118  PML     3'  GGCTGCTCAATAAACACTTGTT 52669          C        _
            GAA                    TTCAACAAGT TTTATTGAGCA CC
                                |||||||||| |||||||||| ||
                                AAGTTGTTCA AAATAACTCGT GG
                                     C         C
GAM118  PML     3'  GGCTGCTCAATAAACACTTGTT 52678          C        _
            GAA                    TTCAACAAGT TTTATTGAGCA CC
                                |||||||||| |||||||||| ||
                                AAGTTGTTCA AAATAACTCGT GG
                                     C         C
GAM118  PML     3'  GGCTGCTCAATAAACACTTGTT 52663          C        _
            GAA                    TTCAACAAGT TTTATTGAGCA CC
                                |||||||||| |||||||||| ||
                                AAGTTGTTCA AAATAACTCGT GG
                                     C         C
GAM118  PX19    3'  CTCAATAAATACTTGTTGAA  25087          C
                                TTCAACAAGT TTTATTGAG
                                |||||||||| |||||||||
                                AAGTTGTTCA AAATAACTC
                                     T
GAM118  SNAP25  3'  TGCTCAATGTGCTGTTGA   55527       A  CTT
                                TCAACA GT   TATTGAGCA
                                |||||| ||   |||||||||
                                AGTTGT CG   GTAACTCGT
                                   _ T___
GAM118  SNAP25  3'  TGCTCAATGTGCTGTTGA   11834       A  CTT
                                TCAACA GT   TATTGAGCA
                                |||||| ||   |||||||||
                                AGTTGT CG   GTAACTCGT
                                   _ T___
GAM118  SOD3    5'  GCACCCAATAAACATTTGTTG 11863        C      A___
                                CAACAAGT TTTATTG   GC
                                |||||||| |||||||   ||
                                GTTGTTTA AAATAAC   CG
                                     C      CCA
GAM118  TLR9    3'  GGCACTCAATAAATGCT     33851     C       CA
                                AGT TTTATTGAG  CC
                                ||| |||||||||  ||
                                TCG AAATAACTC  GG
                                  T        AC
GAM118  YWHAZ   3'  TGCTCAATAAATATTG      12706     GTC
                                CAA   TTTATTGAGCA
                                |||   ||||||||||
                                GTT   AAATAACTCGT
                                  AT_
GAM118  Z39IG   3'  GGTGCTCAATAAATATCT    23435    TC_
                                AG   TTTATTGAGCACC
                                ||   |||||||||||||
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                                TC   AAATAACTCGTGG
                                 TAT
GAM118  ZNF2     3'  GGTGCTCAATAAATATTT    40806      C
                                AAGT TTTATTGAGCACC
                                |||| ||||||||||||
                                TTTA AAATAACTCGTGG
                                  T
GAM118  AKAP6    3'  GGTATTCAATAAAAATTTACTG 14992      AC   C       C
           AA                    TTCA  AAGT TTTATTGAG ACC
                                |||| |||| ||||||||| |||
                                AAGT  TTTA AAATAACTT TGG
                                  CA   A       A
GAM118  CROC4    3'  GTCTTCAATAAAGACTCTTGAA 21020       CA          C
                                TTCAA  AGTCTTTATTGAG AC
                                ||||| ||||||||||||| ||
                                AAGTT  TCAGAAATAACTT TG
                                   C_          C
GAM118  DIS3     3'  GGCACTCAATAAATGTTGA    30232       AGTC       CA
                                TCAACA   TTTATTGAG  CC
                                ||||||   |||||||||  ||
                                AGTTGT   AAATAACTC  GG
                                   ____       AC
GAM118  DKFZp434A1520 3'  TGCTCAATAGATGTTTGTTGAA 61118         TC
                                TTCAACAAG  TTTATTGAGCA
                                |||||||||  ||||||||||
                                AAGTTGTTT  AGATAACTCGT
                                     GT
GAM118  E2F6     3'  GTGCTCAATAAATGTCTGAA   8717      _  AGTC
                                TTCA ACA   TTTATTGAGCAC
                                |||| |||   ||||||||||||
                                AAGT TGT   AAATAACTCGTG
                                  C  ____
GAM118  FLJ13352 3'  GGTGCTCAATAACTGTTTGTTG 44757        TCT
                                CAACAAG   TTATTGAGCACC
                                |||||||   ||||||||||||
                                GTTGTTT   AATAACTCGTGG
                                    GTC
GAM118  FLJ20255 3'  TGCTCAATAAAGCTATTCAGTG 34800      ACA___  T
           AA                    TTCA     AG CTTTATTGAGCA
                                ||||     || ||||||||||||
                                AAGT     TC GAAATAACTCGT
                                  GACTTA  _
GAM118  FLJ20276 5'  TGCAAAAATAAAGACCTTTGAA 34832       CAA       GA_
                                TTCAA   GTCTTTATT   GCA
                                |||||   |||||||||   |||
                                AAGTT   CAGAAATAA   CGT
                                   TC_       AAA
GAM118  FLJ21820 3'  GATAAAGAATTGTTGAA     41623         G
                                TTCAACAA TCTTTATT
                                |||||||| ||||||||
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                                AAGTTGTT AGAAATAG
                                    A
GAM118  GIT2     3'  TAATAAAAACTTGTTGA     57582          C
                                TCAACAAGT TTTATTG
                                ||||||||| |||||||
                                AGTTGTTCA AAATAAT
                                    A
GAM118  GOA      3'  TGCTCAATAAACACTTGTTGAA 78078          C
                                TTCAACAAGT TTTATTGAGCA
                                |||||||||| ||||||||||
                                AAGTTGTTCA AAATAACTCGT
                                    C
GAM118  KIAA0830 3'  TGCTCAATAAAGTAATTACTGA 69704     AC  GT_
                                TCA  AA   CTTTATTGAGCA
                                |||  ||   ||||||||||||
                                AGT  TT   GAAATAACTCGT
                                  CA  AAT
GAM118  KIAA0924 3'  CTCAGACTTGTGGAA      29715     A      TTATT
                                TTC ACAAGTCT    GAG
                                ||| ||||||||    |||
                                AAG TGTTCAGA    CTC
                                  G      _____
GAM118  KIAA1161 5'  CTTCCTAGAGACTTGTT     81750           TT
                                AACAAGTCTTTA  GAG
                                ||||||||||||  |||
                                TTGTTCAGAGAT  TTC
                                    CC
GAM118  KIAA1184 3'  GGCGCTCAATAAATGTTGAA   42616       AGTC       A
                                TTCAACA    TTTATTGAGC CC
                                |||||||    |||||||||| ||
                                AAGTTGT    AAATAACTCG GG
                                   ____         C
GAM118  KIAA1219 3'  GGCGCCCAGTAAATACTTGTTG 61370          C     A  A
            AA                    TTCAACAAGT TTTATTG GC CC
                                |||||||||| ||||||| || ||
                                AAGTTGTTCA AAATGAC CG GG
                                    T      C  C
GAM118  KIAA1497 3'  GTGCTCAATAAAATGATT    67516      __
                                AGTC  TTTATTGAGCAC
                                ||||  ||||||||||||
                                TTAG  AAATAACTCGTG
                                  TA
GAM118  KIAA1877 3'  GTACAGTTAAGACTTGTTG   66174          T   A
                                CAACAAGTCTT ATTG GC
                                |||||||||||| |||| ||
                                GTTGTTCAGAA TGAC TG
                                    T   A
GAM118  KLK15    3'  GGCGCTCAAGGTCACCTGTT  56748     A  CTTTA     A
                                AACA GT    TTGAGC CC
                                |||| ||    |||||| ||
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                                TTGT CA    AACTCG GG
                                  C  CTGG_    C
GAM118  KLK15   3' GGCGCTCAAGGTCACCTGTT  33999     A  CTTTA    A
                                AACA GT    TTGAGC CC
                                |||| ||    |||||| ||
                                TTGT CA    AACTCG GG
                                  C  CTGG_    C
GAM118  KLK15   3' GGCGCTCAAGGTCACCTGTT  56746     A  CTTTA    A
                                AACA GT    TTGAGC CC
                                |||| ||    |||||| ||
                                TTGT CA    AACTCG GG
                                  C  CTGG_    C
GAM118  KLK15   3' GGCGCTCAAGGTCACCTGTT  43435     A  CTTTA    A
                                AACA GT    TTGAGC CC
                                |||| ||    |||||| ||
                                TTGT CA    AACTCG GG
                                  C  CTGG_    C
GAM118  LEC3    3' GGCACTCATTGTGGCCTTGTTG 30861        T  T  T   CA
           AA                     TTCAACAAG CT TA TGAG  CC
                                |||||||||  || || ||||  ||
                                AAGTTGTTC GG GT ACTC  GG
                                     C  T  T   AC
GAM118  MGC32043 3' CTCAATAAATGTTTGTT    58048       TC
                                AACAAG  TTTATTGAG
                                ||||||  |||||||||
                                TTGTTT  AAATAACTC
                                   GT
GAM118  MGC5576  3' GGCACTCAATAAAGATTTGCAG 43922     AA          CA
           AA                     TTC  CAAGTCTTTATTGAG  CC
                                |||  ||||||||||||||  ||
                                AAG  GTTTAGAAATAACTC  GG
                                  AC           AC
GAM118  OSBPL11  3' GGTGCTCAACACTTGTT    42891       CTTTA
                                AACAAGT    TTGAGCACC
                                |||||||    |||||||||
                                TTGTTCA    AACTCGTGG
                                   C____
GAM118  PDGFC    3' TGCAAAGACTTTTTGAA    32501      C      ATTGA
                                TTCAA AAGTCTTT    GCA
                                ||||| ||||||||    |||
                                AAGTT TTCAGAAA    CGT
                                   T      _____
GAM118  RHOBTB3  3' TGTAAGTCAAAGACTTGTT   29745         _  GA
                                AACAAGTCTTT ATT  GCA
                                |||||||||| |||  |||
                                TTGTTCAGAAA TGA  TGT
                                      C  A_
GAM118  SC65    3' GGTGCTCAATAAATGTTTGTTG 21293       TC
                                CAACAAG  TTTATTGAGCACC
                                |||||||  ||||||||||||
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                                GTTGTTT  AAATAACTCGTGG
                                    GT
GAM118  SH3BGRL2  3'  TAAAGAACTTGTTGAA      48888          _
                                TTCAACAAGT CTTTA
                                |||||||||| |||||
                                AAGTTGTTCA GAAAT
                                      A
GAM118  TRIM26    3'  GGTGCTCAATAAAGACTTGTTG 12892
            AA                    TTCAACAAGTCTTTATTGAGCACC
                                |||||||||||||||||||||||
                                AAGTTGTTCAGAAATAACTCGTGG

GAM118  VEST1     5'  TAATAAAGACTTCTGAA     53687      AC
                                TTCA  AAGTCTTTATTG
                                ||||  ||||||||||||
                                AAGT  TTCAGAAATAAT
                                  C_
GAM118  ZFP95     3'  TGCCCAATAAATATTTGTTGA  27381          C      A
                                TCAACAAGT TTTATTG GCA
                                ||||||||| ||||||| |||
                                AGTTGTTTA AAATAAC CGT
                                      T      C
GAM118  ZFP95     3'  TGCCCAATAAATATTTGTTGA  59025          C      A
                                TCAACAAGT TTTATTG GCA
                                ||||||||| ||||||| |||
                                AGTTGTTTA AAATAAC CGT
                                      T      C
GAM118  LOC145482 3'  GGCACTTTGTAAAGATTTGTT  77232            T   CA
                                AACAAGTCTTTAT GAG  CC
                                |||||||||||| |||  ||
                                TTGTTTAGAAATG TTC  GG
                                        T   AC
GAM118  LOC145482 3'  GGCACTGAGTAAAGATTTGTTG 77231               G  CA
            AA                    TTCAACAAGTCTTTATT AG  CC
                                |||||||||||||||| ||  ||
                                AAGTTGTTTAGAAATGA TC  GG
                                          G  AC
GAM118  LOC148645 5'  GGTGCTCAGAAAACGTGCT    84184     C__   A
                                AGT   TTT TTGAGCACC
                                |||   ||| |||||||||
                                TCG   AAA GACTCGTGG
                                  TGC   A
GAM118  LOC149535 3'  GTGCTCAATAAATGTGT     79419     AGTC
                                ACA    TTTATTGAGCAC
                                |||    ||||||||||||
                                TGT    AAATAACTCGTG
                                  GT__
GAM118  LOC150630 3'  GTGCTCAATAAATACTGAGTGA 85111      ACA   C
            A                     TTCA   AGT TTTATTGAGCAC
                                ||||   ||| ||||||||||||
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                                AAGT   TCA AAATAACTCGTG
                                  GAG   T
GAM118   LOC152225 5'  GGTGCTCAATAAAAGCTTGTT  85594       TC
                                AACAAG  TTTATTGAGCACC
                                ||||||  ||||||||||||
                                TTGTTC  AAATAACTCGTGG
                                   GA
GAM118   LOC154141 5'  GTGCTGAGAAGACTTGT     86172          AT G
                                ACAAGTCTTT  T AGCAC
                                ||||||||||  | |||||
                                TGTTCAGAAG  A TCGTG
                                      __ G
GAM118   LOC154562 3'  GGCACTCAATAAATACTTGTT  81092        C        CA
                                AACAAGT TTTATTGAG  CC
                                |||||||  |||||||||  ||
                                TTGTTCA AAATAACTC  GG
                                    T        AC
GAM118   LOC157660 3'  GGCACTCAACAAATATTTGTTG 86509          C   A     CA
           AA                     TTCAACAAGT TTT TTGAG  CC
                                |||||||||| ||| |||||  ||
                                AAGTTGTTTA AAA AACTC  GG
                                      T   C     AC
GAM118   LOC158310 3'  GGTGCTCAATAAATATCTGCCG 86760    AA  AG C
           A                     TC  CA  T TTTATTGAGCACC
                                ||  ||  | ||||||||||||
                                AG  GT  A AAATAACTCGTGG
                                 CC  CT T
GAM118   LOC197125 3'  GGCACTCAGTAAATACTTGTTG 87904          C        CA
           AA                     TTCAACAAGT TTTATTGAG  CC
                                |||||||||| |||||||||  ||
                                AAGTTGTTCA AAATGACTC  GG
                                      T        AC
GAM118   LOC203411 3'  TGCTCAGTCAGACCTGTT    90632      A    TT
                                AACA GTCT  ATTGAGCA
                                ||||  ||||  ||||||||
                                TTGT CAGA  TGACTCGT
                                  C    C_
GAM118   LOC256338 3'  CTCAATAAATAATTGTTGAA   94610         GTC
                                TTCAACAA   TTTATTGAG
                                ||||||||   |||||||||
                                AAGTTGTT   AAATAACTC
                                     AAT
GAM118   LOC257494 3'  GGTGCTCAATAAAGACTTGTTG 97796
           AA                     TTCAACAAGTCTTTATTGAGCACC
                                ||||||||||||||||||||||||
                                AAGTTGTTCAGAAATAACTCGTGG

GAM118   LOC56267  3'  TGCTAAGAGTTGTTGAA     39016         G    TATTG
                                TTCAACAA TCTT     AGCA
                                ||||||||  ||||     ||||
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                                AAGTTGTT AGAA    TCGT
                                    G  _____
GAM118  LOC90874  5'  GGCTCGGACTTGGTGAA    64259     A     TTATT   A
                                TTCA CAAGTCT    GAGC C
                                |||| |||||||    |||| |
                                AAGT GTTCAGG    CTCG G
                                  G     _____   C
GAM118  LOC91907  3'  GTGCTCAATAAAATGATT    67494     __
                                AGTC  TTTATTGAGCAC
                                ||||  ||||||||||||
                                TTAG  AAATAACTCGTG
                                  TA
GAM119  CNGA1     3'  CAACTGATAATGTGCAAA    59507         GC   A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                      A_  _
GAM119  ESRRG     3'  TGGCAGTCTTATGTGCAAA   66396       TAGCT
                                TTTGCACAT    AGATTGCCA
                                |||||||||    |||||||||
                                AAACGTGTA    TCTGACGGT
                                     T____
GAM119  KCNJ3     3'  GCAATAATGTGCAAA      9525          GCTAGA
                                TTTGCACATTA     TTGC
                                ||||||||||     ||||
                                AAACGTGTAAT     AACG
                                     _______
GAM119  SDC2      3'  GCAAATTAATGTGTAAA     67132          CTAGA
                                TTTGCACATTAG    TTGC
                                ||||||||||||    ||||
                                AAATGTGTAATT    AACG
                                      A____
GAM119  USP9X     3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
          A                      TTTGCACATTAGC     GCCAT
                                 ||||||||||||      |||||
                                 AAATGTGTAATCG     CGGTA
                                       TAGTC_
GAM119  AMOTL1    3'  GGCAAGTAATGTGCAAA     73650         G  AGAT
                                TTTGCACATTA CT    TGCC
                                |||||||||| ||    ||||
                                AAACGTGTAAT GA    ACGG
                                     _ _____
GAM119  BCAR3     3'  AGTAATAATGTGCAAA      13098         __
                                TTTGCACATTA  GCT
                                ||||||||||  |||
                                AAACGTGTAAT  TGA
                                      AA
GAM119  DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930         AGCTA    C
                                TTTGCACATT    GATTG CA
                                |||||||||     ||||| ||
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                                AGACGTGTAA     TTAAC GT
                                     A____     A
GAM119  MGC3184   3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                TTTGCACATTAG  AGA TG CAT
                                ||||||||||||  ||| || |||
                                AGACGTGTAATC  TTT AC GTA
                                      __   T  A
GAM119  PTD012    3'  ATGGCAATCTAGCTAATGTGCA 25891
           AA                    TTTGCACATTAGCTAGATTGCCAT
                                 ||||||||||||||||||||||||
                                 AAACGTGTAATCGATCTAACGGTA

GAM120  CDH6      3'  CATCAACTACTATTCAAAACC  17027    C     GTTGC
                                GG TTTGGA     AGTTGATG
                                || ||||||     ||||||||
                                CC AAACTT     TCAACTAC
                                 A     ATCA_
GAM120  KIAA0172  5'  CATCAACTCCAATCTCAAAGCC 64968         GA    C
           AC                    GTGGCTTTG  GTTG AGTTGATG
                                 |||||||||  |||| ||||||||
                                 CACCGAAAC  TAAC TCAACTAC
                                      TC    C
GAM120  KIAA1210  3'  GAGTGCAATCCCAAAGCCAC   96331          AG    G
                                GTGGCTTTGG  TTGCA TT
                                ||||||||||  ||||| ||
                                CACCGAAACC  AACGT AG
                                      CT     G
GAM120  LOC121512 5'  CAGCTGCAAGTCCAAAGCCAC  57643           G
                                GTGGCTTTGGA TTGCAGTTG
                                ||||||||||| |||||||||
                                CACCGAAACCT AACGTCGAC
                                       G
GAM120  LOC154089 3'  CAGAAACAACTCCAGAGCCAC  81037              CAG
                                GTGGCTTTGGAGTTG   TTG
                                ||||||||||||||   |||
                                CACCGAGACCTCAAC   GAC
                                       AAA
GAM120  LOC221362 5'  CACCTGAACTCCCAAAGCCAC  93757          _   G   T
                                GTGGCTTTGG AGTT CAG TG
                                |||||||||| |||| ||| ||
                                CACCGAAACC TCAA GTC AC
                                      C    _   C
GAM120  LOC257486 3'  GAGTGCAATCCCAAAGCCAC   69246          AG    G
                                GTGGCTTTGG  TTGCA TT
                                ||||||||||  ||||| ||
                                CACCGAAACC  AACGT AG
                                      CT     G
GAM120  LOC91522  3'  ACCCAGCCCCAAAGCCAC    66313          A   CA
                                GTGGCTTTGG GTTG  GT
                                |||||||||| ||||  ||
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                                CACCGAAACC CGAC  CA
                                      C   C_
GAM121  AKR1B1   3'  GTCCCCAAGTGACCTATACC  7891    C      AAA   A
                                GG ATAGGTCAC  TGGG GAC
                                || |||||||||  |||| |||
                                CC TATCCAGTG  ACCC CTG
                                 A       A__   _
GAM121  CD28     3'  GTCTCCCACTCATGAAATGAGC 20441     A  GG   CAAA
           CA                     TGGC TA  TCA   TGGGAGAC
                                |||| ||  |||   ||||||||
                                ACCG GT  AGT   ACCCTCTG
                                  A  AA   ACTC
GAM121  DRD3     3'  CCCTGTGATCTATACCA    53355    C       AAT
                                TGG ATAGGTCACA  GGG
                                ||| ||||||||||  |||
                                ACC TATCTAGTGT  CCC
                                  A       ___
GAM121  DRD3     3'  CCCTGTGATCTATACCA    53357    C       AAT
                                TGG ATAGGTCACA  GGG
                                ||| ||||||||||  |||
                                ACC TATCTAGTGT  CCC
                                  A       ___
GAM121  EXTL3    3'  TCTCCCATCCTCCCCAGCGCCA 7537     ATA  TCACAA
                                TGGC  GG    ATGGGAGA
                                ||||  ||    ||||||||
                                ACCG  CC    TACCCTCT
                                  CGA  CCTCC_
GAM121  GUCY1B2  3'  TCTCCCACTTCGGCAGCCA   14687    ATAG  ACAAA
                                TGGC   GTC   TGGGAGA
                                ||||   |||   |||||||
                                ACCG   CGG   ACCCTCT
                                  A___   CTTC_
GAM121  RHO      3'  TCTCCCATCCCCTACACC    5021    CA   TCACAA
                                GG  TAGG    ATGGGAGA
                                ||  ||||    ||||||||
                                CC  ATCC    TACCCTCT
                                 AC   CC____
GAM121  SOX10    3'  TCTGACATGCCCATGCCA    22689      A  CACAA  GG
                                TGGCAT GGT   ATG  AGA
                                |||||| |||   |||  |||
                                ACCGTA CCG   TAC  TCT
                                   C   _____  AG
GAM121  SOX10    3'  CCCATGCCACCTATGCCA    22684       CACAA
                                TGGCATAGGT   ATGGG
                                ||||||||||   |||||
                                ACCGTATCCA   TACCC
                                      CCG__
GAM121  SSX3     3'  TCTCCCATCTGCTTTTCCCATT 40670      TA_  TCA__  A
           GCCA                   TGGCA  GG   CA ATGGGAGA
                                |||||  ||   || ||||||||
```

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                                ACCGT   CC    GT TACCCTCT
                                   TAC  TTTTC  C
GAM121  WNT4     3'  TCTCCCACCACCTACCCCA   47762     CA    CACAAA
                                TGG  TAGGT     TGGGAGA
                                |||  |||||     |||||||
                                ACC  ATCCA     ACCCTCT
                                  CC    CC____
GAM121  CORO1A   3'  CTCCCATTCCCAGCCA     22988     ATA  TCACA
                                TGGC   GG    AATGGGAG
                                ||||   ||    ||||||||
                                ACCG   CC    TTACCCTC
                                  AC_  _____
GAM121  DDR2     3'  TCACCCATGCCTATGCCA    20524         CACAA    A
                                TGGCATAGGT    ATGGG GA
                                ||||||||||    ||||| ||
                                ACCGTATCCG    TACCC CT
                                      _____    A
GAM121  DKFZP434G1411 3'  CTTCTGTAACCTATGC      92104        C   AATG
                                GCATAGGT ACA    GGAG
                                |||||||| |||    ||||
                                CGTATCCA TGT    CTTC
                                     A  ____
GAM121  FLJ10726 3'  TCCCCCATTTGCACTACTGGCC 36508      A   GTCA_      A
           A                     TGGC TAG     CAAATGGG GA
                                |||| |||     |||||||| ||
                                ACCG GTC     GTTTACCC CT
                                  _  ATCAC       C
GAM121  ILF2     3'  GTCTCCCATTTGTGACCTATGC 66941
           CA                    TGGCATAGGTCACAAATGGGAGAC
                                |||||||||||||||||||||||
                                ACCGTATCCAGTGTTTACCCTCTG

GAM121  KIAA0222 3'  CTCCCACCTGTGACCTGGCC   27681     A       AA
                                GGC TAGGTCACA  TGGGAG
                                |||  |||||||||  ||||||
                                CCG GTCCAGTGT  ACCCTC
                                  _       CC
GAM121  KIAA0556 3'  CTCTTGTGACCCAAACCA    69083     CATA      AATG
                                TGG    GGTCACA    GGAG
                                |||    |||||||    ||||
                                ACC    CCAGTGT    TCTC
                                  AAAC      ____
GAM121  KIAA0836 3'  TTTATCTGTGACCTATATCA   64566    GC        A
                                TG  ATAGGTCACA ATGGG
                                ||  |||||||||| |||||
                                AC  TATCCAGTGT TATTT
                                  TA        C
GAM121  KIAA1396 3'  TCCCCCTTGGGTGCCTATGCCA 62995         T   AAAT   A
                                TGGCATAGG CAC    GGG GA
                                |||||||| |||    ||| ||
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                                ACCGTATCC GTG    CCC CT
                                     _  GGTT   C
GAM121  MRPL45   3'  GTCTCCCATTCCCCTCATGCTA 50375       _   TCACA
                                TGGCAT AGG     AATGGGAGAC
                                ||||||| |||    ||||||||||
                                ATCGTA TCC     TTACCCTCTG
                                   C   CC___
GAM121  SIRPB1   3'  TCATTCTGTGACCTTTACCA   20264     CAT       _
                                TGG   AGGTCACA AATGG
                                |||   |||||||| |||||
                                ACC   TCCAGTGT TTACT
                                  ATT       C
GAM121  SNAP29   3'  CCCATGTGACCTTTGCCA     16539       T       AA
                                TGGCA AGGTCACA  TGGG
                                ||||| ||||||||  ||||
                                ACCGT TCCAGTGT  ACCC
                                   T       __
GAM121  TRIM29   3'  TCTCCCATTCACATGGCCCACC 23961    CATA     CA__
                                GG    GGTCA    AATGGGAGA
                                ||    |||||    |||||||||
                                CC    CCGGT    TTACCCTCT
                                 AC__     ACAC
GAM121  UPK1A    3'  CTCCCATTCACAGATACC    22796    C  AG  CACA
                                GG AT  GT    AATGGGAG
                                || ||  ||    ||||||||
                                CC TA  CA    TTACCCTC
                                 A  GA  C___
GAM121  LOC115294 3'  TTTGGGACCTATGCCA      73020           A
                                TGGCATAGGTC CAAA
                                |||||||||||| ||||
                                ACCGTATCCAG GTTT
                                       G
GAM121  LOC143458 3'  CCCAGCATCACCTATGCCA    76572          CACAAA
                                TGGCATAGGT     TGGG
                                ||||||||||     ||||
                                ACCGTATCCA     ACCC
                                      CTACG_
GAM121  LOC146138 3'  GTCTCCCACTCGATCCCTTCGC 83616      AT   TCACAAA
           CA                   TGGC  AGG      TGGGAGAC
                                ||||  |||      ||||||||
                                ACCG  TCC      ACCCTCTG
                                  CT   CTAGCTC
GAM121  LOC146784 5'  CTCCCATTTATGTGATC     78111        __
                                GGTCACA  AATGGGAG
                                |||||||  ||||||||
                                CTAGTGT  TTACCCTC
                                    AT
GAM121  LOC201220 5'  CCTATGCCTATGCCA       87346          CACAA
                                TGGCATAGGT    ATGGG
                                ||||||||||    |||||
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                                ACCGTATCCG    TATCC
                                      _____
GAM121  LOC202460 5'  CTCCCATTTATGACTTA     89182        C
                                TAGGTCA AAATGGGAG
                                ||||||| |||||||||
                                ATTCAGT TTTACCCTC
                                    A
GAM121  LOC90408  3'  TCTCTGTGACCCATACC     62670    C  A      AAT
                                GG AT GGTCACA   GGGA
                                || || |||||||   ||||
                                CC TA CCAGTGT   CTCT
                                 A  C      ___
GAM121  LOC90917  3'  TCCTCTTGCAGCCTACGCCA  64340     A    CA   AT
                                TGGC TAGGT  CAA  GGGA
                                |||| |||||  |||  ||||
                                ACCG ATCCG  GTT  TCCT
                                  C     AC   C_
GAM122  EBAF      3'  CAGCTGAGCAATGCAC      65423        A
                                GTGCATTG TTAGTTG
                                |||||||| |||||||
                                CACGTAAC AGTCGAC
                                    G
GAM122  MBNL      5'  TGCCAAACTAATCAAT      40732          GAACT
                                ATTGATTAGTT    GCA
                                ||||||||||     |||
                                TAACTAATCAA    CGT
                                      AC___
GAM122  PTGS1     3'  GCAGTGAGTAATCAATACA   54571    C      G  GA
                                TG ATTGATTA TT  ACTGC
                                || |||||||| ||  |||||
                                AC TAACTAAT AG  TGACG
                                 A       G  __
GAM122  PTGS1     3'  GCAGTGAGTAATCAATACA   6352     C      G  GA
                                TG ATTGATTA TT  ACTGC
                                || |||||||| ||  |||||
                                AC TAACTAAT AG  TGACG
                                 A       G  __
GAM122  MLLT10    3'  GCAACAAGAAACTCAATGCAC  16168         _  AG   AAC
                                GTGCATTGA TT  TTG   TGC
                                ||||||||| ||  |||   |||
                                CACGTAACT AA  AAC   ACG
                                    C  AG   A__
GAM122  RTN4IP1   5'  GCAGTTCAACCAGTGTTTAC  51194    __     ATTA
                                GT  GCATTG   GTTGAACTGC
                                ||  ||||||   ||||||||||
                                CA  TGTGAC   CAACTTGACG
                                 TT     _____
GAM123  TNFAIP1   3'  CATCAGCTGAGGACAGCAAACT 40917     AG     G
                CC                  GGA  TTGCTG CTTCAGCTGATG
                                ||| ||||||  ||||||||||||
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                                CCT  AACGAC GGAGTCGACTAC
                                  CA     A
GAM123  C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 21681    AA      _ ___
            CCC                    GG  GTTGCTGG CT   TCAGCTG
                                || ||||||| ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM123  C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 94622    AA      _ ___
            CCC                    GG  GTTGCTGG CT   TCAGCTG
                                || ||||||| ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM123  C20orf59  3'  CATCCCTAGCCAGCAGCTCC   41992     A       TC  CT
                                GGA GTTGCTGGCT  AG  GATG
                                ||| ||||||||||  ||  ||||
                                CCT CGACGACCGA  TC  CTAC
                                 _       __ C_
GAM123  FLJ20079  3'  CATTCTGGTAAACCAGCAGCCT 34490     A      CT__   CT
            CC                     GGA GTTGCTGG   TCAG  GATG
                                ||| ||||||||   ||||  ||||
                                CCT CGACGACC   GGTC  TTAC
                                  C       AAAT   __
GAM123  SSAT2     3'  CATCAGCTGAAGCACTCTTC   56041     TTGCTG
                                GAAG     GCTTCAGCTGATG
                                ||||     ||||||||||||
                                CTTC     CGAAGTCGACTAC
                                  TCA___
GAM123  SYNJ2     3'  ATCAGCTTAAGCAATTCC    61763     GTTGCTG   C
                                GGAA      GCTT AGCTGAT
                                ||||      |||| |||||||
                                CCTT      CGAA TCGACTA
                                  AA_____   T
GAM123  LOC162333 5'  CTGAAGCCAGCAATTCC     87131     G
                                GGAA TTGCTGGCTTCAG
                                |||| ||||||||||||
                                CCTT AACGACCGAAGTC
                                  _
GAM123  LOC222060 5'  CACCTCCCACCAGCAACCCCC  94104    AA      CTTC  C
                                GG  GTTGCTGG   AG TG
                                ||  ||||||||   || ||
                                CC  CAACGACC   TC AC
                                 CC       ACCC  C
GAM123  LOC255650 3'  CATCAGCCCCAGGCAACTTCC  96711        _  CTTCA
                                GGAAGTTGC TGG    GCTGATG
                                |||||||||  |||    |||||||
                                CCTTCAACG ACC    CGACTAC
                                     G  C____
GAM124  GPR56     3'  CCACCTGCCCATGTGATGAA   19068    G   T   AAA   A
                                TT ATCA CGTG   GCAG TGG
                                || |||| ||||   |||| |||
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                                AA TAGT GTAC   CGTC ACC
                                 G   _   C__   C
GAM124  KAL1     3'  TCCAGTATTATTCAAATGATCA 4017        CG   AGCAGA
                A                TTGATCAT  TGAA     TGGA
                                 ||||||||  ||||     ||||
                                 AACTAGTA  ACTT     ACCT
                                     A_    ATTATG
GAM124  FLJ14107 3'  GCTTCCAGGATGATCAA     46695        G  A
                                 TTGATCATC TG AAGC
                                 |||||||||  || ||||
                                 AACTAGTAG AC TTCG
                                      G  C
GAM124  PRO2325   5'  CCATCTGCCTCAGTCTGGGCCA 37588     AT ATCG_   AA
                A                TTG  C    TGA  GCAGATGG
                                 |||  |    |||  ||||||||
                                 AAC  G    ACT  CGTCTACC
                                   CG GTCTG   C_
GAM124  LOC119369 3'  CCAAAGGCCTTCAAATGATCAA 75510        CG   A  AGA
                                 TTGATCAT  TGAA GC   TGG
                                 ||||||||  |||| ||   |||
                                 AACTAGTA  ACTT CG   ACC
                                     A_    C  GAA
GAM125  DTNB     3'  TACTTAAAACCAGAGCTT    52499      ACA  A   C
                                 AAGC   TC TGG TTTAAGTA
                                 ||||   || ||| ||||||||
                                 TTCG   AG ACC AAATTCAT
                                   ___  _   A
GAM125  EIF2C1    3'  TGAAGCCATGATTACTTTA    24181       CAC
                                 TAAAG   ATCATGGCTTTA
                                 |||||   ||||||||||||
                                 ATTTC   TAGTACCGAAGT
                                    AT_
GAM125  FLT1     3'  AGGCCATGATGGCCTTA     8912      A  A
                                 TAA GC CATCATGGCTT
                                 ||| || ||||||||||
                                 ATT CG GTAGTACCGGA
                                   C  _
GAM125  HTLF     3'  AAAGCCATAATGGACTT     9282      CA   C
                                 AAG  CAT ATGGCTTT
                                 |||  ||| ||||||||
                                 TTC  GTA TACCGAAA
                                   AG   A
GAM125  P4HB     3'  TGAAACCATGATGTACTTT    6220       C        C
                                 AAAG ACATCATGG TTTA
                                 |||| ||||||||| ||||
                                 TTTC TGTAGTACC AAGT
                                   A        A
GAM125  PPP1R2    3'  CTATGACAAACGTGCTTTA    20690        A____
                                 TAAAGCAC     TCATGG
                                 ||||||||     ||||||
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                                ATTTCGTG    AGTATC
                                    CAAAC
GAM125  RNF28    3'  ACTCACAGGGACGATGTGCT  50860       ATGG   A__
                                AGCACATC   CTTT  AGT
                                ||||||||   ||||  |||
                                TCGTGTAG   GGGA  TCA
                                    CA__   CAC
GAM125  USH2A    5'  ACTTAAAGTACCCTGCTT   23062     CATCATG
                                AAGCA     GCTTTAAGT
                                |||||     |||||||||
                                TTCGT     TGAAATTCA
                                  CCCA___
GAM125  ZNF192   3'  ACTTAAAGTATTTATGCTT  20852     CATCATG
                                AAGCA     GCTTTAAGT
                                |||||     |||||||||
                                TTCGT     TGAAATTCA
                                  ATTTA__
GAM125  ELL2     3'  ACTTAAAAGTTGTATGTGTTT  23869       C TG   _
                                AAGCACAT A  GCTTT AAGT
                                |||||||| |  ||||| ||||
                                TTTGTGTA T  TGAAA TTCA
                                    _ GT    A
GAM125  FLJ23445 3'  TACATGACCATAATGTGTTT  89034       C   CT   A
                                AAGCACAT ATGG  TTA GTA
                                |||||||| ||||  ||| |||
                                TTTGTGTA TACC  AGT CAT
                                    A   __  A
GAM125  HEI10    5'  TACCTAAAGCCTGGT     40999     T     A
                                ATCA GGCTTTA GTA
                                |||| ||||||| |||
                                TGGT CCGAAAT CAT
                                  _     C
GAM125  KIAA0547 3'  ACTTAAAGCCAGGAGTTT   28906     ACA  A
                                AAGC   TC TGGCTTTAAGT
                                ||||   || ||||||||||
                                TTTG   AG ACCGAAATTCA
                                  ___  G
GAM125  PRO1600  3'  ACTTAAAGGCCATATGACCTT  26032    CA   C    _
                                AAG  CAT ATGGC TTTAAGT
                                |||  ||| ||||| |||||||
                                TTC  GTA TACCG AAATTCA
                                  CA   _    G
GAM125  LOC120196 3'  ACTTGTACATGTGCTTTA    75546       TCA  GCTT
                                TAAAGCACA   TG   TAAGT
                                |||||||||   ||   |||||
                                ATTTCGTGT   AC   GTTCA
                                    ____ AT__
GAM125  LOC135307 3'  TACTTAAAGACAATGTCACTTT 75226      C_   CA  G
          A                      TAAAG  ACAT  TG CTTTAAGTA
                                |||||  ||||  || |||||||||
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                                ATTTC  TGTA  AC GAAATTCAT
                                  AC   __  A
GAM125  LOC257017 5'  TACTTAATTTCTTATTATGTGC 97377    A    C   CT__
           CTTA                   TAA GCACAT ATGG   TTAAGTA
                                ||| |||||| ||||   |||||||
                                ATT CGTGTA TATT   AATTCAT
                                  C     T   CTTT
GAM125  LOC51336  5'  ACTTAGCATAATGTGC     33575      C   GCT
                                GCACAT ATG   TTAAGT
                                |||||| |||   ||||||
                                CGTGTA TAC   GATTCA
                                   A  ___
GAM126  TNFAIP1   3'  CATCAGCTGAGGACAGCAAACT 40917    AG    G
           CC                     GGA  TTGCTG CTTCAGCTGATG
                                |||  |||||| ||||||||||||
                                CCT  AACGAC GGAGTCGACTAC
                                  CA     A
GAM126  C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 21681    AA      _ ___
           CCC                    GG  GTTGCTGG CT   TCAGCTG
                                ||  |||||||| ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM126  C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 94622    AA      _ ___
           CCC                    GG  GTTGCTGG CT   TCAGCTG
                                ||  |||||||| ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM126  C20orf59  3'  CATCCCTAGCCAGCAGCTCC   41992    A       TC  CT
                                GGA GTTGCTGGCT  AG  GATG
                                ||| ||||||||||  ||  ||||
                                CCT CGACGACCGA  TC  CTAC
                                  _        __ C_
GAM126  FLJ20079  3'  CATTCTGGTAAACCAGCAGCCT 34490    A      CT__   CT
           CC                     GGA GTTGCTGG   TCAG  GATG
                                ||| ||||||||   ||||  ||||
                                CCT CGACGACC   GGTC  TTAC
                                  C       AAAT   __
GAM126  SSAT2     3'  CATCAGCTGAAGCACTCTTC   56041     TTGCTG
                                GAAG     GCTTCAGCTGATG
                                ||||     ||||||||||||||
                                CTTC     CGAAGTCGACTAC
                                   TCA___
GAM126  SYNJ2     3'  ATCAGCTTAAGCAATTCC    61763     GTTGCTG   C
                                GGAA      GCTT AGCTGAT
                                ||||      |||| |||||||
                                CCTT      CGAA TCGACTA
                                  AA_____   T
GAM126  LOC162333 5'  CTGAAGCCAGCAATTCC     87131      G
                                GGAA TTGCTGGCTTCAG
                                |||| ||||||||||||
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                                CCTT AACGACCGAAGTC
                                   _
GAM126  LOC222060 5'  CACCTCCCACCAGCAACCCCC  94104    AA      CTTC  C
                                GG  GTTGCTGG    AG TG
                                ||  ||||||||    || ||
                                CC  CAACGACC    TC AC
                                 CC       ACCC  C
GAM126  LOC255650 3'  CATCAGCCCCAGGCAACTTCC  96711        _  CTTCA
                                GGAAGTTGC TGG    GCTGATG
                                ||||||||| |||    |||||||
                                CCTTCAACG ACC    CGACTAC
                                      G  C____
GAM127  AQP6    3'  CAGGAAACCCTTGGTCCAGAGA 7942     C      CAA   GA
                                TC CTGGACCA   GTTT  CCTG
                                || ||||||||   ||||  ||||
                                AG GACCTGGT   CAAA  GGAC
                                 A       TCC   __
GAM127  AQP6    3'  CAGGAAACCCTTGGTCCAGAGA 53913    C      CAA   GA
                                TC CTGGACCA   GTTT  CCTG
                                || ||||||||   ||||  ||||
                                AG GACCTGGT   CAAA  GGAC
                                 A       TCC   __
GAM127  COG8    5'  CAGCGCCCCTTGTGGTCCGG   50481          TTTGAC
                                CTGGACCACAAG     CTG
                                ||||||||||||     |||
                                GGCCTGGTGTTC     GAC
                                      CCCGC_
GAM127  CORO2A  3'  CAAACTGTGGTCCAGAGA    53401    C       A
                                TC CTGGACCACA GTTTG
                                || ||||||||||  |||||
                                AG GACCTGGTGT CAAAC
                                 A       _
GAM127  CORO2A  3'  CAAACTGTGGTCCAGAGA    12645    C       A
                                TC CTGGACCACA GTTTG
                                || ||||||||||  |||||
                                AG GACCTGGTGT CAAAC
                                 A       _
GAM127  CYP1A2  3'  CAGGTCAACCATGACCCAG   69104     AC  CAA   T
                                CTGG  CA   GTT GACCTG
                                ||||  ||   ||| ||||||
                                GACC  GT   CAA CTGGAC
                                  CA  AC_  _
GAM127  GDF5    3'  CAGGCACAGGTCCAGGGA    5102          ACAA
                                TCCCTGGACC    GTTTG
                                ||||||||||    |||||
                                AGGGACCTGG    CGGAC
                                      ACA_
GAM127  GHR     3'  CAGGTGGCTTTTGCGGTTCAGG 3879         A    TTTG
                                CCTGGACC CAAG    ACCTG
                                |||||||| ||||    |||||
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                                GGACTTGG GTTT    TGGAC
                                     C    TCGG
GAM127  GRLF1    3'  CAGGTCAGAAAGTGGCCCAGG  78553      A    AAG
                                CCTGG CCAC   TTTGACCTG
                                ||||| ||||   |||||||||
                                GGACC GGTG   AGACTGGAC
                                   C    AA_
GAM127  IFNAR2   3'  AGGGCCTGTGGTCCGAAGA   6038     CC       A  TTGA
                                TC  TGGACCACA GT    CCT
                                ||  |||||||| ||    |||
                                AG  GCCTGGTGT CG    GGA
                                 AA        C  ____
GAM127  NEO1     3'  CAAAATTTTGTGTCCAGGGA   10200         C    __
                                TCCCTGGAC ACAAG  TTTG
                                ||||||||| |||||  ||||
                                AGGGACCTG TGTTT  AAAC
                                      _    TA
GAM127  PAX2     3'  CAAGGTTGGGACCCAAGGA   14331     C  A_ A  G
                                TCC TGG  CC CAA TTTG
                                ||| |||  || ||| ||||
                                AGG ACC  GG GTT GAAC
                                  A  CA  _  G
GAM127  PAX2     3'  CAAGGTTGGGACCCAAGGA   14322     C  A_ A  G
                                TCC TGG  CC CAA TTTG
                                ||| |||  || ||| ||||
                                AGG ACC  GG GTT GAAC
                                  A  CA  _  G
GAM127  PCSK5    5'  CAGGTCCCGGCAGCCCCAGGGA 20574       ACCACAA  T_
                                TCCCTGG      GTT  GACCTG
                                |||||||      |||  ||||||
                                AGGGACC      CGG  CTGGAC
                                    CCGA___   CC
GAM127  PIK3R3   3'  CAGGGGCCCTGTGGTCCAGGG  61053          A_  TGA
                                CCCTGGACCACA  GTT   CCTG
                                ||||||||||||  |||   ||||
                                GGGACCTGGTGT  CGG   GGAC
                                      CC   ___
GAM127  PTGFRN   5'  CAGATGCCACTGTCCAGGGA  67186        CACAA_
                                TCCCTGGAC     GTTTG
                                |||||||||     |||||
                                AGGGACCTG     TAGAC
                                     TCACCG
GAM127  ZNF135   3'  CAAATGTAGTGGATCCAGGGA  12850        _   AA_
                                TCCCTGGA CCAC   GTTTG
                                |||||||| ||||   |||||
                                AGGGACCT GGTG   TAAAC
                                    A    ATG
GAM127  ZNF76    5'  CAGATTTGTGACCCAG      12807      AC
                                CTGG  CACAAGTTTG
                                ||||  ||||||||||
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                                GACC  GTGTTTAGAC
                                  CA
GAM127  CTPS2    3'  CAGATTTGTGTGTGGTCCA   39084        ____
                                TGGACCACA   AGTTTG
                                |||||||||   ||||||
                                ACCTGGTGT   TTAGAC
                                     GTGT
GAM127  EZF-2    5'  CAGGCGCTGCGGTCCGGG    37097       A  A_
                                CCTGGACC CA  GTTTG
                                |||||||| ||  |||||
                                GGGCCTGG GT  CGGAC
                                     C  CG
GAM127  FLJ12577 3'  CAAACCATGGGTCCAGGGA   48154         ACAA
                                TCCCTGGACC   GTTTG
                                ||||||||||   |||||
                                AGGGACCTGG   CAAAC
                                      GTAC
GAM127  FLJ13166 3'  CAAACTATGGTCCAGG      46563        CA
                                CCTGGACCA  AGTTTG
                                |||||||||  ||||||
                                GGACCTGGT  TCAAAC
                                     A_
GAM127  FLJ20727 5'  CAGACTTCTGATCCAG      35615      C  C
                                CTGGA CA AAGTTTG
                                |||||  || |||||||
                                GACCT GT TTCAGAC
                                   A  C
GAM127  FLJ23563 3'  CAAATTGTGGCACAGAGA    67589    C   GA     G
                                TC CTG  CCACAA TTTG
                                ||  |||  |||||| ||||
                                AG GAC  GGTGTT AAAC
                                  A   AC     _
GAM127  GMEB2    5'  CGGGAGCCTGCGTCCAGGGA   24729        CA  A   TGA
                                TCCCTGGAC  CA GTT   CCTG
                                |||||||||  ||  |||   ||||
                                AGGGACCTG  GT CGA   GGGC
                                     C_  C   ___
GAM127  KIAA1615 5'  CAAATTTGGAGTCCAGG     68700        CA
                                CCTGGAC  CAAGTTTG
                                |||||||  ||||||||
                                GGACCTG  GTTTAAAC
                                    AG
GAM127  KIAA1668 3'  GGGTCCCAGGGTCCAGGGA   66480         ACAAGTTT
                                TCCCTGGACC       GACCT
                                ||||||||||       |||||
                                AGGGACCTGG       CTGGG
                                      GACC____
GAM127  MGC16025 3'  CAGATGAGGCTACATCCAGGGA 51914        _____  ACAA
                                TCCCTGGA    CC    GTTTG
                                ||||||||    ||    |||||
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                                AGGGACCT    GG    TAGAC
                                    ACATC  AG__
GAM127  MGC2306  3'  CAGGTCAGGACCAGGACCCAGG 50958       A_  ACAAG
          GA                    TCCCTGG  CC    TTTGACCTG
                                |||||||  ||    |||||||||
                                AGGGACC  GG    GGACTGGAC
                                   CA  ACCA_
GAM127  MGC2452  5'  AGGAGATGTGGTCCAGG     50976         AGT  GA
                                CCTGGACCACA   TT  CCT
                                ||||||||||   ||  |||
                                GGACCTGGTGT   AG  GGA
                                      ___  A_
GAM127  MGC3178  3'  CAGGCCTGGGTATCCAGGGA   47983        __  A  A
                                TCCCTGGA  CC CA GTTTG
                                ||||||||  || || |||||
                                AGGGACCT  GG GT CGGAC
                                    AT  _  C
GAM127  NPAS3    3'  CAGTCTTGTGGTCAAGAGA   42096    C  G       T
                                TC CT GACCACAAG TTG
                                || || |||||||||| |||
                                AG GA CTGGTGTTC GAC
                                 A  A        T
GAM127  NXPH3    3'  CAGGCATCCCTTGGTCCAGG   65753         CAAGTT  A
                                CCTGGACCA     TG CCTG
                                |||||||||     || ||||
                                GGACCTGGT     AC GGAC
                                     TCCCT_ _
GAM127  OSMR     3'  CAGGGTGGCTGTGGTCCTAG   14346    _      A   TGA
                                CT GGACCACA GTT   CCTG
                                || ||||||||| |||   ||||
                                GA CCTGGTGT CGG   GGAC
                                 T       _   TG_
GAM127  PLPL     3'  CAGGTCACTCTGTGGTCCA    39430         A TT
                                TGGACCACA G  TGACCTG
                                ||||||||| |  |||||||
                                ACCTGGTGT C  ACTGGAC
                                     _ TC
GAM127  PRTD-NY3 3'  GTCATGACTCCAGGGA      48150         CCACAA  _
                                TCCCTGGA     GTT TGAC
                                ||||||||     ||| ||||
                                AGGGACCT     CAG ACTG
                                     _______  T
GAM127  SCYA14   5'  CAAACCCAGTGGTCCGGG    51999         AA_
                                CCTGGACCAC   GTTTG
                                ||||||||||   |||||
                                GGGCCTGGTG   CAAAC
                                     ACC
GAM127  SCYA14   5'  CAAACCCAGTGGTCCGGG    14787         AA_
                                CCTGGACCAC   GTTTG
                                ||||||||||   |||||
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                                GGGCCTGGTG  CAAAC
                                     ACC
GAM127  SDCCAG10  5'  TAGAGTTGTGGTCCAAAGA   19644   CC       G
                                TC  TGGACCACAA TTTG
                                ||  |||||||||| ||||
                                AG  ACCTGGTGTT AGAT
                                 AA        G
GAM127  ZNF185    3'  AGGAGCTTGTGAATCCAGG   23107     C_     TGA
                                CCTGGA  CACAAGTT  CCT
                                ||||||  ||||||||  |||
                                GGACCT  GTGTTCGA  GGA
                                   AA      ____
GAM127  LOC115219 5'  CAGGCTGGGTCCAGG      73299       A  A
                                CCTGGACC CA GTTTG
                                |||||||| || |||||
                                GGACCTGG GT CGGAC
                                   _  _
GAM127  LOC115399 3'  CAGACCTGCAGTCCAGGGG   73425       CA  A
                                TCCCTGGAC  CA GTTTG
                                |||||||||  || |||||
                                GGGGACCTG  GT CAGAC
                                     AC  C
GAM127  LOC129011 5'  CAGACCTGCGGTCCAGG     74864       A  A
                                CCTGGACC CA GTTTG
                                |||||||| || |||||
                                GGACCTGG GT CAGAC
                                     C  C
GAM127  LOC145608 5'  CAGACCAGAGTTTGTGGCACAG 83381     GA     _   AC
          G                      CCTG  CCACAAG TTTG  CTG
                                ||||  ||||||| ||||  |||
                                GGAC  GGTGTTT AGAC  GAC
                                  AC      G   CA
GAM127  LOC148738 3'  CAGATGAGGCTGCAGTCCAGGG 59201       CACA    GAC
                                CCCTGGAC   AGTTT   CTG
                                ||||||||   |||||  |||
                                GGGACCTG   TCGGA   GAC
                                     ACG_    GTA
GAM127  LOC149127 3'  CAGGCCTGTGGTCCCAGG    84344     _    A
                                CCTGG ACCACA GTTTG
                                ||||| |||||| |||||
                                GGACC TGGTGT CGGAC
                                   C     C
GAM127  LOC150622 5'  TGAACCTGGTGGTCCAGGGA  79965         AA_
                                TCCCTGGACCAC  GTTTG
                                ||||||||||||  |||||
                                AGGGACCTGGTG  CAAGT
                                      GTC
GAM127  LOC150935 3'  GGCCAAGGCCCGGGGA     80035       A  ACAAGT  A
                                TCCCTGG CC     TTG CC
                                ||||||| ||     ||| ||
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                                AGGGGCC GG     AAC GG
                                    C _______  C
GAM127  LOC151318 3'  CAGGTCAAACGTTTTCAGG   80226       CCACAA
                                CCTGGA     GTTTGACCTG
                                ||||||     ||||||||||
                                GGACTT     CAAACTGGAC
                                   TTG___
GAM127  LOC151361 3'  CAGGCGCACGAGGTCCAGGGA  85321          ACAA  T  A
                                TCCCTGGACC    GT TG CCTG
                                ||||||||||    || || ||||
                                AGGGACCTGG    CA GC GGAC
                                      AG__  C  _
GAM127  LOC154739 5'  CAAATTGTGGTCCAGAGA    86226    C         G
                                TC CTGGACCACAA TTTG
                                || ||||||||||| ||||
                                AG GACCTGGTGTT AAAC
                                 A         _
GAM127  LOC154862 5'  AGCTTTGATCCAGGGA      81166         C  C
                                TCCCTGGA CA AAGTT
                                |||||||| || |||||
                                AGGGACCT GT TTCGA
                                     A  _
GAM127  LOC159199 5'  TAAACTTGTGGCTCAGAGA   82187    C   GA
                                TC CTG  CCACAAGTTTG
                                || |||  ||||||||||
                                AG GAC  GGTGTTCAAAT
                                 A   TC
GAM127  LOC200000 3'  CAGAGTTTCAGTGGTCCAAAGA 89918    CC       AAGTTT  _
                                TC  TGGACCAC      GAC CTG
                                ||  ||||||||      ||| |||
                                AG  ACCTGGTG      TTG GAC
                                 AA       ACT___   A
GAM127  LOC200230 3'  AGGCCAAGGTGGTCCGG     88648          AAG    A
                                CTGGACCAC   TTTG CCT
                                |||||||||   |||| |||
                                GGCCTGGTG   GAAC GGA
                                     ___    C
GAM127  LOC256158 5'  CAAGTCTCTGTGGTCCAGG   97647           _ _
                                CCTGGACCACA AG TTTG
                                |||||||||| || ||||
                                GGACCTGGTGT TC GAAC
                                      C  T
GAM127  LOC51027  3'  CAGGTCAAAGTGAACC      59363    AC   AAG
                                GG  CAC   TTTGACCTG
                                ||  |||   |||||||||
                                CC  GTG   AAACTGGAC
                                 AA  ___
GAM127  LOC51145  3'  AACTCCTGATAATCCAGGGA   32391         C___  CA
                                TCCCTGGA    CA  AGTT
                                ||||||||    ||  ||||
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                                AGGGACCT   GT  TCAA
                                    AATA  CC
GAM127  LOC51195  3'  CAGGCCTCTGGAAGGTCCAGGG 32936         ACA_  TTTGA
           A                     TCCCTGGACC   AG    CCTG
                                 ||||||||||   ||    ||||
                                 AGGGACCTGG   TC    GGAC
                                      AAGG  TCC__
GAM127  LOC90719  5'  CAGATTTGCAGCCCGGGA    63881     T  ACCA
                                 TCCC GG   CAAGTTTG
                                 |||| ||   ||||||||
                                 AGGG CC   GTTTAGAC
                                   C  GAC_
GAM127  LOC90843  5'  CAGAAGTCCTTATAGTCCAGGG 64205        CAC   TTT   __
                                 CCCTGGAC   AAG   GAC  CTG
                                 ||||||||   |||   |||  |||
                                 GGGACCTG   TTC   CTG  GAC
                                      ATA   ___   AA
GAM128  ADAMTS8   5'  TCGGGCCGCCAGCACCTG    22886     _      ATAAG
                                 CAG TGCTGGC    CTGA
                                 ||| |||||||    ||||
                                 GTC ACGACCG    GGCT
                                   C      CCG__
GAM128  BAP1      3'  TCAGGGACCCAGCACTGG     16219          CATAAG
                                 CCAGTGCTGG     CTGA
                                 ||||||||||     ||||
                                 GGTCACGACC     GACT
                                      CAGG__
GAM128  BF        5'  TTCAGCTTGGACACTG      8140       CTGGCA
                                 CAGTG     TAAGCTGAA
                                 |||||     |||||||||
                                 GTCAC     GTTCGACTT
                                    AG____
GAM128  C1QB      3'  TTCAACTCTGTGTCCCAGCACT 4923     A        __    _  C
              GGC                   G CCAGTGCTGG  CATA AG TGAA
                                 | ||||||||||  |||| || ||||
                                 C GGTCACGACC  GTGT TC ACTT
                                 _         CT    C  A
GAM128  CHC1      3'  CAGCCCTGAGCACTGTGTC    7020      _      __  CATAA
                                 GAC CAGTGCT  GG     GCTG
                                 ||| |||||||  ||     ||||
                                 CTG GTCACGA  CC     CGAC
                                   T      GT  _____
GAM128  CMRF35    5'  CAGAGCTGTCAGCACCGG     21929     A       TAAG
                                 CC GTGCTGGCA    CTG
                                 || |||||||||    |||
                                 GG CACGACTGT    GAC
                                  C        CGA_
GAM128  EPHB6     3'  TCAGCCCTGGACACTGGTC    15466         _ TG CATAA
                                 GACCAGTG C  G    GCTGA
                                 |||||||| |  |    |||||
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                                CTGGTCAC G  C    CGACT
                                    A GT C____
GAM128  EVPL    5'  CAGCCTGAGCCAGCACT    8803         A  A
                                AGTGCTGGC TA GCTG
                                ||||||||| || ||||
                                TCACGACCG GT CGAC
                                    A  C
GAM128  GARP    3'  CAGCCCAGCACTGG       18594         CATAA
                                CCAGTGCTGG    GCTG
                                ||||||||||    ||||
                                GGTCACGACC    CGAC
                                      _____
GAM128  GJB5    3'  CAGCTCGACGGCACTGG     17945         GCATA
                                CCAGTGCTG    AGCTG
                                |||||||||    |||||
                                GGTCACGGC    TCGAC
                                    AGC__
GAM128  GPR81   3'  CTTACCAGCATTAGTC     50757     C      CA
                                GAC AGTGCTGG  TAAG
                                ||| ||||||||  ||||
                                CTG TTACGACC  ATTC
                                  A      __
GAM128  IFI16   5'  AGCAAGCCAGCACTAGTC    71221     C       ATAA
                                GAC AGTGCTGGC    GCT
                                ||| |||||||||    |||
                                CTG TCACGACCG    CGA
                                  A       AA__
GAM128  KRT4    3'  CAGCTGGGCCCAGCACTGGT  9635          _ ATA
                                ACCAGTGCTGG C   AGCTG
                                |||||||||||  |   |||||
                                TGGTCACGACC G   TCGAC
                                     C GG_
GAM128  MAP3K9  3'  TTCAGCTTCCCAAACACCAGT  60709    CA  C_  CAT
                                AC  GTG  TGG   AAGCTGAA
                                ||  |||  |||   ||||||||
                                TG  CAC  ACC   TTCGACTT
                                 AC   AA   C__
GAM128  MGAT5   5'  TCAGCTTACAGTTCCTG     10028     T_   GCA
                                CAG  GCTG   TAAGCTGA
                                |||  ||||   ||||||||
                                GTC  TGAC   ATTCGACT
                                  CT    ___
GAM128  MOCS1   3'  TTCAGCTTAACAGTTGCCCGGT 92037      A_  _   GCA
          C                      GACC  GTG CTG   TAAGCTGAA
                                ||||  ||| |||   |||||||||
                                CTGG  CGT GAC   ATTCGACTT
                                  CC   T   A__
GAM128  P23     3'  TCAGCTTATACCCGGGCT    21719     G   C_
                                AGT CTGG  ATAAGCTGA
                                ||| ||||  |||||||||
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                                TCG GGCC  TATTCGACT
                                  _   CA
GAM128  PFKFB4   3'  TCAGCCACATGCAACACTGTGT 15874    _    CTG   AA_
            C                    GAC CAGTG  GCAT  GCTGA
                                 ||| |||||  ||||  |||||
                                 CTG GTCAC  CGTA  CGACT
                                   T    AA_   CAC
GAM128  PTPRK    3'  TTCAGCCTGTGGCCCAGCACTG 11125          __   A
            GTC                    GACCAGTGCTGG  CATA GCTGAA
                                 ||||||||||||  |||| ||||||
                                 CTGGTCACGACC  GTGT CGACTT
                                       CG   C
GAM128  RNPEPL1  3'  CGGATGCCAGCACCTG     36676    _       AAG
                                 CAG TGCTGGCAT   CTG
                                 ||| |||||||||   |||
                                 GTC ACGACCGTA   GGC
                                   C       ___
GAM128  UBE2L3   3'  TCAGCCCTGGCACTGGC     12507   A     TG CATAA
                                 G CCAGTGC  G    GCTGA
                                 | |||||||  |    |||||
                                 C GGTCACG  C    CGACT
                                  _      GT C____
GAM128  APXL2    5'  CAGCCTCAGCACTCATC     75185   CC      CATAA
                                 GA  AGTGCTGG    GCTG
                                 ||  ||||||||    ||||
                                 CT  TCACGACT    CGAC
                                   AC       C____
GAM128  ARHGEF9  3'  TTCAGCTTACCAAGCA     30824     _ CA
                                 TGCT GG  TAAGCTGAA
                                 |||| ||  |||||||||
                                 ACGA CC  ATTCGACTT
                                   A  __
GAM128  CEGP1    3'  TTCAGCTTCCTCTAGCCCGG  40589    AGT    CAT
                                 CC   GCTGG   AAGCTGAA
                                 ||   |||||   ||||||||
                                 GG   CGATC   TTCGACTT
                                  CC_    TCC
GAM128  DKFZp547D155 3'  CAGCCCTGAGACCACTGGTC  70435        CTGG  TAA
                                 GACCAGTG    CA   GCTG
                                 ||||||||    ||   ||||
                                 CTGGTCAC    GT   CGAC
                                      CAGA  CC_
GAM128  DKFZP727G051 3'  TTCAGCCCATCAACCAGCATTG 69483           CATAA__
            GTC                    GACCAGTGCTGG      GCTGAA
                                 ||||||||||||      ||||||
                                 CTGGTTACGACC      CGACTT
                                       AACTACC
GAM128  DUSP14   5'  CACTGTCACCAGCACTGCTC  22834    C       CATA  C
                                 GA CAGTGCTGG    AG TG
                                 || |||||||||    || ||
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                                CT GTCACGACC    TC AC
                                 C        ACTG  _
GAM128  FLJ10206  5'  CAGCTTATGCCAGGAGTC    35898     CAGTG
                                GAC    CTGGCATAAGCTG
                                |||    ||||||||||||
                                CTG    GACCGTATTCGAC
                                  AG___
GAM128  FLJ20967  5'  GGCGCCCAGCACTGGTT     41962          CATAA
                                GACCAGTGCTGG    GCT
                                ||||||||||||    |||
                                TTGGTCACGACC    CGG
                                       CG___
GAM128  FLJ22569  3'  TTCAGCTTACTAAACTG     43679     GC   CA
                                CAGT  TGG  TAAGCTGAA
                                ||||  |||  |||||||||
                                GTCA  ATC  ATTCGACTT
                                  A_  __
GAM128  FOXN4     3'  TTCAGCTTGGACACACTGG    75574       C  GCA
                                CCAGTG TG   TAAGCTGAA
                                |||||| ||   |||||||||
                                GGTCAC AC   GTTCGACTT
                                   _ AG_
GAM128  GW112     3'  TTCAACTGAAGCCAGCACTGGT 21194           ATA  C
           T                     GACCAGTGCTGGC   AG TGAA
                                ||||||||||||   || ||||
                                TTGGTCACGACCG   TC ACTT
                                       AAG  A
GAM128  HOOK2     3'  CAGCTCACATGGCGCCCAGCAC 25256         _____  A__
           TGG                    CCAGTGCTGG    CAT   AGCTG
                                ||||||||||    |||   |||||
                                GGTCACGACC    GTA   TCGAC
                                      CGCG   CAC
GAM128  jdp2      3'  TTCAGCACAGCCAGCAT     55327        ATAA
                                GTGCTGGC    GCTGAA
                                ||||||||    ||||||
                                TACGACCG    CGACTT
                                    ACA_
GAM128  KIAA0767  3'  TCTGCTGCCAGCACAGG     60632    A       TAA  T
                                CC GTGCTGGCA   GC GA
                                || |||||||||   || ||
                                GG CACGACCGT   CG CT
                                 A        ___  T
GAM128  KIAA0923  3'  TCAGCTTGATGCATGGTC    25838      G   TGGCA
                                GACCA TGC    TAAGCTGA
                                ||||| |||    ||||||||
                                CTGGT ACG    GTTCGACT
                                   _  TA___
GAM128  KIAA0982  3'  TTCACTGTTTGCCAGCAC    25852         TA_  C
                                GTGCTGGCA   AG TGAA
                                |||||||||   || ||||
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                                CACGACCGT   TC ACTT
                                     TTG  _
GAM128  KIAA1000  3'  TTCAGCTTTGCAAAGTACTGG  65281        G_   T
                                CCAGTGCT  GCA AAGCTGAA
                                ||||||||  ||| ||||||||
                                GGTCATGA  CGT TTCGACTT
                                    AA  _
GAM128  MAP3K3   3'  TCAGCCTGGGCGCTGGTC    9999          GG  TAA
                                GACCAGTGCT  CA   GCTGA
                                ||||||||||  ||   |||||
                                CTGGTCGCGG  GT   CGACT
                                     __  C__
GAM128  MGC16037  5'  CTTGTCCAGCACTAGTC     51821     C       C
                                GAC AGTGCTGG ATAAG
                                ||| |||||||| |||||
                                CTG TCACGACC TGTTC
                                  A       _
GAM128  MIDORI   3'  TCAGCTTATCCTGCAACT    73792     _  T  C
                                AGT GC GG ATAAGCTGA
                                ||| || || |||||||||
                                TCA CG CC TATTCGACT
                                  A  T  _
GAM128  MtFMT    5'  CAGTGGCGAGCACTGG      57651         G  ATAA
                                CCAGTGCT GC    GCTG
                                |||||||| ||    ||||
                                GGTCACGA CG    TGAC
                                     G  G___
GAM128  PCDH16   5'  TCAGTTCCAACCACTGG     72826       C_   CATA
                                CCAGTG  TGG    AGCTGA
                                ||||||  |||    ||||||
                                GGTCAC  ACC    TTGACT
                                   CA  _____
GAM128  QKI      3'  CAGCTTATCAACTCGTC     65439     C   GCTGGC
                                GAC AGT      ATAAGCTG
                                ||| |||      ||||||||
                                CTG TCA      TATTCGAC
                                  C   AC_____
GAM128  TNRC6    3'  CAACTTTTAGCACTG       70506         CAT   C
                                CAGTGCTGG   AAG TG
                                |||||||||   ||| ||
                                GTCACGATT   TTC AC
                                     ___   A
GAM128  TOB2     3'  CAGCCCAGGCCAGCACTG    95618          ATAA
                                CAGTGCTGGC    GCTG
                                ||||||||||    ||||
                                GTCACGACCG    CGAC
                                      GACC
GAM128  TU12B1-TY 3'  TCAGCCCACAGCACTGTC    33406     C      GCATAA
                                GAC AGTGCTG     GCTGA
                                ||| |||||||     |||||
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                                CTG TCACGAC     CGACT
                                  _     ACC___
GAM128  TUSP     3'  TCAGCCTAAGAGCGCAGCACTG 39641        _ A__  A
                                CAGTGCTG GC   TA GCTGA
                                |||||||| ||   || |||||
                                GTCACGAC CG   AT CGACT
                                     G  AGA  C
GAM128  USP19    3'  TCAGCTTATGCATCTGGT    88959      TGCTG
                                ACCAG    GCATAAGCTGA
                                |||||    ||||||||||
                                TGGTC    CGTATTCGACT
                                   TA___
GAM128  ZD52F10  3'  CAGCCTGTGCCAGCCCTGG   52819     T       A
                                CCAG GCTGGCATA GCTG
                                |||| ||||||||| ||||
                                GGTC CGACCGTGT CGAC
                                   C       C
GAM128  LOC145268 3'  TCAGCTTACAAGAGCCACTG   77062      _ GGCA
                                CAGTG CT    TAAGCTGA
                                ||||| ||    ||||||||
                                GTCAC GA    ATTCGACT
                                   C  GAAC
GAM128  LOC149296 5'  CAGCTTATGGGCAGCA      79256      G_
                                TGCTG  CATAAGCTG
                                |||||  |||||||||
                                ACGAC  GTATTCGAC
                                   GG
GAM128  LOC161877 5'  TCAGGGCAGGCCAGCGCTGG   82326          ATAAG
                                CCAGTGCTGGC    CTGA
                                ||||||||||     ||||
                                GGTCGCGACCG    GACT
                                      GACGG
GAM128  LOC163115 5'  TCAGCCCCTGACAGCACTGG   82413        G  TAA
                                CCAGTGCTG CA   GCTGA
                                |||||||| ||   |||||
                                GGTCACGAC GT   CGACT
                                     A  CCC
GAM128  LOC196500 3'  TCAGCTCACTCAGTGGTC    87744     AGT    CATA
                                GACC   GCTGG    AGCTGA
                                ||||   |||||    ||||||
                                CTGG   TGACT    TCGACT
                                  ___    CAC_
GAM128  LOC197287 3'  TCAGCTCATGTGTTTTGCACTG 60865       T_    __
                                CAGTGC  GGCATA  AGCTGA
                                ||||||  ||||||  ||||||
                                GTCACG  TTGTGT  TCGACT
                                   TT     AC
GAM128  LOC200470 5'  TCAGCCTGCGGCGCTGG     90069         G  TAA
                                CCAGTGCTG CA   GCTGA
                                |||||||| ||   |||||
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                                GGTCGCGGC GT   CGACT
                                     _ C__
GAM128  LOC221584 3'  CAGCTTATGTGGCAC      93828       G
                                GTGCTG CATAAGCTG
                                |||||| |||||||||
                                CACGGT GTATTCGAC
                                     _
GAM128  LOC51716  3'  CAGCTCATGGCCCTAGCA    32787       ___  A
                                TGCTGG   CAT AGCTG
                                ||||||   ||| |||||
                                ACGATC   GTA TCGAC
                                   CCG   C
GAM128  LOC92196  5'  CAGAGCACCAGCACTGGC    68456   A       CATAAG
                                G CCAGTGCTGG     CTG
                                | ||||||||||     |||
                                C GGTCACGACC     GAC
                                _        ACGA__
GAM129  BPAG1    3'  TCTGGGGTTAAAGTCACAT    31432     A  C     T
                                ATGT ACT TAGCTT CAGA
                                |||| ||| |||||| ||||
                                TACA TGA ATTGGG GTCT
                                  C  A    _
GAM129  ITPR1    3'  TTCTGAAAGAGCCACATT    9443       AA   AGCT
                                AATGT  CTCT   TTCAGAA
                                |||||  ||||   |||||||
                                TTACA  GAGA   AAGTCTT
                                  CC   _____
GAM129  LPIN1    5'  TCTGAAAGCTAAGGTAAC    67395    A  TC
                                GT AC  TAGCTTTCAGA
                                || ||  ||||||||||
                                CA TG  ATCGAAAGTCT
                                 A  GA
GAM129  PLN      3'  TCTGAGCTAGAGTTAC      10649         TT
                                GTAACTCTAGC  TCAGA
                                ||||||||||  |||||
                                CATTGAGATCG  AGTCT
                                     __
GAM129  SSPN     3'  TTCTGAAAGCCAAGCACCACA  17448     AACT  A_
                                TGT   CT  GCTTTCAGAA
                                |||   ||  ||||||||||
                                ACA   GA  CGAAAGTCTT
                                  CCAC  AC
GAM129  TRO      3'  TTTGGTATCAGAGTTACATTA  32390          AGCTT
                                TAATGTAACTCT    TCAGA
                                ||||||||||||    |||||
                                ATTACATTGAGA    GGTTT
                                       CTAT_
GAM129  WDR1     3'  TTCTGAAAGCTTTAGACA    33984     AA  CT
                                TGT  CT  AGCTTTCAGAA
                                |||  ||  ||||||||||
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                              ACA  GA  TCGAAAGTCTT
                                __  TT
GAM129  ZNF195   3' TTCTGAAAAAAATGTTACA   23120       TCTAGC
                              TGTAAC     TTTCAGAA
                              ||||||     ||||||||
                              ACATTG     AAAGTCTT
                                 TAAAA_
GAM129  ATP10B   3' TCTGAAAGCTGTAACA      63370     A  TCT
                              TGT AC   AGCTTTCAGA
                              ||| ||   ||||||||||
                              ACA TG   TCGAAAGTCT
                                A ___
GAM129  FLJ10052 3' TCTGAAAGCATGTCACAT    35774     A  TCTA
                              ATGT AC    GCTTTCAGA
                              |||| ||    |||||||||
                              TACA TG    CGAAAGTCT
                                C  TA__
GAM129  FLJ12903 3' CTGAAAGCCAGCATTA      42772      TAACT  A
                              TAATG    CT GCTTTCAG
                              ||||||    || ||||||||
                              ATTAC    GA CGAAAGTC
                                 _____ C
GAM129  HYA22    3' TTTCCAAAAGCTGGATACA   19434     AC       CA
                              TGTA  TCTAGCTTT  GAAA
                              ||||  |||||||||  ||||
                              ACAT  AGGTCGAAA  CTTT
                                __       AC
GAM129  KIAA0016 3' CTGAAACATAGTTACAT     28645       CTAGC
                              ATGTAACT    TTTCAG
                              ||||||||    ||||||
                              TACATTGA    AAAGTC
                                 TAC__
GAM129  KIAA0268 3' TTTCTGAGAGTGAGTTTACATT 70008        _  TA
           A                   TAATGTAA CTC  GCTTTCAGAAA
                              ||||||||  |||  ||||||||||
                              ATTACATT GAG  TGAGAGTCTTT
                                 T  __
GAM129  KIAA0438 3' TTCCCAAATGCAGAGTTACAT  29076         A  _  CA
                              ATGTAACTCT GC TTT  GAA
                              |||||||||| || |||  |||
                              TACATTGAGA CG AAA  CTT
                                    _ T  CC
GAM129  KIAA0678 3' TTCTGAAAGCTCACAGT     66852     CT_
                              ACT   AGCTTTCAGAA
                              |||   ||||||||||
                              TGA   TCGAAAGTCTT
                                CAC
GAM129  KIAA1374 3' TTCTGAAAATGGTACATTA   61244       ACT   GC
                              TAATGTA   CTA  TTTCAGAA
                              |||||||   |||  ||||||||
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                                ATTACAT  GGT  AAAGTCTT
                                   ___  A_
GAM129  MBD2     3'  TGAAAACTAGCATTACATTA  31719       CT   C
                                TAATGTAA  CTAG TTTCA
                                ||||||||  |||| |||||
                                ATTACATT  GATC AAAGT
                                    AC   A
GAM129  SENP2    3'  TTTCTGAAAGGAATGTTAC   76346     TCTAG
                                GTAAC    CTTTCAGAAA
                                |||||    ||||||||||
                                CATTG    GAAAGTCTTT
                                  TAAG_
GAM129  ZFP91    3'  TTTCTGAAAGAGGCTTAC    53822     CT  AG
                                GTAA  CT  CTTTCAGAAA
                                ||||  ||  ||||||||||
                                CATT  GA  GAAAGTCTTT
                                  CG  __
GAM129  LOC129868 5'  TTCCGAAAGCTACCAGCA    57130     AACTC      A
                                TGT    TAGCTTTC GAA
                                |||    |||||||| |||
                                ACG    ATCGAAAG CTT
                                  ACC__       C
GAM129  LOC130633 5'  TTCCGAAAGCTACCAGCA    74966     AACTC      A
                                TGT    TAGCTTTC GAA
                                |||    |||||||| |||
                                ACG    ATCGAAAG CTT
                                  ACC__       C
GAM129  LOC146485 5'  CTGTGCTGAGTTACA      59787       T   TTT
                                TGTAACTC AGC   CAG
                                |||||||| |||   |||
                                ACATTGAG TCG   GTC
                                    _   T__
GAM129  LOC168576 5'  TCTGAAAGCCCACGGTCACA  82719     A   CTA_
                                TGT ACT    GCTTTCAGA
                                ||| |||    |||||||||
                                ACA TGG    CGAAAGTCT
                                  C   CACC
GAM129  LOC200107 3'  TTTGAGACAGAGTCACATTA  88580       A    AGC
                                TAATGT ACTCT   TTTCAGA
                                |||||| |||||   |||||||
                                ATTACA TGAGA   AGAGTTT
                                   C    C__
GAM129  LOC51320  3'  TTGAAGAGTTACATT      33548          AGCTT
                                AATGTAACTCT    TCAG
                                ||||||||||||    ||||
                                TTACATTGAGA    AGTT
                                      _____
GAM129  LOC51762  3'  TCTGAAAGCACAGGTCAC    33271    A   CTA
                                GT ACT   GCTTTCAGA
                                || |||   |||||||||
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                                CA TGG   CGAAAGTCT
                                 C   ACA
GAM130  LDLR     3'  CTACCCACTTCCATTCC     4984       C_  C
                                GGAA  GA AGTGGGTAG
                                ||||  || |||||||||
                                CCTT  CT TCACCCATC
                                  AC  _
GAM130  FLJ14824 3'  AAATTATTCCCCCTATCATTCC 51637      C  C  T   TA
                                GGAA GA AG GGG  GATGATTT
                                |||| || || |||  ||||||||
                                CCTT CT TC CCC  TTATTAAA
                                  A  A  _   C_
GAM130  HAK      3'  TCTTCCCACTGTCATTCC    53642      C        T
                                GGAA GACAGTGGG AGA
                                |||| ||||||||| |||
                                CCTT CTGTCACCC TCT
                                  A        T
GAM130  KIAA1813 3'  CTACCCACTTCATTCC      70296      C  C
                                GGAA GA AGTGGGTAG
                                |||| || |||||||||
                                CCTT CT TCACCCATC
                                  A  _
GAM130  LOC152359 5'  TCTACCCAGTGTCGTCC     85705     A    G
                                GGA CGACA TGGGTAGA
                                ||| ||||| ||||||||
                                CCT GCTGT ACCCATCT
                                  _    G
GAM130  LOC201283 3'  AAATCATCTAAGAAATCGTTC  60411       CAGTGGG
                                GAACGA      TAGATGATTT
                                ||||||      ||||||||||
                                CTTGCT      ATCTACTAAA
                                   AAAGA__
GAM131  CNGA1    3'  CAACTGATAATGTGCAAA    59507          GC   A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                      A_  _
GAM131  ESRRG    3'  TGGCAGTCTTATGTGCAAA   66396         TAGCT
                                TTTGCACAT    AGATTGCCA
                                |||||||||    |||||||||
                                AAACGTGTA    TCTGACGGT
                                     T_____
GAM131  KCNJ3    3'  GCAATAATGTGCAAA       9525           GCTAGA
                                TTTGCACATTA     TTGC
                                ||||||||||     ||||
                                AAACGTGTAAT     AACG
                                                _______
GAM131  SDC2     3'  GCAAATTAATGTGTAAA     67132           CTAGA
                                TTTGCACATTAG    TTGC
                                ||||||||||||    ||||
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                                AAATGTGTAATT    AACG
                                      A____
GAM131  USP9X    3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
              A                  TTTGCACATTAGC     GCCAT
                                 ||||||||||||     |||||
                                 AAATGTGTAATCG     CGGTA
                                       TAGTC_
GAM131  AMOTL1   3'  GGCAAGTAATGTGCAAA    73650         G  AGAT
                                 TTTGCACATTA CT    TGCC
                                 |||||||||| ||    ||||
                                 AAACGTGTAAT GA    ACGG
                                      _ ____
GAM131  BCAR3    3'  AGTAATAATGTGCAAA     13098         __
                                 TTTGCACATTA  GCT
                                 ||||||||||  |||
                                 AAACGTGTAAT  TGA
                                       AA
GAM131  DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930        AGCTA    C
                                 TTTGCACATT    GATTG CA
                                 |||||||||     ||||| ||
                                 AGACGTGTAA    TTAAC GT
                                      A____    A
GAM131  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                 TTTGCACATTAG  AGA TG CAT
                                 ||||||||||||  ||| || |||
                                 AGACGTGTAATC  TTT AC GTA
                                       __  T  A
GAM131  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
              AA                   TTTGCACATTAGCTAGATTGCCAT
                                   ||||||||||||||||||||||||
                                   AAACGTGTAATCGATCTAACGGTA

GAM132  CNGA1    3'  CAACTGATAATGTGCAAA    59507         GC   A
                                 TTTGCACATTA  TAG TTG
                                 ||||||||||  ||| |||
                                 AAACGTGTAAT  GTC AAC
                                      A_  _
GAM132  ESRRG    3'  TGGCAGTCTTATGTGCAAA   66396        TAGCT
                                 TTTGCACAT    AGATTGCCA
                                 |||||||||    |||||||||
                                 AAACGTGTA    TCTGACGGT
                                      T____
GAM132  KCNJ3    3'  GCAATAATGTGCAAA      9525          GCTAGA
                                 TTTGCACATTA     TTGC
                                 ||||||||||     ||||
                                 AAACGTGTAAT     AACG
                                      _______
GAM132  SDC2     3'  GCAAATTAATGTGTAAA     67132          CTAGA
                                 TTTGCACATTAG    TTGC
                                 ||||||||||||    ||||
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                                AAATGTGTAATT    AACG
                                      A____
GAM132  USP9X    3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
              A                  TTTGCACATTAGC     GCCAT
                                 ||||||||||||     |||||
                                 AAATGTGTAATCG     CGGTA
                                       TAGTC_
GAM132  AMOTL1   3'  GGCAAGTAATGTGCAAA    73650         G  AGAT
                                 TTTGCACATTA CT    TGCC
                                 |||||||||| ||    ||||
                                 AAACGTGTAAT GA    ACGG
                                      _ ____
GAM132  BCAR3    3'  AGTAATAATGTGCAAA     13098         __
                                 TTTGCACATTA  GCT
                                 ||||||||||  |||
                                 AAACGTGTAAT  TGA
                                       AA
GAM132  DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930        AGCTA    C
                                 TTTGCACATT    GATTG CA
                                 |||||||||    ||||| ||
                                 AGACGTGTAA    TTAAC GT
                                      A____    A
GAM132  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                 TTTGCACATTAG  AGA TG CAT
                                 ||||||||||||  ||| || |||
                                 AGACGTGTAATC  TTT AC GTA
                                       __  T  A
GAM132  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
              AA                   TTTGCACATTAGCTAGATTGCCAT
                                   ||||||||||||||||||||||||
                                   AAACGTGTAATCGATCTAACGGTA

GAM133  B4GALT1  3'  CAAGAGTCAGAACTGTAGA   7666        GTCAA  TG
                                 TCTACAGT    TG  TCTTG
                                 ||||||||    ||  |||||
                                 AGATGTCA    AC  AGAAC
                                      AG___  TG
GAM133  DGKA     3'  CAAAACACATACATTG      7201        CA     C
                                 CAGTGT  ATGTGT TTG
                                 ||||||  |||||| |||
                                 GTTACA  TACACA AAC
                                      __     A
GAM133  MTMR6    3'  CTCAAAACACAATTTGCACTGT 93549        C  _   C
              A                   TACAGTGT AAT GTGT TTGAG
                                  |||||||| ||| |||| |||||
                                  ATGTCACG TTA CACA AACTC
                                       T  A   A
GAM133  SLC4A4   3'  CTCAAGACACAGACACCCACAG 13635     ACA_    AA
              A                   TCT   GTGTC  TGTGTCTTGAG
                                  |||   |||||  ||||||||||
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                                AGA   CACAG  ACACAGAACTC
                                  CACC    __
GAM133  CUL4A    3'  CTCAAGACTTCAACCTGCAGA  13153     A   T  CAA  T_
                                TCT CAG GT   TG  GTCTTGAG
                                ||| ||| ||   ||  ||||||||
                                AGA GTC CA   AC  CAGAACTC
                                  C   _ ___  TT
GAM133  FLJ11301 3'  CAAGACACTAGCACTGTAGA   37226         CAAT
                                TCTACAGTGT   GTGTCTTG
                                ||||||||||   ||||||||
                                AGATGTCACG   CACAGAAC
                                      AT__
GAM133  GPR105   3'  GACACACCCACACCGTAGA   29655      A   CAA
                                TCTAC GTGT   TGTGTC
                                ||||| ||||   ||||||
                                AGATG CACA   ACACAG
                                   C   CCC
GAM133  LAP1B    5'  CTCAAGACACACCATGGGC   64584     AA___
                                GTC    TGTGTCTTGAG
                                |||    ||||||||||
                                CGG    ACACAGAACTC
                                  GTACC
GAM133  PRDM10   3'  CTCAAGACACATTGACACTGTA 39578
                GA                TCTACAGTGTCAATGTGTCTTGAG
                                ||||||||||||||||||||||
                                AGATGTCACAGTTACACAGAACTC

GAM133  SEMA3C   3'  CTCTTCTACATTGACAC     21061          TCTT
                                GTGTCAATGTG    GAG
                                ||||||||||    |||
                                CACAGTTACAT    CTC
                                      CTT_
GAM133  LOC255654 3'  GACATCCACACTGTAGA     96887         CAAT
                                TCTACAGTGT    GTGTC
                                ||||||||||    |||||
                                AGATGTCACA    TACAG
                                      CC__
GAM133  LOC96652  3'  CTCAAGACAGGACACTGCGGA  65467    TA     AATG
                                TC  CAGTGTC   TGTCTTGAG
                                ||  |||||||   |||||||||
                                AG  GTCACAG   ACAGAACTC
                                  GC      G___
GAM134  CCR2     3'  CAATCTCTGATTCTGTCA    5386         CG   GG
                                TGACAGAA  AGAG  TG
                                ||||||||  ||||  ||
                                ACTGTCTT  TCTC  AC
                                     AG   TA
GAM134  CYP51    5'  AGCTTCTCTCGTTCCGTC    5779     A        T
                                GAC GAACGAGAGGG GCT
                                ||| |||||||||| |||
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                                CTG CTTGCTCTCTT CGA
                                  C         _
GAM134  GABRP    3'  TCAGAGAGTCGCTGTCATTCTG 26402         C  G  _  TG
                TCA                    TGACAGAA GA AG GG  CTCTGA
                                |||||||| || || ||  ||||||
                                ACTGTCTT CT TC CT  GAGACT
                                    A  G  G  GA
GAM134  GMPS     5'  GGCACCCTCCCGCCCCGTC   13918     AGAA  A
                                GAC    CG GAGGGTGCT
                                |||    || |||||||||
                                CTG    GC CTCCCACGG
                                  CCCC  C
GAM134  LIMD1    3'  GGGGACCCTCTCTTCCCATCA  26463     CA_  C       G
                                TGA   GAA GAGAGGGT CTC
                                |||   ||| |||||||| |||
                                ACT   CTT CTCTCCCA GGG
                                  ACC   _       G
GAM134  OCRL     3'  CACTCCCCTCGTTCTGTCA   4259           A  _
                                TGACAGAACGAG GG GTG
                                |||||||||||| || |||
                                ACTGTCTTGCTC CC CAC
                                      C  T
GAM134  OCRL     3'  CACTCCCCTCGTTCTGTCA   7825           A  _
                                TGACAGAACGAG GG GTG
                                |||||||||||| || |||
                                ACTGTCTTGCTC CC CAC
                                      C  T
GAM134  PYGO2    3'  GCTCCCTCTCGCTCTCTCA   63987     C   A       T
                                TGA AGA CGAGAGGG GC
                                ||| ||| |||||||| ||
                                ACT TCT GCTCTCCC CG
                                  C   C       T
GAM134  TCFL4    3'  TCAAAATCACCCTTTCTGTCA  63465        ACGA      CTC_
                                TGACAGA    GAGGGTG    TGA
                                |||||||    |||||||    |||
                                ACTGTCT    TTCCCAC    ACT
                                    _____      TAAA
GAM134  BIRC1    3'  CAGTCTCTCCCATTCTGT    15787       C__     G
                                ACAGAA   GAGAGG TG
                                ||||||   |||||| ||
                                TGTCTT   CTCTCT AC
                                   ACC     G
GAM134  CHERP    3'  AGCGCCTTCCACTCCATCA   21096     CA  ACGA
                                TGA  GA    GAGGGTGCT
                                |||  ||    |||||||||
                                ACT  CT    CTTCCGCGA
                                  AC  CAC_
GAM134  DKFZP564K2062 3'  TCAGAAGTCTCAGTTCTGTCA  31238         GA    GTGC
                                TGACAGAAC  GAGG    TCTGA
                                |||||||||  ||||    |||||
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                                ACTGTCTTG CTCT   AGACT
                                     A_   GA__
GAM134  FLJ10482  3'  TCAGAGTGATCTGTCCTGCCA 36165   A  AAC  G  GG
                                TG CAG   GA AG  TGCTCTGA
                                || |||   || ||  ||||||||
                                AC GTC   CT TC  GTGAGACT
                                 C   ___  G  TA
GAM134  FLJ13848  3'  CAGAAGGACTTCTCGTTCCTCA 45461    CA       GTGC
                                TGA  GAACGAGAGG   TCTG
                                |||  ||||||||||   ||||
                                ACT  CTTGCTCTTC   AGAC
                                  C_       AGGA
GAM134  FLJ21802  3'  CAGAGCACCAACTTCATC    44980    AC   AG
                                GA  GAG  GGTGCTCTG
                                ||  |||  |||||||||
                                CT  TTC  CCACGAGAC
                                 AC   AA
GAM134  KIAA1458  3'  CAGGACCTCCATTCTGTCA   69002       CGA   GTGC
                                TGACAGAA   GAGG   TCTG
                                ||||||||   ||||   ||||
                                ACTGTCTT   CTCC   GGAC
                                     AC_   A___
GAM134  MGC10500  3'  GTCCCCCTCGTTCTGT     48935        A   TG
                                ACAGAACGAG GGG  C
                                |||||||||| |||  |
                                TGTCTTGCTC CCC  G
                                      _  CT
GAM134  NDP52     3'  CATCCTCTCACCTGTCA     19526       AAC
                                TGACAG   GAGAGGGTG
                                ||||||   |||||||||
                                ACTGTC   CTCTCCTAC
                                   CA_
GAM134  SEC24C    3'  TCAAGTATCCTGCCACTCTGTC 17000       ACGAG      C
           A                     TGACAGA    AGGGTGCT TGA
                                |||||||    |||||||| |||
                                ACTGTCT    TCCTATGA ACT
                                    CACCG      _
GAM134  SNRPD3    5'  CAGAGCCGAACTCTCTTCCTGC 14800    A  AAC      ___
           CA                     TG CAG   GAGAGGGT   GCTCTG
                                || |||   ||||||||   ||||||
                                AC GTC   TTCTCTCA   CGAGAC
                                 C  C__       AGC
GAM134  LOC152328 3'  CAAGTGCCCTCCCCTATCA   80523    C  AACGA    TG  C
                                TGA AG    GAGGG  CT TG
                                ||| ||    |||||  || ||
                                ACT TC    CTCCC  GA AC
                                  A  CC___    GT  _
GAM134  LOC158835 3'  CATCCCTCTCATTCCATC    82009    CA   C     _
                                GA  GAA GAGAGGG TG
                                ||  ||| ||||||| ||
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                                CT  CTT CTCTCCC AC
                                 AC   A      T
GAM134  LOC197003 3'  CAGACCTTCTCACACTGCCA  87871    A   AAC      TGC
                                TG CAG   GAGAGGG   TCTG
                                || |||   |||||||   ||||
                                AC GTC   CTCTTCC   AGAC
                                 C   ACA      ___
GAM134  LOC257443 3'  CAGGACCTCCATTCTGTCA   95846        CGA    GTGC
                                TGACAGAA   GAGG   TCTG
                                ||||||||   ||||   ||||
                                ACTGTCTT   CTCC   GGAC
                                     AC_   A___
GAM134  LOC257451 3'  GCTCCCTCTCGCTCTCTCA   95557     C   A       T
                                TGA AGA CGAGAGGG GC
                                ||| ||| |||||||| ||
                                ACT TCT GCTCTCCC CG
                                  C   C       T
GAM134  LOC92609  5'  CAAAGTCTCTCGTTC       72844         GGT   C
                                GAACGAGAG   GCT TG
                                |||||||||   ||| ||
                                CTTGCTCTC   TGA AC
                                     ___   A
GAM135  ACP2     3'  AGAAAGTTCTAGACTG      7851       GC  TC
                                CAGT  CT  AGAACTTTCT
                                ||||  ||  ||||||||||
                                GTCA  GA  TCTTGAAAGA
                                   __  __
GAM135  APTX     5'  AAGAGAAAGAGATCAGGCA   34655       TCAGAA
                                TGCCT     CTTTCTCTT
                                |||||     |||||||||
                                ACGGA     GAAAGAGAA
                                   CTAGA_
GAM135  BCL7A    3'  AGGCTGTCTCCTTAAGGCACTG 40637          C  A__  TT
                                CAGTGCCTT AG   AC  TCT
                                ||||||||| ||   ||  |||
                                GTCACGGAA TC   TG  GGA
                                      T  CTC  TC
GAM135  CLC      3'  AAGAGAAAATACTGAAAGCACA 25105    A    C     AAC
             GG                   CC GTGC TTCAG   TTTCTCTT
                                || |||| |||||   ||||||||
                                GG CACG AAGTC   AAAGAGAA
                                 A    A     ATA
GAM135  CNK      3'  AAGCCCTGAAGGCCTG      14517     T       AA
                                CAG GCCTTCAG  CTT
                                ||| ||||||||  |||
                                GTC CGGAAGTC  GAA
                                  _       CC
GAM135  COL4A3   3'  AAGTGCAGGTTCTGAGGGCACC 48549    A           TCT
             GG                   CC GTGCCTTCAGAACTT   CTT
                                || ||||||||||||||   |||
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                                GG CACGGGAGTCTTGGA   GAA
                                 C            CGT
GAM135  CSPG4    3'  AAGAGAGACCTGGAGACAC    8570     C     AAC
                                GTG CTTCAG   TTTCTCTT
                                ||| ||||||   ||||||||
                                CAC GAGGTC   AGAGAGAA
                                  A     C__
GAM135  CYP1B1   3'  AAGAGAAAAGAGAGAAACACTG 3651       CC   AGAAC
                                CAGTG  TTC    TTTCTCTT
                                |||||  |||    ||||||||
                                GTCAC  AAG    AAAGAGAA
                                   A_   AGAGA
GAM135  DLG3     3'  AAGAGAAAAGAGGAGGACTG   40880     G    AGAAC
                                CAGT CCTTC    TTTCTCTT
                                |||| |||||    ||||||||
                                GTCA GGAGG    AAAGAGAA
                                  _    AGA__
GAM135  DLG5     5'  AGGCAGACTCTGAAGGC     82909         A_  T
                                GCCTTCAGA  CT TCT
                                |||||||||  || |||
                                CGGAAGTCT  GA GGA
                                     CA  C
GAM135  FLT1     3'  AAGAGAAACCGGGAGAAGGCAT 8910         AGAAC_
                                GTGCCTTC     TTTCTCTT
                                ||||||||     ||||||||
                                TACGGAAG     AAAGAGAA
                                    AGGGCC
GAM135  GRB10    3'  AGAGAAAATGGCACCTGG    17971     _   TTCAGAAC
                                CCAG TGCC       TTTCTCT
                                |||| ||||       |||||||
                                GGTC ACGG       AAAGAGA
                                  C   TA_______
GAM135  LFG      3'  AAGAGAAAAGGAGCCAAGAACT 76711      GC   CAGAA   _
           GG                   CCAGT  CTT    CTTT CTCTT
                                |||||  |||    |||| |||||
                                GGTCA  GAA    GAAA GAGAA
                                  A_   CCGAG   A
GAM135  MAN2A2   3'  AAGAGAAAGTTCATTCAC    20391     CCTTCA
                                GTG     GAACTTTCTCTT
                                |||     ||||||||||||
                                CAC     CTTGAAAGAGAA
                                  TTA___
GAM135  NLGN3    3'  AAGAAAAGTTCTTAAAACACT  38596     CC  C       C
                                AGTG  TT AGAACTTT TCTT
                                ||||  || |||||||| ||||
                                TCAC  AA TCTTGAAA AGAA
                                  AA  T       _
GAM135  NPAS1    5'  AAGGTCTCCCGAGGGCACT    59879         A_  _
                                AGTGCCTTC  GA ACTTT
                                |||||||||  || |||||
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                                TCACGGGAG  CT TGGAA
                                     CC  C
GAM135  PLAG1    3'  AGTGTGTTCCAAAGGCATT   10605        CA   TTT
                                AGTGCCTT  GAAC   CT
                                ||||||||  ||||   ||
                                TTACGGAA  CTTG   GA
                                    AC    TGT
GAM135  PLXNA1   3'  AGAAAATGAAGGCAGTGG    72309     G       GAAC
                                CCA TGCCTTCA    TTTCT
                                ||| ||||||||    |||||
                                GGT ACGGAAGT    AAAGA
                                  G       A___
GAM135  PPP4R1   3'  AAGAGAAAGTACAGTAAACACT 17620      CCTTCAGA
                                AGTG       ACTTTCTCTT
                                ||||       ||||||||||
                                TCAC       TGAAAGAGAA
                                  AAATGACA
GAM135  ACYP2    3'  AAGAGAAAAATTGTAACACACT 56612      CC  _   AAC
             G                   CAGTG  TT CAG   TTTCTCTT
                                 |||||  || |||   ||||||||
                                 GTCAC  AA GTT   AAAGAGAA
                                   AC  T   AA_
GAM135  B3GNT6   3'  AGAAATCAGATGAAGGCAT    22503         GAAC_
                                GTGCCTTCA     TTTCT
                                |||||||||     |||||
                                TACGGAAGT     AAAGA
                                     AGACT
GAM135  BAG5     3'  AAGAGAAGGGATAAAGGAC    16835    G    CAGAA
                                GT CCTT     CTTTCTCTT
                                || ||||     |||||||||
                                CA GGAA     GGAAGAGAA
                                 _    ATAG_
GAM135  BIVM     3'  AAGAGAAAAGACTCAAGAAACT 34665      GC   C  AAC
             G                   CAGT  CTT AG   TTTCTCTT
                                 ||||  ||| ||   ||||||||
                                 GTCA  GAA TC   AAAGAGAA
                                   AA   C  AGA
GAM135  C15orf5  3'  AGAGAAAAGAAAGCAC      48195      C   AGAAC
                                GTGC TTC     TTTCTCT
                                |||| |||     |||||||
                                CACG AAG     AAAGAGA
                                  A   A_____
GAM135  C20orf80 5'  AAGAGAAGAAGATGAAGAAAC  65282    GC     GAAC
                                GT  CTTCA    TTTCTCTT
                                ||  |||||    ||||||||
                                CA  GAAGT    GAAGAGAA
                                 AA     AGAA
GAM135  CLSTN1   3'  AGTTCTGAGGACACTGG     30103        C
                                CCAGTG CTTCAGAACT
                                |||||| ||||||||||
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                                GGTCAC GGAGTCTTGA
                                   A
GAM135  DKFZP434P0111 3'  AAGAGAAAGTTTCTGCAC    67368      CTTCA
                                GTGC    GAACTTTCTCTT
                                ||||    ||||||||||||
                                CACG    TTTGAAAGAGAA
                                  TC___
GAM135  DORFIN   5'  AGAATTCTCTGAAGGAAC    31257    G       ACT
                                GT CCTTCAGA   TTCT
                                || ||||||||   ||||
                                CA GGAAGTCT   AAGA
                                 A       CTT
GAM135  FLJ10300 5'  AAGAGAAAGATGAAGACTCTG  35997     TGC     GAA
                                CAG   CTTCA   CTTTCTCTT
                                |||   |||||   |||||||||
                                GTC   GAAGT   GAAAGAGAA
                                  TCA    A__
GAM135  FLJ20373  3'  AAGAGAAGAAGGAAAGGCACAG 35070    A      _ AGAAC
           G                     CC GTGCCTT C     TTTCTCTT
                                || |||||||  |     ||||||||
                                GG CACGGAA G     GAAGAGAA
                                 A      A GAA__
GAM135  FLJ23511  5'  AGAGAAAAACAAGGCAT     49956        CAGAAC
                                GTGCCTT     TTTCTCT
                                |||||||     |||||||
                                TACGGAA     AAAGAGA
                                    CAA___
GAM135  FLJ30681  3'  AGAGAAGAAAGACCACTGG    91782       CCT  AGAAC
                                CCAGTG   TC    TTTCTCT
                                ||||||   ||    |||||||
                                GGTCAC   AG    GAAGAGA
                                   C__  AAA__
GAM135  HDAC11    3'  GAGCTATAGGCACTGG      45717         TC  AACTTT
                                CCAGTGCCT  AG     CTC
                                |||||||||  ||     |||
                                GGTCACGGA  TC     GAG
                                     TA  _______
GAM135  IKKE     5'  AGTGAGCCCTGAAAGCTCTGG  25745      T  C    AA   T
                                CCAG GC TTCAG  CTT CT
                                |||| || |||||  ||| ||
                                GGTC CG AAGTC  GAG GA
                                  T  A    CC   T
GAM135  KIAA0680  3'  AGAGAAAATTGAAGCAT     28232      C     AAC
                                GTGC TTCAG   TTTCTCT
                                |||| |||||   |||||||
                                TACG AAGTT   AAAGAGA
                                  _     A__
GAM135  KIAA1228  3'  AGGGGGTGATTCTGAGGCACTG 65035         T    ___   TT
                                CAGTGCCT CAGA   ACT  CT
                                |||||||| ||||   |||  ||
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                                GTCACGGA GTCT   TGG  GA
                                     _   TAG   GG
GAM135  KIAA1300  5'  AGGAACCCTGAAGGCA     62860         AAC
                                TGCCTTCAG   TTTCT
                                |||||||||   |||||
                                ACGGAAGTC   AAGGA
                                     CC_
GAM135  KIAA1805  3'  AAGAGAAAGTAGAAGCAGCA   79966     __    AGA
                                TGC  CTTC   ACTTTCTCTT
                                |||  ||||   ||||||||||
                                ACG  GAAG   TGAAAGAGAA
                                  AC    A__
GAM135  LENG1     5'  AAGAGAAAGCTCTGGGCATCCT 84074     __    TT    A
          G                      CAG  TGCC  CAGA CTTTCTCTT
                                |||  ||||  |||| |||||||||
                                GTC  ACGG  GTCT GAAAGAGAA
                                  CT    __    C
GAM135  LHX6      3'  AAGAGAAAACTCTGGGGTCA   26854    C      AC
                                TG CTTCAGA  TTTCTCTT
                                || |||||||  ||||||||
                                AC GGGGTCT  AAAGAGAA
                                 T      CA
GAM135  N4BP3     3'  AGCTCCAGAAGGCACTGG     66250          A_  A
                                CCAGTGCCTTC  GA CT
                                ||||||||||  || ||
                                GGTCACGGAAG  CT GA
                                       AC  C
GAM135  NASP      3'  AGAGGGTGAAGAAACTG     67966      GC    AGA
                                CAGT  CTTC   ACTTTCT
                                ||||  ||||   |||||||
                                GTCA  GAAG   TGGGAGA
                                  AA    ___
GAM135  SMARCF1   3'  AAAATTCTGAAGGAC       57480    G       C
                                GT CCTTCAGAA TTT
                                || |||||||| |||
                                CA GGAAGTCTT AAA
                                 _       A
GAM135  SMARCF1   3'  AAAATTCTGAAGGAC       37430    G       C
                                GT CCTTCAGAA TTT
                                || |||||||| |||
                                CA GGAAGTCTT AAA
                                 _       A
GAM135  SMARCF1   3'  AAAATTCTGAAGGAC       20034    G       C
                                GT CCTTCAGAA TTT
                                || |||||||| |||
                                CA GGAAGTCTT AAA
                                 _       A
GAM135  TED       3'  AAGAGAAAGTCCAGGGACTGG  31630      G   TCA  A
                                CCAGT CCT   GA CTTTCTCTT
                                ||||| |||   || |||||||||
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                                GGTCA GGA   CT GAAAGAGAA
                                   G   C__ _
GAM135  TGIF2     3'  AGAAGGGTGCTGAAGGC     41447         AA_
                                GCCTTCAG   CTTTCT
                                ||||||||   ||||||
                                CGGAAGTC   GGAAGA
                                    GTG
GAM135  WBSCR20A  3'  AAGAGAAAGAAGAGACAGCA   35958     CT  AGAA
                                TGC  TC    CTTTCTCTT
                                |||  ||    |||||||||
                                ACG  AG    GAAAGAGAA
                                  AC  AGAA
GAM135  LOC115273 3'  AGAAAGTTCTGATGGCCAGG   73356     AGT   T
                                CC   GCC TCAGAACTTTCT
                                ||   ||| ||||||||||||
                                GG   CGG AGTCTTGAAAGA
                                  AC_   T
GAM135  LOC145761 5'  AAGAGAAAGTGGAAGGCATGG  83472     G      AGA
                                CCA TGCCTTC   ACTTTCTCTT
                                ||| |||||||   ||||||||||
                                GGT ACGGAAG   TGAAAGAGAA
                                  _     G__
GAM135  LOC146179 5'  AGAAAGTTTTGGGCCT      77700     T   TT
                                AG GCC  CAGAACTTTCT
                                || |||  ||||||||||
                                TC CGG  GTTTTGAAAGA
                                  _  __
GAM135  LOC147072 3'  AAGAGAAAGTGAGAAGAAACTG 60407      GC    AGA
                                CAGT  CTTC   ACTTTCTCTT
                                ||||  ||||   ||||||||||
                                GTCA  GAAG   TGAAAGAGAA
                                   AA    AG_
GAM135  LOC148758 5'  AGAAAGTTCTGAGAAAC     78962     GCC
                                GT   TTCAGAACTTTCT
                                ||   ||||||||||||
                                CA   GAGTCTTGAAAGA
                                  AA_
GAM135  LOC148932 3'  AGGAATCTGAAGGCACTGG    79103            AC
                                CCAGTGCCTTCAGA  TTTCT
                                ||||||||||||||  |||||
                                GGTCACGGAAGTCT  AAGGA
                                                __
GAM135  LOC149386 5'  AAGTTTTGAAAGCACT      84400       C
                                AGTGC TTCAGAACTT
                                ||||| ||||||||||
                                TCACG AAGTTTTGAA
                                   A
GAM135  LOC150139 3'  AGAAAATAGAAAAAGGCGCTGG 79583          CAGAAC_
                                CCAGTGCCTT       TTTCT
                                ||||||||||       |||||
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                                GGTCGCGGAA      AAAGA
                                      AAAGATA
GAM135  LOC152756 3'  AAGATGCAGTTCTGAAAACCTG 85871     TGCC       TTC
                                CAG    TTCAGAACT   TCTT
                                |||    |||||||||   ||||
                                GTC    AAGTCTTGA   AGAA
                                  CAA_        CGT
GAM135  LOC162333 5'  AAGAGAAAGCGATGACACTG   87114      CCT   GAA
                                CAGTG   TCA   CTTTCTCTT
                                |||||   |||   |||||||||
                                GTCAC   AGT   GAAAGAGAA
                                   ___   AGC
GAM135  LOC199221 3'  AAGAGAAGCTCGAAAGCATGG  80347     G   C   A A   T
                                CCA TGC TTC GA CTT CTCTT
                                ||| ||| ||| || ||| |||||
                                GGT ACG AAG CT GAA GAGAA
                                  _   A   _ C   _
GAM135  LOC203339 3'  AGAGAAAATTGGGCCTG     90542     T   TCAGAAC
                                CAG GCCT      TTTCTCT
                                ||| ||||      |||||||
                                GTC CGGG      AAAGAGA
                                  _    TTA____
GAM135  LOC255017 3'  AGAAAGAGGAACTGG       94624       G   TCAGAA
                                CCAGT CCT     CTTTCT
                                ||||| |||     ||||||
                                GGTCA GGA     GAAAGA
                                   A  _______
GAM135  LOC256021 3'  AAGAGAAACAAAGACAACACTG 96512       CCT  AGAAC
            G                    CCAGTG   TC    TTTCTCTT
                                ||||||  ||    ||||||||
                                GGTCAC   AG    AAAGAGAA
                                   AAC  AAAC_
GAM135  LOC90139  3'  AGAATCCCGAAGGCAT      55396        A_  ACT
                                GTGCCTTC  GA   TTCT
                                ||||||||  ||   ||||
                                TACGGAAG  CT   AAGA
                                     CC  ___
GAM136  AQP3     3'  TTCACGATCCACCCTTTC     59593      T_   _
                                GAAA  GTGG TCGTGAA
                                ||||  |||| |||||||
                                CTTT  CACC AGCACTT
                                  CC    T
GAM136  ARSB     3'  TCACGACTCTTGTC        3502         AATGTG
                                GACAAGA     GTCGTGA
                                |||||||     |||||||
                                CTGTTCT     CAGCACT
                                          _______
GAM136  B4GALT5   3'  TTTTCACAAAAATAGTCCTTTG 16519        AAA_   GGTC
            TCA                    TGACAAG    TGT    GTGAAAA
                                |||||||    |||    |||||||
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                                ACTGTTT   ATA   CACTTTT
                                    CCTG  AAAA
GAM136  CHRNA3   3'  TCGTTACCCATTTCTT     5610        T  CG
                                AAGAAATG GGT  TGA
                                |||||||| |||  |||
                                TTCTTTAC CCA  GCT
                                     _  TT
GAM136  DRD1     3'  TTACAACCACATTTCTGGCCA  5840     ACA        C
                                TG  AGAAATGTGGT GTGA
                                ||  |||||||||||| ||||
                                AC  TCTTTACACCA CATT
                                 CGG         A
GAM136  FUT1     3'  TCTGATCACATCCCCTGTC   3798      AGAA       T
                                GACA   ATGTGGTCG GA
                                ||||   ||||||||| ||
                                CTGT   TACACTAGT CT
                                  CCCC       _
GAM136  IRF1     3'  GCCACATTTCTGATCA     64345     CA
                                TGA  AGAAATGTGGT
                                |||  ||||||||||
                                ACT  TCTTTACACCG
                                  AG
GAM136  MAP3K8   5'  TCACGACCACCTCATG      17791    A  AAT
                                CA GA   GTGGTCGTGA
                                || ||   ||||||||||
                                GT CT   CACCAGCACT
                                 A  C__
GAM136  NGFR     3'  TTCTGACCACACTTCCTGTC   10231     A  A      T
                                GACA GAA TGTGGTCG GAA
                                |||| ||| |||||||| |||
                                CTGT CTT ACACCAGT CTT
                                  C   C      _
GAM136  OLR1     3'  TTCACAACAGTTCTTGTTA    10341        ATGTG  C
                                TGACAAGAA    GT GTGAA
                                |||||||||    || |||||
                                ATTGTTCTT    CA CACTT
                                     GA___  A
GAM136  POU4F1   3'  CACTGAAAACATTTTTGTCA   20660        A  GG  _
                                TGACAAGAA TGT  TC GTG
                                ||||||||| |||  || |||
                                ACTGTTTTT ACA  AG CAC
                                     _  AA  T
GAM136  SMP1     3'  TTTCACATGAATAATTTTTGTC 26705        A  GGTC
          A                      TGACAAGAA TGT    GTGAAA
                                |||||||||  |||    ||||||
                                ACTGTTTTT ATA    CACTTT
                                     A  AGTA
GAM136  ZNF264   3'  TTCTATTAACATTTCTTTTCA  12769     C       GGTCGT
                                TGA AAGAAATGT     GAA
                                ||| |||||||||     |||
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                                ACT TTCTTTACA     CTT
                                  T       ATTAT_
GAM136  C20orf175 3'  CGAGCTCCACGTTTCCTGCCA  55063    A  A      ___
                                TG CA GAAATGTGG   TCG
                                || || |||||||||   |||
                                AC GT CTTTGCACC   AGC
                                 C  C        TCG
GAM136  CAPNS2   3'  TTTCACAACCCTACATATTTCT 50323     CA      ____  C
           GATCA                   TGA  AGAAATGT    GGT GTGAAA
                                |||  ||||||||   ||| ||||||
                                ACT  TCTTTATA    CCA CACTTT
                                  AG       CATC   A
GAM136  CLDN6    3'  TTTACACTCACATTTTTATCA  41041     CA       _  C
                                TGA  AGAAATGTG GT GTGAA
                                |||  ||||||||| || |||||
                                ACT  TTTTTACAC CA CATTT
                                  A_       T  _
GAM136  DKFZP564L0864 3'  GCACCAATTTCTTGCCA     72555    A      G    C
                                TG CAAGAAAT TGGT GT
                                || |||||||| |||| ||
                                AC GTTCTTTA ACCA CG
                                 C       _   _
GAM136  DKFZP566B183 3'  TTTCCATAAACATTTCTTTTCA 31330     C       GGTCGT
                                TGA AAGAAATGT     GAAA
                                ||| |||||||||     ||||
                                ACT TTCTTTACA     CTTT
                                  T       AATAC_
GAM136  GTF2E1   3'  TACAGACCTCTTGTCA      18616        AATGT   _
                                TGACAAGA    GGTC GTG
                                ||||||||    |||| |||
                                ACTGTTCT    CCAG CAT
                                     _____   A
GAM136  KIAA0089  3'  TTTTAATTCACATTTCTT    69967          TCG
                                AAGAAATGTGG   TGAAA
                                ||||||||||   |||||
                                TTCTTTACACT   ATTTT
                                      TA_
GAM136  KIAA0373  5'  TTTTCAAAGTAACATTTCTT   28015         GGTCG
                                AAGAAATGT    TGAAAA
                                |||||||||    ||||||
                                TTCTTTACA    ACTTTT
                                     ATGAA
GAM136  KIAA1813  3'  TTTTCACACTGTAAATTTCTTG 70314         __ TG  C
           T                    ACAAGAAAT  G  GT GTGAAAA
                                |||||||||  |  || |||||||
                                TGTTCTTTA  T  CA CACTTTT
                                     AA GT  _
GAM136  KIAA1951  3'  TTCCAGGCTTCTCTTGTCA   73766        AATGT   GT
                                TGACAAGA    GGTC  GAA
                                ||||||||    ||||  |||
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                                ACTGTTCT    TCGG  CTT
                                    CT___    AC
GAM136  MGC4170   3'  TTCACCATTTCTTGTC      44227          TGGTC
                                GACAAGAAATG    GTGAA
                                ||||||||||    |||||
                                CTGTTCTTTAC    CACTT
                                      _____
GAM136  NRN1      3'  CACTGCACATTTCTCCTCA   33432     CA       GTC
                                TGA  AGAAATGTG   GTG
                                |||  |||||||||   |||
                                ACT  TCTTTACAC   CAC
                                  CC        GT_
GAM136  PLA2G12   3'  TTTTCACAACCACATTT     48028         C
                                AAATGTGGT GTGAAAA
                                ||||||||| |||||||
                                TTTACACCA CACTTTT
                                      A
GAM136  PPY2      3'  CACTCCACATTCCTGGCCA   40819    ACA  A      TC
                                TG   AG AATGTGG  GTG
                                ||   || |||||||  |||
                                AC   TC TTACACC  CAC
                                 CGG  C      T_
GAM136  ZNF31     3'  TTTGTAGACCACATTTCCTGTT 64992       A         _ TG
            A                    TGACA GAAATGTGGTC G  AA
                                |||||| |||||||||| |  ||
                                ATTGT CTTTACACCAG T  TT
                                   C          A GT
GAM136  LOC115219 3'  CACGACAACGGGTCCTCA    73295     CAA  AA   G
                                TGA   GA  TGT GTCGTG
                                |||   ||  ||| ||||||
                                ACT   CT  GCA CAGCAC
                                  C__  GG   A
GAM136  LOC120376 5'  TTCAGAGCATTTCTTTCA    75986     C       GG  G
                                TGA AAGAAATGT  TC TGAA
                                ||| |||||||||  || ||||
                                ACT TTCTTTACG  AG ACTT
                                  _       __  _
GAM136  LOC133418 3'  TTTCATATACATTTTTTGCCA  75094    A        GTC
                                TG CAAGAAATGTG   GTGAAA
                                || ||||||||||   ||||||
                                AC GTTTTTTACAT   TACTTT
                                 C          A__
GAM136  LOC151199 3'  TTAAAACCACAGCTCTTGCCA  80174    A    AA     CG
                                TG CAAGA  TGTGGT  TGA
                                || |||||  ||||||  |||
                                AC GTTCT  ACACCA  ATT
                                 C    CG     AA
GAM136  LOC152317 5'  TCACACTGACTTTTGTCA    85649         AATG   C
                                TGACAAGA    TGGT GTGA
                                ||||||||    |||| ||||
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                                ACTGTTTT   GTCA CACT
                                    CA__   _
GAM136  LOC152674 3'  TTCAACCCACCCTCTTGTCA  85841       AAT   TCG
                                TGACAAGA  GTGG  TGAA
                                ||||||||  ||||  ||||
                                ACTGTTCT  CACC  ACTT
                                    CC_   CA_
GAM136  LOC152845 5'  CATGACCACATTTTTCA    60330    CAA
                                TGA  GAAATGTGGTCGTG
                                |||  ||||||||||||||
                                ACT  TTTTACACCAGTAC
                                  ___
GAM136  LOC154743 3'  TTTAGTCCACATTGTCTTGTCA 81118       _     TCG
                                TGACAAGA AATGTGG  TGAA
                                |||||||| |||||||  ||||
                                ACTGTTCT TTACACC  ATTT
                                    G      TG_
GAM136  LOC165476 5'  TTCACGGCACCTTCT      87201     AT  G
                                AGAA  GTG TCGTGAA
                                ||||  ||| |||||||
                                TCTT  CAC GGCACTT
                                  C_  _
GAM136  LOC254266 5'  TTTTCGGTCACACATCTTATCA 97356    C   AA   GT  T
                                TGA AAGA  TGTG  CG GAA
                                ||| ||||  ||||  || |||
                                ACT TTCT  ACAC  GC TTT
                                  A   AC   TG  T
GAM136  LOC255919 3'  TTTCATTCTTACATTTCTAATC 95043    CA       TC
          A                      TGA  AGAAATGTGG  GTGAAA
                                ||| ||||||||||  ||||||
                                ACT  TCTTTACATT  TACTTT
                                  AA        CT
GAM136  LOC51754  5'  CACGGCCACATCTCTGTCA   71027      A  A
                                TGACA GA ATGTGGTCGTG
                                ||||| || ||||||||||
                                ACTGT CT TACACCGGCAC
                                  _ C
GAM136  LOC55862  3'  ACCTCATTTCTTGCCA     37485    A       T
                                TG CAAGAAATG GGT
                                || |||||||| |||
                                AC GTTCTTTAC CCA
                                 C       T
GAM136  LOC55954  3'  CACGTGGTCACTTTTCTCATCA 38877    CA    T   GT __
                                TGA  AGAAA GTG  C  GTG
                                |||  ||||| |||  |  |||
                                ACT  TCTTT CAC  G  CAC
                                  AC    T   TG TG
GAM137  CACNB3   3'  ACAGTGACCGGAACTGGCAG  61332     _  GAGG
                                CTGC AGT   GGTCACTGT
                                |||| |||   |||||||||
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                                GACG TCA    CCAGTGACA
                                  G  AGG_
GAM137  EVC      3'  CAGCCCTCTCACTACAG     27289     C       TCA
                                CTG AGTGAGGGG  CTG
                                ||| |||||||||  |||
                                GAC TCACTCTCC  GAC
                                  A       C__
GAM137  EVC      3'  CAGCCCCTCTCACCACAG    27285     CA      TCA
                                CTG  GTGAGGGG  CTG
                                |||  ||||||||  |||
                                GAC  CACTCTCC  GAC
                                  AC      CC_
GAM137  EVC      3'  CAGCCCTCTCACTACAG     27290     C       TCA
                                CTG AGTGAGGGG  CTG
                                ||| |||||||||  |||
                                GAC TCACTCTCC  GAC
                                  A       C__
GAM137  EVC      3'  CAGCCCCTCTCACCACAG    27287     CA      TCA
                                CTG  GTGAGGGG  CTG
                                |||  ||||||||  |||
                                GAC  CACTCTCC  GAC
                                  AC      CC_
GAM137  RAB5B    3'  CAGTTTCCCCTCACGCAG    11189     A       TC
                                CTGC GTGAGGGG  ACTG
                                |||| ||||||||  ||||
                                GACG CACTCCCC  TGAC
                                  _       TT
GAM137  ROCK2    3'  CTACAGTGATATTGACTGCA   66010       G  GG
                                TGCAGT AG  GTCACTGTAG
                                |||||| ||  ||||||||||
                                ACGTCA TT  TAGTGACATC
                                   G  A_
GAM137  TXNIP    3'  TGGCCCCTCACTGCAG      21354
                                CTGCAGTGAGGGGTCA
                                ||||||||||||||||
                                GACGTCACTCCCCGGT

GAM137  WSX1     3'  GCAAGACCCCTCACTACA    16735     C         AC
                                TG AGTGAGGGGTC  TGT
                                || ||||||||||  |||
                                AC TCACTCCCCAG  ACG
                                 A          A_
GAM137  C11orf21 3'  GTGACCCCCACTGCAG      26246         A
                                CTGCAGTG GGGGTCAC
                                |||||||| ||||||||
                                GACGTCAC CCCCAGTG
                                         _
GAM137  C22orf4  3'  ACAGTGCTCTTCTCACCGCAG 60639      A       T_
                                CTGC GTGAGGGG  CACTGT
                                |||| ||||||||  ||||||
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                                GACG CACTCTTC  GTGACA
                                  C       TC
GAM137  CENTA2    3'  GCTACAGTGACCCCTCATTGCA 37267
                                TGCAGTGAGGGGTCACTGTAGC
                                ||||||||||||||||||||||
                                ACGTTACTCCCCAGTGACATCG

GAM137  CSAD      3'  GCCACAGTGACCTGCGC     32030     AG        A
                                GTG  GGGTCACTGT GC
                                |||  |||||||||| ||
                                CGC  TCCAGTGACA CG
                                  G_         C
GAM137  DKFZP434H132 5'  GCTACAGCCCAGCACTCCCACT 73608         A     CA____
            GCAG                    CTGCAGTG GGGGT     CTGTAGC
                                |||||||| |||||     |||||||
                                GACGTCAC CCTCA     GACATCG
                                     _    CGACCC
GAM137  DKFZp761H079 3'  CACAGCGACCTAACAGT     58730      CAGTGAG    A   A
                                ACTG       GGGTC CTGT G
                                ||||       ||||| |||| |
                                TGAC       TCCAG GACA C
                                  AA_____     C    C
GAM137  DNAJA3    3'  ACAGCCCATTGCAG        60482         A  GGTCA
                                CTGCAGTG GG     CTGT
                                |||||||| ||     ||||
                                GACGTTAC CC     GACA
                                     _ _____
GAM137  FLJ20555  3'  GCTCTCTGGACCCCTCCTACAG 35394     C  T       ACTGT
                                CTG AG GAGGGGTC     AGC
                                ||| || ||||||||     |||
                                GAC TC CTCCCCAG     TCG
                                  A  _       GTCTC
GAM137  LATS1     3'  CTACAACAGTCACTGCA     60274         GGG  CAC
                                TGCAGTGA   GT   TGTAG
                                ||||||||   ||   |||||
                                ACGTCACT   CA   ACATC
                                     GA_  ___
GAM137  MGC4294   3'  GCTAGGGAACCCCTCACTGC   44231           CA  G
                                GCAGTGAGGGGT  CT TAGC
                                ||||||||||||  || ||||
                                CGTCACTCCCCA  GG ATCG
                                       A_  G
GAM137  PTPNS1    3'  CACAGTGACCCAGCCAC     54995     AG_        A
                                GTG   GGGTCACTGT G
                                |||   |||||||||| |
                                CAC   CCCAGTGACA C
                                  CGA         C
GAM137  RCD-8     3'  ACAGTGACCCCATCACT     26747       _
                                AGTGA GGGGTCACTGT
                                ||||| ||||||||||
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                                TCACT CCCCAGTGACA
                                   A
GAM137  SDC3     3'  ACAGTGACCCTGGCCTCAG   27737     C  TGA
                                CTG AG   GGGGTCACTGT
                                ||| ||   ||||||||||
                                GAC TC   TCCCAGTGACA
                                  _  CGG
GAM137  TRIM6    3'  CTACAATCTTCACTACA     54138    C      GTCAC
                                TG AGTGAGGG    TGTAG
                                || ||||||||    |||||
                                AC TCACTTCT    ACATC
                                 A      A____
GAM137  LOC143451 3' GCCACTCCTCCCCACTGCAG  76566        A   TCACT  A
                                CTGCAGTG GGGG    GT GC
                                |||||||| ||||    || ||
                                GACGTCAC CCCT    CA CG
                                     _   CCT__  C
GAM137  LOC145125 3' GCCACTCCTCCCCACTGCAG  77009        A   TCACT  A
                                CTGCAGTG GGGG    GT GC
                                |||||||| ||||    || ||
                                GACGTCAC CCCT    CA CG
                                     _   CCT__  C
GAM137  LOC149149 3' ACAGTAACAACTCTCGCTGCA  84364          __  C
                                TGCAGTGAGGG  GT ACTGT
                                ||||||||||  || |||||
                                ACGTCGCTCTC  CA TGACA
                                      AA  A
GAM137  LOC151963 5' GCCACACACGCACCCTCGCTGC 80402           _  CAC   A
           AGT                    ACTGCAGTGAGGG GT   TGT GC
                                ||||||||||||| ||   ||| ||
                                TGACGTCGCTCCC CG   ACA CG
                                      A  CAC   C
GAM137  LOC202908 5' GCTACAAGTTGACCACTGCAG  89237       GAGG    _ _
                                CTGCAGT    GGTCA CT GTAGC
                                |||||||    ||||| || |||||
                                GACGTCA    CCAGT GA CATCG
                                     ____     T  A
GAM137  LOC253205 5' CTACACCTGCACTACAGT    97570      C    A   GTCAC
                                ACTG AGTG GGG    TGTAG
                                |||| |||| |||    |||||
                                TGAC TCAC TCC    ACATC
                                  A    G  _____
GAM137  LOC254440 3' GCCACTCCTCCCCACTGCAG  97068        A   TCACT  A
                                CTGCAGTG GGGG    GT GC
                                |||||||| ||||    || ||
                                GACGTCAC CCCT    CA CG
                                     _   CCT__  C
GAM137  LOC257222 5' GCGGTCAGACCCCTCACTGCGG 97593             __
           T                    ACTGCAGTGAGGGGTC  ACTGT
                                ||||||||||||||||  |||||
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                                TGGCGTCACTCCCCAG  TGGCG
                                        AC
GAM137  LOC58489 3' GCTACAACAATGAACTGCAG  72528      GAGGG  CAC
                                CTGCAGT    GT   TGTAGC
                                |||||||    ||   ||||||
                                GACGTCA    CA   ACATCG
                                    AGTAA  ___
GAM137  LOC93276 5' GCTACAAGTTGACCACTGCAG 71891       GAGG    _ _
                                CTGCAGT    GGTCA CT GTAGC
                                |||||||    ||||| || |||||
                                GACGTCA    CCAGT GA CATCG
                                    _____    T  A
GAM138  ADD2     3' TCTAGCCTGGTATGA      33933        ACT   TT
                                TCATATCAG   GCT  GA
                                |||||||||   |||  ||
                                AGTATGGTC   CGA  CT
                                     ___   T_
GAM138  ADD2     3' TCTAGCCTGGTATGA      33961        ACT   TT
                                TCATATCAG   GCT  GA
                                |||||||||   |||  ||
                                AGTATGGTC   CGA  CT
                                     ___   T_
GAM138  ADD2     3' TCTAGCCTGGTATGA      33944        ACT   TT
                                TCATATCAG   GCT  GA
                                |||||||||   |||  ||
                                AGTATGGTC   CGA  CT
                                     ___   T_
GAM138  HK2      3' CTTGGAGCCTGAACATGA    3952      A_   ACT   TG
                                TCAT  TCAG   GCTT  AG
                                ||||  ||||   ||||  ||
                                AGTA  AGTC   CGAG  TC
                                  CA    ___    GT
GAM138  PDL2     3' CAGGGTGACCTGATATGA    47479         AC
                                TCATATCAG  TGCTTTG
                                |||||||||  |||||||
                                AGTATAGTC  GTGGGAC
                                     CA
GAM138  CDC14B   3' AGGCTGGTCTGACATG      52844     A     _
                                CAT TCAGACT GCTT
                                ||| ||||||| ||||
                                GTA AGTCTGG CGGA
                                  C      T
GAM138  EHM2     3' CAAAGTAGGAAATGATA     38913       A  AGA
                                TATCAT TC   CTGCTTTG
                                ||||||  ||  ||||||||
                                ATAGTA AG   GATGAAAC
                                   A  ___
GAM138  FLJ20105 5' CTCAGAGGAAATCTGATAT   34570        CTG_
                                ATATCAGA    CTTTGAG
                                ||||||||    |||||||
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                                TATAGTCT   GAGACTC
                                    AAAG
GAM138  HAT     5'  TCAAAGCAGTTGAGTA     14935    CA
                                TAT  GACTGCTTTGA
                                |||  ||||||||||
                                ATG  TTGACGAAACT
                                  AG
GAM138  KIAA0746 3'  TCAAAGCTGAATTGATA    69455     TA  GACT
                                TATCA  TCA   GCTTTGA
                                |||||  |||   |||||||
                                ATAGT  AGT   CGAAACT
                                   TA  ____
GAM138  KIAA1795 3'  CAAGGTAACCCGATATGAT   72149       AGAC
                                ATCATATC   TGCTTTG
                                ||||||||   |||||||
                                TAGTATAG   ATGGAAC
                                    CCCA
GAM138  KIAA1879 5'  CAAAGCAGTATCCTGATTA   73561   T   ___
                                A ATCAG   ACTGCTTTG
                                | |||||   |||||||||
                                A TAGTC   TGACGAAAC
                                 T    CTA
GAM138  LAMB4    3'  TCAAAGTGAGCATGATA    81176     GA  _
                                TATCA  CT GCTTTGA
                                |||||  || |||||||
                                ATAGT  GA TGAAACT
                                   AC  G
GAM138  PDCD7    5'  CTCAAAGCAGCCGCTGATG   72137      A__
                                TATCAG   CTGCTTTGAG
                                ||||||   ||||||||||
                                GTAGTC   GACGAAACTC
                                    GCC
GAM138  PPP4R1L  5'  CTCAAAGCTTTCTGACATGA  79502     A    CT
                                TCAT TCAGA  GCTTTGAG
                                |||| |||||  ||||||||
                                AGTA AGTCT  CGAAACTC
                                  C    TT
GAM138  PRMT6    3'  CAAAGCAGCCTGACCTG    36270    TA   A
                                CA  TCAG CTGCTTTG
                                ||  |||| ||||||||
                                GT  AGTC GACGAAAC
                                 CC   C
GAM138  PRO0902  3'  CTCAAAGACAGATATGGTA   53896       AGAC  _
                                TATCATATC   TG CTTTGAG
                                |||||||||   || |||||||
                                ATGGTATAG   AC GAAACTC
                                     ____  A
GAM138  PRO1728  5'  CTCAAAGCAGAAAGATGT    37538     AGA
                                ATATC   CTGCTTTGAG
                                |||||   ||||||||||
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                                TGTAG  GACGAAACTC
                                   AAA
GAM138  PRSS12   3'  TCAAAGTGATCTGATA     13248       CT
                                TATCAGA  GCTTTGA
                                |||||||  |||||||
                                ATAGTCT  TGAAACT
                                    AG
GAM138  SCMH1    5'  GCAGCCTAATGTGATA     24255       C  A
                                TATCATAT AG CTGC
                                |||||||| || ||||
                                ATAGTGTA TC GACG
                                     A  C
GAM138  SSH2     3'  CTCAAAGCAATGCTGGTG    62204      AC_
                                TATCAG   TGCTTTGAG
                                ||||||   |||||||||
                                GTGGTC   ACGAAACTC
                                   GTA
GAM138  LOC118668 5'  CAAAGCAGGATATG       75480      AGA
                                CATATC   CTGCTTTG
                                ||||||   ||||||||
                                GTATAG   GACGAAAC
                                   ___
GAM138  LOC127841 5'  CTCAAAGCAGCTGCTA     74694    T   A
                                TA CAG CTGCTTTGAG
                                || ||| ||||||||||
                                AT GTC GACGAAACTC
                                 C  _
GAM138  LOC137472 3'  CAAAGCCCTGATATG      75267       ACT
                                CATATCAG   GCTTTG
                                ||||||||   ||||||
                                GTATAGTC   CGAAAC
                                     C__
GAM138  LOC146783 5'  CAAAGCAGTGGTAT       83788      AG
                                ATATC  ACTGCTTTG
                                |||||  |||||||||
                                TATGG  TGACGAAAC
                                   __
GAM138  LOC147353 3'  CATGGAAACCTGATATGATA  84008          ACTG  T
                                TATCATATCAG    CT TG
                                ||||||||||    || ||
                                ATAGTATAGTC    GG AC
                                      CAAA  T
GAM138  LOC157657 3'  CTCAAAGCAATGTTATG     81517      T  GAC
                                CATA CA   TGCTTTGAG
                                ||||  ||   |||||||||
                                GTAT GT   ACGAAACTC
                                  T  A__
GAM138  LOC157922 3'  CTCACTGTATGTTTGATATGAT 86633           _   TT
          A                      TATCATATCAGAC TGC  TGAG
                                ||||||||||||| |||  ||||
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                                ATAGTATAGTTTG ATG  ACTC
                                       T   TC
GAM138  LOC161321 5'  CTCAAAGCAATCTGTCTCTGA  87086     TAT_   C
                                TCA    CAGA TGCTTTGAG
                                |||    |||| |||||||||
                                AGT    GTCT ACGAAACTC
                                  CTCT    A
GAM138  LOC221154 3'  CTTAGACACTCTAATATGATA  93545        C   C  C
                                TATCATAT AGA TG TTTGAG
                                |||||||| ||| || ||||||
                                ATAGTATA TCT AC AGATTC
                                     A   C  _
GAM138  LOC90408  5'  CGAGGCCTCATATGATA     62660        C  ACT
                                TATCATAT AG   GCTTTG
                                |||||||| ||   ||||||
                                ATAGTATA TC   CGGAGC
                                     C  ___
GAM139  ASPH      5'  TGGATTGAAGAAATCAA     50634     GC      _
                                TTG  TTCTTCAA CCA
                                |||  |||||||| |||
                                AAC  AAGAAGTT GGT
                                  TA       A
GAM139  ASPH      5'  TGGATTGAAGAAATCAA     39396     GC      _
                                TTG  TTCTTCAA CCA
                                |||  |||||||| |||
                                AAC  AAGAAGTT GGT
                                  TA       A
GAM139  ASPH      5'  TGGATTGAAGAAATCAA     50626     GC      _
                                TTG  TTCTTCAA CCA
                                |||  |||||||| |||
                                AAC  AAGAAGTT GGT
                                  TA       A
GAM139  FOS       5'  GCGAGCAACTGAGAAGCCAA  17906        T  ACCA  A_
                                TTGGCTTCT CA    GC  GT
                                ||||||||| ||    ||  ||
                                AACCGAAGA GT    CG  CG
                                     _  CAA_  AG
GAM139  FSTL1     3'  ATACTGCTAGTTAACCCAG   23010     C  CTTC   C
                                TTGG TT    AAC AGCAGTAT
                                |||| ||    ||| ||||||||
                                GACC AA    TTG TCGTCATA
                                  C  _____   A
GAM139  NR4A2     3'  TGAGTTGAAGAAGGCAA     20535     G       _
                                TTG CTTCTTCAAC CA
                                ||| |||||||||| ||
                                AAC GAAGAAGTTG GT
                                  G        A
GAM139  NXF5      3'  CTGGCTGACCAAGAAGCCAA  51966        ___   A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
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                                AACCGAAGA  AGT GGTC
                                     ACC  C
GAM139  NXF5    3' CTGGCTGACCAAGAAGCCAA  52508       ___  A
                                TTGGCTTCT  TCA CCAG
                                |||||||||  ||| ||||
                                AACCGAAGA  AGT GGTC
                                     ACC  C
GAM139  NXF5    3' CTGGCTGACCAAGAAGCCAA  52513       ___  A
                                TTGGCTTCT  TCA CCAG
                                |||||||||  ||| ||||
                                AACCGAAGA  AGT GGTC
                                     ACC  C
GAM139  NXF5    3' CTGGCTGACCAAGAAGCCAA  52517       ___  A
                                TTGGCTTCT  TCA CCAG
                                |||||||||  ||| ||||
                                AACCGAAGA  AGT GGTC
                                     ACC  C
GAM139  NXF5    3' CTGGCTGACCAAGAAGCCAA  52521       ___  A
                                TTGGCTTCT  TCA CCAG
                                |||||||||  ||| ||||
                                AACCGAAGA  AGT GGTC
                                     ACC  C
GAM139  POLG     5' GCCAGTAAAAGAAGCCAA   10680       CA  CA
                                TTGGCTTCTT  AC  GC
                                ||||||||||  ||  ||
                                AACCGAAGAA  TG  CG
                                     AA  AC
GAM139  FLJ12377 3' TGTTGGATAAAGAAGCCAA  46487       CAA
                                TTGGCTTCTT  CCAGCA
                                ||||||||||  ||||||
                                AACCGAAGAA  GGTTGT
                                     ATA
GAM139  FLJ13102 3' ACGGCGATTGAGAAGCCAA  46002       T  CCA  A
                                TTGGCTTCT CAA  GC GT
                                |||||||||  |||  || ||
                                AACCGAAGA GTT  CG CA
                                     _  AG_  G
GAM139  FLJ23120 3' CATACTAAATGAAAGAAGCCAG 85145       CAAC  GC_
                                TTGGCTTCTT   CA  AGTATG
                                ||||||||||   ||  ||||||
                                GACCGAAGAA   GT  TCATAC
                                     A___  AAA
GAM139  FREQ     3' GCGGCCAAGAAGCCAA     26582       CAA  A
                                TTGGCTTCTT  CC GC
                                ||||||||||  || ||
                                AACCGAAGAA  GG CG
                                     CC_  _
GAM139  KIAA0232 3' TTGCTAACTGAAGAAGCCAA  72764         ACC
                                TTGGCTTCTTCA  AGCAG
                                ||||||||||||  |||||
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                                AACCGAAGAAGT  TCGTT
                                      CAA
GAM139  KIAA0987  3'  GCAATTAAAGAGGCCAA    24563        C  CCA
                                TTGGCTTCTT AA  GC
                                |||||||||| ||  ||
                                AACCGGAGAA TT  CG
                                     A  AA_
GAM139  PPFIA2   5'  ATTGATCAATTGAAGAAGC   13261        CCAG_
                                GCTTCTTCAA   CAGT
                                ||||||||||   ||||
                                CGAAGAAGTT   GTTA
                                     AACTA
GAM139  SNPH     3'  ACAGCTTACTGAAAAAGCCAG  28236      C   ACC  A
                                TTGGCTT TTCA  AGC GT
                                ||||||| ||||  ||| ||
                                GACCGAA AAGT  TCG CA
                                    A   CAT  A
GAM139  LOC134957 3'  ACGTGACAGATGAAGAAACCAA 57661    C     ACCAG  _
                                TTGG TTCTTCA   CA GT
                                |||| |||||||   || ||
                                AACC AAGAAGT   GT CA
                                  A     AGACA  G
GAM139  LOC136895 5'  CTGCCAAAGAAGCCAA     57168        CAACCA
                                TTGGCTTCTT    GCAG
                                ||||||||||    ||||
                                AACCGAAGAA    CGTC
                                     AC____
GAM139  LOC162333 5'  ACTAAGCTGAAGAGGCCAA   87115         ACCA  __
                                TTGGCTTCTTCA   GC  AGT
                                ||||||||||||   ||  |||
                                AACCGGAGAAGT   CG  TCA
                                      ____  AA
GAM139  LOC253227 5'  ACTACTGGTAAGAAGCCA    97506       CA   C
                                TGGCTTCTT  ACCAG AGT
                                |||||||||  ||||| |||
                                ACCGAAGAA  TGGTC TCA
                                     __    A
GAM139  LOC255452 3'  GCAGCCGAAGAAGCCA     97538        AACCA  A
                                TGGCTTCTTC    GC GT
                                ||||||||||    || ||
                                ACCGAAGAAG    CG CG
                                     C____  A
GAM140  A1BG     3'  CAGGGTCTCACTGTGTTGC   55413       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM140  ACPT     3'  CACCCCGCCATATGCTGC    54980    ACA     TTT
                                GCA  CATATGGC  GTG
                                |||  ||||||||  |||
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                                CGT   GTATACCG   CAC
                                  C__       CCC
GAM140  ACPT     3'  CACCCCGCCATATGCTGC    54986     ACA       TTT
                                GCA   CATATGGC   GTG
                                |||   ||||||||   |||
                                CGT   GTATACCG   CAC
                                  C__       CCC
GAM140  AHCY     3'  CACAAAGCCCATGTGTTTTGC  5473       C       _
                                GCAA ACATATGG CTTTGTG
                                |||| |||||||| |||||||
                                CGTT TGTGTACC GAAACAC
                                  T       C
GAM140  BCL7A    3'  CAGGATTCCATTTGTGTTGCT  40638          T    CT  G
                                AGCAACACA ATGG  TT TG
                                ||||||||| ||||  || ||
                                TCGTTGTGT TACC  AG AC
                                      T    TT  G
GAM140  CDK5R2   3'  CACAAAGCCACCGCCGCTGTT  14132      ACACATA
                                AGCA      TGGCTTTGTG
                                ||||      ||||||||||
                                TTGT      ACCGAAACAC
                                  CGCCGCC
GAM140  CHC1     3'  CACAAAGCATACTCTTGC    7019       CACA    G
                                GCAA    TATG CTTTGTG
                                ||||    |||| |||||||
                                CGTT    ATAC GAAACAC
                                  CTC_   _
GAM140  CIT      3'  CACAAGGCATCTGTTGCT    69741        CATATG
                                AGCAACA     GCTTTGTG
                                |||||||     ||||||||
                                TCGTTGT     CGGAACAC
                                    CTA___
GAM140  COL6A2   5'  CAGGGCCACAGGTGCTGC    54168     A   ATA
                                GCA CAC   TGGCTTTG
                                ||| |||   ||||||||
                                CGT GTG   ACCGGGAC
                                  C   GAC
GAM140  COL6A2   5'  CAGGGCCACAGGTGCTGC    8480      A   ATA
                                GCA CAC   TGGCTTTG
                                ||| |||   ||||||||
                                CGT GTG   ACCGGGAC
                                  C   GAC
GAM140  EYA1     3'  CACAGCGTTATGTGTCTGC   4952      AC       T
                                GCA  ACATATGGC TTGTG
                                |||  ||||||||| |||||
                                CGT  TGTGTATTG GACAC
                                  C_        C
GAM140  FBN2     3'  CAAGGAACCATATGTG      8844          __
                                CACATATGG  CTTTG
                                |||||||||  |||||
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                                GTGTATACC  GGAAC
                                     AA
GAM140  FMO1    3'  CACAAATGATTGTGTTGT    8924        TATGGC
                                GCAACACA    TTTGTG
                                ||||||||    ||||||
                                TGTTGTGT    AAACAC
                                     TAGT__
GAM140  GALNT2  3'  CACAAAGCCGAGTCGTGT    15593     _ A
                                ACAC AT TGGCTTTGTG
                                |||| || ||||||||||
                                TGTG TG GCCGAAACAC
                                  C  A
GAM140  GALNT2  3'  CACAAAGCCGTTCGCAGCT   15594    AACACAT
                                AGC     ATGGCTTTGTG
                                |||     ||||||||||
                                TCG     TGCCGAAACAC
                                  ACGCT__
GAM140  GPR4    3'  CAGGGTCTCACTGTGTTGC    59902       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                     CACT
GAM140  HNMT    3'  CACAAAGCCTGTGTTACT    22567    C     TAT
                                AG AACACA  GGCTTTGTG
                                || ||||||  |||||||||
                                TC TTGTGT  CCGAAACAC
                                 A    ____
GAM140  IL1RN   3'  CACAAAGCCCTTCCATGTCGC 5141     A   CATAT_
                                GC ACA     GGCTTTGTG
                                || |||     |||||||||
                                CG TGT     CCGAAACAC
                                 C  ACCTTC
GAM140  IL2RB   3'  CACAAAGTGGATGCCTGCT   6069      ACA  ATG
                                AGCA  CAT  GCTTTGTG
                                ||||  |||  ||||||||
                                TCGT  GTA  TGAAACAC
                                  CC_  GG_
GAM140  ITSN2   3'  CACAAAGCCATGCACGCT    38971     AACACA
                                AGC     TATGGCTTTGTG
                                |||     ||||||||||||
                                TCG     GTACCGAAACAC
                                  CAC____
GAM140  JRK     3'  CAGGGTCTCACTGTGTTGC    86524       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                     CACT
GAM140  LANCL1  3'  CACAATTTTATATGTATGCT   20210     AC      CT
                                AGCA  ACATATGG  TTGTG
                                ||||  ||||||||  |||||
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                                TCGT  TGTATATT  AACAC
                                  A_       TT
GAM140  LGR6    5'  GGCCATCGTGTTGCT      84200        AT
                                AGCAACAC  ATGGCT
                                ||||||||  ||||||
                                TCGTTGTG  TACCGG
                                    C_
GAM140  LRRC2    3'  CAAGGCACCATGTGTTACT   44465    C      ATG
                                AG AACACAT   GCTTTG
                                || |||||||   ||||||
                                TC TTGTGTA   CGGAAC
                                 A      CCA
GAM140  MYBL2    3'  CAGGGCCATGTGCTGC      10154     ACA
                                GCA   CATATGGCTTTG
                                |||   ||||||||||||
                                CGT   GTGTACCGGGAC
                                  C__
GAM140  OCLN     3'  CACAAAGTTTTGGTTGCT    10314       A  TAT
                                AGCAAC CA   GGCTTTGTG
                                |||||| ||   |||||||||
                                TCGTTG GT   TTGAAACAC
                                   _  T__
GAM140  OSR1     3'  CACAAAGTAATATGTG      17566        G
                                CACATAT GCTTTGTG
                                ||||||| ||||||||
                                GTGTATA TGAAACAC
                                    A
GAM140  PCDH9    5'  CACAAAGTGACAGTGCTGGCT  82794     AA_   ATATG
                                AGC   CAC    GCTTTGTG
                                |||   |||    ||||||||
                                TCG   GTG    TGAAACAC
                                  GTC   ACAG_
GAM140  PRDM2    5'  CACAAAGCCACATCCTGC    24246     ACAC  A
                                GCA    AT TGGCTTTGTG
                                |||    || ||||||||||
                                CGT    TA ACCGAAACAC
                                  CC__  C
GAM140  PRDM2    5'  CACAAAGCCACATCCTGC    31847     ACAC  A
                                GCA    AT TGGCTTTGTG
                                |||    || ||||||||||
                                CGT    TA ACCGAAACAC
                                  CC__  C
GAM140  PRG4     3'  CACAAAGCTTTATCGTGTTGT  19415        _   T
                                GCAACAC ATA GGCTTTGTG
                                ||||||| ||| |||||||||
                                TGTTGTG TAT TCGAAACAC
                                    C   T
GAM140  RXRB     3'  CACAAAGCACTGGCCTTGC    41757      CA_  TATG
                                GCAA   CA    GCTTTGTG
                                ||||   ||    ||||||||
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                                CGTT  GT   CGAAACAC
                                  CCG  CA__
GAM140  SMARCD1  3'  CACAAAGTTCCCATGTG    11811       ___
                                CATATGG  CTTTGTG
                                |||||||  |||||||
                                GTGTACC  GAAACAC
                                    CTT
GAM140  SMARCD1  3'  CACAAAGTTCCCATGTG    57429       ___
                                CATATGG  CTTTGTG
                                |||||||  |||||||
                                GTGTACC  GAAACAC
                                    CTT
GAM140  SMURF1   3'  CACGTGTGATCTGTGTTGC   92448        T  G  TT
                                GCAACACA AT GC  TGTG
                                |||||||| || ||  ||||
                                CGTTGTGT TA TG  GCAC
                                     C  G  T_
GAM140  STX7     3'  CACCAAGATGTGTGTTACT   13108    C       GG   T
                                AG AACACATAT  CTT GTG
                                || |||||||||  ||| |||
                                TC TTGTGTGTA  GAA CAC
                                 A        __  C
GAM140  TAF4B    3'  CACAAAGCATTGTTGC      87167       CATATG
                                GCAACA     GCTTTGTG
                                ||||||     ||||||||
                                CGTTGT     CGAAACAC
                                   TA____
GAM140  TF       3'  CACAGCTCTGTGTTGC      6512         TAT   T
                                GCAACACA   GGCT TG
                                ||||||||   |||| ||
                                CGTTGTGT   TCGA AC
                                     C__   C
GAM140  TLR4     5'  CACAGGGCCACTGCTGCT    12317      A  CATA
                                AGCA CA    TGGCTTTGTG
                                |||| ||    ||||||||||
                                TCGT GT    ACCGGGACAC
                                  C  C___
GAM140  TLR4     5'  CACAGGGCCACTGCTGCT    56727      A  CATA
                                AGCA CA    TGGCTTTGTG
                                |||| ||    ||||||||||
                                TCGT GT    ACCGGGACAC
                                  C  C___
GAM140  TLR4     5'  CACAGGGCCACTGCTGCT    56736      A  CATA
                                AGCA CA    TGGCTTTGTG
                                |||| ||    ||||||||||
                                TCGT GT    ACCGGGACAC
                                  C  C___
GAM140  TLR4     5'  CACAGGGCCACTGCTGCT    56732      A  CATA
                                AGCA CA    TGGCTTTGTG
                                |||| ||    ||||||||||
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                                TCGT GT   ACCGGGACAC
                                  C  C___
GAM140  VIPR2    3' CACAGTCTCCATGTGTGTGC  12605    A      CT_
                                GCA CACATATGG  TTGTG
                                ||| |||||||||  |||||
                                CGT GTGTGTACC  GACAC
                                  _      TCT
GAM140  ANKT     3' CAGGGTCTCACTGTGTTGC   33024      TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM140  ATP9A    3' CACAAAGCCAGTGGCTGTT   62039    A_  ATA
                                AGCA  CAC  TGGCTTTGTG
                                ||||  |||  ||||||||||
                                TTGT  GTG  ACCGAAACAC
                                  CG  ___
GAM140  CETN2    3' CACATGTTACACCTGTGTTGC 15093      TA  GCTT_
                                GCAACACA TG   TGTG
                                |||||||| ||   ||||
                                CGTTGTGT AC   ACAC
                                    CC  ATTGT
GAM140  CYLD     3' CACAAGGTTTTATACTGCT   30883    ACAC  TG
                                AGCA   ATA  GCTTTGTG
                                ||||   |||  ||||||||
                                TCGT   TAT  TGGAACAC
                                  CA__   TT
GAM140  DKFZP586A0522 3' CAGGGTCTCACTGTGTTGC  25871      TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM140  DKFZp762K222 3' ACAGATGCGTGTTGCT     71116      ATATG  _
                                AGCAACAC    GC TTTGT
                                ||||||||    || |||||
                                TCGTTGTG    CG AGACA
                                    _____  T
GAM140  FLJ10297  3' CAGGGCTTCACTGTGTTGC  35979      TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   TCGGGAC
                                    CACT
GAM140  FLJ10511  3' CACATGTGTATGTGCAGCT  36204    AA     G TT
                                AGC  CACATATG C  TGTG
                                |||  |||||||| |  ||||
                                TCG  GTGTATGT G  ACAC
                                  AC      _ T_
GAM140  FLJ11029  5' CACTAGCACCTGTGTTGCT  60973      TATG  TT
                                AGCAACACA   GCT  GTG
                                |||||||||   |||  |||
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                                TCGTTGTGT   CGA  CAC
                                     CCA_   T_
GAM140  FLJ11117  3'  CACAAAGCTTGTATGTG     37073        _
                                CACATATG GCTTTGTG
                                |||||||| ||||||||
                                GTGTATGT CGAAACAC
                                     T
GAM140  FLJ11715  3'  CAGGGTCTCCATATGTTGC   44668      C  AT_
                                GCAACA AT   GGCTTTG
                                |||||| ||   |||||||
                                CGTTGT TA   CTGGGAC
                                   A  CCT
GAM140  FLJ20275  3'  CACAAAGGGCTTTATGTGTCAG 34819    A_     T   __
          CT                      AGC  ACACATA GGCT  TTGTG
                                |||  ||||||| ||||  |||||
                                TCG  TGTGTAT TCGG  AACAC
                                  AC      T   GA
GAM140  FLJ20413  3'  CAGAGCCGCATGCACTGCT   35131     ACA   A
                                AGCA   CAT TGGCTTTG
                                ||||   ||| ||||||||
                                TCGT   GTA GCCGAGAC
                                  CAC   C
GAM140  FLJ20450  3'  CACCTGGGACCTGTGTTGCT   35192        TAT  _   T_
                                AGCAACACA   GG CTT  GTG
                                |||||||||   || |||  |||
                                TCGTTGTGT   CC GGG  CAC
                                     ___  A   TC
GAM140  FLJ20671  3'  CAATTCAAATGTGTTGC     35516        A   CT
                                GCAACACAT TGG  TTG
                                ||||||||| |||  |||
                                CGTTGTGTA ACT  AAC
                                     A   T_
GAM140  FLJ23598  3'  CACAAAGAGAGGCTGTGCTGC  45521     A    TATGG_
                                GCA CACA     CTTTGTG
                                ||| ||||     |||||||
                                CGT GTGT     GAAACAC
                                  C    CGGAGA
GAM140  FRSB      3'  CATAGGCCATACATGTTACT   19090    C    CA      T
                                AG AACA  TATGGCTT GTG
                                || ||||  |||||||| |||
                                TC TTGT  ATACCGGA TAC
                                 A    AC      _
GAM140  H2AV      3'  CACAGCCATATGTATTGTT    56845      C        T
                                AGCAA ACATATGGCT TG
                                ||||| |||||||||| ||
                                TTGTT TGTATACCGA AC
                                   A        C
GAM140  HIC2      3'  CACAAAGTCTGTACCGC     65256    AAC   TAT
                                GC   ACA   GGCTTTGTG
                                ||   |||   |||||||||
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                              CG  TGT  CTGAAACAC
                               CCA  ___
GAM140  KIAA0140 3' CACATGGCCATGTCTTGC   27806    CAC      T
                              GCAA  ATATGGCT TGTG
                              ||||  |||||||| ||||
                              CGTT  TGTACCGG ACAC
                                C__      T
GAM140  KIAA0215 3' CAAATTCCATATGTAATGC  28416    AC      C_
                              GCA  ACATATGG  TTTG
                              |||  ||||||||  ||||
                              CGT  TGTATACC  AAAC
                                AA      TT
GAM140  KIAA0254 3' AGCCACCTGTGTTGCT     28595        TA
                              AGCAACACA  TGGCT
                              |||||||||  |||||
                              TCGTTGTGT  ACCGA
                                   CC
GAM140  KIAA0618 3' CACAAAAACATGTGTTGT   29162       TA  GC
                              GCAACACA  TG  TTTGTG
                              ||||||||  ||  ||||||
                              TGTTGTGT  AC  AAACAC
                                   __  AA
GAM140  KIAA0953 3' AGCTTTCATAGTGTTGCT   66778       A   ___
                              AGCAACAC TATG  GCT
                              |||||||| ||||  |||
                              TCGTTGTG ATAC  CGA
                                   _  TTT
GAM140  KIAA1193 3' CACAGAGCCATATACCTCGCT 67630    AACAC
                              AGC    ATATGGCTTTGTG
                              |||    |||||||||||||
                              TCG    TATACCGAGACAC
                                CTCCA
GAM140  KIAA1281 3' CACAGAGTAACAAATGTTGCT 89151       CATATG
                              AGCAACA     GCTTTGTG
                              |||||||     ||||||||
                              TCGTTGT     TGAGACAC
                                  AAACAA
GAM140  KIAA1466 5' AGCCATATGTGCGCT      71913    AA
                              AGC  CACATATGGCT
                              |||  ||||||||||
                              TCG  GTGTATACCGA
                                C_
GAM140  KIAA1821 3' CAGGGTCTCACTGTGTTGC  71780       TAT_
                              GCAACACA   GGCTTTG
                              ||||||||   |||||||
                              CGTTGTGT   CTGGGAC
                                   CACT
GAM140  KIF13B   3' CACAAAGTCCGTGGTGC    30904    A  ATAT
                              GCA CAC   GGCTTTGTG
                              ||| |||   |||||||||
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                              CGT GTG   CTGAAACAC
                                G  C___
GAM140  KIF13B   3' CACAAAGTCCGTGGTGC    82820    A  ATAT
                              GCA CAC   GGCTTTGTG
                              ||| |||   |||||||||
                              CGT GTG   CTGAAACAC
                                G  C___
GAM140  MGC12921 3' CACAAAGGCCGTTATTGC    63775     CACAT   _
                              GCAA    ATGGC TTTGTG
                              ||||    ||||| ||||||
                              CGTT    TGCCG AAACAC
                                AT___    G
GAM140  MGC14836 5' CACAAAGCTATCATCCTGC   53035    ACACAT
                              GCA     ATGGCTTTGTG
                              |||     ||||||||||
                              CGT     TATCGAAACAC
                                CCTAC_
GAM140  MGC15429 3' CACATTGTCATGTGCAGCT   51249    AACA      TT
                              AGC   CATATGGC  TGTG
                              |||   ||||||||  ||||
                              TCG   GTGTACTG  ACAC
                                AC__       TT
GAM140  MGC15875 3' CGAGGCCATAATGCT      51908     ACACA
                              AGCA    TATGGCTTTG
                              ||||    ||||||||||
                              TCGT    ATACCGGAGC
                                A____
GAM140  MGC16279 5' GAAGCCATCGTGTCGCT    51888    A   AT
                              AGC ACAC  ATGGCTTT
                              ||| ||||  ||||||||
                              TCG TGTG  TACCGAAG
                                C   C_
GAM140  MGC27434 3' CACAATAAGTATGTGTT    58947        GGCT
                              AACACATAT   TTGTG
                              |||||||||   |||||
                              TTGTGTATG   AACAC
                                   AAT_
GAM140  MGC3048  3' CACAAAGCATGAATGTT    43899     CA   G
                              AACA  TATG CTTTGTG
                              ||||  |||| |||||||
                              TTGT  GTAC GAAACAC
                                AA   _
GAM140  MIG-6    3' CACAAGCTGGCCTTGTGTTGCT 38486        TAT   ___
                              AGCAACACA   GGCT   TTGTG
                              |||||||||   ||||   |||||
                              TCGTTGTGT   CCGG   AACAC
                                   T__    TCG
GAM140  MUC17    3' CACTGCCCCATATGTGTCCCT  94271    CA       CTTT
                              AG  ACACATATGG   GTG
                              ||  ||||||||||   |||
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                                TC  TGTGTATACC   CAC
                                 CC        CCGT
GAM140  MYO3B    3'  CACTCTCCCACATGTGTTGT  57301        A   CTTT
                                GCAACACAT TGG   GTG
                                ||||||||| |||   |||
                                TGTTGTGTA ACC   CAC
                                     C   CTCT
GAM140  NS1-BP   3'  CACAAAGCTTTTGCATATTGC  72542     CA__  TAT
                                GCAA   CA   GGCTTTGTG
                                ||||   ||   |||||||||
                                CGTT   GT   TCGAAACAC
                                  ATAC  TT_
GAM140  OR51E2   3'  CACAGGTTTTATGTGTTCT   47791    C      TG   T
                                AG AACACATA  GCTT GTG
                                || ||||||||  |||| |||
                                TC TTGTGTAT  TGGA CAC
                                 _       TT   _
GAM140  PRDM11   3'  CAGGTGCTCCATGTGTTGC   39581        AT  _
                                GCAACACAT  GGC TTTG
                                |||||||||  ||| ||||
                                CGTTGTGTA  TCG GGAC
                                     CC   T
GAM140  PRO0943  5'  CACAAAAGTGTTATATGTG   37701         ___
                                CACATATGGC   TTTGTG
                                ||||||||||   ||||||
                                GTGTATATTG   AAACAC
                                      TGA
GAM140  SULT1C2  5'  CACAACGCAGCCATATGCTG  21674    _      ___
                                CA CATATGGCT   TTGTG
                                || |||||||||   |||||
                                GT GTATACCGA   AACAC
                                 C        CGC
GAM140  VEST1    3'  CACCTGCCATACATGTTGT   53685      CA     TTT
                                GCAACA  TATGGC   GTG
                                ||||||  ||||||   |||
                                TGTTGT  ATACCG   CAC
                                   AC     TC_
GAM140  ZFP100   3'  AGTCACCTGTGTTGCT     70049        TA
                                AGCAACACA  TGGCT
                                |||||||||  |||||
                                TCGTTGTGT  ACTGA
                                     CC
GAM140  ZNF363   5'  AGCCATATTGTCGCT      73452     A  C
                                AGC ACA ATATGGCT
                                ||| ||| ||||||||
                                TCG TGT TATACCGA
                                  C  _
GAM140  LOC118611 5'  CACAGAGCATTTGCGTTACT  75469    C   A  TATG
                                AG AAC CA    GCTTTGTG
                                || ||| ||    ||||||||
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                                TC TTG GT    CGAGACAC
                                 A   C  TTA_
GAM140   LOC120526 3'  CAGGGCCATTGCACTGCT    74015      ACA  T
                                AGCA   CA ATGGCTTTG
                                ||||   || |||||||||
                                TCGT   GT TACCGGGAC
                                  CAC  _
GAM140   LOC126669 3'  CACAAAGTTCCATATGT     75399         __
                                ACATATGG  CTTTGTG
                                ||||||||  |||||||
                                TGTATACC  GAAACAC
                                     TT
GAM140   LOC139840 5'  CACAAGAGCCATGGGT      76266    A        _
                                AC TATGGCTTT GTG
                                || |||||||| |||
                                TG GTACCGAGA CAC
                                 G        A
GAM140   LOC143465 5'  CACATGCACATATGTG      82962         _  TT
                                CACATATG GC  TGTG
                                |||||||| ||  ||||
                                GTGTATAC CG  ACAC
                                     A  T_
GAM140   LOC146774 3'  CACTGACATGTGTGTGC     78094     A       GCTTT
                                GCA CACATATG    GTG
                                ||| ||||||||    |||
                                CGT GTGTGTAC    CAC
                                  _       AGT__
GAM140   LOC147407 5'  CACAAAGCTATCATCCTGC    76322     ACACAT
                                GCA     ATGGCTTTGTG
                                |||     ||||||||||
                                CGT     TATCGAAACAC
                                  CCTAC_
GAM140   LOC151057 3'  ACAGAGCACATACTGT      85199     _   _
                                ACA TATG GCTTTGT
                                ||| |||| |||||||
                                TGT ATAC CGAGACA
                                  C    A
GAM140   LOC151473 3'  CACAACAACCTATGTGTT     80254         T  CT_
                                AACACATA GG   TTGTG
                                |||||||| ||   |||||
                                TTGTGTAT CC   AACAC
                                     _ AAC
GAM140   LOC154739 5'  CACAAAGTTCAAATGTATGC   86227     AC    A  _
                                GCA  ACAT TGG CTTTGTG
                                |||  |||| ||| |||||||
                                CGT  TGTA ACT GAAACAC
                                  A_   A  T
GAM140   LOC157507 5'  CACAGCTGTGTATGTGTGCT   81454      A      __    T
                                AGCA CACATAT  GGCT TG
                                |||| |||||||  |||| ||
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                                TCGT GTGTATG  TCGA AC
                                  _     TG   C
GAM140  LOC161734 3'  CACAAACATTTAGTGTTGCT  87097       AT_  GC
                                AGCAACAC  ATG  TTTGTG
                                ||||||||  |||  ||||||
                                TCGTTGTG  TAC  AAACAC
                                    ATT  __
GAM140  LOC196410 3'  CACAAAAGTCATGGTG     87657    A      _
                                CAC TATGGCTTT GTG
                                ||| ||||||||| |||
                                GTG GTACTGAAA CAC
                                  _       A
GAM140  LOC196485 3'  CACAAAAACCTGTGTTGT    87730       TAT  C_
                                GCAACACA  GG  TTTGTG
                                ||||||||  ||  ||||||
                                TGTTGTGT  CC  AAACAC
                                    ___  AA
GAM140  LOC196529 3'  CAGGGTCTCACTGTGTTGC   87771       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM140  LOC197003 5'  CACAAAGCTCCATGCTGT    87870    _  AT
                                ACA CAT  GGCTTTGTG
                                ||| |||  |||||||||
                                TGT GTA  TCGAAACAC
                                  C   CC
GAM140  LOC202025 5'  CACAGTTGTATGGTTGCT    90281      A   TG  T
                                AGCAAC CATA  GCT TG
                                ||||||| ||||  ||| ||
                                TCGTTG GTAT  TGA AC
                                   _   GT   C
GAM140  LOC203276 3'  CACAAAGTTCAAGTGTATGC  90475    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM140  LOC203292 3'  CAGGGTTTCATATGTGTT    90509        __
                                AACACATATG  GCTTTG
                                ||||||||||  ||||||
                                TTGTGTATAC  TGGGAC
                                     TT
GAM140  LOC203305 3'  CACAAAGTTCAAGTGTATGC  90519    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM140  LOC221354 3'  CACAAAAACATGTGTTGT    92409       TA  GC
                                GCAACACA  TG  TTTGTG
                                ||||||||  ||  ||||||
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                                TGTTGTGT  AC  AAACAC
                                     __ AA
GAM140  LOC254243 3'  CACAAAGTTCAAGTGTATGC  97404    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM140  LOC255870 3'  CACAACTGGCCATGTCCTGC  94657    ACAC      __
                                GCA   ATATGGCT  TTGTG
                                |||   ||||||||  |||||
                                CGT   TGTACCGG  AACAC
                                  CC__      TC
GAM140  LOC90038  3'  CACAAAGTTCAAGTGTATGC  61148    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM140  LOC90321  3'  CACAAATGGATTGTGTGTGC  62262    A    TGGC_
                                GCA CACATA    TTTGTG
                                ||| ||||||    ||||||
                                CGT GTGTGT    AAACAC
                                  _     TAGGT
GAM140  LOC90750  3'  CACAAAGTTAAGATTGCT   63917     CACATA
                                AGCAA     TGGCTTTGTG
                                |||||     ||||||||||
                                TCGTT     ATTGAAACAC
                                   AGA___
GAM140  LOC91069  3'  GAAGCCATCGTGTCACT    64778   CA   AT
                                AG  ACAC  ATGGCTTT
                                ||  ||||  ||||||||
                                TC  TGTG  TACCGAAG
                                 AC   C_
GAM140  LOC92539  3'  CACAAAGCCACTGTAGC    69630   A  CATA
                                GC ACA   TGGCTTTGTG
                                || |||   ||||||||||
                                CG TGT   ACCGAAACAC
                                 A  C___
GAM141  CD79A   3'  GCTCACTTCCCTGGGAC    8357    A_  A
                                GT  CAG GAAGTGAGC
                                ||  ||| |||||||||
                                CA  GTC CTTCACTCG
                                 GG  C
GAM141  CD79A   3'  GCTCACTTCCCTGGGAC    41206   A_  A
                                GT  CAG GAAGTGAGC
                                ||  ||| |||||||||
                                CA  GTC CTTCACTCG
                                 GG  C
GAM141  CYP2C9  3'  TTCTCCATACTCTGTAA    5749        CA
                                TTGCAGAGTA  GAGAA
                                ||||||||||  |||||
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                                AATGTCTCAT  CTCTT
                                      AC
GAM141  DIO1    3'  GCTCTCTGTACCCTG      5820     A       A
                                CAG GTACAGAGA GT
                                ||| ||||||||| ||
                                GTC CATGTCTCT CG
                                  C       _
GAM141  EPO     3'  AGCTCACTCGGCACCCTGCAA  5852       A  ACAGA  A
                                TTGCAG GT    GA GTGAGCT
                                |||||| ||    || |||||||
                                AACGTC CA    CT CACTCGA
                                   C  CGG__  _
GAM141  HDAC4   3'  GCTCACTCCAGCTTCACAA   20111    CA   ACAGA  A
                                TTG  GAGT    GA GTGAGC
                                |||  ||||    || ||||||
                                AAC  TTCG    CT CACTCG
                                  AC   AC___  _
GAM141  HUNK    3'  AGCTCACTGTTCACTGTGCAA  27439     G   ACA   A
                                TTGCA AGT   GAG AGTGAGCT
                                ||||| |||   ||| ||||||||
                                AACGT TCA   CTT TCACTCGA
                                   G   ___   G
GAM141  MXI1    3'  AGCTCATTTCATGCTCTGCAA  55258         CAGA
                                TTGCAGAGTA   GAAGTGAGCT
                                ||||||||||   ||||||||||
                                AACGTCTCGT   CTTTACTCGA
                                      A___
GAM141  MXI1    3'  AGCTCATTTCATGCTCTGCAA  19897         CAGA
                                TTGCAGAGTA   GAAGTGAGCT
                                ||||||||||   ||||||||||
                                AACGTCTCGT   CTTTACTCGA
                                      A___
GAM141  MYO1C   3'  AGCCCACTGCTGACACTTCTGC 61200       _ A_  AGA   A
           AA                     TTGCAGA GT  CAG   AGTG GCT
                                |||||||  ||  |||   |||| |||
                                AACGTCT CA  GTC   TCAC CGA
                                    T  CA   G__    C
GAM141  NTE     3'  AGCTCACTCCCCCTCCTGCTGC 21985     AGTACA  A___
                                GCAG     GAG    AGTGAGCT
                                ||||     |||    ||||||||
                                CGTC     CTC    TCACTCGA
                                  GTC___   CCCC
GAM141  PKD2L2  3'  TCTCTGTACTCCTCAA     26895     CA
                                TTG  GAGTACAGAGA
                                |||  ||||||||||
                                AAC  CTCATGTCTCT
                                  TC
GAM141  SI      3'  CTTGGTTCTTGTACTCTACAA  6438      C       G   G
                                TTG AGAGTACA AGAA TGAG
                                ||| |||||||| |||| ||||
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                                AAC TCTCATGT TCTT GTTC
                                  A       _   G
GAM141  FLJ10415  3'  TCCCTGACTCTGCAA      36100        A  A
                                TTGCAGAGT CAG GA
                                ||||||||| ||| ||
                                AACGTCTCA GTC CT
                                      _  C
GAM141  FLJ14084  3'  ACTCTACCTGTTCTCTGCAA  41295       T   __  A
                                TTGCAGAG ACAG  AGA GT
                                |||||||| ||||  ||| ||
                                AACGTCTC TGTC  TCT CA
                                     T   CA  _
GAM141  FLJ20093  3'  ACTAGTGGTTATACTCTGCAA  34552        C  AGA__
                                TTGCAGAGTA AG    AGT
                                |||||||||| ||    |||
                                AACGTCTCAT TT    TCA
                                      A  GGTGA
GAM141  MGC3329   3'  AGCTCTGGACTGCCTCTGCAA  44013       TA   AGAAGT
                                TTGCAGAG  CAG     GAGCT
                                ||||||||  |||     |||||
                                AACGTCTC  GTC     CTCGA
                                     C_   AGGT__
GAM141  MGC34923  5'  ACCTCTCTGTACTCTCAA    58517     C         A
                                TTG AGAGTACAGAGA GT
                                ||| ||||||||||| ||
                                AAC TCTCATGTCTCT CA
                                  _         C
GAM141  P2RX5     3'  GCCCACTCCCCTCTGCAA    10371       TACAGA  A   A
                                TTGCAGAG     GA GTG GC
                                ||||||||     || ||| ||
                                AACGTCTC     CT CAC CG
                                     CC_____  _   C
GAM141  PPY2      3'  AGCTCACTCCCTGTTCCTGCA  40818      AGT    A  A
                                TGCAG   ACAG GA GTGAGCT
                                |||||   |||| || |||||||
                                ACGTC   TGTC CT CACTCGA
                                   CT_   C  _
GAM141  SYT13     3'  AGCCCTGACCCGTCCTCTGCAA 93449       T  AGAGA  TGA
                                TTGCAGAG AC    AG   GCT
                                |||||||| ||    ||   |||
                                AACGTCTC TG    TC   CGA
                                     C  CCCAG  C__
GAM141  LOC145314 3'  CTCCTCCATGCTCTGCAA    77087        CA   A
                                TTGCAGAGTA  GAG AG
                                ||||||||||  ||| ||
                                AACGTCTCGT  CTC TC
                                      AC   C
GAM141  LOC145720 5'  AGCTCACTTCCCTTTCCTGC   83427     AGTAC  A
                                GCAG    AG GAAGTGAGCT
                                ||||    || ||||||||||
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                                CGTC    TC CTTCACTCGA
                                  CTT__  C
GAM141  LOC149194 3'  CTCACTTAACTTGCAA     79224      GAGTAC  AG
                                TTGCA     AG  AAGTGAG
                                |||||     ||  |||||||
                                AACGT     TC  TTCACTC
                                  _______  AA
GAM141  LOC154877 3'  AGCTCACTTCCCTCTCTACTG  86280     _  TAC  A
                                CAG AG   AG GAAGTGAGCT
                                ||| ||   || ||||||||||
                                GTC TC   TC CTTCACTCGA
                                  A  TC_  C
GAM141  LOC92578  3'  TCCCTATACTCTGCAG     69831          C  A
                                TTGCAGAGTA AG GA
                                |||||||||| || ||
                                GACGTCTCAT TC CT
                                      A  C
GAM142  FDFT1     3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                           _
GAM142  GCKR      3'  ATTTCAGAAATAAAATGAAATG 7635        C   CACTG
                                CATTTCA TTT     TCTGAAAT
                                ||||||| |||     ||||||||
                                GTAAAGT AAA     AGACTTTA
                                    A   TAA__
GAM142  GLO1      3'  TTTCAGAAGAAAGGAAA     22001      A    ACTG
                                TTTC CTTTC    TCTGAAA
                                |||| |||||    |||||||
                                AAAG GAAAG    AGACTTT
                                  _     A___
GAM142  JTB       3'  TCAGACAGTGAAAGTGAAATG  21962
                                CATTTCACTTTCACTGTCTGA
                                |||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACT

GAM142  LUZP1     3'  TGGGCAACAAGAGTGAAATG   53302          CAC
                                CATTTCACTTT   TGTCTG
                                ||||||||||   ||||||
                                GTAAAGTGAGA   ACGGGT
                                      ACA
GAM142  PHYH      3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM142  WRN       3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
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                                AAAGT AAAGTGACGGG
                                   A
GAM142  COASTER  3'  TTTTAGCAGTGAAAATGAA   31452      C       T
                                TTCA TTTCACTG CTGAAA
                                |||| |||||||| ||||||
                                AAGT AAAGTGAC GATTTT
                                   A      _
GAM142  DJ971N18.2 3'  CAGTACCTGAAAGTGAAA    40958          CT  _
                                TTTCACTTTCA  GT CTG
                                ||||||||||  || |||
                                AAAGTGAAAGT  CA GAC
                                      C_  T
GAM142  DKFZP586M1120 3'  AGTAGTGAAAATGAAA     48451       C       T
                                TTTCA TTTCACTG CT
                                ||||| |||||||| ||
                                AAAGT AAAGTGAT GA
                                   A       _
GAM142  ENDOFIN  3'  TTCAAACAGCAAAAAAGTGGGG 28389    TT     CA__    C
                                T  CACTTT    CTGT TGAA
                                |  ||||||    |||| ||||
                                G  GTGAAA    GACA ACTT
                                 GG     AAAC    A
GAM142  FLJ14909  3'  TTCATGAATGTGAAATG     51695         T    CTGTC
                                CATTTCAC TTCA     TGAA
                                |||||||| ||||     ||||
                                GTAAAGTG AAGT     ACTT
                                     T   _____
GAM142  FLJ20323  3'  TTTCTGACAAGTGAAA      38661         _   T
                                TTTCACT GTC GAAA
                                ||||||| ||| ||||
                                AAAGTGA CAG CTTT
                                    A   T
GAM142  FLJ23510  3'  TCAGACAGTGACTGAAATG    45289        CTT
                                CATTTCA   TCACTGTCTGA
                                |||||||   ||||||||||
                                GTAAAGT   AGTGACAGACT
                                    C__
GAM142  GPCR150   5'  ATTGAAGGCAGTAAAAGTGAAA 26876          C      GA
          T                      ATTTCACTTT ACTGTCT  AAT
                                |||||||||| |||||||  |||
                                TAAAGTGAAA TGACGGA  TTA
                                      A      AG
GAM142  HSPC019   3'  ATTTCAATCAGATGAAAGTGA  25856         _   TC
                                TCACTTTCA CTG  TGAAAT
                                ||||||||| |||  ||||||
                                AGTGAAAGT GAC  ACTTTA
                                      A   TA
GAM142  KIAA0574  3'  TTTCCTGTGAAAGGAAAT    69285       A      TGTCT
                                ATTTC CTTTCAC     GAAA
                                ||||| |||||||     ||||
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                                TAAAG GAAAGTG    CTTT
                                  _      TC___
GAM142  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAA
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM142  MGC27044  5'  TTGGTGTTGAAAGTGAAATG   58675          CTGT TG
                                CATTTCACTTTCA   C  A
                                ||||||||||||   | |
                                GTAAAGTGAAAGT   G  T
                                       TGT_ GT
GAM142  MRPL44    3'  GAGAGCGAAAGTGAGAT    43320         A  G
                                ATTTCACTTTC CT TC
                                |||||||||| || ||
                                TAGAGTGAAAG GA AG
                                       C  G
GAM142  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM142  PORIMIN   3'  TCAGAGGGCCAAAGTGAA   53608       CA  G
                                TTCACTTT  CT TCTGA
                                ||||||||  || |||||
                                AAGTGAAA  GG AGACT
                                     CC  G
GAM142  PRTD-NY3  3'  TCATTGCAATAAGTGAAATG  48151        TCAC   C_
                                CATTTCACTT   TGT  TGA
                                ||||||||||   |||  |||
                                GTAAAGTGAA   ACG  ACT
                                      TA__   TT
GAM142  SEP15     3'  TCCTACAGTAAGAGTGAAA   14934       C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                      A    TC
GAM142  SFXN2     3'  TCAGGGGAAAAAAGTGAAA   73954       CACTG
                                TTTCACTTT    TCTGA
                                |||||||||    |||||
                                AAAGTGAAA    GGACT
                                      AAAGG
GAM142  SGT1      3'  ATTTCAGACATGGTGAAACTG  21992    C     __
                                CA TTTCACT  GTCTGAAAT
                                || |||||||  |||||||||
                                GT AAAGTGG  CAGACTTTA
                                 C      TA
GAM142  UPK3      3'  TTCAGGGAAGGTGAAA      22722         ACTG
                                TTTCACTTTC   TCTGAA
                                ||||||||||   ||||||
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                                AAAGTGGAAG   GGACTT
                                     ____
GAM142  ZMPSTE24  3'  ATTTCAGTTCTGCAAAAGTGAA 19594        CACTGT_
            A                    TTTCACTTT     CTGAAAT
                                 |||||||||     |||||||
                                 AAAGTGAAA     GACTTTA
                                     ACGTCTT
GAM142  LOC123283 3'  TTCATCGAGAAAGTGAAA    76013         AC  TC
                                 TTTCACTTTC  TG  TGAA
                                 ||||||||||  ||  ||||
                                 AAAGTGAAAG  GC  ACTT
                                     A_  T_
GAM142  LOC145674 5'  ATTTCTGACTTGAAGTGAAAT  63200        T  CT   T
                                 ATTTCACTT CA  GTC GAAAT
                                 |||||||||  ||  |||  |||||
                                 TAAAGTGAA GT  CAG CTTTA
                                     _  T_   T
GAM142  LOC202908 5'  CAGAGGGGTGACAGTGAAA   89227       T   _ G
                                 TTTCACT TCAC T TCTG
                                 |||||||  ||||  |  ||||
                                 AAAGTGA AGTG G AGAC
                                     C    G G
GAM142  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                 CATTTCACTT CACTGT
                                 ||||||||||  ||||||
                                 GTAAAGTGAA GTGACA
                                     _
GAM142  LOC255338 5'  TTTGGACAAAAGTGAA      95935        CAC    TG
                                 TTCACTTT   TGTC  AA
                                 ||||||||   ||||  ||
                                 AAGTGAAA   ACAG  TT
                                     ___    GT
GAM143  ABCB10   3'  ATGAACTGCTAGGTATTATT   23886        AG    A
                                 AATAATAC  GGTA GTTCAT
                                 ||||||||  ||||  ||||||
                                 TTATTATG  TCGT CAAGTA
                                     GA    _
GAM143  BPAG1    3'  GCACCTGTATCATTGAA     31429        A      _
                                 TTCAAT ATACAGG GT
                                 ||||||  |||||||  ||
                                 AAGTTA TATGTCC CG
                                    C      A
GAM143  EML1     3'  ACCATGTATTATTGAA      59728           G
                                 TTCAATAATACA GGT
                                 ||||||||||||  |||
                                 AAGTTATTATGT CCA
                                       A
GAM143  HEM1     5'  ATGAACTTCTCAACACCATTGA 18049       AATACA   T
                                 TCAAT     GGG AAGTTCAT
                                 |||||     |||  ||||||||
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                                AGTTA     CTC TTCAAGTA
                                   CCACAA  _
GAM143  TTC3      5'  ATCCTTATTATTGAA       12416          C
                                TTCAATAATA AGGGT
                                |||||||||| |||||
                                AAGTTATTAT TCCTA
                                          _
GAM143  FLJ10468  3'  ATGTTTATCCCTGTTTACTGAA 36144      A   T     TAAGTT
                                TTCA TAA ACAGGG     CAT
                                |||| ||| ||||||     |||
                                AAGT ATT TGTCCC     GTA
                                  C  _     TATTT_
GAM143  KIAA1280  5'  AACTTACCCAGATTGAG     69707       AATACA
                                TTCAAT     GGGTAAGTT
                                ||||||     |||||||||
                                GAGTTA     CCCATTCAA
                                   GA_____
GAM143  NEUROD6   5'  TGAAAACTGATTATTGAA     42688         A   GGTAAG
                                TTCAATAAT CAG     TTCA
                                ||||||||| |||     ||||
                                AAGTTATTA GTC     AAGT
                                      _   AA_____
GAM143  LOC144202 5'  TGAACTGCACATTGTTGAA    76710         ACAGG   A
                                TTCAATAAT     GTA GTTCA
                                |||||||||     ||| |||||
                                AAGTTGTTA     CGT CAAGT
                                      CA___   _
GAM143  LOC221552 3'  AACTTACCTATCATTTGAA    93804       TAATACA
                                TTCAA      GGGTAAGTT
                                |||||      |||||||||
                                AAGTT      TCCATTCAA
                                   TACTA__
GAM143  LOC257493 3'  AACTTACCTATCATTTGAA    97799       TAATACA
                                TTCAA      GGGTAAGTT
                                |||||      |||||||||
                                AAGTT      TCCATTCAA
                                   TACTA__
GAM143  LOC257609 3'  AACTTACCTATCATTTGAA    97939       TAATACA
                                TTCAA      GGGTAAGTT
                                |||||      |||||||||
                                AAGTT      TCCATTCAA
                                   TACTA__
GAM143  LOC90768  5'  ATGAACTTACTGCGCCATTTGA 63951       TAATACAG
          A                      TTCAA       GGTAAGTTCAT
                                |||||       ||||||||||
                                AAGTT       TCATTCAAGTA
                                   TACCGCG_
GAM144  HPGD      3'  CAAACCAGATGTAAAACACTCA 5979        A   CT  GTA
                                TGGGT TTT  CA   CTGGTTTG
                                ||||| |||  ||   ||||||||
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                                ACTCA AAA  GT   GACCAAAC
                                  C   AT  A__
GAM144  RASGRP1  3'  CAAATTTAAACTCAGAAATACC 19203          C   ACT
          CA                    TGGGTATTTCT AGT   GGTTTG
                                |||||||||||| |||   ||||||
                                ACCCATAAAGA TCA   TTAAAC
                                      C   AAT
GAM144  APOARGC  3'  CAAACCAGCACCAACAGAGCC  44416     ATT   CA__  A
                                GGT   TCT    GT CTGGTTTG
                                |||   |||    || ||||||||
                                CCG   AGA    CA GACCAAAC
                                  ___   CAAC  C
GAM144  COE2     3'  CAAACCAATGAAGAAATACC   64248         CA  AC
                                GGTATTTCT  GT  TGGTTTG
                                |||||||||  ||  |||||||
                                CCATAAAGA  TA  ACCAAAC
                                     AG  __
GAM144  KIAA1559  3'  GACCAACACTGAGAAACCCCA  73065      TA        AC
                                TGGG  TTTCTCAGT  TGGTT
                                ||||  |||||||||  |||||
                                ACCC  AAAGAGTCA  ACCAG
                                  C_        CA
GAM144  ZNF84    3'  ATGGGTACCAAAAATACCCA   12815         CTCA    G
                                TGGGTATTT    GTACT GT
                                |||||||||    ||||| ||
                                ACCCATAAA    CATGG TA
                                     AAC_    G
GAM144  LOC151056 3'  CAAACCAGTCACCAAATTCCCA 80108      T    CTCA  _
                                TGGG ATTT    GT ACTGGTTTG
                                |||| ||||    || |||||||||
                                ACCC TAAA    CA TGACCAAAC
                                  T   C___  C
GAM144  LOC157603 5'  CAAACCAGCACTGATCTCCC   86491     TATTTC    A
                                GGG     TCAGT CTGGTTTG
                                |||     ||||| ||||||||
                                CCC     AGTCA GACCAAAC
                                  TCT___     C
GAM144  LOC253263 3'  AGGCACTGAGAAAAACCCA    97026       A       A_
                                TGGGT TTTCTCAGT  CT
                                ||||| |||||||||  ||
                                ACCCA AAAGAGTCA  GA
                                   A       CG
GAM145  AXL      3'  TCTCACACTCAGTTG       8111       A
                                CAAC TGAGTGTGAGA
                                |||| ||||||||||
                                GTTG ACTCACACTCT
                                  _
GAM145  AXL      3'  TCTCACACTCAGTTG       41608      A
                                CAAC TGAGTGTGAGA
                                |||| ||||||||||
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                                GTTG ACTCACACTCT
                                  _
GAM145  MCC     3'  ACTTAGCTCCTGTTGTCATG  9957      GTGTG  A
                                CATGA    AG AGCTAAGT
                                ||||||    || ||||||||
                                GTACT    TC TCGATTCA
                                   GTTG_  C
GAM145  MPP5    3'  ACTTAGCTTCCCTTCCCTCATC 42483   C    TGTGA_
          A                      A ATGAG     GAAGCTAAGT
                                | |||||     ||||||||||
                                A TACTC     CTTCGATTCA
                                 C    CCTTCC
GAM145  MS4A7   3'  TTTTCACACTCATATTG    41067    C
                                CAA ATGAGTGTGAGAA
                                ||| ||||||||||||
                                GTT TACTCACACTTTT
                                  A
GAM145  STAU    3'  CTTAGCTTTCACTACACT    33901      A__
                                AGTGTG  GAAGCTAAG
                                ||||||  |||||||||
                                TCACAT  TTTCGATTC
                                   CAC
GAM145  STAU    3'  CTTAGCTTTCACTACACT    33908      A__
                                AGTGTG  GAAGCTAAG
                                ||||||  |||||||||
                                TCACAT  TTTCGATTC
                                   CAC
GAM145  STAU    3'  CTTAGCTTTCACTACACT    33895      A__
                                AGTGTG  GAAGCTAAG
                                ||||||  |||||||||
                                TCACAT  TTTCGATTC
                                   CAC
GAM145  STAU    3'  CTTAGCTTTCACTACACT    16004      A__
                                AGTGTG  GAAGCTAAG
                                ||||||  |||||||||
                                TCACAT  TTTCGATTC
                                   CAC
GAM145  TZFP    5'  ACTTACAAACCACACTCAT   26888        AGAAGC
                                ATGAGTGTG     TAAGT
                                |||||||||     |||||
                                TACTCACAC     ATTCA
                                    CAAAC_
GAM145  VNN2    3'  ACTCAGCTTCTGCATCAT    16237     G  G     A
                                ATGA TGT AGAAGCT AGT
                                |||| ||| ||||||| |||
                                TACT ACG TCTTCGA TCA
                                  _  _     C
GAM145  VNN2    3'  ACTCAGCTTCTGCATCAT    54356     G  G     A
                                ATGA TGT AGAAGCT AGT
                                |||| ||| ||||||| |||
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                                TACT ACG TCTTCGA TCA
                                  _  _     C
GAM145  APXL2    5'  AGCCTCAGCACTCAT      75184       _   AA
                                ATGAGTG TGAG  GCT
                                ||||||| ||||  |||
                                TACTCAC ACTC  CGA
                                   G   __
GAM145  FKSG87   3'  ACTCAGCCTCCCATTCACATGT 49325    __    T   AA   A
                                ACA  TGAGTG GAG  GCT AGT
                                |||  |||||| |||  ||| |||
                                TGT  ACTTAC CTC  CGA TCA
                                  AC     C  __  C
GAM145  FLJ10359 3'  ACTCAGAGTTCACACTCAT   36065         AAG  A
                                ATGAGTGTGAG   CT AGT
                                ||||||||||   || |||
                                TACTCACACTT   GA TCA
                                      GA_  C
GAM145  FLJ12568 3'  GGGATCTCACACCCATGTT   46500      A      AG
                                AACATG GTGTGAGA  CT
                                |||||| ||||||||  ||
                                TTGTAC CACACTCT  GG
                                   C       AG
GAM145  GHITM    3'  ACTCAGCTTCTGGCTTCTCTG  26913    T   T_  G     A
                                CA GAG  GT AGAAGCT AGT
                                || |||  || ||||||| |||
                                GT CTC  CG TCTTCGA TCA
                                 _  TT  G      C
GAM145  KIAA0092 3'  ACTTAGTTGCCACACTCATG   27966        AGA
                                CATGAGTGTG   AGCTAAGT
                                ||||||||||   ||||||||
                                GTACTCACAC   TTGATTCA
                                      CG_
GAM145  KIAA1817 3'  CTTGGGCTCACACTCA      68229         AAG
                                TGAGTGTGAG   CTAAG
                                ||||||||||   |||||
                                ACTCACACTC   GGTTC
                                      G__
GAM145  KSR      5'  AGCTTCCCCACACTCA      64042        A_
                                TGAGTGTG  GAAGCT
                                ||||||||  ||||||
                                ACTCACAC  CTTCGA
                                     CC
GAM145  MGC5528  3'  ACTTAGCTAATGAACTCAT   44042       GTGAGA
                                ATGAGT     AGCTAAGT
                                ||||||     ||||||||
                                TACTCA     TCGATTCA
                                   AGTAA_
GAM145  PRO2037  3'  AGCTTGAGACCTCATGT     37784        T  GAG
                                ACATGAG GT   AAGCT
                                ||||||| ||   |||||
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                                TGTACTC CA   TTCGA
                                    _ GAG
GAM145  SHANK3    3'  ACTCGGTCTCACACTCA     65487          AA  TA
                                TGAGTGTGAG  GC  AGT
                                ||||||||||  ||  |||
                                ACTCACACTC  TG  TCA
                                      __ GC
GAM145  LOC116437 3'  TTTCCACTCATGCTG       73894     A       T
                                CA CATGAGTG GAGA
                                || ||||||||| ||||
                                GT GTACTCAC CTTT
                                 C       _
GAM145  LOC146909 3'  ACTCAGCTTCTTGGCATGT    78161       AGTGT       A
                                ACATG     GAGAAGCT AGT
                                |||||     |||||||| |||
                                TGTAC     TTCTTCGA TCA
                                   GG___       C
GAM145  LOC147093 5'  CTCTTCACCTCATGCTG     83943     A     T    GA
                                CA CATGAG GTGA  AG
                                || |||||| ||||  ||
                                GT GTACTC CACT  TC
                                 C      _    TC
GAM145  LOC154386 3'  AGCTCTCACACTCATTTG    81080     C          A
                                CAA ATGAGTGTGAGA GCT
                                ||| |||||||||||| |||
                                GTT TACTCACACTCT CGA
                                  _          _
GAM145  LOC159121 5'  AGCCACACCATGTCA       86989    A    A    AGAA
                                C ACATG GTGTG    GCT
                                | ||||| |||||    |||
                                A TGTAC CACAC    CGA
                                 C    _    _____
GAM146  8D6A      3'  CTCGAACCCGAGCTCCTG     33421          AA  CTATTG
                                CAGGAGCTC  GG      TGAG
                                |||||||||  ||      ||||
                                GTCCTCGAG  CC      GCTC
                                      C_  AA____
GAM146  ACADSB    3'  GCTCACTGCAGCCTTGACCTCC 7847        C       ATT
              TG                  CAGGAG TCAAGGCT   GTGAGC
                                  |||||| ||||||||   ||||||
                                  GTCCTC AGTTCCGA   CACTCG
                                     C       CGT
GAM146  ADRBK1    3'  GCCCCGCTTGCCTCGGCTCCTG 7869         CA    TATT   A_
                                CAGGAGCT  AGGC    GTG  GC
                                ||||||||  ||||    |||  ||
                                GTCCTCGG  TCCG    CGC  CG
                                     C_    TT__   CC
GAM146  AQP6      3'  AGCCTCTGAGCTCCTG       7939           _
                                CAGGAGCTCA AGGCT
                                |||||||||| |||||
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                                GTCCTCGAGT TCCGA
                                      C
GAM146  AQP6    3'  AGCCTCTGAGCTCCTG     53910        _
                                CAGGAGCTCA AGGCT
                                |||||||||| |||||
                                GTCCTCGAGT TCCGA
                                      C
GAM146  ATM     3'  GCCCAGGGTGGTCTCAAACTCC 56305      CTCA      G  A
           TG                    CAGGAG   AGGCTATT TG GC
                                ||||||   |||||||| || ||
                                GTCCTC   TCTGGTGG AC CG
                                   AAAC      G  C
GAM146  CH25H   3'  GCTCACCTCAATAGCCTTGAAT 14210      GC        ___
           CCTG                   CAGGA  TCAAGGCTATT   GTGAGC
                                |||||  ||||||||||   ||||||
                                GTCCT  AGTTCCGATAA   CACTCG
                                   A_         CTC
GAM146  CLECSF11 5'  TAGTCTTGAACTCCTG     55276      C
                                CAGGAG TCAAGGCTA
                                ||||||| |||||||||
                                GTCCTC AGTTCTGAT
                                   A
GAM146  CREBL2  3'  CTCCCTTAGCCTGAGCTCCT   7145        A    TTGT
                                AGGAGCTCA GGCTA   GAG
                                ||||||||| |||||   |||
                                TCCTCGAGT CCGAT   CTC
                                   _    TCC_
GAM146  EPB49   3'  GCTCGCAAACCCCGAGCTTC  8788       AA  CTA
                                GGAGCTC  GG   TTGTGAGC
                                |||||||  ||   ||||||||
                                CTTCGAG  CC   AACGCTCG
                                   CC  A__
GAM146  FOLR1   3'  GTTCAGCCCCACAGCTCC    33614      CAA_   ATTGT
                                GGAGCT   GGCT    GAGC
                                ||||||   ||||    ||||
                                CCTCGA   CCGA    CTTG
                                   CACC   _____
GAM146  FOLR1   3'  GTTCAGCCCCACAGCTCC    33615      CAA_   ATTGT
                                GGAGCT   GGCT    GAGC
                                ||||||   ||||    ||||
                                CCTCGA   CCGA    CTTG
                                   CACC   _____
GAM146  FOLR1   3'  GTTCAGCCCCACAGCTCC    33609      CAA_   ATTGT
                                GGAGCT   GGCT    GAGC
                                ||||||   ||||    ||||
                                CCTCGA   CCGA    CTTG
                                   CACC   _____
GAM146  FOLR1   3'  GTTCAGCCCCACAGCTCC    33610      CAA_   ATTGT
                                GGAGCT   GGCT    GAGC
                                ||||||   ||||    ||||
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                                CCTCGA   CCGA    CTTG
                                   CACC   _____
GAM146  FOLR1    3'  GTTCAGCCCCACAGCTCC    33611       CAA_   ATTGT
                                GGAGCT   GGCT    GAGC
                                ||||||   ||||    ||||
                                CCTCGA   CCGA    CTTG
                                   CACC   _____
GAM146  FSHPRH1  5'  GCCCAGACTGGTCTTGAACTCC 22115      C       TTG  A
           T                    AGGAG TCAAGGCTA   TG GC
                                ||||| |||||||||   || ||
                                TCCTC AGTTCTGGT   AC CG
                                   A       CAG  C
GAM146  FTSJ2    3'  GTAGCCTGAGCTCCTG      25435          A
                                CAGGAGCTCA GGCTAT
                                |||||||||| ||||||
                                GTCCTCGAGT CCGATG

                                   _
GAM146  GAB2     3'  GCTCACAGGCCCCAAACTACC  24495    _  CTCAA    AT
                                GG AG    GGCT  TGTGAGC
                                || ||    ||||  |||||||
                                CC TC    CCGG  ACACTCG
                                 A  AAACC   __
GAM146  GAB2     3'  GCTCACAGGCCCCAAACTACC  54452    _  CTCAA    AT
                                GG AG    GGCT  TGTGAGC
                                || ||    ||||  |||||||
                                CC TC    CCGG  ACACTCG
                                 A  AAACC   __
GAM146  GLTSCR1  5'  CTCTGCAGCCTCAAACTCCTG  31671       CTCA    ATTGT
                                CAGGAG    AGGCT    GAG
                                ||||||    |||||    |||
                                GTCCTC    TCCGA    CTC
                                   AAAC    CGT__
GAM146  HUNK     3'  GCTCAGGCTGATCTCAAACTCC 27455      CTCAA____   ATTG
           TG                     AGGAG       GGCT    TGAGC
                                |||||       ||||    |||||
                                TCCTC       TCGG    ACTCG
                                   AAACTCTAG   ____
GAM146  IL2      5'  CTCACAGTAACCTCAACTCCTG 64647       CTCA   C
                                CAGGAG    AGG TATTGTGAG
                                ||||||    ||| |||||||||
                                GTCCTC    TCC ATGACACTC
                                   AAC_   A
GAM146  INSRR    3'  ACAACCCTGGGCTCC       68464         A  CTA
                                GGAGCTCA GG   TTGT
                                |||||||| ||   ||||
                                CCTCGGGT CC   AACA
                                     C  ___
GAM146  MAFF     3'  CAGAGCCCGAGCTCCTG     24643          AA    A
                                CAGGAGCTC  GGCT TTG
                                |||||||||  |||| |||
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                                GTCCTCGAG  CCGA GAC
                                     C_   _
GAM146  MBTPS1   5'  GCCCGCCGGCCCTGAGCTCC   13704        A   ATT   A
                                GGAGCTCA GGCT   GTG GC
                                |||||||| ||||   ||| ||
                                CCTCGAGT CCGG   CGC CG
                                     C   C__   C
GAM146  MMP15    3'  GCAGCAGCCCCCAGCTCC    10073       CAA   A
                                GGAGCT   GGCT TTGT
                                ||||||   |||| ||||
                                CCTCGA   CCGA GACG
                                   CCC   C
GAM146  MOX2     3'  GCTCACAGACTGACTTGGGCTC 66929          GCTA_
           CT                     AGGAGCTCAAG    TTGTGAGC
                                ||||||||||    ||||||||
                                TCCTCGGGTTC    GACACTCG
                                      AGTCA
GAM146  NFE2     3'  CTCCCCAACCCTGAGTCCC   20489    AG   A  CTA   T_
                                GG  CTCA GG   TTG  GAG
                                ||  |||| ||   |||  |||
                                CC  GAGT CC   AAC  CTC
                                 CT   C ___   CC
GAM146  PTPN18   3'  GCCCAGACTGGTCTTGAACTCC 26866     C       TTG  A
                                GGAG TCAAGGCTA   TG GC
                                |||| |||||||||   || ||
                                CCTC AGTTCTGGT   AC CG
                                  A       CAG  C
GAM146  RAB36    3'  GCCCCACAGCCCCAGGCTCCTG 16964        CAA   ATT   A_
                                CAGGAGCT   GGCT   GTG  GC
                                ||||||||   ||||   |||  ||
                                GTCCTCGG   CCGA   CAC  CG
                                     ACC    ___   CC
GAM146  SLC25A17 5'  CTCACACCCTGAGCTCC     20997        A  CTAT
                                GGAGCTCA GG    TGTGAG
                                |||||||| ||    ||||||
                                CCTCGAGT CC    ACACTC
                                     C  ____
GAM146  SLC8A2   3'  CACTCCTTGGGCCCCT      66328     A      CTATT
                                AGG GCTCAAGG     GTG
                                ||| ||||||||     |||
                                TCC CGGGTTCC     CAC
                                  C       T____
GAM146  TAL1     3'  GCTGTCTGCAGCCTTGAACTCT 12109      C       ATTGTG
                                GGAG TCAAGGCT     AGC
                                |||| ||||||||     |||
                                TCTC AGTTCCGA     TCG
                                  A       CGTCTG
GAM146  USP7     5'  CTCGCAGCCCCGGCCCC     12954    A  CAA   ATT
                                GG GCT   GGCT   GTGAG
                                || |||   ||||   |||||
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                                CC CGG   CCGA   CGCTC
                                 C   CC_   ___
GAM146  VWF      3'  GCCCACAATAAAGGCTGAGCTC 5094          A G __     A
              TT                  AGGAGCTCA G CT  ATTGTG GC
                                  ||||||||| | ||  |||||| ||
                                  TTCTCGAGT C GA  TAACAC CG
                                       _ G  AA     C
GAM146  XRCC2    3'  GCTCACTGCAGCCTTGAACTCC 18325       C       ATT
              TG                  CAGGAG TCAAGGCT   GTGAGC
                                  |||||| ||||||||   ||||||
                                  GTCCTC AGTTCCGA   CACTCG
                                     A       CGT
GAM146  C(27)-3BETA-HSD 3'  GCTCAGGCTGGTCTTGAACTCC 47274       C       TTG
              TG                  CAGGAG TCAAGGCTA   TGAGC
                                  |||||| |||||||||   |||||
                                  GTCCTC AGTTCTGGT   ACTCG
                                     A        CGG
GAM146  C1orf34   3'  TAGTCTTGAACTCCTG      60680       C
                                  CAGGAG TCAAGGCTA
                                  |||||| |||||||||
                                  GTCCTC AGTTCTGAT
                                     A
GAM146  C20orf27  5'  CTCGGCGTTGAGCTCCTG    35384          G   ATTGT
                                  CAGGAGCTCAA GCT    GAG
                                  |||||||||| |||    |||
                                  GTCCTCGAGTT CGG    CTC
                                        G  _____
GAM146  C21orf69  3'  GCCCTGGCCTTGACCTCC    54212      C       TT
                                  GGAG TCAAGGCTA  GT
                                  |||| |||||||||  ||
                                  CCTC AGTTCCGGT  CG
                                    C        CC
GAM146  CDC42BPB  5'  GCTCGCAGCCGCCGAGCCCC   20100    A    AA   TA
                                  GG GCTC  GGC  TTGTGAGC
                                  || ||||  |||  ||||||||
                                  CC CGAG  CCG  GACGCTCG
                                   C   __   CC
GAM146  DKFZP566I1024 3'  GCCCAGGGTGGTCTCGAACTCC 70103       C  A       G  A
              TG                  CAGGAG TC AGGCTATT TG GC
                                  |||||| || |||||||| || ||
                                  GTCCTC AG TCTGGTGG AC CG
                                     A  C       G  C
GAM146  DKFZP566I1024 3'  GCTCACTCTAGCCTTGAATTCC 70104       C       TT
              TG                  CAGGAG TCAAGGCTA  GTGAGC
                                  |||||| |||||||||  ||||||
                                  GTCCTT AGTTCCGAT  CACTCG
                                     A        CT
GAM146  DKFZP761F241 3'  CTCACACGGCCAAGCTTCTG  48793        CAA    AT
                                  CAGGAGCT   GGCT  TGTGAG
                                  ||||||||   ||||  ||||||
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                                GTCTTCGA  CCGG  ACACTC
                                    A__   C_
GAM146  DNAJA3   3' ACAGCAGCACTGAGCTCC    60481       AG  A
                                GGAGCTCA  GCT TTGT
                                ||||||||  ||| ||||
                                CCTCGAGT  CGA GACA
                                    CA  C
GAM146  FLJ00007 3' CAGAGCCCCAGCTCCTG     71271       CAA   A
                                CAGGAGCT  GGCT TTG
                                ||||||||  |||| |||
                                GTCCTCGA  CCGA GAC
                                    CC_   _
GAM146  FLJ00007 3' GCCAGGGAAGCCTTGACCCCC 71276    AGC      A  G  A
                                GG  TCAAGGCT TT TG GC
                                ||  |||||||| || || ||
                                CC  AGTTCCGA GG AC CG
                                 CCC      A  G  _
GAM146  FLJ10847 3' GCTCACTGCAGCCTCGAACTCT 36751      C  A    ATT
          TG                    CAGGAG TC AGGCT   GTGAGC
                                ||||||| || |||||  ||||||
                                GTTCTC AG TCCGA   CACTCG
                                   A  C    CGT
GAM146  FLJ11155 5' GCCATAACCCATAAGCTCCTG  37118       CAA  CTA    A
                                CAGGAGCT  GG  TTGTG GC
                                ||||||||  ||  ||||| ||
                                GTCCTCGA  CC  AATAC CG
                                    ATA  C__   _
GAM146  FLJ11467 3' GCTCACTGCAGCCTTGACCTCC 46377     C      ATT
                                GGAG TCAAGGCT  GTGAGC
                                ||||  ||||||||  ||||||
                                CCTC AGTTCCGA  CACTCG
                                  C      CGT
GAM146  FLJ11710 3' GCTCACTGCAGCCTTGAATTCC 45829      C      ATT
          TG                    CAGGAG TCAAGGCT  GTGAGC
                                ||||||  ||||||||  ||||||
                                GTCCTT AGTTCCGA  CACTCG
                                   A      CGT
GAM146  FLJ12150 5' GCTCTGGGCACCTCCAGCTCCT 45351       CA  CTATTGT
          G                     CAGGAGCT  AGG     GAGC
                                ||||||||  |||     ||||
                                GTCCTCGA  TCC     CTCG
                                    CC  ACGGGT_
GAM146  FLJ14107 3' GCCCAGCTTGCCCTGATCCCCT 46694    AGC  A  TATT  GA_
          G                     CAGG  TCA GGC   GT  GC
                                ||||  ||| |||   ||  ||
                                GTCC  AGT CCG   CG  CG
                                  CCT  C  TT__  ACC
GAM146  FLJ14213 3' AATAGCCTGAAGCCCCT    45791    A  CA
                                AGG GCT  AGGCTATT
                                ||| |||  ||||||||
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                                TCC CGA  TCCGATAA
                                  C   AG
GAM146  FLJ20542  3'  GCCAAGAAGCCTCGGCTCCTG  49785       CA    ATTG  A
                                CAGGAGCT  AGGCT    TG GC
                                ||||||||  |||||    || ||
                                GTCCTCGG  TCCGA    AC CG
                                    C_     AGA_  _
GAM146  FLJ20584  5'  GCTCAGCTGAGCCCATGAGCTC 35430       A_   ATTG
          C                      GGAGCTCA  GGCT    TGAGC
                                ||||||||  ||||    |||||
                                CCTCGAGT  CCGA    ACTCG
                                    AC    GTCG
GAM146  FLJ22688  3'  GCTCACAATAATACACAGCCCC 47098     A   CAAGGC
          TG                     CAGG GCT     TATTGTGAGC
                                |||| |||     ||||||||||
                                GTCC CGA     ATAACACTCG
                                  C   CACATA
GAM146  FLJ23168  3'  GCTCAACAAGCCCTTGAGCCCC 46823    A      CTA   _
                                GG GCTCAAGG   TTGT GAGC
                                || ||||||||   |||| ||||
                                CC CGAGTTCC   AACA CTCG
                                 C       CG_   A
GAM146  FLJ23416  3'  GCTCACTGCAGCCTTGAACTCC 49951       C       ATT
          TG                     CAGGAG TCAAGGCT   GTGAGC
                                ||||||  ||||||||   ||||||
                                GTCCTC AGTTCCGA   CACTCG
                                   A       CGT
GAM146  FLJ32499  3'  GCTCACTGCAGCCTGGAGCTCC 58158        A    ATT
          TG                     CAGGAGCTC AGGCT   GTGAGC
                                |||||||||  |||||   ||||||
                                GTCCTCGAG TCCGA   CACTCG
                                    G    CGT
GAM146  GP5     3'  CTCCTGGTCTTGAACTCCTG   15643       C       TTGT
                                CAGGAG TCAAGGCTA    GAG
                                ||||||  |||||||||   |||
                                GTCCTC AGTTCTGGT    CTC
                                   A       C___
GAM146  GPS2    5'  CACCACCCTCGAGTTCCTG    15662        A   CTATT
                                CAGGAGCTC AGG    GTG
                                |||||||||  |||    |||
                                GTCCTTGAG TCC    CAC
                                    C   CAC__
GAM146  IKKE    5'  CACTAGTCCCAGCTCCTG    25747        CAA    TT
                                CAGGAGCT   GGCTA  GTG
                                ||||||||   |||||  |||
                                GTCCTCGA   CTGAT  CAC
                                    CC_    __
GAM146  IL1F10   3'  GCGTTTTAGCCTTGTGCCCC   50773    A  T      TTGTGA
                                GG GC CAAGGCTA     GC
                                || || ||||||||     ||
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                                CC CG GTTCCGAT     CG
                                 C  T      TTTG__
GAM146  KIAA0737 3' GCCCAGTCTAGTCTTGAACTCC 29138      C       TTG  A
            TG                   CAGGAG TCAAGGCTA   TG GC
                                 |||||| |||||||||   || ||
                                 GTCCTC AGTTCTGAT   AC CG
                                    A       CTG  C
GAM146  KIAA1030 3' CTCTCACCCCAGCTCCTG    93333        CAA  CTAT  T
                                 CAGGAGCT   GG    TG GAG
                                 ||||||||   ||    || |||
                                 GTCCTCGA   CC    AC CTC
                                      CC_  ____  T
GAM146  KIAA1040 3' GCCATTCTAGTCTTGAACTCCT 72228      C       TT   A
            G                    CAGGAG TCAAGGCTA  GTG GC
                                 |||||| |||||||||  ||| ||
                                 GTCCTC AGTTCTGAT  TAC CG
                                    A       CT  _
GAM146  KIAA1219 3' GCTCACAATAACATCTGCCC   61369    A  TCAAGGC
                                 GG GC      TATTGTGAGC
                                 || ||      ||||||||||
                                 CC CG      ATAACACTCG
                                  _  TCTACA_
GAM146  KIAA1271 3' CAACTGCCTTGAGTTCCTG    69538           TA
                                 CAGGAGCTCAAGGC  TTG
                                 ||||||||||||||  |||
                                 GTCCTTGAGTTCCG  AAC
                                        TC
GAM146  KIAA1297 3' CCCACCCCTAGCTCCTG     72173        CA   CTATT   A_
                                 CAGGAGCT  AGG     GTG  G
                                 ||||||||  |||     |||  |
                                 GTCCTCGA  TCC     CAC  C
                                      __   C_____   CC
GAM146  KIAA1396 3' GCCCAGGGTGGTCTCAAACTCC 62989       CTCA       G  A
            TG                   CAGGAG    AGGCTATT TG GC
                                 ||||||    |||||||| || ||
                                 GTCCTC    TCTGGTGG AC CG
                                    AAAC       G  C
GAM146  KIAA1641 3' GCTCACATTATCACCTGAGCTC 80210         A  C__  T
            T                    GGAGCTCA GG   TA TGTGAGC
                                 ||||||||  ||   || |||||||
                                 TCTCGAGT CC   AT ACACTCG
                                      _  ACT  T
GAM146  KIAA1649 3' CAGGATGGTCTTGAACTCCTG  50248       C         G
                                 CAGGAG TCAAGGCTATT TG
                                 |||||| |||||||||| ||
                                 GTCCTC AGTTCTGGTAG AC
                                    A         G
GAM146  KIAA1727 3' GCTCAGGCTGATCTCGAGCTCC 64058         A  GC  TTG
            TG                   CAGGAGCTC AG  TA   TGAGC
                                 |||||||| ||  ||   |||||
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                                GTCCTCGAG TC  GT   ACTCG
                                     C  TA  CGG
GAM146  KIAA1755  3'  GCAATCATAGCCTTAAATTCCT 61347       CTC       T  GA
            G                    CAGGAG   AAGGCTAT GT  GC
                                 ||||||   |||||||| ||  ||
                                 GTCCTT   TTCCGATA TA  CG
                                    AAA       C  A_
GAM146  KIAA1962  3'  GCCCAGACTGGTCTTGAACTCC 81917       C       TTG  A
            TG                   CAGGAG TCAAGGCTA   TG GC
                                 |||||| |||||||||   || ||
                                 GTCCTC AGTTCTGGT   AC CG
                                    A        CAG  C
GAM146  LNIR     3'  GCTCAGGCTGGCCTTGAACTCC 48132       C       TTG
            TG                   CAGGAG TCAAGGCTA   TGAGC
                                 |||||| |||||||||   |||||
                                 GTCCTC AGTTCCGGT   ACTCG
                                    A        CGG
GAM146  MGC15873  5'  GCTCACTGCAGCCTTGACCTCC 51905       C       ATT
            TG                   CAGGAG TCAAGGCT   GTGAGC
                                 |||||| ||||||||   ||||||
                                 GTCCTC AGTTCCGA   CACTCG
                                    C       CGT
GAM146  MRPL4    5'  GCTCCAGTGGCCTTGACCTCC  31981      C          T
                                 GGAG TCAAGGCTATTG GAGC
                                 |||| ||||||||||| ||||
                                 CCTC AGTTCCGGTGAC CTCG
                                   C          _
GAM146  MRPL44   3'  TAGTCTTGAACTCCTG      43325       C
                                 CAGGAG TCAAGGCTA
                                 |||||| |||||||||
                                 GTCCTC AGTTCTGAT
                                    A
GAM146  N4BP3    3'  CCACACCTGAGCTCCTG     66257          A  CTAT    A
                                 CAGGAGCTCA GG    TGTG G
                                 |||||||||| ||    |||| |
                                 GTCCTCGAGT CC    ACAC C
                                       _ _____    C
GAM146  PRO0478  3'  GCTCACAGCAACTTCAAACTCC 26192       CTC_  GCTA
            TG                   CAGGAG    AAG    TTGTGAGC
                                 ||||||    |||    ||||||||
                                 GTCCTC    TTC    GACACTCG
                                    AAAC   AAC_
GAM146  PRO0611  3'  TAGAACCTGAGCTCCT      26013          A  __
                                 AGGAGCTCA GG  CTA
                                 |||||||||  ||  |||
                                 TCCTCGAGT CC  GAT
                                       _  AA
GAM146  SNAPC1   3'  GCTCAGGCTGGTCTTGAACTCC 11843       C       TTG
            TG                   CAGGAG TCAAGGCTA   TGAGC
                                 |||||| |||||||||   |||||
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                                GTCCTC AGTTCTGGT   ACTCG
                                   A        CGG
GAM146  TOMM34    3'  ACAACCTGAGCTCCTG      22330          A  CTA
                                CAGGAGCTCA GG   TTGT
                                |||||||||| ||   ||||
                                GTCCTCGAGT CC   AACA
                                      _  ___
GAM146  LOC126526 3'  GCCCTGGCCGCCCCAGGCTCCT 74535        CAA___    TT
           G                     CAGGAGCT     GGCTA  GT
                                |||||||      |||||  ||
                                GTCCTCGG     CCGGT  CG
                                     ACCCCG     CC
GAM146  LOC143153 3'  GCCCACACAGAGCCTGAGCTCC 76465         A   AT_   A
           TG                     CAGGAGCTCA GGCT   TGTG GC
                                |||||||||| ||||   |||| ||
                                GTCCTCGAGT CCGA   ACAC CG
                                      _   GAC    C
GAM146  LOC143154 3'  GCCCACACAGAGCCTGAGCTCC 76481         A   AT_   A
           TG                     CAGGAGCTCA GGCT   TGTG GC
                                |||||||||| ||||   |||| ||
                                GTCCTCGAGT CCGA   ACAC CG
                                      _   GAC    C
GAM146  LOC144667 3'  GCTCACTGCAGCCTTGACCTCC 83169      C       ATT
                                GGAG TCAAGGCT   GTGAGC
                                |||| ||||||||   ||||||
                                CCTC AGTTCCGA   CACTCG
                                  C       CGT
GAM146  LOC144776 5'  GCTCACTGCAGCCTTGAACACC 76960      AGC       ATT
           TG                     CAGG   TCAAGGCT   GTGAGC
                                ||||   ||||||||   ||||||
                                GTCC   AGTTCCGA   CACTCG
                                  ACA       CGT
GAM146  LOC145813 5'  GCCCACGCTGGTCTTGAACTCC 83510       C       T    A
           TG                     CAGGAG TCAAGGCTA TGTG GC
                                |||||| ||||||||| |||| ||
                                GTCCTC AGTTCTGGT GCAC CG
                                   A        C    C
GAM146  LOC147817 3'  CAGCTGGTCTCGAGCTCCTG   78492         A     _
                                CAGGAGCTC AGGCTA TTG
                                ||||||||| |||||| |||
                                GTCCTCGAG TCTGGT GAC
                                     C     C
GAM146  LOC148137 3'  GCCACGAAACCTTGGGCTCCT  58430          CTA    A
                                AGGAGCTCAAGG   TTGTG GC
                                ||||||||||||   ||||| ||
                                TCCTCGGGTTCC   AGCAC CG
                                      AA_    _
GAM146  LOC148223 3'  GCCCACAAACCCTGTGCCCC   78742    A  T  A  CTA    A
                                GG GC CA GG   TTGTG GC
                                || || || ||   ||||| ||
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                                CC CG GT CC   AACAC CG
                                 C  T  C  A__    C
GAM146   LOC148231 3'  GCTCACAGTGACCGAGCTCCTG 78752         AA  C
                                CAGGAGCTC  GG TATTGTGAGC
                                |||||||||  || ||||||||||
                                GTCCTCGAG  CC GTGACACTCG
                                     __  A
GAM146   LOC148266 3'  CACAACACTTGAGCTCCT     78769          GCTA
                                AGGAGCTCAAG    TTGTG
                                ||||||||||    |||||
                                TCCTCGAGTTC    AACAC
                                      AC__
GAM146   LOC148709 5'  GCTCACTGTAAACTCAAGCTCC 78946        CA  GC   T
            TG                    CAGGAGCT  AG  TAT GTGAGC
                                ||||||||  ||  ||| ||||||
                                GTCCTCGA  TC  ATG CACTCG
                                     AC  AA   T
GAM146   LOC150933 5'  CAGAGCCTGAGCTCC       85157         A   A
                                GGAGCTCA GGCT TTG
                                |||||||| |||| |||
                                CCTCGAGT CCGA GAC
                                     _   _
GAM146   LOC152445 3'  GCTCACTGCAGCCTTGAACTCC 85754       C       ATT
            T                    AGGAG TCAAGGCT   GTGAGC
                                ||||| ||||||||   ||||||
                                TCCTC AGTTCCGA   CACTCG
                                   A       CGT
GAM146   LOC152698 3'  GCTCCTTGGCCTCCAGCTCCTG 60426         CA     TTGT
                                CAGGAGCT  AGGCTA    GAGC
                                ||||||||  ||||||    ||||
                                GTCCTCGA  TCCGGT    CTCG
                                     CC     TC__
GAM146   LOC152794 5'  TAGTCTTGAACTCCTG      80681        C
                                CAGGAG TCAAGGCTA
                                |||||| |||||||||
                                GTCCTC AGTTCTGAT
                                   A
GAM146   LOC157638 5'  GGTAGCCTCAGCCCCTG     81514      A   CA
                                CAGG GCT  AGGCTATT
                                |||| |||  ||||||||
                                GTCC CGA  TCCGATGG
                                  C   C_
GAM146   LOC158332 3'  CTCTCTGTGCCTGGAGCTCCTG 81888         A    T  TGT
                                CAGGAGCTC AGGC AT   GAG
                                ||||||||| |||| ||   |||
                                GTCCTCGAG TCCG TG   CTC
                                     G    _  TCT
GAM146   LOC159193 5'  CTCGCTGCCTCAACTCCTG    82177       CTCA    TATT
                                CAGGAG    AGGC    GTGAG
                                ||||||    ||||    |||||
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                                GTCCTC   TCCG   CGCTC
                                  AAC_   T___
GAM146  LOC162461 5'  GCTCACTGCAGCCTTGAACTCC 82362      C      ATT
          T                    AGGAG TCAAGGCT   GTGAGC
                               ||||| ||||||||   ||||||
                               TCCTC AGTTCCGA   CACTCG
                                  A       CGT
GAM146  LOC164714 5'  ACATCGGCAACTTCGAGCTCCT 87220        _  __  AT
          G                    CAGGAGCTC AAG  GCT  TGT
                               ||||||||| |||  |||  |||
                               GTCCTCGAG TTC  CGG  ACA
                                    C   AA   CT
GAM146  LOC166879 5'  GCCGCGCCTCGGCTCCTG    87261       CA   TATT   A
                               CAGGAGCT  AGGC   GTG GC
                               ||||||||  ||||   ||| ||
                               GTCCTCGG  TCCG   CGC CG
                                    C_   ____  _
GAM146  LOC200782 5'  CACCCAGTCCTGAGCTCT    89506       A   ATT
                               GGAGCTCA GGCT   GTG
                               ||||||||| ||||  |||
                               TCTCGAGT CTGA   CAC
                                    C   CC_
GAM146  LOC201292 3'  GCTCACTGCAGCCTCGAGCTCC 88190        A    ATT
          TG                   CAGGAGCTC AGGCT   GTGAGC
                               ||||||||| |||||  ||||||
                               GTCCTCGAG TCCGA   CACTCG
                                    C    CGT
GAM146  LOC202451 5'  GCTCCTTTACAGCCTTGGCTCC 90354       T     ATTGT_
          TG                   CAGGAGC CAAGGCT     GAGC
                               ||||||| |||||||     ||||
                               GTCCTCG GTTCCGA     CTCG
                                  _     CATTTC
GAM146  LOC202908 5'  GCTCACTGCAGCCTTGAACTCC 89240      C      ATT
          TG                   CAGGAG TCAAGGCT   GTGAGC
                               |||||| ||||||||   ||||||
                               GTCCTC AGTTCCGA   CACTCG
                                  A       CGT
GAM146  LOC202908 5'  GCTCAGGCTGGTCTTGAACTCC 89242      C       TTG
          TG                   CAGGAG TCAAGGCTA   TGAGC
                               |||||| |||||||||   |||||
                               GTCCTC AGTTCTGGT   ACTCG
                                  A       CGG
GAM146  LOC202934 3'  GCTCACTGCAGCCTTGAACTCC 90418      C      ATT
          TG                   CAGGAG TCAAGGCT   GTGAGC
                               |||||| ||||||||   ||||||
                               GTCCTC AGTTCCGA   CACTCG
                                  A       CGT
GAM146  LOC221576 3'  GCCCGCCACCCTGAGCTCC   93704       A  CTATT   A
                               GGAGCTCA GG    GTG GC
                               |||||||| ||    ||| ||
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                                CCTCGAGT CC     CGC CG
                                    C  AC___   C
GAM146  LOC255465 3'  GCTCACTGCAGCCTTGAACTCC 97291       C       ATT
           TG                    CAGGAG TCAAGGCT   GTGAGC
                                 |||||| ||||||||   ||||||
                                 GTCCTC AGTTCCGA   CACTCG
                                    A       CGT
GAM146  LOC256923 5'  GCTCCCTGCAGCCTTGACCTCC 95139       C       ATTGT
           TG                    CAGGAG TCAAGGCT    GAGC
                                 |||||| ||||||||    ||||
                                 GTCCTC AGTTCCGA    CTCG
                                    C       CGTCC
GAM146  LOC257458 5'  GTTCTCAGCCCCGGCTCCTG  67794        CAA    ATT T
                                 CAGGAGCT   GGCT   G GAGC
                                 |||||||   ||||   | ||||
                                 GTCCTCGG   CCGA   C CTTG
                                    CC_    ___ T
GAM146  LOC257458 5'  GTTCTCAGCCCTGGCTCCTG  67795       T  A    ATT T
                                 CAGGAGC CA GGCT   G GAGC
                                 ||||||| || ||||   | ||||
                                 GTCCTCG GT CCGA   C CTTG
                                    _ C    ___ T
GAM146  LOC257515 3'  GCCCGCCACCCTGAGCTCC   97784        A  CTATT   A
                                 GGAGCTCA GG    GTG GC
                                 |||||||| ||    ||| ||
                                 CCTCGAGT CC    CGC CG
                                    C  AC___   C
GAM146  LOC257572 3'  GCCCGCCACCCTGAGCTCC   97913        A  CTATT   A
                                 GGAGCTCA GG    GTG GC
                                 |||||||| ||    ||| ||
                                 CCTCGAGT CC    CGC CG
                                    C  AC___   C
GAM146  LOC90719  3'  ACTGAGCCTTGAACTCCT    63880      C       ATT
                                 AGGAG TCAAGGCT   GT
                                 ||||| ||||||||   ||
                                 TCCTC AGTTCCGA   CA
                                    A       GT_
GAM146  LOC90785  3'  CACAGCCCTGGCTCCTG     64011       T  A    ATT
                                 CAGGAGC CA GGCT   GTG
                                 ||||||| || ||||   |||
                                 GTCCTCG GT CCGA   CAC
                                    _ C    ___
GAM146  LOC91380  3'  CTCACTGCAGCCTTGAACACCT 65859     AGC       ATT
           G                     CAGG   TCAAGGCT   GTGAG
                                 ||||   ||||||||   |||||
                                 GTCC   AGTTCCGA   CACTC
                                   ACA       CGT
GAM146  LOC91547  3'  GCTCAGGATGGTCTTGAACTCC 66406       C         G
           TG                    CAGGAG TCAAGGCTATT TGAGC
                                 |||||| |||||||||| |||||
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                                GTCCTC AGTTCTGGTAG ACTCG
                                   A         G
GAM146  LOC92609  3'  ACAACAGCCTTGACCTCC    72843     C       A
                                GGAG TCAAGGCT TTGT
                                |||| |||||||| ||||
                                CCTC AGTTCCGA AACA
                                  C       C
GAM147  ADAM19   3'  CAGTTCTACTAATGCTTCA   52704       G_   CCAA
                                TGAAGCA  GGTA   AACTG
                                |||||||  ||||   |||||
                                ACTTCGT  TCAT   TTGAC
                                   AA   C___
GAM147  ECHS1    3'  CAGCTGCCCCTGCTTCA    14565         TAC  AAA
                                TGAAGCAGGG   CA   CTG
                                ||||||||||   ||   |||
                                ACTTCGTCCC   GT   GAC
                                      C__  C__
GAM147  GABRB1   3'  ATCAGTTTTATTACTGCACCAT 5869     AA   GGTACC
                                ATG  GCAG     AAAACTGAT
                                |||  ||||     |||||||||
                                TAC  CGTC     TTTTGACTA
                                  CA   ATTA__
GAM147  KIF5C    3'  ATCAGTTTTAAATACTGTTCAT 15732      G   GGTACC
                                ATGAA CAG     AAAACTGAT
                                |||||  |||     |||||||||
                                TACTT GTC     TTTTGACTA
                                   _  ATAAA_
GAM147  KLRA1    5'  ATCAGTTTTCTCCACCTGC   21740      GTACC
                                GCAGG    AAAACTGAT
                                |||||    |||||||||
                                CGTCC    TTTTGACTA
                                   ACCTC
GAM147  KRT14    3'  CAGCTGGACCCTGCTTCA    4979          A   AAA
                                TGAAGCAGGGT CCA   CTG
                                |||||||||||  |||   |||
                                ACTTCGTCCCA GGT   GAC
                                      _  C__
GAM147  LIPA     3'  TTTTAATACACCTGCTTCA   4085         _   CC
                                TGAAGCAGG GTA  AAAA
                                |||||||||  |||  ||||
                                ACTTCGTCC CAT  TTTT
                                      A   AA
GAM147  LZTR1    3'  CAGTCTGCAACCCTGCTCTAT  22232     A       AC  AA
                                ATG AGCAGGGT  CA  ACTG
                                |||  ||||||||  ||  ||||
                                TAT TCGTCCCA  GT  TGAC
                                  C       AC  C_
GAM147  MEF2D    3'  CAGTTTTGCCCTCTGCCTCAT  96910      A     TAC
                                ATGA GCAGGG   CAAAACTG
                                |||| ||||||   ||||||||
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                                TACT CGTCTC   GTTTTGAC
                                  C     CC_
GAM147  PAPSS1   3'  ATCAGTTTTGGTCTGCCTTAT  18376      A    GGT
                                ATGA GCAG   ACCAAAACTGAT
                                |||| ||||   ||||||||||||
                                TATT CGTC   TGGTTTTGACTA
                                  C   ____
GAM147  PCSK1    3'  TGGCACCCTGCTCCAT      4776      A       A
                                ATG AGCAGGGT CCA
                                ||| |||||||| |||
                                TAC TCGTCCCA GGT
                                  C       C
GAM147  PTGER2   3'  TCAGTTTTGTTTACTC      6308       C_
                                GGGTA  CAAAACTGA
                                |||||  |||||||||
                                CTCAT  GTTTTGACT
                                   TT
GAM147  TCL1B    3'  ATCAGTCCTGTCCTGTCCCA   16983    AA     TAC  AA
                                TG  GCAGGG   CA  ACTGAT
                                ||  ||||||   ||  ||||||
                                AC  TGTCCT   GT  TGACTA
                                 CC      ____  CC
GAM147  DKFZP564A2416 3'  ATCAGCTCTAGCTTGCTTCAT  31387          G  CCAAAA
                                ATGAAGCAGG TA     CTGAT
                                |||||||||| ||     |||||
                                TACTTCGTTC AT     GACTA
                                     G  CTC___
GAM147  DRIL2    3'  CAGCCCTGGCACCTGCTTCA   21324         GTA   AAA
                                TGAAGCAGG   CCA   CTG
                                |||||||||   |||   |||
                                ACTTCGTCC   GGT   GAC
                                     AC_   CCC
GAM147  FLJ13154 3'  TCAGTTTTCTCCACTTC     44801      CA   TACC
                                GAAG  GGG    AAAACTGA
                                ||||  |||    ||||||||
                                CTTC  CTC    TTTTGACT
                                  AC  _____
GAM147  FLJ20174 3'  ATCAATCTTGGTGCTGTTTCA  34685        GG      AAC
                                TGAAGCA  GTACCAA   TGAT
                                |||||||  |||||||   ||||
                                ACTTTGT  CGTGGTT   ACTA
                                    __      CTA
GAM147  FLJ20291 3'  CAGTGTTCAAAGTGACCCTGCT 34866           _  CAAA___
           TCAT                   ATGAAGCAGGGT AC      ACTG
                                |||||||||||| ||      ||||
                                TACTTCGTCCCA TG      TGAC
                                      G  AAACTTG
GAM147  GPS2     3'  TGGTACCCCTCTTCAT      50575       CA
                                ATGAAG  GGGTACCA
                                ||||||  ||||||||
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                                TACTTC  CCCATGGT
                                   TC
GAM147  GPS2     3'  TGGTACCCCTCTTCAT     87165       CA
                                ATGAAG  GGGTACCA
                                ||||||  ||||||||
                                TACTTC  CCCATGGT
                                   TC
GAM147  JM11     3'  GGTGTCTGACACCCTGCTTC  53267         AC  AA_
                                GAAGCAGGGT  CA   ACT
                                ||||||||||  ||   |||
                                CTTCGTCCCA  GT   TGG
                                      CA  CTG
GAM147  KIAA0912 3'  ATCAGTTTCCTATTGCTGCTTC 64406        _   CCA
                                GAAGCAG GGTA   AAACTGAT
                                ||||||| ||||   ||||||||
                                CTTCGTC TTAT   TTTGACTA
                                    G   CC_
GAM147  KIAA0987 3'  ATCAGTTTTGGCAGTGTTTCA  24559       GG TA
                                TGAAGCA  G  CCAAAACTGAT
                                |||||||  |  ||||||||||
                                ACTTTGT  C  GGTTTTGACTA
                                    GA __
GAM147  MAFB     3'  ATCAATTTCAAACCCTGCTT   18409        ACCA   C
                                AAGCAGGGT    AAA TGAT
                                |||||||||    ||| ||||
                                TTCGTCCCA    TTT ACTA
                                     AAC_   A
GAM147  MAFB     3'  ATCAGTTTTATTGCCTGCTCG  18410     A    G  CC
                                TGA GCAGG TA  AAAACTGAT
                                ||| ||||| ||  |||||||||
                                GCT CGTCC GT  TTTTGACTA
                                  _    _ TA
GAM147  ZNF213   3'  ATCAGCACTAACGCCCTGCTCC 65089     A       ACCAAAA
            AT                   ATG AGCAGGGT      CTGAT
                                ||| ||||||||      |||||
                                TAC TCGTCCCG      GACTA
                                  C       CAATCAC
GAM147  ZNF213   3'  ATCGGCCCCGGCACCCTGCTCC 65090     A       A  AAAA
            AT                   ATG AGCAGGGT CC    CTGAT
                                ||| ||||||| ||    |||||
                                TAC TCGTCCCA GG    GGCTA
                                  C       C  CCCC
GAM147  ZNF213   3'  TTGGTGCCCCACTCCAT     65107     A  CA
                                ATG AG  GGGTACCAA
                                ||| ||  |||||||||
                                TAC TC  CCCGTGGTT
                                  C  AC
GAM147  LOC149830 3'  CAGCCCTTTGCTTCCTGCTTC  84722         TAC    A__
                                GAAGCAGGG   CAAA   CTG
                                |||||||||   ||||   |||
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                                CTTCGTCCT  GTTT  GAC
                                     TC_   CCC
GAM147  LOC199796 5'  CAGTTTTGTCCGCTGC     74451     _  TAC
                                GCAG GG  CAAAACTG
                                |||| ||  ||||||||
                                CGTC CC  GTTTTGAC
                                  G  T__
GAM147  LOC51337  3'  CAGCCTGGCCCACCCTGCTCCA 33585   A     A__  AAA
                                TG AGCAGGGT  CCA  CTG
                                || ||||||||  |||  |||
                                AC TCGTCCCA  GGT  GAC
                                 C      CCC  CC_
GAM147  LOC90183  3'  ATCAGTTTTATTGCCTGCTCG  61731    A    G  CC
                                TGA GCAGG TA  AAAACTGAT
                                ||| ||||| ||  |||||||||
                                GCT CGTCC GT  TTTTGACTA
                                 _    _  TA
GAM147  LOC92539  5'  CAGTTTTAAACACCTGCTTC  69631       _  ACC
                                GAAGCAGG GT  AAAACTG
                                |||||||| ||  |||||||
                                CTTCGTCC CA  TTTTGAC
                                     A  AA_
GAM148  ABCB9    3'  CTGGCTGGCAGCCTCC     39034    A      G
                                GGA GCTGCCAG CAG
                                ||| |||||||| |||
                                CCT CGACGGTC GTC
                                  C      G
GAM148  ATP11A   3'  ACAAGGCCACGCCGGCAGCTTC 77013        A  AGAA  A
           C                     GGAAGCTGCC GGC   CT TGT
                                ||||||||||  |||   || |||
                                CCTTCGACGG CCG   GG ACA
                                      _  CACC  A
GAM148  CARD15   3'  ACATAATTCAGGAAGCAGCTTT 42209        CAGGCA  C
           C                     GGAAGCTGC     GAA TATGT
                                |||||||||     ||| |||||
                                CTTTCGACG     CTT ATACA
                                     AAGGA_   A
GAM148  HMOX2    3'  TCTGCCTGACAGCATCC     65159    A   C
                                GGA GCTG CAGGCAGA
                                ||| |||| ||||||||
                                CCT CGAC GTCCGTCT
                                  A   A
GAM148  MFNG     5'  CTGCCTGACCAGCTTCC     10004       C_
                                GGAAGCTG  CAGGCAG
                                ||||||||  |||||||
                                CCTTCGAC  GTCCGTC
                                     CA
GAM148  S100A10  3'  TCTGCCCCACAGCTTCC     59323       CCA
                                GGAAGCTG  GGCAGA
                                ||||||||  ||||||
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                                CCTTCGAC  CCGTCT
                                     ACC
GAM148  ESDN     3'  CTCCTGGCAGCTTCC      55171           C
                                GGAAGCTGCCAGG AG
                                |||||||||||| ||
                                CCTTCGACGGTCC TC
                                          _
GAM148  FGD3     3'  GGTTCTGCCTGCAGCCCCC   72899    AA    C
                                GG  GCTGC AGGCAGAACT
                                ||  ||||| ||||||||||
                                CC  CGACG TCCGTCTTGG
                                 CC    _
GAM148  FLJ21135 5'  TCTGCCTGCAGCTCC      45887    A    C
                                GGA GCTGC AGGCAGA
                                ||| ||||| |||||||
                                CCT CGACG TCCGTCT
                                  _   _
GAM148  FLJ21916 3'  TTCCGGCCAGCAGCTTCC   43648        CA  A_
                                GGAAGCTGC  GGC  GAA
                                |||||||||  |||  |||
                                CCTTCGACG  CCG  CTT
                                     A_  GC
GAM148  KIAA0472 3'  CATAATTAGGGCAGCTT    71861        AGGCAG  C
                                AAGCTGCC    AA TATG
                                ||||||||    || ||||
                                TTCGACGG    TT ATAC
                                    GA____  A
GAM148  KIAA1508 3'  AGTTCTGCTGGCAGCTTCC  61876          G
                                GGAAGCTGCCAG CAGAACT
                                |||||||||||| |||||||
                                CCTTCGACGGTC GTCTTGA
                                          _
GAM148  KIAA1786 3'  ACATAGCCCTGCCTGGGGTTCC 66020     G  G      AA
                                GGAA CT CCAGGCAG  CTATGT
                                |||| || ||||||||  ||||||
                                CCTT GG GGTCCGTC  GATACA
                                  _ _      CC
GAM148  LGALS12  5'  AGTTCTGCTGACAGCCCCC   52387    AA   CCA
                                GG  GCTG   GGCAGAACT
                                ||  ||||   |||||||||
                                CC  CGAC   TCGTCTTGA
                                 CC   AG_
GAM148  NKIR     3'  CTGCCTGGAGCCTCC       57355    A  G
                                GGA GCT CCAGGCAG
                                ||| ||| ||||||||
                                CCT CGA GGTCCGTC
                                  C  _
GAM148  NXPH3    3'  CACAGTTCTGCCTGCACC     65752    AAGC  C       A
                                GG   TGC AGGCAGAACT TG
                                ||   ||| |||||||||| ||
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                                CC    ACG TCCGTCTTGA AC
                                 ____  _         C
GAM148  SARM     3'  ACACAGTTCTGCTGCCATAGTT 30593      G   CCA_       A
              CC                   GGAA CTG    GGCAGAACT TGT
                                |||| |||    ||||||||| |||
                                CCTT GAT    TCGTCTTGA ACA
                                  _  ACCG        C
GAM148  TLN1     3'  CTGCCAGCAGCTTCC       20818          CA
                                GGAAGCTGC  GGCAG
                                |||||||||  |||||
                                CCTTCGACG  CCGTC
                                     A_
GAM148  ULK2     5'  TCCGCGCGGCAGCTTCC     28009          AG  A
                                GGAAGCTGCC  GC GA
                                ||||||||||  || ||
                                CCTTCGACGG  CG CT
                                      CG  C
GAM148  LOC115939 3'  ACATAAATGGGCCTGGCAGCCT 73661     A         AGAAC
              C                    GA GCTGCCAGGC     TATGT
                                || ||||||||||     |||||
                                CT CGACGGTCCG     ATACA
                                 C         GGTAA
GAM148  LOC116411 5'  TCTGCCTGGCAACTGCC     73875     A  C
                                GG AG TGCCAGGCAGA
                                || || ||||||||||
                                CC TC ACGGTCCGTCT
                                 G  A
GAM148  LOC144699 3'  CTGCCTAGCAGTTTCC      76914          C
                                GGAAGCTGC AGGCAG
                                ||||||||| ||||||
                                CCTTTGACG TCCGTC
                                     A
GAM148  LOC196214 5'  AGTTCTGCCCTGGCAGCCTCC  89616     A       _
                                GGA GCTGCCAGG CAGAACT
                                ||| ||||||||| |||||||
                                CCT CGACGGTCC GTCTTGA
                                  C        C
GAM148  LOC255031 5'  AGGGCTCCTGGCAGCCCCC    97229     AA       C  AA
                                GG  GCTGCCAGG AG  CT
                                ||  ||||||||| ||  ||
                                CC  CGACGGTCC TC  GA
                                 CC        _ GG
GAM148  LOC57115  3'  TCTGCCTGGCAGCCCCC     39862     AA
                                GG  GCTGCCAGGCAGA
                                ||  ||||||||||||
                                CC  CGACGGTCCGTCT
                                 CC
GAM148  LOC91355  5'  GTCCTGCCTGGGAGCCCCC    65719     AA  G       A
                                GG  GCT CCAGGCAG AC
                                ||  ||| |||||||| ||
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                              CC  CGA GGTCCGTC TG
                               CC   G      C
GAM149  ALEX1    3'  CTCTACCTAAACTGAC     33501       CAGC   AGC
                              GTCAGTT   AGG   AGAG
                              |||||||   |||   ||||
                              CAGTCAA   TCC   TCTC
                                 A___   A__
GAM149  BAI2     5'  GCTCCTGCTGCTGA      8119      TT
                              TCAG  CAGCAGGAGC
                              ||||  ||||||||||
                              AGTC  GTCGTCCTCG
                                 __
GAM149  CXCL13   3'  CTCTGCTTAAAAACTCACTA  21196     C   CAGCAG
                              TAGT AGTT     GAGCAGAG
                              |||| ||||     ||||||||
                              ATCA TCAA     TTCGTCTC
                                C   AAA___
GAM149  DGKQ     3'  CTCTGCTCCCGCCAGC     7209     CA  A
                              GTT  GC GGAGCAGAG
                              |||  || |||||||||
                              CGA  CG CCTCGTCTC
                               C_  C
GAM149  PCDHA1   3'  TCCCTGCTCCTTTTTCCTATCT 48596    TC  TTCAGC      A
          A                    TAG  AG     AGGAGCAG GA
                              |||  ||     |||||||| ||
                              ATC  TC     TCCTCGTC CT
                                TA  CTTTT_      C
GAM149  PCDHA1   3'  TCCCTGCTCCTTTTTCCTATCT 38185    TC  TTCAGC      A
          A                    TAG  AG     AGGAGCAG GA
                              |||  ||     |||||||| ||
                              ATC  TC     TCCTCGTC CT
                                TA  CTTTT_      C
GAM149  PCDHA10  3'  TCCCTGCTCCTTTTTCCTATCT 38193    TC  TTCAGC      A
          A                    TAG  AG     AGGAGCAG GA
                              |||  ||     |||||||| ||
                              ATC  TC     TCCTCGTC CT
                                TA  CTTTT_      C
GAM149  PCDHA10  3'  TCCCTGCTCCTTTTTCCTATCT 49029    TC  TTCAGC      A
          A                    TAG  AG     AGGAGCAG GA
                              |||  ||     |||||||| ||
                              ATC  TC     TCCTCGTC CT
                                TA  CTTTT_      C
GAM149  PCDHA11  3'  TCCCTGCTCCTTTTTCCTATCT 38204    TC  TTCAGC      A
          A                    TAG  AG     AGGAGCAG GA
                              |||  ||     |||||||| ||
                              ATC  TC     TCCTCGTC CT
                                TA  CTTTT_      C
GAM149  PCDHA12  3'  TCCCTGCTCCTTTTTCCTATCT 38212    TC  TTCAGC      A
          A                    TAG  AG     AGGAGCAG GA
                              |||  ||     |||||||| ||
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                                ATC  TC     TCCTCGTC CT
                                  TA  CTTTT_      C
GAM149  PCDHA13  3'  TCCCTGCTCCTTTTTCCTATCT 38221    TC  TTCAGC      A
          A                      TAG  AG     AGGAGCAG GA
                                 |||  ||     |||||||| ||
                                ATC  TC     TCCTCGTC CT
                                  TA  CTTTT_      C
GAM149  PCDHA2   3'  TCCCTGCTCCTTTTTCCTATCT 38229    TC  TTCAGC      A
          A                      TAG  AG     AGGAGCAG GA
                                 |||  ||     |||||||| ||
                                ATC  TC     TCCTCGTC CT
                                  TA  CTTTT_      C
GAM149  PCDHA3   3'  TCCCTGCTCCTTTTTCCTATCT 38237    TC  TTCAGC      A
          A                      TAG  AG     AGGAGCAG GA
                                 |||  ||     |||||||| ||
                                ATC  TC     TCCTCGTC CT
                                  TA  CTTTT_      C
GAM149  PCDHA4   3'  TCCCTGCTCCTTTTTCCTATCT 38245    TC  TTCAGC      A
          A                      TAG  AG     AGGAGCAG GA
                                 |||  ||     |||||||| ||
                                ATC  TC     TCCTCGTC CT
                                  TA  CTTTT_      C
GAM149  PCDHA5   3'  TCCCTGCTCCTTTTTCCTATCT 38253    TC  TTCAGC      A
          A                      TAG  AG     AGGAGCAG GA
                                 |||  ||     |||||||| ||
                                ATC  TC     TCCTCGTC CT
                                  TA  CTTTT_      C
GAM149  PCDHA6   3'  TCCCTGCTCCTTTTTCCTATCT 38261    TC  TTCAGC      A
          A                      TAG  AG     AGGAGCAG GA
                                 |||  ||     |||||||| ||
                                ATC  TC     TCCTCGTC CT
                                  TA  CTTTT_      C
GAM149  PCDHA6   3'  TCCCTGCTCCTTTTTCCTATCT 49002    TC  TTCAGC      A
          A                      TAG  AG     AGGAGCAG GA
                                 |||  ||     |||||||| ||
                                ATC  TC     TCCTCGTC CT
                                  TA  CTTTT_      C
GAM149  PCDHA7   3'  TCCCTGCTCCTTTTTCCTATCT 38269    TC  TTCAGC      A
          A                      TAG  AG     AGGAGCAG GA
                                 |||  ||     |||||||| ||
                                ATC  TC     TCCTCGTC CT
                                  TA  CTTTT_      C
GAM149  PCDHA8   3'  TCCCTGCTCCTTTTTCCTATCT 38277    TC  TTCAGC      A
          A                      TAG  AG     AGGAGCAG GA
                                 |||  ||     |||||||| ||
                                ATC  TC     TCCTCGTC CT
                                  TA  CTTTT_      C
GAM149  PCDHA9   3'  TCCCTGCTCCTTTTTCCTATCT 49019    TC  TTCAGC      A
          A                      TAG  AG     AGGAGCAG GA
                                 |||  ||     |||||||| ||
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                                ATC  TC     TCCTCGTC CT
                                  TA  CTTTT_       C
GAM149  PCDHAC1  3'  TCCCTGCTCCTTTTTCCTATCT 38168     TC  TTCAGC       A
            A                    TAG  AG     AGGAGCAG GA
                                 |||  ||     |||||||| ||
                                ATC  TC     TCCTCGTC CT
                                  TA  CTTTT_       C
GAM149  PCDHAC2  3'  TCCCTGCTCCTTTTTCCTATCT 38177     TC  TTCAGC       A
            A                    TAG  AG     AGGAGCAG GA
                                 |||  ||     |||||||| ||
                                ATC  TC     TCCTCGTC CT
                                  TA  CTTTT_       C
GAM149  POLR2H   3'  CTCCACTCAATGGGAAACTGAC 20644         _ AGCAG   CA
            T                    AGTCAGTT C     GAG  GAG
                                 |||||||| |     |||  |||
                                TCAGTCAA G     CTC  CTC
                                     A GGTAA   AC
GAM149  SLC1A2   5'  TCTCTGCTCCCGCCACTCGC   61930    C   TCA  A
                                GT AGT   GC GGAGCAGAGA
                                || |||   || ||||||||||
                                CG TCA   CG CCTCGTCTCT
                                 C   C__  C
GAM149  SLC9A5   3'  TCCCTGCTCCTAACCCCTGC   59773   T   TTCAGC       A
                                G CAG     AGGAGCAG GA
                                | |||     |||||||| ||
                                C GTC     TCCTCGTC CT
                                _  CCCAA_       C
GAM149  SLC9A5   3'  TCCCTGCTCCTAACCCCTGC   15984   T   TTCAGC       A
                                G CAG     AGGAGCAG GA
                                | |||     |||||||| ||
                                C GTC     TCCTCGTC CT
                                _  CCCAA_       C
GAM149  DRF1     3'  CTCTGCTCCTACCTGACT    47031       TTCAGC
                                AGTCAG     AGGAGCAGAG
                                ||||||     ||||||||||
                                TCAGTC     TCCTCGTCTC
                                   CA____
GAM149  FLJ14009  5'  TCTCACCTGCTGAACCAGC   45412    CA        AGCA
                                GT  GTTCAGCAGG   GAGA
                                ||  ||||||||||   ||||
                                CG  CAAGTCGTCC   CTCT
                                 AC        A___
GAM149  FLJ14249  3'  CTCTGCTCCTCGTGGCTGC   42405   T    CA  _
                                G CAGTT  GC AGGAGCAGAG
                                | |||||  || ||||||||||
                                C GTCGG  TG TCCTCGTCTC
                                _    __  C
GAM149  FLJ14249  3'  CTCTGCTCCTCGTGGCTGC   55212   T    CA  _
                                G CAGTT  GC AGGAGCAGAG
                                | |||||  || ||||||||||
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                                C GTCGG  TG TCCTCGTCTC
                                _    __ C
GAM149  KIAA0469  3'  CTGCTCCTACCCCCTGACTG  29329       TTCAGC
                                TAGTCAG     AGGAGCAG
                                |||||||     ||||||||
                                GTCAGTC     TCCTCGTC
                                    CCCCA_
GAM149  MGC10765  3'  CTCTGCTCCTGCTGATCTGTGC 44300    _  T
                                GT CAG TCAGCAGGAGCAGAG
                                || ||| ||||||||||||||
                                CG GTC AGTCGTCCTCGTCTC
                                 T  T
GAM149  MGC27044  3'  CTCTGCTAGAAAACTACTA   58672     C   CAGCAGG
                                TAGT AGTT      AGCAGAG
                                |||| ||||      |||||||
                                ATCA TCAA      TCGTCTC
                                  _   AAGA___
GAM149  RTBDN     5'  TTCCTGCTGCACTGAC      48690       T
                                GTCAGT CAGCAGGAG
                                ||||||| |||||||||
                                CAGTCA GTCGTCCTT
                                   C
GAM149  SDS3      3'  CTCTGCTTTTGTGAAGCAACTA 69229     CA  CA
                                TAGT  GTT  GCAGGAGCAGAG
                                ||||  |||  ||||||||||||
                                ATCA  CGA  TGTTTTCGTCTC
                                  A_  AG
GAM149  STK29     3'  CTCCGCTCCTGCTGTTGCTG  87575     T_       A
                                CAGT  CAGCAGGAGC GAG
                                ||||  |||||||||| |||
                                GTCG  GTCGTCCTCG CTC
                                  TT        C
GAM149  LOC129676 5'  TCCTGCTGAACTGCTA     75736     T
                                TAG CAGTTCAGCAGGA
                                ||| ||||||||||||
                                ATC GTCAAGTCGTCCT
                                  _
GAM149  LOC138429 3'  CTGCTCCTGGCCTGAT     75340      TTCAG
                                GTCAG    CAGGAGCAG
                                |||||    |||||||||
                                TAGTC    GTCCTCGTC
                                  CG___
GAM149  LOC146901 5'  TCTCTACTCCCTTGTTTCTGAC 83851      TT_  CA   C
                                GTCAG   CAG  GGAG AGAGA
                                |||||   |||  |||| |||||
                                CAGTC   GTT  CCTC TCTCT
                                  TTT   C_   A
GAM149  LOC155036 5'  TCTCTGCTCCCGCCTGG     86346     TTCA  A
                                TCAG    GC GGAGCAGAGA
                                ||||    || ||||||||||
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                                GGTC    CG CCTCGTCTCT
                                  ____  C
GAM149  LOC253027 5'  CTCTGCTCCCCAGCTCTGC   96991    TC   A__
                                GT  AGC   GGAGCAGAG
                                ||  |||   |||||||||
                                CG  TCG   CCTCGTCTC
                                 TC   ACC
GAM149  LOC255446 3'  CTCTGCTCCCTTCTCCTCACTA 97154      C  TTCAGCA
                                TAGT AG      GGAGCAGAG
                                ||||  ||      |||||||||
                                ATCA TC      CCTCGTCTC
                                  C  CTCTTC_
GAM149  LOC91097  5'  CTGCCCCTGCTGGCAC      64836    _      A
                                GT TCAGCAGG GCAG
                                ||  |||||||| ||||
                                CA GGTCGTCC CGTC
                                 C       C
GAM149  LOC92230  5'  TCTCTGCCCCTGCCCAGAC   68546    AGTTCA    A
                                GTC     GCAGG GCAGAGA
                                |||     ||||| |||||||
                                CAG     CGTCC CGTCTCT
                                  ACC___    C
GAM150  ATF7    3'  ATCTTTGGTCATTTTTCTG   22464    CT   A
                                CAG  AGAT ACCAAAGAT
                                |||  |||| |||||||||
                                GTC  TTTA TGGTTTCTA
                                  TT   C
GAM150  GABRA2   3'  GTTATCTTTGGGATGTATAGC  5866      G   A_
                                GCTA ATA  CCAAAGATAAC
                                ||||  |||  ||||||||||
                                CGAT TGT  GGTTTCTATTG
                                  A   AG
GAM150  SH3GL2   3'  TCTATTTATCTAGCTGTA    11629          CCAA
                                TACAGCTAGATAA    AGA
                                ||||||||||||    |||
                                ATGTCGATCTATT    TCT
                                        TA__
GAM150  SLC38A2  3'  TTGGTCATCTGGCTGTA     38595          A
                                TACAGCTAGAT ACCAA
                                ||||||||||| |||||
                                ATGTCGGTCTA TGGTT
                                       C
GAM150  AKAP11   3'  CTTTGGTTACTTGTGC      32708    _  A
                                GC TAG TAACCAAAG
                                ||  ||| |||||||||
                                CG GTT ATTGGTTTC
                                 T   C
GAM150  CAMKK2   3'  ATCTCTGGTTATTTGTT     21576     T       A
                                AGC AGATAACCA AGAT
                                |||  ||||||||| ||||
```

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                                TTG TTTATTGGT TCTA
                                  _       C
GAM150  DJ328E19.C1.1 3' ATCTTTGTGTTTAGCTCA    31151   C       AC
                                A AGCTAGATA  CAAAGAT
                                | |||||||||  |||||||
                                A TCGATTTGT  GTTTCTA
                                 C       __
GAM150  DKFZp434D177 3' ATCTTTGTGTTTAGCTCA    50052   C       AC
                                A AGCTAGATA  CAAAGAT
                                | |||||||||  |||||||
                                A TCGATTTGT  GTTTCTA
                                 C       __
GAM150  KIAA0853  3' GTTATTCCAGATTATCTAGCTT 30543   C       CCAAA
            A                    A AGCTAGATAA    GATAAC
                                | ||||||||||    ||||||
                                A TCGATCTATT    TTATTG
                                 T        AGACC
GAM150  MGC13071  3' TTATCTTTGACTGCTGT    51092      T  ATAAC
                                ACAGC AG    CAAAGATAA
                                ||||| ||    |||||||||
                                TGTCG TC    GTTTCTATT
                                  _ A____
GAM150  MKRN2    3' ATCTATTATCTAGCTG      72412          CCAA
                                CAGCTAGATAA    AGAT
                                ||||||||||    ||||
                                GTCGATCTATT    TCTA
                                       A___
GAM150  RA-GEF-2  3' TCTAATCAAGTGTTTAGCTGT  32957          ACCAA__
                                ACAGCTAGATA      AGA
                                ||||||||||       |||
                                TGTCGATTTGT      TCT
                                      GAACTAA
GAM150  STRN     3' ATCTTCACCTTCTAGCTGT    12040         TAACCA
                                ACAGCTAGA     AAGAT
                                |||||||||     |||||
                                TGTCGATCT     TTCTA
                                     TCCAC_
GAM150  LOC129607 3'  TGGTATCTAGCTGTA       74888           A
                                TACAGCTAGATA CCA
                                |||||||||||| |||
                                ATGTCGATCTAT GGT
                                          _
GAM150  LOC133418 3'  TTATCCCAACATCTAGCTG    75092         AACCAAA
                                CAGCTAGAT      GATAA
                                |||||||||      |||||
                                GTCGATCTA      CTATT
                                     CAACC__
GAM150  LOC144248 5'  TATCTTTGGTCACCTACATGT  76745     GC   ATA
                                ACA  TAG   ACCAAAGATA
                                |||  |||   ||||||||||
```

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                                TGT  ATC   TGGTTTCTAT
                                  AC   CAC
GAM150   LOC146050 3'  TTATCTTTGGCCAGTGGAGCTG 77655      AG  AA_
                                CAGCT  AT   CCAAAGATAA
                                ||||||  ||  ||||||||||
                                GTCGA  TG   GGTTTCTATT
                                   GG  ACC
GAM150   LOC149010 3'  ATCTTTGTGTTTAGCTCA    79127   C       AC
                                A AGCTAGATA  CAAAGAT
                                | |||||||||  |||||||
                                A TCGATTTGT  GTTTCTA
                                 C       __
GAM150   LOC149013 3'  ATCTTTGTGTTTAGCTCA    79130   C       AC
                                A AGCTAGATA  CAAAGAT
                                | |||||||||  |||||||
                                A TCGATTTGT  GTTTCTA
                                 C       __
GAM150   LOC149317 3'  ATCTTTGTGTTTAGCTCA    79287   C       AC
                                A AGCTAGATA  CAAAGAT
                                | |||||||||  |||||||
                                A TCGATTTGT  GTTTCTA
                                 C       __
GAM150   LOC220638 3'  ATCTTTGTGTTTAGCTCA    73909   C       AC
                                A AGCTAGATA  CAAAGAT
                                | |||||||||  |||||||
                                A TCGATTTGT  GTTTCTA
                                 C       __
GAM150   LOC91496  5'  TTATCTTTGGACATGTACTG   66227    C  G  AA
                                CAG TA AT  CCAAAGATAA
                                ||| || ||  ||||||||||
                                GTC AT TA  GGTTTCTATT
                                  _  G  CA
GAM151   ARHGEF6   3'  CAAACTTGAAGCCAGGC     68198       ACCA
                                GCCTGG    CAAGTTTG
                                ||||||    ||||||||
                                CGGACC    GTTCAAAC
                                   GAA_
GAM151   BIG1      3'  TCAAACTTGCAACACTCCAG   21205      CCA___
                                CTGGA     CAAGTTTGA
                                |||||     |||||||||
                                GACCT     GTTCAAACT
                                   CACAAC
GAM151   CABC1     5'  TCAAGCTGACCCAGGCGG    39658        ACCACA
                                TCGCCTGG     AGTTTGA
                                ||||||||     |||||||
                                GGCGGACC     TCGAACT
                                    CAG___
GAM151   CORO2A    3'  TCAAACTGTGGTCCAGAGA   53403    GC        A
                                TC  CTGGACCACA GTTTGA
                                ||  |||||||||| ||||||
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                                AG  GACCTGGTGT CAAACT
                                 A_       _
GAM151  CORO2A   3'  TCAAACTGTGGTCCAGAGA   12647    GC       A
                                TC  CTGGACCACA GTTTGA
                                ||  |||||||||| ||||||
                                AG  GACCTGGTGT CAAACT
                                 A_       _
GAM151  DISC1    3'  TCAAACTCCTGACCTCAGGCGA 37892       _ AC  CA
                                TCGCCTG G  CA  AGTTTGA
                                ||||||| |  ||  |||||||
                                AGCGGAC C  GT  TCAAACT
                                    T CA  CC
GAM151  EN2      5'  CGGGCGGCCCAGGCGG      7459         A  ACAA
                                TCGCCTGG CC    GTTTG
                                |||||||| ||    |||||
                                GGCGGACC GG    CGGGC
                                     C  ____
GAM151  FOXD2    5'  CAGAGGGGGCCCAGGCGA    15562        A  ACAAG
                                TCGCCTGG CC     TTTG
                                |||||||| ||     ||||
                                AGCGGACC GG     AGAC
                                     C  GGG__
GAM151  GPX3     5'  TCAGGCAGCGGCTCAGGCGA   9125         GA  ACAA
                                TCGCCTG  CC    GTTTGA
                                |||||||  ||    ||||||
                                AGCGGAC  GG    CGGACT
                                    TC  CGA_
GAM151  HNF3G    3'  AACTCTGGTCCAGGAGA     72339    G       CA
                                TC CCTGGACCA  AGTT
                                || |||||||||  ||||
                                AG GGACCTGGT  TCAA
                                 A        C_
GAM151  IL13RA1  3'  TCAAACTTGAGTCACAAAGA   7778     GCC  _   CA
                                TC   TG GAC  CAAGTTTGA
                                ||   || |||  |||||||||
                                AG   AC CTG  GTTCAAACT
                                 AA_  A  A_
GAM151  KCNS2    3'  CAAACTTGTATTGAAGGGA    68300    G   GGACC
                                TC CCT     ACAAGTTTG
                                || |||     |||||||||
                                AG GGA     TGTTCAAAC
                                 _   AGTTA
GAM151  LMO4     5'  CAAACTTGCAGCAGCGA      22251      __   GACCA
                                TCGC  CTG     CAAGTTTG
                                ||||  |||     ||||||||
                                AGCG  GAC     GTTCAAAC
                                  AC  _____
GAM151  LZTS1    3'  TCAAACTTGTGGCCTCAAGC   40695    CT__  A
                                GC    GG CCACAAGTTTGA
                                ||    || ||||||||||||
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                                CG   CC GGTGTTCAAACT
                                 AACT  _
GAM151  MATK    3'  CAAGGAGGGTCCAGGCGG    57816          ACAAG
                                TCGCCTGGACC    TTTG
                                ||||||||||    ||||
                                GGCGGACCTGG    GAAC
                                      GAG__
GAM151  MATK    3'  CAAGGAGGGTCCAGGCGG    57819          ACAAG
                                TCGCCTGGACC    TTTG
                                ||||||||||    ||||
                                GGCGGACCTGG    GAAC
                                      GAG__
GAM151  MATK    3'  CAAGGAGGGTCCAGGCGG    9915           ACAAG
                                TCGCCTGGACC    TTTG
                                ||||||||||    ||||
                                GGCGGACCTGG    GAAC
                                      GAG__
GAM151  MIR16   3'  TCAAACTTGTGGCCA      33565     A
                                TGG CCACAAGTTTGA
                                ||| ||||||||||||
                                ACC GGTGTTCAAACT
                                 _
GAM151  PIK3C2B  3'  AGCTCGGTCCAGGTGA      10559          ACA
                                TCGCCTGGACC   AGTT
                                ||||||||||   ||||
                                AGTGGACCTGG   TCGA
                                      C__
GAM151  PLCG2    5'  CAAACCCGGGGCAGGCGG    72463       GA  ACAA
                                TCGCCTG  CC    GTTTG
                                |||||||  ||    |||||
                                GGCGGAC  GG    CAAAC
                                    GG  CC__
GAM151  PLIN    3'  CAAACTTGTGGCCAAAAGA   10640    GCC   A
                                TC   TGG CCACAAGTTTG
                                ||   ||| ||||||||||
                                AG   ACC GGTGTTCAAAC
                                 AAA  _
GAM151  POU2AF1  3'  CAGATTTACAGTCCAGGC    20648        CAC
                                GCCTGGAC   AAGTTTG
                                ||||||||   |||||||
                                CGGACCTG   TTTAGAC
                                     ACA
GAM151  SLC6A12  3'  CGAATGTGCTCCAGGCGA    11734         C    AG
                                TCGCCTGGA CACA  TTTG
                                ||||||||| ||||  ||||
                                AGCGGACCT GTGT  AAGC
                                      C   __
GAM151  STARD4   3'  TCAAACTTGTAGTACTACAGA  57516    GCC  _  C
                                TC   TGG AC ACAAGTTTGA
                                ||   ||| || ||||||||||
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                                AG  ATC TG TGTTCAAACT
                                 AC_  A  A
GAM151  TP53     3'  TCAAACTCCTGGGCTCAGGCGA 5043        A_  CA
                                TCGCCTGG  CCA  AGTTTGA
                                ||||||||  |||  |||||||
                                AGCGGACT  GGT  TCAAACT
                                    CG   CC
GAM151  TR2      5'  CAAACTTTCCAGGC       72314       CCAC
                                GCCTGGA   AAGTTTG
                                |||||||   |||||||
                                CGGACCT   TTCAAAC
                                    ____
GAM151  C21orf42  5'  TCAAACTTGTAGCTGTATGA  54207    CC  ACC
                                TCG  TGG  ACAAGTTTGA
                                |||  |||  ||||||||||
                                AGT  GTC  TGTTCAAACT
                                  AT  GA_
GAM151  DAZAP1   3'  CAAACTTGTGAACTCGTGA   38536     CT  AC
                                TCGC  GG  CACAAGTTTG
                                ||||  ||  ||||||||||
                                AGTG  TC  GTGTTCAAAC
                                  C_  AA
GAM151  DBR1     3'  AACTCCTGACCTCAGGCGA   32523       _ AC  CA
                                TCGCCTG G  CA  AGTT
                                |||||||  |  ||  ||||
                                AGCGGAC C  GT  TCAA
                                    T CA  CC
GAM151  DC-TM4F2  3'  CAAACTTGTGACTGC      48171    CT  AC
                                GC  GG  CACAAGTTTG
                                ||  ||  ||||||||||
                                CG  TC  GTGTTCAAAC
                                 __  A_
GAM151  DKFZp434N2030 5'  TCAAACTTGTCCTCGC     65525    CT   CAC
                                GC  GGAC   AAGTTTGA
                                ||  ||||   ||||||||
                                CG  CCTG   TTCAAACT
                                 CT   ___
GAM151  DKFZP564I1171 3'  TCAGAAGCTGAGTCCAGGC   71592        _  CAAG
                                GCCTGGAC CA    TTTGA
                                |||||||  ||    |||||
                                CGGACCTG GT    AGACT
                                    A  CGA_
GAM151  DKFZP564O0423 3'  TCAAACTCCTGGCCTCAGGCGA 91699       _ A   CA
                                TCGCCTG G CCA  AGTTTGA
                                |||||||  |  |||  |||||||
                                AGCGGAC C GGT  TCAAACT
                                    T C   CC
GAM151  EPN2     5'  CAAACTTGTGGACAGG     30321     GA
                                CCTG  CCACAAGTTTG
                                ||||  ||||||||||
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                                GGAC  GGTGTTCAAAC
                                  A_
GAM151  EREG     3'  TCAAACTTATGGGCAGGGA   7510     G   GA  C
                                TC CCTG  CCA AAGTTTGA
                                || ||||  ||| ||||||||
                                AG GGAC  GGT TTCAAACT
                                 _   G_  A
GAM151  FLJ10718 3'  TCAAACTCTTAGGCTCAGGCGA 36496       GA  ACA_
                                TCGCCTG  CC   AGTTTGA
                                |||||||  ||   |||||||
                                AGCGGAC  GG   TCAAACT
                                    TC  ATTC
GAM151  FLJ10803 3'  TCAAACTTGTATGGATGA    36671    _ TGGACC
                                TCG CC     ACAAGTTTGA
                                ||| ||     ||||||||||
                                AGT GG     TGTTCAAACT
                                  A  TA____
GAM151  FLJ20312 5'  TCAAACTTGTGTGCTGAGG   34928    _ AC
                                CCT GG  CACAAGTTTGA
                                ||| ||  ||||||||||
                                GGA TC  GTGTTCAAACT
                                  G  GT
GAM151  FLJ23420 3'  CAAGTGGGTCCAGGC      46846        A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                          _ __
GAM151  FREQ     3'  TCAGCTGCTGGCCCGGGCGA  26585       A   CA   T
                                TCGCCTGG CCA  AGTT GA
                                |||||||| |||  |||| ||
                                AGCGGGCC GGT  TCGA CT
                                    C   CG   _
GAM151  H2AV     3'  TCAAACTCCTGACCTCAGGCGA 56858       _ AC  CA
                                TCGCCTG G  CA  AGTTTGA
                                ||||||| |  ||  |||||||
                                AGCGGAC C  GT  TCAAACT
                                    T CA  CC
GAM151  HSA249128 5'  GGCGCGGTCCAGGCGG     34153         ACAA
                                TCGCCTGGACC   GTT
                                ||||||||||    |||
                                GGCGGACCTGG   CGG
                                      CG__
GAM151  KIAA0089 5'  AAGCACGGTCCAGGCGG     69960         ACAA
                                TCGCCTGGACC   GTTT
                                ||||||||||    ||||
                                GGCGGACCTGG   CGAA
                                      CA__
GAM151  KIAA0256 3'  CAAACTTGTCCTGAGTGC    64417    _ __   CAC
                                GC CT  GGAC   AAGTTTG
                                || ||  ||||   |||||||
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                                CG GA  CCTG   TTCAAAC
                                 T  GT   ___
GAM151  KIAA1026 3'  TCAACTCCTGACCTCAGGCGA  71207       _ AC  CA   T
                                TCGCCTG G  CA  AGTT GA
                                ||||||| |  ||  |||| ||
                                AGCGGAC C  GT  TCAA CT
                                    T CA  CC   _
GAM151  KIAA1981 3'  CAGAGGATGATTCAGGCGA   88341        C  CAAG
                                TCGCCTGGA CA    TTTG
                                ||||||||| ||    ||||
                                AGCGGACTT GT    AGAC
                                     A  AGG_
GAM151  MGC13090 5'  TCAAACTTGTCCGCCAAGT   51141    C   ACC
                                GC TGG   ACAAGTTTGA
                                || |||   ||||||||||
                                TG ACC   TGTTCAAACT
                                 A   GCC
GAM151  MGC2452  5'  TCAAGGAGATGTGGTCCAGG   50990         AG__
                                CCTGGACCACA    TTTGA
                                ||||||||||    |||||
                                GGACCTGGTGT    GAACT
                                      AGAG
GAM151  MYT1L    5'  TCAAACTTGTGGTGG      66825    TGG
                                CC   ACCACAAGTTTGA
                                ||   ||||||||||||
                                GG   TGGTGTTCAAACT
                                 ___
GAM151  NUDT13   3'  TCAGTTTGTGACCCAGGGA   63215    G    AC    AGT
                                TC CCTGG  CACA   TTGA
                                || |||||  ||||   ||||
                                AG GGACC  GTGT   GACT
                                 _    CA    TT_
GAM151  PCDH17   3'  CAAACTTGTATTAGG      27087      ACC
                                CCTGG   ACAAGTTTG
                                |||||   |||||||||
                                GGATT   TGTTCAAAC
                                   A__
GAM151  PGRMC1   3'  TCAAACTTGTAATTGTGGT   21895     TG  CC
                                GCC  GA  ACAAGTTTGA
                                |||  ||  ||||||||||
                                TGG  TT  TGTTCAAACT
                                  TG  AA
GAM151  PTDSS2   3'  CATGGTGTGGTCCAGGC     47884          AGTT
                                GCCTGGACCACA   TG
                                ||||||||||||   ||
                                CGGACCTGGTGT   AC
                                       GGT_
GAM151  RPS6KB1  3'  TCAAACTTTTCCCAGGC     12038       ACCAC
                                GCCTGG    AAGTTTGA
                                ||||||    ||||||||
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                                CGGACC    TTCAAACT
                                   CTT__
GAM151  USP22    3'  TCAAACTCCTGACCTCAGGCGA 68023       _ AC  CA
                                TCGCCTG G  CA  AGTTTGA
                                ||||||| |  ||  |||||||
                                AGCGGAC C  GT  TCAAACT
                                    T CA  CC
GAM151  LOC129011 5' CAGACCTGCGGTCCAGGC    74865        A  A
                                GCCTGGACC CA GTTTG
                                ||||||||| || |||||
                                CGGACCTGG GT CAGAC
                                     C  C
GAM151  LOC130595 5' CAGGCTCAGTCCAGGC      75748        CACA
                                GCCTGGAC    AGTTTG
                                ||||||||    ||||||
                                CGGACCTG    TCGGAC
                                    AC__
GAM151  LOC131873 5' CTGGTGGTCCAGGAGA      75879    G       A
                                TC CCTGGACCAC AG
                                || ||||||||| ||
                                AG GGACCTGGTG TC
                                 A        G
GAM151  LOC145978 3' TCAAACTTTAACAGGTGA    77600       GACCAC
                                TCGCCTG     AAGTTTGA
                                |||||||     ||||||||
                                AGTGGAC     TTCAAACT
                                    AAT___
GAM151  LOC146890 5' TCAGAAGTAGTCAGGCGA    83854       G  C  AAG
                                TCGCCTG AC AC   TTTGA
                                ||||||| || ||   |||||
                                AGCGGAC TG TG   AGACT
                                   _  A  A__
GAM151  LOC150622 5' CTGGTGGTCCAGGGA       79957    G       A
                                TC CCTGGACCAC AG
                                || ||||||||| ||
                                AG GGACCTGGTG TC
                                 _        G
GAM151  LOC152002 3' CAAACCAGCTCCAGGTGA    80431        CCACAA
                                TCGCCTGGA     GTTTG
                                |||||||||     |||||
                                AGTGGACCT     CAAAC
                                     CGAC__
GAM151  LOC153474 3' TCAGAAGCTGAGTCCAGGC   80847       _ CAAG
                                GCCTGGAC CA    TTTGA
                                |||||||| ||    |||||
                                CGGACCTG GT    AGACT
                                    A  CGA_
GAM151  LOC154007 3' TCAAACTCCTAGGCTCAGGCGA 81021       GA  ACA_
                                TCGCCTG  CC    AGTTTGA
                                |||||||  ||    |||||||
```

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                                AGCGGAC  GG   TCAAACT
                                    TC  ATCC
GAM151  LOC154789 5'  TCAAACTTGAGCAGGC     81141      GACCA
                                GCCTG    CAAGTTTGA
                                |||||    |||||||||
                                CGGAC    GTTCAAACT
                                  GA___
GAM151  LOC158301 3'  CAAACCTGTGGTTCCA      81869     _    A
                                TGGA CCACA GTTTG
                                |||| ||||| |||||
                                ACCT GGTGT CAAAC
                                  T    C
GAM151  LOC199906 3'  TCAAACTCCTGACCTCAGGCGA 88487       _ AC  CA
                                TCGCCTG G  CA  AGTTTGA
                                ||||||| |  ||  |||||||
                                AGCGGAC C  GT  TCAAACT
                                    T CA  CC
GAM151  LOC199991 5'  TCAGAGCGTTCCAGGCGA    89916        CC  AAG
                                TCGCCTGGA  AC   TTTGA
                                |||||||||  ||   |||||
                                AGCGGACCT  TG   AGACT
                                     __ CG_
GAM151  LOC219529 5'  TCAAACTCCTGAGCCCAGGTGA 92974        AC_  CA
                                TCGCCTGG   CA  AGTTTGA
                                ||||||||   ||  |||||||
                                AGTGGACC   GT  TCAAACT
                                    CGA  CC
GAM151  LOC220753 3'  CAAACTTGTAGAGGTGGGC   92941     GG  ___
                                GCCT  ACC   ACAAGTTTG
                                ||||  |||   |||||||||
                                CGGG  TGG   TGTTCAAAC
                                  __  AGA
GAM151  LOC221718 3'  TCAAACTTATTGGTGAAG    93632    GG   C_
                                CT  ACCA  AAGTTTGA
                                ||  ||||  ||||||||
                                GA  TGGT  TTCAAACT
                                 AG   TA
GAM151  LOC253927 3'  TCAAACTTAGACTTCAGGC   95025       CCAC
                                GCCTGGA    AAGTTTGA
                                |||||||    ||||||||
                                CGGACTT    TTCAAACT
                                    CAGA
GAM151  LOC51028  3'  CAAATATGGTCCAGG      32179        CAA
                                CCTGGACCA  GTTTG
                                |||||||||  |||||
                                GGACCTGGT  TAAAC
                                     A__
GAM152  ACVR1B   3'  CAGGAAGATAGCTTGAGCTCA  39740    A      TCA   CC
                                TGA CTCAGGCT   GTC  CCTG
                                ||| ||||||||   |||  ||||
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                                ACT GAGTTCGA   TAG  GGAC
                                  C       ___   AA
GAM152  AK1     3'  CAGGAGGATCACCTGAGGTCA  4882     A     CTTCA   C
                                TGA CTCAGG    GTCC CCTG
                                ||| ||||||    |||| ||||
                                ACT GAGTCC    TAGG GGAC
                                  G     AC___   A
GAM152  B3GAT1   3'  CAGGAGGGAGGCCTGAG     37825        TCAG   _
                                CTCAGGCT   TCCC CCTG
                                ||||||||   |||| ||||
                                GAGTCCGG   AGGG GGAC
                                     _____   A
GAM152  B3GAT1   3'  CAGGAGGGAGGCCTGAG     53970        TCAG   _
                                CTCAGGCT   TCCC CCTG
                                ||||||||   |||| ||||
                                GAGTCCGG   AGGG GGAC
                                     _____   A
GAM152  CDH15    3'  AGAGGCAGCCTGAGGTCA    17029     A      TCA   CCC
                                TGA CTCAGGCT   GTC   CT
                                ||| ||||||||   |||   ||
                                ACT GAGTCCGA   CGG   GA
                                  G       ___   A__
GAM152  CHC1L    5'  GGGACTGCCCAGGACTGAGTCC 7016     A     G   ___
            A                    TG ACTCAG CTT   CAGTCCC
                                || |||||| |||   |||||||
                                AC TGAGTC GGA   GTCAGGG
                                  C     A   CCC
GAM152  DHCR24   3'  GACAAGCCTGAGTCCA      28627    A        CA
                                TG ACTCAGGCTT  GTC
                                || ||||||||||  |||
                                AC TGAGTCCGAA  CAG
                                  C        __
GAM152  IL6R     3'  CAGGAGGATCACTTGAGTCCA  5118     A     CTTCA   C
                                TG ACTCAGG    GTCC CCTG
                                || |||||||    |||| ||||
                                AC TGAGTTC    TAGG GGAC
                                  C      AC___   A
GAM152  IPP      3'  CAGGGGGATCGCTTGAGCCCA  19725    AA     TTCA
                                TG  CTCAGGC   GTCCCCCTG
                                ||  |||||||   |||||||||
                                AC  GAGTTCG   TAGGGGGAC
                                  CC      C___
GAM152  KCND3    3'  GGGGCACCTGAGGTTCA     17144      _    CTTCA
                                TGAAC TCAGG    GTCCC
                                ||||| |||||    |||||
                                ACTTG AGTCC    CGGGG
                                   G    A____
GAM152  KRT8     3'  CAGGAGACCCACCTGAGGCTCA 9638     A_     CTTCA   CC
                                TGA  CTCAGG    GTC  CCTG
                                |||  ||||||    |||  ||||
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                                ACT  GAGTCC    CAG  GGAC
                                  CG     ACC__   A_
GAM152  LAMC1    3'  AGAGGACTGAAGATTGA     9674       G        CC
                                TCAG CTTCAGTCC  CT
                                |||| |||||||||  ||
                                AGTT GAAGTCAGG  GA
                                  A        A_
GAM152  LDLR     3'  AGAGGCAGAGCCTGAGTCA    4982      A        CAGTC  C
                                TGA CTCAGGCTT    CC CT
                                ||| |||||||||    || ||
                                ACT GAGTCCGAG    GG GA
                                  _        AC___  A
GAM152  LMO2     5'  AGAGGGAAGCCTGAG       18739         TCAG    C
                                CTCAGGCT    TCCC CT
                                ||||||||    |||| ||
                                GAGTCCGA    AGGG GA
                                     _____    A
GAM152  LPP      3'  CAGGAGGATTGCCTGAGGCCA  18745    AA      TTC     C
                                TG  CTCAGGC   AGTCC CCTG
                                ||  |||||||   ||||| ||||
                                AC  GAGTCCG   TTAGG GGAC
                                 CG       ___     A
GAM152  MYLK     5'  GGGACAACGCCTGAGTCCA    53833    A       TTCA
                                TG ACTCAGGC    GTCCC
                                || ||||||||    |||||
                                AC TGAGTCCG    CAGGG
                                 C       CAA_
GAM152  MYLK     5'  GGGACAACGCCTGAGTCCA    53831    A       TTCA
                                TG ACTCAGGC    GTCCC
                                || ||||||||    |||||
                                AC TGAGTCCG    CAGGG
                                 C       CAA_
GAM152  MYO1B    5'  CAGGGGGACTTCCTTGAGCTC  24233    A     CTTC
                                GA CTCAGG    AGTCCCCCTG
                                || ||||||    ||||||||||
                                CT GAGTTC    TCAGGGGGAC
                                 C     CT__
GAM152  NUP98    3'  AGGAGGGTTGGCCTGAGTT    32858          TCAGT   _
                                AACTCAGGCT     CCC CCT
                                ||||||||||     ||| |||
                                TTGAGTCCGG     GGG GGA
                                      TT___    A
GAM152  PPAT     3'  CTGAAGTCTGAATTCA      10697      C
                                TGAA TCAGGCTTCAG
                                |||| ||||||||||
                                ACTT AGTCTGAAGTC
                                  A
GAM152  PPT1     3'  GCCCAAGCCTGAGCTCA     61804     A       CA
                                TGA CTCAGGCTT  GT
                                ||| |||||||||  ||
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                                ACT GAGTCCGAA  CG
                                  C        CC
GAM152  RAD52    3'  GCTCCCGAAGCCTGAGCTCA   56205     A        ___
                                TGA CTCAGGCTTC   AGT
                                ||| ||||||||||   |||
                                ACT GAGTCCGAAG   TCG
                                  C         CCC
GAM152  RAD52    3'  GCTCCCGAAGCCTGAGCTCA   56214     A        ___
                                TGA CTCAGGCTTC   AGT
                                ||| ||||||||||   |||
                                ACT GAGTCCGAAG   TCG
                                  C         CCC
GAM152  RAD52    3'  GCAGAAGCCTGAGCTCA     56195     A        A
                                TGA CTCAGGCTTC GT
                                ||| |||||||||| ||
                                ACT GAGTCCGAAG CG
                                  C         A
GAM152  RERE     5'  CAGAAGACTGAAGCCCAGGCTC 23963     A  CA        CCC
              A                  TGA CT  GGCTTCAGTC   CTG
                                ||| ||  ||||||||||   |||
                                ACT GG  CCGAAGTCAG   GAC
                                  C  AC         AA_
GAM152  TACC1    3'  CAGGAGGATCACTTGAGTCCA  20793    A      CTTCA    C
                                TG ACTCAGG     GTCC CCTG
                                || |||||||     |||| ||||
                                AC TGAGTTC     TAGG GGAC
                                  C       AC___    A
GAM152  TRPM1    3'  GAAAGATAGCTTGAGTCCA    10058    A       _  AG
                                TG ACTCAGGCT TC  TC
                                || |||||||| ||  ||
                                AC TGAGTTCGA AG  AG
                                  C        T  AA
GAM152  TRPM7    3'  CAGAGGTATGAGAAGCCTGA   62128          A_  C  C
                                TCAGGCTTC  GT CC CTG
                                |||||||||  || || |||
                                AGTCCGAAG  TA GG GAC
                                      AG  T  A
GAM152  VIPR2    3'  GCCCCCTGCAATAAAGCCTGAT 12611   AC      T_________   TCCCC
              CTCA                    TCAGGCT        CAG     C
                                 |||||||        |||     |
                                 AGTCCGA        GTC     G
                                CT      AATAACIII   CCCCT
GAM152  WW45     3'  AGAGGATGGCTTGAGCCCA   41519    AA       TCA    CC
                                TG  CTCAGGCT   GTCC  CT
                                ||  ||||||||   ||||  ||
                                AC  GAGTTCGG   TAGG  GA
                                  CC        ___    A_
GAM152  ZNF16    3'  GACCGAAAGCCTGGACTCA    22723     AC       _ A
                                TGA  TCAGGCTT C GTC
                                |||  |||||||| | |||
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                                ACT  GGTCCGAA G CAG
                                  CA       A C
GAM152  APPD     3'  GGGACTGCAGCCTGAGCTC   44216    A       T
                                GA CTCAGGCT CAGTCCC
                                || |||||||| |||||||
                                CT GAGTCCGA GTCAGGG
                                 C       C
GAM152  BICD2    3'  GGGGCAGAACCTGAGTT     70399        C   A
                                AACTCAGG TTC GTCCC
                                |||||||| ||| |||||
                                TTGAGTCC AAG CGGGG
                                     _   A
GAM152  BRAG     3'  CAGGGAAATCTGGCCTGAG   29473       TT   TCC_
                                CTCAGGC  CAG    CCCTG
                                |||||||  |||    |||||
                                GAGTCCG  GTC    GGGAC
                                   __   TAAA
GAM152  BRPF3    3'  CAGGGGGAATCTCCCCAAGCTC 92312     A  CA  CTTCAG
              A                  TGA CT  GG     TCCCCCTG
                                ||| ||  ||     ||||||||
                                ACT GA  CC     AGGGGGAC
                                  C  AC  CTCTA_
GAM152  CHCR     3'  AGAGGGAGCCTGAGTACA    37234    A      TTCAG    C
                                TG ACTCAGGC     TCCC CT
                                || ||||||||     |||| ||
                                AC TGAGTCCG     AGGG GA
                                 A       _____    A
GAM152  CHERP    3'  CAGGAAGGGTTGGCCTGAG    21098        TCAGT   __
                                CTCAGGCT     CCC  CCTG
                                ||||||||     |||  ||||
                                GAGTCCGG     GGG  GGAC
                                     TT___    AA
GAM152  DKFZP434N1511 3'  CTGAACCTGAGTTCA       91416          C
                                TGAACTCAGG TTCAG
                                |||||||||| |||||
                                ACTTGAGTCC AAGTC
                                          _
GAM152  DKFZP564O0423 3'  AGGGAGAGGCCTGAG       91678          AGTCC
                                CTCAGGCTTC     CCCT
                                |||||||||     ||||
                                GAGTCCGGAG     GGGA
                                      A____
GAM152  FLJ00001  3'  CAGGAGAACTGAGGCATGA   81812     G       CCC
                                TCA GCTTCAGT   CCTG
                                ||| ||||||||   ||||
                                AGT CGGAGTCA   GGAC
                                  A       AGA
GAM152  FLJ10057  5'  AGGAGGGGCAACCTGAGTT    35779        CTTCA    _
                                AACTCAGG     GTCCC CCT
                                ||||||||     ||||| |||
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                                TTGAGTCC    CGGGG GGA
                                    AA___    A
GAM152  FLJ10569  5' AGGGGGACTGCGAGTTC    36300      AGGCTT
                                GAACTC    CAGTCCCCCT
                                ||||||    ||||||||||
                                CTTGAG    GTCAGGGGGA
                                   C_____
GAM152  FLJ12476  5' GGACTGAAGTGGGGTT     42950      AG
                                AACTC  GCTTCAGTCC
                                |||||  ||||||||||
                                TTGGG  TGAAGTCAGG
                                  G_
GAM152  FLJ12987  3' CAGGGGGACATCCTGTATTCA  47194     CT   CTTCA
                                TGAA  CAGG    GTCCCCCTG
                                ||||  ||||    |||||||||
                                ACTT  GTCC    CAGGGGGAC
                                  AT   TA___
GAM152  FLJ13072  5' AGGAGGGGCTGAGTCC     89801    C      _
                                GG TTCAGTCCC CCT
                                || |||||||| |||
                                CC GAGTCGGGG GGA
                                 T       A
GAM152  FLJ13902  3' CAGGAGGACCGCTTGAGTCCA  45041    A      TTCA   C
                                TG ACTCAGGC   GTCC CCTG
                                || ||||||||   |||| ||||
                                AC TGAGTTCG   CAGG GGAC
                                 C      C___   A
GAM152  FLJ22479  3' GCCCCCTGCAAAAAAGCCTGAT 46075  AC     T_________  TCCCC
           CTCA                   TCAGGCT       CAG    C
                                  |||||||       |||    |
                                  AGTCCGA       GTC    G
                                CT     AAAAACIII  CCCCT
GAM152  FLJ23042  3' AGAGGATCGCTTGAGCCCA   47167    AA     TTCA   CC
                                TG  CTCAGGC   GTCC  CT
                                ||  |||||||   ||||  ||
                                AC  GAGTTCG   TAGG  GA
                                 CC     C___   A_
GAM152  FLJ23447  3' CAGGAGGATCGCTTGAGCCCA  45711    AA     TTCA   C
                                TG  CTCAGGC   GTCC CCTG
                                ||  |||||||   |||| ||||
                                AC  GAGTTCG   TAGG GGAC
                                 CC     C___   A
GAM152  FLJ23604  3' GCCCCCTGCAGAAAGACCTGAG 46860       _ T________  TCCCC
           TTCA                   ACTCAGG CT       CAG    C
                                  ||||||| ||       |||    |
                                  TGAGTCC GA       GTC    G
                                     A  AAGACIII  CCCCT
GAM152  GCN2     3' CAGGAAGACTGCTTGA     62770       TTC   CC
                                TCAGGC   AGTC  CCTG
                                ||||||   ||||  ||||
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                                AGTTCG  TCAG  GGAC
                                   ___   AA
GAM152  ICK     3' TTGAAGCTGAATTCA      29938     C   G
                                TGAA TCAG CTTCAG
                                |||| |||| ||||||
                                ACTT AGTC GAAGTT
                                  A   _
GAM152  KIAA0226 3' CAGCTTCTGAAGCCGAACTCA 63513    AC  A      TCCCC
                                TGA  TC GGCTTCAG    CTG
                                |||  || ||||||||    |||
                                ACT  AG CCGAAGTC    GAC
                                  CA  _       TTC__
GAM152  KIAA0285 3' CAGAAGGAAGCTGGCCTGAG  29013       TCAG  CC
                                CTCAGGCT    TCC  CTG
                                ||||||||    |||  |||
                                GAGTCCGG    AGG  GAC
                                     TCGA   AA
GAM152  KIAA0298 3' GGAGAGATGCCTGTGTTCA   76580     T    T  AG
                                TGAAC CAGGC TC  TCC
                                ||||| ||||| ||  |||
                                ACTTG GTCCG AG  AGG
                                   T    T  AG
GAM152  KIAA0953 3' CAGGAGGACTGCTTGAGCCCA 66781    AA     TTC    C
                                TG  CTCAGGC   AGTCC CCTG
                                ||  |||||||   ||||| ||||
                                AC  GAGTTCG   TCAGG GGAC
                                 CC      ___     A
GAM152  KIAA1033 3' GGAATGAGCCTGAAGTTCA   64516      _     T  G
                                TGAACT CAGGCT CA TCC
                                |||||| |||||| || |||
                                ACTTGA GTCCGA GT AGG
                                   A     _ A
GAM152  KIAA1463 5' GGACTGAAGCCTGAGGCCA   72277    AA
                                TG  CTCAGGCTTCAGTCC
                                ||  ||||||||||||||
                                AC  GAGTCCGAAGTCAGG
                                 CG
GAM152  KIAA1500 3' GGGGAGACTGAAACCCGAGTT 64121      A  C     _
                                AACTC GG TTCAGTC CCCC
                                ||||| || ||||||| ||||
                                TTGAG CC AAGTCAG GGGG
                                   C  A      A
GAM152  KIAA1666 3' GGACTTAAGCCTGAGTT     65249          C
                                AACTCAGGCTT AGTCC
                                |||||||||||| |||||
                                TTGAGTCCGAA TCAGG
                                       T
GAM152  KR18    3' CAGGAGAATTGCTTGAGTCCA 52741    A      TTCAG  CC
                                TG ACTCAGGC    TC  CCTG
                                || ||||||||    ||  ||||
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                                AC TGAGTTCG    AG  GGAC
                                 C       TTA__  A_
GAM152  LIMR     5'  GAAGCCTGCTGAGTTCA     36189         ___
                                TGAACTCA   GGCTTC
                                ||||||||   ||||||
                                ACTTGAGT   CCGAAG
                                     CGT
GAM152  MGC13183 3'  CAGAAAATGTAAACCTGAGTT  50390        C  _  GTCCCC
                                AACTCAGG TT CA     CTG
                                |||||||| || ||     |||
                                TTGAGTCC AA GT     GAC
                                     A  T  AAAA__
GAM152  MRF-1    3'  AGGCAGCAGCCTGAGCCCA   71324    AA      TCA  CCC
                                TG  CTCAGGCT   GT   CCT
                                ||  ||||||||   ||   |||
                                AC  GAGTCCGA   CG   GGA
                                 CC       ___  AC_
GAM152  OBTP     3'  CAGAGGGGGCTGCCTGG     34241       TTC      _
                                TCAGGC   AGTCCCC CTG
                                ||||||   ||||||| |||
                                GGTCCG   TCGGGGG GAC
                                    ___      A
GAM152  POMT2    3'  GATTCCAGCCTGGGTCCA    25395    A       TC
                                TG ACTCAGGCT  AGTC
                                || |||||||||  ||||
                                AC TGGGTCCGA  TTAG
                                 C        CC
GAM152  PP1665   3'  AGGAGGCACCTGAGTTC     47910         CTTCA T  C
                                GAACTCAGG     G CC CCT
                                |||||||||     | || |||
                                CTTGAGTCC     C GG GGA
                                     A____ _  A
GAM152  PRO2037  3'  AGAGGATTGCTTGAGTCCA   37783    A      TTC    CC
                                TG ACTCAGGC   AGTCC  CT
                                || ||||||||   |||||  ||
                                AC TGAGTTCG   TTAGG  GA
                                 C       ___     A_
GAM152  SEC14L2  3'  AGGAGGTGGCCTGAGTCA    24871     A      TCAGT  C
                                TGA CTCAGGCT     CC CCT
                                ||| ||||||||     || |||
                                ACT GAGTCCGG     GG GGA
                                  _       T____  A
GAM152  TSGA2    3'  CAGGAGGATTGCTTGAGTCCA  55093    A      TTC    C
                                TG ACTCAGGC   AGTCC CCTG
                                || ||||||||   ||||| ||||
                                AC TGAGTTCG   TTAGG GGAC
                                 C       ___     A
GAM152  TXNL2    3'  GATTCAGAAGCCATGAGTTCA  21551         _     __
                                TGAACTCA GGCTTC  AGTC
                                |||||||| ||||||  ||||
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                                ACTTGAGT CCGAAG  TTAG
                                     A     AC
GAM152  LOC115574 3'  GGCGCAGCTCTGAGTTCA    73468         _  TCA
                                TGAACTCAG GCT   GTC
                                ||||||||| |||   |||
                                ACTTGAGTC CGA   CGG
                                      T  CG_
GAM152  LOC130162 3'  CAGGAGGATCGCTTGAGCCCA  74910    AA     TTCA   C
                                TG  CTCAGGC    GTCC CCTG
                                ||  |||||||    |||| ||||
                                AC  GAGTTCG    TAGG GGAC
                                 CC      C___    A
GAM152  LOC130535 3'  CAGGAGGATTGCCTGAGCCCA  76149    AA     TTC    C
                                TG  CTCAGGC   AGTCC CCTG
                                ||  |||||||   ||||| ||||
                                AC  GAGTCCG   TTAGG GGAC
                                 CC      ___     A
GAM152  LOC132625 3'  CAGGAGGATAGCTTGAGCCCA  75901    AA      TCA   C
                                TG  CTCAGGCT   GTCC CCTG
                                ||  ||||||||   |||| ||||
                                AC  GAGTTCGA   TAGG GGAC
                                 CC       ___    A
GAM152  LOC134265 3'  CAGGAGGACCGCTTGAGCCCA  75173    AA     TTCA   C
                                TG  CTCAGGC    GTCC CCTG
                                ||  |||||||    |||| ||||
                                AC  GAGTTCG    CAGG GGAC
                                 CC      C___    A
GAM152  LOC139770 3'  CAGAAGAATAGCTTGAGCCCA  75387    AA      TCAG  CCC
                                TG  CTCAGGCT    TC   CTG
                                ||  ||||||||    ||   |||
                                AC  GAGTTCGA    AG   GAC
                                 CC       TA__  AA_
GAM152  LOC144481 3'  CAGGAAGATGGCTTGAGCCCA  83095    AA      TCA   CC
                                TG  CTCAGGCT   GTC  CCTG
                                ||  ||||||||   |||  ||||
                                AC  GAGTTCGG   TAG  GGAC
                                 CC       ___   AA
GAM152  LOC150221 3'  GGACTTAAGCCTGAGTT     65275          C
                                AACTCAGGCTT AGTCC
                                |||||||||| |||||
                                TTGAGTCCGAA TCAGG
                                       T
GAM152  LOC152426 5'  CAGGGAGACTGGTGCTGA    85711      G T     C
                                TCAG C TCAGTC CCCTG
                                |||| | |||||| |||||
                                AGTC G GGTCAG GGGAC
                                  _ T     A
GAM152  LOC153243 3'  CAGGAGACCCACCTGAGGCTCA 80794     A_     CTTCA   CC
                                TGA  CTCAGG    GTC  CCTG
                                |||  ||||||    |||  ||||
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                                ACT  GAGTCC    CAG  GGAC
                                  CG     ACC__   A_
GAM152   LOC157556 3'  CAGAGGAGGCCAGCCTGAGT   86481        TCA   _  C
                                ACTCAGGCT   GTC CC CTG
                                |||||||||   ||| || |||
                                TGAGTCCGA   CGG GG GAC
                                     C__   A  A
GAM152   LOC199733 3'  CAGGAGGATGGCTTGAGCCCA  89846    AA       TCA    C
                                TG  CTCAGGCT   GTCC CCTG
                                ||  ||||||||   |||| ||||
                                AC  GAGTTCGG   TAGG GGAC
                                 CC       ___    A
GAM152   LOC201305 5'  CAGAAGGCGCAGCTGAGTTCA  88235        G  TCA T  CC
                                TGAACTCAG CT   G CC  CTG
                                |||||||||  ||   | ||  |||
                                ACTTGAGTC GA   C GG  GAC
                                     _  CG_ _  AA
GAM152   LOC202781 3'  CAGGAGGATTGCTTGAGCCCA  90364    AA     TTC    C
                                TG  CTCAGGC   AGTCC CCTG
                                ||  |||||||   ||||| ||||
                                AC  GAGTTCG   TTAGG GGAC
                                 CC       ___    A
GAM152   LOC203276 3'  CAGGAGGATCCCTTGAGTTCA  90477        CTTCA   C
                                TGAACTCAGG    GTCC CCTG
                                ||||||||||    |||| ||||
                                ACTTGAGTTC    TAGG GGAC
                                     CC___    A
GAM152   LOC203305 3'  CAGGAGGATCCCTTGAGTTCA  90521        CTTCA   C
                                TGAACTCAGG    GTCC CCTG
                                ||||||||||    |||| ||||
                                ACTTGAGTTC    TAGG GGAC
                                     CC___    A
GAM152   LOC219405 3'  GAAAGGCACCTGGGTTCA    90772         CT  AG
                                TGAACTCAGG  TC  TC
                                ||||||||||  ||  ||
                                ACTTGGGTCC  GG  AG
                                     AC  AA
GAM152   LOC221946 3'  AGAGGACTGCTTGAGGCCA    93975    AA     TTC    CC
                                TG  CTCAGGC   AGTCC  CT
                                ||  |||||||   |||||  ||
                                AC  GAGTTCG   TCAGG  GA
                                 CG       ___    A_
GAM152   LOC221954 5'  CAGGAGAATGGCTTGAGCCCA  93999    AA      TCAG  CC
                                TG  CTCAGGCT   TC  CCTG
                                ||  ||||||||   ||  ||||
                                AC  GAGTTCGG   AG  GGAC
                                 CC       TA__  A_
GAM152   LOC253906 3'  CAGAAGGATTGCTTGAGCCCA  96532    AA     TTC    CC
                                TG  CTCAGGC   AGTCC  CTG
                                ||  |||||||   |||||  |||
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                                AC  GAGTTCG   TTAGG  GAC
                                 CC      ___     AA
GAM152  LOC254045 3'  CAGGAAGATGGCTTGAGCCCA  96504    AA      TCA   CC
                                TG  CTCAGGCT   GTC  CCTG
                                ||  ||||||||   |||  ||||
                                AC  GAGTTCGG   TAG  GGAC
                                 CC       ___   AA
GAM152  LOC254243 3'  CAGGAGGATCCCTTGAGTTCA  97406         CTTCA   C
                                TGAACTCAGG    GTCC CCTG
                                ||||||||||    |||| ||||
                                ACTTGAGTTC    TAGG GGAC
                                      CC___    A
GAM152  LOC51107  3'  AGGAGCAGCCTGGGTTCA    32060          TCA  CCC
                                TGAACTCAGGCT   GT   CCT
                                ||||||||||||  ||   |||
                                ACTTGGGTCCGA   CG   GGA
                                      ___  A__
GAM152  LOC57118  3'  CAGGAGGACTGTTTGAGTTCA  39866          TTC    C
                                TGAACTCAGGC   AGTCC CCTG
                                ||||||||||   ||||| ||||
                                ACTTGAGTTTG   TCAGG GGAC
                                      ___    A
GAM152  LOC90038  3'  CAGGAGGATCCCTTGAGTTCA  61150         CTTCA   C
                                TGAACTCAGG    GTCC CCTG
                                ||||||||||    |||| ||||
                                ACTTGAGTTC    TAGG GGAC
                                      CC___    A
GAM152  LOC92606  3'  CAGAAGGGTTCTGTAAAGCCTG 69986    AC      __   TC   __
            AACTC                  GA  TCAGGCTT  CAG  CCC  CTG
                                ||  ||||||||  |||  |||  |||
                                CT  AGTCCGAA  GTC  GGG  GAC
                                 CA       AT   TT   AA
GAM152  LOC92771  3'  CAGGAGGATTGCCTGAGGCCA  53074    AA     TTC    C
                                TG  CTCAGGC   AGTCC CCTG
                                ||  |||||||   ||||| ||||
                                AC  GAGTCCG   TTAGG GGAC
                                 CG      ___    A
GAM153  ADAM12    5'  CAACGGTCAAGGCTGGC     12968          TA_
                                GTCAGCCTTG   GTTG
                                ||||||||||   ||||
                                CGGTCGGAAC   CAAC
                                      TGG
GAM153  CASP7     5'  CGATGCAAAACATGAGAAAGCC 52897     A  ___  TG AG_
            GAC                    GTC GC   CT  T   TTGCATCG
                                ||| ||   ||  |  ||||||||
                                CAG CG   GA  A   AACGTAGC
                                  C  AAA  GT CAA
GAM153  DIA1      5'  CGACCCTGACAGGCTGAC    23643         T  A___
                                GTCAGCCT GT    GTTG
                                ||||||||  ||    ||||
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                                CAGTCGGA CA    CAGC
                                     _ GTCC
GAM153  DXYS155E  3'  GCCTACAAGGATGAC      17453      G       TT
                                GTCA CCTTGTAG  GC
                                |||| ||||||||  ||
                                CAGT GGAACATC  CG
                                  A      __
GAM153  EGR2      3'  ATGTTACAAGGCTG       4626          GTT
                                CAGCCTTGTA   GCAT
                                ||||||||||   ||||
                                GTCGGAACAT   TGTA
                                     ____
GAM153  HYAL1     3'  CAATCACAAAGGCTGAC     23606          _  A
                                GTCAGCCTT GT GTTG
                                ||||||||| || ||||
                                CAGTCGGAA CA TAAC
                                     A  C
GAM153  HYAL1     3'  CAATCACAAAGGCTGAC     52535          _  A
                                GTCAGCCTT GT GTTG
                                ||||||||| || ||||
                                CAGTCGGAA CA TAAC
                                     A  C
GAM153  INSRR     3'  GATGCAGAGCCTGAC       68465       C   GTAGT
                                GTCAG CTT    TGCATC
                                ||||| |||    ||||||
                                CAGTC GAG    ACGTAG
                                  C  ______
GAM153  KCNK4     3'  CGAGGGGTACAAGGCCAGC   33505    CA       G TGCA
                                GT  GCCTTGTA T    TCG
                                ||  |||||||| |    |||
                                CG  CGGAACAT G    AGC
                                 AC       G GG__
GAM153  NXF3      3'  CAACTCACAGGGCTGAC     41900          _
                                GTCAGCCTTGT AGTTG
                                |||||||||| |||||
                                CAGTCGGGACA TCAAC
                                     C
GAM153  PTPRA     5'  CGATGCCTTCTACAAGGC    11091          TT_
                                GCCTTGTAG   GCATCG
                                |||||||||   ||||||
                                CGGAACATC   CGTAGC
                                     TTC
GAM153  TLR5      5'  CAACTCCAACAGGCTGAC    79425          __  T
                                GTCAGCCT  TG AGTTG
                                ||||||||  || |||||
                                CAGTCGGA  AC TCAAC
                                     CA  C
GAM153  A4GALT    5'  ATGGGCTGCCCAGGCTGAC   33834          T_     G
                                GTCAGCCT  GTAGTT CAT
                                ||||||||  |||||| |||
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                                CAGTCGGA  CGTCGG GTA
                                     CC     _
GAM153  ARGBP2   5'  CGGCTACAAGGCAGAC      40773     A
                                GTC GCCTTGTAGTTG
                                ||| ||||||||||||
                                CAG CGGAACATCGGC
                                  A
GAM153  CDK5RAP3 5'  CAACTACAGGACTAAC      47281     C  C
                                GT AG CTTGTAGTTG
                                || || ||||||||||
                                CA TC GGACATCAAC
                                 A  A
GAM153  CNNM4    3'  ATGACAGTCAAGGCTGAC     39475          TAG  _
                                GTCAGCCTTG   TTG CAT
                                ||||||||||   ||| |||
                                CAGTCGGAAC   GAC GTA
                                      T__   A
GAM153  DUSP14   5'  CGATGCAAGTGTGACTG     22835     CC TG  G
                                CAG  T  TA TTGCATCG
                                |||  |  || ||||||||
                                GTC  A  GT AACGTAGC
                                  __ GT  G
GAM153  KIAA0410 3'  CGACTTACAAGGCTGA      28773          _
                                TCAGCCTTGTA GTTG
                                |||||||||| ||||
                                AGTCGGAACAT CAGC
                                       T
GAM153  KIAA0753 3'  CAACACAAGTGCGGC       28997     A _    A
                                GTC GC CTTGT GTTG
                                ||| || ||||| ||||
                                CGG CG GAACA CAAC
                                  _  T    _
GAM153  KIAA0931 3'  CGGGGGCCCAAGGCTGAC    67418          TAGTT  A_
                                GTCAGCCTTG    GC  TCG
                                ||||||||||    ||  |||
                                CAGTCGGAAC    CG  GGC
                                      C____  GG
GAM153  KIAA1036 5'  GCCTCCAAGGCTGAC       29822          T  TT
                                GTCAGCCTTG AG  GC
                                |||||||||| ||  ||
                                CAGTCGGAAC TC  CG
                                      C  __
GAM153  KIAA1200 5'  CGACGCAAGGTCGGC       62371     A      A
                                GTC GCCTTGT GTTG
                                ||| ||||||| ||||
                                CGG TGGAACG CAGC
                                  C      _
GAM153  PRPF8    3'  CGATACAAATACAAGCTGAT   61189       C    G   C
                                GTCAGC TTGTA TTG ATCG
                                |||||| ||||| ||| ||||
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                                TAGTCG AACAT AAC TAGC
                                  _    A  A
GAM153  PSR      3'  CAACCACAAGGCTGGC      65175          A
                                GTCAGCCTTGT GTTG
                                |||||||||| ||||
                                CGGTCGGAACA CAAC
                                      C
GAM153  STARD7   5'  CGAGGAGCCACAGGGCTGAC  57697          A   GCA
                                GTCAGCCTTGT GTT   TCG
                                |||||||||| |||   |||
                                CAGTCGGGACA CGA   AGC
                                      C   GG_
GAM153  STARD7   5'  CGAGGAGCCACAGGGCTGAC  39330          A   GCA
                                GTCAGCCTTGT GTT   TCG
                                |||||||||| |||   |||
                                CAGTCGGGACA CGA   AGC
                                      C   GG_
GAM153  STX12    3'  CAACACTTTGGAAGGCTGA   66348        G  ____
                                TCAGCCTT TA    GTTG
                                |||||||| ||    ||||
                                AGTCGGAA GT    CAAC
                                     G  TTCA
GAM153  LOC126520 5'  GCTGCTACAAGCTGAC     74524        C      T
                                GTCAGC TTGTAGT GC
                                |||||| ||||||| ||
                                CAGTCG AACATCG CG
                                   _      T
GAM153  LOC143282 3'  CGATGCAGAGGGAGGCTGA   76514         GTAG
                                TCAGCCTT    TTGCATCG
                                ||||||||    ||||||||
                                AGTCGGAG    GACGTAGC
                                     GGA_
GAM153  LOC143425 3'  CGGCTGGCAGGCTGAC      87635         TG
                                GTCAGCCT  TAGTTG
                                ||||||||  ||||||
                                CAGTCGGA  GTCGGC
                                     CG
GAM153  LOC148946 5'  CAACACCAGGGCTGAC      84308          TA
                                GTCAGCCTTG  GTTG
                                ||||||||||  ||||
                                CAGTCGGGAC  CAAC
                                      CA
GAM153  LOC149711 3'  ATGACTTGCAAGGTGAC     84672      G       TTG
                                GTCA CCTTGTAG   CAT
                                |||| ||||||||   |||
                                CAGT GGAACGTT   GTA
                                  _       CA_
GAM153  LOC197414 3'  CGATGTCTCCTACAAGGC    88064         TT_
                                GCCTTGTAG   GCATCG
                                |||||||||   ||||||
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                                CGGAACATC   TGTAGC
                                     CTC
GAM153  LOC202986 5'  CAACTACAAGCCGAC      90440     A  C
                                GTC GC TTGTAGTTG
                                ||| || |||||||||
                                CAG CG AACATCAAC
                                  C  _
GAM153  LOC220045 3'  CAACACAAACAGGGCTGA    93406          A___
                                TCAGCCTTGT    GTTG
                                ||||||||||    ||||
                                AGTCGGGACA    CAAC
                                      AACA
GAM153  LOC222602 5'  CAAATACAAGGTGAC       92858      G      G
                                GTCA CCTTGTA TTG
                                |||| ||||||| |||
                                CAGT GGAACAT AAC
                                  _      A
GAM153  LOC255461 5'  CGATAGAAGAAAGGCTGAC   97318         GTAG  GC
                                GTCAGCCTT    TT  ATCG
                                |||||||||    ||  ||||
                                CAGTCGGAA    AG  TAGC
                                     AGA_  A_
GAM153  LOC255516 5'  CGATAGAAGAAAGGCTGAC   97331         GTAG  GC
                                GTCAGCCTT    TT  ATCG
                                |||||||||    ||  ||||
                                CAGTCGGAA    AG  TAGC
                                     AGA_  A_
GAM153  LOC91421  3'  CGATGCAATGGAGGC       65991       GTA
                                GCCTT   GTTGCATCG
                                |||||   |||||||||
                                CGGAG   TAACGTAGC
                                   G__
GAM153  LOC93190  5'  CAACTCTCCCTAAAGGCTGAC  71658         GT_____
                                GTCAGCCTT      AGTTG
                                |||||||||      |||||
                                CAGTCGGAA      TCAAC
                                     ATCCCTC
GAM154  AOAH      5'  ACAGACTCCCTCCAGCTCT    91114      AA    A  A  A
                                AGA  TGGAG GA GT TGT
                                |||  ||||| || || |||
                                TCT  ACCTC CT CA ACA
                                  CG    C  _  G
GAM154  CCND2     3'  ATACTCCTCCCCTCTTCT     8286       AT  A   A
                                AGAA  GG GAG AGTAT
                                ||||  || ||| |||||
                                TCTT  CC CTC TCATA
                                  CT  C   C
GAM154  CD209     3'  ACAGTTCCTTCTCTCCAT     40956          TA__
                                ATGGAGAGAAG    TGT
                                ||||||||||    |||
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                                TACCTCTCTTC   ACA
                                      CTTG
GAM154  CD209L   3'  GCGCTTCTTCTCTCCAT    26520         TATGTA
                                ATGGAGAGAAG    CGC
                                ||||||||||     |||
                                TACCTCTCTTC    GCG
                                      TTC___
GAM154  CHRNB4   3'  CATCTCTCTCCACTTC     5628     A      A T
                                GAA TGGAGAGA G ATG
                                ||| |||||||| | |||
                                CTT ACCTCTCT C TAC
                                  C      _ _
GAM154  CXCR4    3'  GCATAGATAATCTCTCCATT   12951        AG   G  C
                                AATGGAGAGA  TAT TA GC
                                ||||||||||  ||| || ||
                                TTACCTCTCT  ATA AT CG
                                      A_   G  A
GAM154  DDOST    3'  ACTCCTCTCATTTCT      17815       G    A
                                AGAAATG AGAG AGT
                                ||||||| |||| |||
                                TCTTTAC TCTC TCA
                                   _   C
GAM154  DTNB     3'  GCACATTCCTCTCCATCTTT   41580     A      A   A
                                AGA ATGGAGAG AGT TGT
                                ||| |||||||| ||| |||
                                TTT TACCTCTC TTA ACG
                                  C       C   C
GAM154  DTNB     3'  GCACATTCCTCTCCATCTTT   52502     A      A   A
                                AGA ATGGAGAG AGT TGT
                                ||| |||||||| ||| |||
                                TTT TACCTCTC TTA ACG
                                  C       C   C
GAM154  GCK      3'  ACATGCCACCCTCTCCAT    53170        AA__
                                ATGGAGAG    GTATGT
                                ||||||||    ||||||
                                TACCTCTC    CGTACA
                                     CCAC
GAM154  GCK      3'  ACATGCCACCCTCTCCAT    53175        AA__
                                ATGGAGAG    GTATGT
                                ||||||||    ||||||
                                TACCTCTC    CGTACA
                                     CCAC
GAM154  GCK      3'  ACATGCCACCCTCTCCAT    3863         AA__
                                ATGGAGAG    GTATGT
                                ||||||||    ||||||
                                TACCTCTC    CGTACA
                                     CCAC
GAM154  GORASP1  3'  GTGTACTTGCCCCCATCTCC   49113      GAA__   T
                                GGAGA    GTA GTACGC
                                |||||    ||| ||||||
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                                CCTCT    CGT CATGTG
                                   ACCCC  T
GAM154  GSPT1   5' CGCCCCTGCCTCCATTTCT  9141        AGAA  TGTA
                                AGAAATGGAG   GTA   CG
                                ||||||||||   |||   ||
                                TCTTTACCTC   CGT   GC
                                     ____  CCCC
GAM154  HCN4    3' ACGTTCTCTCTCCAGTCCT  18487   AAA      A T
                                AG  TGGAGAGA G ATGT
                                ||  |||||||| | ||||
                                TC  ACCTCTCT C TGCA
                                 CTG      _ T
GAM154  HRB     3' ACATTACATCTCTCCACCTCT 15703    AA      A  _
                                AGA  TGGAGAGA GTA TGT
                                |||  |||||||| ||| |||
                                TCT  ACCTCTCT CAT ACA
                                  CC       A  T
GAM154  IL2RB   3' GCACACTTGGTCCATCCATTTC 6071       GA  ___  A
                                GAAATGGA  GA   AGT TGT
                                ||||||||  ||   ||| |||
                                CTTTACCT  CT   TCA ACG
                                     AC  GGT   C
GAM154  KCNJ5   3' GCATCTGTTCTCTCCAT    6092         GT_
                                ATGGAGAGAA   ATGT
                                ||||||||||   ||||
                                TACCTCTCTT   TACG
                                      GTC
GAM154  KLF7    5' GCTGGATGCCTCTCTCCAT   13542       A   G  C
                                ATGGAGAGA GTAT TA GC
                                ||||||||| |||| || ||
                                TACCTCTCT CGTA GT CG
                                     C   G  _
GAM154  LRP1    3' GCACAGTATTATTTCTCCAT  9803         _   GTAC
                                ATGGAGAGA AGTAT   GC
                                ||||||||| |||||   ||
                                TACCTCTTT TTATG   CG
                                     A    ACA_
GAM154  MAP1A   3' GCACCCTTTCCTCCATTTC   9898        AG  TA
                                GAAATGGAG  AAG  TGT
                                |||||||||  |||  |||
                                CTTTACCTC  TTC  ACG
                                     CT   CC
GAM154  MYD88   3' ACAGCTGTTCTCTCCCTCTCT 10160    AAT      GTA_
                                AGA   GGAGAGAA   TGT
                                |||   ||||||||   |||
                                TCT   CCTCTCTT   ACA
                                  CTC      GTCG
GAM154  MYL3    5' GCATTCTTCTCTCCACATC   63900    AA       T
                                GA  TGGAGAGAAG ATGT
                                ||  |||||||||| ||||
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                                CT  ACCTCTCTTC TACG
                                 AC         T
GAM154  OPRM1    3'  GCATCATTTTCACCTCCATTTC 6202          A_   T   TAC
            T                    AGAAATGGAG  GAAG ATG   GC
                                 ||||||||||  |||| |||   ||
                                 TCTTTACCTC  CTTT TAC   CG
                                       CA    _   TA_
GAM154  PLP2     3'  GCGAACTTCCCTCATTTCT    10652        G  A    A
                                 AGAAATG AG GAAGT TGT
                                 ||||||| || ||||| |||
                                 TCTTTAC TC CTTCA GCG
                                     _ C    A
GAM154  POLG     5'  ACGTGTCTCTCTCCACGTCT   10677     AA       AG
                                 AGA  TGGAGAGA  TATGT
                                 |||  ||||||||  |||||
                                 TCT  ACCTCTCT  GTGCA
                                   GC       CT
GAM154  PTTG1IP  3'  GCTGCAGCTCTCTCCAGCCCT  15092    AAA      A  A    C
                                 AG   TGGAGAGA GT TGTA GC
                                 ||   |||||||| || |||| ||
                                 TC   ACCTCTCT CG ACGT CG
                                  CCG       _ _    _
GAM154  SERPINB6 3'  GCAGCCCCTCTCCTCTCT    15878     AAT     AA  A
                                 AGA   GGAGAG  GT TGT
                                 |||   ||||||  || |||
                                 TCT   CCTCTC  CG ACG
                                   CT_     CC  _
GAM154  SFN      3'  GCTACTTCTCCCCTCCTCT    74561     AAT  A      T
                                 AGA   GG GAGAAGTA GT
                                 |||   || |||||||| ||
                                 TCT   CC CTCTTCAT CG
                                   CCT  C       _
GAM154  SLC16A2  3'  ACTTCTCTCCATACTCT     21499     A_
                                 AGA  ATGGAGAGAAGT
                                 |||  ||||||||||||
                                 TCT  TACCTCTCTTCA
                                   CA
GAM154  SLC7A8   3'  ACACACCCCTCTCTCTGCTTTT 24273      AT      A__  A
                                 AGAA  GGAGAGA   GT TGT
                                 ||||  |||||||   || |||
                                 TTTT  TCTCTCT   CA ACA
                                    CG      CCC  C
GAM154  ACAS2L   3'  GCATTGCCATCTCCATTCCT   68075    A      GAAGT
                                 AG AATGGAGA     ATGT
                                 || ||||||||     ||||
                                 TC TTACCTCT     TACG
                                  C       ACCGT
GAM154  APOA5    3'  GCATACTGTGTGCTCTCCCCAT 53729    A   A   _______
            CTC                    GA ATGG GAGA     AGTATGT
                                 || |||| ||||     |||||||
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                                CT TACC CTCT     TCATACG
                                 C   C   CGTGTG
GAM154  ATP9A    3'  TATTTCTCCCCCTTCT     62051     AT  A
                                AGAA  GG GAGAAGTA
                                ||||  || ||||||||
                                TCTT  CC CTCTTTAT
                                  CC  _
GAM154  BBX      5'  GCGAGCTTCTCTCCACTTTC   39589     _       A
                                GAAA TGGAGAGAAGT TGT
                                |||| |||||||||| |||
                                CTTT ACCTCTCTTCG GCG
                                  C         A
GAM154  CLSTN3   5'  ACTTCTCTCCTTTCT      28203      T
                                AGAAA GGAGAGAAGT
                                ||||| ||||||||||
                                TCTTT CCTCTCTTCA

                                  _
GAM154  CYP2S1   3'  ACACGCCCTCTCCATTC     47611     A     AA TA
                                GAA TGGAGAG  G  TGT
                                ||| |||||||  |  |||
                                CTT ACCTCTC  C  ACA
                                  _     C_ GC
GAM154  DKFZP564F0522 3'  ACATAACATCTCTCCTTTCT   68584      T     AG_
                                AGAAA GGAGAGA   TATGT
                                ||||| |||||||   |||||
                                TCTTT CCTCTCT   ATACA
                                  _      ACA
GAM154  DKFZP761E1824 3'  GCAACTTTCTCCATT      66439         A  A
                                AATGGAGAGA GT TGT
                                |||||||||| || |||
                                TTACCTCTTT CA ACG

                                     _ _
GAM154  EPB41L1  3'  ACACCCTTCTCTCCTTTCT    70586      T       TA
                                AGAAA GGAGAGAAG  TGT
                                ||||| |||||||||  |||
                                TCTTT CCTCTCTTC  ACA
                                  _       CC
GAM154  FLJ10525 5'  ACGTTTTCTCTCCCCTTTCT   36222      T_       T
                                AGAAA  GGAGAGAAG ATGT
                                |||||  ||||||||| ||||
                                TCTTT  CCTCTCTTT TGCA
                                   CC       _
GAM154  FLJ10853 3'  GCATTGAACTCCTCTCATTTCT 36769       G   A  ___
                                AGAAATG AGAG AGT   ATGT
                                ||||||| |||| |||   ||||
                                TCTTTAC TCTC TCA   TACG
                                    _   C   AGT
GAM154  FLJ13154 3'  GCATCAGTTTTCTCCACTTCT  44798     A       GT_
                                AGAA TGGAGAGAA   ATGT
                                |||| |||||||||   ||||
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                                TCTT ACCTCTTTT   TACG
                                  C        GAC
GAM154  FLJ13848 3'  ACATCCATCTTTCTCCACTTC  45458     A       AG __
                                GAA TGGAGAGA  T  ATGT
                                ||| ||||||||  |  ||||
                                CTT ACCTCTTT  A  TACA
                                  C       CT CC
GAM154  FLJ22169 3'  GCTCACCTCTCTCCGCTTCT   44005     A       A  AT
                                AGAA TGGAGAGA GT  GT
                                |||| |||||||| ||  ||
                                TCTT GCCTCTCT CA  CG
                                  C       C  CT
GAM154  FLJ22644 3'  ACCTCTGCTCCATTTCT     47000          _   A
                                AGAAATGGAG AGA GT
                                |||||||||| ||| ||
                                TCTTTACCTC TCT CA
                                      G   C
GAM154  GOLGB1   3'  ACAGGTCTTCTCTCCAACTCT  15631     AA        TA_
                                AGA  TGGAGAGAAG   TGT
                                |||  ||||||||||   |||
                                TCT  ACCTCTCTTC   ACA
                                  CA         TGG
GAM154  HBOA     3'  ACGAACTCCTCCTCCATTTC   22963         _ A   A
                                GAAATGGAG AG AGT TGT
                                ||||||||| || ||| |||
                                CTTTACCTC TC TCA GCA
                                      C  C   A
GAM154  ING4     3'  ACACTTTTCTTCTCCATT     59702         _    TA
                                AATGGAGA GAAG  TGT
                                |||||||| ||||  |||
                                TTACCTCT CTTT  ACA
                                     T    TC
GAM154  ITGA10   5'  CATCACTCCTCCCATTCCT    59376    A    A  A  _
                                AG AATGG GAG AGT ATG
                                || ||||| ||| ||| |||
                                TC TTACC CTC TCA TAC
                                 C     _  C   C
GAM154  ITM3     3'  ACATGTCTCTCCATTCCT     48161    A        AG
                                AG AATGGAGAGA  TATGT
                                || ||||||||||  |||||
                                TC TTACCTCTCT  GTACA
                                 C         __
GAM154  KIAA0247 3'  ACATAACAATGTCGCCTCCATT 28390         A_  AG____
           TC                     GAAATGGAG  GA     TATGT
                                |||||||||  ||     |||||
                                CTTTACCTC  CT     ATACA
                                      CG  GTAACA
GAM154  KIAA0254 3'  GCTCACTTCTCTCCCACTTCT  28598     AT_        AT
                                AGAA   GGAGAGAAGT  GT
                                ||||   ||||||||||  ||
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                                TCTT  CCTCTCTTCA  CG
                                  CAC        CT
GAM154  KIAA0286 3' ACATGCTCTGTCCATTCCT   68316   A    G  A
                                AG AATGGA AGA GTATGT
                                || |||||| ||| ||||||
                                TC TTACCT TCT CGTACA
                                 C     G  _
GAM154  KIAA0431 3' CGACATGCTCCTTTCT     30891      A     A
                                GGAGAG AGTATGT CG
                                |||||| ||||||| ||
                                TCTTTC TCGTACA GC
                                   C      _
GAM154  KIAA0523 3' ACATTCATTCCTCCATTTC   67725        A  GT_
                                GAAATGGAG GAA  ATGT
                                ||||||||| |||  ||||
                                CTTTACCTC CTT  TACA
                                     _  ACT
GAM154  KIAA0748 3' ACATCTCTTCATTTCT     28931          A
                                AGAAATGGAGAGA GT
                                |||||||||||| ||
                                TCTTTACTTCTCT CA
                                       A
GAM154  KIAA1029 3' GCACACACACTCTCTCTTTCT  23475     AT     A  A  AC
                                AGAA  GGAGAGA GT TGT  GC
                                ||||  ||||||| || |||  ||
                                TCTT  TCTCTCT CA ACA  CG
                                  __      _  C  CA
GAM154  KIAA1305 3' ACCCACATTCTCTCCAACTCT  46926    AA       _  AT
                                AGA  TGGAGAGAA GT  GT
                                |||  ||||||||| ||  ||
                                TCT  ACCTCTCTT CA  CA
                                  CA       A  CC
GAM154  KIAA1317 5' ACATCTCTCCATCTTT     86028    A       A
                                AGA ATGGAGAGA GT
                                ||| ||||||||| ||
                                TTT TACCTCTCT CA
                                  C       A
GAM154  KIAA1319 3' GCATGGCTCTACCCATTTCT  40407       AG  AG
                                AGAAATGG  AGA  TATGT
                                ||||||||  |||  |||||
                                TCTTTACC  TCT  GTACG
                                     CA  CG
GAM154  KIAA1915 3' GCATTACCTTCCTCCCATTTCT 73282       _  A   T__
                                AGAAATGG AG GAAG  ATGT
                                |||||||| || ||||  ||||
                                TCTTTACC TC CTTC  TACG
                                     C  _   CAT
GAM154  LASP1    3' GCATATGTTTCCCCATCTCT  20457    A   A   A
                                AGA ATGG GAGA GTATGT
                                ||| |||| |||| ||||||
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                                TCT TACC CTTT TATACG
                                  C   C   G
GAM154  MGC13053 3' ACTCAATTCTCTCCAATTCT  51130     A       GTAT
                                AGAA TGGAGAGAA   GT
                                |||| |||||||||   ||
                                TCTT ACCTCTCTT   CA
                                  A       AACT
GAM154  MGC2477  5' ACATACACATCCCTCTCCAT  44056       AA____
                                ATGGAGAG    GTATGT
                                ||||||||    ||||||
                                TACCTCTC    CATACA
                                    CCTACA
GAM154  MGC26988 5' GCAGTTACCTTCTCTCCGTCTC 55654    A        TA___
          T                      AGA ATGGAGAGAAG    TGT
                                ||| ||||||||||    |||
                                TCT TGCCTCTCTTC    ACG
                                  C         CATTG
GAM154  MGC33182 3' GCATTTGTTTCTCCCCACATCT 75577    AA  A    T__
                                AGA  TGG GAGAAG  ATGT
                                |||  ||| ||||||  ||||
                                TCT  ACC CTCTTT  TACG
                                  AC  C    GTT
GAM154  P66      3' GCATAACCCTTCTCTCCA   40366        ___
                                TGGAGAGAAG  TATGT
                                |||||||||  |||||
                                ACCTCTCTTC  ATACG
                                    CCA
GAM154  PRDM15   3' ACATTTTCTCCTCACTTCT   61711    A  GA    T
                                AGAA TG  GAGAAG ATGT
                                |||| ||  |||||| ||||
                                TCTT AC  CTCTTT TACA
                                  C  TC    _
GAM154  PRO1580  5' ACTTCTCTTCACTTCT     37529     A
                                AGAA TGGAGAGAAGT
                                |||| ||||||||||
                                TCTT ACTTCTCTTCA
                                  C
GAM154  SEPT3    3' ACATTGCTTTCTCTCC     38881       _  _
                                GGAGAGAA GTA TGT
                                |||||||| ||| |||
                                CCTCTCTT CGT ACA
                                    T  T
GAM154  SFRS6    3' GCATGAAGACCCTCTCCCTTCT 20782     AT    AAG___
                                AGAA  GGAGAG    TATGT
                                ||||  ||||||    |||||
                                TCTT  CCTCTC    GTACG
                                  C_    CCAGAA
GAM154  SOX17    3' ACAGCTTCCTCCATTTC    42395       A   A
                                GAAATGGAG GAAGT TGT
                                ||||||||| ||||| |||
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                                CTTTACCTC CTTCG ACA
                                      _   _
GAM154  STAG2     5'  GCATCGATCTCTCCATCCCT  70566    AA       AGT
                                AG  ATGGAGAGA   ATGT
                                ||  |||||||||   ||||
                                TC  TACCTCTCT   TACG
                                 CC        AGC
GAM154  SUPT4H1   3'  GCATCTTTGCTCTCCACCTC  12062    AA     _   T
                                GA  TGGAGAG AAG ATGT
                                ||  ||||||| ||| ||||
                                CT  ACCTCTC TTT TACG
                                 CC      G   C
GAM154  ZNF333    3'  ACATCTCTCCACTTCT     50567     A      A
                                AGAA TGGAGAGA GT
                                ||||| |||||||| ||
                                TCTT ACCTCTCT CA
                                  C       A
GAM154  LOC116349 5'  GCATTTTCTCTCCTTTC     73833     T      T
                                GAAA GGAGAGAAG ATGT
                                |||| |||||||||| ||||
                                CTTT CCTCTCTTT TACG
                                  _       _
GAM154  LOC121506 3'  ACACACAGAGCTTCATTTC   74093        AGAA  A
                                GAAATGGAG    GT TGT
                                |||||||||    || |||
                                CTTTACTTC    CA ACA
                                     GAGA  C
GAM154  LOC143451 3'  ACAGCTCTTCTCTCCTTCTCT  76561    AAT      TA_
                                AGA   GGAGAGAAG   TGT
                                |||   |||||||||   |||
                                TCT   CCTCTCTTC   ACA
                                  CTT       TCG
GAM154  LOC145125 3'  ACAGCTCTTCTCTCCTTCTCT  77003    AAT      TA_
                                AGA   GGAGAGAAG   TGT
                                |||   |||||||||   |||
                                TCT   CCTCTCTTC   ACA
                                  CTT       TCG
GAM154  LOC145547 3'  ACCCACATTCTCTCCAACTCT  77262    AA       _ AT
                                AGA  TGGAGAGAA GT  GT
                                |||  ||||||||| ||  ||
                                TCT  ACCTCTCTT CA  CA
                                  CA       A  CC
GAM154  LOC145601 3'  ACATTCTCTCTCCATCTC    83360    A      A T
                                GA ATGGAGAGA G ATGT
                                || ||||||||| | ||||
                                CT TACCTCTCT C TACA
                                 C       _ T
GAM154  LOC145845 3'  ACATCTGTCTCCATTCCT    83549    A      GA  T
                                AG AATGGAGA  AG ATGT
                                || ||||||||  || ||||
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                                TC TTACCTCT  TC TACA
                                 C       G_ _
GAM154   LOC145955 5' ACAGACCTCTCTCCAGCCCT   83583    AAA      A  A
                                AG   TGGAGAGA GT TGT
                                ||   |||||||| || |||
                                TC   ACCTCTCT CA ACA
                                 CCG       C  G
GAM154   LOC148137 3' GCGTGCCTCTCCCCAGCTTCT  58433     A_   A    A
                                AGAA  TGG GAGA GTATGT
                                ||||  ||| |||| ||||||
                                TCTT  ACC CTCT CGTGCG
                                  CG   C    C
GAM154   LOC148764 5' ATTTCTCCCACTTCT       78981      A   A
                                AGAA TGG GAGAAGT
                                |||| ||| |||||||
                                TCTT ACC CTCTTTA
                                  C   _
GAM154   LOC149506 3' ACCTGCTTCCCCCCATTTTT   84443        AGA     T
                                AGAAATGG   GAAGTA GT
                                ||||||||   |||||| ||
                                TTTTTACC   CTTCGT CA
                                     CCC     C
GAM154   LOC154739 5' ACATACATTTTCTCCACTTCT  86222      A       _
                                AGAA TGGAGAGAA GTATGT
                                |||| ||||||||| ||||||
                                TCTT ACCTCTTTT CATACA
                                  C        A
GAM154   LOC158364 5' ACTTCTCTCCACCCTCT     81872     AA_
                                AGA   TGGAGAGAAGT
                                |||   ||||||||||
                                TCT   ACCTCTCTTCA
                                  CCC
GAM154   LOC169181 5' GCATTCCCTCCTCTCCAT    82734        A  T__
                                ATGGAGAG AG   ATGT
                                |||||||| ||   ||||
                                TACCTCTC TC   TACG
                                     C  CCT
GAM154   LOC170221 3' GCCTCATTTTCTTTCCAT    82578          T   TAC
                                ATGGAGAGAAG ATG   GC
                                |||||||||| |||   ||
                                TACCTTTCTTT TAC   CG
                                       _   TC_
GAM154   LOC196860 3' ACATGCTTCTCTCCACTTCT   89640      A
                                AGAA TGGAGAGAAGTATGT
                                |||| ||||||||||||||
                                TCTT ACCTCTCTTCGTACA
                                  C
GAM154   LOC200197 3' ACGCCCTTCTCTCCACTTT    88611     A        TA
                                GAA TGGAGAGAAG  TGT
                                ||| |||||||||  |||
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                                TTT ACCTCTCTTC  GCA
                                  C         CC
GAM154   LOC203276 3'  ACATATATTTTCTCCACTTCT  90470      A       _
                                AGAA TGGAGAGAA GTATGT
                                |||| ||||||||| ||||||
                                TCTT ACCTCTTTT TATACA
                                  C         A
GAM154   LOC203305 3'  ACATATATTTTCTCCACTTCT  90514      A       _
                                AGAA TGGAGAGAA GTATGT
                                |||| ||||||||| ||||||
                                TCTT ACCTCTTTT TATACA
                                  C         A
GAM154   LOC219653 3'  ACGTGTTTCCCCTCTCCTTTCT 91289       T    ___
                                AGAAA GGAGA   GAAGTATGT
                                ||||| |||||   |||||||||
                                TCTTT CCTCT   CTTTGTGCA
                                  _    CCC
GAM154   LOC221656 3'  CAAGCCCCTCTCCACTTCT    92227      A      AA  A
                                AGAA TGGAGAG  GT TG
                                |||| |||||||  || ||
                                TCTT ACCTCTC  CG AC
                                  C      CC  A
GAM154   LOC221882 5'  ACATCCTCTCCTCTCTCCTTCT 92499      AAT      ____  T
           CT                     AGA   GGAGAGA    AG ATGT
                                |||   |||||||    || ||||
                                TCT   CCTCTCT    TC TACA
                                  CTT      CCTC  C
GAM154   LOC222899 5'  ACATCCTGCTTCTCCATCTC   94364    A       A_  T
                                GA ATGGAGAG  AG ATGT
                                || ||||||||  || ||||
                                CT TACCTCTT  TC TACA
                                 C       CG  C
GAM154   LOC254243 3'  ACATATATTTTCTCCACTTCT  97399      A       _
                                AGAA TGGAGAGAA GTATGT
                                |||| ||||||||| ||||||
                                TCTT ACCTCTTTT TATACA
                                  C         A
GAM154   LOC254440 3'  ACAGCTCTTCTCTCCTTCTCT  97063     AAT       TA_
                                AGA   GGAGAGAAG   TGT
                                |||   |||||||||   |||
                                TCT   CCTCTCTTC   ACA
                                  CTT        TCG
GAM154   LOC51125  3'  ACATACCATTGGTTCTCTTCAT 32246    A         _______
           TCCT                    AG AATGGAGAGAA     GTATGT
                                || ||||||||||     ||||||
                                TC TTACTTCTCTT     CATACA
                                 C          GGTTAC
GAM154   LOC51195  3'  GCGGGGTGCTTTCTCCA     32946        A    GTA
                                TGGAGAGA GTAT   CGC
                                |||||||| ||||   |||
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                                ACCTCTTT CGTG   GCG
                                     _   GG_
GAM154  LOC90038  3'  ACATATATTTTCTCCACTTCT  61143      A       _
                                AGAA TGGAGAGAA GTATGT
                                |||| ||||||||| ||||||
                                TCTT ACCTCTTTT TATACA
                                  C        A
GAM155  ADH5      3'  AGCCTCATACTTGCTCATTCT  5416         ___ A    A
                                AGAATGA   AG ATGAG CT
                                |||||||   || ||||| ||
                                TCTTACT   TC TACTC GA
                                    CGT  A    C
GAM155  ALEX3     3'  GAGTAAGCTCCCTTCTGTCA  33499         TGA  AATGAG
                                TGACAGAA   AG     ACTC
                                ||||||||   ||     ||||
                                ACTGTCTT   TC     TGAG
                                     CCC  GAA___
GAM155  APPBP2    3'  GTTCTTCATTGTGTCA      21079       G
                                TGACA AATGAAGAAT
                                ||||| ||||||||||
                                ACTGT TTACTTCTTG
                                   G
GAM155  ARSB      5'  GTTCCTCATTCTATCA      3501      C      A
                                TGA AGAATGA GAAT
                                ||| ||||||| ||||
                                ACT TCTTACT CTTG
                                  A      C
GAM155  BCL2L2    3'  GAGACTCTTCTGTCA       14468        TGAAGAAT   A
                                TGACAGAA       GAG CTC
                                ||||||||       ||| |||
                                ACTGTCTT       CTC GAG
                                     _________  A
GAM155  CASP10    3'  AGTCTCATTCTGTCA       52097        ATGAAGA
                                TGACAGA      ATGAGACT
                                |||||||      ||||||||
                                ACTGTCT      TACTCTGA
                                     ________
GAM155  CASP10    3'  AGTCTCATTCTGTCA       52115        ATGAAGA
                                TGACAGA      ATGAGACT
                                |||||||      ||||||||
                                ACTGTCT      TACTCTGA
                                     ________
GAM155  CHRNA4    3'  GAGTCTCATTCCTCTGTC    5616         ATGAA
                                GACAGA    GAATGAGACTC
                                ||||||    ||||||||||
                                CTGTCT    CTTACTCTGAG
                                   C_____
GAM155  COL4A1    3'  TATTCCTCATTCTGCA      8465     A       A
                                TG CAGAATGA GAATG
                                || |||||||| |||||
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                                AC GTCTTACT CTTAT
                                 _       C
GAM155  CRIM1    3'  TCTCATTCTACCTGCA      33179    A   AATGA
                                TG CAG     AGAATGAGA
                                || |||     |||||||||
                                AC GTC     TCTTACTCT
                                 _   CA___
GAM155  EIF4EBP2 3'  AGCCTCATTCTTTTCTGT     14587       AT        A
                                ACAGA  GAAGAATGAG CT
                                |||||  |||||||||| ||
                                TGTCT  TTTCTTACTC GA
                                   __         C
GAM155  GABRP    3'  GAGTCGCTGTCATTCTGTCA   26400           AGAATGA
                                TGACAGAATGA      GACTC
                                ||||||||||       |||||
                                ACTGTCTTACT      CTGAG
                                       GTCG___
GAM155  GAS1     3'  AGTCCCACTTACCGATTCATTC 8991      C       _____  A  A
           TTTCA                    TGA AGAATGAA     GA TG GACT
                                ||| ||||||||     || || ||||
                                ACT TCTTACTT     TT AC CTGA
                                  T       AGCCA  C  C
GAM155  GPR81    3'  GAGTCTCACTCTGTGTC     50758      GAATGA   A
                                GACA     AGA TGAGACTC
                                ||||     ||| ||||||||
                                CTGT     TCT ACTCTGAG
                                  G_____   C
GAM155  GTF2H1   3'  CATCCTTCATTCTTCA      18006     C        A
                                TGA AGAATGAAG ATG
                                ||| ||||||||| |||
                                ACT TCTTACTTC TAC
                                  _       C
GAM155  HAS2     3'  GTTTATTTTCATTCTGCCA    18035    A         ATG
                                TG CAGAATGAAGA   AGAC
                                || ||||||||||   ||||
                                AC GTCTTACTTTT   TTTG
                                 C         A__
GAM155  HSPA1L   3'  GAGTCTCATGCACCACCTATCA 92020     C  AA  AAGA
                                TGA AG  TG    ATGAGACTC
                                ||| ||  ||    |||||||||
                                ACT TC  AC    TACTCTGAG
                                  A  C_  CACG
GAM155  HSPA1L   3'  GAGTCTCATGCACCACCTATCA 97767     C  AA  AAGA
                                TGA AG  TG    ATGAGACTC
                                ||| ||  ||    |||||||||
                                ACT TC  AC    TACTCTGAG
                                  A  C_  CACG
GAM155  IGFBP4   3'  TCTCATTCCCAGAGTCA     7765       AGAA  AA
                                TGAC    TG  GAATGAGA
                                ||||    ||  ||||||||
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                                ACTG    AC  CTTACTCT
                                  AG__  C_
GAM155  ITGA9    3'  TCTTCTTCATTCTATCA     9383      C         T
                                TGA AGAATGAAGAA GA
                                ||| |||||||||| ||
                                ACT TCTTACTTCTT CT
                                  A         _
GAM155  KIF3B    3'  TTTACTCTTCATTTGTCA     16617        A     A
                                TGACAGA TGAAGA TGAG
                                ||||||| |||||| ||||
                                ACTGTTT ACTTCT ATTT
                                     _     C
GAM155  MLF2     3'  ATTTTTCATTCTGCCA      18372     A
                                TG CAGAATGAAGAAT
                                || ||||||||||||
                                AC GTCTTACTTTTTA
                                 C
GAM155  MOG      3'  TTTCCCTTCTTCTGTCA     10108         T    AAT
                                TGACAGAA GAAG   GAGA
                                |||||||| ||||   ||||
                                ACTGTCTT CTTC   CTTT
                                     _    C__
GAM155  MYO1F    3'  CTTTGCTCATTCTGTCA     82425           A AAT
                                TGACAGAATGA G   GAG
                                |||||||||| |   |||
                                ACTGTCTTACT C   TTC
                                       _ GT_
GAM155  NAGA     3'  TCACCCTTCATTCTTTCA     4237      C        AA
                                TGA AGAATGAAG  TGA
                                ||| |||||||||  |||
                                ACT TCTTACTTC  ACT
                                  T        CC
GAM155  NAPB     3'  GAATCTCATTCCTCATATTTCA 70182     C  A    A       C
                                TGA AG ATGA GAATGAGA TC
                                ||| || |||| |||||||| ||
                                ACT TT TACT CTTACTCT AG
                                  _ A    C       A
GAM155  OSR1     3'  AGTCTTTATGTTCTTCCTGCCA 17565    A   AAT      ___
                                TG CAG   GAAGAAT   GAGACT
                                || |||   |||||||   ||||||
                                AC GTC   CTTCTTG   TTCTGA
                                 C   ___       TAT
GAM155  PLCD1    3'  GAGCTGTCCTTCATTCCGTTA  20630      A       A  G  A
                                TGAC GAATGAAG AT AG CTC
                                |||| |||||||| || || |||
                                ATTG CTTACTTC TG TC GAG
                                  C       C _ _
GAM155  POU2AF1  3'  GAGTCTCACTCCATT       20651      AA  A
                                AATG  GA TGAGACTC
                                ||||  || ||||||||
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                                TTAC  CT ACTCTGAG
                                  __ C
GAM155  REV3L    3'  ATTCCTCATTCTGTCA      11295          A
                                TGACAGAATGA GAAT
                                |||||||||| ||||
                                ACTGTCTTACT CTTA
                                       C
GAM155  SACM1L   3'  TGTTTTTCACTCTGTCA     25827        A
                                TGACAGA TGAAGAATG
                                ||||||| |||||||||
                                ACTGTCT ACTTTTTGT
                                    C
GAM155  SMARCD1  3'  GAGCCTCACATTCTTCTTC   57434     T    __   A
                                GAA GAAGAA  TGAG CTC
                                ||| ||||||  |||| |||
                                CTT CTTCTT  ACTC GAG
                                  _     AC   C
GAM155  SMARCD1  3'  GAGCCTCACATTCTTCTTC   11816     T    __   A
                                GAA GAAGAA  TGAG CTC
                                ||| ||||||  |||| |||
                                CTT CTTCTT  ACTC GAG
                                  _     AC   C
GAM155  WHSC1    3'  TTCGACTTCATTTTGCCA    55856    A       AA
                                TG CAGAATGAAG  TGAG
                                || ||||||||||  ||||
                                AC GTTTTACTTC  GCTT
                                 C        A_
GAM155  WHSC1    3'  TTCGACTTCATTTTGCCA    55839    A       AA
                                TG CAGAATGAAG  TGAG
                                || ||||||||||  ||||
                                AC GTTTTACTTC  GCTT
                                 C        A_
GAM155  WHSC1    3'  TTCGACTTCATTTTGCCA    29921    A       AA
                                TG CAGAATGAAG  TGAG
                                || ||||||||||  ||||
                                AC GTTTTACTTC  GCTT
                                 C        A_
GAM155  ZFP36L1  3'  AGTCCCATATTTTGTCA     17003        GAAGA  A
                                TGACAGAAT    ATG GACT
                                |||||||||    ||| ||||
                                ACTGTTTTA    TAC CTGA
                                      _____  C
GAM155  ZNF8     5'  CATTCTTCCTCTGCCA      64069    A   AT
                                TG CAGA  GAAGAATG
                                || ||||  ||||||||
                                AC GTCT  CTTCTTAC
                                 C   C_
GAM155  ARHF     3'  GAGTCTCATTCTGTCACTC   38742    A  _
                                GA TGA AGAATGAGACTC
                                || ||| ||||||||||||
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                                CT ACT TCTTACTCTGAG
                                 C   G
GAM155  CALN1    3'  AGCTCACCCCTCATTCTGTC  48853          AGAA    A
                                GACAGAATGA    TGAG CT
                                ||||||||||    |||| ||
                                CTGTCTTACT    ACTC GA
                                      CCCC    _
GAM155  CHL1     3'  TATTCTCCTTCTGTCA      21750         T  A
                                TGACAGAA GA GAATG
                                |||||||| || |||||
                                ACTGTCTT CT CTTAT
                                     C  _
GAM155  CPR2     5'  AGTCTTGTCTCTCTGCCA    48090    A    AT  A A TG
                                TG CAGA  GA G A  AGACT
                                || ||||  || | |  |||||
                                AC GTCT  CT C T  TCTGA
                                 C    __  _ _ GT
GAM155  FLJ20298 5'  GAGTCCCTGGGCTCATTCTGCA 34902    A       AGAATGA
                                TG CAGAATGA      GACTC
                                || ||||||||      |||||
                                AC GTCTTACT      CTGAG
                                 _       CGGGTCC
GAM155  FLJ20449 3'  GAGTTTCCTTCTTCATTC    35187          T
                                GAATGAAGAA GAGACTC
                                |||||||||| |||||||
                                CTTACTTCTT CTTTGAG
                                      C
GAM155  FLJ22167 5'  GAGTCTCACTCTTCACTC    44574    A     A
                                GA TGAAGA TGAGACTC
                                || |||||| ||||||||
                                CT ACTTCT ACTCTGAG
                                 C     C
GAM155  FLJ22624 5'  CTCAGTTCTTCATCCCTCA    45652     CA  A      _
                                TGA  GA TGAAGAA TGAG
                                |||  || ||||||| ||||
                                ACT  CT ACTTCTT ACTC
                                  CC  _      G
GAM155  GABARAPL3 3'  GTGTCAGTTCTGTCA       50802         GAAGAA   G
                                TGACAGAAT      TGA AC
                                |||||||||      ||| ||
                                ACTGTCTTG      ACT TG
                                      _______  G
GAM155  KIAA0010 3'  AGCTCCTTCTTTCATTCTGCCA 27893    A       _  T   A
                                TG CAGAATGAA GAA GAG CT
                                || ||||||||| ||| ||| ||
                                AC GTCTTACTT CTT CTC GA
                                 C        T   C   _
GAM155  KIAA0220 5'  GAGCCCCTGTTCTCATTCTGCA 95082    A       A    G  A__
                                TG CAGAATGA GAAT AG   CTC
                                || |||||||| |||| ||   |||
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                                AC GTCTTACT CTTG TC   GAG
                                 _       _   _ CCC
GAM155  KIAA0564  3'  AGCCTCATTCTCTTTTCTTTCA 66206     C    TGA       A
                                TGA AGAA   AGAATGAG CT
                                ||| ||||   |||||||| ||
                                ACT TCTT   TCTTACTC GA
                                  T    TTC       C
GAM155  KIAA0935  3'  CTCTCCTCTTCTGTCA      72722         T  A  AT
                                TGACAGAA GA GA  GAG
                                |||||||| || ||  |||
                                ACTGTCTT CT CT  CTC
                                     _ C  __
GAM155  PDZD2     5'  GAGTCCAGGCCACTTCTGTCA  80871         _  AAGAA  A
                                TGACAGAA TG     TG GACTC
                                |||||||| ||     || |||||
                                ACTGTCTT AC     AC CTGAG
                                     C  CGG__  _
GAM155  PELI2     3'  AGTCTAGTCATTCTGCA     41178    A      AGAATG
                                TG CAGAATGA     AGACT
                                || |||||||      |||||
                                AC GTCTTACT     TCTGA
                                 _       GA____
GAM155  PPP1R16B  3'  GAGTCTCATTACCACTGCCA  61387    A   AA  AAG
                                TG CAG  TG   AATGAGACTC
                                || |||  ||   ||||||||||
                                AC GTC  AC   TTACTCTGAG
                                 C   __  CA_
GAM155  SCAND2    3'  GAGTCTCATTCTATCA      41888    _
                                TGA AGAATGAGACTC
                                ||| ||||||||||||
                                ACT TCTTACTCTGAG
                                  A
GAM155  SCYA16    3'  GGGTCTTACTCTGTCA      15964        ATGAAGAA
                                TGACAGA       TGAGACTC
                                |||||||       ||||||||
                                ACTGTCT       ATTCTGGG
                                    C________
GAM155  SDCCAG28  5'  CATTTCCTCATTCTGCA     21822    A      A_
                                TG CAGAATGA  GAATG
                                || ||||||||  |||||
                                AC GTCTTACT  TTTAC
                                 _       CC
GAM155  SLC26A9   3'  AGCCTCATTCTCCTTTTGTT   53616       T  A     A
                                GACAGAA GA GAATGAG CT
                                ||||||| || ||||||| ||
                                TTGTTTT CT CTTACTC GA
                                    C _      C
GAM155  SLC26A9   3'  AGCCTCATTCTCCTTTTGTT   56177       T  A     A
                                GACAGAA GA GAATGAG CT
                                ||||||| || ||||||| ||
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                                TTGTTTT CT CTTACTC GA
                                    C _      C
GAM155  SUCLA2   3'  AGTCTTCATGATTCTGTCA   13892         GAAGA   _
                                TGACAGAAT    ATGA GACT
                                |||||||||    |||| ||||
                                ACTGTCTTA    TACT CTGA
                                     G____   T
GAM155  SV2B     3'  GTTTACTCTCCTTCTGTCA   29299         T  A  ATG
                                TGACAGAA GA GA   AGAC
                                |||||||| || ||   ||||
                                ACTGTCTT CT CT   TTTG
                                    C  _  CA_
GAM155  WNT16    3'  GAATCTCATTTATTCTCTCA  32228     C      AGA     C
                                TGA AGAATGA   ATGAGA TC
                                ||| |||||||   |||||| ||
                                ACT TCTTATT   TACTCT AG
                                  C      ___      A
GAM155  WNT16    3'  GAATCTCATTTATTCTCTCA  54073     C      AGA     C
                                TGA AGAATGA   ATGAGA TC
                                ||| |||||||   |||||| ||
                                ACT TCTTATT   TACTCT AG
                                  C      ___      A
GAM155  ZNF333   3'  TCTTTGTCATTCTGTCA     50571           AGAAT
                                TGACAGAATGA    GAGA
                                ||||||||||    ||||
                                ACTGTCTTACT    TTCT
                                     GT___
GAM155  LOC115286 3'  AGCCTCACCTCCACTTCTGTCA 73371         _  A  AA    A
                                TGACAGAA TG AG  TGAG CT
                                |||||||| || ||  |||| ||
                                ACTGTCTT AC TC  ACTC GA
                                    C  C  C_   C
GAM155  LOC126031 5'  AGCCTCATCGTTCTGCA     74432     A       AGAA    A
                                TG CAGAATGA    TGAG CT
                                || ||||||||    |||| ||
                                AC GTCTTGCT    ACTC GA
                                 _      _____    C
GAM155  LOC138654 5'  GAGCCTCATTCTGACTACATCA 75949     CAGAATGA       A
                                TGA       AGAATGAG CTC
                                |||       |||||||| |||
                                ACT       TCTTACTC GAG
                                  ACATCAG_       C
GAM155  LOC144920 3'  TCATTCTTCCTCTGCCA     83192     A    AT
                                TG CAGA  GAAGAATGA
                                || ||||  |||||||||
                                AC GTCT  CTTCTTACT
                                 C    C_
GAM155  LOC145739 3'  TCTCAATTTCATTCTATC     77444     C       AA
                                GA AGAATGAAG  TGAGA
                                || |||||||||  |||||
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                                CT TCTTACTTT  ACTCT
                                 A        A_
GAM155  LOC146136 5'  GAGCCCCTGTTCTCATTCTGCA 72943    A       A    G  A__
                                TG CAGAATGA GAAT AG   CTC
                                || |||||||| |||| ||   |||
                                AC GTCTTACT CTTG TC   GAG
                                 _       _    _ CCC
GAM155  LOC146181 3'  GAGCCCCTGTTCTCATTCTGCA 68592    A       A    G  A__
                                TG CAGAATGA GAAT AG   CTC
                                || |||||||| |||| ||   |||
                                AC GTCTTACT CTTG TC   GAG
                                 _       _    _ CCC
GAM155  LOC146346 5'  GAGTCTCACTCCGTT       77842      AA  A
                                AATG  GA TGAGACTC
                                ||||  || ||||||||
                                TTGC  CT ACTCTGAG
                                  __  C
GAM155  LOC147741 3'  GAGTCTCACTCTGCACTC     78473    A  A   A
                                GA TG AGA TGAGACTC
                                || || ||| ||||||||
                                CT AC TCT ACTCTGAG
                                 C  G   C
GAM155  LOC148223 3'  GAGTCTCATAGCCACCCTGCCA 78740    A   AA  AAGA
                                TG CAG  TG    ATGAGACTC
                                || |||  ||   |||||||||
                                AC GTC  AC    TACTCTGAG
                                 C   CC  CGA_
GAM155  LOC152220 3'  GAGTCTCACTCTGTCACTC    85582    A  _  A
                                GA TGA AGA TGAGACTC
                                || ||| ||| ||||||||
                                CT ACT TCT ACTCTGAG
                                 C   G   C
GAM155  LOC157867 5'  AGTCTTTTTCCACTCTGTTA   86555       A  AA   T
                                TGACAGA TG  GAA GAGACT
                                ||||||| ||  ||| ||||||
                                ATTGTCT AC  CTT TTCTGA
                                     C  __   T
GAM155  LOC196955 3'  CATCCTCCATTCTGTC       77369         A  A
                                GACAGAATG AG ATG
                                ||||||||| || |||
                                CTGTCTTAC TC TAC
                                      C  C
GAM155  LOC197419 3'  GTCCCATTTCTGTTA        89755        TGAAGA   A
                                TGACAGAA      ATG GAC
                                ||||||||      ||| |||
                                ATTGTCTT      TAC CTG
                                     _______  C
GAM155  LOC200339 3'  AGTCTCACTCTTGTCG       90031       GAATGA   A
                                TGACA      AGA TGAGACT
                                |||||      ||| |||||||
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                                GCTGT     TCT ACTCTGA
                                  _______  C
GAM155  LOC202908 5'  GGGTCTCACCCTGTCA     89245       AATGAAGAA
                                TGACAG       TGAGACTC
                                ||||||       ||||||||
                                ACTGTC       ACTCTGGG
                                   CC_______
GAM155  LOC253666 5'  GAGCCCCTGTTCTCATTCTGCA 95062    A      A   G  A__
                                TG CAGAATGA GAAT AG   CTC
                                || |||||||| |||| ||   |||
                                AC GTCTTACT CTTG TC   GAG
                                 _      _   _ CCC
GAM155  LOC255465 3'  AGTCTCATCTTGAATTC     97278      G_   A
                                GAAT  AAGA TGAGACT
                                ||||  |||| |||||||
                                CTTA  TTCT ACTCTGA
                                  AG   _
GAM155  LOC256476 5'  AGGATCTCATTCTGTCA     96817          AGAAT  GA
                                TGACAGAATGA    GA  CT
                                ||||||||||    ||  ||
                                ACTGTCTTACT    CT  GA
                                      _____ AG
GAM155  LOC257618 3'  GAGTCTCATGCACCACCTATCA 97854     C  AA  AAGA
                                TGA AG  TG    ATGAGACTC
                                ||| ||  ||    |||||||||
                                ACT TC  AC    TACTCTGAG
                                 A  C_  CACG
GAM155  LOC90777  3'  GAGTCTCAGATATTCTGTTA   63968         AAGAA
                                TGACAGAATG    TGAGACTC
                                ||||||||||    ||||||||
                                ATTGTCTTAT    ACTCTGAG
                                      AG___
GAM156  CNGA1     3'  CAACTGATAATGTGCAAA    59507          GC   A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                      A_   _
GAM156  ESRRG     3'  TGGCAGTCTTATGTGCAAA   66396        TAGCT
                                TTTGCACAT    AGATTGCCA
                                |||||||||    |||||||||
                                AAACGTGTA    TCTGACGGT
                                     T_____
GAM156  KCNJ3     3'  GCAATAATGTGCAAA       9525           GCTAGA
                                TTTGCACATTA     TTGC
                                ||||||||||     ||||
                                AAACGTGTAAT     AACG
                                       _______
GAM156  SDC2      3'  GCAAATTAATGTGTAAA     67132           CTAGA
                                TTTGCACATTAG    TTGC
                                ||||||||||||    ||||
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                                AAATGTGTAATT    AACG
                                      A____
GAM156  USP9X    3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
              A                  TTTGCACATTAGC     GCCAT
                                 ||||||||||||     |||||
                                 AAATGTGTAATCG     CGGTA
                                       TAGTC_
GAM156  AMOTL1   3'  GGCAAGTAATGTGCAAA    73650         G  AGAT
                                 TTTGCACATTA CT    TGCC
                                 |||||||||| ||    ||||
                                 AAACGTGTAAT GA    ACGG
                                      _ ____
GAM156  BCAR3    3'  AGTAATAATGTGCAAA     13098         __
                                 TTTGCACATTA  GCT
                                 ||||||||||  |||
                                 AAACGTGTAAT  TGA
                                       AA
GAM156  DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930        AGCTA    C
                                 TTTGCACATT    GATTG CA
                                 |||||||||     ||||| ||
                                 AGACGTGTAA    TTAAC GT
                                      A____    A
GAM156  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                 TTTGCACATTAG  AGA TG CAT
                                 ||||||||||||  ||| || |||
                                 AGACGTGTAATC  TTT AC GTA
                                       __  T  A
GAM156  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
              AA                   TTTGCACATTAGCTAGATTGCCAT
                                   ||||||||||||||||||||||||
                                   AAACGTGTAATCGATCTAACGGTA

GAM157  ABCC3    3'  TACCGGCCGGGCCTAGACCTGG 39161          AA_  _ A_
              TG                   CACCAGGTCTA   CTG C  GTA
                                   ||||||||||   ||| |  |||
                                   GTGGTCCAGAT   GGC G  CAT
                                         CCG   C GC
GAM157  ABCC3    3'  TACCGGCCGGGCCTAGACCTGG 39142          AA_  _ A_
              TG                   CACCAGGTCTA   CTG C  GTA
                                   ||||||||||   ||| |  |||
                                   GTGGTCCAGAT   GGC G  CAT
                                         CCG   C GC
GAM157  ANGPT1   3'  CAGTTTCAAACTTGGTGA    6702         CT_
                                   TCACCAGGT   AAACTG
                                   |||||||||   ||||||
                                   AGTGGTTCA   TTTGAC
                                         AAC
GAM157  BLNK     3'  TATTGCCTGACCTGATGA    25257     C     TAAACT
                                   TCA CAGGTC     GCAGTA
                                   ||| ||||||     ||||||
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                                AGT GTCCAG     CGTTAT
                                  A     TC____
GAM157  CELSR1   3'  CTGTCAGACCTGGTGA      26483          AAACT
                                TCACCAGGTCT    GCAG
                                ||||||||||    ||||
                                AGTGGTCCAGA    TGTC
                                      C____
GAM157  DGCR2    3'  TACTGCAGCTCAGTGCCCAGTG 17630     CA  _  AAA
                                CAC  GGT CT   CTGCAGTA
                                |||  ||| ||   ||||||||
                                GTG  CCG GA   GACGTCAT
                                  AC   T  CTC
GAM157  FGF2     3'  ACTGCAGTCCAGCCTAGG    8865     _   T  AA
                                CC AGG CT  ACTGCAGT
                                || ||| ||  ||||||||
                                GG TCC GA  TGACGTCA
                                 A  _  CC
GAM157  GRIN2B   3'  TACTGGGGGCAACCCTGGTGA  5906         TCTAAA  G
                                TCACCAGG     CT CAGTA
                                ||||||||     || |||||
                                AGTGGTCC     GG GTCAT
                                     CAACG_  G
GAM157  GTF2H1   3'  TTACTGCAGTTGCTCAGG    18009    A_  CTA
                                CC  GGT   AACTGCAGTAA
                                ||  |||   ||||||||||
                                GG  TCG   TTGACGTCATT
                                 AC  ____
GAM157  HOXD4    3'  ACTGCAGTCCCTAGGCT     27518       A__
                                GGTCTA   ACTGCAGT
                                ||||||   ||||||||
                                TCGGAT   TGACGTCA
                                   CCC
GAM157  IFNAR1   3'  ACTGCACTCCAGCCTGGTGA   5280          CTAAAC
                                TCACCAGGT     TGCAGT
                                |||||||||     ||||||
                                AGTGGTCCG     ACGTCA
                                      ACCTC_
GAM157  IFNGR2   5'  ACTGCACTCCAGCCTGGTGA   18648         CTAAAC
                                TCACCAGGT     TGCAGT
                                |||||||||     ||||||
                                AGTGGTCCG     ACGTCA
                                      ACCTC_
GAM157  KPNB1    5'  TACCCAGACAGAGCCGGTGA   9626       A  _   AAA   CA
                                TCACC GG TCT   CTG  GTA
                                ||||| || |||   |||  |||
                                AGTGG CC AGA   GAC  CAT
                                   _  G   CA_   C_
GAM157  LPHH1    3'  TACTGCAGCAGTCTGTGA    24539      C   T  AAA
                                TCAC AGG CT   CTGCAGTA
                                |||| ||| ||   ||||||||
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                                AGTG TCT GA   GACGTCAT
                                  _  _ C__
GAM157  MAPT     3'  TTGCAGACCTGGGA       33702    A      AAACT
                                TC CCAGGTCT    GCAG
                                || ||||||||    ||||
                                AG GGTCCAGA    CGTT
                                _      _____
GAM157  MAPT     3'  TTGCAGACCTGGGA       33693    A      AAACT
                                TC CCAGGTCT    GCAG
                                || ||||||||    ||||
                                AG GGTCCAGA    CGTT
                                _      _____
GAM157  MAPT     3'  TTGCAGACCTGGGA       33712    A      AAACT
                                TC CCAGGTCT    GCAG
                                || ||||||||    ||||
                                AG GGTCCAGA    CGTT
                                _      _____
GAM157  MAPT     3'  TTGCAGACCTGGGA       19782    A      AAACT
                                TC CCAGGTCT    GCAG
                                || ||||||||    ||||
                                AG GGTCCAGA    CGTT
                                _      _____
GAM157  MSL3L1   3'  ACTGCAGTCGAGCCTGG     54360      T  AA
                                CCAGG CT  ACTGCAGT
                                ||||| ||  ||||||||
                                GGTCC GA  TGACGTCA
                                  _ GC
GAM157  MYO1E    3'  TTATTGTATTTAAACCTGGTGA 17192          C   C
                                TCACCAGGT TAAA TGCAGTAA
                                ||||||||| |||| ||||||||
                                AGTGGTCCA ATTT ATGTTATT
                                     A   _
GAM157  NR3C1    3'  TACTGCAGCTTTACAT      3925     C   _
                                GT TAAA CTGCAGTA
                                || |||| ||||||||
                                TA ATTT GACGTCAT
                                 C   C
GAM157  PXN      3'  TGCCCTAGGCCTGGCGA     11164    A       AACT
                                TC CCAGGTCTA    GCA
                                || |||||||||    |||
                                AG GGTCCGGAT    CGT
                                 C       CC__
GAM157  RGS6     3'  ACCGCAGTCCAGGGCCTGG   15026        AA_    A
                                CCAGGTCT   ACTGC GT
                                ||||||||   ||||| ||
                                GGTCCGGG   TGACG CA
                                     ACC    C
GAM157  UBE2G2   3'  TTACTGCAGTTTTAC      64865    CT
                                GT  AAACTGCAGTAA
                                ||  ||||||||||||
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                                CA  TTTGACGTCATT
                                 T_
GAM157  UBE3A   3'  TTACTGTAGATCAACCTGATGA 55583     C    CTAAA
                                TCA CAGGT    CTGCAGTAA
                                ||| |||||    |||||||||
                                AGT GTCCA    GATGTCATT
                                  A    ACTA_
GAM157  UBE3A   3'  TTACTGTAGATCAACCTGATGA 4871      C    CTAAA
                                TCA CAGGT    CTGCAGTAA
                                ||| |||||    |||||||||
                                AGT GTCCA    GATGTCATT
                                  A    ACTA_
GAM157  UBE3A   3'  TTACTGTAGATCAACCTGATGA 55596     C    CTAAA
                                TCA CAGGT    CTGCAGTAA
                                ||| |||||    |||||||||
                                AGT GTCCA    GATGTCATT
                                  A    ACTA_
GAM157  WNT5A   3'  ACTGCAGTCCAGTTGGGA    12660    A   GT  AA
                                TC CCAG  CT  ACTGCAGT
                                || ||||  ||  ||||||||
                                AG GGTT  GA  TGACGTCA
                                 _   __  CC
GAM157  ZNF215  5'  TTACTGCAATCTAGTAAGGCGG 25120    A  AGGT   AAC
                                TC CC    CTA   TGCAGTAA
                                || ||    |||   ||||||||
                                GG GG    GAT   ACGTCATT
                                 C  AAT_  CTA
GAM157  AAMP    3'  TTGCCCAGACCTGGTGG     6561          AAACT
                                TCACCAGGTCT    GCAG
                                ||||||||||    ||||
                                GGTGGTCCAGA    CGTT
                                      CC___
GAM157  ADMP    5'  TACTGCAGCTTGAAGG      58869    AGG  T  A
                                CC   TC AA CTGCAGTA
                                ||   || || ||||||||
                                GG   AG TT GACGTCAT
                                 A__  _  C
GAM157  AKR1D1  3'  ACTGCAGTCCGGCCTGGGTGA  19971      _    TAA
                                TCACC AGGTC   ACTGCAGT
                                ||||| |||||   ||||||||
                                AGTGG TCCGG   TGACGTCA
                                   G    CC_
GAM157  AP1GBP1 3'  ACTGCAGTGTGCAGTGA     54514     CAG  CTAA
                                TCAC   GT    ACTGCAGT
                                ||||   ||    ||||||||
                                AGTG   CG    TGACGTCA
                                  A__  TG__
GAM157  AP1GBP1 3'  ACTGCAGTGTGCAGTGA     23388     CAG  CTAA
                                TCAC   GT    ACTGCAGT
                                ||||   ||    ||||||||
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                                AGTG  CG   TGACGTCA
                                  A__ TG__
GAM157  C20orf121 5'  ACTGACAGAAGACCTGGT   44275        AAA  _
                                ACCAGGTCT  CTG CAGT
                                |||||||||  ||| ||||
                                TGGTCCAGA  GAC GTCA
                                     A__  A
GAM157  CPR2    3'  ACTGCAGTCCAGCCTGG    48087      T  AA
                                CCAGG CT  ACTGCAGT
                                ||||| ||  ||||||||
                                GGTCC GA  TGACGTCA
                                   _ CC
GAM157  DIS3    3'  ACTGCAGTTCAGCCTGGATGA  30225    _    T  A
                                TCA CCAGG CT AACTGCAGT
                                ||| ||||| || |||||||||
                                AGT GGTCC GA TTGACGTCA
                                  A   _ C
GAM157  DNAJB5  3'  ACTGCAGTGGCTGGAGA    24352    A   G  TAA
                                TC CCAG TC  ACTGCAGT
                                || |||| ||  ||||||||
                                AG GGTC GG  TGACGTCA
                                 A  _ ___
GAM157  ELF4    5'  TTACTGCAGCTCAGGGGGT   7440     AGG  AAA
                                ACC  TCT  CTGCAGTAA
                                |||  |||  |||||||||
                                TGG  GGA  GACGTCATT
                                  G__  CTC
GAM157  FIGN    5'  TGGTCTCGACCTGGTGA    95646        TAA
                                TCACCAGGTC  ACTG
                                ||||||||||  ||||
                                AGTGGTCCAG  TGGT
                                      CTC
GAM157  FLJ10597 3'  ACTGCATCACACAGACTGGTGA 36313       G  AAAC__
                                TCACCAG TCT    TGCAGT
                                ||||||| |||    ||||||
                                AGTGGTC AGA    ACGTCA
                                    _  CACACT
GAM157  FLJ12750 3'  ACTGCAGCCCTGGTGA    45120       TCTAAA
                                TCACCAGG    CTGCAGT
                                ||||||||    |||||||
                                AGTGGTCC    GACGTCA
                                    C_____
GAM157  FLJ14117 3'  ACTGCACTCCAGCCTGGTGA  42897       CTAAAC
                                TCACCAGGT    TGCAGT
                                |||||||||    ||||||
                                AGTGGTCCG    ACGTCA
                                     ACCTC_
GAM157  FLJ14457 3'  TACTAGCTGGAAACTCTGGTGA 51388        ___   AACT  _
                                TCACCAGG  TCTA   GC AGTA
                                ||||||||  ||||   || ||||
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                                AGTGGTCT   AGGT    CG TCAT
                                     CAA    ____  A
GAM157   FLJ20340  3'  ACTGTACTCCAGCCTGGTGA   34971          CTAAAC
                                TCACCAGGT     TGCAGT
                                |||||||||     ||||||
                                AGTGGTCCG     ATGTCA
                                     ACCTC_
GAM157   FLJ20825  3'  ACTGCAGTCCAGCCTGG     35692       T  AA
                                CCAGG CT  ACTGCAGT
                                ||||| ||  ||||||||
                                GGTCC GA  TGACGTCA
                                   _  CC
GAM157   H-L(3)MBT 3'  TTACTGCAAGGATCCT      31310     _   AAAC
                                AGG TCT    TGCAGTAA
                                ||| |||    ||||||||
                                TCC AGG    ACGTCATT
                                  T   A___
GAM157   HEYL     3'  ACCACAGCCAAGGCCTGGAGA  27388    A       AAA   CA
                                TC CCAGGTCT   CTG  GT
                                || ||||||||   |||  ||
                                AG GGTCCGGA   GAC  CA
                                 A       ACC   AC
GAM157   HNRPA3   3'  TTACTGCAGCTTAAACAGG    19263    AG  C   A
                                CC  GT TAA CTGCAGTAA
                                ||  || ||| |||||||||
                                GG  CA ATT GACGTCATT
                                 A_  A   C
GAM157   HSA250303 3'  TACTGCAGTCCAGCCTGG     37412       T  AA
                                CCAGG CT  ACTGCAGTA
                                ||||| ||  |||||||||
                                GGTCC GA  TGACGTCAT
                                   _  CC
GAM157   HSGP25L2G 3'  CAGCCTAGACCTGCTGA     62166     C       AA
                                TCA CAGGTCTA  CTG
                                ||| ||||||||  |||
                                AGT GTCCAGAT  GAC
                                  C       CC
GAM157   HSH2     3'  ACTGCAGTCCAGCCTGGATGA  51670     _    T  AA
                                TCA CCAGG CT  ACTGCAGT
                                ||| ||||| ||  ||||||||
                                AGT GGTCC GA  TGACGTCA
                                  A    _  CC
GAM157   KIAA1909  5'  CTGCATTTAGGCCTG       73839          C
                                CAGGTCTAAA TGCAG
                                |||||||||| |||||
                                GTCCGGATTT ACGTC
                                           _
GAM157   LIM      3'  ACTGCACTCCAGCCTGGTGA   21300          CTAAAC
                                TCACCAGGT     TGCAGT
                                |||||||||     ||||||
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                                AGTGGTCCG     ACGTCA
                                     ACCTC_
GAM157  LIMK2    3'  TTGTACATAGACCTGATGA   33631     C      AAC
                                TCA CAGGTCTA   TGCAG
                                ||| ||||||||   |||||
                                AGT GTCCAGAT   ATGTT
                                  A       AC_
GAM157  LIMK2    3'  TTGTACATAGACCTGATGA   18731     C      AAC
                                TCA CAGGTCTA   TGCAG
                                ||| ||||||||   |||||
                                AGT GTCCAGAT   ATGTT
                                  A       AC_
GAM157  LSM5     3'  TACTGCAGTAGCCAGTGG    24639     CA  T  AA
                                TCAC  GG CT  ACTGCAGTA
                                ||||  || ||  |||||||||
                                GGTG  CC GA  TGACGTCAT
                                  A_  _  __
GAM157  MACMARCKS 3' ACTGCCTGGACCTGGTG     43447          AACT
                                CACCAGGTCTA    GCAGT
                                ||||||||||    |||||
                                GTGGTCCAGGT    CGTCA
                                     C___
GAM157  MGC17998 3'  ACTCCAGCCTGGTGA       58740        TCTAAA   C
                                TCACCAGG     CTG AGT
                                ||||||||     ||| |||
                                AGTGGTCC     GAC TCA
                                    _______  C
GAM157  MGC23280 5'  ACTACAACCTGGTGA       58391        CTAAAC  C
                                TCACCAGGT     TG AGT
                                |||||||||     || |||
                                AGTGGTCCA     AC TCA
                                    _______ A
GAM157  MGC2474  3'  ACTGCAGCCTAGACCTGCTGG  43712     C       AA
                                TCA CAGGTCTA  CTGCAGT
                                ||| ||||||||  |||||||
                                GGT GTCCAGAT  GACGTCA
                                  C       CC
GAM157  MGC4663  3'  ACTGCCAACTTGGTGA      44503        CTAAACT
                                TCACCAGGT      GCAGT
                                |||||||||      |||||
                                AGTGGTTCA      CGTCA
                                     AC_____
GAM157  NFAT5    5'  GCGCGGACCTAGACCTGG     56944         AA_   A
                                CCAGGTCTA   CTGC GT
                                |||||||||   |||| ||
                                GGTCCAGAT   GGCG CG
                                     CCA    _
GAM157  PTK9L    3'  ACTGCAGTTTGGGATGGTTGA  23466     _   GG
                                TCA CCA  TCTAAACTGCAGT
                                ||| |||  |||||||||||||
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                                AGT GGT  GGGTTTGACGTCA
                                  T  A_
GAM157  PTR4     3'  TTACTGCAGCGTGTCTCCTGG  74057      TC_  AA
                                CCAGG  TA  CTGCAGTAA
                                |||||  ||  |||||||||
                                GGTCC  GT  GACGTCATT
                                   TCT  GC
GAM157  RAB35    3'  GCGCCTGGACCTGGCGA     22480    A       AAC
                                TC CCAGGTCTA  TGC
                                || |||||||||  |||
                                AG GGTCCAGGT  GCG
                                 C       CC_
GAM157  SCN12A   3'  ACTGCACTCCAGCCTGGTGA  26221        CTAAAC
                                TCACCAGGT     TGCAGT
                                |||||||||     ||||||
                                AGTGGTCCG     ACGTCA
                                      ACCTC_
GAM157  SULT1C2  3'  CAGCCTAGACCTGCTGA     21675     C      AA
                                TCA CAGGTCTA  CTG
                                ||| ||||||||  |||
                                AGT GTCCAGAT  GAC
                                  C       CC
GAM157  TOMM34   3'  ACTGCAGTTCATCTG       22332      CTA
                                CAGGT  AACTGCAGT
                                |||||  |||||||||
                                GTCTA  TTGACGTCA
                                   C__
GAM157  VEZATIN  3'  TTACTGCAGCTTAGGGATGG  34229     GG    A
                                CCA  TCTAA CTGCAGTAA
                                |||  ||||| |||||||||
                                GGT  GGATT GACGTCATT
                                  AG    C
GAM157  ZFP106   3'  ACTGCACTCCAGCCTGGTGA  42460        CTAAAC
                                TCACCAGGT     TGCAGT
                                |||||||||     ||||||
                                AGTGGTCCG     ACGTCA
                                      ACCTC_
GAM157  LOC120227 5'  ACTGCCAACTTGGTGA      74006         CTAAACT
                                TCACCAGGT      GCAGT
                                |||||||||      |||||
                                AGTGGTTCA      CGTCA
                                      AC_____
GAM157  LOC124411 3'  ACTTCAGAAAAGCCTGGTGA  74282        T  AAA  C
                                TCACCAGG CT  CTG AGT
                                |||||||| ||  ||| |||
                                AGTGGTCC GA  GAC TCA
                                     _ AAA  T
GAM157  LOC126282 3'  ACTGCACTTCAGCCTGGTGA  74468        T  A  C
                                TCACCAGG CT AA TGCAGT
                                |||||||| || || ||||||
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                                AGTGGTCC GA TT ACGTCA
                                    _ C  C
GAM157  LOC127281 3'  TAGTCCAGACCTGGGGA     74650    A       AA
                                TC CCAGGTCT  ACTG
                                || ||||||||  ||||
                                AG GGTCCAGA  TGAT
                                 G       CC
GAM157  LOC142779 3'  ACTGCATTGCAGCCTGGTGA   76390         CTA  C
                                TCACCAGGT   AA TGCAGT
                                |||||||||   || ||||||
                                AGTGGTCCG   TT ACGTCA
                                     ACG  _
GAM157  LOC145078 3'  TTACTGCAGCTTAAACAGG    60294    AG  C   A
                                CC  GT TAA CTGCAGTAA
                                ||  || ||| |||||||||
                                GG  CA ATT GACGTCATT
                                 A_  A   C
GAM157  LOC148137 3'  CTGTAACCTAGACCTGG      58427         AAC
                                CCAGGTCTA   TGCAG
                                |||||||||   |||||
                                GGTCCAGAT   ATGTC
                                     CCA
GAM157  LOC148981 3'  TTACTGCAGCTTAAACAGG    84319    AG  C   A
                                CC  GT TAA CTGCAGTAA
                                ||  || ||| |||||||||
                                GG  CA ATT GACGTCATT
                                 A_  A   C
GAM157  LOC149332 5'  TTACTGCATTTAACATGATGA  84399     C  G  C    C
                                TCA CA GT TAAA TGCAGTAA
                                ||| || || |||| ||||||||
                                AGT GT CA ATTT ACGTCATT
                                  A  A  _    _
GAM157  LOC150481 3'  ACTGCATTCCAGCCTGGTGA   79880         CTAAAC
                                TCACCAGGT     TGCAGT
                                |||||||||     ||||||
                                AGTGGTCCG     ACGTCA
                                     ACCTT_
GAM157  LOC150935 3'  GGTTCTAGTACCTGGTGA     80037          _  _
                                TCACCAGGT CTA AACT
                                ||||||||| ||| ||||
                                AGTGGTCCA GAT TTGG
                                     T   C
GAM157  LOC151248 3'  ACTGCACTCCAGCCTGGTGA   80182         CTAAAC
                                TCACCAGGT     TGCAGT
                                |||||||||     ||||||
                                AGTGGTCCG     ACGTCA
                                     ACCTC_
GAM157  LOC151258 5'  TTACTGCAGAAATGATGACCTG 80197         TAAA___
           GT                    ACCAGGTC      CTGCAGTAA
                                ||||||||      |||||||||
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                                TGGTCCAG      GACGTCATT
                                     TAGTAAA
GAM157   LOC153883 5'  TACTGCAGTTTTTAGTG     80985     CAGGTCT
                                CAC       AAACTGCAGTA
                                |||       ||||||||||
                                GTG       TTTGACGTCAT
                                  ATT_____
GAM157   LOC158450 3'  TACTGAACAGCCTGGTGA     81932         CTAAACTG
                                TCACCAGGT       CAGTA
                                |||||||||       |||||
                                AGTGGTCCG       GTCAT
                                     ACAA_____
GAM157   LOC158504 3'  TACTGAACAGCCTGGTGA     81940         CTAAACTG
                                TCACCAGGT       CAGTA
                                |||||||||       |||||
                                AGTGGTCCG       GTCAT
                                     ACAA_____
GAM157   LOC166979 5'  CTGACTTAGACCTGGGA      82669     A        ACTG
                                TC CCAGGTCTAA    CAG
                                || ||||||||||    |||
                                AG GGTCCAGATT    GTC
                                 _        CA__
GAM157   LOC202404 5'  TTGTGTTCAGCCTGGTGA     89169         T  A   T
                                TCACCAGG CT AAC GCAG
                                |||||||| || ||| ||||
                                AGTGGTCC GA TTG TGTT
                                     _  C   _
GAM157   LOC202934 3'  TACTGCAGCACCACCTAGTGG  90426      C    CTAAA
                                TCAC AGGT    CTGCAGTA
                                |||| ||||    ||||||||
                                GGTG TCCA    GACGTCAT
                                  A    CCAC_
GAM157   LOC220988 3'  TTACTGCAGCTTAAACAGG    90849     AG  C   A
                                CC  GT TAA CTGCAGTAA
                                ||  || ||| |||||||||
                                GG  CA ATT GACGTCATT
                                 A_  A   C
GAM157   LOC253981 3'  TTACTTTTCCCTTTAGGCCTGG 95835           CTGC__
                                CCAGGTCTAAA      AGTAA
                                ||||||||||      |||||
                                GGTCCGGATTT      TCATT
                                      CCCTTT
GAM157   LOC255190 3'  TTACTGCAGCTTAAACAGG    97690     AG  C   A
                                CC  GT TAA CTGCAGTAA
                                ||  || ||| |||||||||
                                GG  CA ATT GACGTCATT
                                 A_  A   C
GAM157   LOC255465 3'  TACTGCAGCGCCACCTAGTGG  97300      C    CTAAA
                                TCAC AGGT    CTGCAGTA
                                |||| ||||    ||||||||
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                                GGTG TCCA    GACGTCAT
                                  A   CCGC_
GAM157  LOC256433 5'  ACTGTAGTAAAACCCAGTGA  97475     CA  CTAA
                                TCAC  GGT   ACTGCAGT
                                ||||  |||   ||||||||
                                AGTG  CCA   TGATGTCA
                                  AC  AAA_
GAM157  LOC57149  3'  ACTGCAGTCACCTTTGG     39935    __  CTAA
                                CCA  GGT   ACTGCAGT
                                |||  |||   ||||||||
                                GGT  CCA   TGACGTCA
                                 TT  C___
GAM157  LOC92521  3'  TACTGCAGCTTTTCCTGG    69598     TCT  A
                                CCAGG   AA CTGCAGTA
                                |||||   || ||||||||
                                GGTCC   TT GACGTCAT
                                   TT_  C
GAM157  LOC92979  3'  ACCACGGTGACTTGGTGA    56436       TAA   CA
                                TCACCAGGTC   ACTG  GT
                                ||||||||||   ||||  ||
                                AGTGGTTCAG   TGGC  CA
                                     ___    AC
GAM158  AQP3      3'  TTCACGATCCACCCTTTC     59593     T_   _
                                GAAA  GTGG TCGTGAA
                                ||||  |||| |||||||
                                CTTT  CACC AGCACTT
                                  CC    T
GAM158  ARSB      3'  TCACGACTCTTGTC        3502        AATGTG
                                GACAAGA     GTCGTGA
                                |||||||     |||||||
                                CTGTTCT     CAGCACT
                                     _______
GAM158  B4GALT5   3'  TTTTCACAAAAATAGTCCTTTG 16519       AAA_  GGTC
           TCA                    TGACAAG   TGT   GTGAAAA
                                |||||||   |||   |||||||
                                ACTGTTT   ATA   CACTTTT
                                   CCTG   AAAA
GAM158  CHRNA3    3'  TCGTTACCCATTTCTT      5610        T  CG
                                AAGAAATG GGT  TGA
                                |||||||| |||  |||
                                TTCTTTAC CCA  GCT
                                   _  TT
GAM158  DRD1      3'  TTACAACCACATTTCTGGCCA  5840     ACA        C
                                TG   AGAAATGTGGT GTGA
                                ||   |||||||||| ||||
                                AC   TCTTTACACCA CATT
                                 CGG         A
GAM158  FUT1      3'  TCTGATCACATCCCCTGTC   3798      AGAA       T
                                GACA   ATGTGGTCG GA
                                ||||   ||||||||| ||
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                                CTGT    TACACTAGT CT
                                  CCCC       _
GAM158  IRF1     3'  GCCACATTTCTGATCA     64345     CA
                                TGA  AGAAATGTGGT
                                |||  ||||||||||
                                ACT  TCTTTACACCG
                                  AG
GAM158  MAP3K8   5'  TCACGACCACCTCATG      17791    A  AAT
                                CA GA   GTGGTCGTGA
                                || ||   ||||||||||
                                GT CT   CACCAGCACT
                                 A  C__
GAM158  NGFR     3'  TTCTGACCACACTTCCTGTC   10231      A   A       T
                                GACA GAA TGTGGTCG GAA
                                |||| ||| |||||||| |||
                                CTGT CTT ACACCAGT CTT
                                  C   C       _
GAM158  OLR1     3'  TTCACAACAGTTCTTGTTA    10341         ATGTG  C
                                TGACAAGAA    GT GTGAA
                                |||||||||    || |||||
                                ATTGTTCTT    CA CACTT
                                     GA___  A
GAM158  POU4F1   3'  CACTGAAAACATTTTTGTCA   20660         A   GG  _
                                TGACAAGAA TGT  TC GTG
                                ||||||||| |||  || |||
                                ACTGTTTTT ACA  AG CAC
                                     _  AA  T
GAM158  SMP1     3'  TTTCACATGAATAATTTTTGTC 26705         A   GGTC
           A                     TGACAAGAA TGT    GTGAAA
                                |||||||||| |||    ||||||
                                ACTGTTTTT ATA    CACTTT
                                     A   AGTA
GAM158  ZNF264   3'  TTCTATTAACATTTCTTTTCA  12769     C        GGTCGT
                                TGA AAGAAATGT     GAA
                                ||| |||||||||     |||
                                ACT TTCTTTACA     CTT
                                  T       ATTAT_
GAM158  C20orf175 3'  CGAGCTCCACGTTTCCTGCCA  55063    A  A       ___
                                TG CA GAAATGTGG   TCG
                                || || |||||||||   |||
                                AC GT CTTTGCACC   AGC
                                 C  C        TCG
GAM158  CAPNS2   3'  TTTCACAACCCTACATATTTCT 50323     CA       ____  C
           GATCA                   TGA  AGAAATGT    GGT GTGAAA
                                |||  ||||||||   ||| ||||||
                                ACT  TCTTTATA    CCA CACTTT
                                  AG       CATC   A
GAM158  CLDN6    3'  TTTACACTCACATTTTTATCA  41041     CA       _  C
                                TGA  AGAAATGTG GT GTGAA
                                |||  ||||||||| || |||||
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                                ACT  TTTTTACAC CA CATTT
                                  A_       T  _
GAM158  DKFZP564L0864 3'  GCACCAATTTCTTGCCA     72555    A      G   C
                                TG CAAGAAAT TGGT GT
                                || |||||||| |||| ||
                                AC GTTCTTTA ACCA CG
                                 C       _   _
GAM158  DKFZP566B183 3'  TTTCCATAAACATTTCTTTTCA 31330     C       GGTCGT
                                TGA AAGAAATGT     GAAA
                                ||| |||||||||     ||||
                                ACT TTCTTTACA     CTTT
                                  T       AATAC_
GAM158  GTF2E1   3'  TACAGACCTCTTGTCA      18616        AATGT   _
                                TGACAAGA    GGTC GTG
                                ||||||||    |||| |||
                                ACTGTTCT    CCAG CAT
                                     _____   A
GAM158  KIAA0089  3'  TTTTAATTCACATTTCTT    69967          TCG
                                AAGAAATGTGG   TGAAA
                                ||||||||||   |||||
                                TTCTTTACACT   ATTTT
                                      TA_
GAM158  KIAA0373  5'  TTTTCAAAGTAACATTTCTT   28015         GGTCG
                                AAGAAATGT    TGAAAA
                                |||||||||    ||||||
                                TTCTTTACA    ACTTTT
                                     ATGAA
GAM158  KIAA1813  3'  TTTTCACACTGTAAATTTCTTG 70314         __ TG  C
            T                    ACAAGAAAT  G  GT GTGAAAA
                                |||||||||  |  || |||||||
                                TGTTCTTTA  T  CA CACTTTT
                                     AA GT  _
GAM158  KIAA1951  3'  TTCCAGGCTTCTCTTGTCA   73766        AATGT   GT
                                TGACAAGA    GGTC  GAA
                                ||||||||    ||||  |||
                                ACTGTTCT    TCGG  CTT
                                     CT___    AC
GAM158  MGC4170   3'  TTCACCATTTCTTGTC      44227          TGGTC
                                GACAAGAAATG    GTGAA
                                ||||||||||    |||||
                                CTGTTCTTTAC    CACTT
                                      _____
GAM158  NRN1     3'  CACTGCACATTTCTCCTCA   33432     CA       GTC
                                TGA  AGAAATGTG   GTG
                                |||  |||||||||  |||
                                ACT  TCTTTACAC   CAC
                                  CC        GT_
GAM158  PLA2G12   3'  TTTTCACAACCACATTT     48028         C
                                AAATGTGGT GTGAAAA
                                ||||||||| |||||||
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                                TTTACACCA CACTTTT
                                     A
GAM158  PPY2     3'  CACTCCACATTCCTGGCCA   40819    ACA  A      TC
                                TG   AG AATGTGG  GTG
                                ||   || |||||||  |||
                                AC   TC TTACACC  CAC
                                 CGG  C      T_
GAM158  ZNF31    3'  TTTGTAGACCACATTTCCTGTT 64992       A         _ TG
           A                     TGACA GAAATGTGGTC G  AA
                                |||||| |||||||||||  |  ||
                                ATTGT CTTTACACCAG T  TT
                                   C          A GT
GAM158  LOC115219 3' CACGACAACGGGTCCTCA    73295     CAA  AA   G
                                TGA   GA  TGT GTCGTG
                                |||   ||  ||| ||||||
                                ACT   CT  GCA CAGCAC
                                 C__  GG   A
GAM158  LOC120376 5' TTCAGAGCATTTCTTTCA    75986     C       GG  G
                                TGA AAGAAATGT  TC TGAA
                                ||| |||||||||  || ||||
                                ACT TTCTTTACG  AG ACTT
                                  _        __ _
GAM158  LOC133418 3' TTTCATATACATTTTTTGCCA  75094    A         GTC
                                TG CAAGAAATGTG   GTGAAA
                                || ||||||||||   ||||||
                                AC GTTTTTTACAT   TACTTT
                                 C          A__
GAM158  LOC151199 3' TTAAAACCACAGCTCTTGCCA  80174    A    AA     CG
                                TG CAAGA  TGTGGT  TGA
                                || |||||  ||||||  |||
                                AC GTTCT  ACACCA  ATT
                                 C    CG     AA
GAM158  LOC152317 5' TCACACTGACTTTTGTCA    85649        AATG   C
                                TGACAAGA   TGGT GTGA
                                ||||||||   |||| ||||
                                ACTGTTTT   GTCA CACT
                                     CA__   _
GAM158  LOC152674 3' TTCAACCCACCCTCTTGTCA   85841        AAT    TCG
                                TGACAAGA   GTGG   TGAA
                                ||||||||   ||||   ||||
                                ACTGTTCT   CACC   ACTT
                                     CC_    CA_
GAM158  LOC152845 5' CATGACCACATTTTTCA     60330     CAA
                                TGA   GAAATGTGGTCGTG
                                |||   ||||||||||||||
                                ACT   TTTTACACCAGTAC
                                  ____
GAM158  LOC154743 3' TTTAGTCCACATTGTCTTGTCA 81118         _      TCG
                                TGACAAGA AATGTGG   TGAA
                                |||||||| |||||||   ||||
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                                ACTGTTCT TTACACC   ATTT
                                    G      TG_
GAM158  LOC165476 5'  TTCACGGCACCTTCT      87201      AT   G
                                AGAA  GTG TCGTGAA
                                ||||  ||| |||||||
                                TCTT  CAC GGCACTT
                                  C_  _
GAM158  LOC254266 5'  TTTTCGGTCACACATCTTATCA 97356     C    AA    GT  T
                                TGA AAGA  TGTG  CG GAA
                                ||| ||||  ||||  || |||
                                ACT TTCT  ACAC  GC TTT
                                  A   AC    TG  T
GAM158  LOC255919 3'  TTTCATTCTTACATTTCTAATC 95043     CA        TC
           A                     TGA  AGAAATGTGG  GTGAAA
                                |||  ||||||||||  ||||||
                                ACT  TCTTTACATT  TACTTT
                                  AA         CT
GAM158  LOC51754  5'  CACGGCCACATCTCTGTCA    71027      A  A
                                TGACA GA ATGTGGTCGTG
                                ||||| || ||||||||||
                                ACTGT CT TACACCGGCAC
                                   _  C
GAM158  LOC55862  3'  ACCTCATTTCTTGCCA      37485    A       T
                                TG CAAGAAATG GGT
                                || |||||||| |||
                                AC GTTCTTTAC CCA
                                 C        T
GAM158  LOC55954  3'  CACGTGGTCACTTTTCTCATCA 38877     CA    T   GT __
                                TGA  AGAAA GTG  C  GTG
                                |||  ||||| |||  |  |||
                                ACT  TCTTT CAC  G  CAC
                                  AC     T   TG TG
GAM159  ADD2      3'  TGGGTCCCTGCCCTGCTCGTC  33948     A       A T  TA
                                GAC AGCAGGGCA G GA  CA
                                ||| ||||||||| | ||  ||
                                CTG TCGTCCCGT C CT  GT
                                  C        _ C  GG
GAM159  ADD2      3'  TGGGTCCCTGCCCTGCTCGTC  33954     A       A T  TA
                                GAC AGCAGGGCA G GA  CA
                                ||| ||||||||| | ||  ||
                                CTG TCGTCCCGT C CT  GT
                                  C        _ C  GG
GAM159  ADD2      3'  TGGGTCCCTGCCCTGCTCGTC  33965     A       A T  TA
                                GAC AGCAGGGCA G GA  CA
                                ||| ||||||||| | ||  ||
                                CTG TCGTCCCGT C CT  GT
                                  C        _ C  GG
GAM159  ADD2      3'  TGGGTCCCTGCCCTGCTCGTC  33937     A       A T  TA
                                GAC AGCAGGGCA G GA  CA
                                ||| ||||||||| | ||  ||
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                                CTG TCGTCCCGT C CT  GT
                                  C       _ C  GG
GAM159  ARNT2    3'  CACCCTCGCCCTGCTTGCCC  29454    A       AA__
                                GG CAAGCAGGGC   GTG
                                || ||||||||||   |||
                                CC GTTCGTCCCG   CAC
                                 C        CTCC
GAM159  ATP2A3   3'  CACTCGCCCACTTGCCCA   17721    A   CA   A
                                TGG CAAG  GGGC AGTG
                                ||| ||||  |||| ||||
                                ACC GTTC  CCCG TCAC
                                  C   A_   C
GAM159  CD34     3'  CACAGCCCTGCTTACCA    8339     AC       AA
                                TGG  AAGCAGGGC  GTG
                                |||  |||||||||  |||
                                ACC  TTCGTCCCG  CAC
                                  A_       A_
GAM159  CHRNB1   3'  GTACCACTTGCCCCCTCCA   60537    CAAGCA       A
                                TGGA     GGGCAAGTG TAC
                                ||||     ||||||||| |||
                                ACCT     CCCGTTCAC ATG
                                  CC____        C
GAM159  CRAT     3'  CATCTGTACCCTGCTTCCCA  14350    AC      __ AG
                                TGG  AAGCAGGG  CA  TG
                                |||  ||||||||  ||  ||
                                ACC  TTCGTCCC  GT  AC
                                  C_       AT  CT
GAM159  CRAT     3'  CATCTGTACCCTGCTTCCCA  5658     AC      __ AG
                                TGG  AAGCAGGG  CA  TG
                                |||  ||||||||  ||  ||
                                ACC  TTCGTCCC  GT  AC
                                  C_       AT  CT
GAM159  DAP      3'  ACTGTCCTGCTCACCCA    72551    ACA       A
                                TGG   AGCAGGGCA GT
                                |||   |||||||||  ||
                                ACC   TCGTCCTGT CA
                                  CAC       _
GAM159  DAZ      3'  GCTTACTCTGCTTATCCA    82114    C       C
                                TGGA AAGCAGGG AAGT
                                |||| ||||||||  ||||
                                ACCT TTCGTCTC TTCG
                                   A       A
GAM159  EXTL3    3'  TACTTATCCCTGCTCTCC    7536     CA      C_
                                GGA  AGCAGGG  AAGTG
                                |||  |||||||  |||||
                                CCT  TCGTCCC  TTCAT
                                  C_       TA
GAM159  GLUL     3'  TGGGTTTCTGCCCTGCCCACCC 9048    ACAA       A T  TA
                                GG    GCAGGGCA G GA  CA
                                ||    |||||||| | ||  ||
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                                CC   CGTCCCGT C TT  GT
                                 CACC       _ T  GG
GAM159  GYS1    3'  CACTCCCCGCCTGTCC      88398      A  A   CA
                                GGACA GC GGG  AGTG
                                ||||| || |||  ||||
                                CCTGT CG CCC  TCAC
                                  C  C  __
GAM159  KHK     3'  TCCTCTGCCCTGCCCACCA   21403     ACAA      _ T
                                TGG   GCAGGGCA AG GA
                                |||   |||||||| || ||
                                ACC   CGTCCCGT TC CT
                                 ACC_       C  _
GAM159  KHK     3'  TCCTCTGCCCTGCCCACCA   4033      ACAA      _ T
                                TGG   GCAGGGCA AG GA
                                |||   |||||||| || ||
                                ACC   CGTCCCGT TC CT
                                 ACC_       C  _
GAM159  MAT1A   3'  CACCTGCCCTACCTGCCCCA  90827     ACA  C_     A
                                TGG   AG  AGGGCA GTG
                                |||   ||  |||||| |||
                                ACC   TC  TCCCGT CAC
                                 CCG  CA     C
GAM159  MAT1A   3'  TACCTGCCCCACTTGTCC    90836       CA    A
                                GGACAAG  GGGCA GTG
                                |||||||  ||||| |||
                                CCTGTTC  CCCGT CAT
                                    AC    C
GAM159  MCL1    3'  ACTGCCCTGCCTGCCCA     41712     A  A      A
                                TGG CA GCAGGGCA GT
                                ||| || |||||||| ||
                                ACC GT CGTCCCGT CA
                                 C  C       _
GAM159  PDGFB   3'  CACCCCTCCCTGCTTGCACA  10495    GA       CAA_
                                TG  CAAGCAGGG   GTG
                                ||  |||||||||   |||
                                AC  GTTCGTCCC   CAC
                                 AC        TCCC
GAM159  PFKFB4  3'  TGTAATCGGGTGCCCTGCTGTC 15875       A      AG   _
           CA                    TGGACA GCAGGGCA  TGAT ACA
                                ||||||  ||||||||  |||| |||
                                ACCTGT CGTCCCGT  GCTA TGT
                                   _       GG    A
GAM159  RAI14   3'  TCATCACCCTGCTTATC     31482    C       CAA
                                GA AAGCAGGG   GTGA
                                || ||||||||   ||||
                                CT TTCGTCCC   TACT
                                 A       AC_
GAM159  SFRP1   3'  ACTTTACCCTTCTTGTCCA   11563        C    C_
                                TGGACAAG AGGG  AAGT
                                |||||||| ||||  ||||
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                                ACCTGTTC TCCC  TTCA
                                     T   AT
GAM159  SLA2     3'  CTTGCCCTGTTGCCCA     49898     ACA
                                TGG   AGCAGGGCAAG
                                |||   ||||||||||
                                ACC   TTGTCCCGTTC
                                  CG_
GAM159  SLC25A11 3'  GCTTGCCCTGCTCGTCC     13091      A
                                GGAC AGCAGGGCAAGT
                                |||| ||||||||||||
                                CCTG TCGTCCCGTTCG
                                  C
GAM159  SLC7A4   3'  CACTTGCCCCGCCCTCC     65203     CAA  A
                                GGA   GC GGGCAAGTG
                                |||   || |||||||||
                                CCT   CG CCCGTTCAC
                                  CC_  C
GAM159  TEAD3    3'  ATCACCCTGCTCTGCCCA    12207     ACAA       A_
                                TGG   GCAGGGCA  GTGAT
                                |||   ||||||||  |||||
                                ACC   CGTCTCGT  CACTA
                                  ____       CC
GAM159  TFE3     3'  TGCCCTGCTCTGCCCA      21513     A  _
                                TGG CA AGCAGGGCA
                                ||| || |||||||||
                                ACC GT TCGTCCCGT
                                  C  C
GAM159  TRPM6    3'  TGCTTGCCCTGCCTGCCA    34550     A  A
                                TGG CA GCAGGGCAAGTG
                                ||| || ||||||||||||
                                ACC GT CGTCCCGTTCGT
                                  _  C
GAM159  VDR      3'  TGCAGGCCCCGCTTGTCCA   4573          A    AA
                                TGGACAAGC GGGC  GTG
                                ||||||||| ||||  |||
                                ACCTGTTCG CCCG  CGT
                                      C   GA
GAM159  VIPR1    3'  GCTGCCCTCCTTGTCCA     16114         C     A
                                TGGACAAG AGGGCA GT
                                |||||||| |||||| ||
                                ACCTGTTC TCCCGT CG
                                     C     _
GAM159  AP3D1    3'  CGCATCCCCTGCTTGCCA    14136     A       CAA
                                TGG CAAGCAGGG   GTG
                                ||| |||||||||   |||
                                ACC GTTCGTCCC   CGC
                                  _       CTA
GAM159  ATP9A    3'  GCCAGCCCTGCTTATCCA    62044      C       AA
                                TGGA AAGCAGGGC  GT
                                |||| |||||||||  ||
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                                ACCT TTCGTCCCG  CG
                                  A        AC
GAM159  B3GNT7   3'  CGCACCCTGCTTCTCCA     71127      C       CAA
                                TGGA AAGCAGGG   GTG
                                |||| ||||||||   |||
                                ACCT TTCGTCCC   CGC
                                  C       A__
GAM159  BAGE     3'  CACATCTTCCTGCTTTGTCCA  6807         _     CAA_
                                TGGACAA GCAGGG    GTG
                                |||||||  ||||||    |||
                                ACCTGTT CGTCCT    CAC
                                    T     TCTA
GAM159  BCAN     3'  CACTGCCCTGTCACCCA     41689     ACAA       A
                                TGG    GCAGGGCA GTG
                                |||    ||||||||  |||
                                ACC    TGTCCCGT CAC
                                  CAC_       _
GAM159  BLP2     3'  ATCACTTGTATCTCCAGCCCA  54333     ACAA  A  ____
                                TGG    GC GG    GCAAGTGAT
                                |||    || ||    |||||||||
                                ACC    CG CC    TGTTCACTA
                                  ____  A  TCTA
GAM159  BLP2     3'  ATCACTTGTATCTCCAGCCCA  47115     ACAA  A  ____
                                TGG    GC GG    GCAAGTGAT
                                |||    || ||    |||||||||
                                ACC    CG CC    TGTTCACTA
                                  ____  A  TCTA
GAM159  BTBD3    3'  ATCTAGCTCCCTTACTTGTCCA 30305         C_    CAAGT
                                TGGACAAG  AGGG     GAT
                                ||||||||  ||||     |||
                                ACCTGTTC  TCCC     CTA
                                    AT    TCGAT
GAM159  C19orf7  3'  CACACCCTGCTTGCCCA     61126     A       CAA
                                TGG CAAGCAGGG   GTG
                                ||| |||||||||   |||
                                ACC GTTCGTCCC   CAC
                                  C       A__
GAM159  C9orf16  3'  CACTTGCCTGCCCACCCA    44114     ACAA    G
                                TGG    GCAGG CAAGTG
                                |||    ||||| ||||||
                                ACC    CGTCC GTTCAC
                                  CACC    _
GAM159  CENTB5   3'  CGCGGCCCTGCTCGCCCA    95484     ACA       AA
                                TGG   AGCAGGGC  GTG
                                |||   ||||||||  |||
                                ACC   TCGTCCCG  CGC
                                  CGC       G_
GAM159  CXYorf1  5'  TCTCTGCCCTGCTGCCCA    82054     ACA       A T
                                TGG   AGCAGGGCA G GA
                                |||   |||||||||  | ||
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                                ACC   TCGTCCCGT C CT
                                  CG_       _ T
GAM159  CYP2C18   3'  GTATCACTTGTATTGACCA   5750     ACAAG   G
                                TGG    CAG GCAAGTGATAC
                                |||    ||| ||||||||||
                                ACC    GTT TGTTCACTATG
                                  A____   A
GAM159  DCOHM     3'  TGCCTGCCCTGCCCACCA    49615    ACAA      A
                                TGG    GCAGGGCA GTG
                                |||    |||||||| |||
                                ACC    CGTCCCGT CGT
                                  ACC_      C
GAM159  DKFZp547E052 3'  GTACCAGCCACTTGTCC     50099       CAG   AAG  A
                                GGACAAG   GGC   TG TAC
                                |||||||   |||   || |||
                                CCTGTTC   CCG   AC ATG
                                    A__   ___  C
GAM159  DKFZp547O146 3'  CGCCTGTCCTGCCCGCCCA   39566    ACAA      A
                                TGG    GCAGGGCA GTG
                                |||    |||||||| |||
                                ACC    CGTCCTGT CGC
                                  CGCC      C
GAM159  DKFZP564O0423 3'  CGCTTTGGCCTGCTTGTCCA   91683          G   _
                                TGGACAAGCAGG CAA GTG
                                |||||||||||| ||| |||
                                ACCTGTTCGTCC GTT CGC
                                       G   T
GAM159  DKFZP566N034 3'  CACACCACTGCTTGCCC     80139    A     _  CAA
                                GG CAAGCAG GG   GTG
                                || ||||||| ||   |||
                                CC GTTCGTC CC   CAC
                                 C      A  A__
GAM159  ERF       3'  TGCCTGCCCTGCCCCTCCA   21439     CAA      A
                                TGGA   GCAGGGCA GTG
                                ||||   |||||||| |||
                                ACCT   CGTCCCGT CGT
                                  CCC      C
GAM159  FBXO29    3'  TACGGTCCCTGCTTAGCCA   76758    AC      CAA
                                TGG  AAGCAGGG   GTG
                                |||  ||||||||   |||
                                ACC  TTCGTCCC   CAT
                                  GA       TGG
GAM159  FIBL-6    5'  ATCCCTGCCCTGCCCA     72914    ACAA      A T
                                TGG    GCAGGGCA G GAT
                                |||    |||||||| | |||
                                ACC    CGTCCCGT C CTA
                                  _____       _ C
GAM159  FLJ14810  3'  CACCCTCTGCCCTGCCCGGCCA 51623    ACAA      A___
                                TGG    GCAGGGCA    GTG
                                |||    ||||||||    |||
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                                ACC   CGTCCCGT   CAC
                                  GGCC      CTCC
GAM159  FLJ20542  3'  TGTCACCTGCCTGCCCA    49787    ACAA    G  A
                                TGG   GCAGG CA GTGATA
                                |||   ||||| || ||||||
                                ACC   CGTCC GT CACTGT
                                 ____    _ C
GAM159  FLJ22955  5'  CACTTGCCCTGCTCTCCA    95117     CA
                                TGGA  AGCAGGGCAAGTG
                                ||||  ||||||||||||
                                ACCT  TCGTCCCGTTCAC
                                  C_
GAM159  GAL3ST2   3'  GTCCTGCCCTGCCCTCC     52313     CAA      A T
                                GGA   GCAGGGCA G GAT
                                |||   |||||||| | |||
                                CCT   CGTCCCGT C CTG
                                  CC_      _ _
GAM159  HSA250839 3'  GTCTCTGCCCTGCCCACCCA   37260     ACAA      A T
                                TGG   GCAGGGCA G GAT
                                |||   |||||||| | |||
                                ACC   CGTCCCGT C CTG
                                  CACC      _ T
GAM159  IRO039700 3'  CACACAGCCCTGCTTGGCCA   37909     A        AA_
                                TGG CAAGCAGGGC   GTG
                                ||| ||||||||||   |||
                                ACC GTTCGTCCCG   CAC
                                  G         ACA
GAM159  KIAA0427  3'  CACAGCCCTGCTCCCCA     28718     ACA      AA
                                TGG   AGCAGGGC  GTG
                                |||   ||||||||  |||
                                ACC   TCGTCCCG  CAC
                                  CC_       A_
GAM159  KIAA0495  3'  TGGAGTCTTGCCCTGTCACCCA 62600     ACAA       TGATA
                                TGG   GCAGGGCAAG    CA
                                |||   ||||||||||    ||
                                ACC   TGTCCCGTTC    GT
                                  CAC_        TGAG_
GAM159  KIAA1041  3'  TGGAGTCTTGCCCTGTTGCCCA 30144     ACA        TGATA
                                TGG   AGCAGGGCAAG    CA
                                |||   ||||||||||    ||
                                ACC   TTGTCCCGTTC    GT
                                  CG_         TGAG_
GAM159  KIAA1111  3'  TCACCCCAGCTTGCCCA     96208     A    A   CAA
                                TGG CAAGC GGG   GTGA
                                ||| ||||| |||   ||||
                                ACC GTTCG CCC   CACT
                                  C    A  ___
GAM159  KIAA1321  3'  TGTATCACTTCTCTGTCTGTCC 62228       AG    C
              A                   TGGACA  CAGGG AAGTGATACA
                                ||||||  ||||| ||||||||||
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                                ACCTGT  GTCTC TTCACTATGT
                                   CT    _
GAM159  KIAA1437  3'  TGCCTGCCCTGCCTCTCCA   60595     CAA      A
                                TGGA   GCAGGGCA GTG
                                ||||   |||||||| |||
                                ACCT   CGTCCCGT CGT
                                  CTC       C
GAM159  KIAA1464  3'  GGAGCTGCCCTGCCCTCCA   68271     CAA      A  GATA
                                TGGA   GCAGGGCA GT    C
                                ||||   |||||||| ||    |
                                ACCT   CGTCCCGT CG    G
                                  CC_       _ AG__
GAM159  KIAA1560  3'  CACTCTGCCCTGCCTGTC    64174     A      _
                                GACA GCAGGGCA AGTG
                                |||| |||||||| ||||
                                CTGT CGTCCCGT TCAC
                                  C       C
GAM159  KIAA1881  3'  CGCGGGGTCGCCCTGCTCTGTC 95338       _      AA____
            CA                    TGGACA AGCAGGGC     GTG
                                |||||| ||||||||     |||
                                ACCTGT TCGTCCCG     CGC
                                   C       CTGGGG
GAM159  LASP1     3'  TGTGATTTTGCCCTCCTGCCCA 20464     ACA  C       TGA
                                TGG   AG AGGGCAAG   TACA
                                |||   || ||||||||   ||||
                                ACC   TC TCCCGTTT   GTGT
                                  CG_  C       TA_
GAM159  MGC3130   3'  TGGTTGCTCTGCTCATCCA   43822     CA       G
                                TGGA  AGCAGGGCAA TG
                                ||||  |||||||||| ||
                                ACCT  TCGTCTCGTT GT
                                  AC         G
GAM159  RAB1B     3'  CACCTGTGCCCTGCCCTCCA   48284     CAA      A__
                                TGGA   GCAGGGCA   GTG
                                ||||   ||||||||   |||
                                ACCT   CGTCCCGT   CAC
                                  CC_       GTC
GAM159  VI        3'  TGTATCACCTGGGTTCTGTCC  25560       _  AG  CAA
                                GGACA AGC  GG   GTGATACA
                                ||||| |||  ||   ||||||||
                                CCTGT TTG  TC   CACTATGT
                                   C   GG  ___
GAM159  LOC128977 3'  TGCTAGCCCTACTTGCCCA   74829     A   C    A
                                TGG CAAG AGGGC AGTG
                                ||| |||| ||||| ||||
                                ACC GTTC TCCCG TCGT
                                  C   A    A
GAM159  LOC132671 3'  TGCTTTCTACCCTGCCTGGCCA 59172     A  A     C___
                                TGG CA GCAGGG    AAGTG
                                ||| || ||||||    |||||
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                                ACC GT CGTCCC    TTCGT
                                  G  C     ATCT
GAM159  LOC143153 3'  GTAGCAGCTGTCCTGCTCACCC 76468     ACA       A  GA_
            A                      TGG   AGCAGGGCA GT   TAC
                                   |||   ||||||||| ||   |||
                                   ACC   TCGTCCTGT CG   ATG
                                     CAC       _  ACG
GAM159  LOC144583 3'  TGTCTGCCCTGCTCTCC     76896     CA       AGT
                                   GGA  AGCAGGGCA   GATA
                                   |||  |||||||||   ||||
                                   CCT  TCGTCCCGT   CTGT
                                     C_       ___
GAM159  LOC145333 5'  CATTCTCCCACTTGTCCA    83324        CA   CA
                                   TGGACAAG  GGG  AGTG
                                   ||||||||  |||  ||||
                                   ACCTGTTC  CCC  TTAC
                                        A_   TC
GAM159  LOC147975 3'  TACAGTCCCTGCTTATTCA    84085      C       CAA
                                   TGGA AAGCAGGG   GTG
                                   |||| ||||||||   |||
                                   ACTT TTCGTCCC   CAT
                                     A       TGA
GAM159  LOC148137 3'  ATGGCTCTGCCCTGCCCCCCA  58420     ACAA      _   G
                                   TGG    GCAGGGCA AGT AT
                                   |||    |||||||| ||| ||
                                   ACC    CGTCCCGT TCG TA
                                     CCC_       C   G
GAM159  LOC151405 5'  TGTATCACTGTTTAATGTTACC 85340     ACA   __    A
            CA                       TGG   AGCA  GGGCA GTGATACA
                                     |||   ||||  ||||| ||||||||
                                     ACC   TTGT  TTTGT CACTATGT
                                       CA_    AA    _
GAM159  LOC152271 3'  CATCTGCCCTGCCTGCCCA    80514     A  A       AG
                                   TGG CA GCAGGGCA  TG
                                   ||| || ||||||||  ||
                                   ACC GT CGTCCCGT  AC
                                     C  C       CT
GAM159  LOC152282 5'  CTTGCCCTGTTGCCCA      80552     ACA
                                   TGG   AGCAGGGCAAG
                                   |||   ||||||||||
                                   ACC   TTGTCCCGTTC
                                     CG_
GAM159  LOC154547 5'  CGCACCCTCTCCCCTTGTCCA  76052         C____    CAA
                                   TGGACAAG    AGGG   GTG
                                   ||||||||    ||||   |||
                                   ACCTGTTC    TCCC   CGC
                                        CCCTC    A__
GAM159  LOC158629 3'  TATCACTTACTATATGTC    86884      AGCAG  C
                                   GACA    GG AAGTGATA
                                   ||||    || ||||||||
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                                CTGT    TC TTCACTAT
                                  ATA__  A
GAM159  LOC200093 5'  GTCTCTGCCCTGCTGCCCA   63098    ACA       A T
                                TGG   AGCAGGGCA G GAT
                                |||   ||||||||| | |||
                                ACC   TCGTCCCGT C CTG
                                  CG_       _ T
GAM159  LOC200470 5'  CACCTCCTCACTTGTCCA    90057        CA   CAA
                                TGGACAAG  GGG   GTG
                                ||||||||  |||   |||
                                ACCTGTTC  TCC   CAC
                                     AC   TC_
GAM159  LOC219295 5'  GTAGCAGCTGTCCTGCTCGCCC 92995     ACA       A  GA_
          A                      TGG   AGCAGGGCA GT   TAC
                                |||   ||||||||| ||   |||
                                ACC   TCGTCCTGT CG   ATG
                                  CGC       _  ACG
GAM159  LOC221466 5'  TGTATCACCTGGTGACTTGTC  93697       _  GGG  A
                                GACAAG CA   CA GTGATACA
                                |||||| ||   || ||||||||
                                CTGTTC GT   GT CACTATGT
                                   A  G__  C
GAM159  LOC221561 5'  CGCACCCTCTCCCCTTGTCCA  92132        C____    CAA
                                TGGACAAG    AGGG   GTG
                                ||||||||    ||||   |||
                                ACCTGTTC    TCCC   CGC
                                     CCCTC    A__
GAM159  LOC222066 5'  CACCTGCCCTGCCTGTT     92742      A       A
                                GACA GCAGGGCA GTG
                                |||| |||||||| |||
                                TTGT CGTCCCGT CAC
                                  C       C
GAM159  LOC253187 5'  TATCCTCTTGCTTACCCA    97116     AC      GCA  T
                                TGG  AAGCAGG   AG GATA
                                |||  |||||||   || ||||
                                ACC  TTCGTTC   TC CTAT
                                  CA      ___  _
GAM159  LOC253558 5'  GCGTGCCCTGCTTGTC      95673           A
                                GACAAGCAGGGCA GT
                                |||||||||||| ||
                                CTGTTCGTCCCGT CG
                                       G
GAM159  LOC257591 5'  CGCACCCTCTCCCCTTGTCCA  97842        C____    CAA
                                TGGACAAG    AGGG   GTG
                                ||||||||    ||||   |||
                                ACCTGTTC    TCCC   CGC
                                     CCCTC    A__
GAM159  LOC90139  3'  ATCACATTCCCTTGTCCA    55398       AGC    CAA
                                TGGACA   AGGG   GTGAT
                                ||||||   ||||   |||||
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                                ACCTGT   TCCC   CACTA
                                   ___    TTA
GAM159  LOC90750  3'  CACAGCCCTGCCCTGCC     63918    A  A_      AA
                                GG CA  GCAGGGC  GTG
                                || ||  |||||||  |||
                                CC GT  CGTCCCG  CAC
                                 _ CC      A_
GAM159  LOC91040  5'  GTCTCTGCCCTGCTGCCCA   64722     ACA       A T
                                TGG   AGCAGGGCA G GAT
                                |||   |||||||||| | |||
                                ACC   TCGTCCCGT C CTG
                                  CG_        _ T
GAM159  LOC91574  3'  CACTGCACTCCACCTGTCCA   66519       AGCA_ _   A
                                TGGACA    GG GCA GTG
                                ||||||    || ||| |||
                                ACCTGT    TC CGT CAC
                                   CCACC  A   _
GAM160  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A     T__
GAM160  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM160  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM160  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM160  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM160  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM160  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
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                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM160  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM160  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM160  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM160  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM160  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM160  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM160  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM160  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM160  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM160  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598         CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
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                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM160  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM160  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                     TA__    TT
GAM160  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A     TC
GAM160  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                     AAAGG
GAM160  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM160  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM160  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM160  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                      _
GAM161  SLC17A4   3'  CAACAGTTCTTCATGTAGC    18525       CAGT
                                GCTGC    TGAAGAACTGTTG
                                |||||    ||||||||||||||
                                CGATG    ACTTCTTGACAAC
                                  T____
GAM161  CITED1    5'  CAACAGCTCCAGCTGGCAGC   14729          AA  A
                                GCTGCCAGTTG  GA CTGTTG
                                ||||||||||  || ||||||
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                                CGACGGTCGAC  CT GACAAC
                                      __ C
GAM161  FLJ10900  5'  CAACAGTTCTTGCTGAAGCAGT 65590       __   TG
           T                   AGCTGC  CAGT  AAGAACTGTTG
                               ||||||  ||||  ||||||||||
                               TTGACG  GTCG  TTCTTGACAAC
                                  AA   __
GAM161  HS6ST    3'  CAACAGTTCCTTTGCCAGCAGC 62025      CA  T  A
                               GCTGC  GT GA GAACTGTTG
                               |||||  || || |||||||||
                               CGACG  CG TT CTTGACAAC
                                  AC  T  C
GAM161  MGC4638  3'  CAACAGTTCTTCAAGTG    48939    G
                               CA TTGAAGAACTGTTG
                               || ||||||||||||||
                               GT AACTTCTTGACAAC
                                G
GAM161  ZNF262   3'  TTCCCCAATGGCAGCTT    17492        G   AA
                               AAGCTGCCA TTG  GAA
                               ||||||||| |||  |||
                               TTCGACGGT AAC  CTT
                                     _  CC
GAM161  LOC115051 3'  CAACAGTTCCTTTGCCAGCAGC 60036     CA  T  A
                               GCTGC  GT GA GAACTGTTG
                               |||||  || || |||||||||
                               CGACG  CG TT CTTGACAAC
                                  AC  T  C
GAM161  LOC143153 3'  CAGCCTCAAGCTGGCAGC    76463        GA  AA
                               GCTGCCAGTT  AG  CTG
                               ||||||||||  ||  |||
                               CGACGGTCGA  TC  GAC
                                     AC  C_
GAM161  LOC168512 5'  CAACAGCCTCTCTGGCAGCTT  82714        TTGA  A_
                               AAGCTGCCAG   AGA  CTGTTG
                               ||||||||||   |||  ||||||
                               TTCGACGGTC   TCT  GACAAC
                                     ____  CC
GAM161  LOC199923 3'  AACAGTTCCAGACCAGC    88494     CCA  GAA
                               GCTG  GTT  GAACTGTT
                               ||||  |||  ||||||||
                               CGAC  CAG  CTTGACAA
                                  ___  AC_
GAM161  LOC199926 3'  TAGTCCTTCAACTCACAGCTT  89880      CC      A
                               AAGCTG  AGTTGAAG ACTG
                               ||||||  |||||||| ||||
                               TTCGAC  TCAACTTC TGAT
                                  AC      C
GAM161  LOC202316 3'  TAGTCCTTCAACTCACAGCTT  90340      CC      A
                               AAGCTG  AGTTGAAG ACTG
                               ||||||  |||||||| ||||
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                                TTCGAC  TCAACTTC TGAT
                                   AC       C
GAM161  LOC221479 3'  CAACAACTACAGCAGCAGC   92222      CA   A  AAC
                                GCTGC  GTTG AG   TGTTG
                                |||||  |||| ||   |||||
                                CGACG  CGAC TC   ACAAC
                                   A_    A  A__
GAM162  C8orf13   5'  GACCCAACTGTGCCACCCA   81573     ACATT  TA
                                TGG    GC  AGTTGGGTC
                                |||    ||  |||||||||
                                ACC    CG  TCAACCCAG
                                  CAC__  TG
GAM162  CHST3     3'  GACACAGCAGCGTCCAATG   14974        A    AA
                                CATTGGAC TTGCT  GTT
                                |||||||| |||||  |||
                                GTAACCTG GACGA  CAG
                                     C    CA
GAM162  FLJ11175  3'  GACTTTGGACAGCAGCACCCAA 37135      ACA    AAGTT
           T                     ATTGG   TTGCT    GGGTC
                                |||||   |||||    |||||
                                TAACC   GACGA    TTCAG
                                   CAC    CAGGT
GAM162  KIAA0022  3'  AACTACAATGTCCAATG     29657          CTA
                                CATTGGACATTG   AGTT
                                ||||||||||||   ||||
                                GTAACCTGTAAC   TCAA
                                       A__
GAM162  STIP-1    3'  ACCCAACTCACAGCCCTATG   69661     T  ACATT   A__
                                CAT GG    GCT   AGTTGGGT
                                ||| ||    |||   ||||||||
                                GTA CC    CGA   TCAACCCA
                                  T _____   CAC
GAM163  ADH1B     3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                   A    T__
GAM163  AHR       3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM163  FDFT1     3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM163  JTB       3'  ATCTCAGACAGTGAAAGTGAAA 21959
           TG                     CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
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                                GTAAAGTGAAAGTGACAGACTCTA

GAM163  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM163  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM163  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM163  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM163  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_   CG_
GAM163  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM163  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                |||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM163  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                 ||||||        |||||||||
                                 GTAAAG        CAGACTCTA
                                    AAACATTT_
GAM163  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                    C__
GAM163  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
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                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM163  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM163  NIR3     3'  GCAGTGAAAGTGCAAT      66242      T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM163  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598         CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM163  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM163  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__   TT
GAM163  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM163  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                      AAAGG
GAM163  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC       CTGTCTGAGAT
                                ||||       ||||||||||||
                                AAAG       GACAGACTCTA
                                  GTTTGCC
GAM163  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM163  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
```

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                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM163  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM164  ADAMTS8   5'  TCGGGCCGCCAGCACCTG    22886    _     ATAAG
                                CAG TGCTGGC    CTGA
                                ||| |||||||    ||||
                                GTC ACGACCG    GGCT
                                  C      CCG__
GAM164  BAP1      3'  TCAGGGACCCAGCACTGG    16219          CATAAG
                                CCAGTGCTGG     CTGA
                                ||||||||||     ||||
                                GGTCACGACC     GACT
                                      CAGG__
GAM164  BF        5'  TTCAGCTTGGACACTG      8140       CTGGCA
                                CAGTG     TAAGCTGAA
                                |||||     |||||||||
                                GTCAC     GTTCGACTT
                                   AG____
GAM164  C1QB      3'  TTCAACTCTGTGTCCCAGCACT 4923    A        __   _ C
           GGC                    G CCAGTGCTGG  CATA AG TGAA
                                | ||||||||||  |||| || ||||
                                C GGTCACGACC  GTGT TC ACTT
                                _        CT    C  A
GAM164  CHC1      3'  CAGCCCTGAGCACTGTGTC    7020     _     __ CATAA
                                GAC CAGTGCT  GG    GCTG
                                ||| |||||||  ||    ||||
                                CTG GTCACGA  CC    CGAC
                                  T      GT _____
GAM164  CMRF35    5'  CAGAGCTGTCAGCACCGG    21929    A       TAAG
                                CC GTGCTGGCA    CTG
                                || |||||||||    |||
                                GG CACGACTGT    GAC
                                 C        CGA_
GAM164  EPHB6     3'  TCAGCCCTGGACACTGGTC    15466        _ TG CATAA
                                GACCAGTG C  G    GCTGA
                                |||||||| |  |    |||||
                                CTGGTCAC G  C    CGACT
                                     A GT C____
GAM164  EVPL      5'  CAGCCTGAGCCAGCACT     8803          A  A
                                AGTGCTGGC TA GCTG
                                ||||||||| || ||||
                                TCACGACCG GT CGAC
                                      A  C
GAM164  GARP      3'  CAGCCCAGCACTGG        18594          CATAA
                                CCAGTGCTGG    GCTG
                                ||||||||||    ||||
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                                GGTCACGACC    CGAC
                                      _____
GAM164  GJB5    3'  CAGCTCGACGGCACTGG     17945        GCATA
                                CCAGTGCTG    AGCTG
                                |||||||||    |||||
                                GGTCACGGC    TCGAC
                                     AGC__
GAM164  GPR81   3'  CTTACCAGCATTAGTC     50757    C      CA
                                GAC AGTGCTGG  TAAG
                                ||| ||||||||  ||||
                                CTG TTACGACC  ATTC
                                  A      __
GAM164  IFI16   5'  AGCAAGCCAGCACTAGTC    71221    C       ATAA
                                GAC AGTGCTGGC   GCT
                                ||| |||||||||   |||
                                CTG TCACGACCG   CGA
                                  A       AA__
GAM164  KRT4    3'  CAGCTGGGCCCAGCACTGGT  9635          _ ATA
                                ACCAGTGCTGG C   AGCTG
                                |||||||||||  |  |||||
                                TGGTCACGACC G   TCGAC
                                      C GG_
GAM164  MAP3K9  3'  TTCAGCTTCCCAAACACCAGT  60709   CA  C_  CAT
                                AC  GTG  TGG   AAGCTGAA
                                ||  |||  |||   ||||||||
                                TG  CAC  ACC   TTCGACTT
                                 AC   AA   C__
GAM164  MGAT5   5'  TCAGCTTACAGTTCCTG    10028    T_   GCA
                                CAG  GCTG   TAAGCTGA
                                |||  ||||   ||||||||
                                GTC  TGAC   ATTCGACT
                                  CT   ____
GAM164  MOCS1   3'  TTCAGCTTAACAGTTGCCCGGT 92037     A_  _   GCA
            C                    GACC  GTG CTG   TAAGCTGAA
                                ||||  ||| |||   |||||||||
                                CTGG  CGT GAC   ATTCGACTT
                                   CC   T   A__
GAM164  P23     3'  TCAGCTTATACCCGGGCT    21719    G   C_
                                AGT CTGG  ATAAGCTGA
                                ||| ||||  |||||||||
                                TCG GGCC  TATTCGACT
                                  _    CA
GAM164  PFKFB4  3'  TCAGCCACATGCAACACTGTGT 15874    _    CTG   AA_
            C                    GAC CAGTG   GCAT   GCTGA
                                ||| |||||   ||||   |||||
                                CTG GTCAC   CGTA   CGACT
                                  T    AA_    CAC
GAM164  PTPRK   3'  TTCAGCCTGTGGCCCAGCACTG 11125          __   A
            GTC                    GACCAGTGCTGG  CATA GCTGAA
                                ||||||||||||  |||| ||||||
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                                CTGGTCACGACC  GTGT CGACTT
                                      CG    C
GAM164  RNPEPL1   3'  CGGATGCCAGCACCTG     36676     _       AAG
                                CAG TGCTGGCAT   CTG
                                ||| |||||||||   |||
                                GTC ACGACCGTA   GGC
                                  C       ___
GAM164  UBE2L3    3'  TCAGCCCTGGCACTGGC     12507    A      TG CATAA
                                G CCAGTGC  G    GCTGA
                                | |||||||  |    |||||
                                C GGTCACG  C    CGACT
                                 _      GT C____
GAM164  APXL2     5'  CAGCCTCAGCACTCATC     75185    CC       CATAA
                                GA  AGTGCTGG    GCTG
                                ||  ||||||||    ||||
                                CT  TCACGACT    CGAC
                                  AC       C____
GAM164  ARHGEF9   3'  TTCAGCTTACCAAGCA      30824     _  CA
                                TGCT GG  TAAGCTGAA
                                |||| ||  |||||||||
                                ACGA CC  ATTCGACTT
                                  A  __
GAM164  CEGP1     3'  TTCAGCTTCCTCTAGCCCGG   40589    AGT    CAT
                                CC   GCTGG   AAGCTGAA
                                ||   |||||   ||||||||
                                GG   CGATC   TTCGACTT
                                 CC_    TCC
GAM164  DKFZp547D155 3'  CAGCCCTGAGACCACTGGTC   70435        CTGG  TAA
                                GACCAGTG    CA   GCTG
                                ||||||||    ||   ||||
                                CTGGTCAC    GT   CGAC
                                     CAGA  CC_
GAM164  DKFZP727G051 3'  TTCAGCCCATCAACCAGCATTG 69483           CATAA__
           GTC                    GACCAGTGCTGG      GCTGAA
                                ||||||||||||      ||||||
                                CTGGTTACGACC      CGACTT
                                      AACTACC
GAM164  DUSP14    5'  CACTGTCACCAGCACTGCTC   22834    C       CATA  C
                                GA CAGTGCTGG    AG TG
                                || |||||||||    || ||
                                CT GTCACGACC    TC AC
                                 C       ACTG  _
GAM164  FLJ10206  5'  CAGCTTATGCCAGGAGTC    35898     CAGTG
                                GAC    CTGGCATAAGCTG
                                |||    |||||||||||||
                                CTG    GACCGTATTCGAC
                                  AG___
GAM164  FLJ20967  5'  GGCGCCCAGCACTGGTT     41962           CATAA
                                GACCAGTGCTGG    GCT
                                ||||||||||||    |||
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                                TTGGTCACGACC    CGG
                                      CG___
GAM164  FLJ22569  3'  TTCAGCTTACTAAACTG    43679     GC  CA
                                CAGT  TGG  TAAGCTGAA
                                ||||  |||  |||||||||
                                GTCA  ATC  ATTCGACTT
                                  A_  __
GAM164  FOXN4     3'  TTCAGCTTGGACACACTGG   75574       C  GCA
                                CCAGTG TG   TAAGCTGAA
                                |||||| ||   |||||||||
                                GGTCAC AC   GTTCGACTT
                                   _ AG_
GAM164  GW112     3'  TTCAACTGAAGCCAGCACTGGT 21194           ATA  C
           T                     GACCAGTGCTGGC   AG TGAA
                                ||||||||||||   || ||||
                                TTGGTCACGACCG   TC ACTT
                                      AAG  A
GAM164  HOOK2     3'  CAGCTCACATGGCGCCCAGCAC 25256         _____  A__
           TGG                    CCAGTGCTGG    CAT   AGCTG
                                ||||||||||    |||  |||||
                                GGTCACGACC    GTA   TCGAC
                                     CGCG   CAC
GAM164  jdp2      3'  TTCAGCACAGCCAGCAT     55327        ATAA
                                GTGCTGGC    GCTGAA
                                ||||||||    ||||||
                                TACGACCG    CGACTT
                                    ACA_
GAM164  KIAA0767  3'  TCTGCTGCCAGCACAGG     60632    A       TAA  T
                                CC GTGCTGGCA   GC GA
                                || |||||||||   || ||
                                GG CACGACCGT   CG CT
                                 A        ___  T
GAM164  KIAA0923  3'  TCAGCTTGATGCATGGTC    25838      G   TGGCA
                                GACCA TGC     TAAGCTGA
                                ||||| |||     ||||||||
                                CTGGT ACG     GTTCGACT
                                   _   TA___
GAM164  KIAA0982  3'  TTCACTGTTTGCCAGCAC    25852         TA_  C
                                GTGCTGGCA   AG TGAA
                                |||||||||   || ||||
                                CACGACCGT   TC ACTT
                                     TTG  _
GAM164  KIAA1000  3'  TTCAGCTTTGCAAAGTACTGG  65281         G_   T
                                CCAGTGCT  GCA AAGCTGAA
                                ||||||||  ||| ||||||||
                                GGTCATGA  CGT TTCGACTT
                                     AA  _
GAM164  MAP3K3    3'  TCAGCCTGGGCGCTGGTC    9999          GG  TAA
                                GACCAGTGCT  CA   GCTGA
                                ||||||||||  ||   |||||
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                                CTGGTCGCGG  GT   CGACT
                                      __  C__
GAM164  MGC16037  5'  CTTGTCCAGCACTAGTC     51821     C       C
                                GAC AGTGCTGG ATAAG
                                ||| |||||||| |||||
                                CTG TCACGACC TGTTC
                                  A       _
GAM164  MIDORI    3'  TCAGCTTATCCTGCAACT    73792     _  T  C
                                AGT GC GG ATAAGCTGA
                                ||| || || |||||||||
                                TCA CG CC TATTCGACT
                                  A  T  _
GAM164  MtFMT     5'  CAGTGGCGAGCACTGG      57651        G  ATAA
                                CCAGTGCT GC    GCTG
                                |||||||| ||    ||||
                                GGTCACGA CG    TGAC
                                     G  G___
GAM164  PCDH16    5'  TCAGTTCCAACCACTGG     72826       C_  CATA
                                CCAGTG  TGG    AGCTGA
                                ||||||  |||    ||||||
                                GGTCAC  ACC    TTGACT
                                   CA  _____
GAM164  QKI       3'  CAGCTTATCAACTCGTC     65439     C   GCTGGC
                                GAC AGT      ATAAGCTG
                                ||| |||      ||||||||
                                CTG TCA      TATTCGAC
                                  C   AC_____
GAM164  TNRC6     3'  CAACTTTTAGCACTG       70506         CAT   C
                                CAGTGCTGG   AAG TG
                                |||||||||   ||| ||
                                GTCACGATT   TTC AC
                                      ___   A
GAM164  TOB2      3'  CAGCCCAGGCCAGCACTG    95618          ATAA
                                CAGTGCTGGC    GCTG
                                ||||||||||    ||||
                                GTCACGACCG    CGAC
                                      GACC
GAM164  TU12B1-TY 3'  TCAGCCCACAGCACTGTC    33406     C      GCATAA
                                GAC AGTGCTG     GCTGA
                                ||| |||||||     |||||
                                CTG TCACGAC     CGACT
                                  _      ACC____
GAM164  TUSP      3'  TCAGCCTAAGAGCGCAGCACTG 39641         _  A__  A
                                CAGTGCTG GC   TA GCTGA
                                |||||||| ||   || |||||
                                GTCACGAC CG   AT CGACT
                                     G  AGA  C
GAM164  USP19     3'  TCAGCTTATGCATCTGGT    88959       TGCTG
                                ACCAG    GCATAAGCTGA
                                |||||    ||||||||||
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                                TGGTC    CGTATTCGACT
                                  TA___
GAM164  ZD52F10  3'  CAGCCTGTGCCAGCCCTGG   52819     T       A
                                CCAG GCTGGCATA GCTG
                                |||| ||||||||| ||||
                                GGTC CGACCGTGT CGAC
                                  C       C
GAM164  LOC145268 3'  TCAGCTTACAAGAGCCACTG  77062     _ GGCA
                                CAGTG CT   TAAGCTGA
                                ||||| ||   ||||||||
                                GTCAC GA   ATTCGACT
                                  C  GAAC
GAM164  LOC149296 5'  CAGCTTATGGGCAGCA     79256      G_
                                TGCTG  CATAAGCTG
                                |||||  |||||||||
                                ACGAC  GTATTCGAC
                                  GG
GAM164  LOC161877 5'  TCAGGGCAGGCCAGCGCTGG  82326          ATAAG
                                CCAGTGCTGGC    CTGA
                                ||||||||||    ||||
                                GGTCGCGACCG    GACT
                                     GACGG
GAM164  LOC163115 5'  TCAGCCCCTGACAGCACTGG  82413        G  TAA
                                CCAGTGCTG CA   GCTGA
                                |||||||| ||   |||||
                                GGTCACGAC GT   CGACT
                                     A  CCC
GAM164  LOC196500 3'  TCAGCTCACTCAGTGGTC    87744     AGT    CATA
                                GACC   GCTGG    AGCTGA
                                ||||   |||||    ||||||
                                CTGG   TGACT    TCGACT
                                  ___    CAC_
GAM164  LOC197287 3'  TCAGCTCATGTGTTTTGCACTG 60865       T_    __
                                CAGTGC  GGCATA  AGCTGA
                                ||||||  ||||||  ||||||
                                GTCACG  TTGTGT  TCGACT
                                   TT     AC
GAM164  LOC200470 5'  TCAGCCTGCGGCGCTGG     90069        G  TAA
                                CCAGTGCTG CA   GCTGA
                                |||||||| ||   |||||
                                GGTCGCGGC GT   CGACT
                                     _ C__
GAM164  LOC221584 3'  CAGCTTATGTGGCAC       93828       G
                                GTGCTG CATAAGCTG
                                |||||| |||||||||
                                CACGGT GTATTCGAC
                                  _
GAM164  LOC51716  3'  CAGCTCATGGCCCTAGCA    32787       ___  A
                                TGCTGG   CAT AGCTG
                                ||||||   ||| |||||
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                                ACGATC   GTA TCGAC
                                   CCG   C
GAM164  LOC92196  5'  CAGAGCACCAGCACTGGC    68456   A       CATAAG
                                G CCAGTGCTGG     CTG
                                | ||||||||||     |||
                                C GGTCACGACC     GAC
                                _       ACGA__
GAM165  CSNK1D    5'  CCCGGAAGATCCGAGTCCATCC 8549        G  CTC     A
                                GGATGGAC CG   TCTTCC GG
                                |||||||| ||   |||||| ||
                                CCTACCTG GC   AGAAGG CC
                                     A  CT_     C
GAM165  CSNK1D    5'  CCCGGAAGATCCGAGTCCATCC 57405       G  CTC     A
                                GGATGGAC CG   TCTTCC GG
                                |||||||| ||   |||||| ||
                                CCTACCTG GC   AGAAGG CC
                                     A  CT_     C
GAM165  MATN1     5'  CCTGGAAGAGCCACCCCCCACC 9919     A   ACGCGCT
              CA                  TGG TGG      CTCTTCCAGG
                                ||| |||      ||||||||||
                                ACC ACC      GAGAAGGTCC
                                  C   CCCCACC
GAM165  TMPRSS3   3'  GAAAGAGGCACCCTTCCA    43795     T  AC  G    C
                                TGGA GG  GC CTCT TTC
                                |||| ||  || |||| |||
                                ACCT CC  CG GAGA AAG
                                  T  CA  _    _
GAM165  TMPRSS3   3'  GAAAGAGGCACCCTTCCA    50506     T  AC  G    C
                                TGGA GG  GC CTCT TTC
                                |||| ||  || |||| |||
                                ACCT CC  CG GAGA AAG
                                  T  CA  _    _
GAM165  TMPRSS3   3'  GAAAGAGGCACCCTTCCA    50527     T  AC  G    C
                                TGGA GG  GC CTCT TTC
                                |||| ||  || |||| |||
                                ACCT CC  CG GAGA AAG
                                  T  CA  _    _
GAM165  CARD9     3'  CTGGAAGATGGCTCACCCA    42286     A   ACGC   C
                                TGG TGG    GCT TCTTCCAG
                                ||| |||    ||| ||||||||
                                ACC ACT    CGG AGAAGGTC
                                  C   _____   T
GAM165  FLJ12572  3'  CCCGGAAGAGAGCCCTCACCA  43249     A   ACGC        A
                                TGG TGG    GCTCTCTTCC GG
                                ||| |||    |||||||||| ||
                                ACC ACT    CGAGAGAAGG CC
                                  _   CC__         C
GAM165  PMX2B     3'  CTGAAAGATGCCCTATCCA    14082       AC   CTC    C
                                TGGATGG  GCG   TCTT CAG
                                |||||||  |||   |||| |||
```

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                                ACCTATC  CGT   AGAA GTC
                                   C_  ___   A
GAM165  LOC149837 5'  CTGGAAGAATCCCATGCA    84733    G   ACGCGCTC
                                TG ATGG       TCTTCCAG
                                || ||||       ||||||||
                                AC TACC       AGAAGGTC
                                 G   CTA_____
GAM165  LOC152348 3'  CTGGAAGAGAGCCTCACCA    85693    A   ACGC
                                TGG TGG    GCTCTCTTCCAG
                                ||| |||    ||||||||||||
                                ACC ACT    CGAGAGAAGGTC
                                  _  C___
GAM165  LOC90835  5'  CTGGAAGAGAGGGCGCCCA    64128    A   G
                                TGG CGC CTCTCTTCCAG
                                ||| ||| ||||||||||
                                ACC GCG GAGAGAAGGTC
                                  C   G
GAM165  LOC91748  3'  GAAGAGAGTCCCCA       67055    AT    GCGC
                                TGG  GGAC    TCTCTTC
                                |||  ||||    |||||||
                                ACC  CCTG    AGAGAAG
                                  __   _____
GAM165  LOC92080  3'  CCTGTGAGGGAGGGCACCCACC 68046    A   AC  G     TC
           CA                     TGG TGG  GC CTCTCT  CAGG
                                ||| |||  || ||||||  ||||
                                ACC ACC  CG GAGGGA  GTCC
                                  C   CA  G     GT
GAM166  ABCC4    5'  TGCTTGAGGTCCAGG      19575         G
                                CCTGGACCT CAAGTG
                                ||||||||| ||||||
                                GGACCTGGA GTTCGT
                                     _
GAM166  ALPI     3'  AGGTCACCAGATCCAAGG    7895    C   C   CAA   TTA
                                CC TGGA CTG   GTG   CT
                                || |||| |||   |||   ||
                                GG ACCT GAC   CAC   GA
                                 A   A  ___   TG_
GAM166  BCL11B   3'  CAGTTTCCTACCTGCAGATCCA 43185        C    A   TT__
           GGGG                    CCCCTGGA CTGCA GTG   ACTG
                                ||||||| ||||| |||   ||||
                                GGGGACCT GACGT CAT    TGAC
                                    A    C   CCTT
GAM166  CUTL1    3'  CAGGCCCGCTAGGTCCAG    8590         GCA   TTA
                                CTGGACCT   AGTG   CTG
                                ||||||||   ||||   |||
                                GACCTGGA   TCGC   GAC
                                    ___    CCG
GAM166  CYLN2    3'  TAAAGCTTGTGACAGGTCCAGG 12637          ___    G
                                CCTGGACCTG   CAAGT TTA
                                ||||||||||   ||||| |||
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                                GGACCTGGAC  GTTCG AAT
                                     AGT    A
GAM166  DIA1    3'  GCTGCAGGTCCCAGGG     23646      _     A
                                CCCTGG ACCTGCA GT
                                |||||| ||||||| ||
                                GGGACC TGGACGT CG
                                   C     _
GAM166  GBA     3'  AGCGACGTAAGCCCAGGGG   76336      ACCT  AAG   TA
                                CCCCTGG   GC   TGT  CT
                                |||||||   ||   |||  ||
                                GGGGACC   CG   GCA  GA
                                   ____ AAT   GC
GAM166  GDF5    3'  GGCACAGGTCCAGGG      5108         GCAA
                                CCCTGGACCT   GTGTT
                                ||||||||||   |||||
                                GGGACCTGGA   CACGG
                                     ____
GAM166  GNB3    3'  AGCCCTTTGCAGGCCCAG   9073      A     _ T
                                CTGG CCTGCAA G GTT
                                |||| ||||||| | |||
                                GACC GGACGTT C CGA
                                  C      T C
GAM166  MARK1   3'  ATTTACAGGTTCAGGG     37843         C
                                CCCTGGACCTG AAGT
                                |||||||||| ||||
                                GGGACTTGGAC TTTA
                                     A
GAM166  NUDT2   3'  CACCCTCAGGTCCAGGG    6743          CAA
                                CCCTGGACCTG  GTG
                                ||||||||||  |||
                                GGGACCTGGAC  CAC
                                     TCC
GAM166  PIK3R3  3'  CAGTAAATCACAGACCCAGGGG 61054       AC  CAAGTG
                                CCCCTGG  CTG    TTACTG
                                |||||||  |||    ||||||
                                GGGGACC  GAC    AATGAC
                                   CA  ACTA__
GAM166  POU2F2  3'  GACCCCTGGAGGTCCAGGGG  10690         G  AGT
                                CCCCTGGACCT CA  GTT
                                |||||||||| ||  |||
                                GGGGACCTGGA GT  CAG
                                     G  CCC
GAM166  SERPINB5 3' CAGGCTACTATAGGTCCAG   10548       CA   TTA
                                CTGGACCTG  AGTG  CTG
                                |||||||||  ||||  |||
                                GACCTGGAT  TCAT  GAC
                                   A_   CG_
GAM166  SOST    3'  TGGCCTTGCAGGCCCGAGGG  47471     _  A     T
                                CCCT GG CCTGCAAG GTTA
                                |||| || |||||||| ||||
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                                GGGA CC GGACGTTC CGGT
                                  G C      _
GAM166  USP6    5' GATAGTTTGCAGGCACAGG   91146     GA      _
                                CCTG  CCTGCAAG TGTT
                                ||||  |||||||| ||||
                                GGAC  GGACGTTT ATAG
                                  AC       G
GAM166  BICD2   3' TACTTGCAAATTCAGGGG    70401       CC
                                CCCCTGGA  TGCAAGTG
                                ||||||||  ||||||||
                                GGGGACTT  ACGTTCAT
                                     AA
GAM166  BOP     5' TGAGGTCTTAAAGTCCAGGG  85054       C GC  _ G
                                CCCTGGAC T  AAG T TTA
                                |||||||| |  ||| | |||
                                GGGACCTG A  TTC G AGT
                                     _ AA   T G
GAM166  EIF2C2  3' AGCATTTCCAGGTCCAG    71945       C
                                CTGGACCTG AAGTGTT
                                ||||||||| |||||||
                                GACCTGGAC TTTACGA
                                     C
GAM166  FAM8A1  5' CAGTAACAAGTATCCCAGAGG 32722   _   ACC   AAG
                                CC CTGG   TGC   TGTTACTG
                                || ||||   |||   ||||||||
                                GG GACC   ATG   ACAATGAC
                                 A   CT_   A__
GAM166  FLJ10520 3' TAACACTTGTGTTCCAGG   36214      CCT
                                CCTGGA   GCAAGTGTTA
                                ||||||   ||||||||||
                                GGACCT   TGTTCACAAT
                                   TG_
GAM166  FLJ12768 3' GGTGGCCCAGATCCAGGGG  47185       C   CAAGT
                                CCCCTGGA CTG    GTTACT
                                |||||||| |||    ||||||
                                GGGGACCT GAC    CGGTGG
                                     A   C____
GAM166  FLJ14117 3' CGGATCACAAGGTCCAG    42905       GCAA   TTA
                                CTGGACCT   GTG   CTG
                                ||||||||   |||   |||
                                GACCTGGA   CAC   GGC
                                     A___   TA_
GAM166  FLJ20208 5' AACAGAAGCAGGTCCGAGG  34737    _      AAG
                                CCT GGACCTGC   TGTT
                                ||| ||||||||   ||||
                                GGA CCTGGACG   ACAA
                                  G       AAG
GAM166  FLJ22582 3' CAGCAACAGCAGCAGATCCA  46778     C   AAG   A
                                TGGA CTGC   TGTT CTG
                                |||| ||||   |||| |||
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                                ACCT GACG   ACAA GAC
                                  A   ACG   C
GAM166  GRAP     3' AGGAACTGAGGTCCAG     21741        G  A  GTTA
                                CTGGACCT CA GT   CT
                                |||||||| || ||   ||
                                GACCTGGA GT CA   GA
                                    _ _ AG__
GAM166  KIAA0444 3' CACTTGAGGCCCAAGG     62336    C   A   G
                                CC TGG CCT CAAGTG
                                || ||| ||| ||||||
                                GG ACC GGA GTTCAC
                                 A   C   _
GAM166  KIAA0542 3' AGCAGCAGGTCCAGG      66079          AAG
                                CCTGGACCTGC   TGTT
                                ||||||||||   ||||
                                GGACCTGGACG   ACGA

                                    ___
GAM166  KIAA0542 3' AGCAGCTGCAGGCCCAG     66080     A     AG
                                CTGG CCTGCA  TGTT
                                |||| ||||||  ||||
                                GACC GGACGT  ACGA
                                  C     CG
GAM166  KIAA0993 3' CAGAACACACAAATCCAGGGG  64139        CC  CAA    A
                                CCCCTGGA  TG   GTGTT CTG
                                ||||||||  ||   ||||| |||
                                GGGGACCT  AC   CACAA GAC
                                    AA  A__    _
GAM166  KIAA1202 3' AGCAGCAAGTTCAGGGG     72016         C   AAG
                                CCCCTGGAC TGC   TGTT
                                |||||||| |||   ||||
                                GGGGACTTG ACG   ACGA
                                    A   ___
GAM166  KIAA1464 3' CAGAGAACTACAGGGCCAAGGG 68261     C   A    CA   GTTA
                                CCC TGG CCTG  AGT    CTG
                                ||| ||| ||||  |||    |||
                                GGG ACC GGAC  TCA    GAC
                                  A   G    A_   AGA_
GAM166  MAP3K3   3' TGGCACCGAAGCCCAGAGG    10000    _    AC  GCAA
                                CC CTGG  CT    GTGTTA
                                || ||||  ||    ||||||
                                GG GACC  GA    CACGGT
                                 A    C_  AGC_
GAM166  MGC12466 5' TGGGACCTGCAGGTCCCGG    52632    T       A  G
                                CC GGACCTGCA GT TTA
                                || ||||||||| || |||
                                GG CCTGGACGT CA GGT
                                 C        C  G
GAM166  OSR2     3' CACCTGCAGCTCCAGGG     53804        C     A
                                CCCTGGA CTGCA GTG
                                ||||||| ||||| |||
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                                GGGACCT GACGT CAC
                                    C     C
GAM166   LOC115399 3'  GACCTGCAGTCCAGGGG     73431          C    A T
                                CCCCTGGAC TGCA G GTT
                                ||||||||| |||| | |||
                                GGGGACCTG ACGT C CAG
                                          _    _ _
GAM166   LOC147174 3'  GCTGTCCCAGATCCAGGGG   64769          C   CA__
                                CCCCTGGA CTG    AGT
                                |||||||| |||    |||
                                GGGGACCT GAC    TCG
                                    A   CCTG
GAM166   LOC147515 3'  AGCAGCAAGTCTAGGGG     84018          C   AAG
                                CCCCTGGAC TGC   TGTT
                                ||||||||| |||   ||||
                                GGGGATCTG ACG   ACGA
                                     A  ____
GAM166   LOC148938 5'  CATCACAGGTCCAGAGG     84268    _       CAA
                                CC CTGGACCTG   GTG
                                || |||||||||   |||
                                GG GACCTGGAC   TAC
                                 A        AC_
GAM166   LOC149271 3'  AGTGATTGCTGGTCCAGGG   79237          T   AGT
                                CCCTGGACC GCA   GTTACT
                                ||||||||| |||   ||||||
                                GGGACCTGG CGT   TAGTGA
                                     T  ____
GAM166   LOC149995 3'  AGCAGCAAGTCTAGGGG     84840          C   AAG
                                CCCCTGGAC TGC   TGTT
                                ||||||||| |||   ||||
                                GGGGATCTG ACG   ACGA
                                     A  ____
GAM166   LOC154790 5'  CACCATCGCAGGTCCAGGGG   81147            AA__
                                CCCCTGGACCTGC    GTG
                                ||||||||||||    |||
                                GGGGACCTGGACG    CAC
                                      CTAC
GAM166   LOC157349 5'  GCTGAGGTCCAGGG         81415          G  A
                                CCCTGGACCT CA GT
                                |||||||||| || ||
                                GGGACCTGGA GT CG
                                          _  _
GAM166   LOC201931 5'  GAGGCTTACAGGTCCAGG     89112          C   G
                                CCTGGACCTG AAGT TT
                                |||||||||| |||| ||
                                GGACCTGGAC TTCG AG
                                     A   G
GAM166   LOC256112 3'  CAGAGAACACATCCAGGGG   96363          CCTGCAA    A_
                                CCCCTGGA      GTGTT  CTG
                                ||||||||      |||||  |||
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                                GGGGACCT      CACAA  GAC
                                   A_______    GA
GAM166  LOC256158 5'  CACCTGCAGGTCCAGG      97649          A
                                CCTGGACCTGCA GTG
                                |||||||||||| |||
                                GGACCTGGACGT CAC
                                   C
GAM166  LOC256218 3'  GCTGTCCCAGATCCAGGGG   95194        C   CA__
                                CCCCTGGA CTG    AGT
                                |||||||| |||    |||
                                GGGGACCT GAC    TCG
                                   A   CCTG
GAM166  LOC256228 5'  AGCAAGCAGGTCCAGG      96234          AAG
                                CCTGGACCTGC   TGTT
                                ||||||||||   ||||
                                GGACCTGGACG   ACGA
                                   A__
GAM166  LOC91149  3'  AGTCTCTGCAGGTCAGG     65069      G      A TGTT
                                CCTG ACCTGCA G    ACT
                                |||| ||||||| |    |||
                                GGAC TGGACGT C    TGA
                                  _      _ TC__
GAM166  LOC92973  5'  CAGTAACACCTGCTCTTTCT   71037     CCT_   A
                                GGA    GCA GTGTTACTG
                                |||    ||| |||||||||
                                TCT    CGT CACAATGAC
                                  TTCT   C
GAM167  AXL       3'  TCTCACACTCAGTTG       8111       A
                                CAAC TGAGTGTGAGA
                                |||| ||||||||||
                                GTTG ACTCACACTCT
                                  _
GAM167  AXL       3'  TCTCACACTCAGTTG       41608      A
                                CAAC TGAGTGTGAGA
                                |||| ||||||||||
                                GTTG ACTCACACTCT
                                  _
GAM167  MCC       3'  ACTTAGCTCCTGTTGTCATG   9957       GTGTG  A
                                CATGA     AG AGCTAAGT
                                |||||     || ||||||||
                                GTACT     TC TCGATTCA
                                   GTTG_  C
GAM167  MPP5      3'  ACTTAGCTTCCCTTCCCTCATC 42483    C     TGTGA_
          A                      A ATGAG      GAAGCTAAGT
                                | |||||      ||||||||||
                                A TACTC      CTTCGATTCA
                                 C     CCTTCC
GAM167  MS4A7     3'  TTTTCACACTCATATTG     41067     C
                                CAA ATGAGTGTGAGAA
                                ||| ||||||||||||
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                                GTT TACTCACACTTTT
                                  A
GAM167  STAU    3' CTTAGCTTTCACTACACT    33908      A__
                                AGTGTG  GAAGCTAAG
                                ||||||  |||||||||
                                TCACAT  TTTCGATTC
                                   CAC
GAM167  STAU    3' CTTAGCTTTCACTACACT    33895      A__
                                AGTGTG  GAAGCTAAG
                                ||||||  |||||||||
                                TCACAT  TTTCGATTC
                                   CAC
GAM167  STAU    3' CTTAGCTTTCACTACACT    33901      A__
                                AGTGTG  GAAGCTAAG
                                ||||||  |||||||||
                                TCACAT  TTTCGATTC
                                   CAC
GAM167  STAU    3' CTTAGCTTTCACTACACT    16004      A__
                                AGTGTG  GAAGCTAAG
                                ||||||  |||||||||
                                TCACAT  TTTCGATTC
                                   CAC
GAM167  TZFP    5' ACTTACAAACCACACTCAT   26888        AGAAGC
                                ATGAGTGTG    TAAGT
                                |||||||||    |||||
                                TACTCACAC    ATTCA
                                     CAAAC_
GAM167  VNN2    3' ACTCAGCTTCTGCATCAT    54356    G  G     A
                                ATGA TGT AGAAGCT AGT
                                |||| ||| ||||||| |||
                                TACT ACG TCTTCGA TCA
                                  _  _     C
GAM167  VNN2    3' ACTCAGCTTCTGCATCAT    16237    G  G     A
                                ATGA TGT AGAAGCT AGT
                                |||| ||| ||||||| |||
                                TACT ACG TCTTCGA TCA
                                  _  _     C
GAM167  APXL2   5' AGCCTCAGCACTCAT       75184       _   AA
                                ATGAGTG TGAG  GCT
                                ||||||| ||||  |||
                                TACTCAC ACTC  CGA
                                   G   __
GAM167  FKSG87  3' ACTCAGCCTCCCATTCACATGT 49325    __    T  AA  A
                                ACA  TGAGTG GAG  GCT AGT
                                |||  |||||| |||  ||| |||
                                TGT  ACTTAC CTC  CGA TCA
                                  AC     C  __  C
GAM167  FLJ10359 3' ACTCAGAGTTCACACTCAT   36065         AAG  A
                                ATGAGTGTGAG   CT AGT
                                ||||||||||   || |||
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                                TACTCACACTT  GA TCA
                                      GA_  C
GAM167  FLJ12568  3'  GGGATCTCACACCCATGTT   46500      A      AG
                                AACATG GTGTGAGA  CT
                                |||||| ||||||||  ||
                                TTGTAC CACACTCT  GG
                                   C       AG
GAM167  GHITM    3'  ACTCAGCTTCTGGCTTCTCTG  26913    T  T_  G     A
                                CA GAG  GT AGAAGCT AGT
                                || |||  || ||||||| |||
                                GT CTC  CG TCTTCGA TCA
                                 _  TT  G     C
GAM167  KIAA0092  3'  ACTTAGTTGCCACACTCATG  27966        AGA
                                CATGAGTGTG  AGCTAAGT
                                ||||||||||  ||||||||
                                GTACTCACAC  TTGATTCA
                                      CG_
GAM167  KIAA1817  3'  CTTGGGCTCACACTCA     68229        AAG
                                TGAGTGTGAG  CTAAG
                                ||||||||||  |||||
                                ACTCACACTC  GGTTC
                                      G__
GAM167  KSR      5'  AGCTTCCCCACACTCA     64042       A_
                                TGAGTGTG  GAAGCT
                                ||||||||  ||||||
                                ACTCACAC  CTTCGA
                                     CC
GAM167  MGC5528  3'  ACTTAGCTAATGAACTCAT   44042      GTGAGA
                                ATGAGT     AGCTAAGT
                                ||||||     ||||||||
                                TACTCA     TCGATTCA
                                   AGTAA_
GAM167  PRO2037  3'  AGCTTGAGACCTCATGT     37784       T  GAG
                                ACATGAG GT   AAGCT
                                ||||||| ||   |||||
                                TGTACTC CA   TTCGA
                                    _  GAG
GAM167  SHANK3   3'  ACTCGGTCTCACACTCA     65487        AA  TA
                                TGAGTGTGAG  GC  AGT
                                ||||||||||  ||  |||
                                ACTCACACTC  TG  TCA
                                      __  GC
GAM167  LOC116437 3'  TTTCCACTCATGCTG      73894    A      T
                                CA CATGAGTG GAGA
                                || |||||||| ||||
                                GT GTACTCAC CTTT
                                 C       _
GAM167  LOC146909 3'  ACTCAGCTTCTTGGCATGT   78161      AGTGT      A
                                ACATG    GAGAAGCT AGT
                                |||||    |||||||| |||
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                                TGTAC     TTCTTCGA TCA
                                   GG___       C
GAM167   LOC147093 5'  CTCTTCACCTCATGCTG     83943    A     T   GA
                                CA CATGAG GTGA  AG
                                || |||||| ||||  ||
                                GT GTACTC CACT  TC
                                 C     _    TC
GAM167   LOC154386 3'  AGCTCTCACACTCATTTG    81080     C          A
                                CAA ATGAGTGTGAGA GCT
                                ||| |||||||||||| |||
                                GTT TACTCACACTCT CGA
                                  _          _
GAM167   LOC159121 5'  AGCCACACCATGTCA       86989    A    A    AGAA
                                C ACATG GTGTG    GCT
                                | ||||| |||||    |||
                                A TGTAC CACAC    CGA
                                 C    _    _____
GAM168   PPAT     3'  AGGAAAATAATACTGTGA     10694            C
                                TCACAGTGTTATT TTCT
                                |||||||||||| ||||
                                AGTGTCATAATAA AGGA
                                        A
GAM168   PROC     3'  ATGAAAAAGAATAAAAAACAC  4341       ____      C
                                GTGT    TATTCTT TTCAT
                                ||||    ||||||| |||||
                                CACA    ATAAGAA AAGTA
                                   AAAA       A
GAM168   BIRC3    3'  GAAAAAGAGGTAGCACT      67197         _    C
                                AGTGTTAT TCTT TTC
                                |||||||| |||| |||
                                TCACGATG AGAA AAG
                                     G    A
GAM168   DDX21    5'  AAGGGGAGACACTGCGA      16383    A      AT
                                TC CAGTGTT  TCTTCTT
                                || |||||||  |||||||
                                AG GTCACAG  AGGGGAA
                                 C      __
GAM168   DDX32    3'  AGAAAATAACACTGTG       36417            C
                                CACAGTGTTATT TTCT
                                |||||||||||| ||||
                                GTGTCACAATAA AAGA
                                              _
GAM168   DKK4     3'  AAGAAGAATCCACATTG      27012        T_
                                CAGTGT  ATTCTTCTT
                                ||||||  |||||||||
                                GTTACA  TAAGAAGAA
                                    CC
GAM168   EFA6R    3'  AGAATAACCCCGTGATA      30977        AGT
                                TATCAC   GTTATTCT
                                ||||||   ||||||||
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                                ATAGTG   CAATAAGA
                                   CCC
GAM168  FLJ22746  3'  ATGAAGAAGAATTCTTTAT   45551     TT__
                                GTG    ATTCTTCTTCAT
                                |||    ||||||||||||
                                TAT    TAAGAAGAAGTA
                                  TTCT
GAM168  FLJ23053  3'  ATGAAGTTTTTTTAACATTGT  43261         TTCTT_
                                ACAGTGTTA     CTTCAT
                                |||||||||     ||||||
                                TGTTACAAT     GAAGTA
                                      TTTTTT
GAM168  HBXAP     5'  AAGAAGAATTGACAGATA    33416     ACAG    _
                                TATC    TGTTA TTCTTCTT
                                ||||    ||||| ||||||||
                                ATAG    ACAGT AAGAAGAA
                                  _____    T
GAM168  KIAA0970  3'  GAAGAAAAGCTTCTTTGATA   29959      C  T_   A
                                TATCA AG  GTT TTCTTC
                                ||||| ||  ||| ||||||
                                ATAGT TC  CGA AAGAAG
                                   T  TT   A
GAM168  KIAA1018  3'  GGCAGAATAACACCGTG     30352     A        T
                                CAC GTGTTATTCT CT
                                ||| |||||||||| ||
                                GTG CACAATAAGA GG
                                  C         C
GAM168  PLAC3     3'  ATGAAGAAGAACAATCATG    69342    GT   A
                                CA  GTT TTCTTCTTCAT
                                ||  ||| ||||||||||||
                                GT  TAA AAGAAGAAGTA
                                 AC   C
GAM168  RASGRF2   3'  TGAAAAAGACCTGTGATG    61043        T TTAT    C
                                TATCACAG G    TCTT TTCA
                                |||||||| |    |||| ||||
                                GTAGTGTC C    AGAA AAGT
                                    _ _____    A
GAM168  TGOLN2    3'  ATGAAGAAAAAAGTACTGTGA  64046          A  C
                                TCACAGTGTT TT TTCTTCAT
                                |||||||||| || ||||||||
                                AGTGTCATGA AA AAGAAGTA
                                      _  A
GAM168  ZDHHC7    3'  GAAGAAAAACAGTGA       34839      AG    A
                                TCAC  TGTT TTCTTC
                                ||||  |||| ||||||
                                AGTG  ACAA AAGAAG
                                   __    A
GAM168  LOC124145 3'  GAAGAAAAACATTTAATGATA  74254       C__     A
                                TATCA   AGTGTT TTCTTC
                                |||||   |||||| ||||||
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                                ATAGT   TTACAA AAGAAG
                                   AAT     A
GAM168  LOC145748 3'  ATGAAGAAAAACAACAC     83463       A  C
                                GTGTT TT TTCTTCAT
                                |||||| || ||||||||
                                CACAA AA AAGAAGTA
                                   C  A
GAM168  LOC148894 3'  AGAAAATAACATTGTAATA    84254     C         C
                                TAT ACAGTGTTATT TTCT
                                ||| |||||||||| ||||
                                ATA TGTTACAATAA AAGA
                                  A         _
GAM168  LOC153020 3'  ATGAAGCTCAACACTGTGGTA  80763           ATTCTT
                                TATCACAGTGTT     CTTCAT
                                ||||||||||||     ||||||
                                ATGGTGTCACAA     GAAGTA
                                       CTC___
GAM168  LOC202309 5'  AAGAATTACACTGTGA      90333         T
                                TCACAGTGT ATTCTT
                                ||||||||| ||||||
                                AGTGTCACA TAAGAA
                                      T
GAM168  LOC219392 5'  ATGAAGAAGAAGCAACCGATA  91131      ACAG   TA
                                TATC    TGT  TTCTTCTTCAT
                                ||||    |||  ||||||||||||
                                ATAG    ACG  AAGAAGAAGTA
                                  CCA_  __
GAM168  LOC222068 3'  TGAAAAAGAATAAGTCAC    92714     __      C
                                GTG  TTATTCTT TTCA
                                |||  |||||||| ||||
                                CAC  AATAAGAA AAGT
                                  TG       A
GAM168  LOC51218  3'  AAGAAACTGTGATA        33104         GTTA
                                TATCACAGT    TTCTT
                                |||||||||    |||||
                                ATAGTGTCA    AAGAA
                                       ____
GAM168  LOC93538  5'  ATGAAGAAAAATAACAGCATGA 72559      CAG      C
           T                     ATCA   TGTTATT TTCTTCAT
                                ||||   ||||||| ||||||||
                                TAGT   ACAATAA AAGAAGTA
                                  ACG      A
GAM169  HCS       3'  ACTAACCACATGTGGCTGT    38455        AG    AAC
                                ACAGCTAT  ATGT   TAGT
                                ||||||||  ||||   ||||
                                TGTCGGTG  TACA   ATCA
                                     __   CCA
GAM169  PCDHA1    3'  TACTAGTTATTACAGCTGTA   38184        A  GAT
                                TACAGCT TA   GTAACTAGTA
                                ||||||| ||   ||||||||||
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                              ATGTCGA AT  TATTGATCAT
                                 C ___
GAM169  PCDHA1   3' TACTAGTTATTACAGCTGTA  48595     A GAT
                              TACAGCT TA  GTAACTAGTA
                              ||||||| ||  ||||||||||
                              ATGTCGA AT  TATTGATCAT
                                 C ___
GAM169  PCDHA10  3' TACTAGTTATTACAGCTGTA  49028     A GAT
                              TACAGCT TA  GTAACTAGTA
                              ||||||| ||  ||||||||||
                              ATGTCGA AT  TATTGATCAT
                                 C ___
GAM169  PCDHA10  3' TACTAGTTATTACAGCTGTA  38192     A GAT
                              TACAGCT TA  GTAACTAGTA
                              ||||||| ||  ||||||||||
                              ATGTCGA AT  TATTGATCAT
                                 C ___
GAM169  PCDHA11  3' TACTAGTTATTACAGCTGTA  38203     A GAT
                              TACAGCT TA  GTAACTAGTA
                              ||||||| ||  ||||||||||
                              ATGTCGA AT  TATTGATCAT
                                 C ___
GAM169  PCDHA12  3' TACTAGTTATTACAGCTGTA  38211     A GAT
                              TACAGCT TA  GTAACTAGTA
                              ||||||| ||  ||||||||||
                              ATGTCGA AT  TATTGATCAT
                                 C ___
GAM169  PCDHA13  3' TACTAGTTATTACAGCTGTA  38220     A GAT
                              TACAGCT TA  GTAACTAGTA
                              ||||||| ||  ||||||||||
                              ATGTCGA AT  TATTGATCAT
                                 C ___
GAM169  PCDHA2   3' TACTAGTTATTACAGCTGTA  38228     A GAT
                              TACAGCT TA  GTAACTAGTA
                              ||||||| ||  ||||||||||
                              ATGTCGA AT  TATTGATCAT
                                 C ___
GAM169  PCDHA3   3' TACTAGTTATTACAGCTGTA  38236     A GAT
                              TACAGCT TA  GTAACTAGTA
                              ||||||| ||  ||||||||||
                              ATGTCGA AT  TATTGATCAT
                                 C ___
GAM169  PCDHA4   3' TACTAGTTATTACAGCTGTA  38244     A GAT
                              TACAGCT TA  GTAACTAGTA
                              ||||||| ||  ||||||||||
                              ATGTCGA AT  TATTGATCAT
                                 C ___
GAM169  PCDHA5   3' TACTAGTTATTACAGCTGTA  38252     A GAT
                              TACAGCT TA  GTAACTAGTA
                              ||||||| ||  ||||||||||
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                                ATGTCGA AT   TATTGATCAT
                                   C ___
GAM169  PCDHA6   3' TACTAGTTATTACAGCTGTA  38260      A  GAT
                                TACAGCT TA   GTAACTAGTA
                                ||||||| ||   ||||||||||
                                ATGTCGA AT   TATTGATCAT
                                   C ___
GAM169  PCDHA6   3' TACTAGTTATTACAGCTGTA  49001      A  GAT
                                TACAGCT TA   GTAACTAGTA
                                ||||||| ||   ||||||||||
                                ATGTCGA AT   TATTGATCAT
                                   C ___
GAM169  PCDHA7   3' TACTAGTTATTACAGCTGTA  38268      A  GAT
                                TACAGCT TA   GTAACTAGTA
                                ||||||| ||   ||||||||||
                                ATGTCGA AT   TATTGATCAT
                                   C ___
GAM169  PCDHA8   3' TACTAGTTATTACAGCTGTA  38276      A  GAT
                                TACAGCT TA   GTAACTAGTA
                                ||||||| ||   ||||||||||
                                ATGTCGA AT   TATTGATCAT
                                   C ___
GAM169  PCDHA9   3' TACTAGTTATTACAGCTGTA  49018      A  GAT
                                TACAGCT TA   GTAACTAGTA
                                ||||||| ||   ||||||||||
                                ATGTCGA AT   TATTGATCAT
                                   C ___
GAM169  PCDHAC1  3' TACTAGTTATTACAGCTGTA  38167      A  GAT
                                TACAGCT TA   GTAACTAGTA
                                ||||||| ||   ||||||||||
                                ATGTCGA AT   TATTGATCAT
                                   C ___
GAM169  PCDHAC2  3' TACTAGTTATTACAGCTGTA  38176      A  GAT
                                TACAGCT TA   GTAACTAGTA
                                ||||||| ||   ||||||||||
                                ATGTCGA AT   TATTGATCAT
                                   C ___
GAM169  PMX1     3' ACTAAAGTCTACATCTAAGCT  22585     A     _  __
                                AGCT TAGATGTA ACT  AGT
                                |||| |||||||| |||  |||
                                TCGA ATCTACAT TGA  TCA
                                   _      C   AA
GAM169  PMX1     3' ACTAAAGTCTACATCTAAGCT  42653     A     _  __
                                AGCT TAGATGTA ACT  AGT
                                |||| |||||||| |||  |||
                                TCGA ATCTACAT TGA  TCA
                                   _      C   AA
GAM169  RGS1     3' ACTGACATCTATGCT      11325     T     AAC
                                AGC ATAGATGT   TAGT
                                ||| ||||||||   ||||
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                                TCG TATCTACA   GTCA
                                  _     ___
GAM169  ZNF266    3'  TTACACTATAACTGTA      88324       C    A
                                TACAG TATAG TGTAA
                                ||||| ||||| |||||
                                ATGTC ATATC ACATT
                                   A    _
GAM169  BTN2A2    3'  TACATCTATATCTGTA      22780       C
                                TACAG TATAGATGTA
                                ||||| ||||||||||
                                ATGTC ATATCTACAT
                                   T
GAM169  DKFZP564D1378 3'  TTGGTTACTACAGCTGTA    49530        ATAGAT
                                TACAGCT     GTAACTAG
                                |||||||     ||||||||
                                ATGTCGA     CATTGGTT
                                    CAT___
GAM169  FLJ10376  3'  ACTAGTTGATTGCTGTA     36075       TATAGATG
                                TACAGC      TAACTAGT
                                ||||||      ||||||||
                                ATGTCG      GTTGATCA
                                   TTA_____
GAM169  FLJ20274  3'  ACTAATATTTGTCATGCTGTA  62642       T__      AAC
                                TACAGC   ATAGATGT   TAGT
                                ||||||   ||||||||   ||||
                                ATGTCG   TGTTTATA   ATCA
                                   TAC      ___
GAM169  HSPC228   3'  ACTAGCCATCTCAATAGTT    33225       __    TAA
                                AGCTAT  AGATG   CTAGT
                                ||||||  |||||   |||||
                                TTGATA  TCTAC   GATCA
                                   AC    C__
GAM169  KIAA0993  3'  ACTAATGTTCTACTATAGCTTA 64137    C       A  T   __
                                A AGCTATAG TG AAC  TAGT
                                | |||||||| || |||  ||||
                                A TCGATATC AT TTG  ATCA
                                 T       _  C   TA
GAM169  KIAA1010  3'  TTAGTTACATCCATAGATG    72075    G    A
                                CA CTAT GATGTAACTAG
                                || |||| ||||||||||
                                GT GATA CTACATTGATT
                                 A    C
GAM169  MGC10067  3'  ACTAGTTACATTTCTA      58933    T
                                TA AGATGTAACTAGT
                                || ||||||||||||
                                AT TTTACATTGATCA
                                 C
GAM169  LOC126669 3'  TACTAGTTACATTTGACTGTA  75416       CTA
                                TACAG   TAGATGTAACTAGTA
                                |||||   |||||||||||||||
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                                ATGTC   GTTTACATTGATCAT
                                  A__
GAM169  LOC153387 5'  TACTAGTTCATAACCAGCT   86039     ATAG   T
                                AGCT    ATG AACTAGTA
                                ||||    ||| ||||||||
                                TCGA    TAC TTGATCAT
                                  CCAA   _
GAM170  ABCC12    5'  TCCCAACCAAAACCACAC    52648      ATGG
                                GTGTGG    TTGGTTGGGA
                                ||||||    ||||||||||
                                CACACC    AACCAACCCT
                                  AA__
GAM170  CYP1A2    3'  CCCAAGTTATCCACCTGC    69105     T     GG TGG
                                GCAG GTGGAT  T   TTGGG
                                |||| ||||||  |   |||||
                                CGTC CACCTA  G   AACCC
                                  _     TT ____
GAM170  CYP1A2    3'  CCCAAGTTATCCACCTGC    5685      T     GG TGG
                                GCAG GTGGAT  T   TTGGG
                                |||| ||||||  |   |||||
                                CGTC CACCTA  G   AACCC
                                  _     TT ____
GAM170  EFNB1     3'  CCACCTCCACACTGC       15395          T   T
                                GCAGTGTGGA GGT GG
                                |||||||||| ||| ||
                                CGTCACACCT CCA CC
                                          _  _
GAM170  HRC       5'  CCCAACGTTTGTCCACATTGC  9279           TG TTG
                                GCAGTGTGGA  G   GTTGGG
                                ||||||||||  |   ||||||
                                CGTTACACCT  T   CAACCC
                                      GT TG_
GAM170  MAFF      3'  CCCAACACTGTCCACACTGC   24644            TG
                                GCAGTGTGGATGGT  GTTGGG
                                ||||||||||||||  ||||||
                                CGTCACACCTGTCA  CAACCC
                                          __
GAM170  ODF2      5'  TCCCAAGTTTTCATCCAACTGC 10327       G      TTGG
                                GCAGT TGGATGG    TTGGGA
                                |||||  |||||||   ||||||
                                CGTCA ACCTACT    AACCCT
                                  _      TTTG
GAM170  PODXL     3'  TCCATTTGCACCATGCCACACT 18238          _    TGGT_
              GCT                 AGCAGTGTGG ATGGT    TGGG
                                ||||||||||  |||||    ||||
                                TCGTCACACC TACCA     ACCT
                                      G    CGTTT
GAM170  ARSDR1    3'  TCCCAACCAACCAGTCTTCACT 32076      T   _
                                AGTG GGA TGGTTGGTTGGGA
                                ||||  ||| ||||||||||||
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                                TCAC TCT ACCAACCAACCCT
                                  T  G
GAM170  CBARA1   3'  TCAGGGAACCATCCACAC    20293          GG
                                GTGTGGATGGTT  TTGG
                                ||||||||||||  ||||
                                CACACCTACCAA  GACT
                                      GG
GAM170  CYP2S1   3'  CCCAACCACTTGTCCACACAGC 47613     A      TG T
           T                     AGC GTGTGGA  G TGGTTGGG
                                ||| |||||||  | ||||||||
                                TCG CACACCT  T ACCAACCC
                                  A      GT C
GAM170  DKFZP434J193 3'  CCCAACCAGGGCACCCAC    71003      A  G _
                                GTGG TG T TGGTTGGG
                                |||| || | ||||||||
                                CACC AC G ACCAACCC
                                  C  G G
GAM170  DKFZP566G1424 5'  CCCATCCAGCCACACCAC    84781      A_      T
                                GTGG  TGGTTGG TGGG
                                ||||  ||||||| ||||
                                CACC  ACCGACC ACCC
                                  AC      T
GAM170  GAL3ST-4  3'  CCCAAGGCAGATCCACAT    44935        G_  GG
                                GTGTGGAT  GTT  TTGGG
                                ||||||||  |||  |||||
                                TACACCTA  CGG  AACCC
                                    GA  __
GAM170  KIAA1280  5'  CAAACAACCATCCACACTGC   69711             G
                                GCAGTGTGGATGGTTG TTG
                                |||||||||||||||| |||
                                CGTCACACCTACCAAC AAC
                                          A
GAM170  KIAA1957  3'  CCCTTTGCCCCTCCACACTGC  75716          T  TT   T__
                                GCAGTGTGGA GG  GGT   GGG
                                |||||||||| ||  |||   |||
                                CGTCACACCT CC  CCG   CCC
                                    _  __   TTT
GAM170  PARD6A   3'  CCCATGCCACTCCACACTGCT  33769           _   TGGT
                                AGCAGTGTGGA TGGT    TGGG
                                |||||||||| ||||    ||||
                                TCGTCACACCT ACCG    ACCC
                                      C    T___
GAM170  PRKRI    5'  CCCAGCTCACCCACCCAC    20755      A   T  _
                                GTGG TGG TG GTTGGG
                                |||| ||| || ||||||
                                CACC ACC AC CGACCC
                                  C   C  T
GAM170  SDC3     3'  CCCAAATACACCCACACTCT   27744    C      A  GTTGG
                                AG AGTGTGG TG     TTGGG
                                || ||||||| ||     |||||
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                                TC TCACACC AC    AACCC
                                 _     C  ATA__
GAM170  WIT-1    5'  CCCAACGGATCCACATGC    31822    G    TGG  G
                                GCA TGTGGA   TT GTTGGG
                                ||| ||||||   || ||||||
                                CGT ACACCT   AG CAACCC
                                 _    ___  G
GAM170  LOC148753 3'  CCCGCACACACACCCACACTGC 84215         A  GT  GT
           T                     AGCAGTGTGG TG  TG  TGGG
                                ||||||||||  ||  ||  ||||
                                TCGTCACACC AC  AC  GCCC
                                      C  AC  AC
GAM170  LOC149345 3'  CCCAATATCCACTCTAC     79306      _  TTG
                                GTGGA TGG   GTTGGG
                                ||||| |||   ||||||
                                CATCT ACC   TAACCC
                                   C   TA_
GAM170  LOC200597 3'  TCCCAACCCCACCCCAC     88844     T  A   TT
                                GTG GG TGG  GGTTGGGA
                                ||| || |||  ||||||||
                                CAC CC ACC  CCAACCCT
                                 _ C  __
GAM170  LOC255990 5'  CCCAACCAACCAGAGC      96235    GGA
                                GT   TGGTTGGTTGGG
                                ||   ||||||||||||
                                CG   ACCAACCAACCC
                                 AG_
GAM170  LOC93259  5'  CCCGTAGCCACCACCACACTGC 71811         A   T  __
           T                     AGCAGTGTGG TGGT GGT  TGGG
                                ||||||||||  |||| |||  ||||
                                TCGTCACACC ACCA CCG  GCCC
                                      _   _  AT
GAM171  DBT      3'  CCAAAAAGCCAAGTGTGGTG   8609         CCA  C  GA
                                CATCACAC   GC TT  GG
                                ||||||||   || ||  ||
                                GTGGTGTG   CG AA  CC
                                     AAC  A  AA
GAM171  DBT      3'  TCAGCCAGGTGTGATG      8612          CA  CT
                                CATCACACC  GC  TGA
                                |||||||||  ||  |||
                                GTAGTGTGG  CG  ACT
                                     AC  __
GAM171  DDX3     3'  CCTTGGCACACAGGTGTGAT   7223         CA___  TT
                                ATCACACC    GCC  GAGG
                                ||||||||    |||  ||||
                                TAGTGTGG    CGG  TTCC
                                     ACACA  __
GAM171  DGKI     5'  AAATCAATTCAGGCCAAGTGTG 16340         CCA   T  __
              GTG                   CATCACAC   GCCT GAG  GATTT
                                ||||||||   |||| |||  |||||
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                                GTGGTGTG  CGGA CTT  CTAAA
                                    AAC   _  AA
GAM171  EFG2     5' TTCAAGGCCAGGCATGGTG  50479      CA  CA
                                CATCA  CC  GCCTTGAG
                                |||||  ||  ||||||||
                                GTGGT  GG  CGGAACTT
                                   AC  AC
GAM171  LPP      3' TAAGGCCAGGTGTGGTG    18750        CA
                                CATCACACC  GCCTTG
                                |||||||||  ||||||
                                GTGGTGTGG  CGGAAT
                                     AC
GAM171  RANBP2L1 3' TTTCAAGGCCAGGTGTGGTG  17316        CA
                                CATCACACC  GCCTTGAGG
                                |||||||||  |||||||||
                                GTGGTGTGG  CGGAACTTT
                                     AC
GAM171  SIGLEC11 3' AAGGCTGGGCATGGTG     53541      CA
                                CATCA  CCCAGCCTT
                                |||||  |||||||||
                                GTGGT  GGGTCGGAA
                                   AC
GAM171  SLC14A1  3' AGGGCTGAGTGTGGTG     31835        C
                                CATCACAC CAGCCTT
                                ||||||||  |||||||
                                GTGGTGTG GTCGGGA
                                     A
GAM171  SLC16A2  3' AAATCCTCAAGGAGTTTGG  21496      ___
                                CCAG   CCTTGAGGATTT
                                ||||   ||||||||||||
                                GGTT   GGAACTCCTAAA
                                  TGA
GAM171  ATP1B4   3' AAATCTGCCTAAGCCGGGTGTG 23810          A  CTTGA_
           GTG                    CATCACACCC GC     GGATTT
                                ||||||||||  ||     ||||||
                                GTGGTGTGGG CG     TCTAAA
                                     C  AATCCG
GAM171  C20orf121 3' TGAGGCTGGATGAAATG     44278     CA  C
                                CAT  CA CCAGCCTTG
                                |||  ||  |||||||||
                                GTA  GT GGTCGGAGT
                                  AA  A
GAM171  C22orf19  3' AAATAAGATGGGCTGGGCACAG 13416     A___      TGAGG
           TG                     CAC    CCCAGCCT    ATTT
                                |||    ||||||||    ||||
                                GTG    GGGTCGGG    TAAA
                                  ACAC       TAGAA
GAM171  C22orf19  3' TCAGCCAGGTGTGGTG      13433        CA  CT
                                CATCACACC  GC  TGA
                                |||||||||  ||  |||
```

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                                GTGGTGTGG  CG  ACT
                                     AC  __
GAM171  CFLAR    3'  CCAAAAGGCTGGGCGTAGTG  13928    C  A      GA
                                CAT AC CCCAGCCTT  GG
                                ||| || |||||||||  ||
                                GTG TG GGGTCGGAA  CC
                                  A  C       AA
GAM171  DKFZP564M182 3'  TGAGGCTGGGCGTGGTG    78044      A
                                CATCAC CCCAGCCTTG
                                |||||| ||||||||||
                                GTGGTG GGGTCGGAGT
                                   C
GAM171  ET       3'  AAATAGCAAAGCTGGGTGTGGT 44219          C  AGG
           G                     CATCACACCCAGC TTG  ATTT
                                ||||||||||||| |||  ||||
                                GTGGTGTGGGTCG AAC  TAAA
                                       A  GA_
GAM171  FLJ00060  3'  TTCAAGGCTGGGTGCGGTG   61107    A
                                CATC CACCCAGCCTTGAG
                                |||| ||||||||||||||
                                GTGG GTGGGTCGGAACTT
                                  C
GAM171  FLJ10738  3'  AAATCCTTTTCTGGACATGA  36526    CAC   CCTT
                                TCA  CCAG   GAGGATTT
                                |||  ||||   ||||||||
                                AGT  GGTC   TTCCTAAA
                                  ACA   TT__
GAM171  FLJ13153  5'  AAATCCTCAGGGGAACTGATG  45554     CACCCAG
                                CATCA     CCTTGAGGATTT
                                |||||     ||||||||||||
                                GTAGT     GGGACTCCTAAA
                                   CAAG___
GAM171  FLJ13193  3'  TTTTCAAGCTGGGCGTAGTG  49777    C  A    C
                                CAT AC CCCAGC TTGAGGA
                                ||| || |||||| |||||||
                                GTG TG GGGTCG AACTTTT
                                  A  C    _
GAM171  FLJ13448  3'  CTTTGGGCTGGGCACAGTG   47136    A___      T
                                CAC   CCCAGCCT GAG
                                |||   |||||||| |||
                                GTG   GGGTCGGG TTC
                                  ACAC       T
GAM171  FLJ13842  3'  AAATCCTCAATGAGTGTGATG  44981       C  GCC
                                CATCACAC CA  TTGAGGATTT
                                |||||||| ||  ||||||||||
                                GTAGTGTG GT  AACTCCTAAA
                                     A  ___
GAM171  FLJ14117  3'  TCAGCTGGGTGTGGTG     42916          CT
                                CATCACACCCAGC  TGA
                                ||||||||||||  |||
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                                GTGGTGTGGGTCG  ACT
                                      __
GAM171  FLJ20059  3'  AAATATTTCAGGCTGGGCGTGG 34445       A      T   _
              TG                  CATCAC CCCAGCCT GAGG ATTT
                                  |||||| |||||||| |||| ||||
                                  GTGGTG GGGTCGGA CTTT TAAA
                                     C       _   A
GAM171  FLJ23499  3'  AAATCTTGGTGGGCTGGGTACG 42815     AC       TG_
              GTG                  CATC  ACCCAGCCT   AGGATTT
                                  ||||  |||||||||   |||||||
                                  GTGG  TGGGTCGGG   TTCTAAA
                                    CA       TGG
GAM171  FLJ25012  3'  GAGGCCAGGTGTGATG     58091         CA
                                  CATCACACC  GCCTT
                                  |||||||||  |||||
                                  GTAGTGTGG  CGGAG
                                       AC
GAM171  FLJ30681  3'  CCTCTTGGCCGGGTGTGGT   91785         A   TT
                                  ATCACACCC GCC  GAGG
                                  ||||||||| |||  ||||
                                  TGGTGTGGG CGG  CTCC
                                       C   TT
GAM171  JAM1      3'  CTGGAGGCTGGGCGCAGTG   57897     A___       G
                                  CAC    CCCAGCCTT AG
                                  |||    ||||||||| ||
                                  GTG    GGGTCGGAG TC
                                    ACGC       G
GAM171  JAM1      3'  CTGGAGGCTGGGCGCAGTG   57926     A___       G
                                  CAC    CCCAGCCTT AG
                                  |||    ||||||||| ||
                                  GTG    GGGTCGGAG TC
                                    ACGC       G
GAM171  JAM1      3'  CTGGAGGCTGGGCGCAGTG   57952     A___       G
                                  CAC    CCCAGCCTT AG
                                  |||    ||||||||| ||
                                  GTG    GGGTCGGAG TC
                                    ACGC       G
GAM171  JAM1      3'  CTGGAGGCTGGGCGCAGTG   33759     A___       G
                                  CAC    CCCAGCCTT AG
                                  |||    ||||||||| ||
                                  GTG    GGGTCGGAG TC
                                    ACGC       G
GAM171  KIAA0336  3'  TTTCAAGGCCAGGTGTGGTG  27591         CA
                                  CATCACACC  GCCTTGAGG
                                  |||||||||  |||||||||
                                  GTGGTGTGG  CGGAACTTT
                                       AC
GAM171  KIAA0355  3'  GAGGCTGGGCGTGGTG      28027        A
                                  CATCAC CCCAGCCTT
                                  |||||| |||||||||
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                                GTGGTG GGGTCGGAG
                                   C
GAM171  KIAA0447 3' AAGACTGGGTGTGGTG     71661          C
                                CATCACACCCAG CTT
                                |||||||||||| |||
                                GTGGTGTGGGTC GAA
                                     A
GAM171  KIAA0530 3' AAATCCTTTGTGAATGTGAT  70864      CC  GCCTT
                                ATCACA  CA    GAGGATTT
                                ||||||  ||    ||||||||
                                TAGTGT  GT    TTCCTAAA
                                   AA  GT___
GAM171  KIAA1277 3' CTCTGGCTGGGTGTG       64453          TT
                                CACACCCAGCC  GAG
                                ||||||||||  |||
                                GTGTGGGTCGG  CTC
                                     T_
GAM171  KIAA1649 5' CCACAATTAGCCAGGTGTGGTG 50250        CA  C__   A
                                CATCACACC  GC   TTG GG
                                |||||||||  ||   ||| ||
                                GTGGTGTGG  CG   AAC CC
                                     AC  ATT   A
GAM171  KIAA1715 3' GGGGCCAGGTGTGGTG      68124         CA
                                CATCACACC  GCCTT
                                |||||||||  |||||
                                GTGGTGTGG  CGGGG
                                     AC
GAM171  KIAA1879 3' CCAGGCCAAGTGTGGTG     73564         CCA   TGA
                                CATCACAC   GCCT   GG
                                ||||||||   ||||   ||
                                GTGGTGTG   CGGA   CC
                                     AAC   ___
GAM171  KIAA1975 5' AAATCCTTGTTAGGTTTGATG  73966      C   C   CTT
                                CATCA ACC AGC   GAGGATTT
                                ||||| ||| |||   ||||||||
                                GTAGT TGG TTG   TTCCTAAA
                                   T   A  ___
GAM171  LIM      3' AGGGCCAGGTGTGGTG      21301          CA
                                CATCACACC  GCCTT
                                |||||||||  |||||
                                GTGGTGTGG  CGGGA
                                     AC
GAM171  MGC12538 3' AAATCTTCAAGCTGAGTG    51239     C   C
                                CAC CAGC TTGAGGATTT
                                ||| |||| ||||||||||
                                GTG GTCG AACTTCTAAA
                                  A   _
GAM171  MGC13053 3' TTTAAGGCCGGGCACGGTG   51135      ACA   A
                                CATC   CCC GCCTTGAG
                                ||||   ||| ||||||||
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                              GTGG  GGG CGGAATTT
                                CAC  C
GAM171  MGC39350 3'  CCAGGCCAGGTGTGATG    58653        CA   TGA
                              CATCACACC  GCCT  GG
                              |||||||||  ||||  ||
                              GTAGTGTGG  CGGA  CC
                                   AC   ___
GAM171  OS4      3'  AAATCCTCAAAGCGTGGACGTG 19174      __  _ C
           TG                   CACAC  CCA GC TTGAGGATTT
                              |||||  ||| || ||||||||||
                              GTGTG  GGT CG AACTCCTAAA
                                CA  G  A
GAM171  OSBPL11  3'  AAATCCTCAAAATGAGT    42889    C  GCC
                              AC CA  TTGAGGATTT
                              || ||  ||||||||||
                              TG GT  AACTCCTAAA
                               A  AA_
GAM171  PAFAH2   3'  AAGGCTGGGCGTGGTG     4757       A
                              CATCAC CCCAGCCTT
                              |||||| |||||||||
                              GTGGTG GGGTCGGAA
                                 C
GAM171  PRO0233  3'  AATCCTCTTAGGATGTGTG   26114      CCAG  T_
                              CACAC   CCT  GAGGATT
                              |||||   |||  |||||||
                              GTGTG   GGA  CTCCTAA
                                 TA__  TT
GAM171  PRO2730  3'  CCTCAAGGCTGGGCGCGGTG  47413     ACA
                              CATC  CCCAGCCTTGAGG
                              ||||  ||||||||||||
                              GTGG  GGGTCGGAACTCC
                                CGC
GAM171  Rpo1-2   3'  AAGGCTGGGTGTGGTG     38695
                              CATCACACCCAGCCTT
                              ||||||||||||||||
                              GTGGTGTGGGTCGGAA

GAM171  SCIN    3'  TTAAGGCTGGGCGCGGTG    52427     ACA
                              CATC  CCCAGCCTTGA
                              ||||  ||||||||||
                              GTGG  GGGTCGGAATT
                                CGC
GAM171  TTY7     5'  AAATCCCCCATGCCCAGGTGTG 49175       CA_  CT  A_
           GTG                   CATCACACC  GC  TG  GGATTT
                              |||||||||  ||  ||  ||||||
                              GTGGTGTGG  CG  AC  CCTAAA
                                   ACC  T_  CC
GAM171  TXNL2    3'  AAGTGCCAGGCTGGG      21547       TGA  _
                              CCCAGCCT  GG ATTT
                              ||||||||  || ||||
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                                GGGTCGGA   CC TGAA
                                   ___  G
GAM171  ust3     3'  CAAGGCTGGGTGCGGTG     93227      A
                                CATC CACCCAGCCTTG
                                |||| ||||||||||||
                                GTGG GTGGGTCGGAAC
                                  C
GAM171  LOC144501 3'  AAATCCTCAGTGGG        83102      GCC
                                CCCA   TTGAGGATTT
                                ||||   ||||||||||
                                GGGT   GACTCCTAAA
                                  ___
GAM171  LOC146958 3'  AAATCCTCCAATGGGCTGGG   83880        T___
                                CCCAGCCT    GAGGATTT
                                ||||||||    ||||||||
                                GGGTCGGG    CTCCTAAA
                                     TAAC
GAM171  LOC148293 3'  TCAGGCCAGGTGTGGTG     78784         CA    T
                                CATCACACC  GCCT GA
                                |||||||||  |||| ||
                                GTGGTGTGG  CGGA CT
                                     AC   _
GAM171  LOC149086 5'  CAGGGCTGGGCATGAT      84336      CA
                                ATCA  CCCAGCCTTG
                                ||||  ||||||||||
                                TAGT  GGGTCGGGAC
                                  AC
GAM171  LOC150519 3'  TCCTCAAGGTAGGCATGATG   79923      CAC  A
                                CATCA   CC GCCTTGAGGA
                                |||||   || ||||||||||
                                GTAGT   GG TGGAACTCCT
                                   AC_  A
GAM171  LOC150577 3'  CTTAGCTGGGTGTGGTG     85074           CT
                                CATCACACCCAGC  TGAG
                                ||||||||||||  ||||
                                GTGGTGTGGGTCG  ATTC
                                      __
GAM171  LOC151068 3'  CTTAGCTGGGTGTGGTG     85220           CT
                                CATCACACCCAGC  TGAG
                                ||||||||||||  ||||
                                GTGGTGTGGGTCG  ATTC
                                      __
GAM171  LOC151446 3'  TCAGCCGGGTGTGGTG      85378         A  CT
                                CATCACACCC GC  TGA
                                |||||||||| ||  |||
                                GTGGTGTGGG CG  ACT
                                     C  __
GAM171  LOC152348 3'  AAATCCTAATCCCCAGTGTGAT 85690         CCAGCCTTG
           G                     CATCACAC        AGGATTT
                                ||||||||        |||||||
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                                GTAGTGTG       TCCTAAA
                                    ACCCCTAA_
GAM171  LOC153218 5' CTCAAGGCTAGTTGTGA    80776      CCC
                                TCACA  AGCCTTGAG
                                |||||  |||||||||
                                AGTGT  TCGGAACTC
                                   TGA
GAM171  LOC153218 5' CTCAAGGCTAGTTGTGA    80777      CCC
                                TCACA  AGCCTTGAG
                                |||||  |||||||||
                                AGTGT  TCGGAACTC
                                   TGA
GAM171  LOC154877 3' CCTCTCTTGGCTGGGTGTGGTG 86290            TT__
                                CATCACACCCAGCC   GAGG
                                ||||||||||||||   ||||
                                GTGGTGTGGGTCGG   CTCC
                                      TTCT
GAM171  LOC158677 5' AAATTTTAGCTGGGTGTTATG  86887    C       CTTG
                                CAT ACACCCAGC   AGGATTT
                                ||| |||||||||   |||||||
                                GTA TGTGGGTCG   TTTTAAA
                                  T       A___
GAM171  LOC167555 3' TCAGCCAGGTGTGATG      82680        CA  CT
                                CATCACACC  GC  TGA
                                |||||||||  ||  |||
                                GTAGTGTGG  CG  ACT
                                     AC  __
GAM171  LOC197201 3' AAGGCTGGGTGTGATG      87927
                                CATCACACCCAGCCTT
                                ||||||||||||||||
                                GTAGTGTGGGTCGGAA

GAM171  LOC219406 3' CAAGGCTGGGTGCAGTG     93556     CA
                                CAT  CACCCAGCCTTG
                                |||  ||||||||||||
                                GTG  GTGGGTCGGAAC
                                  AC
GAM171  LOC220001 3' CCCAAGGCTGGATGT       91633     C       A
                                ACA CCAGCCTTG GG
                                ||| ||||||||| ||
                                TGT GGTCGGAAC CC
                                  A       _
GAM171  LOC220692 3' TTTCAAGGCCAGGTGTGGTG   91223         CA
                                CATCACACC  GCCTTGAGG
                                |||||||||  |||||||||
                                GTGGTGTGG  CGGAACTTT
                                     AC
GAM171  LOC221263 3' AAATCCTCAGTGAGTG      93611     C  GCC
                                CAC CA   TTGAGGATTT
                                ||| ||   ||||||||||
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                                GTG GT   GACTCCTAAA
                                  A ___
GAM171  LOC221787 3'  CAAAGCCAGGTGTGGTG     92467         CA  C
                                CATCACACC  GC TTG
                                |||||||||  || |||
                                GTGGTGTGG  CG AAC
                                     AC  A
GAM171  LOC257095 5'  CCAGGCTGGGTGCAATG     96936     CA        TGA
                                CAT  CACCCAGCCT   GG
                                |||  ||||||||||   ||
                                GTA  GTGGGTCGGA   CC
                                  AC        ___
GAM171  LOC91250  5'  AAATCAAGAATAGGCTAGGTGT 65318         C    TGAG__
           GGTG                    CATCACACC AGCCT     GATTT
                                |||||||||| |||||     |||||
                                GTGGTGTGG TCGGA     CTAAA
                                     A    TAAGAA
GAM171  LOC91565  3'  AAGGCTGGGTGCAGTG      66457     CA
                                CAT  CACCCAGCCTT
                                |||  ||||||||||
                                GTG  GTGGGTCGGAA
                                  AC
GAM171  LOC93132  5'  TCAGCCGGGTGTGGTG      71502          A  CT
                                CATCACACCC GC  TGA
                                |||||||||| ||  |||
                                GTGGTGTGGG CG  ACT
                                     C  __
GAM172  ARSE      5'  GCCCAGGAGCAGAGGAAGTAGA 3503        _         A
                                TCTATT CCTCTGCTCCT GGC
                                |||||| |||||||||| |||
                                AGATGA GGAGACGAGGA CCG
                                   A         C
GAM172  FZD4      3'  CCCTAGAGGAATAGACT     24132            CTCCTA
                                AGTCTATTCCTCTG     GG
                                ||||||||||||||     ||
                                TCAGATAAGGAGAT     CC
                                        C_____
GAM172  GSBS      3'  CCTAGAGAAAAAATAGACT   91092        CCTCTG   C
                                AGTCTATT     CTC TAGG
                                ||||||||     ||| ||||
                                TCAGATAA     GAG ATCC
                                     AAAA__   _
GAM172  LDHB      5'  GCTGGAAGAGGAATAAATTA  9714       C       GC   TA
                                TAGT TATTCCTCT  TCC  GGC
                                |||| |||||||||  |||  |||
                                ATTA ATAAGGAGA  AGG  TCG
                                  A       __  __
GAM172  LDHB      5'  GCTGGAAGAGGAATAAATTA  9715       C       GC   TA
                                TAGT TATTCCTCT  TCC  GGC
                                |||| |||||||||  |||  |||
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                                ATTA ATAAGGAGA  AGG  TCG
                                  A       __   __
GAM172  PCDH11X  5' GCCCAGAGCTGAAGAAATGGAC 27240        _ C  T   CTA
                TA                  TAGTCTATT C TC GCTC   GGC
                                    |||||||||  | || ||||   |||
                                    ATCAGGTAA G AG CGAG   CCG
                                         A A  T    AC_
GAM172  PCDH11X  5' GCCCAGAGCTGAAGAAATGGAC 52022        _ C  T   CTA
                TA                  TAGTCTATT C TC GCTC   GGC
                                    |||||||||  | || ||||   |||
                                    ATCAGGTAA G AG CGAG   CCG
                                         A A  T    AC_
GAM172  PCDH11X  5' GCCCAGAGCTGAAGAAATGGAC 52044        _ C  T   CTA
                TA                  TAGTCTATT C TC GCTC   GGC
                                    |||||||||  | || ||||   |||
                                    ATCAGGTAA G AG CGAG   CCG
                                         A A  T    AC_
GAM172  PCDH11Y  5' GCCCAGAGCTGAAGAAATGGAC 52067        _ C  T   CTA
                TA                  TAGTCTATT C TC GCTC   GGC
                                    |||||||||  | || ||||   |||
                                    ATCAGGTAA G AG CGAG   CCG
                                         A A  T    AC_
GAM172  PCDH11Y  5' GCCCAGAGCTGAAGAAATGGAC 52079        _ C  T   CTA
                TA                  TAGTCTATT C TC GCTC   GGC
                                    |||||||||  | || ||||   |||
                                    ATCAGGTAA G AG CGAG   CCG
                                         A A  T    AC_
GAM172  FLJ12770 3' CCCAGGAGCAGAGTGGTGGAC  49739       TC        A
                                    GTCTAT  CTCTGCTCCT GG
                                    ||||||  |||||||||| ||
                                    CAGGTG  GAGACGAGGA CC
                                       GT        C
GAM172  FLJ13231 3' GCCTAGGAGTGAAAAGA     43551     A   CTCT
                                    TCT TTC    GCTCCTAGGC
                                    ||| |||    ||||||||||
                                    AGA AAG    TGAGGATCCG
                                      A  _____
GAM172  FLJ13352 3' CCTAGTAGGAATGGACTA    44753           CTGCTC
                                    TAGTCTATTCCT     CTAGG
                                    ||||||||||||     |||||
                                    ATCAGGTAAGGA     GATCC
                                           T_____
GAM172  FLJ14966 5' CAGGAGCAGAAGAC       51767      ATTCC       A
                                    GTCT     TCTGCTCCT G
                                    ||||     ||||||||| |
                                    CAGA     AGACGAGGA C
                                      _____        C
GAM172  KIAA0040 5' GCTGGAAGAGGAATAAATTA  27788      C       GC   TA
                                    TAGT TATTCCTCT  TCC  GGC
                                    |||| |||||||||  |||  |||
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                                ATTA ATAAGGAGA  AGG  TCG
                                  A       __   __
GAM172  MRF-1    3'  GCCCAGGAGCAGAGGA      71325           A
                                TCCTCTGCTCCT GGC
                                |||||||||||| |||
                                AGGAGACGAGGA CCG
                                       C
GAM172  RBM11    3'  CCCATTGGCAACAAATAGACTA 58582         CCTC    CCTA
                                TAGTCTATT    TGCT    GG
                                |||||||||    ||||    ||
                                ATCAGATAA    ACGG    CC
                                     ACA_    TTAC
GAM172  SYT12    3'  CCCAGAAGCAGAGGGGCTG   94727      TATT       C  A
                                TAGTC    CCTCTGCT CT GG
                                |||||    |||||||| || ||
                                GTCGG    GGAGACGA GA CC
                                  _____       A  C
GAM172  TSGA14   3'  CTTCTGCAGAGGAAAGAC    38046     A       TCCT
                                GTCT TTCCTCTGC    AG
                                |||| |||||||||    ||
                                CAGA AAGGAGACG    TC
                                  _       TCT_
GAM173  ATF7     3'  ATCTTTGGTCATTTTTCTG   22464     CT    A
                                CAG  AGAT ACCAAAGAT
                                |||  |||| |||||||||
                                GTC  TTTA TGGTTTCTA
                                  TT    C
GAM173  GABRA2   3'  GTTATCTTTGGGATGTATAGC  5866      G   A_
                                GCTA ATA  CCAAAGATAAC
                                |||| |||  ||||||||||
                                CGAT TGT  GGTTTCTATTG
                                  A   AG
GAM173  SH3GL2   3'  TCTATTTATCTAGCTGTA    11629           CCAA
                                TACAGCTAGATAA    AGA
                                ||||||||||||    |||
                                ATGTCGATCTATT    TCT
                                       TA__
GAM173  SLC38A2  3'  TTGGTCATCTGGCTGTA     38595           A
                                TACAGCTAGAT ACCAA
                                |||||||||| |||||
                                ATGTCGGTCTA TGGTT
                                       C
GAM173  AKAP11   3'  CTTTGGTTACTTGTGC      32708    _   A
                                GC TAG TAACCAAAG
                                || ||| |||||||||
                                CG GTT ATTGGTTTC
                                 T   C
GAM173  CAMKK2   3'  ATCTCTGGTTATTTGTT     21576     T       A
                                AGC AGATAACCA AGAT
                                ||| ||||||||| ||||
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                                TTG TTTATTGGT TCTA
                                  _       C
GAM173  DJ328E19.C1.1 3' ATCTTTGTGTTTAGCTCA    31151   C       AC
                                A AGCTAGATA  CAAAGAT
                                | |||||||||  |||||||
                                A TCGATTTGT  GTTTCTA
                                 C       __
GAM173  DKFZp434D177 3' ATCTTTGTGTTTAGCTCA    50052   C       AC
                                A AGCTAGATA  CAAAGAT
                                | |||||||||  |||||||
                                A TCGATTTGT  GTTTCTA
                                 C       __
GAM173  KIAA0853  3' GTTATTCCAGATTATCTAGCTT 30543   C       CCAAA
            A                    A AGCTAGATAA    GATAAC
                                | ||||||||||    ||||||
                                A TCGATCTATT    TTATTG
                                 T        AGACC
GAM173  MGC13071  3' TTATCTTTGACTGCTGT     51092      T  ATAAC
                                ACAGC AG    CAAAGATAA
                                ||||| ||    |||||||||
                                TGTCG TC    GTTTCTATT
                                  _ A____
GAM173  MKRN2    3' ATCTATTATCTAGCTG      72412          CCAA
                                CAGCTAGATAA   AGAT
                                ||||||||||   ||||
                                GTCGATCTATT   TCTA
                                       A___
GAM173  RA-GEF-2  3' TCTAATCAAGTGTTTAGCTGT  32957          ACCAA__
                                ACAGCTAGATA      AGA
                                ||||||||||      |||
                                TGTCGATTTGT      TCT
                                      GAACTAA
GAM173  STRN     3' ATCTTCACCTTCTAGCTGT   12040         TAACCA
                                ACAGCTAGA     AAGAT
                                |||||||||     |||||
                                TGTCGATCT     TTCTA
                                     TCCAC_
GAM173  LOC129607 3' TGGTATCTAGCTGTA       74888           A
                                TACAGCTAGATA CCA
                                |||||||||||| |||
                                ATGTCGATCTAT GGT
                                          _
GAM173  LOC133418 3' TTATCCCAACATCTAGCTG   75092         AACCAAA
                                CAGCTAGAT      GATAA
                                |||||||||      |||||
                                GTCGATCTA      CTATT
                                     CAACC__
GAM173  LOC144248 5' TATCTTTGGTCACCTACATGT  76745     GC   ATA
                                ACA  TAG   ACCAAAGATA
                                |||  |||   ||||||||||
```

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                                TGT  ATC   TGGTTTCTAT
                                  AC   CAC
GAM173  LOC146050 3'  TTATCTTTGGCCAGTGGAGCTG 77655      AG  AA_
                                CAGCT  AT   CCAAAGATAA
                                |||||  ||   ||||||||||
                                GTCGA  TG   GGTTTCTATT
                                   GG  ACC
GAM173  LOC149010 3'  ATCTTTGTGTTTAGCTCA    79127   C       AC
                                A AGCTAGATA  CAAAGAT
                                | |||||||||  |||||||
                                A TCGATTTGT  GTTTCTA
                                 C       __
GAM173  LOC149013 3'  ATCTTTGTGTTTAGCTCA    79130   C       AC
                                A AGCTAGATA  CAAAGAT
                                | |||||||||  |||||||
                                A TCGATTTGT  GTTTCTA
                                 C       __
GAM173  LOC149317 3'  ATCTTTGTGTTTAGCTCA    79287   C       AC
                                A AGCTAGATA  CAAAGAT
                                | |||||||||  |||||||
                                A TCGATTTGT  GTTTCTA
                                 C       __
GAM173  LOC220638 3'  ATCTTTGTGTTTAGCTCA    73909   C       AC
                                A AGCTAGATA  CAAAGAT
                                | |||||||||  |||||||
                                A TCGATTTGT  GTTTCTA
                                 C       __
GAM173  LOC91496  5'  TTATCTTTGGACATGTACTG   66227    C  G  AA
                                CAG TA AT  CCAAAGATAA
                                ||| || ||  ||||||||||
                                GTC AT TA  GGTTTCTATT
                                  _  G  CA
GAM174  ADAMTS8   5'  TCGGGCCGCCAGCACCTG    22886    _     ATAAG
                                CAG TGCTGGC    CTGA
                                ||| |||||||    ||||
                                GTC ACGACCG    GGCT
                                  C      CCG__
GAM174  BAP1      3'  TCAGGGACCCAGCACTGG    16219         CATAAG
                                CCAGTGCTGG     CTGA
                                ||||||||||     ||||
                                GGTCACGACC     GACT
                                     CAGG__
GAM174  BF        5'  TTCAGCTTGGACACTG      8140       CTGGCA
                                CAGTG     TAAGCTGAA
                                |||||     |||||||||
                                GTCAC     GTTCGACTT
                                   AG____
GAM174  C1QB      3'  TTCAACTCTGTGTCCCAGCACT 4923    A       __   _  C
            GGC                   G CCAGTGCTGG  CATA AG TGAA
                                | ||||||||||  |||| || ||||
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                                C GGTCACGACC  GTGT TC ACTT
                                _        CT    C  A
GAM174  CHC1     3'  CAGCCCTGAGCACTGTGTC    7020      _      __  CATAA
                                GAC CAGTGCT  GG     GCTG
                                ||| |||||||  ||     ||||
                                CTG GTCACGA  CC     CGAC
                                  T      GT  _____
GAM174  CMRF35   5'  CAGAGCTGTCAGCACCGG    21929    A        TAAG
                                CC GTGCTGGCA    CTG
                                || |||||||||    |||
                                GG CACGACTGT    GAC
                                 C        CGA_
GAM174  EPHB6    3'  TCAGCCCTGGACACTGGTC    15466         _ TG CATAA
                                GACCAGTG C  G    GCTGA
                                |||||||| |  |    |||||
                                CTGGTCAC G  C    CGACT
                                     A GT C____
GAM174  EVPL     5'  CAGCCTGAGCCAGCACT     8803          A  A
                                AGTGCTGGC TA GCTG
                                ||||||||| || ||||
                                TCACGACCG GT CGAC
                                     A  C
GAM174  GARP     3'  CAGCCCAGCACTGG        18594          CATAA
                                CCAGTGCTGG    GCTG
                                ||||||||||    ||||
                                GGTCACGACC    CGAC
                                              _____
GAM174  GJB5     3'  CAGCTCGACGGCACTGG     17945         GCATA
                                CCAGTGCTG    AGCTG
                                |||||||||    |||||
                                GGTCACGGC    TCGAC
                                     AGC__
GAM174  GPR81    3'  CTTACCAGCATTAGTC      50757     C       CA
                                GAC AGTGCTGG  TAAG
                                ||| ||||||||  ||||
                                CTG TTACGACC  ATTC
                                  A       __
GAM174  IFI16    5'  AGCAAGCCAGCACTAGTC    71221     C       ATAA
                                GAC AGTGCTGGC    GCT
                                ||| |||||||||    |||
                                CTG TCACGACCG    CGA
                                  A        AA__
GAM174  KRT4     3'  CAGCTGGGCCCAGCACTGGT   9635           _ ATA
                                ACCAGTGCTGG C   AGCTG
                                |||||||||||| |   |||||
                                TGGTCACGACC G   TCGAC
                                       C GG_
GAM174  MAP3K9   3'  TTCAGCTTCCCAAACACCAGT  60709    CA   C_   CAT
                                AC  GTG  TGG   AAGCTGAA
                                ||  |||  |||   ||||||||
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                                TG  CAC  ACC   TTCGACTT
                                 AC   AA   C__
GAM174  MGAT5    5'  TCAGCTTACAGTTCCTG     10028     T_   GCA
                                CAG  GCTG   TAAGCTGA
                                |||  ||||   ||||||||
                                GTC  TGAC   ATTCGACT
                                  CT   ___
GAM174  MOCS1    3'  TTCAGCTTAACAGTTGCCCGGT 92037      A_  _   GCA
            C                    GACC  GTG CTG   TAAGCTGAA
                                ||||  ||| |||   |||||||||
                                CTGG  CGT GAC   ATTCGACTT
                                  CC   T   A__
GAM174  P23      3'  TCAGCTTATACCCGGGCT    21719     G   C_
                                AGT CTGG  ATAAGCTGA
                                |||  ||||  |||||||||
                                TCG GGCC  TATTCGACT
                                  _    CA
GAM174  PFKFB4   3'  TCAGCCACATGCAACACTGTGT 15874     _    CTG    AA_
            C                    GAC CAGTG   GCAT   GCTGA
                                |||  |||||   ||||   |||||
                                CTG GTCAC   CGTA   CGACT
                                  T    AA_    CAC
GAM174  PTPRK    3'  TTCAGCCTGTGGCCCAGCACTG 11125           __    A
            GTC                    GACCAGTGCTGG  CATA GCTGAA
                                ||||||||||||  ||||  ||||||
                                CTGGTCACGACC  GTGT CGACTT
                                       CG    C
GAM174  RNPEPL1  3'  CGGATGCCAGCACCTG      36676     _       AAG
                                CAG TGCTGGCAT   CTG
                                |||  |||||||||   |||
                                GTC ACGACCGTA   GGC
                                  C       ___
GAM174  UBE2L3   3'  TCAGCCCTGGCACTGGC     12507    A      TG CATAA
                                G CCAGTGC  G    GCTGA
                                |  |||||||  |    |||||
                                C GGTCACG  C    CGACT
                                 _      GT C____
GAM174  APXL2    5'  CAGCCTCAGCACTCATC     75185    CC       CATAA
                                GA  AGTGCTGG    GCTG
                                ||  ||||||||    ||||
                                CT  TCACGACT    CGAC
                                  AC       C____
GAM174  ARHGEF9  3'  TTCAGCTTACCAAGCA      30824     _  CA
                                TGCT GG  TAAGCTGAA
                                ||||  ||  |||||||||
                                ACGA CC  ATTCGACTT
                                  A  __
GAM174  CEGP1    3'  TTCAGCTTCCTCTAGCCCGG   40589    AGT    CAT
                                CC   GCTGG   AAGCTGAA
                                ||   |||||   ||||||||
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                                GG  CGATC  TTCGACTT
                                 CC_    TCC
GAM174  DKFZp547D155 3' CAGCCCTGAGACCACTGGTC  70435       CTGG  TAA
                                GACCAGTG   CA  GCTG
                                ||||||||   ||  ||||
                                CTGGTCAC   GT  CGAC
                                    CAGA  CC_
GAM174  DKFZP727G051 3' TTCAGCCCATCAACCAGCATTG 69483          CATAA__
          GTC                    GACCAGTGCTGG     GCTGAA
                                ||||||||||||     ||||||
                                CTGGTTACGACC     CGACTT
                                      AACTACC
GAM174  DUSP14   5' CACTGTCACCAGCACTGCTC  22834    C       CATA  C
                                GA CAGTGCTGG   AG TG
                                || |||||||||   || ||
                                CT GTCACGACC   TC AC
                                 C       ACTG  _
GAM174  FLJ10206 5' CAGCTTATGCCAGGAGTC   35898    CAGTG
                                GAC    CTGGCATAAGCTG
                                |||    ||||||||||||||
                                CTG    GACCGTATTCGAC
                                 AG___
GAM174  FLJ20967 5' GGCGCCCAGCACTGGTT    41962          CATAA
                                GACCAGTGCTGG    GCT
                                ||||||||||||    |||
                                TTGGTCACGACC    CGG
                                      CG___
GAM174  FLJ22569 3' TTCAGCTTACTAAACTG    43679     GC  CA
                                CAGT  TGG  TAAGCTGAA
                                ||||  |||  |||||||||
                                GTCA  ATC  ATTCGACTT
                                  A_  __
GAM174  FOXN4    3' TTCAGCTTGGACACACTGG   75574       C  GCA
                                CCAGTG TG   TAAGCTGAA
                                |||||| ||   |||||||||
                                GGTCAC AC   GTTCGACTT
                                   _  AG_
GAM174  GW112    3' TTCAACTGAAGCCAGCACTGGT 21194           ATA  C
          T                     GACCAGTGCTGGC   AG TGAA
                                ||||||||||||   || ||||
                                TTGGTCACGACCG   TC ACTT
                                      AAG  A
GAM174  HOOK2    3' CAGCTCACATGGCGCCCAGCAC 25256         _____  A__
          TGG                     CCAGTGCTGG   CAT   AGCTG
                                ||||||||||   |||  |||||
                                GGTCACGACC   GTA   TCGAC
                                     CGCG   CAC
GAM174  jdp2     3' TTCAGCACAGCCAGCAT     55327        ATAA
                                GTGCTGGC   GCTGAA
                                ||||||||   ||||||
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                                TACGACCG   CGACTT
                                    ACA_
GAM174  KIAA0767 3' TCTGCTGCCAGCACAGG    60632   A      TAA  T
                                CC GTGCTGGCA  GC GA
                                || |||||||||  || ||
                                GG CACGACCGT  CG CT
                                 A       ___  T
GAM174  KIAA0923 3' TCAGCTTGATGCATGGTC    25838     G  TGGCA
                                GACCA TGC    TAAGCTGA
                                ||||| |||    ||||||||
                                CTGGT ACG    GTTCGACT
                                   _  TA___
GAM174  KIAA0982 3' TTCACTGTTTGCCAGCAC    25852       TA_  C
                                GTGCTGGCA  AG TGAA
                                |||||||||  || ||||
                                CACGACCGT  TC ACTT
                                     TTG  _
GAM174  KIAA1000 3' TTCAGCTTTGCAAAGTACTGG 65281       G_  T
                                CCAGTGCT  GCA AAGCTGAA
                                ||||||||  ||| ||||||||
                                GGTCATGA  CGT TTCGACTT
                                    AA  _
GAM174  MAP3K3   3' TCAGCCTGGGCGCTGGTC    9999        GG  TAA
                                GACCAGTGCT  CA  GCTGA
                                ||||||||||  ||  |||||
                                CTGGTCGCGG  GT  CGACT
                                     __  C__
GAM174  MGC16037 5' CTTGTCCAGCACTAGTC    51821    C      C
                                GAC AGTGCTGG ATAAG
                                ||| |||||||| |||||
                                CTG TCACGACC TGTTC
                                  A      _
GAM174  MIDORI   3' TCAGCTTATCCTGCAACT    73792    _  T  C
                                AGT GC GG ATAAGCTGA
                                ||| || || |||||||||
                                TCA CG CC TATTCGACT
                                  A  T  _
GAM174  MtFMT    5' CAGTGGCGAGCACTGG      57651       G  ATAA
                                CCAGTGCT GC   GCTG
                                |||||||| ||   ||||
                                GGTCACGA CG   TGAC
                                    G  G___
GAM174  PCDH16   5' TCAGTTCCAACCACTGG     72826      C_  CATA
                                CCAGTG  TGG   AGCTGA
                                ||||||  |||   ||||||
                                GGTCAC  ACC   TTGACT
                                   CA  _____
GAM174  QKI      3' CAGCTTATCAACTCGTC     65439    C  GCTGGC
                                GAC AGT     ATAAGCTG
                                ||| |||     ||||||||
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                                CTG TCA     TATTCGAC
                                  C  AC____
GAM174  TNRC6    3'  CAACTTTTAGCACTG       70506         CAT  C
                                CAGTGCTGG  AAG TG
                                |||||||||  ||| ||
                                GTCACGATT  TTC AC
                                     ___  A
GAM174  TOB2     3'  CAGCCCAGGCCAGCACTG    95618          ATAA
                                CAGTGCTGGC   GCTG
                                ||||||||||   ||||
                                GTCACGACCG   CGAC
                                     GACC
GAM174  TU12B1-TY 3'  TCAGCCCACAGCACTGTC    33406     C      GCATAA
                                GAC AGTGCTG     GCTGA
                                ||| |||||||     |||||
                                CTG TCACGAC     CGACT
                                  _      ACC___
GAM174  TUSP     3'  TCAGCCTAAGAGCGCAGCACTG 39641         _  A__  A
                                CAGTGCTG GC   TA GCTGA
                                |||||||| ||   || |||||
                                GTCACGAC CG   AT CGACT
                                     G  AGA  C
GAM174  USP19    3'  TCAGCTTATGCATCTGGT    88959       TGCTG
                                ACCAG    GCATAAGCTGA
                                |||||    ||||||||||
                                TGGTC    CGTATTCGACT
                                   TA___
GAM174  ZD52F10  3'  CAGCCTGTGCCAGCCCTGG   52819     T       A
                                CCAG GCTGGCATA GCTG
                                |||| ||||||||| ||||
                                GGTC CGACCGTGT CGAC
                                  C        C
GAM174  LOC145268 3'  TCAGCTTACAAGAGCCACTG  77062      _ GGCA
                                CAGTG CT    TAAGCTGA
                                ||||| ||    ||||||||
                                GTCAC GA    ATTCGACT
                                   C  GAAC
GAM174  LOC149296 5'  CAGCTTATGGGCAGCA      79256      G_
                                TGCTG  CATAAGCTG
                                |||||  |||||||||
                                ACGAC  GTATTCGAC
                                   GG
GAM174  LOC161877 5'  TCAGGGCAGGCCAGCGCTGG  82326          ATAAG
                                CCAGTGCTGGC    CTGA
                                ||||||||||     ||||
                                GGTCGCGACCG    GACT
                                     GACGG
GAM174  LOC163115 5'  TCAGCCCCTGACAGCACTGG  82413         G  TAA
                                CCAGTGCTG CA   GCTGA
                                |||||||| ||   |||||
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                                GGTCACGAC GT   CGACT
                                     A  CCC
GAM174  LOC196500 3'  TCAGCTCACTCAGTGGTC    87744     AGT    CATA
                                GACC   GCTGG    AGCTGA
                                ||||   |||||    ||||||
                                CTGG   TGACT    TCGACT
                                  ___    CAC_
GAM174  LOC197287 3'  TCAGCTCATGTGTTTTGCACTG 60865       T_     __
                                CAGTGC  GGCATA  AGCTGA
                                ||||||  ||||||  ||||||
                                GTCACG  TTGTGT  TCGACT
                                   TT     AC
GAM174  LOC200470 5'  TCAGCCTGCGGCGCTGG     90069         G  TAA
                                CCAGTGCTG CA   GCTGA
                                ||||||||| ||   |||||
                                GGTCGCGGC GT   CGACT
                                     _ C__
GAM174  LOC221584 3'  CAGCTTATGTGGCAC       93828       G
                                GTGCTG CATAAGCTG
                                |||||| |||||||||
                                CACGGT GTATTCGAC
                                  _
GAM174  LOC51716  3'  CAGCTCATGGCCCTAGCA    32787       ___  A
                                TGCTGG   CAT AGCTG
                                ||||||   ||| |||||
                                ACGATC   GTA TCGAC
                                   CCG   C
GAM174  LOC92196  5'  CAGAGCACCAGCACTGGC    68456   A       CATAAG
                                G CCAGTGCTGG     CTG
                                | ||||||||||     |||
                                C GGTCACGACC     GAC
                                _        ACGA__
GAM175  CD74     3'  GAACAGCAGATAACA      15129     CA
                                TGT  GTCTGCTGTTT
                                |||  ||||||||||
                                ACA  TAGACGACAAG
                                  A_
GAM175  MFAP4    3'  CCTGTCCCAACAGCTGACAG   69254       T   C  TTT
                                CTGTCAG CTG TG   GCAGG
                                ||||||| ||| ||   |||||
                                GACAGTC GAC AC   TGTCC
                                   _   A  CC_
GAM175  SLC20A1   3'  TGTTAACAGAAGACTGACA   59391         G    T
                                TGTCAGTCT CTGTT GCA
                                ||||||||| ||||| |||
                                ACAGTCAGA GACAA TGT
                                     A    T
GAM175  WNT14    3'  CCTGCAAGGACTGAGAG     12676    G     GCTGT
                                CT TCAGTCT    TTGCAGG
                                || |||||||    |||||||
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                                GA AGTCAGG     AACGTCC
                                 G      _____
GAM175  ATF3     5'  CGCCCGCCGGCCAGACAAACAG 14431      CA    _  TTT  A
                                CTGT  GTCTG CTG   GC GGCG
                                ||||  ||||| |||   || ||||
                                GACA  CAGAC GGC   CG CCGC
                                  AA    C  ___  C
GAM175  CXorf9   3'  CGCCCTCCACCAGCGACTGACA 38623         T   TTTGCA
              G                  CTGTCAGTC GCTG     GGCG
                                |||||||||| ||||     ||||
                                GACAGTCAG CGAC     CCGC
                                     _   CACCTC
GAM175  FLJ20195 3'  CCAGCCCCAGCAGACCACAG   34708      CA       TTT  A
                                CTGT  GTCTGCTG   GC GG
                                ||||  ||||||||   || ||
                                GACA  CAGACGAC   CG CC
                                  C_       CC_  A
GAM175  MAP3K6   5'  CGCCTGCAGCGGAGACTGGACA 16245      _    G    T
              G                  CTGTC AGTCT CTGTT GCAGGCG
                                ||||| ||||| ||||| |||||||
                                GACAG TCAGA GGCGA CGTCCGC
                                  G    _    _
GAM175  SRF      5'  GCCCTAGCAGACGGACAG    11950       A       TTTGCA
                                CTGTC GTCTGCTG     GGC
                                ||||| ||||||||     |||
                                GACAG CAGACGAT     CCG
                                  G       C_____
GAM175  LOC115004 3'  CCTGCTGCTCAGACTGA     73174         CT  TT
                                TCAGTCTG  GT  GCAGG
                                ||||||||  ||  |||||
                                AGTCAGAC  CG  CGTCC
                                     T_  T_
GAM175  LOC118611 5'  CACCCATGCAGACGACA     75470      A     _  TT
                                TGTC GTCTGC TG  TG
                                |||| ||||||  ||  ||
                                ACAG CAGACG AC  AC
                                  _      T  CC
GAM175  LOC197342 3'  CCTGGGCTGCAGACAGACA    87998      A     T   TG
                                TGTC GTCTGC GTT  CAGG
                                |||| ||||||  |||  ||||
                                ACAG CAGACG CGG  GTCC
                                  A     T  __
GAM175  LOC204084 5'  TTTGTACAGACTGACA      89450          CTGTT
                                TGTCAGTCTG    TGCAGG
                                ||||||||||    ||||||
                                ACAGTCAGAC    ATGTTT
                                              _____
GAM175  LOC83690  5'  CGCCCACCCTGGCAGACTAACG 48814      C       GTTTGCA
                                TGT AGTCTGCT      GGCG
                                |||  ||||||||      ||||
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                                GCA TCAGACGG      CCGC
                                  A       TCCCAC_
GAM175  LOC90515  3'  CGCCTGCAACCTTGATCGACAG 63123      A   TGCTGT
                                CTGTC GTC     TTGCAGGCG
                                ||||| |||     |||||||||
                                GACAG TAG     AACGTCCGC
                                   C   TTCC__
GAM176  FLJ22672  3'  AACCAGGCCGAGAGGCCAC   46066       ___
                                GTGGTC   CGGCCTGGTT
                                ||||||   ||||||||||
                                CACCGG   GCCGGACCAA
                                    AGA
GAM176  RBT1      3'  AACCAGGCCGGACCACGTGCAA 25348
              TA                  TATTGCACGTGGTCCGGCCTGGTT
                                ||||||||||||||||||||||||
                                ATAACGTGCACCAGGCCGGACCAA

GAM177  ATP11A    3'  TGGCACCCTGGCCGCCTGGA   77037      CA      A
                                TTCAG  GTGGCCAG GTGCCA
                                |||||  |||||||| ||||||
                                AGGTC  CGCCGGTC CACGGT
                                   __       C
GAM177  GPRK6     3'  CGTGGCAGAGGAGCCACTGC   9110         CAGAG
                                GCAGTGGC    TGCCACG
                                ||||||||    |||||||
                                CGTCACCG    ACGGTGC
                                     AGGAG
GAM177  NOS1      3'  GGGACAGACACTGCTGAA    5251          GCCAGA  G  A
                                TTCAGCAGTG     GT CC C
                                ||||||||||     || || |
                                AAGTCGTCAC     CA GG G
                                      AGA___  _  C
GAM177  PTGS1     3'  TTCTGGCCTCTGCTGAA     6358          T
                                TTCAGCAG GGCCAGAG
                                |||||||| ||||||||
                                AAGTCGTC CCGGTCTT
                                     T
GAM177  PTGS1     3'  TTCTGGCCTCTGCTGAA     54577         T
                                TTCAGCAG GGCCAGAG
                                |||||||| ||||||||
                                AAGTCGTC CCGGTCTT
                                     T
GAM177  TOP3A     3'  ACCATAGCCACTGCTGAA    16069           CAGA
                                TTCAGCAGTGGC    GT
                                ||||||||||||    ||
                                AAGTCGTCACCG    CA
                                       ATAC
GAM177  AFAP      3'  GTGGCACAGCACTGCAGAA   41307     A     G CAGA
                                TTC GCAGTG C    GTGCCAC
                                ||| ||||||  |    |||||||
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                                AAG CGTCAC G    CACGGTG
                                  A     _ A___
GAM177  CSMD1    3' GTACCGGCACTGCTGAA     73127         G  AGA
                                TTCAGCAGTG CC   GTGC
                                |||||||||| ||   ||||
                                AAGTCGTCAC GG   CATG
                                      _  C__
GAM177  FLJ11151 3' GCTTCTGACCACTGCT      67880        C    T
                                AGCAGTGG CAGAG GC
                                |||||||| ||||| ||
                                TCGTCACC GTCTT CG
                                    A    _
GAM177  FLJ12076 3' CACCTGGCCAGTGCTGAA    47233        G     A
                                TTCAGCA TGGCCAG GTG
                                ||||||| ||||||| |||
                                AAGTCGT ACCGGTC CAC
                                   G     _
GAM177  FLJ20004 5' GGCCTGGCCACCGCCGGA    95298    A  A      AGT
                                TTC GC GTGGCCAG   GCC
                                ||| || ||||||||   |||
                                AGG CG CACCGGTC   CGG
                                  C  C      ___
GAM177  FLJ20004 3' GGCCTGGCCACCGCCGGA    34314    A  A      AGT
                                TTC GC GTGGCCAG   GCC
                                ||| || ||||||||   |||
                                AGG CG CACCGGTC   CGG
                                  C  C      ___
GAM177  FYCO1    5' TGGAGTCTGACCACTGCTGAG  44499         C   GTG
                                TTCAGCAGTGG CAGA   CCA
                                |||||||||| ||||   |||
                                GAGTCGTCACC GTCT   GGT
                                      A   GA_
GAM177  KIAA0415 3' GCTGCTGACCCTGCTGAA    92578        T  C   AGT
                                TTCAGCAG GG CAG   GC
                                |||||||| || |||   ||
                                AAGTCGTC CC GTC   CG
                                     _  A   GT_
GAM177  KIAA1377 3' TGGCACTTTGGCATAC      67180    _
                                GTG GCCAGAGTGCCA
                                ||| ||||||||||||
                                CAT CGGTTTCACGGT
                                  A
GAM177  KIAA1853 3' CACGGGACCATCTGCTGAA   69389        _  _ AGA
                                TTCAGCAG TGG CC   GTG
                                |||||||| ||| ||   |||
                                AAGTCGTC ACC GG   CAC
                                     T  A  G__
GAM177  MGC16824 5' TTTGCAGCCACTGCTGA     39727          __
                                TCAGCAGTGGC  CAGA
                                ||||||||||  ||||
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                                AGTCGTCACCG  GTTT
                                      AC
GAM177  MYL9     3'  CACCCTGACCGGCCACTGC    59934         ____  A
                                GCAGTGGCC    AG GTG
                                |||||||||    || |||
                                CGTCACCGG    TC CAC
                                     CCAG  C
GAM177  LOC145719 5' GGTCCCTGGCCCCTGCTGAA   83454        T     AGT
                                TTCAGCAG GGCCAG   GCC
                                |||||||| ||||||   |||
                                AAGTCGTC CCGGTC   TGG
                                     C     CC_
GAM177  LOC145720 5' GGTCCCTGGCCCCTGCTGAA   83436        T     AGT
                                TTCAGCAG GGCCAG   GCC
                                |||||||| ||||||   |||
                                AAGTCGTC CCGGTC   TGG
                                     C     CC_
GAM177  LOC157927 5' GTGGCACCCCCATGATGAA    86670     GCA    CCAGA
                                TTCA   GTGG    GTGCCAC
                                ||||   ||||    |||||||
                                AAGT   TACC    CACGGTG
                                  AG_    CC___
GAM177  LOC170392 3' GGTCACAGCACTGCTGAA     76365         G CAGA  _
                                TTCAGCAGTG C    GTG CC
                                |||||||||| |    ||| ||
                                AAGTCGTCAC G    CAC GG
                                      _ A___   T
GAM177  LOC197114 5' GGTCCCTGGCCCCTGCTGAA   89708        T     AGT
                                TTCAGCAG GGCCAG   GCC
                                |||||||| ||||||   |||
                                AAGTCGTC CCGGTC   TGG
                                     C     CC_
GAM177  LOC197117 5' GGTCCCTGGCCCCTGCTGAA   89722        T     AGT
                                TTCAGCAG GGCCAG   GCC
                                |||||||| ||||||   |||
                                AAGTCGTC CCGGTC   TGG
                                     C     CC_
GAM177  LOC200583 5' GTGCTCTGGCCACCATGAA    88835     GCA        TG
                                TTCA   GTGGCCAGAG  C
                                ||||   ||||||||||  |
                                AAGT   CACCGGTCTC  G
                                  AC_         GT
GAM177  LOC221656 3' GGTTCAACTACTGCTGAA     92229         CCA  GT
                                TTCAGCAGTGG   GA  GCC
                                ||||||||||   ||  |||
                                AAGTCGTCATC   CT  TGG
                                      AA_  __
GAM177  LOC257319 3' TACTCTACCACTGCT       95779        CC
                                AGCAGTGG  AGAGTG
                                ||||||||  ||||||
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                                TCGTCACC  TCTCAT
                                    A_
GAM177  LOC90333  3'  GTGGCACCCCATACTAGAA   62294     _ CA   CCAGA
                                TTC AG  GTGG    GTGCCAC
                                ||| ||  ||||    |||||||
                                AAG TC  TACC    CACGGTG
                                  A A_   C____
GAM178  CNGA1     3'  CAACTGATAATGTGCAAA    59507         GC   A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                    A_  _
GAM178  ESRRG     3'  TGGCAGTCTTATGTGCAAA   66396        TAGCT
                                TTTGCACAT    AGATTGCCA
                                |||||||||    |||||||||
                                AAACGTGTA    TCTGACGGT
                                    T____
GAM178  KCNJ3     3'  GCAATAATGTGCAAA      9525          GCTAGA
                                TTTGCACATTA     TTGC
                                ||||||||||     ||||
                                AAACGTGTAAT     AACG
                                    _______
GAM178  SDC2      3'  GCAAATTAATGTGTAAA     67132          CTAGA
                                TTTGCACATTAG    TTGC
                                ||||||||||||    ||||
                                AAATGTGTAATT    AACG
                                    A____
GAM178  USP9X     3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
          A                      TTTGCACATTAGC     GCCAT
                                ||||||||||||     |||||
                                AAATGTGTAATCG     CGGTA
                                    TAGTC_
GAM178  AMOTL1    3'  GGCAAGTAATGTGCAAA     73650         G  AGAT
                                TTTGCACATTA CT    TGCC
                                ||||||||||| ||    ||||
                                AAACGTGTAAT GA    ACGG
                                    _ ____
GAM178  BCAR3     3'  AGTAATAATGTGCAAA      13098         __
                                TTTGCACATTA  GCT
                                ||||||||||  |||
                                AAACGTGTAAT  TGA
                                    AA
GAM178  DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930        AGCTA    C
                                TTTGCACATT    GATTG CA
                                ||||||||||    ||||| ||
                                AGACGTGTAA    TTAAC GT
                                    A____     A
GAM178  MGC3184   3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                TTTGCACATTAG  AGA TG CAT
                                ||||||||||||  ||| || |||
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                                AGACGTGTAATC  TTT AC GTA
                                      __  T  A
GAM178  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
            AA                  TTTGCACATTAGCTAGATTGCCAT
                                ||||||||||||||||||||||
                                AAACGTGTAATCGATCTAACGGTA

GAM179  ABCD4    3'  GCCCACTACTCATAGCA     39739       GAAAGA   _
                                TGCTATG     AGTA TGGGC
                                |||||||     |||| |||||
                                ACGATAC     TCAT ACCCG
                                   _______   C
GAM179  APXL     3'  ACTTCTCCCATAGCA      7924         AA
                                TGCTATGG  AGAAGT
                                ||||||||  ||||||
                                ACGATACC  TCTTCA
                                     C_
GAM179  BAP1     3'  ACTGCTCTCCATAGCA      16212        A  A
                                TGCTATGGA AG AGT
                                ||||||||| || |||
                                ACGATACCT TC TCA
                                     C  G
GAM179  CYP2B6   3'  GCTTCCTTCCCCTCCATGGCA  5737         AA_   TAT
                                TGCTATGGA   GAAG   GGGC
                                |||||||||   ||||   ||||
                                ACGGTACCT   CTTC   TTCG
                                     CCC    C__
GAM179  DSCR3    3'  GCCAGGGACTCCCCATAGCA   20182        AAA  A  ATG_
                                TGCTATGG   GA GT    GGC
                                ||||||||   || ||    |||
                                ACGATACC   CT CA    CCG
                                     C__  _  GGGA
GAM179  EPB72    3'  GCTTTCTTTCCCAGCA      14607      AT      _
                                TGCT  GGAAAGAA GT
                                ||||  |||||||| ||
                                ACGA  CCTTTCTT CG
                                  C_       T
GAM179  HUNK     3'  GCCCTGCCTTTCATAGCA    27453         AGAA   T
                                TGCTATGGAA    GTA GGGC
                                ||||||||||    ||| ||||
                                ACGATACTTT    CGT CCCG
                                     C____  _
GAM179  IL1R1    3'  GCCCATGCTTTCCCACCAGCA  6060      A_  AAA
                                TGCT  TGG   GAAGTATGGGC
                                ||||  |||   ||||||||||||
                                ACGA  ACC   TTTCGTACCCG
                                  CC   C__
GAM179  MEF2D    5'  GCCCCTCCCCTCCGTAGCA   19798         AAGA  TAT
                                TGCTATGGA    AG   GGGC
                                |||||||||    ||   ||||
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                                ACGATGCCT   TC  CCCG
                                     CCCC ___
GAM179  NXT1    5' GCCCTCCTTCCATAG      25114       A  AGTAT
                                CTATGGAA GA    GGGC
                                |||||||| ||    ||||
                                GATACCTT CT    CCCG
                                     C _____
GAM179  PCDH11Y  3' ATTTTCTTCCATAGCA     52076        AG
                                TGCTATGGAA  AAGT
                                ||||||||||  ||||
                                ACGATACCTT  TTTA
                                      CT
GAM179  RAG1    3' GCCCTTCTTCTTTCCA     4815         TAT
                                TGGAAAGAAG  GGGC
                                ||||||||||  ||||
                                ACCTTTCTTC  CCCG
                                      TT_
GAM179  RRM2B   3' GGCTCCATTCTTTCCATAACA 67828   C       GTAT
                                TG TATGGAAAGAA   GGGCC
                                || ||||||||||   |||||
                                AC ATACCTTTCTT   CTCGG
                                 A        AC__
GAM179  SLC17A4  3' ATTTCTTTCCAAAGCA     18524     A
                                TGCT TGGAAAGAAGT
                                |||| ||||||||||
                                ACGA ACCTTTCTTTA
                                  A
GAM179  STK10   3' CCCAGTCTGCTCCATAGCA   19983       A_  AGTA
                                TGCTATGGA  AGA   TGGG
                                |||||||||  |||   ||||
                                ACGATACCT  TCT   ACCC
                                     CG  G___
GAM179  ABLIM   3' CTCTTTCTGCTTCCCATAGCA 9766       A  A  TAT
                                TGCTATGG AAG AG   GGG
                                |||||||| ||| ||   |||
                                ACGATACC TTC TC   CTC
                                     C  G  TTT
GAM179  ABLIM   3' GCTTCTTTCCATATCA     9772     C
                                TG TATGGAAAGAAGT
                                || ||||||||||||
                                AC ATACCTTTCTTCG
                                 T
GAM179  ABLIM   3' CTCTTTCTGCTTCCCATAGCA 22027       A  A  TAT
                                TGCTATGG AAG AG   GGG
                                |||||||| ||| ||   |||
                                ACGATACC TTC TC   CTC
                                     C  G  TTT
GAM179  ABLIM   3' GCTTCTTTCCATATCA     22033    C
                                TG TATGGAAAGAAGT
                                || ||||||||||||
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                                AC ATACCTTTCTTCG
                                 T
GAM179  AD034    5'  CCGTTCCTTTCCATCGCA    48945     T      AAGT
                                TGC ATGGAAAG    ATGG
                                ||| ||||||||    ||||
                                ACG TACCTTTC    TGCC
                                  C       CT__
GAM179  AP1S2    3'  GCTTCCTTTCTTTCCATGGCA  14041             TAT
                                TGCTATGGAAAGAAG   GGGC
                                ||||||||||||||   ||||
                                ACGGTACCTTTCTTT   TTCG
                                          CC_
GAM179  ATP6M8-9 3'  ACTTCTTTACACAGCA      19272      A  G
                                TGCT TG AAAGAAGT
                                |||| || ||||||||
                                ACGA AC TTTCTTCA
                                  C  A
GAM179  C1orf34  3'  GGCTTCATCCCCTGCCCATAGC 60677         AA  AAGT   _
           A                     TGCTATGG  AG    ATGG GCC
                                ||||||||  ||    |||| |||
                                ACGATACC  TC    TACT CGG
                                     CG  CCC_    T
GAM179  CSEN     3'  GGCCCCATTCTCCCTCCATGGC 25532          A__    GTAT
           A                     TGCTATGGA   AGAA    GGGCC
                                |||||||||   ||||    |||||
                                ACGGTACCT   TCTT    CCCGG
                                     CCC    AC__
GAM179  Cyt19    3'  CCTGCTTTTCCCCATAGCA   72936        AA      T
                                TGCTATGG  AGAAGTA GG
                                ||||||||  |||||||  ||
                                ACGATACC  TTTTCGT CC
                                     CC      _
GAM179  DCTN3    3'  ATGCTTCTCTCCAAGCA     44306      A    A
                                TGCT TGGA AGAAGTAT
                                |||| |||| ||||||||
                                ACGA ACCT TCTTCGTA
                                  _    C
GAM179  DMWD     3'  CCCCTTTTCATAGCA       60878           AAGTAT
                                TGCTATGGAAAG     GGG
                                ||||||||||||     |||
                                ACGATACTTTTC     CCC
                                         _______
GAM179  FLJ00001 3'  CCATCTTCTCCATAGCA     81814          AA    T
                                TGCTATGGA  GAAG ATGG
                                |||||||||  |||| ||||
                                ACGATACCT  CTTC TACC
                                         __   _
GAM179  FLJ10769 3'  GCATCTTTCCACAGCA      36597      A       A
                                TGCT TGGAAAGA GT
                                |||| |||||||| ||
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                                ACGA ACCTTTCT CG
                                  C       A
GAM179  FLJ20281  3'  CCTGTCTCTCATAGCA      90981        GAA   A T
                                TGCTATG   AGA G ATGGG
                                |||||||   ||| | |||||
                                ACGATAC   TCT C TGTCC
                                    ____  _ _
GAM179  FLJ20477  5'  GCCCCGCCCCTCCGCCATAGCA 35242         AA_  AA  AT
                                TGCTATGG   AG  GT  GGGC
                                ||||||||   ||  ||  ||||
                                ACGATACC   TC  CG  CCCG
                                     GCC  CC  C_
GAM179  FLJ22555  5'  ACTTCCTTTCCATACA      44512    C       _
                                TG TATGGAAAG AAGT
                                || |||||||| ||||
                                AC ATACCTTTC TTCA
                                 _       C
GAM179  FREQ      3'  GCCCGTGCGCCTCTCCACAGC  26580     A    A  AA
                                GCT TGGA AG  GTATGGGC
                                ||| |||| ||  ||||||||
                                CGA ACCT TC  CGTGCCCG
                                  C    C  CG
GAM179  GIT2      3'  CCATATGTTCTGTCCCATAGCA 28757         AA_   _
                                TGCTATGG   AGAA GTATGG
                                ||||||||   |||| ||||||
                                ACGATACC   TCTT TATACC
                                     CTG    G
GAM179  GIT2      3'  CCATATGTTCTGTCCCATAGCA 54079         AA_   _
                                TGCTATGG   AGAA GTATGG
                                ||||||||   |||| ||||||
                                ACGATACC   TCTT TATACC
                                     CTG    G
GAM179  GIT2      3'  CCATATGTTCTGTCCCATAGCA 54092         AA_   _
                                TGCTATGG   AGAA GTATGG
                                ||||||||   |||| ||||||
                                ACGATACC   TCTT TATACC
                                     CTG    G
GAM179  HEMK      3'  GCCCATACCTCTGCTGGCA    32434       TGGAA   A
                                TGCTA     AGA GTATGGGC
                                |||||     ||| ||||||||
                                ACGGT     TCT CATACCCG
                                   CG___   C
GAM179  KIAA0057  3'  GCCAGTGGTCCTTTCCACAGC  24431     A      AAG   G
                                GCT TGGAAAG   TAT GGC
                                ||| |||||||   ||| |||
                                CGA ACCTTTC   GTG CCG
                                  C      CTG   A
GAM179  KIAA1018  3'  GCCCAGCTCCCCATAGCA    30351         AAA  A  A
                                TGCTATGG   GA GT TGGGC
                                ||||||||   || || |||||
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                                ACGATACC   CT CG ACCCG
                                    C__  _ _
GAM179  KIAA1069  3'  GCGTCCTTTCTCATAGCA    67937       _    AA_
                                TGCTATG GAAAG   GT
                                ||||||| |||||   ||
                                ACGATAC CTTTC   CG
                                    T    CTG
GAM179  KIAA1449  3'  GGCCTGCCTCCACCATAGCA  40453       AAA  A  AT
                                TGCTATGG   GA GT  GGGCC
                                ||||||||   || ||  |||||
                                ACGATACC   CT CG  TCCGG
                                    AC_  C  __
GAM179  KIAA1538  3'  CCCATACTCCTCTGAGGCA   71535     A    AA A
                                TGCT TGGA  G AGTATGGG
                                |||| ||||  | ||||||||
                                ACGG GTCT  C TCATACCC
                                  A   __ C
GAM179  NECL1     3'  ACCTCTCTTCCATAGCA     41023         _  A
                                TGCTATGGAA AGA GT
                                |||||||||| ||| ||
                                ACGATACCTT TCT CA
                                    C   C
GAM179  NECL1     3'  CCACTCCTCCCATGGCA     41024        AA  A   AT
                                TGCTATGG  AG AGT  GG
                                ||||||||  || |||  ||
                                ACGGTACC  TC TCA  CC
                                    C_  C  __
GAM179  Nup43     5'  GGCCCTGCAGTCCTTCCTATAG 45005       _   A  A_   T
          CA                      TGCTAT GGAA GA  GTA GGGCC
                                |||||| |||| ||  ||| |||||
                                ACGATA CCTT CT  CGT CCCGG
                                   T   C  GA  _
GAM179  ORMDL2    3'  ACTCTCCTCCATAGCA      26359         A_  A
                                TGCTATGGA  AGA GT
                                |||||||||  ||| ||
                                ACGATACCT  TCT CA
                                    CC  _
GAM179  PADI1     3'  GGCCCATGTCCCCTCCCACAGT 61998      A  AAAGAAG
          A                      TGCT TGG      TATGGGCC
                                |||| |||      ||||||||
                                ATGA ACC      GTACCCGG
                                  C  CTCCCCT
GAM179  PDE10A    3'  GCTTTCTGTCCATAGCA     21864         A   _
                                TGCTATGGA AGAA GT
                                ||||||||| |||| ||
                                ACGATACCT TCTT CG
                                    G   T
GAM179  PP1201    3'  GCTATTTCTTCCCCCAGCA   42193      AT  A      ATG
                                TGCT  GG AAGAAGT   GGC
                                ||||  || |||||||   |||
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                                ACGA  CC TTCTTTA   TCG
                                  CC  C      ___
GAM179  SCDGF-B  3' GCTTTTTCCTCTCATAGCA   47378       _ __
                                TGCTATG GA  AAGAAGT
                                ||||||| ||  |||||||
                                ACGATAC CT  TTTTTCG
                                    T  CC
GAM179  SCDGF-B  3' GCTTTTTCCTCTCATAGCA   52450       _ __
                                TGCTATG GA  AAGAAGT
                                ||||||| ||  |||||||
                                ACGATAC CT  TTTTTCG
                                    T  CC
GAM179  ZAK      3' GCACAGGTCCTTTCCATATCA  56128    C       AAGTA  G
                                TG TATGGAAAG     TG GC
                                || |||||||||     || ||
                                AC ATACCTTTC     AC CG
                                 T        CTGG_  A
GAM179  ZNF185   3' GCCCATGCTCTTCCCAGAGCA  23113     A   A    A
                                TGCT TGG AAGA GTATGGGC
                                |||| ||| |||| ||||||||
                                ACGA ACC TTCT CGTACCCG
                                  G   C   _
GAM179  LOC130951 3' GCCTGTGCCCTTCCCA      57145     A   AA
                                TGG AAG  GTATGGGC
                                ||| |||  ||||||||
                                ACC TTC  CGTGTCCG
                                  C   C_
GAM179  LOC134111 3' GCTTCTTTCCATGACA      75138    C
                                TG TATGGAAAGAAGT
                                || ||||||||||||
                                AC GTACCTTTCTTCG
                                 A
GAM179  LOC138240 5' CCCAGGAAAATTTCCATAGTA  75305          GAAGTA
                                TGCTATGGAAA     TGGG
                                ||||||||||     ||||
                                ATGATACCTTT     ACCC
                                      AAAAGG
GAM179  LOC143451 3' GCCACTCCTCCCCACTGCA    76565    TA   AA  A   ATG
                                TGC  TGG  AG AGT   GGC
                                |||  |||  || |||   |||
                                ACG  ACC  TC TCA   CCG
                                  TC   CC  C  ___
GAM179  LOC143451 3' GCCAGTGTCTCCATAGCA     76567         AA  AGTATG
                                TGCTATGGA  GA     GGC
                                |||||||||  ||     |||
                                ACGATACCT  CT     CCG
                                     __ GTGA__
GAM179  LOC145125 3' GCCACTCCTCCCCACTGCA    77008    TA   AA  A   ATG
                                TGC  TGG  AG AGT   GGC
                                |||  |||  || |||   |||
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                                ACG  ACC  TC TCA   CCG
                                  TC   CC  C  ___
GAM179  LOC145125 3'  GCCAGTGTCTCCATAGCA    77010         AA  AGTATG
                                TGCTATGGA  GA     GGC
                                |||||||||  ||     |||
                                ACGATACCT  CT     CCG
                                     __  GTGA__
GAM179  LOC148638 3'  GCTCACTCTCTTTCCACGCA   78920     TA       A TA
                                TGC  TGGAAAGA G  TGGGC
                                |||  ||||||||  |  |||||
                                ACG  ACCTTTCT C  ACTCG
                                  C_       _ TC
GAM179  LOC149132 5'  GGCCCATACCCTACGTCACGGC 79177     TA   AAAGAA
              A                   TGC  TGG     GTATGGGCC
                                |||  |||     |||||||||
                                ACG  ACT     CATACCCGG
                                  GC   GCATCC
GAM179  LOC151996 5'  GGCCCATACCCCTCCAGACA   85536    CTA    AAGAA
                                TG   TGGA    GTATGGGCC
                                ||   ||||    |||||||||
                                AC   ACCT    CATACCCGG
                                 AG_    CCC__
GAM179  LOC154222 3'  ACATTCCATCCATAGCA     86186         AA   _
                                TGCTATGGA  GAA GT
                                |||||||||  |||  ||
                                ACGATACCT  CTT CA
                                     AC   A
GAM179  LOC157931 3'  GCCCAAAGCTTCATAGCA    86664       GGAAA    A_
                                TGCTAT    GAAGT  TGGGC
                                ||||||    |||||  |||||
                                ACGATA    CTTCG  ACCCG
                                   ______     AA
GAM179  LOC200492 3'  GGCCATTGTTCTTTCCACCGCA 90088     TA       GTATG
                                TGC  TGGAAAGAA    GGCC
                                |||  |||||||||    ||||
                                ACG  ACCTTTCTT    CCGG
                                  CC       GTTA_
GAM179  LOC219848 3'  CCCCCTCCCATAGCA       91492         AAA  A TAT
                                TGCTATGG   GA G   GGG
                                ||||||||   || |   |||
                                ACGATACC   CT C   CCC
                                     ___  _ C__
GAM179  LOC221415 5'  GCCCAGATGTCCATAGCA    93874         AAGAAGTA
                                TGCTATGGA       TGGGC
                                |||||||||       |||||
                                ACGATACCT       ACCCG
                                     GTAG____
GAM179  LOC221510 3'  CCCATATTCCCACAGCA     91057      A   AAA   G
                                TGCT TGG   GAA TATGGG
                                ||||  |||   |||  ||||||
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                                ACGA ACC   CTT ATACCC
                                  C  ___   _
GAM179  LOC222134 5'  GCCCATGTGTCCCATA      94140      AAA  AG
                                TATGG   GA  TATGGGC
                                |||||   ||  |||||||
                                ATACC   CT  GTACCCG
                                   ___  GT
GAM179  LOC222488 5'  GCCCTGCCGTCCATAGCA    94345        AAGAA   T
                                TGCTATGGA    GTA GGGC
                                |||||||||    ||| ||||
                                ACGATACCT    CGT CCCG
                                     GC___   _
GAM179  LOC253424 5'  GGCCCATACCTCTGTTGTG    97577    TG AA   A
                                TA  G  AGA GTATGGGCC
                                ||  |  ||| |||||||||
                                GT  T  TCT CATACCCGG
                                 GT G_   C
GAM179  LOC254440 3'  GCCAGTGTCTCCATAGCA    97069        AA  AGTATG
                                TGCTATGGA  GA     GGC
                                |||||||||  ||     |||
                                ACGATACCT  CT     CCG
                                     __ GTGA__
GAM179  LOC254440 3'  GCCACTCCTCCCCACTGCA    97067     TA   AA  A   ATG
                                TGC  TGG  AG AGT   GGC
                                |||  |||  || |||   |||
                                ACG  ACC  TC TCA   CCG
                                  TC   CC  C  ___
GAM179  LOC57109  3'  GCTTCTCCCCATAGCA      39851        AA
                                TGCTATGG  AGAAGT
                                ||||||||  ||||||
                                ACGATACC  TCTTCG
                                     CC
GAM179  LOC91923  5'  CCACTGTTTTCCATAGCA    67550          A   AT
                                TGCTATGGAAAG AGT  GG
                                |||||||||||| |||  ||
                                ACGATACCTTTT TCA  CC
                                       G  __
GAM179  LOC93444  3'  GGTATCTTTTTTCCACAGCA   72389     A        TATGG
                                TGCT TGGAAAGAAG    GCC
                                ||||  ||||||||||    |||
                                ACGA ACCTTTTTTC    TGG
                                  C        TA___
GAM180  ADAMTS8   5'  TCGGGCCGCCAGCACCTG    22886    _      ATAAG
                                CAG TGCTGGC    CTGA
                                |||  |||||||    ||||
                                GTC ACGACCG    GGCT
                                  C      CCG__
GAM180  BAP1      3'  TCAGGGACCCAGCACTGG    16219          CATAAG
                                CCAGTGCTGG     CTGA
                                ||||||||||     ||||
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                                GGTCACGACC     GACT
                                      CAGG__
GAM180  BF      5'  TTCAGCTTGGACACTG     8140       CTGGCA
                                CAGTG     TAAGCTGAA
                                |||||     |||||||||
                                GTCAC     GTTCGACTT
                                   AG_____
GAM180  C1QB    3'  TTCAACTCTGTGTCCCAGCACT 4923    A        __   _ C
           GGC                     G CCAGTGCTGG  CATA AG TGAA
                                | ||||||||||  |||| || ||||
                                C GGTCACGACC  GTGT TC ACTT
                                _         CT    C  A
GAM180  CHC1    3'  CAGCCCTGAGCACTGTGTC    7020     _      __ CATAA
                                GAC CAGTGCT  GG     GCTG
                                ||| |||||||  ||     ||||
                                CTG GTCACGA  CC     CGAC
                                  T       GT  _____
GAM180  CMRF35  5'  CAGAGCTGTCAGCACCGG    21929    A        TAAG
                                CC GTGCTGGCA    CTG
                                || |||||||||    |||
                                GG CACGACTGT    GAC
                                 C        CGA_
GAM180  EPHB6   3'  TCAGCCCTGGACACTGGTC    15466         _ TG CATAA
                                GACCAGTG C  G     GCTGA
                                |||||||| |  |     |||||
                                CTGGTCAC G  C     CGACT
                                     A GT C____
GAM180  EVPL    5'  CAGCCTGAGCCAGCACT     8803          A  A
                                AGTGCTGGC TA GCTG
                                ||||||||| || ||||
                                TCACGACCG GT CGAC
                                     A  C
GAM180  GARP    3'  CAGCCCAGCACTGG        18594          CATAA
                                CCAGTGCTGG    GCTG
                                ||||||||||    ||||
                                GGTCACGACC    CGAC
                                      _____
GAM180  GJB5    3'  CAGCTCGACGGCACTGG     17945          GCATA
                                CCAGTGCTG    AGCTG
                                |||||||||    |||||
                                GGTCACGGC    TCGAC
                                     AGC__
GAM180  GPR81   3'  CTTACCAGCATTAGTC      50757     C       CA
                                GAC AGTGCTGG  TAAG
                                ||| ||||||||  ||||
                                CTG TTACGACC  ATTC
                                  A       __
GAM180  IFI16   5'  AGCAAGCCAGCACTAGTC    71221     C        ATAA
                                GAC AGTGCTGGC   GCT
                                ||| |||||||||   |||
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                                CTG TCACGACCG    CGA
                                  A       AA__
GAM180  KRT4     3'  CAGCTGGGCCCAGCACTGGT  9635          _ ATA
                                ACCAGTGCTGG C   AGCTG
                                |||||||||||  |   |||||
                                TGGTCACGACC G   TCGAC
                                      C GG_
GAM180  MAP3K9   3'  TTCAGCTTCCCAAACACCAGT  60709    CA   C_   CAT
                                AC  GTG  TGG   AAGCTGAA
                                ||  |||  |||   ||||||||
                                TG  CAC  ACC   TTCGACTT
                                 AC   AA   C__
GAM180  MGAT5    5'  TCAGCTTACAGTTCCTG     10028     T_    GCA
                                CAG  GCTG   TAAGCTGA
                                |||  ||||   ||||||||
                                GTC  TGAC   ATTCGACT
                                  CT   ____
GAM180  MOCS1    3'  TTCAGCTTAACAGTTGCCCGGT 92037      A_   _   GCA
            C                    GACC  GTG CTG   TAAGCTGAA
                                ||||  ||| |||   |||||||||
                                CTGG  CGT GAC   ATTCGACTT
                                  CC   T   A__
GAM180  P23      3'  TCAGCTTATACCCGGGCT    21719     G    C_
                                AGT CTGG  ATAAGCTGA
                                ||| ||||  |||||||||
                                TCG GGCC  TATTCGACT
                                  _    CA
GAM180  PFKFB4   3'  TCAGCCACATGCAACACTGTGT 15874     _     CTG    AA_
            C                    GAC CAGTG   GCAT   GCTGA
                                ||| |||||   ||||   |||||
                                CTG GTCAC   CGTA   CGACT
                                  T    AA_    CAC
GAM180  PTPRK    3'  TTCAGCCTGTGGCCCAGCACTG 11125           __    A
            GTC                    GACCAGTGCTGG  CATA GCTGAA
                                ||||||||||||  |||| ||||||
                                CTGGTCACGACC  GTGT CGACTT
                                      CG    C
GAM180  RNPEPL1  3'  CGGATGCCAGCACCTG      36676     _       AAG
                                CAG TGCTGGCAT   CTG
                                |||  |||||||||   |||
                                GTC ACGACCGTA   GGC
                                  C       ___
GAM180  UBE2L3   3'  TCAGCCCTGGCACTGGC     12507    A      TG CATAA
                                G CCAGTGC  G    GCTGA
                                | |||||||  |    |||||
                                C GGTCACG  C    CGACT
                                 _      GT C____
GAM180  APXL2    5'  CAGCCTCAGCACTCATC     75185    CC       CATAA
                                GA  AGTGCTGG    GCTG
                                ||  ||||||||    ||||
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                                CT  TCACGACT    CGAC
                                 AC       C____
GAM180  ARHGEF9  3'  TTCAGCTTACCAAGCA     30824      _  CA
                                TGCT GG  TAAGCTGAA
                                |||| ||  |||||||||
                                ACGA CC  ATTCGACTT
                                  A  __
GAM180  CEGP1    3'  TTCAGCTTCCTCTAGCCCGG   40589    AGT    CAT
                                CC   GCTGG   AAGCTGAA
                                ||   |||||   ||||||||
                                GG   CGATC   TTCGACTT
                                 CC_    TCC
GAM180  DKFZp547D155 3'  CAGCCCTGAGACCACTGGTC   70435        CTGG  TAA
                                GACCAGTG    CA   GCTG
                                ||||||||    ||   ||||
                                CTGGTCAC    GT   CGAC
                                     CAGA  CC_
GAM180  DKFZP727G051 3'  TTCAGCCCATCAACCAGCATTG 69483           CATAA__
           GTC                    GACCAGTGCTGG      GCTGAA
                                ||||||||||||      ||||||
                                CTGGTTACGACC      CGACTT
                                      AACTACC
GAM180  DUSP14   5'  CACTGTCACCAGCACTGCTC   22834    C       CATA  C
                                GA CAGTGCTGG    AG TG
                                || |||||||||    || ||
                                CT GTCACGACC    TC AC
                                 C       ACTG  _
GAM180  FLJ10206  5'  CAGCTTATGCCAGGAGTC    35898     CAGTG
                                GAC    CTGGCATAAGCTG
                                |||    ||||||||||||||
                                CTG    GACCGTATTCGAC
                                  AG___
GAM180  FLJ20967  5'  GGCGCCCAGCACTGGTT     41962          CATAA
                                GACCAGTGCTGG    GCT
                                ||||||||||||    |||
                                TTGGTCACGACC    CGG
                                      CG___
GAM180  FLJ22569  3'  TTCAGCTTACTAAACTG     43679      GC   CA
                                CAGT  TGG  TAAGCTGAA
                                ||||  |||  |||||||||
                                GTCA  ATC  ATTCGACTT
                                  A_  __
GAM180  FOXN4    3'  TTCAGCTTGGACACACTGG    75574       C  GCA
                                CCAGTG TG   TAAGCTGAA
                                |||||| ||   |||||||||
                                GGTCAC AC   GTTCGACTT
                                   _ AG_
GAM180  GW112    3'  TTCAACTGAAGCCAGCACTGGT 21194           ATA  C
           T                    GACCAGTGCTGGC   AG TGAA
                                ||||||||||||||   || ||||
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                                TTGGTCACGACCG  TC ACTT
                                      AAG  A
GAM180  HOOK2    3'  CAGCTCACATGGCGCCCAGCAC 25256        _____  A__
            TGG                  CCAGTGCTGG   CAT  AGCTG
                                 ||||||||||   |||  |||||
                                 GGTCACGACC   GTA  TCGAC
                                      CGCG  CAC
GAM180  jdp2     3'  TTCAGCACAGCCAGCAT    55327       ATAA
                                 GTGCTGGC   GCTGAA
                                 ||||||||   ||||||
                                 TACGACCG   CGACTT
                                     ACA_
GAM180  KIAA0767 3'  TCTGCTGCCAGCACAGG    60632    A      TAA  T
                                 CC GTGCTGGCA  GC GA
                                 || |||||||||  || ||
                                 GG CACGACCGT  CG CT
                                  A       ___  T
GAM180  KIAA0923 3'  TCAGCTTGATGCATGGTC    25838     G   TGGCA
                                 GACCA TGC    TAAGCTGA
                                 ||||| |||    ||||||||
                                 CTGGT ACG    GTTCGACT
                                    _  TA___
GAM180  KIAA0982 3'  TTCACTGTTTGCCAGCAC    25852       TA_  C
                                 GTGCTGGCA  AG TGAA
                                 |||||||||  || ||||
                                 CACGACCGT  TC ACTT
                                      TTG  _
GAM180  KIAA1000 3'  TTCAGCTTTGCAAAGTACTGG  65281       G_   T
                                 CCAGTGCT  GCA AAGCTGAA
                                 ||||||||  ||| ||||||||
                                 GGTCATGA  CGT TTCGACTT
                                     AA  _
GAM180  MAP3K3   3'  TCAGCCTGGGCGCTGGTC    9999        GG  TAA
                                 GACCAGTGCT  CA  GCTGA
                                 ||||||||||  ||  |||||
                                 CTGGTCGCGG  GT  CGACT
                                      __  C__
GAM180  MGC16037 5'  CTTGTCCAGCACTAGTC    51821    C      C
                                 GAC AGTGCTGG ATAAG
                                 ||| |||||||| |||||
                                 CTG TCACGACC TGTTC
                                   A      _
GAM180  MIDORI   3'  TCAGCTTATCCTGCAACT    73792    _  T  C
                                 AGT GC GG ATAAGCTGA
                                 ||| || || |||||||||
                                 TCA CG CC TATTCGACT
                                   A  T  _
GAM180  MtFMT    5'  CAGTGGCGAGCACTGG      57651       G  ATAA
                                 CCAGTGCT GC   GCTG
                                 |||||||| ||   ||||
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                                GGTCACGA CG    TGAC
                                    G  G___
GAM180  PCDH16    5'  TCAGTTCCAACCACTGG     72826       C_   CATA
                                CCAGTG  TGG    AGCTGA
                                ||||||  |||    ||||||
                                GGTCAC  ACC    TTGACT
                                   CA   _____
GAM180  QKI       3'  CAGCTTATCAACTCGTC     65439     C   GCTGGC
                                GAC AGT     ATAAGCTG
                                ||| |||     ||||||||
                                CTG TCA     TATTCGAC
                                  C   AC_____
GAM180  TNRC6     3'  CAACTTTTAGCACTG       70506         CAT   C
                                CAGTGCTGG   AAG TG
                                |||||||||   ||| ||
                                GTCACGATT   TTC AC
                                    ___   A
GAM180  TOB2      3'  CAGCCCAGGCCAGCACTG    95618          ATAA
                                CAGTGCTGGC    GCTG
                                ||||||||||    ||||
                                GTCACGACCG    CGAC
                                     GACC
GAM180  TU12B1-TY 3'  TCAGCCCACAGCACTGTC    33406     C      GCATAA
                                GAC AGTGCTG     GCTGA
                                ||| |||||||     |||||
                                CTG TCACGAC     CGACT
                                  _      ACC___
GAM180  TUSP      3'  TCAGCCTAAGAGCGCAGCACTG 39641         _  A__  A
                                CAGTGCTG GC   TA GCTGA
                                |||||||| ||   || |||||
                                GTCACGAC CG   AT CGACT
                                    G  AGA  C
GAM180  USP19     3'  TCAGCTTATGCATCTGGT    88959       TGCTG
                                ACCAG    GCATAAGCTGA
                                |||||    ||||||||||
                                TGGTC    CGTATTCGACT
                                   TA___
GAM180  ZD52F10   3'  CAGCCTGTGCCAGCCCTGG    52819     T       A
                                CCAG GCTGGCATA GCTG
                                |||| ||||||||| ||||
                                GGTC CGACCGTGT CGAC
                                  C        C
GAM180  LOC145268 3'  TCAGCTTACAAGAGCCACTG   77062      _ GGCA
                                CAGTG CT    TAAGCTGA
                                ||||| ||    ||||||||
                                GTCAC GA    ATTCGACT
                                   C  GAAC
GAM180  LOC149296 5'  CAGCTTATGGGCAGCA      79256       G_
                                TGCTG  CATAAGCTG
                                |||||  |||||||||
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                                ACGAC  GTATTCGAC
                                   GG
GAM180  LOC161877 5'  TCAGGGCAGGCCAGCGCTGG  82326          ATAAG
                                CCAGTGCTGGC    CTGA
                                ||||||||||    ||||
                                GGTCGCGACCG    GACT
                                     GACGG
GAM180  LOC163115 5'  TCAGCCCCTGACAGCACTGG  82413        G  TAA
                                CCAGTGCTG CA   GCTGA
                                ||||||||| ||   |||||
                                GGTCACGAC GT   CGACT
                                     A  CCC
GAM180  LOC196500 3'  TCAGCTCACTCAGTGGTC    87744     AGT    CATA
                                GACC   GCTGG   AGCTGA
                                ||||   |||||   ||||||
                                CTGG   TGACT   TCGACT
                                  ___    CAC_
GAM180  LOC197287 3'  TCAGCTCATGTGTTTTGCACTG 60865       T_    __
                                CAGTGC  GGCATA  AGCTGA
                                ||||||  ||||||  ||||||
                                GTCACG  TTGTGT  TCGACT
                                   TT     AC
GAM180  LOC200470 5'  TCAGCCTGCGGCGCTGG     90069        G  TAA
                                CCAGTGCTG CA   GCTGA
                                ||||||||| ||   |||||
                                GGTCGCGGC GT   CGACT
                                     _ C__
GAM180  LOC221584 3'  CAGCTTATGTGGCAC       93828       G
                                GTGCTG CATAAGCTG
                                |||||| |||||||||
                                CACGGT GTATTCGAC
                                  _
GAM180  LOC51716  3'  CAGCTCATGGCCCTAGCA    32787       ___  A
                                TGCTGG   CAT AGCTG
                                ||||||   ||| |||||
                                ACGATC   GTA TCGAC
                                   CCG   C
GAM180  LOC92196  5'  CAGAGCACCAGCACTGGC    68456   A       CATAAG
                                G CCAGTGCTGG     CTG
                                | ||||||||||     |||
                                C GGTCACGACC     GAC
                                _        ACGA__
GAM181  AAT1     5'  TGGCGGGAGGAAAGAGGCGGCA 80495         ___  GT  G
                                TGCTGCCTC   CCT  TT GCCA
                                |||||||||   |||  || ||||
                                ACGGCGGAG   GGA  GG CGGT
                                     AAA   __  G
GAM181  ACCN2    3'  TTGGATAGGGGAACAGCA    39171      CC      TG
                                TGCTG  TCCCTGTT  G
                                |||||  ||||||||  |
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                                ACGAC  GGGGATAG  T
                                  AA       GT
GAM181  ADAM11   3'  GCCACGGAGGGAGGCACCA   9967     C       GTT
                                TG TGCCTCCCT   TGGC
                                || |||||||||   ||||
                                AC ACGGAGGGA   ACCG
                                 C        GGC
GAM181  ADAM11   3'  GCCACGGAGGGAGGCACCA   41214    C       GTT
                                TG TGCCTCCCT   TGGC
                                || |||||||||   ||||
                                AC ACGGAGGGA   ACCG
                                 C        GGC
GAM181  ADAMTS8  3'  TTGGCCATATCAAGGCAGCA  22888        CCC  TT_
                                TGCTGCCT   TG   TGGCCAA
                                ||||||||   ||   |||||||
                                ACGACGGA   AC   ACCGGTT
                                     ___  TAT
GAM181  AKAP2    3'  GAACAGAGGAGGCAGCA     23261         _
                                TGCTGCCTCC CTGTTT
                                |||||||||| ||||||
                                ACGACGGAGG GACAAG
                                      A
GAM181  ALOX12B  5'  GGCCACCAAGGGCAGCA     6682         CCC  TT
                                TGCTGCCT   TG  TGGCC
                                ||||||||   ||  |||||
                                ACGACGGG   AC  ACCGG
                                     A__  C_
GAM181  ALX4     3'  TGGGAGGGAGGGGGCAGCA   41631        T   G   GG
                                TGCTGCC CCCT TTT  CCA
                                ||||||| |||| |||  |||
                                ACGACGG GGGA GGA  GGT
                                     _   G   G_
GAM181  AMN      3'  TGGCCACTGCTGGAGGCAGC  48194         CT  T_
                                GCTGCCTCC  GT  TGGCCA
                                |||||||||  ||  ||||||
                                CGACGGAGG  CG  ACCGGT
                                      T_  TC
GAM181  AOAH     3'  TGGGGAGCACAGGGAGGCAG  91118          _  GG
                                CTGCCTCCCTGT TT  CCA
                                ||||||||||| ||  |||
                                GACGGAGGGACA GA  GGT
                                       C  GG
GAM181  AQP6     3'  GGCACTGGGGAAGCAGGCA   53937    _  C     TTTG
                                TGC TGC TCCCTG    GCC
                                ||| ||| ||||||    |||
                                ACG ACG AGGGGT    CGG
                                  G  A     CA__
GAM181  ARCN1    5'  GTCAAGGGGGCAGCA       7982         T   GTT
                                TGCTGCC CCCT   TGGC
                                ||||||| ||||   ||||
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                                ACGACGG GGGA   ACTG
                                      _   ___
GAM181  ARF4L    3'  TCAAGAGGAAGAAGGCAGC   69815       C___   G
                                GCTGCCT   CCT TTTGG
                                |||||||   ||| |||||
                                CGACGGA   GGA GAACT
                                    AGAA  _
GAM181  ARNT2    3'  CCGACTGGAGGAACAGCA    29457      __    CT   T
                                TGCTG  CCTCC  GTT GG
                                |||||  |||||  ||| ||
                                ACGAC  GGAGG  CAG CC
                                   AA    T_  _
GAM181  ATP1A2   3'  GGCAGACAGGAAGGAAGCA   5526      G  C      G
                                TGCT CCT CCTGTTTG CC
                                |||| ||| |||||||| ||
                                ACGA GGA GGACAGAC GG
                                  A  A      _
GAM181  ATP6V0A4 5'  CCGAGTGGAGGGAGGCA    55598        G__
                                TGCCTCCCT   TTTGG
                                |||||||||   |||||
                                ACGGAGGGA   GAGCC
                                     GGT
GAM181  ATP6V0A4 5'  CCGAGTGGAGGGAGGCA    40188        G__
                                TGCCTCCCT   TTTGG
                                |||||||||   |||||
                                ACGGAGGGA   GAGCC
                                     GGT
GAM181  AVP      5'  CCAGCAGAGGCAGCA       4920         CC    T
                                TGCTGCCTC  TGTT GG
                                |||||||||  |||| ||
                                ACGACGGAG  ACGA CC
                                     __   _
GAM181  AXIN1    3'  GCCCCCAAGGAGGCAGC     60857        C  TTT
                                GCTGCCTCC TG   GGC
                                ||||||||| ||   |||
                                CGACGGAGG AC   CCG
                                     A  CC_
GAM181  B4GALT4  3'  GGCTGCAAAGGCAGCA      13673        CCC   TT
                                TGCTGCCT   TGT  GGCC
                                |||||||   |||  ||||
                                ACGACGGA   ACG  TCGG
                                     A__   __
GAM181  BAZ2A    3'  CAGGCAAGGGAACAACA     25597    C  CC    _
                                TG TG  TCCCT GTTTG
                                || ||  ||||| |||||
                                AC AC  AGGGA CGGAC
                                 A  A_    A
GAM181  BAZ2B    3'  GGTAGAACAGGGAAGCACA   25622    C   C       G
                                TG TGC TCCCTGTTT GCC
                                || ||| ||||||||| |||
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                                AC ACG AGGGACAAG TGG
                                 _  A       A
GAM181  BDNF    5'  CCGGCGGGGAGCAGCA     59600      C      T
                                TGCTGC TCCCTGTT GG
                                |||||| |||||||| ||
                                ACGACG AGGGGCGG CC
                                   _      _
GAM181  BMP7    3'  TGGCCAGGAACCAGCA     8167      CC   CTGTT
                                TGCTG  TCC    TGGCCA
                                |||||  |||    ||||||
                                ACGAC  AGG    ACCGGT
                                  CA  ______
GAM181  CALR    3'  CCAGAGGAGGGCAGCA     62974       TC   GT
                                TGCTGCC  CCT  TTGG
                                |||||||  |||  ||||
                                ACGACGG  GGA  GACC
                                    GA  __
GAM181  CAPN1   3'  TTGGAGCAGAGAGGCAGC    17753        C    TGG
                                GCTGCCTC CTGTT   CCAA
                                |||||||| |||||   ||||
                                CGACGGAG GACGA   GGTT
                                    A    ___
GAM181  CAPN10  3'  GGCCAGACGGCGGGGGGCAGCA 43602          __
                                TGCTGCCTCCC  TGTTTGGCC
                                ||||||||||  |||||||||
                                ACGACGGGGGG  GCAGACCGG
                                      CG
GAM181  CBFA2T2 3'  GCCAGGCTGGAGGCGGCA    17468         CT
                                TGCTGCCTCC  GTTTGGC
                                ||||||||||  |||||||
                                ACGGCGGAGG  CGGACCG
                                      T_
GAM181  CBFA2T3 3'  TGGCCTGCCGGACACAGCA   17763      CC   CT  TT
                                TGCTG  TCC  GT  GGCCA
                                |||||  |||  ||  |||||
                                ACGAC  AGG  CG  CCGGT
                                  AC   C_  T_
GAM181  CCK     3'  CCAACCCAGAGGAGGCAG    5585         _   T_
                                CTGCCTCC CTG  TTGG
                                |||||||| |||  ||||
                                GACGGAGG GAC  AACC
                                    A   CC
GAM181  CCND2   3'  TTGAGCTTAAACAGAAGCAGCA 8301        CTCC      _ _
                                TGCTGC    CTGTTTG GC CAA
                                ||||||    ||||||| || |||
                                ACGACG    GACAAAT CG GTT
                                   AA__       T  A
GAM181  CCND3   3'  CCAGCAGGGAAAATGCAGCA  8304        C___       T
                                TGCTGC    TCCCTGTT GG
                                ||||||    |||||||| ||
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                              ACGACG   AGGGACGA CC
                                 TAAA     _
GAM181  CENTD2   3' GGCAGGGGTGGGAGGCAGCA  30872        TGTTTG
                              TGCTGCCTCCC    GCC
                              ||||||||||    |||
                              ACGACGGAGGG    CGG
                                    TGGGGA
GAM181  CENTD2   3' GGCAGGGGTGGGAGGCAGCA  57556        TGTTTG
                              TGCTGCCTCCC    GCC
                              ||||||||||    |||
                              ACGACGGAGGG    CGG
                                    TGGGGA
GAM181  CGTHBA   3' TGGCCCTCCAGCAAGGCAGCA 23865       CC  TTT
                              TGCTGCCT CTG  GGCCA
                              ||||||| |||  |||||
                              ACGACGGA GAC  CCGGT
                                   AC  CTC
GAM181  CHGA     3' GGTAGGGAGGCAGC      7044         GTTTG
                              GCTGCCTCCCT   GCC
                              ||||||||||   |||
                              CGACGGAGGGA   TGG
                                    _____
GAM181  COG6     5' TGGCTGAGGTGGCAGCA    72880       T CTGT TG
                              TGCTGCC CC   T GCCA
                              ||||||| ||   | ||||
                              ACGACGG GG   A CGGT
                                  T ____ GT
GAM181  COLQ     3' TTGGCCAAACAACCGGCTACA 54473   CT  TCCC
                              TG GCC  TGTTTGGCCAA
                              || |||  ||||||||||
                              AC CGG  ACAAACCGGTT
                               AT  CCA_
GAM181  COLQ     3' TTGGCCAAACAACCGGCTACA 54479   CT  TCCC
                              TG GCC  TGTTTGGCCAA
                              || |||  ||||||||||
                              AC CGG  ACAAACCGGTT
                               AT  CCA_
GAM181  COLQ     3' TTGGCCAAACAACCGGCTACA 54485   CT  TCCC
                              TG GCC  TGTTTGGCCAA
                              || |||  ||||||||||
                              AC CGG  ACAAACCGGTT
                               AT  CCA_
GAM181  COLQ     3' TTGGCCAAACAACCGGCTACA 54491   CT  TCCC
                              TG GCC  TGTTTGGCCAA
                              || |||  ||||||||||
                              AC CGG  ACAAACCGGTT
                               AT  CCA_
GAM181  COLQ     3' TTGGCCAAACAACCGGCTACA 54499   CT  TCCC
                              TG GCC  TGTTTGGCCAA
                              || |||  ||||||||||
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                                AC  CGG    ACAAACCGGTT
                                 AT   CCA_
GAM181   COLQ     3'  TTGGCCAAACAACCGGCTACA  19050    CT   TCCC
                                TG  GCC    TGTTTGGCCAA
                                ||  |||    ||||||||||
                                AC  CGG    ACAAACCGGTT
                                 AT   CCA_
GAM181   CPSF4    3'  CCAGGGAGGGAGGCAGC     21953          G
                                GCTGCCTCCCT TTTGG
                                |||||||||| |||||
                                CGACGGAGGGA GGACC
                                       G
GAM181   CSRP1    3'  TTGGAGGCAGAGAGGCATGCA  14538     _     C     GG
                                TGC TGCCTC CTGTTT  CCAA
                                ||| |||||| ||||||  ||||
                                ACG ACGGAG GACGGA  GGTT
                                  T     A     __
GAM181   CTLA4    3'  TGGACAGAAGAAGGCAGCA    17812        CC  G    G
                                TGCTGCCT  CT TTTG CCA
                                ||||||||  || |||| |||
                                ACGACGGA  GA AGAC GGT
                                     A_  _    A
GAM181   DAP      3'  AGGCAGGGAACAGCA       72552       CC
                                TGCTG  TCCCTGTTT
                                |||||  |||||||||
                                ACGAC  AGGGACGGA
                                   A_
GAM181   DDEF2    3'  TGGAAAGTGAGGCAGCA     13956         C  GTTTGG
                                TGCTGCCTC CT     CCA
                                ||||||||| ||     |||
                                ACGACGGAG GA     GGT
                                      T  AA_____
GAM181   DGCR2    3'  GCTTCAGGGAGGCAGC      17627           TTT
                                GCTGCCTCCCTG   GGC
                                ||||||||||||   |||
                                CGACGGAGGGAC   TCG
                                       T__
GAM181   DISC1    3'  GTCAGAGACAGGCAGCA     37888         CCCTG
                                TGCTGCCT    TTTGGC
                                ||||||||    ||||||
                                ACGACGGA    AGACTG
                                     CAG__
GAM181   DLG5     5'  GGCCCCCCAGGAGGCAGCA   82918          C  TTT
                                TGCTGCCTCC TG   GGCC
                                |||||||||| ||   ||||
                                ACGACGGAGG AC   CCGG
                                       _ CCC
GAM181   DNAJB1   3'  TGGCCAGGGGTGAGAGGCAG  20449        ___   GT
                                CTGCCTC   CCT  TTGGCCA
                                |||||||   |||  |||||||
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                                GACGGAG  GGG  GACCGGT
                                   AGT  __
GAM181  DTNBP1   5'  GGCGACAGAGGCAGCA     49526        CC   TG
                                TGCTGCCTC  TGTT  GCC
                                |||||||||  ||||  |||
                                ACGACGGAG  ACAG  CGG
                                      __   __
GAM181  DYRK1A   5'  TTGGCCAACATATGCAACA   55254    C  CTCCC   T
                                TG TGC    TGTT GGCCAA
                                || |||    |||| ||||||
                                AC ACG    ACAA CCGGTT
                                 A  TAT__   _
GAM181  EDAR     3'  TTGACCTTTTAGGGGCAGCA  42270       TC   TTT  C
                                TGCTGCC  CCTG  GG CAA
                                |||||||  ||||  || |||
                                ACGACGG  GGAT  CC GTT
                                   __   TTT  A
GAM181  EFNA1    3'  GGTACAGGAGAGGCAGCA    15391        _    TTG
                                TGCTGCCTC CCTGT  GCC
                                |||||||||  |||||  |||
                                ACGACGGAG GGACA  TGG
                                     A   ___
GAM181  EFNA3    3'  CTAGATGGGCAAGGGGCAGCA  17066         ___
                                TGCTGCCTC  CCTGTTTGG
                                |||||||||  |||||||||
                                ACGACGGGG  GGGTAGATC
                                     AAC
GAM181  EFNB1    3'  TTGGCCTGGTGGGGAAACAG  15401     CC   TG TT
                                CTG  TCCC  T  GGCCAA
                                |||  ||||  |  ||||||
                                GAC  AGGG  G  CCGGTT
                                  AA   GT GT
GAM181  EGFL5    5'  AGGGAGGAAGGCAGCA      86610        C  G
                                TGCTGCCT CCT TTT
                                |||||||| ||| |||
                                ACGACGGA GGA GGA
                                     A  G
GAM181  EIF2C1   3'  CCAAAAGGGGCAGCA       24167        TC  G
                                TGCTGCC  CCT TTTGG
                                |||||||  ||| |||||
                                ACGACGG  GGA AAACC
                                      __  _
GAM181  EMD      3'  CCACCAGGGAGGCAGCA     3680           TT
                                TGCTGCCTCCCTG  TGG
                                ||||||||||||  |||
                                ACGACGGAGGGAC  ACC
                                       C_
GAM181  EPHA8    3'  TTGGCAGGCAGGGAAGCAG   40068     C       G
                                CTGC TCCCTGTTTG CCAA
                                |||| |||||||||| ||||
```

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                                GACG AGGGACGGAC GGTT
                                  A       _
GAM181  EPM2A   5'  GGCACAAAGAGGCAGC     19032       CCTG   _
                                GCTGCCTC   TTTG GCC
                                ||||||||   |||| |||
                                CGACGGAG   AAAC CGG
                                    _____   A
GAM181  F2RL3   3'  GCCACTCAAGAGGCACA    14183   C    CC  TT
                                TG TGCCTC  TG  TGGC
                                || ||||||  ||  ||||
                                AC ACGGAG  AC  ACCG
                                 _    A_  TC
GAM181  F7      5'  AACAGGCAGGGGCAGCA    3715        __
                                TGCTGCCTC  CCTGTT
                                |||||||||  ||||||
                                ACGACGGGG  GGACAA
                                     AC
GAM181  F7      5'  AACAGGCAGGGGCAGCA    39025       __
                                TGCTGCCTC  CCTGTT
                                |||||||||  ||||||
                                ACGACGGGG  GGACAA
                                     AC
GAM181  FGF1    3'  CCAGGTTAGGAAGGCAGCA   5856       C  _ TT
                                TGCTGCCT CCT G  TGG
                                |||||||| ||| |  |||
                                ACGACGGA GGA T  ACC
                                     A   T GG
GAM181  FGF1    3'  CCAGGTTAGGAAGGCAGCA   52456      C  _ TT
                                TGCTGCCT CCT G  TGG
                                |||||||| ||| |  |||
                                ACGACGGA GGA T  ACC
                                     A   T GG
GAM181  FGF1    3'  CCAGGTTAGGAAGGCAGCA   52459      C  _ TT
                                TGCTGCCT CCT G  TGG
                                |||||||| ||| |  |||
                                ACGACGGA GGA T  ACC
                                     A   T GG
GAM181  FKBP10  3'  TGGCCAGGCCTGAGACACA   41649   C  C   CCT
                                TG TG CTC   GTTTGGCCA
                                || || |||   |||||||||
                                AC AC GAG   CGGACCGGT
                                 _  A   TC_
GAM181  FMNL    3'  TTGGCCACAGAGGGCAGCA   19707      CC    TT
                                TGCTGCCT  CTGT  GGCCAA
                                ||||||||  ||||  ||||||
                                ACGACGGG  GACA  CCGGTT
                                     A_   __
GAM181  FOXE3   3'  TTGGAGATTTCAGACAGGCAGC 24107      CC   TTTGG_
          A                      TGCTGCCT  CTG     CCAA
                                ||||||||  |||     ||||
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                                ACGACGGA  GAC     GGTT
                                    CA   TTTAGA
GAM181  G22P1    5'  TCGGGAAGGAGGCGGCA     7603          CTG
                                TGCTGCCTCC   TTTGG
                                ||||||||||   |||||
                                ACGGCGGAGG   GGGCT
                                     AA_
GAM181  GAB2     3'  GGCAGGACAAGGAGAAAGCA   24501     GC   C   TG
                                TGCT  CTCC TGTT  GCC
                                ||||  |||| ||||  |||
                                ACGA  GAGG ACAG  CGG
                                  AA   A   GA
GAM181  GAB2     3'  GGCAGGACAAGGAGAAAGCA   54458     GC   C   TG
                                TGCT  CTCC TGTT  GCC
                                ||||  |||| ||||  |||
                                ACGA  GAGG ACAG  CGG
                                  AA   A   GA
GAM181  GABRE    5'  CCAGCAAAGGCAGCA       41772        CCC   T
                                TGCTGCCT   TGTT GG
                                ||||||||   |||| ||
                                ACGACGGA   ACGA CC
                                    A__   _
GAM181  GABRE    5'  CCAGCAAAGGCAGCA       41781        CCC   T
                                TGCTGCCT   TGTT GG
                                ||||||||   |||| ||
                                ACGACGGA   ACGA CC
                                    A__   _
GAM181  GABRE    5'  CCAGCAAAGGCAGCA       41801        CCC   T
                                TGCTGCCT   TGTT GG
                                ||||||||   |||| ||
                                ACGACGGA   ACGA CC
                                    A__   _
GAM181  GALNS    3'  GCCAGACAGACAGCA       4965       CCTCC
                                TGCTG    CTGTTTGGC
                                |||||    |||||||||
                                ACGAC    GACAGACCG
                                  A____
GAM181  GALNT7   3'  CCAGCACTTTGGGAGGCAG   54017         T__ _
                                CTGCCTCCC   GT TTGG
                                |||||||||   || ||||
                                GACGGAGGG   CA GACC
                                     TTT  C
GAM181  GORASP1  3'  GGCTTCCCAGGAGGCAGCA   49112          C  TTT
                                TGCTGCCTCC TG   GGCC
                                |||||||||| ||   ||||
                                ACGACGGAGG AC   TCGG
                                     _  CCT
GAM181  GPC1     3'  GGCCCAGGGAGGCAGC      9102           TTT
                                GCTGCCTCCCTG   GGCC
                                ||||||||||||   ||||
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                                CGACGGAGGGAC  CCGG
                                      ___
GAM181  GPRK7   3'  CCAGACAGGCAGCA       57626        CCCT
                                TGCTGCCT   GTTTGG
                                ||||||||   ||||||
                                ACGACGGA   CAGACC
                                     _____
GAM181  GRLF1   3'  CCGGGAGGGAGGGAGGCA    78556     G_     G
                                TGCT  CCTCCCT TTTGG
                                ||||  ||||||| |||||
                                ACGG  GGAGGGA GGGCC
                                  AG      _
GAM181  GYG     3'  TGTGTACAGTAAGGCAGCA    14693        CC    TTG  _
                                TGCTGCCT  CTGT   GC CA
                                ||||||||  ||||   || ||
                                ACGACGGA  GACA   TG GT
                                     AT    ___  T
GAM181  HBE1    5'  CCAGACAGAGAGGCAGCA     18044         C
                                TGCTGCCTC CTGTTTGG
                                |||||||||  ||||||||
                                ACGACGGAG GACAGACC
                                      A
GAM181  HIP12   3'  TGGCCAAGGTCAGGAGGAGCA  66232     G    C  __
                                TGCT CCTCC TG  TTTGGCCA
                                |||| |||||  ||  ||||||||
                                ACGA GGAGG AC  GAACCGGT
                                  _    _  TG
GAM181  HIS1    5'  TGGCCCCTCGGAGGCAGC    21317         CTGTTT
                                GCTGCCTCC     GGCCA
                                |||||||||     |||||
                                CGACGGAGG     CCGGT
                                      CTCC__
GAM181  HMG20A  3'  CCAAATGAGGGAGCAGCA    36534       C    _
                                TGCTGC TCCCT GTTTGG
                                ||||||  ||||| ||||||
                                ACGACG AGGGA TAAACC
                                   _    G
GAM181  HOXB3   5'  TGGCCAAATGTCACAGCA    9263       CCTCCCT
                                TGCTG      GTTTGGCCA
                                |||||      |||||||||
                                ACGAC      TAAACCGGT
                                   ACTG___
GAM181  HSD3B2  3'  TCATACAGAAGGCAACA     3976     C    CC    T
                                TG TGCCT  CTGT TGG
                                || |||||  |||| |||
                                AC ACGGA  GACA ACT
                                 A    A_   T
GAM181  HTR2C   3'  TGGCCAAACATCAGT       6025       CCTCCC
                                GCTG     TGTTTGGCCA
                                ||||     ||||||||||
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                                TGAC     ACAAACCGGT
                                  T_____
GAM181  HUNK     3'  TGGCGAGAAGGCAGCA      27463        CCCTG   G
                                TGCTGCCT     TTT GCCA
                                ||||||||     ||| ||||
                                ACGACGGA     AGA CGGT
                                     _____   G
GAM181  IL1RAPL2 5'  AGACAGAGGCAGCA       33789        CC
                                TGCTGCCTC  TGTTT
                                |||||||||  |||||
                                ACGACGGAG  ACAGA
                                     __
GAM181  INSR     3'  TGGCCAAGGGAGGAGCA     70982      G      GTT
                                TGCT CCTCCCT   TGGCCA
                                |||| |||||||   ||||||
                                ACGA GGAGGGA   ACCGGT
                                  _     ___
GAM181  ITPKB    3'  TGGCCCCAGGGAGGAGCA    9438       G       TTT
                                TGCT CCTCCCTG   GGCCA
                                |||| ||||||||   |||||
                                ACGA GGAGGGAC   CCGGT
                                  _       C__
GAM181  JJAZ1    5'  TGGCGGGGGGGAGGAGGCAG   31081         _ G   G
                                CTGCCTCC CT TTTG CCA
                                |||||||| || |||| |||
                                GACGGAGG GG GGGC GGT
                                     A  G   _
GAM181  KCNA7    3'  GGACCCAAAGGAAATAGCA   49055      CC   CTG    __
                                TGCTG  TCC   TTTGG  CC
                                |||||  |||   |||||  ||
                                ACGAT  AGG   AAACC  GG
                                   AA   ___     CA
GAM181  KCND2    5'  CCGAGGAGTAGAGGCAGCA   24395         C_  G
                                TGCTGCCTC  CT TTTGG
                                |||||||||  ||  |||||
                                ACGACGGAG  GA GAGCC
                                     AT  G
GAM181  KCND2    3'  CCATTCAGGAAGGCAGCA    24394         C    TT
                                TGCTGCCT CCTG  TGG
                                |||||||| ||||  |||
                                ACGACGGA GGAC  ACC
                                     A    TT
GAM181  KCNK6    3'  TGGCAGGCAGGAAACAGACA  16697    _   CCTC       G
                                TG CTG    CCTGTTTG CCA
                                || |||    |||||||| |||
                                AC GAC    GGACGGAC GGT
                                  A  AAA_       _
GAM181  KIP2     3'  CCAAGAGGGAAAAGCA      21089      GCC     G
                                TGCT   TCCCT TTTGG
                                ||||   ||||| |||||
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                                ACGA   AGGGA GAACC
                                  AA_    _
GAM181  LARS2    3'  CCAGTAGGGATGCAGCA     31052       C       T
                                TGCTGC TCCCTGTT GG
                                |||||| |||||||| ||
                                ACGACG AGGGATGA CC
                                   T      _
GAM181  LIF      3'  TGGCACCCGGGGAGGTAGCA   9740            TTTG
                                TGCTGCCTCCCTG   GCCA
                                ||||||||||||   ||||
                                ACGATGGAGGGGC   CGGT
                                       CCA_
GAM181  LOH11CR2A 5'  CCAACCTGGGTCGAAGGCGGCA 27538         ____   TGT
                                TGCTGCCT   CCC   TTGG
                                ||||||||   |||  ||||
                                ACGGCGGA   GGG   AACC
                                     AGCT   TCC
GAM181  LRP1     3'  GCCTTCAGGGAGACAGGCA   9804      GC_     TTT
                                TGCT   CTCCCTG   GGC
                                ||||   |||||||   |||
                                ACGG   GAGGGAC   CCG
                                  ACA      TT_
GAM181  LZTS1    3'  TGGCTGGAGGAGCAGCA     40699       C   CTG  TG
                                TGCTGC TCC   TT  GCCA
                                |||||| |||   ||  ||||
                                ACGACG AGG   AG  CGGT
                                   _   ___  GT
GAM181  MAD1L1   3'  GCCCCACAGGGCAGCA      87488        TCC    TT
                                TGCTGCC   CTGT  GGC
                                |||||||   ||||  |||
                                ACGACGG   GACA  CCG
                                    ___    CC
GAM181  MAML1    5'  GGCTTGAGGTAGGCAGCA    28593         C   GTTT
                                TGCTGCCT CCT    GGCC
                                |||||||| |||    ||||
                                ACGACGGA GGA    TCGG
                                     T   GT__
GAM181  MAN1A1   5'  GCCTAGGAAAGAGGCAGCA   91903          ___    TTT
                                TGCTGCCTC   CCTG   GGC
                                |||||||||   ||||   |||
                                ACGACGGAG   GGAT   CCG
                                     AAA    ___
GAM181  MARK3    5'  CTAGAGAGGGAGAAGCA     9913       GC     G
                                TGCT  CTCCCT TTTGG
                                ||||  |||||| |||||
                                ACGA  GAGGGA AGATC
                                  A_     G
GAM181  MCCC2    5'  CCAGCCAGGGAAGCGGCA    42137       C     T
                                TGCTGC TCCCTG TTGG
                                |||||| |||||| ||||
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                                ACGGCG AGGGAC GACC
                                   A     C
GAM181  MEF2C   3' CTAGACAAGAAGGAAGCA   9988      G   CCC
                                TGCT CCT   TGTTTGG
                                |||| |||   |||||||
                                ACGA GGA   ACAGATC
                                  A   AGA
GAM181  MEF2D   3' TGACTGGGTGGGGACAGCA   96920     CC    TG  TG C
                                TGCTG  TCCC  TT  G CA
                                |||||  ||||  ||  | ||
                                ACGAC  AGGG  GG  C GT
                                   __   GT  GT A
GAM181  MEOX1   3' TCAATTTAGGGATACAGCA   15757     CC     T_
                                TGCTG  TCCCTG  TTGG
                                |||||  ||||||  ||||
                                ACGAC  AGGGAT  AACT
                                   AT     TT
GAM181  MEOX1   3' TCAATTTAGGGATACAGCA   25731     CC     T_
                                TGCTG  TCCCTG  TTGG
                                |||||  ||||||  ||||
                                ACGAC  AGGGAT  AACT
                                   AT     TT
GAM181  MEST    5' GGCAGGGAGAAGGCGGCA    69901       ___
                                TGCTGCC   TCCCTGTT
                                |||||||   ||||||||
                                ACGGCGG   AGGGACGG
                                    AAG
GAM181  MID2    5' CCAACCCGCTGCGGAGGCAG  53387       CT_ ___
                                CTGCCTCC   GT   TTGG
                                ||||||||   ||   ||||
                                GACGGAGG   CG   AACC
                                     CGT  CCC
GAM181  MID2    5' CCAACCCGCTGCGGAGGCAG  24222       CT_ ___
                                CTGCCTCC   GT   TTGG
                                ||||||||   ||   ||||
                                GACGGAGG   CG   AACC
                                     CGT  CCC
GAM181  MLH3    3' CTGAGCAGAGAGCAGCA     26885      C  C    TG
                                TGCTGC TC CTGTT  G
                                |||||| || |||||  |
                                ACGACG AG GACGA  C
                                   _ A    GT
GAM181  MNT     3' TTGGCTTCCAGAAGGCAGCA  39720       CC   TTT
                                TGCTGCCT  CTG   GGCCAA
                                ||||||||  |||   ||||||
                                ACGACGGA  GAC   TCGGTT
                                     A_   CT_
GAM181  MPST    3' TGGAGGAGGGAGGCCACA    40888    CT      G  TGG
                                TG  GCCTCCCT TT   CCA
                                ||  |||||||| ||   |||
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                                AC  CGGAGGGA GA   GGT
                                 AC       G ___
GAM181  MUCDHL   3' GCTCTGGGGGAGGCACA     48372    C       GTTT
                                TG TGCCTCCCT    GGC
                                || |||||||||    |||
                                AC ACGGAGGGG    TCG
                                 _       GTC_
GAM181  MUCDHL   3' GCTCTGGGGGAGGCACA     87302    C       GTTT
                                TG TGCCTCCCT    GGC
                                || |||||||||    |||
                                AC ACGGAGGGG    TCG
                                 _       GTC_
GAM181  NFIC     3' GGAATCCCAGGGGGCAGCA    18795        T    TTTGG
                                TGCTGCC CCCTG    CC
                                ||||||| |||||    ||
                                ACGACGG GGGAC    GG
                                    _    CCTAA
GAM181  NKX3A    3' TGGCTAAAAGACATGCA     20504     _ C  CCCTG
                                TGC TG CT    TTTGGCCA
                                ||| || ||    ||||||||
                                ACG AC GA    AAATCGGT
                                  T  A _____
GAM181  NSF      3' TTGGCCGATTAGAAGGCAG   63073       CC   T
                                CTGCCT  CTG TTGGCCAA
                                ||||||  ||| ||||||||
                                GACGGA  GAT AGCCGGTT
                                   A_   T
GAM181  P2RX7    3' CCAGCCTGGGAGGCACA     10373    C       TGT
                                TG TGCCTCCC   TTGG
                                || ||||||||   ||||
                                AC ACGGAGGG   GACC
                                 _       TCC
GAM181  PACE4    3' TTGAATAGGGAAGTAACA    10404    C  C       TG
                                TG TGC TCCCTGTT  G
                                || ||| ||||||||  |
                                AC ATG AGGGATAA  T
                                 A   A       GT
GAM181  PACE4    3' TTGAATAGGGAAGTAACA    56349    C  C       TG
                                TG TGC TCCCTGTT  G
                                || ||| ||||||||  |
                                AC ATG AGGGATAA  T
                                 A   A       GT
GAM181  PAX4     5' GACAGCCTGGGGGCAGCA    20555          ___
                                TGCTGCCTCC   CTGTT
                                ||||||||||   |||||
                                ACGACGGGGG   GACAG
                                      TCC
GAM181  PCDH7    5' TGGCAGGCGGGGGAGGCTGCA 50599     T      _    G
                                TGC GCCTCCCT GTTTG CCA
                                ||| |||||||| ||||| |||
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                                ACG CGGAGGGG CGGAC GGT
                                  T       G    _
GAM181  PCDH7    5'  TGGCAGGCGGGGGAGGCTGCA  50605     T      _    G
                                TGC GCCTCCCT GTTTG CCA
                                ||| |||||||| ||||| |||
                                ACG CGGAGGGG CGGAC GGT
                                  T       G    _
GAM181  PCDH7    5'  TGGCAGGCGGGGGAGGCTGCA  10461     T      _    G
                                TGC GCCTCCCT GTTTG CCA
                                ||| |||||||| ||||| |||
                                ACG CGGAGGGG CGGAC GGT
                                  T       G    _
GAM181  PCDHAC1  5'  GGCGTTCGGGAGGCGCA     49040     T      T TTTG
                                TGC GCCTCCC G    GCC
                                ||| ||||||| |    |||
                                ACG CGGAGGG C    CGG
                                  _      _ TTG_
GAM181  PCDHAC1  5'  GGCGTTCGGGAGGCGCA     38166     T      T TTTG
                                TGC GCCTCCC G    GCC
                                ||| ||||||| |    |||
                                ACG CGGAGGG C    CGG
                                  _      _ TTG_
GAM181  PFKFB4   3'  TTGGTCCCAGAGAGGCAGC   15876         C   TTT
                                GCTGCCTC CTG   GGCCAA
                                |||||||| |||   ||||||
                                CGACGGAG GAC   CTGGTT
                                     A   C__
GAM181  PIAS3    3'  TGGCCAAGGGCCAGACAG    20342     C  __   GTT
                                CTG CT  CCCT   TGGCCA
                                ||| ||  ||||   ||||||
                                GAC GA  GGGA   ACCGGT
                                  A  CC   ___
GAM181  PLA2G2A  5'  CCACCAAGGAGGAGCA      4319      G    C  TT
                                TGCT CCTCC TG  TGG
                                |||| ||||| ||  |||
                                ACGA GGAGG AC  ACC
                                  _    A  C_
GAM181  PLCB4    3'  TTGGCCAAACAAAAATAGC    6255      CCTCCC
                                GCTG     TGTTTGGCCAA
                                ||||     ||||||||||
                                CGAT     ACAAACCGGTT
                                   AAAA__
GAM181  PLXNB3   3'  TGGCTCAGACAGCAGCA     18228       CTCCC    _
                                TGCTGC    TGTTTG GCCA
                                ||||||    |||||| ||||
                                ACGACG    ACAGAC CGGT
                                    _____     T
GAM181  POLG     5'  GGCCGGGTGGAGGCCACA    10681    CT     CT TT
                                TG  GCCTCC  G  TGGCC
                                ||  ||||||  |  |||||
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                                AC  CGGAGG  T  GCCGG
                                 AC     __ GG
GAM181  POLR2E   3'  CTAAGAAAGGGAGACAG     59918     C     G_
                                CTG CTCCCT  TTTGG
                                ||| ||||||  |||||
                                GAC GAGGGA  GAATC
                                  A     AA
GAM181  PPEF1    5'  TTGGCCAAGCAGAAGAAACAG  20683     CC  C_
                                CTG  TC  CTGTTTGGCCAA
                                |||  ||  ||||||||||||
                                GAC  AG  GACGAACCGGTT
                                  AA  AA
GAM181  PROK1    3'  TCAGACCAGGGAGGCA      50557          _
                                TGCCTCCCTG TTTGG
                                |||||||||| |||||
                                ACGGAGGGAC AGACT
                                       C
GAM181  PROK1    3'  TTGGCTCTTCCCAGAGGGCAGC 50558        CC   TTT__
              A                  TGCTGCCT  CTG    GGCCAA
                                |||||||  |||    ||||||
                                ACGACGGG  GAC    TCGGTT
                                     A_   CCTTC
GAM181  PSMD9    3'  CCACCAGAGGGCAGCA      10982        CC   TT
                                TGCTGCCT  CTG  TGG
                                |||||||  |||  |||
                                ACGACGGG  GAC  ACC
                                     A_   C_
GAM181  PTPRO    3'  ACAGAAAGGAGGCAGCA     47711          ___
                                TGCTGCCTCC   CTGT
                                ||||||||||   ||||
                                ACGACGGAGG   GACA
                                       AAA
GAM181  RAD50    5'  CCGGCGGGGAAAGCAGC     56008      C_      T
                                GCTGC  TCCCTGTT GG
                                |||||  |||||||| ||
                                CGACG  AGGGGCGG CC
                                   AA       _
GAM181  RAD50    5'  CCGGCGGGGAAAGCAGC     19194      C_      T
                                GCTGC  TCCCTGTT GG
                                |||||  |||||||| ||
                                CGACG  AGGGGCGG CC
                                   AA       _
GAM181  RAGE     5'  GGTGACAGGGACACAACA    26446    C  CC      TG
                                TG TG  TCCCTGTT  GCC
                                || ||  ||||||||  |||
                                AC AC  AGGGACAG  TGG
                                 A  AC       __
GAM181  RASSF1   3'  CCAGGTGGAAGGCAGACA    23208    _     CC TG
                                TG CTGCCT  C  TTTGG
                                || ||||||  |  |||||
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                                AC GACGGA  G  GGACC
                                 A     A_ GT
GAM181  RECK    3'  TTGGCCAAGGAAAGGCACA   40875    C    C_  GTT
                                TG TGCCT  CCT   TGGCCAA
                                || |||||  |||   |||||||
                                AC ACGGA  GGA   ACCGGTT
                                 _    AA  ___
GAM181  REPS2   5'  TGGCCCCATGGAGGCGGCA   16374         C  TTT
                                TGCTGCCTCC TG   GGCCA
                                |||||||||| ||   |||||
                                ACGGCGGAGG AC   CCGGT
                                      T  C__
GAM181  RPL10   3'  GCCCTGCTCATGAGGCAGCA  20029        CCT_  TT
                                TGCTGCCTC    GT  GGC
                                |||||||||    ||  |||
                                ACGACGGAG    CG  CCG
                                      TACT  TC
GAM181  RUNX3   3'  CCAGAGAGAGGCAGCA      15112         CC G
                                TGCTGCCTC  T TTTGG
                                |||||||||  | |||||
                                ACGACGGAG  A AGACC
                                     __ G
GAM181  SDC1    3'  TGGTCGGGAGACAGCA      11474      C    TGTTT
                                TGCTG CTCCC    GGCCA
                                ||||| |||||    |||||
                                ACGAC GAGGG    CTGGT
                                   A    _____
GAM181  SELE    5'  AGACAGAGGCAGCA        4826          CC
                                TGCTGCCTC  TGTTT
                                |||||||||  |||||
                                ACGACGGAG  ACAGA
                                     __
GAM181  SIAT1   3'  TCAGTGAGAGAGGCAGACA   11663    _     C  GT
                                TG CTGCCTC CT  TTGG
                                || ||||||| ||  ||||
                                AC GACGGAG GA  GACT
                                 A      A  GT
GAM181  SLC13A3 3'  TTGGCCAGCTGGGAAGGCAGC  60472       _  T  T
                                GCTGCCT CCC GTT GGCCAA
                                ||||||| ||| ||| ||||||
                                CGACGGA GGG CGA CCGGTT
                                    A  T  _
GAM181  SLC21A9 3'  GCTCGGGAGGCAGCA      23421          TGTTT
                                TGCTGCCTCCC    GGC
                                ||||||||||    |||
                                ACGACGGAGGG    TCG
                                      C____
GAM181  SLC25A11 3' GGGGACAGGGAGGAGCA    13092     G         GG
                                TGCT CCTCCCTGTTT  CC
                                |||| ||||||||||  ||
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                                ACGA GGAGGGACAGG  GG
                                  _      __
GAM181  SLC2A6   3'  GGACCAAGAGGCAGCA      34158        CCTGT   _
                                TGCTGCCTC    TTGG CC
                                |||||||||    |||| ||
                                ACGACGGAG    AACC GG
                                     _____   A
GAM181  SLC6A6   3'  CCAGGCAGAGAAGGAGCA    11729      G  _ C
                                TGCT CCT C CTGTTTGG
                                |||| ||| | ||||||||
                                ACGA GGA G GACGGACC
                                  _  A A
GAM181  SLC7A7   5'  TGGCTGGGAAGGAGGAGCA   14295      G    CTG  TG
                                TGCT CCTCC   TT  GCCA
                                |||| |||||   ||  ||||
                                ACGA GGAGG   GG  CGGT
                                  _    AA_  GT
GAM181  SLC7A8   5'  TTAGAAAGGGAGGCAGC     24286          G
                                GCTGCCTCCCT TTTGG
                                |||||||||| |||||
                                CGACGGAGGGA AGATT
                                      A
GAM181  SMOH     3'  TGGCCAGGGAGGCAGC      18873          GTTT
                                GCTGCCTCCCT   GGCCA
                                ||||||||||   |||||
                                CGACGGAGGGA   CCGGT
                                     ____
GAM181  SORCS2   3'  GCCCAGAGGGGCAGCA      40419        C   TTT
                                TGCTGCCTC CTG   GGC
                                ||||||||| |||   |||
                                ACGACGGGG GAC   CCG
                                     A  ___
GAM181  ST3GALVI 5'  GCGAGAGAGGCAGCA       20343        CCTG   G
                                TGCTGCCTC    TTT GC
                                |||||||||    ||| ||
                                ACGACGGAG    AGA CG
                                     _____  G
GAM181  STARD5   3'  CCAACCAGAGGCGGCA      47557        CC  T
                                TGCTGCCTC  TG TTGG
                                |||||||||  || ||||
                                ACGGCGGAG  AC AACC
                                     __  C
GAM181  STK11    3'  CCGGGCAGGGGGGACAGCA    4847       C
                                TGCTG CTCCCTGTTTGG
                                ||||| ||||||||||||
                                ACGAC GGGGGACGGGCC
                                   A
GAM181  SURF5    3'  CAGACATGAGGCAGCA       22179        CC
                                TGCTGCCTC  TGTTTG
                                |||||||||  ||||||
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                                ACGACGGAG  ACAGAC
                                     T_
GAM181  SYNGR1   3' CTAAGCAGAGAAGTAGCA    16315       C  C
                                TGCTGC TC CTGTTTGG
                                |||||| || ||||||||
                                ACGATG AG GACGAATC
                                   A  A
GAM181  SYNGR1   3' TGGGGTAGGGAGACAGC     16324      C      TTTGG
                                GCTG CTCCCTG    CCA
                                |||| |||||||    |||
                                CGAC GAGGGAT    GGT
                                  A      GG___
GAM181  SYNGR3   3' TGGCCAGGAAGGCACA      14857    C    C   GTTT
                                TG TGCCT CCT    GGCCA
                                || ||||| |||    |||||
                                AC ACGGA GGA    CCGGT
                                 _    A  _____
GAM181  TARBP2   3' CCACCAGGGAGGCAGC      56164          TT
                                GCTGCCTCCCTG  TGG
                                ||||||||||||  |||
                                CGACGGAGGGAC  ACC
                                      C_
GAM181  TBX5     5' GCCAAACGTGACAGC       54890      CC  CC
                                GCTG  TC  TGTTTGGC
                                ||||  ||  ||||||||
                                CGAC  AG  GCAAACCG
                                  __  T_
GAM181  TBX5     5' GCCAAACGTGACAGC       3958       CC  CC
                                GCTG  TC  TGTTTGGC
                                ||||  ||  ||||||||
                                CGAC  AG  GCAAACCG
                                  __  T_
GAM181  TCF1     3' AACAGGGAAGGCAGGCA     5031      _    _
                                TGC TGCCT CCCTGTT
                                ||| ||||| |||||||
                                ACG ACGGA GGGACAA
                                  G    A
GAM181  TCF2     3' TCGACTCAGGCAGACAGCA   21386      C  C   T_
                                TGCTG CT CCTG  TTGG
                                ||||| || ||||  ||||
                                ACGAC GA GGAC  AGCT
                                   A  C    TC
GAM181  TCF7     3' TGGGTAACAGGGAGACTGCA  12164     TGC       T G
                                TGC   CTCCCTGTT G CCA
                                |||   ||||||||| | |||
                                ACG   GAGGGACAA T GGT
                                  TCA        _ G
GAM181  TFE3     5' AGCGGAGGAGGCGGCA      21510          _
                                TGCTGCCTCC CTGTT
                                |||||||||| |||||
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                                ACGGCGGAGG GGCGA
                                     A
GAM181  TGFBR2   3' CCAAAGAACAGAGGCAGCA   12265        CCTG_
                                TGCTGCCTC    TTTGG
                                |||||||||    |||||
                                ACGACGGAG    AAACC
                                     ACAAG
GAM181  TNFRSF8  3' GGCTAGGAGGGCAGCA     6962        TC   GTTT
                                TGCTGCC  CCT   GGCC
                                |||||||  |||   ||||
                                ACGACGG  GGA   TCGG
                                   GA  ____
GAM181  TNFSF8   3' TCAGACAGAGACAGCA     6967       CC  C
                                TGCTG  TC CTGTTTGG
                                |||||  || ||||||||
                                ACGAC  AG GACAGACT
                                  __  A
GAM181  TOP1     3' TGGGGGAGAGAGGCAGCA    12360        C  G  TGG
                                TGCTGCCTC CT TT   CCA
                                |||||||||| || ||   |||
                                ACGACGGAG GA GG   GGT
                                     A  G  ___
GAM181  UBE2B    3' CCAGCACTTTGGGAGGCA    12473        T__  _
                                TGCCTCCC   GT TTGG
                                ||||||||   || ||||
                                ACGGAGGG   CA GACC
                                     TTT  C
GAM181  ZNF9     3' TGGCCAAAGGTTGGCAG     12773      TC   GT
                                CTGCC  CCT  TTGGCCA
                                |||||  |||  |||||||
                                GACGG  GGA  AACCGGT
                                   TT  __
GAM181  BHLHB2   3' CTAACATGGGGAGGTAGCA   13378           _
                                TGCTGCCTCCCTGT TTGG
                                |||||||||||||| ||||
                                ACGATGGAGGGGTA AATC
                                        C
GAM181  C16orf5  3' GCCCTGGGGAGGCGCA      25450     T       TTT
                                TGC GCCTCCCTG   GGC
                                ||| |||||||||   |||
                                ACG CGGAGGGGT   CCG
                                  _       C__
GAM181  C17orf1A 3' CTATCCAGTAGAGGCAGCA   21087        C_  TT
                                TGCTGCCTC  CTG  TGG
                                |||||||||  |||  |||
                                ACGACGGAG  GAC  ATC
                                     AT   CT
GAM181  C1QR1    3' GGTGGCAAGGAGGCAG      23843        C    TG
                                CTGCCTCC TGTT  GCC
                                |||||||| ||||  |||
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                                GACGGAGG ACGG  TGG
                                    A   __
GAM181  C20orf175 5'  CCAGAGAGAGGCAGC      55062        CC G
                                GCTGCCTC  T TTTGG
                                ||||||||  | |||||
                                CGACGGAG  A AGACC
                                    __ G
GAM181  C20orf54  3'  TCAAATGGAGGCAACA     53008    C     CT
                                TG TGCCTCC  GTTTGG
                                || |||||||  ||||||
                                AC ACGGAGG  TAAACT
                                 A      __
GAM181  C6.1A     3'  GCTACTAGGGAGGCAG      44283          TT
                                CTGCCTCCCTG  TGGC
                                ||||||||||  ||||
                                GACGGAGGGAT  ATCG
                                      C_
GAM181  C8orf17   5'  TTGACCTTACAGGGAGG     39606        TT  C
                                CCTCCCTGT  GG CAA
                                |||||||||  || |||
                                GGAGGGACA  CC GTT
                                     TT  A
GAM181  CALN1     3'  CCAGACCAAGGAGGCAGCA   48860         CT_
                                TGCTGCCTCC   GTTTGG
                                ||||||||||   ||||||
                                ACGACGGAGG   CAGACC
                                      AAC
GAM181  CAP350    3'  TGGCCAAGGAAAAGCA      29047     GCC   CTGT
                                TGCT   TCC    TTGGCCA
                                ||||   |||    |||||||
                                ACGA   AGG    AACCGGT
                                  AA_   _____
GAM181  CBARA1    3'  GCTCTAGGAAGGCAGCA     20291        C    TTT
                                TGCTGCCT CCTG   GGC
                                |||||||| ||||   |||
                                ACGACGGA GGAT   TCG
                                     A   C__
GAM181  CFDP1     5'  GTCGAGCGGCAGCA       20903       TCCCT
                                TGCTGCC    GTTTGGC
                                |||||||    |||||||
                                ACGACGG    CGAGCTG
                                     _____
GAM181  CG012     3'  TCAACCCAGGAGGCAG      83227        C  T_
                                CTGCCTCC TG  TTGG
                                |||||||| ||  ||||
                                GACGGAGG AC  AACT
                                     _  CC
GAM181  CLDN4     3'  CCAGGCAGGAAGGCAGCA    7136         C
                                TGCTGCCT CCTGTTTGG
                                |||||||| |||||||||
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                                ACGACGGA GGACGGACC
                                    A
GAM181  COE2     5'  CTTTCAGGAGGCAGCA      64252          C  TTT
                                TGCTGCCTCC TG   GG
                                |||||||||| ||   ||
                                ACGACGGAGG AC   TC
                                     _  TT_
GAM181  CPVL     5'  GGCTCAGGGAGGAGCA      48547      G       TTT
                                TGCT CCTCCCTG   GGCC
                                |||| ||||||||   ||||
                                ACGA GGAGGGAC   TCGG
                                  _      ____
GAM181  CSR1     3'  GCCAGGGAGGCAGC        32688           GTTT
                                GCTGCCTCCCT    GGC
                                ||||||||||    |||
                                CGACGGAGGGA    CCG
                                     _____
GAM181  CYB5-M   5'  GGTGGAGAGGCAGTA       47568          _  TGTTTG
                                TGCTGCCTC CC     GCC
                                |||||||| ||      |||
                                ATGACGGAG GG     TGG
                                    A _______
GAM181  CYB5-M   5'  GGTGGAGAGGCAGTA       94565          _  TGTTTG
                                TGCTGCCTC CC     GCC
                                |||||||| ||      |||
                                ATGACGGAG GG     TGG
                                    A _______
GAM181  DCAMKL1  5'  GCCCGGCGAGGACAGCA     16411       _   C   TTT
                                TGCTG CCTC CTG   GGC
                                ||||| |||| |||   |||
                                ACGAC GGAG GGC   CCG
                                   A   C  ____
GAM181  DKFZp434C0923 3'  GCCAATGCTTGAACCAGCA   34213       CC  CCT  _
                                TGCTG  TC   GT TTGGC
                                |||||  ||   || |||||
                                ACGAC  AG   CG AACCG
                                   CA  TT_  T
GAM181  DKFZP434J214 3'  TCAGTTCAGAGAGGTAGCA   60930         C   T_
                                TGCTGCCTC CTG  TTGG
                                |||||||| |||  ||||
                                ACGATGGAG GAC  GACT
                                    A   TT
GAM181  DKFZP434P0111 3'  TGGCAAGGGGAGGCAG     67375          GTTTG
                                CTGCCTCCCT    GCCA
                                ||||||||||    ||||
                                GACGGAGGGG    CGGT
                                    AA___
GAM181  DKFZP564I122 3'  TTGAACCAGGGAGGCAG     63179           _  TG
                                CTGCCTCCCTG TT  G
                                |||||||||| ||  |
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                                GACGGAGGGAC AA  T
                                      C  GT
GAM181  DKFZP586D2223 3'  CCAACACTTTGGGAGGCAG   37681         T__ _
                                CTGCCTCCC   GT TTGG
                                |||||||||   || ||||
                                GACGGAGGG   CA AACC
                                     TTT  C
GAM181  DKFZp586G0123 5'  CCAGGCAGAGAGAAGCA    95416     GC   C
                                TGCT  CTC CTGTTTGG
                                ||||  ||| ||||||||
                                ACGA  GAG GACGGACC
                                  A_   A
GAM181  DKFZP586G1517 3'  TCGGGCAGGGAAACACA    81032    C  CC
                                TG TG  TCCCTGTTTGG
                                || ||  ||||||||||
                                AC AC  AGGGACGGGCT
                                 _  AA
GAM181  DKFZP586M1120 3'  GGGCGAGTGAGGCAGCA    48468         CCTG    G
                                TGCTGCCTC    TTTG CC
                                |||||||||    |||| ||
                                ACGACGGAG    GAGC GG
                                     T___    G
GAM181  DKFZp762A227 3'  TGGGAAAAAGAGGAGCA    26037     G    CCTG   GG
                                TGCT CCTC    TTT  CCA
                                |||| ||||    |||  |||
                                ACGA GGAG    AAA  GGT
                                  _    A___   AG
GAM181  DKFZp762A227 3'  TGGGAAAAAGAGGAGCA    34287     G    CCTG   GG
                                TGCT CCTC    TTT  CCA
                                |||| ||||    |||  |||
                                ACGA GGAG    AAA  GGT
                                  _    A___   AG
GAM181  DKFZp762M136 3'  TTGGCCAGCGTAGACAGCAGCA 64691       C_  CC    T
                                TGCTGC  TC  TGTT GGCCAA
                                ||||||  ||  |||| ||||||
                                ACGACG  AG  GCGA CCGGTT
                                    AC  AT   _
GAM181  DNAM-1    5'  CTAATTAAGGGAGGGAGCA   21639      G      GT_
                                TGCT CCTCCCT   TTGG
                                |||| |||||||   ||||
                                ACGA GGAGGGA   AATC
                                  G      ATT
GAM181  ELF1     3'  TTAAATAGAAGGCAACA    71459    C    CC
                                TG TGCCT  CTGTTTGG
                                || |||||  ||||||||
                                AC ACGGA  GATAAATT
                                 A    A_
GAM181  EPHA7    3'  TGGCCAGGAAAATAGCA     15435      CC_   CTGTT
                                TGCTG   TCC    TGGCCA
                                |||||   |||    ||||||
```

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                              ACGAT  AGG   ACCGGT
                                AAA  _____
GAM181  FADS2   5' GGCGCGGGGAGGCCGCA    14956    T      TTG
                              TGC GCCTCCCTGT  GCC
                              ||| ||||||||||  |||
                              ACG CGGAGGGGCG  CGG
                                C       ___
GAM181  FADS2   5' GGCTGGGAGGCAGC      14957        TGTTT
                              GCTGCCTCCC   GGCC
                              ||||||||||   ||||
                              CGACGGAGGG   TCGG
                                           _____
GAM181  FHX     3' TGGCAGTGGGGAAAGAGCA  37310    GCC  TG TG
                              TGCT  TCCC  TT  GCCA
                              ||||  ||||  ||  ||||
                              ACGA  AGGG  GA  CGGT
                                GAA   GT  __
GAM181  FLJ00001 3' TGGCAGGTGGGGGCAGCA   81822      T  TGTTTG
                              TGCTGCC CCC    GCCA
                              ||||||| |||    ||||
                              ACGACGG GGG    CGGT
                                 _  TGGA__
GAM181  FLJ10101 3' TTGGAAGGAAGGCGGCA    45275      C  G  TG
                              TGCTGCCT CCT TT  G
                              |||||||| ||| ||  |
                              ACGGCGGA GGA AG  T
                                   A  _  GT
GAM181  FLJ10120 3' GCCAAGAGCATAAGGCAGCA  35832      CCCTG_
                              TGCTGCCT    TTTGGC
                              ||||||||    ||||||
                              ACGACGGA    GAACCG
                                   ATACGA
GAM181  FLJ10261 3' TTAAGCAGGAAACAGCA    35956     CCTC
                              TGCTG   CCTGTTTGG
                              |||||   |||||||||
                              ACGAC   GGACGAATT
                                AAA_
GAM181  FLJ10330 3' CCAATGTACAAGAAGGCAGCA 36032      CCC  ___
                              TGCTGCCT  TGT  TTGG
                              ||||||||  |||  ||||
                              ACGACGGA  ACA  AACC
                                   AGA  TGT
GAM181  FLJ10420 3' GGCCAGGTAGGCAACA    36109   C   C  GTTT
                              TG TGCCT CCT   GGCC
                              || ||||| |||   ||||
                              AC ACGGA GGA   CCGG
                               A   T  ____
GAM181  FLJ10432 3' TGGCCAAGATTCAGGCTGCA  38829   T  CCCTG
                              TGC GCCT    TTTGGCCA
                              ||| ||||    ||||||||
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                              ACG CGGA    GAACCGGT
                                T   CTTA_
GAM181  FLJ10811 3' AGCAGGAGCAGCAGCA     36681      __   C
                              TGCTGC  CTCC TGTT
                              ||||||  |||| ||||
                              ACGACG  GAGG ACGA
                                 AC   _
GAM181  FLJ10815 3' TGGCCACTTCCAAAGGTAGCA 36697       CCCTGTT
                              TGCTGCCT     TGGCCA
                              ||||||||     ||||||
                              ACGATGGA     ACCGGT
                                   AACCTTC
GAM181  FLJ10898 5' GCACAGAGGGCAGCA      59432       CC   TTG
                              TGCTGCCT  CTGT   GC
                              ||||||||  ||||   ||
                              ACGACGGG  GACA   CG
                                   A_   ___
GAM181  FLJ11301 3' TTGAACCAGGGAGGCAG    37228         _ TG
                              CTGCCTCCCTG TT  G
                              |||||||||||  ||  |
                              GACGGAGGGAC AA  T
                                    C  GT
GAM181  FLJ11506 3' TTGGGAGGAAAGGAGGCAGC  45116       CTG  GG
                              GCTGCCTCC   TTT  CCAA
                              |||||||||   |||  ||||
                              CGACGGAGG   AGG  GGTT
                                   AA_   AG
GAM181  FLJ11608 3' GGCCAGGAAGCCAGCA     44650     C  C   GTTT
                              TGCTG CT CCT    GGCC
                              |||||  ||  |||    ||||
                              ACGAC GA GGA    CCGG
                                 C  A  _____
GAM181  FLJ11722 5' GCCAGAGGGCAGCA       46393       CCCTG
                              TGCTGCCT    TTTGGC
                              ||||||||    ||||||
                              ACGACGGG    AGACCG
                                          ______
GAM181  FLJ12529 3' CTGAAGGAGGAGGCAGCA    45659         _  G  TG
                              TGCTGCCTCC CT TT  G
                              ||||||||||  ||  ||  |
                              ACGACGGAGG GG AA  C
                                    A  _  GT
GAM181  FLJ13441 3' TTGGCATGCGGGAAGCAGC   43675      C   T  TTG
                              GCTGC TCCC GT   GCCAA
                              |||||  ||||  ||   |||||
                              CGACG AGGG CG   CGGTT
                                 A    _  TA_
GAM181  FLJ13710 3' TGGAGAGTCCAAGGAGGCAGC 45685        C  T_  GG
                              GCTGCCTCC TG  TT  CCA
                              |||||||||  ||  ||  |||
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                                CGACGGAGG AC  GA  GGT
                                     A  CT  GA
GAM181  FLJ13855  5' CCGACTGAGGAGGCGGCA    43584          CT T
                                TGCTGCCTCC  G TTGG
                                ||||||||||  | ||||
                                ACGGCGGAGG  T AGCC
                                     AG C
GAM181  FLJ14166  3' GCCAAGTGAGGCAGCA      44685         CCTG
                                TGCTGCCTC    TTTGGC
                                |||||||||    ||||||
                                ACGACGGAG    GAACCG
                                     T___
GAM181  FLJ14327  3' CCAGAGAGAGGCGGCA      46131         CC G
                                TGCTGCCTC  T TTTGG
                                |||||||||  | |||||
                                ACGGCGGAG  A AGACC
                                     __ G
GAM181  FLJ14642  3' CCAGCACTTTGGGAAGCAG    51497     C    T__ _
                                CTGC TCCC   GT TTGG
                                |||| ||||   || ||||
                                GACG AGGG   CA GACC
                                  A    TTT  C
GAM181  FLJ14816  3' TGGAGGGAGACAGGGTGACAGC 51636       CCT       GG__
          A                      TGCTG   CCCTGTTT    CCA
                                |||||   ||||||||    |||
                                ACGAC   GGGACAGA    GGT
                                   AGT       GGGA
GAM181  FLJ20069  3' TGACCCAGGAGGCAG       34470        C  TTT  C
                                CTGCCTCC TG   GG CA
                                |||||||| ||   || ||
                                GACGGAGG AC   CC GT
                                     _ ___  A
GAM181  FLJ20154  3' CTGAATGGAGGCAGCA      72926         CT   TG
                                TGCTGCCTCC  GTT  G
                                ||||||||||  |||  |
                                ACGACGGAGG  TAA  C
                                     __  GT
GAM181  FLJ20254  5' GGCCGAGGAGGCGGCA      34795         CTGT
                                TGCTGCCTCC    TTGGCC
                                ||||||||||    ||||||
                                ACGGCGGAGG    AGCCGG
                                     _____
GAM181  FLJ20257  5' GGCCTTCAAGAGGCGCA     38997     T    CC  TTT
                                TGC GCCTC  TG   GGCC
                                ||| |||||  ||   ||||
                                ACG CGGAG  AC   CCGG
                                  _    A_  TT_
GAM181  FLJ20359  3' GGCTGCAGGGAGACA       35045    C       TT
                                TG CTCCCTGT  GGCC
                                || ||||||||  ||||
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                                AC GAGGGACG  TCGG
                                 A      __
GAM181  FLJ20456  5' GACAGTGGGGAAAGCAGC    35212      ___   _
                                GCTGC   CTCC CTGTT
                                |||||   |||| |||||
                                CGACG   GGGG GACAG
                                   AAA   T
GAM181  FLJ20464  5' CCAGCTCCGGGAGGCGACA   35231    C       TGT_
                                TG TGCCTCCC   TTGG
                                || ||||||||   ||||
                                AC GCGGAGGG   GACC
                                 A       CCTC
GAM181  FLJ20671  3' CCAGCACTTTGGGAGGCAG   35519         T__ _
                                CTGCCTCCC   GT TTGG
                                |||||||||   || ||||
                                GACGGAGGG   CA GACC
                                      TTT  C
GAM181  FLJ20825  3' CCAACTCTTGGGGAGGCAG   35695          T___
                                CTGCCTCCCTG   TTGG
                                ||||||||||    ||||
                                GACGGAGGGGT   AACC
                                       TCTC
GAM181  FLJ21156  3' CCAAGAAGGAAGCAGTA     44807       C   CTG
                                TGCTGC TCC   TTTGG
                                |||||| |||   |||||
                                ATGACG AGG   GAACC
                                   A   AA_
GAM181  FLJ21162  3' TTGAGCCCAGGGAGGCAG    45898          TTT   _
                                CTGCCTCCCTG   GGC CAA
                                ||||||||||   ||| |||
                                GACGGAGGGAC   CCG GTT
                                      ___   A
GAM181  FLJ21369  3' CTGGATAGAGGCAGCA      45635         CC    TG
                                TGCTGCCTC  TGTT  G
                                |||||||||  ||||  |
                                ACGACGGAG  ATAG  C
                                      __    GT
GAM181  FLJ21709  3' TTGACCTGAGCAGCAACAGCA  77923      CCTCC     _  C
                                TGCTG    CTGTTT GG CAA
                                |||||    |||||| || |||
                                ACGAC    GACGAG CC GTT
                                   AAC__     T  A
GAM181  FLJ21865  3' CCAGGCAGGAAGCAGCA     42807       CTC
                                TGCTGC   CCTGTTTGG
                                ||||||   |||||||||
                                ACGACG   GGACGGACC
                                   AA_
GAM181  FLJ21977  3' CCGACAGGGGGCAGCA      49883        T      T
                                TGCTGCC CCCTGTT GG
                                ||||||| ||||||| ||
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                                ACGACGG GGGACAG CC
                                  _     _
GAM181  FLJ22031  3'  CCAGGGCAGGGAGACAGC    46888     C       _
                                GCTG CTCCCTGTT TGG
                                |||| ||||||||| |||
                                CGAC GAGGGACGG ACC
                                  A       G
GAM181  FLJ22215  5'  TGGCCAGGAGGGCAGCA     96839       TC   GTTT
                                TGCTGCC  CCT   GGCCA
                                |||||||  |||   |||||
                                ACGACGG  GGA   CCGGT
                                   GA  ____
GAM181  FLJ22215  3'  TGGCCAGGAGGGCAGCA     43095       TC   GTTT
                                TGCTGCC  CCT   GGCCA
                                |||||||  |||   |||||
                                ACGACGG  GGA   CCGGT
                                   GA  ____
GAM181  FLJ22639  3'  AGCAGAGAGGGCAGCA      45608       _ C
                                TGCTGCC TC CTGTT
                                ||||||| || |||||
                                ACGACGG AG GACGA
                                   G  A
GAM181  FLJ23251  5'  GGCTAGGAAGGCAGC       45687       C   GTTT
                                GCTGCCT CCT   GGCC
                                ||||||| |||   ||||
                                CGACGGA GGA   TCGG
                                   A  ____
GAM181  FLJ23441  3'  TGGTTAAGGAAAAGCA      45171     GCC   CTGT
                                TGCT   TCC   TTGGCCA
                                ||||   |||   |||||||
                                ACGA   AGG   AATTGGT
                                  AA_  ____
GAM181  FLJ31952  5'  TTGGTGGAAGAAGACAGCA   58390      C  CC  GT  G
                                TGCTG CT  CT  TT GCCAA
                                ||||| ||  ||  || |||||
                                ACGAC GA  GA  AG TGGTT
                                   A  A_  __  G
GAM181  FXYD5     3'  TGGCCAGAGAGGGAAGACACA  26343    C  C  _   G
                                TG TG CT CCCT TTTGGCCA
                                || || || |||| ||||||||
                                AC AC GA GGGA AGACCGGT
                                 _  A  A   G
GAM181  GLIO703   3'  CCAGGTTAGGAAGGCAGCA   25438        C  _ TT
                                TGCTGCCT CCT G  TGG
                                |||||||| ||| |  |||
                                ACGACGGA GGA T  ACC
                                    A   T GG
GAM181  GPT2      3'  CCGAGGAGTGAGGCAGCA    55953         C  G
                                TGCTGCCTC CT TTTGG
                                ||||||||| || |||||
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                                ACGACGGAG GA GAGCC
                                     T  G
GAM181  GRIP1    5' CCAAAACAGAGAGGCAGC    70625        C     _
                                GCTGCCTC CTGTTT GG
                                |||||||| |||||| ||
                                CGACGGAG GACAAA CC
                                     A     A
GAM181  GTPBG3   3' TCAAATAGTGAAGCAACA    50908    C   C  C
                                TG TGC TC CTGTTTGG
                                || ||| || ||||||||
                                AC ACG AG GATAAACT
                                 A  A  T
GAM181  HCNGP    3' CCAGATGGAAGGACAGGCAGCA 25151        __   __
                                TGCTGCC  TCC  CTGTTTGG
                                |||||||  |||  ||||||||
                                ACGACGG  AGG  GGTAGACC
                                     AC   AA
GAM181  HEYL     3' CCGGAGGGAGGCAG       27394         GT
                                CTGCCTCCCT  TTGG
                                ||||||||||  ||||
                                GACGGAGGGA  GGCC
                                          __
GAM181  HNK-1ST  3' CCAGCAGGGAGGAAGCA     16768      G        T
                                TGCT CCTCCCTGTT GG
                                |||| |||||||||| ||
                                ACGA GGAGGGACGA CC
                                  A        _
GAM181  HRIHFB2436 5' GGCCGGCTTCAGAGGCAGCA  26795         CCTGT
                                TGCTGCCTC    TTGGCC
                                |||||||||    ||||||
                                ACGACGGAG    GGCCGG
                                     ACTTC
GAM181  IGF2AS   3' GGCATAGGGAGGCAG      33100           TTG
                                CTGCCTCCCTGT   GCC
                                ||||||||||||   |||
                                GACGGAGGGATA   CGG
                                          ____
GAM181  IL-17RE  3' CCGGGGTAGGGAGGCAG    58292          TT _
                                CTGCCTCCCTG  T GG
                                ||||||||||  | ||
                                GACGGAGGGAT  G CC
                                      GG G
GAM181  IL1F10   5' CCAACTGTGAGGGAGGCTACA  50772    CT      GT___
                                TG  GCCTCCCT    TTGG
                                ||  ||||||||    ||||
                                AC  CGGAGGGA    AACC
                                 AT       GTGTC
GAM181  IMP13    5' GCCAGGGAGGGAGCA      27733      G      GTTT
                                TGCT CCTCCCT    GGC
                                |||| |||||||    |||
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                                ACGA GGAGGGA   CCG
                                  G     ____
GAM181  ITPK1    3'  TTGAGGAGGGAGGCACA     26418    C       G  TG
                                TG TGCCTCCCT TT  G
                                || |||||||| ||  |
                                AC ACGGAGGGA GA  T
                                 _       G  GT
GAM181  JM5      3'  CCAGAGACCCAGGAAGGCAGC  22989       C   ____
                                GCTGCCT CCTG   TTTGG
                                ||||||| ||||   |||||
                                CGACGGA GGAC   AGACC
                                    A   CCAG
GAM181  KATII    3'  CCAGCACTTTGGGAGGCAG   32644        T__ _
                                CTGCCTCCC  GT TTGG
                                |||||||||  || ||||
                                GACGGAGGG  CA GACC
                                     TTT  C
GAM181  KCNN1    5'  GGACAGGAAAGGCAGCA     9558        C_
                                TGCTGCCT  CCTGTTT
                                ||||||||  |||||||
                                ACGACGGA  GGACAGG
                                    AA
GAM181  KIAA0121 3'  TGGGGCAGAGGAGGCAGCA   72664         _    TGG
                                TGCTGCCTCC CTGTT   CCA
                                |||||||||| |||||  |||
                                ACGACGGAGG GACGG   GGT
                                     A   ___
GAM181  KIAA0140 3'  GCCGGCAGGGATGCAGCA    27810       C       T
                                TGCTGC TCCCTGTT GGC
                                |||||| |||||||| |||
                                ACGACG AGGGACGG CCG
                                   T      _
GAM181  KIAA0169 3'  GGCCAGGGGAGAGGCGGCA   72820         _  GT
                                TGCTGCCTC CCT  TTGGCC
                                ||||||||| |||  ||||||
                                ACGGCGGAG GGG  GACCGG
                                     A  __
GAM181  KIAA0210 3'  TGGCCATCCCTGGGCAGCA   28490        CCCTGTT
                                TGCTGCCT      TGGCCA
                                ||||||||      ||||||
                                ACGACGGG      ACCGGT
                                     TCCCT__
GAM181  KIAA0218 3'  GCCAAAATGCTCCAGGGTAGGC 28620        _   _______
           AGCA                    TGCTGCCT CCCTG     TTTGGC
                                ||||||||| |||||     ||||||
                                ACGACGGA GGGAC     AAACCG
                                     T    CTCGTA
GAM181  KIAA0258 3'  CCAGCAAGGAGGCAG      28812        C   T
                                CTGCCTCC TGTT GG
                                |||||||| |||| ||
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                                GACGGAGG ACGA CC
                                    A   _
GAM181  KIAA0261  3'  CCAGCCAGGTGCAAAGGCAGC  68180       C____   T
                                GCTGCCT    CCTG TTGG
                                |||||||    |||| ||||
                                CGACGGA    GGAC GACC
                                    AACGT   C
GAM181  KIAA0323  3'  CCAGGCGAAAGGGCAGCA    63260       CCC
                                TGCTGCCT   TGTTTGG
                                ||||||||   |||||||
                                ACGACGGG   GCGGACC
                                    AAA
GAM181  KIAA0397  3'  GGCCAGGAGGCAGCA      61676         CTGTT
                                TGCTGCCTCC    TGGCC
                                ||||||||||    |||||
                                ACGACGGAGG    ACCGG

                                    _____
GAM181  KIAA0415  3'  GCCCAGGGAGGAGCA      92577     G      TTT
                                TGCT CCTCCCTG   GGC
                                |||| ||||||||   |||
                                ACGA GGAGGGAC   CCG

                                  _      ___
GAM181  KIAA0430  3'  TGTGTCGAGAGGCAGCA     38843        CCTGT    _
                                TGCTGCCTC    TTGGC CA
                                |||||||||    ||||| ||
                                ACGACGGAG    AGCTG GT
                                    _____    T
GAM181  KIAA0436  3'  CCAGAAAGAAGGCAACA     60054    C    CC  G
                                TG TGCCT  CT TTTGG
                                || |||||  || |||||
                                AC ACGGA  GA AGACC
                                 A    A_  A
GAM181  KIAA0450  5'  TTGGCAGGGCTCAGGGGGCAGC 27658       T    TTTG__
          A                      TGCTGCC CCCTG     GCCAA
                                |||||||  |||||     |||||
                                ACGACGG GGGAC     CGGTT
                                   _    TCGGGA
GAM181  KIAA0450  3'  CCAGCAGGCAGGAGACA     27625    _  G   C     T
                                TG CT CCT CCTGTT GG
                                || || ||| |||||| ||
                                AC GA GGA GGACGA CC
                                 A  _   C     _
GAM181  KIAA0494  3'  TCAGAGAGGCAAAAAGGTAGCA 28748       C____   G
                                TGCTGCCT    CCT TTTGG
                                ||||||||    ||| |||||
                                ACGATGGA    GGA AGACT
                                    AAAAC   G
GAM181  KIAA0542  3'  TGGCAGCCAGGAGGCAG     66089       C  TTTG
                                CTGCCTCC TG    GCCA
                                ||||||||  ||    ||||
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                                GACGGAGG AC    CGGT
                                    _  CGA_
GAM181  KIAA0544  3'  CCAGGCAGGGAGACAG      70898     C
                                CTG CTCCCTGTTTGG
                                ||| ||||||||||||
                                GAC GAGGGACGGACC
                                  A
GAM181  KIAA0545  3'  TGGCCGAAGATAGCAGCA    63150       CTCCCTG
                                TGCTGC      TTTGGCCA
                                ||||||      ||||||||
                                ACGACG      AAGCCGGT
                                   ATAG___
GAM181  KIAA0561  5'  CCAACGGCAGGCAGCA      65877        C  T   T
                                TGCTGCCT CC GTT GG
                                |||||||| || ||| ||
                                ACGACGGA GG CAA CC
                                     C  _   _
GAM181  KIAA0607  3'  TTGGCTCCCTTGGGCAGACAGC 72573      C  _   TGTTT
            A                    TGCTG CT CCC     GGCCAA
                                ||||| || |||     ||||||
                                ACGAC GA GGG     TCGGTT
                                   A  C   TTCCC
GAM181  KIAA0660  3'  GCAACAGGAGGCAACA      24514    C      C    TG
                                TG TGCCTCC TGTT  GC
                                || |||||| ||||  ||
                                AC ACGGAGG ACAA  CG
                                 A      _   __
GAM181  KIAA0788  3'  GCTCCTGGGAGGCAGCA     71337          TGTTT
                                TGCTGCCTCCC     GGC
                                ||||||||||     |||
                                ACGACGGAGGG     TCG
                                      TCC__
GAM181  KIAA0800  3'  CTATAACAGGGAGGCAG     28146           _
                                CTGCCTCCCTGTT TGG
                                |||||||||||| |||
                                GACGGAGGGACAA ATC
                                       T
GAM181  KIAA0882  3'  GCTAAGTAAGGCAGCA      82646        CC  GTT
                                TGCTGCCT  CT   TGGC
                                ||||||||  ||   ||||
                                ACGACGGA  GA   ATCG
                                     AT  ____
GAM181  KIAA0884  3'  CCAGCACTTTGGGAGGCA    70202        T__  _
                                TGCCTCCC   GT TTGG
                                ||||||||   || ||||
                                ACGGAGGG   CA GACC
                                     TTT  C
GAM181  KIAA0935  3'  CCAGGACAGGGAAAAGCA    72721      GCC       _
                                TGCT   TCCCTGTT TGG
                                ||||   |||||||| |||
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                                ACGA   AGGGACAG ACC
                                  AA_       G
GAM181  KIAA0939 3' GCCAAGCAGGAAGCACA     62016    C   CTC
                                TG TGC   CCTGTTTGGC
                                || |||   ||||||||||
                                AC ACG   GGACGAACCG
                                 _   AA_
GAM181  KIAA0939 3' GGCCAGGTGAGGTCAGCA    62017      _   _  GTTT
                                TGCTG CCTC CCT    GGCC
                                ||||| |||| |||    ||||
                                ACGAC GGAG GGA    CCGG
                                  T    T  ____
GAM181  KIAA1054 3' TTGGAGAACAAAGACAGCA   68455      C  CCC    GG
                                TGCTG CT   TGTTT  CCAA
                                ||||| ||   |||||  ||||
                                ACGAC GA   ACAAG  GGTT
                                   A  A__     A_
GAM181  KIAA1068 3' GCCACTGCAGGCAGCA      31033        CCCT  T_
                                TGCTGCCT    GT  TGGC
                                ||||||||    ||  ||||
                                ACGACGGA    CG  ACCG
                                     ____  TC
GAM181  KIAA1110 3' GCCAGACGAGAGGCAGC     61846         CC
                                GCTGCCTC  TGTTTGGC
                                ||||||||  ||||||||
                                CGACGGAG  GCAGACCG
                                     A_
GAM181  KIAA1115 5' TTGGAGGAGGGAGGCAG     30022          G  TGG
                                CTGCCTCCCT TT   CCAA
                                |||||||||| ||   ||||
                                GACGGAGGGA GA   GGTT
                                      G  ___
GAM181  KIAA1140 3' TGGCCAGAGGGAGAGGCAGCA 62776         C  G
                                TGCTGCCTC CT TTTGGCCA
                                ||||||||| || ||||||||
                                ACGACGGAG GG AGACCGGT
                                     A  G
GAM181  KIAA1196 3' GCTCAGGGAGGCAGTA      61469           TTT
                                TGCTGCCTCCCTG   GGC
                                ||||||||||||   |||
                                ATGACGGAGGGAC   TCG
                                        ___
GAM181  KIAA1239 3' GCTGTGTGGTGAGGCAGCA   71332         C TG T
                                TGCTGCCTC C  T TGGC
                                ||||||||| |  | ||||
                                ACGACGGAG G  G GTCG
                                     T GT T
GAM181  KIAA1274 3' GGACAGGGAGACAGCA      91365       C
                                TGCTG CTCCCTGTTT
                                ||||| ||||||||||
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                                ACGAC GAGGGACAGG
                                   A
GAM181  KIAA1274  3'  TGACCTCCAGGGAGGAGCA   91371     G      TTT  C
                                TGCT CCTCCCTG   GG CA
                                |||| ||||||||   || ||
                                ACGA GGAGGGAC   CC GT
                                  _      CT_  A
GAM181  KIAA1280  5'  CTGTTCAGGGAGGCAGC     69715          TT
                                GCTGCCTCCCTG  TGG
                                ||||||||||||  |||
                                CGACGGAGGGAC  GTC
                                       TT
GAM181  KIAA1332  3'  CCAAGTAGGCAGGCAACA    71164    C    C
                                TG TGCCT CCTGTTTGG
                                || ||||| |||||||||
                                AC ACGGA GGATGAACC
                                 A    C
GAM181  KIAA1405  3'  GCCCTGATGGAGAGGGCAGCA  61040       _ C    T_
                                TGCTGCC TC CTGTT  GGC
                                ||||||| || |||||  |||
                                ACGACGG AG GGTAG  CCG
                                    G  A    TC
GAM181  KIAA1464  3'  TGACCCATGGAGGCAG      68276        C  TTT  C
                                CTGCCTCC TG   GG CA
                                |||||||| ||   || ||
                                GACGGAGG AC   CC GT
                                     T ___  A
GAM181  KIAA1473  3'  CCAGCACTTTGGGAGGCA    70665        T__  _
                                TGCCTCCC   GT TTGG
                                ||||||||   || ||||
                                ACGGAGGG   CA GACC
                                     TTT  C
GAM181  KIAA1486  3'  CCAGCACTCTGGGAGGCAG   67378         T__  _
                                CTGCCTCCC   GT TTGG
                                |||||||||   || ||||
                                GACGGAGGG   CA GACC
                                      TCT  C
GAM181  KIAA1500  5'  CTAGACCAGGAGGCAGCA    64119          CT
                                TGCTGCCTCC  GTTTGG
                                ||||||||||  ||||||
                                ACGACGGAGG  CAGATC
                                      AC
GAM181  KIAA1508  3'  GCTCAGGGAGGCAG        61886          TTT
                                CTGCCTCCCTG   GGC
                                ||||||||||   |||
                                GACGGAGGGAC   TCG
                                        ___
GAM181  KIAA1549  3'  TTGGCCAAAAGCCAGCAGCA  69349       CTCCCTG
                                TGCTGC      TTTGGCCAA
                                ||||||      |||||||||
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                                ACGACG      AAACCGGTT
                                   ACCGA__
GAM181  KIAA1582 5' GGTCAAACAGAAGGACAGCA  65373      _  CC
                                TGCTG CCT  CTGTTTGGCC
                                ||||| |||  ||||||||||
                                ACGAC GGA  GACAAACTGG
                                   A  A_
GAM181  KIAA1607 3' GAAGAGAGAGGCAGCA      63798        C  G
                                TGCTGCCTC CT TTT
                                ||||||||| || |||
                                ACGACGGAG GA AAG
                                     A  G
GAM181  KIAA1649 5' CTAGATAAGGAAGCAG      50256      C   C
                                CTGC TCC TGTTTGG
                                |||| ||| |||||||
                                GACG AGG ATAGATC
                                  A  A
GAM181  KIAA1737 3' TGAGTGGCAGGGAGAAGCA   67366     GC       TG _
                                TGCT  CTCCCTGTT  GC CA
                                ||||  |||||||||  || ||
                                ACGA  GAGGGACGG  TG GT
                                  A_       __ A
GAM181  KIAA1813 3' GCCAGAGGGGCAGCA       70300         CCTG
                                TGCTGCCTC    TTTGGC
                                |||||||||    ||||||
                                ACGACGGGG    AGACCG
                                             ____
GAM181  KIAA1813 5' GCTTCCAGGAAGGAGCA     70305     G   C    TTT
                                TGCT CCT CCTG   GGC
                                |||| ||| ||||   |||
                                ACGA GGA GGAC   TCG
                                  _  A   CT_
GAM181  KIAA1878 3' CCGACCATTCAGGCAGCA    91710        CCC  T
                                TGCTGCCT   TG TTGG
                                ||||||||   || ||||
                                ACGACGGA   AC AGCC
                                     CTT  C
GAM181  KIAA1879 3' CCGAGCACGAAGAAACAGCA  73565      CC  CC__
                                TGCTG  TC    TGTTTGG
                                |||||  ||    |||||||
                                ACGAC  AG    ACGAGCC
                                   AA  AAGC
GAM181  KIAA1938 3' GCTCAGGAGAGGCAGC      92198        _   TTT
                                GCTGCCTC CCTG   GGC
                                |||||||| ||||   |||
                                CGACGGAG GGAC   TCG
                                     A   ___
GAM181  KIAA1940 3' CTGGGAGGGAGGCACA      79982    C       G  TG
                                TG TGCCTCCCT TT  G
                                || |||||||| ||  |
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                                AC ACGGAGGGA GG  C
                                 _       _ GT
GAM181  KIAA1940 3' GCCAAAAGCTGGGGGCAGCA  79984         CTG_
                                TGCTGCCTCC   TTTGGC
                                ||||||||||   ||||||
                                ACGACGGGGG   AAACCG
                                     TCGA
GAM181  KIAA1958 3' TTGACCTTTTCAAAGGTAGCA 81912        CCC  TTT_  C
                                TGCTGCCT   TG   GG CAA
                                ||||||||   ||   || |||
                                ACGATGGA   AC   CC GTT
                                    A__  TTTT  A
GAM181  KIAA1981 3' TTGACCAGCTACGCAGGCAGCA 88349        CCC  T   C
                                TGCTGCCT   TG TTGG CAA
                                ||||||||   || |||| |||
                                ACGACGGA   AT GACC GTT
                                    CGC  C   A
GAM181  LHFPL2   3' TGACCAAAGGGGTCAGCA   69955      C T   GT   C
                                TGCTG C CCCT  TTGG CA
                                ||||| | ||||  |||| ||
                                ACGAC G GGGA  AACC GT
                                  T _   __   A
GAM181  LIPG     3' GCCAGCAAGGCAGCA      20097        CCC   T
                                TGCTGCCT   TGTT GGC
                                ||||||||   |||| |||
                                ACGACGGA   ACGA CCG
                                           ___   _
GAM181  LMOD1    3' GGCCCAGGAAGGCGGCA    24046        C   TTT
                                TGCTGCCT CCTG   GGCC
                                |||||||| ||||   ||||
                                ACGGCGGA GGAC   CCGG
                                    A   ___
GAM181  MAPKAP1  5' CTAACCCGGGAAGCGGCA   44140       C   TGT
                                TGCTGC TCCC   TTGG
                                |||||| ||||   ||||
                                ACGGCG AGGG   AATC
                                   A   CCC
GAM181  MARK2    5' GGCCGAAAGGCGGCA      65606        CCCTG
                                TGCTGCCT    TTTGGCC
                                ||||||||    |||||||
                                ACGGCGGA    AAGCCGG
                                           _____
GAM181  MGC10854 5' CAAACAGGGAGGAAACA    50202    CTG
                                TG   CCTCCCTGTTTG
                                ||   ||||||||||||
                                AC   GGAGGGACAAAC
                                 AAA
GAM181  MGC1136  3' TTGACCAGGGAAGGAGGCAGC 43806         CTG    C
                                GCTGCCTCC   TTTGG CAA
                                |||||||||   ||||| |||
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                                CGACGGAGG  GGACC GTT
                                     AAG    A
GAM181  MGC12435 3' GCTCAGAAGGCAGCA      48689       CC  TTT
                                TGCTGCCT  CTG  GGC
                                ||||||||  |||  |||
                                ACGACGGA  GAC  TCG
                                    A_  ___
GAM181  MGC12760 3' TGGCCCCCTAGGAGGCAGCA  51177        CTGTTT
                                TGCTGCCTCC    GGCCA
                                ||||||||||    |||||
                                ACGACGGAGG    CCGGT
                                     ATCCC_
GAM181  MGC13071 3' CCAGCCAGGTGAGCAACA    51086    C  C _   T
                                TG TGC TC CCTG TTGG
                                || ||| || |||| ||||
                                AC ACG AG GGAC GACC
                                 A  _ T   C
GAM181  MGC14425 3' GGCCCTGCGGAGGCGGCA    51866        CT  TT
                                TGCTGCCTCC  GT  GGCC
                                ||||||||||  ||  ||||
                                ACGGCGGAGG  CG  CCGG
                                     __  TC
GAM181  MGC14480 3' TGGTGTGGGAAGGGGCAGCA  58750        __  TG TTG
                                TGCTGCCTC  CC  T   GCCA
                                |||||||||  ||  |   ||||
                                ACGACGGGG  GG  G   TGGT
                                     AA  GT ___
GAM181  MGC15416 3' TGGCCTGGGAGGCAGCA     56546         TGTTT
                                TGCTGCCTCCC    GGCCA
                                ||||||||||     |||||
                                ACGACGGAGGG    CCGGT
                                     T____
GAM181  MGC15716 3' GGTGGATACCAGGAGGCAGCA 50425         CT  _  G
                                TGCTGCCTCC  GT TT GCC
                                ||||||||||  || || |||
                                ACGACGGAGG  CA AG TGG
                                     AC  T  G
GAM181  MGC15730 5' GGCCAGTGGCCGGAGGCAG   51803       CTGT_
                                CTGCCTCC    TTGGCC
                                ||||||||    ||||||
                                GACGGAGG    GACCGG
                                    CCGGT
GAM181  MGC15854 3' TTGACCTTGGAGTGGAGGCAGC 58854         _  GTTT  C
          A                      TGCTGCCTCC CT    GG CAA
                                 ||||||||||  ||    || |||
                                 ACGACGGAGG GA    CC GTT
                                      T  GGTT  A
GAM181  MGC16291 5' TGGAGGCAGTGAGGCAGCA   51308        C     GG
                                TGCTGCCTC CTGTTT  CCA
                                |||||||||  ||||||  |||
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                                ACGACGGAG GACGGA  GGT
                                     T     __
GAM181  MGC19570 3' TGGCCACTAGGTGGCAGCA   59007       TC   TT
                                TGCTGCC  CCTG  TGGCCA
                                |||||||  ||||  ||||||
                                ACGACGG  GGAT  ACCGGT
                                    T_   C_
GAM181  MGC3036  3' GCTGTTGGGAGACAGTA     43747      C    TGTT
                                TGCTG CTCCC   TGGC
                                ||||| |||||   ||||
                                ATGAC GAGGG   GTCG
                                   A    TT__
GAM181  MGC3079  3' CCAGCACTTTGGGAGGCAG   50951        T__ _
                                CTGCCTCCC   GT TTGG
                                |||||||||   || ||||
                                GACGGAGGG   CA GACC
                                     TTT  C
GAM181  MGC4368  5' GCCTCAGGCAGGAAACAGCA  44462      ___  C   TTT
                                TGCTG   CCT CCTG   GGC
                                |||||   ||| ||||   |||
                                ACGAC   GGA GGAC   CCG
                                   AAA   C   T__
GAM181  MGC4796  3' TGGCCGAGCAACAGCA      61497      CCTCCC
                                TGCTG     TGTTTGGCCA
                                |||||     ||||||||||
                                ACGAC     ACGAGCCGGT
                                   A_____
GAM181  MGC4840  3' CCAGAGGGAGGCAGC       71566          GT
                                GCTGCCTCCCT  TTGG
                                ||||||||||  ||||
                                CGACGGAGGGA  GACC
                                      __
GAM181  MIDORI   3' TTGGAATGCAATAAAGGCAGCA 73796        CCC_  TTGG
                                TGCTGCCT   TGT   CCAA
                                |||||||   |||   ||||
                                ACGACGGA   ACG   GGTT
                                     AATA  TAA_
GAM181  MRPL20   3' TTGGCCAGTAGGAGGCGACA  35742   C      CTGT
                                TG TGCCTCC   TTGGCCAA
                                || |||||||   ||||||||
                                AC GCGGAGG   GACCGGTT
                                 A      AT__
GAM181  MRPL35   3' TGGGCAGGGAAGCAGCA     33545      C      TT
                                TGCTGC TCCCTGT  G
                                |||||| |||||||  |
                                ACGACG AGGGACG  T
                                   A      GG
GAM181  NAV3     3' TGGTCTCCAAGGAGGCAGCA  29776         C  TTT
                                TGCTGCCTCC TG  GGCCA
                                |||||||||| ||  |||||
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                                ACGACGGAGG AC   CTGGT
                                      A  CT_
GAM181  NIN283   3'  GGGCAGGGAGCAGCA       50074        C
                                TGCTGC TCCCTGTTT
                                |||||| |||||||||
                                ACGACG AGGGACGGG
                                   _
GAM181  NR1I3    5'  TGACCACTGCTGGGCAGCA   17604         CCCT  T_   C
                                TGCTGCCT    GT  TGG CA
                                ||||||||    ||  ||| ||
                                ACGACGGG    CG  ACC GT
                                     T___  TC   A
GAM181  NXPH3    3'  GGCTCTCTTGGGAGGGCAGCA  65766         _    TGTTT
                                TGCTGCC TCCC     GGCC
                                ||||||| ||||     ||||
                                ACGACGG AGGG     TCGG
                                    G    TTCTC
GAM181  OBTP     3'  CCAAGCAGAGGACAGCA     34242       _    CC
                                TGCTG CCTC  TGTTTGG
                                ||||| ||||  |||||||
                                ACGAC GGAG  ACGAACC
                                  A   __
GAM181  ORMDL3   5'  CCAGCGGGGAGGCTGCA     74310     T         T
                                TGC GCCTCCCTGTT GG
                                ||| |||||||||| ||
                                ACG CGGAGGGGCGA CC
                                 T         _
GAM181  PADI3    3'  TTGGCCAGGTGGTGGAGACAG  32662     C    _ TG
                                CTG CTCC C  TTTGGCCAA
                                ||| |||| |  |||||||||
                                GAC GAGG G  GGACCGGTT
                                  A    T GT
GAM181  PARVB    3'  CCAGCAAGAAAGGCGGCA    25292         CC  GT
                                TGCTGCCT  CT  TTGG
                                ||||||||  ||  ||||
                                ACGGCGGA  GA  GACC
                                     AA  AC
GAM181  PB1      3'  GCCAAACAGGAAGAAGG     37023     GC  C
                                CT  CT CCTGTTTGGC
                                ||  || ||||||||||
                                GG  GA GGACAAACCG
                                 AA  A
GAM181  PEAS     5'  TGGCAGATAGCAGAGGCAGCA  54070         C_      G
                                TGCTGCCTC  CTGTTTG CCA
                                |||||||||  ||||||| |||
                                ACGACGGAG  GATAGAC GGT
                                     AC      _
GAM181  PIP3-E   3'  TGGCCGAAAGACAGTA      66815       C  CCCTG
                                TGCTG CT    TTTGGCCA
                                ||||| ||    ||||||||
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                                ATGAC GA    AAGCCGGT
                                  A _____
GAM181  PIP5K2B  3'  TGGCCAGGAGAGAAACAGC   13081     CC  C  G
                                GCTG  TC CT TTTGGCCA
                                ||||  || || ||||||||
                                CGAC  AG GA GGACCGGT
                                  AA  A  _
GAM181  PIPPIN   3'  TGGGTGGCAGGGGGGCAGCA  79698          TGG
                                TGCTGCCTCCCTGTT  CCA
                                ||||||||||||||  |||
                                ACGACGGGGGGACGG  GGT
                                        TG_
GAM181  PLPL     3'  TTGACCTGGAGGGGGAGGCAG  39437        G  TG C_
                                CTGCCTCCCT TT  G  CAA
                                |||||||||| ||  |  |||
                                GACGGAGGGG AG  C  GTT
                                      G  GT CA
GAM181  PNMA5    3'  CCAGACACGGGAAGGAGCA   73595     G  _  _
                                TGCT CCT CCC TGTTTGG
                                |||| ||| ||| |||||||
                                ACGA GGA GGG ACAGACC
                                  _  A  C
GAM181  PPFIA2   3'  GCCACTCAAAGGAGGCAGCA  13262        C_  TT
                                TGCTGCCTCC  TG  TGGC
                                ||||||||||  ||  ||||
                                ACGACGGAGG  AC  ACCG
                                      AA  TC
GAM181  PPFIA4   3'  TTGGCCATGTCGTAAGGCAGCA 70338       CCCTGTT
                                TGCTGCCT     TGGCCAA
                                ||||||||     |||||||
                                ACGACGGA     ACCGGTT
                                     ATGCTGT
GAM181  PPIE     3'  GCCTCAGAGGAGGCAGCA    20362        _  TTT
                                TGCTGCCTCC CTG  GGC
                                |||||||||| |||  |||
                                ACGACGGAGG GAC  CCG
                                      A  T__
GAM181  PRDM14   3'  CCAGCACTTTGGGAGGCAG   44445       T__  _
                                CTGCCTCCC  GT TTGG
                                |||||||||  || ||||
                                GACGGAGGG  CA GACC
                                      TTT  C
GAM181  PREI3    3'  TTAACCAGCTAGGCAGCA    66325       CC  T
                                TGCTGCCT  CTG TTGG
                                ||||||||  ||| ||||
                                ACGACGGA  GAC AATT
                                     TC  C
GAM181  PRO2015  5'  TTGGCCAAACCCAGGCAG   37563      CCCT
                                CTGCCT   GTTTGGCCAA
                                ||||||   ||||||||||
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                                GACGGA   CAAACCGGTT
                                   CC__
GAM181  PRSS21   5' GGCGCGAGAGGAGGCAG    58618       CTG   _
                                CTGCCTCC  TTTG GCC
                                ||||||||  |||| |||
                                GACGGAGG  GAGC CGG
                                    A__   G
GAM181  PRSS21   5' GGCGCGAGAGGAGGCAG    22307       CTG   _
                                CTGCCTCC  TTTG GCC
                                ||||||||  |||| |||
                                GACGGAGG  GAGC CGG
                                    A__   G
GAM181  PSMD12   5' CCGAAGCAGGGGGACAGCA  10998     C       _
                                TGCTG CTCCCTGTTT GG
                                ||||| |||||||||| ||
                                ACGAC GGGGGACGAA CC
                                   A        G
GAM181  PTRF     3' CCAGAAGGGGGCAGCA     63499       T   G
                                TGCTGCC CCCT TTTGG
                                ||||||| |||| |||||
                                ACGACGG GGGA AGACC
                                    _   _
GAM181  PTRF     5' GGCCAAACTGAGCATCA    63505    C  C  CCT
                                TG TGC TC  GTTTGGCC
                                || ||| ||  ||||||||
                                AC ACG AG  CAAACCGG
                                 T  _ T__
GAM181  RA-GEF-2 3' TGACCAAACAGAAGTCA    32958    C  CC     C
                                TG CT  CTGTTTGG CA
                                || ||  |||||||| ||
                                AC GA  GACAAACC GT
                                 T  A_      A
GAM181  RAB9B    5' GGACGAGGAGGCAGCA     33036         C
                                TGCTGCCTCC TGTTT
                                |||||||||| |||||
                                ACGACGGAGG GCAGG
                                      A
GAM181  RHOBTB2  3' GCCCCCATGGGGCAGCA    60943       T  C  TTT
                                TGCTGCC CC TG  GGC
                                ||||||| || ||  |||
                                ACGACGG GG AC  CCG
                                   _ T  CC_
GAM181  RHOBTB2  3' CCAGAGGGAGGAGCA      60942     G     GT
                                TGCT CCTCCCT  TTGG
                                |||| |||||||  ||||
                                ACGA GGAGGGA  GACC
                                  _     __
GAM181  RoXaN    3' TCACACAGCGAGGCAGCA    46658       C   T
                                TGCTGCCTC CTGT TGG
                                ||||||||| |||| |||
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                                ACGACGGAG GACA ACT
                                     C   C
GAM181  RP4-622L5 3'  CTAAAGAGGGGAGGCAGCA   38930          G_
                                TGCTGCCTCCCT  TTTGG
                                ||||||||||||  |||||
                                ACGACGGAGGGG  AAATC
                                      AG
GAM181  SDR1    3'  TGACCCCCACAGGGAGGCAG   16464          TT_  C
                                CTGCCTCCCTGT   GG CA
                                ||||||||||||   || ||
                                GACGGAGGGACA   CC GT
                                       CCC  A
GAM181  SEC61A1  3'  CCAGCAGCAAGGGCAGCA    25308        CC_    T
                                TGCTGCCT   CTGTT GG
                                ||||||||   ||||| ||
                                ACGACGGG   GACGA CC
                                     AAC    _
GAM181  SEC8    3'  GGTCATAGAAGGCAGCA     41442        CC   TT
                                TGCTGCCT  CTG  TGGCC
                                ||||||||  |||  |||||
                                ACGACGGA  GAT  ACTGG
                                     A_  __
GAM181  SEMA5A   3'  CCAAATAGAAAAGAAGCA    14253     GC  CC_
                                TGCT  CT   CTGTTTGG
                                ||||  ||   ||||||||
                                ACGA  GA   GATAAACC
                                  A_  AAA
GAM181  SLC26A9  3'  TGGCCAAGAGCCAACA     53623    C  C   CCTGT
                                TG TG CTC    TTGGCCA
                                || || |||    |||||||
                                AC AC GAG    AACCGGT
                                 A  C  _____
GAM181  SLC26A9  3'  TGGCCAAGAGCCAACA     56184    C  C   CCTGT
                                TG TG CTC    TTGGCCA
                                || || |||    |||||||
                                AC AC GAG    AACCGGT
                                 A  C  _____
GAM181  SLC39A3  3'  GGCCAAACAAGGGGTTTGG   57977     CC    _
                                CTG  TCCCT GTTTGGCC
                                |||  ||||| ||||||||
                                GGT  GGGGA CAAACCGG
                                  TT    A
GAM181  SNAPC4   3'  GCCTGCAAGAGAGGCAGC    11849        C  _  TT
                                GCTGCCTC CT GT  GGC
                                |||||||| || ||  |||
                                CGACGGAG GA CG  CCG
                                     A  A  T_
GAM181  SPPL2A   5'  GGCCACGGAGGCAGC       51430         CTGTT
                                GCTGCCTCC    TGGCC
                                |||||||||    |||||
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                                CGACGGAGG    ACCGG
                                     C____
GAM181  SRCAP    5'  CCGGAGGGAGGAGCA      21867     G     GT
                                TGCT CCTCCCT  TTGG
                                |||| |||||||  ||||
                                ACGA GGAGGGA  GGCC
                                  _      __
GAM181  STAG3    3'  TTGGAGTGGAGAAGGGCAGCA 24913       CC  GTTTGG
                                TGCTGCCT  CT     CCAA
                                ||||||||  ||     ||||
                                ACGACGGG  GA     GGTT
                                     AA  GGTGA_
GAM181  TCL6     3'  GAGCAGAGGCAGCA       40134        CC
                                TGCTGCCTC  TGTTT
                                |||||||||  |||||
                                ACGACGGAG  ACGAG
                                     __
GAM181  TCL6     3'  GAGCAGAGGCAGCA       40102        CC
                                TGCTGCCTC  TGTTT
                                |||||||||  |||||
                                ACGACGGAG  ACGAG
                                     __
GAM181  TESK2    3'  CTATGCAAGGGGACAGCA    63181      C   C   T
                                TGCTG CTCC TGT TGG
                                ||||| |||| ||| |||
                                ACGAC GGGG ACG ATC
                                   A   A   T
GAM181  TESK2    3'  TGTGTATGACGGGAGGCAGCA 63184         T   TG  _
                                TGCTGCCTCCC GTT  GC CA
                                |||||||||||| |||  || ||
                                ACGACGGAGGG CAG  TG GT
                                      _  TA  T
GAM181  TNRC3    3'  AGGGAGGGAGGCTGCA      19656     T      G
                                TGC GCCTCCCT TTT
                                ||| ||||||| |||
                                ACG CGGAGGGA GGA
                                  T       G
GAM181  TRAD     3'  CTAAAAGGAGGCAGC       22952         CTG
                                GCTGCCTCC   TTTGG
                                |||||||||   |||||
                                CGACGGAGG   AAATC
                                     A__
GAM181  TREX1    5'  CCAGCAGAGGGAGGCAG     53279         GT_
                                CTGCCTCCCT   TTGG
                                ||||||||||   ||||
                                GACGGAGGGA   GACC
                                      GAC
GAM181  TREX1    5'  CCAGCAGAGGGAGGCAG     53289         GT_
                                CTGCCTCCCT   TTGG
                                ||||||||||   ||||
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                                GACGGAGGGA  GACC
                                      GAC
GAM181  TRIAD3   3'  CTACTCAGATGAGGCAGCA   94503        C_  TT
                                TGCTGCCTC  CTG  TGG
                                |||||||||  |||  |||
                                ACGACGGAG  GAC  ATC
                                      TA   TC
GAM181  TRIM4    5'  CCGCGGCAGGGAAGCAGC    52253      C      _
                                GCTGC TCCCTGTT TGG
                                ||||| |||||||| |||
                                CGACG AGGGACGG GCC
                                   A       C
GAM181  TTY7     3'  TGGCCAAACAAAGGTACA    49182    C    CCC
                                TG TGCCT   TGTTTGGCCA
                                || |||||   ||||||||||
                                AC ATGGA   ACAAACCGGT
                                 _    A__
GAM181  WDR9     3'  GTCAAAGAGGCAGTA      53352        CCTG
                                TGCTGCCTC   TTTGGC
                                |||||||||   ||||||
                                ATGACGGAG   AAACTG
                                      ____
GAM181  ZF5128   3'  CCAAAGAGGTAGCA       26802        CCTG
                                TGCTGCCTC   TTTGG
                                |||||||||   |||||
                                ACGATGGAG   AAACC
                                      ____
GAM181  ZIN      3'  GCTTTCCAGAGGGCAGCA    25492       CC   TTT
                                TGCTGCCT  CTG   GGC
                                ||||||||  |||   |||
                                ACGACGGG  GAC   TCG
                                     A_   CTT
GAM181  ZNF271   3'  CCAACACTTTGGGAGGCAG   95249        T__  _
                                CTGCCTCCC   GT TTGG
                                |||||||||   || ||||
                                GACGGAGGG   CA AACC
                                      TTT  C
GAM181  ZNF282   5'  CCGAGCGGGGAACAGCA     89211      CC
                                TGCTG  TCCCTGTTTGG
                                |||||  ||||||||||
                                ACGAC  AGGGGCGAGCC
                                   A_
GAM181  LOC112724 5'  TTGGCCAGGAGAGGAGGCAACA 56505    C     _  G
                                TG TGCCTCC CT TTTGGCCAA
                                || ||||||| || |||||||||
                                AC ACGGAGG GA GGACCGGTT
                                 A      A  _
GAM181  LOC112817 5'  CAAGTCAGGGAGGCCGCA    56506     T      _
                                TGC GCCTCCCTG TTTG
                                ||| ||||||||| ||||
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                                ACG CGGAGGGAC GAAC
                                  C       T
GAM181   LOC114987 3'  CCAGAAGGGAGAGAGGCAGCA  59122          ___   G
                                TGCTGCCTC   CCT TTTGG
                                |||||||||   ||| |||||
                                ACGACGGAG   GGG AGACC
                                     AGA   A
GAM181   LOC115110 3'  GCCCAGAGAGGCAGC       71717        C   TTT
                                GCTGCCTC CTG   GGC
                                |||||||| |||   |||
                                CGACGGAG GAC   CCG
                                     A   ___
GAM181   LOC115399 3'  CCAGCCAGGGAGGCAGCA    73428           T
                                TGCTGCCTCCCTG TTGG
                                |||||||||||| ||||
                                ACGACGGAGGGAC GACC
                                       C
GAM181   LOC115399 5'  TGGCTGGAGAAAGGCAGGCA  73439      C   G__  TG
                                TGCCT CCT   TT  GCCA
                                ||||| |||   ||  ||||
                                ACGGA GGA   AG  CGGT
                                   C   AAG  GT
GAM181   LOC121512 5'  GCTTTTATAAGGCAGCA     57645        CCC   TT_
                                TGCTGCCT   TGT   GGC
                                ||||||||   |||   |||
                                ACGACGGA   ATA   TCG
                                     ___   TTT
GAM181   LOC122886 3'  CCAAAGAGAGGCAGCA      75582         C  GT
                                TGCTGCCTC CT  TTGG
                                ||||||||| ||  ||||
                                ACGACGGAG GA  AACC
                                     A  __
GAM181   LOC122970 3'  GCCAAACATGGTACA       74179    C    TCCC
                                TG TGCC    TGTTTGGC
                                || ||||    ||||||||
                                AC ATGG    ACAAACCG
                                 _   T___
GAM181   LOC124460 3'  TTAGGCAAAGAGGTAGCA    76048         CC
                                TGCTGCCTC  TGTTTGG
                                |||||||||  |||||||
                                ACGATGGAG  ACGGATT
                                     AA
GAM181   LOC128387 3'  TCAACTGCAGGGGGCAGCA   74751        T     __
                                TGCTGCC CCCTGT  TTGG
                                ||||||| ||||||  ||||
                                ACGACGG GGGACG  AACT
                                    _     TC
GAM181   LOC129228 5'  CCAGACAGACAGGCAGCA    75808         CC
                                TGCTGCCT  CTGTTTGG
                                ||||||||  ||||||||
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                                ACGACGGA  GACAGACC
                                    CA
GAM181   LOC129228 5'  CCGGACAGGGAGACAG      75809     C
                                CTG CTCCCTGTTTGG
                                ||| ||||||||||||
                                GAC GAGGGACAGGCC
                                  A
GAM181   LOC129433 5'  TGACCAAACAGCAGTA      75727       CTCCC      C
                                TGCTGC    TGTTTGG CA
                                ||||||    ||||||| ||
                                ATGACG    ACAAACC GT
                                   _____      A
GAM181   LOC129676 5'  GGACAGGGAGGGAGCA      75734      G
                                TGCT CCTCCCTGTTT
                                |||| ||||||||||
                                ACGA GGAGGGACAGG
                                  G
GAM181   LOC138429 3'  GCCAGAGGGCAGCA        75341        CCCTG
                                TGCTGCCT    TTTGGC
                                ||||||||    ||||||
                                ACGACGGG    AGACCG
                                    _____
GAM181   LOC139941 5'  TGGGCAGGAAGGGCAGCA    75390        C_    TT
                                TGCTGCCT  CCTGT  G
                                ||||||||  |||||  |
                                ACGACGGG  GGACG  T
                                     AA    GG
GAM181   LOC142955 3'  AGCGTGGGAAGGCAGC      76441        _  _
                                GCTGCCT CCC TGTT
                                ||||||| ||| ||||
                                CGACGGA GGG GCGA
                                    A  T
GAM181   LOC143425 3'  GCTAAATAGGCAGCA       87637        CCCT
                                TGCTGCCT   GTTTGGC
                                ||||||||   |||||||
                                ACGACGGA   TAAATCG
                                    _____
GAM181   LOC144262 5'  GCTCAGAAAAGGTAGCA     76752        CC_   TTT
                                TGCTGCCT   CTG   GGC
                                ||||||||   |||   |||
                                ACGATGGA   GAC   TCG
                                    AAA   ___
GAM181   LOC144319 3'  TGGCCCCAGGGCAGCA      83060       TCC   TTT
                                TGCTGCC   CTG   GGCCA
                                |||||||   |||   |||||
                                ACGACGG   GAC   CCGGT
                                    ___   C__
GAM181   LOC145814 5'  CTGAGCCAGGGAGGCGCA    77505     T       _  TG
                                TGC GCCTCCCTG TT  G
                                ||| |||||||| ||  |
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                                ACG CGGAGGGAC GA  C
                                  _       C  GT
GAM181  LOC145820 3'  TGGCCAAAATGGAAAACTGCA  77518     TGCC_   CTG
                                TGC    TCC   TTTGGCCA
                                |||    |||   ||||||||
                                ACG    AGG   AAACCGGT
                                  TCAAA   TA_
GAM181  LOC145945 5'  CCAGCAGGGGAGGCAACA    83572    C       GT
                                TG TGCCTCCCT  TTGG
                                || |||||||||  ||||
                                AC ACGGAGGGG  GACC
                                 A        AC
GAM181  LOC146013 5'  CCAGACCAAGAAGGCAGCA   83610        _ CCT
                                TGCTGCCT C   GTTTGG
                                |||||||| |   ||||||
                                ACGACGGA G   CAGACC
                                     A AAC
GAM181  LOC146092 5'  GGTCAAGGGGCAGCA       83613         CCTGT
                                TGCTGCCTC    TTGGCC
                                |||||||||    ||||||
                                ACGACGGGG    AACTGG
                                             _____
GAM181  LOC146226 5'  TTGGCAGGATGAGAGGCAGCA 83625         CC   TG
                                TGCTGCCTC  TGTT  GCCAA
                                |||||||||  ||||  |||||
                                ACGACGGAG  GTAG  CGGTT
                                     A_   GA
GAM181  LOC146714 5'  TGGGAAAAAGGGAGCA      83743     C    G   GG
                                TGC TCCCT TTT  CCA
                                ||| ||||| |||  |||
                                ACG AGGGA AAA  GGT
                                  _    _  AG
GAM181  LOC146756 3'  CCAGGAAGAAGGCAGC      83774       CC  G
                                GCTGCCT  CT TTTGG
                                |||||||  || |||||
                                CGACGGA  GA GGACC
                                    A_  A
GAM181  LOC146890 5'  CCAAGCAGAGAAGCAGC     83853      C  C
                                GCTGC TC CTGTTTGG
                                ||||| || ||||||||
                                CGACG AG GACGAACC
                                   A  A
GAM181  LOC147042 3'  CTGGAAGAGAGGCAGTA     83913        C  G  TG
                                TGCTGCCTC CT TT  G
                                ||||||||| || ||  |
                                ATGACGGAG GA AG  C
                                     A  _  GT
GAM181  LOC147228 3'  GGAGGCAGGGAGGCAGC     66902            GG
                                GCTGCCTCCCTGTTT  CC
                                ||||||||||||||  ||
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                                CGACGGAGGGACGGA  GG
                                          __
GAM181   LOC147299 5'  TCAACAAGGGAAGCACCA    78349    C  C    GT
                                TG TGC TCCCT  TTGG
                                || ||| |||||  ||||
                                AC ACG AGGGA  AACT
                                 C   A     AC
GAM181   LOC147343 5'  GAGCAGGGAGGAAGCA      84000      G
                                TGCT CCTCCCTGTTT
                                |||| ||||||||||
                                ACGA GGAGGGACGAG
                                  A
GAM181   LOC147381 5'  TCAAACTTGAGAGAGGCA    84013       C  ___
                                TGCCTC CT   GTTTGG
                                |||||| ||   ||||||
                                ACGGAG GA   CAAACT
                                    A  GTT
GAM181   LOC147991 5'  TGACCAGGAGGCACCA      78605    C      CTGTT   C
                                TG TGCCTCC     TGG CA
                                || |||||||     ||| ||
                                AC ACGGAGG     ACC GT
                                 C      ______   A
GAM181   LOC148089 3'  CCAGCAGATGAGGCAGCA    78628         C_    T
                                TGCTGCCTC  CTGTT GG
                                |||||||||  ||||| ||
                                ACGACGGAG  GACGA CC
                                      TA    _
GAM181   LOC148198 3'  CCAGCACTTTGGGAGGCA    70679        T__ _
                                TGCCTCCC   GT TTGG
                                ||||||||   || ||||
                                ACGGAGGG   CA GACC
                                     TTT  C
GAM181   LOC148397 3'  GGTGCACAGGGAACAGCA    78821      CC      TTG
                                TGCTG  TCCCTGT   GCC
                                |||||  |||||||   |||
                                ACGAC  AGGGACA   TGG
                                   A_      CG_
GAM181   LOC148413 3'  TGTGTGCAGAAGGCAGCA    78832        CC    TTG  _
                                TGCTGCCT  CTGT   GC CA
                                ||||||||  ||||   || ||
                                ACGACGGA  GACG   TG GT
                                     A_   ___  T
GAM181   LOC148529 5'  TGGCAGACAGGAAGACA     84173    C  C      G
                                TG CT CCTGTTTG CCA
                                || || |||||||| |||
                                AC GA GGACAGAC GGT
                                 A  A       _
GAM181   LOC149305 5'  TGGCCAGGCGACAGCAGCA   79267       CTCCC
                                TGCTGC     TGTTTGGCCA
                                ||||||     ||||||||||
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                                ACGACG    GCGGACCGGT
                                   ACA__
GAM181  LOC149414 3'  CTGAACTAGAGAGGCAGTA   84413        C _  TG
                                TGCTGCCTC CT GTT  G
                                ||||||||| || |||  |
                                ATGACGGAG GA CAA  C
                                     A  T   GT
GAM181  LOC149579 3'  GCGTGAAAAGGAGGCAGCA   71134         CTG  _
                                TGCTGCCTCC   TTTG GC
                                ||||||||||   |||| ||
                                ACGACGGAGG   AAGT CG
                                     AA_   G
GAM181  LOC150150 3'  TGGCCAGGCGGGGGAGGCGCA  84869    T      _
                                TGC GCCTCCCT GTTTGGCCA
                                ||| |||||||| |||||||||
                                ACG CGGAGGGG CGGACCGGT
                                  _      G
GAM181  LOC150225 3'  CAGGCAGGAGAGGCAGC     84985        _
                                GCTGCCTC CCTGTTTG
                                |||||||| ||||||||
                                CGACGGAG GGACGGAC
                                     A
GAM181  LOC150225 3'  CTAACCTGGGTGGGGCAGCA   84989         _  GT_
                                TGCTGCCTC CCT   TTGG
                                ||||||||| |||   ||||
                                ACGACGGGG GGG   AATC
                                     T   TCC
GAM181  LOC150290 3'  CCAGAAGAAAGAGGGCAGCA   79769       _ CCTG_
                                TGCTGCC TC    TTTGG
                                ||||||| ||    |||||
                                ACGACGG AG    AGACC
                                   G  AAAGA
GAM181  LOC150418 5'  CCAGCAGGGAGACAG       65508    C       T
                                CTG CTCCCTGTT GG
                                ||| ||||||||| ||
                                GAC GAGGGACGA CC
                                  A       _
GAM181  LOC150481 3'  GGCTCAGAAGGCAGCA      79893        CC   TTT
                                TGCTGCCT  CTG   GGCC
                                ||||||||  |||   ||||
                                ACGACGGA  GAC   TCGG
                                     A_  ____
GAM181  LOC150998 3'  TGGCCGGCTGGAGGCTGCA   85188    T     CT   T
                                TGC GCCTCC  GTT GGCCA
                                ||| ||||||  ||| |||||
                                ACG CGGAGG  CGG CCGGT
                                  T     T_  _
GAM181  LOC150998 3'  TTGACCAAACAGAAAGAGGC   85189      C__      C
                                GCCTC   CTGTTTGG CAA
                                |||||   |||||||| |||
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                                CGGAG   GACAAACC GTT
                                  AAA       A
GAM181   LOC151005 3'  CCAATAGGGAAAAGACA     80096    _ GCC       T
                                TG CT   TCCCTGTT GG
                                || ||   |||||||| ||
                                AC GA   AGGGATAA CC
                                 A  AA_       _
GAM181   LOC151438 5'  GCCAAGCTTTGAGAAGCA    85366     GC   CCT
                                TGCT  CTC   GTTTGGC
                                ||||  |||   |||||||
                                ACGA  GAG   CGAACCG
                                  A_   TTT
GAM181   LOC151742 3'  TTGACAATGGAAAGGCAGCA   57674        CC    T GC
                                TGCTGCCT  CTGTT G  CAA
                                ||||||||  ||||| |  |||
                                ACGACGGA  GGTAA C  GTT
                                     AA    _ A_
GAM181   LOC151904 5'  GCCTTCTGCAGGAGGCAGC   80391        C   TT__
                                GCTGCCTCC TGT    GGC
                                |||||||||| |||    |||
                                CGACGGAGG ACG    CCG
                                     _   TCTT
GAM181   LOC152190 5'  GCCAAACAAGAAGTAG      69658      C  CC
                                CTGC TC  TGTTTGGC
                                |||| ||  ||||||||
                                GATG AG  ACAAACCG
                                  A  A_
GAM181   LOC152271 3'  CCAACCTGCGCAGGCAGCA   80515        CCC   ___
                                TGCTGCCT   TGT   TTGG
                                ||||||||   |||   ||||
                                ACGACGGA   GCG   AACC
                                     C__   TCC
GAM181   LOC152317 3'  TGGCCAAACAGTGGCAG     85651      TCC
                                CTGCC   CTGTTTGGCCA
                                |||||   ||||||||||
                                GACGG   GACAAACCGGT
                                   T__
GAM181   LOC152762 3'  GGCCCAGGATAGGCAGCA    80655        C_   TTT
                                TGCTGCCT  CCTG   GGCC
                                |||||||  ||||   ||||
                                ACGACGGA  GGAC   CCGG
                                     TA   ___
GAM181   LOC152860 3'  CCAGCACTTTGGGAGGCAG   80698        T__  _
                                CTGCCTCCC   GT TTGG
                                |||||||||   || ||||
                                GACGGAGGG   CA GACC
                                     TTT  C
GAM181   LOC153196 5'  TTGGCCAAAGGAAACAGC    85983     CC   CTG
                                GCTG  TCC   TTTGGCCAA
                                ||||  |||   |||||||||
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                                CGAC  AGG   AAACCGGTT
                                  AA  ___
GAM181   LOC153727 3'  TTGAACCTAGGGAGGCAG    86155         __  TG
                                CTGCCTCCCT  GTT  G
                                ||||||||||  |||  |
                                GACGGAGGGA  CAA  T
                                     TC   GT
GAM181   LOC153910 3'  GCCAAGTAGACCAGCA      80996      CCTCC
                                TGCTG    CTGTTTGGC
                                |||||    |||||||||
                                ACGAC    GATGAACCG
                                   CA___
GAM181   LOC154141 5'  GCCTCAGAAAGGCAGCA     86169        CC   TTT
                                TGCTGCCT  CTG   GGC
                                ||||||||  |||   |||
                                ACGACGGA  GAC   CCG
                                     AA   T__
GAM181   LOC154282 3'  CTAAAAGAAAGGCAGCA     86197        CC  G
                                TGCTGCCT  CT TTTGG
                                ||||||||  ||  |||||
                                ACGACGGA  GA AAATC
                                     AA  _
GAM181   LOC155006 3'  CCAGCACTTTGGGAGGCAG    81233         T__  _
                                CTGCCTCCC   GT TTGG
                                |||||||||   ||  ||||
                                GACGGAGGG   CA GACC
                                     TTT  C
GAM181   LOC157273 3'  TCAAACAGGAAGACACA     86434    C  C  C
                                TG TG CT CCTGTTTGG
                                ||  ||  ||  |||||||||
                                AC AC GA GGACAAACT
                                 _  A  A
GAM181   LOC157349 5'  GGAGAGCAGGAAGGGAGCA   81418     G   C      GG
                                TGCT CCT CCTGTTT  CC
                                ||||  |||  |||||||  ||
                                ACGA GGA GGACGAG  GG
                                  G   A      A_
GAM181   LOC157638 5'  TGGCTGAGGAGGGGCAGCA   81515        TC   G  TG
                                TGCTGCC  CCT TT  GCCA
                                |||||||  |||  ||  ||||
                                ACGACGG  GGA GA  CGGT
                                    __   G  GT
GAM181   LOC157848 3'  CCAGGAGGGAGGCACA      81616    C       G
                                TG TGCCTCCCT TTTGG
                                ||  |||||||||  |||||
                                AC ACGGAGGGA GGACC
                                 _       _
GAM181   LOC157848 3'  CCAGGGAGGGAGGCAGC     81617          G
                                GCTGCCTCCCT TTTGG
                                ||||||||||  |||||
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                                CGACGGAGGGA GGACC
                                      G
GAM181  LOC158191 3'  GGCTCAGAAGGCAGCA      81781        CC   TTT
                                TGCTGCCT  CTG   GGCC
                                ||||||||  |||   ||||
                                ACGACGGA  GAC   TCGG
                                    A_   ___
GAM181  LOC158308 5'  GGTGCAGGGAGGCAG       86744           TTG
                                CTGCCTCCCTGT   GCC
                                ||||||||||||   |||
                                GACGGAGGGACG   TGG
                                       ___
GAM181  LOC158377 5'  TTGGCACGAGGGGGGCAGCA   86795          C   TTG
                                TGCTGCCTCC TGT   GCCAA
                                ||||||||||| |||   |||||
                                ACGACGGGGG GCA   CGGTT
                                    A   ___
GAM181  LOC158572 3'  CCGGGGGAGGGGGGGCAGCA   81955          G   _
                                TGCTGCCTCCCT TTT GG
                                |||||||||||| ||| ||
                                ACGACGGGGGGA GGG CC
                                      G   G
GAM181  LOC158572 3'  TGGCACTGGGCAGCAGCA    81957       CT   T  TTG
                                TGCTGC  CCC GT   GCCA
                                ||||||  ||| ||   ||||
                                ACGACG  GGG CA   CGGT
                                   AC   T  ___
GAM181  LOC158722 3'  TCAACTCCAGGAAGGCAGTA   81997        C    T__
                                TGCTGCCT CCTG   TTGG
                                |||||||| ||||   ||||
                                ATGACGGA GGAC   AACT
                                    A    CTC
GAM181  LOC162333 5'  TTGACCAAACATCAGTCAAGCA 87147      GCCTCCC      C
                                TGCT      TGTTTGG CAA
                                ||||      ||||||| |||
                                ACGA      ACAAACC GTT
                                  ACTGACT      A
GAM181  LOC164582 5'  GGCCAGAGGCTGGAGGCAGACA 82544    _      CTG_
                                TG CTGCCTCC    TTTGGCC
                                || ||||||||    |||||||
                                AC GACGGAGG    AGACCGG
                                 A       TCGG
GAM181  LOC164714 3'  GGCAGCAGGGGGGGGCAGCA   87237          GTTTG
                                TGCTGCCTCCCT    GCC
                                ||||||||||||    |||
                                ACGACGGGGGGG    CGG
                                      ACGA_
GAM181  LOC165476 5'  TGGCCAAGAAGGCAG       87199       CCCTG
                                CTGCCT    TTTGGCCA
                                ||||||    ||||||||
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                                GACGGA    GAACCGGT
                                   A____
GAM181  LOC166341 3'  TGGCCACGAGGCAGCA     82633        CCTGTT
                                TGCTGCCTC     TGGCCA
                                |||||||||     ||||||
                                ACGACGGAG     ACCGGT
                                    C_____
GAM181  LOC169611 3'  CCGGAGAGGGGCAGCA     82761       TC   G
                                TGCTGCC  CCT TTTGG
                                |||||||  ||| |||||
                                ACGACGG  GGA AGGCC
                                   __  G
GAM181  LOC196214 5'  TGGCCAAATCAGAGCA     89623     GCCTCC  _
                                TGCT     CTG TTTGGCCA
                                ||||     ||| ||||||||
                                ACGA     GAC AAACCGGT
                                  _______  T
GAM181  LOC196337 3'  TGGCTGGAGAGGCAGCA     87652        CCTG  TG
                                TGCTGCCTC    TT  GCCA
                                |||||||||    ||  ||||
                                ACGACGGAG    AG  CGGT
                                     _____ GT
GAM181  LOC196410 3'  TGACCCAGGGAGGAAACA    87659    CTG      TTT  C
                                TG   CCTCCCTG   GG CA
                                ||   ||||||||   || ||
                                AC   GGAGGGAC   CC GT
                                 AAA       ___  A
GAM181  LOC197201 3'  TTGAACCAGGGAGGCAG     87950          _  TG
                                CTGCCTCCCTG TT  G
                                |||||||||||  ||  |
                                GACGGAGGGAC AA  T
                                      C  GT
GAM181  LOC197273 5'  TGGCCCTAGGGCAGCA      67400       TCC   TTT
                                TGCTGCC   CTG   GGCCA
                                |||||||   |||   |||||
                                ACGACGG   GAT   CCGGT
                                   ___   C__
GAM181  LOC197408 5'  TCAAGCAGGAGGCAGCA     89753          C
                                TGCTGCCTCC TGTTTGG
                                |||||||||| |||||||
                                ACGACGGAGG ACGAACT
                                           _
GAM181  LOC199692 3'  CCATACAGGGAGACAGC     59239     C       T
                                GCTG CTCCCTGT TGG
                                |||| |||||||| |||
                                CGAC GAGGGACA ACC
                                  A       T
GAM181  LOC200093 3'  CCAGGCAGGACGACAGCA    63091       CCTC
                                TGCTG    CCTGTTTGG
                                |||||    |||||||||
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                                ACGAC    GGACGGACC
                                   AGCA
GAM181   LOC200163 5'  CTAAACAGATAAGGCAGCA    88589        CC_
                                TGCTGCCT   CTGTTTGG
                                ||||||||   ||||||||
                                ACGACGGA   GACAAATC
                                     ATA
GAM181   LOC200931 3'  TGACCAAATGGGAAGCA     88944     C    T     C
                                TGC TCCC GTTTGG CA
                                ||| |||| |||||| ||
                                ACG AGGG TAAACC GT
                                  A    _     A
GAM181   LOC201191 5'  CCGGAAGGAGAAAGGCAGCA   89769        __  _   G
                                TGCTGCC  TC CCT TTTGG
                                |||||||  || ||| |||||
                                ACGACGG  AG GGA AGGCC
                                     AA  A   _
GAM181   LOC201191 3'  GCCAGGCAGAGAGGCA      89771       C
                                TGCCTC CTGTTTGGC
                                |||||| |||||||||
                                ACGGAG GACGGACCG
                                   A
GAM181   LOC201252 3'  TGGCCAAGAAGGGAGCA     88171     C     G
                                TGC TCCCT TTTGGCCA
                                ||| ||||| ||||||||
                                ACG AGGGA GAACCGGT
                                  _     A
GAM181   LOC202301 3'  TGGTTAAGAAAGGAAGCA    89162     C   CTG
                                TGC TCC   TTTGGCCA
                                ||| |||   ||||||||
                                ACG AGG   GAATTGGT
                                  A   AAA
GAM181   LOC203052 3'  CCAGAGGAAGGCAGGCA     90452     _     C   GT
                                TGC TGCCT CCT  TTGG
                                ||| ||||| |||  ||||
                                ACG ACGGA GGA  GACC
                                  G     A   __
GAM181   LOC203286 5'  CCGACATTGAGAGGCAGCA    90495         CC__    T
                                TGCTGCCTC    TGTT GG
                                |||||||||    |||| ||
                                ACGACGGAG    ACAG CC
                                     AGTT    _
GAM181   LOC203286 3'  CCGGCAAGAGGTAGCA      90496         CC    T
                                TGCTGCCTC  TGTT GG
                                |||||||||  |||| ||
                                ACGATGGAG  ACGG CC
                                     A_    _
GAM181   LOC204161 5'  GGCCAAGGGGCAGCA       90660         CCTGT
                                TGCTGCCTC    TTGGCC
                                |||||||||    ||||||
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                                ACGACGGGG    AACCGG
                                      _____
GAM181  LOC204285 5'  AAACAGGGGACAGCA      89452      C T
                                TGCTG C CCCTGTTT
                                ||||| | ||||||||
                                ACGAC G GGGACAAA
                                   A _
GAM181  LOC204804 3'  GCCAGATGACAGCA       89473      CC  CCT
                                TGCTG  TC   GTTTGGC
                                |||||  ||   |||||||
                                ACGAC  AG   TAGACCG
                                   __  ___
GAM181  LOC206426 3'  TCAAGGAAGGGAGGCAGC    89536          G_
                                GCTGCCTCCCT  TTTGG
                                ||||||||||  |||||
                                CGACGGAGGGA  GAACT
                                      AG
GAM181  LOC219848 3'  GCCAATGATTGGGGAGGCAGC  91493          GT___
                                GCTGCCTCCCT    TTGGC
                                ||||||||||    |||||
                                CGACGGAGGGG    AACCG
                                      TTAGT
GAM181  LOC220143 3'  TGGCCAGTCACTAGGGGGCAGC 93593          CT __
          A                      TGCTGCCTCC  GT  TTGGCCA
                                ||||||||||  ||  |||||||
                                ACGACGGGGG  CA  GACCGGT
                                      AT  CT
GAM181  LOC220824 3'  AGCAGAGAGGGCAGCA      90804        _  C
                                TGCTGCC TC CTGTT
                                ||||||| || |||||
                                ACGACGG AG GACGA
                                    G  A
GAM181  LOC221178 3'  CTAGAAAGAGGGCAGCA     93532         CC  G
                                TGCTGCCT  CT TTTGG
                                ||||||||  || |||||
                                ACGACGGG  GA AGATC
                                    A_  A
GAM181  LOC221398 3'  TTGGCCAGACCACAGCAGCA   91020       CTCCCT
                                TGCTGC     GTTTGGCCAA
                                ||||||     ||||||||||
                                ACGACG     CAGACCGGTT
                                   ACAC__
GAM181  LOC221415 5'  CCAAGGGGAAAGGGCAGCA    93873        ___    GT
                                TGCTGCC   TCCCT  TTGG
                                |||||||   |||||  ||||
                                ACGACGG   AGGGG  AACC
                                    GAA    __
GAM181  LOC221495 5'  GCCCAGGGAGGCAG        93858          TTT
                                CTGCCTCCCTG   GGC
                                ||||||||||   |||
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                                GACGGAGGGAC   CCG
                                      ___
GAM181   LOC221495 3'  TTGGCCTCTGGGGAGGCA    93868         TTT
                                TGCCTCCCTG   GGCCAA
                                ||||||||||   ||||||
                                ACGGAGGGGT   CCGGTT
                                     CT_
GAM181   LOC221927 3'  GGACCAAGGGAGGCAGCA    92651          GTT  _
                                TGCTGCCTCCCT   TGG CC
                                ||||||||||||   ||| ||
                                ACGACGGAGGGA   ACC GG
                                       ___   A
GAM181   LOC222008 5'  GCCAAGCAAGCAGCA      94011       CTCCC
                                TGCTGC    TGTTTGGC
                                ||||||    ||||||||
                                ACGACG    ACGAACCG
                                   A____
GAM181   LOC222159 5'  CCAAACAGGATTAGTA     94076      CCTC
                                TGCTG   CCTGTTTGG
                                |||||   |||||||||
                                ATGAT   GGACAAACC
                                  TA__
GAM181   LOC222493 5'  TTGGCCAATCCCAGGCACCA  94349    C    CCCTGT
                                TG TGCCT     TTGGCCAA
                                || |||||     ||||||||
                                AC ACGGA     AACCGGTT
                                 C    CCCT__
GAM181   LOC253142 3'  TGGCGAGAGGCAGCA      97383         CCTGTT G
                                TGCTGCCTC     T GCCA
                                |||||||||     | ||||
                                ACGACGGAG     A CGGT
                                      _______ G
GAM181   LOC253666 3'  TCAGGAAGGAAGGAGCA     95070     G   C   G
                                TGCT CCT CCT TTTGG
                                |||| ||| ||| |||||
                                ACGA GGA GGA GGACT
                                  _   A   A
GAM181   LOC253893 3'  CCAGGAGGGAGGCACA      96110    C       G
                                TG TGCCTCCCT TTTGG
                                || |||||||| |||||
                                AC ACGGAGGGA GGACC
                                  _       _
GAM181   LOC253893 3'  CCAGGGAGGGAGGCAGC     96111          G
                                GCTGCCTCCCT TTTGG
                                |||||||||| |||||
                                CGACGGAGGGA GGACC
                                       G
GAM181   LOC253955 3'  CCGGGTAGGAAGGTAGCA    94426        C    TT
                                TGCTGCCT CCTG  TGG
                                |||||||| ||||  |||
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                                ACGATGGA GGAT  GCC
                                    A    GG
GAM181   LOC253955 5'  TGGCACCCAAGAGGCAGC    94434        CC  TTTG
                                GCTGCCTC  TG    GCCA
                                ||||||||  ||    ||||
                                CGACGGAG  AC    CGGT
                                    A_  CCA_
GAM181   LOC254015 3'  CCAGGAAGAAGGCAGC      96702        CC  G
                                GCTGCCT  CT TTTGG
                                |||||||  || |||||
                                CGACGGA  GA GGACC
                                    A_  A
GAM181   LOC254057 5'  CCAGCGCGGGAGGCAG      96996         _   T
                                CTGCCTCCC TGTT GG
                                ||||||||| |||| ||
                                GACGGAGGG GCGA CC
                                     C   _
GAM181   LOC254105 5'  TGGCTTGGGAGGTAACA     94772    C       TGTTT
                                TG TGCCTCCC    GGCCA
                                || ||||||||    |||||
                                AC ATGGAGGG    TCGGT
                                 A       T____
GAM181   LOC254173 5'  GGCCGGGAGGCACCA       96844    C       TGTTT
                                TG TGCCTCCC    GGCC
                                || ||||||||    ||||
                                AC ACGGAGGG    CCGG
                                 C      _____
GAM181   LOC254207 3'  GGAGGCAGGGAGGCAGC     94586             GG
                                GCTGCCTCCCTGTTT  CC
                                ||||||||||||||  ||
                                CGACGGAGGGACGGA  GG
                                          __
GAM181   LOC254268 5'  CCAGCTCAGGAGGCAG      95404        C  T_
                                CTGCCTCC TG  TTGG
                                |||||||| ||  ||||
                                GACGGAGG AC  GACC
                                    _  TC
GAM181   LOC254485 5'  GGCTCAGAAAGGTAGCA     95015        CC   TTT
                                TGCTGCCT  CTG   GGCC
                                ||||||||  |||   ||||
                                ACGATGGA  GAC   TCGG
                                    AA  ____
GAM181   LOC254842 5'  TTGGCCGAGAGAGCAGGCAGCA 97598         CCCTG
                                TGCTGCCT    TTTGGCCAA
                                ||||||||    |||||||||
                                ACGACGGA    GAGCCGGTT
                                    CGAGA
GAM181   LOC255520 3'  CTAAAATCTCAGGAGGGCAGCA 95855         TC   _____
                                TGCTGCC  CCTG    TTTGG
                                |||||||  ||||    |||||
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                                ACGACGG  GGAC    AAATC
                                    GA    TCTA
GAM181   LOC255654 5'  GGAGACAGAAGGCAGCA     96888        CC     GG
                                TGCTGCCT  CTGTTT  CC
                                ||||||||  ||||||  ||
                                ACGACGGA  GACAGA  GG
                                    A_     __
GAM181   LOC255671 3'  CCAGCACTTTGGGAGGCAG    97253         T__  _
                                CTGCCTCCC   GT TTGG
                                |||||||||   || ||||
                                GACGGAGGG   CA GACC
                                    TTT  C
GAM181   LOC255671 3'  GCTGCTCGGGAGGCAG      97259         T TT
                                CTGCCTCCC G  TGGC
                                |||||||||  |  ||||
                                GACGGAGGG C  GTCG
                                    _ TC
GAM181   LOC255704 3'  CCAACACAGATGGAGGCAGCA  95281          __   _
                                TGCTGCCTCC  CTGT TTGG
                                ||||||||||  |||| ||||
                                ACGACGGAGG  GACA AACC
                                    TA    C
GAM181   LOC256880 5'  GAACAGGGAAGCCAGCA     97094       _ C
                                TGCTG C TCCCTGTTT
                                |||||  |  |||||||||
                                ACGAC G AGGGACAAG
                                   C A
GAM181   LOC257465 3'  GTCAAATGAGGCAACA      81598     C     CCT
                                TG TGCCTC   GTTTGGC
                                ||  ||||||   |||||||
                                AC ACGGAG   TAAACTG
                                 A     ____
GAM181   LOC57795  3'  TGGCACAGGGAGGCTACA    69324     CT        TTG
                                TG  GCCTCCCTGT   GCCA
                                ||  ||||||||||   ||||
                                AC  CGGAGGGACA   CGGT
                                 AT         ____
GAM181   LOC58525  3'  CCAGCAGGGGCAGCA       78643        TC     T
                                TGCTGCC  CCTGTT GG
                                |||||||  ||||||  ||
                                ACGACGG  GGACGA CC
                                    __     _
GAM181   LOC90233  3'  GCCAGGCGTGGCAGCA      56383        TCCC
                                TGCTGCC    TGTTTGGC
                                |||||||    ||||||||
                                ACGACGG    GCGGACCG
                                    T____
GAM181   LOC90462  3'  CCAGCAGAGGGCAGCA      62902        CC     T
                                TGCTGCCT  CTGTT GG
                                ||||||||  |||||  ||
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                                ACGACGGG  GACGA CC
                                    A_    _
GAM181  LOC90906  5' CTAAGAGGGCAGGCAGCA    64296        _   G
                                TGCTGCCT CCCT TTTGG
                                |||||||| |||| |||||
                                ACGACGGA GGGA GAATC
                                    C   _
GAM181  LOC90906  5' TAAACAGGGATGCAGCA     64312       C
                                TGCTGC TCCCTGTTTG
                                |||||| ||||||||||
                                ACGACG AGGGACAAAT
                                   T
GAM181  LOC91040  3' CCAGGCAGGACGACAGCA    64712      CCTC
                                TGCTG   CCTGTTTGG
                                |||||   |||||||||
                                ACGAC   GGACGGACC
                                  AGCA
GAM181  LOC91300  5' GGCTTCCAGGCGGAAACAGCA  57070      CC  _ GTTT
                                TGCTG  TCC CT   GGCC
                                |||||  ||| ||   ||||
                                ACGAC  AGG GG   TCGG
                                  AA   C  ACCT
GAM181  LOC91300  5' GGCTTCCAGGCGGAAACAGCA  94597      CC  _ GTTT
                                TGCTG  TCC CT   GGCC
                                |||||  ||| ||   ||||
                                ACGAC  AGG GG   TCGG
                                  AA   C  ACCT
GAM181  LOC91547  3' CCAGCACTTTGGGAGGCAG   66401        T__ _
                                CTGCCTCCC   GT TTGG
                                |||||||||   || ||||
                                GACGGAGGG   CA GACC
                                     TTT  C
GAM181  LOC91960  3' CTAAAAGGAAGCCAGCA     67659      C  C   G
                                TGCTG CT CCT TTTGG
                                ||||| || ||| |||||
                                ACGAC GA GGA AAATC
                                  C  A  _
GAM181  LOC91974  3' TCAGAGTAAGGAAGGTAGCA  67761        C   G__
                                TGCTGCCT CCT   TTTGG
                                |||||||| |||   |||||
                                ACGATGGA GGA   AGACT
                                    A   ATG
GAM181  LOC91974  5' TGGTTGAAGGAGAGCAGCA   67763      _   CTG  TG
                                TGCTGC CTCC   TT  GCCA
                                |||||| ||||   ||  ||||
                                ACGACG GAGG   AA  TGGT
                                  A   ____  GT
GAM181  LOC92305  3' AGCAGGTGAAGGCAGCA     56410        _ _
                                TGCTGCCT C CCTGTT
                                |||||||| | ||||||
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                                ACGACGGA G GGACGA
                                    A T
GAM181  LOC92497  5'  GCCTGCACAGAGGCAGCA    69533        CC   TT
                                TGCTGCCTC  TGT  GGC
                                |||||||||  |||  |||
                                ACGACGGAG  ACG  CCG
                                     AC   T_
GAM181  LOC93613  5'  CAGGCAGAGAAGGCAGCA    72697        _ C
                                TGCTGCCT C CTGTTTG
                                |||||||| | |||||||
                                ACGACGGA G GACGGAC
                                    A A
GAM181  LOC96597  3'  CCAGCAACAAGGCAGCA     66908        CCC    T
                                TGCTGCCT   TGTT GG
                                ||||||||   |||| ||
                                ACGACGGA   ACGA CC
                                    ACA   _
GAM181  LOC96597  5'  GGTCAGAGAGGCAGC       66917        CCTG
                                GCTGCCTC    TTTGGCC
                                ||||||||    |||||||
                                CGACGGAG    AGACTGG
                                     _____
GAM182  ADH1B     3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM182  AHR       3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM182  FDFT1     3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                     _
GAM182  JTB       3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                ||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM182  KLF4      3'  TCCCAGACAGTGGATATG     14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||  ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM182  PHYH      3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
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                                TAAAGTGAAA TGACA
                                      A
GAM182  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM182  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM182  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_   CG_
GAM182  CG012   5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM182  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                      G  TC
GAM182  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM182  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                      C__
GAM182  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                   A       CT
GAM182  KLHL6   3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                   _  G
GAM182  NIR3    3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
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                                TAA GTGAAAGTGACG
                                  C
GAM182  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM182  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM182  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__    TT
GAM182  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                      A     TC
GAM182  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941          CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                      AAAGG
GAM182  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647       ACTTTCA
                                TTTC       CTGTCTGAGAT
                                ||||       ||||||||||||
                                AAAG       GACAGACTCTA
                                  GTTTGCC
GAM182  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT      GT TGAGAT
                                |||||||      || ||||||
                                AAAGTGA      CA ACTCTA
                                     TTTCC_  A
GAM182  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM182  LOC222134 5'  ACAGTGAAGTGAAATG       94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM183  BAZ2A    3'  GCAGAGAGCTGAGGCAT     25604          AC_
                                ATGCCTCAGC   CTGC
                                ||||||||||   ||||
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                                TACGGAGTCG  GACG
                                      AGA
GAM183  BUB1B   5'  GCAGCAGGACGAGGACCTGA  6855    AATG  AGCA
                                TCA   CCTC   CCTGCTGC
                                |||   ||||   ||||||||
                                AGT   GGAG   GGACGACG
                                  CCA_   CA__
GAM183  CASQ1   3'  GCTGGGTGCTGAGACACTGA  6931    AA  C      _
                                TCA  TG CTCAGCACCT GC
                                |||  || ||||||||||  ||
                                AGT  AC GAGTCGTGGG CG
                                  C_ A        T
GAM183  COL5A3  3'  GCATTTGGTGCTGAGGCTTTGA 31694     T       TGC
                                TCAAA GCCTCAGCACC  TGC
                                ||||| ||||||||||  |||
                                AGTTT CGGAGTCGTGG  ACG
                                  _         TTT
GAM183  FBN2    3'  CAGCCAGTCTGCAGAAGCATTT 8845       C  A  C_  _
            GA                    TCAAATGC TC GCA  CTG CTG
                                |||||||| || |||  ||| |||
                                AGTTTACG AG CGT  GAC GAC
                                     A  A   CT   C
GAM183  GPR44   3'  CAGCAGGTGCTGAGCA     16525    C
                                TGC TCAGCACCTGCTG
                                ||| ||||||||||||
                                ACG AGTCGTGGACGAC
                                _
GAM183  GPR91   3'  GCAACAAGTTGTCTGCATTTGA 52332       CT_   ACC_
                                TCAAATGC   CAGC   TGC
                                ||||||||   ||||   |||
                                AGTTTACG   GTTG   ACG
                                     TCT   AACA
GAM183  GUCY1A3 5'  GCAGCAGGGTAAGAGACA   63489   C  A_  A
                                TG CTC  GC CCTGCTGC
                                || |||  || ||||||||
                                AC GAG  TG GGACGACG
                                 A  AA  _
GAM183  GYPC    3'  CAGCAGGTGCCAGAGC     33652   _  CA
                                GC CT  GCACCTGCTG
                                || ||  ||||||||||
                                CG GA  CGTGGACGAC
                                 A  C_
GAM183  GYPC    3'  CAGCAGGTGCCAGAGC     9162    _  CA
                                GC CT  GCACCTGCTG
                                || ||  ||||||||||
                                CG GA  CGTGGACGAC
                                 A  C_
GAM183  LIPA    3'  CAGCAGGTGCATAGTCA    4080    C  CA
                                TG CT  GCACCTGCTG
                                || ||  ||||||||||
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                                AC GA  CGTGGACGAC
                                 T  TA
GAM183  NAB2     5'  GCAGCAGGCGCCGAGCGC    19915    _  A  A
                                GC CTC GC CCTGCTGC
                                || ||| || ||||||||
                                CG GAG CG GGACGACG
                                 C  C  C
GAM183  PDHA1    5'  GCGTCTGCTGGGGCACCTGA  4294      AA        CC
                                TCA  TGCCTCAGCA  TGC
                                |||  ||||||||||  |||
                                AGT  ACGGGGTCGT  GCG
                                  CC         CT
GAM183  PLCG1    3'  GCAGCAGGTGCTGTGCGCCTTG 10621     A_   CT
                                CAA  TGC  CAGCACCTGCTGC
                                |||  |||  |||||||||||||
                                GTT  GCG  GTCGTGGACGACG
                                  CC   T_
GAM183  SCAMP1   3'  CAACAGGTGCTAGTTTTGA   53404      TGC  C       C
                                TCAAA   CT AGCACCTG TG
                                |||||   || ||||||| ||
                                AGTTT   GA TCGTGGAC AC
                                   T__  _       A
GAM183  SERPINA4 3'  CAGCAGGTGCTGGC       20610     TC
                                GCC  AGCACCTGCTG
                                |||  ||||||||||
                                CGG  TCGTGGACGAC
                                   __
GAM183  SLC9A6   3'  GCAACGAGCTGATGGCATTTGA 21005         _    ACC_
                                TCAAATGCC TCAGC    TGC
                                ||||||||| |||||    |||
                                AGTTTACGG AGTCG    ACG
                                     T     AGCA
GAM183  SORBS1   3'  GCAAAACTGAGGCACCTGA   31155     AA       CACC
                                TCA  TGCCTCAG    TGC
                                |||  ||||||||    |||
                                AGT  ACGGAGTC    ACG
                                  CC       AAA_
GAM183  TRIM9    3'  GCTGGTGCCAAAGCATTCTGA  53759     _    CTCA    T
                                TCA AATGC    GCACC GC
                                ||| |||||    ||||| ||
                                AGT TTACG    CGTGG CG
                                  C    AAAC    T
GAM183  WISP2    3'  GCAGCAGGTGCTGGGC      13934     T
                                GCC CAGCACCTGCTGC
                                ||| ||||||||||||
                                CGG GTCGTGGACGACG
                                   _
GAM183  C11orf16 3'  CAGCAGGAAGGCACCTG     40217     AA    CAGCA
                                CA  TGCCT    CCTGCTG
                                ||  |||||    |||||||
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                                GT  ACGGA    GGACGAC
                                 CC    A____
GAM183  C17orf31  3'  CAGCCCAGCCTGAGGCATT   34118         CACCT
                                AATGCCTCAG    GCTG
                                ||||||||||    ||||
                                TTACGGAGTC    CGAC
                                     CGACC
GAM183  DKFZp434N2435 5'  GCAGCAGCGGCAGAAGTATTTG 96339        C  A  AC
           A                     TCAAATGC TC GC  CTGCTGC
                                ||||||||  || ||  |||||||
                                AGTTTATG AG CG  GACGACG
                                     A  A  GC
GAM183  FLJ10120  3'  GCAGCAGGAAGTAAAGGCATCT 35831    A     CA  A_
           G                     CA ATGCCT  GC  CCTGCTGC
                                || ||||||  ||  ||||||||
                                GT TACGGA  TG  GGACGACG
                                 C     AA  AA
GAM183  FLJ11252  3'  GCAACAGGTGCTAGAG      67608     _      C
                                CTC AGCACCTG TGC
                                ||| |||||||| |||
                                GAG TCGTGGAC ACG
                                  A       A
GAM183  FLJ20485  3'  AGCAGGAGTATTTGA       38763        CTCAGCA
                                TCAAATGC      CCTGCT
                                ||||||||      ||||||
                                AGTTTATG      GGACGA
                                     A_______
GAM183  FLJ22127  3'  CAGCAGGTGCTGCCAT      42882     CCT
                                ATG   CAGCACCTGCTG
                                |||   ||||||||||||
                                TAC   GTCGTGGACGAC
                                  C__
GAM183  FLJ31952  5'  CAGCAGGCGGTGGGCATT    58382        CA  A_
                                AATGCCT  GC  CCTGCTG
                                |||||||  ||  |||||||
                                TTACGGG  TG  GGACGAC
                                     __  GC
GAM183  KIAA0350  3'  CAGCAGGTGAACATTT      61168      CCTCAG
                                AAATG     CACCTGCTG
                                |||||     |||||||||
                                TTTAC     GTGGACGAC
                                   AA____
GAM183  KIAA0779  5'  GCAGCAGGCGCTGTAGT     85727    CT    A
                                GC  CAGC CCTGCTGC
                                ||  |||| ||||||||
                                TG  GTCG GGACGACG
                                 AT    C
GAM183  KIAA1046  3'  GCAGCAGGATGCTGGCATCTG  29997    A    TC    _
                                CA ATGCC  AGCA CCTGCTGC
                                || |||||  |||| ||||||||
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                                GT TACGG  TCGT GGACGACG
                                 C    __   A
GAM183  KIAA1706 3'  GCAGCAGGGTTAGCATT    92787      CTC  A
                                AATGC  AGC CCTGCTGC
                                ||||||  ||| ||||||||
                                TTACG  TTG GGACGACG
                                  A__  _
GAM183  MGC10854 3'  CAAGGGATGCTGAGGCTTCTGA 50203    AAT       _  GC
                                TCA  GCCTCAGCA CCT  TG
                                |||  ||||||||| |||  ||
                                AGT  CGGAGTCGT GGG  AC
                                  CTT       A  A_
GAM183  MGC15631 3'  GCAGCAGGAGGGGGCCCTGA  51265    AAT    AGCA
                                TCA  GCCTC   CCTGCTGC
                                |||  |||||   ||||||||
                                AGT  CGGGG   GGACGACG
                                  CC_    GA__
GAM183  MGC2752  5'  GCAACAAGTGCTGAGATCAGCG 78448    _____      C  C
                                TGC   CTCAGCAC TG TGC
                                |||   |||||||| || |||
                                GCG   GAGTCGTG AC ACG
                                  ACTA       A  A
GAM183  MGC2752  5'  GCGATTACTGAGGCATCTGG  78449    A       CACC
                                TCA ATGCCTCAG   TGC
                                ||| |||||||||   |||
                                GGT TACGGAGTC   GCG
                                  C        ATTA
GAM183  MSTP032  5'  GCAGAACTAACTGAGGCATTT  47441          CACCTG
                                AAATGCCTCAG     CTGC
                                ||||||||||     ||||
                                TTTACGGAGTC     GACG
                                      AATCAA
GAM183  OIP5     3'  CAACAGGTGCTGCTTAGTCAT  62783    C ___       C
                                ATG CT   CAGCACCTG TG
                                ||| ||   |||||||| ||
                                TAC GA   GTCGTGGAC AC
                                  T  TTC       A
GAM183  PNMA5    3'  CAGCAGGGACATTTGA     73594       CCTCAGCA
                                TCAAATG       CCTGCTG
                                |||||||       |||||||
                                AGTTTAC       GGACGAC
                                   AG_______
GAM183  PPP1R15A 5'  GCTTGTCGCCACGGCACTTGA  59895    A   TCA  _  CT
                                TCAA TGCC   GC AC  GC
                                ||||  ||||   ||  ||  ||
                                AGTT ACGG   CG TG  CG
                                  C    CAC  C  TT
GAM183  QKI      3'  GCAGCGAGCTGAGGCACTTG  65443    A       ACC
                                CAA TGCCTCAGC   TGCTGC
                                |||  |||||||||   ||||||
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                                GTT ACGGAGTCG   GCGACG
                                  C       A__
GAM183  LOC128402 3'  GCTTTGCTGAGGCCCTGA    75783     AAT       CCT
                                TCA   GCCTCAGCA   GC
                                |||   |||||||||   ||
                                AGT   CGGAGTCGT   CG
                                  CC_       TT_
GAM183  LOC147172 3'  GCAGCAGGAAGCAAAGGCATTG 78296     A    CA  A_
          A                      TCAA TGCCT  GC  CCTGCTGC
                                |||| |||||  ||  ||||||||
                                AGTT ACGGA  CG  GGACGACG
                                  _    AA  AA
GAM183  LOC148166 5'  GCAGGACGCTGAGGCTCTGA   78691     AAT       A_
                                TCA   GCCTCAGC  CCTGC
                                |||   ||||||||  |||||
                                AGT   CGGAGTCG  GGACG
                                  CT_       CA
GAM183  LOC149570 3'  GCAGTGGCGCTGAGGCCCTGA  84501     AAT       A  T
                                TCA   GCCTCAGC CC GCTGC
                                |||   |||||||| || |||||
                                AGT   CGGAGTCG GG TGACG
                                  CC_       C  _
GAM183  LOC155006 5'  GCAGCAGGCACTCGGCA     81238      TC  CA
                                TGCC  AG  CCTGCTGC
                                ||||  ||  ||||||||
                                ACGG  TC  GGACGACG
                                  C_  AC
GAM183  LOC155438 3'  CAGCAGGTGTCCTTGCGTCTGA 86392     A    CTCA
                                TCA ATGC    GCACCTGCTG
                                ||| ||||    ||||||||||
                                AGT TGCG    TGTGGACGAC
                                  C    TTCC
GAM183  LOC219541 5'  GCGGTGCCTGAGGCAT      91568          _    T
                                ATGCCTCAG CACC GC
                                ||||||||| |||| ||
                                TACGGAGTC GTGG CG
                                      C    _
GAM183  LOC253039 3'  GTATAACTGAAGCATTTGA    96160         C    CACC
                                TCAAATGC TCAG    TGC
                                ||||||| ||||    |||
                                AGTTTACG AGTC    ATG
                                     A    AAT_
GAM183  LOC51125  5'  GCAGCAGGCGCCGGTGTCCGGA 32249    AA_    TCA  A
                                TC   ATGCC   GC CCTGCTGC
                                ||   |||||   || ||||||||
                                AG   TGTGG   CG GGACGACG
                                  GCC    C__  C
GAM184  ARHGEF6   3'  CAAACTTGAAGCCAGGC     68197       ACCA
                                GCCTGG    CAAGTTTG
                                ||||||    ||||||||
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                                CGGACC   GTTCAAAC
                                   GAA_
GAM184  CNTN2    3'  GTCACAACCCAGGTGA     17411       ACCACAA  _
                                TCGCCTGG     GTT TGAC
                                ||||||||     ||| ||||
                                AGTGGACC     CAA ACTG
                                   ________  C
GAM184  CORO2A   3'  AAACTGTGGTCCAGAGA    53398   GC       A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_       _
GAM184  CORO2A   3'  AAACTGTGGTCCAGAGA    12642   GC       A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_       _
GAM184  GRLF1    3'  AGGTCAGAAAGTGGCCCAGG  78551     A   AAG
                                CCTGG CCAC   TTTGACCT
                                ||||| ||||   ||||||||
                                GGACC GGTG   AGACTGGA
                                   C   AA_
GAM184  LAPTM5   3'  AGGCTTGTGGTCAAGC     22199   CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCGGA
                                 AA_
GAM184  POU2AF1  3'  AGATTTACAGTCCAGGC     20647       CAC
                                GCCTGGAC   AAGTTT
                                ||||||||   ||||||
                                CGGACCTG   TTTAGA
                                     ACA
GAM184  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  54574       C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM184  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  6355        C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM184  TRIM34   5'  AGGTCAAGTTGAGCCCAG    55224     ACCA   G
                                CTGG    CAA TTTGACCT
                                ||||    ||| ||||||||
                                GACC    GTT GAACTGGA
                                  CGA_   _
GAM184  TRIM9    5'  AGGCCAGGCAAGTCCAGGC   30749       CACAA    A
                                GCCTGGAC    GTTTG CCT
                                ||||||||    ||||| |||
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                                CGGACCTG    CGGAC GGA
                                    AA___    C
GAM184  ABLIM    5'  GATATGTAACCCAGGCGG    22030        ACC   A
                                TCGCCTGG   ACA GTT
                                ||||||||   ||| |||
                                GGCGGACC   TGT TAG
                                    CAA   A
GAM184  AMOT     3'  AGGCATCTTCATGGTCCAGGGA 55716    G       C_   TT  A
                                TC CCTGGACCA  AAG  TG CCT
                                || |||||||||  |||  || |||
                                AG GGACCTGGT  TTC  AC GGA
                                 _       AC   T_ _
GAM184  DKFZp434D177 5'  TTAGACCCAGGCGA       50056        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                ________
GAM184  DKFZp434D177 5'  TTAGACCCAGGCGA       79443        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                ________
GAM184  FLJ23420  3'  CAAGTGGGTCCAGGC       46845         A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                    _ __
GAM184  HSA249128 5'  GGCGCGGTCCAGGCGG      34152          ACAA
                                TCGCCTGGACC    GTT
                                ||||||||||    |||
                                GGCGGACCTGG    CGG
                                      CG__
GAM184  MGC15668  5'  AGACCCGGTGGTCCAGACG    51277    C       AA_
                                CG CTGGACCAC   GTTT
                                || |||||||||   ||||
                                GC GACCTGGTG   CAGA
                                 A        GCC
GAM184  MGC22014  3'  AGGTCCCGAGTGTAACCCAGGT 64486        ACC   AGTTT
          GA                     TCGCCTGG   ACA    GACCT
                                ||||||||   |||    |||||
                                AGTGGACC   TGT    CTGGA
                                    CAA   GAGCC
GAM184  SDCCAG10  5'  AGAGTTGTGGTCCAAAGA    19641    GCC        G
                                TC   TGGACCACAA TTT
                                ||   |||||||||| |||
                                AG   ACCTGGTGTT AGA
                                 AA_         G
GAM184  LOC115442 3'  AGGTCAGGGATGGTCCAG    72676        CAAG
                                CTGGACCA    TTTGACCT
                                ||||||||    ||||||||
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                                GACCTGGT   GGACTGGA
                                    AG__
GAM184  LOC129011 5'  AGACCTGCGGTCCAGGC    74862        A  A
                                GCCTGGACC CA GTTT
                                ||||||||| || ||||
                                CGGACCTGG GT CAGA
                                    C  C
GAM184  LOC130536 5'  GCAAAGTCCAGGCG       75746        CACAAG   A
                                CGCCTGGAC    TTTG C
                                |||||||||    |||| |
                                GCGGACCTG    AAAC G
                                    _______  C
GAM184  LOC149108 3'  AGACTTCACTGTGGTCCA    84357        ____
                                TGGACCACA   AGTTT
                                |||||||||   |||||
                                ACCTGGTGT   TCAGA
                                    CACT
GAM184  LOC221688 5'  AGACTCGGGCCCAGACGA    93674    C   A  ACA
                                TCG CTGG CC   AGTTT
                                ||| |||| ||   |||||
                                AGC GACC GG   TCAGA
                                  A   C  GC_
GAM184  LOC256228 5'  AGACTTGTGGTCAAAGC     96233    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCAGA
                                 AAA
GAM184  LOC257441 5'  TTAGACCCAGGCGA        95566        ACCACAA
                                TCGCCTGG     GTTTGA
                                ||||||||     ||||||
                                AGCGGACC     CAGATT
                                    ________
GAM184  LOC91960  3'  AGGTGCCTCTCGTGGTCCAAGC 67657    C       A  TTTG
                                GC TGGACCAC AG    ACCT
                                || |||||||| ||    ||||
                                CG ACCTGGTG TC    TGGA
                                 A       C  TCCG
GAM184  LOC92840  3'  GTCCCTCGGGTCCAGGC     56435        ACA  TTT
                                GCCTGGACC   AG   GAC
                                |||||||||   ||   |||
                                CGGACCTGG   TC   CTG
                                    GC_  C__
GAM185  C8orf13   5'  GACCCAACTGTGCCACCCA    81573    ACATT  TA
                                TGG    GC  AGTTGGGTC
                                |||    ||  |||||||||
                                ACC    CG  TCAACCCAG
                                  CAC__  TG
GAM185  CHST3     3'  GACACAGCAGCGTCCAATG    14974        A    AA
                                CATTGGAC TTGCT  GTT
                                |||||||| |||||  |||
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                                GTAACCTG GACGA  CAG
                                     C    CA
GAM185  FLJ11175  3'  GACTTTGGACAGCAGCACCCAA 37135      ACA    AAGTT
            T                    ATTGG   TTGCT    GGGTC
                                 |||||   |||||    |||||
                                 TAACC   GACGA    TTCAG
                                   CAC    CAGGT
GAM185  KIAA0022  3'  AACTACAATGTCCAATG    29657          CTA
                                 CATTGGACATTG   AGTT
                                 ||||||||||||   ||||
                                 GTAACCTGTAAC   TCAA
                                       A__
GAM185  STIP-1   3'  ACCCAACTCACAGCCCTATG   69661    T  ACATT   A__
                                 CAT GG    GCT   AGTTGGGT
                                 ||| ||    |||   ||||||||
                                 GTA CC    CGA   TCAACCCA
                                   T _____  CAC
GAM186  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                 ATTT ACTTT   TGTCTGAG
                                 |||| |||||   ||||||||
                                 TAAA TGAAA   ACAGATTC
                                   A    T__
GAM186  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                 CATTT   TTT AC GTCTGAGAT
                                 |||||   ||| || |||||||||
                                 GTAAA   AAA TG TAGACTCTA
                                    TA_   T  _
GAM186  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                 CATTTCACTTTC CTG
                                 ||||||||||||| |||
                                 GTAAAGTGAAAG GAT
                                       _
GAM186  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                     CATTTCACTTTCACTGTCTGAGAT
                                 ||||||||||||||||||||||||
                                 GTAAAGTGAAAGTGACAGACTCTA

GAM186  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                 CA  TTCACTGTCTG GA
                                 ||  ||||||||||| ||
                                 GT  AGGTGACAGAC CT
                                  AT         C
GAM186  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                 ATTTCACTTT ACTGT
                                 |||||||||| |||||
                                 TAAAGTGAAA TGACA
                                       A
GAM186  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                 TTTCACTTTCA   TCTG GA
                                 ||||||||||   |||| ||
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                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM186  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM186  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017        CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM186  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM186  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM186  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM186  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM186  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM186  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM186  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM186  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
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                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM186  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM186  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__    TT
GAM186  SEP15     3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                      A     TC
GAM186  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                      AAAGG
GAM186  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM186  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM186  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM186  LOC222134 5'  ACAGTGAAGTGAAATG       94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                      _
GAM187  APXL      3'  TAGGACTTTCTCTTCTA      7932      A       C
                                TA AGGAGAAAG CCTG
                                || |||||||| ||||
                                AT TTCTCTTTC GGAT
                                 C        A
GAM187  CFL1      5'  TCGGTGCCCTCTCCTTT      18574         AA  C
                                AAAGGAGA  GC CTGA
                                ||||||||  || ||||
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                                TTTCCTCT  CG GGCT
                                     CC  T
GAM187  CORO2B   3'  GGGCCTTTCCTTTATG      64576          AA
                                CATAAAGGAGA  GCCC
                                ||||||||||  ||||
                                GTATTTCCTTT  CGGG
                                      C_
GAM187  DGCR2    3'  TCACTGTCTTCTCCTTTAT    17632          AG CC
                                ATAAAGGAGAA  C  TGA
                                ||||||||||  |  |||
                                TATTTCCTCTT  G  ACT
                                      CT TC
GAM187  DNAI2    3'  AGGGTTTCTCCTCCATG     43523     AA      G
                                CAT  AGGAGAAA CCCT
                                |||  |||||||| ||||
                                GTA  TCCTCTTT GGGA
                                  CC       _
GAM187  HS2ST1   3'  CAGGTGCTTCTCCTTTATG   24333          A  _
                                CATAAAGGAGAA GC CCTG
                                |||||||||||| || ||||
                                GTATTTCCTCTT CG GGAC
                                      _  T
GAM187  IFI16    5'  CAAGGCCTTTTTTCCTT     71222         __  C
                                AAGGAGAAA  GCC TG
                                |||||||||  ||| ||
                                TTCCTTTTT  CGG AC
                                     TC   A
GAM187  IL1B     3'  TCAGCTCTCTCCTTTCA     5139    T      A   CC
                                A AAAGGAGA AGC  TGA
                                | ||||||||| |||  |||
                                A TTTCCTCT TCG  ACT
                                 C       C  __
GAM187  OGDH     3'  TCTTTCTTTCTCCTTTA     91109          CCCT
                                TAAAGGAGAAAG   GA
                                ||||||||||||   ||
                                ATTTCCTCTTTC   CT
                                      TTT_
GAM187  OTOF     3'  GTTGGGGCTCTTCCTCTA    16645    A    AA    TG
                                TA AGGAG  AGCCC  AT
                                || |||||  |||||  ||
                                AT TCCTT  TCGGG  TG
                                 C    C_    GT
GAM187  PTPRG    5'  CGATCGGCTCTCTCCTTT    11110        A   CT
                                AAAGGAGA AGCC  GATCG
                                |||||||| ||||  |||||
                                TTTCCTCT TCGG  CTAGC
                                     C   __
GAM187  SYNGR1   3'  CGTGGCACCCTCCTTTATG   16314         AAA  C
                                CATAAAGGAG   GCC TG
                                ||||||||||   ||| ||
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                                GTATTTCCTC  CGG GC
                                     CCA  T
GAM187  VIL2    3'  TCGTGCACTGCTTTCTCCTT  12601        CC  AT
                                AAGGAGAAAGC  TG  CGA
                                ||||||||||  ||  |||
                                TTCCTCTTTCG  AC  GCT
                                     TC  GT
GAM187  ABCA6   5'  TGATTACTTTCTCCTT     54413        CCC
                                AAGGAGAAAG   TGATCG
                                |||||||||   ||||||
                                TTCCTCTTTC   ATTAGT
                                     ___
GAM187  C20orf26 3'  CAGGGTCTCCCCTTTATG    70174       A  AA
                                CATAAAGG GA  GCCCTG
                                ||||||||  ||  ||||||
                                GTATTTCC CT  TGGGAC
                                     C  C_
GAM187  CIP29   3'  TCAGGAGGGAGCCCTCTCCTTT 50409        AA  _____
           AT                    ATAAAGGAGA  GC    CCTGA
                                ||||||||||  ||    |||||
                                TATTTCCTCT  CG    GGACT
                                     CC  AGGGA
GAM187  CYorf15B 3'  TCATTGCCTTCTCCTTTCA   50818   T      A  CC
                                A AAAGGAGAA GC  TGA
                                | |||||||||  ||  |||
                                A TTTCCTCTT CG  ACT
                                 C       C  TT
GAM187  DKFZp434C0328 3'  GGCTTCCTTCTTTATG     34134         A
                                CATAAAGGAG AAGCC
                                ||||||||||  |||||
                                GTATTTCTTC TTCGG
                                     C
GAM187  FLJ11539 3'  CGCTCGCTTTCTCCT      45375         CCT  T
                                AGGAGAAAGC   GA CG
                                ||||||||||   || ||
                                TCCTCTTTCG   CT GC
                                     ___  C
GAM187  FLJ12707 3'  AGAGCTCTCTCTTTATG    41946       G  A  C
                                CATAAAG AGA AGC CT
                                |||||||  |||  |||  ||
                                GTATTTC TCT TCG GA
                                    _  C  A
GAM187  FLJ22615 3'  CAGGGGGACCCTCTCCTTTCTG 68516    T      AAG___
                                CA AAAGGAGA     CCCTG
                                ||  ||||||||     |||||
                                GT TTTCCTCT     GGGAC
                                 C       CCCAGG
GAM187  GGA2    3'  CAGGCTTTCTCCCCTAT    30460     AA        C
                                ATA  GGAGAAAGCC TG
                                |||  ||||||||||  ||
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                                TAT  CCTCTTTCGG AC
                                  CC        _
GAM187  GGA2     3'  CAGGCTTTCTCCCCTAT     56874     AA        C
                                ATA  GGAGAAAGCC TG
                                |||  |||||||||| ||
                                TAT  CCTCTTTCGG AC
                                  CC        _
GAM187  HCRTR2   5'  CGGACGTAGCTTTCTCCT    7730          CC  A
                                AGGAGAAAGC  TG TCG
                                ||||||||||  || |||
                                TCCTCTTTCG  GC GGC
                                      AT  A
GAM187  HRI      3'  CGGTACTTCCTCCTTTAT    26983         A   CC
                                ATAAAGGAG AAG  CTG
                                ||||||||| |||  |||
                                TATTTCCTC TTC  GGC
                                      C   AT
GAM187  KIAA1055 3'  CAGGTGACTCTCTCCTTTTA  66058   T      A  C__
                                A AAAGGAGA AG   CCTG
                                | ||||||||  ||   ||||
                                A TTTCCTCT TC   GGAC
                                 T       C  AGT
GAM187  KIAA1069 3'  TCAACTTGCTTCTCCTTTA   67940         A  CC__
                                TAAAGGAGAA GC    TGA
                                |||||||||| ||    |||
                                ATTTCCTCTT CG    ACT
                                      _  TTCA
GAM187  MGC10646 3'  TCTGGTAACTCCTCCTTTAT  51109         AAA__   CT
                                ATAAAGGAG    GCC  GA
                                |||||||||    |||  ||
                                TATTTCCTC    TGG  CT
                                      CTCAA   T_
GAM187  MGC20460 5'  CGACCGGCTTCTGCTTCATG  53846     A   G    A   CTGA
                                CAT AAG AGAA GCC    TCG
                                ||| ||| |||| |||    |||
                                GTA TTC TCTT CGG    AGC
                                  C   G    _   CC__
GAM187  MGC23445 3'  TCGACGGTCTTTGCTCCTTTA  58154         _    C  T A
                                TAAAGGAG AAAG CC G TCGA
                                |||||||| |||| || | ||||
                                ATTTCCTC TTTC GG C AGCT
                                     G    T  _ _
GAM187  MGC2488  3'  GGAGTTTCTCCTTTATG     43874           GC
                                CATAAAGGAGAAA  CC
                                ||||||||||||  ||
                                GTATTTCCTCTTT  GG
                                       GA
GAM187  MGC3123  3'  GGTCTTTCTCCTTTATG     44098           C
                                CATAAAGGAGAAAG CC
                                ||||||||||||| ||
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                                GTATTTCCTCTTTC GG
                                         T
GAM187  NCKX3    3'  GGGGCCTTCCCCTTTTA     40352   T    A   A
                                A AAAGG GAA GCCCT
                                | ||||| ||| |||||
                                A TTTCC CTT CGGGG
                                 T    C   C
GAM187  NET-2    5'  TGGGGCTTCTCCCTTA      24706    A     A
                                TAA GGAGAA GCCCTG
                                ||| |||||| ||||||
                                ATT CCTCTT CGGGGT
                                  C     _
GAM187  ROBO4    3'  CACTGCTTTCTCCTCTGTG   38791     A        CC
                                CATA AGGAGAAAGC  TG
                                |||| ||||||||||  ||
                                GTGT TCCTCTTTCG  AC
                                   C         TC
GAM187  TTTY9    3'  CAGGGCTCCTCCTTTA      49184         AA
                                TAAAGGAG  AGCCCTG
                                ||||||||  |||||||
                                ATTTCCTC  TCGGGAC
                                     C_
GAM187  YAP1     3'  TCGATTATCTGCTCTCTCTTTT 20358          A   CC_
             AT                   ATAAAGGAGA AGC   TGATCGA
                                ||||||||||| |||   |||||||
                                TATTTTCTCT TCG   ATTAGCT
                                      C   TCT
GAM187  LOC124512 5'  TCTGGGCTTTCCCCTTCTTG   74303    TA   A      T
                                CA  AAGG GAAAGCCC GA
                                ||  |||| |||||||| ||
                                GT  TTCC CTTTCGGG CT
                                 TC    C       T
GAM187  LOC128272 3'  TGGGGCCCTCTCCTTT      74731         AA
                                AAAGGAGA  GCCCTG
                                ||||||||  ||||||
                                TTTCCTCT  CGGGGT
                                     CC
GAM187  LOC130074 3'  CAGGACTTTCTTCTTAATG    76128     A        C
                                CAT AAGGAGAAAG CCTG
                                ||| |||||||||| ||||
                                GTA TTCTTCTTTC GGAC
                                  A         A
GAM187  LOC132321 3'  CGATCATTTTTTCCTCTAT    75058     A       CCC
                                ATA AGGAGAAAG   TGATCG
                                ||| |||||||||   ||||||
                                TAT TCCTTTTTT   ACTAGC
                                  C        ____
GAM187  LOC136337 3'  TCAATCAGGGCAAGATCTTC   76210       AA__       C
                                GGAGA    GCCCTGAT GA
                                |||||    |||||||| ||
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                                CTTCT   CGGGACTA CT
                                  AGAA      A
GAM187  LOC146138 3'  TCAGTTTCTCCTTTAT     83617          GCC
                                ATAAAGGAGAAA  CTGA
                                ||||||||||||  ||||
                                TATTTCCTCTTT  GACT
                                    ____
GAM187  LOC148479 3'  GGGGCTTCCCCTTCATG     78874    A   A  A
                                CAT AAGG GAA GCCCT
                                ||| |||| ||| |||||
                                GTA TTCC CTT CGGGG
                                  C   C  _
GAM187  LOC151438 5'  TCGATCAGGTGGTCCCT     85370    A  AA  C
                                AGG GA  GCC TGATCGA
                                ||| ||  ||| |||||||
                                TCC CT  TGG ACTAGCT
                                  _  GG  _
GAM187  LOC151446 5'  TCGAGGACTTTCTCCT      85379        C  TGA
                                AGGAGAAAG CC   TCGA
                                |||||||||  ||   ||||
                                TCCTCTTTC GG   AGCT
                                     A  ____
GAM187  LOC158696 3'  TCAGTTAAAACTCTTTCCTTTA 81976         A  CC_____
          T                      ATAAAGGAGA AG     CTGA
                                ||||||||||  ||     ||||
                                TATTTCCTTT TC     GACT
                                     C  AAAATT
GAM187  LOC201456 3'  CAGCCTTTCTCCTCTA     88244    A       CC
                                TA AGGAGAAAG  CTG
                                ||  |||||||||  |||
                                AT TCCTCTTTC  GAC
                                 C        C_
GAM187  LOC221468 3'  TCGGCTGCTTCCTCCTTTAT  59292        A   C_
                                ATAAAGGAG AAGC  CTGA
                                |||||||||  ||||  ||||
                                TATTTCCTC TTCG  GGCT
                                     C    TC
GAM187  LOC222166 3'  CGAAAACCTCTCTCCTTTAT  94095         A  CCCTGA
                                ATAAAGGAGA AG     TCG
                                |||||||||  ||     |||
                                TATTTCCTCT TC     AGC
                                     C  CAAA__
GAM187  LOC257309 3'  AGGGTTTCTCCTCCATG     94636    AA      G
                                CAT  AGGAGAAA CCCT
                                |||  ||||||||  ||||
                                GTA  TCCTCTTT GGGA
                                  CC       _
GAM187  LOC91813  5'  CATGGATCTCTCCTTTATG   67247          AAG  C
                                CATAAAGGAGA   CC TG
                                ||||||||||   || ||
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                                GTATTTCCTCT  GG AC
                                     CTA  T
GAM187  LOC93097  5' CGAGCTCTCTCCCCTTTGTG  71360      __    A  CCTGA
                                CATAAA  GGAGA AGC    TCG
                                ||||||  ||||| |||    |||
                                GTGTTT  CCTCT TCG    AGC
                                   CC    C  _____
GAM188  ABCA1    3' AGTCTTATTTTTCTAGTCA   18545         TCCTTCA
                                TGACTAGAAAA     GCT
                                ||||||||||      |||
                                ACTGATCTTTT     TGA
                                     TATTC__
GAM188  AKAP2    3' CTGAGGATTTCTAGCCA    23260    A     A   T
                                TG CTAGAAA TCCT CAG
                                || ||||||| |||| |||
                                AC GATCTTT AGGA GTC
                                 C      _   _
GAM188  EGFL6    3' TTAGCTGGGTCTTTCATAGCCA 31325    A  _   AT  TT
                                TG CTA GAAA  CC  CAGCTAA
                                || ||| ||||  ||  |||||||
                                AC GAT CTTT  GG  GTCGATT
                                 C  A   CT  __
GAM188  ERBB2IP  3' AGTTTTTAATTTTTTAGTCA  37983          CCTTC
                                TGACTAGAAAAT    AGCT
                                ||||||||||||    ||||
                                ACTGATTTTTTA    TTGA
                                     ATTT_
GAM188  GRB10    3' TGAAGAATTTTCTAGCA    17986    A       C
                                TG CTAGAAAAT CTTCA
                                || |||||||| |||||
                                AC GATCTTTTA GAAGT
                                 _       A
GAM188  LMO7     3' TAGTTTGACTTTCTAGTTA   18091         A  CTTC
                                TGACTAGAAA TC   AGCTA
                                |||||||||| ||   |||||
                                ATTGATCTTT AG   TTGAT
                                     C  T___
GAM188  LMO7     3' TAGTTTGACTTTCTAGTTA   31767         A  CTTC
                                TGACTAGAAA TC   AGCTA
                                |||||||||| ||   |||||
                                ATTGATCTTT AG   TTGAT
                                     C  T___
GAM188  LRAT     3' GATTTGTTTTCTAGTCA    60105          CCT
                                TGACTAGAAAAT  TC
                                ||||||||||||  ||
                                ACTGATCTTTTG  AG
                                     TTT
GAM188  NUMB     3' TAGCTTGTTTTCTGTCA    13626     T     CCTTC
                                TGAC AGAAAAT    AGCTA
                                |||| |||||||    |||||
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                                ACTG TCTTTTG     TCGAT
                                  _      T_____
GAM188  PAICS     3'  TTTAGCTGAAGGAAAATCAAGC 21265     A  A  AAA
              A                    TG CT GA   TCCTTCAGCTAAA
                                   || || ||   ||||||||||||
                                   AC GA CT   AGGAAGTCGATTT
                                    _ A  AAA
GAM188  TOX       3'  AGCTGGTTCTAGTCA       28288          AATCCT
                                   TGACTAGAA     TCAGCT
                                   |||||||||     ||||||
                                   ACTGATCTT     GGTCGA
                                             _______
GAM188  USH3A     3'  TTTAGCTGAAATGGTCCAGTAC 53786    _   A  AA  CC
              A                    TG ACT GA  AT  TTCAGCTAAA
                                   || ||| ||  ||  ||||||||||
                                   AC TGA CT  TA  AAGTCGATTT
                                    A   C  GG  __
GAM188  ZNF36     3'  CTTAAGGATCCTTCTAGTCA   93963          A_     C
                                   TGACTAGAA  ATCCTT AG
                                   |||||||||  ||||||  ||
                                   ACTGATCTT  TAGGAA TC
                                         CC      T
GAM188  C20orf45  3'  TTAGTGTGATAAACTTCTAGTC 32108          AATCCT   _
              A                    TGACTAGAA     TCA GCTAA
                                   |||||||||     |||  |||||
                                   ACTGATCTT     AGT TGATT
                                         CAAAT_   G
GAM188  C8orf13   3'  TAGCTGAATGTAGTCA      81578        GAAAATCC
                                   TGACTA       TTCAGCTA
                                   ||||||       ||||||||
                                   ACTGAT       AAGTCGAT
                                      GT_______
GAM188  DCNP1     3'  AGCTAGGGCCCTCTGGTCA    55619         AAAT    C
                                   TGACTAGA    CCTT AGCT
                                   ||||||||    ||||  ||||
                                   ACTGGTCT    GGGA TCGA
                                        CCC_    _
GAM188  EVI5      3'  AGCTGAAGAATTTCTTCA     18989      CT    ATC
                                   TGA  AGAAA   CTTCAGCT
                                   |||  |||||   ||||||||
                                   ACT  TCTTT   GAAGTCGA
                                     __     AA_
GAM188  GTPBP1    3'  AGCTGTTTCTAGTTA       15012          ATCCTT
                                   TGACTAGAAA     CAGCT
                                   ||||||||||     |||||
                                   ATTGATCTTT     GTCGA
                                             _______
GAM188  HSA243666 3'  AGGACTACTTTTCTAGTCA    34144           _____
                                   TGACTAGAAAA    TCCT
                                   ||||||||||    ||||
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                                ACTGATCTTTT   AGGA
                                      CATC
GAM188  KIAA1364  3'  TTAGCCTCATCTTCTAGTCA  63600        A  CCTTCA
                                TGACTAGAA AT    GCTAA
                                ||||||||| ||    |||||
                                ACTGATCTT TA    CGATT
                                     C  CTC___
GAM188  MGC11352  5'  TAGCTGGGCTACTTTCTA   64806      ATCC
                                TAGAAA   TTCAGCTA
                                ||||||   ||||||||
                                ATCTTT   GGGTCGAT
                                   CATC
GAM188  PGR1      3'  AGCCAATGGATTCTGGTCA   52755       AA   TTCA
                                TGACTAGA  ATCC   GCT
                                ||||||||  ||||   |||
                                ACTGGTCT  TAGG   CGA
                                     __   TAAC
GAM188  SNX11     3'  TAGTGTCTTCTAGTCA     25275        A  CCTTCA
                                TGACTAGAA AT    GCTA
                                ||||||||| ||    ||||
                                ACTGATCTT TG    TGAT
                                     C  _______
GAM188  TMSNB     5'  GGCTATCTTCTAGTCA     41812        A  CCTTC
                                TGACTAGAA AT    AGCT
                                ||||||||| ||    ||||
                                ACTGATCTT TA    TCGG
                                     C  ______
GAM188  LOC149134 5'  AGAGATTTTCTAGCCA     84360    A       _
                                TG CTAGAAAATC CT
                                || ||||||||||  ||
                                AC GATCTTTTAG GA
                                  C        A
GAM188  LOC149175 3'  AGCTGAGGTTGTAGCCA     79206    A   G  AATC
                                TG CTA AA    CTTCAGCT
                                || ||| ||    ||||||||
                                AC GAT TT    GGAGTCGA
                                  C   G  _____
GAM188  LOC149722 5'  TAGCTGAAGTCACTTATCA   84607     CT  AAAATC
                                TGA  AG     CTTCAGCTA
                                |||  ||     |||||||||
                                ACT  TC     GAAGTCGAT
                                  AT  ACT___
GAM188  LOC150279 3'  AGCTGTTTAATTTCTAGTCA  79662         ATCCTT
                                TGACTAGAAA     CAGCT
                                ||||||||||     |||||
                                ACTGATCTTT     GTCGA
                                     AATTT_
GAM188  LOC220370 3'  GGAGGATTTTCCAGCCA     92829    A  A
                                TG CT GAAAATCCTTC
                                || || ||||||||||
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                                AC GA CTTTTAGGAGG
                                 C  C
GAM188  LOC255481 3'  AGCTGGGGGCTCCTAGCA    94438    A    AAAAT
                                TG CTAG    CCTTCAGCT
                                || ||||    |||||||||
                                AC GATC    GGGGGTCGA
                                 _   CTC__
GAM188  LOC257444 3'  TTAACTGAAGGAAAATCT    81114     AAA       C
                                AGA   TCCTTCAG TAA
                                |||   |||||||| |||
                                TCT   AGGAAGTC ATT
                                  AAA       A
GAM189  ADRA1A   3'  GCACAAATCCAACATG      52784      AAGCC  A
                                CATGT    TG ATTTGTGC
                                |||||    || ||||||||
                                GTACA    AC TAAACACG
                                  _____  C
GAM189  AEGL1    5'  GCACAAATACACTACAT     6679       AGCC  A
                                ATGTA    TG ATTTGTGC
                                |||||    || ||||||||
                                TACAT    AC TAAACACG
                                  C___  A
GAM189  CDH2     3'  GCACAAATGTTTTACAT     8377        CCTGA
                                ATGTAAG    ATTTGTGC
                                |||||||    ||||||||
                                TACATTT    TAAACACG
                                   TG___
GAM189  CHRNE    3'  GCCCTCAGGCCCACAGGT    3586     A   AA     ATTTGT
                                ACC TGT  GCCTGA     GC
                                ||| |||  ||||||     ||
                                TGG ACA  CGGACT     CG
                                 _  CC     CC_____
GAM189  COL4A3   3'  GGCCATGGCTCACATGGT    3622        A   TGAATT  T
                                ACCATGT AGCC     TG GCC
                                ||||||| ||||     || |||
                                TGGTACA TCGG     AC CGG
                                   C    T_____  _
GAM189  COL4A3   3'  GGCCATGGCTCACATGGT    48557       A   TGAATT  T
                                ACCATGT AGCC     TG GCC
                                ||||||| ||||     || |||
                                TGGTACA TCGG     AC CGG
                                   C    T_____  _
GAM189  COL4A3   3'  GGCCATGGCTCACATGGT    48568       A   TGAATT  T
                                ACCATGT AGCC     TG GCC
                                ||||||| ||||     || |||
                                TGGTACA TCGG     AC CGG
                                   C    T_____  _
GAM189  CYP3A4   3'  ACAAGCCTGGCCTACATGGT   33923        A   TGAA
                                ACCATGTA GCC    TTTGT
                                |||||||| |||    |||||
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                                TGGTACAT CGG    GAACA
                                    C   TCC_
GAM189  HIVEP3   5'  GGCACAAACCCAGCAGCCTCA  44439    TAA __   AA
                                TG   GC  CTG  TTTGTGCC
                                ||   ||  |||  ||||||||
                                AC   CG  GAC  AAACACGG
                                 TC_  AC   CC
GAM189  RECK     3'  GCAACAGGCTCACTGGT     40869      T  A     AAT
                                ACCA GT AGCCTG   TTGT
                                |||| || ||||||   ||||
                                TGGT CA TCGGAC   AACG
                                  _ C     ___
GAM189  TNFSF8   3'  GCACAAATTTAATACA      6966       AGCC
                                TGTA    TGAATTTGTGC
                                ||||    ||||||||||
                                ACAT    ATTTAAACACG
                                  A___
GAM189  ADAR3    3'  CACAAATTCAGAACGTG     38018       AAGC
                                CATGT    CTGAATTTGTG
                                |||||    ||||||||||
                                GTGCA    GACTTAAACAC
                                   A___
GAM189  BIVM     3'  CACAAATTCACTTA        34667      CC
                                TAAG  TGAATTTGTG
                                ||||  ||||||||||
                                ATTC  ACTTAAACAC
                                   __
GAM189  C20orf160 3'  GCAGTTACAGGATTACATGGT  54648          G    AAT
                                ACCATGTAA CCTG   TTGT
                                ||||||||| ||||   ||||
                                TGGTACATT GGAC   GACG
                                     A    ATT
GAM189  EPHA7    3'  CACAAATTTGCTGCACA     15433     A_   CT
                                TGT  AGC  GAATTTGTG
                                |||  |||  |||||||||
                                ACA  TCG  TTTAAACAC
                                  CG  __
GAM189  FLJ12783  3'  AGTTCAGGCTCACTG       48675     T  A
                                CA GT AGCCTGAATT
                                || || ||||||||||
                                GT CA TCGGACTTGA
                                 _ C
GAM189  HSC3     3'  CACAGGTTCAGACTACA      59067      A C
                                TGTA G CTGAATTTGTG
                                |||| | ||||||||||
                                ACAT C GACTTGGACAC
                                  _ A
GAM189  KIAA0316  3'  GCACAAATGCTCTTCACAGTGG 69674      _   _   CCTGA
             T                   ACCA TGT AAG     ATTTGTGC
                                ||||  ||| |||     ||||||||
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                                TGGT ACA TTC     TAAACACG
                                  G   C   TCG__
GAM189  KIAA0453  3'  GCACAAGTAGCTACATAGT   69047    C     A  CTGA
                                AC ATGTA GC    ATTTGTGC
                                || ||||| ||    ||||||||
                                TG TACAT CG    TGAACACG
                                 A     _  A___
GAM189  KIAA1423  3'  AATTCAAGTTTACATG      61719         C
                                CATGTAAGC TGAATT
                                ||||||||| ||||||
                                GTACATTTG ACTTAA
                                      A
GAM189  KIAA1691  3'  GCACAAATGCTGTCCATGG   92556      TA_   CTGA
                                CCATG   AGC    ATTTGTGC
                                |||||   |||    ||||||||
                                GGTAC   TCG    TAAACACG
                                   CTG   _____
GAM189  PPP1R3B   3'  GCCAGGTTCAGATTACA     44820      GC        T
                                TGTAA  CTGAATTTG GC
                                |||||  ||||||||| ||
                                ACATT  GACTTGGAC CG
                                   A_        _
GAM189  SFXN2     3'  GCAGCAGAGTTACATGGT    73946        GC   AATTTG
                                ACCATGTAA  CTG     TGC
                                |||||||||  |||     |||
                                TGGTACATT  GAC     ACG
                                     GA   G_____
GAM189  TBC1D2    5'  TAAATTCAGACCTACTGGT   37321     T   AGC
                                ACCA GTA   CTGAATTTG
                                ||||| |||   |||||||||
                                TGGT CAT   GACTTAAAT
                                  _   CCA
GAM189  ZNF347    3'  GGCTTTATTCAGGCCTCACA  50848     AA_      TTGT
                                TGT   GCCTGAAT    GCC
                                |||   ||||||||    |||
                                ACA   CGGACTTA    CGG
                                  CTC       TTT_
GAM189  LOC134147 3'  CACAAATTCAGTAGGACGT   57158     AAGC
                                ATGT    CTGAATTTGTG
                                ||||    ||||||||||
                                TGCA    GACTTAAACAC
                                  GGAT
GAM189  LOC151195 5'  GCACAAATTTATTTACA     80169       CC
                                TGTAAG  TGAATTTGTGC
                                ||||||  ||||||||||
                                ACATTT  ATTTAAACACG
                                        __
GAM189  LOC152860 3'  AATTCCAGCTTACATGG     80695         CT
                                CCATGTAAGC  GAATT
                                ||||||||||  |||||
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                                GGTACATTCG  CTTAA
                                      AC
GAM189  LOC200382 3'  ACAGGGGCCAGACTTACATG   88801        C   AA_
                                CATGTAAG CTG   TTTGT
                                |||||||| |||   |||||
                                GTACATTC GAC   GGACA
                                     A   CGG
GAM189  LOC93622  3'  ACAGTCATTCCAGGCTTAGATG 56929     G      _  __
                                CAT TAAGCCTG AAT  TTGT
                                ||| |||||||| |||  ||||
                                GTA ATTCGGAC TTA  GACA
                                  G       C   CT
GAM190  GM2A     3'  GTCACAACCTCTGATC      67782         TC  GTTCT
                                GATCAGAG  TG     TGAC
                                ||||||||  ||     ||||
                                CTAGTCTC  AC     ACTG
                                     CA  _____
GAM190  SLC35A2  3'  GGGACCAAACTCTGATC     18980         C
                                GATCAGAGT TGGTTCT
                                ||||||||| |||||||
                                CTAGTCTCA ACCAGGG
                                      A
GAM190  ASB16    3'  CATGCCAAGAACCAGTGATT   55104       GAGT        A
                                GATCA    CTGGTTCTTG CATG
                                |||||    |||||||||| ||||
                                TTAGT    GACCAAGAAC GTAC
                                   ____         C
GAM190  DDM36    3'  TCAAGAGTTAACTCTG      40577        C GG
                                CAGAGT T  TTCTTGA
                                |||||| |  |||||||
                                GTCTCA A  GAGAACT
                                   _ TT
GAM190  FLJ11181  5'  AACTCAAACTCTGATC      37136         C  _
                                GATCAGAGT TG GTT
                                ||||||||| || |||
                                CTAGTCTCA AC CAA
                                      A  T
GAM190  PDE8A    3'  GAGAACCGGACCCTAATC     62635     C  A
                                GAT AG GTCTGGTTCTT
                                ||| || ||||||||||
                                CTA TC CAGGCCAAGAG
                                  A  C
GAM190  PRDM14   3'  AGAACCAGACCCTGTC      44442     T   A
                                GA CAG GTCTGGTTCT
                                || ||| ||||||||||
                                CT GTC CAGACCAAGA
                                 _  C
GAM190  LOC143425 3'  CATGCCAAGAACCAAGATCGGA 87633     AGA   _       A
                                TC   GTCT GGTTCTTG CATG
                                ||   |||| |||||||| ||||
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                                AG   TAGA CCAAGAAC GTAC
                                 GC_    A       C
GAM190  LOC221893 3'  TGTTGGGAACCAAACTCTGTC  92493    T     C      TG
                                GA CAGAGT TGGTTCT  ACA
                                || |||||| |||||||  |||
                                CT GTCTCA ACCAAGG  TGT
                                 _      A       GT
GAM190  LOC253805 3'  AGGAACCAAACTCTGGTC    96425          C
                                GATCAGAGT TGGTTCTT
                                ||||||||| ||||||||
                                CTGGTCTCA ACCAAGGA
                                      A
GAM191  ADAMTS8   5'  TCGGGCCGCCAGCACCTG    22886     _      ATAAG
                                CAG TGCTGGC    CTGA
                                ||| |||||||    ||||
                                GTC ACGACCG    GGCT
                                  C      CCG__
GAM191  BAP1      3'  TCAGGGACCCAGCACTGG    16219          CATAAG
                                CCAGTGCTGG     CTGA
                                ||||||||||     ||||
                                GGTCACGACC     GACT
                                      CAGG__
GAM191  BF        5'  TTCAGCTTGGACACTG      8140       CTGGCA
                                CAGTG     TAAGCTGAA
                                |||||     |||||||||
                                GTCAC     GTTCGACTT
                                   AG____
GAM191  C1QB      3'  TTCAACTCTGTGTCCCAGCACT 4923     A        __    _ C
            GGC                    G CCAGTGCTGG  CATA AG TGAA
                                | ||||||||||  |||| || ||||
                                C GGTCACGACC  GTGT TC ACTT
                                _        CT    C  A
GAM191  CHC1      3'  CAGCCCTGAGCACTGTGTC    7020      _      __ CATAA
                                GAC CAGTGCT  GG     GCTG
                                ||| |||||||  ||     ||||
                                CTG GTCACGA  CC     CGAC
                                  T      GT  _____
GAM191  CMRF35    5'  CAGAGCTGTCAGCACCGG    21929    A        TAAG
                                CC GTGCTGGCA    CTG
                                || |||||||||    |||
                                GG CACGACTGT    GAC
                                 C        CGA_
GAM191  EPHB6     3'  TCAGCCCTGGACACTGGTC    15466         _ TG CATAA
                                GACCAGTG C  G     GCTGA
                                |||||||| |  |     |||||
                                CTGGTCAC G  C     CGACT
                                     A GT C____
GAM191  EVPL      5'  CAGCCTGAGCCAGCACT     8803           A  A
                                AGTGCTGGC TA GCTG
                                ||||||||| || ||||
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                                TCACGACCG GT CGAC
                                     A  C
GAM191  GARP     3'  CAGCCCAGCACTGG       18594          CATAA
                                CCAGTGCTGG    GCTG
                                ||||||||||    ||||
                                GGTCACGACC    CGAC
                                      _____
GAM191  GJB5     3'  CAGCTCGACGGCACTGG     17945         GCATA
                                CCAGTGCTG    AGCTG
                                |||||||||    |||||
                                GGTCACGGC    TCGAC
                                     AGC__
GAM191  GPR81    3'  CTTACCAGCATTAGTC      50757     C       CA
                                GAC AGTGCTGG  TAAG
                                ||| ||||||||  ||||
                                CTG TTACGACC  ATTC
                                  A       __
GAM191  IFI16    5'  AGCAAGCCAGCACTAGTC    71221     C       ATAA
                                GAC AGTGCTGGC    GCT
                                ||| |||||||||    |||
                                CTG TCACGACCG    CGA
                                  A        AA__
GAM191  KRT4     3'  CAGCTGGGCCCAGCACTGGT   9635           _ ATA
                                ACCAGTGCTGG C   AGCTG
                                ||||||||||| |   |||||
                                TGGTCACGACC G   TCGAC
                                      C GG_
GAM191  MAP3K9   3'  TTCAGCTTCCCAAACACCAGT  60709    CA   C_   CAT
                                AC  GTG  TGG   AAGCTGAA
                                ||  |||  |||   ||||||||
                                TG  CAC  ACC   TTCGACTT
                                 AC   AA   C__
GAM191  MGAT5    5'  TCAGCTTACAGTTCCTG     10028     T_   GCA
                                CAG  GCTG   TAAGCTGA
                                |||  ||||   ||||||||
                                GTC  TGAC   ATTCGACT
                                  CT   ____
GAM191  MOCS1    3'  TTCAGCTTAACAGTTGCCCGGT 92037      A_   _   GCA
           C                     GACC  GTG CTG   TAAGCTGAA
                                ||||  ||| |||   |||||||||
                                CTGG  CGT GAC   ATTCGACTT
                                  CC   T   A__
GAM191  P23      3'  TCAGCTTATACCCGGGCT    21719     G    C_
                                AGT CTGG  ATAAGCTGA
                                ||| ||||  |||||||||
                                TCG GGCC  TATTCGACT
                                  _    CA
GAM191  PFKFB4   3'  TCAGCCACATGCAACACTGTGT 15874     _    CTG    AA_
           C                     GAC CAGTG   GCAT   GCTGA
                                ||| |||||   ||||   |||||
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                                CTG GTCAC   CGTA   CGACT
                                  T    AA_    CAC
GAM191  PTPRK    3'  TTCAGCCTGTGGCCCAGCACTG 11125          __    A
                GTC                   GACCAGTGCTGG  CATA GCTGAA
                                |||||||||||  |||| ||||||
                                CTGGTCACGACC  GTGT CGACTT
                                      CG    C
GAM191  RNPEPL1  3'  CGGATGCCAGCACCTG      36676    _       AAG
                                CAG TGCTGGCAT   CTG
                                ||| |||||||||   |||
                                GTC ACGACCGTA   GGC
                                  C       ___
GAM191  UBE2L3   3'  TCAGCCCTGGCACTGGC     12507    A      TG CATAA
                                G CCAGTGC  G    GCTGA
                                | |||||||  |    |||||
                                C GGTCACG  C    CGACT
                                _      GT C____
GAM191  APXL2    5'  CAGCCTCAGCACTCATC     75185    CC       CATAA
                                GA  AGTGCTGG    GCTG
                                ||  ||||||||    ||||
                                CT  TCACGACT    CGAC
                                 AC       C____
GAM191  ARHGEF9  3'  TTCAGCTTACCAAGCA      30824     _ CA
                                TGCT GG  TAAGCTGAA
                                |||| ||  |||||||||
                                ACGA CC  ATTCGACTT
                                  A __
GAM191  CEGP1    3'  TTCAGCTTCCTCTAGCCCGG   40589    AGT    CAT
                                CC   GCTGG   AAGCTGAA
                                ||   |||||   ||||||||
                                GG   CGATC   TTCGACTT
                                 CC_    TCC
GAM191  DKFZp547D155 3'  CAGCCCTGAGACCACTGGTC   70435        CTGG  TAA
                                GACCAGTG    CA   GCTG
                                ||||||||    ||   ||||
                                CTGGTCAC    GT   CGAC
                                     CAGA  CC_
GAM191  DKFZP727G051 3'  TTCAGCCCATCAACCAGCATTG 69483           CATAA__
                GTC                   GACCAGTGCTGG      GCTGAA
                                ||||||||||||      ||||||
                                CTGGTTACGACC      CGACTT
                                      AACTACC
GAM191  DUSP14   5'  CACTGTCACCAGCACTGCTC   22834    C       CATA  C
                                GA CAGTGCTGG    AG TG
                                || |||||||||    || ||
                                CT GTCACGACC    TC AC
                                 C       ACTG  _
GAM191  FLJ10206 5'  CAGCTTATGCCAGGAGTC    35898     CAGTG
                                GAC    CTGGCATAAGCTG
                                |||    |||||||||||||
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                                CTG    GACCGTATTCGAC
                                  AG___
GAM191  FLJ20967  5'  GGCGCCCAGCACTGGTT     41962          CATAA
                                GACCAGTGCTGG    GCT
                                ||||||||||||   |||
                                TTGGTCACGACC    CGG
                                      CG___
GAM191  FLJ22569  3'  TTCAGCTTACTAAACTG     43679     GC   CA
                                CAGT  TGG  TAAGCTGAA
                                ||||  |||  |||||||||
                                GTCA  ATC  ATTCGACTT
                                  A_  __
GAM191  FOXN4     3'  TTCAGCTTGGACACACTGG    75574       C  GCA
                                CCAGTG TG   TAAGCTGAA
                                ||||||  ||   |||||||||
                                GGTCAC AC   GTTCGACTT
                                   _  AG_
GAM191  GW112     3'  TTCAACTGAAGCCAGCACTGGT 21194           ATA  C
           T                     GACCAGTGCTGGC   AG TGAA
                                ||||||||||||||   || ||||
                                TTGGTCACGACCG   TC ACTT
                                      AAG  A
GAM191  HOOK2     3'  CAGCTCACATGGCGCCCAGCAC 25256         _____  A__
           TGG                    CCAGTGCTGG    CAT   AGCTG
                                ||||||||||    |||   |||||
                                GGTCACGACC    GTA   TCGAC
                                     CGCG   CAC
GAM191  jdp2      3'  TTCAGCACAGCCAGCAT     55327        ATAA
                                GTGCTGGC    GCTGAA
                                ||||||||    ||||||
                                TACGACCG    CGACTT
                                    ACA_
GAM191  KIAA0767  3'  TCTGCTGCCAGCACAGG     60632    A       TAA  T
                                CC GTGCTGGCA   GC GA
                                || |||||||||   || ||
                                GG CACGACCGT   CG CT
                                 A        ___  T
GAM191  KIAA0923  3'  TCAGCTTGATGCATGGTC    25838      G   TGGCA
                                GACCA TGC    TAAGCTGA
                                |||||  |||    ||||||||
                                CTGGT ACG    GTTCGACT
                                   _   TA___
GAM191  KIAA0982  3'  TTCACTGTTTGCCAGCAC    25852         TA_  C
                                GTGCTGGCA   AG TGAA
                                |||||||||   || ||||
                                CACGACCGT   TC ACTT
                                     TTG  _
GAM191  KIAA1000  3'  TTCAGCTTTGCAAAGTACTGG  65281         G_   T
                                CCAGTGCT  GCA AAGCTGAA
                                ||||||||  |||  ||||||||
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                                GGTCATGA  CGT TTCGACTT
                                    AA  _
GAM191  MAP3K3   3'  TCAGCCTGGGCGCTGGTC    9999         GG  TAA
                                GACCAGTGCT  CA   GCTGA
                                ||||||||||  ||   |||||
                                CTGGTCGCGG  GT   CGACT
                                    __  C__
GAM191  MGC16037 5'  CTTGTCCAGCACTAGTC     51821     C       C
                                GAC AGTGCTGG ATAAG
                                ||| |||||||| |||||
                                CTG TCACGACC TGTTC
                                  A       _
GAM191  MIDORI   3'  TCAGCTTATCCTGCAACT    73792     _  T  C
                                AGT GC GG ATAAGCTGA
                                ||| || || |||||||||
                                TCA CG CC TATTCGACT
                                  A  T  _
GAM191  MtFMT    5'  CAGTGGCGAGCACTGG      57651        G  ATAA
                                CCAGTGCT GC    GCTG
                                |||||||| ||    ||||
                                GGTCACGA CG    TGAC
                                    G  G___
GAM191  PCDH16   5'  TCAGTTCCAACCACTGG     72826       C_  CATA
                                CCAGTG  TGG    AGCTGA
                                ||||||  |||    ||||||
                                GGTCAC  ACC    TTGACT
                                   CA  _____
GAM191  QKI      3'  CAGCTTATCAACTCGTC     65439     C   GCTGGC
                                GAC AGT      ATAAGCTG
                                ||| |||      ||||||||
                                CTG TCA      TATTCGAC
                                  C   AC_____
GAM191  TNRC6    3'  CAACTTTTAGCACTG       70506         CAT   C
                                CAGTGCTGG   AAG TG
                                |||||||||   ||| ||
                                GTCACGATT   TTC AC
                                    ___  A
GAM191  TOB2     3'  CAGCCCAGGCCAGCACTG    95618          ATAA
                                CAGTGCTGGC    GCTG
                                ||||||||||    ||||
                                GTCACGACCG    CGAC
                                     GACC
GAM191  TU12B1-TY 3'  TCAGCCCACAGCACTGTC    33406     C      GCATAA
                                GAC AGTGCTG      GCTGA
                                ||| |||||||      |||||
                                CTG TCACGAC      CGACT
                                  _      ACC____
GAM191  TUSP     3'  TCAGCCTAAGAGCGCAGCACTG 39641         _  A__  A
                                CAGTGCTG GC   TA GCTGA
                                |||||||| ||   || |||||
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                                GTCACGAC CG   AT CGACT
                                    G  AGA  C
GAM191  USP19     3'  TCAGCTTATGCATCTGGT    88959      TGCTG
                                ACCAG    GCATAAGCTGA
                                |||||    ||||||||||
                                TGGTC    CGTATTCGACT
                                  TA___
GAM191  ZD52F10   3'  CAGCCTGTGCCAGCCCTGG   52819     T       A
                                CCAG GCTGGCATA GCTG
                                |||| ||||||||| ||||
                                GGTC CGACCGTGT CGAC
                                  C       C
GAM191  LOC145268 3'  TCAGCTTACAAGAGCCACTG  77062      _ GGCA
                                CAGTG CT    TAAGCTGA
                                ||||| ||    ||||||||
                                GTCAC GA    ATTCGACT
                                  C  GAAC
GAM191  LOC149296 5'  CAGCTTATGGGCAGCA     79256      G_
                                TGCTG  CATAAGCTG
                                |||||  |||||||||
                                ACGAC  GTATTCGAC
                                  GG
GAM191  LOC161877 5'  TCAGGGCAGGCCAGCGCTGG  82326          ATAAG
                                CCAGTGCTGGC    CTGA
                                ||||||||||    ||||
                                GGTCGCGACCG    GACT
                                     GACGG
GAM191  LOC163115 5'  TCAGCCCCTGACAGCACTGG  82413        G  TAA
                                CCAGTGCTG CA   GCTGA
                                |||||||| ||   |||||
                                GGTCACGAC GT   CGACT
                                    A  CCC
GAM191  LOC196500 3'  TCAGCTCACTCAGTGGTC    87744     AGT    CATA
                                GACC   GCTGG   AGCTGA
                                ||||   |||||   ||||||
                                CTGG   TGACT   TCGACT
                                  ___    CAC_
GAM191  LOC197287 3'  TCAGCTCATGTGTTTTGCACTG 60865       T_     __
                                CAGTGC  GGCATA  AGCTGA
                                ||||||  ||||||  ||||||
                                GTCACG  TTGTGT  TCGACT
                                   TT     AC
GAM191  LOC200470 5'  TCAGCCTGCGGCGCTGG     90069        G  TAA
                                CCAGTGCTG CA   GCTGA
                                |||||||| ||   |||||
                                GGTCGCGGC GT   CGACT
                                     _ C__
GAM191  LOC221584 3'  CAGCTTATGTGGCAC       93828       G
                                GTGCTG CATAAGCTG
                                ||||||  |||||||||
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                                CACGGT GTATTCGAC
                                    _
GAM191  LOC51716 3' CAGCTCATGGCCCTAGCA    32787      ___  A
                                TGCTGG  CAT AGCTG
                                ||||||  ||| |||||
                                ACGATC  GTA TCGAC
                                   CCG  C
GAM191  LOC92196 5' CAGAGCACCAGCACTGGC    68456   A       CATAAG
                                G CCAGTGCTGG     CTG
                                | ||||||||||     |||
                                C GGTCACGACC     GAC
                                _       ACGA__
GAM192  APOB48R  3' TGTATCATTCATGGAGCAGGCA 37961         CAGT   _
                                TGCCTGCTCC   ATGG ACA
                                ||||||||||   |||| |||
                                ACGGACGAGG   TACT TGT
                                      TACT   A
GAM192  ARHGEF12 3' CATACTAAATAGCAGGCA    30996       CCC_
                                TGCCTGCT   AGTATG
                                ||||||||   ||||||
                                ACGGACGA   TCATAC
                                     TAAA
GAM192  ARSD     3' ATGTGTCTCCTGAGACAAGCA  23794    C  C  C   TAT
                                TGC TG TC CAG   GGACACAT
                                ||| || || |||   ||||||||
                                ACG AC AG GTC   TCTGTGTA
                                  A  _  A   C__
GAM192  BAK1     3' TGTGTCCCAGGAGCAGG     91995       CAGTAT
                                CCTGCTCC     GGACACA
                                ||||||||     |||||||
                                GGACGAGG     CCTGTGT
                                     AC_____
GAM192  EPHA8    3' GTGAGGGGCTGGCAGCAGGCA  40064       C    ATGGA
                                TGCCTGCT CCAGT    CAC
                                |||||||| |||||    |||
                                ACGGACGA GGTCG    GTG
                                     C    GGGA_
GAM192  ERBB2    3' ATGTGTCCTCAGGGAGCAGG   15472       AGTAT
                                CCTGCTCCC    GGACACAT
                                |||||||||    ||||||||
                                GGACGAGGG    CCTGTGTA
                                      ACT__
GAM192  ITPKB    3' ATGTGATCTGGAAGGCAGGCA  9420       C_   TATGGA
                                TGCCTGCT  CCAG     CACAT
                                ||||||||  ||||     |||||
                                ACGGACGG  GGTC     GTGTA
                                     AA   TA_____
GAM192  KCNA7    3' TGTATCTGGGAGCATGCA    49063     C       TATGG
                                TGC TGCTCCCAG     ACA
                                ||| |||||||||     |||
```

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                                ACG ACGAGGGTC    TGT
                                  T       TA___
GAM192  KIF3B   3'  TGTGTCTGTAAGAGAGACA   16614   _  CCAG
                                TG CTC   TATGGACACA
                                || |||   ||||||||||
                                AC GAG   ATGTCTGTGT
                                 A  AGA_
GAM192  KIF5C   3'  TGACATACTGGGAAAGGCA   15743     GC       GA
                                TGCCT  TCCCAGTATG  CA
                                |||||  |||||||||  ||
                                ACGGA  AGGGTCATAC  GT
                                   A_       A_
GAM192  MAT1A   3'  GTGCTGGGAGAGGCA      90835     G
                                TGCCT CTCCCAGTAT
                                ||||| ||||||||||
                                ACGGA GAGGGTCGTG
                                   _
GAM192  PCSK1   3'  TGTTACCTAGAGCAGGCA   4778        CC  TATG
                                TGCCTGCTC  AG   GACA
                                |||||||||  ||   ||||
                                ACGGACGAG  TC   TTGT
                                     A_  CA__
GAM192  SPINK2  3'  CATTTTCTGAGAGCAGGTA   40877       C   T__
                                TGCCTGCTC CAG   ATG
                                ||||||||| |||   |||
                                ATGGACGAG GTC   TAC
                                     A   TTT
GAM192  SULT1C1 3'  GTTCACCCTGGGAGCAGACA  6469    C       TA
                                TG CTGCTCCCAG  TGGAC
                                || ||||||||||  |||||
                                AC GACGAGGGTC  ACTTG
                                 A        CC
GAM192  TOP3B   5'  ATGTGCCTGCAGGGAGCAGGC  14128         A   T  A
                                GCCTGCTCCC GTA GG CACAT
                                |||||||||| ||| || |||||
                                CGGACGAGGG CGT CC GTGTA
                                     A  _ _
GAM192  CARD11  3'  TGTAATGCTGGGGACAGGCA  50559      CT      GG
                                TGCCTG  CCCAGTAT  ACA
                                ||||||  ||||||||  |||
                                ACGGAC  GGGTCGTA  TGT
                                   AG       A_
GAM192  FBXO29  3'  ATGTGCCTCAGTTGGGAGCAAG 76755    _      TAT_  A
          G                      CCT GCTCCCAG    GG CACAT
                                ||| ||||||||    || |||||
                                GGA CGAGGGTT    CC GTGTA
                                  A       GACT  _
GAM192  GMFB    3'  CCATACTGGAATCAGACA    14666    C   CTC
                                TG CTG   CCAGTATGG
                                || |||   |||||||||
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                                AC GAC   GGTCATACC
                                 A   TAA
GAM192  KIAA1550 3' ATGTGTTTCATTTACAAGCAAG 66541    C   CCCAGT   _
            CA                    TGC TGCT     ATGGA CACAT
                                  ||| ||||     ||||| |||||
                                  ACG ACGA     TACTT GTGTA
                                    A   ACATT_    T
GAM192  KIAA1550 3' ATGTGTTTCATTTACAAGCAAG 66542    C   CCCAGT   _
            CA                    TGC TGCT     ATGGA CACAT
                                  ||| ||||     ||||| |||||
                                  ACG ACGA     TACTT GTGTA
                                    A   ACATT_    T
GAM192  KIAA1550 3' ATGTGTTTCATTTACAAGCAAG 66543    C   CCCAGT   _
            CA                    TGC TGCT     ATGGA CACAT
                                  ||| ||||     ||||| |||||
                                  ACG ACGA     TACTT GTGTA
                                    A   ACATT_    T
GAM192  KIAA1550 3' ATGTGTTTCATTTACAAGCAAG 66544    C   CCCAGT   _
            CA                    TGC TGCT     ATGGA CACAT
                                  ||| ||||     ||||| |||||
                                  ACG ACGA     TACTT GTGTA
                                    A   ACATT_    T
GAM192  KIAA1550 3' ATGTGTTTCATTTACAAGCAAG 66545    C   CCCAGT   _
            CA                    TGC TGCT     ATGGA CACAT
                                  ||| ||||     ||||| |||||
                                  ACG ACGA     TACTT GTGTA
                                    A   ACATT_    T
GAM192  LGP1    5' CGTGCCAGGAGTAGGCA    50651        CA
                                  TGCCTGCTCC  GTATG
                                  ||||||||||  |||||
                                  ACGGATGAGG  CGTGC
                                        AC
GAM192  MGC16291 3' CATGCTGGGAACAGGC     51305      C
                                  GCCTG TCCCAGTATG
                                  ||||| ||||||||||
                                  CGGAC AGGGTCGTAC
                                     A
GAM192  PNAS-131 5' GTGTCCATACTGTTTCCAGC   48750    C  CTCC
                                  GC TG    CAGTATGGACAC
                                  || ||    ||||||||||||
                                  CG AC    GTCATACCTGTG
                                   _  CTTT
GAM192  TBX19    3' TGTATTGGTCAAGGCAGGCA   17653        C___
                                  TGCCTGCT    CCAGTATG
                                  ||||||||    ||||||||
                                  ACGGACGG    GGTTATGT
                                       AACT
GAM192  THEA    3' CATGTTGGGAGCAAGC     66278    C
                                  GC TGCTCCCAGTATG
                                  || ||||||||||||
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                                CG ACGAGGGTTGTAC
                                 A
GAM192  LOC127696 5'  CGTATTGGGACAAGCA     75453     C  C
                                TGC TG TCCCAGTATG
                                ||| || ||||||||||
                                ACG AC AGGGTTATGC
                                  A  _
GAM192  LOC131744 5'  TGTATTGGGAAAAGGCA     75873       GC
                                TGCCT  TCCCAGTATG
                                |||||  ||||||||||
                                ACGGA  AGGGTTATGT
                                   AA
GAM192  LOC146713 3'  TGTGCTGGGAAAGGCA      83736       GC
                                TGCCT  TCCCAGTATG
                                |||||  ||||||||||
                                ACGGA  AGGGTCGTGT
                                   A_
GAM192  LOC149010 5'  TGTATTGGGAAAGACA      79128     C  GC
                                TG CT  TCCCAGTATG
                                || ||  ||||||||||
                                AC GA  AGGGTTATGT
                                 A  A_
GAM192  LOC149276 3'  CATCCTGGGAGCAAGC      84382     C        T
                                GC TGCTCCCAG ATG
                                || ||||||||| |||
                                CG ACGAGGGTC TAC
                                 A        C
GAM192  LOC149566 3'  GTGCCCAGGCAGGCA       84493         CCCAGTA   A
                                TGCCTGCT      TGG CAC
                                ||||||||      ||| |||
                                ACGGACGG      ACC GTG
                                     ________  C
GAM192  LOC164397 5'  CCAGCGGCGAGAGCAGGC    82522         ___  A  A
                                GCCTGCTC   CC GT TGG
                                ||||||||   || || |||
                                CGGACGAG   GG CG ACC
                                     AGC  _  _
GAM192  LOC165140 5'  TCCACTGGGAGCAG        82466           AT
                                CTGCTCCCAGT  GGA
                                ||||||||||  |||
                                GACGAGGGTCA  CCT
                                      __
GAM192  LOC220567 3'  TGTATCATTCATGGAGCAGGCA 90739          CAGT   _
                                TGCCTGCTCC    ATGG ACA
                                ||||||||||    |||| |||
                                ACGGACGAGG    TACT TGT
                                      TACT    A
GAM192  LOC256812 5'  CCATACTGGAAACGGGCA    97547       CTC
                                TGCCTG   CCAGTATGG
                                ||||||   |||||||||
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                                ACGGGC  GGTCATACC
                                   AAA
GAM192  LOC51691  3' ATGTGTTTGCTTGAGAAAAGCA 32479    CTG_  CC   TG
                                TGC   CTC  AGTA  GACACAT
                                |||   |||  ||||  |||||||
                                ACG   GAG  TCGT  TTGTGTA
                                  AAAA  T_   __
GAM192  LOC57862  3' TGCGTATACTGGGAACAGG   41022     C        GA
                                CCTG TCCCAGTATG  CA
                                |||| ||||||||||  ||
                                GGAC AGGGTCATAT  GT
                                  A        GC
GAM192  LOC90148  3' TGTGTTCAAAAGGAGACA    61668    _   CAGTA
                                TG CTCC    TGGACACA
                                || ||||    ||||||||
                                AC GAGG    ACTTGTGT
                                 A   AAA__
GAM192  LOC90826  5' CATGTTGGGAACAGGC      64088      C
                                GCCTG TCCCAGTATG
                                ||||| ||||||||||
                                CGGAC AGGGTTGTAC
                                   A
GAM193  AXL     3'  TCTCACACTCAGTTG       8111       A
                                CAAC TGAGTGTGAGA
                                |||| ||||||||||
                                GTTG ACTCACACTCT
                                  _
GAM193  AXL     3'  TCTCACACTCAGTTG       41608      A
                                CAAC TGAGTGTGAGA
                                |||| ||||||||||
                                GTTG ACTCACACTCT
                                  _
GAM193  MCC     3'  ACTTAGCTCCTGTTGTCATG   9957       GTGTG  A
                                CATGA    AG AGCTAAGT
                                |||||    || ||||||||
                                GTACT    TC TCGATTCA
                                   GTTG_  C
GAM193  MPP5    3'  ACTTAGCTTCCCTTCCCTCATC 42483   C    TGTGA_
          A                      A ATGAG     GAAGCTAAGT
                                | |||||     ||||||||||
                                A TACTC     CTTCGATTCA
                                 C    CCTTCC
GAM193  MS4A7   3'  TTTTCACACTCATATTG     41067     C
                                CAA ATGAGTGTGAGAA
                                ||| ||||||||||||
                                GTT TACTCACACTTTT
                                  A
GAM193  STAU    3'  CTTAGCTTTCACTACACT    33895       A__
                                AGTGTG  GAAGCTAAG
                                ||||||  |||||||||
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                                TCACAT   TTTCGATTC
                                   CAC
GAM193  STAU    3' CTTAGCTTTCACTACACT    33901      A__
                                AGTGTG   GAAGCTAAG
                                ||||||   |||||||||
                                TCACAT   TTTCGATTC
                                   CAC
GAM193  STAU    3' CTTAGCTTTCACTACACT    33908      A__
                                AGTGTG   GAAGCTAAG
                                ||||||   |||||||||
                                TCACAT   TTTCGATTC
                                   CAC
GAM193  STAU    3' CTTAGCTTTCACTACACT    16004      A__
                                AGTGTG   GAAGCTAAG
                                ||||||   |||||||||
                                TCACAT   TTTCGATTC
                                   CAC
GAM193  TZFP    5' ACTTACAAACCACACTCAT   26888        AGAAGC
                                ATGAGTGTG     TAAGT
                                |||||||||     |||||
                                TACTCACAC     ATTCA
                                     CAAAC_
GAM193  VNN2    3' ACTCAGCTTCTGCATCAT    54356     G  G      A
                                ATGA TGT AGAAGCT AGT
                                |||| ||| ||||||| |||
                                TACT ACG TCTTCGA TCA
                                  _  _      C
GAM193  VNN2    3' ACTCAGCTTCTGCATCAT    16237     G  G      A
                                ATGA TGT AGAAGCT AGT
                                |||| ||| ||||||| |||
                                TACT ACG TCTTCGA TCA
                                  _  _      C
GAM193  APXL2   5' AGCCTCAGCACTCAT       75184       _   AA
                                ATGAGTG TGAG  GCT
                                |||||||  ||||  |||
                                TACTCAC ACTC  CGA
                                    G   __
GAM193  FKSG87  3' ACTCAGCCTCCCATTCACATGT 49325     __     T   AA   A
                                ACA  TGAGTG GAG  GCT AGT
                                |||  |||||| |||  ||| |||
                                TGT  ACTTAC CTC  CGA TCA
                                  AC     C   __   C
GAM193  FLJ10359 3' ACTCAGAGTTCACACTCAT   36065          AAG  A
                                ATGAGTGTGAG   CT AGT
                                ||||||||||   || |||
                                TACTCACACTT   GA TCA
                                      GA_  C
GAM193  FLJ12568 3' GGGATCTCACACCCATGTT   46500       A       AG
                                AACATG GTGTGAGA  CT
                                ||||||  ||||||||  ||
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                                TTGTAC CACACTCT  GG
                                   C       AG
GAM193  GHITM    3'  ACTCAGCTTCTGGCTTCTCTG  26913    T  T_  G      A
                                CA GAG  GT AGAAGCT AGT
                                || |||  || ||||||| |||
                                GT CTC  CG TCTTCGA TCA
                                 _   TT  G      C
GAM193  KIAA0092 3'  ACTTAGTTGCCACACTCATG   27966         AGA
                                CATGAGTGTG   AGCTAAGT
                                ||||||||||   ||||||||
                                GTACTCACAC   TTGATTCA
                                      CG_
GAM193  KIAA1817 3'  CTTGGGCTCACACTCA      68229          AAG
                                TGAGTGTGAG   CTAAG
                                ||||||||||   |||||
                                ACTCACACTC   GGTTC
                                      G__
GAM193  KSR      5'  AGCTTCCCCACACTCA      64042         A_
                                TGAGTGTG  GAAGCT
                                ||||||||  ||||||
                                ACTCACAC  CTTCGA
                                     CC
GAM193  MGC5528  3'  ACTTAGCTAATGAACTCAT   44042       GTGAGA
                                ATGAGT     AGCTAAGT
                                ||||||     ||||||||
                                TACTCA     TCGATTCA
                                   AGTAA_
GAM193  PRO2037  3'  AGCTTGAGACCTCATGT     37784        T  GAG
                                ACATGAG GT   AAGCT
                                ||||||| ||   |||||
                                TGTACTC CA   TTCGA
                                    _  GAG
GAM193  SHANK3   3'  ACTCGGTCTCACACTCA     65487          AA  TA
                                TGAGTGTGAG  GC  AGT
                                ||||||||||  ||  |||
                                ACTCACACTC  TG  TCA
                                      __  GC
GAM193  LOC116437 3'  TTTCCACTCATGCTG       73894    A       T
                                CA CATGAGTG GAGA
                                || |||||||| ||||
                                GT GTACTCAC CTTT
                                 C       _
GAM193  LOC146909 3'  ACTCAGCTTCTTGGCATGT    78161       AGTGT       A
                                ACATG     GAGAAGCT AGT
                                |||||     |||||||| |||
                                TGTAC     TTCTTCGA TCA
                                   GG___       C
GAM193  LOC147093 5'  CTCTTCACCTCATGCTG      83943    A     T   GA
                                CA CATGAG GTGA  AG
                                || |||||| ||||  ||
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                                GT GTACTC CACT  TC
                                 C      _    TC
GAM193  LOC154386 3'  AGCTCTCACACTCATTTG    81080     C          A
                                CAA ATGAGTGTGAGA GCT
                                ||| |||||||||||| |||
                                GTT TACTCACACTCT CGA
                                  _          _
GAM193  LOC159121 5'  AGCCACACCATGTCA       86989    A    A    AGAA
                                C ACATG GTGTG    GCT
                                | ||||| |||||    |||
                                A TGTAC CACAC    CGA
                                 C    _    _____
GAM194  DPYSL2    3'  ACACCCAAGACTACCCAC     7289      CAAGAC       A
                                GTG      AGTCTTGG TGT
                                |||      |||||||| |||
                                CAC      TCAGAACC ACA
                                  CCA___       C
GAM194  NR2E1     3'  CAGGACCGCCTGCACTGA     12323         AGACA
                                TCAGTGCA     GTCTTG
                                ||||||||     ||||||
                                AGTCACGT     CAGGAC
                                     CCGC_
GAM194  UCP3      3'  CACCTTTGTTTTGCACTGA    12535             TCTT  A
                                TCAGTGCAAGACAG    GG TG
                                ||||||||||||||    || ||
                                AGTCACGTTTTGTT    CC AC
                                       T___  _
GAM194  CNNM4     3'  CCAGGGATTGTCTTGCAC     39479              _
                                GTGCAAGACAGTCT TGG
                                |||||||||||||| |||
                                CACGTTCTGTTAGG ACC
                                       G
GAM194  DDX8      3'  GACTGTCTTAACTGA       17052       GC
                                TCAGT  AAGACAGTC
                                |||||  |||||||||
                                AGTCA  TTCTGTCAG
                                   A_
GAM194  DKFZP727M111 5'  ACATCACTGCTGTCTTGACT   31403     G       CTTG
                                AGT CAAGACAGT    GATGT
                                ||| |||||||||    |||||
                                TCA GTTCTGTCG    CTACA
                                  _        TCA_
GAM194  EVI5      3'  ACACCCAAATTATACTTGCACT 18985         ACAGTC    A
                                AGTGCAAG     TTGG TGT
                                ||||||||     |||| |||
                                TCACGTTC     AACC ACA
                                     ATATTA    C
GAM194  KIAA0237  3'  GGACTGTCTTTCACTGA     28528       C
                                TCAGTG AAGACAGTCT
                                |||||| ||||||||||
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                                AGTCAC TTCTGTCAGG
                                   T
GAM194  NFX1     3'  CATACTGTCTTGTACTGA    10215            CT
                                TCAGTGCAAGACAGT  TG
                                |||||||||||||||  ||
                                AGTCATGTTCTGTCA  AC
                                       T_
GAM194  SCYA2    5'  CATCCAATTCTCAAACTGA   11446     GCA   CAGTC
                                TCAGT   AGA    TTGGATG
                                |||||   |||    |||||||
                                AGTCA   TCT    AACCTAC
                                   AAC   T____
GAM194  SHARP    3'  CAGAACTGCCTTTGCACT    30395       A_   CT
                                AGTGCAAG  CAGT  TG
                                ||||||||  ||||  ||
                                TCACGTTT  GTCA  AC
                                     CC    AG
GAM194  LOC115273 5'  CATCCAAGACTGGCAC     73358     AAGA
                                GTGC   CAGTCTTGGATG
                                ||||   ||||||||||||
                                CACG   GTCAGAACCTAC
                                  ____
GAM194  LOC149386 5'  ATCTAGACTGTTTCACAC    84403     CA       T
                                GTG  AGACAGTCT GGAT
                                |||  ||||||||| ||||
                                CAC  TTTGTCAGA TCTA
                                  AC       _
GAM194  LOC152627 5'  CTAGACCTCTTGCAC       80628       CA   T
                                GTGCAAGA  GTCT GG
                                ||||||||  |||| ||
                                CACGTTCT  CAGA TC
                                     C_   _
GAM194  LOC63904  3'  ACATCTGCCATCGATCTTGCAC 41975        CAGTCTT_
                                GTGCAAGA       GGATGT
                                ||||||||       ||||||
                                CACGTTCT       TCTACA
                                     AGCTACCG
GAM195  ARSF     5'  GGCCCTTCTGTTACTTTTC   64602        AATGT   A
                                GAAAAGTAA    GAAG GCC
                                |||||||||    |||| |||
                                CTTTTCATT    CTTC CGG
                                     GT___   C
GAM195  CALR     3'  GGCTCTTCTCATTTCAC     62976    A    T
                                GT AAATG GAAGAGCC
                                || ||||| ||||||||
                                CA TTTAC CTTCTCGG
                                 C    T
GAM195  CBFB     3'  GCTCCTTGGTTTTTTACTTCTG 43142      AA      TG G  _
                                TAGA  AGTAAAA  T AAG AGC
                                ||||  |||||||  | ||| |||
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                                GTCT  TCATTTT  G TTC TCG
                                  __      TT G   C
GAM195  CBFB     3'  GCTCCTTGGTTTTTTACTTCTG 8275       AA      TG G  _
                                TAGA  AGTAAAA  T AAG AGC
                                ||||  |||||||  | ||| |||
                                GTCT  TCATTTT  G TTC TCG
                                  __      TT G   C
GAM195  CENPF    3'  CACATTTTATTCTTCTA     32965       A
                                TAGAA AGTAAAATGTG
                                ||||| ||||||||||
                                ATCTT TTATTTTACAC
                                   C
GAM195  DISC1    3'  GCTTTTCACCTTACTTCTC   37884    A     AAT
                                GA AAGTAA   GTGAAGAGC
                                || ||||||   |||||||||
                                CT TTCATT   CACTTTTCG
                                 C     C__
GAM195  DPYS     3'  GCTCTGTGATTTTACTTTTT   7284           GTGA
                                GAAAAGTAAAAT    AGAGC
                                ||||||||||||    |||||
                                TTTTTCATTTTA    TCTCG
                                      GTG_
GAM195  HMGA2    3'  CTGGACATTTAACTTTTCTA   12999         A     GA
                                TAGAAAAGT AAATGT  AG
                                |||||||| ||||||  ||
                                ATCTTTTCA TTTACA  TC
                                     A     GG
GAM195  JMJ      5'  GGCTCTTTTTTTTTCCTT    17133     T    TGT
                                AAG AAAA   GAAGAGCC
                                ||| ||||   ||||||||
                                TTC TTTT   TTTCTCGG
                                  C   TT_
GAM195  MRE11A   3'  GCTACCATTTTACATTTCTA   18788       A       TGAAG
                                TAGAAA GTAAAATG     AGC
                                |||||| ||||||||     |||
                                ATCTTT CATTTTAC     TCG
                                   A       CA___
GAM195  PAX2     3'  GCTCTTCACTGCTCCTC     14325    AA    AAAT
                                GA  AGTA    GTGAAGAGC
                                ||  ||||    |||||||||
                                CT  TCGT    CACTTCTCG
                                 CC   _____
GAM195  PAX2     3'  GCTCTTCACTGCTCCTC     14334    AA    AAAT
                                GA  AGTA    GTGAAGAGC
                                ||  ||||    |||||||||
                                CT  TCGT    CACTTCTCG
                                 CC   _____
GAM195  PPP1R3C  3'  GGCTAGCATCCATACTTTTCTA 18250          AAAT   AAG
                                TAGAAAAGTA    GTG   AGCC
                                ||||||||||    |||   ||||
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                                ATCTTTTCAT   TAC  TCGG
                                     ACC_  GA_
GAM195  SCG3     5'  GGCTCTTCCTGTTTTTACTCCT 25100    AA     TGT_
            C                    GA  AGTAAAA   GAAGAGCC
                                 ||  |||||||   ||||||||
                                 CT  TCATTTT   CTTCTCGG
                                  CC      TGTC
GAM195  SWAP70   3'  CTCTTGGTTTTACTTTTGTA  71347    G        GTG
                                 TA AAAAGTAAAAT  AAGAG
                                 ||  ||||||||||  |||||
                                 AT TTTTCATTTTG  TTCTC
                                  G        G__
GAM195  VASP     3'  GCTCCTTCCCCTTTTCTA    12567        TAAAATGT   _
                                 TAGAAAAG       GAAG AGC
                                 ||||||||       |||| |||
                                 ATCTTTTC       CTTC TCG
                                      CC_______    C
GAM195  A2BP1    5'  GGCTCTCCTTTGTTTATTTTCT 38062        G   ATGTGA
            A                    TAGAAAA TAAA     AGAGCC
                                 |||||||  ||||     ||||||
                                 ATCTTTT ATTT     TCTCGG
                                     _   GTTTCC
GAM195  AF9Q34   3'  CTCTTCACAGATTTTT      50736       GTAAAA
                                 GAAAA     TGTGAAGAG
                                 |||||     |||||||||
                                 TTTTT     ACACTTCTC
                                    AG____
GAM195  APOL4    5'  CTTTCATTTTACCTTTC     47623      A       T
                                 GAAA GTAAAATG GAAG
                                 ||||  |||||||| ||||
                                 CTTT CATTTTAC TTTC
                                    C       _
GAM195  C(27)-3BETA-HSD 3'  GCCCTCCACATTTTCTTTTTCT 47272         T       A  A
                                 AGAAAAG AAAATGTG AG GC
                                 |||||||  |||||||  ||  ||
                                 TCTTTTT TTTTACAC TC CG
                                      C       C  C
GAM195  DCNP1    3'  TCGCATTCCTCTGCTTTTC    55628         A___
                                 GAAAAGTA    AATGTGA
                                 ||||||||    |||||||
                                 CTTTTCGT    TTACGCT
                                      CTCC
GAM195  DJ971N18.2 3'  GGCTCTCCACACTCTTC     40960     A   AAAAT   A
                                 GAA AGT     GTG AGAGCC
                                 |||  |||     |||  ||||||
                                 CTT TCA     CAC TCTCGG
                                   C  _____   C
GAM195  DKFZP434F1735 5'  GGCTCTTCAGCAAACCACTTTT 31500         AAAA  _
            C                    GAAAAGT    TG TGAAGAGCC
                                 |||||||    ||  |||||||||
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                                CTTTTCA    AC ACTTCTCGG
                                    CCAA  G
GAM195  DKFZP434P211 3'  GGTTCCCACACCTCACTTTTC  27267       AAAA    AA
                                GAAAAGT    TGTG  GAGCC
                                |||||||    ||||  |||||
                                CTTTTCA    ACAC  CTTGG
                                    CTCC    C_
GAM195  DKFZp761N1114 3'  GGCTCTTCCAACCTCACTTTTC 79021       AAAA_  T
                                GAAAAGT    TG GAAGAGCC
                                |||||||    || ||||||||
                                CTTTTCA    AC CTTCTCGG
                                    CTCCA  _
GAM195  FLJ10482  3'  CTTCACATCTACTCTTC     36162     A    AA
                                GAA AGTA  ATGTGAAG
                                ||| ||||  ||||||||
                                CTT TCAT  TACACTTC
                                  C    C_
GAM195  FLJ10713  3'  CTCATTCATACTACTTTTCTA  36467         AAA     _
                                TAGAAAAGTA   TGTGAA GAG
                                ||||||||||   |||||| |||
                                ATCTTTTCAT   ATACTT CTC
                                     C__     A
GAM195  FLJ10874  3'  GGCTCTACTTTTCACTTTTT   36781       A   T  GA
                                GAAAAGT AAA GT  AGAGCC
                                ||||||| ||| ||  ||||||
                                TTTTTCA TTT CA  TCTCGG
                                    C   T  __
GAM195  FLJ20694  3'  CTCTTCACCTCCTCTG      35547      AA  TAAAAT
                                TAGA  AG     GTGAAGAG
                                ||||  ||     ||||||||
                                GTCT  TC     CACTTCTC
                                  CC  _______
GAM195  HDAC11    3'  GGCCCTTCCTCTACTTTTC    45719        AAATGT    A
                                GAAAAGTA     GAAG GCC
                                ||||||||     |||| |||
                                CTTTTCAT     CTTC CGG
                                     CTC___    C
GAM195  HT002     3'  GGCTCCACGGCCCCTACTTTTC 25944        AAA__    AA
                                GAAAAGTA    TGTG  GAGCC
                                ||||||||    ||||  |||||
                                CTTTTCAT    GCAC  CTCGG
                                    CCCCG   __
GAM195  KIAA0286  3'  GCTCTTTGGGTCCCACTGTTC  68327     A   AAA  G
                                GAA AGT   AT TGAAGAGC
                                ||| |||   || ||||||||
                                CTT TCA   TG GTTTCTCG
                                  G   CCC  G
GAM195  KIAA0329  3'  CTTCACACTTCCCTTTTCTA   29274        TA  A
                                TAGAAAAG  AA TGTGAAG
                                ||||||||  || |||||||
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                                ATCTTTTC  TT ACACTTC
                                    CC  C
GAM195  KIAA0377 3' GGGTCTTCACTTTTCTG     27796        AAAATGT    G
                                TAGAAAAGT      GAAGA CC
                                |||||||||      ||||| ||
                                GTCTTTTCA      CTTCT GG
                                    ________    G
GAM195  KIAA0721 3' GCCTCACTCCACTTTTCTA   41341        AAAAT   A A
                                TAGAAAAGT    GTGA G GC
                                |||||||||    |||| | ||
                                ATCTTTTCA    CACT C CG
                                    CCT__   _ _
GAM195  KIAA0721 3' GCCTCACTCCACTTTTCTA   95969        AAAAT   A A
                                TAGAAAAGT    GTGA G GC
                                |||||||||    |||| | ||
                                ATCTTTTCA    CACT C CG
                                    CCT__   _ _
GAM195  KIAA0889 3' CTCAAACATTCTACTTTTCTA 31135         A    GAA
                                TAGAAAAGTA AATGT   GAG
                                |||||||||| |||||   |||
                                ATCTTTTCAT TTACA   CTC
                                    C    AA_
GAM195  KIAA1677 3' GCCCTTCACTTATCTTTTCTA 67068        TAAAAT    A
                                TAGAAAAG     GTGAAG GC
                                ||||||||     |||||| ||
                                ATCTTTTC     CACTTC CG
                                    TATT__     C
GAM195  KIAA1678 3' TATATTTTACTTTTCTG     72307
                                TAGAAAAGTAAAATGTG
                                |||||||||||||||||
                                GTCTTTTCATTTTATAT

GAM195  KIAA1742 3' GGCTCTTCATCAGGACACTTCC 77659    AA   AAAA _
          CT                  AG  AAGT    TG TGAAGAGCC
                              ||  ||||    || |||||||||
                              TC  TTCA    AC ACTTCTCGG
                               CC    CAGG  T
GAM195  KIAA1771 3' GGCTTATGACCCTACTTTTCT  79138        AAAT  GAA
                              AGAAAAGTA    GT   GAGCC
                              |||||||||    ||   |||||
                              TCTTTTCAT    CA   TTCGG
                                   CC__  GTA
GAM195  KRTAP4-13 3' CACATTTTACCTCTCTA     52595      AAA
                              TAGA   GTAAAATGTG
                              ||||   ||||||||||
                              ATCT   CATTTTACAC
                                CTC
GAM195  KRTAP4-4  3' CACATTTTACCTCTCTA     50717      AAA
                              TAGA   GTAAAATGTG
                              ||||   ||||||||||
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                                ATCT   CATTTTACAC
                                  CTC
GAM195  LRBA     3'  GGTGTATAATTCTACTTTTCTA 22053          A   GTGAAGA
                                TAGAAAAGTA AAT      GCC
                                |||||||||| |||      |||
                                ATCTTTTCAT TTA      TGG
                                     C   ATATG__
GAM195  LRPPRC   3'  GGCTCTTCGGCACACTT     55709      AAAA  _
                                AAGT    TGT GAAGAGCC
                                ||||    ||| ||||||||
                                TTCA    ACG CTTCTCGG
                                  C___   G
GAM195  MR       5'  GCTCTTAACGTTACTTTTC    48321        AA   G
                                GAAAAGTA  ATGT AAGAGC
                                ||||||||  |||| ||||||
                                CTTTTCAT  TGCA TTCTCG
                                     __   A
GAM195  PRO1853  3'  GCTTGGACATTTTACCCTTC   58571     AA       GAA
                                GAA  GTAAAATGT   GAGC
                                |||  |||||||||   ||||
                                CTT  CATTTTACA   TTCG
                                  CC        GG_
GAM195  PRO1853  3'  GCTTGGACATTTTACCCTTC   37773     AA       GAA
                                GAA  GTAAAATGT   GAGC
                                |||  |||||||||   ||||
                                CTT  CATTTTACA   TTCG
                                  CC        GG_
GAM195  TAF9L    3'  CTCTTCCATGTTTCACATTTCT 32004       A  A      _
           A                     TAGAAA GT AAATGTG AAGAG
                                |||||| || ||||||| |||||
                                ATCTTT CA TTTGTAC TTCTC
                                   A  C      C
GAM195  TPD52L1  3'  GCTCTTCATGACTGTCT     12363     AA   AAAA
                                AGA  AGT    TGTGAAGAGC
                                |||  |||    ||||||||||
                                TCT  TCA    GTACTTCTCG
                                  G_  _____
GAM195  TRIM22   3'  CTCTTCACATTGTCTTT     20287      TAA
                                AAAG   AATGTGAAGAG
                                ||||   ||||||||||
                                TTTC   TTACACTTCTC
                                  TG_
GAM195  TUSP     3'  GCCTCATCATTCCACTTTTC   39636        AA   _  A A
                                GAAAAGT  AATG TGA G GC
                                |||||||  |||| ||| | ||
                                CTTTTCA  TTAC ACT C CG
                                    CC    T  _ _
GAM195  LOC129852 3'  GGCCCTCACATTTACTTTTCTG 74899           A    A A
                                TAGAAAAGTAAA TGTGA G GCC
                                |||||||||||| ||||| | |||
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                                GTCTTTTCATTT ACACT C CGG
                                      _    _ C
GAM195  LOC145368 3'  TCACATTTTTCTTCCCTA    77096    AA  T
                                TAG  AAG AAAATGTGA
                                |||  ||| |||||||||
                                ATC  TTC TTTTACACT
                                  CC   T
GAM195  LOC150174 3'  GGTTCCCACACCTCACTTTTC  79610      AAAA   AA
                                GAAAAGT   TGTG  GAGCC
                                |||||||   ||||  |||||
                                CTTTTCA   ACAC  CTTGG
                                    CTCC   C_
GAM195  LOC150213 3'  GGTTCCCACACCTCACTTTTC  74858      AAAA   AA
                                GAAAAGT   TGTG  GAGCC
                                |||||||   ||||  |||||
                                CTTTTCA   ACAC  CTTGG
                                    CTCC   C_
GAM195  LOC150236 5'  GGTTCCCACACCTCACTTTTC  79688      AAAA   AA
                                GAAAAGT   TGTG  GAGCC
                                |||||||   ||||  |||||
                                CTTTTCA   ACAC  CTTGG
                                    CTCC   C_
GAM195  LOC150423 3'  TCACATTTTTCTTCCCTA    79867    AA  T
                                TAG  AAG AAAATGTGA
                                |||  ||| |||||||||
                                ATC  TTC TTTTACACT
                                  CC   T
GAM195  LOC151242 5'  GCTCTTCACATCTCTGACT   80178    AAA__
                                AGT    ATGTGAAGAGC
                                |||    ||||||||||
                                TCA    TACACTTCTCG
                                  GTCTC
GAM195  LOC152804 3'  GGCTTGCTATTTTACTTTCT   85889     A      TGAA
                                AGAAA GTAAAATG   GAGCC
                                ||||| ||||||||   |||||
                                TCTTT CATTTTAT   TTCGG
                                   _      CG__
GAM195  LOC157627 5'  GGCTCTTCATTTGCCCTCCTA  81505    AAAA   AAT
                                TAG   GTAA   GTGAAGAGCC
                                |||   ||||   ||||||||||
                                ATC   CGTT   TACTTCTCGG
                                  CTCC   ___
GAM195  LOC160414 3'  GGCTCTTCAAAACCTTTTC   87068      TAAAATG
                                GAAAAG      TGAAGAGCC
                                ||||||      |||||||||
                                CTTTTC      ACTTCTCGG
                                   CAAA___
GAM195  LOC219627 3'  CTCTTTGAAATTACTTTTT   92176       AATG
                                GAAAAGTAA   TGAAGAG
                                |||||||||   |||||||
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                                TTTTTCATT   GTTTCTC
                                     AAA_
GAM195  LOC221773 3'  CACATTTCACTTTTCTG    91038        A
                                TAGAAAAGT AAATGTG
                                ||||||||| |||||||
                                GTCTTTTCA TTTACAC
                                     C
GAM195  LOC222057 3'  CTCTTCACACCCAGCTCTTC  92774    A  AAAA
                                GAA AGT   TGTGAAGAG
                                ||| |||   |||||||||
                                CTT TCG   ACACTTCTC
                                  C  ACCC
GAM195  LOC256008 3'  CTCTTCACTTTCACCTCTCTG 95224     AAA  A  T
                                TAGA  GT AAA GTGAAGAG
                                ||||  || ||| ||||||||
                                GTCT  CA TTT CACTTCTC
                                   CTC  C  _
GAM195  LOC257449 3'  GGCTCTTCATCAGGACACTTCC 62720   AA   AAAA  _
            CT                   AG  AAGT   TG TGAAGAGCC
                                ||  ||||   || |||||||||
                                TC  TTCA   AC ACTTCTCGG
                                 CC   CAGG  T
GAM195  LOC51667  3'  GCTCTTTCTGTTCTTACTTTTT 32274       _  GT
                                GAAAAGTAA AAT  GAAGAGC
                                ||||||||| |||  |||||||
                                TTTTTCATT TTG  TTTCTCG
                                     C  TC
GAM195  LOC89919  3'  GGCCCCTTTTGTTCTCTTTTCT 60726       TA  ATGT   A_
            A                    TAGAAAAG  AA   GAAG  GCC
                                ||||||||  ||   ||||  |||
                                ATCTTTTC  TT   TTTC  CGG
                                     TC  GT__   CC
GAM195  LOC90072  3'  CTCAAACATTCTACTTTTCTA  61294       A   GAA
                                TAGAAAAGTA AATGT   GAG
                                |||||||||| |||||   |||
                                ATCTTTTCAT TTACA   CTC
                                     C    AA_
GAM195  LOC91923  5'  CACCATTTTACTTTTCTA    67549          _
                                TAGAAAAGTAAAATG TG
                                |||||||||||||| ||
                                ATCTTTTCATTTTAC AC
                                       C
GAM195  LOC93097  5'  TTCACATTTTCTTTTCTA    71365       T
                                TAGAAAAG AAAATGTGAA
                                |||||||| ||||||||||
                                ATCTTTTC TTTTACACTT
                                     _
GAM196  CD74     3'  GAACAGCAGATAACA      15129     CA
                                TGT  GTCTGCTGTTT
                                |||  ||||||||||
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                                ACA  TAGACGACAAG
                                  A_
GAM196  MFAP4    3'  CCTGTCCCAACAGCTGACAG   69254       T   C  TTT
                                CTGTCAG CTG TG   GCAGG
                                ||||||| ||| ||   |||||
                                GACAGTC GAC AC   TGTCC
                                   _   A  CC_
GAM196  SLC20A1  3'  TGTTAACAGAAGACTGACA    59391        G    T
                                TGTCAGTCT CTGTT GCA
                                ||||||||| ||||| |||
                                ACAGTCAGA GACAA TGT
                                     A    T
GAM196  WNT14    3'  CCTGCAAGGACTGAGAG     12676    G     GCTGT
                                CT TCAGTCT    TTGCAGG
                                || |||||||    |||||||
                                GA AGTCAGG    AACGTCC
                                 G     _____
GAM196  ATF3     5'  CGCCCGCCGGCCAGACAAACAG 14431     CA    _   TTT  A
                                CTGT  GTCTG CTG   GC GGCG
                                ||||  ||||| |||   || ||||
                                GACA  CAGAC GGC   CG CCGC
                                  AA    C   ___  C
GAM196  CXorf9   3'  CGCCCTCCACCAGCGACTGACA 38623         T    TTTGCA
           G                     CTGTCAGTC GCTG     GGCG
                                ||||||||| ||||     ||||
                                GACAGTCAG CGAC     CCGC
                                     _   CACCTC
GAM196  FLJ20195 3'  CCAGCCCCAGCAGACCACAG   34708     CA      TTT  A
                                CTGT  GTCTGCTG   GC GG
                                ||||  ||||||||   || ||
                                GACA  CAGACGAC   CG CC
                                  C_       CC_  A
GAM196  MAP3K6   5'  CGCCTGCAGCGGAGACTGGACA 16245      _    G    T
           G                     CTGTC AGTCT CTGTT GCAGGCG
                                ||||| ||||| ||||| |||||||
                                GACAG TCAGA GGCGA CGTCCGC
                                  G    _    _
GAM196  SRF      5'  GCCCTAGCAGACGGACAG    11950      A      TTTGCA
                                CTGTC GTCTGCTG     GGC
                                ||||| ||||||||     |||
                                GACAG CAGACGAT     CCG
                                  G       C_____
GAM196  LOC115004 3' CCTGCTGCTCAGACTGA     73174        CT  TT
                                TCAGTCTG  GT  GCAGG
                                ||||||||  ||  |||||
                                AGTCAGAC  CG  CGTCC
                                     T_  T_
GAM196  LOC118611 5'  CACCCATGCAGACGACA     75470     A     _  TT
                                TGTC GTCTGC TG  TG
                                |||| ||||||  ||  ||
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                                ACAG CAGACG AC  AC
                                  _     T  CC
GAM196  LOC197342 3'  CCTGGGCTGCAGACAGACA   87998      A     T   TG
                                TGTC GTCTGC GTT  CAGG
                                |||| |||||| |||  ||||
                                ACAG CAGACG CGG  GTCC
                                  A     T  __
GAM196  LOC204084 5'  TTTGTACAGACTGACA      89450          CTGTT
                                TGTCAGTCTG    TGCAGG
                                ||||||||||    ||||||
                                ACAGTCAGAC    ATGTTT
                                      _____
GAM196  LOC83690  5'  CGCCCACCCTGGCAGACTAACG 48814     C       GTTTGCA
                                TGT AGTCTGCT      GGCG
                                ||| ||||||||      ||||
                                GCA TCAGACGG      CCGC
                                  A       TCCCAC_
GAM196  LOC90515  3'  CGCCTGCAACCTTGATCGACAG 63123       A   TGCTGT
                                CTGTC GTC     TTGCAGGCG
                                ||||| |||     |||||||||
                                GACAG TAG     AACGTCCGC
                                   C   TTCC__
GAM197  ARHGEF6   3'  CAAACTTGAAGCCAGGC     68197       ACCA
                                GCCTGG    CAAGTTTG
                                ||||||    ||||||||
                                CGGACC    GTTCAAAC
                                    GAA_
GAM197  CNTN2     3'  GTCACAACCCAGGTGA      17411        ACCACAA  _
                                TCGCCTGG      GTT TGAC
                                ||||||||      ||| ||||
                                AGTGGACC      CAA ACTG
                                      ________  C
GAM197  CORO2A    3'  AAACTGTGGTCCAGAGA     12642    GC        A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM197  CORO2A    3'  AAACTGTGGTCCAGAGA     53398    GC        A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM197  GRLF1     3'  AGGTCAGAAAGTGGCCCAGG   78551      A   AAG
                                CCTGG CCAC   TTTGACCT
                                ||||| ||||   ||||||||
                                GGACC GGTG   AGACTGGA
                                   C    AA_
GAM197  LAPTM5    3'  AGGCTTGTGGTCAAGC      22199    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
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                                CG  CTGGTGTTCGGA
                                 AA_
GAM197  POU2AF1  3' AGATTTACAGTCCAGGC    20647       CAC
                                GCCTGGAC  AAGTTT
                                ||||||||  ||||||
                                CGGACCTG  TTTAGA
                                    ACA
GAM197  PTGS1    3' GTCTCCTGTCTTATGGTCCAG 54574       C  TTT___
                                CTGGACCA AAG    GAC
                                |||||||| |||    |||
                                GACCTGGT TTC    CTG
                                    A  TGTCCT
GAM197  PTGS1    3' GTCTCCTGTCTTATGGTCCAG 6355        C  TTT___
                                CTGGACCA AAG    GAC
                                |||||||| |||    |||
                                GACCTGGT TTC    CTG
                                    A  TGTCCT
GAM197  TRIM34   5' AGGTCAAGTTGAGCCCAG   55224    ACCA  G
                                CTGG   CAA TTTGACCT
                                ||||   ||| ||||||||
                                GACC   GTT GAACTGGA
                                  CGA_  _
GAM197  TRIM9    5' AGGCCAGGCAAGTCCAGGC   30749       CACAA   A
                                GCCTGGAC    GTTTG CCT
                                ||||||||    ||||| |||
                                CGGACCTG    CGGAC GGA
                                    AA___    C
GAM197  ABLIM    5' GATATGTAACCCAGGCGG    22030       ACC  A
                                TCGCCTGG  ACA GTT
                                ||||||||  ||| |||
                                GGCGGACC  TGT TAG
                                    CAA  A
GAM197  AMOT     3' AGGCATCTTCATGGTCCAGGGA 55716   G       C_  TT  A
                                TC CCTGGACCA  AAG  TG CCT
                                || |||||||||  |||  || |||
                                AG GGACCTGGT  TTC  AC GGA
                                 _       AC  T_ _
GAM197  DKFZp434D177 5' TTAGACCCAGGCGA       50056       ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                        _______
GAM197  DKFZp434D177 5' TTAGACCCAGGCGA       79443       ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                        _______
GAM197  FLJ23420  3' CAAGTGGGTCCAGGC       46845        A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
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                                CGGACCTGG GT  GAAC
                                      _  __
GAM197  HSA249128 5'  GGCGCGGTCCAGGCGG      34152          ACAA
                                TCGCCTGGACC    GTT
                                ||||||||||    |||
                                GGCGGACCTGG    CGG
                                      CG__
GAM197  MGC15668  5'  AGACCCGGTGGTCCAGACG    51277    C       AA_
                                CG CTGGACCAC   GTTT
                                || |||||||||   ||||
                                GC GACCTGGTG   CAGA
                                 A        GCC
GAM197  MGC22014  3'  AGGTCCCGAGTGTAACCCAGGT 64486        ACC   AGTTT
           GA                     TCGCCTGG   ACA    GACCT
                                ||||||||   |||    |||||
                                AGTGGACC   TGT    CTGGA
                                     CAA   GAGCC
GAM197  SDCCAG10  5'  AGAGTTGTGGTCCAAAGA    19641    GCC        G
                                TC   TGGACCACAA TTT
                                ||   |||||||||| |||
                                AG   ACCTGGTGTT AGA
                                 AA_         G
GAM197  LOC115442 3'  AGGTCAGGGATGGTCCAG    72676        CAAG
                                CTGGACCA    TTTGACCT
                                ||||||||    ||||||||
                                GACCTGGT    GGACTGGA
                                     AG__
GAM197  LOC129011 5'  AGACCTGCGGTCCAGGC     74862         A  A
                                GCCTGGACC CA GTTT
                                ||||||||| || ||||
                                CGGACCTGG GT CAGA
                                      C  C
GAM197  LOC130536 5'  GCAAAGTCCAGGCG        75746         CACAAG    A
                                CGCCTGGAC      TTTG C
                                |||||||||      |||| |
                                GCGGACCTG      AAAC G
                                     _______   C
GAM197  LOC149108 3'  AGACTTCACTGTGGTCCA    84357          _____
                                TGGACCACA    AGTTT
                                |||||||||    |||||
                                ACCTGGTGT    TCAGA
                                      CACT
GAM197  LOC221688 5'  AGACTCGGGCCCAGACGA    93674     C    A  ACA
                                TCG CTGG CC   AGTTT
                                ||| |||| ||   |||||
                                AGC GACC GG   TCAGA
                                  A   C  GC_
GAM197  LOC256228 5'  AGACTTGTGGTCAAAGC     96233    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
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                                CG   CTGGTGTTCAGA
                                 AAA
GAM197  LOC257441 5'  TTAGACCCAGGCGA       95566        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                          ________
GAM197  LOC91960  3'  AGGTGCCTCTCGTGGTCCAAGC 67657    C       A  TTTG
                                GC TGGACCAC AG    ACCT
                                || |||||||| ||    ||||
                                CG ACCTGGTG TC    TGGA
                                 A       C  TCCG
GAM197  LOC92840  3'  GTCCCTCGGGTCCAGGC     56435         ACA  TTT
                                GCCTGGACC   AG   GAC
                                |||||||||   ||   |||
                                CGGACCTGG   TC   CTG
                                      GC_  C__
GAM198  ANK2      3'  ACTTGAAGCAAGAGGCCAAGTG 6708          ATAG  T
              A                  TCACTTGGC    TG CTTCAAGT
                                 |||||||||    || ||||||||
                                 AGTGAACCG    AC GAAGTTCA
                                      GAGA  _
GAM198  ANK2      3'  ACTTGAAGCAAGAGGCCAAGTG 40602         ATAG  T
              A                  TCACTTGGC    TG CTTCAAGT
                                 |||||||||    || ||||||||
                                 AGTGAACCG    AC GAAGTTCA
                                      GAGA  _
GAM198  DAAM2     3'  TGAAGGTGCCAAGGA       92293     A       AGTGT
                                TC CTTGGCAT     CTTCA
                                || ||||||||     |||||
                                AG GAACCGTG     GAAGT
                                 _      ______
GAM198  FAAH      3'  ACTTAAAAAACTCGCCAAGTG  44193         AT   GTC  C
                                CACTTGGC  AGT   TT AAGT
                                ||||||||  |||   || ||||
                                GTGAACCG  TCA   AA TTCA
                                     C_   AA_  A
GAM198  GLS       3'  CTTGAAGATTACCAATGA     29789      C    CATAGT
                                TCA TTGG      GTCTTCAAG
                                ||| ||||      |||||||||
                                AGT AACC      TAGAAGTTC
                                  _    AT_____
GAM198  GPR87     5'  ACTTGAAGACACCGTATGAGGT 43654        GG   __
              GA                   TCACTT  CATA  GTGTCTTCAAGT
                                   ||||||  ||||  ||||||||||||
                                   AGTGGA  GTAT  CACAGAAGTTCA
                                      __    GC
GAM198  LPIN1     3'  ACTTGAGCACACTTATGCCAAA 67390      C       _    C
              TGA                    TCA TTGGCATA GTGT TTCAAGT
                                     ||| |||||||| |||| |||||||
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                                AGT AACCGTAT CACA GAGTTCA
                                  A       T   C
GAM198  PODXL    3'  CTCGAAGGTGCCAGAATGA   18232    C_     AGTGT   A
                                TCA  TTGGCAT    CTTC AG
                                |||  |||||||    |||| ||
                                AGT  GACCGTG    GAAG TC
                                  AA      _____   C
GAM198  ARHE     3'  ACTTGAAAAATATGCCAA    17710        GTGTC
                                TTGGCATA    TTCAAGT
                                ||||||||    |||||||
                                AACCGTAT    AAGTTCA
                                     AAA__
GAM198  BHC80    3'  GCACCATGCCAAGTGA      33535          A
                                TCACTTGGCAT GTGT
                                |||||||||| ||||
                                AGTGAACCGTA CACG
                                       C
GAM198  FLJ30927 3'  ACTTGAAGAATGTAATGCCAGT 58412      T    AGTG_
            GA                    TCACT GGCAT    TCTTCAAGT
                                ||||| |||||    |||||||||
                                AGTGA CCGTA    AGAAGTTCA
                                   _    ATGTA
GAM198  GAB3     3'  ACTTGAAAGATGTGCATGTCAA 54623          A_ TG   _
            GTGA                   TCACTTGGCAT  G  TCTT CAAGT
                                |||||||||| |  |||| |||||
                                AGTGAACTGTA  T  AGAA GTTCA
                                       CG GT   A
GAM198  KIAA1374 3'  CTTGAAAACACTATGCTAAGTG 61242             C
            A                     TCACTTGGCATAGTGT TTCAAG
                                |||||||||||||||| ||||||
                                AGTGAATCGTATCACA AAGTTC
                                          A
GAM198  LOC148708 3'  GATGTATGCCAAGCGG      78952    A       G
                                TC CTTGGCATA TGTC
                                || ||||||||| ||||
                                GG GAACCGTAT GTAG
                                 C       _
GAM198  LOC221975 5'  GAAGGCACCGCCAAGGA     92605    A     ATA
                                TC CTTGGC   GTGTCTTC
                                || ||||||   ||||||||
                                AG GAACCG   CACGGAAG
                                  _     C__
GAM198  LOC253832 3'  ACCTGAAACTATGCCAA     94919          GTC   A
                                TTGGCATAGT   TTCA GT
                                ||||||||||   |||| ||
                                AACCGTATCA   AAGT CA
                                       ___   C
GAM199  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
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                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM199  AHR     3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM199  FDFT1   3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                      _
GAM199  JTB     3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM199  KLF4    3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM199  PHYH    3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM199  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                       T__    _
GAM199  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM199  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_    CG_
GAM199  CG012   5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM199  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
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                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM199  FLJ23462  3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
            G                    CATTTC        GTCTGAGAT
                                 ||||||        |||||||||
                                 GTAAAG        CAGACTCTA
                                    AAACATTT_
GAM199  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                 CATTTCA   TCACTGTCTGAGAT
                                 |||||||   ||||||||||||||
                                 GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM199  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                 TTCA TTTCACTG  TGAG
                                 |||| ||||||||  ||||
                                 AAGT AAAGTGAC  GTTT
                                   A       CT
GAM199  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                 TTTC CTG TCTGAGAT
                                 |||| ||| ||||||||
                                 AAAG GAC AGACTCTA
                                   _  G
GAM199  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                 ATT CACTTTCACTGT
                                 ||| ||||||||||||
                                 TAA GTGAAAGTGACG
                                   C
GAM199  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                 TTCACTTT  CT TCTGAGAT
                                 ||||||||  || ||||||||
                                 AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM199  PP35      3'  ATCTCAGACTGAAA       22814      CT
                                 TTTCA  GTCTGAGAT
                                 |||||  |||||||||
                                 AAAGT  CAGACTCTA
                                    __
GAM199  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148         TCAC  C_
                                 CATTTCACTT   TGT  TGAG
                                 ||||||||||   |||  ||||
                                 GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM199  SEP15     3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                 TTTCACTTT ACTGT  GA
                                 ||||||||| |||||  ||
                                 AAAGTGAGA TGACA  CT
                                      A    TC
GAM199  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                 TTTCACTTT    TCTGAG
                                 |||||||||    ||||||
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                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM199  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM199  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM199  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226     A      GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM199  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM200  D12S2489E 3'  GCCTTAAGATCTTAGG      23743         C   A
                                CCTGAGATCT AAG GT
                                |||||||||| ||| ||
                                GGATTCTAGA TTC CG
                                     A   _
GAM200  GPR34     3'  ACTCAGATCTCAAAGC      17960    CC      CAA
                                GC  TGAGATCT   GAGT
                                ||  ||||||||   ||||
                                CG  ACTCTAGA   CTCA
                                 AA       ___
GAM200  LNK       3'  GTCACCCTTTCAGGG       18468       GATCTC   A
                                CCCTGA     AAG GTGAC
                                ||||||     ||| |||||
                                GGGACT     TTC CACTG
                                   _______  C
GAM200  LZTS1     3'  GCTTTGAAACCTCAGGGC    40693        ATC   A
                                GCCCTGAG   TCA GAGT
                                ||||||||   ||| ||||
                                CGGGACTC   AGT TTCG
                                     CAA   _
GAM200  SOLH      3'  ACGCTTGAGCCAGAATCTCAGG 18874        _____     A
                                CCTGAGAT    CTCAAG GT
                                ||||||||    |||||| ||
                                GGACTCTA    GAGTTC CA
                                     AGACC     G
GAM200  SORCS1    3'  ATGTGGAAGGTAAGATTCAGGG 53580        A   CAAGAGTG
              C                  GCCCTGAG TCT       ACAT
                                ||||||||| |||       ||||
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                                CGGGACTT AGA       TGTA
                                     _  ATGGAAGG
GAM200  SORD     3'  CAGTCTTGGGATCTCAGGGC  11869              G
                                GCCCTGAGATCTCAAGA TG
                                |||||||||||||||| ||
                                CGGGACTCTAGGGTTCT AC
                                          G
GAM200  BDH      3'  CTCTAAATCTCAGGGC      14474          CTCA
                                GCCCTGAGAT   AGAG
                                ||||||||||   ||||
                                CGGGACTCTA   TCTC
                                     AA__
GAM200  CAMP-GEFII 3'  CATCCTGAGACACCTCAGGGC 22826        A__    A AG
                                GCCCTGAG  TCTCA G  TG
                                ||||||||  ||||| |  ||
                                CGGGACTC  AGAGT C  AC
                                     CAC    _ CT
GAM200  FLJ22362  3'  ATGCCACTCCCACAATCTCAGG 43069        CTCAA    A
                                CCTGAGAT    GAGTG CAT
                                ||||||||    ||||| |||
                                GGACTCTA    CTCAC GTA
                                     ACACC    C
GAM200  FLJ22690  3'  TGATCAGAAATCTCAGGGC   45250         C  AAGAG  _
                                GCCCTGAGAT TC    TGA CA
                                |||||||||| ||    ||| ||
                                CGGGACTCTA AG    ACT GT
                                     A ______  A
GAM200  KIAA1143  3'  ATGTCACTCTTGAACTTCAGG  68669       ATC
                                CCTGAG   TCAAGAGTGACAT
                                ||||||   ||||||||||||||
                                GGACTT   AGTTCTCACTGTA
                                   CA_
GAM200  KIAA1297  3'  CGCTCGGTGCAGGACCTCAGGG 72176        A  __  A_
             C                   GCCCTGAG TCT  CA  GAGTG
                                ||||||||  |||  ||  |||||
                                CGGGACTC AGG  GT  CTCGC
                                     C   AC  GG
GAM200  KIAA1322  3'  CAGTCTAAGACTTCAGGGC   72734        A   CA   G
                                GCCCTGAG TCT  AGA TG
                                ||||||||  |||  |||  ||
                                CGGGACTT AGA  TCT AC
                                     C   A_   G
GAM200  SMCR7    3'  CACCTGATACCTCAGGGC    57505        ATC   A A
                                GCCCTGAG   TCA G GTG
                                ||||||||   |||  |  |||
                                CGGGACTC   AGT C CAC
                                     CAT   _ _
GAM200  TBX19    3'  ATGTCACTCCTCTGCTCAG   17648       ATCTCAA
                                CTGAG      GAGTGACAT
                                |||||      |||||||||
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                                GACTC      CTCACTGTA
                                  GTCTC__
GAM200  VIT1     3'  ACTCAGGATCTCAAAGC     37971    CC       CAA
                                GC  TGAGATCT   GAGT
                                ||  ||||||||   ||||
                                CG  ACTCTAGG   CTCA
                                 AA       A__
GAM200  LOC115330 3' ATGCCACTCTTGGGCCAAGGC  56608     C  AGAT        A
                                GCC TG    CTCAAGAGTG CAT
                                ||| ||    |||||||||| |||
                                CGG AC    GGGTTCTCAC GTA
                                  A  C___         C
GAM200  LOC116166 3' TCTCGGGATCTCAGGGC     59763            A
                                GCCCTGAGATCTC AGA
                                |||||||||||| |||
                                CGGGACTCTAGGG TCT
                                        C
GAM200  LOC138389 3' CACTCTGAAAATCTCAGGGC   76220          CTCA
                                GCCCTGAGAT    AGAGTG
                                ||||||||||    ||||||
                                CGGGACTCTA    TCTCAC
                                      AAAG
GAM200  LOC146268 3' ATGTCACTCTCATTCAACAGGG 77801       A_  TCTCA
                                CCCTG  GA     AGAGTGACAT
                                |||||  ||    ||||||||||
                                GGGAC  CT    TCTCACTGTA
                                   AA  TAC__
GAM200  LOC148438 3' CATTTTCCAAGATCTCA     84157         CA_
                                TGAGATCT   AGAGTG
                                ||||||||   ||||||
                                ACTCTAGA   TTTTAC
                                     ACC
GAM200  LOC199675 3' ATGCCACCCTGTGTGCTCAGGG 88260         ATCTCA  A   A
           C                     GCCCTGAG     AG GTG CAT
                                ||||||||     || ||| |||
                                CGGGACTC     TC CAC GTA
                                     GTGTG_  C   C
GAM200  LOC199958 3' ATGTCACTCCTCATTCAG    89883       ATCTCAA
                                CTGAG      GAGTGACAT
                                |||||      |||||||||
                                GACTT      CTCACTGTA
                                   ACTC____
GAM200  LOC222029 5' ATGTCACTCCCACTCCCAGC   94034    CCT   ATCTCAA
                                GC   GAG      GAGTGACAT
                                ||   |||      |||||||||
                                CG   CTC      CTCACTGTA
                                 ACC   ACC_____
GAM200  LOC255326 3' ATGTCATTGTGAAACCTCACAG 96374    CC    ATC   AG
           C                     GC  TGAG   TCA  AGTGACAT
                                ||  ||||   |||  ||||||||
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                                CG  ACTC   AGT  TTACTGTA
                                 AC    CAA   G_
GAM200  LOC256905 3'  ATGTTGAGTGCTGAGATTTCAA 96864     C        A AG__
           GGC                    GCC TGAGATCTCA G    TGACAT
                                ||| |||||||||| |    ||||||
                                CGG ACTTTAGAGT C    GTTGTA
                                  A         _ GTGA
GAM201  ACP5     5'  GGGAATAAAGGCTCAGGGACCG 7856          ___  T   CAC
           GC                     GCTGGTCCT   GC CTT   TCCC
                                |||||||||   || |||   ||||
                                CGGCCAGGG   CG GAA   AGGG
                                     ACT  _   ATA
GAM201  ATP8A2    3'  GGAAGTGAAGAGCGGAATC    93514     C          _
                                GGT CTGCTCTTCACT CC
                                ||| ||||||||||| ||
                                CTA GGCGAGAAGTGA GG
                                  A          A
GAM201  BACH2     3'  AGGAGCCAGGACCAGC      41485          _
                                GCTGGTCCTG CTCTT
                                |||||||||| |||||
                                CGACCAGGAC GAGGA
                                      C
GAM201  BAIAP3    3'  GGGAGTGAAAAGGGTGCCA    14127      _  GCTC
                                TGGT CCT    TTCACTCCC
                                |||| |||    |||||||||
                                ACCG GGG    AAGTGAGGG
                                  T   AA__
GAM201  BLTR2     5'  GAGAACAGAAGCAGGACCAG   39041          _ TCA
                                CTGGTCCTGCT CT   CTC
                                |||||||||| ||   |||
                                GACCAGGACGA GA   GAG
                                      A  CAA
GAM201  CBFA2T2   3'  GGAATGATTGCAGGGACCAG   17474        _   TCT   C
                                CTGGTCC TGC   TCA TCC
                                ||||||| |||   ||| |||
                                GACCAGG ACG   AGT AGG
                                    G   TT_   A
GAM201  CD4       3'  GGGAGTGTTCAGGGCCAGC    5226          CTCTT
                                GCTGGTCCTG    CACTCCC
                                |||||||||     |||||||
                                CGACCGGGAC    GTGAGGG
                                      TT___
GAM201  CDC25A    3'  GGGCGGCAGGACCAGC      8365           C
                                GCTGGTCCTGCT TTC
                                |||||||||||| |||
                                CGACCAGGACGG GGG
                                       C
GAM201  CHRM1     3'  GAAGTCAGGAGCCAGC      94790      _    CT
                                GCTGG TCCTG  CTTC
                                ||||| |||||  ||||
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                                CGACC AGGAC  GAAG
                                  G    T_
GAM201  CML66    3'  GAGTGAAGATAGTACTAGC   68233      C  C
                                GCTGGT CTG TCTTCACTC
                                |||||| ||| |||||||||
                                CGATCA GAT AGAAGTGAG
                                   T  _
GAM201  COL4A2   3'  GAAAGCCAGGAGCAGC     8467      G   _ C
                                GCTG TCCTG CT TTC
                                |||| ||||| || |||
                                CGAC AGGAC GA AAG
                                  G    C _
GAM201  CYP1A1   3'  GAGTGAAGGGAAGAGACAGC  4942     G _ G
                                GCTG TC CT CTCTTCACTC
                                |||| || || ||||||||||
                                CGAC AG GA GGGAAGTGAG
                                  _ A  A
GAM201  CYP1A2   3'  GGGAGCGAGTGGGGGCCAGC  5699       _ TG  TTCA
                                GCTGGTC C  CTC   CTCCC
                                ||||||| |  |||   |||||
                                CGACCGG G  GAG   GAGGG
                                    G GT  C___
GAM201  CYP1A2   3'  GGGAGCGAGTGGGGGCCAGC  69119      _ TG  TTCA
                                GCTGGTC C  CTC   CTCCC
                                ||||||| |  |||   |||||
                                CGACCGG G  GAG   GAGGG
                                    G GT  C___
GAM201  DYRK2    5'  GAAGTAGCAGCAGGACCGGC  21390        ____
                                GCTGGTCCTGCT   CTTC
                                ||||||||||||   ||||
                                CGGCCAGGACGA   GAAG
                                       CGAT
GAM201  DYRK2    5'  GAAGTAGCAGCAGGACCGGC  13126        ____
                                GCTGGTCCTGCT   CTTC
                                ||||||||||||   ||||
                                CGGCCAGGACGA   GAAG
                                       CGAT
GAM201  EFNB1    3'  GAGAGGGAGCAGAACAGC   15398     GTC      CA
                                GCTG  CTGCTCTT  CTC
                                ||||  ||||||||  |||
                                CGAC  GACGAGGG  GAG
                                  AA_      A_
GAM201  EIF2C1   3'  GAGTGGGGAACAGGGCCAGC  24177        C
                                GCTGGTCCTG TCTTCACTC
                                |||||||||| |||||||||
                                CGACCGGGAC AGGGGTGAG
                                       A
GAM201  EVX1     3'  GAGGGCGGAAAAGGACCAGC  8808        GC  TCA
                                GCTGGTCCT  TCT  CTC
                                |||||||||  |||  |||
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                                CGACCAGGA  AGG   GAG
                                     AA   CGG
GAM201   EXTL1    5'  GGAGTGGGAAGACCAGC     15495        CTGC   T
                                GCTGGTC    TCT CACTCC
                                |||||||    ||| ||||||
                                CGACCAG    AGG GTGAGG
                                    A___   _
GAM201   F8       3'  AGTGAGGAGAAACCTGC     3722     T   CCTG
                                GC GGT    CTCTTCACT
                                || |||    |||||||||
                                CG CCA    GAGGAGTGA
                                 T   AA__
GAM201   FCER2    5'  GAGAATCCAAGCAGGACCGC   8861     T       CTTCA_
                                GC GGTCCTGCT     CTC
                                || |||||||||      |||
                                CG CCAGGACGA     GAG
                                 _        ACCTAA
GAM201   FEN1     5'  GAGCGAGCTTAGGACCGC    14644    T     __   _
                                GC GGTCCT  GCTC TTC
                                || ||||||  |||| |||
                                CG CCAGGA  CGAG GAG
                                 _     TT    C
GAM201   FLG      5'  GGCGGACCAGGACCAGC     70878          C   TCACT
                                GCTGGTCCTG TCT    CC
                                |||||||||| |||    ||
                                CGACCAGGAC AGG    GG
                                      C   C_____
GAM201   FPGS     3'  GGACGAAGAGCAGGCCAGC   17089      T        AC
                                GCTGG CCTGCTCTTC  TCC
                                ||||| ||||||||||  |||
                                CGACC GGACGAGAAG  AGG
                                   _        C_
GAM201   FUT7     3'  GGGGAGCAAACCAGC       15587       CC
                                GCTGGT  TGCTCTTC
                                ||||||  ||||||||
                                CGACCA  ACGAGGGG
                                   A_
GAM201   FZD7     3'  AGTGAAGAGCAGTGTGC     13044    TGGTC
                                GC    CTGCTCTTCACT
                                ||    ||||||||||||
                                CG    GACGAGAAGTGA
                                 TGT__
GAM201   GAB2     3'  GGAGTCAAGGACCAGC      24500         GCTCTTC
                                GCTGGTCCT      ACTCC
                                |||||||||      |||||
                                CGACCAGGA      TGAGG
                                      AC_____
GAM201   GAB2     3'  GGAGTCAAGGACCAGC      54457         GCTCTTC
                                GCTGGTCCT      ACTCC
                                |||||||||      |||||
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                                CGACCAGGA      TGAGG
                                     AC_____
GAM201  GABRG3   3'  GAGTGAAGAGCATTTGGT    52638    TG TCC
                                GC  G   TGCTCTTCACTC
                                ||  |   ||||||||||||
                                TG  T   ACGAGAAGTGAG
                                 GT T__
GAM201  GAGED2   5'  GAGTGAAGAGGAACCAGC    55932       CCTG
                                GCTGGT    CTCTTCACTC
                                ||||||    ||||||||||
                                CGACCA    GAGAAGTGAG
                                   AG__
GAM201  GPRK5    5'  GGGCTGAGAGCAGGAACA    17962    G       T  CT
                                TG TCCTGCTCT CA  CC
                                || |||||||| ||  ||
                                AC AGGACGAGA GT  GG
                                 A        _  CG
GAM201  GRM1     5'  GGGAGCCTGCAGCGGGACCAGC 5917            CTTCA
                                GCTGGTCCTGCT    CTCCC
                                ||||||||||||    |||||
                                CGACCAGGGCGA    GAGGG
                                      CGTCC
GAM201  GRM3     5'  GGAAATGAGAGAGGACTAGC   5919         G    CAC
                                GCTGGTCCT CTCTT   TCC
                                ||||||||| |||||   |||
                                CGATCAGGA GAGAG   AGG
                                     _    TAA
GAM201  HAP1     3'  GAGGACAGGACCAGC       14168          C
                                GCTGGTCCTG TCTTC
                                |||||||||| |||||
                                CGACCAGGAC AGGAG
                                     _
GAM201  HD       3'  GAAAGCAGGAGCAGC       9184       G      C
                                GCTG TCCTGCT TTC
                                |||| ||||||| |||
                                CGAC AGGACGA AAG
                                  G      _
GAM201  HOXD4    5'  GGGAGTGAGGTACAAGGCCAGC 27528        C  CT
                                GCTGGTC TG  CTTCACTCCC
                                ||||||| ||  ||||||||||
                                CGACCGG AC  GGAGTGAGGG
                                    A  AT
GAM201  HSD17B3  3'  GAGGAGCAGACCAGC       3973         C
                                GCTGGTC TGCTCTTC
                                ||||||| ||||||||
                                CGACCAG ACGAGGAG
                                     _
GAM201  KIF3B    3'  GGAGTCACCTTAGCAGGACCA  16609          CTTC__
                                TGGTCCTGCT     ACTCC
                                ||||||||||     |||||
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                                ACCAGGACGA     TGAGG
                                     TTCCAC
GAM201  KIF3C    5'  GGATAGCAGGACCGC      9607     T       C
                                GC GGTCCTGCT TTC
                                || ||||||||| |||
                                CG CCAGGACGA AGG
                                 _       T
GAM201  KRTHA2   3'  GAAGAGCAGGGCCAGC      9643
                                GCTGGTCCTGCTCTTC
                                ||||||||||||||||
                                CGACCGGGACGAGAAG

GAM201  KRTHA8   3'  GGAAGTGAAGAACAGACT    22260      C  C       _
                                GGTC TG TCTTCACT CC
                                |||| || |||||||| ||
                                TCAG AC AGAAGTGA GG
                                  _ A       A
GAM201  LRP1     5'  GAAGTAGCAGGACCAG      9802            _
                                CTGGTCCTGCT CTTC
                                |||||||||| ||||
                                GACCAGGACGA GAAG
                                       T
GAM201  MAP3K1   5'  GAGTGTGGAGCTGGACCAGC   67815         T    T
                                GCTGGTCC GCTCT CACTC
                                |||||||| ||||| |||||
                                CGACCAGG CGAGG GTGAG
                                     T    T
GAM201  MAT1A    3'  AGTGAAGACAGAACCA      90826      C   C
                                TGGT CTG TCTTCACT
                                |||| ||| ||||||||
                                ACCA GAC AGAAGTGA
                                  A  _
GAM201  MGAT5    5'  GGGAGTGAAAGTGAGAACCA   10026      _ CT   C
                                TGGT C  GCT TTCACTCCC
                                |||| |  ||| |||||||||
                                ACCA G  TGA AAGTGAGGG
                                  A AG  _
GAM201  MNT      3'  GGAGACATGGACCAGC      39715         _  C
                                GCTGGTCC TG TCTTC
                                |||||||| || |||||
                                CGACCAGG AC AGAGG
                                     T  _
GAM201  MYD88    3'  GAGACTAAGAAGGACCAGC   10168          GC    CA_
                                GCTGGTCCT  TCTT   CTC
                                |||||||||  ||||   |||
                                CGACCAGGA  AGAA   GAG
                                      __   TCA
GAM201  MYD88    3'  GGACACTATAGAACAGGACCAG 10170           C   TCAC__
            C                    GCTGGTCCTG TCT      TCC
                                ||||||||||| |||      |||
```

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                                CGACCAGGAC AGA     AGG
                                      A   TATCAC
GAM201   NAPB     3'  GGAAGTGGGAAGGGCCAGC   70187        GC   T   _
                                GCTGGTCCT  TCT CACT CC
                                |||||||||  ||| |||| ||
                                CGACCGGGA  AGG GTGA GG
                                      __  _   A
GAM201   NCOA3    3'  GAAGAAAGGACCAGC      21531        GC
                                GCTGGTCCT  TCTTC
                                |||||||||  |||||
                                CGACCAGGA  AGAAG
                                      A_
GAM201   NTSR1    3'  GAAGCTGGCCGGGACCAGC   10293         _ __
                                GCTGGTCCTG CT  CTTC
                                |||||||||| ||  ||||
                                CGACCAGGGC GG  GAAG
                                      C  TC
GAM201   OPCML    3'  GGAGAGCAAACCAGC      10345       CC
                                GCTGGT  TGCTCTTC
                                ||||||  ||||||||
                                CGACCA  ACGAGAGG
                                   A_
GAM201   PIG8     3'  GAAGGCAGGACCCGC      16870    T      T
                                GC GGTCCTGC CTTC
                                || |||||||| ||||
                                CG CCAGGACG GAAG
                                 C      _
GAM201   PITX3    3'  AGCCAGGAACAGGGACCAGC  17264        GC_   CA
                                GCTGGTCCT   TCTT  CT
                                |||||||||   ||||  ||
                                CGACCAGGG   AGGA  GA
                                      ACA   CC
GAM201   PKP1     5'  GAAGCGCCAGGAGCAGC     4316      G    _ T
                                GCTG TCCTG C CTTC
                                |||| ||||| | ||||
                                CGAC AGGAC G GAAG
                                  G    C C
GAM201   PRDM4    3'  AGTTTAAAGCAGGACCTGC   24822    T      CTTC
                                GC GGTCCTGCT   ACT
                                || |||||||||   |||
                                CG CCAGGACGA   TGA
                                 T       AATT
GAM201   PSG4     3'  GGAATCACGAAGAGCAAGACC  10938     C      AC___
                                GGTC TGCTCTTC    TCC
                                |||| ||||||||    |||
                                CCAG ACGAGAAG    AGG
                                  A      CACTA
GAM201   PTPRA    3'  GGAGTAATAGGACCAG      11095        CTCTTC
                                CTGGTCCTG    ACTCC
                                |||||||||    |||||
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                                GACCAGGAT     TGAGG
                                    AA____
GAM201   PTPRA    3'  GGAGTAATAGGACCAG      55083         CTCTTC
                                CTGGTCCTG     ACTCC
                                |||||||||     |||||
                                GACCAGGAT     TGAGG
                                    AA____
GAM201   PTPRA    3'  GGAGTAATAGGACCAG      55091         CTCTTC
                                CTGGTCCTG     ACTCC
                                |||||||||     |||||
                                GACCAGGAT     TGAGG
                                    AA____
GAM201   PTPRS    3'  GGAGTGCTCCCCAGAACCAG  55644      C  CTCTT
                                CTGGT CTG     CACTCC
                                |||||  |||     ||||||
                                GACCA GAC     GTGAGG
                                   A   CCCTC
GAM201   PTPRS    3'  GGAGTGCTCCCCAGAACCAG  55647      C  CTCTT
                                CTGGT CTG     CACTCC
                                |||||  |||     ||||||
                                GACCA GAC     GTGAGG
                                   A   CCCTC
GAM201   PTPRS    3'  GGAGTGCTCCCCAGAACCAG  55650      C  CTCTT
                                CTGGT CTG     CACTCC
                                |||||  |||     ||||||
                                GACCA GAC     GTGAGG
                                   A   CCCTC
GAM201   PTPRS    3'  GGAGTGCTCCCCAGAACCAG  11140      C  CTCTT
                                CTGGT CTG     CACTCC
                                |||||  |||     ||||||
                                GACCA GAC     GTGAGG
                                   A   CCCTC
GAM201   PXF      3'  GAGAATGGGGAGAAACAGC   11150     GTCCTG     __
                                GCTG     CTCTTCA  CTC
                                ||||     |||||||  |||
                                CGAC     GAGGGGT  GAG
                                  AAA___      AA
GAM201   RASD1    3'  GGAGCGAGGGCCCAGC      32223      TCCT  T    A
                                GCTGG    GC CTTC CTCC
                                |||||    || |||| ||||
                                CGACC    CG GGAG GAGG
                                  _____  _    C
GAM201   RFNG     3'  GAGAACGAAGACAGCCAG    88175      TC   C     A__
                                CTGG  CTG TCTTC   CTC
                                ||||  ||| |||||   |||
                                GACC  GAC AGAAG   GAG
                                  __   _    CAA
GAM201   RRM2B    5'  GAAAGCAGGACCGGC       67826           C
                                GCTGGTCCTGCT TTC
                                |||||||||||| |||
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                                CGGCCAGGACGA AAG
                                           _
GAM201  RXRA    3'  GGAGTGAAGATGCCA      11412     CCTGC
                                TGGT    TCTTCACTCC
                                ||||    ||||||||||
                                ACCG    AGAAGTGAGG
                                  T_____
GAM201  SLC4A4  5'  GAGTGGTGGAGAACCA     13639     CCTG  _
                                TGGT   CTCT TCACTC
                                ||||   |||| ||||||
                                ACCA   GAGG GGTGAG
                                  A___   T
GAM201  SRGAP2  3'  GGAGTATCAGGACCAG     74607        CTCTTC
                                CTGGTCCTG    ACTCC
                                |||||||||    |||||
                                GACCAGGAC    TGAGG
                                     TA____
GAM201  STAT6   5'  GGGAGGTGCTAGCAGGGCCAGC 12024          CTTCA
                                GCTGGTCCTGCT   CTCCC
                                ||||||||||||   |||||
                                CGACCGGGACGA   GAGGG
                                       TCGTG
GAM201  STK38   3'  GGTGAAGGAACCAGC      23443      CCTGC
                                GCTGGT    TCTTCACT
                                ||||||    ||||||||
                                CGACCA    GGAAGTGG
                                   A____
GAM201  TCN2    5'  GAGCCTCAGCAGGGCCAGC   4480          CTTCA
                                GCTGGTCCTGCT   CTC
                                ||||||||||||   |||
                                CGACCGGGACGA   GAG
                                       CTCC_
GAM201  TDE1    5'  AAGCAGCCTCAGGACCGGC   22340        ___  _
                                GCTGGTCCT  GCT CTT
                                |||||||||  ||| |||
                                CGGCCAGGA  CGA GAA
                                     CTC  C
GAM201  TFE3    3'  AGTGAGGATGAGACCCAGC   21511     TC  GC
                                GCTGG  CT  TCTTCACT
                                |||||  ||  ||||||||
                                CGACC  GA  AGGAGTGA
                                  CA  GT
GAM201  TMSB4Y  5'  GAGCGCCGGCAGGACTAGC   14842          CTTCA
                                GCTGGTCCTGCT   CTC
                                ||||||||||||   |||
                                CGATCAGGACGG   GAG
                                       CCGC_
GAM201  TOP3A   3'  GAGTTAACCAGGACCA     16072       CTC  C
                                TGGTCCTG   TT ACTC
                                ||||||||   || ||||
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                                ACCAGGAC   AA TGAG
                                    C__  T
GAM201  TRPC5   5' GGAATAAAGAACAGGAGCAG  25000    G    C   CAC
                                CTG TCCTG TCTT   TCC
                                ||| ||||| ||||   |||
                                GAC AGGAC AGAA   AGG
                                  G    A   ATA
GAM201  TYRO3   3' GGAGGGCAGGTCCAGC     20845      T
                                GCTGG CCTGCTCTTC
                                ||||| ||||||||||
                                CGACC GGACGGGAGG
                                   T
GAM201  TZFP    3' GAAAAGCGGGCCGGC      26890      T    C
                                GCTGG CCTGCT TTC
                                ||||| |||||| |||
                                CGGCC GGGCGA AAG
                                   _     A
GAM201  WASF3   3' AGTGAAGAACAGAGTCCA   21824    TC_  C
                                TGG   CTG TCTTCACT
                                |||   ||| ||||||||
                                ACC   GAC AGAAGTGA
                                  TGA   A
GAM201  WBSCR1  3' GGTTAGAGCAGGACCA     42230          TCACT
                                TGGTCCTGCTCT    CC
                                ||||||||||||    ||
                                ACCAGGACGAGA    GG
                                      TT___
GAM201  WBSCR1  3' GGTTAGAGCAGGACCA     49262          TCACT
                                TGGTCCTGCTCT    CC
                                ||||||||||||    ||
                                ACCAGGACGAGA    GG
                                      TT___
GAM201  WNT11   5' GGCGGCGTGCAGGACCAGC  16123          TCT  A
                                GCTGGTCCTGC   TC CT
                                ||||||||||   || ||
                                CGACCAGGACG   GG GG
                                      TGC  C
GAM201  ZNF74   3' GGAGTCTAGGACCAGC     12800          CT
                                GCTGGTCCTG  CTTC
                                |||||||||  ||||
                                CGACCAGGAT  GAGG
                                     CT
GAM201  BCMP1   3' GTTAAGAGCAGGACCA     48737           C
                                TGGTCCTGCTCTT AC
                                |||||||||||| ||
                                ACCAGGACGAGAA TG
                                      T
GAM201  BEX1    5' GGAAAGCGGACCAGC      37479         T   C
                                GCTGGTCC GCT TTC
                                |||||||| ||| |||
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                                CGACCAGG CGA AGG
                                    _  A
GAM201  C1orf34  3' GAGGGCGGCAGGACCA     60672          __
                                TGGTCCTGCT  CTTC
                                ||||||||||  ||||
                                ACCAGGACGG  GGAG
                                      CG
GAM201  C22orf5  3' GGAGTGGTCAGGACCA     24343        CTCT
                                TGGTCCTG   TCACTCC
                                ||||||||   |||||||
                                ACCAGGAC   GGTGAGG
                                    T___
GAM201  CMRF-35H 3' GAGTGAAGAGAGTGCCA    70418    TC  G
                                TGG  CT CTCTTCACTC
                                |||  || ||||||||||
                                ACC  GA GAGAAGTGAG
                                  GT  _
GAM201  CNTNAP1  5' AAGAGCGGAGGACCAG     13274         __
                                CTGGTCCT  GCTCTT
                                ||||||||  ||||||
                                GACCAGGA  CGAGAA
                                    GG
GAM201  CREB-H   3' AGCAAAGAGCAGACACA    50882   _  C      CA
                                TG GTC TGCTCTT  CT
                                || ||| |||||||  ||
                                AC CAG ACGAGAA  GA
                                 A  _      AC
GAM201  CSE-C    3' GGAATGAAAAGCAAGGGCCAG 91482         _  C   C
                                CTGGTCCT GCT TTCA TCC
                                |||||||| ||| |||| |||
                                GACCGGGA CGA AAGT AGG
                                    A  A   A
GAM201  CSMD1    5' GGAACCTTACGCGGGACCAGC  73124          TCTTCAC
                                GCTGGTCCTGC      TCC
                                ||||||||||      |||
                                CGACCAGGGCG      AGG
                                      CATTCCA
GAM201  DC2      3' GAATGAAGAGCAGCAGT     64264     GTC       C
                                GCTG   CTGCTCTTCA TC
                                ||||   |||||||||| ||
                                TGAC   GACGAGAAGT AG
                                  ___        A
GAM201  DDX37    3' GGAGCACCCCAGGCAGGACCA 51025         CTTCA__
                                TGGTCCTGCT      CTCC
                                ||||||||||      ||||
                                ACCAGGACGG      GAGG
                                      ACCCCAC
GAM201  DIS3     3' GGTGAACAGGACCA       30233        CTC
                                TGGTCCTG   TTCACT
                                ||||||||   ||||||
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                                ACCAGGAC   AAGTGG
                                     ___
GAM201   DJ667H12.2 5'  GAGCCCAGAGCGGACCAGC   38984        T    TCA
                                GCTGGTCC GCTCT   CTC
                                |||||||| |||||   |||
                                CGACCAGG CGAGA   GAG
                                     _    CCC
GAM201   DKFZP564D166 3'  GAGATGAGAACAGGACCAG   47678        C   T _
                                CTGGTCCTG TCT CA CTC
                                ||||||||| ||| || |||
                                GACCAGGAC AGA GT GAG
                                      A   _  A
GAM201   DKFZP564M182 3'  GAGAAGTAGGACCAGC      78035          CT
                                GCTGGTCCTGCT  TC
                                ||||||||||||  ||
                                CGACCAGGATGA  AG
                                       AG
GAM201   DKFZp761B0514 5'  GGAGTCCCAGGAGCAGC     50157     G    CTCTTC
                                GCTG TCCTG     ACTCC
                                |||| |||||     |||||
                                CGAC AGGAC     TGAGG
                                  G    CC____
GAM201   DKFZP761I2123 3'  AGTGAAGAATTAGTACAGC   48754     GTC   C_
                                GCTG   CTG  TCTTCACT
                                ||||   |||  ||||||||
                                CGAC   GAT  AGAAGTGA
                                  AT_   TA
GAM201   DKFZp761O17121 3'  AGTGCGGCAGGACCAGC     50135          CTT
                                GCTGGTCCTGCT   CACT
                                ||||||||||||   ||||
                                CGACCAGGACGG   GTGA
                                       C__
GAM201   FLJ10201  3'  AGTGAAGATGCCAGC      35891       CCTGC
                                GCTGGT    TCTTCACT
                                ||||||    ||||||||
                                CGACCG    AGAAGTGA
                                   T____
GAM201   FLJ10613  5'  GGAAGTGAAGAGAGCAAGC   38823     GGTC  G       _
                                GCT    CT CTCTTCACT CC
                                |||    || |||||||| ||
                                CGA    GA GAGAAGTGA GG
                                  AC__  _        A
GAM201   FLJ10751  3'  AGGAGCCCGAGGACCAGC    36566         ___
                                GCTGGTCCT   GCTCTT
                                |||||||||   ||||||
                                CGACCAGGA   CGAGGA
                                      GCC
GAM201   FLJ10751  3'  AGGAGCCCGAGGACCAGC    36727         ___
                                GCTGGTCCT   GCTCTT
                                |||||||||   ||||||
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                                CGACCAGGA   CGAGGA
                                     GCC
GAM201  FLJ11342  3' GTGAAGAAGGACCAGC      37249         GC
                                GCTGGTCCT  TCTTCAC
                                |||||||||  |||||||
                                CGACCAGGA  AGAAGTG
                                     __
GAM201  FLJ12592  3' GGAGTTCAGGACCAGC      49698         CT
                                GCTGGTCCTG  CTTC
                                ||||||||||  ||||
                                CGACCAGGAC  GAGG
                                      TT
GAM201  FLJ13105  5' GGGGAGCTGGACCAGC      46546         T
                                GCTGGTCC GCTCTTC
                                |||||||| |||||||
                                CGACCAGG CGAGGGG
                                     T
GAM201  FLJ13111  3' AGGAGCACAAGGACCCAGC    46935      _   ___
                                GCTGG TCCT   GCTCTT
                                ||||| ||||   ||||||
                                CGACC AGGA   CGAGGA
                                   C    ACA
GAM201  FLJ13204  3' GAAAGAAGGACCAGC       45417         G  C
                                GCTGGTCCT CT TTC
                                ||||||||| || |||
                                CGACCAGGA GA AAG
                                      A  _
GAM201  FLJ13231  3' GGAGTGAAAAGAAAAACCA   43553      CCTG  C
                                TGGT    CT TTCACTCC
                                ||||    || ||||||||
                                ACCA    GA AAGTGAGG
                                  AAAA  A
GAM201  FLJ14596  3' GGAAGCAGAGGCCAGGACCAGT 51462          CT   CA  _
                                GCTGGTCCTG  CTT  CT CC
                                ||||||||||  |||  || ||
                                TGACCAGGAC  GAG  GA GG
                                      CG   AC  A
GAM201  FLJ20085  5' GAGCCGGGAGCAGGTCCA    34516     T       CA
                                TGG CCTGCTCTT  CTC
                                ||| |||||||||  |||
                                ACC GGACGAGGG  GAG
                                  T        CC
GAM201  FLJ20195  5' GATGTGGAGCAGGGCCA     34710           T  C
                                TGGTCCTGCTCT CA TC
                                |||||||||||| || ||
                                ACCGGGACGAGG GT AG
                                       T  _
GAM201  FLJ20421  5' GGAAGTCGGACCAGC       35147         T   C
                                GCTGGTCC GCT TTC
                                |||||||| ||| |||
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                                CGACCAGG TGA AGG
                                     C   _
GAM201  FLJ20695  3'  GGAAACAAAGCAGGACCAGC  35558          CTTCAC
                                GCTGGTCCTGCT     TCC
                                ||||||||||||    |||
                                CGACCAGGACGA     AGG
                                      AACAA_
GAM201  FLJ21736  3'  AAGAGCACCCACCAAGACACAG 46223     _  C_______
           C                    GCTG GTC       TGCTCTT
                                |||| |||       |||||||
                                CGAC CAG       ACGAGAA
                                  A  AACCACCC
GAM201  FLJ21865  3'  GGAGCTGCAGGACCCGC    42809    T      TCTTCA
                                GC GGTCCTGC     CTCC
                                || ||||||||     ||||
                                CG CCAGGACG     GAGG
                                 C       TC____
GAM201  FLJ22035  5'  GAAGCCTTGGCAGGACGAGC  44537    G      ____
                                GCT GTCCTGCT    CTTC
                                ||| ||||||||    ||||
                                CGA CAGGACGG    GAAG
                                  G       TTCC
GAM201  FLJ22938  3'  AAGAGCGAGAAGGAGCAGC   45154     G   ____
                                GCTG TCCT    GCTCTT
                                |||| ||||    ||||||
                                CGAC AGGA    CGAGAA
                                  G    AGAG
GAM201  FOXJ1     3'  GAGGGCCCAGGACCAG      7573        __
                                CTGGTCCT  GCTCTT
                                ||||||||  ||||||
                                GACCAGGA  CGGGAG
                                     CC
GAM201  GALNT11   3'  GGGTGGAGCAGAACCA     42006     C     TT
                                TGGT CTGCTC  CACTC
                                |||| ||||||  |||||
                                ACCA GACGAG  GTGGG
                                  A     __
GAM201  GBTS1     3'  GGGAGCCAGCACCAGC      59059       C  _
                                GCTGGT CTG CTCTT
                                |||||| ||| |||||
                                CGACCA GAC GAGGG
                                    C   C
GAM201  GENX-3414 3'  GGGAGCATCTGTAGGACCA   14147         TCTTCA
                                TGGTCCTGC     CTCCC
                                |||||||||     |||||
                                ACCAGGATG     GAGGG
                                      TCTAC_
GAM201  GTSE1     3'  GGAGTTCGGGACCAGC      33140          CT
                                GCTGGTCCTG  CTTC
                                ||||||||||  ||||
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                                CGACCAGGGC  GAGG
                                      TT
GAM201  H2AFY    5'  GGAAGCGAAGAGGCGGGCGGGC 56811       ___    _    A _
           CAGC                    GCTGGT   CCTGC TCTTC CT CC
                                |||||||   ||||| ||||| || ||
                                CGACCG   GGGCG AGAAG GA GG
                                   GGC    G    C A
GAM201  H2AFY    5'  GGAAGCGAAGAGGCGGGCGGGC 56814       ___    _    A _
           CAGC                    GCTGGT   CCTGC TCTTC CT CC
                                |||||||   ||||| ||||| || ||
                                CGACCG   GGGCG AGAAG GA GG
                                   GGC    G    C A
GAM201  HIC2     3'  GGAAGTCGTGTGCAGGAGCCAG 65265       _     TCTTC  _
           C                     GCTGG TCCTGC     ACT CC
                                |||||  ||||||     |||  ||
                                CGACC AGGACG     TGA GG
                                   G     TGTGC   A
GAM201  HSPC019  3'  GAGGGGTAAAACCAGC      25858       CC
                                GCTGGT  TGCTCTTC
                                |||||||  ||||||||
                                CGACCA  ATGGGGAG
                                   AA
GAM201  HUMAGCGB  5'  GGAAGGGGACTGGACCAGC    25232        TG_    CAC
                                GCTGGTCC   CTCTT   TCC
                                |||||||||   |||||   |||
                                CGACCAGG   GGGGA   AGG
                                     TCA    ___
GAM201  IMAGE:4907098 3'  GGGAGCCAGGATCAGC      91663          _
                                GCTGGTCCTG CTCTT
                                ||||||||||| |||||
                                CGACTAGGAC GAGGG
                                      C
GAM201  IMAGE3451454 5'  GGAAACGGTGAGGACCAGC    53872          _  C  CAC
                                GCTGGTCCT GCT TT   TCC
                                |||||||||  |||  ||   |||
                                CGACCAGGA TGG AA   AGG
                                     G   C  ___
GAM201  KCNN1    3'  GAATAAAGCAGGACCCGC     9557     T       C__
                                GC GGTCCTGCT   TTC
                                ||  |||||||||   |||
                                CG CCAGGACGA   AAG
                                 C        AAT
GAM201  KIAA0391  3'  AGGAAATAGGACCAGC      27903          C_
                                GCTGGTCCTG  TCTT
                                ||||||||||  ||||
                                CGACCAGGAT  AGGA
                                      AA
GAM201  KIAA0418  5'  GGAAGTGAGGAGAACCTGC    27558    T   CCTG       _
                                GC GGT    CTCTTCACT CC
                                ||  |||    |||||||||  ||
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                                CG CCA    GAGGAGTGA GG
                                 T  A___        A
GAM201  KIAA0427  3'  GGGAGTGGACGACAGGACC    28721        C  _
                                GGTCCTG TC TTCACTCCC
                                ||||||| || |||||||||
                                CCAGGAC AG AGGTGAGGG
                                    _  C
GAM201  KIAA0515  3'  GGGAACAGGTGGAGACCAGC   63813        _ TG T  TCAC
                                GCTGGTC C  C CT    TCCC
                                ||||||| |  | ||    ||||
                                CGACCAG G  G GA    AGGG
                                    A GT _  CA__
GAM201  KIAA0542  3'  GGAGGCAGGAGCAGC       66087      G     T
                                GCTG TCCTGC CTTC
                                |||| |||||| ||||
                                CGAC AGGACG GAGG
                                  G     _
GAM201  KIAA0638  3'  GAGTGGAGGACCAG        72398         GCTCT
                                CTGGTCCT     TCACTC
                                ||||||||     ||||||
                                GACCAGGA     GGTGAG
                                      _____
GAM201  KIAA0672  3'  GGAAGCAGGACAGC        29412      G      C
                                GCTG TCCTGCT TTC
                                |||| ||||||| |||
                                CGAC AGGACGA AGG
                                  _      _
GAM201  KIAA0773  3'  GGAAATGGAGGACCAG      28056         G  C  CAC
                                CTGGTCCT CT TT   TCC
                                |||||||| || ||   |||
                                GACCAGGA GG AA   AGG
                                    _  T  ___
GAM201  KIAA0820  5'  GGCGAGCAGGGACCAGC     69027         _    T
                                GCTGGTCC TGCTC TC
                                |||||||| ||||| ||
                                CGACCAGG ACGAG GG
                                     G    C
GAM201  KIAA0841  3'  GGGTGAGCAGGAGCA       71393     G       TTC
                                TG TCCTGCTC   ACTC
                                || ||||||||   ||||
                                AC AGGACGAG   TGGG
                                 G       ___
GAM201  KIAA0864  5'  GAAGACAAGGCCAGC       63249        C  C
                                GCTGGTC TG TCTTC
                                ||||||| || |||||
                                CGACCGG AC AGAAG
                                    A  _
GAM201  KIAA0930  3'  GAGAGCGGAAGGAGCAGC    70543      G    ___
                                GCTG TCCT   GCTCTT
                                |||| ||||   ||||||
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                                CGAC AGGA   CGAGAG
                                  G    AGG
GAM201  KIAA0931  3'  GAGCCAGCAGGAGCAGC     67420      G      CTTCA
                                GCTG TCCTGCT     CTC
                                |||| |||||||     |||
                                CGAC AGGACGA     GAG
                                  G      CC___
GAM201  KIAA0939  3'  AGTCAGAGCAGGCCAGC     62004       T       TC
                                GCTGG CCTGCTCT  ACT
                                ||||| ||||||||  |||
                                CGACC GGACGAGA  TGA
                                  _       C_
GAM201  KIAA1030  3'  GGAAGTGAAACCCCCAGGGACC 93337          GCTC___     _
           AGC                    GCTGGTCCT      TTCACT CC
                                |||||||||       |||||| ||
                                CGACCAGGG       AAGTGA GG
                                     ACCCCCA     A
GAM201  KIAA1045  3'  GAAAGCACGAAGGAGCAGC    71051      G    _____   C
                                GCTG TCCT    GCT TTC
                                |||| ||||    ||| |||
                                CGAC AGGA    CGA AAG
                                  G    AGCA  _
GAM201  KIAA1056  3'  AGTGGGGAGGAGCCAGC     29690       TC  G
                                GCTGG  CT CTCTTCACT
                                |||||  || |||||||||
                                CGACC  GA GAGGGGTGA
                                  __  G
GAM201  KIAA1115  5'  AGGAGCTTCAGGACCAGC    30017          ___
                                GCTGGTCCT   GCTCTT
                                |||||||||   ||||||
                                CGACCAGGA   CGAGGA
                                     CTT
GAM201  KIAA1194  5'  GGGAACAAAGAGCAGCGACTA  95939       _       CAC
                                TGGTC CTGCTCTT   TCCC
                                ||||| ||||||||   ||||
                                ATCAG GACGAGAA   AGGG
                                  C       ACA
GAM201  KIAA1204  3'  GAAGTTATTACAGGGCCAGC   69217          CT_____
                                GCTGGTCCTG     CTTC
                                ||||||||||     ||||
                                CGACCGGGAC     GAAG
                                     ATTATT
GAM201  KIAA1228  3'  GGAGTGAAGCCACCA       65045      CCT   CT
                                TGGT   GCT  TCACTCC
                                ||||   |||  |||||||
                                ACCA   CGA  AGTGAGG
                                  C__   __
GAM201  KIAA1535  3'  GAAGGGCAGGCCAGC       79412       T
                                GCTGG CCTGCTCTTC
                                ||||| ||||||||||
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                                CGACC GGACGGGAAG
                                     _
GAM201  KIAA1649 3' GGGAGTGAAGAGAATCCAG   50277     TCCTG
                                CTGG    CTCTTCACTCCC
                                ||||    ||||||||||||
                                GACC    GAGAAGTGAGGG
                                  TAA__
GAM201  KIAA1649 3' GGGAGTGAAGAGAATCCAG   66982     TCCTG
                                CTGG    CTCTTCACTCCC
                                ||||    ||||||||||||
                                GACC    GAGAAGTGAGGG
                                  TAA__
GAM201  KIAA1822 3' GAAGGTGCAAGAACAGC     67567     G  C  _
                                GCTG TC TGC TCTTC
                                |||| || ||| |||||
                                CGAC AG ACG GGAAG
                                  A  A   T
GAM201  KIAA1877 3' GGGAGTGAGGTGGGACCAG   66173       TG  CT
                                CTGGTCC  CT  TCACTCCC
                                |||||||  ||  ||||||||
                                GACCAGG  GG  AGTGAGGG
                                    GT  __
GAM201  KIAA1950 5' GAGAGCGTCCAGGACCAG    92591       _____
                                CTGGTCCT    GCTCTT
                                ||||||||    ||||||
                                GACCAGGA    CGAGAG
                                     CCTG
GAM201  KIAA1958 5' GGAGTAGATGGACCAGC     81905       TGC   TC
                                GCTGGTCC   TCT  ACTCC
                                ||||||||   |||  |||||
                                CGACCAGG   AGA  TGAGG
                                    T__   __
GAM201  KIAA1958 3' GGAGTTCAAGATCAGGACCA  81906       C    C_
                                TGGTCCTG TCTT  ACTCC
                                |||||||| ||||  |||||
                                ACCAGGAC AGAA  TGAGG
                                     T    CT
GAM201  KLHL6    3' AGTTAGAGCAGGCCCAGC    55298      T       TC
                                GCTGG CCTGCTCT  ACT
                                ||||| ||||||||  |||
                                CGACC GGACGAGA  TGA
                                   C       T_
GAM201  LANCL2   3' GGACGGACAGGACCAGC     38001         C   TCAC
                                GCTGGTCCTG TCT    TCC
                                |||||||||| |||    |||
                                CGACCAGGAC AGG    AGG
                                      _  C___
GAM201  MGC11296 5' GAAAATGAGGGGAGCAGC    50377     G   G  ___
                                GCTG TCCT CTC   TTC
                                |||| |||| |||   |||
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                                CGAC AGGG GAG   AAG
                                  G   _  TAA
GAM201  MGC13064  3'  GGGAATGGACTGCAGAAC    50353    C   TC   C
                                GT CTGC  TTCA TCCC
                                || ||||  |||| ||||
                                CA GACG  AGGT AGGG
                                 A   TC   A
GAM201  MGC14407  3'  GGAGTTCGGGACCAGC      51878         CTCTTC
                                GCTGGTCCTG     ACTCC
                                ||||||||||     |||||
                                CGACCAGGGC     TGAGG
                                      T_____
GAM201  MGC15437  3'  GGAGTGTGCCCAGACCAGC   51783       C  CTCTT
                                GCTGGTC TG    CACTCC
                                ||||||| ||    ||||||
                                CGACCAG AC    GTGAGG
                                   _ CCGT_
GAM201  MGC26954  5'  GGAAGCGAAGGGCACCA     58837     CCT     A _
                                TGGT   GCTCTTC CT CC
                                ||||   ||||||| || ||
                                ACCA   CGGGAAG GA GG
                                  ___      C  A
GAM201  MRF2      5'  GAAGAGAGGACCAGC       76520         G
                                GCTGGTCCT CTCTTC
                                ||||||||| ||||||
                                CGACCAGGA GAGAAG
                                          _
GAM201  MRP63     3'  GAAAATGAGCCTTTGGACCAGT 43808        T___   ___
                                GCTGGTCC   GCTC   TTC
                                ||||||||   ||||   |||
                                TGACCAGG   CGAG   AAG
                                     TTTC   TAA
GAM201  OSBPL2    3'  AGTGAAGAGTTTCAG      29199     TCCT
                                CTGG   GCTCTTCACT
                                ||||   ||||||||||
                                GACT   TGAGAAGTGA
                                  T___
GAM201  OSBPL2    3'  AGTGAAGAGTTTCAG      57850     TCCT
                                CTGG   GCTCTTCACT
                                ||||   ||||||||||
                                GACT   TGAGAAGTGA
                                  T___
GAM201  PGLYRP    3'  GGAGGGCAGACCCAGC     53577      TC
                                GCTGG  CTGCTCTTC
                                |||||  |||||||||
                                CGACC  GACGGGAGG
                                   CA
GAM201  PHF7      3'  GGAAGCAGGGCCAGC      33224          C
                                GCTGGTCCTGCT TTC
                                |||||||||||| |||
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                                CGACCGGGACGA AGG
                                           _
GAM201  PILR(ALPHA) 3'  GGAGTTCAGGGCCAGC      25547          CT
                                GCTGGTCCTG  CTTC
                                ||||||||||  ||||
                                CGACCGGGAC  GAGG
                                      TT
GAM201  PTRF    3'  GGAGTTCGGGACCAGC      63504          CT
                                GCTGGTCCTG  CTTC
                                ||||||||||  ||||
                                CGACCAGGGC  GAGG
                                      TT
GAM201  RASSF2  3'  GAGTGAAGAAATTGGCCA    28434       CTGC
                                TGGTC   TCTTCACTC
                                |||||   |||||||||
                                ACCGG   AGAAGTGAG
                                   TTAA
GAM201  RNF9    5'  GGAAGCCATAGCAGCAGGACCA 22281           _  TCAC__
           GC                     GCTGGTCCTGCT CT     TCC
                                ||||||||||||  ||      |||
                                CGACCAGGACGA GA     AGG
                                      C  TACCGA
GAM201  RNF9    5'  GGAAGCCATAGCAGCAGGACCA 53413           _  TCAC__
           GC                     GCTGGTCCTGCT CT     TCC
                                ||||||||||||  ||      |||
                                CGACCAGGACGA GA     AGG
                                      C  TACCGA
GAM201  SBBI31  3'  GGAGTGAAGCGCCCACCCAGC  25877       TCCT  T
                                GCTGG   GC CTTCACTCC
                                |||||   ||  |||||||||
                                CGACC   CG GAAGTGAGG
                                   CACC  C
GAM201  SDC3    3'  GAGTTCAGTGAGGACCAGC   27753         _  CTTC
                                GCTGGTCCT GCT   ACTC
                                |||||||||  |||   ||||
                                CGACCAGGA TGA   TGAG
                                      G   CT__
GAM201  SLC37A1  5'  GGAAGGGGACAAGACCCAGC  38565       _  C  C    AC
                                GCTGG TC TG TCTTC  TCC
                                |||||  ||  ||  |||||  |||
                                CGACC AG AC AGGGG  AGG
                                   C  A  _    A_
GAM201  SMUG1   5'  GGGATGGGGAGCTGGACCAGC  26693         T       C
                                GCTGGTCC GCTCTTCA TCCC
                                ||||||||  ||||||||  ||||
                                CGACCAGG CGAGGGGT AGGG
                                      T       _
GAM201  SNFT    3'  GGAGCTCCAGGACCAGC     37899          CTCTTCA
                                GCTGGTCCTG      CTCC
                                ||||||||||      ||||
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                                CGACCAGGAC      GAGG
                                      CTC____
GAM201  SPEC1    5'  GGAGTGAAGCTGGAACCA    39612      _ T  CT
                                TGGT CC GCT  TCACTCC
                                |||| || |||  |||||||
                                ACCA GG CGA  AGTGAGG
                                  A  T  __
GAM201  STIM2    3'  GGGAGCTCTGGAGCAGGACCAG 40477            TCA_
          C                      GCTGGTCCTGCTCT   CTCCC
                                |||||||||||||   |||||
                                CGACCAGGACGAGG   GAGGG
                                       TCTC
GAM201  STX5A    3'  GGGAGCAGAGGCCAGC      12044        _
                                GCTGGTC CTGCTCTT
                                ||||||| ||||||||
                                CGACCGG GACGAGGG
                                    A
GAM201  SYNCOILIN 5'  GAAGCAGAAGGAGCAGC     47896      G   G  _
                                GCTG TCCT CT CTTC
                                |||| |||| || ||||
                                CGAC AGGA GA GAAG
                                  G   A  C
GAM201  TIAM2    3'  GGGAGTGAAGTGCACCACGC   24933    _   CCT  T
                                GC TGGT   GC CTTCACTCCC
                                || ||||   || ||||||||||
                                CG ACCA   CG GAAGTGAGGG
                                 C   ___  T
GAM201  XYLT1    3'  GGTCAAAGCAGGATCAGC    77851          C  C
                                GCTGGTCCTGCT TT ACT
                                |||||||||||| || |||
                                CGACTAGGACGA AA TGG
                                       _  C
GAM201  ZF       3'  AAGAGACGGGACCAGC      41084          _
                                GCTGGTCCTG CTCTT
                                |||||||||| |||||
                                CGACCAGGGC GAGAA
                                      A
GAM201  ZNF384   5'  GGGAACGAACAAGGACCAGT   55985        GCTC   AC
                                GCTGGTCCT    TTC  TCCC
                                |||||||||    |||  ||||
                                TGACCAGGA    AAG  AGGG
                                     AC__    CA
GAM201  LOC115129 3'  GAAGCCCCAGGACCAGC     73233         CT_
                                GCTGGTCCTG   CTTC
                                ||||||||||   ||||
                                CGACCAGGAC   GAAG
                                      CCC
GAM201  LOC119587 3'  GGGAGTGAGAGAACTCAGC   73997      TCCTG    T
                                GCTGG    CTCT CACTCCC
                                |||||    |||| |||||||
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                                CGACT    GAGA GTGAGGG
                                  CAA__   _
GAM201   LOC124411 3'  GATAGAGCAGGACAGC      74285      G       _
                                GCTG TCCTGCTCT TC
                                |||| ||||||||| ||
                                CGAC AGGACGAGA AG
                                  _       T
GAM201   LOC124470 3'  GGGAGCAGAGGGGCAGGACCTG 75639    T          A_
           C                     GC GGTCCTGCTCTTC  CTCCC
                                || ||||||||||||  |||||
                                CG CCAGGACGGGGAG  GAGGG
                                 T           AC
GAM201   LOC124590 3'  AGGAGCAAGGACCAGT      75650         _
                                GCTGGTCCT GCTCTT
                                ||||||||| ||||||
                                TGACCAGGA CGAGGA
                                     A
GAM201   LOC124739 5'  GAGGAACAGGAGCAGC      74327      G    C
                                GCTG TCCTG TCTTC
                                |||| ||||| |||||
                                CGAC AGGAC AGGAG
                                  G    A
GAM201   LOC129831 5'  AGCAAAGAGCAGTGAGGC    74891     GG _      CA
                                GCT  TC CTGCTCTT  CT
                                |||  || ||||||||  ||
                                CGG  AG GACGAGAA  GA
                                  __ T       AC
GAM201   LOC130564 5'  AGCAAAGAGCAGACTCGGC   75747     _  C      CA
                                GCTG GTC TGCTCTT  CT
                                |||| ||| |||||||  ||
                                CGGC CAG ACGAGAA  GA
                                  T  _      AC
GAM201   LOC130813 3'  GGGAGCATGTCAGGACCA    75774        _ TCTTCA
                                TGGTCCTG C     CTCCC
                                |||||||| |     |||||
                                ACCAGGAC G     GAGGG
                                     T TAC___
GAM201   LOC143310 3'  GGAGTGGGCCTGAGGAGCAGC  76536     G   GCTC
                                GCTG TCCT    TTCACTCC
                                |||| ||||    ||||||||
                                CGAC AGGA    GGGTGAGG
                                  G    GTCC
GAM201   LOC143785 5'  GGGAGCAGCAAGCCAGC     76607       C__
                                GCTGGT   CTGCTCTT
                                ||||||   ||||||||
                                CGACCG   GACGAGGG
                                   AAC
GAM201   LOC145371 3'  GGAAATGAAGGACTAGC     77157         GCTCT  C_
                                GCTGGTCCT    TCA  TCC
                                |||||||||    |||  |||
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                                CGATCAGGA    AGT  AGG
                                     _____  AA
GAM201   LOC145601 3'  GGAGCGGCAGGACCTGC    83367    T       CTTCA
                                GC GGTCCTGCT    CTCC
                                || |||||||||    ||||
                                CG CCAGGACGG    GAGG
                                 T       C____
GAM201   LOC148183 3'  GAGAGTTTCAGGACCAG    84119         ___
                                CTGGTCCTG   CTCTT
                                |||||||||   |||||
                                GACCAGGAC   GAGAG
                                      TTT
GAM201   LOC148490 5'  GGAGCGTGAGGAGCAG     78886          __
                                CTGCTCTTCAC  TCC
                                ||||||||||  |||
                                GACGAGGAGTG  AGG
                                       CG
GAM201   LOC148697 5'  GAGTGAAGAGCCGGAGC    78925    TGG   T
                                GC   TCC GCTCTTCACTC
                                ||   ||| ||||||||||
                                CG   AGG CGAGAAGTGAG
                                 ___  C
GAM201   LOC148758 3'  GAGAACCCCAGACAGGGACCAG 78970         GC   TCA___
            C                    GCTGGTCCT  TCT     CTC
                                |||||||||  |||     |||
                                CGACCAGGG  AGA     GAG
                                      AC   CCCCAA
GAM201   LOC148864 5'  AAGAGCTCGGACCAGC     79040        T_
                                GCTGGTCC  GCTCTT
                                ||||||||  ||||||
                                CGACCAGG  CGAGAA
                                     CT
GAM201   LOC148918 5'  GGAATAGTGTTAGGATCA    79077        _ T  TCAC
                                TGGTCCTG C CT    TCC
                                |||||||| | ||    |||
                                ACTAGGAT G GA    AGG
                                     T T  TA__
GAM201   LOC149478 5'  GAAGAGCAGAACCGGC     79379       C
                                GCTGGT CTGCTCTTC
                                ||||||  |||||||||
                                CGGCCA GACGAGAAG
                                   A
GAM201   LOC149577 3'  GGAAGCGACGTGGCAGGGCCAG 84518           CT_  A  _
            C                    GCTGGTCCTGCT   TC CT CC
                                ||||||||||||   || || ||
                                CGACCGGGACGG   AG GA GG
                                       TGC  C  A
GAM201   LOC149706 5'  GATGGGCAGGACAAGC     84643     G       T
                                GCT GTCCTGCTC TC
                                ||| |||||||||  ||
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                                CGA CAGGACGGG AG
                                  A        T
GAM201   LOC150343 5'  GGGAGGTGTGGCGGACCAGC   79676         T   CTTCA
                                GCTGGTCC GCT     CTCCC
                                |||||||| |||     |||||
                                CGACCAGG CGG     GAGGG
                                     _   TGTG_
GAM201   LOC150481 3'  GGAAGTGATGACCCAGGAGCAG 79890      G     C_  T     _
           C                     GCTG TCCTG  TC TCACT CC
                                |||| |||||  || ||||| ||
                                CGAC AGGAC  AG AGTGA GG
                                  G     CC  T     A
GAM201   LOC151429 3'  GGGAGTAGACGGCAAAACCTGC 85359    T   CC    C TC
                                GC GGT  TGCT T  ACTCCC
                                || |||  |||| |  ||||||
                                CG CCA  ACGG A  TGAGGG
                                 T   AA    C GA
GAM201   LOC152765 5'  GGGAGGTGGGCAGGGCCA    80661           TTCA
                                TGGTCCTGCTC    CTCCC
                                ||||||||||    |||||
                                ACCGGGACGGG    GAGGG
                                       TG__
GAM201   LOC153546 5'  GAGAGGGTCGCAGGACCG    80886         TC   A
                                TGGTCCTGC  TTC CTC
                                |||||||||  ||| |||
                                GCCAGGACG  GGG GAG
                                     CT   A
GAM201   LOC153688 3'  GAGTGACGGGGAGCAGC     86108      G    GCT T
                                GCTG TCCT   C TCACTC
                                |||| ||||   | ||||||
                                CGAC AGGG   G AGTGAG
                                  G    ___ C
GAM201   LOC157247 5'  GGAGTTCAGGACTAGC      81374           CT
                                GCTGGTCCTG  CTTC
                                ||||||||||  ||||
                                CGATCAGGAC  GAGG
                                       TT
GAM201   LOC157918 3'  GAGGTCAGCAGGACCCGC    86645    T        __
                                GC GGTCCTGCT  CTTC
                                || |||||||||  ||||
                                CG CCAGGACGA  GGAG
                                 C        CT
GAM201   LOC157919 5'  GAGGTCAGCAGGACCCGC    81634    T        __
                                GC GGTCCTGCT  CTTC
                                || |||||||||  ||||
                                CG CCAGGACGA  GGAG
                                 C        CT
GAM201   LOC158191 3'  AGTGATGACCCAGGAGCAGC   81770      G     C_  T
                                GCTG TCCTG  TC TCACT
                                |||| |||||  || |||||
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                                CGAC AGGAC  AG AGTGA
                                  G    CC  T
GAM201  LOC164714 5'  GAAGCAAGCCCAGGGACCAG  87230       ___  __
                                CTGGTCCT  GCT  CTTC
                                ||||||||  |||  ||||
                                GACCAGGG  CGA  GAAG
                                    ACC  AC
GAM201  LOC166793 5'  AGTGAAGAAGTCGTCAGT   59225     TCCT  _
                                GCTGG   GCT CTTCACT
                                |||||   ||| |||||||
                                TGACT   TGA GAAGTGA
                                  GC__  A
GAM201  LOC169693 5'  GAAGCAGAGGAGCAGC     87292     G   G  _
                                GCTG TCCT CT CTTC
                                |||| |||| || ||||
                                CGAC AGGA GA GAAG
                                  G   _ C
GAM201  LOC169696 5'  GGAAGTGAAAGGGGACGAGC  87296    G    G  C    _
                                GCT GTCCT CT TTCACT CC
                                ||| ||||| || |||||| ||
                                CGA CAGGG GA AAGTGA GG
                                 G    _ _    A
GAM201  LOC196540 3'  GGAGCATGGACACAGGACCAG  89636       C_  TCA
                                CTGGTCCTG  TCT  CTCC
                                |||||||||  |||  ||||
                                GACCAGGAC  AGG  GAGG
                                    AC  TAC
GAM201  LOC197003 3'  AGTGAAGGTCAAGACCAG    87866      C  CT
                                CTGGTC TG  CTTCACT
                                ||||||  ||  |||||||
                                GACCAG AC  GAAGTGA
                                   A  TG
GAM201  LOC200473 3'  AGTGCAGAGCCAGGACCAGC  90072        _   T
                                GCTGGTCCTG CTCT CACT
                                |||||||||| |||| ||||
                                CGACCAGGAC GAGA GTGA
                                    C   C
GAM201  LOC201161 3'  GGAATGATTGGGGCCAGC    88128       GCTCT  C
                                GCTGGTCCT    TCA TCC
                                |||||||||    ||| |||
                                CGACCGGGG    AGT AGG
                                    TT___  A
GAM201  LOC202459 3'  GAATGAAGAGCAGCAGT     59253     GTC       C
                                GCTG  CTGCTCTTCA TC
                                ||||  |||||||||| ||
                                TGAC  GACGAGAAGT AG
                                  ___       A
GAM201  LOC203350 3'  GAGAGCCAAGGACCAGC     90568       __
                                GCTGGTCCT  GCTCTT
                                |||||||||  ||||||
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                                CGACCAGGA  CGAGAG
                                     AC
GAM201   LOC203636 3'  GAGTGAAGGAGTCACCCGC   89426    T  CCT   _
                                GC GGT   GCTC TTCACTC
                                || |||   |||| |||||||
                                CG CCA   TGAG AAGTGAG
                                 C  C__   G
GAM201   LOC205251 5'  GGGTGGAACAGGCCCAGC    90672      T   CTC
                                GCTGG CCTG   TTCACTC
                                ||||| ||||   |||||||
                                CGACC GGAC   AGGTGGG
                                   C   A__
GAM201   LOC219511 5'  TGGTAGCAGGGCCAGC      92821          CT
                                GCTGGTCCTGCT  TCA
                                ||||||||||||  |||
                                CGACCGGGACGA  GGT
                                       T_
GAM201   LOC219920 5'  GGGAGCCAGGGACCAGC     93317         __
                                GCTGGTCCT  GCTCTT
                                |||||||||  ||||||
                                CGACCAGGG  CGAGGG
                                     AC
GAM201   LOC219920 5'  GGGCCAGGGCAGGACCAGC   93318           TCACT
                                GCTGGTCCTGCTCT    CCC
                                ||||||||||||||    |||
                                CGACCAGGACGGGA    GGG
                                      CC___
GAM201   LOC253039 3'  GGAAACCAAGAAAGACCAGC  96157       CTGC   CAC_
                                GCTGGTC   TCTT   TCC
                                |||||||   ||||   |||
                                CGACCAG   AGAA   AGG
                                    AA__   CCAA
GAM201   LOC256715 3'  GGAGACAGGACCAGC       97273          C
                                GCTGGTCCTG TCTTC
                                |||||||||| |||||
                                CGACCAGGAC AGAGG
                                          _
GAM201   LOC257106 5'  GAAGCAGCAGGAGCAGC     95388      G     _
                                GCTG TCCTGCT CTTC
                                |||| ||||||| ||||
                                CGAC AGGACGA GAAG
                                  G      C
GAM201   LOC257408 5'  GGAGTGAAGAGCGGTGGGGAAC 96070      _  ____
           CAG                    CTGGT CCT   GCTCTTCACTCC
                                |||||| |||   ||||||||||||
                                GACCA GGG   CGAGAAGTGAGG
                                  A  GTGG
GAM201   LOC51161  5'  GGGAGTGAGAGGAACCAG    32515      _  GCTC
                                CTGGT CCT   TTCACTCCC
                                ||||| |||   |||||||||
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                                GACCA GGA    GAGTGAGGG
                                  A  ____
GAM201  LOC90019  5' GGAAGTGATGGGACCGC     56765    T      CTCT    _
                                GC GGTCCTG    TCACT CC
                                || |||||||    ||||| ||
                                CG CCAGGGT    AGTGA GG
                                 _     ____    A
GAM201  LOC90670  3' GGAAGTGAAGGGTACAAC    63741    CC         _
                                GT  TGCTCTTCACT CC
                                ||  ||||||||||| ||
                                CA  ATGGGAAGTGA GG
                                 AC          A
GAM201  LOC91582  3' GATGGCGATGCAGGACCAGC   66538          _ T   C
                                GCTGGTCCTGC TC TCA TC
                                |||||||||| || ||| ||
                                CGACCAGGACG AG GGT AG
                                       T  C  _
GAM201  LOC91828  5' GGAGCTCAGGACCAGT      67277          CT
                                GCTGGTCCTG  CTTC
                                |||||||||  ||||
                                TGACCAGGAC  GAGG
                                      TC
GAM201  LOC92017  5' GGAGTGAAGCCCACCAGC    67893       CCT   CT
                                GCTGGT   GCT  TCACTCC
                                ||||||   |||  |||||||
                                CGACCA   CGA  AGTGAGG
                                   CC_   __
GAM201  LOC92078  3' GGAGGGCAGGGCCAGC      67984
                                GCTGGTCCTGCTCTTC
                                ||||||||||||||||
                                CGACCGGGACGGGAGG

GAM201  LOC92492  5' AAGAGCATGGAGAGCCAGC   69524        ___ _
                                GCTGGT   CC TGCTCTT
                                ||||||   || |||||||
                                CGACCG   GG ACGAGAA
                                   AGA  T
GAM201  LOC93259  5' GGAGTGGGCAAGACCA      71823       C    CTT
                                TGGTC TGCT   CACTCC
                                ||||| ||||   ||||||
                                ACCAG ACGG   GTGAGG
                                  A   ___
GAM202  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM202  GCKR     3'  ATTTCAGAAATAAAATGAAATG 7635         C   CACTG
                                CATTTCA TTT     TCTGAAAT
                                ||||||| |||     ||||||||
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                                GTAAAGT AAA     AGACTTTA
                                    A   TAA__
GAM202  GLO1     3'  TTTCAGAAGAAAGGAAA     22001      A     ACTG
                                TTTC CTTTC    TCTGAAA
                                |||| |||||    |||||||
                                AAAG GAAAG    AGACTTT
                                  _     A___
GAM202  JTB      3'  TCAGACAGTGAAAGTGAAATG  21962
                                CATTTCACTTTCACTGTCTGA
                                ||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACT

GAM202  LUZP1    3'  TGGGCAACAAGAGTGAAATG   53302          CAC
                                CATTTCACTTT   TGTCTG
                                ||||||||||   ||||||
                                GTAAAGTGAGA   ACGGGT
                                      ACA
GAM202  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM202  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM202  COASTER  3'  TTTTAGCAGTGAAAATGAA   31452      C       T
                                TTCA TTTCACTG CTGAAA
                                |||| |||||||| ||||||
                                AAGT AAAGTGAC GATTTT
                                  A       _
GAM202  DJ971N18.2 3'  CAGTACCTGAAAGTGAAA    40958          CT  _
                                TTTCACTTTCA  GT CTG
                                ||||||||||  || |||
                                AAAGTGAAAGT  CA GAC
                                      C_  T
GAM202  DKFZP586M1120 3'  AGTAGTGAAAATGAAA      48451       C       T
                                TTTCA TTTCACTG CT
                                ||||| |||||||| ||
                                AAAGT AAAGTGAT GA
                                   A       _
GAM202  ENDOFIN  3'  TTCAAACAGCAAAAAAGTGGGG 28389    TT     CA__    C
                                T  CACTTT    CTGT TGAA
                                |  ||||||    |||| ||||
                                G  GTGAAA    GACA ACTT
                                 GG     AAAC    A
GAM202  FLJ14909 3'  TTCATGAATGTGAAATG     51695         T    CTGTC
                                CATTTCAC TTCA     TGAA
                                |||||||| ||||     ||||
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                                GTAAAGTG AAGT    ACTT
                                    T  _____
GAM202  FLJ20323  3'  TTTCTGACAAGTGAAA     38661       _  T
                                TTTCACT GTC GAAA
                                ||||||| ||| ||||
                                AAAGTGA CAG CTTT
                                    A  T
GAM202  FLJ23510  3'  TCAGACAGTGACTGAAATG   45289       CTT
                                CATTTCA  TCACTGTCTGA
                                |||||||  ||||||||||
                                GTAAAGT  AGTGACAGACT
                                    C__
GAM202  GPCR150   5'  ATTGAAGGCAGTAAAAGTGAAA 26876         C     GA
          T                      ATTTCACTTT ACTGTCT  AAT
                                ||||||||| |||||||  |||
                                TAAAGTGAAA TGACGGA  TTA
                                      A      AG
GAM202  HSPC019   3'  ATTTCAATCAGATGAAAGTGA  25856       _  TC
                                TCACTTTCA CTG  TGAAAT
                                ||||||||| |||  ||||||
                                AGTGAAAGT GAC  ACTTTA
                                     A  TA
GAM202  KIAA0574  3'  TTTCCTGTGAAAGGAAAT    69285      A     TGTCT
                                ATTTC CTTTCAC    GAAA
                                ||||| |||||||    ||||
                                TAAAG GAAAGTG    CTTT
                                   _      TC___
GAM202  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAA
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A      CT
GAM202  MGC27044  5'  TTGGTGTTGAAAGTGAAATG  58675          CTGT TG
                                CATTTCACTTTCA   C  A
                                ||||||||||||   |  |
                                GTAAAGTGAAAGT   G  T
                                       TGT_ GT
GAM202  MRPL44    3'  GAGAGCGAAAGTGAGAT    43320         A  G
                                ATTTCACTTTC CT TC
                                |||||||||| || ||
                                TAGAGTGAAAG GA AG
                                     C  G
GAM202  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM202  PORIMIN   3'  TCAGAGGGCCAAAGTGAA   53608       CA  G
                                TTCACTTT  CT TCTGA
                                ||||||||  || |||||
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                                AAGTGAAA  GG AGACT
                                    CC  G
GAM202  PRTD-NY3 3'  TCATTGCAATAAGTGAAATG   48151         TCAC   C_
                                CATTTCACTT   TGT  TGA
                                ||||||||||   |||  |||
                                GTAAAGTGAA   ACG  ACT
                                   TA__   TT
GAM202  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                    A    TC
GAM202  SFXN2    3'  TCAGGGGAAAAAAGTGAAA   73954        CACTG
                                TTTCACTTT    TCTGA
                                |||||||||    |||||
                                AAAGTGAAA    GGACT
                                   AAAGG
GAM202  SGT1     3'  ATTTCAGACATGGTGAAACTG  21992    C     __
                                CA TTTCACT  GTCTGAAAT
                                || |||||||  |||||||||
                                GT AAAGTGG  CAGACTTTA
                                 C      TA
GAM202  UPK3     3'  TTCAGGGAAGGTGAAA      22722         ACTG
                                TTTCACTTTC   TCTGAA
                                ||||||||||   ||||||
                                AAAGTGGAAG   GGACTT
                                    ____
GAM202  ZMPSTE24  3'  ATTTCAGTTCTGCAAAAGTGAA 19594        CACTGT_
           A                     TTTCACTTT     CTGAAAT
                                 |||||||||     |||||||
                                 AAAGTGAAA     GACTTTA
                                    ACGTCTT
GAM202  LOC123283 3'  TTCATCGAGAAAGTGAAA    76013         AC  TC
                                TTTCACTTTC  TG  TGAA
                                ||||||||||  ||  ||||
                                AAAGTGAAAG  GC  ACTT
                                   A_  T_
GAM202  LOC145674 5'  ATTTCTGACTTGAAGTGAAAT  63200        T  CT   T
                                ATTTCACTT CA  GTC GAAAT
                                ||||||||| ||  ||| |||||
                                TAAAGTGAA GT  CAG CTTTA
                                   _ T_   T
GAM202  LOC202908 5'  CAGAGGGGTGACAGTGAAA   89227       T   _ G
                                TTTCACT TCAC T TCTG
                                ||||||| |||| | ||||
                                AAAGTGA AGTG G AGAC
                                    C   G G
GAM202  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
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                                GTAAAGTGAA GTGACA
                                          _
GAM202  LOC255338 5'  TTTGGACAAAAGTGAA     95935       CAC   TG
                                TTCACTTT  TGTC  AA
                                ||||||||  ||||  ||
                                AAGTGAAA  ACAG  TT
                                    ___   GT
GAM203  ASPH    3'  CATCATTTTGAAAGG      50629     TA
                                CCTT  TCAGGATGATG
                                ||||  ||||||||||
                                GGAA  AGTTTTACTAC
                                  __
GAM203  ASPH    3'  CATCATTTTGAAAGG      50616     TA
                                CCTT  TCAGGATGATG
                                ||||  ||||||||||
                                GGAA  AGTTTTACTAC
                                  __
GAM203  DDX6    5'  CTGCATTGCAATAAAGG     15287       CAGGAT
                                CCTTTAT     GATGCAG
                                |||||||     |||||||
                                GGAAATA     TTACGTC
                                   ACG___
GAM203  TRIP15   3'  CTGCAGTGTAGTAAAGGTTT  14893         CAGGATGA
                                AAACCTTTAT      TGCAG
                                ||||||||||      |||||
                                TTTGGAAATG      ACGTC
                                     ATGTG___
GAM203  FLJ13593  3'  CAGACCTGGCAAAGGTTT    45503       AT   A_
                                AAACCTTT  CAGG  TG
                                ||||||||  ||||  ||
                                TTTGGAAA  GTCC  AC
                                    CG    AG
GAM203  FLJ21988  3'  CTGCATCATCCCCCAGCCAGGT 42554   A   TTATCA_
          CC                      A ACCT      GGATGATGCAG
                                | ||||      ||||||||||
                                C TGGA      CCTACTACGTC
                                 C    CCGACCC
GAM203  HIRIP5   5'  CTGCATCAGTTTGTACAAAG  31653     AT_   A
                                CTTT   CAGG TGATGCAG
                                ||||   |||| ||||||||
                                GAAA   GTTT ACTACGTC
                                  CAT    G
GAM203  KIAA0547  3'  TGCATCATCCCAGGTTT     28917      TTATCA
                                AAACCT     GGATGATGCA
                                ||||||     ||||||||||
                                TTTGGA     CCTACTACGT
                                   C_____
GAM203  KIAA1223  3'  CTGCAGTTCCCTGATAAA    71145       ATGA
                                TTTATCAGG    TGCAG
                                |||||||||    |||||
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                                AAATAGTCC   ACGTC
                                     CTTG
GAM203  KIAA1951  3'  CTGCATCACCCTGGTG     73759       A
                                TATCAGG TGATGCAG
                                ||||||| ||||||||
                                GTGGTCC ACTACGTC
                                    C
GAM203  PFDN1    3'  CTGCATCACCCTGAGCCCCATT 10511     CCTTTA    A
           TG                    CAAA     TCAGG TGATGCAG
                                ||||     ||||| |||||||||
                                GTTT     AGTCC ACTACGTC
                                  ACCCCG    C
GAM203  SLC22A6  3'  CATCATTAAAAGGTTTG     16570        ATCAG
                                CAAACCTTT    GATGATG
                                |||||||||    |||||||
                                GTTTGGAAA    TTACTAC
                                     A____
GAM203  LOC90835  3'  CATTTTCCCCAATAAAGGTCTG 64127    A      CA_  T
                                CA ACCTTTAT   GGA GATG
                                || ||||||||   ||| ||||
                                GT TGGAAATA   CCT TTAC
                                 C       ACC   T
GAM203  LOC92218  3'  CTGCACTTTCTTGATAAATATT 68505     CC        TGA
           TG                    CAAA  TTTATCAGGA   TGCAG
                                ||||  ||||||||||   |||||
                                GTTT  AAATAGTTCT   ACGTC
                                  AT        TTC
GAM204  MMP20    3'  TCCAAATCAACACAATGCAC   16484          CAGGA
                                GTGCATTGTGTTG    TTGGG
                                ||||||||||||    |||||
                                CACGTAACACAAC    AACCT
                                       TA___
GAM204  PIM2     3'  TCCCAATCCTACAAAGGAGC   59991    A  GTG   C
                                GC TT   TTG AGGATTGGGA
                                || ||   ||| ||||||||||
                                CG AG   AAC TCCTAACCCT
                                 _  GA_   A
GAM204  RXRA     3'  CCCAATCCTTAGCAATGC    11405       GTTGC
                                GCATTGT    AGGATTGGG
                                |||||||    |||||||||
                                CGTAACG    TCCTAACCC
                                    AT___
GAM204  BRAG     3'  TCCCAATTCCAAAACACAATGC 29477          GCA
           AC                    GTGCATTGTGTT   GGATTGGGA
                                ||||||||||||  |||||||||
                                CACGTAACACAA   CTTAACCCT
                                       AAC
GAM204  DKFZp547O146 5'  CCCAATCCCCCAACAC      39564       CA
                                GTGTTG  GGATTGGG
                                ||||||  ||||||||
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                                CACAAC  CCTAACCC
                                   CC
GAM204  KIAA1762  3'  TCCCAATCCCCACAGACACACA 63792     CAT     GCA__
            C                    GTG   TGTGTT    GGATTGGGA
                                 |||   ||||||    |||||||||
                                 CAC   ACACAG    CCTAACCCT
                                  ___     ACACC
GAM204  LOC145820 3'  CCCAATCCTTAAGCAATCAC   77512     C    GTTGC
                                 GTG ATTGT    AGGATTGGG
                                 ||| |||||    |||||||||
                                 CAC TAACG    TCCTAACCC
                                  _    AAT__
GAM204  LOC253980 3'  TCCCAACCCCATTGCTAACAA  95076      GTT  ___  A
                                 TTGT   GCA   GG TTGGGA
                                 ||||   |||   || ||||||
                                 AACA   CGT   CC AACCCT
                                   AT_   TAC  C
GAM205  ABCC3    3'  AGTCCTGTACTCTGGGGTG   13692     A   CAGC
                                 CACC CAGA    TGCAGGACT
                                 |||| ||||    |||||||||
                                 GTGG GTCT    ATGTCCTGA
                                   G    C___
GAM205  ABCC3    3'  AGTCCTGTACTCTGGGGTG   39139     A   CAGC
                                 CACC CAGA    TGCAGGACT
                                 |||| ||||    |||||||||
                                 GTGG GTCT    ATGTCCTGA
                                   G    C___
GAM205  ABCC3    3'  AGTCCTGTACTCTGGGGTG   39151     A   CAGC
                                 CACC CAGA    TGCAGGACT
                                 |||| ||||    |||||||||
                                 GTGG GTCT    ATGTCCTGA
                                   G    C___
GAM205  ARVCF    3'  AGCCCTGCAGTCACGTGAGG   8026     A  GACA      A
                                 CC CA    GCTGCAGG CT
                                 || ||    |||||||| ||
                                 GG GT    TGACGTCC GA
                                  A  GCAC       C
GAM205  CCS      3'  AGCTGCTGTGGTGTT       17609          A
                                 AACACCACAG CAGCT
                                 |||||||||| |||||
                                 TTGTGGTGTC GTCGA
                                            _
GAM205  CELSR1   3'  TTTGTACTTCTGCGGTG     26492      A   C  C
                                 CACC CAGA AG TGCAGG
                                 |||| |||| || ||||||
                                 GTGG GTCT TC ATGTTT
                                   C    _  _
GAM205  CELSR3   3'  GCAAAAGTTGTCTGTGGTG   7401             ___
                                 CACCACAGACAGCT   GC
                                 ||||||||||||||   ||
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                                GTGGTGTCTGTTGA  CG
                                       AAA
GAM205  COL19A1  3'  AGCCACCAAGCTGTCTTTGGT  8506      C      GCA_  A
                                ACCA AGACAGCT   GG CT
                                |||| ||||||||   || ||
                                TGGT TCTGTCGA   CC GA
                                  T       ACCA  _
GAM205  DDC      3'  CTCAGCTGTCTGTGG       5797            C
                                CCACAGACAGCTG AG
                                |||||||||||| ||
                                GGTGTCTGTCGAC TC
                                          _
GAM205  DLEC1    3'  AGTCCTGCACCCTGCGG     23685    A  ACAGC
                                CC CAG    TGCAGGACT
                                || |||    |||||||||
                                GG GTC    ACGTCCTGA
                                 C  CC___
GAM205  DLEC1    3'  AGTCCTGCACCCTGCGG     23696    A  ACAGC
                                CC CAG    TGCAGGACT
                                || |||    |||||||||
                                GG GTC    ACGTCCTGA
                                 C  CC___
GAM205  DUSP2    3'  GCCCTGTCTGTGGGTT      15347    A       CT
                                AAC CCACAGACAG  GC
                                ||| ||||||||||  ||
                                TTG GGTGTCTGTC  CG
                                  _       C_
GAM205  ERN2     5'  AGCCGTGCAGCTGCCCAGG   52701    ACAGA      _  A
                                CC    CAGCTGCA GG CT
                                ||    |||||||| || ||
                                GG    GTCGACGT CC GA
                                 ACCC_      G  _
GAM205  EZH1     3'  TCTGCTTTCCTGTCTGTAGTG  8830     C      CT__
                                CAC ACAGACAG   GCAGG
                                ||| ||||||||   |||||
                                GTG TGTCTGTC   CGTCT
                                  A       CTTT
GAM205  FUT4     3'  AGTCCTGCAGGAGTGCTG    8961     _  AG
                                CAG AC  CTGCAGGACT
                                ||| ||  ||||||||||
                                GTC TG  GACGTCCTGA
                                  G  AG
GAM205  GGA3     3'  AGCCCTGGGAATGTCTGTGG  56825        GCTG   A
                                CCACAGACA   CAGG CT
                                |||||||||   |||| ||
                                GGTGTCTGT   GTCC GA
                                      AAGG   C
GAM205  GGA3     3'  AGCCCTGGGAATGTCTGTGG  25741        GCTG   A
                                CCACAGACA   CAGG CT
                                |||||||||   |||| ||
```

```
                                GGTGTCTGT   GTCC GA
                                     AAGG   C
GAM205  GPC1    3'  AGCCCCGCACGGGCTGTCTGGG 9098       A       ___  A  A
          TGT                    ACACC CAGACAGCT   GC GG CT
                                 ||||| |||||||||   || || ||
                                 TGTGG GTCTGTCGG   CG CC GA
                                   _       GCA  C  C
GAM205  HMGN3   3'  AGTCCTGTGCATACTGTGGTGT 14902          ACA  T
          T                     AACACCACAG   GC GCAGGACT
                                 ||||||||||   || ||||||||
                                 TTGTGGTGTC   CG TGTCCTGA
                                      ATA  _
GAM205  HPS1    3'  AGCCTCCTGTCTGCAGTG    3964     CA     CTGC   A
                                 CAC  CAGACAG    AGG CT
                                 |||  |||||||    ||| ||
                                 GTG  GTCTGTC    TCC GA
                                   AC      C___   _
GAM205  IGFBP1  3'  TCAAAGCTACCTGTGGTG    5180        AC    GCAG
                                 CACCACAG  AGCT    GA
                                 ||||||||  ||||    ||
                                 GTGGTGTC  TCGA    CT
                                      CA    AA__
GAM205  IGFBP3  3'  AGCTCACAGCCTTCTGTGGTGT 5185         CA    CA  A
                                 ACACCACAGA  GCTG  GG CT
                                 ||||||||||  ||||  || ||
                                 TGTGGTGTCT  CGAC  TC GA
                                      TC    AC  _
GAM205  IGFBP4  3'  AGTCCTGTCTCTGCCTGCGG   7758     A   A   CT
                                 CC CAG CAG  GCAGGACT
                                 || ||| |||  ||||||||
                                 GG GTC GTC  TGTCCTGA
                                  C   C   TC
GAM205  IL19    3'  GTCCATGTCTGTGATGT     25360     C       GCTGCA
                                 ACA CACAGACA     GGAC
                                 ||| ||||||||     ||||
                                 TGT GTGTCTGT     CCTG
                                   A       A_____
GAM205  INPP5B  5'  AGTCCCGTGCGCCCTGTGGTG  95521        ACA  T  A
                                 CACCACAG   GC GC GGACT
                                 ||||||||   || || |||||
                                 GTGGTGTC   CG TG CCTGA
                                      CCG  _  C
GAM205  ISLR    3'  CTCACTGTCTGCGGTG      18669      A      C  C
                                 CACC CAGACAG TG AG
                                 |||| ||||||| || ||
                                 GTGG GTCTGTC AC TC
                                   C       _ _
GAM205  KAI1    3'  AGCCCTGGCTGTTCTGTGGT   9495          _    TG    A
                                 ACCACAGA CAGC  CAGG CT
                                 |||||||| ||||  |||| ||
```

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                                TGGTGTCT GTCG  GTCC GA
                                     T   __   C
GAM205  KDR     3'  TGAAGCTGTGTGTGGTGT    9596         G     G
                                ACACCACA ACAGCT CA
                                |||||||| ||||||  ||
                                TGTGGTGT TGTCGA GT
                                     G     A
GAM205  MLLT4   3'  AGTTATGGGCTCTCTGCAGTGT 72482      CA    C    G  G
          T                      AACAC  CAGA AGCT CA GACT
                                |||||  |||| |||| || ||||
                                TTGTG  GTCT TCGG GT TTGA
                                   AC    C    _  A
GAM205  MPO     3'  TCCTGGCTCTGTGG       4204        CA  TG
                                CCACAGA  GC  CAGGA
                                |||||||  ||  |||||
                                GGTGTCT  CG  GTCCT
                                     __  __
GAM205  PACSIN1  3'  AGTCCTGCAGCACCAGGTG   92253     ACAGACA
                                CACC      GCTGCAGGACT
                                ||||      ||||||||||||
                                GTGG      CGACGTCCTGA
                                  ACCA___
GAM205  PCLO    3'  CAGTGTCTGTGATGTT      94224      C       G
                                AACA CACAGACA CTG
                                |||| |||||||| |||
                                TTGT GTGTCTGT GAC
                                  A       _
GAM205  PLOD3   5'  TCCTCGCCTTGTCTGTGG    6558          CT  _
                                CCACAGACAG  GC AGGA
                                ||||||||||  || ||||
                                GGTGTCTGTT  CG TCCT
                                      C_  C
GAM205  PPP1R8  5'  AGCCCCGCATCCCTCTGTGGT  10722         CAGC   A  A
                                ACCACAGA    TGC GG CT
                                ||||||||    ||| || ||
                                TGGTGTCT    ACG CC GA
                                     CCCT   C  C
GAM205  PPP2R2B  3'  TGAGGTTGTCTGTAGT      15909    C        G
                                AC ACAGACAGCT CA
                                || ||||||||||  ||
                                TG TGTCTGTTGG GT
                                 A         A
GAM205  RAX     3'  AGCCCTGCAGCTGGAGGG    25536    ACAGA        A
                                CC     CAGCTGCAGG CT
                                ||     ||||||||||  ||
                                GG     GTCGACGTCC GA
                                 GAG__         C
GAM205  REGL    3'  AGTCCTGCAGCCAGGAGGGT   21485     ACAGACA
                                ACC       GCTGCAGGACT
                                |||       ||||||||||
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                                TGG      CGACGTCCTGA
                                  GAGGAC_
GAM205  RFC1     3'  GTCCTGTCCTGTGATGG     11302     CAG    CT
                                CCA   ACAG  GCAGGAC
                                |||   ||||  |||||||
                                GGT   TGTC  TGTCCTG
                                  AG_   C_
GAM205  RRM2     3'  AGTCCTGTCTGTTTATAGTG  6407      CAC     CT
                                CAC   AGACAG  GCAGGACT
                                |||   ||||||  ||||||||
                                GTG   TTTGTC  TGTCCTGA
                                  ATA     __
GAM205  RU2      5'  AGTCCTGCAAGCTCCTAGTG  33020     _ AC    _
                                CAC AG  AGCT GCAGGACT
                                ||| ||  |||| ||||||||
                                GTG TC  TCGA CGTCCTGA
                                  A  C_   A
GAM205  RXRA     3'  CCTGCAGCCATCTGTG      11407       CA
                                CACAGA  GCTGCAGG
                                ||||||  ||||||||
                                GTGTCT  CGACGTCC
                                   AC
GAM205  SH3BP2   3'  AGCCCTGCAGCTACAGCTG   11589     AC__       A
                                CAG    AGCTGCAGG CT
                                |||    |||||||||| ||
                                GTC    TCGACGTCC GA
                                  GACA        C
GAM205  SLC1A4   3'  TTGTATGTCTGTGGT       11721          GC
                                ACCACAGACA  TGCAG
                                ||||||||||  |||||
                                TGGTGTCTGT  ATGTT
                                      __
GAM205  TBXA2R   5'  AGCCTGCCCTGTCTG       6478        CT     A
                                CAGACAG  GCAGG CT
                                |||||||  ||||| ||
                                GTCTGTC  CGTCC GA
                                   C_    _
GAM205  TEM7     3'  AGCCCCAGCTTCTGT       39880       C     CA  A
                                ACAGA AGCTG  GG CT
                                ||||| |||||  || ||
                                TGTCT TCGAC  CC GA
                                  _    C_ _
GAM205  UNC13    3'  AGTCCTGCTCATCTGTGG    21055        CAGCT
                                CCACAGA    GCAGGACT
                                |||||||    ||||||||
                                GGTGTCT    CGTCCTGA
                                   ACT__
GAM205  WASF3    3'  AGCCCTGCAGCTGTAGTACAGT 21823     CACAG_         A
          G                     CAC      ACAGCTGCAGG CT
                                |||      |||||||||| ||
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                                GTG     TGTCGACGTCC GA
                                  ACATGA         C
GAM205  ZNF138   5' AGGCCCAGCCTCTGTGG     81184        CA    CA  A
                                CCACAGA  GCTG  GG CT
                                |||||||  ||||  || ||
                                GGTGTCT  CGAC  CC GA
                                    C_   __  G
GAM205  ABCA9    3' AGTCCATGTTTTGTCTGTTGTG 54409     C       CT  _
                                CAC ACAGACAG  GCA GGACT
                                ||| ||||||||  ||| |||||
                                GTG TGTCTGTT  TGT CCTGA
                                  T       T_  A
GAM205  APCL     5' GTTCAGCTGTCTGT       19684          CAG
                                ACAGACAGCTG   GAC
                                ||||||||||   |||
                                TGTCTGTCGAC   TTG
                                       ___
GAM205  BRD1     5' AGTCCTGCAACTGTGG      27413       ACAGC
                                CCACAG    TGCAGGACT
                                ||||||    |||||||||
                                GGTGTC    ACGTCCTGA
                                   A____
GAM205  C16orf5  3' AGTCCCCAGGCCTGTGG     25445       ACA   GCA
                                CCACAG   GCT   GGACT
                                ||||||   |||   |||||
                                GGTGTC   CGG   CCTGA
                                   ___   ACC
GAM205  C1orf24  3' AGTCTCTGCTTTCTGCAGTG   53707     CA    CAGCT   _
                                CAC  CAGA    GCAG GACT
                                |||  ||||    |||| ||||
                                GTG  GTCT    CGTC CTGA
                                  AC   TT___    T
GAM205  C1orf34  3' AGTCCCGGTCTGCTGTGGTGTT 60661          A  _  CA
                                AACACCACAG CAG CTG  GGACT
                                |||||||||| ||| |||  |||||
                                TTGTGGTGTC GTC GGC  CCTGA
                                      _  T  __
GAM205  C20orf82 5' AGTCTCTGGTCTGTCTG     84711        CTG  _
                                CAGACAG   CAG GACT
                                |||||||   ||| ||||
                                GTCTGTC   GTC CTGA
                                   TG_   T
GAM205  DKFZP434C171 3' AGTCCTGATAGTCTGTGG    31551        AGCTG
                                CCACAGAC    CAGGACT
                                ||||||||    |||||||
                                GGTGTCTG    GTCCTGA
                                    ATA__
GAM205  DKFZP434P211 3' AGTCCTGCGATGCTAAGTG   27260     CAC  A  GC
                                CAC   AG CA  TGCAGGACT
                                |||   || ||  |||||||||
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                                GTG   TC GT  GCGTCCTGA
                                  AA_  _  A_
GAM205  DMWD     3' AGCCCCAGGTCTGCAGTGT   60876     CA    AG   CA  A
                                ACAC  CAGAC  CTG  GG CT
                                ||||  |||||  |||  || ||
                                TGTG  GTCTG  GAC  CC GA
                                  AC    ___   C_  _
GAM205  DOCK3    3' AGTCCTGCATGTTCAGG    66495    ACA   GC
                                CC   GACA  TGCAGGACT
                                ||   ||||  |||||||||
                                GG   TTGT  ACGTCCTGA
                                 AC_   ___
GAM205  FLJ10094 3' AGTTATATCTGTGGCGTT    35807     A      C__
                                AAC CCACAGA   AGCT
                                ||| |||||||   ||||
                                TTG GGTGTCT   TTGA
                                  C      ATA
GAM205  FLJ10178 3' AGCCCTATAGTTCTGTG     35869       CA   C   A
                                CACAGA  GCTG AGG CT
                                ||||||  |||| ||| ||
                                GTGTCT  TGAT TCC GA
                                   __    A   C
GAM205  FLJ10637 5' AGTCCCCTGTCTGTGG      68586          CTGCA
                                CCACAGACAG    GGACT
                                ||||||||||    |||||
                                GGTGTCTGTC    CCTGA
                                      C_____
GAM205  FLJ12891 5' AGTCCTGCAGCCTCGCTGG   46336    CA  CA
                                CCA  GA  GCTGCAGGACT
                                |||  ||  ||||||||||
                                GGT  CT  CGACGTCCTGA
                                  CG  C_
GAM205  FLJ12903 3' GTGCTATTGTGGTGT       42778         AC   T
                                ACACCACAG  AGC GC
                                |||||||||  ||| ||
                                TGTGGTGTT  TCG TG
                                     A_   _
GAM205  FLJ13902 3' AGCCCTGTAGCATCTGTG    45038       CA       A
                                CACAGA  GCTGCAGG CT
                                ||||||  |||||||| ||
                                GTGTCT  CGATGTCC GA
                                   A_       C
GAM205  FLJ20033 3' TTTTGCTAGCTGTGGTGTT   34351          ACAGCT
                                AACACCACAG     GCAGGA
                                ||||||||||     ||||||
                                TTGTGGTGTC     CGTTTT
                                      GAT___
GAM205  FLJ20315 3' CCAGCTGCTGCCTGTGGCGT  34933    A     A   T  A
                                AC CCACAG CAGC GC GG
                                || |||||| |||| || ||
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                                TG GGTGTC GTCG CG CC
                                 C     C    T  A
GAM205  FLJ20374  3'  AGCCCTGCAGCTGGCTGGAGT  35077    CA   A        A
                                AC  CAG CAGCTGCAGG CT
                                ||  ||| |||||||||| ||
                                TG  GTC GTCGACGTCC GA
                                 AG   G         C
GAM205  FLJ22127  3'  AGTCCTGTGGCTGGCCCGTGAT 42881    C   AGA_   TG
          G                      CA CAC    CAGC  CAGGACT
                                || |||    ||||  |||||||
                                GT GTG    GTCG  GTCCTGA
                                 A  CCCG    GT
GAM205  FLJ23185  5'  GTCCTGCAGTATGGCGT     46833    A   CAGACA
                                AC CCA     GCTGCAGGAC
                                || |||     ||||||||||
                                TG GGT     TGACGTCCTG
                                 C  A_____
GAM205  FLJ31762  5'  AGTCCTGCAGATGTGCGTG    58139    _    GACAG
                                CAC CACA    CTGCAGGACT
                                ||| ||||    ||||||||||
                                GTG GTGT    GACGTCCTGA
                                 C   A____
GAM205  GIOT-2    3'  CCTTCAGTTATCTGCAGT    32749    CA   C    C
                                AC  CAGA AGCTG AGG
                                ||  |||| ||||| |||
                                TG  GTCT TTGAC TCC
                                 AC    A    T
GAM205  HRH3      3'  AGCCCCGCCGTGTCTGTGG    23364        G T  A  A
                                CCACAGACA C GC GG CT
                                ||||||||| | || || ||
                                GGTGTCTGT G CG CC GA
                                      _ C  C  C
GAM205  HYA22     3'  TCCTACGTGTTGGTCTGTGGT  19429        _  _  C
                                ACCACAGAC AGC TG AGGA
                                ||||||||| ||| || ||||
                                TGGTGTCTG TTG GC TCCT
                                      G   T  A
GAM205  KCNB2     5'  TCCCACAGCCCTTTGTGGTG   96102        CA   CA
                                CACCACAGA  GCTG  GGA
                                |||||||||  ||||  |||
                                GTGGTGTTT  CGAC  CCT
                                      CC    AC
GAM205  KCNT1     3'  AGTCCTGCAGATCCCTCTGTGG 61826        CAG__
          T                     ACCACAGA    CTGCAGGACT
                                ||||||||    ||||||||||
                                TGGTGTCT    GACGTCCTGA
                                     CCCTA
GAM205  KIAA0218  3'  GTCCCTCGTCTGTGGT      28623         _  CTGCA
                                ACCACAGAC AG    GGAC
                                ||||||||| ||    ||||
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                                TGGTGTCTG TC    CCTG
                                    C _____
GAM205  KIAA0828 3' TCCTGTGCCTGTAGTGTT   81199     C   ACA  T
                                AACAC ACAG  GC GCAGGA
                                ||||| ||||  || ||||||
                                TTGTG TGTC  CG TGTCCT
                                  A  ___ _
GAM205  KIAA0953 3' AGTCCTGCATGTAGTTGGTG  66780     CAG  GC
                                CACCA  ACA  TGCAGGACT
                                |||||  |||  |||||||||
                                GTGGT  TGT  ACGTCCTGA
                                  TGA  __
GAM205  KIAA1157 3' AGTCCGTCCATGCTCTGTGG  72239      _ GCT  A
                                CCACAGA CA  GC GGACT
                                ||||||| ||  || |||||
                                GGTGTCT GT  TG CCTGA
                                    C  ACC  _
GAM205  KIAA1183 3' GCAGCCTGTGGTGTT      62535       ACA
                                AACACCACAG  GCTGC
                                ||||||||||  |||||
                                TTGTGGTGTC  CGACG
                                     ___
GAM205  KIAA1280 5' AGCCTGACTGTCCGTGGTG  69710     A   CTG   A
                                CACCAC GACAG  CAGG CT
                                |||||| |||||  |||| ||
                                GTGGTG CTGTC  GTCC GA
                                   C   A__  _
GAM205  KIAA1336 3' TCCTGGGTTTTGTAATGTT  72325    CC   CA  G
                                AACA  ACAGA  GCT CAGGA
                                ||||  |||||  ||| |||||
                                TTGT  TGTTT  TGG GTCCT
                                  AA   __  _
GAM205  KIAA1505 5' AGTCCCACCCATCTGTGGT  94185      CAGC  CA
                                ACCACAGA   TG  GGACT
                                ||||||||   ||  |||||
                                TGGTGTCT   AC  CCTGA
                                    ACCC  __
GAM205  KIAA1786 3' AGTCCTTCCTTATCTGTGGT  66022      CAGCTGC
                                ACCACAGA    AGGACT
                                ||||||||    ||||||
                                TGGTGTCT    TCCTGA
                                    ATTCCT_
GAM205  MAD4    3' CCTGTACCGGTCTGTGG    21271      AGC
                                CCACAGAC  TGCAGG
                                ||||||||  ||||||
                                GGTGTCTG  ATGTCC
                                    GCC
GAM205  MGC10940 3' AGCCCCCCAATCTGTGGT   50214      CAGC  CA  A
                                ACCACAGA   TG  GG CT
                                ||||||||   ||  || ||
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                                TGGTGTCT   AC  CC GA
                                    A___  CC  C
GAM205  MGC2654  5' AGCTTGGACCTGTCTGCAGT  44103   CA     CTG   A
                                AC  CAGACAG   CAGG CT
                                ||  |||||||   |||| ||
                                TG  GTCTGTC   GTTC GA
                                 AC      CAG   _
GAM205  MVD      3' AGTCCTGCGGCCGCCCAGGTGT 10138      ACAGACA
                                ACACC      GCTGCAGGACT
                                ||||||      ||||||||||||
                                TGTGG      CGGCGTCCTGA
                                   ACCCGC_
GAM205  NIN283   3' AGCCCTCTGCCGGCTGTGGTGT 50065        ACA  TGC   A
                                ACACCACAG   GC   AGG CT
                                |||||||||   ||   ||| ||
                                TGTGGTGTC   CG   TCC GA
                                     GGC  TC_   C
GAM205  NTT5     3' AGTCCTGCTACTTCTGGGGTG  25880     A   C  CT
                                CACC CAGA AG  GCAGGACT
                                |||| |||| ||  ||||||||
                                GTGG GTCT TC  CGTCCTGA
                                  G   _ AT
GAM205  P2RX1    3' TCCTGGGCTCCCTGCCTGTGG  67172      A  ____  G
                                CCACAG CA   GCT CAGGA
                                |||||| ||   ||| |||||
                                GGTGTC GT   CGG GTCCT
                                   C  CCCT  _
GAM205  PMAIP1   5' TGCAGCTGTCCGAGGTG    40892     ACA
                                CACC   GACAGCTGCA
                                ||||   ||||||||||
                                GTGG   CTGTCGACGT
                                  AGC
GAM205  PMVK     3' AGTCCCCTCAGCCTGTGGTG  21610       ACA   CA_
                                CACCACAG   GCTG   GGACT
                                ||||||||   ||||   |||||
                                GTGGTGTC   CGAC   CCTGA
                                     ___    TCC
GAM205  PMVK     3' AGTCCCCTCAGCCTGTGGTG  94612       ACA   CA_
                                CACCACAG   GCTG   GGACT
                                ||||||||   ||||   |||||
                                GTGGTGTC   CGAC   CCTGA
                                     ___    TCC
GAM205  POLD3    3' TCTGAGCTGTCTGCAAGG    91646    A__       G
                                CC   CAGACAGCT CAGG
                                ||   ||||||||| ||||
                                GG   GTCTGTCGA GTCT
                                 AAC       _
GAM205  PRO2958  3' AGTCCTAAACTGGCATCTGT  37651      CA   C___
                                ACAGA  GCTG   AGGACT
                                |||||  ||||   ||||||
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                                TGTCT  CGGT   TCCTGA
                                  A_   CAAA
GAM205  RAN     3'  GCAGCTGTCCTGTGATGT   20907    C   _
                                ACA CACAG ACAGCTGC
                                ||| ||||| ||||||||
                                TGT GTGTC TGTCGACG
                                  A    C
GAM205  RMP     3'  AGTTTTGTGCCAGCTGTG   13707     ACA  T
                                CACAG   GC GCAGGACT
                                |||||   || ||||||||
                                GTGTC   CG TGTTTTGA
                                  GAC  _
GAM205  RMP     3'  AGTTTTGTGCCAGCTGTG   56242     ACA  T
                                CACAG   GC GCAGGACT
                                |||||   || ||||||||
                                GTGTC   CG TGTTTTGA
                                  GAC  _
GAM205  SCYD1   3'  AGTCACCCCGGCCACCTGCGGT 90924     A  ACA   CAG_
          G                      CACC CAG   GCTG   GACT
                                |||| |||   ||||   ||||
                                GTGG GTC   CGGC   CTGA
                                  C   CAC   CCCA
GAM205  SHAPY   5'  AGTCCCGCCTGTCTGT     57108       CT  A
                                ACAGACAG  GC GGACT
                                ||||||||  || |||||
                                TGTCTGTC  CG CCTGA
                                    __  C
GAM205  SMOC1   3'  AGTCCTGCAATTGTACTGCGG  42147   A  _   C
                                CC CAG ACAG TGCAGGACT
                                || ||| |||| |||||||||
                                GG GTC TGTT ACGTCCTGA
                                 C  A   A
GAM205  SRPUL   3'  TCCTGCAGTGTTTCCAGG   27101   AC_   G
                                CC   AGACA CTGCAGGA
                                ||   ||||| ||||||||
                                GG   TTTGT GACGTCCT
                                 ACC    _
GAM205  SSH-3   3'  AGCCCTGCACACTCACCTGTGG 35339      AC_  C_    A
                                CCACAG   AG  TGCAGG CT
                                ||||||   ||  |||||| ||
                                GGTGTC   TC  ACGTCC GA
                                   CAC  AC     C
GAM205  TOSO    3'  CCCAGGCTCGGACTGTGGTG   18389       AC__   GCA
                                CACCACAG    AGCT   GG
                                ||||||||    ||||   ||
                                GTGGTGTC    TCGG   CC
                                    AGGC    AC_
GAM205  TPC2    3'  CCTGCAGCTTCCGTGGTG    57446      A  C
                                CACCAC GA AGCTGCAGG
                                |||||| || |||||||||
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                                GTGGTG CT TCGACGTCC
                                   C  _
GAM205  TRIM11   3'  CCATGCCTGTCTGTG      72831        CT  _
                                CACAGACAG  GCA GG
                                |||||||||  ||| ||
                                GTGTCTGTC  CGT CC
                                     __  A
GAM205  UGT2B10  3'  AGCCCCAGTAATGCTCTGTGG  6540       _ __   CA  A
                                CCACAGA CA  GCTG  GG CT
                                |||||||  ||  ||||  || ||
                                GGTGTCT GT  TGAC  CC GA
                                    C  AA   C_  _
GAM205  LOC113386 3'  AGTCCTGCATGTGTTGATG   57077   CA   GC
                                CA  GACA  TGCAGGACT
                                ||  ||||  |||||||||
                                GT  TTGT  ACGTCCTGA
                                  AG   GT
GAM205  LOC130814 3'  AGTGCTCAGACATCTGCAGTGT 74984     CA   CAG   C  G
           T                     AACAC  CAGA   CTG AG ACT
                                |||||  ||||   ||| || |||
                                TTGTG  GTCT   GAC TC TGA
                                   AC   ACA  _  G
GAM205  LOC131870 3'  AGTCCTGCAGCCTCATATGG   75013    CAGACA
                                CCA     GCTGCAGGACT
                                |||     ||||||||||
                                GGT     CGACGTCCTGA
                                  ATACTC
GAM205  LOC133491 5'  GTCTGGCGCCTGTGGCGT    75096    A    ACA  T  A
                                AC CCACAG   GC GC GGAC
                                || ||||||   || || ||||
                                TG GGTGTC   CG CG TCTG
                                 C     ___  _  G
GAM205  LOC139065 3'  TCCTTTTGATTTGTGG     75817       _  CTGC
                                CCACAGA CAG    AGGA
                                ||||||| |||    ||||
                                GGTGTTT GTT    TCCT
                                    A  T___
GAM205  LOC145622 5'  AGTCCTGCAAAGGTGATGGTGG 77291     AGA  G  __
           T                     ACCAC   CA CT  GCAGGACT
                                |||||   ||  ||  ||||||||
                                TGGTG   GT GA  CGTCCTGA
                                   GTA  G  AA
GAM205  LOC145676 5'  AGTCCTGTCCAGGGTCT    77333     AG  __
                                AGAC  CTG  CAGGACT
                                ||||  |||  |||||||
                                TCTG  GAC  GTCCTGA
                                  G_   CT
GAM205  LOC145955 5'  AGCCCTGAGATGTCCATGGT   83586     CA   G  G   A
                                ACCA  GACA CT CAGG CT
                                ||||  |||| || |||| ||
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                                TGGT  CTGT GA GTCC GA
                                  AC   A _   C
GAM205  LOC145957 5' CTGCTGTTGTCTGCGGT    56794    A      T
                                ACC CAGACAGC GCAG
                                ||| |||||||| ||||
                                TGG GTCTGTTG CGTC
                                  C       T
GAM205  LOC146287 5' TTGCAGCTGCCTCGGT     83654    AC  A
                                ACC  AG CAGCTGCAG
                                |||  || |||||||||
                                TGG  TC GTCGACGTT
                                  C_  C
GAM205  LOC146669 3' AGCCCTGCAGCCTGGG     78049    A   ACA      A
                                CC CAG   GCTGCAGG CT
                                || |||   |||||||| ||
                                GG GTC   CGACGTCC GA
                                 _  ___       C
GAM205  LOC147040 3' CAGTGTCTGTGATGT      78230    C      G
                                ACA CACAGACA CTG
                                ||| |||||||| |||
                                TGT GTGTCTGT GAC
                                  A       _
GAM205  LOC147160 5' AGCCCTGCAGTGCGTGTACAGG 83956    ACAG  ___      A
                                CC    ACA   GCTGCAGG CT
                                ||    |||   |||||||| ||
                                GG    TGT   TGACGTCC GA
                                 ACA_   GCG       C
GAM205  LOC149111 3' CCTGCGTGTCTGTG       79181        GC
                                CACAGACA  TGCAGG
                                ||||||||  ||||||
                                GTGTCTGT  GCGTCC
                                     __
GAM205  LOC150174 3' AGTCCTGCGATGCTAAGTG   79604    CAC  A  GC
                                CAC   AG CA  TGCAGGACT
                                |||   || ||  |||||||||
                                GTG   TC GT  GCGTCCTGA
                                  AA_  _  A_
GAM205  LOC150213 3' AGTCCTGCGATGCTAAGTG   74851    CAC  A  GC
                                CAC   AG CA  TGCAGGACT
                                |||   || ||  |||||||||
                                GTG   TC GT  GCGTCCTGA
                                  AA_  _  A_
GAM205  LOC150236 3' AGTCCTGCGATGCTAAGTG   79683    CAC  A  GC
                                CAC   AG CA  TGCAGGACT
                                |||   || ||  |||||||||
                                GTG   TC GT  GCGTCCTGA
                                  AA_  _  A_
GAM205  LOC154559 3' GCAGCTGTCCTGTGATGT    81096    C    _
                                ACA CACAG ACAGCTGC
                                ||| ||||| ||||||||
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                                TGT GTGTC TGTCGACG
                                  A    C
GAM205  LOC158117 3'  CCTGGTCTGTTCTGTATTGTT  81703     CC    _  CTG
                                AACA  ACAGA CAG   CAGG
                                ||||  ||||| |||   ||||
                                TTGT  TGTCT GTC   GTCC
                                  TA    T   TG_
GAM205  LOC160897 3'  CCAGCTATTGTCTGTTGTGTT  82245      C      CT  A
                                AACAC ACAGACAG  GC GG
                                ||||| ||||||||  || ||
                                TTGTG TGTCTGTT  CG CC
                                   T       AT  A
GAM205  LOC161482 3'  GCACTTACCTGTGGTGTT    87089         AC_  C
                                AACACCACAG   AG TGC
                                ||||||||||   || |||
                                TTGTGGTGTC   TC ACG
                                      CAT  _
GAM205  LOC164382 3'  AGTCTCCCTGTCTGTGGT    87203         CTGCA
                                ACCACAGACAG    GGACT
                                ||||||||||    |||||
                                TGGTGTCTGTC    TCTGA
                                      CC___
GAM205  LOC200301 5'  AGCCTGTCTGTGTGTT      88736      C      _
                                AACAC ACAGACAG CT
                                ||||| |||||||| ||
                                TTGTG TGTCTGTC GA
                                  _       C
GAM205  LOC203275 3'  CCTGGTCTGTTCTGTATTGTT  89319     CC    _  CTG
                                AACA  ACAGA CAG   CAGG
                                ||||  ||||| |||   ||||
                                TTGT  TGTCT GTC   GTCC
                                  TA    T   TG_
GAM205  LOC219920 5'  TTGGGCACTGCCTGTGG     93323       A  C  AG
                                CCACAG CAG TGC  GA
                                |||||| ||| |||  ||
                                GGTGTC GTC ACG  TT
                                   C   _  GG
GAM205  LOC220932 3'  AGTCCTGTTCTCTGTTAATGT  93135     __    CT_
                                ACA  GACAG   GCAGGACT
                                |||  |||||   ||||||||
                                TGT  TTGTC   TGTCCTGA
                                  AA    TCT
GAM205  LOC221466 5'  GTCCTGTGTCCAGGGTG     93693     ACA   AGCT
                                CACC   GAC    GCAGGAC
                                ||||   |||    |||||||
                                GTGG   CTG    TGTCCTG
                                  GAC   _____
GAM205  LOC221547 3'  GCAGCTGTCCTGTGATGT    91007     C    _
                                ACA CACAG ACAGCTGC
                                ||| ||||| ||||||||
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                                TGT GTGTC TGTCGACG
                                  A     C
GAM205  LOC221935 3'  AGCCGTCACTGTCTGTG     92615          CT  A  A
                                CACAGACAG  GC GG CT
                                |||||||||  || || ||
                                GTGTCTGTC  TG CC GA
                                     AC  _  _
GAM205  LOC253681 3'  CAGTGTCTGTGATGT       95127     C       G
                                ACA CACAGACA CTG
                                ||| |||||||| |||
                                TGT GTGTCTGT GAC
                                  A       _
GAM205  LOC257115 3'  AGTCCTGCAAGGTGAAGGCGTT 96523     A  ACAGA  G  _
                                AAC CC     CA CT GCAGGACT
                                ||| ||     || || ||||||||
                                TTG GG     GT GA CGTCCTGA
                                  C  AA___  G  A
GAM205  LOC257577 3'  GCAGCTGTCCTGTGATGT     97838     C     _
                                ACA CACAG ACAGCTGC
                                ||| ||||| ||||||||
                                TGT GTGTC TGTCGACG
                                  A     C
GAM205  LOC51112  5'  AGTCCTGCGGGCCGTGG      32082      AGACAG
                                CCAC      CTGCAGGACT
                                ||||      ||||||||||
                                GGTG      GGCGTCCTGA
                                  CCG___
GAM205  LOC51236  3'  TCCTGCAGCTGTCTGCAGG    33205    A_
                                CC  CAGACAGCTGCAGGA
                                ||  ||||||||||||||
                                GG  GTCTGTCGACGTCCT
                                 AC
GAM205  LOC51713  3'  TTTGTACTGTCTGCGG      32762     A      C
                                CC CAGACAG TGCAGG
                                || ||||||| ||||||
                                GG GTCTGTC ATGTTT
                                 C      _
GAM205  LOC56920  3'  AGCCTTCCAGCCTGCGGTG    39379      A  ACA   C_  A
                                CACC CAG   GCTG  AGG CT
                                |||| |||   ||||  ||| ||
                                GTGG GTC   CGAC  TCC GA
                                  C  ___    CT  _
GAM205  LOC90408  3'  AGTCCTGTGGTCCTGTG     62655      ACA  TG
                                CACAG   GC  CAGGACT
                                |||||   ||  |||||||
                                GTGTC   TG  GTCCTGA
                                   C__  GT
GAM205  LOC91397  5'  GCAGTATCTGTGGTG       65910          CA
                                CACCACAGA  GCTGC
                                |||||||||  |||||
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                                GTGGTGTCT  TGACG
                                     A_
GAM206  ADH1B   3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM206  AHR     3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM206  FDFT1   3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT

                                     _
GAM206  JTB     3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM206  KLF4    3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM206  PHYH    3'  ACAGTAAAAGTGAAAT     20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                     A
GAM206  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM206  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM206  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM206  CG012   5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
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                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM206  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                |||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM206  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
          G                      CATTTC       GTCTGAGAT
                                 ||||||       |||||||||
                                 GTAAAG       CAGACTCTA
                                    AAACATTT_
GAM206  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM206  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM206  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM206  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM206  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM206  PP35     3'  ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM206  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG 48148         TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM206  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
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                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM206  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM206  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM206  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM206  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226     A      GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM206  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM207  DDEF1    3'  GAGCTTTAGCAGCCTC      59564    A  AGATAC      A
                                GA GCT     CTAAAGCT C
                                || |||     |||||||| |
                                CT CGA     GATTTCGA G
                                 C  C_____       C
GAM207  DDX3     3'  GAGCCTTAGGTATTTG      43759          A  A
                                TAGATACCTAA GCT C
                                |||||||||| ||| |
                                GTTTATGGATT CGA G
                                       C  C
GAM207  GRAF     3'  GGTAACTCCCTCCCTAGCTTC  30573        ATACCTAA  C
                                GAAGCTAG       AG TACC
                                ||||||||       || ||||
                                CTTCGATC       TC ATGG
                                     CCTCCC__  A
GAM207  MAT1A    3'  AGCTTTAGAATCCCAGC     90825     A_  AC
                                GCT  GAT  CTAAAGCT
                                |||  |||  ||||||||
                                CGA  CTA  GATTTCGA
                                  CC  A_
GAM207  MYLK     3'  AGCTTCAGACATTTGGTT    97018        AC  A
                                AGCTAGAT  CT AAGCT
                                ||||||||  || |||||
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                                TTGGTTTA  GA TTCGA
                                    CA  C
GAM207  RGL     3'  GTAGCTAAAACTTAGCTTCA  30736        ATACCTAA
                                TGAAGCTAG      AGCTAC
                                |||||||||      ||||||
                                ACTTCGATT      TCGATG
                                    CAAAA___
GAM207  ZFP93   3'  GTAGCCTTAATAACGTTAGTTT 14887        ATACC_  A
           CA                    TGAAGCTAG     TAA GCTAC
                                |||||||||     ||| |||||
                                ACTTTGATT     ATT CGATG
                                    GCAATA  C
GAM207  C3orf4  3'  AGCATTGACACATAGCTTCA  39118        GATACC  A
                                TGAAGCTA     TAA GCT
                                ||||||||     ||| |||
                                ACTTCGAT     GTT CGA
                                    ACACA_  A
GAM207  D2S448  3'  GGCAGGAGTCCTAGCTTCA  73527        _  A  AAA
                                TGAAGCTAG AT CCT  GCT
                                ||||||||| || |||  |||
                                ACTTCGATC TG GGA  CGG
                                    C  A  ___
GAM207  FLJ12604 3' AGCTTTAGTATTGACTTCA  64436      CTA    C
                                TGAAG  GATAC TAAAGCT
                                |||||  ||||| |||||||
                                ACTTC  TTATG ATTTCGA
                                   AG_   _
GAM207  FLJ14280 5' GGTAGCTCCTGGCCAGCTCA  45999    A  AGATA  TAA
                                TGA GCT    CC  AGCTACC
                                ||| |||    ||  |||||||
                                ACT CGA    GG  TCGATGG
                                  _  CC___  TCC
GAM207  H2AFJ   3'  GTTGTCAAGTTTCTAGCTTCA 36842        T  CTAA_
                                TGAAGCTAGA AC    AGC
                                |||||||||| ||    |||
                                ACTTCGATCT TG    TTG
                                     T  AACTG
GAM207  KIAA0441 3' TAGCTTTGTTAATCTAGCCTC 28960    A     ACC
                                GA GCTAGAT  TAAAGCTA
                                || |||||||  ||||||||
                                CT CGATCTA  GTTTCGAT
                                 C      ATT
GAM207  KIAA1128 3' TAGCTTTATGTGCAGCTTGCA 68483    _    AGA  C
                                TG AAGCT  TAC TAAAGCTA
                                || |||||  ||| ||||||||
                                AC TTCGA  GTG ATTTCGAT
                                 G    C__  T
GAM207  KIAA1750 3' TAGCCCCAGGAGTGGGCTTTA 68254       AG  A  AAA
                                TGAAGCT  AT CCT  GCTA
                                |||||||  || |||  ||||
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                                ATTTCGG  TG GGA   CGAT
                                    G_  A   CCC
GAM207  KPNA5    3'  GGTAGCTTCAGGTAACT     9629     A    A
                                AG TACCT AAGCTACC
                                || ||||| ||||||||
                                TC ATGGA TTCGATGG
                                 A    C
GAM207  MAGEH1   5'  GGTAGCTTCAGCGGCAGCAGCT 25924       AGATAC_  A
           TC                     GAAGCT      CT AAGCTACC
                                ||||||      || ||||||||
                                CTTCGA      GA TTCGATGG
                                   CGACGGC  C
GAM207  MGC12921 3'  AGCCCTATTTAGCTTC      63774          CCTAAA
                                GAAGCTAGATA     GCT
                                ||||||||||     |||
                                CTTCGATTTAT     CGA
                                      CC____
GAM207  MGC30052 3'  AGCTTTAGAATAGCTTC     58532        GATAC
                                GAAGCTA    CTAAAGCT
                                |||||||    ||||||||
                                CTTCGAT    GATTTCGA
                                    AA___
GAM207  RNF34    3'  AGCAAGGGCTGCATCTAGCTTC 47094         A___   AAA
                                GAAGCTAGAT   CCT   GCT
                                |||||||||   |||  |||
                                CTTCGATCTA   GGG   CGA
                                      CGTC   AA_
GAM207  TNFRSF19L 3' GTAGCTTTTATCCCAGC     51779     A_   CCT
                                GCT  GATA   AAAGCTAC
                                |||  ||||  ||||||||
                                CGA  CTAT   TTTCGATG
                                  CC   ___
GAM207  LOC121536 3' AGCAAATCACATTTAGCTTCA  74082          ACCTAAA
                                TGAAGCTAGAT      GCT
                                ||||||||||      |||
                                ACTTCGATTTA      CGA
                                      CACTAAA
GAM207  LOC255452 3' TAGGTACCTACCTTCA      97544      C   A
                                TGAAG TAG TACCTA
                                ||||| ||| ||||||
                                ACTTC ATC ATGGAT
                                   C   C
GAM207  LOC257396 3' GGCAGCTTTAGGCTTAACTT  97139     C   ATA       A
                                AAG TAG   CCTAAAGCT CC
                                ||| |||   ||||||||| ||
                                TTC ATT   GGATTTCGA GG
                                  A   C__        C
GAM207  LOC92710  3' GTACAAGGCATCTAGCTT    70359         A   AAAGC
                                AAGCTAGAT CCT     TAC
                                ||||||||| |||     |||
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                                TTCGATCTA GGA    ATG
                                     C  AC___
GAM208  ATP7A    3'  AGTGGACGATGTTGTGCA   3517       AGCAGT  _
                                TGCACA    GCA CGTCCACT
                                ||||||    ||| ||||||||
                                ACGTGT    TGT GCAGGTGA
                                   _______  A
GAM208  LRP6     3'  CAGCAGATTTGCTGCTTGTGC  9806         GT  C  CA
                                GCACAAGCA  GCA GTC  CTG
                                |||||||||  ||| |||  |||
                                CGTGTTCGT  CGT TAG  GAC
                                     __  T  AC
GAM208  FLJ12572 3'  CAGCCCGGCATCTGCTTGTACA 43248    C      _  A  TCCA
                                TG ACAAGCAG TGC CG   CTG
                                || |||||||| ||| ||   |||
                                AC TGTTCGTC ACG GC   GAC
                                 A      T  _ CC__
GAM208  KIAA0552 3'  CAGCAGACGTGCAGTGC    28308    G      CA
                                GCA TGCACGTC  CTG
                                ||| ||||||||  |||
                                CGT ACGTGCAG  GAC
                                  G       AC
GAM208  KIAA0844 3'  CAGTGGACTGCACGCTTGGTGC 30199      _   A    C
           A                     TGCAC AAGC GTGCA GTCCACTG
                                ||||| |||| ||||| ||||||||
                                ACGTG TTCG CACGT CAGGTGAC
                                   G   _    _
GAM208  KIAA1277 3'  TAGTGGATGTGCACTGCCTGTA 64460    C  A
           CA                     TG ACA GCAGTGCACGTCCACTG
                                || ||| ||||||||||||||||
                                AC TGT CGTCACGTGTAGGTGAT
                                 A  C
GAM208  KIAA1554 5'  ACGTGCACTGCCTGCGC    95144    A  A
                                GC CA GCAGTGCACGT
                                || || ||||||||||
                                CG GT CGTCACGTGCA
                                 C  C
GAM208  KIAA1679 3'  CAGTGGATAGCAACCTGTGCA  70150      A CAG   AC
                                TGCACA G   TGC  GTCCACTG
                                |||||| |   |||  ||||||||
                                ACGTGT C   ACG  TAGGTGAC
                                   _ CA_   A_
GAM208  MGC16279 5'  CAGCAGACGTGCTGTATTGC  51886      ___      CA
                                GCAGT   GCACGTC  CTG
                                |||||   |||||||  |||
                                CGTTA   CGTGCAG  GAC
                                   TGT      AC
GAM208  PLAGL2   3'  CAGTGGACTCGGCCACTGTGCA 70442     ACAA     _ AC_
                                TGC    GCAGTG C   GTCCACTG
                                |||    |||||| |   ||||||||
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                                ACG   TGTCAC G   CAGGTGAC
                                 _____     C GCT
GAM208  PTRF     3'  CAGTGGACAGCCCCCGCTTGGA 63498    CA    AGT_  AC
              CA                  TG  CAAGC   GC  GTCCACTG
                                ||  |||||   ||  ||||||||
                                AC  GTTCG   CG  CAGGTGAC
                                 AG    CCCC  A_
GAM208  SAMHD1   3'  ACTGCACTGCCTGTGC     61306      A      C
                                GCACA GCAGTGCA GT
                                ||||| |||||||| ||
                                CGTGT CGTCACGT CA
                                   C       _
GAM208  TUSP     3'  CAGTGGCGTGCACTGCTTGTGC 39627              T
              A                   TGCACAAGCAGTGCACG CCACTG
                                |||||||||||||||| ||||||
                                ACGTGTTCGTCACGTGC GGTGAC
                                                 _
GAM208  LOC147929 5'  CGCGCACACCCACTTGTGCA   78574        CA___   A
                                TGCACAAG    GTGC CG
                                ||||||||    |||| ||
                                ACGTGTTC    CACG GC
                                     ACCCA   C
GAM208  LOC150299 3'  GGAGCACTGCTCATGCA     84972     CA      ACG
                                TGCA  AGCAGTGC   TCC
                                ||||  ||||||||  |||
                                ACGT  TCGTCACG   AGG
                                  AC       ___
GAM208  LOC220692 5'  ACCTGCTCTGCTTGTACA    91216    C      T   C
                                TG ACAAGCAG GCA GT
                                || |||||||| ||| ||
                                AC TGTTCGTC CGT CA
                                 A       T   C
GAM208  LOC256158 5'  CAGTGCTGGCCACTACTCCTGC 97651     CA  C    CA  TC
              A                   TGCA  AG AGTG  CG  CACTG
                                ||||  || ||||  ||  |||||
                                ACGT  TC TCAC  GT  GTGAC
                                  CC  A    CG  C_
GAM208  LOC256730 3'  ATGGCACTGCTTGTACA     95228    C        A
                                TG ACAAGCAGTGC CGT
                                || ||||||||||| |||
                                AC TGTTCGTCACG GTA
                                 A        _
GAM208  LOC91069  3'  CAGCAGACGTGCTGTATTGC   64773      ___      CA
                                GCAGT   GCACGTC  CTG
                                |||||   |||||||  |||
                                CGTTA   CGTGCAG  GAC
                                   TGT      AC
GAM209  FCMD     3'  ACAACTATTCACCCTACCT   22086    C    GTTAGT
                                AG TAGGG     ATAGTTGT
                                || |||||     ||||||||
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                                TC ATCCC     TATCAACA
                                 C    ACT___
GAM209  MPDZ     3'  CAACCCAACCCCTAGCT     13817          AGTATA
                                AGCTAGGGGTT     GTTG
                                ||||||||||     ||||
                                TCGATCCCCAA     CAAC
                                      CC____
GAM209  C12orf4   3'  ACTGGTGATCAACCCCTAACTT 39809      C       AGTA__
          A                     TAAG TAGGGGTT     TAGT
                                |||| ||||||||     ||||
                                ATTC ATCCCCAA     GTCA
                                  A       CTAGTG
GAM209  DKFZP434F0318 3'  CAACCATTCCCTAACTCC    48005        T__  A
                                GGGGTTAG   AT GTTG
                                ||||||||   || ||||
                                CCTCAATC   TA CAAC
                                     CCT  C
GAM209  U5-100K   3'  ACAATCCAACTCCCTAGC    59678       GTT   ATA
                                GCTAGGG   AGT   GTTGT
                                |||||||   |||   |||||
                                CGATCCC   TCA   TAACA
                                    ___   ACC
GAM210  CEP2     3'  TCCTGCCTCATCCCTAG     22284         TAC
                                CTAGGGATG   TAGGG
                                |||||||||   |||||
                                GATCCCTAC   GTCCT
                                     TCC
GAM210  C6orf35   3'  CCCTAATAGCAATAGTACTG   37451        GGGA   AC
                                CAGTACTA    TGT  TAGGG
                                ||||||||    |||  |||||
                                GTCATGAT    ATA  ATCCC
                                    AACG   __
GAM210  FLJ10933  3'  AGTAATCCCTAGTACT      36900          G
                                AGTACTAGGGAT TACT
                                |||||||||||| ||||
                                TCATGATCCCTA ATGA
                                          _
GAM210  FLJ12484  3'  TCCCCAGTCCACCCAGTACTGG 42858        A   A  T   A
                                TCAGTACT GGG TG ACT GGGA
                                |||||||| ||| || ||| ||||
                                GGTCATGA CCC AC TGA CCCT
                                    _   _  C   C
GAM210  FLJ12484  3'  TCCCCAGTCCACCCAGTACTGG 69655        A   A  T   A
                                TCAGTACT GGG TG ACT GGGA
                                |||||||| ||| || ||| ||||
                                GGTCATGA CCC AC TGA CCCT
                                    _   _  C   C
GAM210  FLJ20519  3'  TCCCTTCATCCCTAAGACTGA  35346      AC       TACT
                                TCAGT  TAGGGATG   AGGGA
                                |||||  ||||||||   |||||
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                                AGTCA  ATCCCTAC    TCCCT
                                  GA       T___
GAM210  FLJ32926  3'  CCCAAGAGCCCCCCAGTGCTGA 58019         A   AT  A  A
                                TCAGTACT GGG  GT CT GGG
                                |||||||| |||  || || |||
                                AGTCGTGA CCC  CG GA CCC
                                     _  CC  A  A
GAM210  KIAA0534  3'  TACATCCTAATACTGA      71433       CTA
                                TCAGTA   GGGATGTA
                                ||||||   ||||||||
                                AGTCAT   TCCTACAT
                                   AA_
GAM210  PRO0246   5'  TCCCTAGTATGATGGTACT   26140        GGGAT
                                AGTACTA    GTACTAGGGA
                                |||||||    ||||||||||
                                TCATGGT    TATGATCCCT
                                    AG___
GAM210  LOC169245 5'  CCCCAGTAGCATCTCTATCAC  87282    AC       _  A
                                GT  TAGGGATGT ACT GGG
                                ||  ||||||||| ||| |||
                                CA  ATCTCTACG TGA CCC
                                 CT       A   C
GAM210  LOC91252  3'  CCCCAGCTCCTAGTAGTGA   65338    G       ATGTA  A
                                TCA TACTAGGG    CT GGG
                                ||| ||||||||    || |||
                                AGT ATGATCCT    GA CCC
                                  G       C____  C
GAM211  ADH4      3'  TAAAAAGATTTTTACTGGA   5409         CGT
                                TCCAGTGG   TCTTTTTA
                                ||||||||   ||||||||
                                AGGTCATT   AGAAAAAT
                                     TTT
GAM211  ADRA2B    3'  GGGGGAACACACTAGAG     5465     C    GC
                                CTC AGTG  GTTCTTTT
                                ||| ||||  ||||||||
                                GAG TCAC  CAAGGGGG
                                  A   A_
GAM211  CTBP1     3'  AAAAAGAAAACCTGAAGGAG   67942     AGT_  CG
                                CTCC    GG  TTCTTTTT
                                ||||    ||  ||||||||
                                GAGG    CC  AAGAAAAA
                                  AAGT  AA
GAM211  EGFL5     5'  GTAAAAAGAAAAATATGGGGA  86626     T   GTGGCG
                                TCC CCA     TTCTTTTTAC
                                ||| |||     ||||||||||
                                AGG GGT     AAGAAAAATG
                                  _  ATAAA_
GAM211  ENPP3     3'  TAAAAAGAACAGCAGAGAG   17227     CAGTG  _
                                CTC    GC GTTCTTTTTA
                                |||    || ||||||||||
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                                GAG    CG CAAGAAAAAT
                                  AGA__  A
GAM211  F8      3'  TAAAAAAATAAGTCAGGAGGA  3733       AG   GTTC_
                                TCCTCC  TGGC    TTTTTA
                                ||||||  ||||    ||||||
                                AGGAGG  ACTG    AAAAAT
                                   __   AATAA
GAM211  ID4     3'  AAAAAAAGCCACCGGAGGA   7752       A    GTTC
                                TCCTCC GTGGC   TTTTT
                                |||||| |||||   |||||
                                AGGAGG CACCG   AAAAA
                                   C    AA__
GAM211  PITX1   3'  AAAAAGACGTCGGAG      10596     AGT    T
                                CTCC   GGCGT CTTTTT
                                ||||   ||||| ||||||
                                GAGG   CTGCA GAAAAA
                                  ___    _
GAM211  TDG     3'  AAAAAGATGCTGGAG      12184       GCGT
                                CTCCAGTG   TCTTTTT
                                ||||||||   |||||||
                                GAGGTCGT   AGAAAAA
                                    _____
GAM211  XRCC2   3'  AAAAAGAACAAAGCTGGAGG  18314       GGC
                                CCTCCAGT   GTTCTTTTT
                                ||||||||   |||||||||
                                GGAGGTCG   CAAGAAAAA
                                     AAA
GAM211  ABCA10  5'  AAAAAGAGACCAGTGGA    54406     G   CG
                                TCCA TGG  TTCTTTTT
                                ||||  |||  ||||||||
                                AGGT ACC  GAGAAAAA
                                  G   A_
GAM211  ABCC13  3'  AAAAGTTTTCCACTGGGGA  56988     T     CGTT
                                TCC CCAGTGG   CTTTT
                                ||| |||||||   |||||
                                AGG GGTCACC   GAAAA
                                  _     TTTT
GAM211  ARFGAP1 3'  GGAACACCCTGGAAGA     36593    C    T  C
                                TC TCCAG GG GTTCT
                                || ||||| || |||||
                                AG AGGTC CC CAAGG
                                 A    _  A
GAM211  BA526D8.4 5'  TAAAAAAATTCATACTGGAGGG 70385         GCGTTC
                                TCCTCCAGTG     TTTTTA
                                ||||||||||     ||||||
                                GGGAGGTCAT     AAAAAT
                                     ACTTAA
GAM211  DKFZP727M111 5'  AAAAGGAAAAGCCCTGAAG   31402    C   T   G_
                                CT CAG GGC  TTCTTTTT
                                || ||| |||  ||||||||
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                                GA GTC CCG  AAGGAAAA
                                 A  _  AA
GAM211  DKFZp761H079 3'  AAAAAGAGCCAATGGA     58727     G   GT
                                TCCA TGGC  TCTTTTT
                                |||| ||||  |||||||
                                AGGT ACCG  AGAAAAA
                                  A  __
GAM211  FLJ10648  3'  AAAAAGAACAAAGTCCTGGAGG 36377       T  ___
          A                      TCCTCCAG GGC  GTTCTTTTT
                                 |||||||| |||  |||||||||
                                 AGGAGGTC CTG  CAAGAAAAA
                                     _  AAA
GAM211  FLJ20151  3'  AAAGACCCTGGAGGA      34649       T  CGT
                                 TCCTCCAG GG  TCTTT
                                 |||||||| ||  |||||
                                 AGGAGGTC CC  AGAAA
                                     _ ___
GAM211  FLJ20190  5'  AAAGGACACCATTGGAG    34702        C
                                 CTCCAGTGG GTTCTTT
                                 ||||||||| |||||||
                                 GAGGTTACC CAGGAAA
                                      A
GAM211  FLJ20435  3'  TAAAAAGAGCCATCTGGAGGA  35163       _  GT
                                 TCCTCCAG TGGC  TCTTTTTA
                                 |||||||| ||||  ||||||||
                                 AGGAGGTC ACCG  AGAAAAAT
                                     T  __
GAM211  FLJ22477  5'  GACACCATCTGGAGGA     45343       _  C
                                 TCCTCCAG TGG GTT
                                 |||||||| ||| |||
                                 AGGAGGTC ACC CAG
                                     T  A
GAM211  HNRPA3   3'  GTAAAAATCTGTCACAGAAGGA 19256     CCA    TTC
                                 TCCT  GTGGCG  TTTTTAC
                                 ||||  ||||||  |||||||
                                 AGGA  CACTGT  AAAAATG
                                   AGA    CT_
GAM211  KIAA1091  3'  GTAAAAAGAAAACTAGAGGA  69685     CAG  CG
                                 TCCTC  TGG  TTCTTTTTAC
                                 |||||  |||  ||||||||||
                                 AGGAG  ATC  AAGAAAAATG
                                    ___  AA
GAM211  KIAA1546  3'  AAAAAGAAGGTGGGGA     67900      CAGTG  G
                                 TCCTC    GC TTCTTTTT
                                 |||||    || ||||||||
                                 AGGGG    TG AAGAAAAA
                                    _____  G
GAM211  KIAA1956  3'  GTAAAACATAACACTGGAGGA  78439        GC  TCT
                                 TCCTCCAGTG  GT  TTTTAC
                                 ||||||||||  ||  ||||||
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                                AGGAGGTCAC  TA   AAAATG
                                      AA  C__
GAM211  MDS024   3'  AAAAAGAATTGCCAAGGA    41523     AG    _
                                TCC  TGGCG TTCTTTTT
                                |||  ||||| ||||||||
                                AGG  ACCGT AAGAAAAA
                                  A_    T
GAM211  MEGF11   3'  AAAAGGAGACTGGGGA     50576     T    GGCG
                                TCC CCAGT    TTCTTTTT
                                ||| |||||    ||||||||
                                AGG GGTCA    GAGGAAAA
                                  _    _____
GAM211  MGC11082 5'  AAAAAAAAGGCGGAGGG     51098       AGTG  G  C
                                TCCTCC    GC TT TTTTT
                                ||||||    || || |||||
                                GGGAGG    CG AA AAAAA
                                     _____  G  A
GAM211  MGC13105 3'  AAAAAGTCACACTAGAGGA   71477      C    GCGTT
                                TCCTC AGTG     CTTTTT
                                ||||| ||||     ||||||
                                AGGAG TCAC     GAAAAA
                                   A    ACT__
GAM211  RPL13    3'  AAAAAGAGCCAAGGA      78080     AG    GT
                                TCC  TGGC  TCTTTTT
                                |||  ||||  |||||||
                                AGG  ACCG  AGAAAAA
                                  A_    __
GAM211  ShrmL    5'  AGAGCGCCACTGAAGGA     40464      C
                                TCCT CAGTGGCGTTCT
                                |||| ||||||||||||
                                AGGA GTCACCGCGAGA
                                  A
GAM211  SIAT8C   5'  TAAAAAAGCCCCACAGAGGA   31884       CA    C   C
                                TCCTC  GTGG GTT TTTTTA
                                |||||  |||| ||| ||||||
                                AGGAG  CACC CGA AAAAAT
                                   A_    C   _
GAM211  VEST1    5'  AAAAAGATGCACTGGGGA    53679     T     G   T
                                TCC CCAGTG CGT CTTTTT
                                ||| |||||| ||| ||||||
                                AGG GGTCAC GTA GAAAAA
                                  _     _  _
GAM211  ZFD25    5'  AAAAAGAGCCCTGGA       32574       T   GT
                                TCCAG GGC  TCTTTTT
                                ||||| |||  |||||||
                                AGGTC CCG  AGAAAAA
                                     _  __
GAM211  LOC124626 3'  GTAAGACCAAACCACTGGA   74315         CGTTCT
                                TCCAGTGG     TTTTAC
                                ||||||||     ||||||
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                                AGGTCACC     AGAATG
                                    AAACC_
GAM211  LOC126302 3'  AAAAAGAAGCAGGAGGA     74486       AGTG  G
                                TCCTCC    GC TTCTTTTT
                                ||||||    || ||||||||
                                AGGAGG    CG AAGAAAAA
                                   A___  _
GAM211  LOC132332 5'  AAAAAGAAGGCTGGA       76159      GTG  G
                                TCCA   GC TTCTTTTT
                                ||||   || ||||||||
                                AGGT   CG AAGAAAAA
                                  ___ G
GAM211  LOC144577 3'  TAAAAAGAAGCCACAAAGAG   76903     CA_    G
                                CTC   GTGGC TTCTTTTTA
                                |||   ||||| |||||||||
                                GAG   CACCG AAGAAAAAT
                                  AAA    _
GAM211  LOC145078 3'  GTAAAAATCTGCCACAGAAGGA 60292      CCA     TTC
                                TCCT   GTGGCG   TTTTTAC
                                ||||   ||||||   |||||||
                                AGGA   CACCGT   AAAAATG
                                  AGA     CT_
GAM211  LOC145837 5'  AAAAAGAACCAAAGAGGA    83540      CAG   CG
                                TCCTC   TGG  TTCTTTTT
                                |||||   |||  ||||||||
                                AGGAG   ACC  AAGAAAAA
                                  AA_   __
GAM211  LOC148753 3'  AAAAGGAGCACCAGGGA     84207     AG   C
                                TCC  TGG GTTCTTTTT
                                |||  ||| |||||||||
                                AGG  ACC CGAGGAAAA
                                  G_   A
GAM211  LOC148981 3'  GTAAAAATCTGCCACAGAAGGA 84317      CCA     TTC
                                TCCT   GTGGCG   TTTTTAC
                                ||||   ||||||   |||||||
                                AGGA   CACCGT   AAAAATG
                                  AGA     CT_
GAM211  LOC153711 5'  AAAAGCGTCCCGCCAGAGGA   86129      CA    C TT
                                TCCTC  GTGG G  CTTTT
                                |||||  |||| |  |||||
                                AGGAG  CGCC T  GAAAA
                                  AC    C GC
GAM211  LOC154789 5'  GTAAAATCTCAGGCCACTAGAG 81140     C     GTTCT_
                                CTC AGTGGC     TTTTAC
                                ||| ||||||     ||||||
                                GAG TCACCG     AAAATG
                                  A     GACTCT
GAM211  LOC197322 3'  AAAGACTCCACTGGAGGA    89737          C  T
                                TCCTCCAGTGG GT CTTT
                                |||||||||| || ||||
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                                AGGAGGTCACC CA GAAA
                                       T  _
GAM211  LOC220988 3'  GTAAAAATCTGCCACAGAAGGA 90848     CCA     TTC
                                TCCT   GTGGCG   TTTTTAC
                                ||||   ||||||   |||||||
                                AGGA   CACCGT   AAAAATG
                                  AGA     CT_
GAM211  LOC221596 3'  TAAAAACCTCACACTGGAGAGA 91981    _      GCGTTC
                                TC CTCCAGTG     TTTTTA
                                || ||||||||     ||||||
                                AG GAGGTCAC     AAAAAT
                                 A       ACTCC_
GAM211  LOC255190 3'  GTAAAAATCTGCCACAGAAGGA 97689     CCA     TTC
                                TCCT   GTGGCG   TTTTTAC
                                ||||   ||||||   |||||||
                                AGGA   CACCGT   AAAAATG
                                  AGA     CT_
GAM211  LOC91796  3'  AAAAAGAACAAGGCTGGA    67207       GGC
                                TCCAGT   GTTCTTTTT
                                ||||||   |||||||||
                                AGGTCG   CAAGAAAAA
                                   GAA
GAM211  LOC92539  5'  TAAAAAGTGTCACTG       69639        TT
                                CAGTGGCG  CTTTTTA
                                ||||||||  |||||||
                                GTCACTGT  GAAAAAT
                                          __
GAM211  LOC93444  3'  GAACCCACTGGAAGA       72387    C       C
                                TC TCCAGTGG GTTC
                                || |||||||| ||||
                                AG AGGTCACC CAAG
                                 A       _
GAM211  LOC93538  5'  GTAAAGCTTCAGCGACTGAAGG 72562      C    G  GTTCT
           A                     TCCT CAGT GC     TTTTAC
                                ||||  |||| ||    ||||||
                                AGGA GTCA CG     GAAATG
                                  A    G  ACTTC
GAM212  ADRBK1    3'  CCCACTTCCCCTCCTACC     7866     C    TGAT  CAT
                                GG AGGA    GG   AAGTGGG
                                || ||||    ||   |||||||
                                CC TCCT    CC   TTCACCC
                                 A   _____  CC_
GAM212  ALPP      3'  CCCACCTCCTGTCGTCCTGCC  68833           CATAA
                                GGCAGGATGATGG    GTGGG
                                ||||||||||||     |||||
                                CCGTCCTGCTGTC    CACCC
                                        CTC__
GAM212  ALPPL2    3'  CCCACCTCCAGTCGTCCTGCC  68839          _  CATAA
                                GGCAGGATGA TGG    GTGGG
                                |||||||||| |||     |||||
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                                CCGTCCTGCT ACC    CACCC
                                     G  TC___
GAM212  BF      5'  CCAGGACACACCATCCTGCC  8138         A  GCATAAG
                                GGCAGGATG TG     TGG
                                ||||||||| ||     |||
                                CCGTCCTAC AC     ACC
                                     C  ACAGG__
GAM212  CYFIP2  3'  TCCATCCCATCATCCCACC   73587    CA       CATAA
                                GG  GGATGATGG    GTGGG
                                ||  |||||||||    |||||
                                CC  CCTACTACC    TACCT
                                 AC       C____
GAM212  DDIT3   3'  CCCACTTGGGCCACACTACC  14558    C  GA  A    A
                                GG AG  TG TGGC TAAGTGGG
                                || ||  || |||| ||||||||
                                CC TC  AC ACCG GTTCACCC
                                 A  __  _   G
GAM212  FAAH    3'  TCCCACCCCCTCCGTCCTGCC  44195         AT  CATAA
                                GGCAGGATG  GG    GTGGGA
                                |||||||||  ||    ||||||
                                CCGTCCTGC  CC    CACCCT
                                     CT  CC___
GAM212  FGFR3   3'  CCCACTTCCCACCCTGCC    3768       ATGA   CAT
                                GGCAGG   TGG   AAGTGGG
                                ||||||   |||   |||||||
                                CCGTCC   ACC   TTCACCC
                                   C___   C__
GAM212  HMGA1   3'  TCCCACTTAGCCGCACCCTGC  76936      A  A   A
                                GCAGG TG TGGC TAAGTGGGA
                                ||||| || |||| |||||||||
                                CGTCC AC GCCG ATTCACCCT
                                  C  _   _
GAM212  IGF2    3'  CCGGCGCCACCATCCTGC    5218         A   ATAA  G
                                GCAGGATG TGGC    GT GG
                                |||||||| ||||    || ||
                                CGTCCTAC ACCG    CG CC
                                     C    ____  G
GAM212  ITGAM   3'  CCCACTTACTTACCCTCACC  71837    A   T  CA__
                                GG TGA GG    TAAGTGGG
                                || ||| ||    ||||||||
                                CC ACT CC    ATTCACCC
                                 _   C  ATTC
GAM212  PEX14   3'  CCCACTCATGCCCCGTCGTCCT 63640    C      __    A
            CC                    GG AGGATGAT  GGCAT AGTGGG
                                || ||||||||  ||||| ||||||
                                CC TCCTGCTG  CCGTA TCACCC
                                 _       CC    C
GAM212  RAD18   3'  TCCCACCCCTCTGCCATCACCC 39398     A  A       TAA__
            AGCC                    GGC GG TGATGGCA    GTGGGA
                                ||| || ||||||||    ||||||
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                                CCG CC ACTACCGT    CACCCT
                                  A  C      CTCCC
GAM212  RGS16    5'  TCCTGGAGCCTGCCACCATCCT 11340        A    TAAGT_
             GCC                   GGCAGGATG TGGCA     GGGA
                                |||||||||  |||||     ||||
                                CCGTCCTAC ACCGT     TCCT
                                     C    CCGAGG
GAM212  RGS5     3'  CCCACTCAATTCTTCCTGCC  13237       T  TGGCATA
                                GGCAGGA GA      AGTGGG
                                |||||||  ||      ||||||
                                CCGTCCT CT      TCACCC
                                    T  TAAC___
GAM212  CSEN     3'  CCCAAGAAACCTCCATCCTGCC 25530        AT  CATAAG
                                GGCAGGATG  GG     TGGG
                                |||||||||  ||     ||||
                                CCGTCCTAC  CC     ACCC
                                     CT  AAAGA_
GAM212  FLJ20309 3'  TCCCAGAGGCCACATCCTGCC  34923        A   ATAAG
                                GGCAGGATG TGGC    TGGGA
                                |||||||||  ||||    |||||
                                CCGTCCTAC ACCG    ACCCT
                                     _   GAG__
GAM212  KIAA0455 3'  CCCACTTCTCACCACCACCGCC 72468    A  A  A   CAT_
                                GGC GG TG TGG    AAGTGGG
                                |||  ||  ||  |||   |||||||
                                CCG CC AC ACC    TTCACCC
                                  _  _  C   ACTC
GAM212  KIAA0652 3'  CCCACCCCTCATCCTGCT    28461         T  CATAA
                                GGCAGGATGA GG    GTGGG
                                ||||||||||  ||    |||||
                                TCGTCCTACT CC    CACCC
                                     C  _____
GAM212  KIAA1205 3'  CCCACCCACTGCCCATCCCC   70042    CA    AT    TAA_
                                GG  GGATG  GGCA   GTGGG
                                ||  |||||  ||||   |||||
                                CC  CCTAC  CCGT   CACCC
                                 __    __   CACC
GAM212  MAPKAPK2 3'  CCCCTGCCGCCCTCACCCTGCC 16471       A   T   ATA  T
                                GGCAGG TGA GGC   AG GGG
                                ||||||  |||  |||   ||  |||
                                CCGTCC ACT CCG   TC CCC
                                   C   C   CCG  _
GAM212  MGC3101  3'  TCCCACCTTGATTTCCATCCTG 43885        AT  _  TAA
             CC                    GGCAGGATG  GG CA   GTGGGA
                                |||||||||  ||  ||   ||||||
                                CCGTCCTAC  TT GT   CACCCT
                                     CT  A  TC_
GAM212  MPPE1    5'  CCTGAATGCCATCACCCTCC   43562    C   A       AAG
                                GG AGG TGATGGCAT   TGGG
                                ||  |||  |||||||||   ||||
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                                CC TCC ACTACCGTA   GTCC
                                 _  C       A__
GAM212  NOPAR    5'  CCACCCCCATCCTGC      53807        AT  CATAA
                                GCAGGATG  GG    GTGG
                                ||||||||  ||    ||||
                                CGTCCTAC  CC    CACC
                                    C_  _____
GAM212  PADI3    3'  CCCACCCACCATCCTGTC    32656         A   CATAA
                                GGCAGGATG TGG    GTGGG
                                ||||||||| |||    |||||
                                CTGTCCTAC ACC    CACCC
                                    C  _____
GAM212  PRTD-NY3  5'  TCCCACCACCACCATCATCCTG 48152    G         CATAA
              GC                  G CAGGATGATGG    GTGGGA
                                | ||||||||||    ||||||
                                C GTCCTACTACC    CACCCT
                                 G         ACCAC
GAM212  SCAM-1   3'  CCACCCCCATCCTGCT     19325         AT  CATAA
                                GGCAGGATG  GG    GTGG
                                |||||||||  ||    ||||
                                TCGTCCTAC  CC    CACC
                                    C_  _____
GAM212  SEPT6    3'  CCACCCCTATCCTGCC     30697         AT  CATAA
                                GGCAGGATG  GG    GTGG
                                |||||||||  ||    ||||
                                CCGTCCTAT  CC    CACC
                                    C_  _____
GAM212  YKT6     3'  CCCACAGATCCCCTGCT     21602       ATGAT  C  AA
                                GGCAGG    GG AT  GTGGG
                                ||||||    || ||  |||||
                                TCGTCC    CC TA  CACCC
                                   _____  _  GA
GAM212  LOC124470 3'  CCACTTTCCCCTGCC      75635       ATGAT  CAT
                                GGCAGG    GG   AAGTGG
                                ||||||    ||   ||||||
                                CCGTCC    CC   TTCACC
                                   _____  T__
GAM212  LOC132228 3'  CCAGATGCCACCACCCCCC   75044    CA  A  A     AAGTG
                                GG  GG TG TGGCAT    GG
                                ||  || || ||||||    ||
                                CC  CC AC ACCGTA    CC
                                 CC  _  C     GA___
GAM212  LOC149711 3'  TCCCACTTATCACACTCTACC  84691    C  GA  A  GC
                                GG AG  TG TG  ATAAGTGGGA
                                || ||  || ||  ||||||||||
                                CC TC  AC AC  TATTCACCCT
                                 A  TC  _  __
GAM212  LOC157931 3'  CCCACTTGCCACCATCCCC   86658    CA    A    TA
                                GG  GGATG TGGCA  AGTGGG
                                ||  ||||| |||||  ||||||
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                                CC  CCTAC ACCGT  TCACCC
                                 __     C     __
GAM212  LOC158062 5'  TCCCGTACACACACCATCCTGC 86679          A  GCATAAG
          C                      GGCAGGATG TG       TGGGA
                                 |||||||||  ||      |||||
                                 CCGTCCTAC AC       GCCCT
                                       C  ACACAT_
GAM212  LOC161357 3'  CCCACCTTATCCCCATCCCACC 82271    CA     AT  C    _
                                 GG  GGATG  GG ATAAG TGGG
                                 ||  |||||  ||  ||||| ||||
                                 CC  CCTAC  CC TATTC ACCC
                                  AC     C_  _     C
GAM212  LOC196205 3'  CCCAGCCCTCATCCTGCC    87590          T   ATAAG
                                 GGCAGGATGA GGC     TGGG
                                 ||||||||||  |||     ||||
                                 CCGTCCTACT CCG     ACCC
                                       C   _____
GAM212  LOC207092 5'  CCCTTTGCCATCATCT      90703          TAAGT
                                 GGATGATGGCA     GGG
                                 ||||||||||     |||
                                 TCTACTACCGT     CCC
                                       TT___
GAM212  LOC51336  5'  CCCCTGGCAACCACCATCCTAC 33576    C     A   CATA_  T
          T                      GG AGGATG TGG     AG GGG
                                 ||  ||||||  |||     ||  |||
                                 TC  TCCTAC ACC     TC  CCC
                                  A      C   AACGG  _
GAM213  ADRA2A    3'  CCGGGCGCTGCCTGCTCTG    5450          A     A
                                 CAGAGCAG CAGCG CTTGG
                                 ||||||||  |||||  |||||
                                 GTCTCGTC GTCGC GGGCC
                                       C     _
GAM213  B4GALT6   3'  TCACCCGTCCTCCCTGCTCTGA 59867          AC  C   TT  C
                                 TCAGAGCAG  AG GAC  GG GA
                                 |||||||||  ||  |||  ||  ||
                                 AGTCTCGTC  TC CTG  CC CT
                                       CC  _   C_  A
GAM213  BN51T     3'  CCACGGCTGCTGCCTGCTC    87493        A     A  _
                                 GAGCAG CAGCG CT TGG
                                 ||||||  |||||  ||  |||
                                 CTCGTC GTCGT GG ACC
                                     C     C  C
GAM213  CACNG7    3'  TCGTTCTCCACCTGCTCTGA   49098          AC____
                                 TCAGAGCAG      AGCGA
                                 |||||||||      |||||
                                 AGTCTCGTC      TTGCT
                                       CACCTC
GAM213  GNB5      5'  TCACCTCTCACCATCTGCTCTG 32468          CAGC  CTT  C
                                 CAGAGCAGA    GA   GG GA
                                 |||||||||    ||   ||  ||
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                                GTCTCGTCT   CT  CC CT
                                     ACCA  CT_  A
GAM213  KLHL3   3'  TCACCAAAGCCAATCTGCTCT 87466       CA_ GAC   C
                                AGAGCAGA  GC  TTGG GA
                                ||||||||  ||  |||| ||
                                TCTCGTCT  CG  AACC CT
                                     AAC  A__   A
GAM213  LAMP2   5'  CGCCGTCGCCGCCTGCTCTG  25710       ACA   TT
                                CAGAGCAG  GCGAC  GGCG
                                ||||||||  |||||  ||||
                                GTCTCGTC  CGCTG  CCGC
                                     CGC   __
GAM213  LAMP2   5'  CGCCGTCGCCGCCTGCTCTG  9683        ACA   TT
                                CAGAGCAG  GCGAC  GGCG
                                ||||||||  |||||  ||||
                                GTCTCGTC  CGCTG  CCGC
                                     CGC   __
GAM213  NAPB    3'  TCGCCAAGTCTGTGTTGCTGTG 70190    G   A  GC
            A                    TCA AGCAG CA  GACTTGGCGA
                                ||| ||||| ||  ||||||||||
                                AGT TCGTT GT  CTGAACCGCT
                                  G    _ GT
GAM213  PCSK2   3'  CCCAGCTGCTGCTCTGA    10465        A   GACT  C
                                TCAGAGCAG CAGC   TGG G
                                |||||||| ||||   ||| |
                                AGTCTCGTC GTCG   ACC C
                                     _   ____  A
GAM213  PLIN    3'  CCAGAGCCGCAGCCTGCTCTGA 10641       ACA  A  _
                                TCAGAGCAG  GCG CT TGG
                                |||||||||  ||| || |||
                                AGTCTCGTC  CGC GA ACC
                                     CGA  C  G
GAM213  PPP1R2  3'  CCCAATGTCTGCTCTG     20687         GCGAC   C
                                CAGAGCAGACA    TTGG G
                                ||||||||||    |||| |
                                GTCTCGTCTGT    AACC C
                                     _____  A
GAM213  PTMA    5'  CCACTGGCTGCTCTGA     11030        A  CGACT
                                TCAGAGCAG CAG    TGG
                                |||||||| |||    |||
                                AGTCTCGTC GTC    ACC
                                     G  _____
GAM213  RECQL   5'  TCACTGCCCTGCTCTGA    11284        A_  C
                                TCAGAGCAG  CAG GA
                                |||||||||  ||| ||
                                AGTCTCGTC  GTC CT
                                     CC   A
GAM213  C20orf18 3'  CCACGTCAACTGCCTGCTCTG  48338       A  C_  T
                                CAGAGCAG CAG  GAC TGG
                                |||||||| |||  ||| |||
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                                GTCTCGTC GTC  CTG ACC
                                     C   AA   C
GAM213  C20orf59  5'  TCATGAGTCGCCATCTGCCCTG 41997     A    CA      GC
              A                   TCAG GCAGA  GCGACTTG  GA
                                  |||| |||||  ||||||||  ||
                                  AGTC CGTCT  CGCTGAGT  CT
                                    C     AC       A_
GAM213  C9orf9    5'  TCGCGCGGGTCGCCCCCGC   38529    AGACA      _
                                  GC    GCGACTTG GCGA
                                  ||    |||||||| ||||
                                  CG    CGCTGGGC CGCT
                                   CCCC_       G
GAM213  CLIPR-59  5'  CCAGCGCTGTCTGC       31370          A  T
                                  GCAGACAGCG CT GG
                                  |||||||||| || ||
                                  CGTCTGTCGC GA CC
                                        _ _
GAM213  CXYorf1   3'  CAGGGCCGCTGCCCGCCCTGG  82039      A  AGA    A_
                                  TCAG GC   CAGCG  CTTG
                                  |||| ||   |||||  ||||
                                  GGTC CG   GTCGC  GGAC
                                    C  CCC    CG
GAM213  DNAJC6    3'  GTCAGTATCTGCTCTGA     28847          CA  _
                                  TCAGAGCAGA  GC GAC
                                  ||||||||||  || |||
                                  AGTCTCGTCT  TG CTG
                                        A_  A
GAM213  FLJ10656  3'  GCCAGTATCTGCTCT       36388         CAGCG   T
                                  AGAGCAGA    ACT GGC
                                  ||||||||    ||| |||
                                  TCTCGTCT    TGA CCG
                                      A____   _
GAM213  FLJ10901  3'  GCTATGCTTCTGCTCTGA    36827          C    ACT
                                  TCAGAGCAGA AGCG   TGGC
                                  |||||||||| ||||   ||||
                                  AGTCTCGTCT TCGT   ATCG
                                        _   ____
GAM213  FLJ12056  3'  TCCTGCCTGCTCTGA       46257          A   C
                                  TCAGAGCAG CAG GA
                                  |||||||| ||| ||
                                  AGTCTCGTC GTC CT
                                        C   _
GAM213  FLJ14154  3'  CGCCTTCCTGTCCATCTGA   45816       GCA    C  CTT
                                  TCAGA   GACAG GA   GGCG
                                  |||||   ||||| ||   ||||
                                  AGTCT   CTGTC CT   CCGC
                                     AC_     _ T__
GAM213  HRH3      5'  CGGCACCGCCTGCTCTGG    23367          ACA   ACT  G
                                  TCAGAGCAG   GCG   TG CG
                                  |||||||||   |||   || ||
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                                GGTCTCGTC  CGC  AC GC
                                    ___  C__  G
GAM213  HSU79266  3'  CGCCTGTTCCGTCTGCTC   25250       AGC  TT
                                GAGCAGAC  GAC  GGCG
                                ||||||||  |||  ||||
                                CTCGTCTG  TTG  CCGC
                                    CC_  T_
GAM213  KIAA0355  3'  CGGCACCGCCTTGCTCTGA   28024       ACA  ACT  G
                                TCAGAGCAG  GCG  TG CG
                                |||||||||  |||  || ||
                                AGTCTCGTT  CGC  AC GC
                                    C__  C__  G
GAM213  MGC10500  3'  CCAGTGCACCGTCTGCTCTG  48933       A__  G  T
                                CAGAGCAGAC  GC ACT GG
                                ||||||||||  || ||| ||
                                GTCTCGTCTG  CG TGA CC
                                    CCA  _  _
GAM213  MGC3178  3'  CCACTTATACTGTCTGTCTGA  47984     G     CGACT_
                                TCAGA CAGACAG     TGG
                                |||||  |||||||     |||
                                AGTCT GTCTGTC     ACC
                                   _     ATATTC
GAM213  MIG2     3'  TCACCAGCATAATCACTGTCTG 72425    A     C  C____   C
          CCT                    AG GCAGACAG GA    TTGG GA
                                || ||||||| ||    |||| ||
                                TC CGTCTGTC CT    GACC CT
                                 _      A  AATAC   A
GAM213  PIGQ     3'  GCCAGCCATCTGCTCTG     14850        CA  GACT
                                CAGAGCAGA  GC   TGGC
                                |||||||||  ||   ||||
                                GTCTCGTCT  CG   ACCG
                                    AC  ____
GAM213  RASGRP4  3'  CCAGCGCCATCTGCTC     53650       CA  A  T
                                GAGCAGA  GCG CT GG
                                |||||||  ||| || ||
                                CTCGTCT  CGC GA CC
                                    AC  _  _
GAM213  SLC2A11  5'  CGCCAAGTCTCTCGCTCTG   47964      _  CAGC
                                CAGAGC AGA   GACTTGGCG
                                ||||||  |||   |||||||||
                                GTCTCG TCT   CTGAACCGC
                                   C  ____
GAM213  LOC138307 3'  CCCTGCACCTGCTCTGA    75313       ACA  ACTT  C
                                TCAGAGCAG  GCG   GG G
                                |||||||||  |||   || |
                                AGTCTCGTC  CGT   CC C
                                    CA_  ____  A
GAM213  LOC144266 5'  TCACTCCCTCGCTGTCTCTCTG 76764      C       CTT  C
          A                     TCAGAG AGACAGCGA  GG GA
                                ||||||  |||||||||  || ||
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                                AGTCTC TCTGTCGCT   TC CT
                                  _       CCC  A
GAM213  LOC145123 5'  CCACTGGCTGCTCTGA      67526         A   CGACT
                                TCAGAGCAG CAG     TGG
                                ||||||||| |||     |||
                                AGTCTCGTC GTC     ACC
                                   G  _____
GAM213  LOC145226 3'  CGAATCCTGCCTGCTCTGA   77047         A   C  C
                                TCAGAGCAG CAG GA TTG
                                ||||||||| ||| || |||
                                AGTCTCGTC GTC CT AGC
                                   C   _  A
GAM213  LOC145725 3'  TCGCCATGTGCTCTGA      77416       AGACAGCG  T
                                TCAGAGC       AC TGGCGA
                                |||||||       || ||||||
                                AGTCTCG       TG ACCGCT
                                  _________  T
GAM213  LOC145732 3'  TCGCCATGTGCTCTGA      77438       AGACAGCG  T
                                TCAGAGC       AC TGGCGA
                                |||||||       || ||||||
                                AGTCTCG       TG ACCGCT
                                  _________  T
GAM213  LOC196411 3'  CGTCATCATCTGCTCTGA    87671         CAGC  CT
                                TCAGAGCAGA    GA  TGGCG
                                ||||||||||    ||  |||||
                                AGTCTCGTCT    CT  ACTGC
                                   A___  __
GAM213  LOC196961 3'  TCGCCATGTGCTCTGA      87853       AGACAGCG  T
                                TCAGAGC       AC TGGCGA
                                |||||||       || ||||||
                                AGTCTCG       TG ACCGCT
                                  _________  T
GAM213  LOC197138 3'  TCGCCATGTGCTCTGA      87926       AGACAGCG  T
                                TCAGAGC       AC TGGCGA
                                |||||||       || ||||||
                                AGTCTCG       TG ACCGCT
                                  _________  T
GAM213  LOC219920 5'  CCACCATCTTCCTGCTCTGA  93306         AC  CGACT
                                TCAGAGCAG  AG    TGG
                                |||||||||  ||    |||
                                AGTCTCGTC  TC    ACC
                                   CT  TACC_
GAM213  LOC255043 3'  CGCCCCCTGCTGCTGCTCTGA 95329         A    ACTT
                                TCAGAGCAG CAGCG    GGCG
                                ||||||||| |||||    ||||
                                AGTCTCGTC GTCGT    CCGC
                                   _    CCC_
GAM213  LOC257468 5'  TCGCCAAGCAGGTTCGCTCTGA 95189        AG  AGCGA
                                TCAGAGC  AC    CTTGGCGA
                                |||||||  ||    ||||||||
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                                AGTCTCG  TG    GAACCGCT
                                    CT  GAC__
GAM214  ACK1     3'  GGAGGACCCGCTGCTCCT    19344        G CAC  G  _
                                AGGAGCAG C   GT CC CC
                                |||||||| |   || || ||
                                TCCTCGTC G   CA GG GG
                                    _ CC_  _  A
GAM214  ADAM19   3'  GGGCACGCAAGAGAGCTTCCC  52709    A    AGGCCA_
                                GG GGAGC      CGTGCCC
                                || |||||      |||||||
                                CC CTTCG      GCACGGG
                                 _    AGAGAAC
GAM214  ADCY8    5'  CGTGACCCCCTCCTCCT     6653         CA  C
                                AGGAGGAG  GG CACG
                                ||||||||  || ||||
                                TCCTCCTC  CC GTGC
                                    CC  A
GAM214  AGPAT2   3'  GGGAATCGGGGCCTGCTGCTCC 21156      G      A  TG_
           T                     AGGAG AGCAGGCC CG   CCC
                                ||||| |||||||| ||   |||
                                TCCTC TCGTCCGG GC   GGG
                                   G       G  TAA
GAM214  AGPAT2   3'  GGGAATCGGGGCCTGCTGCTCC 65823      G      A  TG_
           T                     AGGAG AGCAGGCC CG   CCC
                                ||||| |||||||| ||   |||
                                TCCTC TCGTCCGG GC   GGG
                                   G       G  TAA
GAM214  AMT      5'  GGGGCTGCCCACGCCCCCT   4905     A  A  A__   CACGT
                                AGG GG GC   GGC    GCCCC
                                ||| || ||   |||    |||||
                                TCC CC CG   CCG    CGGGG
                                 _ _  CAC   T____
GAM214  ATP4A    3'  GGGCACGTGGGACCCTCT    5531       AGCAGG
                                GGAGG     CCACGTGCCC
                                |||||     ||||||||||
                                TCTCC     GGTGCACGGG
                                   CAG___
GAM214  ATRN     3'  TGGGACAGTCCCCTGCTCCTCT 57806          CC  G  C
                                GGAGGAGCAGG  AC TG CCCA
                                ||||||||||  || || ||||
                                TCTCCTCGTCC  TG AC GGGT
                                     CC  _  A
GAM214  BAALC    3'  TGAAGCAGTCATACCTGCTCCT 45666         CC__  G   CC
           C                     GAGGAGCAGG   AC TGC  CA
                                ||||||||||   || |||  ||
                                CTCCTCGTCC   TG ACG  GT
                                     ATAC  _   AA
GAM214  BGN      3'  GTTCATGGCCTGTCCCTCC   8144       AG      CGT
                                GGAGG  CAGGCCA   GC
                                |||||  |||||||   ||
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                                CCTCC  GTCCGGT   TG
                                   CT      ACT
GAM214  C1orf6   5'  GCTGCGGCCCGCCCGCC     39283    A  A  A    A  T
                                GG GG GC GGCC CG GC
                                || || || |||| || ||
                                CC CC CG CCGG GT CG
                                 G  _  C    C  _
GAM214  C1orf6   5'  GGCCCGCCCGCCCCTCCT    39285       A  A   CAC T
                                AGGAGG GC GGC   G GCC
                                |||||| || |||   | |||
                                TCCTCC CG CCG   C CGG
                                   C  C   ___ C
GAM214  CACNG7   3'  GGAGCTCCCCCTGCCTCCTCCT 49096         _   CCACGT  C
                                AGGAGGAG CAGG     GC CC
                                |||||||| ||||      || ||
                                TCCTCCTC GTCC     CG GG
                                     C    CCCT__  A
GAM214  CBFA2T3  5'  GCTGGCCCAGCCCCTCCT    17757       A  A_    C
                                AGGAGG GC  GGCCA GT
                                |||||| ||  ||||| ||
                                TCCTCC CG  CCGGT CG
                                   C  AC    _
GAM214  CD244    5'  GGCAGTTCTGCTCCCC      33062    A      CC  G
                                GG GGAGCAGG  AC TGCC
                                || ||||||||  || ||||
                                CC CCTCGTCT  TG ACGG
                                 _       __  _
GAM214  CDC42    3'  TGGAGCCCATCTTGCCCCTCCT 8372        A    CCACGT  C
                                AGGAGG GCAGG     GC CCA
                                |||||| |||||      || |||
                                TCCTCC CGTTC     CG GGT
                                   C    TACC__  A
GAM214  CLDN14   3'  CACAGCCTGCTTCTCC      24031           CAC
                                GGAGGAGCAGGC   GTG
                                ||||||||||||   |||
                                CCTCTTCGTCCG   CAC
                                       A__
GAM214  CLDN14   3'  CACAGCCTGCTTCTCC      57837           CAC
                                GGAGGAGCAGGC   GTG
                                ||||||||||||   |||
                                CCTCTTCGTCCG   CAC
                                       A__
GAM214  CRB1     5'  GGGCACCCGCTCCTCT      23867        A  CCAC    C
                                GGAGGAGC GG    GTGCC C
                                |||||||| ||    ||||| |
                                TCTCCTCG CC    CACGG G
                                     _ _____     A
GAM214  CRSP8    3'  ATGTGTACAGCTGCTCCTCC   80962          GC___
                                GGAGGAGCAG     CACGT
                                ||||||||||     |||||
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                                CCTCCTCGTC    GTGTA
                                      GACAT
GAM214  DAG1    3'  GGCAGCCTGCTCCCCT     15280     A       CACG
                                AGG GGAGCAGGC    TGCC
                                ||| |||||||||    ||||
                                TCC CCTCGTCCG    ACGG
                                  _       _____
GAM214  DAZ     5'  CACTGCCTCTGTTCCTCCT    14548          _ C  C
                                AGGAGGAGCAG G CA GTG
                                |||||||||||| | || |||
                                TCCTCCTTGTC C GT CAC
                                      T C  _
GAM214  DCN     5'  GCACCTACCCCCTCCTCCT    8618         CA  CCAC
                                AGGAGGAG  GG    GTGC
                                ||||||||  ||    ||||
                                TCCTCCTC  CC    CACG
                                     CC  ATC_
GAM214  DYRK1B  3'  GGGGAGATGGCCTTGCTCCTCC 16329          _    CGTG
          T                      AGGAGGAGCA GGCCA    CCCC
                                ||||||||||| |||||    ||||
                                TCCTCCTCGT CCGGT    GGGG
                                      T    AGA_
GAM214  EIF4EBP1 3'  GGGCACCTGCCCCCTCCT    14585       A_    CCACG
                                AGGAGG  GCAGG    TGCCC
                                ||||||  |||||    |||||
                                TCCTCC  CGTCC    ACGGG
                                   CC    ______
GAM214  EMD     3'  GTAGTGCTTGCTCCCCCT    3685      A       C  G
                                AGG GGAGCAGGC AC TGC
                                ||| ||||||||| || |||
                                TCC CCTCGTTCG TG ATG
                                  C       _ _
GAM214  GAB2    3'  GCTGCACCTCTCCTCCT     54453        C   CCA  T
                                AGGAGGAG AGG   CG GC
                                |||||||| |||   || ||
                                TCCTCCTC TCC   GT CG
                                     _   AC_  _
GAM214  GAB2    3'  GCTGCACCTCTCCTCCT     24496        C   CCA  T
                                AGGAGGAG AGG   CG GC
                                |||||||| |||   || ||
                                TCCTCCTC TCC   GT CG
                                     _   AC_  _
GAM214  GDF2    5'  GGGAGATGCCGGCCCGCTCCTT 32493         A   A_   GC
          C                      GGAGGAGC GGCC  CGT  CCC
                                |||||||| ||||  |||  |||
                                CTTCCTCG CCGG  GTA  GGG
                                     C    CC   GA
GAM214  HD      3'  GCAGCCCCTCCTCCT      9185         CA   CACG
                                AGGAGGAG  GGC    TGC
                                ||||||||  |||    |||
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                                TCCTCCTC  CCG   ACG
                                    C_  ____
GAM214  HDAC5   3'  GGGTCTCTCAGCCTTGCCCCTC 57611      A  _  CACGT_
            CT                   AGGAGG GCA GGC     GCCC
                                ||||||| ||| |||     ||||
                                TCCTCC CGT CCG     TGGG
                                   C   T   ACTCTC
GAM214  IL1F5   5'  GGGAATCCTGCTCCTCCT    24382          CCAC  GC
                                AGGAGGAGCAGG   GT  CCC
                                ||||||||||||   ||  |||
                                TCCTCCTCGTCC   TA  GGG
                                      ____  A_
GAM214  IMMP2L   5'  GGAGCTGGCCCGCTCCTCC   50730       A    CGT  C
                                GGAGGAGC GGCCA   GC CC
                                |||||||| |||||   || ||
                                CCTCCTCG CCGGT   CG GG
                                    C    ___  A
GAM214  ITPKB   3'  CGGAGGCCTGCTGCCCC    9428    A  _      A_
                                GG GG AGCAGGCC  CG
                                || || ||||||||  ||
                                CC CC TCGTCCGG  GC
                                 _  G       AG
GAM214  LAPTM5   3'  CGCTGGCCTGCTCCTCCT    22203            C
                                AGGAGGAGCAGGCCA GTG
                                |||||||||||||| |||
                                TCCTCCTCGTCCGGT CGC
                                                _
GAM214  LOH11CR2A 5'  TGTGGCCTACTCACCCT    27543    AG   C
                                AGG  GAG AGGCCACG
                                |||  ||| ||||||||
                                TCC  CTC TCCGGTGT
                                  CA   A
GAM214  LY9     3'  GGATGTGGCCCCTCCCCCT   71684    A   CA      G
                                AGG GGAG  GGCCACGT CC
                                ||| ||||  |||||||| ||
                                TCC CCTC  CCGGTGTA GG
                                  C   C_      _
GAM214  LZTR1   3'  TGGGGAAGTGACCTGCTCTCCT 22246      G    C  GTG
                                AGGAG AGCAGG CAC   CCCCA
                                ||||| |||||| |||   |||||
                                TCCTC TCGTCC GTG   GGGGT
                                   _     A   AA_
GAM214  MBD3    3'  GGGCTCGAGGCCAGCTCCTCC  14096       A   A  T
                                GGAGGAGC GGCC CG GCCC
                                |||||||| |||| || ||||
                                CCTCCTCG CCGG GC CGGG
                                    A   A  T
GAM214  MCC     3'  GGTGCCCGCTCTTCC      9959         A  CACGT
                                GGAGGAGC GGC    GCC
                                |||||||| |||    |||
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                                CCTTCTCG CCG    TGG
                                    C  _____
GAM214  MGAT1   3'  GGGCACGAGCCCTCCT    10010     CA  CA
                                AGGAG  GGC  CGTGCCC
                                |||||  |||  |||||||
                                TCCTC  CCG  GCACGGG
                                  __  A_
GAM214  MYO1C   3'  GGACACCTCTCCTCCT     61208       C  CCAC  G
                                AGGAGGAG AGG   GT CC
                                |||||||| |||   || ||
                                TCCTCCTC TCC   CA GG
                                    _  A___  _
GAM214  NCF4    3'  GGCTCGTGGCCTCCCCTCC   25510     AGC     T
                                GGAGG  AGGCCACG GCC
                                |||||  |||||||| |||
                                CCTCC  TCCGGTGC CGG
                                  CC_      T
GAM214  OGT     5'  CACACAACCTCCTCCTCCT   13200       C  CCAC
                                AGGAGGAG AGG   GTG
                                |||||||| |||   |||
                                TCCTCCTC TCC   CAC
                                    C  AACA
GAM214  OIP2    5'  GGGAGACCCGCTCCTTCT    76984       A  CCAC  GC
                                AGGAGGAGC GG   GT  CCC
                                ||||||||| ||   ||  |||
                                TCTTCCTCG CC   CA  GGG
                                    _ ____  GA
GAM214  PCDH11X 3'  GGCACATGACTGCTTCT    52026       GC  C
                                AGGAGCAG  CA GTGCC
                                ||||||||  || |||||
                                TCTTCGTC  GT CACGG
                                    A_  A
GAM214  PCDH11X 3'  GGCACATGACTGCTTCT    52048       GC  C
                                AGGAGCAG  CA GTGCC
                                ||||||||  || |||||
                                TCTTCGTC  GT CACGG
                                    A_  A
GAM214  PCDH11Y 3'  GGCACATGACTGCTTCT    52082       GC  C
                                AGGAGCAG  CA GTGCC
                                ||||||||  || |||||
                                TCTTCGTC  GT CACGG
                                    A_  A
GAM214  PDGFRB  5'  GGCGGCTCTGCTCCTCC    65979         _  ACGT
                                GGAGGAGCAG GCC   GCC
                                |||||||||| |||   |||
                                CCTCCTCGTC CGG   CGG
                                     T  ____
GAM214  PFKL    3'  CACTGTGACCTGCTCCTGCC  10515   _      C  _
                                GG AGGAGCAGG CAC GTG
                                || ||||||||| ||| |||
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                                CC TCCTCGTCC GTG CAC
                                 G       A  T
GAM214  PIK4CB   3'  TGGGGCTTCCCTGCCCCTCCT  10595       A    CCACGT
                                AGGAGG GCAGG     GCCCCA
                                |||||| |||||     ||||||
                                TCCTCC CGTCC     CGGGGT
                                   C    CTT___
GAM214  PK428    5'  GGAAGCACCCCTCCTCCT    13212        CA  CCAC   C_
                                AGGAGGAG  GG   GTGC  CC
                                ||||||||  ||   ||||  ||
                                TCCTCCTC  CC   CACG  GG
                                    __  ____   AA
GAM214  PMX1     5'  CACCCTCTCCTCCT       22590        C   CCAC
                                AGGAGGAG AGG   GTG
                                |||||||| |||   |||
                                TCCTCCTC TCC   CAC
                                    _  ____
GAM214  PMX1     5'  CACCCTCTCCTCCT       42658        C   CCAC
                                AGGAGGAG AGG   GTG
                                |||||||| |||   |||
                                TCCTCCTC TCC   CAC
                                    _  ____
GAM214  PROX1    5'  GCGCTCCGCTCCTCC      10894        A  CCAC
                                GGAGGAGC GG   GTGC
                                |||||||| ||   ||||
                                CCTCCTCG CC   CGCG
                                    _  T___
GAM214  PRX      3'  TGGAGCCCCGGCCCGCTGCTCC 40542      G   A   ACGT  C
           T                     AGGAG AGC GGCC   GC CCA
                                ||||| ||| ||||   || |||
                                TCCTC TCG CCGG   CG GGT
                                  G   C   CCC_  A
GAM214  PTPRK    5'  GGCCCGGCCCGCTCCTCC    11124        A   ACGT
                                GGAGGAGC GGCC   GCC
                                |||||||| ||||   |||
                                CCTCCTCG CCGG   CGG
                                    C   CC__
GAM214  RHO      3'  GGGATGTGTGCCCCTCCTCCT  5020        CA  _    G
                                AGGAGGAG  GGC CACGT CCC
                                ||||||||  ||| ||||| |||
                                TCCTCCTC  CCG GTGTA GGG
                                    C_  T    _
GAM214  ROR2     3'  GGCCCTGCTCCTCT       15854          CCACGT  C
                                GGAGGAGCAGG     GC C
                                ||||||||||     || |
                                TCTCCTCGTCC     CG G
                                      _____  A
GAM214  RPH3AL   3'  GGGCACGTGGCTCCCTC     22752      AGCA
                                GAGG   GGCCACGTGCCC
                                ||||   ||||||||||||
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                                CTCC    TCGGTGCACGGG
                                  C___
GAM214  SELPLG   3'  TGAGGCTGTTTCCTGCTGCTCC 59691      G     CC   T   C
            T                    AGGAG AGCAGG  ACG GCC CA
                                 ||||| ||||||  ||| ||| ||
                                 TCCTC TCGTCC  TGT CGG GT
                                    G     TT   _   A
GAM214  SERPINB9 3'  CACTGCAACCTCCTCCTCCT   14750        C   C__  C
                                 AGGAGGAG AGG   CA GTG
                                 |||||||| |||   || |||
                                 TCCTCCTC TCC   GT CAC
                                     C   AAC  _
GAM214  SH2D2A   3'  TGCGGAGCCTGCTCCCTCC    14275      _      CA
                                 GGAGG AGCAGGC  CGTG
                                 ||||| |||||||  ||||
                                 CCTCC TCGTCCG  GCGT
                                    C       AG
GAM214  SLC2A2   5'  GGGTAGCCCAACTCCTCC    4421        CA_   CACG
                                 GGAGGAG   GGC    TGCCC
                                 |||||||   |||    |||||
                                 CCTCCTC   CCG    ATGGG
                                     AAC   _____
GAM214  SLC9A1   3'  TGAGGCCGGCCCTGCCCCTCC  70413      A    CCA  T   C
                                 GGAGG GCAGG   CG GCC CA
                                 ||||| |||||   || ||| ||
                                 CCTCC CGTCC   GC CGG GT
                                    C     CG_  _   A
GAM214  SNTB1    3'  GGACATTTTTACCTACTCCTCC 40704        C   CCAC_   _
            T                    AGGAGGAG AGG     GTG CC
                                 |||||||| |||     ||| ||
                                 TCCTCCTC TCC     TAC GG
                                     A   ATTTT   A
GAM214  SOX12    3'  CGGAGGACCCGCCCCCTCCT   22695       A_  A  _  A_
                                 AGGAGG  GC GG CC  CG
                                 ||||||  || || ||  ||
                                 TCCTCC  CG CC GG  GC
                                    CC  C  A  AG
GAM214  TARBP2   5'  GGAGGGCCCGCTCCTCC     56167        A    ACGTG
                                 GGAGGAGC GGCC     CC
                                 |||||||| ||||     ||
                                 CCTCCTCG CCGG     GG
                                     C    GA___
GAM214  TARBP2   5'  GGAGGGCCCGCTCCTCC     56159        A    ACGTG
                                 GGAGGAGC GGCC     CC
                                 |||||||| ||||     ||
                                 CCTCCTCG CCGG     GG
                                     C    GA___
GAM214  TCP10    3'  GCCTGGCCTGCTCCCCT     16044     A         C
                                 AGG GGAGCAGGCCA GT
                                 ||| ||||||||||| ||
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                                TCC CCTCGTCCGGT CG
                                  _        C
GAM214  TMEPAI   3' CGTGTGGCCCTCCCCTCC    39445      AGCA
                                GGAGG   GGCCACGTG
                                |||||   |||||||||
                                CCTCC   CCGGTGTGC
                                   CCTC
GAM214  TMSB4Y   3' TGGAGGCCACGCCTGCTTCTCC 14845          CAC  _ _
                                GGAGGAGCAGGC  GTG CC CCA
                                ||||||||||||  ||| || |||
                                CCTCTTCGTCCG  CAC GG GGT
                                      ___  C  A
GAM214  TNFSF4   3' TGGGTGCACCTGGCCTGCTCTT 12447           C   _
           CC                     GGAGGAGCAGGCCA GTGC CCCA
                                ||||||||||||| |||| ||||
                                CCTTCTCGTCCGGT CACG GGGT
                                      C   T
GAM214  TRPV2    5' GCAGCCTCCTCCTCCT     32267       C   CACG
                                AGGAGGAG AGGC   TGC
                                |||||||| ||||   |||
                                TCCTCCTC TCCG   ACG
                                    C   ____
GAM214  ZFP103   5' GGCGGCCGCTCCTCC      19024       A   ACGT
                                GGAGGAGC GGCC   GCC
                                |||||||| ||||   |||
                                CCTCCTCG CCGG   CGG
                                   _   _____
GAM214  ZNF131   5' GCCTGGGCCGCTCCTCCT    70159        A   A  T
                                AGGAGGAGC GGCC CG GC
                                ||||||||| |||| || ||
                                TCCTCCTCG CCGG GT CG
                                    _   _ C
GAM214  A4GALT   3' TGGGGCACTGGGCCGCCCTTCC 33841      A  A   AC
                                GGAGG GC GGCC  GTGCCCCA
                                ||||| || ||||  ||||||||
                                CCTTC CG CCGG  CACGGGGT
                                  C  _   GT
GAM214  BIRC5    3' GGGGCACATGCTGGCCGCTCCT 6750        A   C___
           CC                     GGAGGAGC GGCCA   GTGCCCC
                                |||||||| |||||   |||||||
                                CCTCCTCG CCGGT   CACGGGG
                                   _    CGTA
GAM214  BRD1     5' GGGCCGGACCCCTCCTCCT   27416       CA  CCA  T
                                AGGAGGAG  GG   CG GCCC
                                ||||||||  ||   || ||||
                                TCCTCCTC  CC   GC CGGG
                                   C_  AG_  _
GAM214  C12orf22 5' GGGACTCGCTCGCTCCTCC   47980       AG  CAC  G
                                GGAGGAGC  GC   GT CCC
                                ||||||||  ||   || |||
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                                  CCTCCTCG  CG   CA GGG
                                       CT  CT_  _
GAM214  C17orf31  3'  GGGGGACCTGCTCCTC      34126          CCACG G
                                  GAGGAGCAGG    T CCCC
                                  ||||||||||    | ||||
                                  CTCCTCGTCC    A GGGG
                                        _____ G
GAM214  C20orf100 3'  CGGAGCACTGCTCTCCT     51810      G    _ CA
                                  AGGAG AGCAG GC  CG
                                  ||||| ||||| ||  ||
                                  TCCTC TCGTC CG  GC
                                     _    A  AG
GAM214  C20orf39  3'  GCCCGGGACCTGCCCCTCTT   46044       A    _ A  T
                                  AGGAGG GCAGG CC CG GC
                                  |||||| ||||| || || ||
                                  TTCTCC CGTCC GG GC CG
                                      C    A  _  C
GAM214  CAMKK1    3'  GGAACCCAGCCTCTCCTCCT   50174        C   CAC  G
                                  AGGAGGAG AGGC   GT CC
                                  |||||||| ||||   || ||
                                  TCCTCCTC TCCG   CA GG
                                       _   ACC  A
GAM214  CAMTA2    3'  GGAGCCCTGCCTGCCCCTGCT  61221    G   A     CACGT  C
                                  AG AGG GCAGGC    GC CC
                                  || ||| ||||||    || ||
                                  TC TCC CGTCCG    CG GG
                                   G   C     TCC__  A
GAM214  CARD9     5'  GGCGTCCGGCGTGCTCCTCC   53375        G   ACG
                                  GGAGGAGCA GCC   TGCC
                                  ||||||||| |||   ||||
                                  CCTCCTCGT CGG   GCGG
                                       G   CCT
GAM214  CARD9     5'  GGCGTCCGGCGTGCTCCTCC   53381        G   ACG
                                  GGAGGAGCA GCC   TGCC
                                  ||||||||| |||   ||||
                                  CCTCCTCGT CGG   GCGG
                                       G   CCT
GAM214  CARD9     5'  GGCGTCCGGCGTGCTCCTCC   42288        G   ACG
                                  GGAGGAGCA GCC   TGCC
                                  ||||||||| |||   ||||
                                  CCTCCTCGT CGG   GCGG
                                       G   CCT
GAM214  CIC       3'  GGAATGAGGCCTGCTCCTCTT  30675           A   G
                                  AGGAGGAGCAGGCC CGT CC
                                  |||||||||||||| ||| ||
                                  TTCTCCTCGTCCGG GTA GG
                                         A   A
GAM214  DAZ2      5'  CACTGCCTCTGTTCCTCCT    39798          _ C  C
                                  AGGAGGAGCAG G CA GTG
                                  |||||||||| | || |||
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                                TCCTCCTTGTC C GT CAC
                                      T C  _
GAM214  DAZ3     5'  CACTGCCTCTGTTCCTCCT   39801          _ C  C
                                AGGAGGAGCAG G CA GTG
                                |||||||||||  | || |||
                                TCCTCCTTGTC C GT CAC
                                      T C  _
GAM214  DAZ3     5'  CACTGCCTCTGTTCCTCCT   60532          _ C  C
                                AGGAGGAGCAG G CA GTG
                                |||||||||||  | || |||
                                TCCTCCTTGTC C GT CAC
                                      T C  _
GAM214  DCAMKL1  3'  GGCGCAGCCAGCTCCTCC    16414        A   CAC
                                GGAGGAGC GGC   GTGCC
                                ||||||||  |||   |||||
                                CCTCCTCG CCG   CGCGG
                                     A   A__
GAM214  DKFZP434B103 3'  CGAGGCTCCTGCTCTCCT    31590      G    __   A
                                AGGAG AGCAG  GCC CG
                                |||||  |||||  |||  ||
                                TCCTC TCGTC  CGG GC
                                   _    CT   A
GAM214  DKFZp434I1930 3'  TGGGGCACCCCTCTGCCTCCCC 50034    A   _   CCAC
          C                      GG GGAG CAGG    GTGCCCCA
                                || |||| ||||   ||||||||
                                CC CCTC GTCT    CACGGGGT
                                 C   C   CCC_
GAM214  DKFZP434N178 3'  GGGAGGCCTGCTCCCTCT    71907    GA       ACGTGC
                                AG  GGAGCAGGCC     CCC
                                ||  ||||||||||     |||
                                TC  CCTCGTCCGG     GGG
                                 TC        A_____
GAM214  DKFZP434O047 5'  GGAACAAGCCCCTCCTCCT   31515        CA   CAC  G
                                AGGAGGAG  GGC   GT CC
                                ||||||||  |||   || ||
                                TCCTCCTC  CCG   CA GG
                                     C_   AA_  A
GAM214  DKFZP564J157 3'  GGAACCTTACCTCTCCTCCT   37456        C   CCAC  G
                                AGGAGGAG AGG    GT CC
                                ||||||||  |||    || ||
                                TCCTCCTC TCC    CA GG
                                     _   ATTC  A
GAM214  DKFZP586J1624 3'  GGGTGGGGCCTGCTCCTC    31396          ACGT
                                GAGGAGCAGGCC    GCCC
                                ||||||||||||    ||||
                                CTCCTCGTCCGG    TGGG
                                      GG__
GAM214  DKFZP586M1120 3'  GGGACGCGCCGGGCCTGCTCCT 48467           A__   C
          CC                     GGAGGAGCAGGCC   CGTG CCC
                                ||||||||||||   |||| |||
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                                CCTCCTCGTCCGG  GCGC GGG
                                       GCC   A
GAM214  DKFZp762K222 5'  GCCGTGGCCTCCCCTCC    71118      AGC      T
                                GGAGG  AGGCCACG GC
                                |||||  |||||||| ||
                                CCTCC  TCCGGTGC CG
                                  CC_      _
GAM214  DNAJC5   3'  CACGACCCCTCCTCCT     61448        CA  CCA
                                AGGAGGAG  GG  CGTG
                                ||||||||  ||  ||||
                                TCCTCCTC  CC  GCAC
                                    C_  A__
GAM214  DOC-1R   3'  GCACCCGCTTCTCC       19580        A  CCAC
                                GGAGGAGC GG   GTGC
                                |||||||| ||   ||||
                                CCTCTTCG CC   CACG
                                  _ _____
GAM214  DPYSL4   3'  GGGCACTCGCCCCCCTCCT   21217      AGCA  CAC
                                AGGAGG   GGC  GTGCCC
                                ||||||   |||  ||||||
                                TCCTCC   CCG  CACGGG
                                   CC__  CT_
GAM214  DRIL2    3'  GGGCAGCTCTGTCCCCTCCT  21327      A_   _ CACG
                                AGGAGG  GCAG GC   TGCCC
                                ||||||  |||| ||   |||||
                                TCCTCC  TGTC CG   ACGGG
                                   CC   T _____
GAM214  EFS2     3'  GGCACAGCTCTGCTCCTCC   19624        _ CAC
                                GGAGGAGCAG GC  GTGCC
                                |||||||||| ||  |||||
                                CCTCCTCGTC CG  CACGG
                                     T  A__
GAM214  EFS2     5'  GGCCCGCCCCGCTCCTCCT   19625        A  CCA  T
                                AGGAGGAGC GG  CG GCC
                                ||||||||| ||  || |||
                                TCCTCCTCG CC  GC CGG
                                     C  C__  C
GAM214  EIF4B    3'  GGAGGCTGCCAGCCCCTCCT  75969      A  A  CACGT  _
                                AGGAGG GC GGC   GCC CC
                                |||||| || |||   ||| ||
                                TCCTCC CG CCG   CGG GG
                                   C  A  T_____  A
GAM214  EPI64    3'  TGGGGCCTCCTTCAGCCCCCTC 49196       CA  CACGT___
           CTCCT               AGGAGGAG  GGC      GCCCCA
                                ||||||||  |||      ||||||
                                TCCTCCTC  CCG      CGGGGT
                                    CC   ACTTCCTC
GAM214  EPS8R1   5'  GGCAGCCTGTCCTCCT     57602       G    CACG
                                AGGAGGA CAGGC   TGCC
                                ||||||| |||||   ||||
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                                TCCTCCT GTCCG   ACGG
                                    _   _____
GAM214  EVI5    3'  TGGGGCACACCCATGCTCACCC 19019    AG    _ CCAC
            T                    AGG  GAGCA GG   GTGCCCCA
                                 |||  ||||| ||   ||||||||
                                 TCC  CTCGT CC   CACGGGGT
                                   CA    A  CA__
GAM214  FATE    3'  TGGAGCCCTCCCTGCTTCCCCT 52361    A      CCACGT  C
                                 AGG GGAGCAGG     GC CCA
                                 ||| ||||||||     || |||
                                 TCC CTTCGTCC     CG GGT
                                   C       CTCC__  A
GAM214  FBP17   3'  ATGGGACACACGCCCCTACCTG 72779       CCA___   C__   III
            CTCCTTC                 AGCAGG     CGTG   CCCA   T
                                 ||||||     ||||   ||||  |
                                 TCGTCC     GCAC   GGGT   A
                                    ATCCCC    ACA   III
GAM214  FER1L4  3'  ATGTGCCTGCTCCACC     47333    A       C
                                 GG GGAGCAGGC ACGT
                                 || |||||||| ||||
                                 CC CCTCGTCCG TGTA
                                  A       _
GAM214  FLJ10008 3'  GTGGACTTGCTCCCCCT     35730     A      _
                                 AGG GGAGCAGG CCAC
                                 ||| |||||||| ||||
                                 TCC CCTCGTTC GGTG
                                   C       A
GAM214  FLJ10803 5'  GGTGCCTGCTTCCCCT      36670     A       CACGT
                                 AGG GGAGCAGGC    GCC
                                 ||| |||||||||    |||
                                 TCC CTTCGTCCG    TGG
                                   C       _____
GAM214  FLJ11280 3'  GGCTGGCCTGCCCCTTCT    37210       A       CGT
                                 AGGAGG GCAGGCCA   GCC
                                 |||||| ||||||||   |||
                                 TCTTCC CGTCCGGT   CGG
                                    C       ___
GAM214  FLJ11301 3'  ATGTGCCTGCTTCTCCT     37225           C
                                 AGGAGGAGCAGGC ACGT
                                 |||||||||||| ||||
                                 TCCTCTTCGTCCG TGTA
                                                _
GAM214  FLJ11383 3'  CACATGGACTCCCTCTTCCT   46282        CA _   C
                                 AGGAGGAG  GG CCA GTG
                                 ||||||||  || ||| |||
                                 TCCTTCTC  TC GGT CAC
                                      CC  A   A
GAM214  FLJ12057 3'  TGCGAGCCCCTCCTCCT     45442        CA   CA
                                 AGGAGGAG  GGC  CGTG
                                 ||||||||  |||  ||||
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                                TCCTCCTC  CCG  GCGT
                                    C_   A_
GAM214  FLJ12387  3'  GGGACCTTCTCGCGCTCCTCCT 43068        A_  CCAC  G
                                AGGAGGAGC  GG    GT CCC
                                |||||||||  ||    || |||
                                TCCTCCTCG  CT    CA GGG
                                    CG  CTTC  _
GAM214  FLJ13052  3'  TGGAGCACGTGGATGCTGCCTA 43474    _  _   GG      C
          CC                     GG AGG AGCA  CCACGTGC CCA
                                || ||| ||||  |||||||| |||
                                CC TCC TCGT  GGTGCACG GGT
                                 A  G   A_      A
GAM214  FLJ13310  3'  GGTGCCTGCTTCTCCT      47084           CACGT
                                AGGAGGAGCAGGC    GCC
                                ||||||||||||     |||
                                TCCTCTTCGTCCG    TGG
                                      _____
GAM214  FLJ13848  3'  GGTATCAGCTGCTCCTCCT   45471          G CAC
                                AGGAGGAGCAG C   GTGCC
                                ||||||||||| |   |||||
                                TCCTCCTCGTC G   TATGG
                                      _ AC_
GAM214  FLJ20397  3'  GTCGCAGCCGCTCCTCC     35123        A   CA  T
                                GGAGGAGC GGC  CG GC
                                |||||||| |||  || ||
                                CCTCCTCG CCG  GC TG
                                    _   AC  _
GAM214  FLJ21019  3'  GGGAGAGAGCCAGCTCCTCCT  46245        A   CACGTG
                                AGGAGGAGC GGC     CCC
                                ||||||||| |||     |||
                                TCCTCCTCG CCG     GGG
                                    A   AGAGA_
GAM214  FLJ22671  3'  GTGTGTGGCCCCTCCCCCT   45867     A    CA      TG
                                AGG GGAG  GGCCACG  C
                                ||| ||||  |||||||  |
                                TCC CCTC  CCGGTGT  G
                                  C    C_      GT
GAM214  FOXH1     3'  ACAGGGGCCGCTCCTCC     14069        A    AC_
                                GGAGGAGC GGCC   GT
                                |||||||| ||||   ||
                                CCTCCTCG CCGG   CA
                                    _    GGA
GAM214  GNG3      3'  TGAGGCACCCTTTGCTCCACC  24192    A      CCAC     C
                                GG GGAGCAGG    GTGCC CA
                                || ||||||||    ||||| ||
                                CC CCTCGTTT    CACGG GT
                                 A       CC__     A
GAM214  HAND2     3'  GGGCATCTGCTCCCC       41749    A      GCCAC    C
                                GG GGAGCAG     GTGCC C
                                || |||||||     ||||| |
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                                CC CCTCGTC     TACGG G
                                 _      _____     A
GAM214  HCC-4     3'  TGGGACAGGTTGCTGGCCCTCC 56820       A A   C  G  C
                                GGAGG GC GGC AC TG CCCA
                                ||||| || ||| || || ||||
                                CCTCC CG TCG TG AC GGGT
                                  _ G   T  G  A
GAM214  HS6ST     3'  GGAAGCCTGCTCCCCT      62029     A       CACGTG
                                AGG GGAGCAGGC      CC
                                ||| |||||||||      ||
                                TCC CCTCGTCCG      GG
                                  _        AA____
GAM214  HS6ST1    3'  GGAAGCCTGCTCCCCT      16660     A       CACGTG
                                AGG GGAGCAGGC      CC
                                ||| |||||||||      ||
                                TCC CCTCGTCCG      GG
                                  _        AA____
GAM214  HSA243666 3'  CACCTGGTCTGCCCCT      34146     A       C
                                AGG GCAGGCCA GTG
                                ||| |||||||| |||
                                TCC CGTCTGGT CAC
                                  C        C
GAM214  HSJ1      3'  GGAGCCTCCTGCTCTCCT     22134      G     CCACGT  C
                                AGGAG AGCAGG      GC CC
                                ||||| ||||||      || ||
                                TCCTC TCGTCC      CG GG
                                   _      TC____  A
GAM214  HSPC065   3'  GCTGCAACCTCCTCCTCCT    26313        C   CCA  T
                                AGGAGGAG AGG   CG GC
                                |||||||| |||   || ||
                                TCCTCCTC TCC   GT CG
                                     C   AAC  _
GAM214  IKKE      3'  GGGGCACATGAGGCATCCT    25749      _ AGGC  C
                                AGGA GC    CA GTGCCCC
                                |||| ||    || |||||||
                                TCCT CG    GT CACGGGG
                                  A  GA__  A
GAM214  IL18BP    3'  GGAACCAGGGCCTACTCCTCTT 19109        C    AC_  G
                                AGGAGGAG AGGCC   GT CC
                                |||||||| |||||   || ||
                                TTCTCCTC TCCGG   CA GG
                                     A     GAC  A
GAM214  KHDRBS3   5'  GCCCGCGCCCGCTCCTCCT    21619         A   CA  T
                                AGGAGGAGC GGC  CG GC
                                ||||||||| |||  || ||
                                TCCTCCTCG CCG  GC CG
                                     C   C_  C
GAM214  KIAA0016  5'  TGAGGGTTCGTGGCCCACCGCT 28647       A___      T   _
            CCT                    AGGAGC    GGCCACG GCCC CA
                                ||||||    ||||||| |||| ||
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                                TCCTCG   CCGGTGC TGGG GT
                                   CCAC     T   A
GAM214  KIAA0056 3' TGGAACACGAGAGCTCCTCCT 91555       AGGCCA   CC
                                AGGAGGAGC     CGTG  CCA
                                |||||||||     ||||  |||
                                TCCTCCTCG     GCAC  GGT
                                     AGA___    AA
GAM214  KIAA0133 3' GGGCTCCTGCCTGCTCCTCCT 28769          CACGT
                                AGGAGGAGCAGGC    GCCC
                                ||||||||||||     ||||
                                TCCTCCTCGTCCG    CGGG
                                       TCCT_
GAM214  KIAA0285 3' GGAACAGGCTGCTCCTTCT   29019         G  AC  G
                                AGGAGGAGCAG CC  GT CC
                                |||||||||| ||  || ||
                                TCTTCCTCGTC GG  CA GG
                                      _ A_  A
GAM214  KIAA0322 5' GGGGCACGTGCGCCCCCC    92753    A  AGCA  _
                                GG GG    GGC CACGTGCCCC
                                || ||    ||| ||||||||||
                                CC CC    CCG GTGCACGGGG
                                 _ _____  C
GAM214  KIAA0450 5' GGCCGCCTCACCTGCTCCCCCT 27642     A       CCA__  T
                                AGG GGAGCAGG     CG GCC
                                ||| ||||||||     || |||
                                TCC CCTCGTCC     GC CGG
                                  C       ACTCC  _
GAM214  KIAA0513 3' GGGCACTGCTCTCCTCCT    28367        CA   CAC
                                AGGAGGAG  GGC   GTGCCC
                                ||||||||  |||   ||||||
                                TCCTCCTC  TCG   CACGGG
                                     __   T__
GAM214  KIAA0632 3' TGGGGCACTGCTCGCTGCTCC 31428     G   AG  CAC
                                GGAG AGC  GC   GTGCCCCA
                                ||||  |||  ||   ||||||||
                                CCTC TCG  CG   CACGGGGT
                                  G   CT  T__
GAM214  KIAA0978 3' GCCATGCCTGCTCCTGCC    70481    _       CACGT
                                GG AGGAGCAGGC     GC
                                || ||||||||||     ||
                                CC TCCTCGTCCG     CG
                                 G         TAC__
GAM214  KIAA1028 3' GCACACTTGGCTACTCTTCCT  91939        CA    C__
                                AGGAGGAG  GGCCA   GTGC
                                ||||||||  |||||   ||||
                                TCCTTCTC  TCGGT   CACG
                                     A_     TCA
GAM214  KIAA1037 3' TGGAGCACCCTCGCTCCTCT   30437        _  CCAC    C
                                GGAGGAGC AGG    GTGC CCA
                                |||||||| |||    |||| |||
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                                TCTCCTCG TCC    CACG GGT
                                    C  ____   A
GAM214  KIAA1055 3' GGGACGGAGCCAACTCCTCCT 66065       CA  CA  G
                                AGGAGGAG  GGC  CGT CCC
                                ||||||||  |||  ||| |||
                                TCCTCCTC  CCG  GCA GGG
                                    AA  AG  _
GAM214  KIAA1171 3' CACCATTGCCTGCTCCTCC   87978         CAC_
                                GGAGGAGCAGGC   GTG
                                ||||||||||||   |||
                                CCTCCTCGTCCG   CAC
                                      TTAC
GAM214  KIAA1388 5' GCAGCCGCTCCTCT      93579       A  CACG
                                GGAGGAGC GGC   TGC
                                |||||||| |||   |||
                                TCTCCTCG CCG   ACG
                                  _  ____
GAM214  KIAA1538 3' ATGTCTAACCTGCTCCCCT   71530    A     CC__
                                AGG GGAGCAGG   ACGT
                                ||| ||||||||   ||||
                                TCC CCTCGTCC   TGTA
                                  _      AATC
GAM214  KIAA1655 5' GGGCTCCAACTCCTCCT    66621       CA  CCACGT
                                AGGAGGAG  GG    GCCC
                                ||||||||  ||    ||||
                                TCCTCCTC  CC    CGGG
                                    AA  T_____
GAM214  KIAA1753 3' GGGCAGGCCCTGCTCCCCCT  64886    A     _  ACG
                                AGG GGAGCAGG CC  TGCCC
                                ||| |||||||| ||  |||||
                                TCC CCTCGTCC GG  ACGGG
                                  C      C  ___
GAM214  KIAA1813 5' TGGAGCCTCCACTTGCCCCTCC 70313      A    CCACGT  C
            T                    AGGAGG GCAGG     GC CCA
                                ||||||  |||||     || |||
                                TCCTCC CGTTC     CG GGT
                                   C    ACCTC_  A
GAM214  KIAA1862 3' GGGAGCCTCTCCTCCT     68929       C   CACGTG
                                AGGAGGAG AGGC     CCC
                                ||||||||  ||||     |||
                                TCCTCCTC TCCG     GGG
                                   _   A_____
GAM214  KIAA1904 3' GGATGGTCTGGGCCTGCTCCTC 73493          A  T  __
            CT                    AGGAGGAGCAGGCC CG GCC  CC
                                ||||||||||||||  ||  |||  ||
                                TCCTCCTCGTCCGG GT TGG  GG
                                      _  C   TA
GAM214  KIAA1958 3' GGTGTGGCCTGCCCTCC     81910      A       GT
                                GGAGG GCAGGCCAC  GCC
                                |||||  |||||||||  |||
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                              CCTCC CGTCCGGTG  TGG
                                _      __
GAM214  KRTHB5   3' GCAGCCCCCTCCTCCT     9654        CA   CACG
                              AGGAGGAG  GGC    TGC
                              ||||||||  |||    |||
                              TCCTCCTC  CCG    ACG
                                  CC  ____
GAM214  LANCL2   5' GCGCGCGGCCTCGCTCCTCCT 37999         _    A
                              AGGAGGAGC AGGCC CGTGC
                              |||||||||| ||||| |||||
                              TCCTCCTCG TCCGG GCGCG
                                   C    C
GAM214  LASP1    3' TAGGTGGCCGCTCCTCC     20461        A     G
                              GGAGGAGC GGCCAC TG
                              |||||||| |||||| ||
                              CCTCCTCG CCGGTG AT
                                  _     G
GAM214  MGC10902 3' ACGTGCCTGCTTCCCCT     47546     A       C
                              AGG GGAGCAGGC ACGT
                              ||| ||||||||| ||||
                              TCC CTTCGTCCG TGCA
                                C       _
GAM214  MGC11257 3' TGGGGCATGCTGGCTCCTCC   50374        A   CAC
                              GGAGGAGC GGC   GTGCCCCA
                              |||||||| |||   ||||||||
                              CCTCCTCG TCG   TACGGGGT
                                  G  ___
GAM214  MGC15827 3' GGGGCCTCCTCTCCTCCT    51806        C   CCACGT
                              AGGAGGAG AGG     GCCCC
                              |||||||| |||     |||||
                              TCCTCCTC TCC     CGGGG
                                  _  TC_____
GAM214  MGC16703 5' GGGCACGTAGCCCTCT      73103      CA   C
                              GGAG  GGC ACGTGCCC
                              ||||  ||| ||||||||
                              TCTC  CCG TGCACGGG
                                __  A
GAM214  MGC16703 5' GGGGCCAGGCCCGTCTCCTCC  73104        _ A    ACGT
                              GGAGGAG C GGCC    GCCCC
                              ||||||| | ||||    |||||
                              CCTCCTC G CCGG    CGGGG
                                  T C    AC__
GAM214  MGC2605  3' TGGGGCACACGGGGGCCTCCC   50221    AGC    AC__
                              GG   AGGCC    GTGCCCCA
                              ||   |||||    ||||||||
                              CC   TCCGG    CACGGGGT
                               C__     GGCA
GAM214  MGC3047  3' GGAGTCCCACTCCTCCT      50361        CA  CCACGT  C
                              AGGAGGAG  GG     GC CC
                              ||||||||  ||     || ||
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                                TCCTCCTC  CC     TG GG
                                    AC  _______  A
GAM214  MGC5457  3'  GTGTAAACCCTCTCCTCCT   50947        C   C_____
                                AGGAGGAG AGG    CAC
                                |||||||| |||    |||
                                TCCTCCTC TCC    GTG
                                    _   CAAAT
GAM214  MIG-6    5'  GGGGCAGCCGCCGCTCCTCC   38489        A   CACG
                                GGAGGAGC GGC    TGCCCC
                                |||||||| |||    ||||||
                                CCTCCTCG CCG    ACGGGG
                                    _   CCG_
GAM214  MRPL24   3'  TGGGGCAGAGCAGCTCCTCC   73510        AG  CACG
                                GGAGGAGC  GC    TGCCCCA
                                ||||||||  ||    |||||||
                                CCTCCTCG  CG    ACGGGGT
                                    A_  AG__
GAM214  MYLE     3'  GGCCTACCTGCTCCCCT     25817     A      CCACGT
                                AGG GGAGCAGG      GCC
                                ||| ||||||||      |||
                                TCC CCTCGTCC      CGG
                                  _       ATC___
GAM214  MYLE     3'  GGAGCGCACCTGCTTCCCC   25816    A      CCAC   C
                                GG GGAGCAGG    GTGC CC
                                || ||||||||    |||| ||
                                CC CTTCGTCC    CGCG GG
                                 C       A___    A
GAM214  NECL1    3'  CGCAGGGCCGCCCCTCC     41025      A  A   AC
                                GGAGG GC GGCC  GTG
                                ||||| || ||||  |||
                                CCTCC CG CCGG  CGC
                                   C  _    GA
GAM214  NECL1    3'  GTGGCTGCCCCTCCT       41026       A   G
                                AGGAGG GCAG CCAC
                                |||||| |||| ||||
                                TCCTCC CGTC GGTG
                                    C   _
GAM214  NRM      3'  GGGGCTCCCTGCTCTCCC    92026    AG     CCACGT
                                GG  GAGCAGG     GCCCC
                                ||  |||||||     |||||
                                CC  CTCGTCC     CGGGG
                                 CT      CT_____
GAM214  NRM      3'  GGGGCTCCCTGCTCTCCC    97891    AG     CCACGT
                                GG  GAGCAGG     GCCCC
                                ||  |||||||     |||||
                                CC  CTCGTCC     CGGGG
                                 CT      CT_____
GAM214  NRM      3'  GGGGCTCCCTGCTCTCCC    97765    AG     CCACGT
                                GG  GAGCAGG     GCCCC
                                ||  |||||||     |||||
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                                CC  CTCGTCC     CGGGG
                                 CT      CT____
GAM214  NXN      3'  ACTCAGCCTTCTCCTCCT    42415        C    CAC
                                AGGAGGAG AGGC   GT
                                |||||||| ||||   ||
                                TCCTCCTC TCCG   CA
                                     T    ACT
GAM214  OBTP     3'  CGGGCCGCGCTCCTCC      34245        A_   A
                                GGAGGAGC  GGCC CG
                                ||||||||  |||| ||
                                CCTCCTCG  CCGG GC
                                     CG    _
GAM214  PAK6     3'  GGACTTGCCTGCCTCCTCCT   39409        _    CAC  G
                                AGGAGGAG CAGGC   GT CC
                                |||||||| |||||   || ||
                                TCCTCCTC GTCCG   CA GG
                                     C     TT_  _
GAM214  PDE4DIP  3'  GGAAAGGTTGGCCTGTCCCCCT 95439     A  AG      CGT  ___
                                AGG GG  CAGGCCA   GCC   CC
                                ||| ||  |||||||   |||   ||
                                TCC CC  GTCCGGT   TGG   GG
                                  _ CT      ___   AAA
GAM214  PDZ-GEF1 3'  CACCTCATCTGCTCCTTC    26494          CCAC
                                GGAGGAGCAGG    GTG
                                ||||||||||    |||
                                CTTCCTCGTCT    CAC
                                       ACTC
GAM214  PP1665   3'  TGAAGCAACTCTGCTCTTCCT  47922          CCACG   CC
                                AGGAGGAGCAGG     TGC  CA
                                ||||||||||||     |||  ||
                                TCCTTCTCGTCT     ACG  GT
                                       CA___   AA
GAM214  PPFIA4   3'  GGGCTTAAAGCCCGCTGCTCCT 70328      G   A   CACGT
                                AGGAG AGC GGC     GCCC
                                ||||| ||| |||     ||||
                                TCCTC TCG CCG     CGGG
                                   G   C   AAATT
GAM214  PPM1A    5'  GGACGCAGCCCGGCTCCTCC   40659        A_   CA   G
                                GGAGGAGC  GGC  CGT CC
                                ||||||||  |||  ||| ||
                                CCTCCTCG  CCG  GCA GG
                                     GC   AC   _
GAM214  PRO1866  5'  ACGTTACTTGCTCCTCCT    37550          CC
                                AGGAGGAGCAGG  ACGT
                                ||||||||||||  ||||
                                TCCTCCTCGTTC  TGCA
                                       AT
GAM214  PTPRU    3'  TGGGGCACACTGACTGTCCTCC 55692       G   GCCAC
                                GGAGGA CAG     GTGCCCCA
                                ||||||  |||    ||||||||
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                                CCTCCT GTC    CACGGGGT
                                   _  AGTCA
GAM214  PTPRU    3'  TGGGGCACACTGACTGTCCTCC 55698      G  GCCAC
                                GGAGGA CAG    GTGCCCCA
                                |||||| |||    ||||||||
                                CCTCCT GTC    CACGGGGT
                                   _  AGTCA
GAM214  PTPRU    3'  TGGGGCACACTGACTGTCCTCC 19119      G  GCCAC
                                GGAGGA CAG    GTGCCCCA
                                |||||| |||    ||||||||
                                CCTCCT GTC    CACGGGGT
                                   _  AGTCA
GAM214  RAB10    5'  GCCCGAGCCGCTCCTCC    85175       A  CA  T
                                GGAGGAGC GGC  CG GC
                                |||||||| |||  || ||
                                CCTCCTCG CCG  GC CG
                                     _  A_  C
GAM214  RNPC1    3'  GGGCACGTGGGCGGCTTCCT  33991      A_  AGG
                                AGGAGG  GC   CCACGTGCCC
                                ||||||  ||   ||||||||||
                                TCCTTC  CG   GGTGCACGGG
                                   GG  ___
GAM214  SEMA4B   5'  GGGACACCGTCGCTCCTGCT  69038    G     A  CAC  C
                                AG AGGAGC GGC   GTG CCC
                                || |||||| |||   ||| |||
                                TC TCCTCG CTG   CAC GGG
                                 G     _  C__   A
GAM214  STK25    3'  GGGCAGCTCTGCCTCCTCCT  21052        _  _  CACG
                                AGGAGGAG CAG GC    TGCCC
                                |||||||| ||| ||    |||||
                                TCCTCCTC GTC CG    ACGGG
                                     C  T  _____
GAM214  T1A-2    5'  GGGGCTCCTGCTCCCACC    21356    A_      CCACGT
                                GG  GGAGCAGG     GCCCC
                                ||  ||||||||     |||||
                                CC  CCTCGTCC     CGGGG
                                 AC       T_____
GAM214  TNFRSF19L 3'  CATGTGCCTGCCCCTCC     51773      A     C
                                GGAGG GCAGGC ACGTG
                                ||||| |||||| |||||
                                CCTCC CGTCCG TGTAC
                                   C     _
GAM214  TOMM34   3'  TGTGGCTGCTCCTCCT      22337          G
                                AGGAGGAGCAG CCACG
                                |||||||||||| |||||
                                TCCTCCTCGTC GGTGT
                                           _
GAM214  TRIP3    3'  GGAACCTGCCTGCTCCCTCT  78219    GA       CAC  G
                                AG  GGAGCAGGC   GT CC
                                ||  |||||||||   || ||
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                                TC  CCTCGTCCG   CA GG
                                 TC       TC_  A
GAM214  TTTY14   3'  GGCCTCGAGCCTGCTCCGCCT  49189     A       CA  T_
                                AGG GGAGCAGGC  CG  GCC
                                ||| |||||||||  ||  |||
                                TCC CCTCGTCCG  GC  CGG
                                  G        A_  TC
GAM214  VPS4A    3'  ATGGGGCACACAGTGGACACTG 25101      G__   ___      III
           CTCTTCCT                AGCAG   CCAC   GTGCCCCA  T
                                |||||   ||||   ||||||||  |
                                TCGTC   GGTG   CACGGGGT   A
                                   ACA    ACA       III
GAM214  WBSCR20A  5'  GGGGTGGCCTGCCCCTCC    49654      A      ACGT
                                GGAGG GCAGGCC    GCCCC
                                ||||| |||||||    |||||
                                CCTCC CGTCCGG    TGGGG
                                   C      _____
GAM214  ZFP100   5'  GGGACTTGTCCTCCTCCTCCT  70056        C   C  C  G
                                AGGAGGAG AGG CA GT CCC
                                |||||||| ||| || || |||
                                TCCTCCTC TCC GT CA GGG
                                     C   T  T  _
GAM214  ZNF282   3'  GGGAAGCTGCTGGCCTGGCCCT 89216       AG      C  _  __
           CCT                    AGGAGG  CAGGCCA GT GC  CCC
                                ||||||  ||||||| || ||  |||
                                TCCTCC  GTCCGGT CG CG  GGG
                                   CG       _  T  AA
GAM214  LOC112885 3'  TGGGGCACACAGTCTCCCCCC  56532    A  AGC    CAC
                                GG GG   AGGC   GTGCCCCA
                                || ||   ||||   ||||||||
                                CC CC   TCTG   CACGGGGT
                                 _  CC_    ACA
GAM214  LOC115051 3'  GGAAGCCTGCTCCCCT      60040     A       CACGTG
                                AGG GGAGCAGGC      CC
                                ||| |||||||||      ||
                                TCC CCTCGTCCG      GG
                                  _        AA_____
GAM214  LOC115399 3'  GGGCGGCCCGTCCCCTCCT   73435       A_  A   ACGT
                                AGGAGG  GC GGCC    GCCC
                                ||||||  || ||||    ||||
                                TCCTCC  TG CCGG    CGGG
                                   CC  C    _____
GAM214  LOC115757 3'  GGGGCAGTCCGCTCCTCC    73577        A   CACG
                                GGAGGAGC GGC    TGCCCC
                                |||||||| |||    ||||||
                                CCTCCTCG CTG    ACGGGG
                                     C   _____
GAM214  LOC116071 3'  CACCACCCTCTGCTCCTCCT   56623           CCAC_
                                AGGAGGAGCAGG     GTG
                                ||||||||||||     |||
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                                TCCTCCTCGTCT    CAC
                                      CCCAC
GAM214  LOC118472 3'  GGACGGCCTGTCTCCTCCT   73916       _    AC  G
                                AGGAGGAG CAGGCC  GT CC
                                |||||||| ||||||  || ||
                                TCCTCCTC GTCCGG  CA GG
                                    T    __ _
GAM214  LOC121457 5'  GGCGGCCACGTCCTGCTCCCCC 74071    A      CC   _ _
          T                      AGG GGAGCAGG  ACGTG CC CC
                                 ||| ||||||||  ||||| || ||
                                 TCC CCTCGTCC  TGCAC GG GG
                                   C       __    C C
GAM214  LOC124930 3'  GGCACGGCCTGGTCCCCCT   74359    A  G    AC
                                AGG GGA CAGGCC  GTGCC
                                ||| ||| ||||||  |||||
                                TCC CCT GTCCGG  CACGG
                                  C  G    __
GAM214  LOC130355 5'  GGGCGGGACCCGCTCCTCC   74931       A _ ACG
                                GGAGGAGC GG CC   TGCCC
                                |||||||| || ||   |||||
                                CCTCCTCG CC GG   GCGGG
                                    C A ___
GAM214  LOC136319 5'  GGCAGCCTAACCCTCCT    75259      AGC   CACG
                                AGGAGG   AGGC   TGCC
                                ||||||   ||||   ||||
                                TCCTCC   TCCG   ACGG
                                   CAA   _____
GAM214  LOC138399 5'  GGAAGTGCCTGCTCCCACT   75329   GA      C  GTG
                                AG  GGAGCAGGC AC   CC
                                ||  ||||||||| ||   ||
                                TC  CCTCGTCCG TG   GG
                                 AC       _ AA_
GAM214  LOC139673 3'  GGAGGCTGCCAGCCCCTCCT   75977      A  A   CACGT  _
                                AGGAGG GC GGC    GCC CC
                                |||||| || |||    ||| ||
                                TCCTCC CG CCG    CGG GG
                                   C  A   T_____   A
GAM214  LOC139770 3'  GGACACATGACCTAGTTTCTTC 75389        _  C  C  _
          T                      AGGAGGAGC AGG CA GTG CC
                                 |||||||| ||| || ||| ||
                                 TCTTCTTTG TCC GT CAC GG
                                     A  A A  A
GAM214  LOC144519 5'  ACATGCCTGCTCCCCCT    76863    A      CAC
                                AGG GGAGCAGGC   GT
                                ||| |||||||||   ||
                                TCC CCTCGTCCG   CA
                                  C       TA_
GAM214  LOC144866 5'  TGGGGAGGAGCCTGGCCCCTCC 83207      A  _   CACGTG
          T                      AGGAGG GC AGGC     CCCCA
                                 |||||| || ||||     |||||
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                                TCCTCC CG TCCG     GGGGT
                                   C  G   AGGA__
GAM214  LOC145195 3'  GCCTGGCCTGCTCCTCTT    83272            C
                                AGGAGGAGCAGGCCA GT
                                ||||||||||||||| ||
                                TTCTCCTCGTCCGGT CG
                                        C
GAM214  LOC145919 3'  TGAGGCAGCAAGACCAGCCCCT 77572       A  A  CCACG_   C
           CCT                    AGGAGG GC GG     TGCC CA
                                ||||||  || ||     |||| ||
                                TCCTCC CG CC     ACGG GT
                                   C  A  AGAACG    A
GAM214  LOC147004 3'  GGACCTCACTCCCAGCTCCTCC 83902         A  CCAC   CC__
           T                    AGGAGGAGC GG    GTG    CC
                                |||||||| ||    |||    ||
                                TCCTCCTCG CC    CAC    GG
                                     A  CT__   TCCA
GAM214  LOC147229 5'  TGTGGCCTGCTCCCC       78324    A
                                GG GGAGCAGGCCACG
                                || ||||||||||||
                                CC CCTCGTCCGGTGT
                                 _
GAM214  LOC148697 3'  GTGCAGCCTGCTCCCTCC    78931      _      CAC TG
                                GGAGG AGCAGGC   G  C
                                ||||| |||||||   |  |
                                CCTCC TCGTCCG   C  G
                                   C      A__ GT
GAM214  LOC149372 5'  GGGGCAGGCCCACCCTCCT   79327       AGCA    ACG
                                AGGAGG   GGCC   TGCCCC
                                ||||||   ||||   ||||||
                                TCCTCC   CCGG   ACGGGG
                                   CAC_   ____
GAM214  LOC149386 5'  GCTGGCCCCTCCTCCT      84406        CA     C
                                AGGAGGAG  GGCCA GT
                                ||||||||  ||||| ||
                                TCCTCCTC  CCGGT CG
                                     C_    _
GAM214  LOC150378 5'  CAGTGTGGCCCAGTCCTCC   79741       GCA      _
                                GGAGGA   GGCCACG TG
                                ||||||   ||||||| ||
                                CCTCCT   CCGGTGT AC
                                   GAC      G
GAM214  LOC151736 5'  TGAAGCTTGTTCCCTCTCCTCC 82606        C   CC   T  CC
           T                    AGGAGGAG AGG  ACG GC  CA
                                |||||||| |||  ||| ||  ||
                                TCCTCCTC TCC  TGT CG  GT
                                     _  CT   T  AA
GAM214  LOC152426 5'  GGACAGCCATCCTCCT      85717        GCA   CACG  C
                                AGGAGGA   GGC    TG CC
                                |||||||   |||    || ||
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                                TCCTCCT  CCG   AC GG
                                   A__  ____  A
GAM214  LOC152765 5'  GGCCTTCAGCCTGCTCTCCT  80660      G     CACGT
                                AGGAG AGCAGGC    GCC
                                ||||| |||||||    |||
                                TCCTC TCGTCCG    CGG
                                  _      ACTTC
GAM214  LOC157254 5'  GGAGCCTTTGCCTGCTCCTCCT 81387          CACGT  C
                                AGGAGGAGCAGGC    GC CC
                                ||||||||||||    || ||
                                TCCTCCTCGTCCG    CG GG
                                       TTTC_  A
GAM214  LOC158377 5'  CGAGGCCCAGCTCCTCCT   86793        A_   A
                                AGGAGGAGC  GGCC CG
                                |||||||||  |||| ||
                                TCCTCCTCG  CCGG GC
                                     AC   A
GAM214  LOC158972 3'  GGTCTCGTCCCGCCCCTCCT  86955      A  A  CC   T_
                                AGGAGG GC GG  ACG  GCC
                                |||||| || ||  |||  |||
                                TCCTCC CG CC  TGC  TGG
                                   C  C  __   TC
GAM214  LOC159199 5'  GTGCCTGCTCCTCCT      82185           C
                                AGGAGGAGCAGGC AC
                                |||||||||||| ||
                                TCCTCCTCGTCCG TG
                                                _
GAM214  LOC161753 3'  TGGGGCACTCACTGCCCCTC  82297     A   GCCAC
                                GAGG GCAG    GTGCCCCA
                                |||| ||||    ||||||||
                                CTCC CGTC    CACGGGGT
                                  C   ACT__
GAM214  LOC163782 5'  GGAGCCACCGGCCTCCTCCTCC 82158        C    AC   _ C
          T                      AGGAGGAG AGGCC  GTG C CC
                                |||||||| |||||  ||| | ||
                                TCCTCCTC TCCGG  CAC G GG
                                     C    C_   C A
GAM214  LOC166316 5'  GGCACACTTTCTGCTCCTCTT  87260          CCAC
                                AGGAGGAGCAGG   GTGCC
                                ||||||||||||   |||||
                                TTCTCCTCGTCT   CACGG
                                       TTCA
GAM214  LOC196746 3'  GGGCTGGGCCTGCTCCCCC   87512   A       A  T
                                GG GGAGCAGGCC CG GCCC
                                || ||||||||| || ||||
                                CC CCTCGTCCGG GT CGGG
                                 C        _ _
GAM214  LOC196812 3'  GTGGCCACTCCTCCT      89575        CA
                                AGGAGGAG  GGCCAC
                                ||||||||  ||||||
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                                TCCTCCTC  CCGGTG
                                    A_
GAM214  LOC196890 3'  TGGGGCACCCCTGACCCTCC  89652     AG   CCAC
                                GGAGG  CAGG   GTGCCCCA
                                |||||  ||||   ||||||||
                                CCTCC  GTCC   CACGGGGT
                                  CA   C___
GAM214  LOC200531 3'  GGCGCCCTGCTCTTCC     88823         CCAC
                                GGAGGAGCAGG   GTGCC
                                ||||||||||   |||||
                                CCTTCTCGTCC   CGCGG
                                          ____
GAM214  LOC200734 3'  ACATGGCCTGCTCCCC     88856    A        C
                                GG GGAGCAGGCCA GT
                                || ||||||||||| ||
                                CC CCTCGTCCGGT CA
                                 _         A
GAM214  LOC200734 3'  ACATGGCCTGCTCCCC     88857    A        C
                                GG GGAGCAGGCCA GT
                                || ||||||||||| ||
                                CC CCTCGTCCGGT CA
                                 _         A
GAM214  LOC200779 5'  ACCTGCCTGCTCGCTCCT    88872      _      CAC
                                AGGAG GAGCAGGC   GT
                                ||||| ||||||||   ||
                                TCCTC CTCGTCCG   CA
                                  G       TC_
GAM214  LOC200782 5'  GGGACTCTGGCCTGCCCCTACC 89508    _  A      C_  G
                                GG AGG GCAGGCCA  GT CCC
                                || ||| ||||||||  || |||
                                CC TCC CGTCCGGT  CA GGG
                                 A  C       CT  _
GAM214  LOC201242 3'  GTACCCTGCTCCCCCT     87361     A      CCAC
                                AGG GGAGCAGG   GTGC
                                ||| ||||||||   ||||
                                TCC CCTCGTCC   CATG
                                  C      ____
GAM214  LOC202126 3'  GGGGCCTCCTGTTCCTCCT   90316          CCACGT
                                AGGAGGAGCAGG    GCCCC
                                ||||||||||||    |||||
                                TCCTCCTTGTCC    CGGGG
                                       TC____
GAM214  LOC202518 5'  TGGCCCGGCTCCTCCT     87487        A_
                                AGGAGGAGC  GGCCA
                                |||||||||  |||||
                                TCCTCCTCG  CCGGT
                                      GC
GAM214  LOC203339 3'  GTACAGCCCTCTCCTCCT    90548       CA  CAC
                                AGGAGGAG  GGC  GTGC
                                ||||||||  |||  ||||
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                                TCCTCCTC  CCG   CATG
                                    TC   A__
GAM214   LOC206372 5'  GGAGGTGCGGGGCCTGCTCCCG 89531    A_       A  TG  _
            CC                    GG  GGAGCAGGCC CG  CC CC
                                  ||  |||||||||| ||  || ||
                                  CC  CCTCGTCCGG GC  GG GG
                                   GC        G  GT  A
GAM214   LOC219513 3'  GGAGAACAGCCTGCTCCACCT  94332     A       CAC  GCC
                                  AGG GGAGCAGGC   GT   CC
                                  ||| |||||||||   ||   ||
                                  TCC CCTCGTCCG   CA   GG
                                    A       A__  AGA
GAM214   LOC220370 3'  CACACCTGCTCCTCC       92825          CCAC
                                  GGAGGAGCAGG    GTG
                                  ||||||||||    |||
                                  CCTCCTCGTCC    CAC
                                        A___
GAM214   LOC221119 3'  TGGGGGACACCCCCTCCTCCT  93443        CA  CCAC  G
                                  AGGAGGAG  GG    GT CCCCA
                                  ||||||||  ||    || |||||
                                  TCCTCCTC  CC    CA GGGGT
                                       CC  A___  G
GAM214   LOC221596 5'  GGCATGCCTGCTTCCCCT    91979     A       CAC
                                  AGG GGAGCAGGC   GTGCC
                                  ||| |||||||||   |||||
                                  TCC CTTCGTCCG   TACGG
                                    C        ___
GAM214   LOC221882 3'  GGCCCTGTTCCTCC        92500          CCACGT  C
                                  GGAGGAGCAGG      GC C
                                  ||||||||||      || |
                                  CCTCCTTGTCC     CG G
                                         _______  A
GAM214   LOC222031 3'  GGCTGGCCCCCTCCTCCT    94026        CA    CGT
                                  AGGAGGAG  GGCCA   GCC
                                  ||||||||  |||||   |||
                                  TCCTCCTC  CCGGT   CGG
                                       CC    ___
GAM214   LOC222166 5'  GGGGTGCCGGCCGCTCCTCC   94097        A   AC TG
                                  GGAGGAGC GGCC  G  CCCC
                                  ||||||||  ||||  |  ||||
                                  CCTCCTCG CCGG  C  GGGG
                                       _   C_ GT
GAM214   LOC253148 3'  GGGAGGCCCGGCTCCTCCT   96879        A_   ACGTG
                                  AGGAGGAGC  GGCC    CCC
                                  |||||||||  ||||    |||
                                  TCCTCCTCG  CCGG    GGG
                                        GC    A____
GAM214   LOC254911 5'  GGAGACGCCGGCTGCTCCTCC  97054         G  A_   GC
                                  GGAGGAGCAG CC  CGT  CC
                                  ||||||||||  ||  |||  ||
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                                CCTCCTCGTC GG  GCA  GG
                                      _ CC   GA
GAM214  LOC255187 5'  ACTGGCCTGCCACCCCT     97181     A  A_       C
                                AGG GG  GCAGGCCA GT
                                ||| ||  |||||||| ||
                                TCC CC  CGTCCGGT CA
                                  _ AC       _
GAM214  LOC255520 5'  GGCAGCTCCTGCTCCCCCT    95861     A       CCACG
                                AGG GGAGCAGG     TGCC
                                ||| ||||||||     ||||
                                TCC CCTCGTCC     ACGG
                                  C       TCG__
GAM214  LOC256789 3'  GGCGCCAGCCTGCTCCACC    97449     A        CAC
                                GG GGAGCAGGC   GTGCC
                                || |||||||||   |||||
                                CC CCTCGTCCG   CGCGG
                                 A        AC_
GAM214  LOC256815 5'  GGCAGCCTGCTCTCCT       94709       G      CACG
                                AGGAG AGCAGGC    TGCC
                                ||||| |||||||    ||||
                                TCCTC TCGTCCG    ACGG
                                  _      _____
GAM214  LOC256980 3'  GGCCTGGCCTGCCCTCC      95221       A       CGT
                                GGAGG GCAGGCCA   GCC
                                ||||| ||||||||   |||
                                CCTCC CGTCCGGT   CGG
                                  _       C__
GAM214  LOC257619 5'  TGGCCCGGCTCCTCCT       97812         A_
                                AGGAGGAGC  GGCCA
                                |||||||||  |||||
                                TCCTCCTCG  CCGGT
                                     GC
GAM214  LOC51087  3'  GTACCCTGCTCCCCCT       32014     A       CCAC
                                AGG GGAGCAGG    GTGC
                                ||| ||||||||    ||||
                                TCC CCTCGTCC    CATG
                                  C       _____
GAM214  LOC51117  3'  GGGGCCTGGCCTACCTCC     32093      AGC     CGT
                                GGAGG   AGGCCA   GCCCC
                                |||||   ||||||   |||||
                                CCTCC   TCCGGT   CGGGG
                                   A__      C__
GAM214  LOC51279  3'  CACAGACCGCTCCTCCT      33308         A  CCAC
                                AGGAGGAGC GG    GTG
                                ||||||||| ||    |||
                                TCCTCCTCG CC    CAC
                                     _ AGA_
GAM214  LOC51619  3'  CACTACCGCCCGCTCCTCC    32016         A   CAC_
                                GGAGGAGC GGC    GTG
                                |||||||| |||    |||
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                                CCTCCTCG CCG    CAC
                                    C   CCAT
GAM214  LOC59346  5'  CGCGCGGCCCGCCCTCC     41275       A  A    A
                                GGAGG GC GGCC CGTG
                                ||||| || |||| ||||
                                CCTCC CG CCGG GCGC
                                  _ C    C
GAM214  LOC90381  3'  TGGAACAGCGTCCGCTCCTCCT 62547          A  CC    GCC_
                                AGGAGGAGC GG  ACGT    CCA
                                ||||||||| ||  ||||    |||
                                TCCTCCTCG CC  TGCG    GGT
                                    _ __    ACAA
GAM214  LOC91464  3'  TGGAGGACAGGGCCTGCTCCCC 66146     A        AC  G  _
          T                      AGG GGAGCAGGCC  GT CC CCA
                                ||| ||||||||||  || || |||
                                TCC CCTCGTCCGG  CA GG GGT
                                  _         GA  _  A
GAM214  LOC93268  3'  TACAGCCTGCTCCCC       71886     A        CAC
                                GG GGAGCAGGC   GTG
                                || |||||||||   |||
                                CC CCTCGTCCG   CAT
                                  _        A__
GAM215  ABCC1     3'  TGATGTGGGGTAAATATTAAGG 17183     CA       AAA  C
          A                      TCC  AATATTTAC   GC ATCA
                                ||| |||||||||   || ||||
                                AGG  TTATAAATG   TG TAGT
                                  AA        GGG  _
GAM215  ABCC1     3'  TGATGTGGGGTAAATATTAAGG 39128     CA       AAA  C
          A                      TCC  AATATTTAC   GC ATCA
                                ||| |||||||||   || ||||
                                AGG  TTATAAATG   TG TAGT
                                  AA        GGG  _
GAM215  ABCC1     3'  TGATGTGGGGTAAATATTAAGG 39136     CA       AAA  C
          A                      TCC  AATATTTAC   GC ATCA
                                ||| |||||||||   || ||||
                                AGG  TTATAAATG   TG TAGT
                                  AA        GGG  _
GAM215  ASIC4     3'  TTTGTAAATATTTAGGG     37924     _
                                CCC AAATATTTACAAA
                                ||| |||||||||||||
                                GGG TTTATAAATGTTT
                                  A
GAM215  CREBBP    3'  GATAACTTTGTGATGTTTCGGG 15207     _      T     CC
          A                      TCCC AAATATT ACAAAG  ATC
                                |||| ||||||| ||||||  |||
                                AGGG TTTGTAG TGTTTC  TAG
                                  C       _     AA
GAM215  CTSS      3'  TGATGGCTTAAAAATA      14545       ACA
                                TATTT   AAGCCATCA
                                |||||   |||||||||
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                                ATAAA  TTCGGTAGT
                                  AA_
GAM215  EYA1    5'  GATGGCTCCGAGTTTGGGG  4954        ATTTACAA
                                TCCCAAAT      AGCCATC
                                ||||||||      |||||||
                                GGGGTTTG      TCGGTAG
                                    AGCC____
GAM215  FBXW1B  3'  TGACAGCTTTGTACTGTGG  24527    AATATT      CA
                                CCA    TACAAAGC  TCA
                                |||    ||||||||  |||
                                GGT    ATGTTTCG  AGT
                                  GTC___      AC
GAM215  FBXW1B  3'  TGACAGCTTTGTACTGTGG  53331    AATATT      CA
                                CCA    TACAAAGC  TCA
                                |||    ||||||||  |||
                                GGT    ATGTTTCG  AGT
                                  GTC___      AC
GAM215  FBXW1B  3'  TGACAGCTTTGTACTGTGG  53342    AATATT      CA
                                CCA    TACAAAGC  TCA
                                |||    ||||||||  |||
                                GGT    ATGTTTCG  AGT
                                  GTC___      AC
GAM215  GCN5L2  3'  TGATGGCTTCAGGGGTTGG  59841     ATA  ACA
                                CCAA  TTT  AAGCCATCA
                                ||||  |||  |||||||||
                                GGTT  GGA  TTCGGTAGT
                                  GG_  C__
GAM215  GSPT1   3'  GCTTTGTAAGTGATGTGG   9143     AA_
                                CCA  TATTTACAAAGC
                                |||  ||||||||||||
                                GGT  GTGAATGTTTCG
                                  GTA
GAM215  PTPN11  3'  TGATGAGAAGAAATGATTTGGG 11085        _   ACAAAGC
          A                      TCCCAAAT ATTT      CATCA
                                 |||||||| ||||      |||||
                                 AGGGTTTA TAAA      GTAGT
                                     G   GAAGA__
GAM215  RNMT    3'  TGATAGCTTTGTAGGTACAGGA 13725    CAAA         C
                                TCC   TATTTACAAAGC ATCA
                                |||   |||||||||||| ||||
                                AGG   ATGGATGTTTCG TAGT
                                  AC__          A
GAM215  ROR2    3'  TGACAGCTTTGTATTTGGTGA  15855   _   TATT      CA
                                TC CCAAA   TACAAAGC  TCA
                                || |||||   ||||||||  |||
                                AG GGTTT   ATGTTTCG  AGT
                                 T    _____      AC
GAM215  STAM    3'  TTGTAATTATTTGGGA     12964         T
                                TCCCAAATA TTACAA
                                ||||||||| ||||||
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                                AGGGTTTAT AATGTT
                                     T
GAM215  TGFBR2   3' CTTTATAAATATTTGG      12267          C
                                CCAAATATTTA AAAG
                                |||||||||| ||||
                                GGTTTATAAAT TTTC
                                     A
GAM215  ZNF14    3' TGTAAGACATTTGGGA      40718        A_
                                TCCCAAAT  TTTACA
                                ||||||||  ||||||
                                AGGGTTTA  GAATGT
                                    CA
GAM215  DKFZP434L1123 5' TGGTTTGTAAATATTTG     49585            G
                                CAAATATTTACAAA CCA
                                |||||||||||||| |||
                                GTTTATAAATGTTT GGT
                                              _
GAM215  DKFZP434O047 5'  TGATGGCTCCACATCTTGGGG  31517       ATATTTACAA
                                TCCCAA         AGCCATCA
                                ||||||         ||||||||
                                GGGGTT         TCGGTAGT
                                   CTACACC___
GAM215  DKFZP564G092 5'  TGGACAGTAAATATTTG     31539          AAAG
                                CAAATATTTAC    CCA
                                ||||||||||    |||
                                GTTTATAAATG    GGT
                                     ACA_
GAM215  DKFZP564O0823 3'  ATGGCTGTAAAATGTTT     59519        ACAA
                                AAATATTT    AGCCAT
                                ||||||||    ||||||
                                TTTGTAAA    TCGGTA
                                    ATG_
GAM215  FLJ10036  3' GCTTTGTAAATATTTCAGA   94950    CC
                                TC  AAATATTTACAAAGC
                                ||  ||||||||||||||
                                AG  TTTATAAATGTTTCG
                                 AC
GAM215  FLJ11267  5'  TGATGGCTCTAGAATGTCTAGG 39007     CAA     ACAA
           A                     TCC   ATATTT    AGCCATCA
                                |||   ||||||   ||||||||
                                AGG   TGTAAG    TCGGTAGT
                                  ATC     ATC_
GAM215  FLJ11730  3'  TGGAGGCTGTAAATATCTGG   42798     A       AA   AT
                                CCA ATATTTACA  GCC  CA
                                ||| |||||||||  |||  ||
                                GGT TATAAATGT  CGG  GT
                                  C        __   AG
GAM215  FLJ13194  3'  TGATAACTTTGTAAGATGGGA  47131       AATA       CC
                                TCCCA    TTTACAAAG  ATCA
                                |||||    |||||||||  ||||
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                                AGGGT   GAATGTTTC  TAGT
                                  A___       AA
GAM215  FLJ14564  3'  ATGGGGAAAATATTTGGGA   76499          ACAAAG
                                TCCCAAATATTT     CCAT
                                ||||||||||||     ||||
                                AGGGTTTATAAA     GGTA
                                      AGG___
GAM215  FLJ22596  5'  TGATGGCTTGATGGTATCTGG  46964    A    TACA
                                CCA ATATT   AAGCCATCA
                                ||| |||||   |||||||||
                                GGT TATGG   TTCGGTAGT
                                  C    TAG_
GAM215  FLJ25200  5'  TGATGGCTTCATTAACTATCTG 58514    A  T  CA_
          G                      CCA ATA TTA   AAGCCATCA
                                ||| ||| |||   |||||||||
                                GGT TAT AAT   TTCGGTAGT
                                  C  C   TAC
GAM215  FRAT1    3'  TGAGGGCCAAAATATTTGG   18496         ACAAA  A
                                CCAAATATTT    GCC TCA
                                ||||||||||    ||| |||
                                GGTTTATAAA    CGG AGT
                                      AC___   G
GAM215  GLUC     3'  ATGGCCTTTATTTGTATTTGG  40586        TTAC   _
                                CCAAATAT    AAAG CCAT
                                ||||||||    |||| ||||
                                GGTTTATG    TTTC GGTA
                                     TTTA   C
GAM215  GPR      3'  GGATTGTAAATTCTTGG     23336     AT      AG
                                CCAA  ATTTACAA  CC
                                ||||  ||||||||  ||
                                GGTT  TAAATGTT  GG
                                  CT       A_
GAM215  GSPT2    3'  GCTTTGTAAGTGATGTGG    36120     AA_
                                CCA   TATTTACAAAGC
                                |||   ||||||||||||
                                GGT   GTGAATGTTTCG
                                  GTA
GAM215  KIAA0453 3'  GTGTGTTTGTAAATATATAGGA 69051    CAA        GC
                                TCC   ATATTTACAAA  CAT
                                |||   ||||||||||  |||
                                AGG   TATAAATGTTT  GTG
                                  ATA         GT
GAM215  KIAA0746 3'  GCTTTGTAAATTGG       69454     AAT
                                CCA   ATTTACAAAGC
                                |||   ||||||||||
                                GGT   TAAATGTTTCG
                                      ___
GAM215  KIAA0884 3'  TGATTATTGTAAATATTTTGGA 70207    C         AGCC
                                TCC AAATATTTACAA    ATCA
                                ||| ||||||||||||    ||||
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                                AGG TTTATAAATGTT   TAGT
                                  T         AT__
GAM215  KIAA0930  3'  TGATGGCTTTGCCCTGGGCTGG 70554      AATATTTA
                GA                  TCCCA       CAAAGCCATCA
                                    |||||       ||||||||||||
                                    AGGGT       GTTTCGGTAGT
                                       CGGGTCCC
GAM215  KIAA1052  3'  TGATGGCTTTTATCCTCCTGGG 30252      AATATT  C
                A                   TCCCA     TA AAAGCCATCA
                                    |||||     || ||||||||||
                                    AGGGT     AT TTTCGGTAGT
                                       CCTCCT  _
GAM215  KIAA1557  3'  TTGTAAATATTTGTGA     61140    C
                                    TC CAAATATTTACAA
                                    || ||||||||||||
                                    AG GTTTATAAATGTT
                                     T
GAM215  KIAA1587  3'  TGATAGCTCTATAAAATGTTTT 40512     C       ACAA_  C
                GGA                   TCC AAATATTT     AGC ATCA
                                    ||| ||||||||     ||| ||||
                                    AGG TTTGTAAA     TCG TAGT
                                      T       ATATC   A
GAM215  LIPI     3'  ATGACTTTGTAAATATTT    79564             C
                                    AAATATTTACAAAG CAT
                                    |||||||||||||| |||
                                    TTTATAAATGTTTC GTA
                                              A
GAM215  MARCKS   3'  GTTTTGTAAATACTGGAGA   9870     _  AA
                                    TC CCA  TATTTACAAAGC
                                    || |||  ||||||||||||
                                    AG GGT  ATAAATGTTTTG
                                     A  C_
GAM215  MED6     3'  TGATGGCTTTGTTGCAGCTGAG 18439    C  AATATTT
                A                   TC CA      ACAAAGCCATCA
                                    || ||      ||||||||||||
                                    AG GT      TGTTTCGGTAGT
                                     A  CGACGT_
GAM215  MGC17330  3'  GTTTTTAAAATATTTGGGA   53531           AC
                                    TCCCAAATATTT  AAAGC
                                    ||||||||||||  |||||
                                    AGGGTTTATAAA  TTTTG
                                            AT
GAM215  OR51E2   3'  ATGGCTTTGTACTTGTGATG  47790    A_  TT
                                    CA  ATA  TACAAAGCCAT
                                    ||  |||  ||||||||||||
                                    GT  TGT  ATGTTTCGGTA
                                     AG   TC
GAM215  PSTPIP2  3'  CTTTCACAAATATTTGGG    44389          AC_
                                    CCCAAATATTT   AAAG
                                    ||||||||||   ||||
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                                GGGTTTATAAA  TTTC
                                      CAC
GAM215  PURG     3'  ATGGCTTTGCTATGG      25336     AATATT  _
                                CCA     TA CAAAGCCAT
                                |||     || |||||||||
                                GGT     AT GTTTCGGTA
                                 _______ C
GAM215  VDU1     3'  TGATGGCTTTGTTTTGGTTTGG 30431         ATTT
           GG                     TCCCAAAT    ACAAAGCCATCA
                                |||||||||   ||||||||||||
                                GGGGTTTG    TGTTTCGGTAGT
                                    GTTT
GAM215  ZNF294   3'  GCTTTGTAAATGTTTGG     70828
                                CCAAATATTTACAAAGC
                                |||||||||||||||||
                                GGTTTGTAAATGTTTCG

GAM215  LOC127162 3'  TGATGGCTACATATACTAGGGA 74638      AAA   TTACAA
                                TCCC   TAT     AGCCATCA
                                ||||   |||     ||||||||
                                AGGG   ATA     TCGGTAGT
                                  ATC   TACA__
GAM215  LOC148936 5'  TGATGGCTCTATAAGGGGGA   84303     AAA   TTACAA
                                TCCC   TAT     AGCCATCA
                                ||||   |||     ||||||||
                                AGGG   ATA     TCGGTAGT
                                  GGA   TC____
GAM215  LOC148938 5'  TGATGGCTCTATAAGGGGGA   84284     AAA   TTACAA
                                TCCC   TAT     AGCCATCA
                                ||||   |||     ||||||||
                                AGGG   ATA     TCGGTAGT
                                  GGA   TC____
GAM215  LOC152084 5'  GATGGCTTTCCTCAGCCTGGGA 85553       AATATTTAC
                                TCCCA        AAAGCCATC
                                |||||        |||||||||
                                AGGGT        TTTCGGTAG
                                   CCGACTCC_
GAM215  LOC152573 3'  GATGACTATATATTTGGG    80618         TTACAA  C
                                CCCAAATAT     AG CATC
                                |||||||||     || ||||
                                GGGTTTATA     TC GTAG
                                     TA____  A
GAM215  LOC152627 5'  ATGGCTTCTAAGTATTCAGG   80627    CA       CA
                                CC  AATATTTA  AAGCCAT
                                ||  ||||||||  |||||||
                                GG  TTATGAAT  TTCGGTA
                                 AC       C_
GAM215  LOC200301 3'  GCTTGTTATTTGGGG       88748         TTT    A
                                TCCCAAATA   ACAA GC
                                |||||||||   |||| ||
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                                GGGGTTTAT   TGTT CG
                                    ___   _
GAM216  AKAP13   3'  TCACCCCCCACACCTTCCC   89686    A   ACA    A
                                GG AAG   TGGGG GGTGG
                                || |||   ||||| |||||
                                CC TTC   ACCCC CCACT
                                  C   CAC    _
GAM216  ALX4     3'  CCACGCCCATGTTTTCCA    41630      A      GAG
                                TGGAA GACATGGG   GTGG
                                ||||| ||||||||   ||||
                                ACCTT TTGTACCC   CACC
                                   _      G__
GAM216  ARCN1    3'  ACCACCTCCCTCTTCCA     7966       A  CATG
                                TGGAA GA    GGGAGGTGGT
                                ||||| ||    ||||||||||
                                ACCTT CT    CCCTCCACCA
                                   _ _____
GAM216  ARCN1    3'  TCACGTATACCCCATTTCCTTC 7984       A  C     AG___
              CA                  TGGAA GA ATGGGG     GTGG
                                ||||| || ||||||     ||||
                                ACCTT CT TACCCC     CACT
                                   C  T     ATATG
GAM216  ARHC     5'  ACCACCTCCCTTAGCCTCC    17707     AAGACAT
                                GGA      GGGGAGGTGGT
                                |||      ||||||||||
                                CCT      TCCCTCCACCA
                                  CCGAT__
GAM216  ASPH     3'  ACCACCTTCCCTCCTCTCCA   39394     A  ACAT
                                TGGA AG    GGGGAGGTGGT
                                |||| ||    ||||||||||
                                ACCT TC    CCCTTCCACCA
                                  C  CT__
GAM216  ASPH     3'  ACCACCTTCCCTCCTCTCCA   50622     A  ACAT
                                TGGA AG    GGGGAGGTGGT
                                |||| ||    ||||||||||
                                ACCT TC    CCCTTCCACCA
                                  C  CT__
GAM216  BCL11B   3'  ACCACCTCTCCCGCCCTTACCA 43182     A   ACAT
                                TGG AAG    GGGGAGGTGGT
                                ||| |||    ||||||||||
                                ACC TTC    CCTCTCCACCA
                                  A   CCGC
GAM216  CANX     3'  GCAGACCCATACCTTTCCA    87481       AC    GAG
                                TGGAAAG  ATGGG   GT
                                |||||||  |||||   ||
                                ACCTTTC  TACCC   CG
                                    CA    AGA
GAM216  COL6A2   3'  CCAGCCCCAGGTCTCCCCA    8481      AA   A    AGG
                                TGG  AGAC TGGGG   TGG
                                |||  |||| |||||   |||
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                                ACC  TCTG ACCCC   ACC
                                  CC   G    G__
GAM216  DBY     3'  CCACCACTAAAAATGCCTCTCC 16227     A  A   GG__  A
                                GGA AG CAT    GG GGTGG
                                ||| || |||    || |||||
                                CCT TC GTA    TC CCACC
                                  C  C   AAAA  A
GAM216  DES     3'  CCACCTCCCCACGCCCTCC    72122     AAGACA
                                GGA     TGGGGAGGTGG
                                |||     ||||||||||
                                CCT     ACCCCTCCACC
                                  CCCGC_
GAM216  DPYSL2  3'  TCACCACCCTTGTCTCTCTA   7303      A    T    A
                                TGGA AGACA GGGG GGTGG
                                |||| ||||| |||| |||||
                                ATCT TCTGT TCCC CCACT
                                  C    _   A
GAM216  GRAF    3'  TTTCCCCATGTCCTCC      30583     AA
                                GGA  GACATGGGGAGG
                                |||  ||||||||||||
                                CCT  CTGTACCCCTTT
                                  C_
GAM216  HTR6    5'  CCCCGCCCATGTCCCCCCA    6032      AAA       GA  T
                                TGG   GACATGGG  GG GG
                                |||   ||||||||  || ||
                                ACC   CTGTACCC  CC CC
                                  CCC       G_ _
GAM216  IDH3B   3'  CCACACTCCCCATACCCTTC   22577     AGAC       _
                                GAA    ATGGGGAG GTGG
                                |||    |||||||| ||||
                                CTT    TACCCCTC CACC
                                  CCCA       A
GAM216  LCN1    3'  TACCACCCCCCGCCTTCCC    64230    A   ACA    A
                                GG AAG   TGGGG GGTGGTA
                                || |||   ||||| |||||||
                                CC TTC   GCCCC CCACCAT
                                 C   C__    _
GAM216  LCN1    3'  TACCACCCCCCGCCTTCCC    9690     A   ACA    A
                                GG AAG   TGGGG GGTGGTA
                                || |||   ||||| |||||||
                                CC TTC   GCCCC CCACCAT
                                 C   C__    _
GAM216  MDFI    3'  CTACCCACCCATGTCCTCT    18771     AA       GA
                                GGA  GACATGGG  GGTGG
                                |||  ||||||||  |||||
                                TCT  CTGTACCC  CCATC
                                  C_       AC
GAM216  MGAT1   3'  CCAGGCGCCCCATGTCCTC    10006    AA       AGG_
                                GA  GACATGGGG    TGG
                                ||  |||||||||    |||
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                                CT  CTGTACCCC   ACC
                                 C_      GCGG
GAM216  MLLT2   3' CCGCCCCCAATCTCCCCA   19844    AA  CATG  A
                                TGG  AGA   GGG GGTGG
                                |||  |||   ||| |||||
                                ACC  TCT   CCC CCGCC
                                  CC  AA__  _
GAM216  MMP19   3' CCACCACCCACCCTTTC    10081     ACA   GA
                                GAAAG  TGGG  GGTGG
                                |||||  ||||  |||||
                                CTTTC  ACCC  CCACC
                                  CC_   A_
GAM216  MMP19   3' CCACCACCCACCCTTTC    42968     ACA   GA
                                GAAAG  TGGG  GGTGG
                                |||||  ||||  |||||
                                CTTTC  ACCC  CCACC
                                  CC_   A_
GAM216  MMP19   3' CCACCACCCACCCTTTC    42977     ACA   GA
                                GAAAG  TGGG  GGTGG
                                |||||  ||||  |||||
                                CTTTC  ACCC  CCACC
                                  CC_   A_
GAM216  MMP19   3' CCACCACCCACCCTTTC    42982     ACA   GA
                                GAAAG  TGGG  GGTGG
                                |||||  ||||  |||||
                                CTTTC  ACCC  CCACC
                                  CC_   A_
GAM216  MN1     5' CCTCCCCATTCCCCCCA    10088    AAA  C
                                TGG   GA ATGGGGAGG
                                |||   || |||||||||
                                ACC   CT TACCCCTCC
                                  CCC  _
GAM216  MPL     3' CCACTTCCCCACACTTCCCA  18136    A   ACA
                                TGG AAG   TGGGGAGGTGG
                                ||| |||   ||||||||||
                                ACC TTC   ACCCCTTCACC
                                  C   AC_
GAM216  MUC4    5' CTTCCCCATTCTTCCCA    37272    A   C
                                TGG AAGA ATGGGGAGG
                                ||| |||| |||||||||
                                ACC TTCT TACCCCTTC
                                  C   _
GAM216  MUC4    5' CTTCCCCATTCTTCCCA    56325    A   C
                                TGG AAGA ATGGGGAGG
                                ||| |||| |||||||||
                                ACC TTCT TACCCCTTC
                                  C   _
GAM216  PAK4    3' GCCCCCCACCCTCTCCA    19688     A  ACA   A
                                TGGA AG   TGGGG GGT
                                |||| ||   ||||| |||
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                                ACCT TC   ACCCC CCG
                                  C  CC_    _
GAM216  PCDH7    5'  TCATTCCCCACCTCTTCCCA  10460     A    CA      G
                                TGG AAGA  TGGGGAG TGG
                                ||| ||||  ||||||| |||
                                ACC TTCT  ACCCCTT ACT
                                  C    CC      _
GAM216  PCDH7    3'  CTTCCCCACCCCTCTCCA    50603      A  ACA
                                TGGA AG   TGGGGAGG
                                |||| ||   ||||||||
                                ACCT TC   ACCCCTTC
                                  C  CCC
GAM216  PCDH7    5'  TCATTCCCCACCTCTTCCCA  50604     A    CA      G
                                TGG AAGA  TGGGGAG TGG
                                ||| ||||  ||||||| |||
                                ACC TTCT  ACCCCTT ACT
                                  C    CC      _
GAM216  PCDH7    5'  TCATTCCCCACCTCTTCCCA  50598     A    CA      G
                                TGG AAGA  TGGGGAG TGG
                                ||| ||||  ||||||| |||
                                ACC TTCT  ACCCCTT ACT
                                  C    CC      _
GAM216  PCOLN3   3'  CCACACCCCAATGCCTTCCCA  10908     A  A  _   AG
                                TGG AAG CAT GGGG  GTGG
                                ||| ||| ||| ||||  ||||
                                ACC TTC GTA CCCC  CACC
                                  C  C  A   A_
GAM216  PCTK3    3'  CCACCCTCCACTCCTCCCCA  72964     AA  ACA    A
                                TGG  AG   TGGGG GGTGG
                                |||  ||   ||||| |||||
                                ACC  TC   ACCTC CCACC
                                  CC  CTC    _
GAM216  PIG3     3'  CCACCCCAGGCCTTTCCA    16875        ACA    A
                                TGGAAAG   TGGGG GG
                                |||||||   ||||| ||
                                ACCTTTC   ACCCC CC
                                    CGG    A
GAM216  PRKACA   3'  CCACCCCTCCCATGTCCCCCCA 10787     AAA       _ A
                                TGG   GACATGGG G GGTGG
                                |||   |||||||| | |||||
                                ACC   CTGTACCC C CCACC
                                  CCC       T C
GAM216  SELP     3'  TACCACCCCTTCCTGTCCCA  11537     AAA   T   A
                                TGG   GACA GGGG GGTGGTA
                                |||   |||| |||| |||||||
                                ACC   CTGT CTTC CCACCAT
                                  ___   C   C
GAM216  SLC16A2  3'  TTACCACCCAATGTGTCTCCCA 21505     AA      GGGA
                                TGG  AGACATG    GGTGGTAA
                                |||  |||||||   ||||||||
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                                ACC  TCTGTGT   CCACCATT
                                  C_     AAC_
GAM216  SLC22A12  3'  CCTCCCCATGTCCCTCCA   58067     AA
                                TGGA  GACATGGGGAGG
                                ||||  ||||||||||||
                                ACCT  CTGTACCCCTCC
                                  CC
GAM216  SLC9A5    3'  ACCACCTCCCTGCTCC     59767     AAGACAT
                                GGA     GGGGAGGTGGT
                                |||     ||||||||||
                                CCT     TCCCTCCACCA
                                  CG_____
GAM216  SLC9A5    3'  ACCACCTCCCTGCTCC     15980     AAGACAT
                                GGA     GGGGAGGTGGT
                                |||     ||||||||||
                                CCT     TCCCTCCACCA
                                  CG_____
GAM216  SNX5      3'  TCACCTGGCCCATGTCCC    27036    AAA      G_
                                GG   GACATGGG  AGGTGG
                                ||   ||||||||  ||||||
                                CC   CTGTACCC  TCCACT
                                  ___       GG
GAM216  SNX9      3'  CCATCCCATGTCCCTCCA    32591     AA      GA
                                TGGA  GACATGGG  GG
                                ||||  ||||||||  ||
                                ACCT  CTGTACCC  CC
                                  CC       TA
GAM216  STIM1     3'  CCACTTTCCCCCACCCTTCCCA 60146     A   ACAT_
                                TGG AAG    GGGGAGGTGG
                                ||| |||    ||||||||||
                                ACC TTC    CCCTTTCACC
                                  C   CCACC
GAM216  TAF10     3'  TTATCTGTCCCCATGTCCCCA  20805     AAA       GGT
                                TGG   GACATGGGGA   GGTAA
                                |||   ||||||||||   |||||
                                ACC   CTGTACCCCT   CTATT
                                  C__        GT_
GAM216  TBL1X     3'  CTCCCCCTGTCTTTCCA     18931         T
                                TGGAAAGACA GGGGAG
                                |||||||||| ||||||
                                ACCTTTCTGT CCCCTC
                                       C
GAM216  TCF7      3'  CTACATCCCCAGGTCTCTCCA  12160     A   A     G
                                TGGA AGAC TGGGGA GTGG
                                |||| |||| |||||| ||||
                                ACCT TCTG ACCCCT CATC
                                  C   G     A
GAM216  TLE2      5'  CCACCACCCCACTTCAGCC   12307    AAA  CA    A
                                GG   GA  TGGGG GGTGG
                                ||   ||  ||||| |||||
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                                CC  CT  ACCCC CCACC
                                 GA_ TC    A
GAM216  UBE2V1   3' TCACCACCCAACACCTTCCA  12520     AGACA   GA
                                TGGAA   TGGG GGTGG
                                |||||   |||| |||||
                                ACCTT   ACCC CCACT
                                  CCACA   A_
GAM216  UBE2V1   3' TCACCACCCAACACCTTCCA  42372     AGACA   GA
                                TGGAA   TGGG GGTGG
                                |||||   |||| |||||
                                ACCTT   ACCC CCACT
                                  CCACA   A_
GAM216  UBE2V1   3' TCACCACCCAACACCTTCCA  41795     AGACA   GA
                                TGGAA   TGGG GGTGG
                                |||||   |||| |||||
                                ACCTT   ACCC CCACT
                                  CCACA   A_
GAM216  VDR      3' CCACCTGGCCCCATGTCTCTC 4567     A       __
                                GA AGACATGGGG AGGTGG
                                || |||||||||| ||||||
                                CT TCTGTACCCC TCCACC
                                 C        GG
GAM216  AP1GBP1  3' TCACCATGACATCTCTCTCCA 54524     A  C  GGGA
                                TGGA AGA ATG   GGTGG
                                |||| ||| |||   |||||
                                ACCT TCT TAC   CCACT
                                  C  C  AGTA
GAM216  AP1GBP1  3' TCACCATGACATCTCTCTCCA 54535     A  C  GGGA
                                TGGA AGA ATG   GGTGG
                                |||| ||| |||   |||||
                                ACCT TCT TAC   CCACT
                                  C  C  AGTA
GAM216  AP1GBP1  3' TCACCATGACATCTCTCTCCA 23399     A  C  GGGA
                                TGGA AGA ATG   GGTGG
                                |||| ||| |||   |||||
                                ACCT TCT TAC   CCACT
                                  C  C  AGTA
GAM216  AP3D1    3' CCAAGGTTTCCCCACATCCTTC 14135     A  CA     ___
           C                     GGAA GA  TGGGGAGG  TGG
                                |||| ||  ||||||||  |||
                                CCTT CT  ACCCCTTT  ACC
                                  C AC      GGA
GAM216  ASB16    3' ACCACCTCCCTCTCCTGCCA  55102    AAA  CAT
                                TGG  GA  GGGGAGGTGGT
                                |||  ||  ||||||||||
                                ACC  CT  TCCCTCCACCA
                                 GTC  C__
GAM216  C20orf102 3' ACCACCTCCTGGCGAGTCCTTC 54613     A  A  __
           C                     GGAA GAC TG  GGGAGGTGGT
                                |||| ||| ||  ||||||||||
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                                CCTT CTG GC  TCCTCCACCA
                                  C   A  GG
GAM216  CDC42BPB  3'  GCTTCCCCTGTCCTCC     20101     AA   T
                                GGA  GACA GGGGAGGT
                                |||  |||| ||||||||
                                CCT  CTGT CCCCTTCG
                                  C_   _
GAM216  CINP      3'  TCACCAGCCCCATGGCCTCTCC 50939     A  A_     A_
            A                    TGGA AG  CATGGGG  GGTGG
                                |||| ||  |||||||  |||||
                                ACCT TC  GTACCCC  CCACT
                                  C  CG      GA
GAM216  COL12A1   3'  TCACCTCCTCATCTTTCCA   15184        CA
                                TGGAAAGA  TGGGGAGGTGG
                                ||||||||  ||||||||||
                                ACCTTTCT  ACTCCTCCACT
                                    __
GAM216  COL12A1   3'  TCACCTCCTCATCTTTCCA   54666        CA
                                TGGAAAGA  TGGGGAGGTGG
                                ||||||||  ||||||||||
                                ACCTTTCT  ACTCCTCCACT
                                    __
GAM216  DCOHM     3'  CTACCTTCCCTCACCTCTCCA  49597      A  ACAT
                                TGGA AG    GGGGAGGTGG
                                |||| ||    ||||||||||
                                ACCT TC    CCCTTCCATC
                                  C  CACT
GAM216  DEFB118   5'  TACCACCTCCTGCTTCCCA   54027     A   A  TGG
                                TGG AAG CA   GGAGGTGGTA
                                ||| ||| ||   ||||||||||
                                ACC TTC GT   CCTCCACCAT
                                  C  _ ___
GAM216  DKFZP434P1750 3'  TCACCAGGACCCATACCTTTC  31379       AC     GA__
                                GAAAG  ATGGG    GGTGG
                                |||||  |||||    |||||
                                CTTTC  TACCC    CCACT
                                   CA     AGGA
GAM216  DKFZP547E1010 5'  TTACCACCTCCCTATCTTACCA 31546     A    CA
                                TGG AAGA  TGGGGAGGTGGTAA
                                ||| ||||  ||||||||||||||
                                ACC TTCT  ATCCCTCCACCATT
                                  A   __
GAM216  DKFZP547E1010 5'  TTACCACCTCCCTATCTTACCA 66939     A    CA
                                TGG AAGA  TGGGGAGGTGGTAA
                                ||| ||||  ||||||||||||||
                                ACC TTCT  ATCCCTCCACCATT
                                  A   __
GAM216  DKFZP566K1924 5'  ACCACCTCCCTCACCCTCCCC  73774     AA  ACAT
                                GG  AG    GGGGAGGTGGT
                                ||  ||    ||||||||||
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                                CC  TC    TCCCTCCACCA
                                 CC  CCAC
GAM216  ENAH     5'  ACCACCTCCTGCCCCACCCCTC 36612     AAGACA    _____
              C                   GGA     TGGGG    AGGTGGT
                                  |||     |||||    |||||||
                                  CCT     ACCCC    TCCACCA
                                    CCCC__     GTCC
GAM216  FBXO32   5'  ACCAGGCCGGCCCCGTCTCCCC 54256     AA    AT    A_  __
              A                   TGG  AGAC  GGGG  GGT  GGT
                                  |||  ||||  ||||  |||  |||
                                  ACC  TCTG  CCCC  CCG  CCA
                                    CC    __    GG   GA
GAM216  FGF19    3'  CCACCTCACATGCCTCCCCA  17586     AA  A    GG
                                  TGG  AG CATG  GAGGTGG
                                  |||  || ||||  |||||||
                                  ACC  TC GTAC  CTCCACC
                                    CC  C    A_
GAM216  FKBP4    3'  CTGCCCCCCAGTCTCCCCA   8900      AA    A     A  TG
                                  TGG  AGAC TGGGG GG  G
                                  |||  |||| ||||| ||  |
                                  ACC  TCTG ACCCC CC  C
                                    CC    _     _ GT
GAM216  FLJ10044 3'  CTTCCCCATGTCTCTCC     35766     A
                                  GGA AGACATGGGGAGG
                                  ||| ||||||||||||
                                  CCT TCTGTACCCCTTC
                                    C
GAM216  FLJ10193 3'  CCAGGCCCCATACTCCCTCCA  56553      AA  C_     AGG
                                  TGGA  GA  ATGGGG   TGG
                                  ||||  ||  ||||||   |||
                                  ACCT  CT  TACCCC   ACC
                                     CC  CA     GG_
GAM216  FLJ10276 3'  TCCCCATGCCTTCCCA      35966     A   A
                                  TGG AAG CATGGGGA
                                  ||| ||| ||||||||
                                  ACC TTC GTACCCCT
                                    C   C
GAM216  FLJ12700 3'  TCACCAGGACATTCTTTCCA   46121         C   GGGA
                                  TGGAAAGA ATG    GGTGG
                                  |||||||| |||    |||||
                                  ACCTTTCT TAC    CCACT
                                        _   AGGA
GAM216  FLJ20273 3'  CCACTCCCACATCTCTCA    38727    A   C   _    G
                                  A AGA ATG GGGAG TGG
                                  | ||| ||| ||||| |||
                                  A TCT TAC CCCTC ACC
                                   C   C   A    _
GAM216  GS3955   5'  TTACACGCCCCCCCACCCTTTCC 41323         ACA    A    _
              A                   TGGAAAG   TGGGG GGTG GTAA
                                  |||||||   ||||| |||| ||||
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                                ACCTTTC   ACCCC CCGC CATT
                                   CC_    _   A
GAM216  HRD1     3'  TCCCCCACCCCTTTCCA     69560       ACA    A
                                TGGAAAG   TGGGG GG
                                |||||||   ||||| ||
                                ACCTTTC   ACCCC CT
                                   CCC    _
GAM216  HS6ST    3'  TTTCCCCATGCTCCCCA     62033     AA  A
                                TGG  AG CATGGGGAGG
                                |||  || ||||||||||
                                ACC  TC GTACCCCTTT
                                  CC  _
GAM216  HSPB7    3'  CCTCCCCACGTCTTCCA     27026      A   A
                                TGGAA GAC TGGGGAGG
                                ||||| ||| ||||||||
                                ACCTT CTG ACCCCTCC
                                   _  C
GAM216  KIAA0254 3'  TCTCCCCATACCTTCCC     28602    A   AC
                                GG AAG  ATGGGGAGG
                                || |||  |||||||||
                                CC TTC  TACCCCTCT
                                 C   CA
GAM216  KIAA0370 3'  CCACCACAGATGTCTCCCA   73206     AA     GGGGA
                                TGG  AGACAT    GGTGG
                                |||  ||||||    |||||
                                ACC  TCTGTA    CCACC
                                  C_     GACA_
GAM216  KIAA0416 3'  ACCACCACTACCCACTCCA   31461     AAGACA   GA__
                                TGGA     TGGG   GGTGGT
                                ||||     ||||   ||||||
                                ACCT     ACCC   CCACCA
                                  C_____   ATCA
GAM216  KIAA0451 3'  CCTCCCCACTCTCCCCA     29104     AA   CA
                                TGG  AGA  TGGGGAGG
                                |||  |||  ||||||||
                                ACC  TCT  ACCCCTCC
                                  CC   C_
GAM216  KIAA0522 3'  CCTCCCCATGTCCTCC      71967     AA
                                GGA  GACATGGGGAGG
                                |||  ||||||||||||
                                CCT  CTGTACCCCTCC
                                  C_
GAM216  KIAA0630 3'  ACCACCTCTACCCCTTTCCA  89387       ACAT  __
                                TGGAAAG   GGG  GAGGTGGT
                                |||||||   |||  ||||||||
                                ACCTTTC   CCC  CTCCACCA
                                   ____  AT
GAM216  KIAA0644 3'  TCACCACCCACCTTTTCA    29064       ACA   GA
                                TGGAAAG   TGGG  GGTGG
                                |||||||   ||||  |||||
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                                ACTTTTC  ACCC  CCACT
                                   C__   A_
GAM216  KIAA0674  5'  TCACCACCCACATCAATACCTT 60617      AC____  _  A
              TC                  GAAAG     ATG GGG GGTGG
                                  |||||     ||| ||| |||||
                                  CTTTC     TAC CCC CCACT
                                     CATAAC   A   A
GAM216  KIAA1069  3'  CTCCCCATGCCCTTCCCA    67935    A  A_
                                  TGG AAG  CATGGGGAG
                                  ||| |||  |||||||||
                                  ACC TTC  GTACCCCTC
                                    C   CC
GAM216  KIAA1138  3'  CCCCATGCCTCTTCCA      62138      _  A
                                  TGGAA AG CATGGGG
                                  ||||| || |||||||
                                  ACCTT TC GTACCCC
                                     C  C
GAM216  KIAA1202  3'  TACCACCTCTTGTTTCATCTTT 72021        CATG__
              CC                  GGAAAGA     GGGAGGTGGTA
                                  |||||||     ||||||||||
                                  CCTTTCT     TTCTCCACCAT
                                     ACTTTG
GAM216  KIAA1205  3'  ACTCCCTCCCCATTCCTCC   70040     AA  C       TG
                                  GGA  GA ATGGGGAGG  GT
                                  |||  || |||||||||  ||
                                  CCT  CT TACCCCTCC  CA
                                    C_  _        CT
GAM216  KIAA1305  3'  CTACACCCACATTCTCTCCA  46930     A   C   _   AG
                                  TGGA AGA ATG GGG  GTGG
                                  |||| ||| ||| |||  ||||
                                  ACCT TCT TAC CCC  CATC
                                    C   _   A   A_
GAM216  KIAA1416  5'  ACCACCCCTCTACTGCTCTCCA 86453      A  A  _    A
                                  TGGA AG CA TGGGG GGTGGT
                                  |||| || || ||||| ||||||
                                  ACCT TC GT ATCTC CCACCA
                                    C  _  C    C
GAM216  KIAA1553  3'  ACCACCTCCCCCTTCCCA    91913    A   ACAT
                                  TGG AAG    GGGGAGGTGGT
                                  ||| |||    ||||||||||
                                  ACC TTC    CCCCTCCACCA
                                    C  _____
GAM216  KIAA1656  3'  TCACCCCCACTTCCTTCCA    65807      A  CATG   A
                                  TGGAA GA    GGG GGTGG
                                  ||||| ||    ||| |||||
                                  ACCTT CT    CCC CCACT
                                     C  TCA_  _
GAM216  KIAA1765  3'  ACCACCTTGGGAATCTGTCCA  70608      A   CATGGG
                                  TGGA AGA     GAGGTGGT
                                  |||| |||     ||||||||
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                                ACCT TCT     TTCCACCA
                                  G  AAGGG_
GAM216  KIAA1817  3'  CCTCTCCATATCTCCCCA   68226    AA  C
                                TGG  AGA ATGGGGAGG
                                |||  ||| |||||||||
                                ACC  TCT TACCTCTCC
                                  CC   A
GAM216  KIAA1879  3'  TACCACCTCAACAGACACCTCC 73572     AAGACA  GG
          A                      TGGA     TG  GAGGTGGTA
                                ||||     ||  |||||||||
                                ACCT     AC  CTCCACCAT
                                  CCACAG  AA
GAM216  KIAA1883  5'  ACCACCTCCACCTCCCTGCCA  73417    AAAGACAT  _
                                TGG       GG GGAGGTGGT
                                |||       || |||||||||
                                ACC       CC CCTCCACCA
                                  GTCCCT__  A
GAM216  MGC10540  3'  TTACCTCCCACCTTTCCA   50383       ACATG
                                TGGAAAG    GGGAGGTGG
                                |||||||    |||||||||
                                ACCTTTC    CCCTCCATT
                                    CA___
GAM216  MGC16025  3'  CCGTCCCCATGACCCTCCA   51917     AAGA      _
                                TGGA   CATGGGGA GG
                                ||||   |||||||| ||
                                ACCT   GTACCCCT CC
                                  CCCA       G
GAM216  MGC21738  3'  TCAGTTTCCCCATTCCCCCCA  58919    AAA  C       _
                                TGG   GA ATGGGGAGG TGG
                                |||   || ||||||||| |||
                                ACC   CT TACCCCTTT ACT
                                  CCC  _       G
GAM216  MGC2562   3'  TCAAGAAGCCCCACATCTTCC  50448     A  CA    AGG__
                                GGAA GA  TGGGG    TGG
                                |||| ||  |||||    |||
                                CCTT CT  ACCCC    ACT
                                  _  AC    GAAGA
GAM216  MGC2574   3'  CCAGCTTCCCCCACACCTTCCC 44052     A   ACAT_     _
          A                      TGG AAG    GGGGAGG TGG
                                ||| |||    ||||||| |||
                                ACC TTC    CCCCTTC ACC
                                  C   CACAC      G
GAM216  PDE2A     3'  CCACCTCCCACAGCCCTCCA   10470     AAGACA  _
                                TGGA     TG GGGAGGTGG
                                ||||     || |||||||||
                                ACCT     AC CCCTCCACC
                                  CCCG__  A
GAM216  PEG10     3'  ACCACCGCCGCCGCCTCCA   30516     AAGACA  _  A
                                TGGA     TGG GG GGTGGT
                                ||||     ||| || ||||||
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                                ACCT     GCC CC CCACCA
                                  CC____  G  G
GAM216  PPP1R16B  3'  CCACCTCCCACCCCCTTCCA  61382      AGACATG
                                TGGAA     GGGAGGTGG
                                |||||     |||||||||
                                ACCTT     CCCTCCACC
                                   CCCCCA_
GAM216  PRKWNK2  3'  ACCACCTCAGTATTTCTCTCCA 90536     A  C  GG
                                TGGA AGA ATG  GAGGTGGT
                                |||| ||| |||  ||||||||
                                ACCT TCT TAT  CTCCACCA
                                  C  T  GA
GAM216  PRO2325  3'  ACCACCTCCTGAGCCTCCA   96300     AAGACATG
                                TGGA      GGGAGGTGGT
                                ||||      ||||||||||
                                ACCT      TCCTCCACCA
                                  CCGAG___
GAM216  Rab11-FIP2 3'  TTACATATTCCCCAATCTTTCC 29784        CA     GTG
           A                     TGGAAAGA  TGGGGAG   GTAA
                                |||||||| |||||||  ||||
                                ACCTTTCT  ACCCCTT   CATT
                                    A_     ATA
GAM216  Rab11-FIP3 3'  ACACCCTCCCCACGCACTTCCC 28121     A  ACA_      TG
           A                     TGG AAG   TGGGGAGG  GT
                                ||| |||   |||||||| ||
                                ACC TTC   ACCCCTCC  CA
                                  C  ACGC      CA
GAM216  RBM14    3'  CCACTTCCCCATCTCCCCA   20909    AA  CA
                                TGG  AGA  TGGGGAGGTGG
                                |||  |||  ||||||||||
                                ACC  TCT  ACCCCTTCACC
                                  CC  __
GAM216  RBM14    3'  TACTCTGGCCCATACCTTTCC  20911      AC    GA  T
                                GGAAAG  ATGGG  GG GGTA
                                ||||||  |||||  || ||||
                                CCTTTC  TACCC  TC TCAT
                                   CA    GG  _
GAM216  SAMP14   3'  CCATGTCCCCATGTCCTTCC   56052     A       G
                                GGAA GACATGGGGA GTGG
                                |||| |||||||||| ||||
                                CCTT CTGTACCCCT TACC
                                  C        G
GAM216  SCGF     3'  CCACCACCCGGCCTTTCC    11438      ACA   GA
                                GGAAAG   TGGG  GGTGG
                                ||||||   ||||  |||||
                                CCTTTC   GCCC  CCACC
                                   CG_   A_
GAM216  SE70-2   5'  ACCACCTCCACTTCCA     42088     AAGACAT  _
                                TGGA      GG GGAGGTGGT
                                ||||      || |||||||||
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                                ACCT      TC CCTCCACCA
                                  _______ A
GAM216  SERPINB7 3' TACCACCATGTGTCTCACC   13689    AA     GGGA
                                GG  AGACATG   GGTGGTA
                                ||  |||||||   |||||||
                                CC  TCTGTGT   CCACCAT
                                 AC      A___
GAM216  SEZ6    5' ACCACCGGCCGCATCGTCTCTC 74362     A   _  G  A_
           CA                     TGGA AGAC ATG GG  GGTGGT
                                |||| |||| ||| ||  ||||||
                                ACCT TCTG TAC CC  CCACCA
                                  C   C  G  GG
GAM216  SIRPB1   3' ACCACCCCTCCCTGTCCCA   20236    AAA   T   A
                                TGG   GACA GGGG GGTGGT
                                |||   |||| |||| ||||||
                                ACC   CTGT CCTC CCACCA
                                  ___   C   C
GAM216  SLC2A4RG 3' TACCACCTTCTCCCTCCCCA  39173    AA  ACAT
                                TGG  AG   GGGGAGGTGGTA
                                |||  ||   ||||||||||||
                                ACC  TC   CTCTTCCACCAT
                                  CC  C___
GAM216  SNAP29   3' CTTCCCCACGTGCTCCCA    16542    AA  _  A
                                TGG  AG AC TGGGGAGG
                                |||  || || ||||||||
                                ACC  TC TG ACCCCTTC
                                  C_  G  C
GAM216  TED     3' CCACCACCCTAATCTTCCA   31632      A  CA    A
                                TGGAA GA  TGGGG GGTGG
                                |||||  ||  ||||| |||||
                                ACCTT CT  ATCCC CCACC
                                   _ A_    A
GAM216  TRAF3    3' CCACCACCCCTTCCTCCCCA  59738    AA  ACAT   A
                                TGG  AG   GGGG GGTGG
                                |||  ||   |||| |||||
                                ACC  TC   CCCC CCACC
                                  CC  CTT_   A
GAM216  TRPM3    3' TACCTAACGTCCCACATCCTTC 64912   GA  AC  _   G  __
           TCA                    TG  AAG  ATG GGGA GT  GGTA
                                ||  |||  ||| |||| ||  ||||
                                AC  TTC  TAC CCCT CA  CCAT
                                 TC   C_   A   G  AT
GAM216  WIRE     3' CTACCACCCTTGCCTTCCCA  78302    A  A  T   A
                                TGG AAG CA GGGG GGTGG
                                ||| ||| || |||| |||||
                                ACC TTC GT TCCC CCATC
                                  C   C  _   A
GAM216  WIT-1    5' CCACCACCCCTCTACCTCTTCA 31821     A  ACAT_   A
                                TGGA AG    GGGG GGTGG
                                ||||  ||    |||| |||||
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                                ACTT TC    CCCC CCACC
                                  C  CATCT   A
GAM216  ZNF185   3'  CTACAGAGCCCATGCTCTTCCC 23111    A   _    GAG_
            A                    TGG AAGA CATGGG   GTGG
                                ||| |||| ||||||   ||||
                                ACC TTCT GTACCC   CATC
                                  C   C    GAGA
GAM216  LOC115051 3'  TTTCCCCATGCTCCCCA    60044    AA  A
                                TGG  AG CATGGGGAGG
                                |||  || ||||||||||
                                ACC  TC GTACCCCTTT
                                  CC  _
GAM216  LOC116071 3'  CCACCACTGATGCCTCCCA   56624    AA  A   G  GA
                                TGG  AG CAT GG  GGTGG
                                |||  || ||| ||  |||||
                                ACC  TC GTA TC  CCACC
                                  C_  C   G  A_
GAM216  LOC145547 3'  CTACACCCACATTCTCTCCA   77265    A   C   _   AG
                                TGGA AGA ATG GGG  GTGG
                                |||| ||| ||| |||  ||||
                                ACCT TCT TAC CCC  CATC
                                  C   _   A  A_
GAM216  LOC147958 3'  CTACCTCCCCAGATCTCTCCA  87178     A   CA
                                TGGA AGA  TGGGGAGGTGG
                                |||| |||  ||||||||||
                                ACCT TCT  ACCCCTCCATC
                                  C   AG
GAM216  LOC149466 3'  CCTCCCCACTCCCTCCA    79395     AA  CA
                                TGGA  GA  TGGGGAGG
                                ||||  ||  ||||||||
                                ACCT  CT  ACCCCTCC
                                  CC  C_
GAM216  LOC158117 3'  CCACCACCTATGTCCTC    81702    AA      GA
                                GA  GACATGGG  GGTGG
                                ||  ||||||||  |||||
                                CT  CTGTATCC  CCACC
                                 C_       A_
GAM216  LOC159199 5'  TACCACCTTCGCCTCGCCCA  82188    AAA  CAT  _
                                TGG   GA   GG GGAGGTGGTA
                                |||   ||   || ||||||||||
                                ACC   CT   CC CTTCCACCAT
                                  CG_  ___  G
GAM216  LOC165741 3'  CCAGCAAGCCCCATTCTCTCCA 87255     A   C    AG_ _
                                TGGA AGA ATGGGG   G TGG
                                |||| ||| ||||||   | |||
                                ACCT TCT TACCCC   C ACC
                                  C   _    GAA G
GAM216  LOC200316 3'  ACCACCTCCTCCCCGCTCTCC  88763    A  ACAT
                                GGA AG   GGGGAGGTGGT
                                ||| ||   ||||||||||
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                                CCT TC    CTCCTCCACCA
                                  C  GCCC
GAM216  LOC200574 3'  CTACTCCCCATTCTTTCCA   88830        C      G
                                TGGAAAGA ATGGGGAG TGG
                                |||||||| |||||||| |||
                                ACCTTTCT TACCCCTC ATC
                                      _      _
GAM216  LOC202404 5'  ACCAGCTTCCATGTGTCCCCA  89168     AAA    _    G
                                TGG   GACATG GGGAG TGGT
                                |||   |||||| ||||| ||||
                                ACC   CTGTGT CCTTC ACCA
                                  C__     A    G
GAM216  LOC203275 3'  CCACCACCTATGTCCTC     89318    AA      GA
                                GA  GACATGGG  GGTGG
                                ||  ||||||||  |||||
                                CT  CTGTATCC  CCACC
                                 C_       A_
GAM216  LOC221922 5'  CCCCCCATGCCTCTCCA     92690      A  A      A
                                TGGA AG CATGGGG GG
                                |||| || ||||||| ||
                                ACCT TC GTACCCC CC
                                  C  C      _
GAM216  LOC255952 5'  CCACCACCTTTGTTTCCCA   97633     AA    T   GA
                                TGG  AGACA GGG  GGTGG
                                |||  ||||| |||  |||||
                                ACC  TTTGT TCC  CCACC
                                  C_    T   A_
GAM216  LOC256849 5'  CCTCCCCATTTCCTCC      96949     AA  C
                                GGA  GA ATGGGGAGG
                                |||  || |||||||||
                                CCT  CT TACCCCTCC
                                  C_  T
GAM216  LOC257200 3'  CCACCACCCTCATCTTCCA   95651       A  CAT    A
                                TGGAA GA   GGGG GGTGG
                                |||||  ||   |||| |||||
                                ACCTT CT   TCCC CCACC
                                   _  AC_    A
GAM216  LOC51279  3'  CCAGCCCCCACATCCTTACCA  33310     A   AC   _   A  _
                                TGG AAG  ATG GGG GG TGG
                                ||| |||  ||| ||| || |||
                                ACC TTC  TAC CCC CC ACC
                                  A   C_   A   _  G
GAM216  LOC56965  5'  ACCATATCATCCCACGCCTTTC 39526        ACA    AG__
            CA                    TGGAAAG   TGGGG   GTGGT
                                |||||||   |||||   |||||
                                ACCTTTC   ACCCT   TACCA
                                    CGC    ACTA
GAM216  LOC90288  3'  CCAGCCCCATGTCTACCCA   62085     AA        AGG
                                TGG  AGACATGGGG   TGG
                                |||  ||||||||||   |||
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                                ACC  TCTGTACCCC   ACC
                                  CA         G__
GAM216  LOC91813  5'  CCACCCCCCACACCTTCCCA  67248     A   ACA     A
                                TGG AAG   TGGGG GGTGG
                                ||| |||   ||||| |||||
                                ACC TTC   ACCCC CCACC
                                  C   CAC    _
GAM216  LOC91974  5'  CCTCCCCAGTGTCTTCCCA   67754     A     _
                                TGG AAGACA TGGGGAGG
                                ||| |||||| ||||||||
                                ACC TTCTGT ACCCCTCC
                                  C     G
GAM216  LOC92710  3'  CCACATCCCCCACATGCCTCCC 70354     AA  A  ___    G
             A                   TGG  AG CAT   GGGGA GTGG
                                ||| || |||   ||||| ||||
                                ACC  TC GTA   CCCCT CACC
                                  C_  C   CAC    A
GAM217  ALX3     3'  CAAACTGAGTCCCCTCA     21418      A_  AG
                                TGAG  GA  TCAGTTTG
                                ||||  ||  ||||||||
                                ACTC  CT  AGTCAAAC
                                  CC  G_
GAM217  HNF3G    3'  TGAAGCCCACCCTTTC      72345     GTC  TT
                                GAA   AG  TGGGCTTCA
                                |||   ||  |||||||||
                                CTT   TC  ACCCGAAGT
                                  ___  CC
GAM217  IL1R1    3'  GAAGCCCATGCTTTC       6059      GTC   T
                                GAA   AGT TGGGCTTC
                                |||   ||| ||||||||
                                CTT   TCG ACCCGAAG
                                  ___   T
GAM217  NGFR     3'  GAAGCTCAGCCCACCCCCCTCA 10228      AGAA  CA   T
                                TGAG    GT  GTT GGGCTTC
                                ||||    ||  ||| |||||||
                                ACTC    CA  CGA CTCGAAG
                                  CCCC  CC   _
GAM217  PLA2G2D  3'  TGAAGCTTTCCGAATCCTCCCA 24801    A   AAG  AGTTT
                                TG GAG   TC    GGGCTTCA
                                || |||   ||    ||||||||
                                AC CTC   AG    TTCGAAGT
                                 C   CTA  CCT__
GAM217  SLC7A8   3'  TGAAGCCCAGTTCCTTTC    24285      AAGTCAGT
                                GAGAG       TTGGGCTTCA
                                |||||       ||||||||||
                                CTTTC       GACCCGAAGT
                                   CTT_____
GAM217  SOX13    3'  AAGCCCCCACTTCTCTC     19078         CAGTTT
                                GAGAGAAGT     GGGCTT
                                |||||||||     ||||||
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                                CTCTCTTCA     CCCGAA
                                     CC____
GAM217  ATP1B4   3'  AAACTGCCTCCTCTCA      23809       A  T
                                TGAGAG AG CAGTTT
                                |||||| || ||||||
                                ACTCTC TC GTCAAA
                                   C  C
GAM217  C20orf44 3'  TCAAACCGCTTCTCTCA     36762          CA
                                TGAGAGAAGT  GTTTGG
                                ||||||||||  ||||||
                                ACTCTCTTCG  CAAACT
                                      C_
GAM217  CYP2A7   5'  AAGCCCAAGTGCTC       47584     AAGT  G
                                GAG    CA TTTGGGCTT
                                |||    || |||||||||
                                CTC    GT GAACCCGAA
                                 _____  _
GAM217  CYP2A7   5'  AAGCCCAAGTGCTC       5713      AAGT  G
                                GAG    CA TTTGGGCTT
                                |||    || |||||||||
                                CTC    GT GAACCCGAA
                                 _____  _
GAM217  DSCR1L1  3'  AAGCTGACTCTTCTCA      19492       GA
                                TGAGA  AGTCAGTTT
                                |||||  |||||||||
                                ACTCT  TCAGTCGAA
                                   TC
GAM217  FLJ10287 3'  GAAACCAAAAACCTTCTC    38845       TCAG    GC
                                GAGAAG   TTTGG  TTC
                                ||||||   |||||  |||
                                CTCTTC   AAACC  AAG
                                   CAA_    A_
GAM217  FLJ12783 3'  TGAAACCTGACTCTGCTTCTCT 48685         T   T_ TG  C
           CA                    TGAGAGAAG CAG  T  GG TTCA
                                |||||||||  |||  |  || ||||
                                ACTCTCTTC GTC  A  CC AAGT
                                     _  TC GT  A
GAM217  FLJ14107 3'  TGAAATGTGTCCAAACTCCTCT 46700       AAGTC       _____
           CA                    GAGAG    AGTTTGGGC    TTCA
                                |||||    |||||||||   ||||
                                CTCTC    TCAAACCTG    AAGT
                                  C_____        TGTA
GAM217  FLJ14124 5'  AAGCCCAGGCCTTC       45888      TCA
                                GAAG   GTTTGGGCTT
                                ||||   ||||||||||
                                CTTC   CGGACCCGAA
                                  ___
GAM217  FLJ20086 3'  AAGCCTTTCAAACTTCCATCA  34520     GA    CAGTTT
                                TGA  GAAGT     GGGCTT
                                |||  |||||     ||||||
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                                ACT  CTTCA     TCCGAA
                                  AC     AACTT_
GAM217  FLJ23191  3'  AAGTATAAACTGACTACTCCCA 44707    A   A        G
                                TG GAG AGTCAGTTTG GCTT
                                || ||| |||||||||| ||||
                                AC CTC TCAGTCAAAT TGAA
                                 C   A         A
GAM217  GAB3      3'  GAAATTCTGACTTCTCTC    54627           TTTGGGC
                                GAGAGAAGTCAG      TTC
                                ||||||||||||      |||
                                CTCTCTTCAGTC      AAG
                                       TTA____
GAM217  HSU24186  5'  AAGCCCACCTTCTCCTCA    25323      _    TCAGTT
                                TGAG AGAAG     TGGGCTT
                                |||| |||||     |||||||
                                ACTC TCTTC     ACCCGAA
                                  C    C_____
GAM217  KIAA1975  5'  AAGCTGACTTTTCCCA     73967    A
                                TG GAGAAGTCAGTTT
                                || ||||||||||||
                                AC CTTTTCAGTCGAA
                                 C
GAM217  SFRS12    3'  AAGCTTTTAATTCTCTCA    57525         GTCAGTTT
                                TGAGAGAA       GGGCTT
                                ||||||||       ||||||
                                ACTCTCTT       TTCGAA
                                     AATT____
GAM217  LOC149271 5'  AAATCCAAGCTCTCTCA     79234        AGTCA     GC
                                TGAGAGA    GTTTGG  TT
                                |||||||    ||||||  ||
                                ACTCTCT    CGAACC  AA
                                   _____      TA
GAM217  LOC151512 5'  AAGCCTGAGGTGACCCTC    85425     AA    G  TG
                                GAG  GTCA TT  GGCTT
                                |||  |||| ||  |||||
                                CTC  CAGT GA  CCGAA
                                  C_   G  GT
GAM217  LOC159199 5'  AAGCCCAGCTCCTATCA     82179     G  A   CAGTT
                                TGA AG AGT     TGGGCTT
                                ||| || |||     |||||||
                                ACT TC TCG     ACCCGAA
                                  A  C  _____
GAM217  LOC161357 5'  TGAAGTCCGACTGACTCCTCTC 82274       A       T
          A                      TGAGAG AGTCAGTT GGGCTTCA
                                ||||||| |||||||| ||||||||
                                ACTCTC TCAGTCAG CCTGAAGT
                                   C       _
GAM217  LOC199918 5'  AAGTCCTGCTTCTCTCA     89875         T  GTTT
                                TGAGAGAAG CA    GGGCTT
                                ||||||||| ||    ||||||
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                                ACTCTCTTC GT    CCTGAA
                                      _ ____
GAM217  LOC220469 3'  AAGCCCAACCTTCTCCA     76381    A     TCAGT
                                TG GAGAAG    TTGGGCTT
                                || ||||||    ||||||||
                                AC CTCTTC    AACCCGAA
                                 _     C____
GAM217  LOC55885  3'  GAACAAACTTCTCTCA      37816         CA
                                TGAGAGAAGT  GTTT
                                ||||||||||  ||||
                                ACTCTCTTCA  CAAG
                                      AA
GAM217  LOC90139  3'  TGAAGCCTGAAGACTC      55405    A   AG  TG
                                GA GTC  TT  GGCTTCA
                                || |||  ||  |||||||
                                CT CAG  AA  CCGAAGT
                                 _  __  GT
GAM217  LOC92578  5'  AAGCCAGAAACTTCTCTCA    69820         CAG   G
                                TGAGAGAAGT   TTT GGCTT
                                ||||||||||   ||| |||||
                                ACTCTCTTCA   AAG CCGAA
                                      ___   A
GAM218  PDE6D     3'  GGAAACAAACACATACCACA   10493         AG__
                                TGTGGTATGT    GTTTCT
                                ||||||||||    ||||||
                                ACACCATACA    CAAAGG
                                      CAAA
GAM218  SFRP1     3'  GAAACAGACTCATACCACA    11568         T  GTT    C
                                TGTGGTATG AG   TCTG TTC
                                ||||||||| ||   |||| |||
                                ACACCATAC TC   AGAC AAG
                                      _ ___    A
GAM218  SLC4A4    3'  GAAGCAGAATGAAACCACA    13638       ATGTAGGT
                                TGTGGT       TTCTGCTTC
                                ||||||       |||||||||
                                ACACCA       AAGACGAAG
                                   AAGT_____
GAM218  TRIM39    3'  GGAAACAGAAACCCCTGCA    41172      __       C
                                TGTA  GGTTTCTG TTCC
                                ||||  |||||||| ||||
                                ACGT  CCAAAGAC AAGG
                                  CC       A
GAM218  TRPM7     3'  AAGCAGAAACCTAACTCAC    62124      TATG
                                GTGG   TAGGTTTCTGCTT
                                ||||   |||||||||||||
                                CACT   ATCCAAAGACGAA
                                  CA__
GAM218  UBE3A     3'  CAAAAACAACTCATGCCACA   55587         TAG_   C
                                TGTGGTATG    GTTT TG
                                |||||||||    |||| ||
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                                ACACCGTAC   CAAA AC
                                     TCAA   A
GAM218  UBE3A    3'  CAAAAACAACTCATGCCACA  4865        TAG_   C
                                TGTGGTATG   GTTT TG
                                |||||||||   |||| ||
                                ACACCGTAC   CAAA AC
                                     TCAA   A
GAM218  UBE3A    3'  CAAAAACAACTCATGCCACA  55577       TAG_   C
                                TGTGGTATG   GTTT TG
                                |||||||||   |||| ||
                                ACACCGTAC   CAAA AC
                                     TCAA   A
GAM218  FLJ10724 3'  GAAGCAGAATTTAGAAACCACA 36501     ATG    T
                                TGTGGT   TAGGTT CTGCTTC
                                ||||||   |||||| |||||||
                                ACACCA   ATTTAA GACGAAG
                                   AAG    _
GAM218  FLJ13315 3'  GAAGCAGAAGTTAGATCCCACA 46569     T  G   G  T
                                TGTGG AT TAG TT CTGCTTC
                                ||||| || ||| || |||||||
                                ACACC TA ATT AA GACGAAG
                                  C  G   G  _
GAM218  KIAA0450 3'  GAAGCAAAACTTATACAACA  27638    GGTA      C
                                TGT   TGTAGGTTT TGCTTC
                                |||   ||||||||| ||||||
                                ACA   ATATTCAAA ACGAAG
                                 AC__       _
GAM218  NYD-SP21 3'  GAATCTACCCAATACCACA   50874       ___
                                TGTGGTAT   GTAGGTTT
                                ||||||||   ||||||||
                                ACACCATA   CATCTAAG
                                     ACC
GAM218  PTD002   3'  GGAAACAAAAGTGAATACCATA 32347      GTAG____
                                TGTGGTAT      GTTTCT
                                ||||||||      ||||||
                                ATACCATA      CAAAGG
                                     AGTGAAAA
GAM218  LOC151126 5' AGGCAGTACATGCCACA    80124        GGTTT
                                TGTGGTATGTA    CTGCTT
                                ||||||||||    ||||||
                                ACACCGTACAT    GACGGA
                                              _____
GAM218  LOC200488 5' GAAGCAGAAACTCAGGTCCACA 90086     TA_  TA
                                TGTGG   TG  GGTTTCTGCTTC
                                |||||   ||  ||||||||||||
                                ACACC   AC  TCAAAGACGAAG
                                   TGG  __
GAM218  LOC221688 3' CAGAAACCCTGAGCCGCA    93676      ATGTA
                                TGTGGT    GGTTTCTG
                                ||||||    ||||||||
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                                ACGCCG    CCAAAGAC
                                   AGTC_
GAM219  CCND2    3'  ATCCTGGATTTTGCCCT    8287    A    TGT
                                AG GCAAA   TTCAGGAT
                                || |||||   ||||||||
                                TC CGTTT   AGGTCCTA
                                 C    T__
GAM219  CTLA4    5'  GGATCCTGAAAGGTTTTGCTCT 17809         _ G
             AC                   GTAGAGCAAA T TTTCAGGATCC
                                ||||||||||| | ||||||||||
                                CATCTCGTTT G AAAGTCCTAGG
                                      T G
GAM219  CYP1A1   3'  GATCCTGCCTGCCCCTAC    4943      A_   AATGTTT
                                GTAG  GCA     CAGGATC
                                ||||  |||     |||||||
                                CATC  CGT     GTCCTAG
                                  CC   CC_____
GAM219  ETF1     3'  CCTGAAGCTGATGCTTCAC   16395    AG    AAT
                                GT  AGCA   GTTTCAGG
                                ||  ||||   ||||||||
                                CA  TCGT   CGAAGTCC
                                 CT    AGT
GAM219  HDAC4    3'  GGATCCTGCCACCTGCCCT   20113    A   AA  TTT
                                AG GCA  TG   CAGGATCC
                                || |||  ||   ||||||||
                                TC CGT  AC   GTCCTAGG
                                 C   CC  C__
GAM219  KRTHA8   3'  ATCCTGAGTTTTCTCTAC    22256      C    GTT
                                GTAGAG AAAT   TCAGGAT
                                |||||| ||||   |||||||
                                CATCTC TTTG   AGTCCTA
                                   T   ____
GAM219  MAP3K9   3'  GGACCCCCTGAGATCCAGCCCT 60707     A  AAAT      A__
             AC                   GTAG GC    GTTTCAGG   TCC
                                |||| ||    ||||||||   |||
                                CATC CG    TAGAGTCC   AGG
                                  C  ACC_      CCC
GAM219  PLCB2    3'  GGATCCTGGCCCCACTCTGC   15893      CAAA  TT_
                                GTAGAG    TG   TCAGGATCC
                                ||||||    ||   |||||||||
                                CGTCTC    AC   GGTCCTAGG
                                    ____  CCC
GAM219  SH3GL1   3'  GGACCCCAGGCTCTGCTCTGC  11626        AAT    CA  A
                                GTAGAGCA   GTTT  GG TCC
                                ||||||||   ||||  || |||
                                CGTCTCGT   CGGA  CC AGG
                                     CT_    CC  _
GAM219  STK6     3'  GGAACACGTGCTCTAC      13188        AA
                                GTAGAGCA  TGTTTC
                                ||||||||  ||||||
```

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                                CATCTCGT  ACAAGG
                                     GC
GAM219  TMOD2    5' GGATCCTGGCCCCGCTCCAC  27250    A   AAATGTT
                                GT GAGC      TCAGGATCC
                                || ||||      |||||||||
                                CA CTCG      GGTCCTAGG
                                 C   CCCC___
GAM219  DIO2     3' GAATCTGGACATTTGTTCCAC  5832     A        T   A
                                GT GAGCAAATGTT CAGG TC
                                || |||||||||| |||| ||
                                CA CTTGTTTACAG GTCT AG
                                 C         _   A
GAM219  DIO2     3' GAATCTGGACATTTGTTCCAC  25684    A        T   A
                                GT GAGCAAATGTT CAGG TC
                                || |||||||||| |||| ||
                                CA CTTGTTTACAG GTCT AG
                                 C         _   A
GAM219  DKFZP434K1421 3'  GGAAAATTTGCTCCAC     49554    A      G
                                GT GAGCAAAT TTTC
                                || |||||||| ||||
                                CA CTCGTTTA AAGG
                                 C       A
GAM219  DKFZP566D193 3'  GGTTAAACATTTGCCTCTAC  85569       _       CAG
                                GTAGAG CAAATGTTT   GATC
                                |||||| |||||||||   ||||
                                CATCTC GTTTACAAA   TTGG
                                   C        ___
GAM219  EST-YD1  3' GACCTCGACATTTGCTC     41081          TC   A
                                GAGCAAATGTT  AGG TC
                                ||||||||||  ||| ||
                                CTCGTTTACAG  TCC AG
                                      C_  _
GAM219  FLJ10482 3' GGATCCTGCCACTTCACATCTA 36164      GCAAAT  TT
           C                     GTAGA     GT  CAGGATCC
                                |||||     ||  ||||||||
                                CATCT     CA  GTCCTAGG
                                   ACACTT  CC
GAM219  FLJ11026 5' GGATCACCAGTTTGCTCCAC  36994    A      GTTTCAG
                                GT GAGCAAAT      GATCC
                                || ||||||||      |||||
                                CA CTCGTTTG      CTAGG
                                 C       ACCA___
GAM219  FLJ13769 3' GACCCTGAAACACTCAGC    46610    A  CAAA       A
                                GT GAG    TGTTTCAGG TC
                                || |||    |||||||| ||
                                CG CTC    ACAAAGTCC AG
                                 A  _____        C
GAM219  FLJ20294 3' GGATCCTGCTGCACCCCTCCAC 34880    A  CAAA  TT
                                GT GAG    TGT  CAGGATCC
                                || |||    |||  ||||||||
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                              CA CTC    ACG  GTCCTAGG
                               C   CCC_   TC
GAM219  FLJ21918  3'  ATCCCAATGTTCTAC      46286        AA  TTTCA
                              GTAGAGCA  TG    GGAT
                              ||||||||  ||    ||||
                              CATCTTGT  AC    CCTA
                                  A_  _____
GAM219  FLJ22269  3'  CTGGAACATCTGGTCCAC    49913    A  G  A
                              GT GA CA ATGTTTCAG
                              || || || |||||||||
                              CA CT GT TACAAGGTC
                               C  G  C
GAM219  GAB1      3'  GAAACATTTGTTCCAC      8978     A
                              GT GAGCAAATGTTTC
                              || ||||||||||||
                              CA CTTGTTTACAAAG
                               C
GAM219  HSMPP8    3'  TCTAAAACATTTGCTT      93486          C
                              GAGCAAATGTTT AGG
                              |||||||||||| |||
                              TTCGTTTACAAA TCT
                                    A
GAM219  KIAA0310  3'  GACCCCAACCCCTGCTCTGC   81676        AAT   TCA  A
                              GTAGAGCA   GTT   GG TC
                              ||||||||   |||   || ||
                              CGTCTCGT   CAA   CC AG
                                   CCC   C__  C
GAM219  KIAA0759  3'  GATCCTGGGCCAGCCCCTCCAC 67324    A   CAAA  TT
                              GT GAG    TG  TCAGGATC
                              || |||    ||  ||||||||
                              CA CTC    AC  GGTCCTAG
                               C  CCCG  CG
GAM219  KIAA1211  3'  GTCCAAAACATTTACTCTAC   68896      C       CA
                              GTAGAG AAATGTTT  GGAT
                              |||||| ||||||||  ||||
                              CATCTC TTTACAAA  CCTG
                                  A       A_
GAM219  KIAA1373  3'  GGATCCTGATTAATGCTCTA   70947       AATGTT
                              TAGAGCA     TCAGGATCC
                              |||||||     |||||||||
                              ATCTCGT     AGTCCTAGG
                                  AATT__
GAM219  KIAA1586  5'  GATCATGCCATTGTGCTCTAC  92331        _   TTT  G
                              GTAGAGCA AATG   CA GATC
                              |||||||| ||||   || ||||
                              CATCTCGT TTAC   GT CTAG
                                   G   C__  A
GAM219  KIAA1987  3'  GACCCACATTTGCTC       88017         TTCA  A
                              GAGCAAATGT    GG TC
                              ||||||||||    || ||
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                                CTCGTTTACA   CC AG
                                     _____ C
GAM219  MESDC2   3' GGATGGGACATTTGCCCTGC  72495     A      TT  GGA
                                GTAG GCAAATGT  CA   TCC
                                |||| ||||||||  ||   |||
                                CGTC CGTTTACA  GT   AGG
                                  C       GG  ___
GAM219  MGC9753  5' GGATCCTGCCCCCGCCCTGC  53054     A  AAATGTTT
                                GTAG GC       CAGGATCC
                                |||| ||       ||||||||
                                CGTC CG       GTCCTAGG
                                  C  CCCCC___
GAM219  NFKBIE   3' GGACCCTGAAACACCGTTGTTT 15852      A__       A
                                GAGCAA   TGTTTCAGG TCC
                                ||||||   ||||||||| |||
                                TTTGTT   ACAAAGTCC AGG
                                    GCC        C
GAM219  LOC123016 3' GATCCTGAAACTGTCTCTC   58105   T   _ AAT
                                G AGAG CA   GTTTCAGGATC
                                | |||| ||   ||||||||||
                                C TCTC GT   CAAAGTCCTAG
                                 _    T ___
GAM219  LOC123435 5' GGACCCTGGGATTTTGCTCT  74207       T  TT   A
                                AGAGCAAA GT  CAGG TCC
                                |||||||| ||  |||| |||
                                TCTCGTTT TA  GTCC AGG
                                     _ GG   C
GAM219  LOC136895 5' GACCCTATTTGCTCTGC     57169         GTTTC  A
                                GTAGAGCAAAT     AGG TC
                                ||||||||||     ||| ||
                                CGTCTCGTTTA     TCC AG
                                       ______  C
GAM219  LOC144248 5' ATCCACCCTTATTTGCTCT   76734         TTTCA
                                AGAGCAAATG     GGAT
                                ||||||||||     ||||
                                TCTCGTTTAT     CCTA
                                      TCCCA
GAM219  LOC148189 5' GATCCGCACCGCCCTAC     78709     A  AAA   TTCA
                                GTAG GC   TGT    GGATC
                                |||| ||   |||    |||||
                                CATC CG   ACG    CCTAG
                                  C  CC_  _____
GAM219  LOC149711 5' ATCCACTATCTGCTCTAC    84671       A   TTTCA
                                GTAGAGCA ATG     GGAT
                                |||||||| |||     ||||
                                CATCTCGT TAT     CCTA
                                     C   CA___
GAM219  LOC153910 3' GATCCTGAGAGCACTC      80995     CAAA  _
                                GAG    TG TTTCAGGATC
                                |||    || ||||||||||
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                                CTC    AC AGAGTCCTAG
                                  _____  G
GAM219  LOC165693 3'  ACCTGAAACAGCTC       82591      AAA        A
                                GAGC   TGTTTCAGG T
                                ||||   |||||||||| |
                                CTCG   ACAAAGTCC A
                                  ___         C
GAM219  LOC199800 5'  GGATCCTGACCCGCCCTGC    89859      A  AAAT TT
                                GTAG GC    G  TCAGGATCC
                                |||| ||    |  |||||||||
                                CGTC CG    C  AGTCCTAGG
                                  C _____ CC
GAM219  LOC253985 5'  ATCCACCATGCTCTAC      96483         AAT  TTCA
                                GTAGAGCA   GT    GGAT
                                ||||||||   ||    ||||
                                CATCTCGT   CA    CCTA
                                     AC_  _____
GAM219  LOC256568 3'  GACACATTGCTCTAC       94842         A   T
                                GTAGAGCAA TGT TC
                                ||||||||| ||| ||
                                CATCTCGTT ACA AG
                                     _   C
GAM219  LOC90906  5'  GATCCTGAGAGCGCTC      64300      AAATG
                                GAGC     TTTCAGGATC
                                ||||     ||||||||||
                                CTCG     AGAGTCCTAG
                                  CG___
GAM219  LOC91266  5'  CCTGAAACATGTTC        65413      AA
                                GAGCA  TGTTTCAGG
                                |||||  |||||||||
                                CTTGT  ACAAAGTCC
                                  __
GAM220  ALPP      3'  CTACCCCAACCCCAGGGACTG  68834       G  CCAAC  AA
                                CAGTCT TG     TG  GTAG
                                |||||| ||     ||  ||||
                                GTCAGG AC     AC  CATC
                                   G  CCCA_  CC
GAM220  APLP2     3'  CTACCCACTATGCACAGATT   90895         CAAC  AA
                                AGTCTGTGC    TG  GTAG
                                |||||||||    ||  ||||
                                TTAGACACG    AC  CATC
                                     TATC  C_
GAM220  CASP7     3'  CTACTTCAGTCAATAGC     52901    T   GCCA
                                G CTGT    ACTGAAGTAG
                                | ||||    ||||||||||
                                C GATA    TGACTTCATC
                                 _    AC__
GAM220  COL3A1    3'  CTACCTCAACTGGTCAGA     3615       T   AC   A
                                TCTG GCCA  TGA GTAG
                                |||| ||||  ||| ||||
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                                AGAC TGGT  ACT CATC
                                  _   CA   C
GAM220  CYB5     3'  TACTTCAACTGACAGA      8595       GC  AC
                                TCTGT  CA  TGAAGTA
                                |||||  ||  |||||||
                                AGACA  GT  ACTTCAT
                                  __  CA
GAM220  PPEF2    3'  ACTTCAGTTAAGAACCACTG   20666      CT  GCC_
                                CAGT  GT    AACTGAAGT
                                ||||  ||    |||||||||
                                GTCA  CA    TTGACTTCA
                                  C_  AGAA
GAM220  DKFZP434C171 5'  GCTTCGAGACAGACTGGA    31557          GCCAA  _
                                TCCAGTCTGT     CT GAAGT
                                ||||||||||     || |||||
                                AGGTCAGACA     GA CTTCG
                                      _____  G
GAM220  DKFZP586P0123 3'  CGGTCAGCCCAGACTGGA    94838         T  CA
                                TCCAGTCTG GC  ACTG
                                ||||||||| ||  ||||
                                AGGTCAGAC CG  TGGC
                                     C  AC
GAM220  FLJ12389  3'  CTTTATTGCACAGACTG     60267          C  C
                                CAGTCTGTGC AA TGAAG
                                |||||||||| || |||||
                                GTCAGACACG TT ATTTC
                                      _  _
GAM220  FLJ20811  5'  AGGCTGGCACAGACTTGA    67126    C         A_
                                TC AGTCTGTGCCA  CT
                                || ||||||||||  ||
                                AG TCAGACACGGT  GA
                                  T         CG
GAM220  FLJ22059  5'  CAGCCCCAGCAGAGACTGGA   42767        G   CAA__
                                TCCAGTCT TGC     CTG
                                |||||||| |||    |||
                                AGGTCAGA ACG     GAC
                                     G   ACCCC
GAM220  HYA22     3'  TGGCATTAACAAGACTGGA    19433         _____
                                TCCAGTCT    GTGCCA
                                ||||||||    ||||||
                                AGGTCAGA    TACGGT
                                     ACAAT
GAM220  KIAA0062  3'  CTATGAAAAACTGACACAGACT 70238          C  ACTGAA_
          G                      CAGTCTGTG CA      GTAG
                                |||||||||  ||      ||||
                                GTCAGACAC GT      TATC
                                     A  CAAAAAG
GAM220  KIAA0286  3'  CTACCTCAGTTGGCAGGAAAGA 68323     CAG   G        A
                                TC   TCT TGCCAACTGA GTAG
                                ||   ||| ||||||||||  ||||
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                                AG   AGG ACGGTTGACT CATC
                                 AA_  _        C
GAM220  KIAA0475  3'  TAGTGTGCCAGCACAGGCCAGA 29504    CA      CA____
                                TC  GTCTGTGC     ACTG
                                ||  ||||||||     ||||
                                AG  CGGACACG     TGAT
                                 AC       ACCGTG
GAM220  KIAA1280  5'  TCACACCAGCTACAAACTGGA  69731       C  _  CAAC_
                                TCCAGT TGT GC    TGA
                                |||||| ||| ||    |||
                                AGGTCA ACA CG    ACT
                                   A   T  ACCAC
GAM220  KIAA1677  3'  CTATATCTGATACAGACTAGA  67066    C       C  ACT  A
                                TC AGTCTGTG CA   GA GTAG
                                || |||||||| ||   || ||||
                                AG TCAGACAT GT   CT TATC
                                 A       A ___  A
GAM220  KIAA1870  5'  CTACTTCAATTGTGCCCA    51829    T  _  C
                                TG GC CAA TGAAGTAG
                                || || ||| ||||||||
                                AC CG GTT ACTTCATC
                                 C  T   A
GAM220  MGC22805  3'  ACTTCAGTCAGAAACTG     58079     __    TGCCA
                                CAG  TCTG    ACTGAAGT
                                |||  ||||    ||||||||
                                GTC  AGAC    TGACTTCA
                                 AA   _____
GAM220  NYD-SP25  3'  CTACTTTGAACACAAACTG    53186      C    CCAACT
                                CAGT TGTG     GAAGTAG
                                |||| ||||     |||||||
                                GTCA ACAC     TTTCATC
                                  A    AAG___
GAM220  LOC122886 3'  CTACTTCAGTCAGCTAGCCAGA 75584      T___  CA
                                TCTG    GC  ACTGAAGTAG
                                ||||    ||  ||||||||||
                                AGAC    CG  TGACTTCATC
                                   CGAT  AC
GAM220  LOC145676 5'  CTACTTTCTCTGCAGCCAGACT 77339         T  __  ACT
           GGA                    TCCAGTCTG GC  CA   GAAGTAG
                                |||||||| ||  ||   |||||||
                                AGGTCAGAC CG  GT   TTTCATC
                                      _  AC  CTC
GAM220  LOC151248 5'  CTACTTCAGTATGAGAGCAGA  80185      GC_  _
                                TCTGT   CA ACTGAAGTAG
                                |||||   || ||||||||||
                                AGACG   GT TGACTTCATC
                                   AGA  A
GAM220  LOC256922 3'  CTACTTCAGTTAGTCTCTATG  94943    GTCTGT  C
                                CA     GC AACTGAAGTAG
                                ||     || ||||||||||
```

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                                GT     TG TTGACTTCATC
                                 ATCTC_  A
GAM221  ARHGAP6  5'  GCCCCGCCTGGCACCTTT    6763      T   G   T  A_
                                AAAG GTG TCA GC  GGC
                                |||| ||| ||| ||  |||
                                TTTC CAC GGT CG  CCG
                                  _  _   C  CC
GAM221  ARHGAP6  5'  GCCCCGCCTGGCACCTTT    20407     T   G   T  A_
                                AAAG GTG TCA GC  GGC
                                |||| ||| ||| ||  |||
                                TTTC CAC GGT CG  CCG
                                  _  _   C  CC
GAM221  CELSR2   3'  GTCCTGCCCGCACTGCC     7410      CA   A
                                GGT  TGC GGCAGGAC
                                |||  ||| ||||||||
                                CCG  ACG CCGTCCTG
                                  TC   C
GAM221  CLN6     3'  CCTCCTCTGCACCTGACCACAC 35404    A        __    _ C
           TCC                    A AGTGTGGTCA  TGCAG G AGG
                                | ||||||||||  ||||| | |||
                                C TCACACCAGT  ACGTC C TCC
                                 C         CC     T C
GAM221  DAG1     3'  TCCTGCCCCGACCCAC      15282     T    ATGCA
                                GTG GGTC     GGCAGGA
                                ||| ||||     |||||||
                                CAC CCAG     CCGTCCT
                                  _    CC___
GAM221  FGFR1    3'  CCTGCCTGCCCCGACAC     43631      _  TCAT
                                GTGT GG    GCAGGCAGG
                                |||| ||    |||||||||
                                CACA CC    CGTCCGTCC
                                  G  C___
GAM221  G6PT1    3'  GTCCTGCCCGCATCCTAC    7599       TC    A
                                GTGG  ATGC GGCAGGAC
                                ||||  |||| ||||||||
                                CATC  TACG CCGTCCTG
                                  C_    C
GAM221  GADD45B  3'  CCTCGACAAGACCACACTTT  31615           A  CA GC
                                AAAGTGTGGTC TG  G  AGG
                                |||||||||| ||  |  |||
                                TTTCACACCAG AC  C  TCC
                                      A  AG __
GAM221  GRB10    3'  GTCTACAGACCACACT      17983         A  C
                                AGTGTGGTC TG AGGC
                                |||||||| || ||||
                                TCACACCAG AC TCTG
                                      _ A
GAM221  ITPKB    3'  CCTGCCTGCATACATGGGCTCC 9425    A   G  _  C
                                A AGT TG GT ATGCAGGCAGG
                                | ||| || || ||||||||||
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                                C TCG GT CA TACGTCCGTCC
                                 C  G  A  _
GAM221  KCND3   5'  TCCTGCCCGACGCCACTT   17146     TG  ATGCA
                                AAGTG  GTC   GGCAGGA
                                |||||  |||   |||||||
                                TTCAC  CAG   CCGTCCT
                                   CG  C____
GAM221  KCNN4   5'  CCTGCCTGGCCGTCACCAC   9568      C  __
                                GTGGT ATG  CAGGCAGG
                                ||||| |||  ||||||||
                                CACCA TGC  GTCCGTCC
                                   C  CG
GAM221  KIF1B   3'  GTCCCCATCATGACCACCT   30591   T      CA  CA
                                AG GTGGTCATG  GG  GGAC
                                || |||||||||  ||  ||||
                                TC CACCAGTAC  CC  CCTG
                                 _       TA  __
GAM221  LY6E    3'  GTCCTGCCCCAGCCCAC    9830     T  CA  CA
                                GTG GGT  TG  GGCAGGAC
                                ||| |||  ||  ||||||||
                                CAC CCG  AC  CCGTCCTG
                                  _  __  C_
GAM221  MAGEA10  5'  GTCCTGCCCACACTCCCACCT  40737   T   TCA  CA
                                AG GTGG   TG  GGCAGGAC
                                || ||||   ||  ||||||||
                                TC CACC   AC  CCGTCCTG
                                 _   CTC  AC
GAM221  MAPK4   3'  CTCACATGACCAACTTT    10827      G      CA
                                AAAGT TGGTCATG  GG
                                ||||| ||||||||  ||
                                TTTCA ACCAGTAC  TC
                                   _      AC
GAM221  MMP2    3'  CCTGGTGCTGCCACACTT    15763       T  T   GG
                                AAGTGTGG CA GCA  CAGG
                                |||||||| || |||  ||||
                                TTCACACC GT CGT  GTCC
                                    _ _  G_
GAM221  NLGN2   3'  CCTGCCTGCCCGCCCGACTACA 88156       AT____
            C                    GTGTGGTC    GCAGGCAGG
                                ||||||||    |||||||||
                                CACATCAG    CGTCCGTCC
                                     CCCGCC
GAM221  OSR1    3'  TCCTGCCTGTTCCCCCACAC   17569      TCAT
                                GTGTGG   GCAGGCAGGA
                                ||||||   ||||||||||
                                CACACC   TGTCCGTCCT
                                   CCCT
GAM221  PFKP    3'  GTCCCGCCTGCATGTGCC    10523    _      A
                                GGT CATGCAGGC GGAC
                                ||| ||||||||| ||||
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                                CCG GTACGTCCG CCTG
                                  T       C
GAM221  PHKA2    3'  CCTGGAAACATGATCACACT  4305           CAGG
                                AGTGTGGTCATG   CAGG
                                ||||||||||||  ||||
                                TCACACTAGTAC   GTCC
                                      AAAG
GAM221  PIG8     3'  TCCTGCCTTCTACCACCCTT  16873    T    CATGC
                                AAG GTGGT    AGGCAGGA
                                ||| |||||    ||||||||
                                TTC CACCA    TCCGTCCT
                                  C    TCT__
GAM221  SIX3     3'  CCCACCTGCATGACGAT    18275    G       CA
                                GT GTCATGCAGG  GG
                                || ||||||||||  ||
                                TA CAGTACGTCC  CC
                                 G         AC
GAM221  SMARCB1  3'  GTCCTGCCCCCCACCCCACCCT 65585    T   TCATGCA
                                AG GTGG      GGCAGGAC
                                || ||||      ||||||||
                                TC CACC      CCGTCCTG
                                 C   CCACCCC
GAM221  SNCG     5'  GTCCTGCCTGCAGCAGCAC   11851     G  CA
                                GTGT GT  TGCAGGCAGGAC
                                |||| ||  ||||||||||||
                                CACG CG  ACGTCCGTCCTG
                                  A  __
GAM221  SRC      3'  CCCGCCTGCCTGCCACCCT   18284    T   T T    A
                                AG GTGG CA GCAGGC GG
                                || |||| || |||||| ||
                                TC CACC GT CGTCCG CC
                                 C   _ C     C
GAM221  SYNGR1   3'  GTCCTGCCTGCACGGCT    16323     A
                                GGTC TGCAGGCAGGAC
                                |||| ||||||||||||
                                TCGG ACGTCCGTCCTG
                                  C
GAM221  TRPM6    3'  CCTGCCTGCCAGGAACTCT   34537    T  GG  AT
                                AG GT  TC  GCAGGCAGG
                                || ||  ||  |||||||||
                                TC CA  GG  CGTCCGTCC
                                 T  A_  AC
GAM221  TUBG1    3'  CCTGCCTGACTGACCAC     63398       TG
                                GTGGTCA  CAGGCAGG
                                |||||||  ||||||||
                                CACCAGT  GTCCGTCC
                                    CA
GAM221  ZFHX1B   5'  TCCTGCCTCCCGACACT     28925      _  TCATGC
                                AGTGT GG     AGGCAGGA
                                ||||| ||     ||||||||
```

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                                TCACA CC     TCCGTCCT
                                  G  C_____
GAM221  C16orf7   3'  CCCACCCCAGAGGCCACAC   16937       A_  CA  CA
                                GTGTGGTC  TG  GG  GG
                                ||||||||  ||  ||  ||
                                CACACCGG  AC  CC  CC
                                    AG  C_  AC
GAM221  C1orf29   3'  GTCCTACTGCAAACCAC    22371      CA    GC
                                GTGGT  TGCAG  AGGAC
                                |||||  |||||  |||||
                                CACCA  ACGTC  TCCTG
                                  A_    A_
GAM221  C8orf2    3'  GCCCTCCATGACCACCT    23165    T       CA_
                                AG GTGGTCATG   GGC
                                || |||||||||   |||
                                TC CACCAGTAC   CCG
                                 _       CTC
GAM221  DECR2     3'  CCTGTTTGCATAAACACACTTT 40334        GTC
                                AAAGTGTG   ATGCAGGCAGG
                                ||||||||   ||||||||||
                                TTTCACAC   TACGTTTGTCC
                                    AAA
GAM221  DKFZp434C0923 3'  GCCCGGAGCATGACCCCACT   34214     T      A___
                                AGTG GGTCATGC    GGC
                                |||| ||||||||    |||
                                TCAC CCAGTACG    CCG
                                  C       AGGC
GAM221  FBP17     3'  TCCCGCCGCCACCACCCTT   72809    T    CAT  A   A
                                AAG GTGGT   GC GGC GGA
                                ||| |||||   || ||| |||
                                TTC CACCA   CG CCG CCT
                                  C    C__  _   C
GAM221  FEM-2     3'  CCTACCTGCATGCCCAGCCTT  27572     TG   T      C
                                AAG  TGG CATGCAGG AGG
                                |||  ||| ||||||||| |||
                                TTC  ACC GTACGTCC TCC
                                  CG   C       A
GAM221  FLJ14346  3'  GCCCCGTGGCCACACTCC    46711   A         CA
                                A AGTGTGGTCATG  GGC
                                | ||||||||||||  |||
                                C TCACACCGGTGC  CCG
                                 C          C_
GAM221  FLJ14827  3'  CCTGTCTCAACCATACTCC   51651   A      CA  C
                                A AGTGTGGT  TG AGGCAGG
                                | ||||||||  || |||||||
                                C TCATACCA  AC TCTGTCC
                                 C       __  _
GAM221  FLJ20113  3'  GTCCCAGGGCCACCCACACTT  34577        TCAT  AGGCA
                                AAGTGTGG   GC    GGAC
                                ||||||||   ||    ||||
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                                TTCACACC   CG    CCTG
                                    CAC_  GGAC_
GAM221  FLJ22127  3'  CCTGCCCTCACCCACCCT   42884    T   TCA  CA
                                AG GTGG   TG  GGCAGG
                                || ||||   ||  ||||||
                                TC CACC   AC  CCGTCC
                                 C    C__  TC
GAM221  FLJ22418  3'  CCTGCCTGGCCACA       44891       CATG
                                TGTGGT    CAGGCAGG
                                ||||||    ||||||||
                                ACACCG    GTCCGTCC
                                    ____
GAM221  FLJ22678  3'  GCCGTGGCATGGCCACAC    60497           A__
                                GTGTGGTCATGC   GGC
                                ||||||||||||   |||
                                CACACCGGTACG   CCG
                                       GTG
GAM221  GOLGA3    3'  CCTGCCCACCAGAACACA    19715      G  A  CA_
                                TGTG TC TG   GGCAGG
                                |||| || ||   ||||||
                                ACAC AG AC   CCGTCC
                                  A  _  CAC
GAM221  GPR107    3'  CCTGCCTGCTGATTTAACACAC 40561         ____   T
           TTT                    AAAGTGTG    GTCA GCAGGCAGG
                                |||||||||    |||| |||||||||
                                TTTCACAC    TAGT CGTCCGTCC
                                    AATT   _
GAM221  jdp2      3'  GTCCTGCCTGGGGCCCCACTTT 55326       T   ATG
                                AAAGTG GGTC   CAGGCAGGAC
                                |||||| ||||   ||||||||||
                                TTTCAC CCGG   GTCCGTCCTG
                                   C   G__
GAM221  JIK       3'  CCTGCAAAACCACATTCC    32797   A       CA
                                A AGTGTGGT  TGCAGG
                                | ||||||||  ||||||
                                C TTACACCA  ACGTCC
                                 C       AA
GAM221  KIAA0475  3'  CCAGTAAATGACCACAC     29488          GCAG  A
                                GTGTGGTCAT    GC GG
                                ||||||||||    || ||
                                CACACCAGTA    TG CC
                                      AA__  A
GAM221  KIAA0534  3'  TCCTAATACTGACCACAGTT   71435    G       TGCAGGC
                                AA TGTGGTCA      AGGA
                                || ||||||||      ||||
                                TT ACACCAGT      TCCT
                                 G       CATAA__
GAM221  KIAA0662  3'  GCCCTGCTGGCCACACT     81855          T    _
                                AGTGTGGTCA GCAGG C
                                |||||||||| ||||| |
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                                TCACACCGGT CGTCC G
                                      _    C
GAM221  KIAA0767  3'  CCTGCCTGCGCTCCACACTCG  60626   A     TCA
                                A AGTGTGG   TGCAGGCAGG
                                | |||||||   ||||||||||
                                G TCACACC   GCGTCCGTCC
                                 C      TC_
GAM221  KIAA0937  3'  TCCTGCCCTCCCAACTTT    91591     G   TCATGCA
                                AAAGT TGG      GGCAGGA
                                ||||| |||      |||||||
                                TTTCA ACC      CCGTCCT
                                   _  CTC____
GAM221  KIAA1283  5'  CCTCTTTCACAACCAGAC    72058    G    CA  C   C
                                GT TGGT  TG AGG AGG
                                || ||||  || ||| |||
                                CA ACCA  AC TTC TCC
                                 G   AC  T   _
GAM221  KIAA1303  3'  CCTGCCTGGTCACATTT     66001       GT  TGCA
                                AAGTGTG  CA    GGCAGG
                                |||||||  ||    ||||||
                                TTTACAC  GT    CCGTCC
                                    TG  _____
GAM221  KIAA1857  3'  GTCCTGCCTCCCACCACACTT  50721         CATGC
                                AAGTGTGGT    AGGCAGGAC
                                |||||||||    |||||||||
                                TTCACACCA    TCCGTCCTG
                                     CCC__
GAM221  LAGY      5'  GTCCTGCCCGCCCCACGC    50675       TCAT  A
                                GTGTGG    GC GGCAGGAC
                                ||||||    || ||||||||
                                CGCACC    CG CCGTCCTG
                                   C___  C
GAM221  LMOD1     3'  GTCCCACAGGGACCACATCC   24047   A       A_  CA  _
                                A GTGTGGTC  TG  GG C
                                | ||||||||  ||  || |
                                C TACACCAG  AC  CC G
                                 C       GG  AC  T
GAM221  MDS028    3'  TCTGGGACATGACCCACTCC   37465   A   T     CAGG
                                A AGTG GGTCATG    CAGG
                                | |||| |||||||    ||||
                                C TCAC CCAGTAC    GTCT
                                 C   _      AGG_
GAM221  MGC4737   3'  CCTGCCTGGCCTCCCACAC    48847       TCATG
                                GTGTGG    CAGGCAGG
                                ||||||    ||||||||
                                CACACC    GTCCGTCC
                                   CTCCG
GAM221  NR6A1     3'  GTCCTGCCTACACCCAGG    52874   G   TCA  C
                                T TGG   TG AGGCAGGAC
                                | |||   || |||||||||
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                                G ACC   AC TCCGTCCTG
                                 G   C__  A
GAM221  NR6A1    3'  GTCCTGCCTACACCCAGG    52886   G   TCA  C
                                T TGG   TG AGGCAGGAC
                                | |||   || |||||||||
                                G ACC   AC TCCGTCCTG
                                 G   C__  A
GAM221  NR6A1    3'  GTCCTGCCTACACCCAGG    7649    G   TCA  C
                                T TGG   TG AGGCAGGAC
                                | |||   || |||||||||
                                G ACC   AC TCCGTCCTG
                                 G   C__  A
GAM221  POLR2D   3'  GTCACATAACCACACT      16657       C   CA
                                AGTGTGGT ATG  GGC
                                |||||||| |||  |||
                                TCACACCA TAC  CTG
                                     A   A_
GAM221  RAI17    3'  CCTGCCTGCACTCCTCCAC   91278     TCA__
                                GTGG    TGCAGGCAGG
                                ||||    ||||||||||
                                CACC    ACGTCCGTCC
                                  TCCTC
GAM221  RASSF2   3'  GTAATGCAGACCACACTTT   28440         A   G_
                                AAAGTGTGGTC TGCA  GC
                                |||||||||| ||||  ||
                                TTTCACACCAG ACGT  TG
                                       _   AA
GAM221  SHANK3   3'  GCCCTAGCGTGACCACCTCC  65499   A  T       A__
                                A AG GTGGTCATGC   GGC
                                | || ||||||||||   |||
                                C TC CACCAGTGCG   CCG
                                 C _        ATC
GAM221  SLC5A7   3'  TCCCAACAACCACACTT     41515        CA  CAGGCA
                                AAGTGTGGT  TG     GGA
                                |||||||||  ||     |||
                                TTCACACCA  AC     CCT
                                     __  AAC___
GAM221  TRAF3    3'  CCACACATGACCAGACTCC   59737   A   G      CA_
                                A AGT TGGTCATG   GG
                                | ||| ||||||||   ||
                                C TCA ACCAGTAC   CC
                                 C   G       ACA
GAM221  VPS45A   3'  TGTACATACCACACTCC     23427   A      C   CAG
                                A AGTGTGGT ATG   GCA
                                | |||||||| |||   |||
                                C TCACACCA TAC   TGT
                                 C       _   A__
GAM221  VR22     3'  TCCTGCCTAACCACACT     25170        CATGC
                                AGTGTGGT    AGGCAGGA
                                ||||||||    ||||||||
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                                TCACACCA    TCCGTCCT
                                   A____
GAM221  ZNF297B  3'  TTGCACCACCACACTCC    25791   A      CA
                                A AGTGTGGT  TGCAG
                                | ||||||||  |||||
                                C TCACACCA  ACGTT
                                 C       CC
GAM221  LOC113763 3'  CCTGCCTGCCATCACCCTT   56577    T    CAT
                                AAG GTGGT   GCAGGCAGG
                                ||| |||||   |||||||||
                                TTC CACTA   CGTCCGTCC
                                  C    C__
GAM221  LOC118611 3'  GCCCTGCTGACCACACT    75475         T    _
                                AGTGTGGTCA GCAGG C
                                |||||||||| ||||| |
                                TCACACCAGT CGTCC G
                                      _    C
GAM221  LOC120406 3'  TTGCACCACCACACTCC    75549   A      CA
                                A AGTGTGGT  TGCAG
                                | ||||||||  |||||
                                C TCACACCA  ACGTT
                                 C       CC
GAM221  LOC126695 3'  TCTTAACATGACCACAGTTT  75429    G       CAGGC
                                AAA TGTGGTCATG    AGGA
                                ||| ||||||||||    ||||
                                TTT ACACCAGTAC    TTCT
                                  G        AA___
GAM221  LOC145601 5'  GTCCTGCCTCTCTGCTCACAC  83370     GT  TGC
                                GTGTG  CA   AGGCAGGAC
                                |||||  ||   |||||||||
                                CACAC  GT   TCCGTCCTG
                                   TC  CTC
GAM221  LOC150142 5'  GTCCTGCCCACACCTCACTTT  79578      T   CA  CA
                                AAAGTG GGT  TG  GGCAGGAC
                                |||||| |||  ||  ||||||||
                                TTTCAC CCA  AC  CCGTCCTG
                                    T   C_  __
GAM221  LOC150271 3'  TCCCCACTGACCACACTTT   84957         TGCA  CA
                                AAAGTGTGGTCA   GG  GGA
                                ||||||||||||   ||  |||
                                TTTCACACCAGT   CC  CCT
                                      CA__  __
GAM221  LOC150951 5'  CCCACCTGTCACATTCC    85168   A    GTCAT    CA
                                A AGTGTG    GCAGG  GG
                                | ||||||    |||||  ||
                                C TTACAC    TGTCC  CC
                                 C     _____    AC
GAM221  LOC152271 3'  CCTGCCTGCCCACAT      80517       TCAT
                                GTGTGG   GCAGGCAGG
                                ||||||   |||||||||
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                                TACACC   CGTCCGTCC
                                    ____
GAM221  LOC153027 3'  CCGATGCATACACCACAC    67432       C_    GGCA
                                GTGTGGT  ATGCA   GG
                                |||||||  |||||   ||
                                CACACCA  TACGT   CC
                                    CA    AG__
GAM221  LOC158056 5'  CCTGACCACGACCACAC     81683       ATGCA  _
                                GTGTGGTC    GG CAGG
                                ||||||||    || ||||
                                CACACCAG    CC GTCC
                                     CA___  A
GAM221  LOC200311 3'  TCCCCACTGACCACACTTT   89983          TGCA  CA
                                AAAGTGTGGTCA   GG  GGA
                                ||||||||||||   ||  |||
                                TTTCACACCAGT   CC  CCT
                                       CA__  __
GAM221  LOC201305 3'  TCCTGCCTGCAAGCC      88237     CA
                                GGT  TGCAGGCAGGA
                                |||  ||||||||||
                                CCG  ACGTCCGTCCT
                                  A_
GAM221  LOC201510 3'  CCTGCAAAACCACACTTT    88250         CA
                                AAAGTGTGGT  TGCAGG
                                |||||||||  ||||||
                                TTTCACACCA  ACGTCC
                                       AA
GAM221  LOC203052 3'  GTCCTGCCCACATGGGGCCCAC 90458     T   __    CA
           T                     AGTG GGT  CATG  GGCAGGAC
                                ||||  |||  ||||  ||||||||
                                TCAC CCG  GTAC  CCGTCCTG
                                  _   GG    AC
GAM221  LOC221002 3'  CCTGCCTGCTCGGACGCCTT   91476     T   GT AT
                                AAG GTG  C  GCAGGCAGG
                                |||  |||  |  |||||||||
                                TTC CGC  G  CGTCCGTCC
                                  _   AG CT
GAM221  LOC253805 3'  TCCTGCCTGTCCACAC      96438       TCAT
                                GTGTGG    GCAGGCAGGA
                                ||||||    ||||||||||
                                CACACC    TGTCCGTCCT
                                    ____
GAM221  LOC253891 3'  CCTGCCCATGGCCAC       94413         CA
                                GTGGTCATG  GGCAGG
                                |||||||||  ||||||
                                CACCGGTAC  CCGTCC
                                     __
GAM221  LOC51716  3'  CCTGTCTGTGACCACACTCC   32791    A       AT
                                A AGTGTGGTC  GCAGGCAGG
                                | |||||||||  |||||||||
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                                C TCACACCAG  TGTCTGTCC
                                 C       __
GAM221  LOC91565  3'  GCCTGCGTGACACAACCACACT 66462       _____
                                AGTGTGG    TCATGCAGGC
                                |||||||    ||||||||||
                                TCACACC    AGTGCGTCCG
                                    AACAC
GAM221  LOC92661  3'  TCCTGCCTTGCCCCAC     70088     TCAT  _
                                GTGG   GCA GGCAGGA
                                ||||   ||| |||||||
                                CACC   CGT CCGTCCT
                                  C___  T
GAM222  ACCN2     3'  CCCTGCTCCTCCTATCCCA   39167   A  GA   GAG
                                TG GA  AGGA  GGAGCAGGG
                                || ||  ||||  |||||||||
                                AC CT  TCCT  CCTCGTCCC
                                 C  A_  ___
GAM222  ACRV1     3'  TCCCTGCTCCAACTCTTTCTCT 39179          AG
          CA                      TGAGAGAAGGAG  GGAGCAGGGA
                                |||||||||||  |||||||||
                                ACTCTCTTTCTC  CCTCGTCCCT
                                      AA
GAM222  ACRV1     3'  TCCCTGCTCCAACTCTTTCTCT 39184          AG
          CA                      TGAGAGAAGGAG  GGAGCAGGGA
                                |||||||||||  |||||||||
                                ACTCTCTTTCTC  CCTCGTCCCT
                                      AA
GAM222  ACRV1     3'  TCCCTGCTCCAACTCTTTCTCT 39189          AG
          CA                      TGAGAGAAGGAG  GGAGCAGGGA
                                |||||||||||  |||||||||
                                ACTCTCTTTCTC  CCTCGTCCCT
                                      AA
GAM222  ACRV1     3'  TCCCTGCTCCAACTCTTTCTCT 39194          AG
          CA                      TGAGAGAAGGAG  GGAGCAGGGA
                                |||||||||||  |||||||||
                                ACTCTCTTTCTC  CCTCGTCCCT
                                      AA
GAM222  ACRV1     3'  TCCCTGCTCCAACTCTTTCTCT 39199          AG
          CA                      TGAGAGAAGGAG  GGAGCAGGGA
                                |||||||||||  |||||||||
                                ACTCTCTTTCTC  CCTCGTCCCT
                                      AA
GAM222  ACRV1     3'  TCCCTGCTCCAACTCTTTCTCT 39204          AG
          CA                      TGAGAGAAGGAG  GGAGCAGGGA
                                |||||||||||  |||||||||
                                ACTCTCTTTCTC  CCTCGTCCCT
                                      AA
GAM222  ACRV1     3'  TCCCTGCTCCAACTCTTTCTCT 39209          AG
          CA                      TGAGAGAAGGAG  GGAGCAGGGA
                                |||||||||||  |||||||||
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                                ACTCTCTTTCTC  CCTCGTCCCT
                                      AA
GAM222  ACRV1    3'  TCCCTGCTCCAACTCTTTCTCT 39214          AG
           CA                   TGAGAGAAGGAG  GGAGCAGGGA
                                ||||||||||||  ||||||||||
                                ACTCTCTTTCTC  CCTCGTCCCT
                                      AA
GAM222  ACRV1    3'  TCCCTGCTCCAACTCTTTCTCT 39219          AG
           CA                   TGAGAGAAGGAG  GGAGCAGGGA
                                ||||||||||||  ||||||||||
                                ACTCTCTTTCTC  CCTCGTCCCT
                                      AA
GAM222  ACRV1    3'  TCCCTGCTCCAACTCTTTCTCT 7863           AG
           CA                   TGAGAGAAGGAG  GGAGCAGGGA
                                ||||||||||||  ||||||||||
                                ACTCTCTTTCTC  CCTCGTCCCT
                                      AA
GAM222  ALDH3B1  3'  TTCCCTCTCCCTGCCTCA    91534     AGAA
                                TGAG   GGAGAGGGAG
                                ||||   ||||||||||
                                ACTC   CCTCTCCCTT
                                  CGTC
GAM222  ALDOC    3'  TCCCTTCCCCTCTCTCA     17702       A  AG
                                TGAGAGA GG  AGGGA
                                |||||||  ||  |||||
                                ACTCTCT CC  TCCCT
                                    C  CT
GAM222  AR       5'  CCCTGCCTTCCCCCCCTCC   3490      A__   __
                                GGAG   GGGA  GCAGGG
                                ||||   ||||  ||||||
                                CCTC   CCCT  CGTCCC
                                  CCC    TC
GAM222  ARF3     3'  GCCCCTCTCTCTCTCTCA    8002        AG      A
                                TGAGAGA  GAGAGGG GC
                                |||||||  |||||||  ||
                                ACTCTCT  CTCTCCC CG
                                    CT      _
GAM222  ARIH1    5'  CCCTCGCTCCCTCCCTCCCTC  19229     A  A  A      _
                                GAG GA GG GAGGGAGC AGGG
                                |||  ||  ||  ||||||||  ||||
                                CTC CT CC CTCCCTCG TCCC
                                  C  _  _       C
GAM222  ATP2A3   3'  CCCTACGCCTCACCCCTCCTCC 17723       A_    A  _   _ __
           CTCTCA                  GAGAG  AGGAG GG GAG C  AGGG
                                |||||  |||||  ||  |||  |  ||||
                                CTCTC  TCCTC CC CTC G  TCCC
                                   CC    C  A   C CA
GAM222  ATRN     3'  CCTGTCCCTCTCCTTCTCCA   57797    A          G
                                TG GAGAAGGAGAGGGA CAGG
                                ||  ||||||||||||||  ||||
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                                AC CTCTTCCTCTCCCT GTCC
                                 _         _
GAM222  ATRN    3'  CTCACCCTCCCTCTCTCA    57799       A  A    AGCA
                                TGAGAGA GG GAGGG   GGG
                                ||||||| || |||||   |||
                                ACTCTCT CC CTCCC   CTC
                                   _ _    A___
GAM222  B4GALT1  3'  CCCCACCCCCTTCTTTCA    7667          AGA  AGCA
                                TGAGAGAAGG  GGG   GGG
                                ||||||||||  |||   |||
                                ACTTTCTTCC  CCC   CCC
                                      ____  AC__
GAM222  B4GALT3  3'  CCCAAGCCCCTCCCTCTTCCA 13678    AG  A A    A A_
                                TG  AGA GG GAGGG GC  GGG
                                ||  ||| || ||||| ||  |||
                                AC  TCT CC CTCCC CG  CCC
                                 CT  _ _   _ AA
GAM222  BAI2    5'  CCCCTTTCTCTCCCTCTCA   8116       AA    GG  CA
                                TGAGAG  GGAGAG  AG  GGG
                                ||||||  ||||||  ||  |||
                                ACTCTC  CCTCTC  TC  CCC
                                   __     TT  __
GAM222  BAK1    3'  CCCTGCTCCCATTCCTCCCTC  91988    A  A   A
                                GAG GA GGAG GGGAGCAGGG
                                ||| || |||| ||||||||||
                                CTC CT CCTT CCCTCGTCCC
                                  C  _   A
GAM222  BAP1    3'  TCCCTGCCCCACTTCCCCTTTT 16220    A     A ___  A
           CCCA                   TG GAGAAGG GA   GGG GCAGGGA
                                || ||||||| ||   ||| |||||||
                                AC CTTTTCC CT   CCC CGTCCCT
                                 C      C  TCA  _
GAM222  BCL2L2  5'  CCCTCTCTCCCTCCCT     14466    A     C_
                                AGG GAGGGAG  AGGG
                                ||| |||||||  ||||
                                TCC CTCCCTC  TCCC
                                  _      TC
GAM222  BIN1    5'  CCCTCCCCTCTCCCTCCCTC   15037    A  A      AGC
                                GAG GA GGAGAGGG   AGGG
                                ||| || ||||||||   ||||
                                CTC CT CCTCTCCC   TCCC
                                  C  C       C__
GAM222  BIN1    5'  CCCTCCCCTCTCCCTCCCTC   57810    A  A      AGC
                                GAG GA GGAGAGGG   AGGG
                                ||| || ||||||||   ||||
                                CTC CT CCTCTCCC   TCCC
                                  C  C       C__
GAM222  BSN     3'  TCCCTGCTCACCCCCTTCTCCA 12929    A     AGA  _
                                TG GAGAAGG   GG GAGCAGGGA
                                || |||||||   || |||||||||
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                                AC CTCTTCC   CC CTCGTCCCT
                                 _      C__  A
GAM222  BTG1     5'  CCCTCACGCCCTCTCTTCCTCT 8190        A       AGC_
            CA                    TGAGAG AGGAGAGGG    AGGG
                                |||||| |||||||||    ||||
                                ACTCTC TTCTCTCCC    TCCC
                                   C        GCAC
GAM222  CACNA1B  3'  TCCCTCCCCCTCCTCCCCTCT  5554      AA   _   AGC
                                AGAG  GGAG AGGG   AGGGA
                                ||||  |||| ||||   |||||
                                TCTC  CCTC TCCC   TCCCT
                                  C_   C   CC_
GAM222  CALU     3'  TCCCCATTCCTCCTCCTCTCT  6891      A   AG   CA
                                AGAGA GGAG  GGAG  GGGA
                                ||||| ||||  ||||  ||||
                                TCTCT CCTC  CCTT  CCCT
                                  _   CT   AC
GAM222  CAPN1    3'  TCCTGTCCCCTCTCCT     17751         AG
                                AGGAGAGGG  CAGGG
                                |||||||||  |||||
                                TCCTCTCCC  GTCCT
                                     CT
GAM222  CAPS     3'  CCCTGGGCCCCTTCTCTC    14479         AGAG  AG
                                GAGAGAAGG   GG  CAGGG
                                |||||||||   ||  |||||
                                CTCTCTTCC   CC  GTCCC
                                     ____  GG
GAM222  CBFA2T3  5'  CCCTCCTCTTTCCCTCA     17756     A     _
                                TGAG GAAGGAG AGGG
                                |||| ||||||| ||||
                                ACTC CTTTCTC TCCC
                                  C      C
GAM222  CD34     3'  CCCACCTCCCCCTCCCCCT   8341     AA   A    CA
                                AG  GGAG GGGAG  GGG
                                ||  |||| |||||  |||
                                TC  CCTC CCCTC  CCC
                                 CC   C    CA
GAM222  CD34     3'  CCCTACCCCCTCCTCTCT    8342       A   A   AGC
                                AGAGA GGAG GGG   AGGG
                                ||||| |||| |||   ||||
                                TCTCT CCTC CCC   TCCC
                                  _   _   CA_
GAM222  CD3E     3'  CCCCGCTCCCTCCTCC      5590      _     A
                                GGAG AGGGAGC GGG
                                |||| ||||||| |||
                                CCTC TCCCTCG CCC
                                  C      C
GAM222  CDKN1C   5'  TCCGCCCTCTCCTCCTCTC   3576       A       AGCA
                                GAGAG AGGAGAGGG    GGG
                                ||||| |||||||||    |||
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                                CTCTC TCCTCTCCC    CCT
                                  C        G___
GAM222  CDS1     5'  TCCCCGCCCCTTCTCCTCCTC  7006      A        A  A
                                GAG AGGAGAGGG GC GGGA
                                ||| ||||||||| || ||||
                                CTC TCCTCTTCC CG CCCT
                                  C        C  C
GAM222  CELSR2   3'  TCCCCACCTCTCCTCCCCTCTC 7412        A__       GAGCA
                                GAGAG   AGGAGAGG    GGGA
                                |||||   ||||||||    ||||
                                CTCTC   TCCTCTCC    CCCT
                                   CCC       AC___
GAM222  CENTD2   5'  CCCAGCCTCCCTCTCC      57553          _ A
                                GGAGAGGGAG C GGG
                                |||||||||| | |||
                                CCTCTCCCTC G CCC
                                      C A
GAM222  CFL1     3'  CCCTGGATTTTCCTTCTC     18571          GGAG
                                GAGAAGGAGAG    CAGGG
                                ||||||||||    |||||
                                CTCTTCCTTTT    GTCCC
                                      AG__
GAM222  CHRM1    5'  CCCTTTCCTCCCTCCCTCT    94788     A  A      C__
                                AGA GG GAGGGAG   AGGG
                                ||| || |||||||   ||||
                                TCT CC CTCCCTC   TCCC
                                  _ _      CTT
GAM222  CHRNE    3'  CCCTGCTCCCTCCCT       3585      A
                                AGG GAGGGAGCAGGG
                                ||| ||||||||||||
                                TCC CTCCCTCGTCCC
                                  _
GAM222  CORO2B   3'  CCCACCCCCTCTTCCCTC     64568     AA       AGCA
                                GAG  GGAGAGGG    GGG
                                |||  ||||||||    |||
                                CTC  CTTCTCCC    CCC
                                  C_       CCA_
GAM222  DDX3     5'  TCCCTCTCCTCCCCTTCCCTC  7226      A    A   G  C
                                GAG GAAGG GAGG AG AGGGA
                                ||| ||||| |||| || |||||
                                CTC CTTCC CTCC TC TCCCT
                                  C    C   _ _
GAM222  DDX3     5'  TCCCTCTCCTCCCCTTCCCTC  43760     A    A   G  C
                                GAG GAAGG GAGG AG AGGGA
                                ||| ||||| |||| || |||||
                                CTC CTTCC CTCC TC TCCCT
                                  C    C   _ _
GAM222  DLX4     3'  CCCCACTCCTTCTTCCCTCTCT 56277       A  _      CA
              C                   GAGAGA GGA GAGGGAG  GGG
                                ||||||| ||| |||||||  |||
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                                CTCTCT CCT CTTCCTC  CCC
                                   C  T      AC
GAM222  DLX4     3'  CCCCACTCCTTCTTCCCTCTCT 8654        A  _      CA
              C                    GAGAGA GGA GAGGGAG  GGG
                                   |||||| ||| |||||||  |||
                                   CTCTCT CCT CTTCCTC  CCC
                                      C  T      AC
GAM222  DNASE1L1 5'  TCCCTGGGTCTCCTCCTCTCT  22083      A   AG  AG
                                   AGAGA GGAG  GG  CAGGGA
                                   ||||| ||||  ||  ||||||
                                   TCTCT CCTC  CT  GTCCCT
                                     _   CT  GG
GAM222  DRPLA    3'  CCCTGCTTTTCTCCT      8668         G
                                   AGGAGAGG AGCAGGG
                                   |||||||| |||||||
                                   TCCTCTTT TCGTCCC
                                            _
GAM222  EHD3     3'  TCCCTGCTCTGCCTCC     27483      AG
                                   GGAG  GGAGCAGGGA
                                   ||||  ||||||||||
                                   CCTC  TCTCGTCCCT
                                     CG
GAM222  EIF5A    3'  CCCTCCTCTTCTCCCCTC    8765      AA      G  C
                                   GAG  GGAGAGG AG AGGG
                                   |||  ||||||| || ||||
                                   CTC  CCTCTTC TC TCCC
                                    C_      _ C
GAM222  EPHA2    3'  CCTTCCCTCCGCCTTCTCCCA  15404    A      A_     GC
                                   TG GAGAAGG  GAGGGA  AGG
                                   || |||||||  ||||||  |||
                                   AC CTCTTCC  CTCCCT  TCC
                                    C      GC     __
GAM222  EPHB1    3'  TCCCTGAGAGTCCCCTCCCTTC 15439    A      A     AG____
              TCCCA                   G GAGAAGG GAGGG      CAGGGA
                                   | ||||||| |||||      ||||||
                                   C CTCTTCC CTCCC      GTCCCT
                                    C      _     CTGAGA
GAM222  ERBB3    3'  TCCCTATTCCCTCTCTCTCCCA 8798     A   AG       C
                                   TG GAGA  GAGAGGGAG AGGGA
                                   || ||||  |||||||||| |||||
                                   AC CTCT  CTCTCCCTT TCCCT
                                    C   __        A
GAM222  FAAH     3'  TCCCTGCTCTGGTCCCCTCTC  7539       AA   GAG
                                   GAGAG  GGA   GGAGCAGGGA
                                   |||||  |||   ||||||||||
                                   CTCTC  CCT   TCTCGTCCCT
                                     C_   GG_
GAM222  FACL2    3'  TCCCTGCTACTGTCCCTTCTC  40884        A  G  _
                                   GAGAAGG GA GG AGCAGGGA
                                   ||||||| || || ||||||||
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                                CTCTTCC CT TC TCGTCCCT
                                    _ G A
GAM222  FE65L2  3'  CCCTGCCCCTCCCCCTGCTC  55678    A  A_   A
                                GAG AGG  GAGGG GCAGGG
                                ||| |||  ||||| ||||||
                                CTC TCC  CTCCC CGTCCC
                                  G  CC   _
GAM222  FE65L2  3'  CCCTGCCCCTCCCCCTGCTC  55683    A  A_   A
                                GAG AGG  GAGGG GCAGGG
                                ||| |||  ||||| ||||||
                                CTC TCC  CTCCC CGTCCC
                                  G  CC   _
GAM222  FGD1    5'  CCCTCCTCTCCCCTCCCCTCT  15521     AA   A   C__
                                AGAG  GGAG GGGAG  AGGG
                                ||||  |||| |||||  ||||
                                TCTC  CCTC CCCTC  TCCC
                                  C_  _   TCC
GAM222  FGD1    5'  TTCCCTCCCCTCCTCTC    15526     A  A
                                GAGAG AGG GAGGGAG
                                ||||| ||| |||||||
                                CTCTC TCC CTCCCTT
                                   C  C
GAM222  FLNA    3'  CCCCGCCCTCTTCCCCTC   7578     AA      AGCA
                                GAG  GGAGAGGG   GGG
                                |||  ||||||||   |||
                                CTC  CTTCTCCC   CCC
                                  CC      GC__
GAM222  GALR1   5'  TCCCGAACCCACCCTCTCTCA  7619       A  AGA  AGCA
                                TGAGAGA GG  GGG   GGGA
                                ||||||| ||  |||   ||||
                                ACTCTCT CC  CCC   CCCT
                                    C  A__  AAG_
GAM222  GAP43   3'  CCCCACCCTCCCCTCTC    8984      AA  A   AGCA
                                GAGAG  GG GAGGG   GGG
                                |||||  || |||||   |||
                                CTCTC  CC CTCCC   CCC
                                  __  _   AC__
GAM222  GDI1    3'  TCCAGCATCCTCTGCTTC   59981     G   GA  AG
                                GAAG AGAGG  GC  GGA
                                |||| |||||  ||  |||
                                CTTC TCTCC  CG  CCT
                                  G   TA  A_
GAM222  GJB1    3'  TCCCTCTTCCCTCTCCCTCTCT 59973      A       C
          C                      GAGAGA GGAGAGGGAG AGGGA
                                ||||||| |||||||||| |||||
                                CTCTCT CCTCTCCCTT TCCCT
                                   C       C
GAM222  GPR44   3'  CCCTGCTCCCTCCCATCCCT  16526   A  A  A
                                AG GA GG GAGGGAGCAGGG
                                || || || ||||||||||||
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                                TC CT CC CTCCCTCGTCCC
                                 C  A  _
GAM222  GPR56    3'  TCCCTGGGGTTCTCCTCCTCTC 19075      A     GGAG
                                GAGAG AGGAGAG   CAGGGA
                                ||||| |||||||   ||||||
                                CTCTC TCCTCTT   GTCCCT
                                   C      GGG_
GAM222  GRIK5    3'  CCCCTTCTTCCCCTTCTCCCA  9134     A     A     CA
                                TG GAGAAGG GAGGGAG  GGG
                                || ||||||| |||||||  |||
                                AC CTCTTCC CTTCTTC  CCC
                                 C      C      __
GAM222  GTF2IRD1  5'  TCCCTCTGCCTCTCCTTC    32895         G  C
                                GAAGGAGAGG AG AGGGA
                                |||||||||| || |||||
                                CTTCCTCTCC TC TCCCT
                                      G  _
GAM222  HHIP     5'  TCCAACTCCTTCTCCTCCTCCC 42489    A  A        CAG
              A                  TG GAG AGGAGAGGGAG   GGA
                                || ||| ||||||||||   |||
                                AC CTC TCCTCTTCCTC   CCT
                                 C  C         AA_
GAM222  HMGA2    3'  CTCCCTCTCCCTCTCTC     12997       A
                                GAGAGA GGAGAGGGAG
                                |||||| ||||||||||
                                CTCTCT CCTCTCCCTC
                                   C
GAM222  HOXB9    3'  CCCTGCTCCCCTACTTCTC    43776       G  A
                                GAGAAG AG GGGAGCAGGG
                                |||||| || ||||||||||
                                CTCTTC TC CCCTCGTCCC
                                   A  _
GAM222  HOXC6    3'  CCCTGCCACCCCTCTCTCC    15701    A      A__
                                A GGAGAGGG   GCAGGG
                                | ||||||||   ||||||
                                C TCTCTCCC   CGTCCC
                                 C       CAC
GAM222  HRMT1L2  3'  CCCCTTCCTCTCCCTCCCTC   7737     A  A       CA
                                GAG GA GGAGAGGGAG  GGG
                                ||| || ||||||||||  |||
                                CTC CT CCTCTCCTTC  CCC
                                  C  C        __
GAM222  HYAL2    3'  TCCCTGGGAGGCCCCTTCTCTC 13666         AGAG  AG___
                                GAGAGAAGG   GG    CAGGGA
                                |||||||||   ||    ||||||
                                CTCTCTTCC   CC    GTCCCT
                                      _____  GGAGG
GAM222  HYAL2    3'  TCCCTGGGAGGCCCCTTCTCTC 52533         AGAG  AG___
                                GAGAGAAGG   GG    CAGGGA
                                |||||||||   ||    ||||||
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                                CTCTCTTCC   CC    GTCCCT
                                     ____  GGAGG
GAM222  HYOU1    3'  CCCTCCCTTCCTCTCC      59650          C_
                                GGAGAGGGAG  AGGG
                                ||||||||||  ||||
                                CCTCTCCTTC  TCCC
                                      CC
GAM222  IGFBP2   3'  CCCTGCCCCCCGCCCCTCTC   5182       AA  AGA   A
                                GAGAG  GG   GGG GCAGGG
                                |||||  ||   ||| ||||||
                                CTCTC  CC   CCC CGTCCC
                                   C_  GCC   _
GAM222  IL1F8    5'  CCCCACTCTGTCTTTCTC    27056         G    AGCA
                                GAGAAGGA AGGG    GGG
                                ||||||||| ||||    |||
                                CTCTTTCT TCTC    CCC
                                     G    AC__
GAM222  JJAZ1    5'  TCCCTTCCCCTCTCCTCCCCTC 31080      A__        AGC
             T                   AGAG   AGGAGAGGG   AGGGA
                                ||||   |||||||||   |||||
                                TCTC   TCCTCTCCC   TCCCT
                                  CCC        CT_
GAM222  JUNB     3'  CCCCGCCCCCTGCCCTCCCCTC 9482       AA   ___    A  A
             T                   AGAG  GGAG   AGGG GC GGG
                                ||||  ||||   |||| || |||
                                TCTC  CCTC   TCCC CG CCC
                                  C_    CCG    C  C
GAM222  JUNB     3'  CCCTGCCCTCCCCTCTCTGCA  9483     _    A  A    GA
                                TG AGAGA GG GAGG  GCAGGG
                                || ||||| || ||||  ||||||
                                AC TCTCT CC CTCC  CGTCCC
                                 G    C  _    __
GAM222  KIAA0442 5'  TCCCCGTCCCTCCTCCCCTCT  31474      AA   _    G A
                                AGAG  GGAG AGGGA C GGGA
                                ||||  |||| ||||| | ||||
                                TCTC  CCTC TCCCT G CCCT
                                  C_   C     _ C
GAM222  KIFC3    3'  CCCCGCCCCTCTCCTTC     18686          A  A
                                GAAGGAGAGGG GC GGG
                                |||||||||| || |||
                                CTTCCTCTCCC CG CCC
                                      _  C
GAM222  KIP2     3'  CCCTGCCTGTTCCCCTTCTCCC 21090    A      A  _  A
             G                   TG GAGAAGG GAG GG GCAGGG
                                || ||||||| ||| || ||||||
                                GC CTCTTCC CTT TC CGTCCC
                                 C      C  G  _
GAM222  KRT17    3'  CCCTGCTTCAGTCCCTTC    4706       A  G_
                                GAAGG GA  GGAGCAGGG
                                ||||| ||  |||||||||
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                                CTTCC CT  CTTCGTCCC
                                  _ GA
GAM222  LCN1    3'  CCCTGCCCTGCGCCCCCTCTC  9688      AA  AGA   A
                                GAGAG  GG   GGG GCAGGG
                                |||||  ||   ||| ||||||
                                CTCTC  CC   TCC CGTCCC
                                  CC  GCG  _
GAM222  LCN1    3'  CCCTGCCCTGCGCCCCCTCTC  64228     AA  AGA   A
                                GAGAG  GG   GGG GCAGGG
                                |||||  ||   ||| ||||||
                                CTCTC  CC   TCC CGTCCC
                                  CC  GCG  _
GAM222  LMO1    5'  CCCTTCTCTCTCCCTCTC    9790       AA       GC
                                GAGAG  GGAGAGGGA  AGGG
                                |||||  |||||||||  ||||
                                CTCTC  CCTCTCTCT  TCCC
                                  __       __
GAM222  LMO1    5'  CTCCCTCTCCCTCTCTC     9791        A
                                GAGAGA GGAGAGGGAG
                                |||||| ||||||||||
                                CTCTCT CCTCTCCCTC
                                   C
GAM222  LRP1    3'  CCCTGCTTGCCCGCTCC     9798       A  __
                                GGAG GGG  AGCAGGG
                                |||| |||  |||||||
                                CCTC CCC  TCGTCCC
                                  G  GT
GAM222  LRP4    3'  TCCTGACCCCTCTCTCCCTC   64446     AA      AG
                                GAG  GGAGAGGG  CAGGG
                                |||  ||||||||  |||||
                                CTC  TCTCTCCC  GTCCT
                                  CC       CA
GAM222  MADH7   3'  CCCTGCCCCTCCTCTCCCTCA  19744     A  AG A    A
                                TGAG GA  G GAGGG GCAGGG
                                |||| ||  | ||||| ||||||
                                ACTC CT  C CTCCC CGTCCC
                                  C  CT _    _
GAM222  MGAT1   3'  CCCCACTTAGCCCTTCTCTC   10007         AGAGG   CA
                                GAGAGAAGG    GAG  GGG
                                |||||||||    |||  |||
                                CTCTCTTCC    TTC  CCC
                                     CGA__   AC
GAM222  MTMR3   3'  CCCTACTCCCTCCCT      40812     A     C
                                AGG GAGGGAG AGGG
                                ||| ||||||| ||||
                                TCC CTCCCTC TCCC
                                  _      A
GAM222  MUTYH   5'  CCCGAGGCCTTCCCCTCTCCCA 24230    A   A  A    AGCA
                                TG GAGA GG GAGGG    GGG
                                || |||| || |||||    |||
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                                AC CTCT CC CTTCC    CCC
                                 C   C  _    GGAG
GAM222  MYO1C    3'  CCTGCTCCTACCCTC      61204     AA  AGA
                                GAG  GG   GGGAGCAGG
                                |||  ||   |||||||||
                                CTC  CC   TCCTCGTCC
                                  __  A__
GAM222  MYO3A    3'  CCCGCACCCTCCTTTCTC    60136       A    A  A
                                GAGAAGG GAGGG GC GGG
                                ||||||| ||||| || |||
                                CTCTTTC CTCCC CG CCC
                                    _    A  _
GAM222  MYO9A    3'  CCCACCCTCTTTTCCCTTC   22581      AG     CA_
                                GAAGG  AGGGAG   GGG
                                |||||  ||||||   |||
                                CTTCC  TTTCTC   CCC
                                   CT     CCA
GAM222  NAV2     3'  TCCTCCTCCCCTCCTCTCT   60161      A   A    C
                                AGAGA GGAG GGGAG AGGG
                                ||||| |||| ||||| ||||
                                TCTCT CCTC CCCTC TCCT
                                  _   _    C
GAM222  NDP      5'  TCCCTCTCTCTCTCCCTCTCTC 4244        A        C
                                GAGAGA GGAGAGGGAG AGGGA
                                |||||| |||||||||| |||||
                                CTCTCT CCTCTCTCTC TCCCT
                                   C         _
GAM222  NEUD4    3'  CCCTCCCTCCCTCCCTCT    16195     A  A      C_
                                AGA GG GAGGGAG  AGGG
                                ||| || |||||||  ||||
                                TCT CC CTCCCTC  TCCC
                                  _ _      CC
GAM222  NEUROD2  3'  CCCTCCTCCTCTCTCC      20480       _    C
                                GGAGAG GGAG AGGG
                                |||||| |||| ||||
                                CCTCTC CCTC TCCC
                                   T    C
GAM222  NEUROD2  5'  CCCCTCCCCTCCCCTCT     20479      AA    A    CA
                                AGAG  GGAG GGGAG  GG
                                ||||  |||| |||||  ||
                                TCTC  CCTC CCCTC  CC
                                  C_   _    C_
GAM222  NF1      5'  CCCTTTCCCTCTCCCCCTCCCG 4247     A   AA        C
                                TG GAG  GGAGAGGGAG AGGG
                                || |||  |||||||||| ||||
                                GC CTC  CCTCTCCCTT TCCC
                                 C   CC         _
GAM222  NOTCH3   3'  TCCCCACTTCTCTCTTCCCTCA 4749       A   _     GAGCA
                                TGAG GAAG GAGAGG     GGGA
                                |||| |||| ||||||     ||||
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                                ACTC CTTC CTCTTC    CCCT
                                  C   T     AC___
GAM222  NPTX1    3'  TCCCTCTCCCCCTCC      10266     A    C
                                GGAG GGGAG AGGGA
                                |||| ||||| |||||
                                CCTC CCCTC TCCCT
                                  C    _
GAM222  NR4A2    5'  CCCTGCTCCCTCCCT      20530     A
                                AGG GAGGGAGCAGGG
                                ||| ||||||||||||
                                TCC CTCCCTCGTCCC
                                  _
GAM222  NRXN2    3'  CCCCACCCTCCTTCCCT     30626    A      A  GAGCA
                                AG GAAGGAG GG     GGG
                                || ||||||| ||     |||
                                TC CTTCCTC CC     CCC
                                 C      _  AC___
GAM222  NRXN2    5'  CCCGCGCTCCCCTCCCTCTCCA 57024    A   A   A     A_
                                TG GAGA GGAG GGGAGC  GGG
                                || |||| |||| ||||||  |||
                                AC CTCT CCTC CCCTCG  CCC
                                 _   C   _     CG
GAM222  NRXN2    3'  CCCCACCCTCCTTCCCT     57012    A      A  GAGCA
                                AG GAAGGAG GG     GGG
                                || ||||||| ||     |||
                                TC CTTCCTC CC     CCC
                                 C      _  AC___
GAM222  NRXN2    3'  CCCCACCCTCCTTCCCT     57023    A      A  GAGCA
                                AG GAAGGAG GG     GGG
                                || ||||||| ||     |||
                                TC CTTCCTC CC     CCC
                                 C      _  AC___
GAM222  PACSIN1  3'  CCCTGCCCTGCTTCCCTTCCTC 92257     A    AG __ A
                                GAG GAAGG  AG  GG GCAGGG
                                ||| |||||  ||  || ||||||
                                CTC CTTCC  TC  CC CGTCCC
                                  _    CT  GT  _
GAM222  PAFAH1B1 5'  TCCCTCCCCTCTCCCTC     4733      AA      AGC
                                GAG  GGAGAGGG   AGGGA
                                |||  ||||||||   |||||
                                CTC  CCTCTCCC   TCCCT
                                  __       C__
GAM222  PBX1     3'  TCCCGGGGTCCCCGCCCTCTCT 10439       A  AGA   GCA_
           CA                    TGAGAGA GG   GGGA   GGGA
                                ||||||| ||   ||||   ||||
                                ACTCTCT CC   CCCT   CCCT
                                    C  GC_   GGGG
GAM222  PCDH11X  5'  CCCTCTCCTCTCCCA      27239    A   A
                                TG GAGA GGAGAGGG
                                || |||| ||||||||
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                                AC CTCT CCTCTCCC
                                 C   _
GAM222  PCDH11X  5' CCCTCTCCTCTCCCA      52020    A   A
                                TG GAGA GGAGAGGG
                                || |||| ||||||||
                                AC CTCT CCTCTCCC
                                 C   _
GAM222  PCDH11X  5' CCCTCTCCTCTCCCA      52042    A   A
                                TG GAGA GGAGAGGG
                                || |||| ||||||||
                                AC CTCT CCTCTCCC
                                 C   _
GAM222  PCDH11Y  5' CCCTCTCCTCTCCCA      52065    A   A
                                TG GAGA GGAGAGGG
                                || |||| ||||||||
                                AC CTCT CCTCTCCC
                                 C   _
GAM222  PCDH11Y  5' CCCTCTCCTCTCCCA      52077    A   A
                                TG GAGA GGAGAGGG
                                || |||| ||||||||
                                AC CTCT CCTCTCCC
                                 C   _
GAM222  PCMT1    3' CCTTCTCTCTCTCTCA     18221    A       C
                                A GGAGAGGGAG AGG
                                | |||||||||| |||
                                A TCTCTCTCTC TCC
                                 C         T
GAM222  PFKFB3   3' TCCAGGGCCCCTCTCTCCTCCC 82875    A   AA      A  AG_
           A                     TG GAG  GGAGAGGG GC   GGA
                                || |||  |||||||| ||   |||
                                AC CTC  TCTCTCCC CG   CCT
                                 C   C_       _  GGA
GAM222  PLAT     3' TCCCCACTCCCTGGCTCTCA   6253       AAGGAG     CA
                                TGAGAG     AGGGAG  GGGA
                                ||||||     ||||||  ||||
                                ACTCTC     TCCCTC  CCCT
                                    GG____     AC
GAM222  PLAT     3' TCCCCACTCCCTGGCTCTCA   52236       AAGGAG     CA
                                TGAGAG     AGGGAG  GGGA
                                ||||||     ||||||  ||||
                                ACTCTC     TCCCTC  CCCT
                                    GG____     AC
GAM222  PLOD3    3' TCCCCGCCTCTCTCCT      6557          A  A
                                AGGAGAGGG GC GGGA
                                ||||||||| || ||||
                                TCCTCTCTC CG CCCT
                                      _  C
GAM222  PMX1     5' CCCCACTCGGCTCCTCTC    22592      A   AGG   CA
                                GAGA GGAG   GAG  GGG
                                |||| ||||   |||  |||
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                                CTCT CCTC  CTC  CCC
                                  _  GG_  AC
GAM222  PMX1    5'  CCCCACTCGGCTCCTCTC   42660     A   AGG  CA
                                GAGA GGAG  GAG  GGG
                                |||| ||||  |||  |||
                                CTCT CCTC  CTC  CCC
                                  _  GG_  AC
GAM222  PPP1R11  3'  TCCAGCCCCCTCCTTCCCTC  41708    A     A  A  AG
                                GAG GAAGGAG GGG GC  GGA
                                ||| ||||||| ||| ||  |||
                                CTC CTTCCTC CCC CG  CCT
                                  C     _  _ A_
GAM222  PPP1R11  3'  TCCAGCCCCCTCCTTCCCTC  96010    A     A  A  AG
                                GAG GAAGGAG GGG GC  GGA
                                ||| ||||||| ||| ||  |||
                                CTC CTTCCTC CCC CG  CCT
                                  C     _  _ A_
GAM222  PRKAR1A  3'  CCCTTTTCTCCTCTCC     10801       _  C
                                GGAGAGG GAG AGGG
                                ||||||| ||| ||||
                                CCTCTCC CTT TCCC
                                   T  T
GAM222  PTK7    3'  TCCCCACCCTTCTCTCCTTTCC 11020     AG       AGCA_
          TCA                    TGAG  AAGGAGAGGG   GGGA
                                ||||  ||||||||||   ||||
                                ACTC  TTCCTCTCTT   CCCT
                                  CT       CCCAC
GAM222  PTMS    3'  TCCCTCAGATCCCCTCTTCTC  11035     G  A   GC__
                                GAGAAG AG GGGA   AGGGA
                                |||||| || ||||   |||||
                                CTCTTC TC CCCT   TCCCT
                                   _ _   AGAC
GAM222  PTPRS   5'  CCCTGCTCCATGTGACCCTCCC 11139    A  A  AGAG__
          TC                    GAG GA GG    GGAGCAGGG
                                ||| || ||    |||||||||
                                CTC CT CC    CCTCGTCCC
                                  C  C  AGTGTA
GAM222  PTPRS   5'  CCCTGCTCCATGTGACCCTCCC 55649    A  A  AGAG__
          TC                    GAG GA GG    GGAGCAGGG
                                ||| || ||    |||||||||
                                CTC CT CC    CCTCGTCCC
                                  C  C  AGTGTA
GAM222  PTPRS   5'  CCCTGCTCCATGTGACCCTCCC 55643    A  A  AGAG__
          TC                    GAG GA GG    GGAGCAGGG
                                ||| || ||    |||||||||
                                CTC CT CC    CCTCGTCCC
                                  C  C  AGTGTA
GAM222  PTPRS   5'  CCCTGCTCCATGTGACCCTCCC 55646    A  A  AGAG__
          TC                    GAG GA GG    GGAGCAGGG
                                ||| || ||    |||||||||
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                                CTC CT CC     CCTCGTCCC
                                  C  C  AGTGTA
GAM222  PYGO2    3'  TCTGCTCCCTCTCGCTCTCTCA 63992       AG
                                TGAGAGA  GAGAGGGAGCAGG
                                |||||||  |||||||||||||
                                ACTCTCT  CTCTCCCTCGTCT
                                    CG
GAM222  PYGO2    3'  CCCTACCCCCACTTCTCTCA  63983        GAGA   AGC
                                TGAGAGAAG   GGG   AGGG
                                |||||||||   |||   ||||
                                ACTCTCTTC   CCC   TCCC
                                     AC__   CA_
GAM222  RUNX3    3'  TCCCCGCCCCCTCTCC      15119        A  A
                                GGAGAGGG GC GGGA
                                |||||||| || ||||
                                CCTCTCCC CG CCCT
                                     C  C
GAM222  RXRA     3'  CCCTGCTCAGGCCTTCTCTC   11406        AGAGG
                                GAGAGAAGG    GAGCAGGG
                                |||||||||    ||||||||
                                CTCTCTTCC    CTCGTCCC
                                     GGA__
GAM222  RYR2     3'  CCCCTCTCTCTCCCTCTCTCA  6412        A        CA
                                TGAGAGA GGAGAGGGAG  GGG
                                ||||||| ||||||||||  |||
                                ACTCTCT CCTCTCTCTC  CCC
                                    C        __
GAM222  S100A5   3'  CCCTGCCCTCCTCTCCCTCCCA 11426    A   AA     _ A
                                TG GAG  GGAGAGG G GCAGGG
                                || |||  ||||||| | ||||||
                                AC CTC  CCTCTCC C CGTCCC
                                 C  __      T C
GAM222  SC5DL    3'  TCCTCCTCTTCTCCCCTC    90884     AA      G  C
                                GAG  GGAGAGG AG AGGG
                                |||  ||||||| || ||||
                                CTC  CCTCTTC TC TCCT
                                  C_      _ C
GAM222  SCD      3'  TCTCTCCCTCCCTCTCTCA   17350        A  A     C
                                TGAGAGA GG GAGGGAG AGG
                                ||||||| || ||||||| |||
                                ACTCTCT CC CTCCCTC TCT
                                     _ _     _
GAM222  SHMT2    3'  CCCTCTCCTCTCTCA       18263        A
                                TGAGAGA GGAGAGGG
                                ||||||| ||||||||
                                ACTCTCT CCTCTCCC
                                     _
GAM222  SIT      3'  CCCCGCTCCCTCATAGTCT   27076     AGGA       A
                                AGA   GAGGGAGC GGG
                                |||   |||||||| |||
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                                TCT    CTCCCTCG CCC
                                  GATA       C
GAM222  SIX2     3'  CCCTCCTCCTTCTCTC      33722          _
                                GAGAGAAGGAG AGGG
                                |||||||||| ||||
                                CTCTCTTCCTC TCCC
                                      C
GAM222  SIX3     5'  TCCCTGAATTTTCTCCTCTCCT 18278      A     _  ____
              CTC                   GAGA GGAGAGG GAG    CAGGGA
                                |||| ||||||| |||    ||||||
                                CTCT CCTCTCC CTT    GTCCCT
                                  _      T   TTAA
GAM222  SLC2A4   3'  CCCCTCCCTCTTCCTTC     6440        _      CA
                                GAAGGA GAGGGAG  GGG
                                |||||| |||||||  |||
                                CTTCCT CTCCCTC  CCC
                                   T      __
GAM222  SLC6A3   3'  CCCTGCTCCCTGCTCC      6447       _
                                GGAG AGGGAGCAGGG
                                |||| ||||||||||
                                CCTC TCCCTCGTCCC
                                  G
GAM222  SLC7A8   3'  CTTCCTCCCCTCCTTC      24280        A    C
                                GAAGGAG GGGAG AGG
                                ||||||| ||||| |||
                                CTTCCTC CCCTC TTC
                                    _    C
GAM222  SLC9A5   3'  TCCCTGCTCCTAACCCCT    15983     AGA_
                                AGG    GGGAGCAGGGA
                                |||    ||||||||||
                                TCC    TCCTCGTCCCT
                                  CCAA
GAM222  SLC9A5   3'  TCCCTGCTCCTAACCCCT    59772     AGA_
                                AGG    GGGAGCAGGGA
                                |||    ||||||||||
                                TCC    TCCTCGTCCCT
                                  CCAA
GAM222  SMARCD1  3'  TTCCCTCTCCCTGCCTCA    57440      AGAA
                                TGAG    GGAGAGGGAG
                                ||||    ||||||||||
                                ACTC    CCTCTCCCTT
                                  CGTC
GAM222  SMARCD1  3'  TTCCCTCTCCCTGCCTCA    11822      AGAA
                                TGAG    GGAGAGGGAG
                                ||||    ||||||||||
                                ACTC    CCTCTCCCTT
                                  CGTC
GAM222  SMCX     3'  CCCTGCCCCCACTCTCCT    14825        _ A_
                                AGGAGAG GG  GCAGGG
                                ||||||| ||  ||||||
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                                TCCTCTC CC  CGTCCC
                                    A  CC
GAM222  SMCX     3'  CCCCACTCTCCTCCCCTCT   14824      AA   A    CA
                                AGAG  GGAG GGGAG  GGG
                                ||||  |||| |||||  |||
                                TCTC  CCTC CTCTC  CCC
                                  C_   _    AC
GAM222  SOX9     5'  CCCCTCCTCCTCCTCTCCA   4437     A   A   AG   CA
                                TG GAGA GGAG  GGAG  GGG
                                || |||| ||||  ||||  |||
                                AC CTCT CCTC  CCTC  CCC
                                 _   _   CT   __
GAM222  SP3      5'  CCCTGTCTCCCTCTCT      82497          _
                                GGAGAGGGAG CAGGG
                                |||||||||| |||||
                                TCTCTCCCTC GTCCC
                                      T
GAM222  SPTBN2   3'  CCCCGCCGACTTCTCCCCTTTC 22704       AA      GA_  A
                                GAGAG  GGAGAGG   GC GGG
                                |||||  |||||||   || |||
                                CTTTC  CCTCTTC   CG CCC
                                   C_      AGC  C
GAM222  SRGAP2   3'  TCCCACTGCCCTCTGCTTC   74608      G     AGCA
                                GAAG AGAGGG    GGGA
                                |||| ||||||    ||||
                                CTTC TCTCCC    CCCT
                                  G     GTCA
GAM222  STXBP1   3'  TCCCTACCCCTCAGTGCCTGCT 12049       A   A___     AGC
           CTCA                    TGAGAG AGG    GAGGG   AGGGA
                                ||||||| |||    |||||   |||||
                                ACTCTC TCC    CTCCC   TCCCT
                                   G   GTGA    CA_
GAM222  TCF3     3'  TCCCTGCCGCATCCTCTCCCCT 70735     AA       A___
           C                     GAG  GGAGAGGG    GCAGGGA
                                |||  ||||||||    |||||||
                                CTC  CCTCTCCT    CGTCCCT
                                  C_       ACGC
GAM222  TGFB1    3'  CCCCACTCCCACTCCCTCTCTC 5401        A   A    CA
                                GAGAGA GGAG GGGAG  GGG
                                |||||| |||| |||||  |||
                                CTCTCT CCTC CCCTC  CCC
                                   C   A    AC
GAM222  TLR9     3'  CCCTGCTCGCCTCCCTC     33850    A  A   _
                                GA GG GAGG GAGCAGGG
                                || || |||| ||||||||
                                CT CC CTCC CTCGTCCC
                                 _ _   G
GAM222  TP53     3'  CCTGTTCCCTCTCCCTCTC   5039       AA
                                GAGAG  GGAGAGGGAGCAGG
                                |||||  ||||||||||||||
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                                CTCTC  CCTCTCCCTTGTCC
                                  __
GAM222  UBE2I    5'  CCCTGCTCCCCGCCCCCTC   12491     AA  AGA
                                GAG  GG   GGGAGCAGGG
                                |||  ||   ||||||||||
                                CTC  CC   CCCTCGTCCC
                                  CC  GC_
GAM222  UBQLN2   3'  CCCACTCCCTCCCTCT      25566     A  A      CA
                                AGA GG GAGGGAG  GG
                                ||| || |||||||  ||
                                TCT CC CTCCCTC  CC
                                  _ _      AC
GAM222  UBQLN2   3'  TCCCTCCTACTTCCCTCA    25569      A    GA_
                                TGAG GAAG   GAGGGA
                                |||| ||||   ||||||
                                ACTC CTTC   CTCCCT
                                  C    ATC
GAM222  UNRIP    5'  CCCTACTTTCCTCCCTCCCTC  23200     A  A    A GG  C
                                GAG GA GGAG G  AG AGGG
                                ||| || |||| |  || ||||
                                CTC CT CCTC C  TC TCCC
                                  C  C    _ TT  A
GAM222  VTN      3'  TCCCTCCTCCCATCTCCTTC   5315          _     C
                                GAAGGAGA GGGAG AGGGA
                                |||||||| ||||| |||||
                                CTTCCTCT CCCTC TCCCT
                                     A    C
GAM222  WNT8B    3'  TCCTCTGCCCCCTCCTTTTCCC 59596    A       A   A   _
            A                    TG GAGAAGGAG GGG GCAG GGA
                                || |||||||| ||| |||| |||
                                AC CTTTTCCTC CCC CGTC CCT
                                 C       _  _   T
GAM222  XT3      3'  TCCCTGCTGACCTTCTTC    39525         __
                                GGAGAGGG  AGCAGGGA
                                ||||||||  ||||||||
                                CTTCTTCC  TCGTCCCT
                                     AG
GAM222  ZFP103   5'  CCCCGCCCTCGACCCTTCTCTC 19022          A__    AGCA
                                GAGAGAAGG   GAGGG   GGG
                                |||||||||   |||||   |||
                                CTCTCTTCC   CTCCC    CCC
                                     CAG    GC__
GAM222  ACYP2    5'  TCCCATGTGTCCCCTCCCTCTC 56613    A   A   A   _  _
            GCA                    TG GAGA GGAG GGGA GCA GGGA
                                || |||| |||| |||| ||| ||||
                                AC CTCT CCTC CCCT TGT CCCT
                                 G   C    _   G  A
GAM222  AIF1     5'  TCCCTTCTGCTCTCTCCCCTC  51979     AA       _ C
                                GAG  GGAGAGGG AG AGGGA
                                |||  |||||||| || |||||
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                                CTC  CCTCTCTC TC TCCCT
                                  C_       G  T
GAM222  AKAP11   3'  CCCACCCCCCACTCTCTCTCA  32703        AG   A   AGCA
                                TGAGAGA  GAG GGG    GGG
                                |||||||  ||| |||    |||
                                ACTCTCT  CTC CCC    CCC
                                   __   A   CCCA
GAM222  AKAP3    3'  CCCCGCCCTTCTTTCTC     21210      AG      A  A
                                GAGA  GAGAGGG GC GGG
                                ||||  ||||||| || |||
                                CTCT  TTCTTCC CG CCC
                                  __      _ C
GAM222  ALOXE3   3'  CCCCAAACTCCTTCTCCT    41263          CA__
                                AGGAGAGGGAG    GGG
                                ||||||||||    |||
                                TCCTCTTCCTC    CCC
                                      AAAC
GAM222  ARHGEF2  3'  TCCCTTTCTCCTCTCCCCTC   16364     AA      _  C
                                GAG  GGAGAGG GAG AGGGA
                                |||  ||||||| ||| |||||
                                CTC  CCTCTCC CTT TCCCT
                                  C_      T  _
GAM222  ASB10    5'  TCCCCACTCCCCTTTCC     55129         _ CA
                                GGAGAGGG AG  GGGA
                                ||||||||  ||  ||||
                                CCTTTCCC TC  CCCT
                                     C  AC
GAM222  BA108L7.2 3'  TCCATTTCCCCTCCTCCTCTC  48268       A    A    CAG
                                GAGAG AGGAG GGGAG   GGA
                                |||||  |||||  |||||   |||
                                CTCTC TCCTC CCCTT   CCT
                                   C     _    TA_
GAM222  BSPECV   5'  TCCTGATGTCCCTCTCCCTCCC 33566     A  A       G__
            TC                    GAG GA GGAGAGGGA   CAGGG
                                ||| ||  |||||||||   |||||
                                CTC CT CCTCTCCCT   GTCCT
                                  C  C        GTA
GAM222  C16orf7   5'  TCCCTGGCTCTCTCTCTCTCTC 16944        AG        _
            A                     TGAGAGA  GAGAGGGAGC AGGGA
                                |||||||  ||||||||||  |||||
                                ACTCTCT  CTCTCTCTCG TCCCT
                                   __         G
GAM222  C20orf27  3'  TCCCTCGTCCTCCTCTC     35386       A   _
                                GAGAG AGGA GAGGGA
                                |||||  ||||  ||||||
                                CTCTC TCCT CTCCCT
                                   C    G
GAM222  C21orf57  5'  CCCTCTCCTGTCCCTC      74797      A  _
                                GAG GA AGGAGAGGG
                                |||  ||  |||||||||
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                                CTC CT TCCTCTCCC
                                  C  G
GAM222  C6orf28   3'  TCCTCTTCCCCTCCCTCTTTCA 40996        A   A    C
                                TGAGAGA GGAG GGGAG AGGG
                                ||||||| |||| ||||| ||||
                                ACTTTCT CCTC CCCTT TCCT
                                    C   _    C
GAM222  CALN1     3'  TCCCTACTCCCAGCCCCTTCTC 48877    A      AGA_    C
            CCA                   TG GAGAAGG    GGGAG AGGGA
                                || |||||||    ||||| |||||
                                AC CTCTTCC    CCCTC TCCCT
                                  C      CCGA    A
GAM222  CECR6     3'  CCCTGCCCCCACTGACTCCTCT 49082      A  G_  A   A
            C                    GAGAG AG  AG GGG GCAGGG
                                ||||| ||  || ||| ||||||
                                CTCTC TC  TC CCC CGTCCC
                                   C  AG  A   C
GAM222  CHL1      3'  TCCCCGATATTCTCCTTCTGTC 21752     G        GGAGCA
            A                    TGA AGAAGGAGAG     GGGA
                                ||| ||||||||||     ||||
                                ACT TCTTCCTCTT     CCCT
                                  G         ATAGC_
GAM222  CTRP5     3'  CCCCACCCCCTCCTGCTC    31594     A    A   AGCA
                                GAG AGGAG GGG    GGG
                                ||| ||||| |||    |||
                                CTC TCCTC CCC    CCC
                                  G    _   CAC_
GAM222  dA141H5.1 3'  TCTCTCCCTCCCTCTCTCA    59107        A  A      C
                                TGAGAGA GG GAGGGAG AGG
                                ||||||| || ||||||| |||
                                ACTCTCT CC CTCCCTC TCT
                                     _ _      _
GAM222  DEFCAP    5'  TCCCTGCTCTGCGGCTCCT    52233       AG__
                                AGGAG    GGAGCAGGGA
                                |||||    ||||||||||
                                TCCTC    TCTCGTCCCT
                                   GGCG
GAM222  DKFZP434E2135 5'  TCCCTCTCTTCCCTCA      47957      A    G
                                TGAG GAAG AGAGGGA
                                |||| |||| |||||||
                                ACTC CTTC TCTCCCT
                                  C   _
GAM222  DKFZp434K1210 3'  CCCTTCCCCTCTCCCTC     34274      AA       AGC
                                GAG  GGAGAGGG   AGGG
                                |||  ||||||||   ||||
                                CTC  CCTCTCCC   TCCC
                                  __       CT_
GAM222  DKFZP434M154 3'  CCCCGCTCCCTTCTGCTCCTTC 72338         ____      A
                                GAAGGAG    AGGGAGC GGG
                                |||||||    ||||||| |||
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                                CTTCCTC    TCCCTCG CCC
                                    GTCT      C
GAM222  DKFZP434P1750 3'  GCCCCCCTCTTTCCCTCA    31376     A      A  A
                                TGAG GAAGGAG GGG GC
                                |||| ||||||| ||| ||
                                ACTC CTTTCTC CCC CG
                                  C      _  C
GAM222  DKFZp547H236 3'  CCCTACCTCCCTTCTCT     78541        A   GAGC
                                AGAGAAGG GAGG   AGGG
                                |||||||| ||||   ||||
                                TCTCTTCC CTCC   TCCC
                                     _   A___
GAM222  DKFZP586G1122 3'  TCCCTAAATGATCTCTCCTTC  61288         GAGC__
                                GAAGGAGAGG     AGGGA
                                ||||||||||     |||||
                                CTTCCTCTCT     TCCCT
                                      AGTAAA
GAM222  DKFZp761G2113 3'  TCCCCACTCCCCTCCCTCT   69910     AA   A    CA
                                AGAG  GGAG GGGAG  GGGA
                                ||||  |||| |||||  ||||
                                TCTC  CCTC CCCTC  CCCT
                                  __   _    AC
GAM222  DPCR1    3'  TCCCCATTCTCTCTCCT     55123          CA
                                AGGAGAGGGAG  GGGA
                                ||||||||||  ||||
                                TCCTCTCTCTT  CCCT
                                      AC
GAM222  ELF4     3'  TCCCTGCTTCCCCCTTCCCTC  7438     A    AGA
                                GAG GAAGG   GGGAGCAGGGA
                                ||| |||||   ||||||||||
                                CTC CTTCC   CCTTCGTCCCT
                                  C    C__
GAM222  FEM-2    3'  CCCTGCCCTCCCCTTCCTC   27571     A    A   GA
                                GAG GAAGG GAGG  GCAGGG
                                ||| ||||| ||||  ||||||
                                CTC CTTCC CTCC  CGTCCC
                                  _    C   __
GAM222  FLJ10074  5'  TCCCCGGTCCCTCCCCTC    35797     AA  A     GCA
                                GAG  GG GAGGGA   GGGA
                                |||  || ||||||   ||||
                                CTC  CC CTCCCT   CCCT
                                  __ _     GGC
GAM222  FLJ10079  3'  CTCCTTCCCCTTCTCCCA    60202    A      A
                                TG GAGAAGG GAGGGAG
                                || ||||||| |||||||
                                AC CTCTTCC CTTCCTC
                                 C      C
GAM222  FLJ10647  3'  TCCCCACTCCCTCTCTGGGGTC 36376    GAA_        CA
                                GA   GGAGAGGGAG  GGGA
                                ||   ||||||||||  ||||
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                              CT   TCTCTCCCTC  CCCT
                               GGGG        AC
GAM222  FLJ10759  5' CCCTGCCCCTCGGGCCCCCCTC 36575      AA  A___    A
          TC                   GAGAG  GG   GAGGG GCAGGG
                              ||||| ||   ||||| ||||||
                              CTCTC  CC   CTCCC CGTCCC
                                CC  CGGG   _
GAM222  FLJ10815  3' TCCCTCTCCTCCTCCA     36696    A  A
                              TG GAG AGGAGAGGGA
                              || ||| ||||||||||
                              AC CTC TCCTCTCCCT
                               _  C
GAM222  FLJ10898  3' CCCTGCTCCGCTCCTCTC    59428     A   AG
                              GAGA GGAG  GGAGCAGGG
                              |||| ||||  |||||||||
                              CTCT CCTC  CCTCGTCCC
                                _   G_
GAM222  FLJ12076  3' CCCTGCCCACATCCCCTCTC   47234      AA   GAG  A
                              GAGAG  GGA   GG GCAGGG
                              |||||  |||   || ||||||
                              CTCTC  CCT   CC CGTCCC
                                C_   ACA  _
GAM222  FLJ12221  3' CCCTGCCGCCCTCTCT      62549        A_
                              GGAGAGGG  GCAGGG
                              ||||||||  ||||||
                              TCTCTCCC  CGTCCC
                                   GC
GAM222  FLJ12287  3' CCCTTCACCTCTCCCCCTC   42311     AA     _ GC
                              GAG  GGAGAGG GA  AGGG
                              |||  ||||||| ||  ||||
                              CTC  CCTCTCC CT  TCCC
                                CC      A  __
GAM222  FLJ12581  3' CCCTCCTCCCATCCCTC     45877     AA   GA    C
                              GAG  GGA  GGGAG AGGG
                              |||  |||  ||||| ||||
                              CTC  CCT  CCCTC TCCC
                                __  A_    C
GAM222  FLJ13154  3' CCCTCCTGTCTCTCCTCCCCTC 44793     AGA      G  C
                              GAG   AGGAGAGG AG AGGG
                              |||   |||||||| || ||||
                              CTC   TCCTCTCT TC TCCC
                                CCC       G  C
GAM222  FLJ13154  3' CCCTCCTGTCTCTCCTCCCCTC 44794     AGA      G  C
                              GAG   AGGAGAGG AG AGGG
                              |||   |||||||| || ||||
                              CTC   TCCTCTCT TC TCCC
                                CCC       G  C
GAM222  FLJ13612  3' CCCAGTCCCTCCCTCTTC    47312    GA   A     G A
                              GA  AGG GAGGGA C GGG
                              ||  ||| |||||| | |||
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                                CT  TCC CTCCCT G CCC
                                 TC  _    _ A
GAM222  FLJ13782  3'  CCCTCTCCTTCTCCA      46164    A
                                TG GAGAAGGAGAGGG
                                || ||||||||||||
                                AC CTCTTCCTCTCCC
                                 _
GAM222  FLJ13848  3'  TCCCCACAGCCACCCTCCCTCT 45472    GA   A    A_  A___
              TC                  GA  AGG GAGGG  GC    GGGA
                                || ||| |||||  ||   ||||
                                CT  TCC CTCCC  CG    CCCT
                                 TC  _    AC  ACAC
GAM222  FLJ14126  3'  CCCAGCCCCCTCTCCT      45842         A  A
                                AGGAGAGGG GC GGG
                                ||||||||| || |||
                                TCCTCTCCC CG CCC
                                     C  A
GAM222  FLJ14251  3'  CTTTGCCTCCTCTTCCCTC    45971     AA      GA
                                GAG  GGAGAGG  GCAGGG
                                |||  |||||||  ||||||
                                CTC  CTTCTCC  CGTTTC
                                  C_      TC
GAM222  FLJ14442  3'  CCCTCTCTTCTCTCA      51364         G
                                TGAGAGAAG AGAGGG
                                ||||||||| ||||||
                                ACTCTCTTC TCTCCC
                                      _
GAM222  FLJ14721  3'  CCCTGTTCCTCCTTCCCCT    51580    A_     GAG
                                AG  GAAGGA   GGAGCAGGG
                                ||  ||||||   |||||||||
                                TC  CTTCCT   CCTTGTCCC
                                 CC     ____
GAM222  FLJ20320  3'  CCCTGCTTGGAGGCCCTTCTCT 34940         AGAGG_
                                AGAGAAGG     GAGCAGGG
                                ||||||||     ||||||||
                                TCTCTTCC     TTCGTCCC
                                     CGGAGG
GAM222  FLJ20359  3'  CCCACCCTCTCTCCTCCCA   35038    A   AA       AGCA
                                TG GAG  GGAGAGGG    GGG
                                || |||  ||||||||    |||
                                AC CTC  TCTCTCCC    CCC
                                 C   C_       A___
GAM222  FLJ20378  5'  CCTTTTCCCTCTCCTCCCCTC  35089     AGA         C
                                GAG   AGGAGAGGGAG AGG
                                |||   |||||||||| |||
                                CTC   TCCTCTCCCTT TCC
                                  CCC          T
GAM222  FLJ20507  3'  CCCTGGCCCCTTCCCTCT    35278     A  AG    AG
                                AGA GG  AGGG  CAGGG
                                ||| ||  ||||  |||||
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                                TCT CC  TCCC  GTCCC
                                  _ CT    CG
GAM222  FLJ20507  3'  CCCTGGCCCCTTCCCTCT    60213     A  AG    AG
                                AGA GG  AGGG  CAGGG
                                ||| ||  ||||  |||||
                                TCT CC  TCCC  GTCCC
                                  _ CT    CG
GAM222  FLJ20548  3'  CCCTGCCCCTTTTCCTTC    35376           A
                                GAAGGAGAGGG GCAGGG
                                |||||||||||| ||||||
                                CTTCCTTTTCC CGTCCC
                                       C
GAM222  FLJ21820  3'  TCCCTGCAGGCTCCTCCTCTC  41628       A     AGGGA
                                GAGAG AGGAG     GCAGGGA
                                ||||| |||||     |||||||
                                CTCTC TCCTC     CGTCCCT
                                   C    GGA__
GAM222  FLJ22596  5'  CCCTGCCACCTTCTCTC     46961          AGAGGGA
                                GAGAGAAGG       GCAGGG
                                |||||||||       ||||||
                                CTCTCTTCC       CGTCCC
                                      AC_____
GAM222  FLJ22795  3'  CCCACTGCCTTTTCTCA     46942           _  A
                                TGAGAGAAGG AG GGG
                                |||||||||| || |||
                                ACTCTTTTCC TC CCC
                                       G  A
GAM222  FLJ23058  3'  CCCTCCCCTTCTCCCA      45202     A      A
                                TG GAGAAGG GAGGG
                                || ||||||| |||||
                                AC CTCTTCC CTCCC
                                  C      C
GAM222  FLJ23416  3'  TCCTACTCCCTCTCCTCCCCTC 49954       A__          C
          T                      AGAG   AGGAGAGGGAG AGGG
                                ||||   |||||||||||| ||||
                                TCTC   TCCTCTCCCTC TCCT
                                   CCC          A
GAM222  FLJ23590  5'  TCCCTGCCCCGGGCCTTCTTCA 45023     G     AGA   A
                                TGA AGAAGG   GGG GCAGGGA
                                ||| ||||||   ||| |||||||
                                ACT TCTTCC   CCC CGTCCCT
                                  _     GGG  _
GAM222  FLJ32468  3'  CCCCACCCCCTCTCTTTTCCA  59041    A     G     AGCA
                                TG GAGAAG AGAGGG    GGG
                                || |||||| ||||||    |||
                                AC CTTTTC TCTCCC    CCC
                                  _     _     CCAC
GAM222  FREQ      3'  TCTGCCCCCTCCTCTC      26587      A    A   A
                                GAGA GGAG GGG GCAGG
                                |||| |||| ||| |||||
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                                CTCT CCTC CCC CGTCT
                                  _   _  _
GAM222  GDAP1L1  3'  CCCCTCACCTCCCCTTCCCTC  43829     A    A   _  CA
                                GAG GAAGG GAGG GAG  GGG
                                ||| ||||| |||| |||  |||
                                CTC CTTCC CTCC CTC  CCC
                                  C    C   A  __
GAM222  GIT1     3'  TCCCCACTCTCGCCCCTTCTCT 25869         AGA    CA
                                AGAGAAGG   GGGAG  GGGA
                                ||||||||   |||||  ||||
                                TCTCTTCC   CTCTC  CCCT
                                     CCG    AC
GAM222  H17      3'  CCCAGTGTCCTCTCCTCTC   34086      A      GA  A
                                GAGA GGAGAGG  GC GGG
                                |||| |||||||  || |||
                                CTCT CCTCTCC  TG CCC
                                  _      TG  A
GAM222  HYA22    5'  CCCCGCTCCCCTCTCC      19421         _  A
                                GGAGAGGG AGC GGG
                                |||||||| ||| |||
                                CCTCTCCC TCG CCC
                                     C   C
GAM222  IGF2AS   3'  CCCTGCCTAGAGCTCCCTCTTT 33096        A   AG__  A
           CA                     TGAGAGA GGAG   GG GCAGGG
                                |||||||| ||||   || ||||||
                                ACTTTCT CCTC   TC CGTCCC
                                     C   GAGA  _
GAM222  IMUP     5'  CCCTGCTCCGCTCCTCT     78595     A   AG
                                AGA GGAG  GGAGCAGGG
                                ||| ||||  |||||||||
                                TCT CCTC  CCTCGTCCC
                                  _   G_
GAM222  ING4     3'  TCCCTTCTCCTCCCCTCTC   59705       AA  A   G  C
                                GAGAG  GG GAGG AG AGGGA
                                |||||  || |||| || |||||
                                CTCTC  CC CTCC TC TCCCT
                                   __  _   _  T
GAM222  KIAA0057 3'  CTCCCTCTCCTTCCCT      24422     A
                                AG GAAGGAGAGGGAG
                                || ||||||||||||
                                TC CTTCCTCTCCCTC
                                 C
GAM222  KIAA0258 3'  TCCCTGCCCACATGTTCCCTCT 28822         A   AG___  A
           CTCA                    TGAGAGA GGAG    GG GCAGGGA
                                |||||||| ||||    || |||||||
                                ACTCTCT CCTT    CC CGTCCCT
                                     C   GTACA  _
GAM222  KIAA0293 3'  CCCAGCTCCCCTTCTC      60606         AGAG    A
                                GAGAAGG    GGAGC GGG
                                |||||||    ||||| |||
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                                CTCTTCC    CCTCG CCC
                                    ____     A
GAM222  KIAA0429  5'  CCCTAACCCTCTGCTTCTCTCA 28553         G     AGC
                                TGAGAGAAG AGAGGG   AGGG
                                ||||||||| ||||||   ||||
                                ACTCTCTTC TCTCCC   TCCC
                                     G     AA_
GAM222  KIAA0450  3'  CCCTGCCTCCCTCTCT      27630          _
                                GGAGAGGGAG CAGGG
                                |||||||||| |||||
                                TCTCTCCCTC GTCCC
                                      C
GAM222  KIAA0450  5'  CCCTCCTATCCCCCTCCTTCTC 27629          A   GC__
            TC                    GAGAGAAGGAG GGGA    AGGG
                                ||||||||||| ||||    ||||
                                CTCTCTTCCTC CCCT    TCCC
                                      C    ATCC
GAM222  KIAA0451  3'  TCCCCACCCTCCCCTCCTCTC  29115      A   A    AGCA
                                GAGAG AGG GAGGG    GGGA
                                ||||| ||| |||||    ||||
                                CTCTC TCC CTCCC    CCCT
                                   C   C     AC__
GAM222  KIAA0469  3'  TCAGGCCCCCTCCTCTC     29354      A    A   A  AG
                                GAGA GGAG GGG GC  GG
                                |||| |||| ||| ||  ||
                                CTCT CCTC CCC CG  CT
                                  _   _   _  GA
GAM222  KIAA0544  3'  CCCCGCTCCCTCCTTCCCT    70900    A     GA     A
                                AG GAAGGA  GGGAGC GGG
                                || ||||||  |||||| |||
                                TC CTTCCT  CCCTCG CCC
                                 C      __      C
GAM222  KIAA0552  3'  TCCCCAGTGTCCCCTCCCCTCC 28321    A   AA  A    AG  ___
            A                     TG GAG  GG GAGGG  CA   GGGA
                                || |||  || |||||  ||   ||||
                                AC CTC  CC CTCCC  GT   CCCT
                                 _  __ _     CT  GAC
GAM222  KIAA0556  3'  CCCTTCTCCCCCTTC       69082       AGA    C
                                GAAGG   GGGAG AGGG
                                |||||   ||||| ||||
                                CTTCC   CCCTC TCCC
                                   ___     T
GAM222  KIAA0557  3'  CCCAGGCCCCTCTCTCA     77993    A       A  A_
                                A GGAGAGGG GC  GGG
                                | ||||||||  ||  |||
                                A TCTCTCCC CG  CCC
                                 C       _  GA
GAM222  KIAA0599  3'  CCCTGTTTATTCCCCTCCTGTC 77173    GA    A   ____
                                GA  AGGAG GGGA    GCAGGG
                                ||  ||||| ||||    ||||||
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                              CT  TCCTC CCCT    TGTCCC
                               G_    _    TATT
GAM222  KIAA0682 3' CCCTGCTCCCCCTGTCC    32474     G __
                              GGA A  GGGAGCAGGG
                              ||| |  ||||||||||
                              CCT T  CCCTCGTCCC
                                G CC
GAM222  KIAA0712 3' TCCCTGCTTCATTACCCCCTCT 28199       AA  A  G
          T                    GAGAG  GG GA GGAGCAGGGA
                              |||||  || || ||||||||||
                              TTCTC  CC TT CTTCGTCCCT
                                 CC  A  A
GAM222  KIAA0721 3' CCTCCTCCTCCCCTCT      41338      AA  A    G  C
                              AGAG  GG GAGG AG AGG
                              ||||  || |||| || |||
                              TCTC  CC CTCC TC TCC
                                __  _   _ C
GAM222  KIAA0721 3' TCCCTCCCCCTCTCCCTCCCA 41346    A   AA       AGC
                              TG GAG  GGAGAGGG   AGGGA
                              || |||  ||||||||   |||||
                              AC CTC  CCTCTCCC   TCCCT
                               C   __       CC_
GAM222  KIAA0721 3' CCCTCTCCCTCCCCCTCTC   41337      AA  A      C
                              GAGAG  GG GAGGGAG AGGG
                              |||||  || ||||||| ||||
                              CTCTC  CC CTCCCTC TCCC
                                 C_  _      _
GAM222  KIAA0721 3' CCCTCTCCCTCCCCCTCTC   95964      AA  A      C
                              GAGAG  GG GAGGGAG AGGG
                              |||||  || ||||||| ||||
                              CTCTC  CC CTCCCTC TCCC
                                 C_  _      _
GAM222  KIAA0721 3' CCTCCTCCTCCCCTCT      95965      AA  A    G  C
                              AGAG  GG GAGG AG AGG
                              ||||  || |||| || |||
                              TCTC  CC CTCC TC TCC
                                __  _   _ C
GAM222  KIAA0721 3' TCCCTCCCCCTCTCCCTCCCA 95974    A   AA       AGC
                              TG GAG  GGAGAGGG   AGGGA
                              || |||  ||||||||   |||||
                              AC CTC  CCTCTCCC   TCCCT
                               C   __       CC_
GAM222  KIAA0918 3' CCCTCCCCTCCCTTCTC     73133        A    AGC
                              GAGAAGG GAGGG   AGGG
                              ||||||| |||||   ||||
                              CTCTTCC CTCCC   TCCC
                                  _    C__
GAM222  KIAA0918 3' TCCGCCCCTCTCCTTCTCTC   73135             A  A
                              GAGAGAAGGAGAGGG GC GGG
                              |||||||||||||| || |||
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                                CTCTCTTCCTCTCCC CG CCT
                                      _ _
GAM222  KIAA0939 3' CCCTGCCCCATCCCATCCCCCT 62011      AA  ___ _  A
            CTC                   GAGAG  GGA   GA GGG GCAGGG
                                  ||||| |||   || ||| ||||||
                                  CTCTC  CCT   CT CCC CGTCCC
                                    CC   ACC  A  _
GAM222  KIAA1030 3' TCCCTTTTTTTTCTCCTCTTCCC 93340    A  GA        C
            A                     TG GA  AGGAGAGGGAG AGGGA
                                  || ||  |||||||||||| |||||
                                  AC CT  TCCTCTTTTTT TCCCT
                                   C  TC         _
GAM222  KIAA1030 3' CCCAGCTCCCTCCCTGTCCCA  93331    A  GA   A      A
                                  TG GA  AGG GAGGGAGC GGG
                                  || ||  ||| |||||||| |||
                                  AC CT  TCC CTCCCTCG CCC
                                   C  G_  _       A
GAM222  KIAA1030 3' TCCATTGACCCTCTCCTTTCCC 93339    A   A      AG  _
            A                     TG GAGA GGAGAGGG  CAG GGA
                                  || |||| ||||||||  ||| |||
                                  AC CTTT CCTCTCCC  GTT CCT
                                   C   _       A_  A
GAM222  KIAA1042 3' TCCCACCTCCCTCTCTT     30345          CA
                                  AGGAGAGGGAG  GGGA
                                  ||||||||||  ||||
                                  TTCTCTCCCTC  CCCT
                                         CA
GAM222  KIAA1115 3' CCCAGCTCCCTCCTCC      30018      _      A
                                  GGAG AGGGAGC GGG
                                  |||| ||||||| |||
                                  CCTC TCCCTCG CCC
                                    C      A
GAM222  KIAA1130 3' CCCTGCTCACCCTCCTC     62415    A    A  _
                                  GA GGAG GG GAGCAGGG
                                  || |||| || ||||||||
                                  CT CCTC CC CTCGTCCC
                                   _   _  A
GAM222  KIAA1183 3' CCCGCCCTCCCCTCCCCTCT   62529      AA   A    CA_
                                  AGAG  GGAG GGGAG   GGG
                                  ||||  |||| |||||   |||
                                  TCTC  CCTC CCCTC   CCC
                                    C_   _    CCG
GAM222  KIAA1384 5' TCCCTCTCTCTCTCCCTCTCTC 64579       A        C
                                  GAGAGA GGAGAGGGAG AGGGA
                                  |||||| |||||||||| |||||
                                  CTCTCT CCTCTCTCTC TCCCT
                                     C        _
GAM222  KIAA1462 3' CCCTCCCTCCCTCCCT      91384     A      C_
                                  AGG GAGGGAG  AGGG
                                  ||| |||||||  ||||
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                                TCC CTCCCTC  TCCC
                                  _      CC
GAM222  KIAA1538 5' TCCTCTTCCTCTCCCCCTCCA 71557    A   AA        C
                                TG GAG  GGAGAGGGAG AGGG
                                || |||  |||||||||| ||||
                                AC CTC  CCTCTCCTTC TCCT
                                  _   CC         _
GAM222  KIAA1753 3' TCCCTGCCCCCTCCCCTCTCT  64887       A A    A
                                AGAGA GG GAGGG GCAGGGA
                                ||||| || ||||| |||||||
                                TCTCT CC CTCCC CGTCCCT
                                   C _    C
GAM222  KIAA1775 3' CCCTGCTCCCTGCTTTC     52378       AG
                                GAAGG  AGGGAGCAGGG
                                |||||  ||||||||||
                                CTTTC  TCCCTCGTCCC
                                   G_
GAM222  KIAA1870 5' CCACTGGGACCTCTCTTCTCCC 51827    A     G    GAG  _
              A                  TG GAGAAG AGAGG   CAG GG
                                || |||||| |||||   ||| ||
                                AC CTCTTC TCTCC   GTC CC
                                 C     _    AGG   A
GAM222  KIAA1904 3' CCCTTCCTCCCTCCCTCT    73481     A A      C_
                                AGA GG GAGGGAG  AGGG
                                ||| || |||||||  ||||
                                TCT CC CTCCCTC  TCCC
                                  _ _      CT
GAM222  KIAA1922 3' CCCTGCCTCTCTCTCC      73620          _
                                GGAGAGGGAG CAGGG
                                ||||||||| |||||
                                CCTCTCTCTC GTCCC
                                      C
GAM222  KIAA1938 3' CCCCGCCCCTCTGCTTCCCTC  92192     A   G     A A
                                GAG GAAG AGAGGG GC GGG
                                ||| |||| |||||| || |||
                                CTC CTTC TCTCCC CG CCC
                                  C   G     _ C
GAM222  KIAA1938 3' TCCCTCTCATCCTCCCCCTCCC 92202    A   AA   A _  C
              A                  TG GAG  GGAG GG GAG AGGGA
                                || |||  |||| || ||| |||||
                                AC CTC  CCTC CT CTC TCCCT
                                 C  CC   _ A  _
GAM222  KIAA1949 5' TCCCCAGTGCTCCCTACCCTC  97755    A  AG       ___
                                GA GG  AGGGAGCA   GGGA
                                || ||  ||||||||   ||||
                                CT CC  TCCCTCGT   CCCT
                                 _ CA       GAC
GAM222  KIAA1949 5' TCCCTCCTCCTCTCCCTCCCTC 97756     A  A      G  C
                                GAG GA GGAGAGG AG AGGGA
                                ||| || ||||||| || |||||
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                                CTC CT CCTCTCC TC TCCCT
                                  C  C      _  C
GAM222  KIAA1949  5'  TCCCCAGTGCTCCCTACCCTC  97877    A  AG      ___
                                GA GG  AGGGAGCA   GGGA
                                || ||  ||||||||   ||||
                                CT CC  TCCCTCGT   CCCT
                                 _  CA       GAC
GAM222  KIAA1949  5'  TCCCTCCTCCTCTCCCTCCCTC 97878     A  A     G  C
                                GAG GA GGAGAGG AG AGGGA
                                ||| || ||||||| || |||||
                                CTC CT CCTCTCC TC TCCCT
                                  C  C      _  C
GAM222  KIAA1949  5'  TCCCCAGTGCTCCCTACCCTC  92087    A  AG      ___
                                GA GG  AGGGAGCA   GGGA
                                || ||  ||||||||   ||||
                                CT CC  TCCCTCGT   CCCT
                                 _  CA       GAC
GAM222  KIAA1949  5'  TCCCTCCTCCTCTCCCTCCCTC 92088     A  A     G  C
                                GAG GA GGAGAGG AG AGGGA
                                ||| || ||||||| || |||||
                                CTC CT CCTCTCC TC TCCCT
                                  C  C      _  C
GAM222  KIAA1951  3'  TCCTAAAGCCTCCCTTCTCCCA 73765    A      A   GAGC
                                TG GAGAAGG GAGG    AGGG
                                || ||||||| ||||    ||||
                                AC CTCTTCC CTCC    TCCT
                                 C      _   GAAA
GAM222  LASP1     3'  CTCTGTTCTCTCCCCTC     20453     AA  A
                                GAG  GG GAGGGAGCAGGG
                                |||  || ||||||||||||
                                CTC  CC CTCTCTTGTCTC
                                   __  _
GAM222  MCAM      3'  TCCCTGCTCACTCTTCTCTC   21460      A     G
                                GAGA GGAGAG GAGCAGGGA
                                |||| |||||| |||||||||
                                CTCT CTTCTC CTCGTCCCT
                                  _     A
GAM222  MEIS3     3'  CCCCACCTCCCTTCTCT     78278         A   GAGCA
                                AGAGAAGG GAGG     GGG
                                |||||||| ||||     |||
                                TCTCTTCC CTCC     CCC
                                     _    AC___
GAM222  MGC11115  3'  TCCCTGCTGCCCCTCCCTCTCT 50243       A   A  _
          C                      GAGAGA GGAG GGG AGCAGGGA
                                ||||||| |||| ||| ||||||||
                                CTCTCT CCTC CCC TCGTCCCT
                                   C   _  G
GAM222  MGC13064  3'  TTCCCTCTCCATCCCTCA    50356      A  A
                                TGAG GA GGAGAGGGAG
                                |||| || ||||||||||
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                                ACTC CT CCTCTCCCTT
                                  C  A
GAM222  MGC13251  3'  CCGGCTCCCCCTCCTGCTCCCA 51147    A  A    A     A
                                TG GAG AGGAG GGGAGC GG
                                || ||| ||||| |||||| ||
                                AC CTC TCCTC CCCTCG CC
                                 C  G    C     G
GAM222  MGC15407  5'  CCCTACTCCCTCTCGGCTC   54730    AAG       C
                                GAG   GAGAGGGAG AGGG
                                |||   ||||||||| ||||
                                CTC   CTCTCCCTC TCCC
                                  GG_       A
GAM222  MGC20255  3'  TCCCTTTCTCCCCCTCTCTC   53446       A  AGA    C_
                                GAGAGA GG   GGGAG  AGGGA
                                |||||| ||   |||||  |||||
                                CTCTCT CC   CCCTC  TCCCT
                                   _ ____    TT
GAM222  MGC2574   3'  TCCCTCCTTCCTCTCCTTCTCC 44055    A           C
            A                    TG GAGAAGGAGAGGGAG AGGGA
                                || ||||||||||||||| |||||
                                AC CTCTTCCTCTCCTTC TCCCT
                                 _           C
GAM222  MGC26914  3'  CCCGTGCCCCCCCTCTCC    58665        A__  _
                                GGAGAGGG   GCA GGG
                                ||||||||   ||| |||
                                CCTCTCCC   CGT CCC
                                     CCC   G
GAM222  MGC3047   3'  TCCCTACCCTAGCCTTGCTCTC 50364       _   AG   AGC
            A                    TGAGAG AAGG  AGGG   AGGGA
                                |||||| ||||  ||||   |||||
                                ACTCTC TTCC  TCCC   TCCCT
                                   G   GA   A__
GAM222  MGC5338   3'  CCCTTCCTCTTTCTCC      43938          C_
                                GGAGAGGGAG  AGGG
                                ||||||||||  ||||
                                CCTCTTTCTC  TCCC
                                      CT
GAM222  NCOA2     3'  TCCCTTCCCCTCTCTCA     21546        A  AG
                                TGAGAGA GG  AGGGA
                                |||||||  ||  |||||
                                ACTCTCT CC  TCCCT
                                    C  CT
GAM222  NOL4      5'  CCCTCCTCCCCTCTT       13694       A    C
                                AGGAG GGGAG AGGG
                                ||||| ||||| ||||
                                TTCTC CCCTC TCCC
                                   _    C
GAM222  NR5A1     3'  TCCCTGCTCCCAGCTCTCTCTC 17104       AG AGA
                                GAGAGA  G   GGGAGCAGGGA
                                ||||||  |   ||||||||||
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                                CTCTCT  C   CCCTCGTCCCT
                                   CT GA_
GAM222  NR5A1    3'  CCCCGCCCCCTCCCTGCTCCCA 17100    A   A   A    A  A
                                TG GAG AGG GAGGG GC GGG
                                || ||| ||| ||||| || |||
                                AC CTC TCC CTCCC CG CCC
                                 C   G   _    C  C
GAM222  NXPH3    3'  TCCCTTCCCCCCCTTC      65769      AGA    GC
                                GAAGG   GGGA  AGGGA
                                |||||   ||||  |||||
                                CTTCC   CCCT  TCCCT
                                   CC_   __
GAM222  PADI1    3'  TCCCCGCTCTAGGTTTCTTCTC 62000    A       AG_    A
            CCA                    TG GAGAAGGAG   GGAGC GGGA
                                || |||||||||   ||||| ||||
                                AC CTCTTCTTT   TCTCG CCCT
                                 C       GGA    C
GAM222  PCDH17   5'  TCCCTGCTCCCTCCCCCACTC  27090     AA  A
                                GAG  GG GAGGGAGCAGGGA
                                |||  || ||||||||||||
                                CTC  CC CTCCCTCGTCCCT
                                  AC  C
GAM222  PFTK1    3'  CCCTCTCTCCTTCCCCT     24756     A      C_
                                AGG GAGGGAG  AGGG
                                ||| |||||||  ||||
                                TCC CTTCCTC  TCCC
                                  C      TC
GAM222  PHYHIP   3'  CCCTGCTCCCTCCACTCT    28607     A GA
                                AGA G  GAGGGAGCAGGG
                                ||| |  ||||||||||||
                                TCT C  CTCCCTCGTCCC
                                  _ AC
GAM222  PKMYT1   5'  CCCTGCTCCTGCCTCC      14846      A_
                                GGAG  GGGAGCAGGG
                                ||||  ||||||||||
                                CCTC  TCCTCGTCCC
                                   CG
GAM222  PMFBP1   3'  CCCAGCCCTCCCTCTCTC    48447       A  A    AGCA
                                GAGAGA GG GAGGG    GGG
                                |||||| || |||||    |||
                                CTCTCT CC CTCCC    CCC
                                   _ _     GA__
GAM222  PMX2B    5'  TCCCCACTCCAGCCACCTTCTC 14088    A      AGAG_   CA
            CA                    TG GAGAAGG     GGAG  GGGA
                                || |||||||    ||||  ||||
                                AC CTCTTCC    CCTC  CCCT
                                 _      ACCGA    AC
GAM222  PPFIA4   3'  TCCCTTCCCCTTCTCTC     70332          A_
                                GAGAGAAGG  GAGGGA
                                |||||||||  ||||||
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                                CTCTCTTCC  TTCCCT
                                     CC
GAM222  PPIL4    3'  TCCCTAAGGCCCTCTCCCTCTC 57478       AA      AGC_
            A                    TGAGAG  GGAGAGGG   AGGGA
                                 ||||||  ||||||||   |||||
                                 ACTCTC  CCTCTCCC   TCCCT
                                    __      GGAA
GAM222  PRO2214  3'  TCCCCATTTCCTCTCCTTC   37567           CA
                                 GAAGGAGAGGGAG  GGGA
                                 ||||||||||||  ||||
                                 CTTCCTCTCCTTT  CCCT
                                       AC
GAM222  PSMF1    5'  CCCCGCCCCCTTCTTTCCTC   22350    AG     A  A  A
                                 GAG  AAGGAG GGG GC GGG
                                 |||  |||||| ||| || |||
                                 CTC  TTCTTC CCC CG CCC
                                   CT     _  _  C
GAM222  QKI      5'  CCCCGCCCCTCCCTCCTCTC   65440      A  A    A  A
                                 GAGAG AGG GAGGG GC GGG
                                 ||||| ||| ||||| || |||
                                 CTCTC TCC CTCCC CG CCC
                                    C  _    _ C
GAM222  RAB14    5'  CCCCGCCCCCTCTCCCGCT   32871    AA      A  A
                                 AG  GGAGAGGG GC GGG
                                 ||  |||||||| || |||
                                 TC  CCTCTCCC CG CCC
                                  GC       C  C
GAM222  RAB2     3'  CCCTCTCCTCCTGCTCA     11180     _ A
                                 TGAG AG AGGAGAGGG
                                 |||| || |||||||||
                                 ACTC TC TCCTCTCCC
                                   G  C
GAM222  RBAF600  3'  CCCCGCCCTCCCCTCTCTCA   68532       A  A    AGCA
                                 TGAGAGA GG GAGGG    GGG
                                 |||||||  || |||||    |||
                                 ACTCTCT CC CTCCC    CCC
                                     C  _    GC__
GAM222  RILP     5'  TCCCTACCCCACGCCTTCTC   48695       AGA   AGC
                                 GAGAAGG   GGG   AGGGA
                                 |||||||   |||   |||||
                                 CTCTTCC   CCC   TCCCT
                                     GCA   CA_
GAM222  SCAMP5   3'  CCCTGCCTTCTCCTCCTTCTCT 57256          AG   _
            C                    GAGAGAAGGAG  GGAG CAGGG
                                 ||||||||||  |||| |||||
                                 CTCTCTTCCTC  CTTC GTCCC
                                       CT    C
GAM222  SCAMP5   3'  CCCACCTTCCCTTCTCCCA   57255    A     A    AGCA
                                 TG GAGAAGG GAGGG    GGG
                                 || |||||| |||||    |||
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                                AC CTCTTCC CTTCC    CCC
                                 C      _    A___
GAM222  SEMA4G   5'  CCCCACTCCATACCCTTCTCCC 94675    A     AGAG    CA
            A                    TG GAGAAGG    GGAG  GGG
                                || |||||||    ||||  |||
                                AC CTCTTCC    CCTC  CCC
                                 C      CATA    AC
GAM222  SENP7    5'  TCCTTTCCCCTCCCCCTC    40303     AA    A    C
                                GAG  GGAG GGGAG AGGG
                                |||  |||| ||||| ||||
                                CTC  CCTC CCCTT TCCT
                                  CC   _    _
GAM222  SEPT1    3'  TCCGGAGTCCCCCTTCTTCTCC 53424    A       A   AG AG_
            CA                    TG GAGAAGGAG GGG  C   GGA
                                || |||||||| |||  |   |||
                                AC CTCTTCTTC CCC  G   CCT
                                 C        _  CT AGG
GAM222  SET07    3'  TCCCCGCCCCACTTTCCCTTCT 39847     G     _   _  A  A
            TCA                    TGA AGAAGG AGAG GG GC GGGA
                                ||| |||||| |||| || || ||||
                                ACT TCTTCC TTTC CC CG CCCT
                                  _     C    A  C  C
GAM222  SIAT8C   5'  CCCTACTCCCTCCCTCTC    31878      A  A      C
                                GAGA GG GAGGGAG AGGG
                                |||| || ||||||| ||||
                                CTCT CC CTCCCTC TCCC
                                  _ _      A
GAM222  SLC17A6  5'  CTCCCTCCCTTCTCTCA     39742          A
                                TGAGAGAAGG GAGGGAG
                                |||||||||| |||||||
                                ACTCTCTTCC CTCCCTC
                                          _
GAM222  SSBP3    3'  TCCCTGCTCCCCTCAACCCCCT 36062     AGAAG_   A
            C                    GAG     GAG GGGAGCAGGGA
                                |||     ||| ||||||||||
                                CTC     CTC CCCTCGTCCCT
                                  CCCCAA  _
GAM222  STK39    3'  CCCTACTCCCTTCAACCCTCCC 25073     A  A  A__      C
            TC                    GAG GA GG   GAGGGAG AGGG
                                ||| || ||   ||||||| ||||
                                CTC CT CC   TTCCCTC TCCC
                                  C  C  AAC      A
GAM222  STX1B2   3'  CCCTGCTCCAGGCTCACTCCCA 53515    A   AAG   AG_
                                TG GAG   GAG   GGAGCAGGG
                                || |||   |||   |||||||||
                                AC CTC   CTC   CCTCGTCCC
                                 C  A__   GGA
GAM222  SUI1     5'  CCCTGCCCGCCTTCTCC     19402         A__
                                GGAGAGGG   GCAGGG
                                ||||||||   ||||||
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                                CCTCTTCC  CGTCCC
                                    GCC
GAM222  SV2     5'  CCCTGCTCCCCCTGTCC    29307    G __
                                GGA A  GGGAGCAGGG
                                ||| |  ||||||||||
                                CCT T  CCCTCGTCCC
                                  G CC
GAM222  SYT12   3'  CCCTGCCCTCTCCCCTCTCTC  94728      A_     GA
                                GAGAGA  GGAGAGG  GCAGGG
                                ||||||  |||||||  ||||||
                                CTCTCT  CCTCTCC  CGTCCC
                                   CC     __
GAM222  TBX21   5'  CCCTGCTCCCTGCCCATC    25326    A  AG
                                GA GG  AGGGAGCAGGG
                                || ||  ||||||||||
                                CT CC  TCCCTCGTCCC
                                 A  CG
GAM222  THG-1   5'  CCCTGCTCCCCCCTCC     48183     A_
                                GGAG  GGGAGCAGGG
                                ||||  ||||||||||
                                CCTC  CCCTCGTCCC
                                  CC
GAM222  TIGD5   3'  CCCATCTCTCCTCCCCTC    51700     AA   A    CA
                                GAG  GGAG GGGAG  GGG
                                |||  |||| |||||  |||
                                CTC  CCTC CTCTC  CCC
                                  C_   _    TA
GAM222  TM9SF2  5'  TCCCCACCCCTCCTTCCCTC   16628    A     A  AGCA
                                GAG GAAGGAG GGG   GGGA
                                ||| ||||||| |||   ||||
                                CTC CTTCCTC CCC   CCCT
                                  C      _  AC__
GAM222  TNKS1BP1 5'  CCCACTCCAAGTTCTCTC    53004       ___   A
                                GAGAGAA   GGAG GGG
                                |||||||   |||| |||
                                CTCTCTT   CCTC CCC
                                    GAA   A
GAM222  ZNF177  3'  CCCTCATGCCTCCTTTCTC    12898       A   GAGC
                                GAGAAGG GAGG   AGGG
                                ||||||| ||||   ||||
                                CTCTTTC CTCC   TCCC
                                   _   GTAC
GAM222  LOC113386 3'  CCCTGACCCCTTCTTTC    57078       G   AG
                                GAAGGA AGGG  CAGGG
                                |||||| ||||  |||||
                                CTTTCT TCCC  GTCCC
                                   _   CA
GAM222  LOC121133 5'  CCACCCCCTCCTCTCCTCA   75989     _  A   A  AGCAG
                                TGAG AGA GGAG GGG    GG
                                |||| ||| |||| |||    ||
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                                ACTC TCT CCTC CCC    CC
                                  C  _  _  CA___
GAM222  LOC126526 3'  TCCAGGACTCCCCTTCTCTCA  74537         AGAG   CAG_
                                TGAGAGAAGG   GGAG   GGA
                                ||||||||||   ||||   |||
                                ACTCTCTTCC   CCTC   CCT
                                      _____  AGGA
GAM222  LOC130644 3'  TCCCTATCTCCCCTCCT     75755      A    C_
                                AGGAG GGGAG  AGGGA
                                ||||| |||||  |||||
                                TCCTC CCCTC  TCCCT
                                   _    TA
GAM222  LOC133688 3'  TCCCCATTTCTCCTTCTATCA  75116     G         GAGCA
                                TGA AGAAGGAGAGG    GGGA
                                ||| ||||||||||     ||||
                                ACT TCTTCCTCTTT    CCCT
                                  A         AC___
GAM222  LOC138389 5'  TCCCTTTCTCCCTCCCTCCCTC 76234    A  A  A     C_
                                GAG GA GG GAGGGAG  AGGGA
                                ||| || || |||||||  |||||
                                CTC CT CC CTCCCTC  TCCCT
                                  C  _  _      TT
GAM222  LOC143243 3'  CCCTCCTCTTCTCCCCTC    60304     AA     G  C
                                GAG  GGAGAGG AG AGGG
                                |||  ||||||| || ||||
                                CTC  CCTCTTC TC TCCC
                                  C_      _  C
GAM222  LOC144512 5'  CCCTGCTGGCCATCTCC     83115      G  __
                                GGAGA GG  AGCAGGG
                                |||||  ||  |||||||
                                CCTCT CC  TCGTCCC
                                   A  GG
GAM222  LOC145717 3'  CCCACTGCCTTTTCTCA     66828          _  A
                                TGAGAGAAGG AG GGG
                                |||||||||| || |||
                                ACTCTTTTCC TC CCC
                                      G  A
GAM222  LOC145717 3'  TCCCACCCCCCTCCCTCTCTC  66833       A   A  AGCA
                                GAGAGA GGAG GGG   GGGA
                                ||||||  |||| |||   ||||
                                CTCTCT CCTC CCC    CCCT
                                   C    _  CCA_
GAM222  LOC145725 3'  CCCACTGCCTTTTCTCA     77402          _  A
                                TGAGAGAAGG AG GGG
                                |||||||||| || |||
                                ACTCTTTTCC TC CCC
                                      G  A
GAM222  LOC145732 3'  CCCACTGCCTTTTCTCA     77424          _  A
                                TGAGAGAAGG AG GGG
                                |||||||||| || |||
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                                ACTCTTTTCC TC CCC
                                      G  A
GAM222  LOC146315 3'  CCCTGCTGACTGCCCTTCTCTC 60887         AG  GG
                                GAGAGAAGG  AG  AGCAGGG
                                |||||||||  ||  |||||||
                                CTCTCTTCC  TC  TCGTCCC
                                     CG  AG
GAM222  LOC146378 3'  CCCTGCTTTCCTCCTCCCT   77853    A  A    A GG
                                AG GA GGAG G  AGCAGGG
                                || || |||| |  |||||||
                                TC CT CCTC C  TCGTCCC
                                 C  _   _ TT
GAM222  LOC146713 3'  TCCTGATCCTTTCCCTC     83734     AA       AG
                                GAG  GGAGAGGG  CAGGG
                                |||  ||||||||  |||||
                                CTC  CCTTTCCT  GTCCT
                                  __       A_
GAM222  LOC146856 3'  CCCTGGCTTCCTCCCCTC    82800     AA  A      _
                                GAG  GG GAGGGAGC AGGG
                                |||  || ||||||||| ||||
                                CTC  CC CTCCTTCG TCCC
                                  __ _       G
GAM222  LOC147228 3'  CCCTGCTTCAGTCCCTTC    66901      A  G_
                                GAAGG GA  GGAGCAGGG
                                |||||  ||  |||||||||
                                CTTCC CT  CTTCGTCCC
                                   _  GA
GAM222  LOC147650 5'  CCCTGCTCCCTCCCTC      78386    A  A
                                GA GG GAGGGAGCAGGG
                                || || ||||||||||||
                                CT CC CTCCCTCGTCCC

                                 _  _
GAM222  LOC147917 3'  CCCTCCTTTCTCCCA       78566    A      A
                                TG GAGAAGG GAGGG
                                || ||||||| |||||
                                AC CTCTTTC CTCCC
                                 C      _
GAM222  LOC148645 3'  CCCTTGGCCCCTCCCTCTTC   84179    GA   A    A __
                                GA  AGG GAGGG GC  AGGG
                                ||  ||| ||||| ||  ||||
                                CT  TCC CTCCC CG  TCCC
                                 TC   _    _  GT
GAM222  LOC148764 5'  CCCACCCACCTTCTCCCA    78983    A      AGA   AGCA
                                TG GAGAAGG   GGG    GGG
                                || |||||||   |||    |||
                                AC CTCTTCC   CCC    CCC
                                 C      A__   A____
GAM222  LOC148870 3'  CCCCACCATGCGTCCTGCTCTC 79044       A    GAG__  AGCA
           A                     TGAGAG AGGA    GG    GGG
                                ||||||| ||||    ||    |||
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                                ACTCTC TCCT    CC   CCC
                                   G   GCGTA  AC__
GAM222  LOC149386 5'  TCCCTAGGCCTCTCCCTCTTCA 84409     G  A      GAGC
                                TGA AGA GGAGAGG   AGGGA
                                ||| ||| |||||||   |||||
                                ACT TCT CCTCTCC   TCCCT
                                  _  C      GGA_
GAM222  LOC149506 5'  TCCCCACCCCTCTCCTCT    84483     A       AGCA
                                AGA GGAGAGGG   GGGA
                                ||| ||||||||   ||||
                                TCT CCTCTCCC   CCCT
                                  _      CAC_
GAM222  LOC149670 3'  TCCCTGCTCCTGCTCACCTCTC 79493        AG_  A
           TCA                    TGAGAGA   GAG GGGAGCAGGGA
                                |||||||   ||| ||||||||||
                                ACTCTCT   CTC TCCTCGTCCCT
                                    CCA   G
GAM222  LOC150319 3'  CCCTCCTCTCTCCCT      79651     A     C
                                AGG GAGGGAG AGGG
                                ||| ||||||| ||||
                                TCC CTCTCTC TCCC
                                  _      C
GAM222  LOC152220 3'  CCCTTCTCCCCTCCCCTC    85580     AA   A    C
                                GAG  GGAG GGGAG AGGG
                                |||  |||| ||||| ||||
                                CTC  CCTC CCCTC TCCC
                                  C_   _    T
GAM222  LOC152286 3'  CCCCATTCCCTCCCTCTGTCA  85627     G  A A     CA
                                TGA AGA GG GAGGGAG  GGG
                                ||| ||| || |||||||  |||
                                ACT TCT CC CTCCCTT  CCC
                                  G  _ _      AC
GAM222  LOC153338 5'  TTCCCCCTCCTTTTCTCA    86003          A
                                TGAGAGAAGGAG GGGAG
                                |||||||||||| |||||
                                ACTCTTTTCCTC CCCTT
                                       C
GAM222  LOC153339 5'  TCCCTGCTCTTCTCCCTCCTC  86014     A  A     G
                                GAG GA GGAGAGG AGCAGGGA
                                ||| || ||||||| ||||||||
                                CTC CT CCTCTTC TCGTCCCT
                                  _ C      _
GAM222  LOC155006 3'  CCCCACCTCAGGTCCTTCTCCA 81235    A      ___   GAGCA
                                TG GAGAAGGA   GAGG    GGG
                                || ||||||||   ||||    |||
                                AC CTCTTCCT   CTCC    CCC
                                  _      GGA   AC___
GAM222  LOC155066 3'  CCCTACACTCCCTCTCT     81279          C__
                                GGAGAGGGAG   AGGG
                                ||||||||||   ||||
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                                TCTCTCCCTC   TCCC
                                     ACA
GAM222   LOC157247 5'  CCCTTTTCTCCCTCTCC     81362          C__
                                GGAGAGGGAG   AGGG
                                ||||||||||   ||||
                                CCTCTCCCTC   TCCC
                                     TTT
GAM222   LOC158722 5'  TTCCCTCTTCTTCCCTCA     81998      A
                                TGAG GAAGGAGAGGGAG
                                |||| ||||||||||||
                                ACTC CTTCTTCTCCCTT
                                  C
GAM222   LOC159090 5'  TCCCTCCTCTCTCCTCTTC    82091      GA      C
                                GAAG  GAGGGAG AGGGA
                                ||||  ||||||| |||||
                                CTTC  CTCTCTC TCCCT
                                  TC      C
GAM222   LOC196382 5'  TCCCCGCCCCACTTTCCCTTCT 89625     G     _   _ A  A
           TCA                     TGA AGAAGG AGAG GG GC GGGA
                                ||| |||||| |||| || || ||||
                                ACT TCTTCC TTTC CC CG CCCT
                                 _     C    A C  C
GAM222   LOC196957 3'  CCCACTGCCTTTTCTCA     87819          _ A
                                TGAGAGAAGG AG GGG
                                |||||||||| || |||
                                ACTCTTTTCC TC CCC
                                     G  A
GAM222   LOC196961 3'  CCCACTGCCTTTTCTCA     87840          _ A
                                TGAGAGAAGG AG GGG
                                |||||||||| || |||
                                ACTCTTTTCC TC CCC
                                     G  A
GAM222   LOC197044 3'  CCTCCTCCCTCTCTCC      87875    A        C
                                A GGAGAGGGAG AGG
                                | ||||||||||  |||
                                C TCTCTCCCTC TCC
                                 C         C
GAM222   LOC197138 3'  CCCACTGCCTTTTCTCA     87913          _ A
                                TGAGAGAAGG AG GGG
                                |||||||||| || |||
                                ACTCTTTTCC TC CCC
                                     G  A
GAM222   LOC200382 3'  CCCTCCTCCTCTTCTCCCA    88802    A     GA    GAGC
                                TG GAGAAG  GAGG    AGGG
                                || ||||||  ||||    ||||
                                AC CTCTTC  CTCC    TCCC
                                 C     TC   _____
GAM222   LOC200597 5'  CCCTGTCTCCTCTCCTCCTCCA 88838    A  A       GA
                                TG GAG AGGAGAGG  GCAGGG
                                || ||| ||||||||  ||||||
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                                AC CTC TCCTCTCC  TGTCCC
                                 _  C       TC
GAM222  LOC201456 3'  CCCCTACTCATCTTCTCT    88245       GA   GG  CA
                                AGAGAAG  GAG  AG  GGG
                                |||||||  |||  ||  |||
                                TCTCTTC  CTC  TC  CCC
                                    TA   A_  __
GAM222  LOC201911 3'  TCCCGATCCCTCCCTCCCTC   90266    A  A  A     GCA
                                GAG GA GG GAGGGA   GGGA
                                ||| || || ||||||   ||||
                                CTC CT CC CTCCCT   CCCT
                                  C  _  _     AG_
GAM222  LOC201911 3'  CCCTCCCTCCCTCTCC      90258          C_
                                GGAGAGGGAG  AGGG
                                ||||||||||  ||||
                                CCTCTCCCTC  TCCC
                                      CC
GAM222  LOC219649 5'  CCCTGCCCTGCCCTCTCTC   92953       A  AGA   A
                                GAGAGA GG   GGG GCAGGG
                                ||||||  ||   |||  ||||||
                                CTCTCT CC   TCC CGTCCC
                                    _  CG_   _
GAM222  LOC219700 3'  CTCCCTCTGCCTTCTCTCA   93063          _
                                TGAGAGAAGG AGAGGGAG
                                |||||||||| ||||||||
                                ACTCTCTTCC TCTCCCTC
                                      G
GAM222  LOC219942 3'  CCCCGCTTCCTTCCTTC     93343       G      A
                                GAAGGA AGGGAGC GGG
                                ||||||  |||||||  |||
                                CTTCCT TCCTTCG CCC
                                    _      C
GAM222  LOC219997 3'  CCCTACTCCACTCTCC      91617       _   C
                                GGAGAG GGAG AGGG
                                ||||||  ||||  ||||
                                CCTCTC CCTC TCCC
                                   A   A
GAM222  LOC220020 5'  CCCTCTCCTCTCCCA       93419    A   A
                                TG GAGA GGAGAGGG
                                ||  ||||  ||||||||
                                AC CTCT CCTCTCCC
                                 C   _
GAM222  LOC220537 3'  CCCACTGCCTTTTCTCA     90728          _ A
                                TGAGAGAAGG AG GGG
                                ||||||||||  ||  |||
                                ACTCTTTTCC TC CCC
                                      G  A
GAM222  LOC221042 3'  CCCCTCACCTCTCCCTCTC   93183       AA      _   CA
                                GAGAG  GGAGAGG GAG  GGG
                                |||||  |||||||  |||  |||
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                                CTCTC  CCTCTCC CTC  CCC
                                  __      A  __
GAM222  LOC221296 3'  TCTTACGCCCCTCCCCTTCTT  91973       A    A  A_
                                GAGAAGG GAGGG GC  GGGA
                                ||||||| ||||| ||  ||||
                                TTCTTCC CTCCC CG  TTCT
                                   C    _  CA
GAM222  LOC221337 5'  CCCTCCCTCCCTCCCT     92107     A     C_
                                AGG GAGGGAG  AGGG
                                ||| |||||||  ||||
                                TCC CTCCCTC  TCCC
                                  _     CC
GAM222  LOC221337 5'  CCCTCCCTCCCTCCCT     92108     A     C_
                                AGG GAGGGAG  AGGG
                                ||| |||||||  ||||
                                TCC CTCCCTC  TCCC
                                  _     CC
GAM222  LOC221463 3'  CCCCACCGTCTCTCCCTCTCA  92069       AA    G  AGCA
                                TGAGAG  GGAGA GG    GGG
                                ||||||  ||||| ||    |||
                                ACTCTC  TCTCT CC    CCC
                                   CC    G  AC__
GAM222  LOC221486 3'  TCCCTTTCTCTCTCC       91016          C
                                GGAGAGGGAG AGGGA
                                |||||||||| |||||
                                CCTCTCTCTT TCCCT
                                          _
GAM222  LOC221486 3'  TCCCTGCCCTCCCCTGCTCCCA 91015    A   A   A   GA
                                TG GAG AGG GAGG  GCAGGGA
                                || ||| ||| ||||  |||||||
                                AC CTC TCC CTCC  CGTCCCT
                                 C   G   C   __
GAM222  LOC221641 5'  TCCTGATCCTCTCCCTCCTC   93730     A  A       AG
                                GAG GA GGAGAGGG  CAGGG
                                ||| ||  ||||||||  |||||
                                CTC CT CCTCTCCT  GTCCT
                                  _  C       A_
GAM222  LOC221876 5'  CCCCACCTTCCCTCTCTC    93920       A  A    AGCA
                                GAGAGA GG GAGGG    GGG
                                |||||| || |||||    |||
                                CTCTCT CC CTTCC    CCC
                                   _  _     AC__
GAM222  LOC221975 5'  CCCTCTCTCCCTCCCTCT    92604     A  A      C_
                                AGA GG GAGGGAG  AGGG
                                ||| ||  |||||||  ||||
                                TCT CC CTCCCTC  TCCC
                                  _  _      TC
GAM222  LOC222060 5'  TCCCTGCTCAGCTTCTGCTC  94110     A    AGG
                                GAG AGGAG   GAGCAGGGA
                                ||| |||||   |||||||||
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                                CTC TCTTC   CTCGTCCCT
                                  G     GA_
GAM222   LOC245727 3'  CCCACTGCCTTTTCTCA     91123          _  A
                                TGAGAGAAGG AG GGG
                                |||||||||| || |||
                                ACTCTTTTCC TC CCC
                                      G  A
GAM222   LOC253367 3'  CCCTGCTCCCTTCATCCCTCCC 97581    A   AA   __
           G                     TG GAG  GGA  GAGGGAGCAGGG
                                || |||  |||  ||||||||||||
                                GC CTC  CCT  TTCCCTCGTCCC
                                 C   __   AC
GAM222   LOC254143 5'  CCCTGCTGGCCATCTCC     96497       G  __
                                GGAGA GG  AGCAGGG
                                ||||| ||  |||||||
                                CCTCT CC  TCGTCCC
                                   A  GG
GAM222   LOC254873 3'  CCCCTCCCTCTTCCTTC     94570       _      CA
                                GAAGGA GAGGGAG  GGG
                                |||||| |||||||  |||
                                CTTCCT CTCCCTC  CCC
                                   T      __
GAM222   LOC255096 5'  TCCAGAACCCATCCTTCTCTCA 97625           GA   AGCAG
                                TGAGAGAAGGA  GGG    GGA
                                ||||||||||  |||    |||
                                ACTCTCTTCCT  CCC    CCT
                                      A_   AAGA_
GAM222   LOC255270 3'  CCCTGCCCTCCTCTCCCTCCCA 94604    A   AA      _ A
                                TG GAG  GGAGAGG G GCAGGG
                                || |||  ||||||| | ||||||
                                AC CTC  CCTCTCC C CGTCCC
                                 C   __      T C
GAM222   LOC256980 3'  CCCTACTCCCTGGTTCTCTC   95216       GGAG     C
                                GAGAGAA    AGGGAG AGGG
                                |||||||    |||||| ||||
                                CTCTCTT    TCCCTC TCCC
                                    GG__     A
GAM222   LOC257451 3'  CCCTACCCCCACTTCTCTCA   95553        GAGA   AGC
                                TGAGAGAAG    GGG   AGGG
                                |||||||||    |||   ||||
                                ACTCTCTTC    CCC   TCCC
                                     AC__   CA_
GAM222   LOC257451 3'  TCTGCTCCCTCTCGCTCTCTCA 95562        AG
                                TGAGAGA  GAGAGGGAGCAGG
                                |||||||  ||||||||||||
                                ACTCTCT  CTCTCCCTCGTCT
                                    CG
GAM222   LOC257468 3'  CCCCACCTCCCTTCTCT     95185        A    GAGCA
                                AGAGAAGG GAGG    GGG
                                |||||||| ||||    |||
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                                TCTCTTCC CTCC    CCC
                                    _   AC___
GAM222  LOC257471 5'  CCCTGTCTCCCTCTCT     95688          _
                                GGAGAGGGAG CAGGG
                                |||||||||| |||||
                                TCTCTCCCTC GTCCC
                                     T
GAM222  LOC51195  3'  CCCTGCCCCCTCCCTGCT    32938    A  A    A
                                AG AGG GAGGG GCAGGG
                                || ||| ||||| ||||||
                                TC TCC CTCCC CGTCCC
                                 G  _    C
GAM222  LOC51195  3'  CCTTTACTCCCTCCCTCTCCCA 32941    A   A A     C_
                                TG GAGA GG GAGGGAG  AGGG
                                || |||| || |||||||  ||||
                                AC CTCT CC CTCCCTC  TTCC
                                 C   _ _      AT
GAM222  LOC56963  3'  CCCGGCCCCTCCCTCTC     71452     A A    A A
                                GAGA GG GAGGG GC GGG
                                |||| || ||||| || |||
                                CTCT CC CTCCC CG CCC
                                  _ _    _ G
GAM222  LOC57149  5'  CCCTCCCTCCCTCTCC     39936          C_
                                GGAGAGGGAG  AGGG
                                ||||||||||  ||||
                                CCTCTCCCTC  TCCC
                                     CC
GAM222  LOC90408  5'  TCCCCACTACCATCTCCCTCTC 62669        A    G _ CA
           TCA                    TGAGAGA GGAGA GG AG  GGGA
                                |||||||  ||||| || ||  ||||
                                ACTCTCT CCTCT CC TC  CCCT
                                   C    A A  AC
GAM222  LOC90630  5'  CCCCACCCCATCTCCTCTC   63629     A    _  AGCA
                                GAGA GGAGA GGG   GGG
                                |||| ||||| |||   |||
                                CTCT CCTCT CCC   CCC
                                  _    A  CAC_
GAM222  LOC90736  3'  TCCCTGTGTCCTCTCTCCCTCT 63903       A    _  _
           CTC                    GAGAGA GGAGAG GGA GCAGGGA
                                |||||| |||||| ||| |||||||
                                CTCTCT CCTCTC CCT TGTCCCT
                                   C     T  G
GAM222  LOC91208  5'  CCCCACCCCATCTCCTCTC   65244     A    _  AGCA
                                GAGA GGAGA GGG   GGG
                                |||| ||||| |||   |||
                                CTCT CCTCT CCC   CCC
                                  _    A  CAC_
GAM222  LOC92340  3'  CCCCACCCTCTCTCCCTC    68989     AA      AGCA
                                GAG  GGAGAGGG   GGG
                                |||  ||||||||   |||
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                                CTC  TCTCTCCC   CCC
                                  CC       AC__
GAM222  LOC92697  5'  TCCCTCTCCCTCTCCCTCTC   70281      AA       C
                                GAGAG  GGAGAGGGAG AGGGA
                                |||||  |||||||||| |||||
                                CTCTC  CCTCTCCCTC TCCCT
                                  __        _
GAM222  LOC92697  5'  TCCCTCTCCCTCTCCCTCTC   70282      AA       C
                                GAGAG  GGAGAGGGAG AGGGA
                                |||||  |||||||||| |||||
                                CTCTC  CCTCTCCCTC TCCCT
                                  __        _
GAM222  LOC95633  3'  CCCTGCCCCAAACCTCTCTC   59870       A  AGA   A
                                GAGAGA GG   GGG GCAGGG
                                ||||||  ||   ||| ||||||
                                CTCTCT CC   CCC CGTCCC
                                   _  AAA   _
GAM223  ABR       3'  TCTCTTGGCCCTGCTCCCA   41731       G     A  T
                                TGGGAG CAGGGC CG GGGA
                                |||||| |||||| ||  ||||
                                ACCCTC GTCCCG GT CTCT
                                   _      _  T
GAM223  ABR       3'  TCTCTTGGCCCTGCTCCCA   6579        G     A  T
                                TGGGAG CAGGGC CG GGGA
                                |||||| |||||| ||  ||||
                                ACCCTC GTCCCG GT CTCT
                                   _      _  T
GAM223  APLP1     3'  CCCACGTGGCACCTCCTC    17704      C   _  _
                                GAGG AGG GC ACGTGGG
                                ||||  ||| ||  |||||||
                                CTCC TCC CG TGCACCC
                                   _  A  G
GAM223  AR        5'  TCTCCACCCCGCCTCCC     3496         A   CAC    _
                                GGGAGGC GGG   GTGG GA
                                |||||||  |||   ||||  ||
                                CCCTCCG CCC   CACC CT
                                   _  ____    T
GAM223  ARHG      3'  CCCTGCCCTCCCCCCA      8015       A  C     CGT
                                TGGG GG AGGGCA   GGG
                                ||||  ||  ||||||   |||
                                ACCC CC TCCCGT   CCC
                                   _  C      ___
GAM223  ATP5J     5'  CCCCCTCCCGCCTCCCA     8071         A   CACGT
                                TGGGAGGC GGG     GGG
                                ||||||||  |||     |||
                                ACCCTCCG CCC     CCC
                                    _   TCC__
GAM223  ATP6V0C   3'  CCCCGGCGCCCCACCCCC    87314     A  CA   A_  T
                                GGG GG  GGGC  CG GGG
                                |||  ||  ||||  ||  |||
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                                CCC CC  CCCG  GC CCC
                                  _ AC    CG  _
GAM223  BAK1     3'  TCCAAGCCTGCCTCCCA     91994          GCACG
                                TGGGAGGCAGG    TGGG
                                ||||||||||    ||||
                                ACCCTCCGTCC    ACCT
                                      GA___
GAM223  BTEB1    5'  CCCTTCCCTGCCTCCCA     6842           CACGT
                                TGGGAGGCAGGG    GGG
                                ||||||||||||    |||
                                ACCCTCCGTCCC    CCC
                                       TT___
GAM223  CA3      5'  TTCCTCTACCCGGCCTCCCA  17738        A  CACGT
                                TGGGAGGC GGG    GGGAA
                                ||||||||| |||    |||||
                                ACCCTCCG CCC    TCCTT
                                     G  ATC__
GAM223  CACNA2D2 3'  CTTTCCCACCCTCCTGCCCC  20085    A     CAC
                                GG GGCAGGG  GTGGGAAAG
                                || |||||||  |||||||||
                                CC CCGTCCT  CACCCTTTC
                                 _     CC_
GAM223  CALM3    3'  CCCACCCCACCCCCCA     17741     A  CA  CAC
                                TGGG GG  GGG  GTGGG
                                |||| ||  |||  |||||
                                ACCC CC  CCC  CACCC
                                  _ CA  ___
GAM223  CELSR1   3'  TCCCCTCACCGCCTCCCA    26488       A  GCACGT
                                TGGGAGGC GG     GGGA
                                |||||||| ||     ||||
                                ACCCTCCG CC     CCCT
                                     _ ACTC__
GAM223  CHRM1    3'  CCTCCGGCCCTGCCCC     94789    A      A  TG
                                GG GGCAGGGC CG  GG
                                || |||||||| ||  ||
                                CC CCGTCCCG GC  CC
                                 _      _  CT
GAM223  CLC      3'  CCCAAGGCCCTGCCCCCCA  25107     A      ACG
                                TGGG GGCAGGGC  TGGG
                                |||| ||||||||  ||||
                                ACCC CCGTCCCG  ACCC
                                  C      GA_
GAM223  CRABP1   3'  CCCACCCCCACCCCCCA     59758     A  CA  CAC
                                TGGG GG  GGG  GTGGG
                                |||| ||  |||  |||||
                                ACCC CC  CCC  CACCC
                                  C  AC  ___
GAM223  DAXX     3'  TCCCCTTCTCCCTGCCTCC   7213          CACGT
                                GGAGGCAGGG    GGGA
                                ||||||||||    ||||
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                                CCTCCGTCCC    CCCT
                                     TCTTC
GAM223  DRPLA   3'  CCCACCCTCCCCCCA      8667      A  C   CACG
                                TGGG GG AGGG   TGGG
                                |||| || ||||   ||||
                                ACCC CC TCCC   ACCC
                                  _  C   ____
GAM223  FAAH    3'  TCCCCCTGCCTCCCA      44196          CACGTG
                                TGGGAGGCAGGG    GGA
                                ||||||||||||    |||
                                ACCCTCCGTCCC    CCT
                                        _______
GAM223  FHL2    5'  TCCTGCCCCAGCCTCCCA   7568        A   CAC TG
                                TGGGAGGC GGG   G  GGA
                                |||||||| |||   |  |||
                                ACCCTCCG CCC   C  CCT
                                     A   ___ GT
GAM223  HD      3'  CCTTGTGCCCTGCCTCC    9183           T
                                GGAGGCAGGGCACG GG
                                |||||||||||||| ||
                                CCTCCGTCCCGTGT CC
                                         T
GAM223  HDAC5   5'  TCCCGTCCCAGCCCCCA    18452     A  A  C  T
                                TGGG GGC GGG ACG GGG
                                |||| ||| ||| ||| |||
                                ACCC CCG CCC TGC CCT
                                  _   A  _  _
GAM223  HDAC5   5'  TCCCGTCCCAGCCCCCA    57614     A  A  C  T
                                TGGG GGC GGG ACG GGG
                                |||| ||| ||| ||| |||
                                ACCC CCG CCC TGC CCT
                                  _   A  _  _
GAM223  IMPDH1  3'  TCCCTGCCCCTAGCCTCCCA  6084        A__   CGT
                                TGGGAGGC  GGGCA  GGGA
                                ||||||||  |||||  ||||
                                ACCCTCCG  CCCGT  CCCT
                                     ATC   ___
GAM223  KAI1    3'  TCCAGGCCTGCCTCCCA    9503          G ACGTG
                                TGGGAGGCAGG C    GGA
                                ||||||||||| |    |||
                                ACCCTCCGTCC G    CCT
                                       _ GA___
GAM223  KHK     3'  TCCTCTGCCCTGCCCACCA  4034     GA      CGT
                                TGG  GGCAGGGCA  GGGA
                                |||  |||||||||  ||||
                                ACC  CCGTCCCGT  TCCT
                                  AC       C__
GAM223  KHK     3'  TCCTCTGCCCTGCCCACCA  21404    GA      CGT
                                TGG  GGCAGGGCA  GGGA
                                |||  |||||||||  ||||
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                                ACC  CCGTCCCGT   TCCT
                                  AC        C__
GAM223  LASS1    3'  TCCCCTGGGACCCCGCCCCC   41199     A   A   CA_  T
                                GGG GGC GGG   CG GGGA
                                ||| ||| |||   || ||||
                                CCC CCG CCC   GT CCCT
                                  _   C   AGG  C
GAM223  LCP1     3'  TTCCTACCCTGCCTCCCA    9696           CACG
                                TGGGAGGCAGGG   TGGGAA
                                ||||||||||||   ||||||
                                ACCCTCCGTCCC   ATCCTT
                                               _____
GAM223  MAP4     3'  TCCCTTCCCTCCTCCCA     9910         C   CACGT
                                TGGGAGG AGGG    GGGA
                                |||||||  ||||    ||||
                                ACCCTCC TCCC    CCCT
                                    _   TT___
GAM223  MFGE8    3'  CTTTCCCACCCTCCACCTCTCA 19812        CA   CAC
                                TGGGAGG  GGG   GTGGGAAAG
                                |||||||  |||   |||||||||
                                ACTCTCC  CTC   CACCCTTTC
                                    AC   C__
GAM223  MUCDHL   3'  CCCCGGCCCTGCCTCCC     48366          A  T
                                GGGAGGCAGGGC CG GGG
                                ||||||||||||  || |||
                                CCCTCCGTCCCG GC CCC
                                              _  _
GAM223  MYO1D    3'  CCCATCCCTGCTTCCCA     71768          CAC
                                TGGGAGGCAGGG   GTGGG
                                ||||||||||||   |||||
                                ACCCTTCGTCCC   TACCC
                                               ___
GAM223  NCOR2    3'  CCCTCCCTCCGCCTCCCA    20879        __   CACGT
                                TGGGAGGC  AGGG    GGG
                                ||||||||  ||||    |||
                                ACCCTCCG  TCCC    CCC
                                    CC    T_____
GAM223  NR1I2    5'  TCCCTGTGTGCCTGCCCCCC   13974     A     _    T
                                GGG GGCAGG GCACG GGGA
                                ||| |||||| ||||| ||||
                                CCC CCGTCC TGTGT CCCT
                                  C     G    _
GAM223  PDE4A    5'  CCCTTGCCCTGCCCCCC     20583     A       CGT
                                GGG GGCAGGGCA   GGG
                                ||| |||||||||   |||
                                CCC CCGTCCCGT   CCC
                                  C        T__
GAM223  PDE4A    3'  TTCCCCCACTGCCCCCCA    20588     A    _ CACGT
                                TGGG GGCAG GG    GGGAA
                                |||| ||||| ||    |||||
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                                ACCC CCGTC CC     CCCTT
                                  C     A _____
GAM223  PDGFB    3'  CTTTCCCCCTTCCCGCCTTCCA 10500         A   CACGT
                                TGGGAGGC GGG     GGGAAAG
                                |||||||| |||     |||||||
                                ACCTTCCG CCC     CCCTTTC
                                    _   TTCC_
GAM223  PIK3CG   3'  TTCCTTTTTCCCTGCCTCCC   10591          CACGT
                                GGGAGGCAGGG     GGGAA
                                ||||||||||     |||||
                                CCCTCCGTCCC     TCCTT
                                      TTTT_
GAM223  PMM2     3'  CCTGCACTCCTGCCTCCCA    72089          CAC TG
                                TGGGAGGCAGGG   G  GG
                                ||||||||||||   |  ||
                                ACCCTCCGTCCT   C  CC
                                      CA_ GT
GAM223  PTGIS    3'  CCCAGCCTGCCCCAGCCTCCCA 6328         A_     C _
                                TGGGAGGC  GGGCA G TGGG
                                ||||||||  ||||| | ||||
                                ACCCTCCG  CCCGT C ACCC
                                    AC     C G
GAM223  PYGB     3'  CCCAAGGCTGGCAACCTGCCTC 11175          __  ACG___
          CCA                    TGGGAGGCAGG  GC     TGGG
                                ||||||||||  ||     ||||
                                ACCCTCCGTCC  CG     ACCC
                                      AA  GTCGGA
GAM223  RFX1     3'  CCCCGGGACACCCTACCCCCA  11310     A  C    CA___  T
                                TGGG GG AGGG     CG GGG
                                |||| || ||||     || |||
                                ACCC CC TCCC     GC CCC
                                  _  A    ACAGG  _
GAM223  SECTM1   3'  TTCCCCTCCACCCCCCA     11532      A  CA   CACGT
                                TGGG GG  GGG     GGGAA
                                |||| ||  |||     |||||
                                ACCC CC  CTC     CCCTT
                                  C  AC   _____
GAM223  SEZ6L    5'  CCCAAGCACGCCTTGCCCCCCA 40878      A       ACG__
                                TGGG GGCAGGGC     TGGG
                                |||| ||||||||     ||||
                                ACCC CCGTTCCG     ACCC
                                  C       CACGA
GAM223  SH3GL1   3'  TCCTGCAGGGCCCTGCCTCCCA 11627           AC_ TG
                                TGGGAGGCAGGGC   G  GGA
                                ||||||||||||   |  |||
                                ACCCTCCGTCCCG   C  CCT
                                      GGA GT
GAM223  SHC1     3'  CCTCTGCCCTGCCTCCC     11647           CGT
                                GGGAGGCAGGGCA   GGG
                                ||||||||||||   |||
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                                CCCTCCGTCCCGT  TCC
                                      C__
GAM223  SLC25A1  3'  CCCTGTGCCCCGCCTCCC   19962      A     T
                                GGGAGGC GGGCACG GGG
                                ||||||| ||||||| |||
                                CCCTCCG CCCGTGT CCC
                                   C     _
GAM223  SLC9A1   3'  CCCACCAGAGCTGCCTCCC   70408       GGCAC
                                GGGAGGCAG    GTGGG
                                |||||||||    |||||
                                CCCTCCGTC    CACCC
                                     GAGAC
GAM223  SMARCD1  3'  TTCCCTCTCCCTGCCTC    57439       CACGT
                                GAGGCAGGG    GGGAA
                                |||||||||    |||||
                                CTCCGTCCC    CCCTT
                                     TCT__
GAM223  SMARCD1  3'  TTCCCTCTCCCTGCCTC    11821       CACGT
                                GAGGCAGGG    GGGAA
                                |||||||||    |||||
                                CTCCGTCCC    CCCTT
                                     TCT__
GAM223  SOCS5    5'  CCCGTCTCGCGCCCTGCCTCCC 25797         A ___
                                GGGAGGCAGGGC CG   TGGG
                                |||||||||||| ||   ||||
                                CCCTCCGTCCCG GC   GCCC
                                      C  TCT
GAM223  SORD     5'  TCCCAGGCCCCACCTTCCA   11872      CA   ACG
                                TGGGAGG  GGGC   TGGGA
                                |||||||  ||||   |||||
                                ACCTTCC  CCCG   ACCCT
                                   AC    G__
GAM223  SOX13    3'  TCCCACCCAGCCCTGCCCCTCA 19086     A      AC_
                                TGGG GGCAGGGC   GTGGGA
                                |||| ||||||||   ||||||
                                ACTC CCGTCCCG   CACCCT
                                  C       ACC
GAM223  TFAP4    3'  TCCCACCCCCCAGCCCCCA   12241     A  A   CAC
                                TGGG GGC GGG   GTGGGA
                                |||| ||| |||   ||||||
                                ACCC CCG CCC   CACCCT
                                  _   A   CC_
GAM223  TIMP3    3'  CTTTCCTCTCCCTGCCTCCCA  4508          CACGT
                                TGGGAGGCAGGG    GGGAAAG
                                ||||||||||||    |||||||
                                ACCCTCCGTCCC    TCCTTTC
                                      TC___
GAM223  TIMP4    3'  CCTGTTGCCCTGCCTCCCA   12291          C TG
                                TGGGAGGCAGGGCA G  GG
                                |||||||||||||| |  ||
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                                ACCCTCCGTCCCGT T  CC
                                       _ GT
GAM223  TMC1     5'  TCTCTGCAACCTCCGCCTCCCA 56907        A   CAC TG _
                                TGGGAGGC GGG   G  G GA
                                |||||||| |||   |  | ||
                                ACCCTCCG CTC   C  C CT
                                     C   CAA GT T
GAM223  TNFAIP2  3'  TCCCCTCTCCTGCCTCCC    20833          CACGT
                                GGGAGGCAGGG    GGGA
                                ||||||||||     ||||
                                CCCTCCGTCCT    CCCT
                                      CTC__
GAM223  TNFRSF10C 3'  TCTCTGCCCTGCCTCCC     13863           CGT
                                GGGAGGCAGGGCA   GGGA
                                ||||||||||||   ||||
                                CCCTCCGTCCCGT   CTCT

                                ___
GAM223  UBE2V1   3'  TCCCCTTACCCTCCCGCCTCCC 42373        ___   CACGT
          A                      TGGGAGGC   AGGG    GGGA
                                ||||||||   ||||    ||||
                                ACCCTCCG   TCCC    CCCT
                                     CCC    ATTC_
GAM223  VPREB3   3'  TCCCCTCTGCCTCCCA      25384          CACGT
                                TGGGAGGCAGGG    GGGA
                                ||||||||||     ||||
                                ACCCTCCGTCTC    CCCT

                                _____
GAM223  WBP2     3'  TCCTGCCTCCCTGCCTCCCA   73030          CAC TG
                                TGGGAGGCAGGG   G  GGA
                                ||||||||||||   |  |||
                                ACCCTCCGTCCC   C  CCT
                                      TC_ GT
GAM223  WNT5A    5'  TCCCGCGTCCTGCCCCCA    12673     A     GC
                                TGGG GGCAGG  ACGTGGGA
                                |||| ||||||  ||||||||
                                ACCC CCGTCC  TGCGCCCT

                                _    ___
GAM223  AKAP11   3'  TCCCCCCTCCTCCCA      32713        C   CACGT
                                TGGGAGG AGGG    GGGA
                                ||||||| ||||    ||||
                                ACCCTCC TCCC    CCCT

                                _   _____
GAM223  APCL     3'  CTGCCAGCCCCGCCTCCCA   19671        A   AC TG
                                TGGGAGGC GGGC  G  G
                                |||||||| ||||  |  |
                                ACCCTCCG CCCG  C  C
                                     C    AC GT
GAM223  ARTN     5'  CCCTCGGCCCGGCCTCCCA   54038        A   A  T
                                TGGGAGGC GGGC CG GGG
                                |||||||| |||| || |||
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                                ACCCTCCG CCCG GC CCC
                                    G   _ T
GAM223  ASB16    3'  TCCTGCCTCTGCCTCCCA    69946          CAC TG
                                TGGGAGGCAGGG  G  GGA
                                ||||||||||||  |  |||
                                ACCCTCCGTCTC  C  CCT
                                      ___ GT
GAM223  C1orf16  5'  TTCCCAGCTGCCTCC      29235        GGCACG
                                GGAGGCAG     TGGGAA
                                ||||||||     ||||||
                                CCTCCGTC     ACCCTT
                                    G_____
GAM223  CAMTA2   3'  CCCACGCCTTGCTCCCA     61220       G     AC
                                TGGGAG CAGGGC  GTGGG
                                |||||| ||||||  |||||
                                ACCCTC GTTCCG  CACCC
                                  _     __
GAM223  CBX6     3'  TCTCTAGTACCCCCGCCTCCCA 26627        A_   C  GT
                                TGGGAGGC  GGG AC  GGGA
                                ||||||||  ||| ||  ||||
                                ACCCTCCG  CCC TG  CTCT
                                    CC   A  AT
GAM223  CLDN6    3'  CCTTCTGCCCTGCCCCCC    41040     A       CGT
                                GGG GGCAGGGCA   GGG
                                ||| |||||||||   |||
                                CCC CCGTCCCGT   TCC
                                  C        CT_
GAM223  DKFZp434M0331 3'  TCCCACAGCACCCTGCCTCCC  34236          CAC_
                                GGGAGGCAGGG   GTGGGA
                                ||||||||||    ||||||
                                CCCTCCGTCCC   CACCCT
                                     ACGA
GAM223  DKFZP566J091 3'  TCCCTCCCCACCTCCCA     48127       CA   CACGT
                                TGGGAGG  GGG    GGGA
                                |||||||  |||    ||||
                                ACCCTCC  CCC    CCCT
                                    AC   T____
GAM223  DNAJB5   3'  TTTCTCAGCCCCACCCCCA   24357     A  CA   ACG
                                TGGG GG  GGGC   TGGGAAA
                                |||| ||  ||||  |||||||
                                ACCC CC  CCCG   ACTCTTT
                                  _  AC   ___
GAM223  EAT2     3'  TCTCCACATCCCCGCCTCCCA  79282        A   CAC   _
                                TGGGAGGC GGG   GTGG GA
                                |||||||| |||   |||| ||
                                ACCCTCCG CCC   CACC CT
                                    C   TA_   T
GAM223  FLJ10604 3'  TTTCCCACAGACCTCCC     36342       CAGGGCAC
                                GGGAGG       GTGGGAAA
                                ||||||       ||||||||
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                                CCCTCC       CACCCTTT
                                   AGA_____
GAM223  FLJ10619  3'  TTCCCTCCCTGCCTCCC     36354          CACGT
                                GGGAGGCAGGG    GGGAA
                                ||||||||||    |||||
                                CCCTCCGTCCC    CCCTT
                                      T____
GAM223  FLJ11294  3'  CTCATTGCCCCAACTCCCA   37221       GCA    C
                                TGGGAG   GGGCA GTGGG
                                ||||||   ||||| |||||
                                ACCCTC   CCCGT TACTC
                                   AAC    _
GAM223  FLJ12190  3'  TTTCACGCCCAGCCTCCCA   46878        A   AC   GG
                                TGGGAGGC GGGC  GTG  A
                                |||||||| ||||  |||  |
                                ACCCTCCG CCCG  CAC  T
                                     A   __   TT
GAM223  FLJ12443  3'  TCTCTGCAGCACTGCCTCCCA  45732         G  ACGT
                                TGGGAGGCAG GC    GGGA
                                |||||||||| ||    ||||
                                ACCCTCCGTC CG    CTCT
                                      A  ACGT
GAM223  FLJ13710  3'  TCTCAGCCCTGCTCCCA     45683       G     ACG
                                TGGGAG CAGGGC   TGGGA
                                ||||||  ||||||   |||||
                                ACCCTC GTCCCG   ACTCT
                                   _     ____
GAM223  FLJ14100  3'  TCCCTTTCCTGCCGCCCA    46686     A      CACGT
                                TGGG GGCAGGG    GGGA
                                ||||  |||||||    ||||
                                ACCC CCGTCCT    CCCT
                                  G      TT___
GAM223  FLJ14129  3'  TCTGAGACTCCCCGCCTCCCA  48072        A   CACGTG
                                TGGGAGGC GGG     GGA
                                |||||||| |||     |||
                                ACCCTCCG CCC     TCT
                                     C   TCAGAG
GAM223  FLJ14249  3'  TCCCAGCCTGCACCGCCTCCCA 42409        A  _   C _
                                TGGGAGGC GG GCA G TGGGA
                                |||||||| || ||| | |||||
                                ACCCTCCG CC CGT C ACCCT
                                     _ A   C G
GAM223  FLJ14249  3'  TCCCAGCCTGCACCGCCTCCCA 55216        A  _   C _
                                TGGGAGGC GG GCA G TGGGA
                                |||||||| || ||| | |||||
                                ACCCTCCG CC CGT C ACCCT
                                     _ A   C G
GAM223  FLJ14524  3'  TCCTGCCCACGCCTCCCA    51410        A_    CGTG
                                TGGGAGGC  GGGCA   GGA
                                ||||||||  |||||   |||
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                                ACCCTCCG  CCCGT   CCT
                                    CA    ____
GAM223  FLJ14888  3' CTTTCCCACACTTGTCCCCCCA 51681     A _   GCAC
                                TGGG GG CAGG   GTGGGAAAG
                                |||| || ||||   |||||||||
                                ACCC CC GTTC   CACCCTTTC
                                  C T   A___
GAM223  FLJ20195  3' TCTGAGCGCGACCCCGCCTCCC 34717       A  CA   ___
          A                      TGGGAGGC GGG  CGTG  GGA
                                |||||||| |||  ||||  |||
                                ACCCTCCG CCC  GCGC  TCT
                                    C  A_   GAG
GAM223  FLJ20257  3' TCTCCCCCAGCCTCCCA    39000       A  CACGT
                                TGGGAGGC GGG    GGGA
                                |||||||| |||    ||||
                                ACCCTCCG CCC    CTCT
                                    A  C____
GAM223  FLJ21324  5' TCCTGCCCCAGCCTCCCA   91210       A  CAC TG
                                TGGGAGGC GGG  G  GGA
                                |||||||| |||  |  |||
                                ACCCTCCG CCC  C  CCT
                                    A  ___ GT
GAM223  FLJ21596  3' CTTTGTCCCTGCCTCCCA   45701         C  T
                                TGGGAGGCAGGG ACG GG
                                |||||||||||| ||| ||
                                ACCCTCCGTCCC TGT TC
                                      _  T
GAM223  FLJ23519  5' TCTTGCCTCTGCCTCCCA   69208         CAC TG
                                TGGGAGGCAGGG  G  GGA
                                ||||||||||||  |  |||
                                ACCCTCCGTCTC  C  TCT
                                      ___ GT
GAM223  FLJ23556  5' TTCCACCCTGCCTCCC     45963         CACG
                                GGGAGGCAGGG   TGGGA
                                ||||||||||    |||||
                                CCCTCCGTCCC   ACCTT
                                      ____
GAM223  FLJ30532  3' TCCTGCCTCTGCCTCCCA   58553         CAC TG
                                TGGGAGGCAGGG  G  GGA
                                ||||||||||||  |  |||
                                ACCCTCCGTCTC  C  CCT
                                      ___ GT
GAM223  FLJ32771  5' CCCCTGGGGCCCTGCCCC   58800   A     A_  T
                                GG GGCAGGGC  CG GGG
                                || ||||||||  || |||
                                CC CCGTCCCG  GT CCC
                                  _      GG  C
GAM223  FLJ32884  3' TTCCCCTAGCCCCCTCCCA  58461       CA   ACGT
                                TGGGAGG  GGGC   GGGAA
                                |||||||  ||||   |||||
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                                ACCCTCC  CCCG   CCCTT
                                   __   ATC_
GAM223  FOXD4   5'  CCTGGACCCCGCCTCCCA   82746       A  CA  T
                                TGGGAGGC GGG  CG GG
                                |||||||| |||  || ||
                                ACCCTCCG CCC  GT CC
                                    C   AG  _
GAM223  GMPPB   5'  CTTTCCGTCTCCCTGCTTCCCA 95739          CACGTG
                                TGGGAGGCAGGG    GGAAAG
                                ||||||||||||    ||||||
                                ACCCTTCGTCCC    CCTTTC
                                      TCTG__
GAM223  GPR     5'  TCCCTCCCCGCCTCCC     23338       A  CACGT
                                GGGAGGC GGG    GGGA
                                ||||||| |||    ||||
                                CCCTCCG CCC    CCCT
                                   _  CT___
GAM223  GTF3C1  3'  TCCCAGCCACCGCCTGCCA  7720     G   AG_  ACG
                                TGG AGGC  GGC  TGGGA
                                ||| ||||  |||  |||||
                                ACC TCCG  CCG  ACCCT
                                  G   CCA  ___
GAM223  HSPC023 3'  TTCCCAGGTCCTGCCTCC   25912         ACG
                                GGAGGCAGGGC  TGGGAA
                                ||||||||||  ||||||
                                CCTCCGTCCTG  ACCCTT
                                      G__
GAM223  ICK     3'  TCTCTGCAACCTCTGCCTCCCA 29935         CAC TG _
                                TGGGAGGCAGGG  G  G GA
                                ||||||||||||  |  | ||
                                ACCCTCCGTCTC  C  C CT
                                      CAA GT T
GAM223  ITM3    3'  CCCAGTCCTGCCCCCCA    48162     A     ACG
                                TGGG GGCAGGGC  TGGG
                                |||| ||||||||  ||||
                                ACCC CCGTCCTG  ACCC
                                  C      ___
GAM223  KIAA0450 3' CCTCCGCCCCTGCCTCCC   27631         CA  TG
                                GGGAGGCAGGG  CG  GG
                                ||||||||||  ||  ||
                                CCCTCCGTCCC  GC  CC
                                      C_  CT
GAM223  KIAA0513 3' CCCACCTCAGCCTCCCA    28348       A  CAC
                                TGGGAGGC GGG  GTGGG
                                |||||||| |||  |||||
                                ACCCTCCG CTC  CACCC
                                   A  ___
GAM223  KIAA0523 3' TTTCCCAGCAACCCCCCA   67746     A  CAGG  ACG
                                TGGG GG   GC  TGGGAAA
                                |||| ||   ||  |||||||
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                                ACCC CC    CG   ACCCTTT
                                  _ CAA_ ___
GAM223  KIAA0628  3'  CCTGGAGCCCTGCCTCCCA   28868          A_  T
                                TGGGAGGCAGGGC  CG GG
                                |||||||||||||  || ||
                                ACCCTCCGTCCCG  GT CC
                                       AG  _
GAM223  KIAA0643  5'  CTCGCTGCGCCTCTGCCTCCCA 45599         _  A _
                                TGGGAGGCAG GGC C GTGGG
                                |||||||||| ||| | |||||
                                ACCCTCCGTC CCG G CGCTC
                                      T   C T
GAM223  KIAA0720  3'  TCCTGCCCTGCCCCCA      62331      A       CGTG
                                TGGG GGCAGGGCA    GGA
                                |||| |||||||||    |||
                                ACCC CCGTCCCGT    CCT
                                  _       _____
GAM223  KIAA0773  3'  CCCAATGCCCTGCCTTCCA    28050           CG
                                TGGGAGGCAGGGCA  TGGG
                                ||||||||||||||  ||||
                                ACCTTCCGTCCCGT  ACCC
                                       A_
GAM223  KIAA0798  3'  CTCACTGCAACCCCGCCTCCCA 27722        A  ___  C
                                TGGGAGGC GG   GCA GTGGG
                                |||||||| ||   ||| |||||
                                ACCCTCCG CC   CGT CACTC
                                     C  CAA  _
GAM223  KIAA0884  3'  TTCCCACATGTCTCCC      70208        GGGCAC
                                GGGAGGCA     GTGGGAA
                                ||||||||     |||||||
                                CCCTCTGT     CACCCTT
                                     A_____
GAM223  KIAA1126  3'  TCCCAGCGGGCCCTGCCTCCCA 71941           A  _
                                TGGGAGGCAGGGC CG TGGGA
                                |||||||||||||| || |||||
                                ACCCTCCGTCCCG GC ACCCT
                                       G  G
GAM223  KIAA1193  3'  TTCCAGCTTGCCCTGCCTCC   67654          C  G
                                GGAGGCAGGGCA GT GGAA
                                |||||||||||| || ||||
                                CCTCCGTCCCGT CG CCTT
                                       T  A
GAM223  KIAA1196  3'  CTCAGGCCCTGCCCCCCA    61465      A       ACG
                                TGGG GGCAGGGC   TGGG
                                |||| ||||||||   ||||
                                ACCC CCGTCCCG   ACTC
                                  C       G__
GAM223  KIAA1545  3'  CCCATGCCCTGCCCCCC     60688     A       CG
                                GGG GGCAGGGCA  TGGG
                                ||| |||||||||  ||||
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                                CCC CCGTCCCGT  ACCC
                                  C       __
GAM223  KIAA1817 3'  CCCAAAGTGCCCTGCCCCTCA  68225      A        G_
                                TGGG GGCAGGGCAC  TGGG
                                |||| ||||||||||  ||||
                                ACTC CCGTCCCGTG  ACCC
                                  C        AA
GAM223  KLF3     3'  TCTCTGTCCTGCCTCCCA    33274           CGT
                                TGGGAGGCAGGGCA   GGGA
                                ||||||||||||||   ||||
                                ACCCTCCGTCCTGT   CTCT

                                    ____
GAM223  LHPP     3'  TCCACCCCTGCCTCCC      42102          CAC
                                GGGAGGCAGGG   GTGGG
                                ||||||||||   |||||
                                CCCTCCGTCCC   CACCT

                                    ____
GAM223  LHPP     3'  TCCACCCCTGCCTCCC      42103          CAC
                                GGGAGGCAGGG   GTGGG
                                ||||||||||   |||||
                                CCCTCCGTCCC   CACCT

                                    ____
GAM223  MAD4     3'  TCCCCCGTGCCCTGCCTCCC   21284            T
                                GGGAGGCAGGGCACG GGGA
                                |||||||||||||| ||||
                                CCCTCCGTCCCGTGC CCCT
                                       C
GAM223  MCF2L    3'  CCCACGCGCCCCCTGCCTCCCA 60841          __   A
                                TGGGAGGCA  GGGC CGTGGG
                                |||||||||  |||| ||||||
                                ACCCTCCGT  CCCG GCACCC
                                     CC   C
GAM223  MGC12217 3'  CTTTCCCACCTCCTTCCCCCCA 51312      A  C   CAC
                                TGGG GG AGGG   GTGGGAAAG
                                |||| || ||||   |||||||||
                                ACCC CC TTCC   CACCCTTTC
                                  _  C   TC_
GAM223  MGC15548 5'  TCCGCGGCGCCGCCTCCCA   51256        A  _  A
                                TGGGAGGC GG GC CGTGGG
                                |||||||| || || ||||||
                                ACCCTCCG CC CG GCGCCT
                                     _  G  _
GAM223  MGC15827 3'  CCCAAGGGGCCCTGCCCACCA  51804     GA       ACG_
                                TGG  GGCAGGGC    TGGG
                                |||  ||||||||    ||||
                                ACC  CCGTCCCG    ACCC
                                  AC       GGGA
GAM223  MGC3262  3'  TCTGCCTGTCCTGCCCCCCA   43817      A        C TG
                                TGGG GGCAGGGCA G  GG
                                |||| |||||||| |  ||
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                                ACCC CCGTCCTGT C  CT
                                  C       C GT
GAM223  MYT1    3'  TCCCTCGCCCTGCCCC     15782    A      ACGT
                                GG GGCAGGGC   GGGA
                                || ||||||||   ||||
                                CC CCGTCCCG   CCCT
                                 _      CT__
GAM223  NINJ2   3'  CTCACTGCACCTCCGCCTCCCA 33283        __  _  C
                                TGGGAGGC  AGG GCA GTGGG
                                ||||||||  ||| ||| |||||
                                ACCCTCCG  TCC CGT CACTC
                                    CC  A  _
GAM223  NPTXR   3'  CCCACCCATGCCTCCC     54175        G  CAC
                                GGGAGGCA GG   GTGGG
                                |||||||| ||   |||||
                                CCCTCCGT CC   CACCC
                                    A  ___
GAM223  NPTXR   3'  CCCACCCATGCCTCCC     26639        G  CAC
                                GGGAGGCA GG   GTGGG
                                |||||||| ||   |||||
                                CCCTCCGT CC   CACCC
                                    A  ___
GAM223  OATL1   3'  TCCCTCCCTGCCTGCCA    70493    G      CACGT
                                TGG AGGCAGGG    GGGA
                                ||| ||||||||    ||||
                                ACC TCCGTCCC    CCCT
                                  G      T____
GAM223  P17.3   3'  CTTCCCCACCCCCTGCCTGCCA 38796    G      CAC    A
                                TGG AGGCAGGG   GTGGG AAG
                                ||| ||||||||   ||||| |||
                                ACC TCCGTCCC   CACCC TTC
                                  G      C__    C
GAM223  P2RX1   3'  TCCCACACACCTGCACCCTA  67171     AG    GCAC
                                TGGG  GCAGG   GTGGGA
                                ||||  |||||   ||||||
                                ATCC  CGTCC   CACCCT
                                   CA    ACA_
GAM223  PADI1   3'  CTTTCCCACCCACAGCCCCCA 61995     A  AG_  CAC
                                TGGG GGC   GG   GTGGGAAAG
                                |||| |||   ||   |||||||||
                                ACCC CCG   CC   CACCCTTTC
                                   _   ACA  ___
GAM223  PDEF    3'  TCCATCCCCCTGCCTCCCA   24752          CAC
                                TGGGAGGCAGGG   GTGGG
                                ||||||||||||   |||||
                                ACCCTCCGTCCC   TACCT
                                       CC_
GAM223  PHRET1  5'  TCCCCCTCCAGCCTCCCA    41064        A  CACGT
                                TGGGAGGC GGG    GGGA
                                |||||||| |||    ||||
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                                ACCCTCCG CCT    CCCT
                                    A  CC___
GAM223  PIP5K2B  3'  TCTCTGTAAAGCCTGCCTCCCA 13079          GC__  T
                                TGGGAGGCAGG   ACG GGGA
                                ||||||||||   ||| ||||
                                ACCCTCCGTCC   TGT CTCT
                                     GAAA  _
GAM223  PLA2G6   3'  TCCCACTAACCCCGCCTTCCA  66491        A  CAC
                                TGGGAGGC GGG  GTGGGA
                                |||||||| |||  ||||||
                                ACCTTCCG CCC  CACCCT
                                    C  AAT
GAM223  PPP1R13B 3'  TCCCCTGCGACCGCCCTGCCCC 31012    A      A__  __
           CC                     GGG GGCAGGGC  CGT  GGGA
                                |||  ||||||||  |||  ||||
                                CCC CCGTCCCG  GCG  CCCT
                                  C       CCA  TC
GAM223  PTGES2   3'  TCCCTGTCCCTGCCTCCC    46883          C  T
                                GGGAGGCAGGG ACG GGGA
                                |||||||||| ||| ||||
                                CCCTCCGTCCC TGT CCCT
                                      _  _
GAM223  RAB1B    3'  CCTGTGCCCTGCCCTCCA    48287    GA        T
                                TGG  GGCAGGGCACG GG
                                |||  |||||||||| ||
                                ACC  CCGTCCCGTGT CC
                                  TC         _
GAM223  RAB22A   3'  TTCTACCCACCCGCCTCCCA  59933        A  CAC
                                TGGGAGGC GGG  GTGGGA
                                |||||||| |||  ||||||
                                ACCCTCCG CCC  CATCTT
                                    _  ACC
GAM223  SCYA22   3'  TCCCACCCCAGCCTCCCA    90962        A  CAC
                                TGGGAGGC GGG  GTGGGA
                                |||||||| |||  ||||||
                                ACCCTCCG CCC  CACCCT
                                    A  ___
GAM223  SGK2     3'  CTTTCCCAAAAGCTCCCCCCA  32778     A  CA   ACG
                                TGGG GG  GGGC  TGGGAAAG
                                |||| ||  ||||  ||||||||
                                ACCC CC  CTCG  ACCCTTTC
                                  _ __   AAA
GAM223  SNAP29   3'  TTCCCCACGTGCTCCCA    16546      GGCAGG       A
                                TGGGA     GCACGTGGG AA
                                |||||     |||||||||  ||
                                ACCCT     CGTGCACCC TT
                                  _______        C
GAM223  STMN3    3'  CCCACCCCCCGCCCCCA     31899      A  A  CAC
                                TGGG GGC GGG  GTGGG
                                |||| ||| |||  |||||
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                                ACCC CCG CCC   CACCC
                                  _   C   ___
GAM223  SV2      3'  CACAACCCTGCCTCCCA     29305          CAC
                                TGGGAGGCAGGG   GTG
                                ||||||||||||   |||
                                ACCCTCCGTCCC   CAC
                                       AA_
GAM223  TED      3'  TCCGGCTGCCCCTGCCTCCCA  31644          _  C  G
                                TGGGAGGCAGGG CA GT GGA
                                |||||||||||| || || |||
                                ACCCTCCGTCCC GT CG CCT
                                       C  _  G
GAM223  TOMM40   3'  CCCTCCTGGCCCCCGCCTTCCA 20370        A_   ACGT_
                                TGGGAGGC  GGGC    GGG
                                ||||||||  ||||    |||
                                ACCTTCCG  CCCG    CCC
                                     CC    GTCCT
GAM223  WBSCR23  3'  TCCTGCCTCCGCCTCCCA    46771        A   CAC TG
                                TGGGAGGC GGG   G  GGA
                                |||||||| |||   |  |||
                                ACCCTCCG CCT   C  CCT
                                     _   C__ GT
GAM223  ZFP106   5'  CCCCTGCCCTGCCTCCC     42465          CGT
                                GGGAGGCAGGGCA   GGG
                                ||||||||||||   |||
                                CCCTCCGTCCCGT   CCC
                                       C__
GAM223  LOC115114 5'  CTTTCCCAGCACGCTGCCTCAC 68758     _      G__  ACG
           CA                    TGG GAGGCAG   GC   TGGGAAAG
                                ||| |||||||   ||   ||||||||
                                ACC CTCCGTC   CG   ACCCTTTC
                                  A      GCA  ___
GAM223  LOC115196 3'  TCCCACCCCAGCCTCCCA    73267        A   CAC
                                TGGGAGGC GGG   GTGGGA
                                |||||||| |||   ||||||
                                ACCCTCCG CCC   CACCCT
                                     A   ___
GAM223  LOC115207 3'  CCCACCCCACCCCCA       56599      A  CA   CAC
                                TGGG GG  GGG   GTGGG
                                |||| ||  |||   |||||
                                ACCC CC  CCC   CACCC
                                  _  A_   ___
GAM223  LOC116113 3'  CCCACATCTGAAACTGCCTCCC 92213         GG_  C__
                                GGGAGGCAG   CA   GTGGG
                                |||||||||   ||   |||||
                                CCCTCCGTC   GT   CACCC
                                      AAA  CTA
GAM223  LOC116113 3'  TCCCCAGCACCTGCCCTCCCA  92220        _    _  ACGT
                                TGGGAGG CAGG GC    GGGA
                                ||||||| |||| ||    ||||
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                                ACCCTCC GTCC CG    CCCT
                                    C    A  AC__
GAM223   LOC123775 3'  TTTCCCACCCACCCCCCA    75625      A  CAG  CAC
                                TGGG GG   GG   GTGGGAAA
                                |||| ||   ||   ||||||||
                                ACCC CC   CC   CACCCTTT
                                  _  CA_  ___
GAM223   LOC126364 3'  TCCCAAATTGCTCCCCACCTCC 75701        CA__     CG_
            CA                    TGGGAGG    GGGCA   TGGGA
                                |||||||    |||||   |||||
                                ACCCTCC    CTCGT   ACCCT
                                    ACCC     TAA
GAM223   LOC126669 3'  TTCCCCATCAGCCTCCCA    75425         A  GCACGT
                                TGGGAGGC GG      GGGAA
                                |||||||| ||      |||||
                                ACCCTCCG CT      CCCTT
                                     A  AC_____
GAM223   LOC130612 3'  TTCCCATCGCCCTGCCTCGCA  74961    G         AC
                                TG GAGGCAGGGC  GTGGGAA
                                || ||||||||||  |||||||
                                AC CTCCGTCCCG  TACCCTT
                                 G         C_
GAM223   LOC143392 3'  TCCCACCACCCCTGCCTGCCA  82952     G       CAC
                                TGG AGGCAGGG   GTGGGA
                                ||| ||||||||   ||||||
                                ACC TCCGTCCC   CACCCT
                                  G       CAC
GAM223   LOC143903 5'  TCCCCCCCCGCCTCCC       76622         A   CACGT
                                GGGAGGC GGG     GGGA
                                ||||||| |||     ||||
                                CCCTCCG CCC     CCCT
                                    C  ______
GAM223   LOC144347 3'  CCCAGAGCCCTGCCACCC     76813     A       ACG
                                GGG GGCAGGGC   TGGG
                                ||| ||||||||   ||||
                                CCC CCGTCCCG   ACCC
                                  A       AG_
GAM223   LOC144766 3'  TTCCCTCTTCCTGCCTGCCA   76956     G       CACGT
                                TGG AGGCAGGG     GGGAA
                                ||| ||||||||     |||||
                                ACC TCCGTCCT     CCCTT
                                  G       TCT__
GAM223   LOC144817 3'  CCCACAAACACACCCTGCCTCC 76965           CAC____
            C                    GGGAGGCAGGG      GTGGG
                                ||||||||||       |||||
                                CCCTCCGTCCC      CACCC
                                       ACACAAA
GAM223   LOC145468 3'  CCCTCCTGGCCCCCGCCTTCCA 73820         A_    ACGT_
                                TGGGAGGC  GGGC     GGG
                                ||||||||  ||||     |||
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                                ACCTTCCG  CCCG    CCC
                                    CC    GTCCT
GAM223   LOC145809 5'  TCTCCACCCTGCCTCCCA    83495          CACG  _
                                TGGGAGGCAGGG    TGG GA
                                ||||||||||||    ||| ||
                                ACCCTCCGTCCC    ACC CT
                                      _____   T
GAM223   LOC146268 3'  TCCCCCAGCTCCTACCTGCCTC 77814          GCAC_ ___
           CCA                    TGGGAGGCAGG    GT   GGGA
                                ||||||||||||    ||   ||||
                                ACCCTCCGTCC    CG   CCCT
                                      ATCCT  ACC
GAM223   LOC147160 5'  TCTCGCCCTGCCCCCA      83975      A       ACGT
                                TGGG GGCAGGGC    GGGA
                                |||| ||||||||    ||||
                                ACCC CCGTCCCG    CTCT

                                  _      _____
GAM223   LOC147429 3'  CCCGCCCCCCGCCTCCCA     78355        A   CAC
                                TGGGAGGC GGG   GTGGG
                                |||||||| |||   |||||
                                ACCCTCCG CCC   CGCCC
                                    C   ___
GAM223   LOC147965 3'  CCCAAATGCCCTGCTCCCA    78597       G      CG
                                TGGGAG CAGGGCA  TGGG
                                |||||| |||||||  ||||
                                ACCCTC GTCCCGT  ACCC
                                  _      AA
GAM223   LOC148193 5'  TCCCCGCCCCGCCTCCC     60338        A    AC T
                                GGGAGGC GGGC  G GGGA
                                ||||||| ||||  | ||||
                                CCCTCCG CCCG  C CCCT
                                    C   __ _
GAM223   LOC148443 3'  TCCCACCTCAGCCTCCCA     78862        A   CAC
                                TGGGAGGC GGG   GTGGGA
                                |||||||| |||   ||||||
                                ACCCTCCG CTC   CACCCT
                                    A   ___
GAM223   LOC148753 3'  TCCCTTGGCCGCCCTACTCCC  84219       GC    A__  T
                                GGGAG  AGGGC   CG GGGA
                                |||||  |||||   || ||||
                                CCCTC  TCCCG   GT CCCT
                                  A_    CCG  T
GAM223   LOC148936 5'  CTTGGTGCCCTGCATCCCA    84291       G       G
                                TGGGA GCAGGGCAC TGGG
                                ||||| ||||||||| ||||
                                ACCCT CGTCCCGTG GTTC
                                  A       _
GAM223   LOC148938 5'  CTTGGTGCCCTGCATCCCA    84271       G       G
                                TGGGA GCAGGGCAC TGGG
                                ||||| ||||||||| ||||
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                                ACCCT CGTCCCGTG GTTC
                                  A       _
GAM223  LOC149276 3'  CTTTCTTAAGTACCCTGCCTCC 84387         C  G
                                GGAGGCAGGG AC TGGGAAAG
                                |||||||||| || ||||||||
                                CCTCCGTCCC TG ATTCTTTC
                                    A  A
GAM223  LOC149506 3'  CCCACACACCTGCTTCCC    84456         GCAC
                                GGGAGGCAGG   GTGGG
                                ||||||||||   |||||
                                CCCTTCGTCC   CACCC
                                    ACA_
GAM223  LOC150155 3'  CCCTCCTGGCCCCCGCCTTCCA 70851        A_   ACGT_
                                TGGGAGGC  GGGC    GGG
                                ||||||||  ||||    |||
                                ACCTTCCG  CCCG    CCC
                                    CC    GTCCT
GAM223  LOC151171 5'  CCCCCCACGCCTCCCA     80143        A_  CACGT
                                TGGGAGGC  GGG    GGG
                                ||||||||  |||    |||
                                ACCCTCCG  CCC    CCC
                                    CA  _____
GAM223  LOC151171 5'  TCTCGGGGGGTGCCCTGCCCC  80146    A       G__
                                GG GGCAGGGCAC   TGGGA
                                || ||||||||||   |||||
                                CC CCGTCCCGTG   GCTCT
                                 _        GGG
GAM223  LOC152402 3'  TCCACTGCGCCCCACCTCCC  85708      CA   A _
                                GGGAGG  GGGC C GTGGG
                                ||||||  |||| | |||||
                                CCCTCC  CCCG G CACCT
                                   AC   C T
GAM223  LOC153443 3'  TCCCACCTCTGCCTCCCA    80827          CAC
                                TGGGAGGCAGGG   GTGGGA
                                ||||||||||||   ||||||
                                ACCCTCCGTCTC   CACCCT
                                      ___
GAM223  LOC154007 3'  CTCTTGCCCTGGCCTCCCA   81018        _    CGT
                                TGGGAGGC AGGGCA   GGG
                                |||||||| ||||||   |||
                                ACCCTCCG TCCCGT   CTC
                                    G     T__
GAM223  LOC158402 5'  TCCCGTCTCCGCCTCCCA    86814        A  C   T
                                TGGGAGGC GGG ACG GGG
                                |||||||| ||| ||| |||
                                ACCCTCCG CTC TGC CCT
                                    C   _  _
GAM223  LOC195977 3'  TTCCCACGGATGCCGCCCA   87544     A   GGGCA
                                TGGG GGCA    CGTGGGAA
                                |||| ||||    ||||||||
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                                ACCC CCGT    GCACCCTT
                                  G   AG___
GAM223  LOC199718 3'  TCCATGCAACCCCACCGCCCA 88336     A  CA   CA_
                                TGGG GG  GGG   CGTGGG
                                |||| ||  |||   ||||||
                                ACCC CC  CCC   GTACCT
                                  G  AC   AAC
GAM223  LOC199796 5'  TCCTCGAGCCCTGCTCCCA   74459      G     A  T
                                TGGGAG CAGGGC CG GGGA
                                |||||| |||||| || ||||
                                ACCCTC GTCCCG GC TCCT
                                   _     A  _
GAM223  LOC199863 5'  TCCCTCCTGCCTCCCA      89867          CACGT
                                TGGGAGGCAGGG    GGGA
                                ||||||||||||    ||||
                                ACCCTCCGTCCT    CCCT
                                        _____
GAM223  LOC203286 5'  TTCCCACACGTGTCCCC     90506    CA     __
                                GG  GGGCAC  GTGGGAA
                                ||  ||||||  |||||||
                                CC  CCTGTG  CACCCTT
                                 __     CA
GAM223  LOC219649 5'  TCCCCCTCGTCCTGCTTCCCA  92963          ACGT
                                TGGGAGGCAGGGC   GGGA
                                ||||||||||||   ||||
                                ACCCTTCGTCCTG   CCCT
                                       CTCC
GAM223  LOC220776 3'  CTCAGCCGCCCTGCCTCCCA   68391          ACG
                                TGGGAGGCAGGGC   TGGG
                                ||||||||||||   ||||
                                ACCCTCCGTCCCG   ACTC
                                       CCG
GAM223  LOC220776 3'  CCCTCTTCTGCCGCGCCTCCCA 68389        AG   CGT__
                                TGGGAGGC  GGCA    GGG
                                ||||||||  ||||    |||
                                ACCCTCCG  CCGT    CCC
                                    CG    CTTCT
GAM223  LOC222136 3'  TCCCACAGCTTGTGCCCTCCA  92720     GA   _   AC
                                TGG  GGCA GGGC  GTGGGA
                                |||  |||| ||||  ||||||
                                ACC  CCGT TTCG  CACCCT
                                  TC   G   A_
GAM223  LOC254207 3'  TTTCCCGGCCGGCCCCCCA   94587     A  AG   ACG
                                TGGG GGC  GGC   TGGGAAA
                                |||| |||  |||   |||||||
                                ACCC CCG  CCG   GCCCTTT
                                  C   G_   ___
GAM223  LOC254219 5'  CCCACGCCCCCACCCCCCA   96547     A  CA   CA
                                TGGG GG  GGG  CGTGGG
                                |||| ||  |||  ||||||
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                                ACCC CC  CCC  GCACCC
                                  _ CA   CC
GAM223   LOC255354 5'  TCTTACCCTGCCTC       97497         CACG
                                GAGGCAGGG    TGGGA
                                |||||||||    |||||
                                CTCCGTCCC    ATTCT
                                     ____
GAM223   LOC255452 3'  CACACACCCTGCCTTCCA    97526           CAC
                                TGGGAGGCAGGG   GTG
                                ||||||||||||   |||
                                ACCTTCCGTCCC   CAC
                                       ACA
GAM223   LOC255919 3'  TTTCTGCAACCTCTGCCTCCCA 95044           CAC TG
                                TGGGAGGCAGGG   G  GGAA
                                ||||||||||||   |  ||||
                                ACCCTCCGTCTC   C  CTTT
                                       CAA GT
GAM223   LOC256789 3'  CCTCTGCCCTGCCTCCC     97444           CGT
                                GGGAGGCAGGGCA   GGG
                                ||||||||||||   |||
                                CCCTCCGTCCCGT   TCC
                                       C__
GAM223   LOC256867 5'  CCCTGTCTGTGCCCTGCCTCTC 94863             T___
           A                     TGGGAGGCAGGGCACG    GGG
                                 ||||||||||||||||    |||
                                 ACTCTCCGTCCCGTGT    CCC
                                       CTGT
GAM223   LOC257054 5'  CCATGTCCCTGCCTCCCA    95657           C
                                TGGGAGGCAGGG ACGTGG
                                |||||||||||| ||||||
                                ACCCTCCGTCCC TGTACC
                                     _
GAM223   LOC257054 5'  TCCCCTGTGGCCCACCCGCC   95670    A  CA   _   T
                                GG GG  GGGC ACG GGGA
                                || ||  |||| ||| ||||
                                CC CC  CCCG TGT CCCT
                                 G  CA   G   C
GAM223   LOC51042  3'  TTCTTGGTGCCCTGCCCCCA   31856      A        G
                                TGGG GGCAGGGCAC TGGGAA
                                |||| ||||||||| ||||||
                                ACCC CCGTCCCGTG GTTCTT
                                   _        _
GAM223   LOC89944  3'  TTCCCACTCGCTGCTTCCCA   91550          _  CAC
                                TGGGAGGCAG GG   GTGGGAA
                                |||||||||| ||   |||||||
                                ACCCTTCGTC CT   CACCCTT
                                      G  ___
GAM223   LOC90529  3'  CTTCCCCACGCACCCATCC    63161     GGCA   CA     A
                                GGA   GGG  CGTGGG AAG
                                |||   |||  |||||| |||
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                                CCT   CCC  GCACCC TTC
                                  A___   AC     C
GAM223  LOC90591  3'  TCCTGCCCCAGCCTCCCA    63446        A   CAC TG
                                TGGGAGGC GGG   G  GGA
                                |||||||| |||   |  |||
                                ACCCTCCG CCC   C  CCT
                                    A   ___ GT
GAM223  LOC90917  5'  TTCCCACTCCTCCCA       64341        CAGGGCAC
                                TGGGAGG       GTGGGAA
                                |||||||       |||||||
                                ACCCTCC       CACCCTT
                                   T_______
GAM223  LOC92162  3'  TTCCGACCTGCCCTGCCCCCA  68365     A       C  G
                                TGGG GGCAGGGCA GT GGAA
                                |||| ||||||||| || ||||
                                ACCC CCGTCCCGT CA CCTT
                                  _       C  G
GAM224  ABCF1     3'  ATTCAGGCACATGAAGGTGGAG 6566           C_      AT
          TG                      CATTTCACTTTCA  TGTCTGAG
                                |||||||||||||  ||||||||
                                GTGAGGTGGAAGT  ACGGACTT
                                       AC       A
GAM224  ACVRL1    5'  GCGGTGGAGGGGAGGTG     3418        A
                                CATTTC CTTTCACTGT
                                |||||| ||||||||||
                                GTGGAG GGAGGTGGCG
                                   G
GAM224  ADRA1A    3'  TCTTGATGGAAGTGAGG     5448          CTG  T
                                TTTCACTTTCA   TC GAGA
                                ||||||||||   || ||||
                                GGAGTGAAGGT   AG TTCT
                                       ___  _
GAM224  AGT       3'  ATTTTAGAGAATGGGGGTGGGG 3453    TT    TT  CTG
                                T  CACT  CA   TCTGAGAT
                                |  ||||  ||   ||||||||
                                G  GTGG  GT   AGATTTTA
                                 GG    GG  AAG
GAM224  AIM1      3'  ATCTCAGGCTGGAGTGCAGTG  91816     T     CACT
                                CATT CACTTT    GTCTGAGAT
                                |||| ||||||    |||||||||
                                GTGA GTGAGG    CGGACTCTA
                                  C     T___
GAM224  AKAP13    3'  GTTTTGGGCATGGATAAAGTGA 58580        ___    C    TG
          AG                      TTTCACT   TTCA TGTC  AGAT
                                |||||||   |||| ||||  ||||
                                GAAGTGA   AGGT ACGG  TTTG
                                    AAT    _    GT
GAM224  AKAP13    3'  GTTTTGGGCATGGATAAAGTGA 22144        ___    C    TG
          AG                      TTTCACT   TTCA TGTC  AGAT
                                |||||||   |||| ||||  ||||
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                                GAAGTGA  AGGT ACGG  TTTG
                                   AAT   _   GT
GAM224  AKAP13   3' GTTTTGGGCATGGATAAAGTGA 23248       ___   C   TG
          AG                    TTTCACT  TTCA TGTC  AGAT
                                |||||||  |||| ||||  ||||
                                GAAGTGA  AGGT ACGG  TTTG
                                   AAT   _   GT
GAM224  ATP11B   3' ATTTCAGGTGTGGCTGTGGAAT 80315       TT   TGT
          G                     CATTTCAC  TCAC  CTGAGAT
                                ||||||||  ||||  |||||||
                                GTAAGGTG  GGTG  GACTTTA
                                   TC   TG_
GAM224  B4GALT4  3' TAGCAGGAGGGTGGAGTG   13674         A   T
                                CATTTCACTTTC CTG CTG
                                |||||||||||| ||| |||
                                GTGAGGTGGGAG GAC GAT
                                      _  _
GAM224  BLAME    3' ATCTGGGAGTGAGGGTGGAG  39239         TG  G
                                TTTCACTTTCAC  TCT AGAT
                                ||||||||||||  ||| ||||
                                GAGGTGGGAGTG  AGG TCTA
                                      __  G
GAM224  C20orf1  5' ATTTCAGAAAAGGGGTGAAA  23999       CACTG
                                TTTCACTTT   TCTGAGAT
                                |||||||||   ||||||||
                                AAAGTGGGG   AGACTTTA
                                    AAA__
GAM224  C21orf5  3' TTTCAGGCTAGGTGCGGTG   17614     TT   __
                                CACT  CACT  GTCTGAGA
                                ||||  ||||  ||||||||
                                GTGG  GTGG  CGGACTTT
                                  C_   AT
GAM224  CAPN10   3' GTCTCAGAACCGAGTGAGGTG 43604        TCACTG
                                CATTTCACTT    TCTGAGAT
                                ||||||||||    ||||||||
                                GTGGAGTGAG    AGACTCTG
                                     CCA___
GAM224  CARPX    3' ATTTCAGATAGTGTCCTAGGA 39415    A  TT__
                                TC CT   CACTGTCTGAGAT
                                || ||   ||||||||||||
                                AG GA   GTGATAGACTTTA
                                 _ TCCT
GAM224  CARPX    5' TCGGGTGGGAGTGCGAGTG   39426     _   TT   TGT
                                CATTT CACT  CAC   CTGA
                                ||||| ||||  |||   ||||
                                GTGAG GTGA  GTG   GGCT
                                  C   GG  ___
GAM224  CASP10   3' TTTTGGACTGGGTGCGGTG   52111     TT   __  TG
                                CACT  CACT  GTC  AGA
                                ||||  ||||  |||  |||
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                                GTGG  GTGG  CAG  TTT
                                  C_   GT   GT
GAM224  CASP10   3'  TTTTGGACTGGGTGCGGTG   52127     TT   __   TG
                                CACT  CACT  GTC  AGA
                                ||||  ||||  |||  |||
                                GTGG  GTGG  CAG  TTT
                                  C_   GT   GT
GAM224  CCND1    3'  GTGGTGGCAGTGGAGGTGGGGT 53891     TT         TGAGAT
           G                     CAT  CACTTTCACTGTC
                                |||  ||||||||||||
                                GTG  GTGGAGGTGACGG
                                  GG          TGGTG
GAM224  CDK4     5'  GTCACATGGTGAGGGTGGGG   53763   TT        C   GAT
                                T  CACTTTCACTGT TGA
                                |  ||||||||||| |||
                                G  GTGGGAGTGGTA ACT
                                 GG         C   G
GAM224  CDK4     5'  GTCACATGGTGAGGGTGGGG   3573    TT        C   GAT
                                T  CACTTTCACTGT TGA
                                |  ||||||||||| |||
                                G  GTGGGAGTGGTA ACT
                                 GG         C   G
GAM224  CDKN2A   5'  GTCCGGGTGGGAGTGGGGGTGG 54229   TT   TT   G___   A
           GGTG                   T  CACT  CACT    TCTG GAT
                                |  ||||  ||||   |||| |||
                                G  GTGG  GTGA   GGGC CTG
                                 GG   GG   GGGT   _
GAM224  CDKN2A   5'  TATCTTGGAGGTCCGGGTGGGA 54230    TT   G_____ TG
           GTGGGG                  ACT  CACT    TC  AGAT   A
                                |||  ||||    ||  ||||  |
                                TGA  GTGG    AG  TCTA   T
                                  GG   GCCTGG  GT
GAM224  CDKN2B   3'  AGGTGGTGGAGTGGAGTG    54353         T   TG
                                CATTTCACTT CAC  TCT
                                ||||||||| |||  |||
                                GTGAGGTGAG GTG  GGA
                                      _  GT
GAM224  CERD4    3'  ATCTCAGAGCAGAGGAGGTGGG 23849   TT     A   _
           G                     T  CACTTTC CTG TCTGAGAT
                                |  ||||||| ||| ||||||||
                                G  GTGGAGG GAC AGACTCTA
                                 GG     A   G
GAM224  CHRM1    3'  TTTTCCTGGGAGTGGGAGTCAA 94794     C   TT   G  T_   T
           GTG                    CATTT ACT  CACT TC  GAGA
                                |||||  |||  ||||  ||  ||||
                                GTGAA TGA  GTGA GG  CTTT
                                  C   GG   G  TC    TA
GAM224  CLASP1   3'  GGGGGTGGGGTGGGGTG    65305    TT    T   G
                                CAT  CACTT CACT TC
                                |||  ||||| |||| ||
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                                GTG  GTGGG GTGG GG
                                  GG    _   G
GAM224  CMAR     5'  ATTTTGGACGGTGCTCTGA   17772    CTTT     TG
                                TCA   CACTGTC  AGAT
                                |||   |||||||  ||||
                                AGT   GTGGCAG  TTTA
                                  CTC_     GT
GAM224  COL1A1   3'  ATCTATGTGATGGGTGGGGTG  3601     TT   _   TGTCTG
                                CAT  CACTT TCAC    AGAT
                                |||  ||||| ||||     ||||
                                GTG  GTGGG AGTG    TCTA
                                  GG    T   TA____
GAM224  COL4A4   5'  CAGGCGGGGAAGTGGGGTG   3626     TT     A
                                CAT  CACTTTC CTGTCTG
                                |||  ||||||| |||||||
                                GTG  GTGAAGG GGCGGAC
                                  GG     _
GAM224  COL4A6   3'  GTCTTAGGCAGGCAAGAGAATT 8473     ___   CA_
           GAAATG                 TCA   CTTT   CTGTCTGAGAT
                                |||   ||||   ||||||||||
                                AGT   GAGA   GACGGATTCTG
                                  TAA    ACG
GAM224  CPT1B    3'  GCCCAGGTGGTGGAGGTGGGGT 15199    TT       TG   AGAT
                                AT  CACTTTCAC  TCTG
                                ||  |||||||||  ||||
                                TG  GTGGAGGTG  GGAC
                                  GG       GT    CCG
GAM224  D10S170  3'  GTTTTGTACTTTGGTAGTGAAG 18367         T   CT  CT
           TG                    CATTTCACT TCA  GT  GAGAT
                                |||||||||  |||  ||  |||||
                                GTGAAGTGA GGT  CA  TTTTG
                                     T   TT  TG
GAM224  DDEF2    3'  ATTTTAGGCGGCCAGTGAACTG 13952    T     TTCA
                                CA TTCACT    CTGTCTGAGAT
                                || ||||||    ||||||||||
                                GT AAGTGA    GGCGGATTTTA
                                 C     CC__
GAM224  DES      3'  TCTCAGGCTGGTGGGAG     72132    TT   _
                                CT  CACT GTCTGAGA
                                ||  |||| ||||||||
                                GA  GTGG CGGACTCT
                                  GG    T
GAM224  DLEC1    3'  TAGAGAGAGTGAGGTG      23706           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTGGAGTGAGAG GAT
                                        A
GAM224  DPYSL3   3'  ATCTCAGCTTATATGAAAGTCA 7311      C      C   ___
           AGTG                    TTT ACTTTCA TGT   CTGAGAT
                                ||| ||||||| |||   |||||||
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                                GAA TGAAAGT ATA   GACTCTA
                                  C      _  TTC
GAM224  DRIL1    3'  GTTTTGGACATTCAGAGAGATG 17831       A  TTCAC    TG
                                CATTTC CT    TGTC  AGAT
                                |||||| ||    ||||  ||||
                                GTAGAG GA    ACAG  TTTG
                                   A  CTT__   GT
GAM224  DXS1283E  3'  GTTTTAGATAGTTTTTGATGGA 70836      CTTTC_
          A                      TTTCA     ACTGTCTGAGAT
                                |||||     ||||||||||||
                                AAGGT     TGATAGATTTTG
                                   AGTTTT
GAM224  EHF      3'  GTCTCAGATGGTTAGGACAAAG 24063      __ ___
          TGGA                    CACTT  TC   ACTGTCTGAGAT
                                |||||  ||   ||||||||||||
                                GTGAA  AG   TGGTAGACTCTG
                                   AC  GAT
GAM224  EIF2B1   5'  CTGCGGAAGTGGAGTG      59658       T   G   _
                                CACTT CACT TCTG AG
                                ||||| |||| |||| ||
                                GTGAG GTGA AGGC TC
                                   _   _   G
GAM224  EPHA1    3'  GTTTTAAAAGGGAGGTGGGG   17861   TT      A  GTC
                                T  CACTTTC CT   TGAGAT
                                |  ||||||| ||   ||||||
                                G  GTGGAGG GA   ATTTTG
                                 GG      _  AA_
GAM224  ESRRA    3'  ATCTCAGGGAGGGAAGGGGATG 15479     TT A    A  G
                                CAT  C CTTTC CT TCTGAGAT
                                |||  | ||||| || ||||||||
                                GTA  G GAAGG GA GGACTCTA
                                  GG _    _  G
GAM224  FCAR     3'  GCACTGAGAGTGAAGTG     55798            C
                                CATTTCACTTTCA TGT
                                |||||||||||| |||
                                GTGAAGTGAGAGT ACG
                                        C
GAM224  FCAR     3'  GCACTGAGAGTGAAGTG     55814            C
                                CATTTCACTTTCA TGT
                                |||||||||||| |||
                                GTGAAGTGAGAGT ACG
                                        C
GAM224  FGF2     3'  GTCTCAGATACTTGGGAGGCTG 8873      _    AC__
          AGGTG                    TTCA CTTTC    TGTCTGAGAT
                                |||| |||||   ||||||||||
                                GAGT GGAGG    ATAGACTCTG
                                  C    GTTC
GAM224  FRAT2    3'  GGCTGGTGAAGGTGGGA     23881    TT       _
                                T  CACTTTCACT GTC
                                |  |||||||||| |||
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                                A  GTGGAAGTGG CGG
                                 GG         T
GAM224  GCKR     3'  ATTTCAGAAATAAAATGAAATG 7635         C   CACTG
                                CATTTCA TTT     TCTGAGAT
                                ||||||| |||     ||||||||
                                GTAAAGT AAA     AGACTTTA
                                   A   TAA__
GAM224  GNPI     3'  GTCTTAGGCCTTCATGGAGTGG 18448         CACT__
             A                   TTCACTTT     GTCTGAGAT
                                 ||||||||     |||||||||
                                 AGGTGAGG     CGGATTCTG
                                      TACTTC
GAM224  GPR61    3'  TGGGCTGGTGGGAGTGGGAT   78914    TT    TT   _
                                AT  CACT  CACT GTCTG
                                ||  ||||  |||| |||||
                                TA  GTGA  GTGG CGGGT
                                 GG    GG    T
GAM224  GUCY1B3  3'  ATCTTGGATTATGGGGTGAAG  5963         T  CT   TG
                                TTTCACTT CA  GTC  AGAT
                                |||||||| ||  |||  ||||
                                GAAGTGGG GT  TAG  TCTA
                                     _  AT   GT
GAM224  GYG2     3'  ATTTCAGGTGAGTCAGGGTTGG 14047      TC     C  _ GT
             ATG                   CATT  ACTTT AC T  CTGAGAT
                                ||||  ||||| || |  |||||||
                                GTAG  TGGGA TG G  GACTTTA
                                  GT     C  A TG
GAM224  HHEX     3'  ATTTCAGGCAGCCTTGGAGT   10784      CA__
                                ACTTT    CTGTCTGAGAT
                                |||||    ||||||||||||
                                TGAGG    GACGGACTTTA
                                   TTCC
GAM224  HMGA2    3'  TCTGGGGTGGGGTGGGGTG    13004     TT    TTCA TG   G
                                CAT  CACT    C  TCT AGA
                                |||  ||||    |  ||| |||
                                GTG  GTGG    G  GGG TCT
                                  GG    ____ GT   G
GAM224  HOXD4    5'  TTTTGGGGTACTAGGGAGTGAG 27534         TT AC_ GT  G   T
             GT                    ATTTCACT  C   T  CT AGA
                                |||||||| |   |  || |||
                                TGGAGTGA  G   A  GG TTT
                                     GG ATC TG  G   TG
GAM224  HPCAL1   3'  TTATGTATGGTGAAGTGGAGTG 9272          T     CTGAGAT
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTGAGGTGAA GTGGTA
                                      _     TGTATTA
GAM224  HPCAL1   5'  GTGGTGACAGGTGAAATG    56190          _    TG
                                CATTTCACTT TCAC  T
                                |||||||||| ||||  |
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                                GTAAAGTGGA AGTG  G
                                      C    GT
GAM224  HPCAL1   3'  TTATGTATGGTGAAGTGGAGTG 56191          T     CTGAGAT
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTGAGGTGAA GTGGTA
                                      _     TGTATTA
GAM224  IGF1R    3'  TTCTCTCAGTGAAGGTGGGG  6049    TT        TCT   T
                                T  CACTTTCACTG   GAGA
                                |  ||||||||||   ||||
                                G  GTGGAAGTGAC   CTCT
                                 GG         T__    TT
GAM224  IL11     3'  ATTTCAGGAGCAGGGGTGGGA  5324    TT     CA  G
                                T  CACTTT  CT TCTGAGAT
                                |  ||||||  || ||||||||
                                A  GTGGGG  GA GGACTTTA
                                 GG     AC  _
GAM224  IL13RA1  3'  TTAGGGGCAGTGGAGGTAGAAT 7782       TC          GAGAT
              G                   CATT  ACTTTCACTGTCT
                                ||||  ||||||||||||||
                                GTAA  TGGAGGTGACGGG
                                   GA           GATTG
GAM224  IL1F5    3'  ATTTCTGTGGGGGTGGGGTG  24377    TT   TT   TGTCT
                                CAT  CACT  CAC    GAGAT
                                |||  ||||  |||    |||||
                                GTG  GTGG  GTG    CTTTA
                                  GG   GG  T____
GAM224  IL1RN    3'  GATGGTGAAAGTAAGTG     5143       C
                                CATTT ACTTTCACTGTC
                                ||||| ||||||||||||
                                GTGAA TGAAAGTGGTAG
                                   _
GAM224  IL24     3'  TTGGGGTGGGGGTAAGGTG   22447      C   TT    GT TG
                                CATTT ACT  CACT  C  A
                                ||||| |||  ||||  |  |
                                GTGGA TGG  GTGG  G  T
                                   A   GG    __ GT
GAM224  IRS1     3'  ATCTTTTTTTTGGATGTGGGAT 18662     TT   T   CTGTCT
              G                   CAT  CAC TTCA     GAGAT
                                |||  ||| ||||     |||||
                                GTA  GTG AGGT     TTCTA
                                  GG   T   TTTTT_
GAM224  IRS2     3'  TCTCAATGGAAGTGAAAT    59723          CTGTC
                                ATTTCACTTTCA    TGAGA
                                ||||||||||||    |||||
                                TAAAGTGAAGGT    ACTCT
                                      A____
GAM224  JTB      3'  CTATCTCAGACAGTGAAAGTGA 21961
              AATG                   CATTTCACTTTCACTGTCTGAGAT
                                ||||||||||||||||||||||||
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                                GTAAAGTGAAAGTGACAGACTCTA
                                                   TCC
GAM224  KCNA7   3'  TCTCAGAGCAGGGGAGTG    49061     TT A  _
                                CACT  C CTG TCTGAGA
                                ||||  | ||| |||||||
                                GTGA  G GAC AGACTCT
                                  GG _   G
GAM224  KCNK6   3'  ATGGAGGAGGTGAGGTG     16690          A
                                CATTTCACTTTC CTGT
                                |||||||||||| ||||
                                GTGGAGTGGAGG GGTA
                                       A
GAM224  KCNK6   3'  TTTCAGGCTGAGTGTGGTG   16699     TT   __
                                CACT  CACT  GTCTGAGA
                                ||||  ||||  ||||||||
                                GTGG  GTGA  CGGACTTT
                                  T_   GT
GAM224  LAMC1   3'  GTCTCAGGCCACAATGGGGTG  9677     TT  CTTTCACT
                                CAT  CA       GTCTGAGAT
                                |||  ||       |||||||||
                                GTG  GT       CGGACTCTG
                                  GG  AACAC___
GAM224  MALT1   3'  ATTTTAGATGCCTGTGAAAT   22291       TTTCACT
                                ATTTCAC      GTCTGAGAT
                                |||||||      |||||||||
                                TAAAGTG      TAGATTTTA
                                    TCCG___
GAM224  MAPK14  3'  TCCTCCATGGTGGAAGGGGGTG 7161      TT A        CT   AT
                                CAT  C CTTTCACTGT  GAG
                                |||  | ||||||||||  |||
                                GTG  G GAAGGTGGTA  CTC
                                  GG _        C_   CTT
GAM224  MAPK14  3'  TCCTCCATGGTGGAAGGGGGTG 57335     TT A        CT   AT
                                CAT  C CTTTCACTGT  GAG
                                |||  | ||||||||||  |||
                                GTG  G GAAGGTGGTA  CTC
                                  GG _        C_   CTT
GAM224  MAPK14  3'  TCCTCCATGGTGGAAGGGGGTG 57346     TT A        CT   AT
                                CAT  C CTTTCACTGT  GAG
                                |||  | ||||||||||  |||
                                GTG  G GAAGGTGGTA  CTC
                                  GG _        C_   CTT
GAM224  MAPRE1  3'  ATTTTTTGGGGAAGTGAGGTG  24661           A  GTCT
                                CATTTCACTTTC CT    GAGAT
                                |||||||||||| ||    |||||
                                GTGGAGTGAAGG GG    TTTTA
                                       _  TT__
GAM224  MBP     5'  TTTTGGAAGGTGGAGTG     89783       T    G  TG
                                CACTT CACT TC  AGA
                                ||||| |||| ||  |||
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                                GTGAG GTGG AG  TTT
                                  _   A  GT
GAM224  MGAT5   5' TGCCTCATGGTGGGAGTGAAA 10030      TT   TC   AT
                                TTTCACT  CACTG  TGAG
                                |||||||  |||||  ||||
                                AAAGTGA  GTGGT  ACTC
                                    GG   __   CGTT
GAM224  MGEA5   3' GTTTCAGAAGTGTCAGGGTGGA 24218        __   G
           GTG                   ATTTCACTTT  CACT TCTGAGAT
                                |||||||||  |||| ||||||||
                                TGAGGTGGGA  GTGA AGACTTTG
                                     CT   _
GAM224  MMP19   3' TCAATGGTGGAGGGAGATG   10086      A       C
                                CATTTC CTTTCACTGT TGA
                                |||||| |||||||||| |||
                                GTAGAG GGAGGTGGTA ACT

                                  _       _
GAM224  MMP19   3' TCAATGGTGGAGGGAGATG   42975      A       C
                                CATTTC CTTTCACTGT TGA
                                |||||| |||||||||| |||
                                GTAGAG GGAGGTGGTA ACT

                                  _       _
GAM224  MMP19   3' TCAATGGTGGAGGGAGATG   42981      A       C
                                CATTTC CTTTCACTGT TGA
                                |||||| |||||||||| |||
                                GTAGAG GGAGGTGGTA ACT

                                  _       _
GAM224  MMP19   3' TCAATGGTGGAGGGAGATG   42985      A       C
                                CATTTC CTTTCACTGT TGA
                                |||||| |||||||||| |||
                                GTAGAG GGAGGTGGTA ACT

                                  _       _
GAM224  MOG     3' TCTTGGCAGGGGTGGAG    10107       TCA  T TG
                                TTTCACTT  CTG C  AGA
                                ||||||||  ||| |  |||
                                GAGGTGGG  GAC G  TCT
                                   ___  _ GT
GAM224  MPP4    5' TATCGGGAGCAGTGAGGTG   52347      T    __   GAT
                                CACTT CACTGT  CTGA
                                ||||| ||||||  ||||
                                GTGGA GTGACG  GGCT
                                  _    AG   ATT
GAM224  MS4A1   3' ATTTTGGGGAGACAAAGGGAAA 3748       A   CA  G  TG
           TG                   CATTTC CTTT  CT TC  AGAT
                                |||||| ||||  || ||  ||||
                                GTAAAG GAAA  GA GG  TTTA
                                   G   CA  G  GT
GAM224  MTNR1A  3' ACAATGAAAGTGGGGTG    19887    TT      C
                                CAT  CACTTTCA TGT
                                |||  |||||||| |||
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                                GTG  GTGAAAGT ACA
                                  GG       A
GAM224  MYOZ1    5'  ATCTCAGGCTCTAGGTGCAATG 41149      T    TCACT
                                CATT CACTT    GTCTGAGAT
                                |||| |||||    |||||||||
                                GTAA GTGGA    CGGACTCTA
                                  C    TCT__
GAM224  NAV2     3'  TTTCATTAGGGGTGGGGTG   60162     TT    TCA   TC
                                CAT  CACTT   CTG  TGAGA
                                |||  |||||   |||  |||||
                                GTG  GTGGG   GAT  ACTTT
                                  GG    ___   T_
GAM224  NDST2    3'  ATCTTGGGAGGTGGGGAGGAAT 13296       AC TT    GT TG
           G                     CATTTC  T  CACT  C  AGAT
                                ||||||  |  ||||  |  ||||
                                GTAAGG  G  GTGG  G  TCTA
                                   A_ GG    AG GT
GAM224  NEBL     3'  TTTTTGTGGTAGGGAAGTGGGA 21126     TT      A  GT _    T
           TG                    CAT  CACTTTC CT  C TGAGA
                                |||  ||||||| ||  | |||||
                                GTA  GTGAAGG GA  G GTTTT
                                  GG      _ TG T     TA
GAM224  NEU1     3'  GTCTTGGGCAGGTCTAGTGAGC 4742     T     TTCA     TG
           TG                    CA TTCACT    CTGTC  AGAT
                                || ||||||    |||||  ||||
                                GT GAGTGA    GACGG  TCTG
                                 C     TCTG    GT
GAM224  NEUROD2  3'  ATTTTGGCGGGAGGGGAAGTG  20478       A    A   T TG
                                CATTTC CTTTC CTG C  AGAT
                                |||||| ||||| ||| |  ||||
                                GTGAAG GGGAG GGC G  TTTA
                                   _    _  _ GT
GAM224  NFE2L1   3'  TGTCTGCCCCAGACAAGTGGGA 12177     TT   _    _____
           GTGAAATG                 ACT  CACT GTCTG    AGAT   G
                                |||  |||| |||||    ||||   |
                                TGA  GTGA CAGAC    TCTG   T
                                  GG   A    CCCG
GAM224  NFRKB    5'  GTCTTAAGGGAAGTGAAAGAGG 20497       A       G_  _
           AGTG                    ATTTC CTTTCACT  TCT GAGAT
                                ||||| ||||||||  ||| |||||
                                TGAGG GAAAGTGA  GGA TTCTG
                                   A       AG   A
GAM224  NGB      3'  GTTTTGGTGGCAGAGGTGGGAT 41188     TT     CA   T TG
           G                     CAT  CACTTT  CTG C  AGAT
                                |||  ||||||  ||| |  ||||
                                GTA  GTGGAG  GGT G  TTTG
                                  GG     AC   _ GT
GAM224  NLGN1    3'  CCTTTTGGTAAGGTGAAGTG   30024          C   GTCT   AT
                                CATTTCACTTT ACT    GAG
                                |||||||||| |||    |||
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                                GTGAAGTGGAA TGG   TTC
                                      _  TT__  CT
GAM224  NPC2    3'  GTCTTAGGTGGTTTCATTAAAT 21223     CACTTTC  TG
           G                   CATTT     AC  TCTGAGAT
                               |||||     ||  ||||||||
                               GTAAA     TG  GGATTCTG
                                  TTACTT_  GT
GAM224  OCRL    3'  GTTTCTTGGTGGGGGTGGGG  7830   TT   TT   GTCT
                               T  CACT  CACT   GAGAT
                               |  ||||  ||||   |||||
                               G  GTGG  GTGG   CTTTG
                                GG   GG   TT__
GAM224  OCRL    3'  GTTTCTTGGTGGGGGTGGGG  4264   TT   TT   GTCT
                               T  CACT  CACT   GAGAT
                               |  ||||  ||||   |||||
                               G  GTGG  GTGG   CTTTG
                                GG   GG   TT__
GAM224  PER2    3'  TTTTTGATGGAGGTGAAAT   43051         CTG  T
                               ATTTCACTTTCA   TC GAGA
                               ||||||||||||   || ||||
                               TAAAGTGGAGGT   AG TTTT
                                     ___  T
GAM224  PGAM1   3'  TTTCATGGCAGTGAAA     76276         _
                               TTTCACTGTC TGAGA
                               |||||||||| |||||
                               AAAGTGACGG ACTTT
                                     T
GAM224  PIGN    5'  GTCTCAGTCCTGTGCAAAGTGA 24672         _  TGT_
           GATG                  ATTTCACTTT CAC   CTGAGAT
                               |||||||||| |||   |||||||
                               TAGAGTGAAA GTG   GACTCTG
                                     C   TCCT
GAM224  PKP4    3'  GAAATGTGAAAGTGAAGTG   13266           TG_
                               CATTTCACTTTCAC   TC
                               ||||||||||||||   ||
                               GTGAAGTGAAAGTG   AG
                                        TAA
GAM224  PRDM2   3'  GTCTCGGAGAAACGGGTGAGCT 24250   T     TCACTG
           G                   CA TTCACTT     TCTGAGAT
                               || |||||||     ||||||||
                               GT GAGTGGG     AGGCTCTG
                                C      CAAAG_
GAM224  PSEN1   5'  ATAGTGGAGGCTGGGATG    23621    TT  _
                               CAT  CA CTTTCACTGT
                               |||  || ||||||||||
                               GTA  GT GGAGGTGATA
                                 GG  C
GAM224  RALB    3'  GTTTTGGAGGAGGGAGTGGAGT 11245       TT A  G  TG
                               ATTTCACT  C CT TC  AGAT
                               ||||||||  | || ||  ||||
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                                TGAGGTGA  G GG AG  TTTG
                                    GG A  _  GT
GAM224  RAMP3    3'  CGGTGAGATGGAGTG       19589        C
                                CATTTCA TTTCACTG
                                ||||||| ||||||||
                                GTGAGGT AGAGTGGC

                                _
GAM224  RANBP7   3'  ATTTTGGGGGGTGGGGGGGA   21113     A  TT   G  TG
                                TTC CT  CACT TC  AGAT
                                ||| ||  |||| ||  ||||
                                AGG GG  GTGG GG  TTTA
                                  _ GG   _ GT
GAM224  RGS19IP1 3'  GATGGTGAGGGGAGGTG     62509       A
                                CATTTC CTTTCACTGTC
                                |||||| ||||||||||
                                GTGGAG GGGAGTGGTAG

                                _
GAM224  RNASE1   3'  ATTTTGGGGGTGAAGAGTGGGT 63875    T      _   G  TG
           TG                     CA TTCACTTT CACT TC  AGAT
                                || |||||||| |||| ||  ||||
                                GT GGGTGAGA GTGG GG  TTTA
                                 T       A   _ GT
GAM224  RNGTT    3'  ATTTTGGACATTGTGAAGGAAA 13729       A  T  __   TG
           TG                     CATTTC CTT CAC  TGTC  AGAT
                                |||||| ||| |||  ||||  ||||
                                GTAAAG GAA GTG  ACAG  TTTA
                                   _  _  TT   GT
GAM224  RXRB     3'  CAGTGGTGGAGGTGGG      41758           T
                                TTCACTTTCACTG CTG
                                |||||||||||| |||
                                GGGTGGAGGTGGT GAC

                                _
GAM224  SEDL     3'  ATTCTGCAGTTGGGAGTGAAAT 27322         TT  _   CT   AT
           G                     CATTTCACT  CA CTGT  GAG
                                |||||||||  || ||||  |||
                                GTAAAGTGA  GT GACG  CTT
                                     GG  T   T_  A
GAM224  SH3BP4   3'  CAGTAGAGTGAGGTG      27232          C
                                CATTTCACTTT ACTG
                                |||||||||| ||||
                                GTGGAGTGAGA TGAC

                                _
GAM224  SIGLEC6  3'  ATTTTAAGACTGAAAGTGAAAT 59926          CT   _
                                ATTTCACTTTCA  GTCT GAGAT
                                |||||||||||  |||| |||||
                                TAAAGTGAAAGT  CAGA TTTTA
                                       __   A
GAM224  SLC17A2  5'  TTTAATGGTGAAGGTAAGTG  19546      C        C
                                CATTT ACTTTCACTGT TGAG
                                ||||| |||||||||| ||||
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                                GTGAA TGGAAGTGGTA ATTT
                                  _       _
GAM224  SLC19A1  5'  GTCTCGGGGCCCTGGGGTGAG  11758       T  CT   _
                                TTCACTT CA  GTCT GAGAT
                                ||||||| ||  |||| |||||
                                GAGTGGG GT  CGGG CTCTG
                                    _ CC    G
GAM224  SLC38A2  3'  TCTCGGGTTAAGGGAAGTG   38593       A  G__
                                CACTTTC CT   TCTGAGA
                                ||||||| ||   |||||||
                                GTGAAGG GA   GGGCTCT
                                    _ ATT
GAM224  SLC6A4   3'  TTTTGGACGTGTGAGGATG   6452     CT    _   TG
                                CA  TTCAC TGTC  AGA
                                ||  ||||| ||||  |||
                                GT  GAGTG GCAG  TTT
                                 AG    T    GT
GAM224  SLC7A8   3'  GTCTTGGGGCAGGGTGAAA   24282       TTCA   _ TG
                                TTTCACT    CTGT C  AGAT
                                |||||||    |||| |  ||||
                                AAAGTGG    GACG G  TCTG
                                    _____   G GT
GAM224  SMARCB1  3'  TCGGGTGGGGGTGGAGTG    65586        TT   TGT
                                CATTTCACT  CAC   CTGA
                                |||||||||  |||   ||||
                                GTGAGGTGG  GTG   GGCT
                                     GG  ___
GAM224  SNCA     3'  TTAATTATTGAAAGTGGGGTG  4433     TT      C  TC
                                CAT  CACTTTCA TG  TGA
                                |||  |||||||| ||  |||
                                GTG  GTGAAAGT AT  ATT
                                  GG       T  TA
GAM224  SRRM2    3'  TTTGGGGTGGGAGGGAATG   32918       A  TT    GT TG
                                CATTTC CT  CACT  C  AG
                                ||||||  ||  ||||  |  ||
                                GTAAGG GA  GTGG  G  TT
                                    _  GG    __ GT
GAM224  SSPN     3'  GTCTTAGAAGAAAGTGGAAT   17445          ACTG
                                ATTTCACTTTC    TCTGAGAT
                                ||||||||||    ||||||||
                                TAAGGTGAAAG    AGATTCTG
                                     A___
GAM224  STAR     3'  ATCTCCATCTGGTGACAGTGGG 4443     TT    T    GTCT_
            ATG                   CAT  CACT TCACT    GAGAT
                                |||  |||| |||||    |||||
                                GTA  GTGA AGTGG    CTCTA
                                  GG   C    TCTAC
GAM224  T        3'  GTCTCAGGTTAAGAAGGAAATG 12077       A    CACTG
                                CATTTC CTTT    TCTGAGAT
                                |||||| ||||    ||||||||
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                                GTAAAG GAAG    GGACTCTG
                                   _   AATT_
GAM224  TAF1C    3'  TGGTGAGGGTGGAGTG     19060
                                CATTTCACTTTCACTG
                                ||||||||||||||||
                                GTGAGGTGGGAGTGGT

GAM224  TIMP3    3'  GTTTTAGTGTCAAAAGTGAGAT 4517          CACTGT
              G                  CATTTCACTTT    CTGAGAT
                                ||||||||||     |||||||
                                GTAGAGTGAAA    GATTTTG
                                      ACTGT_
GAM224  TMOD4    5'  TACCACACAGTGGGAGGGGGTG 25331    TT A  TT    C  AGAT
                                CAT  C CT  CACTGT TG
                                |||  | ||  |||||| ||
                                GTG  G GA  GTGACA AC
                                  GG _  GG     C  CATG
GAM224  TNFRSF4  3'  ATCTTGGCCAGGGTGGAGTG   12451       TTCA   T TG
                                CATTTCACT    CTG C  AGAT
                                |||||||||    ||| |  ||||
                                GTGAGGTGG    GAC G  TCTA
                                     _____  C GT
GAM224  TRH      3'  CAGCCAGTGAGGGTGGGGGTG   23051    TT        T
                                CAT  CACTTTCACTG CTG
                                |||  |||||||||||| |||
                                GTG  GTGGGAGTGAC GAC
                                  GG         C
GAM224  TRHDE    3'  TTTTGGGCAATGTGAGAG    25393       __   TG
                                CTTTCAC  TGTC  AGA
                                |||||||  ||||  |||
                                GAGAGTG  ACGG  TTT
                                    TA    GT
GAM224  TRIM9    3'  GTTTCAAATGGGTGGTGGGGTG 53761    TT    TTCA    C
                                CAT  CACT    CTGT TGAGAT
                                |||  ||||    |||| ||||||
                                GTG  GTGG    GGTA ACTTTG
                                  GG   TG__    A
GAM224  TSG      3'  ATTTCCTACTGTGAGTGGAGTG 40231        TT    T  CT
                                CATTTCAC  TCAC GT  GAGAT
                                ||||||||  |||| ||  |||||
                                GTGAGGTG  AGTG CA  CTTTA
                                     __    T  TC
GAM224  TSLP     5'  TTTAGTGTGAAACTGGGGTG   52310    TT  C     TGT
                                CAT  CA TTTCAC   CTGAG
                                |||  || ||||||   |||||
                                GTG  GT AAAGTG   GATTT
                                  GG  C     T__
GAM224  VDAC1    3'  TTTGGGGTGGAGAAGGTGGA   12583         A TG   G   T
                                TTCACTTTC C  TCT AGA
                                |||||||||  |  ||| |||
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                                AGGTGGAAG G  GGG TTT
                                     A GT   G   T
GAM224  VDR      3'  TCTTTGTGAGAGTGAGCTG   4571     T        TGTCT
                                CA TTCACTTTCAC    GAGA
                                || ||||||||||    ||||
                                GT GAGTGAGAGTG    TTCT
                                 C         T____
GAM224  WNT10B   3'  GGGTGGTGGGGGTCAGGTG   12675      C   TT   TG
                                CATTT ACT  CAC  TCT
                                ||||| |||  |||  |||
                                GTGGA TGG  GTG  GGG
                                   C   GG   GT
GAM224  ZNF239   5'  GTCAGGATAATGGTGGGAATGG 19042   TT  C TT    ____    GAT
           GGTG                    CA T  CACTGT   CTGA
                                 || |  ||||||   ||||
                                 GT A  GTGGTA    GACT
                                GG  A GG     ATAG    G
GAM224  AKAP6    5'  GTTTTGGAAAGAAGTGAGGT   14996        CACTG  TG
                                ATTTCACTTT    TC  AGAT
                                ||||||||||    ||  ||||
                                TGGAGTGAAG    AG  TTTG
                                      AA___  GT
GAM224  APXL2    3'  TAGGTGGAGAGGGTGGGGTG   75196    TT      A TG
                                CAT  CACTTTC C  TCTG
                                |||  ||||||| |  ||||
                                GTG  GTGGGAG G  GGAT
                                  GG      A GT
GAM224  ARFGAP3  3'  ATCTCAGGCGGCAGTGAAGT   27385       TTCA
                                ATTTCACT   CTGTCTGAGAT
                                ||||||||   ||||||||||
                                TGAAGTGA   GGCGGACTCTA
                                     C___
GAM224  ARHGEF9  3'  TTTTAGGTACTGTGAAGG    30827       __ GT
                                CTTTCAC  T  CTGAGA
                                |||||||  |  ||||||
                                GGAAGTG  A  GATTTT
                                    TC TG
GAM224  ARHGEF9  3'  TTTTGGGGAAGTGAAAT     30829         ACTGT TG
                                ATTTCACTTTC    C  AGA
                                ||||||||||    |  |||
                                TAAAGTGAAGG    G  TTT
                                      _____ GT
GAM224  BCL2L1   3'  GTCTGTGTGAAGGTGAAA    56807         TGTCTG
                                TTTCACTTTCAC     AGAT
                                ||||||||||||     ||||
                                AAAGTGGAAGTG     TCTG
                                       TG____
GAM224  C19orf7  3'  AGACAGTGAGAGTGAAA     61124
                                TTTCACTTTCACTGTCT
                                |||||||||||||||||
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                                AAAGTGAGAGTGACAGA

GAM224  C1orf17   3'  TTTCAGAGTGGGGAAGTG    68219        A  _
                                CACTTTC CTG TCTGAGA
                                ||||||| ||| |||||||
                                GTGAAGG GGT AGACTTT
                                    _  G
GAM224  C1orf34   3'  GCAGTGAGGGTGAGCTG     60673    T
                                CA TTCACTTTCACTGT
                                || ||||||||||||||
                                GT GAGTGGGAGTGACG
                                 C
GAM224  C20orf151 3'  TCTGGCAGTGAGGGTGGAG    88703             T
                                TTTCACTTTCACTGTC GA
                                |||||||||||||||| ||
                                GAGGTGGGAGTGACGG CT
                                          T
GAM224  C20orf21  3'  TCTCAGGACAAGTGGAAG     35117        _  _
                                CTTTCACT GTC TGAGA
                                |||||||| ||| |||||
                                GAAGGTGA CAG ACTCT
                                     A  G
GAM224  C20orf29  3'  GTCTCAGACTCCCCTGAGGGTG 37129          CT___
           GAG                     TTTCACTTTCA    GTCTGAGAT
                                |||||||||||    |||||||||
                                GAGGTGGGAGT    CAGACTCTG
                                      CCCCT
GAM224  C20orf60  3'  TAGGGGTGGGGGTGGGATG    53738    TT   TT   G
                                CAT  CACT  CACT TCTG
                                |||  ||||  |||| ||||
                                GTA  GTGG  GTGG GGAT
                                  GG   GG   _
GAM224  C22orf5   5'  GACAGTGAGGGGGGATG     24342     TT A
                                CAT  C CTTTCACTGTC
                                |||  | ||||||||||
                                GTA  G GGGAGTGACAG
                                  GG _
GAM224  C8orf2    3'  ATAGTGAAAGTAAGATG     23157      C
                                CATTT ACTTTCACTGT
                                ||||| ||||||||||
                                GTAGA TGAAAGTGATA
                                   A
GAM224  CCR5      3'  ATTTCAGACTGAATGGGGGTGG 5147    TT   TT  CT__
           GG                     T  CACT  CA   GTCTGAGAT
                                |  ||||  ||   |||||||||
                                G  GTGG  GT   CAGACTTTA
                                 GG   GG  AAGT
GAM224  CCR6      3'  TCTCTTCAGGGTGGGGTG    48589    TT   TTCA   TCT
                                CAT  CACT   CTG   GAGA
                                |||  ||||   |||   ||||
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                                GTG  GTGG   GAC   CTCT
                                  GG   ____   TT_
GAM224  CCR6    3'  TCTCTTCAGGGTGGGGTG   15173    TT   TTCA   TCT
                                CAT  CACT   CTG   GAGA
                                |||  ||||   |||   ||||
                                GTG  GTGG   GAC   CTCT
                                  GG   ____   TT_
GAM224  CECR7   5'  ATAGTGGGAATGAAATG    79615       C TT
                                CATTTCA T  CACTGT
                                |||||||  |  ||||||
                                GTAAAGT A  GTGATA
                                    A GG
GAM224  CENTA2  3'  TCTCAGATGGCTGAAATGT   37269    _    _
                                AC TTTCA CTGTCTGAGA
                                || ||||| ||||||||||
                                TG AAAGT GGTAGACTCT
                                 T    C
GAM224  CEP3    3'  ATCTTGGCAAAAAAAGGAAGTG 21247      A   CAC  T TG
                                CATTTC CTTT   TG C  AGAT
                                ||||||  ||||   ||  |  ||||
                                GTGAAG GAAA   AC G  TCTA
                                   _   AAA  _ GT
GAM224  CHSY1   3'  TTGGGGACAAAAGTGAAATG   29905        CAC    GA  T
                                CATTTCACTTT   TGTCT  GA
                                ||||||||||   |||||  ||
                                GTAAAGTGAAA   ACAGG  TT
                                      ___    GG  T
GAM224  CNNM2   3'  GGACAGTGAGGGAGGAATG   34461      A
                                CATTTC CTTTCACTGTCT
                                ||||||  ||||||||||||
                                GTAAGG GGGAGTGACAGG
                                   A
GAM224  COLEC10 3'  TTTCAGACCATGTGGAATG   21230       TTTCACT
                                CATTTCAC      GTCTGAGA
                                ||||||||      ||||||||
                                GTAAGGTG      CAGACTTT
                                     TAC____
GAM224  CRR9    3'  ATTTCAGGTGGTTTTCTAAGTG 47878      TC___  TG
                                CACTT    AC  TCTGAGAT
                                |||||    ||  ||||||||
                                GTGAA    TG  GGACTTTA
                                   TCTTT  GT
GAM224  CYYR1   3'  ATTTTAGGTGGGTGTGAAGTG  53670       TTTCA TG
                                CATTTCAC    C  TCTGAGAT
                                ||||||||    |  ||||||||
                                GTGAAGTG    G  GGATTTTA
                                     TG___ GT
GAM224  DAPK3   3'  GTCGTGGGACGGGGAGGGTGGG 7211     TT     A     GA_
            ATG                   CAT  CACTTTC CTGTCT   GAT
                                |||  ||||||| ||||||   |||
```

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                                GTA  GTGGGAG GGCAGG   CTG
                                  GG      G     GTG
GAM224   DDX8     3'  GGATGGGAAGGTGGAGTG    17053           A
                                CATTTCACTTTC CTGTCT
                                |||||||||||| ||||||
                                GTGAGGTGGAAG GGTAGG
                                          _
GAM224   DKFZp434B217 3'  GGGTTTGGGCGGGAGTGGGCTG 70701    T      TCA     TG  AT
                                CA TTCACTT   CTGTC  AG
                                || |||||||   |||||  ||
                                GT GGGTGAG   GGCGG  TT
                                 C       ___     GT  GGGT
GAM224   DKFZP434K028 3'  CTTACAGTGGAGGTAAAGTG   93231       C         CT
                                CATTT ACTTTCACTGT  GAG
                                ||||| ||||||||||  |||
                                GTGAA TGGAGGTGACA  TTC
                                   A         __
GAM224   DKFZp434O0320 3'  GGTGGCAGGTGGAGTG      83696          _
                                CATTTCACTT TCACT
                                |||||||||| |||||
                                GTGAGGTGGA GGTGG
                                      C
GAM224   DKFZP434O047 5'  ATTTTGGACAAGGTGCTGAAGT 31503        CTTT   __   TG
   G                             CATTTCA    CACT  GTC  AGAT
                                |||||||    ||||  |||  ||||
                                GTGAAGT    GTGG  CAG  TTTA
                                    C___    AA   GT
GAM224   DKFZp547F072 5'  TCCATGGGCGGGGGTGGGGTG  50094     TT    TT A  GTC  A  T
                                CAT  CACT  C CT   TG GA
                                |||  ||||  | ||   || ||
                                GTG  GTGG  G GG   AC CT
                                  GG    GG C  GT_  _  T
GAM224   DKFZP564C103 3'  TCTTAGATAAGTAAGGTG    31612       C  _
                                CACTTT ACT GTCTGAGA
                                |||||| ||| ||||||||
                                GTGGAA TGA TAGATTCT
                                   _   A
GAM224   DKFZP564I052 3'  GTTTTAGGTGGTGATCTTAAAT 66718      CACTT    TG
   G                             CATTT     TCAC  TCTGAGAT
                                |||||     ||||  |||||||||
                                GTAAA     AGTG  GGATTTTG
                                   TTCT_    GT
GAM224   DKFZP564I052 3'  GTTTTGAGAGGGGAGTAGAAGT 66719       _  TT A  G  T
   G                             CATTTC ACT  C CT TC GAGAT
                                |||||| |||  | || || |||||
                                GTGAAG TGA  G GA AG TTTTG
                                   A   GG _  G  _
GAM224   DKFZP566G1424 3'  ATTTTGGACTCAGTGAAAGTG  84773          __   TG
                                CACTTTCACT  GTC  AGAT
                                ||||||||||  |||  ||||
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                                GTGAAAGTGA  CAG  TTTA
                                      CT   GT
GAM224  DKFZp761N1114 3'  GTTTCAGAAAGCTGGGTGGTGG 79022      _   _ G
                                TCACT TTCA CT TCTGAGAT
                                ||||| |||| || ||||||||
                                GGTGG GGGT GA AGACTTTG
                                   T   C  A
GAM224  DKFZp762P2111 3'  GTCTCAGGTGTTCTGGGGATG  86361     TT ACTTT   TGT
                                CAT  C    CAC   CTGAGAT
                                |||  |    |||   |||||||
                                GTA  G    GTG   GACTCTG
                                  GG GTCTT  ___
GAM224  DKFZp762P2111 3'  TGAGAAACAGTGGAGTGGAGTG 86365          T     CTGAGAT
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTGAGGTGAG GTGACA
                                      _     AAGAGTA
GAM224  DMRTA2   3'  GTTTTGTTTAGGAGGGTGGG   60660         A   TC
                                TTCACTTTC CTG  TGAGAT
                                ||||||||| |||  ||||||
                                GGGTGGGAG GAT  GTTTTG
                                      _  TT
GAM224  DRIL2    3'  ATCGTGGGGGCGGGGAGGTGGA 21322          A     GA__
           GTG                    ATTTCACTTTC CTGTCT    GAT
                                ||||||||||| ||||||    |||
                                TGAGGTGGAGG GGCGGG    CTA
                                      _     GGTG
GAM224  EAT2     3'  TCAGGTGAAGGTGAGG      79281           TGT
                                TTTCACTTTCAC   CTGA
                                ||||||||||||   ||||
                                GGAGTGGAAGTG   GACT
                                      ____
GAM224  EPS8R1   5'  TAGAACATGAAGGTGGGATG   34803     TT       C  _
                                CAT  CACTTTCA TGT CTG
                                |||  |||||||| ||| |||
                                GTA  GTGGAAGT ACA GAT
                                  GG       _  A
GAM224  FBXL3B   5'  ATCTTCTGTATGTAGGAGGTGG 24070          _ TGTCT_
           AATG                    ATTTCACTTTC AC     GAGAT
                                ||||||||||| ||     |||||
                                TAAGGTGGAGG TG     TTCTA
                                      A  TATGTC
GAM224  FHX      3'  TCAAGGGTGAAAGTGATGATG  37307      _        GTC
                                CATT TCACTTTCACT   TGA
                                |||| ||||||||||   |||
                                GTAG AGTGAAAGTGG   ACT
                                  T         GA_
GAM224  FKSG42   3'  GTCTCAGGGTGGGAAGTGGGA  49335   TT      _  GT
                                T  CACTTTC ACT  CTGAGAT
                                |  ||||||| |||  |||||||
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                                A  GTGAAGG TGG  GACTCTG
                                 GG      G  __
GAM224  FLJ00024  3'  GTCTTGGGAGAAGGGTGAGG  63765        CA  G  TG
                                TTTCACTTT  CT TC  AGAT
                                |||||||||  || ||  ||||
                                GGAGTGGGA  GA GG  TCTG
                                     A_  _  GT
GAM224  FLJ10052  3'  ATCTCAGGCTCCACAGTGAGG  35771       TTCACT
                                TTTCACT     GTCTGAGAT
                                |||||||     |||||||||
                                GGAGTGA     CGGACTCTA
                                    CACCT_
GAM224  FLJ11506  3'  TGGGTGGGGAAGTGAAATG   45115          A TG
                                CATTTCACTTTC C  TCTG
                                ||||||||||||| |  ||||
                                GTAAAGTGAAGG G  GGGT
                                       _ GT
GAM224  FLJ12056  3'  TTTGGGGGCAGGGAGGTTGGGT 46258     TC     A     GA  T
          G                      CATT  ACTTTC CTGTCT  GA
                                ||||  |||||| ||||||  ||
                                GTGG  TGGAGG GACGGG  TT
                                  GT     _     GG  TT
GAM224  FLJ12121  3'  GTTTTGGACAGTCATTTGGAAT 46458      CTTTC     TG
                                ATTTCA    ACTGTC  AGAT
                                ||||||    ||||||  ||||
                                TAAGGT    TGACAG  TTTG
                                   TTAC_     GT
GAM224  FLJ12547  3'  ATCTCAGCCAGAGAGAGTGAAC 46489    T       A   T
          TG                     CA TTCACTTTC CTG CTGAGAT
                                || |||||||| ||| |||||||
                                GT AAGTGAGAG GAC GACTCTA
                                 C        A   C
GAM224  FLJ12581  3'  TCTCATGGAGGGTGGAGT    45881          ACTGTC
                                ATTTCACTTTC     TGAGA
                                ||||||||||     |||||
                                TGAGGTGGGAG     ACTCT
                                       GT____
GAM224  FLJ12787  3'  TTTCAGGTCAGAGGAA      49756      A  _
                                TTTC CTG TCTGAGA
                                |||| ||| |||||||
                                AAGG GAC GGACTTT
                                  A   T
GAM224  FLJ12891  3'  ACTGTGGAGGTGGAGTG     46335           T
                                CATTTCACTTTCAC GT
                                |||||||||||||| ||
                                GTGAGGTGGAGGTG CA
                                         T
GAM224  FLJ13072  5'  GACAGTGAGAGTGAAA      89814
                                TTTCACTTTCACTGTC
                                ||||||||||||||||
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                                AAAGTGAGAGTGACAG

GAM224  FLJ13852  3'  TGGGCAGTGGTAGGTGGGGTG  43579     TT    _
                                CAT  CACTT TCACTGTCTG
                                |||  ||||| ||||||||||
                                GTG  GTGGA GGTGACGGGT
                                  GG    T
GAM224  FLJ14107  3'  GCAGGGGAGGTGAAATG     46693           A
                                CATTTCACTTTC CTGT
                                |||||||||||| ||||
                                GTAAAGTGGAGG GACG
                                       G
GAM224  FLJ14346  3'  GGCAGGGAAGTGAGATG     46714           A
                                CATTTCACTTTC CTGTC
                                |||||||||||| |||||
                                GTAGAGTGAAGG GACGG

                                       _
GAM224  FLJ14502  3'  GTTTTGGGCTTAATAAATGGGG 62717     TT  C  TCACT   TG
          TG                      CAT  CA TT    GTC  AGAT
                                |||  || ||    |||  ||||
                                GTG  GT AA    CGG  TTTG
                                  GG  A  TAATT   GT
GAM224  FLJ14641  5'  CGGGGAAGTGGAATG       51483           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAGGTGAAGG GGC

                                       _
GAM224  FLJ14743  3'  GCTCTGGGGTGGGGGTGGGGTG 68064     TT   TT   G  T   AT
                                CAT  CACT  CACT TC GAG
                                |||  ||||  |||| || |||
                                GTG  GTGG  GTGG GG CTC
                                  GG   GG   _  T   GT
GAM224  FLJ20034  3'  TTTGTACGTGAGGGTGGA    34392           T  CT
                                TTCACTTTCAC GT  GAG
                                |||||||||| ||  |||
                                AGGTGGGAGTG CA  TTT
                                       _ TG
GAM224  FLJ20043  3'  GTTTTGGGAAAGGAGTGGGAT  34406    TT     CACTG  TG
                                AT  CACTTT    TC  AGAT
                                ||  ||||||    ||  ||||
                                TA  GTGAGG    GG  TTTG
                                 GG     AAA__  GT
GAM224  FLJ20306  3'  GAAGGTGGAGGTGGAA      34916           G
                                TTTCACTTTCACT TC
                                |||||||||||| ||
                                AAGGTGGAGGTGG AG
                                       A
GAM224  FLJ20340  3'  TTGGAGTGGAGTGGGGTG    34980     TT    T   TG  TG
                                CAT  CACTT CAC  TC  A
                                |||  ||||| |||  ||  |
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                                GTG  GTGAG GTG  AG  T
                                  GG    _  __  GT
GAM224  FLJ20400  3'  TTCTTGACTGAAGGTGAGATG  66514          CT   T   T
                                CATTTCACTTTCA  GTC GAGA
                                |||||||||||||  ||| ||||
                                GTAGAGTGGAAGT  CAG TTCT
                                       __  _   TT
GAM224  FLJ20729  3'  GTCTTGGAGTGCAAGTGGTATG 35649    T    T  TG  TG
                                CAT TCACTT CAC  TC  AGAT
                                ||| |||||| |||  ||  ||||
                                GTA GGTGAA GTG  AG  TCTG
                                  T    C  __ GT
GAM224  FLJ21125  3'  GTTTGGATGCAGGAAGGTGGGA 44892    TT     A   __ TG  AT
          TG                    CAT  CACTTTC CTGT  C  AG
                                |||  ||||||| ||||  |  ||
                                GTA  GTGGAAG GACG  G  TT
                                  GG     _   TA GT  G
GAM224  FLJ21162  3'  TCTTGGGCTGGGTGCAGTG   45896     TT   __  TG
                                CACT  CACT  GTC  AGA
                                ||||  ||||  |||  |||
                                GTGA  GTGG  CGG  TCT
                                  C_   GT   GT
GAM224  FLJ21324  5'  ATCTGCAGGTGGAAGGAGGTG  91189      A     TGT  _
                                CATTTC CTTTCAC   CTG AGAT
                                ||||||| |||||||   ||| ||||
                                GTGGAG GAAGGTG   GAC TCTA
                                   _     ___  G
GAM224  FLJ21736  3'  TTTCAGATGGAAGTGAGA    46234          CTG
                                TTTCACTTTCA   TCTGAGA
                                ||||||||||   |||||||
                                AGAGTGAAGGT   AGACTTT
                                      ___
GAM224  FLJ22378  3'  GTCTCGGGTCCAGGGAGTGGAG 46905        TT ACTG
                                TTTCACT  C    TCTGAGAT
                                |||||||  |   ||||||||
                                GAGGTGA  G    GGGCTCTG
                                    GG ACCT
GAM224  FLJ22659  5'  GTGGTGAAGGTTAAATG     46261      C       TG
                                CATTT ACTTTCAC  T
                                |||||  ||||||||  |
                                GTAAA TGGAAGTG  G
                                   T       GT
GAM224  FLJ23059  3'  ATCTCAGAACAGAAGGGTGGGA 49933    TT     CA   _
                                T  CACTTT  CTGT CTGAGAT
                                |  ||||||  |||| |||||||
                                A  GTGGGA  GACA GACTCTA
                                 GG     A_   A
GAM224  FLJ23091  3'  ACCTCATGTGGGGGTGGGGTG  46124    TT   TT  TGTC   AT
                                CAT  CACT  CAC    TGAG
                                |||  ||||  |||   ||||
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                                GTG  GTGG  GTG   ACTC
                                  GG   GG  T___   CAA
GAM224  FLJ23185  3'  TTTCAGGCAGGTGGAG     46837     CA
                                CTTT  CTGTCTGAGA
                                ||||  ||||||||||
                                GAGG  GACGGACTTT
                                  TG
GAM224  FLJ23309  3'  ATCTTGGGTGATGGAGGAAATG 46061       A   T  C GT TG
                                CATTTC CTT CA T  C  AGAT
                                |||||| ||| || |  |  ||||
                                GTAAAG GAG GT G  G  TCTA
                                   _  _  A TG GT
GAM224  FLJ23476  3'  GTCTCAGGTGGCTGCGTGTGGT 44962     TT   TTT  _ TG
           G                     CAT  CAC   CA C  TCTGAGAT
                                |||  |||   || |  ||||||||
                                GTG  GTG   GT G  GGACTCTG
                                  GT   C__  C GT
GAM224  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM224  FLJ23556  3'  GTTTTAATAAGGGAGGTGGAA  45956         A  GTC
                                TTTCACTTTC CT   TGAGAT
                                |||||||||| ||   ||||||
                                AAGGTGGAGG GA   ATTTTG
                                     _  ATA
GAM224  FLJ31762  3'  TCTTCTGGGGGTGAGATG    58145        TT  CTGTCT
                                CATTTCACT  CA     GAGA
                                |||||||||  ||     ||||
                                GTAGAGTGG  GT     TTCT
                                     GG  C_____
GAM224  FTSJ3     3'  GTCTGAAGAACAGTGAGGTGGA 34455         T     _  G_
           GTG                    ATTTCACTT CACTGT CT  AGAT
                                |||||||||  ||||||  ||  ||||
                                TGAGGTGGA GTGACA GA  TCTG
                                     _     A  AG
GAM224  G4        5'  ATCTCAGATTGTGGGGGTGTGG 90991       _   TT   T
           ATG                    CATTT CACT  CAC GTCTGAGAT
                                |||||  ||||  |||  |||||||||
                                GTAGG GTGG  GTG TAGACTCTA
                                   T   GG   T
GAM224  GBTS1     3'  ATTTTGGGGAGTGGGTGATATG 59050     T    TT   G  TG
                                CAT TCACT  CACT TC  AGAT
                                |||  |||||  ||||  ||  ||||
                                GTA AGTGG  GTGA GG  TTTA
                                  T    __   G  GT
GAM224  GBTS1     3'  TTAGTGAGGGAAGGTGAGATG  59064          A  GT_
                                CATTTCACTTTC CT   CTGA
                                ||||||||||||  ||   ||||
```

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                                GTAGAGTGGAAG GG   GATT
                                      _ AGT
GAM224  GK001    3' TTTCTGGTGGGAGTGGGGTG  39503    TT   TT    TCT   T
                                CAT  CACT  CACTG   GAGA
                                |||  ||||  |||||   ||||
                                GTG  GTGA  GTGGT   CTTT
                                  GG   GG    ___    T
GAM224  GPS2     5' GTCTTTGAGGTGAAAGTGGAA 15671          G  T
                                TTTCACTTTCACT TC GAGAT
                                |||||||||||| || |||||
                                AAGGTGAAAGTGG AG TTCTG
                                      _ T
GAM224  GPT2     3' TTTCAGATCTGGAGAAATG   55962      ACT   CT
                                CATTTC   TTCA  GTCTGAGA
                                ||||||   ||||  ||||||||
                                GTAAAG   AGGT  TAGACTTT
                                   ___   C_
GAM224  GRSF1    3' ATTTTAGAACAAGTAGGGGTG 9139      TC  _ _
                                CACTT  ACT GT CTGAGAT
                                |||||  ||| || |||||||
                                GTGGG  TGA CA GATTTTA
                                   GA   A  A
GAM224  HBXAP    5' CAGTGAAATGAAGTG      33420       C
                                CATTTCA TTTCACTG
                                ||||||| ||||||||
                                GTGAAGT AAAGTGAC
                                      _
GAM224  HIC      5' GTTTCAGGATTGTAGGAGTGGA 67452        TC  TG_
           A                     TTTCACTT  AC   TCTGAGAT
                                ||||||||  ||   ||||||||
                                AAGGTGAG  TG   GGACTTTG
                                     GA  TTA
GAM224  HIF1AN   3' ATCTATTCAGTGGGAGTGGGGT 61968    TT   TT    TCTG
                                AT  CACT  CACTG    AGAT
                                ||  ||||  |||||    ||||
                                TG  GTGA  GTGAC    TCTA
                                 GG   GG    TTA_
GAM224  HSF2     3' TCGGGGGTGGGATGGGATG   15710     TT  C TT   G
                                CAT  CA T  CACT TCTGA
                                |||  || |  |||| |||||
                                GTA  GT A  GTGG GGGCT
                                  GG  _ GG   _
GAM224  HSPC054  3' TTTTACAGCTGTGGAAAGTGAA 26264          _  T T   _   T
           GTG                    ATTTCACTTTC AC G CTG AGA
                                ||||||||||| || | ||| |||
                                TGAAGTGAAAG TG C GAC TTT
                                      G  T _   A   TG
GAM224  HXCP2    3' ATCTCAGTTTGGGAAGTGGGAT 50832     TT      ACTGT
           G                     CAT  CACTTTC    CTGAGAT
                                |||  |||||||    |||||||
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                                GTA  GTGAAGG    GACTCTA
                                  GG      GTTT_
GAM224  HYPK     3'  TCTTGGGTCAAGTAGAGTG   33080       C  _ _  TG
                                CACTTT ACT G TC  AGA
                                |||||| ||| | ||  |||
                                GTGAGA TGA C GG  TCT
                                   _  A T  GT
GAM224  IL18BP   3'  TCTTGGGCAGAGGAGGTG    19113       A    TG
                                CACTTTC CTGTC  AGA
                                ||||||| |||||  |||
                                GTGGAGG GACGG  TCT
                                    A    GT
GAM224  IL22R    3'  GTGGTGAAGATGAAATG     41192       C     TG
                                CATTTCA TTTCAC  T
                                ||||||| ||||||  |
                                GTAAAGT GAAGTG  G
                                    A     GT
GAM224  IMAGE3451454 3'  GTTTTAGCCAAAAGTGAAAT   53873         CAC  T
                                ATTTCACTTT   TG CTGAGAT
                                ||||||||||   || |||||||
                                TAAAGTGAAA   AC GATTTTG
                                     ___  C
GAM224  KIAA0092  3'  ATTTTGGAATAAAGTGAGA   27967        CACTG  TG
                                TTTCACTTT    TC  AGAT
                                |||||||||    ||  ||||
                                AGAGTGAAA    AG  TTTA
                                     TA___  GT
GAM224  KIAA0174  5'  ATTTTGGATGGTGAACCCTGAA 78592       CT_       TG
           GT                    ATTTCA   TTCACTGTC  AGAT
                                ||||||   |||||||||  ||||
                                TGAAGT   AAGTGGTAG  TTTA
                                   CCC       GT
GAM224  KIAA0212  3'  GTGAGACCGTGGTGAAAGGGGG 27940   TT A      ___    GAGAT
           ATG                    T  C CTTTCACT   GTCT
                                |  | ||||||||   ||||
                                A  G GAAAGTGG   CAGA
                                 GG G       TGC    GTG
GAM224  KIAA0284  3'  TGGTGGGGGTGGACGTG     63119     _     TT
                                CAT TTCACT  CACTG
                                ||| ||||||  |||||
                                GTG AGGTGG  GTGGT
                                  C     GG
GAM224  KIAA0285  5'  GGCAGTGGAGGTGAGA      29020
                                TTTCACTTTCACTGTC
                                ||||||||||||||||
                                AGAGTGGAGGTGACGG

GAM224  KIAA0419  5'  ATTTCAGATAGTGTGTGA    28187      TTT
                                TCAC   CACTGTCTGAGAT
                                ||||   ||||||||||||
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                                AGTG  GTGATAGACTTTA
                                  T__
GAM224  KIAA0426 3' GTTTTAGATGGTGTTACTGAGA 28261      CTTT
                                TTTCA   CACTGTCTGAGAT
                                |||||   ||||||||||||||
                                AGAGT   GTGGTAGATTTTG
                                   CATT
GAM224  KIAA0453 3' GTCTTGCTGGGGGGTGGTGATG 69049     _    TT ACT  CT
                                CATT TCACT  C   GT  GAGAT
                                |||| |||||  |   ||  |||||
                                GTAG GGTGG  G   CG  TTCTG
                                  T    GG GT_  __
GAM224  KIAA0459 3' ATTTCAGATGGGATGCAGGTG  60983      T  __
                                CACTT CA  CTGTCTGAGAT
                                |||||| ||  ||||||||||
                                GTGGA GT  GGTAGACTTTA
                                   C  AG
GAM224  KIAA0523 3' ATCTTGGGCTCACAAGTGAGG  67728       TCACT   TG
                                TTTCACTT    GTC  AGAT
                                ||||||||    |||  ||||
                                GGAGTGAA    CGG  TCTA
                                     CACT_   GT
GAM224  KIAA0552 3' GTTTTGGGGGGCAAGGTGGAG  28320        CA  G  TG
                                TTTCACTTT  CT TC  AGAT
                                |||||||||  || ||  ||||
                                GAGGTGGAA  GG GG  TTTG
                                     C_  G  GT
GAM224  KIAA0660 3' GTTTCAGGCAGGAGTGGGGT   24515    TT    TCA
                                AT  CACTT   CTGTCTGAGAT
                                ||  |||||   ||||||||||||
                                TG  GTGAG   GACGGACTTTG
                                 GG    ____
GAM224  KIAA0759 3' GTTTCTGTTTTGAAAGTGAAAT 67329           CTGTCT
           G                     CATTTCACTTTCA     GAGAT
                                ||||||||||||||     |||||
                                GTAAAGTGAAAGT     CTTTG
                                       TTTGT_
GAM224  KIAA0795 3' ATTTCAGGGAAGAGGTGGGAT  46588    TT     CA  GT
                                AT  CACTTT  CT  CTGAGAT
                                ||  ||||||  ||  |||||||
                                TA  GTGGAG  GG  GACTTTA
                                 GG     AA  __
GAM224  KIAA0830 3' ATTTCAGCAGTGTGAAGGTAAA 69694      CA   _    T
           TG                    CATTT  CTTT CACTG CTGAGAT
                                |||||  |||| ||||| |||||||
                                GTAAA  GAAG GTGAC GACTTTA
                                   TG   T    _
GAM224  KIAA0871 3' ATTTCAGAATAGGAAGTAAATG 30299      C     ACTG
                                CATTT ACTTTC    TCTGAGAT
                                ||||| ||||||    ||||||||
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                                GTAAA TGAAGG    AGACTTTA
                                  _     ATA_
GAM224  KIAA0893  3'  GTTTCAGGCTAAAAGGTAAATG 30360      C    CACT
                                CATTT ACTTT    GTCTGAGAT
                                ||||| |||||    |||||||||
                                GTAAA TGGAA    CGGACTTTG
                                  _    AAT_
GAM224  KIAA0918  3'  GTTTCAACGTTTAGGGTGAAGT 73134          CAC   C
          G                      CATTTCACTTT   TGT TGAGAT
                                ||||||||||   ||| ||||||
                                GTGAAGTGGGA   GCA ACTTTG
                                      TTT   _
GAM224  KIAA0931  3'  ATCTCAGACTAATGGGGTGTGA 67412     _ TT  CT_
                                TCAC T  CA   GTCTGAGAT
                                |||| |  ||   |||||||||
                                AGTG G  GT   CAGACTCTA
                                  T GG  AAT
GAM224  KIAA0934  3'  GGCATGGGGGTGAAATG     64223        TT  C
                                CATTTCACT  CA TGTC
                                |||||||||  || ||||
                                GTAAAGTGG  GT ACGG
                                     GG  _
GAM224  KIAA0978  3'  CTCGACGTGAGGGTGAAATG   70480           T   T
                                CATTTCACTTTCAC GTC GAG
                                |||||||||||||| ||| |||
                                GTAAAGTGGGAGTG CAG CTC
                                          _  _
GAM224  KIAA1036  3'  TGATGGGGGGTGGGGGTGGGGT 29831     TT    TT    G    AGAT
          G                      CAT  CACT  CACT TCTG
                                |||  ||||  |||| ||||
                                GTG  GTGG  GTGG GGGT
                                  GG   GG   G   AGTG
GAM224  KIAA1046  3'  ATCTTAGAAGAGGGGTGGG   29990        CACTG
                                TTCACTTT    TCTGAGAT
                                ||||||||    ||||||||
                                GGGTGGGG    AGATTCTA
                                     AGA__
GAM224  KIAA1046  3'  TTTCAGATGTTGGAAATG    30002    C    CT
                                CA TTTCA  GTCTGAGA
                                || |||||  ||||||||
                                GT AAGGT  TAGACTTT
                                 A    TG
GAM224  KIAA1237  3'  TTTTGGATGAAGTGAGGG    80476        __  TG
                                CTTTCACT  GTC  AGA
                                ||||||||  |||  |||
                                GGGAGTGA  TAG  TTT
                                     AG   GT
GAM224  KIAA1257  3'  GTTGGCACGACTGAGAGTGGGA 62755     TT      CT  _  A_
          TG                     CAT  CACTTTCA  GTC TG  GAT
                                |||  ||||||||  ||| ||  |||
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                                GTA  GTGAGAGT  CAG AC  TTG
                                  GG       __   C  GG
GAM224  KIAA1456 3' GTTTTGGAGGAAGGAGGAAATG 67006       A_    A TG  TG
                                CATTTC  CTTTC C  TC  AGAT
                                ||||||  ||||| |  ||  ||||
                                GTAAAG  GGAAG G  AG  TTTG
                                   GA    _ __  GT
GAM224  KIAA1538 3' GTTTTAGACAGGCTCCCTGAA  71556     CTTTCA
                                TTCA     CTGTCTGAGAT
                                ||||     ||||||||||
                                AAGT     GACAGATTTTG
                                  CCCTCG
GAM224  KIAA1559 3' TTGGAGACAGTGAGGGAAGTG  73078       A   T      GAGAT
                                CATTTC CTT CACTGTCT
                                |||||| ||| ||||||||
                                GTGAAG GGA GTGACAGA
                                   _  _       GGTTT
GAM224  KIAA1560 3' TTTGGGAGAGGGAGGGA     64183    A    A  G   G
                                TC CTTTC CT TCT AGA
                                || ||||| || ||| |||
                                AG GGAGG GA AGG TTT
                                 _    _ G   G
GAM224  KIAA1655 5' ATCTCACCTCCAGTGGGAGGGA 66590       A  TT    TC__
           AGTG                    ATTTC CT  CACTG    TGAGAT
                                |||||  ||  |||||    ||||||
                                TGAAG GA  GTGAC    ACTCTA
                                   G  GG    CTCC
GAM224  KIAA1655 5' TCTCACTGAGAGTGAGA     66634          CTGTC
                                TTTCACTTTCA     TGAGA
                                ||||||||||     |||||
                                AGAGTGAGAGT     ACTCT
                                      C_____
GAM224  KIAA1729 3' GTCTTAGGCGATTTGTGGGGTG 89130     TT   TTTCAC
                                CAT  CAC     TGTCTGAGAT
                                |||  |||     ||||||||||
                                GTG  GTG     GCGGATTCTG
                                  GG   TTTA__
GAM224  KIAA1799 5' ATCTTATTTCCGGTGGCGGTGA 74634        T     TC__
           GGTG                    ATTTCACT TCACTG    TGAGAT
                                |||||||| ||||||    ||||||
                                TGGAGTGG GGTGGC    ATTCTA
                                    C     CTTT
GAM224  KIAA1808 5' CATTGAGGGTGAGGTG      85861            C
                                CATTTCACTTTCA TG
                                |||||||||||| ||
                                GTGGAGTGGGAGT AC
                                       T
GAM224  KIAA1811 3' ATCTCTCTGCGGGGTGGGGTG  64793     TT   TTCA   CT_
                                CAT  CACT   CTGT   GAGAT
                                |||  ||||   ||||  |||||
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                                GTG  GTGG   GGCG   CTCTA
                                  GG   ____   TCT
GAM224  KIAA1821  3'  GGGCAGTGAGGGTGAGG    71790
                                TTTCACTTTCACTGTCT
                                ||||||||||||||||
                                GGAGTGGGAGTGACGGG

GAM224  KIAA1893  3'  GTCTCGGGCAGCACGTGAGGT  73217       TTTCA
                                ATTTCAC    CTGTCTGAGAT
                                |||||||    ||||||||||
                                TGGAGTG    GACGGGCTCTG
                                    CAC__
GAM224  KPNA6     3'  GCAGAGGAGGGTGGAGTG    24609         A_
                                CATTTCACTTTC  CTGT
                                ||||||||||||  ||||
                                GTGAGGTGGGAG  GACG
                                      GA
GAM224  LMOD1     3'  ATCTTTGAGGTGAGGGTGGGGT 24038    TT       G  T
            G                    CAT  CACTTTCACT TC GAGAT
                                |||  |||||||||| || |||||
                                GTG  GTGGGAGTGG AG TTCTA
                                  GG        _  T
GAM224  LY6G5B    5'  TTTCAGGCTCAGAGAAGTG   41131       CACT_
                                CACTTT    GTCTGAGA
                                ||||||    ||||||||
                                GTGAAG    CGGACTTT
                                   AGACT
GAM224  MAGE-E1   3'  GATTGGACGGTGGAGCTGGGAT 47945    TT  C       TG GAT
            G                    CAT  CA TTTCACTGTC  A
                                |||  || ||||||||||  |
                                GTA  GT GAGGTGGCAG  T
                                  GG  C        GT AG
GAM224  MGC10960  3'  ATCTCCCCAGGAGGGTGAGATG 51003          A   TCT
                                CATTTCACTTTC CTG   GAGAT
                                |||||||||||| |||   |||||
                                GTAGAGTGGGAG GAC   CTCTA
                                      _   CC_
GAM224  MGC2628   3'  ATTTCCGGGTTAGGGTGGAATG 43968          C   GT T
                                CATTTCACTTT ACT  C GAGAT
                                |||||||||||  |||  | |||||
                                GTAAGGTGGGA TGG  G CTTTA
                                      T   __ C
GAM224  MGC27044  5'  CTTGGTGTTGAAAGTGAAATG  58673          CTGT TG
                                CATTTCACTTTCA    C  AG
                                ||||||||||||    |  ||
                                GTAAAGTGAAAGT    G  TC
                                       TGT_ GT
GAM224  MGC35558  3'  TCTCAGGTGGGTGAGGG     58787       _ TG
                                CTTTCA C  TCTGAGA
                                ||||||  |  |||||||
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                                GGGAGT G  GGACTCT
                                   G GT
GAM224  MGC4251  3'  GTTGGCCTGGTGGGGGTGGAGT 50460        TT   __  TGAGAT
                                ATTTCACT  CACT  GTC
                                ||||||||  ||||  |||
                                TGAGGTGG  GTGG  CGG
                                     GG   TC   TTG
GAM224  MLLT10   5'  AGGCGGTGGAGGGGAGGTG   16166       A
                                CATTTC CTTTCACTGTCT
                                |||||| ||||||||||||
                                GTGGAG GGAGGTGGCGGA
                                   G
GAM224  MOCS3    3'  TCTTGGACATGTGAGATGT   27161   _    _   TG
                                AC TTTCAC TGTC  AGA
                                || |||||| ||||  |||
                                TG AGAGTG ACAG  TCT
                                 T    T   GT
GAM224  NR6A1    3'  ATTTTGAGGGAGAGGGTGGGAT 7642     TT     A  G  T
           G                     CAT  CACTTTC CT TC GAGAT
                                |||  ||||||| || || |||||
                                GTA  GTGGGAG GG AG TTTTA
                                  GG     A  G  _
GAM224  NR6A1    3'  ATTTTGAGGGAGAGGGTGGGAT 52867    TT     A  G  T
           G                     CAT  CACTTTC CT TC GAGAT
                                |||  ||||||| || || |||||
                                GTA  GTGGGAG GG AG TTTTA
                                  GG     A  G  _
GAM224  NR6A1    3'  ATTTTGAGGGAGAGGGTGGGAT 52879    TT     A  G  T
           G                     CAT  CACTTTC CT TC GAGAT
                                |||  ||||||| || || |||||
                                GTA  GTGGGAG GG AG TTTTA
                                  GG     A  G  _
GAM224  P450RAI-2 3'  TGGTGGAGATGGAATG     39107       C
                                CATTTCA TTTCACTG
                                ||||||| ||||||||
                                GTAAGGT GAGGTGGT
                                    A
GAM224  PALM     3'  TCTCAGGCAGTTGGGGTGA   10417      TC
                                TCACTT  ACTGTCTGAGA
                                ||||||  ||||||||||
                                AGTGGG  TGACGGACTCT
                                   GT
GAM224  PB1      3'  ATTTTAGTTACTGGGGGTGGGG 36368   TT   TT  C  T
                                T  CACT  CA TG CTGAGAT
                                |  ||||  || || |||||||
                                G  GTGG  GT AT GATTTTA
                                 GG   GG  C  T
GAM224  pcnp     3'  GTTTTGAAATTGGGGTGTGGGG 39789    TT  _ TT  CTG  T
           TG                    CAT  CAC T  CA   TC GAGAT
                                |||  ||| |  ||   || |||||
```

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                                GTG  GTG G  GT   AG TTTTG
                                  GG   T GG  TAA  _
GAM224  PEF      3'  TCTGTGGAGAGTGGAGTG    24754      T   G   _
                                CACTT CACT TCTG AGA
                                ||||| |||| |||| |||
                                GTGAG GTGA AGGT TCT
                                   _   G   G
GAM224  PGGT1B   3'  ATTTTAGATTGGGAGGGTGGGG 17231   TT      ACT
                                T  CACTTTC   GTCTGAGAT
                                |  |||||||   |||||||||
                                G  GTGGGAG   TAGATTTTA
                                 GG      GGT
GAM224  PINK1    3'  GTCTGTGAATGGTGAGGGTGGG 50543   TT         _ TG
           A                     T  CACTTTCACTGT C  AGAT
                                |  ||||||||||| |  ||||
                                A  GTGGGAGTGGTA G  TCTG
                                 GG          A TG
GAM224  PP1057   5'  GTTTTGTGGGGGTGGGAGTGGA 48435       TT   G  _
           G                     TTTCACT  CACT TC TGAGAT
                                |||||||  |||| || ||||||
                                GAGGTGA  GTGG GG GTTTTG
                                    GG   G  T
GAM224  PRMT3    3'  GTTTTTAATGTGGGGGTAGAGT 65025     TC   TT   TGTCT
           G                     CATT  ACT  CAC    GAGAT
                                ||||  |||  |||    |||||
                                GTGA  TGG  GTG    TTTTG
                                  GA   GG   TAAT_
GAM224  PRMT6    3'  GTTTCGCGGGGGAGTGAGG   36272       TT A   CT
                                TTTCACT  C CTGT  GAGAT
                                |||||||  | ||||  |||||
                                GGAGTGA  G GGCG  CTTTG
                                    GG _   __
GAM224  PRO2900  5'  TTCAACTGAGAGTGAGGTG   37809          CT  C
                                CATTTCACTTTCA  GT TGAG
                                ||||||||||||  || ||||
                                GTGGAGTGAGAGT  CA ACTT
                                              __  _
GAM224  PSMF1    3'  GTCTTAGGTGTTCTATGGGAGG 22354    A  TT  C____ GT
           AAGTG                   TC CT  CA    T  CTGAGAT
                                || ||  ||    |  |||||||
                                AG GA  GT    G  GATTCTG
                                 _  GG  ATCTT TG
GAM224  PXR2b    3'  ATTTTTAACTTGGGGGTGAAA  33338       TT  CT  CT
                                TTTCACT  CA  GT  GAGAT
                                |||||||  ||  ||  |||||
                                AAAGTGG  GT  CA  TTTTA
                                    GG  T_  AT
GAM224  RAB6B    3'  GTCTTTAGGAGTAGGGTGGGAT 33414    TT     C  G    _
           G                     CAT  CACTTT ACT TCTGA GAT
                                |||  |||||| ||| ||||| |||
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                                GTA  GTGGGA TGA GGATT CTG
                                  GG     _  _    T
GAM224  RACGAP1  3'  GTCTCAGGGTGGGAAGTGGGA  25200   TT     _  GT
                                T  CACTTTC ACT  CTGAGAT
                                |  ||||||| |||  |||||||
                                A  GTGAAGG TGG  GACTCTG
                                 GG      G  __
GAM224  RAD51    3'  TTTCAGGCCAGTGTGGTG    11229     TT    _
                                CACT  CACTG TCTGAGA
                                ||||  ||||| |||||||
                                GTGG  GTGAC GGACTTT
                                  T_    C
GAM224  RAD51    3'  TTTCAGGCCAGTGTGGTG    56023     TT    _
                                CACT  CACTG TCTGAGA
                                ||||  ||||| |||||||
                                GTGG  GTGAC GGACTTT
                                  T_    C
GAM224  RASSF2   3'  GTTTCAGGTTGAAGGGAAATG  28443       A     CTG
                                CATTTC CTTTCA   TCTGAGAT
                                |||||| ||||||   ||||||||
                                GTAAAG GGAAGT   GGACTTTG
                                   _     T__
GAM224  RBM7     3'  ATTTTAGACACTTTAGGAGGGG 32235    TT A    CAC__
           GTG                    AT  C CTTT     TGTCTGAGAT
                                ||  | ||||    ||||||||||
                                TG  G GAGG    ACAGATTTTA
                                 GG _    ATTTC
GAM224  RIL      3'  GGGGGTGGTGGTGGGGTG    13488     TT    T    G
                                CAT  CACT TCACT TC
                                |||  |||| ||||| ||
                                GTG  GTGG GGTGG GG
                                  GG    T     G
GAM224  RILP     5'  GTCCCAGTGGAGGGTGGGGTG  48694     TT      ACTGT   A
                                CAT  CACTTTC     CTG GAT
                                |||  |||||||    ||| |||
                                GTG  GTGGGAG     GAC CTG
                                  GG      GT___   C
GAM224  RNO2     5'  ATTTTTTTAGTGGAGATGGGGT 52762     TT  C       TCT
           G                     CAT  CA TTTCACTG   GAGAT
                                |||  || ||||||||   |||||
                                GTG  GT GAGGTGAT   TTTTA
                                  GG  A       TT_
GAM224  RoXaN    3'  ACAGTGGGTGTGAGATG     46627         T
                                CATTTCAC TTCACTGT
                                |||||||| ||||||||
                                GTAGAGTG GGGTGACA
                                     T
GAM224  SAE1     3'  TTTTGGGAGAAAGGAGATG    18537       A    ACTG  TG
                                CATTTC CTTTC    TC  AGA
                                |||||| |||||    ||  |||
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                                GTAGAG GAAAG   GG  TTT
                                  _    A___  GT
GAM224  SDS3    3'  ATTTTTCCATTGAAGGTGGAGT 69223          C  TCT
                                ATTTCACTTTCA TG   GAGAT
                                |||||||||||| ||   |||||
                                TGAGGTGGAAGT AC   TTTTA
                                       T  CT_
GAM224  SEMA4C  3'  ACATATGGAGGTGGGGTG   35052    TT      C_
                                CAT  CACTTTCA  TGT
                                |||  ||||||||  |||
                                GTG  GTGGAGGT  ACA
                                  GG       AT
GAM224  SFXN5   3'  TCTTAGGGTAGGGGAAGTG   58040       A  GT _
                                CACTTTC CT  C TGAGA
                                |||||||  ||  | |||||
                                GTGAAGG GA  G ATTCT
                                    G  TG G
GAM224  SGT1    3'  ATTTCAGACATGGTGAAACTG  21992    C     __
                                CA TTTCACT  GTCTGAGAT
                                || |||||||  |||||||||
                                GT AAAGTGG  CAGACTTTA
                                 C      TA
GAM224  SH3BGRL2 3'  ATCTCAGACAGTGATCAGGA   48883    ACTT
                                TC    TCACTGTCTGAGAT
                                ||    ||||||||||||||
                                AG    AGTGACAGACTCTA
                                 GACT
GAM224  SMC1L1  3'  GTCTTAGGCAGTTACCTGAAA  71960      CTTTC
                                TTTCA     ACTGTCTGAGAT
                                |||||     ||||||||||||
                                AAAGT     TGACGGATTCTG
                                   CCAT_
GAM224  SPTLC2  5'  GTTTCGGGGAGGTGGGTGGGGT 16809     TT    TCA  G
          G                     CAT  CACTT   CT TCTGAGAT
                                |||  |||||   || ||||||||
                                GTG  GTGGG   GA GGGCTTTG
                                  GG    TG_  G
GAM224  STK29   3'  GTCTCAGGCAGTGGGGG     87579    TT
                                CT  CACTGTCTGAGAT
                                ||  ||||||||||||
                                GG  GTGACGGACTCTG
                                 GG
GAM224  TA-PP2C 3'  GTAGACGCGGTGGGGGCGGGGT 57759     TT A  TT   __    AGAT
          G                     CAT  C CT  CACT  GTCTG
                                |||  | ||  ||||  |||||
                                GTG  G GG  GTGG  CAGAT
                                  GG C  GG    CG    G
GAM224  THEA    3'  TTTTAGGCCAGGTGTGGTG   66305     TT   __
                                CACT  CACT  GTCTGAGA
                                ||||  ||||  ||||||||
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                                GTGG  GTGG  CGGATTTT
                                  T_   AC
GAM224  TIAM2    3'  ATCTTGGGCTGTATCAAGGGAG 24931      A  TC_ T  TG
           TG                    CATTTC CTT  AC GTC  AGAT
                                 |||||| |||  || |||  ||||
                                 GTGAGG GAA  TG CGG  TCTA
                                   _  CTA  T  GT
GAM224  TP53TG3  3'  ATCTTGGACATCTTGGAGATG  31102      ACTTTCAC   TG
                                 CATTTC      TGTC  AGAT
                                 ||||||      ||||  ||||
                                 GTAGAG      ACAG  TCTA
                                    GTTCT___   GT
GAM224  TRIP3    3'  GTTTCAGGCAGACTTGGGGT  78220    TT  CTTTCA
                                 AT  CA     CTGTCTGAGAT
                                 ||  ||     ||||||||||
                                 TG  GT     GACGGACTTTG
                                  GG  TCA___
GAM224  VIAAT    3'  GTTTTGGGGGGAGGCGGGGTG  54541    TT A    A  GT TG
                                 CAT  C CTTTC CT  C  AGAT
                                 |||  | ||||| ||  |  ||||
                                 GTG  G GGAGG GG  G  TTTG
                                  GG C    _ __ GT
GAM224  VPS39    3'  GTCTTTGATGGTGGTGAGGGTG 62849          ___  T
           GG                    TTCACTTTCACT  GTC GAGAT
                                 ||||||||||||  ||| |||||
                                 GGGTGGGAGTGG  TAG TTCTG
                                       TGG  T
GAM224  ZAP3     3'  GTTTTGGGGAGGGAGGGAG   77224    A    A  G  TG
                                 TTC CTTTC CT TC  AGAT
                                 ||| ||||| || ||  ||||
                                 GAG GGAGG GA GG  TTTG
                                  _    _  G  GT
GAM224  ZNF297B  3'  ATTTCAGTACTAAGGTGGTGA  25775      T  ACT  _
                                 TCACT TC   GT CTGAGAT
                                 ||||| ||   || |||||||
                                 AGTGG GG   CA GACTTTA
                                    T  AAT  T
GAM224  ZNF323   5'  ATCTTAAGATTGTGAAAGTGGA 48077          T   _
           G                     TTTCACTTTCAC GTCT GAGAT
                                 |||||||||||| |||| |||||
                                 GAGGTGAAAGTG TAGA TTCTA
                                       T   A
GAM224  ZNF84    3'  TCTTGGACTTCAGGAAATG   12817      A  TTCACT   TG
                                 CATTTC CT     GTC  AGA
                                 |||||| ||     |||  |||
                                 GTAAAG GA     CAG  TCT
                                    _ CTT___   GT
GAM224  LOC114987 3'  TCTTGAGGGGAGTGGGATG   59124    TT   TT A  GTC
                                 CAT  CACT  C CT   TGAGA
                                 |||  ||||  | ||   |||||
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                                GTA  GTGA  G GA   GTTCT
                                  GG   GG _  ___
GAM224   LOC115219 5'  GGCGGTGGAGGGGAGATG    73312       A
                                CATTTC CTTTCACTGTC
                                ||||||| ||||||||||
                                GTAGAG GGAGGTGGCGG
                                   G
GAM224   LOC115297 3'  ATCTCAGATATCCTACGGTGAG 72884       TTCAC_
           A                     TTTCACT     TGTCTGAGAT
                                |||||||     ||||||||||
                                AGAGTGG     ATAGACTCTA
                                    CATCCT
GAM224   LOC116150 3'  TCTTACTTGAGAGTGAG     56638         CT  CT
                                TTCACTTTCA  GT  GAGA
                                ||||||||||  ||  ||||
                                GAGTGAGAGT  CA  TTCT
                                      T_  __
GAM224   LOC124446 3'  TTTTAGAAAAAGTGAAG     74293         CACTG
                                TTTCACTTT    TCTGAGA
                                |||||||||    |||||||
                                GAAGTGAAA    AGATTTT
                                     A____
GAM224   LOC126964 3'  GTTTTGGTGGGATGGGGGGAGG 74622       A  TT  _  GT TG
           TG                     CATTTC CT  CA CT  C  AGAT
                                |||||| ||  || ||  |  ||||
                                GTGGAG GG  GT GG  G  TTTG
                                   _  GG  A  GT GT
GAM224   LOC128977 3'  GTCTGTGAACAGTGGGGGTGGG 74827    TT    TT     _ TG
           G                      T  CACT  CACTGT C  AGAT
                                |  ||||  |||||| |  ||||
                                G  GTGG  GTGACA G  TCTG
                                 GG    GG     A TG
GAM224   LOC130940 5'  GTCTCGGGCGCGGGAGGGGGTG 57139     TT A  TT AC
                                CAT  C CT  C  TGTCTGAGAT
                                |||  | ||  |  ||||||||||
                                GTG  G GA  G  GCGGGCTCTG
                                  GG _  GG C_
GAM224   LOC131368 3'  ATTTCAGATACTTTAAGTGAAT 75858    T      TCAC
           TG                     CA TTCACTT    TGTCTGAGAT
                                || |||||||    ||||||||||
                                GT AAGTGAA    ATAGACTTTA
                                 T      TTTC
GAM224   LOC134288 3'  TCCACAGAGGTGAGAGTCGGGT 75178      TC       G    AGAT
           G                      CATT  ACTTTCACT TCTG
                                ||||  ||||||||| ||||
                                GTGG  TGAGAGTGG AGAC
                                  GC        _    ACCTT
GAM224   LOC142948 3'  GTCTTGGCAGCATGGAAGTGAG 82891          __   T TG
           A                      TTTCACTTTCA  CTG C  AGAT
                                ||||||||||  ||| |  ||||
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                                AGAGTGAAGGT  GAC G  TCTG
                                      AC   _ GT
GAM224   LOC143279 5'  GTCCTGGTGGTGGAGGTGGGG  76511    TT       TG  TGA
                                T  CACTTTCAC  TC   GAT
                                |  |||||||||  ||   |||
                                G  GTGGAGGTG  GG   CTG
                                 GG        GT  TC_
GAM224   LOC144483 3'  TTTCATGGCAGTGAAA      60179          _
                                TTTCACTGTC TGAGA
                                |||||||||| |||||
                                AAAGTGACGG ACTTT
                                      T
GAM224   LOC144486 3'  TTTTGGTGTGAAGGTGAAAT   83090           TGT TG   T
                                ATTTCACTTTCAC   C  AGA
                                ||||||||||||   |  |||
                                TAAAGTGGAAGTG   G  TTT
                                       T__ GT   T
GAM224   LOC144845 5'  GTGGGGCAAGGTGGGGGTGAAG 56664         TT   __   GAGAT
           TG                    CATTTCACT  CACT  GTCT
                                |||||||||  ||||  ||||
                                GTGAAGTGG  GTGG  CGGG
                                     GG    AA    GTG
GAM224   LOC144845 5'  TCGCTCAGGGAGGTGGAGTG   56665           A   TC
                                CATTTCACTTTC CTG  TGA
                                ||||||||||||| |||  |||
                                GTGAGGTGGAGG GAC  GCT
                                      _   TC
GAM224   LOC145828 5'  GTTTTGGAAGGGAGAGGAGGTG 83538       A    A  G  TG
                                CATTTC CTTTC CT TC  AGAT
                                ||||||| ||||| || ||  ||||
                                GTGGAG GAGAG GG AG  TTTG
                                   _    _ A  GT
GAM224   LOC146050 3'  ATCTCAGATGATTTAGGAAGTG 77625        ACT___
                                CACTTTC     GTCTGAGAT
                                |||||||     |||||||||
                                GTGAAGG     TAGACTCTA
                                     ATTTAG
GAM224   LOC146229 3'  GTGGTAGAGTGGAATG      77769           C  TG
                                CATTTCACTTT AC  T
                                |||||||||||  ||  |
                                GTAAGGTGAGA TG  G
                                      _  GT
GAM224   LOC146336 3'  GACAGTGAGGCTGAAATG    77832         C
                                CATTTCA TTTCACTGTC
                                ||||||| ||||||||||
                                GTAAAGT GGAGTGACAG
                                     C
GAM224   LOC146728 5'  TCGGAGTGGGGTGGAGTG    83753           T   TG
                                CATTTCACTT CAC  TCTGA
                                |||||||||| |||  |||||
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                                GTGAGGTGGG GTG  AGGCT
                                      _  __
GAM224  LOC146990 5'  ATCTCGGGCGGCTGGAGGGGTG 83884       __   _
          AGG                   TTCACT  TTCA CTGTCTGAGAT
                                |||||| |||| ||||||||||
                                GAGTGG  AGGT GGCGGGCTCTA
                                   GG   C
GAM224  LOC147632 5'  TGGTGGAATGAGATG      56670       C
                                CATTTCA TTTCACTG
                                ||||||| ||||||||
                                GTAGAGT AAGGTGGT
                                   _
GAM224  LOC148413 3'  GCAGTGAGGATGGAGTG    78830       CT
                                CATTTCA  TTCACTGT
                                ||||||| ||||||||
                                GTGAGGT  GAGTGACG
                                    AG
GAM224  LOC148479 3'  GTTCCCTGCAGTGGAGGTGGAC 78879    T          CT_  AT
          TG                     CA TTCACTTTCACTGT  GAG
                                || ||||||||||||||  |||
                                GT AGGTGGAGGTGACG  CTT
                                 C          TCC  G
GAM224  LOC148529 5'  TCTTAGGCGAGTGGGAG    84172    TT  _
                                CT  CACT GTCTGAGA
                                ||  |||| ||||||||
                                GA  GTGA CGGATTCT
                                 GG   G
GAM224  LOC149076 3'  ATCTTGGAGGCAGGGAGGTGAG 79148         A    __
          G                     TTTCACTTTC CTGTCT  GAGAT
                                |||||||||| ||||||  |||||
                                GGAGTGGAGG GACGGA  TTCTA
                                      _    GG
GAM224  LOC149182 5'  TCTTGTGCAGGGTGAGATG   84379        TTCA   CT
                                CATTTCACT   CTGT  GAGA
                                |||||||||   ||||  ||||
                                GTAGAGTGG   GACG  TTCT
                                     ____   TG
GAM224  LOC149711 3'  ATTTCACCTGCTTGGAAAGTGA 84673         ACT  C__
          GATG                    ATTTCACTTTC  GT  TGAGAT
                                |||||||||||  ||  ||||||
                                TAGAGTGAAAG  CG  ACTTTA
                                      GTT  TCC
GAM224  LOC149837 5'  GTTTTGAGGGTGGAATGAGGTG 84745       C     G  T
                                CATTTCA TTTCACT TC GAGAT
                                ||||||| ||||||| || |||||
                                GTGGAGT AAGGTGG AG TTTTG
                                   _     G  _
GAM224  LOC149844 5'  GGTGGTGGGGGTGGTGGTG   79519     _   TT  TG
                                CATT TCACT  CAC  TC
                                |||| |||||  |||  ||
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                                GTGG GGTGG  GTG  GG
                                  T    GG   GT
GAM224  LOC149844 3'  TGGTGAGTGAGATG       79521        TT
                                CATTTCAC  TCACTG
                                ||||||||  ||||||
                                GTAGAGTG  AGTGGT
                                    __
GAM224  LOC150225 3'  GTCTTTTGCAGGTGAAGGTGGG 85009   TT      _  CT
          A                      T  CACTTTCAC TGT  GAGAT
                                |  |||||||||  |||  |||||
                                A  GTGGAAGTG ACG  TTCTG
                                 GG       G   TT
GAM224  LOC150351 5'  TTTTAGATAGTACGAAGT    60249      C_
                                ACTTT  ACTGTCTGAGA
                                |||||  ||||||||||
                                TGAAG  TGATAGATTTT
                                   CA
GAM224  LOC150358 3'  TCTCAGAGAGTGAAGTGA    84928       T   G
                                TCACTT CACT TCTGAGA
                                |||||| |||| |||||||
                                AGTGAA GTGA AGACTCT
                                   _   G
GAM224  LOC150819 5'  GTTAGGGAGCAGTGAAAGTGAG 85122            ___   GAT
          G                      TTTCACTTTCACTGT   CTGA
                                ||||||||||||||   ||||
                                GGAGTGAAAGTGACG   GATT
                                        AGG   G
GAM224  LOC150933 3'  ATTTCAGTCACAGGAAATGGGG 85156    TT  C   A   __
          TG                     CAT  CA TTTC CTGT  CTGAGAT
                                |||  || |||| ||||  |||||||
                                GTG  GT AAAG GACA  GACTTTA
                                  GG  _   _   CT
GAM224  LOC151056 3'  ATCTTTTTTGGGAGTGAACTG  80106    T     TT  CTGTCT
                                CA TTCACT  CA     GAGAT
                                || ||||||  ||     |||||
                                GT AAGTGA  GT     TTCTA
                                 C     GG  TTT___
GAM224  LOC151176 3'  GTTTTGATAAGGGGGTGATGTG 85263    T    TT AC   T
                                CAT TCACT  C  TGTC GAGAT
                                ||| |||||  |  |||| |||||
                                GTG AGTGG  G  ATAG TTTTG
                                  T    GG A_   _
GAM224  LOC151194 3'  ATTTTAGATGGTGAAATTAGAA 59213      AC_
          GT                     ATTTC   TTTCACTGTCTGAGAT
                                |||||   ||||||||||||||||
                                TGAAG   AAAGTGGTAGATTTTA
                                   ATT
GAM224  LOC151414 3'  ATTTTGGCATATGGGGGTGGAG 80235       TT  C  _ TG
                                TTTCACT  CA TGT C  AGAT
                                |||||||  || ||| |  ||||
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                                GAGGTGG  GT ATA G  TTTA
                                    GG  _  C GT
GAM224  LOC151438 5'  TTTTCGGTGTGAAGGTGGGATG 85373     TT       TGT     T
                                CAT  CACTTTCAC   CTGAGA
                                |||  |||||||||   ||||||
                                GTA  GTGGAAGTG   GGCTTT
                                  GG       T__     TT
GAM224  LOC151610 3'  GGATGGTGGGAGTGAAG     80288        TT
                                TTTCACT  CACTGTCT
                                |||||||  ||||||||
                                GAAGTGA  GTGGTAGG
                                    GG
GAM224  LOC151658 5'  GTGGTGGAGTGGAGTG      85481          T   TG
                                CATTTCACTT CAC  T
                                |||||||||| |||  |
                                GTGAGGTGAG GTG  G
                                      _  GT
GAM224  LOC151826 3'  TTTTAGGCTAGTGAAA      80370        _
                                TTTCACT GTCTGAGA
                                |||||||  ||||||||
                                AAAGTGA CGGATTTT
                                    T
GAM224  LOC151904 5'  CCCTGCGTGGTGGAGGGAGGTG 80387        A      TG CTGAGAT
                                CATTTC CTTTCAC  T
                                ||||||  |||||||  |
                                GTGGAG GGAGGTG  G
                                    _      GT CGTCCCT
GAM224  LOC152274 3'  TCTTGGATTGGATGAGATG    80509        CT    CT   TG
                                CATTTCA  TTCA  GTC  AGA
                                |||||||  ||||  |||  |||
                                GTAGAGT  AGGT  TAG  TCT
                                    __   __  GT
GAM224  LOC152275 3'  GGGGGCGACAGGGAGGTGGGAT 85620     TT      A     TGAGAT
          G                      CAT  CACTTTC CTGTC
                                |||  ||||||| |||||
                                GTA  GTGGAGG GACAG
                                  GG      _     CGGGGGT
GAM224  LOC152633 5'  GTCTTGCTGTGCTGGGGGTGGG 85817     TT    TT  CTGTCT_
          GTG                     CAT  CACT  CA      GAGAT
                                |||  ||||  ||      |||||
                                GTG  GTGG  GT      TTCTG
                                  GG   GG  CGTGTCG
GAM224  LOC152805 5'  TCTCAGGATGAGTGAGG     80689         TCACTG
                                TTTCACTT      TCTGAGA
                                ||||||||      |||||||
                                GGAGTGAG      GGACTCT
                                    TA____
GAM224  LOC153196 5'  GTCTTAGAGCTAGAGATGAGGT 85975        C    ACTG
          G                      CATTTCA TTTC    TCTGAGAT
                                |||||||  ||||    ||||||||
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                                GTGGAGT AGAG   AGATTCTG
                                   _   ATCG
GAM224  LOC153222 3'  TTTTGGAGGAGTGAAAT    80791         CACTG  TG
                                ATTTCACTTT    TC  AGA
                                ||||||||||    ||  |||
                                TAAAGTGAGG    AG  TTT
                                     _____  GT
GAM224  LOC153339 5'  GTTTTGGTGGGGTGGTGGGATG 86012    TT   T  A   T TG
                                CAT  CACT TC CTG C  AGAT
                                |||  |||| || ||| |  ||||
                                GTA  GTGG GG GGT G  TTTG
                                  GG   T _  _ GT
GAM224  LOC153651 3'  TTTTAGATGGTGATTGT    80918    TT
                                AC  TCACTGTCTGAGA
                                ||  ||||||||||||
                                TG  AGTGGTAGATTTT
                                 TT
GAM224  LOC153711 3'  TCGGGTGGGAGAGGGA     86138    A    A TG
                                TTC CTTTC C  TCTGA
                                ||| ||||| |  |||||
                                AGG GAGAG G  GGGCT
                                  _    _ GT
GAM224  LOC153811 3'  GCAGTGGGGGTAAGGTG    80950      C   TT
                                CATTT ACT  CACTGT
                                ||||| |||  ||||||
                                GTGGA TGG  GTGACG
                                   A   GG
GAM224  LOC154386 3'  GTTTCAGTTCTGGAAGGTGAAA 81084         ACTGT
                                TTTCACTTTC    CTGAGAT
                                ||||||||||    |||||||
                                AAAGTGGAAG    GACTTTG
                                     GTCTT
GAM224  LOC154792 3'  TTTTGGATATGTGAGAG    86250       _   TG
                                CTTTCAC TGTC  AGA
                                ||||||| ||||  |||
                                GAGAGTG ATAG  TTT
                                    T   GT
GAM224  LOC154877 3'  GTCTTTACTGAGGGTGGCAGTG 86306    T    G  T___
                                CACT TCACT TC   GAGAT
                                |||| ||||| ||   |||||
                                GTGA GGTGG AG   TTCTG
                                  C    G  TCAT
GAM224  LOC157623 5'  CAACGAGGCGGTGTGGGTGGAG 81493        TT      GAGAT
          TG                    CATTTCACT  CACTGTCT
                                |||||||||  ||||||||
                                GTGAGGTGG  GTGGCGGA
                                     GT      GCAACT
GAM224  LOC157693 3'  TCTTGGACGCAGTGAAGT   81558        TTCAC   TG
                                ATTTCACT    TGTC  AGA
                                ||||||||    ||||  |||
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                                TGAAGTGA    GCAG  TCT
                                    C____   GT
GAM224  LOC157918 3'  GTCTTGGGCACAGGTGGGGT  86649   TT   TCAC   TG
                                AT  CACTT   TGTC  AGAT
                                ||  |||||   ||||  ||||
                                TG  GTGGA   ACGG  TCTG
                                 GG    C___   GT
GAM224  LOC157919 3'  GTTTCAGACAGTGGAA     81637
                                TTTCACTGTCTGAGAT
                                ||||||||||||||||
                                AAGGTGACAGACTTTG

GAM224  LOC158117 3'  GGCGTGGTGGAATGGAATG   81709       C     __
                                CATTTCA TTTCACT  GTC
                                |||||||  |||||||  |||
                                GTAAGGT AAGGTGG  CGG
                                    _      TG
GAM224  LOC158382 5'  ACGGGGGAAGTGAGGTG     86782          A
                                CATTTCACTTTC CTGT
                                ||||||||||||  ||||
                                GTGGAGTGAAGG GGCA
                                      G
GAM224  LOC158382 5'  GTGGTGGAAGATGAAGTG    86789       _     TG
                                CATTTCA CTTTCAC  T
                                |||||||  |||||||  |
                                GTGAAGT GAAGGTG  G
                                    A      GT
GAM224  LOC158954 3'  TTTTGGGTGGGGGGGAAGTG  60437      A  TT   TGT TG
                                CATTTC CT  CAC   C  AGA
                                ||||||  ||  |||   |  |||
                                GTGAAG GG  GTG   G  TTT
                                   G  GG   ___ GT
GAM224  LOC159184 5'  TCAATGGTGAAGGTGAAGT   60051            C
                                ATTTCACTTTCACTGT TGA
                                ||||||||||||||||  |||
                                TGAAGTGGAAGTGGTA ACT
                                                  _
GAM224  LOC163882 3'  ATGCTGGCAGTGAGAGTGAAA  82163            TGAGAT
                                TTTCACTTTCACTGTC
                                ||||||||||||||||
                                AAAGTGAGAGTGACGG
                                      TCGTA
GAM224  LOC166983 5'  GTCTGGCCCAAGGGGAGGTGGA 87266         A  ___   T  GAT
          GTG                    TTTCACTTTC CT   GTC GA
                                ||||||||||  ||   |||  ||
                                GAGGTGGAGG GA   CGG CT
                                      G  ACC   T  G
GAM224  LOC169436 5'  GGGGTAGATGTGGGGGTGGAAT 82743         TT   T    AGAT
          G                     CATTTCACT  CAC GTCTG
                                |||||||||  |||  |||||
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                                GTAAGGTGG  GTG TAGAT
                                     GG  _    GGGGT
GAM224  LOC196761 3'  GTTTTGGGCAGTGGAG     89556         TG
                                TTTCACTGTC  AGAT
                                ||||||||||  ||||
                                GAGGTGACGG  TTTG
                                      GT
GAM224  LOC197379 3'  GATGGTGAGGGTGGGGT    89742    TT
                                AT  CACTTTCACTGTC
                                ||  ||||||||||||
                                TG  GTGGGAGTGGTAG
                                 GG
GAM224  LOC197414 3'  ATTTTGGGCAGGCGCTGAGTGG 88061   TT    TCA__    TG
           GG                     T  CACTT    CTGTC  AGAT
                                |  |||||    |||||  ||||
                                G  GTGAG    GACGG  TTTA
                                 GG    TCGCG    GT
GAM224  LOC201203 3'  ATCTCAGATTGTGAGGTAAATG 88140      C   T   T
                                CATTT ACTT CAC GTCTGAGAT
                                ||||| |||| ||| |||||||||
                                GTAAA TGGA GTG TAGACTCTA
                                   _   _  T
GAM224  LOC201895 3'  TCTTAGGCCAGTGCAGTG    89094     TT   _
                                CACT  CACTG TCTGAGA
                                ||||  ||||| |||||||
                                GTGA  GTGAC GGATTCT
                                   C_    C
GAM224  LOC202152 3'  ATCTCAGATTTAAAAACGTGGG 89157    TT  _  CACT
           ATG                    CAT  CAC TTT   GTCTGAGAT
                                |||  ||| |||   |||||||||
                                GTA  GTG AAA    TAGACTCTA
                                  GG   C   AATT
GAM224  LOC203275 3'  GGCGTGGTGGAATGGAATG   89325       C     __
                                CATTTCA TTTCACT  GTC
                                |||||||  |||||||  |||
                                GTAAGGT AAGGTGG  CGG
                                     _      TG
GAM224  LOC203317 5'  GTCTTGCCAATGGAAGTTGGAG 89333       _    C  TC
           TG                     CATTTCA CTTTCA TG  TGAGAT
                                |||||||  ||||||  ||  ||||||
                                GTGAGGT GAAGGT AC  GTTCTG
                                    T     A  C_
GAM224  LOC219333 3'  GTCAGGGCAGTGGAAGTGGA  93542             GA
                                TTCACTTTCACTGTCT  GAT
                                ||||||||||||||||  |||
                                AGGTGAAGGTGACGGG  CTG
                                          A_
GAM224  LOC219529 3'  GTCTCAGGTGAGTGGAGG    92972       _ GT
                                CTTTCAC T  CTGAGAT
                                |||||||  |  |||||||
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                                GGAGGTG G  GACTCTG
                                    A TG
GAM224   LOC220143 5'  GCGGGAGGGTGAAATG      93589           A
                                CATTTCACTTTC CTGT
                                |||||||||||| ||||
                                GTAAAGTGGGAG GGCG
                                                _
GAM224   LOC220549 5'  GCGGTGAGAGAGAGGTG     92919       A
                                CATTTC CTTTCACTGT
                                |||||| ||||||||||
                                GTGGAG GAGAGTGGCG
                                   A
GAM224   LOC220739 5'  ATTTCCCATGGGAGTGGAGT   92925        TT  C  TCT
                                ATTTCACT  CA TG   GAGAT
                                ||||||||  || ||   |||||
                                TGAGGTGA  GT AC   CTTTA
                                     GG  _  C__
GAM224   LOC221400 3'  GTCTCAGGTTGATGGTGGGGTG 92299     TT   T   CTG
                                CAT  CACT TCA   TCTGAGAT
                                |||  |||| |||   ||||||||
                                GTG  GTGG AGT   GGACTCTG
                                  GG   T   T__
GAM224   LOC221405 3'  TTTTAGATTAGTGGAA      93892         _
                                TTTCACTG TCTGAGA
                                |||||||| |||||||
                                AAGGTGAT AGATTTT
                                     T
GAM224   LOC221415 3'  TTTCCTGGGGGTTGAGGTG   93878       C   G  T_
                                CACTTT ACT TC  GAGA
                                |||||| ||| ||  ||||
                                GTGGAG TGG GG  CTTT
                                   T   G  TC
GAM224   LOC221584 3'  TCTCGAGAGAAAGGGAGTG   93833       A    A  GTC
                                CATTTC CTTTC CT   TGAGA
                                |||||| ||||| ||   |||||
                                GTGAGG GAAAG GA   GCTCT
                                   _    A  ____
GAM224   LOC221683 5'  GTCTTAGGTTTTGGTGTGA   93717     TT   CT
                                TCAC  TCA  GTCTGAGAT
                                ||||  |||  |||||||||
                                AGTG  GGT  TGGATTCTG
                                  T_   TT
GAM224   LOC221865 3'  ATTTTGGGTATATGGGGTGAAA 92486          CAC GT TG
           T                     ATTTCACTTT   T  C  AGAT
                                ||||||||||   |  |  ||||
                                TAAAGTGGGG   A  G  TTTA
                                      TAT TG GT
GAM224   LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
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                                GTAAAGTGAA GTGACA
                                      _
GAM224  LOC245728 5'  TTCAGGCAATGAAGTG      91135       T  C
                                CACTT CA TGTCTGAG
                                ||||| || ||||||||
                                GTGAA GT ACGGACTT
                                  _  A
GAM224  LOC253115 3'  ATTTTTATTGTGGGGTGGGATG 94494     TT    T  TGTCT
                                CAT  CACTT CAC    GAGAT
                                |||  ||||| |||    |||||
                                GTA  GTGGG GTG    TTTTA
                                  GG    _  TTAT_
GAM224  LOC254485 3'  CTGGGAAGTGAGGTG       95013       T   G  G
                                CACTT CACT TCT AG
                                ||||| |||| ||| ||
                                GTGGA GTGA AGG TC
                                  _   _  G
GAM224  LOC254755 3'  GCAGGGAGGTGGGGTG      97369     TT      A
                                CAT  CACTTTC CTGT
                                |||  ||||||| ||||
                                GTG  GTGGAGG GACG
                                  GG     _
GAM224  LOC254756 3'  GCAGGGAGGTGGGGTG      97363     TT      A
                                CAT  CACTTTC CTGT
                                |||  ||||||| ||||
                                GTG  GTGGAGG GACG
                                  GG     _
GAM224  LOC255391 5'  TCTCTGGGGGTGCGGTG     97614      TT    G  T
                                CACT  CACT TC GAGA
                                ||||  |||| || ||||
                                GTGG  GTGG GG CTCT
                                  C_   G  T
GAM224  LOC255394 3'  GTTTCAGACACTGCTTAGGTGC 94886     T     T__  C
          AGTG                    ATT CACTT   CA TGTCTGAGAT
                                ||| |||||   || ||||||||||
                                TGA GTGGA   GT ACAGACTTTG
                                  C    TTC  C
GAM224  LOC255452 5'  GTCTCTATCCGAGAGGGTGGAG 97543           ACTGTCT
          TG                    CATTTCACTTTC      GAGAT
                                ||||||||||||      |||||
                                GTGAGGTGGGAG      CTCTG
                                      AGCCTAT
GAM224  LOC255480 3'  TCTTGAGGAGGTGAAGG     96521        GT  _
                                CTTTCACT  CT GAGA
                                ||||||||  || ||||
                                GGAAGTGG  GA TTCT
                                    AG  G
GAM224  LOC255779 3'  ATTTCCCCATGCAAAGTGGGAT 96013     TT     _  C  TCT
          G                     CAT  CACTTT CA TG   GAGAT
                                |||  |||||| || ||   |||||
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                                GTA  GTGAAA GT AC   CTTTA
                                  GG     C  _  CC_
GAM224   LOC256145 5'  GTCTCGGGCATCGTGGG     96543       __
                                TTCAC  TGTCTGAGAT
                                |||||  ||||||||||
                                GGGTG  ACGGGCTCTG
                                   CT
GAM224   LOC256405 5'  ATCTCAGGACCAGATAGTGGAG 95872         T  ACTG
           TG                     CATTTCACT TC    TCTGAGAT
                                |||||||||  ||    ||||||||
                                GTGAGGTGA AG    GGACTCTA
                                     T  ACCA
GAM224   LOC256639 5'  GTCTTGCTTCAGGAAGGTGAAG 96219           A   TC_
           TG                     CATTTCACTTTC CTG   TGAGAT
                                ||||||||||||  |||   ||||||
                                GTGAAGTGGAAG GAC   GTTCTG
                                      _  TTC
GAM224   LOC257048 3'  TATGTAGGTAGTGGGGGGAAAT 96216       A  TT    GT   AGAT
           G                       CATTTC CT  CACT  CTG
                                ||||||  ||  ||||  |||
                                GTAAAG GG  GTGA  GAT
                                   _  GG    TG   GTATT
GAM224   LOC257554 5'  ATCTCAGATTGTGGGGGTGTGG 97691       _   TT   T
           ATG                      CATTT CACT  CAC GTCTGAGAT
                                |||||  ||||  |||  |||||||||
                                GTAGG GTGG  GTG TAGACTCTA
                                   T   GG   T
GAM224   LOC257556 3'  ATTTTTATTGTGGGGTGGGATG 97707     TT    T  TGTCT
                                CAT  CACTT CAC     GAGAT
                                |||  |||||  |||    |||||
                                GTA  GTGGG GTG     TTTTA
                                  GG     _  TTAT_
GAM224   LOC257617 3'  ATTTTTATTGTGGGGTGGGATG 97813     TT    T  TGTCT
                                CAT  CACTT CAC     GAGAT
                                |||  |||||  |||    |||||
                                GTA  GTGGG GTG     TTTTA
                                  GG     _  TTAT_
GAM224   LOC51107  3'  TTTCTGCTGAGGGTGGAGTG   32064           CT  CT
                                CATTTCACTTTCA  GT  GAGA
                                ||||||||||||  ||  ||||
                                GTGAGGTGGGAGT  CG  CTTT
                                      __  T_
GAM224   LOC51152  3'  GTCTCAAAGGAGAAAGTGAGGT 32454           A  GTC
           G                       CATTTCACTTTC CT   TGAGAT
                                ||||||||||||  ||   ||||||
                                GTGGAGTGAAAG GG   ACTCTG
                                      A  AA_
GAM224   LOC51716  3'  GCAGTGAAGGTGAGGT      32792
                                ATTTCACTTTCACTGT
                                ||||||||||||||||
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                                TGGAGTGGAAGTGACG

GAM224  LOC56912  5' CTCACGAGAGTGGAAG      39336         G _
                                CTTTCACT TC TGAG
                                |||||||| || ||||
                                GAAGGTGA AG ACTC
                                     G  C
GAM224  LOC56959  5' TCTTGACCGGAGGTGGAA    81927          ACT   T
                                TTTCACTTTC   GTC GAGA
                                ||||||||||   ||| ||||
                                AAGGTGGAGG   CAG TTCT
                                      C__  _
GAM224  LOC89135  3' TGGTGAGTGAGATG       60319         TT
                                CATTTCAC  TCACTG
                                ||||||||  ||||||
                                GTAGAGTG  AGTGGT

                                   __
GAM224  LOC90170  5' GGTGGTGAGGGTTAAATG    61710      C      TG
                                CATTT ACTTTCAC  TC
                                ||||| ||||||||  ||
                                GTAAA TGGGAGTG  GG
                                   T       GT
GAM224  LOC90826  5' GTCTTGGGTTTGGAATGTGAAA 64095         _    CTG  TG
           TG                     CATTTCAC TTTCA   TC  AGAT
                                ||||||||| |||||   ||  ||||
                                GTAAAGTG AAGGT   GG  TCTG
                                     T    TT_  GT
GAM224  LOC91363  3' ATCTCAGAACAGAAGGGTGGGA 65776    TT     CA    _
                                T  CACTTT  CTGT CTGAGAT
                                |  ||||||  |||| |||||||
                                A  GTGGGA  GACA GACTCTA
                                 GG     A_    A
GAM224  LOC91450  3' GTTTTGGGCAGAGGAGTGGGG  66076    TT     CA     TG
                                T  CACTTT  CTGTC  AGAT
                                |  ||||||  |||||  ||||
                                G  GTGAGG  GACGG  TTTG
                                 GG     A_    GT
GAM224  LOC91628  3' GCAGTGGATGTGGGATG     66760     TT   T
                                CAT  CAC TTCACTGT
                                |||  ||| ||||||||
                                GTA  GTG AGGTGACG
                                  GG   T
GAM224  LOC92305  3' GTCTCAGACTCCTGGGTAGGGG 56418     TT _    TCACT
           TG                     CAT  C ACTT    GTCTGAGAT
                                |||  | ||||    |||||||||
                                GTG  G TGGG    CAGACTCTG
                                  GG A    TCCT_
GAM224  LOC93349  3' CTTAGGCGGATGGAGG      56457        _
                                CTTTCA CTGTCTGAG
                                |||||| |||||||||
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                                GGAGGT GGCGGATTC
                                   A
GAM224  LOC93587  3'  TAGGAGAAAGTGAGGTG     72648          A_
                                CATTTCACTTTC  CTG
                                ||||||||||||  |||
                                GTGGAGTGAAAG  GAT
                                      AG
GAM225  FCN2      3'  GACAACTTACATACACTCC    31740      A_      A
                                GGAG  TATGTAA TTGTC
                                ||||  ||||||| |||||
                                CCTC  ATACATT AACAG
                                  AC      C
GAM225  KCNJ10    3'  CAATACACATACCTCCCTTA   9533         A     AA
                                TGAGGGAG TATGT  ATTG
                                |||||||| |||||  ||||
                                ATTCCCTC ATACA  TAAC
                                     C    CA
GAM225  MTMR2     3'  GACAATTCACATGTCT      32384        A     C
                                AGATATGT AATTGT C
                                |||||||| |||||| |
                                TCTGTACA TTAACA G
                                     C     A
GAM225  RDBP      3'  TGGAAGCTTACACATCTCCCTC 11275          A     ATTG
          A                      TGAGGGAGAT TGTAA    TCCA
                                 |||||||||| |||||    ||||
                                 ACTCCCTCTA ACATT    AGGT
                                       C    CGA_
GAM225  STIM1     3'  GACAACTCTCTCCCTTA     60149         TAT  AAAT
                                TGAGGGAGA   GT    TGTC
                                |||||||||   ||    ||||
                                ATTCCCTCT   CA    ACAG
                                     CT_ ____
GAM225  TNFSF4    3'  TGGACAAGCTTACATCTTCCTC 12446         TA    A_
          A                      TGAGGGAGA  TGTAA  TTGTCCA
                                 |||||||||  |||||  |||||||
                                 ACTCCTTCT  ACATT  AACAGGT
                                       __    CG
GAM225  AD-020    3'  TTACATACCTCCTTCA      39312         A
                                TGAGGGAG TATGTAA
                                |||||||| |||||||
                                ACTTCCTC ATACATT
                                     C
GAM225  AD-020    3'  TTACATACCTCCTTCA      59388         A
                                TGAGGGAG TATGTAA
                                |||||||| |||||||
                                ACTTCCTC ATACATT
                                     C
GAM225  FLJ13063  5'  GACCACATCTCCCTC       71829         A  TAAATT
                                GAGGGAGAT TG     GTC
                                |||||||||  ||     |||
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                                CTCCCTCTA AC     CAG
                                     C _______
GAM225  KIAA0202  3'  ACAATTTAAATTTCCATCA   64366    G    ATG
                                TGA GGAGAT   TAAATTGT
                                ||| ||||||   ||||||||
                                ACT CCTTTA   ATTTAACA
                                  A     A__
GAM225  KIAA0285  3'  GGGCTCCCACACCTCCCTCA   29021       ATA   AAATT
                                TGAGGGAG   TGT    GTCC
                                ||||||||   |||    ||||
                                ACTCCCTC   ACA    CGGG
                                     C__   CCCT_
GAM225  NGEF      3'  CAGTATTACACCACCTCCCTCA 69162       ATA_    _
                                TGAGGGAG    TGTAA ATTG
                                ||||||||    ||||| ||||
                                ACTCCCTC    ACATT TGAC
                                     CACC     A
GAM225  TAF2      3'  TGGACAATTTACACACCC    12088    AGATA
                                GGG    TGTAAATTGTCCA
                                |||    ||||||||||||
                                CCC    ACATTTAACAGGT
                                  AC___
GAM225  LOC152274 3'  TGGCTATAAACACCTCCCTCA  80510       ATA   AAATT T
                                TGAGGGAG   TGT    G CCA
                                ||||||||   |||    | |||
                                ACTCCCTC   ACA    C GGT
                                     C__   AATAT _
GAM225  LOC222008 3'  GACAATTTACAACCT      94008    AGATA
                                GGG    TGTAAATTGTC
                                |||    ||||||||||
                                TCC    ACATTTAACAG
                                  A____
GAM225  LOC91149  3'  GAGAATACATATTCCCTCA   65076       A    AA  G
                                TGAGGGAG TATGTA  TT TC
                                |||||||| ||||||  || ||
                                ACTCCCTT ATACAT  AA AG
                                     _     __  G
GAM226  BCL11A    3'  AGAGAGAGAAAAAGAC     43157      C
                                GTCTTT TCTCTCTCT
                                |||||| |||||||||
                                CAGAAA AGAGAGAGA
                                   A
GAM226  BCL11A    3'  CTGAGAGAAAAAGAGAGAGAGA 43163         C__
                                TCTTTCTCTCT   TCTCTCAG
                                ||||||||||   ||||||||
                                AGAGAGAGAGA   AGAGAGTC
                                      AAA
GAM226  CALU      3'  CTGAGATTAAAAAAAGACTA  6884        CTCTCTCTC
                                TAGTCTTT       TCTCAG
                                ||||||||       ||||||
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                                ATCAGAAA       AGAGTC
                                    AAAATT___
GAM226  KCNK6    3'  CTGAAAGAAAGAGAGAAAGA  16691          C  C
                                TCTTTCTCTCT TCT TCAG
                                |||||||||| ||| ||||
                                AGAAAGAGAGA AGA AGTC
                                      A  A
GAM226  PRDM2    3'  CTGAGAGAGAGAGAGG     31848
                                TCTCTCTCTCTCTCAG
                                ||||||||||||||||
                                GGAGAGAGAGAGAGTC

GAM226  SIM1     3'  CTGAGAAAGAGAGAGA      17379         C
                                TCTCTCTCT TCTCAG
                                ||||||||| ||||||
                                AGAGAGAGA AGAGTC
                                      A
GAM226  WW45     3'  TGAGAGAGAGAGAGCCAGA   41521     TT
                                TCT  CTCTCTCTCTCTCA
                                |||  ||||||||||||||
                                AGA  GAGAGAGAGAGAGT
                                  CC
GAM226  6H9A     3'  AGAGTAGAAAGATTAA      16930          _
                                TTAGTCTTTCT CTCT
                                |||||||||| ||||
                                AATTAGAAAGA GAGA
                                      T
GAM226  C17      3'  AGAAGAAAAGGACTAA      37856         C  C
                                TTAGTCTTT TCT TCT
                                ||||||||| ||| |||
                                AATCAGGAA AGA AGA
                                      A  _
GAM226  CGI-85   3'  CTGAAAAAGAGAACGAAGACTA 32080         CTC    CTC
           A                     TTAGTCTTT   TCTCT   TCAG
                                |||||||||   |||||  ||||
                                AATCAGAAG   AGAGA   AGTC
                                      CA_    AAA
GAM226  FLJ14327 3'  CTGAGAGAGAAATGTAGAT   46135     TTCTCTC
                                GTCT      TCTCTCTCAG
                                ||||      ||||||||||
                                TAGA      AGAGAGAGTC
                                  TGTAA__
GAM226  G2       3'  AGAAAGAGAGAAGAT       66656      T     C
                                GTCTT CTCTCT TCT
                                ||||| |||||| |||
                                TAGAA GAGAGA AGA
                                  _     A
GAM226  GDAP1L1  3'  GAGAGAGAGAGAGAAA      43832
                                TTTCTCTCTCTCTCTC
                                ||||||||||||||||
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                                AAAGAGAGAGAGAGAG

GAM226  KIAA0907  3'  GAGAGAGAGAGAGAGA      30176
                                TCTTTCTCTCTCTCTC
                                ||||||||||||||||
                                AGAGAGAGAGAGAGAG

GAM226  KIAA1577  3'  CTGAGAGAAAACCTATCAGAAG 64477          CTCTC____
              GACTAA                  TAGTCTTTCT       TCTCTCAG
                                ||||||||||       ||||||||
                                ATCAGGAAGA       AGAGAGTC
                                      CTATCCAAA
GAM226  MGC3020   3'  CTGAGAGAAATGAGGAAA    43894     T   TC_
                                TTTC CTC   TCTCTCAG
                                |||| |||   ||||||||
                                AAAG GAG   AGAGAGTC
                                  _   TAA
GAM226  MGC5508   3'  AGAGAAACAGAGAAAGAC    44031         CTC
                                GTCTTTCTCT   TCTCT
                                ||||||||||   |||||
                                CAGAAAGAGA   AGAGA
                                      CAA
GAM226  RANBP8    5'  CTGAGAGGGTCAAAAGAAAACT 21111      C    CTCT_
              AA                  TTAGT TTTCT    CTCTCTCAG
                                ||||| |||||    |||||||||
                                AATCA AAAGA    GGGAGAGTC
                                  _    AAACT
GAM226  SH3KBP1   3'  AGAAGAAAAAGAAAGAC     66346        CTC   C
                                GTCTTTCT   TCT TCT
                                ||||||||   ||| |||
                                CAGAAAGA   AGA AGA
                                     AAA   _
GAM226  LOC112476 3'  CTGGGGGAAGAAAAAAACTAA  59113      C   C   CTC
                                TTAGT TTT TCT   TCTCTCAG
                                ||||| ||| |||   ||||||||
                                AATCA AAA AGA   AGGGGGTC
                                  A   A   ____
GAM226  LOC147622 3'  CTGGCTTCAGAGAGAAGAGACT 84049          C      CTC_
              AA                  TTAGTCTTT TCTCTCT    TCAG
                                |||||||| |||||||    ||||
                                AATCAGAGA AGAGAGA    GGTC
                                     _      CTTC
GAM226  LOC150538 3'  CTGATATTTAGAGAACAAGACT 79933         TC    CTCTC
              AA                  TTAGTCTT  TCTCT    TCAG
                                ||||||||  |||||    ||||
                                AATCAGAA  AGAGA    AGTC
                                     CA    TTTAT
GAM226  LOC200059 3'  CTGAGAAAAAAAGAGAGGTGA  88552    TT      CTC__
                                TC  TCTCTCT    TCTCAG
                                ||  |||||||    ||||||
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                                AG  GGAGAGA    AGAGTC
                                 T_      AAAAA
GAM226  LOC221395 5'  CTGAAAACTCCAGAAGAGAAAG 92028          C   CTC____
              GC                  GTCTTTCTCT TCT      TCAG
                                  |||||||||| |||      ||||
                                  CGGAAAGAGA AGA      AGTC
                                       _  CCTCAAA
GAM226  LOC221711 3'  CTGAAGACGAAGAGAAAGA   92208         C _  C
                                  TCTTTCTCT TC TCT TCAG
                                  ||||||||| || ||| ||||
                                  AGAAAGAGA AG AGA AGTC
                                       _ C  _
GAM226  LOC57105  3'  AGATTCAGGGAAAGACTAA   39814           CTC
                                  TTAGTCTTTCTCT   TCT
                                  ||||||||||||   |||
                                  AATCAGAAAGGGA   AGA
                                        CTT
GAM227  DACH     3'  TGAGAATGTTTGTAAATGTACA 54974       CATCC   CT
                                  TGTACA    ACA  CATTCTCA
                                  ||||||    |||  ||||||||
                                  ACATGT    TGT  GTAAGAGT
                                     AAA__   TT
GAM227  IL11RA   3'  GGAACGTGTGTAATGTGTACA  15712         C_    TCA
                                  TGTACACAT  CACAC   TTCT
                                  |||||||||  |||||   ||||
                                  ACATGTGTA  GTGTG   AAGG
                                       AT    C__
GAM227  LYPLA1   3'  AGAATGAGGTGGTATTACA   20922      CACAT   A
                                  TGTA    CCAC CTCATTCT
                                  ||||    |||| ||||||||
                                  ACAT    GGTG GAGTAAGA
                                    TAT__   _
GAM227  NAPB     3'  GAGAATGAATGTATGT      70183      CC   C
                                  ACAT  ACA TCATTCTC
                                  ||||  ||| ||||||||
                                  TGTA  TGT AGTAAGAG
                                    __   A
GAM227  NRF1     3'  GAATATATGTATATGTGTACA  60120         CC   CTC
                                  TGTACACAT  ACA   ATTC
                                  |||||||||  |||   ||||
                                  ACATGTGTA  TGT   TAAG
                                       TA   ATA
GAM227  PRKAB1   3'  AGAGGGAATGGACTGTACA   20734       CA   CA   AT
                                  TGTACA  TCCA  CTC  TCT
                                  ||||||  ||||  |||  |||
                                  ACATGT  AGGT  GGG  AGA
                                     C_    AA   __
GAM227  PTGFR    3'  TGAGAGAGATGTGTACA     6319          CACA
                                  TGTACACATC    CTCA
                                  ||||||||||    ||||
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                                ACATGTGTAG   GAGT
                                     AGA_
GAM227  RBBP5    3'  AGATTGGATAGATGTGTACA  17327        CACAC  T
                                TGTACACATC    TCA TCT
                                ||||||||||    ||| |||
                                ACATGTGTAG    GGT AGA
                                     ATA__   T
GAM227  SAT      3'  TGAGTCATTTAAATGTGTACA  11436       CCAC___
                                TGTACACAT     ACTCA
                                |||||||||     |||||
                                ACATGTGTA     TGAGT
                                     AATTTAC
GAM227  TMP21    3'  AATGGTGATGGATGTGACA   22399    A      _  T
                                TGT CACATCCA CAC CATT
                                ||| |||||||| ||| ||||
                                ACA GTGTAGGT GTG GTAA
                                  _      A  _
GAM227  UBE2V1   3'  TGAAATGTGGATGCATAC    41797    CA     C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
                                CAT  GTAGGTGT  AGT
                                  AC       AA
GAM227  UBE2V1   3'  TGAAATGTGGATGCATAC    42374    CA     C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
                                CAT  GTAGGTGT  AGT
                                  AC       AA
GAM227  UBE2V1   3'  TGAAATGTGGATGCATAC    12522    CA     C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
                                CAT  GTAGGTGT  AGT
                                  AC       AA
GAM227  ZIC1     3'  AGAATGTTCTAGTAAATGTGTA 12720       CC  ACT__
           C                     GTACACAT  AC    CATTCT
                                |||||||  ||    ||||||
                                CATGTGTA  TG    GTAAGA
                                     AA  ATCTT
GAM227  AF038169 5'  TGAAAATGAGTGCTGTAGATG  25255     __ _     C
                                CATC  CA CACTCATT TCA
                                ||||  || |||||||| |||
                                GTAG  GT GTGAGTAA AGT
                                  AT  C       A
GAM227  CDC14A   3'  AGAAGTGGATGTATATA     13391     C      ACTCA
                                TGTA ACATCCAC    TTCT
                                |||| ||||||||    ||||
                                ATAT TGTAGGTG    AAGA
                                  A      _____
GAM227  DKFZP564I052 3'  GATGATCATGTGATGTGTACA  66710         C  C__
                                TGTACACATC ACA   TCATT
                                |||||||||| |||   |||||
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                                ACATGTGTAG TGT   AGTAG
                                      _  ACT
GAM227  DKFZP761F241 3'  TGAGAATGAGTGAGGTTTCGTA 48800      ACAT  A
          CA                    TGTAC   CC CACTCATTCTCA
                                ||||||   || ||||||||||||
                                ACATG   GG GTGAGTAAGAGT
                                   CTTT  A
GAM227  FLJ11101  3'  AGAAGTGTTGAGTGTGTACA  37049        TC  _   CAT
                                TGTACACA  CA CACT   TCT
                                ||||||||  || ||||   |||
                                ACATGTGT  GT GTGA   AGA
                                    GA  T   ____
GAM227  FLJ14642  3'  AGTATGGGTGTGTACA     51492          C
                                TGTACACATCCA ACT
                                |||||||||||| |||
                                ACATGTGTGGGT TGA
                                       A
GAM227  FLJ20399  3'  GGTGGCTGTGGATGCCACA   35125    ACA      CT
                                TGT   CATCCACA  CATT
                                |||   ||||||||  ||||
                                ACA   GTAGGTGT  GTGG
                                  CC_      CG
GAM227  GFPT1    3'  GAAGATGGGATGTGTACA    9022          A  C  A
                                TGTACACATCC CA TC TTC
                                |||||||||||  || || |||
                                ACATGTGTAGG GT AG AAG
                                         _  _  _
GAM227  KIAA0450  3'  GAGGGCAGTGTGGATG     27640         CA
                                CATCCACACT  TTCTC
                                ||||||||||  |||||
                                GTAGGTGTGA  GGGAG
                                      C_
GAM227  KIAA0530  3'  GATGGTATGAAAATGTGTACA  70867        C__  C  T
                                TGTACACAT   CA AC CATT
                                |||||||||   || || ||||
                                ACATGTGTA   GT TG GTAG
                                     AAA  A  _
GAM227  KIAA0753  3'  GGGGAGTTAAATGTGTACA   28999        CCAC   ATT
                                TGTACACAT   ACTC   CTC
                                |||||||||   ||||   |||
                                ACATGTGTA   TGAG   GGG
                                     AAT_   ____
GAM227  KIAA0788  3'  TGAATTAGGAATGTGTACA   71339        _  ACAC
                                TGTACACAT CC    TCA
                                |||||||||  ||    |||
                                ACATGTGTA GG    AGT
                                     A  ATTA
GAM227  KIAA0855  3'  AGAATGAGCAGTGTAC     30400       ATCCACA
                                GTACAC      CTCATTCT
                                ||||||      ||||||||
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                                CATGTG      GAGTAAGA
                                  AC_____
GAM227  KIAA0865  5'  GAGCAAGTGGAATGTGTACA  61250        _   A__
                                TGTACACAT CCAC   CTC
                                ||||||||| ||||   |||
                                ACATGTGTA GGTG   GAG
                                    A    AAC
GAM227  KIAA0992  3'  GGAAGTGTGGAGCACACA    32207    ACACA      CAT
                                TGT    TCCACACT   TCT
                                |||    ||||||||   |||
                                ACA    AGGTGTGA   AGG
                                 CACG_      ___
GAM227  MGC16037  5'  TGAGGTGTAGATATGTATA   51822      C  C   _
                                TGTACA ATC ACAC TCA
                                |||||| ||| |||| |||
                                ATATGT TAG TGTG AGT
                                   A  A   G
GAM227  OSRF      3'  TGAAAATGCACACAAATGTGTA 59525       CCACACT   C
          CA                     TGTACACAT      CATT TCA
                                |||||||||      |||| |||
                                ACATGTGTA      GTAA AGT
                                    AACACAC    A
GAM227  RAB3-GAP150 3'  TGAGAATCAGAGATGTGTA   24839       CACA  C
                                TACACATC    CT ATTCTCA
                                ||||||||    || |||||||
                                ATGTGTAG    GA TAAGAGT
                                    A___  C
GAM227  RAP140    3'  GATGGGTAAATGTGTACA    30844       CCAC
                                TGTACACAT    ACTCATT
                                |||||||||    |||||||
                                ACATGTGTA    TGGGTAG
                                    AA__
GAM227  TACTILE   5'  GAGTGCATGTGTACA      19471        CCA
                                TGTACACAT   CACTC
                                |||||||||   |||||
                                ACATGTGTA   GTGAG
                                    C__
GAM227  LOC131873 3'  GATGTATGCATATGTGTACA  75880       CCA  CT
                                TGTACACAT   CA  CATT
                                |||||||||   ||  ||||
                                ACATGTGTA   GT  GTAG
                                    TAC  AT
GAM227  LOC134145 3'  AGCTGTATATGTGTACA     75144       CC  _
                                TGTACACAT  ACA CT
                                |||||||||  ||| ||
                                ACATGTGTA  TGT GA
                                    TA   C
GAM227  LOC145482 3'  AATGGTATGATGTGTACA    77226        CAC  T
                                TGTACACATC   AC CATT
                                ||||||||||   || ||||
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                                ACATGTGTAG   TG GTAA
                                      TA_  _
GAM227  LOC148195 3'  GAAAAGGTGGATGTGTCA    84129    T        A  CA
                                TG ACACATCCAC CT  TTC
                                || |||||||||| ||  |||
                                AC TGTGTAGGTG GA  AAG
                                 _        _ A_
GAM227  LOC152633 5'  TGAGCTGTACATGTAGAGTGTA 85826        A  C   CT__  TT
          CA                     TGTACAC TC ACA    CA  CTCA
                                ||||||| || |||   ||  ||||
                                ACATGTG AG TGT    GT  GAGT
                                    _ A   ACAT  C_
GAM227  LOC153630 5'  AATGAGTGTGCGTAC      86079      ACATC
                                GTAC    CACACTCATT
                                ||||    ||||||||||
                                CATG    GTGTGAGTAA
                                  C____
GAM227  LOC221662 3'  AGAATGAGGGGAATGGGCA   92399    TA  CA   ACA
                                TG  CA  TCC   CTCATTCT
                                ||  ||  |||   ||||||||
                                AC  GT  AGG   GAGTAAGA
                                 GG  A_  G__
GAM227  LOC254659 5'  GAGAATGGAGATGCTACA    95113     CA    CACAC
                                TGTA  CATC    TCATTCTC
                                ||||  ||||    ||||||||
                                ACAT  GTAG    GGTAAGAG
                                  C_   A____
GAM227  LOC83693  3'  AGGGTGTGTGGATGGCACA   48830     ACA       TC
                                TGT   CATCCACAC  ATTCT
                                |||   |||||||||  |||||
                                ACA   GTAGGTGTG  TGGGA
                                 CG_       __
GAM227  LOC90981  3'  AATGGTGATGGATGTGACA   64532     A      _   T
                                TGT CACATCCA CAC CATT
                                ||| |||||||| ||| ||||
                                ACA GTGTAGGT GTG GTAA
                                  _       A  _
GAM228  ADARB1    3'  CTCAAACACTTTACCCCA    31722    A      A
                                TG GGTAAAGT GTTTGAG
                                || |||||||| |||||||
                                AC CCATTTCA CAAACTC
                                 C      _
GAM228  DDX19     3'  AAACTACCTACCTCA       23382        AA
                                TGAGGTA  GTAGTTT
                                |||||||  |||||||
                                ACTCCAT  CATCAAA
                                    C_
GAM228  GAN       3'  CTCAACCCACTTTACCCCA   41862    A      AGT
                                TG GGTAAAGT   TTGAG
                                || ||||||||   |||||
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                                AC CCATTTCA   AACTC
                                 C       CCC
GAM228  HKE4     3'  TAAACTACCCTGCCCCA     22732    A    AA
                                TG GGTA  GTAGTTTG
                                || ||||  ||||||||
                                AC CCGT  CATCAAAT
                                 C   CC
GAM228  ARTN     5'  TTAAACCATTTACCTCA     14277         GTA
                                TGAGGTAAA   GTTTGA
                                |||||||||   ||||||
                                ACTCCATTT   CAAATT
                                      AC_
GAM228  DKFZP434H132 3'  ACAACGCAACCTACCTCA    31314       AAAGT  T   A
                                TGAGGT    AG TTG GTTGT
                                ||||||    || ||| |||||
                                ACTCCA    TC AAC CAACA
                                   _____  C   G
GAM228  DKFZP434H132 3'  ACAACGCAACCTACCTCA    73602       AAAGT  T   A
                                TGAGGT    AG TTG GTTGT
                                ||||||    || ||| |||||
                                ACTCCA    TC AAC CAACA
                                   _____  C   G
GAM228  FLJ11126  3'  AAACTACCTACCTCA      37081        AA
                                TGAGGTA  GTAGTTT
                                |||||||  |||||||
                                ACTCCAT  CATCAAA
                                   C_
GAM228  FLJ25416  5'  CTCAAACTCCCTACCTCA    58808        AAGT
                                TGAGGTA   AGTTTGAG
                                |||||||   ||||||||
                                ACTCCAT   TCAAACTC
                                   CCC_
GAM228  MGC16063  3'  AACTCAAAACCACCTTGCCTCA 53857        A  AG_
                                TGAGGTAA GT   TTTGAGTT
                                |||||||| ||   ||||||||
                                ACTCCGTT CA   AAACTCAA
                                     C  CCA
GAM228  SLC26A9   3'  GACAACTCACTCTCCCCTACTC 53622    AG   AAGT  TT
           CA                    TG  GTA   AG  TGAGTTGTC
                                || |||   ||  |||||||||
                                AC  CAT   TC  ACTCAACAG
                                 CT   CCCC  TC
GAM228  SLC26A9   3'  GACAACTCACTCTCCCCTACTC 56183    AG   AAGT  TT
           CA                    TG  GTA   AG  TGAGTTGTC
                                || |||   ||  |||||||||
                                AC  CAT   TC  ACTCAACAG
                                 CT   CCCC  TC
GAM228  LOC58489  3'  ACAACTTGATCTTACCTCA   72526        AAGT  T TG
                                TGAGGTA   AG T  AGTTGT
                                |||||||   || |  ||||||
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                                ACTCCAT   TC A  TCAACA
                                    ____  T GT
GAM229  AKAP13   3'  CACAAAACCAAACAGCA    22142    G  GCCGG
                                TG TG    TGGTTTTGTG
                                || ||    ||||||||||
                                AC AC    ACCAAAACAC
                                 G  AA___
GAM229  AKAP13   3'  CACAAAACCAAACAGCA    23246    G  GCCGG
                                TG TG    TGGTTTTGTG
                                || ||    ||||||||||
                                AC AC    ACCAAAACAC
                                 G  AA___
GAM229  AKAP13   3'  CACAAAACCAAACAGCA    58577    G  GCCGG
                                TG TG    TGGTTTTGTG
                                || ||    ||||||||||
                                AC AC    ACCAAAACAC
                                 G  AA___
GAM229  ALOX12B  5'  GCACCCACCCCGGCCACCA   6681         T   TTT
                                TGGTGGCCGG GGT   GTGC
                                |||||||||| |||   ||||
                                ACCACCGGCC CCA   CACG
                                     _  CC_
GAM229  CAV3     3'  GCACAAAAATGGGCACCA    52891      G   GTGG
                                TGGTG CCG    TTTTGTGC
                                ||||| |||    ||||||||
                                ACCAC GGT    AAAACACG
                                   G   A___
GAM229  CYP1A1   3'  GCACATATCCAGGCACCA    4944       G  GG   TTT
                                TGGTG CC  TGG   TGTGC
                                ||||| ||  |||   |||||
                                ACCAC GG  ACC   ACACG
                                   _ __   TAT
GAM229  DFFB     3'  ACAGGCACCTACCACCA     87371      CC    GT
                                TGGTGG  GGTG  TTTGT
                                ||||||  ||||  |||||
                                ACCACC  CCAC  GGACA
                                    AT   __
GAM229  FASN     3'  CACAGGGCCCGGCCAC      14632        TG
                                GTGGCCGG  GTTTTGTG
                                ||||||||  ||||||||
                                CACCGGCC  CGGGACAC
                                     __
GAM229  GALGT    3'  GCACAAAAGAAGGGGCACCA  7616       G  GGTGG
                                TGGTG CC    TTTTGTGC
                                ||||| ||    ||||||||
                                ACCAC GG    AAAACACG
                                   G  GAAG_
GAM229  GCH1     3'  GCACAAAACCACTGCCA     3860       C
                                TGGC GGTGGTTTTGTGC
                                |||| |||||||||||||
```

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                                ACCG TCACCAAAACACG
                                  _
GAM229  GRIK3   3' GCACAAACAGAGGCCGCCA  5889       GG  GT
                                TGGTGGCC  TG  TTTGTGC
                                ||||||||  ||  |||||||
                                ACCGCCGG  AC  AAACACG
                                    AG  __
GAM229  ITGA2   3' GCACTGGAAACCACCACCA  9375     GGCC      __
                                TGGT   GGTGGTTTT  GTGC
                                ||||   |||||||||  ||||
                                ACCA   CCACCAAAG  CACG
                                  ____       GT
GAM229  ITPKB   3' GCACAAAACCATCGGGGAACCA 9431     GG_
                                TGGT   CCGGTGGTTTTGTGC
                                ||||   ||||||||||||||
                                ACCA   GGCTACCAAAACACG
                                  AGG
GAM229  LANCL1  3' CACAAAAAATTGCAACCCCCA  20209    T  CCG TG   __
                                TGG GG   G  GTTT  TGTG
                                ||| ||   |  ||||  ||||
                                ACC CC   C  TAAA  ACAC
                                  _  CAA GT    AA
GAM229  MEN1    3' CACAAAACTCCGCCCCCA    55469    T  C   T
                                TGG GG CGG GGTTTTGTG
                                ||| || ||| |||||||||
                                ACC CC GCC TCAAAACAC
                                  _  C  _
GAM229  MEN1    3' CACAAAACTCCGCCCCCA    55470    T  C   T
                                TGG GG CGG GGTTTTGTG
                                ||| || ||| |||||||||
                                ACC CC GCC TCAAAACAC
                                  _  C  _
GAM229  MEN1    3' CACAAAACTCCGCCCCCA    55471    T  C   T
                                TGG GG CGG GGTTTTGTG
                                ||| || ||| |||||||||
                                ACC CC GCC TCAAAACAC
                                  _  C  _
GAM229  MEN1    3' CACAAAACTCCGCCCCCA    55472    T  C   T
                                TGG GG CGG GGTTTTGTG
                                ||| || ||| |||||||||
                                ACC CC GCC TCAAAACAC
                                  _  C  _
GAM229  MEN1    3' CACAAAACTCCGCCCCCA    55473    T  C   T
                                TGG GG CGG GGTTTTGTG
                                ||| || ||| |||||||||
                                ACC CC GCC TCAAAACAC
                                  _  C  _
GAM229  MEN1    3' CACAAAACTCCGCCCCCA    55476    T  C   T
                                TGG GG CGG GGTTTTGTG
                                ||| || ||| |||||||||
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                                ACC CC GCC TCAAAACAC
                                  _ C  _
GAM229  MEN1     3'  CACAAAACTCCGCCCCCA    4158     T C  T
                                TGG GG CGG GGTTTTGTG
                                ||| || ||| |||||||||
                                ACC CC GCC TCAAAACAC
                                  _ C  _
GAM229  PLXNA2   3'  GCACAAATTGCAAAGCCATCA 47210       CG_ TG   T
                                TGGTGGC  G  GTTT GTGC
                                |||||||  |  |||| ||||
                                ACTACCG  C  TAAA CACG
                                   AAA GT   _
GAM229  SH3GL1   3'  GCACAAGCTGCCACCACCA   11624      CC  TG   T
                                TGGTGG  GG  GTTT GTGC
                                ||||||  ||  |||| ||||
                                ACCACC  CC  CGAA CACG
                                   A_  GT   _
GAM229  WWOX     3'  ACCACCACGGCCACCA     33043       __
                                TGGTGGCC  GGTGGT
                                ||||||||  ||||||
                                ACCACCGG  CCACCA
                                    CA
GAM229  WWOX     3'  ACCACCACGGCCACCA     55441       __
                                TGGTGGCC  GGTGGT
                                ||||||||  ||||||
                                ACCACCGG  CCACCA
                                    CA
GAM229  ARGBP2   3'  ACATCTCCACCTGCCACCA   13192      C    TTT
                                TGGTGGC GGTGG  TGT
                                ||||||| |||||  |||
                                ACCACCG CCACC  ACA
                                   T    TCT
GAM229  C11orf17 3'  ACAGGCACCCGCCACCA    40209      C   GT
                                TGGTGGC GGTG  TTTGT
                                ||||||| ||||  |||||
                                ACCACCG CCAC  GGACA
                                   C   __
GAM229  C1QR1    3'  CACTAGAGTCACCAGCCACCA 23838      C   GT  _
                                TGGTGGC GGTG  TTT GTG
                                ||||||| ||||  ||| |||
                                ACCACCG CCAC  AGA CAC
                                   A   TG  T
GAM229  DKFZp547J036 3'  CACAAAACTCAGCCCAGCCA  50126    C_  __
                                TGGC  GGT  GGTTTTGTG
                                ||||  |||  |||||||||
                                ACCG  CCG  TCAAAACAC
                                  AC  AC
GAM229  FHX      3'  CACAAAACTTCCCATCA     37300      CCGGT
                                TGGTGG    GGTTTTGTG
                                ||||||    |||||||||
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                                ACTACC    TCAAAACAC
                                   CT___
GAM229  FLJ10276  3'  CACAAAACAGCTACCA     35963       CGGTG
                                TGGTGGC    GTTTTGTG
                                |||||||    ||||||||
                                ACCATCG    CAAAACAC
                                   A____
GAM229  FLJ11117  3'  CACTCCACCAGCCCCA     37074    T  C    TTTT
                                TGG GGC GGTGG   GTG
                                ||| ||| |||||   |||
                                ACC CCG CCACC   CAC
                                  _  A    T___
GAM229  FLJ12294  3'  CACAAAACCAGAGGACTCA   47007   T  _  GG
                                G GG CC  TGGTTTTGTG
                                | || ||  ||||||||||
                                A TC GG  ACCAAAACAC
                                 C  A  AG
GAM229  FLJ12973  3'  ACAGGCACCTGCCACCA     46097       C   GT
                                TGGTGGC GGTG  TTTGT
                                ||||||| ||||  |||||
                                ACCACCG CCAC  GGACA
                                   T   __
GAM229  FLJ23323  3'  GCAAGCTCCACGGCCACCA   45052        G  T_
                                TGGTGGCCG TGG  TTTGT
                                ||||||||| |||  |||||
                                ACCACCGGC ACC  GAACG
                                     _  TC
GAM229  FREQ     3'  GCAGGCACCAGCCCCA     26579    T  C   GT
                                TGG GGC GGTG  TTTGT
                                ||| ||| ||||  |||||
                                ACC CCG CCAC  GGACG
                                  _  A   __
GAM229  GMPPB    5'  GCAGTTCCACCGGCACCA    95740     G     TT
                                TGGTG CCGGTGG  TTGT
                                ||||| |||||||  ||||
                                ACCAC GGCCACC  GACG
                                   _     TT
GAM229  IFI30    3'  CACAAAATTCCACCCCA     65867    CC   __
                                TGG  GGTGG  TTTTGTG
                                |||  |||||  |||||||
                                ACC  CCACC  AAAACAC
                                  __    TT
GAM229  KIAA0323 3'  GCACTTGACTGGCCACCA    63265         GGTTTT
                                TGGTGGCCGGT    GTGC
                                ||||||||||     ||||
                                ACCACCGGTCA    CACG
                                      GTT____
GAM229  KIAA0459 3'  CACGGAGCACCAGTCACCA   60984       C   G
                                TGGTGGC GGTG TTTTGTG
                                ||||||| |||| |||||||
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                                ACCACTG CCAC GAGGCAC
                                    A   _
GAM229  KIAA0532 3' GCAAGCACCTGCCACCA     70773       C   GT
                                TGGTGGC GGTG  TTTGT
                                ||||||| ||||  |||||
                                ACCACCG CCAC  GAACG
                                    T   __
GAM229  KIAA0618 3' GCACAAAATCAAACCCCA    29163     T  CCGG
                                TGG GG    TGGTTTTGTGC
                                ||| ||    ||||||||||
                                ACC CC    ACTAAAACACG
                                  _ AA__
GAM229  KIAA0960 5' GCAGCGGCCACGGCCACCA   92655         G    _
                                TGGTGGCCG TGGTT TTGT
                                ||||||||| ||||| ||||
                                ACCACCGGC ACCGG GACG
                                     _    C
GAM229  KIAA1084 3' CACAAAACCATTATCCA     29833     CC
                                TGG  GGTGGTTTTGTG
                                |||  ||||||||||||
                                ACC  TTACCAAAACAC
                                  TA
GAM229  KIAA1145 3' GCAGGCACAAGCCACCA     65625       CG   GT
                                TGGTGGC  GTG  TTTGT
                                |||||||  |||  |||||
                                ACCACCG  CAC  GGACG
                                    AA  __
GAM229  KIAA1203 3' GCACAAAATAATCACCA     71640       CCGGTG
                                TGGTGG     GTTTTGTGC
                                ||||||     |||||||||
                                ACCACT     TAAAACACG
                                   AA____
GAM229  KIAA1443 3' ACAGGCACCTGCCACCA     63824       C   GT
                                TGGTGGC GGTG  TTTGT
                                ||||||| ||||  |||||
                                ACCACCG CCAC  GGACA
                                    T   __
GAM229  KIAA1821 3' GCCTTGGCCACCGGCCAGCA  71787    G         TTGT
                                TG TGGCCGGTGGTT    GC
                                || ||||||||||||    ||
                                AC ACCGGCCACCGG    CG
                                 G          TTC_
GAM229  KIAA1883 5' GCACGGGAAACCCGCCACCA  73419       C   GG
                                TGGTGGC GGT  TTTTGTGC
                                ||||||| |||  ||||||||
                                ACCACCG CCA  AGGGCACG
                                    C  A_
GAM229  KIAA1904 3' GCACAAACAGTGAGGCCCCCA 73487     T   GGTG_   T
                                TGG GGCC     GTTT GTGC
                                ||| ||||     |||| ||||
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                                ACC CCGG    CAAA CACG
                                  C   AGTGA   _
GAM229  KIAA1924  3'  GCACAAAAACCACCACCA   73674    CC       _
                                TGG  GGTGGTTTT GTGC
                                |||  ||||||||| ||||
                                ACC  CCACCAAAA CACG
                                  A_       A
GAM229  MGC10870  3'  GCACAAGGAGTCCCAGCCAC   50207      C  TGG_
                                GTGGC GG    TTTTGTGC
                                ||||| ||    ||||||||
                                CACCG CC    GGAACACG
                                   A  CTGA
GAM229  PEG10     3'  GCACAAAATAAGAGGGCCAC   30526      GGTG_
                                GTGGCC    GTTTTGTGC
                                ||||||    |||||||||
                                CACCGG    TAAAACACG
                                    GAGAA
GAM229  PRO2325   3'  CACCAGCCACCGGCCCCA    96301    T        TT
                                TGG GGCCGGTGGTT  GTG
                                ||| ||||||||||  |||
                                ACC CCGGCCACCGA  CAC
                                  _        C_
GAM229  RALGPS1A  3'  GCACAAAACCACCCATTCAT   27603     CC_
                                GTGG   GGTGGTTTTGTGC
                                ||||   |||||||||||||
                                TACT   CCACCAAAACACG
                                  TAC
GAM229  SCYA23    3'  CACAAGTTGCCAGCCACCA    17353       C   GG   T
                                TGGTGGC GGT  TTT GTG
                                ||||||| |||  ||| |||
                                ACCACCG CCG  GAA CAC
                                    A   TT   _
GAM229  SEMA4G    5'  ACAGGGCCACCACCACCA    94669       CC
                                TGGTGG  GGTGGTTTTGT
                                ||||||  ||||||||||
                                ACCACC  CCACCGGGACA
                                    A_
GAM229  SFXN2     3'  ACAGGGCACCTGCCACCA    73935       C   G
                                TGGTGGC GGTG TTTTGT
                                ||||||| |||| ||||||
                                ACCACCG CCAC GGGACA
                                    T   _
GAM229  SMCR5     5'  AGCCACCAGCCAGCCA      58590     _   C
                                TGG TGGC GGTGGTT
                                ||| |||| |||||||
                                ACC ACCG CCACCGA
                                  G   A
GAM229  TP53INP1  3'  CACAAGGCCAACCAC       52723      CCGG
                                GTGG    TGGTTTTGTG
                                ||||    ||||||||||
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                                CACC    ACCGGAACAC
                                  A___
GAM229   TP53INP1  3'  CACAAGGCCAACCAC      72951      CCGG
                                GTGG    TGGTTTTGTG
                                ||||    ||||||||||
                                CACC    ACCGGAACAC
                                  A___
GAM229   LOC113026 3'  ACAGGCACAGGCCACCA     55898        G   GT
                                TGGTGGCC GTG  TTTGT
                                |||||||| |||  |||||
                                ACCACCGG CAC  GGACA
                                    A   __
GAM229   LOC123879 5'  GCCAGGCCACCAGCACCA     75633       G C       T
                                TGGTG C GGTGGTTT GT
                                ||||| | |||||||| ||
                                ACCAC G CCACCGGA CG
                                  _ A       C
GAM229   LOC142955 3'  CACAAAACCAGAGTCCCA     76443     T   CGG
                                TGG GGC   TGGTTTTGTG
                                ||| |||   ||||||||||
                                ACC CTG   ACCAAAACAC
                                  _  AG_
GAM229   LOC143153 3'  ACAGGCCACGGCCACCA     76460         G     T
                                TGGTGGCCG TGGTTT GT
                                |||||||| |||||| ||
                                ACCACCGGC ACCGGA CA
                                      _     _
GAM229   LOC143154 3'  ACAGGCCACGGCCACCA     76476         G     T
                                TGGTGGCCG TGGTTT GT
                                |||||||| |||||| ||
                                ACCACCGGC ACCGGA CA
                                      _     _
GAM229   LOC152274 3'  CATGGAGCCACCAACACCA    80503       GCC       TG
                                TGGTG   GGTGGTTT  TG
                                |||||   ||||||||  ||
                                ACCAC   CCACCGAG  AC
                                  AA_       GT
GAM229   LOC154726 3'  CACAAAATGCAAACACCA     81101       GCCG   G
                                TGGTG    GTG TTTTGTG
                                |||||    ||| |||||||
                                ACCAC    CGT AAAACAC
                                  AAA_  _
GAM229   LOC167153 5'  GCTGTCCCACGGGCCACCA    82675         G    TTTT
                                TGGTGGCC GTGG    GT
                                |||||||| ||||    ||
                                ACCACCGG CACC    CG
                                    G    CTGT
GAM229   LOC200261 5'  GCAGGGGAGCCACCAGCCAC   88656       C       _ G
                                GTGGC GGTGGTTT T TGC
                                ||||| |||||||| | |||
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                                CACCG CCACCGAG G ACG
                                   A       G G
GAM229   LOC200325 5'  GCACTGCTCCCCCGGCCACCA  89989          T  TTTT
                                TGGTGGCCGG GG    GTGC
                                |||||||||| ||    ||||
                                ACCACCGGCC CC    CACG
                                     C  TCGT
GAM229   LOC200471 5'  GCAGCTCACCAGCCCCA     90053     T   C     TT
                                TGG GGC GGTGG  TTGT
                                ||| ||| |||||  ||||
                                ACC CCG CCACT  GACG
                                  _  A     C_
GAM229   LOC203078 3'  CACAGAACCACCGCCACCA    89275        C
                                TGGTGGC GGTGGTTTTGTG
                                ||||||| ||||||||||||
                                ACCACCG CCACCAAGACAC

                                  _
GAM229   LOC204994 5'  ACACTCCACCAGCACCA      89420       G C     TTT
                                TGGTG C GGTGG   TGT
                                ||||| | |||||   |||
                                ACCAC G CCACC   ACA
                                   _ A     TC_
GAM229   LOC219294 3'  ACAGGCCACGGCCACCA      93002          G      T
                                TGGTGGCCG TGGTTT GT
                                ||||||||| |||||| ||
                                ACCACCGGC ACCGGA CA

                                  _     _
GAM229   LOC219295 3'  ACAGGCCACGGCCACCA      92987          G      T
                                TGGTGGCCG TGGTTT GT
                                ||||||||| |||||| ||
                                ACCACCGGC ACCGGA CA

                                  _     _
GAM229   LOC221060 3'  ACAGGCACGGGCCACCA      93204          G   GT
                                TGGTGGCC GTG  TTTGT
                                |||||||| |||  |||||
                                ACCACCGG CAC  GGACA
                                     G   __
GAM229   LOC222159 5'  CACAAATGAGCCATCCA      94075     _   _  GTGGT
                                TGG TGGC CG     TTTGTG
                                ||| |||| ||     ||||||
                                ACC ACCG GT     AAACAC
                                  T   A  _____
GAM229   LOC254549 5'  GCAAGCACCAACCCCA       96238     T  CC    GT
                                TGG GG  GGTG  TTTGT
                                ||| ||  ||||  |||||
                                ACC CC  CCAC  GAACG
                                  _ AA   __
GAM229   LOC257457 3'  CACAAAACCCTTCCCCACC    62627       CC_  T
                                GGTGG   GG GGTTTTGTG
                                |||||   || |||||||||
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                                CCACC   TC CCAAAACAC
                                   CCT  _
GAM229  LOC51162  5'  CACAGCAGCGGCCACCA     32519         G  GTT
                                TGGTGGCCG TG   TTGTG
                                ||||||||| ||   |||||
                                ACCACCGGC AC   GACAC
                                     G  ____
GAM229  LOC51162  5'  CACAGCAGCGGCCACCA     65817         G  GTT
                                TGGTGGCCG TG   TTGTG
                                ||||||||| ||   |||||
                                ACCACCGGC AC   GACAC
                                     G  ____
GAM229  LOC90485  3'  ACAGGCGCCCGGCCACCA    63002          TG   T
                                TGGTGGCCGG  GTTT GT
                                ||||||||||  |||| ||
                                ACCACCGGCC  CGGA CA
                                      CG   _
GAM230  ARHGDIB   3'  GAGAGACACTGTAAACGACAC  6773     A  A  GCT
                                GT TC GT   CAGTGTCTCTC
                                || || ||   ||||||||||
                                CA AG CA   GTCACAGAGAG
                                 C  _  AAT
GAM230  BDKRB2    3'  AGACACTGAGGTCTAGA     5262     _  TG
                                TC AG  CTCAGTGTCT
                                || ||  ||||||||||
                                AG TC  GAGTCACAGA
                                 A  TG
GAM230  NCALD     3'  TAGTGAGCACTAATAC      49378      C       G
                                GTAT AGTGCTCA TG
                                |||| |||||||| ||
                                CATA TCACGAGT AT
                                   A       G
GAM230  TMPRSS4   3'  GAGAGACACAGCCCACTGAAC  39117    A     CTCA
                                GT TCAGTG    GTGTCTCTC
                                || ||||||    |||||||||
                                CA AGTCAC    CACAGAGAG
                                 _      CCGA
GAM230  C17orf31  3'  GAAAAACTGACACTGACAC    34123    A     C    GTC
                                GT TCAGTG TCAGT   TC
                                || |||||| |||||   ||
                                CA AGTCAC AGTCA   AG
                                 C     _     AAA
GAM230  FLJ14075  3'  ATATCAAGCACTGACATGA    46048      A       CA
                                TCGT TCAGTGCT  GTGT
                                |||| ||||||||  ||||
                                AGTA AGTCACGA  TATA
                                   C       AC
GAM230  KIAA1486  5'  AGAAACACTGAGCTGAACTAC  67376     TCAGT        C
                                GTA    GCTCAGTGT TCT
                                |||    ||||||||| |||
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                                CAT     CGAGTCACA AGA
                                  CAAGT        A
GAM230  KOC1     3'  AGATTTTTAAGCACTGATA   91070          CAGT_
                                TATCAGTGCT     GTCT
                                ||||||||||     ||||
                                ATAGTCACGA     TAGA
                                     ATTTT
GAM230  PPP1R1B  5'  AGAGACACCGAGACGC      49823     _   A
                                GTG CTC GTGTCTCT
                                ||| ||| ||||||||
                                CGC GAG CACAGAGA
                                  A   C
GAM230  PPP1R1B  5'  AGAGACACCGAGACGC      49824     _   A
                                GTG CTC GTGTCTCT
                                ||| ||| ||||||||
                                CGC GAG CACAGAGA
                                  A   C
GAM230  LOC146940 5'  ACGAGAACTGATACGA      78196          G   A
                                TCGTATCAGT CTC GT
                                |||||||||| ||| ||
                                AGCATAGTCA GAG CA
                                     A   _
GAM230  LOC152559 3'  AGACACTGAGTAGTTAC     80616     TCAG
                                GTA    TGCTCAGTGTCT
                                |||    ||||||||||||
                                CAT    ATGAGTCACAGA
                                  TG__
GAM230  LOC163882 3'  AGAGGAAAGCACTGAGAC    82162     A       CAGTG
                                GT TCAGTGCT     TCTCT
                                || ||||||||     |||||
                                CA AGTCACGA     GGAGA
                                 G       AA___
GAM230  LOC202754 3'  CTGAAACTGATACGA       82704          GC
                                TCGTATCAGT  TCAG
                                ||||||||||  ||||
                                AGCATAGTCA  AGTC
                                     A_
GAM230  LOC203378 3'  GAAACTTGCTGAGCACCAACAT 90604      ATCA        __  C
           GA                     TCGT    GTGCTCAGT  GT TC
                                ||||    |||||||||  || ||
                                AGTA    CACGAGTCG  CA AG
                                  CAAC        TT  A
GAM230  LOC92900  5'  GAGACACATGAACCTGACAC   70834    A    TGC  _
                                GT TCAG   TCA GTGTCTC
                                || ||||   ||| |||||||
                                CA AGTC   AGT CACAGAG
                                 C    CA_   A
GAM231  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
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                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM231  AHR     3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM231  FDFT1   3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM231  JTB     3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM231  KLF4    3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM231  PHYH    3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM231  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                       T__    _
GAM231  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM231  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_    CG_
GAM231  CG012   5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM231  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
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                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM231  FLJ23462  3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                      CATTTC        GTCTGAGAT
                                  ||||||        |||||||||
                                  GTAAAG        CAGACTCTA
                                     AAACATTT_
GAM231  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                  CATTTCA   TCACTGTCTGAGAT
                                  |||||||   ||||||||||||||
                                  GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM231  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                  TTCA TTTCACTG  TGAG
                                  |||| ||||||||  ||||
                                  AAGT AAAGTGAC  GTTT
                                    A       CT
GAM231  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                  TTTC CTG TCTGAGAT
                                  |||| ||| ||||||||
                                  AAAG GAC AGACTCTA
                                    _  G
GAM231  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                  ATT CACTTTCACTGT
                                  ||| ||||||||||||
                                  TAA GTGAAAGTGACG
                                   C
GAM231  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                  TTCACTTT  CT TCTGAGAT
                                  ||||||||  || ||||||||
                                  AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM231  PP35      3'  ATCTCAGACTGAAA       22814      CT
                                  TTTCA  GTCTGAGAT
                                  |||||  |||||||||
                                  AAAGT  CAGACTCTA
                                    __
GAM231  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148         TCAC  C_
                                  CATTTCACTT   TGT  TGAG
                                  ||||||||||   |||  ||||
                                  GTAAAGTGAA   ACG  ACTC
                                       TA__   TT
GAM231  SEP15     3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                  TTTCACTTT ACTGT  GA
                                  ||||||||| |||||  ||
                                  AAAGTGAGA TGACA  CT
                                       A    TC
GAM231  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                  TTTCACTTT    TCTGAG
                                  |||||||||    ||||||
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                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM231  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM231  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM231  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM231  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM233  AF1Q     3'  TGACTCGACATCTTGTCCC    22370            CG_
                                GGGACAAGATGTTG   CA
                                ||||||||||||||   ||
                                CCCTGTTCTACAGC   GT
                                      TCA
GAM233  AGRN     3'  TGCAACGTCCCGTCCC      78842       AA
                                GGGAC  GATGTTGCG
                                |||||  |||||||||
                                CCCTG  CTGCAACGT
                                   CC
GAM233  ATP6V0C   3'  CATGCGCAGTGTCCT       87313       AGATG
                                GGGACA    TTGCGCATG
                                ||||||    |||||||||
                                TCCTGT    GACGCGTAC
                                          _____
GAM233  BCL11A    3'  GCGCATGCATACACCCATTTTG 43165          TT_________  GCAT
            TCCC                    GACAAGATG         GC    GC
                                ||||||||          ||    ||
                                CTGTTTTAC         CG    CG
                                     CCACATIIIA  TACG
GAM233  BVES     3'  TGCATAACATTTACCC      69316     ACA       C
                                GGG   AGATGTTG GCA
                                |||   |||||||| |||
                                CCC   TTTACAAT CGT
                                  A__       A
GAM233  C21orf33  5'  CGCACGCTCTGTCCC       16197       A  T  _
                                GGGACA GA GT TGCG
                                |||||| || || ||||
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                                CCCTGT CT CG ACGC
                                   _ _  C
GAM233  CD81    3'  TGCACAGCTCACCTTGTTCC  15137       A  TT  GCA
                                GGGACAAG TG  GC   TGCA
                                |||||||| ||  ||   ||||
                                CCTTGTTC AC  CG   ACGT
                                     C  T_  AC_
GAM233  CERD4   3'  TGCAACATTTTATCCC     23856     C
                                GGGA AAGATGTTGCG
                                |||| ||||||||||
                                CCCT TTTTACAACGT
                                  A
GAM233  CKAP1   5'  GCATGCGCGAGTTTACCC   73538     ACA   G
                                GGG   AGAT TTGCGCATGC
                                |||   |||| ||||||||||
                                CCC   TTTG AGCGCGTACG
                                  A__   _
GAM233  CLCN6   3'  GCGCATGCACACAGACACTTTG 41385       A  T_________  GCAT
           TCCC                    GACAAG TG       TGC   GC
                                |||||| ||       |||   ||
                                CTGTTT AC       ACG   CG
                                   C  AGACACIII   TACG
GAM233  CLCN6   3'  GCGCATGCACACAGACACTTTG 41400       A  T_________  GCAT
           TCCC                    GACAAG TG       TGC   GC
                                |||||| ||       |||   ||
                                CTGTTT AC       ACG   CG
                                   C  AGACACIII   TACG
GAM233  CLCN6   3'  GCGCATGCACACAGACACTTTG 7078        A  T_________  GCAT
           TCCC                    GACAAG TG       TGC   GC
                                |||||| ||       |||   ||
                                CTGTTT AC       ACG   CG
                                   C  AGACACIII   TACG
GAM233  EN2     5'  TGCATGCGCGCAGCTCTCGCCC 7471     ACA   T  __
                                GGG   AGA GT  TGCGCATGCA
                                |||   ||| ||  ||||||||||
                                CCC   TCT CG  GCGCGTACGT
                                  GC_   _  AC
GAM233  FGFR2   5'  TGCATGCGGCGTACCTGGCCC  3766     A  AG_   TG
                                GGG CA   ATGT  CGCATGCA
                                ||| ||   ||||  ||||||||
                                CCC GT   TGCG  GCGTACGT
                                  G  CCA   __
GAM233  FGFR2   5'  TGCATGCGGCGTACCTGGCCC  43362    A  AG_   TG
                                GGG CA   ATGT  CGCATGCA
                                ||| ||   ||||  ||||||||
                                CCC GT   TGCG  GCGTACGT
                                  G  CCA   __
GAM233  FGFR2   5'  TGCATGCGGCGTACCTGGCCC  43366    A  AG_   TG
                                GGG CA   ATGT  CGCATGCA
                                ||| ||   ||||  ||||||||
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                                CCC GT  TGCG  GCGTACGT
                                  G CCA  __
GAM233  FGFR2   5' TGCATGCGGCGTACCTGGCCC 43374   A AG_  TG
                                GGG CA  ATGT  CGCATGCA
                                ||| ||  ||||  ||||||||
                                CCC GT  TGCG  GCGTACGT
                                  G CCA  __
GAM233  FGFR2   5' TGCATGCGGCGTACCTGGCCC 43381   A AG_  TG
                                GGG CA  ATGT  CGCATGCA
                                ||| ||  ||||  ||||||||
                                CCC GT  TGCG  GCGTACGT
                                  G CCA  __
GAM233  FGFR2   5' TGCATGCGGCGTACCTGGCCC 43387   A AG_  TG
                                GGG CA  ATGT  CGCATGCA
                                ||| ||  ||||  ||||||||
                                CCC GT  TGCG  GCGTACGT
                                  G CCA  __
GAM233  FGFR2   5' TGCATGCGGCGTACCTGGCCC 43389   A AG_  TG
                                GGG CA  ATGT  CGCATGCA
                                ||| ||  ||||  ||||||||
                                CCC GT  TGCG  GCGTACGT
                                  G CCA  __
GAM233  FGFR2   5' TGCATGCGGCGTACCTGGCCC 43392   A AG_  TG
                                GGG CA  ATGT  CGCATGCA
                                ||| ||  ||||  ||||||||
                                CCC GT  TGCG  GCGTACGT
                                  G CCA  __
GAM233  FGFR2   5' TGCATGCGGCGTACCTGGCCC 43485   A AG_  TG
                                GGG CA  ATGT  CGCATGCA
                                ||| ||  ||||  ||||||||
                                CCC GT  TGCG  GCGTACGT
                                  G CCA  __
GAM233  FGFR2   5' TGCATGCGGCGTACCTGGCCC 43495   A AG_  TG
                                GGG CA  ATGT  CGCATGCA
                                ||| ||  ||||  ||||||||
                                CCC GT  TGCG  GCGTACGT
                                  G CCA  __
GAM233  FGFR2   5' TGCATGCGGCGTACCTGGCCC 43505   A AG_  TG
                                GGG CA  ATGT  CGCATGCA
                                ||| ||  ||||  ||||||||
                                CCC GT  TGCG  GCGTACGT
                                  G CCA  __
GAM233  MCM2    3' TGCTGAACATCTTGCC    67931   A     GC
                                GG CAAGATGTT  GCA
                                || |||||||||  |||
                                CC GTTCTACAA  CGT
                                  _       GT
GAM233  MEST    5' GCATGCGCAACCGGTTCT   69898     AAGAT
                                GGGAC   GTTGCGCATGC
                                |||||   ||||||||||
```

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                                TCTTG    CAACGCGTACG
                                  GC___
GAM233  MNT     3'  CGCACACATCTTACCT     39712    AC     _
                                GGG  AAGATGT TGCG
                                |||  ||||||| ||||
                                TCC  TTCTACA ACGC
                                  A_     C
GAM233  PLA2G4C  5'  GCATGCGCACACGCCCC    73414    ACAAGA   T
                                GGG     TGT GCGCATGC
                                |||     ||| ||||||||
                                CCC     ACA CGCGTACG
                                  CGC___  _
GAM233  PTP4A2   3'  GCACGCGCAGTGTCC      12982      AGATG     A
                                GGACA    TTGCGC TGC
                                |||||    |||||| |||
                                CCTGT    GACGCG ACG
                                  _____     C
GAM233  RANBP3   5'  CATGCAAGGGTCCTTGTCCC  23631        _ G  GC
                                GGGACAAG AT TT  GCATG
                                |||||||| || ||  |||||
                                CCCTGTTC TG GA  CGTAC
                                    C  G  A_
GAM233  RRM2B    3'  TGTTAACATCTCACCC     67830    ACA      C
                                GGG   AGATGTTG GCA
                                |||   |||||||| |||
                                CCC   TCTACAAT TGT
                                  AC_      _
GAM233  SLC13A3  3'  GCAGCTGACATCTCGACCC   60469    ACA      C  A
                                GGG   AGATGTTG GC TGC
                                |||   |||||||| || |||
                                CCC   TCTACAGT CG ACG
                                  AGC      _ _
GAM233  SLC22A12 3'  GCACTGCCACTTGTCCC     58071       ATGT  C  _
                                GGGACAAG    TG GCA TGC
                                ||||||||    || ||| |||
                                CCCTGTTC    AC CGT ACG
                                    _____ _   C
GAM233  VGF      3'  TGCATGCGCCCCGGCCCTGCCC 12595    ACAAGA  TT
                                GGG     TG  GCGCATGCA
                                |||     ||  |||||||||
                                CCC     GC  CGCGTACGT
                                  GTCCCG  CC
GAM233  ZNF261   3'  TGCAGACTCCTGTCCC      17499      A  T   GC
                                GGGACA GA GTT  GCA
                                |||||| || |||  |||
                                CCCTGT CT CAG  CGT
                                   C  _   A_
GAM233  ANKRD6   3'  GCGCATGCATACATGGATCTTG 30085       GT_________   GCAT
            TCTC                  GACAAGAT        TGC    GC
                                ||||||||        |||   ||
```

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                                CTGTTCTA        ACG   CG
                                    GGTACATIII  TACG
GAM233  BAD      5'  CGTAACATCTTGTCCT      15062
                                GGGACAAGATGTTGCG
                                ||||||||||||||||
                                TCCTGTTCTACAATGC

GAM233  BM039    5'  GCATGCGCCGCCTGTCCT    37453       AGAT  T
                                GGGACA   GT GCGCATGC
                                ||||||   || ||||||||
                                TCCTGT   CG CGCGTACG
                                   C___  C
GAM233  C20orf30 3'  TGCATCATTTTGTCCC      26251          T
                                GGGACAAGATG TGCG
                                |||||||||| ||||
                                CCCTGTTTTAC ACGT
                                       T
GAM233  CLPTM1   3'  GTTCATCATCTTGTCCC     7106           T  C
                                GGGACAAGATG TG GC
                                |||||||||| || ||
                                CCCTGTTCTAC AC TG
                                       T  T
GAM233  CNNM1    3'  CCATGCACACATAACTTTGTCC 39770        ___   T____   GCAT
           C                     GGGACAAG   ATG    TGC   G
                                |||||||   |||    |||   |
                                CCCTGTTT   TAC    ACG   C
                                    CAA   ACIII   TACG
GAM233  CNNM3    3'  GCATGCGCCCCAGCCTTTCCC  34339     C  A_  TT
                                GGGA AAG  TG  GCGCATGC
                                |||| |||  ||  ||||||||
                                CCCT TTC  AC  CGCGTACG
                                  _  CG  CC
GAM233  CST7     3'  GCATGCTCCTTGTCCC      13327        ATGTTGC
                                GGGACAAG      GCATGC
                                ||||||||      ||||||
                                CCCTGTTC      CGTACG
                                    CT_____
GAM233  D2S448   3'  CGTCAGCATCTAATCCC     73520      CA      _
                                GGGA  AGATGTTG CG
                                ||||  |||||||| ||
                                CCCT  TCTACGAC GC
                                  AA       T
GAM233  DDX34    3'  TGCATGCGCCCCTCACGCCC  27991     ACAA  TGTT
                                GGG   GA   GCGCATGCA
                                |||   ||   |||||||||
                                CCC   CT   CGCGTACGT
                                 GCA_  CCC_
GAM233  DKFZP564D166 3'  CAGAAGCAACATCCCATCTC  47673      CAA       GCA
                                GGGA  GATGTTGC  TG
                                ||||  ||||||||  ||
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                                CTCT  CTACAACG  AC
                                  ACC      AAG
GAM233  ETL     5'  TGCACCAAGACACCTTGTCTC  42206       A   GCGCA
                                GGGACAAG TGTT    TGCA
                                |||||||| ||||    ||||
                                CTCTGTTC ACAG    ACGT
                                    C   AACC_
GAM233  FBXO21   3'  TGCATGCAGTATTCTCACCC  53244    ACA  TGT  _
                                GGG  AGA  TGC GCATGCA
                                |||  |||  ||| |||||||
                                CCC  TCT  ATG CGTACGT
                                 AC_  T__  A
GAM233  FLJ12681 3'  GCCAACCCTTGTCCC      42873       AT   C
                                GGGACAAG  GTTG GC
                                ||||||||  |||| ||
                                CCCTGTTC  CAAC CG
                                    C_   _
GAM233  FLJ13057 5'  GCATGCGCCCTCCGTCCC    95649     AA  TGTT
                                GGGAC  GA   GCGCATGC
                                |||||  ||   ||||||||
                                CCCTG  CT   CGCGTACG
                                  C_  CC__
GAM233  FLJ14326 3'  TGCAAAGAAAATCTTGTCCC  49819        GTTGCGCA
                                GGGACAAGAT      TGCA
                                ||||||||||      ||||
                                CCCTGTTCTA      ACGT
                                     AAAGAA__
GAM233  FLJ14888 3'  TGCACTTTCCCACACTTGTCCC 51685       A  TGCGCA_
                                GGGACAAG TGT     TGCA
                                |||||||| |||     ||||
                                CCCTGTTC ACA     ACGT
                                    _  CCCTTTC
GAM233  FREQ    3'  TGGCACACCTTGTCCC     26590       A  T  G
                                GGGACAAG TGT GC CA
                                |||||||| ||| || ||
                                CCCTGTTC ACA CG GT
                                    C  _ _
GAM233  GNB4    3'  TGCATCTGAACATCTTTCCC  41274     C      G  C
                                GGGA AAGATGTT CG ATGCA
                                |||| |||||||| || |||||
                                CCCT TTCTACAA GT TACGT
                                  _      _ C
GAM233  KIAA0738 3'  TGGCAACATCCCGTCTC    28221      AA      G
                                GGGAC  GATGTTGC CA
                                |||||  |||||||| ||
                                CTCTG  CTACAACG GT
                                  CC      _
GAM233  KIAA1128 3'  GCGCATGCATACACACGTCTTG 68479  GA     T_________  GCAT
           CACC                   CAAGATG       TGC   GC
                                 |||||||       |||   ||
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                                GTTCTGC       ACG   CG
                               AC      ACACATIII  TACG
GAM233  KIAA1138  3'  TGCACAGCATCTTTCCC    62140     C       C
                               GGGA AAGATGTTG GCA
                               |||| ||||||||| |||
                               CCCT TTCTACGAC CGT
                                 _       A
GAM233  KIAA1530  3'  CATGTGTCCTCTTGTCCC    67948        TGTT
                               GGGACAAGA   GCGCATG
                               |||||||||   |||||||
                               CCCTGTTCT   TGTGTAC
                                    CC__
GAM233  MGC12679  3'  GCATGCGCACGACGTTGACCC  51203    ACAA   __
                               GGG   GATGT  TGCGCATGC
                               |||   |||||  |||||||||
                               CCC   TTGCA  ACGCGTACG
                                 AG__    GC
GAM233  MPPE1     3'  CATGCACGAGAGTCCTTGTTCC 43561       _ G_  C
                               GGGACAAG AT  TTG GCATG
                               |||||||| ||  ||| |||||
                               CCTTGTTC TG  AGC CGTAC
                                    C  AG   A
GAM233  NYD-SP17  5'  TGTTTTCCAACACCTTGCCT   50880    A   A    CGCAT
                               GGG CAAG TGTTG    GCA
                               ||| |||| |||||    |||
                               TCC GTTC ACAAC    TGT
                                 _   C    CTTT_
GAM233  PF1       3'  CATGTTAACTTGTCCC     95120       A  TTGC
                               GGGACAAG TG   GCATG
                               |||||||| ||   |||||
                               CCCTGTTC AT   TGTAC
                                    A  ____
GAM233  PRO1914   3'  GCGCATGCATACAAGCATCTTA 26046    C    T_________  GCAT
           TCCC                   GA AAGATG       TGC   GC
                               || ||||||       |||   ||
                               CT TTCTAC       ACG   CG
                                A     GAACATIII   TACG
GAM233  SIRPB1    3'  GCTTCCAACATCTTATCCC   20259     C       CGCAT
                               GGGA AAGATGTTG    GC
                               |||| |||||||||    ||
                               CCCT TTCTACAAC    CG
                                 A       CTT__
GAM233  SLC12A5   3'  GCACGCGCTTTGTCCT     40382       ATGTT   A
                               GGGACAAG    GCGC TGC
                               ||||||||    |||| |||
                               TCCTGTTT    CGCG ACG
                                    _____   C
GAM233  ZNF297B   5'  CCATGCATACAAATCTTGTCCC 25778        __ T____  GCAT
                               GGGACAAGA  TG    TGC   G
                               |||||||||  ||    |||   |
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                                CCCTGTTCT  AC    ACG   C
                                     AA  ATIII  TACG
GAM233  ZNF304    5'  CACACGTCCTCTTGTCCT    40312        TGTT  CA
                                GGGACAAGA   GCG  TG
                                |||||||||   |||  ||
                                TCCTGTTCT   TGC  AC
                                     CC__   AC
GAM233  LOC112609 3'  TGTATGGTACTCTTGTCCC   72842        T  T  G
                                GGGACAAGA GT GC CATGCA
                                ||||||||| || || ||||||
                                CCCTGTTCT CA TG GTATGT
                                     _ _ _
GAM233  LOC124930 3'  CGCACACCCTTGTCCC      74357        A_   T
                                GGGACAAG  TGT GCG
                                ||||||||  ||| |||
                                CCCTGTTC  ACA CGC
                                     CC  _
GAM233  LOC148987 3'  TGGGCAGCATCCTATCCC    79123     CAA      G
                                GGGA  GATGTTGC CA
                                ||||  |||||||| ||
                                CCCT  CTACGACG GT
                                  ATC       G
GAM233  LOC152641 5'  TGCATGCGCATTCCTCGCGCC  80636    ACAA  TGT_
                                GG   GA   TGCGCATGCA
                                ||   ||   ||||||||||
                                CC   CT   ACGCGTACGT
                                 GCG_  CCTT
GAM233  LOC221178 3'  TGCACACTGGCTTTGTCCC   93541        A_ GT  C
                                GGGACAAG  T  TG GCA
                                ||||||||  |  || |||
                                CCCTGTTT  G  AC CGT
                                     CG TC  A
GAM233  LOC253980 3'  GCCAACACTTGTCCC       95073        A    C
                                GGGACAAG TGTTG GC
                                |||||||| ||||| ||
                                CCCTGTTC ACAAC CG
                                     _    _
GAM233  LOC254556 3'  TGCCTAACATCTGCCC      94620     A  A      C
                                GGG CA GATGTTG GCA
                                ||| || ||||||| |||
                                CCC GT CTACAAT CGT
                                  _ _      C
GAM233  LOC256295 3'  TGCATAGCATCTCATCCT    96591      CA       C
                                GGGA  AGATGTTG GCA
                                ||||  |||||||| |||
                                TCCT  TCTACGAT CGT
                                  AC       A
GAM234  AXL       3'  TCTCACACTCAGTTG       8111       A
                                CAAC TGAGTGTGAGA
                                |||| ||||||||||
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                                GTTG ACTCACACTCT
                                   _
GAM234  AXL     3'  TCTCACACTCAGTTG      41608     A
                                CAAC TGAGTGTGAGA
                                |||| ||||||||||
                                GTTG ACTCACACTCT
                                   _
GAM234  MCC     3'  ACTTAGCTCCTGTTGTCATG  9957      GTGTG  A
                                CATGA    AG AGCTAAGT
                                |||||    || ||||||||
                                GTACT    TC TCGATTCA
                                   GTTG_  C
GAM234  MPP5    3'  ACTTAGCTTCCCTTCCCTCATC 42483   C    TGTGA_
          A                      A ATGAG     GAAGCTAAGT
                                | |||||     ||||||||||
                                A TACTC     CTTCGATTCA
                                 C    CCTTCC
GAM234  MS4A7   3'  TTTTCACACTCATATTG    41067    C
                                CAA ATGAGTGTGAGAA
                                ||| ||||||||||||
                                GTT TACTCACACTTTT
                                  A
GAM234  STAU    3'  CTTAGCTTTCACTACACT    33908      A__
                                AGTGTG   GAAGCTAAG
                                ||||||   |||||||||
                                TCACAT   TTTCGATTC
                                   CAC
GAM234  STAU    3'  CTTAGCTTTCACTACACT    33895      A__
                                AGTGTG   GAAGCTAAG
                                ||||||   |||||||||
                                TCACAT   TTTCGATTC
                                   CAC
GAM234  STAU    3'  CTTAGCTTTCACTACACT    33901      A__
                                AGTGTG   GAAGCTAAG
                                ||||||   |||||||||
                                TCACAT   TTTCGATTC
                                   CAC
GAM234  STAU    3'  CTTAGCTTTCACTACACT    16004      A__
                                AGTGTG   GAAGCTAAG
                                ||||||   |||||||||
                                TCACAT   TTTCGATTC
                                   CAC
GAM234  TZFP    5'  ACTTACAAACCACACTCAT   26888        AGAAGC
                                ATGAGTGTG     TAAGT
                                |||||||||     |||||
                                TACTCACAC     ATTCA
                                     CAAAC_
GAM234  VNN2    3'  ACTCAGCTTCTGCATCAT    54356     G  G      A
                                ATGA TGT AGAAGCT AGT
                                |||| ||| ||||||| |||
```

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                                TACT ACG TCTTCGA TCA
                                  _  _     C
GAM234  VNN2     3'  ACTCAGCTTCTGCATCAT    16237     G  G     A
                                ATGA TGT AGAAGCT AGT
                                |||| ||| ||||||| |||
                                TACT ACG TCTTCGA TCA
                                  _  _     C
GAM234  APXL2    5'  AGCCTCAGCACTCAT      75184       _   AA
                                ATGAGTG TGAG  GCT
                                ||||||| ||||  |||
                                TACTCAC ACTC  CGA
                                   G   __
GAM234  FKSG87   3'  ACTCAGCCTCCCATTCACATGT 49325    __    T   AA   A
                                ACA  TGAGTG GAG  GCT AGT
                                |||  |||||| |||  ||| |||
                                TGT  ACTTAC CTC  CGA TCA
                                  AC     C  __  C
GAM234  FLJ10359 3'  ACTCAGAGTTCACACTCAT   36065         AAG  A
                                ATGAGTGTGAG   CT AGT
                                ||||||||||   || |||
                                TACTCACACTT   GA TCA
                                      GA_  C
GAM234  FLJ12568 3'  GGGATCTCACACCCATGTT   46500      A      AG
                                AACATG GTGTGAGA  CT
                                |||||| ||||||||  ||
                                TTGTAC CACACTCT  GG
                                   C       AG
GAM234  GHITM    3'  ACTCAGCTTCTGGCTTCTCTG  26913    T   T_  G     A
                                CA GAG  GT AGAAGCT AGT
                                || |||  || ||||||| |||
                                GT CTC  CG TCTTCGA TCA
                                  _  TT  G      C
GAM234  KIAA0092 3'  ACTTAGTTGCCACACTCATG   27966        AGA
                                CATGAGTGTG   AGCTAAGT
                                ||||||||||   ||||||||
                                GTACTCACAC   TTGATTCA
                                      CG_
GAM234  KIAA1817 3'  CTTGGGCTCACACTCA      68229         AAG
                                TGAGTGTGAG   CTAAG
                                ||||||||||   |||||
                                ACTCACACTC   GGTTC
                                      G__
GAM234  KSR      5'  AGCTTCCCCACACTCA      64042        A_
                                TGAGTGTG  GAAGCT
                                ||||||||  ||||||
                                ACTCACAC  CTTCGA
                                     CC
GAM234  MGC5528  3'  ACTTAGCTAATGAACTCAT   44042       GTGAGA
                                ATGAGT     AGCTAAGT
                                ||||||     ||||||||
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```
                                TACTCA     TCGATTCA
                                   AGTAA_
GAM234  PRO2037   3'  AGCTTGAGACCTCATGT     37784        T  GAG
                                ACATGAG GT   AAGCT
                                ||||||| ||   |||||
                                TGTACTC CA   TTCGA
                                   _ GAG
GAM234  SHANK3    3'  ACTCGGTCTCACACTCA     65487         AA  TA
                                TGAGTGTGAG  GC  AGT
                                ||||||||||  ||  |||
                                ACTCACACTC  TG  TCA
                                      __ GC
GAM234  LOC116437 3'  TTTCCACTCATGCTG       73894     A       T
                                CA CATGAGTG GAGA
                                || |||||||| ||||
                                GT GTACTCAC CTTT
                                 C       _
GAM234  LOC146909 3'  ACTCAGCTTCTTGGCATGT    78161       AGTGT       A
                                ACATG     GAGAAGCT AGT
                                |||||     |||||||| |||
                                TGTAC     TTCTTCGA TCA
                                   GG___       C
GAM234  LOC147093 5'  CTCTTCACCTCATGCTG     83943     A     T    GA
                                CA CATGAG GTGA  AG
                                || |||||| ||||  ||
                                GT GTACTC CACT  TC
                                 C     _    TC
GAM234  LOC154386 3'  AGCTCTCACACTCATTTG     81080     C          A
                                CAA ATGAGTGTGAGA GCT
                                ||| |||||||||||| |||
                                GTT TACTCACACTCT CGA
                                  _          _
GAM234  LOC159121 5'  AGCCACACCATGTCA       86989    A    A    AGAA
                                C ACATG GTGTG    GCT
                                | ||||| |||||    |||
                                A TGTAC CACAC    CGA
                                 C    _    _____
GAM235  PMX1      3'  TAATACTTACCTACCTCA     22595            C
                                TGAGGTAGGTAAGT ATTG
                                |||||||||||||| ||||
                                ACTCCATCCATTCA TAAT
                                              _
GAM235  PMX1      3'  TAATACTTACCTACCTCA     42662            C
                                TGAGGTAGGTAAGT ATTG
                                |||||||||||||| ||||
                                ACTCCATCCATTCA TAAT
                                              _
GAM235  WIG1      3'  GTGACCTACCTACCCCA     94469     A       A
                                TG GGTAGGTA GTCAT
                                || |||||||| |||||
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                                AC CCATCCAT CAGTG
                                 C       C
GAM235  ABCF2    5'  TGAAACAACAGTAACCTACC  19099        AAGTCA
                                GGTAGGT     TTGTTTCA
                                |||||||     ||||||||
                                CCATCCA     AACAAAGT
                                   ATGAC_
GAM235  CTPS2    3'  AAACCCATACTACTACCTCA  39081        GTA   CATT
                                TGAGGTAG   AGT    GTTT
                                ||||||||   |||    ||||
                                ACTCCATC   TCA    CAAA
                                    A__    TACC
GAM235  CYP4F8   3'  CAGTGACCCACCCACCT    23409      A   AA
                                AGGT GGT  GTCATTG
                                |||| |||  |||||||
                                TCCA CCA  CAGTGAC
                                  C   CC
GAM235  DKFZp761N1114 3'  AGTACCTACCCTACCTCA    79013         TA  TC
                                TGAGGTAGG  AG  ATT
                                |||||||||  ||  |||
                                ACTCCATCC  TC  TGA
                                     CA  CA
GAM235  FLJ11082 3'  TGAAACAATAACTCTGCACCA  37036    AG   GTA   C
                                TG  GTAG   AGT ATTGTTTCA
                                ||  ||||   ||| |||||||||
                                AC  CGTC   TCA TAACAAAGT
                                 CA   ___   A
GAM235  FLJ11560 3'  AGACTCTGACCCACCTACCTCA 47215          AA    TT
                                TGAGGTAGGT  GTCA  GTTT
                                ||||||||||  ||||  ||||
                                ACTCCATCCA  CAGT  CAGA
                                      CC    CT
GAM235  FLJ20485 3'  CAGTGACTCTCCCACCTCA   38765       A  TA
                                TGAGGT GG  AGTCATTG
                                ||||||  ||  ||||||||
                                ACTCCA CC  TCAGTGAC
                                   C  TC
GAM235  FLJ20511 3'  AAACAATGAATGAGCCACCTTA 35316       A   AAG_
                                TGAGGT GGT    TCATTGTTT
                                ||||||  |||   |||||||||
                                ATTCCA CCG    AGTAACAAA
                                   _   AGTA
GAM235  KIAA0557 3'  TGACTTCCTACCTCA      78011         T
                                TGAGGTAGG AAGTCA
                                |||||||||  ||||||
                                ACTCCATCC TTCAGT
                                          _
GAM235  KIAA1274 3'  TAATACTTGCCTACCT      91369           C
                                AGGTAGGTAAGT ATTG
                                ||||||||||||  ||||
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                                TCCATCCGTTCA TAAT
                                           _
GAM235  KIAA1297  3'  TGACTCTCCTACCTCA      72188          TA
                                TGAGGTAGG  AGTCA
                                |||||||||  |||||
                                ACTCCATCC  TCAGT
                                     TC
GAM235  KIAA1571  5'  TAGTGACTGACCCACCTCA   60959       A   A
                                TGAGGT GGT AGTCATTG
                                |||||| ||| ||||||||
                                ACTCCA CCA TCAGTGAT
                                   C   G
GAM235  ZNF396    3'  GAAACAACAAGTGCCTCA    75668        GGTAAGTCA
                                TGAGGTA       TTGTTTC
                                |||||||       |||||||
                                ACTCCGT       AACAAAG
                                    GAAC_____
GAM235  LOC130576 5'  AAACAATAACTGCCTA      74953       A  C
                                TAGGTA GT ATTGTTT
                                |||||| || |||||||
                                ATCCGT CA TAACAAA
                                   _ A
GAM235  LOC153339 3'  TGATTACCTACCTCA       86015           G
                                TGAGGTAGGTAA TCA
                                |||||||||||| |||
                                ACTCCATCCATT AGT
                                           _
GAM235  LOC158563 3'  TAATTGCCCTACCTACCTCA  81952          A_  C
                                TGAGGTAGGTA  GT ATTG
                                ||||||||||  || ||||
                                ACTCCATCCAT  CG TAAT
                                      CC  T
GAM235  LOC200942 3'  TGAAACCTTCCTACCCTACCTA 88949          A_  CATT__
           CCTCA                   TGAGGTAGGTA  GT     GTTTCA
                                ||||||||||  ||     ||||||
                                ACTCCATCCAT  CA     CAAAGT
                                      CC  TCCTTC
GAM235  LOC255349 3'  GAAATCATACCTACCTCA    95612          AGTCAT  _
                                TGAGGTAGGTA     TG TTTC
                                ||||||||||      || ||||
                                ACTCCATCCAT     AC AAAG
                                      _______ T
GAM236  CBFA2T1   3'  TTCTTTAGAGAACTGA      15106       G
                                TCAGT CTCTAAAGAA
                                ||||| ||||||||||
                                AGTCA GAGATTTCTT
                                   A
GAM236  FLNB      3'  ATACAAAGCCCTCCAGCCTG  62173     T  CTAA  AA
                                CAG GCT    AG  CTTTGTAT
                                ||| |||    ||  ||||||||
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                                GTC CGA   TC  GAAACATA
                                  _  CC__  CC
GAM236  LAMA4    3'  ATACAAAGTTCTTTAGAGCACT 9664
                GA                  TCAGTGCTCTAAAGAACTTTGTAT
                                    ||||||||||||||||||||||||
                                    AGTCACGAGATTTCTTGAAACATA

GAM236  LZTS1    3'  ACACAGCCCCTATAGCACTGA  40675        C  AAGAA  T
                                    TCAGTGCT TA    CT TGT
                                    |||||||| ||    || |||
                                    AGTCACGA AT    GA ACA
                                         T  CCCC_  C
GAM236  MCM2     3'  ACAAAACCAGAGCACTTGA   67927    _     AAAGAAC
                                    TCA GTGCTCT     TTTGT
                                    ||| |||||||     |||||
                                    AGT CACGAGA     AAACA
                                      T     CCA____
GAM236  PKD2     3'  ACAAAGTTCTTTATTACT    60090     CTC
                                    AGTG   TAAAGAACTTTGT
                                    ||||   ||||||||||||||
                                    TCAT   ATTTCTTGAAACA
                                      T__
GAM236  YWHAE    3'  AGGTTCTTTAAGACACT     22194     C  _
                                    AGTG TCT AAAGAACTT
                                    |||| ||| |||||||||
                                    TCAC AGA TTTCTTGGA
                                      _  A
GAM236  DKFZp761P1010 3'  ACAAAGTTCTTCAGTCCTGA   37336     TG  CTA
                                    TCAG  CT   AAGAACTTTGT
                                    ||||  ||   ||||||||||||
                                    AGTC  GA   TTCTTGAAACA
                                      CT  C__
GAM236  SSR1     3'  ACAAGTCTTTAGAATACT    11979     C      AC
                                    AGTG TCTAAAGA  TTTGT
                                    |||| ||||||||  |||||
                                    TCAT AGATTTCT  GAACA
                                      A      __
GAM236  LOC150498 3'  AGGTTCTTTAAGACACT     79904     C  _
                                    AGTG TCT AAAGAACTT
                                    |||| ||| |||||||||
                                    TCAC AGA TTTCTTGGA
                                      _  A
GAM236  LOC222933 5'  TTCTCAGAGCACTGA       94361          AA
                                    TCAGTGCTCT  AGAA
                                    ||||||||||  ||||
                                    AGTCACGAGA  TCTT
                                          C_
GAM236  LOC93129  3'  ATACAAAGCTCTTCTGACACTG 71460       C  TA   A
                A                    TCAGTG TC  AAGA CTTTGTAT
                                    ||||||  ||  ||||  ||||||||
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                                AGTCAC AG  TTCT GAAACATA
                                   _ TC   C
GAM237  DACH    3'  TGAGAATGTTTGTAAATGTACA 54974      CATCC  CT
                                TGTACA    ACA  CATTCTCA
                                ||||||    |||  ||||||||
                                ACATGT    TGT  GTAAGAGT
                                   AAA__   TT
GAM237  IL11RA  3'  GGAACGTGTGTAATGTGTACA  15712       C_    TCA
                                TGTACACAT  CACAC   TTCT
                                |||||||||  |||||   ||||
                                ACATGTGTA  GTGTG   AAGG
                                     AT    C__
GAM237  LYPLA1  3'  AGAATGAGGTGGTATTACA   20922     CACAT   A
                                TGTA    CCAC CTCATTCT
                                ||||    |||| ||||||||
                                ACAT    GGTG GAGTAAGA
                                  TAT__   _
GAM237  NAPB    3'  GAGAATGAATGTATGT     70183     CC  C
                                ACAT  ACA TCATTCTC
                                ||||  ||| ||||||||
                                TGTA  TGT AGTAAGAG
                                  __  A
GAM237  NRF1    3'  GAATATATGTATATGTGTACA  60120       CC  CTC
                                TGTACACAT  ACA   ATTC
                                |||||||||  |||   ||||
                                ACATGTGTA  TGT   TAAG
                                     TA   ATA
GAM237  PRKAB1  3'  AGAGGGAATGGACTGTACA   20734      CA   CA  AT
                                TGTACA  TCCA  CTC  TCT
                                ||||||  ||||  |||  |||
                                ACATGT  AGGT  GGG  AGA
                                   C_   AA   __
GAM237  PTGFR   3'  TGAGAGAGATGTGTACA     6319        CACA
                                TGTACACATC    CTCA
                                ||||||||||    ||||
                                ACATGTGTAG    GAGT
                                     AGA_
GAM237  RBBP5   3'  AGATTGGATAGATGTGTACA  17327       CACAC  T
                                TGTACACATC    TCA TCT
                                ||||||||||    ||| |||
                                ACATGTGTAG    GGT AGA
                                     ATA__   T
GAM237  SAT     3'  TGAGTCATTTAAATGTGTACA  11436       CCAC___
                                TGTACACAT     ACTCA
                                |||||||||     |||||
                                ACATGTGTA     TGAGT
                                     AATTTAC
GAM237  TMP21   3'  AATGGTGATGGATGTGACA   22399    A      _  T
                                TGT CACATCCA CAC CATT
                                ||| |||||||| ||| ||||
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                                ACA GTGTAGGT GTG GTAA
                                  _      A  _
GAM237  UBE2V1   3'  TGAAATGTGGATGCATAC    41797     CA      C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
                                CAT  GTAGGTGT  AGT
                                  AC       AA
GAM237  UBE2V1   3'  TGAAATGTGGATGCATAC    42374     CA      C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
                                CAT  GTAGGTGT  AGT
                                  AC       AA
GAM237  UBE2V1   3'  TGAAATGTGGATGCATAC    12522     CA      C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
                                CAT  GTAGGTGT  AGT
                                  AC       AA
GAM237  ZIC1     3'  AGAATGTTCTAGTAAATGTGTA 12720        CC  ACT__
            C                    GTACACAT  AC    CATTCT
                                |||||||  ||    ||||||
                                CATGTGTA  TG    GTAAGA
                                    AA  ATCTT
GAM237  AF038169  5'  TGAAAATGAGTGCTGTAGATG  25255      __  _      C
                                CATC  CA CACTCATT TCA
                                ||||  || ||||||||  |||
                                GTAG  GT GTGAGTAA AGT
                                  AT  C       A
GAM237  CDC14A   3'  AGAAGTGGATGTATATA     13391      C       ACTCA
                                TGTA ACATCCAC     TTCT
                                ||||  ||||||||     ||||
                                ATAT TGTAGGTG     AAGA
                                  A      ______
GAM237  DKFZP564I052 3'  GATGATCATGTGATGTGTACA  66710          C   C__
                                TGTACACATC ACA   TCATT
                                ||||||||||  |||   |||||
                                ACATGTGTAG TGT   AGTAG
                                      _  ACT
GAM237  DKFZP761F241 3'  TGAGAATGAGTGAGGTTTCGTA 48800       ACAT  A
            CA                    TGTAC    CC CACTCATTCTCA
                                |||||    ||  ||||||||||||
                                ACATG    GG GTGAGTAAGAGT
                                   CTTT  A
GAM237  FLJ11101  3'  AGAAGTGTTGAGTGTGTACA   37049        TC  _   CAT
                                TGTACACA  CA CACT   TCT
                                ||||||||  ||  ||||   |||
                                ACATGTGT  GT GTGA   AGA
                                    GA  T   ____
GAM237  FLJ14642  3'  AGTATGGGTGTGTACA      51492           C
                                TGTACACATCCA ACT
                                ||||||||||||  |||
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                                ACATGTGTGGGT TGA
                                      A
GAM237  FLJ20399  3'  GGTGGCTGTGGATGCCACA   35125    ACA      CT
                                TGT  CATCCACA  CATT
                                |||  ||||||||  ||||
                                ACA  GTAGGTGT  GTGG
                                  CC_      CG
GAM237  GFPT1     3'  GAAGATGGGATGTGTACA    9022         A  C  A
                                TGTACACATCC CA TC TTC
                                |||||||||||  || || |||
                                ACATGTGTAGG GT AG AAG
                                         _  _  _
GAM237  KIAA0450  3'  GAGGGCAGTGTGGATG     27640        CA
                                CATCCACACT  TTCTC
                                ||||||||||  |||||
                                GTAGGTGTGA  GGGAG
                                      C_
GAM237  KIAA0530  3'  GATGGTATGAAAATGTGTACA  70867       C__  C  T
                                TGTACACAT   CA AC CATT
                                |||||||||   || || ||||
                                ACATGTGTA   GT TG GTAG
                                     AAA  A  _
GAM237  KIAA0753  3'  GGGGAGTTAAATGTGTACA   28999       CCAC   ATT
                                TGTACACAT   ACTC  CTC
                                |||||||||   ||||  |||
                                ACATGTGTA   TGAG  GGG
                                     AAT_   ____
GAM237  KIAA0788  3'  TGAATTAGGAATGTGTACA   71339       _  ACAC
                                TGTACACAT CC   TCA
                                |||||||||  ||   |||
                                ACATGTGTA GG   AGT
                                     A  ATTA
GAM237  KIAA0855  3'  AGAATGAGCAGTGTAC     30400      ATCCACA
                                GTACAC     CTCATTCT
                                ||||||     ||||||||
                                CATGTG     GAGTAAGA
                                   AC_____
GAM237  KIAA0865  5'  GAGCAAGTGGAATGTGTACA  61250       _   A__
                                TGTACACAT CCAC  CTC
                                |||||||||  ||||  |||
                                ACATGTGTA GGTG  GAG
                                     A   AAC
GAM237  KIAA0992  3'  GGAAGTGTGGAGCACACA   32207    ACACA     CAT
                                TGT   TCCACACT  TCT
                                |||   ||||||||  |||
                                ACA   AGGTGTGA  AGG
                                  CACG_     ____
GAM237  MGC16037  5'  TGAGGTGTAGATATGTATA   51822      C  C   _
                                TGTACA ATC ACAC TCA
                                ||||||  ||| |||| |||
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                                ATATGT TAG TGTG AGT
                                   A  A   G
GAM237  OSRF     3'  TGAAAATGCACACAAATGTGTA 59525        CCACACT   C
            CA                   TGTACACAT      CATT TCA
                                 |||||||||      |||| |||
                                 ACATGTGTA      GTAA AGT
                                      AACACAC   A
GAM237  RAB3-GAP150 3'  TGAGAATCAGAGATGTGTA   24839       CACA  C
                                 TACACATC   CT ATTCTCA
                                 ||||||||   || |||||||
                                 ATGTGTAG   GA TAAGAGT
                                      A___  C
GAM237  RAP140   3'  GATGGGTAAATGTGTACA    30844        CCAC
                                 TGTACACAT   ACTCATT
                                 |||||||||   |||||||
                                 ACATGTGTA   TGGGTAG
                                      AA__
GAM237  TACTILE  5'  GAGTGCATGTGTACA       19471        CCA
                                 TGTACACAT  CACTC
                                 |||||||||  |||||
                                 ACATGTGTA  GTGAG
                                      C__
GAM237  LOC131873 3'  GATGTATGCATATGTGTACA  75880        CCA  CT
                                 TGTACACAT  CA  CATT
                                 |||||||||  ||  ||||
                                 ACATGTGTA  GT  GTAG
                                      TAC  AT
GAM237  LOC134145 3'  AGCTGTATATGTGTACA     75144        CC  _
                                 TGTACACAT  ACA CT
                                 |||||||||  ||| ||
                                 ACATGTGTA  TGT GA
                                      TA  C
GAM237  LOC145482 3'  AATGGTATGATGTGTACA    77226        CAC  T
                                 TGTACACATC  AC CATT
                                 ||||||||||  || ||||
                                 ACATGTGTAG  TG GTAA
                                      TA_ _
GAM237  LOC148195 3'  GAAAAGGTGGATGTGTCA    84129    T       A  CA
                                 TG ACACATCCAC CT  TTC
                                 || ||||||||||  ||  |||
                                 AC TGTGTAGGTG GA  AAG
                                  _        _ A_
GAM237  LOC152633 5'  TGAGCTGTACATGTAGAGTGTA 85826       A  C   CT__  TT
            CA                   TGTACAC TC ACA   CA  CTCA
                                 ||||||| || |||   ||  ||||
                                 ACATGTG AG TGT   GT  GAGT
                                     _ A  ACAT  C_
GAM237  LOC153630 5'  AATGAGTGTGCGTAC      86079      ACATC
                                 GTAC    CACACTCATT
                                 ||||    ||||||||||
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                                CATG    GTGTGAGTAA
                                  C____
GAM237  LOC221662 3'  AGAATGAGGGGAATGGGCA   92399    TA  CA   ACA
                                TG  CA  TCC   CTCATTCT
                                ||  ||  |||   ||||||||
                                AC  GT  AGG   GAGTAAGA
                                 GG  A_  G__
GAM237  LOC254659 5'  GAGAATGGAGATGCTACA    95113     CA    CACAC
                                TGTA  CATC    TCATTCTC
                                ||||  ||||    ||||||||
                                ACAT  GTAG    GGTAAGAG
                                  C_   A____
GAM237  LOC83693  3'  AGGGTGTGTGGATGGCACA   48830     ACA       TC
                                TGT   CATCCACAC  ATTCT
                                |||   |||||||||  |||||
                                ACA   GTAGGTGTG  TGGGA
                                  CG_       __
GAM237  LOC90981  3'  AATGGTGATGGATGTGACA   64532     A      _   T
                                TGT CACATCCA CAC CATT
                                ||| |||||||| ||| ||||
                                ACA GTGTAGGT GTG GTAA
                                  _       A   _
GAM238  ARHI      3'  GTCCTTTTGGTAACCCGATT   16249          ACAT    _
                                AGTCGGGTTA    CCAAA GGAC
                                ||||||||||    ||||| ||||
                                TTAGCCCAAT    GGTTT CCTG
                                      _____    T
GAM238  CDKN2A    3'  GTCCCTCAGACATCCCCGATTG 54228        TTAACA  CAAA
                                CAGTCGGG     TC    GGAC
                                ||||||||     ||    ||||
                                GTTAGCCC     AG    CCTG
                                     CTAC__  ACTC
GAM238  CDKN2A    3'  GTCCCTCAGACATCCCCGATTG 54238        TTAACA  CAAA
                                CAGTCGGG     TC    GGAC
                                ||||||||     ||    ||||
                                GTTAGCCC     AG    CCTG
                                     CTAC__  ACTC
GAM238  CPNE3     3'  TCCTTTGGATATGTGCTG    14034     T  G  TAAC
                                CAG CG GT    ATCCAAAGGA
                                ||| || ||    ||||||||||
                                GTC GT TA    TAGGTTTCCT
                                  _ G  _____
GAM238  EXTL3     3'  GTCCTTCGAGGAACCCACCCG  7535       TAACA   A__
                                CGGGT    TCC   AAGGAC
                                |||||    |||   ||||||
                                GCCCA    AGG   TTCCTG
                                   CCCA_   AGC
GAM238  MUC4      3'  CCAAAGGACGCCCTCCAAACCT 56321        AACA_________   AAA
              GACTG                  TCGGGTT         TCC   GG
                                |||||||          |||   ||
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                                AGTCCAA         AGG  CC
                                   ACCTCCCGIIIC  AAA
GAM238  RHBG    3'  CCAGATGCCCAACCCGACTG  39900        AA_   CAAA
                                CAGTCGGGTT  CATC   GG
                                ||||||||||  ||||   ||
                                GTCAGCCCAA  GTAG   CC
                                     CCC   A___
GAM238  SSPN    3'  GTCCTCTAGATAAAACACCCGA 17444       TAAC_  CAA
          TT                     AGTCGGGT   ATC  AGGAC
                                ||||||||   |||  |||||
                                TTAGCCCA   TAG  TCCTG
                                    CAAAA  ATC
GAM238  SURF5   3'  CCTTTGGATGCCCTCAC    22183   C  TTAA
                                GT GGG   CATCCAAAGG
                                || |||   ||||||||||
                                CA TCC   GTAGGTTTCC
                                 C  C___
GAM238  SURF5   3'  CCTTTGGATGCCCTCAC    56103   C  TTAA
                                GT GGG   CATCCAAAGG
                                || |||   ||||||||||
                                CA TCC   GTAGGTTTCC
                                 C  C___
GAM238  ZNF268  3'  CCTTTGGATGCAGCT     62899    AA
                                GGTT  CATCCAAAGG
                                ||||  ||||||||||
                                TCGA  GTAGGTTTCC
                                  C_
GAM238  BRD3    3'  CTTCAAATGCTAACCCGAT   23758       A  CCA
                                GTCGGGTTA CAT   AAG
                                |||||||| |||   |||
                                TAGCCCAAT GTA   TTC
                                     C  AAC
GAM238  BTN2A2  3'  TTTTAGATGTCAACCTGACTG  22784        A   C
                                CAGTCGGGTT ACATC AAAG
                                |||||||||| ||||| ||||
                                GTCAGTCCAA TGTAG TTTT
                                     C    A
GAM238  C15orf15  3'  CCTTTGGATACTTGGAACTG  32831     __   TAAC
                                CAGT  CGGGT   ATCCAAAGG
                                ||||  |||||   |||||||||
                                GTCA  GTTCA   TAGGTTTCC
                                  AG   _____
GAM238  DKFZp434C0328 5'  CCTTTGATTTAACCTGACT   34132         C  C
                                AGTCGGGTTAA ATC AAAGG
                                |||||||||| ||| |||||
                                TCAGTCCAATT TAG TTTCC
                                      _  _
GAM238  EFNA2   3'  CCTCCGGACCCGGCTG     7392        TTAACA  AA
                                CAGTCGGG    TCC  AGG
                                ||||||||    |||  |||
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                                GTCGGCCC     AGG  TCC
                                   _______  CC
GAM238  FKSG42   3'  TCCTTTGGCATCCCAACT    49336     C   TTAACAT
                                AGT GGG      CCAAAGGA
                                ||| |||      ||||||||
                                TCA CCC      GGTTTCCT
                                  A   TAC_____
GAM238  FLJ00001 3'  CCTTTGGACATCCCATGGACT  81815      ___   TTAACA
                                AGTC   GGG     TCCAAAGG
                                ||||   |||     ||||||||
                                TCAG   CCC     AGGTTTCC
                                  GTA   TAC___
GAM238  FLJ20257 5'  TCCCCCTCGTTACCCCGACTG  38999        T    ATCCAAA
                                CAGTCGGG TAAC      GGA
                                |||||||| ||||      |||
                                GTCAGCCC ATTG      CCT
                                     C    CTCCC__
GAM238  KIAA1870 3'  TCCCCTGGACACAGCCCACCTG 51834     TC     AACA    AA
                                CAG  GGGTT    TCCA  GGA
                                |||  |||||    ||||  |||
                                GTC  CCCGA    AGGT  CCT
                                  CA    CAC_   CC
GAM238  LIG-1    3'  GTCCTTCAAATGTTCCTTTGGC 63898       TT     CCA
                                GTCGGG  AACAT   AAGGAC
                                ||||||  |||||   ||||||
                                CGGTTT  TTGTA   TTCCTG
                                   CC     AAC
GAM238  MGC10940 3'  GTCCTTTGGACATAAGAGAT   50217     GGG   ACA
                                GTC   TTA   TCCAAAGGAC
                                |||   |||   ||||||||||
                                TAG   AAT   AGGTTTCCTG
                                  AG_   AC_
GAM238  MGC20253 3'  GTCCTTTGAATGTTCCAAC    58062    C   TTA    C
                                GT GGG   ACAT CAAAGGAC
                                || |||   |||| ||||||||
                                CA CCT   TGTA GTTTCCTG
                                 A   ___    A
GAM238  RACGAP1  3'  TCCTTTGGCATCCCAACT     25202     C   TTAACAT
                                AGT GGG      CCAAAGGA
                                ||| |||      ||||||||
                                TCA CCC      GGTTTCCT
                                  A   TAC_____
GAM238  SUI1     3'  TCCCCTGGTGTCTCCAACCTGA 19404         A___   T   AA
           CT                     AGTCGGGTT    ACA CCA  GGA
                                |||||||||   ||| |||  |||
                                TCAGTCCAA    TGT GGT  CCT
                                     CCTC   _   CC
GAM238  LOC115207 3'  GTCCTTTGGATATTCTGTGATG 56603    GT_    TTAAC
                                CA   CGGG    ATCCAAAGGAC
                                ||   ||||    ||||||||||
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                                GT   GTCT    TAGGTTTCCTG
                                 AGT    TA___
GAM238   LOC152343 3'  GTCCTTTGGATGTTAATCTGAC 80568
            TG                    CAGTCGGGTTAACATCCAAAGGAC
                                  ||||||||||||||||||||||||
                                  GTCAGTCTAATTGTAGGTTTCCTG

GAM238   LOC154222 3'  CCAAAGGACAGAACATCAGCCC 86190       AACA_________  AAA
            GACTG                   TCGGGTT         TCC   GG
                                  |||||||         |||   ||
                                  AGCCCGA         AGG   CC
                                     CTACAAGAIIIC   AAA
GAM238   LOC203286 3'  CCTCCAAATGTGCCTGACT   90497       TA    CCAA
                                  AGTCGGGT  ACAT    AGG
                                  ||||||||  ||||    |||
                                  TCAGTCCG  TGTA    TCC
                                       __    AACC
GAM238   LOC221688 5'  GTCCTTTGGATGTCATGTCT   93679    T  GGTTA
                                  AG CG     ACATCCAAAGGAC
                                  || ||     ||||||||||||
                                  TC GT     TGTAGGTTTCCTG
                                   T  AC___
GAM239   CD80     3'  AGATCTGAAGGTAGCCTC    17766    A     AG
                                  GA GCTGCC  TCAGATCT
                                  || ||||||  ||||||||
                                  CT CGATGG  AGTCTAGA
                                   C     A_
GAM239   CEACAM5   3'  CTAACTGACAGCTTCA      15159        C    C
                                  TGAAGCTG CAGT AG
                                  |||||||| |||| ||
                                  ACTTCGAC GTCA TC
                                       A    A
GAM239   CX3CR1    5'  AGGGTGGCTGACTGGCAGATCC 70643    AAG        AT_
            A                      TG   CTGCCAGTCAG   CTCT
                                  ||   ||||||||||   ||||
                                  AC   GACGGTCAGTC   GGGA
                                   CTA         GGT
GAM239   DUSP6    5'  ATCTGGGCAGCTTCA       65962          AGT
                                  TGAAGCTGCC   CAGAT
                                  ||||||||||   |||||
                                  ACTTCGACGG   GTCTA
                                               ___
GAM239   FLNB     3'  AGAGAAGGGCAGCAGCTT    62170        CA   AGA
                                  AAGCTGC  GTC   TCTCT
                                  |||||||  |||   |||||
                                  TTCGACG  CGG   AGAGA
                                     A_   GA_
GAM239   HTN1     3'  AGAGGTTTGACTGGCAAATTCA 9284       GC
                                  TGAA  TGCCAGTCAGATCTCT
                                  ||||  ||||||||||||||||
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                                ACTT  ACGGTCAGTTTGGAGA
                                  AA
GAM239  ITPKB    3'  TCCGATTAGCAGCCTCA     9437      A    C    A
                                TGA GCTGC AGTC GA
                                ||| ||||| |||| ||
                                ACT CGACG TTAG CT
                                  C    A   C
GAM239  MAPK1    3'  AGATTTAAAGTGGCAGCTTCA  10818          GTC_
                                TGAAGCTGCCA   AGATCT
                                ||||||||||    ||||||
                                ACTTCGACGGT   TTTAGA
                                      GAAA
GAM239  MAT1A    3'  CTGACCAGCAGCTTTA      90832         CA
                                TGAAGCTGC  GTCAG
                                |||||||||  |||||
                                ATTTCGACG  CAGTC
                                      AC
GAM239  MMP19    3'  GTCTACTGGCGCCTCA      42974     A  T     C
                                TGA GC GCCAGT AGAT
                                ||| || |||||| ||||
                                ACT CG CGGTCA TCTG
                                  C  _     _
GAM239  MMP19    3'  GTCTACTGGCGCCTCA      42980     A  T     C
                                TGA GC GCCAGT AGAT
                                ||| || |||||| ||||
                                ACT CG CGGTCA TCTG
                                  C  _     _
GAM239  NAB1     3'  AGATAACTGACAGCTTTA     19906        C    CAG
                                TGAAGCTG CAGT   ATCT
                                |||||||| ||||   ||||
                                ATTTCGAC GTCA   TAGA
                                     A   A__
GAM239  NEF3     3'  ATGTGATTGGCAGCTTCA     18195            G
                                TGAAGCTGCCAGTCA AT
                                |||||||||||||| ||
                                ACTTCGACGGTTAGT TA
                                        G
GAM239  NHP2L1   3'  AGAGATCTGGTTCCAGCTTT   17200        CC GT
                                GAAGCTG  A  CAGATCTCT
                                |||||||  |  |||||||||
                                TTTCGAC  T  GTCTAGAGA
                                    C_ TG
GAM239  SCN1A    5'  GGACCTGACAGCTTCA      88852        GCCA    A
                                TGAAGCT    GTCAG TCT
                                |||||||    ||||| |||
                                ACTTCGA    CAGTC AGG
                                    _____    C
GAM239  TTC3     3'  CTGTTCTGGTAGCTCCA     12418    A       T_
                                TG AGCTGCCAG  CAG
                                || |||||||||  |||
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                                AC TCGATGGTC  GTC
                                 C        TT
GAM239  ZNF202   3'  AGACTGCTCAACAGCTTCA   12911        CC_  T   A
                                TGAAGCTG   AG CAG TCT
                                ||||||||   || ||| |||
                                ACTTCGAC   TC GTC AGA
                                    AAC  _   _
GAM239  BTN2A1   3'  AGAGACAGAAGTGCAGCTTCA  54338         CAG  AGA
                                TGAAGCTGC   TC   TCTCT
                                |||||||||   ||   |||||
                                ACTTCGACG   AG   AGAGA
                                     TGA  AC_
GAM239  CCR5     5'  AGAGATCTATTCTCCAGCTT   5146        CCAGTC
                                AAGCTG     AGATCTCT
                                ||||||     ||||||||
                                TTCGAC     TCTAGAGA
                                   CTCTTA
GAM239  DKFZP586I2223 5'  ATCTGACTGCAGCCCCA     54917    AA    C
                                TG  GCTGC AGTCAGAT
                                ||  ||||| ||||||||
                                AC  CGACG TCAGTCTA
                                 CC    _
GAM239  FLJ10242  3'  AGAGTCCTGACAGCAGCTTCA  35933         CA    AT
                                TGAAGCTGC  GTCAG  CTCT
                                |||||||||  |||||  ||||
                                ACTTCGACG  CAGTC  GAGA
                                     A_    CT
GAM239  FLJ10314  3'  AGATCTGACCAAGGTGTCA   36009    A   GCCA
                                TGA GCT    GTCAGATCT
                                ||| |||    |||||||||
                                ACT TGG    CAGTCTAGA
                                  G   AAC_
GAM239  FLJ10901  3'  TCTGACTGACAGCCTC      36834    A    C
                                GA GCTG CAGTCAGA
                                || |||| ||||||||
                                CT CGAC GTCAGTCT
                                 C    A
GAM239  FLJ11715  3'  AGAGCTCACTGCAGCTTCA   44666         C   CA  T
                                TGAAGCTGC AGT  GA CTCT
                                ||||||||| |||  || ||||
                                ACTTCGACG TCA  CT GAGA
                                     _   ___  C
GAM239  FLJ13154  3'  AGAAATCTTTTTACAGTTTCA  44789        CC  TC   C
                                TGAAGCTG  AG  AGAT TCT
                                ||||||||  ||  |||| |||
                                ACTTTGAC  TT  TCTA AGA
                                     A_  TT    A
GAM239  FLJ13769  3'  AGAGCTTTCTATCAGCTTCA   46595        CC  TC  AT
                                TGAAGCTG  AG  AG  CTCT
                                ||||||||  ||  ||  ||||
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                                ACTTCGAC  TC  TC  GAGA
                                    TA  TT  __
GAM239  FLJ23132  3'  AGAGACGGCAGGCAGCTT    96133        A   AGA
                                AAGCTGCC GTC   TCTCT
                                |||||||| |||   |||||
                                TTCGACGG CGG   AGAGA
                                    A   C__
GAM239  FUBP3     3'  ATTTGACTGACAATTCA     63731      GC  C
                                TGAA  TG CAGTCAGAT
                                ||||  || |||||||||
                                ACTT  AC GTCAGTTTA
                                  A_  A
GAM239  HSJ1      3'  ATGTGATGGCAGCTCCA     22124    A      G   G
                                TG AGCTGCCA TCA AT
                                || |||||||| ||| ||
                                AC TCGACGGT AGT TA
                                 C       _   G
GAM239  KIAA0607  3'  AGAGACGCGACTGGCGGCTCCA 72566    A         AGA
                                TG AGCTGCCAGTC   TCTCT
                                || ||||||||||   |||||
                                AC TCGGCGGTCAG   AGAGA
                                 C          CGC
GAM239  KIAA0907  3'  AGAGATCTGACTGCTGGCT    30169     GC
                                AGCT  CAGTCAGATCTCT
                                ||||  ||||||||||||
                                TCGG  GTCAGTCTAGAGA
                                  TC
GAM239  KIAA1190  3'  AGGCTGACTGGCAGC       71095          A
                                GCTGCCAGTCAG TCT
                                |||||||||||| |||
                                CGACGGTCAGTC GGA
                                      _
GAM239  KIAA1196  3'  AGGTTGATGGCAGCTCCA    61460    A      GTCA
                                TG AGCTGCCA    GATCT
                                || ||||||||    |||||
                                AC TCGACGGT    TTGGA
                                 C       AG__
GAM239  KIAA1300  3'  AGAGACACTGTGGCAGCT    62859        GT   A_
                                AGCTGCCA  CAG  TCTCT
                                ||||||||  |||  |||||
                                TCGACGGT  GTC  AGAGA
                                    __   AC
GAM239  LBP-9     3'  GGGTTAACTAACAGCTTTA   27280        CC   CA
                                TGAAGCTG  AGT  GATCT
                                ||||||||  |||  |||||
                                ATTTCGAC  TCA  TTGGG
                                    AA   A_
GAM239  MGC14436  5'  AGAATCGATACTGAACAGCTTC 51851        C_   CA_   C
          A                      TGAAGCTG  CAGT   GAT TCT
                                ||||||||  ||||   ||| |||
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                                ACTTCGAC  GTCA   CTA AGA
                                    AA    TAG  _
GAM239  MGC4832  3' AGAGCTGCCTGGTAGCTTCA  58997          T   AT
                                TGAAGCTGCCAG CAG  CTCT
                                |||||||||||| |||  ||||
                                ACTTCGATGGTC GTC  GAGA
                                     C  __
GAM239  P15-2    3' AGATTTTTCTTGGCAGCTCCA 38005    A      _ TC
                                TG AGCTGCCA G  AGATCT
                                || |||||||| |  ||||||
                                AC TCGACGGT C  TTTAGA
                                 C       T TT
GAM239  RGS10    3' AGCCGGGACTGGCAGCTTTA  11331           AGAT
                                TGAAGCTGCCAGTC   CT
                                ||||||||||||||   ||
                                ATTTCGACGGTCAG   GA
                                      GGCC
GAM239  TBDN100  3' AGAGATCTATTTGAAGCTTCA 46948       GC   TC
                                TGAAGCT  CAG  AGATCTCT
                                |||||||  |||  ||||||||
                                ACTTCGA  GTT  TCTAGAGA
                                    A_   TA
GAM239  ZNF238   3' GGATATTGCAGCTTCA     20964         C  CAG
                                TGAAGCTGC AGT   ATCT
                                ||||||||| |||   ||||
                                ACTTCGACG TTA   TAGG
                                      _  ____
GAM239  LOC113763 3' CTGGCTGGCAGCCCCA     56579    AA
                                TG  GCTGCCAGTCAG
                                ||  ||||||||||||
                                AC  CGACGGTCGGTC
                                 CC
GAM239  LOC125061 3' CTGACACTGACAGCTTCA    74390        C  __
                                TGAAGCTG CA  GTCAG
                                |||||||| ||  |||||
                                ACTTCGAC GT  CAGTC
                                    A  CA
GAM239  LOC135293 3' CTGGGTGGCAGTTCA       76180     G     G
                                TGAA CTGCCA TCAG
                                |||| |||||| ||||
                                ACTT GACGGT GGTC
                                  _     G
GAM239  LOC146056 3' GAGAAGCAACAGCTTCA     77617        CCA  CAGA
                                TGAAGCTG   GT    TCTC
                                ||||||||   ||   ||||
                                ACTTCGAC   CG    AGAG
                                    AA_  A___
GAM239  LOC147610 5' GAGACCTACAGCTTCA      87173        CCAGTC  A
                                TGAAGCTG     AG TCTC
                                ||||||||     || ||||
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                                ACTTCGAC     TC AGAG
                                     A_____  C
GAM239   LOC149076 3'  AGAGGGGTGCGGCAGCTTCA   79146          A T  GA
                                TGAAGCTGCC G CA  TCTCT
                                |||||||||| | ||  |||||
                                ACTTCGACGG C GT  GGAGA
                                     _ _  GG
GAM239   LOC153196 5'  CTGACTTGACAGCTTCA     85959        C  _
                                TGAAGCTG CA GTCAG
                                |||||||| || |||||
                                ACTTCGAC GT CAGTC
                                     A  T
GAM239   LOC168975 5'  GAGTTTCCACAGCTTCA     87279        CCAGTC   T
                                TGAAGCTG     AGA CTC
                                ||||||||     ||| |||
                                ACTTCGAC     TTT GAG
                                     ACC___   _
GAM239   LOC199953 3'  CTACTGGCAGCTCCA       88503    A        C
                                TG AGCTGCCAGT AG
                                || ||||||||||  ||
                                AC TCGACGGTCA TC
                                 C        _
GAM239   LOC201194 3'  AGGTAGTGGCAGCTCCA     89774    A       GTCAG
                                TG AGCTGCCA     ATCT
                                || ||||||||     ||||
                                AC TCGACGGT     TGGA
                                 C       GA___
GAM239   LOC219914 5'  AGGTCTGCAGCTTCA       93324          CAGTC
                                TGAAGCTGC     AGATCT
                                |||||||||     ||||||
                                ACTTCGACG     TCTGGA
                                      _____
GAM239   LOC220672 3'  AGACTGATGGCAGCTCG     60423     A      G    A
                                TGA GCTGCCA TCAG TCT
                                ||| ||||||| |||| |||
                                GCT CGACGGT AGTC AGA
                                  _      _    _
GAM239   LOC222662 3'  AGAACTGGCTACCAGCTTCA   92841         CC     A
                                TGAAGCTG  AGTCAG TCT
                                ||||||||  |||||| |||
                                ACTTCGAC  TCGGTC AGA
                                     CA      A
GAM239   LOC245771 5'  TCTGACTGACAGCCTC      92899    A    C
                                GA GCTG CAGTCAGA
                                || |||| ||||||||
                                CT CGAC GTCAGTCT
                                 C    A
GAM239   LOC257239 5'  AGGTCTGCAGCTTCA       97061          CAGTC
                                TGAAGCTGC     AGATCT
                                |||||||||     ||||||
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                                ACTTCGACG    TCTGGA
                                      _____
GAM239  LOC90522 3' GAGATCTCCAGCTGCA     63155    A    CCAGTC
                                TG AGCTG     AGATCTC
                                || |||||     |||||||
                                AC TCGAC     TCTAGAG
                                 G    C_____
GAM239  LOC90750 3' AGAGATCTAACCATGGGCA   63912     A___  C
                                TGCC   GT AGATCTCT
                                ||||   || ||||||||
                                ACGG   CA TCTAGAGA
                                  GTAC  A
GAM240  ABH      3' ACATGGTCTGTTCCT       59749          GTTA
                                AGGAGTAGATT   GTGT
                                ||||||||||   ||||
                                TCCTTGTCTGG   TACA
                                      ____
GAM240  ACAD8    3' CAGTGTTTCTGTTCCTGA    26891          TTGTT  TG
                                TCAGGAGTAGA    AG  TTG
                                ||||||||||    ||  |||
                                AGTCCTTGTCT    TT  GAC
                                      _____ GT
GAM240  ACRV1    5' TAGCACTGGAAGCTTTTG    39177       AGATTG
                                CAGGAGT    TTAGTGTTG
                                |||||||    |||||||||
                                GTTTTCG    GGTCACGAT
                                   AA____
GAM240  ACRV1    5' TAGCACTGGAAGCTTTTG    7861        AGATTG
                                CAGGAGT    TTAGTGTTG
                                |||||||    |||||||||
                                GTTTTCG    GGTCACGAT
                                   AA____
GAM240  ACRV1    5' TAGCACTGGAAGCTTTTG    39182       AGATTG
                                CAGGAGT    TTAGTGTTG
                                |||||||    |||||||||
                                GTTTTCG    GGTCACGAT
                                   AA____
GAM240  ACRV1    5' TAGCACTGGAAGCTTTTG    39187       AGATTG
                                CAGGAGT    TTAGTGTTG
                                |||||||    |||||||||
                                GTTTTCG    GGTCACGAT
                                   AA____
GAM240  ACRV1    5' TAGCACTGGAAGCTTTTG    39192       AGATTG
                                CAGGAGT    TTAGTGTTG
                                |||||||    |||||||||
                                GTTTTCG    GGTCACGAT
                                   AA____
GAM240  ACRV1    5' TAGCACTGGAAGCTTTTG    39197       AGATTG
                                CAGGAGT    TTAGTGTTG
                                |||||||    |||||||||
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                                GTTTTCG     GGTCACGAT
                                   AA____
GAM240  ACRV1    5'  TAGCACTGGAAGCTTTTG    39202       AGATTG
                                CAGGAGT     TTAGTGTTG
                                |||||||     |||||||||
                                GTTTTCG     GGTCACGAT
                                   AA____
GAM240  ACRV1    5'  TAGCACTGGAAGCTTTTG    39207       AGATTG
                                CAGGAGT     TTAGTGTTG
                                |||||||     |||||||||
                                GTTTTCG     GGTCACGAT
                                   AA____
GAM240  ACRV1    5'  TAGCACTGGAAGCTTTTG    39212       AGATTG
                                CAGGAGT     TTAGTGTTG
                                |||||||     |||||||||
                                GTTTTCG     GGTCACGAT
                                   AA____
GAM240  ACRV1    5'  TAGCACTGGAAGCTTTTG    39217       AGATTG
                                CAGGAGT     TTAGTGTTG
                                |||||||     |||||||||
                                GTTTTCG     GGTCACGAT
                                   AA____
GAM240  ACT      3'  TCAGTTGCGGTCTTATTTTTGA 40042        _     TAGTG
                                TCAGGAGTA GATTGT     TTGA
                                ||||||||| ||||||     ||||
                                AGTTTTTAT CTGGCG     GACT
                                     T     TT___
GAM240  ACTN2    3'  CATAAATAGGTTTATTTCTGA  6592          _   A
                                TCAGGAGTAGAT TGTT GTG
                                |||||||||||| |||| |||
                                AGTCTTTATTTG ATAA TAC
                                      G   A
GAM240  ADAMTS4  3'  TTGGCCAGGCTGCTCTTGA   17523         ATT_
                                TCAGGAGTAG   GTTAG
                                ||||||||||   |||||
                                AGTTCTCGTC   CGGTT
                                     GGAC
GAM240  ADAMTS5  3'  TCAACACTGGTATACCTCCT   22896     TAGAT  TT
                                AGGAG    TG  AGTGTTGA
                                |||||    ||  ||||||||
                                TCCTC    AT  TCACAACT
                                   CAT__  GG
GAM240  ADCY7    3'  TCAGCATATTTGTACTCTTGG  6646        GATTGTTA
                                TCAGGAGTA      GTGTTGA
                                |||||||||      |||||||
                                GGTTCTCAT      TACGACT
                                     GTTTA___
GAM240  AGA      3'  GCACTTTCTATATCTGA     3442       A    TTGTT
                                TCAGG GTAGA    AGTGT
                                ||||| |||||    |||||
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                                AGTCT TATCT    TCACG
                                  A    T____
GAM240  AGL     5'  ATATTGAACTCCTGG      5374         AGATTG
                                TCAGGAGT    TTAGTGT
                                ||||||||    |||||||
                                GGTCCTCA    AGTTATA
                                     _______
GAM240  AGTPBP1  3'  TGGCGCTTGTTTTATTTTCGA  30866    AG     TTGTT    TG
                                TC  GAGTAGA    AGTGT  A
                                ||  |||||||    |||||  |
                                AG  TTTATTT    TCGCG  T
                                 CT     TGT__    GT
GAM240  AICDA    3'  CAGCAAATTTGCTTCTGG    40324          GTTAG    A
                                TCAGGAGTAGATT    TGTTG
                                ||||||||||||    |||||
                                GGTCTTCGTTTAA    ACGAC
                                     _____    A
GAM240  ANG     5'  ATTGGCCTAATTTGGTGATGCT 6699     _  _____    T  TG
            GTTCTTGG                TAG ATT    GTTAG GT  A   T
                                ||| |||    ||||| ||  |  |
                                GTC TAG    TAATC CG  T   A
                                  G   TGGTT    _ GT
GAM240  AP1G1    3'  AGGCTGGCTGCTTCTGG     6672         GATT     G
                                TCAGGAGTA    GTTAGT T
                                |||||||||    ||||||  |
                                GGTCTTCGT    CGGTCG A
                                     ____     G
GAM240  APAF1    3'  TCAATAACTAGCTATTTTTGA  6738         GATT     _
                                TCAGGAGTA    GTTAGT GTTGA
                                |||||||||    |||||| |||||
                                AGTTTTTAT    CGATCA TAACT
                                     ____     A
GAM240  APAF1    3'  TCAATAACTAGCTATTTTTGA  25047        GATT     _
                                TCAGGAGTA    GTTAGT GTTGA
                                |||||||||    |||||| |||||
                                AGTTTTTAT    CGATCA TAACT
                                     ____     A
GAM240  APC     3'  TGGCACTTATCTATTCCTGA   3480           TGTT    TG
                                TCAGGAGTAGAT    AGTGT  A
                                ||||||||||||    |||||  |
                                AGTCCTTATCTA    TCACG  T
                                       T___    GT
GAM240  ARAF1    3'  TCAATGTTCGTCTCTGCCCTGA 63940      A    TTGTT  TG
                                TCAGG GTAGA    AG  TTGA
                                ||||| |||||    ||  ||||
                                AGTCC CGTCT    TT  AACT
                                   _    CTGC_  GT
GAM240  ARHGEF7  3'  CAACACTTTCTTTTTTGG    14002        T   TTGTT
                                TCAGGAG AGA    AGTGTTG
                                ||||||| |||    |||||||
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                                GGTTTTT TCT    TCACAAC
                                   _  T____
GAM240  ARSD    5'  TGGCACTAGCGGCGCCC    8024    A  AGA       TG
                                GG GT   TTGTTAGTGT  A
                                || ||   ||||||||||  |
                                CC CG   GGCGATCACG  T
                                 _ C__        GT
GAM240  AS3     3'  ACCTAGTGTTTACTCCTGG   31934          TGT   T
                                TCAGGAGTAGAT   TAG GT
                                ||||||||||||   ||| ||
                                GGTCCTCATTTG   ATC CA
                                      TG_  _
GAM240  B3GALT3  3'  TTAACTGATCAGTTTATTATTG 13682     G       _    GTTGA
          A                      TCAG AGTAGATTG TTAGT
                                 |||| ||||||||| |||||
                                 AGTT TTATTTGAC AGTCA
                                   A       T    ATT
GAM240  B3GALT3  3'  TTAACTGATCAGTTTATTATTG 52553     G       _    GTTGA
          A                      TCAG AGTAGATTG TTAGT
                                 |||| ||||||||| |||||
                                 AGTT TTATTTGAC AGTCA
                                   A       T    ATT
GAM240  B3GALT3  3'  TTAACTGATCAGTTTATTATTG 52554     G       _    GTTGA
          A                      TCAG AGTAGATTG TTAGT
                                 |||| ||||||||| |||||
                                 AGTT TTATTTGAC AGTCA
                                   A       T    ATT
GAM240  B3GALT5  5'  TTGGCATATCTGGTTCTGA   52565      G    _
                                 TCAGGA TAGAT TGTTAG
                                 |||||| ||||| ||||||
                                 AGTCTT GTCTA ACGGTT
                                    G    T
GAM240  B3GALT5  5'  TTGGCATATCTGGTTCTGA   52573      G    _
                                 TCAGGA TAGAT TGTTAG
                                 |||||| ||||| ||||||
                                 AGTCTT GTCTA ACGGTT
                                    G    T
GAM240  B3GALT5  5'  TTGGCATATCTGGTTCTGA   52581      G    _
                                 TCAGGA TAGAT TGTTAG
                                 |||||| ||||| ||||||
                                 AGTCTT GTCTA ACGGTT
                                    G    T
GAM240  B3GALT5  5'  TTGGCATATCTGGTTCTGA   20222      G    _
                                 TCAGGA TAGAT TGTTAG
                                 |||||| ||||| ||||||
                                 AGTCTT GTCTA ACGGTT
                                    G    T
GAM240  BAZ1A    3'  TTTTGTTATTGATGATTTATTT 25586        TG    TTGA
          TT                     AGGAGTAGAT  TTAGTG
                                 ||||||||||  ||||||
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                                TTTTTATTTA  AGTTAT
                                      GT     TGTTTTA
GAM240  BCAS1    3'  AACAATTGCTTTTGA      13337          A
                                TCAGGAGTAG TTGTT
                                |||||||||| |||||
                                AGTTTTCGTT AACAA
                                      _
GAM240  BCL10    3'  TCAGCATTAAGCTGTTCCTG  14062         ATTG
                                CAGGAGTAG   TTAGTGTTGA
                                |||||||||   ||||||||||
                                GTCCTTGTC   AATTACGACT
                                     G___
GAM240  BMP5     5'  AATAACTACTCTTGA      40776          A
                                TCAGGAGTAG TTGTT
                                |||||||||| |||||
                                AGTTCTCATC AATAA
                                      _
GAM240  BN51T    3'  GACATTTTGTTCTTGA     87494          T
                                TCAGGAGTAGA TGTT
                                |||||||||||| ||||
                                AGTTCTTGTTT ACAG
                                       T
GAM240  BTEB1    5'  CAACCAACTTACTTTTGA    6840          A   TTAGT
                                TCAGGAGTAG TTG    GTTG
                                |||||||||| |||    ||||
                                AGTTTTCATT AAC    CAAC
                                     C  _____
GAM240  CADPS    3'  AACAATTAACTTTTGA     65205         A
                                TCAGGAGT GATTGTT
                                |||||||| |||||||
                                AGTTTTCA TTAACAA
                                     A
GAM240  CALU     3'  TTAACATGGCGTGTTTATTTTT 6892          _    G
           G                     CAGGAGTAGAT TGTTA TGTTGA
                                 |||||||||||| ||||| ||||||
                                 GTTTTTATTTG GCGGT ACAATT
                                       T    _
GAM240  CAT      3'  TCATGGCTTAATGTTTATTCCT 8258           TGTT   GT
           GA                    TCAGGAGTAGAT   AGT  TGA
                                 ||||||||||||   |||  |||
                                 AGTCCTTATTTG   TCG  ACT
                                       TAAT   GT
GAM240  CD36     5'  TTAACACTAATTCACCTCCTGA 3570        TA  TT
                                 TCAGGAG  GA  GTTAGTGTTGA
                                 |||||||  ||  ||||||||||||
                                 AGTCCTC  CT  TAATCACAATT
                                     CA  __
GAM240  CDH10    5'  TAGTGACAATTTCTCCTGG   22057        T       G
                                 TCAGGAG AGATTGTTA TG
                                 ||||||| ||||||||| ||
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                                GGTCCTC TTTAACAGT AT
                                   _       G
GAM240  CDH12    5'  CGGTGCTGCTGCTCCTG     14490         ATTGT   TG
                                CAGGAGTAG    TAG  TTG
                                |||||||||    |||  |||
                                GTCCTCGTC    GTC  GGC
                                   _____  GT
GAM240  CEACAM5  3'  TCAATAAAAATCTGCTCTT   15161          GTTAG
                                AGGAGTAGATT    TGTTGA
                                ||||||||||    ||||||
                                TTCTCGTCTAA    ATAACT
                                      AA___
GAM240  CENPA    3'  TTAACATTTTACTCTTG     8415           T
                                CAGGAGTAGA TGTTAG
                                |||||||||| ||||||
                                GTTCTCATTT ACAATT
                                      T
GAM240  CHAC     3'  TTAATATTAATGGACTGTTTC  52795        A TG
                                GGAGTAG T  TTAGTGTTGA
                                ||||||| |  ||||||||||
                                CTTTGTC G  AATTATAATT
                                    A GT
GAM240  CHC1     5'  TTGGCATTGACATTTAATTTTA 7025     AG    A  T       TG
           GG                     TC  GAGT GA TGTTAGTGT  A
                                ||  |||| || |||||||||  |
                                GG  TTTA TT ACAGTTACG  T
                                 AT    A  T       GT
GAM240  CHI3L1   3'  TTGGCGCTTTGCTTTGGTCTAT 7047    GA      ___  T_    TG
           CTTTGA                    GTAGATT   GT  AGTGT  A
                                 |||||||   ||  |||||  |
                                 TATCTGG   CG  TCGCG  T
                                TC      TTT  TT    GT
GAM240  CHRM1    3'  TTAACATTAAGTATTCCT    94793        GATTG
                                AGGAGTA    TTAGTGTTGA
                                |||||||    ||||||||||
                                TCCTTAT    AATTACAATT
                                    G____
GAM240  CKN1     3'  CAGTATTGACTTTCTCTT    3589      T   TT
                                GAG AGA  GTTAGTGTTG
                                ||| |||  ||||||||||
                                TTC TCT  CAGTTATGAC
                                  _   TT
GAM240  CKN1     3'  TCAACTGTATGGTCTATTCCTG 3590           TG TAGT
           A                     TCAGGAGTAGAT  T    GTTGA
                                ||||||||||||  |    |||||
                                AGTCCTTATCTG  A    CAACT
                                       GT TGT_
GAM240  CLCN6    3'  TAAGGGAAACACTCTGCTCCTG 41392          T    AGTGTTGA
           G                     TCAGGAGTAGA TGTT
                                ||||||||||| ||||
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                                GGTCCTCGTCT ACAA
                                      C    AGGGAATT
GAM240  CLCN6    3'  TAAGGGAAACACTCTGCTCCTG 41407          T    AGTGTTGA
              G                    TCAGGAGTAGA TGTT
                                   |||||||||| ||||
                                GGTCCTCGTCT ACAA
                                      C    AGGGAATT
GAM240  CLCN6    3'  TAAGGGAAACACTCTGCTCCTG 7085           T    AGTGTTGA
              G                    TCAGGAGTAGA TGTT
                                   |||||||||| ||||
                                GGTCCTCGTCT ACAA
                                      C    AGGGAATT
GAM240  COX15    3'  TCAGTGTTGGCAAGCTCTTGG  54320        AGA      TG
                                TCAGGAGT   TTGTTAG  TTGA
                                |||||||   |||||||  ||||
                                GGTTCTCG   AACGGTT  GACT
                                    ___      GT
GAM240  COX15    3'  TCGACAGTATAAATTGGTTCCT 54322        TA    GT  G
              GA                   TCAGGAG  GATT  TA TGTTGA
                                   |||||||  ||||  || ||||||
                                AGTCCTT  TTAA  AT ACAGCT
                                    GG    AT  G
GAM240  CPD      3'  TTGACGGTCTCTTTTTGA    7133         T
                                TCAGGAG AGATTGTTAG
                                ||||||| ||||||||||
                                AGTTTTT TCTGGCAGTT
                                    C
GAM240  CR2      3'  TCAATGTTACTATCTGCTTTTG 8534           T  T  TG
              G                    TCAGGAGTAGAT GT AG  TTGA
                                   |||||||||||| || ||  ||||
                                GGTTTTCGTCTA CA TT  AACT
                                      T  _  GT
GAM240  CREB1    3'  TCAATACTGAAAATTTGTCCTT 15203       AG     G
              GG                   TCAGG  TAGATT TTAGTGTTGA
                                   |||||  |||||| ||||||||||
                                GGTTC  GTTTAA AGTCATAACT
                                   CT     A
GAM240  CRIM1    3'  TTGGTAATTAATCCATTCCTGG 33183        A    TTAG  TT
                                TCAGGAGT GATTG    TG  GA
                                |||||||| |||||    ||  ||
                                GGTCCTTA CTAAT    AT  TT
                                    C     TA__  GG
GAM240  CSPG3    3'  TCAATGTTGGCTGAATTCCT   15238       AGATT    TG
                                AGGAGT    GTTAG  TTGA
                                ||||||    |||||  ||||
                                TCCTTA    CGGTT  AACT
                                   AGT__     GT
GAM240  CTBP2    5'  TTAGCACACAGCCAGGTCTGTT 42988          __   A_
              TTTGA                   GGAGTAGATT  GTT  GTGTTGA
                                   ||||||||||  |||  |||||||
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                                TTTTGTCTGG  CGA  CACGATT
                                      AC   CA
GAM240  CTGF     3'  TCAATGTTAGCCTCAATTTCTG 8577         A  TT    TG
             A                  TCAGGAGT GA  GTTAG  TTGA
                                |||||||| ||  |||||  ||||
                                AGTCTTTA CT  CGATT  AACT
                                     A  C_    GT
GAM240  CTLA4    3'  TTGGTGTTGACATGTGCTTTGG 17813    AG    G  T    TG TG
             G                  TC  GAGTA AT GTTAG  T  A
                                ||  ||||| || |||||  |  |
                                GG  TTCGT TA CAGTT  G  T
                                 GT    G  _    GT GT
GAM240  CUL3     3'  TCAGAAATTTGATTTATTCTTG 13166            TTAGTG
             G                  TCAGGAGTAGATTG     TTGA
                                ||||||||||||||     ||||
                                GGTTCTTATTTAGT     GACT
                                      TTAAA_
GAM240  CXCL1    3'  CACTGGTGGCTGTTCCTGA   7697          A TG
                                TCAGGAGTAG T  TTAGTG
                                |||||||||| |  ||||||
                                AGTCCTTGTC G  GGTCAC
                                      _ GT
GAM240  CXorf6   3'  GGCGAGCTGTTCCTGG      18517          A
                                TCAGGAGTAG TTGTT
                                |||||||||| |||||
                                GGTCCTTGTC AGCGG
                                      G
GAM240  CYP1B1   3'  TTAACATTAATGCCTGCTTTT  3656         ATT
                                AGGAGTAG   GTTAGTGTTGA
                                ||||||||   ||||||||||
                                TTTTCGTC   TAATTACAATT
                                     CG_
GAM240  DACH     3'  TCAGCCATTGCTCTGCTCCTGG 54972          TT  TAGT
                                TCAGGAGTAGA  GT   GTTGA
                                ||||||||||  ||   |||||
                                GGTCCTCGTCT  CG   CGACT
                                      __ TTAC
GAM240  DACH     3'  TTAACATTATAGATACTCT   54976       GATTGT
                                GGAGTA     TAGTGTTGA
                                ||||||     |||||||||
                                TCTCAT     ATTACAATT
                                   AGAT__
GAM240  DAZ      3'  TTAACACTGAAACTGTTCTTC  14552      TAGATTG
                                GGAG      TTAGTGTTGA
                                ||||      ||||||||||
                                CTTC      AGTCACAATT
                                  TTGTCAA
GAM240  DDEF2    3'  TTGGCATTGTACTTTTTGTTTT 13957          TT  _     TG
             TG                   CAGGAGTAGA  GT TAGTGT  A
                                |||||||||  || ||||||  |
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                                GTTTTTGTTT  CA GTTACG  T
                                      TT  T     GT
GAM240  DGCR2    3'  TGATACTGTACATTGTCTTGA  17633       G   AT  _     TG
                                TCAGGA TAG  TGT TAGTGT  A
                                |||||| |||  ||| ||||||  |
                                AGTTCT GTT  ACA GTCATA  T
                                   _  __  T     GT
GAM240  DNAH9    3'  TTAATAAAATGATTTACTCTT  16231         TG  AG
                                AGGAGTAGAT  TT  TGTTGA
                                ||||||||||  ||  ||||||
                                TTCTCATTTA  AA  ATAATT
                                      GT  A_
GAM240  DPYSL3   3'  TACAGGCAGTTTGTGTTTGA   7319       AG      TA
                                TCAGG  TAGATTGT  GTG
                                |||||  ||||||||  |||
                                AGTTT  GTTTGACG  CAT
                                   GT       GA
GAM240  DSCR3    3'  TTGATGAATTTGGTCTGCCTCT 20200     GA      TTAG   TG
          GA                      TCAG  GTAGATTG    TGT  A
                                ||||  ||||||||    |||  |
                                AGTC  CGTCTGGT    GTA  T
                                  TC       TTAA   GT
GAM240  DUSP6    3'  AGCAGTTTCTCTTGG       65961        T
                                TCAGGAG AGATTGTT
                                ||||||| ||||||||
                                GGTTCTC TTTGACGA
                                      _
GAM240  DYRK1A   3'  CAGATGCAATCACTTTTGG    7350         A     TAGTG
                                TCAGGAGT GATTGT    TTG
                                |||||||| ||||||     |||
                                GGTTTTCA CTAACG    GAC
                                   _     TA___
GAM240  DYRK1A   3'  CAGATGCAATCACTTTTGG    55200        A     TAGTG
                                TCAGGAGT GATTGT    TTG
                                |||||||| ||||||     |||
                                GGTTTTCA CTAACG    GAC
                                   _     TA___
GAM240  DYRK1A   3'  CAGATGCAATCACTTTTGG    55241        A     TAGTG
                                TCAGGAGT GATTGT    TTG
                                |||||||| ||||||     |||
                                GGTTTTCA CTAACG    GAC
                                   _     TA___
GAM240  DYT1     3'  GCATGGCATTTGTTCCTGA    3673           T   G
                                TCAGGAGTAGAT GTTA TGT
                                |||||||||||| |||| |||
                                AGTCCTTGTTTA CGGT ACG
                                      _   _
GAM240  EFNB2    3'  GACAGCTACTTCTGG       14572          A
                                TCAGGAGTAG TTGTT
                                |||||||||| |||||
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                                GGTCTTCATC GACAG
                                      _
GAM240  EGFL5    3'  AAGCAAATAATCTACTTCTGG  86608              AG    GA
                                TCAGGAGTAGATTGTT  TGTT
                                |||||||||||||||  ||||
                                GGTCTTCATCTAATAA  ACGA
                                      __    AC
GAM240  EHD3     3'  TTAATACAGTACATTTATTCTT 27484          T  TA_
                                AGGAGTAGAT GT   GTGTTGA
                                |||||||||| ||   |||||||
                                TTCTTATTTA CA   CATAATT
                                      _  TGA
GAM240  ELK1     3'  TTGATAGTATAATCTATTTTT  17847           T G   TG
                                AGGAGTAGATTGT A TGT  A
                                |||||||||||| | |||  |
                                TTTTTATCTAATA T ATA  T
                                      _ G   GT
GAM240  ELOVL4   3'  ATTTATGGCTGTTCCTGA    42684          A TG T
                                TCAGGAGTAG T  T AGT
                                |||||||||| |  | |||
                                AGTCCTTGTC G  A TTA
                                      _ GT T
GAM240  EN2      3'  AAATATACATTTTATTTTTGA  7454           T   TA    GA
                                TCAGGAGTAGA TGT  GTGTT
                                |||||||||| |||  |||||
                                AGTTTTTATTT ACA  TATAA
                                      T  __    AA
GAM240  ENC1     3'  TCAAAGTTGGGGTCTGTTCTTG 13285           G    TG
           A                     TCAGGAGTAGATT TTAG  TTGA
                                |||||||||||| ||||  ||||
                                AGTTCTTGTCTGG GGTT  AACT
                                      _   GA
GAM240  EPHA3    3'  TTACATATATTATTTATTTCTG 17872           T  TA   TGA
           G                     TCAGGAGTAGAT GT  GTGT
                                |||||||||||| ||  ||||
                                GGTCTTTATTTA TA  TACA
                                      T  TA   TT
GAM240  ERBB2IP  3'  CGGCAGGATCTGTTCTTG    37985          GTTAG
                                CAGGAGTAGATT    TGTTG
                                ||||||||||||    |||||
                                GTTCTTGTCTAG    ACGGC
                                      G____
GAM240  ERBB2IP  3'  TTAATGTTTTTCTCCTGA    37989       T   TT
                                TCAGGAG AGA  GTTAG
                                ||||||| |||  |||||
                                AGTCCTC TTT  TAATT
                                    T   TG
GAM240  ESR1     3'  TACTGATAATTTACTTTTGA  3708
                                TCAGGAGTAGATTGTTAGTG
                                ||||||||||||||||||||
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                                AGTTTTCATTTAATAGTCAT

GAM240  EVC     3'  TCGCATGGAGCATTTTGCTTCT 27299          T   A_   TGA
            GG                    TCAGGAGTAGA TGTT  GTGT
                                  |||||||||| |||| ||||
                                  GGTCTTCGTTT ACGA  TACG
                                        T   GG   CT
GAM240  F3      3'  TTAGCATTCTGGTTTTGA    67082       G   T
                                  TCAGGA TAGA TGTTAG
                                  |||||| |||| ||||||
                                  AGTTTT GTCT ACGATT
                                     G   T
GAM240  FANCC   3'  CTGATAGTTTAGTTTTTGA   70521       _
                                  TCAGGAG TAGATTGTTAG
                                  ||||||| ||||||||||
                                  AGTTTTT ATTTGATAGTC
                                      G
GAM240  FBXW1B  3'  TTAGCATTCTCCTTTTGA    24530       T   T
                                  TCAGGAG AGA TGTTAG
                                  ||||||| ||| ||||||
                                  AGTTTTC TCT ACGATT
                                      C   T
GAM240  FBXW1B  3'  TTAGCATTCTCCTTTTGA    53334       T   T
                                  TCAGGAG AGA TGTTAG
                                  ||||||| ||| ||||||
                                  AGTTTTC TCT ACGATT
                                      C   T
GAM240  FBXW1B  3'  TTAGCATTCTCCTTTTGA    53345       T   T
                                  TCAGGAG AGA TGTTAG
                                  ||||||| ||| ||||||
                                  AGTTTTC TCT ACGATT
                                      C   T
GAM240  FGF13   3'  TTGATGTTTTCTATCTACGCTT 53322      A     TGTT  TG TG
            GA                    TCAGG GTAGAT   AG  T  A
                                  ||||| ||||||   ||  |  |
                                  AGTTC CATCTA    TT  A  T
                                     G     TCTT  GT GT
GAM240  FIGF    3'  CAGTACTGACTTTCTG      15555      TT
                                  TAGA  GTTAGTGTTG
                                  ||||  ||||||||||
                                  GTCT  CAGTCATGAC
                                    TT
GAM240  FLRT2   3'  ACCATATGCTGATTTGCTTCTG 25054          GTT    _  A
            G                     CAGGAGTAGATT   AGTGT TG
                                  ||||||||||||   ||||| ||
                                  GTCTTCGTTTAG   TCGTA AC
                                         ___     T  CAA
GAM240  FMN2    3'  TCAGTGCTTTCCCAACTCTTGG 79345        AGATTGTT  TG
                                  TCAGGAGT       AG  TTGA
                                  ||||||||       ||  ||||
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                                GGTTCTCA      TC  GACT
                                    ACCCTT__  GT
GAM240  FMR1    3'  TAATGTAACTGCTCTTGG    8940          AT_
                                TCAGGAGTAG   TGTTA
                                ||||||||||   |||||
                                GGTTCTCGTC   GTAAT
                                     AAT
GAM240  FOXF1   3'  TCAGTATTAATGGTGTAACTTT 7570       _ G  TG
                                GGAGT A AT  TTAGTGTTGA
                                ||||| | ||  ||||||||||
                                TTTCA T TG  AATTATGACT
                                   A G  GT
GAM240  G6PD    3'  TTGGCCACTGGGTCTCACTCCT 4636         _    GT    _ TG
            GA                    TCAGGAGT AGATT  TAGTG T  A
                                ||||||||| |||||  |||||  |  |
                                AGTCCTCA TCTGG  GTCAC G  T
                                     C     __     C GT
GAM240  GFRA1   3'  TTAACAGTTTTACTTCTGG    17937          _
                                TCAGGAGTAGA TTGTTAG
                                |||||||||||  |||||||
                                GGTCTTCATTT GACAATT
                                       T
GAM240  GM2A    3'  CACCAGCAGCTGCTTTTGG    67771          A    A
                                TCAGGAGTAG TTGTT GTG
                                ||||||||||  |||||  |||
                                GGTTTTCGTC GACGA CAC
                                     _    C
GAM240  GNAI1   3'  TTGATAGAATAATTTTCTTTTG 9056        T      AG   TG
            A                     TCAGGAG AGATTGTT  TGT  A
                                |||||||  ||||||||  |||  |
                                AGTTTTC TTTAATAA  ATA  T
                                     T      G_  GT
GAM240  GNRHR   5'  TTAACATTGTACCTGCTTT   4644        ATTGT
                                GGAGTAG    TAGTGTTGA
                                |||||||    |||||||||
                                TTTCGTC    GTTACAATT
                                     CAT__
GAM240  GOLGA4  5'  TCAGCAACAGGCTGCTTCTGA  60070         A   TAG
                                TCAGGAGTAG TTGT   TGTTGA
                                ||||||||||  ||||   ||||||
                                AGTCTTCGTC GACA   ACGACT
                                       G   ___
GAM240  GORASP1 3'  CAATGCTAATATTTCC     49107     TAGAT
                                GGAG    TGTTAGTGTTG
                                ||||    ||||||||||
                                CCTT    ATAATCGTAAC
                                  T____
GAM240  GRM8    3'  TTATACAAATAATTTATTTCT  5948            A   TGA
                                AGGAGTAGATTGTT GTGT
                                ||||||||||||| ||||
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                                TCTTTATTTAATAA CATA
                                       A   TT
GAM240  HAS2    3'  AAAATTGAATAGTTTATTTCTG 18034            AGT  GA
                                CAGGAGTAGATTGTT  GTT
                                |||||||||||||||  |||
                                GTCTTTATTTGATAA  TAA
                                       GT_  AAT
GAM240  HAS3    3'  TTAGCACTGAACTGCTTTT   18043       ATTG
                                AGGAGTAG   TTAGTGTTGA
                                ||||||||   ||||||||||
                                TTTTCGTC   AGTCACGATT
                                    A___
GAM240  HCFC1   3'  CGCGCGCCTATTGATTTGTTTC 70992          GT  _  TGA
           TGA                    TCAGGAGTAGATT  TAG TGT
                                |||||||||||||  ||| |||
                                AGTCTTTGTTTAG  ATC GCG
                                       TT  C  CGCT
GAM240  HCK     3'  TTGATATTTCTATTTCCTGG  59935       _   T_
                                TCAGGAG TAGA  TGTTAG
                                |||||||| ||||  ||||||
                                GGTCCTT ATCT  ATAGTT
                                    T   TT
GAM240  HDAC4   3'  ATTAAAAGTCTGCTATTGA   20106     G      G
                                TCAG AGTAGATT TTAGT
                                |||| ||||||||| |||||
                                AGTT TCGTCTGA AATTA
                                  A       A
GAM240  HDAC4   3'  TGACGGTTTATTCTGA     20117     G
                                TCAG AGTAGATTGTTA
                                |||| ||||||||||||
                                AGTC TTATTTGGCAGT
                                  _
GAM240  HDAC5   3'  TCAGCACTGATGGGAGGCT   57613    AGA TG
                                AGT  T  TTAGTGTTGA
                                |||  |  ||||||||||
                                TCG  G  AGTCACGACT
                                  GAG GT
GAM240  HLF     3'  AGCACTGGTCTCTCTTGG    9215       T   TGT
                                TCAGGAG AGAT   TAGTGTT
                                |||||||| ||||  |||||||
                                GGTTCTC TCTG   GTCACGA
                                    _   ___
GAM240  HMGB3   3'  TCTACTATAACAGTCAATTTCT 18072       A      GT  T
           GA                     TCAGGAGT GATTGTTA  GT GA
                                |||||||| |||||||| || ||
                                AGTCTTTA CTGACAAT  CA CT
                                    A       AT  T
GAM240  HMGN2   3'  TAACTGTGTACTTCTGG    18622         G  T
                                TCAGGAGTA AT GTTA
                                ||||||||| || ||||
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                                GGTCTTCAT TG CAAT
                                     G  T
GAM240  HNRPH2   3'  ATTCTGATCACTCTTGG     38976        A   GTT  T
                                TCAGGAGT GATT   AG GT
                                |||||||| ||||   || ||
                                GGTTCTCA CTAG   TC TA
                                    _   ____  T
GAM240  HPGD     3'  TCAATATACATTCTGCTTTGA  5981      G     T   TA
                                TCAG AGTAGA TGT  GTGTTGA
                                |||| |||||| |||  |||||||
                                AGTT TCGTCT ACA  TATAACT
                                  _     T  __
GAM240  HPS1     3'  TCAGTGCTGATAAGCCCTTG   3968      A  AGA     TG
                                CAGG GT   TTGTTAG  TTGA
                                |||| ||   |||||||  ||||
                                GTTC CG   AATAGTC  GACT
                                  C ____      GT
GAM240  HS3ST2   3'  CAAGCAAAGTTGATCTGCTCCT 20155           TTAG   GA
             GG                   TCAGGAGTAGATTG   TGTT
                                |||||||||||||    ||||
                                GGTCCTCGTCTAGT    ACGA
                                       TGAA    ACT
GAM240  HTR1D    5'  AATAGTCTGGTCTTGA      5991       G
                                TCAGGA TAGATTGTT
                                |||||| |||||||||
                                AGTTCT GTCTGATAA
                                   G
GAM240  HTR1D    5'  CACTGTGGTCTGTTCTGG    5992       G    TG T
                                TCAGGA TAGAT  T AGTG
                                |||||| |||||  | ||||
                                GGTCTT GTCTG  G TCAC
                                   _    GT _
GAM240  IARS     3'  TCAGCCCACAGTTTATTTCT   25514          TAGT
                                AGGAGTAGATTGT   GTTGA
                                ||||||||||||    |||||
                                TCTTTATTTGACA   CGACT
                                       CC__
GAM240  IARS     3'  TCAGCCCACAGTTTATTTCT   9294           TAGT
                                AGGAGTAGATTGT   GTTGA
                                ||||||||||||    |||||
                                TCTTTATTTGACA   CGACT
                                       CC__
GAM240  IHPK1    3'  TGGCACCTGTCCTATTCCTGA  95766         _ TGTTA   TG
                                TCAGGAGTAG AT    GTGT  A
                                |||||||||| ||    ||||  |
                                AGTCCTTATC TG    CACG  T
                                      C  TC___   GT
GAM240  IL12B    3'  TCGATGCTAAATGCTCATTGA  9326      _    GATTG
                                TCAG GAGTA    TTAGTGTTGA
                                |||| |||||    ||||||||||
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                                AGTT CTCGT     AATCGTAGCT
                                  A     A____
GAM240  IL13RA1   3'  TTGATGCTGACAGTCATGCAGT 7784      A_  _         TG
             CTGG                   AGG  GTA GATTGTTAGTGT  A
                                |||  ||| ||||||||||||  |
                                TCT  CGT CTGACAGTCGTA  T
                                  GA   A          GT
GAM240  IL17BR   3'  ACGTGGTGGTCTACTTTAGA   38065    AG      TG   G
                                TC  GAGTAGAT  TTA TGT
                                ||  ||||||||  ||| |||
                                AG  TTCATCTG  GGT GCA
                                 AT       GT  _
GAM240  IL17E    3'  TCAGTGAGCATCTACTTTGGG  42966    AG      T   AGTG
                                TC  GAGTAGAT GTT    TTGA
                                ||  |||||||| |||    ||||
                                GG  TTCATCTA CGA    GACT
                                 GT       _   GT__
GAM240  IL8      3'  TCAATATTAGTAATTTCTTGCT 94481      G  T
             GG                   TCAG AG AGATTGTTAGTGTTGA
                                |||| ||  ||||||||||||||||
                                GGTC TT TTTAATGATTATAACT
                                  G  C
GAM240  IL9      3'  TTAACATTGTATGTCTTTATTT 5172        GT_    TGT
             TGA                   TCAGGA   AGAT   TAGTGTTGA
                                ||||||   ||||  |||||||||
                                AGTTTT   TCTG   GTTACAATT
                                    ATT    TAT
GAM240  ISL1     5'  CAGCATTGGCAACCCC      9362     A  AGAT
                                GG GT    TGTTAGTGTTG
                                || ||    ||||||||||
                                CC CA    ACGGTTACGAC
                                 C  _____
GAM240  ITGA1    3'  TAACATAAGTCATTCCTGG    63536         A    GTTA
                                TCAGGAGT GATT    GTGTTG
                                |||||||| ||||    ||||||
                                GGTCCTTA CTGA    TACAAT
                                    _    A___
GAM240  ITGAV    3'  ACACTACAGTTTACTTTT     9397             T
                                AGGAGTAGATTGT AGTGT
                                |||||||||||| |||||
                                TTTTCATTTGACA TCACA
                                          _
GAM240  ITK      3'  CGACACTGGCTTCTACT      18679        TT
                                AGTAGA  GTTAGTGTTG
                                ||||||  ||||||||||
                                TCATCT  CGGTCACAGC
                                   T_
GAM240  ITSN2    3'  TTGATCATTTTATTCCTGA    38974           T  _
                                TCAGGAGTAGA TG TTAG
                                |||||||||| || ||||
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                                AGTCCTTATTT AC AGTT
                                      T  T
GAM240  JAK2    5'  CGGCGCTGACAGGCTG      17125     A
                                TAG TTGTTAGTGTTG
                                ||| ||||||||||||
                                GTC GACAGTCGCGGC
                                  G
GAM240  KAI1    3'  CTAGCGATCTCTCCTGG      9497         T
                                TCAGGAG AGATTGTTAG
                                ||||||| ||||||||||
                                GGTCCTC TCTAGCGATC
                                    _
GAM240  KAL1    3'  CAACACTATTGACTTTTGG    4012          AGATTGT
                                TCAGGAGT      TAGTGTTG
                                ||||||||      ||||||||
                                GGTTTTCA      ATCACAAC
                                     GTT_____
GAM240  KAL1    3'  TTAATACTGTTTTTTTTCTTGA 4018         T   TTGT
                                TCAGGAG AGA    TAGTGTTGA
                                ||||||| |||    |||||||||
                                AGTTCTT TTT    GTCATAATT
                                     T  TT__
GAM240  KCNJ16  3'  TCAACATTGATAATACAATGA  37855     GGA   GA
                                TCA   GTA  TTGTTAGTGTTGA
                                |||   |||  ||||||||||||
                                AGT   CAT  AATAGTTACAACT
                                  AA_  __
GAM240  KERA    5'  AACGGTGTATTCCTGG      22868         G
                                TCAGGAGTA ATTGTT
                                ||||||||| ||||||
                                GGTCCTTAT TGGCAA
                                     G
GAM240  KIF2    3'  TTACACAAATAGTGATTTACTT 15727          TG  ___   TGA
            TTGG                    AGGAGTAGAT  TTA   GTGT
                                ||||||||||  |||   ||||
                                TTTTCATTTA  GAT   CACA
                                      GT   AAA    TT
GAM240  KIF5C   3'  TAACACTAACAATTTA      15739
                                TAGATTGTTAGTGTTG
                                ||||||||||||||||
                                ATTTAACAATCACAAT

GAM240  KIF5C   3'  TGTTGATATGTTTGCTTCTGA  15744           _    GT
                                TCAGGAGTAGAT TGTTA  G
                                |||||||||||| |||||  |
                                AGTCTTCGTTTG ATAGT  T
                                       T    TG
GAM240  KLRD1   5'  CAACGCTGTTCTTTCTGA    23677       GT   TTGT
                                TCAGGA  AGA    TAGTGTTG
                                ||||||  |||    ||||||||
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                                AGTCTT  TCT    GTCGCAAC
                                   __   T___
GAM240   KLRD1    3'  TATTACTAATTGTCTACTTCTG 23682          T      TTGA
              G                    TCAGGAGTAGAT GTTAGTG
                                   |||||||||||| |||||||
                                   GGTCTTCATCTG TAATCAT
                                          T      TATT
GAM240   KLRD1    5'  CAACGCTGTTCTTTCTGA    9618       GT   TTGT
                                   TCAGGA  AGA    TAGTGTTG
                                   ||||||  |||    ||||||||
                                   AGTCTT  TCT    GTCGCAAC
                                      __   T___
GAM240   KLRD1    3'  TATTACTAATTGTCTACTTCTG 9623          T      TTGA
              G                    TCAGGAGTAGAT GTTAGTG
                                   |||||||||||| |||||||
                                   GGTCTTCATCTG TAATCAT
                                          T      TATT
GAM240   LAMC1    3'  TTGACGATATACTCCTGA    9681          G
                                   TCAGGAGTA ATTGTTAG
                                   |||||||||  ||||||||
                                   AGTCCTCAT TAGCAGTT
                                         A
GAM240   LIFR     3'  TCAGCACTGGGCATTCTTGG   9746        TAGAT   _
                                   TCAGGAG     TGTT AGTGTTGA
                                   |||||||     |||| ||||||||
                                   GGTTCTT     ACGG TCACGACT
                                      _____    G
GAM240   LMO7     3'  TTAATAAGGAAGTTTATTTTTG 18093          G  AG
              A                    TCAGGAGTAGATT TT  TGTTGA
                                   |||||||||||||  ||  ||||||
                                   AGTTTTTATTTGA AG  ATAATT
                                          _  GA
GAM240   LMO7     3'  TTAATAAGGAAGTTTATTTTTG 31769          G  AG
              A                    TCAGGAGTAGATT TT  TGTTGA
                                   |||||||||||||  ||  ||||||
                                   AGTTTTTATTTGA AG  ATAATT
                                          _  GA
GAM240   LOH11CR2A 3'  TCAATATTAAAATGACTATTTC 27542        ATTG_
              T                    AGGAGTAG     TTAGTGTTGA
                                   ||||||||     ||||||||||
                                   TCTTTATC     AATTATAACT
                                        AGTAA
GAM240   LZTR1    5'  TCGATGTGAAAGACTGCTCCTG 22244          A  GTTA TG
              G                    TCAGGAGTAG TT    G  TTGA
                                   ||||||||||  ||    |  ||||
                                   GGTCCTCGTC AG    T  AGCT
                                         _  AAAG GT
GAM240   LZTS1    3'  TTGACAGCTTCATTTTATTTTT 40701          T  TT  _   TG
              GA                     TCAGGAGTAGA TG  AG TGT  A
                                   ||||||||||  ||  ||  |||  |
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                                AGTTTTTATTT AC  TC ACA  T
                                      T  T_  G   GT
GAM240   MADH7    3'  TTGGCCATCTGCTCCTGG    19748          T
                                TCAGGAGTAGAT GTTAG
                                |||||||||||| |||||
                                GGTCCTCGTCTA CGGTT
                                      C
GAM240   MAPK10   5'  TTAATTCTGAGTTGCTCTTGG  57294         ATTG    T
                                TCAGGAGTAG    TTAG GTTGA
                                ||||||||||    |||| |||||
                                GGTTCTCGTT    AGTC TAATT
                                      G___    T
GAM240   MAPK9    3'  GGTAGTGCTGCTTCTGA     57412         _
                                TCAGGAGTAG ATTGTT
                                |||||||||| ||||||
                                AGTCTTCGTC TGATGG
                                      G
GAM240   MAPK9    3'  GGTAGTGCTGCTTCTGA     57417         _
                                TCAGGAGTAG ATTGTT
                                |||||||||| ||||||
                                AGTCTTCGTC TGATGG
                                      G
GAM240   MAPK9    3'  GGTAGTGCTGCTTCTGA     57422         _
                                TCAGGAGTAG ATTGTT
                                |||||||||| ||||||
                                AGTCTTCGTC TGATGG
                                      G
GAM240   MAPK9    3'  GGTAGTGCTGCTTCTGA     10852         _
                                TCAGGAGTAG ATTGTT
                                |||||||||| ||||||
                                AGTCTTCGTC TGATGG
                                      G
GAM240   MATN3    3'  TTAATGTTAGTGATCCACCTG  9941       AGTA   TG    TG
                                CAGG    GAT  TTAG  TTGA
                                ||||    |||  ||||  ||||
                                GTCC    CTA  GATT  AATT
                                  AC__   GT    GT
GAM240   MBL2     3'  TAAACATTCTATCTATTCCTGG 4117          TGTT     GA
                                TCAGGAGTAGAT    AGTGTT
                                ||||||||||||    ||||||
                                GGTCCTTATCTA    TTACAA
                                      TC__      ATA
GAM240   MEIS1    3'  ATATGTTGACTTTATTTCTGA  9993          TT    TG TGA
                                TCAGGAGTAGA  GTTAG  T
                                ||||||||||  |||||  |
                                AGTCTTTATTT  CAGTT  A
                                      __    GT TAA
GAM240   MEN1     5'  TATGGGCACATTTGCTTTTGG  93378          _  TA
                                TCAGGAGTAGAT TGT  GTG
                                |||||||||||| |||  |||
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                                GGTTTTCGTTTA ACG  TAT
                                      C   GG
GAM240  MET     3'  CGATATTCTTTGCTCTTG    71268         TTGTT
                                CAGGAGTAGA    AGTGTTG
                                ||||||||||    |||||||
                                GTTCTCGTTT    TTATAGC
                                      C____
GAM240  MGEA5   3'  ATCAGGATTTTTTAGCAAGTTT 24209       _   ____  G
            GCTTTTGG                GTAGATT GTTA    GT TTGA   T
                                ||||||| ||||   || ||||  |
                                CGTTTGA CGAT    TA GACT   A
                                    A   TTTT  G
GAM240  MGEA5   3'  TTAACACTAGTGGACAATTCT  24220      AGA TG
                                GGAGT   T  TTAGTGTTGA
                                |||||  |  ||||||||||
                                TCTTA   G  GATCACAATT
                                   ACA GT
GAM240  MGEA5   3'  TTGAAAAGTGCAGTTACTTCTG 24221        A     TAGTG TG
            G                    TCAGGAGT GATTGT    T  A
                                |||||||| ||||||    | |
                                GGTCTTCA TTGACG    A  T
                                     _     TGAAA GT
GAM240  MHC2TA  3'  TTAACACTAACGATTTGTTAAT 4198     GG
            GA                    TCA  AGTAGATTGTTAGTGTTGA
                                |||  ||||||||||||||||||
                                AGT  TTGTTTAGCAATCACAATT
                                  AA
GAM240  MJD     3'  TTGAAAGATGGTAATCTTTTCT 47684       T     TT GTG_ TG
            GA                    TCAGGAG AGATTG  A   T  A
                                ||||||| ||||||  |   | |
                                AGTCTTT TCTAAT  T   A  T
                                     _     GG AGAA GT
GAM240  MJD     3'  TTGAAAGATGGTAATCTTTTCT 17165       T     TT GTG_ TG
            GA                    TCAGGAG AGATTG  A   T  A
                                ||||||| ||||||  |   | |
                                AGTCTTT TCTAAT  T   A  T
                                     _     GG AGAA GT
GAM240  MORF    5'  TCAACATTGCCTGTTTGTCTGC 24682       TGT____
            TTTTGA                 GAGTAGAT      TAGTGTTGA
                                ||||||||      |||||||||
                                TTCGTCTG      GTTACAACT
                                     TTTGTCC
GAM240  MS4A4A  3'  TCGATACTGATAGACTTGTTGA 43785     _   AGA
                                TCAG GAGT   TTGTTAGTGTTGA
                                ||||  ||||  ||||||||||||
                                AGTT TTCA   GATAGTCATAGCT
                                  G   ___
GAM240  MSR1    3'  TCAATGTTAATGATATGTCTTG 56953      GTAG  TG   TG
            G                    TCAGGA   AT  TTAG  TTGA
                                ||||||   ||  ||||  ||||
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                                GGTTCT   TA  AATT  AACT
                                   GTA_  GT   GT
GAM240  MSR1    3'  TTAACACTAATAATAGTACT  56955     G_
                                AGTA  ATTGTTAGTGTTGA
                                ||||  ||||||||||||||
                                TCAT  TAATAATCACAATT
                                  GA
GAM240  MSR1    3'  TCAATGTTAATGATATGTCTTG 56961      GTAG  TG   TG
           G                     TCAGGA   AT  TTAG  TTGA
                                ||||||   ||  ||||  ||||
                                GGTTCT   TA  AATT  AACT
                                   GTA_  GT   GT
GAM240  MSR1    3'  TTAACACTAATAATAGTACT  56963     G_
                                AGTA  ATTGTTAGTGTTGA
                                ||||  ||||||||||||||
                                TCAT  TAATAATCACAATT
                                  GA
GAM240  MTMR2   3'  CAGTAACTGATTTACCTTGA  32382      A     _   G
                                TCAGG GTAGATT GTTA TG
                                ||||| ||||||| |||| ||
                                AGTTC CATTTAG CAAT AC
                                  _     T   G
GAM240  MTMR6   3'  TCAATGAGTTGCTGTTCCTGG  93552         ATTGTTAG
                                TCAGGAGTAG       TGTTGA
                                ||||||||||       ||||||
                                GGTCCTTGTC       GTAACT
                                     GTTGA___
GAM240  MYF5    3'  CAGTAATACTATTTCTGA    18790         AT    G
                                TCAGGAGTAG  TGTTA TG
                                ||||||||||  ||||| ||
                                AGTCTTTATC  ATAAT AC
                                     __     G
GAM240  NCF2    5'  TCAGCCTTCAGGCTGTTTTTGG 4737          A   TT  T
                                TCAGGAGTAG TTG  AG GTTGA
                                |||||||||| |||  || |||||
                                GGTTTTTGTC GAC  TC CGACT
                                     G   T_  _
GAM240  NCOA4   3'  TCAGTATTATTTCAAGACTATT 18371       A_   T__
           TTTGA                  GGAGTAG  TTG   TAGTGTTGA
                                |||||||  |||   |||||||||
                                TTTTATC  AAC   ATTATGACT
                                   AG   TTT
GAM240  NCOA6   5'  TTAGCACTACTGTTCATTTCTG 25982        AG  T  T
           A                     TCAGGAGT  AT GT AGTGTTGA
                                ||||||||  || || ||||||||
                                AGTCTTTA  TG CA TCACGATT
                                   CT  T  _
GAM240  NDRG3   5'  TCAGAGTTACTGATTTATTCTT 42494          GT   TG
           GA                     TCAGGAGTAGATT  TAG  TTGA
                                ||||||||||||  |||  ||||
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                                AGTTCTTATTTAG  ATT  GACT
                                      TC   GA
GAM240  NDRG3    5'  TCAGAGTTACTGATTTATTCTT 49305          GT   TG
             GA                  TCAGGAGTAGATT  TAG  TTGA
                                 ||||||||||||  |||  ||||
                                 AGTTCTTATTTAG  ATT  GACT
                                       TC   GA
GAM240  NEBL     3'  ATTATACCTTAGCGATTTGCTT 21119             T  TGA
             CTGA                  TCAGGAGTAGATTGTTAG GT
                                   |||||||||||||||||| ||
                                   AGTCTTCGTTTAGCGATT CA
                                         C  TATTAA
GAM240  NEBL     3'  TATACCTTAGCGATTTGCTTCT 21124             T  TGA
             GA                    TCAGGAGTAGATTGTTAG GT
                                   |||||||||||||||||| ||
                                   AGTCTTCGTTTAGCGATT CA
                                         C  TATT
GAM240  NEO1     3'  TTGACAGTGTGGGTCGTTCCTG 10207       GTA   GT  G   TG
             G                     TCAGGA   GATT  TA TGT  A
                                   ||||||   ||||  || |||  |
                                   GGTCCT   CTGG  GT ACA  T
                                      TG_   GT  G   GT
GAM240  NET1     3'  TCAGTGTTGACTATTCTGTGA  19616    _    GATT    TG
                                   TCA GGAGTA    GTTAG  TTGA
                                   ||| ||||||    |||||  ||||
                                   AGT TCTTAT    CAGTT  GACT
                                     G     _____     GT
GAM240  NGFR     3'  TTAGCATGTGTTTGGTTCTGG  10230       G    TGTTA
                                   TCAGGA TAGAT     GTGTTGA
                                   |||||| |||||     |||||||
                                   GGTCTT GTTTG     TACGATT
                                      G    TG___
GAM240  NOLA1    3'  TTAACCTGCATGATCTGTTTCT 52206          TG _  T
                                   AGGAGTAGAT  T TAG GTTGA
                                   ||||||||||  | ||| |||||
                                   TCTTTGTCTA  A GTC CAATT
                                         GT C  _
GAM240  NOLA1    3'  TTAACCTGCATGATCTGTTTCT 38608          TG _  T
                                   AGGAGTAGAT  T TAG GTTGA
                                   ||||||||||  | ||| |||||
                                   TCTTTGTCTA  A GTC CAATT
                                         GT C  _
GAM240  NOVA1    3'  TGATTTACTGTGCAATTTACTT 21411            _    TTGA
             TTGG                  CAGGAGTAGATTGT TAGTG
                                   |||||||||||||| |||||
                                   GTTTTCATTTAACG GTCAT
                                         T    TTAGTT
GAM240  NOVA1    3'  TGATTTACTGTGCAATTTACTT 10249            _    TTGA
             TTGG                  CAGGAGTAGATTGT TAGTG
                                   |||||||||||||| |||||
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                                GTTTTCATTTAACG GTCAT
                                      T    TTAGTT
GAM240  NPC2    3'  TCTACACCTGGAAATTTACTCT 21225          G   _  T
            TGA                   TCAGGAGTAGATT TTAG TGT GA
                                  |||||||||||| |||| ||| ||
                                  AGTTCTCATTTAA GGTC ACA CT
                                        A   C   T
GAM240  NPDC1   3'  TGATGCTGTGTGCTTTTGG   31174        G  TGTT    TG
                                  TCAGGAGTA AT    AGTGT  A
                                  ||||||||| ||    |||||  |
                                  GGTTTTCGT TG    TCGTA  T
                                       G _____    GT
GAM240  NPEPPS  3'  CAACACTGGCTTCTCCCGG   20873    A    TAGATT
                                  TC GGAG     GTTAGTGTTG
                                  || ||||     ||||||||||
                                  GG CCTC     CGGTCACAAC
                                   C   TT____
GAM240  NR1I2   3'  AATAATGTACTTTTGG     41824         G
                                  TCAGGAGTA ATTGTT
                                  |||||||| ||||||
                                  GGTTTTCAT TAATAA
                                       G
GAM240  NR1I2   3'  GGGGCCTGGGTTTGTTCCTGG  41829          GT   T   GA
                                  TCAGGAGTAGATT  TAG GTT
                                  ||||||||||||  ||| |||
                                  GGTCCTTGTTTGG  GTC CGG
                                         __  _  GGT
GAM240  NR1I2   5'  TTAGTGCTGGCAGCCCCCTGA  41832      A_  AGAT    TG
                                  TCAGG  GT   TGTTAG  TTGA
                                  |||||  ||   ||||||  ||||
                                  AGTCC  CG   ACGGTC  GATT
                                     CC _____     GT
GAM240  NR1I2   3'  AATAATGTACTTTTGG     13958         G
                                  TCAGGAGTA ATTGTT
                                  |||||||| ||||||
                                  GGTTTTCAT TAATAA
                                       G
GAM240  NR1I2   3'  GGGGCCTGGGTTTGTTCCTGG  13971          GT   T   GA
                                  TCAGGAGTAGATT  TAG GTT
                                  ||||||||||||  ||| |||
                                  GGTCCTTGTTTGG  GTC CGG
                                         __  _  GGT
GAM240  NR1I2   5'  TCAATATTTCACTTACTCT   13973       AT  TT
                                  GGAGTAG  TG  AGTGTTGA
                                  |||||||  ||  ||||||||
                                  TCTCATT  AC  TTATAACT
                                      C_  T_
GAM240  NRAP    3'  TCAACGTTGGCAGGCTCC    20510      AGA
                                  GGAGT   TTGTTAGTGTTGA
                                  |||||   ||||||||||||
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                              CCTCG   GACGGTTGCAACT
                                   ___
GAM240  NT5E    3'  TTGATATCCACAACTTATTTTT 10282         A   TA   TG
           GG                   TCAGGAGTAG TTGT  GTGT  A
                                |||||||||| ||||  ||||  |
                                GGTTTTTATT AACA  TATA  T
                                     C   CC   GT
GAM240  NUDT2   5'  CGGTGCGTTTGCTTCTGA    6744          TGTTA TG
                                TCAGGAGTAGAT    G  TTG
                                ||||||||||||    |  |||
                                AGTCTTCGTTTG    C  GGC
                                      _____ GT
GAM240  NXF5    3'  TCATGAATGATAAGCTGTTTCT 52511         A    GTGT
           GA                   TCAGGAGTAG TTGTTA   TGA
                                |||||||||| ||||||   |||
                                AGTCTTTGTC AATAGT   ACT
                                     G     AAGT
GAM240  NXF5    3'  TCATGAATGATAAGCTGTTTCT 52524         A    GTGT
           GA                   TCAGGAGTAG TTGTTA   TGA
                                |||||||||| ||||||   |||
                                AGTCTTTGTC AATAGT   ACT
                                     G     AAGT
GAM240  NXF5    3'  ACATTGACAGCTCTGA     52512     G   AGAT
                                TCAG AGT   TGTTAGTGT
                                |||| |||   |||||||||
                                AGTC TCG   ACAGTTACA
                                  _  ____
GAM240  NXF5    3'  TCATGAATGATAAGCTGTTTCT 52516         A    GTGT
           GA                   TCAGGAGTAG TTGTTA   TGA
                                |||||||||| ||||||   |||
                                AGTCTTTGTC AATAGT   ACT
                                     G     AAGT
GAM240  NXF5    3'  TCATGAATGATAAGCTGTTTCT 52520         A    GTGT
           GA                   TCAGGAGTAG TTGTTA   TGA
                                |||||||||| ||||||   |||
                                AGTCTTTGTC AATAGT   ACT
                                     G     AAGT
GAM240  OPHN1   3'  TAGTGGCCATCATTTCTGG   10360        A  T   G
                                TCAGGAGT GAT GTTA TG
                                |||||||| ||| |||| ||
                                GGTCTTTA CTA CGGT AT
                                   _  C   G
GAM240  OPRM1   3'  TTAGGCTTTCAGTGGTTTGTTC 6203          TG ___  GTTGA
           CTGG                  AGGAGTAGAT  TT  AGT
                                 ||||||||||  ||  |||
                                 TCCTTGTTTG  GA  TCG
                                      GT  CTT  GATT
GAM240  ORC5L   3'  TAACACTGAAATTGCCTGA   10366      AGTAGATTG
                                TCAGG       TTAGTGTTG
                                |||||       |||||||||
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                                AGTCC       AGTCACAAT
                                  GTTAA____
GAM240  P2RY1    3'  TGATATTAGTAATTTCTCT   10379     T         TG
                                GGAG AGATTGTTAGTGT  A
                                |||| ||||||||||||  |
                                TCTC TTTAATGATTATA  T
                                  _          GT
GAM240  PACE     3'  TAGATGCTGATGATTTGTTTTT 10398         TG      GA
              G                  CAGGAGTAGAT  TTAGTGTT
                                ||||||||||  ||||||||
                                GTTTTTGTTTA  AGTCGTAG
                                      GT       ATT
GAM240  PAFAH1B1 3'  GAGAACTAATGGCTATTTTTGA 4728          A TG    GTTGA
                                TCAGGAGTAG T  TTAGT
                                |||||||||| |  |||||
                                AGTTTTTATC G  AATCA
                                      _ GT    AGAGT
GAM240  PAWR     3'  TCAATGCTAGCACAATATTCCT 10432       GAT
                                AGGAGTA   TGTTAGTGTTGA
                                |||||||   ||||||||||||
                                TCCTTAT   ACGATCGTAACT
                                    AAC
GAM240  PCDH12   5'  TGAACTCAGGCAGTTTACCTCT 33424     GA        AGT   GA
              GA                  TCAG  GTAGATTGTT   GTT
                                ||||  ||||||||||   |||
                                AGTC  CATTTGACGG   CAA
                                  TC        ACT   GTT
GAM240  PCDHA9   3'  TAGCATTAGCAGCACCT    25767     A  AGAT
                                AGG GT    TGTTAGTGTTG
                                ||| ||    ||||||||||
                                TCC CG    ACGATTACGAT
                                 A _____
GAM240  PCDHAC1  3'  AAGGGACTTATAGTTTATTTTT 49038            T   G  GA
              GA                  TCAGGAGTAGATTGT AGT TT
                                |||||||||||||| ||| ||
                                AGTTTTTATTTGATA TCA GG
                                        T   G  AAC
GAM240  PCDHB15  3'  TTAATAGTATTCATTCCTGA   38429       AG__
                                TCAGGAGT    ATTGTTAG
                                ||||||||    ||||||||
                                AGTCCTTA    TGATAATT
                                    CTTA
GAM240  PCTK3    3'  TCAACACTGGGCTGATCCTGA  72967      G   ATTGT
                                TCAGGA TAG     TAGTGTTGA
                                ||||||  |||    |||||||||
                                AGTCCT GTC     GTCACAACT
                                  A   GG___
GAM240  PIAS3    3'  AGGACACTGGGGTCTGTTTCTG 20340          G       GA
              G                   TCAGGAGTAGATT TTAGTGTT
                                ||||||||||||| ||||||||
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                                GGTCTTTGTCTGG GGTCACAG
                                      _       GAA
GAM240  PIGK     3'  TTAATATTTTACTGCTGG    66703      G     T
                                TCAG AGTAGA TGTTAG
                                |||| |||||| ||||||
                                GGTC TCATTT ATAATT
                                  G     T
GAM240  PIK3R3   3'  CAGTAATGTGTCTGCTCCT   61055          _    G
                                AGGAGTAGAT TGTTA TG
                                |||||||||| ||||| ||
                                TCCTCGTCTG GTAAT AC
                                      T    G
GAM240  PITPNB   3'  TAACTATTTATTTCTGG     24781           T
                                TCAGGAGTAGAT GTTA
                                |||||||||||| ||||
                                GGTCTTTATTTA CAAT
                                       T
GAM240  PLGL     3'  TCGATGTTCAACTATTTTTGG  10638          A   TT  TG
                                TCAGGAGTAG TTG  AG  TTGA
                                |||||||||| |||  ||  ||||
                                GGTTTTTATC AAC  TT  AGCT
                                      _  __ GT
GAM240  PLS1     3'  TTAGCATTAGTCCATTTCTG   10663        A   TGT
                                CAGGAGT GAT   TAGTGTTGA
                                ||||||| |||   |||||||||
                                GTCTTTA CTG   ATTACGATT
                                    C  ___
GAM240  PNN      3'  TTGGCATTTTCTTCCTGA    71115        T   T
                                TCAGGAG AGA TGTTAG
                                ||||||| ||| ||||||
                                AGTCCTT TTT ACGGTT
                                    C   T
GAM240  PPIL1    3'  AACAGTGCTGTTTCTGA     32140          _
                                TCAGGAGTAG ATTGTT
                                |||||||||| ||||||
                                AGTCTTTGTC TGACAA
                                       G
GAM240  PPP2R5C  3'  TTAGTGCTTTGTCTATTCTT  10762          TGTT  TG
                                AGGAGTAGAT    AG  TTGA
                                ||||||||||    ||  ||||
                                TTCTTATCTG    TC  GATT
                                      TT__  GT
GAM240  PRDM2    3'  TCAACTTCAAAAGTAATCTACC 31851    GA       TTAGT___
            TCTGA                   G  GTAGATTG       GTTGA
                                |  ||||||||       |||||
                                C  CATCTAAT       CAACT
                                 TC       GAAAACTT
GAM240  PRKCM    3'  TTAGCACTGTTGATGTATCTGA 10816      GA   G   GT
                                TCAG  GTA ATT  TAGTGTTGA
                                ||||  ||| |||  |||||||||
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                                AGTC  TAT TAG  GTCACGATT
                                  __  G   TT
GAM240  PRKWNK3  3'  ACAGTCTACTTTGTGA     61548    _
                                TCA GGAGTAGATTGT
                                ||| ||||||||||||
                                AGT TTTCATCTGACA
                                  G
GAM240  PRNP     3'  TGGCACTGATGGGCACTGG   4338     GA  AGA TG     TG
                                TCAG  GT   T  TTAGTGT  A
                                ||||  ||   |  |||||||  |
                                GGTC  CG   G  AGTCACG  T
                                  A_  ___ GT     GT
GAM240  PRPS2    3'  AGCAGTGTATTTCTGG     10901        G
                                TCAGGAGTA ATTGTT
                                ||||||||| ||||||
                                GGTCTTTAT TGACGA
                                     G
GAM240  PTBP1    3'  GCCAGTCTGTACCTGG     11007     AG     TTAGT
                                TCAGG  TAGATTG    GT
                                |||||  |||||||    ||
                                GGTCC  GTCTGAC    CG
                                  AT     _____
GAM240  PTBP1    3'  GCCAGTCTGTACCTGG     49252     AG     TTAGT
                                TCAGG  TAGATTG    GT
                                |||||  |||||||    ||
                                GGTCC  GTCTGAC    CG
                                  AT     _____
GAM240  PTGER2   3'  TTAATACTCTTATTATCCTATT 6310       AT  TT___
           TCTGG                  GGAGTAG  TG    AGTGTTGA
                                |||||||  ||    ||||||||
                                CTTTATC  AT    TCATAATT
                                    CT  TATTC
GAM240  PTPN22   3'  GCAATACAAACTGCTCTTGA  31995        A   TAG
                                TCAGGAGTAG TTGT   TGT
                                |||||||||| ||||   |||
                                AGTTCTCGTC AACA   ACG
                                     A   TA_
GAM240  PTPRC    3'  TTAACACTGAAATTATTTTT   55169       ATTG
                                AGGAGTAG   TTAGTGTTGA
                                ||||||||   ||||||||||
                                TTTTTATT   AGTCACAATT
                                    AA__
GAM240  RAB18    3'  TGATACAAAGTCTGCTTTTG  41168         GTTA   TG
                                CAGGAGTAGATT   GTGT  A
                                ||||||||||||   ||||  |
                                GTTTTCGTCTGA   CATA  T
                                      AA__   GT
GAM240  RAB1A    3'  TCAATACTGACTTTTTTTTT  70234    T   TT
                                GAG AGA  GTTAGTGTTGA
                                ||| |||  ||||||||||
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                                TTT TTT  CAGTCATAACT
                                  T  TT
GAM240  RAD23B   3'  GCATGTTTGCTTTTGA     11215          _
                                TCAGGAGTAGAT TGT
                                |||||||||||| |||
                                AGTTTTCGTTTG ACG
                                      T
GAM240  RAD52    3'  CATTGCAATTTATTCTTG    11240           T
                                CAGGAGTAGATTGT AGTG
                                |||||||||||||| ||||
                                GTTCTTATTTAACG TTAC
                                        _
GAM240  RANBP2L1 3'  ACTGAAATTTGCTGCTGA    17312     G      G
                                TCAG AGTAGATT TTAGT
                                |||| |||||||| |||||
                                AGTC TCGTTTAA AGTCA
                                  G      _
GAM240  RBBP2    3'  TTAGTGCTGGCTTCCTCTTT   17325     TA  TT    TG
                                GGAG  GA  GTTAG  TTGA
                                ||||  ||  |||||  ||||
                                TTTC  CT  CGGTC  GATT
                                  TC  T_    GT
GAM240  RBL1     3'  GAGGATAAATAATCTGCTTTTG 11261            A  G  GA
          A                      TCAGGAGTAGATTGTT GT TT
                                 |||||||||||||||| || ||
                                 AGTTTTCGTCTAATAA TA GA
                                       A  G  GT
GAM240  RDX      3'  TTAACACTAATTATCACGTCTG 11280     GA  A   T
          A                      TCAG  GT GAT GTTAGTGTTGA
                                 ||||  || ||| ||||||||||
                                 AGTC  CA CTA TAATCACAATT
                                   TG  _   T
GAM240  RET      3'  TAACCTAATTGTCTATTCCTGA 40599          T    T
                                 TCAGGAGTAGAT GTTAG GTTG
                                 |||||||||||| ||||| ||||
                                 AGTCCTTATCTG TAATC CAAT
                                       T    _
GAM240  RET      3'  TTAACTTCCAAGGTGGTTTTAC 40601      _______  TT  GTTGA
          TTCTGA                    GTAGA     TTG  AGT
                                 |||||     |||  |||
                                 CATTT     AAC  TCA
                                    TGGTGG   CT   ATT   A
GAM240  RET      3'  TAACCTAATTGTCTATTCCTGA 40171          T    T
                                 TCAGGAGTAGAT GTTAG GTTG
                                 |||||||||||| ||||| ||||
                                 AGTCCTTATCTG TAATC CAAT
                                       T    _
GAM240  RET      3'  TAACCTAATTGTCTATTCCTGA 40183          T    T
                                 TCAGGAGTAGAT GTTAG GTTG
                                 |||||||||||| ||||| ||||
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                                AGTCCTTATCTG TAATC CAAT
                                      T    _
GAM240  RET     3'  TTAACTTCCAAGGTGGTTTTAC 40187      _______  TT  GTTGA
            TTCTGA                 GTAGA     TTG  AGT
                                |||||     |||  |||
                                CATTT     AAC  TCA
                                   TGGTGG   CT   ATT   A
GAM240  RET     3'  TAACCTAATTGTCTATTCCTGA 4374           T    T
                                TCAGGAGTAGAT GTTAG GTTG
                                |||||||||||| ||||| ||||
                                AGTCCTTATCTG TAATC CAAT
                                      T    _
GAM240  RPS3A   3'  TGATGGTTTGCTTCTGA     6404           TG
                                TCAGGAGTAGAT  TTA
                                ||||||||||||  |||
                                AGTCTTCGTTTG  AGT
                                      GT
GAM240  S100A4  5'  TCAGCGCTTCTTCTTTCTTGG  11424       T   TTGTT
                                TCAGGAG AGA    AGTGTTGA
                                |||||||| |||    ||||||||
                                GGTTCTT TCT    TCGCGACT
                                    _  TCT__
GAM240  S100B   3'  TCAGCGCTGGCAGCGTCCTGG  20779       _ AGAT
                                TCAGGA GT    TGTTAGTGTTGA
                                |||||| ||    ||||||||||||
                                GGTCCT CG    ACGGTCGCGACT
                                   G  _____
GAM240  SALL1   3'  TCAATGTTAATAAGTTTCTG   11434      GTAGA      TG
                                CAGGA    TTGTTAG  TTGA
                                |||||    |||||||  ||||
                                GTCTT    AATAATT  AACT
                                   TG___      GT
GAM240  SDHC    3'  GTTCTTGGAGCAGCTGCTTTTG 69385          A    AGTGTTGA
            A                    TCAGGAGTAG TTGTT
                                ||||||||||  |||||
                                AGTTTTCGTC GACGA
                                      _    GGTTCTTGA
GAM240  SERPINE1  3'  TTAGTGTTAATGACTCTTTCTG 5197        T  A TG    TG
            A                    TCAGGAG AG T  TTAG  TTGA
                                |||||||  ||  |  ||||  ||||
                                AGTCTTT TC A  AATT  GATT
                                    C  _ GT    GT
GAM240  SFRP1   3'  TCAGAGCTCCAGTTTGCATTTG 11573      A       TT   G
            G                    TCAGG GTAGATTG  AGT TTGA
                                |||||  ||||||||  |||  ||||
                                GGTTT CGTTTGAC  TCG GACT
                                   A       C_   A
GAM240  SLA     3'  CATGTATTTATTCCTGA     22170           TGTTA
                                TCAGGAGTAGAT    GTG
                                ||||||||||||    |||
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                                AGTCCTTATTTA    TAC
                                      TG___
GAM240  SLC1A1   3'  TCAGTATTGACGACCTACATCT 14794     GA   A
            GA                  TCAG  GTAG TTGTTAGTGTTGA
                                |||||  |||| ||||||||||||
                                AGTC  CATC AGCAGTTATGACT
                                  TA   C
GAM240  SLC25A13 3'  TCAACACTAACATGATTT    26504     AGAT
                                GAGT   TGTTAGTGTTGA
                                ||||   ||||||||||||
                                TTTA   ACAATCACAACT
                                  GT__
GAM240  SMARCD1  3'  ACACTGGACAACCTTGG     11808      A  AGAT   _
                                TCAGG GT   TGTT AGTGT
                                ||||| ||   |||| |||||
                                GGTTC CA   ACAG TCACA
                                  _ ____   G
GAM240  SMARCD1  3'  ACACTGGACAACCTTGG     57426      A  AGAT   _
                                TCAGG GT   TGTT AGTGT
                                ||||| ||   |||| |||||
                                GGTTC CA   ACAG TCACA
                                  _ ____   G
GAM240  SMG1     3'  TCGATGCTGTTAACAACTTCTG 30655        AGA   T
            A                   TCAGGAGT   TTG TAGTGTTGA
                                ||||||||   ||| |||||||||
                                AGTCTTCA   AAT GTCGTAGCT
                                     AC_   T
GAM240  SMT3H1   3'  CTAGTATTTGCTTCTGA     59958          TGT
                                TCAGGAGTAGAT   TAG
                                ||||||||||||   |||
                                AGTCTTCGTTTA   ATC
                                      TG_
GAM240  SNX6     3'  TAGTGACAGTTATTCCTGA    41160        A      G
                                TCAGGAGT GATTGTTA TG
                                |||||||| |||||||| ||
                                AGTCCTTA TTGACAGT AT
                                   _       G
GAM240  SON      3'  TCAGCTGAACTCTATTCCTGG  54204         TT   AGT
                                TCAGGAGTAGA  GTT   GTTGA
                                ||||||||||  |||   |||||
                                GGTCCTTATCT  CAA   CGACT
                                     __  GT_
GAM240  SORCS3   3'  TTAAAATGACAATCTGTTTTT  30376           GTG
                                AGGAGTAGATTGTTA   TTGA
                                ||||||||||||||   ||||
                                TTTTTGTCTAACAGT   AATT
                                      AA_
GAM240  SPOCK    3'  TCAATATTTTTTTTCTCTCTTG 62821       T   TTGTT
            A                   TCAGGAG AGA    AGTGTTGA
                                |||||||  |||    ||||||||
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                                AGTTCTC TCT    TTATAACT
                                    _  TTTTT
GAM240  SPRR2C   5' AGCACCGATCTGCTTCGGA  21506   A       TTA
                                TC GGAGTAGATTG  GTGTT
                                || ||||||||||  |||||
                                AG CTTCGTCTAGC  CACGA
                                 G        ___
GAM240  SSPN     3' TGGCAACCAATCTATGTTTGA 17447     A     TTAG  TG
                                TCAGG GTAGATTG   TGT A
                                ||||| ||||||||   ||| |
                                AGTTT TATCTAAC   ACG T
                                   G      CA__  GT
GAM240  ST7      3' CAATATATTTTATTCCTGG   25543         TTGTTA
                                TCAGGAGTAGA    GTGTTG
                                ||||||||||     ||||||
                                GGTCCTTATTT    TATAAC
                                       TA____
GAM240  SURF4    3' TCGATGGCTCAGTCTGCTCTGG 52546   A       TT  _
           A                     TC GGAGTAGATTG  AGT GTTGA
                                 || ||||||||||  ||| |||||
                                 AG TCTCGTCTGAC  TCG TAGCT
                                  G         __  G
GAM240  SYBL1    3' CAACACTAATGCCTCTT     18893      TAGAT
                                AGGAG    TGTTAGTGTTG
                                |||||    ||||||||||
                                TTCTC    GTAATCACAAC
                                   C____
GAM240  SYNGR1   3' CAGCCAGGTCGGCTCCTGG   16311       A   GTTAGT
                                TCAGGAGT GATT    GTTG
                                |||||||| ||||    ||||
                                GGTCCTCG CTGG    CGAC
                                     G   AC____
GAM240  TAF7     3' TCAGCATTAGAAAATTCTTGG  18912       AGATTG
                                TCAGGAGT    TTAGTGTTGA
                                ||||||||    ||||||||||
                                GGTTCTTA    GATTACGACT
                                     AAA___
GAM240  TAL1     3' TCAGTGGACAGTCTGCTCTAGA 12114   A         AGTG
                                TC GGAGTAGATTGTT   TTGA
                                || ||||||||||||   ||||
                                AG TCTCGTCTGACAG   GACT
                                 A          GT__
GAM240  TAL1     5' TTGGACTAAATAGCTATTCCTG 12116        ATTG   GTTGA
           A                     TCAGGAGTAG   TTAGT
                                 ||||||||||   |||||
                                 AGTCCTTATC   AATCA
                                       GATA   GGTT
GAM240  TCEA1    3' TTGATATTAATTAAACTCTTGG 80443       AGATT      TG
                                TCAGGAGT    GTTAGTGT A
                                ||||||||    |||||||| |
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                                GGTTCTCA    TAATTATA  T
                                    AAT__      GT
GAM240  TCF3    3'  TGATGTTGGGGGTTCTCTTGG  70736       TA   G   TG TG
                                TCAGGAG  GATT TTAG  T  A
                                |||||||  |||| ||||  |  |
                                GGTTCTC  TTGG GGTT  A  T
                                   __   G   GT GT
GAM240  TEC     3'  AAACCGGGTAATCTACTTCT   12213           AGT   GA
                                AGGAGTAGATTGTT   GTT
                                ||||||||||||||   |||
                                TCTTCATCTAATGG   CAA
                                      GC_   AT
GAM240  TEM6    3'  CGGTACTGACAAGCTGTTTTTG 42742         A       TT A
            A                    TCAGGAGTAG TTGTTAGTG  G
                                |||||||||| |||||||||  |
                                AGTTTTTGTC AACAGTCAT  C
                                      G       GG C
GAM240  TFDP2   3'  TTGACGATCGTGTTTCTGA   20809       TA_
                                TCAGGAG   GATTGTTAG
                                |||||||   |||||||||
                                AGTCTTT   CTAGCAGTT
                                    GTG
GAM240  TFF3    3'  TCAATACTTGTACTATTCCTGG 63568         ATTGTT
                                TCAGGAGTAG     AGTGTTGA
                                ||||||||||     ||||||||
                                GGTCCTTATC     TCATAACT
                                      ATGT__
GAM240  TIAL1   3'  TAGCACAGATTTGCTTT     12287         GTTA
                                GGAGTAGATT    GTGTTG
                                ||||||||||    ||||||
                                TTTCGTTTAG    CACGAT
                                      A___
GAM240  TIAL1   3'  TAGCACAGATTTGCTTT     42260         GTTA
                                GGAGTAGATT    GTGTTG
                                ||||||||||    ||||||
                                TTTCGTTTAG    CACGAT
                                      A___
GAM240  TLR1    3'  TTGATATTGCTGCTTTTGG    12315         AT_
                                TCAGGAGTAG   TGTTAG
                                ||||||||||   ||||||
                                GGTTTTCGTC   ATAGTT
                                      GTT
GAM240  TLR6    3'  AACAGTCTCTTTTGA       20269        T
                                TCAGGAG AGATTGTT
                                ||||||| ||||||||
                                AGTTTTC TCTGACAA
                                      _
GAM240  TMEM2   3'  TTGCACAAAGGAAGTCTGTTCT 25429           GTTA__    TGA
            TGG                   CAGGAGTAGATT     GTGT
                                ||||||||||||     ||||
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                                GTTCTTGTCTGA     CACG
                                      AGGAAA    TT
GAM240  TMOD2    3'  TTAGCACTACTTATTTATCTTG 27255       G    TGT
              G                  TCAGGA TAGAT   TAGTGTTGA
                                 |||||| |||||   |||||||||
                                 GGTTCT ATTTA   ATCACGATT
                                    _    TTC
GAM240  TNFRSF17  5'  TCAACATTCTAGCTGCTCTTG  6819         ATTGTT
                                 CAGGAGTAG     AGTGTTGA
                                 |||||||||     ||||||||
                                 GTTCTCGTC     TTACAACT
                                       GATC__
GAM240  TNFSF15   5'  TCGATCACTTTAGTCTATTTTG 17598      G       TT   _
              A                  TCAG AGTAGATTG  AGTG TTGA
                                 |||| |||||||||  |||| ||||
                                 AGTT TTATCTGAT  TCAC AGCT
                                   _       T_   T
GAM240  TNR      3'  CGCTGGCTAACATCTGCTCTTG 12353          T     GTTGA
              G                  TCAGGAGTAGAT GTTAGT
                                 |||||||||||| ||||||
                                 GGTTCTCGTCTA CAATCG
                                       _     GTCGCC
GAM240  TOB1     3'  TTGGCACTAATAAGTGGGTTTA 19237     GAGTAGA__       TG
              TTGG                  CAG       TTGTTAGTGT  A
                                 |||       ||||||||||  |
                                 GTT       AATAATCACG  T
                                   ATTTGGGTG        GT
GAM240  TOP3B    5'  TCAGCATTGGTAATAGTGCT   14130     G_   TT
                                 AGTA  ATTG  AGTGTTGA
                                 ||||  ||||  ||||||||
                                 TCGT  TAAT  TTACGACT
                                   GA   GG
GAM240  TPST1    3'  GGCAGTCTCCTTTTGA      13179       T
                                 TCAGGAG AGATTGTT
                                 ||||||| ||||||||
                                 AGTTTTC TCTGACGG
                                     C
GAM240  TRA1     3'  TTAACTGACTATTCTTGA    12382         ATT
                                 TCAGGAGTAG   GTTAG
                                 |||||||||   |||||
                                 AGTTCTTATC   CAATT
                                       AGT
GAM240  TRAM     3'  TCAGCATTAGAGATTTTTCTGT 26658       TTG____
              TCTTGA                 GAGTAGA      TTAGTGTTGA
                                 |||||||      ||||||||||
                                 CTTGTCT      GATTACGACT
                                     TTTTAGA
GAM240  TRHDE    3'  TTGGCACTGACAACTGTGTTCT 25391      __  A       TG
                                 GGAG  TAG TTGTTAGTGT  A
                                 ||||  ||| ||||||||||  |
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                                TCTT  GTC AACAGTCACG  T
                                  GT  _       GT
GAM240  TRIM14   3'  AATAGTTCATTCCTGG     52634        AG
                                TCAGGAGT  ATTGTT
                                ||||||||  ||||||
                                GGTCCTTA  TGATAA
                                    CT
GAM240  TRO      3'  TGGTGCTAAAATGTGTTCCT   32388       G   G    TG TG
                                AGGAGTA ATT TTAG  T  A
                                ||||||| ||| ||||  |  |
                                TCCTTGT TAA AATC  G  T
                                    G   _   GT GT
GAM240  TRPS1    5'  TTGATATTAATAGTGTTGGTGT 26085     G__  _        TG
           CTTGA                 GGA   TAG ATTGTTAGTGT  A
                                |||   ||| ||||||||||  |
                                TCT   GTT TGATAATTATA  T
                                  GTG   G        GT
GAM240  TTK      3'  TGACATCATTTTACTCTTGG   67492         T  TTA    TG
                                TCAGGAGTAGA TG   GTGT  A
                                ||||||||||| ||   ||||  |
                                GGTTCTCATTT AC   TACA  T
                                      T ___   GT
GAM240  UBE2E3   3'  ACCCAGATCTATTTCTGA    20992          GTTA
                                TCAGGAGTAGATT   GT
                                ||||||||||||   ||
                                AGTCTTTATCTAG   CA
                                     ACC_
GAM240  UBE3A    3'  TTAATGATTTGCTTTTGA    4870          TG
                                TCAGGAGTAGAT  TTAG
                                ||||||||||||  ||||
                                AGTTTTCGTTTA  AATT
                                     GT
GAM240  UBE3A    3'  TTAATGATTTGCTTTTGA    55582          TG
                                TCAGGAGTAGAT  TTAG
                                ||||||||||||  ||||
                                AGTTTTCGTTTA  AATT
                                     GT
GAM240  UBE3A    3'  TTAATGATTTGCTTTTGA    55595          TG
                                TCAGGAGTAGAT  TTAG
                                ||||||||||||  ||||
                                AGTTTTCGTTTA  AATT
                                     GT
GAM240  UBL3     5'  TCAAAATCGTGGTTTATTTCTG 23034          TG TAGTG
                                CAGGAGTAGAT  T    TTGA
                                ||||||||||| |    ||||
                                GTCTTTATTTG  G    AACT
                                     GT CTAA_
GAM240  UCP2     3'  TCAGTGCTGGTGGAGTTGACAT 12532      A  AGA__ TG   TG
           TTGA                  CAGG GT    T  TTAG  TTGA
                                |||| ||    |  ||||  ||||
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                                GTTT CA    G  GGTC  GACT
                                  A  GTTGA GT    GT
GAM240  UGT1A1   3'  TCAGTGTTAAATTCATTTTATT 4876         T ___   TG
          CTT                   AGGAGTAGA TG   TTAG  TTGA
                                |||||||||  ||   ||||  ||||
                                TTCTTATTT AC   AATT  GACT
                                    T  TTA    GT
GAM240  UGT1A4   3'  TCAGTGTTAAATTCATTTTATT 23061        T ___   TG
          CTT                   AGGAGTAGA TG   TTAG  TTGA
                                |||||||||  ||   ||||  ||||
                                TTCTTATTT AC   AATT  GACT
                                    T  TTA    GT
GAM240  UGT1A9   3'  TCAGTGTTAAATTCATTTTATT 40712        T ___   TG
          CTT                   AGGAGTAGA TG   TTAG  TTGA
                                |||||||||  ||   ||||  ||||
                                TTCTTATTT AC   AATT  GACT
                                    T  TTA    GT
GAM240  USP14    3'  TTAATACTGTACAATTTCTGA  17663        AGAT  _
                                TCAGGAGT    TGT TAGTGTTGA
                                ||||||||    ||| |||||||||
                                AGTCTTTA    ACA GTCATAATT
                                    ____  T
GAM240  VNN1     3'  AACATTGGTCTTTCTTGG    16238        T    TGT
                                TCAGGAG AGAT   TAGTGTT
                                |||||||  ||||   |||||||
                                GGTTCTT TCTG   GTTACAA
                                   _   ___
GAM240  WASF3    3'  TTAGTGCAGTTTGGGTTTACTC 21829          GTTA__ TG
          TT                    AGGAGTAGATT     G  TTGA
                                ||||||||||     |  ||||
                                TTCTCATTTGG     C  GATT
                                     GTTTGA GT
GAM240  WBSCR1   3'  AGTGCTTCTCTTCTGA     42224        T  TTGTT  TG
                                TCAGGAG AGA    AG  TT
                                |||||||  |||    ||  ||
                                AGTCTTC TCT    TC  GA
                                   _  _____  GT
GAM240  WBSCR1   3'  AGTGCTTCTCTTCTGA     49256        T  TTGTT  TG
                                TCAGGAG AGA    AG  TT
                                |||||||  |||    ||  ||
                                AGTCTTC TCT    TC  GA
                                   _  _____  GT
GAM240  WDR4     3'  TGGCGGTCTGTTTCTG     53358
                                CAGGAGTAGATTGTTA
                                ||||||||||||||||
                                GTCTTTGTCTGGCGGT

GAM240  WNT7A    3'  TTAACAATTTATTCTGA     16121      G
                                TCAG AGTAGATTGTTAG
                                ||||  ||||||||||||
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                                AGTC TTATTTAACAATT
                                   _
GAM240  XPR1     3'  TCAGTGTTAACAATTTA     16430          TG
                                TAGATTGTTAG  TTGA
                                ||||||||||  ||||
                                ATTTAACAATT  GACT
                                      GT
GAM240  ZIC3     3'  TTAACACTTGTCCTGTTTCTTG 12732        TAGATTGTT
           A                     TCAGGAG       AGTGTTGA
                                |||||||       ||||||||
                                AGTTCTT       TCACAATT
                                    TGTCCTGT_
GAM240  ZNF144   5'  TATGTTATAATTTACCCTGG   23081      A       TA_
                                TCAGG GTAGATTGT   GTG
                                ||||| |||||||||   |||
                                GGTCC CATTTAATA   TAT
                                  _       TTG
GAM240  ZNF144   3'  TTACAAATGCAGTTTATCCCTG 23083      AG      TAG   TGA
           G                     TCAGG  TAGATTGT   TGT
                                |||||  ||||||||   |||
                                GGTCC  ATTTGACG   ACA
                                   CT       TAA   TT
GAM240  ZNF184   3'  GATCGGGGATCTAGTATGCTCC 92041      _____    G  AGTGTTGA
           TGG                    GGAGT    AGATT TT
                                |||||    ||||| ||
                                CCTCG    TCTAG GG
                                   TATGA    G  CT   AGT
GAM240  ZNF192   3'  CAGCCCAGCTGCTCTTGA    20854         A   TTAGT
                                TCAGGAGTAG TTG    GTTG
                                |||||||||| |||    ||||
                                AGTTCTCGTC GAC    CGAC
                                      _  C_____
GAM240  ZNF20    3'  TTAGCGAGCCTGTTCTTGA   63403         A_
                                TCAGGAGTAG  TTGTTAG
                                |||||||||  |||||||
                                AGTTCTTGTC  AGCGATT
                                      CG
GAM240  ZNF216   3'  ACTGGCAGTCTACTTCT    20015
                                AGGAGTAGATTGTTAGT
                                |||||||||||||||||
                                TCTTCATCTGACGGTCA

GAM240  ZNF26    3'  TTAACACTGAATAGTATTTCT  72985        GATTG
                                AGGAGTA    TTAGTGTTGA
                                |||||||    ||||||||||
                                TCTTTAT    AGTCACAATT
                                    GATA_
GAM240  ZNF264   3'  CATCTGATAATTTATCCTGG   12747       G        _
                                TCAGGA TAGATTGTTAG TG
                                ||||||||||||||||| ||
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                                GGTCCT ATTTAATAGTC AC
                                   _         T
GAM240  ZNF264   3' CTGGTGGTTTGTCTTGA     12755       G    TG
                                TCAGGA TAGAT  TTAG
                                |||||| |||||  ||||
                                AGTTCT GTTTG  GGTC
                                   _    GT
GAM240  ZNFN2A1  3' TCAAGCCCACCATCTGCTTCTG 60741           T  TA  G
           A                     TCAGGAGTAGAT GT  GT TTGA
                                ||||||||||| ||  || ||||
                                AGTCTTCGTCTA CA  CG AACT
                                      C  CC  _
GAM240  ZNFN2A1  3' TGGCGGTCATTCCTGG      60743         A
                                TCAGGAGT GATTGTTA
                                |||||||| ||||||||
                                GGTCCTTA CTGGCGGT

                                   _
GAM240  ABLIM    3' TGGCGCTGATGTAGCTCATGG  9779      G    AGAT       TG
                                TCA GAGT    TGTTAGTGT  A
                                ||| ||||    |||||||||  |
                                GGT CTCG    GTAGTCGCG  T
                                  A    AT__       GT
GAM240  ABLIM    3' TGGCGCTGATGTAGCTCATGG  22041     G    AGAT       TG
                                TCA GAGT    TGTTAGTGT  A
                                ||| ||||    |||||||||  |
                                GGT CTCG    GTAGTCGCG  T
                                  A    AT__       GT
GAM240  acmsd    5' CAGATGCAAGTAGTTTGCTTTG 56354    AG          A     GA
           GA                     TC  GAGTAGATTGTT GTGTT
                                ||  |||||||||||| |||||
                                AG  TTCGTTTGATGA CGTAG
                                  GT          A     ACT
GAM240  ACTR2    3' TTAATGCTTCTGTTTATTCC   19154         TGTT
                                GGAGTAGAT    AGTGTTGA
                                |||||||||    ||||||||
                                CCTTATTTG    TCGTAATT
                                      TCT_
GAM240  AF093680 5' TCGGTGCCTGTATCTACTCC   25092         TGTTA TG
                                GGAGTAGAT    G  TTGA
                                |||||||||    |  ||||
                                CCTCATCTA    C  GGCT
                                      TGTC_ GT
GAM240  AGPAT1   3' GCAGTCTCCACTCTTGA     51235         __
                                TCAGGAGT  AGATTGT
                                ||||||||  |||||||
                                AGTTCTCA  TCTGACG
                                      CC
GAM240  AGPAT1   3' TCGGTGCAGTTTCCACTCTTGA 21152         A  TTGTTA TG
                                TCAGGAGT GA     G  TTGA
                                |||||||| ||     |  ||||
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                                AGTTCTCA CT     C  GGCT
                                    C  TTGA__ GT
GAM240  AKAP12   3'  GCAATACCTAGTTCTGCTTCTG 17524          TTGTTA     A
            A                    TCAGGAGTAGA     GTGTTG
                                 ||||||||||      ||||||
                                 AGTCTTCGTCT     CATAAC
                                       TGATC_     GG
GAM240  AKAP12   3'  GCAATACCTAGTTCTGCTTCTG 57843          TTGTTA     A
            A                    TCAGGAGTAGA     GTGTTG
                                 ||||||||||      ||||||
                                 AGTCTTCGTCT     CATAAC
                                       TGATC_     GG
GAM240  AKT3     3'  TACTGCAGTTACTTTTGA    18435        A     T
                                 TCAGGAGT GATTGT AGTG
                                 ||||||||| |||||| ||||
                                 AGTTTTCA TTGACG TCAT

                                      _     _
GAM240  ALS2CR3  3'  TGCTGGCACATTTACTTCTGG  30488          _
                                 TCAGGAGTAGAT TGTTAGTG
                                 |||||||||||| ||||||||
                                 GGTCTTCATTTA ACGGTCGT
                                       C
GAM240  AMOT     3'  TCCTATTAACAGTCTTTTTTTG 55726        T          TTGA
            A                    TCAGGAG AGATTGTTAGTG
                                 ||||||| ||||||||||||
                                 AGTTTTT TCTGACAATTAT
                                     T          CCT
GAM240  ANGPTL1  3'  GCACAATTTATTTCT       16246           TAGT
                                 AGGAGTAGATTGT    GT
                                 ||||||||||||    ||
                                 TCTTTATTTAACA    CG

                                        _____
GAM240  AP3M1    3'  AACAATCTATACCTGG      23914       A
                                 TCAGG GTAGATTGTT
                                 ||||| ||||||||||
                                 GGTCC TATCTAACAA
                                    A
GAM240  APCL     3'  CTGGTGGTCTCTTCTGA     19672        T    TG
                                 TCAGGAG AGAT  TTAG
                                 ||||||| ||||  ||||
                                 AGTCTTC TCTG  GGTC
                                     _    GT
GAM240  Apg4B    3'  TCGGCACTGACCGGCCCACCTG 25289       A__  AGATT
            G                    TCAGG   GT    GTTAGTGTTGA
                                 |||||   ||    ||||||||||
                                 GGTCC   CG    CAGTCACGGCT
                                    ACC  GC___
GAM240  API5     3'  TTAAACATCTTGATAATTTGTT 21692    G          __     GA
            GTTGA                    AG AGTAGATTGTTA  GTGTT
                                 || ||||||||||  |||||
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                                TT TTGTTTAATAGT  TACAA
                                 G          TC    ATT
GAM240  APOA5    3'  GCTCTAGTCACTTCTGG     53730        A   TGT   T
                                TCAGGAGT GAT   TAG GT
                                |||||||| |||   ||| ||
                                GGTCTTCA CTG   ATC CG
                                    _  ___   T
GAM240  ARG99    3'  ACTCCAGATTTCTCTTGA    49169        T    GTT
                                TCAGGAG AGATT   AGT
                                ||||||| |||||   |||
                                AGTTCTC TTTAG   TCA
                                    _    ACC
GAM240  ARHGAP5  3'  TGGGCAACTTAATTTACATTCT 77083       _      TTAG   GA
            GG                    TCAGGA GTAGATTG    TGTT
                                |||||| ||||||||    ||||
                                GGTCTT CATTTAAT    ACGG
                                   A       TCA_   GTT
GAM240  ARHGEF15 3'  TGGTGATTGTGCTCCTGA    30263        _   TG
                                TCAGGAGTA GAT  TTA
                                ||||||||| |||  |||
                                AGTCCTCGT TTA  GGT
                                     G   GT
GAM240  ARPP-19  3'  AAAACATGAATTGTTTATTTCT 21781          T   A    GA
            GG                    TCAGGAGTAGAT GTT GTGTT
                                |||||||||||| ||| |||||
                                GGTCTTTATTTG TAA TACAA
                                      T   G    AAT
GAM240  BAG2     3'  TTGACACTGATAGTTGTTTC   91029     TA         TG
                                GAG  GATTGTTAGTGT  A
                                |||  |||||||||||  |
                                CTT  TTGATAGTCACA  T
                                  TG          GT
GAM240  BAG5     3'  CAGTATCTGCTGCTTTTGA   16841          ATTGT  G
                                TCAGGAGTAG     TA TG
                                ||||||||||     || ||
                                AGTTTTCGTC     AT AC
                                      GTCT_  G
GAM240  BDG-29   3'  CAACACTGAAATTGTTGA    72352      G   AGATTG
                                TCAG AGT     TTAGTGTTG
                                |||| |||     |||||||||
                                AGTT TTA     AGTCACAAC
                                  G   A_____
GAM240  BIRC2    3'  TTGGTACTAATAATCTTGTTTC 67204       GT_         TT
            TGA                   TCAGGA   AGATTGTTAGTG  GA
                                ||||||   ||||||||||||  ||
                                AGTCTT   TCTAATAATCAT  TT
                                   TGT          GG
GAM240  BNIP-S   5'  TTAACAGCAGGTAATCTGCTTC 56271           TA _
            T                     AGGAGTAGATTGT  G TGTTGA
                                ||||||||||||  | ||||||
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                                TCTTCGTCTAATG  C ACAATT
                                       GA G
GAM240  BTBD1    3'  TTAGCATTATAATACATCTTGG 47478       GTAG    T
                                TCAGGA    ATTGT AGTGTTGA
                                ||||||    ||||| ||||||||
                                GGTTCT    TAATA TTACGATT
                                   ACA_    _
GAM240  BTN2A2   3'  TAACACTGGGGACTCCT     22779       AGAT G
                                AGGAGT    T TTAGTGTTG
                                ||||||    | |||||||||
                                TCCTCA    G GGTCACAAT
                                   ____ G
GAM240  BZW1     3'  TCTACGTAGTGATCTGCTTTT  27892         TG   G   T
                                AGGAGTAGAT  TTA TGT GA
                                ||||||||||  ||| ||| ||
                                TTTTCGTCTA  GAT GCA CT
                                      GT   _   T
GAM240  C12orf22 3'  ACACCATACTTTACTTCTGG   47973          T   TA
                                TCAGGAGTAGA TGT  GTGT
                                |||||||||||| |||  ||||
                                GGTCTTCATTT ATA  CACA
                                      C   C_
GAM240  C13orf1  3'  TATATTACTGGCAATTTCATTT 39974        _         TTGA
           TTGG                    CAGGAGT AGATTGTTAGTG
                                |||||||  ||||||||||||
                                GTTTTTA TTTAACGGTCAT
                                   C          TATATT
GAM240  C13orf1  3'  TCATTTTTGGCAGTCTATTTCT 39977              TGT
           G                     CAGGAGTAGATTGTTAG   TGA
                                ||||||||||||||||   |||
                                GTCTTTATCTGACGGTT   ACT
                                          TTT
GAM240  C20orf11 3'  TCAATGAACCATCTCTTCTGG  35442       T   T   AG
                                TCAGGAG AGAT GTT  TGTTGA
                                |||||||  |||| |||  ||||||
                                GGTCTTC TCTA CAA  GTAACT
                                   _   C   __
GAM240  C20orf16 5'  CAAAGACAGTCTGCTCATGA   38721     G         AG
                                TCA GAGTAGATTGTT  TG
                                |||  ||||||||||||  ||
                                AGT CTCGTCTGACAG  AC
                                  A          AA
GAM240  C20orf36 3'  TGACAACTATTTGCTTTTGA   36800          T  TAG   TG
                                TCAGGAGTAGAT GT   TGT  A
                                ||||||||||||  ||   |||  |
                                AGTTTTCGTTTA CA   ACA  T
                                      T  ___   GT
GAM240  C2orf6   3'  GTGCTACCTATTCTTGA     36645         ATTGT   TG
                                TCAGGAGTAG    TAG  T
                                ||||||||||    |||  |
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                                AGTTCTTATC    ATC  G
                                      C____   GT
GAM240  C6orf37  3'  TGTGCAATGATGATATGCTCCT 67481        G  TG   G   TGA
            GG                    TCAGGAGTA AT  TTA TGT
                                  ||||||||| ||  ||| |||
                                  GGTCCTCGT TA  AGT ACG
                                        A  GT   A   TGTT
GAM240  C6orf9   5'  CAGCATTTTGTGCTTTTGG   42076        GATTGTT
                                  TCAGGAGTA      AGTGTTG
                                  |||||||||      |||||||
                                  GGTTTTCGT      TTACGAC
                                        GTT____
GAM240  C8orf4   3'  TTGATGCTGATAGAAGAGCCTG 39281      AGTAGA        TG
            G                     TCAGG     TTGTTAGTGT  A
                                  |||||     |||||||||| |
                                  GGTCC     GATAGTCGTA  T
                                     GAGAA_        GT
GAM240  CAGE     5'  TGAATAATAATGATTTGTTCTT 82697          TG   G    GA
            G                     CAGGAGTAGAT  TTA TGTT
                                  |||||||||||  ||| ||||
                                  GTTCTTGTTTA  AAT ATAA
                                        GT   A    GTT
GAM240  CALN1    3'  GACAGTTTGTCTTGG       48870       G
                                  TCAGGA TAGATTGTT
                                  |||||| |||||||||
                                  GGTTCT GTTTGACAG
                                        _
GAM240  CALN1    3'  TGGTGCGTTGTGTGTTCCTGA  48879        G  TGTTA TG TG
                                  TCAGGAGTA AT     G  T  A
                                  ||||||||| ||     |  |  |
                                  AGTCCTTGT TG     C  G  T
                                        G  TTG__ GT GT
GAM240  caspr5   3'  TAGGCACATGACGGTCATTCCT 55383        A       _     GA
            GA                      TCAGGAGT GATTGTTA GTGTT
                                  |||||||| |||||||| |||||
                                  AGTCCTTA CTGGCAGT CACGG
                                        _       A     ATT
GAM240  CBX1     3'  ACTAATGATTTGCTTCT     22325          TG
                                  AGGAGTAGAT  TTAGT
                                  |||||||||  |||||
                                  TCTTCGTTTA  AATCA
                                        GT
GAM240  CBX6     3'  TGCCACAGGTGGTCTGCTTCTG 26628          TG TA   TTGA
                                  CAGGAGTAGAT  T  GTG
                                  ||||||||||| |  |||
                                  GTCTTCGTCTG  G  CAC
                                        GT GA   CGTT
GAM240  CCNA2    3'  TTAATTTTACAATCATTTCTGA 6946         A     TAGT
                                  TCAGGAGT GATTGT    GTTGA
                                  |||||||| ||||||    |||||
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                                AGTCTTTA CTAACA    TAATT
                                    _     TTT_
GAM240  CCNE1    3'  TTAATAAAGATAATACTGTTTT 6952          _     AG
           TGA                    TCAGGAGTAG ATTGTT  TGTTGA
                                  |||||||||| ||||||  ||||||
                                  AGTTTTTGTC TAATAG  ATAATT
                                       A     AA
GAM240  CCNE1    3'  TTAATAAAGATAATACTGTTTT 54119         _     AG
           TGA                    TCAGGAGTAG ATTGTT  TGTTGA
                                  |||||||||| ||||||  ||||||
                                  AGTTTTTGTC TAATAG  ATAATT
                                       A     AA
GAM240  CCNE2    3'  TTGACTAGTGCAATTTGGTTCT 54122      _ G      TAGT  TG
           TGA                    TCAGG A TAGATTGT    GT  A
                                  ||||| | ||||||||    ||  |
                                  AGTTC T GTTTAACG    CA  T
                                     T G       TGAT  GT
GAM240  CCNE2    3'  TTGACTAGTGCAATTTGGTTCT 16294      _ G      TAGT  TG
           TGA                    TCAGG A TAGATTGT    GT  A
                                  ||||| | ||||||||    ||  |
                                  AGTTC T GTTTAACG    CA  T
                                     T G       TGAT  GT
GAM240  CD36L1   3'  AATAATTCACTCTTGA      18564         AG
                                  TCAGGAGT  ATTGTT
                                  ||||||||  ||||||
                                  AGTTCTCA  TAATAA
                                       CT
GAM240  CDA02    5'  GGCAGTTTGCCTTGA       67850       A
                                  TCAGG GTAGATTGTT
                                  ||||| ||||||||||
                                  AGTTC CGTTTGACGG
                                     _
GAM240  CDC14B   3'  TCAGTGACAATGATCTGCTTCT 52838           TG  AG GT
           GG                     TCAGGAGTAGAT  TT  T  TGA
                                  ||||||||||||  ||  |  |||
                                  GGTCTTCGTCTA  AA  G  ACT
                                        GT  CA TG
GAM240  CDC14B   3'  CTAGCAGTCAACTCCTGA     52848         A
                                  TCAGGAGT GATTGTTAG
                                  |||||||| |||||||||
                                  AGTCCTCA CTGACGATC
                                       A
GAM240  CDC14B   3'  TCAGTGACAATGATCTGCTTCT 13389           TG  AG GT
           GG                     TCAGGAGTAGAT  TT  T  TGA
                                  ||||||||||||  ||  |  |||
                                  GGTCTTCGTCTA  AA  G  ACT
                                        GT  CA TG
GAM240  CEP3     5'  TCAGCGGCGGCCGGTTTGTCCT 21251       G      TTA  _
           GG                     TCAGGA TAGATTG   GT GTTGA
                                  |||||| |||||||   || |||||
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                                GGTCCT GTTTGGC  CG CGACT
                                   _     CGG  G
GAM240  cerk     3'  CTACCAATGTTTGCTCCTGG  42845          __  T
                                TCAGGAGTAGAT  TG TAG
                                ||||||||||||  || |||
                                GGTCCTCGTTTG  AC ATC
                                      TA  C
GAM240  CETN2    3'  TGCCACAAGCAGTCATTCTTGA 15094        A     A  TTGA
                                TCAGGAGT GATTGTT GTG
                                |||||||| ||||||| |||
                                AGTTCTTA CTGACGA CAC
                                   _     A  CGTT
GAM240  CGI-01   3'  ATACTGGTTTGCTTTTGA   31941          TGT
                                TCAGGAGTAGAT   TAGTGT
                                ||||||||||||   ||||||
                                AGTTTTCGTTTG   GTCATA
                                      ___
GAM240  CGI-127  3'  CTAGTATTTGCTTCTGG    32155          TGT
                                TCAGGAGTAGAT   TAG
                                ||||||||||||   |||
                                GGTCTTCGTTTA   ATC
                                      TG_
GAM240  CGI-127  3'  TTGATATTAAAAGTGACTTCTG 32157        AG  G     TG
           A                     TCAGGAGT  ATT TTAGTGT  A
                                 ||||||||  ||| |||||||  |
                                 AGTCTTCA  TGA AATTATA  T
                                    G_  A     GT
GAM240  CGI-96   5'  TTGGCGCGCTGATTTGCCTCTG 31665     GA      TTA   TG
           A                     TCAG  GTAGATTG   GTGT  A
                                 ||||  ||||||||   ||||  |
                                 AGTC  CGTTTAGT   CGCG  T
                                   TC       CG_   GT
GAM240  CHM-I    3'  TCAACCTGAGCGGTTATTCTTG 59725        A   _   T
           A                     TCAGGAGT GATTG TTAG GTTGA
                                 |||||||| ||||| |||| |||||
                                 AGTTCTTA TTGGC AGTC CAACT
                                    _    G   _
GAM240  CKS2     3'  TTACTGAAACAGTTTACTTTTG 8436           __    TTGA
                                 CAGGAGTAGATTGT  TAGTG
                                 ||||||||||||||  |||||
                                 GTTTTCATTTGACA  GTCAT
                                       AA    T
GAM240  CLIC2    3'  TTAATATATACATGAGTTTATT 7091         ___  TA
           TCTGA                   GGAGTAGAT   TGT  GTGTTGA
                                   |||||||||   |||  |||||||
                                   CTTTATTTG   ACA  TATAATT
                                      AGT   TA
GAM240  CLIC4    3'  CAATTTAGTCTATCCTGG    25632       G     TTAGT
                                 TCAGGA TAGATTG    GTTG
                                 ||||||  |||||||    ||||
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                                GGTCCT ATCTGAT    TAAC
                                  _     T____
GAM240  CMG2    3'  TTGGTGTTACTGCTACTCCTGG 54167         ATT  T  TG TG
                                TCAGGAGTAG  GT AG  T  A
                                ||||||||||  || ||  |  |
                                GGTCCTCATC  CA TT  G  T
                                   GT_  _  GT GT
GAM240  CNNM1   3'  TCAGTATTTAATGTATTTATTC 39777         _    _
          TTG                  CAGGAGTAGAT TGTTAG TGTTGA
                               |||||||||||| |||||| ||||||
                               GTTCTTATTTA GTAATT ATGACT
                                  T     T
GAM240  CNTN6   5'  TCCCTGGTAAGATCTACTCTTG 27091          GT__  TGTTGA
          A                    TCAGGAGTAGATT   TAG
                               ||||||||||||    |||
                               AGTTCTCATCTAG   GTC
                                  AATG  CCT
GAM240  COPS7B  3'  TTGGCGTTCTCTCCTGG    42695       T  T
                               TCAGGAG AGA TGTTAG
                               ||||||| ||| ||||||
                               GGTCCTC TCT GCGGTT
                                  _  T
GAM240  CRNKL1  3'  GCAGTGATTATATTTCTGA   33599       GATT   G
                               TCAGGAGTA   GTTA TGT
                               |||||||||   |||| |||
                               AGTCTTTAT   TAGT ACG
                                  AT__   G
GAM240  CSMD1   3'  TTAACTCCCAGACTTGCTCTTG 73130       _ A  TT  GTTGA
          G                    TCAGGAGTA G TTG  AGT
                               ||||||||| | |||  |||
                               GGTTCTCGT C GAC  TCA
                                  T A  CC  ATT
GAM240  CSTF3   5'  TGGTGTTGGCGGTCTGGCTC  7175      _       TG TG
                               GAGT AGATTGTTAG  T  A
                               |||| ||||||||||  |  |
                               CTCG TCTGGCGGTT  G  T
                                 G       GT GT
GAM240  CYorf14 3'  TTGGTACTGGCTAGAAATTTCT 37612       AGATT     TT
          G                    CAGGAGT    GTTAGTG  GA
                               |||||||    |||||||  ||
                               GTCTTTA    CGGTCAT  TT
                                  AAGAT     GG
GAM240  CYP4F2  5'  TGTCTGGGACAGACTGCTCCTG 6553         A    AGTGTTGA
          A                    TCAGGAGTAG TTGTT
                               |||||||||| |||||
                               AGTCCTCGTC GACAG
                                  A    GGTCTGTT
GAM240  DAZ2    3'  TTAACACTGAAACTGTTCTTC  39800     TAGATTG
                               GGAG      TTAGTGTTGA
                               ||||      ||||||||||
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                                CTTC      AGTCACAATT
                                  TTGTCAA
GAM240  DCAMKL1   3'  TCAATGAATATGTGATTTGCTC 16415         TG TAG__
           C                     GGAGTAGAT  T    TGTTGA
                                 |||||||||  |    ||||||
                                 CCTCGTTTA  G    GTAACT
                                      GT TATAA
GAM240  DKFZP434A043 3'  CAACAGAAGTTGCTCTTGA   31186          ATTG  AG
                                 TCAGGAGTAG    TT  TGTTG
                                 ||||||||||    ||  |||||
                                 AGTTCTCGTT    AG  ACAAC
                                       GA__  __
GAM240  DKFZp434A171 3'  TTGGTATTTATAGTTTACTTTG 50012      G        T    TT
           A                     TCAG AGTAGATTGT AGTG  GA
                                 |||| ||||||||||  ||||  ||
                                 AGTT TCATTTGATA TTAT  TT
                                   _        T    GG
GAM240  DKFZP434B172 5'  TCAGTACTCAGCATGTTGTGCT 70038       _  _   _
           CCTGA                    GGAGTA GAT TGTT AGTGTTGA
                                 |||||| ||| |||| ||||||||
                                 CCTCGT TTG ACGA TCATGACT
                                    G   T   C
GAM240  DKFZp434D177 5'  TCAGTGCTGTGTGCTCTTGG   50054         G  TGTT  TG
                                 TCAGGAGTA AT    AG  TTGA
                                 |||||||| ||    ||  ||||
                                 GGTTCTCGT TG    TC  GACT
                                       G  ____  GT
GAM240  DKFZp434F1719 3'  ATATTAGCAGGCTTC       49995       AGA
                                 GGAGT   TTGTTAGTGT
                                 |||||   ||||||||||
                                 CTTCG   GACGATTATA
                                   ___
GAM240  DKFZp434F1719 3'  ATTAACACTGAAAAAGATGATC 49996       TG _______
           TGTTCT                   TAGAT  TT     AGTGTTGA   T
                                 |||||  ||     ||||||||  |
                                 GTCTA  AG     TCACAATT   A
                                    GT  AAAAAG
GAM240  DKFZP434J1813 3'  TCCCACTGATAGTTGATTTTTG 61792         A         TTGA
           A                     TCAGGAGT GATTGTTAGTG
                                 ||||||||  ||||||||||
                                 AGTTTTTA TTGATAGTCAC
                                      G          CCT
GAM240  DKFZp434K1210 3'  TGGCACTGGCGGCCTCCT    34277       TAGA        TG
                                 AGGAG    TTGTTAGTGT  A
                                 |||||    ||||||||||  |
                                 TCCTC    GGCGGTCACG  T
                                    C___         GT
GAM240  DKFZP564M182 3'  TTAGCATTTGCTCTGCTACTTG 78047       _     TT  T
           A                     TCAGG AGTAGA  GT AGTGTTGA
                                 ||||| ||||||  || ||||||||
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                                AGTTC TCGTCT  CG TTACGATT
                                   A     __ T
GAM240  DKFZP564P1916 3'  ACTAAATCTGCTTTT      31606          GT
                                AGGAGTAGATT  TAGT
                                ||||||||||  ||||
                                TTTTCGTCTAA  ATCA
                                          __
GAM240  DKFZP566D193 3'  CATGTATATTTATTCCTGG   85567          TGTTA
                                TCAGGAGTAGAT    GTG
                                ||||||||||||    |||
                                GGTCCTTATTTA    TAC
                                      TATG_
GAM240  DKFZP566F2124 3'  TCAATATTATTTCTGTTACTTG 31574      _     TTGT
          A                      TCAGG AGTAGA    TAGTGTTGA
                                ||||| ||||||    |||||||||
                                AGTTC TTGTCT    ATTATAACT
                                   A     TT__
GAM240  DKFZp586H0623 5'  TCAGTGCTGTCAGCTGTTTTT  34074        A   T   TG
                                AGGAGTAG TTG TAG  TTGA
                                |||||||| ||| |||  ||||
                                TTTTTGTC GAC GTC  GACT
                                     _  T   GT
GAM240  DKFZP727C091 3'  TCGGTGTTAGTTCCACTCTTGG 66212        A  TTG    TG
                                TCAGGAGT GA   TTAG  TTGA
                                |||||||| ||   ||||  ||||
                                GGTTCTCA CT   GATT  GGCT
                                     C  T__    GT
GAM240  DKFZp761B1514 3'  TTAGTGTTGACTTTTCCTG    50150       TAGATT    TG
                                CAGGAG     GTTAG  TTGA
                                ||||||     |||||  ||||
                                GTCCTT     CAGTT  GATT
                                   TT____     GT
GAM240  DKFZp761D221 3'  TTAGCATTTTACCATTCCTGA  50166       ___    T
                                TCAGGA   GTAGA TGTTAG
                                ||||||   ||||| ||||||
                                AGTCCT   CATTT ACGATT
                                   TAC    T
GAM240  DKFZp761F2014 3'  GCAAGGCTGTCATCTGCTCTTG 39538          T T   G   A
          G                      TCAGGAGTAGAT G TAGT TTG
                                ||||||||||||| | |||| |||
                                GGTTCTCGTCTA C GTCG AAC
                                      _ T   G   GG
GAM240  DKFZp761G0313 3'  CACTGTGGCTGCTTCTGG    65815         ATTGT
                                TCAGGAGTAG    TAGTG
                                ||||||||||    |||||
                                GGTCTTCGTC    GTCAC
                                      GGT__
GAM240  DKFZp761H079 3'  TAGCAAGATTTACTGTTGA   58737     G      GTTAG
                                TCAG AGTAGATT    TGTTG
                                |||| ||||||||    |||||
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                                AGTT TCATTTAG    ACGAT
                                  G      A____
GAM240  DKFZp761H079 3'  TCAGCACTGTATATATTCTTGG 58738        GATTGT
                                TCAGGAGTA     TAGTGTTGA
                                |||||||||     |||||||||
                                GGTTCTTAT     GTCACGACT
                                    ATAT__
GAM240  DKFZp761K1423 3'  TGGTGGTCTTCTTTTGA     37335       T   TG
                                TCAGGAG AGAT  TTA
                                ||||||| ||||  |||
                                AGTTTTC TCTG  GGT
                                    T   GT
GAM240  DKFZp761K1423 3'  TCGGCATTAGCAGTTT      37334
                                AGATTGTTAGTGTTGA
                                ||||||||||||||||
                                TTTGACGATTACGGCT

GAM240  DKFZp762A227 3'  TTGGTGTTGAAAGTTCTTCCTG 26038      GT   TTG_   TG TG
          G                      TCAGGA  AGA    TTAG  T  A
                                ||||||  |||    ||||  |  |
                                GGTCCT  TCT    AGTT  G  T
                                   __   TGAA    GT GT
GAM240  DKFZp762A227 3'  TTGGTGTTGAAAGTTCTTCCTG 34288      GT   TTG_   TG TG
          G                      TCAGGA  AGA    TTAG  T  A
                                ||||||  |||    ||||  |  |
                                GGTCCT  TCT    AGTT  G  T
                                   __   TGAA    GT GT
GAM240  DPCR1    3'  TTAACCCTTCATCTGTTCTTGA 55125          T TT  T
                                TCAGGAGTAGAT G  AG GTTGA
                                ||||||||||||  |  || |||||
                                AGTTCTTGTCTA C  TC CAATT
                                      _ T_  C
GAM240  DPP8     3'  TAACATCTACTCCTGA      55235          T
                                TCAGGAGTAGAT GTTA
                                |||||||||||| ||||
                                AGTCCTCATCTA CAAT
                                      _
GAM240  DRF1     5'  TGATGCTGTAGCTGCCCTGA   47037      A   ATTGT    TG
                                TCAGG GTAG    TAGTGT  A
                                ||||| ||||    ||||||  |
                                AGTCC CGTC    GTCGTA  T
                                   _   GAT__     GT
GAM240  DSCR6    3'  CTGGCAATTCGTTTTTGG    38546       TA
                                TCAGGAG  GATTGTTAG
                                |||||||  |||||||||
                                GGTTTTT  TTAACGGTC
                                    GC
GAM240  DSCR6    3'  TGATAAACGTGTATTCCTGA   38554        G  T   AG   TG
                                TCAGGAGTA AT GTT  TGT  A
                                ||||||||| || |||  |||  |
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                                AGTCCTTAT TG CAA  ATA  T
                                     G  _  __  GT
GAM240  EML4    3'  TGCTGTGTAGCAGTTTTTTTCT 38813       T       GTGTTGA
          GG                    TCAGGAG AGATTGTTA
                                |||||||  |||||||||
                                GGTCTTT TTTGACGAT
                                   T       GTGTCGTT
GAM240  EPN2    3'  CTAATAGTCTTTTTTTGG    30322       T
                                TCAGGAG AGATTGTTAG
                                |||||||  ||||||||||
                                GGTTTTT TCTGATAATC
                                   T
GAM240  ESM1    3'  TCAGTATTTACCTGTATTTTAT 22881       TT____  T
          TCTTGA                GAGTAGA    GT AGTGTTGA
                                |||||||     || ||||||||
                                CTTATTT    CA TTATGACT
                                   TATGTC  T
GAM240  EVI5    3'  TTAGTGCTAATATTCTACT   19020      T    TG
                                AGTAGA TGTTAG  TTGA
                                ||||||  ||||||  ||||
                                TCATCT ATAATC  GATT
                                   T    GT
GAM240  F23149_1 3'  CTAGTGGTCTGTTTGTGA    69982    G      TG
                                TCA GAGTAGAT  TTAG
                                |||  ||||||||  ||||
                                AGT TTTGTCTG  GATC
                                  G      GT
GAM240  FBXO21  3'  TGCAATAATTTCCTTCTGA   53243       T      A
                                TCAGGAG AGATTGTT GTG
                                |||||||  ||||||||  |||
                                AGTCTTC TTTAATAA CGT
                                   C      _
GAM240  FBXO3   3'  GACAATCTGTCTTTGA     24096      AG
                                TCAGG  TAGATTGTT
                                |||||  |||||||||
                                AGTTT  GTCTAACAG
                                   CT
GAM240  FBXO30  3'  TTAATTTGAAACTGCTCCTGG  49581         ATTG   T
                                TCAGGAGTAG   TTAG GTTGA
                                ||||||||||   ||||  |||||
                                GGTCCTCGTC   AGTT TAATT
                                     AA__   _
GAM240  FBXO4   3'  TTGATACTGACATTTTGTCTGC 53113       ____       TG
          TTCTGG                GAGTAGAT   TGTTAGTGT  A
                                ||||||||   |||||||||  |
                                TTCGTCTG   ACAGTCATA  T
                                     TTTT       GT
GAM240  FBXO9   3'  TTAAAGGGATAGTTGATTCCTG 53107       A      AGTG
          G                     TCAGGAGT GATTGTT   TTGA
                                |||||||| |||||||   ||||
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                                GGTCCTTA TTGATAG    AATT
                                    G      GGA_
GAM240  FEM-2    3'  TTTGCTAATAATTCTGTTCCTG 27586          _       TTGA
            G                    TCAGGAGTAGA TTGTTAGTG
                                 |||||||||| |||||||||
                                 GGTCCTTGTCT AATAATCGT
                                       T        TT
GAM240  FEZ2     3'  TCAGTATTAACAGATCTTGA   17526       GTAGAT
                                 TCAGGA     TGTTAGTGTTGA
                                 ||||||     ||||||||||||
                                 AGTTCT     ACAATTATGACT
                                    AG____
GAM240  FEZ2     3'  TTAGTGCTAACATTGAAACTGT 17527      G   AGAT_     TG
            TGG                    TCAG AGT    TGTTAG  TTGA
                                 |||| |||    ||||||  ||||
                                 GGTT TCA    ACAATC  GATT
                                   G   AAGTT     GT
GAM240  FHX      3'  TCAATGCTAATCCCACCTTTTG 37308        TAGATT
            G                    TCAGGAG     GTTAGTGTTGA
                                 |||||||     ||||||||||||
                                 GGTTTTC     TAATCGTAACT
                                     CACCC_
GAM240  FIGN     3'  TCAGTGCAATTTTGCTTCT    95643         TT   A TG
                                 AGGAGTAGA  GTT G  TTGA
                                 |||||||||  ||| |  ||||
                                 TCTTCGTTT  TAA C  GACT
                                      __   _ GT
GAM240  FKBP9    5'  TCAGTGCTTCATTTTGATGTAC 94069      G    TT____  TG
            TTCTGA                  GAGTA ATTG     AG  TTGA
                                 |||||  ||||     ||  ||||
                                 TTCAT TAGT     TC  GACT
                                    G    TTTACT  GT
GAM240  FKSG14   3'  ATATATTAATCTACTCTTGA   67804            TTA
                                 TCAGGAGTAGATTG   GTGT
                                 ||||||||||||||   ||||
                                 AGTTCTCATCTAAT   TATA
                                         TA_
GAM240  FLJ00024 3'  TCAGGCCGCTGGTTTATTCCTG 63769           TGT    __
            G                    TCAGGAGTAGAT   TAGTG  TTGA
                                 ||||||||||||   |||||  ||||
                                 GGTCCTTATTTG   GTCGC  GACT
                                       ____     CG
GAM240  FLJ10103 3'  TCGGCATTATGGTTTGCATCTG 35818      GA     TG T
            A                    TCAG  GTAGAT  T AGTGTTGA
                                 ||||  ||||||  | ||||||||
                                 AGTC  CGTTTG  A TTACGGCT
                                   TA     GT _
GAM240  FLJ10110 3'  TCAACACTGACAGCACTTT    35824       AGA
                                 GGAGT   TTGTTAGTGTTGA
                                 |||||   ||||||||||||
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                                TTTCA   GACAGTCACAACT
                                  C__
GAM240  FLJ10201  3'  AATAGTCTATACCTGA      35889       A
                                TCAGG GTAGATTGTT
                                ||||| ||||||||||
                                AGTCC TATCTGATAA
                                   A
GAM240  FLJ10201  5'  TCAAAGAACAGTTTGCTCTTGA 35894              AGTG
                                TCAGGAGTAGATTGTT    TTGA
                                ||||||||||||||||   ||||
                                AGTTCTCGTTTGACAA    AACT
                                          GA__
GAM240  FLJ10350  3'  CAGTGTTACTGCATCTGA    95504     GA   ATTGT   TG
                                TCAG  GTAG    TAG  TTG
                                ||||  ||||    |||  |||
                                AGTC  CGTC    ATT  GAC
                                  TA   _____   GT
GAM240  FLJ10466  3'  TTGATACTGGAACTATGCTTTG 36140      G   GATTG      TG
          A                      TCAG AGTA    TTAGTGT  A
                                ||||| ||||    |||||||  |
                                AGTT TCGT    GGTCATA  T
                                  _   ATCAA      GT
GAM240  FLJ10565  5'  TCAGTCATTGTCTATTCCTGG  36288           TGTT   _
                                TCAGGAGTAGAT    AGTG TTGA
                                ||||||||||||   |||| ||||
                                GGTCCTTATCTG    TTAC GACT
                                      _____   T
GAM240  FLJ10724  3'  TCAGCAGGGTGATCTACATTTG 36507      A     TG  AG
          G                      TCAGG GTAGAT  TT  TGTTGA
                                ||||| ||||||  ||  ||||||
                                GGTTT CATCTA  GG  ACGACT
                                   A     GT  G_
GAM240  FLJ10856  3'  TTGCACTTGGCAGTTTATTTTC 36777    AG          _   TGA
          GG                     TC  GAGTAGATTGTTA GTGT
                                ||  |||||||||||| ||||
                                GG  TTTATTTGACGGT CACG
                                 CT          T   TT
GAM240  FLJ11184  3'  ATACTGACATTCTCTT      37140     T   T
                                GAG AGA TGTTAGTGT
                                ||| ||| |||||||||
                                TTC TCT ACAGTCATA
                                  _  T
GAM240  FLJ11186  3'  TCAGTACTAATTGTATTCCT   37148       GATT
                                AGGAGTA   GTTAGTGTTGA
                                |||||||   ||||||||||
                                TCCTTAT   TAATCATGACT
                                    GT__
GAM240  FLJ11193  3'  TTGGCATTGTGGCCCTGCTCTT 37155        ATTGT     TG
          G                      CAGGAGTAG    TAGTGT  A
                                |||||||||    ||||||  |
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                                GTTCTCGTC    GTTACG  T
                                     CCGGT     GT
GAM240  FLJ11259  3' TAACACTAAGATACTCTGA   37193     G   GATTG
                                TCAG AGTA    TTAGTGTTG
                                |||| ||||    |||||||||
                                AGTC TCAT    AATCACAAT
                                  _   AG___
GAM240  FLJ11565  3' TCAATATTAAACTTGTTATTCT 45076        ATTG_
           T                     AGGAGTAG    TTAGTGTTGA
                                |||||||||    ||||||||||
                                TTCTTATT    AATTATAACT
                                     GTTCA
GAM240  FLJ11743  3' TCGGCGCTGGGAGCTATTTTTG 44552         A  G
                                CAGGAGTAG TT TTAGTGTTGA
                                ||||||||| || ||||||||||
                                GTTTTTATC GA GGTCGCGGCT
                                     _  G
GAM240  FLJ11795  5' TAACACTTACTATTTCT     45133        ATTGTT
                                AGGAGTAG     AGTGTTG
                                |||||||||    |||||||
                                TCTTTATC     TCACAAT
                                     AT_____
GAM240  FLJ11848  3' TCAGTACTAAAGCCTGTTCTCT 47164     _     ATTG
           GG                     TCAG GAGTAG    TTAGTGTTGA
                                |||| ||||||    ||||||||||
                                GGTC CTTGTC    AATCATGACT
                                  T     CGA_
GAM240  FLJ12505  3' GCGGTACTGGATTTACCTCTGA 45389     GA     GT    TT A
                                TCAG  GTAGATT  TAGTG  G
                                ||||  |||||||  |||||  |
                                AGTC  CATTTAG  GTCAT  C
                                  TC      __     GG GA
GAM240  FLJ12697  3' TCGGCGTTGGCGGAAGCCCCGG 92571    A  A  AGA
           A                     TC GG GT   TTGTTAGTGTTGA
                                || || ||   ||||||||||||
                                AG CC CG   GGCGGTTGCGGCT
                                 G  C  AA_
GAM240  FLJ12787  3' TTGGCTTTTTGATGTATCTGTT 49755        _     T__  TG
           CCTGA                    GGAGTAGAT TGTTAG   GT  A
                                |||||||| ||||||   ||  |
                                CCTTGTCTA GTAGTT   CG  T
                                     T     TTT  GT
GAM240  FLJ12806  3' TTAGCTTACTATAATTTACTTT 43089           T  __
           TGA                    CAGGAGTAGATTGT AGT  GTTGA
                                |||||||||||||| |||  |||||
                                GTTTTCATTTAATA TCA  CGATT
                                       _  TT
GAM240  FLJ12876  3' TAAGGGCAGTTTGCTTCT    42789           AG
                                AGGAGTAGATTGTT  TG
                                ||||||||||||||  ||
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                                TCTTCGTTTGACGG  AT
                                       GA
GAM240  FLJ13052  3'  TCAATGTTGATAATAAATGTCT 43473     TAG___       TG
              C                 GAG     ATTGTTAG  TTGA
                                |||     ||||||||  ||||
                                CTC     TAATAGTT  AACT
                                  TGTAAA       GT
GAM240  FLJ13081  3'  TTAATATTGATAATGTTGCTGA 45752      G  TAG
                                TCAG AG   ATTGTTAGTGTTGA
                                ||||  ||   ||||||||||||||
                                AGTC TT   TAATAGTTATAATT
                                  G  G__
GAM240  FLJ13102  3'  GATGATTTATTCTTGG      46011           TG
                                TCAGGAGTAGAT  TT
                                ||||||||||||  ||
                                GGTTCTTATTTA  AG
                                       GT
GAM240  FLJ13189  3'  GGCATTTATTCTTGA       45985           T
                                TCAGGAGTAGAT GTT
                                |||||||||||| |||
                                AGTTCTTATTTA CGG
                                          _
GAM240  FLJ13194  3'  TTAACATTGCTGTTACATCTGA 47132      GA    ATT  T
                                TCAG  GTAG   GT AGTGTTGA
                                ||||  ||||   ||  ||||||||
                                AGTC  CATT   CG TTACAATT
                                  TA    GT_  _
GAM240  FLJ13315  3'  TCAGCATTAATTAAGTGTCTGG 46572       AGTAGATT
                                TCAGG       GTTAGTGTTGA
                                |||||       ||||||||||||
                                GGTCT       TAATTACGACT
                                   GTGAAT__
GAM240  FLJ13397  3'  TACTATTGATAAACTACTTTTG 46327          A        TTGA
              G                  TCAGGAGTAG TTGTTAGTG
                                 ||||||||||  |||||||||
                                 GGTTTTCATC AATAGTTAT
                                       A        CATT
GAM240  FLJ13848  3'  CTGGCAGTCTCTCCTGG     45464        T
                                TCAGGAG AGATTGTTAG
                                |||||||  ||||||||||
                                GGTCCTC TCTGACGGTC
                                     _
GAM240  FLJ13848  3'  TGGTGCTGATAGCTCTCT    45476      T  A      TG TG
                                GGAG AG TTGTTAG  T  A
                                ||||  ||  |||||||  |  |
                                TCTC TC GATAGTC  G  T
                                  _  _      GT GT
GAM240  FLJ14082  3'  TCAGCATTGACCACTCCTGA   46675         AGATT
                                TCAGGAGT    GTTAGTGTTGA
                                ||||||||    ||||||||||
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                                AGTCCTCA    CAGTTACGACT
                                    C____
GAM240  FLJ14213  3' ATTAGAATTGTGCTCTTGA   45792        _   G
                                TCAGGAGTA GATT TTAGT
                                ||||||||| |||| |||||
                                AGTTCTCGT TTAA GATTA
                                    G   _
GAM240  FLJ14566  5' TCGGTGCTGGCAGCGGTCCTG  51449     GTAGA     TG
                                CAGGA    TTGTTAG  TTGA
                                |||||    |||||||  ||||
                                GTCCT    GACGGTC  GGCT
                                   GGC__      GT
GAM240  FLJ14600  3' TCAACACTGATTTCACCTCTTG 51468       TA  TT
          A                     TCAGGAG  GA  GTTAGTGTTGA
                                |||||||  ||  ||||||||||
                                AGTTCTC  CT  TAGTCACAACT
                                    CA  T_
GAM240  FLJ14775  3' TTGGCTTTTCAGTCTATATTTG 51607      A      TT  T  TG
          A                     TCAGG GTAGATTG  AG GT  A
                                ||||| ||||||||  || ||  |
                                AGTTT TATCTGAC  TT CG  T
                                   A       TT  _  GT
GAM240  FLJ14855  5' TGACATTGACAAACTGCTGA   52621     G   AGA       TG
                                TCAG AGT   TTGTTAGTGT  A
                                |||| |||   ||||||||||  |
                                AGTC TCA   AACAGTTACA  T
                                  G  ___        GT
GAM240  FLJ14888  3' GACATTTGCTTTTGG      51682          T
                                TCAGGAGTAGAT GTT
                                |||||||||||| |||
                                GGTTTTCGTTTA CAG
                                       _
GAM240  FLJ20085  3' GGGGGCTGGTTCTGCTCCTGG  34519          TT TT   G  GA
                                TCAGGAGTAGA  G  AGT TT
                                |||||||||||  |  ||| ||
                                GGTCCTCGTCT  T  TCG GG
                                      __ GG   G  GT
GAM240  FLJ20154  5' TCAGCGCTGCCATTTTATTTC  72934        T  T
                                GGAGTAGA TG TAGTGTTGA
                                |||||||| || |||||||||
                                CTTTATTT AC GTCGCGACT
                                    T  C
GAM240  FLJ20273  3' AAGAATGTTAGCAGATTTATTT 38723          _     TG  GA
          CTGA                      CAGGAGTAGAT TGTTAG  TT
                                |||||||||||| ||||||  ||
                                GTCTTTATTTA ACGATT  AA
                                      G     GT  GAAG
GAM240  FLJ20275  3' ACATGCAGCTGCTTTTGG    34815          A    TA
                                TCAGGAGTAG TTGT  GTGT
                                |||||||||| ||||  ||||
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                                GGTTTTCGTC GACG  TACA
                                       _   __
GAM240  FLJ20275 3' AGCACTGAAATCCTGG     34817      GTAGATTG
                                TCAGGA      TTAGTGTT
                                ||||||      ||||||||
                                GGTCCT      AGTCACGA
                                   AA_____
GAM240  FLJ20275 3' TCAGTACTGACAGACTAC    34826     A
                                GTAG TTGTTAGTGTTGA
                                |||| ||||||||||||
                                CATC GACAGTCATGACT
                                  A
GAM240  FLJ20422 3' CTGAGGTCTGTTCCTGG     35148          G
                                TCAGGAGTAGATT TTAG
                                |||||||||||| ||||
                                GGTCCTTGTCTGG AGTC
                                       _
GAM240  FLJ20445 3' CAACACTAATGTTTTTA     35176     T_
                                TAGA  TGTTAGTGTTG
                                ||||  ||||||||||
                                ATTT  GTAATCACAAC
                                  TT
GAM240  FLJ20445 5' CAGTGCTATTGTCCCTGG    35177      AGTA  TGT  TG
                                TCAGG   GAT  TAG  TTG
                                |||||   |||  |||  |||
                                GGTCC   CTG  ATC  GAC
                                  _____  TT_  GT
GAM240  FLJ20449 3' TGGCATGGTTTGGCTTCTGA  35189       _   GTTA   TG
                                TCAGGAGT AGATT   GTGT  A
                                |||||||| |||||   ||||  |
                                AGTCTTCG TTTGG   TACG  T
                                    G    _____   GT
GAM240  FLJ20456 3' TTAACGTTAATAATCTTGTATG 35218    GGAGT
           G                     TCA    AGATTGTTAGTGTTGA
                                |||    ||||||||||||||||
                                GGT    TCTAATAATTGCAATT
                                  ATGT_
GAM240  FLJ20507 3' TTGGCAGGTTTACTTGTGG   35305    G     _
                                TCA GAGTAGAT TGTTAG
                                ||| |||||||| ||||||
                                GGT TTCATTTG ACGGTT
                                  G      G
GAM240  FLJ20507 3' TTGGCAGGTTTACTTGTGG   60240    G     _
                                TCA GAGTAGAT TGTTAG
                                ||| |||||||| ||||||
                                GGT TTCATTTG ACGGTT
                                  G      G
GAM240  FLJ20513 3' TCAATACTAGTATCAGTTCTT 35334     TA  TGT
                                AGGAG  GAT   TAGTGTTGA
                                |||||  |||   |||||||||
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                                TTCTT  CTA   ATCATAACT
                                  GA   TG_
GAM240   FLJ20730  3'  TTGATGTCATTACTCCTGA   35621          AT_
                                TCAGGAGTAG   TGTTAG
                                ||||||||||   ||||||
                                AGTCCTCATT   GTAGTT
                                     ACT
GAM240   FLJ21240  5'  CACCTATGATCTGCCCCTGG   45839      A     TG TA
                                TCAGG GTAGAT  T  GTG
                                ||||| ||||||  |  |||
                                GGTCC CGTCTA  A  CAC
                                  C     GT TC
GAM240   FLJ21615  3'  TCAACGTACAGTTTGATCCTGA 49838       G       TAG
                                TCAGGA TAGATTGT   TGTTGA
                                ||||||| ||||||||   ||||||
                                AGTCCT GTTTGACA   GCAACT
                                   A       T__
GAM240   FLJ21709  3'  TCAGTGAGAACGGTTTGTCCCT 77922       AG        AG GT
           GG                    TCAGG  TAGATTGTT  T  TGA
                                ||||||  |||||||||  |  |||
                                GGTCC  GTTTGGCAA  G  ACT
                                  CT        GA TG
GAM240   FLJ21742  3'  TCGACTCTTGGATCTGCTCC   49848          GTT  T
                                GGAGTAGATT   AG GTTGA
                                ||||||||||   || |||||
                                CCTCGTCTAG   TC CAGCT
                                     GT_  T
GAM240   FLJ21934  3'  TCAAGGTGAACAGATTATTTTT 45361          A     AG G
           GG                    TCAGGAGTAG TTGTT  T TTGA
                                ||||||||||| |||||  | ||||
                                GGTTTTTATT GACAA  G AACT
                                     A     GT G
GAM240   FLJ22035  3'  TTGTTTTAATAATATGCTCCTG 44541          G       TGTTGA
           G                     TCAGGAGTA ATTGTTAG
                                ||||||||| ||||||||
                                GGTCCTCGT TAATAATT
                                     A       TTGTT
GAM240   FLJ22301  3'  TTAATGCTACTGTGCTCTCTGG 45759      _     GATT  T
                                TCAG GAGTA    GT AGTGTTGA
                                |||| |||||    || ||||||||
                                GGTC CTCGT    CA TCGTAATT
                                  T     GT__  _
GAM240   FLJ22724  3'  ATTGCTAGTTTATTCCTGG    44562            T
                                TCAGGAGTAGATTG TAGT
                                |||||||||||||| ||||
                                GGTCCTTATTTGAT GTTA
                                          C
GAM240   FLJ22833  3'  TCAATGCTAGCAGTAATTTTTG 43109          AG
           A                     TCAGGAGT  ATTGTTAGTGTTGA
                                ||||||||  ||||||||||||||
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                                AGTTTTTA  TGACGATCGTAACT
                                    A_
GAM240   FLJ22843  3'  TCGACACTTTCATTTATTCCTG 47230          T TT
                                CAGGAGTAGAT G  AGTGTTGA
                                |||||||||||  |  ||||||||
                                GTCCTTATTTA C  TCACAGCT
                                      _ TT
GAM240   FLJ22969  3'  ACACATATCTGCTTTGA     68640      G      TGTTA
                                TCAG AGTAGAT     GTGT
                                ||||  |||||||     ||||
                                AGTT TCGTCTA     CACA
                                  _      TA___
GAM240   FLJ23056  3'  ATACTGATATTTTCCT      44721       TAGAT
                                AGGAG     TGTTAGTGT
                                |||||     |||||||||
                                TCCTT     ATAGTCATA
                                   TT___
GAM240   FLJ23560  3'  TTAATACTTTGATTTTCTCCTG 45193        T     TT
            A                    TCAGGAG AGATTG  AGTGTTGA
                                |||||||  ||||||  ||||||||
                                AGTCCTC TTTAGT  TCATAATT
                                    T     T_
GAM240   FLJ31547  3'  TCAAAAAGTGCAATTTGTCTTG 58833       G       TAGTG
            G                    TCAGGA TAGATTGT     TTGA
                                ||||||  ||||||||     ||||
                                GGTTCT GTTTAACG     AACT
                                   _       TGAAA
GAM240   FLJ32499  3'  CATTACAGTTTGCTCTGA     58155      G        T
                                TCAG AGTAGATTGT AGTG
                                ||||  ||||||||||  ||||
                                AGTC TCGTTTGACA TTAC
                                   _        _
GAM240   FLJ32894  3'  CAACACTGGCTGGTTTTGA    58337       G  GATT
                                TCAGGA TA    GTTAGTGTTG
                                ||||||  ||    ||||||||||
                                AGTTTT GT    CGGTCACAAC
                                   G  _____
GAM240   FOXP1     3'  CTGGCAGTTACTTTTGA      51064         A
                                TCAGGAGT GATTGTTAG
                                |||||||  |||||||||
                                AGTTTTCA TTGACGGTC
                                      _
GAM240   FTSJ3     3'  TCAATGTAGTCAGTCTACACCT 34456       A       TTA TG
            GG                    TCAGG GTAGATTG   G  TTGA
                                |||||  ||||||||   |  ||||
                                GGTCC CATCTGAC   T  AACT
                                   A       TGA GT
GAM240   GAPCENA   3'  TTGGCATTATTCATGTTTCTGA 24164          GATTGT     TG
                                TCAGGAGTA     TAGTGT  A
                                |||||||||     ||||||  |
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                                AGTCTTTGT     ATTACG  T
                                     ACTT__     GT
GAM240  GIOT-3   3'  TTAATACTAAAAGATATGTTTC 32754         GATTG_
           TGA                    TCAGGAGTA     TTAGTGTTGA
                                |||||||||     ||||||||||
                                AGTCTTTGT     AATCATAATT
                                     ATAGAA
GAM240  GL009    3'  ACTATAATTTATTCCTGG    72634             T
                                TCAGGAGTAGATTGT AGT
                                ||||||||||||||| |||
                                GGTCCTTATTTAATA TCA
                                                _
GAM240  GMFB     3'  GGATATTAGCAGTTTATTTATG 14668     G             GA
           A                     TCA GAGTAGATTGTTAGTGTT
                                ||| ||||||||||||||||||
                                AGT TTTATTTGACGATTATAG
                                  A              GT
GAM240  GNRHR2   3'  TTAACATCTCACTTCTACTCCT 54071          TT  T  _
           G                     CAGGAGTAGA  GT AG TGTTGA
                                ||||||||||  || || ||||||
                                GTCCTCATCT  CA TC ACAATT
                                     T_  C  T
GAM240  GPR88    3'  CACACAGTTTGTTTTTGA    41877             TA
                                TCAGGAGTAGATTGT  GTG
                                ||||||||||||||  |||
                                AGTTTTTGTTTGACA  CAC
                                                __
GAM240  GR6      5'  TAGCACTGAGAGTTTTTC    23734     T    G
                                GAG AGATT TTAGTGTTG
                                ||| ||||| |||||||||
                                CTT TTTGA AGTCACGAT
                                  _     G
GAM240  GRO2     3'  TATTGGTGGCTGTTCCTGA   59517          A TG
                                TCAGGAGTAG T  TTAGTG
                                |||||||||| |  ||||||
                                AGTCCTTGTC G  GGTTAT
                                     _ GT
GAM240  GS3955   3'  TTAATGCTTTGCTCCCTGA   41322       _     TT
                                TCAGG AGTAGA  GTTAG
                                ||||| ||||||  |||||
                                AGTCC TCGTTT  TAATT
                                   C     CG
GAM240  H2AFJ    3'  TTAACACTAGTAATCATCTTCT 36844       TA
           G                     CAGGAG  GATTGTTAGTGTTGA
                                ||||||  ||||||||||||||
                                GTCTTC  CTAATGATCACAATT
                                    TA
GAM240  H2AFY    3'  TTAGCACTGATAGTTGGC    16892    A
                                GT GATTGTTAGTGTTGA
                                || ||||||||||||||
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                                CG TTGATAGTCACGATT
                                 G
GAM240  H2AFY    3'  TTAGCACTGATAGTTGGC    56812    A
                                GT GATTGTTAGTGTTGA
                                || ||||||||||||||
                                CG TTGATAGTCACGATT
                                 G
GAM240  H2AFY    3'  TTAGCACTGATAGTTGGC    56815    A
                                GT GATTGTTAGTGTTGA
                                || ||||||||||||||
                                CG TTGATAGTCACGATT
                                 G
GAM240  H2BFQ    3'  CATTGGATTTGCTTTTGA    59358          GT
                                TCAGGAGTAGATT  TAGTG
                                ||||||||||||  |||||
                                AGTTTTCGTTTAG  GTTAC
                                              __
GAM240  HCA4     3'  TTAATGTTGTGTTATTTTGCTC 56939       TTGT__  TG
              C                  GGAGTAGA     TAG  TTGA
                                ||||||||     |||  ||||
                                CCTCGTTT     GTT  AATT
                                     TATTGT   GT
GAM240  HCA4     3'  TTAATGTTGTGTTATTTTGCTC 77595       TTGT__  TG
              C                  GGAGTAGA     TAG  TTGA
                                ||||||||     |||  ||||
                                CCTCGTTT     GTT  AATT
                                     TATTGT   GT
GAM240  HE3-BETA 3'  TCAGCTCATATGGCATCTGTTC 42300         T   GT___
              TTGA                 AGGAGTAGAT GTTA    GTTGA
                                ||||||||||  ||||    |||||
                                TTCTTGTCTA CGGT    CGACT
                                     _   ATACT
GAM240  HIC      3'  AAACGAGGCAGTTTATTTTGA  67442     G        AG   GA
                                TCAG AGTAGATTGTT  TGTT
                                ||||  ||||||||||  ||||
                                AGTT TTATTTGACGG  GCAA
                                  _        A_   AT
GAM240  HIC      3'  TGATATGTATCTATTCATGA   67453    G      TGTTA   TG
                                TCA GAGTAGAT    GTGT  A
                                |||  ||||||||    ||||  |
                                AGT CTTATCTA    TATA  T
                                  A       TG___    GT
GAM240  HIF3A    3'  TCTACAGATGGTGCTACTCTTG 42414         _  TG  A   TTGA
              G                  TCAGGAGTAG AT  TT GTG
                                ||||||||||  ||  ||  |||
                                GGTTCTCATC TG  AG CAT
                                     G  GT  A   CT
GAM240  HINT3    3'  TGGCCTTAAATCTTTTCTGA   56781       T    GTT  T    A
                                TCAGGAG AGATT   AG GTTG
                                |||||||  |||||   ||  ||||
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                                AGTCTTT TCTAA   TC CGGT
                                    _    AT_ _   G
GAM240  HMP19    5'  GCTTGAATCTGCTCTGA    87474     G      GTT
                                TCAG AGTAGATT   AGT
                                |||| ||||||||   |||
                                AGTC TCGTCTAA   TCG
                                  _      GT_
GAM240  HN1L     3'  TGACTCTGGTCTGTTTCTGA   58006          TGT   T  TG
                                TCAGGAGTAGAT   TAG GT  A
                                ||||||||||||   ||| ||  |
                                AGTCTTTGTCTG   GTC CA  T
                                       ___   T  GT
GAM240  HNRPR    3'  AAAAGCCGTGACAATTTGTTCT 19513            GT   GA
            T                    AGGAGTAGATTGTTA  GTT
                                ||||||||||||||  |||
                                TTCTTGTTTAACAGT  CGA
                                       GC   AAAC
GAM240  HSPC065  3'  TCAGCATTCTCAGTTTACTCTT 26325          TT
                                AGGAGTAGATTG  AGTGTTGA
                                ||||||||||||  ||||||||
                                TTCTCATTTGAC  TTACGACT
                                       TC
GAM240  HTMP10   3'  TCAGCATTTCTGTCATTTACTT 52613          TGTT__
            CTG                   CAGGAGTAGAT     AGTGTTGA
                                ||||||||||      ||||||||
                                GTCTTCATTTA     TTACGACT
                                      CTGTCT
GAM240  HYA22    3'  AGCACAGCCTATTTCTGA    19418         ATT   A
                                TCAGGAGTAG   GTT GTGTT
                                ||||||||||   ||| |||||
                                AGTCTTTATC   CGA CACGA
                                       ___   _
GAM240  HYPC     3'  TTGGCACCTCTCAAGGTTGCTC 64613        A_   TTA_   TG
            TTGG                  CAGGAGTAG  TTG   GTGT  A
                                |||||||||  |||   ||||  |
                                GTTCTCGTT  AAC   CACG  T
                                     GG   TCTC   GT
GAM240  INA      3'  TTGACTTGTTAAACAGCCTATT 51190       AT   AGT___  TG
            CCTGA                 GGAGTAG  TGTT     GT  A
                                |||||||  ||||     ||  |
                                CCTTATC  ACAA     CA  T
                                    CG   ATTGTT  GT
GAM240  ITPK1    3'  TTAAGATAGCAGTTTACTTTGA 26417      G         G G
                                TCAG AGTAGATTGTTA T TTGA
                                |||| ||||||||||| | ||||
                                AGTT TCATTTGACGAT A AATT
                                  _          _ G
GAM240  JM11     5'  GACAACTATTTTTGA      53258          A
                                TCAGGAGTAG TTGTT
                                |||||||||| |||||
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                                AGTTTTTATC AACAG
                                          _
GAM240  KEAP1    3'  TCACCATGTGATTTATTCTTGG 24453          TG TA   T
                                TCAGGAGTAGAT  T  GTG TGA
                                ||||||||||||  |  ||| |||
                                GGTTCTTATTTA  G  TAC ACT
                                      GT __   C
GAM240  KHDRBS3  3'  TTGATACTAAATAAACTTTTGA 21621        AGATTG      TG
                                TCAGGAGT     TTAGTGT  A
                                ||||||||     |||||||  |
                                AGTTTTCA     AATCATA  T
                                     AATA__      GT
GAM240  KIAA0022 3'  TCAATATTGAACACTACCCTGG 29670      A    ATTG
                                TCAGG GTAG    TTAGTGTTGA
                                ||||| ||||    ||||||||||
                                GGTCC CATC    AGTTATAACT
                                  _   ACA_
GAM240  KIAA0061 3'  TGGCACTAAATGGCTTTGGG   68295    AG    AGATTG      TG
                                TC  GAGT     TTAGTGT  A
                                ||  ||||     |||||||  |
                                GG  TTCG     AATCACG  T
                                 GT    GTA___      GT
GAM240  KIAA0062 3'  TCAAAAATTGGCAATTTCTTTT 70245        T         G_
            GA                    TCAGGAG AGATTGTTAGT  TTGA
                                ||||||| ||||||||||  ||||
                                AGTTTTC TTTAACGGTTA  AACT
                                      _         AA
GAM240  KIAA0063 3'  TCAGGAAAAAAAAAGTCTGCTTT 29642           GTTAGTG_
            TGA                    TCAGGAGTAGATT       TTGA
                                ||||||||||||||       ||||
                                AGTTTTCGTCTGA       GACT
                                      AAAAAAAG
GAM240  KIAA0125 3'  TTAGCTAACCCAGCTTACTCCT 60508         _ ATT_     GTTGA
            GG                    TCAGGAGTA G    GTTAGT
                                |||||||||  |    ||||||
                                GGTCCTCAT C    CAATCG
                                     T GACC     ATT
GAM240  KIAA0125 5'  TTAGCTAACCCAGCTTGCTCCT 28905         _ ATT_     GTTGA
            GG                    TCAGGAGTA G    GTTAGT
                                |||||||||  |    ||||||
                                GGTCCTCGT C    CAATCG
                                     T GACC     ATT
GAM240  KIAA0143 3'  CAATTTAAGCTGCTTTTGA   64781          ATTGTTAGT
                                TCAGGAGTAG        GTTG
                                ||||||||||        ||||
                                AGTTTTCGTC        TAAC
                                      GAATT_____
GAM240  KIAA0143 3'  TTAACACTGTGTGCTTTTG   64791         G  TGTT
                                CAGGAGTA AT    AGTGTTGA
                                ||||||||  ||    ||||||||
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                                GTTTTCGT TG   TCACAATT
                                    G ____
GAM240  KIAA0179 3' TTAATGCTGGTGATCTTAAC  64832   __   TG
                                GT  AGAT  TTAGTGTTGA
                                ||  ||||  ||||||||||
                                CA  TCTA  GGTCGTAATT
                                 AT   GT
GAM240  KIAA0182 3' TCAAGCCCAGTTTGCTTTTG  72035          TTA  G
                                CAGGAGTAGATTG  GT TTGA
                                ||||||||||||||  || ||||
                                GTTTTCGTTTGAC  CG AACT
                                       C__  _
GAM240  KIAA0205 3' TTGACATTGGCACTAAATGCAT 29592     A  GAT__       TG
           TTGG                   CAGG GTA    TGTTAGTGT  A
                                ||||| |||    |||||||||  |
                                GTTT CGT    ACGGTTACA  T
                                  A  AAATC       GT
GAM240  KIAA0210 5' TCAGTGCTTGTAATCTTTTCTG 28488       T     TT  TG
           A                    TCAGGAG AGATTG  AG  TTGA
                                |||||||  ||||||  ||  ||||
                                AGTCTTT TCTAAT  TC  GACT
                                   _     GT  GT
GAM240  KIAA0210 3' TTGGTTCTGCAATTTGCTCTT  28492          T  TG TG
                                AGGAGTAGATTGT AG  T  A
                                ||||||||||||| ||  |  |
                                TTCTCGTTTAACG TC  G  T
                                      _  TT GT
GAM240  KIAA0240 3' TTAATGTGTTGCCAGAATCTGC 92442        ___  TA_ TG
           TTCTGG                 GAGTAGATT   GT   G  TTGA
                                |||||||||   ||   |  ||||
                                TTCGTCTAA   CG   T  AATT
                                     GAC  TTG GT
GAM240  KIAA0258 3' CAGATACAGCTACTTCTGG   28809         A   TAGTG
                                TCAGGAGTAG TTGT    TTG
                                |||||||||| ||||    |||
                                GGTCTTCATC GACA    GAC
                                     _   TA___
GAM240  KIAA0258 3' GCACTAAAGGCCCTGG     28818      A  AGATTG
                                TCAGG GT     TTAGTGT
                                ||||| ||     |||||||
                                GGTCC CG     AATCACG
                                  _ GA____
GAM240  KIAA0261 3' TTAATGCTAGGGAGGCTCTT  68183       AGA  G
                                AGGAGT   TT TTAGTGTTGA
                                ||||||   || ||||||||||
                                TTCTCG   AG GATCGTAATT
                                   G__  G
GAM240  KIAA0317 5' GCATTGACGGGACCTG     29084      AGTAGA
                                CAGG     TTGTTAGTGT
                                ||||     ||||||||||
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                                GTCC     GGCAGTTACG
                                  AG____
GAM240  KIAA0332  3'  GTGGTTTGCTAACCATTTGCTT 62702          T     TTGA
            TTGA                    TCAGGAGTAGAT GTTAGTG
                                    |||||||||||| |||||||
                                    AGTTTTCGTTTA CAATCGT
                                          C      TTGGTGG
GAM240  KIAA0336  3'  ACTGAAATTTGCTGCTGA    27587     G      G
                                    TCAG AGTAGATT TTAGT
                                    |||| |||||||| |||||
                                    AGTC TCGTTTAA AGTCA
                                      G      _
GAM240  KIAA0354  3'  TTAACAGTTTTTTCTGG     29574       T
                                    TCAGGAG AGATTGTTAG
                                    ||||||| ||||||||||
                                    GGTCTTT TTTGACAATT

                                      _
GAM240  KIAA0408  5'  ATAGTCATCTGACAGTCTCTTT 28131       T       _  TTGA
            TGA                     CAGGAG AGATTGTTAG TG
                                    |||||| |||||||||| ||
                                    GTTTTC TCTGACAGTC AC
                                      _        T  TGATAG
GAM240  KIAA0429  5'  ATTGAGAATGTGCTCCTGA   28550        G   G
                                    TCAGGAGTA ATT TTAGT
                                    ||||||||| ||| |||||
                                    AGTCCTCGT TAA AGTTA
                                         G   G
GAM240  KIAA0446  5'  TGGCATGAGGTTTGCTACTGG  68884     G      GTTA    TG
                                    TCAG AGTAGATT    GTGT  A
                                    |||| ||||||||    ||||  |
                                    GGTC TCGTTTGG    TACG  T
                                      A       AG__    GT
GAM240  KIAA0451  3'  TTAGTGGCCACGTCTATTTCTG 29120          T__    G  TTGA
            A                       TCAGGAGTAGAT   GTTA TG
                                    ||||||||||||   |||| ||
                                    AGTCTTTATCTG   CGGT AT
                                           CAC    G  T
GAM240  KIAA0493  3'  TTAACATACTTACTTCTGG    64284          AT_
                                    TCAGGAGTAG   TGTTAG
                                    ||||||||||   ||||||
                                    GGTCTTCATT   ACAATT
                                          CAT
GAM240  KIAA0495  3'  AATAACTACTTCTGA       62572          A
                                    TCAGGAGTAG TTGTT
                                    |||||||||| |||||
                                    AGTCTTCATC AATAA

                                      _
GAM240  KIAA0534  5'  TTAGCATTGATTCCAGTCTTCT 71437       TAGATT
            G                       CAGGAG     GTTAGTGTTGA
                                    ||||||     ||||||||||
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                                GTCTTC     TAGTTACGATT
                                   TGACCT
GAM240  KIAA0565 3' TCAGAGTAAGAGTCTATTTCTG 66899          G   GTG
             G                  TCAGGAGTAGATT TTA   TTGA
                                |||||||||||| |||   ||||
                                GGTCTTTATCTGA AAT   GACT
                                      G   GA_
GAM240  KIAA0626 5' GAAGCAAGGTGGTTTGCTCGTG 67440     G      TG  AG    GA
             A                  TCA GAGTAGAT  TT  TGTT
                                ||| ||||||||  ||  ||||
                                AGT CTCGTTTG  GG  ACGA
                                  G       GT  A_    AGG
GAM240  KIAA0626 3' TTAATACTAATTGTTCTTTCTG 41335       GT   TT_
             G                  TCAGGA  AGA   GTTAGTGTTGA
                                ||||||  |||   ||||||||||
                                GGTCTT  TCT   TAATCATAATT
                                   __   TGT
GAM240  KIAA0648 3' CAGCATTGTGCTATTT      82652       ATTGT
                                GAGTAG    TAGTGTTG
                                ||||||    ||||||||
                                TTTATC    GTTACGAC
                                   GT___
GAM240  KIAA0669 3' TGGCAATTTACTTATGG     28790     G
                                TCA GAGTAGATTGTTA
                                ||| ||||||||||||
                                GGT TTCATTTAACGGT
                                  A
GAM240  KIAA0716 3' TCAAGGTGCAATTTGCTTC    28167          TAG G
                                GGAGTAGATTGT   T TTGA
                                ||||||||||||   | ||||
                                CTTCGTTTAACG   G AACT
                                      T__ G
GAM240  KIAA0716 3' TCAGTGTTATTTGCTCTTGG   28168          TTGT   TG
                                TCAGGAGTAGA    TAG  TTGA
                                ||||||||||    |||  ||||
                                GGTTCTCGTTT    ATT  GACT
                                      ____   GT
GAM240  KIAA0773 3' TCAGCAGGTCATTTGGCTTCTG 28061        A  T  TTAG
             A                  TCAGGAGT GA TG    TGTTGA
                                ||||||| || ||    ||||||
                                AGTCTTCG TT AC    ACGACT
                                     G  T  TGG_
GAM240  KIAA0783 3' TGACATTCTATTTTTGA     27802          T
                                TCAGGAGTAGA TGTTA
                                |||||||||| |||||
                                AGTTTTTATCT ACAGT
                                      T
GAM240  KIAA0788 3' GCAGTGTCTGCTCCTGG     71336          __
                                TCAGGAGTAGAT  TGT
                                |||||||||||  |||
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                                GGTCCTCGTCTG  ACG
                                      TG
GAM240  KIAA0820 3' TTAATGCTGATATATGGACTCT 69031   _     AGAT_
           TAGA                  C AGGAGT    TGTTAGTGTTGA
                                | ||||||    ||||||||||||
                                G TTCTCA    ATAGTCGTAATT
                                 A     GGTAT
GAM240  KIAA0825 3' TGATAGTTTACTTTTGA     61032
                                TCAGGAGTAGATTGTTA
                                ||||||||||||||||
                                AGTTTTCATTTGATAGT

GAM240  KIAA0825 3' TTGTCGTGATAGTTTACTTTTG 61036              GTGTTGA
           A                   TCAGGAGTAGATTGTTA
                               ||||||||||||||||
                               AGTTTTCATTTGATAGT
                                     GCTGTT
GAM240  KIAA0830 3' GCACTGGTATTTATTTCTGA   69699          T TT
                                TCAGGAGTAGAT G  AGTGT
                                ||||||||||| |  |||||
                                AGTCTTTATTTA T  TCACG
                                      _ GG
GAM240  KIAA0844 3' AAGTATATTAATAATTTATTTT 30196              TGA
           T                    AGGAGTAGATTGTTAGTGT
                                ||||||||||||||||||
                                TTTTTATTTAATAATTATA
                                      TGAAT
GAM240  KIAA0847 3' TCAGTGTTGATCTTCTCTTG   77616      T    GTT  TG
                                CAGGAG AGATT   AG  TTGA
                                |||||| |||||   ||  ||||
                                GTTCTC TCTAG   TT  GACT
                                   T    ___  GT
GAM240  KIAA0852 5' TAATGCTAAAAGCTCCT     30081       AGATTG
                                AGGAGT     TTAGTGTTG
                                ||||||     |||||||||
                                TCCTCG     AATCGTAAT
                                   AA____
GAM240  KIAA0852 5' GCATTATCTTCCTGG       30078       GT   TTGT
                                TCAGGA  AGA    TAGTGT
                                ||||||  |||    ||||||
                                GGTCCT  TCT    ATTACG
                                  __   ____
GAM240  KIAA0884 3' TTGATATTGGTAGTGTTTCCT  70209      TAG   TT    TG
                                AGGAG   ATTG  AGTGT  A
                                |||||   ||||  |||||  |
                                TCCTT   TGAT  TTATA  T
                                  TG_   GG    GT
GAM240  KIAA0888 3' ACACATAAAATCTGTTTCTGA  63228          GTTA
                                TCAGGAGTAGATT    GTGT
                                ||||||||||||    ||||
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                                AGTCTTTGTCTAA    CACA
                                      AATA
GAM240  KIAA0913  3'  ACTGACAGCTGCTCTTGG    68961          A
                                TCAGGAGTAG TTGTTAGT
                                |||||||||| ||||||||
                                GGTTCTCGTC GACAGTCA
                                       _
GAM240  KIAA0931  3'  CATTATAGTGTATTTTTGA   67416        G    T
                                TCAGGAGTA ATTGT AGTG
                                ||||||||| ||||| ||||
                                AGTTTTTAT TGATA TTAC
                                     G    _
GAM240  KIAA0972  3'  GCTGTTAGTTTACTCTTGG   30012           T
                                TCAGGAGTAGATTG TAGT
                                |||||||||||||| ||||
                                GGTTCTCATTTGAT GTCG
                                       T
GAM240  KIAA0976  3'  TCAGTCATTCTGATCTGCTTT  29895         GTT   _
                                GGAGTAGATT   AGTG TTGA
                                ||||||||||   |||| ||||
                                TTTCGTCTAG   TTAC GACT
                                     TC_   T
GAM240  KIAA0979  3'  ACCTAGTGTTTACTCCTGG   30441          TGT   T
                                TCAGGAGTAGAT   TAG GT
                                ||||||||||||   ||| ||
                                GGTCCTCATTTG   ATC CA
                                       TG_  _
GAM240  KIAA0993  3'  GAGCCTACAGTCTATTTATGA  64141    G        T  T   GA
                                TCA GAGTAGATTGT AG GTT
                                ||| |||||||||| || |||
                                AGT TTTATCTGACA TC CGA
                                  A         _ _   GT
GAM240  KIAA1001  5'  TTGACATTGATGTCTAATTATT 30295     GAG_    T      TG
            GA                    TCAG    TAGAT GTTAGTGT  A
                                ||||    ||||| ||||||||  |
                                AGTT    ATCTG TAGTTACA  T
                                  ATTA    _       GT
GAM240  KIAA1018  3'  CACATTAGCAGTGTTACTCTTG 30348          _         TGA
            G                     TCAGGAGTAG ATTGTTAGTGT
                                |||||||||| ||||||||||
                                GGTTCTCATT TGACGATTACA
                                     G         C
GAM240  KIAA1018  3'  TAACGCTCTCTGTTCTGA    30353       G    TTGTT
                                TCAGGA TAGA    AGTGTTG
                                |||||| ||||    |||||||
                                AGTCTT GTCT    TCGCAAT
                                   _   C_____
GAM240  KIAA1030  3'  CGGTGCTGGCCTCTCCTG    93332       T  ATT    TG
                                CAGGAG AG   GTTAG  TTG
                                |||||| ||   |||||  |||
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                                GTCCTC TC   CGGTC  GGC
                                  _ ___     GT
GAM240  KIAA1040 3' TCAAAGGAAAATGGTCTGTTCT 72233          TG  AGTG_
            TGA                   TCAGGAGTAGAT  TT     TTGA
                                  ||||||||||||  ||     ||||
                                  AGTTCTTGTCTG  AA     AACT
                                        GT  AAGGA
GAM240  KIAA1046 3' TTAATATTCATAAGGTATATTT 30001        GA__    T
            TTGA                    CAGGAGTA    TTGT AGTGTTGA
                                  ||||||||    |||| ||||||||
                                  GTTTTTAT    AATA TTATAATT
                                       ATGG    C
GAM240  KIAA1054 3' TCGATAGAGGTTTATTCTTG   68453          GTTAG
                                  CAGGAGTAGATT     TGTTGA
                                  ||||||||||||     ||||||
                                  GTTCTTATTTGG     ATAGCT
                                        AG___
GAM240  KIAA1091 3' TGGAATAAATAATCTATTTTAG 69689     AG         AGTGTTGA
            A                      TC  GAGTAGATTGTT
                                  ||  ||||||||||||
                                  AG  TTTATCTAATAA
                                   AT          ATAAGGTT
GAM240  KIAA1102 3' TCAGCATTTACCTAATTTCTGA 69014         _  ATT  T
                                  TCAGGAGT AG   GT AGTGTTGA
                                  ||||||||  ||   ||  ||||||||
                                  AGTCTTTA TC   CA TTACGACT
                                       A  ___  T
GAM240  KIAA1130 3' TTAACACTGTATCCCTAGCTCC 62430         _  ATTGT
            TGA                     TCAGGAGT AG     TAGTGTTGA
                                  ||||||||  ||     |||||||||
                                  AGTCCTCG TC     GTCACAATT
                                       A  CCTAT
GAM240  KIAA1136 3' TCAACTTTAGTTGATTCTTGA  91321         A     TTAGT
                                  TCAGGAGT GATTG     GTTGA
                                  ||||||||  |||||     |||||
                                  AGTTCTTA TTGAT     CAACT
                                       G     TT___
GAM240  KIAA1145 3' TTAACACGAATCTGTTTC     65630          GTTA
                                  GGAGTAGATT    GTGTTGA
                                  ||||||||||    |||||||
                                  CTTTGTCTAA    CACAATT
                                        G___
GAM240  KIAA1164 5' CAATGTTTTGCTCCTGG      69504          TTGTTA TG
                                  TCAGGAGTAGA     G  TTG
                                  ||||||||||||     |  |||
                                  GGTCCTCGTTT     T  AAC
                                         ______ GT
GAM240  KIAA1164 3' TCAATCCAAGTTTACTCTTGA  69508           GTTAGT
                                  TCAGGAGTAGATT     GTTGA
                                  ||||||||||||||     |||||
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                                AGTTCTCATTTGA     TAACT
                                      ACC___
GAM240  KIAA1196 3' TGGTGCTAAGGGTTTCCTGG  61481      GTA   G   TG TG
                                TCAGGA  GATT TTAG  T  A
                                ||||||  |||| ||||  |  |
                                GGTCCT  TTGG AATC  G  T
                                   ___   G   GT GT
GAM240  KIAA1199 3' TGGTGTTGGCGGTCCCTG   72520     AGTA       TG TG
                                CAGG   GATTGTTAG  T  A
                                ||||   |||||||||  |  |
                                GTCC   CTGGCGGTT  G  T
                                  ____       GT GT
GAM240  KIAA1200 3' TCAATATTTGCTTATTTATTCT 62381         T_  T
           T                    AGGAGTAGAT  GT AGTGTTGA
                                ||||||||||  || ||||||||
                                TTCTTATTTA  CG TTATAACT
                                      TT  T
GAM240  KIAA1228 3' TCAATGTTAGCAATTAAGCT  65049    A_       TG
                                AGT  GATTGTTAG  TTGA
                                |||  |||||||||  ||||
                                TCG  TTAACGATT  AACT
                                  AA        GT
GAM240  KIAA1240 3' GCTATGGTCTGTTCTGG    66734      G    TG T
                                TCAGGA TAGAT  T AGT
                                ||||||  |||||  | |||
                                GGTCTT GTCTG  A TCG
                                   _    GT _
GAM240  KIAA1240 3' TCAACTATGGTCTATTTTGGG  66738    AG      TG TAGT
                                TC  GAGTAGAT  T   GTTGA
                                ||  ||||||||  |   |||||
                                GG  TTTATCTG  A   CAACT
                                 GT       GT T___
GAM240  KIAA1244 3' TGATATGTTTCTAACTCTTGA  71994        _  TTGTTA   TG
                                TCAGGAGT AGA     GTGT  A
                                ||||||||  |||     ||||  |
                                AGTTCTCA TCT     TATA  T
                                     A   TTG___    GT
GAM240  KIAA1254 3' TAAAACTGATGAATTATTTCTG 70023         A TG    GTTGA
           A                     TCAGGAGTAG T  TTAGT
                                ||||||||||  |  |||||
                                AGTCTTTATT A  AGTCA
                                      A GT     AAAT
GAM240  KIAA1255 5' TCAGTGCTCACAAGTTTGTCCT 67167       G     _  T  TG
           GG                     TCAGGA TAGATT GT AG  TTGA
                                ||||||  ||||||  ||  ||  ||||
                                GGTCCT GTTTGA CA TC  GACT
                                   _     A  C  GT
GAM240  KIAA1255 5' TCAGAGAGGATGATGTGTTCCT 67166         G  TG  AGTG
           GA                     TCAGGAGTA AT  TT    TTGA
                                ||||||||  ||  ||    ||||
```

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                                AGTCCTTGT TA  AG    GACT
                                     G  GT  GAGA
GAM240  KIAA1284  3'  TTAATATAGGAAATGTTTATTC 63943          TG__ TA
            TTGA                  CAGGAGTAGAT    T  GTGTTGA
                                ||||||||||    |  |||||||
                                GTTCTTATTTG    G  TATAATT
                                      TAAA GA
GAM240  KIAA1323  5'  TTGACATTTTGAAGTTACTTTT 63047          ATTGTT    TG
            GA                    TCAGGAGTAG     AGTGT  A
                                ||||||||||     |||||  |
                                AGTTTTCATT     TTACA  T
                                     GAAGTT    GT
GAM240  KIAA1349  3'  TAGACCCAGCAGTCTCACTTTT 70758        _      AGT   GA
            GG                    TCAGGAGT AGATTGTT   GTT
                                |||||||| ||||||||   |||
                                GGTTTTCA TCTGACGA   CAG
                                     C       CC_   ATT
GAM240  KIAA1357  3'  TCAACATTTGCTAACTTTTGG  71982        AGATT  T
                                TCAGGAGT    GT AGTGTTGA
                                ||||||||    || ||||||||
                                GGTTTTCA    CG TTACAACT
                                     AT___  T
GAM240  KIAA1361  3'  TCAGTGCTAAAGTACTACTGA  62198     G   GATTG   TG
                                TCAG AGTA    TTAG  TTGA
                                |||| ||||    ||||  ||||
                                AGTC TCAT    AATC  GACT
                                  A   GA___   GT
GAM240  KIAA1374  3'  AATATTCTGTTCTTGA      61239          T
                                TCAGGAGTAGA TGTT
                                |||||||||| ||||
                                AGTTCTTGTCT ATAA
                                       T
GAM240  KIAA1416  3'  GATTAAGCAGTCTGGTTTTGTT 86461    _______       AGTGTTGA
            CCTGA                 AG     TAGATTGTT
                                ||     |||||||||
                                TT     GTCTGACGA
                                 GTTTTG       ATT   AGT
GAM240  KIAA1449  3'  GGATACAACAGTGTGCTTTTGG 40451        G     A    GA
                                TCAGGAGTA ATTGTT GTGTT
                                ||||||||| |||||| |||||
                                GGTTTTCGT TGACAA CATAG
                                     G     _     GT
GAM240  KIAA1456  3'  TTAAAATAATGATGTTACTTTT 67009         _ TG   GTG
            GA                    TCAGGAGTAG AT  TTA   TTGA
                                |||||||||| ||  |||   ||||
                                AGTTTTCATT TA  AAT   AATT
                                      G  GT   AA_
GAM240  KIAA1462  3'  TCATGCACACAATTTACTGTTG 91390      G        TA   _
            G                     TCAG AGTAGATTGT  GTGT TGA
                                |||| ||||||||||  |||| |||
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                                GGTT TCATTTAACA  CACG ACT
                                  G        __   T
GAM240  KIAA1464 3' TTGGCATTAGCATGAAACTTGT 68279    G   AGAT       TG
                GG                  TCA GAGT   TGTTAGTGT  A
                                    ||| ||||   ||||||||| |
                                    GGT TTCA   ACGATTACG  T
                                      G   AAGT       GT
GAM240  KIAA1493 3' TTAATCAAATTGCTTCTGA   64168         A  _
                                    TCAGGAGTAG TTG TTAG
                                    |||||||||| ||| ||||
                                    AGTCTTCGTT AAC AATT
                                          A  T
GAM240  KIAA1497 3' TCAGAGGATATTTTGCTTCTGG 67522          T   AGTG
                                    TCAGGAGTAGA TGTT   TTGA
                                    |||||||||| ||||   ||||
                                    GGTCTTCGTTT ATAG   GACT
                                           T   GA__
GAM240  KIAA1509 3' TCGGGGTGTTGATTTATTTCTG 61618           TTA TG
                A                    TCAGGAGTAGATTG  G  TTGA
                                    |||||||||||||  | ||||
                                    AGTCTTTATTTAGT  T  GGCT
                                             TG_ GG
GAM240  KIAA1530 3' TTAATTGAATGATTTATCTTGA 67963      G    TG  AGT
                                    TCAGGA TAGAT  TT  GTTGA
                                    |||||| |||||  ||  |||||
                                    AGTTCT ATTTA  AA  TAATT
                                       _    GT  GT_
GAM240  KIAA1553 3' CAGTGTTAGCTACTCC     91916      GATT    TG
                                    GGAGTA   GTTAG  TTG
                                    ||||||   |||||  |||
                                    CCTCAT   CGATT  GAC
                                       ____    GT
GAM240  KIAA1560 3' ACTGCAGTCTGTTTTTGA    64171           T
                                    TCAGGAGTAGATTGT AGT
                                    |||||||||||||| |||
                                    AGTTTTTGTCTGACG TCA
                                                 _
GAM240  KIAA1600 3' TAGTAACAGTCTACTTTGA   71446     G        G
                                    TCAG AGTAGATTGTTA TG
                                    |||| |||||||||||| ||
                                    AGTT TCATCTGACAAT AT
                                       _         G
GAM240  KIAA1615 3' TCAGTGCTAATGTTCCTCTTTT 68732       TA  TT    TG
                GG                  TCAGGAG  GA  GTTAG  TTGA
                                    |||||||  ||  |||||  ||||
                                    GGTTTTC  CT  TAATC  GACT
                                       TC  TG    GT
GAM240  KIAA1635 3' TCAAGTATGTGGTAATTTGCTC 67864          TT _  _
                CT                  AGGAGTAGATTG  A GTG TTGA
                                    ||||||||||||  | ||| ||||
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                                TCCTCGTTTAAT  T TAT AACT
                                      GG G   G
GAM240  KIAA1641  3'  TTAACACTGATAAGCTTTTC   80211     T  A
                                GAG AG TTGTTAGTGTTGA
                                ||| || ||||||||||||
                                CTT TC AATAGTCACAATT
                                  T  G
GAM240  KIAA1649  3'  TTGGCGCGCTGATTTGCCTCTG 50281      GA       TTA    TG
          A                      TCAG  GTAGATTG   GTGT  A
                                ||||  ||||||||  ||||  |
                                AGTC  CGTTTAGT   CGCG  T
                                  TC       CG_    GT
GAM240  KIAA1677  3'  TTGCGCATGAGTAGTCTATATC 67073      A       _  _    TGA
          TGA                      CAGG GTAGATTG TTA GTGT
                                |||| |||||||| ||| ||||
                                GTCT TATCTGAT AGT CGCG
                                  A       G   A    TT
GAM240  KIAA1715  3'  TGACATTGAATATTCTCTGA   68127      _    GATTG      TG
                                TCAG GAGTA    TTAGTGT  A
                                |||| |||||    |||||||  |
                                AGTC CTTAT    AGTTACA  T
                                  T    A____      GT
GAM240  KIAA1715  3'  TGGCACTGGTACGAATTCTC   68130     T  A   __     TG
                                GAG AG TTGT  TAGTGT  A
                                ||| || ||||  ||||||  |
                                CTC TT AGCA  GTCACG  T
                                  _ A   TG     GT
GAM240  KIAA1715  3'  TTAGTAAAATGTCCTATTTCTG 68133          _ TG_   G  TTGA
          A                      TCAGGAGTAG AT   TTA TG
                                |||||||||| ||   ||| ||
                                AGTCTTTATC TG   AAT AT
                                      C  TAA   G  T
GAM240  KIAA1750  3'  GGGAGATTGGTAGTCTCTTTTG 68250        T     TT   G  GA
          A                      TCAGGAG AGATTG  AGT TT
                                |||||||  ||||||  ||| ||
                                AGTTTTC TCTGAT  TTA AG
                                    _     GG   G  GGT
GAM240  KIAA1754  3'  CTTGCAGTTTACTTCTGG    63235             T
                                TCAGGAGTAGATTGT AG
                                |||||||||||||| ||
                                GGTCTTCATTTGACG TC
                                          T
GAM240  KIAA1771  3'  GATAATTTATTCTGGA      79136    A
                                TC GGAGTAGATTGTT
                                || ||||||||||||
                                AG TCTTATTTAATAG
                                 G
GAM240  KIAA1912  3'  TTAATATTAACAATTTCAACT  73369     __
                                AGT  AGATTGTTAGTGTTGA
                                |||  ||||||||||||||||
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                                TCA  TTTAACAATTATAATT
                                  AC
GAM240  KIAA1941  3'  ACGCTAAGCCACCCTGG     74834       A  AGATTG
                                TCAGG GT     TTAGTGT
                                ||||| ||     |||||||
                                GGTCC CA     AATCGCA
                                  _  CCG___
GAM240  KIAA1987  3'  CACCACAATCACTTCTGG    88012         A     TA
                                TCAGGAGT GATTGT  GTG
                                |||||||| ||||||  |||
                                GGTCTTCA CTAACA  CAC
                                     _     C_
GAM240  KIF13B    3'  CACTGAGAAGTTTGTTTTTGG 82821           G_
                                TCAGGAGTAGATT  TTAGTG
                                ||||||||||||  ||||||
                                GGTTTTTGTTTGA  AGTCAC
                                       AG
GAM240  KIF13B    3'  CACTGAGAAGTTTGTTTTTGG 30905           G_
                                TCAGGAGTAGATT  TTAGTG
                                ||||||||||||  ||||||
                                GGTTTTTGTTTGA  AGTCAC
                                       AG
GAM240  KLHL8     3'  TGATACTTCCTGCTTTTG    62857         ATTGTT    TG
                                CAGGAGTAG     AGTGT  A
                                |||||||||     |||||  |
                                GTTTTCGTC     TCATA  T
                                     CT_____    GT
GAM240  LAP1B     3'  TCAATTCGTAACAGTTTATTTT 64588    AG          GT_
           GGA                    TC  GAGTAGATTGTTA   GTTGA
                                ||  ||||||||||||   |||||
                                AG  TTTATTTGACAAT   TAACT
                                  GT          GCT
GAM240  LEC3      5'  AACAGTCATTCTTGA      30857         A
                                TCAGGAGT GATTGTT
                                |||||||| |||||||
                                AGTTCTTA CTGACAA
                                         _
GAM240  LIN-7-C   3'  TTAATATTAAAATGTACTTTT  37166        G   G
                                AGGAGTA ATT TTAGTGTTGA
                                ||||||| ||| ||||||||||
                                TTTTCAT TAA AATTATAATT
                                   G  _
GAM240  LOXL4     3'  GGGGCTCTGATTTGCTCTTG   49870           GTT  T   GA
                                CAGGAGTAGATT   AG GTT
                                ||||||||||||   || |||
                                GTTCTCGTTTAG   TC CGG
                                       ___  T   GGT
GAM240  M9        5'  TCAGTGTTAGCCTCCAGCCCTG 61681       A  AGATT    TG
           G                     TCAGG GT    GTTAG  TTGA
                                ||||| ||    |||||  ||||
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                                GGTCC CG    CGATT  GACT
                                  _ ACCTC    GT
GAM240  MAPK8IP3  3'  TCAGCACTGGCCATGACTTCTG 52993        AG  T
            G                    TCAGGAGT  AT GTTAGTGTTGA
                                 ||||||||  || ||||||||||
                                 GGTCTTCA  TA CGGTCACGACT
                                     G_  C
GAM240  MAPK8IP3  3'  TCGGCACTGCTCATCTTTTGG  52995       TAGATT  T
                                 TCAGGAG     GT AGTGTTGA
                                 |||||||     || ||||||||
                                 GGTTTTC     CG TCACGGCT
                                     TACT__ _
GAM240  MBLR    3'  ATTGATACCTTGCAATAGTATT 49625     _____    TA_   TG
            GCTTCTGA               GTAG   ATTGT   GTGT  A   T
                                 ||||   |||||  ||||  |  |
                                 CGTT   TAACG   CATA  T   A
                                   ATGA    TTC    GT
GAM240  MBLR    3'  TTAGCATTGTGATGCTTTCTGA 49628       _  GATTGT
                                 TCAGGA GTA     TAGTGTTGA
                                 ||||||| |||     |||||||||
                                 AGTCTT CGT     GTTACGATT
                                     T   AGT___
GAM240  MEGF10   3'  TCAATATTAGTAGTCCACTTT  50584      A
                                 GGAGT GATTGTTAGTGTTGA
                                 ||||| ||||||||||||||
                                 TTTCA CTGATGATTATAACT
                                   C
GAM240  MEGF10   3'  TGACATTGATGTCACTCTT   50585      A   T      TG
                                 AGGAGT GAT GTTAGTGT  A
                                 |||||| ||| ||||||||  |
                                 TTCTCA CTG TAGTTACA  T
                                     _  _      GT
GAM240  METAP1   3'  GCAGTGATTTAATTCCTGG   72639       AGATT   G
                                 TCAGGAGT    GTTA TGT
                                 ||||||||    |||| |||
                                 GGTCCTTA    TAGT ACG
                                     ATT__   G
GAM240  MGC11034  3'  TTAATATTTTTTGTATTTGCTC 48791         TGTT__
            TTG                   AGGAGTAGAT     AGTGTTGA
                                 ||||||||||     ||||||||
                                 TTCTCGTTTA     TTATAATT
                                     TGTTTT
GAM240  MGC11034  3'  TTAGTGTTAGCAGTTGAC    48792    A       TG
                                 GT GATTGTTAG  TTGA
                                 || |||||||||  ||||
                                 CA TTGACGATT  GATT
                                  G       GT
GAM240  MGC1203   3'  TCAGCATTGAACAATTATTTTT 44155       A    _
                                 AGGAGT GATTGT TAGTGTTGA
                                 |||||| |||||| |||||||||
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                                TTTTTA TTAACA GTTACGACT
                                  _     A
GAM240  MGC1223  3' ACATTGAGAACCCTGA      48239       A  AGAT G
                                TCAGG GT    T TTAGTGT
                                ||||| ||    | |||||||
                                AGTCC CA    A AGTTACA
                                  _ ____ G
GAM240  MGC12945 5' TGCTAAGTGGTCGGTTCCTGG  50299        TA   TG _
                                TCAGGAG  GAT  TT AGTG
                                |||||||  |||  || ||||
                                GGTCCTT  CTG  GA TCGT
                                    GG   GT  A
GAM240  MGC13007 5' TCCTGATGGCATATCTATTCCT 50306           _    GTGTTGA
           GA                     TCAGGAGTAGAT TGTTA
                                |||||||||||| |||||
                                AGTCCTTATCTA ACGGT
                                      T     AGTCCT
GAM240  MGC14161 5' CAGCAGCAATTTATTCTT     51839           TAG
                                AGGAGTAGATTGT   TGTTG
                                ||||||||||||   |||||
                                TTCTTATTTAACG   ACGAC
                                     ___
GAM240  MGC15397 3' TCAGAAAGGACACTCTGCTCTT 54682           T    AGTG
           GA                     TCAGGAGTAGA TGTT    TTGA
                                |||||||||| ||||    ||||
                                AGTTCTCGTCT ACAG    GACT
                                      C    GAAA
GAM240  MGC15606 3' AATAACTACTTTTGG       58873          A
                                TCAGGAGTAG TTGTT
                                |||||||||| |||||
                                GGTTTTCATC AATAA
                                     _
GAM240  MGC16384 5' TCAGTACCTGTCTCTGCTCTT  53869         TTGTTA
                                AGGAGTAGA     GTGTTGA
                                |||||||||     |||||||
                                TTCTCGTCT     CATGACT
                                    CTGTC_
GAM240  MGC20481 3' TTAGTGTTTGACACTACTCCTG 62715          AT    _ TG
           G                      TCAGGAGTAG  TGTTA G  TTGA
                                |||||||||  ||||| |  ||||
                                GGTCCTCATC  ACAGT T  GATT
                                     __     T GT
GAM240  MGC2647  3' TCAACATTCTTTTCTGTTCTTG 73708           TTGTT
           G                      TCAGGAGTAGA     AGTGTTGA
                                ||||||||||     ||||||||
                                GGTTCTTGTCT     TTACAACT
                                      TTTC_
GAM240  MGC27016 3' TATTCAGTGGTTTCTCTTGA   58680        T   TG _
                                TCAGGAG AGAT  TT AGTG
                                ||||||| ||||  || ||||
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                                AGTTCTC TTTG  GA TTAT
                                   _   GT  C
GAM240  MGC2963  3' TATAAATAATTTATATCTGA  48510      A        A
                                TCAGG GTAGATTGTT GTG
                                ||||| |||||||||| |||
                                AGTCT TATTTAATAA TAT
                                   A        A
GAM240  MGC3040  3' TTAATAACTATTCTTGA    66846          A
                                TCAGGAGTAG TTGTTAG
                                |||||||||| |||||||
                                AGTTCTTATC AATAATT
                                      _
GAM240  MGC3771  3' TTGAGTTTGCAACTCTGCTTTT 48248          _   TAGTGTTGA
           GG                    TCAGGAGTAGA TTGT
                                |||||||||| ||||
                                GGTTTTCGTCT AACG
                                      C   TTTGAGTT
GAM240  MGC4189  3' GACATCTGTTCTTGG      50230          T
                                TCAGGAGTAGAT GTT
                                |||||||||| |||
                                GGTTCTTGTCTA CAG
                                      _
GAM240  MGC4504  3' TGACACTGACTTACTACTT   44113      ATT      TG
                                GAGTAG  GTTAGTGT  A
                                ||||||  |||||||  |
                                TTCATC  CAGTCACA  T
                                   ATT      GT
GAM240  MGC4707  3' TAAGAGCAGTCTCTTCTGA   44122       T      AG
                                TCAGGAG AGATTGTT  TG
                                ||||||| |||||||  ||
                                AGTCTTC TCTGACGA  AT
                                   _      GA
GAM240  MGC4734  3' TCAGGCCATGTGTTTGCTTCTG 58951          TGTTA  __
           G                    TCAGGAGTAGAT   GTG  TTGA
                                |||||||||||   |||  ||||
                                GGTCTTCGTTTG   TAC  GACT
                                      TG___  CG
GAM240  MIG-6    3' CAGCATCTTTCTGCTTTGA   38487     G    TTGTTA
                                TCAG AGTAGA    GTGTTG
                                |||| ||||||    ||||||
                                AGTT TCGTCT    TACGAC
                                   _    TTC___
GAM240  MIL1     3' TGGCACTAGTGCTGTTCTGA  31099      G  ATTG     TG
                                TCAGGA TAG   TTAGTGT  A
                                |||||| |||   |||||||  |
                                AGTCTT GTC   GATCACG  T
                                   _  GT__     GT
GAM240  MISS     3' TTAGTAGTTTATTTCTG    58032
                                CAGGAGTAGATTGTTAG
                                |||||||||||||||||
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                                GTCTTTATTTGATGATT

GAM240  MKP-7    3'  GATAATCAGTTCTTGG      66418        TA
                                TCAGGAG  GATTGTT
                                |||||||  |||||||
                                GGTTCTT  CTAATAG
                                    GA
GAM240  MORF4    3'  TTGACAAAGCTGCTTTTGA    90788          A_
                                TCAGGAGTAG  TTGTTAG
                                ||||||||||  |||||||
                                AGTTTTCGTC  AACAGTT
                                      GA
GAM240  MRG15    3'  TTGACAAAGCTGCTTTTGA    22304          A_
                                TCAGGAGTAG  TTGTTAG
                                ||||||||||  |||||||
                                AGTTTTCGTC  AACAGTT
                                      GA
GAM240  MSE55    5'  GAACATCTATAGCTGCTTCTGA 22942          A    TA    GA
                                TCAGGAGTAG TTGT  GTGTT
                                |||||||||| ||||  |||||
                                AGTCTTCGTC GATA  TACAA
                                      _   TC    GT
GAM240  MYH10    3'  TCAGTGTTAATTCTAAATCCTT 69144    _  G_   TT    TG
              GA                  TCA GGA  TAGA  GTTAG  TTGA
                                ||| |||  ||||  |||||  ||||
                                AGT CCT  ATCT  TAATT  GACT
                                  T  AA   __    GT
GAM240  N4BP1    3'  TAGCAGTTACTCTTGA      27835        A
                                TCAGGAGT GATTGTTA
                                |||||||| ||||||||
                                AGTTCTCA TTGACGAT
                                    _
GAM240  N4BP3    3'  CAGCCCCAGTCTGTCTTGG    66253       G      TTAGT
                                TCAGGA TAGATTG    GTTG
                                |||||| |||||||    ||||
                                GGTTCT GTCTGAC    CGAC
                                    _      CC___
GAM240  NDP52    3'  TTAGCACTTTCTACTCTCTGA  19537     _     TTGTT
                                TCAG GAGTAGA    AGTGTTGA
                                |||| |||||||    ||||||||
                                AGTC CTCATCT    TCACGATT
                                  T      T____
GAM240  NET-2    3'  TCAATATTGGTGACTACCT    24705    A    A TG
                                GG GTAG T  TTAGTGTTGA
                                || |||| |  ||||||||||
                                TC CATC A  GGTTATAACT
                                 _   _ GT
GAM240  NETO2    3'  TCAGTATAGGCATTTGTTCTTG 36116          T  TA
              A                  TCAGGAGTAGAT GT  GTGTTGA
                                ||||||||||| ||  |||||||
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                                AGTTCTTGTTTA CG  TATGACT
                                      _  GA
GAM240  NPD009   5'  TCAGTGCTAATCCGTCGTTCTT 95052     GTA  T_   TG
                                AGGA  GAT  GTTAG  TTGA
                                ||||  |||  |||||  ||||
                                TTCT  CTG  TAATC  GACT
                                  TG_  CC    GT
GAM240  NSG-X    3'  GACGGGCTGTTCCTGA     26971         A
                                TCAGGAGTAG TTGTT
                                |||||||||| |||||
                                AGTCCTTGTC GGCAG
                                      G
GAM240  NXPH3    3'  GCGCTGATGTTTGCT      65763        T
                                AGTAGAT GTTAGTGT
                                ||||||| ||||||||
                                TCGTTTG TAGTCGCG
                                      _
GAM240  OAZIN    5'  CAACGCTGAGCCACCTTGG   31874      A  AGATTG
                                TCAGG GT     TTAGTGTTG
                                ||||| ||     |||||||||
                                GGTTC CA     AGTCGCAAC
                                  _  CCG___
GAM240  OBTP     5'  TGTTAGTGGCTACTCCTGG   34251         A TG  GT
                                TCAGGAGTAG T  TTA  G
                                |||||||||| |  |||  |
                                GGTCCTCATC G  GAT  T
                                      _ GT  TG
GAM240  OIP5     3'  TTAATGTTGACTTCTATTACTC 62785        ATT__    TG
           CTG                   CAGGAGTAG    GTTAG  TTGA
                                |||||||||    |||||  ||||
                                GTCCTCATT    CAGTT  AATT
                                     ATCTT    GT
GAM240  OR7C1    3'  TTAATACTTATTATATTTCTGG 33997        GATT  T
                                TCAGGAGTA   GT AGTGTTGA
                                |||||||||   || ||||||||
                                GGTCTTTAT   TA TCATAATT
                                     AT__  T
GAM240  OSBPL1A  3'  TTAGTGCTCTGAATTTACTTTT 55744         GTT  TG
                                AGGAGTAGATT   AG  TTGA
                                ||||||||||   ||  ||||
                                TTTTCATTTAA   TC  GATT
                                      GTC  GT
GAM240  OSBPL1A  3'  TTAGTGCTCTGAATTTACTTTT 35911         GTT  TG
                                AGGAGTAGATT   AG  TTGA
                                ||||||||||   ||  ||||
                                TTTTCATTTAA   TC  GATT
                                      GTC  GT
GAM240  OSBPL1A  3'  TTAGTGCTCTGAATTTACTTTT 54585         GTT  TG
                                AGGAGTAGATT   AG  TTGA
                                ||||||||||   ||  ||||
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                                TTTTCATTTAA  TC  GATT
                                     GTC  GT
GAM240  P15-2   3'  TAATATTTTCTATTCCTG   38009        TTGTT
                                CAGGAGTAGA   AGTGTTG
                                ||||||||||   |||||||
                                GTCCTTATCT   TTATAAT
                                     T____
GAM240  P5326   3'  TGACATGTGCCTGCTCCTGG  48774        ATT  TA   TG
                                TCAGGAGTAG  GT  GTGT  A
                                ||||||||||  ||  ||||  |
                                GGTCCTCGTC  CG  TACA  T
                                     ___ TG   GT
GAM240  PARG1   3'  CAGTGCATTTCCTCTTGA   16681       T   TGTTA TG
                                TCAGGAG AGAT   G  TTG
                                ||||||| ||||   |  |||
                                AGTTCTC TTTA   C  GAC
                                    C   _____ GT
GAM240  PC4     3'  CAATATTAGCAGATCTA    22012      _
                                TAGAT TGTTAGTGTTG
                                ||||| ||||||||||
                                ATCTA ACGATTATAAC
                                   G
GAM240  PCDH19  3'  CACCAATGGTTGGTTCTTGA  63697       TA  TG  A
                                TCAGGAG  GAT  TT GTG
                                |||||||  |||  || |||
                                AGTTCTT  TTG  AA CAC
                                    GG   GT  C
GAM240  PDCD10  3'  TAAATATTGGTGTTTGTTTCTG 23308         TGT     GA
          A                     TCAGGAGTAGAT   TAGTGTT
                                ||||||||||||   |||||||
                                AGTCTTTGTTTG   GTTATAA
                                      TG_      ATG
GAM240  PDCD10  5'  TCAACTGTAGTTGGCTTTTGA  23309       A    TTAGT
                                TCAGGAGT GATTG    GTTGA
                                |||||||| |||||    |||||
                                AGTTTTCG TTGAT    CAACT
                                    G    GT___
GAM240  PHIP    5'  TCAATGCTACAATGTTTGCTGG 35593     G  TAG    T
                                TCAG AG   ATTGT AGTGTTGA
                                |||| ||   ||||| ||||||||
                                GGTC TT   TAACA TCGTAACT
                                  G  TG_   _
GAM240  PLAA    3'  TTGATATTTGGCTGTTTATTTT 14915         T   _  TG
          TG                    CAGGAGTAGAT GTTAG TGT  A
                                |||||||||| ||||| |||  |
                                GTTTTTATTTG CGGTT ATA  T
                                      T    T  GT
GAM240  PLAGL2  3'  GCACTAGAACTCCTGA     70450        AGATTG
                                TCAGGAGT     TTAGTGT
                                ||||||||     |||||||
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                                AGTCCTCA     GATCACG
                                   A_____
GAM240  PLAGL2   3'  TCAGACTAGATGATTTGCTTCT 70457         TG _  G
                                AGGAGTAGAT  TT AGT TTGA
                                ||||||||||  || ||| ||||
                                TCTTCGTTTA  AG TCA GACT
                                   GT  A  _
GAM240  POPX1    3'  TCAACACTGAGTCTAATTTTGA 29802       G    TG
                                TCAGGA TAGAT  TTAGTGTTGA
                                ||||||| |||||  ||||||||||
                                AGTTTT ATCTG  AGTCACAACT
                                   A    __
GAM240  PPP2R3A  3'  CAGCACTCTACACTCTTGA   10749        AGATT  T_
                                TCAGGAGT    GT  AGTGTTG
                                ||||||||    ||  |||||||
                                AGTTCTCA    CA  TCACGAC
                                     _____  TC
GAM240  PRDM13   3'  GGCGGTCTGCTCTTGG     41239
                                TCAGGAGTAGATTGTT
                                ||||||||||||||||
                                GGTTCTCGTCTGGCGG

GAM240  PRO0233  3'  GCACTGATAGAACTCT     26117      AGA
                                GGAGT   TTGTTAGTGT
                                |||||   ||||||||||
                                TCTCA   GATAGTCACG
                                   A__
GAM240  PRO0233  3'  TTAATGCTAAAATACTTCT   26119       GATTG
                                AGGAGTA    TTAGTGTTGA
                                |||||||    ||||||||||
                                TCTTCAT    AATCGTAATT
                                   AA___
GAM240  PRO0628  5'  TCAGCATTAGCTAGACTTATGA 26208     G   AGATT
                                TCA GAGT    GTTAGTGTTGA
                                |||| ||||    ||||||||||
                                AGT TTCA    CGATTACGACT
                                  A   GAT__
GAM240  PRO1430  3'  TTGATGCTGATAGAAGAGCCTG 37750      AGTAGA       TG
          G                      TCAGG     TTGTTAGTGT  A
                                |||||     |||||||||  |
                                GGTCC     GATAGTCGTA  T
                                   GAGAA_        GT
GAM240  PRO1596  5'  CAGTGCTGTTTGCTTTT     48385         TGTT  TG
                                AGGAGTAGAT   AG  TTG
                                ||||||||||   ||  |||
                                TTTTCGTTTG   TC  GAC
                                     _____  GT
GAM240  PRO1770  5'  TCAAATGACAGCTACTCCTGG  26041         A     GTG
                                TCAGGAGTAG TTGTTA   TTGA
                                |||||||||| ||||||   ||||
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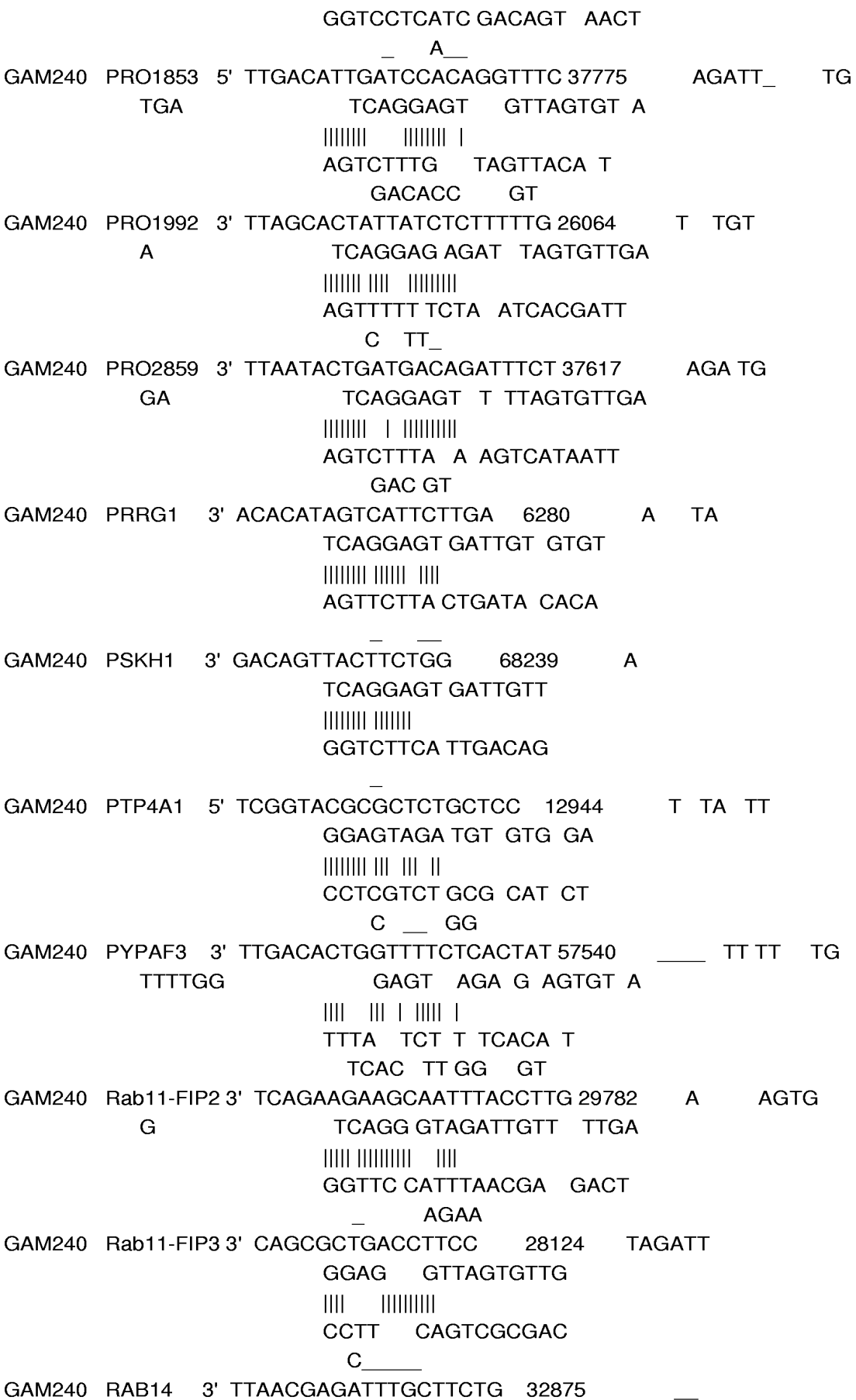
GGTCCTCATC GACAGT AACT
A
GAM240 PRO1853 5' TTGACATTGATCCACAGGTTTC 37775 AGATT TG
TGA TCAGGAGT GTTAGTGT A
AGTCTTTG TAGTTACA T
GACACC GT
GAM240 PRO1992 3' TTAGCACTATTATCTCTTTTTG 26064 T TGT
A TCAGGAG AGAT TAGTGTTGA
AGTTTTT TCTA ATCACGATT
C TT
GAM240 PRO2859 3' TTAATACTGATGACAGATTTCT 37617 AGA TG
GA TCAGGAGT T TTAGTGTTGA
AGTCTTTA A AGTCATAATT
GAC GT
GAM240 PRRG1 3' ACACATAGTCATTCTTGA 6280 A TA
TCAGGAGT GATTGT GTGT
AGTTCTTA CTGATA CACA
GAM240 PSKH1 3' GACAGTTACTTCTGG 68239 A
TCAGGAGT GATTGTT
GGTCTTCA TTGACAG
GAM240 PTP4A1 5' TCGGTACGCGCTCTGCTCC 12944 T TA TT
GGAGTAGA TGT GTG GA
CCTCGTCT GCG CAT CT
C GG
GAM240 PYPAF3 3' TTGACACTGGTTTTCTCACTAT 57540 TT TT TG
TTTTGG GAGT AGA G AGTGT A
TTTA TCT T TCACA T
TCAC TT GG GT
GAM240 Rab11-FIP2 3' TCAGAAGAAGCAATTTACCTTG 29782 A AGTG
G TCAGG GTAGATTGTT TTGA
GGTTC CATTTAACGA GACT
AGAA
GAM240 Rab11-FIP3 3' CAGCGCTGACCTTCC 28124 TAGATT
GGAG GTTAGTGTTG
CCTT CAGTCGCGAC
C
GAM240 RAB14 3' TTAACGAGATTTGCTTCTG 32875
CAGGAGTAGATT GTTAG

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                                GTCTTCGTTTAG  CAATT
                                      AG
GAM240  RAB17    3'  TCAATGCTGGGTTGCTCCCGA  42390    A     ATTGT
                                TC GGAGTAG    TAGTGTTGA
                                || |||||||    |||||||||
                                AG CCTCGTT    GTCGTAACT
                                 C      GG___
GAM240  RAB22A   3'  TCATCCTGGGTTTGCTTCTGA  59932          GT   TGT
                                TCAGGAGTAGATT  TAG   TGA
                                ||||||||||||  |||   |||
                                AGTCTTCGTTTGG  GTC   ACT
                                       __  CT_
GAM240  RAB3GAP  3'  TTAACACACTATTTTGCTTTTG 66951         TT_  TA
                                CAGGAGTAGA   GT  GTGTTGA
                                ||||||||||   ||  |||||||
                                GTTTTCGTTT   CA  CACAATT
                                      TAT  __
GAM240  RAB40B   3'  TTAGTACTCTGCTCGACTCTTG 22377        A  TT  T_
           G                     TCAGGAGT GA  GT  AGTGTTGA
                                |||||||| ||  ||  ||||||||
                                GGTTCTCA CT  CG  TCATGATT
                                     G  __  TC
GAM240  RANBP6   3'  TCAGCACTAGGGAAGATTTTGA 61639       GTAGA  G
                                TCAGGA    TT TTAGTGTTGA
                                ||||||    || ||||||||||
                                AGTTTT    AG GATCACGACT
                                   AGA__  G
GAM240  RBT1     3'  TTAACGAGACTCTGTTTCTGG  25355         TT   AG
                                TCAGGAGTAGA  GTT  TGTTGA
                                ||||||||||  |||  ||||||
                                GGTCTTTGTCT  CAG  GCAATT
                                      __  A_
GAM240  RER1     3'  TTAACTACCATGATTGCTTTTG 22867         AT_  T   GTTGA
           A                     TCAGGAGTAG   TG TAGT
                                ||||||||||   || ||||
                                AGTTTTCGTT   AC ATCA
                                      AGT  C   ATT
GAM240  RI58     3'  AGCACTGAAGTCCTGA     24845       GTAGATTG
                                TCAGGA      TTAGTGTT
                                ||||||      ||||||||
                                AGTCCT      AGTCACGA
                                   GA_______
GAM240  RP4-622L5 3'  AGCATTCCTGCCCTGG     38927      A   ATTGTT
                                TCAGG GTAG     AGTGTT
                                ||||| ||||     ||||||
                                GGTCC CGTC     TTACGA
                                  _   C______
GAM240  RPL34    3'  TCACTAATATAGTATGCTCTTG 53247         GAT__      TTGA
           G                     TCAGGAGTA    TGTTAGTG
                                |||||||||    ||||||||
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                                GGTTCTCGT    ATAATCAC
                                     ATGAT       T
GAM240  RPL34    3'  TCACTAATATAGTATGCTCTTG 6396         GAT__      TTGA
            G                    TCAGGAGTA    TGTTAGTG
                                 |||||||||    ||||||||
                                 GGTTCTCGT    ATAATCAC
                                      ATGAT       T
GAM240  RPS6KA4  3'  GCACAGCTACTCCTGG      14143         ATTGTTA
                                 TCAGGAGTAG      GTGT
                                 ||||||||||      ||||
                                 GGTCCTCATC      CACG
                                       GA_____
GAM240  RTN4IP1  5'  CATGCACTGCGGTTTGCTTCTG 51192             T    TGA
            G                    TCAGGAGTAGATTGT AGTGT
                                 ||||||||||||||| |||||
                                 GGTCTTCGTTTGGCG TCACG
                                        _    TACG
GAM240  S100Z    5'  TTGGTGGCCTGCTTCTGG    55378         A TG
                                 TCAGGAGTAG T  TTAG
                                 |||||||||| |  ||||
                                 GGTCTTCGTC G  GGTT
                                       C GT
GAM240  S164     5'  TTAGCTAAATGTGGTTTGGTTT 60784       G    TG TAGT_
            TGA                    TCAGGA TAGAT  T    GTTGA
                                 |||||| |||||  |    |||||
                                 AGTTTT GTTTG  G    CGATT
                                    G    GT TAAAT
GAM240  SAMHD1   3'  CATTGTGGTTTACTCTGA    61310     G      TG T
                                 TCAG AGTAGAT  T AGTG
                                 |||| |||||||  | ||||
                                 AGTC TCATTTG  G TTAC
                                   _      GT _
GAM240  SAP30    5'  TCAGCACTGTCCACTGTTTC   13914       ATTGT
                                 GGAGTAG    TAGTGTTGA
                                 |||||||    |||||||||
                                 CTTTGTC    GTCACGACT
                                      ACCT_
GAM240  SAST     5'  CACCACGGTCTACTTCT     62977           TA
                                 AGGAGTAGATTGT  GTG
                                 ||||||||||||  |||
                                 TCTTCATCTGGCA  CAC
                                       C_
GAM240  SBB103   3'  TTAATACTGTGGCTTATACCTG 19363      A    A TG T
            A                    TCAGG GTAG T  T AGTGTTGA
                                 ||||| |||| |  | ||||||||
                                 AGTCC TATT G  G TCATAATT
                                   A    C GT _
GAM240  SCYA20   5'  TCAACACTGAGCAGATCTGTTC 15972          _ _
            TT                     AGGAGTAGAT TG TTAGTGTTGA
                                 |||||||||| || ||||||||||
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                                TTCTTGTCTA AC AGTCACAACT
                                      G  G
GAM240  SDCBP    3'  TTGACACTTTATCCTGA     18844       G    T
                                TCAGGA TAGA TGTTAG
                                |||||| |||| ||||||
                                AGTCCT ATTT ACAGTT
                                   _    C
GAM240  SEC15B   3'  TTAATGAGTGATGTAATCACTT 66691       A   __   G_
            CTGA                    AGGAGT GATT  GTTA  TGTTGA
                                |||||| ||||  ||||  ||||||
                                TCTTCA CTAA  TAGT  GTAATT
                                   _   TG   GA
GAM240  SEMA3C   3'  TCAACACTATATATTTTAT   21063      T  _
                                GTAGA TGT TAGTGTTGA
                                ||||| ||| |||||||||
                                TATTT ATA ATCACAACT
                                   T   T
GAM240  SENP2    3'  AACTATTTATTTCTGA      76344           T
                                TCAGGAGTAGAT GTT
                                |||||||||||| |||
                                AGTCTTTATTTA CAA
                                       T
GAM240  SENP8    3'  TTAATACTCTTTTTCCTGA   59092       T_  T
                                TCAGGAG  AGA TGTTAG
                                |||||||  ||| ||||||
                                AGTCCTT  TCT ATAATT
                                     TT   C
GAM240  SERHL    3'  AACACTGGGACTCTGA      95603     G   AGATTGT
                                TCAG AGT      TAGTGTT
                                |||| |||      |||||||
                                AGTC TCA      GTCACAA
                                  _   GG_____
GAM240  Sfmbt    3'  TCAGCACTGATTTGGGACTGTT 32898        ATT___
            CCT                    GGAGTAG     GTTAGTGTTGA
                                |||||||     ||||||||||||
                                CCTTGTC     TAGTCACGACT
                                     AGGGTT
GAM240  SFRS10   3'  TACGATGACTACTTTTGG    15979         A TG  A
                                TCAGGAGTAG T  TT GTG
                                |||||||||| |  || |||
                                GGTTTTCATC A  AG CAT
                                      _ GT  _
GAM240  ShrmL    3'  GGGTTATTGGTGTTTGTTCCTG 40467          TGT    TTGA
            A                   TCAGGAGTAGAT   TAGTG
                                ||||||||||||   |||||
                                AGTCCTTGTTTG   GTTAT
                                       TG_    TGGGT
GAM240  SLC11A2  3'  CTGATGATATTTACTCTTGA  5235          __ TG
                                TCAGGAGTAGA  T  TTAG
                                ||||||||||  |  ||||
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                                AGTTCTCATTT  A  AGTC
                                      AT GT
GAM240  SLC2A10  3'  TCAATATTGCCTTTGCCTCTTG 47826       TA  TT  T
            G                   TCAGGAG  GA  GT AGTGTTGA
                                |||||||  ||  || ||||||||
                                GGTTCTC  TT  CG TTATAACT
                                    CG  TC  _
GAM240  SLC5A7   3'  TTAATGTTACAGCATCTACTCT 41517         T  __  TG
            T                   AGGAGTAGAT GT  TAG  TTGA
                                |||||||||| ||  |||  ||||
                                TTCTCATCTA CG  ATT  AATT
                                      _ AC  GT
GAM240  SP192    3'  TTAATGCTAATAATTTG     41312
                                TAGATTGTTAGTGTTGA
                                ||||||||||||||||
                                GTTTAATAATCGTAATT

GAM240  SPC12    3'  TCAGCACCTGCTTTTGTTTCTG 95826         TT  TA
                                CAGGAGTAGA  GT  GTGTTGA
                                ||||||||||  ||  |||||||
                                GTCTTTGTTT  CG  CACGACT
                                      T_  TC
GAM240  SS18L1   3'  GTTTAGCTGATGGTCATTTCTG 65348        A  TG    GTTGA
            G                   TCAGGAGT GAT  TTAGT
                                |||||||| |||  |||||
                                GGTCTTTA CTG  AGTCG
                                    _  GT    ATTTGT
GAM240  SSH2     3'  GAATGCAACGTTTTATTTTTGG 62206         T   A    GA
                                TCAGGAGTAGA TGTT GTGTT
                                |||||||||||| |||| |||||
                                GGTTTTTATTT GCAA CGTAA
                                      T   _    GT
GAM240  ST13     3'  TTAACTCAAGAACAGTTTCTTC 14119       T      AGT__
            TGG                   CAGGAG AGATTGTT    GTTGA
                                |||||| ||||||||    |||||
                                GTCTTC TTTGACAA    CAATT
                                   _       GAACT
GAM240  STK17A   3'  TCAACACTCTGGTTACCTTGG  16477      A   ATTGTT
                                TCAGG GTAG     AGTGTTGA
                                ||||| ||||     ||||||||
                                GGTTC CATT     TCACAACT
                                   _   GGTC__
GAM240  STK38L   3'  TCTAGTATGGTAACTATTCTTG 69175         A   TT GTGTT
            A                   TCAGGAGTAG TTG  A    GA
                                |||||||||| |||  |    ||
                                AGTTCTTATC AAT  T    CT
                                      _  GG ATGAT
GAM240  SYAP1    3'  TCAAAAATATAATTTATTCCT  51405          TAGTG
                                AGGAGTAGATTGT    TTGA
                                ||||||||||||    ||||
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                                TCCTTATTTAATA    AACT
                                      TAAA_
GAM240  T2BP    3'  TTCAGACTGTCAGTCTATTCCT 69999           T   G
          GG                  TCAGGAGTAGATTG TAGT TTGA
                              |||||||||||||| |||| ||||
                              GGTCCTTATCTGAC GTCA GACT
                                    T   _   TA
GAM240  TA-KRP  3'  CAGCATTTTTTTTTCCTGG   50690       T   TTGTT
                              TCAGGAG AGA    AGTGTTG
                              ||||||| |||    |||||||
                              GGTCCTT TTT    TTACGAC
                                  _  TT___
GAM240  TA-LRRP 3'  TTAACACTAACCTGAAGTTTTG 31073    G   TAGATT_
          TGA                   TCA GAG     GTTAGTGTTGA
                              ||| |||      ||||||||||
                              AGT TTT      CAATCACAATT
                                G   TGAAGTC
GAM240  TAF9L   3'  CTAATATGGCAATTCTGTTTTT 32002         _    G    A
          GA                  TCAGGAGTAGA TTGTTA TGTTG
                              |||||||||| |||||| |||||
                              AGTTTTTGTCT AACGGT ATAAT
                                    T    _    CC
GAM240  TBLR1   3'  CAGCAGTAGTTTGTTCTTG   45099         TGT  G    A
                              CAGGAGTAGAT   TA TGTTG
                              ||||||||||   || |||||
                              GTTCTTGTTTG   AT ACGAC
                                    ___ G    G
GAM240  TIGD5   3'  TTAACACATTAAATCTGTTTTT 51703         GTTA
                              AGGAGTAGATT    GTGTTGA
                              ||||||||||    |||||||
                              TTTTTGTCTAA    CACAATT
                                    ATTA
GAM240  TLR10   5'  TCAACATTAATACTATTATTTG 48230      _    AT
          G                    TCAGG AGTAG  TGTTAGTGTTGA
                              ||||| |||||  ||||||||||||
                              GGTTT TTATC  ATAATTACAACT
                                 A    __
GAM240  TM4-B   5'  TCAGCATTGGCGCCCCTTCCT  24971      TAGAT
                              AGGAG    TGTTAGTGTTGA
                              |||||    ||||||||||||
                              TCCTT    GCGGTTACGACT
                                 CCCC_
GAM240  TP53INP1  3'  TCAGCATTGTTTCTGCTTCTGA 52730         TTGT
                              TCAGGAGTAGA    TAGTGTTGA
                              ||||||||||    |||||||||
                              AGTCTTCGTCT    GTTACGACT
                                    TT__
GAM240  TP53INP1  3'  TCAGCATTGTTTCTGCTTCTGA 72957         TTGT
                              TCAGGAGTAGA    TAGTGTTGA
                              ||||||||||    |||||||||
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                                AGTCTTCGTCT   GTTACGACT
                                      TT__
GAM240  TRAF6   3' GGCAGTTTTTTCCTGG     16094       T
                                TCAGGAG AGATTGTT
                                ||||||| ||||||||
                                GGTCCTT TTTGACGG
                                    T
GAM240  TREX1   5' TTGATAAACCTGCTCCTGA   53284         A_
                                TCAGGAGTAG  TTGTTAG
                                ||||||||||  |||||||
                                AGTCCTCGTC  AATAGTT
                                      CA
GAM240  TREX1   5' TTGATAAACCTGCTCCTGA   53294         A_
                                TCAGGAGTAG  TTGTTAG
                                ||||||||||  |||||||
                                AGTCCTCGTC  AATAGTT
                                      CA
GAM240  TRPV5   3' TTAACATCGCTATCACTCTTGA 39048        A   T  TA
                                TCAGGAGT GAT GT  GTGTTGA
                                |||||||| ||| ||  |||||||
                                AGTTCTCA CTA CG  TACAATT
                                     _  T  C_
GAM240  UBE2D1  3' TCAACATTAGCAGTAAATTGA  12479     GAGTAG
                                TCAG     ATTGTTAGTGTTGA
                                ||||     ||||||||||||||
                                AGTT     TGACGATTACAACT
                                  AAA___
GAM240  UBE2G1  3' TCAATGCTGACAAGAGCCT    12486     AGTAGA
                                AGG     TTGTTAGTGTTGA
                                |||     ||||||||||||
                                TCC     AACAGTCGTAACT
                                  GAG___
GAM240  UBXD2   3' CAAGTCAGTTTGCCTTGA     68342       A       TTAG
                                TCAGG GTAGATTG    TG
                                ||||| ||||||||    ||
                                AGTTC CGTTTGAC    AC
                                   _       TGA_
GAM240  VPS4B   3' TCAGGGAACAGTTTGTCCTGA  16825       G       AGTG
                                TCAGGA TAGATTGTT    TTGA
                                |||||| |||||||||    ||||
                                AGTCCT GTTTGACAA    GACT
                                   _       GG__
GAM240  XPO5    3' TTAGTGCTAACATCCCCTTTAG 91238    AG   TA   T    TG
            A                    TC  GAG  GAT GTTAG  TTGA
                                 ||  |||  ||| |||||  ||||
                                 AG  TTC  CTA CAATC  GATT
                                  AT   CC   _    GT
GAM240  YR-29   5' AGCGGCTGCTCCTGG      29681          A
                                TCAGGAGTAG TTGTT
                                |||||||||| |||||
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                                GGTCCTCGTC GGCGA
                                      _
GAM240  ZER6     3'  TTAGCCCAGCTAACTTTGCTTC 63382         TT     ___
           TGG                    AGGAGTAGA  GTTAGT   GTTGA
                                  |||||||||  ||||||   |||||
                                  TCTTCGTTT  CAATCG   CGATT
                                       __      ACC
GAM240  ZMPSTE24 3'  TCAGGCCTGATTCTACTTTTGA 19596          TT    TG
                                  TCAGGAGTAGA  GTTAG  TTGA
                                  ||||||||||||  |||||  ||||
                                  AGTTTTCATCT  TAGTC  GACT
                                       __    CG    A
GAM240  ZNF238   3'  TCAACACTGCATTGTCTTTTGA 20969        TAGAT   T
                                  TCAGGAG     TGT AGTGTTGA
                                  |||||||     ||| ||||||||
                                  AGTTTTC     ACG TCACAACT
                                      TGTT_  _
GAM240  ZNF294   3'  TTGATGCTGACCTTTTTGCTTG 70833     G      TT_      TG
           TGG                    TCA GAGTAGA   GTTAGTGT  A
                                  ||| |||||||   ||||||||  |
                                  GGT TTCGTTT   CAGTCGTA  T
                                    G      TTC       GT
GAM240  ZNF297   3'  TCAGGTGGTTGTAGTCTGTGCC 18394      AG      TTAGTG_
           TGA                    TCAGG  TAGATTG      TTGA
                                  |||||  |||||||      ||||
                                  AGTCC  GTCTGAT      GACT
                                     GT      GTTGGTG
GAM240  ZNF300   3'  GACACTCTGCTTTTGA      53476          T
                                  TCAGGAGTAGA TGTT
                                  |||||||||||  ||||
                                  AGTTTTCGTCT ACAG
                                        C
GAM240  ZNF317   3'  TTAGTGCTGATAATTCCT     72015       AGAT     TG
                                  AGGAGT    TGTTAG  TTGA
                                  ||||||    ||||||  ||||
                                  TCCTTA    ATAGTC  GATT
                                       ____      GT
GAM240  ZNF323   3'  TCAGCATTATTCTTCTTTTGG  48083       T   TTGT
                                  TCAGGAG AGA    TAGTGTTGA
                                  |||||||  |||    |||||||||
                                  GGTTTTC TCT    ATTACGACT
                                      T   T___
GAM240  LOC115817 3'  TTAGTATTGAAAAATGCTCTTG 56620         GATTG
           G                      TCAGGAGTA     TTAGTGTTGA
                                  |||||||||     ||||||||||
                                  GGTTCTCGT     AGTTATGATT
                                        AAAA_
GAM240  LOC118668 5'  AGCTATTTTATTCCTGA     75479          TT_
                                  TCAGGAGTAGA   GTT
                                  ||||||||||   |||
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                                AGTCCTTATTT   CGA
                                      TAT
GAM240  LOC119467 3'  ATGCTGTACTCCTGA       73982         GATTGT
                                TCAGGAGTA     TAGTGT
                                |||||||||     ||||||
                                AGTCCTCAT     GTCGTA
                                      _______
GAM240  LOC120103 3'  AGCCAAATTCTAATGATTGGCT 74004       A   TG    TG_   A
          CCTGG                   CAGGAGT GAT  TTAG   TTG
                                |||||||| |||  ||||   |||
                                GTCCTCG TTA  AATC   AAC
                                   G   GT    TTA   CGAT
GAM240  LOC120114 3'  CAGTAAGGCTGCTCTTGA    75522         ATTG   G
                                TCAGGAGTAG    TTA TG
                                ||||||||||    ||| ||
                                AGTTCTCGTC    AAT AC
                                      GG__   G
GAM240  LOC120939 5'  TTGGTCACCAGCAATCTGCCTT 76263     GA        A   _ TG
          TGA                     TCAG  GTAGATTGTT GTG T  A
                                ||||  |||||||||| ||| |  |
                                AGTT  CGTCTAACGA CAC G  T
                                  TC         C   T GT
GAM240  LOC121133 3'  CACGCTAATGGGTCTGTTCCTG 75988          _ TG      TGA
          G                       TCAGGAGTAGA T  TTAGTGT
                                ||||||||||| |  |||||||
                                GGTCCTTGTCT G  AATCGCA
                                      G GT      C
GAM240  LOC122792 3'  TTAGCATTTTAATCCATTCTTG 59144        A    TT
          A                       TCAGGAGT GATTG  AGTGTTGA
                                |||||||| |||||  ||||||||
                                AGTTCTTA CTAAT  TTACGATT
                                     C    T_
GAM240  LOC122830 3'  TTGGCATGGCACATTTGTTCTG 74171       G    _    G   TG
          A                       TCAGGA TAGAT TGTTA TGT  A
                                ||||||| ||||| ||||| |||  |
                                AGTCTT GTTTA ACGGT ACG  T
                                   _    C    _   GT
GAM240  LOC122830 3'  TCAATATTAAATTTTCCATTCT 74169        A  TTG_
          TGA                     TCAGGAGT GA    TTAGTGTTGA
                                |||||||| ||    ||||||||||
                                AGTTCTTA CT    AATTATAACT
                                     C  TTTA
GAM240  LOC122830 3'  TCAGCCTTTCAATATGTTTTTG 74170         G    TT  T
          G                       TCAGGAGTA ATTG  AG GTTGA
                                ||||||||| ||||  || |||||
                                GGTTTTTGT TAAC  TC CGACT
                                     A    TT  _
GAM240  LOC124512 3'  TCAATACTGATGAGCAACCTGG 74302       AGTAGA TG
                                TCAGG      T  TTAGTGTTGA
                                |||||      |  ||||||||||
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                                GGTCC     A  AGTCATAACT
                                  AACG__ GT
GAM240   LOC125268 3'  TTAGGACCAGTGGTTTGTCCCT 76083      AG    TG  A  G
           GG                    TCAGG  TAGAT  TT GT TTGA
                                 ||||| |||||  || || ||||
                                 GGTCC  GTTTG  GA CA GATT
                                   CT    GT  C  G
GAM240   LOC126661 3'  GCCAGTCTGGTCTTGA      74551       G      TTAGT
                                 TCAGGA TAGATTG    GT
                                 |||||| |||||||    ||
                                 AGTTCT GTCTGAC    CG
                                   G     _____
GAM240   LOC128977 5'  TTGATGCTCAGTATGTACTTTT 74831         G  TGTT    TG
           GA                    TCAGGAGTA AT   AGTGT  A
                                 ||||||||| ||   ||||| |
                                 AGTTTTCAT TA   TCGTA  T
                                      G  TGAC    GT
GAM240   LOC130074 3'  GCACTGACTGTCCTGG      76133       GTAGATT
                                 TCAGGA      GTTAGTGT
                                 ||||||      ||||||||
                                 GGTCCT      CAGTCACG
                                   GT_____
GAM240   LOC130940 3'  TTGACACTAACTTTTTATTTTT 57140         TT       TG
           G                     CAGGAGTAGA  GTTAGTGT  A
                                 |||||||||  ||||||||  |
                                 GTTTTTATTT  CAATCACA  T
                                      TT       GT
GAM240   LOC131034 3'  TTAATACTTCTACTACTCCTG  55522         ATTGTT
                                 CAGGAGTAG     AGTGTTGA
                                 |||||||||     ||||||||
                                 GTCCTCATC     TCATAATT
                                      ATCT__
GAM240   LOC131870 3'  CAACACTAATACCACTT     75015      AGAT
                                 GAGT    TGTTAGTGTTG
                                 ||||    ||||||||||
                                 TTCA    ATAATCACAAC
                                   CC__
GAM240   LOC133308 3'  TTGACAAGTTTACTTCTGG    75086           _
                                 TCAGGAGTAGATT GTTAG
                                 |||||||||||| |||||
                                 GGTCTTCATTTGA CAGTT
                                        A
GAM240   LOC134957 3'  TTGACTTGTGTATGAGCTACTC 57664         A TG TAGT__  TG
           TTGG                    CAGGAGTAG T  T     GT  A
                                 ||||||||| |  |     ||  |
                                 GTTCTCATC A  A     CA  T
                                      G GT TGTGTT  GT
GAM240   LOC135398 3'  TCAATACTAAGAAATCTCTGA  75937      GAGT    G_
                                 TCAG    AGATT  TTAGTGTTGA
                                 ||||    |||||  ||||||||||
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                                AGTC    TCTAA  AATCATAACT
                                  ____    AG
GAM240   LOC135932 5'  CTGACAGGCTGTTTCTGG    76197         A
                                TCAGGAGTAG TTGTTAG
                                |||||||||| |||||||
                                GGTCTTTGTC GACAGTC
                                     G
GAM240   LOC139221 3'  GACAATGGTTGCTCTTGG    75824         __
                                TCAGGAGTAG  ATTGTT
                                ||||||||||  ||||||
                                GGTTCTCGTT  TAACAG
                                     GG
GAM240   LOC142893 5'  TCAGATATGACAAATTGTTTTT 82879         A     GTG
           GA                     TCAGGAGTAG TTGTTA   TTGA
                                |||||||||| ||||||   ||||
                                AGTTTTTGTT AACAGT   GACT
                                     A     ATA
GAM240   LOC142913 3'  TCAGCACTGTCGTCTTCTTGG  76418       GT    TGT
                                TCAGGA  AGAT   TAGTGTTGA
                                ||||||  ||||   |||||||||
                                GGTTCT  TCTG   GTCACGACT
                                  __    CT_
GAM240   LOC143153 3'  TTGGCAGGGCGAGCTGTTCTTG 76472         A    AG   TG
           G                     TCAGGAGTAG TTGTT  TGT  A
                                |||||||||| |||||  |||  |
                                GGTTCTTGTC AGCGG  ACG  T
                                     G    G_   GT
GAM240   LOC143154 3'  TTGGCAGGGCGAGCTGTTCTTG 76488         A    AG   TG
           G                     TCAGGAGTAG TTGTT  TGT  A
                                |||||||||| |||||  |||  |
                                GGTTCTTGTC AGCGG  ACG  T
                                     G    G_   GT
GAM240   LOC143680 5'  AACAATCTGTTCCTGG      82984
                                TCAGGAGTAGATTGTT
                                ||||||||||||||||
                                GGTCCTTGTCTAACAA

GAM240   LOC143879 3'  TTGGTATTGATAATAGTATTC  76655       G_        TT
                                GAGTA  ATTGTTAGTG  GA
                                |||||  ||||||||||  ||
                                CTTAT  TAATAGTTAT  TT
                                   GA         GG
GAM240   LOC143909 3'  TGACATTTGTTTATTCTTG    82998         TGTT    TG
                                CAGGAGTAGAT    AGTGT  A
                                ||||||||||    |||||  |
                                GTTCTTATTTG    TTACA  T
                                     T___     GT
GAM240   LOC144058 5'  TCAATGGAACGGCTACTTTTGG 76670         A    AG
                                TCAGGAGTAG TTGTT  TGTTGA
                                |||||||||| |||||  ||||||
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                                GGTTTTCATC GGCAA  GTAACT
                                      _    G_
GAM240   LOC144147 3'  TGCTGTAGTCACTTCTGA    71732        A   TGT
                                TCAGGAGT GAT   TAGTG
                                |||||||| |||   |||||
                                AGTCTTCA CTG   GTCGT
                                     _   AT_
GAM240   LOC144161 3'  TTAACACTGATAATCTAGCC   83009    AG
                                GG  TAGATTGTTAGTGTTGA
                                ||  ||||||||||||||||
                                CC  ATCTAATAGTCACAATT
                                 G_
GAM240   LOC144308 3'  CGACATCTCTGCTTTGGG    83044    AG      TTGTTA
                                TC  GAGTAGA     GTGTTG
                                ||  |||||||     ||||||
                                GG  TTCGTCT     TACAGC
                                 GT      C_____
GAM240   LOC144438 3'  ACTGAGTGTTTGCTCCTGA    76830          TG
                                TCAGGAGTAGAT  TTAGT
                                ||||||||||||  |||||
                                AGTCCTCGTTTG  AGTCA
                                       TG
GAM240   LOC144473 3'  TCAGCCAAACATGTCTGCTTTT 83075          _    AGT
            GA                    TCAGGAGTAGAT TGTT   GTTGA
                                ||||||||||||| ||||   |||||
                                AGTTTTCGTCTG ACAA   CGACT
                                       T    AC_
GAM240   LOC144524 3'  TTGGTGTAAATAACTTTACTTC 83142          _    A TG TG
            TGG                    TCAGGAGTAGA TTGTT G  T  A
                                |||||||||||| ||||| |  |  |
                                GGTCTTCATTT AATAA T  G  T
                                       C     A GT GT
GAM240   LOC144558 3'  TCAACATTTCTCCTTTCTTGA  83150        TA  TTGTT
                                TCAGGAG  GA    AGTGTTGA
                                |||||||  ||    ||||||||
                                AGTTCTT  CT    TTACAACT
                                     TC  CT___
GAM240   LOC144558 5'  TTGGCTAATCTGCTTCT     83152          _
                                AGGAGTAGATT GTTAG
                                ||||||||||| |||||
                                TCTTCGTCTAA CGGTT
                                       T
GAM240   LOC144715 5'  TCAGCCTTTGCAAGTTATTTTT 76931          A    T_  T
            GA                    TCAGGAGTAG TTGT  AG GTTGA
                                |||||||||| ||||  || |||||
                                AGTTTTTATT AACG  TC CGACT
                                       G    TT  _
GAM240   LOC144742 5'  TTGGCATTGGTGCTCTCTGCCT 76950       _  T   T GT     TG
            GG                    TCAGG AG AGA T  TAGTGT  A
                                |||||  || |||  |  ||||||  |
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                                GGTCC TC TCT G  GTTACG  T
                                  G  _  C TG     GT
GAM240  LOC145482 3'  TTGACAAGATTTACTCC     77234          __
                                GGAGTAGAT  TGTTAG
                                |||||||||  ||||||
                                CCTCATTTA  ACAGTT
                                     GA
GAM240  LOC145566 5'  CAGCAAAATCACTCTTGG    77272        A   GTTAG
                                TCAGGAGT GATT    TGTTG
                                |||||||| ||||    |||||
                                GGTTCTCA CTAA    ACGAC
                                     _   A____
GAM240  LOC145622 3'  TGGCATATGATCTGCTTCT   77318         TG TA   TG
                                AGGAGTAGAT  T  GTGT  A
                                ||||||||||  |  ||||  |
                                TCTTCGTCTA  A  TACG  T
                                      GT __   GT
GAM240  LOC145623 5'  GACAACTACTTTTGG       83395          A
                                TCAGGAGTAG TTGTT
                                |||||||||| |||||
                                GGTTTTCATC AACAG
                                     _
GAM240  LOC145676 5'  ATTAATTCTGCTCTTGA     77334          TT
                                TCAGGAGTAGA  GTTAGT
                                ||||||||||  ||||||
                                AGTTCTCGTCT  TAATTA
                                     __
GAM240  LOC145773 3'  TTAATATTTAAAACTATTTTTG 77497          A  GTT
          A                      TCAGGAGTAG TT   AGTGTTGA
                                ||||||||||  ||   ||||||||
                                AGTTTTTATC AA   TTATAATT
                                     A  AT_
GAM240  LOC145842 5'  TTGACACTTTTCATTTGCTCCT 77535          TGTT    TG
          G                      CAGGAGTAGAT    AGTGT  A
                                ||||||||||    |||||  |
                                GTCCTCGTTTA    TCACA  T
                                      CTTT    GT
GAM240  LOC146176 5'  CAATGCTTGTTTTTCCTGG   77694        T   TGTT
                                TCAGGAG AGAT    AGTGTTG
                                ||||||| ||||    |||||||
                                GGTCCTT TTTG    TCGTAAC
                                     _   T___
GAM240  LOC146438 3'  TTGAGTTTGCAACTCTGCTTTT 77893          _   TAGTGTTGA
          GG                      TCAGGAGTAGA TTGT
                                ||||||||||| ||||
                                GGTTTTCGTCT AACG
                                      C   TTTGAGTT
GAM240  LOC146520 3'  TCAATGGGCTATTTCATTCCTG 77959        A  TTGT   __
          G                      TCAGGAGT GA    TAGT  GTTGA
                                ||||||| ||    ||||  |||||
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                                GGTCCTTA CT   ATCG  TAACT
                                    _ TT__   GG
GAM240  LOC146956 3'  TTAATGTTCCTCTCCTGG    78212       TA  TT
                                TCAGGAG  GA  GTTAG
                                |||||||  ||  |||||
                                GGTCCTC  CT  TAATT
                                   TC  TG
GAM240  LOC147004 5'  ACACAAATCATTTCTGA     83899       A   GTTA
                                TCAGGAGT GATT   GTGT
                                |||||||| ||||   ||||
                                AGTCTTTA CTAA   CACA
                                    _   A___
GAM240  LOC147124 3'  TCAAGCCACCAGCTGTCTGCTC 76304         T  A  __
          CTGG                    CAGGAGTAGAT GTT GTG  TTGA
                                |||||||||| ||| |||  ||||
                                GTCCTCGTCTG CGA CAC  AACT
                                      T  C  CG
GAM240  LOC147138 5'  TCAGTGCTGGGAGAACTCC   78272     AGA  G   TG
                                GGAGT   TT TTAG  TTGA
                                |||||   || ||||  ||||
                                CCTCA   GA GGTC  GACT
                                  A__  G   GT
GAM240  LOC148195 5'  GCTGTTTAATCACTTCTGA   84134       A   T_
                                TCAGGAGT GATTG  TAGT
                                |||||||| |||||  ||||
                                AGTCTTCA CTAAT  GTCG
                                    _    TT
GAM240  LOC148254 3'  TTGATATTAGGGATATTCCTG  78761       GA  G     TG
                                CAGGAGTA  TT TTAGTGT  A
                                ||||||||  || |||||||  |
                                GTCCTTAT  AG GATTATA  T
                                    __  G     GT
GAM240  LOC148280 3'  TTGACTGATTGGGTGATTGATT 84141    A  _____    GTTGA
          CCTGG                   AGT GATT    GTTAGT
                                ||| ||||    ||||||
                                TTA TTAG    TAGTCA
                                  G   TGGGT    GTT  A
GAM240  LOC148418 3'  TATTTATAATAATTTGTTTCTG 78849            GTGTTGA
          A                      TCAGGAGTAGATTGTTA
                                |||||||||||||||||
                                AGTCTTTGTTTAATAAT
                                       ATTTATT
GAM240  LOC148811 3'  CAATTTATTCTACTTCTGG   79006         TTGTTAGT
                                TCAGGAGTAGA      GTTG
                                ||||||||||       ||||
                                GGTCTTCATCT      TAAC
                                     TATT____
GAM240  LOC148823 3'  ACATTGGCTTTTCTGA     59203       TAGATT
                                TCAGGAG    GTTAGTGT
                                |||||||    ||||||||
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                                AGTCTTT     CGGTTACA
                                   T_____
GAM240  LOC149153 5'  TGATGTTGATAGCTTCTGG   84370       AGAT     TG TG
                                TCAGGAGT   TGTTAG  T  A
                                ||||||||   ||||||  |  |
                                GGTCTTCG   ATAGTT  A  T
                                     ____     GT GT
GAM240  LOC149153 5'  TTGATGTTGATAGCTTCTGG  84371       AGAT     TG TG
                                TCAGGAGT   TGTTAG  T  A
                                ||||||||   ||||||  |  |
                                GGTCTTCG   ATAGTT  A  T
                                     ____     GT GT G
GAM240  LOC149267 5'  ACACTGTCTGCTCCTGA    56672         TGTT
                                TCAGGAGTAGAT   AGTGT
                                ||||||||||||   |||||
                                AGTCCTCGTCTG   TCACA
                                     _____
GAM240  LOC149371 3'  TTGATTGAATTAATTACTCTTG 79318        ATTG_    GTTGA
           G                     TCAGGAGTAG    TTAGT
                                 ||||||||||    |||||
                                 GGTTCTCATT    AGTTA
                                      AATTA    GTT
GAM240  LOC149420 3'  TCAGCACTAAAGGTTTGTTGA  79370     GAG    TG
                                TCAG  TAGAT  TTAGTGTTGA
                                ||||  |||||  ||||||||||
                                AGTT  GTTTG  AATCACGACT
                                   ___    GA
GAM240  LOC149460 5'  TCAGTGCTGACCCCTGGGGCTC 84442       AGATT__    TG
           TTGG                  CAGGAGT      GTTAG  TTGA
                                 |||||||      |||||  ||||
                                 GTTCTCG      CAGTC  GACT
                                    GGGTCCC    GT
GAM240  LOC149535 3'  TCAATGCTAGAAGAACCCTTGG 79420      A  AGATTG
                                TCAGG GT     TTAGTGTTGA
                                ||||| ||     ||||||||||
                                GGTTC CA     GATCGTAACT
                                   C  AGAA__
GAM240  LOC149606 3'  TTGACACTGACAGACCCTGCCT 79457      AGTAGA        TG
           GG                    TCAGG     TTGTTAGTGT  A
                                 |||||     ||||||||||  |
                                 GGTCC     GACAGTCACA  T
                                   GTCCCA         GT
GAM240  LOC149832 5'  TTGATACTGATAATATATTTT  84704       G         TG
                                GGAGTA ATTGTTAGTGT  A
                                ||||||| ||||||||||  |
                                TTTTAT TAATAGTCATA  T
                                   A         GT
GAM240  LOC150271 3'  TCAGCACTGAGCACCTACTTTG 84956    AG     AT  _
           GG                    TC  GAGTAG  TG TTAGTGTTGA
                                 ||  ||||||  || ||||||||||
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                                GG  TTCATC  AC AGTCACGACT
                                 GT     C_  G
GAM240   LOC150350 3'  CACAATATCTATTTTTGA     79762           T   A
                                TCAGGAGTAGAT GTT GTG
                                |||||||||||| ||| |||
                                AGTTTTTATCTA TAA CAC
                                          _   _
GAM240   LOC150384 3'  AACAGTCATTCCTGA       85034         A
                                TCAGGAGT GATTGTT
                                |||||||| |||||||
                                AGTCCTTA CTGACAA
                                          _
GAM240   LOC150568 5'  TTGGTCCTAGATCTGACTTTTG 85046         _    GT   TG TG
           A                     TCAGGAGT AGATT  TAG  T  A
                                |||||||| |||||  |||  |  |
                                AGTTTTCA TCTAG  ATC  G  T
                                     G     __   CT GT
GAM240   LOC150596 3'  TTAAGAGTTTATTCCTGG     79952           G
                                TCAGGAGTAGATT TTAG
                                |||||||||||| ||||
                                GGTCCTTATTTGA AATT
                                        G
GAM240   LOC151176 5'  AGTGCTGTCCTCCTGG      85257        TA   TGTT  TG
                                TCAGGAG  GAT    AG  TT
                                |||||||  |||    ||  ||
                                GGTCCTC  CTG    TC  GA
                                   __   _____  GT
GAM240   LOC151470 3'  TCAGTGCTGGAGAAATCTTGA  80260       GTAGATTG    TG
                                TCAGGA       TTAG  TTGA
                                ||||||       ||||  ||||
                                AGTTCT       GGTC  GACT
                                   AAAGA___    GT
GAM240   LOC151507 3'  TTGCAGCTATAATTTGCTTCTG 80266            T  _   TGA
           A                     TCAGGAGTAGATTGT AG TGT
                                |||||||||||||| || |||
                                AGTCTTCGTTTAATA TC ACG
                                          _  G   TT
GAM240   LOC151521 3'  CAGTGAAATGTCTGTGTCTGA  85436      AG    TG_  G
                                TCAGG  TAGAT   TTA TG
                                |||||  |||||   ||| ||
                                AGTCT  GTCTG   AGT AC
                                   GT    TAA   G
GAM240   LOC151556 5'  GGCATCGCCTTCAATTTTATTC 80280         _   TTA   T  A
           TTGA                    CAGGAGTAGA TTG   GTG TG
                                |||||||||| |||   ||| ||
                                GTTCTTATTT AAC   CGC AC
                                      T   TTC   T  GGT
GAM240   LOC151579 3'  TCTACGTAGTGATCTGCTTTT  69458          TG   G   T
                                AGGAGTAGAT  TTA TGT GA
                                ||||||||||  ||| ||| ||
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                                TTTTCGTCTA  GAT GCA CT
                                      GT   _   T
GAM240   LOC151623 5'  TTGGCTAATCTGCTTCT     85461          _
                                AGGAGTAGATT GTTAG
                                |||||||||| |||||
                                TCTTCGTCTAA CGGTT
                                       T
GAM240   LOC151643 3'  TTAGCATTGATGGGCTATTTTT 80327          A TG
           GA                    TCAGGAGTAG T  TTAGTGTTGA
                                |||||||||| |  ||||||||||
                                AGTTTTTATC G  AGTTACGATT
                                      G GT
GAM240   LOC151657 3'  GCTGTGGTCTGCCTCTGA    85477      GA     TG T
                                TCAG  GTAGAT  T AGT
                                ||||  ||||||  | |||
                                AGTC  CGTCTG  G TCG
                                  TC     GT _
GAM240   LOC151760 5'  AGCATTTGACTCTTGG      85493         AGATTGTT
                                TCAGGAGT       AGTGTT
                                ||||||||       ||||||
                                GGTTCTCA       TTACGA
                                     GT_______
GAM240   LOC152137 3'  TTAACACTTCCTCTGCTTTTG  80485          TTGTT
                                CAGGAGTAGA     AGTGTTGA
                                ||||||||||     ||||||||
                                GTTTTCGTCT     TCACAATT
                                      CCT__
GAM240   LOC152220 3'  TCAAGTATCTGTGGTTTGGTTC 85589       G     TG TA  _
           TGG                   TCAGGA TAGAT  T  GTG TTGA
                                |||||| |||||  |  ||| ||||
                                GGTCTT GTTTG  G  TAT AACT
                                   G    GT TC   G
GAM240   LOC152220 3'  TTATAGAAACTGGTTTATTTCT 85592           _  AGTGTTGA
           GG                    TCAGGAGTAGATT GTT
                                |||||||||||| |||
                                GGTCTTTATTTGG CAA
                                       T   AGATATT
GAM240   LOC152220 3'  TTGACATTAACTGCTGTATTTT 85593       GT_  ATT       TG
           GA                    TCAGGA   AG   GTTAGTGT  A
                                ||||||   ||   ||||||||  |
                                AGTTTT   TC   CAATTACA  T
                                   ATG  GT_       GT
GAM240   LOC152267 3'  TAGCTGTGTACTTCTGG     60398         G  T
                                TCAGGAGTA AT GTTA
                                ||||||||| || ||||
                                GGTCTTCAT TG CGAT
                                      G  T
GAM240   LOC152328 3'  CACCATATTTTACTTTTGA   80524          T   TA
                                TCAGGAGTAGA TGT  GTG
                                |||||||||| |||  |||
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                                AGTTTTCATTT ATA  CAC
                                      T  C_
GAM240  LOC152426 3'  CTAGTGGTCTCTTTCTGG    85713       T   TG
                                TCAGGAG AGAT  TTAG
                                ||||||| ||||  ||||
                                GGTCTTT TCTG  GATC
                                    C   GT
GAM240  LOC152503 3'  TTAGCAATCTCAATTTCATTTT 85772        _    TTAG
           TGA                    TCAGGAGT AGATTG   TGTTGA
                                ||||||||| ||||||   ||||||
                                AGTTTTTA TTTAAC   ACGATT
                                    C     TCTA
GAM240  LOC152719 5'  ACATTGATAAGCACTGA    85842     GA  AGA
                                TCAG  GT   TTGTTAGTGT
                                ||||  ||   ||||||||||
                                AGTC  CG   AATAGTTACA
                                  A_  ___
GAM240  LOC152903 3'  TTAGCATTAATAGTTGTTCTGA 80731       GTA
                                TCAGGA   GATTGTTAGTGTTGA
                                ||||||   ||||||||||||||||
                                AGTCTT   TTGATAATTACGATT
                                   G__
GAM240  LOC152992 3'  TCAGTGCTGTGGTCTCTGCTCT 80759        TTGT_  TG
                                GGAGTAGA    TAG  TTGA
                                ||||||||    |||  ||||
                                TCTCGTCT    GTC  GACT
                                     CTGGT   GT
GAM240  LOC153077 3'  AGAAATTCTGATCAGTCTACTT 85905          _   T   GA
           TTGG                   CAGGAGTAGATTG TTAG GTT
                                ||||||||||||| |||| |||
                                GTTTTCATCTGAC AGTC TAA
                                       T   T   AGAT
GAM240  LOC153339 3'  TTAGCACTGGTAAATAGAATAT 86019      GA____   TT
           TTCT                   GAGTA     TTG  AGTGTTGA
                                |||||     |||  ||||||||
                                TTTAT     AAT  TCACGATT
                                   AAGATA   GG
GAM240  LOC153516 3'  GTGCTAATGTGCCCTGG     56711      A   GAT     TG
                                TCAGG GTA   TGTTAG  T
                                ||||| |||   ||||||  |
                                GGTCC CGT   GTAATC  G
                                   _  ___     GT
GAM240  LOC153682 3'  TTGGTTCTTTGCAGTTTGGTTC 86088       G       T_  TG TG
           TGA                    TCAGGA TAGATTGT  AG  T  A
                                |||||| ||||||||  ||  |  |
                                AGTCTT GTTTGACG  TC  G  T
                                   G       TT  TT GT
GAM240  LOC154084 5'  TAGTGCTGTGCTGCCTGA    86164       _   GATTGT   TG
                                TCAGG AGTA     TAG  TTG
                                ||||| ||||     |||  |||
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                                AGTCC TCGT     GTC  GAT
                                  G   _______  GT
GAM240   LOC154089 3'  GCCAACCGTGATAGTGTGCTCC 81038         G      GT    A
            TGG                    TCAGGAGTA ATTGTTA  GTTG
                                   ||||||||| |||||||  ||||
                                   GGTCCTCGT TGATAGT  CAAC
                                     G      GC    CGA
GAM240   LOC154214 5'  TTGACATTGGCTCTTGA     81060         AGAT
                                   TCAGGAGT    TGTTAG
                                   ||||||||    ||||||
                                   AGTTCTCG    ACAGTT
                                       GTT_
GAM240   LOC154222 3'  CAGCATTCACGCTCCTGA    86188         AGATT  T
                                   TCAGGAGT    GT AGTGTTG
                                   ||||||||    || |||||||
                                   AGTCCTCG    CA TTACGAC
                                       _____  C
GAM240   LOC154760 5'  CTGACAGGCTGTTTCTGG    86244          A
                                   TCAGGAGTAG TTGTTAG
                                   |||||||||| |||||||
                                   GGTCTTTGTC GACAGTC
                                         G
GAM240   LOC154761 3'  TCGGTGTGGCAGCCAATCTGTA 81126    AG      TTA___ TG
            CCTGG                    GG  TAGATTG     G  TTGA
                                   ||  |||||||     |  ||||
                                   CC  GTCTAAC     T  GGCT
                                    AT      CGACGG GT
GAM240   LOC155064 3'  TGATGCTGTAGTTTTTCCTGG  81253        T    TGT     TG
                                   TCAGGAG AGAT   TAGTGT  A
                                   ||||||| ||||   ||||||  |
                                   GGTCCTT TTTG   GTCGTA  T
                                       _   AT_     GT
GAM240   LOC155434 3'  TAACACTGGTAGCTCCTG    86405        AGAT  TT
                                   CAGGAGT    TG  AGTGTTG
                                   |||||||    ||  |||||||
                                   GTCCTCG    AT  TCACAAT
                                       ____  GG
GAM240   LOC157278 3'  TCAACATTTCTCCTTTCTTGA 86427        TA  TTGTT
                                   TCAGGAG  GA    AGTGTTGA
                                   |||||||  ||    ||||||||
                                   AGTTCTT  CT    TTACAACT
                                       TC  CT___
GAM240   LOC157697 3'  TATTCACGTGTTTGTTCCTGG  81554           _   T
                                   TCAGGAGTAGAT TGT AGTG
                                   |||||||||||| ||| ||||
                                   GGTCCTTGTTTG GCA TTAT
                                           T   C
GAM240   LOC157793 5'  TCAGCAAGGCAGTTTACTTCT  81613             AG
                                   AGGAGTAGATTGTT  TGTTGA
                                   ||||||||||||||  ||||||
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                                TCTTCATTTGACGG  ACGACT
                                      A_
GAM240  LOC157867 5'  AACAATCTTACTCCTGG     86553         _
                                TCAGGAGTA GATTGTT
                                ||||||||| |||||||
                                GGTCCTCAT CTAACAA
                                     T
GAM240  LOC158295 5'  TGATGCTAATTATCTCTTT   86736     T   T      TG
                                GGAG AGAT GTTAGTGT  A
                                |||| |||| ||||||||  |
                                TTTC TCTA TAATCGTA  T
                                  _   T      GT
GAM240  LOC158382 5'  TGCAGCATCTGCTTCTGG    86790          T   A
                                TCAGGAGTAGAT GTT GTG
                                |||||||||||| ||| |||
                                GGTCTTCGTCTA CGA CGT
                                      _  _
GAM240  LOC158431 3'  TGGCTATCTACTTCTGA     86831          T
                                TCAGGAGTAGAT GTTA
                                |||||||||||| ||||
                                AGTCTTCATCTA CGGT
                                      T
GAM240  LOC158576 3'  TCAGATTCAGTGGTCTGTTTCT 81958          TG  AGTG
          GG                    TCAGGAGTAGAT  TT   TTGA
                                |||||||||||  ||   ||||
                                GGTCTTTGTCTG  GA   GACT
                                      GT  CTTA
GAM240  LOC161321 5'  AGCAATCTGTCTCTGA     87085      AG
                                TCAGG  TAGATTGTT
                                |||||  |||||||||
                                AGTCT  GTCTAACGA
                                  CT
GAM240  LOC164295 3'  CAGTGCTGTTATTCCT     82508        ATTGT   TG
                                AGGAGTAG    TAG  TTG
                                ||||||||    |||  |||
                                TCCTTATT    GTC  GAC
                                     _____  GT
GAM240  LOC170221 3'  TGGCGCTGTCACCTCTTTTGG  82580       T  AT  T    TG
                                TCAGGAG AG  TG TAGTGT  A
                                ||||||| ||  || ||||||  |
                                GGTTTTC TC  AC GTCGCG  T
                                    _ C_  T    GT
GAM240  LOC196394 3'  TTAATGTTAACACTATTTTT  87656        AT     TG
                                AGGAGTAG  TGTTAG  TTGA
                                ||||||||  ||||||  ||||
                                TTTTTATC  ACAATT  AATT
                                     __    GT
GAM240  LOC196527 3'  GCTAGATCTGTTCC       87756         GT
                                GGAGTAGATT  TAGT
                                ||||||||||  ||||
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                                CCTTGTCTAG  ATCG
                                    __
GAM240  LOC196761 3'  CAAATGTGTCTGCTTCTGA   89551          TGTTAGTG
                                TCAGGAGTAGAT      TTG
                                ||||||||||||      |||
                                AGTCTTCGTCTG      AAC
                                      TGTA____
GAM240  LOC196792 5'  TCGACGCTGGCGGTGGAC    87519    AG
                                GT  ATTGTTAGTGTTGA
                                ||  ||||||||||||||
                                CA  TGGCGGTCGCAGCT
                                 GG
GAM240  LOC196812 3'  ATAATAAAATAATTTGCTTCT  89562           AG    A
                                AGGAGTAGATTGTT  TGTTG
                                ||||||||||||||  |||||
                                TCTTCGTTTAATAA  ATAAT
                                        A_    AT
GAM240  LOC196955 5'  AACAGTTGGCTCCTGG      77356        A
                                TCAGGAGT GATTGTT
                                ||||||||| |||||||
                                GGTCCTCG TTGACAA
                                     G
GAM240  LOC196955 5'  TCAGTATTTGCCTCTTTTCCTG 77388       T   TT  T
           G                     TCAGGAG AGA  GT AGTGTTGA
                                 ||||||| |||  || ||||||||
                                 GGTCCTT TCT  CG TTATGACT
                                     T   C_  T
GAM240  LOC197201 3'  ACCTGATGGTCTGTTCTGA   87929       G    TG    T
                                TCAGGA TAGAT  TTAG GT
                                ||||||| |||||  |||| ||
                                AGTCTT GTCTG  AGTC CA
                                   _    GT   _
GAM240  LOC197414 3'  TCAGCATTAACTTCTGGGTTCC 88070       __    TT
           TG                     CAGGAG  TAGA  GTTAGTGTTGA
                                  ||||||  ||||  ||||||||||
                                  GTCCTT  GTCT  CAATTACGACT
                                     GG    T_
GAM240  LOC197416 5'  GACAGATCTATTCTTGG     89754           _
                                TCAGGAGTAGAT TGTT
                                ||||||||||| ||||
                                GGTTCTTATCTA ACAG
                                      G
GAM240  LOC199678 3'  TAACAACTGTCACTCCTGA   89794        A   T  TAG
                                TCAGGAGT GAT GT   TGTTG
                                |||||||| ||| ||   |||||
                                AGTCCTCA CTG CA   ACAAT
                                     _   T  ___
GAM240  LOC200030 3'  TCAACTCCTTCAGTTTATCTTG 79338       G      TTAGT
           G                     TCAGGA TAGATTG    GTTGA
                                 |||||| |||||||    |||||
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                                GGTTCT ATTTGAC    CAACT
                                   _      TTCCT
GAM240   LOC200030 3'  TCGACTCCTTCAGTTTATCTTG 79339      G     TTAGT
            G                    TCAGGA TAGATTG    GTTGA
                                 |||||| |||||||    |||||
                                GGTTCT ATTTGAC    CAGCT
                                   _      TTCCT
GAM240   LOC200030 3'  TCGACTCCTTCAGTTTATCTTG 79340      G     TTAGT
            G                    TCAGGA TAGATTG    GTTGA
                                 |||||| |||||||    |||||
                                GGTTCT ATTTGAC    CAGCT
                                   _      TTCCT
GAM240   LOC200030 3'  TCGACTCCTTCAGTTTATCTTG 79341      G     TTAGT
            G                    TCAGGA TAGATTG    GTTGA
                                 |||||| |||||||    |||||
                                GGTTCT ATTTGAC    CAGCT
                                   _      TTCCT
GAM240   LOC200845 5'  GGCAGTCTGGTCTTGA     88903      G
                                TCAGGA TAGATTGTT
                                |||||| |||||||||
                                AGTTCT GTCTGACGG
                                   G
GAM240   LOC200933 5'  TCAGCACTAATGACTGCTCC  90201       A TG
                                GGAGTAG T  TTAGTGTTGA
                                ||||||| |  ||||||||||
                                CCTCGTC A  AATCACGACT
                                    _ GT
GAM240   LOC200933 3'  TTAACATTAACTCCTATTTTGA 90202     G    ATT
                                TCAG AGTAG   GTTAGTGTTGA
                                |||| |||||   ||||||||||
                                AGTT TTATC   CAATTACAATT
                                  _    CT_
GAM240   LOC200953 5'  TCAGGGCCAGATGGCTGTTCCT 90212         A TG  A_  G
            GG                    TCAGGAGTAG T  TT  GT TTGA
                                  |||||||||| |  ||  || ||||
                                  GGTCCTTGTC G  AG  CG GACT
                                       _ GT  AC  G
GAM240   LOC201626 3'  TCAGCCCTCCTAGTTATGTTCC 88998        _    TT  T
            TGA                    TCAGGAGTA GATTG  AG GTTGA
                                   ||||||||| |||||  || |||||
                                   AGTCCTTGT TTGAT  TC CGACT
                                      A    CC  C
GAM240   LOC201736 5'  GGCAAACTGCTTCTGA     89052         A
                                TCAGGAGTAG TTGTT
                                |||||||||| |||||
                                AGTCTTCGTC AACGG
                                   A
GAM240   LOC201780 3'  TCAATGCTGTAATATAATTTGC 89054   A      ____
            ACCTGG                 G GTAGATTGT    TAGTGTTGA
                                   | |||||||||    |||||||||
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                                C CGTTTAATA    GTCGTAACT
                                 A        TAAT
GAM240   LOC202134 3'  TACCAAAATGTCTACTTTTGA  90324          TG_  A
                                TCAGGAGTAGAT   TT GTG
                                |||||||||||   || |||
                                AGTTTTCATCTG   AA CAT
                                      TAA  C
GAM240   LOC202266 3'  CAATGCTTCCTAATCCTGA    90330       G   ATTGTT
                                TCAGGA TAG     AGTGTTG
                                |||||| |||     |||||||
                                AGTCCT ATC     TCGTAAC
                                   A   CT_____
GAM240   LOC203084 3'  TTGATATTAATTAAACTCTTGG 87492        AGATT       TG
                                TCAGGAGT    GTTAGTGT  A
                                ||||||||    ||||||||  |
                                GGTTCTCA    TAATTATA  T
                                     AAT__       GT
GAM240   LOC203197 3'  AGTGATCTGCTCCTGA      89283          TG
                                TCAGGAGTAGAT  TT
                                ||||||||||||  ||
                                AGTCCTCGTCTA  GA
                                       GT
GAM240   LOC203246 3'  CAACATCTTTGCTTTTG     89303         TTGTTA
                                CAGGAGTAGA     GTGTTG
                                ||||||||||     ||||||
                                GTTTTCGTTT     TACAAC
                                      C_____
GAM240   LOC204394 5'  TTAGTGTGATAATTTACTTGCT 89464     _          GTGTTGA
           GG                     TCAG GAGTAGATTGTTA
                                ||||| ||||||||||||
                                GGTC TTCATTTAATAGT
                                  G          GTGATT
GAM240   LOC204970 3'  GCCAGTCTGTGCTTGG      89409       AG      TTAGT
                                TCAGG  TAGATTG    GT
                                |||||  |||||||    ||
                                GGTTC  GTCTGAC    CG
                                   GT     _____
GAM240   LOC206324 5'  TAACAGTGTACTTCTGG     90715         G
                                TCAGGAGTA ATTGTTA
                                |||||||| |||||||
                                GGTCTTCAT TGACAAT
                                      G
GAM240   LOC219333 3'  TAACATAACTACTCTTGA    93543         AT_
                                TCAGGAGTAG   TGTTA
                                ||||||||||   |||||
                                AGTTCTCATC   ACAAT
                                      AAT
GAM240   LOC219513 3'  AACGCTAACCCCTGG       94320       AGTAGATT
                                TCAGG       GTTAGTGTT
                                |||||       |||||||||
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                                GGTCC       CAATCGCAA
                                  C_______
GAM240  LOC219673 3'  CAATGCTGATTTTCGCT     93021     A  TT
                                AGT GA  GTTAGTGTTG
                                ||| ||  ||||||||||
                                TCG CT  TAGTCGTAAC
                                  _  TT
GAM240  LOC220114 3'  TTAATACTTAAAATCGTTCTTG 91742       GTA    GTT
          A                      TCAGGA   GATT   AGTGTTGA
                                ||||||   ||||   ||||||||
                                AGTTCT   CTAA   TCATAATT
                                   TG_    AAT
GAM240  LOC220164 3'  TTGACTAGAGAGACAGTCTGTC 91799      G       AGT___  TG
          CTGG                    AGGA TAGATTGTT     GT  A
                                |||| |||||||||     ||  |
                                TCCT GTCTGACAG     CA  T
                                  _       AGAGAT  GT
GAM240  LOC220692 3'  ACTGAAATTTGCTGCTGA    91217      G       G
                                TCAG AGTAGATT TTAGT
                                |||| |||||||| |||||
                                AGTC TCGTTTAA AGTCA
                                  G      _
GAM240  LOC220766 5'  GGCAGCTCTGCTCCTGG     90799           _
                                TCAGGAGTAGA TTGTT
                                |||||||||| |||||
                                GGTCCTCGTCT GACGG
                                      C
GAM240  LOC221312 3'  TCAGCATTGATTATGTTCTTTT 91910        TAGATT
          GA                    TCAGGAG     GTTAGTGTTGA
                                |||||||     ||||||||||
                                AGTTTTC     TAGTTACGACT
                                   TTGTAT
GAM240  LOC221322 5'  TAGCACTGGTGAACTT      91931      AGA TG
                                GAGT   T  TTAGTGTTG
                                ||||   |  |||||||||
                                TTCA   A  GGTCACGAT
                                  ___ GT
GAM240  LOC221399 5'  CGTATTTAATATTCCTGA    93847         GATTGTT    TT
                                TCAGGAGTA      AGTG  G
                                |||||||||      ||||  |
                                AGTCCTTAT      TTAT  C
                                     AAT____    GG
GAM240  LOC221477 3'  TTGATAAGCAGAATCTACTACT 92164      G       GTTAG   TG
          GG                    TCAG AGTAGATT     TGT  A
                                |||| ||||||||     |||  |
                                GGTC TCATCTAA     ATA  T
                                  A       GACGA   GT
GAM240  LOC221576 3'  ACACAATTTTACTTTTGA     93701           TT   A
                                TCAGGAGTAGA  GTT GTGT
                                ||||||||||  ||| ||||
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                                AGTTTTCATTT  TAA CACA
                                   __  _
GAM240  LOC221583 3'  TTAATACTGATGATGCAATTTT 92146       GTAG  TG
            GA                    TCAGGA   AT  TTAGTGTTGA
                                  ||||||   ||  ||||||||||
                                  AGTTTT   TA  AGTCATAATT
                                     AACG  GT
GAM240  LOC221688 3'  TTAACCAGAAATAATTTATTCT 93680            AGT_
            T                     AGGAGTAGATTGTT   GTTGA
                                  ||||||||||||||   |||||
                                  TTCTTATTTAATAA   CAATT
                                           AGAC
GAM240  LOC221751 5'  TGATGCTGGAAGCTCTTGG   92051        AGATTG      TG
                                  TCAGGAGT     TTAGTGT  A
                                  ||||||||     |||||||  |
                                  GGTTCTCG     GGTCGTA  T
                                       AA____      GT
GAM240  LOC221763 5'  GCAACATAGTAATTTATTTTT  93798            G    A
                                  AGGAGTAGATTGTTA TGTTG
                                  |||||||||||||| |||||
                                  TTTTTATTTAATGAT ACAAC
                                           _    GT
GAM240  LOC221895 3'  AGTAATCTACATCTGG      92521      GA
                                  TCAG  GTAGATTGTT
                                  ||||  ||||||||||
                                  GGTC  CATCTAATGA
                                    TA
GAM240  LOC221927 5'  TCGGCGGCCAGTCAGCTCCTGG 92652         A    TTAG
                                  TCAGGAGT GATTG    TGTTGA
                                  |||||||| |||||    ||||||
                                  GGTCCTCG CTGAC    GCGGCT
                                       A    CG__
GAM240  LOC221929 3'  TCAGCGCTGACCCCACCGCCCT 92676      A  AGATT_
            GG                    TCAGG GT     GTTAGTGTTGA
                                  ||||| ||     ||||||||||
                                  GGTCC CG     CAGTCGCGACT
                                    _  CCACCC
GAM240  LOC221943 5'  CAACGCTAGCATCTGTTTCTGG 93987           T        A
                                  TCAGGAGTAGAT GTTAGTGTTG
                                  |||||||||||| ||||||||||
                                  GGTCTTTGTCTA CGATCGCAAC
                                           _        G
GAM240  LOC221962 3'  TCAACATTTCTCCTTTCTTGA  92684       TA  TTGTT
                                  TCAGGAG  GA    AGTGTTGA
                                  |||||||  ||    ||||||||
                                  AGTTCTT  CT    TTACAACT
                                       TC  CT___
GAM240  LOC221975 3'  GATATTTTATTTCTGG      92606           T
                                  TCAGGAGTAGA TGTT
                                  |||||||||| ||||
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                                GGTCTTTATTT ATAG
                                       T
GAM240  LOC221981 3'  TAATGCTAGCTCTCC      93991      TAGATT
                                GGAG     GTTAGTGTTG
                                ||||     ||||||||||
                                CCTC     CGATCGTAAT
                                  T_____
GAM240  LOC222031 3'  TAGTGACAGTTTATTCCTG   94029             G
                                CAGGAGTAGATTGTTA TG
                                |||||||||||||||| ||
                                GTCCTTATTTGACAGT AT
                                       G
GAM240  LOC222060 3'  CAATACGGGTCTATTTTT    94103          TGTTA
                                AGGAGTAGAT    GTGTTG
                                ||||||||||    ||||||
                                TTTTTATCTG    CATAAC
                                      GG___
GAM240  LOC222161 5'  GTAGGTACTAATGATTTATGTT 92799      A     TG      GA
          TGA                     TCAGG GTAGAT  TTAGTGTT
                                |||||| ||||||  ||||||||
                                AGTTT TATTTA  AATCATGG
                                   G     GT       ATGG
GAM240  LOC222224 5'  ACTGAAATTGACTTTTGA    94194        A   G
                                TCAGGAGT GATT TTAGT
                                |||||||| |||| |||||
                                AGTTTTCA TTAA AGTCA
                                     G   _
GAM240  LOC222865 3'  TCAGTGTTAACTGACTGCTGA  92869     G   AGATT    TG
                                TCAG AGT    GTTAG  TTGA
                                |||| |||    |||||  ||||
                                AGTC TCA    CAATT  GACT
                                  G  GT___    GT
GAM240  LOC253220 5'  TCGGACTATGTGGTTTGCCCCT 96370      A     TG _   G
          GG                      TCAGG GTAGAT  T TAGT TTGA
                                |||||| ||||||  | |||| ||||
                                GGTCC CGTTTG  G ATCA GGCT
                                   C     GT T   _
GAM240  LOC253465 5'  TCAACATTTATCTTAATTCTGA 97504      GT_   TGTT
                                TCAGGA   AGAT    AGTGTTGA
                                ||||||   ||||    ||||||||
                                AGTCTT   TCTA    TTACAACT
                                   AAT    T___
GAM240  LOC253539 3'  TCAGTGGGGGAGCTTGCTTCTG 96004         A  G  AG GT
          A                      TCAGGAGTAG TT TT  T  TGA
                                |||||||||| || ||  |  |||
                                AGTCTTCGTT GA GG  G  ACT
                                      C  G  G_ TG
GAM240  LOC253675 5'  CAGCACTGACCACCCTTGA   96773      A  AGATT
                                TCAGG GT    GTTAGTGTTG
                                ||||| ||    ||||||||||
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                                AGTTC CA    CAGTCACGAC
                                  C  C____
GAM240   LOC253716 5'  TTGGCTGAAGCAGTCATTTTTG 94693       A     AGT  TG
                A                  TCAGGAGT GATTGTT   GT  A
                                   |||||||| |||||||   ||  |
                                   AGTTTTTA CTGACGA   CG  T
                                       _      AGT  GT
GAM240   LOC253815 3'  TAACGGAGGTCTGCTCTGA   95598     G      GTTAG
                                   TCAG AGTAGATT    TGTTG
                                   |||| ||||||||    |||||
                                   AGTC TCGTCTGG    GCAAT
                                     _      AG___
GAM240   LOC253832 3'  ATTAATGTTGATGCTTTGCTTT 94921       TT    TG
                                   GGAGTAGA  GTTAG  TTGA   T
                                   ||||||||  |||||  ||||   |
                                   TTTCGTTT  TAGTT  AATT   A
                                       CG    GT
GAM240   LOC253955 3'  CCATGGCAAGTGATCTGTTCTT 94424         TG  A  GT  A
                GG                   TCAGGAGTAGAT  TT GT  TG
                                     ||||||||||||  || ||  ||
                                     GGTTCTTGTCTA  GA CG  AC
                                         GT  A  GT  CT
GAM240   LOC253981 3'  TCAGTGTTGGGGGGTGCCTTGA 95833      A   GA  G    TG
                                   TCAGG GTA  TT TTAG  TTGA
                                   ||||| |||  || ||||  ||||
                                   AGTTC CGT  GG GGTT  GACT
                                     _  G_  G    GT
GAM240   LOC254100 3'  TTAATCTCTCCAATTTACTCCT 96422         TT  T_
                                   AGGAGTAGATTG  AG  GTTGA
                                   ||||||||||||  ||  |||||
                                   TCCTCATTTAAC  TC  TAATT
                                         C_  TC
GAM240   LOC254251 3'  TTAACACTGAAGCTGTTTTGA  95914      G   ATTG
                                   TCAGGA TAG    TTAGTGTTGA
                                   |||||| |||    ||||||||||
                                   AGTTTT GTC    AGTCACAATT
                                      _   GA__
GAM240   LOC254650 5'  TCAGCGTTATCAGTGTGCCTGG 97686      AG  G    T
                                   TCAGG  TA ATTG TAGTGTTGA
                                   |||||  || |||| |||||||||
                                   GGTCC  GT TGAC ATTGCGACT
                                      __  G    T
GAM240   LOC255065 3'  AGTAGTTATACTCCTGG     96579         _
                                   TCAGGAGTA GATTGTT
                                   |||||||||  |||||||
                                   GGTCCTCAT TTGATGA
                                         A
GAM240   LOC255147 3'  ATATAGCTTGTAACTACTTTTG 95700         A   TT   GTTGA
                G                    TCAGGAGTAG TTG  AGT
                                     ||||||||||  |||  |||
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                                GGTTTTCATC AAT  TCG
                                      _  GT   ATATAG
GAM240   LOC255458 3'  TTAATACTTACTATTTGTACTT 97151      AG    T  T
           GA                    TCAGG  TAGAT GT AGTGTTGA
                                 |||||  ||||| || ||||||||
                                 AGTTC  GTTTA CA TCATAATT
                                    AT    T  T
GAM240   LOC255461 5'  TTGGCTAATCTGCTTCT     97323          _
                                 AGGAGTAGATT GTTAG
                                 |||||||||||| |||||
                                 TCTTCGTCTAA CGGTT
                                       T
GAM240   LOC255516 5'  TTGGCTAATCTGCTTCT     97336          _
                                 AGGAGTAGATT GTTAG
                                 |||||||||||| |||||
                                 TCTTCGTCTAA CGGTT
                                       T
GAM240   LOC255650 3'  CACGTGGTCACTCCTGG     96710        A   TG TA
                                 TCAGGAGT GAT  T  GTG
                                 |||||||| |||  |  |||
                                 GGTCCTCA CTG  G  CAC
                                      _  GT __
GAM240   LOC255919 3'  TCAGTGCTTTGGTACTTTTGA  95040         GATTGTT  TG
                                 TCAGGAGTA      AG  TTGA
                                 |||||||||      ||  ||||
                                 AGTTTTCAT      TC  GACT
                                      GGTT___  GT
GAM240   LOC256073 5'  CACCAAACGTTTGCTTTTGG   96661           T   A_
                                 TCAGGAGTAGAT GTT  GTG
                                 |||||||||||| |||  |||
                                 GGTTTTCGTTTG CAA  CAC
                                       _  AC
GAM240   LOC256073 3'  TGGTGCTGGCTGTCATCTGA   96669      AGTA   T    TG TG
                                 TCAGG   GAT GTTAG  T  A
                                 |||||   ||| |||||  |  |
                                 AGTCT   CTG CGGTC  G  T
                                    A___   T    GT GT
GAM240   LOC256096 5'  TCAATGCTGATCTCAGCTTCTG 97200        A  TT
           A                     TCAGGAGT GA  GTTAGTGTTGA
                                 |||||||| ||  ||||||||||
                                 AGTCTTCG CT  TAGTCGTAACT
                                      A  C_
GAM240   LOC256160 3'  TCAATGCTGTAATATAATTTGC 95877   A       ____
           ACCTGG                   G GTAGATTGT    TAGTGTTGA
                                 | |||||||||    |||||||||
                                 C CGTTTAATA    GTCGTAACT
                                  A        TAAT
GAM240   LOC256207 3'  TCAGAGTAAGAGTCTATTTCTG 95178           G   GTG
           G                     TCAGGAGTAGATT TTA   TTGA
                                 |||||||||||| |||   ||||
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                                GGTCTTTATCTGA AAT   GACT
                                      G   GA_
GAM240   LOC256269 3'  TAACTGTGTACTTCTGG     94935         G  T
                                TCAGGAGTA AT GTTA
                                ||||||||| || ||||
                                GGTCTTCAT TG CAAT
                                     G  T
GAM240   LOC256273 5'  CAGTGCTCAGCTGTCTTGA   96405       G   A   TT  TG
                                TCAGGA TAG TTG  AG  TTG
                                |||||| ||| |||  ||  |||
                                AGTTCT GTC GAC  TC  GAC
                                   _  _  __ GT
GAM240   LOC256476 5'  TCAGTGCTGCACCTGCTCTGA  96821      G    AT   T  TG
                                TCAG AGTAG  TGT AG  TTGA
                                |||| |||||  ||| ||  ||||
                                AGTC TCGTC  ACG TC  GACT
                                  _    C_  _ GT
GAM240   LOC256867 3'  TAACGCTAATATTTCC      94867      TAGAT
                                GGAG    TGTTAGTGTTG
                                ||||    ||||||||||
                                CCTT    ATAATCGCAAT
                                  T____
GAM240   LOC256905 3'  AACAGTTTTTCTTGA       96861        T
                                TCAGGAG AGATTGTT
                                ||||||| ||||||||
                                AGTTCTT TTTGACAA
                                       _
GAM240   LOC256937 3'  TCGGCGCTGATACTGCTATTCT 97128    _      AT_
            GTGA                   CA GGAGTAG   TGTTAGTGTTGA
                                || |||||||   ||||||||||||
                                GT TCTTATC   ATAGTCGCGGCT
                                 G      GTC
GAM240   LOC257017 5'  TTACACCAAAATGATTTACTTT 97379     G      TG  A__   TGA
            GA                   TCAG AGTAGAT  TT   GTGT
                                |||| |||||||  ||   ||||
                                AGTT TCATTTA  AA   CACA
                                  _      GT  AAC    TT
GAM240   LOC257031 5'  TCGACTCCTTCAGTTTATCTTG 94608       G      TTAGT
            G                   TCAGGA TAGATTG     GTTGA
                                |||||| |||||||     |||||
                                GGTTCT ATTTGAC     CAGCT
                                   _       TTCCT
GAM240   LOC257463 3'  ACATTAGAGTTTACTCTTGG   71065           G
                                TCAGGAGTAGATT TTAGTGT
                                |||||||||||| |||||||
                                GGTTCTCATTTGA GATTACA
                                        _
GAM240   LOC257465 3'  TTGGCCAGGCTGCTCTTGA   81603          ATT_
                                TCAGGAGTAG    GTTAG
                                ||||||||||    |||||
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                                AGTTCTCGTC    CGGTT
                                      GGAC
GAM240  LOC257466 3'  AATAACTACTGATGGTTTGTTC 95878    G      TG    _   A
              ATGA                    CA GAGTAGAT  TTAGT GTTG
                                || ||||||||  ||||| ||||
                                GT CTTGTTTG  AGTCA CAAT
                                  A       GT    T    AAT
GAM240  LOC257476 3'  TGGCACCTGTCCTATTCCTGA  61261         _ TGTTA    TG
                                TCAGGAGTAG AT    GTGT  A
                                |||||||||| ||    ||||  |
                                AGTCCTTATC TG    CACG  T
                                      C  TC___    GT
GAM240  LOC257515 3'  ACACAATTTTACTTTTGA    97781          TT   A
                                TCAGGAGTAGA  GTT GTGT
                                ||||||||||  ||| ||||
                                AGTTTTCATTT  TAA CACA
                                      __  _
GAM240  LOC257572 3'  ACACAATTTTACTTTTGA    97910          TT   A
                                TCAGGAGTAGA  GTT GTGT
                                ||||||||||  ||| ||||
                                AGTTTTCATTT  TAA CACA
                                      __  _
GAM240  LOC51042  5'  TTGGCTGGCCGGGCTGTTTCTG 31857         ATT_     GTTGA
              G                   TCAGGAGTAG    GTTAGT
                                ||||||||||    ||||||
                                GGTCTTTGTC    CGGTCG
                                      GGGC     GTT
GAM240  LOC51086  3'  TTGACAGCTATGGGTTTATTTC 32009          GT   _   TG
              T                    AGGAGTAGATT  TAG TGT  A
                                ||||||||||  ||| |||  |
                                TCTTTATTTGG  ATC ACA  T
                                      GT   G   GT
GAM240  LOC51133  3'  TCAGTGTTAACAACAATCATGA 32284     G  GTAGA      TG
                                TCA GA     TTGTTAG  TTGA
                                |||  ||    |||||||  ||||
                                AGT CT     AACAATT  GACT
                                  A  AAC__      GT
GAM240  LOC51170  3'  TTAACATATATTTTTATTTTTG 32696          TTGTTA
              A                    TCAGGAGTAGA     GTGTTGA
                                ||||||||||      |||||||
                                AGTTTTTATTT     TACAATT
                                      TTATA_
GAM240  LOC51241  3'  TTGATATTTCATTCTGATTTCT 33207         _  T  TT    TG
              GA                    TCAGGAGT AGA TG  AGTGT  A
                                ||||||||  ||| ||  |||||  |
                                AGTCTTTA TCT AC  TTATA  T
                                     G   T  T_    GT
GAM240  LOC51270  3'  GCCCCTTAACAGTTTTTCCTGA 60011        T        TGTTGA
                                TCAGGAG AGATTGTTAG
                                |||||||  ||||||||||
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                                AGTCCTT TTTGACAATT
                                   _       CCCCGT
GAM240  LOC51315  3' ACAATCTGTTTCTTGA     33529       _
                                TCAGGAG TAGATTGT
                                ||||||| ||||||||
                                AGTTCTT GTCTAACA
                                    T
GAM240  LOC51580  3' TACCGTGCTTTATTCCTGA   31864         TT  TA_
                                TCAGGAGTAGA  GT   GTG
                                |||||||||||  ||   |||
                                AGTCCTTATTT  CG   CAT
                                      __ TGC
GAM240  LOC83468  5' GACATCTGTTCTTGA      48517          T
                                TCAGGAGTAGAT GTT
                                |||||||||||| |||
                                AGTTCTTGTCTA CAG
                                                _
GAM240  LOC90120  5' TCGGTGCTGCTGCTGCTGCTGG 61542     G    ATT  T  TG
                                TCAG AGTAG   GT AG  TTGA
                                |||| |||||   || ||  ||||
                                GGTC TCGTC   CG TC  GGCT
                                  G    GT_ _  GT
GAM240  LOC90139  5' CAACGCTGGCTCTCC      55399      TAGATT
                                GGAG     GTTAGTGTTG
                                ||||     ||||||||||
                                CCTC     CGGTCGCAAC
                                  T_____
GAM240  LOC90148  3' TCAGCATTGATTTCTTAATTTT 61666       GT_  TT
           GA                     TCAGGA   AGA  GTTAGTGTTGA
                                |||||||  |||  ||||||||||||
                                AGTTTT   TCT  TAGTTACGACT
                                   AAT   T_
GAM240  LOC90355  3' AACCATTTACTTTTGA      52622          T
                                TCAGGAGTAGAT GTT
                                |||||||||||| |||
                                AGTTTTCATTTA CAA
                                      C
GAM240  LOC90355  3' TTAAAGGTGCAATTTATTACTG 52625     G       TAGTG
           A                     TCAG AGTAGATTGT    TTGA
                                |||| ||||||||||    ||||
                                AGTC TTATTTAACG    AATT
                                  A        TGGA_
GAM240  LOC90371  5' AGCAATCATTTTTGA      62492        A
                                TCAGGAGT GATTGTT
                                |||||||| |||||||
                                AGTTTTTA CTAACGA
                                                _
GAM240  LOC90494  5' GGCAGTCTTTTCTGG      63055        T
                                TCAGGAG AGATTGTT
                                ||||||| ||||||||
```

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                                GGTCTTT TCTGACGG
                                        _
GAM240  LOC90495  3'  TTGATGCTGATCTTCAATTCTT 63061        A  TT       TG
              GA                  TCAGGAGT GA  GTTAGTGT  A
                                  |||||||| ||  ||||||||  |
                                  AGTTCTTA CT  TAGTCGTA  T
                                       A  TC       GT
GAM240  LOC90639  3'  ATCAAAAACTCATGAATGGTTT 63651       TG  A  _____
              ATTTCTGG               GTAGAT  TT GTG    TTGA  T
                                  ||||||  || |||    ||||  |
                                  TATTTG  AA TAC    AACT  A
                                     GT  G  TCAAA
GAM240  LOC90719  3'  TCAACGTTGAAGCTGCATTTTG 63888       _   ATTG
              G                   TCAGGA GTAG    TTAGTGTTGA
                                  ||||||| ||||    ||||||||||
                                  GGTTTT CGTC    AGTTGCAACT
                                     A   GA__
GAM240  LOC90784  5'  TCAGAGTCCAGACTGCTCTTGA 64006         A   TTAGTG
                                  TCAGGAGTAG TTG     TTGA
                                  |||||||||| |||     ||||
                                  AGTTCTCGTC GAC     GACT
                                       A  CTGA__
GAM240  LOC90786  3'  TACCTATGATCAATTCTTGG  64035        A   TG TA
                                  TCAGGAGT GAT  T  GTG
                                  |||||||| |||  |  |||
                                  GGTTCTTA CTA  A  CAT
                                       A  GT TC
GAM240  LOC90806  3'  TTAGCCAAATTTACTTTTGA  57987           __
                                  TCAGGAGTAGATT  GTTAG
                                  ||||||||||||  |||||
                                  AGTTTTCATTTAA  CGATT
                                         AC
GAM240  LOC90906  3'  ACTCAGTTTACTCT       64292          TT
                                  GGAGTAGATTG  AGT
                                  ||||||||||  |||
                                  TCTCATTTGAC  TCA
                                        __
GAM240  LOC91050  3'  TCGGCGTTCTGTTGCTTCTGG  64752         ATTGTTAG
                                  TCAGGAGTAG       TGTTGA
                                  |||||||||       ||||||
                                  GGTCTTCGTT       GCGGCT
                                       GTCTT___
GAM240  LOC91138  5'  TTAACATGAGTAGTTTATTTTT 65032           TTA
              G                   CAGGAGTAGATTG   GTGTTGA
                                  ||||||||||||   |||||||
                                  GTTTTTATTTGAT   TACAATT
                                         GAG
GAM240  LOC91409  3'  GTACACACAGCTGTTCCTGG  65959         A   TA   TGA
                                  TCAGGAGTAG TTGT  GTGT
                                  |||||||||| ||||  ||||
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                                GGTCCTTGTC GACA  CACA
                                      _   __    TGG
GAM240  LOC91445  3' TTGGTAAGTTGCTTCTGA    60555         A   TT
                                TCAGGAGTAG TTG  AG
                                |||||||||| |||  ||
                                AGTCTTCGTT AAT  TT
                                     G   GG
GAM240  LOC91661  3' TCAGGTGGAACAGTTTAATCCT 56405       G        AGTG
             GA                   TCAGGA TAGATTGTT    TTGA
                                |||||| |||||||||    ||||
                                AGTCCT ATTTGACAA    GACT
                                   A        GGTG
GAM240  LOC91907  3' TCAGAGGATATTTTGCTTCTGG 67497          T    AGTG
                                TCAGGAGTAGA TGTT    TTGA
                                |||||||||| ||||    ||||
                                GGTCTTCGTTT ATAG    GACT
                                       T    GA__
GAM240  LOC91963  5' AGCAATTTCTCCTGG       67689        T
                                TCAGGAG AGATTGTT
                                ||||||| ||||||||
                                GGTCCTC TTTAACGA
                                   _
GAM240  LOC91966  3' TCAGCATTGCTGCTAATTTTGG 67707       G   ATT  T
                                TCAGGA TAG   GT AGTGTTGA
                                |||||| |||   || ||||||||
                                GGTTTT ATC   CG TTACGACT
                                   A   GT_  _
GAM240  LOC92080  3' GCACGTCTGCTCCTGA      68052           TGTTA
                                TCAGGAGTAGAT    GTGT
                                ||||||||||||    ||||
                                AGTCCTCGTCTG    CACG
                                      ______
GAM240  LOC92249  5' GCTGATTCATTCCTGA      68566         A  TT
                                TCAGGAGT GA  GTTAGT
                                |||||||| ||  ||||||
                                AGTCCTTA CT  TAGTCG
                                   _  __
GAM240  LOC92270  5' GGCAGTTTTCTTCTGA      68632         T
                                TCAGGAG AGATTGTT
                                ||||||| ||||||||
                                AGTCTTC TTTGACGG
                                    T
GAM240  LOC92293  3' TTATATTTAATGTTTATTTCTG 68765           TGTT    TGA
             A                   TCAGGAGTAGAT    AGTGT
                                ||||||||||||    |||||
                                AGTCTTTATTTG    TTATA
                                       TAAT    TT
GAM240  LOC92346  3' TTGACACTGGCACCTTCTCCT  57641       T  AT       TG
                                AGGAG AG  TGTTAGTGT  A
                                ||||| ||  |||||||||  |
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                                TCCTC TC  ACGGTCACA  T
                                   T  C_       GT
GAM240  LOC92379  3'  TTAATATTAGTGGTCT     69150     TG
                                AGAT  TTAGTGTTGA
                                ||||  ||||||||||
                                TCTG  GATTATAATT
                                  GT
GAM240  LOC92492  5'  TCAGCACTACTGTGCTTCTTGG 69528       _  GATT  T
                                TCAGGA GTA    GT AGTGTTGA
                                |||||| |||    || ||||||||
                                GGTTCT CGT    CA TCACGACT
                                   T   GT__  _
GAM240  LOC92565  5'  AACACTGATGTCGTGA      69763     G  GTAGAT
                                TCA GA      TGTTAGTGTT
                                ||| ||      ||||||||||
                                AGT CT      GTAGTCACAA
                                  G  _______
GAM240  LOC93052  3'  TCAGCATTGCTGCTAATTTTGG 71267       G   ATT  T
                                TCAGGA TAG   GT AGTGTTGA
                                |||||| |||   || ||||||||
                                GGTTTT ATC   CG TTACGACT
                                   A   GT_  _
GAM240  LOC93333  5'  AACAACCTGCTCCTGA      72063          A
                                TCAGGAGTAG TTGTT
                                |||||||||| |||||
                                AGTCCTCGTC AACAA
                                      C
GAM240  LOC93613  5'  TCAACATTGAGGTGTCTCCTGA 72701        TAG   G
                                TCAGGAG   ATT TTAGTGTTGA
                                |||||||   ||| ||||||||||
                                AGTCCTC   TGG AGTTACAACT
                                   TG_   _
GAM240  LOC94468  5'  TGATGCTGGTTATCTCTCTGA  60432     G  T   TG     TG
                                TCAG AG AGAT  TTAGTGT  A
                                |||| || ||||  |||||||  |
                                AGTC TC TCTA  GGTCGTA  T
                                  _ _   TT      GT
GAM240  LOC94468  5'  AGCGTCTGGCTATTCTTGG    60430        GATT    _
                                TCAGGAGTA    GTTAG TGTT
                                |||||||||    ||||| ||||
                                GGTTCTTAT    CGGTC GCGA
                                     ____     T
GAM241  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM241  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
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                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM241  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                                _
GAM241  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                   CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM241  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||  ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM241  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM241  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM241  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM241  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_    CG_
GAM241  CG012    5'  CTCACTCTGAAAGTGAA     83218          CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM241  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM241  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
              G                   CATTTC        GTCTGAGAT
                                ||||||        |||||||||
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                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM241  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA  TCACTGTCTGAGAT
                                |||||||  ||||||||||||||
                                GTAAAGT  AGTGACAGACTCTA
                                   C__
GAM241  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM241  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM241  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                 C
GAM241  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM241  PP35      3'  ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM241  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148        TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM241  SEP15     3'  TCCTACAGTAAGAGTGAAA   14934       C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM241  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA  73941       CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM241  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
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                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM241  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM241  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM241  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA

                                        _
GAM242  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A     T__
GAM242  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM242  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT

                                        _
GAM242  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                  CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM242  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM242  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM242  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   ||||| ||
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                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM242  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM242  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM242  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM242  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM242  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||         |||||||||
                                GTAAAG         CAGACTCTA
                                   AAACATTT_
GAM242  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM242  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM242  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM242  NIR3     3'  GCAGTGAAAGTGCAAT      66242      T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM242  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598         CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
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                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM242  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM242  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__    TT
GAM242  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                      A     TC
GAM242  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                      AAAGG
GAM242  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC       CTGTCTGAGAT
                                ||||       ||||||||||
                                AAAG       GACAGACTCTA
                                  GTTTGCC
GAM242  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT      GT TGAGAT
                                |||||||      || ||||||
                                AAAGTGA      CA ACTCTA
                                    TTTCC_  A
GAM242  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM242  LOC222134 5'  ACAGTGAAGTGAAATG       94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                      _
GAM243  EMS1     3'  TGTCACGCGGCAGCTTCA     17856          AG  _
                                TGAAGCTGCC  GTG CA
                                ||||||||||  ||| ||
                                ACTTCGACGG  CAC GT
                                      CG   T
GAM243  EMS1     3'  TGTCACGCGGCAGCTTCA     56756          AG  _
                                TGAAGCTGCC  GTG CA
                                ||||||||||  ||| ||
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                                ACTTCGACGG  CAC GT
                                     CG   T
GAM243  ZNF180   3' ACTTTTCAACCTGGCAATTC  25136    GC      GCATTT
                                GAA  TGCCAGGT     AAGT
                                |||  ||||||||     ||||
                                CTT  ACGGTCCA     TTCA
                                  A_       ACTT__
GAM243  FLJ25193 3' AGTGCACCAGCAGCCCCA   58699    AA    CA
                                TG  GCTGC  GGTGCATT
                                ||  |||||  ||||||||
                                AC  CGACG  CCACGTGA
                                 CC    A_
GAM243  KIAA0794 3' TTAACTAGCAGCTTC      80418        C  GTGCAT
                                GAAGCTGC AG     TTAA
                                |||||||| ||     ||||
                                CTTCGACG TC     AATT
                                    A _______
GAM243  RAB40C   3' AGGTGCACCTGGCAGC     40977
                                GCTGCCAGGTGCATTT
                                ||||||||||||||||
                                CGACGGTCCACGTGGA

GAM244  ARHGEF12 3' GTAAATATAAAAACTTTGCTCT 31002        AT   GGG
                                AGAGCAAG  GTT   ATATTTAC
                                ||||||||  |||   ||||||||
                                TCTCGTTT  CAA   TATAAATG
                                    __   AAA
GAM244  CD81     3' ATCACAACATCCTGACTC    15131    _ A     G
                                GAG CA GATGTTG GAT
                                ||| || ||||||| |||
                                CTC GT CTACAAC CTA
                                  A  C      A
GAM244  MRPL49   3' AAATACCCCCAAGCCTTTGCTC 69561        ATG    A_
           T                     AGAGCAAG   TTGGG  TATTT
                                ||||||||   |||||  |||||
                                TCTCGTTT   AACCC  ATAAA
                                    CCG    CC
GAM244  NCSTN    3' AAATAGAAGCTTCTTGCTC   73753        T  GGGA
                                GAGCAAGA GTT    TATTT
                                |||||||| |||    |||||
                                CTCGTTCT CGA    ATAAA
                                    T   AG__
GAM244  PER2     3' GTTGAAACATTTGCTCT     43041       A     GG
                                AGAGCA GATGTT  GAT
                                |||||| ||||||  |||
                                TCTCGT TTACAA  TTG
                                   _     AG
GAM244  PTPRA    3' GTAAATATCCCTCCCCTCTCTC 55084     CA  ATGTT
                                GAG  AG    GGGATATTTAC
                                |||  ||    ||||||||||
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                                CTC  TC    CCCTATAAATG
                                  TC  CCCT_
GAM244  PTPRA    3'  GTAAATATCCCTCCCCTCTCTC 55092     CA  ATGTT
                                GAG  AG    GGGATATTTAC
                                |||  ||    ||||||||||
                                CTC  TC    CCCTATAAATG
                                  TC  CCCT_
GAM244  PTPRA    3'  GTAAATATCCCTCCCCTCTCTC 11096     CA  ATGTT
                                GAG  AG    GGGATATTTAC
                                |||  ||    ||||||||||
                                CTC  TC    CCCTATAAATG
                                  TC  CCCT_
GAM244  TCF2     3'  GTAAATATCCACAGACTCCCTC 4858      CA  A_  TG
                                GAG  AG  TGT  GGATATTTAC
                                |||  ||  |||  ||||||||||
                                CTC  TC  ACA  CCTATAAATG
                                  CC  AG  __
GAM244  XRCC4    3'  TCCAACATCCTGTCT      42355     G  A
                                AGA CA GATGTTGGG
                                ||| || |||||||||
                                TCT GT CTACAACCT
                                  _  C
GAM244  XRCC4    3'  TCCAACATCCTGTCT      42585     G  A
                                AGA CA GATGTTGGG
                                ||| || |||||||||
                                TCT GT CTACAACCT
                                  _  C
GAM244  XRCC4    3'  TCCAACATCCTGTCT      12685     G  A
                                AGA CA GATGTTGGG
                                ||| || |||||||||
                                TCT GT CTACAACCT
                                  _  C
GAM244  CNNM1    3'  GTCCCAACACCTGCTCT     39776       A A
                                AGAGCA G TGTTGGGAT
                                |||||| | |||||||||
                                TCTCGT C ACAACCCTG
                                   _ C
GAM244  DKFZP434B195 3'  CCCAACATCCTGGTCT     48427     G  A
                                AGA CA GATGTTGGG
                                ||| || |||||||||
                                TCT GT CTACAACCC
                                  G  C
GAM244  DPCR1    3'  AAATATCTCTCATCT      55118      TT
                                AGATG  GGGATATTT
                                |||||  |||||||||
                                TCTAC  CTCTATAAA
                                   T_
GAM244  KIAA0534 3'  TCCCAACATCTCATCT     71434     GCA
                                AGA   AGATGTTGGGA
                                |||   ||||||||||
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                                TCT   TCTACAACCCT
                                  AC_
GAM244  KIAA1024  3'  TCCCAACCTCTTGCTCT     69065         T
                                AGAGCAAGA GTTGGGA
                                ||||||||| |||||||
                                TCTCGTTCT CAACCCT
                                     C
GAM244  KIAA1808  3'  TCCCACACACCTTGCTCT    85869         A  _
                                AGAGCAAG TGT TGGGA
                                |||||||| ||| |||||
                                TCTCGTTC ACA ACCCT
                                    C   C
GAM244  NAPG      5'  TAAATATCTTCAGTCCTCTCT  96728      CAA   GTT
                                AGAG   GAT   GGGATATTTA
                                ||||   |||   ||||||||||
                                TCTC   CTG   TTCTATAAAT
                                  TC_   AC_
GAM244  SCGB1D1   3'  GTAAAGGTTTCAACGTCTTGCT 21593            GG  A
          CT                     AGAGCAAGATGTTG  AT TTTAC
                                ||||||||||||||  || |||||
                                TCTCGTTCTGCAAC  TG AAATG
                                       TT  G
GAM244  SMT3H2    3'  TAAATATCACCTTGTTC     22674        ATGTTGG
                                GAGCAAG      GATATTTA
                                |||||||      ||||||||
                                CTTGTTC      CTATAAAT
                                    CA_____
GAM244  TOSO      3'  AAATAGAAGGCTCTTGCTCT   18387         T   GGGA
                                AGAGCAAGA GTT    TATTT
                                ||||||||| |||    |||||
                                TCTCGTTCT CGG    ATAAA
                                     _   AAG_
GAM244  LOC124649 5'  TCCCAACACCCTAACTCT    75656      CA  A_
                                AGAG  AG  TGTTGGGA
                                ||||  ||  ||||||||
                                TCTC  TC  ACAACCCT
                                  AA  CC
GAM244  LOC129607 3'  AAATATACCAACCTTCTCT    74883      C   AT    G
                                AGAG AAG  GTTGG ATATTT
                                |||| |||  ||||| ||||||
                                TCTC TTC  CAACC TATAAA
                                  _  __    A
GAM244  LOC148304 3'  AAATATACCTGCTCT       78789       AGATGTT  G
                                AGAGCA      GG ATATTT
                                ||||||      || ||||||
                                TCTCGT      CC TATAAA
                                   ________ A
GAM244  LOC157681 5'  TAAATATCTGCCCTTAGCTCT  81543       _   AT  TG
                                AGAGC AAG  GT  GGATATTTA
                                ||||| |||  ||  |||||||||
```

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                                TCTCG TTC  CG  TCTATAAAT
                                  A   C_ __
GAM244   LOC196472 5'  CCCAACACCTGTGCTC      87720       _ A
                                GAGCA AG TGTTGGG
                                ||||| || |||||||
                                CTCGT TC ACAACCC
                                   G  C
GAM244   LOC203232 3'  TTCAGCATCCTGCCCT      71413     A   A
                                AG GCA GATGTTGGG
                                || ||| |||||||||
                                TC CGT CTACGACTT
                                 C   C
GAM244   LOC253936 3'  TTCAGCATCCTGCCCT      94667     A   A
                                AG GCA GATGTTGGG
                                || ||| |||||||||
                                TC CGT CTACGACTT
                                 C   C
GAM244   LOC92691  3'  TCCCAACAACTTACTC      56425     C   A
                                GAG AAG TGTTGGGA
                                ||| ||| ||||||||
                                CTC TTC ACAACCCT
                                  A   A
GAM245   ABCA1     3'  ACTAGTAATAATGTAATACTGT 18544        G       CA  G
                                GCGGTA TTACGTTG  TA TGGT
                                |||||| ||||||||  || ||||
                                TGTCAT AATGTAAT  AT ATCA
                                   _       A_  G
GAM245   ABCD1     3'  GCCAATGTGACTACCGT      3463              _
                                GCGGTAGTTACGTTG C
                                |||||||||||||| |
                                TGCCATCAGTGTAAC G
                                          C
GAM245   ABH       3'  ATTGTGTATTGCCGT       59750         TACGTT
                                GCGGTAGT     GCATAGT
                                ||||||||     |||||||
                                TGCCGTTA     TGTGTTA
                                   _______
GAM245   ABR       3'  GCGCTGTGTAACTGCTGC     41728         TACGT       GT
                                GCGGTAGT    TGCATAGTG
                                ||||||||    |||||||||
                                CGTCGTCA    ATGTGTCGC
                                   _____       GT
GAM245   ABR       3'  GCGCTGTGTAACTGCTGC     6576          TACGT       GT
                                GCGGTAGT    TGCATAGTG
                                ||||||||    |||||||||
                                CGTCGTCA    ATGTGTCGC
                                   _____       GT
GAM245   ACAT1     3'  GCTGTAATCAGTGTGACTACTG 3416              C__     GGT
             T                   GCGGTAGTTACGTTG   ATAGT
                                 ||||||||||||||   |||||
```

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                                TGTCATCAGTGTGAC  TGTCG
                                       TAA
GAM245  ACPP    3' GCTGTTATGCATAGGATGGTTG 66850    TA  ACGT    TG
          T                    GCGG  GTT   TGCATAG  GT
                               |||| |||   ||||||| ||
                               TGTT  TAG   ACGTATT  CG
                                 GG  GAT_    GT
GAM245  ADAM15  3' ACCTGCCGGCGTAGTTGCAGC  13771   G  GT    _ TAGT
                               GC GTA  TACGTTG CA   GGT
                               || |||  ||||||| ||   |||
                               CG CGT  ATGCGGC GT   CCA
                                A  TG    C ____
GAM245  ADAMTS13 3' CCACTGGGGTGCTGCTGT   57373       TACGTT  A_
                               GCGGTAGT    GC  TAGTGG
                               ||||||||    ||  ||||||
                               TGTCGTCG    TG  GTCACC
                                   _______ GG
GAM245  ADAMTS3  3' CGTTGTGTAAATACTGT    26478      GTTACG     TG
                               GCGGTA    TTGCATAG  G
                               ||||||    |||||||| |
                               TGTCAT    AATGTGTT  C
                                  A_____      GT
GAM245  ADAMTS5  3' ATCATTGTTAATGTGGTTAATG 22891    G  TT    C
          C                    GCG TAG  ACGTTG ATAGTGGT
                               ||| |||  |||||| ||||||||
                               CGT ATT  TGTAAT TGTTACTA
                                 A  GG    _
GAM245  ADD3    3' ATTATTATAACAATGTGACATT 33671      A      C_
          GC                   GCGGT GTTACGTTG  ATAGTGGT
                               ||||| |||||||||  ||||||||
                               CGTTA CAGTGTAAC  TATTATTA
                                  _       AA
GAM245  ADRA1A  3' GCTATGTATTATGTGACATCGC 52793     A     __
                               GCGGT GTTACGT  TGCATAGT
                               ||||| |||||||  ||||||||
                               CGCTA CAGTGTA  ATGTATCG
                                  _      TT
GAM245  ANGPT1  3' ACTGTTGTTCTGTGGTTATC  57771     TT  TT  _
                               GGTAG  ACG  GCA TAGT
                               |||||  |||  ||| ||||
                               CTATT  TGT  TGT GTCA
                                  GG  CT  T
GAM245  ANGPT1  5' GCTACTATGCAATAAATATC  57773    GTTAC
                               GGTA    GTTGCATAGTGGT
                               ||||    ||||||||||||
                               CTAT    TAACGTATCATCG
                                 AAA__
GAM245  ANGPT1  5' GCTACTATGCAATAAATATC  6703     GTTAC
                               GGTA    GTTGCATAGTGGT
                               ||||    ||||||||||||
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                                CTAT    TAACGTATCATCG
                                  AAA__
GAM245  APBB2    5'  GTTGCTGTGGGTGAGCTGCTGT 72467        A  TTG     GG
                                GCGGTAGTT CG   CATAGT  T
                                |||||||||  ||   ||||||  |
                                TGTCGTCGA GT   GTGTCG  G
                                     _  GG_     TT
GAM245  APCS     5'  GCCACTGTGTTGTCTGCTACC  7913       T_   TT
                                GGTAGT  ACG  GCATAGTGGT
                                ||||||  |||  ||||||||||
                                CCATCG  TGT  TGTGTCACCG
                                   TC   __
GAM245  ARF3     3'  TATTATTATGTAGTTGTTCAGA 8009     _____   TT_
             AGCTGTTGC               TT    ACG   GCATAGTGGT   A
                                ||    |||   ||||||||||  |
                                GA    TGT   TGTATTATTA   T
                                 AGACT   TGA
GAM245  ARHA     3'  GTACTGTGTAATTAGTGCC   70697     G   C        GG
                                GGTA TTA GTTGCATAGT  T
                                ||||  ||| ||||||||||  |
                                CCGT GAT TAATGTGTCA  G
                                  _   _        TT
GAM245  ARHG     3'  GTTGCTGCCTATTGTGGTGCCG 8016       G    T  CA    GG
             C                   GCGGTA TTACG TG  TAGT  T
                                ||||||  |||||  ||  ||||  |
                                CGCCGT GGTGT AT  GTCG  G
                                   _    T  CC    TT
GAM245  ASL      3'  GCTGCTGTGTGTTTCCTGCC   71899      TT_  GTT     TG
                                GGTAG   AC   GCATAG  GT
                                |||||   ||   ||||||  ||
                                CCGTC   TG   TGTGTC  CG
                                   CTT  ___     GT
GAM245  ATBF1    5'  GTTGCTGTGTAATGTGGATCCC 22551     TA  _         GG
             CG                    CGG  GTT ACGTTGCATAGT  T
                                |||  |||  ||||||||||||  |
                                GCC  TAG TGTAATGTGTCG  G
                                  CC   G          TT
GAM245  ATP2B4   5'  ACTACTACAGTTGCTGGTTGTT 70341    GG   TT C  T  A_
             GC                    GC  TAG  A GT GC  TAGTGGT
                                ||  |||  | || ||  |||||||
                                CG  GTT  T CG TG  ATCATCA
                                 TT   GG _  T  AC
GAM245  ATP2B4   3'  TGTCACGTCAGCTGCTGT    70344         _   T
                                GCGGTAGTT ACGT GCA
                                |||||||||  ||||  |||
                                TGTCGTCGA TGCA TGT
                                     C   C
GAM245  B3GALT3  3'  CTATAATGTGTGATTCTGT   13680      T     GTT    A
                                GCGG AGTTAC   GCAT GTGG
                                ||||  ||||||   ||||  ||||
```

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                                TGTC TTAGTG   TGTA TATC
                                  _     ___    A
GAM245  B4GALT1   3'  ACCATTGTGTAGGGGGCTGT   7664       AGTTACG
                                GCGGT      TTGCATAGTGGT
                                |||||      ||||||||||||
                                TGTCG      GATGTGTTACCA
                                  GGG____
GAM245  B4GALT7   3'  ACCGCTCTAGCTGGTTGTTGC  23412    GG   TT C    CAT
                                GC  TAG  A GTTG   AGTGGT
                                ||  |||  | ||||   ||||||
                                CG  GTT  T CGAT   TCGCCA
                                 TT   GG _   C__
GAM245  BAI3      3'  CTGGACAGTGTGACTATC    8123            CA
                                GGTAGTTACGTTG  TAG
                                ||||||||||||  |||
                                CTATCAGTGTGAC  GTC
                                       AG
GAM245  BAP1      3'  GCTGGCAAGTGTGGCAGCTGC  16217      A     _    A
                                GCGGT GTTACG TTGC TAGT
                                ||||| |||||| |||| ||||
                                CGTCG CGGTGT AACG GTCG
                                  A     G    _
GAM245  BASP1     3'  ATCGTTTGTACCTGAAACTGCC 75965         A  T_    TAG
          GC                    GCGGTAGTT CG  TGCA   TGGT
                                |||||||||  ||  ||||   ||||
                                CGCCGTCAA GT  ATGT   GCTA
                                     A  CC    TT_
GAM245  BAT1      5'  GTCGCTGTTGCTGCCGC     54586         T  _  T
                                GCGGTAGT AC GT GC
                                ||||||||  ||  ||  ||
                                CGCCGTCG TG CG TG
                                     T  T  C
GAM245  BAT1      5'  GTCGCTGTTGCTGCCGC     16162         T  _  T
                                GCGGTAGT AC GT GC
                                ||||||||  ||  ||  ||
                                CGCCGTCG TG CG TG
                                     T  T  C
GAM245  BAZ2A     3'  ATCACTGCCTTACATGTGACTA 25594          TGCA__
          T                     GTAGTTACGT     TAGTGGT
                                ||||||||||     |||||||
                                TATCAGTGTA     GTCACTA
                                     CATTCC
GAM245  BAZ2B     3'  ACCACTGTGTTTTATCTACTGT 25618        TTACGTT
                                GCGGTAG      GCATAGTGGT
                                |||||||      ||||||||||
                                TGTCATC      TGTGTCACCA
                                   TATTT__
GAM245  BCAS2     3'  ATCATAGAAGGTGTAGGCTGCT 19649         _     GCATA
          GT                    GCGGTAGT TACGTT     GTGGT
                                |||||||| ||||||     |||||
```

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                                TGTCGTCG ATGTGG    TACTA
                                    G     AAGA_
GAM245  BDP1    5'  GCTGGTGGTGTGGCTTTGT   37365     T     TT  A
                                GCGG AGTTACG  GC TAGT
                                |||| |||||||  || ||||
                                TGTT TCGGTGT  TG GTCG
                                  _     GG  _
GAM245  BHLHB3  3'  CGCTGCTGTTGCTACTGT    47765       T   TT   TA TG
                                GCGGTAGT ACG  GCA  G  G
                                |||||||| |||  |||  |  |
                                TGTCATCG TGT  CGT  C  C
                                    T   __   __ GT
GAM245  BRCA1   5'  GCCGGGCGTGGTGCCGC    23531      G     __
                                GCGGTA TTACGTT  GC
                                |||||| |||||||  ||
                                CGCCGT GGTGCGG  CG
                                  _     GC
GAM245  BRPF1   3'  GCTGTTGTAAATACTGTAATTA 73088       ____    _   GGT
            TCG                   TAGTTACG    TTGCA TAGT
                                |||||||    ||||| ||||
                                ATTAATGT    AATGT GTCG
                                    CATA    T      T
GAM245  BTAF1   3'  TGTAAATGCAATTGCTGC    72458        A   _
                                GCGGTAGTT CGTT GCA
                                ||||||||| |||| |||
                                CGTCGTTAA GTAA TGT
                                    C    A
GAM245  BTG2    3'  CACTGTGCAATATGCC     22210     GTTAC
                                GGTA    GTTGCATAGTG
                                ||||    ||||||||||
                                CCGT    TAACGTGTCAC
                                  A____
GAM245  BUB3    3'  TGTAACGTAATTGCAGT     16370    G
                                GC GTAGTTACGTTGCA
                                || ||||||||||||||
                                TG CGTTAATGCAATGT
                                 A
GAM245  BYSL    3'  GCTATTGTGTCAGGTCACTG   14477     T  G  _
                                TAGT AC TTG CATAGTGGT
                                |||| || ||| |||||||||
                                GTCA TG GAC GTGTTATCG
                                  C  _   T
GAM245  BZRP    3'  ATCACGCTTGTGATGTGGTGGC 5547      AG     TG  TA_
            CGT                   GCGGT  TTACGT  CA   GTGGT
                                |||||  ||||||  ||   |||||
                                TGCCG  GGTGTA  GT   CACTA
                                   GT     GT  TCG
GAM245  C10orf2 3'  CTACTGAGAAACTACTGT    41544         ACGTTGCA
                                GCGGTAGTT       TAGTGG
                                |||||||||       ||||||
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                                TGTCATCAA      GTCATC
                                     AGA_____
GAM245  C14orf2  3'  ATCATTGTGAAATAATTACC  16893       CGTTG
                                GGTAGTTA    CATAGTGGT
                                ||||||||    |||||||||
                                CCATTAAT    GTGTTACTA
                                     AAA__
GAM245  C8orf1   3'  TCATTATGCCAGAAATTATC  15088       ACGTT      GT
                                GGTAGTT    GCATAGTG
                                |||||||    ||||||||
                                CTATTAA    CGTATTAC
                                    AGAC_      TG
GAM245  CA12     3'  CGCTTGCTGTAACTG      6877        TT   T  TG
                                TAGTTACG  GCA AG  G
                                ||||||||  ||| ||  |
                                GTCAATGT  CGT TC  C
                                     __  _  GT
GAM245  CA2      3'  ACTGCTGTGGCTGGTTGGTGC  3559     G   TT C  TG    TG
                                GCG TAG  A GT  CATAG  GT
                                ||| |||  | ||  |||||  ||
                                CGT GTT  T CG  GTGTC  CA
                                  G   GG _ __    GT
GAM245  CACNB4   3'  ACTGTGCTAATGGGCTGCTGT  5582         A   _
                                GCGGTAGTT CGTT GCATAGT
                                ||||||||| |||| |||||||
                                TGTCGTCGG GTAA CGTGTCA
                                     _   T
GAM245  CALB2    3'  CCAATGGTGTAGCTGTCC    8209     _      GTT  ATAG
                                GG TAGTTAC   GC    TGG
                                || |||||||   ||    |||
                                CC GTCGATG   TG    ACC
                                 T      ____  GTA_
GAM245  CAPN10   3'  ACCGAGTGAGGTGTACATTGCC 43598        _    TG   AG
           GT                     GCGGTAGT TACGT  CAT  TGGT
                                ||||||||| |||||  |||  ||||
                                TGCCGTTA ATGTG  GTG  GCCA
                                     C    GA   A_
GAM245  CARPX    3'  CTCACTGTGTTTGGTTACTGT  39420       TT CGTT       T
                                GCGGTAG  A    GCATAGTGG
                                |||||||  |    |||||||||
                                TGTCATT  T    TGTGTCACT
                                     GG T___        CA
GAM245  CARS     3'  ACCATTGTGGACTAGTGGCTGC 57701          __  G
           TGT                     CGGTAGTTAC  GTT CATAGTGGT
                                ||||||||||  ||| |||||||||
                                GTCGTCGGTG  CAG GTGTTACCA
                                     AT  _
GAM245  CARS     3'  ACCATTGTGGACTAGTGGCTGC 8257          __  G
           TGT                     CGGTAGTTAC  GTT CATAGTGGT
                                ||||||||||  ||| |||||||||
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                                GTCGTCGGTG  CAG GTGTTACCA
                                      AT  _
GAM245  CASP3   3'  CCACTATGAAGCTACC     52193      TACGTTG
                                GGTAGT     CATAGTGG
                                ||||||     ||||||||
                                CCATCG     GTATCACC
                                   AA_____
GAM245  CASP3   3'  CCACTATGAAGCTACC     15097      TACGTTG
                                GGTAGT     CATAGTGG
                                ||||||     ||||||||
                                CCATCG     GTATCACC
                                   AA_____
GAM245  CASP8   3'  CCACTGTGAATAACTG     52943      CGTTG
                                TAGTTA    CATAGTGG
                                ||||||    ||||||||
                                GTCAAT    GTGTCACC
                                   AA___
GAM245  CCND1    3'  TGACTTAATGTGATTACTGC  53892           CAT  GGT
                                GCGGTAGTTACGTTG  AGT
                                ||||||||||||||  |||
                                CGTCATTAGTGTAAT  TCA
                                        ___  GTT
GAM245  CCNT2   3'  GTTATGTGGATTACTGT     54267        _   T
                                GCGGTAGTT ACGT GC
                                ||||||||| |||| ||
                                TGTCATTAG TGTA TG
                                     G   T
GAM245  CD164   3'  GCTATACTGATGTAATTGTC  20050   GT      GC_
                                G  AGTTACGTT  ATAGT
                                |  |||||||||  |||||
                                C  TTAATGTAG  TATCG
                                 TG       TCA
GAM245  CD8A    3'  CGTTGTGCGCACATCGC     8333      A  TAC  T    TG
                                GCGGT GT  GT GCATAG  G
                                ||||| ||  || ||||||  |
                                CGCTA CA  CG CGTGTT  C
                                  _ ___ _     GT
GAM245  CDH1    3'  ATTGTGGGCATGAGCTGCTGT  15141        A  T  ATA TG
                                GCGGTAGTT CGT GC  G  GT
                                ||||||||| ||| ||  |  ||
                                TGTCGTCGA GTA CG  T  TA
                                     _  _ GG_ GT
GAM245  CDH2    5'  CCGCTGTTGGTGCTGCCGC   8375        TA  TTGC
                                GCGGTAGT  CG   ATAGTGG
                                ||||||||  ||   |||||||
                                CGCCGTCG  GT   TGTCGCC
                                    TG  ____
GAM245  CDH5    3'  ACTGTGTTTAACTGCTGC    8382         CGTT
                                GCGGTAGTTA   GCATAGT
                                ||||||||||   |||||||
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                                CGTCGTCAAT    TGTGTCA
                                      T___
GAM245  CDKN2A   3'  GCCCGAGTGGCGGAGCTGCTGC 54236         A   TG ATAGT
                                GCGGTAGTT CGT  C     GGT
                                ||||||||| |||  |    |||
                                CGTCGTCGA GCG  G     CCG
                                     G   GT AGC__
GAM245  CDKN2B   3'  CCGCGTGGCGGAGCTGCTGC   54354         A   TG ATA
                                GCGGTAGTT CGT  C   GTGG
                                ||||||||| |||  |   ||||
                                CGTCGTCGA GCG  G   CGCC
                                     G   GT ___
GAM245  CDX1     3'  TGGGAGTGTGGCTCCTGT    8404       T     _  G
                                GCGG AGTTACG TT CA
                                |||| ||||||| || ||
                                TGTC TCGGTGT AG GT
                                  C      G  G
GAM245  CHRNA5   5'  GCTGCTAGGCTGAGGCTGCTGT 59756         TA  TT  A   TG
                                GCGGTAGT  CG  GC TAG  GT
                                ||||||||  ||  || |||  ||
                                TGTCGTCG  GT  CG ATC  CG
                                     GA  __  G   GT
GAM245  CHST7    3'  ACTGCTGTGCAATTCTGCTG   39109       TTAC        TG
                                CGGTAG   GTTGCATAG  GT
                                ||||||   |||||||||  ||
                                GTCGTC   TAACGTGTC  CA
                                   T___        GT
GAM245  CIT      3'  ACCGTAACACGAAATTGCTGT  69739         A   TGCA  G
                                GCGGTAGTT CGT   TA TGGT
                                ||||||||| |||   || ||||
                                TGTCGTTAA GCA   AT GCCA
                                     A   CA__  _
GAM245  CKTSF1B1  3'  ATGGACATAACTATTGT     25364          C   G
                                GCGGTAGTTA GTT CAT
                                |||||||||| ||| |||
                                TGTTATCAAT CAG GTA
                                     A   _
GAM245  CNR1     3'  ATCACTGTGCAGTTGCTGT   32212        TTACG
                                GCGGTAG    TTGCATAGTGGT
                                |||||||    ||||||||||||
                                TGTCGTT    GACGTGTCACTA
                                     _____          T
GAM245  COL5A3   3'  GCCAATGGGATGTGACTTCGC  31695      T       G   AG
                                GCGG AGTTACGTT CAT  TGGT
                                |||| ||||||||| |||  ||||
                                CGCT TCAGTGTAG GTA  ACCG
                                  _       G   __
GAM245  COL6A1   5'  GCCGCGCTGTGTGGTGACCGC  8478       AG    TT  ATA
                                GCGGT  TTACG  GC   GTGGT
                                |||||  |||||  ||   |||||
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                                CGCCA  GGTGT  CG   CGCCG
                                  GT    GT  ___
GAM245  COL9A2   3'  CTACTAGGTGACTGCTGC    8486          GTTGCA
                                GCGGTAGTTAC     TAGTGG
                                ||||||||||      ||||||
                                CGTCGTCAGTG     ATCATC
                                     G_____
GAM245  COMT     5'  CGCTGGTGGTGCTGCTGC    23602        TAC TT  A   TG
                                GCGGTAGT   G  GC TAG  G
                                ||||||||   |  || |||  |
                                CGTCGTCG   T  TG GTC  C
                                    ___ GG  _   GT
GAM245  CPO      3'  GCCACTGTGTGGCAGTTACCCG 3637       TA  T  _  TG
           T                     GCGG  GT AC GT  CATAGTGGT
                                ||||  || || ||  |||||||||
                                TGCC  CA TG CG  GTGTCACCG
                                  __  T  A  GT
GAM245  CRABP1   5'  GCCGCTGTCCGTACCTGCCGC  59759        T    TTGC
                                GCGGTAG TACG    ATAGTGGT
                                |||||||  ||||    ||||||||
                                CGCCGTC ATGC    TGTCGCCG
                                    C    C___
GAM245  CSNK1A1  3'  GTTGCTTAGATAAATGTAATCA 8548       A       GCAT__   GG
           CTGT                   CGGT GTTACGTT     AGT  T
                                |||| ||||||||      |||  |
                                GTCA TAATGTAA     TCG  G
                                  C       ATAGAT   TT
GAM245  CTNNA1   3'  TAATTACTAATGTACGCTGCTG 65920        _     TGCA
           C                     CGGTAGT TACGT    TAGTGGT
                                |||||||  |||||    |||||||
                                GTCGTCG ATGTA    ATCATTA
                                    C     ____       ATA
GAM245  CTSF     3'  GCTGATCAGAGTGGCTGCTGC  94386          G   CA
                                GCGGTAGTTAC TTG  TAGT
                                ||||||||||| |||  ||||
                                CGTCGTCGGTG GAC  GTCG
                                      A   TA
GAM245  CTSK     3'  GCTAAGAGATGTGACTACAGC  4624     G         GCA
                                GC GTAGTTACGTT   TAGT
                                ||  ||||||||||   ||||
                                CG CATCAGTGTAG   ATCG
                                 A          AGA
GAM245  CTSL2    3'  CCACTACTTTAATTATTGT    7187           CGTTGCA
                                GCGGTAGTTA      TAGTGG
                                ||||||||||      ||||||
                                TGTTATTAAT      ATCACC
                                     TTC____
GAM245  CUL3     3'  ATTGCTGGCGATGTGATGCTGC 13161        G        A   TG
                                GCGGTA TTACGTTGC TAG  GT
                                ||||||  |||||||| |||  ||
```

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                                CGTCGT AGTGTAGCG GTC  TA
                                  _       _  GT
GAM245  CXorf6   3'  GCCACCAAGCTATGTGGCTGCT 18516          T  ATA
          GC                    GCGGTAGTTACGT GC   GTGGT
                                |||||||||||| ||  |||||
                                CGTCGTCGGTGTA CG   CACCG
                                      T  AAC
GAM245  CYFIP1   3'  CCATTAACTGTAACTATT    66456         TTGCA
                                GGTAGTTACG    TAGTGG
                                ||||||||||    ||||||
                                TTATCAATGT    ATTACC
                                     CA___
GAM245  CYP2C9   3'  GCTGCTGTGCAGTCCCTGCAGC 5748    G   TT  GT     TG
                                GC GTAG  AC  TGCATAG  GT
                                || ||||  ||  |||||||  ||
                                CG CGTC  TG  ACGTGTC  CG
                                 A   CC  __      GT
GAM245  CYP4F3   3'  ACCACGTCCAGCTAATTGTTGT 6105    GG    C   CATA
                                GC  TAGTTA GTTG   GTGGT
                                ||  |||||| ||||   |||||
                                TG  GTTAAT CGAC   CACCA
                                 TT     _   CTG_
GAM245  D1S155E  3'  CCCTTGGTGTAGCTTCTGT   23123     T     TT CAT  T
                                GCGG AGTTACG  G   AG GG
                                |||| |||||||  |   || ||
                                TGTC TCGATGT  T   TC CC
                                  T      GG ___  _
GAM245  DAZL     3'  TAACTTAATGTAGTTACTGT   68142      GT     CAT   GGT
                                GCGGTA  TACGTTG   AGT
                                ||||||  |||||||   |||
                                TGTCAT  ATGTAAT   TCA
                                   TG      ___   ATC
GAM245  DBT      3'  CATTGTGCCACTATC      8608       TACGTT
                                GGTAGT     GCATAGTG
                                ||||||     ||||||||
                                CTATCA     CGTGTTAC
                                   C_____
GAM245  DDX3     3'  TCACTGTAGCTTTAGTAATTGC 7225        GTT_ _    GT
                                GTAGTTAC   GC ATAGTG
                                ||||||||   || ||||||
                                CGTTAATG   CG TGTCAC
                                     ATTT  A     TG
GAM245  DFFB     3'  CACGTGAAACTGCTGT      87376        ACG TG ATA
                                GCGGTAGTT   T  C   GTG
                                |||||||||  |  |  |||
                                TGTCGTCAA   A  G   CAC
                                     ___ GT ___
GAM245  DHFR     3'  CATAATGATGTGACTGCT    5800          TG   A
                                GGTAGTTACGT  CAT GTG
                                ||||||||||  ||| |||
```

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                                TCGTCAGTGTA  GTA TAC
                                     __   A
GAM245  DOCK1    3'  CCGGTGGTGTGACTTCGT    7271      T      TT  ATAG
                                GCGG AGTTACG  GC    TGG
                                |||| |||||||  ||    |||
                                TGCT TCAGTGT  TG    GCC
                                  _      GG  ____
GAM245  DPYSL3   3'  CCGCTGTGGCAGCTGTCAC   7313     T _    _
                                GT AC GTTGC ATAGTGG
                                || || ||||| |||||||
                                CA TG CGACG TGTCGCC
                                 C  T    G
GAM245  DRP2     5'  CCGTGTGAGTGGCTATCGT   8662          G TG   AGT
                                GCGGTAGTTAC T  CAT   GG
                                |||||||||||  |  |||   ||
                                TGCTATCGGTG A  GTG   CC
                                      _ GT   ___
GAM245  DUSP4    5'  ACTGCTATGTGACCGCGAGGCT 7334       AGTTAC  TG    TG
            GC                    GCGGT     GT  CATAG  GT
                                |||||     ||  |||||  ||
                                CGTCG     CA  GTATC  CA
                                   GAGCGC  GT    GT
GAM245  DVL1     3'  GCTGCTTCTGTGTAAATGCTGC 59335       G    GTT   T_  TG
                                GCGGTA TTAC   GCA  AG  GT
                                |||||| ||||   |||  ||  ||
                                CGTCGT AATG   TGT  TC  CG
                                   A   ___   CT  GT
GAM245  EIF4G1   3'  TCACTCTCGGACTGCCGT    17071         A  TTGCAT
                                GCGGTAGTT CG     AGTGG
                                |||||||||  ||     |||||
                                TGCCGTCAG GC     TCACT
                                      _  TC_____
GAM245  ELL      3'  CACTTTTAGCTACTGC      21523          CGTTGCAT
                                GCGGTAGTTA       AGTG
                                ||||||||||       ||||
                                CGTCATCGAT       TCAC
                                     TT_______
GAM245  ENTPD5   3'  TAATGTGAACTGCTGC      6975          _
                                GCGGTAGT TACGTTG
                                |||||||| |||||||
                                CGTCGTCA GTGTAAT
                                    A
GAM245  EPHB2    3'  TGCAGTGACTGCCGT       33889          GT
                                GCGGTAGTTAC  TGCA
                                ||||||||||  ||||
                                TGCCGTCAGTG  ACGT
                                      __
GAM245  EPHB2    3'  CTATTGTGAATAGTGCTGC   15444       T  GTTG
                                GTAGT AC    CATAGTGG
                                ||||| ||    ||||||||
```

```
                                CGTCG TG   GTGTTATC
                                   _ ATAA
GAM245  EPHB2    3'  TGCAGTGACTGCCGT      15450          GT
                                GCGGTAGTTAC  TGCA
                                ||||||||||  ||||
                                TGCCGTCAGTG  ACGT
                                    __
GAM245  ESR1     3'  ATTGTTTTCTAAGTAATTGCTG 3699          GTTGCAT  TG
             C                   GCGGTAGTTAC     AG  GT
                                ||||||||||     ||  ||
                                CGTCGTTAATG     TT  TA
                                      AATCTT_  GT
GAM245  F3       3'  ACTGTTGGAGCTACTGC     67079        A  TTGC
                                GCGGTAGTT CG   ATAGT
                                |||||||| ||   |||||
                                CGTCATCGA GT   TGTCA
                                     G _____
GAM245  FABP5    3'  ATTACTGTGTTCAATTATC    7540        ACGTT
                                GGTAGTT    GCATAGTGGT
                                |||||||    ||||||||||
                                CTATTAA    TGTGTCATTA
                                    CT___
GAM245  FACL3    3'  TGTTGCTGTGTAATTATTGT   15501          TT   TAGTGGT
                                GCGGTAGTTACG  GCA
                                ||||||||||||  |||
                                TGTTATTAATGT  CGT
                                      GT   TG   TG
GAM245  FACL4    3'  ATTATTATCAAGTAGACTACTG 15507        _ G   C
             T                   GCGGTAGTT AC TTG ATAGTGGT
                                ||||||||| || ||| ||||||||
                                TGTCATCAG TG AAC TATTATTA
                                     A  _  _
GAM245  FACL4    3'  ATTATTATCAAGTAGACTACTG 43397        _ G   C
             T                   GCGGTAGTT AC TTG ATAGTGGT
                                ||||||||| || ||| ||||||||
                                TGTCATCAG TG AAC TATTATTA
                                     A  _  _
GAM245  FBLN1    3'  ATTGCTGCCAGTGACTGTGGT  21397    G      GTT   TA TG
                                GC GTAGTTAC   GCA  G  GT
                                || ||||||||   |||  |  ||
                                TG TGTCAGTG   CGT  C  TA
                                 G       AC_   __ GT
GAM245  FBN2     3'  CTCAAAGGCAACCGTGGTTACT 8846        TT  _   ATAG   T
             GT                   GCGGTAG  ACG TTGC    TGG
                                |||||||  ||| ||||   |||
                                TGTCATT  TGC AACG    ACT
                                    GG   C    GAA_   CG
GAM245  FBXW1B   3'  ACTGAGCAAATGTAAATTACTG 53335         _    _ A   GGT
             C                   GCGGTAGTT ACGTT GC TAGT
                                |||||||| ||||| || ||||
```

```
                                CGTCATTAA TGTAA CG GTCA
                                     A    A  A
GAM245  FBXW1B   3'  ACTGAGCAAATGTAAATTACTG 53324        _    _ A   GGT
              C                   GCGGTAGTT ACGTT GC TAGT
                                  ||||||||| ||||| || ||||
                                CGTCATTAA TGTAA CG GTCA
                                     A    A  A
GAM245  FBXW1B   3'  ACTGAGCAAATGTAAATTACTG 24520        _    _ A   GGT
              C                   GCGGTAGTT ACGTT GC TAGT
                                  ||||||||| ||||| || ||||
                                CGTCATTAA TGTAA CG GTCA
                                     A    A  A
GAM245  FDFT1    3'  TCGCTGCATATGTGACTGTC  15519   GT      _   TA  GT
                                G  AGTTACGT TGCA  GTG
                                |  |||||||| ||||  |||
                                C  TCAGTGTA ACGT  CGC
                                 TG       T   __  TG
GAM245  FGF5     3'  CTATTGTGAATAGTGCTGC   15541      T  GTTG
                                GTAGT AC   CATAGTGG
                                ||||| ||   ||||||||
                                CGTCG TG   GTGTTATC
                                   _ ATAA
GAM245  FGF5     3'  CTATTGTGAATAGTGCTGC   52487      T  GTTG
                                GTAGT AC   CATAGTGG
                                ||||| ||   ||||||||
                                CGTCG TG   GTGTTATC
                                   _ ATAA
GAM245  FGFR3    3'  GCTGCTGTGCAACGGTCTCC  3772     T  TTA       TG
                                GG AG   CGTTGCATAG  GT
                                || ||   ||||||||||  ||
                                CC TC   GCAACGTGTC  CG
                                 _ TG_        GT
GAM245  FGR      3'  ATCACCGAGGACGTGGCTGCT  17893          GCATA
                                GGTAGTTACGTT    GTGGT
                                ||||||||||||    |||||
                                TCGTCGGTGCAG    CACTA
                                      GAGC_
GAM245  FHL1     3'  CCCTTGTAACGTAGTAGTTGT  7557     GG AG       T  T  T
                                GC  T  TTACGTTGCA AG GG
                                ||  |  |||||||||| || ||
                                TG  G  GATGCAATGT TC CC
                                 TT AT        _ _  T
GAM245  FLT1     3'  GCCGACAGTGGTGTAACTG   8918        TT  ATAG
                                TAGTTACG  GC   TGGT
                                ||||||||  ||   ||||
                                GTCAATGT  TG   GCCG
                                    GG  ACA_
GAM245  FMN2     3'  TCGCTATGTGCAATACTGT   79346      GTTAC  T
                                GCGGTA    GT GCATAGTGG
                                ||||||    || |||||||||
```

```
                                TGTCAT    CG TGTATCGCT
                                   AA___ _
GAM245  FMR1    3'  ACCTTGTAATGTAACTGCT   8935            TA
                                GGTAGTTACGTTGCA  GT
                                |||||||||||||||  ||
                                TCGTCAATGTAATGT  CA
                                         TC
GAM245  FMR2    5'  TCGCTGGGTGCGCGGGCTACCG 8945         A  T   __   GT
          C                      GCGGTAGTT CGT GCAT  AGTG
                                |||||||||  ||| ||||  ||||
                                CGCCATCGG GCG CGTG  TCGC
                                      _  _   GG   TG
GAM245  FN1     3'  ACTACTGTGGAAAGACAACTGT 8946       A  ACG  G
                                GCGGT GTT   TT CATAGTGGT
                                ||||| |||   || |||||||||
                                TGTCA CAG   AA GTGTCATCA
                                   A  A__  G
GAM245  FOG2    3'  GTATTGTGTAGCACATATGGT  23877    G  GTTAC       GG
                                GC GTA    GTTGCATAGT  T
                                || |||    ||||||||||  |
                                TG TAT    CGATGTGTTA  G
                                 G  ACA__        TT
GAM245  FOXD2   5'  GCCACTGTGCGGCGCTGTCG   15565    GT  TTA
                                CG  AG   CGTTGCATAGTGGT
                                ||  ||   ||||||||||||||
                                GC  TC   GCGGCGTGTCACCG
                                 TG  ___
GAM245  FOXO1A  3'  ATCATTATGTTTTATTACT   8903       TACGTT
                                GGTAGT     GCATAGTGGT
                                ||||||     ||||||||||
                                TCATTA     TGTATTACTA
                                   TTT___
GAM245  FRAP1   3'  ATCACTGTGCAGTGGGACC   17096     AGTTA
                                GGT    CGTTGCATAGTGGT
                                |||    ||||||||||||||
                                CCA    GTGACGTGTCACTA
                                  GG___
GAM245  FUS1    3'  TGCAACTAACTGTTGC      23453    GG     C
                                GC  TAGTTA GTTGCA
                                ||  |||||| ||||||
                                CG  GTCAAT CAACGT
                                 TT     _
GAM245  FUT6    3'  ACCGTTTCCAGATGTAATACTG 3805       G      GCAT
          C                      GCGGTA TTACGTT    AGTGGT
                                |||||| |||||||    ||||||
                                CGTCAT AATGTAG    TTGCCA
                                   _      ACCT
GAM245  FUT9    3'  GCTTGTGGTTTGATTATTGT   67845         CG TG  T
                                GCGGTAGTTA  T  CA AGT
                                ||||||||||  |  || |||
```

```
                                TGTTATTAGT  G  GT TCG
                                     TT GT  _
GAM245  FZD1     3'  TCATGGAAAGATGTGGTTACTG 13038       TT    GCATA   GT
                                CGGTAG  ACGTT    GTG
                                ||||||  |||||    |||
                                GTCATT  TGTAG    TAC
                                   GG    AAAGG   TG
GAM245  G6PT1    3'  GCAGTGGGTGACTGCTGT    7598          G__
                                GCGGTAGTTAC   TTGC
                                ||||||||||   ||||
                                TGTCGTCAGTG   GACG
                                      GGT
GAM245  GABRP    3'  GTCGCTGTCATTCTGTCATTGC 26401       T   T__  C     GT
           TGC                    CGGTAGT ACG   TG ATAGTG
                                ||||||| |||   || ||||||
                                GTCGTTA TGT   AC TGTCGC
                                    C   CTT  _     TG
GAM245  GATA6    3'  GCTGACAGAACGTGATTCTCGT 17916     GT       GCA_
                                GCG  AGTTACGTT    TAGT
                                |||  |||||||||    ||||
                                TGC  TTAGTGCAA    GTCG
                                  TC        GACA
GAM245  GEMIN5   5'  GCTGTTTTGGAGGTGAACTGTT 89165    GG   _   G  G  T  TG
           GC                     GC  TAGT TAC TT CA AG  GT
                                ||  |||| ||| || || ||  ||
                                CG  GTCA GTG AG GT TT  CG
                                 TT    A   G  _  T  GT
GAM245  GFRA1    5'  TCGCCGGCGGCGGTGGCTGCTG 17936          _    ATA   GT
           C                      GCGGTAGTTAC GTTGC   GTG
                                ||||||||||| |||||   |||
                                CGTCGTCGGTG CGGCG   CGC
                                      G    GC_   TG
GAM245  GLS      3'  ACTGTGCTATTAACTGCTGC  29787         CGTT
                                GCGGTAGTTA    GCATAGT
                                ||||||||||    |||||||
                                CGTCGTCAAT    CGTGTCA
                                      TAT_
GAM245  GNAS     3'  GCTTCAACGATGTGACTGCC   33440           CAT_
                                GGTAGTTACGTTG    AGT
                                ||||||||||||    |||
                                CCGTCAGTGTAGC    TCG
                                       AACT
GAM245  GNL1     5'  ACTATGGTAACAGCTGC     97887      A    GTTG
                                GCGGT GTTAC    CATAGT
                                ||||| |||||    ||||||
                                CGTCG CAATG    GTATCA
                                   A    _____
GAM245  GNL1     5'  ACTATGGTAACAGCTGC     92038      A    GTTG
                                GCGGT GTTAC    CATAGT
                                ||||| |||||    ||||||
```

```
                                CGTCG CAATG   GTATCA
                                  A   ____
GAM245  GORASP1  3' TTACTATGAAAGCTGCT    49115       ACGTTG
                                GGTAGTT    CATAGTGG
                                |||||||    ||||||||
                                TCGTCGA    GTATCATT
                                   AA____
GAM245  GPR44    3' ACTGCTGTGTTTGAGCTCTGC 16521     T   A TT    TG
                                GCGG AGTT CG  GCATAG  GT
                                |||| |||| ||  ||||||  ||
                                CGTC TCGA GT  TGTGTC  CA
                                  _   _ T_    GT
GAM245  GPR44    5' GCCTCTTGTCTAGCTGCTGT  16528        CGTT  T  T
                                GCGGTAGTTA   GCA AG GGT
                                ||||||||||   ||| || |||
                                TGTCGTCGAT   TGT TC CCG
                                     C___  _ T
GAM245  GPR48    3' CTACTGTGTGTGTAACCGT   37503     AGT  GTT
                                GCGGT  TAC  GCATAGTGG
                                |||||  |||  |||||||||
                                TGCCA  GTG  TGTGTCATC
                                  AT_  ___
GAM245  GRIA3    3' ATCACCGAAAACGTGGCTGCT 23642         GCATA
                                GGTAGTTACGTT   GTGGT
                                ||||||||||||   |||||
                                TCGTCGGTGCAA   CACTA
                                     AAGC_
GAM245  GRINL1A  3' GCTTCCAGGTGTAATTATTGC 69515          GCAT
                                GCGGTAGTTACGTT   AGT
                                ||||||||||||||   |||
                                CGTTATTAATGTGG   TCG
                                       ACCT
GAM245  GRLF1    3' CCACCCCACGTAGCTGCT    78554         TGCATA
                                GGTAGTTACGT    GTGG
                                ||||||||||     ||||
                                TCGTCGATGCA    CACC
                                     CCC___
GAM245  HADH2    3' CATTTTGTAACTGCC      15677         TTGCAT
                                GGTAGTTACG     AGTG
                                |||||||||      ||||
                                CCGTCAATGT     TTAC
                                     T_____
GAM245  HDAC7A   3' CCACTATTCCTGGCTCTGC   33449     T    CGTTGC
                                GCGG AGTTA     ATAGTGG
                                |||| |||||     |||||||
                                CGTC TCGGT     TATCACC
                                  _    CCT___
GAM245  HDAC7A   3' CCACTATTCCTGGCTCTGC   31208     T    CGTTGC
                                GCGG AGTTA     ATAGTGG
                                |||| |||||     |||||||
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```
                                CGTC TCGGT      TATCACC
                                  _     CCT___
GAM245  HMG20A   3'  GCCAGCCCTCAGTGTGGCTTTG 36541      T         CATAG
             T                   GCGG AGTTACGTTG     TGGT
                                 |||| ||||||||||     ||||
                                 TGTT TCGGTGTGAC     ACCG
                                   _         TCCCG
GAM245  HNF3G    3'  ACCATGTGCCATGATGGCTGCT 72341          _  T    G
             GC                    GCGGTAGTTA CGT GCATA TGGT
                                 |||||||||| ||| ||||| ||||
                                 CGTCGTCGGT GTA CGTGT ACCA
                                       A  C    _
GAM245  HNF3G    3'  TTACTGTGATGACTGCTGT    72346          CGTTG       T
                                 GCGGTAGTTA     CATAGTGG
                                 ||||||||||     ||||||||
                                 TGTCGTCAGT     GTGTCATT
                                       A____        C
GAM245  HNRPH3   5'  ACCAGAGTCGGCGTAACTATCG 24199              C  AG
             C                     GCGGTAGTTACGTTG AT  TGGT
                                 ||||||||||||||| ||  ||||
                                 CGCTATCAATGCGGC TG  ACCA
                                          _ AG
GAM245  HPSE     3'  ACCACTGTGTATGTTCTTGTGT 21889     GT  TT    T
                                 GCG  AG  ACGT GCATAGTGGT
                                 |||  ||  |||| ||||||||||
                                 TGT  TC  TGTA TGTGTCACCA
                                   GT  T_   _
GAM245  HS2ST1   3'  ATTGCTGTGAAATGGCAACTGT 24332       A  TA    G     TG
                                 GCGGT GT  CGTT CATAG  GT
                                 ||||| ||  |||| |||||  ||
                                 TGTCA CG  GTAA GTGTC  TA
                                    A  __    A     GT
GAM245  HSPA6    5'  CGCTGTGCAGGCGGCCGT    76332       A  TACG       TG
                                 GCGGT GT    TTGCATAG  G
                                 ||||| ||    ||||||||  |
                                 TGCCG CG    GACGTGTC  C
                                    G  ____        GT
GAM245  HSPA8    3'  ACCAAGTGTAGATGTAGCATTG 21694       A      _     AG
             T                     GCGGT GTTACGT TGCAT  TGGT
                                 ||||| ||||||| |||||  ||||
                                 TGTTA CGATGTA ATGTG  ACCA
                                   _      G     A_
GAM245  IFNAR1   3'  ATCACTGATGCTGCTGGCTACT 5281           C  T   _
             GC                    GCGGTAGTTA GT GCAT AGTGGT
                                 |||||||||| || |||| ||||||
                                 CGTCATCGGT CG CGTA TCACTA
                                       _ T   G
GAM245  IGF1     5'  TGAAATGTGACATTGC      5239        A       G
                                 GCGGT GTTACGTT CA
                                 ||||| |||||||| ||
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```
                                CGTTA CAGTGTAA GT
                                  _      A
GAM245  IK      5'  CGCTGCGGTGTTGCTGT    76347      GTT  TT  TA
                                GCGGTA  ACG  GCA  GTG
                                ||||||  |||  |||  |||
                                TGTCGT  TGT  CGT  CGC
                                  ___  GG  __
GAM245  IKBKG   3'  GCTGCTGTGCCCTGGGAGTGCT 94664      G TA  TT    TG
          GC                  GCGGTA T  CG  GCATAG  GT
                              |||||| |  ||  ||||||  ||
                              CGTCGT A  GT  CGTGTC  CG
                                 G GG  CC    GT
GAM245  IKBKG   3'  GCTGCTGTGCCCTGGGAGTGCT 13312      G TA  TT    TG
          GC                  GCGGTA T  CG  GCATAG  GT
                              |||||| |  ||  ||||||  ||
                              CGTCGT A  GT  CGTGTC  CG
                                 G GG  CC    GT
GAM245  IL17R   3'  GCAGCGGTCTGGTTATCGT   26777      TT ___
                              GCGGTAG  A   CGTTGC
                              |||||||  |   ||||||
                              TGCTATT  T   GCGACG
                                 GG CTG
GAM245  IL1R1   3'  TGTTCTGGAGCTGCTGT    6066        A  TT
                              GCGGTAGTT CG  GCA
                              |||||||||  ||  |||
                              TGTCGTCGA GT  TGT
                                   G  CT
GAM245  IL2RB   3'  GCTATTCCCTGGGGCTGCTGT  6073       TA  TTGC
                              GCGGTAGT  CG   ATAGT
                              ||||||||  ||   |||||
                              TGTCGTCG  GT   TATCG
                                 GG  CCCT
GAM245  INMT    3'  GCTGTTGATGAGAGCTGTTGC  22275   GG   A_   C
                              GC  TAGTT  CGTTG ATAGT
                              ||  |||||  ||||| |||||
                              CG  GTCGA  GTAGT TGTCG
                               TT    GA   _
GAM245  INPP5A  3'  CGCTGCTGTGGTTGCCGC    18658      TT  TT  TA
                              GCGGTAG  ACG  GCA  GTG
                              |||||||  |||  |||  |||
                              CGCCGTT  TGT  CGT  CGC
                                 GG  __  __
GAM245  IRTA2   3'  GCTTCAGCTGTGATTGCTGT   48408        _   CAT
                              GCGGTAGTTAC GTTG  AGT
                              |||||||||| ||||  |||
                              TGTCGTTAGTG CGAC  TCG
                                    T   T__
GAM245  IRTA2   3'  TGCTGTTCTGAGTACTGC    48412      G  CGTTGC   TG
                              GCGGTA TTA    ATAG  G
                              |||||| |||    ||||  |
```

```
                                CGTCAT AGT     TGTC  T
                                   G   CT____    GT
GAM245  ITGA1    3'  GCTGCATGTGTGAACTACTGC  63534        TACG TG    _ TG
                                GCGGTAGT    T  CATA G  GT
                                ||||||||    |  |||| |  ||
                                CGTCATCA    A  GTGT C  CG
                                     ____ GT    A GT
GAM245  ITGAL    3'  CACTACGTGACTGTGGC     9387     G        TGCAT
                                GC GTAGTTACGT     AGTG
                                || ||||||||||     ||||
                                CG TGTCAGTGCA     TCAC
                                 G        _____
GAM245  ITPR3    3'  GCTGCGCTTGCGTGGCTG    9456          T_  A
                                TAGTTACGT  GC TAGT
                                |||||||||  || ||||
                                GTCGGTGCG  CG GTCG
                                      TT  C
GAM245  IVD      5'  GCCGCCTAGGGTGATTGGCTGC 9463          C  TG A_  _
            TGC                    CGGTAGTTA GT  C  TAG TGGT
                                |||||||||  ||  |  ||| ||||
                                GTCGTCGGT TA  G  ATC GCCG
                                     _  GT GG   C
GAM245  KCNAB2   3'  GCCACAAAAAGCGTAGCGGTCG 13304      TA       GCATA
            T                   GCGG  GTTACGTT    GTGGT
                                ||||  ||||||||    |||||
                                TGCT  CGATGCGA    CACCG
                                  GG       AAAA_
GAM245  KCNK10   3'  TATGTGTAACTAGCGT      56344     G      GTT
                                GCG TAGTTAC   GCATA
                                ||| |||||||   |||||
                                TGC ATCAATG   TGTAT
                                  G      ___
GAM245  KCNK10   3'  TATGTGTAACTAGCGT      40972     G      GTT
                                GCG TAGTTAC   GCATA
                                ||| |||||||   |||||
                                TGC ATCAATG   TGTAT
                                  G      ___
GAM245  KCNK10   3'  TATGTGTAACTAGCGT      56339     G      GTT
                                GCG TAGTTAC   GCATA
                                ||| |||||||   |||||
                                TGC ATCAATG   TGTAT
                                  G      ___
GAM245  KCNMA1   3'  GCCACTGTGTGAAACTGTATCT 9555       T    ___ TG
            GC                    GTAG TACG   T  CATAGTGGT
                                |||| ||||   |  |||||||||
                                CGTC ATGT   A  GTGTCACCG
                                  T    CAA GT
GAM245  KERA     3'  ACCATTTCTTGTAGCTGTTGT  22869    GG       TTGCAT
                                GC  TAGTTACG     AGTGGT
                                ||  ||||||||     ||||||
```

```
                                TG  GTCGATGT     TTACCA
                                 TT       TCT___
GAM245  KIF5B    5'  GCAGCTGACTGCTGC       15730          C
                                GCGGTAGTTA GTTGC
                                |||||||||| |||||
                                CGTCGTCAGT CGACG
                                          _
GAM245  KLHL1    3'  GCCAAAGATGCAGTGTAATTAT 40487              AG_
           TG                    CGGTAGTTACGTTGCAT   TGGT
                                |||||||||||||||||  ||||
                                GTTATTAATGTGACGTA   ACCG
                                          GAA
GAM245  KRTHA7   3'  GCTAAAATGTTGTAATTATC   13658          TT   AG
                                GGTAGTTACG  GCAT  TGGT
                                ||||||||||  ||||  ||||
                                CTATTAATGT  TGTA  ATCG
                                      __    AA    T
GAM245  LAMA4    3'  CTACTGGTGAAATTACTGT    9667          ACG TG A     T
                                GCGGTAGTT   T  C TAGTGG
                                |||||||||   |  | ||||||
                                TGTCATTAA   A  G GTCATC
                                      ___ GT _     C
GAM245  LDHB     5'  GCTGCTGTGTGTGGAGGTGCTG 9712        G  ACGT      TG
           T                     GCGGTA TT    TGCATAG  GT
                                |||||| ||    |||||||  ||
                                TGTCGT GA    GTGTGTC  CG
                                   G  GGT_      GT
GAM245  LDHB     5'  GCTGCTGTGTGTGGAGGTGCTG 9713        G  ACGT      TG
           T                     GCGGTA TT    TGCATAG  GT
                                |||||| ||    |||||||  ||
                                TGTCGT GA    GTGTGTC  CG
                                   G  GGT_      GT
GAM245  LEP      3'  GCTGCTGTGTTTTTGCTATC   4052        TACGTT     TG
                                GGTAGT     GCATAG  GT
                                ||||||     ||||||  ||
                                CTATCG     TGTGTC  CG
                                   TTTT__     GT
GAM245  LETM1    3'  TCCACACTGTGGTGTGGCTGCC 24624          TT   TA   T
                                GGTAGTTACG  GCA  GTGG
                                ||||||||||  |||  ||||
                                CCGTCGGTGT  TGT  CACC
                                      GG   CA   TA
GAM245  LHCGR    3'  GCTACGTGTGACTAGTGC    4073      G      GTT  A
                                GCG TAGTTAC   GC TAGT
                                ||| |||||||   || ||||
                                CGT ATCAGTG   TG ATCG
                                  G      ___ C
GAM245  LMO4     5'  GCTGTTGTGTCTGCGACTGCT  22252       TA  T_     TG
                                GGTAGT  CGT  GCATAG  GT
                                ||||||  |||  ||||||  ||
```

```
                                TCGTCA  GCG  TGTGTT  CG
                                   __  TC     GT
GAM245  LNK     3'  CCACTGAGTGGCCACTGT    18461      AGTTAC  TG A
                                GCGGT     GT  C TAGTGG
                                |||||     ||  | ||||||
                                TGTCA     CG  G GTCACC
                                  C_____  GT A
GAM245  LRAT    3'  ACCACTATGAGAACTACCGT   60102        ACGTTG
                                GCGGTAGTT     CATAGTGGT
                                |||||||||     |||||||||
                                TGCCATCAA     GTATCACCA
                                     GA____
GAM245  LYPLA1   3'  ACCATAAAGTGTAGTTACC   20920     GT     GCATA
                                GGTA  TACGTT    GTGGT
                                ||||  ||||||    |||||
                                CCAT  ATGTGA    TACCA
                                  TG     AA___
GAM245  LYPLA1   3'  ACTACTTATTTCGAATTACTGT 20921         A  TTGCAT
                                GCGGTAGTT CG     AGTGGT
                                |||||||||  ||     ||||||
                                TGTCATTAA GC     TCATCA
                                     _  TTTAT_
GAM245  MAD2L1   5'  GCTGTTGGAGCCGCTGTGGTTG 9876       TT  _  T  A_   TG
           CTGT                  CGGTAG  AC GT GC  TAG  GT
                                ||||||  || || ||  |||  ||
                                GTCGTT  TG CG CG  GTT  CG
                                   GG  T  C  AG   GT
GAM245  MADD    3'  CCGCAGTGTTGGCTGCTGC   55333        CGTT   A
                                GCGGTAGTTA    GCAT GTGG
                                ||||||||||    |||| ||||
                                CGTCGTCGGT    TGTG CGCC
                                     _____    A
GAM245  MADD    3'  CCGCAGTGTTGGCTGCTGC   55339        CGTT   A
                                GCGGTAGTTA    GCAT GTGG
                                ||||||||||    |||| ||||
                                CGTCGTCGGT    TGTG CGCC
                                     _____    A
GAM245  MADD    3'  CCGCAGTGTTGGCTGCTGC   55344        CGTT   A
                                GCGGTAGTTA    GCAT GTGG
                                ||||||||||    |||| ||||
                                CGTCGTCGGT    TGTG CGCC
                                     _____    A
GAM245  MADD    3'  CCGCAGTGTTGGCTGCTGC   55349        CGTT   A
                                GCGGTAGTTA    GCAT GTGG
                                ||||||||||    |||| ||||
                                CGTCGTCGGT    TGTG CGCC
                                     _____    A
GAM245  MADD    3'  CCGCAGTGTTGGCTGCTGC   55355        CGTT   A
                                GCGGTAGTTA    GCAT GTGG
                                ||||||||||    |||| ||||
```

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                                CGTCGTCGGT   TGTG CGCC
                                     ____   A
GAM245  MADD    3'  CCGCAGTGTTGGCTGCTGC   13464        CGTT   A
                                GCGGTAGTTA   GCAT GTGG
                                ||||||||||   |||| ||||
                                CGTCGTCGGT   TGTG CGCC
                                     ____   A
GAM245  MADH4   5'  TTCCTTGCAACGTTAGCTGTTG 18096   GG    _     T  T  T
          T                   GC  TAGTTA CGTTGCA AG GG
                              ||  |||||| ||||||| || ||
                              TG  GTCGAT GCAACGT TC CT
                               TT     T      _ _ TT
GAM245  MADH6   3'  TCATTTTTACAATGTAATTATT 18768          CAT_   GT
                                GGTAGTTACGTTG   AGTG
                                ||||||||||||   ||||
                                TTATTAATGTAAC   TTAC
                                       ATTT   TG
GAM245  MAGEA4  3'  ATCGTAGTTAACGTATATTGCT 9882        _     C  AG
          GT                    GCGGTAGT TACGTTG AT  TGGT
                                |||||||| ||||||| ||  ||||
                                TGTCGTTA ATGCAAT TG  GCTA
                                     T      _ AT
GAM245  MAGEC1  3'  GCACATGTATTGCTGT     18421        T   _
                                GCGGTAGT ACGT TGC
                                |||||||| |||| |||
                                TGTCGTTA TGTA ACG
                                     _   C
GAM245  MAL     3'  TGCTCGTGGGTGCTGT     9892       G    TT
                                GCGGTA TTACG  GCA
                                |||||| |||||  |||
                                TGTCGT GGTGC  CGT
                                   G    T_
GAM245  MAL     3'  TGCTCGTGGGTGCTGT     42361      G    TT
                                GCGGTA TTACG  GCA
                                |||||| |||||  |||
                                TGTCGT GGTGC  CGT
                                   G    T_
GAM245  MAL     3'  TGCTCGTGGGTGCTGT     42363      G    TT
                                GCGGTA TTACG  GCA
                                |||||| |||||  |||
                                TGTCGT GGTGC  CGT
                                   G    T_
GAM245  MAL     3'  TGCTCGTGGGTGCTGT     42365      G    TT
                                GCGGTA TTACG  GCA
                                |||||| |||||  |||
                                TGTCGT GGTGC  CGT
                                   G    T_
GAM245  MAP3K1  5'  TGCCGCGGGACTGCTGC    67816        TA   T
                                GCGGTAGT  CGT GCA
                                ||||||||  ||| |||
```

```
                                CGTCGTCA  GCG CGT
                                    GG   C
GAM245  MAPK1    3'  CACTCTGTAGTTACTGT     10819       TTACG    T
                                GCGGTAG    TTGCA AGTG
                                |||||||    ||||| ||||
                                TGTCATT    GATGT TCAC
                                    _____    C
GAM245  MAPK8IP1 3'  GCTGCTGACAGGATGTGGCACT 18404      A      GCA_   TG
          GC                    GCGGT GTTACGTT    TAG  GT
                                ||||| ||||||||   |||  ||
                                CGTCA CGGTGTAG    GTC  CG
                                  _      GACA   GT
GAM245  MAPT     3'  GCCGCTGTGCTGTTGTCTGCCG 33690       TT  TT_
          T                     GCGGTAG  ACG   GCATAGTGGT
                                |||||||  |||   ||||||||||
                                TGCCGTC  TGT   CGTGTCGCCG
                                   __  TGT
GAM245  MAPT     3'  GCCGCTGTGCTGTTGTCTGCCG 33699       TT  TT_
          T                     GCGGTAG  ACG   GCATAGTGGT
                                |||||||  |||   ||||||||||
                                TGCCGTC  TGT   CGTGTCGCCG
                                   __  TGT
GAM245  MAPT     3'  GCCGCTGTGCTGTTGTCTGCCG 33709       TT  TT_
          T                     GCGGTAG  ACG   GCATAGTGGT
                                |||||||  |||   ||||||||||
                                TGCCGTC  TGT   CGTGTCGCCG
                                   __  TGT
GAM245  MAPT     3'  GCCGCTGTGCTGTTGTCTGCCG 19779       TT  TT_
          T                     GCGGTAG  ACG   GCATAGTGGT
                                |||||||  |||   ||||||||||
                                TGCCGTC  TGT   CGTGTCGCCG
                                   __  TGT
GAM245  MASP2    3'  ATTACTGTGGACATGGCAGTTG 21737     TA   C   G
          T                     GCGG  GTTA GTT CATAGTGGT
                                ||||  |||| ||| |||||||||
                                TGTT  CGGT CAG GTGTCATTA
                                  GA   A   _
GAM245  MBD1     3'  TGCAGGCCTGACTACTGC    31775         C  _
                                GCGGTAGTTA GT TGCA
                                |||||||||| || ||||
                                CGTCATCAGT CG ACGT
                                     C  G
GAM245  MBD1     3'  TGCAGGCCTGACTACTGC    31783         C  _
                                GCGGTAGTTA GT TGCA
                                |||||||||| || ||||
                                CGTCATCAGT CG ACGT
                                     C  G
GAM245  MBD1     3'  TGCAGGCCTGACTACTGC    31790         C  _
                                GCGGTAGTTA GT TGCA
                                |||||||||| || ||||
```

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                                CGTCATCAGT CG ACGT
                                      C  G
GAM245  MBD1    3'  TGCAGGCCTGACTACTGC    9949          C  _
                                GCGGTAGTTA GT TGCA
                                |||||||||| || ||||
                                CGTCATCAGT CG ACGT
                                      C  G
GAM245  MBNL    3'  ACTATTATGTAATCACAACT   40724     A  TAC
                                GGT GT   GTTGCATAGTGGT
                                ||| ||   ||||||||||||
                                TCA CA   TAATGTATTATCA
                                  A  C__
GAM245  MBNL    3'  TGTTGTTATGTGATTGTTTTTT 40733    _____  _ TG    TG
            AATTGCTGT               TT    ACG T  CATAG  GT   G
                                ||    ||| |  |||||  ||   |
                                AA    TGT A  GTATT  TG   T
                                 TTTTT   T GT    GT
GAM245  MCCC2   3'  ACTGCTGTGCAGCCATTACC   42135      TAC       TG
                                GGTAGT   GTTGCATAG  GT
                                ||||||   |||||||||  ||
                                CCATTA   CGACGTGTC  CA
                                   C__       GT
GAM245  MDH2    3'  GCTTTGGTGATGATTACTGT   19795       TA   TG AT_
                                GCGGTAGT  CGT  C   AGT
                                ||||||||  |||  |   |||
                                TGTCATTA  GTA  G   TCG
                                    __  GT GTT
GAM245  MEN1    5'  TGCAGGGCTGGTTGCCGT    93382       TT C  __
                                GCGGTAG  A GT  TGCA
                                |||||||  | ||  ||||
                                TGCCGTT  T CG  ACGT
                                   GG _  GG
GAM245  MGA     3'  TGGGATTTAGCTGCTGC     62811         C   G
                                GCGGTAGTTA GTT CA
                                |||||||||| ||| ||
                                CGTCGTCGAT TAG GT
                                      T   G
GAM245  MGAM    3'  ACTGTTGTGCGGCCTCTGCT   72360      TTAC       TG
                                GGTAG    GTTGCATAG  GT
                                |||||    |||||||||  ||
                                TCGTC    CGGCGTGTT  CA
                                  TC__       GT
GAM245  MHC2TA  3'  TGTTAATGATAGCTACTGT   4197          _    _
                                GCGGTAGTTA CGTTG CA
                                |||||||||| ||||| ||
                                TGTCATCGAT GTAAT GT
                                      A    T
GAM245  MICB    3'  ACCGTTATGCATTACTCTGT   19816     T   TACGT
                                GCGG AGT    TGCATAGTGGT
                                |||| |||    ||||||||||
```

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                                TGTC TCA    ACGTATTGCCA
                                  _  TT___
GAM245  MJD     3'  ATCATTATTTCATGACTGGTGC 47682    G    CGTTGC
                                GCG TAGTTA    ATAGTGGT
                                ||| ||||||    ||||||||
                                CGT GTCAGT    TATTACTA
                                  G    ACTT__
GAM245  MJD     3'  ATCATTATTTCATGACTGGTGC 17163    G    CGTTGC
                                GCG TAGTTA    ATAGTGGT
                                ||| ||||||    ||||||||
                                CGT GTCAGT    TATTACTA
                                  G    ACTT__
GAM245  MLANA   3'  GCCACTATGCCTGACTAATTTT 18586    T   C  __
            GT                  GCGG AGTTA GTT  GCATAGTGGT
                                |||| ||||| |||  ||||||||||
                                TGTT TTAAT CAG  CGTATCACCG
                                  _   _  TC
GAM245  MLLT4   3'  ACTGCTGTGCGGTGTTCCTCTC 72481   GT  TT  TT    TG
                                G  AG  ACG  GCATAG  GT
                                |  ||  |||  ||||||  ||
                                C  TC  TGT  CGTGTC  CA
                                 TC  CT   GG    GT
GAM245  MMP13   3'  ACTATTGTGCTCAGAGACACTG 10070     A   ACGTT
            T                   GCGGT GTT    GCATAGTGGT
                                ||||| |||    ||||||||||
                                TGTCA CAG    CGTGTTATCA
                                  _  AGACT
GAM245  MNT     3'  CACTGTGATTCGTTACCGT   39705      GTT   TTG
                                GCGGTA   ACG   CATAGTG
                                ||||||   |||   |||||||
                                TGCCAT   TGC   GTGTCAC
                                   ___   TTA
GAM245  MSR1    3'  ATTGCTAGTACTAGTACTATTG 56952       T  GT_  A   TG
            C                   GCGGTAGT AC   TGC TAG  GT
                                |||||||| ||   ||| |||  ||
                                CGTTATCA TG   ATG ATC  TA
                                     _ ATC   _   GT
GAM245  MSR1    3'  ATTGCTAGTACTAGTACTATTG 56960       T  GT_  A   TG
            C                   GCGGTAGT AC   TGC TAG  GT
                                |||||||| ||   ||| |||  ||
                                CGTTATCA TG   ATG ATC  TA
                                     _ ATC   _   GT
GAM245  MTMR6   3'  TGCTCAATGAGTTGCTGT    93553      GT A    CAT  TG
                                GCGGTA  T CGTTG   AG  G
                                ||||||  | |||||   ||  |
                                TGTCGT  A GTAAC   TC  T
                                   TG _    ___  GT
GAM245  MTMR8   3'  ACCACATAGATTAGCTACTGC  31287        C   GC  A
                                GCGGTAGTTA GTT  AT GTGGT
                                |||||||||| |||  || |||||
```

```
                                CGTCATCGAT TAG  TA CACCA
                                      _   A_  _
GAM245  MYBBP1A  3'  GCCACTGGGGAGGGTGGCTGTT 27230    GG      G  GCA
           GC                    GC  TAGTTAC TT   TAGTGGT
                                 ||  ||||||| ||   |||||||
                                 CG  GTCGGTG GA   GTCACCG
                                  TT      G  GGG
GAM245  MYD88    3'  ACTGCTGTGACCACGACACTGC 10161      A  TA   TG_    TG
                                 GCGGT GT  CGT   CATAG  GT
                                 ||||| ||  |||   |||||  ||
                                 CGTCA CA  GCA   GTGTC  CA
                                   _ __   CCA    GT
GAM245  MYD88    3'  GCTGCGGGAGAGCTGGCTGTTG 10169    GG     C   GCATA TG
           C                     GC  TAGTTA GTT     G  GT
                                 ||  |||||| |||     |  ||
                                 CG  GTCGGT CGA     C  CG
                                  TT     _   GAGGG GT
GAM245  MYH2     3'  TTATTGTGTATTCTACC     34040       TTACGT
                                 GGTAG     TGCATAGTGG
                                 |||||     ||||||||||
                                 CCATC     ATGTGTTATT
                                   TT_____
GAM245  MYL3     3'  ACCTCTCCACGTGGTTGCCGT  63899        TT    T CAT  T
                                 GCGGTAG  ACGT G   AG GGT
                                 |||||||  |||| |   || |||
                                 TGCCGTT  TGCA C   TC CCA
                                     GG    _ C__  T
GAM245  MYO6     3'  GCTAGCACAATGTGTGTTGCTG 17193       GT_     CA_   GGT
           T                     GCGGTA   TACGTTG   TAGT
                                 ||||||   |||||||   ||||
                                 TGTCGT   GTGTAAC   ATCG
                                    TGT      ACG
GAM245  NAB1     3'  GTTGCTAGCTTGAGGTTGATTA 19909        _ G  __  A   GG
           TTGT                    GGTAGTTA C TT  GC TAGT  T
                                 |||||||| | ||  || ||||  |
                                 TTATTAGT G AG  CG ATCG  G
                                      T G  TT  _   TT
GAM245  NBEA     3'  ATCATTATTTATTGATGTGATT 94912           C___
           ACT                     GGTAGTTACGTTG    ATAGTGGT
                                 ||||||||||||    ||||||||
                                 TCATTAGTGTAGT    TATTACTA
                                        TATT
GAM245  NBS1     3'  CCATTGTCCTAGCTACT     69496         CGTTGC
                                 GGTAGTTA     ATAGTGG
                                 ||||||||     |||||||
                                 TCATCGAT     TGTTACC
                                     CC_____
GAM245  NCALD    3'  GCTGTTCATTGTCATTGCTGT  49375         T   T  C
                                 GCGGTAGT ACG TG ATAGT
                                 |||||||| ||| || |||||
```

```
                                TGTCGTTA TGT AC TGTCG
                                    C   T  T
GAM245  NCOA6    5'  ATTACAGGTGTGAGCTACTGT  25955        TACG TG   A_
                                GCGGTAGT    T  CAT  GTGGT
                                ||||||||    |  |||  |||||
                                TGTCATCG    A  GTG  CATTA
                                    _____ GT   GA
GAM245  NCOA6IP  3'  ATTACAGGCGTGAGCTACTGT  45734         ACGT   ATA
                                GCGGTAGTT    TGC   GTGGT
                                |||||||||    |||   |||||
                                TGTCATCGA    GCG   CATTA
                                    GT__   GA_
GAM245  NEURL    3'  GTCAGTGCAGGGGTGGCTGCTG 14864          G _    AGTGGT
          C                      GCGGTAGTTAC T TGCAT
                                ||||||||||| | |||||
                                CGTCGTCGGTG G ACGTG
                                      G G    ACTG
GAM245  NEURL    3'  CCGCTCCTGAGCTGCTGT    14858         ACGTTGCAT
                                GCGGTAGTT        AGTGG
                                |||||||||        |||||
                                TGTCGTCGA        TCGCC
                                    GTCC_____
GAM245  NEUROD1  3'  ACTGTGCTTACAGTGACTGTCG 10208     GT    _ T_     GGT
          T                     GCG  AGTTAC GT  GCATAGT
                                |||  |||||| ||  |||||||
                                TGC  TCAGTG CA  CGTGTCA
                                  TG     A  TT
GAM245  NKTR     3'  ATTGCTGTGTGACAAATTACC  18199       AC  TG    TG
                                GGTAGTT  GT  CATAG  GT
                                |||||||  ||  |||||  ||
                                CCATTAA  CA  GTGTC  TA
                                    A_  GT    GT
GAM245  NKX3A    3'  ACCATTATGATCAAAAACTGCC 20500        ACGTTG
                                GGTAGTT     CATAGTGGT
                                |||||||     |||||||||
                                CCGTCAA     GTATTACCA
                                    AAACTA
GAM245  NLGN1    3'  ACCATTATCACATAAGTGCTGT 30023       G   C  T C
                                GCGGTA TTA GT G ATAGTGGT
                                |||||| ||| || | ||||||||
                                TGTCGT AAT CA C TATTACCA
                                   G   A  _ _
GAM245  NLVCF    3'  GCTGCTATCCTTAACATGCTGC 13668       _   CGTTGC    TG
                                GCGGTA GTTA     ATAG  GT
                                |||||| ||||     ||||  ||
                                CGTCGT CAAT     TATC  CG
                                    A   TCC___    GT
GAM245  NOS2A    3'  ACCACTGTGTATTTAACTGCC  5269         CGT
                                GGTAGTTA   TGCATAGTGGT
                                ||||||||   ||||||||||
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```
                                CCGTCAAT   ATGTGTCACCA
                                     TT_
GAM245  NPHP1    3'  ACTGTTGTTTTTTATTACCGC  62478        TACGTT  _
                                GCGGTAGT     GCA TAGT
                                ||||||||     ||| ||||
                                CGCCATTA     TGT GTCA
                                     TTTTT_   T
GAM245  NPR2L    3'  ACTAGCAGCCGCGGTGTGACTG 21557       _______    A    GGT
            GTGC                    AGTTAC     GTTGC TAGT
                                ||||||     ||||| ||||
                                TCAGTG     CGACG ATCA
                                   TGGCGC    _      T
GAM245  NPTX1    3'  CCACCCGTGTAGCTACTG    10260         GTT  ATA
                                CGGTAGTTAC   GC   GTGG
                                ||||||||||   ||   ||||
                                GTCATCGATG   TG   CACC
                                     ___  CC_
GAM245  Nrap     3'  CTATTAGAGCAGTTACTGT    57634        TTACG    A_
                                GCGGTAG    TTGC  TAGTGG
                                |||||||    ||||  ||||||
                                TGTCATT    GACG  ATTATC
                                     _____    AG
GAM245  NRCAM    3'  ACTATGTATAGCTGTCGT    17205     GT    CGT
                                GCG  AGTTA   TGCATAGT
                                |||  |||||   ||||||||
                                TGC  TCGAT   ATGTATCA
                                  TG    ___
GAM245  NRCAM    3'  ATTGTTGTGAAATTGGTGACTA 17207         __   G    TG
            T                    GTAGTTAC  GTT CATAG  GT
                                ||||||||  ||| |||||  ||
                                TATCAGTG  TAA GTGTT  TA
                                     GT   A    GT
GAM245  NRXN3    5'  GCTGCGGTGGCTGCTGC     57279          _  T
                                GCGGTAGTTAC GT GC
                                |||||||||||  || ||
                                CGTCGTCGGTG CG CG
                                       G  T
GAM245  ODF2     5'  GTGCTGTGCGACTTGGAC    10326     AC_        GG
                                GTT   GTTGCATAGT  T
                                |||   ||||||||||  |
                                CAG   CAGCGTGTCG  G
                                  GTT         TT
GAM245  OPCML    3'  ATCAATCTATCAATGTAATTGT 10343    GT        C   __
            C                    G  AGTTACGTTG ATAG  TGGT
                                |  ||||||||||  ||||  ||||
                                C  TTAATGTAAC TATC  ACTA
                                 TG         _    TA
GAM245  OPHN1    3'  CTATTGTGAATAGTGCCGC   10356      AGTT  GTTG
                                GCGGT    AC    CATAGTGG
                                |||||    ||    ||||||||
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                              CGCCG   TG   GTGTTATC
                                 ____ ATAA
GAM245  P23     3' TCACCCCACAATGTCACTGTTG 21718   GG   T    CATA  GT
           C                   GC  TAGT ACGTTG   GTG
                               ||  |||| ||||||   |||
                               CG  GTCA TGTAAC   CAC
                                TT   C    ACCC  TG
GAM245  PCDH1   5' ACTGTTGTGCTTGTGAATTATT 50561      _   TT    TG
           G                   CGGTAGT TACG  GCATAG  GT
                               |||||||  ||||  ||||||  ||
                               GTTATTA GTGT  CGTGTT  CA
                                   A   T_    GT
GAM245  PCDH11X 3' GTAGTGTAAATACTGC     52028      G
                               GCGGTA TTACGTTGC
                               ||||||  |||||||||
                               CGTCAT AATGTGATG
                                   A
GAM245  PCDH11X 3' TGATATTGTGGCTATTGT    52031         TTG_
                               GCGGTAGTTACG   CA
                               ||||||||||||   ||
                               TGTTATCGGTGT   GT
                                     TATA
GAM245  PCDH11X 3' GCTATTGTGTAATGGTAGC   52045     _
                               GTTAC GTTGCATAGTGGT
                               |||||  |||||||||||||
                               CGATG TAATGTGTTATCG
                                  G
GAM245  PCDH11X 5' GCTGAAGAAATGGACTACTGT  52046       A   GCA_
                               GCGGTAGTT CGTT   TAGT
                               |||||||||  ||||   ||||
                               TGTCATCAG GTAA   GTCG
                                     _   AGAA
GAM245  PCDH11X 3' GTAGTGTAAATACTGC     52050      G
                               GCGGTA TTACGTTGC
                               ||||||  |||||||||
                               CGTCAT AATGTGATG
                                   A
GAM245  PCDH11X 3' TGATATTGTGGCTATTGT    52053         TTG_
                               GCGGTAGTTACG   CA
                               ||||||||||||   ||
                               TGTTATCGGTGT   GT
                                     TATA
GAM245  PCDH11X 5' GCTGAAGAAATGGACTACTGT  27241       A   GCA_
                               GCGGTAGTT CGTT   TAGT
                               |||||||||  ||||   ||||
                               TGTCATCAG GTAA   GTCG
                                     _   AGAA
GAM245  PCDH11X 3' GCTATTGTGTAATGGTAGC   52023     _
                               GTTAC GTTGCATAGTGGT
                               |||||  |||||||||||||
```

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                              CGATG TAATGTGTTATCG
                                 G
GAM245  PCDH11X  5' GCTGAAGAAATGGACTACTGT  52024        A   GCA_
                              GCGGTAGTT CGTT    TAGT
                              ||||||||| ||||    ||||
                              TGTCATCAG GTAA    GTCG
                                   _   AGAA
GAM245  PCDH11Y  3' GCTATTGTGTAATGGTAGC    52080      _
                              GTTAC GTTGCATAGTGGT
                              ||||| ||||||||||||
                              CGATG TAATGTGTTATCG
                                 G
GAM245  PCDH11Y  3' GTAGTGTAAATACTGC      52084       G
                              GCGGTA TTACGTTGC
                              |||||| |||||||||
                              CGTCAT AATGTGATG
                                  A
GAM245  PCDH11Y  3' TGATATTGTGGCTATTGT    52087          TTG_
                              GCGGTAGTTACG    CA
                              ||||||||||||    ||
                              TGTTATCGGTGT    GT
                                    TATA
GAM245  PCDHA1   3' GCCACTGGGTATGTGTGGCTAC 38183          GT_  A
           CGC                   GCGGTAGTTAC   TGC TAGTGGT
                              |||||||||||   ||| |||||||
                              CGCCATCGGTG   ATG GTCACCG
                                    TGT   G
GAM245  PCDHA1   3' GCCACTGGGTATGTGTGGCTAC 48594          GT_  A
           CGC                   GCGGTAGTTAC   TGC TAGTGGT
                              |||||||||||   ||| |||||||
                              CGCCATCGGTG   ATG GTCACCG
                                    TGT   G
GAM245  PCDHA10  3' GCCACTGGGTATGTGTGGCTAC 49027          GT_  A
           CGC                   GCGGTAGTTAC   TGC TAGTGGT
                              |||||||||||   ||| |||||||
                              CGCCATCGGTG   ATG GTCACCG
                                    TGT   G
GAM245  PCDHA10  3' GCCACTGGGTATGTGTGGCTAC 38191          GT_  A
           CGC                   GCGGTAGTTAC   TGC TAGTGGT
                              |||||||||||   ||| |||||||
                              CGCCATCGGTG   ATG GTCACCG
                                    TGT   G
GAM245  PCDHA11  3' GCCACTGGGTATGTGTGGCTAC 38201          GT_  A
           CGC                   GCGGTAGTTAC   TGC TAGTGGT
                              |||||||||||   ||| |||||||
                              CGCCATCGGTG   ATG GTCACCG
                                    TGT   G
GAM245  PCDHA12  3' GCCACTGGGTATGTGTGGCTAC 38210          GT_  A
           CGC                   GCGGTAGTTAC   TGC TAGTGGT
                              |||||||||||   ||| |||||||
```

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                                CGCCATCGGTG   ATG GTCACCG
                                      TGT   G
GAM245  PCDHA13  3'  GCCACTGGGTATGTGTGGCTAC 38219          GT_  A
          CGC                   GCGGTAGTTAC   TGC TAGTGGT
                                ||||||||||   ||| |||||||
                                CGCCATCGGTG   ATG GTCACCG
                                      TGT   G
GAM245  PCDHA2   3'  GCCACTGGGTATGTGTGGCTAC 38227          GT_  A
          CGC                   GCGGTAGTTAC   TGC TAGTGGT
                                ||||||||||   ||| |||||||
                                CGCCATCGGTG   ATG GTCACCG
                                      TGT   G
GAM245  PCDHA3   3'  GCCACTGGGTATGTGTGGCTAC 38235          GT_  A
          CGC                   GCGGTAGTTAC   TGC TAGTGGT
                                ||||||||||   ||| |||||||
                                CGCCATCGGTG   ATG GTCACCG
                                      TGT   G
GAM245  PCDHA4   3'  GCCACTGGGTATGTGTGGCTAC 38243          GT_  A
          CGC                   GCGGTAGTTAC   TGC TAGTGGT
                                ||||||||||   ||| |||||||
                                CGCCATCGGTG   ATG GTCACCG
                                      TGT   G
GAM245  PCDHA5   3'  GCCACTGGGTATGTGTGGCTAC 38251          GT_  A
          CGC                   GCGGTAGTTAC   TGC TAGTGGT
                                ||||||||||   ||| |||||||
                                CGCCATCGGTG   ATG GTCACCG
                                      TGT   G
GAM245  PCDHA6   3'  GCCACTGGGTATGTGTGGCTAC 49000          GT_  A
          CGC                   GCGGTAGTTAC   TGC TAGTGGT
                                ||||||||||   ||| |||||||
                                CGCCATCGGTG   ATG GTCACCG
                                      TGT   G
GAM245  PCDHA6   3'  GCCACTGGGTATGTGTGGCTAC 38259          GT_  A
          CGC                   GCGGTAGTTAC   TGC TAGTGGT
                                ||||||||||   ||| |||||||
                                CGCCATCGGTG   ATG GTCACCG
                                      TGT   G
GAM245  PCDHA7   3'  GCCACTGGGTATGTGTGGCTAC 38267          GT_  A
          CGC                   GCGGTAGTTAC   TGC TAGTGGT
                                ||||||||||   ||| |||||||
                                CGCCATCGGTG   ATG GTCACCG
                                      TGT   G
GAM245  PCDHA8   3'  GCCACTGGGTATGTGTGGCTAC 38275          GT_  A
          CGC                   GCGGTAGTTAC   TGC TAGTGGT
                                ||||||||||   ||| |||||||
                                CGCCATCGGTG   ATG GTCACCG
                                      TGT   G
GAM245  PCDHA9   3'  ATCACTATCATTTATTTATTGC 25757        TTACGT  C
                                GCGGTAG     TG ATAGTGGT
                                |||||||     || ||||||||
```

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                                CGTTATT     AC TATCACTA
                                    TATTT_ _
GAM245  PCDHA9   3'  GCCACTGGGTATGTGTGGCTAC 49017          GT_  A
            CGC                   GCGGTAGTTAC   TGC TAGTGGT
                                  ||||||||||   ||| |||||||
                                  CGCCATCGGTG   ATG GTCACCG
                                        TGT   G
GAM245  PCDHAC1  3'  GCCACTGGGTATGTGTGGCTAC 38165          GT_  A
            CGC                   GCGGTAGTTAC   TGC TAGTGGT
                                  ||||||||||   ||| |||||||
                                  CGCCATCGGTG   ATG GTCACCG
                                        TGT   G
GAM245  PCDHAC2  3'  GCCACTGGGTATGTGTGGCTAC 38175          GT_  A
            CGC                   GCGGTAGTTAC   TGC TAGTGGT
                                  ||||||||||   ||| |||||||
                                  CGCCATCGGTG   ATG GTCACCG
                                        TGT   G
GAM245  PCDHB6   3'  TGCTATGTAGGACTG      38439      ACG      TG
                                  TAGTT   TTGCATAG  G
                                  |||||   ||||||||  |
                                  GTCAG   GATGTATC  T
                                     ___       GT
GAM245  PCM1     5'  GTGCGGGCTGACTGTCGC    20570     GT    CG
                                  GCG  AGTTA  TTGCAT
                                  |||  |||||  ||||||
                                  CGC  TCAGT  GGCGTG
                                    TG    CG
GAM245  PDE4B    5'  GCTGTTTTCAATGTAATGCTGC 10481       G      CAT  TG
                                  GCGGTA TTACGTTG   AG  GT
                                  ||||||  ||||||||   ||  ||
                                  CGTCGT AATGTAAC   TT  CG
                                     _      TT_  GT
GAM245  PDE4B    3'  GCTGTTTTCAATGTAATGCTGC 10482       G      CAT  TG
                                  GCGGTA TTACGTTG   AG  GT
                                  ||||||  ||||||||   ||  ||
                                  CGTCGT AATGTAAC   TT  CG
                                     _      TT_  GT
GAM245  PDGFRA   3'  CCTGATGTCAGCTGCTGT    20596        ACGTT    AGT
                                  GCGGTAGTT    GCAT   GG
                                  |||||||||    ||||   ||
                                  TGTCGTCGA    TGTA   CC
                                       C_____    GT_
GAM245  PDZK1    3'  TTCACCATGTGTGATTGTC    10507   GT     GTT    A    T
                                  G  AGTTAC   GCAT GTGG
                                  |  ||||||   |||| ||||
                                  C  TTAGTG   TGTA CACT
                                   TG     ___    C    TA
GAM245  PFN2     3'  ACTATTGTTAAAATGAACTGTT 10524    GG    A    GC_
            GC                    GC  TAGTT CGTT   ATAGTGGT
                                  ||  ||||| ||||   ||||||||
```

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                                CG  GTCAA GTAA   TGTTATCA
                                 TT    _   AAT
GAM245  PFN2    3'  ATTATTGTGGACTTGGCTGTC  10525   GT    C   G
                                G  AGTTA GTT CATAGTGGT
                                |  ||||| ||| |||||||||
                                C  TCGGT CAG GTGTTATTA
                                 TG    T  _
GAM245  PFN2    3'  ACTATTGTTAAAATGAACTGTT 53823    GG    A   GC_
            GC                    GC  TAGTT CGTT   ATAGTGGT
                                ||  ||||| ||||   ||||||||
                                CG  GTCAA GTAA   TGTTATCA
                                 TT    _   AAT
GAM245  PFN2    3'  ATTATTGTGGACTTGGCTGTC  53824   GT    C   G
                                G  AGTTA GTT CATAGTGGT
                                |  ||||| ||| |||||||||
                                C  TCGGT CAG GTGTTATTA
                                 TG    T  _
GAM245  PGAM1   3'  ACCTGCGTGGTGATGTGACAAC 76273      A      TG ATA  _
            TGT                   GCGGT GTTACGT  C   GT GGT
                                ||||| |||||||  |   || |||
                                TGTCA CAGTGTA  G   CG CCA
                                   A      GT GTG  T
GAM245  PHF1    5'  CCGCTGCTTTGGCTGCTGC   44148         CGTT   TA
                                GCGGTAGTTA   GCA  GTGG
                                ||||||||||   |||  ||||
                                CGTCGTCGGT   CGT  CGCC
                                      TT__   __
GAM245  PITX2   3'  ACTGCTATGTACAACCTACC   4378       TTACGT      TG
                                GGTAG     TGCATAG  GT
                                |||||     |||||||  ||
                                CCATC     ATGTATC  CA
                                   CAAC__      GT
GAM245  PLA2G2D  3'  GCCATTTGTGTGTGGCTAGCTG 24794      _     GTT     _
            T                    GCGGT AGTTAC   GCATAG TGGT
                                ||||| ||||||   |||||| ||||
                                TGTCG TCGGTG   TGTGTT ACCG
                                   A      ___      T
GAM245  PLAG1   3'  CCATTGTGGAACTGCAGC    10607    G    TACGT G
                                GC GTAGT    T CATAGTGG
                                || |||||    | ||||||||
                                CG CGTCA    A GTGTTACC
                                 A    _____ G
GAM245  PLCG1   3'  GCCATTAATGAGATGTTATTAC 10622        T   TG  _
            TGT                   GCGGTAGT ACGT  CAT AGTGGT
                                ||||||||  ||||  |||  ||||||
                                TGTCATTA TGTA  GTA TTACCG
                                     T   GA  A
GAM245  PLIN    3'  GTACTATAAGAGTAATTGCC   10644         G  GC    GG
                                GGTAGTTAC TT  ATAGT  T
                                |||||||||  ||  |||||  |
```

```
                                CCGTTAATG AG  TATCA  G
                                     _ AA     TT
GAM245  POLR2G   3'  GCTTCTTGTAGCTTAACTACTG 10685          C     T  T
            C                    GCGGTAGTTA GTTGCA AG GGT
                                 |||||||||| |||||| || |||
                                 CGTCATCAAT CGATGT TC TCG
                                      T     _ T
GAM245  POU3F2   3'  GCTGCTGTGTTTATTTATTGT  18813        TTACGTT     TG
                                 GCGGTAG      GCATAG  GT
                                 |||||||      ||||||  ||
                                 TGTTATT      TGTGTC  CG
                                     TATT___      GT
GAM245  PPP1R2   5'  CGTTGTGTCGTGACAACCGC   20689      A     TT
                                 GCGGT GTTACG  GCATAGTG
                                 ||||| ||||||  ||||||||
                                 CGCCA CAGTGC  TGTGTTGC
                                    A     __
GAM245  PPP2R5C  3'  CCATTATGAAAACTATC     10755        ACGTTG
                                 GGTAGTT     CATAGTGG
                                 |||||||     ||||||||
                                 CTATCAA     GTATTACC
                                     AA____
GAM245  PPP6C    3'  ACTGCTGCATGTAGCTCTTGC  10766     T       T   TA TG
                                 GCGG AGTTACGT GCA  G  GT
                                 |||| |||||||| |||  |  ||
                                 CGTT TCGATGTA CGT  C  CA
                                   C       _  __ GT
GAM245  PRKCN    3'  ACCATTATGTGATGTTACTAT  19442      T    TG
                                 GTAGT ACGT  CATAGTGGT
                                 ||||| ||||  |||||||||
                                 TATCA TGTA  GTATTACCA
                                    T    GT
GAM245  PRKCN    3'  ACTAGGAAAGTGTTAACTATCG 19443          _    GCA_    GGT
            T                    GCGGTAGTTA CGTT    TAGT
                                 |||||||||| ||||    ||||
                                 TGCTATCAAT GTGA    ATCA
                                      T    AAGG
GAM245  PSEN1    5'  CCGTTGTGGTCAGCTCTGC    23622      T    _ GTTG
                                 GCGG AGTT AC    CATAGTGG
                                 |||| |||| ||    ||||||||
                                 CGTC TCGA TG    GTGTTGCC
                                    _    C ____
GAM245  PSMC1    3'  TCACTGTGCAGCAGTCTGCT   10967      TTAC         GT
                                 GGTAG    GTTGCATAGTG
                                 |||||    ||||||||||
                                 TCGTC    CGACGTGTCAC
                                    TGA_          TG
GAM245  PTGFR    3'  ATTATTATGAAGGTCGATTGTT 6316     GG    _ G  G
            GT                     GC  TAGTT AC TT CATAGTGGT
                                 ||  ||||| || || |||||||||
```

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                                TG  GTTAG TG AA GTATTATTA
                                 TT    C  G  _
GAM245  PTPN6    5'  GCCACTGTGCACAGCTGTGCCG 54509      __    ACGT
              C                   GCGGT  AGTT    TGCATAGTGGT
                                  |||||  ||||    ||||||||||
                                  CGCCG  TCGA    ACGTGTCACCG
                                    TG    C___
GAM245  RAB23    5'  ACCACCCCCGGCGGAGCTGCTG 32781         A    CATA
              C                   GCGGTAGTT CGTTG    GTGGT
                                  |||||||||  |||||    |||||
                                  CGTCGTCGA GCGGC    CACCA
                                       G    CCC_
GAM245  RAB36    3'  CCATGGTGGACTGTCGT     16952     GT   ACGTTG   A
                                  GCG  AGTT     CAT GTGG
                                  |||  ||||     ||| ||||
                                  TGC  TCAG     GTG TACC
                                    TG   _______   G
GAM245  RABGGTB  3'  ATCGAATCTAAAAGTGACTACT 15929          GTTGCATAG
              GT                   GCGGTAGTTAC        TGGT
                                   ||||||||||         ||||
                                   TGTCATCAGTG        GCTA
                                        AAAATCTAA
GAM245  RAD51L1  3'  ACCATTATGCAAGTGTTCCTAT 56059      TT   _
              T                    GGTAG  ACG TTGCATAGTGGT
                                   |||||  ||| ||||||||||||
                                   TTATC  TGT AACGTATTACCA
                                     CT   G
GAM245  RAD51L1  3'  ACCATTATGCAAGTGTTCCTAT 11230      TT   _
              T                    GGTAG  ACG TTGCATAGTGGT
                                   |||||  ||| ||||||||||||
                                   TTATC  TGT AACGTATTACCA
                                     CT   G
GAM245  RARB     3'  ACTATTGACAGGACTATTGT   6370         AC    C
                                   GCGGTAGTT  GTTG ATAGT
                                   |||||||||  |||| |||||
                                   TGTTATCAG  CAGT TATCA
                                        GA   _
GAM245  RARB     3'  ACTATTGACAGGACTATTGT   32365         AC    C
                                   GCGGTAGTT  GTTG ATAGT
                                   |||||||||  |||| |||||
                                   TGTTATCAG  CAGT TATCA
                                        GA   _
GAM245  RBL2     3'  CCACTCAGTGATTACTGT    18829          GTTGCAT
                                   GCGGTAGTTAC      AGTGG
                                   ||||||||||       |||||
                                   TGTCATTAGTG      TCACC
                                         AC_____
GAM245  RENT1    3'  GCTGATGGGGTGATTGCTGC   11291          G  GCA
                                   GCGGTAGTTAC TT   TAGT
                                   |||||||||| ||   ||||
```

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                                CGTCGTTAGTG GG   GTCG
                                      G  TA_
GAM245  REPS2    5'  ATTGCCCTGAAATTAATTGCTG 16371          C   G  TA TG
              C                   GCGGTAGTTA GTT CA  G  GT
                                  |||||||||| ||| ||  |  ||
                                  CGTCGTTAAT TAA GT  C  TA
                                        _   A  CC GT
GAM245  RET      3'  GCCATTGAGTGCAGCAGTGTGC 40175      _  _      __
              TGTTGC                TAGT TAC GTTGCAT  AGTGGT
                                  |||| ||| |||||||  ||||||
                                  GTCG GTG CGACGTG  TTACCG
                                    T  A      AG
GAM245  RGS5     3'  ATCATGTAAAATGAAACTGTTG 13236    GG    A   GCATA
              C                   GC  TAGTT CGTT    GTGGT
                                  ||  ||||| ||||    |||||
                                  CG  GTCAA GTAA    TACTA
                                   TT    A   AATG_
GAM245  RHD      3'  ACTGCTATGTGTCACACTTTGC 32295     T   TACGT     TG
                                  GCGG AGT    TGCATAG  GT
                                  |||| |||    |||||||  ||
                                  CGTT TCA    GTGTATC  CA
                                    _  CACT_     GT
GAM245  RHD      3'  ACTGCTATGTGTCACACTTTGC 32604     T   TACGT     TG
                                  GCGG AGT    TGCATAG  GT
                                  |||| |||    |||||||  ||
                                  CGTT TCA    GTGTATC  CA
                                    _  CACT_     GT
GAM245  RNMT     3'  CACTTGTGTAACTGACTGC   13712       C      _
                                  GTAGTTA GTTGCATA GTG
                                  ||||||| |||||||| |||
                                  CGTCAGT CAATGTGT CAC
                                       _       T
GAM245  RNTRE    3'  TGCATTAGCAGTGTGGTTACT  28041      TT     A    GT
                                  GGTAG  ACGTTGC TAGTG
                                  |||||  ||||||| |||||
                                  TCATT  TGTGACG ATTAC
                                     GG      _    GTC
GAM245  RNTRE    3'  TGCTATGTTCATAATTGC    28042       CGTT     TG
                                  GTAGTTA   GCATAG  G
                                  |||||||   ||||||  |
                                  CGTTAAT   TGTATC  T
                                      ACT_     GT
GAM245  RP2      3'  ATTACAGGTGTGAGCTACCGC  22614        TACG TG   A_
                                  GCGGTAGT   T  CAT  GTGGT
                                  ||||||||   |  |||  |||||
                                  CGCCATCG   A  GTG  CATTA
                                       ____ GT   GA
GAM245  RP42     3'  TGATTTAATGTGGTGTGATTAT 40208         TT   AGTGGT
              T                   GGTAGTTACG  GCAT
                                  ||||||||||  ||||
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```
                                TTATTAGTGT  TGTA
                                      GG   ATTTAGTC
GAM245  RPL10    3'  CCATAAATGTGATTATAGT   20028    G        GCATA
                                GC GTAGTTACGTT    GTGG
                                || ||||||||||    ||||
                                TG TATTAGTGTAA    TACC
                                 A         A____
GAM245  RTN3     3'  CGCTGTGCACTGCTGT     73898        TACGTT     TG
                                GCGGTAGT    GCATAG  G
                                ||||||||    ||||||  |
                                TGTCGTCA    CGTGTC  C
                                     _______    GT
GAM245  SACM1L   3'  TGCTAATGTGGCTGCT     25826          _
                                GGTAGTTACGTT GCA
                                |||||||||||| |||
                                TCGTCGGTGTAA CGT
                                       T
GAM245  SBF1     5'  GCTGCTCGATGTGATTGTTGC  65458    GG        CAT  TG
                                GC  TAGTTACGTTG   AG  GT
                                ||  ||||||||||   ||  ||
                                CG  GTTAGTGTAGC   TC  CG
                                 TT         ___  GT
GAM245  SCD      3'  ACCACTGTGCCACTGACTTGCT 17344       _   C  T
             GT                   GCGGTA GTTA GT GCATAGTGGT
                                |||||| |||| || ||||||||||
                                TGTCGT CAGT CA CGTGTCACCA
                                   T   _ C
GAM245  SCG3     3'  CCGCTGTGGAAGCTTTGT    25098     T   TACG  G
                                GCGG AGT    TT CATAGTGG
                                |||| |||    || ||||||||
                                TGTT TCG    AA GTGTCGCC
                                  _   ____  G
GAM245  SCN4A    3'  ACCACTGTGTGAACCACTGT   4406       A  TACG TG
                                GCGGT GT    T  CATAGTGGT
                                ||||| ||    |  |||||||||
                                TGTCA CA    A  GTGTCACCA
                                  C  ____ GT
GAM245  SCN8A    3'  GCTTGGGCAGGTGGTTACTGC  26385       TT  G   AT_
                                GCGGTAG  AC TTGC   AGT
                                |||||||  || ||||   |||
                                CGTCATT  TG GACG   TCG
                                    GG  _    GGT
GAM245  SEL1L    3'  ACTGCTGTGTAATGGGCTTTGT 17356     T   A       TG
                                GCGG AGTT CGTTGCATAG  GT
                                |||| |||| ||||||||||  ||
                                TGTT TCGG GTAATGTGTC  CA
                                  _   _        GT
GAM245  SEL1L    3'  GCTACTATGCTTCAGGATTGTC 17360   GT   ACGTT
                                G  AGTT    GCATAGTGGT
                                |  ||||    ||||||||||
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```
                                C  TTAG    CGTATCATCG
                                 TG   GACTT
GAM245  SELE    3'  ACTACTGTGATCAGGCTAT   4825       ACGTTG
                                GTAGTT    CATAGTGGT
                                ||||||    |||||||||
                                TATCGG    GTGTCATCA
                                   ACTA__
GAM245  SELPLG  3'  GCCATTGTCTTTTGGTTGCC  59689     TT CGTTGC
                                GGTAG  A    ATAGTGGT
                                |||||  |    ||||||||
                                CCGTT  T    TGTTACCG
                                   GG TTTC__
GAM245  SERPIND1  3'  GTCACTGTAACTGTAGTGTGTC 3946     T      ____    GT
           TGCTGT                 TAG TACGTTGCA   TAGTG
                                ||| |||||||||   |||||
                                GTC GTGTGATGT   GTCAC
                                  T       CAAT    TG
GAM245  SERPINE2  3'  GCTGTTGTGCAGTGTGCCTGTC 74922   GT  T        TG
                                G  AG TACGTTGCATAG  GT
                                |  || ||||||||||||  ||
                                C  TC GTGTGACGTGTT  CG
                                 TG  C          GT
GAM245  SERPINI1  3'  GTCATTGTGTTTGTGTGCTGTT 17235   GG   _   TT      GT
           GT                    GC  TAGT TACG  GCATAGTG
                                ||  |||| ||||  ||||||||
                                TG  GTCG GTGT  TGTGTTAC
                                 TT   T   T_      TG
GAM245  SFRP1   3'  ACTCTGAGTAACTGGTTGCTGT 11562       TT C    A   T
                                GCGGTAG  A GTTGC TAG GGT
                                |||||||  | ||||| ||| |||
                                TGTCGTT  T CAATG GTC TCA
                                   GG _    A   _
GAM245  SFRS1   3'  ACTGTTAATGTGTGACCTGCTG 22636       _   GTT   _ TG
           T                    GCGGTAG TTAC   GCAT AG  GT
                                |||||||  ||||   ||||  ||  ||
                                TGTCGTC AGTG   TGTA TT  CA
                                   C    ___    A  GT
GAM245  SFRS2   3'  GCTGTTAAGGTGGCGTGTTGC  65189   GG  _    G   C
                                GC  TA GTTAC TTG ATAGT
                                ||  ||  |||||  |||  |||||
                                CG  GT CGGTG AAT TGTCG
                                 TT  G    G   _
GAM245  SHMT2   3'  GCTTCTTGTAGCTTAACTACTG 18267         C     T  T
           C                    GCGGTAGTTA GTTGCA AG GGT
                                ||||||||||  ||||||  ||  |||
                                CGTCATCAAT CGATGT TC TCG
                                      T     _  T
GAM245  SIM2    3'  ATTGCACCGAGACCTAACTGCC 23781          C   GCATA TG
           GC                    GCGGTAGTTA GTT    G  GT
                                ||||||||||  |||    |  ||
```

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                                CGCCGTCAAT CAG    C  TA
                                      C   AGCCA GT
GAM245  SLC12A7  3' ATTGCTGTAGAGTGACGGCTGC 21698      A    G  GC    TG
                                GCGGT GTTAC TT  ATAG  GT
                                ||||| ||||| ||  ||||  ||
                                CGTCG CAGTG AG  TGTC  TA
                                   G    _ A_   GT
GAM245  SLC13A1  3' ATCAGTTATGGTGTAGCTGCTG 42376          TTG   _
           C                    GCGGTAGTTACG   CATAG TGGT
                                ||||||||||||   ||||| ||||
                                CGTCGTCGATGT   GTATT ACTA
                                       G__    G
GAM245  SLC16A1  3' ATTGTTGTGCTTAGAATTGCTG 11739        ACGTT     TG
                                CGGTAGTT    GCATAG  GT
                                ||||||||    ||||||  ||
                                GTCGTTAA    CGTGTT  TA
                                     GATT_     GT
GAM245  SLC18A1  3' GTGTAATGTGACATTGT     11750      A
                                GCGGT GTTACGTTGCAT
                                ||||| ||||||||||||
                                TGTTA CAGTGTAATGTG
                                  _
GAM245  SLC19A2  3' ACTAGGATAGATGTGATTCCTG 68975     T       GC  AG
           C                    GCGG AGTTACGTT  AT  TGGT
                                |||| |||||||||  ||  ||||
                                CGTC TTAGTGTAG  TA  ATCA
                                  C       A_  GG
GAM245  SLC20A2  3' ACTGTGTATTGATTGTTGT   22175    GG     CGT
                                GC  TAGTTA   TGCATAGT
                                ||  ||||||   ||||||||
                                TG  GTTAGT   ATGTGTCA
                                 TT     T__
GAM245  SLC21A2  3' GCCACTGTGTACCCGGGCTGT  18862      AGTTACGT
                                GCGGT       TGCATAGTGGT
                                |||||       ||||||||||
                                TGTCG       ATGTGTCACCG
                                   GGCCC___
GAM245  SLC4A7   3' TGGAAATGTAGCTGCT      13230          G_
                                GGTAGTTACGTT  CA
                                ||||||||||||  ||
                                TCGTCGATGTAA  GT
                                       AG
GAM245  SLC4A7   3' GCTGTTTATGTGTGACTACCG  13227         GTT    _ TG
                                CGGTAGTTAC   GCATA G  GT
                                ||||||||||   ||||| |  ||
                                GCCATCAGTG   TGTAT T  CG
                                      ___     T GT
GAM245  SLIT3    5' CCGCCGATGGAGCTGCTGT   11767         A    CATA
                                GCGGTAGTT CGTTG   GTGG
                                ||||||||| |||||   ||||
```

```
                                TGTCGTCGA GTAGC   CGCC
                                     G    ____
GAM245  SLIT3    5'  GCTGCTGTTGCTGCCGC     11768        T _ T
                                GCGGTAGT AC GT GC
                                |||||||| || || ||
                                CGCCGTCG TG CG CG
                                     T  T  T
GAM245  SMARCA3  3'  ATTGTTTAAATGTAACTTGCTG 11788       _      GC_    GGT
           T                    GCGGTA GTTACGTT   ATAGT
                                |||||| ||||||||   |||||
                                TGTCGT CAATGTAA   TGTTA
                                   T       ATT
GAM245  SOCS5    3'  TTGATGTGCAGTCTAATTGTTG 25803    GG     CG      GTGGT
           T                    GC  TAGTTA  TTGCATA
                                ||  ||||||  |||||||
                                TG  GTTAAT  GACGTGT
                                 TT     CT      AGTTG
GAM245  SORCS2   3'  CCGCCCCACGTGCTGTCGC   40416    GT   T   TGCATA
                                GCG  AGT ACGT     GTGG
                                |||  ||| ||||     ||||
                                CGC  TCG TGCA     CGCC
                                  TG   _   CCC___
GAM245  SRD5A1   3'  GCCATTGTGCAGTCATGGCC   6457     A  T  GT
                                GGT GT AC  TGCATAGTGGT
                                ||| || ||  ||||||||||
                                CCG TA TG  ACGTGTTACCG
                                  G  C  __
GAM245  SRGAP2   3'  CCAGATGGTTGGCTACTGC   74605         CGTTG   AG
                                GCGGTAGTTA    CAT  TGG
                                ||||||||||    |||  |||
                                CGTCATCGGT    GTA  ACC
                                      TG___   G_
GAM245  SRR      3'  AAGAACATGTAACGTACTACTG 41685        T       A  GGT
           C                    GCGGTAGT ACGTTGCAT GT
                                |||||||| |||||||| ||
                                CGTCATCA TGCAATGTA CA
                                     _       _  AGAAG
GAM245  SSRP1    3'  ACCTTAAGGATGTAGCTGCTGC 11984           GCA   T
                                GCGGTAGTTACGTT   TAG GGT
                                ||||||||||||||   ||| |||
                                CGTCGTCGATGTAG   ATT CCA
                                       GA_  _
GAM245  ST7      3'  ACTGTAGAAATGTGGCTGCTG  25541          GC_
                                CGGTAGTTACGTT   ATAGT
                                ||||||||||||   |||||
                                GTCGTCGGTGTAA   TGTCA
                                       AGA
GAM245  SURF4    3'  ACCACTTTCCTGAGGCTGTCGC 52539     GT   TA  TTGCAT
                                GCG  AGT  CG     AGTGGT
                                |||  |||  ||     ||||||
```

```
                              CGC  TCG  GT     TCACCA
                                TG   GA  CCTT__
GAM245  SVIL    3'  CGCTATAGATAGCACTGC    12070      A   AC   GC    TG
                              GCGGT GTT  GTT  ATAG  G
                              ||||| |||  |||  ||||  |
                              CGTCA CGA  TAG  TATC  C
                                _  __   A_   GT
GAM245  SVIL    3'  CGCTATAGATAGCACTGC    41409      A   AC   GC    TG
                              GCGGT GTT  GTT  ATAG  G
                              ||||| |||  |||  ||||  |
                              CGTCA CGA  TAG  TATC  C
                                _  __   A_   GT
GAM245  SYNGR1   3'  GCTGTGTGACAGCTGGTTGTTG 16318    GG   TT C__  TG     GGT
          C                    GC  TAG  A   GT  CATAGT
                              ||  |||  |   ||  ||||||
                              CG  GTT  T   CA  GTGTCG
                               TT   GG CGA  GT
GAM245  SYT1    3'  CTATTATGAAGCTACT      18901       TACGTTG
                              GGTAGT      CATAGTGG
                              ||||||      ||||||||
                              TCATCG      GTATTATC
                                 AA_____
GAM245  TACC1    3'  GCTGCGTTGACTACTGC     20800          _  T
                              GCGGTAGTTA CGT GC
                              |||||||||| ||| ||
                              CGTCATCAGT GCG CG
                                    T   T
GAM245  TAF1A    3'  GCTATTGTGTAATAAACTG    19062      AC
                              TAGTT  GTTGCATAGTGGT
                              |||||  ||||||||||||
                              GTCAA  TAATGTGTTATCG
                                 A_
GAM245  TAF1A    3'  GCTATTGTGTAATAAACTG    57814      AC
                              TAGTT  GTTGCATAGTGGT
                              |||||  ||||||||||||
                              GTCAA  TAATGTGTTATCG
                                 A_
GAM245  TAF5    3'  GCTGTAAAAACGTAGTTACTGT 57400       GT     GC_    GGT
                              GCGGTA  TACGTT   ATAGT
                              ||||||  ||||||   |||||
                              TGTCAT  ATGCAA   TGTCG
                                 TG     AAA
GAM245  TAF5    3'  GCTGTAAAAACGTAGTTACTGT 22711       GT     GC_    GGT
                              GCGGTA  TACGTT   ATAGT
                              ||||||  ||||||   |||||
                              TGTCAT  ATGCAA   TGTCG
                                 TG     AAA
GAM245  TAPBP    3'  ATTACAGGCGTGACGACCGC   12120      A      GCA
                              GCGGT GTTACGTT   TAGT
                              ||||| ||||||||   ||||
```

```
                                CGCCA CAGTGCGG   ATTA
                                  G       AC_
GAM245  TARBP2   3'  GCCACTGTGTGTCATGGCTCTG 56165      T    CGT
           C                     GCGG AGTTA   TGCATAGTGGT
                                 |||| |||||   ||||||||||
                                 CGTC TCGGT   GTGTGTCACCG
                                   _    ACT
GAM245  TCEA1    3'  TCTTAGTGTAGTATAGCTATTG 80442          CG     AGTGGT
           T                     GCGGTAGTTA  TTGCAT
                                 ||||||||||  ||||||
                                 TGTTATCGAT  GATGTG
                                       AT     ATTCTA
GAM245  TCF2     3'  GCCAGAAACGTAACTGTGTGC  21382    GG_        GCATAG
                                 GC   TAGTTACGTT     TGGT
                                 ||   ||||||||||     ||||
                                 CG   GTCAATGCAA     ACCG
                                  TGT        AG____
GAM245  TCF7     3'  ATCACATATTCTAGTGTAACAC 12156      A       C_  _
           TGC                     CGGT GTTACGTTG  ATA GTGGT
                                 |||| |||||||||  ||| |||||
                                 GTCA CAATGTGAT  TAT CACTA
                                   _       CT   A
GAM245  TCF8     3'  GCTGCTGCTCTGTGGCTG    47726         TT   TA TG
                                 TAGTTACG  GCA  G  GT
                                 ||||||||  |||  |  ||
                                 GTCGGTGT  CGT  C  CG
                                      CT   __ GT
GAM245  TCP10    3'  CCAATAGTGCAGTTATCGT    16043        TTACG     AG_
                                 GCGGTAG    TTGCAT   TGG
                                 |||||||    ||||||   |||
                                 TGCTATT    GACGTG   ACC
                                      _____      ATA
GAM245  TDG      3'  ATTGCTTTGGTATATAACTATT 12188          CGT   AT_  TG
           GT                      GCGGTAGTTA   TGC   AG  GT
                                 ||||||||||   |||   ||  ||
                                 TGTTATCAAT   ATG   TC  TA
                                       AT_   GTT  GT
GAM245  TDG      5'  CCACTGTCTGGGTACTGC     12189       G   CGTTGC
                                 GCGGTA TTA     ATAGTGG
                                 ||||||  |||     |||||||
                                 CGTCAT GGT     TGTCACC
                                    G   C_____
GAM245  TEGT     3'  GCTGTCCTCTGATTTAGCTGCT 64624          C    C___    GGT
           GC                      CGGTAGTTA GTTG    ATAGT
                                 |||||||||  ||||    |||||
                                 GTCGTCGAT TAGT    TGTCG
                                       T    CTCC
GAM245  TEM8     3'  TGCCGCGTGATTCCCGC     49860      T       T
                                 GCGG AGTTACGT GCA
                                 ||||  ||||||||  |||
```

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                                CGCC TTAGTGCG CGT
                                  C       C
GAM245  TFF3     3'  CCCGGCTGTGATTGCTGC    63565          TT  ATAGT
                                GCGGTAGTTACG  GC    GG
                                ||||||||||||  ||    ||
                                CGTCGTTAGTGT  CG    CC
                                      __  GC___
GAM245  TFG      3'  ACCAATTAATGTAGCTGCTAGC 20274    _         CATAG
                                GC GGTAGTTACGTTG    TGGT
                                || ||||||||||||    ||||
                                CG TCGTCGATGTAAT    ACCA
                                 A          TA___
GAM245  THBD     3'  ATCATAGAAATGTAACTTTTGT 4492      T       GCATA
                                GCGG AGTTACGTT    GTGGT
                                |||| |||||||||    |||||
                                TGTT TCAATGTAA    TACTA
                                  T       AGA__
GAM245  TIA1     5'  GCCGGGCGGTTTAGTGTAATTG 41849         TT__  ATAG
            CCGC                  CGGTAGTTACG   GC   TGGT
                                ||||||||||    ||   ||||
                                GCCGTTAATGT   TG   GCCG
                                      GATT  GCGG
GAM245  TIA1     5'  GCCGGGCGGTTTAGTGTAATTG 42246         TT__  ATAG
            CCGC                  CGGTAGTTACG   GC   TGGT
                                ||||||||||    ||   ||||
                                GCCGTTAATGT   TG   GCCG
                                      GATT  GCGG
GAM245  TIE      3'  CAGAACGTGGCTCTGC      18296      T       GCATAG
                                GCGG AGTTACGTT     TG
                                |||| |||||||||     ||
                                CGTC TCGGTGCAA     AC
                                  _       G_____
GAM245  TIRAP    3'  ATTATGATGTCACTGCTGT    53567        T   TG
                                GCGGTAGT ACGT  CATAGT
                                |||||||| ||||  ||||||
                                TGTCGTCA TGTA  GTATTA
                                    C   __
GAM245  TMEFF2   5'  ATCATGCGCGGGTTTGGCTGCT 32466         CG_   ATA
            GC                    GCGGTAGTTA   TTGC   GTGGT
                                |||||||||   ||||   |||||
                                CGTCGTCGGT   GGCG   TACTA
                                      TTG   CG_
GAM245  TMPRSS4  3'  CGTTGGTATGACTACCGT    39116         CGT   A   TG
                                GCGGTAGTTA   TGC TAG  G
                                ||||||||||   ||| |||  |
                                TGCCATCAGT   ATG GTT  C
                                      ___   _   GT
GAM245  TNFRSF6B 3'  CGCTGGTGCGGCTGCTGC    51982         TACGT    _ TG
                                GCGGTAGT    TGCAT AG  G
                                ||||||||    ||||| ||  |
```

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                                CGTCGTCG    GCGTG TC  C
                                     _____    G  GT
GAM245  TNFRSF6B  3'  ACCTGGTGCCGGCGTGATTGCC 51980          _  AGT
                                GGTAGTTACGTTG CAT   GGT
                                |||||||||||| |||   |||
                                CCGTTAGTGCGGC GTG   CCA
                                      C   GT_
GAM245  TNXB    5'  ATTACTCGCTGGGGCTGCTGT  50637       TA  TT  AT
                                GCGGTAGT  CG  GC  AGTGGT
                                ||||||||  ||  ||  ||||||
                                TGTCGTCG  GT  CG  TCATTA
                                     GG  __  C_
GAM245  TP53BP2  5'  GCTGAAGTGTGGTGTGGCTCTG 18302     T     TT   AG
           T                     GCGG AGTTACG  GCAT  TGGT
                                |||| |||||||  ||||  ||||
                                TGTC TCGGTGT  TGTG  GTCG
                                  _     GG    AA
GAM245  TPD52L2  3'  TCCACGCGGAGATGTGGCTGCC 12367          GCATA   T
           GC                    GCGGTAGTTACGTT    GTGG
                                ||||||||||||||    ||||
                                CGCCGTCGGTGTAG    CACC
                                      AGGCG    TA
GAM245  TPM4    3'  GCCGGGGGTGGCTATTGT    12371         G  __
                                GCGGTAGTTAC TT  GC
                                |||||||||| ||  ||
                                TGTTATCGGTG GG  CG
                                      G  GC
GAM245  TRC8    3'  TTACTGTGATGTGCTACTGT   23311       T   TG
                                GCGGTAGT ACGT  CATAGTGG
                                |||||||| ||||  ||||||||
                                TGTCATCG TGTA  GTGTCATT
                                     _   __
GAM245  TRPC5   5'  GTTATTGTGTGTGACTGGCTGC 25002      _    GTT     GG
                                GCGGT AGTTAC   GCATAGT  T
                                ||||| ||||||   |||||||  |
                                CGTCG TCAGTG   TGTGTTA  G
                                   G     ___      TT
GAM245  TRPM6   3'  ACCACTATGCCTGGCTAATTTT 34524     T    C  __
           GT                    GCGG AGTTA GTT  GCATAGTGGT
                                |||| ||||| |||  ||||||||||
                                TGTT TTAAT CGG  CGTATCACCA
                                  _    _  TC
GAM245  TRPM7   3'  TCATTATGTGATACTGGC    62131   G   TAC  TG
                                G TAGT   GT  CATAGTGG
                                | ||||   ||  ||||||||
                                C GTCA   TA  GTATTACT
                                 G   ___  GT
GAM245  TSPY    3'  GCTATTTTTAAGGGAGTGTGAT 82107       TTGCAT____
           TGCTGC                TAGTTACG       AGTGGT
                                ||||||||       ||||||
```

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                                GTTAGTGT        TTATCG
                                    GAGGGAATTT
GAM245  TUBA2    3'  GCCACCCCCAGCGTGGCTGCT  54405          CATA
                                GGTAGTTACGTTG   GTGGT
                                |||||||||||||   |||||
                                TCGTCGGTGCGAC   CACCG
                                    CCC_
GAM245  TUBA2    3'  GCCACCCCCAGCGTGGCTGCT  20005          CATA
                                GGTAGTTACGTTG   GTGGT
                                |||||||||||||   |||||
                                TCGTCGGTGCGAC   CACCG
                                    CCC_
GAM245  UBE2B    3'  ATTGTTGTGTATAATTTACC  12472      TTACGT     TG
                                GGTAG     TGCATAG  GT
                                |||||     |||||||  ||
                                CCATT     ATGTGTT  TA
                                   TAAT__     GT
GAM245  UBE2G2   5'  CGCTCGGCGCAGCTGTTGC  64854    GG    A    CAT
                                GC  TAGTT CGTTG   AGTG
                                ||  ||||| |||||   ||||
                                CG  GTCGA GCGGC   TCGC
                                 TT    C    ___
GAM245  UBE2L3   3'  TGCCAACGTAGCTCTGC     12508      T        _
                                GCGG AGTTACGTTG CA
                                |||| |||||||||| ||
                                CGTC TCGATGCAAC GT
                                  _        C
GAM245  UBE3A    3'  ACAGTGTGATGCAATTACTGC  4864         A   TG   A
                                GCGGTAGTT CGT  CAT GT
                                |||||||| |||  ||| ||
                                CGTCATTAA GTA  GTG CA
                                     C   GT   A
GAM245  UBE3A    3'  GCTACTGTGCCTTGTGTTACT  4867     AGT    TT
                                GGT   TACG  GCATAGTGGT
                                |||   ||||  ||||||||||
                                TCA   GTGT  CGTGTCATCG
                                  TT_    TC
GAM245  UBE3A    3'  ACAGTGTGATGCAATTACTGC  55576        A   TG   A
                                GCGGTAGTT CGT  CAT GT
                                |||||||| |||  ||| ||
                                CGTCATTAA GTA  GTG CA
                                     C   GT   A
GAM245  UBE3A    3'  GCTACTGTGCCTTGTGTTACT  55579     AGT    TT
                                GGT   TACG  GCATAGTGGT
                                |||   ||||  ||||||||||
                                TCA   GTGT  CGTGTCATCG
                                  TT_    TC
GAM245  UBE3A    3'  ACAGTGTGATGCAATTACTGC  55586        A   TG   A
                                GCGGTAGTT CGT  CAT GT
                                |||||||| |||  ||| ||
```

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                                CGTCATTAA GTA  GTG CA
                                     C   GT   A
GAM245  UBE3A    3'  GCTACTGTGCCTTGTGTTACT  55591     AGT    TT
                                GGT   TACG  GCATAGTGGT
                                |||   ||||  ||||||||||
                                TCA   GTGT  CGTGTCATCG
                                  TT_    TC
GAM245  UCN      3'  ACTGTCTGCGTGACTATT    12529          TGC
                                GGTAGTTACGT   ATAGT
                                ||||||||||   |||||
                                TTATCAGTGCG   TGTCA
                                      TC_
GAM245  UROS     5'  GCCCAGCGCGGGTGGCTGCCGC 4562           G    ATAGT
                                GCGGTAGTTAC TTGC     GGT
                                |||||||||| ||||     |||
                                CGCCGTCGGTG GGCG     CCG
                                      _    CGAC_
GAM245  USP11    3'  ATTGCAGGCTTAGTCGTGGCTA 16201          TT___  ATA TG
            CTGT                  GGTAGTTACG    GC   G  GT
                                |||||||||     ||  |  ||
                                TCATCGGTGC    CG   C  TA
                                     TGATT  GA_ GT
GAM245  UTY      3'  ACCACTGGTTTTGTAGCTG   23067        TT  A
                                TAGTTACG  GC TAGTGGT
                                ||||||||  || |||||||
                                GTCGATGT  TG GTCACCA
                                    TT  _
GAM245  WBSCR14  3'  GCCACTGTGCTCCAGCACCGT  51969      A   ACGTT
                                GCGGT GTT    GCATAGTGGT
                                |||||  |||    ||||||||||
                                TGCCA CGA    CGTGTCACCG
                                   _  CCT__
GAM245  WBSCR14  3'  GCCACTGTGCTCCAGCACCGT  51974      A   ACGTT
                                GCGGT GTT    GCATAGTGGT
                                |||||  |||    ||||||||||
                                TGCCA CGA    CGTGTCACCG
                                   _  CCT__
GAM245  WEE1     3'  ACCACTGTGGTGGTGTGCTGC  12648      T   TT  _
                                GTAGT ACG  GC ATAGTGGT
                                |||||  |||  ||  ||||||||
                                CGTCG TGT  TG TGTCACCA
                                   _  GG  G
GAM245  WHSC1    3'  ACCATTGTAATATGACTCCTGT 23651      T    CG    TA
                                GCGG AGTTA  TTGCA  GTGGT
                                ||||  |||||  |||||  |||||
                                TGTC TCAGT  AATGT  TACCA
                                  C    AT    __
GAM245  WHSC1    3'  CATTTGGGGCTGCTGC      23655        TA  TTGCAT
                                GCGGTAGT  CG     AGTG
                                ||||||||  ||     ||||
```

```
                              CGTCGTCG GT    TTAC
                                  GG _______
GAM245  WHSC1    3' GCTTTAGCAGCGTGGCTGCC 29912          AT_
                              GGTAGTTACGTTGC AGT
                              ||||||||||||||  |||
                              CCGTCGGTGCGACG TCG
                                   ATT
GAM245  WHSC1L1  3' CCACAGAACGTGGCTAT   35029        GCATA
                              GTAGTTACGTT   GTGG
                              ||||||||||    ||||
                              TATCGGTGCAA   CACC
                                   GA___
GAM245  WT1      3' ACCGTTGCTTGAAATTACTGT 4584        A TT  TAG
                              GCGGTAGTT CG GCA  TGGT
                              ||||||||| || |||  ||||
                              TGTCATTAA GT CGT  GCCA
                                   A T_  T__
GAM245  WT1      3' ATTACTGTGTAAATATATGTC 4585   GT GTTACG
                              G A    TTGCATAGTGGT
                              | |    ||||||||||||
                              C T    AATGTGTCATTA
                               TG ATATA_
GAM245  WT1      3' ACCGTTGCTTGAAATTACTGT 44349       A TT  TAG
                              GCGGTAGTT CG GCA  TGGT
                              ||||||||| || |||  ||||
                              TGTCATTAA GT CGT  GCCA
                                   A T_  T__
GAM245  WT1      3' ATTACTGTGTAAATATATGTC 44350   GT GTTACG
                              G A    TTGCATAGTGGT
                              | |    ||||||||||||
                              C T    AATGTGTCATTA
                               TG ATATA_
GAM245  WT1      3' ACCGTTGCTTGAAATTACTGT 44359       A TT  TAG
                              GCGGTAGTT CG GCA  TGGT
                              ||||||||| || |||  ||||
                              TGTCATTAA GT CGT  GCCA
                                   A T_  T__
GAM245  WT1      3' ATTACTGTGTAAATATATGTC 44360   GT GTTACG
                              G A    TTGCATAGTGGT
                              | |    ||||||||||||
                              C T    AATGTGTCATTA
                               TG ATATA_
GAM245  WT1      3' ACCGTTGCTTGAAATTACTGT 44369       A TT  TAG
                              GCGGTAGTT CG GCA  TGGT
                              ||||||||| || |||  ||||
                              TGTCATTAA GT CGT  GCCA
                                   A T_  T__
GAM245  WT1      3' ATTACTGTGTAAATATATGTC 44370   GT GTTACG
                              G A    TTGCATAGTGGT
                              | |    ||||||||||||
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```
                                C  T     AATGTGTCATTA
                                 TG ATATA_
GAM245  WWP2     3'  CCACTGGGGGTGGCTG      61087        G  GCA
                                TAGTTAC TT   TAGTGG
                                ||||||| ||   ||||||
                                GTCGGTG GG   GTCACC
                                   G  ___
GAM245  XRCC5    3'  AGCCCTTGTGATGTGATTAGTG 40930     G       TG  T  T
           T                     GCG TAGTTACGT  CA AG GGT
                                ||| |||||||||  || || |||
                                TGT ATTAGTGTA  GT TC CCG
                                  G       GT  _  _   AC
GAM245  YWHAG    3'  CATTATGTAGCTGTCGT     25018     GT   TACGT
                                GCG  AGT    TGCATAGTG
                                |||  |||    |||||||||
                                TGC  TCG    ATGTATTAC
                                  TG  ______
GAM245  YWHAZ    3'  CTACTAATATAACTACTGT    12701          CG TGCA
                                GCGGTAGTTA  T    TAGTGG
                                ||||||||||  |    ||||||
                                TGTCATCAAT  A    ATCATC
                                      AT _____
GAM245  ZFP36L1  3'  ATTAAGATGAATGTAATTATT  17004           G   AG
                                GGTAGTTACGTT CAT  TGGT
                                |||||||||||| |||  ||||
                                TTATTAATGTAA GTA  ATTA
                                      _  GA
GAM245  ZIC3     3'  ATCGTTTGTAATTTAATTATTG 12728          C     TAG
           C                     GCGGTAGTTA GTTGCA   TGGT
                                ||||||||||| ||||||   ||||
                                CGTTATTAAT TAATGT   GCTA
                                      T     TT_
GAM245  ZNF135   3'  ATCACTGTGGATACTGACTGTC 12849    GT    C  TG_
                                G  AGTTA GT   CATAGTGGT
                                |  ||||| ||   |||||||||
                                C  TCAGT CA   GTGTCACTA
                                 TG    _  TAG
GAM245  ZNF137   3'  ACCACTATGCCCGGCTAACTTT 12857      T    C  __
           GT                     GCGG AGTTA GTT  GCATAGTGGT
                                |||| ||||| |||  ||||||||||
                                TGTT TCAAT CGG  CGTATCACCA
                                  _    _  CC
GAM245  ZNF141   3'  ATTATAAATGTAATTTCTGT   12871      T       GC
                                GCGG AGTTACGTT  ATAGT
                                |||| |||||||||  |||||
                                TGTC TTAATGTAA  TATTA
                                  T       A_
GAM245  ZNF155   3'  CCAATCAGTGTAATTGGTGT   12875     G        CATAG
                                GCG TAGTTACGTTG    TGG
                                ||| ||||||||||    |||
```

```
                                TGT GTTAATGTGAC    ACC
                                  G         TA___
GAM245  ZNF22    3'  GTTCTTTGTGATGGTAACTGCT 91464          _ TG  T  TGGT
                GT                  GCGGTAGTTAC GT  CA AG
                                    |||||||||| ||  || ||
                                    TGTCGTCAATG TA  GT TC
                                          G  GT  T  TTG
GAM245  ZNF264   3'  CTACTAATGTAACTATC     12751          TGCA
                                    GGTAGTTACGT   TAGTGG
                                    ||||||||||    ||||||
                                    CTATCAATGTA   ATCATC
                                                  ____
GAM245  ZNF274   5'  GCCATTGTGCGGCGCGCGCCG  56056     A  TA
                                    CGGT GT  CGTTGCATAGTGGT
                                    |||| ||  ||||||||||||||
                                    GCCG CG  GCGGCGTGTTACCG
                                      _  C_
GAM245  ZNF274   5'  GCCATTGTGCGGCGCGCGCCG  32882     A  TA
                                    CGGT GT  CGTTGCATAGTGGT
                                    |||| ||  ||||||||||||||
                                    GCCG CG  GCGGCGTGTTACCG
                                      _  C_
GAM245  ZNF42    3'  TCGCCCAGGGCTTGGCTACTGT 12787         C   GCATA   GT
                                    GCGGTAGTTA GTT    GTG
                                    |||||||||| |||    |||
                                    TGTCATCGGT CGG    CGC
                                          T   GACC_   TG
GAM245  3-PAP    5'  GCCGCTAGTGCTGGTGGCCGCC 38804     TA    GTT   _
                GC                  GCGG  GTTAC   GCAT AGTGGT
                                    ||||  |||||   |||| ||||||
                                    CGCC  CGGTG   CGTG TCGCCG
                                      GC    GT_   A
GAM245  ACAS2L   3'  TGTAGTGTAGCTACAGT     68078    G
                                    GC GTAGTTACGTTGCA
                                    || ||||||||||||||
                                    TG CATCGATGTGATGT
                                     A
GAM245  ACP33    3'  ATTGTTTTGAGTGTTAGCTACT 33556         _ TTG  T  TG
                GC                  GCGGTAGTTA CG   CA AG  GT
                                    |||||||||| ||   || ||  ||
                                    CGTCATCGAT GT   GT TT  TA
                                          T  GA_  T  GT
GAM245  AKAP7    3'  GTTGCTATGCAGTGTGAT    33050           GG
                                    GTTACGTTGCATAGT  T
                                    |||||||||||||||  |
                                    TAGTGTGACGTATCG  G
                                              TT
GAM245  AKAP7    3'  TTATAAATGTAATTATTGC   33053           GC
                                    GCGGTAGTTACGTT  ATAG
                                    ||||||||||||||  ||||
```

```
                                CGTTATTAATGTAA  TATT
                                       A_
GAM245  AKAP7    3'  TTATAAATGTAATTATTGC   16728          GC
                                GCGGTAGTTACGTT  ATAG
                                |||||||||||||  ||||
                                CGTTATTAATGTAA  TATT
                                       A_
GAM245  AKAP7    3'  GTTGCTATGCAGTGTGAT    56838          GG
                                GTTACGTTGCATAGT  T
                                |||||||||||||  |
                                TAGTGTGACGTATCG  G
                                        TT
GAM245  AKAP7    3'  TTATAAATGTAATTATTGC   56841          GC
                                GCGGTAGTTACGTT  ATAG
                                |||||||||||||  ||||
                                CGTTATTAATGTAA  TATT
                                       A_
GAM245  AKAP7    3'  GTTGCTATGCAGTGTGAT    16725          GG
                                GTTACGTTGCATAGT  T
                                |||||||||||||  |
                                TAGTGTGACGTATCG  G
                                        TT
GAM245  ALS2CR3  3'  TCAGATGACGTGGCTTTGT   30487     T     TG  AG
                                GCGG AGTTACGT  CAT  TGG
                                |||| ||||||||  |||  |||
                                TGTT TCGGTGCA  GTA  ACT
                                  _      __  G_
GAM245  ALS2CR3  3'  CGTTGTGTAATGTCTCT    30483    TT       TG
                                AG  ACGTTGCATAG  G
                                ||  ||||||||||  |
                                TC  TGTAATGTGTT  C
                                 TC         GT
GAM245  ALTE     3'  ATGTGTGACTTCTGC      16388     T    GTT
                                GCGG AGTTAC   GCAT
                                |||| ||||||   ||||
                                CGTC TCAGTG   TGTA
                                  T     ____
GAM245  AMOTL1   3'  ATCACTGTAAACTGGCTCTGT  73648     T   C  GC
                                GCGG AGTTA GTT  ATAGTGGT
                                |||| ||||| |||  ||||||||
                                TGTC TCGGT CAA  TGTCACTA
                                  _    _  A_
GAM245  AP3S2    3'  ACCATGCCCAGCTAATTGTTGT 19515    GG    C   CATA
                                GC  TAGTTA GTTG   GTGGT
                                ||  |||||| ||||   |||||
                                TG  GTTAAT CGAC   TACCA
                                 TT     _   CCG_
GAM245  Apg4B    3'  GCCGCTGTGCTGGGAGCTGCAG 25286    G    ACGTT
          T                     GC GTAGTT    GCATAGTGGT
                                || ||||||    ||||||||||
```

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                                TG CGTCGA    CGTGTCGCCG
                                 A     GGGT_
GAM245  APOARGC  3'  CCTGACAATGAACTACTGC   44419         A    _  TAGT
                                GCGGTAGTT CGTTG CA   GG
                                ||||||||| ||||| ||   ||
                                CGTCATCAA GTAAC GT   CC
                                      _    A  ____
GAM245  APOL2    5'  GCTGGGGAGCAGCGTGTTTACT 48051       T      A___   GGT
          GT                    CGGTAG TACGTTGC   TAGT
                                |||||| ||||||||   ||||
                                GTCATT GTGCGACG   GTCG
                                   T      AGGG
GAM245  APOL4    5'  GCTGGGGAGCAGCGTGTTTGCT 47625       T      A___   GGT
          GT                    CGGTAG TACGTTGC   TAGT
                                |||||| ||||||||   ||||
                                GTCGTT GTGCGACG   GTCG
                                   T      AGGG
GAM245  APOL6    3'  ATTGCATTGTAGTGTGATTATC 47617            TA TG
                                GGTAGTTACGTTGCA  G  GT
                                |||||||||||||||  |  ||
                                CTATTAGTGTGATGT  C  TA
                                         TA GT
GAM245  APOL6    3'  TACTGTATACTACTGT     47621        TACGTTGC
                                GCGGTAGT      ATAGTG
                                ||||||||      ||||||
                                TGTCATCA      TGTCAT
                                    TA_______
GAM245  ARHGAP5  3'  ATTACTATAAGTGACTGCTGC  77070          GTTGC
                                GCGGTAGTTAC    ATAGTGGT
                                ||||||||||    ||||||||
                                CGTCGTCAGTG    TATCATTA
                                      AA___
GAM245  ARHGEF10 3'  GCCATGCTGGCTGCTGT    60422          _  T
                                GCGGTAGTTA CGT GC
                                |||||||||| ||| ||
                                TGTCGTCGGT GTA CG
                                      C  C
GAM245  ARHGEF11 5'  GCTGTTGTGTACATACTATTGT 28805        TAC  T    TG
                                GCGGTAGT   GT GCATAG  GT
                                |||||||   || ||||||  ||
                                TGTTATCA   CA TGTGTT  CG
                                    TA_ _     GT
GAM245  ARHGEF16 5'  ACCATTGTGGTCAAGAGCTACC 27068        ACGTTG
          G                     CGGTAGTT     CATAGTGGT
                                ||||||||     |||||||||
                                GCCATCGA     GTGTTACCA
                                    GAACTG
GAM245  ARHGEF4  3'  CGCTGTGCGGTAGCTCC     52211    T    GT     TG
                                GG AGTTAC  TGCATAG  G
                                || ||||||  |||||||  |
```

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                                CC TCGATG  GCGTGTC  C
                                 _    __      GT
GAM245  ASB13    3'  GCAGCGTGATTGCTGT     45218
                                GCGGTAGTTACGTTGC
                                ||||||||||||||||
                                TGTCGTTAGTGCGACG

GAM245  ASB13    3'  GCTGCTCTGCTGGCTGCTGT  45220         CGTT  T  TG
                                GCGGTAGTTA   GCA AG  GT
                                ||||||||||   ||| ||  ||
                                TGTCGTCGGT   CGT TC  CG
                                      _____  C  GT
GAM245  ATF3     3'  GCCACAAGGACGCTGGCTACTG 14432          _   GCATA
           T                     GCGGTAGTTA CGTT    GTGGT
                                ||||||||||| ||||    |||||
                                TGTCATCGGT GCAG    CACCG
                                      C   GAA__
GAM245  ATP6V1B2 3'  ATTGCTGGGCTGTGCTGCTGC  8085        T  TT  A  TG
                                GCGGTAGT ACG  GC TAG  GT
                                |||||||| |||  || |||  ||
                                CGTCGTCG TGT  CG GTC  TA
                                     _  __ G  GT
GAM245  ATP6V1D  3'  GCTGTTGTCTGAGATTGCTGC  32041         A  TT  _
                                GCGGTAGTT CG  GCA TAGT
                                ||||||||| ||  ||| ||||
                                CGTCGTTAG GT  TGT GTCG
                                      A  C_  T
GAM245  ATP9A    3'  ATTGTTTGCCAGCGTGGCTCGT 62038   GG _       _  T  TG
           TGC                    C  T AGTTACGTTG CA AG  GT
                                |  | ||||||||||| || ||  ||
                                G  G TCGGTGCGAC GT TT  TA
                                 TT C        C  _  GT
GAM245  ATP9A    3'  CCATGTCAGTGACTGTTGT   62040   GG     GTT  TAG
                                GC  TAGTTAC   GCA   TGG
                                ||  |||||||   |||   |||
                                TG  GTCAGTG   TGT   ACC
                                 TT      AC_  ____
GAM245  AXOT     5'  GCCATTGTGCTTCGCTGCCG  43079       TACGTT
                                CGGTAGT     GCATAGTGGT
                                |||||||     ||||||||||
                                GCCGTCG     CGTGTTACCG
                                    CTT____
GAM245  B3GNT1   3'  ACTATTACTTATATGTACTATT 52682         T   TGCA_
           GT                     GCGGTAGT ACGT    TAGTGGT
                                ||||||||| ||||    |||||||
                                TGTTATCA TGTA    ATTATCA
                                     _   TATTC
GAM245  B3GNT1   3'  ATTATTATTGAGTAGTAACTGC 52684         GTTG  _
                                GTAGTTAC    CA TAGTGGT
                                ||||||||    || |||||||
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                                CGTCAATG   GT ATTATTA
                                     ATGA  T
GAM245  B3GNT1   3'  ATTATTGAGTAGTAACTGCT  52685        GT   A
                                GGTAGTTAC  TGC TAGTGGT
                                |||||||||  ||| |||||||
                                TCGTCAATG  ATG GTTATTA
                                     __   A
GAM245  B3GNT1   3'  ACTATTACTTATATGTACTATT 21657        T   TGCA_
           GT                    GCGGTAGT ACGT    TAGTGGT
                                |||||||| ||||    |||||||
                                TGTTATCA TGTA    ATTATCA
                                     _   TATTC
GAM245  B3GNT1   3'  ATTATTATTGAGTAGTAACTGC 21659        GTTG  _
                                GTAGTTAC   CA TAGTGGT
                                ||||||||   || |||||||
                                CGTCAATG   GT ATTATTA
                                     ATGA  T
GAM245  B3GNT1   3'  ATTATTGAGTAGTAACTGCT  21660        GT   A
                                GGTAGTTAC  TGC TAGTGGT
                                |||||||||  ||| |||||||
                                TCGTCAATG  ATG GTTATTA
                                     __   A
GAM245  B3GNT5   3'  ACCACATCCATGTAGCTACTG  49423          T C  A
                                CGGTAGTTACGT G AT GTGGT
                                |||||||||||| | || |||||
                                GTCATCGATGTA C TA CACCA
                                      _ C  _
GAM245  bA430M15.1 3'  TATGTTAATGAAACTGTTGC   76979    GG    A    _
                                GC  TAGTT CGTTG CATA
                                ||  ||||| ||||| ||||
                                CG  GTCAA GTAAT GTAT
                                 TT    A    T
GAM245  BCAA     3'  TGGAATGGAACTACTGT     33049         A   G
                                GCGGTAGTT CGTT CA
                                ||||||||| |||| ||
                                TGTCATCAA GTAA GT
                                     G   G
GAM245  BCAR3    3'  ATTATTAAGGTAACTACTGC   13099          G   C
                                GCGGTAGTTAC TTG ATAGT
                                |||||||||| ||| |||||
                                CGTCATCAATG AAT TATTA
                                      G   _
GAM245  BDG-29   5'  ACCGCTGGTTCTCGGAGCTGCC 72351         A  TT_  A
           GT                    GCGGTAGTT CG   GC TAGTGGT
                                ||||||||| ||   || |||||||
                                TGCCGTCGA GC   TG GTCGCCA
                                     G  TCT  _
GAM245  BG1      5'  CGCTTATGACTGCTGC     87309          CGTTGCAT
                                GCGGTAGTTA       AGTG
                                ||||||||||       ||||
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                                CGTCGTCAGT      TCGC
                                     AT_____
GAM245  BICD2   3' TCATTGTGCAAAATTCTGT   70403     T   ACG       GT
                                GCGG AGTT   TTGCATAGTG
                                |||| ||||   ||||||||||
                                TGTC TTAA   AACGTGTTAC
                                  _   ___        TG
GAM245  BRAG    3' ATGTGGTGTAATTCTGC    29470     T     TT
                                GCGG AGTTACG  GCAT
                                |||| |||||||  ||||
                                CGTC TTAATGT  TGTA
                                  _     GG
GAM245  BTBD2   3' CCACGAGTGTGGCTGCTG    35105        GTT  ATA
                                CGGTAGTTAC   GC   GTGG
                                ||||||||||   ||   ||||
                                GTCGTCGGTG   TG   CACC
                                     ___  AG_
GAM245  BZW1    3' GCTATTAACATACCCTAGTTGC 27890      GT  C_  TGCA
           CGT                    GCGGTA  TA  GT    TAGTGGT
                                ||||||  ||  ||    |||||||
                                TGCCGT  AT  CA    ATTATCG
                                   TG  CC  TACA
GAM245  C13orf1 3' ACCACGCCCGTGTAATTTTTGT 39962     T     TT_  ATA
                                GCGG AGTTACG   GC   GTGGT
                                |||| |||||||   ||   |||||
                                TGTT TTAATGT   CG   CACCA
                                  T     GCC  ___
GAM245  C16orf7 3' GCTACGTGGAGCTGCTGC    16941        __    T
                                GCGGTAGT  TACGT GC
                                ||||||||  ||||| ||
                                CGTCGTCG  GTGCA CG
                                     AG    T
GAM245  C1orf22 3' TCACTAATGTAATTACT     47256          TGCA
                                GGTAGTTACGT    TAGTGG
                                ||||||||||    ||||||
                                TCATTAATGTA    ATCACT
                                               ____
GAM245  C1orf22 3' TCCTGGAGTAACTACTGT    47257         GTTGCA   TG
                                GCGGTAGTTAC     TAG  G
                                ||||||||||     |||  |
                                TGTCATCAATG     GTC  T
                                     AG____   CT
GAM245  C1orf22 3' TGACTGGCGTAGTTATCGT   47259      GT    TGCA   GGT
                                GCGGTA  TACGT   TAGT
                                ||||||  |||||   ||||
                                TGCTAT  ATGCG   GTCA
                                   TG    _____   GTC
GAM245  C1orf24 3' ACTGCTGTGCTGGGGCTATT  53706      TA  TT    TG
                                GGTAGT  CG  GCATAG  GT
                                ||||||  ||  ||||||  ||
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                                TTATCG  GT  CGTGTC  CA
                                   GG  __     GT
GAM245  C20orf129 3'  ACCATTATGTTACAGTTGCC   61396      TTAC  T
                                GGTAG   GT GCATAGTGGT
                                |||||   || ||||||||||
                                CCGTT   CA TGTATTACCA
                                   GA__  T
GAM245  C20orf150 3'  TGCCACTGTGTGGTATTCGAGG 65404     A_  ____ TG
           ATTATTGC               GTT  CG   T  CATAGTGGT  G
                                |||  ||   |  |||||||||  |
                                TAG  GC   G  GTGTCACCG  T
                                  GA  TTAT GT
GAM245  C20orf16  5'  GCTCATGATGTAGCTTCTGC   38722      T       ____
                                GCGG AGTTACGTT   GC
                                |||| |||||||||   ||
                                CGTC TCGATGTAG   CG
                                   T       TACT
GAM245  C20orf177 3'  GCTTAGCATGATTACTGC    62151         CGT   AT
                                GCGGTAGTTA   TGC  AGT
                                ||||||||||   |||  |||
                                CGTCATTAGT   ACG  TCG
                                      ___  AT
GAM245  C20orf31  5'  TGCAGTGGCTGCTGC       36640          GT
                                GCGGTAGTTAC  TGCA
                                ||||||||||  ||||
                                CGTCGTCGGTG  ACGT
                                          __
GAM245  C20orf82  3'  ATTATTGTGCATCAAGCAATTG 84712       A   ACGT
           T                    GCGGT GTT   TGCATAGTGGT
                                |||||  |||   ||||||||||
                                TGTTA CGA   ACGTGTTATTA
                                   A  ACT_
GAM245  C21orf108 3'  ATGTAAGATGTGGCTTTGC   88716      T       __
                                GCGG AGTTACGTT  GCAT
                                |||| |||||||||  ||||
                                CGTT TCGGTGTAG  TGTA
                                  _       AA
GAM245  C21orf7   3'  GCCAATGCTAACTGGCTGTTGT 39334    GG     C  _   AG
                                GC  TAGTTA GTT GCAT  TGGT
                                ||  |||||| ||| ||||  ||||
                                TG  GTCGGT CAA CGTA  ACCG
                                 TT     _  T   __
GAM245  C22orf20  3'  ATTGCTGTGTAGTGACCCCTGC 47427      TA    GT     TG
                                GCGG  GTTAC  TGCATAG  GT
                                ||||  |||||  |||||||  ||
                                CGTC  CAGTG  ATGTGTC  TA
                                   CC    __      GT
GAM245  C22orf20  5'  GCCGGGCGGAGCTGCTGC    47432         A   __
                                GCGGTAGTT CGTT  GC
                                |||||||| ||||  ||
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                                CGTCGTCGA GCGG  CG
                                     G   GC
GAM245  C9orf5   3'  GGCACGGTGGTGTGGCTATAGT 49279    G       TT  ATA   GT
                                GC GTAGTTACG  GC   GTG
                                || |||||||||  ||   |||
                                TG TATCGGTGT  TG   CAC
                                 A        GG  G__   GGG
GAM245  CABYR    3'  TATTGCTGGGGAGGTAACCGTG 24111       _   A____   TG
           ACTACTGC                GTTACG TTGC    TAG  GT   A
                                |||||| ||||    |||  ||  |
                                CAGTGC AATG    GTC  TA   T
                                   C    GAGGG   GT
GAM245  CAMKK2   3'  CCATGGAGGTGGTTGCTGC   21579        TT  G  GCATA
                                GCGGTAG  AC TT    GTGG
                                |||||||  || ||    ||||
                                CGTCGTT  TG AG    TACC
                                    GG  G  G____
GAM245  CAMTA1   3'  CCCTTAGCAATGTGACATTGC  67916      A        AT  T  T
                                GCGGT GTTACGTTGC  AG GG
                                ||||| ||||||||||  || ||
                                CGTTA CAGTGTAACG  TC CC
                                   _        AT  _  T
GAM245  CAS1     3'  TCATTGTTGATGTTATTGTTGC 43205    GG    T     C     GT
                                GC  TAGT ACGTTG ATAGTG
                                ||  |||| |||||| ||||||
                                CG  GTTA TGTAGT TGTTAC
                                 TT   T     _     TG
GAM245  CBX8     5'  GTGCGCTGGCTGCTGC      40242          C  T
                                GCGGTAGTTA GT GCAT
                                |||||||||| || ||||
                                CGTCGTCGGT CG CGTG
                                      _ _
GAM245  CCNE1    3'  TGTTTTGTAAGTGCTGC     6951        G    TT
                                GCGGTA TTACG  GCA
                                |||||| |||||  |||
                                CGTCGT AATGT  TGT
                                   G    TT
GAM245  CCNE1    3'  TGTTTTGTAAGTGCTGC     54118       G    TT
                                GCGGTA TTACG  GCA
                                |||||| |||||  |||
                                CGTCGT AATGT  TGT
                                   G    TT
GAM245  CCT4     3'  ACCATTATGATCACCAGTATTG 21219       GTTACGTTG
           T                     GCGGTA       CATAGTGGT
                                ||||||       |||||||||
                                TGTTAT       GTATTACCA
                                   GACCACTA_
GAM245  CCT6B    3'  ACTATTGTGTAGCCTGAGCC   59813     AG   C
                                GGT  TTA GTTGCATAGTGGT
                                |||  ||| ||||||||||||
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                                CCG  AGT CGATGTGTTATCA
                                  __  C
GAM245  CDA02    5'  CACTAACAAGGGACTACTGC  67849        ACG  CA
                                GCGGTAGTT  TTG  TAGTG
                                |||||||||  |||  |||||
                                CGTCATCAG  AAC  ATCAC
                                    GG_  A_
GAM245  CDC14A   3'  TGTAAAGTTGACTACTGT    13395        CG_
                                GCGGTAGTTA  TTGCA
                                ||||||||||  |||||
                                TGTCATCAGT  AATGT
                                     TGA
GAM245  CDC14B   3'  ACTGTTGTAATGTTAACTCTGT 13384     T   _    _
                                GCGG AGTTA CGTTGCA TAGT
                                |||| ||||| ||||||| ||||
                                TGTC TCAAT GTAATGT GTCA
                                  _   T     T
GAM245  CDC14B   3'  ACTGTTGTAATGTTAACTCTGT 52831     T   _    _
                                GCGG AGTTA CGTTGCA TAGT
                                |||| ||||| ||||||| ||||
                                TGTC TCAAT GTAATGT GTCA
                                  _   T     T
GAM245  CDH22    5'  ATCGTTGTGCGACCAAGC    41153     AC
                                GTT  GTTGCATAGTGGT
                                |||  |||||||||||||
                                CGA  CAGCGTGTTGCTA
                                  AC
GAM245  CDW92    3'  ATCCTCCAGTGTGACTGTTGT  54505    GG       CAT  T
                                GC  TAGTTACGTTG  AG GGT
                                ||  ||||||||||  || |||
                                TG  GTCAGTGTGAC  TC CTA
                                 TT       C__  _
GAM245  CECR7    3'  ATTGCTGTGTTGTTGTAACTAT 79616        TT_    TG
          C                      GGTAGTTACG  GCATAG  GT
                                ||||||||||  ||||||  ||
                                CTATCAATGT  TGTGTC  TA
                                     TGT    GT
GAM245  CENTB5   3'  TCACTATGCAATGCTGCC    95487      TAC       GT
                                GGTAGT  GTTGCATAGTG
                                ||||||  ||||||||||
                                CCGTCG  TAACGTATCAC
                                   ___        TG
GAM245  cerk     3'  GCCAGGAGGCTGTGGCTGCTGT 42848         TT  ATAG
                                GCGGTAGTTACG  GC   TGGT
                                ||||||||||||  ||   ||||
                                TGTCGTCGGTGT  CG   ACCG
                                      __ GAGG
GAM245  CFDP1    5'  GCCGTTGGAGGCGGCTGCTGC  20900       TA   GCA
                                GCGGTAGT  CGTT  TAGTGGT
                                |||||||  ||||  |||||||
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                                CGTCGTCG  GCGG   GTTGCCG
                                    __    AG_
GAM245  CGI-142  3'  ATTATTATGTGTACATTATTGT 32175    GG    TAC  _
            TGC                   GC  TAGT   GT TGCATAGTGGT
                                  ||  ||||   || ||||||||||
                                  CG  GTTA   CA GTGTATTATTA
                                   TT    TTA  T
GAM245  CHL1     3'  ACCACGAAATACTTAACTACTG 21743          C  TGCATA
            T                     GCGGTAGTTA GT     GTGGT
                                  ||||||||||  ||     |||||
                                  TGTCATCAAT CA     CACCA
                                        T  TAAAG_
GAM245  CHST3    3'  ACAGTGTGGTGTGACTATTG   14964          TT    A
                                  CGGTAGTTACG  GCAT GT
                                  ||||||||||  ||||  ||
                                  GTTATCAGTGT  TGTG CA
                                         GG    A
GAM245  CILP     3'  CCATTGTGAGACTGAT      13221      C  TG
                                  GTTA GT  CATAGTGG
                                  ||||  ||  ||||||||
                                  TAGT CA  GTGTTACC
                                    _  GA
GAM245  CLECSF9  3'  CTATTGTGAATAGTGCTGC   26839       T  GTTG
                                  GTAGT AC    CATAGTGG
                                  |||||  ||    ||||||||
                                  CGTCG TG    GTGTTATC
                                    _  ATAA
GAM245  CLIC4    3'  CTGGCAGCTATTGT        25634         TACGT   A
                                  GCGGTAGT     TGC TAG
                                  ||||||||     ||| |||
                                  TGTTATCG     ACG GTC
                                       ______  _
GAM245  CNK2     3'  CCGCAGTGTGTGGTATTGC    75961       G    GTT    A
                                  GCGGTA TTAC   GCAT GTGG
                                  ||||||  ||||   ||||  ||||
                                  CGTTAT GGTG   TGTG CGCC
                                    _    ____    A
GAM245  CNNM3    3'  GCCACCTTGTGAGTGCAGTTAC 34340       T__   G TG  TA
            TGC                   CGGTAG   TAC T  CA  GTGGT
                                  ||||||   ||| |  ||  |||||
                                  GTCATT   GTG A  GT  CACCG
                                     GAC   _ GT  TC
GAM245  CPSF2    5'  CCACTGTGGGGCTTCTGC     61575      TTAC   G
                                  GTAG    GTT CATAGTGG
                                  ||||    ||| ||||||||
                                  CGTC    CGG GTGTCACC
                                    TT__   G
GAM245  CRK7     3'  ATCATCTGCATTTGGCTACTGC 33252          CGT    TA
                                  GCGGTAGTTA   TGCA  GTGGT
                                  ||||||||||   ||||  |||||
```

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                                CGTCATCGGT   ACGT  TACTA
                                     TT_   C_
GAM245  CSMD1    3'  ACATTAGTGTGGCAGCTGC   73116      A    GTT  A    GT
                                GCGGT GTTAC   GC TAGTG
                                ||||| |||||   || |||||
                                CGTCG CGGTG   TG ATTAC
                                   A    ___ _    AG
GAM245  CTCF     3'  TGTAGCTGATTGTTGT     21638    GG     C
                                GC  TAGTTA GTTGCA
                                ||  |||||| ||||||
                                TG  GTTAGT CGATGT
                                 TT     _
GAM245  CTPS2    3'  CACTGTGCCTTTGCTGT     39083       TTACGTT
                                GCGGTAG      GCATAGTG
                                |||||||      ||||||||
                                TGTCGTT      CGTGTCAC
                                    TC_____
GAM245  CUGBP2   3'  ATTTTTGTAATGTATGTTATTG 21626       GT_       TAGTGGT
           T                     GCGGTA   TACGTTGCA
                                ||||||   |||||||||
                                TGTTAT   ATGTAATGT
                                   TGT       TTTTA
GAM245  CXorf15  5'  CCGCTTGTTTGGCTGCTGC   37162         CGTT   T
                                GCGGTAGTTA    GCA AGTGG
                                ||||||||||    ||| |||||
                                CGTCGTCGGT    TGT TCGCC
                                     T___   _
GAM245  CYLD     5'  GCTGTGACAGAATGTGGTAATT 30887      AG     __ _     GGT
           GT                    CGGT  TTACGT  TG CATAGT
                                ||||  ||||||  || ||||||
                                GTTA  GGTGTA  AC GTGTCG
                                  AT     AG  A
GAM245  D2S448   3'  GCCACTGTGCGGGATCGCTGT  73524     TA   ACG
                                GCGG  GTT   TTGCATAGTGGT
                                ||||  |||   ||||||||||||
                                TGTC  TAG   GGCGTGTCACCG
                                  GC   ___
GAM245  DATF1    5'  GTTGTTGTGAGCCTGGCTGTCT 55006     _     C   G    TG
           GC                    GCGG TAGTTA GTT CATAG  GT
                                |||| |||||| ||| |||||  ||
                                CGTC GTCGGT CGA GTGTT  TG
                                  T     C   _     GT
GAM245  DATF1    5'  GTTGTTGTGAGCCTGGCTGTCT 55009     _     C   G    TG
           GC                    GCGG TAGTTA GTT CATAG  GT
                                |||| |||||| ||| |||||  ||
                                CGTC GTCGGT CGA GTGTT  TG
                                  T     C   _     GT
GAM245  DATF1    5'  GTTGTTGTGAGCCTGGCTGTCT 42071     _     C   G    TG
           GC                    GCGG TAGTTA GTT CATAG  GT
                                |||| |||||| ||| |||||  ||
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                                CGTC GTCGGT CGA GTGTT  TG
                                  T     C  _    GT
GAM245  DCOHM    3'  ATTGCTTGATATGTAGTTGCC  49593     GT    TG  T  TG
                                GGTA  TACGT  CA AG  GT
                                ||||  |||||  || ||  ||
                                CCGT  ATGTA  GT TC  TA
                                  TG    TA  _  GT
GAM245  DD5      3'  ATTGCTGTGTAATATTACTAGC 31911    _     TAC       TG
                                GC GGTAGT   GTTGCATAG  GT
                                || ||||||   |||||||||  ||
                                CG TCATTA   TAATGTGTC  TA
                                 A      ___        GT
GAM245  DDR1     3'  TCTCTAGTGTAGCTGCC     25698         GTT  A   T
                                GGTAGTTAC   GC TAG GG
                                |||||||||   || ||| ||
                                CCGTCGATG   TG ATC CT
                                     ___  _   T
GAM245  DDR1     3'  TCTCTAGTGTAGCTGCC     25707         GTT  A   T
                                GGTAGTTAC   GC TAG GG
                                |||||||||   || ||| ||
                                CCGTCGATG   TG ATC CT
                                     ___  _   T
GAM245  DDR1     3'  TCTCTAGTGTAGCTGCC     8725          GTT  A   T
                                GGTAGTTAC   GC TAG GG
                                |||||||||   || ||| ||
                                CCGTCGATG   TG ATC CT
                                     ___  _   T
GAM245  DDX17    5'  ACCAATATTGGTGTAACTCCTG 48036     T      TT C   G
            T                    GCGG AGTTACG  G ATA TGGT
                                ||||  |||||||  |  ||| ||||
                                TGTC TCAATGT  T TAT ACCA
                                  C      GG  _   A
GAM245  DDX18    3'  ATTGCTGTGCTCACTGCTGT   22263        TACGTT     TG
                                GCGGTAGT     GCATAG  GT
                                ||||||||     ||||||  ||
                                TGTCGTCA     CGTGTC  TA
                                     CT____     GT
GAM245  DDX25    5'  GCCATGGCGTCGTTACTGT   25167       TT    GCATA
                                GCGGTAG  ACGTT    GTGGT
                                |||||||  |||||    |||||
                                TGTCATT  TGCGG    TACCG
                                    GC    _____     A
GAM245  DEPC-1   3'  TCATGATGTGGCTGTTG    57548   GG       GCATA
                                C  TAGTTACGTT    GTGG
                                |  ||||||||||    ||||
                                G  GTCGGTGTAG    TACT
                                 TT        _____
GAM245  DGKD     3'  CCGCACCGTGTGGCTCCGC   59400     T    GTT  ATA
                                GCGG AGTTAC   GC   GTGG
                                |||| ||||||   ||   ||||
```

```
                                CGCC TCGGTG   TG   CGCC
                                  _     ___  CCA
GAM245  DGKD     3'  CGCTGGGCGTGATGTCGC    59402     GT G      GCA   TG
                                GCG  A TTACGTT   TAG  G
                                |||  | |||||||   |||  |
                                CGC  T AGTGCGG   GTC  C
                                  TG _      ___   GT
GAM245  DHRS2    5'  ACTATTGCCAAGCAGTGAGACT 19378        A     A___
            ATTGC                  GTAGTT CGTTGC    TAGTGGT
                                |||||| ||||||   |||||||
                                TATCAG GTGACG    GTTATCA
                                   A     AACC
GAM245  DHRS2    5'  ATCACCAAGTGGTGAGACTATT 19380          A  TT  ATA
            GC                    GCGGTAGTT CG  GC   GTGGT
                                ||||||||| ||  ||   |||||
                                CGTTATCAG GT  TG   CACTA
                                      A  GG  AAC
GAM245  DJ473B4  3'  ATCATTATAAATGGTTGCC    38957     GTTA   GC
                                GGTA   CGTT  ATAGTGGT
                                ||||   ||||  ||||||||
                                CCGT   GTAA  TATTACTA
                                  TG__   A_
GAM245  DKFZP434A0225 3'  TGCTGTGTGATTACTGT     93910           TT
                                GCGGTAGTTACG  GCA
                                ||||||||||||  |||
                                TGTCATTAGTGT  CGT
                                      GT
GAM245  DKFZP434A043 5'  TCAAGGTGCGGTTAGCTGCCGT 31194          C TT    AG  GT
                                GCGGTAGTTA G  GCAT  TG
                                ||||||||||  |  ||||  ||
                                TGCCGTCGAT T  CGTG  AC
                                      _ GG    GA  TG
GAM245  DKFZp434A1520 3'  TGAATGTTAACTGCTGT     61117          _   G
                                GCGGTAGTTA CGTT CA
                                |||||||||| |||| ||
                                TGTCGTCAAT GTAA GT
                                      T   _
GAM245  DKFZP434C0826 5'  ACTGTTGTGTGATGTTGTCTAC 84031      TT_   TG    TG
                                GTAG   ACGT  CATAG  GT
                                ||||   ||||  |||||  ||
                                CATC   TGTA  GTGTT  CA
                                  TGT    GT    GT
GAM245  DKFZp434C0923 3'  GTTACTAGTTGTGTGATTTCTG 34219      T      TT  A    GG
            T                   GCGG AGTTACG  GC TAGT  T
                                |||| |||||||  || ||||  |
                                TGTC TTAGTGT  TG ATCA  G
                                  T      GT  _    TT
GAM245  DKFZP434D146 3'  TTACTAAGGTGACTGTC     31529    GT     G TGCA
                                G  AGTTAC T    TAGTGG
                                |  ||||||  |    ||||||
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                                C  TCAGTG A    ATCATT
                                 TG     G ____
GAM245  DKFZp434D177 3'  GCTGAGAGATGTCATTGCTGC  50053         T    GCA
                                GCGGTAGT ACGTT   TAGT
                                |||||||| |||||   ||||
                                CGTCGTTA TGTAG   GTCG
                                     C     AGA
GAM245  DKFZP434F0318 3'  CTACTGTGTGAGTGTAGC    48008       _ TG
                                GTTACG T  CATAGTGG
                                |||||| |  ||||||||
                                CGATGT A  GTGTCATC
                                   G GT
GAM245  DKFZP434H0820 3'  TCACTCTGGGCCTGGCTGTCGT 63854     GT    C   G  T   GT
                                GCG  AGTTA GTT CA AGTG
                                |||  ||||| ||| || ||||
                                TGC  TCGGT CGG GT TCAC
                                  TG    C   _  C    TG
GAM245  DKFZP434L0117 5'  CCGCAGACGTAGTGGCTGC   42918      AG      GCATA
                                GCGGT  TTACGTT    GTGG
                                |||||  |||||||    ||||
                                CGTCG  GATGCAG    CGCC
                                   GT      A____
GAM245  DKFZP434L1435 5'  GCTGCCTGGAGATGTGGCTGTG 92172    G         GCATA TG
           GC                    GC GTAGTTACGTT     G  GT
                                || ||||||||||    |  ||
                                CG TGTCGGTGTAG    C  CG
                                 G          AGGTC GT
GAM245  DKFZp434N035 3'  GCTGCGCGCTAACGGGCTGCTG 50050         A   _  ATA TG
           C                     GCGGTAGTT CGTT GC   G  GT
                                ||||||||| |||| ||   |  ||
                                CGTCGTCGG GCAA CG   C  CG
                                      _   T  CG_ GT
GAM245  DKFZp434O0320 3'  GTCATTGTGACTGCTGC     83697          T  _
                                GCGGTAGTTACG TG C
                                |||||||||||| || |
                                CGTCGTCAGTGT AC G
                                       T  T
GAM245  DKFZP434O047 5'  GCTGTTGCAGGTGGTGGGCTAC 31514     ____  G   _   GGT
           TGC                    TAGT    TAC TTGCA TAGT
                                ||||    ||| ||||| ||||
                                ATCG    GTG GACGT GTCG
                                  GGTG   _     T      T
GAM245  DKFZP434P211 3'  TGCTATGCGAGTGGCTGCCGT  27270          G
                                GCGGTAGTTAC TTGCATAGTG
                                |||||||||| ||||||||||
                                TGCCGTCGGTG AGCGTATCGT
                                          _
GAM245  DKFZp547F072 5'  CGCATGCGAAGCTGCCGC    50093         ACG     A TG
                                GCGGTAGTT   TTGCAT G  G
                                |||||||||   |||||| |  |
```

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                                CGCCGTCGA   AGCGTA C  C
                                    ___     _ GT
GAM245  DKFZp547J036 3'  TGCTATGTTAACTATT      50131         CGTT     TG
                                GGTAGTTA    GCATAG  G
                                ||||||||    ||||||  |
                                TTATCAAT    TGTATC  T
                                    _____     GT
GAM245  DKFZP564C186 3'  GCTGGGCTGGTGTGGCTGCTG  72408           TT_  A
                                CGGTAGTTACG   GC TAGT
                                ||||||||||   || ||||
                                GTCGTCGGTGT   CG GTCG
                                      GGT  G
GAM245  DKFZP564D0764 5'  TTATTATGTGGACTACCG    88243        TACG TG
                                CGGTAGT    T  CATAGTGG
                                |||||||    |  ||||||||
                                GCCATCA    G  GTATTATT
                                    ____ GT
GAM245  DKFZP564D172 3'  TCACTATTTAATTGCC      49391         CGTTGC
                                GGTAGTTA     ATAGTGG
                                ||||||||     |||||||
                                CCGTTAAT     TATCACT
                                     T_____
GAM245  DKFZP564I052 5'  GCTGTTATAAACTGTGATGACT 66712       A    _  GC    TG
           GT                     GCGGT GTTAC GTT  ATAG  GT
                                |||||  ||||| |||  ||||  ||
                                TGTCA TAGTG CAA  TATT  CG
                                   G    T  A_   GT
GAM245  DKFZP564I1171 5'  GCTGCTGAAGCTGGCGTCGCTG 71589        T    _ A_   TG
           CCGC                    CGGTAGT ACGTT GC  TAG  GT
                                ||||||| |||||  ||  |||  ||
                                GCCGTCG TGCGG CG  GTC  CG
                                    C    T  AA   GT
GAM245  DKFZP564K0822 3'  ACCACCCTGGTGTGACTGCTG  94041           TT CATA
                                CGGTAGTTACG  G    GTGGT
                                ||||||||||  |   |||||
                                GTCGTCAGTGT  T    CACCA
                                      GG CC__
GAM245  DKFZP564O123 3'  CCCTTTGATGTCACTACTGT   59467         T    GCAT  T
                                GCGGTAGT ACGTT    AG GG
                                |||||||  |||||   || ||
                                TGTCATCA TGTAG    TC CC
                                     C    TT__  _
GAM245  DKFZP566C243 3'  GCCACTGAGCTGTAGCTGC    31169          TT  A
                                GTAGTTACG  GC TAGTGGT
                                |||||||||  || |||||||
                                CGTCGATGT  CG GTCACCG
                                      __  A
GAM245  DKFZP586D0623 3'  GCTGCTGTGCTTCATATTGTTG 71975    GG    TACGTT     TG
           C                     GC  TAGT     GCATAG  GT
                                ||  ||||     ||||||  ||
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                                CG  GTTA     CGTGTC  CG
                                 TT    TACTT_     GT
GAM245   DKFZP667O116 3'  CCTTTCAACGTAGCTACT    94281           CATAGT
                                GGTAGTTACGTTG     GG
                                ||||||||||||      ||
                                TCATCGATGCAAC     CC
                                     TTT___
GAM245   DKFZP667O116 3'  GCTTTTTGTGGGTGGCTGCTGC 94283          G TG  TAGT
                                GCGGTAGTTAC T  CA    GGT
                                |||||||||||  |  ||    |||
                                CGTCGTCGGTG G  GT    TCG
                                      _ GT  TTT_
GAM245   DKFZp761B0514 3'  ATTATATACATGTACTACTGT  50151         T   _  C
                                GCGGTAGT ACGT TG ATAGT
                                ||||||||  ||||  ||  |||||
                                TGTCATCA TGTA AT TATTA
                                     _   C  A
GAM245   DKFZp761D112 3'  GCCATTATCTTGTGGTTGTC   50190    GT  TT   TTGC
                                G  AG  ACG    ATAGTGGT
                                |  ||  |||    ||||||||
                                C  TT  TGT    TATTACCG
                                 TG  GG   TC__
GAM245   DKFZp761F2014 3'  ACTTTGTTAGCGTTGCTGCTGT 39532         T     _  T
                                GCGGTAGT ACGTTG CA AGT
                                ||||||||  ||||||  ||  |||
                                TGTCGTCG TGCGAT GT TCA
                                     T     T  T
GAM245   DKFZp761G2113 5'  GCTGTCAAGTGTGGCTACT    69905          _   C
                                GGTAGTTACG TTG ATAGT
                                ||||||||||  |||  |||||
                                TCATCGGTGT AAC TGTCG
                                      G   _
GAM245   DKFZp761H079 3'  ACTATAGTGTAGCTACTG     58729          GTT  _
                                CGGTAGTTAC   GC ATAGT
                                ||||||||||   ||  |||||
                                GTCATCGATG   TG TATCA
                                      ___  A
GAM245   DKFZp761N1114 3'  TACTATATATGATGGTGTGCTA 79023       T   TT _   _
            CTGT                   GGTAGT ACG  G CATA GTGGT
                                |||||| |||  |  ||||  |||||
                                TCATCG TGT  T GTAT TATCA
                                    _   GG A    A     TT
GAM245   DKFZp761O17121 3'  TGTATTGTGACTGCTGT     50144           T
                                GCGGTAGTTACG TGCA
                                ||||||||||||  ||||
                                TGTCGTCAGTGT ATGT
                                       T
GAM245   DKFZP762D096 3'  ACCGCTGTGCAGTGTCATGTTC 65575     TA_  T
            C                   GG   GT ACGTTGCATAGTGGT
                                ||   ||  ||||||||||||||
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                                CC   TA TGTGACGTGTCGCCA
                                 TTG  C
GAM245  DKFZp762L0311 3'  GCTACTGTCGGAAGCGTGACGG 38056      A       GC__
            CCGC                    CGGT GTTACGTT    ATAGTGGT
                                |||| ||||||||    ||||||||
                                GCCG CAGTGCGA    TGTCATCG
                                  G       AGGC
GAM245  DMTF1    3'  ATCACGAAAGCTTAACTGCTGT 40936          C   GCATA
                                GCGGTAGTTA GTT     GTGGT
                                |||||||||| |||     |||||
                                TGTCGTCAAT CGA     CACTA
                                      T   AAG__
GAM245  DNAJC5   3'  ATTTAAAGCAGTGTAGCTACGG 61447    G          ATAGTGGT
            T                    GC GTAGTTACGTTGC
                                || ||||||||||||
                                TG CATCGATGTGACG
                                 G           AAATTTA
GAM245  DRCTNNB1A 3'  ACCACTGTATAATATGTAATTG 50838         TGC__
                                TAGTTACGT     ATAGTGGT
                                |||||||||     ||||||||
                                GTTAATGTA     TGTCACCA
                                      TAATA
GAM245  DXS9928E  5'  GCCGCTGCCGCTGTCGCTGTCG 16287     GT   T  _  T   TA
            C                    GCG  AGT AC GT GCA  GTGGT
                                |||  ||| || || |||  |||||
                                CGC  TCG TG CG CGT  CGCCG
                                  TG   C  T  C  __
GAM245  E2F6     3'  GCTGTCTACCTAATTGCTGT   8714          C  TGC
                                GCGGTAGTTA GT   ATAGT
                                |||||||||| ||   |||||
                                TGTCGTTAAT CA   TGTCG
                                      C  TC_
GAM245  EDR1     3'  ACTGGGGCACATGTGGCTGTTG 15379    GG       _   A_   GGT
            T                    GC  TAGTTACGT TGC  TAGT
                                ||  ||||||||| |||  ||||
                                TG  GTCGGTGTA ACG  GTCA
                                 TT        C   GG
GAM245  EIF4B    3'  TGCCAGTGTGATTAGTGC    75973     G         _
                                GCG TAGTTACGTTG CA
                                ||| ||||||||||| ||
                                CGT ATTAGTGTGAC GT
                                  G         C
GAM245  EPHA7    3'  ACCATATTATTTGATTACTGT  15432          C  TGCATA
                                GCGGTAGTTA GT     GTGGT
                                |||||||||| ||     |||||
                                TGTCATTAGT TA     TACCA
                                      T  TTA___
GAM245  EREG     3'  ACAACATTTATGTGAGGTAATT 7486          G TG    _  GT
            ATTGC                    CGGTAGTTAC T  CATAG TG
                                |||||||||| |  ||||| ||
```

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                                GTTATTAATG A  GTATT AC
                                     G GT    T  AACAT
GAM245  EVI5    3'  ATTACAGGTGCGAGCTACTGC  18991       TACG    A_
                                GCGGTAGT   TTGCAT  GTGGT
                                ||||||||   ||||||  |||||
                                CGTCATCG   AGCGTG  CATTA
                                     _____     GA
GAM245  EZFIT   3'  GTTAGCAAATAACAGTAACTAC 41112         _   CATAGTGGT
           TGC                    GCGGTAGTTAC GTTG
                                ||||||||||| ||||
                                CGTCATCAATG CAAT
                                      A   AAACGATTG
GAM245  FADS2   3'  GCTGCTGTGTGGACGGCGCTGC 14955      TA _ TG    TG
           C                     GGTAGT  CG T  CATAG  GT
                                ||||||  || |  |||||  ||
                                CCGTCG  GC G  GTGTC  CG
                                    CG  A GT    GT
GAM245  FARSL   3'  TGTCCTGTGTGGTGTGTCTACT 15516      T   TT    TGGT
           GT                     GCGGTAG TACG  GCATAG
                                ||||||| ||||  ||||||
                                TGTCATC GTGT  TGTGTC
                                    T   GG    CTGTT
GAM245  FASTK   3'  CACTGTGCCAACTGCGGT   46986   G    ACGTT
                                GC GTAGTT   GCATAGTG
                                || ||||||   ||||||||
                                TG CGTCAA   CGTGTCAC
                                 G    C____
GAM245  FBP17   3'  ATTACAGGTGTGAGCTACCGC  72780       TACG TG  A_
                                GCGGTAGT   T  CAT  GTGGT
                                ||||||||   |  |||  |||||
                                CGCCATCG   A  GTG  CATTA
                                     _____ GT   GA
GAM245  FBXL9   3'  CTACCTACGTGTTGCCGC    24081     AGT    TGCATA
                                GCGGT   TACGT    GTGG
                                |||||   |||||     ||||
                                CGCCG   GTGCA     CATC
                                   TT_    TC_____
GAM245  FBXO30   3'  CCATAAAATGTAACTCTGC   49576     T      GCATA
                                GCGG AGTTACGTT    GTGG
                                |||| |||||||||    ||||
                                CGTC TCAATGTAA    TACC
                                  _       AA___
GAM245  FER1L3   3'  ACCAACATCCAGTGTGATTTTG 25626     T       C  AG
           T                     GCGG AGTTACGTTG AT  TGGT
                                |||| |||||||||| ||  ||||
                                TGTT TTAGTGTGAC TA  ACCA
                                  _       C  CA
GAM245  FHR5    3'  GCCATTATGTAGCCAATTCTGT 47901     T   AC
                                GCGG AGTT  GTTGCATAGTGGT
                                |||| ||||  ||||||||||||
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```
                                TGTC TTAA  CGATGTATTACCG
                                  _   C_
GAM245  FLJ00001  3' CCACTGTGCAGTGGGC     81813     A
                                GTT CGTTGCATAGTGG
                                ||| ||||||||||||
                                CGG GTGACGTGTCACC
                                  _
GAM245  FLJ10055  5' CGCTGAGGTGGCTGTCGC    35776     GT     G  GCAT  TG
                                GCG  AGTTAC TT    AG  G
                                |||  |||||| ||    ||  |
                                CGC  TCGGTG AG    TC  C
                                  TG     G ____  GT
GAM245  FLJ10101  3' ACCGTAGTACCTAATGTAATAC 45263      G       C__  AG
           CGC                    CGGTA TTACGTTG   AT  TGGT
                                |||||| ||||||||   ||  ||||
                                GCCAT AATGTAAT   TG  GCCA
                                  _      CCA  AT
GAM245  FLJ10116  3' ATTGTAGACCAATTTAACTGCT 35827          C    CATA TG
           GT                     GCGGTAGTTA GTTG    G  GT
                                |||||||||| ||||    |  ||
                                TGTCGTCAAT TAAC    T  TA
                                     T    CAGA GT
GAM245  FLJ10199  5' TGTTGTGACTGCTGC       71237           TT
                                GCGGTAGTTACG  GCA
                                ||||||||||||  |||
                                CGTCGTCAGTGT  TGT
                                          __
GAM245  FLJ10290  3' GCCATTAACACATCTGGTTACT 35973        TT CGT  CA_
           GC                     GCGGTAG  A   TG   TAGTGGT
                                |||||||  |   ||   |||||||
                                CGTCATT  T   AC   ATTACCG
                                   GG CT_  ACA
GAM245  FLJ10352  3' GCTTGATGTGACTGCT      49560           __
                                GGTAGTTACGTT  GC
                                ||||||||||||  ||
                                TCGTCAGTGTAG  CG
                                      TT
GAM245  FLJ10357  3' ACTTTATATATGTAATTACTGT 36063           TGCAT_
                                GCGGTAGTTACGT     AGT
                                ||||||||||||      |||
                                TGTCATTAATGTA     TCA
                                     TATATT
GAM245  FLJ10546  3' TGTTATGTAATATTGCC     59481       TAC       TG
                                GGTAGT   GTTGCATAG  G
                                ||||||   |||||||||  |
                                CCGTTA   TAATGTATT  T
                                   ___         GT
GAM245  FLJ10565  5' TGAGCCTGACTACCGC      36289          C   G
                                GCGGTAGTTA GTT CA
                                |||||||||| ||| ||
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```
                                CGCCATCAGT CGA GT
                                      C  _
GAM245  FLJ10604  3'  CCGCCATGTGGATGCTGT    36336       GTTACG TG   A
                                GCGGTA     T  CAT GTGG
                                ||||||     |  ||| ||||
                                TGTCGT     G  GTA CGCC
                                   A_____ GT   C
GAM245  FLJ10604  3'  GCTGTTGTGATTGCTGT     36338           TT_
                                GCGGTAGTTACG   GC
                                ||||||||||||   ||
                                TGTCGTTAGTGT   CG
                                       TGT
GAM245  FLJ10607  3'  ATTACATATGTCGGCTACCGT  77105        TA  TT    _
                                GCGGTAGT  CG  GCATA GTGGT
                                ||||||||  ||  ||||| |||||
                                TGCCATCG  GC  TGTAT CATTA
                                   __  __    A
GAM245  FLJ10702  3'  CATTAAATCAGTGCTGCTGC   36440        T  GTTGCA
                                GCGGTAGT AC     TAGTG
                                |||||||| ||     |||||
                                CGTCGTCG TG     ATTAC
                                   _  ACTAA_
GAM245  FLJ10702  3'  GCCATTAGACATCTTGATTATT 36442          CGT  CA
          GT                     GCGGTAGTTA   TG  TAGTGGT
                                ||||||||||   ||  |||||||
                                TGTTATTAGT   AC  ATTACCG
                                      TCT  AG
GAM245  FLJ10716  3'  ACGGGTGATGTGATTCTGC    36479      T       TG ATA
                                GCGG AGTTACGT  C   GT
                                |||| ||||||||  |   ||
                                CGTC TTAGTGTA  G   CA
                                  _       GT GG_
GAM245  FLJ10759  3'  GCCACTATGCCAGAAAGCTGCT 36576          ACGTT
          G                      CGGTAGTT    GCATAGTGGT
                                ||||||||    ||||||||||
                                GTCGTCGA    CGTATCACCG
                                     AAGAC
GAM245  FLJ10815  3'  GCCAGCCCTAGCGTGACTACC  36695            CATAG
                                GGTAGTTACGTTG    TGGT
                                ||||||||||||     ||||
                                CCATCAGTGCGAT    ACCG
                                       CCCG_
GAM245  FLJ10898  5'  GCCGCTGCCGCCGCAGCTGCTG 59436          A  TT  A_
          C                      GCGGTAGTT CG  GC  TAGTGGT
                                |||||||| ||  ||  |||||||
                                CGTCGTCGA GC  CG  GTCGCCG
                                     C  __  CC
GAM245  FLJ10901  3'  GCCATTGCCAAGTGGCTG    36826       GTT   TA
                                TAGTTAC   GCA  GTGGT
                                |||||||   |||  |||||
```

```
                              GTCGGTG  CGT  TACCG
                                 AAC  __
GAM245  FLJ10904  3' GCTGTTGAAGTGGTGAGTGCTG 36848      G   GTTG_ _   GGT
             T                  GCGGTA TTAC    CA TAGT
                                |||||| ||||    || ||||
                              TGTCGT AGTG    GT GTCG
                                 G   GTGAA  T
GAM245  FLJ10922  3' ATTACATGGGTGAGCTACCGT  36868        A  TTG  A
                              GCGGTAGTT CG   CAT GTGGT
                              |||||||||  ||   ||| |||||
                              TGCCATCGA GT   GTA CATTA
                                   _ GG_  _
GAM245  FLJ10936  3' CCACTGTGCTAGTTGCC    36905     GTT  GTT
                              GGTA  AC   GCATAGTGG
                              ||||  ||   |||||||||
                              CCGT  TG   CGTGTCACC
                                ___ AT_
GAM245  FLJ10936  5' GCTGTCGGGACGTGACTGC   36911         GC_
                              GTAGTTACGTT   ATAGT
                              ||||||||||   |||||
                              CGTCAGTGCAG   TGTCG
                                    GGC
GAM245  FLJ11036  3' ACTGCTGTGCAACCCAGCTGC  36996      AC       TG
                              GTAGTT  GTTGCATAG  GT
                              ||||||  |||||||||  ||
                              CGTCGA  CAACGTGTC  CA
                                 CC       GT
GAM245  FLJ11116  5' GCTGCTGTAAATTGCTGCTGC  82589       TACG    TA TG
                              GCGGTAGT   TTGCA  G  GT
                              ||||||||   |||||  |  ||
                              CGTCGTCG   AATGT  C  CG
                                  TTA_    __ GT
GAM245  FLJ11700  3' ACCAGATGGGCTTGGCTATTGT 46033         C   G   AG
                              GCGGTAGTTA GTT CAT  TGGT
                              |||||||||| ||| |||  ||||
                              TGTTATCGGT CGG GTA  ACCA
                                    T   _   G_
GAM245  FLJ12132  3' CCACTCCCGAGCTGCCGT    46467        A  TTGCAT
                              GCGGTAGTT CG     AGTGG
                              |||||||||  ||     |||||
                              TGCCGTCGA GC     TCACC
                                   _ CC____
GAM245  FLJ12389  3' CCGCAGGTGTGGCACTGT    60266      AGTTAC  TG   A_
                              GCGGT     GT  CAT  GTGG
                              |||||     ||  |||  ||||
                              TGTCA     CG  GTG  CGCC
                                ______  GT   GA
GAM245  FLJ12439  3' GCTGTTATGCTTCAGGGTTGCT 43572      GT ACGTT     TG
             G                  CGGTA  T    GCATAG  GT
                              |||||  |    ||||||  ||
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                                GTCGT G    CGTATT CG
                                  TG GACTT     GT
GAM245  FLJ12529 3' TCCAAATTGTAATGTGGTTGCT 45661       TT      TAG  T
            GC                  GCGGTAG ACGTTGCA  TGG
                                ||||||| |||||||| |||
                                CGTCGTT TGTAATGT  ACC
                                   GG      TAA  TA
GAM245  FLJ12577 3' GTCATTGTGTGTCCTTTGTTGC 48158       TTACGT_      GT
            TGC                 GCGGTAG     TGCATAGTG
                                |||||||     |||||||||
                                CGTCGTT     GTGTGTTAC
                                   GTTTCCT       TG
GAM245  FLJ12750 3' ACCGCCTGACCTGGCTGCTGC  45118         C   CATA
                                GCGGTAGTTA GTTG   GTGGT
                                |||||||||| ||||   |||||
                                CGTCGTCGGT CAGT   CGCCA
                                     C   C___
GAM245  FLJ12787 3' GCCACTGTGTCCAGCCTGTAAC 49749       __   __
            TATT                TAGTTAC  GTTG  CATAGTGGT
                                ||||||| ||||  |||||||||
                                ATCAATG  CGAC  GTGTCACCG
                                   TC   CT
GAM245  FLJ12806 3' CGCAGGCATAACTGCTGT    43085        CGT   ATA TG
                                GCGGTAGTTA   TGC   G  G
                                |||||||||   |||   |  |
                                TGTCGTCAAT   ACG   C  C
                                     ___  GA_ GT
GAM245  FLJ12899 3' GCCACTACCCATATGTAGCTGT 44762   GG       _  CA
            TG                  C  TAGTTACGT TG  TAGTGGT
                                |  ||||||||| ||  |||||||
                                G  GTCGATGTA AC  ATCACCG
                                 TT       T  CC
GAM245  FLJ12960 3' ATTATTTTGTGGCTGCTGT   44946          TTGC
                                GCGGTAGTTACG   ATAGT
                                ||||||||||||   |||||
                                TGTCGTCGGTGT   TATTA
                                     TT__
GAM245  FLJ13072 3' TTTCTCTGCATGTGGCTGCTGC 89833           T   T  TGGT
                                GCGGTAGTTACGT GCA AG
                                |||||||||||| ||| ||
                                CGTCGTCGGTGTA CGT TC
                                     _  C  TTTG
GAM245  FLJ13150 3' CCATAGAATTGGCTACTGC   45669         C   GCATA
                                GCGGTAGTTA GTT    GTGG
                                |||||||||| |||    ||||
                                CGTCATCGGT TAA    TACC
                                     _  GA___
GAM245  FLJ13153 5' CGCTGTGTGGGGGCTGTCG   45556    GT    ACG TG
                                CG  AGTT   T  CATAGTG
                                ||  ||||   |  |||||||
```

```
                              GC  TCGG   G  GTGTCGC
                               TG    G__ GT
GAM245  FLJ13193  5' CCGCTGTGCAGCGCAGC     49762     A
                              GTT CGTTGCATAGTGG
                              ||| ||||||||||||
                              CGA GCGACGTGTCGCC
                                C
GAM245  FLJ13265  3' GCTGCTGTGCCTCGGGCTGCTG 45929        A  TT     TG
                              CGGTAGTT CG  GCATAG  GT
                              |||||||| ||  ||||||  ||
                              GTCGTCGG GC  CGTGTC  CG
                                   _ TC     GT
GAM245  FLJ13305  5' ACCACTGTGCCTGGCCAATTCT 90124      T   AC  __
            GT                   GCGG AGTT  GTT  GCATAGTGGT
                              |||| ||||  |||  ||||||||||
                              TGTC TTAA  CGG  CGTGTCACCA
                                _   C_  TC
GAM245  FLJ13305  5' GCTACTAAAACGAACTGCTGC  90129         A   GCA
                              GCGGTAGTT CGTT   TAGTGGT
                              ||||||||| ||||   |||||||
                              CGTCGTCAA GCAA   ATCATCG
                                   _   A__
GAM245  FLJ13310  3' TGTTAATGAGAGCTGCTGC   47087         A_   _
                              GCGGTAGTT  CGTTG CA
                              |||||||||  ||||| ||
                              CGTCGTCGA  GTAAT GT
                                   GA    T
GAM245  FLJ13385  3' GCTGTGAAGCGAACTATCGC   45850         A   G
                              GCGGTAGTT CGTT CATAGT
                              ||||||||| |||| ||||||
                              CGCTATCAA GCGA GTGTCG
                                   _   A
GAM245  FLJ13441  3' ACTGTGTTCACGTGGCTCCTGC 43656      T      T_
                              GCGG AGTTACGT  GCATAGT
                              |||| ||||||||  |||||||
                              CGTC TCGGTGCA  TGTGTCA
                                C       CT
GAM245  FLJ13491  5' CGCTGCCAGGGCTGCTGC    44884         ACGTT   TA TG
                              GCGGTAGTT    GCA  G  G
                              |||||||||    |||  |  |
                              CGTCGTCGG    CGT  C  C
                                   GAC__   __ GT
GAM245  FLJ13491  5' GCTGTTAGCAGAGGCTGCTGC  44887        TACG   A   TG
                              GCGGTAGT    TTGC TAG  GT
                              ||||||||    |||| |||  ||
                              CGTCGTCG    GACG ATT  CG
                                   GA__    _  GT
GAM245  FLJ13576  3' CTACTTCTGTAGCTGCT     42515          TTGCAT
                              GGTAGTTACG     AGTGG
                              ||||||||||     |||||
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                                TCGTCGATGT     TCATC
                                      CT____
GAM245  FLJ14117 3' ACTGCTGTTCTAGCTGCTG   42898        CGTTGC   TG
                                CGGTAGTTA     ATAG  GT
                                |||||||||     ||||  ||
                                GTCGTCGAT     TGTC  CA
                                      CT____    GT
GAM245  FLJ14117 3' GCTGTGTGTGCACTGCTGT   42911        _  GTT
                                GCGGTAGT TAC   GCATAGT
                                |||||||| |||   |||||||
                                TGTCGTCA GTG   TGTGTCG
                                     C  ___
GAM245  FLJ14146 3' CCACTGTTCTGACTTTGT    45241     T   CGTTGC
                                GCGG AGTTA     ATAGTGG
                                |||| |||||     |||||||
                                TGTT TCAGT     TGTCACC
                                  _    CT____
GAM245  FLJ14225 3' CATTGTGCCCAGAGTGCTGC   45901      G  ACGTT
                                GCGGTA TT    GCATAGTG
                                |||||| ||    ||||||||
                                CGTCGT AG    CGTGTTAC
                                   G  ACC__
GAM245  FLJ14326 3' ACCGAACTGGCTTAGCTGCTGT 49797         CGTT  A   __
                                GCGGTAGTTA   GC TAGT  GGT
                                ||||||||||   || ||||  |||
                                TGTCGTCGAT   CG GTCA  CCA
                                      T___ _   AG
GAM245  FLJ14457 5' GCGGGCGTGGCTGTGGC    51385    G        _
                                GC GTAGTTACGTT GC
                                || ||||||||||| ||
                                CG TGTCGGTGCGG CG
                                 G         G
GAM245  FLJ14524 3' GTTGCTGGAGGCCGGGCTACCG 51409        AC   GCA   GG
           T                     GCGGTAGTT  GTT   TAGT  T
                                |||||||||  |||   ||||  |
                                TGCCATCGG  CGG   GTCG  G
                                     GC   AG_   TT
GAM245  FLJ14547 5' GTGCGGGCGCGTGGCTGCTG   51438         T  ATA  GG
                                CGGTAGTTACGT GC   GT  T
                                |||||||||||| ||   ||  |
                                GTCGTCGGTGCG CG   CG  G
                                      _ GG_  TT
GAM245  FLJ14642 3' TGCAGTGGCTGCTGC       51509         GT
                                GCGGTAGTTAC  TGCA
                                ||||||||||  ||||
                                CGTCGTCGGTG  ACGT
                                      __
GAM245  FLJ14950 3' ACTGCTATGTGGCTTCAACCAG 51712    _  AGTTAC  TG    TG
           C                     GC GGT     GT  CATAG  GT
                                || |||     ||  |||||  ||
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                                CG CCA     CG  GTATC  CA
                                 A  ACTT__  GT    GT
GAM245  FLJ14957  3' CCACTATTTGCATTGCTGT   51743       TTACGT   __
                                GCGGTAG     TGCA  TAGTGG
                                |||||||     ||||  ||||||
                                TGTCGTT     ACGT  ATCACC
                                   _______   TT
GAM245  FLJ14957  3' GCTGTTATGCGTTTTGACAATT 51754      A   CGT     TG
           GC                    GCGGT GTTA   TGCATAG  GT
                                |||||  ||||   |||||||  ||
                                CGTTA CAGT   GCGTATT  CG
                                   A   TTT      GT
GAM245  FLJ14957  3' GTTGCTTGTGTCTGTGACTGCA 51756    G       TT    _  GG
           GC                    GC GTAGTTACG  GCATA GT  T
                                || |||||||||  |||||  ||  |
                                CG CGTCAGTGT  TGTGT CG  G
                                 A       C_    T  TT
GAM245  FLJ20034  3' GCCGCAGATGGTGTAATTGCTG 34373          TT CATA
                                CGGTAGTTACG  G   GTGGT
                                ||||||||||  |   |||||
                                GTCGTTAATGT  T   CGCCG
                                      GG AGA_
GAM245  FLJ20069  3' AACCATTGTGACTATTGT    34466          TTGCATA
                                GCGGTAGTTACG     GTGGT
                                ||||||||||      |||||
                                TGTTATCAGTGT     TACCA
                                      _______    AA
GAM245  FLJ20086  3' GCTATTATGCTTTTAATATTGT 34522       GTTACGTT
                                GCGGTA       GCATAGTGGT
                                ||||||       ||||||||||
                                TGTTAT       CGTATTATCG
                                   AATTTT__
GAM245  FLJ20154  5' GCTGCTGTGTTTGCCACCACCG 72928      A  TA  TT     TG
           C                     GCGGT GT  CG  GCATAG  GT
                                |||||  ||  ||  ||||||  ||
                                CGCCA CA  GT  TGTGTC  CG
                                   C  CC  T_     GT
GAM245  FLJ20211  3' ACTATGTGTGTAGTGCTGC   34749       G    GTT
                                GCGGTA TTAC   GCATAGT
                                ||||||  ||||   |||||||
                                CGTCGT GATG   TGTATCA
                                   _    TG_
GAM245  FLJ20211  3' TGCCATGTGGCTCTGT      34753      T       T
                                GCGG AGTTACGT GCA
                                ||||  |||||||| |||
                                TGTC TCGGTGTA CGT
                                   _       C
GAM245  FLJ20254  5' CACTACATGGTTACCGC     34786        TT C  TGCAT
                                GCGGTAG  A GT    AGTG
                                |||||||  | ||    ||||
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                                CGCCATT  T CA     TCAC
                                   GG A  _____
GAM245  FLJ20257  3'  GCCATTGTACCTAGCTCTTGT  38996      T     C  TGC
                                GCGG AGTTA GT   ATAGTGGT
                                |||| ||||| ||   ||||||||
                                TGTT TCGAT CA   TGTTACCG
                                  C    C  ___
GAM245  FLJ20288  5'  TGCACTGGATGAAGCTGCTGC  45129          A    GCA    GT
                                GCGGTAGTT CGTT   TAGTG
                                ||||||||| ||||   |||||
                                CGTCGTCGA GTAG   GTCAC
                                     A   ___    GTG
GAM245  FLJ20321  3'  GCCGATGGTGGCGGCAGTGGCT 34949          _    _  AG_
           ACTGC                 GTAGTTAC GTTGC AT   TGGT
                                |||||||| ||||| ||   ||||
                                CATCGGTG CGGCG TG   GCCG
                                     A    G  GTA
GAM245  FLJ20331  3'  ATCATCTTAAAAGGTGATTATT 34953          G  GCATA
           GT                   GCGGTAGTTAC TT    GTGGT
                                ||||||||||| ||    |||||
                                TGTTATTAGTG AA    TACTA
                                     G  AATTC
GAM245  FLJ20333  5'  CCGTTGAATGTGGCTGCT    34956          G  TAG
                                GGTAGTTACGTT CA   TGG
                                |||||||||||| ||   |||
                                TCGTCGGTGTAA GT   GCC
                                     _  T__
GAM245  FLJ20378  5'  GCTGCTGTTTTAGTAAGTATTG 35094       G   GTTGC   TG
           T                    GCGGTA TTAC    ATAG  GT
                                |||||| ||||    ||||  ||
                                TGTTAT AATG    TGTC  CG
                                   G   ATTT_   GT
GAM245  FLJ20452  3'  GCCACTAGTCTGTGGCATTGT  35202      A     TT  A
                                GCGGT GTTACG  GC TAGTGGT
                                ||||| ||||||  || |||||||
                                TGTTA CGGTGT  TG ATCACCG
                                   _     C_ _
GAM245  FLJ20502  3'  TCATTATGCAGTGTGTATATT  35263     GT          GT
                                GGTA  TACGTTGCATAGTG
                                ||||  ||||||||||||||
                                TTAT  GTGTGACGTATTAC
                                  AT           TG
GAM245  FLJ20519  3'  ATTACTGTGCAACTATTTTGCT 35344      TTAC
                                GGTAG   GTTGCATAGTGGT
                                |||||   ||||||||||||
                                TCGTT   CAACGTGTCATTA
                                  TTAT
GAM245  FLJ20647  5'  GCCGTGGCGCACGCGGCTGCTG 35495        TA  _  ATAG
           C                    GCGGTAGT  CGT TGC   TGGT
                                ||||||||  ||| |||   ||||
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                                CGTCGTCG  GCA GCG    GCCG
                                    GC   C   GT__
GAM245  FLJ20689  3'  CCACAGACGCAACTACTGC   35538         A    GCATA
                                GCGGTAGTT CGTT     GTGG
                                ||||||||| ||||     ||||
                                CGTCATCAA GCAG     CACC
                                    C    A____
GAM245  FLJ20689  5'  GCCGTTGGAGGTGGCTGCGGC  35539    G       G  GCA
                                GC GTAGTTAC TT   TAGTGGT
                                || |||||||| ||   |||||||
                                CG CGTCGGTG AG   GTTGCCG
                                 G       G ___
GAM245  FLJ20699  3'  TCACAGCCAGTGTGAGTGCTGC 35566       G       CATA   GT
                                GCGGTA TTACGTTG    GTG
                                |||||| ||||||||    |||
                                CGTCGT AGTGTGAC    CAC
                                   G       CGA_   TG
GAM245  FLJ20730  3'  GTTACTAATTCAAGCTGTGACT 35620         _   GCA__    GG
            ATTGT                GTAGTTAC GTT     TAGT  T
                                |||||||| |||     ||||  |
                                TATCAGTG CGA     ATCA  G
                                    T   ACTTA    TT
GAM245  FLJ20739  3'  CGCTGGGGGCTGCCGC      67855         ACGTTGCA
                                GCGGTAGTT       TAGTG
                                |||||||||       |||||
                                CGCCGTCGG       GTCGC
                                    GG_______
GAM245  FLJ20758  3'  GCCTGATGTGCTGCTGT     35643         T     __
                                GCGGTAGT ACGTT  GC
                                |||||||| |||||  ||
                                TGTCGTCG TGTAG  CG
                                    _     TC
GAM245  FLJ20761  5'  TCAAAGTCCGACGTGGTACTGT 35653       G       C  AG  GT
                                GCGGTA TTACGTTG AT  TG
                                |||||| |||||||| ||  ||
                                TGTCAT GGTGCAGC TG  AC
                                   _       C  AA  TG
GAM245  FLJ21172  5'  GCCACCCTCGCGTCAGTTGTCG 45645     GT GT _    TGCATA
            C                    GCG  A  T ACGT     GTGGT
                                ||| |  | ||||     |||||
                                CGC  T  A TGCG     CACCG
                                  TG TG C    CTCC__
GAM245  FLJ21438  5'  CGCCTGCGCGTGCTGCCGT    61520         T    T   TA
                                GCGGTAGT ACGT GCA  GTG
                                |||||||| |||| |||  |||
                                TGCCGTCG TGCG CGT  CGC
                                    _    _   C_
GAM245  FLJ21615  3'  GCTGTGTTAGCTCTTGC     49837      T    CGTT
                                GCGG AGTTA    GCATAGT
                                |||| |||||    |||||||
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                                CGTT TCGAT    TGTGTCG
                                  C    ____
GAM245  FLJ21945  3' CGCTGTGTAGCAGAGCT     47316      AC        TG
                                AGTT  GTTGCATAG  G
                                ||||  |||||||||  |
                                TCGA  CGATGTGTC  C
                                  GA        GT
GAM245  FLJ22009  3' ACTGCTGCCATTGTAGTTTGCT 60282        TT_   T  CA   TG
           GT                    GCGGTAG   ACG TG  TAG  GT
                                |||||||   ||| ||  |||  ||
                                TGTCGTT   TGT AC  GTC  CA
                                   TGA   T  C_   GT
GAM245  FLJ22009  3' ACTTTTTAGTGTAATTACC    60283           CAT
                                GGTAGTTACGTTG   AGT
                                ||||||||||||   |||
                                CCATTAATGTGAT   TCA
                                       TTT
GAM245  FLJ22009  3' GCTGCAGTGAGGTGTGATTGCG 60285     G        TG   A TG
           C                     GCG TAGTTACGT  CAT G  GT
                                ||| |||||||||  ||| |  ||
                                CGC GTTAGTGTG  GTG C  CG
                                  _        GA   A GT
GAM245  FLJ22056  5' GCTGCTGTGTGAGGGCGCGGCC 42535       A  TACG TG     TG
           GC                    GCGGT GT    T  CATAG  GT
                                |||||  ||    |  |||||  ||
                                CGCCG CG    A  GTGTC  CG
                                   G  CGGG GT     GT
GAM245  FLJ22127  3' CATTTGACTGTGACTGTTGC   42883    GG       TTG  T
                                GC  TAGTTACG   CA AGTG
                                ||  ||||||||   || ||||
                                CG  GTCAGTGT   GT TTAC
                                 TT       CA_  _
GAM245  FLJ22191  5' GCTGTCCAAAGGACGCTAGCTG 47446       _  _____  C     GGT
           TTGC                    TAGTTA CGT    TG ATAGT
                                |||||| |||    || |||||
                                GTCGAT GCA    AC TGTCG
                                   C   GGAA  C       T
GAM245  FLJ22215  3' GCCGCTGTGAACCGGCTGTCC  96834    _    AC   G
                                GG TAGTT  GTT CATAGTGGT
                                || |||||  ||| |||||||||
                                CC GTCGG  CAA GTGTCGCCG
                                 T    C_  _
GAM245  FLJ22233  3' ACTGCTGTGTACCTCTTGCTGC 46363       TACGT_      TG
           C                     GGTAGT     TGCATAG  GT
                                ||||||     |||||||  ||
                                CCGTCG     ATGTGTC  CA
                                   TTCTCC      GT
GAM245  FLJ22282  3' ATCATTGTGGGTAGGTAGTTAT 45586      GT   GTTG_
           TG                    CGGTA  TAC    CATAGTGGT
                                |||||  |||    |||||||||
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                              GTTAT  ATG    GTGTTACTA
                                 TG  GATGG
GAM245  FLJ22341  3' GCTGGGGACGTGGCTG     44804         GCA
                              TAGTTACGTT   TAGT
                              ||||||||||   ||||
                              GTCGGTGCAG   GTCG
                                   GG_
GAM245  FLJ22369  5' GCTGTTTGTATTTTGGCTGCTG 49919         CGT   T  TG
           C                   GCGGTAGTTA   TGCA AG  GT
                              ||||||||||   |||| ||  ||
                              CGTCGTCGGT   ATGT TT  CG
                                   TTT   _  GT
GAM245  FLJ22405  5' GCTGTTTGGCCGAGACTACTGT 42521         A  TT  AT  TG
                              GCGGTAGTT CG  GC  AG  GT
                              ||||||||| ||  ||  ||  ||
                              TGTCATCAG GC  CG  TT  CG
                                   A  __  GT  GT
GAM245  FLJ22479  3' ATTGCTGAATGTCGTGGCTGTT 46072   GG      TT   __  TG
           G                    C  TAGTTACG  GCAT  AG  GT
                              |  ||||||||  ||||  ||  ||
                              G  GTCGGTGC  TGTA  TC  TA
                               TT       __    AG  GT
GAM245  FLJ22490  3' TACTAATTACATGATGTAACTA 45581          CA   _
           CT                   GGTAGTTACGTTG  TAGT GGT
                              ||||||||||||  |||| |||
                              TCATCAATGTAGT  ATTA TCA
                                    AC    A   TT
GAM245  FLJ22688  5' GTTACTCTGATTACCGC     47099         C_  T
                              GCGGTAGTTA  GT GC
                              ||||||||||  || ||
                              CGCCATTAGT  CA TG
                                   CT  T
GAM245  FLJ22693  3' GCTGCTGTGTGGTGCCATCG   42760     A  TAC TT     TG
                              CGGT GT   G  GCATAG  GT
                              |||| ||   |  ||||||  ||
                              GCTA CG   T  TGTGTC  CG
                                C  ___ GG     GT
GAM245  FLJ22794  3' CGCTGTTTGACTCCTGC     91606     T    CGTTGC    TG
                              GCGG AGTTA     ATAG  G
                              |||| |||||     ||||  |
                              CGTC TCAGT     TGTC  C
                                C    T_____    GT
GAM245  FLJ22875  3' GCCACTGGCCTGTAATTG    49927        TT  A
                              TAGTTACG  GC TAGTGGT
                              ||||||||  || |||||||
                              GTTAATGT  CG GTCACCG
                                   C_  _
GAM245  FLJ23027  5' ACCTGACCAGTGAGCTGCTGC  49928         A    CATAGT
                              GCGGTAGTT CGTTG     GGT
                              |||||||| |||||     |||
```

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                                CGTCGTCGA GTGAC      CCA
                                      _     CAGT__
GAM245  FLJ23186  3'  ACCTCAGCAGTGTGGTTCTGT  60400      T  TT      ATAGT
                                GCGG AG  ACGTTGC     GGT
                                |||| ||  |||||||     |||
                                TGTC TT  TGTGACG     CCA
                                  _  GG      ACT__
GAM245  FLJ23309  3'  CACTGGAAAGTGATTGCC    46062         GTTGCA
                                GGTAGTTAC     TAGTG
                                |||||||||     |||||
                                CCGTTAGTG     GTCAC
                                      AAAG__
GAM245  FLJ23311  3'  ACTATTATGCAAAGTAACTG   45178        G
                                TAGTTAC TTGCATAGTGGT
                                ||||||| ||||||||||||
                                GTCAATG AACGTATTATCA
                                     A
GAM245  FLJ23322  3'  TGCAATGGAGCTGTCGC     88790     GT    A
                                GCG  AGTT CGTTGCA
                                |||  |||| |||||||
                                CGC  TCGA GTAACGT
                                  TG    G
GAM245  FLJ23360  5'  GCAATGTGAATATTGC      43568       G
                                GCGGTA TTACGTTGC
                                |||||| |||||||||
                                CGTTAT AGTGTAACG
                                    A
GAM245  FLJ23563  3'  GCTAAATGAAACTGCTGC     67595         A    GCA
                                GCGGTAGTT CGTT   TAGT
                                ||||||||| ||||   ||||
                                CGTCGTCAA GTAA   ATCG
                                      A   ___
GAM245  FLJ23563  5'  TTCATTTCGATGTGACATTGT  67607      A       CAT     T
                                GCGGT GTTACGTTG   AGTGG
                                ||||| |||||||||   |||||
                                TGTTA CAGTGTAGC   TTACT
                                  _       T__     TA
GAM245  FLJ23590  3'  ATTACTATGTGAAAGTTAACTG 45018       CG__ TG
          C                      GTAGTTA    T  CATAGTGGT
                                 |||||||    |  |||||||||
                                 CGTCAAT    A  GTATCATTA
                                      TGAA GT
GAM245  FLJ30046  3'  GTTACTGTGTACACTGCTGT   58103        TAC  T      GG
                                GCGGTAGT   GT GCATAGT  T
                                ||||||||   || |||||||  |
                                TGTCGTCA   CA TGTGTCA  G
                                     ___  _      TT
GAM245  FLJ30663  5'  GCCGTTAGGTTGCGGCTGCTGT 78656         TA   T  A
                                GCGGTAGT  CGT GC TAGTGGT
                                ||||||||  ||| || |||||||
```

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                                TGTCGTCG  GCG TG ATTGCCG
                                    __   T  G
GAM245  FLJ31737  3'  GTTACTGGACATTTGAAGCTGC 58697        A  T_  CA    GG
           TGT                    GCGGTAGTT CG  TG  TAGT  T
                                |||||||||  ||  ||  ||||  |
                                TGTCGTCGA GT  AC  GTCA  G
                                     A  TT  AG    TT
GAM245  FOXD4    3'  CGCGTGGAGCTACTGC      82748         ACG TG ATA
                                GCGGTAGTT   T  C   GTG
                                |||||||||   |  |   |||
                                CGTCATCGA   G  G   CGC
                                     ___ GT ___
GAM245  FOXP1    5'  GCCACTGTGCAGCAGGAGTCGC 51068     AG  AC_
           C                     GGT  TT   GTTGCATAGTGGT
                                |||  ||   ||||||||||||
                                CCG  GA   CGACGTGTCACCG
                                  CT  GGA
GAM245  FRAT1    3'  ATCATCCAGATGTGGCTACTG  18494           GCATA
                                CGGTAGTTACGTT    GTGGT
                                ||||||||||||     |||||
                                GTCATCGGTGTAG    TACTA
                                       ACC__
GAM245  FREQ     3'  TGTTAACTGTTGCTGCTGC   26593        T  _   _
                                GCGGTAGT AC GTTG CA
                                |||||||| || |||| ||
                                CGTCGTCG TG CAAT GT
                                     T  T   T
GAM245  FZD9     3'  GCCTGGCGCGGGGTGGCTGCTG 13046          G    ATAGT
           C                     GCGGTAGTTAC TTGC    GGT
                                ||||||||||| ||||    |||
                                CGTCGTCGGTG GGCG    CCG
                                      G   CGGT_
GAM245  GABARAPL2 5'  GCCGCTGCCGCCGTCGTTGTTG 23468    GG   TT   TT  A_
           T                     GC  TAG  ACG  GC  TAGTGGT
                                ||  |||  |||  ||  |||||||
                                TG  GTT  TGC  CG  GTCGCCG
                                 TT   GC   __  CC
GAM245  GDBR1    3'  TGCTGCTTGAATTGCCGT    32422         AC_  T
                                GCGGTAGTT   GT GCA
                                |||||||||   || |||
                                TGCCGTTAA   CG CGT
                                     GTT  T
GAM245  GFR      3'  ATCATTAATTAGGGCTGCTGT  24467         ACGTTGCA
                                GCGGTAGTT       TAGTGGT
                                |||||||||       |||||||
                                TGTCGTCGG       ATTACTA
                                     GATTA___
GAM245  GFR      3'  GTTAGATGCAAATGTATTACTG 24474         T    _    AGTGGT
           T                     GCGGTAGT ACGTT GCAT
                                ||||||||  |||||  ||||
```

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                                TGTCATTA TGTAA CGTA
                                   _    A   GATTG
GAM245  GIT2    3'  ATTATTGTGCCCTTTAAGTGTT 28754    GG  G   CGTT
            GT                   GC  TA TTA   GCATAGTGGT
                                 ||  || |||   ||||||||||
                                 TG  GT AAT   CGTGTTATTA
                                  TT  G   TTCC
GAM245  GIT2    3'  ATTATTGTGCCCTTTAAGTGTT 54076    GG  G   CGTT
            GT                   GC  TA TTA   GCATAGTGGT
                                 ||  || |||   ||||||||||
                                 TG  GT AAT   CGTGTTATTA
                                  TT  G   TTCC
GAM245  GIT2    3'  ATTATTGTGCCCTTTAAGTGTT 54089    GG  G   CGTT
            GT                   GC  TA TTA   GCATAGTGGT
                                 ||  || |||   ||||||||||
                                 TG  GT AAT   CGTGTTATTA
                                  TT  G   TTCC
GAM245  GK001   3'  ACCAGTGACAACGTGAATGCTG 39495       G      _   AG
            T                    GCGGTA TTACGTTG CAT  TGGT
                                 ||||||| |||||||| |||  ||||
                                 TGTCGT AGTGCAAC GTG  ACCA
                                    A       A   __
GAM245  GMEB1   5'  GTGGCGGTAGCTGCCGT     21669          _ TG
                                 GCGGTAGTTAC GT  C
                                 ||||||||||| ||  |
                                 TGCCGTCGATG CG  G
                                       G  GT
GAM245  GMEB1   5'  GTGGCGGTAGCTGCCGT     44403          _ TG
                                 GCGGTAGTTAC GT  C
                                 ||||||||||| ||  |
                                 TGCCGTCGATG CG  G
                                       G  GT
GAM245  GMPPB   5'  ACCACGCCCGGCTAATTGTTGT 95717    GG     C    CATA
                                 GC  TAGTTA GTTG   GTGGT
                                 ||  |||||| ||||   |||||
                                 TG  GTTAAT CGGC   CACCA
                                  TT     _   CCG_
GAM245  GNB1L   5'  GCTGGGGGCGTGGCTGCGC   53811     G        GCA
                                 GCG TAGTTACGTT   TAGT
                                 ||| ||||||||||   ||||
                                 CGC GTCGGTGCGG   GTCG
                                   _         GG_
GAM245  GOLGA1  3'  CACCATGTAGCGCTGC      9087       TAGTTA       A
                                 GCGG     CGTTGCAT GTG
                                 ||||     |||||||| |||
                                 CGTC     GCGATGTA CAC
                                    _______        C
GAM245  GOLGA3  3'  GCCACTATGCCAGGCTAATGT  19718     G    ACGTT
                                 GCG TAGTT    GCATAGTGGT
                                 ||| |||||    ||||||||||
```

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                                TGT ATCGG    CGTATCACCG
                                  A    AC___
GAM245  GP      5'  GCCGCTTTCCACAATGCAGTTG 37373      GT A    CAT__
             CTGT                  CGGTA  T CGTTG    AGTGGT
                                |||||  | |||||    ||||||
                                GTCGT  A GTAAC    TCGCCG
                                   TG C    ACCTT
GAM245  GPR107   3'  TGGGGGTGACTGCTGC     40566          G  G
                                GCGGTAGTTAC TT CA
                                |||||||||| || ||
                                CGTCGTCAGTG GG GT
                                      _  G
GAM245  GPS2    5'  ACGGGCAGCCTGGCTGCTGC   15661          C    ATA
                                GCGGTAGTTA GTTGC   GT
                                |||||||||| |||||   ||
                                CGTCGTCGGT CGACG   CA
                                      C    GG_
GAM245  GPS2    3'  ACGGGCAGCCTGGCTGCTGC   87149          C    ATA
                                GCGGTAGTTA GTTGC   GT
                                |||||||||| |||||   ||
                                CGTCGTCGGT CGACG   CA
                                      C    GG_
GAM245  GPT2    3'  GCCTGGCAGCTTGGCTGCCGT  55957          C    ATAGT
                                GCGGTAGTTA GTTGC    GGT
                                |||||||||| |||||    |||
                                TGCCGTCGGT CGACG    CCG
                                      T    GT___
GAM245  GRIN3A   5'  CGCTCCTCTGTCACTGCTGC   55969        T   TTGCAT
                                GCGGTAGT ACG     AGTG
                                |||||||| |||     ||||
                                CGTCGTCA TGT     TCGC
                                    C   CTCC__
GAM245  GW112    3'  TGCATGTAATTTTTGC     21193      T      T
                                GCGG AGTTACGT GCA
                                |||| |||||||| |||
                                CGTT TTAATGTA CGT
                                  T       _
GAM245  H326    3'  CCAGATGTTGGCTGCTGT    31704          CGTT    AG
                                GCGGTAGTTA    GCAT  TGG
                                ||||||||||    ||||  |||
                                TGTCGTCGGT    TGTA  ACC
                                      _____    G_
GAM245  HABP4    3'  GCTATTGTGTAGCCACTGGCC  70560     _   TAC
                                GGT AGT   GTTGCATAGTGGT
                                ||| |||   ||||||||||||||
                                CCG TCA   CGATGTGTTATCG
                                  G   C__
GAM245  HARS2    3'  ATTACAGGTGTGAACTACCGC  55031        TACG TG   A_
                                GCGGTAGT    T  CAT  GTGGT
                                ||||||||    |  |||  |||||
```

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                                CGCCATCA   A  GTG  CATTA
                                    ____ GT   GA
GAM245  HCC-4    5'  ACCGAAAAATGTTGCTATTGC  56817        T    GCATAG
                                GCGGTAGT ACGTT     TGGT
                                |||||||| |||||     ||||
                                CGTTATCG TGTAA     GCCA
                                    T    AAA___
GAM245  HCF-2    3'  GCTATTGTGATGATGATTATT  25261        _   TG  _
                                GGTAGTTA CGT  CA TAGT
                                |||||||| |||  || ||||
                                TTATTAGT GTA  GT ATCG
                                    A   GT  T
GAM245  HCGIV.9  3'  GCCACTGTGTTACTATATGTTG 38612    GG  GTTAC  T
           T                     GC  TA    GT GCATAGTGGT
                                ||  ||    || ||||||||||
                                TG  GT    CA TGTGTCACCG
                                 TT  ATAT_  T
GAM245  HCGIX    3'  ACCGGGGGATGTGACTGCC   19571          GCATAG
                                GGTAGTTACGTT     TGGT
                                ||||||||||||     ||||
                                CCGTCAGTGTAG     GCCA
                                      GGG___
GAM245  HEMK     3'  TGCTCTGTGTTGGTGAAATTGC 32443        A  TT _    T
           TGT                    CGGTAGTT CG  G CATAG GGT
                                |||||||| ||  | ||||| |||
                                GTCGTTAA GT  T GTGTC TCG
                                    A  GG T    _   TT
GAM245  HEYL     3'  ACTCCTACGATCTGGTTACTGC 27389       TT C    CA   TG
                                GCGGTAG  A GTTG  TAG  GT
                                |||||||  | ||||  |||  ||
                                CGTCATT  T TAGC  ATC  CA
                                    GG C    __   CT
GAM245  HIC      5'  CCGCTGCCGCAGTTGCCGC   67447       TTACG   A_
                                GCGGTAG    TTGC  TAGTGG
                                |||||||    ||||  ||||||
                                CGCCGTT    GACG  GTCGCC
                                    ______   CC
GAM245  HMP19    3'  TGAGATGTGGTACTGC     87476       G     TG
                                GCGGTA TTACGT  CA
                                |||||| ||||||  ||
                                CGTCAT GGTGTA  GT
                                    _     GA
GAM245  HMT-1    3'  GCCCCTGCTAGCGTATTACTGT 38899        T    _   TAGT
                                GCGGTAGT ACGTT GCA    GGT
                                |||||||| ||||| |||    |||
                                TGTCATTA TGCGA CGT    CCG
                                    _    T  CC__
GAM245  HN1L     3'  GCCCTGCTGTGTGGCTGTCGT  57998     GT      TT   TA T
                                GCG  AGTTACG  GCA  G GGT
                                |||  |||||||  |||  | |||
```

```
                                TGC  TCGGTGT  CGT  C CCG
                                  TG      GT  __ _
GAM245  HSA243666 3'  TGTATGTACTTGCTGT     34149        T    T
                                GCGGTAG TACGT GCA
                                ||||||| ||||| |||
                                TGTCGTT ATGTA TGT
                                   C    _
GAM245  HSA404617 5'  CCAAGGATGTTGCTGCTGT   72709        T    GCATAG
                                GCGGTAGT ACGTT     TGG
                                |||||||| |||||     |||
                                TGTCGTCG TGTAG     ACC
                                     T    GA____
GAM245  HSF2     5'  CGCTGCCGTAGCTGCCGC    15709          TT   TA TG
                                GCGGTAGTTACG  GCA  G  G
                                ||||||||||||  |||  |  |
                                CGCCGTCGATGC  CGT  C  C
                                       __  __ GT
GAM245  HSPC049   3'  TGCAGTGGCTACTGT      71922          GT
                                GCGGTAGTTAC  TGCA
                                ||||||||||  ||||
                                TGTCATCGGTG  ACGT
                                       __
GAM245  HSPC065   3'  GCTATGGCGTGGTTTTGC    26306     T  TT   TG
                                GCGG AG  ACGT  CATAGT
                                |||| ||  ||||  ||||||
                                CGTT TT  TGCG  GTATCG
                                  _ GG   __
GAM245  HSPC138   5'  GCTGAACGGAGCTGCCGT    33081         A   __
                                GCGGTAGTT CGTT  GC
                                ||||||||| ||||  ||
                                TGCCGTCGA GCAA  CG
                                     G   GT
GAM245  HT009     5'  ACCAGGAAACGTGACTTTCGT  37470     T       GCATAG
                                GCGG AGTTACGTT     TGGT
                                |||| |||||||||     ||||
                                TGCT TCAGTGCAA     ACCA
                                  T       AGG___
GAM245  HUMNPIIY20 3'  GCTCCTCAGCGTGGTGGCCGT  83347      AG       CAT  TG
                                GCGGT  TTACGTTG   AG  GT
                                |||||  ||||||||   ||  ||
                                TGCCG  GGTGCGAC   TC  CG
                                   GT       ___  CT
GAM245  HXCP2     3'  CTATTGTGAATAGTGCCGC    50835      AGTT  GTTG
                                GCGGT    AC    CATAGTGG
                                |||||    ||    ||||||||
                                CGCCG    TG    GTGTTATC
                                   _____  ATAA
GAM245  IMAGE3451454 3'  CTACTGTGGGGCTGCT      53871        TACGT G
                                GGTAGT     T CATAGTGG
                                ||||||     | ||||||||
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```
                                TCGTCG    G GTGTCATC
                                  _____ G
GAM245  ING3     3'  CGTTATGTAACACTGT     38832      AGTTAC       TG
                                GCGGT     GTTGCATAG  G
                                |||||     |||||||||  |
                                TGTCA     CAATGTATT  C
                                  _______       GT
GAM245  IPLA2(GAMMA) 5'  GCGACCTAGCTGCTGC     60692          C
                                GCGGTAGTTA GTTGC
                                |||||||||| |||||
                                CGTCGTCGAT CAGCG
                                      C
GAM245  IRX3     3'  GCTAAATAAATGAGCTGCTGC  87964         A    GCA_
                                GCGGTAGTT CGTT    TAGT
                                ||||||||| ||||    ||||
                                CGTCGTCGA GTAA    ATCG
                                    _   ATAA
GAM245  KCNMB2   5'  CACTAGGCTGGTTGCTGT    19539       TT CGTT  A
                                GCGGTAG  A    GC TAGTG
                                |||||||  |    || |||||
                                TGTCGTT  T    CG ATCAC
                                   GG ____  G
GAM245  KCNS1    3'  GTTGTTGTCTGACTGTGGCTAT 9581          _   C    TG
          C                      GGTAGTTAC GTTG ATAG  GT
                                |||||||| |||| ||||  ||
                                CTATCGGTG CAGT TGTT  TG
                                     T    C    GT
GAM245  KDELR3   5'  CCGGAGACGTGGCAGCCGC   33606      A       GCATAG
                                GCGGT GTTACGTT     TGG
                                ||||| ||||||||     |||
                                CGCCG CGGTGCAG     GCC
                                   A       AG____
GAM245  KDELR3   5'  CCGGAGACGTGGCAGCCGC   22457      A       GCATAG
                                GCGGT GTTACGTT     TGG
                                ||||| ||||||||     |||
                                CGCCG CGGTGCAG     GCC
                                   A       AG____
GAM245  KIAA0010 3'  GTTATGTGCCATGTGGCTACT  27897          T    GTGGT
                                GGTAGTTACGT GCATA
                                |||||||||| |||||
                                TCATCGGTGTA CGTGT
                                      C     ATTG
GAM245  KIAA0014 3'  TGCATTTGGCTGCCGT      27852          CGT
                                GCGGTAGTTA   TGCA
                                |||||||||   ||||
                                TGCCGTCGGT   ACGT
                                     TT_
GAM245  KIAA0014 3'  TGCGCGGGCTGCTGC       27853          A   T
                                GCGGTAGTT CGT GCA
                                ||||||||| ||| |||
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```
                                CGTCGTCGG GCG CGT
                                      _  _
GAM245  KIAA0022 3' ACTGTGCTGAATACTGC    29658      G  CGTT
                                GCGGTA TTA   GCATAGT
                                |||||| |||   |||||||
                                CGTCAT AGT   CGTGTCA
                                   A  ____
GAM245  KIAA0040 5' GCTGCTGTGTGTGGAGGTGCTG 27787      G  ACGT     TG
           C                    GCGGTA TT   TGCATAG  GT
                                |||||| ||   |||||||  ||
                                CGTCGT GA   GTGTGTC  CG
                                   G  GGT_     GT
GAM245  KIAA0061 3' GCTTTGGGCAGTGTGGCTG   68293          AT__
                                TAGTTACGTTGC   AGT
                                ||||||||||||   |||
                                GTCGGTGTGACG   TCG
                                      GGTT
GAM245  KIAA0062 3' GCTAACGTGGCGGTGTGGCTGC 70241         TT  ATA  _
           C                    GGTAGTTACG  GC   GT GGT
                                ||||||||||  ||   || |||
                                CCGTCGGTGT  CG   CA TCG
                                     GG  GTG  A
GAM245  KIAA0064 3' ATCATTAAACTCAGCCTGACTG 28541         C   CA__
           CTGC                    CGGTAGTTA GTTG   TAGTGGT
                                |||||||| ||||   |||||||
                                GTCGTCAGT CGAC   ATTACTA
                                     C   TCAA
GAM245  KIAA0087 3' ACTACTTAATTATAAGTAATTG 28693   GG     GTTGCAT__
           TTGC                    C  TAGTTAC       AGTGGT
                                |  |||||||       ||||||
                                G  GTTAATG       TCATCA
                                 TT      AATATTAAT
GAM245  KIAA0090 3' ATTACAGGCATGAGCTACTGC  88439         A   T  ATA
                                GCGGTAGTT CGT GC   GTGGT
                                ||||||||| ||| ||   |||||
                                CGTCATCGA GTA CG   CATTA
                                     _  _  GA_
GAM245  KIAA0143 5' GCTGGCGGCGGTAGCTGTCGC  64787     GT    _    A
                                GCG  AGTTAC GTTGC TAGT
                                |||  |||||| ||||| ||||
                                CGC  TCGATG CGGCG GTCG
                                  TG     G    _
GAM245  KIAA0157 3' ACTTATCAGCGTAGTTTCTGT  49792      T GT      CAT
                                GCGG A  TACGTTG   AGT
                                |||| |  |||||||   |||
                                TGTC T  ATGCGAC   TCA
                                  T TG      TAT
GAM245  KIAA0193 3' TGCTGATGTGGCTGCGC     28664     G        _
                                GCG TAGTTACGTT GCA
                                ||| ||||||||| |||
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```
                              CGC GTCGGTGTAG CGT
                                _       T
GAM245  KIAA0217 3' GCTATTATGTAATATAA    67039    CG
                              TTA  TTGCATAGTGGT
                              |||  ||||||||||||
                              AAT  AATGTATTATCG
                                AT
GAM245  KIAA0218 3' GCTGTTATGTTGTCTGTGCTGC 28621      GTT   TT    TG
                              GCGGTA   ACG  GCATAG  GT
                              ||||||   |||  ||||||  ||
                              CGTCGT   TGT  TGTATT  CG
                                 GTC   __     GT
GAM245  KIAA0227 3' ATCATTGTGCAATATGCTGT   60695      GTTAC
                              GCGGTA    GTTGCATAGTGGT
                              ||||||    ||||||||||||
                              TGTCGT    TAACGTGTTACTA
                                 A____
GAM245  KIAA0247 3' CGCTTGCTGTGCTGCTGC    28397       T   TT   T  TG
                              GCGGTAGT ACG  GCA AG  G
                              |||||||| |||  ||| ||  |
                              CGTCGTCG TGT  CGT TC  C
                                   _  __  _ GT
GAM245  KIAA0252 3' ACTAAACAGGCCTGACTGCTGT 62787         C   GCA_
                              GCGGTAGTTA GTT    TAGT
                              |||||||||| |||    ||||
                              TGTCGTCAGT CGG    ATCA
                                    C   ACAA
GAM245  KIAA0258 3' CGTTATGAGGATTACTG     28813        ACGTTG    TG
                              CGGTAGTT     CATAG  G
                              ||||||||     |||||  |
                              GTCATTAG     GTATT  C
                                   GA____     GT
GAM245  KIAA0261 3' GCTGCTGTTAGTGCAACTGCTG 68181         A    C    TG
           T                   GCGGTAGTT CGTTG ATAG  GT
                              ||||||||| ||||| ||||  ||
                              TGTCGTCAA GTGAT TGTC  CG
                                   C    _   GT
GAM245  KIAA0261 3' ACTGCTGTGTATGTTGAGCCAC 68177      A  ACGT_     TG
           TGT                   GCGGT GTT    TGCATAG  GT
                              |||||  |||    |||||||  ||
                              TGTCA CGA    ATGTGTC  CA
                                 C  GTTGT     GT
GAM245  KIAA0276 3' ATTATGTGTATATTGCTGT    70961        _  GTT
                              GCGGTAGT TAC   GCATAGT
                              ||||||||  |||  |||||||
                              TGTCGTTA ATG   TGTATTA
                                   T  ___
GAM245  KIAA0298 3' GTACTGTGCTGTGACCGCTGC  76581     TA    TT     GG
                              GCGG  GTTACG  GCATAGT  T
                              ||||  ||||||  |||||||  |
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```
                              CGTC  CAGTGT  CGTGTCA  G
                                GC     __      TT
GAM245  KIAA0298 3' TGACATAGGTGGCTGCTGT   76582          GT_ _
                              GCGGTAGTTAC   TG CA
                              ||||||||||   || ||
                              TGTCGTCGGTG   AC GT
                                    GAT  A
GAM245  KIAA0310 5' ACCACTGTGAGCCAGAATTACC 81673         AC_  G
           GT                   GCGGTAGTT   GTT CATAGTGGT
                              |||||||||   ||| |||||||||
                              TGCCATTAA   CGA GTGTCACCA
                                  GAC  _
GAM245  KIAA0323 3' ACCACTGTGTGGTTAGTAAT  63252      G__ TG
                              GTTAC   T  CATAGTGGT
                              |||||  |  |||||||||
                              TAATG   G  GTGTCACCA
                                 ATT GT
GAM245  KIAA0329 3' ACCCGTGGCTGGCGTGATTGCT 29268           _ ATAGT
           GC                   GCGGTAGTTACGTT GC    GGT
                              ||||||||||||||  ||    |||
                              CGTCGTTAGTGCGG CG    CCA
                                     T  GTGC_
GAM245  KIAA0349 3' ATTATTATGTACCACACAACTA 92304       AC  __
           CT                   GGTAGTT  GT  TGCATAGTGGT
                              |||||||  ||  ||||||||||
                              TCATCAA  CA  ATGTATTATTA
                                  CA  CC
GAM245  KIAA0410 3' TGTTTACGTAACTTTTGC    28779     T      T_
                              GCGG AGTTACGT  GCA
                              ||||  ||||||||  |||
                              CGTT TCAATGCA  TGT
                                T       TT
GAM245  KIAA0410 3' TTTCTTATGTGACTTAGCTGCT 28785         C  TG    TGGT
           GT                   GCGGTAGTTA GT  CATAG
                              ||||||||||  ||  |||||
                              TGTCGTCGAT CA  GTATT
                                    T  GT    CTTTC
GAM245  KIAA0410 3' GTTACTGTGTAATTGATTTGC  28777     GT    C       GG
                              GCG  AGTTA GTTGCATAGT  T
                              |||  |||||  ||||||||||  |
                              CGT  TTAGT TAATGTGTCA  G
                                __    _        TT
GAM245  KIAA0429 3' ATTATTGTGCTTTAGTTGCTA  28549     T  GTT_
                              TAGT AC    GCATAGTGGT
                              ||||  ||    ||||||||||
                              ATCG TG    CGTGTTATTA
                                T  ATTT
GAM245  KIAA0443 5' CTCTGCTGGTGGTGGGGTTGCT 28184        TA  TT  A   TG T
           GC                   GCGGTAGT  CG  GC TAG  G
                              ||||||||  ||  || |||  |
```

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                                CGTCGTTG  GT  TG GTC  C
                                    GG  GG  _   GT TCG
GAM245  KIAA0446 5' TCCCTGTGATGTGGCTACC   68880          TG    T  T
                                GGTAGTTACGT  CATAG GG
                                ||||||||||  ||||| ||
                                CCATCGGTGTA  GTGTC CC
                                      __    _ TG
GAM245  KIAA0469 3' ACTGTGGATGTCATTGCTGT   29321        T    G
                                GCGGTAGT ACGTT CATAGT
                                |||||||| ||||| ||||||
                                TGTCGTTA TGTAG GTGTCA
                                    C    _
GAM245  KIAA0469 3' GCCAGATGGCGTGGCTGGTTGC 29335    GG _      TG   AG
                                GC  T AGTTACGT  CAT  TGGT
                                ||  | ||||||||  |||  ||||
                                CG  G TCGGTGCG  GTA  ACCG
                                 TT G       __   G_
GAM245  KIAA0493 5' CGCTGTTGGGCTGCTGC     64274         ACGTTGC
                                GCGGTAGTT      ATAGTG
                                |||||||||      ||||||
                                CGTCGTCGG      TGTCGC
                                     GT_____
GAM245  KIAA0495 3' GCTGCTGTGCACGACGTGGATG 62593      G     __      TG
           CCGT                    CGGTA TTACGT  TGCATAG  GT
                                |||||  ||||||  |||||||  ||
                                GCCGT GGTGCA  ACGTGTC  CG
                                   A     GC      GT
GAM245  KIAA0513 5' CAGGTGAGCTGCTGT       28346         ACGTTG   AG
                                GCGGTAGTT     CAT  TG
                                |||||||||     |||  ||
                                TGTCGTCGA     GTG  AC
                                     _______  G_
GAM245  KIAA0544 3' GTCACTGTGGCGGCCTGGCTGT 70907     GT    C    _     GT
           CGC                     GCG  AGTTA GTTGC ATAGTG
                                |||  ||||| ||||| ||||||
                                CGC  TCGGT CGGCG TGTCAC
                                  TG    C    G     TG
GAM245  KIAA0547 3' GTTACTAAGCCATGTGGCTCCG 28915     T      T  A   GG
           C                     GCGG AGTTACGT GC TAGT  T
                                |||| |||||||| || ||||  |
                                CGCC TCGGTGTA CG ATCA  G
                                  _      C  A   TT
GAM245  KIAA0547 3' GCTATTGACAACATGTGACTAT 28911          __   CA
           T                     GGTAGTTAC  GTTG  TAGTGGT
                                |||||||||  ||||  |||||||
                                TTATCAGTG  CAAC  GTTATCG
                                     TA   A_
GAM245  KIAA0556 3' GCTGTGCTCACTGATGTGGCTG 69086          _____     GGT
           CT                     TAGTTACGTT    GCATAGT
                                ||||||||||    |||||||
```

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                                GTCGGTGTAG    CGTGTCG
                                     TCACT        T
GAM245  KIAA0556 3' TCATCTGCGTGCTGCTGC    69088        T   TGCATA
                                GCGGTAGT ACGT     GTGG
                                |||||||| ||||     ||||
                                CGTCGTCG TGCG     TACT
                                    _   TC_____
GAM245  KIAA0560 3' ACCAGTGAATGTGACTAATGT  61499     G        G   AG
                                GCG TAGTTACGTT CAT  TGGT
                                ||| |||||||||| |||  ||||
                                TGT ATCAGTGTAA GTG  ACCA
                                  A        _  __
GAM245  KIAA0561  5' GCCACGCCGAGGACGTGGCTGC 65887            GCATA_
            CGC                   GCGGTAGTTACGTT     GTGGT
                                |||||||||||||     |||||
                                CGCCGTCGGTGCAG     CACCG
                                       GAGCCG
GAM245  KIAA0565 3' ATTGCTATGCAATAGCACAGT  66886    G  A   AC       TG
                                GC GT GTT  GTTGCATAG  GT
                                || || |||  |||||||||  ||
                                TG CA CGA  TAACGTATC  TA
                                 A  _  __       GT
GAM245  KIAA0596 3' CATTTGAAATTACTGC      62827         A  TTGCAT
                                GCGGTAGTT CG     AGTG
                                |||||||| ||     ||||
                                CGTCATTAA GT     TTAC
                                     A  _______
GAM245  KIAA0599 3' GTTGTTGTGCTGACCCTGTGGT 77186   T  TT  ___  _     TG
            TGTCGC                  AG  AC   GTT GCATAG  GT
                                 ||  ||   ||| ||||||  ||
                                 TT  TG   CAG CGTGTT  TG
                                G  GG  TCC   T     GT
GAM245  KIAA0628 3' CCACTGTGCAGCCCTACT    28866      TTAC
                                GGTAG    GTTGCATAGTGG
                                |||||    ||||||||||||
                                TCATC    CGACGTGTCACC
                                   C___
GAM245  KIAA0635 3' ACCATATATAACGTGTTATTGC 27693      AGT      C   G
                                GCGGT   TACGTTG ATA TGGT
                                |||||   ||||||| ||| ||||
                                CGTTA   GTGCAAT TAT ACCA
                                   TT_      A  _
GAM245  KIAA0637 3' CCAGAGGCGTGGCTGCC     29237           GCATAG
                                GGTAGTTACGTT     TGG
                                ||||||||||||     |||
                                CCGTCGGTGCGG     ACC
                                       AG____
GAM245  KIAA0664 3' TACAGGTGCCGACGTGATGTCG 64288     GT G       _   AG  GT
            C                    GCG  A TTACGTTG CAT  TG
                                |||  | ||||||||  |||  ||
```

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                                CGC  T AGTGCAGC GTG  AC
                                  TG _       C   G_  ATT
GAM245  KIAA0664  3'  ACTGGCGTGGTCTGGCTGCTGC 64285          CG TG A_
                                GCGGTAGTTA  T  C  TAGT
                                ||||||||||  |  |  ||||
                                CGTCGTCGGT  G  G  GTCA
                                      CT GT CG
GAM245  KIAA0767  3'  ATCATTGCCAGTGTGACTTTTG 60625      T        CA
              T                  GCGG AGTTACGTTG  TAGTGGT
                                 ||||  ||||||||||  |||||||
                                 TGTT TCAGTGTGAC  GTTACTA
                                   T        C_
GAM245  KIAA0794  3'  ACCACTATGGTTATTGATTGTC 80406    _     CGTTG
              C                   GG TAGTTA    CATAGTGGT
                                  ||  ||||||    |||||||||
                                  CC GTTAGT    GTATCACCA
                                   T     TATTG
GAM245  KIAA0826  3'  CCAGAAATGTAATTAC      82637          GCATAG
                                GTAGTTACGTT     TGG
                                ||||||||||      |||
                                CATTAATGTAA     ACC
                                      AG____
GAM245  KIAA0828  3'  ACCACAGGTGTGTGCTACCGT  81189        T  GTT   A_
                                GCGGTAGT AC   GCAT  GTGGT
                                ||||||||  ||   ||||  |||||
                                TGCCATCG TG   TGTG  CACCA
                                   _  ____    GA
GAM245  KIAA0828  3'  CCAGAGTGTGGTTACTGC    81193       TTACG TG   AG   T
                                GCGGTAG    T  CAT  TGG
                                |||||||    |  |||  |||
                                CGTCATT    G  GTG  ACC
                                   _____ GT   AG   C
GAM245  KIAA0836  3'  GCCTTAACAATGTGGCTGTCC  64564    _        CA   T
                                GG TAGTTACGTTG  TAG GGT
                                ||  ||||||||||  |||  |||
                                CC GTCGGTGTAAC  ATT CCG
                                 T         A_  _
GAM245  KIAA0841  3'  TGCAAGTTAACTGCTGT     71404          CG
                                GCGGTAGTTA  TTGCA
                                ||||||||||  |||||
                                TGTCGTCAAT  AACGT
                                      TG
GAM245  KIAA0844  3'  TGCTGTGAATAGCACTGT    30206      A   CGTTG    TG
                                GCGGT GTTA    CATAG  G
                                |||||  ||||    |||||  |
                                TGTCA CGAT    GTGTC  T
                                   _   AA___    GT
GAM245  KIAA0855  3'  ATTAAAAAATGTAACTGCT   30404           GCA
                                GGTAGTTACGTT   TAGT
                                ||||||||||||   ||||
```

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                                TCGTCAATGTAA  ATTA
                                      AAA
GAM245  KIAA0863  3'  CACTGTGCTGCTCTGC     29874     T  TACGTT
                                GCGG AGT     GCATAGTG
                                |||| |||     ||||||||
                                CGTC TCG     CGTGTCAC
                                  _  T_____
GAM245  KIAA0863  3'  CACTGTGCTGCTCTGC     95243     T  TACGTT
                                GCGG AGT     GCATAGTG
                                |||| |||     ||||||||
                                CGTC TCG     CGTGTCAC
                                  _  T_____
GAM245  KIAA0889  5'  CTATTATTGCACTACTGC    31134       TACGTT  _
                                GCGGTAGT     GCA TAGTGG
                                ||||||||     ||| ||||||
                                CGTCATCA     CGT ATTATC
                                     _______  T
GAM245  KIAA0930  3'  GTTATTAAAAGCGAGCTATTGC 70552        A   GCA    GT
                                GCGGTAGTT CGTT  TAGTG
                                ||||||||| ||||  |||||
                                CGTTATCGA GCGA  ATTAT
                                     _   AA_    TGT
GAM245  KIAA0931  3'  GCAGCGTGGTCATTGC     67422      AG
                                GCGGT  TTACGTTGC
                                |||||  |||||||||
                                CGTTA  GGTGCGACG
                                   CT
GAM245  KIAA0940  3'  CGCTGTGTTTTCTGTGCTGT  29868      GTTACGTT
                                GCGGTA       GCATAGTG
                                ||||||       ||||||||
                                TGTCGT       TGTGTCGC
                                   GTCTTT__
GAM245  KIAA0970  3'  GCTGCTTCTCCCATAACTGCTG 29964        CGTTGCAT  TG
          C                     GCGGTAGTTA       AG  GT
                                ||||||||||       ||  ||
                                CGTCGTCAAT       TC  CG
                                     ACCCTCT_  GT
GAM245  KIAA0972  3'  CCACTGTGCAGTTCAAC    30009     ACG
                                GTT   TTGCATAGTGG
                                |||   ||||||||||
                                CAA   GACGTGTCACC
                                  CTT
GAM245  KIAA0976  3'  GTCATTCGTACCTGCTGT    29894       T   T_ _
                                GCGGTAG TACG  TG C
                                ||||||| ||||  || |
                                TGTCGTC ATGC  AC G
                                    C   TT  T
GAM245  KIAA0976  3'  CAGGTGTAGCTCCCGC     29888     T  TACGT    AG
                                GCGG AGT    TGCAT  TG
                                |||| |||    |||||  ||
```

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                                CGCC TCG    ATGTG  AC
                                  C  _____    G_
GAM245  KIAA0993  3' GCTATTATGTAACTGTGGGCC  64144    AG   _
                                GGT  TTAC GTTGCATAGTGGT
                                |||  |||| ||||||||||||
                                CCG  GGTG CAATGTATTATCG
                                  __   T
GAM245  KIAA1001  5' ATCTCTAGTGGTGGCTGCCGT  30287         GTT  A   T
                                GCGGTAGTTAC   GC TAG GGT
                                ||||||||||   || ||| |||
                                TGCCGTCGGTG   TG ATC CTA
                                      G__  _   T
GAM245  KIAA1009  3' GCTATTGTAAATATTGCTGC   29700       TACG    _
                                GCGGTAGT    TTGCA TAGT
                                ||||||||    ||||| ||||
                                CGTCGTTA    AATGT ATCG
                                     TA__    T
GAM245  KIAA1013  3' ATTGCGTGATGAGCTATTGT   88885        A   TG A
                                GCGGTAGTT CGT  C TAGT
                                ||||||||| |||  | ||||
                                TGTTATCGA GTA  G GTTA
                                     _  GT C
GAM245  KIAA1018  3' ATCACTGTTCTGGCTGTCG   30347    GT    CGTTGC
                                CG  AGTTA     ATAGTGGT
                                ||  |||||     ||||||||
                                GC  TCGGT     TGTCACTA
                                 TG    CT____
GAM245  KIAA1041  3' CCATTATTTGTAACTG      30130        TTGC
                                TAGTTACG    ATAGTGG
                                ||||||||    |||||||
                                GTCAATGT    TATTACC
                                     T___
GAM245  KIAA1079  5' CGCTGGCGTTGCTGCTGT    29883        T    TGCA   TG
                                GCGGTAGT ACGT    TAG  G
                                |||||||| ||||    |||  |
                                TGTCGTCG TGCG    GTC  C
                                     T   _____   GT
GAM245  KIAA1111  3' ATTATCCACGTGGCTGTGGC   96205    G        T C
                                GC GTAGTTACGT G ATAGT
                                || |||||||||| | |||||
                                CG TGTCGGTGCA C TATTA
                                 G        _ C
GAM245  KIAA1126  3' GCCAGGGACAGGCGTGACTGTT 71929    GG        GCATAG
           GT                    GC  TAGTTACGTT     TGGT
                                ||  ||||||||||     ||||
                                TG  GTCAGTGCGG     ACCG
                                 TT         ACAGGG
GAM245  KIAA1143  3' GCCGTTGTGTCTGGTGGTTGCA 68681    G    TT  GTT
           GT                    GC GTAG  AC   GCATAGTGGT
                                || ||||  ||   ||||||||||
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                                TG CGTT  TG   TGTGTTGCCG
                                 A   GG  GTC
GAM245  KIAA1160 3' GCTACTGTGTGGATCCATTTAT 40371      TTACG_ TG
            T                    GGTAG     T  CATAGTGGT
                                 |||||     |  |||||||||
                                 TTATT     G  GTGTCATCG
                                   TACCTA GT
GAM245  KIAA1171 3' ACCAGGAAGACGGATTGCTGC  87977        A   GCATAG
                                 GCGGTAGTT CGTT     TGGT
                                 |||||||||  ||||     ||||
                                 CGTCGTTAG GCAG     ACCA
                                      _   AAGG__
GAM245  KIAA1185 3' GCCCCTCCCCACGTGACTGTCG 62605    GT      TGCAT  T
            T                    GCG  AGTTACGT    AG GGT
                                 |||  ||||||||    || |||
                                 TGC  TCAGTGCA    TC CCG
                                   TG       CCCC_  C   T
GAM245  KIAA1190 3' GCTGCTGTGCCTCACAGCGCTG 71101      A  ACGTT    TG
            T                    GCGGT GTT    GCATAG  GT
                                 |||||  |||    ||||||  ||
                                 TGTCG CGA    CGTGTC  CG
                                   _  CACTC     GT
GAM245  KIAA1219 3' ACCACCTCTTTGGGTGGCTACT 61362         GTTGCATA
            GT                    GCGGTAGTTAC       GTGGT
                                  ||||||||||        |||||
                                  TGTCATCGGTG       CACCA
                                       GGTTTCTC
GAM245  KIAA1228 3' ATTGTTATGCAATTTTTATCCT 65037     TAGTTAC       TG
            GT                    GCGG      GTTGCATAG  GT
                                  ||||      |||||||||  ||
                                  TGTC      TAACGTATT  TA
                                    CTATTTT       GT
GAM245  KIAA1229 5' ATCGCGGCGACGGCGGGCTGTC 62063    GT   TA__     ATA
            GT                    GCG  AGT   CGTTGC   GTGGT
                                  |||  |||   ||||||   |||||
                                  TGC  TCG   GCAGCG   CGCTA
                                    TG   GGCG     G__
GAM245  KIAA1240 3' ACTGTAATTTGTAATATAACTG 66729         CG    TA__ TG
            CTGT                    CGGTAGTTA  TTGCA    G  GT
                                  |||||||||  |||||    |  ||
                                  GTCGTCAAT  AATGT    T  CA
                                       AT     TTAA GT
GAM245  KIAA1255 5' ACTACTGTGCAGAAATTATTGC 67160         ACG
                                  GCGGTAGTT   TTGCATAGTGGT
                                  |||||||||   ||||||||||||
                                  CGTTATTAA   GACGTGTCATCA
                                       A__
GAM245  KIAA1255 5' GCACACTGATGAACTACTGT   67163         A   GCAT   _
                                  GCGGTAGTT CGTT    AGTG GT
                                  |||||||||  ||||    ||||  ||
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                                TGTCATCAA GTAG   TCAC CG
                                   _  ____   A
GAM245  KIAA1257 3' ATTACAGGCATGAGCTGCCGC 62728       A  T  ATA
                                GCGGTAGTT CGT GC  GTGGT
                                ||||||||| ||| ||  |||||
                                CGCCGTCGA GTA CG  CATTA
                                   _  _ GA_
GAM245  KIAA1257 3' ATTACAGGCGTGAGCTACCGC 62729       ACGT  ATA
                                GCGGTAGTT   TGC  GTGGT
                                |||||||||   |||  |||||
                                CGCCATCGA   GCG  CATTA
                                     GT__  GA_
GAM245  KIAA1265 3' GCTTGGCAACCAGTGTAGCTGC 70791       ____   AT  GGT
           TGT                   GTAGTTAC   GTTGC  AGT
                                ||||||||   |||||  |||
                                CGTCGATG   CAACG  TCG
                                     TGAC   GT    T
GAM245  KIAA1266 3' GCCACTTGGCAGTGGGGCTGCT 66122       TA    AT
           GC                    GCGGTAGT  CGTTGC  AGTGGT
                                ||||||||  ||||||  ||||||
                                CGTCGTCG  GTGACG  TCACCG
                                     GG    GT
GAM245  KIAA1284 5' CCACTCGTAGCTATTGC    63942         TTGCAT   T
                                GCGGTAGTTACG    AGTGG
                                ||||||||||||    |||||
                                CGTTATCGATGC    TCACC
                                   ______   T
GAM245  KIAA1322 3' GTTGCTGAGCCAGTGGCTGCC 72741       GTT  A   GG
                                GGTAGTTAC   GC TAGT  T
                                |||||||||   || ||||  |
                                CCGTCGGTG   CG GTCG  G
                                     AC_ A   TT
GAM245  KIAA1337 5' CTGCGCAGCGTGGTGGCCGC  72680     AG       A
                                GCGGT  TTACGTTGC TAG
                                |||||  ||||||||| |||
                                CGCCG  GGTGCGACG GTC
                                   GT       C
GAM245  KIAA1350 3' ACTAATTTAATGTGAATACTGT 72704      G      CA_
                                GCGGTA TTACGTTG   TAGT
                                ||||||| ||||||||  ||||
                                TGTCAT AGTGTAAT   ATCA
                                   A       TTA
GAM245  KIAA1371 3' ATTATTGTGCAATAAATACT  89042     GTTAC
                                GGTA    GTTGCATAGTGGT
                                ||||    ||||||||||||
                                TCAT    TAACGTGTTATTA
                                  AAA__
GAM245  KIAA1388 3' TCGCTGGGTGGCTACGGC    93582    G      GTTGCA
                                GC GTAGTTAC     TAGTGG
                                || ||||||||     ||||||
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```
                                CG CATCGGTG     GTCGCT
                                 G      G_____
GAM245  KIAA1456 5' ACCGTGGGCTGTGACTACTGT  66986          TT  ATA
                                GCGGTAGTTACG  GC   GTGGT
                                ||||||||||||  ||   |||||
                                TGTCATCAGTGT  CG   TGCCA
                                      __  GG_
GAM245  KIAA1464 5' GCTGGGGGCGGGCTGCCGT   68268         A   GCA
                                GCGGTAGTT CGTT   TAGT
                                |||||||||  ||||   ||||
                                TGCCGTCGG GCGG   GTCG
                                      _   GG_
GAM245  KIAA1493 3' CCATCCACGAAGCTGCTGT   64157         A   T CATA
                                GCGGTAGTT CGT G    GTGG
                                |||||||||  ||| |    ||||
                                TGTCGTCGA GCA C    TACC
                                     A   _ C___
GAM245  KIAA1497 5' TCAAGATCTGATGTGGCTATT  67519           C  AG  GT
                                GGTAGTTACGTTG AT  TG
                                ||||||||||||| ||  ||
                                TTATCGGTGTAGT TA  AC
                                      C  GA  TG
GAM245  KIAA1511 3' ATTATTGTAAACTTGTAACTAT 70163         __  GC
          T                      GGTAGTTAC  GTT  ATAGTGGT
                                 |||||||||  |||  ||||||||
                                 TTATCAATG  CAA  TGTTATTA
                                      TT   A_
GAM245  KIAA1522 3' CCACAGCAGCGTGGCTGCC   64972           ATA   T
                                GGTAGTTACGTTGC   GTGG
                                ||||||||||||||   ||||
                                CCGTCGGTGCGACG   CACC
                                      A__    T
GAM245  KIAA1545 3' ACTGCTGTGTGTTTTCTTCCGC 60687     T  TT_  GTT     TG
                                GCGG AG   AC   GCATAG  GT
                                ||||  ||   ||   ||||||  ||
                                CGCC TC   TG   TGTGTC  CA
                                  T  TTT  ___     GT
GAM245  KIAA1560 3' ATTGCTGCAAAGAGCTGCTGC  64173         ACG    TA TG
                                GCGGTAGTT   TTGCA  G  GT
                                |||||||||   |||||  |  ||
                                CGTCGTCGA   AACGT  C  TA
                                     GA_    __ GT
GAM245  KIAA1582 5' CGCTGTTAGTACTGCTGC    65371         T  GTTGC    TG
                                GCGGTAGT AC    ATAG  G
                                ||||||||  ||    ||||  |
                                CGTCGTCA TG    TGTC  C
                                     _  AT___    GT
GAM245  KIAA1596 5' ATCAGATACAGATGAAATTGCT 70913         A    GCATAG
          GC                     GCGGTAGTT CGTT     TGGT
                                 |||||||||  ||||     ||||
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                                CGTCGTTAA GTAG     ACTA
                                     A    ACATAG
GAM245  KIAA1644  3'  GCTGTGGGTGTGGCTG      85029         TTG
                                TAGTTACG   CATAGT
                                ||||||||   ||||||
                                GTCGGTGT   GTGTCG
                                    GG_
GAM245  KIAA1655  5'  ACTGTTATGTAACAGGACC    66587     AGTTAC       TG
                                GGT     GTTGCATAG  GT
                                |||     |||||||||  ||
                                CCA     CAATGTATT  CA
                                  GGA___        GT
GAM245  KIAA1673  3'  GCTACTGTGATTGATAGCATTG 70783       A    _  TTG
            T                    GCGGT GTTA CG   CATAGTGGT
                                ||||| |||| ||   |||||||||
                                TGTTA CGAT GT   GTGTCATCG
                                  _    A  TA_
GAM245  KIAA1674  5'  ACCAAGGAGGATGAGCTGCTGT 68769          A    GCATAG
                                GCGGTAGTT CGTT     TGGT
                                |||||||| ||||     ||||
                                TGTCGTCGA GTAG     ACCA
                                     _   GAGGA_
GAM245  KIAA1674  3'  GCCGGGCGTGGTGGCTGT    68782       AG      __
                                GCGGT  TTACGTT  GC
                                |||||  |||||||  ||
                                TGTCG  GGTGCGG  CG
                                   GT      GC
GAM245  KIAA1676  5'  CAAGTGTTGCTGCTGT      93122         TACGTT    AG
                                GCGGTAGT     GCAT  TG
                                ||||||||     ||||  ||
                                TGTCGTCG     TGTG  AC
                                     T_____    A_
GAM245  KIAA1691  3'  GTCAATGTAATTTCTGT     92563      T        _
                                GCGG AGTTACGTTG C
                                |||| |||||||||| |
                                TGTC TTAATGTAAC G
                                  T        T
GAM245  KIAA1719  3'  ACTGAGGCTCAGGTGACTGCTG 68154           GTT_  A_   GGT
            C                    GCGGTAGTTAC    GC  TAGT
                                ||||||||||    ||  ||||
                                CGTCGTCAGTG    CG  GTCA
                                     GACT  GA
GAM245  KIAA1751  3'  GCTGTCCAGCGTGGCTGTC    71701    GT        C
                                G  AGTTACGTTG ATAGT
                                |  |||||||||| |||||
                                C  TCGGTGCGAC TGTCG
                                 TG        C
GAM245  KIAA1751  3'  GCTCTGCAGCTGTGGCTGTTGT 71700     GG      _     T
                                GC  TAGTTAC GTTGCA AGT
                                ||  ||||||| |||||| |||
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```
                              TG  GTCGGTG CGACGT TCG
                               TT      T     C
GAM245  KIAA1813 5' GCCATTGTGCAGACTCTGCC  70301      TTACG
                              GGTAG    TTGCATAGTGGT
                              |||||    ||||||||||||
                              CCGTC    GACGTGTTACCG
                                 TCA__
GAM245  KIAA1817 3' TGCAGGCTTAGCTGCCGC    68231         C _
                              GCGGTAGTTA GT TGCA
                              |||||||||| || ||||
                              CGCCGTCGAT CG ACGT
                                    T  G
GAM245  KIAA1822 3' GCTATGCCAATAATGTGGCTG  67571          ____     GGT
                              TAGTTACGTT    GCATAGT
                              |||||||||    |||||||
                              GTCGGTGTAA    CGTATCG
                                    TAAC
GAM245  KIAA1826 3' GCTACTGTGCAATGCATACC   67218     GTTA
                              GGTA   CGTTGCATAGTGGT
                              ||||   ||||||||||||||
                              CCAT   GTAACGTGTCATCG
                                AC__
GAM245  KIAA1877 3' ATTATTATGCATGTTTCTGTC  66163   GT  TT   T
                              G  AG  ACGT GCATAGTGGT
                              |  ||  |||| ||||||||||
                              C  TC  TGTA CGTATTATTA
                               TG  TT   _
GAM245  KIAA1877 3' GCCATTGAGTATGTATTACTGC 66172        T   T  A
                              GCGGTAGT ACGT GC TAGTGGT
                              |||||||| |||| || |||||||
                              CGTCATTA TGTA TG GTTACCG
                                   _   _ A
GAM245  KIAA1922 3' ATTGCTGTGTGATGTTAGACTG 73616      AGTT   TG    TG
           C                   GCGGT   ACGT  CATAG  GT
                              |||||   ||||  |||||  ||
                              CGTCA   TGTA  GTGTC  TA
                                 GAT_   GT    GT
GAM245  KIAA1924 3' GCCTCCCTTGATGAGCTGCTGC 73678        A   GCATAGT
                              GCGGTAGTT CGTT      GGT
                              ||||||||| ||||      |||
                              CGTCGTCGA GTAG      CCG
                                   _   TTCCCT_
GAM245  KIAA1948 5' CTACATGTAACGTGACTTCTGT 82401     T         A   T
                              GCGG AGTTACGTTGCAT GTGG
                              |||| |||||||||||| ||||
                              TGTC TCAGTGCAATGTA CATC
                                T          _   C
GAM245  KIAA1969 3' ATCAGAAAGATGTGACTACT   78729          GCATAG
                              GGTAGTTACGTT     TGGT
                              ||||||||||||     ||||
```

```
                                TCATCAGTGTAG     ACTA
                                      AAAG__
GAM245  KIF13B   3'  GCTGGGAATGTGACTGCTG   82825          GCA
                                CGGTAGTTACGTT   TAGT
                                ||||||||||||   ||||
                                GTCGTCAGTGTAA   GTCG
                                      GG_
GAM245  KIF13B   3'  GCTGGGAATGTGACTGCTG   30911          GCA
                                CGGTAGTTACGTT   TAGT
                                ||||||||||||   ||||
                                GTCGTCAGTGTAA   GTCG
                                      GG_
GAM245  LAT1-3TM 5'  CCGAAGATTGGCTACTGT    68600         C   GCATAG
                                GCGGTAGTTA GTT     TGG
                                |||||||||| |||     |||
                                TGTCATCGGT TAG     GCC
                                     _   AA____
GAM245  LIG-1    3'  GCTGCTGTGCGGTGGGACTCC  63897    T   TA  TT     TG
                                GG AGT  CG  GCATAG  GT
                                || |||  ||  ||||||  ||
                                CC TCA  GT  CGTGTC  CG
                                 _  GG  GG     GT
GAM245  LOXL4    3'  GTCACTGCACACTCCTAGCTGC 49871        C__ _    TA   GT
           TGC                    GGTAGTTA   GT TGCA  GTG
                                |||||||   || ||||  |||
                                TCGTCGAT   CA ACGT  CAC
                                     CCT  C    __   TG
GAM245  LRBA     3'  TTACTGTGTGGAATTCTGT    22055     T   ACG TG
                                GCGG AGTT   T  CATAGTGG
                                |||| ||||   |  ||||||||
                                TGTC TTAA   G  GTGTCATT
                                  _   ____ GT
GAM245  LSM1     5'  CGCTGTGCATTGCAGC      27093     A  T
                                GTT CG TGCATAGTG
                                ||| || |||||||||
                                CGA GT ACGTGTCGC
                                  C  T
GAM245  LYPLA3   3'  GCTGCTGATGGTGGAACTGCTG 24631         A  TT CA   TG
           T                     GCGGTAGTT CG  G  TAG  GT
                                |||||||| ||  |  |||  ||
                                TGTCGTCAA GT  T  GTC  CG
                                     G  GG A_   GT
GAM245  M9       5'  GCCGGAAAGCGTGGCGGCTGC  61680      A       GCATAG
                                GCGGT GTTACGTT     TGGT
                                ||||| ||||||||     ||||
                                CGTCG CGGTGCGA     GCCG
                                   G       AAG____
GAM245  MAL2     3'  TCATTATGCAATAATCACATTG 53555      A  TAC_         GT
           C                     GCGGT GT    GTTGCATAGTG
                                ||||| ||    ||||||||||
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                                CGTTA CA   TAACGTATTAC
                                  _ CTAA        TG
GAM245  MAN1    3'  ACTATTATGCAGCTTATTTTAC 26709      T_ C
            C                    GGTAG  TA GTTGCATAGTGGT
                                 |||||  || ||||||||||||
                                 CCATT  AT CGACGTATTATCA
                                   TT  T
GAM245  MAP     3'  ACATTATTGTAACTACCGT   43052          TTGC    GT
                                 GCGGTAGTTACG   ATAGTG
                                 ||||||||||||   ||||||
                                 TGCCATCAATGT   TATTAC
                                       ____     AG
GAM245  MAP2K4  3'  CGCTATGTGACTTGCGC    11546    G   TTAC  TG
                                 GCG TAG   GT  CATAGTG
                                 ||| |||   ||  |||||||
                                 CGC GTT   CA  GTATCGC
                                  _  ____  GT
GAM245  MAP2K4  3'  TCGTGGCACGTATTGCTGT   11551       T   T  ATAG
                                 GCGGTAGT ACGT GC   TGG
                                 |||||||| |||| ||   |||
                                 TGTCGTTA TGCA CG   GCT
                                     _   _ GT__
GAM245  MAP2K6  3'  GCTGTTGTGACTGCTGC    10870          TT_
                                 GCGGTAGTTACG  GC
                                 ||||||||||||  ||
                                 CGTCGTCAGTGT  CG
                                       TGT
GAM245  MAP2K6  3'  GCTGTTGTGACTGCTGC    49244          TT_
                                 GCGGTAGTTACG  GC
                                 ||||||||||||  ||
                                 CGTCGTCAGTGT  CG
                                       TGT
GAM245  MAP3K3  3'  GCTGCTGGGCTCAGTGAAGTTG 9998       __   GTT  A  TG
            CTGC                   CGGTAG  TTAC  GC TAG  GT
                                 ||||||  ||||  || |||  ||
                                 GTCGTT  AGTG  CG GTC  CG
                                    GA   ACT  G  GT
GAM245  MAPK11  3'  GCCGGGGTGGGTGTGCTGTTGC 10848   GG   T  TTG  AG
                                 GC  TAGT ACG  CAT  TGGT
                                 ||  |||| |||  |||  ||||
                                 CG  GTCG TGT  GTG  GCCG
                                  TT   _  GG_  GG
GAM245  MAPK8   3'  CGCTGTAGATGACTACT    10842      TA   GC   TG
                                 GGTAGT  CGTT  ATAG  G
                                 ||||||  ||||  ||||  |
                                 TCATCA  GTAG  TGTC  C
                                    __   A_   GT
GAM245  MAPK8   3'  CGCTGTAGATGACTACT    57392      TA   GC   TG
                                 GGTAGT  CGTT  ATAG  G
                                 ||||||  ||||  ||||  |
```

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                                TCATCA  GTAG  TGTC  C
                                   __   A_   GT
GAM245  MAPKAPK2  3'  GCTGGGGTGAGGCTGCCGT   16472        ACG TG A_
                                GCGGTAGTT   T  C  TAGT
                                |||||||||   |  |  ||||
                                TGCCGTCGG   A  G  GTCG
                                     ___ GT GG
GAM245  MARCKS   3'  TAACTGTGACTATTGT     9871          _
                                GCGGTAGTTAC GTTG
                                |||||||||||  ||||
                                TGTTATCAGTG CAAT
                                       T
GAM245  MBLL39   3'  ACTATAACAATGTAGTTACGC  58602    G  GT     C_
                                GCG TA  TACGTTG  ATAGT
                                |||  ||  |||||||  |||||
                                CGC AT  ATGTAAC  TATCA
                                  _  TG      AA
GAM245  MCF2L    3'  ACTGCCCCGCACGTGGCTGCCG 60840          T  ATA TG
            C                    GCGGTAGTTACGT GC   G  GT
                                |||||||||||||  ||   |  ||
                                CGCCGTCGGTGCA CG   C  CA
                                       _  CCC GT
GAM245  MDS018   3'  GCCATTTGGTGTGGCTGCAGC  41535    G       TT CAT
                                GC GTAGTTACG  G   AGTGGT
                                || |||||||||  |   ||||||
                                CG CGTCGGTGT  T   TTACCG
                                 A        GG ___
GAM245  MEIS3    3'  ATTATTAGTGTTTGACTACTGC 78275         CGT   A
                                GCGGTAGTTA   TGC TAGTGGT
                                ||||||||||   ||| |||||||
                                CGTCATCAGT   GTG ATTATTA
                                      TT_  _
GAM245  MGC:5244  5'  GCCTCCTAACGGGGCTGCTGT  48327        TA    CATAGT
                                GCGGTAGT  CGTTG     GGT
                                ||||||||  |||||     |||
                                TGTCGTCG  GCAAT     CCG
                                     GG    CCT___
GAM245  MGC10067  3'  GTAATGTGACCACTGT      58937      A
                                GCGGT GTTACGTTGC
                                |||||  ||||||||||
                                TGTCA CAGTGTAATG
                                   C
GAM245  MGC10200  3'  ACCCCTTCATGTGGCTGTTGT  58981    GG       TGCAT  T
                                GC  TAGTTACGT    AG GGT
                                ||  |||||||||    || |||
                                TG  GTCGGTGTA    TC CCA
                                 TT       CT___  C
GAM245  MGC11324  3'  ACCATTATGGTTATGGTCTACT 51162       TTA   TG_
            GC                    GCGGTAG   CGT   CATAGTGGT
                                |||||||   |||   |||||||||
```

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                                CGTCATC  GTA  GTATTACCA
                                   TG_  TTG
GAM245  MGC12679  3' GCTGCGGCCGCGTGGCTCCGC  51204     T      T  ATA TG
                                GCGG AGTTACGT GC  G  GT
                                |||| |||||||| ||  |  ||
                                CGCC TCGGTGCG CG  C  CG
                                  _      C  G__ GT
GAM245  MGC12966  3' ATTACTATGCCATGTGCTATT  51122      T   T
                                GGTAGT ACGT GCATAGTGGT
                                |||||| |||| ||||||||||
                                TTATCG TGTA CGTATCATTA
                                   _  C
GAM245  MGC13053  3' GCTTCAGTGTAGCTGCT    51133           CAT
                                GGTAGTTACGTTG  AGT
                                ||||||||||||  |||
                                TCGTCGATGTGAC  TCG
                                      T__
GAM245  MGC13071  3' ACTACGATGAGTGTGTGCTGCC 51084       _   TTG  A
          GT                   GCGGTAGT TACG  CAT GTGGT
                                |||||||| ||||  ||| |||||
                                TGCCGTCG GTGT  GTA CATCA
                                   T  GA_  G
GAM245  MGC13130  5' CGCTGTTGCTACTGC      51835        TACGTTGC
                                GCGGTAGT      ATAGTG
                                ||||||||      ||||||
                                CGTCATCG      TGTCGC
                                   T_______
GAM245  MGC14126  5' TCAGTAGGGCTGTGGCTGTCGC 51857    GT     TT  A_  G  GT
                                GCG  AGTTACG  GC  TA TG
                                |||  |||||||  ||  || ||
                                CGC  TCGGTGT  CG  AT AC
                                  TG     __ GG  G  TG
GAM245  MGC14859  3' GCCATATTCAGGTGTAGCTAAT 61919      _      GCATA
          TGC                  GCGGT AGTTACGTT    GTGGT
                                ||||| |||||||||    |||||
                                CGTTA TCGATGTGG    TACCG
                                   A       ACTTA
GAM245  MGC15416  5' GCTGCTGTGGGTGGCTGCT   56542       GTTG    TG
                                GGTAGTTAC   CATAG  GT
                                |||||||||   |||||  ||
                                TCGTCGGTG   GTGTC  CG
                                   G___    GT
GAM245  MGC15438  5' ACTGCTGTGTCCCTATTGCC  51786      TACGTT    TG
                                GGTAGT    GCATAG  GT
                                ||||||    ||||||  ||
                                CCGTTA    TGTGTC  CA
                                   TCCC__    GT
GAM245  MGC15854  3' GCTGCTGTGTAATTTAACTTGT 58849    GT   C       TG
                                GCG  AGTTA GTTGCATAG  GT
                                |||  ||||| |||||||||  ||
```

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                                TGT  TCAAT TAATGTGTC  CG
                                  __    T       GT
GAM245  MGC16025  5'  GCAGGCGGCGTGTGCTGCTGT  51919        _      ATA
                                GCGGTAGT TACGTTGC   GT
                                |||||||| ||||||||   ||
                                TGTCGTCG GTGCGGCG   CG
                                     T       GA_
GAM245  MGC16063  3'  CGCTGTCCTGGCCACTGC    53858      A   CGTTGC   TG
                                GCGGT GTTA     ATAG  G
                                ||||| ||||     ||||  |
                                CGTCA CGGT     TGTC  C
                                   C    CC____    GT
GAM245  MGC17919  3'  GCCCTAAAATGTGTTGCTGC   58221      AGT    GCA   T
                                GCGGT   TACGTT   TAG GGT
                                |||||   ||||||   ||| |||
                                CGTCG   GTGTAA   ATC CCG
                                   TT_     A__   _
GAM245  MGC19556  5'  ACTGTTGTGTCCTCGCTCTGC  53225     T   TACGTT     TG
                                GCGG AGT     GCATAG  GT
                                |||| |||     ||||||  ||
                                CGTC TCG     TGTGTT  CA
                                  _   CTCC__     GT
GAM245  MGC20496  3'  GTAAAGTGATTGCTGC      53435          G
                                GCGGTAGTTAC TTGC
                                |||||||||| ||||
                                CGTCGTTAGTG AATG
                                      A
GAM245  MGC22014  3'  TTTCCAGAGTTAGGCGGTGTGG 64502     TT   TT  A   ___   T
           TTGCCGT                GTAG  ACG  GC TAG   TGG
                                ||||  |||  || |||   |||
                                CGTT  TGT  CG ATT   ACC
                                  GG   GG  G   GAG   TTTG
GAM245  MGC2306   3'  GCTGCCTCCGCACCTGACTGCT 50964         C  T  ATA_ TG
           GC                   GCGGTAGTTA GT GC    G  GT
                                |||||||||| || ||    |  ||
                                CGTCGTCAGT CA CG    C  CG
                                     C  _  CCTC GT
GAM245  MGC23280  5'  GCTGCTGGGCGCGGGGTTGCTG 58396        TA   T  A   TG
           C                    GCGGTAGT  CGT GC TAG  GT
                                ||||||||  ||| || |||  ||
                                CGTCGTTG  GCG CG GTC  CG
                                     GG   _  G   GT
GAM245  MGC23937  3'  TCACATATGTGGCTATTGC   58955           TGCATA
                                GCGGTAGTTACGT     GTGG
                                ||||||||||||      ||||
                                CGTTATCGGTGTA     CACT
                                       TA____
GAM245  MGC2452   3'  GCGATGATGGCTGCTGT     50986          _
                                GCGGTAGTTA CGTTGC
                                |||||||||| ||||||
```

```
                                TGTCGTCGGT GTAGCG
                                      A
GAM245  MGC2474  3' ACCGCTGCCCGCAGTGTGGCCG 43707     TA        A__
             CTGC                  CGG  GTTACGTTGC   TAGTGGT
                                |||  ||||||||||   |||||||
                                GTC  CGGTGTGACG   GTCGCCA
                                  GC        CCC
GAM245  MGC2650  3' CACTGCCCAGTAGCTGCT    44102         GTT   TA
                                GGTAGTTAC   GCA  GTG
                                |||||||||   |||  |||
                                TCGTCGATG   CGT  CAC
                                     ACC  __
GAM245  MGC26766 5' ACTGCTTACCACTGACTATTGT 58817          C  TGCAT  TG
                                GCGGTAGTTA GT    AG  GT
                                |||||||||| ||    ||  ||
                                TGTTATCAGT CA    TC  CA
                                      _ CCAT_ GT
GAM245  MGC26954 3' ACTATTGAATGTAGCTGTAGT  58835    GG        GC
                                GC  TAGTTACGTT  ATAGT
                                ||  ||||||||||  |||||
                                TG  GTCGATGTAA  TATCA
                                 AT        GT
GAM245  MGC32043 3' ACCTTGATGATGTGGCTTCGC  58043     T      TG   AGT
                                GCGG AGTTACGT  CAT   GGT
                                |||| ||||||||  |||   |||
                                CGCT TCGGTGTA  GTA   CCA
                                  _       __   GTT
GAM245  MGC3207  5' GCGCTGGGCTTGGCTGCTGC  62561         CGTT  A    GT
                                GCGGTAGTTA    GC TAGTG
                                ||||||||||    || |||||
                                CGTCGTCGGT    CG GTCGC
                                      T___  G    GT
GAM245  MGC32104 3' CCATTGTGGAAAGCACTGC   58405      A   ACG  G
                                GCGGT GTT   TT CATAGTGG
                                ||||| |||   || ||||||||
                                CGTCA CGA   AA GTGTTACC
                                  _  ____ G
GAM245  MGC3279  3' CATTATGTAATTATTACC    43814       TAC
                                GGTAGT   GTTGCATAGTG
                                ||||||   ||||||||||
                                CCATTA   TAATGTATTAC
                                   T__
GAM245  MGC3771  5' GACCTCAGCAGTGTAGACTGCT 48245         _      ATAGT
             GT                   CGGTAGTT ACGTTGC     GGT
                                |||||||| |||||||    |||
                                GTCGTCAG TGTGACG    CCA
                                     A      ACT__   GT
GAM245  MGC4309  3' CACAGTGTAGCTACT      44127       TACGT    A
                                GGTAGT    TGCAT GTG
                                ||||||    ||||| |||
```

```
                                TCATCG    ATGTG CAC
                                  _____    A
GAM245  MGC4309  3' GCTGCTGTGTGAATGTTGAC  44130     _  _    TG
                                GTTA CGTT GCATAG  GT
                                |||| |||| ||||||  ||
                                CAGT GTAA TGTGTC  CG
                                  T   G     GT
GAM245  MGC4309  3' GCTGGGGATGGGCTGCTGT   44131        A   GCA
                                GCGGTAGTT CGTT   TAGT
                                ||||||||| ||||   ||||
                                TGTCGTCGG GTAG   GTCG
                                     _   GG_
GAM245  MGC4368  5' GCTGCCAACCAAGTGTGGCTGT 44463    GT     _  CATA TG
           CGC                   GCG  AGTTACG TTG   G  GT
                                ||| ||||||| |||   |  ||
                                CGC  TCGGTGT AAC   C  CG
                                  TG      G   CAAC GT
GAM245  MGC4737  5' ACCACATGTCGGTGGAGCTGCT 48842        A  TT _  A
           GC                    GCGGTAGTT CG  G CAT GTGGT
                                ||||||||| ||  | ||| |||||
                                CGTCGTCGA GT  C GTA CACCA
                                     G  GG T  _
GAM245  MGC4737  5' ATTACTGTGAACGGTTACC   48844    GTTA   G
                                GGTA   CGTT CATAGTGGT
                                ||||   |||| |||||||||
                                CCAT   GCAA GTGTCATTA
                                  TG__   _
GAM245  MGC5302  5' GTCGCGTTGGCTGCTGC    44024         _  T
                                GCGGTAGTTA CGT GC
                                |||||||||| ||| ||
                                CGTCGTCGGT GCG TG
                                     T   C
GAM245  MGC5338  5' CACTGTGCAACTCATCGC   43937      AGTTAC
                                GCGGT     GTTGCATAGTG
                                |||||     ||||||||||
                                CGCTA     CAACGTGTCAC
                                  CT_____
GAM245  MISS     5' CCGCTGCTCTAGCTGCCGT   58029        CGTT   TA
                                GCGGTAGTTA   GCA  GTGG
                                |||||||||    |||  ||||
                                TGCCGTCGAT   CGT  CGCC
                                     CT__   __
GAM245  MO25     3' GCTTTGTGGTGTAGTGCTGT  32811      G    TT   T
                                GCGGTA TTACG  GCA AGT
                                |||||| |||||  ||| |||
                                TGTCGT GATGT  TGT TCG
                                  _    GG   T
GAM245  MO25     3' GTTATTGTAGTAGTATGTAACT 32813         __  _    GG
           ATT                   GTAGTTACGT  TGC ATAGT  T
                                |||||||||  ||| |||||  |
```

```
                                TATCAATGTA  ATG TGTTA  G
                                     TG   A    TT
GAM245  MO25     3'  TGGAGATCGTAGCTGCTGC   32816          __  G
                                GCGGTAGTTACG  TT CA
                                ||||||||||||  || ||
                                CGTCGTCGATGC  GA GT
                                      TA  G
GAM245  moblak   3'  ATTACAGGCATGAGCTACTGC  55486         A   T  ATA
                                GCGGTAGTT CGT GC   GTGGT
                                |||||||||  ||| ||   |||||
                                CGTCATCGA GTA CG   CATTA
                                     _  _  GA_
GAM245  MRPL20   3'  TACTATCTGCTGCCGT     35740         TACGTTGC
                                GCGGTAGT       ATAGTG
                                ||||||||       ||||||
                                TGCCGTCG       TATCAT
                                    TC_______
GAM245  MRPS11   5'  GCCGGCGCAGCTGTGACTGTCG 43118     GT    _    ATAG
          C                      GCG  AGTTAC GTTGC    TGGT
                                |||  ||||||  |||||    ||||
                                CGC  TCAGTG CGACG    GCCG
                                  TG     T    CG__
GAM245  MRPS11   5'  GCCGGCGCAGCTGTGACTGTCG 94560     GT    _    ATAG
          C                      GCG  AGTTAC GTTGC    TGGT
                                |||  ||||||  |||||    ||||
                                CGC  TCAGTG CGACG    GCCG
                                  TG     T    CG__
GAM245  MRPS35   3'  GCTGTGTTCACATGACTGCTGT 41524          C  T_
                                GCGGTAGTTA GT  GCATAGT
                                ||||||||||  ||  |||||||
                                TGTCGTCAGT CA  TGTGTCG
                                     A  CT
GAM245  MST4     3'  ACTATTATGTGGGTGATGCC   33299      G   G TG
                                GGTA TTAC T  CATAGTGGT
                                ||||  ||||  |  |||||||||
                                CCGT AGTG G  GTATTATCA
                                  _   _ GT
GAM245  MSTP043  3'  ATTGTTATGCAATGCTTTGT   49221      T   TAC       TG
                                GCGG AGT   GTTGCATAG  GT
                                ||||  |||   |||||||||  ||
                                TGTT TCG   TAACGTATT  TA
                                  _   ___        GT
GAM245  NBR2     5'  TGCATCACAGTAATTGCTGT   19491          GT___
                                GCGGTAGTTAC     TGCA
                                ||||||||||     ||||
                                TGTCGTTAATG     ACGT
                                      ACACT
GAM245  NCK1     3'  ACTGCTGACCAGAAGTGACTGC 20468          G_   CA   TG
          TGT                    GCGGTAGTTAC  TTG  TAG  GT
                                ||||||||||  |||  |||  ||
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                                TGTCGTCAGTG  GAC  GTC  CA
                                      AA   CA   GT
GAM245  NCK1     3'  ACTGCTGTGTAGCTGTAATTTG 20470   GT  _   _       TG
             TC                   G  AG TTAC GTTGCATAG  GT
                                  |  || |||| |||||||||  ||
                                  C  TT AATG CGATGTGTC  CA
                                   TG  T    T       GT
GAM245  NEDD5    3'  TGCTGTGTCACACTCTGT    15315     T   TAC  T     TG
                                  GCGG AGT   GT GCATAG  G
                                  |||| |||   || ||||||  |
                                  TGTC TCA   CA TGTGTC  T
                                    _  ___  C     GT
GAM245  NET-2    3'  ACTACCTAAATGTGATTTTTGC 24704      T       GCATA
                                  GCGG AGTTACGTT    GTGGT
                                  |||| |||||||||    |||||
                                  CGTT TTAGTGTAA    CATCA
                                    T       ATC__
GAM245  NIR3     3'  ACCAAGTTTTCATGTAACTGTT 66234    GG       TGCATAG
             GC                   GC  TAGTTACGT      TGGT
                                  ||  |||||||||      ||||
                                  CG  GTCAATGTA      ACCA
                                   TT       CTTTTGA
GAM245  NISCH    3'  ACCGTTGTTAACACGTGACACT 23210       A      TGC_
             GT                   GCGGT GTTACGT    ATAGTGGT
                                  ||||| |||||||    ||||||||
                                  TGTCA CAGTGCA    TGTTGCCA
                                    _      CAAT
GAM245  NISCH    3'  GTTGCTGTTGCTGTTGCTGTTG 23213    GG   T  TT  _   GG
             C                    GC  TAGT ACG  GCA TAGT  T
                                  ||  |||| |||  ||| ||||  |
                                  CG  GTCG TGT  CGT GTCG  G
                                   TT   T  __   T   TT
GAM245  NISCH    3'  GTTGCTGTTGCTGTTGCTGTTG 23214    GG   T  TT  _   GG
             C                    GC  TAGT ACG  GCA TAGT  T
                                  ||  |||| |||  ||| ||||  |
                                  CG  GTCG TGT  CGT GTCG  G
                                   TT   T  __   T   TT
GAM245  NJMU-R1  3'  CCAAAAATGTGATAGCTGT   42277      A      GCATAG
                                  GCGGT GTTACGTT     TGG
                                  ||||| ||||||||     |||
                                  TGTCG TAGTGTAA     ACC
                                    A       AA____
GAM245  NMT2     3'  GCTATTGTGTGGAGAGAAATTG 16666        ACG__ TG
             CTGC                   CGGTAGTT    T  CATAGTGGT
                                  ||||||||    |  |||||||||
                                  GTCGTTAA    G  GTGTTATCG
                                       AGAGA GT
GAM245  NP25     5'  CTATTGTGTGGATGCCGC    25148       GTTACG TG
                                  GCGGTA     T  CATAGTGG
                                  ||||||     |  ||||||||
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                                CGCCGT     G  GTGTTATC
                                   A_____ GT
GAM245  NP25     5'  GCTGCTATTGTGTGGATGCCGC 25149       G    GTT  _  TG
                                GCGGTA TTAC   GCA TAG  GT
                                |||||| ||||   ||| |||  ||
                                CGCCGT GGTG   TGT ATC  CG
                                   A   ___   T   GT
GAM245  NS1-BP   3'  GCTTAGTGATGTAATTATGGT  72545    G        TG AT
                                GC GTAGTTACGT  C  AGT
                                || ||||||||||  |  |||
                                TG TATTAATGTA  G  TCG
                                 G        GT AT
GAM245  NT5C1B   3'  CGCTATGGCTAGCTTTGT    71227      T    C  TG    TG
                                GCGG AGTTA GT  CATAG  G
                                |||| ||||| ||  |||||  |
                                TGTT TCGAT CG  GTATC  C
                                  _    _ __    GT
GAM245  OAZ      3'  ATTGTGCATCGTGATGTGATTG 65724      A__     T      GGT
           C                     CGGT   GTTACG TGCATAGT
                                ||||   |||||| ||||||||
                                GTTA   TAGTGC ACGTGTTA
                                  GTG     T         T
GAM245  OLFM3    5'  GCTGTTATTGCTACTGCTGCTG 82145        TAC  T   _   TG
           C                     GCGGTAGT   GT GCA TAG  GT
                                ||||||||   || ||| |||  ||
                                CGTCGTCG   CA CGT ATT  CG
                                     T__  T   T   GT
GAM245  OSBP2    5'  GCCGCGCGCACGTGACTGCGC  47759     G        T  ATA
                                GCG TAGTTACGT GC   GTGGT
                                ||| |||||||| ||   |||||
                                CGC GTCAGTGCA CG   CGCCG
                                  _       _ CG_
GAM245  OSBPL8   3'  GCCATTATGTAATTTGG     40458     C
                                TTA GTTGCATAGTGGT
                                ||| ||||||||||||
                                GGT TAATGTATTACCG
                                  T
GAM245  P311     3'  ACCATTGTCTCGTTGGCTGGCG 16485     G     _  TT   TA
           C                     GCG TAGTTA CG  GCA  GTGGT
                                ||| |||||| ||  |||  |||||
                                CGC GTCGGT GC  TGT  TACCA
                                  G     T  TC  __
GAM245  PCDH10   3'  CCAAAGATGTAGCTATTG    51987           GCATAG
                                CGGTAGTTACGTT     TGG
                                ||||||||||||     |||
                                GTTATCGATGTAG     ACC
                                       AA_____
GAM245  PCDH19   3'  ACTGATGATGCTGACTGTTGC  63693    GG     CGTT   AG_
                                GC  TAGTTA   GCAT   TGGT
                                ||  ||||||   ||||   ||||
```

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                                CG  GTCAGT   CGTA  GTCA
                                 TT     ____   GTA
GAM245  PCNT2    3'  CGTTGTGTGCCTATCG     20091      TTAC  T    TG
                                CGGTAG   GT GCATAG  G
                                ||||||   || ||||||  |
                                GCTATC   CG TGTGTT  C
                                   ____  _    GT
GAM245  PDP      5'  CGCTGTCGCTGCTGCTGC    37422       TA  TTGC   TG
                                GCGGTAGT  CG   ATAG  G
                                ||||||||  ||   ||||  |
                                CGTCGTCG  GC   TGTC  C
                                     TC  ____   GT
GAM245  PDP      5'  GCCGAGCGGTGGCGTCGTTGTC 37423    GT  TT   TG ATAG
             GC                   GCG  AG  ACGT  C   TGGT
                                |||  ||  ||||  |   ||||
                                CGC  TT  TGCG  G   GCCG
                                  TG  GC   GT GCGA
GAM245  PDZD2    5'  GCCACTTCTGTCAAAGTGACTG 80874    GT    G  _  T_
             TCGC                  CG  AGTTAC TTG CA  AGTGGT
                                ||  |||||| ||| ||  ||||||
                                GC  TCAGTG AAC GT  TCACCG
                                 TG     A   T  CT
GAM245  PELI1    5'  ACTGTCAGTCTAATTGTCGT   40252    GT    CG   C
                                GCG  AGTTA  TTG ATAGT
                                |||  |||||  ||| |||||
                                TGC  TTAAT  GAC TGTCA
                                  TG    CT  _
GAM245  PLEKHA3  3'  ATTGCTATGCAAAAGCTGCTGT 38858       TACG      TG
                                GCGGTAGT   TTGCATAG  GT
                                ||||||||   ||||||||  ||
                                TGTCGTCG   AACGTATC  TA
                                     AA__      GT
GAM245  PLEKHA3  3'  GCTGCTGTAATTAAACTATTGT 38863        AC    TA TG
                                GCGGTAGTT  GTTGCA  G  GT
                                |||||||||  ||||||  |  ||
                                TGTTATCAA  TAATGT  C  CG
                                     AT     __ GT
GAM245  PLK      3'  GTTGCTGTGTAAGTTATTTTTG 17267     T   T  G       GG
             T                   GCGG AGT AC TTGCATAGT  T
                                ||||  ||| ||  |||||||||  |
                                TGTT TTA TG AATGTGTCG  G
                                  T   T  _       TT
GAM245  PMX2B    3'  CTATTGTCGTCGCTGCTGC    14081        T   TTGC
                                GCGGTAGT ACG    ATAGTGG
                                ||||||||  |||   |||||||
                                CGTCGTCG TGC    TGTTATC
                                     C  ____
GAM245  PNMA5    5'  ACTGAGCTGATTGCTGC     73590          CGTT  A
                                GCGGTAGTTA    GC TAGT
                                ||||||||||   || ||||
```

```
                                CGTCGTTAGT   CG GTCA
                                     ____ A
GAM245  POLM    3'  ATCACTGTGTGACCCTGGGTCT 91086     TAGTTAC  TG
          GC                   GCGG     GT  CATAGTGGT
                               ||||     ||  |||||||||
                               CGTC     CA  GTGTCACTA
                                 TGGGTCC  GT
GAM245  POPX1   3'  ATTATTATGATTAAAGTTACTG 29795   GG   T  GTTG__
          TTGC                 C  TAGT AC     CATAGTGGT
                               |  |||| ||     |||||||||
                               G  GTCA TG     GTATTATTA
                                TT   T  AAATTA
GAM245  PORIMIN  3'  CTACTGTGAGAATATTGT    53602       GTTACGTTG
                               GCGGTA       CATAGTGG
                               ||||||       ||||||||
                               TGTTAT       GTGTCATC
                                  AAGA_____
GAM245  PP1201   3'  GCTAGGGACTAACTGTTGC   42192    GG     C   GCA
                               GC  TAGTTA GTT   TAGT
                               ||  |||||| |||   ||||
                               CG  GTCAAT CAG   ATCG
                                TT     _  GG_
GAM245  PPAP2B   5'  GCCTGGGTGTGTGGCTGCTGT  13545         GTT   AGT
                               GCGGTAGTTAC   GCAT   GGT
                               ||||||||||   ||||  |||
                               TGTCGTCGGTG   TGTG   CCG
                                     ___   GGT
GAM245  PR48    5'  ACTCCGTCAACGTGGATGCCGT 25089       G      _ AT
                               GCGGTA TTACGTTG C  AGT
                               |||||| |||||||| |  |||
                               TGCCGT GGTGCAAC G  TCA
                                  A       T CC
GAM245  PRDM8   5'  CCAGCGACGTGGTGTTGC    39569    GG  G       ATAG   T
                               GC  TA TTACGTTGC    TGG
                               ||  || |||||||||   |||
                               CG  GT GGTGCAGCG    ACC
                                TT  _        _____  C
GAM245  PREI3   3'  ATTATATATAGCAGTGTAGCTG 66320          _  _
                               TAGTTACGTTGC ATA GTGGT
                               |||||||||||| ||| |||||
                               GTCGATGTGACG TAT TATTA
                                     A   A
GAM245  PRO0097  5'  GCTGTTATGAATATAACTACTG 26098         CG  G    TG
          T                    GCGGTAGTTA  TT CATAG  GT
                               ||||||||||  || |||||  ||
                               TGTCATCAAT  AA GTATT  CG
                                     AT  _    GT
GAM245  PRO0245  5'  ATCAAAATCTATGCAATGTAGC 26125             _____
          TAATGC                 TAGTTACGTTGCATAG    TGGT
                               ||||||||||||||||   ||||
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                                ATCGATGTAACGTATC    ACTA
                                          TAAA
GAM245  PRO0456  3' ATTGCTGTGTACCTGTTAC   26174    T  T_     TG
                                GT ACG  TGCATAG  GT
                                || |||  |||||||  ||
                                CA TGT  ATGTGTC  TA
                                 T  CC      GT
GAM245  PRO0456  5' GCTATTGTGACTAGTGGTGTTG 26178    GG  G    GTTG
           C                     GC  TA TTAC    CATAGTGGT
                                ||  || ||||    |||||||||
                                CG  GT GGTG    GTGTTATCG
                                 TT  _    ATCA
GAM245  PRO0641  5' CATTATGCTGTATTGCC     26211       T   TT
                                GGTAGT ACG  GCATAGTG
                                |||||| |||  ||||||||
                                CCGTTA TGT  CGTATTAC

                                  _   __
GAM245  PRO1787  5' ACCATTCCCTAGGTGTAGCTCT 37766      T       GCAT_
           GT                     GCGG AGTTACGTT     AGTGGT
                                |||| |||||||||     ||||||
                                TGTC TCGATGTGG     TTACCA
                                  _        ATCCC
GAM245  PRO2214  3' CTACTGTGAATAATGCTGC   37566       GTTAC   G
                                GCGGTA     GTT CATAGTGG
                                ||||||     ||| ||||||||
                                CGTCGT     TAA GTGTCATC
                                   AA___   _
GAM245  PRO2714  5' GTCAAATGAAGATGTAACCATT 37595      A      G_   AGTGGT
           GC                     GCGGT GTTACGTT  CAT
                                ||||| ||||||||  |||
                                CGTTA CAATGTAG  GTA
                                   C       AA   AACTG
GAM245  PROL3    3' ACCACTACCCTTGTAACTACTG 21933          TTGCA
           C                      GCGGTAGTTACG     TAGTGGT
                                ||||||||||||     |||||||
                                CGTCATCAATGT     ATCACCA
                                       TCCC_
GAM245  PTP4A1   5' ACTGTAGAAACTGATTACTGC  12934         C   GC_
                                GCGGTAGTTA GTT   ATAGT
                                |||||||||| |||   |||||
                                CGTCATTAGT CAA   TGTCA
                                      _   AGA
GAM245  RA-GEF-2 3' ACTAGGAGATGTGACTGATGC  32952     G        GCA
                                GCG TAGTTACGTT   TAGT
                                ||| ||||||||||   ||||
                                CGT GTCAGTGTAG   ATCA
                                  A         AGG
GAM245  Rab11-FIP2 3' ATTGTATAATGTGACAATTGT  29779      A       C
                                GCGGT GTTACGTTG ATAGT
                                ||||| ||||||||| |||||
```

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                                TGTTA CAGTGTAAT TGTTA
                                   A       A
GAM245  Rab11-FIP3 3'  ACCGCTGTGTGGCGCTCTCTCC 28123    T  TTA_  TG
                                GG AG   CGT  CATAGTGGT
                                || ||   |||  |||||||||
                                CC TC   GCG  GTGTCGCCA
                                 _  TCTC   GT
GAM245  RAB24    3'  ATTACGTCAGTGTGGCTGCC   55387          CATA
                                GGTAGTTACGTTG   GTGGT
                                ||||||||||||   |||||
                                CCGTCGGTGTGAC   CATTA
                                       TG__
GAM245  RAB39    3'  ATTATAGGCATGAGCTGCCGT  76629        A  T  ATA
                                GCGGTAGTT CGT GC   GTGGT
                                ||||||||| ||| ||   |||||
                                TGCCGTCGA GTA CG   TATTA
                                     _  _  GA_
GAM245  RAB40A   5'  ACTGCTGTGTCACTACTCTGT  82067     T   TAC  T     TG
                                GCGG AGT   GT GCATAG  GT
                                |||| |||   || ||||||  ||
                                TGTC TCA   CA TGTGTC  CA
                                  _   T__  C     GT
GAM245  RES4-22  3'  TCATCCACGTGGCTCCGT    13519     T      T CATA
                                GCGG AGTTACGT G    GTGG
                                |||| ||||||||  |    ||||
                                TGCC TCGGTGCA C    TACT
                                  _       _ C___
GAM245  RHOBTB1   5'  ACCGCGCGCAGCCGTGGCTGCT 91438          _   ATA
           GC                    GCGGTAGTTACG TTGC   GTGGT
                                ||||||||||| ||||   |||||
                                CGTCGTCGGTGC GACG   CGCCA
                                       C    CG_
GAM245  RIS1     3'  GCTTCGTGCTGTAGTTATCGT  80583       GT   TT   AGT
                                GCGGTA  TACG  GCAT   GGT
                                ||||||  ||||  ||||   |||
                                TGCTAT  ATGT  CGTG   TCG
                                   TG    __    CT_
GAM245  RNASE3L  3'  GCTCAGTAACTGTGACTGTTGT 25081    GG     _    AT
                                GC  TAGTTAC GTTGC  AGT
                                ||  ||||||| |||||  |||
                                TG  GTCAGTG CAATG  TCG
                                 TT      T    AC
GAM245  RNF24    3'  ACTGTGGTTCCAGTGTAGCTGC 23313          ____     GGT
           TGT                   GTAGTTACGTTG   CATAGT
                                ||||||||||||   ||||||
                                CGTCGATGTGAC   GTGTCA
                                       CTTG       T
GAM245  RNF9     3'  ACTGCTATGCTGCACTGCC   53408       TAC  T     TG
                                GGTAGT   GT GCATAG  GT
                                ||||||   || ||||||  ||
```

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                                CCGTCA  CG CGTATC  CA
                                   ___ T    GT
GAM245  RNPC1   3'  CACTGTCTGCTGCCGC     33986       TACGTTGC
                                GCGGTAGT      ATAGTG
                                ||||||||      ||||||
                                CGCCGTCG      TGTCAC
                                    TC_______
GAM245  RoXaN   3'  CACTGTGGATAGCTGCTGT   46637        CGTTG
                                GCGGTAGTTA    CATAGTG
                                ||||||||||    |||||||
                                TGTCGTCGAT    GTGTCAC
                                    AG___
GAM245  RoXaN   3'  GCTGCTGGTCCTGTGGCTGCTG 46648         TT  A   TG
                                CGGTAGTTACG  GC TAG  GT
                                ||||||||||  || |||  ||
                                GTCGTCGGTGT  TG GTC  CG
                                    CC  _   GT
GAM245  RPL27   5'  GCTGTAGGCCCGGGTGGTTGCT 6390       TT  GTT_ __    GGT
            GC                   CGGTAG  AC    GC  ATAGT
                                ||||||  ||    ||  |||||
                                GTCGTT  TG    CG  TGTCG
                                   GG  GGCC  GA
GAM245  Rpo1-2  3'  GTTAGATGACGATGGATTGCCG 38709        A    _   AGTGGT
            T                    GCGGTAGTT CGTTG CAT
                                |||||||| ||||| |||
                                TGCCGTTAG GTAGC GTA
                                    _    A   GATTG
GAM245  RRP4    3'  CCATAGATGTGATTAT     26562          GCATA
                                GTAGTTACGTT    GTGG
                                ||||||||||    ||||
                                TATTAGTGTAG    TACC
                                    A____
GAM245  RSP3    5'  GCTGCCAGGGGCGTGTTATCGC 49174      AGT     GCATA TG
                                GCGGT   TACGTT    G  GT
                                |||||   ||||||    |  ||
                                CGCTA   GTGCGG    C  CG
                                   TT_     GGAC_ GT
GAM245  RTTN    3'  GCTGTGTGTAGCAGCTGT    91800      A    GTT
                                GCGGT GTTAC   GCATAGT
                                ||||| |||||   |||||||
                                TGTCG CGATG   TGTGTCG
                                   A    ___
GAM245  S164    5'  ACCGTTTCCTCAGCGGCGGACT 60776      A     AT ____
            GCTGC                   TAGTT CGTTGC  AG    TGGT
                                ||||| ||||||  ||    ||||
                                GTCAG GCGGCG  TC    GCCA
                                   _     AC  CTTT
GAM245  SAMHD1  3'  GTACTGAACGTGGTTACC    61319      TT    GCA    GG
                                GGTAG  ACGTT   TAGT  T
                                |||||  |||||   ||||  |
```

```
                                CCATT  TGCAA   GTCA  G
                                  GG    ___    TT
GAM245  SCAM-1   3'  CGCTGTGTGCTGCCCGC    19326     _   TACGTT    TG
                                GCGG TAGT    GCATAG  G
                                |||| ||||    ||||||  |
                                CGCC GTCG    TGTGTC  C
                                  C   _______    GT
GAM245  SCAMP5   3'  GTGCTGTGGCTTGATTCTGC   57262     T    C  TG    GG
                                GCGG AGTTA GT  CATAGT  T
                                |||| ||||| ||  ||||||  |
                                CGTC TTAGT CG  GTGTCG  G
                                  _    T __     TT
GAM245  SCAND2   3'  ATCAGGAGATGTGATTATTGT  53315          GCATAG
                                GCGGTAGTTACGTT    TGGT
                                ||||||||||||||    ||||
                                TGTTATTAGTGTAG    ACTA
                                       AGG___
GAM245  SCYB11   3'  ATTACTATCTGTGGTTACGGT  87440    G   TT   TTGC
                                GC GTAG  ACG   ATAGTGGT
                                || ||||  |||   ||||||||
                                TG CATT  TGT   TATCATTA
                                 G   GG   C___
GAM245  SDCBP    3'  GCCATTGTGATTAGGATGACTG 18842      A   ACGTTG
           T                     GCGGT GTT    CATAGTGGT
                                |||||  |||    |||||||||
                                TGTCA TAG    GTGTTACCG
                                  G   GATTA_
GAM245  SDCCAG3  3'  CCACCGCGTGGCTGCCGC    21818          TGCATA
                                GCGGTAGTTACGT    GTGG
                                ||||||||||||     ||||
                                CGCCGTCGGTGCG    CACC
                                       C_____
GAM245  SEC61A1  5'  GCTGCTGTGCAGTGGAACGC  25310    GTAG   GT     TG
                                GCG   TTAC  TGCATAG  GT
                                |||   ||||  |||||||  ||
                                CGC   GGTG  ACGTGTC  CG
                                  AA__   __     GT
GAM245  SEC61A1  3'  TCATGGCGCGTGCTGCTGC   25313       T   T  ATA
                                GCGGTAGT ACGT GC   GTGG
                                |||||||| |||| ||   ||||
                                CGTCGTCG TGCG CG   TACT
                                     _   _ G__
GAM245  SEF      3'  CACTTTAGCTGCTGC      69463         CGTTGCAT
                                GCGGTAGTTA      AGTG
                                ||||||||||      ||||
                                CGTCGTCGAT      TCAC
                                      T_______
GAM245  SEF      3'  CCATAGTGTGATTGCC     69464       ACGTT   A
                                GGTAGTT    GCAT GTGG
                                |||||||    |||| ||||
```

```
                                CCGTTAG    TGTG TACC
                                   _____   A
GAM245  SEMA3E   5' CTACCGGCGTAGTTGCTG   24880     GT     CATA
                                CGGTA  TACGTTG   GTGG
                                |||||  |||||||   ||||
                                GTCGT  ATGCGGC   CATC
                                  TG     ____
GAM245  SEMA4B   5' ACCGCGGGGCGGAGCTGCCGC 69034       ACG   ATA
                                GCGGTAGTT   TTGC   GTGGT
                                |||||||||   ||||   |||||
                                CGCCGTCGA   GGCG   CGCCA
                                     ___   GGG
GAM245  SEMA4B   3' GCCGAGGATGTAGTTGTTGC  69036   GG  GT    GCATAG
                                GC  TA  TACGTT     TGGT
                                ||  ||  ||||||     ||||
                                CG  GT  ATGTAG     GCCG
                                 TT  TG     GA____
GAM245  SEMA4C   3' GCTCCTAACAGTGTAACTTATT 35053       _       CA   TG
           GT                    GCGGTA GTTACGTTG  TAG  GT
                                ||||||| |||||||||  |||  ||
                                TGTTAT CAATGTGAC  ATC  CG
                                   T       A_   CT
GAM245  SEMA4F   3' ACCACTGCCCTGAGGTTACTGC 14937       TA  TT   TA
                                GCGGTAGT  CG  GCA  GTGGT
                                ||||||||  ||  |||  |||||
                                CGTCATTG  GT  CGT  CACCA
                                     GA  CC  __
GAM245  SEMA4G   5' GCAGGGTGGCTACCGT     94683          G
                                GCGGTAGTTAC TTGC
                                |||||||||||| ||||
                                TGCCATCGGTG GACG
                                      G
GAM245  SENP8    5' TGCGACCGTAGCTGTCGC    59091     GT     _
                                GCG  AGTTACG TTGCA
                                |||  ||||||| |||||
                                CGC  TCGATGC AGCGT
                                  TG     C
GAM245  SEP15    3' ATTACTATGCCTCATGTGCTGT 14933      AGTT   T__
                                GCGGT   ACGT   GCATAGTGGT
                                |||||   ||||   ||||||||||
                                TGTCG   TGTA   CGTATCATTA
                                   _____   CTC
GAM245  SH3BGRL3 5' GCCCGGCAGTGCAGCTGCCGC  48438        A     ATAGT
                                GCGGTAGTT CGTTGC    GGT
                                ||||||||| ||||||    |||
                                CGCCGTCGA GTGACG    CCG
                                     C     GC___
GAM245  SLC15A2  3' GCAATGTAATTATGC      40795     G
                                GCG TAGTTACGTTGC
                                ||| ||||||||||||
```

```
                                CGT ATTAATGTAACG
                                  _
GAM245  SLC26A7  3'  GCTTGATGTGATTATC     53419          __
                                GGTAGTTACGTT  GC
                                ||||||||||||  ||
                                CTATTAGTGTAG  CG
                                      TT
GAM245  SLC2A10  3'  TGCTGGTGTCATTGCTGT    47829       T   TT_
                                GCGGTAGT ACG   GCA
                                |||||||| |||   |||
                                TGTCGTTA TGT   CGT
                                     C   GGT
GAM245  SMAP-5   5'  TGGGATTAGTGAAGCTACTGC 47935        ACG TG A    GGT
                                GCGGTAGTT   T  C TAGT
                                |||||||||   |  | ||||
                                CGTCATCGA   A  G ATTA
                                      ___ GT _    GGGTT
GAM245  SMARCA4  3'  GCTGGCAGTACTGTTGC     11794    GG    T  GT   A
                                GC  TAGT AC  TGC TAGT
                                ||  |||| ||  ||| ||||
                                CG  GTCA TG  ACG GTCG
                                 TT   _ __   _
GAM245  SMARCF1  3'  GCCACTATGGATGACATGTTGT 37437    GG  GTTA    G
                                GC  TA    CGTT CATAGTGGT
                                ||  ||    |||| |||||||||
                                TG  GT    GTAG GTATCACCG
                                 TT  ACA_   _
GAM245  SMCR7    3'  ACCAACAGAATGTGGTTTCTGC 57504     T  TT    GCATAG
                                GCGG AG  ACGTT     TGGT
                                |||| ||  |||||     ||||
                                CGTC TT  TGTAA     ACCA
                                  T  GG    GACA__
GAM245  SNAP91   3'  GCTGTTGTGTGGCGAGCTATT  29266       A   TG    TG
                                GGTAGTT CGT  CATAG  GT
                                |||||||  |||  |||||  ||
                                TTATCGA GCG  GTGTT  CG
                                    _  GT    GT
GAM245  SNAPC1   3'  ATTATAGGTGTGAGCTACTGT  11839       TACG TG   A_
                                GCGGTAGT    T  CAT  GTGGT
                                ||||||||    |  |||  |||||
                                TGTCATCG    A  GTG  TATTA
                                     _____ GT   GA
GAM245  SNX11    5'  CGCTGTGGGGAGCTGGTGC   25268    G    ACG  G
                                GCG TAGTT   TT CATAGTG
                                |||  |||||   ||  |||||||
                                CGT GTCGA   GG GTGTCGC
                                  G    ___  G
GAM245  SSFA2    3'  GCTGTTGAGCTGGGCTACTGT  73768        ACGTT  A   TG
                                GCGGTAGTT    GC TAG  GT
                                |||||||||    ||  |||  ||
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```
                                TGTCATCGG    CG GTT  CG
                                     GT___  A   GT
GAM245  SSTK    3'  TGCCGCGTGCTGCTGC     49346        T   T
                                GCGGTAGT ACGT GCA
                                |||||||| |||| |||
                                CGTCGTCG TGCG CGT
                                     _   C
GAM245  ST7L    3'  GTAATGTGACTTTGT      57001     T
                                GCGG AGTTACGTTGC
                                |||| ||||||||||
                                TGTT TCAGTGTAATG
                                  _
GAM245  ST7L    3'  GTAATGTGACTTTGT      57578     T
                                GCGG AGTTACGTTGC
                                |||| ||||||||||
                                TGTT TCAGTGTAATG
                                  _
GAM245  ST7L    3'  GTAATGTGACTTTGT      34857     T
                                GCGG AGTTACGTTGC
                                |||| ||||||||||
                                TGTT TCAGTGTAATG
                                  _
GAM245  STIM2   3'  ATCATAAGTGATTTGGTTACTG 40471       TT C  TG ATA
           C                     GCGGTAG  A GT  C   GTGGT
                                ||||||| | || |  |||||
                                CGTCATT  T TA  G   TACTA
                                    GG T  GT AA_
GAM245  STK25   3'  ACCCCTGCAGTGTGCTGTTGT  21050    GG   T      TAGT
                                GC  TAGT ACGTTGCA   GGT
                                ||  |||| ||||||||   |||
                                TG  GTCG TGTGACGT   CCA
                                 TT   _      CC__
GAM245  STRBP   5'  GCCACTGTGCCTGGCCTCAACT 37233  G    AC_  __
           GTTGC                   TAGTT   GTT  GCATAGTGGT
                                |||||   |||  ||||||||||
                                GTCAA   CGG  CGTGTCACCG
                                T    CTC   TC
GAM245  STRN3   3'  ATTAAGTTAACTGTAATTACTG 27406          _   _ A   GGT
           T                    GCGGTAGTTAC GTTG C TAGT
                                |||||||||| |||| | ||||
                                TGTCATTAATG CAAT G ATTA
                                      T   T A
GAM245  STX1B2  3'  CGTTGTGTAGACTGCAGC   53516   G    ACGT     TG
                                GC GTAGTT   TGCATAG  G
                                || ||||||   |||||||  |
                                CG CGTCAG   ATGTGTT  C
                                 A    _____     GT
GAM245  TA-KRP  3'  TGTAATGTGATACTGT     50697      G
                                GCGGTA TTACGTTGCA
                                |||||| ||||||||||
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```
                                TGTCAT AGTGTAATGT
                                    _
GAM245  TAF9L    3'  TGAAATGTAGCTGCAGT    32008    G       G
                                GC GTAGTTACGTT CA
                                || |||||||||| ||
                                TG CGTCGATGTAA GT
                                 A        A
GAM245  TBLR1    3'  ATTATGGTAAAAATGTGCACTA 45097     _    G____    GGT
              TTGT                  TAGT TACGTT    CATAGT
                                |||| ||||||    ||||||
                                ATCA GTGTAA    GTATTA
                                  C     AAATG       T
GAM245  TCL6     5'  CGCTGTTTGTTTACCGC    26994      TT  TTGC   TG
                                GCGGTAG  ACG   ATAG  G
                                |||||||  |||   ||||  |
                                CGCCATT  TGT   TGTC  C
                                    __  T___   GT
GAM245  TCL6     5'  CGCTGTTTGTTTACCGC    40081      TT  TTGC   TG
                                GCGGTAG  ACG   ATAG  G
                                |||||||  |||   ||||  |
                                CGCCATT  TGT   TGTC  C
                                    __  T___   GT
GAM245  TCL6     5'  CGCTGTTTGTTTACCGC    40098      TT  TTGC   TG
                                GCGGTAG  ACG   ATAG  G
                                |||||||  |||   ||||  |
                                CGCCATT  TGT   TGTC  C
                                    __  T___   GT
GAM245  TCL6     5'  CGCTGTTTGTTTACCGC    24978      TT  TTGC   TG
                                GCGGTAG  ACG   ATAG  G
                                |||||||  |||   ||||  |
                                CGCCATT  TGT   TGTC  C
                                    __  T___   GT
GAM245  THEA     3'  ATTGCAGGCATGAGCTGCTGC  66276       A   T  ATA TG
                                GCGGTAGTT CGT GC   G  GT
                                ||||||||| ||| ||   |  ||
                                CGTCGTCGA GTA CG   C  TA
                                     _  _  GA_ GT
GAM245  TIMM10   3'  GTCACACTGGAATGTGACTG   90905       G  TA   GT
                                TAGTTACGTT CA  GTG
                                |||||||||| ||  |||
                                GTCAGTGTAA GT  CAC
                                      G  CA   TG
GAM245  TIMM22   3'  ACTGCCTTCACGACGTGACTGC 78310          CATA_ TG
              TG                  CGGTAGTTACGTTG    G  GT
                                ||||||||||||||    |  ||
                                GTCGTCAGTGCAGC    C  CA
                                       ACTTC GT
GAM245  TLR8     3'  ATTGCTATGTAACAAATTATC  33503       AC       TG
                                GGTAGTT  GTTGCATAG  GT
                                |||||||  |||||||||  ||
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                                CTATTAA  CAATGTATC  TA
                                   A_       GT
GAM245  TLR8     3'  ATTGCTATGTAACAAATTATC  56863       AC       TG
                                GGTAGTT  GTTGCATAG  GT
                                |||||||  |||||||||  ||
                                CTATTAA  CAATGTATC  TA
                                   A_       GT
GAM245  TNFRSF21 3'  CCAGGTGTAACTGTTGT    27082    GG   TACGT    AG
                                GC  TAGT    TGCAT  TGG
                                ||  ||||    |||||  |||
                                TG  GTCA    ATGTG  ACC
                                 TT  _____    G_
GAM245  TPARL    3'  ACCGTTGTGCAGTGGGGTCTAC 37477     _ TA
                                GTAG T  CGTTGCATAGTGGT
                                ||||  |  ||||||||||||||
                                CATC G  GTGACGTGTTGCCA
                                  T GG
GAM245  TPD52    3'  CATTATTTAGCACCGT     17425      AGTTAC   C
                                GCGGT     GTTG ATAGTG
                                |||||     |||| ||||||
                                TGCCA     CGAT TATTAC
                                  _______   T
GAM245  TRIM36   3'  ATCATTATGCAATAAAGCTGCT 38011        AC
                                GGTAGTT  GTTGCATAGTGGT
                                |||||||  |||||||||||||
                                TCGTCGA  TAACGTATTACTA
                                   AA
GAM245  TRIM4    3'  CTATTGTGAATAGTGCTGC   52254      T  GTTG
                                GTAGT AC    CATAGTGG
                                |||||  ||    ||||||||
                                CGTCG TG    GTGTTATC
                                  _  ATAA
GAM245  TRIP-Br2 3'  ACTACTCCTCGTAAGTGTTGC  28576    GG  G    TTGCAT
                                GC  TA TTACG     AGTGGT
                                ||  ||  |||||     ||||||
                                CG  GT AATGC     TCATCA
                                 TT  G    TCC___
GAM245  TSC22    3'  TTGTGTATGTAGTGTAACTATT 20067              GTGGT
                                GGTAGTTACGTTGCATA
                                |||||||||||||||||
                                TTATCAATGTGATGTAT
                                         GTGTTT
GAM245  TSC22    3'  CACTGTATTTAACTGTTGC    20062    GG     C  TGC
                                GC  TAGTTA GT   ATAGTG
                                ||  ||||||  ||   ||||||
                                CG  GTCAAT TA   TGTCAC
                                 TT     T  ___
GAM245  TSCOT    5'  CGCTGGGCGGGCTGCTGT    52335         ACGT   A   TG
                                GCGGTAGTT    TGC TAG  G
                                |||||||||    ||| |||  |
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                                TGTCGTCGG   GCG GTC  C
                                    ____  G   GT
GAM245  TTTY2    5'  GCTACTGGGCTGTGTGTTACTG 87005      AGT   TT  A
           T                    GCGGT   TACG  GC TAGTGGT
                                |||||   ||||  || |||||||
                                TGTCA   GTGT  CG GTCATCG
                                  TT_   GT  G
GAM245  UNC5D    3'  ACCACTAACATATGGCTATTGC 55131         CGT  CA
                                GCGGTAGTTA   TG  TAGTGGT
                                ||||||||||   ||  |||||||
                                CGTTATCGGT   AC  ATCACCA
                                      AT_  A_
GAM245  UNC5D    3'  ATTGTCTAACATGTGGGTACTG 55133       G   __   C    GGT
           T                    GCGGTA TTAC  GTTG ATAGT
                                ||||||| ||||  |||| |||||
                                TGTCAT GGTG  CAAT TGTTA
                                   G   TA   C
GAM245  UQCR     3'  ATCATGCTGGTGGCTTGGTTAC 22407       TT C  TG ATA_
           TGT                    GCGGTAG  A GT  C   GTGGT
                                  |||||||  | ||  |   |||||
                                  TGTCATT  T CG  G   TACTA
                                     GG T  GT GTCG
GAM245  USP15    3'  ACTACTATGATATTTAGCTGCA 20882    G     C  TG
           GT                     GC GTAGTTA GT  CATAGTGGT
                                  || |||||||  ||  |||||||||
                                  TG CGTCGAT TA  GTATCATCA
                                   A      T  TA
GAM245  UST      3'  ACCAAGAGCAGTGTAATTATC  19132           ATAG
                                GGTAGTTACGTTGC   TGGT
                                ||||||||||||||   ||||
                                CTATTAATGTGACG   ACCA
                                       AGA_
GAM245  VEZATIN  3'  TGCTGCTTCTCTAGTGGAGTTA 34228      __   GTTGCAT  TG
           CTGC                   GGTAG  TTAC      AG  GT
                                  |||||  ||||      ||  ||
                                  TCATT  GGTG      TC  CG
                                     GA   ATCTCT_  GT  TT
GAM245  VPS4B    5'  GCTTCGACGTTGCTGCTGT   16822        T     CAT
                                GCGGTAGT ACGTTG   AGT
                                |||||||| ||||||   |||
                                TGTCGTCG TGCAGC   TCG
                                     T     T__
GAM245  WDR7     3'  CTAGTTAATGTAATTATC    30958           CA
                                GGTAGTTACGTTG  TAG
                                ||||||||||||  |||
                                CTATTAATGTAAT  ATC
                                       TG
GAM245  WS-3     5'  TCGCATGTGGAATTATCGC   21649         ACG TG   A
                                GCGGTAGTT   T  CAT GTGG
                                |||||||||   |  ||| ||||
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                                CGCTATTAA   G  GTA CGCT
                                    ___ GT   _
GAM245  YAP1     3'  CGCTGTTAATGTATTGC     20349       T     C    TG
                                GTAGT ACGTTG ATAG  G
                                ||||| |||||| ||||  |
                                CGTTA TGTAAT TGTC  C
                                  _     _   GT
GAM245  ZAP3     3'  ATCATTGCTTTGTGGCTG    77221         TT   TA
                                TAGTTACG  GCA  GTGGT
                                ||||||||  |||  |||||
                                GTCGGTGT  CGT  TACTA
                                    TT  __
GAM245  ZDHHC5   5'  GCCGCTGTGTGGGCCTGGGCTA 91559    G    AC_ _ TG
             TGC                   CG TAGTT   G T  CATAGTGGT
                                || |||||   | |  |||||||||
                                GT ATCGG   C G  GTGTCGCCG
                                 _    GTC G GT
GAM245  ZDHHC7   3'  GTACTATGAATGTATTGCTGT  34843         T    G     GG
                                GCGGTAGT ACGTT CATAGT  T
                                |||||||| ||||| ||||||  |
                                TGTCGTTA TGTAA GTATCA  G
                                    _    _     TT
GAM245  ZER6     3'  CCACTGTTTATGTTGCTGC   63377       T    TGC
                                GTAGT ACGT   ATAGTGG
                                ||||| ||||   |||||||
                                CGTCG TGTA   TGTCACC
                                   T   TT_
GAM245  ZFP      3'  GCTACAATATGTAACTGTGGT  37846    G        TGCATA
                                GC GTAGTTACGT     GTGGT
                                || ||||||||||     |||||
                                TG TGTCAATGTA     CATCG
                                 G        TAA___
GAM245  ZFP106   3'  ATTACTGTTTAAGTGATTATTT 42462      _      G   C
             GC                    GCGG TAGTTAC TTG ATAGTGGT
                                |||| ||||||| ||| ||||||||
                                CGTT ATTAGTG AAT TGTCATTA
                                  T      _  T
GAM245  ZIN      3'  ATCACTGTGTGATGGTCTCAGT 25487    GGT  TTA   TG
                                GC   AG   CGT  CATAGTGGT
                                ||   ||   |||  |||||||||
                                TG   TC   GTA  GTGTCACTA
                                 AC_  TG_   GT
GAM245  ZNF213   3'  TCACTATGTCCAGCTCCGT   65105      T    ACGTT
                                GCGG AGTT    GCATAGTGG
                                |||| ||||    |||||||||
                                TGCC TCGA    TGTATCACT
                                  _    CC___
GAM245  ZNF230   3'  ATCAAATTGATGTAATTAGTGT 20859     G        GCATAG
                                GCG TAGTTACGTT     TGGT
                                ||| ||||||||||     ||||
```

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                                TGT ATTAATGTAG     ACTA
                                  G        TTAA__
GAM245  ZNF238   3'  CATTGTGAGTGATTGCT     20958         GTTG
                                GGTAGTTAC    CATAGTG
                                |||||||||    |||||||
                                TCGTTAGTG    GTGTTAC
                                     A___
GAM245  ZNF304   3'  ACTGTAAACGTGATAGCTGT   40311      A      GC
                                GCGGT GTTACGTT  ATAGT
                                ||||| ||||||||  |||||
                                TGTCG TAGTGCAA  TGTCA
                                  A       A_
GAM245  ZNF333   3'  ATTGTTATGAATAAAGCTGCTG 50569         AC   G    TG
           T                     GCGGTAGTT  GTT CATAG  GT
                                |||||||||  ||| |||||  ||
                                TGTCGTCGA  TAA GTATT  TA
                                     AA  _    GT
GAM245  LOC112703 5'  GCCCCAGCGCTGGCTGCCGC   73500         _    CATAGT
                                GCGGTAGTTA CGTTG     GGT
                                |||||||||| |||||     |||
                                CGCCGTCGGT GCGAC     CCG
                                     C    C_____
GAM245  LOC113523 3'  TCATTGTGTAAACATCATGTTG 73049    GG  GTTACG       GT
           T                     GC  TA     TTGCATAGTG
                                ||  ||     ||||||||||
                                TG  GT     AATGTGTTAC
                                 TT  ACTACA         TG
GAM245  LOC115123 5'  GCCATTAGCAGAGTAATTGCTG 73221          G    A
           T                     GCGGTAGTTAC TTGC TAGTGGT
                                |||||||||||| |||| |||||||
                                TGTCGTTAATG GACG ATTACCG
                                     A   _
GAM245  LOC115265 3'  TGCATGGCTATTGT       73355          CGT
                                GCGGTAGTTA   TGCA
                                ||||||||||   ||||
                                TGTTATCGGT   ACGT
                                     ___
GAM245  LOC115297 3'  TGCATGAGTAATTATTGC    72889          GT_
                                GCGGTAGTTAC   TGCA
                                ||||||||||   ||||
                                CGTTATTAATG   ACGT
                                     AGT
GAM245  LOC115297 3'  ATCACTGTGAAATTGACTG   72883       C   G
                                TAGTTA GTT CATAGTGGT
                                |||||| ||| |||||||||
                                GTCAGT TAA GTGTCACTA
                                   _  A
GAM245  LOC115557 5'  GCTGGCAAAATGCGGCTGCTGC 56011         TA   __   A
                                GCGGTAGT  CGT  TGC TAGT
                                ||||||||  |||  ||| ||||
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                                CGTCGTCG  GTA  ACG GTCG
                                    GC   AA  _
GAM245  LOC115708 3'  GCTGGAATTCAGTGTGGCTGCC 73553          CA___   GGT
                                GGTAGTTACGTTG    TAGT
                                ||||||||||||    ||||
                                CCGTCGGTGTGAC    GTCG
                                      TTAAG
GAM245  LOC116123 3'  ACCACTGTGTAGTATTTTACC  57085     T_  GT
                                GGTAG  TAC  TGCATAGTGGT
                                |||||  |||  ||||||||||
                                CCATT  ATG  ATGTGTCACCA
                                  TT  __
GAM245  LOC116123 5'  GTGCTGTGGAATGACTGT    57088     AGTTA   G    GG
                                GCGGT    CGTT CATAGT  T
                                |||||    |||| ||||||  |
                                TGTCA    GTAA GTGTCG  G
                                  _____   G    TT
GAM245  LOC118668 5'  ACTGTGTTTACTCCGC     75477     T   TACGTT
                                GCGG AGT     GCATAGT
                                |||| |||     |||||||
                                CGCC TCA     TGTGTCA
                                  _  TT____
GAM245  LOC118738 3'  TACTAGTTAGCTATTGT     75495         CGTT  A
                                GCGGTAGTTA    GC TAGTG
                                ||||||||||   || |||||
                                TGTTATCGAT    TG ATCAT
                                      ____ _
GAM245  LOC118812 3'  CCAGTGTAGCCTGCTGT     73929       TTAC     AG
                                GCGGTAG   GTTGCAT  TGG
                                |||||||   |||||||  |||
                                TGTCGTC   CGATGTG  ACC
                                    ____    __
GAM245  LOC120196 3'  GCTTTGAATGTAGCTGTTGT   75548    GG       G  T
                                GC  TAGTTACGTT CA AGT
                                ||  |||||||||| || |||
                                TG  GTCGATGTAA GT TCG
                                 TT        _ T
GAM245  LOC120526 3'  GTTGCTAAAGTTATGGGGCTGT 74017    GG   TA   T  A_   GG
          TGT                    GC  TAGT  CGT GC  TAGT  T
                                ||  ||||  ||| ||  ||||  |
                                TG  GTCG  GTA TG  ATCG  G
                                 TT   GG   T  AA   TT
GAM245  LOC120856 3'  ATGTGATGTAACTGATGT    74026     G       TG
                                GCG TAGTTACGT  CAT
                                ||| |||||||||  |||
                                TGT GTCAATGTA  GTA
                                  A       GT
GAM245  LOC121274 3'  CACTGCCAGGGCTGCCGT    74061         ACGTT   TA
                                GCGGTAGTT    GCA  GTG
                                |||||||||    |||  |||
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                                TGCCGTCGG    CGT  CAC
                                     GAC__   __
GAM245  LOC121838 5'  GCTGCTATGGTGTACTA     76001      T   TTG     TG
                                TAGT ACG   CATAG  GT
                                |||| |||   |||||  ||
                                ATCA TGT   GTATC  CG
                                  _   G__     GT
GAM245  LOC122769 5'  GCCAGCTTGACGTGGTTGTGGC 74153    G    TT     CAT  _
                                GC GTAG  ACGTTG   AG TGGT
                                || ||||  ||||||   || ||||
                                CG TGTT  TGCAGT   TC ACCG
                                 G   GG     ___ G
GAM245  LOC123096 5'  ACCAGCGCGGGTCTAGCTGCTG 74196          CG_    ATAG
           C                     GCGGTAGTTA   TTGC    TGGT
                                ||||||||||   ||||    ||||
                                CGTCGTCGAT   GGCG    ACCA
                                      CTG    CG__
GAM245  LOC123242 5'  GCCACTGTGTGGATGCTGCAGC 75601    G     TACG TG
                                GC GTAGT    T  CATAGTGGT
                                || |||||    |  |||||||||
                                CG CGTCG    G  GTGTCACCG
                                 A     TA__ GT
GAM245  LOC124753 3'  ACCACTATGTCCTGGTGACTAC 74316          GTT_
           TG                     CGGTAGTTAC    GCATAGTGGT
                                ||||||||||    ||||||||||
                                GTCATCAGTG    TGTATCACCA
                                      GTCC
GAM245  LOC124977 5'  CACTGGTGAAGCTGCCGT     76056          ACG TG A
                                GCGGTAGTT   T  C TAGTG
                                |||||||||   |  | |||||
                                TGCCGTCGA   A  G GTCAC
                                     ___ GT _
GAM245  LOC126364 5'  GCTGCTGTTGCCGCTGCTGCTG 75692         TA  TT   _   TG
           C                     GCGGTAGT  CG  GCA TAG  GT
                                |||||||  ||  ||| |||  ||
                                CGTCGTCG  GC  CGT GTC  CG
                                     TC  __   T   GT
GAM245  LOC126364 3'  ATTACAGGCGTGGCCACTGC   75683       A       GCA
                                GCGGT GTTACGTT   TAGT
                                ||||| ||||||||   ||||
                                CGTCA CGGTGCGG   ATTA
                                   C       AC_
GAM245  LOC126564 5'  CCACTGTTACTGGCTG      75714        C  TGC
                                TAGTTA GT   ATAGTGG
                                |||||| ||   |||||||
                                GTCGGT CA   TGTCACC
                                   _ T__
GAM245  LOC126823 5'  CACTGTGCGGCCCTGCTCC   74574    T   TAC
                                GG AGT   GTTGCATAGTG
                                || |||   ||||||||||
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                                CC TCG   CGGCGTGTCAC
                                 _  TCC
GAM245  LOC126917 3'  GCCGTGGTGTAATGTGGTTTCT 74585     T  TT       AG
              GC                  GCGG AG  ACGTTGCAT  TGGT
                                  |||| ||  |||||||||  ||||
                                  CGTC TT  TGTAATGTG  GCCG
                                    T  GG        GT
GAM245  LOC129526 3'  CATTGTGGAAAGTTGACTGT   74877      AGTT  G  G
                                  GCGGT    AC TT CATAGTG
                                  |||||    || || |||||||
                                  TGTCA    TG AA GTGTTAC
                                    GT__  A  G
GAM245  LOC129566 5'  CGCTGGCTGTGCTGCTGC    75728        T   TT  A   TG
                                  GCGGTAGT ACG  GC TAG  G
                                  |||||||| |||  || |||  |
                                  CGTCGTCG TGT  CG GTC  C
                                      _  __  _  GT
GAM245  LOC130026 3'  GCTGATAAAAACGTAGCTACCG 56648           GCA__    GGT
              T                   GCGGTAGTTACGTT    TAGT
                                  ||||||||||||||    ||||
                                  TGCCATCGATGCAA    GTCG
                                         AAATA
GAM245  LOC130074 3'  ATTGTTATGTATTAATACTGC  76126       GTTACGT      TG
                                  GCGGTA      TGCATAG  GT
                                  ||||||      |||||||  ||
                                  CGTCAT      ATGTATT  TA
                                     AATT___      GT
GAM245  LOC130436 5'  ATTGTGGGATGTATTATTGT   74933        T    G
                                  GCGGTAGT ACGTT CATAGT
                                  |||||||| ||||| ||||||
                                  TGTTATTA TGTAG GTGTTA
                                      _    G
GAM245  LOC130916 5'  GCTTCCGGCGCCGTAACTGCTG 74992           T   AT__   GGT
              C                    GCGGTAGTTACG TGC    AGT
                                   |||||||||||| |||    |||
                                   CGTCGTCAATGC GCG    TCG
                                         C   GCCT
GAM245  LOC131308 3'  ATTACTATGCAAGCTGTTTACT 75003      T  CG
                                  GGTAG TA  TTGCATAGTGGT
                                  ||||| ||  ||||||||||||
                                  TCATT GT  AACGTATCATTA
                                    T  CG
GAM245  LOC131873 3'  ACCACTGTGGGAGTTGTTTGC  75874     TAGTT  G  G
                                  GCGG     AC TT CATAGTGGT
                                  ||||     || || |||||||||
                                  CGTT     TG AG GTGTCACCA
                                    TGT__  _  G
GAM245  LOC131968 5'  GCCGCTGTGCACGTGACCGTCG 75885      TA      T
              C                    GCGG  GTTACGT GCATAGTGGT
                                   ||||  ||||||| ||||||||||
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                                CGCT  CAGTGCA CGTGTCGCCG
                                  GC      _
GAM245  LOC133121 3'  ACCAAACTTGGAGTGGTTATTG 75080       TT  GTTG  TAG_
            C                    GCGGTAG  AC    CA    TGGT
                                 |||||||  ||    ||    ||||
                                 CGTTATT  TG    GT    ACCA
                                     GG  AG__  TCAA
GAM245  LOC133634 5'  GCCACTGTGTTTCAACTGTCGC 75106     GT    ACGTT
                                 GCG  AGTT    GCATAGTGGT
                                 |||  ||||    ||||||||||
                                 CGC  TCAA    TGTGTCACCG
                                   TG   CTT__
GAM245  LOC133634 5'  GCCGCTGTGTTGGAACTGCCAG 75107    _      ACGTT
            C                    GC GGTAGTT    GCATAGTGGT
                                 || |||||||    ||||||||||
                                 CG CCGTCAA    TGTGTCGCCG
                                  A      GGT__
GAM245  LOC134111 3'  GCTGATTTGTGGTGTGCTGCTG 75137        T   TT   TAG
            T                    GCGGTAGT ACG  GCA   TGGT
                                 ||||||||  |||  |||   ||||
                                 TGTCGTCG TGT  TGT   GTCG
                                     _  GG   TTA
GAM245  LOC134288 3'  TGTTACCTGACAACCGT     75180      A   C  T
                                 GCGGT GTTA GT GCA
                                 |||||  |||| ||  |||
                                 TGCCA CAGT CA TGT
                                   A    C  T
GAM245  LOC134637 3'  TGGAATGTAATTGTGGT     75204    G        G
                                 GC GTAGTTACGTT CA
                                 ||  ||||||||||  ||
                                 TG TGTTAATGTAA GT
                                  G         G
GAM245  LOC135818 3'  CAAAAGCTGCAGTGAGCTACTG 75230         A      TAGTGGT
            T                    GCGGTAGTT CGTTGCA
                                 |||||||||  |||||||
                                 TGTCATCGA GTGACGT
                                     _      CGAAAACT
GAM245  LOC135818 5'  CCCTCGGTGTGCTACTGT     75233        T   TT CAT  T
                                 GCGGTAGT ACG  G   AG GG
                                 |||||||  |||  |   || ||
                                 TGTCATCG TGT  C   TC CC
                                     _  GG ___  _
GAM245  LOC136120 3'  CCATCAACCTGGCTGCTGT    76204          C    CATA
                                 GCGGTAGTTA GTTG    GTGG
                                 ||||||||||  ||||    ||||
                                 TGTCGTCGGT CAAC    TACC
                                      C    ____
GAM245  LOC136319 3'  ACTGTCTGAGCAGTAGTGGCTG 75258          GT_   A   _
            CTGT                   CGGTAGTTAC   TGC TAG TGGT
                                 ||||||||||   ||| ||| ||||
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                                GTCGTCGGTG   ACG GTC GTCA
                                      ATG   A   T
GAM245   LOC138240 3'  ATCACAAAATGATGGCTATTGT 75304          _    GCATA
                                GCGGTAGTTA CGTT    GTGGT
                                |||||||||| ||||    |||||
                                TGTTATCGGT GTAA    CACTA
                                      A   AA___
GAM245   LOC139422 5'  GCCACTGTACCTGGTTACTGT  75841        TT C  TGC
                                GCGGTAG  A GT   ATAGTGGT
                                |||||||  | ||  ||||||||
                                TGTCATT  T CA   TGTCACCG
                                    GG C  ___
GAM245   LOC139673 3'  TGCCAGTGTGATTAGCGC    75982     G         _
                                GCG TAGTTACGTTG CA
                                ||| ||||||||||| ||
                                CGC ATTAGTGTGAC GT
                                  G         C
GAM245   LOC142820 5'  TTACAGGTGAGGCTGCTGT   76400         ACG TG ATA
                                GCGGTAGTT   T  C   GTGG
                                |||||||||   |  |   ||||
                                TGTCGTCGG   A  G   CATT
                                      ___ GT GA_
GAM245   LOC143098 3'  GCTGGTCTCAGGTGTGGCTGCT 76454           GCA___    GGT
           GC                    CGGTAGTTACGTT     TAGT
                                ||||||||||||     ||||
                                GTCGTCGGTGTGG     GTCG
                                      ACTCTG
GAM245   LOC143153 3'  CACTGTTGGTGGCTGCC     76462         GTTGC
                                GGTAGTTAC     ATAGTG
                                |||||||||     ||||||
                                CCGTCGGTG     TGTCAC
                                      GT___
GAM245   LOC143154 3'  CACTGTTGGTGGCTGCC     76479         GTTGC
                                GGTAGTTAC     ATAGTG
                                |||||||||     ||||||
                                CCGTCGGTG     TGTCAC
                                      GT___
GAM245   LOC143392 5'  CCAAGATGTAACTATC      82950           GCATAG
                                GGTAGTTACGTT      TGG
                                ||||||||||||      |||
                                CTATCAATGTAG      ACC
                                      A_____
GAM245   LOC144165 3'  ACAGATGGACGTAGCTGCT   76677           G   AG  GT
                                GGTAGTTACGTT CAT  TG
                                |||||||||||| |||  ||
                                TCGTCGATGCAG GTA  AC
                                      _  G_  AT
GAM245   LOC144305 3'  ACTGCTATGGCCAGCTATT   83031         AC  TG    TG
                                GGTAGTT  GT  CATAG  GT
                                |||||||  ||  |||||  ||
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                                TTATCGA  CG  GTATC  CA
                                   C_  __    GT
GAM245   LOC144363 3'  ATTATTAATGTTGCTGCTGC   76823        T     C
                                GCGGTAGT ACGTTG ATAGT
                                |||||||| |||||| |||||
                                CGTCGTCG TGTAAT TATTA
                                     T     _
GAM245   LOC144483 3'  ACCTGCGTGGTGATGTGACAAC 60176      A      TG ATA  _
           TGT                    GCGGT GTTACGT  C   GT GGT
                                |||||  |||||||  |   || |||
                                TGTCA CAGTGTA  G   CG CCA
                                   A      GT GTG  T
GAM245   LOC144587 5'  ATCACTGTGCGGCTCAAATTCC 67027    T    AC_
                                GG AGTT   GTTGCATAGTGGT
                                || ||||   ||||||||||||
                                CC TTAA   CGGCGTGTCACTA
                                 _    ACT
GAM245   LOC144600 3'  GTTATTAAAAGCGAGCTATTGC 83163         A    GCA     GT
                                GCGGTAGTT CGTT   TAGTG
                                |||||||| ||||   |||||
                                CGTTATCGA GCGA   ATTAT
                                      _    AA_    TGT
GAM245   LOC144755 5'  ACTAGGGGTGAGGCTGCTGC   83183        TA  TTGCA
                                GCGGTAGT  CG     TAGT
                                ||||||||  ||     ||||
                                CGTCGTCG  GT     ATCA
                                     GA  GGGG_
GAM245   LOC144970 5'  CCACTGTGAAGACTGGTGT    76981     G     ACGTTG
                                GCG TAGTT      CATAGTGG
                                ||| |||||      ||||||||
                                TGT GTCAG      GTGTCACC
                                  G    AA____
GAM245   LOC145231 3'  GCCGGATGTGGTGCCGC      83288       G      __
                                GCGGTA TTACGTT  GC
                                |||||| |||||||  ||
                                CGCCGT GGTGTAG  CG
                                    _      GC
GAM245   LOC145371 3'  TGCACTGCGTGGCTGCAGC    77158    G        __
                                GC GTAGTTACGT  TGCA
                                || ||||||||||  ||||
                                CG CGTCGGTGCG  ACGT
                                 A         TC
GAM245   LOC145483 5'  ATCGCTGTCACTGTCGCTGCTG 77240         T   T  C
           C                     GCGGTAGT ACG TG ATAGTGGT
                                |||||||| ||| || ||||||||
                                CGTCGTCG TGT AC TGTCGCTA
                                     C   C  _
GAM245   LOC145483 5'  GCCACTATCGCTGTCACTGTCG 77244     GT   T   TT  _
           C                     GCG  AGT ACG  GC ATAGTGGT
                                |||  ||| |||  || ||||||||
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                                CGC  TCA TGT  CG TATCACCG
                                  TG   C   __ C
GAM245   LOC145566 5'  GCCAGTGAGATGTGATGCCGC  77276       G     TG   AG
                                GCGGTA TTACGT  CAT  TGGT
                                |||||| ||||||  |||  ||||
                                CGCCGT AGTGTA  GTG  ACCG
                                   _     GA   __
GAM245   LOC145623 3'  TCATTGTGTCAATTCCTGC    83401      TTAC   _
                                GTAG    GTTG CATAGTGG
                                ||||    |||| ||||||||
                                CGTC    TAAC GTGTTACT
                                  CT__    T
GAM245   LOC145645 3'  TGTTAATGAGTAATTGCCGT   77326          GTT___
                                GCGGTAGTTAC     GCA
                                ||||||||||      |||
                                TGCCGTTAATG     TGT
                                      AGTAAT
GAM245   LOC145676 5'  AGCATTTCAGTGTGACTGTTGT 77331    GG        CAT    GT
                                GC  TAGTTACGTTG   AGTG
                                ||  ||||||||||   ||||
                                TG  GTCAGTGTGAC   TTAC
                                 TT         T__    GAT
GAM245   LOC145676 5'  TGTGTAATGTGGCTGTGGT    77342    G
                                GC GTAGTTACGTTGCATA
                                || ||||||||||||||||
                                TG TGTCGGTGTAATGTGT
                                 G
GAM245   LOC145725 3'  CGCTGTGCCTGCTCTGC     77405     T   TACGTT     TG
                                GCGG AGT     GCATAG  G
                                |||| |||     ||||||  |
                                CGTC TCG     CGTGTC  C
                                  _   TC_____     GT
GAM245   LOC145732 3'  CGCTGTGCCTGCTCTGC     77427     T   TACGTT     TG
                                GCGG AGT     GCATAG  G
                                |||| |||     ||||||  |
                                CGTC TCG     CGTGTC  C
                                  _   TC_____     GT
GAM245   LOC145790 3'  ACTATAATTGTTTGACTACTGC 77483          CGTT   TA_
                                GCGGTAGTTA    GCA   GTGGT
                                ||||||||||    |||   |||||
                                CGTCATCAGT    TGT   TATCA
                                      T___    TAA
GAM245   LOC145790 3'  ATCACTGTGAAGAAATGCTGT  77485       GTTACGTTG
                                GCGGTA        CATAGTGGT
                                ||||||        |||||||||
                                TGTCGT        GTGTCACTA
                                   AAAGAA___
GAM245   LOC145790 5'  TCACTGTAAAAGTGATTGCT   77489         G  GC     GT
                                GGTAGTTAC TT  ATAGTG
                                ||||||||| ||  ||||||
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                                TCGTTAGTG AA  TGTCAC
                                     A  A_     TG
GAM245  LOC145853 5'  GCCGCTGTGCGCACGCGCCGCC 83559      TA  TA  _
           GC                    GCGG  GT  CGT TGCATAGTGGT
                                 ||||  ||  ||| ||||||||||
                                 CGCC  CG  GCA GCGTGTCGCCG
                                   GC  C_  C
GAM245  LOC145955 3'  ACTGTCTTACGCTGTGACTGTT 83585    GG      T  C___    GGT
           GT                    C  TAGTTACG TG    ATAGT
                                 |  |||||||| ||    |||||
                                 G  GTCAGTGT GC    TGTCA
                                  TT       C  ATTC
GAM245  LOC145980 5'  CCACAGTGGACTGTCGC     83602     GT    ACGTTG   A
                                 GCG  AGTT     CAT GTGG
                                 |||  ||||     ||| ||||
                                 CGC  TCAG     GTG CACC
                                   TG   _______   A
GAM245  LOC146050 3'  ATTGGGAAAATGGACTACTGT  77628         A    GCA_
                                 GCGGTAGTT CGTT    TAGT
                                 |||||||||| ||||    ||||
                                 TGTCATCAG GTAA    GTTA
                                      _    AAGG
GAM245  LOC146108 5'  GCCGCTGTCCCTTAGCTGACGC 77666     G     CGTTGC
                                 GCG TAGTTA     ATAGTGGT
                                 ||| ||||||     ||||||||
                                 CGC GTCGAT     TGTCGCCG
                                   A     TCCC__
GAM245  LOC146136 5'  GCCATGACAGGTGTTGATTGCT 72945          _   GCATA
           GC                    GCGGTAGTTA CGTT     GTGGT
                                 |||||||||| ||||     |||||
                                 CGTCGTTAGT GTGG     TACCG
                                       T    ACAG_
GAM245  LOC146167 3'  GCTGACCCTACGTGGCTGCTGT 77687            TGCA_
                                 GCGGTAGTTACGT     TAGT
                                 ||||||||||||     ||||
                                 TGTCGTCGGTGCA     GTCG
                                         TCCCA
GAM245  LOC146268 3'  ACTAGCCTCAGTGTGGCTGCTG 77798             CA__    GGT
           C                     GCGGTAGTTACGTTG    TAGT
                                 ||||||||||||||    ||||
                                 CGTCGTCGGTGTGAC    ATCA
                                         TCCG
GAM245  LOC146307 5'  CCGCTGTGGGGGTTGTGGC    83656       __  G
                                 GTTACG  TT CATAGTGG
                                 ||||||  || ||||||||
                                 CGGTGT  GG GTGTCGCC
                                    TG  G
GAM245  LOC146346 5'  CCTGTGGTGTGACTTCTGC    77839      T      TT   TAGT
                                 GCGG AGTTACG  GCA    GG
                                 |||| |||||||  |||    ||
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                                CGTC TCAGTGT  TGT    CC
                                  T      GG  ____
GAM245  LOC146733 3'  CTATTGTGAATAGTGCCGC   83761      AGTT  GTTG
                                GCGGT    AC    CATAGTGG
                                ||||||   ||   ||||||||
                                CGCCG    TG    GTGTTATC
                                  ____  ATAA
GAM245  LOC146745 5'  GCCGTTGTCGCCGTCGCTGCTG 78088        T   T  C
          C                      GCGGTAGT ACG TG ATAGTGGT
                                ||||||||| ||| || ||||||||
                                CGTCGTCG TGC GC TGTTGCCG
                                     C   C  _
GAM245  LOC146856 3'  ATTGTTCATAATGTAATGCCGT 82799       G       CAT  TG
                                GCGGTA TTACGTTG   AG  GT
                                ||||||| ||||||||   ||  ||
                                TGCCGT AATGTAAT   TT  TA
                                   _       AC_  GT
GAM245  LOC146990 5'  ACTATTATGCGTGTTGCTGT   83883       TTACGT
                                GCGGTAG     TGCATAGTGGT
                                |||||||     ||||||||||||
                                TGTCGTT     GCGTATTATCA
                                    GT_____
GAM245  LOC147072 3'  GTGCTGCGCAGAACTATCGT   60409         ACG   A   GG
                                GCGGTAGTT   TTGC TAGT  T
                                |||||||||   |||| ||||  |
                                TGCTATCAA   GACG GTCG  G
                                     ___    C    TT
GAM245  LOC147081 3'  ATTATTATTCTAGTACTGCTGT 78240        T  GTTGC
                                GCGGTAGT AC     ATAGTGGT
                                |||||||| ||     ||||||||
                                TGTCGTCA TG     TATTATTA
                                    _  ATCT_
GAM245  LOC147081 5'  GCCACTAGGTGGTGCTGCTGC  78242         TAC TT  A
                                GCGGTAGT   G  GC TAGTGGT
                                ||||||||   |  || |||||||
                                CGTCGTCG   T  TG ATCACCG
                                    ___ GG  G
GAM245  LOC147157 3'  ACCACTGTGTATTTAACTGCC  83978         CGT
                                GGTAGTTA   TGCATAGTGGT
                                ||||||||   ||||||||||||
                                CCGTCAAT   ATGTGTCACCA
                                     TT_
GAM245  LOC147160 5'  ACCACTATACACTGACTG     83955       C  T C
                                TAGTTA GT G ATAGTGGT
                                |||||| || | ||||||||
                                GTCAGT CA C TATCACCA
                                   _  _ A
GAM245  LOC147180 5'  ATTACTATGTATATTTACTATT 83982         TACGT
          G                      CGGTAGT     TGCATAGTGGT
                                |||||||     ||||||||||||
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                                GTTATCA    ATGTATCATTA
                                   TTTAT
GAM245  LOC147229 3'  ACTCAACCTGGCTACTGT    78316         C    CAT
                                GCGGTAGTTA GTTG   AGT
                                |||||||||| ||||   |||
                                TGTCATCGGT CAAC   TCA
                                     C   ___
GAM245  LOC147381 5'  GCTGCTAGCAATGGCGTGCTGC 84012       TA__     A   TG
          TGC                    CGGTAGT    CGTTGC TAG  GT
                                |||||||    |||||| |||  ||
                                GTCGTCG    GTAACG ATC  CG
                                   TGCG     _   GT
GAM245  LOC147495 3'  GCCATTTTCCTGTGGTTGCAGC 84015    G    TT   TTGCAT
                                GC GTAG  ACG     AGTGGT
                                || ||||  |||     ||||||
                                CG CGTT  TGT     TTACCG
                                  A   GG   CCTT__
GAM245  LOC147929 3'  TTTTTAATGTAGTGTAATTAAT 78575     G          AGTGGT
          GT                     GCG TAGTTACGTTGCAT
                                ||| ||||||||||||||
                                TGT ATTAATGTGATGTA
                                  A           ATTTTTA
GAM245  LOC148089 3'  GCTACTTGGCGCGGCTACCGT  78634        TA    CAT
                                GCGGTAGT  CGTTG   AGTGGT
                                ||||||||  |||||   ||||||
                                TGCCATCG  GCGGT   TCATCG
                                     GC    ___
GAM245  LOC148147 3'  CCACAAGTGTGGTGCTGC    78673       GTTACG TG   A_
                                GCGGTA     T  CAT  GTGG
                                ||||||     |  |||  ||||
                                CGTCGT     G  GTG  CACC
                                   _______ GT   AA
GAM245  LOC148193 5'  CGAGGCGTAGCGCTGC      60337       A      TGCATAG
                                GCGGT GTTACGT      TG
                                ||||| |||||||      ||
                                CGTCG CGATGCG      GC
                                   _      GA_____
GAM245  LOC148198 3'  TTAAAGGTGCAATTACTGT   70691       GTTAC      AG_
                                GCGGTA    GTTGCAT   TGG
                                ||||||    |||||||   |||
                                TGTCAT    TAACGTG   ATT
                                   _____      GAA
GAM245  LOC148223 3'  ATTGCTGTACTGTGATTCTGT  78732     T      T    TA TG
                                GCGG AGTTACG TGCA  G  GT
                                |||| ||||||| ||||  |  ||
                                TGTC TTAGTGT ATGT  C  TA
                                   _      C   __ GT
GAM245  LOC148443 3'  TCACTAAGTAGCTGCC      78861         GTTGCA
                                GGTAGTTAC     TAGTGG
                                |||||||||     ||||||
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                                CCGTCGATG     ATCACT
                                     A_____
GAM245  LOC148530 5'  CCACGTGGTGTAGCTCTGC    84162      T      TT  ATA
                                GCGG AGTTACG  GC   GTGG
                                |||| |||||||  ||   ||||
                                CGTC TCGATGT  TG   CACC
                                  _      GG  ___
GAM245  LOC148753 3'  ACTGCTGTCACTGTAGCTGCT  84209          T  C    TG
                                GGTAGTTACG TG ATAG  GT
                                |||||||||| || ||||  ||
                                TCGTCGATGT AC TGTC  CA
                                      C  _    GT
GAM245  LOC148756 5'  TGAACTGACTGCTGT       84222          C   G
                                GCGGTAGTTA GTT CA
                                |||||||||| ||| ||
                                TGTCGTCAGT CAA GT

                                      _  _
GAM245  LOC148758 5'  CCCTTTGATGTGGCTGC     78967          GCAT  T
                                GTAGTTACGTT    AG GG
                                ||||||||||    || ||
                                CGTCGGTGTAG    TC CC
                                       TT__  _
GAM245  LOC148764 5'  GCCAGGTCTTTCATGTAACTGC 78986           TGCATAG_
          TGC                     GCGGTAGTTACGT       TGGT
                                |||||||||||||       ||||
                                CGTCGTCAATGTA       ACCG
                                       CTTTCTGG
GAM245  LOC148809 3'  ACTATGTGTTAGCTGCTGT    78997          CGT
                                GCGGTAGTTA   TGCATAGT
                                |||||||||   ||||||||
                                TGTCGTCGAT   GTGTATCA
                                      T__
GAM245  LOC148898 3'  GCCACTGTGCCTGTGGAGCACT 84252       AG_    TT
          GT                      GCGGT   TTACG  GCATAGTGGT
                                |||||   |||||  ||||||||||
                                TGTCA   GGTGT  CGTGTCACCG
                                  CGA    C_
GAM245  LOC149073 3'  ATTGCTGTGACTCATGGCTTTG 84323      T    CGTTG    TG
          T                       GCGG AGTTA     CATAG  GT
                                |||| |||||    |||||  ||
                                TGTT TCGGT     GTGTC  TA
                                  _    ACTCA     GT
GAM245  LOC149127 3'  GCCACTGTGAGTGGGCTGCC   84347        ACGTTG
                                GGTAGTT      CATAGTGGT
                                |||||||      |||||||||
                                CCGTCGG      GTGTCACCG
                                    GTGA__
GAM245  LOC149194 3'  GCTCATGACGTGGCTTCTGC   79227      T       _____
                                GCGG AGTTACGTT    GC
                                |||| |||||||||    ||
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                                CGTC TCGGTGCAG   CG
                                  T       TACT
GAM245  LOC149372 5'  GCCTCTGTAATGTGGTTCTGC  79325     T  TT      TA T
                                GCGG AG  ACGTTGCA  G GGT
                                |||| ||  ||||||||  | |||
                                CGTC TT  TGTAATGT  C CCG
                                  _  GG       __ T
GAM245  LOC149401 3'  TGCTTTGGATTGCTGC      79337         A  TT
                                GCGGTAGTT CG  GCA
                                ||||||||| ||  |||
                                CGTCGTTAG GT  CGT
                                      _ TT
GAM245  LOC149478 3'  ACCACAACGCCCGGCTAATTGT 79374   GG     C   __ ATA
           TGT                    C  TAGTTA GTT  GC   GTGGT
                                |  |||||| |||  ||   |||||
                                G  GTTAAT CGG  CG   CACCA
                                 TT     _   CC  CAA
GAM245  LOC149535 5'  CCGTTCCATGTACTGCCGC   79416        T   TGCATAG
                                GCGGTAGT ACGT      TGG
                                |||||||| ||||      |||
                                CGCCGTCA TGTA      GCC
                                     _   CCTT___
GAM245  LOC149664 3'  GTTCGAGCGGCGTGGCTGCTGT 79471              ATAGTGGT
                                GCGGTAGTTACGTTGC
                                ||||||||||||||||
                                TGTCGTCGGTGCGGCG
                                        AGCTTG
GAM245  LOC149664 3'  TGCTGTGGTTCGAGCGGCGTGG 79472          _______    GGT
           CTGCTGT                  TTACGTTGC      ATAGT
                                |||||||||      |||||
                                GGTGCGGCG      TGTCG
                                     AGCTTGG       TG
GAM245  LOC149705 3'  GCTGCTGTGGATTCTTGTAGCT 84625   G      TTG___    TG
           ATGC                   G TAGTTACG     CATAG  GT
                                | ||||||||     |||||  ||
                                T ATCGATGT     GTGTC  CG
                                _      TCTTAG    GT
GAM245  LOC149722 5'  GCCACTGTGCAGTCAGAC    84603     ACG
                                GTT   TTGCATAGTGGT
                                |||   ||||||||||||
                                CAG   GACGTGTCACCG
                                  ACT
GAM245  LOC149844 3'  ATTATTATGGTTATGATTACC  79514        CGTTG
                                GGTAGTTA    CATAGTGGT
                                ||||||||    |||||||||
                                CCATTAGT    GTATTATTA
                                     ATTG_
GAM245  LOC149844 5'  GCTGCTCGTGCCTGAGCTACCG 79515         ACGTT   _  TG
           C                    GCGGTAGTT    GCAT AG  GT
                                |||||||||    |||| ||  ||
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                                CGCCATCGA    CGTG TC  CG
                                     GTC__   C  GT
GAM245  LOC150142 5'  CGTTGTGAAAGGTGCCGT    79575      AGTT  G  G    TG
                                GCGGT   AC TT CATAG  G
                                |||||   || || |||||  |
                                TGCCG   TG AA GTGTT  C
                                  ____  G  A    GT
GAM245  LOC150174 3'  TGCTATGCGAGTGGCTGCCGT  79612          G
                                GCGGTAGTTAC TTGCATAGTG
                                |||||||||| ||||||||||
                                TGCCGTCGGTG AGCGTATCGT
                                          _
GAM245  LOC150183 5'  CCCCGTGGGTGGCTACTGC   84910          G TG ATAGT
                                GCGGTAGTTAC T  C    GG
                                |||||||||| |  |    ||
                                CGTCATCGGTG G  G    CC
                                      _ GT CC___
GAM245  LOC150184 5'  CCCCGTGGGTGGCTACTGC   84911          G TG ATAGT
                                GCGGTAGTTAC T  C    GG
                                |||||||||| |  |    ||
                                CGTCATCGGTG G  G    CC
                                      _ GT CC___
GAM245  LOC150185 5'  CCCCGTGGGTGGCTACTGC   84907          G TG ATAGT
                                GCGGTAGTTAC T  C    GG
                                |||||||||| |  |    ||
                                CGTCATCGGTG G  G    CC
                                      _ GT CC___
GAM245  LOC150213 3'  TGCTATGCGAGTGGCTGCCGT  74860          G
                                GCGGTAGTTAC TTGCATAGTG
                                |||||||||| ||||||||||
                                TGCCGTCGGTG AGCGTATCGT
                                          _
GAM245  LOC150236 3'  TGCTATGCGAGTGGCTGCCGT  79691          G
                                GCGGTAGTTAC TTGCATAGTG
                                |||||||||| ||||||||||
                                TGCCGTCGGTG AGCGTATCGT
                                          _
GAM245  LOC150351 5'  ACTGGAGTAACTACTGT     60247          GTTGCA
                                GCGGTAGTTAC     TAGT
                                ||||||||||      ||||
                                TGTCATCAATG     GTCA
                                      AG____
GAM245  LOC150465 3'  GTCACTTTGACTGCTGT     79874          C_  T
                                GCGGTAGTTA  GT GC
                                |||||||||  || ||
                                TGTCGTCAGT  CA TG
                                      TT  C
GAM245  LOC150606 3'  ACTGATGTGATGACTGT     85087       A       GCAT
                                GCGGT GTTACGTT    AGT
                                ||||| ||||||||    |||
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                                TGTCA TAGTGTAG    TCA
                                  G       ____
GAM245  LOC150848 5'  ACCACTGCTCTGTAACTATT   85124          TT   TA
                                GGTAGTTACG  GCA  GTGGT
                                ||||||||||  |||  |||||
                                TTATCAATGT  CGT  CACCA
                                     CT   __
GAM245  LOC150848 5'  ATTATGGGATGTAACTAATGC  85127     G        G
                                GCG TAGTTACGTT CATAGT
                                ||| |||||||||| ||||||
                                CGT ATCAATGTAG GTATTA
                                  A         G
GAM245  LOC150848 3'  TGCTAGTGATTATTGC      85133           GTT
                                GCGGTAGTTAC   GCA
                                ||||||||||   |||
                                CGTTATTAGTG   CGT
                                      AT_
GAM245  LOC150848 5'  TTATTGTGTGAACTATGGT    85139    G    TACG TG
                                GC GTAGT    T  CATAGTGG
                                || |||||    |  ||||||||
                                TG TATCA    A  GTGTTATT
                                 G     _____ GT
GAM245  LOC150862 3'  ACTTCTCACAATGTAACTGCTG 80020             CAT  T
           T                     GCGGTAGTTACGTTG   AG GGT
                                ||||||||||||||   || |||
                                TGTCGTCAATGTAAC   TC TCA
                                        AC_  T
GAM245  LOC150967 5'  GCCACTATATCCTGGCTTTGT  80082      T    CGTTGC
                                GCGG AGTTA      ATAGTGGT
                                ||||  |||||      ||||||||
                                TGTT TCGGT      TATCACCG
                                  _     CCTA__
GAM245  LOC151009 3'  ACCATTGTGTGGCCACACTTGC 85190     GT   TAC  TG
                                GCG  AGT   GT  CATAGTGGT
                                |||  |||   ||  |||||||||
                                CGT  TCA   CG  GTGTTACCA
                                  __   CAC  GT
GAM245  LOC151098 5'  TGAAGCGTAATTAGCTGC     80118       _       G
                                GCGGT AGTTACGTT CA
                                |||||  |||||||||  ||
                                CGTCG TTAATGCGA GT
                                   A        A
GAM245  LOC151174 5'  ATTGCTGTGTAACAAATTGCCC 85249      _    AC        TG
           GC                     GCGG TAGTT  GTTGCATAG  GT
                                ||||  |||||  |||||||||  ||
                                CGCC GTTAA  CAATGTGTC  TA
                                  C     A_        GT
GAM245  LOC151188 5'  GCCACTGCCGCGGATTGGCTGT 80159    GG     CG    A_
           TGC                     GC  TAGTTA  TTGC  TAGTGGT
                                ||  ||||||  ||||  |||||||
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                                CG  GTCGGT  GGCG  GTCACCG
                                 TT     TA    CC
GAM245  LOC151195 3'  ATCATTGTGCACTCACTGCAGC 80165    G    TAC  T
                                GC GTAGT   GT GCATAGTGGT
                                || |||||   || ||||||||||
                                CG CGTCA   CA CGTGTTACTA
                                 A    CT_  _
GAM245  LOC151195 5'  GCTGTATGGAATGTGGACTACT 80170         _    G   G
              GC                  GCGGTAGTT ACGTT CATA TGGT
                                  ||||||||| ||||| |||| ||||
                                  CGTCATCAG TGTAA GTAT GTCG
                                       G    G   _
GAM245  LOC151234 3'  GTGTAATGAGTTACTGC     80176       GT A
                                  GCGGTA  T CGTTGCAT
                                  ||||||  | ||||||||
                                  CGTCAT  A GTAATGTG
                                     TG _
GAM245  LOC151300 5'  ATCATTGCACTGTGACTG     85305        T   TA
                                  TAGTTACG TGCA  GTGGT
                                  |||||||| ||||  |||||
                                  GTCAGTGT ACGT  TACTA
                                       C   __
GAM245  LOC151451 3'  ATGTGGGGTGACTGCTGC     80247          G TG
                                  GCGGTAGTTAC T  CAT
                                  |||||||||||  |  |||
                                  CGTCGTCAGTG G  GTA
                                        G GT
GAM245  LOC151473 3'  ATCATTACAGCTTTGGCTGCTG 80251          C_   CA
              T                    GCGGTAGTTA  GTTG  TAGTGGT
                                   ||||||||||  ||||  |||||||
                                   TGTCGTCGGT  CGAC  ATTACTA
                                        TT   __
GAM245  LOC151534 5'  CGCAGTGCAGCTGCCGC     56683        TACGT    A
                                  GCGGTAGT     TGCAT GTG
                                  ||||||||     ||||| |||
                                  CGCCGTCG     ACGTG CGC
                                       _____     A
GAM245  LOC151568 5'  GCCAGGCCCAGGGTGGCTGCTG 56696          G   CATAG
              C                    GCGGTAGTTAC TTG     TGGT
                                   ||||||||||| |||     ||||
                                   CGTCGTCGGTG GAC     ACCG
                                         G   CCGG_
GAM245  LOC151568 5'  GCTCAGGTGCGGTGTGGCCACC 56698      A     TT    AGT
              GC                    GCGGT GTTACG  GCAT   GGT
                                    ||||| ||||||  ||||   |||
                                    CGCCA CGGTGT  CGTG   TCG
                                      C     GG    GAC
GAM245  LOC151568 3'  GCTTGTACATATGTGATTGCTG 56700          ___   T   GGT
              T                    CGGTAGTTACGT   TGCA AGT
                                   ||||||||||||   |||| |||
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                                GTCGTTAGTGTA  ATGT TCG
                                      TAC   _
GAM245  LOC151571 5'  ACGCACAGCGTGACTCCCGC  85442     T       CATA  GT
                                GCGG AGTTACGTTG   GTG
                                |||| ||||||||||   |||
                                CGCC TCAGTGCGAC   CGC
                                  C       A___  AG
GAM245  LOC151584 3'  TGCGGGGTGTGATGCTGT    85451      GT_  G
                                GCGGTA  TAC TTGCA
                                ||||||  ||| |||||
                                TGTCGT  GTG GGCGT
                                   AGT  G
GAM245  LOC152059 3'  GTGCTAGCTGCTGT       80449         CGTT
                                GCGGTAGTTA   GCAT
                                ||||||||||   ||||
                                TGTCGTCGAT   CGTG
                                     ____
GAM245  LOC152106 3'  GCCGGGGGTGGCTATTGT    70061         G  __
                                GCGGTAGTTAC TT  GC
                                |||||||||| ||  ||
                                TGTTATCGGTG GG  CG
                                      G  GC
GAM245  LOC152179 5'  ACTATTAAGTGTAACCTATTGT 85558       TTAC     __
                                GCGGTAG   GTTGCAT  AGTGGT
                                |||||||   |||||||  ||||||
                                TGTTATC   CAATGTG  TTATCA
                                   ____     AA
GAM245  LOC152200 3'  ACTACTATAAATGTAGTTGCT  85572     GT    GC
                                GGTA  TACGTT  ATAGTGGT
                                ||||  ||||||  ||||||||
                                TCGT  ATGTAA  TATCATCA
                                  TG    A_
GAM245  LOC152273 3'  ATCGCCTCCTGAGGGTGACTGT 80534   GG     G  G  TA__
           TGC                   C  TAGTTAC TT CA   GTGGT
                                |  ||||||| || ||   |||||
                                G  GTCAGTG GA GT   CGCTA
                                 TT     G  _  CCTC
GAM245  LOC152275 3'  ATCATTTCCTATGTGATTACT  85617         TGCAT
                                GGTAGTTACGT    AGTGGT
                                ||||||||||    ||||||
                                TCATTAGTGTA    TTACTA
                                      TCCT_
GAM245  LOC152348 3'  TATTCTATGGCTGATTACTGT  85698        C  TG    TGGT
                                GCGGTAGTTA GT  CATAG
                                |||||||||| ||  |||||
                                TGTCATTAGT CG  GTATC
                                   _  __    TTATA
GAM245  LOC152582 5'  GCCATGTTTGATTGCCGC    85791         __   T
                                GCGGTAGTT  ACGT GC
                                |||||||||  |||| ||
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                                CGCCGTTAG  TGTA CG
                                     TT    C
GAM245  LOC152715 5'  CCCTGTTAATGTGACACTGC  80647      A       C    T
                                GCGGT GTTACGTTG ATAG GG
                                ||||| ||||||||| |||| ||
                                CGTCA CAGTGTAAT TGTC CC
                                   _       _   _
GAM245  LOC152905 3'  CGCTGTGCACTGCTGT     60474        TACGTT     TG
                                GCGGTAGT     GCATAG  G
                                ||||||||     ||||||  |
                                TGTCGTCA     CGTGTC  C
                                     _______     GT
GAM245  LOC152925 3'  GCTGTTATTAGTGATTGCT   80736        GTTGC    TG
                                GGTAGTTAC    ATAG  GT
                                |||||||||    ||||  ||
                                TCGTTAGTG    TATT  CG
                                     AT___    GT
GAM245  LOC152926 3'  TGTGTAGTGAAGCTACTGT   80748        A
                                GCGGTAGTT CGTTGCATA
                                ||||||||| |||||||||
                                TGTCATCGA GTGATGTGT
                                     A
GAM245  LOC153454 3'  TATGTGTAATTGTTGC     80838    GG     GTT
                                GC  TAGTTAC   GCATA
                                ||  |||||||   |||||
                                CG  GTTAATG   TGTAT
                                 TT     ___
GAM245  LOC153454 3'  TCACTGTGTGACACAGATTGC  80839      AC_  TG     GT
                                GTAGTT   GT  CATAGTG
                                ||||||   ||  |||||||
                                CGTTAG   CA  GTGTCAC
                                    ACA  GT      TG
GAM245  LOC153474 5'  GCTGCTGAAGCTGGCGTCGCTG 80846        T    _  A_   TG
           CCGC                     CGGTAGT ACGTT GC  TAG  GT
                                ||||||| ||||| ||  |||  ||
                                GCCGTCG TGCGG CG  GTC  CG
                                    C    T  AA   GT
GAM245  LOC153505 3'  CCGCCTGTGTGCTGCTGT    80848        TACGTT     _
                                GCGGTAGT     GCATAG TGG
                                ||||||||     |||||| |||
                                TGTCGTCG     TGTGTC GCC
                                     _______     C
GAM245  LOC153769 3'  GTTACTGTGTAGAATTTCTATG 80928    G    TTACG       GG
           GT                     GC GTAG    TTGCATAGT  T
                                || ||||    |||||||||  |
                                TG TATC    GATGTGTCA  G
                                 G   TTTAA       TT
GAM245  LOC153810 5'  ACCAGAGAAGTGTGGCACTGC  80932      A       GCATAG
                                GCGGT GTTACGTT     TGGT
                                ||||| ||||||||     ||||
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                                CGTCA CGGTGTGA     ACCA
                                  _       AGAG__
GAM245  LOC154007 3'  CCAGTGGTGACTACTGT     81016          GTTGCA  G
                                GCGGTAGTTAC     TA TGG
                                ||||||||||      || |||
                                TGTCATCAGTG     GT ACC
                                      _______  G
GAM245  LOC154007 3'  GCTGCTATGAATAATTACT    81020        CGTTG    TG
                                GGTAGTTA    CATAG  GT
                                ||||||||    |||||  ||
                                TCATTAAT    GTATC  CG
                                     AA___    GT
GAM245  LOC154449 5'  GCTGGTCAGCGTGACTCTGC   81087     T        CA
                                GCGG AGTTACGTTG  TAGT
                                |||| ||||||||||  ||||
                                CGTC TCAGTGCGAC  GTCG
                                  _        TG
GAM245  LOC154930 3'  ATTATAAATGCAATTACTGT   81177         A    GC
                                GCGGTAGTT CGTT  ATAGT
                                |||||||||  ||||  |||||
                                TGTCATTAA GTAA  TATTA
                                     C    A_
GAM245  LOC155435 3'  GCCGCTGTCCTGCGTAACTG   81350         TGC
                                TAGTTACGT   ATAGTGGT
                                |||||||||   ||||||||
                                GTCAATGCG   TGTCGCCG
                                     TCC
GAM245  LOC157226 5'  GCCGCTGCCGGCCTAGTTACCG 63933       GT  C    CA
          T                      GCGGTA  TA GTTG  TAGTGGT
                                ||||||  || ||||  |||||||
                                TGCCAT  AT CGGC  GTCGCCG
                                   TG  C    C_
GAM245  LOC157567 3'  TGCTAATTGAATTGCTGC    81486         A  TTGCA   TG
                                GCGGTAGTT CG    TAG  G
                                |||||||||  ||    |||  |
                                CGTCGTTAA GT    ATC  T
                                     _  TA___   GT
GAM245  LOC157584 3'  GCCGATACCTCACCGTGGCTGC 81489           T  CATAG_
          TGT                    GCGGTAGTTACG TG     TGGT
                                ||||||||||||  ||     ||||
                                TGTCGTCGGTGC AC     GCCG
                                      C  TCCATA
GAM245  LOC157623 5'  ATTGGAAAACGTGGCTAT    81491          GCA
                                GTAGTTACGTT   TAGT
                                ||||||||||   ||||
                                TATCGGTGCAA   GTTA
                                      AAG
GAM245  LOC157739 3'  ATCACATACAACGTGGATGCCG 81580       G       C  A
          T                      GCGGTA TTACGTTG AT GTGGT
                                ||||||  |||||||  ||  |||||
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                                TGCCGT GGTGCAAC TA CACTA
                                   A       A  _
GAM245  LOC157848 3'  GCCACTGTGATCCAGCTGTTG  81618    GG    ACGTTG
                                C  TAGTT     CATAGTGGT
                                |  |||||     |||||||||
                                G  GTCGA     GTGTCACCG
                                 TT    CCTA__
GAM245  LOC157918 3'  ACTACTGTTTCAGAATGTTGCT 86639      T    GC___
              GCTGC                 GTAGT ACGTT     ATAGTGGT
                                |||||| |||||     ||||||||
                                CGTCG TGTAA     TGTCATCA
                                   T     GACTT
GAM245  LOC157918 3'  GCTGTCCTCAGCTGTAACTACT 86648          _    C__    GGT
              GT                    CGGTAGTTAC GTTG   ATAGT
                                |||||||||| ||||   |||||
                                GTCATCAATG CGAC   TGTCG
                                      T    TCC
GAM245  LOC157919 5'  ACTACTGTTTCAGAATGTTGCT 81630      T    GC___
              GCTGC                 GTAGT ACGTT     ATAGTGGT
                                |||||| |||||     ||||||||
                                CGTCG TGTAA     TGTCATCA
                                   T     GACTT
GAM245  LOC157919 5'  GCTGTCCTCAGCTGTAACTACT 81635          _    C__    GGT
              GT                    CGGTAGTTAC GTTG   ATAGT
                                |||||||||| ||||   |||||
                                GTCATCAATG CGAC   TGTCG
                                      T    TCC
GAM245  LOC157927 3'  GCTATTGTGTGTCACTTGCTG  86668      _  T  GTT
                                CGGTA GT AC   GCATAGTGGT
                                ||||| || ||   ||||||||||
                                GTCGT CA TG   TGTGTTATCG
                                   T  C  ___
GAM245  LOC157983 3'  GCCACTAGCCACATGTGGCTAT 81640           T__  A
              TG                    CGGTAGTTACGT   GC TAGTGGT
                                ||||||||||||   || |||||||
                                GTTATCGGTGTA   CG ATCACCG
                                      CAC  _
GAM245  LOC158055 3'  CGCTGGTGCTTGCTGT      81668        TTACGTT   _
                                GCGGTAG      GCAT AGTG
                                |||||||      |||| ||||
                                TGTCGTT      CGTG TCGC
                                   ________   G
GAM245  LOC158230 3'  GCTCACAGCGTAGCTGTTCC   81800    __        CAT
                                GG  TAGTTACGTTG   AGT
                                ||  ||||||||||   |||
                                CC  GTCGATGCGAC   TCG
                                 TT         AC_
GAM245  LOC158267 3'  CTACTATGCAGATGAT      81829      CG
                                GTTA  TTGCATAGTGG
                                ||||  ||||||||||
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                                TAGT  GACGTATCATC
                                  A_
GAM245  LOC158281 3'  TCACCCCACAATGTCACTGTTG 81853    GG   T    CATA   GT
            C                      GC  TAGT ACGTTG   GTG
                                   ||  |||| ||||||   |||
                                   CG  GTCA TGTAAC   CAC
                                    TT   C    ACCC   TG
GAM245  LOC158722 3'  CCACTGTATTTAATACTGT   81993      G   C  TGC
                                   GCGGTA TTA GT   ATAGTGG
                                   |||||| ||| ||   |||||||
                                   TGTCAT AAT TA   TGTCACC
                                      _  T ___
GAM245  LOC158835 3'  TTACTGCAGTGTGAGCTGCTGC 82013       _       TA   T
                                   GCGGTAG TTACGTTGCA  GTGG
                                   ||||||| ||||||||||  ||||
                                   CGTCGTC AGTGTGACGT  CATT
                                       G        __   T
GAM245  LOC158848 3'  ACACTGATGTAGCTGGCGT   82030    G       GCAT   GT
                                   GCG TAGTTACGTT   AGTG
                                   ||| ||||||||||   ||||
                                   TGC GTCGATGTAG   TCAC
                                     G        _____   AC
GAM245  LOC158954 3'  ATCACTATGGATACTGACTGTC 60434   GT    C  TG_
                                   G  AGTTA GT   CATAGTGGT
                                   |  ||||| ||   |||||||||
                                   C  TCAGT CA   GTATCACTA
                                    TG    _  TAG
GAM245  LOC159089 3'  ATCACTGTTTCATGATTACTGC 86984         CGTTGC
                                   GCGGTAGTTA     ATAGTGGT
                                   ||||||||||     ||||||||
                                   CGTCATTAGT     TGTCACTA
                                         ACTT__
GAM245  LOC159148 5'  GCTACTGGGCTGTGTGTTACTG 87014      AGT   TT  A
            T                      GCGGT   TACG  GC TAGTGGT
                                   |||||   ||||  || |||||||
                                   TGTCA   GTGT  CG GTCATCG
                                      TT_   GT  G
GAM245  LOC159184 5'  GCTACAGCCCTTCATGTGGCTG 60050         T____  ATA
            CTGC                     GTAGTTACGT    GC   GTGGT
                                   ||||||||||    ||   |||||
                                   CGTCGGTGTA    CG   CATCG
                                        CTTCC  A__
GAM245  LOC160418 5'  GCCATTACTATGTACTACTGC  82214        T   TGCA
                                   GCGGTAGT ACGT    TAGTGGT
                                   |||||||| ||||   |||||||
                                   CGTCATCA TGTA    ATTACCG
                                        _   TC__
GAM245  LOC161734 3'  CTACTATCTTGGATACCGT   87100       GTTA  TTGC
                                   GCGGTA   CG   ATAGTGG
                                   ||||||   ||   |||||||
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                                TGCCAT   GT   TATCATC
                                  AG__  TC__
GAM245  LOC161823 3' ACTGGGTGGGACTTGACTGTTG 82299   GG    C  G  AG
           T                   GC  TAGTTA GTT CAT  TGGT
                               ||  |||||| ||| |||  ||||
                               TG  GTCAGT CAG GTG  GTCA
                                TT    T  G  G_
GAM245  LOC163782 3' ACCAATGAAGACATGGCTGTTG 82153   GG    C  GCATAG
           T                   GC  TAGTTA GTT    TGGT
                               ||  |||||| |||    ||||
                               TG  GTCGGT CAG    ACCA
                                TT    A  AAGTA_
GAM245  LOC163915 5' GCTGCTGTGTCTCCAACTGATG 87047    G   ACGTT    TG
           C                   GCG TAGTT   GCATAG  GT
                               ||| |||||   ||||||  ||
                               CGT GTCAA   TGTGTC  CG
                                 A   CCTC_    GT
GAM245  LOC164295 3' CCACAGTGTGGCTGCCGT   82509       ACGTT   A
                               GCGGTAGTT   GCAT GTGG
                               |||||||||   |||| ||||
                               TGCCGTCGG   TGTG CACC
                                    _____   A
GAM245  LOC164584 5' TCGCTAACGAGGTTGCCGC   82547       TA  TGCA
                               GCGGTAGT  CGT   TAGTGG
                               ||||||||  |||   ||||||
                               CGCCGTTG  GCA   ATCGCT
                                   GA  ____
GAM245  LOC164714 5' CGCTGTGCCAGGCTCTGC    87227    T   ACGTT    TG
                               GCGG AGTT   GCATAG  G
                               |||| ||||   ||||||  |
                               CGTC TCGG   CGTGTC  C
                                 _   AC___    GT
GAM245  LOC165552 3' GTCAACAGCTGGCGCAGCTGCC 82489        A   _  ATAGTGGT
           GC                    GCGGTAGTT CGTT GC
                               |||||||| |||| ||
                               CGCCGTCGA GCGG CG
                                    C   T  ACAACTG
GAM245  LOC166219 5' GCCGCGGTGGCTGCCGC    82625         _  T
                               GCGGTAGTTAC GT GC
                               |||||||||| || ||
                               CGCCGTCGGTG CG CG
                                     G  C
GAM245  LOC169026 3' CGCTATGCAGTTTCTGC    82724    TT  GT    TG
                               GTAG  AC  TGCATAG  G
                               ||||  ||  |||||||  |
                               CGTC  TG  ACGTATC  C
                                 TT  __     GT
GAM245  LOC170063 3' TGCACATGTAATTATT     87248         _
                               GGTAGTTACGT TGCA
                               |||||||||| ||||
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                                TTATTAATGTA ACGT
                                      C
GAM245  LOC195977 3' GCTGCTGTGTTGTGTCTGGCGG 87540     A  __  TT    TG
           CTGT                  CGGT GTT  ACG  GCATAG  GT
                                 |||| |||  |||  ||||||  ||
                                 GTCG CGG  TGT  TGTGTC  CG
                                   G   TC   GT     GT
GAM245  LOC196337 5' GCCATTATGCCCAAGCTGCAGC 87648    G     ACGTT
                                 GC GTAGTT    GCATAGTGGT
                                 || ||||||    ||||||||||
                                 CG CGTCGA    CGTATTACCG
                                  A     ACC__
GAM245  LOC196411 3' TATGTATGTAGTCTGTTGC    87684    GG  _     T
                                 GC  TAG TTACGT GCATA
                                 ||  ||| |||||| |||||
                                 CG  GTC GATGTA TGTAT
                                  TT   T     _
GAM245  LOC196478 5' GCCACTGTTTTTGTAACATGTT 87726    GG  _     TTGC
           GC                    GC  TA GTTACG    ATAGTGGT
                                 ||  || ||||||    ||||||||
                                 CG  GT CAATGT    TGTCACCG
                                  TT  A     TTT_
GAM245  LOC196528 3' ATCCTTTGTGGTTTAGCTATTG 87762          CG TG  T  T
           C                     GCGGTAGTTA  T  CA AG GGT
                                 ||||||||||  |  || || |||
                                 CGTTATCGAT  G  GT TC CTA
                                       TT GT  T  _  T
GAM245  LOC196951 5' ACTGTCAAGGCGTAGTTGCAGT 87809    G   GT     GC_
                                 GC GTA  TACGTT   ATAGT
                                 || |||  ||||||   |||||
                                 TG CGT  ATGCGG   TGTCA
                                  A  TG     AAC
GAM245  LOC196957 3' CGCTGTGCCTGCTCTGC     87822     T  TACGTT     TG
                                 GCGG AGT     GCATAG  G
                                 |||| |||     ||||||  |
                                 CGTC TCG     CGTGTC  C
                                   _  TC_____     GT
GAM245  LOC196961 3' CGCTGTGCCTGCTCTGC     87843     T  TACGTT     TG
                                 GCGG AGT     GCATAG  G
                                 |||| |||     ||||||  |
                                 CGTC TCG     CGTGTC  C
                                   _  TC_____     GT
GAM245  LOC196996 3' GCTGCTGTGCTAAGACTGCC   87861       ACGTT     TG
                                 GGTAGTT    GCATAG  GT
                                 |||||||    ||||||  ||
                                 CCGTCAG    CGTGTC  CG
                                     AAT__     GT
GAM245  LOC197138 3' CGCTGTGCCTGCTCTGC     87916     T  TACGTT     TG
                                 GCGG AGT     GCATAG  G
                                 |||| |||     ||||||  |
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                                CGTC TCG     CGTGTC  C
                                  _  TC____     GT
GAM245  LOC197201 3' ACTATTATAAATGATTGCC   87930       TA   GC
                                GGTAGT  CGTT  ATAGTGGT
                                ||||||  ||||  ||||||||
                                CCGTTA  GTAA  TATTATCA
                                   __    A_
GAM245  LOC197201 3' GCTGCTATAAGCTGTGATTG   87939       _  GC   TG
                                TAGTTAC GTT  ATAG  GT
                                |||||||  |||  ||||  ||
                                GTTAGTG CGA  TATC  CG
                                    T   A_    GT
GAM245  LOC197202 5' GCCGTTCCAGCTGGACTGCCGC 87959         AC   CATAG
                                GCGGTAGTT  GTTG    TGGT
                                |||||||||  ||||    ||||
                                CGCCGTCAG  CGAC    GCCG
                                     GT    CTT__
GAM245  LOC197342 3' CCGCTGTGCCGCAGCTG     87997      A  TT
                                TAGTT CG  GCATAGTGG
                                |||||  ||  |||||||||
                                GTCGA GC  CGTGTCGCC
                                  C  __
GAM245  LOC197414 3' GCAGTGTGACGCTGT       88067      A
                                GCGGT GTTACGTTGC
                                |||||  ||||||||||
                                TGTCG CAGTGTGACG
                                  _
GAM245  LOC197423 5' CCGAAGATTGGCTACTGT    77859         C   GCATAG
                                GCGGTAGTTA GTT     TGG
                                ||||||||||  |||     |||
                                TGTCATCGGT TAG     GCC
                                     _   AA____
GAM245  LOC199777 3' ACTGCACAGTGTGGCTGCT   59245           CA
                                GGTAGTTACGTTG  TAGT
                                ||||||||||||  ||||
                                TCGTCGGTGTGAC  GTCA
                                       AC
GAM245  LOC199858 5' GCTGCTGTGGAAGCTGCTGT  88421        TACG  G    TG
                                GCGGTAGT    TT CATAG  GT
                                ||||||||    ||  |||||  ||
                                TGTCGTCG    AA GTGTC  CG
                                    ____  G    GT
GAM245  LOC199958 3' CCACTCCGTGGCTTGCTGT   89885       _     TTGCAT
                                GCGGTA GTTACG     AGTGG
                                ||||||  ||||||     |||||
                                TGTCGT CGGTGC     TCACC
                                   T     C_____
GAM245  LOC199991 5' CGCTGTGGGGCACCGC      89913       AGTTAC   G
                                GCGGT     GTT CATAGTG
                                |||||     ||| |||||||
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                                CGCCA     CGG GTGTCGC
                                  _______  G
GAM245  LOC200138 5'  CCAGACCGACGTGACCGTTGT  89932     TA       CATAG   T
                                GCGG  GTTACGTTG    TGG
                                ||||  |||||||||    |||
                                TGTT  CAGTGCAGC    ACC
                                  GC       CAG__   C
GAM245  LOC200312 3'  GCCAGTGTAGCTGTCGC     89994     GT        _
                                GCG  AGTTACGTTG C
                                |||  |||||||||| |
                                CGC  TCGATGTGAC G
                                  TG        C
GAM245  LOC201203 3'  ACTGCTATGAAGAATGACTGT  88139      A   ACGTTG    TG
                                GCGGT GTT     CATAG  GT
                                ||||| |||     |||||  ||
                                TGTCA TAA     GTATC  CA
                                   G   GAA___    GT
GAM245  LOC201220 5'  GCCATTGTGTGACAGTTGCC   87351      TTAC  TG
                                GGTAG   GT  CATAGTGGT
                                ||||||   ||  |||||||||
                                CCGTT   CA  GTGTTACCG
                                   GA__  GT
GAM245  LOC201229 3'  GCTGCTTTTCCTGACTACTGT  88144         CGTTGCAT  TG
                                GCGGTAGTTA       AG  GT
                                ||||||||||       ||  ||
                                TGTCATCAGT       TC  CG
                                      CCTTT___  GT
GAM245  LOC201243 5'  GCCGTTGTCGCCGTCGCTGCTG 88160        T   T  C
            C                    GCGGTAGT ACG TG ATAGTGGT
                                ||||||||| ||| || ||||||||
                                CGTCGTCG TGC GC TGTTGCCG
                                     C   C  _
GAM245  LOC201283 3'  CATTATGCAAATAGTACGGT   60412    G   G   CG
                                GC GTA TTA  TTGCATAGTG
                                || ||| |||  ||||||||||
                                TG CAT GAT  AACGTATTAC
                                 G   _   A_
GAM245  LOC201294 3'  GCCATTATGCCTGGCTAATTGT 88210      _    CGTT
                                GCGGT AGTTA    GCATAGTGGT
                                |||||  |||||    ||||||||||
                                TGTTA TCGGT    CGTATTACCG
                                   A    C___
GAM245  LOC201696 3'  TGTGATGTGGCTGTGGT     63140    G        TG
                                GC GTAGTTACGT  CA
                                || ||||||||||  ||
                                TG TGTCGGTGTA  GT
                                 G         GT
GAM245  LOC202025 5'  GCCACAGTTGTATGGTTGCTGC 90291        TT CGT    TA_
                                GCGGTAG  A   TGCA   GTGGT
                                |||||||  |   ||||   |||||
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                                CGTCGTT  T   ATGT   CACCG
                                    GG ___    TGA
GAM245  LOC202052 3'  TCATTAAGTGACTGTAGC    90312      _  TG A
                                GTTAC GT  C TAGTGG
                                |||||| ||  | ||||||
                                CGATG CA  G ATTACT
                                   T  GT A
GAM245  LOC202347 3'  TCACTGCTTGGTAGTTGCTGT  90348      GT   GTT   TA   GT
                                GCGGTA  TAC   GCA  GTG
                                ||||||  |||   |||  |||
                                TGTCGT  ATG   CGT  CAC
                                   TG   GTT   __   TG
GAM245  LOC203084 3'  TCTTAGTGTAGTATAGCTATTG 87491         CG     AGTGGT
          T                      GCGGTAGTTA  TTGCAT
                                ||||||||||  ||||||
                                TGTTATCGAT  GATGTG
                                      AT     ATTCTA
GAM245  LOC203197 3'  CGCTCTATGTGGCATTGC    89285      A      TGCAT  TG
                                GCGGT GTTACGT    AG  G
                                ||||| |||||||    ||  |
                                CGTTA CGGTGTA    TC  C
                                  _      TC___  GT
GAM245  LOC203260 3'  CCATCCACGAGCTGCTGC    89316         A   T CATA
                                GCGGTAGTT CGT G   GTGG
                                ||||||||| ||| |   ||||
                                CGTCGTCGA GCA C    TACC
                                     _  _ C___
GAM245  LOC203289 3'  GCCACTAGCCACATGTGGCTAT 89331           T__  A
          TG                     CGGTAGTTACGT   GC TAGTGGT
                                ||||||||||||   || |||||||
                                GTTATCGGTGTA   CG ATCACCG
                                      CAC  _
GAM245  LOC203292 5'  ACTGCTGACTGTTTGGTGGTTG 90508      TT  GTT   __   TG
          CCGT                     CGGTAG  AC   GCA  TAG  GT
                                ||||||  ||   |||  |||  ||
                                GCCGTT  TG   TGT  GTC  CA
                                   GG  GTT   CA   GT
GAM245  LOC204084 5'  TCAATATTGTGGCTACTGT   89447          TTGC   G
                                GCGGTAGTTACG    ATA TGG
                                ||||||||||||   ||| |||
                                TGTCATCGGTGT    TAT ACT
                                      _____  A
GAM245  LOC205103 5'  ACTGTTCACTGAGCTGCTGT   89509         A  T  C
                                GCGGTAGTT CG TG ATAGT
                                ||||||||| || || |||||
                                TGTCGTCGA GT AC TGTCA
                                     _ C  T
GAM245  LOC205251 5'  ATTACAGGCATGAGCTGTCGC  90667     GT   A   T  ATA
                                GCG  AGTT CGT GC   GTGGT
                                |||  |||| ||| ||   |||||
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                                CGC  TCGA GTA CG   CATTA
                                  TG   _  _  GA_
GAM245  LOC205327 3'  ATTGTGTTTGTGACTAGCTACT 89501         C  TG  TA_ TG
                GC                  GCGGTAGTTA GT  CA   G  GT
                                    |||||||||| ||  ||   |  ||
                                    CGTCATCGAT CA  GT   T  TA
                                          _  GT  TTG GT
GAM245  LOC219294 3'  CACTGTTGGTGGCTGCC     93005        GTTGC
                                    GGTAGTTAC    ATAGTG
                                    |||||||||    ||||||
                                    CCGTCGGTG    TGTCAC
                                         GT___
GAM245  LOC219295 3'  CACTGTTGGTGGCTGCC     92989        GTTGC
                                    GGTAGTTAC    ATAGTG
                                    |||||||||    ||||||
                                    CCGTCGGTG    TGTCAC
                                         GT___
GAM245  LOC219401 3'  ATCACTACGAGTTTAATTGCTG 92813         CG  GCA
                T                    GCGGTAGTTA  TT   TAGTGGT
                                     ||||||||||  ||   |||||||
                                     TGTCGTTAAT  GA   ATCACTA
                                          TT  GC_
GAM245  LOC219649 3'  ACTGCTATACTGGACGTGGCTG 92948          GC__   TG
                CC                   GGTAGTTACGTT   ATAG  GT
                                     ||||||||||||   ||||  ||
                                     CCGTCGGTGCAG   TATC  CA
                                           GTCA   GT
GAM245  LOC219672 5'  ACTCGATGGAGCTGCTGT    91326         A    CAT
                                    GCGGTAGTT CGTTG   AGT
                                    |||||||||| |||||   |||
                                    TGTCGTCGA GTAGC   TCA
                                         G    ___
GAM245  LOC219686 3'  GCTAATACATGTGACTATCGT  90842           TGCA
                                    GCGGTAGTTACGT    TAGT
                                    ||||||||||||    ||||
                                    TGCTATCAGTGTA    ATCG
                                          CATA
GAM245  LOC219722 3'  ACCGTTACAACATTGAATTATC 93077         AC__   CA
                GT                   GCGGTAGTT    GTTG  TAGTGGT
                                     |||||||||    ||||  |||||||
                                     TGCTATTAA    CAAC  ATTGCCA
                                          GTTA   __
GAM245  LOC219857 3'  CCAGTGTGTTGCTGC      91509       GTTACGTT    G
                                    GCGGTA       GCATA TGG
                                    ||||||       ||||| |||
                                    CGTCGT       TGTGT ACC
                                       _________    G
GAM245  LOC220000 5'  CCATGAAGTGGCTGCTGC    91597          GTTGCATA
                                    GCGGTAGTTAC       GTGG
                                    ||||||||||        ||||
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                                CGTCGTCGGTG       TACC
                                      AAG_____
GAM245  LOC220003 5' ACCGTCAGCCTTAGCGTCACTG 91640   GT   T    ___ ATAG
              TCGT                    G  AGT ACGTT   GC    TGGT
                                |  ||| |||||  ||   ||||
                                C  TCA TGCGA   CG    GCCA
                                 TG   C    TTC  ACT_
GAM245  LOC220020 5' ACTGTTCAGGTGGCTGTTGC  93416    GG      G   C
                                GC  TAGTTAC TTG ATAGT
                                ||  ||||||| ||| |||||
                                CG  GTCGGTG GAC TGTCA
                                 TT      _   T
GAM245  LOC220020 5' ACACTAGCGTGGCTGCTG    93415          TGCA    GT
                                CGGTAGTTACGT    TAGTG
                                ||||||||||||    |||||
                                GTCGTCGGTGCG    ATCAC
                                      _____     AG
GAM245  LOC220021 3' GTTGCTGTCCAGGTAAATGCTG 93398       G    G   C    GG
              C                   GCGGTA TTAC TTG ATAGT  T
                                ||||||| |||| ||| |||||  |
                                CGTCGT AATG GAC TGTCG  G
                                   A    _  C    TT
GAM245  LOC220032 5' GCTCCCAGCGTGATTGACGC   91670     G         CAT
                                GCG TAGTTACGTTG   AGT
                                ||| ||||||||||   |||
                                CGC GTTAGTGCGAC   TCG
                                  A         CC_
GAM245  LOC220081 5' GTGACGTTGGCTGCTGC     91746          _   TG
                                GCGGTAGTTA CGT  C
                                |||||||||| |||  |
                                CGTCGTCGGT GCA  G
                                      T   GT
GAM245  LOC220115 5' ACTGCTGTTACTGTGATTATT  91743          T  C    TG
                                GGTAGTTACG TG ATAG  GT
                                |||||||||| || ||||  ||
                                TTATTAGTGT AT TGTC  CA
                                      C  _    GT
GAM245  LOC220164 3' ATTGTTATGTTGAATAGCTATT 91795        CGTT     TG
                                GGTAGTTA    GCATAG  GT
                                ||||||||    ||||||  ||
                                TTATCGAT    TGTATT  TA
                                     AAGT     GT
GAM245  LOC220469 3' CCAAAGTGGTGACTGCTGC    76385          GTTG   AG
                                GCGGTAGTTAC    CAT  TGG
                                ||||||||||    |||  |||
                                CGTCGTCAGTG    GTG  ACC
                                      ____   AA
GAM245  LOC220469 3' ACTGCTGCAGTGTGTGGCTATC 76382           __    TA TG
                                GGTAGTTACG  TTGCA  G  GT
                                |||||||||  |||||  |  ||
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                                CTATCGGTGT  GACGT  C  CA
                                      GT    __ GT
GAM245  LOC220522 3'  ATCGCTGTGGTGCAAGCCATCG 60520      A   AC  TG
          T                    GCGGT GTT  GT  CATAGTGGT
                               ||||| |||  ||  |||||||||
                               TGCTA CGA  CG  GTGTCGCTA
                                  C   A_  TG
GAM245  LOC220827 3'  GTGGAATGTAGCTGCC      91244           G
                               GGTAGTTACGTT CAT
                               |||||||||||| |||
                               CCGTCGATGTAA GTG
                                      G
GAM245  LOC220932 3'  GCCGTCCTTGGCGTGGCCGCCG 93136      TA       GCATAG
          C                    GCGG  GTTACGTT     TGGT
                               ||||  ||||||||     ||||
                               CGCC  CGGTGCGG     GCCG
                                 GC       TTCCT_
GAM245  LOC220963 3'  CTGCTGGTGTAGGCTGTTGC   91447    GG    TACG     _  TG T
                               GC  TAGT    TTGCAT AG  G
                               ||  ||||    |||||| ||  |
                               CG  GTCG    GATGTG TC  C
                                TT   _____     G  GT T
GAM245  LOC220980 5'  ACCGCTGAAGTGAACTGCTGC  93142         _   GTTGCA
                               GCGGTAGT TAC     TAGTGGT
                               |||||||| |||     |||||||
                               CGTCGTCA GTG     GTCGCCA
                                    A   AA_____
GAM245  LOC221060 3'  ATTACAGGCATGAGCTACTGT  93206         A   T  ATA
                               GCGGTAGTT CGT GC   GTGGT
                               ||||||||| ||| ||   |||||
                               TGTCATCGA GTA CG   CATTA
                                     _   _  GA_
GAM245  LOC221271 3'  TCATATCGTAGTTACCGT    91878       GT    TTGCATA
                               GCGGTA  TACG      GTGG
                               ||||||  ||||      ||||
                               TGCCAT  ATGC      TACT
                                  TG    TA_____
GAM245  LOC221272 3'  TGCCTCATGTAATTATTGT   93609           T__
                               GCGGTAGTTACGT   GCA
                               ||||||||||||   |||
                               TGTTATTAATGTA   CGT
                                     CTC
GAM245  LOC221336 3'  ACCACTGTGCAATGCGAAGCC  92268     AG TA
                               GGT  T  CGTTGCATAGTGGT
                               |||  |  ||||||||||||||
                               CCG  A  GTAACGTGTCACCA
                                 A_ GC
GAM245  LOC221463 3'  GCTTGATGTGGCTCCGT     92072      T       __
                               GCGG AGTTACGTT  GC
                               |||| |||||||||  ||
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                                TGCC TCGGTGTAG  CG
                                  _       TT
GAM245  LOC221510 3'  CCACTATTCTTAACTATT    91056        CGTTGC
                                GGTAGTTA     ATAGTGG
                                ||||||||     |||||||
                                TTATCAAT     TATCACC
                                    TCT___
GAM245  LOC221692 3'  TTTGCATTGCAGCTGGCTGCTG 92245          C     TA TG T
          T                      GCGGTAGTTA GTTGCA  G  G
                                ||||||||||| ||||||  |  |
                                TGTCGTCGGT CGACGT  C  T
                                      _     TA GT TC
GAM245  LOC221749 5'  CCTCGACGTCGACTACCGC   92003          _     CATAGT
                                GCGGTAGTT ACGTTG     GG
                                ||||||||| ||||||     ||
                                CGCCATCAG TGCAGC     CC
                                     C     T_____
GAM245  LOC221763 3'  ATCATTGTTAAAGGATTGCTGC 93796         ACG   C
                                GCGGTAGTT   TTG ATAGTGGT
                                |||||||||   ||| ||||||||
                                CGTCGTTAG   AAT TGTTACTA
                                     GA_  _
GAM245  LOC221766 3'  GCGGCGAGCTGCTGC       93777         A
                                GCGGTAGTT CGTTGC
                                ||||||||| ||||||
                                CGTCGTCGA GCGGCG
                                          _
GAM245  LOC221766 3'  ATCTGTACAGTGTACATTACTG 93775         _     C    TGGT
          C                      GCGGTAGT TACGTTG ATAG
                                ||||||||| ||||||| ||||
                                CGTCATTA ATGTGAC TGTC
                                     C      A   TA
GAM245  LOC221810 3'  GTACTATGTGATCTTATC    93932       TTAC  TG     GG
                                GGTAG   GT  CATAGT  T
                                |||||   ||  ||||||  |
                                CTATT    TA  GTATCA  G
                                   C___  GT     TT
GAM245  LOC221946 3'  ATCACTGTGGATAGTTACC    93976      GT  CGTTG
                                GGTA  TA    CATAGTGGT
                                ||||  ||    |||||||||
                                CCAT  AT    GTGTCACTA
                                  TG  AG___
GAM245  LOC222160 5'  ATTACTTGCTTATGACTATTGC 94119         CGTT   T
                                GCGGTAGTTA    GCA AGTGGT
                                ||||||||||    ||| ||||||
                                CGTTATCAGT    CGT TCATTA
                                      ATT_  _
GAM245  LOC222169 5'  CTCAGGTGGCGGTGCGACTGCC 94085         TA  TT  ATAG   T
          GC                     GCGGTAGT  CG  GC    TGG
                                ||||||||  ||  ||    |||
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                                CGCCGTCA  GT  CG   ACT
                                    GC  GG  GTGG   CA
GAM245  LOC245727 3'  CGCTGTGCCTGCTCTGC    91125     T   TACGTT     TG
                                GCGG AGT     GCATAG  G
                                |||| |||     ||||||  |
                                CGTC TCG     CGTGTC  C
                                  _   TC____     GT
GAM245  LOC245771 3'  GCCATTGCCAAGTGGCTG    92893       GTT   TA
                                TAGTTAC   GCA  GTGGT
                                |||||||   |||  |||||
                                GTCGGTG   CGT  TACCG
                                    AAC   __
GAM245  LOC245806 3'  CTAAAATGCAGCTGTTGT    91890    GG    TACGT    AG
                                GC  TAGT    TGCAT  TGG
                                ||  ||||    |||||  |||
                                TG  GTCG    ACGTA  ATC
                                 TT   _____    AA
GAM245  LOC253001 5'  GCCACTGTGTGGATGCTGCAGC 96259    G    TACG TG
                                GC GTAGT    T  CATAGTGGT
                                || |||||    |  |||||||||
                                CG CGTCG    G  GTGTCACCG
                                 A    TA__ GT
GAM245  LOC253150 3'  GCTGCTGGGCACTGAGCTGCCG 95517         A  T   A   TG
          C                      GCGGTAGTT CG TGC TAG  GT
                                |||||||| || ||| |||  ||
                                CGCCGTCGA GT ACG GTC  CG
                                     _ C   G   GT
GAM245  LOC253461 3'  GTTGTGTGCAAACGTAGTTAT  96284     GT     _    GTGGT
                                GTA  TACGTT GCATA
                                |||  |||||| |||||
                                TAT  ATGCAA CGTGT
                                  TG     A    GTTG
GAM245  LOC253573 3'  CGCTGTGAGAACAATTGT    97049      A   ACGTTG    TG
                                GCGGT GTT     CATAG  G
                                ||||| |||     |||||  |
                                TGTTA CAA     GTGTC  C
                                   A   GA____     GT
GAM245  LOC253776 3'  TCACTATGTATCTATC      97431       TTACGT
                                GGTAG     TGCATAGTGG
                                |||||     ||||||||||
                                CTATC     ATGTATCACT
                                   T_____
GAM245  LOC253782 5'  ACTATTACATCCTGGAGCTGTC 95693     GT   ACGTTGCA
          GT                     GCG  AGTT      TAGTGGT
                                |||  ||||      |||||||
                                TGC  TCGA      ATTATCA
                                  TG   GGTCCTAC
GAM245  LOC253893 3'  GCCACTGTGATCCAGCTGTTG  96112   GG    ACGTTG
                                C  TAGTT     CATAGTGGT
                                |  |||||     |||||||||
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                                G  GTCGA     GTGTCACCG
                                 TT    CCTA__
GAM245  LOC254020 5'  GCTGGGCCTAGCTGCCGC    96142         CGTT  A
                                GCGGTAGTTA    GC TAGT
                                ||||||||||    || ||||
                                CGCCGTCGAT    CG GTCG
                                      C___  G
GAM245  LOC254096 3'  GCTGCTGTGATCCCGACTGCAG 94906    G     ACGTTG    TG
              C                  GC GTAGTT     CATAG  GT
                                 || ||||||     |||||  ||
                                 CG CGTCAG     GTGTC  CG
                                  A     CCCTA_    GT
GAM245  LOC254228 3'  TGCTTGTGACTGGTGT      95959     G       TT
                                GCG TAGTTACG  GCA
                                ||| ||||||||  |||
                                TGT GTCAGTGT  CGT
                                  G       T_
GAM245  LOC254266 3'  CCAGTGGGTTGATTACTGT    97351         CGTT  A  G
                                GCGGTAGTTA    GC TA TGG
                                ||||||||||    || || |||
                                TGTCATTAGT    TG GT ACC
                                      _____ G  G
GAM245  LOC254532 5'  CATTGTGGTGGCTGCCGC    96632         GTTG
                                GCGGTAGTTAC    CATAGTG
                                ||||||||||    |||||||
                                CGCCGTCGGTG    GTGTTAC
                                       ____
GAM245  LOC254700 5'  TTACTGTGAAGAGTGTCGC    96223     TAGT   GTTG
                                GCGG    TAC    CATAGTGG
                                ||||    |||    ||||||||
                                CGCT    GTG    GTGTCATT
                                  _____  AGAA
GAM245  LOC254778 3'  ACTGCTATGTGTGACTGCCGC  96126         GTT     TG
                                GCGGTAGTTAC   GCATAG  GT
                                ||||||||||    ||||||  ||
                                CGCCGTCAGTG   TGTATC  CA
                                      ___      GT
GAM245  LOC255043 3'  ATCATTGTGATAAACCATCGC  95328      A   ACGTTG
                                GCGGT GTT     CATAGTGGT
                                ||||| |||     |||||||||
                                CGCTA CAA     GTGTTACTA
                                   C   ATA___
GAM245  LOC255127 5'  GCTACCTTCGTGCGGCTGTTGC 96286    GG    TACGT    A___
                                GC  TAGT    TGCAT    GTGGT
                                ||  ||||    |||||    |||||
                                CG  GTCG    GCGTG    CATCG
                                 TT    ______    CTTC
GAM245  LOC255131 5'  ATTAAGTGTCAGTGTAGCTACT 96000           _   AGTGGT
              GT                  GCGGTAGTTACGTTG CAT
                                ||||||||||||||| |||
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                                TGTCATCGATGTGAC GTG
                                       T  AATTA
GAM245  LOC255520 5'  GCTCCTGTGAGGTGGCTGCTGT 95858          GTTG    TG
                                GCGGTAGTTAC   CATAG  GT
                                ||||||||||   |||||  ||
                                TGTCGTCGGTG   GTGTC  CG
                                      GA__    CT
GAM245  LOC255721 5'  CCATGAAGTGGCTGCTGC    94831          GTTGCATA
                                GCGGTAGTTAC      GTGG
                                ||||||||||       ||||
                                CGTCGTCGGTG      TACC
                                      AAG_____
GAM245  LOC255862 3'  ATTATTATGATTGTACTATTGT 94486        T  TTG
                                GCGGTAGT ACG   CATAGTGGT
                                |||||||| |||   |||||||||
                                TGTTATCA TGT   GTATTATTA
                                     _  TA_
GAM245  LOC255974 3'  ACCACTAGCTTGGTGTTTACTG 97476        T  GTT  A
           T                     GCGGTAG TAC   GC TAGTGGT
                                |||||||  |||   || |||||||
                                TGTCATT GTG   CG ATCACCA
                                    T  GTT  _
GAM245  LOC256207 3'  GTGCTATGCAATAGCACAGT   95173    G  A   AC        GG
                                GC GT GTT  GTTGCATAGT  T
                                || || |||  ||||||||||  |
                                TG CA CGA  TAACGTATCG  G
                                 A  _  __         TT
GAM245  LOC256322 5'  CCGCTGTGCCGCCGCCGC    96278      TA  TACGTT
                                GCGG  GT     GCATAGTGG
                                ||||  ||     |||||||||
                                CGCC  CG     CGTGTCGCC
                                  GC  C_____
GAM245  LOC256502 3'  CCATTCTTGTGGCTGTCC    94549    _      TTGCAT
                                GG TAGTTACG     AGTGG
                                || ||||||||     |||||
                                CC GTCGGTGT     TTACC
                                 T       TC____
GAM245  LOC256544 3'  GCCACTAGCCACATGTGGCTAT 96201           T__  A
           TG                    CGGTAGTTACGT   GC TAGTGGT
                                ||||||||||||   || |||||||
                                GTTATCGGTGTA   CG ATCACCG
                                      CAC  _
GAM245  LOC256586 3'  ATTATGTGAAAATATGGTTGCT 94945       TT CG___ TG     GGT
           GT                    CGGTAG  A    T  CATAGT
                                ||||||  |    |  ||||||
                                GTCGTT  T    A  GTATTA
                                   GG ATAAA GT
GAM245  LOC256848 5'  CCAAGGTGCGGCTGCTGC    97513        TACGT    AG
                                GCGGTAGT    TGCAT  TGG
                                ||||||||    |||||  |||
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                                CGTCGTCG    GCGTG  ACC
                                   _____    GA
GAM245  LOC256905 3'  GCTATTGTAAATAGCACTGC  96868      A   CG    _
                                GCGGT GTTA  TTGCA TAGT
                                ||||| ||||  ||||| ||||
                                CGTCA CGAT  AATGT ATCG
                                   _   A_    T
GAM245  LOC257103 5'  ACTGCTGTGGGTCTTGACACTG 95595      A   CGTTG    TG
          C                      GCGGT GTTA    CATAG  GT
                                ||||| ||||    |||||  ||
                                CGTCA CAGT    GTGTC  CA
                                   _   TCTGG    GT
GAM245  LOC257289 5'  ACACTGGGTGGCTGCTGT    97491          GTTGCA    GT
                                GCGGTAGTTAC     TAGTG
                                ||||||||||     |||||
                                TGTCGTCGGTG     GTCAC
                                      G_____    AG
GAM245  LOC257357 5'  ACCACTGAGTGTTACTGCTGT  95594        T  GTT  A
                                GCGGTAGT AC   GC TAGTGGT
                                |||||||| ||   || |||||||
                                TGTCGTCA TG   TG GTCACCA
                                     T ___  A
GAM245  LOC257463 3'  ATCATACAAAATAATGTGACTG 71067           CATA__
          CC                     GGTAGTTACGTTG     GTGGT
                                ||||||||||||     |||||
                                CCGTCAGTGTAAT     TACTA
                                      AAAACA
GAM245  LOC257468 3'  ATTATTAGTGTTTGACTACTGC 95182          CGT   A
                                GCGGTAGTTA   TGC TAGTGGT
                                ||||||||||   ||| |||||||
                                CGTCATCAGT   GTG ATTATTA
                                      TT_  _
GAM245  LOC257541 5'  ACTATGGTAACAGCTGC     97761       A    GTTG
                                GCGGT GTTAC    CATAGT
                                ||||| |||||    ||||||
                                CGTCG CAATG    GTATCA
                                   A    _____
GAM245  LOC51008  5'  ATTACAGGCGTGACGACTGC   31958       A       GCA
                                GCGGT GTTACGTT   TAGT
                                ||||| ||||||||   ||||
                                CGTCA CAGTGCGG   ATTA
                                   G       AC_
GAM245  LOC51014  3'  ACCATTGCCACTGTAATATTGC 65847       G   _  T   TA
                                GCGGTA TTAC GT GCA  GTGGT
                                |||||| |||| || |||  |||||
                                CGTTAT AATG CA CGT  TACCA
                                   _   T  C   __
GAM245  LOC51019  5'  TGAGACGTGATTACCG      32129           TG
                                CGGTAGTTACGT  CA
                                ||||||||||||  ||
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                                GCCATTAGTGCA  GT
                                      GA
GAM245  LOC51097  3' GTTACTGTCGGGCAGTAACTGC 32050          _  GC    GG
             CGC                  GCGGTAGTTAC GTT  ATAGT  T
                                  ||||||||||| |||  |||||  |
                                  CGCCGTCAATG CGG  TGTCA  G
                                        A  GC    TT
GAM245  LOC51117  5' GCTGAGTGAGCGTGGTTGC   32092     TT   _ A
                                  GTAG  ACGTT GC TAGT
                                  ||||  ||||| || ||||
                                  CGTT  TGCGA TG GTCG
                                    GG    G  A
GAM245  LOC51133  3' CCACTATGTAGTAA       32280     GT
                                  TTAC  TGCATAGTGG
                                  ||||  ||||||||||
                                  AATG  ATGTATCACC
                                    __
GAM245  LOC51193  3' GCCATTATGCCTGACTCTTGC  32908     T    CGTT
                                  GCGG AGTTA    GCATAGTGGT
                                  |||| |||||    ||||||||||
                                  CGTT TCAGT    CGTATTACCG
                                    C    C___
GAM245  LOC51198  3' GCTGTCTTCCATGCGATGAAAT 32985      A      ___  _
             TGTTGT                 TAGTT CGTTGCAT   AG TGGT
                                  ||||| ||||||||   || ||||
                                  GTTAA GTAGCGTA   TC GTCG
                                     A       CCT  T
GAM245  LOC51608  3' GCTCAGGGTGGCGCGGCTGCTG 63674        TA   TG AT__   GGT
             C                     GCGGTAGT  CGT  C    AGT
                                  ||||||||  |||  |   |||
                                  CGTCGTCG  GCG  G    TCG
                                       GC   GT GGAC
GAM245  LOC51608  3' GCTGCTGTGCTGGAAATGCCGC 63675       GTTA  TT     TG
                                  GCGGTA    CG  GCATAG  GT
                                  ||||||    ||  ||||||  ||
                                  CGCCGT    GT  CGTGTC  CG
                                     AAAG  __     GT
GAM245  LOC51631  3' TGTTTGTAATGACCGT      68084      A     TT
                                  GCGGT GTTACG  GCA
                                  ||||| ||||||  |||
                                  TGCCA TAATGT  TGT
                                    G     T_
GAM245  LOC51667  3' ATCATTATGAAAAGGCTAATGC 32270     G    ACG  G
                                  GCG TAGTT   TT CATAGTGGT
                                  ||| |||||   || |||||||||
                                  CGT ATCGG   AA GTATTACTA
                                    A    AA_  _
GAM245  LOC54103  5' ACTGCTCAGAGCCTAACTATTG 94209          C   GCAT  TG
             C                     GCGGTAGTTA GTT    AG  GT
                                  |||||||||| |||    ||  ||
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                                CGTTATCAAT CGA   TC  CA
                                     C  GAC_  GT
GAM245  LOC54543  5' CCGACGCTGTGGTTGCTGT   38802      TT  TT  ATAG  T
                                GCGGTAG  ACG  GC   TGG
                                |||||||  |||  ||   |||
                                TGTCGTT  TGT  CG   GCC
                                   GG  __  CA__  C
GAM245  LOC56920  3' ATTACTGTGTATCTGTGTATTG 39381     GT   T_
           T                    GCGGTA  TACG  TGCATAGTGGT
                                ||||||  ||||  ||||||||||
                                TGTTAT  GTGT  ATGTGTCATTA
                                   __   CT
GAM245  LOC57086  3' CTATTGTGAATAGTGCCGC   39779     AGTT  GTTG
                                GCGGT   AC   CATAGTGG
                                |||||   ||   ||||||||
                                CGCCG   TG   GTGTTATC
                                  _____  ATAA
GAM245  LOC57105  3' ACTACTATCACCATGACCATTG 39813     A   CGT  C
           T                    GCGGT GTTA   TG ATAGTGGT
                                ||||| ||||   || ||||||||
                                TGTTA CAGT   AC TATCATCA
                                  C   ACC  _
GAM245  LOC57107  3' ATGTGGTGTAATTACAGC    39829    G      TT
                                GC GTAGTTACG  GCAT
                                || |||||||||  ||||
                                CG CATTAATGT  TGTA
                                 A       GG
GAM245  LOC57107  5' GCCGCTTCCTTTTAGTTACTGT 39837     GT  CGTTGCAT
                                GCGGTA  TA      AGTGGT
                                ||||||  ||      ||||||
                                TGTCAT  AT      TCGCCG
                                   TG  TTTCCT__
GAM245  LOC57228  3' GCCAACAAGATGTGGCTATGC  40000    G       GCATAG
                                GCG TAGTTACGTT     TGGT
                                |||  ||||||||||     ||||
                                CGT ATCGGTGTAG     ACCG
                                  _        AACA__
GAM245  LOC63920  5' GCATGTGATGTGGCTTTGT   42024     T      TG  A
                                GCGG AGTTACGT  CAT GT
                                ||||  ||||||||  |||  ||
                                TGTT TCGGTGTA  GTA CG
                                  _       GT  _
GAM245  LOC81034  3' CCATTGTTTAAATACCGC    47847      G  CGTTGC
                                GCGGTA TTA     ATAGTGG
                                ||||||  |||     |||||||
                                CGCCAT AAT     TGTTACC
                                   A  T_____
GAM245  LOC81537  3' GCTACTATACATTGATTTACTG 47908       TTA  T  C
           C                    GCGGTAG   CG TG ATAGTGGT
                                |||||||   || ||  ||||||||
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                                CGTCATT  GT AC TATCATCG
                                   TA_  T  A
GAM245  LOC85569  3' ATTATAACACGAGCTATTGC  52409        A  TGC
                                GCGGTAGTT CGT  ATAGT
                                ||||||||| |||  |||||
                                CGTTATCGA GCA  TATTA
                                    _  CAA
GAM245  LOC89135  3' ATTATTATGGTTATGATTACC  60316       CGTTG
                                GGTAGTTA   CATAGTGGT
                                ||||||||   |||||||||
                                CCATTAGT   GTATTATTA
                                   ATTG_
GAM245  LOC90019  5' CCCTGGCTGGCTGCTGC    56758        CGTT  A  TG
                                GCGGTAGTTA   GC TAG  G
                                ||||||||||   || |||  |
                                CGTCGTCGGT   CG GTC  C
                                    ____ _  CT
GAM245  LOC90072  5' CTATTATTGCACTACTGC    61293       TACGTT  _
                                GCGGTAGT    GCA TAGTGG
                                ||||||||    ||| ||||||
                                CGTCATCA    CGT ATTATC
                                    _______  T
GAM245  LOC90092  5' GTACTCTGTTGTAGTTGCC   61415    GT   TT  T  GG
                                GGTA  TACG  GCA AGT  T
                                ||||  ||||  ||| |||  |
                                CCGT  ATGT  TGT TCA  G
                                  TG   __  C  TT
GAM245  LOC90110  3' ATTGTTATGTAACTATTATTGT 61506       TAC      TG
                                GCGGTAGT  GTTGCATAG  GT
                                ||||||||  |||||||||  ||
                                TGTTATTA  CAATGTATT  TA
                                   T__      GT
GAM245  LOC90288  3' ATCATTATCTGTGTAGCTGGCT 62079     _    TTGC
          GT                  GCGGT AGTTACG   ATAGTGGT
                              |||||  |||||||   ||||||||
                              TGTCG TCGATGT   TATTACTA
                                G     GTC_
GAM245  LOC90459  5' GCCGCTGGAGTTTGTGTGGCCG 62889    TA    TT_  A_
          CCGC                 CGG  GTTACG  GC  TAGTGGT
                               |||  ||||||  ||  |||||||
                               GCC  CGGTGT  TG  GTCGCCG
                                 GC    GTT  AG
GAM245  LOC90499  5' ACTGCTGACTGTTTGGTGGTTG 63062     TT  GTT  __  TG
          CTGT                 CGGTAG  AC  GCA  TAG  GT
                               ||||||  ||  |||  |||  ||
                               GTCGTT  TG  TGT  GTC  CA
                                  GG  GTT  CA  GT
GAM245  LOC90499  3' TCCTGGTGTGGACTACTGT   63067       TACG TG  AGT  T
                               GCGGTAGT   T  CAT  GG
                               ||||||||   |  |||  ||
```

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                                TGTCATCA   G  GTG   CC
                                    ____ GT   GT_  TG
GAM245  LOC90522  3' ACCGCCCCAGGGCGTGGCCGCT 63152     TA      GCATA
             GT                   GCGG  GTTACGTT    GTGGT
                                  ||||  ||||||||    |||||
                                  TGTC  CGGTGCGG    CGCCA
                                    GC       GACCC
GAM245  LOC90693  3' GCCACTGTCCATTACCTATCGT 57064       TTACGT  C
                                  GCGGTAG     TG ATAGTGGT
                                  |||||||     || ||||||||
                                  TGCTATC     AC TGTCACCG
                                      CATT__  C
GAM245  LOC90835  5' CATTATGCTTACTAACGT    64126     G    TACGTT
                                  GCG TAGT     GCATAGTG
                                  ||| ||||     ||||||||
                                  TGC ATCA     CGTATTAC
                                    A   TT_____
GAM245  LOC90850  5' CCACCCGGTGTGCTACCGC    64211        T   TT CATA
                                  GCGGTAGT ACG  G    GTGG
                                  |||||||| |||  |    ||||
                                  CGCCATCG TGT  C    CACC
                                       _   GG C___
GAM245  LOC91056  3' TGTTACAGTGGCAATCGC    94765       A    _  T
                                  GCGGT GTTAC GT GCA
                                  ||||| ||||| || |||
                                  CGCTA CGGTG CA TGT
                                     A    A  T
GAM245  LOC91137  3' CCCTATGTAACTATC       57065       TACGT      T
                                  GGTAGT    TGCATAG GG
                                  ||||||    ||||||| ||
                                  CTATCA    ATGTATC CC
                                      ______     _
GAM245  LOC91363  3' ACTGCTGTGCGCCATGTGTTGC 65774      TAGT    __      TG
                                  GCGG   TACGT  TGCATAG  GT
                                  ||||   |||||  |||||||  ||
                                  CGTT   GTGTA  GCGTGTC  CA
                                    ____    CC      GT
GAM245  LOC91380  5' GCTATGTCACATTATC      65861       TAC  T
                                  GGTAGT   GT GCATAGT
                                  ||||||   || |||||||
                                  CTATTA   CA TGTATCG
                                      ___  C
GAM245  LOC91445  3' TGAGACTGACTACTGT      60552          C  TG
                                  GCGGTAGTTA GT  CA
                                  |||||||||| ||  ||
                                  TGTCATCAGT CA  GT
                                        _  GA
GAM245  LOC91517  3' ATCAAGAGACCTGACTGCCGC  66308          C   GCATAG
                                  GCGGTAGTTA GTT     TGGT
                                  |||||||||| |||     ||||
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                                CGCCGTCAGT CAG     ACTA
                                      C   AGA___
GAM245  LOC91632  5' GCCTCCTAACGGGGCTGCTGT  66774        TA    CATAGT
                                GCGGTAGT  CGTTG     GGT
                                ||||||||  |||||     |||
                                TGTCGTCG  GCAAT     CCG
                                    GG    CCT___
GAM245  LOC91661  3' ATGGGGCTGCGTGATGTGGCTG 56398           TG A    GGT
           CTGT                  GCGGTAGTTACGT  C TAGT
                                ||||||||||||||  | ||||
                                TGTCGTCGGTGTA  G GTCG
                                      GT C    GGGTAC
GAM245  LOC91661  3' GCTGCGTGATGTGGCTGCTGT  56401           TG A
                                GCGGTAGTTACGT  C TAGT
                                ||||||||||||||  | ||||
                                TGTCGTCGGTGTA  G GTCG
                                      GT C
GAM245  LOC91923  5' CTATTGTGAATAATGCTGC    67551       GTTAC   G
                                GCGGTA     GTT CATAGTGG
                                ||||||     ||| ||||||||
                                CGTCGT     TAA GTGTTATC
                                   AA___   _
GAM245  LOC91923  5' GCTATTGTGAATAATGCTGGCT 67553        _    __
           ATTGT                  GTAGTTA CGTTG  CATAGTGGT
                                ||||||| |||||  |||||||||
                                TATCGGT GTAAT  GTGTTATCG
                                   C     AA
GAM245  LOC91974  5' TTATGTTGTGCTGCTGT     67764        T   TT
                                GCGGTAGT ACG  GCATAG
                                ||||||||| |||  ||||||
                                TGTCGTCG TGT  TGTATT
                                   _   __
GAM245  LOC92017  3' GCTACTGTTAAATATTTGCTGT 67892        TTACG   C
                                GCGGTAG    TTG ATAGTGGT
                                |||||||    ||| ||||||||
                                TGTCGTT    AAT TGTCATCG
                                   TATA_   _
GAM245  LOC92095  3' ACCACTTCAGTGTGATTATT   68090           CAT
                                GGTAGTTACGTTG   AGTGGT
                                ||||||||||||   ||||||
                                TTATTAGTGTGAC   TCACCA
                                      T__
GAM245  LOC92096  3' ACCACTTCATTGTGATTATT   68096         T  CAT
                                GGTAGTTACG TG   AGTGGT
                                ||||||||||  ||   ||||||
                                TTATTAGTGT AC   TCACCA
                                      T  T__
GAM245  LOC92154  5' CCACCGTGCTGGCTGCTGT   68356         CGTT   TA
                                GCGGTAGTTA   GCA  GTGG
                                ||||||||||   |||  ||||
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                                TGTCGTCGGT   CGT  CACC
                                     ____   GC
GAM245  LOC92340  3' GCTGTTGAATGTGGCTGTGGC  68994    G       GC
                                GC GTAGTTACGTT  ATAGT
                                || ||||||||||  |||||
                                CG TGTCGGTGTAA  TGTCG
                                 G        GT
GAM245  LOC92370  3' GTACTATGTGATGGAACCAGC  69135   _  AGTTA  TG    GG
                                GC GGT    CGT  CATAGT  T
                                || |||    |||  ||||||  |
                                CG CCA    GTA  GTATCA  G
                                 A  AG___  GT    TT
GAM245  LOC92379  3' ATGAACGTACTATTGT     69147       T   G
                                GCGGTAGT ACGTT CAT
                                |||||||| ||||| |||
                                TGTTATCA TGCAA GTA

                                     _    _
GAM245  LOC92465  5' GTTGCTGTGTCACGACTGTTGC 69413   GG   TA  T    GG
                                GC  TAGT  CGT GCATAGT  T
                                ||  ||||  ||| |||||||  |
                                CG  GTCA  GCA TGTGTCG  G
                                 TT   __  C     TT
GAM245  LOC92573  5' TGCAGAATCTGACTGCCGT   69812        CG__
                                GCGGTAGTTA   TTGCA
                                ||||||||||   |||||
                                TGCCGTCAGT   GACGT
                                     CTAA
GAM245  LOC92578  5' TTTTGTTGCAGTTTAGCTGCTG 69835        CG   TAGTGGT
           T                     GCGGTAGTTA  TTGCA
                                ||||||||||  |||||
                                TGTCGTCGAT  GACGT
                                     TT   TGTTTTG
GAM245  LOC92912  5' GCGGGGGCGGCGTCGCTGTTGC 70844   GG   T    ATA_
                                GC  TAGT ACGTTGC   GT
                                ||  |||| |||||||   ||
                                CG  GTCG TGCGGCG   CG
                                 TT   C     GGGG
GAM245  LOC93070  3' CCACTGTGCTAGTTGCC    71290    GTT  GTT
                                GGTA  AC  GCATAGTGG
                                ||||  ||  |||||||||
                                CCGT  TG  CGTGTCACC
                                  ___  AT_
GAM245  LOC93070  5' GCTGTCGGGACGTGACTGC   71296        GC_
                                GTAGTTACGTT  ATAGT
                                ||||||||||  |||||
                                CGTCAGTGCAG  TGTCG
                                     GGC
GAM245  LOC93082  5' GCTGAACAAGCTGCGTAACTGT 56446    GT     T  ATAG_
           CGT                    GCG  AGTTACGT GC    TGGT
                                |||  |||||||| ||    ||||
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                                TGC  TCAATGCG CG    GTCG
                                  TG       T  AACAA
GAM245  LOC93550  5'  GCTGTTGTCACGCGGACTGCTG 72585        A  _  C    TG
              T                    GCGGTAGTT CGT TG ATAG  GT
                                   ||||||||| ||| || ||||  ||
                                   TGTCGTCAG GCG AC TGTT  CG
                                         _  C  _    GT
GAM246  NCALD    3'  TGCTTTTCTGAGCAGATCAATA 49380          CC   CCTGT
                                   TATTGATCTGT  CAG    GCA
                                   ||||||||||| |||    |||
                                   ATAACTAGACG  GTC    CGT
                                         A_   TTTT_
GAM246  FLJ10242  5'  TACTTCCTGAAGCAGATCAA   35934         CC   CCT
                                   TTGATCTGT  CAG   GTG
                                   |||||||||  |||   |||
                                   AACTAGACG  GTC   CAT
                                         AA   CTT
GAM246  FLJ13842  3'  TGCACAGAACTGGAACAGATCA 44990         C    C_
                                   TGATCTGT CCAG  CTGTGCA
                                   |||||||| ||||  |||||||
                                   ACTAGACA GGTC  GACACGT
                                        A    AA
GAM246  GPR88    3'  CACAGTCAAGACGGATCAATA  41878           CCAGC
                                   TATTGATCTGTC    CTGTG
                                   ||||||||||||    |||||
                                   ATAACTAGGCAG    GACAC
                                         AACT_
GAM246  KIAA0415  3'  TGCACCGTGGAGCAGATCAA   92582        TC   GCCT
                                   TTGATCTG  CCA    GTGCA
                                   ||||||||  |||   |||||
                                   AACTAGAC  GGT    CACGT
                                        GA   GC__
GAM246  KIAA0513  3'  GCACAGGCTAAGACCACAGA   28359       CCC___
                                   TCTGT     AGCCTGTGC
                                   |||||     |||||||||
                                   AGACA     TCGGACACG
                                      CCAGAA
GAM246  TCL6     3'  GCACAGGCTGGTCTCAA     40135      TCTGTC
                                   TTGA     CCAGCCTGTGC
                                   ||||     ||||||||||
                                   AACT     GGTCGGACACG
                                     CT_____
GAM246  TCL6     3'  GCACAGGCTGGTCTCAA     40103      TCTGTC
                                   TTGA     CCAGCCTGTGC
                                   ||||     ||||||||||
                                   AACT     GGTCGGACACG
                                     CT_____
GAM246  LOC219529 5'  TGCAACAGAAGACAGATTAA   92975          CCAGC   _
                                   TTGATCTGTC    CTGT GCA
                                   ||||||||||    |||| |||
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                                AATTAGACAG    GACA CGT
                                     AA___    A
GAM246  LOC253281 5'  CACAGGCTGGAGGTGCTCA   97343     TC GT _
                                TGA  T  C CCAGCCTGTG
                                |||  |  | ||||||||||
                                ACT  G  G GGTCGGACAC
                                  C_ TG A
GAM247  AF1Q     3'  GGTTATCTGCTACGAAACAGT  22365      G    ACCCT TG
                                ACTG TTTT    G  GATAATC
                                |||| ||||    |  |||||||
                                TGAC AAAG    C  CTATTGG
                                   _   CAT__ GT
GAM247  APM1     3'  GGTTATTCCTTTGTGGAACCAG 16599          CCTGT
                                CTGGTTTTAC    GGATAATC
                                ||||||||||    ||||||||
                                GACCAAGGTG    CTTATTGG
                                      TTTC_
GAM247  ARHGEF12 3'  CCCAGAGTGGGACTAGT     30997          C   T
                                ACTGGTTTTAC CTG GG
                                |||||||||| ||| ||
                                TGATCAGGGTG GAC CC
                                      A  _
GAM247  ASCL2    5'  GGTTATCTATACATTTAAAAAC 17717        ACCC__
           CAG                    CTGGTTTT     TGTGGATAATC
                                ||||||||     ||||||||||
                                GACCAAAA     ATATCTATTGG
                                     ATTTAC
GAM247  ASCL2    5'  GGTTATCTATACATTTAAAAAC 87586        ACCC__
           CAG                    CTGGTTTT     TGTGGATAATC
                                ||||||||     ||||||||||
                                GACCAAAA     ATATCTATTGG
                                     ATTTAC
GAM247  BACH2    3'  GGTTGTTGGGGCAGAGCCAGT  41491          A    GTG
                                ACTGGTTTT CCCT   GATAATC
                                ||||||||| ||||   |||||||
                                TGACCGAGA GGGG   TTGTTGG
                                     C   ___
GAM247  BCRP2    3'  GTTATCTATGAAGGGT      62405       __
                                ACCCT  GTGGATAAT
                                |||||  |||||||||
                                TGGGA  TATCTATTG
                                   AG
GAM247  CA12     3'  GGTTATCTGTGCAGGGGGCTGG 6880     TG   TTA     __
                                C  GTT   CCCTGT  GGATAATC
                                |  |||   ||||||  ||||||||
                                G  CGG   GGGACG  TCTATTGG
                                 GT   ___     TG
GAM247  CACNA2D2 3'  CTATGGGGTGGGGTGGGT    20083     G TT
                                ACT G  TTACCCTGTGG
                                ||| |  ||||||||||
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                                TGG T  GGTGGGGTATC
                                  G GG
GAM247  CAV3     3'  CACAGGGAGAGTTGGT     52890     GG    A
                                ACT  TTTT CCCTGTG
                                |||  |||| |||||||
                                TGG  GAGA GGGACAC
                                  TT   _
GAM247  CBFA2T2  3'  CATGTCTAGGGTGAGACCAGT  17459           GT    ATC
                                ACTGGTTTTACCCT  GGATA
                                ||||||||||||||  |||||
                                TGACCAGAGTGGGA  TCTGT
                                        __    ACA
GAM247  CBFA2T2  3'  TTATTTCTAGGGCAGT     17481     GTTTTA    TG
                                ACTG     CCCTG  GATAA
                                ||||     |||||  |||||
                                TGAC     GGGAT  TTATT
                                  _______    CT
GAM247  CDH11    3'  ATTATCTACAGAACTGG     53362   TG   TTACC
                                C  GTT    CTGTGGATAAT
                                |  |||    ||||||||||
                                G  CAA    GACATCTATTA
                                 GT  _____
GAM247  CEACAM1  3'  GGTTGTCTACCTGTAGGATCAG 8150          CCT
                                CTGGTTTTAC   GTGGATAATC
                                |||||||||   |||||||||
                                GACTAGGATG   CATCTGTTGG
                                      TC_
GAM247  CLASP1   3'  GGTCTGGGCAGGGTGCAGCCGG 65306       T      __    AATC
           T                     ACTGGTT TACCCTGT  GGAT
                                |||||||  ||||||||  ||||
                                TGGCCGA GTGGGACG  TCTG
                                    C       GG   G
GAM247  COL17A1  3'  GATTGTCCGTAGGCCCATACTA 4933       TTTAC
           G                     CTGGT    CCTGTGGATAATC
                                |||||    ||||||||||||
                                GATCA    GGATGCCTGTTAG
                                   TACCC
GAM247  COL4A5   3'  ATTATCTCTTAAGACCA     4938        CCCTGT
                                TGGTTTTA     GGATAAT
                                ||||||||     |||||||
                                ACCAGAAT     TCTATTA
                                    TC_____
GAM247  COL4A5   3'  ATTATCTCTTAAGACCA     52968       CCCTGT
                                TGGTTTTA     GGATAAT
                                ||||||||     |||||||
                                ACCAGAAT     TCTATTA
                                    TC_____
GAM247  COL4A5   3'  ATTATCTCTTAAGACCA     52972       CCCTGT
                                TGGTTTTA     GGATAAT
                                ||||||||     |||||||
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                                ACCAGAAT     TCTATTA
                                   TC____
GAM247  CORO2B   3'  GAGCCAGGCAGGGTAGGGATTA 64574       _      __ ATAATC
           GT                    CTGGTTT TACCCTGT  GG
                                 ||||||| ||||||||  ||
                                 GATTAGG ATGGGACG  CC
                                    G       GA  GAG
GAM247  CPNE7    3'  CGTAGGGTGGGGGCAGT     27038     G
                                 ACTG TTTTACCCTGTG
                                 |||| ||||||||||||
                                 TGAC GGGGTGGGATGC
                                   G
GAM247  CRIM1    3'  TATTTGGGGTGGGGACAGT   33177     GT      GT
                                 ACTG  TTTACCCT  GGATA
                                 ||||  ||||||||  |||||
                                 TGAC  GGGTGGGG  TTTAT
                                   AG       __
GAM247  CTNNB1   3'  GTAGGGTAAATCAGT      8580         T
                                 ACTGGTTT ACCCTGT
                                 |||||||| |||||||
                                 TGACTAAA TGGGATG
                                          _
GAM247  DAAM2    3'  GGTTATTGCCAGTGGAGACTGG 92292    TG   TA _  TG
           T                      AC  GTTT  CC CTG  GATAATC
                                  ||  ||||  || |||  |||||||
                                  TG  CAGA  GG GAC  TTATTGG
                                   GT   __ T   CG
GAM247  DBH      3'  GGTTCCACGTGGGGTGGAATTA 5791           __    TAATC
                                 TGGTTTTACCCT  GTGGA
                                 ||||||||||||  |||||
                                 ATTAAGGTGGGG  CACCT
                                       TG    TGG
GAM247  DMD      5'  GGTTATCTCCTATTAGGAATCA 14398         ACCCTGT
           GT                     ACTGGTTTT      GGATAATC
                                  |||||||||      ||||||||
                                  TGACTAAGG      TCTATTGG
                                      ATTATCC
GAM247  DMD      5'  GGTTATCTCCTATTAGGAATCA 14420         ACCCTGT
           GT                     ACTGGTTTT      GGATAATC
                                  |||||||||      ||||||||
                                  TGACTAAGG      TCTATTGG
                                      ATTATCC
GAM247  DMD      5'  GGTTATCTCCTATTAGGAATCA 14427         ACCCTGT
           GT                     ACTGGTTTT      GGATAATC
                                  |||||||||      ||||||||
                                  TGACTAAGG      TCTATTGG
                                      ATTATCC
GAM247  DSCR3    3'  TGCAGGGTGGGCTGGT     20196    TG   T
                                 AC  GTTT ACCCTGTG
                                 ||  |||| ||||||||
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                                TG  CGGG TGGGACGT
                                 GT   _
GAM247  EDN3    3'  GATTATTTATTGTGAAACT   3675        CCT
                                GGTTTTAC  GTGGATAATC
                                ||||||||  ||||||||||
                                TCAAAGTG  TATTTATTAG
                                    T__
GAM247  EPB49   3'  TACAGGGCAAAGCCAGT    8791         A
                                ACTGGTTTT CCCTGTG
                                ||||||||| |||||||
                                TGACCGAAA GGGACAT
                                      C
GAM247  ESRRA   3'  CAAGGGGTGGGACTGGT    15480   TG       G
                                AC  GTTTTACCCT TG
                                ||  |||||||||| ||
                                TG  CAGGGTGGGG AC
                                 GT        A
GAM247  ESRRG   3'  CACAGGGTAGAATTAG     66388
                                CTGGTTTTACCCTGTG
                                ||||||||||||||||
                                GATTAAGATGGGACAC

GAM247  FEZ1    3'  GATGCATGATGGGGCAGGGCCG 17529       A   ___  G  AATC
           GT                    CTGGTTTT CCCT  GTG AT
                                 |||||||| ||||  ||| ||
                                 GGCCGGGA GGGG  TAC TA
                                      C   TAG  G  G
GAM247  GARP    3'  CCCTTATTTGTGGGGTGAGATT 18595   TG       TG    TC
           GG                    C  GTTTTACCCTG  GATAA
                                 |  ||||||||||  |||||
                                 G  TAGAGTGGGGT  TTATT
                                  GT        GT    CCCG
GAM247  GAS11   3'  GGCTCCAGTGTGGGGTGAGGCA 7626     G       ___   TAATC
           GT                    CTG TTTTACCCTG  TGGA
                                 ||| ||||||||||  ||||
                                 GAC GGAGTGGGGT  ACCT
                                   _       GTG   CGG
GAM247  GPR61   3'  TATGGGGCTGGGGCCAGT    78913         _
                                ACTGGTTTTA CCCTGTG
                                ||||||||| |||||||
                                TGACCGGGGT GGGGTAT
                                      C
GAM247  GRAF    3'  TTGGAGGGTGGGATGAGT    30582    G       G
                                ACT GTTTTACCCT TGG
                                ||| |||||||||| |||
                                TGA TAGGGTGGGA GTT
                                  G       G
GAM247  HYAL4   3'  ATCTGGGGTAAAGTCA     24372    GT      GT
                                TG  TTTACCCT  GGAT
                                ||  ||||||||  ||||
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                                AC  AAATGGGG  TCTA
                                 TG       __
GAM247  IL10RA   3'  GATTATTTGCTCAGGGGAACCA 59643       TA   __ TG
                                TGGTTT  CCCT  G  GATAATC
                                ||||||  ||||  |  |||||||
                                ACCAAG  GGGA  C  TTATTAG
                                    __   CT GT
GAM247  IL20RA   3'  GATTATCCGCAAATGCAAACAG 27047     GTTTTACCC
          T                      ACTG       TGTGGATAATC
                                 ||||       ||||||||||
                                 TGAC       ACGCCTATTAG
                                   AAACGTAA_
GAM247  ITGA3    3'  GGTTGTCTACGGGGGCACTTGG 18539    TG TTTTA
                                C  G    CCCTGTGGATAATC
                                |  |    ||||||||||||||
                                G  T    GGGGCATCTGTTGG
                                 GT CACG_
GAM247  ITGA3    3'  GGTTGTCTACGGGGGCACTTGG 9377    TG TTTTA
                                C  G    CCCTGTGGATAATC
                                |  |    ||||||||||||||
                                G  T    GGGGCATCTGTTGG
                                 GT CACG_
GAM247  LDLR     3'  GATTATTTGCACGAACTGG   4987    TG   TACCC  TG
                                C  GTTT    TG  GATAATC
                                |  ||||    ||  |||||||
                                G  CAAG    AC  TTATTAG
                                 GT   C____  GT
GAM247  M17S2    3'  GTTGATGGGTGGGACCTGT   49035    T       T  G
                                AC GGTTTTACCC GT GAT
                                || |||||||||| || |||
                                TG CCAGGGTGGG TA TTG
                                 T        _  G
GAM247  NAPB     3'  GATTATTTTGATGGTGCTAGT  70184      TTT   CTGT
                                ACTGGT   ACC    GGATAATC
                                ||||||   |||    ||||||||
                                TGATCG   TGG    TTTATTAG
                                    ___   TAGT
GAM247  NAV2     3'  CCACAGGGAGAACTGGT     60157    TG    A
                                AC  GTTTT CCCTGTGG
                                ||  ||||| ||||||||
                                TG  CAAGA GGGACACC
                                 GT    _
GAM247  NOVA1    3'  GGTTGAGTATGGTGGGGTCAGT 21410      TT    CT   GA
                                ACTGG  TTACC  GTG  TAATC
                                |||||  |||||  |||  |||||
                                TGACT  GGTGG  TAT  GTTGG
                                   GG    __   GA
GAM247  NOVA1    3'  GGTTGAGTATGGTGGGGTCAGT 10248      TT    CT   GA
                                ACTGG  TTACC  GTG  TAATC
                                |||||  |||||  |||  |||||
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                                TGACT  GGTGG  TAT  GTTGG
                                  GG    __   GA
GAM247  PATE    3'  GATTGTCTGCCTTCTAGAATCA 56314        CCCT TG
          G                      CTGGTTTTA   G  GATAATC
                                 |||||||||   |  |||||||
                                 GACTAAGAT   C  CTGTTAG
                                     CTTC GT
GAM247  PIK3R3  3'  GGTTATAGCGGGTGGGGTTG  61063   GG      T  GG
                                 T  TTTTACCC GT  ATAATC
                                 |  ||||||||  ||  |||||||
                                 G  GGGGTGGG CG  TATTGG
                                  TT       _  A_
GAM247  PRX     3'  ATCCCCGAGGTGGAGCTGGT  40520    TG      C  T
                                 AC  GTTTTACC TG GGAT
                                 ||  ||||||||  || ||||
                                 TG  CGAGGTGG GC CCTA
                                  GT       A  C
GAM247  PSME3   3'  CCCAGGGTGAGTTGGT     19369     GG   T     T
                                 ACT  TTT ACCCTG GG
                                 |||  |||  |||||||  ||
                                 TGG  GAG TGGGAC CC
                                   TT  _     _
GAM247  PYCR1   3'  GGTTACTGTGGGTGGAATAGT  70091      G       T TG A
                                 ACTG TTTTACCC G  G TAATC
                                 ||||  ||||||||  |  |  |||||
                                 TGAT AAGGTGGG T  C ATTGG
                                   _       _ GT _
GAM247  RAMP1   3'  CTGCAGGGTGAGGCCAG     19583            TG
                                 CTGGTTTTACCCTG  G
                                 ||||||||||||||  |
                                 GACCGGAGTGGGAC  C
                                          GT
GAM247  RECQL   5'  CTGCAGGGCGAGGCCGGT    11283         TA     TG
                                 ACTGGTTT  CCCTG  G
                                 ||||||||  |||||  |
                                 TGGCCGGA  GGGAC  C
                                      GC     GT
GAM247  SCML2   3'  GGTTGTTTGGATGGAGTCAG  20323     GT    C  TGT
                                 CTG  TTTA CC   GGATAATC
                                 |||  ||||  ||   ||||||||
                                 GAC  AGGT GG   TTTGTTGG
                                   TG    A  ___
GAM247  SCN1A   3'  GATTATTTGTGGGTAGGCCAGT 88851         T    T TG
                                 ACTGGTTT ACCC G  GATAATC
                                 ||||||||  ||||  |  |||||||
                                 TGACCGGA TGGG T  TTATTAG
                                      _    _ GT
GAM247  SCP2    3'  GTCTGGGGTAAAATTGAGT    11444     _         GT
                                 ACT GGTTTTACCCT  GGAT
                                 |||  ||||||||||  ||||
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                                TGA TTAAAATGGGG  TCTG
                                  G        __
GAM247  SDPR     3'  GGTTGTTTACTTGCTAGAAACC 16225        ACCCT_
              A                   TGGTTTT     GTGGATAATC
                                  |||||||     ||||||||||
                                  ACCAAAG     CATTTGTTGG
                                     ATCGTT
GAM247  SLC12A7  3'  GGTTGTCCATAAAGAGGTTGCT 21706     TTT  _ __
                                  GGT   ACC CT  GTGGATAATC
                                  |||   ||| ||  ||||||||||
                                  TCG   TGG GA  TACCTGTTGG
                                    T__   A  AA
GAM247  SLC19A2  3'  GATTATTTATTTCTGTAAAATT 68979    TG      CCT_
              TGT                   AC  GTTTTAC    GTGGATAATC
                                  ||  |||||||    ||||||||||
                                  TG  TAAAATG    TATTTATTAG
                                    TT      TCTT
GAM247  SLC19A2  5'  GGCGTCTGTAGGGTAAAGCTGG 68980   TG        TG   AATC
                                  C  GTTTTACCCTG  GAT
                                  |  ||||||||||  |||
                                  G  CGAAATGGGAT  CTG
                                   GT         GT   CGG
GAM247  SLC38A3  3'  GGTTCTGCTGAGGGTGGGGCTG 22424    TG        __ TG  TAATC
              GT                    AC  GTTTTACCCT  G  GA
                                  ||  ||||||||||  |  ||
                                  TG  CGGGGTGGGA  C  CT
                                    GT        GT GT  TGG
GAM247  SUV39H1  3'  CTACGGGCTGAGGCTGGT    12069    TG     C
                                  AC  GTTTTA CCTGTGG
                                  ||  |||||| |||||||
                                  TG  CGGAGT GGGCATC
                                    GT     C
GAM247  TFDP1    3'  GATTGTTTCCCGTAGGATTAG  23048         CCTGT
                                  CTGGTTTTAC    GGATAATC
                                  ||||||||||    ||||||||
                                  GATTAGGATG    TTTGTTAG
                                        CCC__
GAM247  TGIF     3'  GATTATTCATAATGTGAGAT   12277       CC
                                  GTTTTAC  TGTGGATAATC
                                  |||||||  ||||||||||
                                  TAGAGTG  ATACTTATTAG
                                     TA
GAM247  TNFSF9   3'  TTGTTTACATGCCAGT      13760       TTTACCC
                                  ACTGGT      TGTGGATAA
                                  ||||||      |||||||||
                                  TGACCG      ACATTTGTT
                                     T_______
GAM247  TRIM9    3'  GGTTCACATCAGGGTAGGATC  30763          ___     AATC
                                  GGTTTTACCCT   GTGGAT
                                  ||||||||||   ||||||
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                                CTAGGATGGGA  CACTTG
                                     CTA    G
GAM247  TRPC1    5'  CGGGGTCGGGGCCGGT     12387        _
                                ACTGGTTTT ACCCTG
                                ||||||||| ||||||
                                TGGCCGGGG TGGGGC
                                    C
GAM247  WHSC1    3'  GGTTAAGACAGGGTGGGAGTAG 55832     G        GGA
          T                      ACTG TTTTACCCTGT  TAATC
                                ||||| |||||||||||  |||||
                                TGAT AGGGTGGGACA  ATTGG
                                  G         GA_
GAM247  WHSC1    3'  GGTTAAGACAGGGTGGGAGTAG 55849     G        GGA
          T                      ACTG TTTTACCCTGT  TAATC
                                ||||| |||||||||||  |||||
                                TGAT AGGGTGGGACA  ATTGG
                                  G         GA_
GAM247  WHSC1    3'  GGTTAAGACAGGGTGGGAGTAG 29914     G        GGA
          T                      ACTG TTTTACCCTGT  TAATC
                                ||||| |||||||||||  |||||
                                TGAT AGGGTGGGACA  ATTGG
                                  G         GA_
GAM247  AASDHPPT 3'  GATTATCTGCAGTTTATTACT  31245    TT  CC   TG
                                GGT  TA  CTG  GATAATC
                                |||  ||  |||  |||||||
                                TCA  AT  GAC  CTATTAG
                                  TT  TT   GT
GAM247  ALS2CR3  3'  GTTGGTGGGGTAAGCTCAGT   30485     GT      TG G
                                ACTG  TTTACCC  T GAT
                                ||||  |||||||  | |||
                                TGAC  GAATGGG  G TTG
                                  TC      GT G
GAM247  ALS2CR8  3'  GATTATCTAATAAGGCCAGT   45363         CCCTG
                                ACTGGTTTTA    TGGATAATC
                                ||||||||||    |||||||||
                                TGACCGGAAT    ATCTATTAG
                                     A____
GAM247  BDH      3'  GATTATCCACGTGTGGA     14475      CC
                                TTTAC  TGTGGATAATC
                                |||||  ||||||||||
                                AGGTG  GCACCTATTAG
                                   T_
GAM247  BICD2    3'  GCAGGGAAGAGCTAGT      70395         A
                                ACTGGTTTT CCCTGT
                                ||||||||| ||||||
                                TGATCGAGA GGGACG
                                     A
GAM247  BMF      3'  GATTATTTACAGCAGCCA    53157       TTACC
                                TGGTT    CTGTGGATAATC
                                |||||    ||||||||||||
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                                ACCGA    GACATTTATTAG
                                  C____
GAM247  C20orf110 3'  ACACACCATGGGGTGAAGCCA  79540            ATAATC
                                TGGTTTTACCCTGTGG
                                ||||||||||||||||
                                ACCGAAGTGGGGTACC
                                      ACACAG
GAM247  C20orf38  3'  GGTTATCCAAAGGAAACCA   37065      TAC   G
                                TGGTTT   CCT TGGATAATC
                                ||||||   ||| |||||||||
                                ACCAAA   GGA ACCTATTGG
                                   ___   A
GAM247  C21orf93  3'  TCCACGGTGTGAGGCCAGT   59089          C
                                ACTGGTTTTAC CTGTGGA
                                |||||||||| |||||||
                                TGACCGGAGTG GGCACCT
                                      T
GAM247  C8orf17   5'  GCGGGTGTGGGACCAGT     39601          _
                                ACTGGTTTTAC CCTGT
                                |||||||||| |||||
                                TGACCAGGGTG GGGCG
                                      T
GAM247  CEPT1     3'  TTGTGAGGTGGAACTAGT    20329          CT TG
                                ACTGGTTTTACC  G  G
                                |||||||||||  |  |
                                TGATCAAGGTGG  T  T
                                      AG GT
GAM247  CHST8     5'  AGCCGCGCGCAGGGAAGAACTA 42436        A      GATAATC
           GT                     ACTGGTTTT CCCTGTG
                                |||||||| |||||||
                                TGATCAAGA GGGACGC
                                     A      GCGCCGAG
GAM247  CLPTM1    3'  GGTTGGGCGGGGGTGGGGCCGG 7104            G  GA
                                CTGGTTTTACCCT TG  TAATC
                                |||||||||||| ||  |||||
                                GGCCGGGGTGGGG GC  GTTGG
                                      _  GG
GAM247  CMG1      5'  GGTTGTCCCATAGGGACTGGT  47022    TG  TTTA      _
                                AC  GT    CCCTGTGG ATAATC
                                ||  ||    |||||||| ||||||
                                TG  CA    GGGATACC TGTTGG
                                 GT  ____       C
GAM247  COLEC10   3'  GGTTGTCTATATGTCAAATGAG 21229     G    T  CC
           T                     ACT GTTT AC  TGTGGATAATC
                                ||| |||| ||  ||||||||||
                                TGA TAAA TG  ATATCTGTTGG
                                  G    C  T_
GAM247  CST9L     5'  TGTGGGGTGAGACAAGT     54620     G       TG
                                ACT GTTTTACCC  TG
                                ||| |||||||||  ||
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                                TGA CAGAGTGGG  GT
                                  A        GT
GAM247  DC-TM4F2 3'  GGTTGTTTGCAGGATCCTCAG  48173      TTTTAC    TG
                                CTGG     CCTG  GATAATC
                                ||||     ||||  |||||||
                                GACT     GGAC  TTGTTGG
                                  CCTA__    GT
GAM247  DDR1     3'  ATCCAGGGGAAGCCAGT     8721          A    GT
                                ACTGGTTTT CCCT  GGAT
                                ||||||||| ||||  ||||
                                TGACCGAAG GGGA  CCTA
                                     _   __
GAM247  DDR1     3'  ATCCAGGGGAAGCCAGT     25694         A    GT
                                ACTGGTTTT CCCT  GGAT
                                ||||||||| ||||  ||||
                                TGACCGAAG GGGA  CCTA
                                     _   __
GAM247  DDR1     3'  ATCCAGGGGAAGCCAGT     25703         A    GT
                                ACTGGTTTT CCCT  GGAT
                                ||||||||| ||||  ||||
                                TGACCGAAG GGGA  CCTA
                                     _   __
GAM247  DKFZP434C171 3'  TTGTCTGAAGGCCAG       31563      TTTTAC   G
                                CTGG     CCT TGGATAA
                                ||||     ||| |||||||
                                GACC     GGA GTCTGTT
                                  _______  A
GAM247  DKFZP434N1511 3'  GGTGTACCAGTGGTGAAGTCAG 91421      GT     _  _  G  AATC
           T                     ACTG  TTTACC CTG TG AT
                                ||||  |||||| ||| || ||
                                TGAC  AAGTGG GAC AT TG
                                  TG     T   C  G  G
GAM247  DKFZP564O0463 3'  ATTGTCCAGAAGACTCAGT   26277      _     ACCCTG
                                ACTG GTTTT     TGGATAAT
                                |||| |||||     ||||||||
                                TGAC CAGAA     ACCTGTTA
                                  T    G_____
GAM247  DKFZP761E2110 3'  GGTTATTCACAGGCATGATTA  48226       TTAC
                                TGGTT    CCTGTGGATAATC
                                |||||    ||||||||||||||
                                ATTAG    GGACACTTATTGG
                                   TAC_
GAM247  DNAL4    3'  CGTGGGGTGGGGCGGT      19215      G       TG
                                ACTG TTTTACCC  TG
                                |||| ||||||||  ||
                                TGGC GGGGTGGG  GC
                                  _       GT
GAM247  EDG1     3'  TGTTGGTGGGTAGAGTTAGT   59331     GG       TGTG
                                ACT  TTTTACCC    GATA
                                |||  ||||||||    ||||
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                                TGA  GAGATGGG    TTGT
                                  TT       TGG_
GAM247  ELOVL2    3'  GGTTATTTAAGTTCTTGAAGCT 34960    TG     CCCTG_
              GG                   C  GTTTTA     TGGATAATC
                                | ||||||     |||||||||
                                G  CGAAGT     ATTTATTGG
                                 GT     TCTTGA
GAM247  EMILIN-2  3'  GCAGGGGAGAGCCGGT      49430          A
                                ACTGGTTTT CCCTGT
                                ||||||||| ||||||
                                TGGCCGAGA GGGACG
                                     G
GAM247  FHX       3'  ATTTGCAAGGGTAGGATCA    37299           _ TG
                                TGGTTTTACCCT G  GAT
                                |||||||||||| |  |||
                                ACTAGGATGGGA C  TTA
                                       A GT
GAM247  FKSG42    3'  GGTTAATTTGGGGTCAAAGTCA 49334      GT  _     TGGA
              GT                   ACTG  TTT ACCCTG    TAATC
                                ||||  ||| ||||||    |||||
                                TGAC  AAA TGGGGT    ATTGG
                                  TG   C     TTA_
GAM247  FLJ00024  5'  CGATTGTCTGTGGGCTGCTGAA 63757     AC_____    TG
              GAGCTGGT                TTT      CCTG  GATAATC   G
                                |||      ||||  |||||||   |
                                AGA      GGGT  CTGTTAG   C
                                  AGTCGTC    GT
GAM247  FLJ10468  3'  GATTGTTCTAATCAGAGCTGGT 36148    TG    ACCCTGT
                                AC  GTTTT      GGATAATC
                                ||  |||||      ||||||||
                                TG  CGAGA      CTTGTTAG
                                 GT    CTAAT__
GAM247  FLJ10647  5'  GTTGTCAGGCGGAGCTGGT    36375    TG    TA  CTGTG
                                AC  GTTT  CC     GATAAT
                                ||  ||||  ||    ||||||
                                TG  CGAG  GG    CTGTTG
                                 GT    GC  A____
GAM247  FLJ10932  3'  GAGCTTCGTAGAGGTGAGGCTG 36893    TG       _      TAATC
              GT                   AC  GTTTTACC CTGTGGA
                                ||  |||||||| |||||||
                                TG  CGGAGTGG GATGCTT
                                 GT       A      CGAG
GAM247  FLJ10936  3'  TCCACAGGTTGAAACTGGT    36912    TG     C
                                AC  GTTTTA CCTGTGGA
                                ||  |||||| ||||||||
                                TG  CAAAGT GGACACCT
                                 GT     T
GAM247  FLJ12057  3'  CCATGGGGGTGAAACCAGT    45436            _
                                ACTGGTTTTACCCT GTGG
                                |||||||||||||| ||||
```

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                                TGACCAAAGTGGGG TACC
                                       G
GAM247  FLJ12355  5' GCGGGGCTGGGGCCGGT    46482          _
                                ACTGGTTTTA CCCTGT
                                |||||||||| ||||||
                                TGGCCGGGGT GGGGCG
                                      C
GAM247  FLJ12681  3' GTCCAGGGTGGGGTCTGT   42874   T  TT     GT
                                AC GG  TTACCCT  GGAT
                                || ||  |||||||  ||||
                                TG CT  GGTGGGA  CCTG
                                 T  GG     __
GAM247  FLJ20034  3' CCTCGGGGTGGGATTGGT   34367   TG        T
                                AC  GTTTTACCCTG GG
                                ||  |||||||||| ||
                                TG  TAGGGTGGGGC CC
                                 GT         T
GAM247  FLJ20232  3' GTTTCTGGGAGTGAGGCTGGT 38674   TG     _   TG
                                AC  GTTTTAC CCTG  GAT
                                ||  ||||||| ||||  |||
                                TG  CGGAGTG GGGT  TTG
                                 GT      A   CT
GAM247  FLJ20619  3' ATTGGCACGGGTGGAATCAG  35461          _  G
                                CTGGTTTTACCC TGT GAT
                                |||||||||||| ||| |||
                                GACTAAGGTGGG ACG TTA
                                      C   G
GAM247  FLJ20802  5' TGCAGGGGGGACCAGT     35671         A
                                ACTGGTTTT CCCTGTG
                                ||||||||| |||||||
                                TGACCAGGG GGGACGT
                                      _
GAM247  FLJ21156  3' GATTTTGCACAGGTTAAGGCCA 44809         C     GAT
           GT                    ACTGGTTTTA CCTGTG   AATC
                                ||||||||| ||||||   ||||
                                TGACCGGAAT GGACAC   TTAG
                                      T     GTT
GAM247  FLJ21596  3' CACGGGGTGGAGCGGGT    45699     G
                                ACT GTTTTACCCTGTG
                                ||| ||||||||||||
                                TGG CGAGGTGGGGCAC
                                  G
GAM247  FLJ21865  3' GTCTGGGGTGGGGTCTGT   42810   T  TT     GT
                                AC GG  TTACCCT  GGAT
                                || ||  |||||||  ||||
                                TG CT  GGTGGGG  TCTG
                                 T  GG     __
GAM247  FLJ22282  3' CATGGGGTGGGATCGGT    45587
                                ACTGGTTTTACCCTGTG
                                |||||||||||||||||
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                                TGGCTAGGGTGGGGTAC

GAM247  FLJ22282  3'  GTGGAAGCATGGGGTGGGATCG 45592              GATAATC
              GT                  ACTGGTTTTACCCTGTG
                                  ||||||||||||||||
                                  TGGCTAGGGTGGGGTAC
                                        GAAGGTGG
GAM247  FLJ22940  3'  ACAGGGTGAGCCAGT       44695        T
                                  ACTGGTTT ACCCTGT
                                  |||||||| |||||||
                                  TGACCGAG TGGGACA
                                     _
GAM247  FLJ23058  3'  GTTGTCTGGGGAGGTGG     45203      _  G
                                  TTACC CT TGGATAAT
                                  ||||| || ||||||||
                                  GGTGG GG GTCTGTTG
                                     A  G
GAM247  FLJ31564  5'  GTTAGCACGGTGGAGCTGGT   58529    TG      C   G
                                  AC  GTTTTACC TGT GAT
                                  ||  |||||||| ||| |||
                                  TG  CGAGGTGG ACG TTG
                                   GT       C   A
GAM247  FREQ      3'  CTGCAGGGATGGGGTCAGT    26575      TT  _    TG
                                  ACTGG  TTA CCCTG  G
                                  |||||  ||| |||||  |
                                  TGACT  GGT GGGAC  C
                                     GG   A    GT
GAM247  GAB3      3'  GATTATCTGACAAAGGCTGGT  54629    TG    ACCC  _
                                  AC  GTTTT    TGT GGATAATC
                                  ||  |||||    ||| ||||||||
                                  TG  CGGAA    ACA TCTATTAG
                                   GT    _____   G
GAM247  GFR       3'  TTGCAGGTGAAATTAGT     24478           C  TG
                                  ACTGGTTTTACC TG  G
                                  |||||||||||| ||  |
                                  TGATTAAAGTGG AC  T
                                         _  GT
GAM247  GTF3C2    3'  ATCCTTGGAGTGAAGTCGGT   7721       GT    _  TGT
                                  ACTG  TTTAC CC   GGAT
                                  ||||  ||||| ||   ||||
                                  TGGC  AAGTG GG   CCTA
                                    TG    A  TT_
GAM247  GW112     3'  GGTTATTTATTCAACTGAAGCC 21191          CCCT_
              AG                  CTGGTTTTA    GTGGATAATC
                                  |||||||||    ||||||||||
                                  GACCGAAGT    TATTTATTGG
                                       CAACT
GAM247  HRB2      3'  ATTATCCATTAAATCCAGT   22905       T   CCCT
                                  ACTGG TTTA   GTGGATAAT
                                  ||||| ||||   |||||||||
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                                TGACC AAAT    TACCTATTA
                                  T  ____
GAM247  HS6ST    3'  GGTTATTCATACAAAAAAATGA 62031     G    ACCC
              GT                   ACT GTTTT    TGTGGATAATC
                                   ||| |||||    ||||||||||
                                   TGA TAAAA    ATACTTATTGG
                                     G    AAAC
GAM247  HSH2     3'  CCATGGGGTGAGCTGGT     51673    TG   T
                                   AC  GTTT ACCCTGTGG
                                   ||  |||| |||||||||
                                   TG  CGAG TGGGGTACC
                                    GT   _
GAM247  HSPC055  5'  ATTTTAAGGGTGGGGTCA    26266     TT     GT
                                   TGG  TTACCCT  GGAT
                                   |||  |||||||  ||||
                                   ACT  GGTGGGA  TTTA
                                     GG      AT
GAM247  IDI1     5'  GGTTGTCTGTGGCCGGAGGCT  67045       ACC   TG
                                   GGTTTT   CTG  GATAATC
                                   ||||||   |||  |||||||
                                   TCGGAG   GGT  CTGTTGG
                                      GCC   GT
GAM247  IL-17RC  3'  CGTGGGGTGGGACCAG      51200           TG
                                   CTGGTTTTACCC  TG
                                   ||||||||||||  ||
                                   GACCAGGGTGGG  GC
                                         GT
GAM247  IL1F10   3'  GGTTATCCTTGTGGGCTCAGT  50774      TTTTA   TGT_
                                   ACTGG    CCC    GGATAATC
                                   |||||    |||    ||||||||
                                   TGACT    GGG    CCTATTGG
                                     C____   TGTT
GAM247  KIAA0164 3'  TCACAGGTAAAATCAGT     28452           C
                                   ACTGGTTTTACC TGTGG
                                   |||||||||||| |||||
                                   TGACTAAAATGG ACACT
                                                _
GAM247  KIAA0193 3'  GCCGGGTGGGACCAGT      28655           T
                                   ACTGGTTTTACCC GT
                                   |||||||||||| ||
                                   TGACCAGGGTGGG CG
                                          C
GAM247  KIAA0232 3'  GGTTGGGGCGGGTAGAGTCA  72754    GT     T  GGA
                                   TG  TTTACCC GT   TAATC
                                   ||  ||||||| ||   |||||
                                   AC  AGATGGG CG   GTTGG
                                    TG      _ GG_
GAM247  KIAA0258 3'  GTCTGGGGTGGAGACAGT    28821     G       GT
                                   ACTG TTTTACCCT  GGAT
                                   ||||  |||||||||  ||||
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                                TGAC GAGGTGGGG  TCTG
                                  A       __
GAM247  KIAA0319 5' TTTGCTGGGGTGGGGCT     29042          _ TG
                                GGTTTTACCCT G  GA
                                |||||||||||  |  ||
                                TCGGGGTGGGG C  TT
                                      T GT
GAM247  KIAA0377 3' GATTTCCTTGGGGTGGGTTGGT 27795    TG TT T     T   T
                                AC  G  T ACCCTG GGA AATC
                                ||  |  | ||||||| ||| |||||
                                TG  T  G TGGGGT CCT TTAG
                                 GT GG _     T  _
GAM247  KIAA0427 3' TGTGGGGTGGAACAGGT     28724     G        TG
                                ACT GTTTTACCC  TG
                                ||| |||||||||  ||
                                TGG CAAGGTGGG  GT
                                  A        GT
GAM247  KIAA0475 3' CTACAGGGGAAGGCCAGT    29490          A
                                ACTGGTTTT CCCTGTGG
                                ||||||||| ||||||||
                                TGACCGGAA GGGACATC
                                     G
GAM247  KIAA0514 3' GAAACTCATAGAGTAGAGCTGG 28082    TG      C     ATAATC
           T                     AC  GTTTTAC CTGTGG
                                ||  ||||||| ||||||
                                TG  CGAGATG GATACT
                                 GT      A     CAAAG
GAM247  KIAA0515 3' GTCCAGGGTGAGGCTGG     63814    TG         GT
                                C  GTTTTACCCT  GGAT
                                |  ||||||||||  ||||
                                G  CGGAGTGGGA  CCTG
                                GT        __
GAM247  KIAA0836 3' GATTGTTTGTGCTTAATGTAAA 64562        CCT____ TG
           GCC                     GTTTTAC      G  GATAATC
                                |||||||      |  |||||||
                                CGAAATG      T  TTGTTAG
                                     TAATTCG GT
GAM247  KIAA0861 3' GCGGGGTGGGAATCGGT     88926          _
                                ACTGGTTTT ACCCTGT
                                ||||||||| |||||||
                                TGGCTAAGG TGGGGCG
                                     G
GAM247  KIAA0930 3' GGTGTCTGATGTGGGGTGGGGC 70549  TG       TG ___    ATC
           TGG                      GTTTTACCC  T   GGATA
                                 |||||||||  |  |||||
                                 CGGGGTGGG  G   TCTGT
                                GT       GT TAG    GG
GAM247  KIAA0930 3' GGTTGTCTCCTCTGGGGCCAG  70550      TTTA   TGT__
                                CTGGT    CCC    GGATAATC
                                |||||    |||    ||||||||
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                                GACCG   GGG    TCTGTTGG
                                  ____  TCTCC
GAM247  KIAA0970 5' GATTATGAAAGGTAAAACTA  29960         CTGTGG
                                TGGTTTTACC     ATAATC
                                ||||||||||     ||||||
                                ATCAAAATGG     TATTAG
                                    AAAG__
GAM247  KIAA1040 3' ATTATTCATAAGAAATCA    72221        ACCC
                                TGGTTTT   TGTGGATAAT
                                |||||||   ||||||||||
                                ACTAAAG   ATACTTATTA
                                   A___
GAM247  KIAA1173 5' GTTTTGGCAGAGGGTGGGGCCG 40377            G  GATAATC
           GT                    ACTGGTTTTACCCT TG
                                ||||||||||||| ||
                                TGGCCGGGGTGGGA AC
                                       G  GGTTTTGG
GAM247  KIAA1193 3' GCGGGGTGGGGACAGT     67640     GT
                                ACTG  TTTACCCTGT
                                ||||  ||||||||||
                                TGAC  GGGTGGGGCG
                                  AG
GAM247  KIAA1199 3' GATTAGGAGCTGGGGTAGAACT 72515   TG       _  GGA
           GG                    C  GTTTTACCCT GT   TAATC
                                |  |||||||||| ||   |||||
                                G  CAAGATGGGG CG   ATTAG
                                 GT        T  AGG
GAM247  KIAA1388 3' CCACAGGGAGGGGCTGGT    93577    TG   TA
                                AC  GTTT  CCCTGTGG
                                ||  ||||  ||||||||
                                TG  CGGG  GGGACACC
                                 GT   GA
GAM247  KIAA1399 3' GCGGGAGTGAGGCTGGT     70251    TG     _
                                AC  GTTTTAC CCTGT
                                ||  ||||||| |||||
                                TG  CGGAGTG GGGCG
                                 GT      A
GAM247  KIAA1486 3' GGTTGTGGATGGGGAATTAGT  67385       TTA     GG
                                ACTGGTT   CCCTGT  ATAATC
                                |||||||   ||||||  ||||||
                                TGATTAA   GGGGTA  TGTTGG
                                    ___     GG
GAM247  KIAA1643 3' GCAGGTGAAGCCGGT      64552           C
                                ACTGGTTTTACC TGT
                                |||||||||||| |||
                                TGGCCGAAGTGG ACG
                                          _
GAM247  KIAA1679 3' CACAGGGTGGAGTCTGT     70148    T GT
                                AC G  TTTACCCTGTG
                                || |  ||||||||||
```

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                                TG C  AGGTGGGACAC
                                 T TG
GAM247  KIAA1887  5'  GGTGGGGCTGGGGTGGGGCCAG 76777          _  GGATAATC
                                CTGGTTTTACCCT GT
                                |||||||||||| ||
                                GACCGGGGTGGGG CG
                                      T  GGGTGG
GAM247  KIAA1956  3'  GGTTATCTGGCAAAAGCCA   78438      AC  TGT
                                TGGTTTT  CC   GGATAATC
                                |||||||  ||   ||||||||
                                ACCGAAA  GG   TCTATTGG
                                   AC  ____
GAM247  LHFP      5'  GATTATCTGTGGGTCCCTGGT  19336    TG TTTT    T TG
                                AC  G    ACCC G  GATAATC
                                ||  |    |||| |  |||||||
                                TG  C    TGGG T  CTATTAG
                                 GT CC__    _ GT
GAM247  LIMR      3'  GCCTCAGCATGGGGTAGGGCTG 36190    TG          GATAATC
          G                      C  GTTTTACCCTGTG
                                |  ||||||||||||
                                G  CGGGATGGGGTAC
                                 GT           GACTCCGG
GAM247  LRRFIP2   3'  ATTCTAGGGTAGAACCAGT   34781             T
                                ACTGGTTTTACCCTG GGAT
                                |||||||||||||| ||||
                                TGACCAAGATGGGAT CTTA
                                                _
GAM247  MAP2K6    3'  GTTTCGGGGTGAAGCAAGT   49247     G         T
                                ACT GTTTTACCCTG GGAT
                                ||| |||||||||| ||||
                                TGA CGAAGTGGGGC TTTG
                                  A         _
GAM247  MAP2K6    3'  GTTTCGGGGTGAAGCAAGT   10872     G         T
                                ACT GTTTTACCCTG GGAT
                                ||| |||||||||| ||||
                                TGA CGAAGTGGGGC TTTG
                                  A         _
GAM247  MAST205   5'  CCGCGGGCTGGGGTCGGT    30666      TT   C
                                ACTGG  TTA CCTGTGG
                                |||||  ||| |||||||
                                TGGCT  GGT GGGCGCC
                                   GG   C
GAM247  MBC3205   5'  TCCTAACGGTGGGATCGGT   53006           CTGT
                                ACTGGTTTTACC    GGA
                                ||||||||||||    |||
                                TGGCTAGGGTGG    CCT
                                       CAAT
GAM247  MGC10715  5'  GGTTGTTTGTAGGTACCAGT   44250       TTTAC    TG
                                ACTGGT    CCTG  GATAATC
                                ||||||    ||||  |||||||
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                                TGACCA    GGAT  TTGTTGG
                                   T____    GT
GAM247  MGC13040  5'  CTGTGGGTGGGATCGGT     51939           T TG
                                ACTGGTTTTACCC G  G
                                |||||||||||| |  |
                                TGGCTAGGGTGGG T  C
                                       _ GT
GAM247  MGC3329   3'  GGTTGTTTGTGGAGTCTGGGCT 44018   TG   T_  C   TG
           GG                     C  GTTT  AC CTG  GATAATC
                                |  ||||  || |||  |||||||
                                G  CGGG  TG GGT  TTGTTGG
                                 GT    TC  A   GT
GAM247  MGC4607   3'  GCAGGGAGAGCCAGT      48741         A
                                ACTGGTTTT CCCTGT
                                ||||||||| ||||||
                                TGACCGAGA GGGACG
                                      _
GAM247  MLN64     3'  CTGTGGGGTGGAGCAGT     94410      G        TG
                                ACTG TTTTACCCTG  G
                                |||| ||||||||||  |
                                TGAC GAGGTGGGGT  C
                                  _        GT
GAM247  NMA       3'  GGTTATTTGCATCCAAGGGAGC 24713     TTA   _____ TG
           TGG                    GTT   CCCT    G  GATAATC
                                |||   ||||    |  |||||||
                                CGA   GGGA    C  TTATTGG
                                  ___    ACCTA GT
GAM247  NUDEL     3'  GTTCCAGGGTGGGCCGGT    47971         T     T
                                ACTGGTTT ACCCTG GGAT
                                |||||||| |||||| ||||
                                TGGCCGGG TGGGAC CTTG
                                      _     _
GAM247  ORNT2     3'  ATGTACAGGGTGGGCTGGT   49207    TG   T       G
                                AC  GTTT ACCCTGTG AT
                                ||  |||| |||||||| ||
                                TG  CGGG TGGGACAT TA
                                 GT   _       G
GAM247  PDE11A    5'  CCACGGGGTGGGGTCGG     33777      TT
                                CTGG  TTACCCTGTGG
                                ||||  ||||||||||
                                GGCT  GGTGGGGCACC
                                  GG
GAM247  PJA1      3'  GATTATTTCCAATGTGAAAACA 42324      G     CC  TG
           GT                     ACTG TTTTAC  TG  GATAATC
                                |||| ||||||  ||  |||||||
                                TGAC AAAGTG  AC  TTATTAG
                                  A     TA  CT
GAM247  PPP1R13B  3'  GGTTGGGGCTGGGGGTGGACTG 31010    TG   TA   _  GGA
           GT                     AC  GTTT  CCCT GT   TAATC
                                ||  ||||  |||| ||   |||||
```

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                                TG  CAGG  GGGG CG   GTTGG
                                 GT    TG    T GG_
GAM247  RACGAP1  3'  GGTTCATTTGGGGTCAAAGCCA 25199        _    __     AATC
           GT                    CTGGTTTT ACCCT  GTGGAT
                                 |||||||| |||||  ||||||
                                 GACCGAAA TGGGG  TACTTG
                                     C    TT     G
GAM247  RAD51    5'  CCGCGGGGTGAAGTCGG     56014     GT
                                 CTG  TTTACCCTGTGG
                                 |||  ||||||||||||
                                 GGC  AAGTGGGGCGCC
                                   TG
GAM247  RAD51    5'  CCGCGGGGTGAAGTCGG     11220     GT
                                 CTG  TTTACCCTGTGG
                                 |||  ||||||||||||
                                 GGC  AAGTGGGGCGCC
                                   TG
GAM247  RBAF600  3'  GGTTGTCTGTAACCCAAGCCA  68533       TACCC  TG
                                 TGGTTT    TG  GATAATC
                                 ||||||    ||  |||||||
                                 ACCGAA    AT  CTGTTGG
                                    CCCA_  GT
GAM247  RGS17    3'  GGTTGTTCACTGCCAAAACT   24842       ACCCT
                                 GGTTTT    GTGGATAATC
                                 ||||||    ||||||||||
                                 TCAAAA    CACTTGTTGG
                                    CCGT_
GAM247  RNPC1    3'  GGTTGGTGGAGGGTGGAGGCAG 33993     G       G  GA
           T                      ACTG TTTTACCCT TG  TAATC
                                 |||| ||||||||| ||  |||||
                                 TGAC GAGGTGGGA GT  GTTGG
                                   G       G  G_
GAM247  SARM     3'  ATTTACTGGGGTGGGCTGGT   30597    TG    T    _
                                 AC  GTTT ACCCT GTGGAT
                                 ||  |||| ||||| ||||||
                                 TG  CGGG TGGGG CATTTA
                                  GT   _    T
GAM247  SEC14L1  3'  GTTAGTAGGTAGGGCTAGT   11517          C  TG
                                 ACTGGTTTTACC TG  GAT
                                 ||||||||||| ||  |||
                                 TGATCGGGATGG AT  TTG
                                        _  GA
GAM247  SEC14L1  3'  GTTAGTAGGTAGGGCTAGT   11513          C  TG
                                 ACTGGTTTTACC TG  GAT
                                 ||||||||||| ||  |||
                                 TGATCGGGATGG AT  TTG
                                        _  GA
GAM247  SEC14L1  3'  CTAGTAGGTAGGGCTAGT    11501          CTG
                                 ACTGGTTTTACC   TGG
                                 ||||||||||||   |||
```

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                                TGATCGGGATGG  ATC
                                      ATG
GAM247  SEC14L1  3' CTAGTAGGTAGGGCTAGT   11496        CTG
                                ACTGGTTTTACC  TGG
                                ||||||||||||  |||
                                TGATCGGGATGG  ATC
                                      ATG
GAM247  SEC14L1  3' CTAGTAGGTAGGGCTAGT   11497        CTG
                                ACTGGTTTTACC  TGG
                                ||||||||||||  |||
                                TGATCGGGATGG  ATC
                                      ATG
GAM247  SEC14L1  3' CTAGTAGGTAGGGCTAGT   11491        CTG
                                ACTGGTTTTACC  TGG
                                ||||||||||||  |||
                                TGATCGGGATGG  ATC
                                      ATG
GAM247  SEC14L1  3' CTAGTAGGTAGGGCTAGT   11492        CTG
                                ACTGGTTTTACC  TGG
                                ||||||||||||  |||
                                TGATCGGGATGG  ATC
                                      ATG
GAM247  SEC14L1  3' CTAGTAGGTAGGGCTAGT   11494        CTG
                                ACTGGTTTTACC  TGG
                                ||||||||||||  |||
                                TGATCGGGATGG  ATC
                                      ATG
GAM247  SEC14L1  3' CTAGTAGGTAGGGCTAGT   11499        CTG
                                ACTGGTTTTACC  TGG
                                ||||||||||||  |||
                                TGATCGGGATGG  ATC
                                      ATG
GAM247  SEC14L1  3' TAGGGTTCGTAGGTAGGGCTAG 11519        C     AATC
           T                     ACTGGTTTTACC TGTGGAT
                                ||||||||||||  |||||||
                                TGATCGGGATGG ATGCTTG
                                      _      GGATG
GAM247  SEC14L1  3' TAGGGTTCGTAGGTAGGGCTAG 11520        C     AATC
           T                     ACTGGTTTTACC TGTGGAT
                                ||||||||||||  |||||||
                                TGATCGGGATGG ATGCTTG
                                      _      GGATG
GAM247  SEC14L1  3' TAGGGTTCGTAGGTAGGGCTAG 11521        C     AATC
           T                     ACTGGTTTTACC TGTGGAT
                                ||||||||||||  |||||||
                                TGATCGGGATGG ATGCTTG
                                      _      GGATG
GAM247  SEC14L1  3' TAGGGTTCGTAGGTAGGGCTGG 11525    TG      C     AATC
           T                     AC  GTTTTACC TGTGGAT
                                ||  ||||||||  |||||||
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                                TG  CGGGATGG ATGCTTG
                                 GT       _      GGATG
GAM247  SEC14L1  3' TAGGGTTCGTAGGTAGGGTTAG 11526      TT    C      AATC
           T                     ACTGG  TTACC TGTGGAT
                                 |||||  ||||| |||||||
                                TGATT  GATGG ATGCTTG
                                  GG    _      GGATG
GAM247  SEC14L1  3' TAGGGTTCGTAGGTAGGGCTGG 11522    TG      C      AATC
           T                     AC  GTTTTACC TGTGGAT
                                 ||  |||||||| |||||||
                                TG  CGGGATGG ATGCTTG
                                 GT       _      GGATG
GAM247  SEC14L1  3' TAGGGTTCGTAGGTAGGGCTGG 11523    TG      C      AATC
           T                     AC  GTTTTACC TGTGGAT
                                 ||  |||||||| |||||||
                                TG  CGGGATGG ATGCTTG
                                 GT       _      GGATG
GAM247  SEC14L1  3' TAGGGTTCGTAGGTAGGGCTGG 11524    TG      C      AATC
           T                     AC  GTTTTACC TGTGGAT
                                 ||  |||||||| |||||||
                                TG  CGGGATGG ATGCTTG
                                 GT       _      GGATG
GAM247  SEC14L1  3' GTTAGTAGGTAGGGCTAGT   11516         C  TG
                                ACTGGTTTTACC TG  GAT
                                ||||||||||||  ||  |||
                                TGATCGGGATGG AT  TTG
                                       _  GA
GAM247  SEC14L1  3' CTAGTAGGTAGGGCTAGT    11490         CTG
                                ACTGGTTTTACC   TGG
                                ||||||||||||   |||
                                TGATCGGGATGG   ATC
                                       ATG
GAM247  SEC14L1  3' CTAGTAGGTAGGGCTAGT    11495         CTG
                                ACTGGTTTTACC   TGG
                                ||||||||||||   |||
                                TGATCGGGATGG   ATC
                                       ATG
GAM247  SEC14L1  3' GTTAGTAGGTAGGGCTAGT   11512         C  TG
                                ACTGGTTTTACC TG  GAT
                                ||||||||||||  ||  |||
                                TGATCGGGATGG AT  TTG
                                       _  GA
GAM247  SEC14L1  3' CTAGTAGGTAGGGCTAGT    11500         CTG
                                ACTGGTTTTACC   TGG
                                ||||||||||||   |||
                                TGATCGGGATGG   ATC
                                       ATG
GAM247  SEC14L1  3' GTTAGTAGGTAGGGCTAGT   11515         C  TG
                                ACTGGTTTTACC TG  GAT
                                ||||||||||||  ||  |||
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                                TGATCGGGATGG AT  TTG
                                       _ GA
GAM247  SEC14L1  3'  GTTAGTAGGTAGGGCTAGT   11511          C  TG
                                ACTGGTTTTACC TG  GAT
                                |||||||||||| ||  |||
                                TGATCGGGATGG AT  TTG
                                       _ GA
GAM247  SEC14L1  3'  GTTAGTAGGTAGGGCTAGT   11514          C  TG
                                ACTGGTTTTACC TG  GAT
                                |||||||||||| ||  |||
                                TGATCGGGATGG AT  TTG
                                       _ GA
GAM247  SEC14L1  3'  CTAGTAGGTAGGGCTAGT    11498          CTG
                                ACTGGTTTTACC   TGG
                                ||||||||||||   |||
                                TGATCGGGATGG   ATC
                                       ATG
GAM247  SEC14L1  3'  GTTAGTAGGTAGGGCTAGT   11510          C  TG
                                ACTGGTTTTACC TG  GAT
                                |||||||||||| ||  |||
                                TGATCGGGATGG AT  TTG
                                       _ GA
GAM247  SEC14L1  3'  CTAGTAGGTAGGGCTAGT    11493          CTG
                                ACTGGTTTTACC   TGG
                                ||||||||||||   |||
                                TGATCGGGATGG   ATC
                                       ATG
GAM247  SIL1     5'  TACAGGTGGAGCTGGT     42430    TG      C
                                AC  GTTTTACC TGTG
                                ||  |||||||| ||||
                                TG  CGAGGTGG ACAT
                                 GT      _
GAM247  SLB      5'  TCACAGGGGAAGTTGGT     88845    GG    A
                                ACT  TTTT CCCTGTGG
                                |||  |||| ||||||||
                                TGG  GAAG GGGACACT
                                  TT   _
GAM247  SMBP     3'  ATGGGGTAAAAGTGGT      72159      G
                                ACTG TTTTACCCTGT
                                |||| ||||||||||
                                TGGT AAAATGGGGTA
                                  G
GAM247  SS-56    3'  GGTTGTTGTGCTGAGGCCAGT  59608          CCCT  _
                                ACTGGTTTTA    GTG GATAATC
                                ||||||||||    ||| |||||||
                                TGACCGGAGT    CGT TTGTTGG
                                       _____  G
GAM247  SSH2     3'  GGTTATTTACATAGCTGAGCAG 62210      G  TTACCC
           T                     ACTG TT     TGTGGATAATC
                                ||||  ||     ||||||||||
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                                TGAC AG     ACATTTATTGG
                                  G  TCGAT_
GAM247  TCL6     5'  GCAGTGGTGAGGCCAGT     40083          _
                                ACTGGTTTTACC CTGT
                                |||||||||||| ||||
                                TGACCGGAGTGG GACG
                                       T
GAM247  TCL6     5'  GCAGTGGTGAGGCCAGT     26996          _
                                ACTGGTTTTACC CTGT
                                |||||||||||| ||||
                                TGACCGGAGTGG GACG
                                       T
GAM247  TCL6     5'  GCAGTGGTGAGGCCAGT     24980          _
                                ACTGGTTTTACC CTGT
                                |||||||||||| ||||
                                TGACCGGAGTGG GACG
                                       T
GAM247  TCL6     5'  GCAGTGGTGAGGCCAGT     40104          _
                                ACTGGTTTTACC CTGT
                                |||||||||||| ||||
                                TGACCGGAGTGG GACG
                                       T
GAM247  TRF4-2   5'  AGTATTTACAGGTGGAATTGGT 42385    TG       C       ATC
                                AC  GTTTTACC TGTGGATA
                                ||  |||||||| ||||||||
                                TG  TAAGGTGG ACATTTAT
                                  GT       _       GAA
GAM247  UACA     5'  GGTGGCAGGCAGGTGGGGCTGG 72392   TG       ___    GGATAATC
           T                     C  GTTTTACC   CTGT
                                |  |||||||||   ||||
                                G  CGGGGTGG   GACG
                                 GT       ACG    GTGG   C
GAM247  ZAK      3'  GATTATTTACTTCAAAACTAG  56126         ACCCT
                                CTGGTTTT    GTGGATAATC
                                ||||||||    ||||||||||
                                GATCAAAA    CATTTATTAG
                                     CTT__
GAM247  ZNF212   3'  GGTTGTTCACCTTGTACCAGT  24307       TTT  CCT
                                ACTGGT   AC   GTGGATAATC
                                ||||||   ||   ||||||||||
                                TGACCA   TG   CACTTGTTGG
                                   ___  TTC
GAM247  LOC115051 3'  GGTTATTCATACAAAAAAATGA 60042     G     ACCC
           GT                    ACT GTTTT    TGTGGATAATC
                                ||| |||||    ||||||||||
                                TGA TAAAA    ATACTTATTGG
                                  G     AAAC
GAM247  LOC118812 3'  GATAAGTATTGGGTAAAGCCAG 73931            T   GATAATC
           T                     ACTGGTTTTACCC GTG
                                ||||||||||||| |||
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                                TGACCGAAATGGG TAT
                                      T  GAATAG
GAM247  LOC121512 5'  GATTATCTGCAATGGACCGG  57644       TACCC  TG
                                CTGGTTT    TG  GATAATC
                                |||||||    ||  |||||||
                                GGCCAGG    AC  CTATTAG
                                    TA___  GT
GAM247  LOC124470 3'  GTCAGGCAGGGTAAGCCAGT  75640        T     G_
                                ACTGGTTT ACCCTGT  GAT
                                |||||||| |||||||  |||
                                TGACCGAA TGGGACG  CTG
                                     _      GA
GAM247  LOC129293 3'  GGTTATCCAACTTTGGGGGCAG 74870    G TTTA   TG___
                                CTG T   CCC    TGGATAATC
                                ||| |   |||    |||||||||
                                GAC G   GGG    ACCTATTGG
                                  G ____   TTTCA
GAM247  LOC143914 5'  GGTTGTGGTTAGGTCAAACTGG 76613    TG   TAC   TGG
           T                     AC  GTTT   CCTG   ATAATC
                                 ||  ||||   ||||   ||||||
                                 TG  CAAA   GGAT   TGTTGG
                                  GT   CT_   TGG
GAM247  LOC144147 3'  ATTGTGAAGGTAGAACCA    71729         CTGTGG
                                TGGTTTTACC     ATAAT
                                ||||||||||     |||||
                                ACCAAGATGG     TGTTA
                                      AAG___
GAM247  LOC144600 3'  GGTGTCTGATGTGGGGTGGGGC 83162   TG       TG ___    ATC
           TGG                     GTTTTACCC  T   GGATA
                                  |||||||||  |   |||||
                                  CGGGGTGGG  G   TCTGT
                                 GT        GT TAG    GG
GAM247  LOC144667 3'  GAAATGCATGGGGTGGGACAGG 83167     G          G  AATC
           T                      ACT GTTTTACCCTGTG AT
                                 ||| ||||||||||||| ||
                                 TGG CAGGGTGGGGTAC TA
                                   A           G  AAG
GAM247  LOC145813 5'  ATTCACAGGGTGTGGTCAGT   83503     GT T
                                ACTG  T TACCCTGTGGAT
                                ||||  | ||||||||||||
                                TGAC  G GTGGGACACTTA
                                   TG T
GAM247  LOC147081 3'  GGTTATCCCTCAGTAAAGCT   78244       CC  T_
                                GGTTTTAC  TG  GGATAATC
                                ||||||||  ||  ||||||||
                                TCGAAATG  AC  CCTATTGG
                                     __  TC
GAM247  LOC148809 3'  GTAGGGTGGGGCAGT       79005      G
                                ACTG TTTTACCCTGT
                                |||| ||||||||||
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                                TGAC GGGGTGGGATG
                                   _
GAM247  LOC149276 5' CTGTGGGGGGAAACCAGT    84386       TA    TG
                                ACTGGTTT  CCCTG  G
                                ||||||||  |||||  |
                                TGACCAAA  GGGGT  C
                                    GG    GT
GAM247  LOC149832 5' GATTATTTCCTGGGTATTAGT  84701      TTT    TGT
                                ACTGGT   ACCC   GGATAATC
                                ||||||   ||||  ||||||||
                                TGATTA   TGGG   TTTATTAG
                                   ___   TCC
GAM247  LOC149910 3' GATTGTTCATTCCCTAGGGCTA 79532        CCCT
           GT                    ACTGGTTTTA   GTGGATAATC
                                 ||||||||||   ||||||||||
                                 TGATCGGGAT   TACTTGTTAG
                                      CCCT
GAM247  LOC150290 5' GGTTGAGCCAGGGTGGGGCT   79777         TGGA
                                 GGTTTTACCCTG   TAATC
                                 ||||||||||||   |||||
                                 TCGGGGTGGGAC   GTTGG
                                       CGA_
GAM247  LOC150295 5' TCTGGTTCTGGGGTGGAGTTGG 84963    GG       T   AATC
           T                     ACT  TTTTACCCTG GGAT
                                 |||  ||||||||||  ||||
                                 TGG  GAGGTGGGGT CTTG
                                   TT        _   GTCTG
GAM247  LOC151031 5' GTCTGGGGTGGGCCAGT     87191       T    GT
                                 ACTGGTTT ACCCT  GGAT
                                 ||||||||  |||||  ||||
                                 TGACCGGG TGGGG  TCTG
                                      _    __
GAM247  LOC152245 3' GTTATATTGGAGAGCCAGT    85604        A  CTGTGG
                                 ACTGGTTTT CC     ATAAT
                                 |||||||||  ||     |||||
                                 TGACCGAGA GG     TATTG
                                      _  TTA___
GAM247  LOC153328 3' ATGGGGAGGGGCCAGT      80808       TA
                                 ACTGGTTT  CCCTGT
                                 ||||||||  ||||||
                                 TGACCGGG  GGGGTA
                                    GA
GAM247  LOC154043 3' GTTATTTGTGTGGGGTGG    81030       __ TG
                                 TTACCCT  G  GATAAT
                                 |||||||  |  ||||||
                                 GGTGGGG  T  TTATTG
                                    TG GT
GAM247  LOC154184 3' GGTTGTCTGCAAGCTGGAGAAC 86181       A  C___  TG
           CAG                     TGGTTTT CC    TG  GATAATC
                                   |||||||  ||    ||  |||||||
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                                ACCAAGA GG    AC  CTGTTGG
                                    _ TCGA  GT
GAM247  LOC155038 3'  ATAAGCAGGCTGGGGCTGGT   81256    TG     C     GG
                                AC  GTTTTA CCTGT  AT
                                ||  |||||| |||||  ||
                                TG  CGGGGT GGACG  TA
                                 GT     C     AA
GAM247  LOC155054 3'  TGAAGGATTCACAGGGTAAGAT 81277                AATC
           CGG                    CTGGTTTTACCCTGTGGAT
                                ||||||||||||||||||
                                GGCTAGAATGGGACACTTA
                                          GGAAGTT
GAM247  LOC157624 5'  GTTTTAGGGGTGCAAGCCAGT  86499         _     GT
                                ACTGGTTT TACCCT  GGAT
                                |||||||| ||||||  ||||
                                TGACCGAA GTGGGG  TTTG
                                     C     AT
GAM247  LOC158314 3'  GTCTAGGGTAGTGCTGGT    86772    TG  T      GT
                                AC  GT TTACCCT  GGAT
                                ||  || |||||||  ||||
                                TG  CG GATGGGA  TCTG
                                 GT  T     __
GAM247  LOC168667 3'  GTAGGGAAAATCAGT       92758          A
                                ACTGGTTTT CCCTGT
                                |||||||| ||||||
                                TGACTAAAA GGGATG
                                          _
GAM247  LOC196872 3'  GCGTGGAGTGAGACCAGT    87798           _ _
                                ACTGGTTTTAC CC TGT
                                |||||||||| || |||
                                TGACCAGAGTG GG GCG
                                       A  T
GAM247  LOC197201 3'  GGCGTGTGCAGGGCTGGGGCCA 87942          _      G  AATC
           GT                    ACTGGTTTTA CCCTGTG AT
                                |||||||||| ||||||| ||
                                TGACCGGGGT GGGACGT TG
                                     C      G  CGG
GAM247  LOC200261 3'  CGATTGTTGGTGCTGTGGGGAG 88654     A     TG _____
           AAGCTGGT                TTT CCCTG  G     ATAATC   G
                                ||| |||||  |    ||||||  |
                                AAG GGGGT  C     TGTTAG   C
                                  A     GT GTGGT
GAM247  LOC200844 5'  GGTTGTCTGTGGCTCCGCGACT 88910    TG   TTACC_   TG
           GG                    C  GTT     CTG  GATAATC
                                |  |||     |||  |||||||
                                G  CAG     GGT  CTGTTGG
                                 GT   CGCCTC   GT
GAM247  LOC201102 3'  GGTTCCCCGGTGAGGGTAAGGT 88097    TG TT      G__   AT
           TGGT                    C  G  TTACCCT   TGG  AATC
                                |  |  |||||||   |||  ||||
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                                G  T  AATGGGA   GCC  TTGG
                                 GT GG      GTG   CC
GAM247   LOC201706 5'  GAGTGCCACAGGGTGGCACTGG 89521    TG  T         ATAATC
             T                    AC  GT TTACCCTGTGG
                                  ||  || ||||||||||
                                  TG  CA GGTGGGACACC
                                   GT  C          GTGAG
GAM247   LOC201799 3'  GATTATTCAAGTCGTGGGACAG 89062     G      CCTG
             GT                    ACT GTTTTAC    TGGATAATC
                                   ||| |||||||    |||||||||
                                   TGG CAGGGTG    ACTTATTAG
                                     A      CTGA
GAM247   LOC203286 3'  GGTTGGGTGGGTGAGGCCAG   90501           TGTGGA
                                   CTGGTTTTACCC      TAATC
                                   ||||||||||||      |||||
                                   GACCGGAGTGGG      GTTGG
                                          TGG___
GAM247   LOC219894 3'  GGTTATCCACACACTAATCA   93284       TTACCC
                                   TGGTT     TGTGGATAATC
                                   ||||||     ||||||||||
                                   ACTAA     ACACCTATTGG
                                      TCAC__
GAM247   LOC221601 3'  GGTTGTCTGCAAGCTGGAGAAC 93649        A  C___  TG
             CAG                     TGGTTTT CC    TG  GATAATC
                                   ||||||| ||    ||  |||||||
                                   ACCAAGA GG    AC  CTGTTGG
                                       _  TCGA  GT
GAM247   LOC222112 3'  CATAGGGAAGGGTCAGT     92803       TT  A
                                   ACTGG  TT CCCTGTG
                                   |||||  || |||||||
                                   TGACT  GA GGGATAC
                                      GG  A
GAM247   LOC253115 3'  GATTTTTATTGTGGGGTGGGAT 94496     G         TG AT__
             GAGT                     CT GTTTTACCCTG  G    AATC
                                   || ||||||||||  |    ||||
                                   GA TAGGGTGGGGT  T    TTAG
                                    G          GT ATTT
GAM247   LOC253502 3'  CGTAGGGTGGGGGCAGT     94578      G
                                   ACTG TTTTACCCTGTG
                                   |||| ||||||||||||
                                   TGAC GGGGTGGGATGC
                                     G
GAM247   LOC253981 3'  GGTGAGCTGTGGGGGAGGCCAG 95832          A     TG ATA
             T                     ACTGGTTTT CCCTG  G   ATC
                                   |||||||||  |||||  |  |||
                                   TGACCGGAG GGGGT  C   TGG
                                         _    GT GAG
GAM247   LOC254302 5'  GTTGTCTTAGAAACCAGT     96186          ACCCTGT
                                   ACTGGTTTT      GGATAAT
                                   |||||||||      |||||||
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                                TGACCAAAG      TCTGTTG
                                     AT_____
GAM247  LOC254874 5'  GTTGTCTTAGAAACCAGT    96183         ACCCTGT
                                ACTGGTTTT      GGATAAT
                                |||||||||      |||||||
                                TGACCAAAG      TCTGTTG
                                     AT_____
GAM247  LOC255452 3'  TCCTGGGGGAAAACCAGT    97545         A    GT
                                ACTGGTTTT CCCT  GGA
                                ||||||||| ||||  |||
                                TGACCAAAA GGGG  CCT
                                     _   GT
GAM247  LOC255520 3'  TTATAGGGTCAAGTTGGT    95867     GG   T
                                ACT  TTT ACCCTGTGG
                                |||  ||| |||||||||
                                TGG  GAA TGGGATATT
                                  TT   C
GAM247  LOC257556 3'  GATTTTTATTGTGGGGTGGGAT 97709    G         TG AT__
           GAGT                   CT GTTTTACCCTG  G    AATC
                                || ||||||||||  |    ||||
                                GA TAGGGTGGGGT  T    TTAG
                                 G         GT ATTT
GAM247  LOC257617 3'  GATTTTTATTGTGGGGTGGGAT 97815    G         TG AT__
           GAGT                   CT GTTTTACCCTG  G    AATC
                                || ||||||||||  |    ||||
                                GA TAGGGTGGGGT  T    TTAG
                                 G         GT ATTT
GAM247  LOC51076  3'  GATTGTCATCATGGTTAAAGCT 31991    TG     _  C  TG
           GGT                    AC  GTTTTA CC TG  GATAATC
                                ||  |||||| || ||  |||||||
                                TG  CGAAAT GG AC  CTGTTAG
                                 GT     T  T  TA
GAM247  LOC51157  5'  ATTGTCTGCTGGGGTGGG    32488         _ TG
                                TTTACCCT G  GATAAT
                                |||||||| |  ||||||
                                GGGTGGGG C  CTGTTA
                                     T GT
GAM247  LOC51204  3'  GCAATCTCTGAGGGTAAAGCCG 33028            GT_    AATC
           GT                     ACTGGTTTTACCCT   GGAT
                                ||||||||||||||   ||||
                                TGGCCGAAATGGGA   TCTA
                                       GTC    ACG
GAM247  LOC90092  3'  ACATGGTGTAAGGCCAGT    61397          _ _
                                ACTGGTTTTAC CC TGT
                                |||||||||||| || |||
                                TGACCGGAATG GG ACA
                                       T  T
GAM247  LOC90288  3'  ATCTGGGGTGAGGCC       62080          GT
                                GGTTTTACCCT  GGAT
                                ||||||||||  ||||
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                              CCGGAGTGGGG  TCTA
                                        __
GAM247  LOC90321  3' GATTGTCTGATTTAGAGACCA  62263       ACCCTG
                              TGGTTTT     TGGATAATC
                              |||||||     |||||||||
                              ACCAGAG     GTCTGTTAG
                                  ATTTA_
GAM247  LOC91010  3' GGTTGTTCGCCACCAAGCCAG  64617       TACCCT
                              CTGGTTT     GTGGATAATC
                              |||||||     ||||||||||
                              GACCGAA     CGCTTGTTGG
                                  CCAC__
GAM247  LOC91035  5' GATCCAGGGTGGGGTGAAGCCC 64670   T        ___    AATC
            GT                  C GGTTTTACCCTG   TGGAT
                              | ||||||||||||   |||||
                              G CCGAAGTGGGGT   ACCTA
                               C         GGG    G
GAM247  LOC91431  5' GGTTGTCCATGCGTTATTGGT  56925    TG  TTT  CCT
                              AC  GT   AC   GTGGATAATC
                              ||  ||   ||   ||||||||||
                              TG  TA   TG   TACCTGTTGG
                               GT  T__  CG_
GAM247  LOC92080  3' TACTGGGGTGAAGTTGG     68059    GG       _
                              CT  TTTTACCCT GTG
                              ||  ||||||||| |||
                              GG  GAAGTGGGG CAT
                               TT       T
GAM247  LOC93070  3' TCCACAGGTTGAAACTGGT    71297    TG     C
                              AC  GTTTTA CCTGTGGA
                              ||  |||||| ||||||||
                              TG  CAAAGT GGACACCT
                               GT     T
GAM248  BAI2     5' CCGTGGCCGCCCCCGCCA    8117      A  A  A  _
                              TGGC GG GC GGC ACGG
                              |||| || || ||| ||||
                              ACCG CC CG CCG TGCC
                                C  C  _  G
GAM248  CAPG     3' CCATGCTCCCCTGCCCCCCACC 8247     CA_  A    CAC
            A                  TGG   GG GCAGG   GGGCATGG
                              |||   || |||||   ||||||||
                              ACC   CC CGTCC   CTCGTACC
                                ACC  C    C__
GAM248  CARD15   5' CCATGCCTGCTCCCCCA     42211     CA       C
                              TGG  GGAGCAGGCA GG
                              |||  |||||||||| ||
                              ACC  CCTCGTCCGT CC
                                C_        A
GAM248  CD7      3' CATGCCCCCCCACCCTGCCA   20427       AGCA  CAC
                              TGGCAGG   GG   GGGCATG
                              |||||||   ||   |||||||
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                                ACCGTCC   CC  CCCGTAC
                                   CA__  C__
GAM248  CHAD    3'  CATGCCCCAACTCTGCCA   7010      GAGC  GCAC
                                TGGCAG   AG   GGGCATG
                                ||||||   ||   |||||||
                                ACCGTC   TC   CCCGTAC
                                   _____ AAC_
GAM248  HIP12   3'  CCATGCCCTCCTGCTCCCCCCA 66230    CA      CAC
                                TGG  GGAGCAGG  GGGCATGG
                                |||  ||||||||  ||||||||
                                ACC  CCTCGTCC  CCCGTACC
                                  CC      T__
GAM248  HMGA2   5'  CCGCTGCCTGCTCCCGCCA   12995    A       _
                                TGGC GGAGCAGGCA CGG
                                |||| |||||||||| |||
                                ACCG CCTCGTCCGT GCC
                                   C        C
GAM248  HSPB1   3'  CCACTGGCTGTGCCTCCCCCGC 7740      A  AGC      G  _
            CA                    TGGC GG   AGGCACGG CA TGG
                                |||| ||   |||||||| || |||
                                ACCG CC   TCCGTGTC GT ACC
                                  C  CC_      G  C
GAM248  IGHMBP2 3'  CATGCTCCGCCTCCACCA   9302    CA  GCA  AC
                                TGG  GGA  GGC  GGGCATG
                                |||  |||  |||  |||||||
                                ACC  CCT  CCG  CTCGTAC
                                  A_  ____  C_
GAM248  KRT2A   3'  CCATGCCCATTCCCGCCCCCAC 4708    CA  A  A  CAC
            CA                    TGG  GG GC GG   GGGCATGG
                                |||  || || ||   ||||||||
                                ACC  CC CG CC   CCCGTACC
                                  AC  C  C  TTA
GAM248  M11S1   3'  CCAAATGCCTGCTGCTACCA   19732    C  G      CG_
                                TGG AG AGCAGGCA   GG
                                ||| || ||||||||   ||
                                ACC TC TCGTCCGT   CC
                                  A  G      AAA
GAM248  MAPRE3  3'  CAGCCACCTGCTCCTGACA   24664    G       CACG  A
                                TG CAGGAGCAGG   GGC TG
                                || ||||||||||   ||| ||
                                AC GTCCTCGTCC   CCG AC
                                  A        A___  _
GAM248  MHC2TA  3'  CCACACCCAGCCCACTTCTGCC 4167        CA  AC  CA
            A                    TGGCAGGAG  GGC  GGG  TGG
                                |||||||||  |||  |||  |||
                                ACCGTCTTC  CCG  CCC  ACC
                                     AC  A_  AC
GAM248  MICB    3'  CTCACGACTGCTCCTGCCA   19825          GCAC
                                TGGCAGGAGCAG   GGG
                                ||||||||||||   |||
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                                ACCGTCCTCGTC   CTC
                                       AGCA
GAM248  NTSR1    5'  CCTGAGACGCGCCCACTCCTGC 10290        CA  A  GG_  T
             C                   GGCAGGAG  GGC CG   CA GG
                                 ||||||||  ||| ||   || ||
                                 CCGTCCTC  CCG GC   GT CC
                                      AC   C  AGA  _
GAM248  PAG      5'  CCAGTGCCTGCTCCTGCC    37401             G
                                 GGCAGGAGCAGGCAC GG
                                 ||||||||||||||| ||
                                 CCGTCCTCGTCCGTG CC
                                        A
GAM248  PFKL     3'  CCATGCCCACGCCCCTCCCCA  10517     CA   CA   AC
                                 TGG  GGAG  GGC  GGGCATGG
                                 |||  ||||  |||  ||||||||
                                 ACC  CCTC  CCG  CCCGTACC
                                   __   C_  CA
GAM248  PLXNA1   3'  CCATGCCCGCTGCACCGCTGCC 72310      __ A   GCA
             A                   TGGCA  GG GCAG   CGGGCATGG
                                 |||||  || ||||   |||||||||
                                 ACCGT  CC CGTC   GCCCGTACC
                                    CG  A   ____
GAM248  PRDM4    5'  CCTGATGCCTGTCCCCACCA   24823     CA  AG     _
                                 TGG  GG  CAGGCA CGGG
                                 |||  ||  ||||||  ||||
                                 ACC  CC  GTCCGT GTCC
                                   AC  CT     A
GAM248  RARG     3'  CCTGCCCTGCTCCCACCA    6378      CA       CA
                                 TGG  GGAGCAGG  CGGG
                                 |||  ||||||||  ||||
                                 ACC  CCTCGTCC  GTCC
                                   AC       C_
GAM248  RFP      5'  CCATGCCCGTGCGCCCCCGC   21491    A  A  AG
                                 GC GG GC  GCACGGGCATGG
                                 || || ||  ||||||||||||
                                 CG CC CG  CGTGCCCGTACC
                                  C  C  __
GAM248  SYNGR1   3'  CCACACCCAGCCCCTGCTCCTG 16313          CAC_   CA
             CC                    GGCAGGAGCAGG    GGG  TGG
                                   ||||||||||||    |||  |||
                                   CCGTCCTCGTCC    CCC  ACC
                                          CCGA   AC
GAM248  TCF20    3'  CCGCGTGCCTGCCCATGCCA   66955      _ A       _
                                 TGGCA GG GCAGGCACG GG
                                 ||||| || ||||||||| ||
                                 ACCGT CC CGTCCGTGC CC
                                    A _        G
GAM248  WDR1     3'  CATGCCCCCACCCCACCA    33983     CA  AGCA  CAC
                                 TGG  GG   GG   GGGCATG
                                 |||  ||   ||   |||||||
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                                ACC  CC   CC   CCCGTAC
                                  AC  CA__  ___
GAM248  C14orf4   5'  CCGACGCCTGCTCCCCCA    67335    CA       A_
                                TGG  GGAGCAGGC  CGG
                                |||  |||||||||  |||
                                ACC  CCTCGTCCG  GCC
                                  C_       CA
GAM248  C16orf5   3'  CCTGCTCACACCTGCTCCTGC  25447          CAC    T
                                GCAGGAGCAGG   GGGCA GG
                                ||||||||||   ||||| ||
                                CGTCCTCGTCC   CTCGT CC
                                      ACA    _
GAM248  C20orf150 3'  CCGCGCCTCCTCCTGCCA    65394         C    A
                                TGGCAGGAG AGGC CGG
                                |||||||| |||| |||
                                ACCGTCCTC TCCG GCC
                                     C   C
GAM248  C20orf20  5'  CCGCGCCTGCTCCCGCC     36853     A       A
                                GGC GGAGCAGGC CGG
                                ||| |||||||| |||
                                CCG CCTCGTCCG GCC
                                  C       C
GAM248  CL24751   5'  CCGTGCCCACCTACTCCCACCA 64686     CA   C   CAC
                                TGG  GGAG AGG   GGGCATGG
                                |||  |||| |||   ||||||||
                                ACC  CCTC TCC   CCCGTGCC
                                  AC   A  A__
GAM248  CXYorf1   5'  CCAACTCCACCCTCTCCTGCCA 82040         C   CAC   CA
                                TGGCAGGAG AGG   GGG  TGG
                                |||||||| |||   |||  |||
                                ACCGTCCTC TCC   CCT  ACC
                                     _  CA_  CA
GAM248  DKFZp434F142 5'  CACACCCAGCTCCTGCCA    50015          AGGCAC   CA
                                TGGCAGGAGC     GGG  TG
                                ||||||||||     |||  ||
                                ACCGTCCTCG     CCC  AC
                                     A_____   AC
GAM248  DKFZp434P2235 3'  CATGCCCAGCCCCTCC      50040     CA   AC
                                GGAG  GGC  GGGCATG
                                ||||  |||  |||||||
                                CCTC  CCG  CCCGTAC
                                  C_  A_
GAM248  DKFZP586B1621 3'  TCATGCCCTCCCCTGCCA    31385       AGCA  CAC
                                TGGCAGG   GG   GGGCATGG
                                |||||||   ||  ||||||||
                                ACCGTCC   CC   CCCGTACT
                                    _____ T__
GAM248  DKFZp761B0514 3'  CCATGCCCAGGTCTCCTGCC   50152        CAG  AC
                                GGCAGGAG   GC  GGGCATGG
                                ||||||||   ||  ||||||||
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                                CCGTCCTC   TG  CCCGTACC
                                     ___  GA
GAM248  DKFZP761I2123 3'  CCACCCCTGCCTGCCCCCACC  48758    CA  A      C   CA
                                GG  GG GCAGGCA GGG  TGG
                                ||  || ||||||| |||  |||
                                CC  CC CGTCCGT CCC  ACC
                                 AC  C      C  __
GAM248  DPYSL4   5'  GCTTGTGCCGCCCCTACCA   21216     C   A  A
                                TGG AGG GC GGCACGGGC
                                ||| ||| || |||||||||
                                ACC TCC CG CCGTGTTCG
                                  A   C  _
GAM248  DXS9928E  3'  CTCGTGTCCTGCCCCTGCCA   16286        A    _
                                TGGCAGG GCAGG CACGGG
                                ||||||| ||||| ||||||
                                ACCGTCC CGTCC GTGCTC
                                    C    T
GAM248  FLJ13769  3'  CACACCACCCTCCTGCCA    46602         CA  CAC  GCA
                                TGGCAGGAG  GG   GG   TG
                                |||||||||  ||   ||   ||
                                ACCGTCCTC  CC   CC   AC
                                     __  A__  AC_
GAM248  FLJ22301  5'  CATGCGGCTACTCCTGCC    45757        CA   A GG
                                GGCAGGAG  GGC C  GCATG
                                ||||||||  ||| |  |||||
                                CCGTCCTC  TCG G  CGTAC
                                    A_   _ __
GAM248  FLJ23392  3'  CATGCCCAGCCTCCTACC    45529    C   GCA   AC
                                GG AGGA   GGC  GGGCATG
                                || ||||   |||  |||||||
                                CC TCCT   CCG  CCCGTAC
                                 A   ____   A_
GAM248  IL22R    3'  CCATGCCTGCCCATGCCA    41190      _ A      C
                                TGGCA GG GCAGGCA GG
                                ||||| || ||||||| ||
                                ACCGT CC CGTCCGT CC
                                   A  _      A
GAM248  KIAA0152  3'  CCATGTCCCACCCCACTCCCAC 28296     CA   CA  CAC
          CA                     TGG  GGAG  GG   GGGCATGG
                                |||  ||||  ||   ||||||||
                                ACC  CCTC  CC   CCTGTACC
                                  AC    AC  CAC
GAM248  KIAA0978  3'  CCATGCCTGCTCCTGCC     70478            C
                                GGCAGGAGCAGGCA GG
                                |||||||||||||| ||
                                CCGTCCTCGTCCGT CC
                                        A
GAM248  KIAA1056  3'  CCTAACTCCTGCTCCCGCCA   29693      A       CAC_
                                TGGC GGAGCAGG    GGG
                                |||| ||||||||    |||
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                                ACCG CCTCGTCC    TCC
                                  C       TCAA
GAM248  KIAA1171  3'  CCACACCATTGCCTGCTCCTCC 87979     C        CG  CA
            CA                    TGG AGGAGCAGGCA  GG  TGG
                                  ||| ||||||||||  ||  |||
                                  ACC TCCTCGTCCGT  CC  ACC
                                    C         TA  AC
GAM248  KIAA1656  3'  CCAACTGCTGCACCTGCTCCTC 65784     C       CA   G  __
            CA                    TGG AGGAGCAGG  CGG CA  TGG
                                  ||| |||||||||  ||| ||  |||
                                  ACC TCCTCGTCC  GTC GT  ACC
                                    _       AC   _  CA
GAM248  KIAA1831  5'  CACCCAGCCTGCTCCTCCA   63781     C        AC   CA
                                  TGG AGGAGCAGGC  GGG  TG
                                  ||| ||||||||||  |||  ||
                                  ACC TCCTCGTCCG  CCC  AC
                                    _       A_  __
GAM248  MGC15873  3'  CCTGGTTAAGCCCGCTCCCACC 51902     CA    A   AC  G  T
            A                     TGG  GGAGC GGC  GG CA GG
                                  |||  ||||| |||  || || ||
                                  ACC  CCTCG CCG  TT GT CC
                                    AC    C   AA  G  _
GAM248  MGC20255  3'  CCACACCCGGCTCCTGCTCCCC 53441     CA      CA_   CA
            CA                    TGG  GGAGCAGG   CGGG  TGG
                                  |||  ||||||||   ||||  |||
                                  ACC  CCTCGTCC   GCCC  ACC
                                    C_      TCG    AC
GAM248  MGC2306   3'  CCGACACCACTCCTGCCA    50959        CA  CA_
                                  TGGCAGGAG  GG   CGG
                                  |||||||||  ||   |||
                                  ACCGTCCTC  CC   GCC
                                       A_  ACA
GAM248  MGC2668   3'  CCACACCCCTCCTGCTCCCCCC 60574     CA      CAC   CA
            A                     TGG  GGAGCAGG   GGG  TGG
                                  |||  ||||||||   |||  |||
                                  ACC  CCTCGTCC   CCC  ACC
                                    CC       TC_   AC
GAM248  MGC3222   3'  CCATGCTTTGCCACCACCACCA 44294     CA  AGCA   C
                                  TGG  GG    GGCA GGGCATGG
                                  |||  ||    |||| ||||||||
                                  ACC  CC    CCGT TTCGTACC
                                    A_  ACCA   _
GAM248  MGC4707   3'  CCTGTACCTGCTCCCACC    44121    CA       C
                                  GG  GGAGCAGG ACGGG
                                  ||  |||||||| |||||
                                  CC  CCTCGTCC TGTCC
                                   AC       A
GAM248  MGC5508   3'  CATGCAGCCCTCCTGCCA    44035        CA   ACGG
                                  TGGCAGGAG  GGC    GCATG
                                  |||||||||  |||    |||||
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                                ACCGTCCTC  CCG    CGTAC
                                     __   A___
GAM248  MOT8     5'  CCTCTCGTGCCCGCCTCCTGCC 38118         _ A       CAT
            A                    TGGCAGGAG C GGCACGGG   GG
                                 ||||||||| | ||||||||   ||
                                 ACCGTCCTC G CCGTGCTC   CC
                                      C C       T__
GAM248  RASGRP4  3'  CCATGCCCACCTGAGCCCTGAC 53651    G    AG_   CAC
            A                    TG CAGG   CAGG   GGGCATGG
                                 || ||||   ||||   ||||||||
                                 AC GTCC   GTCC   CCCGTACC
                                  A   CGA   A__
GAM248  SKIP     3'  CATGCCTCCACCCTGCCA    55367       AGCA  CAC
                                 TGGCAGG    GG   GGGCATG
                                 |||||||    ||   |||||||
                                 ACCGTCC    CC   TCCGTAC
                                     CA__  ___
GAM248  SKIP     3'  CATGCCTCCACCCTGCCA    33275       AGCA  CAC
                                 TGGCAGG    GG   GGGCATG
                                 |||||||    ||   |||||||
                                 ACCGTCC    CC   TCCGTAC
                                     CA__  ___
GAM248  SSH2     3'  CCAATCACCAGCTCCTGCCA   62203         A  CACG_
                                 TGGCAGGAGC GG     GG
                                 |||||||||| ||     ||
                                 ACCGTCCTCG CC     CC
                                       A  ACTAA
GAM248  TSGA14   3'  CCGTGTGCCTGTCCCTGCCA   38043       AG       _
                                 TGGCAGG  CAGGCACG GG
                                 |||||||  |||||||| ||
                                 ACCGTCC  GTCCGTGT CC
                                     CT       G
GAM248  LOC112724 3'  CCATGCCCGCAGCTTCCTGGCA 56493    G    GCA   A_
                                 TG CAGGA   GGC  CGGGCATGG
                                 || |||||   |||  |||||||||
                                 AC GTCCT   TCG  GCCCGTACC
                                  G    ____   AC
GAM248  LOC119214 3'  CCTAGCACCTTCTCCTGCCA   73965         C   CAC_
                                 TGGCAGGAG AGG    GGG
                                 ||||||||| |||    |||
                                 ACCGTCCTC TCC    TCC
                                       T   ACGA
GAM248  LOC123242 5'  CCATGCCCATCTTGCCTACCA  75595     CA  A    CAC
                                 TGG  GG GCAGG   GGGCATGG
                                 |||  || |||||   ||||||||
                                 ACC  TC CGTTC   CCCGTACC
                                   A_  _    TA_
GAM248  LOC124997 3'  CGTTGTCTGCCCACCCCTACCA 74387     C   A_____      _
                                 TGG AGG    GCAGGCA CG
                                 ||| |||    ||||||| ||
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                                ACC TCC    CGTCTGT GC
                                  A  CCACC     T
GAM248  LOC138612 3'  CCACCCTGTGCCCGCCCCTGCC 76237      A  A      CA
                                GGCAGG GC GGCACGGG  TGG
                                |||||| || ||||||||  |||
                                CCGTCC CG CCGTGTCC  ACC
                                   C  C      C_
GAM248  LOC144501 3'  CCATGCCCACTCCCCCTGCC  83105      AGCA  CAC
                                GGCAGG   GG   GGGCATGG
                                ||||||   ||   ||||||||
                                CCGTCC   CC   CCCGTACC
                                   C___  TCA
GAM248  LOC146733 3'  CCTGTGCCTGCCCCTGCC    83760      A
                                GGCAGG GCAGGCACGGG
                                |||||| ||||||||||
                                CCGTCC CGTCCGTGTCC
                                   C
GAM248  LOC146782 3'  CATGCCCAGCCCCTCC     76292     CA  AC
                                GGAG  GGC  GGGCATG
                                ||||  |||  |||||||
                                CCTC  CCG  CCCGTAC
                                  C_  A_
GAM248  LOC148147 3'  CCACACTTCCTCCTGCTCCAGC 78675     A      CAC  CA
          CA                     TGGC GGAGCAGG   GGG  TGG
                                |||| ||||||||   |||  |||
                                ACCG CCTCGTCC   TTC  ACC
                                  A      TCC   AC
GAM248  LOC148870 3'  CCAGAACCACCCGCCCCCACCA 79042    CA  A  A  CAC  GCA
                                TGG  GG GC GG   GG   TGG
                                |||  || || ||   ||   |||
                                ACC  CC CG CC   CC   ACC
                                  AC  C  C  A__  AAG
GAM248  LOC151361 3'  CCTCAACCACCTGCTCCCGCCA 85324     A      CAC  GCAT
                                TGGC GGAGCAGG   GG    GG
                                |||| ||||||||   ||    ||
                                ACCG CCTCGTCC   CC    CC
                                  C      A__  AACT
GAM248  LOC152992 3'  CCGACGCCTGCCCCACCA    80757    CA  A    A_
                                TGG  GG GCAGGC  CGG
                                |||  || ||||||  |||
                                ACC  CC CGTCCG  GCC
                                  AC  _     CA
GAM248  LOC158298 3'  CCACCCTGTGCCCGCCCCTGCC 86737      A  A      CA
                                GGCAGG GC GGCACGGG  TGG
                                |||||| || ||||||||  |||
                                CCGTCC CG CCGTGTCC  ACC
                                   C  C      C_
GAM248  LOC162952 5'  CCTCTACACCTGCTCCTTCCA  82379    C      CAC__
                                TGG AGGAGCAGG    GGG
                                ||| |||||||||    |||
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                                ACC TCCTCGTCC    TCC
                                  T       ACATC
GAM248  LOC170221 3'  CCTGCCCATGCCTACCACCCGC 82577     A  AGC_    C    T
            CA                    TGGC GG   AGGCA GGGCA GG
                                  |||| ||   ||||| ||||| ||
                                  ACCG CC   TCCGT CCCGT CC
                                    C  ACCA    A    _
GAM248  LOC197114 5'  CCATGCCCACACCTACGCCCT  89703    A __   CAC
                                  AGG GC  AGG   GGGCATGG
                                  ||| ||  |||   ||||||||
                                  TCC CG  TCC   CCCGTACC
                                    _ CA   ACA
GAM248  LOC200093 5'  CCAACTCCACCCTCTCCTGCCA 63089        C   CAC   CA
                                  TGGCAGGAG AGG   GGG  TGG
                                  ||||||||| |||   |||  |||
                                  ACCGTCCTC TCC   CCT  ACC
                                        _  CA_   CA
GAM248  LOC202915 3'  CACCCACCAACTCCTGCCA   90387        CA  CAC   CA
                                  TGGCAGGAG  GG   GGG  TG
                                  |||||||||  ||   |||  ||
                                  ACCGTCCTC  CC   CCC  AC
                                       AA  A__   __
GAM248  LOC219562 3'  CATGCCCAGCCCCTCC     90769     CA   AC
                                  GGAG  GGC  GGGCATG
                                  ||||  |||  |||||||
                                  CCTC  CCG  CCCGTAC
                                    C_   A_
GAM248  LOC220001 5'  CCAATGTCTGCTCCTGCCA   91632            CG
                                  TGGCAGGAGCAGGCA  GG
                                  ||||||||||||||  ||
                                  ACCGTCCTCGTCTGT  CC
                                           AA
GAM248  LOC223009 5'  CACACCCAGCTCCTGCCA    94371         AGGCAC   CA
                                  TGGCAGGAGC     GGG  TG
                                  ||||||||||     |||  ||
                                  ACCGTCCTCG     CCC  AC
                                       A_____   AC
GAM248  LOC253001 5'  CCATGCCCATCTTGCCTACCA  96253    CA  A    CAC
                                  TGG  GG GCAGG   GGGCATGG
                                  |||  || |||||   ||||||||
                                  ACC  TC CGTTC   CCCGTACC
                                    A_  _    TA_
GAM248  LOC253461 3'  CATACCCACTTCTGCCA     96281         CAGGCAC   C
                                  TGGCAGGAG      GGG ATG
                                  |||||||||      ||| |||
                                  ACCGTCTTC      CCC TAC
                                       A_______   A
GAM248  LOC253805 3'  CATGTCCACTCCTGCCA     96426         CAGGCAC
                                  TGGCAGGAG      GGGCATG
                                  |||||||||      |||||||
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                                ACCGTCCTC      CCTGTAC
                                     A_______
GAM248  LOC254266 5'  CAGGACTCCTGCTCCTGC    97349          CAC  GCA
                                GCAGGAGCAGG   GG   TG
                                ||||||||||   ||   ||
                                CGTCCTCGTCC   TC   AC
                                      ___  AGG
GAM248  LOC255975 5'  CACACCCAGCTCCTGCCA    95880         AGGCAC   CA
                                TGGCAGGAGC     GGG  TG
                                ||||||||||     |||  ||
                                ACCGTCCTCG     CCC  AC
                                     A_____   AC
GAM248  LOC257181 3'  CATGCCCAGCCCCTCC      94592      CA   AC
                                GGAG  GGC  GGGCATG
                                ||||  |||  |||||||
                                CCTC  CCG  CCCGTAC
                                  C_   A_
GAM248  LOC92578  3'  CCAAATGCCTGTCCTGCCA    69825        G     CG_
                                TGGCAGGA CAGGCA   GG
                                |||||||| ||||||   ||
                                ACCGTCCT GTCCGT   CC
                                     _     AAA
GAM248  LOC92841  5'  TCATGCCTCTCCTGCCA     70723         C    C
                                TGGCAGGAG AGGCA GG
                                ||||||||| ||||| ||
                                ACCGTCCTC TCCGT CT
                                     _    A
GAM249  ADAM19    3'  CAGGAAGAAGACTGGCCATTAT 52703      C    CTGAG
          G                      CATGA GGCT     TTCTTCCTG
                                |||||  ||||    |||||||||
                                GTATT CCGG     AAGAAGGAC
                                  A    TCAG_
GAM249  FACL5     5'  CAGGAAGAACTCAGAGCCG   64186
                                CGGCTCTGAGTTCTTCCTG
                                ||||||||||||||||||
                                GCCGAGACTCAAGAAGGAC

GAM249  GNAL      5'  CAGGAAAGAGAGGAGCCGTCG  9058          GAG TC
                                TGACGGCTCT   T  TTCCTG
                                ||||||||||   |  ||||||
                                GCTGCCGAGG   A  AAGGAC
                                     AG_ GA
GAM249  KAL1      3'  CAGGAAGAACTTCTGTCA    4013        CTCT
                                TGACGG   GAGTTCTTCCTG
                                ||||||   ||||||||||||
                                ACTGTC   TTCAAGAAGGAC
                                     ____
GAM249  MYO1E     3'  CAGGAGGACAAAACCACCATG  17187      AC  CTC  AGT
                                CATG  GG   TG   TCTTCCTG
                                ||||  ||   ||   ||||||||
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                                GTAC  CC   AC   AGGAGGAC
                                  CA  AAA  ___
GAM249  PRKAR2B  3'  CAGAAAGAACTCAGATGT    10804    _        C
                                GC TCTGAGTTCTT CTG
                                || |||||||||| |||
                                TG AGACTCAAGAA GAC
                                 T         A
GAM249  PUM2     3'  AGGATCAAAGCTGTCATG    31014         C   GTTCT
                                CATGACGGCT TGA    TCCT
                                |||||||||| |||    ||||
                                GTACTGTCGA ACT    AGGA
                                      A  _____
GAM249  SKI      3'  CAGGAAGTGCAGAGCCGCA   11701    A      AGTT
                                TG CGGCTCTG   CTTCCTG
                                || ||||||||   |||||||
                                AC GCCGAGAC   GAAGGAC
                                 _      GT__
GAM249  TEM8     3'  AGGAAGATGCAACCCCATG   36326     AC  CTC  AGT
                                CATG  GG   TG   TCTTCCT
                                ||||  ||   ||   |||||||
                                GTAC  CC   AC   AGAAGGA
                                  C_  A__  GT_
GAM249  ARHGEF4  5'  AGAAAAAACTCAGGGC     52207         C  C
                                GCTCTGAGTT TT CT
                                |||||||||| || ||
                                CGGGACTCAA AA GA
                                      A  A
GAM249  FLJ31978 3'  CAGGAAGGAACAAGCGCC   58348     T  GAG
                                GGC CT   TTCTTCCTG
                                ||| ||   |||||||||
                                CCG GA   AGGAAGGAC
                                  C  ACA
GAM249  HSU24186 5'  AGAACTCAAAGCCGTC     25324        C
                                GACGGCT TGAGTTCT
                                ||||||| ||||||||
                                CTGCCGA ACTCAAGA
                                    A
GAM249  KCNT1    3'  AGCTCCCAGGGCCGCCA     61825    A     __
                                TG CGGCTCT  GAGTT
                                || |||||||  |||||
                                AC GCCGGGA  CTCGA
                                 C      CC
GAM249  KIAA1867 3'  CAGGAAGAACCCAAGAGCTCAT 94822      CG    GA_
                                ATGA  GCTCT   GTTCTTCCTG
                                ||||  |||||   ||||||||||
                                TACT  CGAGA   CAAGAAGGAC
                                  __    ACC
GAM249  KIAA1878 3'  AATTCAGAGAATCGTCATG   91707        __
                                CATGACGG  CTCTGAGTT
                                ||||||||  |||||||||
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                                GTACTGCT  GAGACTTAA
                                     AA
GAM249  MFN1     3'  CAGGAAGAACTCATGA      35541    _
                                TC TGAGTTCTTCCTG
                                || ||||||||||||
                                AG ACTCAAGAAGGAC
                                 T
GAM249  MIDORI   3'  CAGGGCCCTTCCAGAGCCTGTC 73784       _      AGTTCT
           ATG                    CATGAC GGCTCTG     TCCTG
                                |||||| |||||||      |||||
                                GTACTG CCGAGAC      GGGAC
                                   T       CTTCCC
GAM249  MYH7B    3'  CAGGAAGAACCTGGCTCGCATG 70530      A  _   CTGA
                                CATG CG GCT    GTTCTTCCTG
                                |||| || |||    ||||||||||
                                GTAC GC CGG    CAAGAAGGAC
                                  _  T   TC__
GAM249  RNAHP    3'  AGAAAGCAGCAGCCGTCAT    23761          _   AG
                                ATGACGGCT CTG  TTCT
                                |||||||| |||  ||||
                                TACTGCCGA GAC  AAGA
                                     C   GA
GAM249  SLC37A1  3'  AGACGGAGCTCAGACCC     38561    C        TC
                                GG TCTGAGTTCT  CT
                                || ||||||||||  ||
                                CC AGACTCGAGG  GA
                                 C         CA
GAM249  LOC116236 3'  CAGGAAAAGCACAAACCTCAT  73809      C  CTC  A   C
                                ATGA GG   TG GTT TTCCTG
                                |||| ||   || ||| ||||||
                                TACT CC   AC CGA AAGGAC
                                  _  AA_  A   A
GAM249  LOC124801 3'  CAGGAAGAACTCTCTTGCATG  74336      A   CTCT
                                CATG CGG    GAGTTCTTCCTG
                                |||| |||    ||||||||||||
                                GTAC GTT    CTCAAGAAGGAC
                                  _   CT__
GAM249  LOC222160 5'  AGGAAGAACTCACCCC      94117    CTC
                                GG   TGAGTTCTTCCT
                                ||   ||||||||||||
                                CC   ACTCAAGAAGGA
                                 CC_
GAM249  LOC51094  3'  CAGGAAGAATAAAGCC      32045      CTGA
                                GGCT    GTTCTTCCTG
                                ||||    ||||||||||
                                CCGA    TAAGAAGGAC
                                  AA__
GAM249  LOC92078  3'  CAGGAAGAAGAATCGACCGTC  67977       C  T  G__
                                GACGG TC GA   TTCTTCCTG
                                ||||| || ||   |||||||||
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                                CTGCC AG CT   AAGAAGGAC
                                  _ _  AAG
GAM250  ACP2    3' AGAAAGTTCTAGACTG      7851       GC  TC
                                CAGT  CT  AGAACTTTCT
                                ||||  ||  ||||||||||
                                GTCA  GA  TCTTGAAAGA
                                  __  __
GAM250  APTX    5' AAGAGAAAGAGATCAGGCA   34655      TCAGAA
                                TGCCT     CTTTCTCTT
                                |||||     |||||||||
                                ACGGA     GAAAGAGAA
                                   CTAGA_
GAM250  BCL7A   3' AGGCTGTCTCCTTAAGGCACTG 40637         C  A__  TT
                                CAGTGCCTT AG   AC  TCT
                                ||||||||| ||   ||  |||
                                GTCACGGAA TC   TG  GGA
                                      T  CTC  TC
GAM250  CLC     3' AAGAGAAAATACTGAAAGCACA 25105    A   C    AAC
           GG                     CC GTGC TTCAG   TTTCTCTT
                                || |||| |||||   ||||||||
                                GG CACG AAGTC   AAAGAGAA
                                 A   A    ATA
GAM250  CNK     3' AAGCCCTGAAGGCCTG      14517     T      AA
                                CAG GCCTTCAG  CTT
                                ||| ||||||||  |||
                                GTC CGGAAGTC  GAA
                                  _       CC
GAM250  COL4A3  3' AAGTGCAGGTTCTGAGGGCACC 48549    A           TCT
           GG                     CC GTGCCTTCAGAACTT   CTT
                                || ||||||||||||||   |||
                                GG CACGGGAGTCTTGGA   GAA
                                 C            CGT
GAM250  CSPG4   3' AAGAGAGACCTGGAGACAC   8570     C     AAC
                                GTG CTTCAG   TTTCTCTT
                                ||| ||||||   ||||||||
                                CAC GAGGTC   AGAGAGAA
                                  A     C__
GAM250  CYP1B1  3' AAGAGAAAAGAGAGAAACACTG 3651       CC   AGAAC
                                CAGTG  TTC    TTTCTCTT
                                |||||  |||    ||||||||
                                GTCAC  AAG    AAAGAGAA
                                   A_   AGAGA
GAM250  DLG3    3' AAGAGAAAAGAGGAGGACTG   40880     G    AGAAC
                                CAGT CCTTC    TTTCTCTT
                                |||| |||||    ||||||||
                                GTCA GGAGG    AAAGAGAA
                                  _    AGA__
GAM250  DLG5    5' AGGCAGACTCTGAAGGC     82909         A_  T
                                GCCTTCAGA  CT TCT
                                |||||||||  || |||
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                                CGGAAGTCT  GA GGA
                                     CA  C
GAM250  FLT1     3'  AAGAGAAACCGGGAGAAGGCAT 8910         AGAAC_
                                GTGCCTTC     TTTCTCTT
                                ||||||||     ||||||||
                                TACGGAAG     AAAGAGAA
                                   AGGGCC
GAM250  GRB10    3'  AGAGAAAATGGCACCTGG    17971     _   TTCAGAAC
                                CCAG TGCC       TTTCTCT
                                |||| ||||       |||||||
                                GGTC ACGG       AAAGAGA
                                  C   TA______
GAM250  LFG      3'  AAGAGAAAAGGAGCCAAGAACT 76711      GC   CAGAA   _
           GG                     CCAGT  CTT    CTTT CTCTT
                                |||||  |||    |||| |||||
                                GGTCA  GAA    GAAA GAGAA
                                   A_   CCGAG    A
GAM250  MAN2A2   3'  AAGAGAAAGTTCATTCAC    20391     CCTTCA
                                GTG     GAACTTTCTCTT
                                |||     ||||||||||||
                                CAC     CTTGAAAGAGAA
                                  TTA___
GAM250  NLGN3    3'  AAGAAAAGTTCTTAAAACACT  38596     CC  C       C
                                AGTG  TT AGAACTTT TCTT
                                ||||  || |||||||| ||||
                                TCAC  AA TCTTGAAA AGAA
                                  AA  T       _
GAM250  NPAS1    5'  AAGGTCTCCCGAGGGCACT    59879         A_  _
                                AGTGCCTTC  GA ACTTT
                                |||||||||  || |||||
                                TCACGGGAG  CT TGGAA
                                     CC  C
GAM250  PLAG1    3'  AGTGTGTTCCAAAGGCATT    10605         CA    TTT
                                AGTGCCTT  GAAC   CT
                                ||||||||  ||||   ||
                                TTACGGAA  CTTG   GA
                                     AC    TGT
GAM250  PLXNA1   3'  AGAAAATGAAGGCAGTGG    72309     G       GAAC
                                CCA TGCCTTCA    TTTCT
                                ||| ||||||||    |||||
                                GGT ACGGAAGT    AAAGA
                                  G       A___
GAM250  PPP4R1   3'  AAGAGAAAGTACAGTAAACACT 17620      CCTTCAGA
                                AGTG       ACTTTCTCTT
                                ||||       ||||||||||
                                TCAC       TGAAAGAGAA
                                  AAATGACA
GAM250  ACYP2    3'  AAGAGAAAAATTGTAACACACT 56612       CC  _   AAC
           G                     CAGTG  TT CAG   TTTCTCTT
                                |||||  || |||   ||||||||
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                                GTCAC  AA GTT   AAAGAGAA
                                  AC  T   AA_
GAM250  B3GNT6   3'  AGAAATCAGATGAAGGCAT   22503        GAAC_
                                GTGCCTTCA    TTTCT
                                |||||||||    |||||
                                TACGGAAGT    AAAGA
                                     AGACT
GAM250  BAG5     3'  AAGAGAAGGGATAAAGGAC   16835    G   CAGAA
                                GT CCTT    CTTTCTCTT
                                || ||||    |||||||||
                                CA GGAA    GGAAGAGAA
                                 _   ATAG_
GAM250  BIVM     3'  AAGAGAAAAGACTCAAGAAACT 34665     GC   C  AAC
           G                     CAGT  CTT AG   TTTCTCTT
                                ||||  ||| ||   ||||||||
                                GTCA  GAA TC   AAAGAGAA
                                  AA   C  AGA
GAM250  C15orf5  3'  AGAGAAAAGAAAGCAC     48195     C   AGAAC
                                GTGC TTC    TTTCTCT
                                |||| |||    |||||||
                                CACG AAG    AAAGAGA
                                  A  A____
GAM250  C20orf80  5'  AAGAGAAGAAGATGAAGAAAC  65282    GC    GAAC
                                GT  CTTCA    TTTCTCTT
                                ||  |||||    ||||||||
                                CA  GAAGT    GAAGAGAA
                                 AA    AGAA
GAM250  CLSTN1   3'  AGTTCTGAGGACACTGG     30103       C
                                CCAGTG CTTCAGAACT
                                |||||| ||||||||||
                                GGTCAC GGAGTCTTGA
                                   A
GAM250  DKFZP434P0111 3'  AAGAGAAAGTTTCTGCAC    67368      CTTCA
                                GTGC    GAACTTTCTCTT
                                ||||    ||||||||||||
                                CACG    TTTGAAAGAGAA
                                  TC___
GAM250  DORFIN   5'  AGAATTCTCTGAAGGAAC    31257    G       ACT
                                GT CCTTCAGA   TTCT
                                || ||||||||   ||||
                                CA GGAAGTCT   AAGA
                                 A       CTT
GAM250  FLJ10300  5'  AAGAGAAAGATGAAGACTCTG  35997     TGC    GAA
                                CAG   CTTCA   CTTTCTCTT
                                |||   |||||   |||||||||
                                GTC   GAAGT   GAAAGAGAA
                                  TCA    A__
GAM250  FLJ20373  3'  AAGAGAAGAAGGAAAGGCACAG 35070    A      _ AGAAC
           G                     CC GTGCCTT C    TTTCTCTT
                                || |||||| |    ||||||||
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                                GG CACGGAA G    GAAGAGAA
                                 A      A GAA__
GAM250  FLJ23511  5'  AGAGAAAAACAAGGCAT    49956       CAGAAC
                                GTGCCTT     TTTCTCT
                                |||||||     |||||||
                                TACGGAA     AAAGAGA
                                    CAA___
GAM250  FLJ30681  3'  AGAGAAGAAAGACCACTGG   91782      CCT  AGAAC
                                CCAGTG   TC    TTTCTCT
                                ||||||  ||    |||||||
                                GGTCAC   AG    GAAGAGA
                                   C__  AAA__
GAM250  HDAC11    3'  GAGCTATAGGCACTGG      45717       TC  AACTTT
                                CCAGTGCCT  AG     CTC
                                |||||||||  ||     |||
                                GGTCACGGA  TC     GAG
                                     TA  _______
GAM250  IKKE      5'  AGTGAGCCCTGAAAGCTCTGG  25745     T  C    AA   T
                                CCAG GC TTCAG  CTT CT
                                ||||  || |||||  ||| ||
                                GGTC CG AAGTC  GAG GA
                                  T  A    CC   T
GAM250  KIAA0680  3'  AGAGAAAATTGAAGCAT     28232      C    AAC
                                GTGC TTCAG   TTTCTCT
                                ||||  |||||   |||||||
                                TACG AAGTT   AAAGAGA
                                  _    A__
GAM250  KIAA1228  3'  AGGGGGTGATTCTGAGGCACTG 65035       T   ___   TT
                                CAGTGCCT CAGA   ACT  CT
                                ||||||||  ||||   |||  ||
                                GTCACGGA GTCT   TGG  GA
                                    _   TAG   GG
GAM250  KIAA1300  5'  AGGAACCCTGAAGGCA      62860       AAC
                                TGCCTTCAG   TTTCT
                                |||||||||   |||||
                                ACGGAAGTC   AAGGA
                                     CC_
GAM250  KIAA1805  3'  AAGAGAAAGTAGAAGCAGCA   79966    __   AGA
                                TGC  CTTC   ACTTTCTCTT
                                |||  ||||   ||||||||||
                                ACG  GAAG   TGAAAGAGAA
                                  AC    A__
GAM250  LENG1     5'  AAGAGAAAGCTCTGGGCATCCT 84074    __   TT   A
          G                      CAG  TGCC  CAGA CTTTCTCTT
                                |||  ||||  |||| |||||||||
                                GTC  ACGG  GTCT GAAAGAGAA
                                  CT    __    C
GAM250  LHX6      3'  AAGAGAAAACTCTGGGGTCA   26854    C      AC
                                TG CTTCAGA  TTTCTCTT
                                || |||||||  ||||||||
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                                AC GGGGTCT  AAAGAGAA
                                 T      CA
GAM250  N4BP3    3'  AGCTCCAGAAGGCACTGG    66250          A_  A
                                CCAGTGCCTTC  GA CT
                                ||||||||||  || ||
                                GGTCACGGAAG  CT GA
                                      AC  C
GAM250  NASP     3'  AGAGGGTGAAGAAACTG     67966      GC   AGA
                                CAGT  CTTC   ACTTTCT
                                ||||  ||||   |||||||
                                GTCA  GAAG   TGGGAGA
                                  AA   ___
GAM250  SMARCF1  3'  AAAATTCTGAAGGAC       57480    G       C
                                GT CCTTCAGAA TTT
                                || |||||||| |||
                                CA GGAAGTCTT AAA
                                 _       A
GAM250  SMARCF1  3'  AAAATTCTGAAGGAC       37430    G       C
                                GT CCTTCAGAA TTT
                                || |||||||| |||
                                CA GGAAGTCTT AAA
                                 _       A
GAM250  SMARCF1  3'  AAAATTCTGAAGGAC       20034    G       C
                                GT CCTTCAGAA TTT
                                || |||||||| |||
                                CA GGAAGTCTT AAA
                                 _       A
GAM250  TED      3'  AAGAGAAAGTCCAGGGACTGG  31630      G   TCA  A
                                CCAGT CCT   GA CTTTCTCTT
                                ||||| |||   || |||||||||
                                GGTCA GGA   CT GAAAGAGAA
                                   G   C__  _
GAM250  TGIF2    3'  AGAAGGGTGCTGAAGGC     41447        AA_
                                GCCTTCAG   CTTTCT
                                ||||||||   ||||||
                                CGGAAGTC   GGAAGA
                                     GTG
GAM250  WBSCR20A 3'  AAGAGAAAGAAGAGACAGCA   35958     CT  AGAA
                                TGC  TC    CTTTCTCTT
                                |||  ||    |||||||||
                                ACG  AG    GAAAGAGAA
                                  AC  AGAA
GAM250  LOC115273 3' AGAAAGTTCTGATGGCCAGG   73356    AGT   T
                                CC   GCC TCAGAACTTTCT
                                ||   ||| ||||||||||||
                                GG   CGG AGTCTTGAAAGA
                                 AC_   T
GAM250  LOC145761 5' AAGAGAAAGTGGAAGGCATGG  83472     G      AGA
                                CCA TGCCTTC   ACTTTCTCTT
                                ||| |||||||   ||||||||||
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                                GGT ACGGAAG   TGAAAGAGAA
                                  _     G__
GAM250   LOC146179 5'  AGAAAGTTTTGGGCCT     77700    T   TT
                                AG GCC  CAGAACTTTCT
                                || |||  ||||||||||
                                TC CGG  GTTTTGAAAGA
                                 _  __
GAM250   LOC147072 3'  AAGAGAAAGTGAGAAGAAACTG 60407     GC    AGA
                                CAGT  CTTC   ACTTTCTCTT
                                ||||  ||||   ||||||||||
                                GTCA  GAAG   TGAAAGAGAA
                                  AA   AG_
GAM250   LOC148758 5'  AGAAAGTTCTGAGAAAC     78962    GCC
                                GT   TTCAGAACTTTCT
                                ||   |||||||||||||
                                CA   GAGTCTTGAAAGA
                                 AA_
GAM250   LOC148932 3'  AGGAATCTGAAGGCACTGG    79103            AC
                                CCAGTGCCTTCAGA  TTTCT
                                ||||||||||||||  |||||
                                GGTCACGGAAGTCT  AAGGA
                                                __
GAM250   LOC149386 5'  AAGTTTTGAAAGCACT      84400       C
                                AGTGC TTCAGAACTT
                                ||||| ||||||||||
                                TCACG AAGTTTTGAA
                                   A
GAM250   LOC150139 3'  AGAAAATAGAAAAAGGCGCTGG 79583          CAGAAC_
                                CCAGTGCCTT      TTTCT
                                ||||||||||      |||||
                                GGTCGCGGAA      AAAGA
                                      AAAGATA
GAM250   LOC152756 3'  AAGATGCAGTTCTGAAAACCTG 85871     TGCC        TTC
                                CAG    TTCAGAACT   TCTT
                                |||    |||||||||   ||||
                                GTC    AAGTCTTGA   AGAA
                                  CAA_        CGT
GAM250   LOC162333 5'  AAGAGAAAGCGATGACACTG   87114      CCT   GAA
                                CAGTG   TCA   CTTTCTCTT
                                |||||   |||   |||||||||
                                GTCAC   AGT   GAAAGAGAA
                                   ___   AGC
GAM250   LOC199221 3'  AAGAGAAGCTCGAAAGCATGG  80347     G   C   A  A   T
                                CCA TGC TTC GA CTT CTCTT
                                ||| ||| ||| || ||| |||||
                                GGT ACG AAG CT GAA GAGAA
                                  _   A   _  C   _
GAM250   LOC203339 3'  AGAGAAAATTGGGCCTG     90542     T   TCAGAAC
                                CAG GCCT      TTTCTCT
                                ||| ||||      |||||||
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                                GTC CGGG      AAAGAGA
                                  _   TTA____
GAM250  LOC255017 3'  AGAAAGAGGAACTGG      94624      G   TCAGAA
                                CCAGT CCT     CTTTCT
                                ||||| |||     ||||||
                                GGTCA GGA     GAAAGA
                                  A  _______
GAM250  LOC256021 3'  AAGAGAAACAAAGACAACACTG 96512       CCT  AGAAC
          G                      CCAGTG   TC    TTTCTCTT
                                ||||||  ||    ||||||||
                                GGTCAC   AG    AAAGAGAA
                                   AAC  AAAC_
GAM250  LOC90139  3'  AGAATCCCGAAGGCAT     55396        A_  ACT
                                GTGCCTTC  GA   TTCT
                                ||||||||  ||   ||||
                                TACGGAAG  CT   AAGA
                                     CC  ___
GAM251  AQP3     3'  TTCACGATCCACCCTTTC     59593      T_   _
                                GAAA  GTGG TCGTGAA
                                ||||  |||| |||||||
                                CTTT  CACC AGCACTT
                                  CC    T
GAM251  ARSB     3'  TCACGACTCTTGTC       3502        AATGTG
                                GACAAGA     GTCGTGA
                                |||||||     |||||||
                                CTGTTCT     CAGCACT
                                          _______
GAM251  B4GALT5  3'  TTTTCACAAAAATAGTCCTTTG 16519       AAA_   GGTC
          TCA                    TGACAAG    TGT    GTGAAAA
                                |||||||    |||    |||||||
                                ACTGTTT    ATA    CACTTTT
                                    CCTG   AAAA
GAM251  CHRNA3   3'  TCGTTACCCATTTCTT      5610         T   CG
                                AAGAAATG GGT  TGA
                                |||||||| |||  |||
                                TTCTTTAC CCA  GCT
                                     _  TT
GAM251  DRD1     3'  TTACAACCACATTTCTGGCCA  5840     ACA         C
                                TG   AGAAATGTGGT GTGA
                                ||   |||||||||||| ||||
                                AC   TCTTTACACCA CATT
                                 CGG         A
GAM251  FUT1     3'  TCTGATCACATCCCCTGTC    3798      AGAA       T
                                GACA    ATGTGGTCG GA
                                ||||    ||||||||| ||
                                CTGT    TACACTAGT CT
                                  CCCC       _
GAM251  IRF1     3'  GCCACATTTCTGATCA      64345     CA
                                TGA  AGAAATGTGGT
                                |||  ||||||||||
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                                ACT  TCTTTACACCG
                                  AG
GAM251  MAP3K8   5'  TCACGACCACCTCATG      17791    A  AAT
                                CA GA   GTGGTCGTGA
                                || ||   ||||||||||
                                GT CT   CACCAGCACT
                                 A  C__
GAM251  NGFR     3'  TTCTGACCACACTTCCTGTC   10231      A   A       T
                                GACA GAA TGTGGTCG GAA
                                |||| ||| |||||||| |||
                                CTGT CTT ACACCAGT CTT
                                  C   C       _
GAM251  OLR1     3'  TTCACAACAGTTCTTGTTA    10341          ATGTG  C
                                TGACAAGAA     GT GTGAA
                                |||||||||     || |||||
                                ATTGTTCTT     CA CACTT
                                      GA___  A
GAM251  POU4F1   3'  CACTGAAAACATTTTTGTCA   20660          A   GG  _
                                TGACAAGAA TGT  TC GTG
                                ||||||||| |||  || |||
                                ACTGTTTTT ACA  AG CAC
                                      _  AA  T
GAM251  SMP1     3'  TTTCACATGAATAATTTTTGTC 26705          A   GGTC
           A                     TGACAAGAA TGT    GTGAAA
                                ||||||||| |||    ||||||
                                ACTGTTTTT ATA    CACTTT
                                      A   AGTA
GAM251  ZNF264   3'  TTCTATTAACATTTCTTTTCA  12769     C        GGTCGT
                                TGA AAGAAATGT      GAA
                                ||| |||||||||      |||
                                ACT TTCTTTACA      CTT
                                  T        ATTAT_
GAM251  C20orf175 3'  CGAGCTCCACGTTTCCTGCCA  55063    A  A        ___
                                TG CA GAAATGTGG   TCG
                                || || |||||||||   |||
                                AC GT CTTTGCACC   AGC
                                 C  C        TCG
GAM251  CAPNS2   3'  TTTCACAACCCTACATATTTCT 50323     CA       ____  C
           GATCA                    TGA  AGAAATGT    GGT GTGAAA
                                |||  ||||||||    ||| ||||||
                                ACT  TCTTTATA    CCA CACTTT
                                  AG       CATC   A
GAM251  CLDN6    3'  TTTACACTCACATTTTTATCA  41041     CA       _  C
                                TGA  AGAAATGTG GT GTGAA
                                |||  ||||||||| || |||||
                                ACT  TTTTTACAC CA CATTT
                                  A_        T  _
GAM251  DKFZP564L0864 3'  GCACCAATTTCTTGCCA     72555     A       G    C
                                TG CAAGAAAT TGGT GT
                                || |||||||| |||| ||
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                                AC GTTCTTTA ACCA CG
                                 C      _   _
GAM251  DKFZP566B183 3'  TTTCCATAAACATTTCTTTTCA 31330     C       GGTCGT
                                TGA AAGAAATGT     GAAA
                                ||| |||||||||     ||||
                                ACT TTCTTTACA     CTTT
                                  T       AATAC_
GAM251  GTF2E1   3'  TACAGACCTCTTGTCA      18616        AATGT   _
                                TGACAAGA    GGTC GTG
                                ||||||||    |||| |||
                                ACTGTTCT    CCAG CAT
                                     _____   A
GAM251  KIAA0089 3'  TTTTAATTCACATTTCTT    69967          TCG
                                AAGAAATGTGG   TGAAA
                                ||||||||||   |||||
                                TTCTTTACACT   ATTTT
                                       TA_
GAM251  KIAA0373 5'  TTTTCAAAGTAACATTTCTT   28015         GGTCG
                                AAGAAATGT    TGAAAA
                                |||||||||    ||||||
                                TTCTTTACA    ACTTTT
                                     ATGAA
GAM251  KIAA1813 3'  TTTTCACACTGTAAATTTCTTG 70314          __ TG  C
   T                             ACAAGAAAT  G  GT GTGAAAA
                                |||||||||  |  || |||||||
                                TGTTCTTTA  T  CA CACTTTT
                                     AA GT  _
GAM251  KIAA1951 3'  TTCCAGGCTTCTCTTGTCA   73766        AATGT   GT
                                TGACAAGA    GGTC  GAA
                                ||||||||    ||||  |||
                                ACTGTTCT    TCGG  CTT
                                     CT___    AC
GAM251  MGC4170  3'  TTCACCATTTCTTGTC      44227          TGGTC
                                GACAAGAAATG    GTGAA
                                ||||||||||    |||||
                                CTGTTCTTTAC    CACTT
                                      _____
GAM251  NRN1     3'  CACTGCACATTTCTCCTCA   33432     CA       GTC
                                TGA  AGAAATGTG   GTG
                                |||  |||||||||   |||
                                ACT  TCTTTACAC   CAC
                                  CC        GT_
GAM251  PLA2G12  3'  TTTTCACAACCACATTT     48028         C
                                AAATGTGGT GTGAAAA
                                ||||||||| |||||||
                                TTTACACCA CACTTTT
                                     A
GAM251  PPY2     3'  CACTCCACATTCCTGGCCA   40819    ACA  A      TC
                                TG   AG AATGTGG  GTG
                                ||   || |||||||  |||
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                                AC   TC TTACACC  CAC
                                 CGG  C      T_
GAM251   ZNF31     3'  TTTGTAGACCACATTTCCTGTT 64992       A         _ TG
            A                    TGACA GAAATGTGGTC G  AA
                                 |||||| |||||||||||| |  ||
                                 ATTGT CTTTACACCAG T  TT
                                    C          A GT
GAM251   LOC115219 3'  CACGACAACGGGTCCTCA    73295     CAA  AA   G
                                 TGA   GA  TGT GTCGTG
                                 |||   ||  ||| ||||||
                                 ACT   CT  GCA CAGCAC
                                  C__  GG   A
GAM251   LOC120376 5'  TTCAGAGCATTTCTTTCA    75986     C       GG  G
                                 TGA AAGAAATGT  TC TGAA
                                 ||| |||||||||  || ||||
                                 ACT TTCTTTACG  AG ACTT
                                   _       __ _
GAM251   LOC133418 3'  TTTCATATACATTTTTTGCCA  75094    A         GTC
                                 TG CAAGAAATGTG   GTGAAA
                                 || ||||||||||   ||||||
                                 AC GTTTTTTACAT   TACTTT
                                  C          A__
GAM251   LOC151199 3'  TTAAAACCACAGCTCTTGCCA  80174    A    AA     CG
                                 TG CAAGA  TGTGGT  TGA
                                 || |||||  ||||||  |||
                                 AC GTTCT  ACACCA  ATT
                                  C    CG     AA
GAM251   LOC152317 5'  TCACACTGACTTTTGTCA    85649        AATG   C
                                 TGACAAGA    TGGT GTGA
                                 ||||||||    |||| ||||
                                 ACTGTTTT    GTCA CACT
                                      CA__    _
GAM251   LOC152674 3'  TTCAACCCACCCTCTTGTCA   85841        AAT    TCG
                                 TGACAAGA   GTGG   TGAA
                                 ||||||||   ||||   ||||
                                 ACTGTTCT   CACC   ACTT
                                      CC_    CA_
GAM251   LOC152845 5'  CATGACCACATTTTTCA     60330     CAA
                                 TGA   GAAATGTGGTCGTG
                                 |||   ||||||||||||||
                                 ACT   TTTTACACCAGTAC
                                   ____
GAM251   LOC154743 3'  TTTAGTCCACATTGTCTTGTCA 81118        _      TCG
                                 TGACAAGA AATGTGG   TGAA
                                 |||||||| |||||||   ||||
                                 ACTGTTCT TTACACC   ATTT
                                      G      TG_
GAM251   LOC165476 5'  TTCACGGCACCTTCT       87201      AT   G
                                 AGAA  GTG TCGTGAA
                                 ||||  ||| |||||||
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                                TCTT  CAC GGCACTT
                                  C_  _
GAM251  LOC254266 5'  TTTTCGGTCACACATCTTATCA 97356     C    AA    GT  T
                                TGA AAGA  TGTG  CG GAA
                                ||| ||||  ||||  || |||
                                ACT TTCT  ACAC  GC TTT
                                  A    AC    TG  T
GAM251  LOC255919 3'  TTTCATTCTTACATTTCTAATC 95043     CA        TC
           A                     TGA  AGAAATGTGG  GTGAAA
                                |||  ||||||||||  ||||||
                                ACT  TCTTTACATT  TACTTT
                                  AA         CT
GAM251  LOC51754  5'  CACGGCCACATCTCTGTCA    71027      A  A
                                TGACA GA ATGTGGTCGTG
                                ||||| || ||||||||||
                                ACTGT CT TACACCGGCAC
                                  _ C
GAM251  LOC55862  3'  ACCTCATTTCTTGCCA      37485     A       T
                                TG CAAGAAATG GGT
                                || |||||||| |||
                                AC GTTCTTTAC CCA
                                 C        T
GAM251  LOC55954  3'  CACGTGGTCACTTTTCTCATCA 38877     CA    T   GT __
                                TGA  AGAAA GTG  C  GTG
                                |||  ||||| |||  |  |||
                                ACT  TCTTT CAC  G  CAC
                                  AC     T   TG TG
GAM252  PLN       3'  AACAACAGAATCTAATCTTC   10646       CTAGT
                                GAAGA    GATTTTGTTGTT
                                |||||    ||||||||||||
                                CTTCT    CTAAGACAACAA
                                   AAT__
GAM252  cerk      3'  AACAACAAAAAAAGTTTCCCA  42840     A    AGTGA
                                TGG AGACT    TTTTGTTGTT
                                ||| |||||    ||||||||||
                                ACC TTTGA    AAAACAACAA
                                  C    AA___
GAM252  KIAA0087  3'  ACAACAAAAGACCTTTCA    28692       ACTA  GA
                                TGGAAG   GT  TTTTGTTGT
                                ||||||   ||  |||||||||
                                ACTTTC   CA  AAAACAACA
                                   ____  G_
GAM252  KIAA0924  3'  GGCTAAATCACTTACCTCCCA  29721     A  ACT      T
                                TGG AG   AGTGATTT GTT
                                ||| ||   |||||||| |||
                                ACC TC   TCACTAAA CGG
                                  C  CAT       T
GAM252  TOPBP1    3'  AACAACAAAATACAACTCCTC  22837    CT  _ _
                                GA  AGT G ATTTTGTTGTT
                                ||  ||| | ||||||||||
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                                CT  TCA C TAAAACAACAA
                                 CC   A A
GAM252  XLKD1    3'  AACAAATGTATCACTAGCCCTC 21947     AGA      TTTG
              C                   GGA   CTAGTGAT    TTGTT
                                  |||   ||||||||    |||||
                                  CCT   GATCACTA    AACAA
                                    CCC       TGTA
GAM253  AGRN     3'  CAGCTCTGCGTTGCTC      78833      AGATG   G
                                  GAGCA     ATG AGAGCTG
                                  |||||     ||| |||||||
                                  CTCGT     TGC TCTCGAC
                                     _____  G
GAM253  ASNA1    3'  CTCTCCCACCTCTTGCTC    62978        TGAT
                                  GAGCAAGA    GGAGAG
                                  ||||||||    ||||||
                                  CTCGTTCT    CCTCTC
                                       CCAC
GAM253  BCLG     3'  ACAGATACCATCATCCTGC    47776     A      AGAG
                                  GCA GATGATGG    CTGT
                                  ||| ||||||||    ||||
                                  CGT CTACTACC    GACA
                                    C       ATA_
GAM253  BCLG     3'  ACAGATACCATCATCCTGC    56972     A      AGAG
                                  GCA GATGATGG    CTGT
                                  ||| ||||||||    ||||
                                  CGT CTACTACC    GACA
                                    C       ATA_
GAM253  BCLG     3'  ACAGATACCATCATCCTGC    56978     A      AGAG
                                  GCA GATGATGG    CTGT
                                  ||| ||||||||    ||||
                                  CGT CTACTACC    GACA
                                    C       ATA_
GAM253  C14orf1  3'  CAGCTCTCCTTCTATC      23174     _ T
                                  GAT GA GGAGAGCTG
                                  ||| || |||||||||
                                  CTA CT CCTCTCGAC
                                    T  T
GAM253  CLCN6    3'  ACAGCTCTGCGGACCTTG    7073      ATGA  G
                                  CAAG    TG AGAGCTGT
                                  ||||    || ||||||||
                                  GTTC    GC TCTCGACA
                                    CAG_  G
GAM253  CLCN6    3'  ACAGCTCTGCGGACCTTG    41380     ATGA  G
                                  CAAG    TG AGAGCTGT
                                  ||||    || ||||||||
                                  GTTC    GC TCTCGACA
                                    CAG_  G
GAM253  CLCN6    3'  ACAGCTCTGCGGACCTTG    41395     ATGA  G
                                  CAAG    TG AGAGCTGT
                                  ||||    || ||||||||
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                                GTTC    GC TCTCGACA
                                  CAG_  G
GAM253  DISC1    3'  ACAGCTTTTCACCTTACTT   37866     C   ATGA
                                GAG AAG    TGGAGAGCTGT
                                ||| |||    ||||||||||
                                TTC TTC    ACTTTTCGACA
                                  A   C___
GAM253  DNMT3B   3'  CAGCTCTCCAATACTC      22563     CAAGA  A
                                GAG    TG TGGAGAGCTG
                                |||    || ||||||||||
                                CTC    AT ACCTCTCGAC
                                  _____  A
GAM253  DSP      5'  CAGCTTTCCTCCCGCTC     15339     AAGAT  T
                                GAGC    GA GGAGAGCTG
                                ||||    || |||||||||
                                CTCG    CT CCTTTCGAC
                                  CC___  _
GAM253  FUT6     5'  CAGCTCTGCCTCCTCT      3809      T  T  _
                                AGA GA GG AGAGCTG
                                ||| || || |||||||
                                TCT CT CC TCTCGAC
                                  C  _  G
GAM253  HAGH     5'  ACAGCTCTCCCGGCGCAGCTC  18027     AAGA  AT_
                                GAGC   TG   GGAGAGCTGT
                                ||||   ||   ||||||||||
                                CTCG   GC   CCTCTCGACA
                                  AC__  GGC
GAM253  HUS1     3'  ACAGCCTCTGTCACCCCGCC   91097   A  AAGA      A
                                G GC    TGATGGAG GCTGT
                                | ||    |||||||| |||||
                                C CG    ACTGTCTC CGACA
                                 _  CCCC       _
GAM253  IKBKB    3'  ACAGCCTGTCCTCTCCTGCTC  63201      A  T  T   G  _
                                GAGCA GA GA GGA AG CTGT
                                ||||| || || ||| || ||||
                                CTCGT CT CT CCT TC GACA
                                   C  _  _   G  C
GAM253  IL10RA   3'  GCCCCACCATCTTGCT      59644         A   AGA
                                AGCAAGATG TGG   GC
                                |||||||| |||   ||
                                TCGTTCTAC ACC   CG
                                     C   C__
GAM253  LIMK1    3'  ACAGCCCCTTCTCTCGCTT    9782      A   T  T  AGA
                                GAGC AGA GA GG   GCTGT
                                |||| ||| || ||   |||||
                                TTCG TCT CT CC   CGACA
                                  C   _  T  C__
GAM253  LIMK1    3'  ACAGCCCCTTCTCTCGCTT    33640     A   T  T  AGA
                                GAGC AGA GA GG   GCTGT
                                |||| ||| || ||   |||||
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                                TTCG TCT CT CC   CGACA
                                  C   _  T  C__
GAM253  MATN2    5'  ACAGCCTTGCCCCTCTTGCTC  9930         TGATG   A
                                GAGCAAGA    GAG GCTGT
                                ||||||||    ||| |||||
                                CTCGTTCT    TTC CGACA
                                    CCCCG  _
GAM253  MAX      3'  ACAGCTCTCGTTCTCCTT    9942      AT  TG
                                AAG  GA  GAGAGCTGT
                                |||  ||  |||||||||
                                TTC  CT  CTCTCGACA
                                  CT  TG
GAM253  MAX      3'  ACAGCTCTCGTTCTCCTT    59035     AT  TG
                                AAG  GA  GAGAGCTGT
                                |||  ||  |||||||||
                                TTC  CT  CTCTCGACA
                                  CT  TG
GAM253  NT5C2    3'  TCCCATCATCTACTC       24241     CA       A
                                GAG  AGATGATGG GA
                                |||  |||||||||  ||
                                CTC  TCTACTACC CT
                                  A_       _
GAM253  PAG      3'  ACAGCCATGTCATCTT      37397         GAGA
                                AAGATGATG    GCTGT
                                |||||||||    |||||
                                TTCTACTGT    CGACA
                                     AC__
GAM253  PLCB2    3'  AGGTCAGCATCATTTGCTC    15889      A      GA  G
                                GAGCA GATGATG  GA CT
                                ||||| |||||||  || ||
                                CTCGT TTACTAC  CT GA
                                   _      GA  G
GAM253  PNOC     5'  ACAGCTCTCAGCACCTGCTT   20640       A A  ATG
                                GAGCA G TG   GAGAGCTGT
                                ||||| | ||   |||||||||
                                TTCGT C AC   CTCTCGACA
                                   _ C  GA_
GAM253  RARG     3'  AGCCCACCTTCTTGCTC      6376         TGA   AGA
                                GAGCAAGA   TGG   GCT
                                ||||||||   |||   |||
                                CTCGTTCT   ACC   CGA
                                     TCC  ___
GAM253  SCNN1A   3'  AGCCCATCATCCTGCTT     6421       A      AGA
                                GAGCA GATGATGG   GCT
                                ||||| ||||||||   |||
                                TTCGT CTACTACC   CGA
                                   C       ___
GAM253  SF3B3    3'  ACAGCTCTTTCCCCTCAGCTC  24855      AAGA   T  ___
                                GAGC    TGA GG   AGAGCTGT
                                ||||    ||| ||   ||||||||
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                                CTCG   ACT CC   TCTCGACA
                                  ____  C  CTT
GAM253  SHMT1   3'  ACAGCTTGTACACACTGC    14789    A A  A  GA_
                                GCA G TG TG   GAGCTGT
                                ||| | || ||   |||||||
                                CGT C AC AC   TTCGACA
                                  _ _ _ ATG
GAM253  SPAG11  5'  CAGCTCTTCCCACGCTC    33258    AAGA  AT
                                GAGC   TG  GGAGAGCTG
                                ||||   ||  |||||||||
                                CTCG   AC  CTTCTCGAC
                                  C___  C_
GAM253  SPAG11  5'  CAGCTCTTCCCACGCTC    54241    AAGA  AT
                                GAGC   TG  GGAGAGCTG
                                ||||   ||  |||||||||
                                CTCG   AC  CTTCTCGAC
                                  C___  C_
GAM253  SPAG11  5'  CAGCTCTTCCCACGCTC    54243    AAGA  AT
                                GAGC   TG  GGAGAGCTG
                                ||||   ||  |||||||||
                                CTCG   AC  CTTCTCGAC
                                  C___  C_
GAM253  SPAG11  5'  CAGCTCTTCCCACGCTC    54247    AAGA  AT
                                GAGC   TG  GGAGAGCTG
                                ||||   ||  |||||||||
                                CTCG   AC  CTTCTCGAC
                                  C___  C_
GAM253  SPAG11  5'  CAGCTCTTCCCACGCTC    54249    AAGA  AT
                                GAGC   TG  GGAGAGCTG
                                ||||   ||  |||||||||
                                CTCG   AC  CTTCTCGAC
                                  C___  C_
GAM253  TBR1    3'  CAGCTCTTCCCCAGCTC    21683    AAGA  AT
                                GAGC   TG  GGAGAGCTG
                                ||||   ||  |||||||||
                                CTCG   AC  CTTCTCGAC
                                  ____ CC
GAM253  TCFL4   3'  TTCCATCACCTTCCTC     63466    C  A
                                GAG AAG TGATGGAG
                                ||| ||| ||||||||
                                CTC TTC ACTACCTT
                                  C  C
GAM253  THBD    3'  ACAGCTCTCCGGTCTCTCTC  4490    CA   GA
                                GAG  AGAT  TGGAGAGCTGT
                                |||  ||||  ||||||||||||
                                CTC  TCTG  GCCTCTCGACA
                                  TC   __
GAM253  AQP10   3'  ACAGCTCTCCTGCCGCTC   54429    AAGATGAT
                                GAGC      GGAGAGCTGT
                                ||||      ||||||||||
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                                CTCG       CCTCTCGACA
                                  CCGT____
GAM253  ATF3     5'  ACAGCTCTCTTCTCTCGCC   14430   A  A   T  T
                                G GC AGA GA GGAGAGCTGT
                                | || ||| || ||||||||||
                                C CG TCT CT TCTCTCGACA
                                 _ C  _ _
GAM253  BRD2     3'  ACACTTCTTCATCTC       17534    T       C
                                GA GATGGAGAG TGT
                                || ||||||||| |||
                                CT CTACTTCTT ACA
                                  _       C
GAM253  BTN2A1   3'  ACAGCCCCATCTTCATCTGC  54337    A    T  GA__
                                GCA GATGA GGA    GCTGT
                                ||| ||||| |||    |||||
                                CGT CTACT TCT    CGACA
                                  _    _  ACCC
GAM253  C17orf31 5'  ACAGCTTTGACCATCCTC    34117    T    __
                                GA GATGG  AGAGCTGT
                                || |||||  ||||||||
                                CT CTACC  TTTCGACA
                                 C    AG
GAM253  C6orf9   3'  CAGCTCTACCCTTCCTC     42077    C   ATGAT  _
                                GAG AAG     GG AGAGCTG
                                ||| |||     || |||||||
                                CTC TTC     CC TCTCGAC
                                  C  _____  A
GAM253  COLEC10  3'  AGCCTCCATCATCATGCTC   21227      A        A
                                GAGCA GATGATGGAG GCT
                                ||||| |||||||||| |||
                                CTCGT CTACTACCTC CGA
                                   A        _
GAM253  DCOHM    3'  ACAGTCTCACTATCTTGCTC  49590         ATG    G
                                GAGCAAGATG   GAGA CTGT
                                ||||||||||   |||| ||||
                                CTCGTTCTAT   CTCT GACA
                                      CA_   _
GAM253  DKFZP566C243 5'  GGCCCACATCTTGC       31172        A   AGA
                                GCAAGATG TGG   GCT
                                |||||||| |||   |||
                                CGTTCTAC ACC   CGG
                                     _  ___
GAM253  DT1P1A10 3'  ACAGCTCTGTACCCCTGCCC  61563   A   AGATGA  G
                                G GCA     TG AGAGCTGT
                                | |||     || ||||||||
                                C CGT     AT TCTCGACA
                                 C  CCCC__  G
GAM253  DZIP1    5'  ACAGCTCTTGTTCCCGCT    30032     AAGAT  TG
                                AGC    GA  GAGAGCTGT
                                |||    ||  |||||||||
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                                TCG    CT  TTCTCGACA
                                  CC___  TG
GAM253  FLJ12221  3'  GCCCCTTCATCTTACTC    62551    C     T  AGA
                                GAG AAGATGA GG   GC
                                ||| ||||||| ||   ||
                                CTC TTCTACT CC   CG
                                  A      T  C__
GAM253  FLJ12875  3'  ACAGCTCTTTTTTTATTGC   44607     GAT  TG
                                GCAA   GA  GAGAGCTGT
                                ||||   ||  |||||||||
                                CGTT   TT  TTCTCGACA
                                  AT_  TT
GAM253  FLJ20152  3'  ACAGCTCTATTCTGCCTGCTC  38645      AGAT  TGG
                                GAGCA    GA   AGAGCTGT
                                |||||    ||   ||||||||
                                CTCGT    CT   TCTCGACA
                                   CCGT  TA_
GAM253  FLJ20625  3'  CAGCTCTTCTCCTCT      35468     T  T
                                AGA GA GGAGAGCTG
                                ||| || |||||||||
                                TCT CT CTTCTCGAC
                                  C  _
GAM253  FLJ22557  3'  ACAGCTCTAAATCTTACTT   45253    C    GATGG
                                GAG AAGAT    AGAGCTGT
                                ||| |||||    ||||||||
                                TTC TTCTA    TCTCGACA
                                  A    AA___
GAM253  FYCO1     3'  ACAGCTCTTCGTCCCTTGTTC  44484       AT
                                GAGCAAG  GATGGAGAGCTGT
                                |||||||  ||||||||||||
                                CTTGTTC  CTGCTTCTCGACA
                                    C_
GAM253  GGA2      3'  ACAGCTCTGGTTCTTGCC    30455   A    TGATGG
                                G GCAAGA     AGAGCTGT
                                | ||||||     ||||||||
                                C CGTTCT     TCTCGACA
                                 _     TGG___
GAM253  GGA2      3'  ACAGCTCTGGTTCTTGCC    56867   A    TGATGG
                                G GCAAGA     AGAGCTGT
                                | ||||||     ||||||||
                                C CGTTCT     TCTCGACA
                                 _     TGG___
GAM253  GREB1     3'  CAGTGATCATCTTGTTC     27866          GGAGA
                                GAGCAAGATGAT    GCTG
                                ||||||||||||    ||||
                                CTTGTTCTACTA    TGAC
                                       G____
GAM253  H2AV      3'  ACAGCTCTCTATACTC      56842    TG
                                GA  ATGGAGAGCTGT
                                ||  ||||||||||||
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                                CT  TATCTCTCGACA
                                 CA
GAM253  KIAA0298 3' ACAGCTCTCCCTGGTCCTGT  76574    A  GAT
                                GCA GAT  GGAGAGCTGT
                                ||| |||  ||||||||||
                                TGT CTG  CCTCTCGACA
                                  C  GTC
GAM253  KIAA1040 3' ACAGCTCTCCAAGCTTTC   72216   GC  ATGA
                                GA  AAG   TGGAGAGCTGT
                                ||  |||   ||||||||||
                                CT  TTC   ACCTCTCGACA
                                 __  GA__
GAM253  KIAA1203 3' ACAGCCCTACATCTTGC    71633       A  AGA
                                GCAAGATG TGG  GCTGT
                                |||||||| |||  |||||
                                CGTTCTAC ATC  CGACA
                                     _  C__
GAM253  KIAA1237 3' ACAGCTGACAAATCATCTCCTC 80463    CA     GGAG_
                                GAG  AGATGAT    AGCTGT
                                |||  |||||||    ||||||
                                CTC  TCTACTA    TCGACA
                                  C_     AACAG
GAM253  KIAA1388 3' ACAGCCCTCTCCGTCTGCTC  93576     AGAT     __
                                GAGCA   GATGGAGA  GCTGT
                                |||||   ||||||||  |||||
                                CTCGT   CTGCCTCT  CGACA
                                  _____      CC
GAM253  KIAA1691 3' ACAGCTCTCCTTCCTCCCGC  92549   AA  T  T
                                GC  GA GA GGAGAGCTGT
                                ||  || || ||||||||||
                                CG  CT CT CCTCTCGACA
                                 CC  C  T
GAM253  KIAA1737 3' CTCCCATCATCCCACTC    67354    CAA     A
                                GAG   GATGATGG GAG
                                |||   |||||||| |||
                                CTC   CTACTACC CTC
                                  ACC      _
GAM253  KIAA1937 3' ACATATTCATCATCCACTC   73691    CAA      GAGC
                                GAG   GATGATGGA   TGT
                                |||   |||||||||   |||
                                CTC   CTACTACTT   ACA
                                  AC_       AT__
GAM253  KSR     5' ACAGCTTCATCACCCCGC    64041    AAGA    GA
                                GC   TGATG  GAGCTGT
                                ||   |||||  |||||||
                                CG   ACTAC  TTCGACA
                                 CCCC    __
GAM253  LEFTB   5' ACAGCCCCACTCTGCCTCTTGC 40652        TGA    A___
           TC                    GAGCAAGA   TGGAG    GCTGT
                                ||||||||   |||||   |||||
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                                CTCGTTCT  GTCTC   CGACA
                                    CC_   ACCC
GAM253  MGC1842  3' ACAGCCCTCCAGGTCCTCCAGC 65636     AA  T __   A
          TC                    GAGC  GA GA  TGGAG GCTGT
                                |||| || ||  ||||| |||||
                                CTCG  CT CT  ACCTC CGACA
                                  AC  C  GG    C
GAM253  MGC2615  3' ACAGGATTTCATCATGTTGC  44084     G       AG
                                GCAA ATGATGGAG  CTGT
                                |||| |||||||||  ||||
                                CGTT TACTACTTT  GACA
                                  G       AG
GAM253  MGC2628  3' ACAGCTCCCCAAGTGTTC    43965     AGATGA  A
                                GAGCA     TGG GAGCTGT
                                |||||     ||| |||||||
                                CTTGT     ACC CTCGACA
                                   GA____  C
GAM253  NETO1    3' TCTCCATCATCTCATC     57315    GCA
                                GA  AGATGATGGAGA
                                ||  ||||||||||||
                                CT  TCTACTACCTCT
                                 AC_
GAM253  NPTXR    3' CAGCTGCATCTTGCTT     54173         ATGGAG
                                GAGCAAGATG    AGCTG
                                ||||||||||    |||||
                                TTCGTTCTAC    TCGAC
                                     G_____
GAM253  NPTXR    3' CAGCTGCATCTTGCTT     26637         ATGGAG
                                GAGCAAGATG    AGCTG
                                ||||||||||    |||||
                                TTCGTTCTAC    TCGAC
                                     G_____
GAM253  NR4A3    5' ACAGCTCTCTAGAAACTCGCTC 22735     A  ATGA
                                GAGC AG   TGGAGAGCTGT
                                |||| ||   ||||||||||
                                CTCG TC   ATCTCTCGACA
                                  C  AAAG
GAM253  PISD     3' ACATTCACCTCATCCTGCTC  26769     A   T  A  C
                                GAGCA GATGA GG GAG TGT
                                ||||| ||||| || ||| |||
                                CTCGT CTACT CC CTT ACA
                                   C    _ A  _
GAM253  QKI      3' CTCCCCCACCATCTTGT    65441       A  A_
                                GCAAGATG TGG  GAG
                                |||||||| |||  |||
                                TGTTCTAC ACC  CTC
                                     C  CC
GAM253  RAB20    3' ACAACTCTGACATTTCTTGTTC 35153       T   G_   C
                                GAGCAAGA GATG  AGAG TGT
                                |||||||| ||||  |||| |||
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                                CTTGTTCT TTAC  TCTC ACA
                                     _   AG   A
GAM253  RDH-E2   3' ACAGCTCTGGATTTCT     57268     T  GG
                                AGA GAT  AGAGCTGT
                                ||| |||  ||||||||
                                TCT TTA  TCTCGACA
                                  _  GG
GAM253  Rpo1-2   3' ACAACTCTCCATTTCCCTGGC  38696    A  AT_       C
                                GC AG   GATGGAGAG TGT
                                || ||   ||||||||| |||
                                CG TC   TTACCTCTC ACA
                                 G  CCT       A
GAM253  Rpo1-2   3' ACAACTCTCCATTTCCCTGGC  49874    A  AT_       C
                                GC AG   GATGGAGAG TGT
                                || ||   ||||||||| |||
                                CG TC   TTACCTCTC ACA
                                 G  CCT       A
GAM253  S100Z    5' ACAGCAGGGCCTCTTGCTC    55375        TGAT  AGA_
                                GAGCAAGA   GG   GCTGT
                                ||||||||   ||   |||||
                                CTCGTTCT   CC   CGACA
                                     _____ GGGA
GAM253  SMURF2   3' ACAGCTCCTGTACTTGCTC    42714       ATG   A
                                GAGCAAG   ATGG GAGCTGT
                                |||||||   |||| |||||||
                                CTCGTTC   TGTC CTCGACA
                                    A__   _
GAM253  SP140    3' AGTGTCCATCATCTGACTC    23374     CA       GA
                                GAG  AGATGATGGA  GCT
                                |||  ||||||||||  |||
                                CTC  TCTACTACCT  TGA
                                  AG        G_
GAM253  SP192    5' ACAGCTCTTTCCCCTT      41311     AT  TG
                                AAG  GA  GAGAGCTGT
                                |||  ||  |||||||||
                                TTC  CT  TTCTCGACA
                                  CC  __
GAM253  STAF65(gamma) 3'  ACAGCTCTCTATCTC       29419    T
                                GA GATGGAGAGCTGT
                                || ||||||||||||
                                CT CTATCTCTCGACA
                                 _
GAM253  STX1B2   3' ACAGCAGTCCATCACGC     53513    AAGA     GA
                                GC   TGATGGA  GCTGT
                                ||   |||||||  |||||
                                CG   ACTACCT  CGACA
                                 C___      GA
GAM253  ZNF263   3' ACAGCTCTGGAGTCTTGTTC  19221         GATGG
                                GAGCAAGAT    AGAGCTGT
                                |||||||||    ||||||||
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                                CTTGTTCTG    TCTCGACA
                                     AGG__
GAM253  LOC115399 3'  ACAGCTCTGACTTCCTGGC   73421    A  AT  TGG_
                                GC AG  GA    AGAGCTGT
                                || ||  ||    ||||||||
                                CG TC  CT    TCTCGACA
                                 G  __  TCAG
GAM253  LOC115400 3'  CTCTCCATCACCTGCTC     73442      A A
                                GAGCA G TGATGGAGAG
                                ||||| | ||||||||||
                                CTCGT C ACTACCTCTC
                                   _ C
GAM253  LOC143381 5'  CTCCACCACCTTGTTC      76546      A  A
                                GAGCAAG TG TGGAG
                                ||||||| || |||||
                                CTTGTTC AC ACCTC
                                     C  C
GAM253  LOC143451 3'  ACAGCTCTTCTCTCCTTCTC  76560    C   AT  T
                                GAG AAG  GA GGAGAGCTGT
                                ||| |||  || ||||||||||
                                CTC TTC  CT CTTCTCGACA
                                  _   CT  _
GAM253  LOC144404 5'  CTGACCATCATCCTGCTC    76828      A       AG
                                GAGCA GATGATGG  AG
                                ||||| ||||||||  ||
                                CTCGT CTACTACC  TC
                                   C       AG
GAM253  LOC145125 3'  ACAGCTCTTCTCTCCTTCTC  77002    C   AT  T
                                GAG AAG  GA GGAGAGCTGT
                                ||| |||  || ||||||||||
                                CTC TTC  CT CTTCTCGACA
                                  _   CT  _
GAM253  LOC145231 5'  CAGCTCTTTGCCTGCTC     83281      A ATGA GG
                                GAGCA G    T  AGAGCTG
                                ||||| |    |  |||||||
                                CTCGT C    G  TCTCGAC
                                   _ C___ TT
GAM253  LOC146237 3'  ACAGCTCCCCGTCATC      83628       A
                                GATGATGG GAGCTGT
                                |||||||| |||||||
                                CTACTGCC CTCGACA
                                     C
GAM253  LOC146237 3'  ACAGCTCTCACATTCCTT    83629     AT   _
                                AAG  GATG GAGAGCTGT
                                |||  |||| |||||||||
                                TTC  TTAC CTCTCGACA
                                  C_    A
GAM253  LOC147160 3'  ACAGCCTGGTTTCATCTTTCTC 83954     C      TGG_  A
                                GAG AAGATGA    AG GCTGT
                                ||| |||||||    || |||||
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                                CTC TTCTACT    TC CGACA
                                  T      TTGG  _
GAM253   LOC148979 5'  CTCCATCATCCGCTC       84320      AA
                                GAGC  GATGATGGAG
                                ||||  ||||||||||
                                CTCG  CTACTACCTC
                                  C_
GAM253   LOC158308 3'  ACAGCTCTGTCTGCCTTGTTC  86740        AT_   GG
                                GAGCAAG   GAT  AGAGCTGT
                                |||||||   |||  ||||||||
                                CTTGTTC   CTG  TCTCGACA
                                    CGT   __
GAM253   LOC159765 5'  ACAGCTCAACCGTCATCCTC   82195     CAA       A_
                                GAG   GATGATGG  GAGCTGT
                                |||   ||||||||  |||||||
                                CTC   CTACTGCC  CTCGACA
                                  ____       AA
GAM253   LOC160646 3'  CAGCTCTCCAGGTGCT      82224      AGATGA
                                AGCA     TGGAGAGCTG
                                ||||     ||||||||||
                                TCGT     ACCTCTCGAC
                                  GG_____
GAM253   LOC166341 3'  CAGCCCCACTCTGGCTC     82629      A   TGA   AGA
                                GAGC AGA   TGG   GCTG
                                |||| |||   |||   ||||
                                CTCG TCT   ACC   CGAC
                                  G   C__   C__
GAM253   LOC200609 5'  ACAACTCTCCATTCTCTTATC  90093    GC    T       C
                                GA  AAGA GATGGAGAG TGT
                                ||  |||| ||||||||| |||
                                CT  TTCT TTACCTCTC ACA
                                 A_   C        A
GAM253   LOC202908 5'  CTCTCCATCACCTGCTC      89234       A A
                                GAGCA G TGATGGAGAG
                                ||||| | ||||||||||
                                CTCGT C ACTACCTCTC
                                   _ C
GAM253   LOC253786 5'  ACAGCTCCCTGCCCCTGCTC   97041       AGATGAT  A
                                GAGCA      GG GAGCTGT
                                |||||      || |||||||
                                CTCGT      CC CTCGACA
                                   CCCCGT_  _
GAM253   LOC254428 3'  ACAGCTCTAACCTCACCT    95453    A   T  __
                                AG TGA GG  AGAGCTGT
                                || ||| ||  ||||||||
                                TC ACT CC  TCTCGACA
                                 C   _  AA
GAM253   LOC254440 3'  ACAGCTCTTCTCTCCTTCTC   97062     C   AT  T
                                GAG AAG  GA GGAGAGCTGT
                                ||| |||  || ||||||||||
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                                CTC TTC  CT CTTCTCGACA
                                  _  CT  _
GAM253  LOC255696 5'  CAGCTCTTCCTATGC      97498    _ ATGAT
                                GCA AG    GGAGAGCTG
                                ||| ||    |||||||||
                                CGT TC    CTTCTCGAC
                                  A _____
GAM253  LOC256905 5'  ACAGCTCTGGCTCCTGCTC   96862     A  TGATGG
                                GAGCA GA    AGAGCTGT
                                ||||| ||    ||||||||
                                CTCGT CT    TCTCGACA
                                   C  CGG___
GAM253  LOC91012  3'  ACAGCTGCCAATACCCTGCTC 64638     AGA  A   AG
                                GAGCA   TG TGG  AGCTGT
                                |||||   || |||  ||||||
                                CTCGT   AT ACC  TCGACA
                                   CCC  A   G_
GAM253  LOC92379  3'  CAGCTCTCTCCTTTCTC    69148    C   ATGAT
                                GAG AAG    GGAGAGCTG
                                ||| |||    |||||||||
                                CTC TTC    TCTCTCGAC
                                  T   C____
GAM253  LOC92912  3'  ACAGCCTTTGCATTTTGCTC  70842        A GG  A
                                GAGCAAGATG T  AG GCTGT
                                |||||||||| |  || |||||
                                CTCGTTTTAC G  TC CGACA
                                      _ TT  _
GAM254  CNGA1     3'  CAACTGATAATGTGCAAA    59507        GC   A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                      A_  _
GAM254  ESRRG     3'  TGGCAGTCTTATGTGCAAA   66396       TAGCT
                                TTTGCACAT    AGATTGCCA
                                |||||||||    |||||||||
                                AAACGTGTA    TCTGACGGT
                                     T____
GAM254  KCNJ3     3'  GCAATAATGTGCAAA      9525         GCTAGA
                                TTTGCACATTA     TTGC
                                ||||||||||     ||||
                                AAACGTGTAAT     AACG
                                               _______
GAM254  SDC2      3'  GCAAATTAATGTGTAAA     67132         CTAGA
                                TTTGCACATTAG    TTGC
                                ||||||||||||    ||||
                                AAATGTGTAATT    AACG
                                      A____
GAM254  USP9X     3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
            A                    TTTGCACATTAGC     GCCAT
                                ||||||||||||     |||||
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                                AAATGTGTAATCG     CGGTA
                                      TAGTC_
GAM254  AMOTL1   3'  GGCAAGTAATGTGCAAA     73650          G  AGAT
                                TTTGCACATTA CT    TGCC
                                |||||||||| ||    ||||
                                AAACGTGTAAT GA    ACGG
                                      _ ____
GAM254  BCAR3    3'  AGTAATAATGTGCAAA      13098          __
                                TTTGCACATTA  GCT
                                |||||||||| |||
                                AAACGTGTAAT  TGA
                                      AA
GAM254  DKFZP434B044 3'  TGACAATTAAATGTGCAGA    48930          AGCTA    C
                                TTTGCACATT     GATTG CA
                                |||||||||     ||||| ||
                                AGACGTGTAA     TTAAC GT
                                      A____     A
GAM254  MGC3184   3'  ATGACATTTTCTAATGTGCAGA 48235           CT   T  C
                                TTTGCACATTAG  AGA TG CAT
                                |||||||||||  ||| || |||
                                AGACGTGTAATC  TTT AC GTA
                                      __  T  A
GAM254  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
          AA                    TTTGCACATTAGCTAGATTGCCAT
                                ||||||||||||||||||||||||
                                AAACGTGTAATCGATCTAACGGTA

GAM255  ATRX     3'  TTCATGTACAATTTTGGTT    56249         GTTG
                                AACCAAGAT    GCATGAA
                                |||||||||    |||||||
                                TTGGTTTTA    TGTACTT
                                     ACA_
GAM255  ATRX     3'  TTCATGTACAATTTTGGTT    4918          GTTG
                                AACCAAGAT    GCATGAA
                                |||||||||    |||||||
                                TTGGTTTTA    TGTACTT
                                     ACA_
GAM255  CD4      3'  GTTCAGGGCCAGCCCTGG    5227      AGAT     A_
                                CCA    GTTGGC  TGAAC
                                |||    ||||||  |||||
                                GGT    CGACCG  ACTTG
                                  CC__     GG
GAM255  CDYL     3'  TTCATGCTGAGATATC      16700       __
                                GATGTT  GGCATGAA
                                ||||||  ||||||||
                                CTATAG  TCGTACTT
                                   AG
GAM255  DISC1    3'  TGTGGAAATCTTGGTT      37896         G  G
                                AACCAAGAT TT GCA
                                ||||||||| || |||
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                                TTGGTTCTA AG TGT
                                     A  G
GAM255  DLEU1    3'  TTCATGCCAAGTATCT      19698       _
                                AGATG TTGGCATGAA
                                ||||| ||||||||||
                                TCTAT AACCGTACTT
                                   G
GAM255  DSC3     3'  GTTCATGCCATTCTCCTG    8680     A  TGT
                                CA GA   TGGCATGAAC
                                || ||   ||||||||||
                                GT CT   ACCGTACTTG
                                 C  CTT
GAM255  DSC3     3'  GTTCATGCCATTCTCCTG    44345    A  TGT
                                CA GA   TGGCATGAAC
                                || ||   ||||||||||
                                GT CT   ACCGTACTTG
                                 C  CTT
GAM255  EFEMP1   3'  TGTACAACATGCTGGTT     38155      AG     _
                                AACCA  ATGTTG GCA
                                |||||  |||||| |||
                                TTGGT  TACAAC TGT
                                   CG     A
GAM255  EFEMP1   3'  TGTACAACATGCTGGTT     14639      AG     _
                                AACCA  ATGTTG GCA
                                |||||  |||||| |||
                                TTGGT  TACAAC TGT
                                   CG     A
GAM255  ELAVL3   3'  GTTCACTCTCTCGTCTTGGTT  7427          TT  CA
                                AACCAAGATG  GG  TGAAC
                                ||||||||||  ||  |||||
                                TTGGTTCTGC  TC  ACTTG
                                      TC  TC
GAM255  FECH     3'  TTCATTGGTCATCTTGGT    3758          TTGGC
                                ACCAAGATG    ATGAA
                                |||||||||    |||||
                                TGGTTCTAC    TACTT
                                      TGGT_
GAM255  FKBP1B   3'  GTTCATGCGAATTCTTG     54011      T   G
                                CAAGA GTT GCATGAAC
                                ||||| ||| ||||||||
                                GTTCT TAA CGTACTTG
                                   _  G
GAM255  FKBP1B   3'  GTTCATGCGAATTCTTG     14650      T   G
                                CAAGA GTT GCATGAAC
                                ||||| ||| ||||||||
                                GTTCT TAA CGTACTTG
                                   _  G
GAM255  GCS1     3'  TCATGCCACTCTGG        20869     A  T  T
                                CCA GA GT GGCATGA
                                ||| || || |||||||
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                                GGT CT CA CCGTACT
                                  _ _ _
GAM255  GGA3    3'  TATGGACATCTTGG       25744          GG
                                CCAAGATGTT  CATG
                                ||||||||||  ||||
                                GGTTCTACAG  GTAT
                                   __
GAM255  GGA3    3'  TATGGACATCTTGG       56828          GG
                                CCAAGATGTT  CATG
                                ||||||||||  ||||
                                GGTTCTACAG  GTAT
                                   __
GAM255  HMG20A  5'  CATACACCATCTTGGTT    36533          T  GC
                                AACCAAGATG TG  ATG
                                ||||||||||  ||  |||
                                TTGGTTCTAC AC  TAC
                                      C  A_
GAM255  HSD17B1 5'  TCATGTCTGTTTTGG      4690         GTT
                                CCAAGAT   GGCATGA
                                |||||||   |||||||
                                GGTTTTG   CTGTACT
                                    T__
GAM255  IGFBP3  3'  TCACCACATGTTGGT      5187       G   T  CA
                                ACCAA ATGT GG  TGA
                                |||||  |||| ||  |||
                                TGGTT TACA CC  ACT
                                  G   _ __
GAM255  ITGAL   3'  GTTCACCAGCCTCTCTTGGTT  9394         T__    CA
                                AACCAAGA   GTTGG  TGAACC
                                ||||||||   |||||  |||||
                                TTGGTTCT   CGACC  ACTTG
                                    CTC    __
GAM255  KIF5C   3'  TCATGAATATGATTTTGGTT   15741         _  TGG
                                AACCAAGAT GT   CATGA
                                |||||||||  ||   |||||
                                TTGGTTTTA TA   GTACT
                                     G  TAA
GAM255  LHX2    5'  TTGATGAACATTTTGGTT    16568          GG   G
                                AACCAAGATGTT  CAT AA
                                ||||||||||||  ||| ||
                                TTGGTTTTACAA  GTA TT
                                      __  G
GAM255  LPXN    3'  TTCATGCCAACACTGGTT    16678       A A
                                AACCA G TGTTGGCATGAA
                                |||||  |  ||||||||||||
                                TTGGT C ACAACCGTACTT
                                  _ _
GAM255  MDM1    3'  GTTCATGTCCACCACT      39274     A  T  _
                                AG TG TGG CATGAAC
                                ||  ||  |||  |||||||
```

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                                TC AC ACC GTACTTG
                                 _ C   T
GAM255  MTR      3'  GTTCATGCCATTCTCCTG    4216     A  TGT
                                CA GA   TGGCATGAAC
                                || ||   ||||||||||
                                GT CT   ACCGTACTTG
                                 C  CTT
GAM255  NAB1     3'  TCATATAACATCTGGTT     19911      A      GC
                                AACCA GATGTTG  ATGA
                                ||||| |||||||  ||||
                                TTGGT CTACAAT  TACT
                                   _      A_
GAM255  ORC4L    3'  CACGTAACATTTTGGT      62055           G A
                                ACCAAGATGTTG C TG
                                |||||||||||| | ||
                                TGGTTTTACAAT G AC
                                       _ C
GAM255  RAB36    3'  GTTCATGCCATTCTCCTG    16970    A  TGT
                                CA GA   TGGCATGAAC
                                || ||   ||||||||||
                                GT CT   ACCGTACTTG
                                 C  CTT
GAM255  RPP30    3'  GTTCATGCCATTCTCCTG    21171    A  TGT
                                CA GA   TGGCATGAAC
                                || ||   ||||||||||
                                GT CT   ACCGTACTTG
                                 C  CTT
GAM255  SDHB     3'  GTTCCTTTAAAGATCTTGGTT  60510         G  GGCAT
                                AACCAAGAT TT     GAAC
                                ||||||||| ||     ||||
                                TTGGTTCTA AA     CTTG
                                     G  ATTTC
GAM255  SECTM1   3'  GTTCATGCTTTTGTCTTCGT   11530    C     TT
                                AC AAGATG  GGCATGAAC
                                || ||||||  |||||||||
                                TG TTCTGT  TCGTACTTG
                                 C     TT
GAM255  SLC6A3   3'  TTCATGCCTCAAGTCGGT    6450      AA   GTT_
                                ACC  GAT    GGCATGAA
                                |||  |||    ||||||||
                                TGG  CTG    CCGTACTT
                                  __   AACT
GAM255  SNX6     3'  TTCATGTATCCTGGT       41163      A   GTTG
                                ACCA GAT    GCATGAA
                                |||| |||    |||||||
                                TGGT CTA    TGTACTT
                                  C  ____
GAM255  SWAP70   3'  GCCAACAGAACTCTTGGTT   71349         ____
                                AACCAAGA    TGTTGGC
                                ||||||||    |||||||
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                                TTGGTTCT   ACAACCG
                                    CAAG
GAM255  TCL1B    3'  GTTCTGCTGACACTTTGG    16986      A  TG  T
                                CCAAG TGT  GCA GAAC
                                ||||| |||  ||| ||||
                                GGTTT ACA  CGT CTTG
                                   C  GT  _
GAM255  TEM6     3'  GCCTCTAGCATCTCGGTT    42745      A     ___
                                AACC AGATGTT  GGC
                                |||| |||||||  |||
                                TTGG TCTACGA  CCG
                                  C      TCT
GAM255  THBD     3'  TTCATGCCAATTAGCAATTG  4497      GAT___
                                CAA     GTTGGCATGAA
                                |||     ||||||||||
                                GTT     TAACCGTACTT
                                  AACGAT
GAM255  TM7SF3   3'  GTTCATGCCTGGAGTGGTT   59669      AGATGTT
                                AACCA      GGCATGAAC
                                |||||      |||||||||
                                TTGGT      CCGTACTTG
                                   GAGGT__
GAM255  TNFRSF6B 3'  CATGCCAGCCGGCTTGG     31603      AT_
                                CCAAG   GTTGGCATG
                                |||||   |||||||||
                                GGTTC   CGACCGTAC
                                   GGC
GAM255  TNFRSF6B 3'  CATGCCAGCCGGCTTGG     33164      AT_
                                CCAAG   GTTGGCATG
                                |||||   |||||||||
                                GGTTC   CGACCGTAC
                                   GGC
GAM255  TP53     3'  GTTCATGCCACCATGG      5042      AGA  T
                                CCA   TG TGGCATGAAC
                                |||   || ||||||||||
                                GGT   AC ACCGTACTTG
                                  ___  C
GAM255  VHL      3'  GTTCATGCTCCTCTTG      5082       TGTT
                                CAAGA   GGCATGAAC
                                |||||   |||||||||
                                GTTCT   TCGTACTTG
                                   CC__
GAM255  ZFP103   3'  GTCCAGCACCTCTTGGTT    19025        __    _
                                AACCAAGA  TGTTGG C
                                ||||||||  |||||| |
                                TTGGTTCT  ACGACC G
                                     CC     T
GAM255  ARHGAP11A 3' GTTCATGCCATTTTCCTG    28800    A  TGT
                                CA GA   TGGCATGAAC
                                || ||   ||||||||||
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                                GT CT   ACCGTACTTG
                                 C  TTT
GAM255  CLSTN2   3'  GTTCCCCAGCATCCTG     42133    A      CAT
                                CA GATGTTGG   GAAC
                                || ||||||||   ||||
                                GT CTACGACC   CTTG
                                 C       C__
GAM255  DIO2     3'  TCATAACATCTGGGT      25687     A      GGC
                                ACC AGATGTT   ATGA
                                ||| |||||||   ||||
                                TGG TCTACAA   TACT
                                  G     ___
GAM255  DIO2     3'  TCATAACATCTGGGT      5835      A      GGC
                                ACC AGATGTT   ATGA
                                ||| |||||||   ||||
                                TGG TCTACAA   TACT
                                  G     ___
GAM255  DKFZP434B195 3'  TCACCCAACATCCTGGT     48430      A      CA
                                ACCA GATGTTGG  TGA
                                |||| ||||||||  |||
                                TGGT CTACAACC  ACT
                                  C       C_
GAM255  DKFZP434P211 3'  GTTCATGTCCGTCT       27268       TT
                                AGATG  GGCATGAAC
                                |||||  |||||||||
                                TCTGC  CTGTACTTG
                                   __
GAM255  DKFZp547C176 3'  GTTCATGCTTGGACCTC     67230     T  __
                                GA GTT  GGCATGAAC
                                || |||  |||||||||
                                CT CAG  TCGTACTTG
                                 C  GT
GAM255  DKFZp564O1278 5'  TCTGTTAAACATCTTG      63723          _   T
                                CAAGATGTT GGCA GA
                                ||||||||| |||| ||
                                GTTCTACAA TTGT CT
                                     A   _
GAM255  ELF4     3'  GTTCATGCCGAGATTCAGTT   7437      CAA   G
                                AAC   GAT TTGGCATGAAC
                                |||   ||| ||||||||||
                                TTG   TTA AGCCGTACTTG
                                  AC_   G
GAM255  FLB6421  3'  GTTCATGCCCTGGGCTC     39231     T  ___
                                GA GTT   GGCATGAAC
                                || |||   |||||||||
                                CT CGG   CCGTACTTG
                                 _  GTC
GAM255  FLJ10508  3'  GTTCATGCCCACGTGTG     36201     AG    T
                                CA  ATGT GGCATGAAC
                                ||  |||| |||||||||
```

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                              GT  TGCA CCGTACTTG
                               G_   C
GAM255  FLJ10846 3' GTTCATGCCATTCTCCTG    36742    A  TGT
                              CA GA   TGGCATGAAC
                              || ||   ||||||||||
                              GT CT   ACCGTACTTG
                               C  CTT
GAM255  FLJ11149 3' GTTCAGCATCATCTTGGTT    37112         TTG  A
                              AACCAAGATG   GC TGAAC
                              ||||||||||   || |||||
                              TTGGTTCTAC   CG ACTTG
                                    TA_  _
GAM255  FLJ11710 3' GTTCATGCCCTTTGG      45831      ATGTT
                              CCAAG    GGCATGAAC
                              |||||    |||||||||
                              GGTTT    CCGTACTTG
                                 C____
GAM255  FLJ11722 3' GTTCATGCCAATGTGCCAGG   46397    AAG_
                              CC    ATGTTGGCATGAAC
                              ||    ||||||||||||||
                              GG    TGTAACCGTACTTG
                               ACCG
GAM255  FLJ12171 3' GTTCACGTTGATGCTTCTTGGT 44873         __   TG  A
           T                   AACCAAGA  TGT  GC TGAAC
                              ||||||||  |||  || |||||
                              TTGGTTCT  GTA  TG ACTTG
                                   TC   GT  C
GAM255  FLJ12960 3' GTTCATGCCATTCTCCTG    44952    A  TGT
                              CA GA   TGGCATGAAC
                              || ||   ||||||||||
                              GT CT   ACCGTACTTG
                               C  CTT
GAM255  FLJ13868 3' TCATCAGCATCCAGGT      42732     AA      GC
                              ACC  GATGTTG  ATGA
                              |||  |||||||  ||||
                              TGG  CTACGAC  TACT
                                AC       __
GAM255  FLJ20174 3' GCTCAGCATCTGGGTT      34690      A       _
                              AACC AGATGTTG GC
                              |||| |||||||| ||
                              TTGG TCTACGAC CG
                                G       T
GAM255  FLJ20511 3' GTTCATGCCATTCTCCTG    35330    A  TGT
                              CA GA   TGGCATGAAC
                              || ||   ||||||||||
                              GT CT   ACCGTACTTG
                               C  CTT
GAM255  FLJ20574 3' GTTCAGCAGTACATGTTG    35421     G    TG_  A
                              CAA ATGT   GC TGAAC
                              ||| ||||   || |||||
```

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                                GTT TACA   CG ACTTG
                                  G    TGA  _
GAM255  FLJ21603  3'  GTTCATGCCATTCTCCTG    45425    A  TGT
                                CA GA   TGGCATGAAC
                                || ||   ||||||||||
                                GT CT   ACCGTACTTG
                                 C  CTT
GAM255  FLJ22378  3'  TCATGCTGCTCTTG       46907      T  T
                                CAAGA GT GGCATGA
                                ||||| || |||||||
                                GTTCT CG TCGTACT
                                  _  _
GAM255  FLJ23519  3'  GTTCATGCCATTCTCCTG    49971    A  TGT
                                CA GA   TGGCATGAAC
                                || ||   ||||||||||
                                GT CT   ACCGTACTTG
                                 C  CTT
GAM255  FLJ31709  3'  TTCCTGATACATTTTGGTT    58274          TGG  T
                                AACCAAGATGT   CA GAA
                                ||||||||||   || |||
                                TTGGTTTTACA   GT CTT
                                      TA_  C
GAM255  HARC      5'  TTCACGCCAAGTCTGTTGG    35485     __   G    A
                                CCA  AGAT TTGGC TGAA
                                |||  |||| ||||| ||||
                                GGT  TCTG AACCG ACTT
                                  TG   _    C
GAM255  HEMK      3'  TCCTGCCAATACCTTG      32441      A       T
                                CAAG TGTTGGCA GA
                                |||| |||||||| ||
                                GTTC ATAACCGT CT
                                  C       C
GAM255  HEYL      3'  TCTTTCAGCATCTTGGTT    27400           CAT
                                AACCAAGATGTTGG   GA
                                ||||||||||||||   ||
                                TTGGTTCTACGACT   CT
                                       TT_
GAM255  HSA6591   3'  TTCATGTCACCTTGAGTT    72874     _   ATGT
                                AAC CAAG    TGGCATGAA
                                ||| ||||    |||||||||
                                TTG GTTC    ACTGTACTT
                                  A   C___
GAM255  HSU53209  3'  GTTAAACATCTTGAGT      25240    _       _
                                AC CAAGATGTT GGC
                                || |||||||| |||
                                TG GTTCTACAA TTG
                                 A        A
GAM255  HTCD37    3'  GTTCATGGCGTGTTG       67678     G   TGG
                                CAA ATGT   CATGAAC
                                ||| ||||   |||||||
```

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                                GTT TGCG   GTACTTG
                                  G   ___
GAM255  HYPK     3'  GTTCATAGGCCACCTTGAGTT  33079    _   ATGT   __
                                AAC CAAG   TGGC  ATGAAC
                                ||| ||||   ||||  ||||||
                                TTG GTTC   ACCG  TACTTG
                                  A   C___   GA
GAM255  KIAA0265 3'  GCCCAGCAACTCTTGGTT    69880       __    _
                                AACCAAGA  TGTTGG C
                                ||||||||  ||||||  |
                                TTGGTTCT  ACGACC G
                                     CA     C
GAM255  KIAA0349 3'  TTCATGTTTATTTTGG     92311       TT
                                CCAAGATG  GGCATGAA
                                ||||||||  ||||||||
                                GGTTTTAT  TTGTACTT

                                     __
GAM255  KIAA0438 3'  TCATAACCTCTTGGTT     29072       T   GGC
                                AACCAAGA GTT   ATGA
                                ||||||||  |||   ||||
                                TTGGTTCT CAA   TACT
                                     C   ___
GAM255  KIAA0649 3'  GTTCATGTCCAATCTTG     29051      GTT
                                CAAGAT   GGCATGAAC
                                ||||||   |||||||||
                                GTTCTA   CTGTACTTG
                                   AC_
GAM255  KIAA0716 3'  CATGTTCATGTTGGTT     28164      G   TT
                                AACCAA ATG  GGCATG
                                ||||||  |||  ||||||
                                TTGGTT TAC  TTGTAC
                                   G   __
GAM255  KIAA0888 3'  GTTCATGAAGATATTTTGGTT  63232          GG
                                AACCAAGATGTT  CATGAAC
                                ||||||||||||  |||||||
                                TTGGTTTTATAG  GTACTTG
                                      AA
GAM255  KIAA1163 3'  GTTGGTGAAACCCTTGGTT   78903       AT   GG   G
                                AACCAAG  GTT  CAT AAC
                                |||||||  |||  ||| |||
                                TTGGTTC  CAA  GTG TTG
                                   C_   A_   G
GAM255  KIAA1323 5'  GTTTGTGGAACATCTTGG    63046        GG  TG
                                CCAAGATGTT  CA  AAC
                                ||||||||||  ||  |||
                                GGTTCTACAA  GT  TTG
                                      G_  GT
GAM255  KIAA1405 3'  CATGCCCACCAGTGTTGGT   61038      G  __  T
                                ACCAA AT  GT GGCATG
                                |||||  ||  ||  ||||||
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                                TGGTT TG  CA CCGTAC
                                   G  AC  C
GAM255  KIAA1409 3'  TCAGTGTCAACACTCTGGTT  61217      A _      _
                                AACCA GA TGTTGGCA TGA
                                ||||| || |||||||| |||
                                TTGGT CT ACAACTGT ACT
                                  _ C       G
GAM255  KIAA1443 3'  GTTCATGCCATTCTCCTG    63838    A  TGT
                                CA GA   TGGCATGAAC
                                || ||   ||||||||||
                                GT CT   ACCGTACTTG
                                 C  CTT
GAM255  KIAA1600 3'  TTCATAGCTTTTTGGTT     71448        TGTT  _
                                AACCAAGA    GGC ATGAA
                                ||||||||    ||| |||||
                                TTGGTTTT    TCG TACTT
                                    ____  A
GAM255  KIAA1613 3'  TCATGCCATCTTGG       64818       TGT
                                CCAAGA   TGGCATGA
                                ||||||   ||||||||
                                GGTTCT   ACCGTACT
                                   ___
GAM255  KIAA1822 3'  CAGCACAGATATCTTGGTT   67561          _ _  A
                                AACCAAGATGT TG GC TG
                                |||||||||||  || || ||
                                TTGGTTCTATA AC CG AC
                                      G  A  _
GAM255  KIAA1877 3'  TCTGCACATCTTGG        66179         TG   T
                                CCAAGATGT  GCA GA
                                |||||||||  ||| ||
                                GGTTCTACA  CGT CT
                                    __  _
GAM255  KR18     3'  CATGCTATGCATCTTGGTT   52742          _
                                AACCAAGATGT TGGCATG
                                |||||||||||  |||||||
                                TTGGTTCTACG ATCGTAC
                                      T
GAM255  MAL2     3'  TGTTAGATCTTGGTT       53558         G
                                AACCAAGAT TTGGCA
                                |||||||||  ||||||
                                TTGGTTCTA GATTGT
                                   _
GAM255  MDS006   3'  GTTCATGTCTATCCTG      39586    A   TT
                                CA GATG  GGCATGAAC
                                || ||||  |||||||||
                                GT CTAT  CTGTACTTG
                                 C   __
GAM255  MGC10812 3'  TCCTCTAACATCTCAGGT    48670     A_       CAT
                                ACC  AGATGTTGG   GA
                                |||  |||||||||   ||
```

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                                TGG  TCTACAATC   CT
                                  AC        TC_
GAM255  MGC11082  3'  TCCTGCCAACATCGTGG     51101     A         T
                                CCA GATGTTGGCA GA
                                ||| |||||||||| ||
                                GGT CTACAACCGT CT
                                  G         C
GAM255  MGC16142  3'  GTTCAAGGCCAGCCTGG     51294     AGAT      A_
                                CCA    GTTGGC  TGAAC
                                |||    ||||||  |||||
                                GGT    CGACCG  ACTTG
                                  C___      GA
GAM255  MGC17299  3'  GTTCATGGCTATCATGGTT    58239       A   GTT   _
                                AACCA GAT   GGC ATGAAC
                                ||||| |||   ||| ||||||
                                TTGGT CTA   TCG TACTTG
                                   A  ___  G
GAM255  MGC35558  3'  GTCCAGCCATCTTGGTT     58786          _   _
                                AACCAAGATG TTGG C
                                |||||||||| |||| |
                                TTGGTTCTAC GACC G
                                     C   T
GAM255  P1P373C6  3'  TTCATGCCAACATTGGT     38907      AG
                                ACCA  ATGTTGGCATGAA
                                ||||  ||||||||||||
                                TGGT  TACAACCGTACTT
                                  __
GAM255  p25       3'  TCATGGCTCCCATCTTGG     22856        TT  _
                                CCAAGATG  GGC ATGA
                                ||||||||  ||| ||||
                                GGTTCTAC  TCG TACT
                                    CC   G
GAM255  PAGE-5    5'  GTTCTTTCCAACATCTTCGTT  55321     C         CAT
                                AAC AAGATGTTGG   GAAC
                                ||| ||||||||||   ||||
                                TTG TTCTACAACC   CTTG
                                  C         TTT
GAM255  PP3501    5'  CAGCCACCATCTTGGTT     41368          T   A
                                AACCAAGATG TGGC TG
                                |||||||||| |||| ||
                                TTGGTTCTAC ACCG AC
                                     C   _
GAM255  PRO0132   5'  CATGTCAAATGCTTGGTT    26102        ATG
                                AACCAAG   TTGGCATG
                                |||||||   ||||||||
                                TTGGTTC   AACTGTAC
                                   GTA
GAM255  PRPF8     3'  CATGCCAAGATCATGG      61186     A   G
                                CCA GAT TTGGCATG
                                ||| ||| ||||||||
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                                GGT CTA AACCGTAC
                                  A   G
GAM255  SEC24A   3'  GTTCATGTATAATACTTG    82683     A    _
                                CAAG TGTTG GCATGAAC
                                |||| ||||| ||||||||
                                GTTC ATAAT TGTACTTG
                                  _    A
GAM255  SHAPY    3'  TTCATGTCAGCACCTGAGT   57115    CA  A
                                AC  AG TGTTGGCATGAA
                                ||  || ||||||||||||
                                TG  TC ACGACTGTACTT
                                 AG  C
GAM255  SS18L1   3'  TCATGCCAACAGTCTTTA    65349   C   _
                                C AAGA TGTTGGCATGA
                                | |||| ||||||||||
                                A TTCT ACAACCGTACT
                                 T   G
GAM255  TADA3L   3'  GTTCATGCCATTCTCCTG    55997    A  TGT
                                CA GA   TGGCATGAAC
                                || ||   ||||||||||
                                GT CT   ACCGTACTTG
                                 C  CTT
GAM255  TM4SF3   5'  TTCACGGCATCTGG       16067     A     GCA
                                CCA GATGTTG   TGAA
                                ||| |||||||   ||||
                                GGT CTACGGC   ACTT
                                  _     ____
GAM255  TOLLIP   3'  CGTGTAGCATCTTGG       38681          G
                                CCAAGATGTTG CATG
                                |||||||||||| ||||
                                GGTTCTACGAT GTGC
                                      _
GAM255  TOR2A    3'  TCATGCTGCCACTTGG      55317      A  TT
                                CCAAG TG  GGCATGA
                                ||||| ||  |||||||
                                GGTTC AC  TCGTACT
                                   _ CG
GAM255  TP53INP1 3'  TTCAGTTGAAACTCTTGGTT  52733        TG_ TG  A
                                AACCAAGA   T  GC TGAA
                                ||||||||   |  || ||||
                                TTGGTTCT   A  TG ACTT
                                     CAA GT  _
GAM255  TP53INP1 3'  TTCAGTTGAAACTCTTGGTT  72960        TG_ TG  A
                                AACCAAGA   T  GC TGAA
                                ||||||||   |  || ||||
                                TTGGTTCT   A  TG ACTT
                                     CAA GT  _
GAM255  TRAF3    3'  ATGCAACATCTTGGT       59733          G
                                ACCAAGATGTTG CAT
                                |||||||||||| |||
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                                TGGTTCTACAAC GTA
                                             _
GAM255  TUSP     3'  GTTCATGTCCAGACCTCGG   39640    A  ATG   _
                                CC AG   TTGG CATGAAC
                                || ||   |||| |||||||
                                GG TC   GACC GTACTTG
                                 C  CA_   T
GAM255  UBE3B    3'  TTCACATTGGCATCCTGGTT   76927      A     TG CA
                                AACCA GATGT  G  TGAA
                                ||||| |||||  |  ||||
                                TTGGT CTACG  T  ACTT
                                   C     GT AC
GAM255  ZNF212   3'  TTCATGCCAATGCTT      24310     A
                                AAG TGTTGGCATGAA
                                ||| ||||||||||||
                                TTC GTAACCGTACTT
                                 _
GAM255  ZNF361   5'  GTTAAACATCTTAGGT     37664     _      _
                                ACC AAGATGTT GGC
                                ||| |||||||| |||
                                TGG TTCTACAA TTG
                                  A       A
GAM255  LOC118987 3'  TCATGCCAATCGGGTT     73959      AAGAT
                                AACC     GTTGGCATGA
                                ||||     ||||||||||
                                TTGG     TAACCGTACT
                                  GC___
GAM255  LOC125194 3'  TCATGCCAACAGCTTG     74398      A
                                CAAG TGTTGGCATGA
                                |||| ||||||||||
                                GTTC ACAACCGTACT
                                  G
GAM255  LOC129450 5'  GTTCATGCAGCACCTCT    74875     __    G
                                AGA  TGTTG CATGAAC
                                |||  ||||| |||||||
                                TCT  ACGAC GTACTTG
                                  CC    _
GAM255  LOC129676 5'  GTTCACGGGCATCTTG     75735         GGCA
                                CAAGATGTT    TGAAC
                                |||||||||    |||||
                                GTTCTACGG    ACTTG
                                     GC__
GAM255  LOC143279 5'  GTTCACCTGCACATCTTG   76512        TG  __
                                CAAGATGT  GCA  TGAAC
                                ||||||||  |||  |||||
                                GTTCTACA  CGT  ACTTG
                                     __  CC
GAM255  LOC145622 3'  TCATGCCAGATACTTAGT   77314    C   ATG
                                AC AAG   TTGGCATGA
                                || |||   |||||||||
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                                TG TTC   GACCGTACT
                                 A   ATA
GAM255   LOC145748 3'  TTCATGCCAGCACATCT     83471       __
                                AGATGT  TGGCATGAA
                                ||||||  |||||||||
                                TCTACA  ACCGTACTT
                                   CG
GAM255   LOC145820 3'  TTCATGTTACGATCCTGG    77519     A   GT
                                CCA GAT  TGGCATGAA
                                ||| |||  |||||||||
                                GGT CTA  ATTGTACTT
                                  C   GC
GAM255   LOC146839 3'  GTTCATGCCATTCTCCTG    83814    A  TGT
                                CA GA   TGGCATGAAC
                                || ||   ||||||||||
                                GT CT   ACCGTACTTG
                                 C  CTT
GAM255   LOC147694 3'  GTTCATGCCATTCTCCTG    78454    A  TGT
                                CA GA   TGGCATGAAC
                                || ||   ||||||||||
                                GT CT   ACCGTACTTG
                                 C  CTT
GAM255   LOC148223 3'  TTCATGCCGAGTTGGT      78747      GATG
                                ACCAA    TTGGCATGAA
                                |||||    ||||||||||
                                TGGTT    AGCCGTACTT
                                   G___
GAM255   LOC148479 3'  GTCGGACACCTTGGTT      78877       A   _
                                AACCAAG TGTT GGC
                                ||||||| |||| |||
                                TTGGTTC ACAG CTG
                                    C   G
GAM255   LOC149386 5'  GTTCATGCGCGTCT       84408       TG
                                AGATGT  GCATGAAC
                                ||||||  ||||||||
                                TCTGCG  CGTACTTG
                                    __
GAM255   LOC149668 5'  GCCATAGCATCTTGGT      84542         __
                                ACCAAGATGT  TGGC
                                ||||||||||  ||||
                                TGGTTCTACG  ACCG
                                      AT
GAM255   LOC149711 5'  CATGCTTCTCATCTTGGTT   84677         TT_
                                AACCAAGATG   GGCATG
                                ||||||||||   ||||||
                                TTGGTTCTAC   TCGTAC
                                      TCT
GAM255   LOC151571 5'  GTTCATATAGCAACATCT    85446        GC__
                                AGATGTTG    ATGAAC
                                ||||||||    ||||||
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                                TCTACAAC   TACTTG
                                    GATA
GAM255  LOC153146 3' GTTCATTTTATCTTGG     85933       TTGGC
                                CCAAGATG   ATGAAC
                                ||||||||   ||||||
                                GGTTCTAT   TACTTG
                                    TT___
GAM255  LOC153338 3' GTTCAACGCCAGCCTGG    86001    AGAT    A_
                                CCA   GTTGGC  TGAAC
                                |||   ||||||  |||||
                                GGT   CGACCG  ACTTG
                                  C___    CA
GAM255  LOC153910 3' TTCATGTTTCTGGGTT     81001    A  TGTT
                                AACC AGA   GGCATGAA
                                |||| |||   ||||||||
                                TTGG TCT   TTGTACTT
                                  G  ____
GAM255  LOC154739 5' CATGCATCCGTGTTGGTT   86229      G  TTG
                                AACCAA ATG  GCATG
                                |||||| |||  |||||
                                TTGGTT TGC  CGTAC
                                   G  CTA
GAM255  LOC158230 3' TTCATGTTTTCTTGG      81804      TGTT
                                CCAAGA   GGCATGAA
                                ||||||   ||||||||
                                GGTTCT   TTGTACTT
                                   T___
GAM255  LOC161190 5' TCATGCCGGCGGTT       82264     AAGAT
                                AACC    GTTGGCATGA
                                ||||    ||||||||||
                                TTGG    CGGCCGTACT
                                  _____
GAM255  LOC163994 5' GTTCATGCCCAGGATCT    87050     G  _
                                AGAT TTGG CATGAAC
                                |||| |||| |||||||
                                TCTA GACC GTACTTG
                                  G   C
GAM255  LOC165552 3' TCATCCCATCTTGG       82490       TT  C
                                CCAAGATG  GG ATGA
                                ||||||||  || ||||
                                GGTTCTAC  CC TACT
                                   __  _
GAM255  LOC170082 5' GTTCATGCCATTCTCCTG   82563   A  TGT
                                CA GA   TGGCATGAAC
                                || ||   ||||||||||
                                GT CT   ACCGTACTTG
                                 C  CTT
GAM255  LOC196707 3' GTTCATGCAGGGTCCTTGG  87531     _  G  G
                                CCAAG AT TTG CATGAAC
                                ||||| || ||| |||||||
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                                GGTTC TG GAC GTACTTG
                                  C  G  _
GAM255  LOC200035 5'  CATGCCTGGGACCATCTTGG  73252       TT____
                                CCAAGATG    GGCATG
                                ||||||||    ||||||
                                GGTTCTAC    CCGTAC
                                    CAGGGT
GAM255  LOC200078 3'  CATACTCAGCATCTCGG    88570   A     _ C
                                CC AGATGTTG G ATG
                                || |||||||| | |||
                                GG TCTACGAC C TAC
                                 C       T A
GAM255  LOC201191 3'  GTTCATGTGTGGCGCTGGT   89772     A A   _
                                ACCA G TGTTG GCATGAAC
                                |||| | ||||| ||||||||
                                TGGT C GCGGT TGTACTTG
                                  _ _    G
GAM255  LOC201952 5'  GTTCATGCCGTTCATTT    90274     T_
                                AGATG  TGGCATGAAC
                                |||||  ||||||||||
                                TTTAC  GCCGTACTTG
                                   TT
GAM255  LOC203276 3'  CATGCATCCATGTTGGTT    90480      G  TTG
                                AACCAA ATG   GCATG
                                |||||| |||   |||||
                                TTGGTT TAC   CGTAC
                                   G   CTA
GAM255  LOC203305 3'  CATGCATCCATGTTGGTT    90524      G  TTG
                                AACCAA ATG   GCATG
                                |||||| |||   |||||
                                TTGGTT TAC   CGTAC
                                   G   CTA
GAM255  LOC203411 3'  TTCTTTTCAGCATCTCAGTT  90633    CA      CAT
                                AAC  AGATGTTGG   GAA
                                |||  |||||||||   |||
                                TTG  TCTACGACT   CTT
                                  AC        TTT
GAM255  LOC219735 3'  GTTCATGCCATTCTCCTG    93112    A  TGT
                                CA GA   TGGCATGAAC
                                || ||   ||||||||||
                                GT CT   ACCGTACTTG
                                 C  CTT
GAM255  LOC220776 3'  CATGCCAGGTTACGGT      68388    AA   G
                                ACC  GAT TTGGCATG
                                |||  ||| ||||||||
                                TGG  TTG GACCGTAC
                                  CA   _
GAM255  LOC221337 5'  TTCATCTTAACATCTCTGTT  92117    CA      C
                                AAC  AGATGTTGG ATGAA
                                |||  ||||||||| |||||
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                                TTG  TCTACAATT TACTT
                                  TC       C
GAM255  LOC221839 5'  TCATACCAACATTGTCGT    92497    CAA      C
                                AC   GATGTTGG ATGA
                                ||   |||||||| ||||
                                TG   TTACAACC TACT
                                 CTG       A
GAM255  LOC222224 5'  GTTCATGTCGATCCTT     94202     AT
                                AAG  GTTGGCATGAAC
                                |||  ||||||||||||
                                TTC  TAGCTGTACTTG
                                  C_
GAM255  LOC254243 3'  GTTCATGCCACTGCACTT    97417     A  __
                                AAG TGT  TGGCATGAAC
                                ||| |||  ||||||||||
                                TTC ACG  ACCGTACTTG
                                  _  TC
GAM255  LOC254243 3'  CATGCATCCATGTTGGTT    97409      G   TTG
                                AACCAA ATG   GCATG
                                |||||| |||   |||||
                                TTGGTT TAC   CGTAC
                                   G   CTA
GAM255  LOC255645 3'  GTTCATGCTTCCTCTTG     96654      TGTT
                                CAAGA    GGCATGAAC
                                |||||    |||||||||
                                GTTCT    TCGTACTTG
                                   CCT_
GAM255  LOC257160 3'  TCATGCCATGTACATTT     94852      ___
                                AGATGT   TGGCATGA
                                ||||||   ||||||||
                                TTTACA   ACCGTACT
                                   TGT
GAM255  LOC51631  3'  GTTCATGTGGGCCCCTTG    68083     AT   G
                                CAAG  GTT GCATGAAC
                                ||||  ||| ||||||||
                                GTTC  CGG TGTACTTG
                                  CC   G
GAM255  LOC51725  3'  CAGGGCTCATTTTGGTT     69864        TT   A_
                                AACCAAGATG  GGC  TG
                                ||||||||||  |||  ||
                                TTGGTTTTAC  TCG  AC
                                      __  GG
GAM255  LOC57099  3'  GCCTGAAGCAAATCTTGGTT   39806       __   ___
                                AACCAAGA  TGTT   GGC
                                ||||||||  ||||   |||
                                TTGGTTCT  ACGA   CCG
                                     AA    AGT
GAM255  LOC90038  3'  CATGCATCCATGTTGGTT    61153      G   TTG
                                AACCAA ATG   GCATG
                                |||||| |||   |||||
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                                TTGGTT TAC   CGTAC
                                   G   CTA
GAM255  LOC90333  3'  GTTCATGCCTTGCATTT     62295       T_
                                AGATGT  GGCATGAAC
                                ||||||  |||||||||
                                TTTACG  CCGTACTTG
                                   TT
GAM255  LOC90362  5'  GTTCATGCAATTTCCTG     62444    A  T    G
                                CA GA GTTG CATGAAC
                                || || |||| |||||||
                                GT CT TAAC GTACTTG
                                 C  T   _
GAM255  LOC91893  3'  GTTCATGCCATTCTCCTG    67462    A  TGT
                                CA GA   TGGCATGAAC
                                || ||   ||||||||||
                                GT CT   ACCGTACTTG
                                 C  CTT
GAM256  G2        3'  CTCTTCAACAATGATGTC    66659    G     A
                                GA ATCATT TTGAAGAG
                                || |||||| ||||||||
                                CT TAGTAA AACTTCTC
                                 G     C
GAM256  MYH10     3'  GTCGCTCTGCATGCTCTC    69142     T   TATTGA
                                GAGA CAT     AGAGCGAC
                                |||| |||     ||||||||
                                CTCT GTA     TCTCGCTG
                                  C   CG____
GAM256  TOR2A     3'  CGGGGCCAATAATGAT      55313         AAGA  GA
                                ATCATTATTG   GC  CCG
                                ||||||||||   ||  |||
                                TAGTAATAAC   CG  GGC
                                     ____  G_
GAM256  LOC124145 3'  GTCGCTCTTCCCCCAATCT   74255     CATTATT
                                AGAT      GAAGAGCGAC
                                ||||      ||||||||||
                                TCTA      CTTCTCGCTG
                                  ACCCC__
GAM256  LOC91442  5'  GCCACCAGTAACATGATCTC  66050         __    AAGA
                                GAGATCAT  TATTG   GC
                                ||||||||  |||||   ||
                                CTCTAGTA  ATGAC   CG
                                    CA    CAC_
GAM257  A1BG      3'  CAGGGTCTCACTGTGTTGC   55413        TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM257  ACPT      3'  CACCCCGCCATATGCTGC    54980     ACA      TTT
                                GCA   CATATGGC   GTG
                                |||   ||||||||   |||
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                                CGT   GTATACCG   CAC
                                  C__       CCC
GAM257  ACPT     3'  CACCCCGCCATATGCTGC    54986     ACA       TTT
                                GCA   CATATGGC   GTG
                                |||   ||||||||   |||
                                CGT   GTATACCG   CAC
                                  C__       CCC
GAM257  AHCY     3'  CACAAAGCCCATGTGTTTTGC  5473       C       _
                                GCAA ACATATGG CTTTGTG
                                |||| |||||||| |||||||
                                CGTT TGTGTACC GAAACAC
                                  T       C
GAM257  BCL7A    3'  CAGGATTCCATTTGTGTTGCT  40638          T    CT  G
                                AGCAACACA ATGG  TT TG
                                ||||||||| ||||  || ||
                                TCGTTGTGT TACC  AG AC
                                      T    TT  G
GAM257  CDK5R2   3'  CACAAAGCCACCGCCGCTGTT  14132      ACACATA
                                AGCA      TGGCTTTGTG
                                ||||      ||||||||||
                                TTGT      ACCGAAACAC
                                  CGCCGCC
GAM257  CHC1     3'  CACAAAGCATACTCTTGC    7019       CACA    G
                                GCAA    TATG CTTTGTG
                                ||||    |||| |||||||
                                CGTT    ATAC GAAACAC
                                  CTC_   _
GAM257  CIT      3'  CACAAGGCATCTGTTGCT    69741        CATATG
                                AGCAACA     GCTTTGTG
                                |||||||     ||||||||
                                TCGTTGT     CGGAACAC
                                    CTA___
GAM257  COL6A2   5'  CAGGGCCACAGGTGCTGC    8480      A   ATA
                                GCA CAC   TGGCTTTG
                                ||| |||   ||||||||
                                CGT GTG   ACCGGGAC
                                  C   GAC
GAM257  COL6A2   5'  CAGGGCCACAGGTGCTGC    54168     A   ATA
                                GCA CAC   TGGCTTTG
                                ||| |||   ||||||||
                                CGT GTG   ACCGGGAC
                                  C   GAC
GAM257  EYA1     3'  CACAGCGTTATGTGTCTGC   4952      AC       T
                                GCA  ACATATGGC TTGTG
                                |||  ||||||||| |||||
                                CGT  TGTGTATTG GACAC
                                  C_        C
GAM257  FBN2     3'  CAAGGAACCATATGTG      8844          __
                                CACATATGG  CTTTG
                                |||||||||  |||||
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                                GTGTATACC  GGAAC
                                     AA
GAM257  FMO1    3'  CACAAATGATTGTGTTGT    8924        TATGGC
                                GCAACACA    TTTGTG
                                ||||||||    ||||||
                                TGTTGTGT    AAACAC
                                    TAGT__
GAM257  GALNT2  3'  CACAAAGCCGAGTCGTGT    15593     _ A
                                ACAC AT TGGCTTTGTG
                                |||| || ||||||||||
                                TGTG TG GCCGAAACAC
                                  C  A
GAM257  GALNT2  3'  CACAAAGCCGTTCGCAGCT   15594    AACACAT
                                AGC     ATGGCTTTGTG
                                |||     ||||||||||
                                TCG     TGCCGAAACAC
                                  ACGCT__
GAM257  GPR4    3'  CAGGGTCTCACTGTGTTGC   59902       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM257  HNMT    3'  CACAAAGCCTGTGTTACT    22567    C    TAT
                                AG AACACA  GGCTTTGTG
                                || ||||||  |||||||||
                                TC TTGTGT  CCGAAACAC
                                 A    ____
GAM257  IL1RN   3'  CACAAAGCCCTTCCATGTCGC 5141    A  CATAT_
                                GC ACA     GGCTTTGTG
                                || |||     |||||||||
                                CG TGT     CCGAAACAC
                                 C  ACCTTC
GAM257  IL2RB   3'  CACAAAGTGGATGCCTGCT   6069     ACA  ATG
                                AGCA  CAT  GCTTTGTG
                                ||||  |||  ||||||||
                                TCGT  GTA  TGAAACAC
                                  CC_  GG_
GAM257  ITSN2   3'  CACAAAGCCATGCACGCT    38971    AACACA
                                AGC     TATGGCTTTGTG
                                |||     ||||||||||||
                                TCG     GTACCGAAACAC
                                  CAC____
GAM257  JRK     3'  CAGGGTCTCACTGTGTTGC   86524       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM257  LANCL1  3'  CACAATTTTATATGTATGCT  20210     AC     CT
                                AGCA  ACATATGG  TTGTG
                                ||||  ||||||||  |||||
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                                TCGT  TGTATATT  AACAC
                                  A_       TT
GAM257  LGR6    5'  GGCCATCGTGTTGCT      84200        AT
                                AGCAACAC  ATGGCT
                                ||||||||  ||||||
                                TCGTTGTG  TACCGG
                                    C_
GAM257  LRRC2    3'  CAAGGCACCATGTGTTACT   44465    C      ATG
                                AG AACACAT   GCTTTG
                                || |||||||   ||||||
                                TC TTGTGTA   CGGAAC
                                 A      CCA
GAM257  MYBL2    3'  CAGGGCCATGTGCTGC     10154     ACA
                                GCA   CATATGGCTTTG
                                |||   ||||||||||||
                                CGT   GTGTACCGGGAC
                                  C__
GAM257  OCLN     3'  CACAAAGTTTTGGTTGCT    10314       A  TAT
                                AGCAAC CA   GGCTTTGTG
                                |||||| ||   |||||||||
                                TCGTTG GT   TTGAAACAC
                                   _  T__
GAM257  OSR1     3'  CACAAAGTAATATGTG      17566        G
                                CACATAT GCTTTGTG
                                ||||||| ||||||||
                                GTGTATA TGAAACAC
                                    A
GAM257  PCDH9    5'  CACAAAGTGACAGTGCTGGCT  82794     AA_   ATATG
                                AGC   CAC    GCTTTGTG
                                |||   |||    ||||||||
                                TCG   GTG    TGAAACAC
                                  GTC   ACAG_
GAM257  PRDM2    5'  CACAAAGCCACATCCTGC    31847     ACAC  A
                                GCA    AT TGGCTTTGTG
                                |||    || ||||||||||
                                CGT    TA ACCGAAACAC
                                  CC__  C
GAM257  PRDM2    5'  CACAAAGCCACATCCTGC    24246     ACAC  A
                                GCA    AT TGGCTTTGTG
                                |||    || ||||||||||
                                CGT    TA ACCGAAACAC
                                  CC__  C
GAM257  PRG4     3'  CACAAAGCTTTATCGTGTTGT  19415        _   T
                                GCAACAC ATA GGCTTTGTG
                                ||||||| ||| |||||||||
                                TGTTGTG TAT TCGAAACAC
                                    C   T
GAM257  RXRB     3'  CACAAAGCACTGGCCTTGC    41757      CA_  TATG
                                GCAA   CA    GCTTTGTG
                                ||||   ||    ||||||||
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                                CGTT  GT   CGAAACAC
                                  CCG CA__
GAM257  SMARCD1  3'  CACAAAGTTCCCATGTG    11811       ___
                                CATATGG  CTTTGTG
                                |||||||  |||||||
                                GTGTACC  GAAACAC
                                   CTT
GAM257  SMARCD1  3'  CACAAAGTTCCCATGTG    57429       ___
                                CATATGG  CTTTGTG
                                |||||||  |||||||
                                GTGTACC  GAAACAC
                                   CTT
GAM257  SMURF1   3'  CACGTGTGATCTGTGTTGC  92448        T  G  TT
                                GCAACACA AT GC  TGTG
                                |||||||| || ||  ||||
                                CGTTGTGT TA TG  GCAC
                                     C  G  T_
GAM257  STX7     3'  CACCAAGATGTGTGTTACT   13108   C      GG   T
                                AG AACACATAT  CTT GTG
                                || |||||||||  ||| |||
                                TC TTGTGTGTA  GAA CAC
                                 A       __  C
GAM257  TAF4B    3'  CACAAAGCATTGTTGC     87167      CATATG
                                GCAACA     GCTTTGTG
                                ||||||     ||||||||
                                CGTTGT     CGAAACAC
                                   TA____
GAM257  TF       3'  CACAGCTCTGTGTTGC     6512        TAT   T
                                GCAACACA   GGCT TG
                                ||||||||   |||| ||
                                CGTTGTGT   TCGA AC
                                     C__   C
GAM257  TLR4     5'  CACAGGGCCACTGCTGCT    12317     A  CATA
                                AGCA CA    TGGCTTTGTG
                                |||| ||    ||||||||||
                                TCGT GT    ACCGGGACAC
                                  C  C___
GAM257  TLR4     5'  CACAGGGCCACTGCTGCT    56736     A  CATA
                                AGCA CA    TGGCTTTGTG
                                |||| ||    ||||||||||
                                TCGT GT    ACCGGGACAC
                                  C  C___
GAM257  TLR4     5'  CACAGGGCCACTGCTGCT    56732     A  CATA
                                AGCA CA    TGGCTTTGTG
                                |||| ||    ||||||||||
                                TCGT GT    ACCGGGACAC
                                  C  C___
GAM257  TLR4     5'  CACAGGGCCACTGCTGCT    56727     A  CATA
                                AGCA CA    TGGCTTTGTG
                                |||| ||    ||||||||||
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                                TCGT GT   ACCGGGACAC
                                  C  C___
GAM257  VIPR2    3' CACAGTCTCCATGTGTGTGC  12605    A      CT_
                                GCA CACATATGG  TTGTG
                                ||| |||||||||  |||||
                                CGT GTGTGTACC  GACAC
                                  _      TCT
GAM257  ANKT     3' CAGGGTCTCACTGTGTTGC   33024      TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM257  ATP9A    3' CACAAAGCCAGTGGCTGTT   62039    A_  ATA
                                AGCA  CAC  TGGCTTTGTG
                                ||||  |||  ||||||||||
                                TTGT  GTG  ACCGAAACAC
                                  CG  ___
GAM257  CETN2    3' CACATGTTACACCTGTGTTGC 15093      TA  GCTT_
                                GCAACACA TG   TGTG
                                |||||||| ||   ||||
                                CGTTGTGT AC   ACAC
                                    CC  ATTGT
GAM257  CYLD     3' CACAAGGTTTTATACTGCT   30883    ACAC  TG
                                AGCA   ATA  GCTTTGTG
                                ||||   |||  ||||||||
                                TCGT   TAT  TGGAACAC
                                  CA__   TT
GAM257  DKFZP586A0522 3' CAGGGTCTCACTGTGTTGC  25871      TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM257  DKFZp762K222 3' ACAGATGCGTGTTGCT     71116      ATATG  _
                                AGCAACAC    GC TTTGT
                                ||||||||    || |||||
                                TCGTTGTG    CG AGACA
                                    _____  T
GAM257  FLJ10297  3' CAGGGCTTCACTGTGTTGC  35979      TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   TCGGGAC
                                    CACT
GAM257  FLJ10511  3' CACATGTGTATGTGCAGCT  36204    AA     G TT
                                AGC  CACATATG C  TGTG
                                |||  |||||||| |  ||||
                                TCG  GTGTATGT G  ACAC
                                  AC      _ T_
GAM257  FLJ11029  5' CACTAGCACCTGTGTTGCT  60973      TATG  TT
                                AGCAACACA   GCT  GTG
                                |||||||||   |||  |||
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                                TCGTTGTGT   CGA  CAC
                                     CCA_   T_
GAM257  FLJ11117  3'  CACAAAGCTTGTATGTG     37073        _
                                CACATATG GCTTTGTG
                                |||||||| ||||||||
                                GTGTATGT CGAAACAC
                                     T
GAM257  FLJ11715  3'  CAGGGTCTCCATATGTTGC   44668      C  AT_
                                GCAACA AT   GGCTTTG
                                |||||| ||   |||||||
                                CGTTGT TA   CTGGGAC
                                   A  CCT
GAM257  FLJ20275  3'  CACAAAGGGCTTTATGTGTCAG 34819    A_     T   __
           CT                     AGC  ACACATA GGCT  TTGTG
                                |||  ||||||| ||||  |||||
                                TCG  TGTGTAT TCGG  AACAC
                                  AC      T   GA
GAM257  FLJ20413  3'  CAGAGCCGCATGCACTGCT   35131     ACA   A
                                AGCA   CAT TGGCTTTG
                                ||||   ||| ||||||||
                                TCGT   GTA GCCGAGAC
                                  CAC   C
GAM257  FLJ20450  3'  CACCTGGGACCTGTGTTGCT   35192        TAT  _   T_
                                AGCAACACA   GG CTT  GTG
                                |||||||||   || |||  |||
                                TCGTTGTGT   CC GGG  CAC
                                     ___  A   TC
GAM257  FLJ20671  3'  CAATTCAAATGTGTTGC     35516        A   CT
                                GCAACACAT TGG  TTG
                                ||||||||| |||  |||
                                CGTTGTGTA ACT  AAC
                                     A   T_
GAM257  FLJ23598  3'  CACAAAGAGAGGCTGTGCTGC  45521     A    TATGG_
                                GCA CACA     CTTTGTG
                                ||| ||||     |||||||
                                CGT GTGT     GAAACAC
                                  C    CGGAGA
GAM257  FRSB      3'  CATAGGCCATACATGTTACT   19090    C    CA      T
                                AG AACA  TATGGCTT GTG
                                || ||||  |||||||| |||
                                TC TTGT  ATACCGGA TAC
                                 A    AC      _
GAM257  H2AV      3'  CACAGCCATATGTATTGTT    56845      C        T
                                AGCAA ACATATGGCT TG
                                ||||| |||||||||| ||
                                TTGTT TGTATACCGA AC
                                   A        C
GAM257  HIC2      3'  CACAAAGTCTGTACCGC     65256    AAC   TAT
                                GC   ACA   GGCTTTGTG
                                ||   |||   |||||||||
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                              CG  TGT  CTGAAACAC
                               CCA  ___
GAM257  KIAA0140 3' CACATGGCCATGTCTTGC   27806    CAC     T
                              GCAA  ATATGGCT TGTG
                              ||||  |||||||| ||||
                              CGTT  TGTACCGG ACAC
                                C__      T
GAM257  KIAA0215 3' CAAATTCCATATGTAATGC  28416    AC     C_
                              GCA  ACATATGG  TTTG
                              |||  ||||||||  ||||
                              CGT  TGTATACC  AAAC
                                AA      TT
GAM257  KIAA0254 3' AGCCACCTGTGTTGCT     28595       TA
                              AGCAACACA  TGGCT
                              |||||||||  |||||
                              TCGTTGTGT  ACCGA
                                   CC
GAM257  KIAA0618 3' CACAAAAACATGTGTTGT   29162       TA  GC
                              GCAACACA  TG  TTTGTG
                              ||||||||  ||  ||||||
                              TGTTGTGT  AC  AAACAC
                                   __  AA
GAM257  KIAA0953 3' AGCTTTCATAGTGTTGCT   66778       A   ___
                              AGCAACAC TATG   GCT
                              |||||||| ||||   |||
                              TCGTTGTG ATAC   CGA
                                   _   TTT
GAM257  KIAA1193 3' CACAGAGCCATATACCTCGCT 67630    AACAC
                              AGC    ATATGGCTTTGTG
                              |||    ||||||||||||
                              TCG    TATACCGAGACAC
                                CTCCA
GAM257  KIAA1281 3' CACAGAGTAACAAATGTTGCT 89151      CATATG
                              AGCAACA     GCTTTGTG
                              |||||||     ||||||||
                              TCGTTGT     TGAGACAC
                                  AAACAA
GAM257  KIAA1466 5' AGCCATATGTGCGCT      71913    AA
                              AGC  CACATATGGCT
                              |||  ||||||||||
                              TCG  GTGTATACCGA
                                C_
GAM257  KIAA1821 3' CAGGGTCTCACTGTGTTGC  71780       TAT_
                              GCAACACA   GGCTTTG
                              ||||||||   |||||||
                              CGTTGTGT   CTGGGAC
                                   CACT
GAM257  KIF13B   3' CACAAAGTCCGTGGTGC    82820    A  ATAT
                              GCA CAC   GGCTTTGTG
                              ||| |||   |||||||||
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                              CGT GTG   CTGAAACAC
                                G  C___
GAM257  KIF13B   3' CACAAAGTCCGTGGTGC    30904    A  ATAT
                              GCA CAC   GGCTTTGTG
                              ||| |||   |||||||||
                              CGT GTG   CTGAAACAC
                                G  C___
GAM257  MGC12921 3' CACAAAGGCCGTTATTGC   63775    CACAT   _
                              GCAA   ATGGC TTTGTG
                              ||||   ||||| ||||||
                              CGTT   TGCCG AAACAC
                                AT___   G
GAM257  MGC14836 5' CACAAAGCTATCATCCTGC  53035    ACACAT
                              GCA    ATGGCTTTGTG
                              |||    ||||||||||
                              CGT    TATCGAAACAC
                                CCTAC_
GAM257  MGC15429 3' CACATTGTCATGTGCAGCT  51249    AACA     TT
                              AGC   CATATGGC  TGTG
                              |||   ||||||||  ||||
                              TCG   GTGTACTG  ACAC
                                AC__      TT
GAM257  MGC15875 3' CGAGGCCATAATGCT     51908    ACACA
                              AGCA   TATGGCTTTG
                              ||||   ||||||||||
                              TCGT   ATACCGGAGC
                                A____
GAM257  MGC16279 5' GAAGCCATCGTGTCGCT    51888    A   AT
                              AGC ACAC  ATGGCTTT
                              ||| ||||  ||||||||
                              TCG TGTG  TACCGAAG
                                C   C_
GAM257  MGC27434 3' CACAATAAGTATGTGTT    58947       GGCT
                              AACACATAT   TTGTG
                              |||||||||   |||||
                              TTGTGTATG   AACAC
                                   AAT_
GAM257  MGC3048  3' CACAAAGCATGAATGTT    43899    CA   G
                              AACA  TATG CTTTGTG
                              ||||  |||| |||||||
                              TTGT  GTAC GAAACAC
                                AA   _
GAM257  MIG-6    3' CACAAGCTGGCCTTGTGTTGCT 38486       TAT   ___
                              AGCAACACA  GGCT  TTGTG
                              |||||||||  ||||  |||||
                              TCGTTGTGT  CCGG  AACAC
                                   T__   TCG
GAM257  MUC17    3' CACTGCCCCATATGTGTCCCT  94271   CA      CTTT
                              AG  ACACATATGG   GTG
                              ||  ||||||||||   |||
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                                TC  TGTGTATACC   CAC
                                 CC        CCGT
GAM257  MYO3B    3'  CACTCTCCCACATGTGTTGT  57301        A   CTTT
                                GCAACACAT TGG   GTG
                                ||||||||| |||   |||
                                TGTTGTGTA ACC   CAC
                                     C   CTCT
GAM257  NS1-BP   3'  CACAAAGCTTTTGCATATTGC  72542     CA__  TAT
                                GCAA   CA   GGCTTTGTG
                                ||||   ||   |||||||||
                                CGTT   GT   TCGAAACAC
                                  ATAC  TT_
GAM257  OR51E2   3'  CACAGGTTTTATGTGTTCT   47791    C      TG   T
                                AG AACACATA  GCTT GTG
                                || ||||||||  |||| |||
                                TC TTGTGTAT  TGGA CAC
                                 _       TT   _
GAM257  PRDM11   3'  CAGGTGCTCCATGTGTTGC   39581        AT  _
                                GCAACACAT  GGC TTTG
                                |||||||||  ||| ||||
                                CGTTGTGTA  TCG GGAC
                                     CC   T
GAM257  PRO0943  5'  CACAAAAGTGTTATATGTG   37701         ___
                                CACATATGGC   TTTGTG
                                ||||||||||   ||||||
                                GTGTATATTG   AAACAC
                                      TGA
GAM257  SULT1C2  5'  CACAACGCAGCCATATGCTG  21674    _      ___
                                CA CATATGGCT   TTGTG
                                || |||||||||   |||||
                                GT GTATACCGA   AACAC
                                 C        CGC
GAM257  VEST1    3'  CACCTGCCATACATGTTGT   53685      CA     TTT
                                GCAACA  TATGGC   GTG
                                ||||||  ||||||   |||
                                TGTTGT  ATACCG   CAC
                                   AC     TC_
GAM257  ZFP100   3'  AGTCACCTGTGTTGCT     70049        TA
                                AGCAACACA  TGGCT
                                |||||||||  |||||
                                TCGTTGTGT  ACTGA
                                     CC
GAM257  ZNF363   5'  AGCCATATTGTCGCT      73452     A  C
                                AGC ACA ATATGGCT
                                ||| ||| ||||||||
                                TCG TGT TATACCGA
                                  C  _
GAM257  LOC118611 5'  CACAGAGCATTTGCGTTACT  75469    C   A  TATG
                                AG AAC CA    GCTTTGTG
                                || ||| ||    ||||||||
```

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                                TC TTG GT    CGAGACAC
                                 A   C  TTA_
GAM257   LOC120526 3'  CAGGGCCATTGCACTGCT    74015      ACA  T
                                AGCA   CA ATGGCTTTG
                                ||||   || |||||||||
                                TCGT   GT TACCGGGAC
                                  CAC  _
GAM257   LOC126669 3'  CACAAAGTTCCATATGT     75399         __
                                ACATATGG  CTTTGTG
                                ||||||||  |||||||
                                TGTATACC  GAAACAC
                                     TT
GAM257   LOC139840 5'  CACAAGAGCCATGGGT      76266    A        _
                                AC TATGGCTTT GTG
                                || |||||||| |||
                                TG GTACCGAGA CAC
                                 G        A
GAM257   LOC143465 5'  CACATGCACATATGTG      82962         _  TT
                                CACATATG GC  TGTG
                                |||||||| ||  ||||
                                GTGTATAC CG  ACAC
                                     A  T_
GAM257   LOC146774 3'  CACTGACATGTGTGTGC     78094     A       GCTTT
                                GCA CACATATG    GTG
                                ||| ||||||||    |||
                                CGT GTGTGTAC    CAC
                                  _       AGT__
GAM257   LOC147407 5'  CACAAAGCTATCATCCTGC    76322     ACACAT
                                GCA     ATGGCTTTGTG
                                |||     ||||||||||
                                CGT     TATCGAAACAC
                                  CCTAC_
GAM257   LOC151057 3'  ACAGAGCACATACTGT      85199     _   _
                                ACA TATG GCTTTGT
                                ||| |||| |||||||
                                TGT ATAC CGAGACA
                                  C    A
GAM257   LOC151473 3'  CACAACAACCTATGTGTT     80254        T  CT_
                                AACACATA GG   TTGTG
                                |||||||| ||   |||||
                                TTGTGTAT CC   AACAC
                                     _ AAC
GAM257   LOC154739 5'  CACAAAGTTCAAATGTATGC   86227     AC    A  _
                                GCA  ACAT TGG CTTTGTG
                                |||  |||| ||| |||||||
                                CGT  TGTA ACT GAAACAC
                                  A_   A  T
GAM257   LOC157507 5'  CACAGCTGTGTATGTGTGCT   81454      A      __    T
                                AGCA CACATAT  GGCT TG
                                |||| |||||||  |||| ||
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                                TCGT GTGTATG  TCGA AC
                                  _     TG   C
GAM257  LOC161734 3'  CACAAACATTTAGTGTTGCT  87097       AT_  GC
                                AGCAACAC  ATG  TTTGTG
                                ||||||||  |||  ||||||
                                TCGTTGTG  TAC  AAACAC
                                    ATT  __
GAM257  LOC196410 3'  CACAAAAGTCATGGTG     87657    A      _
                                CAC TATGGCTTT GTG
                                ||| ||||||||| |||
                                GTG GTACTGAAA CAC
                                  _       A
GAM257  LOC196485 3'  CACAAAAACCTGTGTTGT    87730       TAT  C_
                                GCAACACA  GG  TTTGTG
                                ||||||||  ||  ||||||
                                TGTTGTGT  CC  AAACAC
                                    ___  AA
GAM257  LOC196529 3'  CAGGGTCTCACTGTGTTGC   87771       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM257  LOC197003 5'  CACAAAGCTCCATGCTGT    87870    _  AT
                                ACA CAT  GGCTTTGTG
                                ||| |||  |||||||||
                                TGT GTA  TCGAAACAC
                                  C   CC
GAM257  LOC202025 5'  CACAGTTGTATGGTTGCT    90281      A   TG  T
                                AGCAAC CATA  GCT TG
                                |||||| ||||  ||| ||
                                TCGTTG GTAT  TGA AC
                                   _   GT   C
GAM257  LOC203276 3'  CACAAAGTTCAAGTGTATGC  90475    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM257  LOC203292 3'  CAGGGTTTCATATGTGTT    90509        __
                                AACACATATG  GCTTTG
                                ||||||||||  ||||||
                                TTGTGTATAC  TGGGAC
                                     TT
GAM257  LOC203305 3'  CACAAAGTTCAAGTGTATGC  90519    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM257  LOC221354 3'  CACAAAAACATGTGTTGT    92409       TA  GC
                                GCAACACA  TG  TTTGTG
                                ||||||||  ||  ||||||
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                                TGTTGTGT  AC  AAACAC
                                    __  AA
GAM257  LOC254243 3'  CACAAAGTTCAAGTGTATGC  97404    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM257  LOC255870 3'  CACAACTGGCCATGTCCTGC  94657    ACAC     __
                                GCA   ATATGGCT  TTGTG
                                |||   ||||||||  |||||
                                CGT   TGTACCGG  AACAC
                                  CC__      TC
GAM257  LOC90038  3'  CACAAAGTTCAAGTGTATGC  61148    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM257  LOC90321  3'  CACAAATGGATTGTGTGTGC  62262    A    TGGC_
                                GCA CACATA    TTTGTG
                                ||| ||||||    ||||||
                                CGT GTGTGT    AAACAC
                                  _    TAGGT
GAM257  LOC90750  3'  CACAAAGTTAAGATTGCT   63917     CACATA
                                AGCAA    TGGCTTTGTG
                                |||||    ||||||||||
                                TCGTT    ATTGAAACAC
                                   AGA___
GAM257  LOC91069  3'  GAAGCCATCGTGTCACT    64778   CA   AT
                                AG  ACAC  ATGGCTTT
                                ||  ||||  ||||||||
                                TC  TGTG  TACCGAAG
                                 AC   C_
GAM257  LOC92539  3'  CACAAAGCCACTGTAGC    69630   A  CATA
                                GC ACA   TGGCTTTGTG
                                || |||   ||||||||||
                                CG TGT   ACCGAAACAC
                                 A  C___
GAM258  CNGA1    3'  CAACTGATAATGTGCAAA   59507        GC  A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                      A_  _
GAM258  ESRRG    3'  TGGCAGTCTTATGTGCAAA  66396       TAGCT
                                TTTGCACAT   AGATTGCCA
                                |||||||||   |||||||||
                                AAACGTGTA   TCTGACGGT
                                     T____
GAM258  KCNJ3    3'  GCAATAATGTGCAAA     9525         GCTAGA
                                TTTGCACATTA    TTGC
                                ||||||||||    ||||
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                                AAACGTGTAAT     AACG
                                        _______
GAM258  SDC2     3'  GCAAATTAATGTGTAAA     67132          CTAGA
                                TTTGCACATTAG     TTGC
                                ||||||||||||    ||||
                                AAATGTGTAATT    AACG
                                      A_____
GAM258  USP9X    3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
              A                  TTTGCACATTAGC     GCCAT
                                ||||||||||||||     |||||
                                AAATGTGTAATCG     CGGTA
                                       TAGTC_
GAM258  AMOTL1   3'  GGCAAGTAATGTGCAAA     73650          G  AGAT
                                TTTGCACATTA CT    TGCC
                                |||||||||||| ||    ||||
                                AAACGTGTAAT GA    ACGG
                                        _ _____
GAM258  BCAR3    3'  AGTAATAATGTGCAAA      13098          __
                                TTTGCACATTA  GCT
                                ||||||||||  |||
                                AAACGTGTAAT  TGA
                                      AA
GAM258  DKFZP434B044 3'  TGACAATTAAATGTGCAGA    48930          AGCTA    C
                                TTTGCACATT     GATTG CA
                                |||||||||     ||||| ||
                                AGACGTGTAA     TTAAC GT
                                      A_____     A
GAM258  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                TTTGCACATTAG  AGA TG CAT
                                ||||||||||||  ||| || |||
                                AGACGTGTAATC  TTT AC GTA
                                       __  T  A
GAM258  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
              AA                   TTTGCACATTAGCTAGATTGCCAT
                                ||||||||||||||||||||||||||||
                                AAACGTGTAATCGATCTAACGGTA

GAM259  ACCN2    3'  ACATCCCTCTGAGAAG      39165          T
                                CTTCTCAGA GGATGT
                                |||||||| ||||||
                                GAAGAGTCT CCTACA
                                      C
GAM259  CDKN1A   3'  AATTCTTTTTCATTTGAGAAGT 54290            TGTT
              A                   TACTTCTCAGATGGA    GAATT
                                ||||||||||||||    |||||
                                ATGAAGAGTTTACTT    CTTAA
                                       TTT_
GAM259  CUL3     3'  AATTCAGCCCCTCTGAAAAG   13158     C    T  AT
                                CTT TCAGA GG  GTTGAATT
                                ||| ||||| ||  ||||||||
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                                GAA AGTCT CC  CGACTTAA
                                  A    _ C_
GAM259  CARHSP1  3'  TCTCACCATCTGAAGAG    26708    TC      A  TT
                                CT  TCAGATGG TG  GA
                                ||  |||||||| ||  ||
                                GA  AGTCTACC AC  CT
                                 GA       _  T_
GAM259  CDC14A   3'  AATTCAGATGACATTTGAGAAG 13390           GATG
           TA                    TACTTCTCAGATG    TTGAATT
                                ||||||||||||    |||||||
                                ATGAAGAGTTTAC    GACTTAA
                                       AGTA
GAM259  FLJ14356 5'  ATTCAAGATCTGAGAA      48030         TGGA G
                                TTCTCAGA    T TTGAAT
                                ||||||||    | ||||||
                                AAGAGTCT    A AACTTA
                                     ____ G
GAM259  KIAA0976 3'  AGCATCCATCTAAAAAG     29885     CTC
                                CTT   AGATGGATGTT
                                |||   ||||||||||
                                GAA   TCTACCTACGA
                                  AAA
GAM259  KIAA1301 3'  AACTCCATCACTTGAGAAGTA  66338         ___     T
                                TACTTCTCA   GATGGA GTT
                                |||||||||   |||||| |||
                                ATGAAGAGT   CTACCT CAA
                                      TCA     _
GAM259  KIAA1655 5'  AACGTCTACCTGAAAAG     66583     C    A
                                CTT TCAG TGGATGTT
                                ||| |||| ||||||||
                                GAA AGTC ATCTGCAA
                                  A    C
GAM259  POLE3    3'  TCAGAGCATCTGAGTAG     33859    T       GATG
                                CT CTCAGATG    TTGA
                                || ||||||||    ||||
                                GA GAGTCTAC    GACT
                                 T       GA__
GAM259  RAB40B   3'  AATTCAATGGAATTTGAGAAG  22374          GGA
                                CTTCTCAGAT   TGTTGAATT
                                ||||||||||   |||||||||
                                GAAGAGTTTA   GTAACTTAA
                                      AG_
GAM259  ROBO2    3'  TTGACCCATCTGAGAA      62489          AT  TG
                                TTCTCAGATGG  GT  A
                                ||||||||||  ||  |
                                AAGAGTCTACC  CA  T
                                      __ GT
GAM259  RoXaN    3'  AATGAGACTCCATCTGA     46626         T   GA
                                TCAGATGGA GTT  ATT
                                ||||||||| |||  |||
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                                AGTCTACCT CAG  TAA
                                    _  AG
GAM259  TCL6    5'  AATGGCCATCTGAGAA     40121          AT
                                TTCTCAGATGG  GTT
                                ||||||||||  |||
                                AAGAGTCTACC  TAA
                                    GG
GAM259  TCL6    5'  AATGGCCATCTGAGAA     40153          AT
                                TTCTCAGATGG  GTT
                                ||||||||||  |||
                                AAGAGTCTACC  TAA
                                    GG
GAM259  LOC203536 3'  GGCATCCAAGAAGTA      89380        CAGA
                                TACTTCT   TGGATGTT
                                |||||||   ||||||||
                                ATGAAGA   ACCTACGG

                                ____
GAM259  LOC56906  3'  ATTCTACATTTGAGAA      39314         GATGTT
                                TTCTCAGATG    GAAT
                                ||||||||||    ||||
                                AAGAGTTTAC    CTTA
                                    AT____
GAM260  A1BG    3'  CCATCTGACATCTGATGCCT   55414       GT    CTTCT
                                GGGCATT  ATGTTG   GTGG
                                |||||||  ||||||   ||||
                                TCCGTAG  TACAGT   TACC
                                   TC    C____   G
GAM260  ABCB4   5'  GAGAAACATATGGTGTCC    38141       TG    G
                                GGGCAT  TATGTT CTT
                                ||||||  |||||| |||
                                CCTGTG  ATACAA GAG
                                   GT    A
GAM260  ABCB4   5'  TACTCCAGCATGCAGT      38144         CTTCT
                                ATTGTATGTTG   GTG
                                ||||||||||    |||
                                TGACGTACGAC   CAT
                                    CT___
GAM260  ABCB4   5'  GAGAAACATATGGTGTCC    4792        TG    G
                                GGGCAT  TATGTT CTT
                                ||||||  |||||| |||
                                CCTGTG  ATACAA GAG
                                   GT    A
GAM260  ABCB4   5'  TACTCCAGCATGCAGT      4795          CTTCT
                                ATTGTATGTTG   GTG
                                ||||||||||    |||
                                TGACGTACGAC   CAT
                                    CT___
GAM260  ABCB9   3'  CCACGGAGGCCCCCAGCTGCCC 39033      _  TATGTT
                                GGGCA TTG    GCTTCTGTGG
                                ||||| |||    ||||||||||
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                                CCCGT GAC     CGGAGGCACC
                                  C  CCC___
GAM260  ABCC3    3'  TCGTGGGGAACTGCGTGGTGCT 39143      TG AT_  G  TC  TGG
           C                     GGGCAT  T   GTT CT  TG
                                 ||||||  |   ||| ||  ||
                                 CTCGTG  G   CAA GG  GC
                                   GT CGT   G  GT  T
GAM260  ABCC3    3'  TCGTGGGGAACTGCGTGGTGCT 39162      TG AT_  G  TC  TGG
           C                     GGGCAT  T   GTT CT  TG
                                 ||||||  |   ||| ||  ||
                                 CTCGTG  G   CAA GG  GC
                                   GT CGT   G  GT  T
GAM260  ABCD4    3'  CTGCAGCCGAAGTACGCAGTGC 39737       ATGT    ___  TG
           TT                    GGCATTGT   TGCTTC  TG  G
                                 ||||||||   ||||||  ||  |
                                 TCGTGACG   ATGAAG  AC  C
                                    C___     CCG  GT
GAM260  ABL1     3'  CAGCACATGCGGGCTC     17674     A     T  TCT
                                 GGGC TTGTATGT GCT   G
                                 |||| |||||||| |||   |
                                 CTCG GGCGTACA CGA   C
                                   _      _  ___
GAM260  ABL1     3'  CAGCACATGCGGGCTC     23611     A     T  TCT
                                 GGGC TTGTATGT GCT   G
                                 |||| |||||||| |||   |
                                 CTCG GGCGTACA CGA   C
                                   _      _  ___
GAM260  ACPT     3'  TGGACCCCAACATGTATGCTC  52350     TGT    CT_
                                 GGGCAT  ATGTTG  TCTG
                                 ||||||  ||||||  ||||
                                 CTCGTA  TACAAC  AGGT
                                    TG_    CCC
GAM260  ACPT     3'  TGGACCCCAACATGTATGCTC  54984     TGT    CT_
                                 GGGCAT  ATGTTG  TCTG
                                 ||||||  ||||||  ||||
                                 CTCGTA  TACAAC  AGGT
                                    TG_    CCC
GAM260  ACPT     3'  TGGACCCCAACATGTATGCTC  54991     TGT    CT_
                                 GGGCAT  ATGTTG  TCTG
                                 ||||||  ||||||  ||||
                                 CTCGTA  TACAAC  AGGT
                                    TG_    CCC
GAM260  ACPT     3'  TGGACCCCAACATGTATGCTC  54993     TGT    CT_
                                 GGGCAT  ATGTTG  TCTG
                                 ||||||  ||||||  ||||
                                 CTCGTA  TACAAC  AGGT
                                    TG_    CCC
GAM260  ACTN2    3'  TTGCGGAAGCTTTACATATGTT 6596      _   TGTT     TG
           T                     GGGCAT TGTA   GCTTCTG  G
                                 |||||| ||||   |||||||  |
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                                TTTGTA ACAT   CGAAGGC  T
                                   T   TT__     GT
GAM260  ACVRL1   3' GGGGGCAGTGGATGGTGCCC  3419       TG A GT
                                GGGCAT  T T  TGCTTCT
                                ||||||  | |  |||||||
                                CCCGTG  A G  ACGGGGG
                                   GT G TG
GAM260  ADAM11   3' CTGCGGGCCTAACATGTTGTGC 41213      TG     CT   TG
           CT                    GGGCAT  TATGTTG  TCTG  G
                                ||||||  |||||||  ||||  |
                                TCCGTG  GTACAAT  GGGC  C
                                   TT     CC   GT
GAM260  ADAM12   3' TTACAGAATTTTATGGTGC   12974     TG  TGTTGC
                                GCAT  TA     TTCTGTGG
                                ||||  ||     ||||||||
                                CGTG  AT     AAGACATT
                                  GT  TTT___
GAM260  ADAR     3' CCACGGAAGTGTGATTGGAGCC 31746     A  GT  GT
           T                     GGGC TT  AT  TGCTTCTGTGG
                                ||||  ||  ||  ||||||||||
                                TCCG AG  TA  GTGAAGGCACC
                                  _  GT  GT
GAM260  ADAR     3' CCACGGAAGTGTGATTGGAGCC 31756     A  GT  GT
           T                     GGGC TT  AT  TGCTTCTGTGG
                                ||||  ||  ||  ||||||||||
                                TCCG AG  TA  GTGAAGGCACC
                                  _  GT  GT
GAM260  ADAR     3' CCACGGAAGTGTGATTGGAGCC 6621      A  GT  GT
           T                     GGGC TT  AT  TGCTTCTGTGG
                                ||||  ||  ||  ||||||||||
                                TCCG AG  TA  GTGAAGGCACC
                                  _  GT  GT
GAM260  ADARB1   3' CTGCAGAGGCGTGACCCAGGCC 6632      A   TATGT      TG
           C                     GGGC TTG    TGCTTCTG  G
                                ||||  |||    ||||||||  |
                                CCCG GAC    GCGGAGAC  C
                                  _  CCAGT      GT
GAM260  ADARB1   3' CTGCAGAGGCGTGACCCAGGCC 31723     A   TATGT      TG
           C                     GGGC TTG    TGCTTCTG  G
                                ||||  |||    ||||||||  |
                                CCCG GAC    GCGGAGAC  C
                                  _  CCAGT      GT
GAM260  ADCY2    3' CGAGCAACAGTGCCC      65016       TGTA      CT
                                GGGCAT   TGTTGCTT  G
                                ||||||   ||||||||  |
                                CCCGTG   ACAACGAG  C
                                   ____      __
GAM260  ADCY6    5' CCGCGGGGGCGGCGGGGCGGGG 40615    A_   A_
           GCCC                   GGC  TTGT  TGTTGCTTCTGTGG
                                |||  ||||  ||||||||||||||
```

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                              CCG GGCG GCGGCGGGGGCGCC
                                GG  GG
GAM260 ADD2   3' CTGCAGGAGTGATGCGGCC  33930   AT AT TG   TG
                              GGC TGT GT CTTCTG G
                              ||| ||| || |||||| |
                              CCG GCG TA GAGGAC C
                                __ __ GT   GT
GAM260 ADD2   3' CTGCAGGAGTGATGCGGCC  33941   AT AT TG   TG
                              GGC TGT GT CTTCTG G
                              ||| ||| || |||||| |
                              CCG GCG TA GAGGAC C
                                __ __ GT   GT
GAM260 ADD2   3' CTGCAGGAGTGATGCGGCC  33958   AT AT TG   TG
                              GGC TGT GT CTTCTG G
                              ||| ||| || |||||| |
                              CCG GCG TA GAGGAC C
                                __ __ GT   GT
GAM260 ADH1B  3' CTACAGTAAATGGCAGTGTTT 72643      ATG   TCT
                              GGGCATTGT  TTGCT  GTGG
                              |||||||||  |||||  ||||
                              TTTGTGACG  AATGA  CATC
                                   GTA   ___
GAM260 ADORA1  3' CTACGGAGGGACCAGGTGTCT 5424      GTAT  G
                              GGGCATT   GTT CTTCTGTGG
                              |||||||   ||| |||||||||
                              TCTGTGG   CAG GGAGGCATC
                                  AC__  _
GAM260 ADRA2B  3' GCGACATGCAGGTGGTGTTT  5461      ____
                              GGGCAT   TGTATGTTGC
                              ||||||   ||||||||||
                              TTTGTG   ACGTACAGCG
                                 GTGG
GAM260 ADRBK1  3' CAGAGGGGCAGGCCC     7865     A  ATGTTG
                              GGGC TTGT    CTTCTG
                              |||| ||||    ||||||
                              CCCG GACG    GGAGAC
                                _  G_____
GAM260 AGL    3' CTATAGTATTCTTAGAATACAG 5370       GTTGCTT___
          TGCTC               CATTGTAT      CTGTGG
                              ||||||||      ||||||
                              GTGACATA      GATATC
                                   AGATTCTTAT
GAM260 AGL    3' CTATAGTATTCTTAGAATACAG 5378       GTTGCTT___
          TGCTC               CATTGTAT      CTGTGG
                              ||||||||      ||||||
                              GTGACATA      GATATC
                                   AGATTCTTAT
GAM260 AGL    5' CGCGGGTCCTGCAGTGCCC  5348        TGTTGCT
                              GGGCATTGTA    TCTGTG
                              ||||||||||    ||||||
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                              CCCGTGACGT      GGGCGC
                                   CCT____
GAM260  AGL     3' CTATAGTATTCTTAGAATACAG 5349        GTTGCTT___
           TGCTC                CATTGTAT       CTGTGG
                              ||||||||       ||||||
                              GTGACATA       GATATC
                                   AGATTCTTAT
GAM260  AGL     3' CTATAGTATTCTTAGAATACAG 5357        GTTGCTT___
           TGCTC                CATTGTAT       CTGTGG
                              ||||||||       ||||||
                              GTGACATA       GATATC
                                   AGATTCTTAT
GAM260  AGL     3' CTATAGTATTCTTAGAATACAG 5364        GTTGCTT___
           TGCTC                CATTGTAT       CTGTGG
                              ||||||||       ||||||
                              GTGACATA       GATATC
                                   AGATTCTTAT
GAM260  AGL     3' CTATAGTATTCTTAGAATACAG 3450        GTTGCTT___
           TGCTC                CATTGTAT       CTGTGG
                              ||||||||       ||||||
                              GTGACATA       GATATC
                                   AGATTCTTAT
GAM260  AGR2    3' CTATGGTGCTGTATATAATGCT 21144         TT  TT
           T                  GGGCATTGTATG  GC  CTGTGG
                              ||||||||||||  ||  ||||||
                              TTCGTAATATAT  CG  GGTATC
                                    GT  T_
GAM260  AICDA   3' CTACATTTTGTATGTGTGTGAT 40325     TG  TG _  TTC_
           GCTT                 GGCAT  TA  T TGC   TGTGG
                              |||||  ||  | |||   |||||
                              TCGTA  GT  G ATG   ACATC
                                 GT  GT T   TTTT
GAM260  AK3     5' CTGTAGGGGCGGCCGGCGAGTC 25497     A   AT       TG
           C                  GGGC TTGT  GTTGCTTCTG  G
                              |||| ||||  ||||||||||  |
                              CCTG AGCG  CGGCGGGGAT  C
                                _   GC        GT
GAM260  AKAP13  3' CATGGCCTTGACAGTGCTC   89681        ATGTT  TCT
                              GGGCATTGT    GCT   GTG
                              |||||||||    |||   |||
                              CTCGTGACA    CGG   TAC
                                   GTTC_   ___
GAM260  ALB     3' CGTGGAAGTTCCAGTGTTC   4890        TATGTT     TG
                              GGGCATTG     GCTTCTG  G
                              ||||||||     ||||||| |
                              CTTGTGAC     TGAAGGT  C
                                   CT_____      GT
GAM260  ALDH3B2 3' TCACAGGGGCAGTGTCACCC   5509     CAT  T TG
                              GGG   TG A  TTGCTTCTGTGG
                              |||   || |  ||||||||||||
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                                CCC   AC T  GACGGGGACACT
                                  ___  _ GT
GAM260  AMPD3    3'  TCAGATGCCAAGTAACATGTGG 4901    TG       _____    TGG
              TTTTC                  T  TATGTTGCT    TCTG
                                |  |||||||||    ||||
                                G  GTACAATGA    AGAC
                                 GT       ACCGT   T  G
GAM260  ANK3     3'  GTATATTAGCAATTATAATGTT 40629         T     TC   G
              T                  GGGCATTGTA GTTGCT  TGTG
                                ||||||||||  ||||||  ||||
                                TTTGTAATAT TAACGA  ATAT
                                      _     TT   GT
GAM260  ANKTM1   3'  TCATTCTCAAACATACTGATGT 23676        _      GCTTCT
              TC                   GGGCATT GTATGTT     GTGG
                                |||||||  |||||||     ||||
                                CTTGTAG CATACAA     TACT
                                    T      ACTCT_
GAM260  ANXA5    3'  TCATAGAAGAAAATAGTGGTGC 6717        TG ATGTTG
              TT                   GGGCAT  T     CTTCTGTGG
                                ||||||  |     |||||||||
                                TTCGTG  G     GAAGATACT
                                   GT ATAAAA
GAM260  ANXA7    3'  AGTAATATTGCAATGTTT    6719          _
                                GGGCATTGTA TGTTGCT
                                ||||||||||  |||||||
                                TTTGTAACGT ATAATGA
                                      T
GAM260  ANXA7    3'  AGTAATATTGCAATGTTT    14451          _
                                GGGCATTGTA TGTTGCT
                                ||||||||||  |||||||
                                TTTGTAACGT ATAATGA
                                      T
GAM260  ANXA8    5'  CTGCAGGAGCCAGACGTGTGGA 7893      A TG     __      TG
              GTCC                   GGC T  TATGTT  GCTTCTG  G
                                |||  |  ||||||  |||||||  |
                                CTG G  GTGCAG  CGAGGAC  C
                                  A GT     AC      GT
GAM260  AP1B1    3'  ACAGAAGCTGTGCCT      6665        TGTATGTT
                                GGGCAT       GCTTCTGT
                                ||||||       ||||||||
                                TCCGTG       CGAAGACA
                                   T_______
GAM260  AP2B1    3'  CACACTGCAAATAGTGTTC    7058          ATG    TTC
                                GGGCATTGT   TTGC   TGTG
                                |||||||||   ||||   ||||
                                CTTGTGATA   AACG   ACAC
                                      ___    TC_
GAM260  APG5L    3'  CAGTACAGCATACAATCTC    16759     C         CTT
                                GGG ATTGTATGTTG   CTG
                                ||| ||||||||||   |||
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                                CTC TAACATACGAC   GAC
                                  _        AT_
GAM260  APLP2    3'  TACAGTTGATGTCGATGCTC   90899       T    GCTT    G
                                GGGCATTG ATGTT   CTGTG
                                |||||||| |||||   |||||
                                CTCGTAGC TGTAG   GACAT
                                    _    TT__    G
GAM260  APLP2    3'  TCACAGGAGTCTTTGTAATGCT 90900        TGTT
           T                     GGGCATTGTA   GCTTCTGTGG
                                ||||||||||   ||||||||||
                                TTCGTAATGT   TGAGGACACT
                                     TTC_
GAM260  APPBP1   5'  CGCAGGGGCTCGGCTGTTT   14022     TT  ATGTT
                                GGGCA  GT    GCTTCTGTG
                                |||||  ||    |||||||||
                                TTTGT  CG    CGGGGACGC
                                  __  GCT__
GAM260  APPBP2   3'  CTGTAGTAGCCCATCTGATGCT 21075      GT   TT   T   TG
           T                     GGGCATT  ATG  GCT CTG  G
                                |||||||  |||  ||| |||  |
                                TTCGTAG  TAC  CGA GAT  C
                                    TC   C_   T   GT
GAM260  APXL     3'  CTGTGGGCTGGGCCTGTGGTGC 7928       TG  T  __   CTGTGG
           CT                     GGGCAT  TA GTT  GCTT
                                ||||||  || |||  ||||
                                TCCGTG  GT CGG  CGGG
                                   GT  C   GT    TGTC
GAM260  AQP6     5'  TTACGGGCACGGTGTGGTGTC  53946     TG   GT   TT
                                GGCAT  TAT  TGC  CTGTGG
                                |||||  |||  |||  ||||||
                                CTGTG  GTG  ACG  GGCATT
                                   GT   GC   __
GAM260  ARF1     5'  TTGTGGGAGCAAAACCAACGCC 70661     A   TATG       TG
           T                     GGGC TTG    TTGCTTCTG  G
                                |||| |||    |||||||||  |
                                TCCG AAC    AACGAGGGT  T
                                  C   CAA_       GT
GAM260  ARG2     3'  TATAGAAGTTCAATGGCT    6755     G    TATGTT
                                GG CATTG     GCTTCTGTG
                                || |||||     |||||||||
                                TC GTAAC     TGAAGATAT
                                 G    T_____
GAM260  ARHGDIA  3'  AGCGGGCAGTGCCC       15041         ATG
                                GGGCATTGT   TTGCT
                                |||||||||   |||||
                                CCCGTGACG   GGCGA
                                     ___
GAM260  ARHGEF12 3'  CTACAGGGTAATTATGTAATTC 30998     C      _    T
           TC                     GGG ATTGTATG TTGCT CTGTGG
                                ||| |||||||| ||||| ||||||
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                                CTC TAATGTAT AATGG GACATC
                                  T      T    _
GAM260  ARHGEF12 3'  TATGGAAGTGACCTGCTGT   31004    TT   T  TG
                                GCA  GTA GT  CTTCTGTG
                                |||  ||| ||  ||||||||
                                TGT  CGT CA  GAAGGTAT
                                  __   C  GT
GAM260  ARHGEF6  3'  CCGTAGAGGCCTTTCAGTTCCT 68201    C    TATGTT
                                GGG ATTG     GCTTCTGTGG
                                ||| ||||     ||||||||||
                                TCC TGAC     CGGAGATGCC
                                  T   TTTC__
GAM260  ARL4     3'  TTGTGGAAGATGAGTAAATGCA 19199       GTTG____     TG
            GTGCTT                 ATTGTAT      CTTCTG  G
                                |||||||      ||||||  |
                                TGACGTA      GAAGGT  T
                                    AATGAGTA     GT
GAM260  ARNT2    3'  CCATACTGTGATGTCGATGCCC 29456       T    TG TTC
                                GGGCATTG ATGT  C   TGTGG
                                |||||||| ||||  |  |||||
                                CCCGTAGC TGTA  G   ATACC
                                    _   GT TC_
GAM260  ARNT2    3'  CGTAGATGCATGCAGTGTTC   29458          TGCT   TG
                                GGGCATTGTATGT    TCTG  G
                                ||||||||||||    ||||  |
                                CTTGTGACGTACG    AGAT  C
                                      T___    GT
GAM260  ARSB     5'  GGCACTAATTATAATGTCT    3499          TGT__
                                GGGCATTGTA     TGCT
                                ||||||||||     ||||
                                TCTGTAATAT     ACGG
                                     TAATC
GAM260  AS3      3'  TGAAAGTGTAATGTGCGATGGC 31935    G          TT  GTGG
            T                    GG CATTGTATGTTGC  CT
                                || ||||||||||||  ||
                                TC GTAGCGTGTAATG  GA
                                 G          T_  AAGTG
GAM260  ASPH     5'  CCGCGTCGACATGCAGTGTGC  50623   G          CTTC
                                G GCATTGTATGTTG    TGTGG
                                | ||||||||||||    |||||
                                C TGTGACGTACAGC    GCGCC
                                 G          T___
GAM260  ATM      3'  CTACAGGAGCATACCACCATGC 56302       T  ATGT
            CT                    GGGCAT GT    TGCTTCTGTGG
                                ||||||| ||    ||||||||||
                                TCCGTA CA    ACGAGGACATC
                                   C  CCAT
GAM260  ATP11A   3'  CCGCAGAAGTGCCAGGATGTCC 77027       GTA  TT
                                GGGCATT   TG  GCTTCTGTGG
                                |||||||   ||  ||||||||||
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                                CCTGTAG  AC  TGAAGACGCC
                                   G__  CG
GAM260  ATP11A   3'  CTGTGGAGACTGTGCACGTGCC 77028      _   _  GCT   TG
           T                    GGGCAT TGTAT GTT  TCTG  G
                                |||||| ||||| |||  ||||  |
                                TCCGTG ACGTG CAG  AGGT  C
                                   C    T  ___   GT
GAM260  ATP11A   3'  TTGCAGGGTCTTCATGCAATTT 77039    C     TT_  T  TG
           TC                    GGG ATTGTATG  GCT CTG  G
                                 ||| ||||||||  ||| |||  |
                                 CTT TAACGTAC  TGG GAC  T
                                   T      TTC  _  GT
GAM260  ATP1B1   3'  CAGGAGTACAGTGCTC     8040         ATGTT
                                 GGGCATTGT    GCTTCTG
                                 |||||||||    |||||||
                                 CTCGTGACA    TGAGGAC
                                      _____
GAM260  ATP1B3   3'  ATAGTGTTCAGTGTCC     8058        TATGTT  TT
                                 GGGCATTG     GC  CTGT
                                 ||||||||     ||  ||||
                                 CCTGTGAC     TG  GATA
                                    T_____  T_
GAM260  ATP2B2   3'  TTACGGGAGTGAGCGGTTTTC  8070     C    ATG TG
                                 GGG ATTGT   T  CTTCTGTGG
                                 ||| |||||   |  |||||||||
                                 CTT TGGCG   A  GAGGGCATT
                                   T    ___ GT
GAM260  ATP6V0C  3'  GTACATGCGCAGTGTCC     87315        __   T
                                 GGGCATTGT  ATGT GC
                                 |||||||||  |||| ||
                                 CCTGTGACG  TACA TG
                                      CG   _
GAM260  ATP7A    3'  TTGTAGTCTCAAGATGTATGGT 3538      TG    GCTT__  TG
           GT                    GCAT  TATGTT     CTG  G
                                 ||||  ||||||     |||  |
                                 TGTG  ATGTAG     GAT  T
                                   GT     AACTCT   GT
GAM260  ATP8B2   5'  CCGTGGGATGAGGCAGTGGACA 65219      A GT   ____  TG
           GTGCCT                  ATTGT T  TGCT   TC  TGG
                                 |||||  |  ||||   ||  |||
                                 TGACA G  ACGG   GG  GCC
                                    G TG    AGTA  GT
GAM260  ATRN     3'  CGCTGGACAGCAATGCTC    57798        ATGT  C   T
                                 GGGCATTGT    TG TTC GTG
                                 |||||||||    || ||| |||
                                 CTCGTAACG    AC AGG CGC
                                      ____  _   T
GAM260  ATSV     3'  CCGTGGGAGCAGTTACATCGGG 15053    AT__   TGT    TG
           TCT                     GGC   TGTA  TGCTTC  TGG
                                 |||   ||||  ||||||  |||
```

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                                CTG   ACAT  ACGAGG  GCC
                                  GGCT   TG_    GT
GAM260  AVP     5' CTATGGGGGTGCGGGGGTGTCA 4921     TG  G ___
             TGTCT                 CAT  TAT TT  GCTTCTGTGG
                                |||  ||| ||  ||||||||||
                                GTA  GTG GG  TGGGGGTATC
                                  CT   G  GCG
GAM260  AXL     3' CCGCAGGGGATGGACGATCTCC 8095     C    ATGTTG
                                GGG ATTGT    CTTCTGTGG
                                ||| |||||    |||||||||
                                CCT TAGCA    GGGGACGCC
                                  C    GGTA__
GAM260  AXL     3' CCGCAGGGGATGGACGATCTCC 41592    C    ATGTTG
                                GGG ATTGT    CTTCTGTGG
                                ||| |||||    |||||||||
                                CCT TAGCA    GGGGACGCC
                                  C    GGTA__
GAM260  B29     5' CAGGAGCCGCAGTTCC     49197    C    ATGTT
                                GGG ATTGT    GCTTCTG
                                ||| |||||    |||||||
                                CCT TGACG    CGAGGAC
                                  _    C____
GAM260  B3GALT5  3' CCACGCCAGAATGTCGGTGTTC 20217       T    G  TC
                                GGGCATTG ATGTT CT  TGTGG
                                |||||||| ||||| ||  |||||
                                CTTGTGGC TGTAA GA  GCACC
                                     _    _ CC
GAM260  B3GALT5  3' CCACGCCAGAATGTCGGTGTTC 52567       T    G  TC
                                GGGCATTG ATGTT CT  TGTGG
                                |||||||| ||||| ||  |||||
                                CTTGTGGC TGTAA GA  GCACC
                                     _    _ CC
GAM260  B3GALT5  3' CCACGCCAGAATGTCGGTGTTC 52575       T    G  TC
                                GGGCATTG ATGTT CT  TGTGG
                                |||||||| ||||| ||  |||||
                                CTTGTGGC TGTAA GA  GCACC
                                     _    _ CC
GAM260  B3GALT5  3' CCACGCCAGAATGTCGGTGTTC 52555       T    G  TC
                                GGGCATTG ATGTT CT  TGTGG
                                |||||||| ||||| ||  |||||
                                CTTGTGGC TGTAA GA  GCACC
                                     _    _ CC
GAM260  B3GALT5  3' CCACGCCAGAATGTCGGTGTTC 52559       T    G  TC
                                GGGCATTG ATGTT CT  TGTGG
                                |||||||| ||||| ||  |||||
                                CTTGTGGC TGTAA GA  GCACC
                                     _    _ CC
GAM260  B4GALT3  5' CCAAGATGGCGGCAGCGATGCC 13677        A     _  G
             T                  GGGCATTGT TGTTGCT TCT TGG
                                |||||||| ||||||| ||| |||
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                                TCCGTAGCG ACGGCGG AGA ACC
                                    _     T  _
GAM260  B4GALT5  3' CTGTGGGAGTGATTGGCCAGGC 16499     ATT  AT  TG    TG
           CT                    GGGC  GT  GT  CTTCTG  G
                                 ||||  ||  ||  ||||||  |
                                 TCCG  CG  TA  GAGGGT  C
                                   GAC  GT  GT    GT
GAM260  BACE    5' CGCAGGAGCCCGGAGCCC    23978     A  TATGTT
                                 GGGC TTG    GCTTCTGTG
                                 |||| |||    |||||||||
                                 CCCG GGC    CGAGGACGC
                                   A  C_____
GAM260  BACE    3' CTATTGGTAATATAATAATGTC 23979        _     TCTGTGG
           C                     GGGCATTGT ATGTTGCT
                                 |||||||||  ||||||||
                                 CCTGTAATA TATAATGG
                                      A      TTATC
GAM260  BACE    3' CTATTGGTAATATAATAATGTC 57289        _     TCTGTGG
           C                     GGGCATTGT ATGTTGCT
                                 |||||||||  ||||||||
                                 CCTGTAATA TATAATGG
                                      A      TTATC
GAM260  BACE    5' CGCAGGAGCCCGGAGCCC    57288     A  TATGTT
                                 GGGC TTG    GCTTCTGTG
                                 |||| |||    |||||||||
                                 CCCG GGC    CGAGGACGC
                                   A  C_____
GAM260  BBS2    3' TTATGGAATAGGATGAATGCTT 49042      G  G  C
                                 GGGCATT TAT TTG TTCTGTGG
                                 |||||||  |||  |||  ||||||||
                                 TTCGTAA GTA GAT AAGGTATT
                                    _  G  _
GAM260  BCL11A  3' AAGAGTAGCAGTATATATGTCT 43155      T       T  GTGG
                                 GGGCAT GTATGTTGCT CT
                                 ||||||  ||||||||||  ||
                                 TCTGTA TATATGACGA GA
                                    _        T  GAAT
GAM260  BCR     5' CCATGGGGGCCGCCCGGCGCCC 15074     A  TAT  T
                                 GGGC TTG  GT GCTTCTGTGG
                                 |||| |||  ||  ||||||||||
                                 CCCG GGC  CG CGGGGGTACC
                                   C  C__  C
GAM260  BCR     5' CCATGGGGGCCGCCCGGCGCCC 41205     A  TAT  T
                                 GGGC TTG  GT GCTTCTGTGG
                                 |||| |||  ||  ||||||||||
                                 CCCG GGC  CG CGGGGGTACC
                                   C  C__  C
GAM260  BHLHB3  3' CACTTTTGTTACAATGCTT   47764        TGTT  TTCT
                                 GGGCATTGTA   GC   GTG
                                 ||||||||||   ||   |||
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                                TTCGTAACAT   TG   CAC
                                     ____ TTTT
GAM260  BLAME   3' CACAGGCACACGATGCTC   39240        A  TGCTT
                                GGGCATTGT TGT   CTGTG
                                |||||||||| |||    |||||
                                CTCGTAGCA ACG   GACAC
                                    C  _____
GAM260  BLK     3' TTGTAGAGGGCTGTAACAGTGA 8156    G    A  TT  _   TG
           CC                    GG CATTGT TG  GCT TCTG  G
                                || |||||| ||  ||| ||||  |
                                CC GTGACA AT  CGG AGAT  T
                                 A     _ GT   G   GT
GAM260  BMP1    3' CCGCGGGGGCTGTGAGCAGCGG 20421      A  ____
           TGCCT                  ATTGT TGTT   GCTTCTGTGG
                                ||||| ||||   ||||||||||
                                TGGCG ACGA   CGGGGGCGCC
                                  _   GTGT
GAM260  BMPR1A  3' TGCATTTGATAGCAATGTAAGT 15079     G      _ T_  G
           GCCT                   GCATT TATGTTGCT TC  GTG
                                ||||| ||||||||| ||  |||
                                CGTGA ATGTAACGA AG  TAC
                                  _       T  TT   GTC
GAM260  BMX     5' CCACGCGTCCGGTGATGGTGCC 8169       TG ATG   CTTC
           T                    GGGCAT  T   TTG   TGTGG
                                ||||||  |   |||   |||||
                                TCCGTG  A   GGC   GCACC
                                   GT GT_   CTGC
GAM260  BPAG1   3' CCACAGCCTTCAAGCTGCAGTG 8172        T   GCTT__
           TTT                    GGCATTGTA GTT    CTGTGG
                                |||||||||| |||     ||||||
                                TTGTGACGT CGA     GACACC
                                     _   ACTTCC
GAM260  C20orf1  5' GCTTCTGAGGCGGTTGCGGTGC 24001         T TT    TGTGG
           TC                     GGGCATTGTA G  GCTTC
                                |||||||||| |  |||||
                                CTCGTGGCGT T  CGGAG
                                     _ GG    TCTTCGG
GAM260  CA14    3' CTGTAGGAGTAGTAAGCAGATG 24003      _  A        TG
           TC                     GGCAT TGT TGTTGCTTCTG  G
                                ||||| ||| ||||||||||  |
                                CTGTA ACG ATGATGAGGAT  C
                                   G   A         GT
GAM260  CACNA1C  5' CCATGGACTCAATGTCAATGCT 5558        T    CT
           T                    GGGCATTG ATGTTG  TCTGTGG
                                ||||||||  ||||||  |||||||
                                TTCGTAAC TGTAAC  AGGTACC
                                     _     TC
GAM260  CACNA2D3 3' CCGCAAGTGGTAGGCAGTGTCC 37254        A  TT   TC
                                GGGCATTGT TG  GCT  TGTGG
                                |||||||||  ||  |||  |||||
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                                CCTGTGACG AT  TGA  ACGCC
                                     G  GG  __
GAM260  CACNB1   3'  TCACACCTGACATGTATGTCC  5574       TGT    CTTC
                                GGGCAT  ATGTTG   TGTGG
                                ||||||  ||||||   |||||
                                CCTGTA  TACAGT   ACACT
                                   TG_    CC__
GAM260  CACNB2   3'  CCACCCAGGTGATGTTAGTGTT 5578        T   TG  CT
           T                    GGGCATTG ATGT  CTT  GTGG
                                |||||||| ||||  |||  ||||
                                TTTGTGAT TGTA  GGA  CACC
                                     _   GT   CC
GAM260  CACNG3   5'  CTGTGGAAGCAGTGAACACTC  21541    CAT   A GT     TG
                                GGG   TGT T  TGCTTCTG  G
                                |||   ||| |  ||||||||  |
                                CTC   ACA G  ACGAAGGT  C
                                  ___   A TG      GT
GAM260  CALB1    3'  TATACTGTTTGTAATATACAGT 17025          TTCT_  G
                                ATTGTATGTTGC    GTG
                                ||||||||||||    |||
                                TGACATATAATG    CAT
                                      TTTGT   ATC
GAM260  CALCB    3'  CCGTGGAAGATACACATGTTT  87571      _    GTTG   TG
                                GGGCAT TGTAT    CTTC  TGG
                                |||||| |||||    ||||  |||
                                TTTGTA ACATA    GAAG  GCC
                                   C     _____   GT
GAM260  CALD1    3'  CGCGGAATGTGTGCAGTATCT  52463    GC     GTT  _    TG
                                GG  ATTGTAT   GC TTCTG  G
                                ||  |||||||   || |||||  |
                                TC  TGACGTG   TG AAGGC  C
                                 TA      ___  T    GT
GAM260  CALD1    3'  CGCGGAATGTGTGCAGTATCT  52468    GC     GTT  _    TG
                                GG  ATTGTAT   GC TTCTG  G
                                ||  |||||||   || |||||  |
                                TC  TGACGTG   TG AAGGC  C
                                 TA      ___  T    GT
GAM260  CALD1    3'  CGCGGAATGTGTGCAGTATCT  52527    GC     GTT  _    TG
                                GG  ATTGTAT   GC TTCTG  G
                                ||  |||||||   || |||||  |
                                TC  TGACGTG   TG AAGGC  C
                                 TA      ___  T    GT
GAM260  CALU     3'  TTATGAGTTTGGTTGCAGTGTT 6893          TGTT_   CTGTGG
           C                    GGGCATTGTA    GCTT
                                ||||||||||    ||||
                                CTTGTGACGT    TGAG
                                      TGGTT    TATT
GAM260  CAPN11   5'  ACAGGAGGATAAGCCT     22938      A   ATGTTG
                                GGGC TTGT     CTTCTGT
                                |||| ||||     |||||||
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                                TCCG AATA     GAGGACA
                                  _   G_____
GAM260  CAPNS1   3'  CTATAGGAGTCACCTGGAGCCT 8250      AT G  T  T
                                GGGC  T TA GT GCTTCTGTGG
                                ||||  | || || ||||||||||
                                TCCG  A GT CA TGAGGATATC
                                  __ G  C  C
GAM260  CAPZA1   5'  TTGTAGGAGTAGCAACAGCT   72629     AT   A        TG
                                GGC  TGT TGTTGCTTCTG  G
                                |||  ||| ||||||||||  |
                                TCG  ACA ACGATGAGGAT  T
                                  __  _        GT
GAM260  CARKL    3'  CCGTCCTGGTATCACAGTGCTT 25187        ATGT    TCTG
                                GGGCATTGT    TGCT    TGG
                                |||||||||    ||||    |||
                                TTCGTGACA    ATGG    GCC
                                     CT__    TCCT
GAM260  CASP10   3'  CACAGCCCTGCAGTGCCC    52099         TGTTGCTT
                                GGGCATTGTA       CTGTG
                                ||||||||||       |||||
                                CCCGTGACGT       GACAC
                                     CCC_____
GAM260  CASP2    3'  CCACAGGAGGTGTGATAGAGCC 52138     A    ATGTTG
          T                      GGGC TTGT     CTTCTGTGG
                                ||||  ||||     |||||||||
                                TCCG GATA     GAGGACACC
                                  A    GTGTG_
GAM260  CASP2    3'  TTACAGGATCATGTAAATGCTC 52148       G     T C
                                GGGCATT TATGT G TTCTGTGG
                                |||||||  |||||  |  ||||||||
                                CTCGTAA ATGTA C AGGACATT
                                   _     _ T
GAM260  CASP2    3'  CCACAGGAGGTGTGATAGAGCC 52151     A    ATGTTG
          T                      GGGC TTGT     CTTCTGTGG
                                ||||  ||||     |||||||||
                                TCCG GATA     GAGGACACC
                                  A    GTGTG_
GAM260  CASP2    3'  TTACAGGATCATGTAAATGCTC 52162       G     T C
                                GGGCATT TATGT G TTCTGTGG
                                |||||||  |||||  |  ||||||||
                                CTCGTAA ATGTA C AGGACATT
                                   _     _ T
GAM260  CASP2    3'  CCACAGGAGGTGTGATAGAGCC 52166     A    ATGTTG
          T                      GGGC TTGT     CTTCTGTGG
                                ||||  ||||     |||||||||
                                TCCG GATA     GAGGACACC
                                  A    GTGTG_
GAM260  CASP2    3'  TTACAGGATCATGTAAATGCTC 52176       G     T C
                                GGGCATT TATGT G TTCTGTGG
                                |||||||  |||||  |  ||||||||
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                                CTCGTAA ATGTA C AGGACATT
                                   _    _ T
GAM260  CASP2    3'  CCACAGGAGGTGTGATAGAGCC 6896      A   ATGTTG
            T                    GGGC TTGT     CTTCTGTGG
                                 |||| ||||     |||||||||
                                 TCCG GATA     GAGGACACC
                                   A   GTGTG_
GAM260  CASP2    3'  TTACAGGATCATGTAAATGCTC 6905       G    T C
                                 GGGCATT TATGT G TTCTGTGG
                                 ||||||| ||||| | ||||||||
                                 CTCGTAA ATGTA C AGGACATT
                                    _    _ T
GAM260  CASP3    3'  CGTAAGGTGCTACAATGCCC   52195        T  T   C  TG
                                 GGGCATTGTA GT GCTT TG  G
                                 |||||||||| || |||| ||  |
                                 CCCGTAACAT CG TGGA AT  C
                                      _ _   _ GT
GAM260  CASP3    3'  CGTAAGGTGCTACAATGCCC   15100        T  T   C  TG
                                 GGGCATTGTA GT GCTT TG  G
                                 |||||||||| || |||| ||  |
                                 CCCGTAACAT CG TGGA AT  C
                                      _ _   _ GT
GAM260  CAV3     3'  TCACAGGGGCTGCTGGCGAGCT 52893     A   AT  T
            C                    GGGC TTGT  GT GCTTCTGTGG
                                 |||| ||||  || ||||||||||
                                 CTCG AGCG  CG CGGGGACACT
                                   _   GT  T
GAM260  CBLB     5'  CACAGGGGTGGGGTGTCC    15121       GTATG TG
                                 GGGCATT    T  CTTCTGTG
                                 |||||||    |  ||||||||
                                 CCTGTGG    G  GGGGACAC
                                      _____ GT
GAM260  CCND2    3'  GCCATTACAGTATCCAATGTCT 8291        TATGT   TCT
                                 GGGCATTG    TGCT   GTGG
                                 ||||||||    ||||   ||||
                                 TCTGTAAC    ATGA   TACC
                                      CT___    CAT    GA
GAM260  CCR9     3'  GGCTCTTGACTGTGATGCCC   21816      TG  T  ____
                                 GGGCAT  TA GTT    GCT
                                 ||||||  || |||    |||
                                 CCCGTA  GT CAG    CGG
                                    GT  _   TTCT
GAM260  CCR9     3'  GGCTCTTGACTGTGATGCCC   48301      TG  T  ____
                                 GGGCAT  TA GTT    GCT
                                 ||||||  || |||    |||
                                 CCCGTA  GT CAG    CGG
                                    GT  _   TTCT
GAM260  CCT2     3'  CTGTGGAATCTGTTTATCGGTG 21221      T   TT  ___    TG
            CCC                    GCATTG ATG  GC   TTCTG  G
                                 ||||||  |||  ||   |||||  |
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                                CGTGGC TAT  TG   AAGGT  C
                                   _  T_  TCT    GT
GAM260  CD59    3'  CCATGGAGGCATGCCAAATGTT 5212        GTATGT
            C                   GGGCATT     TGCTTCTGTGG
                                |||||||     ||||||||||
                                CTTGTAA     ACGGAGGTACC
                                   ACCGT_
GAM260  CD59    3'  CCGAGTGCAATGAATGATGCTT 5213       TG A     TT  G
                                GGGCAT  T TGTTGC  CT TGG
                                ||||||  | ||||||  || |||
                                TTCGTA  A GTAACG  GA GCC
                                   GT A     T_  _
GAM260  CD81    3'  CCACAGGGACCTCTGCAGTGCC 15133         TGTTG  T
            C                   GGGCATTGTA    CT CTGTGG
                                ||||||||||    || ||||||
                                CCCGTGACGT    GG GACACC
                                     CTCCA  _
GAM260  CDC25B  3'  CCATGGGAAAGATGGTGTGGTG 41562       TG  _  GC
            TCC                   GGGCAT  TAT GTT  TTCTGTGG
                                ||||||  |||  |||  ||||||||
                                CCTGTG  GTG TAG  AGGGTACC
                                   GT   G   AA
GAM260  CDC25B  3'  CGTGGATGCGCAGTGCCT    41563        ATGTT  T  TG
                                GGGCATTGT    GC TC  TG
                                |||||||||    || ||  ||
                                TCCGTGACG    CG AG  GC
                                     _____  T  GT
GAM260  CDC25B  3'  CCATGGGAAAGATGGTGTGGTG 41566       TG  _  GC
            TCC                   GGGCAT  TAT GTT  TTCTGTGG
                                ||||||  |||  |||  ||||||||
                                CCTGTG  GTG TAG  AGGGTACC
                                   GT   G   AA
GAM260  CDC25B  3'  CGTGGATGCGCAGTGCCT    41567        ATGTT  T  TG
                                GGGCATTGT    GC TC  TG
                                |||||||||    || ||  ||
                                TCCGTGACG    CG AG  GC
                                     _____  T  GT
GAM260  CDC2L1  5'  GGCGGCGTAGGGTGTTT     8362        G
                                GGGCATT TATGTTGCT
                                ||||||| |||||||||
                                TTTGTGG ATGCGGCGG
                                   G
GAM260  CDC2L1  5'  GGCGGCGTAGGGTGTTT     53115       G
                                GGGCATT TATGTTGCT
                                ||||||| |||||||||
                                TTTGTGG ATGCGGCGG
                                   G
GAM260  CDC2L1  5'  GGCGGCGTAGGGTGTTT     53116       G
                                GGGCATT TATGTTGCT
                                ||||||| |||||||||
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                                TTTGTGG ATGCGGCGG
                                    G
GAM260  CDC2L2   5' CCGCGGCCCCGTAGGGTGTTT 53194      G   TT  TCT
                                GGGCATT TATG  GCT  GTGG
                                ||||||| ||||  |||  ||||
                                TTTGTGG ATGC  CGG  CGCC
                                    G   CC  ___
GAM260  CDC2L2   5' CCGCGGCCCCGTAGGGTGTTT 53195      G   TT  TCT
                                GGGCATT TATG  GCT  GTGG
                                ||||||| ||||  |||  ||||
                                TTTGTGG ATGC  CGG  CGCC
                                    G   CC  ___
GAM260  CDC2L2   5' CCGCGGCCCCGTAGGGTGTTT 53196      G   TT  TCT
                                GGGCATT TATG  GCT  GTGG
                                ||||||| ||||  |||  ||||
                                TTTGTGG ATGC  CGG  CGCC
                                    G   CC  ___
GAM260  CDC2L2   5' CCGCGGCCCCGTAGGGTGTTT 53197      G   TT  TCT
                                GGGCATT TATG  GCT  GTGG
                                ||||||| ||||  |||  ||||
                                TTTGTGG ATGC  CGG  CGCC
                                    G   CC  ___
GAM260  CDC2L2   5' CCGCGGCCCCGTAGGGTGTTT 43775      G   TT  TCT
                                GGGCATT TATG  GCT  GTGG
                                ||||||| ||||  |||  ||||
                                TTTGTGG ATGC  CGG  CGCC
                                    G   CC  ___
GAM260  CDC42    3' TTGCAGCTCAGTAGTATATGGT 8373      TG      T__  TG
           GTTC                  GGCAT  TATGTTGCT  CTG  G
                                |||||  |||||||||  |||  |
                                TTTGTG  ATATGATGA  GAC  T
                                   GT       CTC  GT
GAM260  CDH16    3' CCATGGGAGTGCTCCAAATGTC 14497      GTAT  T
                                GGCATT   GT GCTTCTGTGG
                                ||||||   || ||||||||||
                                CTGTAA   CG TGAGGGTACC
                                    ACCT  _
GAM260  CDH5     3' CAGAAGGCAAGGCCC      8384      A   ATGTTG
                                GGGC TTGT     CTTCTG
                                |||| ||||     ||||||
                                CCCG AACG     GAAGAC
                                   G   _______
GAM260  CDK10    3' CTGCAGGGGTCTCATGTGGTCC 53769    C  TG   TT     TG
           T                     GGG AT  TATG  GCTTCTG  G
                                ||| ||  ||||  |||||||  |
                                TCC TG  GTAC  TGGGGAC  C
                                  _ GT   TC     GT
GAM260  CDK10    3' CTGCAGGGGTCTCATGTGGTCC 53778    C  TG   TT     TG
           T                     GGG AT  TATG  GCTTCTG  G
                                ||| ||  ||||  |||||||  |
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                                TCC TG  GTAC  TGGGGAC  C
                                  _ GT   TC     GT
GAM260  CDK10    3'  CTGCAGGGGTCTCATGTGGTCC 13402    C  TG   TT     TG
            T                    GGG AT  TATG  GCTTCTG  G
                                |||  ||  ||||  |||||||  |
                                TCC TG  GTAC  TGGGGAC  C
                                  _ GT   TC     GT
GAM260  CDKN1A   3'  CCACAGGAAGCCTGCAGTCCT  54293    C     T   GC
                                GGG ATTGTA GTT  TTCTGTGG
                                |||  ||||||  |||  ||||||||
                                TCC TGACGT CGA  AGGACACC
                                  _     C   __
GAM260  CDR2     5'  CCACAGGGGTAAGACGCGCCT  76021     AT   ATG
                                GGGC  TGT   TTGCTTCTGTGG
                                ||||  |||   ||||||||||||
                                TCCG  GCA   AATGGGGACACC
                                  C_   G__
GAM260  CDS2     5'  CCGTGGGAGTCCGCGCGTGCCC 13776      T TA  TT    TG
                                GGGCAT G  TG  GCTTC  TGG
                                ||||||  |  ||  |||||  |||
                                CCCGTG C  GC  TGAGG  GCC
                                   _ GC  C_    GT
GAM260  CENPB    3'  CCGTGGAAGTAACCAAGGGCGC 69535   G  A_   TAT      TG
                                G GC  TTG   GTTGCTTC  TGG
                                | ||  |||   ||||||||  |||
                                C CG  AAC   CAATGAAG  GCC
                                 G  GG  ____      GT
GAM260  CENTD2   5'  TGTGGGGGTGCCCAGCTGCCT  30876     _   TAT  T     TG
                                GGGCA TTG   GT GCTTCTG  G
                                |||||  |||   ||  |||||||  |
                                TCCGT GAC   CG TGGGGGT  T
                                   C   C__  _      GT
GAM260  CGTHBA   3'  CCACAGAAGCCACAAACAGGCT 23860     A    A   T
            C                    GGGC TTGT TGT GCTTCTGTGG
                                ||||  ||||  |||  ||||||||||
                                CTCG GACA ACA CGAAGACACC
                                  _   A   C
GAM260  CHIC2    3'  CTACAGAATCGTGTGGTGTTT  23996      TG   TTGC
                                GGGCAT  TATG   TTCTGTGG
                                ||||||  ||||   ||||||||
                                TTTGTG  GTGC   AAGACATC
                                   GT   T____
GAM260  CHRNA2   3'  CGCAGGGGCTCCATATGTCC   5603      TTG   TT     TG
                                GGGCA   TATG  GCTTCTG  G
                                |||||   ||||  |||||||  |
                                CCTGT   ATAC  CGGGGAC  C
                                   ____   CT     GT
GAM260  CHST1    3'  TGCGGACGGTGACAATGTTT   13335      TGTA   TG  _    G
                                GGGCAT    TGT  CT TCTGTG
                                ||||||    |||  || ||||||
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                                TTTGTA   ACA  GG AGGCGT
                                   ____  GT  C    G
GAM260  CHST7   3'  TGGGGGCAATCTGTC      39110     TTGTAT
                                GGCA     GTTGCTTCTG
                                ||||     ||||||||||
                                CTGT     TAACGGGGGT
                                  C_____
GAM260  CLC     3'  TCTTCCAGTATTACGGTGCCT  25110         TGT   TCTGTGG
                                GGGCATTGTA   TGCT
                                ||||||||||   ||||
                                TCCGTGGCAT   ATGA
                                     T__   CCTTCTG
GAM260  CLCA2   3'  CTATATTTTATATATGAAGCCC 21536     A TG    TGCTTC
                                GGGC T  TATGT     TGTGG
                                |||| |  |||||     |||||
                                CCCG A  ATATA     ATATC
                                  A GT    TTTT__
GAM260  CLCN6   3'  CCGTGGAGGTTGCCCACGGGCC 41383     A   AT  T    TG
            T                    GGGC TTGT  GT GCTTC  TGG
                                ||||  ||||  ||  |||||  |||
                                TCCG GGCA  CG TGGAG  GCC
                                  _   CC  T    GT
GAM260  CLCN6   3'  CCGTGGAGGTTGCCCACGGGCC 41398     A   AT  T    TG
            T                    GGGC TTGT  GT GCTTC  TGG
                                ||||  ||||  ||  |||||  |||
                                TCCG GGCA  CG TGGAG  GCC
                                  _   CC  T    GT
GAM260  CLCN6   3'  CCGTGGAGGTTGCCCACGGGCC 7076      A   AT  T    TG
            T                    GGGC TTGT  GT GCTTC  TGG
                                ||||  ||||  ||  |||||  |||
                                TCCG GGCA  CG TGGAG  GCC
                                  _   CC  T    GT
GAM260  CLDN11  3'  CCACAGAGGTGCTGTAGATGCT 18810       G    TT
                                GGCATT TATG  GCTTCTGTGG
                                ||||||  ||||  ||||||||||
                                TCGTAG ATGT  TGGAGACACC
                                   _   CG
GAM260  CLECSF11 5' CATGGTGTGCGGTGCCC     55274          GTT   TC
                                GGGCATTGTAT   GCT  TG
                                ||||||||||   |||  ||
                                CCCGTGGCGTG   TGG  AC
                                      ___   T_
GAM260  CLN5    5'  CCATAGGCTTACAAACATTATG 21424    TG  _   GCT___
            ATGCTT                  AT  TA TGTT     TCTGTGG
                                ||  ||  ||||     |||||||
                                TA  AT ACAA     GGATACC
                                 GT  T   ACATTC
GAM260  CLN5    3'  CTACAGATAGATATGGTGTGCC 21425      TG     GCT
                                GGCAT  TATGTT   TCTGTGG
                                |||||  ||||||   |||||||
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                              CCGTG  GTATAG   AGACATC
                                 TG     AT_
GAM260  CLN6     3'  CCACAGGAAGTCACAGTGGTGC 35402       TG A   T    _
             CC                   GGGCAT  T TGT GCTTC TGTGG
                                  ||||||  | ||| ||||| |||||
                                  CCCGTG  G ACA TGAAG ACACC
                                     GT _  C    G
GAM260  CLOCK    3'  TCATAGGGGCACAGCCAGTTCT 16912     C   TA   T
                                  GGG ATTG  TGT GCTTCTGTGG
                                  ||| ||||  ||| ||||||||||
                                  TCT TGAC  ACA CGGGGATACT
                                    _   CG  _
GAM260  CLTC     3'  TACACTGGATTGCAGTGCTT   16782         TGTTG  TC   G
                                  GGGCATTGTA    CT  TGTG
                                  ||||||||||    ||  ||||
                                  TTCGTGACGT    GG  ACAT
                                        TA___  TC   G
GAM260  CLU      3'  TTACGGGGGCATCTTGAGTCC  8448      A   TATGT
                                  GGGC TTG    TGCTTCTGTGG
                                  |||| |||    ||||||||||
                                  CCTG AGT    ACGGGGGCATT
                                    _   TCT__
GAM260  CMAR     3'  CCGCAGAGGTGGATCGACGCCC 17773     A   TATG TG
                                  GGGC TTG    T  CTTCTGTGG
                                  |||| |||    |  |||||||||
                                  CCCG AGC    G  GGAGACGCC
                                    C   TA__ GT
GAM260  CMAR     3'  TGGGGAAGGTTATCAGTGCTT  17779        T   TTG    GTGG
                                  GGGCATTG ATG   CTTCT
                                  |||||||| |||   |||||
                                  TTCGTGAC TAT   GAAGG
                                       _   TG_    GGTA
GAM260  CNR1     3'  CATCAAATGAATAATGCCT   32213         A    GCTTCT
                                  GGGCATTGT TGTT     GTG
                                  ||||||||| ||||     |||
                                  TCCGTAATA GTAA     TAC
                                       A    AC____
GAM260  CNTFR    3'  CCACAGTATTTAATGCCC    8455         T   TTGCTT
                                  GGGCATTG ATG     CTGTGG
                                  |||||||| |||     ||||||
                                  CCCGTAAT TAT     GACACC
                                       T   _______
GAM260  CNTN2    3'  TCACAACCCAGGTGACGATGCC 17412         ATG   CTTC
             C                    GGGCATTGT   TTG    TGTGG
                                  |||||||||   |||    |||||
                                  CCCGTAGCA   GAC    ACACT
                                       GTG   CCA_
GAM260  CNTNAP2  3'  CAGAGGTTAGTGCT       26229        TATGTT
                                  GGCATTG     GCTTCTG
                                  |||||||     |||||||
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```
                              TCGTGAT     TGGAGAC
                                   ______
GAM260  COG3     3'  TCATAGATACGTGCAGTATCT  48701    GC       TGCT
                              GG  ATTGTATGT   TCTGTGG
                              ||  |||||||||   |||||||
                              TC  TGACGTGCA   AGATACT
                               TA       T___
GAM260  COL11A1  3'  GCCACATGCAAGTTT      8495      A      T
                              GGGC TTGTATGT GC
                              |||| |||||||| ||
                              TTTG AACGTACA CG
                                _      C
GAM260  COL11A1  3'  GCCACATGCAAGTTT      54654     A      T
                              GGGC TTGTATGT GC
                              |||| |||||||| ||
                              TTTG AACGTACA CG
                                _      C
GAM260  COL17A1  3'  ACAGTAGTTGCAATGTTT    4932         TGTT   T
                              GGGCATTGTA    GCT CTGT
                              ||||||||||    ||| ||||
                              TTTGTAACGT    TGA GACA
                                    ____   T
GAM260  COL1A1   3'  TATAGAAATTGAGATGCCC    3608        GTAT   GCT
                              GGGCATT    GTT   TCTGTG
                              |||||||    |||   ||||||
                              CCCGTAG    TAA   AGATAT
                                  AGT_   ___
GAM260  COL6A1   3'  ACAGAGGGCTGTGTCT      8475        T  ATGTTG
                              GGGCAT GT     CTTCTGT
                              |||||| ||     |||||||
                              TCTGTG CG     GGAGACA
                                 T _______
GAM260  COL8A1   5'  CGTGGGAGCCAGCGAGCCT   8482      A    A  TT    TG
                              GGGC TTGT TG  GCTTC  TG
                              |||| |||| ||  |||||  ||
                              TCCG AGCG AC  CGAGG  GC
                                _   _ __     GT
GAM260  COLQ     3'  CTACGGGGAATCTGTGTATGGG 54495     A TG  TG TGC__
           CCC                   GGC T  TA  T    TTCTGTGG
                              |||  |  ||  |    ||||||||
                              CCG G  AT  G    GGGGCATC
                                _ GT  GT TCTAA
GAM260  CORO2B   5'  CTGGGATGGTGATGTGAGTGCC 64573        G    TG  _   GTGG
           T                   GGGCATT TATGT  CT TCT
                              |||||||  |||||  ||  |||
                              TCCGTGA GTGTA  GG AGG
                                 _    GT  T   GTC
GAM260  CPNE3    3'  GGCTGTAACTCTGTATACAGTG 14030         _____    TTCTGTGG
           CTT                   CATTGTAT    GTTGC
                              ||||||||    |||||
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                                GTGACATA    CAATG
                                    TGTCT    TC  GGT
GAM260  CREBBP   3'  CCATGGAAGGGTGGATTGATGT 15206       TATGTTG
           TT                    GGGCATTG     CTTCTGTGG
                                 ||||||||     |||||||||
                                 TTTGTAGT     GAAGGTACC
                                    TAGGTGG
GAM260  CRY2     3'  CTACAGAAGTACACACAGATAC 72208    GCA   A  T
           C                     GG   TTGT TGT GCTTCTGTGG
                                 ||   |||| ||| ||||||||||
                                 CC   GACA ACA TGAAGACATC
                                  ATA   C  _
GAM260  CRYGS    3'  GCTGACTATAATGCCT     34077         T  _
                                 GGGCATTGTA GTT GC
                                 |||||||||| ||| ||
                                 TCCGTAATAT CAG CG
                                       _  T
GAM260  CSNK1G3  3'  TTGCAGAAGTGGCAAAAGCGCT 15223     A  GTA  TG    TG
           T                     GGGC TT   TGT  CTTCTG  G
                                 |||| ||   |||  ||||||  |
                                 TTCG GA   ACG  GAAGAC  T
                                   C  AA_  GT    GT
GAM260  CSNK1G3  3'  TTGTAGAAAGCAGTACAGTATC 15224    GC     GT    _  TG
           T                     GG  ATTGTAT  TGCTT CTG  G
                                 ||  |||||||  ||||| |||  |
                                 TC  TGACATG  ACGAA GAT  T
                                  TA      __     A   GT
GAM260  CSNK2A1  3'  CTATAGGAGCAGTGGACTGCTT 8556      TT  A GT
                                 GGGCA  GT T  TGCTTCTGTGG
                                 |||||  || |  ||||||||||
                                 TTCGT  CA G  ACGAGGATATC
                                    __  G TG
GAM260  CSNK2A1  3'  TCATCTCCCAACATGCTGTGCT 8557       T      CTTCT
           C                     GGGCAT GTATGTTG    GTGG
                                 ||||||  ||||||||    ||||
                                 CTCGTG CGTACAAC    TACT
                                    T      CCTC_
GAM260  CSPG3    3'  GAGCTGCAGTGTTC       15231          TGTT
                                 GGGCATTGTA    GCTT
                                 ||||||||||    ||||
                                 CTTGTGACGT    CGAG
                                               ____
GAM260  CSPG3    3'  TTGCGGGGGGCTGGGGATGCAG 15242        G  __     _ TG
           TGTTT                    CATTGTAT TT  GCTTCT G  G
                                 ||||||||  ||  ||||||  |  |
                                 GTGACGTA GG  CGGGGG C  T
                                      G  GT     G GT
GAM260  CST3     3'  TCATAGCCCCGGTGTGCGGTGC 3644         TG   CTT
                                 GCATTGTA  TTG   CTGTGG
                                 ||||||||  |||   ||||||
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                                CGTGGCGT  GGC   GATACT
                                    GT   CCC
GAM260  CTNNA1   3'  TCACTTCTAATAACTGCAGTGT 65921          T   CTTCT_
           TT                    GGGCATTGTA GTTG     GTGG
                                 |||||||||| ||||     ||||
                                 TTTGTGACGT CAAT     CACT
                                     _   AATCTT
GAM260  CTSS     5'  CCGTGGGAGCAACTGCTGGTTC 14541      ATT   T      TG
                                 GGGC   GTA GTTGCTTC  TGG
                                 ||||   ||| ||||||||  |||
                                 CTTG   CGT CAACGAGG  GCC
                                   GT_  _      GT
GAM260  CYP1B1   3'  GCAATAAAGTATAATGTTT   3655          ___
                                 GGGCATTGTAT   GTTGC
                                 ||||||||||   |||||
                                 TTTGTAATATG   TAACG
                                       AAA
GAM260  CYP2B6   3'  TTACAGGCATAATATGTGATCT 5746      C  TG      CT
           T                     GGG AT  TATGTTG  TCTGTGG
                                 ||| ||  |||||||  |||||||
                                 TTC TA  GTATAAT  GGACATT
                                   _ GT      AC
GAM260  DAB2     5'  TCACGGAGGCAATAGCTAGCCG 7198       TA____
           GTGTCT                  ATTG     TGTTGCTTCTGTGG
                                 ||||     ||||||||||||||
                                 TGGC     ATAACGGAGGCACT
                                   CGATCG
GAM260  DACH     3'  GGAAGTAAAGCGGCAAACAGTG 54969          A       CTGTGG
           CTT                     GGGCATTGT TGTTGCTT
                                 |||||||||  ||||||||
                                 TTCGTGACA ACGGCGAA
                                     A       ATGAAGGT
GAM260  DAPK1    3'  CAGAAGAGGGTGTGTTT     17047        TGT  G  G
                                 GGGCAT   AT TT CTTCTG
                                 ||||||   || || ||||||
                                 TTTGTG   TG GA GAAGAC
                                    ___  G  _
GAM260  DDEF2    5'  GGCAGCGGCGGTGTCC      13954          A
                                 GGGCATTGT TGTTGCT
                                 |||||||||  |||||||
                                 CCTGTGGCG GCGACGG
                                     _
GAM260  DDX6     3'  TTGCAGGAGCCATATGACAAGC 15293      A   _   T      TG
           CT                      GGGC TTGT ATGT GCTTCTG  G
                                 ||||  ||||  ||||  |||||||  |
                                 TCCG AACA TATA CGAGGAC  T
                                   _   G   C      GT
GAM260  DGAT2    5'  TCACAGGAGTGGCCTGCAGTGC 50791          T  TG
           C                       GGCATTGTA GT  CTTCTGTGG
                                 |||||||||  ||  |||||||||
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                                CCGTGACGT CG  GAGGACACT
                                     C  GT
GAM260  DGKB    3'  TCATGGAAGTGGTTTAACAGT  92535      AT_ TT
                                ATTGT   G  GCTTCTGTGG
                                ||||||  |  ||||||||||
                                TGACA   T  TGAAGGTACT
                                   ATT GG
GAM260  DHCR24  3'  TCATAGGAGACCCATGTGCTT  28635      TGT   TTG
                                GGGCAT   ATG   CTTCTGTGG
                                ||||||  |||  |||||||||
                                TTCGTG   TAC   GAGGATACT
                                   ___  CCA
GAM260  DMD     5'  CGCAGAATTTGAAATGTCT   14375       GTATGTTGC
                                GGGCATT       TTCTGTG
                                |||||||       |||||||
                                TCTGTAA       AAGACGC
                                    AGTTT____
GAM260  DMRT1   3'  TCACGGAGTTTAAATAATAGTG 41700        A   GC__
           TTC                    GGCATTGT TGTT   TTCTGTGG
                                |||||||| ||||   ||||||||
                                TTGTGATA ATAA   GAGGCACT
                                   _   ATTT
GAM260  DNCI1   3'  TGGGTGCAGATGTGGTGTTC  91065      TG  G   T
                                GGGCAT  TAT TTGC TCTG
                                ||||||  ||| |||| ||||
                                CTTGTG  GTA GACG GGGT
                                   GT  _   T
GAM260  DNMT1   3'  TCACATGTGTGGTACATGGTGT 7270       TG A  TT  TTC
           TT                    GGGCAT  T TG  GC   TGTGG
                                ||||||  | ||  ||   |||||
                                TTTGTG  A AT  TG   ACACT
                                   GT C  GG  TGT
GAM260  DNMT3B  3'  TTGCAGGGGTAGCCTGAGGTGC 22566      TG  T       TG
           C                     GGCAT  TA GTTGCTTCTG  G
                                |||||  || ||||||||||  |
                                CCGTG  GT CGATGGGGAC  T
                                   GA  C        GT
GAM260  DPYD    3'  GCACATACGGGCTC       60442     A      T
                                GGGC TTGTATGT GC
                                |||| |||||||| ||
                                CTCG GGCATACA CG
                                   _       _
GAM260  DRD2    3'  CCACAGGAGGCAAGCAAGCTC  5841      A   A   TG
                                GGGC TTGT TGT  CTTCTGTGG
                                |||| |||| |||  |||||||||
                                CTCG AACG ACG  GAGGACACC
                                   _   A   __
GAM260  DRP2    5'  CACAGAGGCAGCCCAGCCC   8661      AT  TAT
                                GGGC  TG   GTTGCTTCTGTG
                                ||||  ||   ||||||||||||
```

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                                CCCG  AC   CGACGGAGACAC
                                  __ C__
GAM260  DSCR2    5'  TCGCGCAAGCGGCGTGCGGTCC 13558     C          C
            C                    GGG ATTGTATGTTGCTT TGTGG
                                 ||| |||||||||||||| |||||
                                 CCC TGGCGTGCGGCGAA GCGCT
                                  _           C
GAM260  DTNB     5'  CCGCGGGGGGTGGCTCCGGGGCC 41579     A   TAT  TG
            T                    GGGC TTG   GT  CTTCTGTGG
                                 |||| |||   ||  |||||||||
                                 TCCG GGC   CG  GGGGGCGCC
                                   G   CT_  GT
GAM260  DTNB     5'  CCGCGGGGGGTGGCTCCGGGGCC 52497     A   TAT  TG
            T                    GGGC TTG   GT  CTTCTGTGG
                                 |||| |||   ||  |||||||||
                                 TCCG GGC   CG  GGGGGCGCC
                                   G   CT_  GT
GAM260  DTNB     5'  CCGCGGGGGGTGGCTCCGGGGCC 52501     A   TAT  TG
            T                    GGGC TTG   GT  CTTCTGTGG
                                 |||| |||   ||  |||||||||
                                 TCCG GGC   CG  GGGGGCGCC
                                   G   CT_  GT
GAM260  DTR      5'  GGGCGGCAGACGGTGCCC    8691          A
                                 GGGCATTGT TGTTGCTT
                                 ||||||||| ||||||||
                                 CCCGTGGCA ACGGCGGG
                                       G
GAM260  DTX1     5'  CCGCAGGAGCAGCAGGCTGTGG 15343    G   T  A
            CC                     GG CAT GT TGTTGCTTCTGTGG
                                 || ||| || ||||||||||||||
                                 CC GTG CG ACGACGAGGACGCC
                                  G   T  G
GAM260  DUOX1    3'  CCAATACCTATGTATGCAATGC 33829           TTGCTTCTG
            TC                     GGGCATTGTATG        TGG
                                 ||||||||||||        |||
                                 CTCGTAACGTAT        ACC
                                        GTATCCATA
GAM260  DUSP11   3'  CTAGACTTGTGATATGCGTGTG 13132      _      TG T__    TGG
            TTT                    GCAT TGTATGT  C   TCTG
                                 |||| |||||||  |   ||||
                                 TGTG GCGTATA  G   AGAT
                                   T      GT TTC    C
GAM260  DUSP3    3'  CTGTTTCTGTAACTTATGATGT 14563       TG  T    TTCT TG
            CT                     GGGCAT  TA GTTGC    G  G
                                 ||||||  || |||||    |  |
                                 TCTGTA  AT CAATG    T  C
                                    GT  T    TCTT GT
GAM260  DUSP4    5'  TTACAAATGTAATACAATGCCC 54060          GT   TTC
                                 GGGCATTGTAT  TGC   TGTGG
                                 ||||||||||  |||   |||||
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                                CCCGTAACATA ATG  ACATT
                                      __  TAA
GAM260  DYRK1A   3' TTATAGAAGTGGTGTTTTTTTT 55250    CATTGT TG TG
           CC                   GGG    A  T  CTTCTGTGG
                                |||    | |  |||||||||
                                CCT    T  G  GAAGATATT
                                  TTTTTT GT GT
GAM260  DYRK1A   3' TCACAGAAGTAGTGGTTTGCTT 55206      TTGTA GT
                                GGGCA   T  TGCTTCTGTGG
                                |||||   |  ||||||||||
                                TTCGT   G  ATGAAGACACT
                                  TTG__ TG
GAM260  DYRK1A   3' TTATAGAAGTGGTGTTTTTTTT 55207    CATTGT TG TG
           CC                   GGG    A  T  CTTCTGTGG
                                |||    | |  |||||||||
                                CCT    T  G  GAAGATATT
                                  TTTTTT GT GT
GAM260  DYRK1A   3' TCACAGAAGTAGTGGTTTGCTT 55248      TTGTA GT
                                GGGCA   T  TGCTTCTGTGG
                                |||||   |  ||||||||||
                                TTCGT   G  ATGAAGACACT
                                  TTG__ TG
GAM260  DYRK1A   3' TCACAGAAGTAGTGGTTTGCTT 7355       TTGTA GT
                                GGGCA   T  TGCTTCTGTGG
                                |||||   |  ||||||||||
                                TTCGT   G  ATGAAGACACT
                                  TTG__ TG
GAM260  DYRK1A   3' TTATAGAAGTGGTGTTTTTTTT 7356     CATTGT TG TG
           CC                   GGG    A  T  CTTCTGTGG
                                |||    | |  |||||||||
                                CCT    T  G  GAAGATATT
                                  TTTTTT GT GT
GAM260  DYRK3    5' CGCGGAGGCAGCCGTCC    13123     ATTGTAT
                                GGGC    GTTGCTTCTGTG
                                ||||    ||||||||||||
                                CCTG    CGACGGAGGCGC
                                  C_______
GAM260  E2F1     3' CTGTGGTCCCTCCTGCAGTGTC 84798        TGTTGCTT   TG
           T                    GGGCATTGTA      CTG  G
                                ||||||||||      |||  |
                                TCTGTGACGT      GGT  C
                                     CCTCCCT_   GT
GAM260  ECH1     5' TGTCAGGTTGCGGCATCGGTGC 59878       T     T_   TGG
           CC                   GGGCATTG ATGTTGC  TCTG
                                |||||||| |||||||  ||||
                                CCCGTGGC TACGGCG  GGAC
                                     _     TT    TGTC
GAM260  ED1      3' CGCAGGAGGGTTGGAGTGCTC  7367       G  TGTTG    TG
                                GGGCATT TA    CTTCTG  G
                                ||||||| ||    ||||||  |
```

```
                                CTCGTGA GT    GAGGAC  C
                                   G  TGG__     GT
GAM260  EFG2    5' CGTGGAGAGACTATGAGGCCC  50474     A TG  T   GC    TG
                                GGGC T  TA GTT  TTCTG  G
                                |||| |  || |||  |||||  |
                                CCCG A  AT CAG  GAGGT  C
                                  G GT  _   A_    GT
GAM260  EGFL4   5' CATGGTGTGTGCAGTGGCC   61808    G      GTT  TT
                                GG CATTGTAT   GC  CTGTG
                                || |||||||   ||  |||||
                                CC GTGACGTG   TG  GGTAC
                                 G       ___  T_
GAM260  EGFL4   3' CTGTGGGGGTGGTGGGGGTGCT 61809       GTA  TT     TG
                                GGCATT   TG  GCTTCTG  G
                                ||||||   ||  |||||||  |
                                TCGTGG   GT  TGGGGGT  C
                                   GG_  GG     GT
GAM260  EGFR    3' CCACGGAGGATAGTATGAGCCC 17836     A TG   GTTG
                                GGGC T  TAT    CTTCTGTGG
                                |||| |  |||    |||||||||
                                CCCG A  ATG    GGAGGCACC
                                  _ GT   ATA_
GAM260  EGLN2   5' CCATGGGCCCGGGCGGTGCCC  54927         A  TT  TT
                                GGGCATTGT TG  GC  CTGTGG
                                |||||||| ||  ||  ||||||
                                CCCGTGGCG GC  CG  GGTACC
                                     G  C_  __
GAM260  EGLN2   5' CCATGGGCCCGGGCGGTGCCC  53853         A  TT  TT
                                GGGCATTGT TG  GC  CTGTGG
                                |||||||| ||  ||  ||||||
                                CCCGTGGCG GC  CG  GGTACC
                                     G  C_  __
GAM260  EHD2    3' CACGGGAGGGACAAGGCTT   27488     ATTGTA   G
                                GGGC     TGTT CTTCTGTG
                                ||||     |||| ||||||||
                                TTCG     ACAG GAGGGCAC
                                  GA_____   G
GAM260  EHD3    3' CACCTGGCCTATGATGTTT   27476       TG  TGTT  TCT
                                GGGCAT  TA   GCT   GTG
                                ||||||  ||   |||   |||
                                TTTGTA  AT   CGG   CAC
                                   GT  C___   TC_
GAM260  EHD3    3' TCACAGAAGCAAACCGTGCCT  27481       T  ATG
                                GGGCAT GT   TTGCTTCTGTGG
                                |||||| ||   ||||||||||||
                                TCCGTG CA   AACGAAGACACT
                                   C  ___
GAM260  EHD4    3' CCTAGTGTGTGCAGTGTCT   57690         GTT  TT   T
                                GGGCATTGTAT   GC  CTG GG
                                ||||||||||   ||  ||| ||
```

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                                TCTGTGACGTG   TG  GAT CC
                                      ___  T_  _
GAM260  EIF2AK3  5'  CTCAATGGGCGATGTCC     16711         A     CTTCT
                                GGGCATTGT TGTTG     G
                                |||||||||  |||||     |
                                CCTGTAGCG GTAAC     C
                                     G     T____
GAM260  EIF2C1   3'  CCAGCAGCTGTAATGTACAGTT 24168     C          TT  _
           CCT                    GGG ATTGTATGTTGC  CTG TGG
                                |||  ||||||||||||  |||  |||
                                TCC TGACATGTAATG  GAC ACC
                                  T          TC   G
GAM260  EIF2C1   3'  CTATAGAGGTGGTGTAAGAGTG 24172      G_  TG TG
                                CATT  TA  T  CTTCTGTGG
                                ||||  ||  |  |||||||||
                                GTGA  AT  G  GGAGATATC
                                  GA  GT GT
GAM260  EIF4G2   5'  CTATGGAGGTGGCAGCGGGTAC 7423     GCA    A   TG
           C                     GG   TTGT TGT  CTTCTGTGG
                                ||   ||||  |||  |||||||||
                                CC   GGCG ACG  GGAGGTATC
                                 ATG    _   GT
GAM260  EIF5A2   3'  TTACATGATACTATGCAATGCT 39858           TTGCT  _
           T                     GGGCATTGTATG     TC TGTGG
                                ||||||||||||     ||  |||||
                                TTCGTAACGTAT     AG ACATT
                                       CAT__  T
GAM260  EN2      5'  CCGCGGAGCTCTGCGGGGCTC  7457      A     TGTT   T
                                GGGC TTGTA    GCT CTGTGG
                                ||||  |||||    |||  ||||||
                                CTCG GGCGT    CGA GGCGCC
                                  G     CT__   _
GAM260  ENPP2    3'  CCAAATCTGACATATTATGCCT 20601       T      GCTTCTG
                                GGGCAT GTATGTT       TGG
                                ||||||  |||||||       |||
                                TCCGTA TATACAG       ACC
                                    T      TCTAA__
GAM260  ENTPD6   3'  TTGCAGAAGGCCTGGTGCTGCC 6973       TT    GTT  _    TG
           C                     GGGCA  GTAT   GC TTCTG  G
                                |||||  ||||   ||  |||||  |
                                CCCGT  CGTG   CG AAGAC  T
                                   __    GTC  G     GT
GAM260  ENTPD6   3'  CTGCTTCAGTGAATGTACAGTG 6969             _   TCT TG
           CCC                     GGGCATTGTATGTT GCT   G  G
                                ||||||||||||||  |||   |  |
                                CCCGTGACATGTAA TGA   C  C
                                       G   CTT GT
GAM260  EPB49    5'  TCGCGGCCCCAAGCGCGCAGTG 8792          TA    GCTT_
           CCC                     GGGCATTG  TGTT     CTGTGG
                                ||||||||  ||||     ||||||
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                                CCCGTGAC  GCGA    GGCGCT
                                    GC    ACCCC
GAM260  EPB72    3'  TCACAGTATATTGACTATATAG 14609        _  GCTT__
          TGTCT                   CATTGTAT GTT     CTGTGG
                                |||||||| |||     ||||||
                                GTGATATA CAG     GACACT
                                    T   TTATAT
GAM260  EPHA8    3'  CCATGGGGGCGGGGGAGAGGCT 40055      A  GTATG
          C                     GGGC TT    TTGCTTCTGTGG
                                ||||| ||    ||||||||||||
                                CTCG AG    GGCGGGGGTACC
                                  G  AGGG_
GAM260  EPHA8    3'  TCACTCTAGTGTGTGGTCCC   40066    C  TG   GTT   TCT
                                GGG AT  TAT   GCT   GTGG
                                ||| ||  |||   |||   ||||
                                CCC TG  GTG   TGA   CACT
                                  _  GT   ___   TCT
GAM260  EPHA8    3'  TCATGGAGGCACCGTGGGCCT  40067     ATTG    T
                                GGGC    TATG TGCTTCTGTGG
                                ||||    |||| ||||||||||||
                                TCCG    GTGC ACGGAGGTACT
                                  G___    C
GAM260  EPHX1    5'  AGAGGGAAGCGACAGCAGTGCT 3693          A        GTGG
          T                     GGGCATTGT TGTTGCTTCT
                                |||||||||| ||||||||||
                                TTCGTGACG ACAGCGAAGG
                                      _        GAGAT
GAM260  EPM2A    3'  TAGTATAATATGCAGTTCCT   19034     C        CTT
                                GGG ATTGTATGTTG   CTG
                                ||| ||||||||||||  |||
                                TCC TGACGTATAAT   GAT
                                  T         AT_
GAM260  ERBB2    3'  CCGCAGAAGCCCTGATGTGTCC 15473       TGTATGTT
                                GGGCAT       GCTTCTGTGG
                                ||||||       ||||||||||
                                CCTGTG       CGAAGACGCC
                                    TAGTCC__
GAM260  ERBB2IP  3'  CCATAGAAGACCAATAACTGTT 37984      TTG   GTTG
          T                     GGGCA   TAT    CTTCTGTGG
                                |||||   |||    |||||||||
                                TTTGT   ATA    GAAGATACC
                                  CA_   ACCA
GAM260  ERCC3    5'  CGTGGGAGCGGGGTCA      3696     T  G       TG
                                TG AT TTGCTTCTG  G
                                || || |||||||||  |
                                AC TG GGCGAGGGT  C
                                  _  G        GT
GAM260  ESR1     3'  TCACAGGTGATAAACAATGCTT 3709          A   TG TT
                                GGGCATTGT TGT  C  CTGTGG
                                ||||||||| |||  |  ||||||
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                                TTCGTAACA ATA  G  GACACT
                                     A   GT __
GAM260  ESRRA    3'  TGCATTGGGCATTAGTGTCC   15484        T   TG  TC  TG
                                GGGCATTG ATGT  CT  TG  G
                                |||||||| ||||  ||  ||  |
                                CCTGTGAT TACG  GG  AC  T
                                     _   __  TT  GT
GAM260  ESRRBL1  5'  CGCAGAGGTCTGTGGGCCT   35848     A TG  TGTT
                                GGGC T  TA   GCTTCTGTG
                                |||| |  ||   |||||||||
                                TCCG G  GT   TGGAGACGC
                                  _ GT  C___
GAM260  EVC      3'  TCACAGGATGTTCCAGTGTCC  27298        TATGTT  _
                                GGGCATTG     GC TTCTGTGG
                                ||||||||     || ||||||||
                                CCTGTGAC     TG AGGACACT
                                     CT____  T
GAM260  EZH1     3'  CCATAGAGGCAAGGCCCAATGG 8815     G    TATG
             CC                   GG CATTG   TTGCTTCTGTGG
                                || |||||   ||||||||||||
                                CC GTAAC   AACGGAGATACC
                                 G    CCGG
GAM260  F2R      3'  GATTTAATATGCAAAGTCT   8839       A        CT
                                GGGC TTGTATGTTG  TC
                                |||| ||||||||||  ||
                                TCTG AACGTATAAT  AG
                                  A        TT
GAM260  F2RL3    5'  CGCGGGGGCAGGGGCAGCCT   14175     AT   ATG       TG
                                GGGC  TGT   TTGCTTCTG  G
                                ||||  |||   |||||||||  |
                                TCCG  ACG   GACGGGGGC  C
                                  __  GG_       GT
GAM260  F2RL3    3'  TAGAAGCGAGTGGCC      14191    G   TGTATG
                                GG CAT     TTGCTTCTG
                                || |||     |||||||||
                                CC GTG     AGCGAAGAT
                                 G  _______
GAM260  F2RL3    3'  TTACATCCAGTGTGGGTGGTGT 14198       TG ATGT    TC_
             CC                   GGGCAT  T    TGCT   TGTGG
                                ||||||  |    ||||   |||||
                                CCTGTG  G    GTGA   ACATT
                                   GT GGT_    CCT
GAM260  FACL4    3'  GAATAATTACAGTGCCT     15509          T    C
                                GGGCATTGTA GTTG TTC
                                |||||||||| |||| |||
                                TCCGTGACAT TAAT AAG
                                     _   _
GAM260  FACL4    3'  GAATAATTACAGTGCCT     43399          T    C
                                GGGCATTGTA GTTG TTC
                                |||||||||| |||| |||
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                                TCCGTGACAT TAAT AAG
                                      _   _
GAM260  FACL5   3' TTATATTGAGACATATAATGT 64189          GCTTC
                                GCATTGTATGTT    TGTGG
                                ||||||||||||    |||||
                                TGTAATATACAG    ATATT
                                      AGTT_
GAM260  FASN    3' AGGCAGCGTGTGGGTCC    14631     A TG
                                GGGC T  TATGTTGCTT
                                |||| |  ||||||||||
                                CCTG G  GTGCGACGGA
                                  _ GT
GAM260  FBXL11  3' CCATGGTCCCCAGCAGTGCCT 24568        A  TTGCTT
                                GGGCATTGT TG    CTGTGG
                                ||||||||| ||    ||||||
                                TCCGTGACG AC    GGTACC
                                     _ CCCT__
GAM260  FBXL5   3' CCATGGAGGTGATTGGTTC  24076    ATTGTAT  TG
                                GGGC     GT  CTTCTGTGG
                                ||||     ||  |||||||||
                                CTTG     TA  GGAGGTACC
                                  GT_____  GT
GAM260  FBXL5   3' CCATGGAGGTGATTGGTTC  53201    ATTGTAT  TG
                                GGGC     GT  CTTCTGTGG
                                ||||     ||  |||||||||
                                CTTG     TA  GGAGGTACC
                                  GT_____  GT
GAM260  FBXL7   5' GCAGCTATGGAGTGTCC    24550      G  _
                                GGGCATT TAT GTTGC
                                ||||||| ||| |||||
                                CCTGTGA GTA CGACG
                                    G  T
GAM260  FBXW1B  3' CGCAGTATTCATACAGTGTTT 24523        TTGCTT  TG
                                GGGCATTGTATG    CTG  G
                                ||||||||||||    |||  |
                                TTTGTGACATAC    GAC  C
                                      TTAT__  GT
GAM260  FBXW1B  3' CGCAGTATTCATACAGTGTTT 53327        TTGCTT  TG
                                GGGCATTGTATG    CTG  G
                                ||||||||||||    |||  |
                                TTTGTGACATAC    GAC  C
                                      TTAT__  GT
GAM260  FBXW1B  3' CGCAGTATTCATACAGTGTTT 53338        TTGCTT  TG
                                GGGCATTGTATG    CTG  G
                                ||||||||||||    |||  |
                                TTTGTGACATAC    GAC  C
                                      TTAT__  GT
GAM260  FETUB   3' TAGGGGTATGGTGCGCC    26882    ATT   GT
                                GGC  GTAT  TGCTTCTG
                                |||  ||||  ||||||||
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                                CCG   CGTG  ATGGGGAT
                                  ___   GT
GAM260   FGF5     3'  CTATGAGTGAGAATATGTGGTG 52485      TG     G  _ _
              TTT                   GGCAT  TATGTT CTT CT GTGG
                                |||||  |||||| ||| || ||||
                                TTGTG  GTATAA GAG GA TATC
                                  GT     _  T  G
GAM260   FGF5     3'  CACTGAATGCATAATGTTT    52479        TATGT  _  T
                                GGGCATTG    TGC TTC GTG
                                ||||||||    ||| ||| |||
                                TTTGTAAT    ACG AAG CAC
                                    _____  T  T
GAM260   FGF5     3'  CCACAGCAGGCCCCGGTATGTG 52480    TG   TT___   _
              ATGTTC                AT  TATG    GCTT CTGTGG
                                ||  ||||    |||| ||||||
                                TA  GTAT    CGGA GACACC
                                 GT   GGCCC   C
GAM260   FGF5     3'  CACTGAATGCATAATGTTT    15533        TATGT  _  T
                                GGGCATTG    TGC TTC GTG
                                ||||||||    ||| ||| |||
                                TTTGTAAT    ACG AAG CAC
                                    _____  T  T
GAM260   FGF5     3'  CCACAGCAGGCCCCGGTATGTG 15534    TG   TT___   _
              ATGTTC                AT  TATG    GCTT CTGTGG
                                ||  ||||    |||| ||||||
                                TA  GTAT    CGGA GACACC
                                 GT   GGCCC   C
GAM260   FGF5     3'  CTATGAGTGAGAATATGTGGTG 15539      TG     G  _ _
              TTT                   GGCAT  TATGTT CTT CT GTGG
                                |||||  |||||| ||| || ||||
                                TTGTG  GTATAA GAG GA TATC
                                  GT     _  T  G
GAM260   FGR1     5'  CATGGAGATGTGGAGCCT    43629      A TG   GTTGC
                                GGGC T  TAT    TTCTGTG
                                |||| |  |||    |||||||
                                TCCG G  GTA    GAGGTAC
                                  A GT  _____
GAM260   FGFR1    3'  CCACCAGAGTGATGTGTGGTCT 43630     C  TG    TG   CT
              T                  GGG AT  TATGT  CTT  GTGG
                                ||| ||  |||||  |||  ||||
                                TTC TG  GTGTA  GAG  CACC
                                  _ GT    GT   AC
GAM260   FGFR1    3'  GCTGGCATGCAGTGCCC     43633           _
                                GGGCATTGTATGTT GC
                                |||||||||||||| ||
                                CCCGTGACGTACGG CG
                                         T
GAM260   FGFR1    5'  CATGGAGATGTGGAGCCT    43613      A TG   GTTGC
                                GGGC T  TAT    TTCTGTG
                                |||| |  |||    |||||||
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                                TCCG G  GTA    GAGGTAC
                                  A GT  _____
GAM260  FGFR1   5'  CATGGAGATGTGGAGCCT   43620     A TG   GTTGC
                                GGGC T  TAT    TTCTGTG
                                |||| |  |||    |||||||
                                TCCG G  GTA    GAGGTAC
                                  A GT  _____
GAM260  FGFR1   5'  CATGGAGATGTGGAGCCT   43636     A TG   GTTGC
                                GGGC T  TAT    TTCTGTG
                                |||| |  |||    |||||||
                                TCCG G  GTA    GAGGTAC
                                  A GT  _____
GAM260  FGFR1   5'  CATGGAGATGTGGAGCCT   5203      A TG   GTTGC
                                GGGC T  TAT    TTCTGTG
                                |||| |  |||    |||||||
                                TCCG G  GTA    GAGGTAC
                                  A GT  _____
GAM260  FGFR1   5'  CATGGAGATGTGGAGCCT   31796     A TG   GTTGC
                                GGGC T  TAT    TTCTGTG
                                |||| |  |||    |||||||
                                TCCG G  GTA    GAGGTAC
                                  A GT  _____
GAM260  FKBP1A  3'  CCATGGAGGGATCTGGTGCCT  5858         TAT   G
                                GGGCATTG   GTT CTTCTGTGG
                                ||||||||   ||| |||||||||
                                TCCGTGGT   TAG GGAGGTACC
                                    C__   _
GAM260  FLNB    3'  TCACAGATGACAGCAGGCGGTG 62180         A    CT_
          CTC                     GGGCATTGT TGTTG   TCTGTGG
                                |||||||||| |||||   |||||||
                                CTCGTGGCG ACGAC   AGACACT
                                    G    AGT
GAM260  FLRT2   3'  AGTCATGTGCAATGCTT     25055           T
                                GGGCATTGTATGT GCT
                                |||||||||||||| |||
                                TTCGTAACGTGTA TGA
                                       C
GAM260  FLT1    3'  CATGGGAGCCAGCTGCTT    8915       TTGTAT   _
                                GGGCA     GTTG CTTCTGTG
                                |||||     |||| ||||||||
                                TTCGT     CGAC GAGGGTAC
                                  _______   C
GAM260  FLT1    3'  CTATGGAAGTGGTTCTATGTCC 8917        TGTAT TT
                                GGGCAT    G  GCTTCTGTGG
                                ||||||    |  ||||||||||
                                CCTGTA    T  TGAAGGTATC
                                   TCT__ GG
GAM260  FMNL    5'  GAGCGGCGGTGATGCTC     19704       TG A
                                GGGCAT  T TGTTGCTT
                                ||||||  | ||||||||
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                                CTCGTA  G GCGGCGAG
                                   GT _
GAM260  FMR1    3'  TATAGAAGAATGCATGC     8941       TG_
                                GTATGT   CTTCTGTG
                                ||||||   ||||||||
                                CGTACG   GAAGATAT
                                   TAA
GAM260  FOSB    5'  TCACAGGGGCCCCCCTGTGCCC 22111      TGTATGTT
                                GGGCAT      GCTTCTGTGG
                                ||||||      ||||||||||
                                CCCGTG      CGGGGACACT
                                   TCCCCC__
GAM260  FOXD2   5'  TGCAGGAGCCTGGGTGAGTTC  15572     A TG ATGTT     TG
                                GGGC T  T    GCTTCTG  G
                                ||||  |  |    |||||||  |
                                CTTG A  G    CGAGGAC  T
                                  _ GT GGTC_      GT
GAM260  FRK     3'  AGGTGATATATAATTTCC    8960     C       TG
                                GGG ATTGTATGT  CTT
                                |||  |||||||||  |||
                                CCT TAATATATA  GGA
                                  T       GT
GAM260  FUT5    3'  CGTGGATGTGTTGCGATGCCT  8966         TGTT  T   TG
                                GGGCATTGTA    GC TCTG  G
                                ||||||||||    ||  ||||  |
                                TCCGTAGCGT    TG AGGT  C
                                      TG__  T   GT
GAM260  FUT9    3'  TCACTAAGTATTACAATGTCT  67847        TGT    CT
                                GGGCATTGTA   TGCTT  GTGG
                                ||||||||||   |||||  ||||
                                TCTGTAACAT   ATGAA  CACT
                                      T__    T_
GAM260  GA      3'  CTATGGAGAGCTACACTGCTT  25174      T   TGTT  _
                                GGGCA TGTA    GCT TCTGTGG
                                |||||  ||||    |||  |||||||
                                TTCGT ACAT    CGA AGGTATC
                                   C    _____   G
GAM260  GALR1   5'  CTGCAGGAGCCGCACAGTGC   7618       AT  T     TG
                                GCATTGT  GT GCTTCTG  G
                                |||||||  ||  |||||||  |
                                CGTGACA  CG CGAGGAC  C
                                    __ C      GT
GAM260  GAN     3'  CGCAGAAATTAGATAATGTTT  41861       ATGTTGC    TG
                                GGGCATTGT      TTCTG  G
                                |||||||||      |||||  |
                                TTTGTAATA      AAGAC  C
                                     GATTA__     GT
GAM260  GAP43   3'  TGTTCCAAGTGTGTGTGCAATG 8985         TG _    CTGTGG
            TTC                   GGGCATTGTA  T TGCTT
                                ||||||||||  |  |||||
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                                CTTGTAACGT  G GTGAA
                                     GT T    CCTTGTC
GAM260  GASC1   3'  CACAGAGGAGGCGGGTCC   64243     A   ATGTTG
                                GGGC TTGT     CTTCTGTG
                                |||| ||||     ||||||||
                                CCTG GGCG     GGAGACAC
                                  _   GA____
GAM260  GCDH    3'  CGTAGGAGCGCTGTGCTC    3854       T  ATGTT
                                GGGCAT GT    GCTTCTGTG
                                |||||| ||    |||||||||
                                CTCGTG CG    CGAGGATGC
                                   T _____
GAM260  GFAP    3'  CCATGGGGGCAGGGCATG    9012       __
                                TATGT  TGCTTCTGTGG
                                |||||  ||||||||||
                                GTACG  ACGGGGGTACC
                                   GG
GAM260  GGT2    5'  CCGCGGATGCCAAGCAGTGCTT 73710         A  TT  T
                                GGGCATTGT TG  GC TCTGTGG
                                ||||||||| ||  || |||||||
                                TTCGTGACG AC  CG AGGCGCC
                                     A  __  T
GAM260  GIPR    5'  CAGGAGCAAGTGACC      3896     G   TGTATG
                                GG CAT     TTGCTTCTG
                                || |||     |||||||||
                                CC GTG     AACGAGGAC
                                 A  _______
GAM260  GJA5    3'  TACCCAGTATACGAAGCCT    17943      A       CTTCT
                                GGGC TTGTATGTTG    GTG
                                |||| ||||||||||    |||
                                TCCG AGCATATGAC    CAT
                                  A        C____
GAM260  GLA     5'  CCGCGGAAATTTATGCTGTCC  3913       TT    TTGC
                                GGGCA  GTATG   TTCTGTGG
                                |||||  |||||   ||||||||
                                CCTGT  CGTAT   AAGGCGCC
                                   __    TTA_
GAM260  GLI2    5'  TGTGAAAGAAAGTGATGATGCG 47529         _ TG  _ GTGG
            ATGTCT                  GCATTGTAT GT  CTT CT
                                |||||||| ||  ||| ||
                                TGTAGCGTA TA  GAA GA
                                     G  GT   A  AAGTGTC
GAM260  GLTSCR1  3'  CCAGCCTCCCAGCGTGCTGTGC 31669       T      CTTCTG
            CC                    GGGCAT GTATGTTG     TGG
                                ||||||| ||||||||     |||
                                CCCGTG CGTGCGAC     ACC
                                   T       CCTCCG
GAM260  GNAI3   3'  TTATAGGGAGTTTTGTACATGG 21445      __     TT     GTGG
            TGCCT                   GCAT  TGTATG  GCTTCT
                                ||||  ||||||  ||||||
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                                CGTG  ACATGT  TGAGGG
                                  GT     TT     ATATT
GAM260  GPC5    3'  TAGAAGGAAATGTCT       15553        GTATGT G
                                GGGCATT     T CTTCTG
                                |||||||     | ||||||
                                TCTGTAA     A GAAGAT
                                   _______ G
GAM260  GPC6    3'  CGCAGAAGTAAAGGAATCTC  19124     C   GTATG       TG
                                GGG ATT    TTGCTTCTG  G
                                ||| |||    |||||||||  |
                                CTC TAA    AATGAAGAC  C
                                  _  GGA__       GT
GAM260  GPR17   3'  CGCAGGGGCTTGTGATGGCT  17953    G   TG  TGTT      TG
                                GG CAT  TA   GCTTCTG  G
                                || |||  ||   |||||||  |
                                TC GTA  GT   CGGGGAC  C
                                 G   GT  T___      GT
GAM260  GPR61   5'  CACAGAGTTAGTAATGCCC   78910        TATGTT   T
                                GGGCATTG     GCT CTGTG
                                ||||||||     ||| |||||
                                CCCGTAAT     TGA GACAC
                                     GAT___  _
GAM260  GPX3    3'  GCAGCTGTGTAGTGCT      9120          _
                                GGCATTGTAT GTTGC
                                |||||||||| |||||
                                TCGTGATGTG CGACG
                                      T
GAM260  GRAF    3'  GTGGCTGTGCGGTGCCC     30574          _  TG
                                GGGCATTGTAT GT  C
                                |||||||||||  ||  |
                                CCCGTGGCGTG CG  G
                                      T  GT
GAM260  GRB10   3'  TTGTAGGAGGGGGATGTGGCGT 17989      A TG   G  G     TG
          TT                     GGGC T  TAT TT CTTCTG  G
                                |||| |  ||| || ||||||  |
                                TTTG G  GTA GG GAGGAT  T
                                  C GT   G  G     GT
GAM260  GRF2    3'  CTGTGGGAGCAGACCCGTGGGC 17993      ATTGTATG       TG
          CT                     GGGC       TTGCTTCTG  G
                                ||||       |||||||||  |
                                TCCG       GACGAGGGT  C
                                  GGTGCCCA        GT
GAM260  GRIN2B  3'  GTTTATATATAAGCCC      5905       A       T_
                                GGGC TTGTATGT  GC
                                |||| ||||||||  ||
                                CCCG AATATATA  TG
                                  _       TT
GAM260  GRIN2C  3'  GCCATGGGACCCCAGTGACAGA 5911    TG A   TG  _____
          TGATGTCT                  T TGT  CT     TCTGTGG   C
                                | |||  ||    |||||||  |
```

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                                A ACA  GA    GGGTACC   G
                               GT G   GT  CCCCA
GAM260  GRINL1A  3'  CAGAAGCTTCAGTCCC     69513     C    TATGTT
                               GGG ATTG     GCTTCTG
                               ||| ||||     |||||||
                               CCC TGAC     CGAAGAC
                                 _    TT____
GAM260  GRLF1    3'  TCATAGGAGCAGCTCGCTGGCC 78564     ATT  AT
                               GGC   GT  GTTGCTTCTGTGG
                               |||   ||  ||||||||||||
                               CCG   CG  CGACGAGGATACT
                                 GT_  CT
GAM260  GRM6     3'  CCGATTCCAGCATGTGAGCTT  5931      A TG      CTTCTG
                               GGGC T  TATGTTG     TGG
                               |||| |  |||||||     |||
                               TTCG A  GTACGAC     GCC
                                 _ GT      CTTA__
GAM260  GTF2E2   3'  CATGGGCAATGTGATGTTC   9145       TG AT     TC
                               GGGCAT  T  GTTGCT  TG
                               ||||||  |  ||||||  ||
                               CTTGTA  G  TAACGG  AC
                                  GT __     GT
GAM260  GUCY1B2  3'  CAGAAGCAAGTGCTC      14684       TGTATG
                               GGGCAT     TTGCTTCTG
                               ||||||     |||||||||
                               CTCGTG     AACGAAGAC
                                          _______
GAM260  GUCY1B2  5'  CGCAGAAGTACAAGATGCCT  14686       GTA   T     TG
                               GGGCATT   TGT GCTTCTG  G
                               |||||||   ||| |||||||  |
                               TCCGTAG   ACA TGAAGAC  C
                                  A__   _     GT
GAM260  HAO2     3'  TCACAGCACAGTGTGTGATGCT 33267      TG  TG   CTT
                               GGCAT  TA  TTG   CTGTGG
                               |||||  ||  |||   ||||||
                               TCGTA  GT  GAC   GACACT
                                  GT  GT   AC_
GAM260  HCN4     5'  CGCGGGGGCGGGGCGCCT    18489     ATT  ATGT
                               GGGC   GT    TGCTTCTGTG
                               ||||   ||    ||||||||||
                               TCCG   CG    GCGGGGGCGC
                                 ___  GG__
GAM260  HD       3'  GCCGCGGGCGGCCAGGCAACGT 9186          _______
            GCGTGTCT                GTATGTTGCT     TCTGTGG   C
                               ||||||||||     |||||||  |
                               CGTGCAACGG     GGGCGCC   G
                                     ACCGGC
GAM260  HDAC4    3'  CTGCAGGGAGGGTATGATTGCC 20109      _ TG   G  G  T   TG
            T                   GGGCA T  TAT TT CT CTG  G
                               |||||  |  ||| || || |||  |
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                                TCCGT A  ATG GA GG GAC  C
                                  T GT   G  _  _   GT
GAM260  HDAC5    3'  CGCAGGGGGTGGTGGTGTCT   57609      TG ATGTTG     TG
                                GGGCAT  T     CTTCTG  G
                                ||||||  |     ||||||  |
                                TCTGTG  G     GGGGAC  C
                                   GT GTG___      GT
GAM260  HELLS    3'  CTGTGGAAGTTTAGTAAATGTC 36035       G   GTT      TG
           T                     GGGCATT TAT   GCTTCTG  G
                                ||||||| |||   |||||||  |
                                TCTGTAA ATG   TGAAGGT  C
                                    _  ATT      GT
GAM260  HEM1     5'  CTGTGGAAGCTGTGTCTGCAGG 18052     A    TGTT__      TG
           GCTC                    GGC TTGTA     GCTTCTG  G
                                ||| |||||     |||||||  |
                                TCG GACGT     CGAAGGT  C
                                  G    CTGTGT      GT
GAM260  HEM1     5'  CGTGGAAGTAATGGAGCGC    18051    G  ATTGTA        TG
                                G GC     TGTTGCTTCTG  G
                                | ||     ||||||||||  |
                                C CG     GTAATGAAGGT  C
                                 G  AG____         GT
GAM260  HERC2    3'  GTCATGGAAAGTGTACTATATA 16241        __   ___
           TAATGTTT                TGTATGT  TGC   TTCTGTGG   T
                                |||||||  |||   ||||||||  |
                                ATATATA  ATG   AAGGTACT   G
                                    TC   TGA
GAM260  HIVEP3   5'  CCGTAGGAGTGGACATGAATGC 44433       G    _ TG
           T                     GGCATT TATG T  CTTCTGTGG
                                ||||||| |||| |  |||||||||
                                TCGTAA GTAC G  GAGGATGCC
                                   _   A GT
GAM260  HK1      5'  TTGCAAGGACAGTGTATGTTGT 53129      TT   TG   C    _ TG
           CC                    GGGCA  GTA  TTG TTCT G  G
                                |||||  |||  ||| |||| |  |
                                CCTGT  TAT  GAC AGGA C  T
                                   TG   GT   _   A GT
GAM260  HK1      5'  TTGCAAGGACAGTGTATGTTGT 53134      TT   TG   C    _ TG
           CC                    GGGCA  GTA  TTG TTCT G  G
                                |||||  |||  ||| |||| |  |
                                CCTGT  TAT  GAC AGGA C  T
                                   TG   GT   _   A GT
GAM260  HLA-DQA1 3'  CCATGGAAGCAACAAATTCCC  97900     C   GTA
                                GGG ATT   TGTTGCTTCTGTGG
                                ||| |||   ||||||||||||||
                                CCC TAA   ACAACGAAGGTACC
                                  T  ___
GAM260  HLA-G    3'  CTACTCTAGGCAGTGACAGTGC 9225          ATG     CT_
           CC                    GGGCATTGT   TTGCTT   GTGG
                                |||||||||   ||||||   ||||
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                                CCCGTGACA  GACGGA  CATC
                                    GT_    TCT
GAM260  HMGN1   3'  TTACAGATTTGAACATGTAGTG 17119         GCT_
          T                  GCATTGTATGTT  TCTGTGG
                             ||||||||||||  |||||||
                             TGTGATGTACAA  AGACATT
                                 GTTT
GAM260  HNRPDL  3'  GTGTGGTCAGTAGGTGCGGTGT 18429        G   T_ TG  G
          CT                  GGGCATTGTAT TTGCT  C  TG
                             |||||||||||| |||||  |  ||
                             TCTGTGGCGTG GATGA  G  GT
                                   _   CT GT  GT
GAM260  HNRPK   3'  TTATGGAAGTGACTAATGCT  9250       TAT  TG
                             GGCATTG  GT  CTTCTGTGG
                             |||||||  ||  |||||||||
                             TCGTAAT  CA  GAAGGTATT
                                ___  GT
GAM260  HNRPK   3'  TTATGGAAGTGACTAATGCT  48360      TAT  TG
                             GGCATTG  GT  CTTCTGTGG
                             |||||||  ||  |||||||||
                             TCGTAAT  CA  GAAGGTATT
                                ___  GT
GAM260  HOXA3   5'  CCGCGGGGGCGTGCCAATGTGC 47687   G    TATGT
                             G GCATTG    TGCTTCTGTGG
                             | ||||||    ||||||||||
                             C TGTAAC    GCGGGGGCGCC
                              G    CGT__
GAM260  HOXA7   3'  TCACAGAATACCTGAATGCCC  22572      G  T  TGC
                             GGGCATT TA GT   TTCTGTGG
                             ||||||| || ||   ||||||||
                             CCCGTAA GT CA   AAGACACT
                                _  C  T__
GAM260  HOXD3   3'  CAATCTGGTAATGGTGTCC   22573      GTAT    TCTG
                             GGGCATT   GTTGCT   TG
                             |||||||   ||||||   ||
                             CCTGTGG   TAATGG   AC
                                 ____     TCTA
GAM260  HPCAL1  3'  GGTGACATGCAGGGTTC    56188    A     TG
                             GGGC TTGTATGT  CT
                             |||| ||||||||  ||
                             CTTG GACGTACA  GG
                               G      GT
GAM260  HPCAL1  3'  GGTGACATGCAGGGTTC    9270     A     TG
                             GGGC TTGTATGT  CT
                             |||| ||||||||  ||
                             CTTG GACGTACA  GG
                               G      GT
GAM260  HS2ST1  3'  GCAGCCCATACGGTCTC    24334    C     __
                             GGG ATTGTAT  GTTGC
                             ||| |||||||  |||||
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                                CTC TGGCATA  CGACG
                                  _     CC
GAM260  HSD11B2  3'  TCACAGGACTCTGCAGATAGTG 3972         A   TGC_
            CCT                   GGGCATTGT TGT    TTCTGTGG
                                  ||||||||| |||    ||||||||
                                  TCCGTGATA ACG    AGGACACT
                                     G   TCTC
GAM260  HTR2C    3'  GCACATACAGATGGTGTCC    6022       ____      T
                                  GGGCAT    TGTATGT GC
                                  ||||||    ||||||| ||
                                  CCTGTG    ACATACA CG
                                     GTAG     _
GAM260  HTR2C    5'  TCGTGGCGCTCGTGTGATGGCC 6024     G   TG    TT  TT TG
                                  GG CAT  TATG  GC  C  TGG
                                  || |||  ||||  ||  |  |||
                                  CC GTA  GTGC  CG  G  GCT
                                   G   GT    T_  C_ GT
GAM260  HYAL4    5'  CTGCAGGAGCATGCCATCATGC 24373       T T   T__       TG
            CC                    GGGCAT G ATG   TGCTTCTG  G
                                  |||||| | |||   ||||||||  |
                                  CCCGTA C TAC   ACGAGGAC  C
                                     _ _  CGT       GT
GAM260  ICA1     3'  TATGGAAGCAGCCATAT     42253      _
                                  GTATG TTGCTTCTGTG
                                  ||||| ||||||||||
                                  TATAC GACGAAGGTAT
                                     C
GAM260  ICA1     3'  GCATGTGCAGTCCC       42256     C       T
                                  GGG ATTGTATGT GC
                                  ||| |||||||| ||
                                  CCC TGACGTGTA CG
                                    _       _
GAM260  IDH3G    5'  AACATGGCGGCAGCGGTGCTC  14705         A      TC   GG
                                  GGGCATTGT TGTTGCT  TGT
                                  ||||||||| |||||||  |||
                                  CTCGTGGCG ACGGCGG  ACA
                                        _      T_   AC
GAM260  IFNA16   3'  TTACAGATGACCATGCTGATGT 9297         _    TTGCT
            CT                    GGGCATT GTATG    TCTGTGG
                                  ||||||| |||||    |||||||
                                  TCTGTAG CGTAC    AGACATT
                                     T    CAGT_
GAM260  IFNA17   3'  TTACAGATGACCATGCTGATGT 41201        _    TTGCT
            CT                    GGGCATT GTATG    TCTGTGG
                                  ||||||| |||||    |||||||
                                  TCTGTAG CGTAC    AGACATT
                                     T    CAGT_
GAM260  IFNAR2   3'  TTACAGGGGTGAGCCGCTGTGC 6047       T  ATG TG
            CT                    GGGCAT GT   T  CTTCTGTGG
                                  |||||| ||   |  |||||||||
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                                TCCGTG CG   A  GGGGACATT
                                   T  CCG GT
GAM260  IFNGR2   3'  TCATGGGGGTGACAAGC     18649    A   TG
                                GT TGT  CTTCTGTGG
                                || |||  |||||||||
                                CG ACA  GGGGGTACT
                                 A   GT
GAM260  IFNW1    5'  CCATGCATACAAGCAATGTCT  9300         A  _  TTCT
                                GGGCATTGT TGT TGC    GTGG
                                |||||||||  ||| |||    ||||
                                TCTGTAACG ACA ACG    TACC
                                     A   T  _____
GAM260  IGHMBP2  3'  CGCTGGTGACTGCAGTGTTC   9303          T  TG  TCT TG
                                GGGCATTGTA GT  CT   G  G
                                ||||||||||  ||  ||   |  |
                                CTTGTGACGT CA  GG   C  C
                                      _  GT  T__ GT
GAM260  IHPK1    3'  TCACAGGGACGTGGTATGGGCC 95763     A TG   GT  CT
             C                   GGGC T  TAT  TG  TCTGTGG
                                ||||  |  |||  ||  |||||||
                                CCCG G  ATG  GC  GGACACT
                                  _ GT   GT  AG
GAM260  IL11     3'  CTGTGGAGGCAGGGTCTGAGCC 5327      A  GT  G       TG
             T                   GGGC TT  AT TTGCTTCTG  G
                                ||||  ||  ||  |||||||||  |
                                TCCG AG  TG GACGGAGGT  C
                                  _  TC  G        GT
GAM260  IL17BR   3'  ACAGGGAAAAAACGTGTGATG  38064     TG     GC    G  G
                                CAT  TATGTT  TTCT TG
                                |||  ||||||  |||| ||
                                GTA  GTGCAA  AAGG AC
                                  GT     AA    G  AT
GAM260  IL17E    5'  GACTGAGTGTGCAGTGCCC   42963          GTT    CT  GG
                                GGGCATTGTAT   GCTT  GT
                                ||||||||||   ||||  ||
                                CCCGTGACGTG   TGAG  CA
                                      ___    T_  GT
GAM260  IL18R1   3'  TGTGGGAGCAACATGAATGTTC 13909        G         TG
                                GGGCATT TATGTTGCTTC  TG
                                |||||||  ||||||||||  ||
                                CTTGTAA GTACAACGAGG  GT
                                   _         GT
GAM260  IL1A     3'  CCAACACTAACATATAATGTT  62465            CTTCTG
                                GGCATTGTATGTTG     TGG
                                ||||||||||||||     |||
                                TTGTAATATACAAT     ACC
                                       CACA__
GAM260  IL1A     3'  CCACAATAGCAGACAGTGTTT  62466         ATG    TC
                                GGGCATTGT   TTGCT  TGTGG
                                |||||||||   |||||  |||||
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                                TTTGTGACA  GACGA  ACACC
                                   ___     TA
GAM260  IMMP2L   5'  TGGGGGCGCGCTGCCT     50732      T   ATGTT
                                GGGCA TGT    GCTTCTG
                                ||||| |||    |||||||
                                TCCGT GCG    CGGGGGT
                                  C  _____
GAM260  INSL5    3'  TCACATGTTTAATTACAGTGTT 18493         T    CTTC
           T                     GGGCATTGTA GTTG   TGTGG
                                ||||||||||| ||||   |||||
                                TTTGTGACAT TAAT    ACACT
                                     _   TTGT
GAM260  IRS2     3'  CCGTGGGGGCTTCCCCAGTGCC 59717        TATGTT    TG
           T                     GGGCATTG     GCTTC  TGG
                                ||||||||     |||||  |||
                                TCCGTGAC     CGGGG  GCC
                                    CCCTT_    GT
GAM260  IRTA2    5'  CTTGGAGCTGGTGTGCAGTGTC 48405         TG  _    TGTGG
           C                     GGGCATTGTA  TT GCTTC
                                ||||||||||  || |||||
                                CCTGTGACGT  GG CGAGG
                                     GT  T    TTC
GAM260  ITGA2    3'  CTACAGAAGTGGAAGTGCTT   9373        TGTATG TG
                                GGGCAT     T  CTTCTGTGG
                                ||||||     |  |||||||||
                                TTCGTG     G  GAAGACATC
                                   AA____ GT
GAM260  ITGA4    3'  TCATGATCTTGTGACATATTAT 6087       T     TG TTCT__
           GTCT                   GGCAT GTATGT  C     GTGG
                                ||||| ||||||  |     ||||
                                CTGTA TATACA  G     TACT
                                   T     GT TTCTAG
GAM260  ITGB1    3'  CTGTAGGGGCAAAAATCAGTG  53370      TATG       TG
                                CATTG    TTGCTTCTG  G
                                |||||    |||||||||  |
                                GTGAC    AACGGGGAT  C
                                   TAAA       GT
GAM260  ITGB3BP  5'  AGCGGCAGTGGTGCTT     26598       TG A
                                GGGCAT  T TGTTGCT
                                ||||||  | |||||||
                                TTCGTG  G ACGGCGA
                                   GT _
GAM260  ITK      3'  CCATGGAAGCAGCATCCTGACC 18677    G  TTGT
                                GG CA    ATGTTGCTTCTGTGG
                                || ||    ||||||||||||||
                                CC GT    TACGACGAAGGTACC
                                 A  CC__
GAM260  ITPKB    3'  CGGAGGCCTGCTGCCC      9427       TT   TGTT
                                GGGCA  GTA    GCTTCTG
                                |||||  |||    |||||||
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                                CCCGT  CGT    CGGAGGC
                                  __   C___
GAM260  ITPKB    3'  CTATGGACCAAGGTGTGTGTGT 9429        TG_   G   CT
              CT                  GGGCAT   TAT TTG  TCTGTGG
                                  ||||||   ||| |||  |||||||
                                  TCTGTG   GTG AAC  AGGTATC
                                     TGT   G   C_
GAM260  JAK2     3'  CCACAGTGGATGTATAATACCT 17124     C        GCTT
                                  GGG ATTGTATGTT    CTGTGG
                                  ||| ||||||||||    ||||||
                                  TCC TAATATGTAG    GACACC
                                    A         GT__
GAM260  JAM3     3'  CTGCTGATCGGTGTTGCAGTGT 51423          _ TG   CT  T TG
              CC                  GGGCATTGT A  TTG  TC G  G
                                  |||||||||  |  |||  ||  |  |
                                  CCTGTGACG T  GGC  AG C  C
                                        T GT   T_  T GT
GAM260  JAM3     3'  TCATGGAAGTTTACTGTGATGT 51429       TG  T  T_
              TC                  GGGCAT  TA GT  GCTTCTGTGG
                                  ||||||  ||  ||  ||||||||||
                                  CTTGTA  GT CA  TGAAGGTACT
                                     GT  _  TT
GAM260  JDP1     3'  CTATGCTGCCAACATGCAGTCT 41436     C         _ TTC
              T                   GGG ATTGTATGTTG C   TGTGG
                                  ||| ||||||||||| |   |||||
                                  TTC TGACGTACAAC G   GTATC
                                  _          C TC_
GAM260  KAL1     3'  CCACAGAGCCTCACTGCAGTGT 4014           _ TT   T
              CT                  GGGCATTGTA TG  GCT CTGTGG
                                  ||||||||||  ||  |||  ||||||
                                  TCTGTGACGT AC  CGA GACACC
                                        C  TC  _
GAM260  KCNA3    3'  AAGTGACATGCTGTGCTC    9504         T     TG
                                  GGGCAT GTATGT  CTT
                                  ||||||  ||||||  |||
                                  CTCGTG CGTACA  GAA
                                     T     GT
GAM260  KCNA3    5'  CAGCGAGCAGCGGCGGTGCCC  9506           A       _
                                  GGGCATTGT TGTTGCTT CTG
                                  |||||||||  ||||||||  |||
                                  CCCGTGGCG GCGACGAG GAC
                                        _       C
GAM260  KCNA5    3'  GGATGTGGTATTGGTGCTT    59707         T   TT  T
                                  GGGCATTG ATG  GC TCT
                                  ||||||||  |||  ||  |||
                                  TTCGTGGT TAT  TG AGG
                                        _  GG  T
GAM260  KCND2    5'  CCGCGGGAGCGGCGCGTTCTGC 24396     TT TA
                                  GCA  G  TGTTGCTTCTGTGG
                                  |||  |  ||||||||||||||
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                                CGT  T  GCGGCGAGGGCGCC
                                  CT GC
GAM260  KCNJ12   3'  GGCTAGCTGCGGTGCTC     40667          T  _
                                GGGCATTGTA GTT GCT
                                |||||||||| ||| |||
                                CTCGTGGCGT CGA CGG
                                      _  T
GAM260  KCNJ15   3'  TCACAGGGGCGCCATCCAGGTT 9546       A  T  T
           T                     GGGC TTG ATG TGCTTCTGTGG
                                |||| ||| ||| ||||||||||
                                TTTG GAC TAC GCGGGGACACT
                                  _  C  C
GAM260  KCNJ6    3'  GTACATATATATGCCT      9531        _      T
                                GGGCAT TGTATGT GC
                                |||||| ||||||| ||
                                TCCGTA ATATACA TG
                                   T     _
GAM260  KCNK2    3'  AAGCAATGTCTGATGCCT    26419        GT
                                GGGCATT  ATGTTGCTT
                                |||||||  |||||||||
                                TCCGTAG  TGTAACGAA
                                    TC
GAM260  KDR      3'  AGGCAACGTAAGTGTTC     9590         G
                                GGGCATT TATGTTGCTT
                                ||||||| |||||||||
                                CTTGTGA ATGCAACGGA
                                      _
GAM260  KIAA0442 3'  CAGATGTTGTGCGGTGTTT   31468           TT  T
                                GGGCATTGTATG  GC TCTG
                                ||||||||||||  || ||||
                                TTTGTGGCGTGT  TG AGAC
                                      __  T
GAM260  KIF5C    3'  TAGAATTATACATGTCT     15740        T    TTGC
                                GGGCAT GTATG    TTCTG
                                |||||| |||||    |||||
                                TCTGTA CATAT    AAGAT
                                   _    T___
GAM260  KLF8     3'  CTGTGAACAAACATACGCTGCT 23404       T      GC   TGTGG
           T                     GGGCA TGTATGTT  TTC
                                ||||| ||||||||  |||
                                TTCGT GCATACAA  AAG
                                   C       AC   TGTC
GAM260  KRT9     3'  GACTTGGCATATGTGCCT    76298        T      CT
                                GGGCAT GTATGTTG  TC
                                |||||| ||||||||  ||
                                TCCGTG TATACGGT  AG
                                   _       TC
GAM260  LAMC2    3'  CCATTCAGAGCTATGGTGCTT  18711       TG  TGTT   CT_
                                GGGCAT  TA   GCTT   GTGG
                                ||||||  ||   ||||   ||||
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                                TTCGTG AT   CGAG  TACC
                                   GT ____   ACT
GAM260  LAMC3   5' CGCAGGGGAAGGCGGGTCC  20226    A   ATGTTG
                                GGGC TTGT    CTTCTGTG
                                |||| ||||    ||||||||
                                CCTG GGCG    GGGGACGC
                                  _   GAA___
GAM260  LAMP2   3' GATGTGGTATAAATGCCC   9684       G   TT  T
                                GGGCATT TATG  GC TC
                                ||||||| ||||  || ||
                                CCCGTAA ATAT  TG AG
                                    _   GG  T
GAM260  LANCL1  3' CCAAGCATCGTGATAGCAATGC 20211       ____  T   CTGTGG
           TT                    GCATTGT   ATG TGCTT
                                |||||||   ||| |||||
                                CGTAACG   TGC ACGAA
                                    ATAG  T   CC  G
GAM260  LAPTM5  3' CACGGAGGCAGGGTCTC    22201    CATTGT  G
                                GGG    AT TTGCTTCTGTG
                                |||    || ||||||||||
                                CTC    TG GACGGAGGCAC
                                 _______ G
GAM260  LARS2   3' CTGCAGGACTCAGGTGCAATGT 31055   G      G  C_   TG
           GC                   G GCATTGTAT TTG  TTCTG  G
                                | |||||||| |||  |||||  |
                                C TGTAACGTG GAC  AGGAC  C
                                 G       _  TC    GT
GAM260  LBR     3' CCATTTAGATATGCAGTGTT  59352          GCTTCT
                                GGCATTGTATGTT    GTGG
                                ||||||||||||    ||||
                                TTGTGACGTATAG    TACC
                                       ATT___
GAM260  LDHB    5' CCATGGAGAGAATCAGTGCCT  9707       TATG  GC
                                GGGCATTG   TT  TTCTGTGG
                                ||||||||   ||  ||||||||
                                TCCGTGAC   AG  GAGGTACC
                                    TA__  A_
GAM260  LDHB    5' CTATGTGTCCAATAGCAATGCT 9710        A   CTTCT
           C                    GGGCATTGT TGTTG    GTGG
                                |||||||| |||||    ||||
                                CTCGTAACG ATAAC    TATC
                                    _    CTGTG
GAM260  LDHB    5' TTACAGAGGTCTCCAGAGCCT  9718     A  TATGTT
                                GGGC TTG    GCTTCTGTGG
                                |||| |||    ||||||||||
                                TCCG GAC    TGGAGACATT
                                  A  CTC___
GAM260  LDOC1   3' CGCAGGGGCGCGGTGTGCCT  24618     TGTA  T    TG
                                GGGCAT   TGT GCTTCTG  G
                                ||||||   ||| |||||||  |
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                                TCCGTG   GCG CGGGGAC  C
                                   TG__  _     GT
GAM260  LENG4   5'  GGCAACTGCAGTGTCC     44167         T
                                GGGCATTGTA GTTGCT
                                |||||||||| ||||||
                                CCTGTGACGT CAACGG
                                        _
GAM260  LFNG    3'  CAGGGATGCGATGC       92637        GTTGC
                                GCATTGTAT    TTCTG
                                |||||||||    |||||
                                CGTAGCGTA    GGGAC
                                        _____
GAM260  LHCGR   3'  TTATAGAGACTTTTATGTATGC 4074       _   TGTTG  T
            CC                    GGGCAT TGTA    CT CTGTGG
                                |||||| ||||    || ||||||
                                CCCGTA GTAT    GA GATATT
                                   T   TTTCA  _
GAM260  LIG4    5'  TCACAGAGGTAACGGAGCTTGC 9755      TT  A_
            CC                    GGGCA  GT  TGTTGCTTCTGTGG
                                |||||  ||  ||||||||||||||
                                CCCGT  CG  GCAATGGAGACACT
                                  T_  AG
GAM260  LILRB1  3'  TGGATGTGGTGGCAGTGCCT  21904        ATG TG T
                                GGGCATTGT   T  C TCTG
                                |||||||||   |  | ||||
                                TCCGTGACG   G  G AGGT
                                     GT_ GT T
GAM260  LIMD1   3'  CTATGGGAGTAAAACATAC   26459      __
                                GTATGT  TGCTTCTGTGG
                                ||||||  ||||||||||||
                                CATACA  ATGAGGGTATC
                                   AA
GAM260  LIPA    3'  CGCACTAACAGTACAATGCTT  4081         _   CTTC  TG
                                GGGCATTGTA TGTTG   TG  G
                                |||||||||| |||||   ||  |
                                TTCGTAACAT ACAAT    AC  C
                                     G    C___  GT
GAM260  LMO7    5'  TGGAAGAACAAAGCCC     31768     A  GTA   G
                                GGGC TT   TGTT CTTCTG
                                |||| ||   |||| ||||||
                                CCCG AA   ACAA GAAGGT
                                  _ ___   _
GAM260  LMO7    5'  TGGAAGAACAAAGCCC     18092     A  GTA   G
                                GGGC TT   TGTT CTTCTG
                                |||| ||   |||| ||||||
                                CCCG AA   ACAA GAAGGT
                                  _ ___   _
GAM260  LPHH1   3'  ACTGTATACAGTGTTC     24536         TTGCTTCT
                                GGGCATTGTATG      GT
                                ||||||||||||      ||
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                                CTTGTGACATAT       CA
                                      GT_______
GAM260  LRAT     3'  TCATTTCTTAAAAATATAGTGT 60107          GTTGCTTCT
              CC                    GGGCATTGTAT        GTGG
                                    ||||||||||         ||||
                                    CCTGTGATATA        TACT
                                          AAAATTCTT
GAM260  LSS      3'  CTACAGGGTTTATAGTAGTCT  9815      _     TGTT   T
                                    GGGC ATTGTA    GCT CTGTGG
                                    |||| ||||||    ||| ||||||
                                    TCTG TGATAT    TGG GACATC
                                      A     T____  _
GAM260  LTBP2    3'  GCGAGCATGCAAGGCCC     4724       A       _
                                    GGGC TTGTATGTT GC
                                    |||| ||||||||| ||
                                    CCCG AACGTACGA CG
                                      G        G
GAM260  LTBR     3'  GGCTGGGTACGGTGCCC     9823           GTT
                                    GGGCATTGTAT   GCT
                                    ||||||||||   |||
                                    CCCGTGGCATG   CGG
                                          GGT
GAM260  LYPLA1   3'  AGTCACCATGCAGTGTCT    20923           T _
                                    GGGCATTGTATG TG CT
                                    |||||||||||| || ||
                                    TCTGTGACGTAC AC GA
                                          C  T
GAM260  LZTR1    5'  CTATGGGAGCAGCATGTTTGTC 22235      TTG
              T                      GGGCA   TATGTTGCTTCTGTGG
                                    |||||   ||||||||||||||||
                                    TCTGT   GTACGACGAGGGTATC
                                       TT_
GAM260  MADH2    3'  TCATAGCATTGTGTGTGGTCCC 19734     C  TG  TG TGCTT
                                    GGG AT  TA  T    CTGTGG
                                    ||| ||  ||  |    ||||||
                                    CCC TG  GT  G    GATACT
                                      _  GT  GT TTAC_
GAM260  MADH3    3'  AGTGCATATGCAATGTATAGTG 19735             TTC    G
              TCT                     GGGCATTGTATGTTGC   TGTG
                                    ||||||||||||||||   ||||
                                    TCTGTGATATGTAACG   ACGT
                                             TAT    GAC
GAM260  MADH4    3'  CAAAGGTGGCAATGCTT     18094       TGTA   TG   C
                                    GGGCAT    TGT  CTT TG
                                    ||||||    |||  ||| ||
                                    TTCGTA    ACG  GGA AC
                                       _____  GT   A
GAM260  MADH4    3'  CCACAGACACAATATGTATGCT 18095       TGT     CT
              T                      GGGCAT   ATGTTG  TCTGTGG
                                    ||||||   ||||||  |||||||
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                                TTCGTA  TATAAC  AGACACC
                                   TG_     AC
GAM260  MADH7    3'  TGCAGTCCCAAGCGGTGTCT  19747        ATG  CTT  TG
                                GGGCATTGT  TTG  CTG  G
                                |||||||||  |||  |||  |
                                TCTGTGGCG  AAC  GAC  T
                                     ___  CCT  GT
GAM260  MAGEC1   3'  TCACAGGTTAATGTGGTGTT  18423     TG  GTTGCT
                                GGCAT  TAT    TCTGTGG
                                |||||  |||    |||||||
                                TTGTG  GTA    GGACACT
                                  GT  ATT___
GAM260  MAN2A2   3'  CGCAGAGGTATTCAGTTCCT  20394    C   TATGT     TG
                                GGG ATTG    TGCTTCTG  G
                                ||| ||||    ||||||||  |
                                TCC TGAC    ATGGAGAC  C
                                 T   TT___      GT
GAM260  MAOB     3'  TCATAGTTACCGATGGTGTCC  59999      TG AT  TGCTT
                                GGGCAT  T  GT    CTGTGG
                                ||||||  |  ||    ||||||
                                CCTGTG  A  CA    GATACT
                                   GT GC  TT___
GAM260  MAP2K1   3'  TTGTAAACAACGTGTATAGTGC 10860         __   CTTCTGTGG
           CT                    GGGCATTGTAT  GTTG
                                ||||||||||  ||||
                                TCCGTGATATG  CAAC
                                      TG   AAATGTT
GAM260  MAP3K7   3'  TCATGGTGGACATACAAT    12100        GCTT
                                ATTGTATGTT   CTGTGG
                                ||||||||||   ||||||
                                TAACATACAG   GGTACT
                                     GT__
GAM260  MAP3K7IP1 3'  CGGGAGAGCAGGGCCT     20377     ATTGTA   G
                                GGGC     TGTT CTTCTG
                                ||||     |||| ||||||
                                TCCG     ACGA GAGGGC
                                  GG____   _
GAM260  MAP3K7IP2 3'  AAGCAGCATGCATTGTCT    30659      T
                                GGGCA TGTATGTTGCTT
                                ||||| ||||||||||||
                                TCTGT ACGTACGACGAA
                                   T
GAM260  MAP3K8   3'  CACAGAAGGATCGTGTCT    17789      TGTAT   G
                                GGGCAT    GTT CTTCTGTG
                                ||||||    ||| ||||||||
                                TCTGTG    TAG GAAGACAC
                                   C____  _
GAM260  MAPK10   5'  CTACAGTGCCGCGTATGATGCT 57291      TG    T  TT
                                GGCAT  TATGT GC  CTGTGG
                                |||||  ||||| ||  ||||||
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                                TCGTA  ATGCG CG  GACATC
                                  GT    C  T_
GAM260  MAPK14   3'  TTACAGGAGGTTGTGGATGCTC 57337       G   TTG
                                GGGCATT TATG   CTTCTGTGG
                                ||||||| ||||   |||||||||
                                CTCGTAG GTGT   GAGGACATT
                                    _   TG_
GAM260  MAPK14   3'  TTACAGGAGGTTGTGGATGCTC 57348       G   TTG
                                GGGCATT TATG   CTTCTGTGG
                                ||||||| ||||   |||||||||
                                CTCGTAG GTGT   GAGGACATT
                                    _   TG_
GAM260  MAPK14   3'  TTACAGGAGGTTGTGGATGCTC 7163        G   TTG
                                GGGCATT TATG   CTTCTGTGG
                                ||||||| ||||   |||||||||
                                CTCGTAG GTGT   GAGGACATT
                                    _   TG_
GAM260  MAPK4    3'  CCACAGAAGTCCAGCCAGTTTC 10825    C   TA  TT
            C                    GGG ATTG  TG  GCTTCTGTGG
                                ||| ||||  ||  ||||||||||
                                CCT TGAC  AC  TGAAGACACC
                                  T   CG  C_
GAM260  MBD1     3'  CGCAGAAGAAGCTGGTGCCC   31773       TAT   G    TG
                                GGGCATTG   GTT CTTCTG  G
                                ||||||||   ||| ||||||  |
                                CCCGTGGT   CGA GAAGAC  C
                                    ___   A    GT
GAM260  MBD1     3'  CGCAGAAGAAGCTGGTGCCC   31781       TAT   G    TG
                                GGGCATTG   GTT CTTCTG  G
                                ||||||||   ||| ||||||  |
                                CCCGTGGT   CGA GAAGAC  C
                                    ___   A    GT
GAM260  MBD1     3'  CGCAGAAGAAGCTGGTGCCC   31788       TAT   G    TG
                                GGGCATTG   GTT CTTCTG  G
                                ||||||||   ||| ||||||  |
                                CCCGTGGT   CGA GAAGAC  C
                                    ___   A    GT
GAM260  MBD1     3'  CGCAGAAGAAGCTGGTGCCC   9947        TAT   G    TG
                                GGGCATTG   GTT CTTCTG  G
                                ||||||||   ||| ||||||  |
                                CCCGTGGT   CGA GAAGAC  C
                                    ___   A    GT
GAM260  MCC      3'  GGTTAGCATATGGTGCTT    9961        TG    _
                                GGGCAT  TATGTTG CT
                                ||||||  ||||||| ||
                                TTCGTG  ATACGAT GG
                                  GT      T
GAM260  MDM1     3'  TCATAGAAGCAGTGTGCAGGT  39276    A    TG
                                GC TTGTA  TTGCTTCTGTGG
                                || |||||  ||||||||||||
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                                TG GACGT  GACGAAGATACT
                                 _    GT
GAM260  MEL     3'  ACGGAAGCGAGGTCCC     18119     CATTGT  G
                                GGG     AT TTGCTTCTGT
                                |||     || ||||||||||
                                CCC     TG AGCGAAGGCA
                                 _______ G
GAM260  MFAP2    3'  GCAGGCTGCGGTGCCT     33921         TG
                                GGGCATTGTA  TTGC
                                ||||||||||  ||||
                                TCCGTGGCGT  GACG
                                      CG
GAM260  MFI2     3'  CTGTGGGAAGGCAAATGATGCC 52813       TG A    GC    TG
           C                     GGGCAT  T TGTT  TTCTG  G
                                ||||||  | ||||  |||||  |
                                CCCGTA  A ACGG  AGGGT  C
                                   GT A    A_    GT
GAM260  MGEA5    5'  CCGCAGAGGTGGCAGCGGCC  24210    ATTGTA  TG
                                GGC     TGT  CTTCTGTGG
                                |||     |||  |||||||||
                                CCG     ACG  GGAGACGCC
                                 GCG___  GT
GAM260  MID2     5'  CGCGGAGGCAGACGAGAGCCC  24224     A_   ATG      TG
                                GGGC  TTGT   TTGCTTCTG  G
                                ||||  ||||   |||||||||  |
                                CCCG  AGCA   GACGGAGGC  C
                                  AG   ___       GT
GAM260  MID2     5'  CGCGGAGGCAGACGAGAGCCC  53389     A_   ATG      TG
                                GGGC  TTGT   TTGCTTCTG  G
                                ||||  ||||   |||||||||  |
                                CCCG  AGCA   GACGGAGGC  C
                                  AG   ___       GT
GAM260  MLC1     5'  CAGCACAGCTGTGGTGTCC   30777      TG  T   CTT
                                GGGCAT  TA GTTG   CTG
                                ||||||  || ||||   |||
                                CCTGTG  GT CGAC   GAC
                                   GT  _   AC_
GAM260  MLC1     5'  CAGCACAGCTGTGGTGTCC   57589      TG  T   CTT
                                GGGCAT  TA GTTG   CTG
                                ||||||  || ||||   |||
                                CCTGTG  GT CGAC   GAC
                                   GT  _   AC_
GAM260  MLLT2    5'  CCGCAGAGGCCCCAGTGCCC   19843       TATGTT
                                GGGCATTG    GCTTCTGTGG
                                ||||||||    ||||||||||
                                CCCGTGAC    CGGAGACGCC
                                    CC____
GAM260  MLLT4    3'  CCACACTGCTGTGCGGTGTTC  72484         GTT  TTC
                                GGGCATTGTAT   GC   TGTGG
                                ||||||||||   ||   |||||
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                                CTTGTGGCGTG  CG  ACACC
                                      T__  TC_
GAM260  MME     3'  CTATAGAGCCTTCTGATGTCT  23497      GTATGTT  T
                                GGGCATT     GCT CTGTGG
                                |||||||     ||| ||||||
                                TCTGTAG     CGA GATATC
                                   TCTTC__  _
GAM260  MME     3'  CTATAGAGCCTTCTGATGTCT  23508      GTATGTT  T
                                GGGCATT     GCT CTGTGG
                                |||||||     ||| ||||||
                                TCTGTAG     CGA GATATC
                                   TCTTC__  _
GAM260  MME     3'  CTATAGAGCCTTCTGATGTCT  6140       GTATGTT  T
                                GGGCATT     GCT CTGTGG
                                |||||||     ||| ||||||
                                TCTGTAG     CGA GATATC
                                   TCTTC__  _
GAM260  MME     3'  CTATAGAGCCTTCTGATGTCT  23487      GTATGTT  T
                                GGGCATT     GCT CTGTGG
                                |||||||     ||| ||||||
                                TCTGTAG     CGA GATATC
                                   TCTTC__  _
GAM260  MMP15   3'  CGGGGGTTCCGTGTCC     10072      TGTAT TT
                                GGGCAT   G  GCTTCTG
                                ||||||   |  |||||||
                                CCTGTG   C  TGGGGGC
                                   _____ CT
GAM260  MMP8    3'  TTACAGAAAATATGGTGCT   10066     TG  GTTGC
                                GGCAT  TAT   TTCTGTGG
                                |||||  |||   ||||||||
                                TCGTG  ATA   AAGACATT
                                  GT   A____
GAM260  MMP8    3'  TTGCAGAGGCTTATTCAGTTCT 10068    C   T   TT    TG
          T                      GGG ATTG ATG  GCTTCTG  G
                                 ||| |||| |||  |||||||  |
                                 TTC TGAC TAT  CGGAGAC  T
                                   T   T  T_     GT
GAM260  MOCS1   3'  TTATGGAAAGGATGCAGGGTCC 92036    A    G  GC
                                GGGC TTGTAT TT  TTCTGTGG
                                |||| ||||||  ||  ||||||||
                                CCTG GACGTA GA  AAGGTATT
                                  G     G  __
GAM260  MPL     3'  CTACTACAGCACTGTGATGCTT 18139      TG  T  T  TCT
                                GGGCAT  TA GT GCT   GTGG
                                ||||||  ||  ||  |||   ||||
                                TTCGTA  GT CA CGA   CATC
                                   GT  _  _   CAT
GAM260  MPP4    5'  GGATAGGAGCAACATGCATGTT 52345      T          GG
          T                      GGGCAT GTATGTTGCTTCTGT
                                 ||||||  ||||||||||||||
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                                TTTGTA CGTACAACGAGGATA
                                   _           GGT
GAM260  MSF     3'  AGTTACATTAATGCCC      88077        T   T
                                GGGCATTG ATGT GCT
                                |||||||| |||| |||
                                CCCGTAAT TACA TGA
                                   _   T
GAM260  MSH6    5'  CCGCGCGGTAGATGCGGTGCTT 3933          G    TC
                                GGGCATTGTAT TTGCT  TGTGG
                                |||||||||| |||||  |||||
                                TTCGTGGCGTA GATGG  GCGCC
                                      _    C_
GAM260  MTMR3   5'  CCGTGGAGGGCCTCGCCATGTC 40813       T  AT_  TG   TG
            C                    GGGCAT GT   GT  CTTC  TGG
                                |||||| ||   ||  ||||  |||
                                CCTGTA CG   CG  GGAG  GCC
                                   C  CTC  __   GT
GAM260  MTMR6   3'  TAGAAGTACACTGTTC     93551       T   ATGTT
                                GGGCA TGT    GCTTCTG
                                ||||| |||    |||||||
                                CTTGT ACA    TGAAGAT
                                  C  ______
GAM260  MTR     3'  TAGAGGAGCAGGGTCT     4218       ATTGTA   G
                                GGGC     TGTT CTTCTG
                                ||||     |||| ||||||
                                TCTG     ACGA GGAGAT
                                  GG____   _
GAM260  MUC4    3'  GCTACATACAGGCCC      56329      A       T
                                GGGC TTGTATGT GC
                                |||| |||||||| ||
                                CCCG GACATACA CG
                                  _       T
GAM260  MUCDHL  3'  CCGCGGAGGCACCGATGCCC   48367        TATGT
                                GGGCATTG    TGCTTCTGTGG
                                ||||||||    ||||||||||
                                CCCGTAGC    ACGGAGGCGCC
                                     C____
GAM260  MX2     3'  CCGTAGCACACAGTTACAGTGT 10148          __  _   TCTGTGG
            CC                    GGCATTGTA  TGT TGCT
                                |||||||||  ||| ||||
                                CTGTGACAT  ACA ACGA
                                     TG   C    TGCC
GAM260  MYBL2   3'  TGTGGGGGCAGAGGGGGTCT   10155     ATTGTATG       TG
                                GGGC       TTGCTTCTG  G
                                ||||       |||||||||  |
                                TCTG       GACGGGGGT  T
                                  GGGGA___        GT
GAM260  MYCBP   3'  TTGTAGGTATAATTATATAGTG 24698          _  CT    TG
            CTT                   GGGCATTGTATG TTG  TCTG  G
                                |||||||||||| |||  ||||  |
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                                TTCGTGATATAT AAT  GGAT  T
                                      T  AT   GT
GAM260  NAB1    3'  CACTTTATTGTGCGATGTCC  19908          TTGCTTCT  G
                                GGGCATTGTATG      GTG
                                ||||||||||||      |||
                                CCTGTAGCGTGT      CAC
                                      TATTT___  A
GAM260  NAB1    3'  TTATAGAAGTAAAATCTAGATG 19913      GTATG_
           TT                    GGCATT    TTGCTTCTGTGG
                                ||||||    ||||||||||||
                                TTGTAG    AATGAAGATATT
                                   ATCTAA
GAM260  NAGA    5'  CAGAGGGTGTGAGGTCT    4233      A TG  GTTG
                                GGGC T  TAT   CTTCTG
                                |||| |  |||   ||||||
                                TCTG A  GTG   GGAGAC
                                  G GT  _____
GAM260  NAP1L4  3'  GTAACTGAATACAGTGTTT   19922          ___
                                GGGCATTGTAT   GTTGC
                                ||||||||||   |||||
                                TTTGTGACATA   CAATG
                                      AGT
GAM260  NBS1    3'  TTATAGGAATATCAATATAATG 69501          GT_  C
           TTT                   GGGCATTGTAT   TG TTCTGTGG
                                ||||||||||   || ||||||||
                                TTTGTAATATA   AT AGGATATT
                                      ACT  A
GAM260  NCALD   3'  CCGTAGGGGTGATGGATGGCAC 49372    _  ATTGTA   TG
           C                     GG GC     TGT  CTTCTGTGG
                                || ||     |||  |||||||||
                                CC CG     GTA  GGGGATGCC
                                 A  GTAG__   GT
GAM260  NDRG3   3'  CGTAGGGGTAGCCCTGTCC   49296      TTGTAT        TG
                                GGGCA     GTTGCTTCTG  G
                                |||||     ||||||||||  |
                                CCTGT     CGATGGGGAT  C
                                   CC_____         GT
GAM260  NDST2   3'  TCATAGAGCCGAGTATGAGCCC 13298      A TG   GTT   T
                                GGGC T  TAT   GCT CTGTGG
                                |||| |  |||   ||| ||||||
                                CCCG A  ATG   CGA GATACT
                                  _ GT   AGC   _
GAM260  NDUFB9  5'  CCGCAGCAGGCGTGCAGTTTCC 17197     C         GCTT
                                GGG ATTGTATGTT    CTGTGG
                                ||| ||||||||||    ||||||
                                CCT TGACGTGCGG    GACGCC
                                  T         AC__
GAM260  NEBL    3'  TCACGGAATGTTACAATGTT   21125         TGTT  _
                                GGCATTGTA    GC TTCTGTGG
                                |||||||||    || ||||||||
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                                TTGTAACAT   TG AAGGCACT
                                    ____ T
GAM260  NFE2L1   3'  CTGGGGTAGGGTGATGGCAGTG 12171      ____ G     TGTGG
            CTC                   CATTGT   AT TTGCTTC
                                |||||||   || |||||||
                                GTGACG   TG GATGGGG
                                   GTAG  G     TC  G
GAM260  NFE2L2   3'  CTACTGTGATGTGAAATGCTC  20490      G    TG TTCT
                                GGGCATT TATGT  C   GTGG
                                ||||||| |||||  |   ||||
                                CTCGTAA GTGTA  G   CATC
                                   A    GT T___
GAM260  NFIB     3'  ATGGAAGAAATGCCT      18792       GTATGTTG
                                GGGCATT      CTTCTGT
                                |||||||      |||||||
                                TCCGTAA      GAAGGTA
                                   A_______
GAM260  NFYA     3'  TACAATTGCAGCGATGCCT   10218       ATGT  TTC
                                GGGCATTGT   TGC  TGTG
                                |||||||||   |||  ||||
                                TCCGTAGCG   ACG  ACAT
                                    ____  TTA
GAM260  NFYA     3'  TACAATTGCAGCGATGCCT   41353       ATGT  TTC
                                GGGCATTGT   TGC  TGTG
                                |||||||||   |||  ||||
                                TCCGTAGCG   ACG  ACAT
                                    ____  TTA
GAM260  NGFR     3'  CGTGGAGATGGGATGCTT    10226      G  GTTGC  TG
                                GGGCATT TAT    TTC  TG
                                ||||||| |||    |||  ||
                                TTCGTAG GTA    GAG  GC
                                   G  _____  GT
GAM260  NKTR     5'  TGGCTGCAGTGGCAGTGCTT  18204       ATG   TT
                                GGGCATTGT   TTGC  CTG
                                |||||||||   ||||  |||
                                TTCGTGACG   GACG  GGT
                                    GT_   TC
GAM260  NKX2H    5'  CCGTAGGAGCGGCGTCCCGGCC 26844    ATTGT
                                GGC    ATGTTGCTTCTGTGG
                                |||    ||||||||||||||
                                CCG    TGCGGCGAGGATGCC
                                  GCCC_
GAM260  NONO     3'  TTACAGGGGTGAGCCACCGTGC 82027      T  ATG TG
            CC                  GGGCAT GT   T  CTTCTGTGG
                                ||||||  ||   |  |||||||||
                                CCCGTG CA   A  GGGGACATT
                                   C  CCG GT
GAM260  NOTCH2   3'  CCGTCCAGTGCTGTGATGCCC  44313      TG  TGTT  TT  __
                                GGGCAT  TA   GC  CTG  TGG
                                ||||||  ||   ||  |||  |||
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                                CCCGTA  GT   CG  GAC  GCC
                                   GT  ____  T_  CT
GAM260  NPTX1   3'  CGCAGGAGGAGCAGGTGTTT  10261      GTA   G    TG
                                GGGCATT  TGTT CTTCTG  G
                                |||||||  |||| ||||||  |
                                TTTGTGG  ACGA GAGGAC  C
                                   ___   G    GT
GAM260  NPY2R   5'  CCGCGAGTGAGTGCGGTGCCC  6183         G TG  CT
                                GGGCATTGTAT T  CTT  GTGG
                                |||||||||||  |  |||  ||||
                                CCCGTGGCGTG A  GAG  CGCC
                                      _ GT  __   C
GAM260  NR3C2   3'  GTAAAGTGCAATGTCC    6134          G
                                GGGCATTGTAT TTGC
                                |||||||||||  ||||
                                CCTGTAACGTG AATG
                                      A
GAM260  NRG1    3'  CCGTGTCCAGCATGACGGTGTC 25653        _    CTTCTGTGG
          C                      GGGCATTGT ATGTTG
                                |||||||||  ||||||
                                CCTGTGGCA TACGAC
                                     G    CTGTGCC
GAM260  NTE     3'  CCGTGGGGGTAGCTCACTCCCC 21986    CATT  AT      TG
                                GGG   GT  GTTGCTTC  TGG
                                |||   ||  ||||||||  |||
                                CCC   CA  CGATGGGG  GCC
                                  CT__  CT      GT
GAM260  NTF5    5'  CCACAGGGGCCCCCCGAAGCCT 20517     A   TATGTT
                                GGGC TTG     GCTTCTGTGG
                                ||||  |||    ||||||||||
                                TCCG AGC     CGGGGACACC
                                  A  CCCC__
GAM260  NUCB1   3'  TGGAACCAGTGATGCCT    20528       TG ATGT  C
                                GGGCAT  T   TG TTCTG
                                ||||||  |   || |||||
                                TCCGTA  G   AC AAGGT
                                   GT ____  C
GAM260  NUP62   3'  TCGTGGGGGCAGCCACTCTCTC 33330    CATT  AT      TG
          C                      GGG   GT  GTTGCTTC  TGG
                                |||   ||  ||||||||  |||
                                CCT   CA  CGACGGGG  GCT
                                  CTCT  C_      GT
GAM260  NUP98   5'  TCGTGGGGGCCGCGCGCTGCTC 32863      TT TA   T    TG
                                GGGCA  G  TGT GCTTC  TGG
                                |||||  |  ||| |||||  |||
                                CTCGT  C  GCG CGGGG  GCT
                                   __ GC   C    GT
GAM260  NXF3    3'  TCACAATAAAGTATGGTGTCT  41901      TG   G   CTTC
                                GGGCAT  TAT TTG   TGTGG
                                ||||||  ||| |||   |||||
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                                TCTGTG  ATG AAT    ACACT
                                   GT   A   A___
GAM260  NYX      3'  CTTCCAGGCAACAGTGCCT   42600       TGTA       CTGTGG
                                GGGCAT   TGTTGCTT
                                ||||||   ||||||||
                                TCCGTG   ACAACGGA
                                   ____      CCTTCT
GAM260  OAS2     3'  CTGTGGAGGTGGTTGCACTTGC 10304      T_   T TT      TG
           C                     GGCA  TGTA G  GCTTCTG  G
                                ||||  |||| |  |||||||  |
                                CCGT  ACGT T  TGGAGGT  C
                                  TC   _ GG      GT
GAM260  ONECUT1  3'  CCACGAAGGTGTATGGTGTCT  62133       TG  TG TG   T
                                GGGCAT  TA  T  CTTC GTGG
                                ||||||  ||  |  |||| ||||
                                TCTGTG  AT  G  GAAG CACC
                                   GT  GT __   _
GAM260  OPHN1    3'  CTATGAGTGAGAATATGCGGTG 10355           G  _ _
           TTT                   GGCATTGTATGTT CTT CT GTGG
                                ||||||||||||| ||| || ||||
                                TTGTGGCGTATAA GAG GA TATC
                                      _  T  G
GAM260  ORC5L    3'  CCACAGGAGCCTCTGCAGTCGC 10364      _     TGTT
           TT                    GGGC ATTGTA   GCTTCTGTGG
                                |||| ||||||   ||||||||||
                                TTCG TGACGT   CGAGGACACC
                                  C     CTC_
GAM260  OTOR     3'  CCATAGATGTTTGGATGATGTC 39346       TG ATGTT  T
           T                     GGGCAT  T    GC TCTGTGG
                                ||||||  |    || |||||||
                                TCTGTA  A    TG AGATACC
                                   GT GGTT_  T
GAM260  OXTR     3'  GCATTGAAATGCAATGTCT   6209          GT___
                                GGGCATTGTAT    TGC
                                ||||||||||    |||
                                TCTGTAACGTA    ACG
                                      AAGTT
GAM260  P2RY1    3'  CACTGCTGTGCAATGCCT    10377         GTT  TTCT
                                GGGCATTGTAT   GC   GTG
                                ||||||||||  ||   |||
                                TCCGTAACGTG   CG   CAC
                                      T__  T___
GAM260  PAFAH1B1 3'  TCATGGAAGTAGCTGCTTGCTT 4732       TT   T
                                GGGCA  GTA GTTGCTTCTGTGG
                                |||||  ||| ||||||||||||
                                TTCGT  CGT CGATGAAGGTACT
                                   T_  _
GAM260  PAK4     3'  TCGTGGGAGCAAGCGAGGCTC  19692     A   ATG     TG
                                GGGC TTGT   TTGCTTC  TGG
                                |||| ||||   |||||||  |||
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                                CTCG AGCG   AACGAGG  GCT
                                  G   ___      GT
GAM260  PAPPA    3'  GGTTGCATATACAGTGTGC   10425   G       T  TTCTGTGG
                                G GCATTGTATGT GC
                                | ||||||||||| ||
                                C TGTGACATATA CG
                                 G         _ TT   GGT
GAM260  PARG     3'  CCGCAGATGCCCAGCGATGCCC 13270        A  TT  T
                                GGGCATTGT TG  GC TCTGTGG
                                ||||||||| ||  || |||||||
                                CCCGTAGCG AC  CG AGACGCC
                                      _ C_  T
GAM260  PAWR     5'  CTGTGGGAGCGGCGGCCGTCC  10430     ATT  A         TG
                                GGGC   GT TGTTGCTTCTG  G
                                ||||   || ||||||||||  |
                                CCTG   CG GCGGCGAGGGT  C
                                  C__  _         GT
GAM260  PCDH7    3'  ATTAGACGTAACAGTGATGTCT 10457      TG A     T    TGG
                                GGGCAT  T TGTTGC TCTG
                                ||||||  | |||||| ||||
                                TCTGTA  G ACAATG AGAT
                                   GT _     C    TAT
GAM260  PCDH7    5'  CCGAACCCGCGGCGCGCAGTGT 10458       TA     TTCTG
          CC                    GGGCATTG  TGTTGC    TGG
                                ||||||||  ||||||    |||
                                CCTGTGAC  GCGGCG    GCC
                                     GC     CCCAA
GAM260  PCDH7    5'  CCGAACCCGCGGCGCGCAGTGT 50596       TA     TTCTG
          CC                    GGGCATTG  TGTTGC    TGG
                                ||||||||  ||||||    |||
                                CCTGTGAC  GCGGCG    GCC
                                     GC     CCCAA
GAM260  PCDH7    5'  CCGAACCCGCGGCGCGCAGTGT 50601       TA     TTCTG
          CC                    GGGCATTG  TGTTGC    TGG
                                ||||||||  ||||||    |||
                                CCTGTGAC  GCGGCG    GCC
                                     GC     CCCAA
GAM260  PCDHGA1  3'  CCATGGGGGTAGTGGGGTT   38282     ATTGTA GT
                                GGC     T  TGCTTCTGTGG
                                |||     |  ||||||||||
                                TTG     G  ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGA10 3'  CCATGGGGGTAGTGGGGTT   38289     ATTGTA GT
                                GGC     T  TGCTTCTGTGG
                                |||     |  ||||||||||
                                TTG     G  ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGA11 3'  CCATGGGGGTAGTGGGGTT   38296     ATTGTA GT
                                GGC     T  TGCTTCTGTGG
                                |||     |  ||||||||||
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                                TTG     G  ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGA11  3'  CCATGGGGGTAGTGGGGTT   49460    ATTGTA GT
                                GGC     T  TGCTTCTGTGG
                                |||     |  ||||||||||
                                TTG     G  ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGA12  3'  CCATGGGGGTAGTGGGGTT   13592    ATTGTA GT
                                GGC     T  TGCTTCTGTGG
                                |||     |  ||||||||||
                                TTG     G  ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGA2   3'  CCATGGGGGTAGTGGGGTT   38304    ATTGTA GT
                                GGC     T  TGCTTCTGTGG
                                |||     |  ||||||||||
                                TTG     G  ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGA3   3'  CCATGGGGGTAGTGGGGTT   38313    ATTGTA GT
                                GGC     T  TGCTTCTGTGG
                                |||     |  ||||||||||
                                TTG     G  ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGA4   3'  CCATGGGGGTAGTGGGGTT   38320    ATTGTA GT
                                GGC     T  TGCTTCTGTGG
                                |||     |  ||||||||||
                                TTG     G  ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGA5   3'  CCATGGGGGTAGTGGGGTT   38327    ATTGTA GT
                                GGC     T  TGCTTCTGTGG
                                |||     |  ||||||||||
                                TTG     G  ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGA6   3'  CCATGGGGGTAGTGGGGTT   38334    ATTGTA GT
                                GGC     T  TGCTTCTGTGG
                                |||     |  ||||||||||
                                TTG     G  ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGA7   3'  CCATGGGGGTAGTGGGGTT   38341    ATTGTA GT
                                GGC     T  TGCTTCTGTGG
                                |||     |  ||||||||||
                                TTG     G  ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGA7   3'  TTATAGAGGTAAAAATGAGTTT 49447     A TG ATG
                                GGGC T  T   TTGCTTCTGTGG
                                ||||| |  |  ||||||||||||
                                TTTG A  A   AATGGAGATATT
                                  _ GT AA_
GAM260  PCDHGA8   3'  CCATGGGGGTAGTGGGGTT   49452    ATTGTA GT
                                GGC     T  TGCTTCTGTGG
                                |||     |  ||||||||||
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                                TTG    G ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGA9  3' CCATGGGGGTAGTGGGGTT  38348   ATTGTA GT
                                GGC    T TGCTTCTGTGG
                                |||    | ||||||||||
                                TTG    G ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGB1  3' CCATGGGGGTAGTGGGGTT  38355   ATTGTA GT
                                GGC    T TGCTTCTGTGG
                                |||    | ||||||||||
                                TTG    G ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGB2  3' CCATGGGGGTAGTGGGGTT  38362   ATTGTA GT
                                GGC    T TGCTTCTGTGG
                                |||    | ||||||||||
                                TTG    G ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGB3  3' CCATGGGGGTAGTGGGGTT  38369   ATTGTA GT
                                GGC    T TGCTTCTGTGG
                                |||    | ||||||||||
                                TTG    G ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGB4  3' CCATGGGGGTAGTGGGGTT  13599   ATTGTA GT
                                GGC    T TGCTTCTGTGG
                                |||    | ||||||||||
                                TTG    G ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGB5  3' CCATGGGGGTAGTGGGGTT  38376   ATTGTA GT
                                GGC    T TGCTTCTGTGG
                                |||    | ||||||||||
                                TTG    G ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGB6  3' CCATGGGGGTAGTGGGGTT  38383   ATTGTA GT
                                GGC    T TGCTTCTGTGG
                                |||    | ||||||||||
                                TTG    G ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGB7  3' CCATGGGGGTAGTGGGGTT  38390   ATTGTA GT
                                GGC    T TGCTTCTGTGG
                                |||    | ||||||||||
                                TTG    G ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGC3  3' CCATGGGGGTAGTGGGGTT  10453   ATTGTA GT
                                GGC    T TGCTTCTGTGG
                                |||    | ||||||||||
                                TTG    G ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGC3  3' CCATGGGGGTAGTGGGGTT  50516   ATTGTA GT
                                GGC    T TGCTTCTGTGG
                                |||    | ||||||||||
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                                TTG     G  ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGC4  3'  CCATGGGGGTAGTGGGGTT   38397     ATTGTA GT
                                GGC     T  TGCTTCTGTGG
                                |||     |  ||||||||||
                                TTG     G  ATGGGGGTACC
                                  GG____ TG
GAM260  PCDHGC5  3'  CCATGGGGGTAGTGGGGTT   38404     ATTGTA GT
                                GGC     T  TGCTTCTGTGG
                                |||     |  ||||||||||
                                TTG     G  ATGGGGGTACC
                                  GG____ TG
GAM260  PCSK1    3'  GTTACAGGTATTTATAATATAC 4773     _      CT____
            CAATGCTT                TG TATGTTG     TCTGTGG   T
                                || |||||||     |||||||  |
                                AC ATATAAT     GGACATT   G
                                 C      ATTTAT
GAM260  PCTP     3'  GGATGACGTGCCAATGTCC    41100        _      C
                                GGGCATTG TATGTTG TTC
                                |||||||| ||||||| |||
                                CCTGTAAC GTGCAGT AGG
                                     C      _
GAM260  PDE4B    3'  CCACAGGAGTTGCTACAGTCCC 10477     C      T  T
                                GGG ATTGTA GT GCTTCTGTGG
                                ||| |||||| || ||||||||||
                                CCC TGACAT CG TGAGGACACC
                                  _     _ T
GAM260  PDGFRB   3'  CGCTCCTGACGTGTTGTGCCC  65974       TG     GCTTCT TG
                                GGGCAT  TATGTT     G  G
                                ||||||  ||||||     |  |
                                CCCGTG  GTGCAG     C  C
                                   TT     TCCT__ GT
GAM260  PDK4     3'  TCATGGTGGCCTAGTGTTGTGG 97271     TG  TGTT___   T
            TGCTT                  CAT  TA      GCT CTGTGG
                                |||  ||      ||| ||||||
                                GTG  GT      CGG GGTACT
                                  GT  TGTGATC   T
GAM260  PDLIM1   3'  TCACACCAGCTGTGCGATGCCC 40635          GTT   TC
                                GGGCATTGTAT   GCT  TGTGG
                                ||||||||||   |||  |||||
                                CCCGTAGCGTG   CGA  ACACT
                                      T__   CC
GAM260  PEX10    3'  CCATGGGAGGCGGCGCTGCTC  10509      TTGTA        _
                                GGGCA    TGTTGCTTCT GTGG
                                |||||    |||||||||| ||||
                                CTCGT    GCGGCGGAGG TACC
                                   C____         G
GAM260  PHEMX    3'  CAGGAGAGCGATGCT      57363         ATGTTG
                                GGCATTGT     CTTCTG
                                ||||||||     ||||||
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                              TCGTAGCG     GAGGAC
                                   A_____
GAM260  PHEMX    3'  CAGGAGAGCGATGCT      57367        ATGTTG
                              GGCATTGT     CTTCTG
                              ||||||||     ||||||
                              TCGTAGCG     GAGGAC
                                   A_____
GAM260  PHLDA3   3'  TGTGGGGGCACGGCTGTGCTC  24769       T  ATGT      TG
                              GGGCAT GT    TGCTTCTG  G
                              |||||| ||    ||||||||  |
                              CTCGTG CG    ACGGGGGT  T
                                 T  GC__       GT
GAM260  PIGA     3'  TCGTGGAAGCAGCCAGTTGTG  40007     TGTAT      TG
                              CAT    GTTGCTTC  TGG
                              |||    ||||||||  |||
                              GTG    CGACGAAG  GCT
                                TTGAC       GT
GAM260  PIGA     3'  TCGTGGAAGCAGCCAGTTGTG  40016     TGTAT      TG
                              CAT    GTTGCTTC  TGG
                              |||    ||||||||  |||
                              GTG    CGACGAAG  GCT
                                TTGAC       GT
GAM260  PIGR     3'  CAGAAAGGAGAGACGTGCAGCG 72593      A       TG    GTGG
           CCC                   GGGC TTGTATGT  CTTCT
                              |||| ||||||||  |||||
                              CCCG GACGTGCA  GAGGA
                                C       GA     AAGACG
GAM260  PIGR     5'  TGGCAGCAGCGTCCAGTGCCC  72610        T      T
                              GGGCATTG ATGTTGCT CTG
                              |||||||| |||||||| |||
                              CCCGTGAC TGCGACGA GGT
                                   C       C
GAM260  PIK3R1   3'  TCACAGCGCTATGCAATTCTT  68580     C       TT  TT
                              GGG ATTGTATG  GC  CTGTGG
                              ||| ||||||||  ||  ||||||
                              TTC TAACGTAT  CG  GACACT
                                T       __  C_
GAM260  PIK3R1   3'  CCATGGTGCTTGTTAATGCTT  68579        TATGTT  TT
                              GGGCATTG     GC  CTGTGG
                              ||||||||     ||  ||||||
                              TTCGTAAT     CG  GGTACC
                                   TGTT__  T_
GAM260  PITX1    3'  CTGCGGACTGGATGTGCGGGGC 10598      A       GCT   TG
           CT                    GGGC TTGTATGTT   TCTG  G
                              |||| |||||||||   ||||  |
                              TCCG GGCGTGTAG   AGGC  C
                                G       GTC    GT
GAM260  PKIB     3'  GATTGCAATGATGATGTCC   50642       TG A     T_
                              GGGCAT  T TGTTGC  TC
                              ||||||  | ||||||  ||
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                                CCTGTA  A GTAACG  AG
                                   GT _     TT
GAM260  PLA2G2D  3'  CCATGGGGGCAGCTGTGCCT   24791      TGTAT
                                GGGCAT    GTTGCTTCTGTGG
                                ||||||    ||||||||||||||
                                TCCGTG    CGACGGGGGTACC
                                   T_____
GAM260  PLA2G4C  3'  CTGTAGAAGTAAGAACTTGGGC 73413     ATT_  ATG       TG
           TT                    GGGC   GT   TTGCTTCTG  G
                                ||||   ||   |||||||||  |
                                TTCG   CA   AATGAAGAT  C
                                  GGTT  AG_       GT
GAM260  PLAG1    3'  GCAGATTGCAATGTTT     10608         TG
                                GGGCATTGTA  TTGC
                                ||||||||||  ||||
                                TTTGTAACGT  GACG
                                      TA
GAM260  PLEK     3'  CATGTGGTGTGCAAGGTTC    10630      A    TG TG TTCT
                                GGGC TTGTA  T  C    GTG
                                |||| |||||  |  |    |||
                                CTTG AACGT  G  G    TAC
                                  G    GT GT _____
GAM260  PLGL     3'  TACAGAGGGACGATGTCC     10637         ATGTTG
                                GGGCATTGT     CTTCTGTG
                                |||||||||     ||||||||
                                CCTGTAGCA     GGAGACAT
                                     G_____
GAM260  PLIN     3'  GGGGTGTTACGCATGCCT     10643       _   TGTT
                                GGGCAT TGTA    GCTTC
                                |||||| ||||    |||||
                                TCCGTA GCAT    TGGGG
                                   C    TG__
GAM260  PLTP     3'  CCACATTCATAGCCTGTAGTGC 20639         T    CTTC
           CC                     GGGCATTGTA GTTG    TGTGG
                                ||||||||||| ||||    |||||
                                CCCGTGATGT CGAT    ACACC
                                      C    ACTT
GAM260  PLXNA1   3'  CCGCATGCGTGTGGAGTGTCC  72311       G  TG T  TTC
                                GGGCATT TA  T GC   TGTGG
                                |||||||  ||  | ||   |||||
                                CCTGTGA GT  G CG   ACGCC
                                    G  GT _  T__
GAM260  PML      3'  CCATGGAGGCCTCTCAAGTCC  52672      A   TATGTT
                                GGGC TTG     GCTTCTGTGG
                                |||| |||     ||||||||||
                                CCTG AAC     CGGAGGTACC
                                  _   TCTC__
GAM260  PML      3'  CCATGGAGGCCTCTCAAGTCC  52666      A   TATGTT
                                GGGC TTG     GCTTCTGTGG
                                |||| |||     ||||||||||
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                                CCTG AAC     CGGAGGTACC
                                  _  TCTC__
GAM260  PMP22    3'  CTGTAGATGTATATATGGTGCC 4326       TG    T T   TG
            C                    GGGCAT  TATGT GC TCTG  G
                                 ||||||  ||||| || ||||  |
                                 CCCGTG  ATATA TG AGAT  C
                                    GT    _ T   GT
GAM260  PMX1     3'  TCACAGGGGTGTTGTGAGGCTC 22596     A TG  TGTT
                                 GGGC T  TA   GCTTCTGTGG
                                 |||| |  ||   ||||||||||
                                 CTCG A  GT   TGGGGACACT
                                   G GT  TG__
GAM260  PMX1     3'  TCACAGGGGTGTTGTGAGGCTC 42663     A TG  TGTT
                                 GGGC T  TA   GCTTCTGTGG
                                 |||| |  ||   ||||||||||
                                 CTCG A  GT   TGGGGACACT
                                   G GT  TG__
GAM260  PODXL    3'  TTGCAGAGGCCACCCACGATCT 18245     C    AT  T     TG
            T                    GGG ATTGT  GT GCTTCTG  G
                                 ||| |||||  || |||||||  |
                                 TTC TAGCA  CA CGGAGAC  T
                                  _    CC  C     GT
GAM260  POH1     5'  CCACAGAGGCAAGACAAGGGTC 19409     A_   ATG
            C                    GGGC  TTGT   TTGCTTCTGTGG
                                 ||||  ||||   ||||||||||||
                                 CCTG  AACA   AACGGAGACACC
                                   GG   G__
GAM260  POLG     3'  CCATGCTCTGATGCAGTGCCC  10678         GTT_  TTCT
                                 GGGCATTGTAT   GC   GTGG
                                 ||||||||||    ||   ||||
                                 CCCGTGACGTA   CG   TACC
                                       GTCT  _____
GAM260  POLR2E   3'  CAGGAGCCCAGTGTC      59915       TATGTT
                                 GGCATTG     GCTTCTG
                                 |||||||     |||||||
                                 CTGTGAC     CGAGGAC
                                    C_____
GAM260  POLR2E   3'  TCATGGGGGGCAGTGGGGCCT  59922     ATTGTA  TG
                                 GGGC     TGT  CTTCTGTGG
                                 ||||     |||  |||||||||
                                 TCCG     ACG  GGGGGTACT
                                   GGGTG_  __
GAM260  POLS     3'  CACAGAGTTTTAATGTTT    22790       TATGTT  T
                                 GGGCATTG     GCT CTGTG
                                 ||||||||     ||| |||||
                                 TTTGTAAT     TGA GACAC
                                      TT_____  _
GAM260  PPARBP   3'  AAGTAATGTTTGGTGTCT    16489        T
                                 GGGCATTG ATGTTGCTT
                                 |||||||| |||||||||
```

```
                                TCTGTGGT TGTAATGAA
                                     T
GAM260  PPAT    3'  CCATAATTTGATGTATATAGTG 10696          TTGCTTC_
            TCC                   GGGCATTGTATG       TGTGG
                                  ||||||||||||       |||||
                                  CCTGTGATATAT       ATACC
                                        GTAGTTTA
GAM260  PPL     3'  GGACAACTGCGATGCCT     10704         T   C
                                  GGGCATTGTA GTTG TTC
                                  |||||||||| |||| |||
                                  TCCGTAGCGT CAAC AGG
                                       _   _
GAM260  PPP1CB  3'  TCATGATCTGCATATGATGT  10714     TG    TGCT  T
                                  GCAT  TATGT    TC GTGG
                                  ||||  |||||    || ||||
                                  TGTA  ATACG    AG TACT
                                    GT    TCT_ _
GAM260  PPP1R2  3'  TAGAAGTAGCTGTC       20695     TTGTAT
                                  GGCA     GTTGCTTCTG
                                  ||||     ||||||||||
                                  CTGT     CGATGAAGAT
                                       _______
GAM260  PPP2CA  3'  CACAAGAGCACTGCAGTGTTT  10743         T  T   TC    G
                                  GGGCATTGTA GT GCT  TGTG
                                  |||||||||| || |||  ||||
                                  TTTGTGACGT CA CGA  ACAC
                                        _ _  GA   G
GAM260  PPP2R4  3'  TGCAGGGGCGGGTCAGTTTCC  60562     C   TATG       TG
                                  GGG ATTG   TTGCTTCTG  G
                                  ||| ||||   |||||||||  |
                                  CCT TGAC   GGCGGGGAC  T
                                    T   TG__       GT
GAM260  PPP2R5C  3'  AAGGAAAATACAGTGTCT    10752          G  G
                                  GGGCATTGTAT TT CTT
                                  |||||||||| || |||
                                  TCTGTGACATA AA GAA
                                        A  G
GAM260  PPP2R5C  3'  CCGCGGGTTGACGACGGTGTCC 10756         A    GCT
                                  GGGCATTGT TGTT   TCTGTGG
                                  |||||||| ||||   |||||||
                                  CCTGTGGCA GCAG   GGGCGCC
                                        _   TT_
GAM260  PPP3CB  5'  CTACAGAGGGTCCGCCATGTTC 40897       T  ATGTTG
                                  GGGCAT GT     CTTCTGTGG
                                  |||||| ||     |||||||||
                                  CTTGTA CG     GGAGACATC
                                     C  CCTG__
GAM260  PPT2    3'  CTACAGCCAACCAGTGTACAAG 57229     A    TG   CTT__
            CCC                   GGC TTGTA  TTG    CTGTGG
                                  ||| |||||  |||    ||||||
```

```
                                CCG AACAT  GAC    GACATC
                                  _    GT   CAACC
GAM260  PRKAB1   3'  CTATGGAACTAAATACAGTGTT 20735         G   C
                                GGCATTGTAT TTG TTCTGTGG
                                |||||||||| ||| ||||||||
                                TTGTGACATA AAT AAGGTATC
                                      _  C
GAM260  PRKCN    3'  CCATAGAGGCATTGAAGGGTTT 19445     ATTGTATGT
                                GGGC       TGCTTCTGTGG
                                ||||       ||||||||||
                                TTTG       ACGGAGATACC
                                  GGAAGTT__
GAM260  PRKG1    3'  TAGATGACAATAGTGCTC    20748        A    CT
                                GGGCATTGT TGTTG  TCTG
                                ||||||||| |||||  ||||
                                CTCGTGATA ACAGT  AGAT

                                      _    __
GAM260  PRKG1    3'  TCATAGTAGGTATATATGAGTT 20749     A TG    T   _
           T                     GGGC T  TATGT GCTT CTGTGG
                                ||||  |  ||||| |||| ||||||
                                TTTG A  ATATA TGGA GATACT
                                  _ GT    _   T
GAM260  PRPS1    3'  TAGGTGGTATCGTAGTGCCT   10900      TG   T   _
                                GGGCAT  TATG TGCT TCTG
                                ||||||  |||| |||| ||||
                                TCCGTG  ATGC ATGG GGAT
                                   __   T   T
GAM260  PRPSAP1  3'  CATGAGTGATACAGTGTTT   10905       AT  TG   CT
                                GGGCATTGT  GT  CTT  GTG
                                |||||||||  ||  |||  |||
                                TTTGTGACA  TA  GAG  TAC
                                      __ GT  __
GAM260  PSA      3'  GAACAACATACAAAGTTT    54193     A       C
                                GGGC TTGTATGTTG TTC
                                |||| |||||||||| |||
                                TTTG AACATACAAC AAG
                                  A       _
GAM260  PSA      3'  GAACAACATACAAAGTTT    40955     A       C
                                GGGC TTGTATGTTG TTC
                                |||| |||||||||| |||
                                TTTG AACATACAAC AAG
                                  A       _
GAM260  PSCD4    3'  GCAAAACTGCAGTGTTT     25406         TG_
                                GGGCATTGTA   TTGC
                                ||||||||||   ||||
                                TTTGTGACGT   AACG
                                      CAA
GAM260  PSME3    3'  CCGCAGACCCTGGTGCAATGCT 19370          GTTGCT
           C                     GGGCATTGTAT     TCTGTGG
                                ||||||||||     |||||||
```

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                                CTCGTAACGTG     AGACGCC
                                      GTCCC_
GAM260  PTGES    3'  CTGTGGAAGCAAGGCTGGGGTC 16859     ATT_ ATG       TG
              T                  GGGC   GT   TTGCTTCTG  G
                                 ||||   ||   |||||||||  |
                                 TCTG   CG   AACGAAGGT  C
                                   GGGT  G__        GT
GAM260  PTGIS    3'  TCACAGGGAGCTGGCAATGCCC 6342         ATGTT    _
                                 GGGCATTGT    GCTTC TGTGG
                                 |||||||||    ||||| |||||
                                 CCCGTAACG    CGAGG ACACT
                                      GT___     G
GAM260  PTPN23   5'  CTACGGGAGTGGCCGGGTGGCC 63728    G   GTAT  TG
                                 GG CATT    GT  CTTCTGTGG
                                 || ||||    ||  |||||||||
                                 CC GTGG    CG  GAGGGCATC
                                  G   GC__  GT
GAM260  PTPN7    3'  TACAGAGGTGACCAGGCCT    54555     A   TAT  TG
                                 GGGC TTG   GT  CTTCTGTG
                                 |||| |||   ||  ||||||||
                                 TCCG GAC   CA  GGAGACAT
                                   _   ___  GT
GAM260  PTPN7    3'  TACAGAGGTGACCAGGCCT    54566     A   TAT  TG
                                 GGGC TTG   GT  CTTCTGTG
                                 |||| |||   ||  ||||||||
                                 TCCG GAC   CA  GGAGACAT
                                   _   ___  GT
GAM260  PTPN7    3'  TACAGAGGTGACCAGGCCT    11073     A   TAT  TG
                                 GGGC TTG   GT  CTTCTGTG
                                 |||| |||   ||  ||||||||
                                 TCCG GAC   CA  GGAGACAT
                                   _   ___  GT
GAM260  PTPRJ    5'  GGCGACGACGGTGCCC      11119         A
                                 GGGCATTGT TGTTGCT
                                 ||||||||| |||||||
                                 CCCGTGGCA GCAGCGG
                                           _
GAM260  PTPRK    3'  GGCAACATATATGCTT      11122        T
                                 GGGCAT GTATGTTGCT
                                 |||||| ||||||||||
                                 TTCGTA TATACAACGG
                                           _
GAM260  PTPRO    3'  CCACAGATCAACTGTGTAATCT 11133     C      _    CT
              T                  GGG ATTGTAT GTTG  TCTGTGG
                                 ||| ||||||| ||||  |||||||
                                 TTC TAATGTG CAAC  AGACACC
                                   _      T   T_
GAM260  PTPRO    3'  CCACAGATCAACTGTGTAATCT 47714     C      _    CT
              T                  GGG ATTGTAT GTTG  TCTGTGG
                                 ||| ||||||| ||||  |||||||
```

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                                TTC TAATGTG CAAC  AGACACC
                                  _     T   T_
GAM260  PTPRO    3' CCACAGATCAACTGTGTAATCT 47697     C     _   CT
           T                     GGG ATTGTAT GTTG  TCTGTGG
                                 ||| ||||||| ||||  |||||||
                                TTC TAATGTG CAAC  AGACACC
                                  _     T   T_
GAM260  PTPRO    3' CCACAGATCAACTGTGTAATCT 47701     C     _   CT
           T                     GGG ATTGTAT GTTG  TCTGTGG
                                 ||| ||||||| ||||  |||||||
                                TTC TAATGTG CAAC  AGACACC
                                  _     T   T_
GAM260  PTPRO    3' CCACAGATCAACTGTGTAATCT 47706     C     _   CT
           T                     GGG ATTGTAT GTTG  TCTGTGG
                                 ||| ||||||| ||||  |||||||
                                TTC TAATGTG CAAC  AGACACC
                                  _     T   T_
GAM260  PUM1     3' TTATGGTCGTAGCATATAGTGT 27962           TT
           T                     GGCATTGTATGTTGC  CTGTGG
                                 ||||||||||||||  ||||||
                                TTGTGATATACGATG  GGTATT
                                        CT
GAM260  PYCS     3' ACAGCAGTGATGCTT      11166       GTATGTT  T
                                GGGCATT     GCT CTGT
                                |||||||     ||| ||||
                                TTCGTAG     TGA GACA
                                   ________  C
GAM260  PYGB     3' CCATGGGGGTCAGGGTG    11174     G  _
                                TAT TTG CTTCTGTGG
                                ||| ||| |||||||||
                                GTG GAC GGGGGTACC
                                  G   T
GAM260  RAB36    3' TTGCGGGGGTGGGTGTGGTGTC 16980       TG   G TG    TG
           C                     GGGCAT  TAT T  CTTCTG  G
                                 ||||||  |||  |  ||||||  |
                                CCTGTG  GTG G  GGGGGC  T
                                   GT   _ GT     GT
GAM260  RAB3A    3' CACTCAGCTGTGGTGTCT    11181       TG  T   CTTCT
                                GGGCAT  TA GTTG    GTG
                                ||||||  ||  ||||    |||
                                TCTGTG  GT CGAC    CAC
                                   GT  _    T____
GAM260  RAB6A    3' CCATCATGGTAGGCAGTGCTT  11194        ATG    TCT
                                GGGCATTGT   TTGCT   GTGG
                                |||||||||   |||||   ||||
                                TTCGTGACG   GATGG   TACC
                                     ___    TAC
GAM260  RAB7L1   3' AGCTGGCTGTGATGCTT     14102       TG  T  _
                                GGGCAT  TA GTT GCT
                                ||||||  ||  ||| |||
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                                TTCGTA  GT CGG CGA
                                   GT  _   T
GAM260  RAD1     5'  CCGAATGCGCAGTGGACGATGC 55818         A GT   TTCTG
            CC                    GGGCATTGT T  TGC     TGG
                                  |||||||||  |  |||     |||
                                  CCCGTAGCA G  ACG     GCC
                                     G TG   CGTAA
GAM260  RAD23B   5'  TCGCGGAGGCAGCGGCGCGGTC 11218      AT   A
            C                     GGGC  TGT TGTTGCTTCTGTGG
                                  ||||  ||| ||||||||||||||
                                  CCTG  GCG GCGACGGAGGCGCT
                                    GC  _
GAM260  RAD51L3  5'  CACGTGACGTGCAGTCCC    11233     C       TG TTCT
                                  GGG ATTGTATGT  C    GTG
                                  ||| |||||||||  |    |||
                                  CCC TGACGTGCA  G    CAC
                                    _       GT ____
GAM260  RAD51L3  5'  CACGTGACGTGCAGTCCC    56066     C       TG TTCT
                                  GGG ATTGTATGT  C    GTG
                                  ||| |||||||||  |    |||
                                  CCC TGACGTGCA  G    CAC
                                    _       GT ____
GAM260  RAD51L3  5'  CACGTGACGTGCAGTCCC    56073     C       TG TTCT
                                  GGG ATTGTATGT  C    GTG
                                  ||| |||||||||  |    |||
                                  CCC TGACGTGCA  G    CAC
                                    _       GT ____
GAM260  RAD51L3  5'  CACGTGACGTGCAGTCCC    56079     C       TG TTCT
                                  GGG ATTGTATGT  C    GTG
                                  ||| |||||||||  |    |||
                                  CCC TGACGTGCA  G    CAC
                                    _       GT ____
GAM260  RANBP2L1 5'  CGCGGGGCTGAGCGGTGCTC  17314         ATGTT   T   TG
                                  GGGCATTGT    GCT CTG  G
                                  |||||||||    ||| |||  |
                                  CTCGTGGCG    CGG GGC  C
                                       AGT__   _   GT
GAM260  RANBP2L1 5'  CGCGGGGCTGAGCGGTGCTC  50044         ATGTT   T   TG
                                  GGGCATTGT    GCT CTG  G
                                  |||||||||    ||| |||  |
                                  CTCGTGGCG    CGG GGC  C
                                       AGT__   _   GT
GAM260  RAP1GDS1 3'  GCATGCATGTGATGTTC     40966       TG    _
                                  GGGCAT  TATGT TGC
                                  ||||||  ||||| |||
                                  CTTGTA  GTACG ACG
                                     GT    T
GAM260  RBBP9    3'  CAGAAATACAATTTCC      70129     C     GTTGC
                                  GGG ATTGTAT    TTCTG
                                  ||| |||||||    |||||
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                                CCT TAACATA     AAGAC
                                  T     _____
GAM260  RBBP9    5'  CGCGGGAGCAGGCTGGGCTC  70131      ATT  ATG       TG
                                GGGC  GT  TTGCTTCTG  G
                                ||||  ||  |||||||||  |
                                CTCG  CG  GACGAGGGC  C
                                  GGT  ___       GT
GAM260  RBM3     5'  CACAGGAGCATGACTGCCT   70484      TT  ATGT
                                GGGCA  GT   TGCTTCTGTG
                                |||||  ||   ||||||||||
                                TCCGT  CA   ACGAGGACAC
                                  __ GT__
GAM260  REQ      3'  TCACAGGGTTCAAACAGTGTCC 20770         A  TT   T
                                GGGCATTGT TG  GCT CTGTGG
                                |||||||||  ||  ||| ||||||
                                CCTGTGACA AC  TGG GACACT
                                     A  T_  _
GAM260  RFX2     5'  GCGGGAGCCGCTGCCC      5311       TTGTAT  T
                                GGGCA     GT GCTTCTGT
                                |||||     || ||||||||
                                CCCGT     CG CGAGGGCG
                                  _______ C
GAM260  RFX2     3'  TCACAGTTAACGGATTGTAATG 5313       TA___    CTT
           CCC                    GCATTG    TGTTG   CTGTGG
                                |||||||    |||||  ||||||
                                CGTAAT    GCAAT   GACACT
                                   GTTAG    T__
GAM260  RGS14    5'  CGAGGGTAGTGAGCGGTGTTT  21368         A GT    TC
                                GGGCATTGT T  TGCT  TG
                                |||||||||  |  ||||  ||
                                TTTGTGGCG G  ATGG  GC
                                     A TG    GA
GAM260  RGS6     5'  TGGAAGCACGAGCTT       15028      A    ATGTT
                                GGGC TTGT    GCTTCTG
                                |||| ||||    |||||||
                                TTCG AGCA    CGAAGGT
                                  _   ______
GAM260  RNF14    3'  GCAACAGCAGTGTTC       15023          A
                                GGGCATTGT TGTTGC
                                |||||||||  ||||||
                                CTTGTGACG ACAACG
                                     _
GAM260  RNGTT    3'  CTATGGGAGTGATATCAA     13731     T    TG
                                TTG ATGT  CTTCTGTGG
                                |||  ||||  |||||||||
                                AAC TATA  GAGGGTATC
                                  _   GT
GAM260  RPL15    3'  TTATCGGAGTGATGGCAATGCT 11386         A   TG    T
           C                     GGGCATTGT TGT  CTTC GTGG
                                |||||||||  |||  |||| ||||
```

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                                CTCGTAACG GTA  GAGG TATT
                                     _  GT   C
GAM260  RPLP0   5'  TCGTGGAAGTGACATCGTCT  6399     ATT T   TG   TG
                                GGGC  G ATGT  CTTC  TGG
                                ||||  | ||||  ||||  |||
                                TCTG  C TACA  GAAG  GCT
                                  ___ _   GT   GT
GAM260  RREB1   5'  TCGCAGGAGCAACACGTGATGT 11396      TA
                                GCATTG  TGTTGCTTCTGTGG
                                ||||||  ||||||||||||||
                                TGTAGT  ACAACGAGGACGCT
                                   GC
GAM260  RRM2    3'  GTGGCTTGTGTAGTGTCC   6410         __ TG
                                GGGCATTGTAT  GT  C
                                ||||||||||  ||  |
                                CCTGTGATGTG  CG  G
                                      TT  GT
GAM260  RRP22   5'  CGCGGGGCGGAGGCGGTGTCT  21358       ATG   T  TG
                                GGGCATTGT   TTGCT CTG  G
                                |||||||||   ||||| |||  |
                                TCTGTGGCG   GGCGG GGC  C
                                     GA_    _  GT
GAM260  RTDR1   5'  CTGCGGAGGCAGTGAGTGGTTT 27050    C  TG A GT     TG
          CT                    GGG AT  T T  TGCTTCTG  G
                                ||| ||  | |  ||||||||  |
                                TCT TG  G G  ACGGAGGC  C
                                  T  GT A TG      GT
GAM260  RTKN    3'  CGCAGGGGTGGGCAGAAGCCC  52326    A_   ATG TG    TG
                                GGGC  TTGT   T  CTTCTG  G
                                ||||  ||||   |  ||||||  |
                                CCCG  GACG   G  GGGGAC  C
                                  AA   ___ GT    GT
GAM260  RUNX1   3'  CCATGGAAAGAAATATGATTCC 8261    C  TG   G  GC
          C                     GGG AT  TAT TT  TTCTGTGG
                                ||| ||  ||| ||  ||||||||
                                CCC TA  ATA AG  AAGGTACC
                                  T  GT   A  A_
GAM260  RUNX3   3'  TCATAAAGGCTAGCAGCATGCG 15118          __  __
          GT                    ATTGTATGTTGCT  TCT  GTGG
                                ||||||||||||  |||  ||||
                                TGGCGTACGACGA  GGA  TACT
                                      TC   AA
GAM260  RXRA    3'  AGTTGTACAGTGCT      11401         TT
                                GGCATTGTATG  GCT
                                ||||||||||  |||
                                TCGTGACATGT  TGA
                                     __
GAM260  SCAMP1  3'  GCAACAGGTGTGATGTCC   53405      TG __
                                GGGCAT  TA  TGTTGC
                                ||||||  ||  ||||||
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                                CCTGTA  GT  ACAACG
                                   GT  GG
GAM260  SCAP2    3'  TAGAGAGTAATGTATAAT    14112          _
                                ATTGTATGTTGCT TCTG
                                |||||||||||| ||||
                                TAATATGTAATGA AGAT
                                      G
GAM260  SCD      3'  AAGTGGCTGCGGTGTTT     17343         T  TG
                                GGGCATTGTA GT  CTT
                                |||||||||| ||  |||
                                TTTGTGGCGT CG  GAA
                                      _  GT
GAM260  SCD      3'  CAGCTGGCAGTGCAATGCTT   17347         GT   T_
                                GGGCATTGTAT  TGCT  CTG
                                ||||||||||  ||||  |||
                                TTCGTAACGTG  ACGG  GAC
                                      __   TC
GAM260  SCD      3'  TCACAGTGTTGCATATGAGCCT 17349     A TG    T  TT
                                GGGC T  TATGT GC  CTGTGG
                                |||| |  ||||| ||  ||||||
                                TCCG A  ATACG TG  GACACT
                                  _ GT    T  T_
GAM260  SCML1    5'  TTGCCAGGTTATATATGATGCT 22169      TG    T   CT TG
           C                     GGGCAT  TATGT GCTT  G  G
                                ||||||  ||||| ||||  |  |
                                CTCGTA  ATATA TGGA  C  T
                                   GT    T   C_ GT
GAM260  SCN1A    3'  TTACAGAAGCAAACCATAGGCT 88853     A   ATG
           C                     GGGC TTGT   TTGCTTCTGTGG
                                |||| ||||  ||||||||||||
                                CTCG GATA   AACGAAGACATT
                                  _   CCA
GAM260  SCN1B    3'  TTACAGAAGTAGTTTTGTTC   6419      TTGTATG
                                GGGCA      TTGCTTCTGTGG
                                |||||      ||||||||||||
                                CTTGT      GATGAAGACATT
                                   TTT____
GAM260  SCN2B    3'  CCATGCTCTGGGACGTGTGGGC 15937     A TG     G  TC__
           CC                      GGGC T  TATGTT CT    TGTGG
                                |||| |  |||||| ||    |||||
                                CCCG G  GTGCAG GG    GTACC
                                  _ GT     _  TCTC
GAM260  SCO1     3'  TCACAGAAAAGAATATAATTTC 15949     C      G  GC
           C                     GGG ATTGTAT TT  TTCTGTGG
                                ||| |||||||  ||  ||||||||
                                CCT TAATATA AG  AAGACACT
                                  T      _  AA
GAM260  SDHD     3'  TTGCAGAAAATTAGACAGTGTT 11487         AT_   GC    TG
           T                     GGGCATTGT   GTT  TTCTG  G
                                |||||||||   |||  |||||  |
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                                TTTGTGACA  TAA  AAGAC  T
                                     GAT  __    GT
GAM260  SEL1L   3'  TTACAGAGGTAGCATTGGTG  17365     T
                                CATTG ATGTTGCTTCTGTGG
                                ||||| ||||||||||||||
                                GTGGT TACGATGGAGACATT
                                  _
GAM260  SEL1L   3'  TTGTGGGAGCACAGTCAGTGAC 17366    _   TA  T    TG
           CC                     GGG CATTG  TGT GCTTCTG  G
                                ||| |||||  ||| |||||||  |
                                CCC GTGAC  ACA CGAGGGT  T
                                  A   TG  _     GT
GAM260  SELL    3'  TTACCCTGTAACATGCAAT   5395          TTCT
                                ATTGTATGTTGC   GTGG
                                ||||||||||||   ||||
                                TAACGTACAATG   CATT
                                      TCC_
GAM260  SEPN1   3'  CGGGAGCCAGCGCTC     66367     A  TATGTT
                                GGGC TTG     GCTTCTG
                                |||| |||     |||||||
                                CTCG GAC     CGAGGGC
                                  C  _______
GAM260  SEPN1   3'  GGGGAGGGAGGGCGTCTGATGC 66376       GT   G   GTGG
           TC                     GGGCATT  ATGTT CTTCT
                                |||||||  ||||| |||||
                                CTCGTAG  TGCGG GAGGG
                                   TC   _    AGGGGT
GAM260  SERPINE1  3'  TTACAGGAGCTTTTGTGTGCCT 5196       TGTATGTT
                                GGGCAT      GCTTCTGTGG
                                ||||||      ||||||||||
                                TCCGTG      CGAGGACATT
                                   TGTTTT__
GAM260  SET7    3'  GCATCAATAGCAGTGTGTAGGT 47637     A    TG    TC  _  G
           CT                     GGGC TTGTA  TTGCT  TG TG
                                |||| |||||  |||||  || ||
                                TCTG GATGT  GACGA  AC AC
                                  _    GT    TA  T  GT
GAM260  SFRP2   3'  CCACAGGAGTGGATAGCTGTTT 72068      TT  ATG TG
                                GGGCA  GT   T  CTTCTGTGG
                                |||||  ||   |  |||||||||
                                TTTGT  CG   G  GAGGACACC
                                  __  ATA GT
GAM260  SFRS7   3'  AAGGGATTTGTGATGTCT    59444       TG  T   G
                                GGGCAT  TA GTT CTT
                                ||||||  || ||| |||
                                TCTGTA  GT TAG GAA
                                   GT  T   G
GAM260  SH3BP5  3'  TTGTGGAAGCAATAACTAGTTC 16747    C   TA        TG
           CT                     GGG ATTG  TGTTGCTTCTG  G
                                ||| ||||  ||||||||||  |
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                                TCC TGAT  ATAACGAAGGT  T
                                  T   CA         GT
GAM260  SHANK2   3'  CCGTGGAGGTGGTGTCTGCTGT 55735     T __ TG TG   TG
            GC                    GCAT GT  A  T  CTTC  TGG
                                |||| ||  |  |  ||||  |||
                                CGTG CG  T  G  GGAG  GCC
                                  T  TC GT GT   GT
GAM260  SIAT4C   3'  CGTGGGGGTGGCTGGTGCC   20785       TAT  TG    TG
                                GGCATTG   GT  CTTCTG  G
                                |||||||   ||  ||||||  |
                                CCGTGGT   CG  GGGGGT  C
                                    ___  GT    GT
GAM260  SIT     5'  GCGGGGTACGGGCCT      27078     A     G
                                GGGC TTGTAT TTGC
                                |||| |||||| ||||
                                TCCG GGCATG GGCG
                                  _     G
GAM260  SIX3     3'  CATACACACATACAAGTCC    18273     A      _ CTTC
                                GGGC TTGTATGT TG    TGTG
                                |||| |||||||| ||    ||||
                                CCTG AACATACA AC    ATAC
                                  _       C ____
GAM260  SLC12A7  3'  CCACAGGTGCGATCAGTGCCT  21699        TAT    T
                                GGGCATTG   GTTGC TCTGTGG
                                ||||||||   ||||| |||||||
                                TCCGTGAC   TAGCG GGACACC
                                    ___     T
GAM260  SLC13A4  3'  CCACAGGAGCTGCCAGTATCC  24919    GC    TAT  T
                                GG  ATTG   GT GCTTCTGTGG
                                ||  ||||   || ||||||||||
                                CC  TGAC   CG CGAGGACACC
                                 TA   ___  T
GAM260  SLC19A1  3'  CACAGGAGTTGTGAGCCC    11754      A TG  TGTT
                                GGGC T  TA    GCTTCTGTG
                                |||| |  ||    |||||||||
                                CCCG A  GT    TGAGGACAC
                                  _ GT  ____
GAM260  SLC21A3  5'  TCACAGCACACTTACGGTGCTT 56228          T _    TCT
                                GGGCATTGTA GT TGCT   GTGG
                                |||||||||| || ||||   ||||
                                TTCGTGGCAT CA ACGA   CACT
                                     T  C   ___
GAM260  SLC22A12 5'  CGTGGGGGAAACAGGCCC    58069     A   ATGTTG   TG
                                GGGC TTGT     CTTC  TG
                                |||| ||||     ||||  ||
                                CCCG GACA     GGGG  GC
                                  _   AA____    GT
GAM260  SLC25A19 3'  CAGGAGTCAGGTCC       41376      A   TATGTT
                                GGGC TTG     GCTTCTG
                                |||| |||     |||||||
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                                CCTG GAC     TGAGGAC
                                  _  _______
GAM260  SLC25A6  3'  TGTAGGAGCCAAGTCGTGTTC  89384       T TA  TT     TG
                                GGGCAT G  TG  GCTTCTG  G
                                ||||||  |  ||  |||||||  |
                                CTTGTG T  AC  CGAGGAT  T
                                   C GA  __      GT
GAM260  SLC26A4  3'  TCACAGATTTGCTAATAATGTT 4789          AT  TGCT
           C                     GGGCATTGT  GT    TCTGTGG
                                |||||||||  ||   |||||||
                                CTTGTAATA  CG    AGACACT
                                     AT  TTT_
GAM260  SLC2A1   3'  CAGCCAGCAATGATGTCC    21495       TG A    CTT
                                GGGCAT  T TGTTG   CTG
                                ||||||  | |||||   |||
                                CCTGTA  A ACGAC   GAC
                                   GT _    C__
GAM260  SLC39A4  3'  TATAGAGGCCCCAGTCCC    55630     C   TATGTT
                                GGG ATTG     GCTTCTGTG
                                ||| ||||     |||||||||
                                CCC TGAC     CGGAGATAT
                                  _   CC____
GAM260  SLC39A4  3'  TATAGAGGCCCCAGTCCC    34952     C   TATGTT
                                GGG ATTG     GCTTCTGTG
                                ||| ||||     |||||||||
                                CCC TGAC     CGGAGATAT
                                  _   CC____
GAM260  SLC4A4   3'  TCATAGGAGTATTAATAGCCC  13643     ATTG   GT_
                                GGGC   TAT   TGCTTCTGTGG
                                ||||   |||  ||||||||||
                                CCCG   ATA   ATGAGGATACT
                                  ____  ATT
GAM260  SLC4A4   3'  TTACAGAGGTTGACATTGTTC  13645      T   ATGTT
                                GGGCA TGT    GCTTCTGTGG
                                ||||| |||    ||||||||||
                                CTTGT ACA    TGGAGACATT
                                   T  GT___
GAM260  SLC6A4   3'  CCACAGGGACACAGTCTGGTGC 6451         TA_   T CT
           CC                    GGGCATTG   TGT G  TCTGTGG
                                |||||||   ||| |  |||||||
                                CCCGTGGT   ACA C  GGACACC
                                    CTG   _ AG
GAM260  SLC9A5   5'  GGCAGTGTACGTGTCC     59771       T   TG
                                GGGCAT GTA  TTGCT
                                ||||||  |||  |||||
                                CCTGTG CAT  GACGG
                                   _  GT
GAM260  SMAP     3'  CCATGGGCTATGTTAATGTCC  21967        T   T  TT
                                GGGCATTG ATGT GC  CTGTGG
                                |||||||| |||| ||  ||||||
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                                CCTGTAAT TGTA CG  GGTACC
                                    _   T  __
GAM260  SMARCA5  3'  TCATAAGATGTACTGTACAATG 13191          GT   T  _
            CTC                   GGGCATTGTAT  TGC TCT GTGG
                                  ||||||||||  ||| ||| ||||
                                  CTCGTAACATG  ATG AGA TACT
                                       TC   T   A
GAM260  SNAI1    3'  CGCGGAGGCGGTGGCAG     19968      ATG       TG
                                  TTGT   TTGCTTCTG  G
                                  ||||   |||||||||  |
                                  GACG   GGCGGAGGC  C
                                    GT_        GT
GAM260  SNRPN    5'  TTGCGGGGGCAAGGTCAGCTGC 43002       _  T  G       TG
            CC                    GGGCA TTG AT TTGCTTCTG  G
                                  |||||  ||| ||  |||||||||  |
                                  CCCGT GAC TG AACGGGGGC  T
                                    C  _  G        GT
GAM260  SNRPN    5'  TTGCGGGGGCAAGGTCAGCTGC 43010       _  T  G       TG
            CC                    GGGCA TTG AT TTGCTTCTG  G
                                  |||||  ||| ||  |||||||||  |
                                  CCCGT GAC TG AACGGGGGC  T
                                    C  _  G        GT
GAM260  SNRPN    5'  TTGCGGGGGCAAGGTCAGCTGC 43017       _  T  G       TG
            CC                    GGGCA TTG AT TTGCTTCTG  G
                                  |||||  ||| ||  |||||||||  |
                                  CCCGT GAC TG AACGGGGGC  T
                                    C  _  G        GT
GAM260  SNX9     3'  ACGGGATTTGATGCCT      32589         TATGTTGC
                                  GGGCATTG       TTCTGT
                                  ||||||||       ||||||
                                  TCCGTAGT       AGGGCA
                                      TT_______
GAM260  SNX9     3'  CTGCAGCCTCAGCAGTGTACAG 32592    A     TG     T___   TG
            AGTCC                   C TTGTA  TTGCT    CTG  G
                                  | |||||  |||||   |||  |
                                  G GACAT  GACGA    GAC  C
                                   A    GT    CTCC   GT
GAM260  SOCS4    3'  TACAAAGGCAGTGGTGTCC    55113       TG ATGT    C
                                  GGGCAT  T    TGCTT TGTG
                                  ||||||  |    ||||| ||||
                                  CCTGTG  G    ACGGA ACAT
                                     GT _____     A
GAM260  SOD3     5'  TCACGGTGGGCGTGCGGGGCTC 11866      A       TG  T
                                  GGGC TTGTATGT  CT CTGTGG
                                  ||||  ||||||||  ||  ||||||
                                  CTCG GGCGTGCG  GG GGCACT
                                    G        __  T
GAM260  SOLH     5'  TGGAGGCAGCAGCCC       18876      ATTGTA
                                  GGGC     TGTTGCTTCTG
                                  ||||     ||||||||||
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                              CCCG     ACGACGGAGGT
                                 ______
GAM260  SORBS1   3'  CCACATTTGCATATGATGCC  31152      TG    TGCTTC
                              GGCAT  TATGT     TGTGG
                              |||||  |||||     |||||
                              CCGTA  ATACG     ACACC
                                 GT    TTT___
GAM260  SORBS1   3'  TCATAGAACACCAAAAATGATG 31162      TG A__  T  C
           TTC                   GGCAT  T   TG TG TTCTGTGG
                              |||||  |   || || ||||||||
                              TTGTA  A   AC AC AAGATACT
                                 GT AAA  C  _
GAM260  SORCS1   3'  TAACTATACAATGTCT     53586          _
                              GGGCATTGTAT GTTG
                              |||||||||| ||||
                              TCTGTAACATA CAAT
                                    T
GAM260  SOX13    3'  CCACAGGGCCAGATGTGGAGTC 19080     A TG   G   C
           T                   GGGC T  TAT TTG TTCTGTGG
                              |||| |  ||| ||| ||||||||
                              TCTG G  GTA GAC GGGACACC
                                 A GT   _   C
GAM260  SPG7     3'  TGGGGAAGGTTATCAGTGCTT  11905       T   TTG    GTGG
                              GGGCATTG ATG   CTTCT
                              |||||||| |||   |||||
                              TTCGTGAC TAT   GAAGG
                                   _  TG_    GGTA
GAM260  SPINK5   3'  CTATAGAAAACAATACAGAGCT 22428     A     _   GC
           T                   GGGC TTGTAT GTT  TTCTGTGG
                              |||| |||||| |||  ||||||||
                              TTCG GACATA CAA  AAGATATC
                                 A     A  __
GAM260  SPR      3'  CCATAGGGGCAGTCCTGCCT   11932      TTGTATG
                              GGGCA      TTGCTTCTGTGG
                              |||||      ||||||||||||
                              TCCGT      GACGGGGATACC
                                 CCT_____
GAM260  SPTAN1   5'  CCGCGGAGGCTCCTCGGTCC   11935     ATTGTATGTT
                              GGGC         GCTTCTGTGG
                              ||||         ||||||||||
                              CCTG         CGGAGGCGCC
                                 GCTCCT_____
GAM260  SSA1     3'  CGCAGAGGCATCCGGATCCC   11976     C   GTATGT      TG
                              GGG ATT     TGCTTCTG  G
                              ||| |||     ||||||||  |
                              CCC TAG     ACGGAGAC  C
                                _  GCCT__       GT
GAM260  STAC     3'  CACAGAAGTTTGGATGCCT    11989       GTATGTT
                              GGGCATT      GCTTCTGTG
                              |||||||      |||||||||
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                                TCCGTAG      TGAAGACAC
                                   GTT____
GAM260  STAM     3'  AGCAAATGATAATGTTC     12960         ATG
                                GGGCATTGT   TTGCT
                                |||||||||   |||||
                                CTTGTAATA   AACGA
                                     GTA
GAM260  STARD4   5'  TGTTGAGAGCGGTGTGAGGTGC 57521       TG  TG     CTGTGG
           TT                    GGGCAT  TA  TTGCTT
                                |||||| ||  ||||||
                                TTCGTG  GT  GGCGAG
                                   GA  GT     AGTTGTC
GAM260  STAU2    3'  CGTAGTCAACATGTAGAGTCT  26903      A        CTT   TG
                                GGGC TTGTATGTTG   CTG  G
                                |||| ||||||||||   |||  |
                                TCTG GATGTACAAC   GAT  C
                                  A        T__   GT
GAM260  SUFU     3'  CAGGGGCCAGGCTC       32407      A   TATGTT
                                GGGC TTG     GCTTCTG
                                |||| |||     |||||||
                                CTCG GAC     CGGGGAC
                                  _  _______
GAM260  SWAP70   3'  CACTTGACATGGAATGCCT    71346        G     GCTTCT   G
                                GGGCATT TATGTT     GTG
                                ||||||| ||||||     |||
                                TCCGTAA GTACAG     CAC
                                   G     TT____   A
GAM260  SYT1     3'  CCACAAGACAGTAGTGATGCTC 18899       TG ATGT   _  _
                                GGGCAT  T    TGCT TCT GTGG
                                ||||||  |    |||| ||| ||||
                                CTCGTA  G    ATGA AGA CACC
                                   GT ____    C   A
GAM260  SYT4     3'  TTATAGGAAATAGGTATAGTGT 62439    G       GTTGC
           GC                    G GCATTGTAT    TTCTGTGG
                                | |||||||||    ||||||||
                                C TGTGATATG    AGGATATT
                                 G        GATAA
GAM260  TAC3     3'  CTACATTAAAAATATAATGTCT 25123          GTTGCTTC
                                GGGCATTGTAT       TGTGG
                                ||||||||||        |||||
                                TCTGTAATATA       ACATC
                                      AAAATT__
GAM260  TACSTD2  3'  CAGGAGGGCGAGCTC      9855      A   ATGTTG
                                GGGC TTGT     CTTCTG
                                |||| ||||     ||||||
                                CTCG AGCG     GAGGAC
                                  _   G_____
GAM260  TAF12    3'  TACTTTGTAATGTCAGTGTTT  18920        T     TTCT   G
                                GGGCATTG ATGTTGC    GTG
                                |||||||| |||||||    |||
```

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                                TTTGTGAC TGTAATG   CAT
                                   _     TTT_  G
GAM260  TAF1C   3'  CTGTGGGGGCCTCAGGCAGGTC 19059     A   A  TT     TG
          C                     GGGC TTGT TG  GCTTCTG  G
                                |||| |||| ||  |||||||  |
                                CCTG GACG AC  CGGGGGT  C
                                  _   G  TC      GT
GAM260  TAF5    3'  TCATGGAGGGGACATTTATGGT 22713      TG  __   G
          GCTT                   GGCAT  TA  TGTT CTTCTGTGG
                                |||||  ||  |||| |||||||||
                                TCGTG  AT  ACAG GGAGGTACT
                                  GT  TT   G
GAM260  TAF5    3'  TCATGGAGGGGACATTTATGGT 57402      TG  __   G
          GCTT                   GGCAT  TA  TGTT CTTCTGTGG
                                |||||  ||  |||| |||||||||
                                TCGTG  AT  ACAG GGAGGTACT
                                  GT  TT   G
GAM260  TARDBP  5'  TGTGGGAGCGAAGCGGTGGCT  23774   G    ATG      TG
                                GG CATTGT   TTGCTTCTG  G
                                || ||||||   |||||||||  |
                                TC GTGGCG   AGCGAGGGT  T
                                 G    A__       GT
GAM260  TBL1X   3'  CGCAGGAGTCTATATG     18929      T_
                                TATGT  GCTTCTGTG
                                |||||  |||||||||
                                GTATA  TGAGGACGC
                                  TC
GAM260  TBXAS1  5'  TTGTGGGGGCCCACTCCATGTG 6510    TG   TT____     TG
          ATGTTT                 AT  TATG    GCTTCTG  G
                                ||  ||||    |||||||  |
                                TA  GTAC    CGGGGGT  T
                                 GT   CTCACC     GT
GAM260  TBXAS1  5'  TTGTGGGGGCCCACTCCATGTG 48294   TG   TT____     TG
          ATGTTT                 AT  TATG    GCTTCTG  G
                                ||  ||||    |||||||  |
                                TA  GTAC    CGGGGGT  T
                                 GT   CTCACC     GT
GAM260  TCF12   3'  CCGTGGAAGTTGCCTTGTGCCT 12179      TGTAT  T    TG
                                GGGCAT    GT GCTTC  TGG
                                ||||||    || |||||  |||
                                TCCGTG    CG TGAAG  GCC
                                  TTC__  T    GT
GAM260  TCF21   5'  CGCAGAAGTCCTCGGGGTTC   12183     A   TATGTT     TG
                                GGGC TTG    GCTTCTG  G
                                |||| |||    |||||||  |
                                CTTG GGC    TGAAGAC  C
                                  G  TCC___      GT
GAM260  TCF8    3'  TTACAGAGGTAGCACAACTG   47734   _   AT
                                CA TTGT  GTTGCTTCTGTGG
                                || ||||  ||||||||||||
```

```
                                GT AACA  CGATGGAGACATT
                                 C   __
GAM260  TDGF1    3'  TAGAAGACAAAATGTTC     12203        GTATG  _
                                GGGCATT     TTG CTTCTG
                                |||||||     ||| ||||||
                                CTTGTAA     AAC GAAGAT
                                    _____   A
GAM260  TEM8     3'  TCATGGGAGCATCAGCCAGTTT 49857     C    TA  T
              CT                  GGG ATTG  TG TGCTTCTGTGG
                                |||  ||||  || ||||||||||
                                TCT TGAC  AC ACGAGGGTACT
                                  T   CG  T
GAM260  TERF2    3'  CACAGGAGCATGGTTCCT     18945     C  TG ATGTT
                                GGG AT  T    GCTTCTGTG
                                |||  ||  |    |||||||||
                                TCC TG  A    CGAGGACAC
                                  T  GT _____
GAM260  TES      5'  CCGCGGGAGTTCCGCAGGTTT  72001      A    AT TT
                                GGGC TTGT  G  GCTTCTGTGG
                                ||||  ||||  |  ||||||||||
                                TTTG GACG  C  TGAGGGCGCC
                                  _    __ CT
GAM260  TFAP2C   5'  TCGCAGAGCCGCCGATGCGTGT 12233       T   __  T   T
              CC                  GGGCAT GTAT  GT GCT CTGTGG
                                |||||| ||||  ||  ||| ||||||
                                CCTGTG CGTA  CG CGA GACGCT
                                   _   GC  C  _
GAM260  TFDP2    3'  CTACGTTTCAATATGTGATGCT 20808       TG      CTTC
              C                   GGGCAT  TATGTTG    TGTGG
                                ||||||  |||||||    |||||
                                CTCGTA  GTATAAC    GCATC
                                   GT      TTT_
GAM260  TGM2     3'  TCGCAGAGGCTGTCTGGGGCCT 16057      ATTGTATGTT
                                GGGC         GCTTCTGTGG
                                ||||         ||||||||||
                                TCCG         CGGAGACGCT
                                  GGGTCTGT__
GAM260  TIA1     3'  CCACTGAAGTAGTGTGCAGTTC 41848     C     TG      T
              T                   GGG ATTGTA  TTGCTTC GTGG
                                |||  ||||||  |||||||  ||||
                                TCT TGACGT  GATGAAG CACC
                                  _     GT      T
GAM260  TIA1     3'  CCACTGAAGTAGTGTGCAGTTC 42245     C     TG      T
              T                   GGG ATTGTA  TTGCTTC GTGG
                                |||  ||||||  |||||||  ||||
                                TCT TGACGT  GATGAAG CACC
                                  _     GT      T
GAM260  TIMM17B  3'  CCACACTCACATGTACGAAGTT 19542      A       _  CTTC
              C                   GGGC TTGTATGT TG    TGTGG
                                ||||  ||||||||  ||    |||||
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                                CTTG AGCATGTA AC    ACACC
                                  A       C  TC__
GAM260  TIMM23   3'  CGTAGAGGTGTGTCAATCCC   60140     C    TATGT       TG
                                GGG ATTG    TGCTTCTG  G
                                ||| ||||    ||||||||  |
                                CCC TAAC    GTGGAGAT  C
                                  _   TGT__       GT
GAM260  TIMP3    3'  CCACAAGTGGACATCAGTGTCT 4503          T  _ TG  TC
                                GGGCATTG ATG T  CT  TGTGG
                                |||||||| ||| |  ||  |||||
                                TCTGTGAC TAC G  GA  ACACC
                                     _  A GT  __
GAM260  TLE1     3'  TAGAGCAGTGGTGTCT      17415       TG ATGT    T
                                GGGCAT  T    TGCT CTG
                                ||||||  |    |||| |||
                                TCTGTG  G    ACGA GAT
                                   GT _____   _
GAM260  TLL1     5'  GCGACTGGGGGTAACAGGCAGT 24954         A        _  GG
           GCTT                    GGCATTGT TGTTGCTTCT GT
                                ||||||||| ||||||||||  ||
                                TCGTGACG ACAATGGGGG CA
                                    G         T  GCGT
GAM260  TLL1     3'  TGGATATAAATATGGTGTCC   24957       TG   G   CT
                                GGGCAT  TAT TTG  TCTG
                                ||||||  ||| |||  ||||
                                CCTGTG  ATA AAT  AGGT
                                   GT   _   AT
GAM260  TLL1     3'  CTGTGGAACAACTACTTATAAT 24952         T___    C    TG
           GCCT                    GCATTGTA    GTTG TTCTG  G
                                ||||||||    |||| |||||  |
                                CGTAATAT    CAAC AAGGT  C
                                    TCAT    _     GT
GAM260  TLR4     5'  TCACAGAAGCAGTGAGGATGAT 12319       TG ATG__
           GCC                     GGCAT  T    TTGCTTCTGTGG
                                |||||  |    ||||||||||||
                                CCGTA  A    GACGAAGACACT
                                   GT GGAGT
GAM260  TLR4     5'  TCACAGAAGCAGTGAGGATGAT 56738       TG ATG__
           GCC                     GGCAT  T    TTGCTTCTGTGG
                                |||||  |    ||||||||||||
                                CCGTA  A    GACGAAGACACT
                                   GT GGAGT
GAM260  TLR4     5'  TCACAGAAGCAGTGAGGATGAT 56729       TG ATG__
           GCC                     GGCAT  T    TTGCTTCTGTGG
                                |||||  |    ||||||||||||
                                CCGTA  A    GACGAAGACACT
                                   GT GGAGT
GAM260  TLR4     5'  TCACAGAAGCAGTGAGGATGAT 56734       TG ATG__
           GCC                     GGCAT  T    TTGCTTCTGTGG
                                |||||  |    ||||||||||||
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                                CCGTA A    GACGAAGACACT
                                   GT GGAGT
GAM260  TM4SF2   3' CACGTCACGTGTAGTGTCC   16063          T TTCT
                                GGGCATTGTATGT GC   GTG
                                |||||||||||| ||   |||
                                CCTGTGATGTGCA TG   CAC
                                      C _____
GAM260  TM7SF1   5' CCGCGGGGGCGGCGGCGGCC  12329    ATTGTA
                                GGC    TGTTGCTTCTGTGG
                                |||    ||||||||||||||
                                CCG    GCGGCGGGGGCGCC
                                  GCG___
GAM260  TM7SF3   3' TGCATAATATTATGGTGCCC  59671      TG _   CTTC TG
                                GGGCAT TA TGTTG   TG G
                                |||||| || |||||   || |
                                CCCGTG AT ATAAT   AC T
                                   GT T    _____ GT
GAM260  TMEFF2   3' GAAATAGTATACATTGTCT   32467      T       C
                                GGGCA TGTATGTTG TTC
                                ||||| ||||||||| |||
                                TCTGT ACATATGAT AAG
                                   T       A
GAM260  TMEM1    3' TCACGGTCTTAGTGACGTGTGT 12339     TGT   TG T___
          GCCT                   GCAT   ATGT CT   CTGTGG
                                |||| |||| ||   ||||||
                                CGTG   TGCA GA   GGCACT
                                  TG_   GT TTCT
GAM260  TMEPAI   3' CACGGAGGCACCGAGTTC    39441     A  TATGT
                                GGGC TTG    TGCTTCTGTG
                                |||| |||    ||||||||||
                                CTTG AGC    ACGGAGGCAC
                                  _   C_____
GAM260  TMEPAI   3' CCGTGGGGTGGAGCATGGTGCC 39444       TG ATG TG  T TG
          C                     GGGCAT  T   T  CT C  TGG
                                |||||| |   |  || |  |||
                                CCCGTG  A   G  GG G  GCC
                                   GT CGA GT  _ GT
GAM260  TMPRSS3  3' GTAGCATTTGGTGCTT     50510        T
                                GGGCATTG ATGTTGC
                                |||||||| |||||||
                                TTCGTGGT TACGATG
                                     T
GAM260  TMPRSS3  3' GTAGCATTTGGTGCTT     50531        T
                                GGGCATTG ATGTTGC
                                |||||||| |||||||
                                TTCGTGGT TACGATG
                                     T
GAM260  TMPRSS3  3' GTAGCATTTGGTGCTT     43799        T
                                GGGCATTG ATGTTGC
                                |||||||| |||||||
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                                TTCGTGGT TACGATG
                                     T
GAM260  TNFAIP1  3'  CTACAGAGGTGGCACATGCTT  40918      TGTA  TG
                                GGGCAT   TGT  CTTCTGTGG
                                ||||||   |||  |||||||||
                                TTCGTA   ACG  GGAGACATC
                                   C___  GT
GAM260  TNFRSF4  3'  AGCATAACATACAGTGCC    12449          __
                                GGCATTGTATGT  TGCT
                                ||||||||||||  ||||
                                CCGTGACATACA  ACGA
                                      AT
GAM260  TNFRSF8  3'  CGCAGGGGTCTGGTGGTCTC  6960     C  TG ATGTT     TG
                                GGG AT  T    GCTTCTG  G
                                ||| ||  |    |||||||  |
                                CTC TG  G    TGGGGAC  C
                                  _  GT GTC__      GT
GAM260  TNFSF15  5'  TCATGGAGGTGTTTGGATGTCT 17597       GTATGT
                                GGGCATT     TGCTTCTGTGG
                                |||||||     ||||||||||
                                TCTGTAG     GTGGAGGTACT
                                    GTTT__
GAM260  TNFSF4   3'  CCATAGACCATATATAGTCTC  12443     C       TGCT
                                GGG ATTGTATGT    TCTGTGG
                                ||| |||||||||    |||||||
                                CTC TGATATATA    AGATACC
                                  _       CC__
GAM260  TR2      3'  CACTGGTGAACAGTGTCT    72315         ATG TG  TCT
                                GGGCATTGT   T  CT   GTG
                                |||||||||   |  ||   |||
                                TCTGTGACA   A  GG   CAC
                                     ___ GT  T__
GAM260  TRIM37   3'  AGTTCCATTAGTGCCT     30970         T   TT
                                GGGCATTG ATG  GCT
                                |||||||| |||  |||
                                TCCGTGAT TAC  TGA
                                     _   CT
GAM260  TRIM37   3'  CGCCCGGCATTGGTGCTC    30971        T     CTTCT
                                GGGCATTG ATGTTG    GTG
                                |||||||| ||||||    |||
                                CTCGTGGT TACGGC    CGC
                                     _     C____
GAM260  TRIM9    3'  CCGTGGAGGCGCCAGCTGCCT  30757      TT  A  T     TG
                                GGGCA  GT TG TGCTTC  TGG
                                |||||  || || ||||||  |||
                                TCCGT  CG AC GCGGAG  GCC
                                   __  _  C     GT
GAM260  TRIM9    3'  CGCAGGAGGATGTAGCGCCT   53757     ATTG     G     TG
                                GGGC    TATGTT CTTCTG  G
                                ||||    |||||| ||||||  |
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```
                                TCCG   ATGTAG GAGGAC  C
                                  CG__     _     GT
GAM260  TRIP12   3'  TTATAGCAAGAAATGCAGTGTC 14898          GTTG  _
           T                     GGGCATTGTAT   CTT CTGTGG
                                 ||||||||||    ||| ||||||
                                 TCTGTGACGTA   GAA GATATT
                                       AA__   C
GAM260  TRO      5'  CCACAGAAGAGGACAGTGTCC  32387         ATGTTG
                                 GGGCATTGT     CTTCTGTGG
                                 |||||||||     |||||||||
                                 CCTGTGACA     GAAGACACC
                                     GGA___
GAM260  TRPC1    3'  GGAGGCGGCAAGCCC       12389      ATTGTA
                                 GGGC     TGTTGCTTCT
                                 ||||     ||||||||||
                                 CCCG     ACGGCGGAGG
                                   A_____
GAM260  TRPC1    3'  GGGGTACGTGAGATGTTT    12390        G    T
                                 GGGCATT TATGT GCTTC
                                 ||||||| ||||| |||||
                                 TTTGTAG GTGCA TGGGG
                                    A    _
GAM260  TRPM2    3'  CGTGGGGGTACAGGAGCCC   12400     A_   ATGTT    TG
                                 GGGC  TTGT    GCTTC  TG
                                 ||||  ||||    |||||  ||
                                 CCCG  GACA    TGGGG  GC
                                   AG   _____    GT
GAM260  TRPM2    3'  CTGCAGAGGCTCCGGATGGAGC 12402     A TG A  TT      TG
           CT                      GGGC T  T TG  GCTTCTG  G
                                 ||||  |  | ||  |||||||  |
                                 TCCG G  A GC  CGGAGAC  C
                                   A GT G  CT      GT
GAM260  TRPM7    3'  TCACAGAGGTATGAGAAGCCT  62130     A  GTATGT
                                 GGGC TT     TGCTTCTGTGG
                                 |||| ||     ||||||||||
                                 TCCG AG     ATGGAGACACT
                                   A  AGT___
GAM260  TRPS1    3'  TTACATTTCAAATAATGGTGCC 26084       TG A    GCTTC
           T                      GGGCAT  T TGTT    TGTGG
                                 ||||||  | ||||    |||||
                                 TCCGTG  A ATAA    ACATT
                                    GT _    ACTTT
GAM260  TRPV1    5'  CCGTCCTGGTATCACAGTGCTT 54794         ATGT    TCTG
                                 GGGCATTGT    TGCT    TGG
                                 |||||||||    ||||    |||
                                 TTCGTGACA    ATGG    GCC
                                      CT__    TCCT
GAM260  TXNRD1   3'  AGAGGTATTAATGCCT      12454         TATGT
                                 GGGCATTG     TGCTTCT
                                 ||||||||     |||||||
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                                TCCGTAAT    ATGGAGA
                                   T____
GAM260  TXNRD1   3'  CAGAAGTGTTTATGCTT    12457      TGTATGT
                                GGGCAT     TGCTTCTG
                                ||||||     ||||||||
                                TTCGTA     GTGAAGAC
                                  TTT____
GAM260  TYK2     5'  CCGCGGGAGCGGGGAGGGGTCC 59875     ATTGTATG
                                GGGC      TTGCTTCTGTGG
                                ||||      ||||||||||||
                                CCTG      GGCGAGGGCGCC
                                  GGGAGG__
GAM260  UBE2G2   3'  CTGTGGAGGTGGGCATGTGGGC 64857     A TG   _ TG    TG
           CC                     GGGC T  TATG T  CTTCTG  G
                                ||||  |  ||||  |  ||||||  |
                                CCCG G  GTAC G  GGAGGT  C
                                  _ GT    G GT     GT
GAM260  UBE3A    5'  CTACAGGAGACGACGGGGCCT  55589     ATTGTA   _
                                GGGC     TGTTG CTTCTGTGG
                                ||||     ||||| |||||||||
                                TCCG     GCAGC GAGGACATC
                                  GG____    A
GAM260  UBL3     3'  CCATGGAAAAATACAGTATCT  23031    GC     GTTGC
                                GG  ATTGTAT    TTCTGTGG
                                ||  |||||||    ||||||||
                                TC  TGACATA    AAGGTACC
                                 TA      AA___
GAM260  UBQLN2   5'  CACAGAGGTACCGTGC     25565      T
                                GTATG TGCTTCTGTG
                                ||||| ||||||||||
                                CGTGC ATGGAGACAC
                                   C
GAM260  UBQLN2   3'  TCACTGAAAGTGTCATGTGATG 25568      TG   T   _ T
           TTT                    GGGCAT  TATG TGCTT C GTGG
                                ||||||  |||| ||||| | ||||
                                TTTGTA  GTAC GTGAA G CACT
                                   GT   T    A T
GAM260  UBQLN3   3'  CGTGGAGGCAATGTTGTTC   33927     TTGT        TG
                                GGGCA   ATGTTGCTTCTG  G
                                |||||   ||||||||||||  |
                                CTTGT   TGTAACGGAGGT  C
                                  ____          GT
GAM260  UMPK     3'  CATGGAGATGAAATGCCT    25010      G   GTTGC
                                GGGCATT TAT    TTCTGTG
                                ||||||| |||    |||||||
                                TCCGTAA GTA    GAGGTAC
                                   A  _____
GAM260  UPF3A    3'  TAGATATAGCATACAGAGCCT  43454     A       CT
                                GGGC TTGTATGTTG  TCTG
                                |||| ||||||||||  ||||
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                                TCCG GACATACGAT  AGAT
                                  A        AT
GAM260  UPF3A    3'  TAGATATAGCATACAGAGCCT  54777     A        CT
                                GGGC TTGTATGTTG  TCTG
                                |||| ||||||||||  ||||
                                TCCG GACATACGAT  AGAT
                                  A        AT
GAM260  UPK1B    3'  CACACTAACGTGTGTGTCT   22717      TGT     CTTC
                                GGGCAT  ATGTTG   TGTG
                                ||||||  ||||||   ||||
                                TCTGTG  TGCAAT   ACAC
                                   TG_    C___
GAM260  USP9X    3'  CTGCAGTGGAAAGTGTATAGTG 16207        TG  G_  T   TG
            TTT                   GGGCATTGTA  TT  CT CTG  G
                                ||||||||||  ||  || |||  |
                                TTTGTGATAT  GA  GG GAC  C
                                     GT  AA  T   GT
GAM260  USP9Y    3'  TACATGAATGACAGTGCCC   64037        ATGTTGC  _
                                GGGCATTGT     TTC TGTG
                                |||||||||     ||| ||||
                                CCCGTGACA     AAG ACAT
                                     GT_____   T
GAM260  UTY      5'  CTATGGAGGTGACAAGGCCT  23070     ATTGTA   TG
                                GGGC     TGT  CTTCTGTGG
                                ||||     |||  |||||||||
                                TCCG     ACA  GGAGGTATC
                                  GA____   GT
GAM260  VANGL2   3'  CAGGAATCAGTGCCT      71647        T  GTTGC
                                GGGCATTG AT    TTCTG
                                |||||||| ||    |||||
                                TCCGTGAC TA    AGGAC
                                   _ _____
GAM260  VBP1     3'  CAGATAAGTGCAGTGTCT    12570          GTTGCT
                                GGGCATTGTAT     TCTG
                                ||||||||||     ||||
                                TCTGTGACGTG     AGAC
                                     AAT___
GAM260  VCL      3'  CACAGAATCATATGATTCT   12573     C  TG   TTGC
                                GGG AT  TATG   TTCTGTG
                                ||| ||  ||||   |||||||
                                TCT TA  ATAC   AAGACAC
                                  _ GT   T___
GAM260  VCL      3'  CTGCAGAGGTCTGTGCTGAGGC 12574     ATT_   GTT     TG
            CT                    GGGC   GTAT   GCTTCTG  G
                                ||||   ||||  ||||||| |
                                TCCG   CGTG   TGGAGAC  C
                                  GAGT   TC_     GT
GAM260  VCL      3'  CACAGAATCATATGATTCT   25732     C  TG   TTGC
                                GGG AT  TATG   TTCTGTG
                                ||| ||  ||||   |||||||
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                                TCT TA  ATAC   AAGACAC
                                  _ GT   T___
GAM260  VCL     3'  CTGCAGAGGTCTGTGCTGAGGC 25733     ATT_   GTT     TG
             CT                   GGGC   GTAT  GCTTCTG  G
                                ||||   ||||  ||||||| |
                                TCCG   CGTG  TGGAGAC  C
                                  GAGT   TC_     GT
GAM260  VENTX2   3'  TCGCAGAAGGTCTGGAAGTGCC 27120       GTATGTTG
             C                    GGGCATT      CTTCTGTGG
                                |||||||      |||||||||
                                CCCGTGA      GAAGACGCT
                                    AGGTCTG_
GAM260  VHL     3'  TCACTAGGCATTGTGATGTTT  5083       TG  TGT    CT
                                GGGCAT  TA   TGCTT  GTGG
                                ||||||  ||   |||||  ||||
                                TTTGTA  GT   ACGGA  CACT
                                    GT  T__    T_
GAM260  VHL     3'  GTAGCATGAATAATGTTT    5080          __
                                GGGCATTGT  ATGTTGC
                                |||||||||  |||||||
                                TTTGTAATA  TACGATG
                                     AG
GAM260  VIPR2    3'  TGGGAGCCGCAGAGCCT     12619     ATTGTA   T
                                GGGC     TGT GCTTCTG
                                ||||     ||| |||||||
                                TCCG     ACG CGAGGGT
                                  AG____   C
GAM260  VPS41    3'  CACAGAGGTGACTGCCT     26923      TTGTAT  TG
                                GGGCA     GT  CTTCTGTG
                                |||||     ||  ||||||||
                                TCCGT     CA  GGAGACAC
                                  _______  GT
GAM260  WARS     3'  TCACGCAGCATGTGCAGGCCT  67288     A      T   TC
                                GGGC TTGTATGT GCT  TGTGG
                                |||| |||||||| |||  |||||
                                TCCG GACGTGTA CGA  GCACT
                                  _      _  C_
GAM260  WHSC1    3'  CTACAGTAAATGTTTGTGATGT 23658       TG  TGTTGCTT
             TT                   GGGCAT  TA      CTGTGG
                                ||||||  ||      ||||||
                                TTTGTA  GT      GACATC
                                    GT  TTGTAAAT
GAM260  WHSC1    3'  GCAGTGTGAGTAATGCTC    23662        __  TG
                                GGGCATTG  TA  TTGC
                                ||||||||  ||  ||||
                                CTCGTAAT  GT  GACG
                                     GA  GT
GAM260  WHSC1    3'  TCATAAGCGCAGCATTGGTGCT 23669        T      TTC
             C                    GGGCATTG ATGTTGC   TGTGG
                                |||||||| |||||||   |||||
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                                CTCGTGGT TACGACG   ATACT
                                   _     CGA
GAM260  WHSC1    3'  AAACCCCGGCGTGTGCAGTGCC 29906        TG T   TCTGTGG
           C                    GGGCATTGTA  T GCT
                                |||||||||| | |||
                                CCCGTGACGT  G CGG
                                   GT _   CCCCAAAT
GAM260  WHSC1    3'  AAACCCCGGCGTGTGCAGTGCC 55824        TG T   TCTGTGG
           C                    GGGCATTGTA  T GCT
                                |||||||||| | |||
                                CCCGTGACGT  G CGG
                                   GT _   CCCCAAAT
GAM260  WHSC1    3'  AAACCCCGGCGTGTGCAGTGCC 55841        TG T   TCTGTGG
           C                    GGGCATTGTA  T GCT
                                |||||||||| | |||
                                CCCGTGACGT  G CGG
                                   GT _   CCCCAAAT
GAM260  WIF1     3'  TTACAATGCATTTATGGTGTCT 60182      TG  TGT   TTC
                                GGGCAT  TA   TGC   TGTGG
                                |||||| ||   |||   |||||
                                TCTGTG  AT   ACG   ACATT
                                   GT  TT_   TA_
GAM260  XPNPEP2  3'  TCACCCTTCAGCAACATGCAGA 12683     A         TCT__
           GTCC                 GGC TTGTATGTTGCT    GTGG
                                ||| ||||||||||||    ||||
                                CTG GACGTACAACGA    CACT
                                  A          CTTCC
GAM260  ZFP36L1  3'  CTGTAGAAGTAGCTTTAATG   17006      TAT       TG
                                CATTG   GTTGCTTCTG  G
                                |||||   ||||||||||  |
                                GTAAT   CGATGAAGAT  C
                                   TT_        GT
GAM260  ZFP36L1  3'  TTACAGAAGCAACTTAGTGCCT 17008        TAT
                                GGGCATTG   GTTGCTTCTGTGG
                                ||||||||   ||||||||||||
                                TCCGTGAT   CAACGAAGACATT
                                     T__
GAM260  ZNF10    3'  TACAGAAGTAATTGGCCT    31180     ATTGTAT
                                GGGC      GTTGCTTCTGTG
                                ||||      ||||||||||||
                                TCCG      TAATGAAGACAT
                                  GT_____
GAM260  ZNF137   3'  CTATAGAAGATCATAAAGCTT  12861     ATTG   TTG
                                GGGC   TATG   CTTCTGTGG
                                ||||   ||||   |||||||||
                                TTCG   ATAC   GAAGATATC
                                  AA__   TA_
GAM260  ZNF148   3'  TTATAGAAGCAATGCATTACTT 41738     CAT   AT
                                GGG   TGT  GTTGCTTCTGTGG
                                |||   |||  ||||||||||||
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                                TTC   ACG  TAACGAAGATATT
                                  ATT   __
GAM260  ZNF202   3' CAGAAGATACTGTCC      12912      TT   GTTG
                                GGGCA  GTAT   CTTCTG
                                |||||  ||||   ||||||
                                CCTGT  CATA   GAAGAC
                                  __   ____
GAM260  ZNF217   3' GCAACGTAAGATGTCC     21516       G
                                GGGCATT TATGTTGC
                                |||||||  ||||||||
                                CCTGTAG ATGCAACG
                                    A
GAM260  ZNF236   3' ATCGGCGGCGGTGCTC     23712        ATGT   TCT
                                GGGCATTGT   TGCT   GT
                                |||||||||   ||||  ||
                                CTCGTGGCG   GCGG   TA
                                    ____   C__
GAM260  ZNF255   5' AGCAGGTATAATGTTT     19320         G
                                GGGCATTGTAT TTGCT
                                |||||||||||  |||||
                                TTTGTAATATG GACGA
                                    _
GAM260  ZNF257   3' GAATGATGTCACAGTGCTT   53097        _    C
                                GGGCATTGT ATGTTG TTC
                                |||||||||  ||||||  |||
                                TTCGTGACA TGTAGT AAG
                                    C    _
GAM260  ZNF277   3' CCACAGAAGCAATTTTTCATGT 41813      TGTAT
           TT                    GGGCAT    GTTGCTTCTGTGG
                                |||||||    ||||||||||||||
                                TTTGTA    TAACGAAGACACC
                                   CTTTT
GAM260  ZNF38    5' CCACAGGAGCAGGTGGGGCCT  94367     A TG ATG
                                GGGC T  T   TTGCTTCTGTGG
                                ||||  |  |   ||||||||||||
                                TCCG G  G   GACGAGGACACC
                                  G GT ____
GAM260  ZNF80    3' CAGGGTTATATGCAATGTTC   23075          T   T
                                GGGCATTGTATGT GCT CTG
                                ||||||||||||  |||  |||
                                CTTGTAACGTATA TGG GAC
                                      T   _
GAM260  ZNF83    3' CCATACAAATGTAACGTGCATG 36981      T       TTC__
           CTT                    GGCAT GTATGTTGC    TGTGG
                                |||||  |||||||||    |||||
                                TCGTA CGTGCAATG    ATACC
                                  _       TAAAC
GAM260  ZNFN2A1  5' CTGTGGAAGTTTCGTGCAGTCT 60738    C      TT     TG
           T                     GGG ATTGTATG  GCTTCTG  G
                                |||  ||||||||  |||||||  |
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                                TTC TGACGTGC  TGAAGGT  C
                                  _      TT      GT
GAM260  20D7-FC4  5'  CTACAGGTGGCATGTGGAGCCT 60898     A TG    TG TT
                                GGGC T  TATGT  C  CTGTGG
                                |||| |  |||||  |  ||||||
                                TCCG G  GTACG  G  GACATC
                                  A GT    GT __
GAM260  7h3     3'  GCCACAGAGGAGGGAGCAGTTT 52273     TG    _______
           GCAGTGCCC               GTA  TTGCT     TCTGTGG   C
                                |||  |||||     |||||||  |
                                CGT  GACGA     AGACACC   G
                                  TT    GGGAGG
GAM260  AAK1    3'  TTGCAGGGGTGAGCCACCATGC 29859       T  ATG TG     TG
           CC                     GGGCAT GT   T  CTTCTG  G
                                ||||||  ||   |  ||||||  |
                                CCCGTA CA   A  GGGGAC  T
                                   C  CCG GT     GT
GAM260  AASDHPPT  3'  TTACAGAGAAAGGCAATGTCT  31246         ATG  G  T
                                GGGCATTGT   TT CT CTGTGG
                                |||||||||   || || ||||||
                                TCTGTAACG   AA GA GACATT
                                     GA_  _  _
GAM260  ABLIM   3'  ACAGTGGCGGTGCCC      9756        TGTATGT    T
                                GGGCAT      TGCT CTGT
                                ||||||      |||| ||||
                                CCCGTG      GCGG GACA
                                   ________   T
GAM260  ABLIM   3'  ACAGTGGCGGTGCCC      22017       TGTATGT    T
                                GGGCAT      TGCT CTGT
                                ||||||      |||| ||||
                                CCCGTG      GCGG GACA
                                   ________   T
GAM260  ACTR3    5'  TGCGGAAGTGATAGCCGCC   19147     ATT  A   TG     TG
                                GGC   GT TGT  CTTCTG  G
                                |||   || |||  ||||||  |
                                CCG   CG ATA  GAAGGC  T
                                  C__  _   GT     GT
GAM260  AD-020   3'  GGCAGAGTGCATATAATGTCC  59386           T   T   GG
                                GGGCATTGTATGT GCT CTGT
                                |||||||||||| ||| ||||
                                CCTGTAATATACG TGA GACG
                                        _  _   GT
GAM260  AD-020   3'  GGCAGAGTGCATATAATGTCC  39310           T   T   GG
                                GGGCATTGTATGT GCT CTGT
                                |||||||||||| ||| ||||
                                CCTGTAATATACG TGA GACG
                                        _  _   GT
GAM260  AD024   3'  CTAGGAGTGAGAATATGTGGTG 40341     TG     ___      TGG
           TTT                    GCAT  TATGTT   GCTTCTG
                                ||||  ||||||   |||||||
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                                TGTG  GTATAA   TGAGGAT
                                  GT     GAG      C
GAM260  AGXT2L1   3'  TGCATTTTAAAGCAAGATGCGA 48397        G     CT__   G
           TGTCC                  GCATTGTAT TTGCTT    GTG
                                  ||||||||| ||||||    |||
                                  TGTAGCGTA AACGAA    TAC
                                      G     ATTT   GTT
GAM260  AHCYL1    3'  CTGTGGAACAATCTGCAATGTC 21765         T    C     TG
           T                     GGGCATTGTA GTTG TTCTG  G
                                 |||||||||| |||| ||||| |
                                 TCTGTAACGT TAAC AAGGT  C
                                      C    _    GT
GAM260  AKAP11    3'  GCATATACAGTGTCC       57832           T
                                 GGGCATTGTATGT GC
                                 |||||||||||| ||
                                 CCTGTGACATATA CG
                                      _
GAM260  AP1GBP1   3'  CTGCGTCTACCAAGTACGATGT 23392         GTTGCTTC  TG
           CT                    GGGCATTGTAT       TG  G
                                 ||||||||||       ||  |
                                 TCTGTAGCATG       GC  C
                                      AACCATCT  GT
GAM260  AP1GBP1   3'  CTGCGTCTACCAAGTACGATGT 54530         GTTGCTTC  TG
           CT                    GGGCATTGTAT       TG  G
                                 ||||||||||       ||  |
                                 TCTGTAGCATG       GC  C
                                      AACCATCT  GT
GAM260  AP1GBP1   3'  CTGCGTCTACCAAGTACGATGT 54518         GTTGCTTC  TG
           CT                    GGGCATTGTAT       TG  G
                                 ||||||||||       ||  |
                                 TCTGTAGCATG       GC  C
                                      AACCATCT  GT
GAM260  AP3D1     3'  TTACAGAATCCCATGCAGTG   14138         TTGC
                                 CATTGTATG    TTCTGTGG
                                 |||||||||    ||||||||
                                 GTGACGTAC    AAGACATT
                                      CCT_
GAM260  AP4S1     3'  CCACGGCCTTTTCAGTATTTGG 22993       T     CTT___
           TGCCT                  CATTG ATGTTG     CTGTGG
                                  ||||| ||||||     ||||||
                                  GTGGT TATGAC     GGCACC
                                     T     TTTTCC
GAM260  APBA2BP   5'  TCGCTGAACCGTGCAGTGCTC  48353          TTGC   T
                                 GGGCATTGTATG    TTC GTGG
                                 ||||||||||||    ||| ||||
                                 CTCGTGACGTGC    AAG CGCT
                                       C___    T
GAM260  APOL4     3'  TCACGGAACCTACCGATGTGTG 47631     TG      C_____
           ATGTCT                 AT  TATGTTG    TTCTGTGG
                                  ||  |||||||    ||||||||
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                                TA  GTGTAGC    AAGGCACT
                                 GT      CATCC
GAM260  AQP10    3'  CAGAGAAGGCAGTGTTC     54431         ATGTTG    G
                                GGGCATTGT     CTTCT TG
                                |||||||||     ||||| ||
                                CTTGTGACG     GAAGA AC
                                      _______    G
GAM260  ARFGAP1  3'  AGCGACGTGAGGTGTCC     36587       TG
                                GGGCAT  TATGTTGCT
                                ||||||  |||||||||
                                CCTGTG  GTGCAGCGA
                                   GA
GAM260  ARFGAP1  3'  CACGGAGGGTGATGGCC     36588    G   TG ATGTTG
                                GG CAT  T     CTTCTGTG
                                || |||  |     ||||||||
                                CC GTA  G     GGAGGCAC
                                 G   GT _______
GAM260  ARFGAP1  3'  TTGGACAGTGGGATGTGGTGTT 36595       TG   G TG  _    TGG
           C                     GGGCAT  TAT T  CT TCTG
                                ||||||  ||| |  || ||||
                                CTTGTG  GTA G  GA AGGT
                                   GT   G GT  C    T
GAM260  ARG99    3'  TCATAGGATAATGTGGTGCCT  49170       TG   GTTGC
                                GGGCAT  TAT    TTCTGTGG
                                ||||||  |||    ||||||||
                                TCCGTG  GTA    AGGATACT
                                   GT   AT___
GAM260  ARHGAP5  3'  CTATATGAAACATTTAATGCTT 77074        T    GCT  _
                                GGGCATTG ATGTT   TC TGTGG
                                |||||||| |||||   || |||||
                                TTCGTAAT TACAA   AG ATATC
                                     T     ___  T
GAM260  ARHGEF10 3'  CCACAGGAGAAAAGTGTGTGCT 60420       TGT  GTTG
           T                     GGGCAT   AT    CTTCTGTGG
                                ||||||   ||    |||||||||
                                TTCGTG   TG    GAGGACACC
                                   TG_  AAAA
GAM260  ARPP-19  3'  ATAGTCAATGGTGCCT     21788       GTAT    CTT
                                GGGCATT    GTTG   CTGT
                                |||||||    ||||   ||||
                                TCCGTGG    TAAC   GATA
                                     ____    T__
GAM260  ARTS-1   3'  GTATATTGTGGTATACGGTGTC 33186          TT  TTC    G
                                GGCATTGTATG  GC   TGTG
                                ||||||||||  ||   ||||
                                CTGTGGCATAT  TG   ATAT
                                      GG  TT_   GT
GAM260  ASB16    5'  CTACAGGGGCCCTCCTGCTGCT 69934      TT   TGTT_
           C                     GGGCA  GTA    GCTTCTGTGG
                                |||||  |||    ||||||||||
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                                CTCGT  CGT    CGGGGACATC
                                  __  CCTCC
GAM260  ASE-1    3'  AAGAACATGCAATGTTT    23939           G
                                GGGCATTGTATGTT CTT
                                ||||||||||||| |||
                                TTTGTAACGTACAA GAA
                                                _
GAM260  ASPN     5'  TGGGAGCAGTTTATTCC    34603    CATT   TG
                                GGG   GTA  TTGCTTCTG
                                |||   |||  |||||||||
                                CCT   TAT  GACGAGGGT
                                  ____  TT
GAM260  ATP10B   3'  TCATAGAGGAAACAATGTGCC  63369     TGTA   G
                                GGCAT   TGTT CTTCTGTGG
                                |||||   |||| |||||||||
                                CCGTG   ACAA GGAGATACT
                                   TA__   A
GAM260  ATP10D   3'  CCATGCTCATATGCAATGTCT  73142         T_  TTCT
                                GGGCATTGTATGT  GC   GTGG
                                ||||||||||||  ||   ||||
                                TCTGTAACGTATA  CG   TACC
                                       CT  ____
GAM260  ATP6M8-9 3'  GGAGTATATAGATGCTT    19276       G    T
                                GGGCATT TATGT GCTTC
                                ||||||| ||||| |||||
                                TTCGTAG ATATA TGAGG
                                          _    _
GAM260  AUTL1    3'  ATATAAAGCAGTGTAGTGGTGT 51659      TG _ TG    C   G
           TT                    GGGCAT  T A  TTGCTT TGTG
                                ||||||  | |  |||||| ||||
                                TTTGTG  G T  GACGAA ATAT
                                   GT A GT     _    AT
GAM260  B3GNT5   3'  CTACAGAAAGAACTAGGTGGTG 49425      TG AT_   GC
           TCT                   GGGCAT  T   GTT  TTCTGTGG
                                ||||||  |   |||  ||||||||
                                TCTGTG  G   CAA  AAGACATC
                                   GT GAT   GA
GAM260  B3GNT6   3'  TTACAGAGGTAGCTGTGGTGTT 22508     TG  T
                                GGCAT  TA GTTGCTTCTGTGG
                                |||||  || ||||||||||||||
                                TTGTG  GT CGATGGAGACATT
                                  GT  _
GAM260  BA526D8.4 3'  AAGCAATGTATAGTGGCC    70384    G
                                GG CATTGTATGTTGCTT
                                || ||||||||||||||
                                CC GTGATATGTAACGAA
                                 G
GAM260  BCAN     3'  GCAGGATGGAGTGTCT     41690       G  G
                                GGGCATT TAT TTGC
                                ||||||| ||| ||||
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                                TCTGTGA GTA GACG
                                    G   G
GAM260  BCCIP    3'  CTACAAAAATATTCAGTGCCC  54304        T    GCTTC
                                GGGCATTG ATGTT    TGTGG
                                |||||||| |||||    |||||
                                CCCGTGAC TATAA    ACATC
                                     T    AA___
GAM260  BCE-1    3'  CTGTGGACTGCTGATGTACAGT 22799          _  T_   TG
            GCCT                  GGCATTGTATGTT GC  TCTG  G
                                |||||||||||| ||  ||||  |
                                CCGTGACATGTAG CG  AGGT  C
                                       T  TC   GT
GAM260  BCL2L1   3'  TATGGGAGCCCCAGGGTCT   56808     ATTGTA  TT
                                GGGC     TG  GCTTCTGTG
                                ||||     ||  |||||||||
                                TCTG     AC  CGAGGGTAT
                                  GG_____  CC
GAM260  BDG-29   3'  TTACAGTGTTGAAGTAATGGTG 72358   TG A      _____
            ATGCTT                 T  T TGTTGCTTC    TGTGG
                                |  | |||||||||    |||||
                                A  G GTAATGAAG    ACATT
                                 GT _       TTGTG
GAM260  BIK      3'  TCACACCCCTGTGTGATATGTG 6824    TG    TG TTC____
            ATGCCC                 AT  TATGT  C      TGTGG
                                ||  |||||  |      |||||
                                TA  GTATA  G      ACACT
                                 GT    GT TGTCCCC
GAM260  BIRC1    3'  TATATCAATGTCAGTGTCC   15792        T     CTTC
                                GGGCATTG ATGTTG   TGTG
                                |||||||| ||||||   ||||
                                CCTGTGAC TGTAAC   ATAT
                                     _     T___
GAM260  BLZF1    5'  TTACGGAGGCCTTACAGTGT   13370        TGTT
                                GCATTGTA   GCTTCTGTGG
                                ||||||||   ||||||||||
                                TGTGACAT   CGGAGGCATT
                                     TC__
GAM260  BM-002   3'  TCACAGAAGATCATAGTCT   33526     ATTG   TTG
                                GGGC   TATG   CTTCTGTGG
                                ||||   ||||   |||||||||
                                TCTG   ATAC   GAAGACACT
                                  ____   TA_
GAM260  BNIP-S   5'  TACAGAGGTAAATATGAT    56264    TG   G
                                AT  TAT TTGCTTCTGTG
                                ||  ||| ||||||||||
                                TA  ATA AATGGAGACAT
                                 GT  _
GAM260  BNIP-S   3'  TATGGGATATGCAGAGCTC   56265     A       GCTT
                                GGGC TTGTATGTT    CTGTG
                                |||| |||||||||    |||||
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                                CTCG GACGTATAG   GGTAT
                                  A      ____
GAM260  BPESC1   3' CAGGGACCTCAGTGTCC    41472       TAT  GCT
                                GGGCATTG  GTT  TCTG
                                ||||||||  |||  ||||
                                CCTGTGAC  CAG  GGAC
                                    TC_  ___
GAM260  BRD4     3' CGTGGAGGTGTGTGTGTCC  54275      TGTATGT    TG
                                GGGCAT     TGCTTC TG
                                ||||||     ||||||  ||
                                CCTGTG     GTGGAG  GC
                                   TGT____     GT
GAM260  BRPF3    3' GAAGCACATGATGCTC     92317       GT   T
                                GGGCATT  ATGT GCTTC
                                |||||||  |||| |||||
                                CTCGTAG  TACA CGAAG
                                  __   _
GAM260  BTBD2    3' ATGGGAGGGGTGTCC      35103       TGTATGT G
                                GGGCAT     T CTTCTGT
                                ||||||     | |||||||
                                CCTGTG     G GAGGGTA
                                  ________ G
GAM260  BTBD2    3' CAGGTGGTGAGCGGTTTGCAGT 35104         TG    _ TG GG
           GTCC                   GGCATTGTA  TTGCTT C  T
                                |||||||||  ||||||  |  |
                                CTGTGACGT  GGCGAG G  G
                                     TT     T GT GACC
GAM260  C11orf11 3' CAGAGTCAGTGCCC       93249        TATGTT   T
                                GGGCATTG    GCT CTG
                                ||||||||    ||| |||
                                CCCGTGAC    TGA GAC
                                  _______  _
GAM260  C11orf11 3' TACAGAAGCTGCTGGGCTT   93261     ATT   TGTT
                                GGGC  GTA   GCTTCTGTG
                                ||||  |||   |||||||||
                                TTCG  CGT   CGAAGACAT
                                  GGT  ____
GAM260  C11orf21 3' TTACATGCCCAGCCTGCAGTGC 26248         T   CTTC
           TT                    GGGCATTGTA GTTG   TGTGG
                                |||||||||| ||||   |||||
                                TTCGTGACGT CGAC   ACATT
                                     C   CCGT
GAM260  C11orf25 3' CCACAGGGGATTTATGCTGCTT 48640      TT    TTG
                                GGGCA  GTATG  CTTCTGTGG
                                |||||  |||||  |||||||||
                                TTCGT  CGTAT  GGGGACACC
                                  __    TTA
GAM260  C12orf22 3' CGTAGAAGCAGCTGCTGCTC  47978      TT  T       TG
                                GGGCA  GTA GTTGCTTCTG  G
                                |||||  ||| ||||||||||  |
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                                CTCGT  CGT CGACGAAGAT  C
                                  __  _        GT
GAM260  C1orf29   3'  TCACAGAGCTTAGCACAGTGCC 22372         ATGTT   T
           T                     GGGCATTGT    GCT CTGTGG
                                 |||||||||    ||| ||||||
                                 TCCGTGACA    CGA GACACT
                                     CGATT   _
GAM260  C1orf34   3'  CCACAGAAGAAAATGATGCACC 60667    _   TG ATGTTG
                                 GG GCAT  T     CTTCTGTGG
                                 || ||||  |     |||||||||
                                 CC CGTA  A     GAAGACACC
                                  A    GT AAA___
GAM260  C1orf9    3'  GCAAACACTACAATGCTT    32636          _   _
                                 GGGCATTGTA TGTT GC
                                 |||||||||| |||| ||
                                 TTCGTAACAT ACAA CG
                                       C    A
GAM260  C1QTNF7   3'  CTACAGAGAAATGATAAATGTT 49158       GTA    GC
           T                     GGGCATT   TGTT  TTCTGTGG
                                 |||||||   ||||  ||||||||
                                 TTTGTAA   GTAA  GAGACATC
                                     ATA    A_
GAM260  C20orf100 3'  CTGCAGAGGCAGCCCACTGCCC 51812      T  TAT        TG
                                 GGGCA TG   GTTGCTTCTG  G
                                 ||||| ||   ||||||||||  |
                                 CCCGT AC   CGACGGAGAC  C
                                    C  C__         GT
GAM260  C20orf102 3'  CTCAGCATGTAAGCCC      54616      A        CTTCT
                                 GGGC TTGTATGTTG     G
                                 |||| ||||||||||     |
                                 CCCG AATGTACGAC     C
                                   _         T_____
GAM260  C20orf108 3'  CTACAGTTTAATATGCAGCGTT 55044      A         CTT
           C                      GGGC TTGTATGTTG   CTGTGG
                                 |||| ||||||||||   ||||||
                                 CTTG GACGTATAAT   GACATC
                                   C         TT_
GAM260  C20orf110 3'  GCTCTGACCTATAATGTCT    79547          T   ___
                                 GGGCATTGTA GTT   GC
                                 |||||||||| |||   ||
                                 TCTGTAATAT CAG   CG
                                       C   TCT
GAM260  C20orf141 5'  CAGGAGCCTAATTCCC      54948     C    TATGTT
                                 GGG ATTG     GCTTCTG
                                 ||| ||||     |||||||
                                 CCC TAAT     CGAGGAC
                                   T   C_____
GAM260  C20orf142 3'  TCATAGAATACTGCCATGCTT  74786       T   T  TGC
                                 GGGCAT GTA GT   TTCTGTGG
                                 |||||| ||| ||   ||||||||
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                                TTCGTA CGT CA   AAGATACT
                                   C   _  T__
GAM260  C20orf150 3'  CCGGTCTTTGTGATGTGTGAAG 65395    A TG    TG TT___   TGG
            CCT                    GC T  TATGT  C    CTG
                                || |  |||||  |    |||
                                CG A  GTGTA  G    GGC
                                 A GT    GT TTTCT   C
GAM260  C20orf167 3'  CAGACTAGCATGTGGTTCT   53662    C  TG     CT
                                GGG AT  TATGTTG  TCTG
                                ||| ||  |||||||  ||||
                                TCT TG  GTACGAT  AGAC
                                  _ GT      C_
GAM260  C20orf18  5'  TCACCGGGCAGTGTGATGCTT  48345      TG   GT    CT
                                GGGCAT  TAT  TGCTT  GTGG
                                ||||||  |||  |||||  ||||
                                TTCGTA  GTG  ACGGG  CACT
                                   GT   __    C_
GAM260  C20orf18  5'  TCACCGGGCAGTGTGATGCTT  48349      TG   GT    CT
                                GGGCAT  TAT  TGCTT  GTGG
                                ||||||  |||  |||||  ||||
                                TTCGTA  GTG  ACGGG  CACT
                                   GT   __    C_
GAM260  C20orf55  3'  TTACAGAGGCAAGTGGTCCC   48662    C  TG ATG
                                GGG AT  T   TTGCTTCTGTGG
                                ||| ||  |   ||||||||||||
                                CCC TG  G   AACGGAGACATT
                                  _ GT ___
GAM260  C20orf55  3'  TTGTGGGGCTGCATTTGCGGTG 48663        __   T    TGTGG
            CTT                   GGCATTGT  ATGT GCTTC
                                ||||||||  |||| |||||
                                TCGTGGCG  TACG CGGGG
                                     TT   T    TGTT
GAM260  C21orf108 3'  CGTAGGGGACATATGGGTCT   88719     A TG    TG     TG
                                GGGC T  TATGT  CTTCTG  G
                                |||| |  |||||  ||||||  |
                                TCTG G  ATACA  GGGGAT  C
                                  _ GT    __     GT
GAM260  C21orf41  3'  TCACAGAAGTTACCTGGTGCC  56359       TAT  T
                                GGCATTG   GT GCTTCTGTGG
                                |||||||   || ||||||||||
                                CCGTGGT   CA TGAAGACACT
                                   C__  T
GAM260  C21orf6   3'  CCATAAAGGTAATGTTGGTGCT 33744        T       C
            C                    GGGCATTG ATGTTGCTT TGTGG
                                |||||||| ||||||||| |||||
                                CTCGTGGT TGTAATGGA ATACC
                                     _       A
GAM260  C22orf19  3'  TAGAGGCGGGATCCC       13432     CATTGT  G
                                GGG     AT TTGCTTCTG
                                |||     || |||||||||
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                                CCC     TA GGCGGAGAT
                                  _______ G
GAM260  C22orf5  3'  TCGCAGGATCCTGCAGTGCT  24348        TGTTGC
                                GGCATTGTA     TTCTGTGG
                                |||||||||     ||||||||
                                TCGTGACGT     AGGACGCT
                                     CCT___
GAM260  C2orf6   3'  TGGTTGTAATATGTGATG    36646     TG      TT
                                CAT  TATGTTGC  CTG
                                |||  ||||||||  |||
                                GTA  GTATAATG  GGT
                                  GT       TT
GAM260  C5orf5   3'  TCACCCGTGTGTGCAATGCCT  33468         GTT  TTCT
                                GGGCATTGTAT   GC    GTGG
                                ||||||||||   ||    ||||
                                TCCGTAACGTG   TG    CACT
                                      ___  TGCC
GAM260  C5orf5   3'  CCATGTTTTGCATGCAATGACT 33466    G        TGCTTCT
                                GG CATTGTATGT      GTGG
                                || ||||||||||      ||||
                                TC GTAACGTACG      TACC
                                 A        TTTTG__
GAM260  C8orf13  3'  CTGCAGGGGCGTGACCGGGGCC 81572     ATT_  ATGT      TG
           T                     GGGC    GT    TGCTTCTG  G
                                ||||    ||    ||||||||  |
                                TCCG    CA    GCGGGGAC  C
                                  GGGC  GT__       GT
GAM260  C8orf13  3'  CACATGTGTACAGTGCT     81568         GTT  TTC
                                GGCATTGTAT   GC   TGTG
                                ||||||||||   ||   ||||
                                TCGTGACATG   TG   ACAC
                                      ___  T__
GAM260  C8orf2   3'  GCAAGCATATTGGTGCCC    23164         _     _
                                GGGCATTG TATGTT GC
                                |||||||| |||||| ||
                                CCCGTGGT ATACGA CG
                                     T     A
GAM260  C8orf6   5'  CTGCAGGATTTTCGTATGATCT 89269     C  TG    TTGC     TG
           T                     GGG AT  TATG    TTCTG  G
                                |||  ||  ||||    |||||  |
                                TTC TA  ATGC    AGGAC  C
                                  _  GT    TTTT     GT
GAM260  C9orf14  5'  CGCTCTCTGGCAACAGTGCTC  86673       TGTA      TCT__ TG
                                GGGCAT    TGTTGCT     G  G
                                ||||||    |||||||     |  |
                                CTCGTG    ACAACGG     C  C
                                   ____       TCTCT GT
GAM260  C9orf7   3'  GCAGCTGTGCAGTCCT      34173     C      _
                                GGG ATTGTAT GTTGC
                                ||| ||||||| |||||
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                                TCC TGACGTG CGACG
                                  _     T
GAM260  CABP2   3' CACCTGTGTGCAGTGCCC   48302        GTT  TTCT
                                GGGCATTGTAT  GC   GTG
                                ||||||||||  ||   |||
                                CCCGTGACGTG  TG   CAC
                                     ___ TC__
GAM260  CABP2   3' CACCTGTGTGCAGTGCCC   33034        GTT  TTCT
                                GGGCATTGTAT  GC   GTG
                                ||||||||||  ||   |||
                                CCCGTGACGTG  TG   CAC
                                     ___ TC__
GAM260  CALN1   3' CAGAAGCTGCTAAGCTC    48857     ATT  TGTT
                                GGGC  GTA   GCTTCTG
                                ||||  |||   |||||||
                                CTCG  CGT   CGAAGAC
                                  AAT  _____
GAM260  CALN1   3' CGCTTTTGACAATAATGCCC  48864       A   GCTTCT TG
                                GGGCATTGT TGTT    G  G
                                ||||||||| ||||    |  |
                                CCCGTAATA ACAG    C  C
                                     _   TTTT__ GT
GAM260  CAMKK2  3' CCATGGAGGTGGTTGCTGC   21580    TT   T TT
                                GCA  GTA G  GCTTCTGTGG
                                |||  ||| |  ||||||||||
                                CGT  CGT T  TGGAGGTACC
                                  __  _ GG
GAM260  CARD14  3' CGTGGGGGCTTCTGTGTGCCT  44105      TGTATGTT     TG
                                GGGCAT      GCTTCTG  G
                                ||||||      |||||||  |
                                TCCGTG      CGGGGGT  C
                                   TGTCTT__     GT
GAM260  CARD9   3' TTGCGGAGGCCATGCGGGTGCT 53378      _    TT     TG
          C                      GGGCATT GTATG  GCTTCTG  G
                                 |||||||  |||||  |||||||  |
                                 CTCGTGG CGTAC  CGGAGGC  T
                                    G    __      GT
GAM260  CARD9   3' TTGCGGAGGCCATGCGGGTGCT 53383      _    TT     TG
          C                      GGGCATT GTATG  GCTTCTG  G
                                 |||||||  |||||  |||||||  |
                                 CTCGTGG CGTAC  CGGAGGC  T
                                    G    __      GT
GAM260  CARD9   3' TTGCGGAGGCCATGCGGGTGCT 42292      _    TT     TG
          C                      GGGCATT GTATG  GCTTCTG  G
                                 |||||||  |||||  |||||||  |
                                 CTCGTGG CGTAC  CGGAGGC  T
                                    G    __      GT
GAM260  CASPR3  5' CACCTGACTGTGATGCCC   45933      TG  T   CTTCT
                                GGGCAT  TA GTTG    GTG
                                ||||||  || ||||    |||
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                                CCCGTA  GT CAGT    CAC
                                   GT  _   C____
GAM260  CBX6    3'  TGGAAGTCACCAGGCCT    26630     A   TAT  T
                                GGGC TTG   GT GCTTCTG
                                |||| |||   || |||||||
                                TCCG GAC   CA TGAAGGT
                                  _  ___  C
GAM260  CCNE1   3'  TATCAGTTGACAGTGTACAATG 54117         TG   CTT_   TGG
           CCT                    GGGCATTGTA  TTG    CTG
                                |||||||||  |||   |||
                                TCCGTAACAT  GAC    GAC
                                     GT   AGTT   TATT
GAM260  CCNE1   3'  TATCAGTTGACAGTGTACAATG 6950          TG   CTT_   TGG
           CCT                    GGGCATTGTA  TTG    CTG
                                |||||||||  |||   |||
                                TCCGTAACAT  GAC    GAC
                                     GT   AGTT   TATT
GAM260  CD36L1  3'  CACAGGGGCTGTGGGTCC    18565     A TG  TGTT
                                GGGC T  TA   GCTTCTGTG
                                |||| |  ||   |||||||||
                                CCTG G  GT   CGGGGACAC
                                  _ GT  _____
GAM260  CDH24   3'  CAGGGGATGTTGTGCCC     94928      TG   GTTG
                                GGGCAT  TAT   CTTCTG
                                ||||||  |||   ||||||
                                CCCGTG  GTA   GGGGAC
                                   TT  _____
GAM260  CEACAM7 3'  GACAGTAGTGTTAATGCCT   22559       T TG   _
                                GGGCATTG A  TTGCT TC
                                |||||||| |  ||||| ||
                                TCCGTAAT T  GATGA AG
                                     _ GT    C
GAM260  CECR1   3'  CAGACTCCAGCGGTGGTGCTC  33808      TG A    CT_
                                GGGCAT  T TGTTG   TCTG
                                ||||||  | |||||   ||||
                                CTCGTG  G GCGAC   AGAC
                                   GT _    CTC
GAM260  CECR2   3'  TTGTGGAAGTGACTACTCAGGT 48611     ATT_   T  TG    TG
           TT                    GGGC   GTA GT  CTTCTG  G
                                ||||   ||| ||  ||||||  |
                                TTTG   CAT CA  GAAGGT  T
                                  GACT   _  GT     GT
GAM260  CECR7   5'  GCCAGCATGCAGGCCC     79624      A       _
                                GGGC TTGTATGTTG C
                                |||| |||||||||| |
                                CCCG GACGTACGAC G
                                  _        C
GAM260  CENTB5  3'  TGCAGGGCCTGCCAATGCCT  95488       TAT  T_   T   TG
                                GGGCATTG   GT  GCT CTG  G
                                ||||||||   ||  ||| |||  |
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                                TCCGTAAC  CG  CGG GAC  T
                                    ___  TC  _  GT
GAM260  CG005   5'  ACAGAGGTTCGTGTCT    29682      TGTATGTT
                                GGGCAT      GCTTCTGT
                                ||||||      ||||||||
                                TCTGTG      TGGAGACA
                                   CT_______
GAM260  CGGBP1  3'  ACAAAGCAGTGACAAATGATGC 13357      TG A  TG  T  G  G
           CC                    GGGCAT  T TGT  CT CT TG
                                ||||||  | |||  || || ||
                                CCCGTA  A ACA  GA GA AC
                                   GT A  GT  C  A  AT
GAM260  CGGBP1  3'  CTGTGGGGGTGTATAACAAGCC 13363     A   A  _     TG
           T                     GGGC TTGT TGT TGCTTCTG  G
                                |||| |||| ||| ||||||||  |
                                TCCG AACA ATA GTGGGGGT  C
                                  _   _  T      GT
GAM260  CGI-94  3'  GTCAGTCTGACATTTAATGTCT 32097       T    CTT  TGG
                                GGGCATTG ATGTTG  CTG
                                |||||||| ||||||  |||
                                TCTGTAAT TACAGT  GAC
                                     T    CT_  TGT
GAM260  CGR11   3'  CACAGAAGTCTCAGTGCC   21644       TATGTT
                                GGCATTG    GCTTCTGTG
                                |||||||    |||||||||
                                CCGTGAC    TGAAGACAC
                                    TC_____
GAM260  CHK     3'  CCACGGGGGCAGTGTGAGGACC 7049    GCATTG  TG
                                GG    TA  TTGCTTCTGTGG
                                ||    ||  ||||||||||||
                                CC    GT  GACGGGGGCACC
                                 AGGA__  GT
GAM260  CHK     3'  GTTATAGACGGTGCTC     7051         A  T
                                GGGCATTGT TGT GC
                                ||||||||| ||| ||
                                CTCGTGGCA ATA TG
                                     G  T
GAM260  CHST3   3'  TTGCGGAGAACAGGACAGTGCC 14983        A_  G  T  TG
           C                     GGGCATTGT  TGTT CT CTG  G
                                |||||||||  |||| || |||  |
                                CCCGTGACA  ACAA GA GGC  T
                                     GG   _ _  GT
GAM260  CHST3   3'  AGCAGCGTCCAATGCTC    14965        T
                                GGGCATTG ATGTTGCT
                                |||||||| ||||||||
                                CTCGTAAC TGCGACGA
                                    C
GAM260  CHST3   3'  CCGTAGAGGCCAGGTGCGGTGG 14971    G      GTT
           CT                    GG CATTGTAT  GCTTCTGTGG
                                || ||||||||  ||||||||||
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                                TC GTGGCGTG   CGGAGATGCC
                                 G       GAC
GAM260   CHST8    3'  GGAGGCAGCAGGCCC      42439      ATTGTA
                                GGGC     TGTTGCTTCT
                                ||||     ||||||||||
                                CCCG     ACGACGGAGG
                                  G_____
GAM260   CHST8    5'  AGGTGACGGCAGTGCCT     42437         A   TG
                                GGGCATTGT TGT  CTT
                                ||||||||| |||  |||
                                TCCGTGACG GCA  GGA
                                     _  GT
GAM260   CLDN7    3'  CTATGGGAGTGTCTAGATGCCT 7139         GTATGT
                                GGGCATT     TGCTTCTGTGG
                                |||||||     ||||||||||
                                TCCGTAG     GTGAGGGTATC
                                    ATCT__
GAM260   CLDN7    3'  CTATGGGAGTGTCTAGATGCCT 94583        GTATGT
                                GGGCATT     TGCTTCTGTGG
                                |||||||     ||||||||||
                                TCCGTAG     GTGAGGGTATC
                                    ATCT__
GAM260   COE2     3'  TGGATGTGTATAGTGTCT    64256          GTT  T
                                GGGCATTGTAT   GC TCTG
                                ||||||||||   || ||||
                                TCTGTGATATG   TG AGGT
                                     ___  T
GAM260   COPS7B   3'  CCGTGGAGGGACGTGATGCT  42693       GT    G   TG
                                GGCATT  ATGTT CTTC  TGG
                                ||||||  ||||| ||||  |||
                                TCGTAG  TGCAG GGAG  GCC
                                   __    _   GT
GAM260   COPS7B   3'  GGTGGCATCGATGCCC     42694         T   TG
                                GGGCATTG ATGT  CT
                                |||||||| ||||  ||
                                CCCGTAGC TACG  GG
                                    _   GT
GAM260   CPEB1    3'  TGCAGTTGCCATACAGTGCCT  47601          TT  TT   TG
                                GGGCATTGTATG  GC  CTG  G
                                ||||||||||||  ||  |||  |
                                TCCGTGACATAC  CG  GAC  T
                                     __  TT   GT
GAM260   CREB-H   5'  CACAGAGGGCTGTGAGCTT   50883     A TG  T  TG
                                GGGC T  TA GT  CTTCTGTG
                                |||| |  || ||  ||||||||
                                TTCG A  GT CG  GGAGACAC
                                  _ GT  _  __
GAM260   CRSP3    3'  TGTAGGAGCAAACAAGGCTT   60636     A   ATG      TG
                                GGGC TTGT   TTGCTTCTG  G
                                |||| ||||   |||||||||  |
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                                TTCG AACA   AACGAGGAT  T
                                  G  ___       GT
GAM260  CSE-C    3'  AAATAGTGGTAATATGAATGTT 91479       G       T   GG
             T                   GGGCATT TATGTTGCT CTGT
                                 ||||||| ||||||||| ||||
                                 TTTGTAA GTATAATGG GATA
                                    _       T   AAT
GAM260  CTPS2    3'  GCATATACATGCGATATCT   39087    GC       ___
                                 GG  ATTGTATGT   TGC
                                 ||  |||||||||   |||
                                 TC  TAGCGTACA   ACG
                                  TA       TAT
GAM260  CX46.6   3'  CCATGGAGGGCCCAGGGTGCCT 39944       TGTA  TTG
                                 GGGCAT   TG   CTTCTGTGG
                                 ||||||   ||   |||||||||
                                 TCCGTG   AC   GGAGGTACC
                                    GG__  CCG
GAM260  CXYorf1  3'  CAGAAGTCAGTGCCC      82036        TATGTT
                                 GGGCATTG     GCTTCTG
                                 ||||||||     |||||||
                                 CCCGTGAC     TGAAGAC
                                      _______
GAM260  CXYorf1  3'  CTGCGCCTGCAGCGGCAGTGCC 82047        A     TTC  TG
             C                   GGGCATTGT TGTTGC   TG  G
                                 ||||||||| ||||||   ||  |
                                 CCCGTGACG GCGACG   GC  C
                                      _     TCC  GT
GAM260  CYorf14  3'  GGGCAATAAATGTCT      37610       GTA
                                 GGGCATT   TGTTGCTT
                                 |||||||   ||||||||
                                 TCTGTAA   ATAACGGG
                                      ___
GAM260  CYorf14  3'  TGCTAAAGACATATATGCTT   37611      T     TG   CT TG
                                 GGGCAT GTATGT  CTT  G  G
                                 |||||| ||||||  |||  |  |
                                 TTCGTA TATACA  GAA  C  T
                                    _     __   AT GT
GAM260  D2S448   3'  CACTTTGTAATGATGCCT    73516       GTAT    TTCT
                                 GGGCATT    GTTGC    GTG
                                 |||||||    |||||    |||
                                 TCCGTAG    TAATG    CAC
                                      _____     TTT_
GAM260  D2S448   3'  CAGAACAGTGGGCAGTGCCT   73517        A GT  C
                                 GGGCATTGT T  TG TTCTG
                                 |||||||||  |  ||  |||||
                                 TCCGTGACG G  AC AAGAC
                                       G TG  _
GAM260  D2S448   3'  GGGCGCATACAGTGCCT     73529           T
                                 GGGCATTGTATGT GCTT
                                 |||||||||||| ||||
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                                TCCGTGACATACG CGGG
                                              _
GAM260  DC-TM4F2 3'  TTATAGGGGTAAGAATGTTC  48174       GTATG
                                GGGCATT    TTGCTTCTGTGG
                                |||||||    ||||||||||||
                                CTTGTAA    AATGGGGATATT
                                    G____
GAM260  DDM36    3'  TCATAGGAGCATAGAATGTT  40578      G  TGT
                                GGCATT TA   TGCTTCTGTGG
                                |||||| ||   ||||||||||
                                TTGTAA AT   ACGAGGATACT
                                   G  ___
GAM260  DDX17    5'  TTGTAGTAATAAAATATATGAA 48043     A TG     GCTT__   TG
            GCTC                   GGC T  TATGTT     CTG  G
                                ||| |  ||||||     |||  |
                                TCG A  ATATAA     GAT  T
                                  A GT     AATAAT   GT
GAM260  DDX27    3'  TCATGGGGGCAGCCCTTAAATC 35440     C   GTAT_
            CC                   GGG ATT    GTTGCTTCTGTGG
                                ||| |||    ||||||||||||
                                CCC TAA    CGACGGGGGTACT
                                  _  ATTCC
GAM260  DDX33    3'  CCACAGGAGGTTGCGGAGCTT  39370     A    TGTTG
                                GGGC TTGTA    CTTCTGTGG
                                |||| |||||    |||||||||
                                TTCG GGCGT    GAGGACACC
                                  A    TG___
GAM260  DDX34    3'  TTATAGGACACGCATATATGTT 27992       T    _  C
            T                   GGGCAT GTATGT TG TTCTGTGG
                                |||||| |||||| || ||||||||
                                TTTGTA TATACG AC AGGATATT
                                   _     C  _
GAM260  DGKD     3'  AAGTAGCATGGATGTTT     59396       G
                                GGGCATT TATGTTGCTT
                                ||||||| ||||||||||
                                TTTGTAG GTACGATGAA
                                              _
GAM260  DGS-A    3'  CAGAGGCCCAGGCCT      84895     A   TATGTT
                                GGGC TTG     GCTTCTG
                                |||| |||     |||||||
                                TCCG GAC     CGGAGAC
                                  _  C_____
GAM260  Di-Ras2  3'  TCAGGGTAGCATGTATAATGCC 34190           T   T  G
            C                   GGGCATTGTATGT GCT CT TGG
                                |||||||||||| ||| || |||
                                CCCGTAATATGTA CGA GG ACT
                                        _  T  G   G
GAM260  DIO2     3'  CCAGCTTCTAGCCATGTAGTGC 5829           TT   TCT_ _
            TC                   GGGCATTGTATG  GCT    G TGG
                                ||||||||||||  |||    | |||
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                                CTCGTGATGTAC  CGA   C ACC
                                      __  TCTT G
GAM260  DIO2     3'  CCAGCTTCTAGCCATGTAGTGC 25681          TT  TCT_ _
           TC                    GGGCATTGTATG  GCT   G TGG
                                ||||||||||||  |||   | |||
                                CTCGTGATGTAC  CGA   C ACC
                                      __  TCTT G
GAM260  DJ167A19.1 3'  CCATGGAAAATTCTGATGTCC  38605       TAT  GC
                                GGGCATTG  GTT  TTCTGTGG
                                ||||||||  |||  ||||||||
                                CCTGTAGT  TAA  AAGGTACC
                                     CT_  __
GAM260  DJ37E16.5 3'  TTACAAAGACTTGTGATGCTC  39734      TG  T  GCTTC
                                GGGCAT  TA GTT    TGTGG
                                ||||||  || |||    |||||
                                CTCGTA  GT CAG    ACATT
                                   GT  T  AA___
GAM260  DJ434O14.5 3'  CCATCTTCAACAGTAGTGTCT  26897       GTA    CTTCT
                                GGGCATT  TGTTG    GTGG
                                |||||||  |||||    ||||
                                TCTGTGA  ACAAC    TACC
                                     TG_    TTC__
GAM260  dJ55C23.6 3'  CCGTGGACCCCGTGCCAGTGTC 53417        _   TTGCT  TG
           T                     GGGCATTG TATG    TC  TGG
                                ||||||||  ||||    ||  |||
                                TCTGTGAC GTGC    AG  GCC
                                     C   CCC__  GT
GAM260  DKFZP434A043 3'  GCAGGTGCAGTGTTC      31193          G
                                GGGCATTGTAT TTGC
                                ||||||||||| ||||
                                CTTGTGACGTG GACG
                                      _
GAM260  DKFZP434A1315 3'  AACATTTTAATATATAATGT  67704          CTTC  GG
                                GCATTGTATGTTG   TGT
                                ||||||||||||   |||
                                TGTAATATATAAT   ACA
                                       TTT_  AT
GAM260  DKFZp434A1520 3'  CACATATGTGCAGTGTC    61115          TGCTTC
                                GGCATTGTATGT    TGTG
                                ||||||||||||    ||||
                                CTGTGACGTGTA    ACAC
                                       T_____
GAM260  DKFZP434B0335 5'  CCGTGGGAGCAATGTGGCCC  92463     ATTG       TG
                                GGGC   TATGTTGCTTC  TGG
                                ||||   ||||||||||  |||
                                CCCG   GTGTAACGAGG  GCC
                                  ____         GT
GAM260  DKFZP434B044 3'  CGTGGGAGGAATGGAGTCT   48923     ATTGTA   G   TG
                                GGGC    TGTT CTTC  TG
                                ||||    |||| ||||  ||
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                                TCTG     GTAA GAGG  GC
                                  AG_____   G   GT
GAM260  DKFZP434B172 5'  TCAGTACTCAGCATGTTGTGCT 70037       TG      CTT_   TGG
           C                      GGGCAT  TATGTTG    CTG
                                  ||||||  |||||||    |||
                                  CTCGTG  GTACGAC    GAC
                                     TT      TCAT   T
GAM260  DKFZP434B205 3'  CCACGGACCTCTGTGGTGCTC  75318       TG  TGTTGCT
                                  GGGCAT  TA      TCTGTGG
                                  ||||||  ||      |||||||
                                  CTCGTG  GT      AGGCACC
                                     GT  CTCC___
GAM260  DKFZP434C171 3'  GTCACTGCAGTGTCC       31560          T  T
                                  GGGCATTGTA GT GC
                                  |||||||||| || ||
                                  CCTGTGACGT CA TG
                                        _  C
GAM260  DKFZP434C212 3'  CCATGGAGGCACACCAAAGCTT 68908      A   TA   T
                                  GGGC TTG  TGT GCTTCTGTGG
                                  |||| |||  ||| ||||||||||
                                  TTCG AAC  ACA CGGAGGTACC
                                    A  C_  _
GAM260  DKFZP434C212 3'  CGTGGAAGTTTGTGAGCCT    68909      A TG  TGTT    TG
                                  GGGC T  TA    GCTTC  TG
                                  |||| |  ||    |||||  ||
                                  TCCG A  GT    TGAAG  GC
                                    _ GT  T___     GT
GAM260  DKFZP434D146 5'  CACGGGGTAGTGGGTGCTC    31521        GTA GT    T
                                  GGGCATT   T  TGCT CTGTG
                                  |||||||   |  |||| |||||
                                  CTCGTGG   G  ATGG GGCAC
                                      ___ TG   _
GAM260  DKFZP434E2135 3'  CATATATGTATAGTGCCT    47952           TGCTTC
                                  GGGCATTGTATGT     TGTG
                                  ||||||||||||      ||||
                                  TCCGTGATATGTA     ATAC
                                          T_____
GAM260  DKFZP434E2135 3'  GGGCATGTACAAGCTT      47956      A       T
                                  GGGC TTGTATGT GCTT
                                  |||| |||||||| ||||
                                  TTCG AACATGTA CGGG
                                    _       _
GAM260  DKFZp434G179 3'  TACTAGAGCGTGTGTGCCT    80091       TGTATGT    CT
                                  GGGCAT      TGCTT  GTG
                                  ||||||      |||||  |||
                                  TCCGTG      GCGAG  CAT
                                     TGT____     AT
GAM260  DKFZP434H0820 3'  CGGAGGGGAAGTGTCC      63848        GTATG  G
                                  GGGCATT     TT CTTCTG
                                  |||||||     || ||||||
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                                CCTGTGA    AG GGAGGC
                                   _____ G
GAM260  DKFZP434H132 3' GAATTGACATCAGTGCTT    31318       T    GC
                                GGGCATTG ATGTT  TTC
                                |||||||| |||||  |||
                                TTCGTGAC TACAG  AAG
                                   _    TT
GAM260  DKFZP434L1435 3' CGCAGTGACTGTGGTGTCC   97859      TG  T  TG  TCT
                                GGGCAT  TA GT  CT   GTG
                                ||||||  || ||  ||   |||
                                CCTGTG  GT CA  GA   CGC
                                   GT  _  GT  ___
GAM260  DKFZP434L1435 3' CGCAGTGACTGTGGTGTCC   97743      TG  T  TG  TCT
                                GGGCAT  TA GT  CT   GTG
                                ||||||  || ||  ||   |||
                                CCTGTG  GT CA  GA   CGC
                                   GT  _  GT  ___
GAM260  DKFZP434L1435 3' CGCAGTGACTGTGGTGTCC   92171      TG  T  TG  TCT
                                GGGCAT  TA GT  CT   GTG
                                ||||||  || ||  ||   |||
                                CCTGTG  GT CA  GA   CGC
                                   GT  _  GT  ___
GAM260  DKFZP434L1717 3' CTGCAGTTTTACAGATAATGTT 49545       A   TGCTT   TG
           T                     GGGCATTGT TGT    CTG  G
                                |||||||| |||    |||  |
                                TTTGTAATA ACA    GAC  C
                                     G   TTTT_   GT
GAM260  DKFZp434M0331 5'  TCACAACCCTGGATAATGCAGT 34235       GTTG  TC___
           GTCC                    GCATTGTAT    CT    TGTGG
                                |||||||||   ||    |||||
                                TGTGACGTA    GG    ACACT
                                     ATA_  TCCCA
GAM260  DKFZp434N2435 5'  GAGGTGTGCGAAGCCC     96338     A     GTT
                                GGGC TTGTAT   GCTTC
                                |||| ||||||   |||||
                                CCCG AGCGTG   TGGAG
                                  A     ___
GAM260  DKFZp434O0320 3'  CACAGAAGCGTCTGTGCTT   83694      TGTATGT
                                GGGCAT      TGCTTCTGTG
                                ||||||      ||||||||||
                                TTCGTG      GCGAAGACAC
                                   TCT____
GAM260  DKFZP434O047 5'  CACAGGAGTGGGTGTCT     31504       TGTATG TG
                                GGGCAT     T  CTTCTGTG
                                ||||||     |  ||||||||
                                TCTGTG     G  GAGGACAC
                                   _______ GT
GAM260  DKFZP434O125 3'  TTGCAGGCAGCTGACTGTGATG 64963      TG  T  _  _   TG
           TCC                     GGCAT  TA GTT GCT TCTG  G
                                |||||  || ||| ||| ||||  |
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                                CTGTA  GT CAG CGA GGAC  T
                                   GT  _  T  C   GT
GAM260  DKFZP434P0721 3'  TCATAGTTGGTCGGTATGTAGT 63720          TT _  T_
           GCTT                    GGCATTGTATG  G CT  CTGTGG
                                |||||||||||  | ||  ||||||
                                TCGTGATGTAT  C GG  GATACT
                                      GG T  TT
GAM260  DKFZp547C176 3'  GGCATTATGCAGTGTT      67228          T
                                GGCATTGTATG TGCT
                                |||||||||||| ||||
                                TTGTGACGTAT ACGG
                                      T
GAM260  DKFZp547G183 3'  CGCAGGAGCTCCTCAAAGTCT  38025     A   TATGTT      TG
                                GGGC TTG     GCTTCTG  G
                                |||| |||     |||||||  |
                                TCTG AAC     CGAGGAC  C
                                  A   TCCT__      GT
GAM260  DKFZp547I014 5'  TTACAGAACAATTCAGTAGTGT 39549        TAT_   C
           CT                     GGGCATTG    GTTG TTCTGTGG
                                |||||||||    |||| ||||||||
                                TCTGTGAT    TAAC AAGACATT
                                    GACT    _
GAM260  DKFZp547M236 3'  AATAGCTGCGGATACAGTGTTC 38032          G    TT    GG
                                GGGCATTGTAT TTGC  CTGT
                                |||||||||| ||||  ||||
                                CTTGTGACATA GGCG  GATA
                                      _   TC    AC
GAM260  DKFZp547M236 3'  CTAGACTTGCAGCATGCATGCT 38034       T       T__    TGG
           C                      GGGCAT GTATGTTGC   TCTG
                                ||||||| |||||||||   ||||
                                CTCGTA CGTACGACG   AGAT
                                   _       TTC    C
GAM260  DKFZp547M236 3'  GCAGCTATAGAATGTTT     38037        G   _
                                GGGCATT TAT GTTGC
                                ||||||| ||| |||||
                                TTTGTAA ATA CGACG
                                    G   T
GAM260  DKFZp564A176 3'  TTGCAGAAGCAGCACCGCT    49975     ATTGTA         TG
                                GGC     TGTTGCTTCTG  G
                                |||     ||||||||||  |
                                TCG     ACGACGAAGAC  T
                                  CC_____          GT
GAM260  DKFZP564A2416 3'  TTGTAGAATTTAACATCTGGTG 31389        GT     C_    TG
           TTT                    GGGCATT  ATGTTG  TTCTG  G
                                |||||||  ||||||  |||||  |
                                TTTGTGG  TACAAT  AAGAT  T
                                    TC     TT    GT
GAM260  DKFZP564C196 3'  CACGGGTCTGCAGTGTTT    70064          TGTTGCT
                                GGGCATTGTA      TCTGTG
                                ||||||||||      ||||||
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                                TTTGTGACGT      GGGCAC
                                      CT_____
GAM260  DKFZP564C196 3'  GCGGCAGTACAATGCCC     70066          _
                                GGGCATTGTA TGTTGC
                                |||||||||| ||||||
                                CCCGTAACAT ACGGCG
                                      G
GAM260  DKFZP564D166 3'  CAGGAGCACACAGTTCT     47674     C     ATGT
                                GGG ATTGT    TGCTTCTG
                                ||| |||||    ||||||||
                                TCT TGACA    ACGAGGAC
                                  _     C___
GAM260  DKFZP564K0322 5'  CGTGGAAGCCCTAAAGCCC    49359      A   TATGTT     TG
                                GGGC TTG     GCTTC  TG
                                |||| |||     |||||  ||
                                CCCG AAT     CGAAG  GC
                                   A  CC____     GT
GAM260  DKFZP564K0822 3'  TCATGGAAGTGGATACGGAGT  94049     A      G TG
                                GC TTGTAT T  CTTCTGTGG
                                || |||||| |  |||||||||
                                TG GGCATA G  GAAGGTACT
                                 A     _ GT
GAM260  DKFZP564M182 3'  TCGTGGGGGTGACAAAGTCC   78043      A  GTA   TG    TG
                                GGGC TT   TGT  CTTC  TGG
                                |||| ||   |||  ||||  |||
                                CCTG AA   ACA  GGGG  GCT
                                  _ ____   GT    GT
GAM260  DKFZp566H0824 5'  CATGGAGGAAAAATGTCC     34048        GTATGTTG
                                GGGCATT       CTTCTGTG
                                |||||||       ||||||||
                                CCTGTAA       GGAGGTAC
                                    AAA_____
GAM260  DKFZp566H0824 5'  CTGCAGGACTCAGTGATGTATG 34049   A TG     TG ____    TG
          AGCCT                    T  TATGT  CT    TCTG  G
                                | |||||  ||   ||||  |
                                A  ATGTA  GA    GGAC  C
                                _ GT    GT  CTCA    GT
GAM260  DKFZP586J1624 3'  TCATAGAAATAAGTGCAATTTC 31399     C      G   C
          T                      GGG ATTGTAT TTG TTCTGTGG
                                ||| ||||||| ||| ||||||||
                                TCT TAACGTG AAT AAGATACT
                                  T      _   A
GAM260  DKFZP586J1624 3'  TGGAACGATGTACGATACCC   31400     C         C
                                GGG ATTGTATGTTG TTCTG
                                ||| |||||||||| |||||
                                CCC TAGCATGTAGC AAGGT
                                  A         _
GAM260  DKFZP586M1120 3'  CTGCAGAAGCAGCGCACAGTGC 48456         A         TG
          C                      GGCATTGT TGTTGCTTCTG  G
                                |||||||| |||||||||| |
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                                CCGTGACA GCGACGAAGAC  C
                                     C         GT
GAM260  DKFZP586M1120 3'  TTGTAGAGGCAACAAGTGGTGC 48472      TG A        TG
           C                  GGCAT  T TGTTGCTTCTG  G
                              |||||  | ||||||||||| |
                              CCGTG  G ACAACGGAGAT  T
                                 GT A         GT
GAM260  DKFZP727M111 5'  GGCTAGCAGGCAGTGTCT    31413        A   _
                              GGGCATTGT TGTT GCT
                              ||||||||| |||| |||
                              TCTGTGACG ACGA CGG
                                   G   T
GAM260  DKFZP761C169 5'  CCATTTTGGATTTACAGTGTTT 67810         TGTTG  TCT
                              GGGCATTGTA    CT   GTGG
                              ||||||||||    ||  ||||
                              TTTGTGACAT    GG   TACC
                                    TTA__  TTT
GAM260  DKFZp761D112 3'  TTACAGAGGCAGCTTTTTGCT  50193     TTGTAT
                              GGCA     GTTGCTTCTGTGG
                              ||||     |||||||||||||
                              TCGT     CGACGGAGACATT
                                TTTT__
GAM260  DKFZp761D221 3'  TTACAGAGGTAGATTGCA    50165     TG
                              TGTA  TTGCTTCTGTGG
                              ||||  ||||||||||||
                              ACGT  GATGGAGACATT
                                TA
GAM260  DKFZp761F2014 3'  TGCAGGGAATTTGCAGGCCT   39542     A    T   G  T   TG
                              GGGC TTGTA GTT CT CTG  G
                              |||| ||||| ||| || |||  |
                              TCCG GACGT TAA GG GAC  T
                                _    T  _ _  GT
GAM260  DKFZp761G2113 3'  TCACAGGGGCAGCCCTTTCCC  69909     CATTGTAT
                              GGG       GTTGCTTCTGTGG
                              |||       ||||||||||||||
                              CCC       CGACGGGGACACT
                                TTTCC___
GAM260  DKFZp761H079 3'  CCACAGCGACCTAACAGTGATG 58732      TG A    CTT__
           CTC                GGCAT  T TGTTG    CTGTGG
                              |||||  | |||||    ||||||
                              TCGTA  G ACAAT    GACACC
                                 GT _    CCAGC
GAM260  DKFZp761K1423 5'  CGTAGGAGCACTGATGTGCCT  37332      TGTAT  T     TG
                              GGGCAT    GT GCTTCTG  G
                              ||||||    || |||||||  |
                              TCCGTG    CA CGAGGAT  C
                                  TAGT_ _      GT
GAM260  DKFZp761K1824 3'  AGCAATGTGTAGTACCT     34205     C
                              GGG ATTGTATGTTGCT
                              ||| |||||||||||||
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```
                                TCC TGATGTGTAACGA
                                  A
GAM260  DKFZp762A227 5'  CGCAGGTGAATGTGATGTTC  26036      TG  G TG TT  TG
                                GGGCAT  TAT T  C  CTG  G
                                ||||||  ||| |  |  |||  |
                                CTTGTA  GTA A  G  GAC  C
                                   GT  _ GT __  GT
GAM260  DNAJC5   3'  GCAGGGTGGGGTGCCC     61455       G  G
                                GGGCATT TAT TTGC
                                ||||||| ||| ||||
                                CCCGTGG GTG GACG
                                    G  G
GAM260  DNAJC6   3'  CGCAGACCTGTGCTAATGCTT  28846       _  GTTGCT  TG
                                GGGCATT GTAT    TCTG  G
                                ||||||| ||||    ||||  |
                                TTCGTAA CGTG    AGAC  C
                                    T   TCC___  GT
GAM260  DNER     3'  CCACGTAACGTAGCATATGATG 57442     TG      _  C
           T                     GCAT  TATGTTGC TT TGTGG
                                 ||||  |||||||| || |||||
                                 TGTA  ATACGATG AA GCACC
                                   GT      C  T
GAM260  DOC-1R   5'  CGGAGGGCGGTGGCC      19579   G    ATGTTG
                                GG CATTGT    CTTCTG
                                || ||||||    ||||||
                                CC GTGGCG    GGAGGC
                                 G    ______
GAM260  DOCK3    3'  CCACAGGAGCCCCAGTGGTGAC 66500   G  TG A  TT
           T                     GG CAT  T TG  GCTTCTGTGG
                                 || |||  | ||  ||||||||||
                                 TC GTG  G AC  CGAGGACACC
                                  A  GT _  CC
GAM260  DSTN     3'  CAGGAGAATGTGCAGTGTCT  22496          G
                                GGGCATTGTATGTT CTTCTG
                                |||||||||||||| ||||||
                                TCTGTGACGTGTAA GAGGAC
                                              _
GAM260  DUSP10   3'  GCAATAATATGATGTTT    23282      TG  _
                                GGGCAT  TAT GTTGC
                                ||||||  ||| |||||
                                TTTGTA  ATA TAACG
                                   GT   A
GAM260  DUSP10   3'  GCAATAATATGATGTTT    58562      TG  _
                                GGGCAT  TAT GTTGC
                                ||||||  ||| |||||
                                TTTGTA  ATA TAACG
                                   GT   A
GAM260  DUSP12   3'  TGCAGATGATATGTGCTGCCT  23380     TT    TGCT   TG
                                GGGCA  GTATGT   TCTG  G
                                |||||  ||||||   ||||  |
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                                TCCGT  CGTGTA   AGAC  T
                                  __     TAGT   GT
GAM260  E2IG4    3'  CACAGGAGTTGTGGGCCT    90908     A TG  TGTT
                                GGGC T  TA   GCTTCTGTG
                                |||| |  ||   |||||||||
                                TCCG G  GT   TGAGGACAC
                                  _ GT  ____
GAM260  EDG2     5'  CAGGAGGCGAGGCTC      54063     A   ATGTTG
                                GGGC TTGT    CTTCTG
                                |||| ||||    ||||||
                                CTCG AGCG    GAGGAC
                                  G  _______
GAM260  EDG2     5'  CAGGAGGCGAGGCTC      7380      A   ATGTTG
                                GGGC TTGT    CTTCTG
                                |||| ||||    ||||||
                                CTCG AGCG    GAGGAC
                                  G  _______
GAM260  EFNA2    3'  CCATGTACAGCACGTAGTGCTC 7391        TA    CTTC
                                GGGCATTG  TGTTG   TGTGG
                                ||||||||  |||||   |||||
                                CTCGTGAT  ACGAC   GTACC
                                     GC    AT__
GAM260  EIF2S1   3'  GAGTGGCATATAATTTTC    14584     C       TG
                                GGG ATTGTATGT  CTT
                                ||| |||||||||  |||
                                CTT TAATATACG  GAG
                                  T       GT
GAM260  EIF3S1   3'  TTGCAGCAAGGGCATGTGGTGT 63168   G   TG    G  _  TG
          GC                      G GCAT  TATGTT CTT CTG  G
                                | ||||  |||||| ||| |||  |
                                C TGTG  GTACGG GAA GAC  T
                                 G   GT    _  C   GT
GAM260  EIF5     3'  TTGCAGTTTGTTCTGTAATGCC 8762          TGTT  TT_   TG
          T                      GGGCATTGTA   GC   CTG  G
                                ||||||||||   ||  |||  |
                                TCCGTAATGT   TG   GAC  T
                                     CT__  TTT   GT
GAM260  ELKS     5'  GGCGGCGGCGGTGCCC      30504         A
                                GGGCATTGT TGTTGCT
                                |||||||| |||||||
                                CCCGTGGCG GCGGCGG
                                     _
GAM260  ENAH     3'  TCACACTAATATGTAGTGGCC  36617    G         CTTC
                                GG CATTGTATGTTG   TGTGG
                                || ||||||||||||   |||||
                                CC GTGATGTATAAT   ACACT
                                 G         C___
GAM260  EREG     3'  GCAGTCATTTGGTGCTC     7499         T  _
                                GGGCATTG ATG TTGC
                                |||||||| ||| ||||
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                                CTCGTGGT TAC GACG
                                     T  T
GAM260  EREG    3'  GCTAATGTATAATGTGC    7502   G        _
                                G GCATTGTATGTT GC
                                | ||||||||||||| ||
                                C TGTAATATGTAA CG
                                 G          T
GAM260  ERMAP   3'  TTATGGAGGCGGTTAAATCCC  37598    C   GTAT TT
                                GGG ATT   G  GCTTCTGTGG
                                ||| |||   |  ||||||||||
                                CCC TAA   T  CGGAGGTATT
                                  _  AT__ GG
GAM260  ERN1    3'  CGCAGAGGCAGCAGGAGCC   7518     ATTGTA        TG
                                GGC     TGTTGCTTCTG  G
                                |||     ||||||||||  |
                                CCG     ACGACGGAGAC  C
                                  AGG___         GT
GAM260  FADS1   3'  CGCAGAAGATTTAGATGTTT  25475      GTATGTTG     TG
                                GGGCATT       CTTCTG  G
                                |||||||       ||||||  |
                                TTTGTAG       GAAGAC  C
                                    ATTTA___     GT
GAM260  FADS2   3'  CCATAGGGAGCTGATCGTAATG 14952        TATGTT    _
           TTT                    GGGCATTG     GCTTC TGTGG
                                |||||||||     ||||| |||||
                                TTTGTAAT     CGAGG ATACC
                                     GCTAGT     G
GAM260  FAIM    5'  GGCGGCGGGCGGTGTCT    36307         A
                                GGGCATTGT TGTTGCT
                                ||||||||| |||||||
                                TCTGTGGCG GCGGCGG
                                      G
GAM260  FAM3D   3'  GGAGAGAATGGGGTGCTT    57152       G   GTTG
                                GGGCATT TAT    CTTC
                                ||||||| |||    ||||
                                TTCGTGG GTA    GAGG
                                    G   AGA_
GAM260  FASTK   3'  GCCAACTGCGGTGCCT     46989          T   _
                                GGGCATTGTA GTTG C
                                |||||||||| |||| |
                                TCCGTGGCGT CAAC G
                                      _    C
GAM260  FBXO24  3'  GTAGGGTGGATGCCC      24093        G   G
                                GGGCATT TAT TTGC
                                ||||||| ||| ||||
                                CCCGTAG GTG GATG
                                    _  G
GAM260  FEM-2   3'  CTGCAGGGGTGGAGGGCAGTCC 27577     C    ATG TG     TG
           C                     GGG ATTGT   T  CTTCTG  G
                                ||| |||||   |  ||||||  |
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                                CCC TGACG  G  GGGGAC  C
                                  _    GGA GT     GT
GAM260  FER1L4   3'  CTGTAGAGATGGTTACAATGCC 47348         T TT C    TG
           T                     GGGCATTGTA G  G TTCTG  G
                                 |||||||||| |  | |||||  |
                                 TCCGTAACAT T  T GAGAT  C
                                       _ GG A    GT
GAM260  FGD3    3'  TGATGCTAGTGGCACACAGTGC 72900        A   TG  TC   GG
           TT                     GGGCATTGT TGT  CT  TGT
                                  ||||||||| |||  ||  |||
                                  TTCGTGACA ACG  GA  GTA
                                       C   GT  TC   GTC
GAM260  FHOD2   5'  GGGCAACAGTGTCT       73827       TGTA
                                  GGGCAT    TGTTGCTT
                                  ||||||    ||||||||
                                  TCTGTG    ACAACGGG
                                    ____
GAM260  FHR5    3'  CCACAGAAACAGTAAATGTTC  47900       GTA    GCT
                                  GGGCATT   TGTT   TCTGTGG
                                  |||||||   ||||   |||||||
                                  CTTGTAA   ACAA   AGACACC
                                      ATG   ___
GAM260  FHX     3'  CAGAAGCTCACTGCCT     37301      T  TATGTT
                                  GGGCA TG     GCTTCTG
                                  ||||| ||     |||||||
                                  TCCGT AC     CGAAGAC
                                    C  T_____
GAM260  FHX     3'  CATGTTACATCAGTGTCC    37302        T    T  TTCT
                                  GGGCATTG ATGT GC    GTG
                                  |||||||| |||| ||    |||
                                  CCTGTGAC TACA TG    TAC
                                       _    T  ____
GAM260  FKSG28  3'  GAGCGGCTATAGTGTTC     48176         T
                                  GGGCATTGTA GTTGCTT
                                  |||||||||| |||||||
                                  CTTGTGATAT CGGCGAG
                                       _
GAM260  FKSG44  3'  CCACCTCAAGATGGGCAGTGTC 49122         A   GCTTCT
           C                      GGGCATTGT TGTT     GTGG
                                  ||||||||| ||||     ||||
                                  CCTGTGACG GTAG     CACC
                                       G    AACTC_
GAM260  FLJ00007 3'  GTGGGGGAGCCATCACGGTGTT 71279         _  TT     G  G
           C                      GGGCATTGT ATG  GCTTCT TG
                                  ||||||||| |||  |||||| ||
                                  CTTGTGGCA TAC  CGAGGG GT
                                       C   __     G  GT
GAM260  FLJ00060 3'  TCGAAGCTGGCAACAGCAGTGT 61104         A      T_  G
           CT                      GGGCATTGT TGTTGCT  CT TGG
                                  |||||||| |||||||  || |||
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                                TCTGTGACG ACAACGG  GA GCT
                                      _      TC  A
GAM260  FLJ10008  3'  TACCTCGGCGGCGATGCCT   35731        ATGT   TCT
                                GGGCATTGT   TGCT  GTG
                                |||||||||   ||||  |||
                                TCCGTAGCG   GCGG  CAT
                                     ____   CTC
GAM260  FLJ10043  3'  CAGAGATGTGTGAGCTT    35756     A TG    GCT
                                GGGC T  TATGTT  TCTG
                                |||| |  ||||||  ||||
                                TTCG A  GTGTAG  AGAC
                                  _ GT    ___
GAM260  FLJ10052  3'  GCAATGGCAGTGCTT      35772         A
                                GGGCATTGT TGTTGC
                                ||||||||| ||||||
                                TTCGTGACG GTAACG

                                     _
GAM260  FLJ10058  3'  CCATGAGAGGGTATGCAGTCTT 35783     C       TTG    _
                                GGG ATTGTATG  CTTCT GTGG
                                ||| ||||||||  ||||| ||||
                                TTC TGACGTAT  GGAGA TACC
                                  _      G__    G
GAM260  FLJ10094  3'  CTACAGAGTTGTATATGTAATG 35808          TGC_
          T                    GCATTGTATGT   TTCTGTGG
                               ||||||||||    ||||||||
                               TGTAATGTATA   GAGACATC
                                     TGTT
GAM260  FLJ10140  3'  CCATAGAAGACAATAAGGTTC  35845     ATTGTA    _
                                GGGC     TGTTG CTTCTGTGG
                                ||||     ||||| |||||||||
                                CTTG     ATAAC GAAGATACC
                                  GA____     A
GAM260  FLJ10140  3'  CGCAGGGGCCCGGCGAGCCC   35846     A   ATGTT     TG
                                GGGC TTGT    GCTTCTG  G
                                |||| ||||    |||||||  |
                                CCCG AGCG    CGGGGAC  C
                                  _   GCC__      GT
GAM260  FLJ10211  5'  CCATCAAGGCCTACAGTGTCC  35903         TGTT   CT
                                GGGCATTGTA   GCTT  GTGG
                                ||||||||||   ||||  ||||
                                CCTGTGACAT   CGGA  TACC
                                     C___    AC
GAM260  FLJ10305  5'  CAGTAGCGGCATCAGTGTCT   68358        T      T
                                GGGCATTG ATGTTGCT CTG
                                |||||||| |||||||| |||
                                TCTGTGAC TACGGCGA GAC
                                     _       T
GAM260  FLJ10350  3'  CCACAGGAGCCTCAGTGGAGTC 95505     A TG A  TT
          T                     GGGC T  T TG  GCTTCTGTGG
                                |||| |  | ||  ||||||||||
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                                TCTG G  G AC  CGAGGACACC
                                  A GT _  TC
GAM260  FLJ10350  3'  TGGAGGCTCGGTCCC      95511     C    TATGTT
                                GGG ATTG     GCTTCTG
                                ||| ||||     |||||||
                                CCC TGGC     CGGAGGT
                                  _   T_____
GAM260  FLJ10375  5'  CACAGATCGTCAGTGCCT    36071        T   TTGCT
                                GGGCATTG ATG    TCTGTG
                                |||||||| |||    ||||||
                                TCCGTGAC TGC    AGACAC
                                     _  T____
GAM260  FLJ10483  3'  TCATGGAAGGTTGTACAGAGCC 36174     A      TTG
          C                      GGGC TTGTATG   CTTCTGTGG
                                |||| |||||||   |||||||||
                                CCCG GACATGT   GAAGGTACT
                                  A      TG_
GAM260  FLJ10508  3'  TAGTATGGTATGCAGTGGCC   36202    G       TT CTT
                                GG CATTGTATG  G   CTG
                                || |||||||||  |   |||
                                CC GTGACGTAT  T   GAT
                                 G       GG AT_
GAM260  FLJ10546  3'  GCAGCTTTGACAGTGCTT    59477         AT__
                                GGGCATTGT    GTTGC
                                |||||||||    |||||
                                TTCGTGACA    CGACG
                                     GTTT
GAM260  FLJ10565  3'  GAGATGAAGTAAATGCAGTGTT 36287          G      TGTGG
          C                      GGGCATTGTAT TTGCTTC
                                |||||||||||| |||||||
                                CTTGTGACGTA AATGAAG
                                       _      TAGAGT
GAM260  FLJ10607  5'  CCGCAGGGCCTCTACGGTTCCT 77108     C     TGTT   T
                                GGG ATTGTA    GCT CTGTGG
                                ||| ||||||    ||| ||||||
                                TCC TGGCAT    CGG GACGCC
                                  T     CTC_  _
GAM260  FLJ10647  3'  GGGAGGGGGCAGCATGCAGGGT 36373      A            GTGG
          CC                     GGGC TTGTATGTTGCTTCT
                                |||| ||||||||||||||
                                CCTG GACGTACGACGGGGG
                                  G            AGGGG
GAM260  FLJ10656  3'  TGTAGAAGGGACTAAATGTTC  36390       GTAT   G     TG
                                GGGCATT    GTT CTTCTG  G
                                |||||||    ||| ||||||  |
                                CTTGTAA    CAG GAAGAT  T
                                     AT__   G     GT
GAM260  FLJ10697  3'  TTACAGGCTAAAATAATGCCT  36422         ATGTT  TT
                                GGGCATTGT    GC  CTGTGG
                                |||||||||    ||  ||||||
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                                TCCGTAATA    CG  GACATT
                                     AAAT_ __
GAM260  FLJ10700 3' AGTTGAGGTAGTATAGGTGCTC 36425       G        TGTGG
                                GGGCATT TATGTTGCTTC
                                ||||||| ||||||||||
                                CTCGTGG ATATGATGGAG
                                     _        TTGAT
GAM260  FLJ10704 3' CTGCAGGACGAACTGTCGATGT 36453       TAT   GC    TG
           TT                    GGGCATTG   GTT  TTCTG  G
                                ||||||||   |||  |||||  |
                                TTTGTAGC   CAA  AGGAC  C
                                     TGT   GC    GT
GAM260  FLJ10719 3' CCACGGGAGCAAATACAGAGCC 62541     A     G
           T                     GGGC TTGTAT TTGCTTCTGTGG
                                |||| |||||| ||||||||||||
                                TCCG GACATA AACGAGGGCACC
                                  A     _
GAM260  FLJ10724 3' GAGTGACATTGATGTTT     36502        T   TG
                                GGGCATTG ATGT  CTT
                                |||||||| ||||  |||
                                TTTGTAGT TACA  GAG
                                     _   GT
GAM260  FLJ10829 5' CCGCAGAGGTTCAAGCGATTCT 36708     C    A  TT
           C                     GGG ATTGT TG  GCTTCTGTGG
                                ||| ||||| ||  ||||||||||
                                CTC TAGCG AC  TGGAGACGCC
                                  T    A  T_
GAM260  FLJ10846 3' GCATGAGTATAATGCTC     36740         GT_
                                GGGCATTGTAT   TGC
                                ||||||||||   |||
                                CTCGTAATATG   ACG
                                      AGT
GAM260  FLJ10847 3' CTACAGGGGTATGCCACCATGC 36747       T  ATGT
           CC                    GGGCAT GT    TGCTTCTGTGG
                                ||||||  ||    ||||||||||
                                CCCGTA CA    ATGGGGACATC
                                   C  CCGT
GAM260  FLJ10851 3' CGTAGATTCAAAGCGATGTTC  36763        ATG   CT    TG
                                GGGCATTGT   TTG  TCTG  G
                                |||||||||   |||  ||||  |
                                CTTGTAGCG   AAC  AGAT  C
                                     A__   TT    GT
GAM260  FLJ10898 5' TTGCATGCCTGAATGCAATGCT 59439         GTT_  TTC  TG
           T                     GGGCATTGTAT    GC   TG  G
                                ||||||||||    ||   ||  |
                                TTCGTAACGTA    CG   AC  T
                                      AGTC  T__  GT
GAM260  FLJ10932 3' TCGTAGAGGTGAGGCTGGTGCC 36898       _  ATG TG
                                GGCATT GT   T  CTTCTGTGG
                                ||||||  ||   |  |||||||||
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                                CCGTGG CG   A  GGAGATGCT
                                   T  G__ GT
GAM260  FLJ10936 3' CCACCAGAGTGGATAATGCTT  36904        ATG TG   CT
                                GGGCATTGT   T  CTT  GTGG
                                |||||||||   |  |||  ||||
                                TTCGTAATA   G  GAG  CACC
                                     ___ GT   AC
GAM260  FLJ10989 3' CACTAAGTGTACAATACTT   36946    C     GTT    CT
                                GGG ATTGTAT   GCTT  GTG
                                ||| |||||||   ||||  |||
                                TTC TAACATG   TGAA  CAC
                                  A      ___    T_
GAM260  FLJ11000 3' TACAGAGGAGGTGGGGCCC   36963     A TG ATGTTG
                                GGGC T  T     CTTCTGTG
                                |||| |  |     ||||||||
                                CCCG G  G     GGAGACAT
                                  G GT GA____
GAM260  FLJ11113 3' CACTAATGCGCAGTGTTT    59394        ATGTT  TTCT
                                GGGCATTGT    GC    GTG
                                |||||||||    ||    |||
                                TTTGTGACG    CG    CAC
                                     _____  TAAT
GAM260  FLJ11181 3' CTATACTCAACAGCAATGCCT  37137        A    CTTC
                                GGGCATTGT TGTTG    TGTGG
                                ||||||||| |||||    |||||
                                TCCGTAACG ACAAC    ATATC
                                     _    TC__
GAM260  FLJ11191 3' TGTAGAACAAATGCAAGCCC   37151     A     G   C    TG
                                GGGC TTGTAT TTG TTCTG  G
                                |||| |||||| ||| |||||  |
                                CCCG AACGTA AAC AAGAT  T
                                  _     _  _     GT
GAM260  FLJ11193 3' TTGTAGATATCAATAATATAGT 37157         _   CT_   TG
           GCCT                 GGCATTGTAT GTTG   TCTG  G
                                |||||||||| ||||   ||||  |
                                CCGTGATATA TAAC   AGAT  T
                                     A   TAT    GT
GAM260  FLJ11210 3' GTCGATGTGCATGCTT     59576       T      _
                                GGGCAT GTATGTTG C
                                |||||| |||||||| |
                                TTCGTA CGTGTAGC G
                                   _       T
GAM260  FLJ11259 3' CTACAGAGGACAGACAGGGTTT 37186     A   A   TG
                                GGGC TTGT TGT  CTTCTGTGG
                                |||| |||| |||  |||||||||
                                TTTG GACA ACA  GGAGACATC
                                  G   G   __
GAM260  FLJ11267 3' TTATAGATAAATATGATGCC   39008      TG   GTTGCT
                                GGCAT  TAT     TCTGTGG
                                |||||  |||     |||||||
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                                CCGTA  ATA     AGATATT
                                  GT   AAT___
GAM260  FLJ11506  3' TTGTAGCTCTGAGCTATGATGC 45117     TG  TGTT   ____  TG
             TT                  GCAT  TA   GCTT   CTG  G
                                 ||||  ||   ||||   |||  |
                                 CGTA  AT   CGAG   GAT  T
                                   GT  ____   TCTC   GT
GAM260  FLJ11608  3' TGCAGAGAACCGATATAGCAGT 44653        _    C   G  G
             GCCC                  GGCATTGT ATGTTG TTCT TG
                                   ||||||||  ||||||  ||||  ||
                                   CCGTGACG TATAGC AAGA AC
                                        A     C   G  GTT
GAM260  FLJ11710  3' CTGTGGGAGCAGTTAGACAGCT 45827     AT   ATG_      TG
             T                    GGGC  TGT   TTGCTTCTG  G
                                  ||||  |||   |||||||||  |
                                  TTCG  ACA   GACGAGGGT  C
                                    __  GATT       GT
GAM260  FLJ11726  3' GCAATGTACGTGCCT      46413       T
                                  GGGCAT GTATGTTGC
                                  ||||||  |||||||||
                                  TCCGTG CATGTAACG
                                    _
GAM260  FLJ11850  3' CCACAGTCCCCCAGTGTGTGGT 42719    C  TG  TG   CTT__
             CTCC                  GG AT  TA  TTG    CTGTGG
                                   ||  ||  ||  |||    ||||||
                                   CT TG  GT  GAC    GACACC
                                    C  GT  GT   CCCCT
GAM260  FLJ12057  3' CCATGGGGGTGAAACCAGTGCT 45437       TATG TG
                                  GGCATTG    T  CTTCTGTGG
                                  |||||||    |  |||||||||
                                  TCGTGAC    A  GGGGGTACC
                                      CAA_ GT
GAM260  FLJ12057  5' CTGCAGAGGCAGGTGTGATGAC 45438    G   TG   G       TG
             C                     GG CAT  TAT TTGCTTCTG  G
                                   ||  |||  |||  |||||||||  |
                                   CC GTA  GTG GACGGAGAC  C
                                    A  GT   _       GT
GAM260  FLJ12078  3' TCGTGGAGGAAGTGATGCCT   46455       TG ATGTTG   TG
                                  GGGCAT  T     CTTC  TGG
                                  ||||||  |     ||||  |||
                                  TCCGTA  G     GGAG  GCT
                                     GT AA____    GT
GAM260  FLJ12122  5' CAGAGGCCAGGTCT       46461      A   TATGTT
                                  GGGC TTG     GCTTCTG
                                  ||||  |||     |||||||
                                  TCTG GAC     CGGAGAC
                                    _  _______
GAM260  FLJ12242  3' TGGCAGATGTGTGGCAATGTCT 45183         ATGT   T    GG
                                  GGGCATTGT    TGC TCTGT
                                  |||||||||    |||  |||||
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                                TCTGTAACG   GTG AGACG
                                     GT__   T    GTA
GAM260  FLJ12270  3' CTACAGAAGTTGGGTATTGTCT 47572      TT   GTT
                                GGGCA  GTAT   GCTTCTGTGG
                                |||||  ||||   ||||||||||
                                TCTGT  TATG   TGAAGACATC
                                   __    GGT
GAM260  FLJ12331  3' CGGGCATCAGTGCCC       46477        T   TGCTT
                                GGGCATTG ATGT    CTG
                                ||||||||| ||||    |||
                                CCCGTGAC TACG    GGC
                                   _   ______
GAM260  FLJ12355  3' TGTGGGAGGAAGGCGATGTCT  46484        ATG  G    TG
                                GGGCATTGT   TT CTTCTG  G
                                |||||||||   || ||||||  |
                                TCTGTAGCG   AA GAGGGT  T
                                     G__  G    GT
GAM260  FLJ12438  3' CTGTGGAAGTTTGTAAATAAAG 41643     A   A  TT_     TG
           CTC                    GGGC TTGT TG   GCTTCTG  G
                                |||| |||| ||   |||||||  |
                                CTCG AATA AT   TGAAGGT  C
                                  A   A  GTT      GT
GAM260  FLJ12476  5' CCGCGGAGGTAGCCGTTCCC   42949    CAT  TAT
                                GGG   TG   GTTGCTTCTGTGG
                                |||   ||   ||||||||||||
                                CCC   GC   CGATGGAGGCGCC
                                 TT_  ___
GAM260  FLJ12525  3' CCACAGGGGAATTTTGAATGTC 48304       GTAT   G
           T                    GGGCATT    GTT CTTCTGTGG
                                |||||||    ||| |||||||||
                                TCTGTAA    TAA GGGGACACC
                                   GTTT   _
GAM260  FLJ12547  3' CACTCAGCATGCAGTGTTT   46490            CTTCT
                                GGGCATTGTATGTTG    GTG
                                ||||||||||||||    |||
                                TTTGTGACGTACGAC    CAC
                                       T____
GAM260  FLJ12577  3' CAGAAGGTAACGTTAATGTTT  48155        T      _
                                GGGCATTG ATGTTGC TTCTG
                                |||||||| ||||||| |||||
                                TTTGTAAT TGCAATG AAGAC
                                   _      G
GAM260  FLJ12700  3' CCACACGCACATCTGGTGTTT  46116       GT    T  TTC
                                GGGCATT  ATGT GC   TGTGG
                                |||||||  |||| ||   |||||
                                TTTGTGG  TACA CG   ACACC
                                   TC    _  C__
GAM260  FLJ12750  3' TGTGCAAGCAGTGCACGGTGCC 45127         A GT    CTGTGG
           C                    GGGCATTGT T  TGCTT
                                |||||||||  |  |||||
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                                CCCGTGGCA G  ACGAA
                                     C TG    CGTGTT
GAM260  FLJ12750 3' CACCTGGCGTGTTGTGCTC   45122      TG  GTT  TCT
                                GGGCAT  TAT   GCT   GTG
                                ||||||  |||   |||   |||
                                CTCGTG  GTG   CGG   CAC
                                   TT   ___   TC_
GAM260  FLJ12770 3' CCGTAGGCCTCATTAATGCTC 49740       T   TT  TT
                                GGGCATTG ATG  GC  CTGTGG
                                ||||||||  |||  ||  ||||||
                                CTCGTAAT TAC  CG  GATGCC
                                     _  TC  __
GAM260  FLJ12783 3' CACAGGGATTAAGTGCCT    48678      GTAT   GCT
                                GGGCATT    GTT   TCTGTG
                                |||||||    |||   ||||||
                                TCCGTGA    TAG   GGACAC
                                    AT__   ___
GAM260  FLJ12969 5' TGTGGGGGTACAGAATGCT   43115      GTA  T     TG
                                GGCATT   TGT GCTTCTG  G
                                ||||||   ||| |||||||  |
                                TCGTAA   ACA TGGGGGT  T
                                   G__   _      GT
GAM260  FLJ13072 3' TAGTTGTGGTATGGATGTCT   89824       G   TT  TT
                                GGGCATT TATG  GC  CTG
                                |||||||  ||||  ||  |||
                                TCTGTAG GTAT  TG  GAT
                                    _   GG  TT
GAM260  FLJ13105 3' TCCTCAAAGTAGATGCAATGTT 46547          G     C  T
           T                     GGGCATTGTAT TTGCTT TG GG
                                ||||||||||| ||||||  ||  ||
                                TTTGTAACGTA GATGAA AC CC
                                      _     _  T  TT
GAM260  FLJ13114 3' CCATGGAACCACTATAGGCTT  44593     A    T  T C
                                GGGC TTGTA GT G TTCTGTGG
                                ||||  |||||  ||  |  ||||||||
                                TTCG GATAT CA C AAGGTACC
                                  _    _  _ C
GAM260  FLJ13150 3' CAGGAGAGACAATTTCT     45668     C    ATGTTG
                                GGG ATTGT     CTTCTG
                                |||  |||||     ||||||
                                TCT TAACA     GAGGAC
                                  T    GA____
GAM260  FLJ13263 3' GTGCTCTGCAGTGTGCAGGGCC 47093     A    TG   TTCT   G
           T                     GGGC TTGTA  TTGC    GTG
                                ||||  |||||  ||||    |||
                                TCCG GACGT  GACG    CGT
                                  G    GT   TCT_   GT
GAM260  FLJ13265 3' CGTAGGAAGAATAGGGTGTCC  45924       G  GTTGC    TG
                                GGGCATT TAT    TTCTG  G
                                |||||||  |||    |||||  |
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                              CCTGTGG ATA    AGGAT  C
                                  G  AGA__    GT
GAM260  FLJ13273  5' TGGAGGCGAGTGGTC      45392    G  TGTATG
                              GG CAT     TTGCTTCTG
                              || |||     |||||||||
                              CT GTG     AGCGGAGGT
                               G  _______
GAM260  FLJ13725  5' CGTATGAGGCATACTGTGTCC  68288       T  TGT    _ TG
                              GGGCAT GTA   TGCTTC TG  G
                              |||||| |||   |||||| ||  |
                              CCTGTG CAT   ACGGAG AT  C
                                 T  ___     T  GT
GAM260  FLJ13769  3' CCACAGAAGCAGCATGAAAT   46606    G
                              ATT TATGTTGCTTCTGTGG
                              ||| ||||||||||||||||
                              TAA GTACGACGAAGACACC
                                A
GAM260  FLJ13769  5' GCAGTGTGGCAATGCTT     46614        _ TG
                              GGGCATTGT A  TTGC
                              ||||||||| |  ||||
                              TTCGTAACG T  GACG
                                   G GT
GAM260  FLJ13840  5' CATGGAAGGGACGGTACCC   45365    CATTGTA   G
                              GGG      TGTT CTTCTGTG
                              |||      |||| ||||||||
                              CCC      GCAG GAAGGTAC
                                ATG____   G
GAM260  FLJ13842  5' TCGCAGAGACAGGAACGTGTAA 44989  C       G  ___
           TCCT                  ATTGTATGTT CT   TCTGTGG
                                 |||||||||| ||   |||||||
                                 TAATGTGCAA GA   AGACGCT
                                _       G  CAG
GAM260  FLJ13848  3' TCGTGGAGGTCTGTTGGTCCC  45473    C   TATGTT    TG
                              GGG ATTG     GCTTC  TGG
                              ||| ||||     |||||  |||
                              CCC TGGT     TGGAG  GCT
                                _   TGTC__    GT
GAM260  FLJ13868  3' TGTGAGGCTGTGGCTTATGGTG 42733      TG  T  TG T_  GTGG
           TCC                   GGGCAT  TA GT  C  TCT
                              ||||||  || ||  |  |||
                              CCTGTG  AT CG  G  GGA
                                 GT  T  GT TC   GTGTC
GAM260  FLJ14009  5' CAGGAGTCGAGCTT      45410     A   TATGTT
                              GGGC TTG     GCTTCTG
                              |||| |||     |||||||
                              TTCG AGC     TGAGGAC
                                _  _______
GAM260  FLJ14129  3' TTGTAGGACATCGCGTTGGTGT 48073       T   __  C    TG
           CT                    GGGCATTG ATGT  TG TTCTG  G
                              |||||||| ||||  || |||||  |
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                                TCTGTGGT TGCG  AC AGGAT  T
                                    _   CT  _    GT
GAM260  FLJ14166  3' CCGTGGAAGCAATTTTTGTTT  44683      TTGTAT      TG
                                GGGCA     GTTGCTTC  TGG
                                |||||     ||||||||  |||
                                TTTGT     TAACGAAG  GCC
                                   TTT___       GT
GAM260  FLJ14251  3' CCGCAGGAGGATGCGTTGCCT  45969      T    GTTG
                                GGGCA TGTAT    CTTCTGTGG
                                ||||| |||||    |||||||||
                                TCCGT GCGTA    GAGGACGCC
                                   T    G___
GAM260  FLJ14281  3' CCATAGAAATTTGCAGTTTCT  46214     C     T   GCT
                                GGG ATTGTA GTT   TCTGTGG
                                ||| ||||||| |||   |||||||
                                TCT TGACGT TAA   AGATACC
                                  T     T  ___
GAM260  FLJ14437  5' CTATGGTATAATGCATTTAGTG 50825        T    TGCTT_
           TTC                    GGGCATTG ATGT     CTGTGG
                                |||||||| ||||     ||||||
                                CTTGTGAT TACG     GGTATC
                                     T    TAATAT
GAM260  FLJ14525  3' TTGCGGTCAACTCAGCAGTGCC 51419         AT_   CTT   TG
           C                    GGGCATTGT   GTTG   CTG  G
                                |||||||||   ||||   |||  |
                                CCCGTGACG   CAAC   GGC  T
                                      ACT    T__   GT
GAM260  FLJ14596  3' ATGGGGGCAGAGCCT      51458      ATTGTATG
                                GGGC       TTGCTTCTGT
                                ||||       ||||||||||
                                TCCG       GACGGGGGTA
                                  A________
GAM260  FLJ14641  5' CTATAGCAGGAAGCGTGTCGGT 51485        _     G   _
           GCTT                    GGCATTG TATGTT CTT CTGTGG
                                ||||||| |||||| ||| ||||||
                                TCGTGGC GTGCGA GGA GATATC
                                     T     A   C
GAM260  FLJ14681  3' CCATGTGTACATGCGATGCT   51522           T  TTCT
                                GGCATTGTATGT GC    GTGG
                                |||||||||||| ||    ||||
                                TCGTAGCGTACA TG    TACC
                                       _  TG__
GAM260  FLJ14721  3' CCACAGGGGCTAACAGTGGGCC 51579      ATTGTA   _
           T                    GGGC     TGTT GCTTCTGTGG
                                ||||     |||| ||||||||||
                                TCCG     ACAA CGGGGACACC
                                  GGTG__    T
GAM260  FLJ14775  3' CTGCAAGTAAAGTAATATGTAA 51600             C___  TG
           TGACT                   CATTGTATGTTGCTT    TG  G
                                |||||||||||||||    ||  |
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                                GTAATGTATAATGAA   AC  C
                                      ATGA  GT
GAM260  FLJ14824  3'  CCAGATCTAACATTGTAGTGTC 51641      GT_    CT   TGG
          T                    GGGCATT   ATGTTG  TCTG
                               |||||||   ||||||  ||||
                               TCTGTGA   TACAAT  AGAC
                                   TGT     CT    C
GAM260  FLJ20005  3'  CTACGGGGGCCGCGTGGTGCC  34316     TG    T
                               GGCAT  TATGT GCTTCTGTGG
                               |||||  ||||| ||||||||||
                               CCGTG  GTGCG CGGGGGCATC
                                  __    C
GAM260  FLJ20034  3'  CCACAGAAGCACCATGGGGTCC 34363     ATTG   T
                               GGGC    TATG TGCTTCTGTGG
                               ||||    |||| ||||||||||
                               CCTG    GTAC ACGAAGACACC
                                 GG__    C
GAM260  FLJ20040  3'  CGCAGCCGCGTCAGTGTCC   38630       T   T   TCT
                               GGGCATTG ATGT GCT   GTG
                               |||||||| |||| |||   |||
                               CCTGTGAC TGCG CGA   CGC
                                    _   C  ___
GAM260  FLJ20054  3'  CAGAGCAATAATGCCT     38783        ATGT   T
                               GGGCATTGT    TGCT CTG
                               |||||||||    |||| |||
                               TCCGTAATA    ACGA GAC
                                    ____   _
GAM260  FLJ20069  3'  GGACTGGCAACAATGTTC    34468        A   GC
                               GGGCATTGT TGTT  TTC
                               ||||||||| ||||  |||
                               CTTGTAACA ACGG  AGG
                                    _   TC
GAM260  FLJ20085  3'  CTGCAGAGGCAAGACCTCAATT 34515    C   TATG_      TG
          CT                     GGG ATTG    TTGCTTCTG  G
                               ||| ||||    |||||||||  |
                               TCT TAAC    AACGGAGAC  C
                                 _   TCCAG       GT
GAM260  FLJ20094  3'  TCACAGTATTCTGTGATGTCT  34559      TG  TGTTGCTT
                               GGGCAT  TA      CTGTGG
                               ||||||  ||      ||||||
                               TCTGTA  GT      GACACT
                                  GT  CTTAT___
GAM260  FLJ20123  5'  CACTTGACTGTGATGCCC    34584      TG  T   GCTTCT
                               GGGCAT  TA GTT     GTG
                               ||||||  || |||     |||
                               CCCGTA  GT CAG     CAC
                                  GT  _   TT____
GAM260  FLJ20125  3'  TTACAGAAAGTGGATGTGCTGT 34590      TT     _   _
          CC                     GGGCA  GTATGTT GCTT CTGTGG
                               |||||  ||||||| |||| ||||||
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                                CCTGT  CGTGTAG TGAA GACATT
                                  __     G   A
GAM260  FLJ20128  3'  TAGAAGCTCGGTCCC      34599     C   TATGTT
                                GGG ATTG     GCTTCTG
                                ||| ||||     |||||||
                                CCC TGGC     CGAAGAT
                                  _   T_____
GAM260  FLJ20136  3'  TCACAGCTGTTGACAATGTCC  34616        ATGTT  TT
                                GGGCATTGT    GC  CTGTGG
                                |||||||||    ||  ||||||
                                CCTGTAACA    TG  GACACT
                                     GT___  TC
GAM260  FLJ20154  3'  CACAGAGGCCCAGGGCTT    72923     ATTGTA  TT
                                GGGC     TG  GCTTCTGTG
                                ||||     ||  |||||||||
                                TTCG     AC  CGGAGACAC
                                  GG_____  C_
GAM260  FLJ20220  3'  GTAATATATGTGCTC      34761       T
                                GGGCAT GTATGTTGC
                                |||||| |||||||||
                                CTCGTG TATATAATG
                                  _
GAM260  FLJ20255  3'  CAGAGGGGCAGTGGCT     34796    G     ATGTTG
                                GG CATTGT     CTTCTG
                                || ||||||     ||||||
                                TC GTGACG     GGAGAC
                                 G     G_____
GAM260  FLJ20257  5'  CGCAGGGATGAAGTGGTGTCT  38994      TG ATG  GC    TG
                                GGGCAT  T   TT  TTCTG  G
                                ||||||  |   ||  |||||  |
                                TCTGTG  G   AG  GGGAC  C
                                   GT A__  TA    GT
GAM260  FLJ20275  3'  ACACAGCTGACATATAGTGT   34814          CTT    G
                                GCATTGTATGTTG   CTGTG
                                ||||||||||||   |||||
                                TGTGATATACAGT   GACAC
                                       C__     AT
GAM260  FLJ20296  3'  CCACGGAATGTGTGTGAAGCCC 34889     A TG   GTT  _
                                GGGC T  TAT   GC TTCTGTGG
                                |||| |  |||   || ||||||||
                                CCCG A  GTG   TG AAGGCACC
                                  A GT   ___  T
GAM260  FLJ20321  3'  CGCAGGGCATGTGGTGATCC   34947    _  TG    TGCT   TG
                                GGG CAT  TATGT   TCTG  G
                                ||| |||  |||||   ||||  |
                                CCT GTG  GTACG   GGAC  C
                                  A  GT    _____   GT
GAM260  FLJ20323  3'  TCACAGGAGTAAGTTGGATCCC 38660    C   GT  G
                                GGG ATT  AT TTGCTTCTGTGG
                                ||| |||  || ||||||||||||
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                                CCC TAG  TG AATGAGGACACT
                                  _  GT  _
GAM260  FLJ20337  3'  CAGAGGCGGGCAAGCCC     34963      A    ATG
                                GGGC TTGT   TTGCTTCTG
                                |||| ||||   |||||||||
                                CCCG AACG   GGCGGAGAC
                                  _   ____
GAM260  FLJ20337  3'  CCATCCCAAGCATCAGTGTCT  34965        T    GCTTCT
                                GGGCATTG ATGTT     GTGG
                                |||||||| |||||     ||||
                                TCTGTGAC TACGA     TACC
                                    _    ACCC__
GAM260  FLJ20344  3'  CATGGGATTGCAGTGCTT    35007          TGTTGC
                                GGGCATTGTA     TTCTGTG
                                ||||||||||     |||||||
                                TTCGTGACGT     AGGGTAC
                                     T_____
GAM260  FLJ20356  5'  CCGCAGGGCCAGGCATGTGAGG 38616     A TG     __   T
           TCT                    GGC T  TATGTT  GCT CTGTGG
                                ||| |  ||||||  ||| ||||||
                                CTG A  GTACGG  CGG GACGCC
                                  G GT     AC  _
GAM260  FLJ20359  3'  CTGCAGAGGTACCGCCTGCTGC 35042      TT   T __      TG
           CC                     GGGCA  GTA GT  TGCTTCTG  G
                                |||||  ||| ||  ||||||||  |
                                CCCGT  CGT CG  ATGGAGAC  C
                                   __  C  CC       GT
GAM260  FLJ20371  3'  TGTGCTGGCTGCAATACTGTGG 35069     TG  _     TT  _   G
           TGCTT                   GCAT  TA TGTTGC  CT GTG
                                ||||  || ||||||  || |||
                                CGTG  GT ATAACG  GG CGT
                                  GT  C     TC  T   GTC
GAM260  FLJ20378  5'  CGGGAGTTGTGGGTCT      35091      A TG  TGTT
                                GGGC T  TA    GCTTCTG
                                |||| |  ||    |||||||
                                TCTG G  GT    TGAGGGC
                                  _ GT  _____
GAM260  FLJ20432  5'  CAGAGATACATGTCT       35160       T   GTTGC
                                GGGCAT GTAT    TTCTG
                                ||||||| ||||    |||||
                                TCTGTA CATA    GAGAC
                                  _   ______
GAM260  FLJ20436  3'  TTGTGGGTGATGGTATGCAGTG 35174           TT CT_   TG
           TCC                    GGGCATTGTATG  G   TCTG  G
                                ||||||||||||  |   ||||  |
                                CCTGTGACGTAT  T   GGGT  T
                                       GG AGT    GT
GAM260  FLJ20499  3'  GCTTTGTAGCAGTGTCT     35259         _   TT
                                GGGCATTGT ATG  GC
                                |||||||| |||  ||
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                                TCTGTGACG TGT  CG
                                     A   TT
GAM260  FLJ20507 3' CTGCAGGCTGCCTGCTATGTGA 35282    TG  _ T_  T_   TG
            TGCCT                CAT  TAT GT  GC  TCTG  G
                                |||  ||| ||  ||  |||| |
                                GTA  GTA CG  CG  GGAC  C
                                  GT   T  TC  TC    GT
GAM260  FLJ20507 3' CTGCAGGCTGCCTGCTATGTGA 60217    TG  _ T_  T_   TG
            TGCCT                CAT  TAT GT  GC  TCTG  G
                                |||  ||| ||  ||  |||| |
                                GTA  GTA CG  CG  GGAC  C
                                  GT   T  TC  TC    GT
GAM260  FLJ20508 3' CCGCAGGGGTGGGAGAATGCC  35306      GTATG TG
                                GGCATT    T  CTTCTGTGG
                                ||||||    | |||||||||
                                CCGTAA    G  GGGGACGCC
                                   GAG__ GT
GAM260  FLJ20511 3' CATAGAAGCAAAAGTAC    35321     G_
                                GTAT  TTGCTTCTGTG
                                ||||  ||||||||||
                                CATG  AACGAAGATAC
                                  AA
GAM260  FLJ20513 3' TGCATTAGTAAATGATGCCT   35335      TG ATG    TC  TG
                                GGGCAT  T   TTGCT  TG  G
                                |||||| |  ||||| ||  |
                                TCCGTA  A   AATGA  AC  T
                                   GT ___    TT  GT
GAM260  FLJ20527 3' CACATAACTTGCGGTGTTT   35352        T   CTTC
                                GGGCATTGTA GTTG   TGTG
                                |||||||||| ||||   ||||
                                TTTGTGGCGT CAAT   ACAC
                                     T  _____
GAM260  FLJ20533 3' TTATGGGAGCAGTTTTAAGTCT 35360     A  TATG
                                GGGC TTG   TTGCTTCTGTGG
                                |||| |||   ||||||||||||
                                TCTG AAT   GACGAGGGTATT
                                  _  TTT_
GAM260  FLJ20557 3' CGCAGGGAATGTGCCATGTCT  61897      T     G  T  TG
                                GGGCAT GTATGTT CT CTG  G
                                |||||| ||||||| || |||  |
                                TCTGTA CGTGTAA GG GAC  C
                                   C     _ _  GT
GAM260  FLJ20557 3' TTGCAGGAGCTCCTTTGCATGT 61898      T  TGTT_     TG
            TC                 GGGCAT GTA    GCTTCTG  G
                               ||||||| |||    ||||||| |
                               CTTGTA CGT    CGAGGAC  T
                                  _  TTCCT     GT
GAM260  FLJ20623 5' CGCGGAACGGTGATGCTC    35466      TG ATGT  C
                                GGGCAT  T   TG TTCTGTG
                                ||||||  |   || |||||||
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                                CTCGTA  G    GC AAGGCGC
                                   GT _____  _
GAM260   FLJ20624  3'  TTACTTTTGGCAGACAGTGTTT 90998         ATG    TCT_
                                GGGCATTGT   TTGCT    GTGG
                                |||||||||   |||||    ||||
                                TTTGTGACA   GACGG    CATT
                                     ___     TTTT
GAM260   FLJ20625  3'  GCGGCTTATACAGTACCC    35470     C      __
                                GGG ATTGTAT  GTTGC
                                ||| |||||||  |||||
                                CCC TGACATA  CGGCG
                                  A      TT
GAM260   FLJ20643  5'  CCACGGATTTGACGATGGTGTT 35489       TG A    CT
            C                    GGGCAT  T TGTTG  TCTGTGG
                                ||||||  | |||||  |||||||
                                CTTGTG  A GCAGT  AGGCACC
                                   GT _     TT
GAM260   FLJ20727  5'  GCAATGCAGACAATGCTC    35616         A  __
                                GGGCATTGT TGT  TGC
                                ||||||||| |||  |||
                                CTCGTAACA ACG  ACG
                                     G   TA
GAM260   FLJ20729  3'  CTGCAGAAGGGTGTTGTGATGA 35647    G   TG  TGTTG     TG
            CC                   GG CAT  TA    CTTCTG  G
                                || |||  ||    ||||||  |
                                CC GTA  GT    GAAGAC  C
                                 A   GT  TGTGG     GT
GAM260   FLJ20739  3'  CTGCAGCCAGACAGATGGTGCT 67856       TG A    GCTT   TG
            T                    GGGCAT  T TGTT    CTG  G
                                ||||||  | ||||    |||  |
                                TTCGTG  A ACAG    GAC  C
                                   GT G    ACC_   GT
GAM260   FLJ20753  3'  TCACGCCCCCGGCAGCGGTGTT 35634         A    CTTC
            T                    GGGCATTGT TGTTG    TGTGG
                                |||||||||  |||||    |||||
                                TTTGTGGCG ACGGC    GCACT
                                     _     CCCC
GAM260   FLJ20850  3'  CCATGGAGGCGATCAGCGAGGT 35722      A    AT
            TC                   GGGC TTGT  GTTGCTTCTGTGG
                                ||||  ||||  ||||||||||||||
                                CTTG AGCG  TAGCGGAGGTACC
                                  G    AC
GAM260   FLJ20856  5'  CATAGGAGTAACCGGCCC    47118      ATTGTAT
                                GGGC      GTTGCTTCTGTG
                                ||||      ||||||||||||
                                CCCG      CAATGAGGATAC
                                  GC_____
GAM260   FLJ20958  3'  TCACTTTTCAGCAAGTAATGTC 42062         TA    CTTCT
            T                    GGGCATTG  TGTTG    GTGG
                                ||||||||  |||||    ||||
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                                TCTGTAAT  ACGAC    CACT
                                    GA    TTTT_
GAM260  FLJ20967  5'  TCGTGGAAGCGCCCAAGTGCC  41966      GTAT  T    TG
                                GGCATT   GT GCTTC  TGG
                                ||||||   || |||||  |||
                                CCGTGA   CG CGAAG  GCT
                                   ACC_  _    GT
GAM260  FLJ20972  3'  TCAGTTTGTAGTTTGCAGTGCC 46729        TG   TT_  TGG
          C                      GGGCATTGTA  TTGC   CTG
                                ||||||||||  ||||   |||
                                CCCGTGACGT  GATG   GAC
                                     TT    TTT   T
GAM260  FLJ21106  3'  CTGTGGAATAATTTAGCAATGT 46996        AT_   C    TG
          TT                     GGGCATTGT   GTTG TTCTG  G
                                |||||||||   |||| |||||  |
                                TTTGTAACG   TAAT AAGGT  C
                                     ATT   _    GT
GAM260  FLJ21195  5'  CAGGAGCAGCCAGCCT     42449     AT  TAT
                                GGGC  TG   GTTGCTTCTG
                                ||||  ||   ||||||||||
                                TCCG  AC   CGACGAGGAC
                                  __ ___
GAM260  FLJ21272  3'  CTATAGAGGCTGGAACAGGCTC 46736     A    ATGTT
                                GGGC TTGT    GCTTCTGTGG
                                |||| ||||    ||||||||||
                                CTCG GACA    CGGAGATATC
                                  _   AGGT_
GAM260  FLJ21324  5'  GGGGCAGCAGTGTCC      91208        ATGT
                                GGGCATTGT   TGCTTC
                                |||||||||   ||||||
                                CCTGTGACG   ACGGGG
                                     ____
GAM260  FLJ21369  3'  TAGGGGTGAGGTGACCC     45638    _   GTATG TG
                                GGG CATT    T  CTTCTG
                                ||| ||||    |  ||||||
                                CCC GTGG    A  GGGGAT
                                  A   _____ GT
GAM260  FLJ21432  3'  CGGAATGTACAGTGTCT     44633          TGCT
                                GGGCATTGTATGT   TCTG
                                ||||||||||||    ||||
                                TCTGTGACATGTA   AGGC
                                     ____
GAM260  FLJ21438  5'  CCACGCTTCACTTGCGGTGCCT 61518         T  TGCTTC
                                GGGCATTGTA GT    TGTGG
                                |||||||||| ||    |||||
                                TCCGTGGCGT CA    GCACC
                                     T  CTTC__
GAM260  FLJ21588  3'  CAGAACACACAGTGCCT     49832         A   TGCT
                                GGGCATTGT TGT   TCTG
                                |||||||| |||   ||||
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                                TCCGTGACA ACA    AGAC
                                     C  ____
GAM260  FLJ21596 3' TGCTCAGTGACGTGCAGGTTT 45704     A      TG  TCT TG
                                GGGC TTGTATGT  CT   G  G
                                |||| ||||||||  ||   |  |
                                TTTG GACGTGCA  GA   C  T
                                  _      GT  CT_ GT
GAM260  FLJ21791 3' TTGCAGAAGTGGTGTAGTTC  61441     ATTG  TG TG     TG
                                GGGC    TA  T  CTTCTG  G
                                ||||    ||  |  ||||||  |
                                CTTG    AT  G  GAAGAC  T
                                  ____  GT GT     GT
GAM260  FLJ21939 5' CGTGGAAGCGGCGGTGTCT   42410         ATGT      TG
                                GGGCATTGT    TGCTTCTG  G
                                |||||||||    ||||||||  |
                                TCTGTGGCG    GCGAAGGT  C
                                     ____       GT
GAM260  FLJ21939 3' TGCAGAGGTCTTCAGTATCT  42412    GC    TATGTT     TG
                                GG  ATTG     GCTTCTG  G
                                ||  ||||     |||||||  |
                                TC  TGAC     TGGAGAC  T
                                 TA    TTC___      GT
GAM260  FLJ21940 3' CGTGGAAGAACATCATGCCT  43080       T T    G     TG
                                GGGCAT G ATGTT CTTCTG  G
                                |||||| | ||||| ||||||  |
                                TCCGTA C TACAA GAAGGT  C
                                   _ _    _     GT
GAM260  FLJ21940 3' TTATAGAGAATGATTATATGAT 43082      TG    TTGC__
           GTTT                  GGCAT  TATG     TTCTGTGG
                                |||||  ||||     ||||||||
                                TTGTA  ATAT     GAGATATT
                                   GT    TAGTAA
GAM260  FLJ21952 5' CCGCCCCGGATATGCGATGGCT 42556    G         GCTTCT
                                GG CATTGTATGTT     GTGG
                                || ||||||||||      ||||
                                TC GTAGCGTATAG     CGCC
                                 G         GCCC__
GAM260  FLJ22028 3' TTACAGAAGTGATAATGAT   45853    TG A   TG
                                AT  T TGT  CTTCTGTGG
                                ||  | |||  |||||||||
                                TA  A ATA  GAAGACATT
                                 GT _   GT
GAM260  FLJ22031 3' CCACACTTTCAAATATAGTGTC 46887          G   CTTC
           C                     GGGCATTGTAT TTG    TGTGG
                                ||||||||||| |||    |||||
                                CCTGTGATATA AAC    ACACC
                                      _  TTTC
GAM260  FLJ22054 3' GTAATATTAATGCTT      94400         T
                                GGGCATTG ATGTTGC
                                |||||||| |||||||
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                                TTCGTAAT TATAATG
                                        _
GAM260  FLJ22056 3' AATCAAAATGCAATGCTT    42532          G  C
                                GGGCATTGTAT TTG TT
                                |||||||||| ||| ||
                                TTCGTAACGTA AAC AA
                                      A  T
GAM260  FLJ22059 5' CAGAGGTGCCTGTGTCT     42766       T_ ATGTT
                                GGGCAT  GT    GCTTCTG
                                ||||||  ||    |||||||
                                TCTGTG  CG    TGGAGAC
                                   TC  _____
GAM260  FLJ22169 3' TCACAGATCCTGGCACAGTGCC 44007         AT   CT_
          C                     GGGCATTGT  GTTG   TCTGTGG
                                |||||||||  ||||   |||||||
                                CCCGTGACA  CGGT   AGACACT
                                     __   CCT
GAM260  FLJ22202 3' CGTAGGAGGGACAGTAC     45989    _   G
                                GTA TGTT CTTCTGTG
                                ||| |||| ||||||||
                                CAT ACAG GAGGATGC
                                  G   G
GAM260  FLJ22282 3' CCGCAGAAGCAAGGGATGACTT 45588    _   GTATG
                                GGG CATT    TTGCTTCTGTGG
                                ||| ||||    ||||||||||||
                                TTC GTAG    AACGAAGACGCC
                                  A   GG___
GAM260  FLJ22282 3' CGCAGAGTACTTGAGTGCTT   45590       G  T  T   T   TG
                                GGGCATT TA GT GCT CTG  G
                                ||||||| || || ||| |||  |
                                TTCGTGA GT CA TGA GAC  C
                                   _  T  _   _   GT
GAM260  FLJ22378 3' CCGCAGGAGACCCTGTAAGGCC 46897     ATTG  GTTG_
          T                     GGGC   TAT    CTTCTGTGG
                                ||||   |||    |||||||||
                                TCCG   ATG    GAGGACGCC
                                  GA__   TCCCA
GAM260  FLJ22378 3' CGCAGGGGCAGTGACTGCT   46898     TT  ATG       TG
                                GGCA  GT   TTGCTTCTG  G
                                ||||  ||   |||||||||  |
                                TCGT  CA   GACGGGGAC  C
                                  __  GT_       GT
GAM260  FLJ22393 3' TCACAGAAGCCAGCGCGGGTCT 47064     A   AT   _
                                GGGC TTGT  GTTG CTTCTGTGG
                                |||| ||||  |||| |||||||||
                                TCTG GGCG  CGAC GAAGACACT
                                  _   __   C
GAM260  FLJ22494 5' CGTGGAGGAGCGGGGCCC    45674     ATTGTA   G   TG
                                GGGC     TGTT CTTC  TG
                                ||||     |||| ||||  ||
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                                CCCG     GCGA GGAG  GC
                                  GG____   _    GT
GAM260  FLJ22501  5' CTGCAGGAGGCACCTGTAGGCC 45369     A    T  T    _  TG
             C                   GGGC TTGTA GT GCTTC TG  G
                                 |||| ||||| || ||||| ||  |
                                 CCCG GATGT CA CGGAG AC  C
                                   _    C  _    G  GT
GAM260  FLJ22529  3' TTATAGGAGCGTGCCATCATGC 45580      T T   T__
             CC                    GGGCAT G ATG   TGCTTCTGTGG
                                   |||||| | |||   ||||||||||
                                   CCCGTA C TAC   GCGAGGATATT
                                     _ _  CGT
GAM260  FLJ22551  3' CTTGGTAAGCGATGCCT    45238        ATG    TCT
                                 GGGCATTGT   TTGCT   G
                                 |||||||||   |||||  |
                                 TCCGTAGCG   AATGG   C
                                      ___    TT_
GAM260  FLJ22578  3' TCACAGGGTTGTTGTGAGGCTC 45876     A TG  TGTT   T
                                 GGGC T  TA    GCT CTGTGG
                                 |||| |  ||    ||| ||||||
                                 CTCG A  GT    TGG GACACT
                                   G GT  TGT_  _
GAM260  FLJ22671  3' CCATGGGAGGCTCCTGGGATGT 45864       G  TGTT    _
             TT                    GGGCATT TA    GCTTCT GTGG
                                   ||||||| ||    |||||| ||||
                                   TTTGTAG GT    CGGAGG TACC
                                      G  CCT_    G
GAM260  FLJ22679  5' TGCAGGAGTAAGAGATCCC   49924    C  GTATG      TG
                                 GGG ATT    TTGCTTCTG  G
                                 ||| |||    |||||||||  |
                                 CCC TAG    AATGAGGAC  T
                                   _  AG___       GT
GAM260  FLJ22684  3' CTACAGGAGATATGATGCCT   46790      TG   GTTG
                                 GGGCAT  TAT    CTTCTGTGG
                                 ||||||  |||   |||||||||
                                 TCCGTA  ATA    GAGGACATC
                                    GT  _____
GAM260  FLJ22938  3' TGTGGGGGCGGGTATGTCT   45165      TGTATG      TG
                                 GGGCAT     TTGCTTCTG  G
                                 ||||||     |||||||||  |
                                 TCTGTA     GGCGGGGGT  T
                                    TG____       GT
GAM260  FLJ22944  3' CTGTAGCTTGTGGCATGTGATC 47124    C  TG    TG TT_  TG
             CT                    GGG AT  TATGT  C   CTG  G
                                   ||| ||  |||||  |   |||  |
                                   TCC TA  GTACG  G   GAT  C
                                   _ GT    GT TTC   GT
GAM260  FLJ23129  3' ATGTACGGAGCAACAGTAATGT 45427       GTA     T    G
             TC                    GGGCATT   TGTTGCT CTGTG
                                   |||||||   ||||||| |||||
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                                CTTGTAA   ACAACGA GGCAT
                                   TG_      _    GTAA
GAM260  FLJ23132  3' CCACAGCCAATTGTGTGTGCTC 96135      TGTAT   CTT
                                GGGCAT    GTTG   CTGTGG
                                ||||||    ||||  ||||||
                                CTCGTG    TAAC   GACACC
                                   TGTGT   C__
GAM260  FLJ23132  3' GGCAGCATAAAGTGTTT    96136       G
                                GGGCATT TATGTTGCT
                                ||||||| |||||||||
                                TTTGTGA ATACGACGG
                                   A
GAM260  FLJ23132  3' GGCTGCAATTCTGTTTGCAGTG 96137       T_____    TTCTGTGG
           CTT                    CATTGTA     GTTGC
                                |||||||     |||||
                                GTGACGT     TAACG
                                   TTGTCT    TC   GGT
GAM260  FLJ23153  3' CTATAGAGCTGGCATGTAATTC 44926     C        _  T
           TT                    GGG ATTGTATGTT GCT CTGTGG
                                ||| |||||||||| ||| ||||||
                                TTC TAATGTACGG CGA GATATC
                                  T        T  _
GAM260  FLJ23306  3' CTGCATCCCTTGGCTGTGATGC 44557      TG  T   GCTTC_  TG
           CC                    GGGCAT  TA GTT     TG  G
                                ||||||  || |||     ||  |
                                CCCGTA  GT CGG     AC  C
                                   GT  _   TTCCCT  GT
GAM260  FLJ23323  3' TCATGGCCATGAATGGTGCCC  45056      TG A   T   TCT
                                GGGCAT  T TGT GCT   GTGG
                                ||||||  | ||| |||   ||||
                                CCCGTG  A GTA CGG   TACT
                                   GT A   C   ___
GAM260  FLJ23403  3' CTACAATGCAATATACAGCGCT 41953      A        TTC
           C                     GGGC TTGTATGTTGC   TGTGG
                                ||||  ||||||||||   |||||
                                CTCG GACATATAACG   ACATC
                                  C         TA_
GAM260  FLJ23462  3' AACACTTAAGTAGCATACACTG 45799      T        CT   G
           CCC                    GGGCA TGTATGTTGCTT  GTG
                                |||||  ||||||||||||  |||
                                CCCGT ACATACGATGAA  CAC
                                   C          TT   AAC
GAM260  FLJ23468  5' GCACATTTGGTGTCC      44908        T   T
                                GGGCATTG ATGT GC
                                |||||||| |||| ||
                                CCTGTGGT TACA CG
                                    T   _
GAM260  FLJ23510  3' CGTGGGGCATGCAAGCCT    45282      A      TGCT  TG
                                GGGC TTGTATGT    TC  TG
                                |||| ||||||||    ||  ||
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                                TCCG AACGTACG   GG  GC
                                  _      ____  GT
GAM260  FLJ23510  3'  TTATAGAAGAGCTACCAGATGG 45291    TG AT____   G
              TGTTC                 AT  T     GTT CTTCTGTGG
                                ||  |     ||| |||||||||
                                TG  A     CGA GAAGATATT
                                 GT GACCAT  _
GAM260  FLJ23560  3'  TCATGGACAAGGACAGTGTTT  45192        ATG   CT
                                GGGCATTGT   TTG  TCTGTGG
                                |||||||||   |||  |||||||
                                TTTGTGACA   AAC  AGGTACT
                                     GG_  __
GAM260  FLJ23563  3'  TTACAGGGGTGAGCCACTGTGC 67604       T  ATG TG
              CC                  GGGCAT GT   T  CTTCTGTGG
                                ||||||  ||   |  |||||||||
                                CCCGTG CA   A  GGGGACATT
                                    T  CCG GT
GAM260  FLJ30791  5'  AGGAGTGGCGTGTGGGTCT   58444     A TG    TG
                                GGGC T  TATGT  CTTCT
                                ||||  |  |||||  |||||
                                TCTG G  GTGCG  GAGGA
                                  _ GT    GT
GAM260  FLJ31121  3'  TTGCAGAGGTAATGCTGTGGC  58540    ATT_  AT       TG
                                GC   GT  GTTGCTTCTG  G
                                ||   ||  ||||||||||  |
                                CG   CG  TAATGGAGAC  T
                                 GTGT  __        GT
GAM260  FLJ31709  3'  AGTCAGGTGCAATGTTC     58270          GTT
                                GGGCATTGTAT   GCT
                                ||||||||||   |||
                                CTTGTAACGTG   TGA
                                      GAC
GAM260  FLJ31762  5'  CAGATGTGCGTGCCT      58140       T    TTGCT
                                GGGCAT GTATG    TCTG
                                ||||||  |||||    ||||
                                TCCGTG CGTGT    AGAC
                                  _    ______
GAM260  FLJ31890  3'  TCATAGAAGCAACATGGCATAG 91341     AT  _
              TT                  GGC  TGT ATGTTGCTTCTGTGG
                                |||  ||| ||||||||||||||||
                                TTG  ACG TACAACGAAGATACT
                                  AT   G
GAM260  FLJ31952  3'  CCATAGGAGAAGCAGTTGTTT  58383      TTGTA   G
                                GGGCA    TGTT CTTCTGTGG
                                |||||    |||| |||||||||
                                TTTGT    ACGA GAGGATACC
                                   TG___   A
GAM260  FLJ31978  3'  TCACATGAGGACGTGCAGTCTT 58351     C        G   C
                                GGG ATTGTATGTT CTT TGTGG
                                ||| |||||||||| ||| |||||
```

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                                TTC TGACGTGCAG GAG ACACT
                                  _       _  T
GAM260  FLJ32334  3'  CTGCTTCCCGGCCTGCGATGTC 57983        T   CTTCT TG
            C                    GGGCATTGTA GTTG    G  G
                                ||||||||||  ||||    |  |
                                CCTGTAGCGT CGGC    C  C
                                     C   CCTT_ GT
GAM260  FLJ32421  5'  TTGTGGACTCCGATATATTGCC 58450     TT      CT_   TG
            C                    GGGCA  GTATGTTG   TCTG  G
                                |||||  ||||||||   ||||  |
                                CCCGT  TATATAGC   AGGT  T
                                  __      CTC   GT
GAM260  FLJ32430  5'  CTGCAACGCGCAGCGTGCCAGT 58322       _      TTC_  TG
            GCCC                   GGCATTG TATGTTGC    TG  G
                                ||||||| ||||||||   ||  |
                                CCGTGAC GTGCGACG    AC  C
                                    C       CGCA  GT
GAM260  FLJ32452  3'  TCGTAGGAGCACCATATGCCT  58018     TTG   T
                                GGGCA   TATG TGCTTCTGTGG
                                |||||   |||| ||||||||||
                                TCCGT   ATAC ACGAGGATGCT
                                  ____   C
GAM260  FLJ32745  3'  TAATATAGTATATGTGGTGCTT 58676      TG    T  TCTGTGG
                                GGGCAT  TATGT GCT
                                ||||||  ||||| |||
                                TTCGTG  GTATA TGA
                                   GT    _  TATAATT
GAM260  FLJ32783  3'  GCATAGTACAGTGTCT     58645         GT
                                GGGCATTGTAT  TGC
                                ||||||||||  |||
                                TCTGTGACATG  ACG
                                      AT
GAM260  FLJ32884  5'  CTACAGAGGAGTACCAGTGCTC 58458       TAT  TG_
                                GGGCATTG   GT   CTTCTGTGG
                                ||||||||   ||   |||||||||
                                CTCGTGAC   CA   GGAGACATC
                                     ___  TGA
GAM260  FOXH1    5'  TTGTGGAAGCCCTCGGCATGCT 14075      T  ATGTT     TG
            C                    GGGCAT GT    GCTTCTG  G
                                ||||||  ||    |||||||  |
                                CTCGTA CG    CGAAGGT  T
                                   _  GCTCC      GT
GAM260  FOXP1    3'  TCATAGAAGATATCATGTAGGC 51070     A     TTG_
            CC                     GGGC TTGTATG    CTTCTGTGG
                                ||||  |||||||    |||||||||
                                CCCG GATGTAC    GAAGATACT
                                  _      TATA
GAM260  FREQ     3'  TCACGGAGGCTTCCAGCGGTGC 26584        ATGTT
            CT                     GGGCATTGT    GCTTCTGTGG
                                |||||||||    ||||||||||
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                                TCCGTGGCG    CGGAGGCACT
                                     ACCTT
GAM260  FSCN3    5'  CACAGAGGTGCTGGGCCC    39804     ATT  ATGTT
                                GGGC   GT    GCTTCTGTG
                                ||||   ||    |||||||||
                                CCCG   CG    TGGAGACAC
                                  GGT  _____
GAM260  FUK      5'  GGTCACATCCGATGTCC     58976        T    T
                                GGGCATTG ATGT GCT
                                |||||||| |||| |||
                                CCTGTAGC TACA TGG
                                     C    C
GAM260  FUSIP1   3'  CCATAGTCTCTTACAGTGCCT  21773         TGTTGCTT
                                GGGCATTGTA       CTGTGG
                                ||||||||||       ||||||
                                TCCGTGACAT       GATACC
                                     TCTCT___
GAM260  FXYD3    3'  CTACCCTTAATAACATACAATG 19924    G         CTTCT_
           ACC                    GG CATTGTATGTTG     GTGG
                                || ||||||||||||     ||||
                                CC GTAACATACAAT     CATC
                                 A          AATTCC
GAM260  FXYD3    3'  CTACCCTTAATAACATACAATG 41584    G         CTTCT_
           ACC                    GG CATTGTATGTTG     GTGG
                                || ||||||||||||     ||||
                                CC GTAACATACAAT     CATC
                                 A          AATTCC
GAM260  GAB3     3'  TCATGGTCACCTATACAGTGT  54635         TTGCTT
                                GCATTGTATG     CTGTGG
                                ||||||||||     ||||||
                                TGTGACATAT     GGTACT
                                     CCACT_
GAM260  GABARAPL3 3'  TCACAGGAATGCTATGTGATGG 50804    G   TG    T GC
           CC                     GG CAT  TATG T  TTCTGTGG
                                || |||  |||| |  ||||||||
                                CC GTA  GTAT G  AGGACACT
                                 G   GT    C TA
GAM260  GABBR1   3'  CTATGGGGTGGGAGGTGGTGTC 41573       TG ATG TG    T
           C                      GGGCAT  T   T  CTTC GTGG
                                ||||||  |   |  |||| ||||
                                CCTGTG  G   G  GGGG TATC
                                   GT GAG GT   _
GAM260  GABBR1   3'  CTATGGGGTGGGAGGTGGTGTC 7608        TG ATG TG    T
           C                      GGGCAT  T   T  CTTC GTGG
                                ||||||  |   |  |||| ||||
                                CCTGTG  G   G  GGGG TATC
                                   GT GAG GT   _
GAM260  GAL3ST2  5'  CCGCAGGATCCCCCATGAGTGC 52312        G    TTGC_
           CT                     GGGCATT TATG    TTCTGTGG
                                |||||||  ||||    ||||||||
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                                TCCGTGA GTAC    AGGACGCC
                                   _   CCCCT
GAM260  GALNT12  5' CGGACAGTTTACAGTGTCC   44973        TG  CT
                                GGGCATTGTA  TTG  TCTG
                                ||||||||||  |||  ||||
                                CCTGTGACAT  GAC  AGGC
                                     TT  __
GAM260  GAPCENA  3' TTACGGGAGCTGTGGACAGAGC 24163     A   ATGTT
           TC                    GGGC TTGT    GCTTCTGTGG
                                ||||| ||||    ||||||||||
                                CTCG GACA    CGAGGGCATT
                                  A   GGTGT
GAM260  GBTS1    3' CCACAGGGCCTGCAGCAGTGCC 59051        A  T_  T
           C                     GGGCATTGT TGT  GCT CTGTGG
                                |||||||||| |||  ||| ||||||
                                CCCGTGACG ACG  CGG GACACC
                                     _  TC  _
GAM260  GCHFR    3' TGGAGGGGCTGCTGTGGGCCC  17924     A TG  T  T    GTGG
                                GGGC T  TA GT GCTTCT
                                ||||| |  || || ||||||
                                CCCG G  GT CG CGGGGA
                                  _ GT  _  T     GGTG
GAM260  GENX-3414 3' TGCAGAAATATATATGTCT   14151       T      GCT
                                GGGCAT GTATGTT   TCTGTG
                                ||||||| |||||||   ||||||
                                TCTGTA TATATAA   AGACGT
                                   _     ____
GAM260  GIT2     3' CTGCAGGAGGTGAAGCAGTGTT 54081        ATG TG   _  TG
           T                     GGGCATTGT   T  CTTC TG  G
                                |||||||||   |  |||| ||  |
                                TTTGTGACG   A  GGAG AC  C
                                     A__ GT   G  GT
GAM260  GIT2     3' CTGCAGGAGGTGAAGCAGTGTT 54094        ATG TG   _  TG
           T                     GGGCATTGT   T  CTTC TG  G
                                |||||||||   |  |||| ||  |
                                TTTGTGACG   A  GGAG AC  C
                                     A__ GT   G  GT
GAM260  GIT2     3' CTGCAGGAGGTGAAGCAGTGTT 28759        ATG TG   _  TG
           T                     GGGCATTGT   T  CTTC TG  G
                                |||||||||   |  |||| ||  |
                                TTTGTGACG   A  GGAG AC  C
                                     A__ GT   G  GT
GAM260  GK001    5' TCGCGGAGGCGGCGGCCAGGCC 39500     A   TA
                                GGC TTG  TGTTGCTTCTGTGG
                                ||| |||  ||||||||||||||
                                CCG GAC  GCGGCGGAGGCGCT
                                  _  CG
GAM260  GL004    3' TGTAGAAGTAAAGGTATA    65995      G_       TG
                                TGTAT  TTGCTTCTG  G
                                |||||  |||||||||  |
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                                ATATG  AATGAAGAT  T
                                   GA       GT
GAM260  GLCCI1   3'  TGTGGAAAGCAGTAATGCTT  92584       TATG    _  TG
                                GGGCATTG   TTGCTT CTG  G
                                ||||||||   |||||| |||  |
                                TTCGTAAT   GACGAA GGT  T
                                     ____     A   GT
GAM260  GLIS2    3'  GAAATAGCAATAATGTCC    50816        A    C
                                GGGCATTGT TGTTG TTC
                                ||||||||| ||||| |||
                                CCTGTAATA ACGAT AAG
                                     _    A
GAM260  GLIS2    3'  CGCGGACAGTTGTGGTGCCC  50815      TG  TGTT  _   TG
                                GGGCAT  TA   GCT TCTG  G
                                ||||||  ||   ||| ||||  |
                                CCCGTG  GT   TGA AGGC  C
                                   GT  ____  C   GT
GAM260  gm117    3'  TCACATGTTGACATGCCAATGT 78845       _    GCTTC
           TC                    GGGCATTG TATGTT    TGTGG
                                ||||||||| ||||||    |||||
                                CTTGTAAC GTACAG    ACACT
                                    C     TTGT_
GAM260  GMPPB    5'  CAGAAGAAGCAGTCC      95725     ATTGTA   G
                                GGGC     TGTT CTTCTG
                                ||||     |||| ||||||
                                CCTG     ACGA GAAGAC
                                  _______   A
GAM260  GMPPB    3'  CTGTGGAAGTGGCTGTGTTC  95735      TGTAT  TG    TG
                                GGGCAT    GT  CTTCTG  G
                                ||||||    ||  ||||||  |
                                CTTGTG    CG  GAAGGT  C
                                   T____  GT    GT
GAM260  GNG4     3'  CGTAGAGACCATGCATGCTC  15613      T    TTG  T   TG
                                GGGCAT GTATG   CT CTG  G
                                |||||| |||||   || |||  |
                                CTCGTA CGTAC   GA GAT  C
                                   _    CA_ _   GT
GAM260  GOLGA1   3'  CCACAGAAGCCCGTCCGCTGCC 9088      T  T   TT
           T                     GGGCA TG ATG  GCTTCTGTGG
                                ||||| || |||  ||||||||||
                                TCCGT GC TGC  CGAAGACACC
                                   C  C   C_
GAM260  GOLGIN-67 3'  GCAGCATGGATGTCC      94977       G
                                GGGCATT TATGTTGC
                                ||||||| ||||||||
                                CCTGTAG GTACGACG
                                     _
GAM260  GPR64    3'  CCACAGTTAGCTCATACAGTGC 19246          TT   T_
           CT                    GGGCATTGTATG  GCT  CTGTGG
                                ||||||||||||  |||  ||||||
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                                TCCGTGACATAC  CGA  GACACC
                                      T_   TT
GAM260  GRID1    3'  TCATGGAGAAATACAAAGTCC  68502      A     GTTG    T
                                GGGC TTGTAT    CTTC GTGG
                                |||| ||||||    |||| ||||
                                CCTG AACATA    GAGG TACT
                                  A     AA__    _
GAM260  GRIN3A   5'  TCGCGGGGCCGGACGCAGTGCC 55973          ATG   C
           C                     GGGCATTGT   TTG TTCTGTGG
                                |||||||||   ||| ||||||||
                                CCCGTGACG   GGC GGGGCGCT
                                     CA_   C
GAM260  GRP3     3'  CCATGGAAGAAAATTATGCTT  31117        TGTATGTTG
                                GGGCAT        CTTCTGTGG
                                ||||||        |||||||||
                                TTCGTA        GAAGGTACC
                                   TTAAAA___
GAM260  GTF2A2   5'  CCACAGGACATCAATGCAAGCT 15676      A     GT_  C
           T                     GGGC TTGTAT   TG TTCTGTGG
                                |||| ||||||   || ||||||||
                                TTCG AACGTA   AC AGGACACC
                                  _     ACT  _
GAM260  GTPBP5   3'  TCGTGGGAGGATCATGTGAGCC 65362      A TG    TTG    TG
           T                     GGGC T  TATG   CTTC  TGG
                                |||| |  ||||   ||||  |||
                                TCCG A  GTAC   GAGG  GCT
                                  _ GT    TAG    GT
GAM260  GW112    5'  CCGTGGGACCTGCCAGTGCTC  21186        TAT  TGC   TG
                                GGGCATTG   GT   TTC  TGG
                                ||||||||   ||   |||  |||
                                CTCGTGAC   CG   AGG  GCC
                                     ___  TCC   GT
GAM260  GW112    3'  CTGCATCTTATGCATTACAATG 21187          _   TGCTTC  TG
           TCT                     GGGCATTGTA TGT     TG  G
                                |||||||||| |||     ||  |
                                TCTGTAACAT ACG     AC  C
                                     T   TATTCT  GT
GAM260  H11      3'  AAAATGGGTGATATACAGGTCT 26845      A       TG   CTGTGG
                                GGGC TTGTATGT  CTT
                                |||| ||||||||  |||
                                TCTG GACATATA  GGG
                                  _       GT   TAAAAT
GAM260  H11      3'  CCACATAAAAACAAACAGTGCC 26848          A    GC  C
           T                     GGGCATTGT TGTT  TT TGTGG
                                |||||||| ||||  || |||||
                                TCCGTGACA ACAA  AA ACACC
                                     A    A_  T
GAM260  H2AFA    3'  TGGAATACACATACGATGCCT  40739            TGC
                                GGGCATTGTATGT   TTCTG
                                ||||||||||||   |||||
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                                TCCGTAGCATACA  AAGGT
                                      CAT
GAM260  HAND1   3'  TGGATCGCACGTGCAATGTCC  16688          T  T_
                                GGGCATTGTATGT GC  TCTG
                                |||||||||||| ||  ||||
                                CCTGTAACGTGCA CG  AGGT
                                      _  CT
GAM260  HARC    3'  GCACAAATGCAATGTTT    35484          GT_
                                GGGCATTGTAT  TGC
                                ||||||||||  |||
                                TTTGTAACGTA  ACG
                                      AAC
GAM260  HBOA    3'  GTGGGCAGTGGGCAGTGGGCAG 22968        A GT   _   GG
           TGTCT                 GGCATTGT T  TGCTT CTGT
                                |||||||| |  ||||| ||||
                                CTGTGACG G  ACGGG GACG
                                    G TG    T   GGTGT
GAM260  HBOA    3'  TTGCAGGTGCCAAAGTAATGTC 22970        TATGTT  T   TG
            C                    GGGCATTG    GC TCTG  G
                                |||||||     || ||||  |
                                CCTGTAAT    CG GGAC  T
                                    GAAAC_  T   GT
GAM260  HCA4    3'  CTACATTTGTGTATAGTGCTT  77584         GTT  TTC
                                GGGCATTGTAT  GC  TGTGG
                                ||||||||||  ||  |||||
                                TTCGTGATATG  TG  ACATC
                                     ___  TTT
GAM260  HCA4    3'  TGCAGGCATTGTACAGTACTT  77594    C    GT   TT   TG
                                GGG ATTGTAT  TGC  CTG  G
                                ||| |||||||  |||  |||  |
                                TTC TGACATG  ACG  GAC  T
                                  A     TT  __  GT
GAM260  HCRTR1  5'  TAGAGCCTAGGATGCCC    7728        G  TGTT   T
                                GGGCATT TA   GCT CTG
                                ||||||| ||   ||| |||
                                CCCGTAG AT   CGA GAT
                                    G  C___  _
GAM260  HES6    3'  CGCGGGGGTGGGCCCGGCCC  37836     ATT  ATG TG    TG
                                GGGC  GT  T  CTTCTG  G
                                ||||  ||  |  ||||||  |
                                CCCG  CG  G  GGGGGC  C
                                  GCC  ___ GT    GT
GAM260  HEYL    3'  CCATCCTCCAGGCGTGTGGTCC 27393    C  TG    GCTTCT
            C                    GGG AT  TATGTT    GTGG
                                ||| ||  ||||||    ||||
                                CCC TG  GTGCGG    TACC
                                  _  GT    ACCTCC
GAM260  HHLA3   3'  TACAGATCAAACAATGCTT   22983        ATG  CT
                                GGGCATTGT  TTG  TCTGTG
                                |||||||||  |||  ||||||
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                                TTCGTAACA   AAC  AGACAT
                                    ___   T_
GAM260  HIC     3'  AGTTACAGGCGGTGTCC     67446         A   T
                                GGGCATTGT TGT GCT
                                ||||||||| ||| |||
                                CCTGTGGCG ACA TGA
                                    G   T
GAM260  HIC     3'  CGTGGGGACAGATACAATTCC  67448     C     G   CT    TG
                                GGG ATTGTAT TTG  TCTG  G
                                ||| ||||||| |||  ||||  |
                                CCT TAACATA GAC  GGGT  C
                                  _     _  AG   GT
GAM260  HIC2    3'  CCGCGGGGGCCACCGCAGGGCC 65259     A    AT  T
            T                    GGGC TTGT  GT GCTTCTGTGG
                                ||||| ||||  || ||||||||||
                                TCCG GACG  CA CGGGGGCGCC
                                  G   C_ C
GAM260  HIP-55  3'  CGCAGGCCCCAGTGTGTGCCT  25929       TGT TG   CT_   TG
                                GGGCAT   A  TTG   TCTG  G
                                ||||||   |  |||   ||||  |
                                TCCGTG   T  GAC   GGAC  C
                                   ___ GT   CCC    GT
GAM260  HN1L    3'  TCATGGAAGATTGTTTTGGTGC 58004         TATGTTG
            CC                   GGGCATTG      CTTCTGTGG
                                ||||||||      |||||||||
                                CCCGTGGT      GAAGGTACT
                                    TTTGTTA
GAM260  HNRPA3  3'  TCACAGAAGGAACGATGATCC  19260    C  TG A    G
                                GG AT  T TGTT CTTCTGTGG
                                || ||  | |||| |||||||||
                                CC TA  A GCAA GAAGACACT
                                 _ GT _    G
GAM260  HNRPAB  3'  AGGCAGCGTGTGGTGTCT    48374       TG
                                GGGCAT  TATGTTGCTT
                                ||||||  ||||||||||
                                TCTGTG  GTGCGACGGA
                                   GT
GAM260  HRI     3'  CCGCAGAAATTGATGTGTGCTC 26980       TGT    GC_
                                GGGCAT   ATGTT   TTCTGTGG
                                ||||||   |||||   ||||||||
                                CTCGTG   TGTAG   AAGACGCC
                                   ___     TTA
GAM260  HRI     3'  TCACGGTAGATGGCGTATGAT  26987    TG      _ T
                                AT  TATGTTG CT CTGTGG
                                ||  ||||||| || ||||||
                                TA  ATGCGGT GA GGCACT
                                 GT      A  T
GAM260  HRIHFB2122 3'  CTGCAGAGCCTGTGTGTGAGTC 56836      A TG  TG T_   T   TG
            C                    GGGC T  TA  T  GCT CTG  G
                                |||| |  ||  |  ||| |||  |
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                                CCTG A  GT  G  CGA GAC  C
                                  _ GT  GT TC  _  GT
GAM260  HS322B1A  3'  CCATGGCAGCCAACTATAATGT 31110         T   _  T
            CT                    GGGCATTGTA GTTG CT CTGTGG
                                  |||||||||| |||| || ||||||
                                  TCTGTAATAT CAAC GA GGTACC
                                       _   C  C
GAM260  HS322B1A  3'  GCAGGATAAGATGTTC     31112       G   G
                                  GGGCATT TAT TTGC
                                  ||||||| ||| ||||
                                  CTTGTAG ATA GACG
                                      A   G
GAM260  HSA277841 3'  GCAGGAGCTGGCGCCC     37658     ATT  ATGTT
                                  GGGC   GT    GCTTCTGT
                                  ||||   ||    ||||||||
                                  CCCG   CG    CGAGGACG
                                    ___  GT___
GAM260  HSPB7     3'  GGCCTGACACATGATGCCC   27029      TG A   __
                                  GGGCAT  T TGTT  GCT
                                  ||||||  | ||||  |||
                                  CCCGTA  A ACAG  CGG
                                     GT C    TC
GAM260  HSPBP1    3'  CGCAGGGCCTAGGTGCCT    24359       GTATGTT   T
                                  GGGCATT      GCT CTGTG
                                  |||||||      ||| |||||
                                  TCCGTGG      CGG GACGC
                                      ATC____   _
GAM260  HSPBP1    5'  CGTAGGAGCAGCGGCGGCTT  24360     ATTGTA        TG
                                  GGGC     TGTTGCTTCTG  G
                                  ||||     ||||||||||| |
                                  TTCG     GCGACGAGGAT  C
                                    GCG___         GT
GAM260  HSPC009   3'  CACATGGTGGATGATGCCC   25828       TG ATG TG  TC
                                  GGGCAT  T   T  CT  TGTG
                                  ||||||  |   |  ||  ||||
                                  CCCGTA  A   G  GG  ACAC
                                     GT ___ GT  T_
GAM260  HSPC055   5'  GGAGTAGCTTGCAGTGTCT   26269         T
                                  GGGCATTGTA GTTGCTTC
                                  |||||||||| ||||||||
                                  TCTGTGACGT CGATGAGG
                                        T
GAM260  HSPC129   3'  AGTGGCGTGTAATCTCC     33068     C       TG
                                  GGG ATTGTATGT  CT
                                  ||| |||||||||  ||
                                  CCT TAATGTGCG  GA
                                    C        GT
GAM260  HSPC134   3'  GATAGCAGTTATAATGCCC   26345         TGT   _
                                  GGGCATTGTA   TGCT TC
                                  ||||||||||   |||| ||
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                              CCCGTAATAT  ACGA AG
                                   TG_   T
GAM260  HSPC138  5' TCGCGGGGGCAGAGGCA    33082    ATG
                              TGT  TTGCTTCTGTGG
                              |||  ||||||||||||
                              ACG  GACGGGGGCGCT
                                GA_
GAM260  HSPC154  3' TTATAGAACTGCATAATGTCT 26351      TG    TGC
                              GGGCAT  TATGT  TTCTGTGG
                              ||||||  |||||  ||||||||
                              TCTGTA  ATACG  AAGATATT
                                 __    TC_
GAM260  HSPC155  3' CCAGGTGGAGCAACATGCGATT 33088    C          TG_
           CT                   GGG ATTGTATGTTGCTTC  TGG
                              ||| ||||||||||||||  |||
                              TCT TAGCGTACAACGAGG  ACC
                                _          TGG
GAM260  HSU79252 3' CGGAATACAATGTCC      25244         GTTGCT
                              GGGCATTGTAT    TCTG
                              ||||||||||     ||||
                              CCTGTAACATA    AGGC
                                        _______
GAM260  HSU79252 5' TGCAGAGGCCCACGGTCTCC  25246    C    ATGTT    TG
                              GGG ATTGT    GCTTCTG  G
                              ||| |||||    |||||||  |
                              CCT TGGCA    CGGAGAC  T
                                C    CC___     GT
GAM260  HT002    3' CTGCAGGAGTGACGGTGATGAC 25940    _  TG A  TG    TG
           CC                   GGG CAT  T TGT  CTTCTG  G
                              ||| |||  | |||  ||||||  |
                              CCC GTA  G GCA  GAGGAC  C
                                A  GT _  GT    GT
GAM260  HT014    3' CTATAGGAAACTTTCTGATGCC 39795      GTAT_  GC
           T                    GGGCATT    GTT  TTCTGTGG
                              |||||||    |||  ||||||||
                              TCCGTAG    CAA  AGGATATC
                                  TCTTT  __
GAM260  HTATIP   5' CTACAGGGGCTTCGTGAGGCCC 21107     ATTG   TT
                              GGGC   TATG  GCTTCTGTGG
                              ||||   ||||  ||||||||||
                              CCCG   GTGC  CGGGGACATC
                                GA__   TT
GAM260  HTATIP   5' TCACAGGGGCAGTCTTGCCC  21109     TTGTATG
                              GGGCA     TTGCTTCTGTGG
                              |||||     ||||||||||||
                              CCCGT     GACGGGGACACT
                                TCT_____
GAM260  HTCD37   3' TCACTTTGAGGGTGTGATGTCT 67680      TG  GTTG   T__
                              GGGCAT  TAT   CTTC  GTGG
                              ||||||  |||   ||||  ||||
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                                TCTGTA  GTG   GGAG   CACT
                                   GT  ____   TTT
GAM260  HTMP10   5' CAGAAGCCCCCAAGCTC    52609     A  TATGTT
                                GGGC TTG     GCTTCTG
                                |||| |||     |||||||
                                CTCG AAC     CGAAGAC
                                  _  CCC___
GAM260  HUMAGCGB 5' CGCGGCCGTCGCGATGCCC   25230        ATGTT  TT
                                GGGCATTGT    GC  CTGTG
                                |||||||||    ||  |||||
                                CCCGTAGCG    TG  GGCGC
                                     C____  CC
GAM260  HXCP2    3'  CTATGAGTGAGAATATGCGGTG 50834          G  _ _
           TTT                   GGCATTGTATGTT CTT CT GTGG
                                |||||||||||||| ||| || ||||
                                TTGTGGCGTATAA GAG GA TATC
                                      _  T  G
GAM260  HYPC     3'  TCACCCTCTAGCATCAGTGCCT 64611        T     CTTCT
                                GGGCATTG ATGTTG    GTGG
                                |||||||| ||||||    ||||
                                TCCGTGAC TACGAT    CACT
                                   _     CTCC_
GAM260  HYPH     3'  AGCAATGTGAATGCTT      94898        G
                                GGGCATT TATGTTGCT
                                ||||||| |||||||||
                                TTCGTAA GTGTAACGA
                                   _
GAM260  IBTK     3'  CTGCAGTTAAATCATATAATGT 67487          TTGCTT   TG
           TT                    GGGCATTGTATG     CTG  G
                                ||||||||||||     |||  |
                                TTTGTAATATAC     GAC  C
                                      TAAATT   GT
GAM260  ICK      3'  TGTAGGGGTATTGATGTGCCC  29937       TGTATGT      TG
                                GGGCAT      TGCTTCTG  G
                                ||||||      ||||||||  |
                                CCCGTG      ATGGGGAT  T
                                   TAGTT__       GT
GAM260  IDI2     3'  TCGAGTCAGCCATGTGTAATGC 52698          T   T_  GTGG
           CC                    GGGCATTGTATGT GCT  CT
                                ||||||||||||| |||  ||
                                CCCGTAATGTGTA CGA  GA
                                      C   CT  GCT
GAM260  IL-17RC  3'  ACAGGATGGGGTGTCC      51197       G  TGTTGC
                                GGGCATT TA     TTCTGT
                                ||||||| ||     ||||||
                                CCTGTGG GT     AGGACA
                                   G  _______
GAM260  IL14     5'  CGCTCTGTCTGCAGTGCCC   95432         TGTT  TTCT
                                GGGCATTGTA   GC   GTG
                                ||||||||||   ||   |||
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                                CCCGTGACGT   TG   CGC
                                     C___  TCT_
GAM260  IL18BP   3'  TCACAGCCTCCTTATAATGCCT 19112        TGTTGCTT
                                GGGCATTGTA      CTGTGG
                                ||||||||||      ||||||
                                TCCGTAATAT      GACACT
                                     TCCTCC__
GAM260  IL1RAPL1 3'  GTAGCATCAGTGTCC      26546       T
                                GGGCATTG ATGTTGC
                                |||||||| |||||||
                                CCTGTGAC TACGATG
                                     _
GAM260  IL22R    3'  CAGAGGGAGTGGCATGCAGGGC 41189     A      TG    G_  G
             CC                   GGGC TTGTATGT  CTTCT  TG
                                |||| ||||||||  |||||  ||
                                CCCG GACGTACG  GAGGG  AC
                                  G       GT    AG
GAM260  ILT7     3'  CATTAAACTGTGGTGCTT    24387      TG  T   GCTTCT
                                GGGCAT  TA GTT     GTG
                                ||||||  || |||     |||
                                TTCGTG  GT CAA     TAC
                                   GT  _   AT____
GAM260  INDO     3'  CCACAAACTAATACTATGCAAT 9295          _  TGCTTC_
             GTTT                 GGCATTGTAT GT      TGTGG
                                ||||||||||  ||      |||||
                                TTGTAACGTA CA      ACACC
                                     T  TAATCAA
GAM260  INSM2    3'  TCGCGGTGAATGCGTGCATGTC 50870      T     TGCTT
             T                    GGGCAT GTATGT    CTGTGG
                                ||||||  ||||||     ||||||
                                TCTGTA CGTGCG    GGCGCT
                                   _     TAAGT
GAM260  INVS     3'  CTATGGAGGAAGACTGTGTTC  27031      T  ATGTTG
                                GGGCAT GT     CTTCTGTGG
                                ||||||  ||     |||||||||
                                CTTGTG CA     GGAGGTATC
                                   T  GAA___
GAM260  IRF7     5'  CGCAGAAGGAGCAATGGCC    14447    G     ATGT G     TG
                                GG CATTGT    T CTTCTG  G
                                ||  ||||||    | ||||||  |
                                CC GTAACG    A GAAGAC  C
                                 G     _____ G     GT
GAM260  ITGB8    5'  CGCGGAGCCCTTGCAGAGCCC  9404      A    TGTT   T   TG
                                GGGC TTGTA    GCT CTG  G
                                ||||  |||||    |||  |||  |
                                CCCG GACGT    CGA GGC  C
                                  A    TCC_  _   GT
GAM260  ITGB8    5'  CTGTGGAAGCAACTGCGCTG  9405     T   T        TG
                                CA TGTA GTTGCTTCTG  G
                                ||  ||||  ||||||||||  |
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                                GT GCGT CAACGAAGGT  C
                                 C   _       GT
GAM260  ITM3    3'  CTATAGAGGTGACATGTCTCTC 48164    CATTG    TG
              C                   GGG    TATGT  CTTCTGTGG
                                  |||    |||||  |||||||||
                                  CCT    GTACA  GGAGATATC
                                    CTCT_    GT
GAM260  ITM3    3'  CTGTGGGGGCGGGGCGGCATGG 48165    AT_  ATG_      TG
              GCTT                  GGC   TGT   TTGCTTCTG  G
                                  |||   |||   |||||||||  |
                                  TCG   ACG   GGCGGGGGT  C
                                    GGT   GCGG       GT
GAM260  KCNB2   5'  CCACAGCCCTTTGTGGTGCCC  96101      TG  TGTTGCTT
                                  GGGCAT  TA      CTGTGG
                                  ||||||  ||      ||||||
                                  CCCGTG  GT      GACACC
                                     GT  TTCCC___
GAM260  KCNH8   3'  TGTGGGAGTAATACCAGCTT   58260     AT  TA        TG
                                  GGGC  TG  TGTTGCTTCTG  G
                                  ||||  ||  ||||||||||  |
                                  TTCG  AC  ATAATGAGGGT  T
                                    __ C_         GT
GAM260  KCNJ9   5'  CGTGGGGGGGGCGGTGTC    17153        ATGT G    TG
                                  GGCATTGT    T CTTC  TG
                                  ||||||||    | ||||  ||
                                  CTGTGGCG    G GGGG  GC
                                      _____ G    GT
GAM260  KIAA0007 3'  CTGCAATGTACTGACATCAGTG 80111      T    ___  TTC  TG
              TCC                   GCATTG ATGTT   GC   TG  G
                                  ||||||  |||||   ||   ||  |
                                  TGTGAC  TACAG   TG   AC  C
                                     _    TCA  TA_  GT
GAM260  KIAA0008 3'  TCACTTCTATAGCATATAATGT 28546           CTTCT
              TT                    GGGCATTGTATGTTG    GTGG
                                  ||||||||||||||    ||||
                                  TTTGTAATATACGAT    CACT
                                           ATCTT
GAM260  KIAA0010 3'  TGGGAGCAGAGTGACCC     27898     _   GTATG
                                  GGG CATT    TTGCTTCTG
                                  ||| ||||    |||||||||
                                  CCC GTGA    GACGAGGGT
                                    A   ______
GAM260  KIAA0014 3'  CCGCAGCTCCACACGGTGCCC  27839        A  TT   TCT
                                  GGGCATTGT TG  GCT   GTGG
                                  |||||||||  ||  |||   ||||
                                  CCCGTGGCA AC  CGA   CGCC
                                       C  CT   ___
GAM260  KIAA0022 3'  TTGTAGTGAGCAGTGTATGGTC 29675    C  TG  TG    _   TG
              TC                    GGG AT  TA  TTGCTT CTG  G
                                  |||  ||  ||  ||||||  |||  |
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                                CTC TG  AT  GACGAG GAT  T
                                  _ GT  GT     T  GT
GAM260  KIAA0033 5' TGCAGGAGGTTGCAGTACTC  76587    C     TGTTG     TG
                                GGG ATTGTA    CTTCTG  G
                                ||| ||||||    ||||||  |
                                CTC TGACGT    GAGGAC  T
                                  A     TG___     GT
GAM260  KIAA0036 5' CCGTGGAGGCAGTAACAGGC  27675    A   A       TG
                                GC TTGT TGTTGCTTC  TGG
                                || |||| |||||||||  |||
                                CG GACA ATGACGGAG  GCC
                                  _   _       GT
GAM260  KIAA0040 5' CCATGGAGAGAATCAGTGCCT  27781        TATG  GC
                                GGGCATTG   TT  TTCTGTGG
                                ||||||||   ||  ||||||||
                                TCCGTGAC   AG  GAGGTACC
                                     TA__  A_
GAM260  KIAA0040 3' CTACAGGAAAAATATACTGATG 27784        _     GC
           TTC                    GGGCATT GTATGTT  TTCTGTGG
                                ||||||| |||||||  ||||||||
                                CTTGTAG CATATAA  AGGACATC
                                    T     AA
GAM260  KIAA0061 3' CTATGGAGAAACTCAGTGCTC  68290        TAT   GC
                                GGGCATTG   GTT  TTCTGTGG
                                ||||||||   |||  ||||||||
                                CTCGTGAC   CAA  GAGGTATC
                                     T__   A_
GAM260  KIAA0073 5' CGTGGAGGCAACACTGGCC   67802    ATTGTA        TG
                                GGC     TGTTGCTTCTG  G
                                |||     ||||||||||  |
                                CCG     ACAACGGAGGT  C
                                  GTC___         GT
GAM260  KIAA0073 5' GGCAGTAGCAGTGGCGGTGTCC 67803         ATG    T   GG
                                GGGCATTGT   TTGCT CTGT
                                |||||||||   ||||| ||||
                                CCTGTGGCG   GACGA GACG
                                     GT_    T   GT
GAM260  KIAA0090 3' GGGGTACATGAGATGTTT    88446       G    T
                                GGGCATT TATGT GCTTC
                                ||||||| ||||| |||||
                                TTTGTAG GTACA TGGGG
                                    A    _
GAM260  KIAA0092 3' GCTATAGGCAGTGCTT     27968         A   T
                                GGGCATTGT TGT GC
                                ||||||||| ||| ||
                                TTCGTGACG ATA CG
                                     G   T
GAM260  KIAA0121 3' CGTGGAGGTCACAGCTGCTC   72657      TT  A   T     TG
                                GGGCA  GT TGT GCTTCTG  G
                                |||||  || ||| |||||||  |
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                                CTCGT  CG ACA TGGAGGT  C
                                  __ _  C      GT
GAM260  KIAA0121 3' TCACAGAGTGGCTGCAGGCCT  72661     A    T  TG  T
                                GGGC TTGTA GT  CT CTGTGG
                                |||| ||||| ||  || ||||||
                                TCCG GACGT CG  GA GACACT
                                  _    _ GT  _
GAM260  KIAA0125 5' CCATGGAGGTGACAGAGTTGCT 28896      TTGTA   TG
           T                     GGGCA    TGT  CTTCTGTGG
                                |||||    |||  |||||||||
                                TTCGT    ACA  GGAGGTACC
                                   TGAG_   GT
GAM260  KIAA0125 5' CCGCAGAGGCTGCTGAGGCCT  28897     ATTG  T  T
                                GGGC    TA GT GCTTCTGTGG
                                ||||    || || ||||||||||
                                TCCG    GT CG CGGAGACGCC
                                  GA__  _  T
GAM260  KIAA0125 3' CCACAGAGGCTGCTGAGGCCT  60505     ATTG  T  T
                                GGGC    TA GT GCTTCTGTGG
                                ||||    || || ||||||||||
                                TCCG    GT CG CGGAGACACC
                                  GA__  _  T
GAM260  KIAA0141 3' TTGTAGACCAAAGGCAATGGTG 28735      TG A    GCT__    TG
           TCT                    GGCAT  T TGTT    TCTG  G
                                |||||  | ||||    ||||  |
                                CTGTG  A ACGG    AGAT  T
                                   GT _   AAACC    GT
GAM260  KIAA0153 3' TGCAGGGGCAGGGCGGGCCC   30705     A   ATGT      TG
                                GGGC TTGT    TGCTTCTG  G
                                |||| ||||   ||||||||  |
                                CCCG GGCG    ACGGGGAC  T
                                  _   GG__       GT
GAM260  KIAA0157 3' TGGATACAGTGTGCAAGTTT   49793     A    TG   CT
                                GGGC TTGTA  TTG  TCTG
                                |||| |||||  |||  ||||
                                TTTG AACGT  GAC  AGGT
                                  _    GT   AT
GAM260  KIAA0182 3' CCGTGGGGAGCATGTACAGAGC 72025      A      T   _ TG
           TC                    GGGC TTGTATGT GCTT C  TGG
                                |||| |||||||| |||| |  |||
                                CTCG GACATGTA CGAG G  GCC
                                  A       _    G GT
GAM260  KIAA0182 3' CTATGGAGGCAGTGTTTAGAT  72026     GT_ TG
                                ATT   A  TTGCTTCTGTGG
                                |||   |  ||||||||||||
                                TAG   T  GACGGAGGTATC
                                  ATT GT
GAM260  KIAA0184 3' GGTCACACACAGTGCCT     65200         A   T
                                GGGCATTGT TGT GCT
                                ||||||||| ||| |||
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                                TCCGTGACA ACA TGG
                                     C   C
GAM260  KIAA0186 3' AGTATATATAATGTTT      40743           T
                                GGGCATTGTATGT GCT
                                |||||||||||| |||
                                TTTGTAATATATA TGA
                                          _
GAM260  KIAA0186 5' CCGCGGGAGTGGGAAGCGTCC 40746     ATT  ATG TG
                                GGGC   GT   T  CTTCTGTGG
                                ||||   ||   |  |||||||||
                                CCTG   CG   G  GAGGGCGCC
                                  ___  AAG GT
GAM260  KIAA0186 3' TTGTAGTTTTCAGTGTACAGGT 40768     A    TG   CTT_   TG
           CT                    GGGC TTGTA  TTG    CTG  G
                                |||| |||||  |||    |||  |
                                TCTG GACAT  GAC    GAT  T
                                  _    GT   TTTT   GT
GAM260  KIAA0187 3' CGGAGGTAGACAGT       28569      ATG
                                ATTGT   TTGCTTCTG
                                |||||   |||||||||
                                TGACA   GATGGAGGC
                                  ___
GAM260  KIAA0189 3' GACAGCAATGTGTGATCCC    28275     C  TG       _
                                GGG AT  TATGTTGCT TC
                                ||| ||  ||||||||| ||
                                CCC TA  GTGTAACGA AG
                                  _ GT       C
GAM260  KIAA0191 3' TTACAGAACCTTGTAGTGCC   65927         TGTTGC
                                GGCATTGTA     TTCTGTGG
                                |||||||||     ||||||||
                                CCGTGATGT     AAGACATT
                                     TCC___
GAM260  KIAA0193 3' CGCACCACAATTGTGATGTCC  28652       TG  T    CTTC  TG
                                GGGCAT  TA GTTG    TG  G
                                ||||||  || ||||    ||  |
                                CCTGTA  GT TAAC    AC  C
                                   GT  _    ACC_  GT
GAM260  KIAA0193 3' TAGTGCACAGTGTCT       28659         ATGTT  TT
                                GGGCATTGT    GC  CTG
                                |||||||||    ||  |||
                                TCTGTGACA    CG  GAT
                                     _____  T_
GAM260  KIAA0193 3' TTATGGAGGTTCCTTAGTGCTC 28667         TATGTT
                                GGGCATTG     GCTTCTGTGG
                                ||||||||     ||||||||||
                                CTCGTGAT     TGGAGGTATT
                                     TCCT__
GAM260  KIAA0194 3' CCACAGAGGGGATGTGGTCCC  65984     C  TG AT   G
                                GGG AT  T  GTT CTTCTGTGG
                                ||| ||  |  ||| |||||||||
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                                CCC TG  G  TAG GGAGACACC
                                  _ GT __   G
GAM260  KIAA0205 3' CGTGGGGGAAAAGCAGTGTCC 29580        ATG  G     TG
                                GGGCATTGT   TT CTTCTG  G
                                |||||||||   || ||||||  |
                                CCTGTGACG   AA GGGGGT  C
                                     AA_ _     GT
GAM260  KIAA0212 3' CGCAGGGCTTTTGCAGTTTCT 27936     C     TGTT   T   TG
                                GGG ATTGTA    GCT CTG  G
                                ||| ||||||    ||| |||  |
                                TCT TGACGT    CGG GAC  C
                                  T     TTT_  _   GT
GAM260  KIAA0215 3' TCATGCTTATCAGTGTCCAGTG 28421        T TG   CTTCT_
           CCT                    GGGCATTG A  TTG     GTGG
                                ||||||||  |  |||      ||||
                                TCCGTGAC T  GAC     TACT
                                     C GT   TATTCG
GAM260  KIAA0217 3' TCGTAGAGGCAGTGCTGGCC   67041    ATT    GT
                                GGC   GTAT  TGCTTCTGTGG
                                |||   ||||  ||||||||||
                                CCG   CGTG  ACGGAGATGCT
                                  GT_   __
GAM260  KIAA0229 3' GCGCACATGCTGGTGCCC    92428        _     _
                                GGGCATT GTATGT TGC
                                ||||||| |||||| |||
                                CCCGTGG CGTACA GCG
                                     T     C
GAM260  KIAA0232 3' CGTGGAAGAGCAAGTGCCC   72747       GTA    G    TG
                                GGGCATT   TGTT CTTC  TG
                                |||||||   |||| ||||  ||
                                CCCGTGA   ACGA GAAG  GC
                                     ___   _   GT
GAM260  KIAA0237 5' CCGTGGTGGCGGGCGATGCCC  28523        ATG    T TG
                                GGGCATTGT   TTGCT C  TGG
                                |||||||||   ||||| |  |||
                                CCCGTAGCG   GGCGG G  GCC
                                     ___    T GT
GAM260  KIAA0240 5' CTATAGGGGTGACGCATGTGCC 92436       _  AT  TG
           T                    GGGCAT TGT  GT  CTTCTGTGG
                                |||||| |||  ||  |||||||||
                                TCCGTG ACG  CA  GGGGATATC
                                   T   __  GT
GAM260  KIAA0247 3' GCAGGGAAGCAGCATGCAGGCT 28400      A           G  G
           T                    GGGC TTGTATGTTGCTTCT TG
                                |||| |||||||||||||| ||
                                TTCG GACGTACGACGAAGG AC
                                  _           G  GA
GAM260  KIAA0254 3' CTGCAGGAGTCCAGCCAATGT  28597      TA  TT     TG
                                GCATTG  TG  GCTTCTG  G
                                ||||||  ||  |||||||  |
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                                TGTAAC  AC  TGAGGAC  C
                                   CG  C_     GT
GAM260  KIAA0276 3' CATAAAAGTGTGCAAGTCC   70962     A    GTT   C
                                GGGC TTGTAT   GCTT TGTG
                                |||| ||||||   |||| ||||
                                CCTG AACGTG   TGAA ATAC
                                  _    ____   A
GAM260  KIAA0284 3' TCGGCAGTGGCTGTGCAATGTT 63118         _ TG  T   TGG
           T                 GGGCATTGTAT GT  CT CTG
                             |||||||||||  ||  || |||
                             TTTGTAACGTG CG  GA GGC
                                   T  GT  C   T
GAM260  KIAA0298 3' TGCAGAGGCTGGCCGCTGCCT  76584      T  TAT  _     TG
                             GGGCA TG   GTT GCTTCTG  G
                             |||||  ||   |||  |||||||  |
                             TCCGT GC   CGG CGGAGAC  T
                                C  ___   T     GT
GAM260  KIAA0303 5' CTACAGGAGGCTCATGATCGTT 69461     ATTG   TTG
           C                 GGGC   TATG   CTTCTGTGG
                             ||||   ||||   |||||||||
                             CTTG   GTAC   GAGGACATC
                               CTA_   TCG
GAM260  KIAA0316 3' CTAAAGGAGAGCACATATGCAA 69671         _   _  GTGG
           TGCCT               GCATTGTATGT TGCT TCT
                             ||||||||||  |||| |||
                             CGTAACGTATA ACGA AGG
                                   C   G   AAATC
GAM260  KIAA0317 3' CCATAGGAGCAGTCCCGCTGC  29082    T  TATG
                             GCA TG   TTGCTTCTGTGG
                             ||| ||   ||||||||||||
                             CGT GC   GACGAGGATACC
                               C  CCT_
GAM260  KIAA0318 3' CTATTCTGTGGCATATGGTTTT 68953    C  TG    TG TTCT
           C                 GGG AT  TATGT  C   GTGG
                             ||| ||  |||||  |   ||||
                             CTT TG  ATACG  G   TATC
                               T  GT    GT TCT_
GAM260  KIAA0321 3' AGTGATGGCGATGCCC     62388        A  TG
                             GGGCATTGT TGT  CT
                             |||||||| |||  ||
                             CCCGTAGCG GTA  GA
                                   _  GT
GAM260  KIAA0321 3' CCACGCAAGATGTGACAATGTT 62391       ATGTTG  C
           T                 GGGCATTGT     CTT TGTGG
                             |||||||||     ||| |||||
                             TTTGTAACA     GAA GCACC
                                   GTGTA_  C
GAM260  KIAA0322 3' CGCAGAGAGTGATGGTGCTT  92752      GTAT  TG  _   TG
                             GGGCATT   GT  CT TCTG  G
                             |||||||   ||  || ||||  |
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                                TTCGTGG   TA  GA AGAC  C
                                   ____  GT  G   GT
GAM260  KIAA0326 3' ATGGAGGAAGATGCTC     64318       GTATGTTG
                                GGGCATT      CTTCTGT
                                |||||||      |||||||
                                CTCGTAG      GGAGGTA
                                   AA_______
GAM260  KIAA0329 3' CAGACAATGGGCAGTGCCC   29270        A    CT
                                GGGCATTGT TGTTG  TCTG
                                ||||||||| |||||  ||||
                                CCCGTGACG GTAAC  AGAC
                                     G   __
GAM260  KIAA0332 3' TCACAGAAGCAATATGATTTCC 62704    CATTG
                                GGG    TATGTTGCTTCTGTGG
                                |||    ||||||||||||||||
                                CCT    GTATAACGAAGACACT
                                  TTA__
GAM260  KIAA0352 5' GGCGGCGATGGTGCTC     29157       TG A
                                GGGCAT  T TGTTGCT
                                ||||||  | |||||||
                                CTCGTG  A GCGGCGG
                                   GT _
GAM260  KIAA0367 5' CACAGTTTCAGCGATGCCT   67295        A  TTGCTT
                                GGGCATTGT TG     CTGTG
                                ||||||||| ||     |||||
                                TCCGTAGCG AC     GACAC
                                     _ TTT___
GAM260  KIAA0379 5' CAGATGTTAATGCTC      68148        TATGTT  T
                                GGGCATTG     GC TCTG
                                ||||||||     || ||||
                                CTCGTAAT     TG AGAC
                                     _______  T
GAM260  KIAA0406 3' CCACAGAGGCCACCGATCCC  61330    C   TAT  T
                                GGG ATTG   GT GCTTCTGTGG
                                ||| ||||   || ||||||||||
                                CCC TAGC   CA CGGAGACACC
                                  _   ___  C
GAM260  KIAA0408 3' TCAAGACTGTAGCATGGTGATG 28137      TG _     T_  GTGG
           TCT                    GGCAT  T ATGTTGC  TCT
                                |||||  | |||||||  |||
                                CTGTA  G TACGATG  AGA
                                   GT G      TC   ACT
GAM260  KIAA0408 3' TACAGAAGTTCTAGTCCC    28136    C   TATGTT
                                GGG ATTG     GCTTCTGTG
                                ||| ||||     |||||||||
                                CCC TGAT     TGAAGACAT
                                  _   CT_____
GAM260  KIAA0418 3' TCATGGGGGCCTCCAGTGTCC  27565        TATGTT
                                GGGCATTG     GCTTCTGTGG
                                ||||||||     ||||||||||
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                              CCTGTGAC     CGGGGGTACT
                                   CTC___
GAM260  KIAA0419 5' CGTGGGGGATCAGTGCCT    28188        TATGTTG   TG
                              GGGCATTG      CTTC  TG
                              ||||||||      ||||  ||
                              TCCGTGAC      GGGG  GC
                                   TA_____    GT
GAM260  KIAA0427 3' ACAGGGGCAGCTCCC       28717     CATTGTAT
                              GGG       GTTGCTTCTGT
                              |||       ||||||||||
                              CCC       CGACGGGGACA
                                T_______
GAM260  KIAA0429 3' CCATACTGGATTGCAGTGTTT  28552         TGTTG  TC
                              GGGCATTGTA    CT  TGTGG
                              ||||||||||    ||  |||||
                              TTTGTGACGT    GG  ATACC
                                   TA___  TC
GAM260  KIAA0429 3' TCACATTTGAAGACAATAGTGT 28562        A   TG   ___
           TT                   GGCATTGT TGT  CTTC   TGTGG
                              ||||||||  |||  ||||   |||||
                              TTGTGATA ACA  GAAG   ACACT
                                   _  __    TTT
GAM260  KIAA0429 3' TTACAGAATATAAACAACAGTA 28563    GTA    C_____
           GTGCCT                 TT   TGTTG     TTCTGTGG
                              ||   |||||     ||||||||
                              GA   ACAAC     AAGACATT
                               TG_    AAATAT
GAM260  KIAA0431 3' CCGTAGGATTTAAGCAGTAGTG 30890       GTA    GC__
           CTT                   GGCATT   TGTT    TTCTGTGG
                              ||||||   ||||   ||||||||
                              TCGTGA   ACGA    AGGATGCC
                                 TG_    ATTT
GAM260  KIAA0444 3' CCAAAAGTGGTGATGGTGGTGT 62337       TG A   TG  T  G_
           CC                    GGGCAT  T TGT  CT CT  TGG
                              ||||||  | |||  || ||  |||
                              CCTGTG  G GTA  GG GA  ACC
                                 GT _   GT  T  AA
GAM260  KIAA0446 5' AAAGGGAGTGGGTGCAGTGCCC 68849          G TG    GTGG
                              GGGCATTGTAT T  CTTCT
                              ||||||||||| |  |||||
                              CCCGTGACGTG G  GAGGG
                                    _ GT    AAAT
GAM260  KIAA0447 3' CCACGGAGGCCGTTCAGTCGCT 71668     _   T   TT
           T                    GGGC ATTG ATG  GCTTCTGTGG
                              ||||  |||| |||  ||||||||||
                              TTCG TGAC TGC  CGGAGGCACC
                                C   T   __
GAM260  KIAA0450 5' TCATGGGGGCGCGGTGGGTGCT 27648       GTA   T
                              GGCATT   TGT GCTTCTGTGG
                              ||||||   ||| ||||||||||
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                                TCGTGG  GCG CGGGGGTACT
                                   GTG  _
GAM260  KIAA0459 3' CGTAGTCAATGTGCAATTTCT 60990    C       CTT  TG
                                GGG ATTGTATGTTG  CTG  G
                                ||| |||||||||||  |||  |
                                TCT TAACGTGTAAC  GAT  C
                                  T        T__  GT
GAM260  KIAA0469 5' CTATTTATAGCAGCGGTGCCT 29328      TGTA     TCT_
                                GGGCAT   TGTTGCT   GTGG
                                ||||||   |||||||   ||||
                                TCCGTG   GCGACGA   TATC
                                   ____     TATT
GAM260  KIAA0469 5' TCGCGGGGGGCGGTGGCGCCC 29357     A TG A  TG
                                GGGC T  T TGT  CTTCTGTGG
                                |||| |  | |||  |||||||||
                                CCCG G  G GCG  GGGGGCGCT
                                  C GT _  __
GAM260  KIAA0478 3' CCATGGAAGCTTTTATTGCTC 29544     TT  TGTT
                                GGGCA  GTA   GCTTCTGTGG
                                |||||  |||   ||||||||||
                                CTCGT  TAT   CGAAGGTACC
                                   __  TTT_
GAM260  KIAA0478 3' TGGAGGGGAGTGCCT      29563      TGTATG  G
                                GGGCAT     TT CTTCTG
                                ||||||     || ||||||
                                TCCGTG     AG GGAGGT
                                   _______  G
GAM260  KIAA0494 3' TCATGGAAGTAGGATTCTGGTT 28749     ATTGT  G
           C                     GGGC    AT TTGCTTCTGTGG
                                ||||    || ||||||||||||
                                CTTG    TA GATGAAGGTACT
                                  GTCT_  G
GAM260  KIAA0513 3' TTACAGTTTTAGCAACATTGAT 28384      T      T___
           GTCT                   GCATTG ATGTTGCT   CTGTGG
                                ||||||| ||||||||   ||||||
                                TGTAGT TACAACGA   GACATT
                                   _      TTTT
GAM260  KIAA0514 5' TTGTGGAAGCCCAGGGTGATTC 28102    C  TG A_  TT     TG
           TC                    GGG AT  T  TG  GCTTCTG  G
                                ||| ||  |  ||  |||||||  |
                                CTC TA  G  AC  CGAAGGT  T
                                  T  GT GG  C_     GT
GAM260  KIAA0515 3' CAGGGGTGCTGTGTTT     63805      T  ATGTT
                                GGGCAT GT    GCTTCTG
                                |||||| ||    |||||||
                                TTTGTG CG    TGGGGAC
                                   T  _____
GAM260  KIAA0532 3' TAAATGGGTAATATACAGGTTT 70776     A         CTGTGG
                                GGGC TTGTATGTTGCTT
                                |||| ||||||||||||
```

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                                TTTG GACATATAATGGG
                                  _          TAAATT
GAM260  KIAA0537  5'  CCGCGGGCGCCAGATGTGCAGT 29245    C        __ T
                CCC                  GG ATTGTATGTT  GC TCTGTGG
                                || ||||||||||  || |||||||
                                CC TGACGTGTAG  CG GGGCGCC
                                  _        AC  C
GAM260  KIAA0542  3'  TTACAGAAGGACCATATGTTC  66090       TGTAT   G
                                GGGCAT    GTT CTTCTGTGG
                                ||||||    ||| |||||||||
                                CTTGTA    CAG GAAGACATT
                                   TAC__   _
GAM260  KIAA0547  3'  CACGGGGTATAATAATGTTT   28909         ATGT   T    G
                                GGGCATTGT    TGCT CTGTG
                                |||||||||    |||| |||||
                                TTTGTAATA    ATGG GGCAC
                                     AT__    _    G
GAM260  KIAA0553  3'  GCAGTATGTAGTGCCC      69893
                                GGGCATTGTATGTTGC
                                ||||||||||||||||
                                CCCGTGATGTATGACG

GAM260  KIAA0557  3'  TAGGAGCTGTGAGTCC      78006      A TG  TGTT
                                GGGC T  TA    GCTTCTG
                                |||| |  ||    |||||||
                                CCTG A  GT    CGAGGAT
                                  _ GT  _____
GAM260  KIAA0565  5'  CTACCTCTCAAATATATATGTC 66888       T      GCTTCT
                C                    GGGCAT GTATGTT     GTGG
                                |||||| |||||||     ||||
                                CCTGTA TATATAA     CATC
                                   _      ACTCTC
GAM260  KIAA0633  3'  CCACGGTGCCTGTGTACGGAGC 94052      A     TG T_  TT
                CT                   GGGC TTGTA  T  GC  CTGTGG
                                |||| |||||  |  ||  ||||||
                                TCCG GGCAT  G  CG  GGCACC
                                  A     GT TC  T_
GAM260  KIAA0645  3'  CCGTGGGAGGGCTCCAGTGTCT 27820         TAT   G    TG
                                GGGCATTG   GTT CTTC  TGG
                                ||||||||   ||| ||||  |||
                                TCTGTGAC   CGG GAGG  GCC
                                     CT_   _    GT
GAM260  KIAA0648  3'  TTACAGGGGCAGAAAAATCCC  82659     C   GTATG
                                GGG ATT    TTGCTTCTGTGG
                                ||| |||    ||||||||||||
                                CCC TAA    GACGGGGACATT
                                  _  AAA__
GAM260  KIAA0649  3'  TCACAGAGGCTCTGATGCTT   29052        GTATGTT
                                GGGCATT      GCTTCTGTGG
                                |||||||      ||||||||||
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                                TTCGTAG      CGGAGACACT
                                   TCT____
GAM260  KIAA0676 3' ACTGTGTGCAATGCCT      30448          GTT  TTCT
                                GGGCATTGTAT   GC    GT
                                ||||||||||   ||    ||
                                TCCGTAACGTG   TG    CA
                                      ___  T___
GAM260  KIAA0700 3' CCATGGAGGCATCCAAGGCTT  72053      A   TATGT
                                GGGC TTG    TGCTTCTGTGG
                                |||| |||    ||||||||||
                                TTCG AAC    ACGGAGGTACC
                                  G  CT___
GAM260  KIAA0711 3' TCATTCCTGTAATGTTTAGTGT 29527        T      TTCT
           TT                    GGGCATTG ATGTTGC    GTGG
                                |||||||| |||||||    ||||
                                TTTGTGAT TGTAATG    TACT
                                     T      TCCT
GAM260  KIAA0729 3' TATAGAGGCAGATTGCCT     95704       TTGTATG
                                GGGCA      TTGCTTCTGTG
                                |||||      ||||||||||
                                TCCGT      GACGGAGATAT
                                   TA_____
GAM260  KIAA0748 3' GAGCACATGCAGTGCTC      28940            T
                                GGGCATTGTATGT GCTT
                                |||||||||||| ||||
                                CTCGTGACGTACA CGAG
                                          _
GAM260  KIAA0748 3' TGCAGGAAACTGCACTGCCC   28945      T   T   GC    TG
                                GGGCA TGTA GTT  TTCTG  G
                                ||||| |||| |||  |||||  |
                                CCCGT ACGT CAA  AGGAC  T
                                   C   _  __    GT
GAM260  KIAA0757 3' TCACATGTAGATGTACAGTGT  20136           GCTTC
                                GCATTGTATGTT    TGTGG
                                ||||||||||||    |||||
                                TGTGACATGTAG    ACACT
                                      ATGT_
GAM260  KIAA0781 3' CCATGTGAAGTGGTAGTGCGGT 67455         _  TT    _
           GCCT                   GGCATTGTA TG  GCTTC TGTGG
                                |||||||| ||  ||||| |||||
                                CCGTGGCGT AT  TGAAG GTACC
                                     G  GG    T
GAM260  KIAA0781 3' CGCAGAGGCACTGTGCTC     67457       T  ATGTT
                                GGGCAT GT    GCTTCTGTG
                                |||||| ||    |||||||||
                                CTCGTG CA    CGGAGACGC
                                   T _____
GAM260  KIAA0802 3' TTAACTGGCAATGTACAGAGTT 62569      A          TCTGTGG
           T                    GGGC TTGTATGTTGCT
                                |||| ||||||||||||
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                                TTTG GACATGTAACGG
                                  A          TCAATT
GAM260  KIAA0820  3' CTACAGAAGTAAATCAGGTTT  69022     A   TATG
                                GGGC TTG    TTGCTTCTGTGG
                                |||| |||    ||||||||||||
                                TTTG GAC    AATGAAGACATC
                                  _   TA__
GAM260  KIAA0821  3' CACAGGGGTGGCCATAT     29942      _ TG
                                GTATG T  CTTCTGTG
                                ||||| |  ||||||||
                                TATAC G  GGGGACAC
                                  C GT
GAM260  KIAA0844  5' CGCGGAGGTGGCAGCCC     30201      ATTGTA   TG
                                GGGC     TGT  CTTCTGTG
                                ||||     |||  ||||||||
                                CCCG     ACG  GGAGGCGC
                                  _______  GT
GAM260  KIAA0855  3' GCAGCATGGATGTCC       30405        G
                                GGGCATT TATGTTGC
                                ||||||| ||||||||
                                CCTGTAG GTACGACG
                                   _
GAM260  KIAA0861  3' CGCAGAGGCGAGCAGAGCCC   88922      A    ATG       TG
                                GGGC TTGT   TTGCTTCTG  G
                                |||| ||||   |||||||||  |
                                CCCG GACG   AGCGGAGAC  C
                                  A   ___        GT
GAM260  KIAA0870  3' TCACAGAAGGTGGACAGGGCCT 81472      A    ATGTTG
                                GGGC TTGT     CTTCTGTGG
                                |||| ||||     |||||||||
                                TCCG GACA     GAAGACACT
                                  G   GGTG__
GAM260  KIAA0871  3' AGGTGAGGGTTGATATATAATG 30298            GC    GTGG
            TCC                   GGGCATTGTATGTT  TTCT
                                |||||||||||||  ||||
                                CCTGTAATATATAG  GGGA
                                        TT    GTGGAT
GAM260  KIAA0871  3' CATGGAAGTGGAAGATCCT    30301     C   GTATG TG
                                GGG ATT     T  CTTCTGTG
                                ||| |||     |  ||||||||
                                TCC TAG     G  GAAGGTAC
                                  _   AA___ GT
GAM260  KIAA0892  3' TGCCAGGGCAGGCAGTGCCC   71015         ATG    T   TGG
                                GGGCATTGT   TTGCT CTG
                                |||||||||   ||||| |||
                                CCCGTGACG   GACGG GAC
                                     ___    _  CGTG
GAM260  KIAA0907  3' TTGCAGAAGTTAGAGATTCAGT 30184        T  G  __      TG
            GCCC                   GGCATTG AT TT  GCTTCTG  G
                                ||||||| || ||  |||||||  |
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                                CCGTGAC TA AG  TGAAGAC  T
                                    T  G  AT      GT
GAM260  KIAA0907  3'  CTGTAGAGGTACATGGGAT   30175    G    T     TG
                                ATT TATGT GCTTCTG  G
                                ||| ||||| |||||||  |
                                TAG GTACA TGGAGAT  C
                                  G    _      GT
GAM260  KIAA0923  3'  TTATAGAAGCAATGTATTAAAT 25840     __
             G                   CATT  GTATGTTGCTTCTGTGG
                                 ||||  ||||||||||||||||
                                 GTAA  TATGTAACGAAGATATT
                                   AT
GAM260  KIAA0931  3'  TTGTGGGAGCAGTTTAGGAGTC 67429     A  G  TG       TG
             C                   GGGC TT TA  TTGCTTCTG  G
                                 |||| || ||  |||||||||  |
                                 CCTG AG AT  GACGAGGGT  T
                                   _  G  TT       GT
GAM260  KIAA0940  3'  CCTCAGGGCTTACAGTGTTC   29867         TGTT   T   T
                                 GGGCATTGTA    GCT CTG GG
                                 ||||||||||    ||| ||| ||
                                 CTTGTGACAT    CGG GAC CC
                                       T___   _   T
GAM260  KIAA0953  3'  CCGCAGGGGTGAATAAATGCTT 66784       GTATG TG
                                 GGGCATT    T  CTTCTGTGG
                                 |||||||    |  |||||||||
                                 TTCGTAA    A  GGGGACGCC
                                     ATA__ GT
GAM260  KIAA0964  3'  CCGCGCCTGTGTCCGGTGCCC  29759        T TG T_  TTCT
                                 GGGCATTG A  T  GC    GTGG
                                 |||||||| |  |  ||    ||||
                                 CCCGTGGC T  G  CG    CGCC
                                     C GT TC  _____
GAM260  KIAA0972  3'  CAGGGTATGACAGTGCTT    30007         ATGT    T
                                 GGGCATTGT    TGCT CTG
                                 |||||||||    |||| |||
                                 TTCGTGACA    ATGG GAC
                                       GT__    _
GAM260  KIAA0976  3'  TCATGTGTAAAATAATGATGCC 29896       TG ATG_    TTCT
             C                   GGGCAT  T    TTGC    GTGG
                                 |||||| |    ||||    ||||
                                 CCCGTA  A    AATG    TACT
                                    GT ATAA    TG__
GAM260  KIAA0978  3'  TATGGGAGTGGGCATCTCC    70483     CAT   ATG TG
                                 GGG   TGT   T  CTTCTGTG
                                 |||   |||   |  ||||||||
                                 CCT   ACG   G  GAGGGTAT
                                   CT_   ___ GT
GAM260  KIAA0979  3'  TGAAAGTGTAATGTGCGATGGC 30446    G          TT  GTGG
             T                   GG CATTGTATGTTGC  CT
                                 || ||||||||||||  ||
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                                TC GTAGCGTGTAATG  GA
                                 G          T_  AAGTG
GAM260  KIAA0987  3'  GGTGGAGGAGCGGCGTGTGGTG 24565     TG         GTGG
            C                    GCAT  TATGTTGCTTCT
                                 ||||  ||||||||||||
                                 CGTG  GTGCGGCGAGGA
                                   GT          GGTGGT
GAM260  KIAA1018  3'  TTATGGAAAAGGGTGCGATCCT 30354     C      G  GC
                                 GGG ATTGTAT TT  TTCTGTGG
                                 ||| ||||||| ||  ||||||||
                                 TCC TAGCGTG GA  AAGGTATT
                                   _      G  A_
GAM260  KIAA1023  3'  CATGGGAGCAGCAAGC      34256    A
                                 GT TGTTGCTTCTGTG
                                 || ||||||||||||
                                 CG ACGACGAGGGTAC
                                  A
GAM260  KIAA1023  3'  CTGTGGGGGCTGCTGGCAGGGC 34259     A   AT  T     TG
            CT                     GGGC TTGT  GT GCTTCTG  G
                                 |||| ||||  || |||||||  |
                                 TCCG GACG  CG CGGGGGT  C
                                   G   GT  T     GT
GAM260  KIAA1026  3'  ACAGCCAGCAGTGTCC      71186         ATGT  CTT
                                 GGGCATTGT   TG   CTGT
                                 |||||||||   ||   ||||
                                 CCTGTGACG   AC   GACA
                                      ____  C__
GAM260  KIAA1026  3'  CAGAGGCAGGGTGGCCC     71187      ATTG   G
                                 GGGC   TAT TTGCTTCTG
                                 ||||   ||| |||||||||
                                 CCCG   GTG GACGGAGAC
                                   ____  G
GAM260  KIAA1028  3'  TTACTGATCTCAGCATAATAAT 91951         _     CT_  T
            GCTC                    GGCATTGT ATGTTG   TC GTGG
                                 |||||||| ||||||   || ||||
                                 TCGTAATA TACGAC   AG CATT
                                     A     TCT  T
GAM260  KIAA1033  3'  TAGAATGGGTGTACAATGCCC  64518          TG  GC
                                 GGGCATTGTA  TT  TTCTG
                                 ||||||||||  ||  |||||
                                 CCCGTAACAT  GG  AAGAT
                                      GT  GT
GAM260  KIAA1041  3'  ATGGAGGCAAAGCCT      30126      ATTGTATG
                                 GGGC       TTGCTTCTGT
                                 ||||       ||||||||||
                                 TCCG       AACGGAGGTA
                                   A_______
GAM260  KIAA1041  3'  CAGAGTAAATGCTT       30129        GTATGT    T
                                 GGGCATT     TGCT CTG
                                 |||||||     |||| |||
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                                TTCGTAA     ATGA GAC
                                  _______   _
GAM260  KIAA1042 3' CGTAGGAGCGTAAGGAGCCT  30336     A TG  GTT     TG
                                GGGC T  TAT  GCTTCTG  G
                                |||| |  |||  |||||||  |
                                TCCG G  ATG  CGAGGAT  C
                                  A GA  ___      GT
GAM260  KIAA1042 3' GCAGCCATTCAATGCCC     30340        T  _
                                GGGCATTG ATG TTGC
                                |||||||| ||| ||||
                                CCCGTAAC TAC GACG
                                     T  C
GAM260  KIAA1045 3' TCACAGATCAAGGTGATGCCT  71058       GT  G  CT
                                GGGCATT  AT TTG  TCTGTGG
                                |||||||  || |||  |||||||
                                TCCGTAG  TG AAC  AGACACT
                                   __ G  T_
GAM260  KIAA1045 3' TCATAATAAAGCGATTGCGATG 71060        T     C__
           CTC                    GGCATTGTA GTTGCTT  TGTGG
                                |||||||||| |||||||  |||||
                                TCGTAGCGT TAGCGAA  ATACT
                                   _     ATA
GAM260  KIAA1055 3' TCACCGATGTGATGTGCAGGCC 66068     A      TG T  T
           C                    GGGC TTGTATGT  C TC GTGG
                                |||| ||||||||  | || ||||
                                CCCG GACGTGTA  G AG CACT
                                  _      GT T  C
GAM260  KIAA1055 3' ACCCACGGTGGTATGTTAGTGT 66056       TATGT   T
           TT                    GGGCATTG    TGCT CTGTGG
                                |||||||||    |||| ||||||
                                TTTGTGAT    ATGG GGCACC
                                   TGT__   T    CAA
GAM260  KIAA1055 3' CAGAATGTAACGTGTGTGTCC  66057      TGT     _
                                GGGCAT   ATGTTGC TTCTG
                                ||||||   ||||||| |||||
                                CCTGTG   TGCAATG AAGAC
                                   TG_      T
GAM260  KIAA1058 3' CACTGACATTGATGCCT     82253        T     CTTC
                                GGGCATTG ATGTTG   TG
                                |||||||| ||||||   ||
                                TCCGTAGT TACAGT   AC
                                   _     C___
GAM260  KIAA1058 3' CAGGGCAGCGTGAGTGTTC   82254       G       T
                                GGGCATT TATGTTGCT CTG
                                ||||||| ||||||||| |||
                                CTTGTGA GTGCGACGG GAC
                                   _      _
GAM260  KIAA1068 3' TCACAGGGGCTCTGGGTGCCC  31039       GTATGTT
                                GGGCATT      GCTTCTGTGG
                                |||||||      ||||||||||
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                                CCCGTGG      CGGGGACACT
                                    GTCT___
GAM260  KIAA1069 3' CGCAGGAGAGTGTAATTTCC  67934    CATTG  TG  G     TG
                                GGG    TA  TT CTTCTG  G
                                |||    ||  || ||||||  |
                                CCT    AT  GA GAGGAC  C
                                  TTA__  GT  _     GT
GAM260  KIAA1078 3' CTGTTGAGCAATGTACAGTGT  65121             CTGTGG
                                GCATTGTATGTTGCTT
                                ||||||||||||||||
                                TGTGACATGTAACGAG
                                          TTGTC
GAM260  KIAA1084 3' CAGTGTGGCACATAATGTTT   29834         A   TG TT
                                GGGCATTGT TGT  C  CTG
                                ||||||||| |||  |  |||
                                TTTGTAATA ACG  G  GAC
                                      C   GT T_
GAM260  KIAA1084 5' TCGCGGAAGCAGCAGCCGCC   29841     ATT  A
                                GGC   GT TGTTGCTTCTGTGG
                                |||   || ||||||||||||||
                                CCG   CG ACGACGAAGGCGCT
                                  C__  _
GAM260  KIAA1091 5' CGGGGGCTCGGTGCC       69683        TATGTT
                                GGCATTG     GCTTCTG
                                |||||||     |||||||
                                CCGTGGC     CGGGGGC
                                    T_____
GAM260  KIAA1096 3' CCATATCAAAGTGAGCAGTGTT 68528         ATG TG   C__
           T                     GGGCATTGT   T  CTT   TGTGG
                                |||||||||   |  |||   |||||
                                TTTGTGACG   A  GAA   ATACC
                                      ___ GT   ACT
GAM260  KIAA1102 3' TCATGGAGGTGTTTGCTGTTT  69015      TT   TGT
                                GGGCA  GTA   TGCTTCTGTGG
                                |||||  |||   ||||||||||
                                TTTGT  CGT   GTGGAGGTACT
                                   __   TT_
GAM260  KIAA1128 3' AAGTGGGCATACATGTTC     68467       T    _ TG
                                GGGCAT GTATG T  CTT
                                |||||| ||||| |  |||
                                CTTGTA CATAC G  GAA
                                    _    G GT
GAM260  KIAA1130 3' CGCGGGGGCCATGTGGGCCC   62417     A TG    TT      TG
                                GGGC T  TATG  GCTTCTG  G
                                |||| |  ||||  |||||||  |
                                CCCG G  GTAC  CGGGGGC  C
                                  _ GT    __      GT
GAM260  KIAA1130 3' CTACAGGAGCAACTCTTCTCCC 62418     CATTGTAT
                                GGG       GTTGCTTCTGTGG
                                |||       ||||||||||||
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                                CCC       CAACGAGGACATC
                                  TCTTCT__
GAM260  KIAA1136 3' GACATGTAACATGTAAGGTCC 91317      A         TTC   GG
                                GGGC TTGTATGTTGC   TGT
                                |||| ||||||||||   |||
                                CCTG AATGTACAATG   ACA
                                  G         T__   GC
GAM260  KIAA1161 3' CATAGGGGCAGTTTCTCCC   81740     CATTGTATG
                                GGG       TTGCTTCTGTG
                                |||       ||||||||||
                                CCC       GACGGGGATAC
                                  TCTTT____
GAM260  KIAA1161 3' CATAGGGGTGGAGCTGCCC   81741      TTGTATG TG
                                GGGCA      T  CTTCTGTG
                                |||||      |  ||||||||
                                CCCGT      G  GGGGATAC
                                   CGA____ GT
GAM260  KIAA1169 5' CTACAGGAGTGGTATGAGGAGC 35448    A TG    TT
                                GC T  TATG  GCTTCTGTGG
                                || |  ||||  ||||||||||
                                CG G  GTAT  TGAGGACATC
                                 A GA    GG
GAM260  KIAA1169 3' TCACGGGAGCAATGCTGTACGG 35451        ___
           T                     ATTGTAT   GTTGCTTCTGTGG
                                |||||||   ||||||||||||
                                TGGCATG   TAACGAGGGCACT
                                    TCG
GAM260  KIAA1183 3' CACTCAGACTGCAGTGTTT   62526         T   GCTTCT
                                GGGCATTGTA GTT     GTG
                                |||||||||| |||     |||
                                TTTGTGACGT CAG     CAC
                                      _   ACT___
GAM260  KIAA1183 3' CAGGGCGTGGGTGCTC      62527        G    TGCT
                                GGGCATT TATGT    TCTG
                                ||||||| |||||    ||||
                                CTCGTGG GTGCG    GGAC
                                   _    _____
GAM260  KIAA1183 3' CCCTGGGGCAATGTGTGTGCTT 62531       TGT        TGT
                                GGGCAT   ATGTTGCTTC   GG
                                ||||||   ||||||||||   ||
                                TTCGTG   TGTAACGGGG   CC
                                   TG_         TC_  T
GAM260  KIAA1183 3' CGCAGAGGCGAGCAGGGCTC   62532     A    ATG       TG
                                GGGC TTGT   TTGCTTCTG  G
                                |||| ||||   |||||||||  |
                                CTCG GACG   AGCGGAGAC  C
                                  G    ___        GT
GAM260  KIAA1184 3' TCACAGTGGCCTCAAGTGTGAT 42618      TG   GTT__   T
           GCCT                   GGCAT  TAT    GCT CTGTGG
                                |||||  |||    ||| ||||||
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                                CCGTA  GTG    CGG GACACT
                                  GT   AACTC   T
GAM260  KIAA1185  3'  TTATGGGAGAAAAGTACAGTGC 62612         GTTG
            T                    GGCATTGTAT   CTTCTGTGG
                                 ||||||||||   |||||||||
                                 TCGTGACATG   GAGGGTATT
                                      AAAA
GAM260  KIAA1193  5'  TTGCAGACAACAGCAGTGGTGT 67655      TG A    CT_   TG
            CC                   GGGCAT  T TGTTG   TCTG  G
                                 ||||||  | |||||   ||||  |
                                 CCTGTG  G ACGAC   AGAC  T
                                   GT _    AAC    GT
GAM260  KIAA1200  3'  CTATTTCAGGCATGTGGGCCT  62372     A TG     GCTTCT
                                 GGGC T  TATGTT     GTGG
                                 ||||  |  ||||||     ||||
                                 TCCG G  GTACGG     TATC
                                   _ GT     ACTT__
GAM260  KIAA1209  3'  CCATAACCTGACAATAGTGCCC 60753        A   GCTTC
                                 GGGCATTGT TGTT    TGTGG
                                 |||||||||  ||||    |||||
                                 CCCGTGATA ACAG    ATACC
                                      _   TCCA_
GAM260  KIAA1211  3'  CTCGCTCAATATGCAATGTGC  68892   G         CTTCT
                                 G GCATTGTATGTTG    GTGG
                                 | ||||||||||||    ||||
                                 C TGTAACGTATAAC    CGCT
                                  G          T____    CG
GAM260  KIAA1219  3'  TTACAGTGCTACAGTATACACT 61373    T   ___   T  TT
            GCTC                   GCA TGTA   TGT GC  CTGTGG
                                 |||  ||||   ||| ||  ||||||
                                 CGT ACAT   ACA CG  GACATT
                                   C    ATG   T  T_
GAM260  KIAA1228  3'  CCGTAGGAGTCGGATGTGTCT  65039      TGTA  TT
                                 GGGCAT    TG  GCTTCTGTGG
                                 ||||||    ||  ||||||||||
                                 TCTGTG    GC  TGAGGATGCC
                                    TAG_  __
GAM260  KIAA1237  3'  CATTGAACGGACAGTGTTT    80466         A   TGCT  T
                                 GGGCATTGT TGT    TC GTG
                                 |||||||||  |||    || |||
                                 TTTGTGACA GCA    AG TAC
                                      G   ____  T
GAM260  KIAA1244  3'  TTATAGAAGAATCTATAATCCT 71996     C     T   G
                                 GGG ATTGTA GTT CTTCTGTGG
                                 ||| |||||| ||| |||||||||
                                 TCC TAATAT TAA GAAGATATT
                                   _     C   _
GAM260  KIAA1254  3'  CAAGATGACAATGTCT      70015          _  G
                                 GGGCATTGT AT TTG
                                 |||||||||  ||  |||
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                              TCTGTAACA TA AAC
                                   G  G
GAM260  KIAA1255 5' AGCAGATGTGATGTCT     67161       TG   G
                              GGGCAT  TAT TTGCT
                              ||||||  ||| |||||
                              TCTGTA  GTA GACGA
                                 GT   _
GAM260  KIAA1260 3' AGTGATATATCAGTGTTT    60022        _    TG
                              GGGCATTG TATGT  CT
                              |||||||| |||||  ||
                              TTTGTGAC ATATA  GA
                                   T    GT
GAM260  KIAA1260 3' TGTAGGAGGATGTGATGTCC  60032      TG  GTTG    TG
                              GGGCAT  TAT   CTTCTG  G
                              ||||||  |||   ||||||  |
                              CCTGTA  GTA   GAGGAT  T
                                 GT   G___    GT
GAM260  KIAA1271 3' CCACTGGAACATGTGGTGCTT 69540      TG    G  TCT
                              GGGCAT  TATGTT CT   GTGG
                              ||||||  |||||| ||   ||||
                              TTCGTG  GTACAA GG   CACC
                                 GT     _  T__
GAM260  KIAA1274 3' TGCAGAACTACTGTGTGTCT  91372      TGTAT  TGC    TG
                              GGGCAT    GT   TTCTG  G
                              ||||||    ||   |||||  |
                              TCTGTG    CA   AAGAC  T
                                 TGT__  TC_    GT
GAM260  KIAA1280 5' CAGAGGTCAGTCTC      69712     C    TATGTT
                              GGG ATTG     GCTTCTG
                              ||| ||||     |||||||
                              CTC TGAC     TGGAGAC
                                _   _______
GAM260  KIAA1297 3' CGCAGGAGTACGAGGTGCT   72175      GTAT  T     TG
                              GGCATT    GT GCTTCTG  G
                              ||||||    || |||||||  |
                              TCGTGG    CA TGAGGAC  C
                                 AG__  _      GT
GAM260  KIAA1297 3' GTGGGGGGCCGCTTTGATGCCT 72184        TAT  T    GTGG
                              GGGCATTG   GT GCTTCT
                              ||||||||   || ||||||
                              TCCGTAGT   CG CGGGGG
                                   TT_  C     GTGT
GAM260  KIAA1318 3' CTACAAGAGTGTATGGTGT   67307     TG   GTT   TC
                              GCAT  TAT   GCT  TGTGG
                              ||||  |||   |||  |||||
                              TGTG  ATG   TGA  ACATC
                                GT   ___   GA
GAM260  KIAA1320 3' TAGAAGTCACTGCCT      69308      TTGTAT  T
                              GGGCA     GT GCTTCTG
                              |||||     || |||||||
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                                TCCGT     CA TGAAGAT
                                  _______ C
GAM260  KIAA1332 3' CAGAAATGCCAGTGCCT     71161        TAT  TGC
                                GGGCATTG   GT   TTCTG
                                ||||||||   ||   |||||
                                TCCGTGAC   CG   AAGAC
                                    ___  TA_
GAM260  KIAA1340 3' TTACAGAAGTGGAATGGTTTCT 69187     C  TG ATG TG
                                GGG AT  T   T  CTTCTGTGG
                                ||| ||  |   |  |||||||||
                                TCT TG  A   G  GAAGACATT
                                  T  GT A__ GT
GAM260  KIAA1340 3' TTATGGGAGCAAATCCATCTCC 69188     CAT  TATG
                                GGG   TG   TTGCTTCTGTGG
                                |||   ||   ||||||||||||
                                CCT   AC   AACGAGGGTATT
                                  CT_  CTA_
GAM260  KIAA1344 3' GTAGCATGTGATGCCT      72449       TG
                                GGGCAT  TATGTTGC
                                ||||||  ||||||||
                                TCCGTA  GTACGATG
                                   GT
GAM260  KIAA1349 3' TGTAGAGGGGGGCAAAGCCC   70761     A   ATG  G     TG
                                GGGC TTGT   TT CTTCTG  G
                                |||| ||||   || ||||||  |
                                CCCG AACG   GG GGAGAT  T
                                  A   ___  G     GT
GAM260  KIAA1363 5' CGTAGAGGGGGGCATGTCC    69262      TTGTA   G
                                GGGCA    TGTT CTTCTGTG
                                |||||    |||| ||||||||
                                CCTGT    ACGG GGAGATGC
                                   _____   G
GAM260  KIAA1384 3' ATGGAGGTTTGTGCTT      64578       TGTATGTT
                                GGGCAT      GCTTCTGT
                                ||||||      ||||||||
                                TTCGTG      TGGAGGTA
                                   TT_______
GAM260  KIAA1389 3' TGCAGGAACAAATGGTGCCT   69768       TG A   TGC    TG
                                GGGCAT  T TGT   TTCTG  G
                                ||||||  | |||   |||||  |
                                TCCGTG  A ACA   AGGAC  T
                                   GT A   ___     GT
GAM260  KIAA1409 3' TCACAGAAAAGTTGTATAAGTC 61216     A      TTGC
           C                     GGGC TTGTATG    TTCTGTGG
                                ||||  |||||||    ||||||||
                                CCTG AATATGT    AAGACACT
                                  _      TGAA
GAM260  KIAA1414 3' TATATTGGTATTATAGTGCTT  67993         TGT    TC   G
                                GGGCATTGTA   TGCT  TGTG
                                ||||||||||   ||||  ||||
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                                TTCGTGATAT  ATGG  ATAT
                                     T__   TT   G
GAM260  KIAA1466 5' CACAGAGGGAAGCAGGTTT  71914     A   ATG  G
                                GGGC TTGT  TT CTTCTGTG
                                |||| ||||  || ||||||||
                                TTTG GACG  AA GGAGACAC
                                  _   ___ G
GAM260  KIAA1466 3' TATAGAGGCAGTTGTGGCC  71917   G  TGTATG
                                GG CAT     TTGCTTCTGTG
                                || |||     ||||||||||
                                CC GTG     GACGGAGATAT
                                 G  TT____
GAM260  KIAA1524 5' CTACAGAAGTTAACATATAATG 73455          _
           TC                    GGCATTGTATGTTG CTTCTGTGG
                                |||||||||||||| |||||||||
                                CTGTAATATACAAT GAAGACATC
                                       T
GAM260  KIAA1533 5' CCGCGGAAGGCCAGGCCGGTGC 73756       TA_  TTG
           CC                    GGGCATTG  TG  CTTCTGTGG
                                |||||||  ||  |||||||||
                                CCCGTGGC  AC  GAAGGCGCC
                                    CGG  CG_
GAM260  KIAA1538 3' GGGCAGAGGTGACGACAGTGCC 71549       A  TG     GG
           C                     GGGCATTGT TGT  CTTCTGT
                                |||||||| |||  |||||||
                                CCCGTGACA GCA  GGAGACG
                                     _  GT     GGG
GAM260  KIAA1538 3' CGCGGAAGCACCAAGAGGCCC  71541    ATTGTA  T     TG
                                GGGC    TG TGCTTCTG  G
                                ||||    || ||||||||  |
                                CCCG    AC ACGAAGGC  C
                                  GAGA__  C      GT
GAM260  KIAA1538 5' CTGCAGAGGTGACGGACCCGTC 71542    ATT  A  TG    TG
           C                     GGGC  GT TGT  CTTCTG  G
                                ||||  || |||  ||||||  |
                                CCTG  CA GCA  GGAGAC  C
                                  CC_  G  GT    GT
GAM260  KIAA1560 3' CCACAGATAGTTGTAGTGTTT  64175        TGTT  _
                                GGGCATTGTA   GCT TCTGTGG
                                ||||||||||   ||| |||||||
                                TTTGTGATGT   TGA AGACACC
                                     ____  T
GAM260  KIAA1580 5' CGCGGGGGTTGGTGTGTTC   69444      TGTATGTT
                                GGGCAT      GCTTCTGTG
                                ||||||      |||||||||
                                CTTGTG      TGGGGGCGC
                                   TGGT____
GAM260  KIAA1582 3' CACGGCGTGCAGTTTTC    65369    C       CTTC
                                GGG ATTGTATGTTG   TG
                                ||| ||||||||||   ||
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                                CTT TGACGTGCGGC   AC
                                  T       ____
GAM260  KIAA1587 5' CGCGGGCCTGTCGGTGTCT   40510       TATGTT  TT
                                GGGCATTG    GC  CTGTG
                                ||||||||    ||  |||||
                                TCTGTGGC    CG  GGCGC
                                    TGTC__  __
GAM260  KIAA1594 3' GGAGTAACGTAGAATGCTC   72085       G
                                GGGCATT TATGTTGCTTC
                                ||||||| ||||||||||
                                CTCGTAA ATGCAATGAGG
                                    G
GAM260  KIAA1613 3' CATAAAGATACAGTGCCT    64816         G  GCTTC
                                GGGCATTGTAT TT    TGTG
                                |||||||||| ||    ||||
                                TCCGTGACATA AA    ATAC
                                      G _____
GAM260  KIAA1623 3' TCACAGGGGCGGCCGGTCTCC 72069    C   TAT
                                GGG ATTG  GTTGCTTCTGTGG
                                ||| ||||  ||||||||||||
                                CCT TGGC  CGGCGGGGACACT
                                  C   ___
GAM260  KIAA1634 3' TTACAGAGAGAAATATGTGAGT 63395    A TG    G  _
           CC                   GGGC T  TATGTT CT TCTGTGG
                                |||| |  |||||| || |||||||
                                CCTG A  GTATAA GA AGACATT
                                  _ GT    A  G
GAM260  KIAA1638 3' CACGTGCAGATACAATGCTC  47100         G   TTC   G
                                GGGCATTGTAT TTGC  TGTG
                                |||||||||| ||||  ||||
                                CTCGTAACATA GACG  GCAC
                                      _   T__   G
GAM260  KIAA1641 3' CACAGGAGTGAAAATCCT    80206    C  GTATG TG
                                GGG ATT    T  CTTCTGTG
                                ||| |||    |  ||||||||
                                TCC TAA    A  GAGGACAC
                                  _  A____ GT
GAM260  KIAA1649 3' CAGCTTCAGTGTGCAGGCTC  66975    A    TG  CTT
                                GGGC TTGTA  TTG  CTG
                                |||| |||||  |||  |||
                                CTCG GACGT  GAC  GAC
                                  _    GT   TTC
GAM260  KIAA1649 3' TCAGCCTCCCATTGTGCAGTGC 66983        GT  CTT__  TGG
           TT                   GGGCATTGTAT  TG    CTG
                                ||||||||||  ||    |||
                                TTCGTGACGTG  AC    GAC
                                      TT  CCTCC   T
GAM260  KIAA1649 3' CAGCTTCAGTGTGCAGGCTC  50247    A    TG  CTT
                                GGGC TTGTA  TTG  CTG
                                |||| |||||  |||  |||
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                                CTCG GACGT  GAC   GAC
                                  _    GT   TTC
GAM260  KIAA1649 5' CCATCCAGAAGGAACATGCAGT 50253          G    __
                GTTT                GGCATTGTATGTT CTTCTG  TGG
                                    |||||||||||| ||||||  |||
                                    TTGTGACGTACAA GAAGAC  ACC
                                          G     CT
GAM260  KIAA1655 3' TATAGGCCAGGTGGTGTCC   66623       TG A  TT  TT
                                    GGGCAT  T TG  GC  CTGTG
                                    ||||||  | ||  ||  |||||
                                    CCTGTG  G AC  CG  GATAT
                                       GT G  __  __
GAM260  KIAA1671 3' CTGCAGCCCAAGTGGTGGTGCC 65674       TG ATG   CTT   TG
                T                    GGGCAT  T   TTG   CTG  G
                                    ||||||  |   |||   |||  |
                                    TCCGTG  G   AAC   GAC  C
                                       GT GTG   CC_   GT
GAM260  KIAA1677 3' GGTGCAATATTGCAATGCCT   67070          _     T
                                    GGGCATTGTA TGTTGC TC
                                    |||||||||| ||||||  ||
                                    TCCGTAACGT ATAACG GG
                                          T     T
GAM260  KIAA1679 3' CACAGTCATGCGATCCC     70149     C       TTGCTT
                                    GGG ATTGTATG     CTGTG
                                    ||| ||||||||     |||||
                                    CCC TAGCGTAC     GACAC
                                      _       T_____
GAM260  KIAA1691 3' GGCTTTAGTGTACGATGTTT   92562          TG  ___
                                    GGGCATTGTA  TT   GCT
                                    ||||||||||  ||   |||
                                    TTTGTAGCAT  GA   CGG
                                          GT  TTT
GAM260  KIAA1706 3' TTGCAGAGGCGCCTCTCAAGGC 92793     A   TATGT      TG
                CC                    GGGC TTG    TGCTTCTG  G
                                    |||| |||    ||||||||  |
                                    CCCG AAC    GCGGAGAC  T
                                      G   TCTCC       GT
GAM260  KIAA1735 3' CGTGGGAACACAGTGTTC    87626         AT  TGC   TG
                                    GGGCATTGT  GT   TTC  TG
                                    |||||||||  ||   |||  ||
                                    CTTGTGACA  CA   AGG  GC
                                          __  ___   GT
GAM260  KIAA1750 3' CGCAGGGGGAGCATGCCT    68247      TTGTA    G
                                    GGGCA    TGTT CTTCTGTG
                                    |||||    |||| ||||||||
                                    TCCGT    ACGA GGGGACGC
                                       _____   G
GAM260  KIAA1766 3' TCATGTTGTCGGGGTGTGATGT 71356       TG   G   _ TTC
                CC                    GGGCAT  TAT TTG C   TGTGG
                                    ||||||  ||| ||| |   |||||
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                              CCTGTA  GTG GGC G   GTACT
                                 GT   G   T TT_
GAM260  KIAA1776 3' GCAATGTGCAATCCC      50591     C
                              GGG ATTGTATGTTGC
                              ||| ||||||||||||
                              CCC TAACGTGTAACG
                                _
GAM260  KIAA1786 3' GCGGTATCACAGTGCTT     66033         _   TT
                              GGGCATTGT ATG  GC
                              ||||||||| |||  ||
                              TTCGTGACA TAT  CG
                                   C   GG
GAM260  KIAA1786 3' CGCAGAGGTAGTGAGTTC    66025      A TG ATGT       TG
                              GGGC T  T    TGCTTCTG  G
                              |||| |  |    ||||||||  |
                              CTTG A  G    ATGGAGAC  C
                                _ GT ____       GT
GAM260  KIAA1786 3' CTATGGCTTCAGTGTCAATGTT 66026        T TG   CTT
           T                   GGGCATTG A  TTG   CTGTGG
                              |||||||| |  |||   ||||||
                              TTTGTAAC T  GAC   GGTATC
                                  _ GT   TTC
GAM260  KIAA1813 5' TCATGGAAACTGGTATGAGCCT 70309      A TG   GTTGC
                              GGGC T  TAT    TTCTGTGG
                              |||| |  |||    ||||||||
                              TCCG A  ATG    AAGGTACT
                                _ GT   GTCA_
GAM260  KIAA1819 3' CTGTAGAGGCTGAACTGTTGAT 69679       TAT  __     TG
           GTTC                   GGCATTG   GTT  GCTTCTG  G
                              |||||||   |||  |||||||  |
                              TTGTAGT   CAA  CGGAGAT  C
                                  TGT   GT     GT
GAM260  KIAA1838 3' TGGGAGCCAGGCCT       64736     A   TATGTT
                              GGGC TTG     GCTTCTG
                              |||| |||     |||||||
                              TCCG GAC     CGAGGGT
                                _  _______
GAM260  KIAA1838 3' TCATTCATATATATGATGCCT  64735       TG    TGCTTCT
                              GGGCAT  TATGT      GTGG
                              ||||||  |||||      ||||
                              TCCGTA  ATATA      TACT
                                 GT    TACT___
GAM260  KIAA1841 3' CGTGGAAAGTACAATGTT    80045         GTTGC   TG
                              GGCATTGTAT    TTC  TG
                              ||||||||||    |||  ||
                              TTGTAACATG    AAG  GC
                                    A____   GT
GAM260  KIAA1854 3' CAGAGCTTGCAATATCT     71739    GC     TGTT   T
                              GG  ATTGTA    GCT CTG
                              ||  ||||||    ||| |||
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                                TC  TAACGT    CGA GAC
                                 TA     T___  _
GAM260  KIAA1854  5' GGTCGGCCTGCAGTGCCC    71746         T   _
                                GGGCATTGTA GTTG CT
                                |||||||||| |||| ||
                                CCCGTGACGT CGGC GG
                                      C   T
GAM260  KIAA1866  3' CATGGAATGCTACATGC     60933       T _
                                GTATGT GC TTCTGTG
                                |||||| || |||||||
                                CGTACA CG AAGGTAC
                                   T  T
GAM260  KIAA1877  3' CACAGGGCTGCAGGTGCCC   66167       GTA  T  T
                                GGGCATT   TGT GCT CTGTG
                                |||||||   ||| ||| |||||
                                CCCGTGG   ACG CGG GACAC
                                   ___   T  _
GAM260  KIAA1877  3' CATGGAATACCGATGCTC    66170       TAT  TGC
                                GGGCATTG   GT   TTCTGTG
                                ||||||||   ||   |||||||
                                CTCGTAGC   CA   AAGGTAC
                                     ___  T__
GAM260  KIAA1879  5' CAGATGATAGCAATGCCT    73563        A    CT
                                GGGCATTGT TGTTG  TCTG
                                ||||||||| |||||  ||||
                                TCCGTAACG ATAGT  AGAC
                                          _    __
GAM260  KIAA1881  3' CGTGGAGGCTGGCAGGCTC   95339     A   ATGTT    TG
                                GGGC TTGT    GCTTC  TG
                                |||| ||||    |||||  ||
                                CTCG GACG    CGGAG  GC
                                  _   GT___    GT
GAM260  KIAA1881  3' TAGGAGCCTGCAGGCCC     95344     A    TGTT
                                GGGC TTGTA    GCTTCTG
                                |||| |||||   |||||||
                                CCCG GACGT    CGAGGAT
                                  _    C___
GAM260  KIAA1904  3' CGTGGGAGCAGCCTGTGTCC  73482       TGTAT       TG
                                GGGCAT    GTTGCTTCTG  G
                                ||||||    ||||||||||  |
                                CCTGTG    CGACGAGGGT  C
                                   TC___        GT
GAM260  KIAA1906  3' CATGGGAATGGAATGCTC    73191       G   GTTGC
                                GGGCATT TAT    TTCTGTG
                                ||||||| |||    |||||||
                                CTCGTAA GTA    AGGGTAC
                                   G  _____
GAM260  KIAA1915  3' AGGCCACATATGATGTCT    73274       TG    T
                                GGGCAT  TATGT GCTT
                                ||||||  ||||| ||||
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                                TCTGTA  ATACA CGGA
                                   GT    C
GAM260  KIAA1922 5' TACAGGAGCAGGTGGCCC    73638     ATTGTATG
                                GGGC      TTGCTTCTGTG
                                ||||      ||||||||||
                                CCCG      GACGAGGACAT
                                  GTG_____
GAM260  KIAA1922 5' TACAGGAGGAGCAGGCCT    73639     ATTGTA   G
                                GGGC     TGTT CTTCTGTG
                                ||||     |||| ||||||||
                                TCCG     ACGA GAGGACAT
                                  G_____   G
GAM260  KIAA1922 3' CCACAGAATCTGTGTGTGATGT 73619      TG  TG TGC
           CC                    GGGCAT  TA  T   TTCTGTGG
                                ||||||  ||  |   ||||||||
                                CCTGTA  GT  G   AAGACACC
                                   GT  GT TCT
GAM260  KIAA1924 3' GCGAATGGGTTGCAGTGCTC   73680        TG____
                                GGGCATTGTA     TTGC
                                ||||||||||     ||||
                                CTCGTGACGT     AGCG
                                     TGGGTA
GAM260  KIAA1940 5' CCGTGGAGGTGGGGGCGGTGGT 79980      TG ATG__ TG   TG
           GCT                   GGCAT  T    T  CTTC  TGG
                                |||||  |    |  ||||  |||
                                TCGTG  G    G  GGAG  GCC
                                  GT GCGGG GT   GT
GAM260  KIAA1946 3' CCATAGAAGAAATAATGTTT   82469        ATGTTG
                                GGGCATTGT     CTTCTGTGG
                                |||||||||     |||||||||
                                TTTGTAATA     GAAGATACC
                                     AA____
GAM260  KIAA1950 3' CGCAGGAGGTGAGGGTGTCT   92589      G_  GTTG     TG
                                GGGCATT  TAT    CTTCTG  G
                                |||||||  |||   ||||||  |
                                TCTGTGG  GTG   GAGGAC  C
                                   GA  _____     GT
GAM260  KIAA1958 3' CGCAGAAGTTCTCCATGTTC   81901      TGTATGTT      TG
                                GGGCAT       GCTTCTG  G
                                ||||||       |||||||  |
                                CTTGTA       TGAAGAC  C
                                   CCTCT___      GT
GAM260  KIAA1962 5' GGCTGTGTATAGTGCCT     81918        TG T
                                GGGCATTGTA  T GCT
                                ||||||||||  | |||
                                TCCGTGATAT  G CGG
                                     GT T
GAM260  KIAA1975 5' ACGACAGGCGCTGGTGTGTGAT 73968      TG  TG  _  T    GG
           GTTC                  GGCAT  TA  TT GC TCTGT
                                |||||  ||  || || |||||
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                                TTGTA  GT  GG CG GGACA
                                  GT  GT  T  C    GCAC
GAM260  KIAA1987  3'  CTGCAGGGTTGGACGTGGTGCC 88015      TG    __  T  TG
            C                    GGGCAT  TATGTT  GCT CTG  G
                                 ||||||  ||||||  ||| |||  |
                                 CCCGTG  GTGCAG  TGG GAC  C
                                    __     GT  _  GT
GAM260  KLHL4    3'  TCATAGAAGAGACATGTATGTT 38924      TGT   TG
            T                    GGGCAT   ATGT  CTTCTGTGG
                                 ||||||   ||||  |||||||||
                                 TTTGTA   TACA  GAAGATACT
                                    TG_   GA
GAM260  KLHL8    3'  TTACGGAAGTAGAAAAAATGTT 62858       GTATG
            C                    GGGCATT    TTGCTTCTGTGG
                                 |||||||    ||||||||||||
                                 CTTGTAA    GATGAAGGCATT
                                     AAAA_
GAM260  KLK6     3'  CTGCAGAGGCCCAGCCACGTGT 10920       _  TA  TT     TG
            CT                    GGGCAT TG  TG  GCTTCTG  G
                                 ||||||  ||  ||  |||||||  |
                                 TCTGTG AC  AC  CGGAGAC  C
                                    C  CG  C_     GT
GAM260  KNSL7    3'  GTTATGGAAGTTCTAACAATAT 39617   G     _______
            ATGGTG                  TATGTTG     CTTCTGTGG   T
                                  |||||||     |||||||||  |
                                  ATATAAC     GAAGGTATT   G
                                 T      AATCTT
GAM260  KOC1     3'  TCATAGATGGTGTGACAGTGTT 91078         ATGT   _
            T                    GGGCATTGT    TGCT TCTGTGG
                                 |||||||||    |||| |||||||
                                 TTTGTGACA    GTGG AGATACT
                                      GT__    T
GAM260  LBP-9    3'  CCACAGGAGCGATGTGTTTTCT 27276     CATTG
            C                    GGG    TATGTTGCTTCTGTGG
                                 |||    ||||||||||||||||
                                 CTC    GTGTAGCGAGGACACC
                                   TTTT_
GAM260  LC27     3'  CCGTGGGAGCAGTGACCATCTG 60126     T_  TA GT     TG
            CT                    GGCA  TG  T  TGCTTC  TGG
                                 ||||  ||  |  ||||||  |||
                                 TCGT  AC  G  ACGAGG  GCC
                                   CT  CA TG     GT
GAM260  LCE      3'  CCATGGGGGCAGCTCCATCCC  44027     CAT  TAT
                                 GGG   TG   GTTGCTTCTGTGG
                                 |||   ||   ||||||||||||
                                 CCC   AC   CGACGGGGGTACC
                                   T__  CT_
GAM260  LHX6     3'  CTACAGTGTTTGTGGGATGTCC 26856       G   TT  TT
                                 GGGCATT TATG  GC  CTGTGG
                                 |||||||  ||||  ||  ||||||
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                              CCTGTAG GTGT  TG  GACATC
                                  G   T_  T_
GAM260  LIPF     3'  TCATAATGTTTGACATGCAGTG 14828          __  TTC
             CTT                  GGCATTGTATGTT  GC   TGTGG
                              ||||||||||||  ||  |||||
                              TCGTGACGTACAG  TG   ATACT
                                    TT  TA_
GAM260  LMOD1    3'  CATGGGAGCGTCCAGGCCT   24042     A   TATGT
                              GGGC TTG    TGCTTCTGTG
                              |||| |||    ||||||||||
                              TCCG GAC    GCGAGGGTAC
                                _  CT___
GAM260  LNIR     3'  CCGTGGAGGGGTGACTGTGTCC 48129       T  ATGTTG   TG
                              GGGCAT GT     CTTC  TGG
                              |||||| ||     ||||  |||
                              CCTGTG CA     GGAG  GCC
                                  T  GTGG__    GT
GAM260  LNX      3'  TCATAGAGGCCACCCAGATGCC 50920       GTAT  T
             T                   GGGCATT    GT GCTTCTGTGG
                              |||||||    || ||||||||||
                              TCCGTAG    CA CGGAGATACT
                                  ACC_  C
GAM260  LNX      5'  TGTGGGGGCATGGCAAGGTTT  50922     A   ATGT      TG
                              GGGC TTGT    TGCTTCTG  G
                              |||| ||||    ||||||||  |
                              TTTG AACG    ACGGGGGT  T
                                G   GT__      GT
GAM260  LRP1B    5'  CTGCAGAAGCAGCCCTGTGCTC 37669       TGTAT       TG
                              GGGCAT    GTTGCTTCTG  G
                              ||||||    ||||||||||  |
                              CTCGTG    CGACGAAGAC  C
                                 TCC__       GT
GAM260  LUC7L    3'  TCATGTTCTGTGCATATAGTGT 35913          TGCTTCT
             T                   GGCATTGTATGT      GTGG
                              ||||||||||||      ||||
                              TTGTGATATACG      TACT
                                    TGTCTTG
GAM260  M96      3'  TCATAAAGTGCAGTGTATATAA 23740         __   TTC_
             TGCCT                CATTGTATG  TTGC    TGTGG
                              |||||||||  ||||   |||||
                              GTAATATAT  GACG    ATACT
                                   GT    TGAA
GAM260  MACMARCKS 3'  TTAGGTTAGTGATGTGAAATGC 43451       G    TG __   TGG
             TC                   GGGCATT TATGT  CT  TCTG
                              |||||||  |||||  ||  ||||
                              CTCGTAA GTGTA  GA  GGAT
                                  A    GT  TT    T
GAM260  MAD4     3'  CGTAGGGGGCATGGTGCCT   21272       TG    TG     TG
                              GGGCAT  TATGT  CTTCTG  G
                              ||||||  |||||  ||||||  |
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                                TCCGTG  GTACG  GGGGAT  C
                                  __    __     GT
GAM260  MADCAM1  3'  TCACAGAGATGGATGCATGTTC 55360      T   G  GC
                                GGGCAT GTAT TT  TTCTGTGG
                                |||||| |||| ||  ||||||||
                                CTTGTA CGTA GG  GAGACACT
                                   _   _  TA
GAM260  MADCAM1  3'  TCACAGAGATGGATGCATGTTC 55363      T   G  GC
                                GGGCAT GTAT TT  TTCTGTGG
                                |||||| |||| ||  ||||||||
                                CTTGTA CGTA GG  GAGACACT
                                   _   _  TA
GAM260  MADCAM1  3'  TCACAGAGATGGATGCATGTTC 55366      T   G  GC
                                GGGCAT GTAT TT  TTCTGTGG
                                |||||| |||| ||  ||||||||
                                CTTGTA CGTA GG  GAGACACT
                                   _   _  TA
GAM260  MAFB     3'  TAGGAGCCACAGCGCTC     18416      ATT  A   T
                                GGGC   GT TGT GCTTCTG
                                ||||   || ||| |||||||
                                CTCG   CG ACA CGAGGAT
                                  ___  _   C
GAM260  MAIL     3'  TTACAGGAGTGAGCCACCATGC 48655       T  ATG TG
           CC                     GGGCAT GT   T  CTTCTGTGG
                                |||||| ||   |  |||||||||
                                CCCGTA CA   A  GAGGACATT
                                   C  CCG GT
GAM260  MAL2     3'  CACGGTCCATACAGTCTC     53551     C      TTGCTT
                                GGG ATTGTATG     CTGTG
                                ||| ||||||||     |||||
                                CTC TGACATAC     GGCAC
                                  _      CT_____
GAM260  MAP      3'  TCACAGATCATGAAACAGTAGT 43055      GTA   GCT___
           GTTC                   GCATT   TGTT     TCTGTGG
                                |||||   ||||     |||||||
                                TGTGA   ACAA     AGACACT
                                   TG_    AGTACT
GAM260  MAP2K4   3'  AAACAAAAGGGTGTATAGTGTT 11544         TG  G   C   GG
           C                     GGGCATTGTA  TT CTT TGT
                                ||||||||||  || ||| |||
                                CTTGTGATAT  GG GAA ACA
                                     GT  _   A   AAA
GAM260  MAP2K6   3'  TCACAGAAAAAAATGGTGCCT  49248      TG ATG  GC
                                GGGCAT  T   TT  TTCTGTGG
                                ||||||  |   ||  ||||||||
                                TCCGTG  A   AA  AAGACACT
                                   GT ___   AA
GAM260  MAP2K6   3'  TCACAGAAAAAAATGGTGCCT  10873      TG ATG  GC
                                GGGCAT  T   TT  TTCTGTGG
                                ||||||  |   ||  ||||||||
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                                TCCGTG  A   AA  AAGACACT
                                   GT ___  AA
GAM260  MAPK8IP3  3'  ACAGAGGCAGAGCCC      52976      ATTGTATG
                                GGGC       TTGCTTCTGT
                                ||||       ||||||||||
                                CCCG       GACGGAGACA
                                  A________
GAM260  MAPK8IP3  3'  AGCCAGGGGTGTACAGTGCCT  52977          GTT      TGG
                                GGGCATTGTAT   GCTTCTG
                                ||||||||||   |||||||
                                TCCGTGACATG   TGGGGAC
                                      ___      CGAT
GAM260  MAPK8IP3  3'  CGTGGGGGCTGCTGCAGGCTC  52981      A    T  T      TG
                                GGGC TTGTA GT GCTTCTG  G
                                |||| ||||| || |||||||  |
                                CTCG GACGT CG CGGGGGT  C
                                  _    _ T      GT
GAM260  MAPK8IP3  3'  CTACAGGGGGCTGCCGCTGTGT 52982       T  AT  T    _
           CC                     GGGCAT GT  GT GCTTC TGTGG
                                ||||||| ||  || ||||| |||||
                                CCTGTG CG  CG CGGGG ACATC
                                   T  C_  T    G
GAM260  MAT2B     3'  GCTGGCATGTAATGCTT     25224            _
                                GGGCATTGTATGTT GC
                                |||||||||||||| ||
                                TTCGTAATGTACGG CG
                                      T
GAM260  MCF2L     3'  CGCAGGGGTAGCGCGGCCT    60843      ATTGTA        TG
                                GGGC     TGTTGCTTCTG  G
                                ||||     ||||||||||| |
                                TCCG     GCGATGGGGAC  C
                                  GC_____         GT
GAM260  MCOLN3    3'  AAGCAATATTTAATGTCT    36974        T
                                GGGCATTG ATGTTGCTT
                                |||||||| |||||||||
                                TCTGTAAT TATAACGAA
                                     T
GAM260  MEGF11    5'  CCGCGGGAGCAGCTATGCT    50579      TGTAT
                                GGCAT    GTTGCTTCTGTGG
                                |||||    ||||||||||||
                                TCGTA    CGACGAGGGCGCC
                                   T_____
GAM260  MESDC1    5'  AGCGGCATGCCAGTGCCC    42592        _
                                GGGCATTG TATGTTGCT
                                |||||||| |||||||||
                                CCCGTGAC GTACGGCGA
                                     C
GAM260  MESDC2    3'  TACTGGAGAGGCTGCGTACAGT 72499           T     G
           GTTT                    GGGCATTGTATGT GCTTCT TGG
                                ||||||||||||| |||||| |||
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                                TTTGTGACATGCG CGGAGA GTC
                                      T     G   ATA
GAM260  MFN2     3' CACATCACAGGTGATGTCC   29598       TG A   T CTTC
                                GGGCAT  T TGT G    TGTG
                                ||||||  | ||| |    ||||
                                CCTGTA  G ACA C    ACAC
                                   GT G   _ T___
GAM260  MGC10960 3' CTGCAGAAGTCTTCCACAGGCC 51005     A    ATGTT      TG
           T                    GGGC TTGT    GCTTCTG  G
                                |||| ||||    |||||||  |
                                TCCG GACA    TGAAGAC  C
                                  _   CCTTC      GT
GAM260  MGC10966 3' CACAGGGGCTCACTGCCC    48892      T  TATGTT
                                GGGCA TG     GCTTCTGTG
                                ||||| ||     |||||||||
                                CCCGT AC     CGGGGACAC
                                   C  T_____
GAM260  MGC10966 5' TCATGGGAGCTGCGGGTGTTT  48900       GTA   T
                                GGGCATT   TGT GCTTCTGTGG
                                |||||||   ||| ||||||||||
                                TTTGTGG   GCG CGAGGGTACT
                                    ___   T
GAM260  MGC10981 3' CACGGGAGCCACGTGTCT    51013       TGTAT  T
                                GGGCAT    GT GCTTCTGTG
                                ||||||    || |||||||||
                                TCTGTG    CA CGAGGGCAC
                                   _____  C
GAM260  MGC11034 3' CCACAGAGCTGTCTGTGGGTGC 48787      _ TG  TG T   T
           CT                    GGGCA T  TA  T GCT CTGTGG
                                |||||  |  ||  | ||| ||||||
                                TCCGT G  GT  G CGA GACACC
                                   G GT  CT T  _
GAM260  MGC12217 5' CACAGATCGTCAGTGCCT    51310        T   TTGCT
                                GGGCATTG ATG    TCTGTG
                                |||||||| |||    ||||||
                                TCCGTGAC TGC    AGACAC
                                    _   T____
GAM260  MGC1223  3' TACAGAGGTGGTGAGCA     48241     A  TT
                                TGT TG  GCTTCTGTG
                                ||| ||  |||||||||
                                ACG GT  TGGAGACAT
                                  A  GG
GAM260  MGC13033 3' CCATGGGGGACAGCTGGACGGT 48751        AT_   _
           GTCT                   GGCATTGT   GTTG CTTCTGTGG
                                |||||||||   |||| |||||||||
                                CTGTGGCA   CGAC GGGGGTACC
                                     GGT    A
GAM260  MGC13138 3' CTGCAGCCTCAACCTGCAGTGC 53018         T   CTT   TG
           TC                    GGGCATTGTA GTTG   CTG  G
                                |||||||||| ||||   |||  |
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                                CTCGTGACGT CAAC   GAC  C
                                     C    TCC   GT
GAM260  MGC14128 3' CACAGAAGCTCCCAAGCCC   51858     A   TATGTT
                                GGGC TTG     GCTTCTGTG
                                |||| |||     |||||||||
                                CCCG AAC     CGAAGACAC
                                  _  CCT___
GAM260  MGC14386 5' TTGTGGGCCCAGAATGTGGTGC 53209      TG   G   CT    TG
           CC                    GGGCAT  TAT TTG  TCTG  G
                                ||||||  ||| |||  ||||  |
                                CCCGTG  GTA GAC  GGGT  T
                                   GT   A   CC    GT
GAM260  MGC14421 3' CAGAGGCTACTGCCC      51873      TTGTAT  T
                                GGGCA     GT GCTTCTG
                                |||||     || |||||||
                                CCCGT     CA CGGAGAC
                                  _______ T
GAM260  MGC14425 3' CGCGGAGGCGGCAGCGGCC   51865    ATTGTA        TG
                                GGC     TGTTGCTTCTG  G
                                |||     ||||||||||  |
                                CCG     ACGGCGGAGGC  C
                                  GCG___         GT
GAM260  MGC15397 3' TGCATCAATGTGCAGTGTCT   54683           CTTC   G
                                GGGCATTGTATGTTG   TGTG
                                ||||||||||||||   ||||
                                TCTGTGACGTGTAAC   ACGT
                                       T___   G
GAM260  MGC15438 5' CTACAGAGAGAAGTGGTGCTC  51788      TG ATG  GC
                                GGGCAT  T   TT  TTCTGTGG
                                ||||||  |   ||  ||||||||
                                CTCGTG  G   AG  GAGACATC
                                   GT A__  A_
GAM260  MGC15705 3' CTGAAGAGTACTGTGTAATGTC 51280         GT    CTGTGG
           T                     GGGCATTGTAT  TGCTT
                                ||||||||||  |||||
                                TCTGTAATGTG  ATGAG
                                      TC    AAGTC
GAM260  MGC15875 5' CACGTGGTATGCACTGCCC   51907     T    TT  TTCT
                                GGGCA TGTATG  GC   GTG
                                ||||| ||||||  ||   |||
                                CCCGT ACGTAT  TG   CAC
                                   C     GG  ____
GAM260  MGC15906 5' CGAGGGTGACATACAGCGTTT  51816     A      TG  TC
                                GGGC TTGTATGT  CT  TG
                                |||| ||||||||  ||  ||
                                TTTG GACATACA  GG  GC
                                  C       GT  GA
GAM260  MGC16186 5' CGCAGGAGACGCAGCGCTC   50429     A   ATGTTG
                                GGGC TTGT     CTTCTGTG
                                |||| ||||     ||||||||
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                              CTCG GACG     GAGGACGC
                                C    CA____
GAM260  MGC16279 5' CAGAGGCTGGCTGCCT      51885      TT  ATGTT
                              GGGCA  GT    GCTTCTG
                              |||||  ||    |||||||
                              TCCGT  CG    CGGAGAC
                                __  GT___
GAM260  MGC17299 3' TCATGGGAAGGTTAATGTGTGC 58240       TGTATGTTGC
           CT                   GGGCAT        TTCTGTGG
                              ||||||         ||||||||
                              TCCGTG         AGGGTACT
                                 TGTAATTGGA
GAM260  MGC17299 3' CCATAGGGGTGACTGGTGCCC  58236        TAT  TG
                              GGGCATTG   GT  CTTCTGTGG
                              ||||||||   ||  |||||||||
                              CCCGTGGT   CA  GGGGATACC
                                  ___  GT
GAM260  MGC17998 3' CGCAGGAGAAACAGGTCC    58742     A   ATGTTG
                              GGGC TTGT     CTTCTGTG
                              |||| ||||     ||||||||
                              CCTG GACA     GAGGACGC
                                _    AA____
GAM260  MGC18257 3' TAGCATCACAGTGCTC      56780         _
                              GGGCATTGT ATGTTG
                              ||||||||| ||||||
                              CTCGTGACA TACGAT
                                   C
GAM260  MGC1842  3' TCGTGGCTGGCAGCAGTGCTC  65661        ATGT   T_ TG
                              GGGCATTGT   TGCT  C  TGG
                              |||||||||   ||||  |  |||
                              CTCGTGACG   ACGG  G  GCT
                                   ____    TC GT
GAM260  MGC19556 5' CACAGAAACCTCAGTGTTT   53227        TAT   GCT
                              GGGCATTG   GTT   TCTGTG
                              ||||||||   |||   ||||||
                              TTTGTGAC   CAA   AGACAC
                                   TC_   ___
GAM260  MGC19556 5' GCATGTACAGTGCCT       53230           T
                              GGGCATTGTATGT GC
                              |||||||||||| ||
                              TCCGTGACATGTA CG
                                        _
GAM260  MGC20470 3' CAGAGGCTACAATCCC      58960     C     TGTT
                              GGG ATTGTA    GCTTCTG
                              ||| ||||||    |||||||
                              CCC TAACAT    CGGAGAC
                                _     ____
GAM260  MGC21636 5' CAGATAAATATATAGTGTCT   58857           GCT
                              GGGCATTGTATGTT   TCTG
                              ||||||||||||||   ||||
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                                TCTGTGATATATAA  AGAC
                                       AT_
GAM260  MGC21854  3'  TGCAGAGGCAGAATATGCT   53493     TGTATG      TG
                                GGCAT    TTGCTTCTG  G
                                |||||    |||||||||  |
                                TCGTA    GACGGAGAC  T
                                   TAA___       GT
GAM260  MGC22805  5'  CGTAGAGGTGAAGTAAGCCT   58081     ATTG  G TG    TG
                                GGGC   TAT T  CTTCTG  G
                                ||||   ||| |  ||||||  |
                                TCCG   ATG A  GGAGAT  C
                                  A___  A GT    GT
GAM260  MGC23280  3'  CCATGGGAGTAAGGGGACGCCT 58393     ATT  ATG_
                                GGGC  GT   TTGCTTCTGTGG
                                ||||  ||   ||||||||||||
                                TCCG  CA   AATGAGGGTACC
                                  ___ GGGG
GAM260  MGC23284  5'  CTGCAGGGGCAACATGCTTTCC 58703    CATT         TG
           T                     GGG   GTATGTTGCTTCTG  G
                                |||   ||||||||||||||  |
                                TCC   CGTACAACGGGGAC  C
                                  TTT_         GT
GAM260  MGC2474   3'  CACAGGGGCGAGAAGCCC    43713     A  GTATG
                                GGGC TT    TTGCTTCTGTG
                                |||| ||    ||||||||||
                                CCCG AG    AGCGGGGACAC
                                  A _____
GAM260  MGC2508   3'  TATGGGAGCAAATTGCCC    44256     TTGTATG
                                GGGCA     TTGCTTCTGTG
                                |||||     ||||||||||
                                CCCGT     AACGAGGGTAT
                                   TA_____
GAM260  MGC2628   3'  ACAGGAGAAGGTGCCC     43966      GTATGTTG
                                GGGCATT      CTTCTGT
                                |||||||      |||||||
                                CCCGTGG      GAGGACA
                                    AA_______
GAM260  MGC2628   3'  CATGCCATAAATGATGCTC   43970      TG A   T  TTCT
                                GGGCAT  T TGT GC   GTG
                                ||||||  | ||| ||   |||
                                CTCGTA  A ATA CG   TAC
                                   GT A   C  ____
GAM260  MGC2628   3'  CTGTGGGGGCGGTGTGGACTCC 43974    CATTG  TG      TG
           T                     GGG    TA  TTGCTTCTG  G
                                |||    ||  |||||||||  |
                                TCC    GT  GGCGGGGGT  C
                                  TCAG_  GT       GT
GAM260  MGC2647   3'  CCATGGGGTCTGCTGTGGGGTC 73701     A TG  T  T_    T
           T                     GGGC T  TA GT  GCTTC GTGG
                                ||||  |  || ||  ||||| ||||
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```
                                TCTG G  GT CG  TGGGG TACC
                                  G GT  _  TC    _
GAM260  MGC26590  5'  ATCTCAGAGAGTGACGTAAGTG 56287      G    TG  _   T
            TTC                   GGCATT TATGT  CT TCTG GG
                                  |||||| |||||  || |||| ||
                                  TTGTGA ATGCA  GA AGAC CT
                                    _    GT  G   T  AC
GAM260  MGC27016  3'  GACATTAAATATGTGATGCTT  58678      TG    GCTTC   GG
                                  GGGCAT  TATGTT    TGT
                                  ||||||  ||||||    |||
                                  TTCGTA  GTATAA    ACA
                                     GT     ATT__   GT
GAM260  MGC2721   3'  ATGGGGAGTCTGCAGTGGTC   51215    G     TGTT    GTGG
                                  GG CATTGTA    GCTTCT
                                  || |||||||    ||||||
                                  CT GTGACGT    TGAGGG
                                   G      C___     GTAT
GAM260  MGC2731   3'  CAGTGGAGGGTGGTGAGCAGTG 43949        A  TT  _  TG GG
            TCC                   GGGCATTGT TG  GCT TC  T
                                  |||||||||  ||  ||| ||  |
                                  CCTGTGACG GT  TGG AG  G
                                       A  GG   G  GT ACT
GAM260  MGC2848   3'  CAGATGGAAATAATATGTGATG 51891    G   TG     C     GG
            GTC                   GG CAT  TATGTTG TTCTGT
                                  || |||  ||||||| ||||||
                                  CT GTA  GTATAAT AAGGTA
                                   G  GT      A     GACG
GAM260  MGC29891  3'  AGCAGGGTACAATGCTT     58198          G
                                  GGGCATTGTAT TTGCT
                                  |||||||||||  |||||
                                  TTCGTAACATG GACGA
                                         G
GAM260  MGC29891  5'  CCGTGGAAGCGTGGCCGGCAGC 58203     A   ATGT__     TG
            GTCC                    GGC TTGT     TGCTTC  TGG
                                  ||| ||||     ||||||  |||
                                  CTG GACG     GCGAAG  GCC
                                    C    GCCGGT     GT
GAM260  MGC3178   3'  CACAGAGGCCACTGGGTTC   47982     ATTGTAT  T
                                  GGGC      GT GCTTCTGTG
                                  ||||      || |||||||||
                                  CTTG      CA CGGAGACAC
                                    GGT_____  C
GAM260  MGC32043  3'  CACTCCAACTATAGTGCCT   58045         T   CTTCT
                                  GGGCATTGTA GTTG    GTG
                                  |||||||||| ||||    |||
                                  TCCGTGATAT CAAC    CAC
                                         _   CT___
GAM260  MGC32104  3'  CAGAAGATATAATTCT     58402     C     GTTG
                                  GGG ATTGTAT   CTTCTG
                                  ||| |||||||   ||||||
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                                TCT TAATATA    GAAGAC
                                  _     _____
GAM260  MGC32124  3'  CCGTGGCTCGGCGTTGTGGTGC 58161       TG _    CTT TG
            CT                    GGGCAT  TA TGTTG   C  TGG
                                  ||||||  || |||||   |  |||
                                  TCCGTG  GT GCGGC   G  GCC
                                     GT  T    TC_ GT
GAM260  MGC33317  3'  CATGGAGGGGACTGTGTTT    58844       TGTAT   G
                                  GGGCAT    GTT CTTCTGTG
                                  ||||||    ||| ||||||||
                                  TTTGTG    CAG GGAGGTAC
                                     T____   G
GAM260  MGC3413   3'  TACCAAGCAGCAGTGTTC    51049        ATGT    CT
                                  GGGCATTGT    TGCTT  GTG
                                  |||||||||    |||||  |||
                                  CTTGTGACG    ACGAA  CAT
                                       _____    C_
GAM260  MGC35521  3'  CCACATGCCCCGCATGCGTGCA 59009         _   TTC___
            ATGCCT                  ATTGTATGT TGC     TGTGG
                                  |||||||||  |||     |||||
                                  TAACGTGCG ACG     ACACC
                                       T   CCCCGT
GAM260  MGC3771   5'  CCATCTTAATGTGCAGTGACT  48242    G         CTTCT
                                  GG CATTGTATGTTG    GTGG
                                  ||  ||||||||||||    ||||
                                  TC GTGACGTGTAAT    TACC
                                   A          TC___
GAM260  MGC4171   5'  CTGTGGGAGTACGGTCATGAGC 44198     AT_  TA   T     TG
            CT                    GGGC   TG  TGT GCTTCTG  G
                                  ||||   ||  ||| |||||||  |
                                  TCCG   AC  GCA TGAGGGT  C
                                    AGT  TG   _      GT
GAM260  MGC4251   3'  CTACAGAAGTCACATGGGTTC  50458     ATTG    T
                                  GGGC    TATGT GCTTCTGTGG
                                  ||||    ||||| ||||||||||
                                  CTTG    GTACA TGAAGACATC
                                    G___     C
GAM260  MGC4293   3'  CTGCGGGAGGCTCTGGGATGCC 48523       G  TGTT     _ TG
            C                     GGGCATT TA    GCTTCT G  G
                                  |||||||  ||    ||||||  |  |
                                  CCCGTAG GT    CGGAGG C  C
                                      G  CT__     G GT
GAM260  MGC4342   3'  GCTGACATGCGTGTGCCT    44268       _      _
                                  GGGCAT TGTATGTT GC
                                  ||||||  ||||||||  ||
                                  TCCGTG GCGTACAG CG
                                     T       T
GAM260  MGC4342   3'  TATGGAGGTGGCCCGGCCC    44270     ATTGTAT  TG
                                  GGGC      GT  CTTCTGTG
                                  ||||      ||  ||||||||
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                                CCCG      CG  GGAGGTAT
                                  GCC____  GT
GAM260  MGC4368  3' AGTATCGTGCAGTGCTT     44457          T
                                GGGCATTGTATG TGCT
                                |||||||||||| ||||
                                TTCGTGACGTGC ATGA
                                       T
GAM260  MGC4400  5' TCGCGTCTGCAGTGTGTGGGGT 51058     A TG  TG    TTC
          TC                    GGGC T  TA  TTGC   TGTGG
                                |||| |  ||  ||||   |||||
                                CTTG G  GT  GACG   GCGCT
                                  G GT  GT    TCT
GAM260  MGC4415  3' CGCAGAAGCTTTCAGAGTCT   48950     A   TATGTT      TG
                                GGGC TTG     GCTTCTG  G
                                |||| |||     |||||||  |
                                TCTG GAC     CGAAGAC  C
                                  A   TTT___      GT
GAM260  MGC4473  5' TGCAGGAGTAACACAGGC    54895    A    AT        TG
                                GC TTGT  GTTGCTTCTG  G
                                || ||||  ||||||||||  |
                                CG GACA  CAATGAGGAC  T
                                 _   __         GT
GAM260  MGC4663  3' CCACAGGCTGTGGTCAGTGTTT 44504        TAT TT  T_
                                GGGCATTG   G  GC  TCTGTGG
                                ||||||||   |  ||  |||||||
                                TTTGTGAC   T  TG  GGACACC
                                    ___ GG  TC
GAM260  MGC4796  3' CGTGGGAGCCTACTGGAGCCC  61484     ATT_   TGTT      TG
                                GGGC    GTA    GCTTCTG  G
                                ||||    |||    |||||||  |
                                CCCG    CAT    CGAGGGT  C
                                  AGGT   C___      GT
GAM260  MGC4832  5' CGCGGGAAGCTGCGGTCTC    59001     C     TGTT     _ TG
                                GGG ATTGTA    GCTTCT G  G
                                ||| ||||||    ||||||  |  |
                                CTC TGGCGT    CGAAGG C  C
                                  _     _____      G GT
GAM260  MGC5395  3' GGCAACTATGGTGCTC      43932        TG  T
                                GGGCAT  TA GTTGCT
                                ||||||  ||  ||||||
                                CTCGTG  AT CAACGG
                                   GT  _
GAM260  MGC5469  5' CCGTGGAGGCTGCTGCAGTGTT 50393          T  T    TG
                                GGCATTGTA GT GCTTC  TGG
                                |||||||||  ||  |||||  |||
                                TTGTGACGT CG CGGAG  GCC
                                      _ T    GT
GAM260  MGC5576  3' CGCAGGCCATTATCAGTGCCT  43921         T   T  CT    TG
                                GGGCATTG ATG TG  TCTG  G
                                |||||||| ||| ||  ||||  |
```

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                                TCCGTGAC TAT AC  GGAC  C
                                    _  T  C_   GT
GAM260  MGC861   5'  CCGCAGGAGCAACGGTTGGTCC 43902     ATTGTA
                                GGGC     TGTTGCTTCTGTGG
                                ||||     ||||||||||||||
                                CCTG     GCAACGAGGACGCC
                                  GTTG__
GAM260  MGC8974  3'  CTATGGAAGTATGTAATAATTT 53633    C    ATGT
           CT                    GGG ATTGT    TGCTTCTGTGG
                                ||| |||||    ||||||||||
                                TCT TAATA    ATGAAGGTATC
                                  T    ATGT
GAM260  MIC2L1   5'  CTGCAGAGGCGGCGGGGCTC   48822     ATTGTA        TG
                                GGGC     TGTTGCTTCTG  G
                                ||||     ||||||||||  |
                                CTCG     GCGGCGGAGAC  C
                                  GG____         GT
GAM260  MIC2L1   3'  CGCAGAAGCCTGGCGGGCTC   48821     A    ATGTT     TG
                                GGGC TTGT    GCTTCTG  G
                                |||| ||||    |||||||  |
                                CTCG GGCG    CGAAGAC  C
                                  _   GTC__      GT
GAM260  MISS     3'  TCATAATCCAAACAAATGATGC 58031      TG A    GCTTC
           CT                    GGGCAT  T TGTT    TGTGG
                                ||||||  | ||||    |||||
                                TCCGTA  A ACAA    ATACT
                                   GT A    ACCTA
GAM260  MKNK1    3'  CGTTTGAGCAATGCAGTGCCT  13479        AT      CT TG
                                GGGCATTGT  GTTGCTT  G  G
                                |||||||||  |||||||  |  |
                                TCCGTGACG  TAACGAG  T  C
                                     __      TT GT
GAM260  MKRN4    3'  CTACAGGTGCATGCTACAATGC 47742         T  _   T
           CC                    GGGCATTGTA GT TGC TCTGTGG
                                ||||||||||  ||  |||  |||||||
                                CCCGTAACAT CG ACG GGACATC
                                     _  T   T
GAM260  MMP24    3'  ATGGGGGCTGTGCCC      21940       TGTATGTT
                                GGGCAT       GCTTCTGT
                                ||||||       ||||||||
                                CCCGTG       CGGGGGTA
                                   T________
GAM260  MMP24    3'  TCACGGCATCCTGTGGTGTCC  21946      TG  TGT    TCT
                                GGGCAT  TA   TGCT   GTGG
                                ||||||  ||   ||||   ||||
                                CCTGTG  GT   ACGG   CACT
                                   GT  CCT    ___
GAM260  moblak   5'  CCGCGGGAGAGCTGTGGGGCTT 55492     A TG  T   G
                                GGGC T  TA GTT CTTCTGTGG
                                |||| |  || ||| |||||||||
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                                TTCG G  GT CGA GAGGGCGCC
                                  G GT  _  _
GAM260  MOST2   5'  CGGAAGACAGGGCCC      39681     A   ATGTTG
                                GGGC TTGT     CTTCTG
                                |||| ||||     ||||||
                                CCCG GACA     GAAGGC
                                  G   _______
GAM260  MRPL37  3'  CGTGGAGCCTCAGTGCCC    66248       TATGTT   T TG
                                GGGCATTG     GCT C  TG
                                ||||||||     ||| |  ||
                                CCCGTGAC     CGA G  GC
                                    TC____   _ GT
GAM260  MRPL48  3'  ATAGCCAGTAATGTCC      32132       TATG   CTT
                                GGGCATTG   TTG   CTGT
                                ||||||||   |||   ||||
                                CCTGTAAT   GAC   GATA
                                    _____  C__
GAM260  MRPS11  3'  CTACAGGGGCAGCCGTGGCCT  43117     ATTGTAT
                                GGGC      GTTGCTTCTGTGG
                                ||||      ||||||||||||
                                TCCG      CGACGGGGACATC
                                  GTGC___
GAM260  MRPS11  3'  CTACAGGGGCAGCCGTGGCCT  94559     ATTGTAT
                                GGGC      GTTGCTTCTGTGG
                                ||||      ||||||||||||
                                TCCG      CGACGGGGACATC
                                  GTGC___
GAM260  MRPS25  3'  GGCTGGGGTGATGGTGTCT   42561       GTAT  TG   T  GG
                                GGGCATT   GT  CTTC GT
                                |||||||   ||  |||| ||
                                TCTGTGG   TA  GGGG CG
                                    _____ GT   T  GG
GAM260  MRVI1   3'  TTACAGAAGTAGGAAAGGCTT  55220     ATTGTATG
                                GGGC      TTGCTTCTGTGG
                                ||||      ||||||||||||
                                TTCG      GATGAAGACATT
                                  GAAAG___
GAM260  MRVI1   3'  TTACAGAAGTAGGAAAGGCTT  20273     ATTGTATG
                                GGGC      TTGCTTCTGTGG
                                ||||      ||||||||||||
                                TTCG      GATGAAGACATT
                                  GAAAG___
GAM260  MST4    3'  CTACAGTCATGAAACATACAGG 33301     A       GCTT__
          TCT                   GGC TTGTATGTT     CTGTGG
                                ||| |||||||||     ||||||
                                CTG GACATACAA     GACATC
                                  _       AGTACT
GAM260  MUC17   3'  CATGGGAACTCAATGTTC    94273       TAT  TGC
                                GGGCATTG   GT   TTCTGTG
                                ||||||||   ||   |||||||
```

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                                CTTGTAAC  CA  AGGGTAC
                                    T__ ___
GAM260  MY014   5' GTGGTATATAATGTTT     48142          TT
                                GGGCATTGTATG  GC
                                ||||||||||||  ||
                                TTTGTAATATAT  TG
                                     GG
GAM260  MYH7B   3' GGAGTCCCTGCAGGCCT    70533     A    TGTT
                                GGGC TTGTA   GCTTC
                                |||| |||||   |||||
                                TCCG GACGT   TGAGG
                                  _   CCC_
GAM260  MYNN    3' CGCATCACAACTGCAATGTTT 37852        T   CTTC  TG
                                GGGCATTGTA GTTG   TG  G
                                |||||||||| ||||   ||  |
                                TTTGTAACGT CAAC   AC  C
                                     _   ACT_  GT
GAM260  MYOM1   3' TTACAGAGGTGATGTGC    13738      TG
                                GTATGT  CTTCTGTGG
                                ||||||  |||||||||
                                CGTGTA  GGAGACATT
                                   GT
GAM260  MYOZ2   3' ATGGAAGATGATGTAC     33460       _
                                GTATGTTG CTTCTGT
                                |||||||| |||||||
                                CATGTAGT GAAGGTA
                                    A
GAM260  NAC1    5' CCGCGGAGGCGGAGGCCGAGGC 53519     A  TATG
           CC                    GGGC TTG   TTGCTTCTGTGG
                                 |||| |||   ||||||||||||
                                 CCCG AGC   GGCGGAGGCGCC
                                   G  CGGA
GAM260  NAP1L1  3' TTATAGAAGTGGAGGGATGC  57623     GTATG TG
                                GCATT    T  CTTCTGTGG
                                |||||    |  |||||||||
                                CGTAG    G  GAAGATATT
                                   GGA__ GT
GAM260  NAPG    3' GCATTTAAGGACATTGCAGTGT 96725         _  G  CT  G
           TT                    GGGCATTGTA TGTT CTT  GTG
                                 |||||||||| |||| |||  |||
                                 TTTGTGACGT ACAG GAA  TAC
                                      T   _  TT  GT
GAM260  NARF    5' CCGCGGGCGGCGGGCAGTGGTG 49240     TG A  _  _
           TCC                   GGCAT  T TGTT GCT TCTGTGG
                                 |||||  | |||| ||| |||||||
                                 CTGTG  G ACGG CGG GGGCGCC
                                   GT _   G  C
GAM260  NAV3    3' TCACAGGGCTTCAGTAGTGTTT 29775      GTA  TT  T
                                GGGCATT   TG  GCT CTGTGG
                                |||||||   ||  ||| ||||||
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                                TTTGTGA   AC  CGG GACACT
                                   TG_  TT  _
GAM260  NCOA2    3'  AAGGATATCAATGCCT     21543        T    G
                                GGGCATTG ATGTT CTT
                                |||||||| ||||| |||
                                TCCGTAAC TATAG GAA
                                   _    _
GAM260  NDRG4    3'  CCATCAGTAGCAGTGTGGTGTT 43287      TG   GT   T  _
           T                     GGGCAT  TAT  TGCT CTG TGG
                                |||||| |||  |||| ||| |||
                                TTTGTG  GTG  ACGA GAC ACC
                                   GT  __   T  T
GAM260  NDRG4    3'  CCATCAGTAGCAGTGTGGTGTT 39984      TG   GT   T  _
           T                     GGGCAT  TAT  TGCT CTG TGG
                                |||||| |||  |||| ||| |||
                                TTTGTG  GTG  ACGA GAC ACC
                                   GT  __   T  T
GAM260  NDUFB5   3'  TTATAGAAGTCTAATAATGTT  10196        ATGTT
                                GGCATTGT    GCTTCTGTGG
                                ||||||||    ||||||||||
                                TTGTAATA    TGAAGATATT
                                    ATC__
GAM260  NEDD5    3'  CTACAGAAAATAATCTGGTGTT 15311       GT  GTTGC
           C                     GGGCATT  AT    TTCTGTGG
                                ||||||| ||    ||||||||
                                CTTGTGG  TA    AAGACATC
                                    TC  ATAA_
GAM260  NEIL2    3'  CTACAGGCATGTGATATGATGC 58907      TG   GT__   TT
           TC                     GGGCAT  TAT   TGC  CTGTGG
                                ||||||  |||   |||  ||||||
                                CTCGTA  ATA   ACG  GACATC
                                   GT   GTGT  __
GAM260  NEIL2    5'  TGCAGAGGCGGCTTGCTTCCC  58912    CATT   T       TG
                                GGG   GTA GTTGCTTCTG  G
                                |||   ||| ||||||||||  |
                                CCC   CGT CGGCGGAGAC  T
                                  TT__   T        GT
GAM260  NEU4     5'  CCGTGGGAGTGTCCAGGGTCC  54952     A   T  GTT    TG
                                GGGC TTG AT   GCTTC  TGG
                                |||| ||| ||   |||||  |||
                                CCTG GAC TG   TGAGG  GCC
                                  G   C  ___    GT
GAM260  NEUROG3  3'  CCACGGGGGCGGTAGGCTGGGT 40655     ATT  A  TT
           TC                     GGGC   GT TG  GCTTCTGTGG
                                ||||   || ||  ||||||||||
                                CTTG   CG AT  CGGGGGCACC
                                  GGT  G  GG
GAM260  NFASC    3'  TACTCAGTGTTGTGATGCCC  70349      TG  TGTT   TCT   G
                                GGGCAT  TA   GCT   GTG
                                ||||||  ||   |||   |||
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                                CCCGTA  GT   TGA  CAT
                                   GT  TG__  CT_  G
GAM260  NIR3    3'  CATGTGTGAGCAGTGTCC    66238        ATG TG TTCT
                                GGGCATTGT  T  C   GTG
                                |||||||||  | |   |||
                                CCTGTGACG  A  G   TAC
                                     ___ GT TG__
GAM260  NPFF    3'  CCACACCCAAAAGTGTCAATGT 13554       T TG  GCTTC_
          TT                     GGGCATTG A  TT    TGTGG
                                 |||||||| |  ||    |||||
                                 TTTGTAAC T  GA    ACACC
                                     _ GT  AAACCC
GAM260  NPTXR   3'  CCATCTTGTGGCATGTGGTGCC 54174      TG    TG TTCT
          C                      GGGCAT  TATGT  C   GTGG
                                 ||||||  |||||  |   ||||
                                 CCCGTG  GTACG  G   TACC
                                    GT    GT TTC_
GAM260  NPTXR   3'  CCATCTTGTGGCATGTGGTGCC 26638      TG    TG TTCT
          C                      GGGCAT  TATGT  C   GTGG
                                 ||||||  |||||  |   ||||
                                 CCCGTG  GTACG  G   TACC
                                    GT    GT TTC_
GAM260  NTT5    5'  TGCAGAAGCGGGAGCTGCCC  25883     TT  ATG       TG
                                GGGCA  GT   TTGCTTCTG  G
                                |||||  ||   |||||||||  |
                                CCCGT  CG   GGCGAAGAC  T
                                   __  AG_       GT
GAM260  NTT73   3'  TTAACTGCAACACTATAATGTC 36024        _     TTCTGTGG
          T                      GGGCATTGTA TGTTGC
                                 ||||||||||  ||||||
                                 TCTGTAATAT  ACAACG
                                       C     TCAATT
GAM260  NUCKS   3'  CTATAGACACAAGTATCAATGT 42697       T  _  CT
          CT                     GGGCATTG ATG TTG  TCTGTGG
                                 |||||||  |||  |||  |||||||
                                 TCTGTAAC TAT AAC  AGATATC
                                     _  G  AC
GAM260  NXPH3   3'  CAACTGGTAGCAATGCCC    65750       ATGT   TCTG
                                GGGCATTGT   TGCT   TG
                                |||||||||   ||||   ||
                                CCCGTAACG   ATGG   AC
                                     _____   TCA_
GAM260  NXPH3   3'  CATTGGCGAGCAGTGTCC    65754       ATG    TCT
                                GGGCATTGT   TTGCT   GTG
                                |||||||||   |||||  |||
                                CCTGTGACG   AGCGG   TAC
                                     ____    T__
GAM260  NYD-SP25 3' GAAGTAATCTGTAGTGTTT   53187        T
                                GGGCATTGTA GTTGCTTC
                                ||||||||||  ||||||||
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                                TTTGTGATGT TAATGAAG
                                      C
GAM260  ODC-p    3'  CCGCGCTCCACCTGCAGTGTTT 53796          __  TT  TTCT
                                GGGCATTGTA  TG  GC   GTGG
                                ||||||||||  ||  ||   ||||
                                TTTGTGACGT  AC  CG   CGCC
                                      CC  CT  ____
GAM260  OR7C1    5'  CAGAATGTACGCTGTCT     33995       T      TGCT
                                GGGCA TGTATGT    TCTG
                                |||||  |||||||    ||||
                                TCTGT GCATGTA    AGAC
                                  C      ____
GAM260  OS4      3'  CTGTGGCCCCAGTGTATAGTGT 19182          TG   CTT   TG
           TT                     GGGCATTGTA  TTG   CTG  G
                                ||||||||||  |||   |||  |
                                TTTGTGATAT  GAC   GGT  C
                                      GT   CCC   GT
GAM260  OSBPL5   3'  CATGGAGGCAGAGAGGCCC    72684      ATTGTATG
                                GGGC       TTGCTTCTGTG
                                ||||       ||||||||||||
                                CCCG       GACGGAGGTAC
                                  GAGA____
GAM260  P15-2    3'  CTACATTGAACGGTGTGCATTG 38007      T    TG   C   __
           TTC                    GGCA TGTA  TTG TTC  TGTGG
                                |||| ||||  ||| |||  |||||
                                TTGT ACGT  GGC AAG  ACATC
                                  T   GT   _   TT
GAM260  P1P373C6 3'  GCCAACATTGGTGCTC      38903         T     _
                                GGGCATTG ATGTTG C
                                |||||||| |||||| |
                                CTCGTGGT TACAAC G
                                     _     C
GAM260  P2RXL1   3'  CAGGGATGCATGTGTCC      18379        _     GTTGC
                                GGGCAT TGTAT    TTCTG
                                ||||||  |||||    |||||
                                CCTGTG ACGTA    GGGAC
                                   T    ______
GAM260  P37NB    3'  GGTGATATGCAATTCC       19506      C        TG
                                GGG ATTGTATGT  CT
                                |||  |||||||||  ||
                                CCT TAACGTATA  GG
                                  _        GT
GAM260  P450RAI-2 3'  CTACAGTGTTTTTGTGATGTTC 39102       TG  TGTT  TT
                                GGGCAT  TA   GC  CTGTGG
                                ||||||  ||   ||  ||||||
                                CTTGTA  GT   TG  GACATC
                                   GT  TTT_  T_
GAM260  P450RAI-2 3'  TTGCAGGGCCCTGTGTGGTCTC 39108     C  TG   TT   T   TG
           C                     GGG AT  TATG  GCT CTG  G
                                ||| ||  ||||  ||| |||  |
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                                CCT TG  GTGT  CGG GAC  T
                                  C  GT   CC  _  GT
GAM260  P4HA2   5'  TAGGGGATAGCTGTCC     14841      TTGTAT   _
                                GGGCA     GTTG CTTCTG
                                |||||     |||| ||||||
                                CCTGT     CGAT GGGGAT
                                  _______   A
GAM260  P66     3'  GTCGCATGCAGTGCCT     40369          T
                                GGGCATTGTATGT GC
                                |||||||||||| ||
                                TCCGTGACGTACG TG
                                       C
GAM260  PAIP1   3'  TAGTTTGACATTTAGTGTCC  66927       T     CTT
                                GGGCATTG ATGTTG   CTG
                                |||||||| ||||||   |||
                                CCTGTGAT TACAGT   GAT
                                     T     TT_
GAM260  PANX3   3'  TTATGGAGGCAATTCCATATCC 53689    CAT  TAT
                                GGG   TG   GTTGCTTCTGTGG
                                |||   ||   ||||||||||||
                                CCT   AC   TAACGGAGGTATT
                                  AT_  CT_
GAM260  PC326   3'  TTACAGAGCTTTAGTGCAAT   37414      GTT_   T
                                ATTGTAT    GCT CTGTGG
                                |||||||    ||| ||||||
                                TAACGTG    CGA GACATT
                                    ATTT   _
GAM260  PCBP3   5'  TTATGGGGGAAGGTGACGCCT  40072     ATTG   G  G
                                GGGC    TAT TT CTTCTGTGG
                                ||||    ||| || |||||||||
                                TCCG    GTG AA GGGGGTATT
                                  CA__   G  _
GAM260  PCBP4   5'  CAGAGTGATGTGTGGCGCTC   39907     A TG    TG  T
                                GGGC T  TATGT  CT CTG
                                |||| |  |||||  || |||
                                CTCG G  GTGTA  GA GAC
                                  C GT    GT  _
GAM260  PCDH16  3'  CACAGAAGCCCTGTTGCTC    13603      TTGTATGTT
                                GGGCA       GCTTCTGTG
                                |||||       |||||||||
                                CTCGT       CGAAGACAC
                                   TGTCC____
GAM260  PCDH19  3'  CCACAATTGTCTGATGTATGAG 63701     A TG     __  TTC
          TCC                     GGC T  TATGTT  GC   TGTGG
                                |||  |  ||||||  ||   |||||
                                CTG A  ATGTAG  TG   ACACC
                                  _ GT     TC  TTA
GAM260  PCYT1B  3'  TCACAGGGTTGCCTGGGTGGTG 16750      TG AT__  T   T
          TTT                     GGCAT  T    GT GCT CTGTGG
                                |||||  |    || ||| ||||||
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                                TTGTG  G    CG TGG GACACT
                                   GT GGTC  T  _
GAM260  PDCD6    3'  GCCATGAGGTAAATGTAATGTT 59528          G      T
             T                    GGGCATTGTAT TTGCTTC GTGG
                                  |||||||||||| ||||||| ||||
                                  TTTGTAATGTA AATGGAG TACC
                                        _      _   GT
GAM260  PDCD6IP  3'  GAATGCAGTGTATAATTTCT   82286     C     TG   _
                                  GGG ATTGTA  TTGC TTC
                                  ||| ||||||  |||| |||
                                  TCT TAATAT  GACG AAG
                                    T     GT    T
GAM260  PDE10A   3'  CATAGAAGCCTGTGGGTTT   21860      A TG  TGTT
                                  GGGC T  TA    GCTTCTGTG
                                  |||| |  ||    |||||||||
                                  TTTG G  GT    CGAAGATAC
                                    _ GT  C___
GAM260  PDE8A    3'  TCACAGACATGTTTGATGCTT  62637         T    TGCT
                                  GGGCATTG ATGT    TCTGTGG
                                  |||||||| ||||    |||||||
                                  TTCGTAGT TGTA    AGACACT
                                       T    C___
GAM260  PDE8B    5'  CTGCGGAGGTGCGCATCGGGCC 67578      A   T   _      TG
             C                    GGGC TTG ATGT TGCTTCTG  G
                                  |||| ||| |||| ||||||||  |
                                  CCCG GGC TACG GTGGAGGC  C
                                    _  _    C       GT
GAM260  PDEF     3'  TACAGAAGGGCAGTGACTC    24751     _     ATGTTG
                                  GGG CATTGT     CTTCTGTG
                                  ||| ||||||     ||||||||
                                  CTC GTGACG     GAAGACAT
                                    A     G_____
GAM260  PDZ-GEF1 3'  TTATGGAGGCAGGACGGTGTC  26497         ATGT
                                  GGCATTGT    TGCTTCTGTGG
                                  ||||||||    ||||||||||
                                  CTGTGGCA    ACGGAGGTATT
                                       GG__
GAM260  PEG10    3'  CCACACTTGCAAGTGATGCTC  30522       TG ATG    TTC
                                  GGGCAT  T   TTGC   TGTGG
                                  ||||||  |   ||||   |||||
                                  CTCGTA  G   AACG   ACACC
                                     GT ___    TTC
GAM260  PELI1    3'  GAATGACAATAGTGCCC     40268         A    C
                                  GGGCATTGT TGTTG TTC
                                  ||||||||| ||||| |||
                                  CCCGTGATA ACAGT AAG
                                        _    _
GAM260  PER3     3'  CACAGGGTCCTGCAGGCTC   33679      A    TGTT   T
                                  GGGC TTGTA    GCT CTGTG
                                  |||| |||||    ||| |||||
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                                CTCG GACGT    TGG GACAC
                                  _     CC__   _
GAM260  PEX16    3'  CCATAGGAGCGAACACTGCTGC 54100       TT   _    _
              TC                   GGGCA  GTA TGTT GCTTCTGTGG
                                |||||  ||| |||| ||||||||||
                                CTCGT  CGT ACAA CGAGGATACC
                                  __  C    G
GAM260  PEX16    5'  CCGCAGCCTGTCGTACGGTCCT 54101     C       TT  TT_
                                GGG ATTGTATG  GC   CTGTGG
                                ||| ||||||||  ||   ||||||
                                TCC TGGCATGC  TG   GACGCC
                                  _      __ TCC
GAM260  PEX16    5'  CCGCAGCCTGTCGTACGGTCCT 16679     C       TT  TT_
                                GGG ATTGTATG  GC   CTGTGG
                                ||| ||||||||  ||   ||||||
                                TCC TGGCATGC  TG   GACGCC
                                  _      __ TCC
GAM260  PFTK1    3'  GCTATGGAAATACCTTTGTGTA 24758      TG _____  C
              CAGTGTCT                TGTA  T    TG TTCTGTGG   C
                                ||||  |    || ||||||||  |
                                ACAT  G    AT AAGGTATC   G
                                  GT TTTCC  A
GAM260  PHCA     3'  CCACATCCCAGGATTTATGGTG 37175       TG  T   GCTTC_
              TCT                   GGGCAT  TA GTT     TGTGG
                                ||||||  || |||     |||||
                                TCTGTG  AT TAG     ACACC
                                   GT  T   GACCCT
GAM260  phospho1 3'  CCACAGAGGCAGAAGAGGGTCT 82368     ATTGTATG
                                GGGC       TTGCTTCTGTGG
                                ||||       ||||||||||||
                                TCTG       GACGGAGACACC
                                  GGAGAA__
GAM260  phospho1 3'  TCGCAGAGAGTGACGGTGTCT  82372       TGTA   TG  _
                                GGGCAT    TGT  CT TCTGTGG
                                ||||||    |||  || |||||||
                                TCTGTG    GCA  GA AGACGCT
                                   ____   GT  G
GAM260  PHYHIP   3'  CTGTGGGGGTGGCCCACTGCCC 28609      T  TAT  TG     TG
                                GGGCA TG   GT  CTTCTG  G
                                ||||| ||   ||  ||||||  |
                                CCCGT AC   CG  GGGGGT  C
                                   C  C__  GT     GT
GAM260  PIK3R4   5'  CTGCAGCAGCTGAAGTGTAGTG 62181          GTT_  T   TG
              TTT                   GGGCATTGTAT    GCT CTG  G
                                ||||||||||    ||| |||  |
                                TTTGTGATGTG    CGA GAC  C
                                      AAGT   C   GT
GAM260  PINK1    3'  CGCAGATGACGTATGTGCCT   50542       T      CT    TG
                                GGGCAT GTATGTTG  TCTG  G
                                |||||| ||||||||  ||||  |
```

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                                TCCGTG TATGCAGT  AGAC  C
                                  _      __    GT
GAM260  PIP3-E   3'  TTATAGAAGTTCAAATTACTAG 66820     _  TGTT__
           TGTTT                  CATT GTA     GCTTCTGTGG
                                |||| |||     ||||||||||
                                GTGA CAT     TGAAGATATT
                                  T   TAAACT
GAM260  PIP5K1C  3'  TGTTTAAGTGATGTGATGTCT  70769       TG AT  TG   CT TG
                                GGGCAT  T  GT  CTT  G  G
                                ||||||  |  ||  |||  |  |
                                TCTGTA  G  TA  GAA  T  T
                                   GT __  GT   TT GT
GAM260  PIP5K2B  3'  CCATCTTAGAGTGTGGTGTCC  13068       TG   GTTG  TCT
                                GGGCAT  TAT    CT   GTGG
                                ||||||  |||    ||   ||||
                                CCTGTG  GTG    GA   TACC
                                   GT   A___  TTC
GAM260  PIPPIN   3'  CACAGGCCCTGCAGTGCTC   79694         TGTT  TT
                                GGGCATTGTA    GC  CTGTG
                                ||||||||||    ||  |||||
                                CTCGTGACGT    CG  GACAC
                                     CC__  __
GAM260  PISD     5'  GCAGAGGCAGAGGCCC     26771      ATTGTATG
                                GGGC       TTGCTTCTGT
                                ||||       ||||||||||
                                CCCG       GACGGAGACG
                                  GA_______
GAM260  PLA2G6   3'  CGCAGGAGTGGGATGCCC    66489       GTATG TG
                                GGGCATT    T  CTTCTGTG
                                |||||||    |  ||||||||
                                CCCGTAG    G  GAGGACGC
                                    _____ GT
GAM260  PLAGL2   3'  GCAGAATACAAAGTCC      70451      A     G
                                GGGC TTGTAT TTGC
                                |||| |||||| ||||
                                CCTG AACATA GACG
                                  A     A
GAM260  PLAGL2   3'  TACAGAGGCCACTGGGCCT   70456      ATTGTAT  T
                                GGGC      GT GCTTCTGTG
                                ||||      || |||||||||
                                TCCG      CA CGGAGACAT
                                  GGT____  C
GAM260  PME-1    3'  CCTGGAGGTGTGCAGTGCCC   32352          GTT      T
                                GGGCATTGTAT   GCTTCTG GG
                                ||||||||||   ||||||| ||
                                CCCGTGACGTG   TGGAGGT CC
                                      ___      _ T
GAM260  PMFBP1   3'  TTACAGGAGTATATCACGGTCC 48448     C    _    T
           C                    GGG ATTGT ATGT GCTTCTGTGG
                                ||| ||||| |||| ||||||||||
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                                CCC TGGCA TATA TGAGGACATT
                                  _    C   _
GAM260  PMX2B    3'  CTACGTGACCGTATAATGTTT  14080          _ TG TTCT
                                GGGCATTGTATG T  C   GTGG
                                |||||||||||| |  |   ||||
                                TTTGTAATATGC A  G   CATC
                                      C GT ____
GAM260  PNAS-127 5'  CCGCAGAAGCTGCGGGTGTCC  50659       GTA  T
                                GGGCATT  TGT GCTTCTGTGG
                                |||||||  ||| ||||||||||
                                CCTGTGG  GCG CGAAGACGCC
                                   ___  T
GAM260  POLE3    3'  TCACAGAGGCAGCCAAGGCTC  33858     A  TAT
                                GGGC TTG  GTTGCTTCTGTGG
                                |||| |||  ||||||||||||
                                CTCG AAC  CGACGGAGACACT
                                  G  ___
GAM260  POLR2D   3'  CCACAACCAGGTGTGCACTGTT 16655     T   TG  GCTTC
           C                     GGGCA TGTA  TT    TGTGG
                                |||||  ||||  ||    |||||
                                CTTGT ACGT  GG    ACACC
                                   C   GT  ACCA_
GAM260  POLR2D   3'  CCGCAGCAGTCAGCGATGTTT  16656       A  TT   T
                                GGGCATTGT TG  GCT CTGTGG
                                |||||||||  ||  ||| ||||||
                                TTTGTAGCG AC  TGA GACGCC
                                      _ __  C
GAM260  POLR2J2  3'  CCATGGGACTTCTGTAGTGCT  59294       TGTTGC
                                GGCATTGTA     TTCTGTGG
                                |||||||||     ||||||||
                                TCGTGATGT     AGGGTACC
                                     CTTC__
GAM260  PORIMIN  3'  CCATGCATATAATGTACAGTGT 53601          CTTCT
                                GCATTGTATGTTG    GTGG
                                ||||||||||||    ||||
                                TGTGACATGTAAT    TACC
                                       ATACG
GAM260  PORIMIN  3'  CTGCAGTGTTTAACATAATAAT 53603       _    CTT_  TG
           GTTT                  GGCATTGT ATGTTG   CTG  G
                                |||||||| ||||||   |||  |
                                TTGTAATA TACAAT   GAC  C
                                    A     TTGT   GT
GAM260  PORIMIN  3'  TTATAGACCGTTCATACAATG  53610       TT  T_
                                CATTGTATG  GC  TCTGTGG
                                |||||||||  ||  |||||||
                                GTAACATAC  TG  AGATATT
                                     T_  CC
GAM260  POU4F2   3'  GGCAACGTATGCTGCTT     15900      TT
                                GGGCA  GTATGTTGCT
                                |||||  ||||||||||
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                                TTCGT  TATGCAACGG
                                  CG
GAM260  PP1044   3'  CTGTAATCTGTAATTGTGATGC 41366      TG  T    TTC_  TG
           CT                    GGGCAT  TA GTTGC    TG  G
                                ||||||  || |||||    ||  |
                                TCCGTA  GT TAATG    AT  C
                                  GT  _    TCTA  GT
GAM260  PPFIA4   3'  TTGTGGAGGCACCCAGGTTGTC 70339      TTGTA  T_      TG
           C                     GGGCA    TG  TGCTTCTG  G
                                |||||    ||  ||||||||  |
                                CCTGT    AC  ACGGAGGT  T
                                  TGG__  CC       GT
GAM260  PPM1A    3'  TTGCAGGTAATAATACAGTGT  40661         _    TT   TG
                                GCATTGTAT GTTGC  CTG  G
                                |||||||||  |||||  |||  |
                                TGTGACATA TAATG  GAC  T
                                    A    __   GT
GAM260  PPP1R16B 3'  TGCAGGAGTGGTGATGCCC   61391       GTAT TT      TG
                                GGGCATT   G  GCTTCTG  G
                                |||||||   |  |||||||  |
                                CCCGTAG   T  TGAGGAC  T
                                   ____ GG      GT
GAM260  PPP1R16B 3'  CATGGGAGTGACTGCA     61381      T  TG
                                TGTA GT  CTTCTGTG
                                ||||  ||  ||||||||
                                ACGT CA  GAGGGTAC
                                  _  GT
GAM260  PPP2R2A  3'  CTGTGGATTCATCACTGTGGTG 10746       TG  _  T  CT    TG
           TTC                   GGGCAT  TA TG TG  TCTG  G
                                ||||||  || || ||  ||||  |
                                CTTGTG  GT AC AC  AGGT  C
                                   GT  C  T  TT    GT
GAM260  PPP4R1L  3'  CTAAAGCAGCAGCAATAGTGTT 79501         A      T  G
           C                     GGGCATTGT TGTTGCT CT TGG
                                |||||||||  |||||||  ||  |||
                                CTTGTGATA ACGACGA GA ATC
                                    _      C  A
GAM260  PRAM-1   3'  CGCGGGGGTGGCAAGCA     69379     A   TG
                                TGT TGT  CTTCTGTG
                                |||  |||  ||||||||
                                ACG ACG  GGGGGCGC
                                  A   GT
GAM260  PRDM10   3'  AAGTGGCATATTGTGTTC    39576       T     TG
                                GGGCAT GTATGT  CTT
                                ||||||  ||||||  |||
                                CTTGTG TATACG  GAA
                                   T     GT
GAM260  PRDM14   5'  CGCCGAGCGTGCGGTCCC    44446     C       TGCT  T
                                GGG ATTGTATGT    TC GTG
                                |||  |||||||||    ||  |||
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                                CCC TGGCGTGCG   AG CGC
                                  _       _____ C
GAM260  PRO0082  3' CTACTTCCAGATGCAGTGCCT 37733          G   CTTCT
                                GGGCATTGTAT TTG    GTGG
                                |||||||||| |||    ||||
                                TCCGTGACGTA GAC    CATC
                                      _  CTT__
GAM260  PRO0529  5' TCACGGGGGCTCATGATGGAGT 26000     A TG _   TT
          CT                   GGGC T  T ATG  GCTTCTGTGG
                               |||| |  | |||  ||||||||||
                               TCTG G  A TAC  CGGGGGCACT
                                 A GT G   T_
GAM260  PRO0618  3' CAATCAATGTCAGTGTCC    26199        T     CTTCTG
                                GGGCATTG ATGTTG     TG
                                |||||||| ||||||     ||
                                CCTGTGAC TGTAAC     AC
                                     _     TA_____
GAM260  PRO0650  5' CTATGAAACAATGCAATGTTC  26214         AT   C   T
                                GGGCATTGT  GTTG TTC GTGG
                                |||||||||  |||| ||| ||||
                                CTTGTAACG  TAAC AAG TATC
                                     __    A   _
GAM260  PRO1596  3' CAGGCCATATGGTCTC     48384     C  TG    TT  TT
                                GGG AT  TATG  GC  CTG
                                ||| ||  ||||  ||  |||
                                CTC TG  ATAC  CG  GAC
                                  _ GT    __  __
GAM260  PRO1600  3' CCATTCTTAGCATCTAATGCCT 26033         T     CTTCT
                                GGGCATTG ATGTTG    GTGG
                                |||||||| ||||||    ||||
                                TCCGTAAT TACGAT    TACC
                                     C     TCT__
GAM260  PRO1770  3' ATCAAAGGCAGCAATAATGTTC 26040          A       C  TGG
                                GGGCATTGT TGTTGCTT TG
                                ||||||||| |||||||| ||
                                CTTGTAATA ACGACGGA AC
                                     _       A  TAT
GAM260  PRO2015  5' CCATGGAAACACTGCATGTGTT 37556        _    T  T C
          C                    GGGCAT TGTA GT G TTCTGTGG
                               |||||| |||| || | ||||||||
                               CTTGTG ACGT CA C AAGGTACC
                                  T    _ _ A
GAM260  PRO2133  3' CGTGGAAGTTCCAGTGTTC   37787        TATGTT      TG
                                GGGCATTG     GCTTCTG  G
                                ||||||||     |||||||  |
                                CTTGTGAC     TGAAGGT  C
                                     CT_____      GT
GAM260  PRO2266  3' TGTAGGGCATGTGTATGCCC   37585       TGTATGT    T   TG
                                GGGCAT      TGCT CTG  G
                                ||||||      |||| |||  |
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                                CCCGTA      ACGG GAT  T
                                   TGTGT__    _  GT
GAM260  PRO2521  5' TCACAGGGAATATGATGGCT  37593    G   TG   GTTGCT
                                GG CAT  TAT     TCTGTGG
                                || |||  |||     |||||||
                                TC GTA  ATA     GGACACT
                                 G   GT   AG____
GAM260  PRO2900  3' CCACAGGGGACCCAGATGGTGC 37806       TG A  TTG
           CT                    GGGCAT  T TG   CTTCTGTGG
                                |||||||  | ||   |||||||||
                                TCCGTG  A AC   GGGGACACC
                                   GT G  CCA
GAM260  PRO2949  3' TCATTAATGTGATAAATAATGT 37625         A   TG TTCT
           CC                    GGGCATTGT TGT  C    GTGG
                                |||||||||| |||  |    ||||
                                CCTGTAATA ATA  G    TACT
                                      A   GT TAAT
GAM260  PRPF8    3' CATAGAGAATATGATCCT    61184     C  TG   GTTGCT
                                GGG AT  TAT     TCTGTG
                                ||| ||  |||     ||||||
                                TCC TA  ATA     AGATAC
                                 _  GT   AG____
GAM260  PRPF8    3' GGCTGGGCAATGTGGATGCCT  61195       G        CT  GG
                                GGGCATT TATGTTGCTT  GT
                                ||||||| ||||||||||  ||
                                TCCGTAG GTGTAACGGG  CG
                                   _        T_  GC
GAM260  PSMD3    5' CGCGCTCGTGTGCAGGCCC    10972     A     TG T_  TTCT
                                GGGC TTGTA  T  GC    GTG
                                |||| |||||  |  ||    |||
                                CCCG GACGT  G  CG    CGC
                                  _    GT CT  _____
GAM260  PTBP2    3' AGTTGACATACGTGCCT     41033       T      _
                                GGGCAT GTATGTTG CT
                                |||||| |||||||| ||
                                TCCGTG CATACAGT GA
                                   _       T
GAM260  PTE1     5' CCGCGGAGCGGGTGTGCAGGGC 18442      A    TG  _   T
           CT                    GGGC TTGTA  TT GCT CTGTGG
                                |||| |||||  || ||| ||||||
                                TCCG GACGT  GG CGA GGCGCC
                                  G    GT  G  _
GAM260  PTPN3    3' GTGTACATGTGTGTGCCC     11059       TG_    _
                                GGGCAT   TATGT TGC
                                ||||||   ||||| |||
                                CCCGTG   GTACA GTG
                                   TGT    T
GAM260  PTPN3    3' TGTAGAAGCAGGTGTGTCT    11061       TGTATG       TG
                                GGGCAT     TTGCTTCTG  G
                                ||||||     |||||||||  |
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                                TCTGTG     GACGAAGAT  T
                                  TG____       GT
GAM260  PTPRU    3'  CATAGGGTCCTGCAGGCCT   19114     A    TGTT   T
                                GGGC TTGTA    GCT CTGTG
                                |||| |||||    ||| |||||
                                TCCG GACGT    TGG GATAC
                                  _    CC__   _
GAM260  PTPRU    3'  CATAGGGTCCTGCAGGCCT   55687     A    TGTT   T
                                GGGC TTGTA    GCT CTGTG
                                |||| |||||    ||| |||||
                                TCCG GACGT    TGG GATAC
                                  _    CC__   _
GAM260  PTPRU    3'  CATAGGGTCCTGCAGGCCT   55693     A    TGTT   T
                                GGGC TTGTA    GCT CTGTG
                                |||| |||||    ||| |||||
                                TCCG GACGT    TGG GATAC
                                  _    CC__   _
GAM260  PYY2     3'  CTGCAGGGCTGTGTGTGGTCCT 40827     C  TG  TG T   T   TG
                                GGG AT  TA  T GCT CTG  G
                                ||| ||  ||  | ||| |||  |
                                TCC TG  GT  G CGG GAC  C
                                  _ GT  GT T   _   GT
GAM260  QSCN6    3'  CGCAGGAGAAGATGGCTGCTT  11039      TTG   G  G    TG
                                GGGCA   TAT TT CTTCTG  G
                                |||||   ||| || ||||||  |
                                TTCGT   GTA AA GAGGAC  C
                                  CG_   G  _     GT
GAM260  RA-GEF-2  3'  TTACAGAGGTGATATGCTTGAT 32960     _ TT     TG
           CT                    GGG CA  GTATGT  CTTCTGTGG
                                ||| ||  ||||||  |||||||||
                                TCT GT  CGTATA  GGAGACATT
                                  A  T_     GT
GAM260  RA-GEF-2  3'  TTATAGAAGCAGCTGACAGTGG 32961    G     AT
           TC                    GG CATTGT  GTTGCTTCTGTGG
                                || ||||||  ||||||||||||
                                CT GTGACA  CGACGAAGATATT
                                 G     GT
GAM260  Rab11-FIP2 3'  GTGGGAAGTATGTGATTGCCT  29781      TTG    T    GTGG
                                GGGCA   TATGT GCTTCT
                                |||||   ||||| ||||||
                                TCCGT   GTGTA TGAAGG
                                  TA_    _     GTGT
GAM260  Rab11-FIP3 3'  ACAGCCGACAGTGCCC     28122       TGTA    CTT
                                GGGCAT    TGTTG   CTGT
                                ||||||    |||||   ||||
                                CCCGTG    ACAGC   GACA
                                   _____     C__
GAM260  RAB33B   3'  AAGTGACATAAGGTGCTT    48480       TG    TG
                                GGGCAT  TATGT  CTT
                                ||||||  |||||  |||
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                                TTCGTG  ATACA  GAA
                                   GA    GT
GAM260  RAB35    3'  CCACAGAGGTGGCAGGTCTTGC 22476      TTGTA   TG
           CC                    GGGCA    TGT  CTTCTGTGG
                                 |||||    |||  |||||||||
                                 CCCGT    ACG  GGAGACACC
                                   TCTGG   GT
GAM260  RAB35    3'  GGGAGTGCATGCCT       22481       T  ATGTT
                                 GGGCAT GT    GCTTCT
                                 ||||||  ||    ||||||
                                 TCCGTA CG    TGAGGG
                                   _  _____
GAM260  RAB3IL1  3'  CCATGGAGGCAGCACTGAGCC  25462     A  GTA
                                 GGC TT   TGTTGCTTCTGTGG
                                 |||  ||   ||||||||||||||
                                 CCG AG   ACGACGGAGGTACC
                                  _  TC_
GAM260  RAB40B   3'  GCGAATGTGTGCGACGCCT   22376     A     ___
                                 GGGC TTGTATG   TTGC
                                 ||||  |||||||   ||||
                                 TCCG AGCGTGT   AGCG
                                   C      GTA
GAM260  RAB6C    3'  ACGGTAGGCAGTGCTT     49565         ATGTTG  T
                                 GGGCATTGT     CT CTGT
                                 |||||||||     ||  ||||
                                 TTCGTGACG     GA GGCA
                                        _____  T
GAM260  RAB6C    5'  TGCAGGGGCACAGAGAGCTC   49572     A  GTA   T     TG
                                 GGGC TT   TGT GCTTCTG  G
                                 ||||  ||   |||  |||||||  |
                                 CTCG AG   ACA CGGGGAC  T
                                   _  AG_  _      GT
GAM260  RALGPS1A 3'  TTATAGAAGCAGTAAGAGGCTT 27612     ATTG   GT
                                 GGGC    TAT  TGCTTCTGTGG
                                 ||||    |||  ||||||||||
                                 TTCG    ATG  ACGAAGATATT
                                   GAGA   __
GAM260  RASSF2   3'  TAATATCGGTAGCATATAATGC 28445             TC   GG
           CC                    GGGCATTGTATGTTGCT  TGT
                                 ||||||||||||||||  |||
                                 CCCGTAATATACGATGG  ATA
                                          CT   ATC
GAM260  RBT1     3'  TTGTGGGGGCTCGAAGCAGTGA 25357    G     ATGTT     TG
           CT                    GG CATTGT    GCTTCTG  G
                                 ||  ||||||    |||||||  |
                                 TC GTGACG    CGGGGGT  T
                                  A     AAGCT      GT
GAM260  REC8     5'  AATGAGGAGCGAGGTGCGGTGC 17615          G      GTGG
           CC                    GGGCATTGTAT TTGCTTCT
                                 ||||||||||| ||||||||
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                                CCCGTGGCGTG AGCGAGGA
                                      G       GTAAT
GAM260  RER1     3'  CCATGGGAGCAAGGGCGAGTGG 22863    G   _ ATG
              CC                  GG CATT GT   TTGCTTCTGTGG
                                  || |||| ||   ||||||||||||
                                  CC GTGA CG   AACGAGGGTACC
                                   G   G  GG_
GAM260  RGS12    3'  CCGTAGCAGGTGGTGTGGGTGC 11334        G  TG TG  _
              TC                  GGGCATT TA  T  CTT CTGTGG
                                  ||||||| ||  |  ||| ||||||
                                  CTCGTGG GT  G  GGA GATGCC
                                      _ GT GT   C
GAM260  RGS12    3'  TTGCAGGAATGATACGTGGCAG 11336       _   TGC__    TG
              TGCCT                  CATTGT ATGT    TTCTG  G
                                  |||||| ||||    |||||  |
                                  GTGACG TGCA    AGGAC  T
                                     G   TAGTA    GT
GAM260  RGS20    3'  GGTAACAGCAGCAATGCTT   13515         A__
                                  GGGCATTGT   TGTTGCT
                                  |||||||||   |||||||
                                  TTCGTAACG   ACAATGG
                                       ACG
GAM260  RNF2     3'  CATTGTCATGCAATGTTT    23297           TTGCTTCT
                                  GGGCATTGTATG       GTG
                                  ||||||||||||       |||
                                  TTTGTAACGTAC       TAC
                                        TGT_____
GAM260  RNF20    3'  TTACAGGGTTGTTGTGATCCC  38969    C  TG  TGTT   T
                                  GGG AT  TA    GCT CTGTGG
                                  ||| ||  ||    ||| ||||||
                                  CCC TA  GT    TGG GACATT
                                    _  GT  TGT_  _
GAM260  RNF8     3'  TTACAGAGGTGGGTCACTGTTT 14247      T  TATG TG
                                  GGGCA TG    T  CTTCTGTGG
                                  ||||| ||    |  |||||||||
                                  TTTGT AC    G  GGAGACATT
                                     C  TG__ GT
GAM260  RNPC1    3'  CCGTGGAGACGACGACAGTGTT 33987         A    CT  TG
              T                   GGGCATTGT TGTTG  TC  TGG
                                  |||||||| |||||  ||  |||
                                  TTTGTGACA GCAGC  AG  GCC
                                        _    AG  GT
GAM260  ROBO4    3'  TGTGGAGGACAGCAGTGGCT   38793    G     A   TG     TG
                                  GG CATTGT TGT  CTTCTG  G
                                  || |||||| |||  ||||||  |
                                  TC GTGACG ACA  GGAGGT  T
                                   G     _  __     GT
GAM260  RoXaN    3'  CAGAAGAGATAGAGCTC     46638      A    ATGTTG
                                  GGGC TTGT     CTTCTG
                                  |||| ||||     ||||||
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                                CTCG GATA     GAAGAC
                                  A   GA____
GAM260  RPL32    5'  CTACGGAGGTGGCAGCCATCTC 6393      CAT  TA   TG
            CT                    GGG   TG  TGT  CTTCTGTGG
                                |||   ||  |||  |||||||||
                                TCC   AC  ACG  GGAGGCATC
                                  TCT  CG   GT
GAM260  Rpo1-2   3'  CCATGGAAGTGTCTACAAGTCT 38699      A     TGT
                                GGGC TTGTA   TGCTTCTGTGG
                                |||| |||||   ||||||||||
                                TCTG AACAT   GTGAAGGTACC
                                  _    CT_
GAM260  RRP4     3'  TTGCAGGAGTGAAGACTGTGAT 26567      TG  TG__ TG     TG
            GT                    GCAT  TA    T  CTTCTG  G
                                |||| ||    |  ||||||  |
                                TGTA  GT    A  GAGGAC  T
                                  GT  CAGA GT      GT
GAM260  SARM     3'  TAACAATACAGTGTCT      30616           _
                                GGGCATTGTAT GTTG
                                |||||||||||  ||||
                                TCTGTGACATA CAAT
                                      A
GAM260  SAS10    3'  CTATGGGAGCAATATGAAGGTG 39803       TG_
            CT                    GGCAT   TATGTTGCTTCTGTGG
                                |||||   ||||||||||||||||
                                TCGTG   GTATAACGAGGGTATC
                                   GAA
GAM260  SCOP     3'  AGCATGGTTGTATAGTGCCC   91777           GT___
                                GGGCATTGTAT     TGCT
                                ||||||||||     ||||
                                CCCGTGATATG     ACGA
                                      TTGGT
GAM260  SCOP     3'  GAGCAGCTGCAGTGTTT     91780          T
                                GGGCATTGTA GTTGCTT
                                |||||||||| |||||||
                                TTTGTGACGT CGACGAG
                                          _
GAM260  SCYA20   3'  CATGGAGGGTTTAGTGCTT    15971         T  GTTG
                                GGGCATTG AT    CTTCTGTG
                                |||||||| ||    ||||||||
                                TTCGTGAT TG    GGAGGTAC
                                     T  _____
GAM260  SCYA7    3'  TCATGGGGGTATTGTATAAGTC 20780      A     GT
            C                     GGGC TTGTAT  TGCTTCTGTGG
                                |||| ||||||  ||||||||||
                                CCTG AATATG  ATGGGGGTACT
                                  _     TT
GAM260  SDCCAG10 5'  GGGCAGGGGTAGTGTTTGGTGT 19643         T TG         GG
            CC                    GGGCATTG A  TTGCTTCTGT
                                |||||||| |  ||||||||||
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                                CCTGTGGT T  GATGGGGACG
                                     T GT        GGT
GAM260  SDCCAG43  3'  CAGAAGTACAGTGCCT      70370         ATGTT
                                GGGCATTGT    GCTTCTG
                                |||||||||    |||||||
                                TCCGTGACA    TGAAGAC
                                      _____
GAM260  SDF2L1    3'  TGTAGGGGTCCTCAAGTGCCT  41868       GTATGTT      TG
                                GGGCATT      GCTTCTG  G
                                |||||||      |||||||  |
                                TCCGTGA      TGGGGAT  T
                                   ACTCC__      GT
GAM260  SDOS      3'  CCACAGGGGTGGCGCACAGCTC 50366      AT   A   TG
                                GGGC  TGT TGT  CTTCTGTGG
                                ||||  ||| |||  |||||||||
                                CTCG  ACA GCG  GGGGACACC
                                  __  C   GT
GAM260  SEC24A    3'  TGCAGAGGCAAAGTACA     82685      G       TG
                                TGTAT TTGCTTCTG  G
                                ||||| |||||||||  |
                                ACATG AACGGAGAC  T
                                   A       GT
GAM260  SEC63L    3'  AGGCAGTGGCGGTGCCT     23302         ATG
                                GGGCATTGT   TTGCTT
                                |||||||||   ||||||
                                TCCGTGGCG   GACGGA
                                     GT_
GAM260  SEC63L    5'  GGCGGCGGCAGTGTCC      23303         A
                                GGGCATTGT TGTTGCT
                                ||||||||| |||||||
                                CCTGTGACG GCGGCGG
                                      _
GAM260  SEMA3E    3'  TCACAGGGGCCTTACAAAGTTT 24886      A     TGTT
                                GGGC TTGTA    GCTTCTGTGG
                                |||| |||||    ||||||||||
                                TTTG AACAT    CGGGGACACT
                                  A     TC__
GAM260  SEMA4F    3'  CATAGAGGGAATGGCG      14939      A   G
                                TGT TGTT CTTCTGTG
                                ||| |||| ||||||||
                                GCG GTAA GGAGATAC
                                  _   G
GAM260  SEMA5A    3'  TGGGAGTCAAAGCCT       14263      A   TATGTT
                                GGGC TTG     GCTTCTG
                                |||| |||     |||||||
                                TCCG AAC     TGAGGGT
                                  A  _______
GAM260  SENP7     3'  TCACGGAATTTATGTATAGTTT 40302      C       TGC
             CT                   GGG ATTGTATGT   TTCTGTGG
                                ||| |||||||||   ||||||||
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                                TCT TGATATGTA   AAGGCACT
                                  T       TTT
GAM260  SEPT3    3'  TGCAGAAAGCATCAGTGCCT   38896       T    GC    TG
                                GGGCATTG ATGTT  TTCTG  G
                                |||||||| |||||  |||||  |
                                TCCGTGAC TACGA  AAGAC  T
                                    _    __    GT
GAM260  SES2     3'  GGGAGTGGTATCCAGTGTTC   48813       T   TT
                                GGGCATTG ATG  GCTTCT
                                |||||||| |||  ||||||
                                CTTGTGAC TAT  TGAGGG
                                     C   GG
GAM260  Sfmbt    3'  TTCCTAAGGCATATCAGTGCTT 32900       T   T   CTGTGG
                                GGGCATTG ATGT GCTT
                                |||||||| |||| ||||
                                TTCGTGAC TATA CGGA
                                    _   _   ATCCTTG
GAM260  SFRS12   3'  CTATGGGAGCACAAGCTGAAGC 57526     ATT_ A   T
             TT                   GGGC    GT TGT GCTTCTGTGG
                                |||||   || ||| ||||||||||
                                TTCG    CG ACA CGAGGGTATC
                                  AAGT  A   _
GAM260  SFRS5    3'  TTGTAGGGGTAGCATTTAAGAT 22646     CA   T        TG
             TC                   GGG  TTG ATGTTGCTTCTG  G
                                |||  ||| ||||||||||||  |
                                CTT  AAT TACGATGGGGAT  T
                                  AG   T         GT
GAM260  SFXN5    3'  GAGGAGGAGGTAACATAGATGC 58035       G        GTGG
             CT                   GGGCATT TATGTTGCTTCT
                                |||||||| ||||||||||||
                                TCCGTAG ATACAATGGAGG
                                    _         AGGAGG
GAM260  SGK2     5'  CACAGGGGTCTTGTTGCCC   32777      TTGT   TT
                                GGGCA   ATG  GCTTCTGTG
                                |||||   |||  |||||||||
                                CCCGT   TGT  TGGGGACAC
                                   _____  TC
GAM260  SH2D3A   5'  TCGTGGGAGCCCCGCGGGTCC  18509     A   ATGTT    TG
                                GGGC TTGT    GCTTC  TGG
                                |||| ||||    |||||  |||
                                CCTG GGCG    CGAGG  GCT
                                  _   CCC__    GT
GAM260  SIAT8C   5'  TCATATCCAGGCATGCAAGCCT 31885      A       GCTTC
                                GGGC TTGTATGTT    TGTGG
                                |||| |||||||||    |||||
                                TCCG AACGTACGG    ATACT
                                  _       ACCT_
GAM260  SIMRP7   3'  CCACAGGGGCCACCTACAGGTT 92360     A    T  T
             T                    GGGC TTGTA GT GCTTCTGTGG
                                |||| ||||| || ||||||||||
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                                TTTG GACAT CA CGGGGACACC
                                  _    C  C
GAM260  SIMRP7   3'  TCATGGGGGCGGCAGTGGTC  92371     ATTGTA
                                GGC     TGTTGCTTCTGTGG
                                |||     ||||||||||||||
                                CTG     ACGGCGGGGGTACT
                                  GTG___
GAM260  SLC11A2  3'  CTACAGAATGAGTATGCAAGTT 5234       A        GC
           T                     GGGC TTGTATGTT  TTCTGTGG
                                |||| |||||||||  ||||||||
                                TTTG AACGTATGA  AAGACATC
                                  _       GT
GAM260  SLC19A3  3'  CTATGGGCCAGGTGCAGTGGCT 47484    G       G   CT
                                GG CATTGTAT TTG  TCTGTGG
                                || ||||||||| |||  |||||||
                                TC GTGACGTG GAC  GGGTATC
                                 G       _   C_
GAM260  SLC1A7   3'  CGCAGGGGCAGGCGAGGCCT   21906     A    ATG       TG
                                GGGC TTGT   TTGCTTCTG  G
                                |||| ||||   |||||||||  |
                                TCCG AGCG   GACGGGGAC  C
                                  G   ___       GT
GAM260  SLC22A6  5'  CTGCGGAGGCAACGGCAGTGCT 16571         A         TG
                                GGCATTGT TGTTGCTTCTG  G
                                |||||||| ||||||||||  |
                                TCGTGACG GCAACGGAGGC  C
                                     _         GT
GAM260  SLC26A7  3'  TAGAATAACATTTGGTGCCT   56151         T     C
                                GGGCATTG ATGTTG TTCTG
                                |||||||| |||||| |||||
                                TCCGTGGT TACAAT AAGAT
                                     T     _
GAM260  SLC34A1  3'  CATAGATGTTGGTGCCT     11746         TATGTT  T
                                GGGCATTG     GC TCTGTG
                                ||||||||     || ||||||
                                TCCGTGGT     TG AGATAC
                                     _______  T
GAM260  SLC4A11  3'  TTGTAGGGGTGCAGTGGTATGT 49342      TGTA___   T      TG
           GCCC                   GCAT      TGT GCTTCTG  G
                                ||||      ||| |||||||  |
                                CGTG      ACG TGGGGAT  T
                                  TATGGTG  _      GT
GAM260  SLC5A7   3'  CCATCAATTTTAACATTTGATG 41509         T     CTTCT_
           TCT                    GGGCATTG ATGTTG     GTGG
                                |||||||| ||||||     ||||
                                TCTGTAGT TACAAT     TACC
                                     T     TTTAAC
GAM260  SLC7A11  3'  TCATATCTACATGCAATGTT   26756           TGCTTC
                                GGCATTGTATGT     TGTGG
                                ||||||||||||     |||||
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                                TTGTAACGTACA     ATACT
                                      TCT___
GAM260  SLC8A3   5' CCGCGGGGGCGATGAGCCGCT 54263     ATT  A
                                GGC   GT TGTTGCTTCTGTGG
                                |||   || ||||||||||||||
                                TCG   CG GTAGCGGGGGCGCC
                                  C__  A
GAM260  SLC8A3   5' CCGCGGGGGCGATGAGCCGCT 52700     ATT  A
                                GGC   GT TGTTGCTTCTGTGG
                                |||   || ||||||||||||||
                                TCG   CG GTAGCGGGGGCGCC
                                  C__  A
GAM260  SMA3     5' CAATCAGCATGCTGTGTCT   22287       T      CTTCTG
                                GGGCAT GTATGTTG     TG
                                |||||| ||||||||     ||
                                TCTGTG CGTACGAC     AC
                                    T       TA____
GAM260  SMARCF1  3' GTAATAATAATGTCT      20044         A
                                GGGCATTGT TGTTGC
                                ||||||||| ||||||
                                TCTGTAATA ATAATG
                                          _
GAM260  SMARCF1  3' GTAATAATAATGTCT      37441         A
                                GGGCATTGT TGTTGC
                                ||||||||| ||||||
                                TCTGTAATA ATAATG
                                          _
GAM260  SMARCF1  3' TTGTAGAATATTTCCGACGATG 37448         ATGTTGC_    TG
           CCT                    GGGCATTGT      TTCTG  G
                                ||||||||||       |||||  |
                                TCCGTAGCA       AAGAT  T
                                     GCCTTTAT    GT
GAM260  SMARCF1  3' GTAATAATAATGTCT      57490         A
                                GGGCATTGT TGTTGC
                                ||||||||| ||||||
                                TCTGTAATA ATAATG
                                          _
GAM260  SMCR8    3' TTACAGAGGCACCCTGGTGCCC 58601        TAT  T
                                GGGCATTG   GT GCTTCTGTGG
                                ||||||||   || ||||||||||
                                CCCGTGGT   CA CGGAGACATT
                                     CC_  _
GAM260  SMOC1    3' GTAACATAAGTGGTGCCC    42154       TG __
                                GGGCAT  T  ATGTTGC
                                ||||||  |  |||||||
                                CCCGTG  G  TACAATG
                                   GT AA
GAM260  SMOC2    3' CCATGGAAGTTTGTGATGT   72370     TG  TGTT
                                GCAT  TA   GCTTCTGTGG
                                ||||  ||   ||||||||||
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                                TGTA  GT    TGAAGGTACC
                                  GT  T___
GAM260  SMOC2    3'  TCACATACAATGTATGTGTCC  72377       T       CTTC
                                GGGCAT GTATGTTG    TGTGG
                                |||||| ||||||||    |||||
                                CCTGTG TATGTAAC    ACACT
                                   _       AT__
GAM260  SNAP29   3'  CTGCAGCCTATAAACAGTGGTG 16540      TG A    GCTT__   TG
          TCT                     GGCAT  T TGTT     CTG  G
                                |||||  | ||||     |||  |
                                CTGTG  G ACAA     GAC  C
                                  GT _    ATATCC   GT
GAM260  SNAP29   3'  TCACTTAAAATAACAGTGCCT  16545         A    GCTTCT
                                GGGCATTGT TGTT     GTGG
                                |||||||||| ||||     ||||
                                TCCGTGACA ATAA     CACT
                                   _    AATT__
GAM260  SNRK     3'  TATTCAGATGTATATATGGTGC 34771       TG    T  T    TGG
          TC                      GGGCAT  TATGT GC TCTG
                                ||||||  ||||| || ||||
                                CTCGTG  ATATA TG AGAC
                                  GT     _ T    TTATA
GAM260  SNRK     3'  AAGTGACATATTGGTGTTC   34762         _     TG
                                GGGCATTG TATGT  CTT
                                |||||||| |||||  |||
                                CTTGTGGT ATACA  GAA
                                     T    GT
GAM260  SNX11    5'  TAGGGGCGGGGCGTCC     25274      ATT  ATGT
                                GGGC   GT    TGCTTCTG
                                ||||   ||    ||||||||
                                CCTG   CG    GCGGGGAT
                                  ___  GG__
GAM260  SPRY1    3'  CACAGAACTATGCTGCCT    65001       TT    TTGC
                                GGGCA  GTATG    TTCTGTG
                                |||||  |||||    |||||||
                                TCCGT  CGTAT    AAGACAC
                                  __     C___
GAM260  SPTLC2   3'  TTACAGGCCGAGTGCGGTGGCT 16814    G       GTT  TT
                                GG CATTGTAT   GC  CTGTGG
                                || ||||||||   ||  ||||||
                                TC GTGGCGTG   CG  GACATT
                                 G       AGC  __
GAM260  SR-BP1   3'  TCACCTGCAGCTATGATGCCC  19635       TG  T    TTCT
                                GGGCAT  TA GTTGC    GTGG
                                ||||||  || |||||    ||||
                                CCCGTA  AT CGACG    CACT
                                   GT  _     TC__
GAM260  SRF      3'  TCACAGTCCTATGTACAGAGCT 11951      A       TGCTT
          T                      GGGC TTGTATGT    CTGTGG
                                ||||| ||||||||     ||||||
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                                TTCG GACATGTA    GACACT
                                  A      TCCT_
GAM260  SRP54    5'  CACGGCTTTAGCGGTGTCT   11959        A  TT   TCT
                                GGGCATTGT TG  GCT   GTG
                                ||||||||| ||  |||   |||
                                TCTGTGGCG AT  CGG   CAC
                                     _  TT   ___
GAM260  SRPK1    3'  CCACAGAGGTGCAACTTGAGGC 11965     ATTG  T    __
          TC                     GGGC    TA GTTGC  TTCTGTGG
                                ||||   || |||||  ||||||||
                                CTCG    GT CAACG  GAGACACC
                                  GA__  T    TG
GAM260  SS-56    3'  GCATCTTATAGCAGTGCCT   59603         _   T__
                                GGGCATTGT ATG   TGC
                                ||||||||| |||   |||
                                TCCGTGACG TAT   ACG
                                     A   TCT
GAM260  SSB-4    3'  CCATGGGGGCAGCCTTGTGACT 55098    G   TGTAT
                                GG CAT    GTTGCTTCTGTGG
                                || |||    ||||||||||||
                                TC GTG    CGACGGGGGTACC
                                 A  TTC__
GAM260  SSH2     3'  CAGGCATCAGTGCCC      62201        T   TGCTT
                                GGGCATTG ATGT    CTG
                                |||||||| ||||    |||
                                CCCGTGAC TACG    GAC
                                     _   _____
GAM260  SSR1     3'  CTATATCTGTAATATAAAGTGT 11980       G      TTC
          TT                     GGGCATT TATGTTGC   TGTGG
                                ||||||| ||||||||   |||||
                                TTTGTGA ATATAATG   ATATC
                                   A       TCT
GAM260  ST7L     3'  CTGCAGGAGCTAGGCTGAATGC 56998       GTATGTT     TG
          CT                     GGGCATT     GCTTCTG  G
                                |||||||     |||||||  |
                                TCCGTAA     CGAGGAC  C
                                   GTCGGAT     GT
GAM260  ST7L     3'  CTGCAGGAGCTAGGCTGAATGC 34854       GTATGTT     TG
          CT                     GGGCATT     GCTTCTG  G
                                |||||||     |||||||  |
                                TCCGTAA     CGAGGAC  C
                                   GTCGGAT     GT
GAM260  ST7L     3'  CTGCAGGAGCTAGGCTGAATGC 57574       GTATGTT     TG
          CT                     GGGCATT     GCTTCTG  G
                                |||||||     |||||||  |
                                TCCGTAA     CGAGGAC  C
                                   GTCGGAT     GT
GAM260  STAF65(gamma) 3'  TCACAGATAAAATATGATGCT  29443      TG   GTTGCT
                                GGCAT  TAT     TCTGTGG
                                |||||  |||     |||||||
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                                TCGTA  ATA     AGACACT
                                  GT   AAAT__
GAM260  STI2     3'  CTGTGGAAGCCTGGGCAGGTGT 88966       _  ATGTT      TG
            CC                    GGGCAT TGT    GCTTCTG  G
                                ||||||  |||    |||||||  |
                                CCTGTG ACG    CGAAGGT  C
                                   G   GGTC_      GT
GAM260  STRBP    3'  GAAGGATGTATAGAGTCT    37232      A       G
                                GGGC TTGTATGTT CTTC
                                |||| ||||||||| ||||
                                TCTG GATATGTAG GAAG
                                  A       _
GAM260  STRIN    3'  CCATACTAATATACATTGTTT  32767      T       CTTC
                                GGGCA TGTATGTTG    TGTGG
                                ||||| |||||||||    |||||
                                TTTGT ACATATAAT    ATACC
                                   T       C___
GAM260  STX6     3'  GACAGAAAATGCAGTGTTT    19487          GTTGC     GG
                                GGGCATTGTAT    TTCTGT
                                ||||||||||    ||||||
                                TTTGTGACGTA    AAGACA
                                      A____     GT
GAM260  SUPT3H   5'  TCGCGGGAAGCGCAGCAGTGCC 13184         A  T    _
            T                    GGGCATTGT TGT GCTTCT GTGG
                                |||||||| ||| |||||| ||||
                                TCCGTGACG ACG CGAAGG CGCT
                                     _  _     G
GAM260  SV2      3'  GCTGCGTCCAGTGCCC     29311        T   T
                                GGGCATTG ATGT GC
                                |||||||| |||| ||
                                CCCGTGAC TGCG CG
                                    C   T
GAM260  T2BP     3'  TTCCTGGGCAGTAGTATGTGAT 70000       TG       T  GT
            GTCC                   GGGCAT  TATGTTGCT CT  GG
                                ||||||  ||||||||| ||  ||
                                CCTGTA  GTATGATGA GG  CC
                                   GT       C  GT  TTA
GAM260  TA-PP2C  3'  CCATTTTGCAGTGTATAGTTTC 57757    C     TG    TTCT
            C                    GGG ATTGTA  TTGC    GTGG
                                ||| ||||||  ||||   ||||
                                CCT TGATAT  GACG    TACC
                                  T     GT    TTT_
GAM260  TBC1D2   5'  TCGCTTGCACATGTGATGTTC  37326       TG    T  TTCT
                                GGGCAT  TATGT GC    GTGG
                                ||||||  ||||| ||    ||||
                                CTTGTA  GTACA CG    CGCT
                                   GT     _ TT__
GAM260  TBC1D2   5'  TCGCTTGCACATGTGATGTTC  37322       TG    T  TTCT
                                GGGCAT  TATGT GC    GTGG
                                ||||||  ||||| ||    ||||
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                                CTTGTA  GTACA CG   CGCT
                                   GT    _ TT__
GAM260  TBC1D2   5'  TCGCTTGCACATGTGATGTTC 37323      TG    T  TTCT
                                GGGCAT  TATGT GC   GTGG
                                ||||||  ||||| ||   ||||
                                CTTGTA  GTACA CG   CGCT
                                   GT    _ TT__
GAM260  TBC1D2   5'  TCGCTTGCACATGTGATGTTC 37324      TG    T  TTCT
                                GGGCAT  TATGT GC   GTGG
                                ||||||  ||||| ||   ||||
                                CTTGTA  GTACA CG   CGCT
                                   GT    _ TT__
GAM260  TBC1D2   5'  TCGCTTGCACATGTGATGTTC 37325      TG    T  TTCT
                                GGGCAT  TATGT GC   GTGG
                                ||||||  ||||| ||   ||||
                                CTTGTA  GTACA CG   CGCT
                                   GT    _ TT__
GAM260  TBL1Y    5'  CAGTGTGGCATTGATGTCC   56133       T   TG TT
                                GGGCATTG ATGT  C  CTG
                                |||||||| ||||  |  |||
                                CCTGTAGT TACG  G  GAC
                                    _   GT T_
GAM260  TBL1Y    5'  CAGTGTGGCATTGATGTCC   52719       T   TG TT
                                GGGCATTG ATGT  C  CTG
                                |||||||| ||||  |  |||
                                CCTGTAGT TACG  G  GAC
                                    _   GT T_
GAM260  TCF6L1   3'  TGTAGAAGCCACGGTGTTC   12152        ATGTT     TG
                                GGGCATTGT    GCTTCTG  G
                                |||||||||    |||||||  |
                                CTTGTGGCA    CGAAGAT  T
                                    C____      GT
GAM260  TDPGD    3'  GTTTTTAGGCAATATAGGATGT 59727       G        CTGTGG
           CT                     GGGCATT TATGTTGCTT
                                |||||||  ||||||||||
                                TCTGTAG ATATAACGGA
                                   G        TTTTTGC
GAM260  TIGA1    3'  TTACAGCTGTTTCCACGTGCGG 53803         T___  TT
           TGCTC                  CATTGTATGT   GC  CTGTGG
                                ||||||||||   ||  ||||||
                                GTGGCGTGCA   TG  GACATT
                                    CCTT  TC
GAM260  TIMM22   3'  GCACAGAGGTGACAGTGTCT   78312      TGTA  TG      G
                                GGGCAT   TGT  CTTCTGTG
                                ||||||   |||  ||||||||
                                TCTGTG   ACA  GGAGACAC
                                   ____  GT      GG
GAM260  TIX1     5'  CTGCAGAAGCAACATGTGACCT 61743     CA TG          TG
                                GGG  T  TATGTTGCTTCTG  G
                                |||  |  ||||||||||||  |
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                                TCC  A  GTACAACGAAGAC  C
                                  __ GT          GT
GAM260  TLN1     3'  CAGAGTTATAAGCCC      20815      A    TGTT   T
                                GGGC TTGTA    GCT CTG
                                |||| |||||    ||| |||
                                CCCG AATAT    TGA GAC
                                  _    ____  _
GAM260  TLOC1    3'  CCACAGAACATCTGTGATCTT  12311     C  TG  TGT  C
                                GGG AT  TA   TG TTCTGTGG
                                ||| ||  ||   || ||||||||
                                TTC TA  GT   AC AAGACACC
                                  _ GT  CT_ _
GAM260  TMPRSS5  3'  TTATTAAAGTGATATATGGTCT 47787     C  TG    TG   CT
           T                     GGG AT  TATGT  CTT  GTGG
                                ||| ||  |||||  |||  ||||
                                TTC TG  ATATA  GAA  TATT
                                  _ GT    GT   AT
GAM260  TNKS2    3'  CTATAGAAGGAAATGCTGTCC  47453      TT   G  G
                                GGGCA  GTAT TT CTTCTGTGG
                                |||||  |||| || |||||||||
                                CCTGT  CGTA AA GAAGATATC
                                   __   _ G
GAM260  TOB2     3'  CTACCTCCCCCGGCAGGCAATG 95623         A    CTTCT_
           TCC                    GGGCATTGT TGTTG     GTGG
                                |||||||| |||||     ||||
                                CCTGTAACG ACGGC     CATC
                                     G    CCCCTC
GAM260  TOLLIP   3'  CTGTAGAAGCAGCTTGCTGAGC 38682     ATT   T       TG
           CC                     GGGC   GTA GTTGCTTCTG  G
                                ||||   ||| ||||||||||  |
                                CCCG   CGT CGACGAAGAT  C
                                  AGT   T       GT
GAM260  TP53INP1 3'  TGTAGACTGTACATGTGCCT   72959      TGT   T  T_   TG
                                GGGCAT   ATGT GC  TCTG  G
                                ||||||   |||| ||  ||||  |
                                TCCGTG   TACA TG  AGAT  T
                                   ___   _ TC   GT
GAM260  TP53INP1 3'  TGTAGACTGTACATGTGCCT   52732      TGT   T  T_   TG
                                GGGCAT   ATGT GC  TCTG  G
                                ||||||   |||| ||  ||||  |
                                TCCGTG   TACA TG  AGAT  T
                                   ___   _ TC   GT
GAM260  TRIM17   3'  CAGAAGGTGTGGGCCT     32255     A TG   GTTG
                                GGGC T  TAT    CTTCTG
                                |||| |  |||    ||||||
                                TCCG G  GTG    GAAGAC
                                  _ GT  ____
GAM260  TRIM26   5'  ATAGGAGAGCAAGTCC     12886     A   ATGTTG
                                GGGC TTGT     CTTCTGT
                                |||| ||||     |||||||
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                                CCTG AACG     GAGGATA
                                  _   A_____
GAM260  TRIM4    3'  ATACGTGAGAACATGTGATGTT 52250      TG     G  C   G
             T                    GGGCAT  TATGTT CTT TGTG
                                  ||||||  |||||| ||| ||||
                                  TTTGTA  GTACAA GAG GCAT
                                     GT     _  T   AT
GAM260  TRIP-Br2 5'  CACCATTGTATAATGCTC    28578         GT  CTTCT
                                  GGGCATTGTAT  TG    GTG
                                  ||||||||||  ||    |||
                                  CTCGTAATATG  AC    CAC
                                        TT  _____
GAM260  TRIP-Br2 3'  GCAATGTATCATGCTT     28583       T
                                  GGGCAT GTATGTTGC
                                  |||||| |||||||||
                                  TTCGTA TATGTAACG
                                     C
GAM260  TSPAN-3  3'  TTATAGGAGGAGTATAATGT   19162        GTTG
                                  GCATTGTAT   CTTCTGTGG
                                  |||||||||   |||||||||
                                  TGTAATATG   GAGGATATT
                                       AG__
GAM260  TSPAN-5  5'  CCGCGGCCCCGTGCGGTGTCC  19156          TT   TCT
                                  GGGCATTGTATG  GCT   GTGG
                                  ||||||||||||  |||   ||||
                                  CCTGTGGCGTGC  CGG   CGCC
                                        CC  ___
GAM260  TSPAN-5  5'  CGCTCCGAGCAACGGTGCTT   19157      TGTA      CT_ TG
                                  GGGCAT   TGTTGCTT   G  G
                                  ||||||   ||||||||   |  |
                                  TTCGTG   GCAACGAG   C  C
                                     ____       CCT GT
GAM260  TTTY14   3'  CCAGCTTGGTGGCATGCATGTT 49188      T     TG  TCTG
             T                    GGGCAT GTATGT  CT    TGG
                                  ||||||  ||||||  ||    |||
                                  TTTGTA CGTACG  GG    ACC
                                     _     GT  TTCG
GAM260  TTTY2    5'  CTGTGGGAGTGTTGCGAGTGTT 87004      _  TGTT      TG
                                  GGCATT GTA    GCTTCTG  G
                                  |||||| |||    |||||||  |
                                  TTGTGA CGT    TGAGGGT  C
                                     G   TG__      GT
GAM260  TU3A     5'  TTACGGAATCACTGTCGATGCC 23195        T  GT  C
             C                     GGGCATTG AT  TG TTCTGTGG
                                   ||||||||  ||  ||  ||||||||
                                   CCCGTAGC TG  AC AAGGCATT
                                        _  TC  T
GAM260  TU3A     3'  TTATGGAAAGCAAATATACAAT 23196          _   _
             G                     CATTGTATGTT GCTT CTGTGG
                                   ||||||||||| |||| ||||||
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                                GTAACATATAA CGAA GGTATT
                                      A   A
GAM260  TU3A    3'  CCATGGAGGCAACAAGTCATTC 23185    CAT  TA_
           C                   GG   TG   TGTTGCTTCTGTGG
                               ||   ||   ||||||||||||||
                               CC   AC   ACAACGGAGGTACC
                                TT_  TGA
GAM260  TU3A    5'  TCGTGGAAGTGGCCGTGCACC  23192    _   TGTAT  TG   TG
                               GG GCAT    GT  CTTC  TGG
                               || ||||    ||  ||||  |||
                               CC CGTG    CG  GAAG  GCT
                                A   C____  GT   GT
GAM260  TUBGCP2  5'  CTGCGGAGAACATATTGTGATG 21854      ___     G  T   TG
           TTC                   GCATT   GTATGTT CT CTG  G
                               |||||   ||||||| || |||  |
                               TGTAG   TATACAA GA GGC  C
                                  TGT      _ _   GT
GAM260  TUSP    3'  CGGCAGTGGCGTGCACTGCTT  39630      T      TG  T
                               GGGCA TGTATGT  CT CTG
                               ||||| |||||||  || |||
                               TTCGT ACGTGCG  GA GGC
                                  C      GT  C
GAM260  TUSP    3'  CGGGCTGTGCGGTCCT     39631     C      GTT  TT
                               GGG ATTGTAT   GC  CTG
                               ||| |||||||   ||  |||
                               TCC TGGCGTG   CG  GGC
                                 _      T__  __
GAM260  TXNL2   3'  TTACAGGAGTGTCGGCTGTGCC 21555       T  ATGT
           C                   GGGCAT GT    TGCTTCTGTGG
                               ||||||  ||   ||||||||||||
                               CCCGTG CG    GTGAGGACATT
                                  T  GCT_
GAM260  UBE2N   3'  CGCAGGGGTGTGGGTGTTT   12510       G   GTT     TG
                               GGGCATT TAT   GCTTCTG  G
                               ||||||| |||   |||||||  |
                               TTTGTGG GTG   TGGGGAC  C
                                  _  ____      GT
GAM260  UBE2N   3'  CGCAGGGGTGTGGGTGTTT   94540       G   GTT     TG
                               GGGCATT TAT   GCTTCTG  G
                               ||||||| |||   |||||||  |
                               TTTGTGG GTG   TGGGGAC  C
                                  _  ____      GT
GAM260  UBE3B   3'  CGCGGAGGACGGCTGCCT    76920      TTGTAT   _
                               GGGCA     GTTG CTTCTGTG
                               |||||     |||| ||||||||
                               TCCGT     CGGC GGAGGCGC
                                  _______   A
GAM260  UBF-fl  3'  GCTATGGTAATATGGTGGTGTG 51565     TG TG  T_____
           CAGTGCCT                TGTA  T  CT     CTGTGG   C
                               ||||  |  ||     ||||||   |
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                                ACGT  G  GG     GGTATC   G
                                  GT GT  TATAAT
GAM260  UBN1     3'  TCGTGGAGGTGGACTGCATAGC 33734      AT    TG TG    TG
             CC                   GGGC  TGTA  T  CTTC  TGG
                                  ||||  ||||  |  ||||  |||
                                  CCCG  ACGT  G  GGAG  GCT
                                    AT    CA GT    GT
GAM260  UBXD2    3'  TCATAAATGCAGACAATGTTT  68345         ATG    TTC
                                  GGGCATTGT   TTGC   TGTGG
                                  |||||||||   ||||   |||||
                                  TTTGTAACA   GACG   ATACT
                                        ___    TAA
GAM260  ULK2     3'  TTGTAGAAGCAGGAGCAAGAGT 28010       GTA  ___       TG
             GTTT                   GCATT   TGT   TGCTTCTG  G
                                  |||||   |||   ||||||||  |
                                  TGTGA   ACG   ACGAAGAT  T
                                    GA_   AGG       GT
GAM260  UMP-CMPK 3'  CACCTTAGTTATGGTGCTC   32842       TG  TGTT   TCT
                                  GGGCAT  TA    GCT   GTG
                                  ||||||  ||    |||   |||
                                  CTCGTG  AT    TGA   CAC
                                     GT  _____   TTC
GAM260  USP19    3'  CAGGGGCAGAGTATCCT     88956     CATT    G
                                  GGG    GTAT TTGCTTCTG
                                  |||    |||| |||||||||
                                  TCC    TATG GACGGGGAC
                                    _____    A
GAM260  USP22    3'  AGTCTGGAGTAAATGCAGTGTC 68003           G      TGTGG
             T                     GGGCATTGTAT TTGCTTC
                                  ||||||||||| |||||||
                                  TCTGTGACGTA AATGAGG
                                        _      TCTGAC
GAM260  USP22    3'  CGCAGCTCATACGGTGT     68007          TT   TCT TG
                                  GCATTGTATG  GCT   G  G
                                  ||||||||||  |||   |  |
                                  TGTGGCATAC  CGA   C  C
                                        T_   ___ GT
GAM260  USP22    3'  GAATGACATATATTGTTC    68013       T       C
                                  GGGCA TGTATGTTG TTC
                                  |||||  |||||||||  |||
                                  CTTGT  ATATACAGT  AAG
                                     T       _
GAM260  VAMP4    3'  CAGAAATATAGTTCCT      60394     C      GTTGC
                                  GGG  ATTGTAT     TTCTG
                                  |||  |||||||     |||||
                                  TCC  TGATATA     AAGAC
                                    T      _____
GAM260  VCY2     3'  TCACAGAAGTAATTGTGCC    60263       TGTAT
                                  GGCAT     GTTGCTTCTGTGG
                                  |||||     |||||||||||||
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                                CCGTG    TAATGAAGACACT
                                  T____
GAM260  VEGFC    5'  TCGCGGGGTGTTCTGGTGTCC  18308       GTATGT   T
                                GGGCATT     TGCT CTGTGG
                                |||||||     |||| ||||||
                                CCTGTGG     GTGG GGCGCT
                                   TCTT__   _
GAM260  VI       3'  TTGTGGGGGCGGTGGGGAGGTC 25562     ATTGTA GT      TG
           C                     GGGC     T  TGCTTCTG  G
                                ||||     |  ||||||||  |
                                CCTG     G  GCGGGGGT  T
                                  GAGGG_ TG       GT
GAM260  VILL     5'  CAGAAGGCCAATGTTC      68411        TAT  TG
                                GGGCATTG   GT  CTTCTG
                                ||||||||   ||  ||||||
                                CTTGTAAC   CG  GAAGAC
                                    ___  __
GAM260  VMP1     3'  TAGGGTGGAATGTGATGTTC   48189       TG   G TG  T
                                GGGCAT  TAT T  CT CTG
                                ||||||  ||| |  || |||
                                CTTGTA  GTA G  GG GAT
                                   GT   A GT  _
GAM260  VPS28    3'  CTGCAGCTGCCTGTCTGGTGTC 32504       GT  GTT  TT   TG
           T                     GGGCATT  AT   GC  CTG  G
                                |||||||  ||   ||  |||  |
                                TCTGTGG  TG   CG  GAC  C
                                   TC  TC_  TC   GT
GAM260  WBSCR22  3'  CTGCGGAGGTGGGGTGGGATGC 34035       G   G TG     TG
           CT                     GGGCATT TAT T  CTTCTG  G
                                ||||||| ||| |  ||||||  |
                                TCCGTAG GTG G  GGAGGC  C
                                   G   G GT     GT
GAM260  WFDC3    3'  TTGGGTAGTGGGTGTGTGGTGC 96927       TG  TG  _   T  GTGG
           TT                     GGGCAT  TA  TT GCT CT
                                ||||||  ||  || ||| ||
                                TTCGTG  GT  GG TGA GG
                                   GT  GT  G   T  GTT
GAM260  WS-3     3'  CACAGAATAATACATGTTC    21646       T   GTTGC
                                GGGCAT GTAT    TTCTGTG
                                |||||| ||||    |||||||
                                CTTGTA CATA    AAGACAC
                                   _   AT___
GAM260  WWP1     5'  TCACGGGTACTCCAGTAGTGTC 80429       GTA  TTGCT
           T                     GGGCATT   TG    TCTGTGG
                                |||||||   ||    |||||||
                                TCTGTGA   AC    GGGCACT
                                   TG_  CTCAT
GAM260  XT2      3'  CACAGGGCTGCAAGTGCCC   42219       GTA   T   T
                                GGGCATT   TGT GCT CTGTG
                                |||||||   ||| ||| |||||
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                                CCCGTGA   ACG CGG GACAC
                                   ___  T  _
GAM260  XT2     3'  CCATTCTGGGCCTGTGGTGCTC 42221      TG  TGTT   CT_
                                GGGCAT  TA   GCTT   GTGG
                                ||||||  ||   ||||   ||||
                                CTCGTG  GT   CGGG   TACC
                                   GT  C___   TCT
GAM260  YAP1    3'  GGCAATATTCAGTGCTT    20353        T
                                GGGCATTG ATGTTGCT
                                |||||||| ||||||||
                                TTCGTGAC TATAACGG
                                     T
GAM260  YAP1    3'  CTACAGGAGTAATAATGGTTTC 20350    C  TG A
           C                     GGG AT  T TGTTGCTTCTGTGG
                                |||  ||  |  ||||||||||||||
                                CCT TG  A ATAATGAGGACATC
                                  T  GT _
GAM260  YKT6    3'  CCACAGAGGCCACAGGCAGGCC 21601     A   A   T
           C                     GGGC TTGT TGT GCTTCTGTGG
                                |||| |||| ||| ||||||||||
                                CCCG GACG ACA CGGAGACACC
                                  _   G   C
GAM260  ZAK     3'  ATGAATCAGCAAATGTGGTGCC 56119      TG   G    TCTGTGG
           T                     GGGCAT  TAT TTGCT
                                ||||||  ||| |||||
                                TCCGTG  GTA AACGA
                                   GT  _    CTAAGTAT
GAM260  ZDHHC2  3'  TATGGAAGAAACAATGTC    33012       ATGTTG
                                GGCATTGT    CTTCTGTG
                                ||||||||    ||||||||
                                CTGTAACA    GAAGGTAT
                                    AA____
GAM260  ZDHHC5  5'  TCGTGGAGGTACTATAGTATCT 91561    GC    T  T    TG
                                GG  ATTGTA GT GCTTC  TGG
                                ||  |||||| || |||||  |||
                                TC  TGATAT CA TGGAG  GCT
                                 TA    _ _    GT
GAM260  ZDHHC8  3'  GGCCTGGCTGCGGTGCTC    63907         T  __
                                GGGCATTGTA GTT  GCT
                                |||||||||| |||  |||
                                CTCGTGGCGT CGG  CGG
                                      _  TC
GAM260  ZFD25   5'  GAGCAGAGTAATATATAGGGTT 32581     A         T   GG
           T                     GGGC TTGTATGTTGCT CTGT
                                |||| |||||||||||| ||||
                                TTTG GATATATAATGA GACG
                                  G          _   AGT
GAM260  ZFP106  5'  CCAAAGTGTGCAGTGTCC    42464         GTT   CTG
                                GGGCATTGTAT   GCTT   TGG
                                ||||||||||   ||||  |||
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                              CCTGTGACGTG  TGAA  ACC
                                   ___  ___
GAM260  ZFP26   5' CGCAGGGTGCGCGATGCCT  33131       ATGTT _
                              GGGCATTGT   GC TTCTGTG
                              |||||||||   || |||||||
                              TCCGTAGCG   CG GGGACGC
                                   _____ T
GAM260  ZIC4    5' TTACAGAAGTTTTTTTGTGT  49624     TGTATGTT
                              GCAT      GCTTCTGTGG
                              ||||      ||||||||||
                              TGTG      TGAAGACATT
                                TTTTTT__
GAM260  ZIC5    5' CTGTGCAGCTCAAATGTGGTGT 52440     TG ____    TTCTGTGG
           TC                   GCAT  TAT   GTTGC
                              ||||  |||   |||||
                              TGTG  GTA   CGACG
                                GT  AACT    TGTC  G
GAM260  ZNF211  3' TACTGAGAATATGCAATTTCC  21093    C       G  CT  G
                              GGG ATTGTATGTT CTT  GTG
                              ||| ||||||||| |||  |||
                              CCT TAACGTATAA GAG  CAT
                                T       _  T_  G
GAM260  ZNF212  3' CCATAGGGGTGAGCAGCTGCCT 24303     _   ATG TG
                              GGGCA TTGT  T  CTTCTGTGG
                              ||||| ||||  |  |||||||||
                              TCCGT GACG  A  GGGGATACC
                                C   ___ GT
GAM260  ZNF212  3' CTGTGGTCTGGGACTTGCGGTG 24305       T  GCTT_  TG
           TCT                   GGGCATTGTA GTT    CTG  G
                              |||||||||| |||    |||  |
                              TCTGTGGCGT CAG    GGT  C
                                   T  GGTCT  GT
GAM260  ZNF213  3' CCGCTCCTTTGACATTGGTGCC 65095       T   GCTTCT
           C                    GGGCATTG ATGTT     GTGG
                              ||||||||| |||||     ||||
                              CCCGTGGT TACAG     CGCC
                                   _    TTTCCT
GAM260  ZNF228  3' TCATAACGCAATGTAGGTGCTC 59924      G      TTC
                              GGGCATT TATGTTGC  TGTGG
                              ||||||| ||||||||  |||||
                              CTCGTGG ATGTAACG  ATACT
                                   _      CA_
GAM260  ZNF234  5' CGTGGGAGAGCAGAGCCT   68923     ATTGTA   G   TG
                              GGGC     TGTT CTTC  TG
                              ||||     |||| ||||  ||
                              TCCG     ACGA GAGG  GC
                                AG____   _   GT
GAM260  ZNF281  3' CTATTAAGAATAATGTGATGCC 25026      TG  GTTG  CT
           C                    GGGCAT  TAT   CTT  GTGG
                              ||||||  |||   |||  ||||
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                                CCCGTA  GTA   GAA  TATC
                                   GT   ATAA   T_
GAM260   ZNF282   3'  CCATGGGAGCTCCTGGTGCC   89210      GTATGTT
                                GGCATT     GCTTCTGTGG
                                ||||||     ||||||||||
                                CCGTGG     CGAGGGTACC
                                   TCCT___
GAM260   ZNF294   3'  TTATAGATGCAGTGTCC     70832        TGTTGCT
                                GGGCATTGTA     TCTGTGG
                                ||||||||||     |||||||
                                CCTGTGACGT     AGATATT
                                       ________
GAM260   ZNF302   3'  TTACAGAAGAGAAGCAGTGTTT 37930        ATGTTG
                                GGGCATTGT    CTTCTGTGG
                                |||||||||    |||||||||
                                TTTGTGACG    GAAGACATT
                                     AAGA__
GAM260   ZNF302   3'  TTACAGAAGAGAAGCAGTGTTT 37420        ATGTTG
                                GGGCATTGT    CTTCTGTGG
                                |||||||||    |||||||||
                                TTTGTGACG    GAAGACATT
                                     AAGA__
GAM260   ZNF304   3'  TGTGGAAGCAACATAAGTTG  40318   TTG        TG
                                CA  TATGTTGCTTCTG  G
                                ||  ||||||||||||| |
                                GT  ATACAACGAAGGT  T
                                 TGA          GT
GAM260   ZNF33A   3'  GCAGGATACAGTCCT     91350    C     G
                                GGG ATTGTAT TTGC
                                ||| ||||||| ||||
                                TCC TGACATA GACG
                                  _     G
GAM260   ZNF361   5'  GGCTTCGGGAGCGGCGAGCAGT 37663        A        T
            GTCT                  GGGCATTGT TGTTGCTTCTG GG
                                ||||||||| |||||||||| ||
                                TCTGTGACG GCGGCGAGGGC TC
                                     A         T  GGA
GAM260   ZNFN1A2  3'  TTGTGGAGGCAGTGTCATTTGC 32745     T_  T TG       TG
            TC                  GGGCA  TG A  TTGCTTCTG  G
                                |||||  || |  |||||||||  |
                                CTCGT  AC T  GACGGAGGT  T
                                   TT  _ GT       GT
GAM260   ZTL1     5'  CGCAGGAGCCCGACGGGGTCT  43224     A   ATGTT     TG
                                GGGC TTGT    GCTTCTG  G
                                |||| ||||    |||||||  |
                                TCTG GGCA    CGAGGAC  C
                                  G   GCC__      GT
GAM260   ZTL1     5'  CGCAGGAGCCCGACGGGGTCT  43914     A   ATGTT     TG
                                GGGC TTGT    GCTTCTG  G
                                |||| ||||    |||||||  |
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                                TCTG GGCA    CGAGGAC  C
                                  G   GCC__     GT
GAM260  LOC112885 3'  CGCGTGGCTTGCGATGTCC   56523         T  TG TTCT
                                GGGCATTGTA GT  C   GTG
                                |||||||||| ||  |   |||
                                CCTGTAGCGT CG  G   CGC
                                     T  GT ____
GAM260  LOC113146 5'  GAGGGAAGTGCAGTGTCC    72971         G  G
                                GGGCATTGTAT TT CTTC
                                |||||||||| || ||||
                                CCTGTGACGTG AA GGAG
                                     _  G
GAM260  LOC113523 3'  CCACAGAACTATAATATACATT 73043     T       C__
          GCCT                    GGCA TGTATGTTG   TTCTGTGG
                                |||| |||||||||   ||||||||
                                CCGT ACATATAAT   AAGACACC
                                  T       ATC
GAM260  LOC113763 3'  CTACGTGGCTTTGTACATGTGA 56578    TG    T____   TC
          TGCTC                   AT  TATGT    GCT  TGTGG
                                ||  |||||    |||  |||||
                                TA  GTACA    CGG  GCATC
                                 GT    TGTTT   T_
GAM260  LOC115129 3'  CACAGGAGGGTGTTGCCC    73225      TTGT TG  G
                                GGGCA    A  TT CTTCTGTG
                                |||||    |  || ||||||||
                                CCCGT    T  GG GAGGACAC
                                   ____ GT  _
GAM260  LOC115131 5'  CGCCCAGCATACAAGCTT    59125      A       CTTCT
                                GGGC TTGTATGTTG    GTG
                                |||| ||||||||||    |||
                                TTCG AACATACGAC    CGC
                                  _        C____
GAM260  LOC115219 3'  CTACCAAAAAAGTGCAGTGTTC 73303          GTTGCTTCT
                                GGGCATTGTAT       GTGG
                                ||||||||||        ||||
                                CTTGTGACGTG       CATC
                                      AAAAAAC__
GAM260  LOC115399 3'  GGTGATGGGGTGGCTGCAGTGC 73436         T  TG   TGTGG
          CT                    GGGCATTGTA GT  CTTC
                                |||||||||| ||  ||||
                                TCCGTGACGT CG  GGGG
                                     _  GT   TAGTGGG
GAM260  LOC115400 3'  CGTAGAGGTGGCCTGCA     73441      T  TG
                                TGTA GT  CTTCTGTG
                                |||| ||  ||||||||
                                ACGT CG  GGAGATGC
                                  C  GT
GAM260  LOC115442 3'  GACTGCGACGTTGATGTTC   72677        T      T_
                                GGGCATTG ATGTTGC  TC
                                |||||||| |||||||  ||
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                                CTTGTAGT TGCAGCG  AG
                                     _      TC
GAM260  LOC115704 3'  CTACAGGGGTCCTCGGTCTCC  73543     C    TATGTT
                                GGG ATTG     GCTTCTGTGG
                                ||| ||||     ||||||||||
                                CCT TGGC     TGGGGACATC
                                  C    TCC___
GAM260  LOC115708 5'  TCGCGGAGGCACGTGTGGAGCC 73556      A TG     T
              C                    GGGC T  TATGT GCTTCTGTGG
                                |||| |  ||||| ||||||||||
                                CCCG G  GTGCA CGGAGGCGCT
                                  A GT    _
GAM260  LOC116411 3'  CGCGGAAGGCCGCAGGGTCC   73858      A    AT  TG     TG
                                GGGC TTGT  GT  CTTCTG  G
                                |||| ||||  ||  ||||||  |
                                CCTG GACG  CG  GAAGGC  C
                                  G    C_  __     GT
GAM260  LOC118611 3'  GGTGGGTGCAATGCCC      75476          G TG
                                GGGCATTGTAT T  CT
                                |||||||||||  |  ||
                                CCCGTAACGTG G  GG
                                       _ GT
GAM260  LOC118611 5'  CGCAGGAAGACAATGGTGTTC  75473       TG A    GC     TG
                                GGGCAT  T TGTT  TTCTG  G
                                ||||||  | ||||  |||||  |
                                CTTGTG  A ACAG  AGGAC  C
                                   GT _    A_     GT
GAM260  LOC118709 5'  TCATGGAGGCCGAGGCTGTGCT 73927       T  ATGTT
              C                    GGGCAT GT     GCTTCTGTGG
                                ||||||  ||     ||||||||||
                                CTCGTG CG     CGGAGGTACT
                                   T  GAGC_
GAM260  LOC120105 3'  TGCAGAAGTGATATTGC     75516     TTGT    TG     TG
                                GCA    ATGT  CTTCTG  G
                                |||    ||||  ||||||  |
                                CGT    TATA  GAAGAC  T
                                  _____   GT     GT
GAM260  LOC120114 3'  TTACGGCCGCCTGTGCAGTGGC 75543     G       GTT  TT
              C                    GG CATTGTAT   GC  CTGTGG
                                || ||||||||   ||  ||||||
                                CC GTGACGTG   CG  GGCATT
                                 G       TC_  CC
GAM260  LOC120839 5'  CGTGGGAGCAGCAGGC      75987     A         TG
                                GT TGTTGCTTCTG  G
                                || ||||||||||  |
                                CG ACGACGAGGGT  C
                                 G          GT
GAM260  LOC120856 3'  GAAATAACATTAGTGCTT     74029         T     C
                                GGGCATTG ATGTTG TTC
                                |||||||| |||||| |||
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                                TTCGTGAT TACAAT AAG
                                   _     A
GAM260   LOC120856 3'  TTACAGGAGCAGAAACAGGTCT 74034     A    ATG
                                GGGC TTGT   TTGCTTCTGTGG
                                |||| ||||   ||||||||||||
                                TCTG GACA   GACGAGGACATT
                                  _    AA_
GAM260   LOC120892 3'  TAGTGTAAATACAGTGTTC    74037          G    TT
                                GGGCATTGTAT TTGC  CTG
                                |||||||||||| ||||  |||
                                CTTGTGACATA AATG  GAT
                                      _    T_
GAM260   LOC121301 5'  CCATGTCCAGAAACAACAGTGT 75570         A    G  TC_
            CT                    GGGCATTGT TGTT CT   TGTGG
                                |||||||||| |||| ||   |||||
                                TCTGTGACA ACAA GA   GTACC
                                     _    A  CCT
GAM260   LOC122525 5'  CCATGGAGGCCATGCCAGAGCC 76007      A  _    TT
            C                     GGGC TTG TATG  GCTTCTGTGG
                                |||| ||| ||||  ||||||||||
                                CCCG GAC GTAC  CGGAGGTACC
                                  A  C   __
GAM260   LOC123096 3'  CTGCTCCCCAGCAAACGGTGCC 74201         A     CTTCT TG
            T                     GGGCATTGT TGTTG    G  G
                                |||||||||| |||||    | |
                                TCCGTGGCA ACGAC    C  C
                                     A    CCCT_ GT
GAM260   LOC123283 5'  CGCTCGGCGTCGGTGCCT    76011        T     CTTCT
                                GGGCATTG ATGTTG    GTG
                                |||||||| ||||||    |||
                                TCCGTGGC TGCGGC    CGC
                                     _     T____
GAM260   LOC123342 5'  TCATAGGAGCAGCAGAAAAGAG 75605     A_  GTA
            TTC                   GGGC  TT   TGTTGCTTCTGTGG
                                ||||  ||   ||||||||||||||
                                CTTG  AA   ACGACGAGGATACT
                                  AG  AAG
GAM260   LOC123342 3'  TCATATTCAATATACATGTTT  75606       T      CTTC
                                GGGCAT GTATGTTG    TGTGG
                                |||||| ||||||||    |||||
                                TTTGTA CATATAAC    ATACT
                                   _       TT__
GAM260   LOC123872 5'  CAGAAACTGGATGCTC      74236       GTAT   GCT
                                GGGCATT    GTT   TCTG
                                |||||||    |||   ||||
                                CTCGTAG    CAA   AGAC
                                    GT__   ___
GAM260   LOC124044 3'  CAGTGGTAATGGTGCCC     76024       GTAT     T
                                GGGCATT    GTTGCT CTG
                                |||||||    |||||| |||
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                                CCCGTGG   TAATGG GAC
                                   ____     T
GAM260   LOC124145 3'  CCACTTTTAAGCAGTAATGTTT 74253        TATG     CT__
                                GGGCATTG   TTGCTT   GTGG
                                ||||||||   ||||||   ||||
                                TTTGTAAT   GACGAA   CACC
                                   ____     TTTT
GAM260   LOC124460 3'  CACGGAAGTGAAGTGTC     76040       GTATG TG
                                GGCATT    T  CTTCTGTG
                                ||||||    |  ||||||||
                                CTGTGA    A  GAAGGCAC
                                   _____ GT
GAM260   LOC125268 3'  TACGGGGCCCTTGGTGTCT   76079        TATGTT   T
                                GGGCATTG     GCT CTGTG
                                ||||||||     ||| |||||
                                TCTGTGGT     CGG GGCAT
                                     TCC___   _
GAM260   LOC126133 5'  GCGACGCGTGCAGGGCCC    74444      A     __
                                GGGC TTGTAT  GTTGC
                                |||| ||||||  |||||
                                CCCG GACGTG  CAGCG
                                  G     CG
GAM260   LOC126295 3'  TCACATTAATTCATGTATAATG 74481            TGCTTC_
            CTC                   GGGCATTGTATGT      TGTGG
                                |||||||||||||      |||||
                                CTCGTAATATGTA      ACACT
                                      CTTAATT
GAM260   LOC126364 3'  CTGTGGATGTACAGGCAGTGCT 75689         A   T  T    TG
            C                    GGGCATTGT TGT GC TCTG  G
                                |||||||||| ||| || ||||  |
                                CTCGTGACG ACA TG AGGT  C
                                     G   _  T    GT
GAM260   LOC126402 3'  CGGGGCTACAGGCCC       75704      A    TGTT   T
                                GGGC TTGTA    GCT CTG
                                ||||  |||||    |||  |||
                                CCCG GACAT    CGG GGC
                                  _    ____   _
GAM260   LOC126669 3'  CCATAGAGCTGTGTCAGTGTTC 75400         T TG T   T
                                GGGCATTG A  T GCT CTGTGG
                                |||||||| |  | ||| ||||||
                                CTTGTGAC T  G CGA GATACC
                                   _ GT T   _
GAM260   LOC126669 3'  GTAATATAGGTGTCT       75414        G
                                GGGCATT TATGTTGC
                                ||||||| ||||||||
                                TCTGTGG ATATAATG
                                  _
GAM260   LOC126823 5'  CGCGGAAGGCGAGGTGCCT    74575        GTATG   _
                                GGGCATT     TTGC TTCTGTG
                                |||||||     |||| |||||||
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                                TCCGTGG    AGCG AAGGCGC
                                   _____   G
GAM260  LOC126961 3'  CCACAGAGGTGATCTCTACAGT 74626     AT   T__  TG
          CT                    GGGC  TGTA   GT  CTTCTGTGG
                                ||||  ||||   ||  |||||||||
                                TCTG  ACAT   TA  GGAGACACC
                                  __   CTC  GT
GAM260  LOC127162 3'  TTGCAGAAAATTAGACGGTGTT 74639        AT_  GC    TG
          T                     GGGCATTGT   GTT  TTCTG  G
                                |||||||||   |||  |||||  |
                                TTTGTGGCA   TAA  AAGAC  T
                                     GAT   __    GT
GAM260  LOC127281 3'  CCGCATCTGAATGTGTGGTCCC 74645    C  TG    GCTTC
                                GGG AT  TATGTT    TGTGG
                                ||| ||  ||||||    |||||
                                CCC TG  GTGTAA    ACGCC
                                  _ GT    GTCT_
GAM260  LOC127428 3'  GTTCCAGTTGCAATGCTC    74672         __  TT
                                GGGCATTGTA  TG  GC
                                ||||||||||  ||  ||
                                CTCGTAACGT  AC  TG
                                     TG  CT
GAM260  LOC128439 3'  CGGGGAGGCTTAGTGCCC    57351        TATGTT    G
                                GGGCATTG    GCTTCT TG
                                ||||||||    |||||| ||
                                CCCGTGAT    CGGAGG GC
                                   T_____    G
GAM260  LOC129433 5'  CGCAGAGGGTGGCTGCCT    75726      TTGTAT  TG  _
                                GGGCA    GT  CT TCTGTG
                                |||||    ||  || ||||||
                                TCCGT    CG  GG AGACGC
                                  _______ GT  G
GAM260  LOC129566 5'  CTACACCCGCGTGGCAGTGTTC 75729        ATGT   TTC
                                GGGCATTGT   TGC   TGTGG
                                |||||||||   |||   |||||
                                CTTGTGACG   GCG   ACATC
                                     GT__   CCC
GAM260  LOC129607 3'  CTGCAGAGGCTGTCTATGTGTC 74886      TGTATGTT     TG
          C                     GGGCAT      GCTTCTG  G
                                ||||||      |||||||  |
                                CCTGTG      CGGAGAC  C
                                   TATCTGT_     GT
GAM260  LOC129607 3'  CATTTGTTATGCAGTGTTC   74885         TT  TTCT
                                GGGCATTGTATG  GC   GTG
                                ||||||||||||  ||   |||
                                CTTGTGACGTAT  TG   TAC
                                       __  TT__
GAM260  LOC129831 5'  CCGCAGAAGCAAAGAGCAGTG  74894      ATG
                                CATTGT   TTGCTTCTGTGG
                                ||||||   ||||||||||||
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                                GTGACG   AACGAAGACGCC
                                   AGA
GAM260   LOC129881 3'  GTAGCATATATGAGCTT     74904      AT_
                                GGGC   TGTATGTTGC
                                ||||   ||||||||||
                                TTCG   ATATACGATG
                                  AGT
GAM260   LOC130026 3'  CTATATAGTAGTATGCAGT    56645           TC
                                ATTGTATGTTGCT  TGTGG
                                ||||||||||||  |||||
                                TGACGTATGATGA  ATATC
                                       T_
GAM260   LOC130074 3'  CAGGAGGTATTGTCC       76129      TT   GTTG
                                GGGCA  GTAT    CTTCTG
                                |||||  ||||    ||||||
                                CCTGT  TATG    GAGGAC
                                  __   _____
GAM260   LOC130074 3'  CGCAGAAGGGTGGTGTGCTC   76132       TG   GTTG     TG
                                GGGCAT  TAT    CTTCTG  G
                                ||||||  |||    ||||||  |
                                CTCGTG  GTG    GAAGAC  C
                                   TG   G___     GT
GAM260   LOC130436 3'  TCATGAAGGGATATATGGTG   74936     TG     G    T
                                CAT  TATGTT CTTC GTGG
                                |||  |||||| |||| ||||
                                GTG  ATATAG GAAG TACT
                                  GT     G    _
GAM260   LOC130814 3'  GTTAGATGCAGTAATGATGTTT 74986       TG A     T    TGG
                                GGGCAT  T TGTTGC TCTG
                                ||||||  | |||||| ||||
                                TTTGTA  A ATGACG AGAT
                                   GT _     T    TGT
GAM260   LOC131377 3'  TGGATCCAGTTATGGTGCCT   76272       TG  TGT  CT
                                GGGCAT  TA   TG  TCTG
                                ||||||  ||   ||  ||||
                                TCCGTG  AT   AC  AGGT
                                   GT  TG_  CT
GAM260   LOC131870 3'  TGAATTCAGTAACATGAAGTGT 75025        G       TCTGTGG
            TT                   GGGCATT TATGTTGCT
                                ||||||| |||||||||
                                TTTGTGA GTACAATGA
                                    A        CTTAAGTT
GAM260   LOC131873 3'  CTAATTTAGTAATGTCTAATGC 75878        T       TCTG
            TC                   GGGCATTG ATGTTGCT    TGG
                                ||||||||| ||||||||    |||
                                CTCGTAAT TGTAATGA    ATC
                                    C       TTTA
GAM260   LOC132332 3'  TGCAGAGGAGCATAAAGTTC   76164      ATTG     G     TG
                                GGGC    TATGTT CTTCTG  G
                                ||||    |||||| ||||||  |
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                                CTTG    ATACGA GGAGAC  T
                                  AA__      _     GT
GAM260   LOC132617 5'  CGTGGAAGGGGACGACGCCT   75891     A   ATG  G     TG
                                GGGC TTGT   TT CTTCTG  G
                                |||| ||||   || ||||||  |
                                TCCG AGCA   GG GAAGGT  C
                                  C   ___  G     GT
GAM260   LOC132671 3'  TTGCTTTCTTGCAATAAGTAAT 59173       TA     TTCT__ TG
           GTTC                  GGCATTG  TGTTGC     G  G
                                |||||||  ||||||     | |
                                TTGTAAT  ATAACG     C  T
                                   GA     TTCTTT GT
GAM260   LOC133634 3'  TCATAGGTGACTTACACAGTGT 75108        AT__  TG TT
           CC                    GGGCATTGT    GT  C  CTGTGG
                                |||||||||    ||  |  ||||||
                                CCTGTGACA    CA  G  GATACT
                                     CATT  GT __
GAM260   LOC134147 3'  CTACAGGCCGGGTGCGGTGGCT 57160    G      GTT  TT
                                GG CATTGTAT   GC  CTGTGG
                                || ||||||||   ||  ||||||
                                TC GTGGCGTG   CG  GACATC
                                 G       GGC  __
GAM260   LOC134637 3'  TCATTTTTTGCAGCTACGATGT 75203         T    TTCT_
           TC                    GGGCATTGTA GTTGC    GTGG
                                |||||||||| |||||    ||||
                                CTTGTAGCAT CGACG    TACT
                                     _    TTTTT
GAM260   LOC135138 3'  TTACAATAGTGTACTGTGCTT  75209      T   GTT   TC
                                GGGCAT GTAT   GCT  TGTGG
                                |||||| ||||   |||  |||||
                                TTCGTG CATG   TGA  ACATT
                                   T    ___   TA
GAM260   LOC135293 3'  TTACAGGAGCTGGTATGTGATG 76195     TG   TT_
           CC                    GGCAT  TATG   GCTTCTGTGG
                                |||||  ||||   ||||||||||
                                CCGTA  GTAT   CGAGGACATT
                                   GT   GGT
GAM260   LOC135521 3'  CCATGGAGGGATCTGGTGCCT  75227       TAT   G
                                GGGCATTG   GTT CTTCTGTGG
                                |||||||   ||| |||||||||
                                TCCGTGGT   TAG GGAGGTACC
                                     C__   _
GAM260   LOC135932 3'  CGCGTGCGTAGCAGTGTCT   76196        ATGT   TTC
                                GGGCATTGT    TGC   TGTG
                                |||||||||    |||   ||||
                                TCTGTGACG    GCG   GCGC
                                     AT__   T__
GAM260   LOC136288 3'  CTACAGGAGAATGTATGCAATG 75252         TTG_
           T                     GCATTGTATG    CTTCTGTGG
                                ||||||||||    |||||||||
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                                TGTAACGTAT    GAGGACATC
                                      GTAA
GAM260   LOC136288 5'  GCAGCGTGCAGCGCCT      75253      A
                                GGGC TTGTATGTTGC
                                |||| ||||||||||
                                TCCG GACGTGCGACG
                                  C
GAM260   LOC136319 3'  AAGCAATTGCAGTGTTT      75257          T
                                GGGCATTGTA GTTGCTT
                                |||||||||| |||||||
                                TTTGTGACGT TAACGAA
                                      _
GAM260   LOC136442 3'  AGGAGTGGTATTTGATGCTT   54283         T   TT
                                GGGCATTG ATG  GCTTCT
                                |||||||| |||  ||||||
                                TTCGTAGT TAT  TGAGGA
                                     T   GG
GAM260   LOC136555 5'  CGTGGAGGCGTCCGAGCTC    75262      A   TATGT     TG
                                GGGC TTG    TGCTTC  TG
                                |||| |||    ||||||  ||
                                CTCG AGC    GCGGAG  GC
                                  _  CT___     GT
GAM260   LOC137868 3'  AAGCATTATGTAATGCTT     57524           T
                                GGGCATTGTATG TGCTT
                                |||||||||||| |||||
                                TTCGTAATGTAT ACGAA
                                       T
GAM260   LOC138046 3'  CCGTAGGAGAATTCAACATATA 75293          ____
            ATTTCT                 ATTGTATGTTG    CTTCTGTGG
                                |||||||||||   |||||||||
                                TAATATACAAC    GAGGATGCC
                                      TTAA
GAM260   LOC138428 3'  GCCTGACTGTAGTGCCC      75336          T  __
                                GGGCATTGTA GTT  GC
                                |||||||||| |||  ||
                                CCCGTGATGT CAG  CG
                                     _  TC
GAM260   LOC138639 5'  ACAGAATTCAGTGTCT       75361         TATGTTGC
                                GGGCATTG       TTCTGT
                                ||||||||       ||||||
                                TCTGTGAC       AAGACA
                                     TT_______
GAM260   LOC138654 5'  CACAGGAGTTCATTGCCT     75947       TTGT   TT
                                GGGCA    ATG  GCTTCTGTG
                                |||||    |||  |||||||||
                                TCCGT    TAC  TGAGGACAC
                                   _____  T_
GAM260   LOC138835 3'  TCAAATCCGTGACAGCAATGTC 75956          A   TG TTCTG
            C                   GGGCATTGT TGT  C     TGG
                                |||||||| |||  |    |||
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                                CCTGTAACG ACA  G    ACT
                                     _  GT CCTAA
GAM260  LOC142820 3' CGCAGAGGCAGACCATTCCT  76397    CAT  TATG      TG
                                GGG  TG   TTGCTTCTG  G
                                |||  ||   |||||||||  |
                                TCC  AC   GACGGAGAC  C
                                 TT_  CA__       GT
GAM260  LOC142955 3' CTGCGGGAGTGACCCAGTGCTT 76446       TAT  TG    TG
                                GGGCATTG  GT  CTTCTG  G
                                ||||||||  ||  ||||||  |
                                TTCGTGAC  CA  GAGGGC  C
                                    C__  GT    GT
GAM260  LOC142972 5' CTGCAGGAGCCAGACGTGTGGA 65129    A TG    __     TG
           GTCC                   GGC T  TATGTT  GCTTCTG  G
                                ||| |  ||||||  |||||||  |
                                CTG G  GTGCAG  CGAGGAC  C
                                 A GT     AC      GT
GAM260  LOC143101 5' CACGGAGGCCTCAGGCCT   82894     A   TATGTT
                                GGGC TTG     GCTTCTGTG
                                |||| |||     |||||||||
                                TCCG GAC     CGGAGGCAC
                                  _  TC_____
GAM260  LOC143153 5' TGCAGAAGTCCTTGCTGCTC  76471     TT   TGTT     TG
                                GGGCA  GTA   GCTTCTG  G
                                |||||  |||   |||||||  |
                                CTCGT  CGT   TGAAGAC  T
                                  __  TCC_     GT
GAM260  LOC143173 3' ACAGAATTGAATGCCT     60373      TGTATG  GC
                                GGGCAT     TT  TTCTGT
                                ||||||     ||  ||||||
                                TCCGTA     AG  AAGACA
                                   _______  TT
GAM260  LOC143286 5' CACAGAACCTGCAGTGCT   82945        T  TGCT
                                GGCATTGTA GT   TCTGTG
                                |||||||||  ||   ||||||
                                TCGTGACGT CA   AGACAC
                                     C  _____
GAM260  LOC143308 5' CAGGTGCATATAAGTTT    82935     A      TGCT
                                GGGC TTGTATGT   TCTG
                                |||| ||||||||   ||||
                                TTTG AATATACG   GGAC
                                  _      T___
GAM260  LOC143310 5' CCACAGCAGTGTGTGGTATCC  76530   GC  TG  TG   TCT
                                GG  AT  TA  TTGCT   GTGG
                                ||  ||  ||  |||||   ||||
                                CC  TG  GT  GACGA   CACC
                                 TA  GT  GT    ___
GAM260  LOC143524 5' CACCCGGCATACAAGCTT   76593     A       CTTCT
                                GGGC TTGTATGTTG    GTG
                                |||| ||||||||||    |||
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                                TTCG AACATACGGC    CAC
                                  _        C____
GAM260  LOC143712 3'  GGCCCTGCAGCATGTCGTGCTC 76603       TG      TTCT  GG
                                GGGCAT  TATGTTGC    GT
                                ||||||  ||||||||    ||
                                CTCGTG  GTACGACG    CG
                                   CT       TCC_  GT
GAM260  LOC143903 3'  CTGTGGATGAGCATGTGGTCCC 76619     C  TG     GCT    TG
                                GGG AT  TATGTT   TCTG  G
                                ||| ||  ||||||   ||||  |
                                CCC TG  GTACGA   AGGT  C
                                  _ GT     GT_    GT
GAM260  LOC143916 5'  CTATGAGTGAGAACATGCAGTG 76639           G  _  _
           TTT                    GGCATTGTATGTT CTT CT GTGG
                                ||||||||||||| ||| || ||||
                                TTGTGACGTACAA GAG GA TATC
                                       _  T  G
GAM260  LOC144203 5'  CCACCCTTAAGTACAATGTTC  76706          GTTGCTTCT
                                GGGCATTGTAT       GTGG
                                ||||||||||        ||||
                                CTTGTAACATG       CACC
                                      AATTCC___
GAM260  LOC144231 3'  TGCACCTGCAAATGGTGCTT   83021       TG ATG    TTC  TG
                                GGGCAT  T   TTGC   TG  G
                                ||||||  |   ||||   ||  |
                                TTCGTG  A   AACG   AC  T
                                   GT ___    TCC  GT
GAM260  LOC144231 3'  TGTGATGTTGTATATATACAAT 83022          _  TTCTGTGG
           GCCT                   GGCATTGTATGT TGC
                                ||||||||||| |||
                                CCGTAACATATA ATG
                                      T   TTGTAGTGTC
GAM260  LOC144321 3'  CAAAAAGCAATGTATAAT    83063           CTG
                                ATTGTATGTTGCTT   TG
                                ||||||||||||||   ||
                                TAATATGTAACGAA   AC
                                      AA_
GAM260  LOC144455 5'  CAGAGGCAGGAAGCCT      76849      A  GTATG
                                GGGC TT    TTGCTTCTG
                                ||||  ||    |||||||||
                                TCCG AG    GACGGAGAC
                                  A  _____
GAM260  LOC144559 5'  CACCCGGCATACAAGCTT    76880      A        CTTCT
                                GGGC TTGTATGTTG    GTG
                                ||||  ||||||||||    |||
                                TTCG AACATACGGC    CAC
                                  _        C____
GAM260  LOC144559 5'  CCATGTAAAACCTGCAGTGCCT 76881          T   GCTTCT
                                GGGCATTGTA GTT     GTGG
                                |||||||||| |||     ||||
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                                TCCGTGACGT CAA     TACC
                                      C   AATG__
GAM260   LOC144603 5'  TCACGGAGGAGGACTGTGCTC  60369      T  ATGTTG
                                GGGCAT GT     CTTCTGTGG
                                |||||| ||     |||||||||
                                CTCGTG CA     GGAGGCACT
                                   T  GGA___
GAM260   LOC144742 5'  TCACAGTTTGGCATTGGTGCTC 76948       T     CTT
                                GGGCATTG ATGTTG   CTGTGG
                                |||||||| ||||||   ||||||
                                CTCGTGGT TACGGT   GACACT
                                     _     TT_
GAM260   LOC144893 3'  CTGTGGGCTTTTCATATACTGC 83187      T     TT__   CTGTGG
            CT                    GGGCA TGTATG    GCTT
                                |||||| ||||||    ||||
                                TCCGT ATATAC    CGGG
                                   C     TTTT    TGTC
GAM260   LOC145078 3'  CCACAGAAGGAACAATGATCC  60290    C  TG A    G
                                GG AT  T TGTT CTTCTGTGG
                                || ||  | |||| |||||||||
                                CC TA  A ACAA GAAGACACC
                                 _ GT _    G
GAM260   LOC145134 3'  TTATGACGTAACGATATGGTGT 83258       TG  _    T  TGTGG
            CT                    GGGCAT  TAT GTTGC TC
                                ||||||  ||| ||||| ||
                                TCTGTG  ATA CAATG AG
                                   GT   G    C  TATT
GAM260   LOC145225 3'  TTACAGATTGCAATGTGTTGCC 83312      TTG      T_
            C                     GGGCA   TATGTTGC  TCTGTGG
                                |||||   ||||||||  |||||||
                                CCCGT   GTGTAACG  AGACATT
                                   T__       TT
GAM260   LOC145225 3'  CACGGGATCTACAGGTTC    83300     A    TGTTGC
                                GGGC TTGTA     TTCTGTG
                                |||| |||||     |||||||
                                CTTG GACAT     AGGGCAC
                                  _    CT_____
GAM260   LOC145231 3'  CCATAGGAAGCTAATATGTGCT 83283      T   GTT    _
            C                     GGGCAT GTAT   GCTTC TGTGG
                                |||||| ||||   ||||| |||||
                                CTCGTG TATA   CGAAG ATACC
                                   _   AT_    G
GAM260   LOC145355 5'  TTGCAGAAAAGAGCCTGCAGTG 77101        T  GC_    TG
            TTT                   GGGCATTGTA GTT   TTCTG  G
                                |||||||||| |||   |||||  |
                                TTTGTGACGT CGA   AAGAC  T
                                      C  GAA    GT
GAM260   LOC145387 3'  CGGGCACATGTAGTCCT     83353     C       T  TT
                                GGG ATTGTATGT GC  CTG
                                ||| |||||||| ||  |||
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                                TCC TGATGTACA CG  GGC
                                  _       _ __
GAM260  LOC145447 3'  AGGCAGTATGGAATGTTC    77201        G
                                GGGCATT TATGTTGCTT
                                ||||||| ||||||||||
                                CTTGTAA GTATGACGGA
                                    G
GAM260  LOC145447 3'  CCACCTGTGATGTATATTGTTC 77203      T      TG TTCT
                                GGGCA TGTATGT  C    GTGG
                                ||||| |||||||  |   ||||
                                CTTGT ATATGTA  G    CACC
                                   T      GT TC__
GAM260  LOC145497 5'  CTGCAAGCTGATGGGTGTAGTG 77215         __  _  TC  TG
           CCT                    GCATTGTAT  GTT GCT  TG  G
                                |||||||||  ||| |||  ||  |
                                CGTGATGTG  TAG CGA  AC  C
                                     GG   T   __ GT
GAM260  LOC145553 5'  TGCAGAGCCTTGGGGTGCCC   56668       G  TGTT   T   TG
                                GGGCATT TA    GCT CTG  G
                                ||||||| ||    ||| |||  |
                                CCCGTGG GT    CGA GAC  T
                                    G  TC__   _  GT
GAM260  LOC145566 5'  CATGGTTTATATGATGTCC    77273       TG    TTGCTT
                                GGGCAT  TATG     CTGTG
                                ||||||  ||||     |||||
                                CCTGTA  ATAT     GGTAC
                                    GT    TT____
GAM260  LOC145566 5'  GCAGGATCAGTGTCC       77275        T  G
                                GGGCATTG AT TTGC
                                |||||||| || ||||
                                CCTGTGAC TA GACG
                                     _  G
GAM260  LOC145608 3'  CCATACCCGGACATGTGAGGCT 83384      A TG     GCTTC
           C                     GGGC T  TATGTT     TGTGG
                                |||| |  ||||||     |||||
                                CTCG A  GTACAG     ATACC
                                  G GT     GCCC_
GAM260  LOC145609 5'  CAGGAGCCAGGCTC       83376      A   TATGTT
                                GGGC TTG     GCTTCTG
                                |||| |||     |||||||
                                CTCG GAC     CGAGGAC
                                  _  _______
GAM260  LOC145676 5'  GGGCTTGGAGAGTGTGCAGTGC 77340          TG  G    T_  GG
           CT                     GGGCATTGTA  TT CTTC  GT
                                ||||||||||  || ||||  ||
                                TCCGTGACGT  GA GAGG  CG
                                     GT  _    TT  GGT
GAM260  LOC145757 3'  GCATATTAAAGCGATGTAATGC 77462       TG        C__    G
           CT                     GGCAT  TATGTTGCTT   TGTG
                                |||||  ||||||||||   ||||
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                                CCGTA  ATGTAGCGAA   ATAC
                                  __        ATT    GT
GAM260   LOC145758 3'  CGCAGGAGTGCTCATGAGCCC  83484     A TG AT  T      TG
                                GGGC T  T  GT GCTTCTG  G
                                |||| |  |  || |||||||  |
                                CCCG A  A  CG TGAGGAC  C
                                  _ GT CT  _      GT
GAM260   LOC145783 3'  TACAGGGGCATGTGGTCCC   77482     C  TG  TGT
                                GGG AT  TA   TGCTTCTGTG
                                ||| ||  ||   ||||||||||
                                CCC TG  GT   ACGGGGACAT
                                  _  GT  ____
GAM260   LOC145786 5'  TGCAGAGTATTATGGTACCT   83494     C  TG  TGT   T   TG
                                GGG AT  TA   TGCT CTG  G
                                ||| ||  ||   |||| |||  |
                                TCC TG  AT   ATGA GAC  T
                                  A  GT  T__   _  GT
GAM260   LOC145790 3'  CAGTACTCATGTACGATGTCT  77486           TGCTT
                                GGGCATTGTATGT    CTG
                                ||||||||||||    |||
                                TCTGTAGCATGTA    GAC
                                       CTCAT
GAM260   LOC145790 3'  TTACAGAAGCAGAAACAAGAGC 77490      A_   ATG
            CT                    GGGC  TTGT   TTGCTTCTGTGG
                                ||||  ||||   ||||||||||||
                                TCCG  AACA   GACGAAGACATT
                                  AG   AA_
GAM260   LOC145824 5'  TCACAGAGGCATCAGTGATGCT 77527       TG A  T
            T                     GGGCAT  T TG TGCTTCTGTGG
                                ||||||  | || ||||||||||||
                                TTCGTA  G AC ACGGAGACACT
                                   GT _  T
GAM260   LOC145828 5'  CGTGGAGGTGGACGTGTGGT   83536    TG   _ TG     TG
                                AT  TATG T  CTTCTG  G
                                ||  |||| |  ||||||  |
                                TG  GTGC G  GGAGGT  C
                                 GT   A GT     GT
GAM260   LOC145837 5'  TGGAATAACTTGCAGTGTCT   83547          T   C
                                GGGCATTGTA GTTG TTCTG
                                |||||||||| |||| |||||
                                TCTGTGACGT CAAT AAGGT
                                      T   _
GAM260   LOC145845 3'  TAGTTTAATGTTTGGTGCCC   83556        T     CTT
                                GGGCATTG ATGTTG   CTG
                                |||||||| ||||||   |||
                                CCCGTGGT TGTAAT   GAT
                                     T     TT_
GAM260   LOC145858 3'  CTACAGAGGATCGACGAGGCCC 77545      A    A  TTG
                                GGGC TTGT TG   CTTCTGTGG
                                |||| |||| ||   |||||||||
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                                CCCG AGCA GC   GGAGACATC
                                  G    _ TA_
GAM260   LOC145868 3'  CCATGGAGGTAGGGCATGGTC  83561     AT   ATGT
                                GGC  TGT    TGCTTCTGTGG
                                |||  |||    ||||||||||
                                CTG  ACG    ATGGAGGTACC
                                  GT   GG__
GAM260   LOC145870 5'  TCATAGAGGTTCCCAGTGCC   77559       TATGTT
                                GGCATTG     GCTTCTGTGG
                                |||||||     ||||||||||
                                CCGTGAC     TGGAGATACT
                                    CCT___
GAM260   LOC145951 5'  CACAGAGCCTGAGTGCTT    77576       GTATGTT   T
                                GGGCATT      GCT CTGTG
                                |||||||      ||| |||||
                                TTCGTGA      CGA GACAC
                                    GTC____   _
GAM260   LOC145988 3'  GCAGCATGGATGTTC       77608       G
                                GGGCATT TATGTTGC
                                ||||||| ||||||||
                                CTTGTAG GTACGACG
                                    _
GAM260   LOC145989 5'  GTGCTTCGCGCAGACGGTGTCC 59548         A   T  TTCTGTGG
                                GGGCATTGT TGT GC
                                ||||||||| ||| ||
                                CCTGTGGCA ACG CG
                                     G   _  CTTCGTGC
GAM260   LOC146062 5'  CACAGCCGTGGAGTGCCT    77660       G    TTGCTT
                                GGGCATT TATG     CTGTG
                                ||||||| ||||     |||||
                                TCCGTGA GTGC     GACAC
                                    G    C_____
GAM260   LOC146136 5'  CTGCTTCGTAACATGTGAAGTC 72942      A TG       TTCT TG
           C                     GGGC T  TATGTTGC    G  G
                                |||| |  ||||||||    |  |
                                CCTG A  GTACAATG    C  C
                                  A GT       CTT_ GT
GAM260   LOC146159 5'  CTGCAGGAGTCCCAGGAAGTGC 77682       GTA  TT      TG
           CC                    GGGCATT   TG  GCTTCTG  G
                                |||||||   ||  |||||||  |
                                CCCGTGA   AC  TGAGGAC  C
                                    AGG  CC      GT
GAM260   LOC146176 5'  TTGCTGATGCAGTATACAGTGT 77699           T  T TG
                                GCATTGTATGTTGC TC G  G
                                |||||||||||||| || |  |
                                TGTGACATATGACG AG C  T
                                        T  T GT
GAM260   LOC146226 5'  CGCAGAGGTGCCAAGTGCCC   83622       GTA  TT      TG
                                GGGCATT   TG  GCTTCTG  G
                                |||||||   ||  |||||||  |
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                                CCCGTGA  AC  TGGAGAC  C
                                   ___  CG     GT
GAM260  LOC146332 3'  CCACAGGAGCACCACGGTGCCC 77821        AT T
                                GGGCATTGT  G TGCTTCTGTGG
                                |||||||||  | ||||||||||
                                CCCGTGGCA  C ACGAGGACACC
                                    __ C
GAM260  LOC146433 3'  CCACAGGAGTTCAACTGGGTCT 77873     ATT  A  TT
                                GGGC   GT TG  GCTTCTGTGG
                                ||||   || ||  ||||||||||
                                TCTG   CA AC  TGAGGACACC
                                  GGT  _  T_
GAM260  LOC146435 3'  AGTAACATGCATGTTT      77895       T
                                GGGCAT GTATGTTGCT
                                |||||| ||||||||||
                                TTTGTA CGTACAATGA

                                  _
GAM260  LOC146445 3'  GGGCAGCAATGTCT       83682         ATGT
                                GGGCATTGT    TGCTT
                                |||||||||    |||||
                                TCTGTAACG    ACGGG

                                   ____
GAM260  LOC146455 3'  TTACAGGGGTGAGCCACCGTGC 77912       T  ATG TG
          CC                      GGGCAT GT   T  CTTCTGTGG
                                |||||| ||   |  |||||||||
                                CCCGTG CA   A  GGGGACATT
                                   C  CCG GT
GAM260  LOC146481 5'  CTACAGAGGAAAGTGGAGCTC  77926     AT G   GTTG
                                GGGC  T TAT    CTTCTGTGG
                                ||||  | |||    |||||||||
                                CTCG  A GTG    GGAGACATC
                                  __ G   AAA_
GAM260  LOC146488 5'  TCATGAAGGCCGGCAGCATCAA 70815      T      __   __
          TGTCT                    ATTG ATGTTGCT  TCT  GTGG
                                |||| ||||||||  |||  ||||
                                TAAC TACGACGG  GGA  TACT
                                  _       CC   AG
GAM260  LOC146512 3'  CACAGAGGTTGGATGTCC    77940       GTATGTT
                                GGGCATT      GCTTCTGTG
                                |||||||      |||||||||
                                CCTGTAG      TGGAGACAC
                                   GT_____
GAM260  LOC146515 3'  TTACAGAGGTGAGAATGAAGTC 77966     A TG ATG TG
          C                      GGGC T  T   T  CTTCTGTGG
                                |||| |  |   |  |||||||||
                                CCTG A  A   A  GGAGACATT
                                  A GT AG_ GT
GAM260  LOC146517 3'  CGCAGACCATGCACAGTGCCT  77944         AT  TGCT    TG
                                GGGCATTGT  GT    TCTG  G
                                |||||||||  ||    ||||  |
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                                TCCGTGACA  CG    AGAC  C
                                     __  TACC    GT
GAM260   LOC146667 5'  CGCAGGGGGGTGTGTGTGCCT  83704       TGT TG  G     TG
                                GGGCAT   A  TT CTTCTG  G
                                ||||||   |  || ||||||  |
                                TCCGTG   T  GG GGGGAC  C
                                   TG_ GT  _     GT
GAM260   LOC146667 5'  TACAGAGGAAATAATTCCC    83708     C    ATGTTG
                                GGG ATTGT     CTTCTGTG
                                ||| |||||     ||||||||
                                CCC TAATA     GGAGACAT
                                  T    AA____
GAM260   LOC146733 3'  TATGAGTGAGAACATGCGGTGT 83771            G  _  GTGG
            TT                    GGGCATTGTATGTT CTT CT
                                ||||||||||||| ||| ||
                                TTTGTGGCGTACAA GAG GA
                                      _  T  GTATT
GAM260   LOC146850 3'  CACACTGTAATGTACGTGCTC  83821       T       TTC    G
                                GGGCAT GTATGTTGC   TGTG
                                |||||| |||||||||   ||||
                                CTCGTG CATGTAATG   ACAC
                                   _       TC_    G
GAM260   LOC147040 3'  CTGTGTTGCTGACTACAGTGTC 78233          T  _  TTCTGTGG
            T                     GGGCATTGTA GTT GC
                                ||||||||| ||| ||
                                TCTGTGACAT CAG CG
                                      _  T  TTGTGTC
GAM260   LOC147040 3'  TACAGTGTCTGTGATGTCC    78238       TG  TGTT  TT
                                GGGCAT  TA    GC  CTGTG
                                ||||||  ||    ||  |||||
                                CCTGTA  GT    TG  GACAT
                                   GT  C___  T_
GAM260   LOC147071 5'  TACAGAAAATGTGGAGTCC    73004      A TG   GTTGC
                                GGGC T  TAT     TTCTGTG
                                |||| |  |||     |||||||
                                CCTG G  GTA     AAGACAT
                                  A GT   A____
GAM260   LOC147072 3'  TTACGTGAAGTAGTAATGTTC  60410         TATG      _
                                GGGCATTG    TTGCTTC TGTGG
                                ||||||||    ||||||| |||||
                                CTTGTAAT    GATGAAG GCATT
                                     ____       T
GAM260   LOC147123 3'  AGGTGGCACACAGTGCTC     78253         A   TG
                                GGGCATTGT TGT  CTT
                                ||||||||| |||  |||
                                CTCGTGACA ACG  GGA
                                      C   GT
GAM260   LOC147137 3'  CTGCAGGCCATCAGCGTGCACT 78273      T       CT__    TG
            GTTC                    GGCA TGTATGTTG    TCTG  G
                                |||| |||||||||    ||||  |
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                                TTGT ACGTGCGAC   GGAC  C
                                  C       TACC   GT
GAM260   LOC147219 3'  GCTGCATGTAATGTCT     83990          T
                                GGGCATTGTATGT GC
                                |||||||||||| ||
                                TCTGTAATGTACG CG
                                        T
GAM260   LOC147353 3'  GGTACATATGGTGCTT     84010      TG    T
                                GGGCAT  TATGT GCT
                                ||||||  ||||| |||
                                TTCGTG  ATACA TGG
                                   GT    _
GAM260   LOC147429 3'  GAACCAATGTACAATGC     78358          C
                                GCATTGTATGTTG TTC
                                |||||||||||| |||
                                CGTAACATGTAAC AAG
                                        C
GAM260   LOC147463 3'  CCACGAGAAATATATAGGCTT  78370     A       GC   T
                                GGGC TTGTATGTT  TTC GTGG
                                |||| |||||||||  ||| ||||
                                TTCG GATATATAA  GAG CACC
                                  _       A_  _
GAM260   LOC147525 3'  CTGTGAGCACTGGTGTGTGTGT 78375     TG_  TG ___    CTGTGG
            GCCT                  CAT   TA  T   TGCTT
                                |||   ||  |   |||||
                                GTG   GT  G   ACGAG
                                  TGT  GT GTC    TGTC
GAM260   LOC147664 3'  TTACAGAAGACCCACGACGTCC 78411     A   ATGTTG
                                GGGC TTGT     CTTCTGTGG
                                |||| ||||     |||||||||
                                CCTG AGCA     GAAGACATT
                                  C   CCCA__
GAM260   LOC147965 5'  CGGGAGCTGCACTGCCC     78599      T   TGTT
                                GGGCA TGTA    GCTTCTG
                                ||||| ||||   |||||||
                                CCCGT ACGT    CGAGGGC
                                  C   ____
GAM260   LOC148018 3'  CACGTTGCGTGCGGGTTT    82418     A      T  TTCT
                                GGGC TTGTATGT GC    GTG
                                |||| |||||||| ||    |||
                                TTTG GGCGTGCG TG    CAC
                                  _       T ____
GAM260   LOC148029 5'  CCACCTGGGTTTATGGTGCCC  78618      TG  TGTT   CT
                                GGGCAT  TA    GCTT  GTGG
                                ||||||  ||    ||||  ||||
                                CCCGTG  AT    TGGG  CACC
                                   GT  T___    TC
GAM260   LOC148147 5'  CTACAGAGAAGTGTGGTG    78678     TG   GTTG  T
                                CAT  TAT    CT CTGTGG
                                |||  |||    || ||||||
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                                GTG  GTG    GA GACATC
                                  GT   AA__  _
GAM260   LOC148195 3'  CTGTGGAAGTAACATTTGAGCT 84128     A   T         TG
                                GGC TTG ATGTTGCTTCTG  G
                                ||| ||| ||||||||||||  |
                                TCG AGT TACAATGAAGGT  C
                                  _  T          GT
GAM260   LOC148345 3'  GGCTGGGTACAGTGTTC     84142          GTT
                                GGGCATTGTAT   GCT
                                ||||||||||   |||
                                CTTGTGACATG   CGG
                                      GGT
GAM260   LOC148426 5'  CAGACCAACATGCATGCTC    84149       T       CT
                                GGGCAT GTATGTTG  TCTG
                                ||||||| ||||||||  ||||
                                CTCGTA CGTACAAC  AGAC
                                   _       C_
GAM260   LOC148697 3'  GCTTGGCATACAGGGCCT     78928      A        __
                                GGGC TTGTATGTT  GC
                                |||| |||||||||  ||
                                TCCG GACATACGG  CG
                                  G        TT
GAM260   LOC148753 3'  CCATGGGGGTGATGAATGACCC 84214     _   GTA   TG
                                GGG CATT   TGT  CTTCTGTGG
                                ||| ||||   |||  |||||||||
                                CCC GTAA   GTA  GGGGGTACC
                                  A   ____  GT
GAM260   LOC148918 5'  CACAGAGGAATAGTGTT      79063         ATGTTG
                                GGCATTGT     CTTCTGTG
                                ||||||||     ||||||||
                                TTGTGATA     GGAGACAC
                                    A_____
GAM260   LOC148918 5'  CTGCAGGGGCAGAAGTGCATGT 79070        T   G_       TG
            CT                    GGGCAT GTAT  TTGCTTCTG  G
                                ||||||| ||||  |||||||||  |
                                TCTGTA CGTG  GACGGGGAC  C
                                   _   AA        GT
GAM260   LOC148932 3'  CCACAGGGAGACTGGGATGTTC 79104        G  T   GC
                                GGGCATT TA GTT  TTCTGTGG
                                ||||||| || |||  ||||||||
                                CTTGTAG GT CAG  GGGACACC
                                    G  _   A_
GAM260   LOC148932 3'  CGTAGGAGTGATGACAGCTC   79107     AT   A   TG     TG
                                GGGC  TGT TGT  CTTCTG  G
                                ||||  ||| |||  ||||||  |
                                CTCG  ACA GTA  GAGGAT  C
                                  __  _  GT     GT
GAM260   LOC148947 3'  ATGGGAGGTCGTGCCT      79119        TGTAT TTG
                                GGGCAT    G   CTTCTGT
                                ||||||    |  |||||||
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                                TCCGTG    C   GAGGGTA
                                   _____ TG_
GAM260   LOC148981 3'  CCACAGAAGGAGCAATGATCC  84315    C  TG A    G
                                GG AT  T TGTT CTTCTGTGG
                                || ||  | |||| |||||||||
                                CC TA  A ACGA GAAGACACC
                                 _  GT _    G
GAM260   LOC149050 3'  GAACAACATACAAAGTTT    60429      A        C
                                GGGC TTGTATGTTG TTC
                                |||| |||||||||| |||
                                TTTG AACATACAAC AAG
                                  A        _
GAM260   LOC149072 5'  TCACAGGTCTAGAACAGTGCCT 79157         ATG   CT
                                GGGCATTGT   TTG  TCTGTGG
                                |||||||||   |||  |||||||
                                TCCGTGACA   GAT  GGACACT
                                     A__   CT
GAM260   LOC149073 5'  TATTGAAGCAGCAGTGCCC    84333         ATGT     T
                                GGGCATTGT    TGCTTC GTG
                                |||||||||    |||||| |||
                                CCCGTGACG    ACGAAG TAT
                                     _____      T
GAM260   LOC149103 3'  CTGCAGAACTTTAGTGCAGAGT 79195      A     GTTGC     TG
            TT                   GGGC TTGTAT     TTCTG  G
                                |||| ||||||     |||||  |
                                TTTG GACGTG     AAGAC  C
                                  A     ATTTC     GT
GAM260   LOC149103 3'  CTGTAGAGGTGGTTTTAATTCC 79196     C    TAT TT      TG
            T                    GGG ATTG   G  GCTTCTG  G
                                ||| ||||   |  |||||||  |
                                TCC TAAT   T  TGGAGAT  C
                                  T   TT_ GG      GT
GAM260   LOC149149 3'  TAGTAGAAGTGGTTGTAGTGTT 84367         TAT TT     GTGG
            T                    GGGCATTG   G  GCTTCT
                                |||||||||   |  ||||||
                                TTTGTGAT   T  TGAAGA
                                     GT_ GG     TGATG
GAM260   LOC149194 3'  TTGCAGAAGCAGAAAGCAAGCC 79232      A    ATG       TG
            C                    GGGC TTGT   TTGCTTCTG  G
                                |||| ||||   |||||||||  |
                                CCCG AACG   GACGAAGAC  T
                                  _    AAA        GT
GAM260   LOC149319 5'  CCATGGGAGCAGCAGAGCC    79291     ATTGTA
                                GGC     TGTTGCTTCTGTGG
                                |||     ||||||||||||||
                                CCG     ACGACGAGGGTACC
                                  AG____
GAM260   LOC149319 5'  CGCAGATGCCAAGCAGTGCTC  79293         A  TT  T    TG
                                GGGCATTGT TG  GC TCTG  G
                                ||||||||| ||  || ||||  |
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                                CTCGTGACG AC  CG AGAC  C
                                     A  __  T   GT
GAM260  LOC149332 3'  TGCAAAGTATGACAGTGTTT  84398        ATGT    C  TG
                                GGGCATTGT   TGCTT TG  G
                                |||||||||   ||||| ||  |
                                TTTGTGACA   ATGAA AC  T
                                     GT__    _  GT
GAM260  LOC149372 5'  CATTGTAAATAGTGCCT    79322        ATG   TTC
                                GGGCATTGT   TTGC   TG
                                |||||||||   ||||   ||
                                TCCGTGATA   AATG   AC
                                     ___    TT_
GAM260  LOC149372 3'  CTGTGGGGGGCGTTCCAGTGTT 79323        T_   TG    TG
          C                      GGGCATTG  ATGT  CTTCTG  G
                                |||||||||  ||||  ||||||  |
                                CTTGTGAC  TGCG  GGGGGT  C
                                     CT   __     GT
GAM260  LOC149422 3'  TTGGTCTGTGGCATGCAGTTCC 79353    C        TG TT_   TGG
          T                      GGG ATTGTATGT  C   CTG
                                ||| |||||||||  |   |||
                                TCC TGACGTACG  G   GGT
                                  T       GT TCT   T
GAM260  LOC149478 5'  TTGTGGAGGCGTGGAAATGCC  79385       GTATGT      TG
                                GGCATT     TGCTTCTG  G
                                ||||||     ||||||||  |
                                CCGTAA     GCGGAGGT  T
                                    AGGT__       GT
GAM260  LOC149501 3'  CTATGGGGGCCTCACAAGCCC  75274     A    AT TT
                                GGGC TTGT  G  GCTTCTGTGG
                                |||| ||||  |  ||||||||||
                                CCCG AACA  C  CGGGGGTATC
                                  _    __ TC
GAM260  LOC149506 3'  ATGGAAGGAGATGTCT      84451        GTATGT G
                                GGGCATT     T CTTCTGT
                                |||||||     | |||||||
                                TCTGTAG     A GAAGGTA
                                    _______ G
GAM260  LOC149506 5'  CGCGGGGGTTTCACAGTG    84460       AT TT      TG
                                CATTGT  G  GCTTCTG  G
                                ||||||  |  |||||||  |
                                GTGACA  C  TGGGGGC  C
                                    __ TT      GT
GAM260  LOC149578 5'  CCACAGGGCCTGTGCCGTGCCC 79445       T    GTT   T
                                GGGCAT GTAT   GCT CTGTGG
                                |||||| ||||   ||| ||||||
                                CCCGTG CGTG   CGG GACACC
                                    C    TC_   _
GAM260  LOC149579 5'  TACAGGAGCAGGTGGCCC    71139      ATTGTATG
                                GGGC       TTGCTTCTGTG
                                ||||       ||||||||||
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                                CCCG       GACGAGGACAT
                                  GTG_____
GAM260   LOC149606 3'  CCCAGGCAGTAAACAGTGCTC  79447         A     TT   T
                                GGGCATTGT TGTTGC  CTG GG
                                ||||||||| ||||||  ||| ||
                                CTCGTGACA ATGACG  GAC CC
                                     A     __  _ A
GAM260   LOC149650 3'  CGGGAGCAGCATTTCC      79467    CATTGT
                                GG     ATGTTGCTTCTG
                                ||     ||||||||||||
                                CC     TACGACGAGGGC
                                 TT____
GAM260   LOC149668 5'  AAACATAGTGGCAGGCAGTGTC 84531         A   TG  TC   GG
           C                     GGGCATTGT TGT  CT  TGT
                                ||||||||| |||  ||  |||
                                CCTGTGACG ACG  GA  ACA
                                     G   GT  T_  AAT
GAM260   LOC149668 3'  CTGTAGAGGCCCAGATGGGGCT 84539      A TG A  TT      TG
           C                     GGGC T  T TG  GCTTCTG  G
                                |||| |  | ||  |||||||  |
                                CTCG G  A AC  CGGAGAT  C
                                  G GT G  C_      GT
GAM260   LOC149703 5'  CCGTGGAAGCACCGGAAGTCC  84650      ATTGTA  T     TG
                                GGGC     TG TGCTTC  TGG
                                ||||     || ||||||  |||
                                CCTG     GC ACGAAG  GCC
                                  AAG___  C     GT
GAM260   LOC149703 5'  TTACAGATAAAACATGTGAAGC 84662      A TG     GCT
           TC                    GGGC T  TATGTT   TCTGTGG
                                |||| |  ||||||   |||||||
                                CTCG A  GTACAA   AGACATT
                                  A GT     AAT
GAM260   LOC149707 5'  CCATGGAGGCAGGTTTCGGGCC 79485      A   TATG
           T                     GGGC TTG    TTGCTTCTGTGG
                                |||| |||    ||||||||||||
                                TCCG GGC    GACGGAGGTACC
                                  _   TTTG
GAM260   LOC149711 3'  CTGTAGGAGCAGACAGGAATCC 84681     C   GTA  _      TG
           T                     GGG ATT   TGT TGCTTCTG  G
                                ||| |||   ||| ||||||||  |
                                TCC TAA   ACA ACGAGGAT  C
                                  _  GG_  G       GT
GAM260   LOC149721 5'  CCGTCAGCAGTACATACAGTGT 79497           T   T  _
           CC                      GGGCATTGTATGT GCT CTG TGG
                                ||||||||||||| ||| ||| |||
                                CCTGTGACATACA TGA GAC GCC
                                        _  C   T
GAM260   LOC149722 5'  CTGTGGAGTTGTTATAGATGCT 84599       G    TT_    TGTGG
           C                     GGGCATT TATG   GCTTC
                                ||||||| ||||   |||||
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                                CTCGTAG ATAT   TGAGG
                                   _   TGT    TGTC
GAM260  LOC149912 5'  TCATAGAAGGTGATGCAGGTTC 84719     A    GTTG
                                GGGC TTGTAT   CTTCTGTGG
                                |||| ||||||   |||||||||
                                CTTG GACGTA   GAAGATACT
                                  _    GTG_
GAM260  LOC150095 5'  CTATGGGAAAACGATGAAATGC 84857       G  _  GC
          TC                      GGGCATT TAT GTT  TTCTGTGG
                                  ||||||| ||| |||  ||||||||
                                  CTCGTAA GTA CAA  AGGGTATC
                                     A  G  A_
GAM260  LOC150113 5'  TCGTGGGAGCAGCCCTGCCC   87215      TTGTAT      TG
                                GGGCA     GTTGCTTC  TGG
                                |||||     ||||||||  |||
                                CCCGT     CGACGAGG  GCT
                                   CC____       GT
GAM260  LOC150166 5'  CTGTGGGAGGAACATGCAGTCT 84883     C        G     TG
          CC                      GGG ATTGTATGTT CTTCTG  G
                                  ||| ||||||||| ||||||  |
                                  CCT TGACGTACAA GAGGGT  C
                                    C        G     GT
GAM260  LOC150166 5'  TTATAGAAGTAATATGTGTTCC 84892     CAT GT
          C                       GGG   T  ATGTTGCTTCTGTGG
                                  |||   |  ||||||||||||||
                                  CCC   G  TATAATGAAGATATT
                                    TT_ TG
GAM260  LOC150174 3'  CGCGGGAGGAGGGAATGTTC   79608       GTATG  G     TG
                                GGGCATT    TT CTTCTG  G
                                |||||||    || ||||||  |
                                CTTGTAA    GA GAGGGC  C
                                   GG___  G     GT
GAM260  LOC150197 3'  CATAGAGGCAGAGAGCCC    79595     ATTGTATG
                                GGGC       TTGCTTCTGTG
                                ||||       ||||||||||
                                CCCG       GACGGAGATAC
                                  AGA_____
GAM260  LOC150208 3'  CTACAGGAGGAACAGTGGCCT  84916     ATTGTA   G
                                GGGC     TGTT CTTCTGTGG
                                ||||     |||| |||||||||
                                TCCG     ACAA GAGGACATC
                                  GTG___   G
GAM260  LOC150213 3'  CGCGGGAGGAGGGAATGTTC   74855       GTATG  G     TG
                                GGGCATT    TT CTTCTG  G
                                |||||||    || ||||||  |
                                CTTGTAA    GA GAGGGC  C
                                   GG___  G     GT
GAM260  LOC150223 3'  CGCAGAGCATTTGGTGCCC    85021       TATGT   T
                                GGGCATTG    TGCT CTGTG
                                ||||||||    |||| |||||
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                                CCCGTGGT    ACGA GACGC
                                    TT___   _
GAM260  LOC150225 3'  CATAAATCTGCAATGTCT    84986        T  GCTTC
                                GGGCATTGTA GTT    TGTG
                                |||||||||| |||    ||||
                                TCTGTAACGT TAA    ATAC
                                    C  _____
GAM260  LOC150271 5'  TCACAGGGGTAACCAAGGTCC  84955     A  TAT
                                GGGC TTG  GTTGCTTCTGTGG
                                |||| |||  ||||||||||||
                                CCTG AAC  CAATGGGGACACT
                                  G  ___
GAM260  LOC150290 5'  CTACGGAAGCGGTGAGACTGTC 79771      TT  AT_ TT
           T                     GGGCA  GT  G  GCTTCTGTGG
                                |||||  ||  |  ||||||||||
                                TCTGT  CA  T  CGAAGGCATC
                                  __  GAG GG
GAM260  LOC150319 3'  CAGGGGGGCAGTTCCT      79649     C    ATGTTG
                                GGG ATTGT     CTTCTG
                                ||| |||||     ||||||
                                TCC TGACG     GGGGAC
                                  T    G_____
GAM260  LOC150372 5'  CTGCAGGGGCGCCTAGCAGTGC 79799        ATGT       TG
           T                     GGCATTGT    TGCTTCTG  G
                                ||||||||    ||||||||  |
                                TCGTGACG    GCGGGGAC  C
                                    ATCC       GT
GAM260  LOC150519 5'  AGCGGCGTGCAGTGTTC     79913
                                GGGCATTGTATGTTGCT
                                ||||||||||||||||
                                CTTGTGACGTGCGGCGA

GAM260  LOC150519 5'  CTAGGGCAGCGGCGTGCAGTGT 79914              T  G
           TC                      GGGCATTGTATGTTGCT CT TGG
                                |||||||||||||||| || |||
                                CTTGTGACGTGCGGCGA GG ATC
                                          C  G
GAM260  LOC150527 3'  CTGTGGAGGCGAGAAGGCAGTG 79928   G     ATG_       TG
           TGC                    G GCATTGT    TTGCTTCTG  G
                                | |||||||    |||||||||  |
                                C TGTGACG    AGCGGAGGT  C
                                 G      GAAG       GT
GAM260  LOC150538 3'  ATAGAAGGCTGTGCTT      79930       T  ATGTTG
                                GGGCAT GT     CTTCTGT
                                ||||||  ||     |||||||
                                TTCGTG CG     GAAGATA
                                   T  _______
GAM260  LOC150577 3'  CACACCCACATCAATGCTC    85072        T    TGCTTC
                                GGGCATTG ATGT     TGTG
                                |||||||| ||||     ||||
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                                CTCGTAAC TACA     ACAC
                                     _   CCC___
GAM260  LOC150677 3'  CAGGAGTCAGGCCT       85116     A   TATGTT
                                GGGC TTG     GCTTCTG
                                |||| |||     |||||||
                                TCCG GAC     TGAGGAC
                                  _  _______
GAM260  LOC150696 3'  TCACAGCCTGGCTGTGATGCTT 58486       TG  T    CTT
                                GGGCAT  TA GTTG   CTGTGG
                                ||||||  || ||||   ||||||
                                TTCGTA  GT CGGT   GACACT
                                   GT  _    CC_
GAM260  LOC150696 3'  TGTGGGAGTGATCTGGTGGCC  58491    G    TAT  TG     TG
                                GG CATTG   GT  CTTCTG  G
                                || |||||   ||  ||||||  |
                                CC GTGGT   TA  GAGGGT  T
                                 G    C__  GT     GT
GAM260  LOC150951 5'  GGTACTGACGACGATGCTT    85169         A    ___
                                GGGCATTGT TGTT   GCT
                                ||||||||| ||||   |||
                                TTCGTAGCA GCAG   TGG
                                     _   TCA
GAM260  LOC150967 5'  CCACTTGCATTAGTGTCC     80079         T    TGCTTCT
                                GGGCATTG ATGT      GTGG
                                |||||||| ||||      ||||
                                CCTGTGAT TACG      CACC
                                     _   TT_____   G
GAM260  LOC151009 3'  CGCAGAGGAGACGGATGCCC   85194       GTA   TG     TG
                                GGGCATT   TGT  CTTCTG  G
                                |||||||   |||  ||||||  |
                                CCCGTAG   GCA  GGAGAC  C
                                   ___   GA     GT
GAM260  LOC151009 3'  GAGTGGATACAATGCTC     85196          G TG
                                GGGCATTGTAT T  CTT
                                |||||||||||  |  |||
                                CTCGTAACATA G  GAG
                                      _ GT
GAM260  LOC151162 5'  CCACAGAGGAGGGTGTGAAGCC 85242      A TG   G  G
          T                      GGGC T  TAT TT CTTCTGTGG
                                |||| |  ||| || |||||||||
                                TCCG A  GTG GA GGAGACACC
                                  A GT   G  _
GAM260  LOC151361 5'  CTATAGGGGCATTGAGGAGCTT 85325      A  GTATGT
                                GGGC TT      TGCTTCTGTGG
                                |||| ||      ||||||||||
                                TTCG GG      ACGGGGATATC
                                  A  AGTT__
GAM260  LOC151414 3'  CCACCAGAGTGTGCAATACCT  80236     C      GTT    CT
                                GGG ATTGTAT   GCTT  GTGG
                                ||| |||||||   ||||  ||||
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                                TCC TAACGTG   TGAG  CACC
                                  A      ___    AC
GAM260   LOC151429 3'  CTGCAGGGGCAGCAACGGCTGC 85351     _    A         TG
                                GCA TTGT TGTTGCTTCTG  G
                                ||| |||| ||||||||||  |
                                CGT GGCA ACGACGGGGAC  C
                                  C    _          GT
GAM260   LOC151465 3'  ATAGTGTTCAATGTCC      62778         TATGTT  TT
                                GGGCATTG     GC  CTGT
                                ||||||||     ||  ||||
                                CCTGTAAC     TG  GATA
                                     T_____  T_
GAM260   LOC151512 3'  CCTCAGACTGTGATGCTT    85427       TG  T TTGCT    T
                                GGGCAT  TA G     TCTG GG
                                ||||||  || |    |||| ||
                                TTCGTA  GT C     AGAC CC
                                    GT  _ _____    T
GAM260   LOC151512 5'  TCGCAGGGGCTCCGGCGATACC 85433     C     ATGTT
           T                     GGG ATTGT     GCTTCTGTGG
                                ||| |||||     ||||||||||
                                TCC TAGCG     CGGGGACGCT
                                  A    GCCT_
GAM260   LOC151516 3'  CATGGGGGTCACTGGGCTT    80268      ATTGTAT  T
                                GGGC      GT GCTTCTGTG
                                ||||      || |||||||||
                                TTCG      CA TGGGGGTAC
                                  GGT_____  C
GAM260   LOC151521 3'  TAGATAGAATGCAGTGTTC    85438          GTTGCT
                                GGGCATTGTAT     TCTG
                                ||||||||||      ||||
                                CTTGTGACGTA     AGAT
                                      AGAT__
GAM260   LOC151647 5'  CGCAGGAGCTTCGGGCTT     80330      A   TATGTT
                                GGGC TTG     GCTTCTGTG
                                |||| |||     |||||||||
                                TTCG GGC     CGAGGACGC
                                  _   TT_____
GAM260   LOC151647 5'  CTGCAGAGGTGATGGGCCGCTC 80331      ATT  A   TG     TG
                                GGGC   GT TGT  CTTCTG  G
                                ||||   || |||  ||||||  |
                                CTCG   CG GTA  GGAGAC  C
                                  C__  G   GT     GT
GAM260   LOC151902 3'  TGCAGGGGCCCTGGATGTTT   80381        GTATGTT      TG
                                GGGCATT      GCTTCTG  G
                                |||||||      |||||||  |
                                TTTGTAG      CGGGGAC  T
                                    GTCC___      GT
GAM260   LOC151963 3'  CAGGATGGTGCAGGCTC     80399      A     GTTGC
                                GGGC TTGTAT     TTCTG
                                |||| ||||||     |||||
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                                CTCG GACGTG     AGGAC
                                  _     GT___
GAM260   LOC152100 3'  TCATGGAAGTCATTTTATAGTC 80459     C      TGT  _
                 CT                  GGG ATTGTA   TG CTTCTGTGG
                                     ||| ||||||   || |||||||||
                                     TCC TGATAT   AC GAAGGTACT
                                       _     TTT  T
GAM260   LOC152271 3'  CGCAGGGGCTTGAAATGTCC   80518        GTATGTT      TG
                                     GGGCATT      GCTTCTG  G
                                     |||||||      |||||||  |
                                     CCTGTAA      CGGGGAC  C
                                         AGTT___      GT
GAM260   LOC152286 5'  TGGGGGAGGCAAGGTCC     85634      A    ATGTTG
                                     GGGC TTGT     CTTCTG
                                     |||| ||||     ||||||
                                     CCTG AACG     GGGGGT
                                       G    GA____
GAM260   LOC152317 5'  TTGTAGAGGTCCACTAAAATGT 85653        GTAT  T_      TG
                 TT                  GGGCATT    GT  GCTTCTG  G
                                     |||||||    ||  |||||||  |
                                     TTTGTAA    CA  TGGAGAT  T
                                         AAT_  CC      GT
GAM260   LOC152404 5'  TCACAGAGGTTCTCCGCAGTGT 80580        ATGTT
                                     GCATTGT     GCTTCTGTGG
                                     |||||||     ||||||||||
                                     TGTGACG     TGGAGACACT
                                         CCTCT
GAM260   LOC152447 3'  AGGCGCCGGCCGCGTGTGATGT 80586       TG     T   TC   GG
                 CC                  GGGCAT  TATGT GCT  TGT
                                     ||||||  ||||| |||  |||
                                     CCTGTA  GTGCG CGG  GCG
                                        GT    C   CC   GAC
GAM260   LOC152453 3'  GAATGATGTTCAGTGTCC     80598         T      C
                                     GGGCATTG ATGTTG TTC
                                     |||||||| |||||| |||
                                     CCTGTGAC TGTAGT AAG
                                         T     _
GAM260   LOC152573 3'  TTGTTCAGCAACATTTAGTGTT 80620         T       TCTGTGG
                 T                   GGGCATTG ATGTTGCT
                                     |||||||| ||||||||
                                     TTTGTGAT TACAACGA
                                         T       CTTGTT
GAM260   LOC152580 3'  TCATTAACCCTAACATACGGGC 85780      A        CTTCT_
                 TC                  GGGC TTGTATGTTG     GTGG
                                     |||| ||||||||||     ||||
                                     CTCG GGCATACAAT     TACT
                                       _         CCCAAT
GAM260   LOC152897 5'  CTACCTAAAGCATTAATGCCC  80726         T    GCTTCT
                                     GGGCATTG ATGTT     GTGG
                                     |||||||| |||||     ||||
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                                CCCGTAAT TACGA     CATC
                                   _    AATC__
GAM260  LOC153196 5'  CTGGGATATGATGTGTGGTGTT 85960       TG      CT   GTGG
           T                    GGGCAT  TATGTTG  TCT
                                |||||| |||||||  |||
                                TTTGTG  GTGTAGT  AGG
                                   GT      AT   GTC
GAM260  LOC153196 5'  GTACACAGCAGTGTCC      85974         A  _
                                GGGCATTGT TGT TGC
                                ||||||||| ||| |||
                                CCTGTGACG ACA ATG
                                      _  C
GAM260  LOC153243 3'  CGTGGGGGCCTCACAAGCCC   80796     A    AT TT      TG
                                GGGC TTGT  G  GCTTCTG  G
                                |||| ||||  |  |||||||  |
                                CCCG AACA  C  CGGGGGT  C
                                  _   __ TC      GT
GAM260  LOC153338 5'  CTGCAGCAAATACATCAGTGTT 85994        T    TGCTT   TG
           C                    GGGCATTG ATGT    CTG  G
                                |||||||| ||||    |||  |
                                CTTGTGAC TACA    GAC  C
                                   _   TAAAC   GT
GAM260  LOC153416 5'  TAGAAAAATACGATCCT     60541     C      GTTGC
                                GGG ATTGTAT     TTCTG
                                ||| |||||||     |||||
                                TCC TAGCATA     AAGAT
                                  _      AA___
GAM260  LOC153516 3'  CATGGCTACATGATGCCC    56707        GT    T   TCT
                                GGGCATT  ATGT GCT   GTG
                                |||||||  |||| |||   |||
                                CCCGTAG  TACA CGG   TAC
                                   __    T   ___
GAM260  LOC153577 5'  CCACGGCCATACACGGTGCCT  86055         A   T   TCT
                                GGGCATTGT TGT GCT   GTGG
                                ||||||||| ||| |||   ||||
                                TCCGTGGCA ATA CGG   CACC
                                     C   C   ___
GAM260  LOC153577 5'  TAGAGGTCAGTGTTT       86061         TATGTT
                                GGGCATTG     GCTTCTG
                                ||||||||     |||||||
                                TTTGTGAC     TGGAGAT
                                   _______
GAM260  LOC153642 5'  CCATGGATGTAATGTGAATGCC 80905        G       T
           T                    GGGCATT TATGTTGC TCTGTGG
                                ||||||| |||||||| |||||||
                                TCCGTAA GTGTAATG AGGTACC
                                   _       T
GAM260  LOC153768 5'  TCGCGGAGGCGTGGCCGGTGC  56716       TATGT
                                GCATTG    TGCTTCTGTGG
                                ||||||    ||||||||||
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                                CGTGGC    GCGGAGGCGCT
                                   CGGT_
GAM260  LOC153894 3'  TCATAATCCAAACAAGTGATGC 80975       TG A   GCTTC
           CT                    GGGCAT  T TGTT    TGTGG
                                |||||| | ||||    |||||
                                TCCGTA  G ACAA    ATACT
                                   GT A   ACCTA
GAM260  LOC153918 3'  GGTAGATGTGATGTCT      80993       TG  G
                                GGGCAT  TAT TTGCT
                                |||||| ||| |||||
                                TCTGTA  GTA GATGG
                                   GT  _
GAM260  LOC153937 5'  CTGCAGAAAGTAGTTCAATGTC 81005        TATG    _  TG
           T                     GGGCATTG   TTGCTT CTG  G
                                |||||||| ||||||| |||  |
                                TCTGTAAC   GATGAA GAC  C
                                    TT__    A  GT
GAM260  LOC153966 5'  CAATCAGCATGCTGTGTCT   71074       T      CTTCTG
                                GGGCAT GTATGTTG    TG
                                |||||| |||||||     ||
                                TCTGTG CGTACGAC    AC
                                   T      TA____
GAM260  LOC154101 5'  CCGCAGAGGCAGCAGGCACTCC 82686    CAT  A
           C                     GGG  TGT TGTTGCTTCTGTGG
                                |||  ||| ||||||||||||||
                                CCC  ACG ACGACGGAGACGCC
                                  TC_  G
GAM260  LOC154214 5'  TGTAACCTGAAGCATATACAGT 81059          T   T_  GG
           GTCC                    GGCATTGTATGT GCTTC  GT
                                |||||||||||| |||||  ||
                                CTGTGACATATA CGAAG  CA
                                       _    TC  ATGTG
GAM260  LOC154215 3'  AGTGACATGCATGTTT     81052       T    TG
                                GGGCAT GTATGT  CT
                                |||||| ||||||  ||
                                TTTGTA CGTACA  GA
                                   _     GT
GAM260  LOC154641 5'  TCACAATGTTCAGTATGTGGAG 81100     A TG     CTTC_
           CCT                     GGGC T  TATGTTG    TGTGG
                                |||| |  |||||||    |||||
                                TCCG G  GTATGAC    ACACT
                                  A GT      TTGTA
GAM260  LOC154813 5'  CTGCAGGAGCAGAGTCATTGCC 81162      T  TATG       TG
           C                     GGGCA TG    TTGCTTCTG  G
                                ||||| ||    |||||||||  |
                                CCCGT AC    GACGAGGAC  C
                                   T  TGA_       GT
GAM260  LOC154834 5'  CGGGGGCGGGATCCC      86264     CATTGT  G
                                GGG     AT TTGCTTCTG
                                |||     || |||||||||
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                                CCC     TA GGCGGGGGC
                                  _______ G
GAM260  LOC154834 3'  TTGCAGGGGTGTGGACAGAGCC 86270     A   ATGT      TG
            C                    GGGC TTGT   TGCTTCTG  G
                                 |||| ||||   |||||||| |
                                 CCCG GACA   GTGGGGAC  T
                                   A   GGT_      GT
GAM260  LOC154849 5'  TGGGAGCGGCTGCC       60314     TTGTAT
                                 GGCA     GTTGCTTCTG
                                 ||||     ||||||||||
                                 CCGT     CGGCGAGGGT
                                  _______
GAM260  LOC155063 5'  TCGCAGAGGCGGCCTGTGCC   86370     TGTAT
                                 GGCAT    GTTGCTTCTGTGG
                                 |||||    |||||||||||||
                                 CCGTG    CGGCGGAGACGCT
                                   TC___
GAM260  LOC155072 5'  CCACAGACCACTGCATGGTGCT 86373      TG    TGCT_
            T                    GGGCAT  TATGT    TCTGTGG
                                 ||||||  |||||    |||||||
                                 TTCGTG  GTACG    AGACACC
                                   __    TCACC
GAM260  LOC155382 3'  CTACAGGGGCCTGGGAAGATGC 86389       GTATGTT
            CT                   GGGCATT     GCTTCTGTGG
                                 |||||||     ||||||||||
                                 TCCGTAG     CGGGGACATC
                                    AAGGGTC
GAM260  LOC155434 3'  CGCAGGAGCTCTTGTGCTT   86403      TGTATGTT
                                 GGGCAT      GCTTCTGTG
                                 ||||||      |||||||||
                                 TTCGTG      CGAGGACGC
                                   TTCT____
GAM260  LOC157254 3'  CGCCCTTGGCCTGCAGTGCTT  81384        TGTT   TCT_ TG
                                 GGGCATTGTA   GCT   G  G
                                 ||||||||||   |||   | |
                                 TTCGTGACGT   CGG   C  C
                                      C___   TTCC GT
GAM260  LOC157421 5'  TGGATGTGACATAAGATGCTT  86447       G    TG T
                                 GGGCATT TATGT  C TCTG
                                 ||||||| |||||  | ||||
                                 TTCGTAG ATACA  G AGGT
                                    A    GT T
GAM260  LOC157507 5'  CACAGAGGCTTCAATCCC    81453     C   TATGTT
                                 GGG ATTG     GCTTCTGTG
                                 ||| ||||     |||||||||
                                 CCC TAAC     CGGAGACAC
                                   _   TT____
GAM260  LOC157623 5'  CCACAGAAACATAATGCAATCT 81494     C      GT  C
            T                    GGG ATTGTAT  TG TTCTGTGG
                                 ||| |||||||  || ||||||||
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                                TTC TAACGTA  AC AAGACACC
                                  _     AT  A
GAM260   LOC157663 3'  CACTGTTGTACGGTGTCT    81535          TTGCTTCT
                                GGGCATTGTATG      GTG
                                ||||||||||||      |||
                                TCTGTGGCATGT      CAC
                                      TGT_____
GAM260   LOC157663 3'  CAGAATATCATATAATGTTT   81536          T  C
                                GGGCATTGTATG TG TTCTG
                                |||||||||||| || |||||
                                TTTGTAATATAC AT AAGAC
                                      T  _
GAM260   LOC157695 3'  CAGTGTTATCAGTGTCT     86516        T   TT  TT
                                GGGCATTG ATG  GC  CTG
                                |||||||| |||  ||  |||
                                TCTGTGAC TAT  TG  GAC
                                   _   __  T_
GAM260   LOC157753 3'  CACAAATATATGATGTT     81586      TG     GCTTC
                                GGCAT  TATGTT    TGTG
                                |||||  ||||||    ||||
                                TTGTA  ATATAA    ACAC
                                  GT     _____
GAM260   LOC157860 5'  CACAGAGGGGAACAGT      86565      ATG  G
                                ATTGT   TT CTTCTGTG
                                |||||   || ||||||||
                                TGACA   AG GGAGACAC
                                  ___  G
GAM260   LOC157860 3'  TTACAGAAGAAAACTGTGCCT  86573       T  ATGTTG
                                GGGCAT GT     CTTCTGTGG
                                ||||||  ||     |||||||||
                                TCCGTG CA     GAAGACATT
                                   T  AAA___
GAM260   LOC158055 3'  CGCAGGGGGCGCGGCTGTCT   81667      _   AT  TG     TG
                                GGGCA TTGT  GT  CTTCTG  G
                                ||||| ||||  ||  ||||||  |
                                TCTGT GGCG  CG  GGGGAC  C
                                  C    __  __     GT
GAM260   LOC158056 5'  CGCGGGGACCTGTGTGTGCCC  81684       TG_  T   GCT    TG
                                GGGCAT   TA GTT   TCTG  G
                                ||||||   || |||   ||||  |
                                CCCGTG   GT CAG   GGGC  C
                                   TGT  C   ___    GT
GAM260   LOC158230 3'  CAGGAGGGCAAGCCC       81797      A   ATGTTG
                                GGGC TTGT     CTTCTG
                                ||||  ||||     ||||||
                                CCCG AACG     GAGGAC
                                  _    G_____
GAM260   LOC158261 3'  AGGCAATAATGATGCTT     86710       TG A
                                GGGCAT  T TGTTGCTT
                                ||||||  |  ||||||||
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                                TTCGTA  A ATAACGGA
                                   GT _
GAM260   LOC158267 5'  CACGGAAGGGGTGCTGCTT   81825      TT    GT G
                                GGGCA  GTAT  T CTTCTGTG
                                |||||  ||||  | ||||||||
                                TTCGT  CGTG  G GAAGGCAC
                                   __   __ G
GAM260   LOC158295 5'  CACAGAAAAGTGGTGCTC    86733       TG ATGTTGC
                                GGGCAT  T      TTCTGTG
                                ||||||  |      |||||||
                                CTCGTG  G      AAGACAC
                                   GT AA_____
GAM260   LOC158295 5'  CCACAGGGGTAGACAGGGGTCT 86734      A_    ATG
                                GGGC  TTGT   TTGCTTCTGTGG
                                ||||  ||||   ||||||||||||
                                TCTG  GACA   GATGGGGACACC
                                  GG   ___
GAM260   LOC158297 5'  GCAGCTGGCGATGCTC      81867         AT
                                GGGCATTGT  GTTGC
                                |||||||||  |||||
                                CTCGTAGCG  CGACG
                                     GT
GAM260   LOC158308 3'  CAGAGGTCAGTCCT       86742     C    TATGTT
                                GGG ATTG     GCTTCTG
                                ||| ||||     |||||||
                                TCC TGAC     TGGAGAC
                                  _   _______
GAM260   LOC158308 3'  TTACATTGTAATATATATGCCC 86746       T        TTC
                                GGGCAT GTATGTTGC   TGTGG
                                |||||| |||||||||   |||||
                                CCCGTA TATATAATG   ACATT
                                   _       TT_
GAM260   LOC158310 5'  CACAGAGGAGATGTGTTC    86749       TGTAT  TG
                                GGGCAT    GT  CTTCTGTG
                                ||||||    ||  ||||||||
                                CTTGTG    TA  GGAGACAC
                                   _____  GA
GAM260   LOC158310 5'  TCAGTGAGTGGTGAGTGGTGTT 86763       TG A  TT   _   TGG
            C                    GGGCAT  T TG  GCTT CTG
                                ||||||  | ||  |||| |||
                                CTTGTG  G GT  TGAG GAC
                                   GT A  GG   T   T
GAM260   LOC158373 5'  TTACAGGGCCTGGTGGTGTTC  71044       TG ATGTT   T
                                GGGCAT  T    GCT CTGTGG
                                ||||||  |    ||| ||||||
                                CTTGTG  G    CGG GACATT
                                   GT GTC__   _
GAM260   LOC158434 5'  TTGTGGAGACCAGATGCAATGC 86827          G   C_    TG
            CT                   GGGCATTGTAT TTG  TTCTG  G
                                ||||||||||| |||  |||||  |
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                                TCCGTAACGTA GAC  GAGGT  T
                                      _  CA    GT
GAM260  LOC158450 5'  CAGAAGTCAATCCT      81931    C   TATGTT
                                GGG ATTG    GCTTCTG
                                ||| ||||    |||||||
                                TCC TAAC    TGAAGAC
                                  _  ______
GAM260  LOC158504 5'  CAGAAGTCAATCCT      81939    C   TATGTT
                                GGG ATTG    GCTTCTG
                                ||| ||||    |||||||
                                TCC TAAC    TGAAGAC
                                  _  ______
GAM260  LOC158527 5'  GGCTGACGTTTAGTGCCT   81945       T   _
                                GGGCATTG ATGTT GCT
                                |||||||| ||||| |||
                                TCCGTGAT TGCAG CGG
                                     T    T
GAM260  LOC158572 3'  CAGAAGCCCATAGGTCC    81954    ATTG   TT
                                GGGC   TATG  GCTTCTG
                                ||||   ||||  |||||||
                                CCTG   ATAC  CGAAGAC
                                  G___   C_
GAM260  LOC158584 5'  CTGTGGGAGTTGATCAAATGGT 81960     TG A  TT__    TG
          GCCT                   GGCAT  T TG   GCTTCTG  G
                                |||||  | ||   |||||||  |
                                CCGTG  A AC   TGAGGGT  C
                                   GT A  TAGT     GT
GAM260  LOC158629 5'  CCACAGAGGTATTAAACAATGC 86875       A  T
          TC                     GGGCATTGT TG TGCTTCTGTGG
                                |||||||||| || ||||||||||
                                CTCGTAACA AT ATGGAGACACC
                                     A  T
GAM260  LOC158674 3'  ATGGGAGGTCATGCCT     81969     TTGTA  TTG
                                GGGCA    TG   CTTCTGT
                                |||||    ||   |||||||
                                TCCGT    AC   GAGGGTA
                                  _____  TG_
GAM260  LOC158678 3'  ATGGGAGGTCATGCCT     60514     TTGTA  TTG
                                GGGCA    TG   CTTCTGT
                                |||||    ||   |||||||
                                TCCGT    AC   GAGGGTA
                                  _____  TG_
GAM260  LOC158809 3'  CGCAGAGAGTACAAGCCC    86897     A     GTTGCT
                                GGGC TTGTAT     TCTGTG
                                |||| ||||||     ||||||
                                CCCG AACATG     AGACGC
                                  _     AG____
GAM260  LOC158835 3'  CTACAGGAGTAGGACTGGGGCC 82011     ATT_  ATGT
          T                     GGGC   GT   TGCTTCTGTGG
                                ||||   ||   ||||||||||
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                                TCCG   CA   ATGAGGACATC
                                  GGGT  GG__
GAM260  LOC158856 5'  TCACAGGGGTGGGGGTGCCC  86919      GTATG TG
                                GGGCATT    T  CTTCTGTGG
                                |||||||    |  |||||||||
                                CCCGTGG    G  GGGGACACT
                                   G____ GT
GAM260  LOC158969 3'  TCTCGATGGTTGTGATGCCC  82063     TG  TGTT   TC  T
                                GGGCAT  TA   GCT  TG GG
                                ||||||  ||   |||  || ||
                                CCCGTA  GT   TGG  GC CT
                                   GT  ____  TA  T
GAM260  LOC158978 3'  GACCCAACTACAGTGCTC   82076        T   CT
                                GGGCATTGTA GTTG  TC
                                ||||||||||  ||||  ||
                                CTCGTGACAT CAAC  AG
                                      _   CC
GAM260  LOC158987 3'  CCGCAGGGAAGGCAGTGTGATG 86960      TG  _   GC
           TTT                    GGGCAT  TA TGTT  TTCTGTGG
                                ||||||  ||  ||||  ||||||||
                                TTTGTA  GT ACGG  GGGACGCC
                                   GT  G    AA
GAM260  LOC159091 3'  CTACAGAACTTGCGTGTATAAT 57185   C     TG T  ___
           TCTT                    G ATTGTA  T GC   TTCTGTGG
                                |  ||||||  |  ||   ||||||||
                                C TAATAT  G CG   AAGACATC
                                 T     GT _  TTC
GAM260  LOC159121 3'  TATAGAATTACATTGCCT    86998      T   TGTTGC
                                GGGCA TGTA     TTCTGTG
                                |||||  ||||     |||||||
                                TCCGT ACAT     AAGATAT
                                   T   T_____
GAM260  LOC159148 5'  CTGTGGGAGTGTTGCGAGTGTT 87013       _  TGTT      TG
                                GGCATT GTA    GCTTCTG  G
                                ||||||  |||   |||||||  |
                                TTGTGA CGT    TGAGGGT  C
                                   G   TG__      GT
GAM260  LOC159976 5'  CTGCAGAAATCTCATGTTGTGT 87058      TG   TTGC    TG
           TC                     GGGCAT  TATG    TTCTG  G
                                ||||||  ||||    |||||  |
                                CTTGTG  GTAC    AAGAC  C
                                   TT    TCTA     GT
GAM260  LOC160166 5'  CGCTCAAGGTATGTGTGCCC   87061      _    G   CTTCT TG
                                GGGCAT TGTAT TTG    G  G
                                ||||||  |||||  |||    |  |
                                CCCGTG GTATG AAC    C  C
                                   T    G   T____ GT
GAM260  LOC161038 5'  TCGCAGGAAGGGATGATGTCC  87077       GTAT   G   _
                                GGGCATT    GTT CTTC TGTGG
                                |||||||    |||  ||||  |||||
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                                CCTGTAG    TAG GAAG ACGCT
                                   ____  G   G
GAM260  LOC161357 5'  TCGTGTGATCAAATATAGTGCT 82273          ___  TG TTCTGTGG
          C                     GGCATTGTAT   GT  C
                                ||||||||||  ||  |
                                TCGTGATATA   TA  G
                                     AAC  GT TGCT   G
GAM260  LOC161527 5'  CGTAGGGCTGAAGCAGTGCCT  82275        ATGTT   T   TG
                                GGGCATTGT    GCT CTG  G
                                |||||||||    ||| |||  |
                                TCCGTGACG    CGG GAT  C
                                     AAGT_  _   GT
GAM260  LOC161734 5'  CCACAGAGAAGCTATAGTTCC  87099    C     T   GC
                                GGG ATTGTA GTT  TTCTGTGG
                                ||| |||||| |||  ||||||||
                                CCT TGATAT CGA  GAGACACC
                                  _     _  A_
GAM260  LOC161742 3'  GCAACATATATGCTT       82291        T
                                GGGCAT GTATGTTGC
                                |||||| |||||||||
                                TTCGTA TATACAACG
                                   _
GAM260  LOC161829 5'  TCACATTGGTCTGTGGTGTCT  82320       TG  TGTT   TC
                                GGGCAT  TA    GCT  TGTGG
                                ||||||  ||    |||  |||||
                                TCTGTG  GT    TGG  ACACT
                                    GT  C___   TT
GAM260  LOC162333 5'  TCACAGAATGCCAGCAGTGCCC 87139          A  TT  _
                                GGGCATTGT TG  GC TTCTGTGG
                                ||||||||| ||  || ||||||||
                                CCCGTGACG AC  CG AAGACACT
                                     _ __  T
GAM260  LOC162952 3'  CGTGGGGGCAGAAGAGCTC    82380      A  GTATG      TG
                                GGGC TT     TTGCTTC  TG
                                |||| ||     |||||||  ||
                                CTCG AG     GACGGGG  GC
                                  _  AA___       GT
GAM260  LOC163682 3'  CATGGAGGGAGTGGAGCCC    87025      A TG ATGT G
                                GGGC T  T    T CTTCTGTG
                                |||| |  |    | ||||||||
                                CCCG G  G    A GGAGGTAC
                                  A GT ____  G
GAM260  LOC163782 5'  CTGCAGGAGCAGTGGAACTGCC 82156       _  G   GT       TG
          T                     GGGCA TT TAT  TGCTTCTG  G
                                |||||  || |||  ||||||||  |
                                TCCGT AA GTG  ACGAGGAC  C
                                  C  G   __       GT
GAM260  LOC163882 3'  TTACAGAAATTTGGTGATGCTT 82169        TG ATGTTGC
                                GGGCAT  T      TTCTGTGG
                                ||||||  |      ||||||||
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                                TTCGTA  G      AAGACATT
                                   GT GTTTA__
GAM260   LOC163996 5'  CTATAGAGCCTAGTGATGCTT  82171       TG ATGTT   T
                                GGGCAT  T    GCT CTGTGG
                                ||||||  |    ||| ||||||
                                TTCGTA  G    CGA GATATC
                                   GT ATC__   _
GAM260   LOC164118 5'  CCGTGGAGGCCTTCCTGCAGGC 82172     A    TGTT_    TG
            CC                    GGGC TTGTA    GCTTC  TGG
                                ||||  |||||    |||||  |||
                                CCCG GACGT    CGGAG  GCC
                                  _    CCTTC    GT
GAM260   LOC164173 3'  GCAGCGCTTGCAGTGTTT    82175          __
                                GGGCATTGTA  TGTTGC
                                ||||||||||  ||||||
                                TTTGTGACGT  GCGACG
                                      TC
GAM260   LOC164390 5'  CACAGGAGCTCATTGTTT    82514      TTGT   TT
                                GGGCA   ATG  GCTTCTGTG
                                |||||   |||  |||||||||
                                TTTGT   TAC  CGAGGACAC
                                  _____  T_
GAM260   LOC164397 5'  GGTGACTGGTGGCTACGATGCC 82528         T  TG  TCTGTGG
            T                    GGGCATTGTA GT  CT
                                ||||||||||  ||  ||
                                TCCGTAGCAT CG  GG
                                      _  GT  TCAGTGGT
GAM260   LOC164397 5'  TGGGAGCGGCGTATAAGCCC   82532     A
                                GGGC TTGTATGTTGCTTCTG
                                ||||  ||||||||||||||||
                                CCCG AATATGCGGCGAGGGT
                                  _
GAM260   LOC164582 5'  CTGTGGAAGCCCATGAGATGTC 82543       G    TT      TG
            C                     GGGCATT TATG  GCTTCTG  G
                                |||||||  ||||  |||||||  |
                                CCTGTAG GTAC  CGAAGGT  C
                                    A   C_      GT
GAM260   LOC164582 3'  TGTAGAAGGGTTACAGTGGCC  82545    G      TGTTG     TG
                                GG CATTGTA    CTTCTG  G
                                ||  |||||||    ||||||  |
                                CC GTGACAT    GAAGAT  T
                                 G      TGG__     GT
GAM260   LOC164633 3'  ACCGCATGCGGTGCCC      82548           TGCTTCT
                                GGGCATTGTATGT      GT
                                ||||||||||||      ||
                                CCCGTGGCGTACG      CA
                                      C_______
GAM260   LOC164684 3'  TTGTAGATAATTGCATATGATT 82552     C  TG    TGCT_   TG
            CC                    GGG AT  TATGT    TCTG  G
                                |||  ||  |||||    ||||  |
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                                CCT TA  ATACG    AGAT  T
                                  _ GT    TTAAT   GT
GAM260  LOC164714 5' CGTGGAGGCAGCCGGTG    87228      TAT       TG
                                CATTG  GTTGCTTCTG  G
                                ||||||  ||||||||||  |
                                GTGGC  CGACGGAGGT  C
                                  ____       GT
GAM260  LOC165229 5' CCGTGGAACTGTGCAGTCCC  82475    C      TTGC  TG
                                GGG ATTGTATG   TTC  TGG
                                ||| ||||||||   |||  |||
                                CCC TGACGTGT   AAG  GCC
                                  _      C___  GT
GAM260  LOC165568 5' TGGATGGAGTGACAGGTGGTGT 82500      TG A  TG   TGTGG
           CT                     GGGCAT  T TGT  CTTC
                                ||||||  | |||  ||||
                                TCTGTG  G ACA  GAGG
                                   GT G   GT   TAGGTC
GAM260  LOC165721 5' ACAGCGGCAGTGTCC      82601      TGTATGT   T
                                GGGCAT     TGCT CTGT
                                ||||||     |||| ||||
                                CCTGTG     ACGG GACA
                                   ________   C
GAM260  LOC166793 3' TCACAGAAGCGAAGGCTTGATG 59229      __ ATG
           CT                     GGCATT  GT   TTGCTTCTGTGG
                                ||||||  ||  ||||||||||||
                                TCGTAG  CG   AGCGAAGACACT
                                   TT  GA_
GAM260  LOC166867 5' CGCGGGACCTGCTGTGTCC   82667      T   T   GCTT
                                GGGCAT GTA GTT    CTGTG
                                |||||| ||| |||    |||||
                                CCTGTG CGT CAG    GGCGC
                                   T   C   ____
GAM260  LOC169436 5' CGCACCGGCAGATGGTGCCT   82739      TG ATG    TC  TG
                                GGGCAT  T   TTGCT  TG  G
                                ||||||  |   |||||  ||  |
                                TCCGTG  A   GACGG  AC  C
                                   GT ___     CC  GT
GAM260  LOC169981 5' CTGCGGAGGCAACGGCGAGGTG 82557      GTA_       TG
           TC                     GGCATT    TGTTGCTTCTG  G
                                ||||||    ||||||||||||  |
                                CTGTGG    GCAACGGAGGC  C
                                   AGCG         GT
GAM260  LOC170082 3' CCACAGAGGTGTGGTGACATGT 82558      T  ATGT_
           CC                     GGGCAT GT    TGCTTCTGTGG
                                ||||||  ||    ||||||||||
                                CCTGTA CA     GTGGAGACACC
                                   _ GTGGT
GAM260  LOC196027 3' AATTAATAAGTAATATGTGGGT 87545     A TG       CTGTGG
           CC                     GGGC T  TATGTTGCTT
                                ||||  |  ||||||||||
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                                CCTG G  GTATAATGAA
                                  _ GT        TAATTAAC
GAM260  LOC196027 3'  GCCATAGGAGCATTGGATATAG 87548        GT__
          TG                    CATTGTAT   TGCTTCTGTGG   C
                                ||||||||   ||||||||||  |
                                GTGATATA   ACGAGGATACC   G
                                   GGTT
GAM260  LOC196047 5'  GCCTCCCTGGCAATGGGTGATG 89602       TG A      TCTGT
          CTC                   GGGCAT  T TGTTGCT    GG
                                ||||||  | |||||||    ||
                                CTCGTA  G GTAACGG    CC
                                  GT G      TCCCT  GT
GAM260  LOC196047 3'  TACAGATTAGCAATGTCC    89608         ATGTTGCT
                                GGGCATTGT       TCTGTG
                                |||||||||       ||||||
                                CCTGTAACG       AGACAT
                                   ATT_____
GAM260  LOC196283 3'  GCACTTTCATGGCAGTGCTT   87620         _   T___
                                GGGCATTGT ATG    TGC
                                ||||||||| |||    |||
                                TTCGTGACG TAC    ACG
                                   G   TTTC
GAM260  LOC196411 3'  CCATGCTCAATATATAGTCCT  87669     C         CTTC
                                GGG ATTGTATGTTG    TGTGG
                                ||| ||||||||||    |||||
                                TCC TGATATATAAC    GTACC
                                  _         TC__
GAM260  LOC196872 3'  CACAGGGGGTGGTGCC      87794      TG ATGTTG
                                GGCAT  T     CTTCTGTG
                                |||||  |     ||||||||
                                CCGTG  G     GGGGACAC
                                  GT _______
GAM260  LOC197083 3'  TGCAGAAGCACTTGCGGGTCT  87882      A    T  T      TG
                                GGGC TTGTA GT GCTTCTG  G
                                |||| ||||| || |||||||  |
                                TCTG GGCGT CA CGAAGAC  T
                                  _    T  _      GT
GAM260  LOC197342 3'  TGGGAGGCAGTGCCC       88008         ATGTTG
                                GGGCATTGT     CTTCTG
                                |||||||||     ||||||
                                CCCGTGACG     GAGGGT
                                   _______
GAM260  LOC197414 3'  TCATAGTCACATTCGATGTCT  88071         T    TGCTT
                                GGGCATTG ATGT     CTGTGG
                                |||||||| ||||     ||||||
                                TCTGTAGC TACA     GATACT
                                   T   CT___
GAM260  LOC197423 5'  TCACAGGAGAGATCAATGTCT  77863         TAT  TG
                                GGGCATTG   GT  CTTCTGTGG
                                ||||||||   ||  |||||||||
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                                TCTGTAAC   TA  GAGGACACT
                                    ___  GA
GAM260  LOC199675 3'  TCACAGTGAATGTGGCATGCAT 88268     T     TG TT___
           GCCT                   GCAT GTATGT  C     CTGTGG
                                |||| ||||||  |    ||||||
                                CGTA CGTACG  G    GACACT
                                  _     GT TAAGT
GAM260  LOC199692 3'  AGCTCAATGTAATGCCT     59237          GTT
                                GGGCATTGTAT   GCT
                                ||||||||||   |||
                                TCCGTAATGTA   CGA
                                      ACT
GAM260  LOC199704 3'  CGTGGATTAGGTATAGTGCC   88329         GTTGCT   TG
                                GGCATTGTAT     TCTG  G
                                ||||||||||     ||||  |
                                CCGTGATATG     AGGT  C
                                      GATT__   GT
GAM260  LOC199733 3'  CGGAGCTAATAGTGTTT     89848         ATGTT   T
                                GGGCATTGT    GCT CTG
                                |||||||||    ||| |||
                                TTTGTGATA    CGA GGC
                                     AT___  _
GAM260  LOC199745 3'  CCACGCCTGGGTAGTAGCAGTG 88352         A      C__
           CCT                    GGCATTGT TGTTGCTT   TGTGG
                                |||||||| ||||||||  |||||
                                CCGTGACG ATGATGGG   GCACC
                                   _       TCC
GAM260  LOC199786 3'  TTATAGGAGTGATCCACTATGT 88396       T  AT  TG
           CC                     GGGCAT GT  GT  CTTCTGTGG
                                |||||| ||  ||  |||||||||
                                CCTGTA CA  TA  GAGGATATT
                                   T  CC  GT
GAM260  LOC199858 5'  TGGAAGCTGCTGTCC       88424       TTGTAT  T
                                GGGCA     GT GCTTCTG
                                |||||     || |||||||
                                CCTGT     CG CGAAGGT
                                  _______  T
GAM260  LOC199906 3'  CATGGCCCATGTGATGACT    88476    G   TG    TT   TCT
                                GG CAT  TATG  GCT   GTG
                                || |||  ||||  |||   |||
                                TC GTA  GTAC  CGG   TAC
                                 A   GT    C_   ___
GAM260  LOC199907 3'  GCACCAAATACAGTGTTT    88465          GT__
                                GGGCATTGTAT    TGC
                                ||||||||||    |||
                                TTTGTGACATA    ACG
                                      AACC
GAM260  LOC199958 3'  AGTGAATGCGATGCCT      89882          G TG
                                GGGCATTGTAT T  CT
                                |||||||||| |  ||
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                                TCCGTAGCGTA A  GA
                                      _ GT
GAM260  LOC199986 3'  CAGAAATGCGGTGCTT     89900          GTTGC
                                GGGCATTGTAT    TTCTG
                                ||||||||||    |||||
                                TTCGTGGCGTA    AAGAC
                                      _____
GAM260  LOC199991 5'  TACCTGGAGCTGTGGTGCCC   89915      TG  TGTT    T_  G
                                GGGCAT  TA   GCTTC  GTG
                                ||||||  ||   |||||  |||
                                CCCGTG  GT   CGAGG  CAT
                                   GT ____    TC   G
GAM260  LOC200078 3'  TCACAGCCTGCCATCTGGTGCC 88572       GT   TT  TT_
           T                     GGGCATT  ATG  GC   CTGTGG
                                ||||||  |||  ||   ||||||
                                TCCGTGG  TAC  CG   GACACT
                                    TC   __ TCC
GAM260  LOC200081 3'  GCACATGACAGTGTTT     88564         _   T
                                GGGCATTGT ATGT GC
                                |||||||| |||| ||
                                TTTGTGACA TACA CG
                                     G   _
GAM260  LOC200093 3'  CAGAAGTCAGTGCCC      63087        TATGTT
                                GGGCATTG     GCTTCTG
                                ||||||||     |||||||
                                CCCGTGAC     TGAAGAC
                                      _______
GAM260  LOC200093 3'  CTGCGCCTGCAGCGGCAGTGCC 63094         A     TTC  TG
           C                     GGGCATTGT TGTTGC   TG  G
                                ||||||||| ||||||   ||  |
                                CCCGTGACG GCGACG   GC  C
                                     _     TCC  GT
GAM260  LOC200132 5'  CGCGCCGCGCGCAGTGTCT   88583        TA   T  TTCT
                                GGGCATTG  TGT GC    GTG
                                ||||||||  ||| ||    |||
                                TCTGTGAC  GCG CG    CGC
                                     GC   C ____
GAM260  LOC200138 5'  CCACGGAAGCCACCATGGTTCC 89931     C  TG AT  T
           C                     GGG AT  T  GT GCTTCTGTGG
                                ||| ||  |  || ||||||||||
                                CCC TG  A  CA CGAAGGCACC
                                  T  GT C_  C
GAM260  LOC200169 3'  CTACAGAAATGTGTACATGTGT 89947       _   TG TGC
           TC                     GGGCAT TGTA  T   TTCTGTGG
                                ||||||  ||||  |   ||||||||
                                CTTGTG ACAT  G   AAGACATC
                                   T   GT TA_
GAM260  LOC200205 3'  TGGAAGGCTGTGCCC       88629       T  ATGTTG
                                GGGCAT GT     CTTCTG
                                ||||||  ||     ||||||
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                                CCCGTG CG     GAAGGT
                                   T _______
GAM260  LOC200227 5'  CCATGGAGGCAGGTTTCGGGCC 88642      A   TATG
                T                   GGGC TTG    TTGCTTCTGTGG
                                    |||| |||    ||||||||||||
                                    TCCG GGC    GACGGAGGTACC
                                      _   TTTG
GAM260  LOC200230 3'  CGCAGAGGCAGAGCGTCTC    88649     CAT   ATG       TG
                                    GGG   TGT   TTGCTTCTG  G
                                    |||   |||   |||||||||  |
                                    CTC   GCG   GACGGAGAC  C
                                      T__   A__        GT
GAM260  LOC200312 3'  CCACAGGATCAATGTGGTGCCT 89992       TG AT    C
                                    GGGCAT  T  GTTG TTCTGTGG
                                    ||||||  |  |||| ||||||||
                                    TCCGTG  G  TAAC AGGACACC
                                       GT __    T
GAM260  LOC200317 3'  CGTGGAGGCAGCTAGCTC    88793     ATTGTAT      TG
                                    GGGC      GTTGCTTC  TG
                                    ||||      ||||||||  ||
                                    CTCG      CGACGGAG  GC
                                      AT_____       GT
GAM260  LOC200720 5'  CATGGGGGTATGACTGCCT    90110      TT  ATGT
                                    GGGCA  GT    TGCTTCTGTG
                                    |||||  ||    ||||||||||
                                    TCCGT  CA    ATGGGGGTAC
                                      __  GT__
GAM260  LOC200904 5'  CGCAGGGGCTTGAAATGTCC   90187       GTATGTT     TG
                                    GGGCATT      GCTTCTG  G
                                    |||||||      |||||||  |
                                    CCTGTAA      CGGGGAC  C
                                       AGTT___      GT
GAM260  LOC201175 5'  CACAGGTGGGCAATGCCT    88134         ATG TG TT
                                    GGGCATTGT   T  C  CTGTG
                                    |||||||||   |  |  |||||
                                    TCCGTAACG   G  G  GACAC
                                         ___ GT __
GAM260  LOC201194 3'  CCACAGGAGAAGCTGGTGCCT  89776         TAT   G
                                    GGGCATTG   GTT CTTCTGTGG
                                    ||||||||   ||| |||||||||
                                    TCCGTGGT   CGA GAGGACACC
                                         ___   A
GAM260  LOC201229 3'  TGGAAGCTCGTGTGTCT     88147       TGT   TT
                                    GGGCAT   ATG  GCTTCTG
                                    ||||||   |||  |||||||
                                    TCTGTG   TGC  CGAAGGT
                                       ___   T_
GAM260  LOC201287 3'  CGCAGAAGTAGCAGCTGCT    88181      TT  A         TG
                                    GGCA  GT TGTTGCTTCTG  G
                                    ||||  || ||||||||||  |
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                                TCGT  CG ACGATGAAGAC  C
                                  __  _         GT
GAM260  LOC201287 5'  CTACCTCTCAAATATATATGTC 88182       T      GCTTCT
            C                      GGGCAT GTATGTT      GTGG
                                   |||||| |||||||      ||||
                                   CCTGTA TATATAA      CATC
                                     _       ACTCTC
GAM260  LOC201292 5'  CGTGGAGGCCCCAGGTCC    88185      A   TATGTT    TG
                                   GGGC TTG     GCTTC  TG
                                   |||| |||     |||||  ||
                                   CCTG GAC     CGGAG  GC
                                     _  CC____    GT
GAM260  LOC201305 3'  ACAGCAGCAGTGCCT       88234       TGTATGT   T
                                   GGGCAT      TGCT CTGT
                                   ||||||      |||| ||||
                                   TCCGTG      ACGA GACA
                                     ________   C
GAM260  LOC201324 3'  ACGGAGGCCCGTGTCC      68559       TGTATGTT
                                   GGGCAT      GCTTCTGT
                                   ||||||      ||||||||
                                   CCTGTG      CGGAGGCA
                                      CC_______
GAM260  LOC201475 5'  TTGCATTGGAATGTGATGGTGC 88247       TG _    G  TC  TG
            TC                     GGGCAT  T ATGTT CT  TG  G
                                   ||||||  | ||||| ||  ||  |
                                   CTCGTG  A TGTAA GG  AC  T
                                      GT G    _ TT  GT
GAM260  LOC201626 5'  TTGCAGGAGGTTGACCGCGCAG 89000       AT_   G__     TG
            TGTTT                   CATTGT   GTT   CTTCTG  G
                                   ||||||   |||   ||||||  |
                                   GTGACG   CAG   GAGGAC  T
                                      CGC   TTG     GT
GAM260  LOC201627 3'  GCTTTAAGGGTATTATGTAATG 89021           T    TC  TGG
            CCT                      GGGCATTGTATG TGCT  TG
                                   ||||||||||||| ||||  ||
                                   TCCGTAATGTAT ATGG  AT
                                         T    GA  TTCGT
GAM260  LOC201696 3'  CAGGAGACAGGCCC        63131      A    ATGTTG
                                   GGGC TTGT     CTTCTG
                                   |||| ||||     ||||||
                                   CCCG GACA     GAGGAC
                                     _   _______
GAM260  LOC201799 3'  GATCAACATGTGTTGCCT    89061       T GT     CT
                                   GGGCA T  ATGTTG  TC
                                   ||||| |  ||||||  ||
                                   TCCGT G  TACAAC  AG
                                      T TG     T_
GAM260  LOC201910 3'  AGTGGCATGGTAGTGTTC    89097          _    TG
                                   GGGCATTGT ATGT  CT
                                   |||||||| ||||  ||
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                                CTTGTGATG TACG  GA
                                     G    GT
GAM260   LOC201952 3'  CTAAAAAGTAATGTTTAATGTT 90272         T        CTGTGG
                T                    GGGCATTG ATGTTGCTT
                                     |||||||| |||||||||
                                     TTTGTAAT TGTAATGAA
                                          T        AAATC
GAM260   LOC202025 5'  CACGGAACTTGCAGTTCC    90282     C     T  TGCT
                                     GGG ATTGTA GT    TCTGTG
                                     ||| |||||| ||    ||||||
                                     CCT TGACGT CA    AGGCAC
                                       _      T _____
GAM260   LOC202052 3'  TAGGGGACAACTGCTC      90311       TTGTAT    _
                                     GGGCA     GTTG CTTCTG
                                     |||||     |||| ||||||
                                     CTCGT     CAAC GGGGAT
                                       _______    A
GAM260   LOC202754 3'  CTGTGGAAGTGGCAATGGCAGA 82705    A_    A__   TG     TG
                AGCCC                     C  TTGT   TGT  CTTCTG  G
                                     |  ||||   |||  ||||||  |
                                     G  GACG   ACG  GAAGGT  C
                                      AA    GTA   GT     GT
GAM260   LOC202868 5'  CCACAGACCACTGCATGGTGCT 90371       TG     TGCT_
                T                    GGGCAT  TATGT     TCTGTGG
                                     ||||||  |||||     |||||||
                                     TTCGTG  GTACG     AGACACC
                                        __     TCACC
GAM260   LOC202934 5'  CATGGAGGCAGGTATTTCC    90407    CATT    G
                                     GG    GTAT TTGCTTCTGTG
                                     ||    |||| ||||||||||
                                     CC    TATG GACGGAGGTAC
                                      TT__    _
GAM260   LOC202934 3'  CCACAGGAGTGGAGCTGTGGCC 90408    G   T  ATG TG
                                     GG CAT GT   T  CTTCTGTGG
                                     || ||| ||   |  |||||||||
                                     CC GTG CG   G  GAGGACACC
                                      G   T  A__ GT
GAM260   LOC202934 5'  GGTAACAGTTGTAATGTCT    90424        TA__
                                     GGGCATTG    TGTTGCT
                                     ||||||||    |||||||
                                     TCTGTAAT    ACAATGG
                                          GTTG
GAM260   LOC202934 3'  TTATAGCTGTATCTACAGTGTT 90435          TGT   TT
                C                    GGGCATTGTA   TGC  CTGTGG
                                     ||||||||||   |||  ||||||
                                     CTTGTGACAT   ATG  GATATT
                                           CT_   TC
GAM260   LOC202986 5'  CGCCTAGGTATGCAATCCT    90441     C      GTT    CT
                                     GGG ATTGTAT   GCTT  GTG
                                     ||| |||||||   ||||  |||
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                                TCC TAACGTA   TGGA  CGC
                                  _     ___    TC
GAM260   LOC203069 5'  CAGAAGCAGCTGTC       89258      TTGTAT
                                GGCA     GTTGCTTCTG
                                ||||     ||||||||||
                                CTGT     CGACGAAGAC
                                  _______
GAM260   LOC203197 5'  GGGCGGCATATGATGCT     89293       TG
                                GGCAT  TATGTTGCTT
                                |||||  ||||||||||
                                TCGTA  ATACGGCGGG
                                   GT
GAM260   LOC203276 3'  CCACACAAGGGTATGCAAAGCT 90481      A      TTG   C
            T                    GGGC TTGTATG   CTT TGTGG
                                |||| |||||||   ||| |||||
                                TTCG AACGTAT   GAA ACACC
                                   A      GG_   C
GAM260   LOC203286 3'  CCACAGAAGTGAGGAGTGGCC  90494    G    GTATG TG
                                GG CATT     T  CTTCTGTGG
                                || ||||     |  |||||||||
                                CC GTGA     A  GAAGACACC
                                 G    GG___ GT
GAM260   LOC203286 3'  TACAGGGGGATAGTAGCCC    90502      ATTGTA    G
                                GGGC      TGTT CTTCTGTG
                                ||||      |||| ||||||||
                                CCCG      ATAG GGGGACAT
                                   ATG___    _
GAM260   LOC203305 3'  CCACACAAGGGTATGCAAAGCT 90525      A      TTG   C
            T                    GGGC TTGTATG   CTT TGTGG
                                |||| |||||||   ||| |||||
                                TTCG AACGTAT   GAA ACACC
                                   A      GG_   C
GAM260   LOC203369 3'  CTATGAAGACAGTATATAAGCT 89339      A        _    T
            T                    GGGC TTGTATGTTG CTTC GTGG
                                |||| ||||||||| |||| ||||
                                TTCG AATATATGAC GAAG TATC
                                   _         A    _
GAM260   LOC203377 5'  CCACAGAGGAGGGTGTGAAGCC 90580      A TG   G  G
            T                    GGGC T  TAT TT CTTCTGTGG
                                |||| |  ||| || |||||||||
                                TCCG A  GTG GA GGAGACACC
                                   A GT   G  _
GAM260   LOC203378 3'  CTGCAGAAGTTATCCAGTTGCT 90601      _  T   TT      TG
            C                    GGGCA TTG ATG  GCTTCTG  G
                                ||||| ||| |||  |||||||  |
                                CTCGT GAC TAT  TGAAGAC  C
                                   T   C  __      GT
GAM260   LOC203378 3'  TTGCCTTTCTCAGCAGGCAATG 90621         A    CTTCT_ TG
            CCT                    GGGCATTGT TGTTG     G  G
                                |||||||| |||||     |  |
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                                TCCGTAACG ACGAC     C  T
                                     G    TCTTTC GT
GAM260  LOC203447 3'  CAATGGTGTACAATGTCT    89368          GTT   TCTG
                                GGGCATTGTAT   GCT    TG
                                ||||||||||   |||    ||
                                TCTGTAACATG   TGG    AC
                                      ___   TA__
GAM260  LOC203504 5'  TCACAGGGGTGGGGGTGCCC   90642        GTATG TG
                                GGGCATT    T  CTTCTGTGG
                                |||||||    |  |||||||||
                                CCCGTGG    G  GGGGACACT
                                   G____ GT
GAM260  LOC203523 3'  TAACAAATAGTTTATAATGTCC 89377          TGTT   TC_   GG
                                GGGCATTGTA    GCT   TGT
                                ||||||||||    |||   |||
                                CCTGTAATAT    TGA   ACA
                                      T___    TAA   ATA
GAM260  LOC203536 3'  TCAGGAGTGGTGATGTCTGATG 89381      GT    ___      TGG
           CTC                    GCATT  ATGTT   GCTTCTG
                                |||||  |||||   |||||||
                                CGTAG  TGTAG   TGAGGAC
                                   TC     TGG      T
GAM260  LOC204962 5'  CCGTGTTGCTAAACCTACAGTG 89405         T   __  TTCTG
           CCC                    GGCATTGTA GTT  GC     TGG
                                |||||||||  |||  ||     |||
                                CCGTGACAT CAA  CG     GCC
                                     C   AT  TTGT_
GAM260  LOC204970 3'  CGCTTCGGCATGTGGGGCTC   89408     A TG      CTTCT TG
                                GGGC T  TATGTTG    G  G
                                ||||  |  |||||||    |  |
                                CTCG G  GTACGGC    C  C
                                  G GT      TT___ GT
GAM260  LOC205011 3'  CGCAGGAGGTACAGCAAGTCC  90652     A    A   TG     TG
                                GGGC TTGT TGT  CTTCTG  G
                                |||| |||| |||  ||||||  |
                                CCTG AACG ACA  GAGGAC  C
                                  _    _   TG     GT
GAM260  LOC205795 5'  GGTGGCATGCAGAGCTC     90707      A       TG
                                GGGC TTGTATGT  CT
                                |||| ||||||||  ||
                                CTCG GACGTACG  GG
                                  A       GT
GAM260  LOC206426 3'  TCATAAATGGGCATTAGTGCCT 89537         T    GCTTC
                                GGGCATTG ATGTT    TGTGG
                                ||||||||  |||||    |||||
                                TCCGTGAT TACGG    ATACT
                                     _    GTAA_
GAM260  LOC206887 5'  CGCAGAGGTTCCAGTTC     89545      ATTGTA  TT
                                GGGC     TG  GCTTCTGTG
                                ||||     ||  |||||||||
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                                CTTG     AC  TGGAGACGC
                                  _______ CT
GAM260  LOC219347 5'  TCATGGCTCAACTGTGATGCCT 92986      TG  T   CTT
                                GGGCAT  TA GTTG   CTGTGG
                                ||||||  || ||||   ||||||
                                TCCGTA  GT CAAC   GGTACT
                                   GT  _   TC_
GAM260  LOC219513 5'  TCGTGGGGTGCTGCAATGTTC  94334        TGTT  _  TG
                                GGGCATTGTA    GC TTC  TGG
                                ||||||||||    || |||  |||
                                CTTGTAACGT    CG GGG  GCT
                                      ____  T   GT
GAM260  LOC219649 5'  TCATGGGGGTTCTCCTGGGCTC 92962     ATTGTATGTT
                                GGGC        GCTTCTGTGG
                                ||||        ||||||||||
                                CTCG        TGGGGGTACT
                                  GGTCCTCT__
GAM260  LOC219653 3'  CCATGGCTTGTTCATACAAT   91291       TT  TT_
                                ATTGTATG  GC   CTGTGG
                                ||||||||  ||   ||||||
                                TAACATAC  TG   GGTACC
                                    T_  TTC
GAM260  LOC219688 5'  CAGAAGCTGGTGCGCC     93050     ATT   GTT
                                GGC   GTAT   GCTTCTG
                                |||   ||||   |||||||
                                CCG   CGTG   CGAAGAC
                                  ___   GT_
GAM260  LOC219731 5'  TTACAGGAGTGAGCCACCATGT 93100      T  ATG TG
           CT                    GGGCAT GT   T  CTTCTGTGG
                                ||||||  ||   |  |||||||||
                                TCTGTA CA   A  GAGGACATT
                                   C  CCG GT
GAM260  LOC219843 3'  TACGTGAGCGTATAATCCC   91508     C      GTT   C
                                GGG ATTGTAT   GCTT TGTG
                                ||| |||||||   |||| ||||
                                CCC TAATATG   CGAG GCAT
                                  _     ___    T
GAM260  LOC219899 3'  CATAGAAGTATAACTGCCC   91500      TT  ATGT
                                GGGCA  GT    TGCTTCTGTG
                                |||||  ||   ||||||||||
                                CCCGT  CA    ATGAAGATAC
                                  __  AT__
GAM260  LOC219899 3'  CCACATTTCCAGTGTATGTGCC 91501       T   TG   CTTC
           C                     GGGCAT GTA  TTG    TGTGG
                                ||||||  |||  |||    |||||
                                CCCGTG TAT  GAC    ACACC
                                   _  GT   CTTT
GAM260  LOC219899 3'  CTACAGGAGTTACCAGAGTTT  91503      A   TAT  T
                                GGGC TTG   GT GCTTCTGTGG
                                ||||  |||   ||  ||||||||||
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                                TTTG GAC   CA TGAGGACATC
                                  A  ___  T
GAM260  LOC219918 5'  CACCCGGCATACAAGCTT    91539     A       CTTCT
                                GGGC TTGTATGTTG    GTG
                                |||| ||||||||||    |||
                                TTCG AACATACGGC    CAC
                                  _        C____
GAM260  LOC219919 5'  CGCAGGGGCTTGAAATGTCC   93292       GTATGTT     TG
                                GGGCATT      GCTTCTG  G
                                |||||||      |||||||  |
                                CCTGTAA      CGGGGAC  C
                                   AGTT___      GT
GAM260  LOC219942 3'  TTATGGGGGCGGGAAATGGCGG 93351       ATG___
          TGCCC                   CATTGT     TTGCTTCTGTGG
                                |||||||    ||||||||||||
                                GTGGCG     GGCGGGGGTATT
                                   GTAAAG
GAM260  LOC220001 5'  CTGTGGGAGTGGCATCTGCATC 91634     AT  __   TG     TG
          GCTC                    GGC  TGT  ATGT  CTTCTG  G
                                |||  |||  ||||  ||||||  |
                                TCG  ACG  TACG  GAGGGT  C
                                  CT   TC    GT     GT
GAM260  LOC220021 3'  CTGCAGTCCAGGCATGTAGGCC 93394      A       GCTT   TG
          T                     GGGC TTGTATGTT    CTG  G
                                |||| |||||||||    |||  |
                                TCCG GATGTACGG    GAC  C
                                  _       ACCT   GT
GAM260  LOC220045 5'  TTACAGTGAGAACTTATGGTGC 93414       TG  T   G  _
          TT                     GGGCAT  TA GTT CTT CTGTGG
                                ||||||  || ||| ||| ||||||
                                TTCGTG  AT CAA GAG GACATT
                                   GT  T   _   T
GAM260  LOC220071 5'  CGCCCGGCATACAAGCTT    93435     A       CTTCT
                                GGGC TTGTATGTTG    GTG
                                |||| ||||||||||    |||
                                TTCG AACATACGGC    CGC
                                  _        C____
GAM260  LOC220143 5'  CTGCAGACAGGCCCATGGTGAT 93587     TG _  TT  __   TG
          GCTC                    GCAT  T ATG  GCT  TCTG  G
                                ||||  | |||  |||  ||||  |
                                CGTA  G TAC  CGG  AGAC  C
                                  GT G   C_   AC    GT
GAM260  LOC220370 3'  TGCAGAAGCAGTGAAGCC    92836     A TG ATGT      TG
                                GGC T  T    TGCTTCTG  G
                                ||| |  |    ||||||||  |
                                CCG A  G    ACGAAGAC  T
                                  A GT ____       GT
GAM260  LOC220513 3'  CTGTGGAAGTTTAGTAAATGTC 60449       G   GTT     TG
          T                     GGGCATT TAT   GCTTCTG  G
                                |||||||  |||   |||||||  |
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                                TCTGTAA ATG   TGAAGGT  C
                                   _  ATT      GT
GAM260   LOC220522 3'  TCGCAGAGGACGGCAGTGCT   60524        ATGTTG
                                GGCATTGT     CTTCTGTGG
                                ||||||||     |||||||||
                                TCGTGACG     GGAGACGCT
                                   GCA___
GAM260   LOC220549 5'  CATCAGGCGGTAATGCCT    92916        TATG     CT
                                GGGCATTG    TTGCTT  GTG
                                ||||||||    ||||||  |||
                                TCCGTAAT    GGCGGA  TAC
                                   _____     C_
GAM260   LOC220565 5'  TCACAGGAGAGATCGATGTCT  90756        TAT  TG
                                GGGCATTG   GT  CTTCTGTGG
                                ||||||||   ||  |||||||||
                                TCTGTAGC   TA  GAGGACACT
                                   ___  GA
GAM260   LOC220565 3'  CTGCTTCGTAACATGTGAAGTC 90750      A TG       TTCT TG
            C                    GGGC T  TATGTTGC    G  G
                                ||||  |  ||||||||    |  |
                                CCTG A  GTACAATG    C  C
                                  A GT       CTT_ GT
GAM260   LOC220717 5'  TCGTGGAAGTGACATCGTCT   90777      ATT T    TG    TG
                                GGGC   G ATGT  CTTC  TGG
                                ||||   | ||||  ||||  |||
                                TCTG   C TACA  GAAG  GCT
                                  ___ _    GT    GT
GAM260   LOC220739 3'  CAGGGCAGACAGTGCCT     92926        ATG     T
                                GGGCATTGT   TTGCT CTG
                                |||||||||   ||||| |||
                                TCCGTGACA   GACGG GAC
                                   ___     _
GAM260   LOC220753 3'  TAGAGGTGGGCAGTCC      92944      AT   ATG TG
                                GGGC  TGT   T  CTTCTG
                                ||||  |||   |  ||||||
                                CCTG  ACG   G  GGAGAT
                                  __   ___ GT
GAM260   LOC220753 3'  TCAGTCTTGCAGTATACAAGCT 92945      A         TT__   TGG
            T                    GGGC TTGTATGTTGC    CTG
                                ||||  ||||||||||    |||
                                TTCG AACATATGACG    GAC
                                  _         TTCT   T
GAM260   LOC220758 3'  CACAGAGGAGGTGGTCCT    90783     C  TG ATGTTG
                                GGG AT  T     CTTCTGTG
                                ||| ||  |     ||||||||
                                TCC TG  G     GGAGACAC
                                  _  GT GA_____
GAM260   LOC220766 5'  TCACAGAGGGGGGCATGGTGTT 90800        TG     G  _
            C                    GGGCAT  TATGTT CT TCTGTGG
                                ||||||  |||||| ||  |||||||
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                                CTTGTG  GTACGG GG AGACACT
                                   __     G  G
GAM260   LOC220827 3'  CGTGGAATGTAGCTGCCC    91241      TTGTAT    _  TG
                                GGGCA     GTTGC TTC  TG
                                |||||     ||||| |||  ||
                                CCCGT     CGATG AAG  GC
                                   _______    T   GT
GAM260   LOC220883 3'  TCACCTGTGGGCAGTGGGCAGT 91265        A GT    CT__
           GTCT                    GGCATTGT T  TGCTT    GTGG
                                |||||||| |  |||||    ||||
                                CTGTGACG G  ACGGG    CACT
                                     G TG    TGTC
GAM260   LOC220883 3'  TTGCAGATGCCAAAATAATGTC 91266        ATGTT  T    TG
           C                     GGGCATTGT    GC TCTG  G
                                |||||||||    || ||||  |
                                CCTGTAATA    CG AGAC  T
                                     AAAC_  T    GT
GAM260   LOC220980 3'  CCACTCTCCAGGCAGATAGTGC 93149        A    GCTTCT
           CC                    GGGCATTGT TGTT     GTGG
                                |||||||||  ||||     ||||
                                CCCGTGATA ACGG     CACC
                                     G    ACCTCT
GAM260   LOC220988 3'  CCACAGAAGGAACGATGATCC  90846    C  TG A    G
                                GG AT  T TGTT CTTCTGTGG
                                || ||  | |||| |||||||||
                                CC TA  A GCAA GAAGACACC
                                 _  GT _    G
GAM260   LOC221035 3'  TCAGCCTTTGTGATGTACTGTG 93171      T     TG TT___   TGG
           TTT                   GCAT GTATGT  C     CTG
                                |||| ||||||  |    |||
                                TGTG CATGTA  G     GAC
                                  T     GT TTTCC   T
GAM260   LOC221042 5'  CCACGGGGGTGTCCCGGCAGGT 93182      A    ATGT_
           CT                    GGGC TTGT    TGCTTCTGTGG
                                |||| ||||    ||||||||||
                                TCTG GACG    GTGGGGGCACC
                                  _    GCCCT
GAM260   LOC221042 3'  TCACAGAGGTGGCCTTGGAGTC 93191      A   TAT  TG
           T                     GGGC TTG   GT  CTTCTGTGG
                                |||| |||   ||  |||||||||
                                TCTG GGT   CG  GGAGACACT
                                  A   TC_  GT
GAM260   LOC221143 3'  AGGTAACATATGATTTCC    93562     C  TG
                                GGG AT  TATGTTGCTT
                                ||| ||  ||||||||||
                                CCT TA  ATACAATGGA
                                  T  GT
GAM260   LOC221271 3'  TGTCTCAAGTAAAATACAGTGT 91883          G     CTGTGG
           CT                    GGGCATTGTAT TTGCTT
                                ||||||||||| ||||||
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                                TCTGTGACATA AATGAA
                                      A     CTCTGTT
GAM260   LOC221297 5'  CACAGCCGTAACAGTGCCT   91839       TGTA     TT
                                GGGCAT   TGTTGC  CTGTG
                                ||||||   ||||||  |||||
                                TCCGTG   ACAATG  GACAC
                                   ____     CC
GAM260   LOC221302 5'  CCGTGGGAGTAAGGAAGTGCTT 59004        GTATG      TG
                                GGGCATT    TTGCTTC  TGG
                                |||||||    |||||||  |||
                                TTCGTGA    AATGAGG  GCC
                                   AGG__      GT
GAM260   LOC221410 3'  CACAGAGGATAGCAAGCTC   92057      A   ATGTTG
                                GGGC TTGT     CTTCTGTG
                                |||| ||||     ||||||||
                                CTCG AACG     GGAGACAC
                                  _   ATA___
GAM260   LOC221454 5'  TTCAGGGCAGCAGTGGTGTCT  92302       TG A      T   TGG
                                GGGCAT  T TGTTGCT CTG
                                ||||||  | ||||||| |||
                                TCTGTG  G ACGACGG GAC
                                   GT _      _  TTG
GAM260   LOC221466 5'  CCATGGTGTGTCAGTGTCT   93684        T  GTT  TT
                                GGGCATTG AT   GC  CTGTGG
                                |||||||| ||   ||  ||||||
                                TCTGTGAC TG   TG  GGTACC
                                   _ ___  T_     G
GAM260   LOC221474 5'  CTGCAGGGGCAGCCCCGCGTTC 92380     CAT   AT_       TG
            CT                   GGG   TGT   GTTGCTTCTG  G
                                |||   |||   ||||||||||  |
                                TCC   GCG   CGACGGGGAC  C
                                  TT_   CCC        GT
GAM260   LOC221486 5'  CCGGGACAGTGTTGTACAGTGT 91009           TT  _   G
            TT                   GGGCATTGTATG  GCT TCT TGG
                                ||||||||||||  ||| ||| |||
                                TTTGTGACATGT  TGA AGG GCC
                                      TG   C  _
GAM260   LOC221495 3'  TAGGAGCACAGGCTT      93863      A   ATGTT
                                GGGC TTGT    GCTTCTG
                                |||| ||||    |||||||
                                TTCG GACA    CGAGGAT
                                  _   ______
GAM260   LOC221496 3'  CGCAGGAAAATGTGGGCTT   91998      A TG   GTTGC
                                GGGC T  TAT    TTCTGTG
                                |||| |  |||    |||||||
                                TTCG G  GTA    AGGACGC
                                  _ GT   AA___
GAM260   LOC221528 5'  TGGCAAGTGATGTGTGAGTCC  92092      A TG    TG  _
                                GGGC T  TATGT  CTT CTG
                                |||| |  |||||  ||| |||
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                                CCTG A  GTGTA  GAA GGT
                                  _ GT    GT   C
GAM260   LOC221543 3'  CTACAGAGGAAAAGTCAATGCC 93738        T  GTTG
           T                     GGGCATTG AT    CTTCTGTGG
                                 |||||||| ||    |||||||||
                                 TCCGTAAC TG    GGAGACATC
                                    _  AAAA
GAM260   LOC221560 3'  CAGAGTGGCATGGCAATGCCC  93773         _    TG  T
                                 GGGCATTGT ATGT  CT CTG
                                 ||||||||| ||||  || |||
                                 CCCGTAACG TACG  GA GAC
                                      G    GT  _
GAM260   LOC221600 5'  CAATCAGCATGCTGTGTCT    91005       T       CTTCTG
                                 GGGCAT GTATGTTG      TG
                                 |||||| ||||||||      ||
                                 TCTGTG CGTACGAC      AC
                                    T       TA____
GAM260   LOC221688 3'  CCACCCTAACATGCAATCTT   93678     C         CTTCT
                                 GGG ATTGTATGTTG     GTGG
                                 ||| ||||||||||     ||||
                                 TTC TAACGTACAAT     CACC
                                  _          CC___
GAM260   LOC221747 5'  TAGAATGATGACAATGCTT    92356         A     C
                                 GGGCATTGT TGTTG TTCTG
                                 ||||||||| ||||| |||||
                                 TTCGTAACA GTAGT AAGAT
                                           _    _
GAM260   LOC221749 5'  CGCGGAGGCGGCGGGGGC    92004     ATTGTA         TG
                                 GC     TGTTGCTTCTG  G
                                 ||     ||||||||||  |
                                 CG     GCGGCGGAGGC  C
                                  GGG___          GT
GAM260   LOC221756 3'  AGCAGCGTAGAATGTTC     92135        G
                                 GGGCATT TATGTTGCT
                                 ||||||| |||||||||
                                 CTTGTAA ATGCGACGA
                                     G
GAM260   LOC221822 5'  TTGATTCCTCAGCAGCAGTGTC 92871         A     CT___  TGTGG
           C                     GGCATTGT TGTTG     TC
                                 |||||||| |||||     ||
                                 CTGTGACG ACGAC     AG
                                    _     TCCTT  TT
GAM260   LOC221922 5'  CGGGAGGGGCAGCATCATGGTG 92692        TG _         GTGG
           CTC                     GGGCAT  T ATGTTGCTTCT
                                 ||||||  | ||||||||||
                                 CTCGTG  A TACGACGGGGA
                                    GT C          GGGCT
GAM260   LOC221935 3'  CCACAGGGATGGGTGTGCAGAG 92619      A     TG  GC_
           CTC                     GGGC TTGTA  TT   TTCTGTGG
                                 |||| |||||  ||   ||||||||
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                                CTCG GACGT  GG   GGGACACC
                                  A    GT  GTA
GAM260   LOC222166 3'  GGTAGCCTGTGGTGTCC     94098       TG  T
                                GGGCAT  TA GTTGCT
                                ||||||  || ||||||
                                CCTGTG  GT CGATGG
                                   GT  C
GAM260   LOC222174 3'  CAGTTCAAATACAATGTTC    94115          G   CTT
                                GGGCATTGTAT TTG   CTG
                                |||||||||||| |||   |||
                                CTTGTAACATA AAC   GAC
                                      _  TT_
GAM260   LOC222234 3'  CATAGGAGTGATGGCCC     94244      ATTGTA   TG
                                GGGC     TGT  CTTCTGTG
                                ||||     |||  ||||||||
                                CCCG     GTA  GAGGATAC
                                  _______  GT
GAM260   LOC222368 5'  TCATGGAGGTGATGACATCAGT 92820       T    ___
            GC                    GCATTG ATGTT   GCTTCTGTGG
                                ||||||| |||||   ||||||||||
                                CGTGAC TACAG   TGGAGGTACT
                                   _    TAG
GAM260   LOC222444 5'  CCGCAGGGGCAGCGGGGTCT   94343      ATTGTA
                                GGGC     TGTTGCTTCTGTGG
                                ||||     ||||||||||||||
                                TCTG     GCGACGGGGACGCC
                                  GG____
GAM260   LOC222709 5'  CTACGGGGTGCGGATAGTGCTC 92857          ATG   _
                                GGGCATTGT   TTGC TTCTGTGG
                                |||||||||   |||| ||||||||
                                CTCGTGATA   GGCG GGGGCATC
                                     ___   T
GAM260   LOC222999 5'  ATGGAAGTTGCTGCCC      94368       TTGTAT  T
                                GGGCA     GT GCTTCTGT
                                |||||     || ||||||||
                                CCCGT     CG TGAAGGTA
                                  _______ T
GAM260   LOC245757 3'  ATGGGAGGTCATGCCT      90774       TTGTA  TTG
                                GGGCA    TG   CTTCTGT
                                |||||    ||   |||||||
                                TCCGT    AC   GAGGGTA
                                  ______ TG_
GAM260   LOC245771 5'  CTGCGCTACCAGCGTCTGGTGC 92890        GT     CTTC  TG
            CC                    GGGCATT  ATGTTG    TG  G
                                ||||||| ||||||   ||  |
                                CCCGTGG  TGCGAC    GC  C
                                   TC     CATC  GT
GAM260   LOC253069 3'  CACAGGAGCTGTGATCTT    95710     C  TG  TGTT
                                GGG AT  TA    GCTTCTGTG
                                ||| ||  ||    |||||||||
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                                TTC TA  GT    CGAGGACAC
                                  _ GT  _____
GAM260   LOC253187 5'  CGTGGGGGCTATACAGTTCC   97115     C       TT      TG
                                GGG ATTGTATG  GCTTCTG  G
                                ||| ||||||||  |||||||  |
                                CCT TGACATAT  CGGGGGT  C
                                  _       __      GT
GAM260   LOC253187 5'  TCACAGCCCTATATCAGTGCTC 97117         T    TGCTT
                                GGGCATTG ATGT     CTGTGG
                                |||||||| ||||     ||||||
                                CTCGTGAC TATA     GACACT
                                     _   TCCC_
GAM260   LOC253254 3'  GCAAAACATATACTGTCT    97121       T      __
                                GGGCA TGTATGT  TGC
                                ||||| |||||||  |||
                                TCTGT ATATACA  ACG
                                   C       AA
GAM260   LOC253258 3'  CTACGGGGGCTTAGCAGGTGTC 96473        GTA  TT
           C                     GGGCATT   TG  GCTTCTGTGG
                                 |||||||   ||  ||||||||||
                                 CCTGTGG   AT  CGGGGGCATC
                                     ACG  T_
GAM260   LOC253392 5'  TCGCAGGCTTGGGATGGTGTTC 96451       TG ATGTT  TT
                                GGGCAT  T     GC  CTGTGG
                                ||||||  |     ||  ||||||
                                CTTGTG  A     CG  GACGCT
                                    GT GGGTT  __
GAM260   LOC253594 5'  GGGACCTGGGGCAGCATTTGAT 95481        T        T_  GG
           GTCT                     GGCATTG ATGTTGCTTC  GT
                                    |||||||  ||||||||||  ||
                                    CTGTAGT  TACGACGGGG  CA
                                        T         TC  GGGC
GAM260   LOC253681 3'  CTGTGTTGCTGACTACAGTGTC 95130          T  _  TTCTGTGG
           T                        GGGCATTGTA GTT GC
                                    ||||||||||  |||  ||
                                    TCTGTGACAT  CAG  CG
                                          _   T  TTGTGTC
GAM260   LOC253681 3'  TACAGTGTCTGTGATGTCC    95135       TG  TGTT  TT
                                GGGCAT  TA    GC  CTGTG
                                ||||||  ||    ||  |||||
                                CCTGTA  GT    TG  GACAT
                                    GT  C___  T_
GAM260   LOC253842 5'  CTACATTGAAACATGCAAGCCT 97386      A        GCTTC
                                GGGC TTGTATGTT     TGTGG
                                ||||  |||||||||     |||||
                                TCCG  AACGTACAA     ACATC
                                  _        AGTT_
GAM260   LOC253890 5'  CGCAGACTTGTCCAGTGCTC   95677        T   TTGCT    TG
                                GGGCATTG ATG     TCTG  G
                                |||||||| |||     ||||  |
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                                CTCGTGAC TGT    AGAC  C
                                    C   TC___   GT
GAM260   LOC253955 3'  CACGGCCCCAACGATGCTT   94423        A  TT   TCT
                                GGGCATTGT TG  GCT   GTG
                                ||||||||| ||  |||   |||
                                TTCGTAGCA AC  CGG   CAC
                                    _  CC   ___
GAM260   LOC254085 3'  TCATAGAAGCTTTGTCAGGCTT 96120     A   T   TT
                                GGGC TTG ATG  GCTTCTGTGG
                                |||| ||| |||  ||||||||||
                                TTCG GAC TGT  CGAAGATACT
                                  _  _  TT
GAM260   LOC254122 5'  CTGCGGGAGCACGCGGGCAGTG 94752    G     A  _      TG
            GCC                   GG CATTGT TGT TGCTTCTG  G
                                || ||||||| ||| ||||||||  |
                                CC GTGACG GCG ACGAGGGC  C
                                 G     G  C       GT
GAM260   LOC254182 3'  CGCAGAAGCATCCAGAGCCT   96034     A   TATGT      TG
                                GGGC TTG    TGCTTCTG  G
                                |||| |||    ||||||||  |
                                TCCG GAC    ACGAAGAC  C
                                  A  CT___      GT
GAM260   LOC254191 5'  TCACAGAGGGAGTGATAGCTT  94768     _  TG ATGT G
                                GGGC AT  T    T CTTCTGTGG
                                |||| ||  |   | |||||||||
                                TTCG TA  G    A GGAGACACT
                                  A  GT ____ G
GAM260   LOC254228 3'  CGTGGAAGCTCCGTGCCC    95953       TGTAT TT    TG
                                GGGCAT    G  GCTTC  TG
                                ||||||    |  |||||  ||
                                CCCGTG    C  CGAAG  GC
                                   _____ CT    GT
GAM260   LOC254243 3'  CCACACAAGGGTATGCAAAGCT 97410     A      TTG   C
            T                    GGGC TTGTATG   CTT TGTGG
                                |||| |||||||   ||| |||||
                                TTCG AACGTAT   GAA ACACC
                                  A      GG_   C
GAM260   LOC254243 3'  CCATGGAACTTCTCACGGTGTC 97411         ATGTTGC
            T                    GGGCATTGT      TTCTGTGG
                                |||||||||      ||||||||
                                TCTGTGGCA      AAGGTACC
                                    CTCTTC_
GAM260   LOC254249 3'  TGGTGTTTGCACTATGTAATGC 95450          T   TTCTGTGG
            TT                    GGGCATTGTATG TGC
                                ||||||||||| |||
                                TTCGTAATGTAT ACG
                                       C   TTTGTGGTT
GAM260   LOC254381 5'  CCACAGACCCAACGCATACGAG 97460     A      __  CT
            GTCC                  GGC TTGTATGT  TG  TCTGTGG
                                ||| ||||||||  ||  |||||||
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                                CTG AGCATACG  AC  AGACACC
                                  G       CA  CC
GAM260   LOC254532 5'  TCACAGAGGCCTTCACACGTGT 96645       T  A  TT_
           CT                     GGGCAT GT TG   GCTTCTGTGG
                                  |||||| || ||   ||||||||||
                                  TCTGTG CA AC   CGGAGACACT
                                    _ C  TTC
GAM260   LOC254556 3'  TCACGGGAATGTCACAATGCCC 94618         _   TGC
                                  GGGCATTGT ATGT   TTCTGTGG
                                  |||||||||| ||||   ||||||||
                                  CCCGTAACA TGTA   AGGGCACT
                                       C   ___
GAM260   LOC254659 5'  CTGTAGGGGCAGTAAGATTTGC 95112     TTGTA         TG
                                  GCA    TGTTGCTTCTG  G
                                  |||    ||||||||||| |
                                  CGT    ATGACGGGGAT  C
                                    TTAGA         GT
GAM260   LOC254659 5'  CTACAGAAGCCCCCGCAGTCTT 95111     C    ATGTT
                                  GGG ATTGT    GCTTCTGTGG
                                  ||| |||||    ||||||||||
                                  TTC TGACG    CGAAGACATC
                                    _    CCCC_
GAM260   LOC254753 3'  TTGCGGGGGCAACATGAGAGCC 96147      A  G          TG
           C                      GGGC TT TATGTTGCTTCTG  G
                                  |||| || ||||||||||||| |
                                  CCCG AG GTACAACGGGGGC  T
                                    _ A           GT
GAM260   LOC254806 5'  CTACAGGGGTCGGACATGTCC  95784       T  A  TT
                                  GGGCAT GT TG  GCTTCTGTGG
                                  |||||| || ||  ||||||||||
                                  CCTGTA CA GC  TGGGGACATC
                                    _ G  __
GAM260   LOC254822 5'  CCCACCAATATGTGATGCC    97213       TG      CTTCT
                                  GGCAT  TATGTTG    GTGG
                                  |||||  |||||||    ||||
                                  CCGTA  GTATAAC    CACC
                                    GT      _____    CT
GAM260   LOC254848 3'  GCCTCGGTGAGCAGCGTGTGGG 97091     A TG         _   T
           TCT                    GGC T  TATGTTGCTT CTG GG
                                  ||| |  |||||||||| ||| ||
                                  CTG G  GTGCGACGAG GGC CC
                                  _ GT         T   T  GT
GAM260   LOC254938 3'  GAAGTGGAAGCAGCATGAAGTG 97058        G         TG GG
           CTC                    GGGCATT TATGTTGCTTC  T
                                  ||||||| |||||||||| |
                                  CTCGTGA GTACGACGAAG  G
                                     A         GT AAGG
GAM260   LOC255000 3'  CTGTGGGAGCAGTCCAAGCTGC 96831      TT  A  __        TG
           CC                     GGGCA  GT TG  TTGCTTCTG  G
                                  |||||  || ||  ||||||||| |
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                                CCCGT  CG AC  GACGAGGGT  C
                                  __ A  CT       GT
GAM260  LOC255031 5'  TTGCAAACTGTGAAGTGCAGTG 97239          G TG TTC_  TG
           CCT                    GGGCATTGTAT T  C    TG  G
                                |||||||||||  |  |    ||  |
                                TCCGTGACGTG A  G    AC  T
                                     A GT TCAA  GT
GAM260  LOC255040 3'  CGTGGGCAGTGCAGTGCT    96381         GT    TC
                                GGCATTGTAT  TGCT  TG
                                ||||||||||  ||||  ||
                                TCGTGACGTG  ACGG  GC
                                     __    GT
GAM260  LOC255041 3'  CGTGGGCAGTGCAGTGCT    96387         GT    TC
                                GGCATTGTAT  TGCT  TG
                                ||||||||||  ||||  ||
                                TCGTGACGTG  ACGG  GC
                                     __    GT
GAM260  LOC255167 3'  CAGATCAGCGTGTGGTGACT   97162    G   TG      CT
                                GG CAT  TATGTTG  TCTG
                                || |||  |||||||  ||||
                                TC GTG  GTGCGAC  AGAC
                                 A  GT      T_
GAM260  LOC255190 3'  CCACAGAAGGAACGATGATCC  97687    C  TG A    G
                                GG AT  T TGTT CTTCTGTGG
                                || ||  | |||| |||||||||
                                CC TA  A GCAA GAAGACACC
                                 _  GT _    G
GAM260  LOC255218 3'  CCACGCACACAGACAGTGCCC  95770         A   _   TTCT
                                GGGCATTGT TGT TGC    GTGG
                                |||||||||  ||| |||    ||||
                                CCCGTGACA ACA ACG    CACC
                                     G   C   ____
GAM260  LOC255265 5'  TACAGAGATGTGATGCT     95349       TG   GTTGC
                                GGCAT  TAT    TTCTGTG
                                |||||  |||    |||||||
                                TCGTA  GTA    GAGACAT
                                  GT   _____
GAM260  LOC255313 3'  TCATGGATGTATGTGACAGTGT 96204         ATGT   T
           TC                     GGGCATTGT    TGC TCTGTGG
                                |||||||||    ||| |||||||
                                CTTGTGACA    ATG AGGTACT
                                     GTGT   T
GAM260  LOC255328 3'  TCACAGAAGTCTTGCATTCAGT 96564        T    T__
           GCCC                     GGCATTG ATGT   GCTTCTGTGG
                                |||||||  ||||   ||||||||||
                                CCGTGAC TACG   TGAAGACACT
                                     T   TTC
GAM260  LOC255360 3'  TCATGGGGGTTGTCCTGGTGTG 96990      TGTATGTT_
           CC                     GGCAT       GCTTCTGTGG
                                |||||       ||||||||||
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                                CCGTG       TGGGGGTACT
                                   TGGTCCTGT
GAM260  LOC255413 3'  CTGTGGCCGTCGAGCGCGCAGT 97576       TA   __ TT  TG
            GCCT                   GGCATTG  TGTT  GC  CTG  G
                                |||||||  ||||  ||  |||  |
                                CCGTGAC  GCGA  TG  GGT  C
                                    GC   GC  CC   GT
GAM260  LOC255452 3'  CGCAGGGTCCCTGCAAGCCT   97529     A    TGTT  T  TG
                                GGGC TTGTA    GCT CTG  G
                                |||| |||||    ||| |||  |
                                TCCG AACGT    TGG GAC  C
                                  _    CCC_  _   GT
GAM260  LOC255458 5'  CCACGTGCACATGCTGGTGCCT 97147       _     T  TTC
                                GGGCATT GTATGT GC   TGTGG
                                ||||||| |||||| ||   |||||
                                TCCGTGG CGTACA CG   GCACC
                                    T     _ T__
GAM260  LOC255465 5'  CATGGAGGCAGGTATTTCC    97284    CATT    G
                                GG    GTAT TTGCTTCTGTG
                                ||    |||| ||||||||||||
                                CC    TATG GACGGAGGTAC
                                 TT__    _
GAM260  LOC255465 3'  CCACAGGAGTGGAGCTGTGGCC 97285    G   T  ATG TG
                                GG CAT GT   T  CTTCTGTGG
                                || ||| ||   |  |||||||||
                                CC GTG CG   G  GAGGACACC
                                 G   T  A__ GT
GAM260  LOC255465 3'  TTACAGCTGTATCTACAGTGTT 97306         TGT   TT
            C                   GGGCATTGTA   TGC  CTGTGG
                                ||||||||||   |||  ||||||
                                CTTGTGACAT   ATG  GACATT
                                      CT_   TC
GAM260  LOC255481 3'  CCATGGTGGCCTGCAGTATGCA 94439   A        TT____
            GAGCCC                  TTGTATGTTGC     CTGTGG
                                 ||||||||||     ||||||
                                 GACGTATGACG     GGTACC
                                A         TCCGGT
GAM260  LOC255515 3'  CCACAGGGGCACAAGATGGCTC 96092      ATTGTA   T
                                GGGC     TGT GCTTCTGTGG
                                ||||     ||| ||||||||||
                                CTCG     ACA CGGGGACACC
                                  GTAGA_   _
GAM260  LOC255515 3'  CTGTAGAGGTTTGGCACGAGTT 96096      A   ATGTT      TG
            T                   GGGC TTGT    GCTTCTG  G
                                |||| ||||    |||||||  |
                                TTTG AGCA    TGGAGAT  C
                                  _   CGGTT      GT
GAM260  LOC255515 5'  CACCCGGCATACAAGCTT    96091      A        CTTCT
                                GGGC TTGTATGTTG    GTG
                                |||| ||||||||||    |||
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                                TTCG AACATACGGC    CAC
                                  _       C____
GAM260  LOC255631 5'  CTGCAGTTTTCAACTACAGTGT 96230        T   CTT_  TG
          TC                    GGGCATTGTA GTTG   CTG  G
                                |||||||||| ||||   |||  |
                                CTTGTGACAT CAAC   GAC  C
                                     _   TTTT   GT
GAM260  LOC255652 3'  TGCACTGTGCAATATGCAGTGG 96722    G         TTCT  G
          CT                    GG CATTGTATGTTGC   GTG
                                || ||||||||||||   |||
                                TC GTGACGTATAACG   CAC
                                 G          TGT_  GTG
GAM260  LOC255654 5'  TATGGGGGCCACAGGGTCC   96889     ATTGTA  T
                                GGGC     TGT GCTTCTGTG
                                ||||     ||| |||||||||
                                CCTG     ACA CGGGGGTAT
                                  GG____   C
GAM260  LOC255702 3'  CGCAGAGCCTTTTGGTGTCT   95356       TATGTT  T  TG
                                GGGCATTG     GCT CTG  G
                                ||||||||     ||| |||  |
                                TCTGTGGT     CGA GAC  C
                                    TTTC__   _   GT
GAM260  LOC255718 5'  CCGCGGGGGTGGAGCGCTGCCT 97550      T  ATG TG
                                GGGCA TGT   T  CTTCTGTGG
                                ||||| |||   |  |||||||||
                                TCCGT GCG   G  GGGGGCGCC
                                  C   A__ GT
GAM260  LOC255967 5'  CTGCAGCTTATTTATAATGATG 94915      TG _  TTGCTT  TG
          CTT                   GGGCAT  T ATG     CTG  G
                                ||||||  | |||     |||  |
                                TTCGTA  A TAT     GAC  C
                                   GT A   TTATTC   GT
GAM260  LOC256112 3'  CGTAGAGGAATGTGATGCT   96365      TG  GTTG    TG
                                GGCAT  TAT   CTTCTG  G
                                |||||  |||   ||||||  |
                                TCGTA  GTA   GGAGAT  C
                                   GT   A___     GT
GAM260  LOC256145 3'  TCATGGTATTGCAGTGCTT   96544        TGTTGCTT
                                GGGCATTGTA       CTGTGG
                                ||||||||||       ||||||
                                TTCGTGACGT       GGTACT
                                    TAT_____
GAM260  LOC256158 5'  GTCAGCCTGCAGTGCCC     97677         T   _
                                GGGCATTGTA GTTG C
                                |||||||||| |||| |
                                CCCGTGACGT CGAC G
                                     C    T
GAM260  LOC256158 5'  CCATGGAGCTCCTCTGTGATGC 97654      TG  TGTT_    T
          CC                    GGGCAT  TA    GCTTC GTGG
                                ||||||  ||    ||||| ||||
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                                CCCGTA  GT    CGAGG TACC
                                   GT  CTCCT    _
GAM260   LOC256158 5'  CGCAGAGTGCTCCGGTGTTC   97660        TATGTT _    TG
                                GGGCATTG     GC TTCTG  G
                                ||||||||     || |||||  |
                                CTTGTGGC     CG GAGAC  C
                                     CT____  T    GT
GAM260   LOC256158 5'  CGTGGAGGTTCAGGTGCCC    97663       GTA  TT    TG
                                GGGCATT   TG  GCTTC  TG
                                |||||||   ||  |||||  ||
                                CCCGTGG   AC  TGGAG  GC
                                    ___  T_    GT
GAM260   LOC256158 5'  ACAGAAGGGGTGTCT       97640       TGTATGT G
                                GGGCAT      T CTTCTGT
                                ||||||      | |||||||
                                TCTGTG      G GAAGACA
                                   ________ G
GAM260   LOC256207 5'  CTACCTCTCAAATATATATGTC 95167       T      GCTTCT
            C                    GGGCAT GTATGTT     GTGG
                                ||||||| |||||||     ||||
                                CCTGTA TATATAA     CATC
                                   _      ACTCTC
GAM260   LOC256306 5'  CAGAGGCCCCGGGCCC      96680      A   TATGTT
                                GGGC TTG     GCTTCTG
                                |||| |||     |||||||
                                CCCG GGC     CGGAGAC
                                  _  CC____
GAM260   LOC256355 5'  GCGGAGGCAAGGCCC       96038      ATTGTATG
                                GGGC       TTGCTTCTGT
                                ||||       ||||||||||
                                CCCG       AACGGAGGCG
                                  G________
GAM260   LOC256405 5'  CACAGAGGCCCACTGTTC     95873       T  TATGTT
                                GGGCA TG     GCTTCTGTG
                                ||||| ||     |||||||||
                                CTTGT AC     CGGAGACAC
                                   C  C_____
GAM260   LOC256520 5'  TTGCCGGAGCGACGCGCAGTGT 95982         TA       T TG
            TT                   GGGCATTG  TGTTGCTTC G  G
                                |||||||  ||||||||| |  |
                                TTTGTGAC  GCAGCGAGG C  T
                                     GC        C GT
GAM260   LOC256597 5'  CTACAGCCTCAGCTGCGATGCC 96287          T    CTT
            C                    GGGCATTGTA GTTG   CTGTGG
                                |||||||||| ||||   ||||||
                                CCCGTAGCGT CGAC   GACATC
                                      _   TCC
GAM260   LOC256691 3'  CGCAGAATGAATGCAGTCTT   96197     C      GTTGC     TG
                                GGG ATTGTAT     TTCTG  G
                                ||| |||||||     |||||  |
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                                TTC TGACGTA    AAGAC  C
                                  _     AGT__    GT
GAM260  LOC256714 3'  CAGAAATGCATTGCCC     96311      T    GTTGC
                                GGGCA TGTAT    TTCTG
                                ||||| |||||    |||||
                                CCCGT ACGTA    AAGAC
                                   T   _____
GAM260  LOC256730 3'  CTGCCTTTATGACATCAGTGCC 95230       T    GCTTCT TG
          C                      GGGCATTG ATGTT     G  G
                                |||||||| |||||     | |
                                CCCGTGAC TACAG     C  C
                                     _    TATTTC GT
GAM260  LOC256789 3'  CTGTGGAGGCTGCCAGCAAGCT 97445     A   AT  T     TG
          C                      GGGC TTGT  GT GCTTCTG  G
                                |||| ||||  || |||||||  |
                                CTCG AACG  CG CGGAGGT  C
                                  _   AC  T      GT
GAM260  LOC256848 3'  CAGGGGCACGGGGCCC     97512     ATTGTA   T
                                GGGC     TGT GCTTCTG
                                ||||     ||| |||||||
                                CCCG     GCA CGGGGAC
                                  GG____   _
GAM260  LOC256940 3'  CAGAGTATATTGTGTTC     96493      T    TTGC
                                GGGCAT GTATG    TTCTG
                                |||||| |||||    |||||
                                CTTGTG TATAT    GAGAC
                                   T    ____
GAM260  LOC256946 3'  CCATAGTCTCTTACAGTGCCT  94546         TGTTGCTT
                                GGGCATTGTA       CTGTGG
                                ||||||||||       ||||||
                                TCCGTGACAT       GATACC
                                     TCTCT___
GAM260  LOC257017 5'  TGTAGAGCATTGTGCAGGTCC  97378     A     GT    T   TG
                                GGGC TTGTAT  TGCT CTG  G
                                |||| ||||||  |||| |||  |
                                CCTG GACGTG  ACGA GAT  T
                                  _     TT   _  GT
GAM260  LOC257020 5'  CTGCAGGAGCCCTGCGGCTGCC 97489      _    TGTT      TG
          C                      GGGCA TTGTA    GCTTCTG  G
                                ||||| |||||    |||||||  |
                                CCCGT GGCGT    CGAGGAC  C
                                   C    CC__      GT
GAM260  LOC257103 5'  CCGCAGGACTGCTGTGGGTCT  95596     A TG  T  TGC
                                GGGC T  TA GT   TTCTGTGG
                                |||| |  || ||   ||||||||
                                TCTG G  GT CG   AGGACGCC
                                  _ GT  _  TC_
GAM260  LOC257106 3'  CTGCAGCATGAGCAGCTGTAGT 95387       T     ___   TG
          GCCC                    GCATTGTA GTTGCTT   CTG  G
                                |||||||| |||||||   |||  |
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                                CGTGATGT CGACGAG   GAC  C
                                   _     TAC   GT
GAM260   LOC257106 3'  TGGGAGGCACTGCCT      95391      T   ATGTTG
                                GGGCA TGT     CTTCTG
                                ||||| |||     ||||||
                                TCCGT ACG     GAGGGT
                                  C  _______
GAM260   LOC257117 5'  TCAATATGGTATCACAATGCCT 96211         ATGT    TCTG
                                GGGCATTGT    TGCT    TGG
                                |||||||||    ||||    |||
                                TCCGTAACA    ATGG    ACT
                                     CT__    TATA
GAM260   LOC257319 3'  AGGCGATGGTGATGTCT     95772       TG A
                                GGGCAT  T TGTTGCTT
                                ||||||  | ||||||||
                                TCTGTA  G GTAGCGGA
                                   GT _
GAM260   LOC257346 3'  TCATAGGGGGTTGCAGTG    96522       TGTTG
                                CATTGTA    CTTCTGTGG
                                |||||||    |||||||||
                                GTGACGT    GGGGATACT
                                   TG___
GAM260   LOC257395 3'  CCACAGAGGTGATCTCTACAGT 95418     AT    T__  TG
           CT                     GGGC  TGTA   GT  CTTCTGTGG
                                ||||  ||||   ||  |||||||||
                                TCTG  ACAT   TA  GGAGACACC
                                  __    CTC  GT
GAM260   LOC257396 5'  CAGGGGTCTTCAGGCTT     97134     A   TATGTT
                                GGGC TTG     GCTTCTG
                                |||| |||     |||||||
                                TTCG GAC     TGGGGAC
                                  _   TTC___
GAM260   LOC257407 5'  CCATGGTGTGTCTGCAGTGTTC 96987         TGT   TT
                                GGGCATTGTA   TGC  CTGTGG
                                ||||||||||   |||  ||||||
                                CTTGTGACGT   GTG  GGTACC
                                     CT_   T_
GAM260   LOC257415 3'  TTATAAAGAAAGTGCAATGTCT 96080          GTTG   C
                                GGGCATTGTAT    CTT TGTGG
                                ||||||||||    ||| |||||
                                TCTGTAACGTG    GAA ATATT
                                     AAA_   _
GAM260   LOC257429 3'  CCATGGAAGCAACAAATTCCC  96003     C   GTA
                                GGG ATT   TGTTGCTTCTGTGG
                                ||| |||   ||||||||||||||
                                CCC TAA   ACAACGAAGGTACC
                                  T  ___
GAM260   LOC257438 3'  TAGGAGGCGGATGCTT      93974       GTA   TG
                                GGGCATT   TGT  CTTCTG
                                |||||||   |||  ||||||
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                                TTCGTAG   GCG  GAGGAT
                                   ___   __
GAM260   LOC257476 3'  TCACAGGGACGTGGTATGGGCC 61258     A TG   GT  CT
             C                   GGGC T  TAT  TG  TCTGTGG
                                 ||||  |  |||  ||  |||||||
                                 CCCG G  ATG  GC  GGACACT
                                   _ GT   GT  AG
GAM260   LOC257482 3'  CGCAGCCACCAACAGTGTCT   94238        A  T  CTT   TG
                                 GGGCATTGT TG TG   CTG  G
                                 |||||||||  ||  ||   |||  |
                                 TCTGTGACA AC AC   GAC  C
                                      _  C  C__   GT
GAM260   LOC257485 3'  TTGCAGCAAGGGCATGTGATGT 65594   G   TG     G  _   TG
             GC                    G GCAT  TATGTT CTT CTG  G
                                 |  ||||  ||||||  |||  |||  |
                                 C TGTA  GTACGG GAA GAC  T
                                  G   GT     _  C   GT
GAM260   LOC257494 5'  ATAGGAGAGCAAGTCC      97790      A   ATGTTG
                                 GGGC TTGT     CTTCTGT
                                 ||||  ||||     |||||||
                                 CCTG AACG     GAGGATA
                                   _   A_____
GAM260   LOC257535 3'  CAGAGTGGCATGGCAATGCCC  97778         _   TG  T
                                 GGGCATTGT ATGT  CT CTG
                                 |||||||||  ||||  ||  |||
                                 CCCGTAACG TACG  GA GAC
                                      G   GT  _
GAM260   LOC257552 5'  TGGCAAGTGATGTGTGAGTCC  97760     A TG    TG  _
                                 GGGC T  TATGT  CTT CTG
                                 ||||  |  |||||  |||  |||
                                 CCTG A  GTGTA  GAA GGT
                                   _ GT    GT   C
GAM260   LOC257595 3'  CAGAGTGGCATGGCAATGCCC  97942         _   TG  T
                                 GGGCATTGT ATGT  CT CTG
                                 |||||||||  ||||  ||  |||
                                 CCCGTAACG TACG  GA GAC
                                      G   GT  _
GAM260   LOC257596 3'  CTACAGAGGAAAAGTCAATGCC 97931        T  GTTG
             T                    GGGCATTG AT    CTTCTGTGG
                                 ||||||||  ||    |||||||||
                                 TCCGTAAC TG    GGAGACATC
                                      _  AAAA
GAM260   LOC257602 5'  TGGCAAGTGATGTGTGAGTCC  97852     A TG    TG  _
                                 GGGC T  TATGT  CTT CTG
                                 ||||  |  |||||  |||  |||
                                 CCTG A  GTGTA  GAA GGT
                                   _ GT    GT   C
GAM260   LOC51026  3'  CATATTATTTACAATGTCT   32169         T  TGCTTC
                                 GGGCATTGTA GT     TGTG
                                 ||||||||||  ||     ||||
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                                TCTGTAACAT TA     ATAC
                                     T  TT____
GAM260  LOC51035  5' CGCGGAAGCCGCGGTGTC    31817       ATGTT
                                GGCATTGT    GCTTCTGTG
                                ||||||||    |||||||||
                                CTGTGGCG    CGAAGGCGC
                                    C____
GAM260  LOC51049  5' TGGGGGCCATACTGTCT     31889      TT    TT
                                GGGCA  GTATG  GCTTCTG
                                |||||  |||||  |||||||
                                TCTGT  CATAC  CGGGGGT
                                  __    __
GAM260  LOC51054  5' CTGCAGAGGGAGTAGTGCGATC 31907    C     GT_ G     TG
           CT                    GGG ATTGTAT   T CTTCTG  G
                                ||| |||||||   | ||||||  |
                                TCC TAGCGTG   A GGAGAC  C
                                  _      ATG G     GT
GAM260  LOC51117  3' TCATGCTGGGATTGTGCAGTGC 32094          TTG  TC
           TC                    GGGCATTGTATG   CT  TGTGG
                                ||||||||||||  ||  |||||
                                CTCGTGACGTGT   GG  GTACT
                                      TAG  TC
GAM260  LOC51133  5' CCATTTTCAGTTGTGATGCCT  32281      TG  TGTT   TCT_
                                GGGCAT  TA    GCT    GTGG
                                ||||||  ||    |||    ||||
                                TCCGTA  GT    TGA    TACC
                                   GT  _____  CTTT
GAM260  LOC51161  3' TATGGGAAGAGCCGTTCAGTGT 32517       T   TTG    GTGG
           TT                    GGGCATTG ATG   CTTCT
                                |||||||| |||   |||||
                                TTTGTGAC TGC   GAAGG
                                     T   CGA    GTATC
GAM260  LOC51195  5' CTGCAGGAGCTACACCAGTACT 32942    C    TA   T      TG
           T                     GGG ATTG  TGT GCTTCTG  G
                                ||| ||||  ||| |||||||  |
                                TTC TGAC  ACA CGAGGAC  C
                                  A    C_   T      GT
GAM260  LOC51219  5' CTGCAGGTGGGAGCATATGGTG 33120    TG     G  _    TG
                                CAT  TATGTT CT TCTG  G
                                |||  |||||| || ||||  |
                                GTG  ATACGA GG GGAC  C
                                  GT     G  T    GT
GAM260  LOC51279  3' CGCAGAAGCCAGGTGAGCCC   33311     A TG A  TT      TG
                                GGGC T  T TG  GCTTCTG  G
                                ||||  |  | ||  |||||||  |
                                CCCG A  G AC  CGAAGAC  C
                                  _ GT G  __      GT
GAM260  LOC51281  3' GCTTTGTAGCAGTGTCT     33325         _   TT
                                GGGCATTGT ATG  GC
                                |||||||| |||  ||
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                                TCTGTGACG TGT  CG
                                     A   TT
GAM260  LOC51611  3' CATGGGGGCAGTTTCCC     31985     CATTGTATG
                                GGG        TTGCTTCTGTG
                                |||        ||||||||||
                                CCC        GACGGGGGTAC
                                  TTT_______
GAM260  LOC51619  3' CCATAGGAGCCTACACTAAGTC 32017      A   TA   T_
           C                     GGGC TTG  TGT  GCTTCTGTGG
                                ||||  |||  |||  ||||||||||
                                CCTG AAT  ACA  CGAGGATACC
                                  _   C_   TC
GAM260  LOC51631  3' CTGCAGAAGAAACTGGGGTGTT 68082       G  T   G     TG
           T                     GGGCATT TA GTT CTTCTG  G
                                |||||||  ||  |||  ||||||  |
                                TTTGTGG GT CAA GAAGAC  C
                                    G  _   A     GT
GAM260  LOC51634  3' TGCAGAACTTTTTAATGTCT   32066        TATGTTGC    TG
                                GGGCATTG       TTCTG  G
                                ||||||||       |||||  |
                                TCTGTAAT       AAGAC  T
                                    TTTTC___     GT
GAM260  LOC51668  3' CGCAGAAGGAACAGTAGTCT   32325      ATTGTA   G     TG
                                GGGC     TGTT CTTCTG  G
                                ||||     |||| ||||||  |
                                TCTG     ACAA GAAGAC  C
                                  ATG___    G     GT
GAM260  LOC51701  3' CCGTGATGGTGATGTGTGCTGT 32651      T GT    TG  TC GT
           CT                     GGGCA T  ATGT  CT  T  GG
                                |||||  |  ||||  ||  |  ||
                                TCTGT G  TGTA  GG  G  CC
                                  C TG    GT  TA TG
GAM260  LOC51716  3' CCATGTTGGGCAGTGATGGTGT 32789       TG ATG     CT_
           CT                     GGGCAT  T   TTGCTT   GTGG
                                ||||||  |   ||||||   ||||
                                TCTGTG  A   GACGGG   TACC
                                   GT GT_     TTG
GAM260  LOC56181  5' CATAGCCCCTACGGTGCCC    95532         TGTT   TCT
                                GGGCATTGTA    GCT   GTG
                                ||||||||||    |||   |||
                                CCCGTGGCAT    CGA   TAC
                                     CCC_   ____
GAM260  LOC56834  3' CACTCAATAAACAGTGTCT    39340         A     CTTCT
                                GGGCATTGT TGTTG     GTG
                                |||||||||  |||||     |||
                                TCTGTGACA ATAAC     CAC
                                     A    T_____
GAM260  LOC56851  3' GAATTAATTACAGTGTCC     39339         T    C
                                GGGCATTGTA GTTG TTC
                                ||||||||||  ||||  |||
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                                CCTGTGACAT TAAT AAG
                                      _   T
GAM260  LOC57086  5' CGTGGGAGCCAGCGAGCCT   39778     A   A TT   TG
                                GGGC TTGT TG  GCTTC  TG
                                |||| |||| ||  |||||  ||
                                TCCG AGCG AC  CGAGG  GC
                                  _   _ __    GT
GAM260  LOC57107  3' TACAGAGGTTAATGTAT     39841       _
                                GTATGTTG CTTCTGTG
                                |||||||| ||||||||
                                TATGTAAT GGAGACAT
                                     T
GAM260  LOC57109  3' CTACAGAGGCAATGTGACCAGT 39850     ATTG
           C                     GGC   TATGTTGCTTCTGTGG
                                |||   ||||||||||||||||
                                CTG   GTGTAACGGAGACATC
                                  ACCA
GAM260  LOC57333  3' CCGCAGGAGGCAGATGCAGTCC 73714     C     G     _
           C                     GGG ATTGTAT TTGCTTC TGTGG
                                ||| ||||||| ||||||| |||||
                                CCC TGACGTA GACGGAG ACGCC
                                  _     _     G
GAM260  LOC57406  3' TATAGGAGCATTAGTCC     40346     ATTGTA  T
                                GGGC     TG TGCTTCTGTG
                                ||||     || ||||||||||
                                CCTG     AT ACGAGGATAT
                                  _______ T
GAM260  LOC58525  5' CGAGGTCTGCGGTGCCT     78645         TGTT    T
                                GGGCATTGTA    GCTTC G
                                ||||||||||    ||||| |
                                TCCGTGGCGT    TGGAG C
                                     C___    _
GAM260  LOC83690  5' GCAGAGGCGGAGGCTC      48816     ATTGTATG
                                GGGC       TTGCTTCTGT
                                ||||       ||||||||||
                                CTCG       GGCGGAGACG
                                  GA_______
GAM260  LOC83985  3' CCACAGGGGCAGCCCCAAGGGC 49348     A_   TAT
           TC                   GGGC  TTG   GTTGCTTCTGTGG
                                ||||  |||   ||||||||||||
                                CTCG  AAC   CGACGGGGACACC
                                  GG   CC_
GAM260  LOC84548  3' CTACGGGAGTGACTCCATGCTT 71254       T TAT  TG
                                GGGCAT G   GT  CTTCTGTGG
                                |||||| |   ||  |||||||||
                                TTCGTA C   CA  GAGGGCATC
                                   _ CT_  GT
GAM260  LOC85479  5' TCATAGGCCGGGTGCGGTGGCT 52405    G      GTT  TT
                                GG CATTGTAT   GC  CTGTGG
                                || ||||||||   ||  ||||||
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                                TC GTGGCGTG   CG  GATACT
                                 G      GGC  __
GAM260  LOC89919  5' TAACAGGGTAACATACGGTG  60730          T   GG
                                CATTGTATGTTGCT CTGT
                                ||||||||||||| ||||
                                GTGGCATACAATGG GACA
                                       _   ATG
GAM260  LOC89932  5' CCATGGGGGCAGGAGCTTGGGT 60793     ATT_ ATG
           CC                    GGGC   GT  TTGCTTCTGTGG
                                ||||   ||  ||||||||||||
                                CCTG   CG  GACGGGGGTACC
                                  GGTT  AG_
GAM260  LOC89932  5' CTGCAGCCTACCCCGTGCGGTG 60799          TTGCTT_  TG
           CCT                    GGGCATTGTATG     CTG  G
                                ||||||||||||      |||  |
                                TCCGTGGCGTGC     GAC  C
                                      CCCATCC   GT
GAM260  LOC89941  3' CAGGGGCAGCACAGCT     57057     AT   AT
                                GGC  TGT  GTTGCTTCTG
                                |||  |||  ||||||||||
                                TCG  ACA  CGACGGGGAC
                                 __   __
GAM260  LOC90038  3' CCATGGAACTTCTCACGGTGTC 61154         ATGTTGC
           T                     GGGCATTGT      TTCTGTGG
                                |||||||||      ||||||||
                                TCTGTGGCA      AAGGTACC
                                    CTCTTC_
GAM260  LOC90050  3' CGCAGGAGTGTCGAGGTCC   56380     A   T  GTT     TG
                                GGGC TTG AT   GCTTCTG  G
                                |||| ||| ||   |||||||  |
                                CCTG AGC TG   TGAGGAC  C
                                  G   _ ___      GT
GAM260  LOC90050  5' TCATGGAAAGCCTCGTGCAGTG 56381    G       TT   _
           GCC                     GG CATTGTATG  GCTT CTGTGG
                                || |||||||||  |||| ||||||
                                CC GTGACGTGC  CGAA GGTACT
                                 G       TC    A
GAM260  LOC90148  3' CCAGAAAAAAGTAATAATACAG 61662       _    ____   TGG
           TGTTT                   TTGTAT GTTGCT    TCTG
                                |||||| ||||||    ||||
                                GACATA TAATGA    AGAC
                                   A     AAAA    C   G
GAM260  LOC90268  3' ACAGATGTCTGATGCCC     61962       GTATGTT  T
                                GGGCATT      GC TCTGT
                                |||||||      || |||||
                                CCCGTAG      TG AGACA
                                    TC_____  T
GAM260  LOC90268  5' CCGCGGCCCGAGATGCAGTGCC 61963          G   CTT
           C                     GGGCATTGTAT TTG   CTGTGG
                                |||||||||| |||   ||||||
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                                CCCGTGACGTA AGC   GGCGCC
                                      G   CC_
GAM260  LOC90268 3' TGTGGAGGTGGTATTTCCC   61966    CATTGT   TT     TG
                                GGG     ATG  GCTTCTG  G
                                |||     |||  |||||||  |
                                CCC     TAT  TGGAGGT  T
                                  TT_____   GG      GT
GAM260  LOC90297 3' CACACTGGGTGTGGTGCCC   62157      TG   GTTG  TC
                                GGGCAT  TAT    CT  TGTG
                                ||||||  |||    ||  ||||
                                CCCGTG  GTG    GG  ACAC
                                   GT   _____  TC
GAM260  LOC90297 5' TATAGGAGCACAGGGCCC    62160     ATTGTA   T
                                GGGC     TGT GCTTCTGTG
                                ||||     ||| |||||||||
                                CCCG     ACA CGAGGATAT
                                  GG_____   _
GAM260  LOC90333 3' TTACAGGAGTGAGCCACTGTGC 62309       T  ATG TG
           CT                     GGGCAT GT   T  CTTCTGTGG
                                |||||| ||   |  |||||||||
                                TCCGTG CA   A  GAGGACATT
                                   T  CCG GT
GAM260  LOC90381 3' CCACGGAGGCACCACGGTGTCT 62544         AT T
                                GGGCATTGT  G TGCTTCTGTGG
                                |||||||||  | ||||||||||
                                TCTGTGGCA  C ACGGAGGCACC
                                     __ C
GAM260  LOC90381 3' CCGCTGGCGGCATGTGATGGCC 62546    G   TG       TCT
                                GG CAT  TATGTTGCT   GTGG
                                || |||  |||||||||   ||||
                                CC GTA  GTACGGCGG   CGCC
                                 G   GT       T__
GAM260  LOC90393 3' CACTAAAATGACAGTGTCC    62620         A   GCTTCT
                                GGGCATTGT TGTT     GTG
                                ||||||||| ||||     |||
                                CCTGTGACA GTAA     CAC
                                     _    AAT___
GAM260  LOC90408 3' TCACAGAACCTGCCAACATGTG 62666    TG     _ ___
           ATGTCT                  AT  TATGTTG C   TTCTGTGG
                                ||  ||||||| |   ||||||||
                                TA  GTACAAC G   AAGACACT
                                 GT      C TCC
GAM260  LOC90485 3' CTACAGGCCTGAGCTACGGTGC 63014          T   GCT_
           CT                    GGGCATTGTA GTT    TCTGTGG
                                |||||||||| |||    |||||||
                                TCCGTGGCAT CGA    GGACATC
                                     _  GTCC
GAM260  LOC90488 3' TCACAGTTCCATATGTATAATG 63034    G        _  CTT
           TGC                    G GCATTGTATGT TG   CTGTGG
                                | ||||||||||| ||   ||||||
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                                C TGTAATATGTA AC   GACACT
                                 G         T  CTT
GAM260  LOC90520  3' GGCTAATACTGCAATGTTT   63143          _   _
                                GGGCATTGTA TGTT GCT
                                |||||||||| |||| |||
                                TTTGTAACGT ATAA CGG
                                     C   T
GAM260  LOC90529  3' CAGGCAGGTGATGCTT     63160       TG ATG    TT
                                GGGCAT  T   TTGC  CTG
                                ||||||  |   ||||  |||
                                TTCGTA  G   GACG  GAC
                                   GT ___   __
GAM260  LOC90550  3' TCACAGGAGGAATAATTGCCC  73094      TTGTA    G
                                GGGCA    TGTT CTTCTGTGG
                                |||||    |||| |||||||||
                                CCCGT    ATAA GAGGACACT
                                   TA___   G
GAM260  LOC90580  3' TTGTGGCCTGGCATGGTGATGT 63372      TG _    __   TCTGTGG
           CT                    GGCAT  T ATGTT  GCT
                                |||||  | |||||  |||
                                CTGTA  G TACGG  CGG
                                   GT G    TC   TGTT
GAM260  LOC90750  5' TTACAGGACAATAATGCATTGT 63927      T    _   C
           TT                    GGGCA TGTAT GTTG TTCTGTGG
                                ||||| ||||| |||| ||||||||
                                TTTGT ACGTA TAAC AGGACATT
                                   T    A   _
GAM260  LOC90906  5' CTGTGGAGGATCAATGCAGTGG 64298    G      GTTG     TG
           CT                    GG CATTGTAT    CTTCTG  G
                                || ||||||||    ||||||  |
                                TC GTGACGTA    GGAGGT  C
                                 G       ACTA     GT
GAM260  LOC91010  5' CGTGGACTTCGTGGAGTGCCT  64615       G    TTGCT    TG
                                GGGCATT TATG    TCTG  G
                                ||||||| ||||    ||||  |
                                TCCGTGA GTGC    AGGT  C
                                    G   TTC__   GT
GAM260  LOC91035  5' CCACAGGAGGCTTGGATGCTC  64667       GTAT  TG
                                GGGCATT   GT  CTTCTGTGG
                                |||||||   ||  |||||||||
                                CTCGTAG   CG  GAGGACACC
                                    GTT_ __
GAM260  LOC91035  5' GGCAGGAGCAGGTGGTGCCT   64672       TG ATG        GG
                                GGGCAT  T   TTGCTTCTGT
                                ||||||  |   ||||||||||
                                TCCGTG  G   GACGAGGACG
                                   GT ___        GT
GAM260  LOC91040  3' CGGAAGTCAGTGCCC       64716         TATGTT
                                GGGCATTG     GCTTCTG
                                ||||||||     |||||||
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                                CCCGTGAC     TGAAGGC
                                         _______
GAM260  LOC91040  3' CTGCGCCTGCAGCGGCAGTGCC 64718         A     TTC  TG
             C                    GGGCATTGT TGTTGC   TG  G
                                  ||||||||| ||||||   ||  |
                                  CCCGTGACG GCGACG   GC  C
                                        _     TCC  GT
GAM260  LOC91069  3' CGGAGGCTGGCTGCCT      64776       TT  ATGTT
                                  GGGCA  GT    GCTTCTG
                                  |||||  ||    |||||||
                                  TCCGT  CG    CGGAGGC
                                     __  GT___
GAM260  LOC91149  3' AGCAATATATGAGTTC      65066       A TG
                                  GGGC T  TATGTTGCT
                                  |||| |  |||||||||
                                  CTTG A  ATATAACGA
                                    _ GT
GAM260  LOC91149  3' CCACATCTCTTTAAGTGTAATG 65073           GTTGCTTC_
             CTC                    GGGCATTGTAT        TGTGG
                                    ||||||||||         |||||
                                    CTCGTAATGTG        ACACC
                                          AATTTCTCT
GAM260  LOC91179  5' GCTTGACGTGCGAGCCC     65170       A        __
                                  GGGC TTGTATGTT  GC
                                  |||| |||||||||  ||
                                  CCCG AGCGTGCAG  CG
                                    _        TT
GAM260  LOC91286  3' TGGGTGCAATGTATACTGCTC  65455       T        T
                                  GGGCA TGTATGTTGC TCTG
                                  ||||| |||||||||| ||||
                                  CTCGT ATATGTAACG GGGT
                                     C         T
GAM260  LOC91380  3' TTACAGGAGTGAGAAGTCC    65866       A  GTATG TG
                                  GGGC TT     T  CTTCTGTGG
                                  |||| ||     |  |||||||||
                                  CCTG AG     A  GAGGACATT
                                    A  _____ GT
GAM260  LOC91445  3' TTGCAGGGGCCTCTGGAGTGTC 60554        G  TGTT      TG
             T                     GGGCATT TA    GCTTCTG  G
                                   ||||||| ||    |||||||  |
                                   TCTGTGA GT    CGGGGAC  T
                                      G  CTC_      GT
GAM260  LOC91461  3' CATGGGGGTATGACTGCCT    66133       TT  ATGT
                                  GGGCA  GT    TGCTTCTGTG
                                  |||||  ||    ||||||||||
                                  TCCGT  CA    ATGGGGGTAC
                                     __  GT__
GAM260  LOC91496  5' CGCAGGGCTTTTACAGTTTTC  66220     C     TGTT   T   TG
                                  GGG ATTGTA    GCT CTG  G
                                  ||| ||||||    ||| |||  |
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                                CTT TGACAT   CGG GAC  C
                                  T    TTT_  _  GT
GAM260  LOC91496  5' GTAATAATGATAGTGCTC   66223        A__
                                GGGCATTGT  TGTTGC
                                |||||||||  ||||||
                                CTCGTGATA  ATAATG
                                     GTA
GAM260  LOC91548  5' CATAGAAGAAATGGTTTCC   66410    C  TG ATGTTG
                                GGG AT  T    CTTCTGTG
                                ||| ||  |    ||||||||
                                CCT TG  A    GAAGATAC
                                  T  GT AA____
GAM260  LOC91585  5' CGGGCCATGCAGTGCCT    66575         TT  TT
                                GGGCATTGTATG  GC  CTG
                                ||||||||||||  ||  |||
                                TCCGTGACGTAC  CG  GGC
                                              __  __
GAM260  LOC91700  3' CTGCAGGGGGCTCAAATGCGAT 67013   G      GTT_    _  TG
           GACC                   G CATTGTAT   GCTTC TG  G
                                | ||||||||   ||||| ||  |
                                C GTAGCGTA   CGGGG AC  C
                                 A      AACT    G  GT
GAM260  LOC91750  3' CCAGTCCCCAGCATCTGATGTT 67060       GT    CTT_  TGG
           T                    GGGCATT  ATGTTG   CTG
                                |||||||  ||||||   |||
                                TTTGTAG  TACGAC   GAC
                                     TC     CCCT   C
GAM260  LOC91759  3' AGCAGCGTGCAGGGCCT    67083     A
                                GGGC TTGTATGTTGCT
                                |||| ||||||||||||
                                TCCG GACGTGCGACGA
                                  G
GAM260  LOC91768  5' CTGCAGAGGTCCCGACGGCGCC 67114     A   A  TT     TG
           T                    GGGC TTGT TG  GCTTCTG  G
                                |||| |||| ||  |||||||  |
                                TCCG GGCA GC  TGGAGAC  C
                                  C   _  CC      GT
GAM260  LOC91782  3' CTACAGGACCCTGAGATGTCC  67154       GTATGTTGC
                                GGGCATT       TTCTGTGG
                                |||||||       ||||||||
                                CCTGTAG       AGGACATC
                                    AGTCCC___
GAM260  LOC91862  3' TGTGGAAGTTTCCAATGCT   53471       TATGTT     TG
                                GGCATTG    GCTTCTG  G
                                |||||||    |||||||  |
                                TCGTAAC    TGAAGGT  T
                                    CTT___     GT
GAM260  LOC91960  3' TTGGAACGTGGTGTATGGTGGT 67668   G   TG  TG TG _    TGG
           C                    GG CAT  TA  T  C TTCTG
                                || |||  ||  |  | |||||
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                                CT GTG  AT  G  G AAGGT
                                 G   GT  GT GT C    T
GAM260  LOC92017  5' CCATAGAATGTTCTGCAATG   67888       TGTT  _
                                CATTGTA    GC TTCTGTGG
                                |||||||    || ||||||||
                                GTAACGT    TG AAGATACC
                                    CT__  T
GAM260  LOC92078  3' CACCTAAATATGCAGGCTC    67975     A       GCTTCT
                                GGGC TTGTATGTT     GTG
                                |||| |||||||||     |||
                                CTCG GACGTATAA     CAC
                                  _       ATC___
GAM260  LOC92140  3' GGTTTAACAACAGTGCCC    68284         A    CT
                                GGGCATTGT TGTTG  TC
                                ||||||||| |||||  ||
                                CCCGTGACA ACAAT  GG
                                    _    TT
GAM260  LOC92231  3' CTATTGAGTGTGGGTATAGTGT 68552          G TG _   T
           CC                    GGGCATTGTAT T  C TTC GTGG
                                ||||||||||| |  | ||| ||||
                                CCTGTGATATG G  G GAG TATC
                                      _ GT T   T
GAM260  LOC92270  5' CACAGGAACATGTGGAGCCT   68629     A TG    TGC     G
                                GGGC T  TATGT   TTCTGTG
                                |||| |  |||||   |||||||
                                TCCG G  GTACA   AGGACAC
                                  A GT    ___       A
GAM260  LOC92285  3' CGTGGATTAGGTATAGTGCC   68751         GTTGCT    TG
                                GGCATTGTAT     TCTG  G
                                ||||||||||     ||||  |
                                CCGTGATATG     AGGT  C
                                     GATT__    GT
GAM260  LOC92293  3' CAGGAGGAAGATGCCT      68761        GTATG  G
                                GGGCATT    TT CTTCTG
                                |||||||    || ||||||
                                TCCGTAG    AA GAGGAC
                                   _____  G
GAM260  LOC92340  3' TTGCAGAGATGAGTGGTGAATG 69000    TG A  TT  ____    TG
           GTGTCT                 AT  T TG  GCT    TCTG  G
                                ||  | ||  |||    ||||  |
                                TG  A GT  TGA    AGAC  T
                                 GT A  GG   GTAG    GT
GAM260  LOC92465  5' CAGGAGGACAGTGTCT      69404         ATGTTG
                                GGGCATTGT     CTTCTG
                                |||||||||     ||||||
                                TCTGTGACA     GAGGAC
                                     G_____
GAM260  LOC92465  5' CCATGGAGGTGGCGTCATCCTC 69405     CAT  T    TG
                                GGG   TG ATGT  CTTCTGTGG
                                |||   || ||||  |||||||||
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                                CTC   AC TGCG  GGAGGTACC
                                  CT_  _    GT
GAM260  LOC92539  5' CCACAATGACACATATGATGCC 69632       TG    TGCTTC
             C                    GGGCAT  TATGT     TGTGG
                                  ||||||  |||||     |||||
                                  CCCGTA  ATACA     ACACC
                                     GT    CAGTA_
GAM260  LOC92539  5' TTATAGTAAAACAGTGGTGCTT 69644       TG A    GCTT
                                  GGGCAT  T TGTT    CTGTGG
                                  ||||||  | ||||    ||||||
                                  TTCGTG  G ACAA    GATATT
                                     GT _    AAT_
GAM260  LOC92558  3' CTGTGGGGGGCAGCGGGCCAGGC 69752     ATT  A         TG
             CT                     GGGC   GT TGTTGCTTCTG  G
                                  ||||   || ||||||||||  |
                                  TCCG   CG GCGACGGGGGT  C
                                    GAC  G         GT
GAM260  LOC92573  5' CCACAGATGGGACTATAGTGCT 69803         T   GCT
             T                    GGGCATTGTA GTT   TCTGTGG
                                  ||||||||||| |||   |||||||
                                  TTCGTGATAT CAG   AGACACC
                                        _  GGT
GAM260  LOC92703  3' AGTAATGTACATGCTC      56427       T
                                  GGGCAT GTATGTTGCT
                                  |||||| ||||||||||
                                  CTCGTA CATGTAATGA
                                  _
GAM260  LOC92736  3' CTGTACCCAGCGTGCTGGTGTT 70427        _       CTTCTGTGG
             C                    GGGCATT GTATGTTG
                                  |||||||  ||||||||
                                  CTTGTGG CGTGCGAC
                                     T       CCATGTC
GAM260  LOC92997  3' CCATGGTGTGTCTGCAGTGTTC 71088         TGT   TT
                                  GGGCATTGTA   TGC  CTGTGG
                                  ||||||||||   |||  ||||||
                                  CTTGTGACGT   GTG  GGTACC
                                        CT_   T_
GAM260  LOC93070  3' CCACCAGAGTGGATAATGCTT  71289         ATG TG   CT
                                  GGGCATTGT   T  CTT  GTGG
                                  |||||||||   |  |||  ||||
                                  TTCGTAATA   G  GAG  CACC
                                        ___ GT   AC
GAM260  LOC93082  3' CGCAAGGAATGTATAAAGTTC  56441      A       G  TC  TG
                                  GGGC TTGTATGTT CT  TG  G
                                  |||| |||||||||  ||  ||  |
                                  CTTG AATATGTAA GA  AC  C
                                    A       G  __  GT
GAM260  LOC93129  3' TGCAGAAGGGATGGTGCCT   71471       GTAT   G     TG
                                  GGGCATT    GTT CTTCTG  G
                                  |||||||    ||| ||||||  |
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                                TCCGTGG   TAG GAAGAC  T
                                   ____  G     GT
GAM260  LOC93166  3'  CCACGGAAGCAGAGTGAGAGCC 71623     A  G   G
            T                    GGGC TT TAT TTGCTTCTGTGG
                                 |||| || ||| ||||||||||||
                                 TCCG AG GTG GACGAAGGCACC
                                   _ A   A
GAM260  LOC93206  5'  CATGGGAGCCTCAGTTTCC   71726    C   TATGTT
                                 GGG ATTG     GCTTCTGTG
                                 ||| ||||     |||||||||
                                 CCT TGAC     CGAGGGTAC
                                   T   TC____
GAM260  LOC93356  5'  TTACAGGGGAAATGATGTGTGA 72082   A TG     ___
            GGCTC                  C T  TATGTTG   CTTCTGTGG
                                 | |  |||||||   |||||||||
                                 G A  GTGTAGT   GGGGACATT
                                  G GT      AAA
GAM260  LOC93589  3'  CTGTGAGGGCAGTATTAATGCC 72669        T      TC  TG
            C                     GGGCATTG ATGTTGCT  TG  G
                                 |||||||| ||||||||  ||  |
                                 CCCGTAAT TATGACGG  GT  C
                                    _      GA  GT
GAM260  LOC94431  5'  TCATTAAGGAAGGCGATGTAGA 68595     G      _   ___
            TGTTT                   ATT TATGTTGC TTCT   GTGG
                                 ||| |||||||| ||||   ||||
                                 TAG ATGTAGCG AAGG   TACT
                                   _      G    AAT
GAM261  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                 ATTT ACTTT   TGTCTGAG
                                 |||| |||||   ||||||||
                                 TAAA TGAAA   ACAGATTC
                                   A    T__
GAM261  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                 CATTT   TTT AC GTCTGAGAT
                                 |||||   ||| || |||||||||
                                 GTAAA   AAA TG TAGACTCTA
                                    TA_   T  _
GAM261  FDFT1    3'  TAGGAAAGTGAAATG      15518           A
                                 CATTTCACTTTC CTG
                                 |||||||||||| |||
                                 GTAAAGTGAAAG GAT
                                              _
GAM261  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                     CATTTCACTTTCACTGTCTGAGAT
                                 ||||||||||||||||||||||||
                                 GTAAAGTGAAAGTGACAGACTCTA

GAM261  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                 CA  TTCACTGTCTG GA
                                 ||  |||||||||| ||
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                                GT  AGGTGACAGAC CT
                                 AT         C
GAM261  PHYH    3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                     A
GAM261  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM261  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM261  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM261  CG012   5'  CTCACTCTGAAAGTGAA     83218          CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM261  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                |||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM261  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                |||||||       |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM261  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM261  KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM261  KLHL6   3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
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                                AAAG GAC AGACTCTA
                                  _  G
GAM261  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM261  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM261  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM261  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148         TCAC   C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM261  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM261  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM261  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM261  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM261  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||   |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM261  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
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                                GTAAAGTGAA GTGACA
                                      _
GAM262  MMP20    3'  TCCAAATCAACACAATGCAC  16484          CAGGA
                                GTGCATTGTGTTG   TTGGG
                                ||||||||||||   |||||
                                CACGTAACACAAC   AACCT
                                      TA___
GAM262  PIM2     3'  TCCCAATCCTACAAAGGAGC  59991   A  GTG  C
                                GC TT  TTG AGGATTGGGA
                                || ||  ||| ||||||||||
                                CG AG  AAC TCCTAACCCT
                                 _ GA_  A
GAM262  RXRA     3'  CCCAATCCTTAGCAATGC   11405       GTTGC
                                GCATTGT   AGGATTGGG
                                |||||||   |||||||||
                                CGTAACG   TCCTAACCC
                                    AT___
GAM262  BRAG     3'  TCCCAATTCCAAAACACAATGC 29477          GCA
            AC                   GTGCATTGTGTT  GGATTGGGA
                                ||||||||||||  |||||||||
                                CACGTAACACAA  CTTAACCCT
                                      AAC
GAM262  DKFZp547O146 5'  CCCAATCCCCCAACAC     39564       CA
                                GTGTTG  GGATTGGG
                                ||||||  ||||||||
                                CACAAC  CCTAACCC
                                   CC
GAM262  KIAA1762  3'  TCCCAATCCCCACAGACACACA 63792    CAT    GCA__
            C                    GTG  TGTGTT   GGATTGGGA
                                |||  ||||||   |||||||||
                                CAC  ACACAG   CCTAACCCT
                                 ___    ACACC
GAM262  LOC145820 3'  CCCAATCCTTAAGCAATCAC  77512    C    GTTGC
                                GTG ATTGT   AGGATTGGG
                                ||| |||||   |||||||||
                                CAC TAACG   TCCTAACCC
                                  _   AAT__
GAM262  LOC253980 3'  TCCCAACCCCATTGCTAACAA  95076     GTT  ___  A
                                TTGT  GCA  GG TTGGGA
                                ||||  |||  || ||||||
                                AACA  CGT  CC AACCCT
                                  AT_  TAC  C
GAM263  ARCN1    3'  AGACTGCACTCTCTGTCA   7970         CA_
                                TGACAGAGA  CAGTTT
                                |||||||||  ||||||
                                ACTGTCTCT  GTCAGA
                                     CAC
GAM263  CBFA2T2  3'  GAGCAAAACTCTGTCT     17466      C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
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                                TCTGT TCAAAACGAG
                                   C
GAM263  CTLA4    3'  CAGAGCTGGGATGTTTCTGTCA 17807          CAGTTTT
                                TGACAGAGACA      GCTCTG
                                ||||||||||       ||||||
                                ACTGTCTTTGT      CGAGAC
                                     AGGGT__
GAM263  ITK      3'  CAGAACAGGAGTGATGTCTCTG 18674        _ G    C
                                CAGAGACA CA TTTTG TCTG
                                |||||||| || ||||| ||||
                                GTCTCTGT GT AGGAC AGAC
                                     A G    A
GAM263  LAMP2    3'  GGTGAAACCCCATCTCTATCA 25716    C    CACA    TG
                                TGA AGAGA    GTTT  CT
                                ||| |||||    ||||  ||
                                ACT TCTCT    CAAA  GG
                                  A    ACCC    GT
GAM263  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA  40865       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM263  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA  52960       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM263  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA  52963       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM263  PDGFRB   5'  CAGAGCCTGGAACTGTG    65969         __
                                CACAGTTTT  GCTCTG
                                |||||||||  ||||||
                                GTGTCAAGG  CGAGAC
                                     TC
GAM263  PTPRA    3'  AGAGCGGTATCTCTG      55087       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM263  PTPRA    3'  AGAGCGGTATCTCTG      55079       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM263  PTPRA    3'  AGAGCGGTATCTCTG      11088       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
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                                GTCTCT TG    GCGAGA
                                   A _____
GAM263  RAD51L3  3'  CAAAACTCAGGTATGTCTCTGT 56065        C_____
                                ACAGAGACA    AGTTTTG
                                |||||||||    |||||||
                                TGTCTCTGT    TCAAAAC
                                     ATGGAC
GAM263  TBL2     3'  CAGAACTGTGTTCCATCA    52178    CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM263  TBL2     3'  CAGAACTGTGTTCCATCA    24924    CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM263  AGTRL2   5'  CAGAGCAAGAACTGTTC    17691    C     _
                                GA ACAGTTTT GCTCTG
                                || |||||||| ||||||
                                CT TGTCAAGA CGAGAC
                                 _      A
GAM263  CABP5    3'  AGAGCGGTATCTTTGCCA    39079    A    C  AGTTT
                                TG CAGAGA AC    TGCTCT
                                || |||||| ||    ||||||
                                AC GTTTCT TG    GCGAGA
                                 C     A _____
GAM263  CUL4A    5'  AGAGCAGCACCTCCATCA    13149    CA  ACACA  T
                                TGA  GAG    GT TTGCTCT
                                |||  |||    || |||||||
                                ACT  CTC    CA GACGAGA
                                  AC  _____  C
GAM263  DKFZp761O17121 3'  CAGACAGCCCCTGTGTCTCTGT 50136          TT_  C
           C                    GACAGAGACACAG   TTG TCTG
                                ||||||||||||   ||| ||||
                                CTGTCTCTGTGTC   GAC AGAC
                                       CCC  _
GAM263  FLJ10375 3'  CAGAGGCCTGTGTCTGTGCCA  36073    A  G      TTTTG
                                TG CA AGACACAG    CTCTG
                                || || ||||||||    |||||
                                AC GT TCTGTGTC    GAGAC
                                 C  G       CG___
GAM263  FLJ10738 5'  CAAAGCCAGCCCTCTGTCA   36527        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
                                ACTGTCTC    CGAAAC
                                     CCGAC
GAM263  FLJ10803 3'  CAAAACAAAACTCTGTCA    36660        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
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                                ACTGTCTC    CAAAAC
                                    AAAA_
GAM263  FLJ10842  3'  AAAGTGTGCTCTGTCA     36723        A   G
                                TGACAGAG CACA TTT
                                |||||||| |||| |||
                                ACTGTCTC GTGT AAA
                                    _   G
GAM263  FLJ13153  3'  CAGAGCCCAGCATCCATCTCTG 45555        CACA_  TT
          TCA                    TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                    ACCTA   CC
GAM263  FLJ20035  3'  CAAACCTGCCATGTTCTGTCA  34395        A ___  T
                                TGACAGAG CA   CAG TTTG
                                |||||||| ||   ||| ||||
                                ACTGTCTT GT   GTC AAAC
                                    _ ACC   C
GAM263  FLJ22195  5'  CAGAGCAGAGGGAAGTCTCTGC 42800    A     ACAG
          CA                     TG CAGAGAC    TTTTGCTCTG
                                || |||||||    ||||||||||
                                AC GTCTCTG    GAGACGAGAC
                                 C      AAGG
GAM263  FLJ32191  5'  GAACTGCACCTCTGTCA     58411        ACA
                                TGACAGAG   CAGTTT
                                ||||||||   ||||||
                                ACTGTCTC   GTCAAG
                                    CAC
GAM263  KIAA1023  3'  CAAAGCTGTATCTGCTATCA   34255    C  _   C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM263  KIAA1586  5'  AGTGTGATGTGTCTCTG     92326         GTT TG T
                                CAGAGACACA   T  C CT
                                ||||||||||   |  | ||
                                GTCTCTGTGT   A  G GA
                                    ___ GT T
GAM263  KIAA1754  3'  GACTAACGTCTCTGTCA     63236         AC_
                                TGACAGAGAC   AGTT
                                ||||||||||   ||||
                                ACTGTCTCTG   TCAG
                                    CAA
GAM263  LANCL2    3'  CAGAGTGCACTGCAGCTCTGTC 37995        ACA    TTT
          A                     TGACAGAG   CAGT   GCTCTG
                                ||||||||   ||||   ||||||
                                ACTGTCTC   GTCA   TGAGAC
                                    GAC    CG_
GAM263  LIG-1     3'  CAGAGCAGGCCTGTCCATGCCA 63893    A  GAGAC    TT
                                TG CA    ACAG  TTGCTCTG
                                || ||    ||||  ||||||||
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                                AC GT    TGTC  GACGAGAC
                                 C  ACC__   CG
GAM263  MGC5242  3'  AGAGTACATGTCTCTG     43823        CAGTTT
                                CAGAGACA    TGCTCT
                                ||||||||    ||||||
                                GTCTCTGT    ATGAGA
                                    AC____
GAM263  OSMR     3'  CAGAGCTGGCACCCTGTCA   14345       AGACA
                                TGACAG    CAGTTTTG
                                ||||||    ||||||||
                                ACTGTC    GTCGAGAC
                                   CCACG
GAM263  RAB21    3'  CAGAACAAAACTGTGGATC   30383    GA        C
                                GA  CACAGTTTTG TCTG
                                ||  |||||||||| ||||
                                CT  GTGTCAAAAC AGAC
                                 AG         A
GAM263  SPTLC2   3'  CAGAGCAAAACTGTGTCTC   16799
                                GAGACACAGTTTTGCTCTG
                                |||||||||||||||||||
                                CTCTGTGTCAAAACGAGAC

GAM263  TGIF2    3'  GAGTCATGCTCTGTCA      41454        A  CAGTTT  _
                                TGACAGAG CA     TG CTC
                                |||||||| ||     || |||
                                ACTGTCTC GT     AC GAG
                                    _  _______  T
GAM263  WBSCR23  5'  GCTGACTGTGTCTCCATCA   46765     CA        TT
                                TGA  GAGACACAGTT  GC
                                |||  ||||||||||  ||
                                ACT  CTCTGTGTCAG  CG
                                  AC         T_
GAM263  LOC115129 3' GGCAAAACCCCGTCTCT     73235       ACA
                                AGAGAC   GTTTTGCT
                                ||||||   ||||||||
                                TCTCTG   CAAAACGG
                                   CCC
GAM263  LOC129198 3' AGCAAGCTGTGCCTC       76117     A       T
                                GAG CACAGTTT GCT
                                ||| |||||||| |||
                                CTC GTGTCGAA CGA
                                  C       _
GAM263  LOC145231 3' GGTGAAACTATGTCTCT     83293        C     TG
                                AGAGACA AGTTT  CT
                                ||||||| |||||  ||
                                TCTCTGT TCAAA  GG
                                    A    GT
GAM263  LOC145483 3' GAGCAAAACTCTGTCT      77243       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
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                                TCTGT TCAAAACGAG
                                   C
GAM263  LOC146713 3'  GAGCAAAACTCCGTCT      83726      AC
                                AGAC  AGTTTTGCTC
                                ||||  ||||||||||
                                TCTG  TCAAAACGAG
                                  CC
GAM263  LOC149175 3'  CAGGGTGAAACCACGTCTCT   79208       ACA    TG
                                AGAGAC   GTTT  CTCTG
                                ||||||   ||||  |||||
                                TCTCTG   CAAA  GGGAC
                                   CAC    GT
GAM263  LOC150299 3'  CAGAACCTGCATCTTTGTCA   84968         CA   _
                                TGACAGAGA  CAG TTTTG
                                |||||||||  ||| |||||
                                ACTGTTTCT  GTC AAGAC
                                     AC   C
GAM263  LOC153277 3'  TAAAACTGTGCCTGTGCCA    85990    A  G  A
                                TG CA AG CACAGTTTTG
                                || || || ||||||||||
                                AC GT TC GTGTCAAAAT
                                 C  G  C
GAM263  LOC155179 3'  CAAAGCTGTATCTGCTATCA   81312     C  _   C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM263  LOC221074 3'  AAAGTGTGTCTCTTTCA     93177     C        G
                                TGA AGAGACACA TTT
                                ||| ||||||||| |||
                                ACT TCTCTGTGT AAA
                                  T        G
GAM263  LOC221103 5'  AGTTTATGTGTGCTCTGTCA   93244         _     GTTTT
                                TGACAGAG ACACA     GCT
                                |||||||| |||||     |||
                                ACTGTCTC TGTGT     TGA
                                     G     ATT__
GAM263  LOC255988 5'  CAGAGCCCAGCATCCATCTCTG 97608          CACA_   TT
           TCA                    TGACAGAGA     GTT  GCTCTG
                                |||||||||     |||  ||||||
                                ACTGTCTCT     CGA  CGAGAC
                                     ACCTA   CC
GAM264  ABCC3    3'  GCACCTGGAGGACAGCT     39154     AAAAG
                                AGC     CTTTTAGGTGT
                                |||     ||||||||||
                                TCG     GGAGGTCCACG
                                  ACA__
GAM264  ABCC3    3'  ACGCCTAAGGTCACAGCT    39138     AAAA     T
                                AGC    GCTTT AGGTGT
                                |||    ||||| ||||||
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                                TCG    TGGAA TCCGCA
                                  ACAC    _
GAM264   ABCC3    3'  ACGCCTAAGGTCACAGCT    13691     AAAA     T
                                AGC    GCTTT AGGTGT
                                |||    ||||| ||||||
                                TCG    TGGAA TCCGCA
                                  ACAC    _
GAM264   ABCC3    3'  ACGCCTAAGGTCACAGCT    39145     AAAA     T
                                AGC    GCTTT AGGTGT
                                |||    ||||| ||||||
                                TCG    TGGAA TCCGCA
                                  ACAC    _
GAM264   ABCC3    3'  ACGCCTGGGAGCCCAGCTT    39146      AAAA
                                GAGC    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                TTCG    CGAGGGTCCGCA
                                  ACC_
GAM264   ABCC5    3'  ACAAAATTTAGTTTTTGTTC    19093          TTTAGG
                                GAGCAAAAGCT     TGT
                                ||||||||||      |||
                                CTTGTTTTTGA     ACA
                                      TTTAAA
GAM264   ABCD4    3'  GCAGCTCCGTCTTTTGCTC    39738         CTTTT  G
                                GAGCAAAAG     AG TGT
                                |||||||||     || |||
                                CTCGTTTTC     TC ACG
                                     TGCC_  G   T
GAM264   ACOX3    3'  GCGCCTAAACTGCTGATTG    13024     A_   T_
                                CAA  AGC  TTTAGGTGT
                                |||  |||  |||||||||
                                GTT  TCG  AAATCCGCG
                                  AG   TC
GAM264   ACPP     3'  GCATCTAAAGGACAGGCTTTTG 66849   A       _____
            CCA                    GCAAAAGCT     TTTAGGTGT
                                   |||||||||     |||||||||
                                   CGTTTTCGG     AAATCTACG
                                _        ACAGG
GAM264   ACRV1    5'  TAGCACTGGAAGCTTTTGCTC  39203             G
                                GAGCAAAAGCTTTTAG TGT
                                |||||||||||||||| |||
                                CTCGTTTTCGAAGGTC ACG
                                        _   ATT
GAM264   ACRV1    5'  TAGCACTGGAAGCTTTTGCTC  39183             G
                                GAGCAAAAGCTTTTAG TGT
                                |||||||||||||||| |||
                                CTCGTTTTCGAAGGTC ACG
                                        _   ATT
GAM264   ACRV1    5'  TAGCACTGGAAGCTTTTGCTC  39208             G
                                GAGCAAAAGCTTTTAG TGT
                                |||||||||||||||| |||
```

```
                                CTCGTTTTCGAAGGTC ACG
                                      _  ATT
GAM264  ACRV1   5' TAGCACTGGAAGCTTTTGCTC 39188          G
                                GAGCAAAAGCTTTTAG TGT
                                |||||||||||||||| |||
                                CTCGTTTTCGAAGGTC ACG
                                      _  ATT
GAM264  ACRV1   5' TAGCACTGGAAGCTTTTGCTC 39198          G
                                GAGCAAAAGCTTTTAG TGT
                                |||||||||||||||| |||
                                CTCGTTTTCGAAGGTC ACG
                                      _  ATT
GAM264  ACRV1   5' TAGCACTGGAAGCTTTTGCTC 39178          G
                                GAGCAAAAGCTTTTAG TGT
                                |||||||||||||||| |||
                                CTCGTTTTCGAAGGTC ACG
                                      _  ATT
GAM264  ACRV1   5' TAGCACTGGAAGCTTTTGCTC 39218          G
                                GAGCAAAAGCTTTTAG TGT
                                |||||||||||||||| |||
                                CTCGTTTTCGAAGGTC ACG
                                      _  ATT
GAM264  ACRV1   5' TAGCACTGGAAGCTTTTGCTC 39213          G
                                GAGCAAAAGCTTTTAG TGT
                                |||||||||||||||| |||
                                CTCGTTTTCGAAGGTC ACG
                                      _  ATT
GAM264  ACRV1   5' TAGCACTGGAAGCTTTTGCTC 39193          G
                                GAGCAAAAGCTTTTAG TGT
                                |||||||||||||||| |||
                                CTCGTTTTCGAAGGTC ACG
                                      _  ATT
GAM264  ACRV1   5' TAGCACTGGAAGCTTTTGCTC 7862           G
                                GAGCAAAAGCTTTTAG TGT
                                |||||||||||||||| |||
                                CTCGTTTTCGAAGGTC ACG
                                      _  ATT
GAM264  ACTN2   3' GTGTCTAAAGGCCTGCTC   6593     AAA     TG
                                GAGCA  GCTTTTAGG  T
                                |||||  |||||||||  |
                                CTCGT  CGGAAATCT  G
                                   C__      GT
GAM264  ADAM19  3' GCACCTGGAGATGTTTGCT  52707     AGC
                                AGCAAA  TTTTAGGTGT
                                ||||||  ||||||||||
                                TCGTTT  GAGGTCCACG
                                   GTA
GAM264  ADAM28  3' ATGCCTGAGAACCTTTGC   26536     AGC
                                GCAAA  TTTTAGGTGT
                                |||||  ||||||||||
```

```
                                CGTTT  AGAGTCCGTA
                                  CCA
GAM264  ADH5    3' ATATCTGAAGCTCTCGTTCA  5417      AAA    T
                                TGAGC  AGCTTT AGGTGT
                                |||||  |||||| ||||||
                                ACTTG  TCGAAG TCTATA
                                  CTC    _
GAM264  ADORA3  3' ACACTTGAGGGCCTGTATGC  5437     AAA__
                                GCA    GCTTTTAGGTGT
                                |||    ||||||||||||
                                CGT    CGGGAGTTCACA
                                 ATGTC
GAM264  ADORA3  3' ATGCCTAGAAGATGTTG    5439     AAG
                                CAA  CTTTTAGGTGT
                                |||  ||||||||||
                                GTT  GAAGATCCGTA
                                 GTA
GAM264  AGL     3' ATGCTTGAAAGCTCGTGT    5367     AA
                                GCA AGCTTTTAGGTGT
                                ||| ||||||||||||
                                TGT TCGAAAGTTCGTA
                                 GC
GAM264  AGL     3' ATGCTTGAAAGCTCGTGT    5354     AA
                                GCA AGCTTTTAGGTGT
                                ||| ||||||||||||
                                TGT TCGAAAGTTCGTA
                                 GC
GAM264  AGL     3' ATGCTTGAAAGCTCGTGT    5342     AA
                                GCA AGCTTTTAGGTGT
                                ||| ||||||||||||
                                TGT TCGAAAGTTCGTA
                                 GC
GAM264  AGL     3' ATGCTTGAAAGCTCGTGT    3446     AA
                                GCA AGCTTTTAGGTGT
                                ||| ||||||||||||
                                TGT TCGAAAGTTCGTA
                                 GC
GAM264  AGL     3' ATGCTTGAAAGCTCGTGT    5375     AA
                                GCA AGCTTTTAGGTGT
                                ||| ||||||||||||
                                TGT TCGAAAGTTCGTA
                                 GC
GAM264  AGL     3' ATGCTTGAAAGCTCGTGT    5361     AA
                                GCA AGCTTTTAGGTGT
                                ||| ||||||||||||
                                TGT TCGAAAGTTCGTA
                                 GC
GAM264  AGT     3' GCACCTGAATTTCTGTTT    3456      A  CT
                                GAGCA AAG  TTTAGGTGT
                                ||||| |||  |||||||||
```

```
                                TTTGT TTT  AAGTCCACG
                                  C  __
GAM264  AKAP13   3' GTGCCTGAAACTGTGCTTA   89685      AA  C     TG
                                TGAGCA  AG TTTTAGG  T
                                ||||||  || |||||||  |
                                ATTCGT  TC AAAGTCC  G
                                   G_  _     GT
GAM264  AKAP13   3' GCCTGTGCTTTTGCTCA    89683         TTT
                                TGAGCAAAAGC  TAGGT
                                ||||||||||  |||||
                                ACTCGTTTTCG  GTCCG
                                      T__
GAM264  AKAP2    3' ACATCTCTTAACTTTTGCT   23255       CTTTT
                                AGCAAAAG   AGGTGT
                                ||||||||   ||||||
                                TCGTTTTC   TCTACA
                                    AATTC
GAM264  AKAP4    3' ACACTTGAGCAGTTGC     13946     AA   TT
                                GCAA  GCTT  AGGTGT
                                ||||  ||||  ||||||
                                CGTT  CGAG  TTCACA
                                  GA   __
GAM264  AKAP4    3' ACACTTGAGCAGTTGC     57768     AA   TT
                                GCAA  GCTT  AGGTGT
                                ||||  ||||  ||||||
                                CGTT  CGAG  TTCACA
                                  GA   __
GAM264  ALB      3' ACATTTAAAAGCATCTCA    4889      CAAAA
                                TGAG   GCTTTTAGGTGT
                                ||||   ||||||||||||
                                ACTC   CGAAAATTTACA
                                  TA___
GAM264  ALDH3B2  5' GCATCTGGAGGCAGC      5506     AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   CGGAGGTCTACG
                                 A___
GAM264  ANK1     5' GCACTTGGGCGGGCTGCTT   40036      AAA_  TT
                                GAGCA   GCT  TAGGTGT
                                |||||   |||  |||||||
                                TTCGT   CGG  GTTCACG
                                  CGGG  __
GAM264  ANK1     5' GCACTTGGGCGGGCTGCTT   40033      AAA_  TT
                                GAGCA   GCT  TAGGTGT
                                |||||   |||  |||||||
                                TTCGT   CGG  GTTCACG
                                  CGGG  __
GAM264  ANK1     5' GCACTTGGGCGGGCTGCTT   40039      AAA_  TT
                                GAGCA   GCT  TAGGTGT
                                |||||   |||  |||||||
```

```
                              TTCGT   CGG  GTTCACG
                                 CGGG  __
GAM264  ANKRD3   3' ATACCTTATCAGCTGTTGCTT  40196      A   TTT_
                              GAGCAA AGCT   AGGTGT
                              |||||| ||||   ||||||
                              TTCGTT TCGA   TCCATA
                                 G   CTAT
GAM264  APPL     3' ACATCTAAAGGAAACCTGCTC  23922     AAAG_
                              GAGCA   CTTTTAGGTGT
                              |||||   ||||||||||
                              CTCGT   GGAAATCTACA
                                 CCAAA
GAM264  APPL     3' TTTATTAAAAGATTTTTGTTCA 23934        _     GTGT
                              TGAGCAAAAG CTTTTAG
                              |||||||||| |||||||
                              ACTTGTTTTT GAAAATT
                                    A     ATTTA
GAM264  APTX     5' ACATTTGGAAGCAGTTGT   34656     AA
                              GCAA  GCTTTTAGGTGT
                              ||||  ||||||||||||
                              TGTT  CGAAGGTTTACA
                                GA
GAM264  ARHGAP6  3' GCGCCTGGGGGACGCTGGCT  6765     AAAAG_
                              AGC     CTTTTAGGTGT
                              |||     ||||||||||
                              TCG     GGGGGTCCGCG
                                GTCGCA
GAM264  ARHGDIB  3' TGCCTAGATTCTTTTG     6774       CT
                              CAAAAG  TTTAGGTG
                              ||||||  ||||||||
                              GTTTTC  AGATCCGT
                                 TT
GAM264  ARHGEF1  3' ACGCCTGGGAGGGGCCCA    16298    A  AAAAG
                              TG GC    CTTTTAGGTGT
                              || ||    ||||||||||
                              AC CG    GAGGGTCCGCA
                               C  GG___
GAM264  ARHGEF12 3' TACCTGGAGGTTTGACTC    31003    CAA        GT
                              GAG   AAGCTTTTAGGT
                              |||   ||||||||||||
                              CTC   TTTGGAGGTCCA
                                AG_         TG
GAM264  ARHGEF12 3' ATGCCTAAAAGACTTT      30995     _
                              AAAG CTTTTAGGTGT
                              |||| ||||||||||
                              TTTC GAAAATCCGTA
                                A
GAM264  ARHGEF6  3' GCGCTTGGGCATTTGCT     68203      A  TT
                              AGCAAA GCT  TAGGTGT
                              |||||| |||  |||||||
```

```
                                TCGTTT CGG  GTTCGCG
                                   A  __
GAM264  ARHGEF7  5' GCATCTGGGGCAGCGGGCTC  14006     AAAA  __
                                GAGC   GCT  TTTAGGTGT
                                ||||   |||  |||||||||
                                CTCG   CGA  GGGTCTACG
                                  GG__  CG
GAM264  ARHGEF7  3' GCACCTGAATCCTTTGTGT   14005    _   CT
                                GCA AAAG  TTTAGGTGT
                                ||| ||||  |||||||||
                                TGT TTTC  AAGTCCACG
                                  G   CT
GAM264  ARNT2    3' ACTGCAGTTTTTGCTTA     29452          TTTA
                                TGAGCAAAAGCT   GGT
                                ||||||||||||   |||
                                ATTCGTTTTTGA   TCA
                                       CG__
GAM264  ARSD     3' ACCTCGGGGAGTTTTTGCTCA  23793           __   GT
                                TGAGCAAAAGCTTTT  AGGT
                                ||||||||||||||  ||||
                                ACTCGTTTTTGAGGG  TCCA
                                        GC
GAM264  ASCL1    5' GCATTTTCACTTTTTTTGCTC  72777        CTTTT_
                                GAGCAAAAG     AGGTGT
                                |||||||||     ||||||
                                CTCGTTTTT     TTTACG
                                     TTCACT
GAM264  ASCL1    3' ACAGCTGAAAGTTCTTGCTC   72774       A       G
                                GAGCAA AGCTTTTAG TGT
                                |||||| ||||||||| |||
                                CTCGTT TTGAAAGTC ACA
                                   C        G   C
GAM264  ASCL1    3' ATGCCTGAGAGACATGGCTT   72775     AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                TTCG    GAGAGTCCGTA
                                  GTACA
GAM264  ASTN     3' ACATCTAGAGTGTTGTTT    69326       AA    T
                                GAGCAA  GCTTT AGGTGT
                                ||||||  ||||| ||||||
                                TTTGTT  TGAGA TCTACA
                                   G_    _
GAM264  ATP10C   3' ACACTTGAAAAGTGTGTTTA  44406       AAAGC
                                TGAGCA    TTTTAGGTGT
                                ||||||    ||||||||||
                                ATTTGT    AAAGTTCACA
                                   GTGA_
GAM264  ATP10C   3' ACACCTGAGCTGCTGC     44405     AA    TT
                                GCA  AGCTT  AGGTGT
                                |||  |||||  ||||||
```

```
                                CGT  TCGAG  TCCACA
                                  CG    __
GAM264  ATP2B3   5' ACGCTTAGCAGCTTTCTCA   41691     CA     T
                                TGAG  AAAGCT TTAGGTGT
                                ||||  |||||| ||||||||
                                ACTC  TTTCGA GATTCGCA
                                  __     C
GAM264  ATP2B4   3' ACACCTAAAGGCCTGT     70340     AAA
                                GCA   GCTTTTAGGTGT
                                |||   ||||||||||||
                                TGT   CGGAAATCCACA
                                  C__
GAM264  ATP6V1C1 3' ACATTTATACTGTTTTGTTCA 8089         GCTTT
                                TGAGCAAAA    TAGGTGT
                                |||||||||    |||||||
                                ACTTGTTTT    ATTTACA
                                     GTCAT
GAM264  ATP8A2   3' TAGCCTAACTTTTGTTTA    93517         CTT     GT
                                TGAGCAAAAG   TTAGGT
                                ||||||||||   ||||||
                                ATTTGTTTTC   AATCCG
                                     ___     ATT
GAM264  ATRX     3' GTGTAAAGCGTTTTTGCTTA   56248          _    GGTGT
                                TGAGCAAAAGC TTTTA
                                |||||||||||| |||||
                                ATTCGTTTTTG GAAAT
                                      C     GTG
GAM264  ATRX     3' GTGTAAAGCGTTTTTGCTTA   4917           _    GGTGT
                                TGAGCAAAAGC TTTTA
                                |||||||||||| |||||
                                ATTCGTTTTTG GAAAT
                                      C     GTG
GAM264  B2M      3' TATCTGAGCAGGTTGCTC     14461       AA_   TT   GT
                                GAGCAA   GCTT  AGGT
                                ||||||   ||||  ||||
                                CTCGTT   CGAG  TCTA
                                   GGA   __    TG
GAM264  B3GNT4   5' ACACCTGAGACTCATCTC    66445     CAAA  C
                                GAG    AG TTTTAGGTGT
                                |||    || ||||||||||
                                CTC    TC AGAGTCCACA
                                  TAC_  _
GAM264  B4GALT4  3' ATACTTGAAGGACTTT      13670      _
                                AAAG CTTTTAGGTGT
                                |||| ||||||||||
                                TTTC GGAAGTTCATA
                                  A
GAM264  B4GALT7  3' GTGCCTGGGACGCTGCTTGC  23416      A_  _      TG
                                GCAA  AGC TTTTAGG  T
                                ||||  ||| |||||||  |
```

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                                CGTT  TCG AGGGTCC  G
                                  CG  C     GT
GAM264  BACH2   3'  GCATTTGGGAGCTTCAGGT   41489   AA_
                                GC  AAGCTTTTAGGTGT
                                ||  ||||||||||||||
                                TG  TTCGAGGGTTTACG
                                 GAC
GAM264  BARX2   3'  GCGCCTAGGAGCTGCCTGC   13342    AA_
                                GCA  AGCTTTTAGGTGT
                                |||  ||||||||||||
                                CGT  TCGAGGATCCGCG
                                  CCG
GAM264  BAT4    3'  GCAGATCCTGAAGTTTTTGGTC 52583    G       T  ___
          A                      TGA CAAAAGCTTT AGG  TGT
                                ||| |||||||||| |||  |||
                                ACT GTTTTTGAAG TCC  ACG
                                  G       _  TAG
GAM264  BAZ1B   3'  ACACCTGAATTGTTTGTT   50536      AGCT
                                AGCAAA   TTTAGGTGT
                                ||||||   |||||||||
                                TTGTTT   AAGTCCACA
                                   GTT_
GAM264  BCL11A  3'  ATACTTAAGGGAAAAGTTGC  43158    AAG__
                                GCAA   CTTTTAGGTGT
                                ||||   ||||||||||
                                CGTT   GGGAATTCATA
                                  GAAAA
GAM264  BCL11B  3'  GCACTTTAAAGCTTTTGTTT  43191          T
                                GAGCAAAAGCTTT AGGTGT
                                |||||||||||| ||||||
                                TTTGTTTTCGAAA TTCACG
                                        T
GAM264  BCL2    3'  CACCTAAACCTTTTG      5299       CT
                                CAAAAG  TTTAGGTG
                                ||||||  ||||||||
                                GTTTTC  AAATCCAC
                                   C_
GAM264  BCL6    5'  TGGCTTTGAGGGCTTTTGGTT  8128    G         _  GT
                                GA CAAAAGCTTTTAG GT
                                || ||||||||||||| ||
                                TT GTTTTCGGGAGTT CG
                                 G          T  GTG
GAM264  BCLG    3'  ATACCTAGGAAGATGTTGCT  47777     AAG   _
                                AGCAA  CTTT TAGGTGT
                                |||||  |||| |||||||
                                TCGTT  GAAG ATCCATA
                                  GTA  G
GAM264  BCLG    3'  ATACCTAGGAAGATGTTGCT  56979     AAG   _
                                AGCAA  CTTT TAGGTGT
                                |||||  |||| |||||||
```

```
                                TCGTT  GAAG ATCCATA
                                  GTA   G
GAM264  BCLG    3'  ATACCTAGGAAGATGTTGCT  56973     AAG  _
                                AGCAA  CTTT TAGGTGT
                                |||||  |||| |||||||
                                TCGTT  GAAG ATCCATA
                                  GTA   G
GAM264  BDKRB2  3'  ACACCTGAGCCAGCCTGCTC  5261      AAA  __
                                GAGCA  GCT  TTTAGGTGT
                                |||||  |||  |||||||||
                                CTCGT  CGA  GAGTCCACA
                                  C__   CC
GAM264  BIG1    3'  ATGCTTAGAAGTCTTACTCA  21203     CA  AG
                                TGAG  AA  CTTTTAGGTGT
                                ||||  ||  ||||||||||
                                ACTC  TT  GAAGATTCGTA
                                  A_  CT
GAM264  BPGM    5'  CGCCTGGGAAGTTCA      8174      AAAAGC
                                TGAGC    TTTTAGGTG
                                |||||    |||||||||
                                ACTTG    AGGGTCCGC
                                  A_____
GAM264  BRF1    3'  GCACTTGAGAGGCAGCAGCTC  7712      AAAA  _
                                GAGC   GC TTTTAGGTGT
                                ||||   || ||||||||||
                                CTCG   CG AGAGTTCACG
                                  ACGA  G
GAM264  BTEB1   5'  GTCCTGGGGCTTTGGCTC   6850      A      T  TGT
                                GAGC AAAGCTTT AGG
                                |||| |||||||| |||
                                CTCG TTTCGGGG TCC
                                  G      _  TGT
GAM264  C18orf2 3'  ACATTTAGAAGCTTTCTTC  48631     CA
                                GAG  AAAGCTTTTAGGTGT
                                |||  ||||||||||||||
                                CTT  TTTCGAAGATTTACA
                                 C_
GAM264  C21orf2 3'  GCATCTGAGAGGGGTTT    17012     AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                TTTG    GAGAGTCTACG
                                  GG___
GAM264  CA5B    3'  ATATCTAGGCAGTATTTTGCTT 23323       _  _
                                GAGCAAAA GCT TTTAGGTGT
                                |||||||| ||| |||||||||
                                TTCGTTTT TGA GGATCTATA
                                    A  C
GAM264  CACNA1S 3'  ATGCCTGAGGCAGGGTGGTCA  3563     G  AAA_   T
                                TGA CA   GCTTT AGGTGT
                                ||| ||   ||||| ||||||
```

```
                                ACT GT    CGGAG TCCGTA
                                  G  GGGA    _
GAM264  CALB1    3'  ACATCTGAAAAGAAATGCT    17022      AAAGC
                                AGCA    TTTTAGGTGT
                                ||||    ||||||||||
                                TCGT    AAAGTCTACA
                                  AAAGA
GAM264  CAPZA1   3'  ACACCTAAAGAGGCTATGCT   72621      AA     __
                                AGCA  AGCTTT  TAGGTGT
                                ||||  ||||||  |||||||
                                TCGT  TCGGAG  ATCCACA
                                  A_     AA
GAM264  CCNF     3'  ACGCCTGGGGAGCCTGC     8311      AAA     _
                                GCA   GCTTTT AGGTGT
                                |||   |||||| ||||||
                                CGT   CGAGGG TCCGCA
                                  C__     G
GAM264  CCNT2    3'  TACTTAGGAGCCTCTTTGT    54268      A__        GT
                                GCAAA   GCTTTTAGGT
                                |||||   ||||||||||
                                TGTTT   CGAGGATTCA
                                   CTC         TG
GAM264  CD209L   3'  GCATTTAGGGGGCGGGCTT    26519      AAAA    _
                                GAGC    GCTTT TAGGTGT
                                ||||    ||||| |||||||
                                TTCG    CGGGG ATTTACG
                                  GG__     G
GAM264  CD2AP    3'  GTTCTTAAAGTTTTTGTT    24016          T   TGT
                                AGCAAAAGCTTT AGG
                                |||||||||||| |||
                                TTGTTTTTGAAA TCT
                                       T   TG
GAM264  CD8A     3'  ATACCTGGGATACTGTGCCCA  8331     A   AAAGC
                                TG GCA    TTTTAGGTGT
                                || |||    ||||||||||
                                AC CGT    AGGGTCCATA
                                 C   GTCAT
GAM264  CDC25B   3'  GTGCTTGAAGGCCCTGCT    41565      AAA       TG
                                AGCA   GCTTTTAGG  T
                                ||||   |||||||||  |
                                TCGT   CGGAAGTTC  G
                                  CC_       GT
GAM264  CDC25B   3'  GTGCTTGAAGGCCCTGCT    41569      AAA       TG
                                AGCA   GCTTTTAGG  T
                                ||||   |||||||||  |
                                TCGT   CGGAAGTTC  G
                                  CC_       GT
GAM264  CDKN1B   3'  ATGCTTAAAAGGTTGC      14511      AAG
                                GCAA   CTTTTAGGTGT
                                ||||   ||||||||||
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```
                                CGTT   GAAAATTCGTA
                                  G__
GAM264  CELSR2   3'  AGCCCAGGTGTTTGCTCA    7405        A    TTA   GT
                                TGAGCAAA GCTT   GGT
                                |||||||| ||||   |||
                                ACTCGTTT TGGA   CCG
                                     G    C__   AC
GAM264  CENPC1   5'  ACTTAAGGTTATTGCTT     8416       A     T
                                GAGCAA AGCTTT AGGT
                                |||||| |||||| ||||
                                TTCGTT TTGGAA TTCA
                                   A     _
GAM264  CENTD1   3'  ACATTTGGGGGCTACCTGGTC  30850    G  AA_
                                GA CA   AGCTTTTAGGTGT
                                || ||   ||||||||||||
                                CT GT   TCGGGGGTTTACA
                                 G  CCA
GAM264  CENTD1   3'  ACATTTGGGGGCTACCTGGTC  57561    G  AA_
                                GA CA   AGCTTTTAGGTGT
                                || ||   ||||||||||||
                                CT GT   TCGGGGGTTTACA
                                 G  CCA
GAM264  CHST6    3'  ATGTTTAAAAGAAGAGCTCA   41222      AAAAG      TG
                                TGAGC    CTTTTAGG  T
                                |||||    ||||||||  |
                                ACTCG    GAAAATTT  A
                                   AGAA_      GT
GAM264  CHST6    5'  ACGTTTGGGAGCCTTTGCT    41220      A      GG
                                AGCAAA GCTTTTA  TGT
                                ||||||| |||||||  |||
                                TCGTTT CGAGGGT  GCA
                                   C      TT
GAM264  CKMT1    3'  TTCCCAGGAGTTTTGCTCA    40632       G    A  TGT
                                TGAGCAAAA CTTTT GG
                                ||||||||| ||||| ||
                                ACTCGTTTT GAGGA CC
                                     _    C  TTA
GAM264  CKTSF1B1 3'  ATGCCTAAGAGTGAAAGT    25363    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                TG   TGAGAATCCGTA
                                 AAAG
GAM264  CLASP1   3'  ATGCCTGAGATGGCAGTTCA   65296      AAAA  __
                                TGAGC   GCT  TTTAGGTGT
                                |||||   |||  |||||||||
                                ACTTG   CGG  GAGTCCGTA
                                   A___   TA
GAM264  CLCA3    3'  ATACCTAAGGAGCCTGGTTCA  16992      AAAA   _
                                TGAGC   GCTT TTAGGTGT
                                |||||   |||| ||||||||
```

```
                                ACTTG   CGAG AATCCATA
                                  GTC_   G
GAM264  CLCA3   3'  ACATTTGACAGTTTTGCT   16990       G  T
                                AGCAAAA CT TTAGGTGT
                                ||||||| || ||||||||
                                TCGTTTT GA AGTTTACA
                                    _ C
GAM264  CLCN3   3'  GCACCTGGCCTGTTTGCTCA  8439        AGCTT
                                TGAGCAAA    TTAGGTGT
                                ||||||||    ||||||||
                                ACTCGTTT    GGTCCACG
                                     GTCC_
GAM264  CLCN4   5'  ACGCCTGAGGGGCGGCCA   8441    A  AAAAG
                                TG GC    CTTTTAGGTGT
                                || ||    ||||||||||
                                AC CG    GGGAGTCCGCA
                                 _ GCG__
GAM264  CLDN14  5'  GCACCTGAGGAGCGGC     57840    AAAA   _
                                GC   GCTT TTAGGTGT
                                ||   |||| ||||||||
                                CG   CGAG AGTCCACG
                                 G___   G
GAM264  CLDN14  5'  GCACCTGAGGAGCGGC     24033    AAAA   _
                                GC   GCTT TTAGGTGT
                                ||   |||| ||||||||
                                CG   CGAG AGTCCACG
                                 G___   G
GAM264  CLDN14  5'  ATGCCTGGAAGTGC       57836    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   TGAAGGTCCGTA
                                 ____
GAM264  CLN2    3'  GCACCTGGAAGTAGGTG     4614     AAA
                                CA   GCTTTTAGGTGT
                                ||   ||||||||||||
                                GT   TGAAGGTCCACG
                                 GGA
GAM264  CNTNAP2 3'  GTGCCTAATCCTGCTTTGTCA 26232     G   A  TT__    TG
                                TGA CAAA GC    TTAGG  T
                                ||| |||| ||    ||||| |
                                ACT GTTT CG    AATCC  G
                                  _   _ TCCT    GT
GAM264  COG8    3'  ATACCTGAAAGCTGTCTT    50480     CAAA
                                GAG    AGCTTTTAGGTGT
                                |||    ||||||||||||
                                TTC    TCGAAAGTCCATA
                                  TG__
GAM264  COL17A1 3'  GCACTTGGGGGACTGGGCGCA 55385    A  AAA  _
                                TG GC   AG CTTTTAGGTGT
                                || ||   || ||||||||||
```

```
                                AC CG   TC GGGGGTTCACG
                                 G  GG_  A
GAM264  COL17A1  3'  GCACTTGGGGGACTGGGCGCA  4934     A  AAA  _
                                TG GC   AG CTTTTAGGTGT
                                || ||   || ||||||||||
                                AC CG   TC GGGGGTTCACG
                                 G  GG_  A
GAM264  COLQ     3'  ACACCTGGGCAGGCTGTTG   54487     A    __
                                CAA AGCTT  TTAGGTGT
                                ||| |||||  ||||||||
                                GTT TCGGA  GGTCCACA
                                  G    CG
GAM264  COLQ     3'  ACACCCTTGGGTTTTTGT    54474         TTA
                                GCAAAAGCTT   GGTGT
                                ||||||||||   |||||
                                TGTTTTTGGG   CCACA
                                      TTC
GAM264  COLQ     3'  ACACCCTTGGGTTTTTGT    19045         TTA
                                GCAAAAGCTT   GGTGT
                                ||||||||||   |||||
                                TGTTTTTGGG   CCACA
                                      TTC
GAM264  COLQ     3'  ACACCTGGGCAGGCTGTTG   54469     A    __
                                CAA AGCTT  TTAGGTGT
                                ||| |||||  ||||||||
                                GTT TCGGA  GGTCCACA
                                  G    CG
GAM264  COLQ     3'  ACACCCTTGGGTTTTTGT    54486         TTA
                                GCAAAAGCTT   GGTGT
                                ||||||||||   |||||
                                TGTTTTTGGG   CCACA
                                      TTC
GAM264  COLQ     3'  ACACCTGGGCAGGCTGTTG   54475     A    __
                                CAA AGCTT  TTAGGTGT
                                ||| |||||  ||||||||
                                GTT TCGGA  GGTCCACA
                                  G    CG
GAM264  COLQ     3'  ACACCCTTGGGTTTTTGT    54480         TTA
                                GCAAAAGCTT   GGTGT
                                ||||||||||   |||||
                                TGTTTTTGGG   CCACA
                                      TTC
GAM264  COLQ     3'  ACACCCTTGGGTTTTTGT    54492         TTA
                                GCAAAAGCTT   GGTGT
                                ||||||||||   |||||
                                TGTTTTTGGG   CCACA
                                      TTC
GAM264  COLQ     3'  ACACCCTTGGGTTTTTGT    54468         TTA
                                GCAAAAGCTT   GGTGT
                                ||||||||||   |||||
```

```
                                TGTTTTTGGG  CCACA
                                      TTC
GAM264  COLQ    3'  ACACCTGGGCAGGCTGTTG  54493    A   __
                                CAA AGCTT  TTAGGTGT
                                ||| |||||  ||||||||
                                GTT TCGGA  GGTCCACA
                                  G    CG
GAM264  COLQ    3'  ACACCTGGGCAGGCTGTTG  54481    A   __
                                CAA AGCTT  TTAGGTGT
                                ||| |||||  ||||||||
                                GTT TCGGA  GGTCCACA
                                  G    CG
GAM264  COLQ    3'  ACACCTGGGCAGGCTGTTG  19046    A   __
                                CAA AGCTT  TTAGGTGT
                                ||| |||||  ||||||||
                                GTT TCGGA  GGTCCACA
                                  G    CG
GAM264  COPEB   3'  GCGCCTAAGCCTTTGC     82871     A  TT
                                GCAAA GCT  TAGGTGT
                                ||||| |||  |||||||
                                CGTTT CGA  ATCCGCG
                                   C  __
GAM264  CR2     3'  ATGCCTGAAGCCAGGCCA   8533    A  AAAA   T
                                TG GC   GCTTT AGGTGT
                                || ||   ||||| ||||||
                                AC CG   CGAAG TCCGTA
                                 _ GAC_   _
GAM264  CRIM1   3'  ATACTTGGACAGAGGTTGCT  33172     AAG  _
                                AGCAA  CT TTTAGGTGT
                                |||||  || |||||||||
                                TCGTT  GA AGGTTCATA
                                   GGA  C
GAM264  CUL5    3'  ACACTTAAAATTGGTGC    12976    AA  C
                                GCA  AG TTTTAGGTGT
                                |||  || ||||||||||
                                CGT  TT AAAATTCACA
                                  GG  _
GAM264  CXCL13  5'  GCACTTGGGAGAAGATGTTT  21197     AAAG
                                GAGCA   CTTTTAGGTGT
                                |||||   ||||||||||
                                TTTGT   GAGGGTTCACG
                                   AGAA
GAM264  CYB561  5'  GCATCTGGAGGGGGCTGTGC  8599    AA   ___
                                GCA  AGCT   TTTAGGTGT
                                |||  ||||   |||||||||
                                CGT  TCGG   AGGTCTACG
                                  G_   GGG
GAM264  CYB561  5'  GCATCTGGGGGGTGCT     8600     AAAG
                                AGCA   CTTTTAGGTGT
                                ||||   ||||||||||
```

```
                                TCGT   GGGGGTCTACG
                                  G___
GAM264  CYP1B1   3'  ACATTTAGAAGAAAGATGTTT  3652      AAAG_
                                GAGCA    CTTTTAGGTGT
                                |||||    ||||||||||
                                TTTGT    GAAGATTTACA
                                   AGAAA
GAM264  CYP21A2  5'  TACCTGAAGGTGGGGTCA    4950     G AAAA       GT
                                TGA C   GCTTTTAGGT
                                ||| |   ||||||||||
                                ACT G   TGGAAGTCCA
                                  _ GGG_        TG
GAM264  CYP27A1  3'  ACACCCTGAGCTTTTGCCA   5772    A       TTA
                                TG GCAAAAGCTT   GGTGT
                                || ||||||||||   |||||
                                AC CGTTTTCGAG   CCACA
                                 _        TC_
GAM264  CYP39A1  3'  ATACTTAAAGGAATTTG     33443     AG
                                CAAA  CTTTTAGGTGT
                                ||||  ||||||||||
                                GTTT  GGAAATTCATA
                                  AA
GAM264  CYR61    3'  ACAGTTTAAAGCTTTTATTC   7766     C       T  G
                                GAG AAAAGCTTT AG TGT
                                ||| |||||||| || |||
                                CTT TTTTCGAAA TT ACA
                                  A       T  G
GAM264  DAAM2    3'  ACACCTGGCCATTGTT     92283      AA   TTT
                                AGCAA  GCT   AGGTGT
                                |||||  |||   ||||||
                                TTGTT  CGG   TCCACA
                                   AC  ___
GAM264  DAPK1    5'  GCGCCTGGGAGGGATCTGC   17049    AAAG_
                                GCA    CTTTTAGGTGT
                                |||    ||||||||||
                                CGT    GAGGGTCCGCG
                                  CTAGG
GAM264  DDIT3    5'  ACACCTGAAAGCAGATGT    14557    AAA
                                GCA   GCTTTTAGGTGT
                                |||   ||||||||||||
                                TGT   CGAAAGTCCACA
                                  AGA
GAM264  DDT      5'  ACATCTGAGGAGCTGTTT    7218      AAA   _
                                GAGCA   GCTT TTAGGTGT
                                |||||   |||| ||||||||
                                TTTGT   CGAG AGTCTACA
                                   ___   G
GAM264  DDX11    3'  GCACCCTGAAGTTTTTGCTC  47654          TA
                                GAGCAAAAGCTTT  GGTGT
                                ||||||||||||  |||||
```

```
                                CTCGTTTTTGAAG CCACG
                                      TC
GAM264  DGAT1   3' GCACCTGAGGGCCTGGCTT  64542    AAAA
                                GAGC  GCTTTTAGGTGT
                                ||||  ||||||||||||
                                TTCG  CGGGAGTCCACG
                                  GTC_
GAM264  DGCR2   3' ACACCTGATGCGTTTTTG   17625     TT_
                                CAAAAGC  TTAGGTGT
                                |||||||  ||||||||
                                GTTTTTG  AGTCCACA
                                    CGT
GAM264  DISC1   3' GCATTTAGGAAAGCAGTGC  37880    AAA   __
                                GCA  GCTTTT  AGGTGT
                                |||  ||||||  ||||||
                                CGT  CGAAAG  TTTACG
                                  GA_    GA
GAM264  DISC1   3' GCATCTGGTGCTTTGCTCA  37879      A  TT
                                TGAGCAAA GC  TTAGGTGT
                                |||||||| ||  ||||||||
                                ACTCGTTT CG  GGTCTACG
                                     _ T_
GAM264  DMD     5' ACCGAAAGAGGTTTTTGC   14423       TA__  GT
                                GCAAAAGCTTT   GGT
                                ||||||||||   |||
                                CGTTTTTGGAG   CCA
                                      AAAG
GAM264  DMD     5' ACCGAAAGAGGTTTTTGC   14416       TA__  GT
                                GCAAAAGCTTT   GGT
                                ||||||||||   |||
                                CGTTTTTGGAG   CCA
                                      AAAG
GAM264  DMD     5' ACCGAAAGAGGTTTTTGC   14393       TA__  GT
                                GCAAAAGCTTT   GGT
                                ||||||||||   |||
                                CGTTTTTGGAG   CCA
                                      AAAG
GAM264  DMN     3' ATATTTAAGAGTAAATTTTGCT 62366      ___
          T                    GAGCAAAA  GCTTTTAGGTGT
                               ||||||||  ||||||||||||
                               TTCGTTTT  TGAGAATTTATA
                                    AAA
GAM264  DNAJB9  3' ATATCTACTAGTTTTGTTT  24678      G  TT
                                GAGCAAAA CT  TAGGTGT
                                |||||||| ||  |||||||
                                TTTGTTTT GA  ATCTATA
                                     _ TC
GAM264  DPYSL2  3' GCACTTAGAGGAAATTTG   7299     AG_
                                CAAA  CTTTTAGGTGT
                                ||||  ||||||||||
```

```
                                GTTT   GGAGATTCACG
                                  AAA
GAM264   DSC1     3'  GCATCTGCTAATGTTTTTGTTT 44330          TTT__
                A                  TGAGCAAAAGC    TAGGTGT
                                   ||||||||||     |||||||
                                   ATTTGTTTTTG    GTCTACG
                                         TAATC
GAM264   DSC1     3'  GCATCTGCTAATGTTTTTGTTT 17061          TTT__
                A                  TGAGCAAAAGC    TAGGTGT
                                   ||||||||||     |||||||
                                   ATTTGTTTTTG    GTCTACG
                                         TAATC
GAM264   DSC3     3'  ACACCCACTGTGTTTTGCTCA  8673          _ TTTTA
                                   TGAGCAAAA GC    GGTGT
                                   |||||||| ||    |||||
                                   ACTCGTTTT TG    CCACA
                                         G  TCAC_
GAM264   DSC3     3'  ACACCCACTGTGTTTTGCTCA  44336         _ TTTTA
                                   TGAGCAAAA GC    GGTGT
                                   |||||||| ||    |||||
                                   ACTCGTTTT TG    CCACA
                                         G  TCAC_
GAM264   DSCR4    5'  ATGTCTGAGAGCTGGTCTC   19638    CAAA       TG
                                   GAG   AGCTTTTAGG  T
                                   |||   ||||||||||  |
                                   CTC   TCGAGAGTCT  A
                                     TGG_       GT
GAM264   DSCR5    3'  TTTATTTATAAGTTTTTGCCA  33155   A       T    T
                                   TG GCAAAAGCTT TAGGTG
                                   || ||||||||||  ||||||
                                   AC CGTTTTTGAA ATTTAT
                                    _        T     TTA
GAM264   DUT      3'  ACACAAAGAAGTTTTTCTT   8695     C       AG
                                   GAG AAAAGCTTTT  GTGT
                                   ||| ||||||||||  ||||
                                   TTC TTTTTGAAGA  CACA
                                     _        AA
GAM264   EBAF     3'  ATACCTAGGCCCCTGTTC    65422     AAA   TT
                                   GAGCA   GCT  TAGGTGT
                                   |||||   |||  |||||||
                                   CTTGT   CGG  ATCCATA
                                      CCC  __
GAM264   EBAF     3'  ACGCAGAAGGCTTTGGCTC   65421     A       AG
                                   GAGC AAAGCTTTT  GTGT
                                   |||| |||||||||  ||||
                                   CTCG TTTCGGAAG  CGCA
                                     G       A_
GAM264   ECT2     3'  ACATTTAAAGGAGATTGTTT  36136      AAG
                                   GAGCAA   CTTTTAGGTGT
                                   ||||||   ||||||||||
```

```
                                TTTGTT  GGAAATTTACA
                                   AGA
GAM264  EFNB1   3'  GCAGTCGGAAGGGTTTTTGTTT 15399          A_ _
                                GAGCAAAAGCTTTT  GG TGT
                                |||||||||||||  || |||
                                TTTGTTTTTGGGAA  CT ACG
                                      GG  G
GAM264  EFNB2   3'  ACGCCTGGAAGGGCCGGCTT  14569    AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                TTCG    GAAGGTCCGCA
                                  GCCGG
GAM264  EGF     3'  ACGTAGTTGTGCTTTTGTTT  8734        TT__  G  GT
                                GAGCAAAAGC   TTA GT
                                ||||||||||   ||| ||
                                TTTGTTTTCG   GAT CA
                                      TGTT  G
GAM264  EGLN2   5'  ACACCTGAAAATGTTTA    34091      AAAGC
                                TGAGCA    TTTTAGGTGT
                                ||||||    ||||||||||
                                ATTTGT    AAAGTCCACA
                                   A____
GAM264  EGR1    3'  ATGCCTGACCCCTTGCTC    8740       AAGCTT
                                GAGCAA    TTAGGTGT
                                ||||||    ||||||||
                                CTCGTT    AGTCCGTA
                                   CCCC__
GAM264  EGR3    3'  GCGTCTAGCCCGCTTTGTTCA  59556       A  TT_   GT
                                TGAGCAAA GC   TTAG  GT
                                ||||||||  ||   ||||  ||
                                ACTTGTTT CG   GATC  CG
                                     _  CCC    TG
GAM264  EIF4A2  3'  GCATTTGAATGCATTTTGTTT  8755        _  T
                                GAGCAAAA GC TTTAGGTGT
                                ||||||||  || |||||||||
                                TTTGTTTT CG AAGTTTACG
                                     A  T
GAM264  ELAVL2  3'  ACATTTAAAGCATTGCT    15412      AA    T
                                AGCAA  GCTTT AGGTGT
                                |||||  |||||  ||||||
                                TCGTT  CGAAA TTTACA
                                  A_    _
GAM264  ELMO2   3'  CAAGCCTGAGGCTTTTGCTT  55672          T   GT
                                GAGCAAAAGCTTT AGGT
                                ||||||||||||| ||||
                                TTCGTTTTCGGAG TCCG
                                      _   AACA
GAM264  EMR1    3'  ACACCTGGCTACCATTTTGTTT 8772        GCTT__
                                GAGCAAAA    TTAGGTGT
                                ||||||||    ||||||||
```

```
                                TTTGTTTT     GGTCCACA
                                     ACCATC
GAM264  EMS1    3' ATATTTAATACTTTTGCT    56750        CTT
                                AGCAAAAG   TTAGGTGT
                                ||||||||   ||||||||
                                TCGTTTTC   AATTTATA
                                     AT_
GAM264  EMS1    3' ATATTTAATACTTTTGCT    17850        CTT
                                AGCAAAAG   TTAGGTGT
                                ||||||||   ||||||||
                                TCGTTTTC   AATTTATA
                                     AT_
GAM264  ENAM    3' GCACTGTACGTTTTTTGCTT  49077         CTTTTA
                                GAGCAAAAG     GGTGT
                                |||||||||     |||||
                                TTCGTTTTT     TCACG
                                      TGCATG
GAM264  EPHA8   3' ACACCTGGAGGCTGGAGCCA  40052    A  AAA
                                TG GC   AGCTTTTAGGTGT
                                || ||   ||||||||||||
                                AC CG   TCGGAGGTCCACA
                                 _ AGG
GAM264  EPHX1   3' GCCCTCCAGGCTTTTCTT    3694     C       TT   T
                                GAG AAAAGCTT  AGG GT
                                ||| ||||||||  ||| ||
                                TTC TTTTCGGA  TCC CG
                                  _       CC  _
GAM264  EPS15   3' TTTACTGTGAGCTTTTGC    8795          TTA    T
                                GCAAAAGCTT   GGTG
                                ||||||||||   ||||
                                CGTTTTCGAG   TCAT
                                      TG_    TTA
GAM264  ERBB4   3' ACACTTTTTGGTTTTTTTCA  17873     C      TTT
                                TGAG AAAAGCT   AGGTGT
                                |||| |||||||   ||||||
                                ACTT TTTTTGG   TTCACA
                                  _      TTT
GAM264  ERCC6   3' GCACTTGATGTTTGTTT     3697        AGCTT
                                GAGCAAA    TTAGGTGT
                                |||||||    ||||||||
                                TTTGTTT    AGTTCACG
                                    GT___
GAM264  ESR1    5' GTGCCTGGAGTGATGTTTA   3704       AAA    T   TG
                                TGAGCA   GCTTT AGG  T
                                ||||||   ||||| |||  |
                                ATTTGT   TGAGG TCC  G
                                   AG_    _  GT
GAM264  ETF1    3' GCGTTTGGGAGCCCTTTGT   16396      A_     GG
                                GCAAA  GCTTTTA  TGT
                                |||||  |||||||  |||
```

```
                                TGTTT  CGAGGGT  GCG
                                   CC      TT
GAM264   ETS2     3'  ACATTTGGGAGTTTTT      17877
                                AAAAGCTTTTAGGTGT
                                ||||||||||||||||
                                TTTTTGAGGGTTTACA

GAM264   EVA1     3'  ATACAGAAGCATTTGTTCA   19392         A     AG
                                TGAGCAAA GCTTTT  GTGT
                                |||||||| ||||||  ||||
                                ACTTGTTT CGAAGA  CATA
                                     A     __
GAM264   EVA1     3'  GCATCTAAAAGTTTAGGCTCA  19396       AA
                                TGAGC  AAGCTTTTAGGTGT
                                |||||  ||||||||||||||
                                ACTCG  TTTGAAAATCTACG
                                   GA
GAM264   EXTL2    3'  ACGTCTAGTTGTTTGCTT    7521        AA  TT    GT
                                GAGCAA  GC  TTAG  GT
                                ||||||  ||  ||||  ||
                                TTCGTT  TG  GATC  CA
                                   __ TT    TG
GAM264   EYA1     5'  GCGCCTGAGAGCCCCCGC    4955      AAAA
                                GC    GCTTTTAGGTGT
                                ||    ||||||||||||
                                CG    CGAGAGTCCGCG
                                 CCCC
GAM264   F2R      3'  ACATCTAGTAGTTGTTC     8833        AAA   T
                                GAGCA   GCT TTAGGTGT
                                |||||   ||| ||||||||
                                CTTGT   TGA GATCTACA
                                   ____   T
GAM264   FACL3    3'  ATACTTGAAATGCATGTCTCA  15497      _  AAA  _
                                TGAG CA   GC TTTTAGGTGT
                                |||| ||   || ||||||||||
                                ACTC GT   CG AAAGTTCATA
                                  T  A__  T
GAM264   FACL4    3'  ATACCTGTTTAAATTGCTCA   43395        AAGCTTT
                                TGAGCAA       TAGGTGT
                                |||||||       |||||||
                                ACTCGTT       GTCCATA
                                    AAATTT_
GAM264   FACL4    3'  ACACTTGTGACTTTTGCTT    43394         C  T
                                GAGCAAAAG TT TAGGTGT
                                ||||||||| || |||||||
                                TTCGTTTTC AG GTTCACA
                                      _ T
GAM264   FACL4    3'  ACACTTGTGACTTTTGCTT    15504         C  T
                                GAGCAAAAG TT TAGGTGT
                                ||||||||| || |||||||
```

```
                                TTCGTTTTC AG GTTCACA
                                      _ T
GAM264  FACL4    3'  ATACCTGTTTAAATTGCTCA  15505       AAGCTTT
                                TGAGCAA     TAGGTGT
                                |||||||     |||||||
                                ACTCGTT     GTCCATA
                                    AAATTT_
GAM264  FBXW1B   3'  ATGCCTAAGGGAGTTCGTTCA  24521      A  AG
                                TGAGC AA  CTTTTAGGTGT
                                ||||| ||  ||||||||||
                                ACTTG TT  GGGAATCCGTA
                                   C  GA
GAM264  FBXW1B   3'  ATGCCTAAGGGAGTTCGTTCA  53325      A  AG
                                TGAGC AA  CTTTTAGGTGT
                                ||||| ||  ||||||||||
                                ACTTG TT  GGGAATCCGTA
                                   C  GA
GAM264  FBXW1B   3'  ATGCCTAAGGGAGTTCGTTCA  53336      A  AG
                                TGAGC AA  CTTTTAGGTGT
                                ||||| ||  ||||||||||
                                ACTTG TT  GGGAATCCGTA
                                   C  GA
GAM264  FEZ1     3'  ATGCCTGAAACCGCTGCT    42565      AAA __
                                AGCA  GC  TTTTAGGTGT
                                ||||  ||  ||||||||||
                                TCGT  CG  AAAGTCCGTA
                                  ___ CC
GAM264  FGF12    3'  ACACCTGAGAGCATGTTT    40719      AAA
                                GAGCA  GCTTTTAGGTGT
                                |||||  ||||||||||||
                                TTTGT  CGAGAGTCCACA
                                   A__
GAM264  FGF9     3'  GCACTTAAAGGCTTCTCCTC  8890       CAA
                                GAG  AAGCTTTTAGGTGT
                                |||  ||||||||||||||
                                CTC  TTCGGAAATTCACG
                                  CTC
GAM264  FLT1     3'  ACATTTGAGGGCCCAGCCA   8911     A  AAAA
                                TG GC   GCTTTTAGGTGT
                                || ||   ||||||||||||
                                AC CG   CGGGAGTTTACA
                                 _ ACC_
GAM264  FMN2     5'  ACATTTTCAGAAAGCATTTGCT 79344         A    ___
           CA                     TGAGCAAA GCTTTT  AGGTGT
                                ||||||||| ||||||  ||||||
                                ACTCGTTT CGAAAG  TTTACA
                                    A    ACT
GAM264  FMO1     3'  GCATTTGAAGGTTGTTG     8925      A
                                CAA AGCTTTTAGGTGT
                                ||| ||||||||||||
```

```
                                GTT TTGGAAGTTTACG
                                  G
GAM264  FMO5    3' ATGCTTAAGACATTTTGTTT  7588        GC
                                GAGCAAAA  TTTTAGGTGT
                                ||||||||  ||||||||||
                                TTTGTTTT  AGAATTCGTA
                                    AC
GAM264  FOXE3   3' ACACCTGGCTGCCTTCTTCA  24101     CAAAA  TT
                                TGAG    GC  TTAGGTGT
                                ||||    ||  ||||||||
                                ACTT    CG  GGTCCACA
                                  CTTC_  TC
GAM264  FOXI1   3' TACCTGGGAAGTGTTGTTT   24110      AA    _   GT
                                GAGCAA  GCTTTT AGGT
                                ||||||  |||||| ||||
                                TTTGTT  TGAAGG TCCA
                                   G_     G   TG
GAM264  FUT8    3' ATATCTGAGAGACCTGTGT   15590    AAAG_
                                GCA    CTTTTAGGTGT
                                |||    ||||||||||
                                TGT    GAGAGTCTATA
                                  GTCCA
GAM264  FZD10   3' GTACTTAAAGGGTTTTGTTT  23241       G       GT
                                GAGCAAAA CTTTTAGGT
                                |||||||| |||||||||
                                TTTGTTTT GGAAATTCA
                                    G       TG
GAM264  GAA     3' GCACCTGAGCTCCTGCTT    3842      AA    TT
                                GAGCA  AGCTT  AGGTGT
                                |||||  |||||  ||||||
                                TTCGT  TCGAG  TCCACG
                                  CC    __
GAM264  GAB2    3' ATGCCTAGAGGACCACATCA  54443    GCAAAAG
                                TGA     CTTTTAGGTGT
                                |||     ||||||||||
                                ACT     GGAGATCCGTA
                                  ACACCA_
GAM264  GAB2    3' ATGCCTAGAGGACCACATCA  24486    GCAAAAG
                                TGA     CTTTTAGGTGT
                                |||     ||||||||||
                                ACT     GGAGATCCGTA
                                  ACACCA_
GAM264  GABRG2  5' GTATCTGCAAGCGTTTTTGCT 5871       __   T   GT
                                AGCAAAA  GCTT TAGGT
                                |||||||  |||| |||||
                                TCGTTTT  CGAA GTCTA
                                    TG   C    TG
GAM264  GABRP   3' ACTTGGCTTTGCTCA      26395       A   TTT
                                TGAGCAAA GCT   AGGT
                                |||||||| |||   ||||
```

```
                                ACTCGTTT CGG   TTCA
                                   _  ___
GAM264  GABRP    3'  ACATTTTCTAGTTTTTGTTT  26393          TTT
                                GAGCAAAAGCT   AGGTGT
                                ||||||||||   ||||||
                                TTTGTTTTTGA   TTTACA
                                      TCT
GAM264  GABRP    3'  ATATTTGAGTCTTTCTGCTCA  26397       _   CT
                                TGAGCA AAAG  TTTAGGTGT
                                ||||||  ||||  |||||||||
                                ACTCGT TTTC  GAGTTTATA
                                   C   T_
GAM264  GADD45G  3'  GCGCCTAGAGCGCGGCT     21993     AAAA    T
                                AGC   GCTTT AGGTGT
                                |||   ||||| ||||||
                                TCG   CGAGA TCCGCG
                                  GCG_    _
GAM264  GADD45G  3'  GTGTCTGGAGCGGCTGCTC   21994      AAA    T   TG
                                GAGCA   GCTTT AGG  T
                                |||||   ||||| |||  |
                                CTCGT   CGAGG TCT  G
                                   CGG    _  GT
GAM264  GALC     3'  GCACTTAGACATTTGCT     3847       AGCT
                                AGCAAA   TTTAGGTGT
                                ||||||   |||||||||
                                TCGTTT   AGATTCACG
                                   AC__
GAM264  GALNT1   3'  ACATTTGAGGGTTTTTTG    40019       _
                                CAAAAG CTTTTAGGTGT
                                ||||||  ||||||||||
                                GTTTTT GGGAGTTTACA
                                   T
GAM264  GAS11    3'  ACACCTGAGAGAATTCA     7621      CAAAAG
                                TGAG     CTTTTAGGTGT
                                ||||     ||||||||||
                                ACTT     GAGAGTCCACA
                                  AA____
GAM264  GBA      5'  GCATCCTTGTTTTTGTTTA   76338          TTTTA
                                TGAGCAAAAGC    GGTGT
                                ||||||||||    |||||
                                ATTTGTTTTTG    CTACG
                                      TTC__
GAM264  GCH1     3'  ACATTTGAGAGTGCCCATCA  3858     GCAAAA
                                TGA     GCTTTTAGGTGT
                                |||     ||||||||||||
                                ACT     TGAGAGTTTACA
                                  ACCCG_
GAM264  GFAP     3'  GCACTTGGGGGATCTGTTGT  9016      AAG__
                                GCAA    CTTTTAGGTGT
                                ||||    ||||||||||
```

```
                                TGTT    GGGGGTTCACG
                                  GTCTA
GAM264  GFPT2    3'  ACCCAAGTGCTTTTGCTTA   17573          T  A
                                TGAGCAAAAGC TTT GGT
                                |||||||||| ||| |||
                                ATTCGTTTTCG GAA CCA
                                      T  C
GAM264  GLS      3'  ACATTGTTGTTTTTGCT     29786         TTTTA
                                AGCAAAAGC    GGTGT
                                |||||||||    |||||
                                TCGTTTTTG    TTACA
                                     TTG__
GAM264  GM2A     5'  GCATTTAAAGGCACCTC     67779     CAAAA
                                GAG    GCTTTTAGGTGT
                                |||    ||||||||||||
                                CTC    CGGAAATTTACG
                                  CA___
GAM264  GNB1     3'  ACATGCTGAGGGCTTTGTTCA  9068         A      _
                                TGAGCAAA GCTTTTAG GTGT
                                |||||||| |||||||| ||||
                                ACTTGTTT CGGGAGTC TACA
                                     _      G
GAM264  GNS      3'  ACACCTGGAAGAGTTTCT    9082     C   AG
                                AG AAA  CTTTTAGGTGT
                                || |||  ||||||||||
                                TC TTT  GAAGGTCCACA
                                 _  GA
GAM264  GOSR2    3'  ACACTTGGGAGTGATTGT    15020      AA
                                GCAA  GCTTTTAGGTGT
                                ||||  ||||||||||||
                                TGTT  TGAGGGTTCACA
                                  AG
GAM264  GPC4     3'  ACACTCGGGCAAAGTTTTTGT  7550          ___ TA
                                GCAAAAGCTT   T  GGTGT
                                ||||||||||   |  |||||
                                TGTTTTTGAA   G  TCACA
                                      ACG GC
GAM264  GPR61    3'  GCACACAGCTTTTGCTTA    78911          TTTAG
                                TGAGCAAAAGCT    GTGT
                                ||||||||||||    ||||
                                ATTCGTTTTCGA    CACG
                                      CA___
GAM264  GPR81    3'  ATGCCTAGAAGAGGACCTGC   50752     AAAG__
                                GCA     CTTTTAGGTGT
                                |||     ||||||||||||
                                CGT     GAAGATCCGTA
                                  CCAGGA
GAM264  GPR85    5'  ACTGGGAAGTTGTTGCTTA   38577        A     TA
                                TGAGCAA AGCTTT  GGT
                                ||||||| ||||||  |||
```

```
                                ATTCGTT TTGAAG  TCA
                                   G     GG
GAM264  GPR85    3'  GCATCTAAAAGTGCATG    38579    AAA
                                CA  GCTTTTAGGTGT
                                ||  ||||||||||||
                                GT  TGAAAATCTACG
                                 ACG
GAM264  GRB10    3'  ATACTTGAAAAGCTTTCTT   17973    CA      _
                                GAG  AAAGCTTT TAGGTGT
                                |||  |||||||| |||||||
                                TTC  TTTCGAAA GTTCATA
                                  __      A
GAM264  GRIN2C   3'  GGCTGGGCTTTTGCT      5912          TTA  GT
                                AGCAAAAGCTT   GGT
                                ||||||||||   |||
                                TCGTTTTCGGG   TCG
                                      ___  GG
GAM264  GRINL1A  3'  GTGCTTGAAAGTATTTTTGT  69516       __       TG
                                GCAAAA  GCTTTTAGG  T
                                ||||||  |||||||||  |
                                TGTTTT  TGAAAGTTC  G
                                   TA       GT
GAM264  GRM6     3'  GCACCTAGCCTCTTTGATCA  5935     GCA   CTT
                                TGA   AAAG   TTAGGTGT
                                |||   ||||   ||||||||
                                ACT   TTTC   GATCCACG
                                  AG_   TCC
GAM264  GRM7     3'  ATGTCTTGAGGTTTTGTTCA  5943         G   TT   TG
                                TGAGCAAAA CTT  AGG  T
                                ||||||||| |||  |||  |
                                ACTTGTTTT GAG  TCT  A
                                     G   T_  GT
GAM264  GRPR     5'  GCATCTAAGGGAACTTTT    18000      __
                                AAAAG  CTTTTAGGTGT
                                |||||  ||||||||||
                                TTTTC  GGGAATCTACG
                                   AA
GAM264  GSTZ1    3'  TGCCTGGCGTGCTCA       7700        AAA   TTT
                                TGAGCA   GCT   AGGTG
                                ||||||   |||   |||||
                                ACTCGT   CGG   TCCGT
                                   G__   ____
GAM264  GUCY1A3  5'  GCGCCTGGAGGAGCTTA    63490      AAAAG
                                TGAGC    CTTTTAGGTGT
                                |||||    ||||||||||
                                ATTCG    GGAGGTCCGCG
                                   A_____
GAM264  GYG      3'  GCATGCTAAAATGCTTTTGTTC 14690          _    _
           A                    TGAGCAAAAGC TTTTAG GTGT
                                ||||||||||| |||||| ||||
```

```
                                ACTTGTTTTCG AAAATC TACG
                                      T     G
GAM264  HADHB   3' CACTTAAGCCTTGCCA     3939     A   AA  TT
                                TG GCAA  GCT  TAGGTG
                                || ||||  |||  ||||||
                                AC CGTT  CGA  ATTCAC
                                 _   C_  __
GAM264  HAS3    3' GCGCCTGAGATACAAGGCCCA 18039    A  AAAAGC
                                TG GC     TTTTAGGTGT
                                || ||     ||||||||||
                                AC CG     AGAGTCCGCG
                                 C  GAACAT
GAM264  HDAC4   3' ACACCTGGAGGTTGC      20103     AAA
                                GCA   GCTTTTAGGTGT
                                |||   ||||||||||||
                                CGT   TGGAGGTCCACA

                                 ____
GAM264  HEM1    5' ACACCTGAGGACTATGCT    18048     AA  CT
                                AGCA  AG  TTTAGGTGT
                                ||||  ||  |||||||||
                                TCGT  TC  GAGTCCACA
                                  A_  AG
GAM264  HFE     3' GCATCTAGAGGCTTCCTTCA  57320     CAA
                                TGAG   AAGCTTTTAGGTGT
                                ||||   ||||||||||||||
                                ACTT   TTCGGAGATCTACG
                                  CC_
GAM264  HFE     3' ACATCTGAGAAAAGCTTT    4647       ___
                                AAAGCTT   TTAGGTGT
                                |||||||   ||||||||
                                TTTCGAA   AGTCTACA
                                    AAG
GAM264  HFE     3' GCATCTAGAGGCTTCCTTCA  4652      CAA
                                TGAG   AAGCTTTTAGGTGT
                                ||||   ||||||||||||||
                                ACTT   TTCGGAGATCTACG
                                  CC_
GAM264  HFE     3' ACATCTGAGAAAAGCTTT    57318      ___
                                AAAGCTT   TTAGGTGT
                                |||||||   ||||||||
                                TTTCGAA   AGTCTACA
                                    AAG
GAM264  HGF     3' ACACCTAATCTAGGTGTTTA  94231      AAAGCTT
                                TGAGCA     TTAGGTGT
                                ||||||     ||||||||
                                ATTTGT     AATCCACA
                                   GGATCT_
GAM264  HIS1    3' ATACTTAAGTGTGCTTGCTT  21311      AA  T
                                GAGCAA  GC TTTAGGTGT
                                ||||||  || |||||||||
```

```
                                TTCGTT  TG GAATTCATA
                                   CG  T
GAM264  HIVEP1   3'  GCCTTTTAGGAGCTTTATGTTT 9200       _      ___   GT
            A                   TGAGCA AAAGCTTTT   AGGT
                                |||||| |||||||||  ||||
                                ATTTGT TTTCGAGGA   TCCG
                                   A       TTT
GAM264  HIVEP1   3'  ACACTTAAAGGTTTCTTTG   9198     __
                                CAAA  AGCTTTTAGGTGT
                                ||||  ||||||||||||
                                GTTT  TTGGAAATTCACA
                                  CT
GAM264  HK1      5'  ACATCTATCTTGCTGTGTTT   53121     AA   TTT_
                                GAGCA  AGC   TAGGTGT
                                |||||  |||   |||||||
                                TTTGT  TCG   ATCTACA
                                   G_   TTCT
GAM264  HK1      5'  ACATCTATCTTGCTGTGTTT   53125     AA   TTT_
                                GAGCA  AGC   TAGGTGT
                                |||||  |||   |||||||
                                TTTGT  TCG   ATCTACA
                                   G_   TTCT
GAM264  HK1      5'  ACATCTATCTTGCTGTGTTT   53130     AA   TTT_
                                GAGCA  AGC   TAGGTGT
                                |||||  |||   |||||||
                                TTTGT  TCG   ATCTACA
                                   G_   TTCT
GAM264  HLA-DMB  5'  ATATCTAGGGGCTGGGT    9207    AAA
                                GC   AGCTTTTAGGTGT
                                ||   ||||||||||||
                                TG   TCGGGGATCTATA
                                 GG_
GAM264  HLF      5'  ACCCGAAAGTTTTTTTTTA   9213      C       TA
                                TGAG AAAAGCTTT  GGT
                                |||| |||||||||  |||
                                ATTT TTTTTGAAA  CCA
                                   T       GC
GAM264  HLF      3'  GTGCTTGGGGGTTTTTG    9220            TG
                                CAAAAGCTTTTAGG  T
                                ||||||||||||||  |
                                GTTTTTGGGGGTTC  G
                                        GT
GAM264  HMGCR    3'  GTTCAGAGAGGCCTTTTGTTTA 5973          _    AGGTGT
                                TGAGCAAAAG CTTTT
                                |||||||||| |||||
                                ATTTGTTTTC GGAGA
                                      C    GACTTG
GAM264  HMGCR    3'  ATGCTTAAGTGTTGCTC    5971       AAGCT
                                GAGCAA    TTTAGGTGT
                                ||||||    |||||||||
```

```
                                CTCGTT    GAATTCGTA
                                   GT___
GAM264  HNF4A   3'  GCACTTGGGGCACCTTGCTC  4853       AA_    T
                                GAGCAA  GCTTT AGGTGT
                                ||||||  ||||| ||||||
                                CTCGTT  CGGGG TTCACG
                                   CCA    _
GAM264  HNRPD   3'  ATGCCCAGTTTTTGCTTA   48573          TTTA
                                TGAGCAAAAGCT   GGTGT
                                ||||||||||||   |||||
                                ATTCGTTTTTGA   CCGTA
                                      C___
GAM264  HNRPD   3'  ATGCCCAGTTTTTGCTTA   9242           TTTA
                                TGAGCAAAAGCT   GGTGT
                                ||||||||||||   |||||
                                ATTCGTTTTTGA   CCGTA
                                      C___
GAM264  HOXA3   3'  GTTCTTGGGCCTTTTGTTCA  47690         _  TT  TGT
                                TGAGCAAAAG CTT  AGG
                                |||||||||| |||  |||
                                ACTTGTTTTC GGG  TCT
                                      C  T_  TG
GAM264  HPCAL1  3'  GTGCCGTTTAAGCTTTGCTT  56189       A   TTA_ TG
                                GAGCAAA GCTT   GG  T
                                ||||||| ||||   ||  |
                                TTCGTTT CGAA   CC  G
                                   _   TTTG  GT
GAM264  HPCAL1  3'  GTGCCGTTTAAGCTTTGCTT  9271        A   TTA_ TG
                                GAGCAAA GCTT   GG  T
                                ||||||| ||||   ||  |
                                TTCGTTT CGAA   CC  G
                                   _   TTTG  GT
GAM264  HPRT1   3'  GCATCTAAGAAGTTTTGTTC  3962        GC
                                GAGCAAAA  TTTTAGGTGT
                                ||||||||  ||||||||||
                                CTTGTTTT  AGAATCTACG
                                     GA
GAM264  HS2ST1  3'  ATGCCTAAAAGAGTTT     24330     AG
                                AAA  CTTTTAGGTGT
                                |||  ||||||||||
                                TTT  GAAAATCCGTA
                                  GA
GAM264  HS2ST1  3'  ATGCCTCTGCTGCTTTTGCTT  24331         TTTT_
                                GAGCAAAAGC    AGGTGT
                                ||||||||||    ||||||
                                TTCGTTTTCG    TCCGTA
                                      TCGTC
GAM264  HS2ST1  3'  ACACTTAAGATATTGC      24328      AAGC
                                GCAA   TTTTAGGTGT
                                ||||   ||||||||||
```

```
                                CGTT   AGAATTCACA
                                  AT__
GAM264  HSPB3    3'  ACATTTGAAATGATTTGCT   20870      AGC
                                AGCAAA   TTTTAGGTGT
                                ||||||   ||||||||||
                                TCGTTT   AAAGTTTACA
                                   AGT
GAM264  ICMT     3'  ATACCTAAAATGTATGTTCA  24807      AAA  _
                                TGAGCA   GC TTTTAGGTGT
                                ||||||   || ||||||||||
                                ACTTGT   TG AAAATCCATA
                                   A__  T
GAM264  ICOS     3'  ACATCTTCTGCTGGTGTTTTGT 23903      _____  TTTT
            TCA                   AGCAAA    AGC   AGGTGT
                                ||||||    |||   ||||||
                                TTGTTT    TCG   TCTACA
                                   TGTGG   TCT_
GAM264  IHPK3    3'  GCATCTAAAAATGTTTACTC   54025    C   AGC
                                GAG AAA   TTTTAGGTGT
                                ||| |||   ||||||||||
                                CTC TTT   AAAATCTACG
                                  A   GTA
GAM264  IL13     3'  GCACTTGGAGCCAAGGGTTCA  9327      AAAA_    T
                                TGAGC    GCTTT AGGTGT
                                |||||    ||||| ||||||
                                ACTTG    CGAGG TTCACG
                                   GGAAC    _
GAM264  IL1RAPL2 3'  ATACTTAAATATTTTTGTTTA  33791         CT
                                TGAGCAAAAG  TTTAGGTGT
                                ||||||||||  |||||||||
                                ATTTGTTTTT  AAATTCATA
                                      AT
GAM264  IL1RAPL2 5'  GCATCTGAGACCTGCT     33793     AAA C
                                AGCA   G TTTTAGGTGT
                                ||||   | ||||||||||
                                TCGT   C AGAGTCTACG
                                  ___ C
GAM264  IL21R    3'  ACACCTGGGGGAAATTG     41422     AAG
                                CAA   CTTTTAGGTGT
                                |||   ||||||||||
                                GTT   GGGGGTCCACA
                                  AAA
GAM264  IL7      3'  ATACCTAAAAGAGATTTCA    6078      CAAAAG
                                TGAG     CTTTTAGGTGT
                                ||||     ||||||||||
                                ACTT     GAAAATCCATA
                                  TAGA__
GAM264  ILF1     3'  ACCGGGAGAGCTTTTCTT    15716     C        A_   GT
                                GAG AAAAGCTTTT  GGT
                                ||| ||||||||||  |||
```

```
                                TTC TTTTCGAGAG  CCA
                                  _       GG
GAM264  IPP     3'  GCTTGATGATAAGTTTTTGCTT 19727          ____    GT
                                GAGCAAAAGCTT   TTAGGT
                                ||||||||||||  ||||||
                                TTCGTTTTTGAA   AGTTCG
                                      TAGT
GAM264  ITPKB   3'  ACACTTCCTGGCTCTTGTTTA 9417       A   TTT
                                TGAGCAA AGCT   AGGTGT
                                ||||||| ||||  ||||||
                                ATTTGTT TCGG   TTCACA
                                    C   TCC
GAM264  IVD     3'  CACCTGGGGGCATGC      9459     AAA
                                GCA  GCTTTTAGGTG
                                |||  ||||||||||
                                CGT  CGGGGGTCCAC
                                  A__
GAM264  IVD     3'  CACCTGGGGGCATGC      9460     AAA
                                GCA  GCTTTTAGGTG
                                |||  ||||||||||
                                CGT  CGGGGGTCCAC
                                  A__
GAM264  JJAZ1   3'  ATGCTTAAAAGAAGGCT    31078    AAAAG
                                AGC    CTTTTAGGTGT
                                |||    ||||||||||
                                TCG    GAAAATTCGTA
                                  GAA__
GAM264  JRKL    3'  GCACTTTTCTGAAATCTTTTGC 13662        C    ____
            TT                  GAGCAAAAG TTTTAG   GTGT
                                |||||||| ||||||   ||||
                                TTCGTTTTC AAAGTC   CACG
                                     T    TTTT
GAM264  JUP     3'  GTGCTTAGTTGGCTTTGCCCA 9490    A   A  T_   TG
                                TG GCAAA GCT  TTAGG  T
                                || ||||| |||  |||||  |
                                AC CGTTT CGG  GATTC  G
                                 C    _  TT    GT
GAM264  KCNA3   3'  GCATCTGAGAGATAAGCTT   9507     AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                TTCG    GAGAGTCTACG
                                  AATA_
GAM264  KCNA7   3'  GCATTTAGAGGAAGAAGGCT  49053    AAAAG_
                                AGC    CTTTTAGGTGT
                                |||    ||||||||||
                                TCG    GGAGATTTACG
                                  GAAGAA
GAM264  KCNAB2  3'  CGCCTAGAACTCTTG      13303    A  C
                                CAA AG TTTTAGGTG
                                ||| || |||||||||
```

```
                                GTT TC AAGATCCGC
                                  C  _
GAM264  KCNK5   3'  ATACCTGGAATCTGTTGTT   13610      A  C
                                AGCAA AG TTTTAGGTGT
                                ||||| || ||||||||||
                                TTGTT TC AAGGTCCATA
                                   G  T
GAM264  KCNQ1   3'  GCACTTGGGGGCTCAGC    4023     AAA
                                GC   AGCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   TCGGGGGTTCACG
                                 AC_
GAM264  KCNS2   3'  GCATTTGAAGGTTATTGTTT  68307       A
                                GAGCAA AGCTTTTAGGTGT
                                |||||| ||||||||||||
                                TTTGTT TTGGAAGTTTACG
                                    A
GAM264  KDR     3'  CCAAGAGGCTTTGTTTA     9592         A     A
                                TGAGCAAA GCTTTT GG
                                |||||||| |||||| ||
                                ATTTGTTT CGGAGA CC
                                     _     A
GAM264  KIAA0857 3'  ACACTTGGAGGAAAGTTGC   66671      AAG_
                                GCAA   CTTTTAGGTGT
                                ||||   ||||||||||
                                CGTT   GGAGGTTCACA
                                  GAAA
GAM264  KIF3C   5'  GCGCCTGGGGGCTGGGCCG   9604     A  AAA
                                TG GC   AGCTTTTAGGTGT
                                || ||   ||||||||||||
                                GC CG   TCGGGGGTCCGCG
                                 _  GG_
GAM264  KIF5C   3'  ACACTTTGCTTTTGTT      15731         TTTT
                                AGCAAAAGC    AGGTGT
                                |||||||||    ||||||
                                TTGTTTTCG    TTCACA
                                      T___
GAM264  KIF5C   3'  CTTTGGGCTTTTCTCA      15735      C       TT
                                TGAG AAAAGCTT  AG
                                |||| ||||||||  ||
                                ACTC TTTTCGGG  TC
                                  _       TT
GAM264  KIFC3   5'  ACACCTGAAGGAGAAGCTCA  18685      AAAAG
                                TGAGC    CTTTTAGGTGT
                                |||||    ||||||||||
                                ACTCG    GGAAGTCCACA
                                  AAGA_
GAM264  KLF8    3'  ACCTAAAAGTGGTTTG      23402      A_
                                CAAA  GCTTTTAGGT
                                ||||  ||||||||||
```

```
                                GTTT  TGAAAATCCA
                                  GG
GAM264  KLRG1    3'  ATACCTAAGATAGTGCTTA   19436       AAAGC
                                TGAGCA    TTTTAGGTGT
                                ||||||    ||||||||||
                                ATTCGT    AGAATCCATA
                                   GAT__
GAM264  KRT9     5'  GCACTTGGGAGCCGGT     76299    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                TG   CGAGGGTTCACG
                                 GC__
GAM264  KRTHB1   3'  GCGCCTGGAGAAGTGCTCA   9650       AAAG   T
                                TGAGCA   CTTT AGGTGT
                                ||||||   |||| ||||||
                                ACTCGT   GAGG TCCGCG
                                   GAA_   _
GAM264  LAMP2    3'  TTGCCTGTCTGTTTGCTCA   25721       AGCTTT    T
                                TGAGCAAA     TAGGTG
                                ||||||||     ||||||
                                ACTCGTTT     GTCCGT
                                     GTCT__     TT
GAM264  LAMP2    3'  TACTTGCTCCTTTTGCTC    25717       CTTT    GT
                                GAGCAAAAG    TAGGT
                                |||||||||    |||||
                                CTCGTTTTC    GTTCA
                                     CTC_    TG
GAM264  LARS     3'  ACCTAACAGCTTTTTA     39220   C     T
                                G AAAAGCT TTAGGT
                                | ||||||| ||||||
                                A TTTTCGA AATCCA
                                 T      C
GAM264  LCP1     3'  ACCCTTCTCGCTTTTGCCA   9692    A      TTTT   T
                                TG GCAAAAGC    AGG GT
                                || |||||||||   ||| ||
                                AC CGTTTTCG    TCC CA
                                 _       CTCT   _
GAM264  LDB2     3'  GCATCTGAGAGTTTCTTGTTT  7092       _
                                GAGCAA AAGCTTTTAGGTGT
                                |||||| ||||||||||||||
                                TTTGTT TTTGAGAGTCTACG
                                   C
GAM264  LEP      3'  GTGTCTTAAGCCTTTTGCTCA  4055         _  TT   TG
                                TGAGCAAAAG CTT  AGG  T
                                |||||||||| |||  |||  |
                                ACTCGTTTTC GAA  TCT  G
                                     C   T_   GT
GAM264  LHX5     5'  ATGCCTTGTTTTTTTTGCTC   42303        CTTTT
                                GAGCAAAAG    AGGTGT
                                |||||||||    ||||||
```

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                                CTCGTTTTT    TCCGTA
                                     TTTGT
GAM264  LILRB4   3'  ACGTCTTGAAGCTTTTCTCA  22429     C       T  GT
                                TGAG AAAAGCTTT AG  GT
                                |||| ||||||||| ||  ||
                                ACTC TTTTCGAAG TC  CA
                                  _       T  TG
GAM264  LIMD1    3'  ACAAGGAGAGTTTTTGT    26454          AGG
                                GCAAAAGCTTTT   TGT
                                ||||||||||||  |||
                                TGTTTTTGAGAG   ACA
                                       GA_
GAM264  LOXL2    5'  ACGCTTGGTGCTTGCTT    9794      AA   TT
                                GAGCA  AGC  TTAGGTGT
                                |||||  |||  ||||||||
                                TTCGT  TCG  GGTTCGCA
                                  __   T_
GAM264  LRP4     3'  ACGTCTAGTCCTTGTGCTC   64440     A   CTT   GT
                                GAGCA AAG   TTAG  GT
                                ||||| |||   ||||  ||
                                CTCGT TTC   GATC  CA
                                   G   CT_   TG
GAM264  LRP4     3'  GTACCTTTCCTAAGTCTTTGCT 64444       AG   TT___   GT
          CA                      TGAGCAAA  CTT    AGGT
                                ||||||||  |||    ||||
                                ACTCGTTT  GAA    TCCA
                                     CT   TCCTT   TG
GAM264  LRRC2    3'  GGCCTAGGAATGTTCA     44473      AAAGC     TG
                                TGAGCA    TTTTAGG  T
                                ||||||    ||||||| |
                                ACTTGT    AGGATCC  G
                                   A____     GT
GAM264  LTK      5'  CGACCGCAAGGGCTTTTGTT  9827          A_  GT
                                AGCAAAAGCTTTT  GGT
                                ||||||||||||  |||
                                TTGTTTTCGGGAA  CCA
                                       CG   GCG
GAM264  LZTFL1   3'  GTGCCCTTTTGGAGCTTTTGTT 39755         TA___  TG
                                AGCAAAAGCTTT    GG  T
                                ||||||||||||    ||  |
                                TTGTTTTCGAGG    CC  G
                                       TTTTC  GT
GAM264  LZTR1    3'  GCACCTGGAAGTGGAGTGC   22241    AAA_
                                GCA   GCTTTTAGGTGT
                                |||   ||||||||||||
                                CGT   TGAAGGTCCACG
                                  GAGG
GAM264  M11S1    3'  AGCTTGAAAGCTTTTTTTTA  19731     C          GT
                                TGAG AAAAGCTTTTAGGT
                                |||| ||||||||||||||
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```
                                ATTT TTTTCGAAAGTTCG
                                  T          A
GAM264  MAD2L1   5'  CGCGTGCTTTTGTTT      9874          TTTT G
                                GAGCAAAAGC   A GTG
                                ||||||||||   | |||
                                TTTGTTTTCG   T CGC
                                     _____ G
GAM264  MADH6    5'  ACATTTAGGGGTTCGCGC    18763    AAA
                                GC   AGCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   TTGGGGATTTACA
                                 CGC
GAM264  MAF      5'  GCGCTTGGAGGTTTCGGGCCA  18100    A  AA_
                                TG GC   AAGCTTTTAGGTGT
                                || ||   ||||||||||||||
                                AC CG   TTTGGAGGTTCGCG
                                 _  GGC
GAM264  MAGEA3   3'  GTGGTAAAAGTATTTGCTTA   18103        A      GGTGT
                                TGAGCAAA GCTTTTA
                                |||||||| |||||||
                                ATTCGTTT TGAAAAT
                                     A      GGTG
GAM264  MAGEA8   3'  ACCTGAATTTGCTT       18104        AGCT
                                GAGCAAA    TTTAGGT
                                |||||||    |||||||
                                TTCGTTT    AAGTCCA
                                     _____
GAM264  MAGEC1   3'  ATACCTGGTTTGCTTGGCTTA  18419      AA    TT_
                                TGAGC  AAGC   TTAGGTGT
                                |||||  ||||   ||||||||
                                ATTCG  TTCG   GGTCCATA
                                   G_    TTT
GAM264  MAGP2    5'  ACGCCTAGCCTGGCTTTCTT   12989     CA     T__
                                GAG  AAAGCT   TTAGGTGT
                                |||  ||||||   ||||||||
                                TTC  TTTCGG   GATCCGCA
                                  __      TCC
GAM264  MAN1A1   3'  ATACCTTGTGTTTGCTTA    91902        A  TTTT
                                TGAGCAAA GC    AGGTGT
                                |||||||| ||    ||||||
                                ATTCGTTT TG    TCCATA
                                     G  T___
GAM264  MANBA    3'  GCATTTGAGCGATTGCTC    19773       AA    TT
                                GAGCAA  GCTT  AGGTGT
                                ||||||  ||||  ||||||
                                CTCGTT  CGAG  TTTACG
                                   AG    __
GAM264  MAP3K7IP2 3'  GCATCTAGGGGCTAAAGATGC  30661     AA___
                                GCA     AGCTTTTAGGTGT
                                |||     ||||||||||||
```

```
                                CGT    TCGGGGATCTACG
                                  AGAAA
GAM264  MAP4    3' GCGCTTGGGCGCCGTGCT    48061     AAA  T
                                AGCA   GC TTTAGGTGT
                                ||||   || |||||||||
                                TCGT   CG GGGTTCGCG
                                  GC_  C
GAM264  MAP4    3' GCGCTTGGGCGCCGTGCT    9909      AAA  T
                                AGCA   GC TTTAGGTGT
                                ||||   || |||||||||
                                TCGT   CG GGGTTCGCG
                                  GC_  C
GAM264  MAPK9   3' ACACTTCTAGAGATTTTGTTCA 57421        G    T_
                                TGAGCAAAA CTTT  AGGTGT
                                ||||||||| ||||  ||||||
                                ACTTGTTTT GAGA  TTCACA
                                      A    TC
GAM264  MAPK9   3' ACACTTCTAGAGATTTTGTTCA 57411        G    T_
                                TGAGCAAAA CTTT  AGGTGT
                                ||||||||| ||||  ||||||
                                ACTTGTTTT GAGA  TTCACA
                                      A    TC
GAM264  MAPK9   3' ACACTTCTAGAGATTTTGTTCA 10851        G    T_
                                TGAGCAAAA CTTT  AGGTGT
                                ||||||||| ||||  ||||||
                                ACTTGTTTT GAGA  TTCACA
                                      A    TC
GAM264  MAPK9   3' ACACTTCTAGAGATTTTGTTCA 57416        G    T_
                                TGAGCAAAA CTTT  AGGTGT
                                ||||||||| ||||  ||||||
                                ACTTGTTTT GAGA  TTCACA
                                      A    TC
GAM264  MAT2A   3' TCCCTAGGTGTTTTGTTCA   19788        G T     TGT
                                TGAGCAAAA C TTTAGG
                                ||||||||| | ||||||
                                ACTTGTTTT G GGATCC
                                      _ T     CTG
GAM264  MATN1   3' GCGTTTGGGAGCTCGTGT    9922      AA       GG
                                GCA  AGCTTTTA  TGT
                                |||  ||||||||  |||
                                TGT  TCGAGGGT  GCG
                                  GC       TT
GAM264  MATN1   3' GCGCCTGAGGGTGGGC      9920     AAAA
                                GC    GCTTTTAGGTGT
                                ||    ||||||||||||
                                CG    TGGGAGTCCGCG
                                 GG__
GAM264  MATN3   3' ACACTTTTTGTTTTTTGCTTA  9933          CTTTT
                                TGAGCAAAAG    AGGTGT
                                ||||||||||    ||||||
```

```
                                ATTCGTTTTT    TTCACA
                                      TGTTT
GAM264  MBD3    3'  GTGCCTGAGTGGCATGCCCA  14099   A  AAA  _    TG
                                TG GCA  GCT TTTAGG  T
                                || |||  ||| ||||||  |
                                AC CGT  CGG GAGTCC  G
                                 C  A__  T    GT
GAM264  MBNL    3'  ATGCTTGAGAGAGATGCTT  40726     AAAG
                                GAGCA   CTTTTAGGTGT
                                |||||   ||||||||||
                                TTCGT   GAGAGTTCGTA
                                   AGA_
GAM264  MBP     3'  GCACCCTTGCGCTTTTGCT  9951        TTTTA
                                AGCAAAAGC    GGTGT
                                |||||||||    |||||
                                TCGTTTTCG    CCACG
                                     CGTTC
GAM264  MCC     3'  GCATTTAAAAGGACTGCT   9958     AAAG
                                AGCA   CTTTTAGGTGT
                                ||||   ||||||||||
                                TCGT   GAAAATTTACG
                                  CAG_
GAM264  MCF2    5'  GCACCACGGCAGCTTTGTTT  18117      A  TTTA_
                                GAGCAAA GCT    GGTGT
                                ||||||| |||    |||||
                                TTTGTTT CGA    CCACG
                                    _  CGGCA
GAM264  MCL1    3'  ACATTTGATCCCTTGTTTGCTT 41711       AGCTT__
          A                      TGAGCAAA     TTAGGTGT
                                |||||||      ||||||||
                                ATTCGTTT     AGTTTACA
                                     GTTCCCT
GAM264  MCM7    3'  GCACTTACTCCTTTTGCT   19792       CTTT
                                AGCAAAAG   TAGGTGT
                                ||||||||   |||||||
                                TCGTTTTC   ATTCACG
                                     CTC_
GAM264  MEF2A   5'  ATATCTAAGTGCACTTTTTGCT 18779       ___  T
                                AGCAAAA  GC TTTAGGTGT
                                |||||||  || |||||||||
                                TCGTTTT  CG GAATCTATA
                                    TCA  T
GAM264  MFI2    3'  GCACCTGGCAGCTTTTTCA  52816    GC     T
                                TGA  AAAAGCT TTAGGTGT
                                |||  ||||||| ||||||||
                                ACT  TTTTCGA GGTCCACG
                                  __      C
GAM264  MGA     3'  GTGCTTGAAGGTTTCATTCA  62810    CAA        TG
                                TGAG   AAGCTTTTAGG  T
                                ||||   |||||||||||  |
```

```
                                ACTT  TTTGGAAGTTC  G
                                  AC_         GT
GAM264  MGAT5   5' GCACCTAGAGAGGTTGC    10025     AAG   T
                                GCAA  CTTT AGGTGT
                                ||||  |||| ||||||
                                CGTT  GAGA TCCACG
                                  GGA   _
GAM264  MINPP1  3' ACACTTGAAAAGTGCT     16908     AAAGC
                                AGCA    TTTTAGGTGT
                                ||||    ||||||||||
                                TCGT    AAAGTTCACA
                                  GA___
GAM264  MLANA   3' ACACCTGAGACATGCT     18580     AAAGC
                                AGCA    TTTTAGGTGT
                                ||||    ||||||||||
                                TCGT    AGAGTCCACA
                                  AC___
GAM264  MLC1    3' GCACTTGGAGCGTTTTTGCT  57593        _
                                AGCAAAAGC TTTTAGGTGT
                                ||||||||| ||||||||||
                                TCGTTTTTG GAGGTTCACG
                                     C
GAM264  MLC1    3' GCACTTGGAACGTTTTTGCT  30780        _
                                AGCAAAAGC TTTTAGGTGT
                                ||||||||| ||||||||||
                                TCGTTTTTG AAGGTTCACG
                                     C
GAM264  MLLT7   3' ATGCCTGGAAGCTTTGT    19860     A
                                GCAAA GCTTTTAGGTGT
                                ||||| ||||||||||||
                                TGTTT CGAAGGTCCGTA
                                  _
GAM264  MN1     3' GCAGTTAGCAAACTTTTGCTTA 10093        C _   G
                                TGAGCAAAAG TT TTAG TGT
                                |||||||||| || |||| |||
                                ATTCGTTTTC AA GATT ACG
                                     A  C    G
GAM264  MOCS1   3' CACCTGGCCCTGTTCA     92032      AAA   TTT
                                TGAGCA  GCT   AGGTG
                                ||||||  |||  |||||
                                ACTTGT  CGG   TCCAC
                                   CC_  ____
GAM264  MPL     3' GCACCTAGAGTAGTGCTT    18142     AAA    T
                                GAGCA   GCTTT AGGTGT
                                |||||   ||||| ||||||
                                TTCGT   TGAGA TCCACG
                                  GA_    _
GAM264  MPP4    5' GTATCCTACTAAAGCTTTTGT  52346        __   TGT
                                GCAAAAGCTTT  TAGG
                                ||||||||||  ||||
```

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                                TGTTTTCGAAA  ATCC
                                      TC    TATG
GAM264  MPP5     3'  CATTTGACAGTTTTTG      42484         T
                                CAAAAGCT TTAGGTG
                                |||||||| |||||||
                                GTTTTTGA AGTTTAC
                                     C
GAM264  MS4A4A   3'  GCACTTGAAAGTTTTT      43783
                                AAAAGCTTTTAGGTGT
                                ||||||||||||||||
                                TTTTTGAAAGTTCACG

GAM264  MSL3L1   3'  GGCCTGAAAGTGCTC       22310      AAAA       TG
                                GAGC   GCTTTTAGG  T
                                ||||   ||||||||| |
                                CTCG   TGAAAGTCC  G
                                  ____       GT
GAM264  MSL3L1   3'  GGCCTGAAAGTGCTC       54375      AAAA       TG
                                GAGC   GCTTTTAGG  T
                                ||||   ||||||||| |
                                CTCG   TGAAAGTCC  G
                                  ____       GT
GAM264  MSL3L1   3'  GGCCTGAAAGTGCTC       54373      AAAA       TG
                                GAGC   GCTTTTAGG  T
                                ||||   ||||||||| |
                                CTCG   TGAAAGTCC  G
                                  ____       GT
GAM264  MTMR2    3'  GCACCTGGAACAACTGTTC    32385       AAAGC
                                GAGCA    TTTTAGGTGT
                                |||||    ||||||||||
                                CTTGT    AAGGTCCACG
                                   CAAC_
GAM264  MTMR8    3'  ACATCTGATAAAGTTTTGTT   31286        G  __
                                AGCAAAA CTT  TTAGGTGT
                                ||||||| |||  ||||||||
                                TTGTTTT GAA  AGTCTACA
                                    _  AT
GAM264  MUC4     3'  ACATTTAAGGCGCCATTGCTT  56318        AA  _
                                GAGCAA  GC TTTTAGGTGT
                                ||||||  || ||||||||||
                                TTCGTT  CG GGAATTTACA
                                   AC  C
GAM264  MUC4     3'  ACATTTAAGGCGCCATTGCTT  37270        AA  _
                                GAGCAA  GC TTTTAGGTGT
                                ||||||  || ||||||||||
                                TTCGTT  CG GGAATTTACA
                                   AC  C
GAM264  MUS81    3'  GCACCTGGAATTCCCTGGTCA  47097     G  AAAGC
                                TGA CA    TTTTAGGTGT
                                |||  ||    ||||||||||
```

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                                ACT GT    AAGGTCCACG
                                  G  CCCTT
GAM264  MVK     3'  ACCTGAGAGGTTTGT      60648      AG
                                GCAAA  CTTTTAGGT
                                |||||  |||||||||
                                TGTTT  GAGAGTCCA
                                   G_
GAM264  MX2     3'  ATACCTGAGGCTATTGCTCA   10147       A     T
                                TGAGCAA AGCTTT AGGTGT
                                ||||||| |||||| ||||||
                                ACTCGTT TCGGAG TCCATA
                                    A     _
GAM264  MYBL1    3'  GTGCCTAGAAGCCAATGTT   64073     AAA       TG
                                AGCA  GCTTTTAGG  T
                                ||||  |||||||||  |
                                TTGT  CGAAGATCC  G
                                  AAC       GT
GAM264  NAB1    3'  TACCATAGTGTTTTGCTCA   19910        _  TTTA  GT
                                TGAGCAAAA GCT   GGT
                                ||||||||| |||   |||
                                ACTCGTTTT TGA   CCA
                                     G  TA__  TG
GAM264  NBEA    3'  ACATCTGGAAGACAAGTTCA  94911      AAAAG
                                TGAGC    CTTTTAGGTGT
                                |||||    ||||||||||
                                ACTTG    GAAGGTCTACA
                                   AACA_
GAM264  NBS1    3'  ACACCTAGTCTGTGGCTT    69494     AAA  CTT
                                GAGC  AG  TTAGGTGT
                                ||||  ||  ||||||||
                                TTCG  TC  GATCCACA
                                  GTG  T__
GAM264  NCALD    3'  CAAGCTTCAAGGGGCTTTTGTT 49371           __   GT
          T                      GAGCAAAAGCTTTT  AGGT
                                ||||||||||||||  ||||
                                TTTGTTTTCGGGGA  TTCG
                                        AC   AACG
GAM264  NCALD    3'  ATGCCTAGAGGGCAGATGC   49370     AAA  _
                                GCA  GCT TTTAGGTGT
                                |||  ||| |||||||||
                                CGT  CGG AGATCCGTA
                                  AGA  G
GAM264  NCALD    3'  GCTTCAAGGGGCTTTTGTTT  49376          A  T
                                GAGCAAAAGCTTTT GG GT
                                |||||||||||||| || ||
                                TTTGTTTTCGGGGA CT CG
                                        A  T
GAM264  NCAM2    3'  ATACTTGAATTAGTTTGTTT  15798       AGCT
                                GAGCAAA   TTTAGGTGT
                                |||||||   |||||||||
```

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                                TTTGTTT   AAGTTCATA
                                   GATT
GAM264  NCOA3   3' ACATTCCTGGTTTTTGC    21527       TTTA
                                GCAAAAGCT   GGTGT
                                |||||||||   |||||
                                CGTTTTTGG   TTACA
                                   TCC_
GAM264  NCOA6   5' GCGCCTGGCCTGTTGCTTA  25969      AA_  TTT
                                TGAGCAA  GCT  AGGTGT
                                |||||||  |||  ||||||
                                ATTCGTT  CGG  TCCGCG
                                   GTC  ___
GAM264  NCOA6   5' GCACCTAGAACATGCTCA   25966      AAAGC
                                TGAGCA   TTTTAGGTGT
                                ||||||   ||||||||||
                                ACTCGT   AAGATCCACG
                                   AC___
GAM264  NDUFS5  3' ATGTCTGGAGGCTGATTTTC  15846    CAAA       TG
                                GAG   AGCTTTTAGG  T
                                |||   ||||||||||  |
                                CTT   TCGGAGGTCT  A
                                  TTAG       GT
GAM264  NEBL    3' ATATAATTTGGCTTTTGTT   21118        TTTAG
                                AGCAAAAGCT   GTGT
                                |||||||||    ||||
                                TTGTTTTCGG   TATA
                                     TTTAA
GAM264  NEF3    3' GCATTTAAAATGGACTTTTGTT 18196        _ __
          CA                    TGAGCAAAAG CT  TTTAGGTGT
                                |||||||||| ||  |||||||||
                                ACTTGTTTTC GG  AAATTTACG
                                     A  TA
GAM264  NEO1    3' ACATTTGACTGCTTGTTC    10199     AA  TT
                                GAGCA  AGC  TTAGGTGT
                                |||||  |||  ||||||||
                                CTTGT  TCG  AGTTTACA
                                   __  TC
GAM264  NEU1    3' ACGCCTGAAAGACAGTTC    4738     AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                CTTG    GAAAGTCCGCA
                                  ACA__
GAM264  NFYC    3' ATGCCTGGGGGCCGAGATTC  26439    CAAAA
                                GAG    GCTTTTAGGTGT
                                |||    ||||||||||||
                                CTT    CGGGGGTCCGTA
                                  AGAGC
GAM264  NKX3A   3' GCGTCAAGTTTTTGCTT    20503         TTA GT
                                GAGCAAAAGCTT  G  GT
                                ||||||||||||  |  ||
```

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                                TTCGTTTTTGAA  C  CG
                                      ___ TG
GAM264  NORE1   3' ACACTTAAGGGAAGTTTA   48715     AAAAG
                                TGAGC   CTTTTAGGTGT
                                |||||   ||||||||||
                                ATTTG   GGGAATTCACA
                                  AA___
GAM264  NPTX1   3' ACACCTGAGCAGTGTCCA   10255   AG  AAA   TT
                                TG  CA  GCTT  AGGTGT
                                ||  ||  ||||  ||||||
                                AC  GT  CGAG  TCCACA
                                 CT  GA_   __
GAM264  NPTX1   3' ACACTTGGCACTTTGCT    10256     A_  TTT
                                AGCAAA  GCT  AGGTGT
                                ||||||  |||  ||||||
                                TCGTTT  CGG  TTCACA
                                   CA  ___
GAM264  NPY2R   5' GCACCTGTTTTCTTGTGTTTA 6187      A  CTTT
                                TGAGCA AAG   TAGGTGT
                                ||||||| |||   |||||||
                                ATTTGT TTC   GTCCACG
                                   G  TTTT
GAM264  NQO1    3' GCACTGGTGGTTTTTGCTC   6159        TTTA
                                GAGCAAAAGCT   GGTGT
                                ||||||||||   |||||
                                CTCGTTTTTGG   TCACG
                                      TGG_
GAM264  NR1I2   3' ACACCTAAGAACTAGTTT   41825    AAA  C
                                GAGC  AG TTTTAGGTGT
                                ||||  || ||||||||||
                                TTTG  TC AGAATCCACA
                                  A__  A
GAM264  NR1I2   5' ACATTCGGCTTTTGTT     13961       TTTA
                                AGCAAAAGCT   GGTGT
                                ||||||||||   |||||
                                TTGTTTTCGG   TTACA
                                      C___
GAM264  NR1I2   3' ACACCTAAGAACTAGTTT   13959    AAA  C
                                GAGC  AG TTTTAGGTGT
                                ||||  || ||||||||||
                                TTTG  TC AGAATCCACA
                                  A__  A
GAM264  NR5A2   5' GCACTTTTCTTTTGCTCA   13789       CTTTT
                                TGAGCAAAAG   AGGTGT
                                ||||||||||   ||||||
                                ACTCGTTTTC   TTCACG
                                      TT___
GAM264  NRCAM   3' ACACTTAAAATGTAGATGCT  17204    AAA  _
                                AGCA  GC TTTTAGGTGT
                                ||||  || ||||||||||
```

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                                TCGT   TG AAAATTCACA
                                  AGA  T
GAM264  NRF1    3'  ACCCAGTTTTTGTTCA     60118          TTTA
                                TGAGCAAAAGCT   GGT
                                ||||||||||||  |||
                                ACTTGTTTTTGA   CCA
                                      C___
GAM264  NRG1    3'  ACACTTGGGATTGTGCTTA   15687      AAAGC
                                TGAGCA   TTTTAGGTGT
                                ||||||   ||||||||||
                                ATTCGT   AGGGTTCACA
                                   GTT__
GAM264  NXF1    5'  GCGCTTGGGAGTTAGGTTGTT 21017      AA__
                                AGCAA   GCTTTTAGGTGT
                                |||||   ||||||||||||
                                TTGTT   TGAGGGTTCGCG
                                  GGAT
GAM264  OCLN    3'  ATACCTACATGTATTTGTTT  10313       A  TTT
                                GAGCAAA GC   TAGGTGT
                                ||||||| ||   |||||||
                                TTTGTTT TG   ATCCATA
                                    A  TAC
GAM264  OGG1    5'  CGCCTAAAGGCCTTG      33659     AA
                                CAA  GCTTTTAGGTG
                                |||  ||||||||||
                                GTT  CGGAAATCCGC
                                  C_
GAM264  OGG1    5'  CGCCTAAAGGCCTTG      33665     AA
                                CAA  GCTTTTAGGTG
                                |||  ||||||||||
                                GTT  CGGAAATCCGC
                                  C_
GAM264  OGG1    5'  CGCCTAAAGGCCTTG      10329     AA
                                CAA  GCTTTTAGGTG
                                |||  ||||||||||
                                GTT  CGGAAATCCGC
                                  C_
GAM264  OPHN1   5'  ATGCCTAAGGGACATGCT    10353     AAAG
                                AGCA   CTTTTAGGTGT
                                ||||   ||||||||||
                                TCGT   GGGAATCCGTA
                                  ACA_
GAM264  P4HB    3'  ATGCCTGGAAGAGGAGCT    6219      AAAAG
                                AGC    CTTTTAGGTGT
                                |||    ||||||||||
                                TCG    GAAGGTCCGTA
                                  AGGA_
GAM264  P53AIP1 3'  ACACTTAAGAGTGGTCA     42079     G AAAA
                                TGA C   GCTTTTAGGTGT
                                ||| |   ||||||||||||
```

```
                                ACT G   TGAGAATTCACA
                                  G ____
GAM264  PACE     3' ATATCTGAGGGAGGAGGCCA  10389    A  AAAAG
                                TG GC    CTTTTAGGTGT
                                || ||    ||||||||||
                                AC CG    GGGAGTCTATA
                                 _ GAGGA
GAM264  PACSIN1  3' GCACCTGGGAGGGGCTGC    92261     AAAG
                                GCA   CTTTTAGGTGT
                                |||   ||||||||||
                                CGT   GAGGGTCCACG
                                  CGGG
GAM264  PAIP2    3' GCATTGCCAAAGTTTTTGTT  33221          TA_
                                AGCAAAAGCTTT  GGTGT
                                ||||||||||||  |||||
                                TTGTTTTTGAAA  TTACG
                                      CCG
GAM264  PARK2    3' ACACTCTTCAAGTTTTTTTCA 25668     C      TT _
                                TGAG AAAAGCTT  AG GTGT
                                |||| ||||||||  || ||||
                                ACTT TTTTTGAA  TC CACA
                                  _      CT  T
GAM264  PARK2    3' ACACTCTTCAAGTTTTTTTCA 15862     C      TT _
                                TGAG AAAAGCTT  AG GTGT
                                |||| ||||||||  || ||||
                                ACTT TTTTTGAA  TC CACA
                                  _      CT  T
GAM264  PARK2    3' ACACTCTTCAAGTTTTTTTCA 25671     C      TT _
                                TGAG AAAAGCTT  AG GTGT
                                |||| ||||||||  || ||||
                                ACTT TTTTTGAA  TC CACA
                                  _      CT  T
GAM264  PARN     3' ACATTTGGAAGCCGC      10426    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   CGAAGGTTTACA
                                 C___
GAM264  PART1    3' CGCCTGAGTGCTGCT      33434     AAA  T
                                AGCA  GC TTTAGGTG
                                ||||  || ||||||||
                                TCGT  CG GAGTCCGC
                                  ___  T
GAM264  PCDH11X  3' GCATCTGAAAGTGAACAGT  52043    AAAA_
                                GC    GCTTTTAGGTGT
                                ||    ||||||||||||
                                TG    TGAAAGTCTACG
                                 ACAAG
GAM264  PCDH11X  3' GCATCTGAAAGTGAACAGT  52021    AAAA_
                                GC    GCTTTTAGGTGT
                                ||    ||||||||||||
```

```
                                TG    TGAAAGTCTACG
                                 ACAAG
GAM264  PCDH11Y  3' GCATCTGAAAGTGAACAGT  52078   AAAA_
                                GC    GCTTTTAGGTGT
                                ||    ||||||||||||
                                TG    TGAAAGTCTACG
                                 ACAAG
GAM264  PCDHA1   3' ATACCTAAAATCTGCATCA  48591    _  AAA C
                                TGA GCA   G TTTTAGGTGT
                                ||| |||   | ||||||||||
                                ACT CGT   C AAAATCCATA
                                  A  ___ T
GAM264  PCDHA1   3' ATACCTAAAATCTGCATCA  38180    _  AAA C
                                TGA GCA   G TTTTAGGTGT
                                ||| |||   | ||||||||||
                                ACT CGT   C AAAATCCATA
                                  A  ___ T
GAM264  PCDHA1   3' GCATTTAACAGGTTTTGTC  48593   G   G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHA1   3' GCATTTAACAGGTTTTGTC  38182   G   G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHA10  3' GCATTTAACAGGTTTTGTC  38190   G   G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHA10  3' GCATTTAACAGGTTTTGTC  49026   G   G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHA10  3' ATACCTAAAATCTGCATCA  49024    _  AAA C
                                TGA GCA   G TTTTAGGTGT
                                ||| |||   | ||||||||||
                                ACT CGT   C AAAATCCATA
                                  A  ___ T
GAM264  PCDHA10  3' ATACCTAAAATCTGCATCA  38188    _  AAA C
                                TGA GCA   G TTTTAGGTGT
                                ||| |||   | ||||||||||
                                ACT CGT   C AAAATCCATA
                                  A  ___ T
GAM264  PCDHA11  3' GCATTTAACAGGTTTTGTC  38200   G   G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
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```
                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHA11  3' ATACCTAAAATCTGCATCA  38197   _  AAA C
                                TGA GCA  G TTTTAGGTGT
                                ||| |||  | ||||||||||
                                ACT CGT  C AAAATCCATA
                                  A  ___ T
GAM264  PCDHA12  3' GCATTTAACAGGTTTTGTC  38209   G   G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHA12  3' ATACCTAAAATCTGCATCA  38207   _  AAA C
                                TGA GCA  G TTTTAGGTGT
                                ||| |||  | ||||||||||
                                ACT CGT  C AAAATCCATA
                                  A  ___ T
GAM264  PCDHA13  3' GCATTTAACAGGTTTTGTC  38218   G   G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHA13  3' ATACCTAAAATCTGCATCA  38216   _  AAA C
                                TGA GCA  G TTTTAGGTGT
                                ||| |||  | ||||||||||
                                ACT CGT  C AAAATCCATA
                                  A  ___ T
GAM264  PCDHA2   3' ATACCTAAAATCTGCATCA  38224   _  AAA C
                                TGA GCA  G TTTTAGGTGT
                                ||| |||  | ||||||||||
                                ACT CGT  C AAAATCCATA
                                  A  ___ T
GAM264  PCDHA2   3' GCATTTAACAGGTTTTGTC  38226   G   G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHA3   3' ATACCTAAAATCTGCATCA  38232   _  AAA C
                                TGA GCA  G TTTTAGGTGT
                                ||| |||  | ||||||||||
                                ACT CGT  C AAAATCCATA
                                  A  ___ T
GAM264  PCDHA3   3' GCATTTAACAGGTTTTGTC  38234   G   G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHA4   3' GCATTTAACAGGTTTTGTC  38242   G   G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
```

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                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHA4   3' ATACCTAAAATCTGCATCA   38240    _  AAA C
                                TGA GCA   G TTTTAGGTGT
                                ||| |||   | ||||||||||
                                ACT CGT   C AAAATCCATA
                                  A  ___ T
GAM264  PCDHA5   3' ATACCTAAAATCTGCATCA   38248    _  AAA C
                                TGA GCA   G TTTTAGGTGT
                                ||| |||   | ||||||||||
                                ACT CGT   C AAAATCCATA
                                  A  ___ T
GAM264  PCDHA5   3' GCATTTAACAGGTTTTGTC   38250    G   G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHA6   3' GCATTTAACAGGTTTTGTC   38258    G   G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHA6   3' GCATTTAACAGGTTTTGTC   48999    G   G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHA6   3' ATACCTAAAATCTGCATCA   38256    _  AAA C
                                TGA GCA   G TTTTAGGTGT
                                ||| |||   | ||||||||||
                                ACT CGT   C AAAATCCATA
                                  A  ___ T
GAM264  PCDHA6   3' ATACCTAAAATCTGCATCA   48997    _  AAA C
                                TGA GCA   G TTTTAGGTGT
                                ||| |||   | ||||||||||
                                ACT CGT   C AAAATCCATA
                                  A  ___ T
GAM264  PCDHA7   3' ATACCTAAAATCTGCATCA   38264    _  AAA C
                                TGA GCA   G TTTTAGGTGT
                                ||| |||   | ||||||||||
                                ACT CGT   C AAAATCCATA
                                  A  ___ T
GAM264  PCDHA7   3' GCATTTAACAGGTTTTGTC   38266    G   G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHA8   3' GCATTTAACAGGTTTTGTC   38274    G   G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
```

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                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHA8   3' ATACCTAAAATCTGCATCA   38272    _  AAA C
                                TGA GCA   G TTTTAGGTGT
                                ||| |||   | ||||||||||
                                ACT CGT   C AAAATCCATA
                                  A  ___ T
GAM264  PCDHA9   3' GCATTTAACAGGTTTTGTC   49016   G    G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHA9   3' ATACCTAAAATCTGCATCA   49012    _  AAA C
                                TGA GCA   G TTTTAGGTGT
                                ||| |||   | ||||||||||
                                ACT CGT   C AAAATCCATA
                                  A  ___ T
GAM264  PCDHAC1  3' ATACCTAAAATCTGCATCA   38161    _  AAA C
                                TGA GCA   G TTTTAGGTGT
                                ||| |||   | ||||||||||
                                ACT CGT   C AAAATCCATA
                                  A  ___ T
GAM264  PCDHAC1  3' GCATTTAACAGGTTTTGTC   38164   G    G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHAC2  3' GCATTTAACAGGTTTTGTC   38174   G    G  T
                                GA CAAAA CT TTAGGTGT
                                || ||||| || ||||||||
                                CT GTTTT GA AATTTACG
                                 _    G  C
GAM264  PCDHAC2  3' ATACCTAAAATCTGCATCA   38172    _  AAA C
                                TGA GCA   G TTTTAGGTGT
                                ||| |||   | ||||||||||
                                ACT CGT   C AAAATCCATA
                                  A  ___ T
GAM264  PCDHB16  5' ACATTTAGAAGTATTTTGC   40544      _
                                GCAAAA GCTTTTAGGTGT
                                |||||| ||||||||||||
                                CGTTTT TGAAGATTTACA
                                    A
GAM264  PCLO     3' GCATCTTTTGACTTTTGTT   94226       CTTTT
                                AGCAAAAG    AGGTGT
                                ||||||||    ||||||
                                TTGTTTTC    TCTACG
                                     AGTTT
GAM264  PDE4B    5' ACAGGGGTGGGCTTTTGTTCA 10475          TTAGG
                                TGAGCAAAAGCTT    TGT
                                ||||||||||||    |||
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                                ACTTGTTTTCGGG    ACA
                                      TGGGG
GAM264  PDE4B   3' ACAGGGGTGGGCTTTTGTTCA 10476          TTAGG
                                TGAGCAAAAGCTT    TGT
                                |||||||||||||    |||
                                ACTTGTTTTCGGG    ACA
                                      TGGGG
GAM264  PDHA1   5' GCACCTGAAGGAGACTTG   4293     AAG_
                                CAA   CTTTTAGGTGT
                                |||   ||||||||||
                                GTT   GGAAGTCCACG
                                  CAGA
GAM264  PEPD    3' GCACCTGGGGGCCTGGC    59909    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   CGGGGGTCCACG
                                 GTC_
GAM264  PEX14   5' GCGCCTGGGAGAAACCTC   63643    CAAAAG
                                GAG    CTTTTAGGTGT
                                |||    ||||||||||
                                CTC    GAGGGTCCGCG
                                  CAAA__
GAM264  PFKL    3' GTGTTTGGAGGCTGCTGC   10522    AA       TG
                                GCA AGCTTTTAGG T
                                ||| |||||||||| |
                                CGT TCGGAGGTTT G
                                  CG       GT
GAM264  PGF     3' GTTGCCTGGGGGCTTTTGCCA 10536   A          T
                                TG GCAAAAGCTTTTAGGTG
                                || ||||||||||||||||
                                AC CGTTTTCGGGGGTCCGT
                                 _           TGG
GAM264  PIGA    3' ACACCTGGAGGAATGTTGC   40011    AAG_
                                GCAA   CTTTTAGGTGT
                                ||||   ||||||||||
                                CGTT   GGAGGTCCACA
                                  GTAA
GAM264  PIGA    3' ACACCTGGAGGAATGTTGC   40002    AAG_
                                GCAA   CTTTTAGGTGT
                                ||||   ||||||||||
                                CGTT   GGAGGTCCACA
                                  GTAA
GAM264  PIK3R3  3' ATACTTATTGGTCTTTTTGTTT 61051       __  TT
          A                     TGAGCAAAA  GCT  TAGGTGT
                                |||||||||  |||  |||||||
                                ATTTGTTTT  TGG  ATTCATA
                                     TC   TT
GAM264  PIK3R3  3' CACTTGGGCTGGCTT      61052    AAA   TT
                                GAGC   AGCT  TAGGTG
                                ||||   ||||  ||||||
```

```
                                TTCG   TCGG  GTTCAC
                                  G__   __
GAM264  PIP5K1B  5' GCATTTGAGGGCCTTTTCT   13060    C    _
                                AG AAAAG CTTTTAGGTGT
                                || ||||| ||||||||||
                                TC TTTTC GGGAGTTTACG
                                 _    C
GAM264  PKHD1    3' GCATTTGAAGGGACAGTTCA  56915      AAAAG
                                TGAGC    CTTTTAGGTGT
                                |||||    ||||||||||
                                ACTTG    GGAAGTTTACG
                                   ACAG_
GAM264  PKIA     3' ACACCTGAAAATGTCTCA    22378     _ AAAGC
                                TGAG CA    TTTTAGGTGT
                                |||| ||    ||||||||||
                                ACTC GT    AAAGTCCACA
                                  T  A____
GAM264  PKIA     3' TATCTGGAATGCATTTGTTT  22385       A _      GT
                                GAGCAAA GC TTTTAGGT
                                ||||||| || ||||||||
                                TTTGTTT CG AAGGTCTA
                                    A  T       TG
GAM264  PLA2G7   5' GCGCCTGAGAGACTAAGCT   17438     AAA  _
                                AGC   AG CTTTTAGGTGT
                                |||   || ||||||||||
                                TCG   TC GAGAGTCCGCG
                                  AA_  A
GAM264  PLS3     3' GTAATAGAAGCTTTTCTTA   17272     C        GGTGT
                                TGAG AAAAGCTTTTA
                                |||| ||||||||||
                                ATTC TTTTCGAAGAT
                                  _        AATGT
GAM264  PLS3     3' ACGCCTGAAATGTGCTCA    17270      AAAGC
                                TGAGCA    TTTTAGGTGT
                                ||||||    ||||||||||
                                ACTCGT    AAAGTCCGCA
                                   GT___
GAM264  PLSCR1   3' TTTATAAAGGTTTTTGTACA  40858    A         GGTGT
                                TG GCAAAAGCTTTTA
                                || ||||||||||||
                                AC TGTTTTTGGAAAT
                                 A          ATTTA
GAM264  PLXNB2   3' ACCTGAGAGCCCCTCA     24802     CAAAA
                                TGAG    GCTTTTAGGT
                                ||||    ||||||||||
                                ACTC    CGAGAGTCCA
                                  CC___
GAM264  PMCHL1   3' ATGCCTGGCTAGTTTTTG    49069       T_
                                CAAAAGCT  TTAGGTGT
                                ||||||||  ||||||||
```

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                                GTTTTTGA  GGTCCGTA
                                     TC
GAM264  PMX1    3'  ATACCTAAAGGTTTTTCT    22588    C
                                AG AAAAGCTTTTAGGTGT
                                || ||||||||||||||||
                                TC TTTTTGGAAATCCATA
                                 _
GAM264  PMX1    3'  ATACCTAAAGGTTTTTCT    42656    C
                                AG AAAAGCTTTTAGGTGT
                                || ||||||||||||||||
                                TC TTTTTGGAAATCCATA
                                 _
GAM264  POLA    3'  GACCCCAGGCTTTGCTCA    33737        A   TTA  GT
                                TGAGCAAA GCTT   GGT
                                |||||||| ||||   |||
                                ACTCGTTT CGGA   CCA
                                     _   CC_   GT
GAM264  POLRMT  5'  GCGCCTGGAGCGGCGTGC    17274    AAA_    T
                                GCA   GCTTT AGGTGT
                                |||   ||||| ||||||
                                CGT   CGAGG TCCGCG
                                  GCGG   _
GAM264  PON1    3'  AGTGCTGGTGGGTTTTTGTTTA 4801          TTA  TG
                                TGAGCAAAAGCTT   GG  T
                                ||||||||||||   ||  |
                                ATTTGTTTTTGGG   TC  G
                                        TGG  GT AT
GAM264  PPARGC1 3'  ATATTTAGAAGCTGAACTTA  25157     CAAA
                                TGAG   AGCTTTTAGGTGT
                                ||||   ||||||||||||
                                ATTC   TCGAAGATTTATA
                                  AAG_
GAM264  PPID    3'  ATGTAAAGGTTTTTGT      87428          G
                                GCAAAAGCTTTTA GT
                                |||||||||||| ||
                                TGTTTTTGGAAAT TA
                                        G
GAM264  PPIF    3'  GTGCCTGAGGAAGGCTGCT   19171     AAA   ___    TG
                                AGCA   GCTT   TTAGG  T
                                ||||   ||||   |||||  |
                                TCGT   CGGA   AGTCC  G
                                  ___   AGG    GT
GAM264  PPP1R3D 3'  GCTAGGAAAAGCTTTTGC    20703         AGGT
                                GCAAAAGCTTTT   GT
                                ||||||||||||   ||
                                CGTTTTCGAAAA   CG
                                        GGAT
GAM264  PPP2R5C 3'  ACTGAGCTTTTGTTT      10753          TTA
                                GAGCAAAAGCTT   GGT
                                ||||||||||||   |||
```

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                                TTTGTTTTCGAG  TCA
                                    ___
GAM264  PPP3CA   3' ATATTTAGGGGTTTTTGTT  6269
                                AGCAAAAGCTTTTAGGTGT
                                ||||||||||||||||||
                                TTGTTTTTGGGGATTTATA

GAM264  PRDM2    5' ACATCTGAAAGTAGGAGTTT  31842    AAAA
                                GAGC  GCTTTTAGGTGT
                                ||||  ||||||||||||
                                TTTG  TGAAAGTCTACA
                                  AGGA
GAM264  PRDM2    5' ACATCTGAAAGTAGGAGTTT  24245    AAAA
                                GAGC  GCTTTTAGGTGT
                                ||||  ||||||||||||
                                TTTG  TGAAAGTCTACA
                                  AGGA
GAM264  PRELP    3' GCACTTGAAGGCTGGGGCCCA  10770   A  AAA
                                TG GC  AGCTTTTAGGTGT
                                || ||  ||||||||||||
                                AC CG  TCGGAAGTTCACG
                                 C  GGG
GAM264  PRG1     3' ACATCTGAAAAAGAAGCTTA  10775    AAAAGC
                                TGAGC    TTTTAGGTGT
                                |||||    ||||||||||
                                ATTCG    AAAGTCTACA
                                   AAGAA_
GAM264  PRKAR1A  3' ATATTTGGGAGTGACTGC   10800    AAA
                                GCA  GCTTTTAGGTGT
                                |||  ||||||||||||
                                CGT  TGAGGGTTTATA
                                  CAG
GAM264  PRKCB1   3' ATACTTTATGTCTTTGCTCA  70512      AG TTTT
                                TGAGCAAA C   AGGTGT
                                |||||||| |   ||||||
                                ACTCGTTT G   TTCATA
                                     CT TAT_
GAM264  PRKCG    5' GCACCTGGAGGTGCCTTGC   10809    AA_
                                GCAA  GCTTTTAGGTGT
                                ||||  ||||||||||||
                                CGTT  TGGAGGTCCACG
                                   CCG
GAM264  PRKCN    3' GCATTGAAGGGTTTTTCTTA  19447    C       AG
                                TGAG AAAAGCTTTT GTGT
                                |||| ||||||||||  ||||
                                ATTC TTTTTGGGAA TACG
                                   _       GT
GAM264  PRKWNK3  3' GCATCTGAGAGGCATTG    61552    AAG
                                CAA  CTTTTAGGTGT
                                |||  ||||||||||
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                                GTT  GAGAGTCTACG
                                  ACG
GAM264  PRNP    3'  AGACTTAGGAGTTTTGTTTA  4334        G      GT
                                TGAGCAAAA CTTTTAGGT
                                ||||||||| |||||||||
                                ATTTGTTTT GAGGATTCA
                                      _      GAC
GAM264  PROX1   3'  ACATTTAAGTATTTTGTTT   10893       GCT
                                GAGCAAAA  TTTAGGTGT
                                ||||||||  |||||||||
                                TTTGTTTT  GAATTTACA
                                    AT_
GAM264  PRX     3'  ATGCCTGAGATGGCTGTGCCA 40521    A  AA  __
                                TG GCA  AGCT  TTTAGGTGT
                                || |||  ||||  |||||||||
                                AC CGT  TCGG  GAGTCCGTA
                                 _  G_   TA
GAM264  PSG2    3'  CATTTCCTTTTGCTC     48356       CTTTT
                                GAGCAAAAG    AGGTG
                                |||||||||    |||||
                                CTCGTTTTC    TTTAC
                                     C____
GAM264  PTGER4  5'  ACATCTGAGGGCTGACCCT   6313    CAAA
                                AG   AGCTTTTAGGTGT
                                ||   ||||||||||||
                                TC   TCGGGAGTCTACA
                                 CCAG
GAM264  PTGER4  3'  CATTTAGCTGTGCTCA     6314      AA   TTT
                                TGAGCA  AGCT   AGGTG
                                ||||||  ||||   |||||
                                ACTCGT  TCGA   TTTAC
                                   G_   ___
GAM264  PTGFRN  3'  GTGTTTATAGCTTTTGTTT   67193        TT   TG
                                GAGCAAAAGCT  TAGG  T
                                ||||||||||  ||||  |
                                TTTGTTTTCGA  ATTT  G
                                      T_   GT
GAM264  PTGFRN  5'  GCACCTGGGAGGTGGGGTTC  67190     AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                CTTG    GAGGGTCCACG
                                  GGGTG
GAM264  PTPRA   5'  GCGCCTAGAAGACGAGCT    11094    AAAAG
                                AGC    CTTTTAGGTGT
                                |||    ||||||||||
                                TCG    GAAGATCCGCG
                                 AGCA_
GAM264  PTPRC   3'  GAATCTAAAAGCTTTTGCTT  55167          GT
                                GAGCAAAAGCTTTTAGGT
                                ||||||||||||||||||
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                                TTCGTTTTCGAAAATCTA
                                      AGT
GAM264  PTPRC   3'  GAATCTAAAAGCTTTTGCTT  11102            GT
                                GAGCAAAAGCTTTTAGGT
                                ||||||||||||||||||
                                TTCGTTTTCGAAAATCTA
                                      AGT
GAM264  RAB1A   3'  ATCCTAGGGGGTTTTGTTT   70233       G      TGT
                                GAGCAAAA CTTTTAGG
                                |||||||| ||||||||
                                TTTGTTTT GGGGATCC
                                     G       TA
GAM264  RAB23   3'  GCATCTAACACCTTTTGCT   32783       CTT
                                AGCAAAAG  TTAGGTGT
                                ||||||||  ||||||||
                                TCGTTTTC  AATCTACG
                                     CAC
GAM264  RAB26   3'  ACGCCTGGGACAGAAGGCTT  26821     AAAAGC
                                GAGC     TTTTAGGTGT
                                ||||     ||||||||||
                                TTCG     AGGGTCCGCA
                                  GAAGAC
GAM264  RAB36   3'  GCACCTGAAGGAGAGGCCA   16962    A  AAAAG
                                TG GC    CTTTTAGGTGT
                                || ||    ||||||||||
                                AC CG    GGAAGTCCACG
                                 _ GAGA_
GAM264  RAB4A   3'  ATATCTGGAGTACCTGCTC   15921      AAA    T
                                GAGCA  GCTTT AGGTGT
                                |||||  ||||| ||||||
                                CTCGT  TGAGG TCTATA
                                   CCA   _
GAM264  RAB5A   5'  CGCCTGGGCCTTGCT      14780      AA  TT
                                AGCAA  GCT  TAGGTG
                                |||||  |||  ||||||
                                TCGTT  CGG  GTCCGC
                                   C_  __
GAM264  RAB7L1  3'  ATACCTGGGAAGTTTGTT    14103      AGC
                                AGCAAA  TTTTAGGTGT
                                ||||||  ||||||||||
                                TTGTTT  AGGGTCCATA
                                   GA_
GAM264  RABIF   3'  ATATCTGAGAGTGACTTTGT  11205      A__
                                GCAAA  GCTTTTAGGTGT
                                |||||  ||||||||||||
                                TGTTT  TGAGAGTCTATA
                                   CAG
GAM264  RAD54B  3'  ACACCTGGAAGCTTGGTG    56231    A_
                                CA AAGCTTTTAGGTGT
                                ||  ||||||||||||||
```

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                                GT  TTCGAAGGTCCACA
                                 GG
GAM264   RAMP3    3'  GCCCAAGCTCTTTGCTCA    19591        _    TTA
                                TGAGCAAA AGCTT   GGT
                                |||||||| |||||   |||
                                ACTCGTTT TCGAA   CCG
                                     C    C__
GAM264   RAPSN    5'  GTGCCTAGAGGCACGGAGCCA  50991    A  AAAA_      TG
                                TG GC    GCTTTTAGG  T
                                || ||    |||||||||  |
                                AC CG    CGGAGATCC  G
                                 _ AGGCA       GT
GAM264   RASA1    3'  CTTTTGTTAAAAGTTATTTGTT 42635        _       GTGT
            CA                    TGAGCAAA AGCTTTTAG
                                |||||||| |||||||||
                                ACTTGTTT TTGAAAATT
                                     A       GTTTTCG
GAM264   RBBP5    3'  ATACTTATGTTTTGCTCA    17331         GCTTT
                                TGAGCAAAA    TAGGTGT
                                |||||||||    |||||||
                                ACTCGTTTT    ATTCATA
                                     GT___
GAM264   RBBP5    3'  GTATCCTAGGAAAGCTTTTGTT 17339          __  TGT
                                AGCAAAAGCTTTT  AGG
                                ||||||||||||  |||
                                TTGTTTTCGAAAG  TCC
                                       GA   TATG
GAM264   RBBP6    3'  GCACTTAAAATATTGCT     73473      AAGC
                                AGCAA    TTTTAGGTGT
                                |||||    ||||||||||
                                TCGTT    AAAATTCACG
                                   AT__
GAM264   RBBP9    3'  ATACCTAAAGGAGATTCA    70127      CAAAAG
                                TGAG     CTTTTAGGTGT
                                ||||     ||||||||||
                                ACTT     GGAAATCCATA
                                   AGA___
GAM264   RBP3     5'  CACAGTCCAGGGAGCTTTTGTG 11265    A        TA __
            CA                    TG GCAAAAGCTTT  GG  TGT
                                || ||||||||||  ||  |||
                                AC TGTTTTCGAGG  CC  ACA
                                 G         GA  TG   CA
GAM264   RDS      3'  ATCTGAGGGCTGCTC       4358       AAA
                                GAGCA   GCTTTTAGGT
                                |||||   ||||||||||
                                CTCGT   CGGGAGTCTA
                                     ___
GAM264   RELA     3'  GCACTTGGACTCTTGCTC    41754       A  CT
                                GAGCAA AG  TTTAGGTGT
                                ||||||  ||  |||||||||
```

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                                CTCGTT TC  AGGTTCACG
                                   C  __
GAM264  RFNG    3'  GCACCTGGGAGGGAGCTGCCA 88176    A  AAAG_
                                TG GCA    CTTTTAGGTGT
                                || |||    ||||||||||
                                AC CGT    GAGGGTCCACG
                                 _  CGAGG
GAM264  RFNG    3'  GCACGAGTAAAGCTTTTGTTC 88177          TAG_
                                GAGCAAAAGCTTT   GTGT
                                ||||||||||||   ||||
                                CTTGTTTTCGAAA   CACG
                                       TGAG
GAM264  RGL     5'  GCCTTGGCTTTTGCT      30734         TTT
                                AGCAAAAGCT   AGGT
                                |||||||||   ||||
                                TCGTTTTCGG   TCCG
                                      T__
GAM264  RGL     3'  GTGTCTGGAGTCTTTTGCCA  30737    A     C     TG
                                TG GCAAAAG TTTTAGG  T
                                || ||||||| |||||||  |
                                AC CGTTTTC GAGGTCT  G
                                 _      T      GT
GAM264  RLF     3'  GCACCTGAGGGTGCTTTGT   24850      A_
                                GCAAA  GCTTTTAGGTGT
                                |||||  ||||||||||||
                                TGTTT  TGGGAGTCCACG
                                   CG
GAM264  RNGTT   3'  ACGAAAGCAAGCTTTTGCCA  13728    A       TTAGG
                                TG GCAAAAGCTT    TGT
                                || ||||||||||    |||
                                AC CGTTTTCGAA    GCA
                                 _        CGAAA
GAM264  RNGTT   3'  ACATGTGAAAGCTTTTGCTT  13727           G
                                GAGCAAAAGCTTTTA GTGT
                                |||||||||||||| ||||
                                TTCGTTTTCGAAAGT TACA
                                       G
GAM264  RNGTT   5'  CACCTGGTGTTTGCCA     13730    A    A  TTT
                                TG GCAAA GCT   AGGTG
                                || ||||| |||   |||||
                                AC CGTTT TGG   TCCAC
                                 _    G  ___
GAM264  RNH     5'  ACCTGAGCTGTGCTC      11360      AA    TT
                                GAGCA  AGCTT  AGGT
                                |||||  |||||  ||||
                                CTCGT  TCGAG  TCCA
                                   G_    __
GAM264  RNH     5'  ACACCCTGGTCGGTTTTGCTCA 11358         ___  TTTA
                                TGAGCAAAA   GCT   GGTGT
                                |||||||||   |||   |||||
```

```
                              ACTCGTTTT  TGG   CCACA
                                   GGC  TC__
GAM264  RNH    5'  ACACCCTGGTCGGTTTTGCTCA 59613        ___  TTTA
                              TGAGCAAAA  GCT   GGTGT
                              |||||||||  |||   |||||
                              ACTCGTTTT  TGG   CCACA
                                   GGC  TC__
GAM264  RNH    5'  ACCTGAGCTGTGCTC      59615      AA    TT
                              GAGCA  AGCTT  AGGT
                              |||||  |||||  ||||
                              CTCGT  TCGAG  TCCA
                                G_    __
GAM264  RP1    3'  GTATCTATGATTTTTTTTGCTC 20773         CTTT__    GT
          A                    TGAGCAAAAG     TAGGT
                              ||||||||||     |||||
                              ACTCGTTTTT     ATCTA
                                   TTTAGT    TG
GAM264  RPA1   3'  AACTAGGTTTTTGCTT     11377          TTA  GT
                              GAGCAAAAGCTT  GGT
                              ||||||||||||  |||
                              TTCGTTTTTGGA  TCA
                                    ___  AT
GAM264  RPP20  5'  GCGCCTGGAGGGCCCTGT   19550     AAAG
                              GCA   CTTTTAGGTGT
                              |||   ||||||||||
                              TGT   GGAGGTCCGCG
                                CCCG
GAM264  RPP30  5'  ATGCCTGAGGGGCGGGCTCA  21161      AAAA  _
                              TGAGC   GCTT TTAGGTGT
                              |||||   |||| ||||||||
                              ACTCG   CGGG AGTCCGTA
                                GG__   G
GAM264  RS1    3'  GCACTTAGAGCGCACGCT   4394     AAAA   T
                              AGC   GCTTT AGGTGT
                              |||   ||||| ||||||
                              TCG   CGAGA TTCACG
                                CACG   _
GAM264  RXRA   3'  ATGCTTGGAAGCTGGCCTGC  11403    AA__
                              GCA   AGCTTTTAGGTGT
                              |||   ||||||||||||
                              CGT   TCGAAGGTTCGTA
                                CCGG
GAM264  RXRG   5'  ATATTTAGAAGCTGCACA   22624   A  AAA
                              TG GCA  GCTTTTAGGTGT
                              || |||  ||||||||||||
                              AC CGT  CGAAGATTTATA
                               A  ___
GAM264  RYR3   3'  GCACTTGAAGGTTATTCA   6415     CAAA
                              TGAG   AGCTTTTAGGTGT
                              ||||   ||||||||||||
```

```
                                ACTT   TTGGAAGTTCACG
                                  A___
GAM264  SACM1L   3' GCACTTGGAGGGTAACAGCT  25823    AAAAG_
                                AGC    CTTTTAGGTGT
                                |||    ||||||||||
                                TCG    GGAGGTTCACG
                                  ACAATG
GAM264  SC5DL    3' ATACCTAGGCCCATTGCT   90882     AA_  TT
                                AGCAA  GCT  TAGGTGT
                                |||||  |||  |||||||
                                TCGTT  CGG  ATCCATA
                                  ACC  __
GAM264  SCD      3' GCCCAGGCTTTTGCT     17348        TTA
                                AGCAAAAGCTT  GGT
                                ||||||||||  |||
                                TCGTTTTCGGA  CCG
                                      C__
GAM264  SCN3A    3' TAAAATTTTTGCTCA     22632        C
                                TGAGCAAAAG TTTTA
                                |||||||||| |||||
                                ACTCGTTTTT AAAAT
                                      _
GAM264  SCP2     3' GTAAACAAAAAAGCTTTTGTTT 11443          AG  GT
                                GAGCAAAAGCTTTT  GT
                                ||||||||||||||  ||
                                TTTGTTTTCGAAAA  CA
                                      AA  AATGT
GAM264  SDC4     3' TATTTAATGGTTTTTGTTT   11482        T    GT
                                GAGCAAAAGCT TTAGGT
                                |||||||||| ||||||
                                TTTGTTTTTGG AATTTA
                                      T    TG
GAM264  SDF2     3' GTGTTTGGAAGCTTCAGC   22635   AA       TG
                                GC  AAGCTTTTAGG  T
                                ||  ||||||||||  |
                                CG  TTCGAAGGTTT  G
                                 AC        GT
GAM264  SEDL     3' GCACTTGAACAATTTTGTTC  27335       GCT
                                GAGCAAAA  TTTAGGTGT
                                ||||||||  |||||||||
                                CTTGTTTT  AAGTTCACG
                                    AAC
GAM264  SERPINB13 3' GTGCTTATTGGCCATTTGTTT 24771      A_  TT  TG
                                GAGCAAA  GCT  TAGG  T
                                |||||||  |||  ||||  |
                                TTTGTTT  CGG  ATTC  G
                                   AC  TT   GT
GAM264  SERPINF2 3' ACACCCCGACTTTTGTTTA  6256         C  TTA
                                TGAGCAAAAG TT   GGTGT
                                |||||||||| ||   |||||
```

```
                                ATTTGTTTTC AG   CCACA
                                      _ CC_
GAM264  SFRP1    3'  GCATTTGAAAGGTGTGCT    11571     AAAG
                                AGCA   CTTTTAGGTGT
                                ||||   ||||||||||
                                TCGT   GAAAGTTTACG
                                  GTG_
GAM264  SGPL1    3'  ACATCTGGTCTTGCTC     91338      AA  TTT
                                GAGCAA  GCT  AGGTGT
                                ||||||  |||  ||||||
                                CTCGTT  TGG  TCTACA
                                   C_  ___
GAM264  SGT      3'  ACACCTAAGAGACGGCT     11586     AAAAG
                                AGC    CTTTTAGGTGT
                                |||    ||||||||||
                                TCG    GAGAATCCACA
                                  GCA__
GAM264  SIAH1    3'  GCAAATCAGGCTTTTGTTT   11657          TTAGG
                                GAGCAAAAGCTT    TGT
                                ||||||||||||    |||
                                TTTGTTTTCGGA    ACG
                                      CTAA_
GAM264  SIAT4C   5'  GCACTTGGGAGCTGACTGTGCT 20786     AA___
                                AGCA    AGCTTTTAGGTGT
                                ||||    ||||||||||||
                                TCGT    TCGAGGGTTCACG
                                  GTCAG
GAM264  SIAT8E   5'  GCGCCTGGAGGTAAAGGT    59859    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                TG   TGGAGGTCCGCG
                                 GAAA
GAM264  SIP      3'  GTGCTTGAAGGTTGCTGT    26976     AA       TG
                                GCA  AGCTTTTAGG  T
                                |||  ||||||||||  |
                                TGT  TTGGAAGTTC  G
                                  CG       GT
GAM264  SLC12A7  3'  GCATCTGAGGGCAGACGCT   21701     AAAA
                                AGC   GCTTTTAGGTGT
                                |||   ||||||||||||
                                TCG   CGGGAGTCTACG
                                  CAGA
GAM264  SLC20A2  5'  AACCTCAAGCTTTGTTTA    22173       A   TT   GT
                                TGAGCAAA GCTT  AGGT
                                ||||||||  ||||  ||||
                                ATTTGTTT CGAA  TCCA
                                     _   C_   AT
GAM264  SLC21A2  3'  GCACCTGGCCCTTTGCCA    18860    A    A_  TTT
                                TG GCAAA  GCT   AGGTGT
                                || |||||  |||   ||||||
```

```
                                AC CGTTT  CGG   TCCACG
                                 _    CC  ___
GAM264  SLC21A2  3' GCATTTGAAATGGTTCTGCTT 18861     AA   __
                                GAGCA  AGCT  TTTAGGTGT
                                |||||  ||||  |||||||||
                                TTCGT  TTGG  AAGTTTACG
                                   C_    TA
GAM264  SLC21A9  3' ATGCCTGGGCTGGTGTCA    23417    G  AA   TT
                                TGA CA  AGCT  TAGGTGT
                                ||| ||  ||||  |||||||
                                ACT GT  TCGG  GTCCGTA
                                  _ GG   __
GAM264  SLC29A1  3' TAGCCTCGGCATTTGCTT    17077      A  TTT   GT
                                GAGCAAA GCT   AGGT
                                ||||||| |||   ||||
                                TTCGTTT CGG   TCCG
                                    A  C__    ATG
GAM264  SLC2A1   3' ATGCCTGAGGGTGGAGACT   21494    CAAAA
                                AG    GCTTTTAGGTGT
                                ||    ||||||||||||
                                TC    TGGGAGTCCGTA
                                 AGAGG
GAM264  SLC2A2   5' ATGCCTAAGGGACCTGCTC   4420      AAAG
                                GAGCA   CTTTTAGGTGT
                                |||||   ||||||||||
                                CTCGT   GGGAATCCGTA
                                   CCA_
GAM264  SLC4A7   3' ACACTGATTAGTTTTTGT    13223       TTTA
                                GCAAAAGCT   GGTGT
                                |||||||||   |||||
                                TGTTTTTGA   TCACA
                                     TTAG
GAM264  SLC6A2   3' GACTGTAGTTTTTGTTCA    6445         TTTA  GT
                                TGAGCAAAAGCT   GGT
                                ||||||||||||   |||
                                ACTTGTTTTTGA   TCA
                                       TG__  GT
GAM264  SLC7A6   3' ATGCCTAGGATGTTTGTT    14298      AGC
                                AGCAAA   TTTTAGGTGT
                                ||||||   ||||||||||
                                TTGTTT   AGGATCCGTA
                                   GT_
GAM264  SLC7A8   5' ACCTGAGGATTGCTC      24274      AAGC
                                GAGCAA   TTTTAGGT
                                ||||||   ||||||||
                                CTCGTT   GGAGTCCA
                                   A___
GAM264  SLC9A6   3' GCATCTGGAAGACTTTCC    21006   A   _
                                C AAAG CTTTTAGGTGT
                                | |||| ||||||||||
```

```
                                C TTTC GAAGGTCTACG
                                 C   A
GAM264  SLC9A6   3' ATGCTTGGAAGAATGCTT   21000      AAAG
                                GAGCA   CTTTTAGGTGT
                                |||||   ||||||||||
                                TTCGT   GAAGGTTCGTA
                                  AA__
GAM264  SMAC     3' GCATCTGAAAGAGAAAATGC  39112    AAAG__
                                GCA     CTTTTAGGTGT
                                |||     ||||||||||
                                CGT     GAAAGTCTACG
                                  AAAAGA
GAM264  SMAC     3' GCATCTGAAAGAGAAAATGC  57210    AAAG__
                                GCA     CTTTTAGGTGT
                                |||     ||||||||||
                                CGT     GAAAGTCTACG
                                  AAAAGA
GAM264  SMAC     3' GCATCTGAAAGAGAAAATGC  57196    AAAG__
                                GCA     CTTTTAGGTGT
                                |||     ||||||||||
                                CGT     GAAAGTCTACG
                                  AAAAGA
GAM264  SMARCA3  3' TGACTTGGAGTTTTATGTTCA 11793      _      T   GT
                                TGAGCA AAAGCTTT AGGT
                                |||||| |||||||| ||||
                                ACTTGT TTTTGAGG TTCA
                                   A      _   GTA
GAM264  SMARCA5  5' ACGTTTGGGAGTGTGCAGCTC 13190     AAAA_     GG
                                GAGC    GCTTTTA  TGT
                                ||||    |||||||  |||
                                CTCG    TGAGGGT  GCA
                                  ACGTG      TT
GAM264  SMARCAL1 5' CGCCATGCTTTTGCCA     26226    A      TTTTA
                                TG GCAAAAGC    GGTG
                                || ||||||||    ||||
                                AC CGTTTTCG    CCGC
                                 _      TA___
GAM264  SMG1     3' CACTCCCTTTTGCTTA     30649         CTTTTA
                                TGAGCAAAAG     GGTG
                                ||||||||||     ||||
                                ATTCGTTTTC     TCAC
                                      CC_____
GAM264  SMP1     5' GTGTCTGGAGGCTGTGGCC   26702   A  AAA       TG
                                G GC   AGCTTTTAGG  T
                                | ||   ||||||||||  |
                                C CG   TCGGAGGTCT  G
                                 _ GTG        GT
GAM264  SNRPA1   3' ATGCTTAAGACTGCTGCT    11855     AA  C
                                AGCA  AG TTTTAGGTGT
                                ||||  ||  ||||||||||
```

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                                TCGT  TC AGAATTCGTA
                                  CG  _
GAM264  SOCS5    3'  GCGTTTGGAATAGCTGCTGC   25798     AA   __    GG
                                GCA  AGCT  TTTA  TGT
                                |||  ||||  ||||  |||
                                CGT  TCGA  AGGT  GCG
                                  CG    TA    TT
GAM264  SOLH     3'  ATGCCTGGGGCAGGGGCT    18875     AAAA    T
                                AGC    GCTTT AGGTGT
                                |||    ||||| ||||||
                                TCG    CGGGG TCCGTA
                                  GGGA    _
GAM264  SORCS2   3'  GCGCCTGGGAACGAGGCCA   40420    A  AAAAGC
                                TG GC     TTTTAGGTGT
                                || ||     ||||||||||
                                AC CG     AGGGTCCGCG
                                 _ GAGCA_
GAM264  SOS2     3'  ACATCTAGGAGAATTGT     68534      AAG
                                GCAA   CTTTTAGGTGT
                                ||||   ||||||||||
                                TGTT   GAGGATCTACA
                                  AA_
GAM264  SOX10    3'  GTGCCTAAGGGCTAGGCCA   22688    A  AAA        TG
                                TG GC   AGCTTTTAGG  T
                                || ||   ||||||||||  |
                                AC CG   TCGGGAATCC  G
                                 _ GA_        GT
GAM264  SOX9     5'  GCGCCCCCACTTTTGCTC    4438         CTTTTA
                                GAGCAAAAG     GGTGT
                                |||||||||     |||||
                                CTCGTTTTC     CCGCG
                                      ACCC__
GAM264  SPAG6    3'  GCACTTGAAGGAGACTC     24906     CAAAAG
                                GAG     CTTTTAGGTGT
                                |||     ||||||||||
                                CTC     GGAAGTTCACG
                                  AGA___
GAM264  SPON1    3'  ATGTTGGGTGGCTTTTGTTC  62447          TTTA  TG
                                GAGCAAAAGCT    GG  T
                                ||||||||||    ||  |
                                CTTGTTTTCGG    TT  A
                                       TGGG  GT
GAM264  SPRR3    3'  CGTACTATAAAGCTTTTGTTCA 95496            _   GTGT
                                TGAGCAAAAGCTTT TAG
                                |||||||||||||| |||
                                ACTTGTTTTCGAAA ATC
                                         T   ATGCA
GAM264  SRGAP1   3'  GCACCTGAGGCCTTGGTTCA   72262      AAAA    T
                                TGAGC    GCTTT AGGTGT
                                |||||    ||||| ||||||
```

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                                ACTTG   CGGAG TCCACG
                                  GTTC   _
GAM264  ST7     3' ACGTTTATGCTTTTGCCA   25540   A      TTT  GG
                                TG GCAAAAGC   TA  TGT
                                || ||||||||   ||  |||
                                AC CGTTTTCG   AT  GCA
                                 _      T__  TT
GAM264  STCH    3' ATACTTGAAGGACCGTGTT   22708     AAAG
                                AGCA   CTTTTAGGTGT
                                ||||   ||||||||||
                                TTGT   GGAAGTTCATA
                                  GCCA
GAM264  STIM1   3' ATACCTGGGGCTGGTCTTA   60144     CAAA    T
                                TGAG   AGCTTT AGGTGT
                                ||||   |||||| ||||||
                                ATTC   TCGGGG TCCATA
                                  TGG_    _
GAM264  STK24   3' ACACCTAGAGGTTGATTTC   13116    CAAA
                                GAG   AGCTTTTAGGTGT
                                |||   ||||||||||||
                                CTT   TTGGAGATCCACA
                                 TAG_
GAM264  STK38   5' ATACCTAGGGGTGGGATTTC  23442    CAAAA
                                GAG    GCTTTTAGGTGT
                                |||    ||||||||||||
                                CTT    TGGGGATCCATA
                                 TAGGG
GAM264  STS     3' ACGCCTGAGAGTGGC      4446    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   TGAGAGTCCGCA
                                 G___
GAM264  STX7    3' ATATAATAAGCTTTTGCT    13107         TTAG
                                AGCAAAAGCTT   GTGT
                                ||||||||||   ||||
                                TCGTTTTCGAA   TATA
                                      TAA_
GAM264  SWAP70  3' ACATTGTCAAGCTGTTTGTTTA 71345       _    TTA
                                TGAGCAAA AGCTT   GGTGT
                                |||||||| |||||  |||||
                                ATTTGTTT TCGAA   TTACA
                                    G    CTG
GAM264  SYBL1   3' GCCTTAAAAAGGCTTTTGTTTA 18895           ___   GT
                                TGAGCAAAAGCTTTT   AGGT
                                ||||||||||||||   ||||
                                ATTTGTTTTCGGAAA   TCCG
                                         AAT
GAM264  TAF4    3' ACGCCTGGGGACTTTTTA    12089   C    CT
                                G AAAAG  TTTAGGTGT
                                | |||||  |||||||||
```

```
                                A TTTTC  GGGTCCGCA
                                 T    AG
GAM264  TAF7    5'  GCACCTAGAGGTTGGGACTT  18909    CAAA
                                GAG   AGCTTTTAGGTGT
                                |||   ||||||||||||
                                TTC   TTGGAGATCCACG
                                  AGGG
GAM264  TAL1    3'  GCGTCTGGGAGGTTGGTTTA  12108     AA  G     GT
                                TGAGC  AA CTTTTAG  GT
                                |||||  || |||||||  ||
                                ATTTG  TT GAGGGTC  CG
                                   G_  G     TG
GAM264  TBL1X   3'  ACACCTGGGAAAGGGATGCT  18925     AAAGC_
                                AGCA    TTTTAGGTGT
                                ||||    ||||||||||
                                TCGT    AGGGTCCACA
                                  AGGGAA
GAM264  TBL1X   5'  GCGCTTGGGAGCGAGGAGC  18934    AAAA_
                                GC    GCTTTTAGGTGT
                                ||    ||||||||||||
                                CG    CGAGGGTTCGCG
                                 AGGAG
GAM264  TCF2    3'  GCAGATGGAGGTTTTGTTT  21380       G     GG
                                GAGCAAAA CTTTTA  TGT
                                |||||||| ||||||  |||
                                TTTGTTTT GGAGGT  ACG
                                    _     AG
GAM264  TCF8    3'  GTGTTTTTAAGTTTTTGTTT  47730         TT   TG
                                GAGCAAAAGCTT  AGG  T
                                ||||||||||||  |||  |
                                TTTGTTTTTGAA  TTT  G
                                      TT   GT
GAM264  TCFL4   3'  ATACTTAAAAGGGCTC     63457     AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||||
                                CTCG    GAAAATTCATA
                                  G____
GAM264  TDG     3'  ATACCTAAGAAGGGCATGCT  12187     AAA  ___
                                AGCA   GCT   TTTAGGTGT
                                ||||   |||   |||||||||
                                TCGT   CGG   GAATCCATA
                                  A__   GAA
GAM264  TEC     3'  ATACCTATCTTTTGTTT     12215        CTTT
                                GAGCAAAAG    TAGGTGT
                                |||||||||    |||||||
                                TTTGTTTTC    ATCCATA
                                     T___
GAM264  TERF1   3'  TAATTTAAAACTTTTGTTTA  33975         C      GT
                                TGAGCAAAAG TTTTAGGT
                                |||||||||| ||||||||
```

```
                                ATTTGTTTTC AAAATTTA
                                      _       ATG
GAM264  TES     3'  ACCAAGAGATTTTGTTTA    71998         G    A
                                TGAGCAAAA CTTTT GGT
                                ||||||||| ||||| |||
                                ATTTGTTTT GAGAA CCA
                                     A    _
GAM264  TES     3'  ACACTTAAAAGTTAGTGT    71997     AA
                                GCA  AGCTTTTAGGTGT
                                |||  ||||||||||||
                                TGT  TTGAAAATTCACA
                                  GA
GAM264  TFEB    5'  GCACTTGGGGCCTGGCTT    92125     AAAA    T
                                GAGC    GCTTT AGGTGT
                                ||||    ||||| ||||||
                                TTCG    CGGGG TTCACG
                                  GTC_    _
GAM264  TGFA    3'  GCACTTGGATCTGTTCA     12253       AAAGCT
                                TGAGCA     TTTAGGTGT
                                ||||||     |||||||||
                                ACTTGT     AGGTTCACG
                                   CT____
GAM264  THOP1   3'  GCATCTGGAGGGCTTTCGT   73377    A       _
                                GC AAAGCTTTT AGGTGT
                                || ||||||||| ||||||
                                TG TTTCGGGAG TCTACG
                                 C        G
GAM264  TIC     5'  CACTCCTGGGCAGCTTTTGCTC 24935          _     T
          A                      TGAGCAAAAGCT TTTAGG GT
                                ||||||||||| |||||| ||
                                ACTCGTTTTCGA GGGTCC CA
                                       C     T  CG
GAM264  TIRAP   3'  ACCTGGATTTTTTGTTT     53563         CT
                                GAGCAAAAG  TTTAGGT
                                |||||||||  |||||||
                                TTTGTTTTT  AGGTCCA
                                     T_
GAM264  TK2     3'  GTGCCTGGCTGGTTTGCCCA   16060    A    __    TTT   TG
                                TG GCAAA  AGCT   AGG  T
                                || |||||  ||||   |||  |
                                AC CGTTT  TCGG   TCC  G
                                 C    GG    ___   GT
GAM264  TLE2    5'  GCGCCTGGGGGGCTTTTCG   12309   C       _
                                G AAAAGCTTTT AGGTGT
                                | ||||||||| ||||||
                                G TTTTCGGGGG TCCGCG
                                 C        G
GAM264  TLL1    3'  ACTCTACAAGCTTTTGTTCA  24946           T   TGT
                                TGAGCAAAAGCTT TAGG
                                |||||||||||| ||||
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                                ACTTGTTTTCGAA ATCT
                                      C   CA
GAM264  TLL2    5' GCGCCTGAGCCATGCCCA   24964   A  AAA   TT
                                TG GCA  GCTT  AGGTGT
                                || |||  ||||  ||||||
                                AC CGT  CGAG  TCCGCG
                                 C  AC_   __
GAM264  TLL2    3' ACACTTGGCACTTGTTC    24960     AA  TTT
                                GAGCAA  GCT  AGGTGT
                                ||||||  |||  ||||||
                                CTTGTT  CGG  TTCACA
                                   CA  ____
GAM264  TMEM2   3' GCACTTGGGTTTTTTGTT   25420      CT
                                AGCAAAAG  TTTAGGTGT
                                ||||||||  |||||||||
                                TTGTTTTT  GGGTTCACG
                                     T_
GAM264  TMEPAI  3' ATGCTTATTTTCTTTTGTTTA 39440       CTTT
                                TGAGCAAAAG   TAGGTGT
                                ||||||||||   |||||||
                                ATTTGTTTTC   ATTCGTA
                                      TTTT
GAM264  TMPO    5' GTCCGCGAGTTTTTGTTC   12343        TTA  TGT
                                GAGCAAAAGCTT  GG
                                ||||||||||||  ||
                                CTTGTTTTTGAG  CC
                                       CG_  TGT
GAM264  TNFRSF14 3' ATACCTGGAGCGACGGCT   13781    AAAA   T
                                AGC   GCTTT AGGTGT
                                |||   ||||| ||||||
                                TCG   CGAGG TCCATA
                                  GCAG   _
GAM264  TNFRSF6B 3' GCACTGAAAGAGGCTTTTTTTT 51965    C      TA__
          A                      TGAG AAAAGCTTT   GGTGT
                                 |||| |||||||||   |||||
                                 ATTT TTTTCGGAG   TCACG
                                   T       AAAG
GAM264  TNFRSF6B 3' GCACTGAAAGAGGCTTTTTTTT 51983    C      TA__
          A                      TGAG AAAAGCTTT   GGTGT
                                 |||| |||||||||   |||||
                                 ATTT TTTTCGGAG   TCACG
                                   T       AAAG
GAM264  TNFRSF6B 3' GCACTGAAAGAGGCTTTTTTTT 13794    C      TA__
          A                      TGAG AAAAGCTTT   GGTGT
                                 |||| |||||||||   |||||
                                 ATTT TTTTCGGAG   TCACG
                                   T       AAAG
GAM264  TNFRSF9  3' ACACCTGACTAACTTTTTTGTT 7785       CTT___
          T                      GAGCAAAAG    TTAGGTGT
                                 |||||||||    ||||||||
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                                TTTGTTTTT    AGTCCACA
                                     TCAATC
GAM264  TNFSF9   3' ATACTTGGGGGCTAGCTT   13753     AAA
                                GAGC  AGCTTTTAGGTGT
                                ||||  ||||||||||||
                                TTCG  TCGGGGGTTCATA
                                  A__
GAM264  TP63     3' ACACTTGAAACCTTTTTTTA  13565     C    C
                                TGAG AAAAG TTTTAGGTGT
                                |||| ||||| ||||||||||
                                ATTT TTTTC AAAGTTCACA
                                  _    C
GAM264  TP63     3' AAGAATTGAAAAGTTTTTGTTT 13564          AG  GT
                                GAGCAAAAGCTTTT  GT
                                ||||||||||||||  ||
                                TTTGTTTTTGAAAA  TA
                                       GT  AGAAG
GAM264  TRPC5    5' GCGCTTGAAGGGGCTCA    24998     AAAAG
                                TGAGC   CTTTTAGGTGT
                                |||||    ||||||||||
                                ACTCG   GGAAGTTCGCG
                                  G____
GAM264  TRPV1    3' ACACCTGGCTGTTTTCTT   54852    CA   TT
                                GAG  AAAGC  TTAGGTGT
                                |||  |||||  ||||||||
                                TTC  TTTTG  GGTCCACA
                                  __    TC
GAM264  TRPV1    3' ACACCTGGCTGTTTTCTT   54785    CA   TT
                                GAG  AAAGC  TTAGGTGT
                                |||  |||||  ||||||||
                                TTC  TTTTG  GGTCCACA
                                  __    TC
GAM264  TRPV1    3' ACACCTGGCTGTTTTCTT   54820    CA   TT
                                GAG  AAAGC  TTAGGTGT
                                |||  |||||  ||||||||
                                TTC  TTTTG  GGTCCACA
                                  __    TC
GAM264  TRPV1    3' ACACCTGGCTGTTTTCTT   38066    CA   TT
                                GAG  AAAGC  TTAGGTGT
                                |||  |||||  ||||||||
                                TTC  TTTTG  GGTCCACA
                                  __    TC
GAM264  TSG      3' ATTCCAAAAGGTTTTTGCTT  40230          A  TGT
                                GAGCAAAAGCTTTT GG
                                |||||||||||||| ||
                                TTCGTTTTTGGAAA CC
                                       A  TTA
GAM264  TSG      3' GCATTCCAAAAGGTTTTTGCTT 40234          A  __
                                GAGCAAAAGCTTTT GG  TGT
                                |||||||||||||| ||  |||
```

```
                                TTCGTTTTTGGAAA CC  ACG
                                       A  TT
GAM264  TSG     3'  GCATTCCCAAGAGTTTATGTTT 40235       A      A __
           A                    TGAGCA AAGCTTTT GG  TGT
                                |||||| |||||||| ||  |||
                                ATTTGT TTTGAGAA CC  ACG
                                   A       C  TT
GAM264  TSN     3'  ACACTTGGGGAGATTTGCCA  16099    A    AG   _
                                TG GCAAA  CTTTT AGGTGT
                                || |||||  ||||| ||||||
                                AC CGTTT  GAGGG TTCACA
                                 _    A_    G
GAM264  UMPS    5'  GCGCCTGGGAGTTTGAAGC   4552     AA_
                                GC   AAGCTTTTAGGTGT
                                ||   ||||||||||||||
                                CG   TTTGAGGGTCCGCG
                                 AAG
GAM264  UNG     3'  AGATGTTGGGGTGTTTTTGCTT 55154          _     GTGT
           A                    TGAGCAAAAGC TTTTAG
                                |||||||||||| ||||||
                                ATTCGTTTTTG GGGGTT
                                       T     GTAGAC
GAM264  UNG     3'  AGATGTTGGGGTGTTTTTGCTT 12550          _     GTGT
           A                    TGAGCAAAAGC TTTTAG
                                |||||||||||| ||||||
                                ATTCGTTTTTG GGGGTT
                                       T     GTAGAC
GAM264  UNRIP   3'  ATGCCTTTTCTTTTTTTGCTT  23199        CTTTT_
                                GAGCAAAAG     AGGTGT
                                |||||||||     ||||||
                                TTCGTTTTT     TCCGTA
                                      TTCTTT
GAM264  USP18   3'  GCATCTGGGGGCCAAAGGTCA  63617     G AAAA_
                                TGA C     GCTTTTAGGTGT
                                ||| |     ||||||||||||
                                ACT G     CGGGGGTCTACG
                                  _ GAAAC
GAM264  USP6    3'  ATACTTGAAGGAAATGTTT   91144      AAAG
                                GAGCA    CTTTTAGGTGT
                                |||||    ||||||||||
                                TTTGT    GGAAGTTCATA
                                   AAA_
GAM264  VBP1    5'  GCACCTAGAGGTTGGGCT    12571     AAA
                                AGC   AGCTTTTAGGTGT
                                |||   ||||||||||||
                                TCG   TTGGAGATCCACG
                                  GG_
GAM264  VDR     3'  ACATCTGAAAGCCACGTTC   4564      AAAA
                                GAGC    GCTTTTAGGTGT
                                ||||    ||||||||||||
```

```
                                CTTG   CGAAAGTCTACA
                                  CAC_
GAM264  VHL     3'  GTGCTTAGAGGTTCTGCCTC  5081     _ AA       TG
                                GAG CA  AGCTTTTAGG  T
                                ||| ||  ||||||||||  |
                                CTC GT  TTGGAGATTC  G
                                  C  C_       GT
GAM264  VHL     3'  ACAAATAAGTTTTTGCT    5049          TTAGG
                                AGCAAAAGCTT    TGT
                                ||||||||||    |||
                                TCGTTTTTGAA    ACA
                                      TAA__
GAM264  VIPR1   3'  ATTCTGGAGTTTTTGTTT   16112          T  TGT
                                GAGCAAAAGCTTT AGG
                                |||||||||||| |||
                                TTTGTTTTTGAGG TCT
                                      _  TA
GAM264  WISP2   5'  GTGCCTGGGAGTGACCTCA  13938    CAAAA      TG
                                TGAG   GCTTTTAGG  T
                                ||||   |||||||||  |
                                ACTC   TGAGGGTCC  G
                                  CAG__       GT
GAM264  WTAP    5'  ACGCCTGAAAGGCGACTCTC  16928    CAAAA  _
                                GAG    GC TTTTAGGTGT
                                |||    || ||||||||||
                                CTC    CG AAAGTCCGCA
                                  TCAG_  G
GAM264  XT3     3'  ACGGAATAGTTTTTGCTCA   39517          T  AG
                                TGAGCAAAAGCT TT  GT
                                |||||||||||| ||  ||
                                ACTCGTTTTTGA AA  CA
                                      T  GG
GAM264  YES1    3'  ACACTAAATGGGTATTTGTTCA 18345        A   TTA_
                                TGAGCAAA GCTT   GGTGT
                                |||||||| ||||   |||||
                                ACTTGTTT TGGG   TCACA
                                     A   TAAA
GAM264  YES1    3'  ACGCCTGGCTAGTTTTTTG   18346   C     T_
                                G AAAAGCT  TTAGGTGT
                                | |||||||  ||||||||
                                G TTTTTGA  GGTCCGCA
                                 T      TC
GAM264  YWHAE   3'  GCATCTAAGAGAGAGGTT   22195    AAAAG
                                AGC    CTTTTAGGTGT
                                |||    ||||||||||
                                TTG    GAGAATCTACG
                                  GAGA_
GAM264  YWHAG   3'  GCGCCTAAAGTCATTGCCA   25020   A   AA   T
                                TG GCAA  GCTTT AGGTGT
                                || ||||  ||||| ||||||
```

```
                                AC CGTT  TGAAA TCCGCG
                                 _   AC   _
GAM264  YY1     3'  ACACCTAAGGGACATGTTT   12688      AAAG
                                GAGCA   CTTTTAGGTGT
                                |||||   ||||||||||
                                TTTGT   GGGAATCCACA
                                   ACA_
GAM264  ZFHX1B  5'  ACACTCTTGGCGAGGTTTTTGT 28920   A        T___ _
            ACA                   G GCAAAAGCTTT   AG GTGT
                                | ||||||||||   || ||||
                                C TGTTTTTGGAG   TC CACA
                                 A         CGGT  T
GAM264  ZNF147  3'  GCACTTGGGCTGACTGC    17436    AA_   TT
                                GCA   AGCT  TAGGTGT
                                |||   ||||  |||||||
                                CGT   TCGG  GTTCACG
                                  CAG   __
GAM264  ZNF192  3'  ACACTTAAAGTATTTATGCTTA 20851       _  GC
                                TGAGCA AAA  TTTTAGGTGT
                                |||||| |||  ||||||||||
                                ATTCGT TTT  GAAATTCACA
                                   A   AT
GAM264  ZNF2    3'  GCACTTGGAGGTGTGACTTA   40804     _ AAA
                                TGAG CA   GCTTTTAGGTGT
                                |||| ||   ||||||||||||
                                ATTC GT   TGGAGGTTCACG
                                  A  G__
GAM264  ZNF264  5'  GCGTCTGGAACGCCGTTGCCA  12757    A   AA _    GT
                                TG GCAA  GC TTTTAG  GT
                                || ||||  || ||||||  ||
                                AC CGTT  CG AAGGTC  CG
                                 _   GC  C     TG
GAM264  ZNF264  3'  ACACCTTCTGTTTCTTTGCTTA 12740        __  TTTT
                                TGAGCAAA  AGC    AGGTGT
                                ||||||||  |||   ||||||
                                ATTCGTTT  TTG    TCCACA
                                     CT   TCT_
GAM264  ZNF265  3'  GTGCTTGGGGGCTTTTTGTT   18398       _       TG
                                AGCAAAA GCTTTTAGG  T
                                |||||||  |||||||||  |
                                TTGTTTT CGGGGGTTC  G
                                    T       GT
GAM264  ZNF274  5'  GCGTCTGGGAGTTGTAGTTC   32883     AAA       GT
                                GAGC   AGCTTTTAG  GT
                                ||||   |||||||||  ||
                                CTTG   TTGAGGGTC  CG
                                  ATG       TG
GAM264  ZNF274  5'  GCGTCTGGGAGTTGTAGTTC   56057     AAA       GT
                                GAGC   AGCTTTTAG  GT
                                ||||   |||||||||  ||
```

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                                CTTG  TTGAGGGTC CG
                                  ATG       TG
GAM264  ZNF289   3' TACCTAAAGGTTTCATTTG  65335     ___       GT
                                CAAA  AGCTTTTAGGT
                                ||||  ||||||||||
                                GTTT  TTGGAAATCCA
                                  ACT        TG
GAM264  ZNF289   3' GCACTTGGAAGATTGTTT   65333      AAG
                                GAGCAA  CTTTTAGGTGT
                                ||||||  ||||||||||
                                TTTGTT  GAAGGTTCACG
                                   A__
GAM264  ZNF36    3' ACACCTAAGAGGCACTCA   93956     CAAAAG
                                TGAG    CTTTTAGGTGT
                                ||||    ||||||||||
                                ACTC    GAGAATCCACA
                                  ACG___
GAM264  ZNF80    3' ACATCTAGAAGTATAAGC   23072    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   TGAAGATCTACA
                                 AATA
GAM264  A2BP1    5' ACATCTGGAGGGGACAGCCA  38059    A  AAAAG
                                TG GC    CTTTTAGGTGT
                                || ||    ||||||||||
                                AC CG    GGAGGTCTACA
                                 _ ACAGG
GAM264  AD034    3' GCATCTGGAAGATGGCTTA   48946     AAAAG
                                TGAGC    CTTTTAGGTGT
                                |||||    ||||||||||
                                ATTCG    GAAGGTCTACG
                                   GTA__
GAM264  ADAMTSL1 5' GCACTTAGCAGCTTATTCA   57638     CAA    T
                                TGAG  AAGCT TTAGGTGT
                                ||||  ||||| ||||||||
                                ACTT  TTCGA GATTCACG
                                  A__    C
GAM264  ADAMTSL1 5' GCACTTAGCAGCTTATTCA   57688     CAA    T
                                TGAG  AAGCT TTAGGTGT
                                ||||  ||||| ||||||||
                                ACTT  TTCGA GATTCACG
                                  A__    C
GAM264  ADAMTSL1 5' GCACTTAGCAGCTTATTCA   53501     CAA    T
                                TGAG  AAGCT TTAGGTGT
                                ||||  ||||| ||||||||
                                ACTT  TTCGA GATTCACG
                                  A__    C
GAM264  ADNP     3' GCATCTAAATAAATTGCT    31046      AAGCT
                                AGCAA    TTTAGGTGT
                                |||||    |||||||||
```

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                                TCGTT    AAATCTACG
                                   AAAT_
GAM264  AIG-1    3'  ATATAGAGTAAGGCTTTTGT  32258         TAG__
                                GCAAAAGCTTT    GTGT
                                ||||||||||    ||||
                                TGTTTTCGGAA    TATA
                                     TGAGA
GAM264  AK000009 3'  ACATTGTATGGCATTTGTTTA  76998        A   TTTA
                                TGAGCAAA GCT    GGTGT
                                |||||||| |||    |||||
                                ATTTGTTT CGG    TTACA
                                    A   TATG
GAM264  AKAP11   3'  ATCTCGAAGAGTTTTGTTC   57829        G_   T   GT
                                GAGCAAAA  CTTT AGGT
                                ||||||||  |||| ||||
                                CTTGTTTT  GAAG TCTA
                                    GA   C
GAM264  AKAP11   3'  ATACTTTAATTTTGCTC     32700        GCTTTT
                                GAGCAAAA     AGGTGT
                                ||||||||     ||||||
                                CTCGTTTT     TTCATA
                                    AAT___
GAM264  AKL3L    3'  AATCTAACTTTTTGTTCA    32801         CTT     GT
                                TGAGCAAAAG   TTAGGT
                                ||||||||||   ||||||
                                ACTTGTTTTT   AATCTA
                                     C__     AT
GAM264  AKL3L    3'  ATGCCTGGGAAATGCTC     32802      AAAGC
                                GAGCA    TTTTAGGTGT
                                |||||    ||||||||||
                                CTCGT    AGGGTCCGTA
                                   AA___
GAM264  AKT3     3'  ACACTCCAGTTTTTGTTT    18431         TTTA
                                GAGCAAAAGCT    GGTGT
                                ||||||||||    |||||
                                TTTGTTTTTGA    TCACA
                                     CC__
GAM264  ALDH5A1  3'  GCATCTGGAGGTGTTGC     6550      AA
                                GCAA  GCTTTTAGGTGT
                                ||||  ||||||||||||
                                CGTT  TGGAGGTCTACG
                                  G_
GAM264  AMOT     3'  GTGCTCTAAAGCTTATTGTTT  55724       _     TA  TG
                                GAGCAA AAGCTTT  GG  T
                                |||||| |||||||  ||  |
                                TTTGTT TTCGAAA  TC  G
                                   A      TC  GT
GAM264  AP1G2    3'  ACACCTGAGGGCTACCAGC   54500    AAA_
                                GC   AGCTTTTAGGTGT
                                ||   ||||||||||||
```

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                                CG   TCGGGAGTCCACA
                                 ACCA
GAM264  AP1G2    3'  ACACCTGAGGGCTACCAGC   14044    AAA_
                                GC   AGCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   TCGGGAGTCCACA
                                 ACCA
GAM264  AP1GBP1  3'  ATATTTAGAAAGGTGCTTTTGT 54529          ____
              TC                  GAGCAAAAGC   TTTTAGGTGT
                                  ||||||||||   ||||||||||
                                  CTTGTTTTCG   AAGATTTATA
                                       TGGA
GAM264  AP1S2    3'  TACTTAGTTGTTTTTG     14042       TT
                                  CAAAAGC  TTAGGTG
                                  |||||||  |||||||
                                  GTTTTTG  GATTCAT
                                      TT
GAM264  AP3M2    3'  TTATACAAAAGGGTTTTTGTTT 22317            AG
              A                   TGAGCAAAAGCTTTT  GTGT
                                  ||||||||||||||  ||||
                                  ATTTGTTTTTGGGAA  CATA
                                          AA   TTT
GAM264  AP3M2    3'  ATATTGTGCAAAGTTTTTGCT  22313          TA__
                                  AGCAAAAGCTTT   GGTGT
                                  ||||||||||||   |||||
                                  TCGTTTTTGAAA   TTATA
                                       CGTG
GAM264  APELIN   3'  CATCAGCGTTTGCTCA     33783        A   TTTA
                                  TGAGCAAA GCT   GGTG
                                  ||||||||| |||   ||||
                                  ACTCGTTT CGA   CTAC
                                      G  _____
GAM264  ARF4     3'  GCCTGATTTTTTGCTCA     82812         CTT
                                  TGAGCAAAAG   TTAGGT
                                  ||||||||||   ||||||
                                  ACTCGTTTTT   AGTCCG
                                       T__
GAM264  ARFGAP1  3'  ACACCTGAGCTGTCCTCA    36586     CAAA    TT
                                  TGAG   AGCTT  AGGTGT
                                  ||||   |||||  ||||||
                                  ACTC   TCGAG  TCCACA
                                    CTG_    __
GAM264  ARHF     3'  GCGCCTAGGAGTCGGTGTC   38743    G  AAA
                                  GA CA   GCTTTTAGGTGT
                                  || ||   ||||||||||||
                                  CT GT   TGAGGATCCGCG
                                   _ GGC
GAM264  ARHGEF2  3'  ACATTTGAAAGAACTGC     16360     AAAG
                                  GCA    CTTTTAGGTGT
                                  |||    ||||||||||
```

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                                CGT   GAAAGTTTACA
                                  CAA_
GAM264  ARHGEF9  3'  GCATCTAGGAGTTAGTTT   30811     AAA
                                GAGC  AGCTTTTAGGTGT
                                ||||  ||||||||||||
                                TTTG  TTGAGGATCTACG
                                  A__
GAM264  ARHGEF9  3'  GCCAGCTTTTTGCTT      30812       _  TTTA
                                GAGCAAAA GCT   GGT
                                |||||||| |||   |||
                                TTCGTTTT CGA   CCG
                                     T  ____
GAM264  ARL5     3'  AAAAGTATTTTGCTTA     23937       _
                                TGAGCAAAA GCTTTT
                                ||||||||| ||||||
                                ATTCGTTTT TGAAAA
                                     A
GAM264  ARNTL2   3'  ACATTTAAAGGGACAGTGC   39452    AAAG_
                                GCA    CTTTTAGGTGT
                                |||    ||||||||||
                                CGT    GGAAATTTACA
                                  GACAG
GAM264  ARPC5    3'  ATAGCTTTGTTTTTGCTT    19139       TTTT  G
                                GAGCAAAAGC   AG TGT
                                |||||||||   || |||
                                TTCGTTTTTG   TC ATA
                                     TT__  G
GAM264  ATP9A    3'  GCGCCTGGGTACTTCTC     62045    CAA  CT
                                GAG  AAG  TTTAGGTGT
                                |||  |||  |||||||||
                                CTC  TTC  GGGTCCGCG
                                  ___  AT
GAM264  ATP9A    3'  ACCTGGCTTTGCTCG       62035       A  TTT
                                TGAGCAAA GCT  AGGT
                                |||||||| |||  ||||
                                GCTCGTTT CGG  TCCA
                                   _  ___
GAM264  ATPW     5'  ACAGCTCGGTTTTTGCCA    31628    A      TTT  G
                                TG GCAAAAGCT  AG TGT
                                || |||||||||  || |||
                                AC CGTTTTTGG  TC ACA
                                  _       C__  G
GAM264  AUTL1    3'  GTGTTTAGAAGCTGAGGCCA  51662    A  AAA       TG
                                TG GC  AGCTTTTAGG  T
                                || ||  ||||||||||  |
                                AC CG  TCGAAGATTT  G
                                  _ GAG        GT
GAM264  AWP1     5'  ACAGGACAGCTGTTTGCTCA  38662       _   T  AG  GT
                                TGAGCAAA AGCT TT  GT
                                |||||||| |||| ||  ||
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                                ACTCGTTT TCGA AG  CA
                                    G   C  GA
GAM264  BAIAP1   3'  ACATTTCATCCTTTTGCTT   16446        CTTTT
                                GAGCAAAAG    AGGTGT
                                |||||||||    ||||||
                                TTCGTTTTC    TTTACA
                                     CTAC_
GAM264  BAT8     3'  ATGCCTGGGGGGTGCTGCCA   22002    A   AAA
                                TG GCA   GCTTTTAGGTGT
                                || |||   ||||||||||||
                                AC CGT   TGGGGGTCCGTA
                                 _  CG_
GAM264  BCMP1    3'  TACCTTAAAGCTTTTGCTC   48738          T   GT
                                GAGCAAAAGCTTT AGGT
                                |||||||||||||| ||||
                                CTCGTTTTCGAAA TCCA
                                       T   TG
GAM264  BCMP1    3'  ATGCCTAAAGCTGTGC     48731     AA     T
                                GCA  AGCTTT AGGTGT
                                |||  |||||| ||||||
                                CGT  TCGAAA TCCGTA
                                  G_     _
GAM264  BCMP1    3'  ACATTTAGAAGTTCCTTTGC   48728      __
                                GCAAA  AGCTTTTAGGTGT
                                |||||  ||||||||||||
                                CGTTT  TTGAAGATTTACA
                                   CC
GAM264  BCoR     3'  ATACCTAGAAGTGCTGCTTA   40509       AAA
                                TGAGCA   GCTTTTAGGTGT
                                ||||||   ||||||||||||
                                ATTCGT   TGAAGATCCATA
                                   CG_
GAM264  BIKE     3'  ACACTTGAAGGCTTATTTTGCT 34180        ___
              T                  GAGCAAA   AGCTTTTAGGTGT
                                |||||||   ||||||||||||
                                TTCGTTT   TCGGAAGTTCACA
                                    TAT
GAM264  BRD3     3'  ATATCTTCCAGTTTTTGCTT   23756          TTT
                                GAGCAAAAGCT   AGGTGT
                                ||||||||||   ||||||
                                TTCGTTTTTGA   TCTATA
                                      CCT
GAM264  BRD3     3'  TATTTGAAAGCTGTTAGCTT   23760      AAA_        GT
                                GAGC   AGCTTTTAGGT
                                ||||   ||||||||||
                                TTCG   TCGAAAGTTTA
                                  ATTG         TG
GAM264  BS69     3'  ACACAGCGGTTTTTGTTT    21767          TTTAG
                                GAGCAAAAGCT    GTGT
                                ||||||||||    ||||
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                                TTTGTTTTTGG    CACA
                                      CGA__
GAM264  BTBD3    3'  AGGAACTGGGGGCATTTGTTTA 30304        A       GTGT
                                TGAGCAAA GCTTTTAG
                                |||||||| ||||||||
                                ATTTGTTT CGGGGGTC
                                     A       AAGGAA
GAM264  BTN2A1   3'  GCACCTAGGGGAGAGCGTGC   54341     AAAG__
                                GCA     CTTTTAGGTGT
                                |||     ||||||||||||
                                CGT     GGGGATCCACG
                                  GCGAGA
GAM264  BTN2A1   3'  TTCCAAAGAGTTTTTGTTTA   54345            A  TGT
                                TGAGCAAAAGCTTTT GG
                                |||||||||||||| ||
                                ATTTGTTTTTGAGAA CC
                                          A  TTA
GAM264  BTN2A2   3'  ACACTTAGAAGTTATTG     22776     A
                                CAA AGCTTTTAGGTGT
                                ||| ||||||||||||
                                GTT TTGAAGATTCACA
                                  A
GAM264  BTN2A2   3'  ACTTTAAAGAGCTTTTGTTTA  22777            __   GT
                                TGAGCAAAAGCTTTT  AGGT
                                ||||||||||||||  ||||
                                ATTTGTTTTCGAGAA  TTCA
                                          AT
GAM264  C11orf15 3'  ATGCCTGGTGGCTTTTCA    40220    C      T
                                G AAAAGCT TTAGGTGT
                                | ||||||| ||||||||
                                A TTTTCGG GGTCCGTA
                                 C      T
GAM264  C11orf9  3'  ATGCAAATAGCTTTTGCT    25205         TTTAG
                                AGCAAAAGCT    GTGT
                                ||||||||||    ||||
                                TCGTTTTCGA    CGTA
                                      TAAA_
GAM264  C15orf5  5'  ATACTTGAAAGCCTAAACTC   48197     CAAAA
                                GAG    GCTTTTAGGTGT
                                |||    ||||||||||||
                                CTC    CGAAAGTTCATA
                                  AAATC
GAM264  C1orf22  3'  ACGCTTAGAAGCAAATTGTTC  47251       AA_
                                GAGCAA   GCTTTTAGGTGT
                                ||||||   ||||||||||||
                                CTTGTT   CGAAGATTCGCA
                                   AAA
GAM264  C1orf24  3'  ACACTTAGGGGTTGCATGC    53701     AA_
                                GCA   AGCTTTTAGGTGT
                                |||   ||||||||||||
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                                CGT  TTGGGGATTCACA
                                  ACG
GAM264  C1orf9   3' ACGCCTTCTTTGTTTGTTTA  32633       AGCTTTT
                                TGAGCAAA     AGGTGT
                                ||||||||     ||||||
                                ATTTGTTT     TCCGCA
                                    GTTTCT_
GAM264  C1QTNF2  3' GCATCTGAGAACCGCTGCTC  49128      AAAGC
                                GAGCA    TTTTAGGTGT
                                |||||    ||||||||||
                                CTCGT    AGAGTCTACG
                                   CGCCA
GAM264  C1QTNF7  3' ACACTTGGAGGGTTGC     49154     AAG
                                GCAA  CTTTTAGGTGT
                                ||||  ||||||||||
                                CGTT  GGAGGTTCACA
                                  G__
GAM264  C20orf103 3' ATCTGAGGCTTGCTT      24326      AA     T
                                GAGCA  AGCTTT AGGT
                                |||||  |||||| ||||
                                TTCGT  TCGGAG TCTA
                                   __     _
GAM264  C20orf110 3' ATTTTAAAAGGCCTTTTGTTTA 79543          __      TGT
                                TGAGCAAAAG  CTTTTAGG
                                ||||||||||  ||||||||
                                ATTTGTTTTC  GAAAATTT
                                     CG       TA
GAM264  C20orf13  3' TTATCTTTGTTTTTGTTTA   34756         TTTT    T
                                TGAGCAAAAGC    AGGTG
                                ||||||||||    |||||
                                ATTTGTTTTTG    TCTAT
                                     TT__     TA
GAM264  C20orf130 3' ATGCTTGAAGGCCAGGGT    61753    AAAA
                                GC    GCTTTTAGGTGT
                                ||    ||||||||||||
                                TG    CGGAAGTTCGTA
                                  GGAC
GAM264  C20orf142 3' ATGCCTGAAGGACACTCTC    74769     CAAAAG
                                GAG     CTTTTAGGTGT
                                |||     ||||||||||
                                CTC     GGAAGTCCGTA
                                  TCACA_
GAM264  C20orf142 3' ATACCTGGGCCTGTTCA     74768       AAA   TT
                                TGAGCA   GCT  TAGGTGT
                                ||||||   |||  |||||||
                                ACTTGT   CGG  GTCCATA
                                   C__   __
GAM264  C20orf149 3' CACCTGGAACTGTGC       44171     AA  C
                                GCA  AG TTTTAGGTG
                                |||  ||  |||||||||
```

```
                                CGT  TC AAGGTCCAC
                                  G_  _
GAM264  C20orf150 3'  TACCAGGACCTTTTGTTCA   65402          C    A   GT
                                TGAGCAAAAG TTTT GGT
                                |||||||||| |||| |||
                                ACTTGTTTTC AGGA CCA
                                      C    _   TG
GAM264  C20orf162 5'  GTGCCTGGGCGAGCTTGCT   54603      AA    __    TG
                                AGCA  AGCTT  TTAGG  T
                                ||||  |||||  |||||  |
                                TCGT  TCGAG  GGTCC  G
                                  __    CG    GT
GAM264  C20orf175 5'  GTGTCTGGGAGCATCTGGCTT  55067      AAAA_       TG
                                GAGC    GCTTTTAGG  T
                                ||||    |||||||||  |
                                TTCG    CGAGGGTCT  G
                                  GTCTA        GT
GAM264  C20orf183 3'  GCACCTGGAGTCCCAGCT    47804     AAAA    T
                                AGC    GCTTT AGGTGT
                                |||    ||||| ||||||
                                TCG    TGAGG TCCACG
                                  ACCC    _
GAM264  C20orf28  3'  GCGCCTGGAGCACCTGCTC   31225       AAA    T
                                GAGCA   GCTTT AGGTGT
                                |||||   ||||| ||||||
                                CTCGT   CGAGG TCCGCG
                                   CCA    _
GAM264  C20orf3   3'  GCACTTGGAACAGGGCTCA   68073      AAAAGC
                                TGAGC     TTTTAGGTGT
                                |||||     ||||||||||
                                ACTCG     AAGGTTCACG
                                   GGAC__
GAM264  C20orf30  3'  ATGCCTAGAGGACTAGATCA   26249     GCAAAAG
                                TGA      CTTTTAGGTGT
                                |||      ||||||||||
                                ACT      GGAGATCCGTA
                                  AGATCA_
GAM264  C20orf40  5'  GCATTTGGGAGTAGTGGCCA   25916    A  AAAA
                                TG GC    GCTTTTAGGTGT
                                || ||    ||||||||||||
                                AC CG    TGAGGGTTTACG
                                 _  GTGA
GAM264  C20orf7   3'  ACGCTTGGTAGCTTTTTTGTTT 44142        __    T
                                GAGCAAA  AGCT TTAGGTGT
                                |||||||  |||| ||||||||
                                TTTGTTT  TCGA GGTTCGCA
                                     TT    T
GAM264  C20orf80  3'  GCATCTAGGAGCTACCTTGT   65288      A__
                                GCAA   AGCTTTTAGGTGT
                                ||||   ||||||||||||
```

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                                TGTT   TCGAGGATCTACG
                                  CCA
GAM264  C21orf25  3'  GTGCCCGTTTAGATTTTTGCTT 63555        _  TTTA_  TG
                                GAGCAAAAG CT    GG  T
                                ||||||||| ||    ||  |
                                TTCGTTTTT GA    CC  G
                                    A  TTTGC  GT
GAM264  C21orf25  3'  TGGCTTGAGGGCTTTTGTTT  63560             GT
                                GAGCAAAAGCTTTTAGGT
                                ||||||||||||||||||
                                TTTGTTTTCGGGAGTTCG
                                          GTG
GAM264  C21orf61  3'  ACACCTAGCCTGCTTGCTTA  88709      AA  TT_
                                TGAGCA  AGC   TTAGGTGT
                                ||||||  |||   ||||||||
                                ATTCGT  TCG   GATCCACA
                                   __   TCC
GAM264  C5orf6    3'  GCATTTAATAGTTTGCTT    33482      AA  T
                                GAGCAA  GCT TTAGGTGT
                                ||||||  ||| ||||||||
                                TTCGTT  TGA AATTTACG
                                   __   T
GAM264  C6orf26   3'  GCATCTAGGGGCCCTTG    47510    AA
                                CAA  GCTTTTAGGTGT
                                |||  ||||||||||||
                                GTT  CGGGGATCTACG
                                  CC
GAM264  C6orf28   3'  ATACTTGAAGGGGTTTTGTTT  40993       G  _
                                GAGCAAAA CT TTTAGGTGT
                                |||||||| || |||||||||
                                TTTGTTTT GG AAGTTCATA
                                    G  G
GAM264  C8orf13   3'  ATGTCTGAGCTATTTTGCTC  81566       GCT    TG
                                GAGCAAAA   TTTAGG  T
                                ||||||||   ||||||  |
                                CTCGTTTT   GAGTCT  A
                                    ATC     GT
GAM264  C8orf14   5'  GCACTTAGAAAGCTCTCA    54001     CAAA     _
                                TGAG    AGCTTTT AGGTGT
                                ||||    ||||||| ||||||
                                ACTC    TCGAAAG TTCACG
                                  ____      A
GAM264  C9orf14   3'  GCACCTAAGAAGCTCTGTT   86675     AA     _
                                AGCA  AGCTTTT AGGTGT
                                ||||  ||||||| ||||||
                                TTGT  TCGAAGA TCCACG
                                  C_      A
GAM264  C9orf7    3'  ACACCTGGAGTCCTCTGCTC  34162      AAA_    T
                                GAGCA   GCTTT AGGTGT
                                |||||   ||||| ||||||
```

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                                CTCGT   TGAGG TCCACA
                                  CTCC    _
GAM264  CAPN13   3' GCACCTGAGCAGCCATTTCA  58013     CAAAA  _
                                TGAG    GCT TTTAGGTGT
                                ||||    ||| |||||||||
                                ACTT    CGA GAGTCCACG
                                  TAC__  C
GAM264  CAPN6    3' CTCGCTGGGGGTGTTTGTTT  26605       A      GTGT
                                GAGCAAA GCTTTTAG
                                ||||||| ||||||||
                                TTTGTTT TGGGGGTC
                                    G       GCTCA
GAM264  CARD14   3' TCTGACCAGGGGTTTTTGC   53397          A   GT
                                GCAAAAGCTTTT GGT
                                |||||||||||| |||
                                CGTTTTTGGGGA CCA
                                       _  GTCTT
GAM264  CASPR3   3' ACATTTAAGTGCTGCTCA    45931       AAA  T
                                TGAGCA   GC TTTAGGTGT
                                ||||||   || |||||||||
                                ACTCGT   CG GAATTTACA
                                   ___  T
GAM264  CBCIP2   3' ATGCCTTGTCTTTTGTTC    51588        CTTTT
                                GAGCAAAAG    AGGTGT
                                |||||||||    ||||||
                                CTTGTTTTC    TCCGTA
                                     TGT__
GAM264  CBX6     3' GCATCTAAAGGCCCCTTCA   26618     CAAAA
                                TGAG    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                ACTT    CGGAAATCTACG
                                  CCC__
GAM264  CD109    3' ACATCTGATGCTTGCT      56042      AA   TT
                                AGCA  AGC  TTAGGTGT
                                ||||  |||  ||||||||
                                TCGT  TCG  AGTCTACA
                                  __   T_
GAM264  CDC14A   3' GCATTTGAATGAATGTTTGACT 13393      _   AGCT__
           CA                     TGAG CAAA     TTTAGGTGT
                                ||||| ||||     |||||||||
                                ACTC GTTT     AAGTTTACG
                                  A    GTAAGT
GAM264  CDC14B   5' GCACCTGGGGGCGGGCT     52852     AAAA
                                AGC    GCTTTTAGGTGT
                                |||    ||||||||||||
                                TCG    CGGGGGTCCACG
                                  GG__
GAM264  CDC14B   5' GCACCTGGGGGCGGGCT     52833     AAAA
                                AGC    GCTTTTAGGTGT
                                |||    ||||||||||||
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                              TCG   CGGGGGTCCACG
                                GG__
GAM264  CDC14B   5' GCACCTGGGGGCGGGCT    13386    AAAA
                              AGC   GCTTTTAGGTGT
                              |||   ||||||||||||
                              TCG   CGGGGGTCCACG
                                GG__
GAM264  CDC26    5' ACACAAGAAGTGTTTGTTTA  57767       A    AG
                              TGAGCAAA GCTTTT  GTGT
                              |||||||| ||||||  ||||
                              ATTTGTTT TGAAGA  CACA
                                   G     A_
GAM264  CDH26    3' ATATCTAAAAGTCTACAGCCA 41463    A  AAA  _
                              TG GC   AG CTTTTAGGTGT
                              || ||   || ||||||||||
                              AC CG   TC GAAAATCTATA
                               _ ACA  T
GAM264  CECR1    3' CACTTGGAGAGCTCA      33807      AAAAGC
                              TGAGC     TTTTAGGTG
                              |||||     |||||||||
                              ACTCG     GAGGTTCAC
                                A_____
GAM264  CEP3     3' CACCTAAGCCTTTTTG     21248      CT
                              CAAAAG  TTTAGGTG
                              ||||||  ||||||||
                              GTTTTT  GAATCCAC
                                 CC
GAM264  CG012    5' TTCTTTGGGGTTTTTGTTT   83231          TT   TGT
                              GAGCAAAAGCTT  AGG
                              ||||||||||||  |||
                              TTTGTTTTTGGG  TTC
                                     GT   TTG
GAM264  CGBP     5' GCGCCTGAGGGGTCTTG    27472     AAG
                              CAA   CTTTTAGGTGT
                              |||   ||||||||||
                              GTT   GGGAGTCCGCG
                                CTG
GAM264  CGGBP1   3' ATACCTGAAACCTGATGGTTA 13359     G  AA  C
                              TGA CA  AG TTTTAGGTGT
                              ||| ||  || ||||||||||
                              ATT GT  TC AAAGTCCATA
                                G  AG  C
GAM264  CHERP    3' GCACTTGGAAGAACCCTGC   21101     AAAG_
                              GCA    CTTTTAGGTGT
                              |||    ||||||||||
                              CGT    GAAGGTTCACG
                                CCCAA
GAM264  CHK      3' ATATTTGGGGGCTAAGGTTT  7048      AAA
                              GAGC   AGCTTTTAGGTGT
                              ||||   ||||||||||||
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                                TTTG  TCGGGGGTTTATA
                                  GAA
GAM264  CHST3   3'  ATATTTGAAGGCTGCCTCA   14968     CAAA
                                TGAG   AGCTTTTAGGTGT
                                ||||   ||||||||||||
                                ACTC   TCGGAAGTTTATA
                                  CG__
GAM264  CKAP2   3'  ACACTTAAGTACATGCTTA   36561      AAA  TT
                                TGAGCA  GCT  TAGGTGT
                                ||||||  |||  |||||||
                                ATTCGT  TGA  ATTCACA
                                   ACA  __
GAM264  CMG2    3'  TCTAGCTTGAAACTTTTGCTCA 54165         C      GT
                                TGAGCAAAAG TTTTAGGT
                                |||||||||| ||||||||
                                ACTCGTTTTC AAAGTTCG
                                      _      ATCTC
GAM264  CNIL    3'  ACATTGGAAGCTTTTGTTTA  19328             G
                                TGAGCAAAAGCTTTTAG TGT
                                |||||||||||||||| |||
                                ATTTGTTTTCGAAGGTT ACA
                                          _  T
GAM264  COASTER  3'  GTATTTGAAAACATGTTTTTGC 31446         ____      GT
           TT                    GAGCAAAAGC   TTTTAGGT
                                ||||||||||   ||||||||
                                TTCGTTTTTG   AAAGTTTA
                                      TACA      TG
GAM264  COLEC12  3'  ATACTTAAAGAGCTTTT    55221         _
                                AAAAGCTTTT AGGTGT
                                |||||||||| ||||||
                                TTTTCGAGAA TTCATA
                                      A
GAM264  COLEC12  3'  ATACTTAAAGAGCTTTT    47862         _
                                AAAAGCTTTT AGGTGT
                                |||||||||| ||||||
                                TTTTCGAGAA TTCATA
                                      A
GAM264  CPNE1   3'  ATACTTGTTTCTGCTTTTGCT  14037        TTT__
                                AGCAAAAGC    TAGGTGT
                                |||||||||    |||||||
                                TCGTTTTCG    GTTCATA
                                     TCTTT
GAM264  CPR2    3'  GCACTTGGGAGGCGCTGGCTC  48097     AAAA    _
                                GAGC   GCTTTT AGGTGT
                                ||||   |||||| ||||||
                                CTCG   CGGAGG TTCACG
                                  GTCG     G
GAM264  CREG    3'  ACACTTAAAAGGCTTAATGTTT 13893      A_   _
                                GAGCA  AAGC TTTTAGGTGT
                                |||||  |||| ||||||||||
```

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                                TTTGT  TTCG AAAATTCACA
                                   AA   G
GAM264  CREG    3'  GCATTTGAAGGTAGTTG    13894    AA
                                CAA  GCTTTTAGGTGT
                                |||  ||||||||||||
                                GTT  TGGAAGTTTACG
                                  GA
GAM264  CSMD1   3'  GCACCTGGAGGATCTCA    73122     CAAAAG
                                TGAG    CTTTTAGGTGT
                                ||||    ||||||||||
                                ACTC    GGAGGTCCACG
                                  TA____
GAM264  ctm-1   3'  ACACCTCTCCTGGTTTTGTTCA 75248        G  TTT__
                                TGAGCAAAA CT    AGGTGT
                                ||||||||| ||    ||||||
                                ACTTGTTTT GG    TCCACA
                                      _ TCCTC
GAM264  CUGBP2  3'  AAAAGTTGTTTGCTTA     21625       _
                                TGAGCAAA AGCTTTT
                                |||||||| |||||||
                                ATTCGTTT TTGAAAA
                                     G
GAM264  CYB5-M  3'  GTATTTGAAAGTGAGAGTTCA  47569     AAAA      GT
                                TGAGC   GCTTTTAGGT
                                |||||   ||||||||||
                                ACTTG   TGAAAGTTTA
                                   AGAG       TG
GAM264  CYB5-M  3'  GTATTTGAAAGTGAGAGTTCA  94566     AAAA      GT
                                TGAGC   GCTTTTAGGT
                                |||||   ||||||||||
                                ACTTG   TGAAAGTTTA
                                   AGAG       TG
GAM264  D2S448  3'  GCGCCTAAATTGATTTTG    73526     GCT_
                                CAAAA   TTTAGGTGT
                                |||||   |||||||||
                                GTTTT   AAATCCGCG
                                   AGTT
GAM264  DECR2   3'  GTGCCTGAGGGCCAGGTGCCA  40336   A  AAA_     TG
                                TG GCA   GCTTTTAGG  T
                                || |||   |||||||||  |
                                AC CGT   CGGGAGTCC  G
                                  _  GGAC       GT
GAM264  DICER1  3'  ACATTTAGCAAGTGCTCA    47606     AAA  TTT
                                TGAGCA  GCT  AGGTGT
                                ||||||  |||  ||||||
                                ACTCGT  CGA  TTTACA
                                   GAA  ___
GAM264  DJ473B4 3'  ATGCCTGAGGTTGGTTTTTG  38958       ___
                                CAAAAGCT  TTTAGGTGT
                                ||||||||  |||||||||
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                                GTTTTTGG   GAGTCCGTA
                                     TTG
GAM264   DKFZp434F1719 3'  GCACTTGTACTTTTTGTTT   49999        CTTT
                                GAGCAAAAG   TAGGTGT
                                |||||||||   |||||||
                                TTTGTTTTT   GTTCACG
                                     CAT_
GAM264   DKFZP434G072 5'  ACATCTGGAAGTGAGGTCA   49587    G AAAA
                                TGA C   GCTTTTAGGTGT
                                ||| |   ||||||||||||
                                ACT G   TGAAGGTCTACA
                                  _ GAG_
GAM264   DKFZp434G179 3'  ACAGAATTGGAGCTTTGCTTA  80087       A    TAGG_
                                TGAGCAAA GCTTT    TGT
                                |||||||| |||||    |||
                                ATTCGTTT CGAGG    ACA
                                     _    TTAAG
GAM264   DKFZP434I0714 3'  ACACTTGAAAGTGAGCTC    85797     AAAA
                                GAGC   GCTTTTAGGTGT
                                ||||   ||||||||||||
                                CTCG   TGAAAGTTCACA
                                  AG__
GAM264   DKFZp434I1610 3'  ACACTTGGGAGAAACTC     63450     CAAAAG
                                GAG     CTTTTAGGTGT
                                |||     ||||||||||
                                CTC     GAGGGTTCACA
                                  AAA___
GAM264   DKFZp434J0617 3'  ACACCTGAAATGCATGCTC   49979      AAA _
                                GAGCA   GC TTTTAGGTGT
                                |||||   || ||||||||||
                                CTCGT   CG AAAGTCCACA
                                   A__  T
GAM264   DKFZp434J1015 3'  ACGTTTGGGAGCAATGCTC   92631      AAA     GG
                                GAGCA   GCTTTTA  TGT
                                |||||   |||||||  |||
                                CTCGT   CGAGGGT  GCA
                                   AA_     TT
GAM264   DKFZP434J1813 3'  ACTTAGTTTTTGGTCA     61783     G      TTT
                                TGA CAAAAGCT   AGGT
                                ||| ||||||||   ||||
                                ACT GTTTTTGA   TTCA
                                  G      ___
GAM264   DKFZP434K028 3'  GCACCTGAGGGTTAATG     93233    AA
                                CA  AGCTTTTAGGTGT
                                ||  ||||||||||||
                                GT  TTGGGAGTCCACG
                                 AA
GAM264   DKFZP434L0117 3'  GCATCTGGGGGCCAAGGGCT   42919     AAAA_
                                AGC    GCTTTTAGGTGT
                                |||    ||||||||||||
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                                TCG    CGGGGGTCTACG
                                  GGAAC
GAM264  DKFZp434L0850 3'  ACATTTGGAAGCTATTGTTT  34107       A
                                GAGCAA AGCTTTTAGGTGT
                                |||||| ||||||||||||
                                TTTGTT TCGAAGGTTTACA
                                   A
GAM264  DKFZP434L1435 5'  TGACTGAAAAGCTTTTGT    92173          A  GT
                                GCAAAAGCTTTT GGT
                                |||||||||||| |||
                                TGTTTTCGAAAA TCA
                                       G  GTG
GAM264  DKFZp434M0331 5'  GCACCTGGAAGCTATCAGCCA  34233    A  AAA_
                                TG GC   AGCTTTTAGGTGT
                                || ||   ||||||||||||
                                AC CG   TCGAAGGTCCACG
                                 _ ACTA
GAM264  DKFZP434N014 3'  ATGCCTGAGCCTTTGTCCA   60598    AG   A   TT
                                TG  CAAA GCTT  AGGTGT
                                ||  |||| ||||  ||||||
                                AC  GTTT CGAG  TCCGTA
                                 CT   C   __
GAM264  DKFZP434N178 5'  GCACCTGGGGCCCTGCCA    71905    A  AAA    T
                                TG GCA  GCTTT AGGTGT
                                || |||  ||||| ||||||
                                AC CGT  CGGGG TCCACG
                                 _  CC_   _
GAM264  DKFZP434O125 3'  GCACTTGACTTTTTGCCA    64961    A     CTT
                                TG GCAAAAG   TTAGGTGT
                                || |||||||  ||||||||
                                AC CGTTTTT   AGTTCACG
                                 _     C__
GAM264  DKFZP434P0721 3'  ACCCCAAAGAGATTTTGTTTA  63715        G    A  T
                                TGAGCAAAA CTTTT GG GT
                                ||||||||| ||||| || ||
                                ATTTGTTTT GAGAA CC CA
                                      A    A  C
GAM264  DKFZp547D155 3'  ATGCCTGGGAGGAGCTGCCA  70434    A  AAAG
                                TG GCA   CTTTTAGGTGT
                                || |||   ||||||||||
                                AC CGT   GAGGGTCCGTA
                                 _  CGAG
GAM264  DKFZp547D155 3'  ACATTTGAAGGCTGCTGT    70432     AA
                                GCA  AGCTTTTAGGTGT
                                |||  ||||||||||||
                                TGT  TCGGAAGTTTACA
                                  CG
GAM264  DKFZp547H025 3'  ATATCTAGGAGTCTCTTG    39351     A  _
                                CAA AG CTTTTAGGTGT
                                ||| || ||||||||||
```

```
                                GTT TC GAGGATCTATA
                                  C  T
GAM264  DKFZp547I224 3'  ATACTTGGAAGTAAAGCTC   39552      AAAA
                                GAGC   GCTTTTAGGTGT
                                ||||   ||||||||||||
                                CTCG   TGAAGGTTCATA
                                  AAA_
GAM264  DKFZP564D116 3'  ACACCTAGCTGAATGTTTA   72213       AA_   TTT
                                TGAGCA  AGCT  AGGTGT
                                ||||||  ||||  ||||||
                                ATTTGT  TCGA  TCCACA
                                   AAG   ___
GAM264  DKFZP564D172 3'  ACATCTAAATAGCGTTTTG   49383       _  _
                                CAAAA GCT TTTAGGTGT
                                ||||| ||| |||||||||
                                GTTTT CGA AAATCTACA
                                   G   T
GAM264  DKFZP564K2062 3'  GGCCAGAAGTTTTTGTT    31237           A   GT
                                AGCAAAAGCTTTT GGT
                                |||||||||||| |||
                                TTGTTTTTGAAGA CCG
                                        _  GT
GAM264  DKFZP564L2423 3'  GGCCTGGAAGAGTTCA      62365       AAAAG       TG
                                TGAGC    CTTTTAGG  T
                                |||||    ||||||||  |
                                ACTTG    GAAGGTCC  G
                                   A_____       GT
GAM264  DKFZP564O0423 3'  ACACCTGAAGAGCACGCCCA   91673    A  AAAA    _
                                TG GC   GCTTT TAGGTGT
                                || ||   ||||| |||||||
                                AC CG   CGAGA GTCCACA
                                 C  CA__    A
GAM264  DKFZP564O0423 3'  GCGCCTGGACTGAGTGTTTGT  91692       A   ___
                                GCAAA GCTT   TTAGGTGT
                                ||||| ||||   ||||||||
                                TGTTT TGAG   GGTCCGCG
                                   G    TCA
GAM264  DKFZP564O1863 3'  ACCTTAAGTTTATGTTT     68588       A     TT
                                GAGCA AAGCTT  AGGT
                                ||||| ||||||  ||||
                                TTTGT TTTGAA  TCCA
                                   A     T_
GAM264  DKFZP566B183 5'  TTTCAGGGGAGCTCTTTGCTCA 31329         _      AGGTGT
                                TGAGCAAA AGCTTTT
                                |||||||| |||||||
                                ACTCGTTT TCGAGGG
                                     C      GACTTTG
GAM264  DKFZP586A011 3'  ACATCTGTGGGTTTTTGTT   31217          TT
                                AGCAAAAGCT  TAGGTGT
                                ||||||||||  |||||||
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                                TTGTTTTTGG  GTCTACA
                                      GT
GAM264   DKFZP761E1824 3'  ATGCCTGAGGGTCAGCTC    66435      AAAA
                                GAGC    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                CTCG    TGGGAGTCCGTA
                                  AC__
GAM264   DKFZp761G0313 3'  ACACTTAAAAGTTATTCTTA   65811      C  A
                                TGAG AA AGCTTTTAGGTGT
                                |||| || ||||||||||||
                                ATTC TT TTGAAAATTCACA
                                  _ A
GAM264   DKFZP761I2123 3'  GCAGAACGGTTTTTGCT     48765          T  AG
                                AGCAAAAGCT TT  GT
                                |||||||||| ||  ||
                                TCGTTTTTGG AA  CG
                                      C  GA
GAM264   DKFZP761L0424 3'  ACATTTGAAAGTAGTGTTC    91336      AAA
                                GAGCA   GCTTTTAGGTGT
                                |||||   ||||||||||||
                                CTTGT   TGAAAGTTTACA
                                   GA_
GAM264   DKFZp761N1114 3'  ACATCTTTTTTTGTTTTTGTTT 79007          TTTT__
                                GAGCAAAAGC     AGGTGT
                                ||||||||||     ||||||
                                TTTGTTTTTTG     TCTACA
                                      TTTTTT
GAM264   DKFZP762D096 3'  GTGTCTGAGGGTTGAGGTT    65579     AAA        TG
                                AGC   AGCTTTTAGG  T
                                |||   ||||||||||  |
                                TTG   TTGGGAGTCT  G
                                  GAG         GT
GAM264   DKFZp762K2015 3'  ATGCTTATGTCTTGTTTTTGCT 72474          TTT___
            T                    GAGCAAAAGC     TAGGTGT
                                ||||||||||     |||||||
                                TTCGTTTTTG     ATTCGTA
                                      TTCTGT
GAM264   DNAJA2    3'  GTCCTGAAGCTTTGTGTTT    59782       _       T   TGT
                                GAGCA AAAGCTTT AGG
                                ||||| |||||||| |||
                                TTTGT TTTCGAAG TCC
                                   G       _   TG
GAM264   DNAJC5    3'  ACATCTGGACGTGCTTA     61444       AAAGCT
                                TGAGCA     TTTAGGTGT
                                ||||||     |||||||||
                                ATTCGT     AGGTCTACA
                                   GC_____
GAM264   DNAJC5    3'  ACATCTAAGGGCCAGGCT    61443     AAAA
                                AGC    GCTTTTAGGTGT
                                |||    ||||||||||||
```

```
                                TCG   CGGGAATCTACA
                                  GAC_
GAM264  DNAL4   3'  ACACCTGGGCAGGAGTGCTC  19211     AAA__  TT
                                GAGCA    GCT  TAGGTGT
                                |||||    |||  |||||||
                                CTCGT    CGG  GTCCACA
                                   GAGGA  __
GAM264  DNPEP   3'  GCACCTGAGAGGGGAAGTTC  23957     AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                CTTG    GAGAGTCCACG
                                  AAGGG
GAM264  DRIL2   3'  GCATCTGGGACGTGGTGCCA  21326    A  AAA  _
                                TG GCA   GC TTTTAGGTGT
                                || |||   || ||||||||||
                                AC CGT   TG AGGGTCTACG
                                 _   GG_  C
GAM264  DZIP1   5'  AGTCTGGCTTTTCCTCA     30034     C     TTT   TG
                                TGAG AAAAGCT   AGG  T
                                |||| |||||||   |||  |
                                ACTC TTTTCGG   TCT  A
                                  C      ___   GT
GAM264  E2IG4   3'  ACACCTAGGAGCAAAGTCTCA  90906     CAAAA
                                TGAG    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                ACTC    CGAGGATCCACA
                                  TGAAA
GAM264  ECE2    3'  GCACTTAGGGGTGGACTCA   28067     CAAAA
                                TGAG    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                ACTC    TGGGGATTCACG
                                  AGG__
GAM264  EFNA2   3'  GCGCTTGAAGCGGGCT      7393     AAAA    T
                                AGC    GCTTT AGGTGT
                                |||    ||||| ||||||
                                TCG    CGAAG TTCGCG
                                  GG__    _
GAM264  EIF5    3'  ATACCTGGAGGGAATGTGCTT  8758      AAAG_
                                GAGCA    CTTTTAGGTGT
                                |||||    ||||||||||
                                TTCGT    GGAGGTCCATA
                                   GTAAG
GAM264  ELF4    3'  GTGCCTGAGGACCTTTGCT   7436      AGC     TG
                                AGCAAA   TTTTAGG  T
                                ||||||   |||||||  |
                                TCGTTT   GGAGTCC  G
                                   CCA     GT
GAM264  ELL2    3'  GCATCTGGAAGTGTGTGCTC  23871     AAA
                                GAGCA   GCTTTTAGGTGT
                                |||||   ||||||||||||
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                                CTCGT   TGAAGGTCTACG
                                   GTG
GAM264  ELL2     3'  ACACTTAAAAGTTGTATGT   23868     AA_
                                GCA   AGCTTTTAGGTGT
                                |||   ||||||||||||
                                TGT   TTGAAAATTCACA
                                  ATG
GAM264  ESDN     3'  TTTTCCTGGAGGTTTTTGTT   55183             TGT
                                AGCAAAAGCTTTTAGG
                                ||||||||||||||||
                                TTGTTTTTGGAGGTCC
                                         TTTTT
GAM264  ESPL1    5'  ACACTGCCGTCGCTTTTGCT   24456         TTTTA_
                                AGCAAAAGC     GGTGT
                                |||||||||     |||||
                                TCGTTTTCG     TCACA
                                     CTGCCG
GAM264  ESPL1    5'  GCATCTGGGGAGCCTGCT    24458      AAA     _
                                AGCA   GCTTTT AGGTGT
                                ||||   |||||| ||||||
                                TCGT   CGAGGG TCTACG
                                  C__      G
GAM264  EVI5     3'  GTGCTTTGGGGATTTTTGTTC  19008         _  TT   TG
                                GAGCAAAAG CTT  AGG  T
                                ||||||||| |||  |||  |
                                CTTGTTTTT GGG  TTC  G
                                     A   GT   GT
GAM264  FAM8A1   3'  ATATTTGAGAGCTCACTTC   32721     CAAA
                                GAG    AGCTTTTAGGTGT
                                |||    ||||||||||||
                                CTT    TCGAGAGTTTATA
                                  CAC_
GAM264  FBXL3B   5'  ATTAAAAAGCATTTTGCTCA  24071         _     AGGTGT
                                TGAGCAAAA GCTTTT
                                ||||||||| ||||||
                                ACTCGTTTT CGAAAA
                                     A     ATTA
GAM264  FBXO22   3'  CTAAGGCTTTTGCTT       24090           T
                                GAGCAAAAGCTTT AG
                                |||||||||||| ||
                                TTCGTTTTCGGAA TC
                                           _
GAM264  FBXO29   3'  GCGCCTGGGGCAAGCT      76757     AAAA    T
                                AGC    GCTTT AGGTGT
                                |||    ||||| ||||||
                                TCG    CGGGG TCCGCG
                                  AA__    _
GAM264  FEM-2    3'  GCAAGGGGGAGCTTTGCTCA  27580         A     AGG
                                TGAGCAAA GCTTTT   TGT
                                |||||||| ||||||   |||
```

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                                ACTCGTTT CGAGGG   ACG
                                    _     GGA   T
GAM264  FIGN     3' GTGCCTGGAGTGGTGCTT    95642      AAA    T   TG
                                GAGCA   GCTTT AGG  T
                                |||||   ||||| |||  |
                                TTCGT   TGAGG TCC  G
                                   GG_    _   GT
GAM264  FKSG42   3' GCATTCTCCAGGCTTTTACTCA 49333      C       TT  _
                                TGAG AAAAGCTT  AGG TGT
                                |||| ||||||||  ||| |||
                                ACTC TTTTCGGA  TCT ACG
                                  A       CC   T
GAM264  FLJ00024 3' ATGCCTGGGGGGCCGGCCA    63748    A  AAAA
                                TG GC    GCTTTTAGGTGT
                                || ||    ||||||||||||
                                AC CG    CGGGGGTCCGTA
                                 _ GC__
GAM264  FLJ10074 5' ACCAGTTTTTGCCA        35795    A       TTTA
                                TG GCAAAAGCT    GGT
                                || |||||||||    |||
                                AC CGTTTTTGA    CCA
                                 _       _____
GAM264  FLJ10156 3' ATATTTGAGAGCTCTTAGCTC  38692     _ A
                                GAGC AA AGCTTTTAGGTGT
                                |||| || ||||||||||||
                                CTCG TT TCGAGAGTTTATA
                                  A  C
GAM264  FLJ10199 5' GCATTTAAGGGGTTTTTGTT   71233          _
                                AGCAAAAGCTT TTAGGTGT
                                |||||||||||| ||||||||
                                TTGTTTTTGGG AATTTACG
                                       G
GAM264  FLJ10204 3' TAATCGTTTTTGTTCA      35896          TT
                                TGAGCAAAAGC  TTA
                                ||||||||||  |||
                                ACTTGTTTTTG  AAT
                                       CT
GAM264  FLJ10252 3' ATACTTTCCGATGCTTTGCTTA 35947        A  TTTT__
                                TGAGCAAA GC     AGGTGT
                                |||||||| ||     ||||||
                                ATTCGTTT CG     TTCATA
                                     _ TAGCCT
GAM264  FLJ10276 3' ACACCTGGGAAGGGGCTC    35960     AAAAGC
                                GAGC     TTTTAGGTGT
                                ||||     ||||||||||
                                CTCG     AGGGTCCACA
                                  GGGA__
GAM264  FLJ10297 3' ATGCCTGGATCTGTTTTGTTT  35977        GCT_
                                GAGCAAAA    TTTAGGTGT
                                ||||||||    |||||||||
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                                TTTGTTTT   AGGTCCGTA
                                    GTCT
GAM264  FLJ10297 3' GCACCTGGGGAAGTGGTTG  35981    AA   __
                                CAA  GCTTT  TAGGTGT
                                |||  |||||  |||||||
                                GTT  TGAAG  GTCCACG
                                  GG    GG
GAM264  FLJ10346 5' ACGCCTGGCTAATTTTGTTT  36037       GCTT
                                GAGCAAAA   TTAGGTGT
                                ||||||||   ||||||||
                                TTTGTTTT   GGTCCGCA
                                    AATC
GAM264  FLJ10352 3' GTGTCAGAGGCTTCTGCTC   49561     A      A  TG
                                GAGCA AAGCTTTT GG  T
                                ||||| |||||||| ||  |
                                CTCGT TTCGGAGA CT  G
                                   C       _ GT
GAM264  FLJ10352 3' GCAAATTTGAAGCTTTGCTT  49559       A    TAGG_
                                GAGCAAA GCTTT    TGT
                                ||||||| |||||    |||
                                TTCGTTT CGAAG    ACG
                                   _    TTTAA
GAM264  FLJ10415 5' ACGTTTGGAGCTGCTGCT   36092     AA     T GG
                                AGCA  AGCTTT A  TGT
                                ||||  |||||| |  |||
                                TCGT  TCGAGG T  GCA
                                  CG     _ TT
GAM264  FLJ10468 5' GCACAGCGAGGTTTTGCTCA  36149        G   TTAG
                                TGAGCAAAA CTT   GTGT
                                ||||||||| |||   ||||
                                ACTCGTTTT GAG   CACG
                                     G  CGA_
GAM264  FLJ10520 3' ACACCTGGGTGTGCTT     36208      AAAGCT
                                GAGCA     TTTAGGTGT
                                |||||     |||||||||
                                TTCGT     GGGTCCACA
                                  GT____
GAM264  FLJ10546 5' ATGTCTGAAAGCACCCTCA   59475     CAAAA       TG
                                TGAG    GCTTTTAGG  T
                                ||||    |||||||||  |
                                ACTC    CGAAAGTCT  A
                                  CCA__       GT
GAM264  FLJ10587 3' ATACTTGAGCTGGTTTTTGTTT 36311          __
                                GAGCAAAAGCT  TTTAGGTGT
                                ||||||||||  |||||||||
                                TTTGTTTTTGG  GAGTTCATA
                                       TC
GAM264  FLJ10607 3' ACACTTAGGGGTGTATTGTTT  77103       AA_
                                GAGCAA   GCTTTTAGGTGT
                                ||||||   ||||||||||||
```

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                                TTTGTT  TGGGGATTCACA
                                   ATG
GAM264  FLJ10619 3' GCACCTGAGAATGCATCA   36352    _  AAAGC
                                TGA GCA   TTTTAGGTGT
                                ||| |||   ||||||||||
                                ACT CGT   AGAGTCCACG
                                  A  A____
GAM264  FLJ10701 3' ATACCTGGGTATTGCTT    36430      AA  TT
                                GAGCAA  GCT  TAGGTGT
                                ||||||  |||  |||||||
                                TTCGTT  TGG  GTCCATA
                                   A_  __
GAM264  FLJ10704 3' ACATTTGGAAGCTAAAATGT  36447    AA__
                                GCA   AGCTTTTAGGTGT
                                |||   ||||||||||||
                                TGT   TCGAAGGTTTACA
                                  AAAA
GAM264  FLJ10704 3' ACACCTGGAACCTCCTGCT   36446     AA  C
                                AGCA  AG TTTTAGGTGT
                                ||||  || ||||||||||
                                TCGT  TC AAGGTCCACA
                                  CC  C
GAM264  FLJ10743 3' GTGCCTGAGGCTTCCTGCTT  36552      A_     T  TG
                                GAGCA  AAGCTTT AGG  T
                                |||||  ||||||| |||  |
                                TTCGT  TTCGGAG TCC  G
                                   CC      _  GT
GAM264  FLJ10751 3' ACACCTGGGAGCTTGTT    36564     AA
                                AGCA  AGCTTTTAGGTGT
                                ||||  ||||||||||||
                                TTGT  TCGAGGGTCCACA
                                   __
GAM264  FLJ10751 3' ACACCTGGGAGCTTGTT    36725     AA
                                AGCA  AGCTTTTAGGTGT
                                ||||  ||||||||||||
                                TTGT  TCGAGGGTCCACA
                                   __
GAM264  FLJ10774 3' ACACCTGGAAGCTGGCCGC   45080    AAA_
                                GC   AGCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   TCGAAGGTCCACA
                                  CCGG
GAM264  FLJ10786 3' ATATCTGGGAGTGGAGGGTTC 36642     AAAA_
                                GAGC    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                CTTG    TGAGGGTCTATA
                                  GGAGG
GAM264  FLJ10898 5' ATGCCTGAATGCAATGCTT   59420      AAA  T
                                GAGCA   GC TTTAGGTGT
                                |||||   || |||||||||
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                                TTCGT  CG AAGTCCGTA
                                  AA_  T
GAM264  FLJ10948 3' ATGCCTGGAACCAAGGTGCT  36913    AAAGC_
                                AGCA    TTTTAGGTGT
                                ||||    ||||||||||
                                TCGT    AAGGTCCGTA
                                  GGAACC
GAM264  FLJ10971 3' ATATTTGAAAGCGAGTG    36923    AAA
                                CA  GCTTTTAGGTGT
                                ||  ||||||||||||
                                GT  CGAAAGTTTATA
                                 GAG
GAM264  FLJ10979 3' TTTGCCTGGCAGCTTTTGTT  36938        T     T
                                AGCAAAAGCT TTAGGTG
                                |||||||||| |||||||
                                TTGTTTTCGA GGTCCGT
                                      C      TTA
GAM264  FLJ10986 5' ACATCTGGGCTGCGTGCT    36941    AA_   TT
                                AGCA  AGCT  TAGGTGT
                                ||||  ||||  |||||||
                                TCGT  TCGG  GTCTACA
                                  GCG   __
GAM264  FLJ11117 3' ATCTGACTTTTGCTC      37072        CTT
                                GAGCAAAAG  TTAGGT
                                |||||||||  ||||||
                                CTCGTTTTC  AGTCTA
                                       ___
GAM264  FLJ11127 3' ACATTTGGGAGTTGGTGGCTT 38714    AAA_
                                GAGC   AGCTTTTAGGTGT
                                ||||   ||||||||||||||
                                TTCG   TTGAGGGTTTACA
                                  GTGG
GAM264  FLJ11149 3' ATACTTGAAAGAAACCTCA  37107    CAAAAG
                                TGAG    CTTTTAGGTGT
                                ||||    ||||||||||
                                ACTC    GAAAGTTCATA
                                  CAAA__
GAM264  FLJ11362 3' ATGCCTGGGGGCCTGGGGCT  41678    AAAA_
                                AGC   GCTTTTAGGTGT
                                |||   ||||||||||||
                                TCG   CGGGGGTCCGTA
                                 GGGTC
GAM264  FLJ11726 3' ATGCCTAGAGGAAGGGGGTTC 46406    AAAAG_
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                CTTG    GGAGATCCGTA
                                  GGGGAA
GAM264  FLJ11767 3' GCACCTGAAGGCAAGGGTTT  44759    AAAA
                                GAGC   GCTTTTAGGTGT
                                ||||   ||||||||||||
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                                TTTG   CGGAAGTCCACG
                                  GGAA
GAM264  FLJ11773  5' GCATCTGAGAGGCTGGTC   41648   G  AAAG
                                GA CA   CTTTTAGGTGT
                                || ||   ||||||||||
                                CT GT   GAGAGTCTACG
                                 G  CG__
GAM264  FLJ11850  3' GCACTGAGCATTTGTTCA   42722       A   TTA
                                TGAGCAAA GCTT   GGTGT
                                |||||||| ||||  |||||
                                ACTTGTTT CGAG   TCACG
                                    A   ___
GAM264  FLJ12057  3' GTGCTTGGAGCCCCTGCTC   45440     AAA    T   TG
                                GAGCA   GCTTT AGG  T
                                |||||   ||||| |||  |
                                CTCGT   CGAGG TTC  G
                                   CCC    _  GT
GAM264  FLJ12076  3' ACATCTTCCTACTTTTGTT   47231       CTTTT
                                AGCAAAAG    AGGTGT
                                ||||||||    ||||||
                                TTGTTTTC    TCTACA
                                    ATCCT
GAM264  FLJ12078  3' ATACTTAAAAGAATATGTT   46451     AAAG
                                AGCA   CTTTTAGGTGT
                                ||||   ||||||||||
                                TTGT   GAAAATTCATA
                                  ATAA
GAM264  FLJ12078  3' ACACTTAAAGGTTGAACATTA  46449    GCAAA
                                TGA    AGCTTTTAGGTGT
                                |||    ||||||||||||
                                ATT    TTGGAAATTCACA
                                 ACAAG
GAM264  FLJ12294  5' GGCCTAGAACTGTGCT     47016     AA  C     TG
                                AGCA  AG TTTTAGG  T
                                ||||  || |||||||  |
                                TCGT  TC AAGATCC  G
                                  G_  _     GT
GAM264  FLJ12666  3' ATACCTGGAGCAGCAGTTTA  44766     AAAA    T
                                TGAGC   GCTTT AGGTGT
                                |||||   ||||| ||||||
                                ATTTG   CGAGG TCCATA
                                   ACGA   _
GAM264  FLJ12707  3' ACACTTGGATTCTTGCTC   41945     AA  CT
                                GAGCA  AG  TTTAGGTGT
                                |||||  ||  |||||||||
                                CTCGT  TC  AGGTTCACA
                                   __  TT
GAM264  FLJ12747  3' GCACTTAAAAGAGATTTTGT  49716      G__
                                GCAAAA  CTTTTAGGTGT
                                ||||||  ||||||||||
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                                TGTTTT  GAAAATTCACG
                                   AGA
GAM264  FLJ12799  3'  TATCTGAATGTTTTTG     42560       T
                                CAAAAGC TTTAGGTG
                                ||||||| ||||||||
                                GTTTTTG AAGTCTAT
                                    T
GAM264  FLJ12800  3'  ACACCTAAAGTCCCAGCT    43225    AAAA    T
                                AGC   GCTTT AGGTGT
                                |||   ||||| ||||||
                                TCG   TGAAA TCCACA
                                  ACCC   _
GAM264  FLJ12806  3'  ACATCTGTTCACTTTTGCTC  43084       CTTT
                                GAGCAAAAG   TAGGTGT
                                |||||||||   |||||||
                                CTCGTTTTC   GTCTACA
                                     ACTT
GAM264  FLJ12921  3'  GCATCTGGAAGCTAAATTGC  45911    A__
                                GCAA  AGCTTTTAGGTGT
                                ||||  ||||||||||||
                                CGTT  TCGAAGGTCTACG
                                  AAA
GAM264  FLJ12934  3'  TACCTGAGCATTTTGTATCA  43202    _    _   TT   GT
                                TGA GCAAAA GCTT  AGGT
                                ||| |||||| ||||  ||||
                                ACT TGTTTT CGAG  TCCA
                                  A    A   __   TG
GAM264  FLJ13072  5'  GTGCCTGGAGGTGATCTTTG  89822    A___      TG
                                CAAA   GCTTTTAGG  T
                                ||||   |||||||||  |
                                GTTT   TGGAGGTCC  G
                                  CTAG       GT
GAM264  FLJ13105  3'  ATTTTGAGGGTATTTGTTCA  46544       A       TGT
                                TGAGCAAA GCTTTTAGG
                                |||||||| |||||||||
                                ACTTGTTT TGGGAGTTT
                                     A       TA
GAM264  FLJ13110  3'  ATACCTAAAAGCGAATTTGT  43299    A__
                                GCAAA  GCTTTTAGGTGT
                                |||||  ||||||||||||
                                TGTTT  CGAAAATCCATA
                                   AAG
GAM264  FLJ13110  3'  ATATTTGGATTGTATTTGTTC 43300      A  T_
                                GAGCAAA GC  TTTAGGTGT
                                ||||||| ||  |||||||||
                                CTTGTTT TG  AGGTTTATA
                                    A  TT
GAM264  FLJ13110  3'  ATAAACAGAAGCTGTTTGCTCA 43298       _    AGGTGT
                                TGAGCAAA AGCTTTT
                                |||||||| |||||||
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                                ACTCGTTT TCGAAGA
                                    G      CAAATA
GAM264  FLJ13149 3' GCATTTAGGGGCATTTCT    41541    C   A
                                AG AAA GCTTTTAGGTGT
                                || ||| ||||||||||||
                                TC TTT CGGGGATTTACG
                                 _   A
GAM264  FLJ13187 3' AAAACTAGGGTTTTTTGTTCA  44840          C     GTGT
                                TGAGCAAAAG TTTTAG
                                |||||||||| ||||||
                                ACTTGTTTTT GGGATC
                                      T     AAAAC
GAM264  FLJ13194 3' ATACCTAAAAGGAAGCTTA   47126      AAAAG
                                TGAGC    CTTTTAGGTGT
                                |||||    ||||||||||
                                ATTCG    GAAAATCCATA
                                   AAG__
GAM264  FLJ13322 5' GCACCTAAAGGAGGCGCA    45298    A  AAAAG
                                TG GC    CTTTTAGGTGT
                                || ||    ||||||||||
                                AC CG    GGAAATCCACG
                                 G  GA___
GAM264  FLJ13340 3' GCATCTGACTGATTTTGTT    54105       GCTT
                                AGCAAAA    TTAGGTGT
                                |||||||    ||||||||
                                TTGTTTT    AGTCTACG
                                    AGTC
GAM264  FLJ13352 3' ATACTTGGGAGTGGGCT     44751     AAAA
                                AGC    GCTTTTAGGTGT
                                |||    ||||||||||||
                                TCG    TGAGGGTTCATA
                                  GG__
GAM264  FLJ13441 3' ATGCTTGAGGGCTGGAGC    43658    AAA
                                GC   AGCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   TCGGGAGTTCGTA
                                 AGG
GAM264  FLJ13456 3' ATACCTAGAAGTGTGGACT   65933    CAAAA
                                AG    GCTTTTAGGTGT
                                ||    ||||||||||||
                                TC    TGAAGATCCATA
                                 AGGTG
GAM264  FLJ13490 3' ATGCTTAAGAGTATTTG     46299      A
                                CAAA GCTTTTAGGTGT
                                |||| ||||||||||||
                                GTTT TGAGAATTCGTA
                                  A
GAM264  FLJ13615 3' GCATTTGAAAGCCCAAGTT   47080     AAAA
                                AGC    GCTTTTAGGTGT
                                |||    ||||||||||||
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                              TTG   CGAAAGTTTACG
                                AACC
GAM264  FLJ13639 3' AAGCCAGGCTCTTTGCTT   45231       _    TTA  GT
                              GAGCAAA AGCTT   GGT
                              ||||||| |||||   |||
                              TTCGTTT TCGGA   CCG
                                 C    ___   AAG
GAM264  FLJ13769 3' ATACTTGGGAGGCTGAGCCA  46599    A  AAA     _
                              TG GC   AGCTTTT AGGTGT
                              || ||   ||||||| ||||||
                              AC CG   TCGGAGG TTCATA
                               _ AG_     G
GAM264  FLJ13769 3' GTGCCCGAAAGCTTTTTTTA  46623     C       TA  TG
                              TGAG AAAAGCTTT  GG  T
                              |||| |||||||||  ||  |
                              ATTT TTTTCGAAA  CC  G
                                _       GC  GT
GAM264  FLJ13782 3' ATACCTGGGGGCTCGTTC    46161     AAA
                              GAGC   AGCTTTTAGGTGT
                              ||||   ||||||||||||||
                              CTTG   TCGGGGGTCCATA
                                C__
GAM264  FLJ13855 3' ATACCTGGAAGGGAGCTT    43580     AAAAG
                              GAGC    CTTTTAGGTGT
                              ||||    ||||||||||
                              TTCG    GAAGGTCCATA
                                AGG__
GAM264  FLJ13868 3' GCCCCTGAGCTTGTGTTTA   42730      A     TTA
                              TGAGCA AAGCTT   GGT
                              |||||| ||||||   |||
                              ATTTGT TTCGAG   CCG
                                 G     TCC
GAM264  FLJ13912 3' ACATCTGGAAGTCAGGACTT  42859     CAAAA
                              GAG    GCTTTTAGGTGT
                              |||    ||||||||||||
                              TTC    TGAAGGTCTACA
                                AGGAC
GAM264  FLJ13984 3' ACATCTAACCATTTTGCTT   45444       GCTT
                              GAGCAAAA   TTAGGTGT
                              ||||||||   ||||||||
                              TTCGTTTT   AATCTACA
                                  ACC_
GAM264  FLJ14107 3' CACTTGGGGGATTGC       46690     AAG
                              GCAA   CTTTTAGGTG
                              ||||   |||||||||
                              CGTT   GGGGGTTCAC
                                A__
GAM264  FLJ14126 3' GCATCTGAAATGCAGGCCA   45843    A  AAAA  _
                              TG GC   GC TTTTAGGTGT
                              || ||   || ||||||||||
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                              AC CG    CG AAAGTCTACG
                               _ GA__  T
GAM264  FLJ14166 3' ATGCCTGAGTGTTTGC     44681      A    TT
                              GCAAA GCTT  AGGTGT
                              ||||| ||||  ||||||
                              CGTTT TGAG  TCCGTA
                                 G   __
GAM264  FLJ14251 5' GCATCTGGAAGGTGCCCG    45972    A   AAAG
                              TG GCA    CTTTTAGGTGT
                              || |||    ||||||||||
                              GC CGT    GAAGGTCTACG
                               C  G___
GAM264  FLJ14351 3' ATGCTTAGAGGTGCTGCT    45319     AAA
                              AGCA   GCTTTTAGGTGT
                              ||||   ||||||||||||
                              TCGT   TGGAGATTCGTA
                                CG_
GAM264  FLJ14442 3' TACATCTAAACTGAGATTTTTT 51373       __  ___
           GTTT                 GCAAAAG  CTT   TTAGGTGT   A
                              |||||||  |||   ||||||||  |
                              TGTTTTT  GAG   AATCTACA   T
                                  TA   TCA
GAM264  FLJ14494 3' ATACTTAGAGGTTGAATTTG  90868     ___
                              CAAA   AGCTTTTAGGTGT
                              ||||   ||||||||||||
                              GTTT   TTGGAGATTCATA
                                AAG
GAM264  FLJ14494 3' GCACCTGGGAGCGCAGGTT   90871     AAAA
                              AGC    GCTTTTAGGTGT
                              |||    ||||||||||||
                              TTG    CGAGGGTCCACG
                                GACG
GAM264  FLJ14596 3' ATGCCTGGAGGCAGCCTC    51457     CAAAA
                              GAG    GCTTTTAGGTGT
                              |||    ||||||||||||
                              CTC    CGGAGGTCCGTA
                                CGA__
GAM264  FLJ14600 3' ATGCTTCATATGTTTTTGCTT  51467         TTTT_
                              GAGCAAAAGC    AGGTGT
                              ||||||||||    ||||||
                              TTCGTTTTTG    TTCGTA
                                    TATAC
GAM264  FLJ14957 3' ATACCTAGAGACGCTGCT    51739     AAA __
                              AGCA   GC  TTTTAGGTGT
                              ||||   ||  ||||||||||
                              TCGT   CG  GAGATCCATA
                                ___  CA
GAM264  FLJ20035 5' ATCTGTGGTTTTTGCTCA    34394          TT
                              TGAGCAAAAGCT  TAGGT
                              ||||||||||||  |||||
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                                ACTCGTTTTTGG  GTCTA
                                      T_
GAM264  FLJ20038 5' ACACCTAGAAGTGGC      34400    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   TGAAGATCCACA
                                 G___
GAM264  FLJ20038 3' ACATTTAGAGGATTATGCTT  34401      A  G
                                GAGCA AA CTTTTAGGTGT
                                ||||| || ||||||||||
                                TTCGT TT GGAGATTTACA
                                   A  A
GAM264  FLJ20055 3' ACGCCTGAAGTCCCAGCT   34439    AAAA    T
                                AGC   GCTTT AGGTGT
                                |||   ||||| ||||||
                                TCG   TGAAG TCCGCA
                                  ACCC   _
GAM264  FLJ20079 3' ATATCTGGAGGCTGGAAGTC  34486   GCAAA
                                GA    AGCTTTTAGGTGT
                                ||    ||||||||||||
                                CT    TCGGAGGTCTATA
                                 GAAGG
GAM264  FLJ20147 3' ATGCCAGCAAGTTTTTGTTT  34636          TTA
                                GAGCAAAAGCTT   GGTGT
                                ||||||||||||   |||||
                                TTTGTTTTTGAA   CCGTA
                                      CGA
GAM264  FLJ20150 3' ACACCTGGGGTGATGGCTTA  34644      AAAA    T
                                TGAGC   GCTTT AGGTGT
                                |||||   ||||| ||||||
                                ATTCG   TGGGG TCCACA
                                   GTAG   _
GAM264  FLJ20171 3' ATACCTGGCTCTTTGCT     34675      _   TTT
                                AGCAAA AGCT   AGGTGT
                                |||||| ||||   ||||||
                                TCGTTT TCGG   TCCATA
                                   C   ___
GAM264  FLJ20189 5' GCATTTGAAATGCTTTT     34700      _
                                AAAAGC TTTTAGGTGT
                                |||||| ||||||||||
                                TTTTCG AAAGTTTACG
                                   T
GAM264  FLJ20195 3' TACCTGGCCGTTTTTGCCA   34714    A     TT    GT
                                TG GCAAAAGC  TTAGGT
                                || ||||||||  ||||||
                                AC CGTTTTTG  GGTCCA
                                 _      CC    TG
GAM264  FLJ20195 3' TACCTGGGGGTGGCCCGCCA  34715    A  AAAA_      GT
                                TG GC    GCTTTTAGGT
                                || ||    ||||||||||
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                                AC CG    TGGGGGTCCA
                                 _ CCCGG        TG
GAM264  FLJ20209  3'  AAAAGCTCTTTGCTCA     85514        _
                                TGAGCAAA AGCTTTT
                                |||||||| |||||||
                                ACTCGTTT TCGAAAA
                                     C
GAM264  FLJ20232  3'  ATATTTAGAGGTCTTTTTGC  38667      __
                                GCAAAA  GCTTTTAGGTGT
                                ||||||  ||||||||||||
                                CGTTTT  TGGAGATTTATA
                                    TC
GAM264  FLJ20232  3'  ATGCCTTCTGTTTTGCTC    38668       G TTTT
                                GAGCAAAA C    AGGTGT
                                |||||||| |    ||||||
                                CTCGTTTT G    TCCGTA
                                     _ TCT_
GAM264  FLJ20255  5'  GCACCTAAGGAACCTCTGCT  34799     AAAGC_
                                AGCA     TTTTAGGTGT
                                ||||     ||||||||||
                                TCGT     GGAATCCACG
                                  CTCCAA
GAM264  FLJ20273  3'  GTGCCTGTTTAAAGGCTTTTGT 38729          ____   TG
          TTA                     GAGCAAAAGCTTT    TAGG  T
                                ||||||||||||    ||||  |
                                TTTGTTTTCGGAA    GTCC  G
                                       ATTT    GT
GAM264  FLJ20273  3'  ACATTTGTATAGAGGTTTTTGT 38724          ____
          T                      AGCAAAAGCTTTTA    GGTGT
                                ||||||||||||||    |||||
                                TTGTTTTTGGAGAT    TTACA
                                       ATGT
GAM264  FLJ20274  3'  ACAGTAAGGCTTTTGTTCA   62641           TAG
                                TGAGCAAAAGCTTT   GT
                                ||||||||||||||   ||
                                ACTTGTTTTCGGAA   CA
                                       TGA
GAM264  FLJ20275  3'  ACGTGATGCTTTTGTTT     34816        TT   G
                                GAGCAAAAGC  TTA GT
                                ||||||||||  ||| ||
                                TTTGTTTTCG  AGT CA
                                     T_   G
GAM264  FLJ20281  5'  ACACTTAAAAGAAGACAGCTC  90977     AAAAG_
                                GAGC     CTTTTAGGTGT
                                ||||     ||||||||||
                                CTCG     GAAAATTCACA
                                  ACAGAA
GAM264  FLJ20300  5'  ATGCCTGGACAGTTTTTG    34906        _
                                CAAAAGCT TTTAGGTGT
                                |||||||| |||||||||
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                                GTTTTTGA AGGTCCGTA
                                     C
GAM264  FLJ20306  5' ACACCTAGAGCCCGGTCTT   34912    _ AAAA    T
                                GAG C   GCTTT AGGTGT
                                ||| |   ||||| ||||||
                                TTC G   CGAGA TCCACA
                                  T GCC_    _
GAM264  FLJ20323  3' ATGCCTGGAGGTTTTGGC    38659    A
                                GC AAAGCTTTTAGGTGT
                                || ||||||||||||||
                                CG TTTTGGAGGTCCGTA
                                 G
GAM264  FLJ20335  3' ACACTTGGAGGGAAAAGTTC  88911     AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                CTTG    GGAGGTTCACA
                                  AAAAG
GAM264  FLJ20345  3' ATATCTGAGGCCAGTGCTC   35021     AAA    T
                                GAGCA   GCTTT AGGTGT
                                |||||   ||||| ||||||
                                CTCGT   CGGAG TCTATA
                                  GAC    _
GAM264  FLJ20445  3' AACCTGGGTTTTGTTCA     35175       G  TTT   GT
                                TGAGCAAAA CT   AGGT
                                ||||||||| ||   ||||
                                ACTTGTTTT GG   TCCA
                                     G ___    AA
GAM264  FLJ20450  3' ACACCTGGGACCTGTGTT    35190     AA  C
                                AGCA  AG TTTTAGGTGT
                                ||||  || ||||||||||
                                TTGT  TC AGGGTCCACA
                                  G_  C
GAM264  FLJ20502  3' ATACTTGAATATTGCTTA    35261       AAGCT
                                TGAGCAA    TTTAGGTGT
                                |||||||    |||||||||
                                ATTCGTT    AAGTTCATA
                                    AT___
GAM264  FLJ20527  3' GCACTTAGAAGAGTGC      35354     AAAG
                                GCA   CTTTTAGGTGT
                                |||   ||||||||||
                                CGT   GAAGATTCACG
                                  GA__
GAM264  FLJ20604  5' GCGCTTGAGAGCGTCATC    35443    GCAAAA
                                GA     GCTTTTAGGTGT
                                ||     ||||||||||||
                                CT     CGAGAGTTCGCG
                                 ACTG__
GAM264  FLJ20635  5' GCGCCTGGAGGCGGCGTG    35479    AAA_
                                CA   GCTTTTAGGTGT
                                ||   ||||||||||||
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                                GT    CGGAGGTCCGCG
                                 GCGG
GAM264  FLJ20694  3' GATTTAGAGCTTGTGTTTA   35549       A      T   GT
                                TGAGCA AAGCTTT AGGT
                                ||||||| ||||||| ||||
                                ATTTGT TTCGAGA TTTA
                                   G      _   GT
GAM264  FLJ20707  3' ACATAATGAAAAGTTTTTTGTT 35596         _    AG__
           T                     GAGCAAAAG CTTTT   GTGT
                                ||||||||| |||||   ||||
                                TTTGTTTTT GAAAA   TACA
                                      T    GTAA
GAM264  FLJ20730  3' ACACTTAAAAGTGCATG    35617    AAA
                                CA  GCTTTTAGGTGT
                                ||  ||||||||||||
                                GT  TGAAAATTCACA
                                 ACG
GAM264  FLJ20758  5' ACATCTAGGAGGAAAGCT    35640    AAAAG
                                AGC    CTTTTAGGTGT
                                |||    ||||||||||
                                TCG    GAGGATCTACA
                                 AAAG_
GAM264  FLJ20813  3' TATATCTAGAAGTTTAAAAGGG 35688    AA____
           CTC                   AGC    AAGCTTTTAGGTGT  A
                                |||    |||||||||||||  |
                                TCG    TTTGAAGATCTATA  T
                                 GGAAAA
GAM264  FLJ20813  3' GCACCTAAAGGCATGGC    35685    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   CGGAAATCCACG
                                 GTA_
GAM264  FLJ20896  3' ACACTTGGGAGTTACCATCA  44812    GCAAA
                                TGA    AGCTTTTAGGTGT
                                |||    ||||||||||||
                                ACT    TTGAGGGTTCACA
                                 ACCA_
GAM264  FLJ20967  5' ACACCTGGAGGCCAGTTTCA  41960    CAAAA
                                TGAG   GCTTTTAGGTGT
                                ||||   ||||||||||||
                                ACTT   CGGAGGTCCACA
                                  TGAC_
GAM264  FLJ20972  3' ATGTTTGAAAGTGAGTGGTCA 46723    G  AAA      TG
                                TGA CA  GCTTTTAGG  T
                                ||| ||  |||||||||  |
                                ACT GT  TGAAAGTTT  A
                                 G  GAG       GT
GAM264  FLJ20986  3' ATATCTAAAAATAGGTTTTTGT 44543        ____
                                GCAAAAGCT   TTTAGGTGT
                                |||||||||   |||||||||
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                              TGTTTTTGG   AAATCTATA
                                   ATAA
GAM264  FLJ21195  3' GCAAGTGGAGCTTTTGCT   42451         TAGG
                              AGCAAAAGCTTT   TGT
                              ||||||||||||   |||
                              TCGTTTTCGAGG   ACG
                                    TGA_
GAM264  FLJ21240  3' ATGCCTGAATCCTTGCTCA   45836      AA  CT
                              TGAGCA  AG  TTTAGGTGT
                              ||||||  ||  |||||||||
                              ACTCGT  TC  AAGTCCGTA
                                 __  CT
GAM264  FLJ21272  5' ATATCTAAGGGCTAAGTCCA   46734    AG AAA
                              TG  C   AGCTTTTAGGTGT
                              ||  |   ||||||||||||
                              AC  G   TCGGGAATCTATA
                                CT AA_
GAM264  FLJ21313  3' GTGCTTCCCGAGGCGTTTTGTT 43689        _    T__   TG
           T                   GAGCAAAA GCTTT   AGG  T
                              ||||||||  |||||   |||  |
                              TTTGTTTT CGGAG   TTC  G
                                   G    CCC   GT
GAM264  FLJ21610  3' ACACTTGGAGGTGTGC     42765     AAA
                              GCA   GCTTTTAGGTGT
                              |||   ||||||||||||
                              CGT   TGGAGGTTCACA
                                G__
GAM264  FLJ21816  3' ACACTTAAAATGATTGCTT   45152      AAGC
                              GAGCAA   TTTTAGGTGT
                              ||||||   ||||||||||
                              TTCGTT   AAAATTCACA
                                 AGT_
GAM264  FLJ21865  3' ACACCTAAGGGCTGGC     42802    AAA
                              GC   AGCTTTTAGGTGT
                              ||   ||||||||||||
                              CG   TCGGGAATCCACA
                               G__
GAM264  FLJ21934  3' ATGCTTAGAAAAGTTTGCT   45359      AGC
                              AGCAAA   TTTTAGGTGT
                              ||||||   ||||||||||
                              TCGTTT   AAGATTCGTA
                                 GAA
GAM264  FLJ21945  3' GCACCTAAAAGGGTATGTT   47317     AAAG
                              AGCA   CTTTTAGGTGT
                              ||||   ||||||||||
                              TTGT   GAAAATCCACG
                                ATGG
GAM264  FLJ22055  3' ACACTTGGGGGAATTGT     45490     AAG
                              GCAA   CTTTTAGGTGT
                              ||||   ||||||||||
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                                TGTT  GGGGGTTCACA
                                  AA_
GAM264  FLJ22174  3' GCATCTGGAAGACGGGCT   41676    AAAAG
                                AGC   CTTTTAGGTGT
                                |||   ||||||||||
                                TCG   GAAGGTCTACG
                                 GGCA_
GAM264  FLJ22329  3' ACATCTGGCTAGTTTTTG   45060      T_
                                CAAAAGCT TTAGGTGT
                                |||||||| ||||||||
                                GTTTTTGA GGTCTACA
                                     TC
GAM264  FLJ22390  3' ACACTTGAAGCATGGTGTTT  42735     AAA_   T
                                GAGCA   GCTTT AGGTGT
                                |||||   ||||| ||||||
                                TTTGT   CGAAG TTCACA
                                   GGTA   _
GAM264  FLJ22418  3' ATGCCTGAGTTCTAGCTCA   44890     AAA CT
                                TGAGC  AG  TTTAGGTGT
                                |||||  ||  |||||||||
                                ACTCG  TC  GAGTCCGTA
                                   A__  TT
GAM264  FLJ22595  5' ACATCTAGGTTCTTGTTC   46782      A   TT
                                GAGCAA AGCT  TAGGTGT
                                |||||| ||||  |||||||
                                CTTGTT TTGG  ATCTACA
                                   C   __
GAM264  FLJ22686  3' CACCTGAGGTTGCCCA     46362    A   AAGC
                                TG GCAA   TTTTAGGTG
                                || ||||   |||||||||
                                AC CGTT   GGAGTCCAC
                                 C   _____
GAM264  FLJ22690  3' ACATCTGAGAAAGCTTCA   45248   A    __
                                A AAGCTT  TTAGGTGT
                                | ||||||  ||||||||
                                A TTCGAA  AGTCTACA
                                 C     AG
GAM264  FLJ22757  3' ACACCAATAAAGCTTTTGTT  46068         TA_
                                AGCAAAAGCTTT  GGTGT
                                ||||||||||||  |||||
                                TTGTTTTCGAAA  CCACA
                                      TAA
GAM264  FLJ22843  3' GTGCCTGAGGGCACATGTTCA 47229      AAA      TG
                                TGAGCA  GCTTTTAGG  T
                                ||||||  ||||||||| |
                                ACTTGT  CGGGAGTCC  G
                                   ACA       GT
GAM264  FLJ23017  3' ATATTTGGAGTTGTTTGCTC  43122       _    T
                                GAGCAAA AGCTTT AGGTGT
                                ||||||| |||||| ||||||
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                                CTCGTTT TTGAGG TTTATA
                                   G    _
GAM264  FLJ23017  3' GCACTTTCTGGTTTTGCTT   43123       G  TTT
                                GAGCAAAA CT   AGGTGT
                                |||||||| ||   ||||||
                                TTCGTTTT GG   TTCACG
                                   _ TCT
GAM264  FLJ23120  3' ACACTTAGTGGTTGCTTA    85142       AA   TTT
                                TGAGCAA  GCT   AGGTGT
                                |||||||  |||   ||||||
                                ATTCGTT  TGA   TTCACA
                                   GG  ___
GAM264  FLJ23186  3' AACTCTTGGAAGCTTTTGCCA  60399    A          T
                                TG GCAAAAGCTTTTAGG GT
                                || ||||||||||||||| ||
                                AC CGTTTTCGAAGGTTC CA
                                 _          T  AA
GAM264  FLJ23293  3' ACCTCATGTTTTTGTTT     42345         TTTT
                                GAGCAAAAGC    AGGT
                                ||||||||||    ||||
                                TTTGTTTTTG    TCCA
                                     TAC_
GAM264  FLJ23356  5' GCGCTTGGGAGGAAATTGC   49938     AAG_
                                GCAA   CTTTTAGGTGT
                                ||||   ||||||||||
                                CGTT   GAGGGTTCGCG
                                  AAAG
GAM264  FLJ23375  3' GCACTTACCGCTGTGCTT    46357     AA  TTT
                                GAGCA  AGC   TAGGTGT
                                |||||  |||   |||||||
                                TTCGT  TCG   ATTCACG
                                   G_   CC_
GAM264  FLJ23516  3' GTACTCTGTGTGGCTTTTGTTT 44589          TT_   TGT
                                GAGCAAAAGCT   TAGG
                                ||||||||||   ||||
                                TTTGTTTTCGG   GTCT
                                     TGT   CATG
GAM264  FLJ23519  5' ACACCCTGGTCGGTTTTGCTCA 69196         ___  TTTA
                                TGAGCAAAA   GCT   GGTGT
                                |||||||||   |||   |||||
                                ACTCGTTTT   TGG   CCACA
                                     GGC   TC__
GAM264  FLJ23519  5' ACCTGAGCTGTGCTC      69198      AA    TT
                                GAGCA  AGCTT  AGGT
                                |||||  |||||  ||||
                                CTCGT  TCGAG  TCCA
                                   G_    __
GAM264  FLJ23519  5' ACCTGAGCTGTGCTC      49960      AA    TT
                                GAGCA  AGCTT  AGGT
                                |||||  |||||  ||||
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                                CTCGT  TCGAG  TCCA
                                  G_    __
GAM264  FLJ23537  3' GCACTTAGAAGAGACATTCA  46025     CAAAAG
                                TGAG     CTTTTAGGTGT
                                ||||     ||||||||||
                                ACTT     GAAGATTCACG
                                  ACAGA_
GAM264  FLJ23563  3' ATATTTGAGAGCCCGAAGCTT  67587     AAAA_
                                GAGC    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                TTCG    CGAGAGTTTATA
                                  AAGCC
GAM264  FLJ23590  5' ACCTAGGGCGGCTCA      45014      AAAA    T
                                TGAGC    GCTTT AGGT
                                |||||    ||||| ||||
                                ACTCG    CGGGA TCCA
                                  G___    _
GAM264  FLJ23590  5' ATGCCTGGGAGCGAGGGGCT  45016    AAAA_
                                AGC    GCTTTTAGGTGT
                                |||    ||||||||||||
                                TCG    CGAGGGTCCGTA
                                 GGGAG
GAM264  FLJ25461  3' GCACCTGGAATGCGGCT    58634    AAAA _
                                AGC    GC TTTTAGGTGT
                                |||    || ||||||||||
                                TCG    CG AAGGTCCACG
                                 G___  T
GAM264  FLJ30046  3' GCACTTAAATATTTGC     58102      AGCT
                                GCAAA    TTTAGGTGT
                                |||||    |||||||||
                                CGTTT    AAATTCACG
                                  AT__
GAM264  FLJ31168  3' GCACCTGGGCTCCTGCCA    58503    A   AA    TT
                                TG GCA  AGCT  TAGGTGT
                                || |||  ||||  |||||||
                                AC CGT  TCGG  GTCCACG
                                 _   CC   __
GAM264  FLJ31455  3' GCGCTTGGAGGTACCTTG    58625     AA_
                                CAA   GCTTTTAGGTGT
                                |||   ||||||||||||
                                GTT   TGGAGGTTCGCG
                                 CCA
GAM264  FLJ31812  3' ACCTGAAGCCTTTGTTTA    58648        A    T
                                TGAGCAAA GCTTT AGGT
                                |||||||| ||||| ||||
                                ATTTGTTT CGAAG TCCA
                                     C    _
GAM264  FLJ32468  5' GCGCTTGGGAGCCAGGC     59043    AAAA
                                GC    GCTTTTAGGTGT
                                ||    ||||||||||||
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                              CG   CGAGGGTTCGCG
                               GAC_
GAM264  FLJ33069 3' ACACTTGGTGCGTGTTCA   58320      AAA  TT
                              TGAGCA  GC  TTAGGTGT
                              ||||||  ||  ||||||||
                              ACTTGT  CG  GGTTCACA
                                 G__  T_
GAM264  FOXP1    5' TGTCCCAGAAGCTTTTGTT   51073          A  TGT
                              AGCAAAAGCTTTT GG
                              |||||||||||| ||
                              TTGTTTTCGAAGA CC
                                     C  TGTG
GAM264  FREQ     3' GCACCTGGGGGCTGC      26578     AAA
                              GCA  GCTTTTAGGTGT
                              |||  ||||||||||||
                              CGT  CGGGGGTCCACG
                                   ___
GAM264  GAB3     3' ATACTTGAAAGATGTGC     54624     AAAG
                              GCA   CTTTTAGGTGT
                              |||   ||||||||||
                              CGT   GAAAGTTCATA
                                GTA_
GAM264  GALNT12  5' GCACCTGAAGGAGCGCTT    44974      AAAAG
                              GAGC    CTTTTAGGTGT
                              ||||    ||||||||||
                              TTCG    GGAAGTCCACG
                                CGA__
GAM264  GAP1IP4BP 5' GCGCTTGGGGCGAGGCTCG   23754      AAAA    T
                              TGAGC   GCTTT AGGTGT
                              |||||   ||||| ||||||
                              GCTCG   CGGGG TTCGCG
                                 GAG_   _
GAM264  GDAP2    3' GCATTTAGAAAGGGCTTTGTT  34632       A  ___
                              AGCAAA GCT   TTTAGGTGT
                              |||||| |||  |||||||||
                              TTGTTT CGG   AGATTTACG
                                 _  GAA
GAM264  GIOT-2   5' ACATCTGTGGTGGCTTTTGTC  32748    G      TT__
                              GA CAAAAGCT   TAGGTGT
                              || ||||||||   |||||||
                              CT GTTTTCGG   GTCTACA
                               _      TGGT
GAM264  GK001    3' ATACCTGGAAAGGGCTC     39496     AAAAGC
                              GAGC    TTTTAGGTGT
                              ||||    ||||||||||
                              CTCG    AAGGTCCATA
                                GGA___
GAM264  GL009    3' ACATTTGGGCAGCTGCTC    72633      AAA  _
                              GAGCA  GCT TTTAGGTGT
                              |||||  ||| |||||||||
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                                CTCGT   CGA GGGTTTACA
                                   ___  C
GAM264  GLUC    3'  TAAGCTGTTTTTGCTTA    40587          T_
                                TGAGCAAAAGC  TTTA
                                ||||||||||  ||||
                                ATTCGTTTTTG  GAAT
                                      TC
GAM264  GPA33   3'  GCCCTGGGGAGCTTTTGCCCA  19454    A         _  T
                                TG GCAAAAGCTTTT AGG GT
                                || ||||||||||| ||| ||
                                AC CGTTTTCGAGGG TCC CG
                                 C          G  _
GAM264  GR6     3'  GTGCCTGGGGAGCTTGTT    23733      AA     _  TG
                                AGCA  AGCTTTT AGG  T
                                ||||  ||||||| |||  |
                                TTGT  TCGAGGG TCC  G
                                  __      G  GT
GAM264  GREB1   3'  GCGCCTGGACAGTGATCA    27875     GCAAAA  _
                                TGA     GCT TTTAGGTGT
                                |||     ||| |||||||||
                                ACT     TGA AGGTCCGCG
                                  AG____   C
GAM264  GRP3    3'  GCATTTGGGGGCTAAAGTGT   31119     AA__
                                GCA   AGCTTTTAGGTGT
                                |||   ||||||||||||
                                TGT   TCGGGGGTTTACG
                                  GAAA
GAM264  GW112   3'  GCACCTGGAATGATGCTT    21190      AAAGC
                                GAGCA    TTTTAGGTGT
                                |||||    ||||||||||
                                TTCGT    AAGGTCCACG
                                   AGT__
GAM264  H-plk   5'  GTATCTGTTCATGTTTTTGCTT 31810          TTT__    GT
          A                     TGAGCAAAAGC    TAGGT
                                ||||||||||    |||||
                                ATTCGTTTTTG    GTCTA
                                      TACTT    TG
GAM264  HBP1    3'  ACAGCTGCTTTTGCTC      24311         TTTT  G
                                GAGCAAAAGC   AG TGT
                                |||||||||    || |||
                                CTCGTTTTCG   TC ACA
                                     ____ G
GAM264  HBXAP   5'  ATATCTAGAAGTTGTATCTCA  33418     CAAA
                                TGAG   AGCTTTTAGGTGT
                                ||||   ||||||||||||
                                ACTC   TTGAAGATCTATA
                                  TATG
GAM264  HCA127  3'  ACATCTGTGTTGGCTTTTGTTC 37948          TT__
          A                     TGAGCAAAAGCT   TAGGTGT
                                ||||||||||||   |||||||
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                                ACTTGTTTTCGG   GTCTACA
                                     TTGT
GAM264  HCA4    3'  CTGCCTATCTTTTGCTC    77585        CTTT    T
                                GAGCAAAAG   TAGGTG
                                |||||||||   ||||||
                                CTCGTTTTC   ATCCGT
                                    T___    CT
GAM264  HCA4    3'  ACATCTTAAAGTTTTTGCT   77578          T
                                AGCAAAAGCTTT AGGTGT
                                |||||||||||| ||||||
                                TCGTTTTTGAAA TCTACA
                                     T
GAM264  HCNGP   3'  ACCTGAGAGGAGCTTCTGTTT  25150      A    ___    GT
                                GAGCA AAGCTT   TTAGGT
                                ||||| ||||||   ||||||
                                TTTGT TTCGAG   AGTCCA
                                   C    GAG
GAM264  HEY2    3'  GCACGTGAGAGTTTTTGTTTA  24318            G
                                TGAGCAAAAGCTTTTA GTGT
                                |||||||||||||||| ||||
                                ATTTGTTTTTGAGAGT CACG
                                       G
GAM264  HEY2    3'  ATGCCTAAACTAGTGCT    24315     AA  CT
                                AGCA  AG  TTTAGGTGT
                                ||||  ||  |||||||||
                                TCGT  TC  AAATCCGTA
                                  GA  __
GAM264  HEYL    3'  GCGCCTGAGATCCTGTTCA   27398      AAAGC
                                TGAGCA    TTTTAGGTGT
                                ||||||    ||||||||||
                                ACTTGT    AGAGTCCGCG
                                   CCT__
GAM264  HIC2    3'  GCACCTAGGAAGTCGTGTGC  65262    AAA_   _
                                GCA   GCTTT TAGGTGT
                                |||   ||||| |||||||
                                CGT   TGAAG ATCCACG
                                  GTGC    G
GAM264  HMGN4   5'  ACACCTAGAAGTAAAATTGC  20979     AA__
                                GCAA   GCTTTTAGGTGT
                                ||||   ||||||||||||
                                CGTT   TGAAGATCCACA
                                  AAAA
GAM264  HMP19   3'  TGCACCTGACTTTTAAGTTTTT 87477         _____
           GTTT                  GCAAAAGCTT    TTAGGTGT   G
                                ||||||||||    ||||||||  |
                                TGTTTTTGAA    AGTCCACG   T
                                      TTTTC
GAM264  HMP19   3'  ACACCTGGATACTGCCCA   87470    A   AAA CT
                                TG GCA   G  TTTAGGTGT
                                || |||   |  |||||||||
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                                AC CGT   C  AGGTCCACA
                                 C   ___ AT
GAM264  HNK-1ST  3'  CGCTGGCCTTTGCTCA      16769         A   TTTA    T
                                TGAGCAAA GCT    GGTG
                                |||||||| |||    ||||
                                ACTCGTTT CGG    TCGC
                                     C   ____    T
GAM264  HNRPA0   3'  ATGCCTGGGAGTGGCT      22320     AAAA
                                AGC    GCTTTTAGGTGT
                                |||    ||||||||||||
                                TCG    TGAGGGTCCGTA
                                  G___
GAM264  HNRPU    3'  TAACTGGGAAGGTTTTTTCTTA 15694      C        A_   GT
                                TGAG AAAAGCTTTT  GGT
                                |||| ||||||||||  |||
                                ATTC TTTTTGGAAG  TCA
                                   T         GG   ATA
GAM264  HNRPU    3'  TAACTGGGAAGGTTTTTTCTTA 48990      C        A_   GT
                                TGAG AAAAGCTTTT  GGT
                                |||| ||||||||||  |||
                                ATTC TTTTTGGAAG  TCA
                                   T         GG   ATA
GAM264  HPCAL4   3'  GCATTTGGAAGTTTAGGAGCCA 32739    A  AA__
                                TG GC    AAGCTTTTAGGTGT
                                || ||    ||||||||||||||
                                AC CG    TTTGAAGGTTTACG
                                 _  AGGA
GAM264  HPIP     3'  ATACTTCTCCTTTTGCTCA    40047          CTTTT
                                TGAGCAAAAG     AGGTGT
                                ||||||||||     ||||||
                                ACTCGTTTTC     TTCATA
                                      CTC__
GAM264  HRD1     3'  ATGCCTGGGAGTGGGGGTGC   69556     AAA__
                                GCA    GCTTTTAGGTGT
                                |||    ||||||||||||
                                CGT    TGAGGGTCCGTA
                                  GGGGG
GAM264  HRH3     3'  GCACCTGGGTGTGCTC      23368       AAAGCT
                                GAGCA     TTTAGGTGT
                                |||||     |||||||||
                                CTCGT     GGGTCCACG
                                   GT____
GAM264  HSNOV1   3'  ATGCCTGGGAGCCTCCAGCT   34005     AAAA_
                                AGC    GCTTTTAGGTGT
                                |||    ||||||||||||
                                TCG    CGAGGGTCCGTA
                                  ACCTC
GAM264  HSOBRGRP 3'  GCATCGAAACCTTTTGCTT   34033         C    A
                                GAGCAAAAG TTTT GGTGT
                                ||||||||| |||| |||||
```

```
                                TTCGTTTTC AAAG CTACG
                                     C   _
GAM264  HSPC014  3' ACACCTGAGAATTTCTGCTCA 31939       A   C
                                TGAGCA AAG TTTTAGGTGT
                                |||||| ||| ||||||||||
                                ACTCGT TTT AGAGTCCACA
                                   C   A
GAM264  HSPC047  3' GCACCTGGGTGGCTTGCT    26259     AA   _
                                AGCA  AGCT TTTAGGTGT
                                ||||  |||| |||||||||
                                TCGT  TCGG GGGTCCACG
                                  __    T
GAM264  HSPC117  5' GAGCCGGGAGTTTTTGCT    26675          A   GT
                                AGCAAAAGCTTTT GGT
                                |||||||||||| |||
                                TCGTTTTTGAGGG CCG
                                       _  AGG
GAM264  HSPC156  3' ACACTTAGAGTGGTTTTTGTTT 26352          __
                                GAGCAAAAGCT  TTTAGGTGT
                                |||||||||||  |||||||||
                                TTTGTTTTTGG  AGATTCACA
                                      TG
GAM264  HSPC232  3' ACATCTAAAATAGTCTGTTTA  33229       AAAGC
                                TGAGCA    TTTTAGGTGT
                                ||||||    ||||||||||
                                ATTTGT    AAAATCTACA
                                   CTGAT
GAM264  HT002    3' GCACCTGAGATGGTGCCA    25941    A  AAAGC
                                TG GCA    TTTTAGGTGT
                                || |||    ||||||||||
                                AC CGT    AGAGTCCACG
                                 _  GGT__
GAM264  HTEX4    3' GCACTTGAAAATTAGCTTA   97723      AAAAGC
                                TGAGC     TTTTAGGTGT
                                |||||     ||||||||||
                                ATTCG     AAAGTTCACG
                                   ATTA__
GAM264  HTEX4    3' GCACTTGAAAATTAGCTTA   92097      AAAAGC
                                TGAGC     TTTTAGGTGT
                                |||||     ||||||||||
                                ATTCG     AAAGTTCACG
                                   ATTA__
GAM264  HTEX4    3' GCACTTGAAAATTAGCTTA   97898      AAAAGC
                                TGAGC     TTTTAGGTGT
                                |||||     ||||||||||
                                ATTCG     AAAGTTCACG
                                   ATTA__
GAM264  HTEX4    5' ACACTTGAGAAGGGGTTCA   97894      AAAAGC
                                TGAGC     TTTTAGGTGT
                                |||||     ||||||||||
```

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                                ACTTG     AGAGTTCACA
                                  GGGA__
GAM264  HTEX4    5'  ACACTTGAGAAGGGGTTCA   97719      AAAAGC
                                TGAGC     TTTTAGGTGT
                                |||||     ||||||||||
                                ACTTG     AGAGTTCACA
                                  GGGA__
GAM264  HTEX4    5'  ACACTTGAGAAGGGGTTCA   92093      AAAAGC
                                TGAGC     TTTTAGGTGT
                                |||||     ||||||||||
                                ACTTG     AGAGTTCACA
                                  GGGA__
GAM264  HTGN29   3'  ATACCTGAATGAAGTTGTTT   39504       AAGCT
                                GAGCAA    TTTAGGTGT
                                ||||||    |||||||||
                                TTTGTT    AAGTCCATA
                                   GAAGT
GAM264  HU-K4    5'  ACGCCTGAGAGCGAGGC     24365    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   CGAGAGTCCGCA
                                 GAG_
GAM264  I-4      3'  ACGCTTAGAAGATATCTGCTT  47383      AAAG_
                                GAGCA    CTTTTAGGTGT
                                |||||    ||||||||||
                                TTCGT    GAAGATTCGCA
                                  CTATA
GAM264  INVS     3'  GTACCTGAAGGCTGATTCA   27032     CAAA        GT
                                TGAG   AGCTTTTAGGT
                                ||||   ||||||||||
                                ACTT   TCGGAAGTCCA
                                  AG__         TG
GAM264  IRF5     5'  GCGCCTGGAAAGCGAGCTCG  50974      AAAA     _
                                TGAGC   GCTTTT AGGTGT
                                |||||   |||||| ||||||
                                GCTCG   CGAAAG TCCGCG
                                  AG__     G
GAM264  IRX4     5'  GCGCCTAGAAGCCTGCAGCTC  33022     AAAA_
                                GAGC    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                CTCG    CGAAGATCCGCG
                                  ACGTC
GAM264  ITM3     3'  GTCCTCAGAAGCTTTTTCTT   48166     C        _   TGT
                                GAG AAAAGCTTTT AGG
                                ||| |||||||||| |||
                                TTC TTTTCGAAGA TCC
                                  T        C   TG
GAM264  ITPK1    3'  GGTCTGGGCTGTGCTC      26412      AA    TT    TG
                                GAGCA  AGCT  TAGG  T
                                |||||  ||||  ||||  |
```

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                                CTCGT  TCGG  GTCT  G
                                  G_   __   GT
GAM264  JM11     3'  ACACTTGGAAGGACTGC     53248     AAAG
                                GCA   CTTTTAGGTGT
                                |||   ||||||||||
                                CGT   GAAGGTTCACA
                                  CAG_
GAM264  JM5      3'  GTGCTTGGAAGCCACCAGCCA  22991    A  AAAA_       TG
                                TG GC    GCTTTTAGG  T
                                || ||    |||||||||  |
                                AC CG    CGAAGGTTC  G
                                 _ ACCAC       GT
GAM264  KCNS1    3'  GTGCCTGGAGCAATGCTC    9580      AAA    T   TG
                                GAGCA   GCTTT AGG  T
                                |||||   ||||| |||  |
                                CTCGT   CGAGG TCC  G
                                   AA_    _  GT
GAM264  KDELR2   3'  GCCAGAAGGTTTCTGTTTA   22453      A      A
                                TGAGCA AAGCTTTT GGT
                                ||||||| |||||||| |||
                                ATTTGT TTTGGAAG CCG
                                   C       A
GAM264  KEAP1    3'  ATACCTGGGAGGGGGCCA    24451    A  AAAAG
                                TG GC    CTTTTAGGTGT
                                || ||    ||||||||||
                                AC CG    GAGGGTCCATA
                                 _ GGG__
GAM264  KIAA0010 3'  GGCCTGGAGAGCTTTCA     27896   A       _   TG
                                C AAAGCTTTT AGG  T
                                | |||||||| |||  |
                                A TTTCGAGAG TCC  G
                                 C       G  GT
GAM264  KIAA0014 3'  GTGCCTGGAAGTTGAATTTGT  27851      ___       TG
                                GCAAA   AGCTTTTAGG  T
                                |||||   ||||||||||  |
                                TGTTT   TTGAAGGTCC  G
                                   AAG        GT
GAM264  KIAA0016 3'  ATGCTTGTTGCCTTTTGCTT   28643        _ TTT
                                GAGCAAAAG C   TAGGTGT
                                |||||||| |   |||||||
                                TTCGTTTTC G   GTTCGTA
                                     C TT_
GAM264  KIAA0016 3'  ACATTTGAGGACTTTTCTC    28642    C    CT
                                GAG AAAAG  TTTAGGTGT
                                ||| |||||  |||||||||
                                CTC TTTTC  GAGTTTACA
                                  _    AG
GAM264  KIAA0057 3'  GTGCCTAGAAAAGGCCTTTGCT 24439       A  ___     TG
           T                     GAGCAAA GCT   TTTAGG  T
                                |||||||  |||   ||||||  |
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                                TTCGTTT CGG   AGATCC  G
                                    C   AAA     GT
GAM264  KIAA0063 3' GCACTTAAGGCCAGTGGTCA   29628     G  AAA    T
                                TGA CA   GCTTT AGGTGT
                                ||| ||   ||||| ||||||
                                ACT GT   CGGAA TTCACG
                                  G  GAC    _
GAM264  KIAA0090 3' GTGCCTAAAAGTGGAGAGCCA  88448    A  AAAA_       TG
                                TG GC    GCTTTTAGG  T
                                || ||    |||||||||  |
                                AC CG    TGAAAATCC  G
                                 _ AGAGG        GT
GAM264  KIAA0141 3' ATGCCTGGATGTGTCTGCTT   28727      AAA  T
                                GAGCA   GC TTTAGGTGT
                                |||||   || |||||||||
                                TTCGT   TG AGGTCCGTA
                                   CTG  T
GAM264  KIAA0164 3' ACACTTGAGCAAATGCTTA   28448      AAA   TT
                                TGAGCA   GCTT  AGGTGT
                                ||||||   ||||  ||||||
                                ATTCGT   CGAG  TTCACA
                                   AAA   __
GAM264  KIAA0179 3' ATGCCTGAGAGGTCCCGGCT   64825    AAAAG_
                                AGC     CTTTTAGGTGT
                                |||     ||||||||||
                                TCG     GAGAGTCCGTA
                                  GCCCTG
GAM264  KIAA0182 3' ACTTCAGAGGCTTTGTTTA   72023       A    _
                                TGAGCAAA GCTTTT AGGT
                                |||||||| |||||| ||||
                                ATTTGTTT CGGAGA TTCA
                                     _     C
GAM264  KIAA0182 3' GCACCTAAATCTGTTTTCA   72030     CAAA  CT
                                TGAG    AG  TTTAGGTGT
                                ||||    ||  |||||||||
                                ACTT    TC  AAATCCACG
                                  TTG_  T_
GAM264  KIAA0182 3' GCACCTGAAAGCCCTCGGCTC  72031     AAAA_
                                GAGC    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                CTCG    CGAAAGTCCACG
                                  GCTCC
GAM264  KIAA0212 3' CCTCAGGGCTTTTCTT     27935     C       T
                                GAG AAAAGCTTT AGG
                                ||| ||||||||| |||
                                TTC TTTTCGGGA TCC
                                  _       C
GAM264  KIAA0212 3' GTGTCTAGTGTCAGCTTTGCTC 27942        A  T___    TG
           A                     TGAGCAAA GCT    TTAGG  T
                                ||||||||| |||    |||||  |
```

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                                ACTCGTTT CGA   GATCT  G
                                    _  CTGT    GT
GAM264  KIAA0215 3' GCCCAGGGTATTTGCTCA   28418       A    TA
                                TGAGCAAA GCTTT  GGT
                                |||||||| |||||  |||
                                ACTCGTTT TGGGA  CCG
                                    A    C_
GAM264  KIAA0217 3' ACTACTTCAAGAGTTTCTGCTC 67033      A      _    T
          A                      TGAGCA AAGCTTTT AGGTG
                                |||||| |||||||| |||||
                                ACTCGT TTTGAGAA TTCAT
                                   C       C    CAT
GAM264  KIAA0222 3' GCATTTTCTGGCTTTTGTTT  27682         TTT
                                GAGCAAAAGCT   AGGTGT
                                ||||||||||   ||||||
                                TTTGTTTTCGG   TTTACG
                                      TCT
GAM264  KIAA0227 3' ACACTTTTTGTTTTTTGCTC  60693       CTTTT
                                GAGCAAAAG    AGGTGT
                                |||||||||    ||||||
                                CTCGTTTTT    TTCACA
                                     TGTTT
GAM264  KIAA0237 3' GCACTTAAGGGTCTGTTT    28525      AAA
                                GAGCA   GCTTTTAGGTGT
                                |||||   ||||||||||||
                                TTTGT   TGGGAATTCACG
                                  C__
GAM264  KIAA0240 3' GTGCTTATAGGCATTTTGTTTA 92438        _   T   TG
                                TGAGCAAAA GCTT TAGG  T
                                ||||||||| |||| ||||  |
                                ATTTGTTTT CGGA ATTC  G
                                     A   T   GT
GAM264  KIAA0286 3' GCACCTAAACCTTTTGTTT   68326       CT
                                GAGCAAAAG  TTTAGGTGT
                                |||||||||  |||||||||
                                TTTGTTTTC  AAATCCACG
                                     C_
GAM264  KIAA0296 5' ATATTTGGGAAGCTTGTGC   28107    A      _
                                GCA AAGCTTTT AGGTGT
                                ||| |||||||| ||||||
                                CGT TTCGAAGG TTTATA
                                  G       G
GAM264  KIAA0316 3' ATATTTAATTTGGGTTTTTGCT 69669          ___
                                AGCAAAAGCTT   TTAGGTGT
                                ||||||||||   ||||||||
                                TCGTTTTTGGG   AATTTATA
                                      TTT
GAM264  KIAA0317 3' ATACCTAGGAGAGTGTCA    29081    G  AAAG
                                TGA CA    CTTTTAGGTGT
                                ||| ||    ||||||||||
```

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                                ACT GT    GAGGATCCATA
                                  _ GA__
GAM264  KIAA0317 3' GTGTCTGGAGGATTTTGTCA  29090     G    G      TG
                                TGA CAAAA CTTTTAGG  T
                                ||| ||||| ||||||||  |
                                ACT GTTTT GGAGGTCT  G
                                  _    A       GT
GAM264  KIAA0319 3' ATACTTAAAAGAGTTTTG    29029      G_
                                CAAAA  CTTTTAGGTGT
                                |||||  ||||||||||
                                GTTTT  GAAAATTCATA
                                   GA
GAM264  KIAA0321 3' GCATCTGAAAGCTGTGGGT   62395    AAA_
                                GC   AGCTTTTAGGTGT
                                ||   ||||||||||||
                                TG   TCGAAAGTCTACG
                                 GGTG
GAM264  KIAA0329 3' GCTCCAGCTTTTGTT       29276         TTTA  T
                                AGCAAAAGCT   GG GT
                                ||||||||||   || ||
                                TTGTTTTCGA   CC CG
                                      ____  T
GAM264  KIAA0332 3' GCATTCCTGGGGTTTTTTGTTT 62701         C      __
                                GAGCAAAAG TTTTAGG  TGT
                                ||||||||| |||||||  |||
                                TTTGTTTTT GGGGTCC  ACG
                                      T      TT
GAM264  KIAA0332 3' GCACTTGAAAATACTTTTG   62700       C__
                                CAAAAG   TTTTAGGTGT
                                ||||||   ||||||||||
                                GTTTTC   AAAGTTCACG
                                   ATA
GAM264  KIAA0349 3' ACATCTACAAGTTTTGTTC   92303        G   T
                                GAGCAAAA CTT TAGGTGT
                                |||||||| ||| |||||||
                                CTTGTTTT GAA ATCTACA
                                      _  C
GAM264  KIAA0350 3' GCTCCCAGAAGCTTTGCTTA  61175         A     A  T
                                TGAGCAAA GCTTTT GG GT
                                |||||||| |||||| || ||
                                ATTCGTTT CGAAGA CC CG
                                      _     C  T
GAM264  KIAA0367 3' ATATCTAAAGGTTTTTCT    67292    C
                                AG AAAAGCTTTTAGGTGT
                                || ||||||||||||||||
                                TC TTTTTGGAAATCTATA
                                 _
GAM264  KIAA0410 3' TATTCTTGAGGAGCCTTTTGCT 28778          _  _    TGT
            CA                    TGAGCAAAAG CTT TTAGG
                                ||||||||| ||| |||||
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                                ACTCGTTTTC GAG AGTTC
                                      C  G    TTATG
GAM264  KIAA0426 3' TGTAGTAAAAGCTTTAGTTTA 28267      A       GGTGT
                                TGAGC AAAGCTTTTA
                                ||||| ||||||||||
                                ATTTG TTTCGAAAAT
                                   A        GATGTG
GAM264  KIAA0426 3' TAACTGAGGAGGCCTTTGTTCA 28262       A    A_  GT
                                TGAGCAAA GCTTTT  GGT
                                |||||||| ||||||  |||
                                ACTTGTTT CGGAGG  TCA
                                     C     AG  ATA
GAM264  KIAA0429 3' ACATTTAAGAGTAGCCTC    28548    CAAAA
                                GAG    GCTTTTAGGTGT
                                |||    ||||||||||||
                                CTC    TGAGAATTTACA
                                  CGA__
GAM264  KIAA0433 3' CTAAAGCTTTAGCTT      30836     A      T
                                GAGC AAAGCTTT AG
                                |||| |||||||| ||
                                TTCG TTTCGAAA TC
                                  A      _
GAM264  KIAA0433 3' GCATTTGAAATAAATGCTC   30838      AAAGC
                                GAGCA    TTTTAGGTGT
                                |||||    ||||||||||
                                CTCGT    AAAGTTTACG
                                   AAAT_
GAM264  KIAA0441 3' ACGCTTGAAATCAGGCTC    28950     AAAAGC
                                GAGC     TTTTAGGTGT
                                ||||     ||||||||||
                                CTCG     AAAGTTCGCA
                                  GACT__
GAM264  KIAA0446 5' TGGCCAGGAGCTTATGCTTA  68885      A      A  GT
                                TGAGCA AAGCTTTT GGT
                                |||||| |||||||| |||
                                ATTCGT TTCGAGGA CCG
                                   A      _  GTA
GAM264  KIAA0450 3' ACGCCTGGAGCCTGCT     27616     AAA    T
                                AGCA   GCTTT AGGTGT
                                ||||   ||||| ||||||
                                TCGT   CGAGG TCCGCA
                                  C__    _
GAM264  KIAA0450 5' GCATTTGGAGACTGTCGCTCA 27641      AAA  CT
                                TGAGC   AG  TTTAGGTGT
                                |||||   ||  |||||||||
                                ACTCG   TC  AGGTTTACG
                                   CTG  AG
GAM264  KIAA0459 3' GCACTTAGGATGCAGAGCTTA 60997      AAAA  _
                                TGAGC    GC TTTTAGGTGT
                                |||||    || ||||||||||
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                                ATTCG   CG AGGATTCACG
                                  AGA_  T
GAM264  KIAA0471 3' ATCTCTGCTGCTTTTGTTTA  29383        TTT   TGT
                                TGAGCAAAAGC  TAGG
                                ||||||||||  ||||
                                ATTTGTTTTCG  GTCT
                                     TC_   CTAT
GAM264  KIAA0472 3' ATACTTTGCTTTTGTTT    71858        TTTT
                                GAGCAAAAGC   AGGTGT
                                |||||||||   ||||||
                                TTTGTTTTCG   TTCATA
                                     T___
GAM264  KIAA0476 3' ATTTTAGAAGTTTTTGTTT  29376            TGT
                                GAGCAAAAGCTTTTAGG
                                |||||||||||||||||
                                TTTGTTTTTGAAGATTT
                                         TA
GAM264  KIAA0513 3' ACGCCTGAGAGTCACTTA   28324    CAAAA
                                TGAG   GCTTTTAGGTGT
                                ||||   ||||||||||||
                                ATTC   TGAGAGTCCGCA
                                  AC___
GAM264  KIAA0513 3' GAGCCTGGGGCTGTTGCTTA  28358      A    T   GT
                                TGAGCAA AGCTTT AGGT
                                ||||||| |||||| ||||
                                ATTCGTT TCGGGG TCCG
                                    G    _   AGT
GAM264  KIAA0514 3' ACATTTAGGGGCCACCTC   28073    CAAAA
                                GAG   GCTTTTAGGTGT
                                |||   ||||||||||||
                                CTC   CGGGGATTTACA
                                 CAC__
GAM264  KIAA0537 3' ACACTTGGGCTGTTTGC    29240     _   TT
                                GCAAA AGCT  TAGGTGT
                                ||||| ||||  |||||||
                                CGTTT TCGG  GTTCACA
                                  G  __
GAM264  KIAA0537 3' TACCTGAAGCCCCGCTTA   29258     AAAA   T   GT
                                TGAGC   GCTTT AGGT
                                |||||   ||||| ||||
                                ATTCG   CGAAG TCCA
                                  CCC_   _   TG
GAM264  KIAA0544 3' ACATCTGAGTGAATGCT    70881    AAA   TT
                                AGCA  GCTT  AGGTGT
                                ||||  ||||  ||||||
                                TCGT  TGAG  TCTACA
                                  AAG  __
GAM264  KIAA0546 3' ACACTTGCAATGCTTTGTTCA 71303       A  _  T
                                TGAGCAAA GC TT TAGGTGT
                                |||||||| || || |||||||
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                                ACTTGTTT CG AA GTTCACA
                                    _ T  C
GAM264  KIAA0546 3' ATGCCTGAGAGATTCCTGTTT  71306      AAAG_
                                GAGCA    CTTTTAGGTGT
                                |||||    ||||||||||
                                TTTGT    GAGAGTCCGTA
                                   CCTTA
GAM264  KIAA0560 5' ACGCTTGGGCTGTTGT     61500     A   TT
                                GCAA AGCT  TAGGTGT
                                |||| ||||  |||||||
                                TGTT TCGG  GTTCGCA
                                  G   __
GAM264  KIAA0561 3' GCACCTGGGACTCTGTTTGC  65886      AGC__
                                GCAAA    TTTTAGGTGT
                                |||||    ||||||||||
                                CGTTT    AGGGTCCACG
                                   GTCTC
GAM264  KIAA0565 5' ACATCTGAAGGTGTTATCTTA 66884     CAAAA
                                TGAG    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                ATTC    TGGAAGTCTACA
                                  TATTG
GAM264  KIAA0601 3' GCATCTGGGCTCCTGATCA   62512    G  AA   TT
                                TGA CA  AGCT  TAGGTGT
                                ||| ||  ||||  |||||||
                                ACT GT  TCGG  GTCTACG
                                  A  CC   __
GAM264  KIAA0630 3' ACACCTCTGTTTTGCTCA    89385       G TTTT
                                TGAGCAAAA C    AGGTGT
                                ||||||||| |    ||||||
                                ACTCGTTTT G    TCCACA
                                     _ TC__
GAM264  KIAA0635 3' ATACCTGGGGGTGGGC     27695    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   TGGGGGTCCATA
                                 GG__
GAM264  KIAA0635 5' ATACCTATTTTTTTGTTT    27694       CTTT
                                GAGCAAAAG   TAGGTGT
                                |||||||||   |||||||
                                TTTGTTTTT   ATCCATA
                                     TT__
GAM264  KIAA0638 3' GCACAACTGGGGCTTTTGT   72399         TAG_
                                GCAAAAGCTTT   GTGT
                                ||||||||||||  ||||
                                TGTTTTCGGGG   CACG
                                      TCAA
GAM264  KIAA0650 3' ATATCTGTACACTTTTGTTCA 88238         CTTT
                                TGAGCAAAAG   TAGGTGT
                                |||||||||   |||||||
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                                ACTTGTTTTC   GTCTATA
                                     ACAT
GAM264  KIAA0662 3' TTTCTTATGAGCTTTGTTTA  81861       A   T   TGT
                                TGAGCAAA GCTT TAGG
                                |||||||| |||| ||||
                                ATTTGTTT CGAG ATTC
                                     _   T   TTTA
GAM264  KIAA0672 3' GCCTGCTTTGCTCA       29411       A  TTTT
                                TGAGCAAA GC   AGGT
                                |||||||| ||   ||||
                                ACTCGTTT CG   TCCG
                                     _ _____
GAM264  KIAA0672 3' TACCTAAAGGCACCCAGTTC  29417     AAAA_       GT
                                GAGC    GCTTTTAGGT
                                ||||    ||||||||||
                                CTTG    CGGAAATCCA
                                  ACCCA        TG
GAM264  KIAA0680 3' ACACCTAGAGTCTGTTGTCA  28231    G   A  C
                                TGA CAA AG TTTTAGGTGT
                                ||| ||| || ||||||||||
                                ACT GTT TC GAGATCCACA
                                  _  G  T
GAM264  KIAA0682 3' ACATCTAATTCAATTTGTTC  29361       AGCTT
                                GAGCAAA    TTAGGTGT
                                |||||||    ||||||||
                                CTTGTTT    AATCTACA
                                    AACTT
GAM264  KIAA0711 3' GCCTGACCTTTTGCTTA     29522        CTT
                                TGAGCAAAAG   TTAGGT
                                ||||||||||   ||||||
                                ATTCGTTTTC   AGTCCG
                                     C__
GAM264  KIAA0716 3' TACTTAAGGGGTTGC       28166     AAG
                                GCAA   CTTTTAGGTG
                                ||||   ||||||||||
                                CGTT   GGGAATTCAT
                                  G__
GAM264  KIAA0721 3' GGCCTGCTTTTTGCTTA     41343        _ TTTT   GT
                                TGAGCAAAA GC   AGGT
                                ||||||||| ||   ||||
                                ATTCGTTTT CG   TCCG
                                     T _____   GA
GAM264  KIAA0721 3' GGCCTGCTTTTTGCTTA     95971        _ TTTT   GT
                                TGAGCAAAA GC   AGGT
                                ||||||||| ||   ||||
                                ATTCGTTTT CG   TCCG
                                     T _____   GA
GAM264  KIAA0738 3' GCACCTGAAAAGCTTGTCT   28218    CAA     _
                                AG   AAGCTTT TAGGTGT
                                ||   ||||||| |||||||
```

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                                TC   TTCGAAA GTCCACG
                                 TG_      A
GAM264  KIAA0775 3' GCTCCTGGTTTCTGCTTA    28282       A    TTT   T
                                TGAGCA AAGCT   AGG GT
                                |||||| |||||   ||| ||
                                ATTCGT TTTGG   TCC CG
                                   C     ___   T
GAM264  KIAA0793 3' ACATCTGGGAGGGGCTT     29024     AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                TTCG    GAGGGTCTACA
                                  GG___
GAM264  KIAA0794 3' ATATCCAGGCTTTTGTTTA   80408          TTA
                                TGAGCAAAAGCTT   GGTGT
                                ||||||||||||   |||||
                                ATTTGTTTTCGGA   CTATA
                                       C__
GAM264  KIAA0819 3' ATGCCTGGGCCGCTTGCT    63573     AA   T_
                                AGCA  AGC  TTTAGGTGT
                                ||||  |||  |||||||||
                                TCGT  TCG  GGGTCCGTA
                                  __   CC
GAM264  KIAA0825 3' GTGTCTAGCTTCTTTTGCTCA 61029         CTT    TG
                                TGAGCAAAAG   TTAGG  T
                                |||||||||   |||||  |
                                ACTCGTTTTC   GATCT  G
                                      TTC    GT
GAM264  KIAA0826 3' ATGCCTAAAAGAGCACTGC   82636     AAAG_
                                GCA    CTTTTAGGTGT
                                |||    ||||||||||
                                CGT    GAAAATCCGTA
                                  CACGA
GAM264  KIAA0836 3' ACATTTAGGAGCCAGGT     64560    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                TG   CGAGGATTTACA
                                 GAC_
GAM264  KIAA0841 3' GCGCCTGACCACATTGCCA   71386    A   AAGCTT
                                TG GCAA     TTAGGTGT
                                || ||||     ||||||||
                                AC CGTT     AGTCCGCG
                                 _   ACACC_
GAM264  KIAA0843 3' AGATTGAAGGGCTTTTGTT   30110          AG  GT
                                AGCAAAAGCTTTT  GT
                                ||||||||||||  ||
                                TTGTTTTCGGGAA  TA
                                       GT  GAG
GAM264  KIAA0854 3' ATACCTGAGTGCACTTTTTCA 30097     C  AA  T
                                TGAG AA  GC TTTAGGTGT
                                |||| ||  || |||||||||
```

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                                ACTT TT  CG GAGTCCATA
                                  T  CA  T
GAM264  KIAA0855 3' ATACTGAAAGACTTTTGCTTA 30403         _     GTGT
                                TGAGCAAAAG CTTTTAG
                                |||||||||| |||||||
                                ATTCGTTTTC GAAAGTC
                                      A      ATA
GAM264  KIAA0888 3' ACGCCTAGAAGTTTAGACTT  63229     CAA
                                GAG  AAGCTTTTAGGTGT
                                |||  ||||||||||||||
                                TTC  TTTGAAGATCCGCA
                                  AGA
GAM264  KIAA0895 3' ATATCTAGAAGGACTTGC    92723     AAG
                                GCAA  CTTTTAGGTGT
                                ||||  ||||||||||
                                CGTT  GAAGATCTATA
                                  CAG
GAM264  KIAA0923 3' ACATTTGAAAGCCCTTG     25832     AA
                                CAA  GCTTTTAGGTGT
                                |||  ||||||||||||
                                GTT  CGAAAGTTTACA
                                  CC
GAM264  KIAA0931 3' TACTTGGAAGCCACAGGCTC  67424     AAAA_       GT
                                GAGC    GCTTTTAGGT
                                ||||    ||||||||||
                                CTCG    CGAAGGTTCA
                                  GACAC        TG
GAM264  KIAA0931 3' ATTTTTGGGAAGATTTTTGTTC 67414         _    AGGTGT
          A                      TGAGCAAAAG CTTTT
                                |||||||||| |||||
                                ACTTGTTTTT GAAGG
                                      A    GTTTTTAT
GAM264  KIAA0934 3' CTAAAAGAGTTTTGTTT     64218        G_
                                GAGCAAAA  CTTTTAG
                                ||||||||  |||||||
                                TTTGTTTT  GAAAATC
                                     GA
GAM264  KIAA0940 3' ATGCTGCAATAGCTTTTGCT  29864         TTTA_
                                AGCAAAAGCT    GGTGT
                                ||||||||||    |||||
                                TCGTTTTCGA    TCGTA
                                      TAACG
GAM264  KIAA0953 3' GTGTCTGCTGCTTTTGCTTA  66789         TTT   TG
                                TGAGCAAAAGC   TAGG  T
                                ||||||||||   ||||  |
                                ATTCGTTTTCG   GTCT  G
                                      TC_    GT
GAM264  KIAA0961 3' ATATCTGGAATGTCCTTTTGTT 29728         C___
          CA                     TGAGCAAAAG    TTTTAGGTGT
                                ||||||||||    ||||||||||
```

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                                ACTTGTTTTC   AAGGTCTATA
                                     CTGT
GAM264  KIAA0964 3' TACCTGAGGGGCTGCTC    29767      AAAG       GT
                                GAGCA   CTTTTAGGT
                                |||||   |||||||||
                                CTCGT   GGGAGTCCA
                                   CG__       TG
GAM264  KIAA0977 3' TCTGAAAGCTTTGTTCA    29750        A
                                TGAGCAAA GCTTTTAGG
                                |||||||| |||||||||
                                ACTTGTTT CGAAAGTCT
                                      _
GAM264  KIAA0978 3' AGAGTTGAGGGTTCTTGCTTA 70475        A       GTGT
                                TGAGCAA AGCTTTTAG
                                ||||||| |||||||||
                                ATTCGTT TTGGGAGTT
                                     C        GAGAC
GAM264  KIAA0978 3' ATACCTGGGACCATGCTC    70476      AAAGC
                                GAGCA    TTTTAGGTGT
                                |||||    ||||||||||
                                CTCGT    AGGGTCCATA
                                   ACC__
GAM264  KIAA1014 3' GCACTAATAAAGCTTTTTTTA 65352      C       TA_
                                TGAG AAAAGCTTT   GGTGT
                                |||| |||||||||   |||||
                                ATTT TTTTCGAAA   TCACG
                                   _        TAA
GAM264  KIAA1018 3' CCAATTGGATGTTTTTGCTTA 30349          T    G  T
                                TGAGCAAAAGC TTTAG TG
                                |||||||||||| ||||| ||
                                ATTCGTTTTTG AGGTT AC
                                      T    A  CC
GAM264  KIAA1023 3' ACGTCTGGAAGCTGAAATGT   34252     AA__       GT
                                GCA    AGCTTTTAG  GT
                                |||    |||||||||  ||
                                TGT    TCGAAGGTC  CA
                                  AAAG        TG
GAM264  KIAA1025 3' CAACAATTGAAAGTGTTTGCTC 63974        A       G
          A                      TGAGCAAA GCTTTTAG TGT
                                |||||||| |||||||| |||
                                ACTCGTTT TGAAAGTT ACA
                                     G       A   ACA
GAM264  KIAA1026 3' TGTAGTGAAGGCTTTTGTACA  71217    A          GGTGT
                                TG GCAAAAGCTTTTA
                                || ||||||||||||
                                AC TGTTTTCGGAAGT
                                 A           GATGTA
GAM264  KIAA1028 3' GCACTACTCTTTTGCTC     91940         CTTTTA
                                GAGCAAAAG     GGTGT
                                |||||||||     |||||
```

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                                CTCGTTTTC     TCACG
                                     TCA___
GAM264  KIAA1032 3' GCACCTAGGGGGCATTTTG   66155      _    _
                                CAAAA GCTTT TAGGTGT
                                ||||| ||||| |||||||
                                GTTTT CGGGG ATCCACG
                                   A    G
GAM264  KIAA1040 3' GCATTTAGAAGTGCAGTG    72227    AAA_
                                CA   GCTTTTAGGTGT
                                ||   ||||||||||||
                                GT   TGAAGATTTACG
                                 GACG
GAM264  KIAA1046 3' ATGTCTAAATGCTATTGTTT  29992       A  T     TG
                                GAGCAA AGC TTTAGG  T
                                |||||| ||| ||||||  |
                                TTTGTT TCG AAATCT  A
                                   A  T     GT
GAM264  KIAA1055 3' GCACTTAAAAGCCAGAATGT  66062     AAA__
                                GCA    GCTTTTAGGTGT
                                |||    ||||||||||||
                                TGT    CGAAAATTCACG
                                 AAGAC
GAM264  KIAA1058 3' ATGCCTGGGGGGACCTTTTGC  82251        __
                                GCAAAAG  CTTTTAGGTGT
                                |||||||  ||||||||||
                                CGTTTTC  GGGGGTCCGTA
                                    CA
GAM264  KIAA1068 3' GGCCTGAGGCTGCTC       31035      AAA    T  TG
                                GAGCA   GCTTT AGG  T
                                |||||   ||||| |||  |
                                CTCGT   CGGAG TCC  G
                                   ___    _  GT
GAM264  KIAA1089 3' ATATCTGGGAGCAGAGATCA  68842     GCAAAA
                                TGA     GCTTTTAGGTGT
                                |||     ||||||||||||
                                ACT     CGAGGGTCTATA
                                 AGAGA_
GAM264  KIAA1110 3' GCACCTGGGTTTGCCTCA    61845     CAA    TT
                                TGAG   AAGCT  TAGGTGT
                                ||||   |||||  |||||||
                                ACTC   TTTGG  GTCCACG
                                  CG_    __
GAM264  KIAA1110 3' ACACTTGGAGCCTGTGGTTA  61840     G  AAA    T
                                TGA CA   GCTTT AGGTGT
                                ||| ||   ||||| ||||||
                                ATT GT   CGAGG TTCACA
                                 G  GTC    _
GAM264  KIAA1128 3' TCTCCCTTTAAGTTTTTGCT  68485          TT   TGT
                                AGCAAAAGCTT  AGG
                                ||||||||||  |||
```

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                                TCGTTTTTGAA  TCC
                                      TT   CTCTA
GAM264  KIAA1143 3' ATGCCTGGAGGAGCTGCTACA  68668    _   AAAG
                                TG AGCA    CTTTTAGGTGT
                                || ||||    ||||||||||
                                AC TCGT    GGAGGTCCGTA
                                 A    CGA_
GAM264  KIAA1155 3' GCACCTGGAGAGCTTTTTG    62233    C       _
                                G AAAAGCTTTT AGGTGT
                                | ||||||||| ||||||
                                G TTTTCGAGAG TCCACG
                                 T        G
GAM264  KIAA1157 3' GCACTGTGGCTTTTGTCA     72245     G       TTTA
                                TGA CAAAAGCT    GGTGT
                                ||| ||||||||    |||||
                                ACT GTTTTCGG    TCACG
                                  _       TG__
GAM264  KIAA1165 3' GCAGGGTGGTTTTTGCTTA    67407           T  AG
                                TGAGCAAAAGCT TT  GT
                                |||||||||||| ||  ||
                                ATTCGTTTTTGG GG  CG
                                       T  GA
GAM264  KIAA1171 3' GCGTTTGGGAGCTGCT      87983      AAA      GG
                                AGCA   GCTTTTA  TGT
                                ||||   |||||||  |||
                                TCGT   CGAGGGT  GCG
                                  ___      TT
GAM264  KIAA1171 3' GAGCCTGAAGCTTTTGCT     87981           T    GT
                                AGCAAAAGCTTT AGGT
                                |||||||||||| ||||
                                TCGTTTTCGAAG TCCG
                                       _   AGA
GAM264  KIAA1205 3' ATACCTGGGGCAGGGGCTT    70041      AAAA    T
                                GAGC    GCTTT AGGTGT
                                ||||    ||||| ||||||
                                TTCG    CGGGG TCCATA
                                  GGGA    _
GAM264  KIAA1211 3' AAAACTAGAGGGTTTTTTGTTT 68888           _    A  GT
           A                     TGAGCAAAAG CTTTT GGT
                                ||||||||| ||||| |||
                                ATTTGTTTTT GGGAG TCA
                                      T    A  AAAT
GAM264  KIAA1228 3' GGCCTGGAGGTGCTT        65046      AAAA       TG
                                GAGC    GCTTTTAGG  T
                                ||||    |||||||||  |
                                TTCG    TGGAGGTCC  G
                                  _____        GT
GAM264  KIAA1237 3' GCACCTGGGGTGTGTGATTCA  80470      _ AAA    T
                                TGAG CA   GCTTT AGGTGT
                                |||| ||   ||||| ||||||
```

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                                ACTT GT   TGGGG TCCACG
                                  A  GTG    _
GAM264  KIAA1240 3' ACACTTACCAGTTTTGCTTA  66728        G  TT
                                TGAGCAAAA CT  TAGGTGT
                                ||||||||| ||  |||||||
                                ATTCGTTTT GA  ATTCACA
                                     _ CC
GAM264  KIAA1244 3' ACGTTTGAAAGCTTTATCTTA 71984     CA        GG
                                TGAG  AAAGCTTTTA  TGT
                                ||||  ||||||||||  |||
                                ATTC  TTTCGAAAGT  GCA
                                  TA        TT
GAM264  KIAA1260 3' ATATTTAAGAGACTTTGT    60023      AG
                                GCAAA  CTTTTAGGTGT
                                |||||  ||||||||||
                                TGTTT  GAGAATTTATA
                                   CA
GAM264  KIAA1280 5' GCGCCTAGAGGAGGAGCT    69722    AAAAG
                                AGC    CTTTTAGGTGT
                                |||    ||||||||||
                                TCG    GGAGATCCGCG
                                 AGGA_
GAM264  KIAA1297 3' ACATCTGGGGAGCGGGTGT   72163     AAA    _
                                GCA   GCTTTT AGGTGT
                                |||   |||||| ||||||
                                TGT   CGAGGG TCTACA
                                  GGG     G
GAM264  KIAA1322 3' GTGTCTGGAAGCAGGGCCCA  72739    A  AAAA       TG
                                TG GC    GCTTTTAGG  T
                                || ||    |||||||||  |
                                AC CG    CGAAGGTCT  G
                                 C  GGA_       GT
GAM264  KIAA1328 5' GCACCTGGCCTATGTTCA    61651      AAA   TTT
                                TGAGCA   GCT   AGGTGT
                                ||||||   |||   ||||||
                                ACTTGT   CGG   TCCACG
                                   ATC   ___
GAM264  KIAA1354 3' ATACCTGGAAGATTGTCA    60914    G   AAG
                                TGA CAA   CTTTTAGGTGT
                                ||| |||   ||||||||||
                                ACT GTT   GAAGGTCCATA
                                  _   A__
GAM264  KIAA1363 3' ATATCATTAGGTTTTTGTT   69260         TTA
                                AGCAAAAGCTT   GGTGT
                                ||||||||||   |||||
                                TTGTTTTTGGA   CTATA
                                      TTA
GAM264  KIAA1371 3' ATACCTGGAAGAAATCGTCA  89041    GCAAAAG
                                TGA      CTTTTAGGTGT
                                |||      ||||||||||
```

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                                ACT      GAAGGTCCATA
                                  GCTAAA_
GAM264  KIAA1387 3' TATCTAGAAGCCATTTTG    70874      __       GT
                                CAAAA  GCTTTTAGGT
                                |||||  ||||||||||
                                GTTTT  CGAAGATCTA
                                   AC        TG
GAM264  KIAA1396 3' GCGCTTGAGCTCTGCT     62990     AA    TT
                                AGCA  AGCTT  AGGTGT
                                ||||  |||||  ||||||
                                TCGT  TCGAG  TTCGCG
                                  C_    __
GAM264  KIAA1432 5' ACACTTGGAGGAGATTTTGCTT 66745         G__
          A                      TGAGCAAAA   CTTTTAGGTGT
                                |||||||||   ||||||||||
                                ATTCGTTTT   GGAGGTTCACA
                                     AGA
GAM264  KIAA1432 5' ACACTTGATGGGTTTGCT    66744       AG  T
                                AGCAAA  CT TTAGGTGT
                                ||||||  || ||||||||
                                TCGTTT  GG AGTTCACA
                                   G_  T
GAM264  KIAA1437 3' ACACTTAGAGGCTGGTCG    60582     G  AAA
                                TGA CA   GCTTTTAGGTGT
                                ||| ||   ||||||||||||
                                GCT GT   CGGAGATTCACA
                                  G  ___
GAM264  KIAA1462 3' GCGCCTGGAGGTCTTTGT    91386      AG
                                GCAAA  CTTTTAGGTGT
                                |||||  ||||||||||
                                TGTTT  GGAGGTCCGCG
                                   CT
GAM264  KIAA1497 5' ACATCTGCAGGCTTTTTCTTA  67498     C       T
                                TGAG AAAAGCTT TAGGTGT
                                |||| |||||||| |||||||
                                ATTC TTTTCGGA GTCTACA
                                   T       C
GAM264  KIAA1500 3' ACACAGCTTGCTTTTGTTT    64113          TTTTAG
                                GAGCAAAAGC     GTGT
                                ||||||||||     ||||
                                TTTGTTTTCG     CACA
                                     TTCGA_
GAM264  KIAA1508 3' ATGCTGTGAATGTGTTTTTGCT 61877          TTTTA___
          T                      GAGCAAAAGC       GGTGT
                                ||||||||||       |||||
                                TTCGTTTTTG       TCGTA
                                     TGTAAGTG
GAM264  KIAA1508 3' GTGCAATGATAAAGGCCTTTTG 61889          _     GG__
          TTTA                     TGAGCAAAAG CTTTTA    TGT
                                |||||||||| ||||||    |||
```

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                                ATTTGTTTTC GGAAAT   ACG
                                      C     AGTA  TG
GAM264  KIAA1522 3' GCATCTGGAGGGGGGGAGCTT 64974     AAAAG_
                                GAGC     CTTTTAGGTGT
                                ||||     ||||||||||
                                TTCG     GGAGGTCTACG
                                  AGGGGG
GAM264  KIAA1557 3' ACACCTGAGAACTCGTCTCA  61134     CAAA  C
                                TGAG   AG TTTTAGGTGT
                                ||||   || ||||||||||
                                ACTC   TC AGAGTCCACA
                                  TGC_  A
GAM264  KIAA1560 3' TGGTGTTGAAGGCTTTTGCTCA 64181             GTGT
                                TGAGCAAAAGCTTTTAG
                                |||||||||||||||||
                                ACTCGTTTTCGGAAGTT
                                      GTGGTC
GAM264  KIAA1576 3' GGCTTTAGAGCTTTTGTT    65904          T   GT
                                AGCAAAAGCTTT AGGT
                                |||||||||||| ||||
                                TTGTTTTCGAGA TTCG
                                      T   GT
GAM264  KIAA1577 3' ATGCTTAGAGGTATGTTT    64471      AAA
                                GAGCA  GCTTTTAGGTGT
                                |||||  ||||||||||||
                                TTTGT  TGGAGATTCGTA
                                  A__
GAM264  KIAA1596 5' GCACTTGAGAATTTGCTT    70916       AGC
                                GAGCAAA  TTTTAGGTGT
                                |||||||  ||||||||||
                                TTCGTTT  AGAGTTCACG
                                   A__
GAM264  KIAA1615 5' ATATCTGGATTCTGCTCA    68698       AAA CT
                                TGAGCA  G  TTTAGGTGT
                                ||||||  |  |||||||||
                                ACTCGT  C  AGGTCTATA
                                   ___ TT
GAM264  KIAA1649 5' GCCATTGAAGGCTTTTGTT   50266           __  GT
                                AGCAAAAGCTTTTA  GGT
                                ||||||||||||||  |||
                                TTGTTTTCGGAAGT  CCG
                                      TA
GAM264  KIAA1655 5' GCACCTGGGGTGTCCTCTCA  66611     CAAAA    T
                                TGAG    GCTTT AGGTGT
                                ||||    ||||| ||||||
                                ACTC    TGGGG TCCACG
                                  TCCTG    _
GAM264  KIAA1656 3' ACACCTGGAGGCATCTCA    65778     CAAAA
                                TGAG    GCTTTTAGGTGT
                                ||||    ||||||||||||
```

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                                ACTC    CGGAGGTCCACA
                                  TA___
GAM264  KIAA1668 3' GCACTTGAAGCAGGTGCTCA  66472       AAA    T
                                TGAGCA  GCTTT AGGTGT
                                ||||||  ||||| ||||||
                                ACTCGT  CGAAG TTCACG
                                   GGA    _
GAM264  KIAA1671 3' ACACCTGGGAGCCTCATGC   65664     AAA_
                                GCA   GCTTTTAGGTGT
                                |||   ||||||||||||
                                CGT   CGAGGGTCCACA
                                  ACTC
GAM264  KIAA1671 3' ACATCTAAAGGGGATCTGCTT 65665      AAAG_
                                GAGCA    CTTTTAGGTGT
                                |||||    ||||||||||||
                                TTCGT    GGAAATCTACA
                                   CTAGG
GAM264  KIAA1671 3' TACTTTTTGCTTTTGCTCA   65689         TTTT   GT
                                TGAGCAAAAGC   AGGT
                                ||||||||||    ||||
                                ACTCGTTTTCG   TTCA
                                      TTT_   TG
GAM264  KIAA1674 3' ACATTTAAGGTGCGTGTGC   68768     AAA _
                                GCA  GC TTTTAGGTGT
                                |||  || ||||||||||
                                CGT  CG GGAATTTACA
                                  GTG  T
GAM264  KIAA1674 3' ACGCCTGAGGGCAGGC     68770    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   CGGGAGTCCGCA
                                 GA__
GAM264  KIAA1677 3' CTTCATTTGGAGTTTTTGTTTA 67067           T    T
                                TGAGCAAAAGCTTT AGGTG
                                |||||||||||||| |||||
                                ATTTGTTTTTGAGG TTTAC
                                       _    TTCG
GAM264  KIAA1691 3' CACCTGAACGCTGCT      92553     AAA  T
                                AGCA  GC TTTAGGTG
                                ||||  || ||||||||
                                TCGT  CG AAGTCCAC
                                  ___  C
GAM264  KIAA1715 3' ACATTTAGAGGTTTTAATCA  68114    GCA
                                TGA  AAAGCTTTTAGGTGT
                                |||  ||||||||||||||||
                                ACT  TTTTGGAGATTTACA
                                  AA_
GAM264  KIAA1719 3' GCGCTTGGGGGTTGGCTT   68166     AAAA
                                GAGC   GCTTTTAGGTGT
                                ||||   ||||||||||||
```

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                                TTCG    TGGGGGTTCGCG
                                  GT__
GAM264  KIAA1729 3' ACATCCATTTTGTTTTTGCTT  89123          TTTTA_
                                GAGCAAAAGC     GGTGT
                                ||||||||||     |||||
                                TTCGTTTTTG     CTACA
                                     TTTTAC
GAM264  KIAA1751 3' GCACCTGGCTAGTTTTTG    71693        T_
                                CAAAAGCT  TTAGGTGT
                                ||||||||  ||||||||
                                GTTTTTGA  GGTCCACG
                                     TC
GAM264  KIAA1753 3' GCATCTGGGAGCATTTTGC    64882       _
                                GCAAAA GCTTTTAGGTGT
                                ||||||| ||||||||||||
                                CGTTTT CGAGGGTCTACG
                                   A
GAM264  KIAA1755 3' ATACCTAAAATGGCTTCA    61338    A    __
                                A AAGCT  TTTAGGTGT
                                | |||||  |||||||||
                                A TTCGG  AAATCCATA
                                 C    TA
GAM264  KIAA1786 3' ACATTCTACAAGCTCTTGTTTA 66021        A    T   _
                                TGAGCAA AGCTT TAGG TGT
                                ||||||| ||||| |||| |||
                                ATTTGTT TCGAA ATCT ACA
                                    C    C   T
GAM264  KIAA1789 5' TGAATAGTCTTTGCTCA     67105         AG  _
                                TGAGCAAA  CT TTTA
                                ||||||||  || ||||
                                ACTCGTTT  GA AAGT
                                     CT  T
GAM264  KIAA1798 3' ACCCAAAGGTTTTTTTCA    60619      C        A
                                TGAG AAAAGCTTTT GGT
                                |||| |||||||||| |||
                                ACTT TTTTTGGAAA CCA
                                  _        C
GAM264  KIAA1838 3' GTGCAGAAGAGCTTTTGTT   64734            AG TG
                                AGCAAAAGCTTTT  G  T
                                ||||||||||||  |  |
                                TTGTTTTCGAGAA  C  G
                                       GA GT
GAM264  KIAA1877 3' AGAGACTGAAGGCTTCTGTTT  66161       A        GTGT
                                GAGCA AAGCTTTTAG
                                ||||| ||||||||||
                                TTTGT TTCGGAAGTC
                                   C         AGAGAC
GAM264  KIAA1894 3' GCACCTGGGAGCGCTGCTT   73845       AAA
                                GAGCA   GCTTTTAGGTGT
                                |||||   ||||||||||||
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                                TTCGT   CGAGGGTCCACG
                                  CG_
GAM264  KIAA1910 3' GCATTTGAGATGCTGCT     73329      AAA  _
                                AGCA   GC TTTTAGGTGT
                                ||||   || ||||||||||
                                TCGT   CG AGAGTTTACG
                                  ___  T
GAM264  KIAA1912 3' TGAGGCTAAAAGCTCTTGTTCA 73368        A       GTGT
                                TGAGCAA AGCTTTTAG
                                ||||||| |||||||||
                                ACTTGTT TCGAAAATC
                                    C       GGAGTT
GAM264  KIAA1912 3' ACATTTAAAATAAGCTTTTG   73363         ___
                                CAAAAGCTT   TTAGGTGT
                                |||||||||   ||||||||
                                GTTTTCGAA   AATTTACA
                                     TAA
GAM264  KIAA1918 3' GGTCTACGCTTTTGTTT     73163         TTT    TG
                                GAGCAAAAGC   TAGG  T
                                ||||||||||   ||||  |
                                TTTGTTTTCG   ATCT  G
                                     C__    GT
GAM264  KIAA1924 3' GCGTCTGAAGGCTGTCGTCG   73681     G AAA       GT
                                TGA C   AGCTTTTAG  GT
                                ||| |   |||||||||  ||
                                GCT G   TCGGAAGTC  CG
                                  _ CTG       TG
GAM264  KIAA1938 3' GCGTCTGGGGGGGCTCA     92197      AAAAG     GT
                                TGAGC    CTTTTAG  GT
                                |||||    |||||||  ||
                                ACTCG    GGGGGTC  CG
                                   G____      TG
GAM264  KIAA1940 3' ACGCTCTTCTTTTGTTC     79974         CTTTTA
                                GAGCAAAAG     GGTGT
                                |||||||||     |||||
                                CTTGTTTTC     TCGCA
                                     TTC___
GAM264  KIAA1944 5' GCACTTGAGAACAGGTGCTT   75561       AAAGC
                                GAGCA    TTTTAGGTGT
                                |||||    ||||||||||
                                TTCGT    AGAGTTCACG
                                   GGACA
GAM264  KIAA1970 3' ACATTTGGAGGCTAGAAGTTCA 74295       AAA_
                                TGAGC   AGCTTTTAGGTGT
                                |||||   ||||||||||||
                                ACTTG   TCGGAGGTTTACA
                                   AAGA
GAM264  KIAA1977 3' CACCTGGAAAATGCCA      74280    A  AAAGC
                                TG GCA    TTTTAGGTG
                                || |||    |||||||||
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                                AC CGT    AAGGTCCAC
                                 _  AA___
GAM264  KIAA1987 3' GTGTCTAGGGGCTGACTGC   88021    AA_       TG
                                GCA  AGCTTTTAGG  T
                                |||  ||||||||||  |
                                CGT  TCGGGGATCT  G
                                  CAG        GT
GAM264  KIF13B   3' ACATCTAGAAAGCGCTGC    30901    AAA    _
                                GCA  GCTTTT AGGTGT
                                |||  |||||| ||||||
                                CGT  CGAAAG TCTACA
                                  CG_    A
GAM264  KIF13B   3' ACATCTAGAAAGCGCTGC    82817    AAA    _
                                GCA  GCTTTT AGGTGT
                                |||  |||||| ||||||
                                CGT  CGAAAG TCTACA
                                  CG_    A
GAM264  KIF13B   3' ACACCTGGAAAGTCTC      30900    CAAAA    _
                                GAG    GCTTTT AGGTGT
                                |||    |||||| ||||||
                                CTC    TGAAAG TCCACA
                                 _____     G
GAM264  KLHL4    3' GCATTTAAAAATGGTGTTCA  38923      AAAGC
                                TGAGCA    TTTTAGGTGT
                                ||||||    ||||||||||
                                ACTTGT    AAAATTTACG
                                   GGTA_
GAM264  KLHL6    3' GTACTGTTGTGAGTTATTTGCT 55307       _    TTA__  GT
           TA                    TGAGCAAA AGCTT    GGT
                                ||||||||| |||||    |||
                                ATTCGTTT TTGAG    TCA
                                    A    TGTTG  TG
GAM264  KLK6     5' CGCCTGGGCCTGCTC      10919     AAA  TT
                                GAGCA  GCT  TAGGTG
                                |||||  |||  ||||||
                                CTCGT  CGG  GTCCGC
                                  C__  __
GAM264  KOC1     3' AAGGCCAGAGCTTTTCTCA  91067     C      TA  GT
                                TGAG AAAAGCTTT  GGT
                                |||| |||||||||  |||
                                ACTC TTTTCGAGA  CCG
                                  _       __  GAAT
GAM264  KOC1     3' ATACCTAAAGAAAGTGCATCA 91071    _  AAAG   T
                                TGA GCA   CTTT AGGTGT
                                ||| |||   |||| ||||||
                                ACT CGT   GAAA TCCATA
                                  A  GAAA   _
GAM264  KR19     5' ATGCCTGGATTGTGCTCA    81165      AAAGCT
                                TGAGCA    TTTAGGTGT
                                ||||||    |||||||||
```

```
                                ACTCGT     AGGTCCGTA
                                   GTT___
GAM264  KREMEN2  3'  ACACCTGAGATGCTGTGCT   44453     AA  _
                                AGCA  AGC TTTTAGGTGT
                                ||||  ||| ||||||||||
                                TCGT  TCG AGAGTCCACA
                                  G_  T
GAM264  KRTHB2   3'  ACATCTGGGCTTCTGTTCA   52284      A    TT
                                TGAGCA AAGCT  TAGGTGT
                                |||||| |||||  |||||||
                                ACTTGT TTCGG  GTCTACA
                                   C    __
GAM264  KRTHB4   5'  ACACTTGCTCTTTTGCTC    52321        CTTT
                                GAGCAAAAG   TAGGTGT
                                |||||||||   |||||||
                                CTCGTTTTC   GTTCACA
                                     TC__
GAM264  LANCL2   3'  ATGCCTGGAGAGTCTGTTTGC  37993     _ _   _
                                GCAAA AG CTTTT AGGTGT
                                ||||| || ||||| ||||||
                                CGTTT TC GAGAG TCCGTA
                                   G  T    G
GAM264  LAP1B    3'  ACACCCTGAAGCTTTTGTTT   64581          TA
                                GAGCAAAAGCTTT  GGTGT
                                ||||||||||||  |||||
                                TTTGTTTTCGAAG  CCACA
                                      TC
GAM264  LAPTM4A  3'  ATACCAGCTTTTTGTTT     28193        _  TTTA
                                GAGCAAAA GCT   GGTGT
                                |||||||| |||   |||||
                                TTTGTTTT CGA   CCATA
                                     T  _____
GAM264  LATS1    3'  GCACCTGAAGTGTTGCT     60277      AA    T
                                AGCAA  GCTTT AGGTGT
                                |||||  ||||| ||||||
                                TCGTT  TGAAG TCCACG
                                   G_    _
GAM264  LEC3     3'  TCACATAGGGTTTTTGGTCA  30863     G       TAG   T
                                TGA CAAAAGCTTT   GTG
                                ||| ||||||||||   |||
                                ACT GTTTTTGGGA   CAC
                                  G        TA_   TA
GAM264  LEPROTL1 3'  ACACTTAGAAGTGTTTACTTA 31061     C   A
                                TGAG AAA GCTTTTAGGTGT
                                |||| ||| ||||||||||||
                                ATTC TTT TGAAGATTCACA
                                  A  G
GAM264  LHFPL2   3'  CACTGTCTTTTGCTTA      69950          CTTTTA
                                TGAGCAAAAG     GGTG
                                ||||||||||     ||||
```

```
                                ATTCGTTTTC     TCAC
                                     TG____
GAM264  LIMK2    3' ATGCCTAAAACATTTTGC    18723       GC
                                GCAAAA  TTTTAGGTGT
                                ||||||  ||||||||||
                                CGTTTT  AAAATCCGTA
                                   AC
GAM264  LIMK2    3' ATGCCTAAAACATTTTGC    33621       GC
                                GCAAAA  TTTTAGGTGT
                                ||||||  ||||||||||
                                CGTTTT  AAAATCCGTA
                                   AC
GAM264  LOXL4    3' GTCCTCCAGGCTTTGCTCA   49872        A   TT   TGT
                                TGAGCAAA GCTT  AGG
                                ||||||||| ||||  |||
                                ACTCGTTT CGGA  TCC
                                     _   CC   TGT
GAM264  LRPPRC   3' ATGCCTGGAGGCTCTTCG    55703     CAAA
                                TGAG   AGCTTTTAGGTGT
                                ||||   ||||||||||||
                                GCTT   TCGGAGGTCCGTA
                                  C___
GAM264  LSM6     5' GCGCCTGGAGTGAGGGTTC   22998     AAAA    T
                                GAGC   GCTTT AGGTGT
                                ||||   ||||| ||||||
                                CTTG   TGAGG TCCGCG
                                  GGAG   _
GAM264  LTBP4    3' ACGCCTGGAAGCTGC      13112     AAA
                                GCA  GCTTTTAGGTGT
                                |||  ||||||||||||
                                CGT  CGAAGGTCCGCA
                                  ___
GAM264  LY75     3' GCGCCTGGCCTCTGCTTA    9841       AAA  TTT
                                TGAGCA  GCT  AGGTGT
                                ||||||  |||  ||||||
                                ATTCGT  CGG  TCCGCG
                                   CTC  ___
GAM264  MAFB     3' ACACTTGGAAGTTGCATGTTT 18408      AA_
                                GAGCA  AGCTTTTAGGTGT
                                |||||  ||||||||||||
                                TTTGT  TTGAAGGTTCACA
                                  ACG
GAM264  MAFB     3' GCAAGCTGAGGGTCTTTGTTT 18412       AG     G_
                                GAGCAAA  CTTTTAG  TGT
                                |||||||  |||||||  |||
                                TTTGTTT  GGGAGTC  ACG
                                    CT     GA
GAM264  MAP-1    5' GCACCTGGAGTACCGGCATC  42178   _ AAAA    T
                                GA GC   GCTTT AGGTGT
                                || ||   ||||| ||||||
```

```
                                CT CG    TGAGG TCCACG
                                 A  GCCA    _
GAM264  MAPK8IP3 3'  GCATTTGGAGGTCACTGCT   52983      AAA
                                AGCA   GCTTTTAGGTGT
                                ||||   ||||||||||||
                                TCGT   TGGAGGTTTACG
                                  CAC
GAM264  MAT2B    3'  GCACTTGAAAGAGCGTGT    25222     AAAG
                                GCA    CTTTTAGGTGT
                                |||    ||||||||||
                                TGT    GAAAGTTCACG
                                  GCGA
GAM264  MAWBP    3'  TCATTAAGAGTGTTTGTTTA  42109         A       GTGT
                                TGAGCAAA GCTTTTAG
                                |||||||| ||||||||
                                ATTTGTTT TGAGAATT
                                     G       ACTG
GAM264  MBLL39   3'  CCTAGATTTTGCCA       58608    A     GCT
                                TG GCAAAA   TTTAGG
                                || ||||||   ||||||
                                AC CGTTTT   AGATCC
                                 _     ____
GAM264  MCM10    3'  CTGAAGTTTTTGCCCA      37572    A         T
                                TG GCAAAAGCTTT AG
                                || ||||||||||| ||
                                AC CGTTTTTGAAG TC
                                 C         _
GAM264  MCM10    3'  GCACTTGAAACTGATGTTT   37574      AA  C
                                GAGCA  AG TTTTAGGTGT
                                |||||  || ||||||||||
                                TTTGT  TC AAAGTTCACG
                                   AG  _
GAM264  METAP2   3'  ATACCTAAGAGATACTTTTTG 60167    C    ____
                                G AAAAG   CTTTTAGGTGT
                                | |||||   ||||||||||
                                G TTTTC   GAGAATCCATA
                                 T    ATA
GAM264  MGC10715 3'  ACACTTAGGAGAGAAGTTTA  44245      AAAAG
                                TGAGC    CTTTTAGGTGT
                                |||||    ||||||||||
                                ATTTG    GAGGATTCACA
                                   AAGA_
GAM264  MGC10772 5'  GCACCTGAGAGTGTGGC     47531    AAAA
                                GC    GCTTTTAGGTGT
                                ||    ||||||||||||
                                CG    TGAGAGTCCACG
                                 GTG_
GAM264  MGC10870 5'  GCACCTGGGACGATGACTC    50208     _  AAAGC
                                GAG CA    TTTTAGGTGT
                                ||| ||    ||||||||||
```

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                              CTC GT    AGGGTCCACG
                                A  AGC__
GAM264  MGC11034 3' ACTAGGAGGGTTTCTGTTCA  48785      A      A_  GT
                              TGAGCA AAGCTTTT  GGT
                              |||||| ||||||||  |||
                              ACTTGT TTTGGGAG  TCA
                                 C       GA
GAM264  MGC11061 3' ACATCTGATTTAAAGTTTCTGT 50283      A    ____
          TTA                   GAGCA AAGCTT    TTAGGTGT
                              ||||| ||||||    ||||||||
                              TTTGT TTTGAA    AGTCTACA
                                 C     ATTT
GAM264  MGC11324 3' GCCCTTTTTGGCTTTTGTT   51168        TTT_  T
                              AGCAAAAGCT    AGG GT
                              ||||||||||    ||| ||
                              TTGTTTTCGG    TCC CG
                                    TTTT  _  T
GAM264  MGC11335 3' GCACCTGGGCTCCTTGCCA   48019   A   A_   TT
                              TG GCAA  AGCT  TAGGTGT
                              || ||||  ||||  |||||||
                              AC CGTT  TCGG  GTCCACG
                               _   CC   __
GAM264  MGC11349 3' GCACCTGGGATGGGGTTTGT  47076     AG  __
                              GCAAA  CT  TTTAGGTGT
                              |||||  ||  |||||||||
                              TGTTT  GG  GGGTCCACG
                                 GG  TA
GAM264  MGC11352 3' GCACCTGAGGCATCCTGCT   64801     AAA_    T
                              AGCA   GCTTT AGGTGT
                              ||||   ||||| ||||||
                              TCGT   CGGAG TCCACG
                                CCTA   _
GAM264  MGC1223  3' ATATCTTTTCTTTTGCTCA   48240        CTTTT
                              TGAGCAAAAG    AGGTGT
                              ||||||||||    ||||||
                              ACTCGTTTTC    TCTATA
                                    TTT__
GAM264  MGC12837 3' ACATCTGGAAGGATGCTCG   51180      AAAG
                              TGAGCA   CTTTTAGGTGT
                              ||||||   ||||||||||
                              GCTCGT   GAAGGTCTACA
                                 AG__
GAM264  MGC12966 3' ATGCTTAAAAGCACCTCA    51121     CAAAA
                              TGAG    GCTTTTAGGTGT
                              ||||    ||||||||||
                              ACTC    CGAAAATTCGTA
                                CA___
GAM264  MGC13183 3' ACTAGGAAAGCTTTTCTT    50387     C       A_
                              GAG AAAAGCTTTT  GGT
                              ||| ||||||||||  |||
```

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                                TTC TTTTCGAAAG  TCA
                                  _       GA
GAM264  MGC13204 3' TTCCTAGGGTTTTTGTTT   48841          T  TGT
                                GAGCAAAAGCTTT AGG
                                |||||||||||| |||
                                TTTGTTTTTGGGA TCC
                                       _  TTA
GAM264  MGC13523 3' GTTATCTCTAGGTTTTTGT  53030        TT   T
                                GCAAAAGCTT  AGGTG
                                ||||||||||  |||||
                                TGTTTTTGGA  TCTAT
                                      TC    TGT
GAM264  MGC14289 3' GCATCTTTCTATATTTGTTCA 54702       AGCTTTT
                                TGAGCAAA     AGGTGT
                                ||||||||     ||||||
                                ACTTGTTT     TCTACG
                                     ATATCTT
GAM264  MGC14421 5' ATGCTTGAAGGTCTGCT    51872     AAA
                                AGCA  GCTTTTAGGTGT
                                ||||  ||||||||||||
                                TCGT  TGGAAGTTCGTA
                                  C__
GAM264  MGC14793 3' ACATCTAATCTAGCTTTCTTA 51935     CA    T__
                                TGAG  AAAGCT  TTAGGTGT
                                ||||  ||||||  ||||||||
                                ATTC  TTTCGA  AATCTACA
                                  __     TCT
GAM264  MGC14839 3' GCGCTTGGGAGGAAGGCCCA  54696   A  AAAAG
                                TG GC    CTTTTAGGTGT
                                || ||    ||||||||||
                                AC CG    GAGGGTTCGCG
                                 C  GAAG_
GAM264  MGC15416 3' GGCCTGGGACCTGGCTCA    56544     AAA  C     TG
                                TGAGC  AG TTTTAGG  T
                                |||||  || |||||||  |
                                ACTCG  TC AGGGTCC  G
                                   G__  C     GT
GAM264  MGC15606 3' ATGCTTGGAAGAAGCTGCT   58875     AAAG
                                AGCA   CTTTTAGGTGT
                                ||||   ||||||||||
                                TCGT   GAAGGTTCGTA
                                  CGAA
GAM264  MGC15854 5' GGCCTAGAGGTGATTTG     58850     A_      TG
                                CAAA  GCTTTTAGG  T
                                ||||  |||||||||  |
                                GTTT  TGGAGATCC  G
                                  AG       GT
GAM264  MGC16169 5' GCACCTGAAATGCAGCGTC   52412    _ AAAA _
                                GA GC   GC TTTTAGGTGT
                                || ||   || ||||||||||
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                              CT CG   CG AAAGTCCACG
                               G  A___  T
GAM264  MGC16186 5' ACACCTGGGAGACAGCT    50428    AAAAG
                              AGC    CTTTTAGGTGT
                              |||    ||||||||||
                              TCG    GAGGGTCCACA
                                ACA__
GAM264  MGC16372 3' CACCTGGGCCTGCTC      58885     AAA  TT
                              GAGCA  GCT  TAGGTG
                              |||||  |||  ||||||
                              CTCGT  CGG  GTCCAC
                                C__  __
GAM264  MGC16384 3' ATGCCTGGAGGCTGCT     53865     AAA
                              AGCA  GCTTTTAGGTGT
                              ||||  ||||||||||||
                              TCGT  CGGAGGTCCGTA
                                ___
GAM264  MGC17998 3' ATGTTTGAGGGTACCTTTTGCT 58741        ___      TG
                              AGCAAAAG  CTTTTAGG  T
                              ||||||||  ||||||||  |
                              TCGTTTTC  GGGAGTTT  A
                                  CAT      GT
GAM264  MGC1842  3' ACAGTTGGGCTTTGTTCA   65637       A  TT  G
                              TGAGCAAA GCT  TAG TGT
                              |||||||| |||  ||| |||
                              ACTTGTTT CGG  GTT ACA
                                  _  __  G
GAM264  MGC20470 3' ATGCCTACTTGTTTGCTT   58959      AGCTTT
                              GAGCAAA    TAGGTGT
                              |||||||    |||||||
                              TTCGTTT    ATCCGTA
                                 GTTC__
GAM264  MGC20806 3' GCGCCTGGGAAGGGCTC    58753    AAAAGC
                              GAGC    TTTTAGGTGT
                              ||||    ||||||||||
                              CTCG    AGGGTCCGCG
                                GGA___
GAM264  MGC22014 3' CACCTGAGCCTGCTT      64492     AAA  TT
                              GAGCA  GCTT  AGGTG
                              |||||  ||||  |||||
                              TTCGT  CGAG  TCCAC
                                C__  __
GAM264  MGC22014 3' ATACCTGGGGGCGGGTTG   64487    AA_
                              CAA  GCTTTTAGGTGT
                              |||  ||||||||||||
                              GTT  CGGGGGTCCATA
                                GGG
GAM264  MGC23980 3' TACTTAAGAGTTTGTGC    58760    A        GT
                              GCA AAGCTTTTAGGT
                              ||| ||||||||||||
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                                CGT TTTGAGAATTCA
                                  G          TG
GAM264  MGC24447  3'  CCCCCGTGAAAGCTTTTCTTA  56285      C         _  TGT
                                TGAG AAAAGCTTTTA GG
                                |||| |||||||||| ||
                                ATTC TTTTCGAAAGT CC
                                  _         G  CCCA
GAM264  MGC2452   5'  CACCTGAGCCTGCCCA      50980    A   AAA    TT
                                TG GCA   GCTT  AGGTG
                                || |||   ||||  |||||
                                AC CGT   CGAG  TCCAC
                                 C  C__   __
GAM264  MGC2488   3'  AGATATTGAAAGCTTGTGTTTA 43866       A        GTGT
                                TGAGCA AAGCTTTTAG
                                |||||| ||||||||||
                                ATTTGT TTCGAAAGTT
                                    G         ATAGAT
GAM264  MGC2541   3'  ACACCTAGCCTTTGTTC     54743        A   TTT
                                GAGCAAA GCT   AGGTGT
                                ||||||| |||   ||||||
                                CTTGTTT CGA   TCCACA
                                    C  ___
GAM264  MGC2541   3'  ATGCCTAGAGACATGCTC    54745      AAAG   T
                                GAGCA    CTTT AGGTGT
                                |||||    |||| ||||||
                                CTCGT    GAGA TCCGTA
                                   ACA_   _
GAM264  MGC2560   3'  ATGCTTAGATGTGCTC      48779      AAAGCT
                                GAGCA     TTTAGGTGT
                                |||||     |||||||||
                                CTCGT     AGATTCGTA
                                   GT____
GAM264  MGC2647   3'  GCACCTGGCACCTGCTC     73704      AAA   TTT
                                GAGCA   GCT   AGGTGT
                                |||||   |||   ||||||
                                CTCGT   CGG   TCCACG
                                   CCA  ___
GAM264  MGC2663   5'  GCGCCTGAGAGTCTTTTTGC   44095       __
                                GCAAAA  GCTTTTAGGTGT
                                ||||||  ||||||||||||
                                CGTTTT  TGAGAGTCCGCG
                                    TC
GAM264  MGC26655  3'  ATGTCTGAAATTCTATTGCTT  56289       A  C_     TG
                                GAGCAA AG  TTTTAGG  T
                                |||||| ||  ||||||| |
                                TTCGTT TC  AAAGTCT  A
                                    A  TT      GT
GAM264  MGC2705   3'  GGTCTGGAGGCATGTTC     51116      AAA       TG
                                GAGCA   GCTTTTAGG  T
                                |||||   |||||||||  |
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                                CTTGT  CGGAGGTCT  G
                                  A__       GT
GAM264  MGC3101  3' GTGTCTGGGAGCCCCAGCTCA 43884      AAAA       TG
                                TGAGC   GCTTTTAGG  T
                                |||||   |||||||||  |
                                ACTCG   CGAGGGTCT  G
                                  ACCC       GT
GAM264  MGC3207  3' GCACCTAGAGCCAGGCT    62559    AAAA    T
                                AGC   GCTTT AGGTGT
                                |||   ||||| ||||||
                                TCG   CGAGA TCCACG
                                 GAC_    _
GAM264  MGC33182 3' TGATCTGGGATTTTGTTCA   75578        GC      GT
                                TGAGCAAAA  TTTTAGGT
                                |||||||||  ||||||||
                                ACTTGTTTT  AGGGTCTA
                                     __       GTA
GAM264  MGC33182 3' ACATCTAGAAATTGTAGTTCA 75575      AAA  C
                                TGAGC   AG TTTTAGGTGT
                                |||||   || ||||||||||
                                ACTTG   TT AAGATCTACA
                                  ATG  A
GAM264  MGC3329  3' ACATCTGAAGTAGAGCTTGTTT 44008      AA    ____
                                GAGCA  AGCTT    TTAGGTGT
                                |||||  |||||   ||||||||
                                TTTGT  TCGAG    AGTCTACA
                                  __    ATGA
GAM264  MGC35558 3' GATCTGGCATTTTGCTT     58783        _  TTT    GT
                                GAGCAAAA GCT   AGGT
                                |||||||| |||   ||||
                                TTCGTTTT CGG   TCTA
                                    A   ___    GA
GAM264  MGC35558 3' GCACTCTTTTTGCTTTTGTTT  58784         TTTT  _
                                GAGCAAAAGC    AG GTGT
                                ||||||||||    || ||||
                                TTTGTTTTCG    TC CACG
                                     TTTT  T
GAM264  MGC4365  3' GCACCTGAGAGAGGAACTC   44272    CAAAAG
                                GAG     CTTTTAGGTGT
                                |||     ||||||||||
                                CTC     GAGAGTCCACG
                                 AAGGA_
GAM264  MGC4643  3' ACATCTAAAATATGTGCTT   51151      AAAGC
                                GAGCA    TTTTAGGTGT
                                |||||    ||||||||||
                                TTCGT    AAAATCTACA
                                  GTAT_
GAM264  MGC4677  5' CTGTCCTCAGGGCCTTTGCTT  53509       A    T  TGT
                                GAGCAAA GCTTT AGG
                                ||||||| ||||| |||
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                                TTCGTTT CGGGA TCC
                                   C    C  TGTCG
GAM264  MGC4767  3' GCATTTGGTCTGTATCTTTGCT 50286       A__  TT_
          CA                    TGAGCAAA  GC  TTAGGTGT
                                |||||||| ||  ||||||||
                                ACTCGTTT  TG  GGTTTACG
                                    CTA  TCT
GAM264  MGC8721  3' GCATCTAGAAGGTTGTTGT   60358     _ G
                                GCAA AA CTTTTAGGTGT
                                |||| || ||||||||||
                                TGTT TT GAAGATCTACG
                                  G  G
GAM264  MIC2L1   3' ATGCCTGGAAGACCCCTCA   48818     CAAAAG
                                TGAG     CTTTTAGGTGT
                                ||||     ||||||||||
                                ACTC     GAAGGTCCGTA
                                  CCCA__
GAM264  MKP-7    3' GCATTTGAGAGATCAGCT    66419     AAAAG
                                AGC     CTTTTAGGTGT
                                |||     ||||||||||
                                TCG     GAGAGTTTACG
                                 ACTA_
GAM264  MMD      3' GCACTTGGGAGTGGGGT     59807     AAAA
                                GC    GCTTTTAGGTGT
                                ||    ||||||||||||
                                TG    TGAGGGTTCACG
                                 GGG_
GAM264  moblak   3' CGCCTGGGATGGTCA      55495     G  AAAGC
                                TGA CA    TTTTAGGTG
                                ||| ||    |||||||||
                                ACT GT    AGGGTCCGC
                                  G  _____
GAM264  MRAS     3' ACAGGGTCTGGCTTTTGCCA  24225     A       TTTAGG
                                TG GCAAAAGCT     TGT
                                || |||||||||     |||
                                AC CGTTTTCGG     ACA
                                 _       TCTGGG
GAM264  MRP63    3' GATTTGAGGTCTTTGCTTA   43809        AG   T   GT
                                TGAGCAAA  CTTT AGGT
                                ||||||||  |||| ||||
                                ATTCGTTT  GGAG TTTA
                                    CT   _   GT
GAM264  MRPL18   3' GCATCTGGAAGAACAGCCA   26336    A  AAAAG
                                TG GC    CTTTTAGGTGT
                                || ||    ||||||||||
                                AC CG    GAAGGTCTACG
                                 _ ACAA_
GAM264  MRPL20   3' GTGCCCAGCTGGGTTTTTGCT  35739          TTA__  TG
                                AGCAAAAGCTT    GG  T
                                ||||||||||    ||  |
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                                TCGTTTTTGGG    CC  G
                                      TCGAC  GT
GAM264  MRPS10   3' GCAGTTAAAGTTTTTGCT    36294          T  G
                                AGCAAAAGCTTT AG TGT
                                |||||||||||| || |||
                                TCGTTTTTGAAA TT ACG
                                       _  G
GAM264  MRPS10   3' GCATCTGAAAATAAGTGCTT   36295      AAAGC
                                GAGCA    TTTTAGGTGT
                                |||||    ||||||||||
                                TTCGT    AAAGTCTACG
                                   GAATA
GAM264  MRPS11   3' ACACAGTGGCCTTTGCTT    94558       A   TTTAG
                                GAGCAAA GCT    GTGT
                                ||||||| |||    ||||
                                TTCGTTT CGG    CACA
                                    C   TGA__
GAM264  MRPS11   3' ACACAGTGGCCTTTGCTT    43116       A   TTTAG
                                GAGCAAA GCT    GTGT
                                ||||||| |||    ||||
                                TTCGTTT CGG    CACA
                                    C   TGA__
GAM264  MRPS14   3' ACATATAGGGGTTTTTGT    42043          G
                                GCAAAAGCTTTTA GTGT
                                |||||||||||| ||||
                                TGTTTTTGGGGAT TACA
                                       A
GAM264  MRPS33   3' ATACCTAAGTTATTGTTT    53836      A    TT
                                GAGCAA AGCT  TAGGTGT
                                |||||| ||||  |||||||
                                TTTGTT TTGA  ATCCATA
                                   A   __
GAM264  MRPS33   3' ATACCTAAGTTATTGTTT    32164      A    TT
                                GAGCAA AGCT  TAGGTGT
                                |||||| ||||  |||||||
                                TTTGTT TTGA  ATCCATA
                                   A   __
GAM264  MRPS5    3' GCACCTAGGAGAGACTCA    49119     CAAAAG
                                TGAG     CTTTTAGGTGT
                                ||||     ||||||||||
                                ACTC     GAGGATCCACG
                                  AGA___
GAM264  MRPS5    3' TTACCTTGCCTTTTGTTT    49120       CTTTT    T
                                GAGCAAAAG    AGGTG
                                |||||||||    |||||
                                TTTGTTTTC    TCCAT
                                     CGT__    TG
GAM264  MSTP032  3' ATATTTAAGAGCAGCTCA    47439      AAAA
                                TGAGC   GCTTTTAGGTGT
                                |||||   ||||||||||||
```

```
                                ACTCG   CGAGAATTTATA
                                  A___
GAM264  MSTP033  3' ACACTTGACTTCTGCTCA   50780      A  CTT
                                TGAGCA AAG  TTAGGTGT
                                ||||||| |||  ||||||||
                                ACTCGT TTC  AGTTCACA
                                   C  ___
GAM264  MUC13    3' GCGAGAGGGAGCTTGTGCTCA 52330      A      AGG
                                TGAGCA AAGCTTTT  TGT
                                ||||||| ||||||||  |||
                                ACTCGT TTCGAGGG  GCG
                                   G      AGA  T
GAM264  N4BP3    3' ACACCTGAGCTCCTGT     66249    AA    TT
                                GCA  AGCTT  AGGTGT
                                |||  |||||  ||||||
                                TGT  TCGAG  TCCACA
                                  CC    __
GAM264  NAG14    3' TGGAAGCTTTTCTCA      42167     C
                                TGAG AAAAGCTTTTA
                                |||| ||||||||||
                                ACTC TTTTCGAAGGT
                                  _
GAM264  NAP1L1   3' ACACTAAGCATTTTGTTCA  57616        _   TTA
                                TGAGCAAAA GCTT  GGTGT
                                ||||||||| ||||  |||||
                                ACTTGTTTT CGAA  TCACA
                                     A  ___
GAM264  NARF     3' ACACTTAAGAAAACCGCTCA  49239      AAAAGC
                                TGAGC     TTTTAGGTGT
                                |||||     ||||||||||
                                ACTCG     AGAATTCACA
                                   CCAAA_
GAM264  NCBP2    3' ATATCTGAGTTATTGCTCA   23745       A    TT
                                TGAGCAA AGCTT  AGGTGT
                                ||||||| |||||  ||||||
                                ACTCGTT TTGAG  TCTATA
                                    A   __
GAM264  NDUFC2   3' CTTGTCCCAAAAGTTTTTGTTT 15833           A  TGT
                                GAGCAAAAGCTTTT GG
                                |||||||||||||| ||
                                TTTGTTTTTGAAAA CC
                                       C  TGTTCA
GAM264  NEDD5    3' ACACCTAAAACCAGTTTT    15307      ___
                                AAAGCT   TTTAGGTGT
                                ||||||   |||||||||
                                TTTTGA   AAATCCACA
                                   CCA
GAM264  NEDD5    3' ATACTTAAACAGCTTTT     15310       _
                                AAAAGCT TTTAGGTGT
                                ||||||| |||||||||
```

```
                                TTTTCGA AAATTCATA
                                    C
GAM264  NESHBP   5'  ATGCCTAAATATTGATTTGTTT 31250        AGCT__
           A                    TGAGCAAA     TTTAGGTGT
                                ||||||||     |||||||||
                                ATTTGTTT     AAATCCGTA
                                    AGTTAT
GAM264  NETO1    3'  TATTTAACACATTTTGCTCA   57314        GCTT     GT
                                TGAGCAAAA    TTAGGT
                                |||||||||    ||||||
                                ACTCGTTTT    AATTTA
                                     ACAC     TG
GAM264  NFX1     3'  ATACCTAAGTCTTTTGCCA    10214    A      CT
                                TG GCAAAAG  TTTAGGTGT
                                || |||||||  |||||||||
                                AC CGTTTTC  GAATCCATA
                                 _      T_
GAM264  NIBAN    5'  GCGCCTGGAACTATTTTG     42003      GC_
                                CAAAA   TTTTAGGTGT
                                |||||   ||||||||||
                                GTTTT   AAGGTCCGCG
                                   ATC
GAM264  NIBAN    3'  ACACTTAGGGGTTGCATGC    41999     AA_
                                GCA   AGCTTTTAGGTGT
                                |||   ||||||||||||
                                CGT   TTGGGGATTCACA
                                  ACG
GAM264  NIR3     3'  GCACCTGGAAGAGTCTCG     66241      CAAAAG
                                TGAG     CTTTTAGGTGT
                                ||||     ||||||||||
                                GCTC     GAAGGTCCACG
                                  TGA___
GAM264  NLI-IF   5'  GCGCCTGGGTTCCATGTTTGC  41049       AGCT___
                                GCAAA      TTTAGGTGT
                                |||||      |||||||||
                                CGTTT      GGGTCCGCG
                                   GTACCTT
GAM264  NMES1    3'  GCACTGTCTAAAAGTTTGTGCT 50552        A        ___
           TA                     TGAGCA AAGCTTTTAG   GTGT
                                ||||||| ||||||||||   ||||
                                ATTCGT TTTGAAAATC   CACG
                                   G         TGT
GAM264  NMNAT    3'  GTAAGCTAAAATAAGTTTTTGT 42961           ___   GTGT
           TT                     GAGCAAAAGCTT   TTAG
                                ||||||||||||   ||||
                                TTTGTTTTTGAA   AATC
                                       TAA   GAATG
GAM264  NR1H4    5'  ACACTTTGGAGTTTTTTTT    17605     C       TT
                                GAG AAAAGCTT  AGGTGT
                                ||| ||||||||  ||||||
```

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                                TTT TTTTTGAG  TTCACA
                                  _      GT
GAM264  NR6A1   3'  GCAAGAAGAGTTTTTGTTT   7646           AGG
                                GAGCAAAAGCTTTT  TGT
                                |||||||||||||  |||
                                TTTGTTTTTGAGAA  ACG
                                       GA_
GAM264  NR6A1   3'  GCAAGAAGAGTTTTTGTTT   52883          AGG
                                GAGCAAAAGCTTTT  TGT
                                |||||||||||||  |||
                                TTTGTTTTTGAGAA  ACG
                                       GA_
GAM264  NR6A1   3'  GCAAGAAGAGTTTTTGTTT   52871          AGG
                                GAGCAAAAGCTTTT  TGT
                                |||||||||||||  |||
                                TTTGTTTTTGAGAA  ACG
                                       GA_
GAM264  NSG-X   3'  ACGCCTGGAAGTAGCT     26969    AAAA
                                AGC   GCTTTTAGGTGT
                                |||   ||||||||||||
                                TCG   TGAAGGTCCGCA
                                  A___
GAM264  NUDT11  3'  GCACCTATAGCCTTTTGTT   59995       _ TT
                                AGCAAAAG CT  TAGGTGT
                                |||||||| ||  |||||||
                                TTGTTTTC GA  ATCCACG
                                     C  T_
GAM264  NUP54   3'  GCATTTAATGTTTTGTTTTTGT 60099        TT____
          TC                      GAGCAAAAGC     TTAGGTGT
                                |||||||||      ||||||||
                                CTTGTTTTTG     AATTTACG
                                      TTTTGT
GAM264  NXPH3   3'  CTAGGGCTTTGCTTA      65758        A    T
                                TGAGCAAA GCTTT AG
                                |||||||| ||||| ||
                                ATTCGTTT CGGGA TC
                                     _    _
GAM264  NXPH3   3'  GCACCTGGAGGCTGCCTC   65761    CAAA
                                GAG   AGCTTTTAGGTGT
                                |||   ||||||||||||
                                CTC   TCGGAGGTCCACG
                                  CG__
GAM264  OAZ2    3'  GCATTTGGTTAAGCTGGCTTA 10306     AAA   __
                                TGAGC  AGCTT  TTAGGTGT
                                |||||  |||||  ||||||||
                                ATTCG  TCGAA  GGTTTACG
                                   G__    TT
GAM264  OAZ2    3'  GTGTCTGAGACTCTGCTC   10311     AA  C     TG
                                GAGCA  AG TTTTAGG  T
                                |||||  || |||||||  |
```

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                                CTCGT  TC AGAGTCT  G
                                  C_ _      GT
GAM264  OCLM     3'  ACATTTAGAAGTTAATGTT   42346     AA
                                AGCA  AGCTTTTAGGTGT
                                ||||  ||||||||||||
                                TTGT  TTGAAGATTTACA
                                  AA
GAM264  OR2C3    3'  GCGTTGTTGGTTTTTGCT    75446         TT  _
                                AGCAAAAGCT  TAG GT
                                ||||||||||  ||| ||
                                TCGTTTTTGG  GTT CG
                                     TT  G
GAM264  OR7C1    3'  ATACTTCTGTTTTTGCTT    33994         TTTT
                                GAGCAAAAGC   AGGTGT
                                ||||||||||   ||||||
                                TTCGTTTTTG   TTCATA
                                     TC__
GAM264  ORC6L    3'  ACGGCTTTGGGATTTTGTTTA  26719        G  TT  G
                                TGAGCAAAA CTT  AG TGT
                                ||||||||| |||  || |||
                                ATTTGTTTT GGG  TC GCA
                                     A  TT  G
GAM264  OSBPL11  3'  GTGCCTGAAATCAGTGTTTA  42893       AAAGC     TG
                                TGAGCA    TTTTAGG  T
                                ||||||    |||||||  |
                                ATTTGT    AAAGTCC  G
                                   GACT_     GT
GAM264  OSBPL5   3'  ACGCCTGAGTCCTGCCCA    72682    A  AAA CT
                                TG GCA  G  TTTAGGTGT
                                || |||  |  |||||||||
                                AC CGT  C  GAGTCCGCA
                                 C  ___ CT
GAM264  P114-RHO-GEF 3'  GCACCTAGAGACGTTGC     31022     AAG   T
                                GCAA  CTTT AGGTGT
                                ||||  |||| ||||||
                                CGTT  GAGA TCCACG
                                  GCA  _
GAM264  p25      3'  GCCCTCAGGCTTTTCTCA    22852     C      TT  T
                                TGAG AAAAGCTT  AGG GT
                                |||| ||||||||  ||| ||
                                ACTC TTTTCGGA  TCC CG
                                  _      C_  _
GAM264  P450RAI-2 3'  ATATTTAGTATAAAGTTTTTGC 39098          ____
           T                     AGCAAAAGCTTT   TAGGTGT
                                 ||||||||||||   |||||||
                                 TCGTTTTTGAAA   ATTTATA
                                        TATG
GAM264  P5-1     3'  ACATTTAGAGGTGGCAGTGT  21912     AAA__
                                GCA    GCTTTTAGGTGT
                                |||    ||||||||||||
```

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                                TGT    TGGAGATTTACA
                                  GACGG
GAM264  PAK6    5'  GCGCCTAAGAGAGAGGCCCA  39407    A  AAAAG
                                TG GC    CTTTTAGGTGT
                                || ||    ||||||||||
                                AC CG    GAGAATCCGCG
                                 C  GAGA_
GAM264  PAPOLG  3'  GCATTTGGGGGTTTTACTGC  43172     __
                                GCA  AAAGCTTTTAGGTGT
                                |||  ||||||||||||||
                                CGT  TTTTGGGGGTTTACG
                                  CA
GAM264  PARVA   3'  ACATTTGGGAAGGATTTTGTTT 36650         G_    _
          A                      TGAGCAAAA  CTTTT AGGTGT
                                |||||||||  ||||| ||||||
                                ATTTGTTTT  GAAGG TTTACA
                                      AG    G
GAM264  PAXIP1L 3'  ACACCTGGAATCTGCCCA    70124    A   AAA C
                                TG GCA   G TTTTAGGTGT
                                || |||   | ||||||||||
                                AC CGT   C AAGGTCCACA
                                 C   ___ T
GAM264  PB1     3'  TTAGAGGTTTTTGTCTT     36372     _
                                GAG CAAAAGCTTTTAG
                                ||| ||||||||||||
                                TTC GTTTTTGGAGATT
                                  T
GAM264  PB1     3'  ACATTTGAAGGCAGC       36366    AAAA
                                GC    GCTTTTAGGTGT
                                ||    ||||||||||||
                                CG    CGGAAGTTTACA
                                 A___
GAM264  PCANAP7 5'  ATATTGTAGCTTTGCTTA    93362        A   TTTA
                                TGAGCAAA GCT    GGTGT
                                |||||||| |||    |||||
                                ATTCGTTT CGA    TTATA
                                      _   TG__
GAM264  PDE11A  3'  ACATCTAGAAACTATAGTTCA 33774      AAA  C
                                TGAGC   AG TTTTAGGTGT
                                |||||   || ||||||||||
                                ACTTG   TC AAGATCTACA
                                   ATA  A
GAM264  PDE3A   3'  ACATTGTTAAAAACTTTTTGCT 6225          _ C     __
          CA                      TGAGCAAAA G TTTTAG  GTGT
                                |||||||||  | ||||||  ||||
                                ACTCGTTTT C AAAATT  TACA
                                      T A     GT
GAM264  PDE3A   3'  ACACCTAAGAGCTGAAGTCA  6224     G AAA
                                TGA C   AGCTTTTAGGTGT
                                ||| |   ||||||||||||
```

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                                ACT G   TCGAGAATCCACA
                                  _ AAG
GAM264  PDZD2    3'  ACTTAAGTTTTTGCT      80857         TT
                                AGCAAAAGCT  TAGGT
                                ||||||||||  |||||
                                TCGTTTTTGA  ATTCA
                                        __
GAM264  phorbolin-1 3'  TAATTGCTTTTGCTCA     88783          TT
                                TGAGCAAAAGC  TTA
                                ||||||||||||  |||
                                ACTCGTTTTCG  AAT
                                       TT
GAM264  PILR(BETA) 5'  GCACCTAAGGCCCTTTTG    25554       C_
                                CAAAAG  TTTTAGGTGT
                                ||||||  ||||||||||
                                GTTTTC  GGAATCCACG
                                    CC
GAM264  PIP3-E   3'  TTAGCCTAGAAGTTTTTGCTT  66819              GT
                                GAGCAAAAGCTTTTAGGT
                                ||||||||||||||||||
                                TTCGTTTTTGAAGATCCG
                                          ATTA
GAM264  PIP5K2B  3'  GCGCCTGGAGTGCTTTTTA   13074   C     _
                                G AAAAGC TTTTAGGTGT
                                | ||||||  ||||||||||
                                A TTTTCG GAGGTCCGCG
                                 T     T
GAM264  PL6      3'  ACATCTGAAACTGGTTGC    22830      A_  C
                                GCAA  AG TTTTAGGTGT
                                ||||  ||  ||||||||||
                                CGTT  TC AAAGTCTACA
                                  GG  _
GAM264  PLA2G3   3'  ATGCCTGGATGTGGTGTTCA   31684       AAA  T
                                TGAGCA   GC TTTAGGTGT
                                ||||||   ||  |||||||||
                                ACTTGT   TG AGGTCCGTA
                                    GG_  T
GAM264  PLAC3    5'  TATTTGAGAGACTTGGCTCA   69347      AA   _       GT
                                TGAGC  AAG CTTTTAGGT
                                |||||  |||  |||||||||
                                ACTCG  TTC GAGAGTTTA
                                   G_   A        TG
GAM264  PLSCR4   3'  ATATTTGAAAGTGCCATTGC   39784      AA__
                                GCAA    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                CGTT    TGAAAGTTTATA
                                  ACCG
GAM264  PLU-1    3'  ACCAGACTTTTGCTTA      21754          _  TTTA
                                TGAGCAAAAG CT    GGT
                                ||||||||||  ||    |||
```

```
                                ATTCGTTTTC GA    CCA
                                     A  ____
GAM264  PLU-1    3'  TTTCACTTTGGGAGTTTTTGTT 21760              _  T
              T                   GAGCAAAAGCTTTTAG GTG
                                  ||||||||||||||| |||
                                  TTTGTTTTTGAGGGTT CAC
                                        T   TTTT
GAM264  PLU-1    3'  TTTCACTTTGGGAGTTTTTGTT 87418              _  T
              T                   GAGCAAAAGCTTTTAG GTG
                                  ||||||||||||||| |||
                                  TTTGTTTTTGAGGGTT CAC
                                        T   TTTT
GAM264  PLU-1    3'  ACCAGACTTTTGCTTA      87414          _  TTTA
                                  TGAGCAAAAG CT    GGT
                                  |||||||||| ||    |||
                                  ATTCGTTTTC GA    CCA
                                     A  ____
GAM264  POFUT1   3'  GCATTCAGCAGGTGTTTGTTCA 70469         A   _  AG
                                  TGAGCAAA GCTT TT  GTGT
                                  |||||||| |||| ||  ||||
                                  ACTTGTTT TGGA GA  TACG
                                       G    C  CT
GAM264  POFUT1   3'  ACACTTAAAACTTTTTGTT    70463         C
                                  AGCAAAAG TTTTAGGTGT
                                  |||||||| ||||||||||
                                  TTGTTTTT AAAATTCACA
                                       C
GAM264  POLE3    3'  CTGGGGCTTTGCTTA       33855         A     T
                                  TGAGCAAA GCTTT AG
                                  |||||||| ||||| ||
                                  ATTCGTTT CGGGG TC
                                        _    _
GAM264  POLM     3'  GCATTTGAGAGCCATGAGCT   91090      AAAA_
                                  AGC     GCTTTTAGGTGT
                                  |||     ||||||||||||
                                  TCG     CGAGAGTTTACG
                                    AGTAC
GAM264  POLR2D   3'  ACACTTGGGGGACAAGTGCT   16653      AAAG_
                                  AGCA     CTTTTAGGTGT
                                  ||||     ||||||||||||
                                  TCGT     GGGGGTTCACA
                                     GAACA
GAM264  POLR3K   3'  ATGTCTGGGAGTTTTTCT    32846    C          TG
                                  AG AAAAGCTTTTAGG  T
                                  || ||||||||||||  |
                                  TC TTTTTGAGGGTCT  A
                                    _          GT
GAM264  PP1201   3'  ATGCCTGGGGGTCCCTCA     42187      CAAAA
                                  TGAG     GCTTTTAGGTGT
                                  ||||     ||||||||||||
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                                ACTC    TGGGGGTCCGTA
                                  CC___
GAM264  PP1665   5' GCGCCTGAGGGCCAGGC    47916    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   CGGGAGTCCGCG
                                 GAC_
GAM264  PP3111   5' TGACCCGGAGGTGTTTGTTCA 42204        A    TA  GT
                                TGAGCAAA GCTTT  GGT
                                |||||||| |||||  |||
                                ACTTGTTT TGGAG  CCA
                                     G    GC   GTA
GAM264  PPFIA4   3' GGCCTGAAAATGTTCA     70327      AAAGC     TG
                                TGAGCA    TTTTAGG  T
                                ||||||    |||||||  |
                                ACTTGT    AAAGTCC  G
                                   A____      GT
GAM264  PPFIA4   3' CACCTGGGCAGTGCCA     70320    A  AAA  TT
                                TG GCA   GCT  TAGGTG
                                || |||   |||  ||||||
                                AC CGT   CGG  GTCCAC
                                 _  GA_  __
GAM264  PPP1R14C 3' GTTTTAAAGGTTTTTGTT    48203            TGT
                                AGCAAAAGCTTTTAGG
                                ||||||||||||||||
                                TTGTTTTTGGAAATTT
                                          TG
GAM264  PPP1R16B 3' GTGTCTAGAAGACTGTTC    61388      AAAG      TG
                                GAGCA    CTTTTAGG  T
                                |||||    ||||||||  |
                                CTTGT    GAAGATCT  G
                                   CA__       GT
GAM264  PPP1R16B 3' ATGCCTGGGGAGGGGCTC    61379     AAAAG   T
                                GAGC    CTTT AGGTGT
                                ||||    |||| ||||||
                                CTCG    GGGG TCCGTA
                                  GGGA_   _
GAM264  PPY2     3' GCACCTGGGCACAGTGCTT   40822      AAA_  TT
                                GAGCA   GCT  TAGGTGT
                                |||||   |||  |||||||
                                TTCGT   CGG  GTCCACG
                                   GACA  __
GAM264  PRDM13   3' ATACAAACGAGAGTTTTGTTCA 41238         G    AG__
                                TGAGCAAAA CTTTT   GTGT
                                ||||||||| |||||   ||||
                                ACTTGTTTT GAGAG   CATA
                                     _    CAAA
GAM264  PRO0245  5' ACATTTGAGGGCCCAAGCT   26122    AAAA
                                AGC   GCTTTTAGGTGT
                                |||   ||||||||||||
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                                TCG   CGGGAGTTTACA
                                  AACC
GAM264  PRO0245  5' ACACTTAAAAATTGTTGCTC  26121      AAGC
                                GAGCAA   TTTTAGGTGT
                                ||||||   ||||||||||
                                CTCGTT   AAAATTCACA
                                   GTTA
GAM264  PRO0529  5' TGCCTGAGGGCATTGC     26002     AA
                                GCAA  GCTTTTAGGTG
                                ||||  ||||||||||
                                CGTT  CGGGAGTCCGT
                                  A_
GAM264  PRO0800  3' ACATTGCTTTGGCTTTTGT   37738       TTTA_
                                GCAAAAGCT    GGTGT
                                |||||||||    |||||
                                TGTTTTCGG    TTACA
                                     TTTCG
GAM264  PRO1048  3' ATATCTGAGAGCACTGC     37509     AAA
                                GCA   GCTTTTAGGTGT
                                |||   ||||||||||||
                                CGT   CGAGAGTCTATA
                                  CA_
GAM264  PRO1048  3' TGGGGGCTTTGCTCA       37526       A
                                TGAGCAAA GCTTTTA
                                |||||||| |||||||
                                ACTCGTTT CGGGGGT
                                        _
GAM264  PRO1855  3' ATGCCTAAAGGAGTAGGCTT  37545     AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                TTCG    GGAAATCCGTA
                                  GATGA
GAM264  PRO2015  3' GCATCTGGAAGTGAGGGT    37560    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                TG   TGAAGGTCTACG
                                 GGAG
GAM264  PRO2325  3' GCACCTGGAAGGAGCTT     96303     AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                TTCG    GAAGGTCCACG
                                  AG___
GAM264  PRO2730  5' ACATTTGGGGGTTATGCCA   47408    A   AA
                                TG GCA  AGCTTTTAGGTGT
                                || |||  ||||||||||||
                                AC CGT  TTGGGGGTTTACA
                                 _  A_
GAM264  PRO2893  3' ATGCCTGAAGGTTTTAAAAGTT 37802      A___
           CA                     TGAGC   AAAGCTTTTAGGTGT
                                |||||   ||||||||||||||
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                                ACTTG   TTTTGGAAGTCCGTA
                                  AAAA
GAM264  PRO2958  3' ATACCTGAAAATTATTGCT   37652     A  C
                                AGCAA AG TTTTAGGTGT
                                |||||| || ||||||||||
                                TCGTT TT AAAGTCCATA
                                  A  A
GAM264  PSR      3' GCACTTGGAAGCACTGC    65181    AAA
                                GCA  GCTTTTAGGTGT
                                |||  ||||||||||||
                                CGT  CGAAGGTTCACG
                                 CA_
GAM264  PSR      3' ATATCTGAGTGGTGTTGCT  65174     AA  _
                                AGCAA  GCT TTTAGGTGT
                                |||||  ||| |||||||||
                                TCGTT  TGG GAGTCTATA
                                  G_  T
GAM264  PTPNS1   3' ATACCTGGAGGCTGACGTT  54994    AAA
                                AGC  AGCTTTTAGGTGT
                                |||  ||||||||||||
                                TTG  TCGGAGGTCCATA
                                 CAG
GAM264  PXR2b    3' ACATCTGAGGAACTTGTTCA  33335      AAG   T
                                TGAGCAA  CTTT AGGTGT
                                |||||||  |||| ||||||
                                ACTTGTT  GGAG TCTACA
                                   CAA  _
GAM264  RA-GEF-2 3' TATTTGAGAGCTCTTGTT   32956     A       GT
                                AGCAA AGCTTTTAGGT
                                ||||| ||||||||||
                                TTGTT TCGAGAGTTTA
                                  C         TG
GAM264  RAB21    3' ATTTGCCTTTTGGGTTTTTTGT 30382       _  TT_   T
          TT                    GAGCAAAAG CTT  AGGTG
                                ||||||||| |||  |||||
                                TTTGTTTTT GGG  TCCGT
                                     T  TTT   TTAC
GAM264  RAB32    3' ACAATTAGGCTTTTGTCA   22416    G      TTAGG
                                TGA CAAAAGCTT   TGT
                                ||| |||||||||   |||
                                ACT GTTTTCGGA   ACA
                                 _       TTA__
GAM264  RAB34    3' GTGTCTCTGTTCTTTTGCTCA 49195       CTTTT  TG
                                TGAGCAAAAG   AGG  T
                                ||||||||||   |||  |
                                ACTCGTTTTC   TCT  G
                                     TTGTC  GT
GAM264  Rabip4R  5' GCGCCTGGAAGGAGCTGCT  35791    AAAG
                                AGCA   CTTTTAGGTGT
                                ||||   ||||||||||
```

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                              TCGT   GAAGGTCCGCG
                                CGAG
GAM264  RACGAP1  3' GCATTCTCCAGGCTTTTACTCA 25198     C      TT  _
                              TGAG AAAAGCTT  AGG TGT
                              |||| ||||||||  ||| |||
                              ACTC TTTTCGGA  TCT ACG
                                A       CC   T
GAM264  RAGA     3' GTGCTTAAAAGTGGGCTT    21645     AAAA       TG
                              GAGC   GCTTTTAGG  T
                              ||||   |||||||||  |
                              TTCG   TGAAAATTC  G
                                GG__       GT
GAM264  RAI17    3' GCACCTGAGGCGGGTTT     91282     AAAA    T
                              GAGC   GCTTT AGGTGT
                              ||||   ||||| ||||||
                              TTTG   CGGAG TCCACG
                                GG__    _
GAM264  RALGPS1A 3' GCATCTAGAGGCTGAATG    27604    AA_
                              CA  AGCTTTTAGGTGT
                              ||  ||||||||||||
                              GT  TCGGAGATCTACG
                               AAG
GAM264  RALGPS1A 3' GCATTTCTAGTTTTTGCTC   27605         TTT
                              GAGCAAAAGCT   AGGTGT
                              ||||||||||   ||||||
                              CTCGTTTTTGA   TTTACG
                                    TC_
GAM264  RASGRP4  3' GCACCTGGGCTGGCTGC     53653    AA_   TT
                              GCA   AGCT  TAGGTGT
                              |||   ||||  |||||||
                              CGT   TCGG  GTCCACG
                                CGG   __
GAM264  RASGRP4  3' GCGCCTGACAGATGCTT     53655     AAAG  T
                              GAGCA   CT TTAGGTGT
                              |||||   || ||||||||
                              TTCGT   GA AGTCCGCG
                                A___  C
GAM264  RASSF2   5' GCGCCTAGAACGTGTTTTTC  28435    C  A  _
                              GAG AAA GC TTTTAGGTGT
                              ||| ||| || ||||||||||
                              CTT TTT TG AAGATCCGCG
                                _  G  C
GAM264  RBSK     3' TACTTGGGGGTGGCTGCTC   42104     AAA       GT
                              GAGCA  GCTTTTAGGT
                              |||||  ||||||||||
                              CTCGT  TGGGGGTTCA
                                CGG       TG
GAM264  RENT2    3' ACCAGGAAGGCTTTTGTTTA  54588           A_  GT
                              TGAGCAAAAGCTTTT  GGT
                              ||||||||||||||  |||
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                                ATTTGTTTTCGGAAG  CCA
                                       GA
GAM264  RENT2    3'  ACCAGGAAGGCTTTTGTTTA  31417            A_  GT
                                TGAGCAAAAGCTTTT  GGT
                                |||||||||||||||  |||
                                ATTTGTTTTCGGAAG  CCA
                                       GA
GAM264  REPRIMO  3'  TGTGCCGTTTTAAGAGGTTTTG 39056       G     _____ TG
          T                     GCAAAA CTTTTA    GG  T   G
                                ||||||  ||||||    ||  |   |
                                TGTTTT GAGAAT    CC  G   T
                                   G     TTTG  GT
GAM264  RES4-22  5'  GCGTCTGGAACAGCAAGCTC   13518     AAAA  __    GT
                                GAGC    GCT  TTTAG  GT
                                ||||    |||  |||||  ||
                                CTCG    CGA  AGGTC  CG
                                  AA__   CA    TG
GAM264  RFX4     3'  GCAGGAGAGGGTTTTTGTTT   50663           AGG
                                GAGCAAAAGCTTTT   TGT
                                ||||||||||||||   |||
                                TTTGTTTTTGGGAG   ACG
                                       AGG
GAM264  RIP60    3'  ACACCTGGCCTCTGCTT     25453      AAA   TTT
                                GAGCA   GCT   AGGTGT
                                |||||   |||   ||||||
                                TTCGT   CGG   TCCACA
                                  CTC   ___
GAM264  RNAH     3'  ATATTTAGGAGCTATCAATCA  61959     GCAAA
                                TGA     AGCTTTTAGGTGT
                                |||     ||||||||||||
                                ACT     TCGAGGATTTATA
                                  AACTA
GAM264  RNF2     3'  GTGACTATAAGCTTTGTGCTTA 23298       _      T   GTGT
                                TGAGCA AAAGCTT TAG
                                |||||| ||||||| |||
                                ATTCGT TTTCGAA ATC
                                   G      T   AGTG
GAM264  RNF8     3'  GCATTTGAAAGACTGCCA    14226    A   AAAG
                                TG GCA    CTTTTAGGTGT
                                || |||    ||||||||||
                                AC CGT    GAAAGTTTACG
                                 _   CA__
GAM264  RNF9     3'  ATATCTGAAAGAGCTC      53409      AAAAG
                                GAGC     CTTTTAGGTGT
                                ||||     ||||||||||
                                CTCG     GAAAGTCTATA
                                  A____
GAM264  RODH-4   5'  ATGCCTGAGGGCTTCCCTGC   13529     A__
                                GCA   AAGCTTTTAGGTGT
                                |||   ||||||||||||||
```

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                                CGT   TTCGGGAGTCCGTA
                                  CCC
GAM264   RPH3A    3'  GCATTTAGAAGACCAGGGCCA  30244     A  AAAAG_
                                TG GC     CTTTTAGGTGT
                                || ||     ||||||||||
                                AC CG     GAAGATTTACG
                                 _ GGACCA
GAM264   RPL39L   3'  ATATGTGAAAGCTTTTGTTT   53732            G
                                GAGCAAAAGCTTTTA GTGT
                                |||||||||||||| ||||
                                TTTGTTTTCGAAAGT TATA
                                         G
GAM264   RPP14    3'  GCCTGGGTTTTTTGTTT     59501         CT
                                GAGCAAAAG  TTTAGGT
                                |||||||||  |||||||
                                TTTGTTTTT  GGGTCCG
                                     T_
GAM264   RRN3     3'  GCATCTGAAGACTGGGTTT   37357      AAA  CT
                                GAGC   AG  TTTAGGTGT
                                ||||   ||  |||||||||
                                TTTG   TC  AAGTCTACG
                                  GG_  AG
GAM264   RRN3     3'  ACATTTGGAAGGATTTGCTT   37351        AG
                                GAGCAAA  CTTTTAGGTGT
                                |||||||  ||||||||||
                                TTCGTTT  GAAGGTTTACA
                                    AG
GAM264   RYK      3'  AGCAGTTGGAGGCTTTTGCT   82613            G
                                AGCAAAAGCTTTTAG TGT
                                |||||||||||||| |||
                                TCGTTTTCGGAGGTT ACG
                                         G   AT
GAM264   RYK      5'  ATACCTGAAAGATGGTT     82615     AAAAG
                                AGC    CTTTTAGGTGT
                                |||    ||||||||||
                                TTG    GAAAGTCCATA
                                  GTA__
GAM264   RYK      3'  GCACCTAGAATAGTGCT     82621      AAAGC
                                AGCA    TTTTAGGTGT
                                ||||    ||||||||||
                                TCGT    AAGATCCACG
                                  GAT__
GAM264   SAD1     3'  GCGTCTAGGGCTTTGCTC    64022        A    T  GT
                                GAGCAAA GCTTT AG  GT
                                ||||||| ||||| ||  ||
                                CTCGTTT CGGGA TC  CG
                                    _    _ TG
GAM264   SART3    3'  ACATTTGCTGGAGTTTTGTTCA 28170         G_  TT
                                TGAGCAAAA  CT  TAGGTGT
                                |||||||||  ||  |||||||
```

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                                ACTTGTTTT GG GTTTACA
                                    GA TC
GAM264 SB52    3' GTGCCTAAAAGTACAGTTTA 56362     AAAA      TG
                                TGAGC  GCTTTTAGG T
                                |||||  ||||||||| |
                                ATTTG  TGAAAATCC G
                                   ACA_      GT
GAM264 SCDGF-B 3' CAACCTAAAAGCTTTTGT   52447          GT
                                GCAAAAGCTTTTAGGT
                                ||||||||||||||||
                                TGTTTTCGAAAATCCA
                                         ACA
GAM264 SCDGF-B 3' CAACCTAAAAGCTTTTGT   47375          GT
                                GCAAAAGCTTTTAGGT
                                ||||||||||||||||
                                TGTTTTCGAAAATCCA
                                         ACA
GAM264 SCDGF-B 3' GTGTCTGATGTTTTTACTCA 47380    C    TT   TG
                                TGAG AAAAGC TTAGG T
                                |||| ||||||  ||||| |
                                ACTC TTTTTG AGTCT G
                                  A    T_   GT
GAM264 SCDGF-B 3' GTGTCTGATGTTTTTACTCA 52452    C    TT   TG
                                TGAG AAAAGC TTAGG T
                                |||| ||||||  ||||| |
                                ACTC TTTTTG AGTCT G
                                  A    T_   GT
GAM264 SCIN    3' ACGGGAAAAGCTTTTTGCTTA 52422       _    AGGTGT
                                TGAGCAAAA GCTTTT
                                ||||||||| ||||||
                                ATTCGTTTT CGAAAA
                                     T    GGGCA
GAM264 SCYA3   3' TATCGGATGCTTTTGTTCA  59847       TTTTA  GT
                                TGAGCAAAAGC   GGT
                                ||||||||||    |||
                                ACTTGTTTTCG   CTA
                                      TAGG_  TG
GAM264 SDC3    3' GCATTTGAGAGAAGAGGCCA 27754   A AAAAG
                                TG GC   CTTTTAGGTGT
                                || ||   ||||||||||
                                AC CG   GAGAGTTTACG
                                 _ GAGAA
GAM264 SDF1    3' GCACTTGTGGGTTTTTGTTT 90857       TT
                                GAGCAAAAGCT TAGGTGT
                                ||||||||||| |||||||
                                TTTGTTTTTGG GTTCACG
                                      GT
GAM264 SDF1    3' CCTATGTTTTTGTTCA    90856       TTT
                                TGAGCAAAAGC  TAGG
                                ||||||||||  ||||
```

```
                                ACTTGTTTTTG  ATCC
                                      T__
GAM264  SEC14L1  3'  TACCTGAAGCCTTTGCTT   11518       A   T   GT
                                GAGCAAA GCTTT AGGT
                                ||||||| ||||| ||||
                                TTCGTTT CGAAG TCCA
                                    C   _   TG
GAM264  SEEK1    5'  GCATCTAGAAGTAGACGATCA  25952    GCAAAA
                                TGA    GCTTTTAGGTGT
                                |||    ||||||||||||
                                ACT    TGAAGATCTACG
                                  AGCAGA
GAM264  SEF      3'  GTGTCTGGAAGTTTATTCTTA  69467    CAA        TG
                                TGAG  AAGCTTTTAGG  T
                                ||||  |||||||||||  |
                                ATTC  TTTGAAGGTCT  G
                                  TTA        GT
GAM264  SEMA3E   3'  ACATTTAAGTTAAAGTGCTCA  24877      AAAGCT
                                TGAGCA    TTTAGGTGT
                                ||||||    |||||||||
                                ACTCGT    GAATTTACA
                                   GAAATT
GAM264  SEMA4G   5'  ACACCTGGGGCACAGCT    94668    AAAA   T
                                AGC   GCTTT AGGTGT
                                |||   ||||| ||||||
                                TCG   CGGGG TCCACA
                                  ACA_   _
GAM264  SEMA5A   3'  GCATTTAAGAGTGTGCT    14257    AAA
                                AGCA  GCTTTTAGGTGT
                                ||||  ||||||||||||
                                TCGT  TGAGAATTTACG
                                  G__
GAM264  SES2     3'  GCACCAGGGTTCTTGTTT    48811      A    TA
                                GAGCAA AGCTTT  GGTGT
                                |||||| ||||||  |||||
                                TTTGTT TTGGGA  CCACG
                                   C    __
GAM264  SETMAR   3'  ATACCTAAACCCTGCTTGC   73659    A_  CT
                                GCAA  AG  TTTAGGTGT
                                ||||  ||  |||||||||
                                CGTT  TC  AAATCCATA
                                  CG  CC
GAM264  SFRS5    3'  ACACTTAAAAGAGCTC     22642    AAAAG
                                GAGC   CTTTTAGGTGT
                                ||||   ||||||||||
                                CTCG   GAAAATTCACA
                                  A____
GAM264  SIAT4A   3'  GTGCCTAGGAGTTCGAGGCT  11674    AAA_       TG
                                AGC   AGCTTTTAGG  T
                                |||   ||||||||||  |
```

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                                TCG   TTGAGGATCC  G
                                  GAGC        GT
GAM264  SLC19A3  3'  GCCAAGGTGGGAGTTTTGCTT  47489       G    _____  GT
                                GAGCAAAA CTTTTA   GGT
                                |||||||| ||||||   |||
                                TTCGTTTT GAGGGT   CCG
                                     _    GGAA
GAM264  SLC2A12  3'  ACACTTAGGAGGGTGTCTT   59077    _ AAAG
                                GAG CA   CTTTTAGGTGT
                                ||| ||   ||||||||||
                                TTC GT   GAGGATTCACA
                                  T  GG__
GAM264  SLC2A13  3'  ATATCAGGGTCAGTTTTTGTTC 53546          __  TA
            A                    TGAGCAAAAGCT  TT  GGTGT
                                ||||||||||||  ||  |||||
                                ACTTGTTTTTGA  GG  CTATA
                                       CT  GA
GAM264  SLC37A1  3'  ACACCTGGGACTGTTTTT   38558      __
                                AAAAGC  TTTTAGGTGT
                                ||||||  ||||||||||
                                TTTTTG  AGGGTCCACA
                                   TC
GAM264  SLC6A14  3'  ACATTTGAAAGAAAGTGTT   23344     AAAG
                                AGCA   CTTTTAGGTGT
                                ||||   ||||||||||
                                TTGT   GAAAGTTTACA
                                  GAAA
GAM264  SLC6A14  3'  TAGTTAAAAGTTTTTGTCA   23359    G         G GT
                                TGA CAAAAGCTTTTAG T
                                ||| |||||||||||| |
                                ACT GTTTTTGAAAATT A
                                  _          G TG
GAM264  SMOC2    3'  GCGTAAGGCTTCTTGCTTA   72375      _     T G
                                TGAGCAA AAGCTTT A GT
                                ||||||| ||||||| | ||
                                ATTCGTT TTCGGAA T CG
                                     C      _ G
GAM264  SNAP29   3'  GCAGAGCAGCTTTTGTGCA   16544    A       T  AG
                                TG GCAAAAGCT TT  GT
                                || |||||||| ||  ||
                                AC TGTTTTCGA GA  CG
                                  G       C  GA
GAM264  SNAP29   3'  ATGCTTATTAGAGTTTTTGT   16537         __
                                GCAAAAGCTTT  TAGGTGT
                                ||||||||||  |||||||
                                TGTTTTTGAGA  ATTCGTA
                                       TT
GAM264  SNAPC4   3'  ACACTTGGAGGAATAAAGTTC  11848     AAAAG_
                                GAGC     CTTTTAGGTGT
                                ||||     ||||||||||
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                                CTTG     GGAGGTTCACA
                                  AAATAA
GAM264  SNFT     3'  ATACCTGGGAGGAAGGCTT   37897      AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                TTCG    GAGGGTCCATA
                                  GAAG_
GAM264  SNRPD3   3'  ATATCTAGGTATCTTTTGCCA  14799    A      CT_
                                TG GCAAAAG   TTTAGGTGT
                                || |||||||  |||||||||
                                AC CGTTTTC   GGATCTATA
                                 _      TAT
GAM264  SNTG1    5'  ACATCTAATTTCATTGCTCG   38572       AAGCTT
                                TGAGCAA     TTAGGTGT
                                |||||||     ||||||||
                                GCTCGTT     AATCTACA
                                    ACTTT_
GAM264  SNX10    3'  GCATTTAAGAGCGATCCTCA   25264      CAAAA
                                TGAG    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                ACTC    CGAGAATTTACG
                                  CTAG_
GAM264  SOX17    3'  ACTCCTGGGTTTTTGTT     42396         TT   T
                                AGCAAAAGCT  TAGG GT
                                ||||||||||  |||| ||
                                TTGTTTTTGG  GTCC CA
                                      __    T
GAM264  SPHAR    5'  ATGCCTACTGCTTTTGTT    21556         TTT
                                AGCAAAAGC   TAGGTGT
                                |||||||||   |||||||
                                TTGTTTTCG   ATCCGTA
                                     TC_
GAM264  Spir-1   3'  GCACCTAGGAGAATGTGCTT   64701      AAAG
                                GAGCA   CTTTTAGGTGT
                                |||||   ||||||||||
                                TTCGT   GAGGATCCACG
                                  GTAA
GAM264  SPRY2    3'  ACACTCCTAGGCAAAGTTTTTG 19555           ___   T
           TTT                    GAGCAAAAGCTTT   TAGG GT
                                ||||||||||||   |||| ||
                                TTTGTTTTTGAAA   ATCC CA
                                       CGG   T  CA
GAM264  SQRDL    5'  GCACGAGGAAGGTTTTTGCT   41055          AG_
                                AGCAAAAGCTTTT   GTGT
                                ||||||||||||   ||||
                                TCGTTTTTGGAAG   CACG
                                       GAG
GAM264  SRP54    3'  TACTTAAAGGTTTTTAATTA   11961     GC          GT
                                TGA  AAAAGCTTTTAGGT
                                |||  ||||||||||||||
```

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                                ATT  TTTTTGGAAATTCA
                                  AA           TG
GAM264  SRP9    3' ATATCTGAAAGTAATTGT    79189      AA
                                GCAA  GCTTTTAGGTGT
                                ||||  ||||||||||||
                                TGTT  TGAAAGTCTATA
                                  AA
GAM264  SSR1    3' CTTTTGGGAGTTTTGCTT    11981        G       TGT
                                GAGCAAAA CTTTTAGG
                                |||||||| ||||||||
                                TTCGTTTT GAGGGTTT
                                     _       TCT
GAM264  STAG1    5' GCACTTGATTATTTTGCTGCA  19612    _      GCTT
                                TG AGCAAAA    TTAGGTGT
                                || |||||||    ||||||||
                                AC TCGTTTT    AGTTCACG
                                 G      ATT_
GAM264  STAG3    5' ACGCCTGAGAGCTTGAGGCCA  24909    A  AA_
                                TG GC   AAGCTTTTAGGTGT
                                || ||   ||||||||||||||
                                AC CG   TTCGAGAGTCCGCA
                                 _ GAG
GAM264  STAM2    3' TATTTGAAAGCTCAGTTTA    19567      AAA        GT
                                TGAGC   AGCTTTTAGGT
                                |||||   ||||||||||
                                ATTTG   TCGAAAGTTTA
                                   AC_         TG
GAM264  STAT2    3' ACTTGGAGGGCTCA       18293      AAAAG
                                TGAGC    CTTTTAGGT
                                |||||    |||||||||
                                ACTCG    GGAGGTTCA
                                   _____
GAM264  STATI2   3' TACCTAGGAGTTTTGTT     94553        G       GT
                                AGCAAAA CTTTTAGGT
                                ||||||| |||||||||
                                TTGTTTT GAGGATCCA
                                     _       TG
GAM264  STATI2   3' TACCTAGGAGTTTTGTT     13925        G       GT
                                AGCAAAA CTTTTAGGT
                                ||||||| |||||||||
                                TTGTTTT GAGGATCCA
                                     _       TG
GAM264  STIM2    3' ACATCTAGGGAGTTTCTGCTTA 40468        A     _
                                TGAGCA AAGCTTT TAGGTGT
                                |||||| ||||||| |||||||
                                ATTCGT TTTGAGG ATCTACA
                                   C      G
GAM264  STK29    3' GCACCTGGAGGCCTCCTC    87576     CAAAA
                                GAG    GCTTTTAGGTGT
                                |||    ||||||||||||
```

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                                CTC    CGGAGGTCCACG
                                  CTC__
GAM264  STK39   3'  GGCCTGAGGCTGCTT      25077      AAA    T  TG
                                GAGCA   GCTTT AGG  T
                                |||||   ||||| |||  |
                                TTCGT   CGGAG TCC  G
                                  ____    _  GT
GAM264  STX3A   3'  AACATGTGAAGGTTTTTGTT  14801           G
                                AGCAAAAGCTTTTA GTGT
                                |||||||||||||| ||||
                                TTGTTTTTGGAAGT TACA
                                        G   AC
GAM264  STX3A   3'  GCACTTGGGAAAGCTCTTG   14806    A      __
                                CAA AGCTTTT  AGGTGT
                                ||| |||||||  ||||||
                                GTT TCGAAAG  TTCACG
                                  C      GG
GAM264  STX4A   3'  ATGCCTGGGGGAGGCCTGC   16015    AAAG_
                                GCA    CTTTTAGGTGT
                                |||    ||||||||||
                                CGT    GGGGGTCCGTA
                                  CCGGA
GAM264  STXBP3  3'  ATATCTAAAAGTCTCATGCT  23438     AA  _
                                AGCA  AG CTTTTAGGTGT
                                ||||  || ||||||||||
                                TCGT  TC GAAAATCTATA
                                  AC  T
GAM264  SYPL    3'  ATACCTACCACCTGTCTTTGCT 92910        AG TTT___
           TA                     TGAGCAAA  C     TAGGTGT
                                ||||||||  |     |||||||
                                ATTCGTTT  G     ATCCATA
                                    CT TCCACC
GAM264  SYT12   5'  ACACCTGGGAGGCAAGTTG   94720    AA_    _
                                CAA   GCTTTT AGGTGT
                                |||   |||||| ||||||
                                GTT   CGGAGG TCCACA
                                  GAA     G
GAM264  SYTL2   5'  GCACTTAGGATCTTGCT     51960     AA  C
                                AGCA  AG TTTTAGGTGT
                                ||||  || ||||||||||
                                TCGT  TC AGGATTCACG
                                  __  T
GAM264  SZF1    3'  CCAGAGGCTTTTGTCCA     32232    AG        A
                                TG  CAAAAGCTTTT GG
                                ||  |||||||||| ||
                                AC  GTTTTCGGAGA CC
                                  CT         _
GAM264  TBDN100 3'  GCATCTGACTGATTTTGTT   46954       GCTT
                                AGCAAAA    TTAGGTGT
                                |||||||    ||||||||
```

```
                                TTGTTTT   AGTCTACG
                                    AGTC
GAM264  TBLR1   3'  GCACTTGAATTCCTGCTT   45102      AAAGCT
                                GAGCA    TTTAGGTGT
                                |||||    |||||||||
                                TTCGT    AAGTTCACG
                                   CCTT__
GAM264  THEA    3'  GCTGCCTTCAAGCATTTGTTTA 66289        A   TT    T
                                TGAGCAAA GCTT  AGGTG
                                |||||||| ||||  |||||
                                ATTTGTTT CGAA  TCCGT
                                     A   CT    CGT
GAM264  THEA    3'  ACACTTGGAAGCTCTGT    66274    AA
                                GCA  AGCTTTTAGGTGT
                                |||  ||||||||||||
                                TGT  TCGAAGGTTCACA
                                  C_
GAM264  TIAM2   3'  ACATCTGGTAGGCTGCTC   24930      AAA   _
                                GAGCA   GCTT TTAGGTGT
                                |||||   |||| ||||||||
                                CTCGT   CGGA GGTCTACA
                                   ___   T
GAM264  TIMM9   5'  GCGTCTAAGGGTTTAAGT   24944   AA       GT
                                GC  AAGCTTTTAG  GT
                                ||  ||||||||||  ||
                                TG  TTTGGGAATC  CG
                                 AA        TG
GAM264  TIP-1   3'  GCATCTGGAAGCTCAGC    27504   AAA
                                GC   AGCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   TCGAAGGTCTACG
                                 AC_
GAM264  TIP120B 3'  ATGCCTGAAGTTAGTGCTCA  72417      AA    T
                                TGAGCA  AGCTTT AGGTGT
                                ||||||  |||||| ||||||
                                ACTCGT  TTGAAG TCCGTA
                                   GA    _
GAM264  TIP47   3'  ACACCTGAGGTCAGGTGTTC  19477      AAA_   T
                                GAGCA   GCTTT AGGTGT
                                |||||   ||||| ||||||
                                CTTGT   TGGAG TCCACA
                                   GGAC   _
GAM264  TIX1    3'  GCACCTGGGAGAGCTT     61745     AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                TTCG    GAGGGTCCACG
                                  A____
GAM264  TLN2    3'  ACACTTTGGCTTTTGTT     61685         TTT
                                AGCAAAAGCT   AGGTGT
                                |||||||||   ||||||
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                                TTGTTTTCGG  TTCACA
                                      T__
GAM264  TLR10    5' ACACCTGGAAATTGTTT    48229      AAGC
                                GAGCAA   TTTTAGGTGT
                                ||||||   ||||||||||
                                TTTGTT   AAGGTCCACA
                                   A___
GAM264  TNRC3    3' ACATCTGGAAGCCTTTCT   19655   C  A
                                AG AAA GCTTTTAGGTGT
                                || ||| ||||||||||||
                                TC TTT CGAAGGTCTACA
                                 _  C
GAM264  TOMM34   3' ATAATAAAAGTTATTGCTTA  22333      A     GGTGT
                                TGAGCAA AGCTTTTA
                                ||||||| ||||||||
                                ATTCGTT TTGAAAAT
                                     A      AATA
GAM264  TOPBP1   3' ATATCTGAAGCTGTAGCTTA  22838     AAA    T
                                TGAGC  AGCTTT AGGTGT
                                |||||  |||||| ||||||
                                ATTCG  TCGAAG TCTATA
                                   ATG    _
GAM264  TOR1B    3' TACCTGAAAACAGCTGTGC   27204    AA  ___    GT
                                GCA  AGCT  TTTAGGT
                                |||  ||||  |||||||
                                CGT  TCGA  AAGTCCA
                                  G_   CAA     TG
GAM264  TRAF3    3' GTGCTTGGGGGTGCTGCTT   59743     AAA      TG
                                GAGCA  GCTTTTAGG  T
                                |||||  |||||||||  |
                                TTCGT  TGGGGGTTC  G
                                   CG_      GT
GAM264  TRAF6    3' GTACTTTCTTGGGCTTTTGCTC 16095         TT__   GT
                                GAGCAAAAGCTT   AGGT
                                ||||||||||||   ||||
                                CTCGTTTTCGGG   TTCA
                                       TTCT   TG
GAM264  TREH     5' GGCCTGGGCTTGCTCA     23205      AA   TT   TG
                                TGAGCA  AGCT  TAGG  T
                                ||||||  ||||  ||||  |
                                ACTCGT  TCGG  GTCC  G
                                   __   __   GT
GAM264  TRIM15   3' ACATCTAAAATAAAATGTTTA 52651      AAAGC
                                TGAGCA   TTTTAGGTGT
                                ||||||   ||||||||||
                                ATTTGT   AAAATCTACA
                                   AAAAT
GAM264  TRIM15   3' ACATCTAAAATAAAATGTTTA 53374      AAAGC
                                TGAGCA   TTTTAGGTGT
                                ||||||   ||||||||||
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                                ATTTGT    AAAATCTACA
                                   AAAAT
GAM264  TRIM26   3' ACGCCTAAGATCATTTTGCT  12884       GC_
                                AGCAAAA   TTTTAGGTGT
                                |||||||   ||||||||||
                                TCGTTTT   AGAATCCGCA
                                   ACT
GAM264  TRIM5    3' ATACTTAAATGGCTGTGCTTA 52293       AA   _
                                TGAGCA  AGCT TTTAGGTGT
                                ||||||  |||| |||||||||
                                ATTCGT  TCGG AAATTCATA
                                   G_   T
GAM264  TSLRP    3' ACATCTGGCTGCGTTGCCA   25006    A   AA  TT
                                TG GCAA  GC  TTAGGTGT
                                || ||||  ||  ||||||||
                                AC CGTT  CG  GGTCTACA
                                 _   G_  TC
GAM264  TTY7     5' ATATCTGGAAGAAATGCTTA  49177       AAAG
                                TGAGCA   CTTTTAGGTGT
                                ||||||   ||||||||||
                                ATTCGT   GAAGGTCTATA
                                   AAA_
GAM264  TU12B1-TY 3' GCACCTGGCCTGCTTTTTTCA 33384     C     TT_
                                TGAG AAAAGC   TTAGGTGT
                                |||| ||||||   ||||||||
                                ACTT TTTTCG   GGTCCACG
                                  _     TCC
GAM264  TXN2     3' ATGCTTAGAGCCCAGGCTC   25008     AAAA    T
                                GAGC    GCTTT AGGTGT
                                ||||    ||||| ||||||
                                CTCG    CGAGA TTCGTA
                                  GACC    _
GAM264  TXNL2    3' CTTGGGGGCTTTTTTCA     21550     C
                                TGAG AAAAGCTTTTAGG
                                |||| ||||||||||||
                                ACTT TTTTCGGGGGTTC
                                  _
GAM264  U5-116KD 3' GTGTCTGGAAGCTGCTGTT   14910     AA        TG
                                AGCA  AGCTTTTAGG  T
                                ||||  ||||||||||  |
                                TTGT  TCGAAGGTCT  G
                                  CG        GT
GAM264  Ubc6p    3' GTGCTTGGGGGTTTTTGCT   54154            TG
                                AGCAAAAGCTTTTAGG  T
                                ||||||||||||||||  |
                                TCGTTTTTGGGGGTTC  G
                                          GT
GAM264  UBE4B    3' GCATCTGAGGAGCAGCTGC   20164     AAA   _
                                GCA   GCTT TTAGGTGT
                                |||   |||| ||||||||
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                                CGT   CGAG AGTCTACG
                                  CGA    G
GAM264  UBF-fl   3'  ATATTTGAATGCAGTTGTTCA  51549        AA  T
                                TGAGCAA  GC TTTAGGTGT
                                |||||||  || |||||||||
                                ACTTGTT  CG AAGTTTATA
                                    GA  T
GAM264  UBP1     3'  ACGCTTAAAAGTGTGTG     27222     AAA
                                CA   GCTTTTAGGTGT
                                ||   ||||||||||||
                                GT   TGAAAATTCGCA
                                 GTG
GAM264  UBP1     3'  TGTTTTAAAAGTTTTGCTT   27227        G       TGT
                                GAGCAAAA CTTTTAGG
                                |||||||| ||||||||
                                TTCGTTTT GAAAATTT
                                    _       TGTT
GAM264  UHRF1    5'  ACTGATGGGGGTTTTTGCT   25218             GGT
                                AGCAAAAGCTTTTA   GT
                                ||||||||||||||   ||
                                TCGTTTTTGGGGGT   CA
                                        AGT
GAM264  UHRF2    3'  ATATCTAAAGGTAGTTC     73448      AAAA
                                GAGC    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                CTTG    TGGAAATCTATA
                                  A___
GAM264  UHRF2    3'  GCACTTAAAAGAGGTATTCA   73449      CAAAAG
                                TGAG     CTTTTAGGTGT
                                ||||     ||||||||||||
                                ACTT     GAAAATTCACG
                                  ATGGA_
GAM264  ULK2     3'  ACACCTACAGATTTTCTCA   27999      C    G  TT
                                TGAG AAAA CT  TAGGTGT
                                |||| |||| ||  |||||||
                                ACTC TTTT GA  ATCCACA
                                  _   A  C_
GAM264  UMP-CMPK 3'  ACACTTCAAAGGTTTTTTTTT  32841     C         _
                                GAG AAAAGCTTTT AGGTGT
                                ||| |||||||||| ||||||
                                TTT TTTTTGGAAA TTCACA
                                  T         C
GAM264  URB      3'  ACATTTAAAAGAATTGTTT    80377       AAG
                                GAGCAA   CTTTTAGGTGT
                                ||||||   ||||||||||||
                                TTTGTT   GAAAATTTACA
                                   AA_
GAM264  USP22    3'  ATGCCTGAAGGGAGTGCTT    68004       AAAG
                                GAGCA    CTTTTAGGTGT
                                |||||    ||||||||||||
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                              TTCGT   GGAAGTCCGTA
                                GAG_
GAM264  UXS1    3' GTGCCTAAAAGCTCCCCTCA  46890    CAAA       TG
                              TGAG   AGCTTTTAGG T
                              ||||   |||||||||| |
                              ACTC   TCGAAAATCC G
                                CCC_       GT
GAM264  VDAC3   3' ATGCTTGAAGGCATGC     18982    AAA
                              GCA  GCTTTTAGGTGT
                              |||  ||||||||||||
                              CGT  CGGAAGTTCGTA
                               A__
GAM264  VDAC3   3' ATGCCTGGAAGTTGTCATGTT 18981    AA__
                              AGCA   AGCTTTTAGGTGT
                              ||||   ||||||||||||
                              TTGT   TTGAAGGTCCGTA
                                ACTG
GAM264  VIAAT   3' GCGCTTGGGAGGCCAAGCTT  54539    AAAAG
                              GAGC    CTTTTAGGTGT
                              ||||    ||||||||||
                              TTCG    GAGGGTTCGCG
                                AACCG
GAM264  VIT1    3' ACACCTAGACTTGCT      37968      AAGCT
                              AGCAA    TTTAGGTGT
                              |||||    |||||||||
                              TCGTT    AGATCCACA
                                C____
GAM264  WBP11   3' ATGCCAGAAAAGGCTTCTGTTC 32848      A      A__
          A                    TGAGCA AAGCTTTT  GGTGT
                              ||||||| ||||||||  |||||
                              ACTTGT TTCGGAAA  CCGTA
                                 C       AGA
GAM264  WBSCR23 3' ACACCTGGCTAGTTTTTG   46750       T_
                              CAAAAGCT  TTAGGTGT
                              ||||||||  ||||||||
                              GTTTTTGA  GGTCCACA
                                   TC
GAM264  WHIP    3' ATACCTGGCAGCTTTGTGC   39298    _    T
                              GCA AAAGCT TTAGGTGT
                              ||| |||||| ||||||||
                              CGT TTTCGA GGTCCATA
                                G     C
GAM264  WNT2B   3' GCACTGCCTCTTTTGCTTA   44423       CTTTTA
                              TGAGCAAAAG     GGTGT
                              ||||||||||     |||||
                              ATTCGTTTTC     TCACG
                                    TCCG__
GAM264  WNT2B   3' GCACTGCCTCTTTTGCTTA   14819       CTTTTA
                              TGAGCAAAAG     GGTGT
                              ||||||||||     |||||
```

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                                ATTCGTTTTC     TCACG
                                     TCCG__
GAM264  YAP1    3'  ACATCTGAGAAATGAGTGCTC  20347      AAAGC_
                                GAGCA     TTTTAGGTGT
                                |||||     ||||||||||
                                CTCGT     AGAGTCTACA
                                   GAGTAA
GAM264  YAP1    3'  GTGCCTAGGGGAGTGCTC    20355      AAAG       TG
                                GAGCA    CTTTTAGG  T
                                |||||    ||||||||  |
                                CTCGT    GGGGATCC  G
                                   GA__       GT
GAM264  ZDHHC7  5'  GCTGAGGCATTTGCTT      34842       A     TA
                                GAGCAAA GCTTT  GGT
                                ||||||| |||||  |||
                                TTCGTTT CGGAG  TCG
                                    A    __
GAM264  ZER6    3'  TTCCAAAGAGTGTTTGCTTA   63383        A     A  TGT
                                TGAGCAAA GCTTTT GG
                                |||||||| |||||| ||
                                ATTCGTTT TGAGAA CC
                                     G     A  TTG
GAM264  ZER6    3'  CATCTGAGTCTGCTC       63376       AAA    TT
                                GAGCA   GCTT  AGGTG
                                |||||   ||||  |||||
                                CTCGT   TGAG  TCTAC
                                   C__    __
GAM264  ZER6    3'  ACACTTAGAAAACATCTGCTC  63374      AAAGC_
                                GAGCA     TTTTAGGTGT
                                |||||     ||||||||||
                                CTCGT     AAGATTCACA
                                   CTACAA
GAM264  ZF5128  3'  ATACCTGAGGGGATGATGTT   26801      AAAG_
                                AGCA    CTTTTAGGTGT
                                ||||    ||||||||||
                                TTGT    GGGAGTCCATA
                                  AGTAG
GAM264  ZF5128  3'  GCACTCGTTCAGGTTTTTGCCC 26805    A        TTA__
           A                     TG GCAAAAGCTT     GGTGT
                                || ||||||||||     |||||
                                AC CGTTTTTGGA     TCACG
                                 C         CTTGC
GAM264  ZFP100  3'  GCACCTGGAGTTCTGCT     70054      AA     T
                                AGCA  AGCTTT AGGTGT
                                ||||  |||||| ||||||
                                TCGT  TTGAGG TCCACG
                                  C_     _
GAM264  ZFR     3'  TTTAATTTAGAGGTTTTGTTT  32257        G        GT
                                GAGCAAAA CTTTTAGGT
                                |||||||| |||||||||
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                                TTTGTTTT GGAGATTTA
                                   _       ATTTT
GAM264  ZNF17    3' ATATCTAGAAGTCTTTTCA   82386    GCA   _
                                TGA   AAAG CTTTTAGGTGT
                                |||   |||| ||||||||||
                                ACT   TTTC GAAGATCTATA
                                  ___   T
GAM264  ZNF213   3' CATCCTGCTTTGTTCA     65092       A  TTTTA
                                TGAGCAAA GC    GGTG
                                |||||||| ||    ||||
                                ACTTGTTT CG    CTAC
                                   _ TC___
GAM264  ZNF220   3' ATACCTCTAGTTTTTGT    22224        TTT
                                GCAAAAGCT   AGGTGT
                                |||||||||   ||||||
                                TGTTTTTGA   TCCATA
                                    TC_
GAM264  ZNF237   3' ATACCTAAGTTGTTGTTTA   26472       A   TT
                                TGAGCAA AGCT  TAGGTGT
                                ||||||| ||||  |||||||
                                ATTTGTT TTGA  ATCCATA
                                   G   __
GAM264  ZNF262   3' ACATCTAAATCATCCTTTTTGT 17482        CT____
          TC                    GAGCAAAAG     TTTAGGTGT
                                |||||||||     |||||||||
                                CTTGTTTTT     AAATCTACA
                                    CCTACT
GAM264  ZNF282   3' GCGAGGGAGAGGCTTTTGCT  89214          AGG_
                                AGCAAAAGCTTTT    TGT
                                ||||||||||||    |||
                                TCGTTTTCGGAGA    GCG
                                      GGGA
GAM264  ZNF282   5' GCGCCTGGAAAACGTTC     89215     AAAAGC
                                GAGC     TTTTAGGTGT
                                ||||     ||||||||||
                                CTTG     AAGGTCCGCG
                                  CAA___
GAM264  ZNF294   3' ATATCTGGAGGCATGCTC    70827      AAA
                                GAGCA   GCTTTTAGGTGT
                                |||||   ||||||||||||
                                CTCGT   CGGAGGTCTATA
                                  A__
GAM264  ZNF297   3' GTGCCTGAAGTCTGTGTTT   18393      AAA    T   TG
                                GAGCA   GCTTT AGG  T
                                |||||   ||||| |||  |
                                TTTGT   TGAAG TCC  G
                                  GTC    _   GT
GAM264  ZNF31    5' GTGCCTGGGAGTTCCAGTTT  64988     AAA       TG
                                GAGC   AGCTTTTAGG  T
                                ||||   ||||||||||  |
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                                TTTG  TTGAGGGTCC  G
                                  ACC        GT
GAM264  ZNF338   3' ATGCCTGGCCGTGGTTTGCTC 42009       A_  TT
                                GAGCAAA  GC  TTAGGTGT
                                |||||||  ||  ||||||||
                                CTCGTTT  TG  GGTCCGTA
                                    GG  CC
GAM264  ZNF361   5' GCGCCTGAGACCTTGTTTCA  37661     CAA  C
                                TGAG  AAG TTTTAGGTGT
                                ||||  ||| ||||||||||
                                ACTT  TTC AGAGTCCGCG
                                  TG_  C
GAM264  LOC112840 5' ATACCTAAAAGTGGGCTTGCT  54727      AA__
                                AGCAA   GCTTTTAGGTGT
                                |||||   ||||||||||||
                                TCGTT   TGAAAATCCATA
                                   CGGG
GAM264  LOC113026 3' ACACCTGGCTAATGTTTA   55897      AA   TTT
                                TGAGCA  AGCT   AGGTGT
                                ||||||  ||||   ||||||
                                ATTTGT  TCGG   TCCACA
                                   AA   ___
GAM264  LOC113444 3' ACATCTAATTGGCTTTGTT   56555      A  T_
                                AGCAAA GCT  TTAGGTGT
                                |||||| |||  ||||||||
                                TTGTTT CGG  AATCTACA
                                   _  TT
GAM264  LOC113828 5' GCATTTGGAGGCTCCCTC    56585    CAAA
                                GAG   AGCTTTTAGGTGT
                                |||   ||||||||||||
                                CTC   TCGGAGGTTTACG
                                  CC__
GAM264  LOC115219 5' GCACTTGGTCCCCTTTGCTC  73308       AGCTT
                                GAGCAAA    TTAGGTGT
                                |||||||    ||||||||
                                CTCGTTT    GGTTCACG
                                    CCCCT
GAM264  LOC115950 3' GTGCCTGGGGCTGCATTGCT  57084     A__    T  TG
                                AGCAA  AGCTTT AGG  T
                                |||||  |||||| |||  |
                                TCGTT  TCGGGG TCC  G
                                   ACG    _  GT
GAM264  LOC116068 3' ATATTTGAAAGCACTTTTGT  73723      __
                                GCAAAA  GCTTTTAGGTGT
                                ||||||  ||||||||||||
                                TGTTTT  CGAAAGTTTATA
                                   CA
GAM264  LOC116150 3' ATACCTGAGATTTTTACTCA  56630     C   C
                                TGAG AAAAG TTTTAGGTGT
                                |||| ||||| ||||||||||
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                                ACTC TTTTT AGAGTCCATA
                                  A    _
GAM264  LOC116411 5' ACGCCTGACTGGTTTT     73854       T_
                                AAAGCT  TTAGGTGT
                                ||||||  ||||||||
                                TTTTGG  AGTCCGCA
                                   TC
GAM264  LOC116411 3' ATGCTTGAAGGCAGCATGCTC  73855      AAA_
                                GAGCA   GCTTTTAGGTGT
                                |||||   ||||||||||||
                                CTCGT   CGGAAGTTCGTA
                                   ACGA
GAM264  LOC118851 5' ATATTTAAAAGCTAGTGTT   75500     AA
                                AGCA  AGCTTTTAGGTGT
                                ||||  ||||||||||||
                                TTGT  TCGAAAATTTATA
                                  GA
GAM264  LOC118851 3' TATCTGGAAGCTACTGC     75505     AA        GT
                                GCA  AGCTTTTAGGT
                                |||  ||||||||||
                                CGT  TCGAAGGTCTA
                                  CA         TG
GAM264  LOC120939 3' ACACCTGAAATGGCTTTGTTT  76241       A  __
                                GAGCAAA GCT  TTTAGGTGT
                                |||||||  |||  |||||||||
                                TTTGTTT CGG  AAGTCCACA
                                   _  TA
GAM264  LOC121504 3' ACGCTTGGTCTTGCTC      74095       AA   TTT
                                GAGCAA  GCT   AGGTGT
                                ||||||  |||   ||||||
                                CTCGTT  TGG   TTCGCA
                                   C_  ____
GAM264  LOC121838 5' GCACCTAATAGAGTTTTCTTA  76000     C   AG  T
                                TGAG AAA  CT TTAGGTGT
                                |||| |||  || ||||||||
                                ATTC TTT  GA AATCCACG
                                  T   GA  T
GAM264  LOC122553 3' GCACCTGAATTGTGCTT     74132      AAAGCT
                                GAGCA     TTTAGGTGT
                                |||||     |||||||||
                                TTCGT     AAGTCCACG
                                  GTT____
GAM264  LOC122726 3' ACATCTAGAGCAAGCT      75580     AAAA    T
                                AGC    GCTTT AGGTGT
                                |||    ||||| ||||||
                                TCG    CGAGA TCTACA
                                  AA__    _
GAM264  LOC123036 3' GCATTTAGAAGACTTT      74192      _
                                AAAG CTTTTAGGTGT
                                |||| ||||||||||
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                                TTTC GAAGATTTACG
                                  A
GAM264   LOC123876 3'  ACATCTAAGAGACATTCA    74240      CAAAAG
                                TGAG     CTTTTAGGTGT
                                ||||     ||||||||||
                                ACTT     GAGAATCTACA
                                  ACA___
GAM264   LOC124402 3'  GCACCTGGGGGTACCCGC    59149    AAAA
                                GC    GCTTTTAGGTGT
                                ||    ||||||||||||
                                CG    TGGGGGTCCACG
                                 CCCA
GAM264   LOC124460 3'  ACACTTAATGATTTTGCT    76036       GCTT
                                AGCAAAA    TTAGGTGT
                                |||||||    ||||||||
                                TCGTTTT    AATTCACA
                                    AGT_
GAM264   LOC125058 3'  GCACCTGAGACGCAGGCT    59856     AAAA _
                                AGC    GC TTTTAGGTGT
                                |||    || ||||||||||
                                TCG    CG AGAGTCCACG
                                 GA__  C
GAM264   LOC126006 5'  ACACCTGAGAGTCCCTG     74427     AAA
                                CA   GCTTTTAGGTGT
                                ||   ||||||||||||
                                GT   TGAGAGTCCACA
                                 CCC
GAM264   LOC126206 3'  GCACCTGGGAGTTCCTTCTCA  75677      CAAA
                                TGAG    AGCTTTTAGGTGT
                                ||||    ||||||||||||
                                ACTC    TTGAGGGTCCACG
                                  TTCC
GAM264   LOC126669 3'  GCATTTAAGGGTAGGGCTT    75407      AAAA
                                GAGC    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                TTCG    TGGGAATTTACG
                                  GGA_
GAM264   LOC126731 3'  TATTCTTATAAGGTTTTTGTTT 59157            _    TGT
                                GAGCAAAAGCTTT TAGG
                                |||||||||||| ||||
                                TTTGTTTTTGGAA ATTC
                                       T    TTATA
GAM264   LOC126789 3'  GTACCAAGTAGTCTTTTGTTCA 74569          _  T  A   GT
                                TGAGCAAAAG CT TT GGT
                                |||||||||| || || |||
                                ACTTGTTTTC GA GA CCA
                                      T  T  A   TG
GAM264   LOC126961 3'  GCACTTGGAAGAAGCT      74627     AAAAG
                                AGC     CTTTTAGGTGT
                                |||     ||||||||||
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                                TCG    GAAGGTTCACG
                                  AA___
GAM264  LOC127255 3'  AAATTCAGGAGTATTTGCTT  59158       A     AG  GT
                                GAGCAAA GCTTTT  GT
                                ||||||| ||||||  ||
                                TTCGTTT TGAGGA  TA
                                    A     CT  AAT
GAM264  LOC127255 3'  CACTTAAAGACTTTTG     59162       CT
                                CAAAAG  TTTAGGTG
                                ||||||  ||||||||
                                GTTTTC  AAATTCAC
                                   AG
GAM264  LOC127435 3'  GCACCTAGGAGACACCTTTGT  76116      AG___
                                GCAAA    CTTTTAGGTGT
                                |||||    ||||||||||
                                TGTTT    GAGGATCCACG
                                   CCACA
GAM264  LOC127702 3'  ACACTTGAGAAGGTTTTG    75455      G  _
                                CAAAA CT TTTAGGTGT
                                ||||| || |||||||||
                                GTTTT GA GAGTTCACA
                                   G  A
GAM264  LOC127702 3'  ACAAAGCAGGCTGTTTGCTCA  75454        _    TTAGG
                                TGAGCAAA AGCTT    TGT
                                |||||||| |||||    |||
                                ACTCGTTT TCGGA    ACA
                                     G    CGAA_
GAM264  LOC129880 3'  ACACCTGACTGGTTTT     74901       T_
                                AAAGCT  TTAGGTGT
                                ||||||  ||||||||
                                TTTTGG  AGTCCACA
                                   TC
GAM264  LOC130733 3'  GTGCTTAAGAGCTAACTC    74981     CAAA        TG
                                GAG   AGCTTTTAGG  T
                                |||   ||||||||||  |
                                CTC   TCGAGAATTC  G
                                  AA__        GT
GAM264  LOC130752 3'  GCACCTAAGTGGCCATGTTTGC 74982       A___  _
           TCA                    GAGCAAA   GCT TTTAGGTGT
                                |||||||   ||| |||||||||
                                CTCGTTT   CGG GAATCCACG
                                    GTAC   T
GAM264  LOC131870 3'  ACGCCTGGGAGATCAGAGCCA  75011    A  AAAAG_
                                TG GC     CTTTTAGGTGT
                                || ||     ||||||||||
                                AC CG     GAGGGTCCGCA
                                 _ AGACTA
GAM264  LOC131873 3'  TACACCACTGTGGGAGTTGTTT 75882      _      ____
           GCTT                   GCAAA AGCTTTTA   GGTGT   A
                                |||||  ||||||||   |||||  |
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                                CGTTT TTGAGGGT   CCACA  T
                                   G      GTCA
GAM264  LOC132671 3'  CACCTGATGCTTTTCA     59167   C     TT
                                G AAAAGC  TTAGGTG
                                | ||||||  |||||||
                                A TTTTCG  AGTCCAC
                                 C     T_
GAM264  LOC132671 3'  ACATTTAAAAAGTGCTTTTG  59166       ___
                                CAAAAGC   TTTTAGGTGT
                                |||||||   ||||||||||
                                GTTTTCG   AAAATTTACA
                                    TGA
GAM264  LOC133258 5'  ATATCTGGGAGAAGGTTCA   75922      AAAAG
                                TGAGC    CTTTTAGGTGT
                                |||||    ||||||||||
                                ACTTG    GAGGGTCTATA
                                   GAA__
GAM264  LOC133688 3'  ACACCCCCAGAGTTTTTGTTCA 75111            TA_
                                TGAGCAAAAGCTTT   GGTGT
                                ||||||||||||||   |||||
                                ACTTGTTTTTGAGA   CCACA
                                        CCC
GAM264  LOC134121 3'  ACGCCTAGGAGCTTGGCT    75147     AA
                                AGC  AAGCTTTTAGGTGT
                                |||  ||||||||||||||
                                TCG  TTCGAGGATCCGCA
                                  G_
GAM264  LOC134218 3'  GCCTGTGCTTTTGTTT      75157         TTT
                                GAGCAAAAGC   TAGGT
                                ||||||||||   |||||
                                TTTGTTTTCG   GTCCG
                                      T__
GAM264  LOC134266 3'  ATACTAAGGAAGCTTTGGCTCA 75162       A       A_
                                TGAGC AAAGCTTTT  GGTGT
                                ||||| |||||||||  |||||
                                ACTCG TTTCGAAGG  TCATA
                                   G        AA
GAM264  LOC135293 3'  ACACCTGCCCATTTTTGTTT   76168        CTTT
                                GAGCAAAAG    TAGGTGT
                                |||||||||    |||||||
                                TTTGTTTTT    GTCCACA
                                     ACCC
GAM264  LOC136442 3'  GCAAAAAATTTTTGCTCA    54286         C    AG
                                TGAGCAAAAG TTTT  GT
                                |||||||||| ||||  ||
                                ACTCGTTTTT AAAA  CG
                                      _    AA
GAM264  LOC138199 3'  ACATCTGGAGTTGGGACTTTGT 75301       AG  _____
           TCA                    GAGCAAA  CT    TTTAGGTGT
                                |||||||  ||   |||||||||
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                                CTTGTTT  GG   AGGTCTACA
                                   CA  GTTG
GAM264   LOC142937 5'  ATGCCTAGGAGTCCTTTG    56654     A_
                                CAAA  GCTTTTAGGTGT
                                ||||  ||||||||||||
                                GTTT  TGAGGATCCGTA
                                  CC
GAM264   LOC143154 3'  AACTTTGGCTTTTGCT     76475        TTT   GT
                                AGCAAAAGCT   AGGT
                                ||||||||||   ||||
                                TCGTTTTCGG   TTCA
                                     T__   AT
GAM264   LOC143241 3'  GCAATAAATGTTTTTGTTT   57176         T   GG
                                GAGCAAAAGC TTTA  TGT
                                |||||||||| ||||  |||
                                TTTGTTTTTG AAAT  ACG
                                     T   A_
GAM264   LOC143310 5'  GCACTTAGCAGGTGCTCA    76535      AAA   TTT
                                TGAGCA   GCT   AGGTGT
                                ||||||   |||   ||||||
                                ACTCGT   CGA   TTCACG
                                   GGA   ___
GAM264   LOC143381 3'  ACATTTAAGGGCTTTATTC    76543     CA
                                GAG  AAAGCTTTTAGGTGT
                                |||  ||||||||||||||
                                CTT  TTTCGGGAATTTACA
                                  A_
GAM264   LOC143425 3'  GTGTCTGGAAAGCTTTGC    87639      A    _  TG
                                GCAAA GCTTTT AGG  T
                                ||||| |||||| |||  |
                                CGTTT CGAAAG TCT  G
                                   _    G  GT
GAM264   LOC143437 5'  GCACCATGCTAAAAGCTTTTAT 82955     C        ____
            TTA                   GAG AAAAGCTTTTA   GGTGT
                                ||| ||||||||||   |||||
                                TTT TTTTCGAAAAT   CCACG
                                  A         CGTA
GAM264   LOC143451 3'  GTGCCTGGGAGGGCGGGGCTC  76568     AAAA    __  TG
                                GAGC   GCTTTT  AGG  T
                                ||||   ||||||  |||  |
                                CTCG   CGGGAG  TCC  G
                                  GGG_    GG   GT
GAM264   LOC143451 5'  GCACCTTTACCTGTGTTTTGCT 76564        _ TTTT__
            C                    GAGCAAAA GC     AGGTGT
                                ||||||||  ||     ||||||
                                CTCGTTTT TG     TCCACG
                                     G  TCCATT
GAM264   LOC143465 5'  ATGTTTGGTGGCATTTTGTTCA 82960         _  T    TG
                                TGAGCAAAA GCT TTAGG  T
                                |||||||||  ||| |||||  |
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                                ACTTGTTTT CGG GGTTT  A
                                      A  T    GT
GAM264  LOC143666 3'  GCACTTAGAAGAACGATCA   82972    GCAAAAG
                                TGA      CTTTTAGGTGT
                                |||      ||||||||||
                                ACT      GAAGATTCACG
                                  AGCAA__
GAM264  LOC143677 5'  TCACTAGAGGCCTTTGCTCA  82981        A      GTGT
                                TGAGCAAA GCTTTTAG
                                |||||||| ||||||||
                                ACTCGTTT CGGAGATC
                                     C       ACTA
GAM264  LOC143677 3'  GTGCTTCAAAGTTTTTGTTT  82979           T  TG
                                GAGCAAAAGCTTT AGG  T
                                |||||||||||| |||  |
                                TTTGTTTTTGAAA TTC  G
                                        C  GT
GAM264  LOC143689 3'  ACACTTAAAATAAGTGTTTGC  76602      A   ___
                                GCAAA GCTT   TTAGGTGT
                                ||||| ||||  ||||||||
                                CGTTT TGAA   AATTCACA
                                   G   TAA
GAM264  LOC143785 3'  ACATCTAAAAGAGCACAGTTT  76605     AAAAG_
                                GAGC     CTTTTAGGTGT
                                ||||     ||||||||||
                                TTTG     GAAAATCTACA
                                  ACACGA
GAM264  LOC143785 3'  ACACTTGAGTGACTTTGTTT   76604       AGCT
                                GAGCAAA    TTTAGGTGT
                                |||||||    |||||||||
                                TTTGTTT    GAGTTCACA
                                    CAGT
GAM264  LOC143879 5'  ACACCTGATTGATTTGCCA   76652    A    AGCTT
                                TG GCAAA    TTAGGTGT
                                || |||||    ||||||||
                                AC CGTTT    AGTCCACA
                                 _    AGTT_
GAM264  LOC144231 5'  GCACCTGAGTGTCCTTGCTC   83014       AA  T
                                GAGCAA  GC TTTAGGTGT
                                ||||||  || |||||||||
                                CTCGTT  TG GAGTCCACG
                                    CC  T
GAM264  LOC144308 5'  GCGCCACTGAGGGCTTTTCTT  83050     C        __
                                GAG AAAAGCTTTTA  GGTGT
                                ||| ||||||||||  |||||
                                TTC TTTTCGGGAGT  CCGCG
                                  _         CA
GAM264  LOC144321 3'  ACACCTGAGGGAAAAACTT   83061     CAAAAG
                                GAG      CTTTTAGGTGT
                                |||      ||||||||||
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                                TTC     GGGAGTCCACA
                                  AAAAA_
GAM264  LOC144438 3'  ACACCTAAAACTCTTTTCTT  76829    C    C_
                                GAG AAAAG  TTTTAGGTGT
                                ||| |||||  ||||||||||
                                TTC TTTTC  AAAATCCACA
                                  _    TC
GAM264  LOC144453 3'  ATACCTGAAGGCTGGTCG    76845    G  AAA
                                TGA CA   GCTTTTAGGTGT
                                ||| ||   ||||||||||||
                                GCT GT   CGGAAGTCCATA
                                  G ___
GAM264  LOC144481 3'  ACACCTAGAGGCTGGGC     83092    AAA
                                GC   AGCTTTTAGGTGT
                                ||   ||||||||||||||
                                CG   TCGGAGATCCACA
                                 GG_
GAM264  LOC144509 3'  GCATCTATTTCCTCTTTTGTTT 76861         CTTT__
                                GAGCAAAAG     TAGGTGT
                                |||||||||     |||||||
                                TTTGTTTTC     ATCTACG
                                     TCCTTT
GAM264  LOC144577 3'  ACACCTAACTGCATTTGTTT   76899        A  TT
                                GAGCAAA GC  TTAGGTGT
                                ||||||| ||  ||||||||
                                TTTGTTT CG  AATCCACA
                                    A  TC
GAM264  LOC144577 3'  GCGCTTGAAAGACCTC      76901     CAAAAG
                                GAG     CTTTTAGGTGT
                                |||     ||||||||||||
                                CTC     GAAAGTTCGCG
                                  CA____
GAM264  LOC144845 5'  GGCCTAGTTTTGCTC       56661        GCTT    TG
                                GAGCAAAA    TTAGG  T
                                ||||||||    |||||  |
                                CTCGTTTT    GATCC  G
                                     _____    GT
GAM264  LOC145021 3'  ACACTTAAGACTATGC      76985     AA  C
                                GCA  AG TTTTAGGTGT
                                |||  || ||||||||||
                                CGT  TC AGAATTCACA
                                  A_  _
GAM264  LOC145098 3'  ACACTTGAGGTTTCTGTTCA  76987       A      T
                                TGAGCA AAGCTTT AGGTGT
                                |||||| ||||||| ||||||
                                ACTTGT TTTGGAG TTCACA
                                   C      _
GAM264  LOC145125 5'  GCACCTTTACCTGTGTTTTGCT 77007         _  TTTT__
           C                     GAGCAAAA GC     AGGTGT
                                ||||||||  ||     ||||||
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                                CTCGTTTT TG     TCCACG
                                     G  TCCATT
GAM264   LOC145125 3'  GTGCCTGGGAGGGCGGGGCTC  77011     AAAA    __  TG
                                GAGC   GCTTTT  AGG  T
                                ||||   ||||||  |||  |
                                CTCG   CGGGAG  TCC  G
                                  GGG_     GG   GT
GAM264   LOC145188 3'  ATGCCTGAGGGCTTTTGACTT  77046    _
                                GAG CAAAAGCTTTTAGGTGT
                                ||| ||||||||||||||||
                                TTC GTTTTCGGGAGTCCGTA
                                  A
GAM264   LOC145355 3'  GTTTCAGAAGCTTTTTGCTCA  77099        _    AGGTGT
                                TGAGCAAAA GCTTTT
                                ||||||||| ||||||
                                ACTCGTTTT CGAAGA
                                      T     CTTTG
GAM264   LOC145474 5'  AGTCTGGCTTTGCTC      77209       A  TTT  TG
                                GAGCAAA GCT   AGG  T
                                ||||||| |||   |||  |
                                CTCGTTT CGG   TCT  A
                                   _  ___   GT
GAM264   LOC145482 3'  ACGCTTGAGAGGCACTTTGT  77227      A_  _
                                GCAAA  GC TTTTAGGTGT
                                |||||  || ||||||||||
                                TGTTT  CG AGAGTTCGCA
                                   CA  G
GAM264   LOC145483 3'  ACACTTAAAATTACTGCTT   77238      AAAGC
                                GAGCA    TTTTAGGTGT
                                |||||    ||||||||||
                                TTCGT    AAAATTCACA
                                   CATT_
GAM264   LOC145622 5'  GCATCTGGAGGTGGCCCA    77301    A  AAAA
                                TG GC    GCTTTTAGGTGT
                                || ||    ||||||||||||
                                AC CG    TGGAGGTCTACG
                                 C  G___
GAM264   LOC145623 3'  AGTCTTTGCATTTGCTTA    83392       A  TTTT   TG
                                TGAGCAAA GC    AGG  T
                                |||||||| ||    |||  |
                                ATTCGTTT CG    TCT  A
                                     A  TT__   GT
GAM264   LOC145781 3'  GAGCATGAAGGTTTTGTTTA  77491        G    TAG  GT
                                TGAGCAAAA CTTT   GT
                                ||||||||| ||||   ||
                                ATTTGTTTT GAAG   CG
                                      G   TA_  AGA
GAM264   LOC145826 5'  GCATCTAGGGGAGTGCCCA   83531    A   AAAG
                                TG GCA    CTTTTAGGTGT
                                || |||    ||||||||||
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                                AC CGT    GGGGATCTACG
                                 C   GA__
GAM264   LOC146138 3'  GCACCTGAAGGAGCTGT     83615     AAAG
                                GCA    CTTTTAGGTGT
                                |||    ||||||||||
                                TGT    GGAAGTCCACG
                                  CGA_
GAM264   LOC146268 3'  GCACTTGATAGGTGCTTA     77810       AAAG  T
                                TGAGCA    CT TTAGGTGT
                                ||||||    || ||||||||
                                ATTCGT    GA AGTTCACG
                                   G___  T
GAM264   LOC146336 3'  ACATTTAGGGGCATTTTGTT   77831        _
                                AGCAAAA GCTTTTAGGTGT
                                ||||||| ||||||||||||
                                TTGTTTT CGGGGATTTACA
                                    A
GAM264   LOC146784 3'  GCATTTGAAGTCATTGCTTTTG 78117         _____
           CT                     AGCAAAAGC     TTTTAGGTGT
                                |||||||||     ||||||||||
                                TCGTTTTCG     GAAGTTTACG
                                     TTACT
GAM264   LOC146839 3'  ACACCTGGCTAAGTTTTTG    83805         __
                                CAAAAGCTT  TTAGGTGT
                                |||||||||  ||||||||
                                GTTTTTGAA  GGTCCACA
                                     TC
GAM264   LOC146856 5'  GTGCCTGAGGGATGGGCTGCA  82803    _  AAAAG       TG
                                TG AGC     CTTTTAGG  T
                                || |||     ||||||||  |
                                AC TCG     GGGAGTCC  G
                                 G   GGTA_       GT
GAM264   LOC146894 3'  ATACCTGAAGGTGACTC     59184     CAAAA
                                GAG     GCTTTTAGGTGT
                                |||     ||||||||||||
                                CTC     TGGAAGTCCATA
                                  AG___
GAM264   LOC146901 3'  GTGTTGGGAAGCTTTTGCCA   83847    A          AG TG
                                TG GCAAAAGCTTTT  G  T
                                || ||||||||||||  |  |
                                AC CGTTTTCGAAGG  T  G
                                 _          GT GT
GAM264   LOC146957 3'  GCTGGGGAGGGCTGTTGCTT   78205       A      AGGT
                                GAGCAA AGCTTTT    GT
                                ||||||| |||||||    ||
                                TTCGTT TCGGGAG    CG
                                   G      GGGT
GAM264   LOC147081 3'  GCGTCCAGCTTCTGCTT      78243       A     TTTA  _
                                GAGCA AAGCT    GG TGT
                                ||||| |||||    || |||
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                                TTCGT TTCGA    CC GCG
                                  C     _____ T
GAM264   LOC147081 5'  CATCCTCTTTTGTTC       78241          CTTTT   _
                                GAGCAAAAG     AGG TG
                                |||||||||     ||| ||
                                CTTGTTTTC     TCC AC
                                      _____   T
GAM264   LOC147093 5'  GCACCTGGCCAAAGCTTTTGTT 83944             ___
           T                     GAGCAAAAGCTTT   TAGGTGT
                                |||||||||||||   |||||||
                                TTTGTTTTCGAAA   GTCCACG
                                        CCG
GAM264   LOC147124 3'  GCACCTGGGGCGCCAGCT    76302     AAAA    T
                                AGC    GCTTT AGGTGT
                                |||    ||||| ||||||
                                TCG    CGGGG TCCACG
                                  ACCG    _
GAM264   LOC147136 3'  ACGTCTGGGAGCTAGCTT    78256     AAA       GT
                                GAGC   AGCTTTTAG  GT
                                ||||   |||||||||  ||
                                TTCG   TCGAGGGTC  CA
                                  A__        TG
GAM264   LOC147178 3'  CTTTGGTTTTTGTTCA      61324           TTT
                                TGAGCAAAAGCT   AG
                                ||||||||||||   ||
                                ACTTGTTTTTGG   TC
                                       TT_
GAM264   LOC147299 5'  ATGCCTGAGAGCTTGC      78343     AA
                                GCA  AGCTTTTAGGTGT
                                |||  ||||||||||||
                                CGT  TCGAGAGTCCGTA
                                  __
GAM264   LOC147343 5'  GTGCCTGGGAGTGGCTT     84003     AAAA       TG
                                GAGC    GCTTTTAGG  T
                                ||||    |||||||||  |
                                TTCG    TGAGGGTCC  G
                                  G___        GT
GAM264   LOC147622 5'  GTGCCTAAGGGAAGTGTTC    84053      AAAG       TG
                                GAGCA    CTTTTAGG  T
                                |||||    ||||||||  |
                                CTTGT    GGGAATCC  G
                                   GAA_       GT
GAM264   LOC147727 3'  ACACTCAGTCTTTGTTCA    78466        AG  TTTA
                                TGAGCAAA  CT    GGTGT
                                ||||||||  ||    |||||
                                ACTTGTTT  GA    TCACA
                                     CT  C___
GAM264   LOC147791 5'  GCGCTGCTGGTTTTTGC     84072         TTTA
                                GCAAAAGCT    GGTGT
                                |||||||||    |||||
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                                CGTTTTTGG   TCGCG
                                     TCG_
GAM264  LOC148138 5' ACGCCTGAGAGCCGGT     78669    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                TG   CGAGAGTCCGCA
                                 GC__
GAM264  LOC148195 3' ATATCTGAAGGATGTGT     84124    AAAG
                                GCA   CTTTTAGGTGT
                                |||   ||||||||||
                                TGT   GGAAGTCTATA
                                  GTA_
GAM264  LOC148438 3' GCACCTAAAAACCTCTTGC   84158     A  C_
                                GCAA AG  TTTTAGGTGT
                                |||| ||  ||||||||||
                                CGTT TC  AAAATCCACG
                                  C  CA
GAM264  LOC148697 3' GCATTTGAAAGCTTCTGGCT  78926    AA_
                                AGC   AAGCTTTTAGGTGT
                                |||   ||||||||||||||
                                TCG   TTCGAAAGTTTACG
                                  GTC
GAM264  LOC148709 5' GTGTCTGGAGGCGCTGTTC   78949     AAA      TG
                                GAGCA   GCTTTTAGG  T
                                |||||   |||||||||  |
                                CTTGT   CGGAGGTCT  G
                                   CG_      GT
GAM264  LOC148710 3' GCACCTGAGGGCAGTACTGC  84195    AAA__
                                GCA    GCTTTTAGGTGT
                                |||    ||||||||||||
                                CGT    CGGGAGTCCACG
                                  CATGA
GAM264  LOC148823 3' TATTCTATGTGTTTTTGCTT  59211        TTT   TGT
                                GAGCAAAAGC   TAGG
                                ||||||||||   ||||
                                TTCGTTTTTG   ATCT
                                     TGT   TATA
GAM264  LOC148823 3' ATGCCTGAAACAGAGTTTGC  59206     AG  __
                                GCAAA  CT  TTTAGGTGT
                                |||||  ||  |||||||||
                                CGTTT  GA  AAGTCCGTA
                                   GA  CA
GAM264  LOC148946 3' ACACCTAGAAGAGGGCTACA  84306   _  AAAAG
                                TG AGC    CTTTTAGGTGT
                                || |||    ||||||||||
                                AC TCG    GAAGATCCACA
                                 A  GGA__
GAM264  LOC149010 3' ACAATTAAAAGCTTTTGC    79125          G
                                GCAAAAGCTTTTAG TGT
                                |||||||||||||| |||
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                                CGTTTTCGAAAATT ACA
                                       A   T
GAM264   LOC149296 5'  TACCTGGGAGCTACTC      79260     CAAA         GT
                                GAG    AGCTTTTAGGT
                                |||    ||||||||||
                                CTC    TCGAGGGTCCA
                                  A___          TG
GAM264   LOC149301 3'  ACAGTTGAGGGCTTTTGTT    79249              G
                                AGCAAAAGCTTTTAG TGT
                                |||||||||||||| |||
                                TTGTTTTCGGGAGTT ACA
                                       G
GAM264   LOC149332 3'  TGACAGTGTTTGCTCA      84397         A   T
                                TGAGCAAA GCT TTA
                                |||||||| ||| |||
                                ACTCGTTT TGA AGT
                                     G   C
GAM264   LOC149372 3'  GCATGAGAGGTGTTTGTTTA   79324         A     AG
                                TGAGCAAA GCTTTT  GTGT
                                |||||||| ||||||  ||||
                                ATTTGTTT TGGAGA  TACG
                                     G     G_
GAM264   LOC149372 5'  ATATCAAGATGAGGCTTTTGTT 79320           TA___
                                AGCAAAAGCTTT    GGTGT
                                ||||||||||||    |||||
                                TTGTTTTCGGAG    CTATA
                                       TAGAA
GAM264   LOC149420 3'  ATACCTGGATATTTGCT     79368       AGCT
                                AGCAAA    TTTAGGTGT
                                ||||||    |||||||||
                                TCGTTT    AGGTCCATA
                                   AT__
GAM264   LOC149466 5'  GCATCTGGGGGCCTCCTCA    79396      CAAAA
                                TGAG    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                ACTC    CGGGGGTCTACG
                                  CTC__
GAM264   LOC149506 3'  GCGCCTCCCTTGGTCTTTGCTT 84470        AG  TTT__
                                GAGCAAA  CT    AGGTGT
                                |||||||  ||    ||||||
                                TTCGTTT  GG    TCCGCG
                                    CT  TTCCC
GAM264   LOC149506 5'  GCATCTGAGGAGGCTGC     84466     AAA    __
                                GCA   GCTTT  TAGGTGT
                                |||   |||||  |||||||
                                CGT   CGGAG  GTCTACG
                                  ____    GA
GAM264   LOC149566 3'  GCATTTGGAGCTGGTTTCTCA  84489      C  A_     T
                                TGAG AA  AGCTTT AGGTGT
                                |||| ||  |||||| ||||||
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                                ACTC TT  TCGAGG TTTACG
                                  T  GG     _
GAM264   LOC149706 5'  ACACCTGGGGGTGGTCA     84634     G AAAA
                                TGA C    GCTTTTAGGTGT
                                ||| |    ||||||||||||
                                ACT G    TGGGGGTCCACA
                                  G _____
GAM264   LOC149722 5'  GTGCCTGGAGGCTTGGAGATGC 84605    A   A____         TG
           CA                     G GCA     AAGCTTTTAGG  T
                                | |||     |||||||||||  |
                                C CGT     TTCGGAGGTCC  G
                                 _  AGAGG          GT
GAM264   LOC149837 3'  GCACCTAGGGGTGTTGCT     84740       AA
                                AGCAA  GCTTTTAGGTGT
                                |||||  ||||||||||||
                                TCGTT  TGGGGATCCACG
                                   G_
GAM264   LOC149837 3'  ACACCTGGAAGAACAGGTT    84728     AAAAG
                                AGC     CTTTTAGGTGT
                                |||     ||||||||||
                                TTG     GAAGGTCCACA
                                  GACAA
GAM264   LOC149837 5'  GATATTAGAAGCTTTTCTCA   84737      C          GTGT
                                TGAG AAAAGCTTTTAG
                                |||| ||||||||||||
                                ACTC TTTTCGAAGATT
                                   _          ATAGT
GAM264   LOC149910 3'  ACGCCTATGTTTTGTTT     79527         GCTTT
                                GAGCAAAA     TAGGTGT
                                ||||||||     |||||||
                                TTTGTTTT     ATCCGCA
                                     GT___
GAM264   LOC150054 5'  GCACCTGGCCTGTGTATTGTTT 84832        AA_  TT_
                                GAGCAA   GC   TTAGGTGT
                                ||||||   ||   ||||||||
                                TTTGTT   TG   GGTCCACG
                                    ATG  TCC
GAM264   LOC150170 5'  ACACCTAGAATGACTTGT     79588      AAGC
                                GCAA    TTTTAGGTGT
                                ||||    ||||||||||
                                TGTT    AAGATCCACA
                                  CAGT
GAM264   LOC150175 5'  ACACCTAGAATGACTTGT     79629      AAGC
                                GCAA    TTTTAGGTGT
                                ||||    ||||||||||
                                TGTT    AAGATCCACA
                                  CAGT
GAM264   LOC150197 3'  GCTGAGCCTTTGCTCA       79599         A    TTA
                                TGAGCAAA GCTT   GGT
                                |||||||| ||||   |||
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                                ACTCGTTT CGAG   TCG
                                    C   ___
GAM264   LOC150208 3'  TACCTAAGACTAATGCTT    84917      AA  C      GT
                                GAGCA  AG TTTTAGGT
                                |||||  || ||||||||
                                TTCGT  TC AGAATCCA
                                   AA  _       TG
GAM264   LOC150215 5'  ACACCTAGAATGACTTGT    79637     AAGC
                                GCAA    TTTTAGGTGT
                                ||||    ||||||||||
                                TGTT    AAGATCCACA
                                  CAGT
GAM264   LOC150218 5'  ACACCTAGAATGACTTGT    79716     AAGC
                                GCAA    TTTTAGGTGT
                                ||||    ||||||||||
                                TGTT    AAGATCCACA
                                  CAGT
GAM264   LOC150273 5'  GCATTTAGGGGCCATGATGTTT 85020       AAA__
            A                    TGAGCA    GCTTTTAGGTGT
                                |||||||    ||||||||||||
                                ATTTGT    CGGGGATTTACG
                                   AGTAC
GAM264   LOC150280 5'  ATACCTAAGGGGCCTGTTT    79710      AAAG
                                GAGCA    CTTTTAGGTGT
                                |||||    ||||||||||
                                TTTGT    GGGAATCCATA
                                  CCG_
GAM264   LOC150498 3'  GCATCTAAGAGAGGTT      79906     AAAAG
                                AGC     CTTTTAGGTGT
                                |||     ||||||||||
                                TTG     GAGAATCTACG
                                  GA___
GAM264   LOC150538 5'  GCTGGAGGGTTTCTGCTT     79938      A      A
                                GAGCA AAGCTTTT GGT
                                ||||| |||||||| |||
                                TTCGT TTTGGGAG TCG
                                   C       G
GAM264   LOC150622 3'  CACTAGTATTTGCTTA      79956        A   TTTA
                                TGAGCAAA GCT    GGTG
                                |||||||| |||    ||||
                                ATTCGTTT TGA    TCAC
                                    A   ____
GAM264   LOC150848 5'  ATACCTGAAAATTGTGC     85126     A  GC
                                GCA AA  TTTTAGGTGT
                                ||| ||  ||||||||||
                                CGT TT  AAAGTCCATA
                                  G  A_
GAM264   LOC151005 5'  GTGCCTAACGGTTCTGCTCA   80099       AA   T    TG
                                TGAGCA  AGCT TTAGG  T
                                ||||||  |||| |||||  |
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                                ACTCGT  TTGG AATCC  G
                                   C_   C    GT
GAM264   LOC151057 3'  ACATTTGAGACTGTGGCTCA  85200      AAA  C
                                TGAGC   AG TTTTAGGTGT
                                ||||||  || ||||||||||
                                ACTCG   TC AGAGTTTACA
                                   GTG  _
GAM264   LOC151103 3'  GCAAAAAAGTGTTTGCTTA   85226       A     AG
                                TGAGCAAA GCTTTT  GT
                                |||||||| ||||||  ||
                                ATTCGTTT TGAAAA  CG
                                     G     AA
GAM264   LOC151171 5'  GCACCTAAGGGTGCCTCG    80144     CAAAA
                                TGAG    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                GCTC    TGGGAATCCACG
                                  CG___
GAM264   LOC151258 5'  ACATTTGGAAGATTTTGTT   80195       G
                                AGCAAAA CTTTTAGGTGT
                                ||||||| ||||||||||
                                TTGTTTT GAAGGTTTACA
                                    A
GAM264   LOC151414 3'  GCATTTAGGGGAACAGGCTT  80239     AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                TTCG    GGGGATTTACG
                                  GACAA
GAM264   LOC151446 5'  ACGTTTGAAACTATTGCTT   85374      A  C    GG
                                GAGCAA AG TTTTA  TGT
                                |||||| || |||||  |||
                                TTCGTT TC AAAGT  GCA
                                   A  _    TT
GAM264   LOC151473 3'  ACATCTAAGTTAGACTTGCTC  80248      AAG  __
                                GAGCAA   CT  TTTAGGTGT
                                ||||||   ||  |||||||||
                                CTCGTT   GA  GAATCTACA
                                   CA_  TT
GAM264   LOC151489 3'  ATATTTGATGGCTTTGCTT   85424       A   T
                                GAGCAAA GCT TTAGGTGT
                                ||||||| ||| ||||||||
                                TTCGTTT CGG AGTTTATA
                                    _   T
GAM264   LOC151507 3'  GGCCTGAAAGTGTTC      80265     AAAA       TG
                                GAGC    GCTTTTAGG  T
                                ||||    |||||||||  |
                                CTTG    TGAAAGTCC  G
                                  ____         GT
GAM264   LOC151534 5'  ACGTTTGGAAGCTTTGCT    56682       A     GG
                                AGCAAA GCTTTTA  TGT
                                |||||| |||||||  |||
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                                TCGTTT CGAAGGT  GCA
                                   _     TT
GAM264  LOC151568 3'  GCACTTGAGGCTCTGTCCA   56694    AG  AA     T
                                TG  CA  AGCTTT AGGTGT
                                ||  ||  |||||| ||||||
                                AC  GT  TCGGAG TTCACG
                                 CT  C_     _
GAM264  LOC151963 3'  CGATCTTGGGTTTTTGC     80400         TT    GT
                                GCAAAAGCTT  AGGT
                                ||||||||||  ||||
                                CGTTTTTGGG  TCTA
                                      T_   GCG
GAM264  LOC151963 3'  ATACTTGGTGCAAATTTGTTCA 80398        A__  TT
                                TGAGCAAA   GC  TTAGGTGT
                                ||||||||   ||  ||||||||
                                ACTTGTTT   CG  GGTTCATA
                                     AAA  T_
GAM264  LOC151996 5'  GCACCTGGAGGACATGC     85534     AAAG
                                GCA    CTTTTAGGTGT
                                |||    ||||||||||
                                CGT    GGAGGTCCACG
                                  ACA_
GAM264  LOC152110 3'  TACTTGAGGGCTTCATTGC    80457      __         GT
                                GCAA  AAGCTTTTAGGT
                                ||||  ||||||||||||
                                CGTT  TTCGGGAGTTCA
                                   AC          TG
GAM264  LOC152185 3'  AGGCCTGGGAGTGTTTGTTTA  58525        A        GT
                                TGAGCAAA GCTTTTAGGT
                                |||||||| ||||||||||
                                ATTTGTTT TGAGGGTCCG
                                     G         GAT
GAM264  LOC152215 3'  TGCATTTATCTTTTGTTCA    80491         CTTT
                                TGAGCAAAAG    TAGGTGT
                                ||||||||||    |||||||
                                ACTTGTTTTC    ATTTACG
                                      T___      TC
GAM264  LOC152215 3'  ATATAAATTTGTTTTTGCTT   80488         TTTTAG
                                GAGCAAAAGC     GTGT
                                ||||||||||     ||||
                                TTCGTTTTTG     TATA
                                      TTTAAA
GAM264  LOC152215 3'  ACATCTAGACCCCTTGCT    80487      AAGCT
                                AGCAA    TTTAGGTGT
                                |||||    |||||||||
                                TCGTT    AGATCTACA
                                   CCCC_
GAM264  LOC152286 3'  ACACCTGGGGGACCCTCA    85625     CAAAAG
                                TGAG     CTTTTAGGTGT
                                ||||     ||||||||||
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                                ACTC     GGGGGTCCACA
                                  CCA___
GAM264  LOC152316 3'  CACCTGAGAGGTTTG      85610      AG
                                CAAA  CTTTTAGGTG
                                ||||  ||||||||||
                                GTTT  GAGAGTCCAC
                                  G_
GAM264  LOC152316 3'  GTGCTTAGGGGCTTGTGGCCA  85615    A  AA_        TG
                                TG GC   AAGCTTTTAGG  T
                                || ||   ||||||||||  |
                                AC CG   TTCGGGGATTC  G
                                 _ GTG         GT
GAM264  LOC152317 3'  TGTCCTGCAGAGGCTTTGTTT  85652        A    __   TGT
                                GAGCAAA GCTTT  TAGG
                                |||||||  |||||  ||||
                                TTTGTTT CGGAG  GTCC
                                    _    AC    TGTG
GAM264  LOC152317 5'  GCATCAGTCGGGGCTTTTGC   85643          TA__
                                GCAAAAGCTTT    GGTGT
                                ||||||||||    |||||
                                CGTTTTCGGGG    CTACG
                                      CTGA
GAM264  LOC152317 5'  CACCTGGGATAGTTTT      85638       __
                                AAAGCT  TTTAGGTG
                                ||||||  ||||||||
                                TTTTGA  GGGTCCAC
                                   TA
GAM264  LOC152343 3'  ATGCTTAAAAGCTAACTTA   80556     CAAA
                                TGAG    AGCTTTTAGGTGT
                                ||||    ||||||||||||
                                ATTC    TCGAAAATTCGTA
                                  AA__
GAM264  LOC152348 5'  ACATTTAAAAGTGTGTTC    85691      AAA
                                GAGCA   GCTTTTAGGTGT
                                |||||   ||||||||||||
                                CTTGT   TGAAAATTTACA
                                  G__
GAM264  LOC152445 5'  ATACTTAGAAGCTGGTG     85744    AA
                                CA  AGCTTTTAGGTGT
                                ||  ||||||||||||
                                GT  TCGAAGATTCATA
                                 GG
GAM264  LOC152445 3'  ATATTTAAAGGTAACTGC    85745     AAA
                                GCA   GCTTTTAGGTGT
                                |||   ||||||||||||
                                CGT   TGGAAATTTATA
                                  CAA
GAM264  LOC152464 3'  ATGCTTGGAAGCCACTAGCCA  59985    A  AAAA_
                                TG GC    GCTTTTAGGTGT
                                || ||    ||||||||||||
```

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                                AC CG     CGAAGGTTCGTA
                                 _ ATCAC
GAM264   LOC152503 5'  ATGTTCTGGACAGAGTTTTAGC 85768      A       ___    TGT
                TC                    GAGC AAAGCTTT   TAGG
                                      |||| ||||||||   ||||
                                      CTCG TTTTGAGA   GTCT
                                        A       CAG    TGTA
GAM264   LOC152641 3'  GCATTTAGGGCGGCCGCTT    80634      AAAA    T
                                      GAGC    GCTTT AGGTGT
                                      ||||    ||||| ||||||
                                      TTCG    CGGGA TTTACG
                                        CCGG    _
GAM264   LOC152756 3'  ACATCTGAAACAGCAAGTGT   85872     AAA   __
                                      GCA   GCT  TTTAGGTGT
                                      |||   |||  |||||||||
                                      TGT   CGA  AAGTCTACA
                                        GAA   CA
GAM264   LOC152845 5'  GCACCTGAAGGGCCACTCA    60331      CAAAAG
                                      TGAG      CTTTTAGGTGT
                                      ||||      ||||||||||
                                      ACTC      GGAAGTCCACG
                                        ACCG__
GAM264   LOC152897 3'  TACACCTGCCCTTTAAGCTTTT 80730    C       T_____
                TTTTA                   G AAAAGCTT      TAGGTGT   A
                                      | ||||||||     |||||||   |
                                      T TTTTCGAA     GTCCACA   T
                                       T       TTTCCC
GAM264   LOC152905 3'  ATGCCTTCCTTGTTTTTGTTT  60473          TTTT_
                                      GAGCAAAAGC     AGGTGT
                                      ||||||||||     ||||||
                                      TTTGTTTTTG     TCCGTA
                                            TTCCT
GAM264   LOC152920 5'  GCATTTGGAGGTTCTTGCTCA  80741        A
                                      TGAGCAA AGCTTTTAGGTGT
                                      ||||||| ||||||||||||
                                      ACTCGTT TTGGAGGTTTACG
                                           C
GAM264   LOC153453 5'  GTAGTAAAAGTTTCTGCTCA   80840       A       GGTGT
                                      TGAGCA AAGCTTTTA
                                      ||||||  |||||||||
                                      ACTCGT TTTGAAAAT
                                         C        GATG
GAM264   LOC153561 5'  GTGCCTGGGAGTGGTCA     80890     G AAAA       TG
                                      TGA C    GCTTTTAGG  T
                                      ||| |    |||||||||  |
                                      ACT G    TGAGGGTCC  G
                                        G _____        GT
GAM264   LOC153642 3'  CATTTGATGGTGCTC       80904      AAAA   T
                                      GAGC    GCT TTAGGTG
                                      ||||    ||| |||||||
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                                CTCG    TGG AGTTTAC
                                  ____  T
GAM264   LOC153811 3'  ACACCTGGGAGGAACGTTC    80937      AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                CTTG    GAGGGTCCACA
                                  CAAG_
GAM264   LOC154089 3'  ATTACAATAAGGTTATTTGCTC 81036        _     TAG   T
           A                     TGAGCAAA AGCTTT   GTG
                                ||||||||| ||||||   |||
                                ACTCGTTT TTGGAA   CAT
                                    A     TAA   TAT
GAM264   LOC154282 3'  GCACTTGAGCTCTGCT      86201      AA     TT
                                AGCA  AGCTT  AGGTGT
                                ||||  |||||  ||||||
                                TCGT  TCGAG  TTCACG
                                  C_    __
GAM264   LOC154386 3'  ACACTAATGGTATTTTGTTCA  81078         _  T    G
                                TGAGCAAAA GCT TTAG TGT
                                ||||||||| ||| |||| |||
                                ACTTGTTTT TGG AATC ACA
                                    A  T   _
GAM264   LOC154386 3'  TTAATCTTGGGAGTTATTGTTT 81085        A        TGT
           A                     TGAGCAA AGCTTTTAGG
                                ||||||| |||||||||
                                ATTTGTT TTGAGGGTTC
                                    A        TAATTT
GAM264   LOC154442 5'  GCGCCACTGTTTTTGTTT     86219          TTTTA
                                GAGCAAAAGC     GGTGT
                                ||||||||||     |||||
                                TTTGTTTTTG     CCGCG
                                     TCA__
GAM264   LOC154743 3'  GCACTTGGAAGAGAGTTTA    81116      AAAAG
                                TGAGC     CTTTTAGGTGT
                                |||||     ||||||||||
                                ATTTG     GAAGGTTCACG
                                  AGA__
GAM264   LOC154789 5'  GCACCTGGGGCGTGGCTTA    81136      AAAA    T
                                TGAGC    GCTTT AGGTGT
                                |||||    ||||| ||||||
                                ATTCG    CGGGG TCCACG
                                  GTG_    _
GAM264   LOC154860 3'  ACGCTTGTGGCTTTTTGTT    86271       _  TT
                                AGCAAAA GCT  TAGGTGT
                                ||||||| |||  |||||||
                                TTGTTTT CGG  GTTCGCA
                                    T  T_
GAM264   LOC155054 5'  TACCTGGGAGTTGGGTT     81276     AAA        GT
                                AGC   AGCTTTTAGGT
                                |||   ||||||||||
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                                TTG  TTGAGGGTCCA
                                  GG_        TG
GAM264  LOC155060 3' GCACCTAAAGGTTGAGC    86330    AAA
                                GC  AGCTTTTAGGTGT
                                ||  ||||||||||||
                                CG  TTGGAAATCCACG
                                 AG_
GAM264  LOC155064 3' GTGCTTGGGGGCGGAGTTCA  81251      AAAA       TG
                                TGAGC   GCTTTTAGG T
                                |||||   ||||||||| |
                                ACTTG   CGGGGGTTC G
                                   AGG_      GT
GAM264  LOC155064 3' ATATCTGGGCATTGCTTA    81248       AA  TT
                                TGAGCAA  GCT  TAGGTGT
                                |||||||  |||  |||||||
                                ATTCGTT  CGG  GTCTATA
                                    A_  __
GAM264  LOC155081 3' GCATTTGAAGGCACAATGC   81293    AAA_
                                GCA   GCTTTTAGGTGT
                                |||   ||||||||||||
                                CGT   CGGAAGTTTACG
                                  AACA
GAM264  LOC155179 3' ACGTCTGGAAGCTGAAATGT  81307    AA__      GT
                                GCA   AGCTTTTAG  GT
                                |||   |||||||||  ||
                                TGT   TCGAAGGTC  CA
                                  AAAG       TG
GAM264  LOC155376 5' GCACCTGGGAGTTCAGTT    81336    AAA
                                AGC  AGCTTTTAGGTGT
                                |||  ||||||||||||
                                TTG  TTGAGGGTCCACG
                                  AC_
GAM264  LOC155397 3' GCACCTGGGAGTTCAGTT    81328    AAA
                                AGC  AGCTTTTAGGTGT
                                |||  ||||||||||||
                                TTG  TTGAGGGTCCACG
                                  AC_
GAM264  LOC157292 3' TACCTGAGCCTGCTT      86419      AAA   TT
                                GAGCA  GCTT  AGGTG
                                |||||  ||||  |||||
                                TTCGT  CGAG  TCCAT
                                   C__   __
GAM264  LOC157306 3' ATACTTGGGAGTTGGTG    81395    AA
                                CA  AGCTTTTAGGTGT
                                ||  ||||||||||||
                                GT  TTGAGGGTTCATA
                                 GG
GAM264  LOC157355 3' GCACCTAGGATGCCTGC    81427    AAA  _
                                GCA  GC TTTTAGGTGT
                                |||  ||  ||||||||||
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                                CGT   CG AGGATCCACG
                                  C__  T
GAM264   LOC157376 3'  GTACCTCCACTCGGTATTTGCT 81430        A   TTT___   GT
            CA                    TGAGCAAA GCT     AGGT
                                  |||||||| |||     ||||
                                  ACTCGTTT TGG     TCCA
                                      A   CTCACC    TG
GAM264   LOC157507 3'  ATCATAAAAAAGTTTTTGGTCA 81452     G        AG   T
                                  TGA CAAAAGCTTTT  GTG
                                  ||| ||||||||||  |||
                                  ACT GTTTTTGAAAA  TAC
                                    G         AA   TAT
GAM264   LOC157567 3'  GCACCTAAGCTATTGCT     81479      A    TT
                                  AGCAA AGCT  TAGGTGT
                                  ||||| ||||  |||||||
                                  TCGTT TCGA  ATCCACG
                                     A   __
GAM264   LOC157567 3'  ATGTTTGAAGGCCTCTTTTGTT 81477        ___       TG
                                  AGCAAAA   GCTTTTAGG  T
                                  |||||||   |||||||||  |
                                  TTGTTTT   CGGAAGTTT  A
                                      CTC       GT
GAM264   LOC157697 3'  TATCTGAAAGTCTCTGCTT   81553      AAA       GT
                                  GAGCA   GCTTTTAGGT
                                  |||||   ||||||||||
                                  TTCGT   TGAAAGTCTA
                                     CTC        TG
GAM264   LOC157858 5'  ATGCCTGAAGGCAGAAGCT   86582     AAAA
                                  AGC    GCTTTTAGGTGT
                                  |||    ||||||||||||
                                  TCG    CGGAAGTCCGTA
                                    AAGA
GAM264   LOC157909 5'  GTGCTTAAAAGCTGTTCTCA   81628      C  A       TG
                                  TGAG AA AGCTTTTAGG  T
                                  |||| || ||||||||||  |
                                  ACTC TT TCGAAAATTC  G
                                    _  G        GT
GAM264   LOC157918 3'  ACGCCTGACTGCTGTTCA    86638       AAA  TT
                                  TGAGCA   GC  TTAGGTGT
                                  ||||||   ||  ||||||||
                                  ACTTGT   CG  AGTCCGCA
                                      ___  TC
GAM264   LOC157922 3'  GCATCTGGAAGCGCTGC     86634     AAA
                                  GCA   GCTTTTAGGTGT
                                  |||   ||||||||||||
                                  CGT   CGAAGGTCTACG
                                    CG_
GAM264   LOC157931 3'  GCACCTAGGAGTAATCTTA    86662      CAAAA
                                  TGAG    GCTTTTAGGTGT
                                  ||||    ||||||||||||
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                                ATTC    TGAGGATCCACG
                                  TAA__
GAM264  LOC158014 5'  TAAAATTAAAAGTCTTTGTTTA 81657        AG     GTGT
                                TGAGCAAA  CTTTTAG
                                ||||||||  |||||||
                                ATTTGTTT  GAAAATT
                                     CT      AAAATT
GAM264  LOC158117 3'  GCACCTGGAGAGTCCTTGCCA  81707    A   AA    _
                                TG GCAA  GCTTTT AGGTGT
                                || ||||  |||||| ||||||
                                AC CGTT  TGAGAG TCCACG
                                 _   CC     G
GAM264  LOC158117 3'  GCACTTGAAAGCCGTGT     81708     AAA
                                GCA   GCTTTTAGGTGT
                                |||   ||||||||||||
                                TGT   CGAAAGTTCACG
                                  GC_
GAM264  LOC158156 3'  ACATCTGATATTTTTGCT    81723        CTT
                                AGCAAAAG   TTAGGTGT
                                ||||||||   ||||||||
                                TCGTTTTT   AGTCTACA
                                     AT_
GAM264  LOC158191 3'  ACACCTGAGCCGCAGTGT    81769     AAA  T_
                                GCA   GC  TTTAGGTGT
                                |||   ||  |||||||||
                                TGT   CG  GAGTCCACA
                                  GA_  CC
GAM264  LOC158237 5'  ACACCTAAAAGTGGC       60452    AAAA
                                GC    GCTTTTAGGTGT
                                ||    ||||||||||||
                                CG    TGAAAATCCACA
                                 G___
GAM264  LOC158257 3'  GCACTTAGAGAGCTTTT     86709          _
                                AAAAGCTTTT AGGTGT
                                |||||||||| ||||||
                                TTTTCGAGAG TTCACG
                                      A
GAM264  LOC158267 3'  GCACCTGGGAGGTGGGGCT   81832     AAAAG
                                AGC     CTTTTAGGTGT
                                |||     ||||||||||||
                                TCG     GAGGGTCCACG
                                  GGGTG
GAM264  LOC158293 5'  GCGCCTGGAGGCCAGAGGC   81863    AAAA_
                                GC    GCTTTTAGGTGT
                                ||    ||||||||||||
                                CG    CGGAGGTCCGCG
                                 GAGAC
GAM264  LOC158314 3'  ACACTTAGGGGTATGGGTT   86767     AAAA
                                AGC    GCTTTTAGGTGT
                                |||    ||||||||||||
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                                TTG   TGGGGATTCACA
                                  GGTA
GAM264  LOC158332 3'  ATATCTGGGAAAGTTTGCT   81886       AGC
                                AGCAAA  TTTTAGGTGT
                                ||||||  ||||||||||
                                TCGTTT  AGGGTCTATA
                                   GAA
GAM264  LOC158476 3'  ATGCCTGAGTGTTTATGCTT  86837      A   T
                                GAGCA AAGC TTTAGGTGT
                                ||||| |||| |||||||||
                                TTCGT TTTG GAGTCCGTA
                                   A   T
GAM264  LOC158521 3'  ACCAAAGTGTTTGCTT      86863       A    TA
                                GAGCAAA GCTTT  GGT
                                ||||||| |||||  |||
                                TTCGTTT TGAAA  CCA
                                   G    __
GAM264  LOC158563 3'  ATGCCTGAGAGTTGGTG     81949    AA
                                CA  AGCTTTTAGGTGT
                                ||  ||||||||||||
                                GT  TTGAGAGTCCGTA
                                 GG
GAM264  LOC158629 5'  TGGCCCCAGCATTTGCTCA   86885       A  TTTA  GT
                                TGAGCAAA GCT   GGT
                                |||||||| |||   |||
                                ACTCGTTT CGA   CCG
                                     A  CC__  GTA
GAM264  LOC158668 3'  TAATTTAAGACTTTTGTTTA  69373        C      GT
                                TGAGCAAAAG TTTTAGGT
                                |||||||||| ||||||||
                                ATTTGTTTTC AGAATTTA
                                      _      ATG
GAM264  LOC158819 3'  ACATCTCTATTTTGCTTA    86899        GCTTTT
                                TGAGCAAAA     AGGTGT
                                |||||||||     ||||||
                                ATTCGTTTT     TCTACA
                                      ATC___
GAM264  LOC158865 5'  ACACCTGGCTAGTTTTT     86926       T_
                                AAAAGCT  TTAGGTGT
                                |||||||  ||||||||
                                TTTTTGA  GGTCCACA
                                   TC
GAM264  LOC160414 5'  CGCTTTGCTTTTGTCA      87066     G      TTTT
                                TGA CAAAAGC    AGGTG
                                ||| |||||||    |||||
                                ACT GTTTTCG    TTCGC
                                  _      T____
GAM264  LOC161742 3'  ACACTTAAGCTTGTGTT     82288     A    TT
                                AGCA AAGCT  TAGGTGT
                                |||| |||||  |||||||
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                                TTGT TTCGA  ATTCACA
                                  G    __
GAM264   LOC162239 3'  GCACTTAAGATTATATGTTTA  82342      AAAGC
                                TGAGCA    TTTTAGGTGT
                                ||||||    ||||||||||
                                ATTTGT    AGAATTCACG
                                   ATATT
GAM264   LOC162333 5'  GCATTTAAAGGGCAATTTTGC  87134      __  _
                                GCAAAA  GCT TTTAGGTGT
                                ||||||  ||| |||||||||
                                CGTTTT  CGG AAATTTACG
                                   AA  G
GAM264   LOC163115 5'  ATGCCTGGGCCCTGCTCA    82410      AAA  TT
                                TGAGCA  GCT  TAGGTGT
                                ||||||  |||  |||||||
                                ACTCGT  CGG  GTCCGTA
                                   CC_  __
GAM264   LOC163231 5'  ATACCTGGAGGAAGGTGCCCA  82435    A  AAAG
                                TG GCA   CTTTTAGGTGT
                                || |||   ||||||||||
                                AC CGT   GGAGGTCCATA
                                 C  GGAA
GAM264   LOC163341 3'  GCACCTGGAGCACCTGCTCA  82120      AAA   T
                                TGAGCA  GCTTT AGGTGT
                                ||||||  ||||| ||||||
                                ACTCGT  CGAGG TCCACG
                                   CCA   _
GAM264   LOC163412 5'  GCGCCTGGACTTGTGCTCA   82134      A  CT
                                TGAGCA AAG  TTTAGGTGT
                                ||||||| |||  |||||||||
                                ACTCGT TTC  AGGTCCGCG
                                   G  __
GAM264   LOC163590 3'  GTCTCTGATGCTTTTGTTCA  58862        TT   TGT
                                TGAGCAAAAGC  TTAGG
                                ||||||||||  |||||
                                ACTTGTTTTCG  AGTCT
                                      T_    CTGT
GAM264   LOC163682 5'  ACACCTGGGCTCTGC      87019    AA  TT
                                GCA  AGCT  TAGGTGT
                                |||  ||||  |||||||
                                CGT  TCGG  GTCCACA
                                  C_   __
GAM264   LOC163688 5'  GTGCCTCATGCATTTGTTCA  56941      A  TTTT  TG
                                TGAGCAAA GC   AGG  T
                                ||||||||  ||   |||  |
                                ACTTGTTT CG   TCC  G
                                     A  TAC_  GT
GAM264   LOC163882 3'  ACATTTAGGAAGCCTTGCTT  82161      AA   _
                                GAGCAA  GCTTT TAGGTGT
                                ||||||  ||||| |||||||
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                                TTCGTT  CGAAG ATTTACA
                                   C_    G
GAM264   LOC164173 3'  GCACTTAAAATCTCCTGATCA  82174     G  AA  C
                                TGA CA  AG TTTTAGGTGT
                                ||| ||  || ||||||||||
                                ACT GT  TC AAAATTCACG
                                  A  CC  T
GAM264   LOC164397 5'  GTACTTAGAGGCCCAGGGGCTT 82529       AAAA__        GT
           A                     TGAGC     GCTTTTAGGT
                                ||||||     ||||||||||
                                ATTCG     CGGAGATTCA
                                   GGGACC         TG
GAM264   LOC164397 3'  GCATCTGGGAGCCGCT      82527     AAAA
                                AGC    GCTTTTAGGTGT
                                |||    ||||||||||||
                                TCG    CGAGGGTCTACG
                                  C___
GAM264   LOC165257 3'  GTGCCTAGAAGCGGAGGGCTC  82482      AAAA_       TG
                                GAGC    GCTTTTAGG  T
                                ||||    ||||||||| |
                                CTCG    CGAAGATCC  G
                                  GGAGG       GT
GAM264   LOC166341 3'  ACACCTGGGAGAAATTG     82627     AAG
                                CAA   CTTTTAGGTGT
                                |||   ||||||||||
                                GTT   GAGGGTCCACA
                                  AAA
GAM264   LOC167606 5'  ATGCTTGGAAGTGACTCGCT   87272     AAAA_
                                AGC    GCTTTTAGGTGT
                                |||    ||||||||||||
                                TCG    TGAAGGTTCGTA
                                  CTCAG
GAM264   LOC168082 5'  ACACCTGGAAAAGGCTCA    82688      AAAAGC
                                TGAGC     TTTTAGGTGT
                                |||||     ||||||||||
                                ACTCG     AAGGTCCACA
                                   GAA___
GAM264   LOC168667 3'  TGCATTTGGGGGTCTCACTTTT 92760        _____
           GCTTA                  GCAAAAG    CTTTTAGGTGT   G
                                |||||||    |||||||||||  |
                                CGTTTTC    GGGGGTTTACG   T
                                    ACTCT
GAM264   LOC170372 5'  TATCTGGAGGATCCTGCTT    76362      AAAG       GT
                                GAGCA   CTTTTAGGT
                                |||||   |||||||||
                                TTCGT   GGAGGTCTA
                                   CCTA       TG
GAM264   LOC196074 3'  GCATCGTCAAAAGATTTTTGCT 87581          _    A__
           T                    GAGCAAAAG CTTTT   GGTGT
                                ||||||||| |||||   |||||
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                                TTCGTTTTT GAAAA  CTACG
                                     A    CTG
GAM264  LOC196205 3'  GGTCTAGGGGTGATTGT    87592     AA       TG
                                GCAA  GCTTTTAGG  T
                                ||||  |||||||||  |
                                TGTT  TGGGGATCT  G
                                  AG       GT
GAM264  LOC196477 3'  TCAAAGTAATAGCTTTTGTTCA 87722          T   GGTGT
                                TGAGCAAAAGCT TTA
                                |||||||||||| |||
                                ACTTGTTTTCGA AAT
                                       T   GAAACTT
GAM264  LOC196812 3'  ACATTTCTCTTTTGCTC    89560        CTTTT
                                GAGCAAAAG    AGGTGT
                                |||||||||    ||||||
                                CTCGTTTTC    TTTACA
                                     TC___
GAM264  LOC197336 3'  ATACCTGTTGCCCTTTTGC   59236       CTTT_
                                GCAAAAG    TAGGTGT
                                |||||||    |||||||
                                CGTTTTC    GTCCATA
                                    CCGTT
GAM264  LOC197408 5'  ATGCCTGAACCAGGGTTTGTTT 89747        AG __
          A                      TGAGCAAA  CT  TTTAGGTGT
                                 ||||||||  ||  |||||||||
                                 ATTTGTTT  GA  AAGTCCGTA
                                     GG  CC
GAM264  LOC199221 3'  ACACCTGGAATCCCTGCT    80348     AAAGC
                                AGCA    TTTTAGGTGT
                                ||||    ||||||||||
                                TCGT    AAGGTCCACA
                                  CCCT_
GAM264  LOC199704 5'  GCACCTGGACCCTTCTCA    88330     CAA   CT
                                TGAG   AAG  TTTAGGTGT
                                ||||   |||  |||||||||
                                ACTC   TTC  AGGTCCACG
                                  ___   CC
GAM264  LOC199718 3'  ATATCTGAGTGTTTTTCTC   88335     C     T
                                GAG AAAAGC TTTAGGTGT
                                ||| |||||| |||||||||
                                CTC TTTTTG GAGTCTATA
                                  _     T
GAM264  LOC199786 3'  GCACCTGGGTGGCTTGC     88383     AA   _
                                GCA  AGCT TTTAGGTGT
                                |||  |||| |||||||||
                                CGT  TCGG GGGTCCACG
                                  __    T
GAM264  LOC199920 3'  GCACCTAGTCAGTTGTGC    88491     AA   T_
                                GCA  AGCT  TTAGGTGT
                                |||  ||||  ||||||||
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                                CGT  TTGA  GATCCACG
                                  G_   CT
GAM264   LOC200186 3'  ATGCCTAGGGGTGGGC     89962    AAAA
                                GC   GCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   TGGGGATCCGTA
                                 GG__
GAM264   LOC200197 3'  CACTTGGGAGAGCTC      88614     AAAAG
                                GAGC    CTTTTAGGTG
                                ||||    ||||||||||
                                CTCG    GAGGGTTCAC
                                  A____
GAM264   LOC200197 3'  GCACCTGAATTGCATTTTG   88617      _ T_
                                CAAAA GC  TTTAGGTGT
                                ||||| ||  |||||||||
                                GTTTT CG  AAGTCCACG
                                   A  TT
GAM264   LOC200197 3'  GCACCTGGAAGCTTGTTG    88618    _
                                CAA AAGCTTTTAGGTGT
                                ||| ||||||||||||||
                                GTT TTCGAAGGTCCACG
                                  G
GAM264   LOC200298 3'  ACACCTGAGGGACTCTC     89971    CAAA  _
                                GAG   AG CTTTTAGGTGT
                                |||   || ||||||||||
                                CTC   TC GGGAGTCCACA
                                  ____  A
GAM264   LOC200301 5'  ACACTTAAAGGAAGTGCTCA  88734      AAAG
                                TGAGCA   CTTTTAGGTGT
                                ||||||   ||||||||||
                                ACTCGT   GGAAATTCACA
                                   GAA_
GAM264   LOC200301 3'  GCATCTGGGGGCGCCCGTGC  88744    AAA__
                                GCA    GCTTTTAGGTGT
                                |||    ||||||||||
                                CGT    CGGGGGTCTACG
                                  GCCCG
GAM264   LOC200339 3'  GCACTTTTCCCCCTTTTGTTT  90034       CTTTT_
                                GAGCAAAAG     AGGTGT
                                |||||||||     ||||||
                                TTTGTTTTC     TTCACG
                                     CCCCTT
GAM264   LOC200488 5'  ACATCTAAATTGGTTTTTGTTT 90078         __
                                GAGCAAAAGCT  TTTAGGTGT
                                ||||||||||  |||||||||
                                TTTGTTTTTGG  AAATCTACA
                                       TT
GAM264   LOC200531 3'  ACACCTAAGGCGCCCTGCTC  88820      AAA_   T
                                GAGCA   GCTTT AGGTGT
                                |||||   ||||| ||||||
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                                CTCGT    CGGAA TCCACA
                                   CCCG    _
GAM264   LOC200781 3'  GAATTCTGGAAGCTTTTTTCA  90138      C          TGT
                                TGAG AAAAGCTTTTAGG
                                |||| ||||||||||||
                                ACTT TTTTCGAAGGTCT
                                   _          TAAGG
GAM264   LOC200940 3'  GCACCTGGAGGGCCTCA     88953      CAAAAG
                                TGAG     CTTTTAGGTGT
                                ||||     ||||||||||
                                ACTC     GGAGGTCCACG
                                  CG____
GAM264   LOC201164 3'  ACATCTGAATAAACATGTTC   88109       AAAGCT
                                GAGCA     TTTAGGTGT
                                |||||     |||||||||
                                CTTGT     AAGTCTACA
                                   ACAAAT
GAM264   LOC201191 3'  GCACCTAAGTCCTCTTTG    89770      _ CT
                                CAAA AG  TTTAGGTGT
                                |||| ||  |||||||||
                                GTTT TC  GAATCCACG
                                  C  CT
GAM264   LOC201287 5'  ACATCTGAAGGTGTTATCTTA  88180      CAAAA
                                TGAG    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                ATTC    TGGAAGTCTACA
                                  TATTG
GAM264   LOC201510 3'  ACACTTTGAGTTTCTGTTT    88248      A     TT
                                GAGCA AAGCTT  AGGTGT
                                ||||| ||||||  ||||||
                                TTTGT TTTGAG  TTCACA
                                   C     T_
GAM264   LOC201627 3'  CTTGAAGCTTTTCCTTA     89014      C        T
                                TGAG AAAAGCTTT AG
                                |||| ||||||||| ||
                                ATTC TTTTCGAAG TC
                                  C        T
GAM264   LOC201695 5'  ATATCTGGAAGATCGGCCCA   90705    A  AAAAG
                                TG GC    CTTTTAGGTGT
                                || ||    ||||||||||
                                AC CG    GAAGGTCTATA
                                 C  GCTA_
GAM264   LOC201799 3'  GCACTTGGAAGAATGTGC     89063     AAAG
                                GCA    CTTTTAGGTGT
                                |||    ||||||||||
                                CGT    GAAGGTTCACG
                                  GTAA
GAM264   LOC202018 3'  ATACTTAACTGATTTTGCTT   89140        GCTT
                                GAGCAAAA    TTAGGTGT
                                ||||||||    ||||||||
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                                TTCGTTTT    AATTCATA
                                     AGTC
GAM264   LOC202024 3'  ATGCCTGAAACACGAAGTTCA  89146      AAAAGC
                                TGAGC     TTTTAGGTGT
                                |||||     ||||||||||
                                ACTTG     AAAGTCCGTA
                                   AAGCAC
GAM264   LOC202052 3'  ACATCTGAACGGTTGTTC    90304       AAGCT
                                GAGCAA    TTTAGGTGT
                                ||||||    |||||||||
                                CTTGTT    AAGTCTACA
                                   GGC__
GAM264   LOC202052 3'  GCATCTGGAGGCGGGGGCCA   90308    A  AAAA
                                TG GC    GCTTTTAGGTGT
                                || ||    ||||||||||||
                                AC CG    CGGAGGTCTACG
                                 _ GGGG
GAM264   LOC202309 5'  ATGCCTAAAAGAGCTT      90335      AAAAG
                                GAGC     CTTTTAGGTGT
                                ||||     ||||||||||||
                                TTCG     GAAAATCCGTA
                                  A____
GAM264   LOC202451 3'  GCCTTGAAGCATTTTGTTTA   90353         _    T    GT
                                TGAGCAAAA GCTTT AGGT
                                ||||||||| ||||| ||||
                                ATTTGTTTT CGAAG TCCG
                                     A    T
GAM264   LOC202754 3'  GCTTCTGAACTTTTGCTTA    82708          CT     T
                                TGAGCAAAAG  TTTAGG GT
                                ||||||||||  |||||| ||
                                ATTCGTTTTC  AAGTCT CG
                                      __     T
GAM264   LOC202759 5'  ATGCCTGGATTGTGCTCA     73512       AAAGCT
                                TGAGCA     TTTAGGTGT
                                ||||||     |||||||||
                                ACTCGT     AGGTCCGTA
                                   GTT___
GAM264   LOC202775 3'  GCACCTGGGCCATGTTT     90361      AAA   TT
                                GAGCA   GCT  TAGGTGT
                                |||||   |||  |||||||
                                TTTGT   CGG  GTCCACG
                                  AC_  __
GAM264   LOC202802 3'  GCATTTGAAGGCACAATGC    89207     AAA_
                                GCA    GCTTTTAGGTGT
                                |||    ||||||||||||
                                CGT    CGGAAGTTTACG
                                  AACA
GAM264   LOC202934 5'  ATACCTGTCATTTTGTTCA    90402         GCTTT
                                TGAGCAAAA     TAGGTGT
                                |||||||||     |||||||
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                                ACTTGTTTT    GTCCATA
                                     ACT__
GAM264  LOC203052 3' GCACTTGGCATGTTTGCTGC  90454    A_   TT_
                                GCA  AAGC   TTAGGTGT
                                |||  ||||   ||||||||
                                CGT  TTTG   GGTTCACG
                                  CG    TAC
GAM264  LOC203246 3' ACATCTTTGCTTTTGCCA    89301    A      TTTT
                                TG GCAAAAGC    AGGTGT
                                || |||||||||   ||||||
                                AC CGTTTTCG    TCTACA
                                  _       TT__
GAM264  LOC203248 3' ATACCTGGAAGACTCCGGTCA  89309     G AAA  _
                                TGA C   AG CTTTTAGGTGT
                                ||| |   || ||||||||||
                                ACT G   TC GAAGGTCCATA
                                  _ GCC  A
GAM264  LOC203275 3' GCACTTGAAAGCCGTGT     89324     AAA
                                GCA   GCTTTTAGGTGT
                                |||   ||||||||||||
                                TGT   CGAAAGTTCACG
                                  GC_
GAM264  LOC203275 3' GCACCTGGAGAGTCCTTGCCA  89323    A    AA     _
                                TG GCAA  GCTTTT AGGTGT
                                || ||||  |||||| ||||||
                                AC CGTT  TGAGAG TCCACG
                                  _   CC     G
GAM264  LOC203350 3' ATGCTGTAGAGAGTGTTTGCTT 90562         A     A__
             A                   TGAGCAAA GCTTTT   GGTGT
                                 |||||||| ||||||   |||||
                                 ATTCGTTT TGAGAG   TCGTA
                                      G     ATG
GAM264  LOC203365 3' ATACTTGAGTCTTTGCTTA    89347         AG   TT
                                 TGAGCAAA  CTT  AGGTGT
                                 ||||||||  |||  ||||||
                                 ATTCGTTT  GAG  TTCATA
                                      CT  __
GAM264  LOC203378 3' GCACTAGCTTCAGGCTTTTGTT 90606           TT  ____
             T                   GAGCAAAAGCTT  AG   GTGT
                                 ||||||||||||  ||   ||||
                                 TTTGTTTTCGGA  TC   CACG
                                       CT  GAT
GAM264  LOC203429 3' ATACCTAAGCATTTTTTTCA   89362     C   _   TT
                                 TGAG AAAA GCT  TAGGTGT
                                 |||| |||| |||  |||||||
                                 ACTT TTTT CGA  ATCCATA
                                   T   A  __
GAM264  LOC203536 3' CACTTGAAAGGGCTC       89379      AAAAG
                                 GAGC    CTTTTAGGTG
                                 ||||    ||||||||||
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                                CTCG    GAAAGTTCAC
                                  G____
GAM264  LOC204970 3'  GTGCCTGGAGGCCGTCTCA   89416     CAAAA       TG
                                TGAG    GCTTTTAGG  T
                                ||||    |||||||||  |
                                ACTC    CGGAGGTCC  G
                                  TGC__       GT
GAM264  LOC205095 3'  ACACCTGAAAGTGAGTTG    90694     AA_
                                CAA   GCTTTTAGGTGT
                                |||   ||||||||||||
                                GTT   TGAAAGTCCACA
                                  GAG
GAM264  LOC205327 3'  ACACTTAAGCACTATTGTTTA  89498       A  CT
                                TGAGCAA AG  TTTAGGTGT
                                |||||||  ||  |||||||||
                                ATTTGTT TC  GAATTCACA
                                    A  AC
GAM264  LOC205418 5'  ACACCTGTTATTTTTGCT    90678       CTTT
                                AGCAAAAG    TAGGTGT
                                ||||||||    |||||||
                                TCGTTTTT    GTCCACA
                                    ATT_
GAM264  LOC206372 3'  ACCCCAGGGCTTTTGCT     89529         TA
                                AGCAAAAGCTTT  GGT
                                ||||||||||||  |||
                                TCGTTTTCGGGA  CCA
                                      CC
GAM264  LOC206463 3'  GCACTTGGAGACCGGCTC    89539     AAAAG    T
                                GAGC    CTTT AGGTGT
                                ||||    |||| ||||||
                                CTCG    GAGG TTCACG
                                  GCCA_   _
GAM264  LOC206836 5'  GCGCCTGGGAGGGCTGCTC   89544      AAAG
                                GAGCA   CTTTTAGGTGT
                                |||||   ||||||||||
                                CTCGT   GAGGGTCCGCG
                                  CGG_
GAM264  LOC219294 3'  AACTTTGGCTTTTGCT      93001        TTT   GT
                                AGCAAAAGCT   AGGT
                                |||||||||   ||||
                                TCGTTTTCGG   TTCA
                                     T__   AT
GAM264  LOC219348 3'  ATGCCTGGAGGAAGCCTGC   91270     AAAG_
                                GCA    CTTTTAGGTGT
                                |||    ||||||||||
                                CGT    GGAGGTCCGTA
                                  CCGAA
GAM264  LOC219401 5'  GCATCTGGACTCTGCTCA    92815       AA  CT
                                TGAGCA  AG  TTTAGGTGT
                                ||||||  ||  |||||||||
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                                ACTCGT  TC  AGGTCTACG
                                   C_  __
GAM264  LOC219401 5'  ACATTTGGAAGTATTCTGC   92810    _  A
                                GCA AA GCTTTTAGGTGT
                                ||| || ||||||||||||
                                CGT TT TGAAGGTTTACA
                                  C  A
GAM264  LOC219404 3'  ACACCTGAGAGTGACTTTG   93490     A__
                                CAAA   GCTTTTAGGTGT
                                ||||   ||||||||||||
                                GTTT   TGAGAGTCCACA
                                   CAG
GAM264  LOC219445 3'  ACACCACTGTTTTGTTCA    91570         G TTTTA
                                TGAGCAAAA C    GGTGT
                                ||||||||| |    |||||
                                ACTTGTTTT G    CCACA
                                      _ TCA__
GAM264  LOC219505 3'  GCATTCTATGCTTTGCTCA   91267        A  TTT   _
                                TGAGCAAA GC   TAGG TGT
                                |||||||| ||   |||| |||
                                ACTCGTTT CG   ATCT ACG
                                      _  T__    T
GAM264  LOC219529 5'  GCAATAAAGCTTTTACTCA   92971     C        TAGG
                                TGAG AAAAGCTTT    TGT
                                |||| |||||||||    |||
                                ACTC TTTTCGAAA    ACG
                                   A        TA__
GAM264  LOC219673 5'  CACCTGAGCTCTTTTG     93022       CT
                                CAAAAG  TTTAGGTG
                                ||||||  ||||||||
                                GTTTTC  GAGTCCAC
                                    TC
GAM264  LOC219686 3'  ATGCCTAAAAGCGGGT     90839    AAAA
                                GC    GCTTTTAGGTGT
                                ||    ||||||||||||
                                TG    CGAAAATCCGTA
                                  GG__
GAM264  LOC219688 5'  GCGCCTGAATCGGATGCTC   93052      AAAGCT
                                GAGCA     TTTAGGTGT
                                |||||     |||||||||
                                CTCGT     AAGTCCGCG
                                   AGGCT_
GAM264  LOC219700 5'  ATACCTAGAAGTCTGC     93060     AAA
                                GCA   GCTTTTAGGTGT
                                |||   ||||||||||||
                                CGT   TGAAGATCCATA
                                  C__
GAM264  LOC219741 3'  ATATTTGTTTCCTTTTGTTC  93129         CTTT
                                GAGCAAAAG    TAGGTGT
                                |||||||||    |||||||
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                                CTTGTTTTC   GTTTATA
                                     CTTT
GAM264  LOC219908 5'  GCGCCTAGGAAGCGCATC    94316   _ AAAA   _
                                GA GC   GCTTT TAGGTGT
                                || ||   ||||| |||||||
                                CT CG   CGAAG ATCCGCG
                                 A ____    G
GAM264  LOC219942 3'  ATGCCTGGGAGATCTCA     93342     CAAAAG
                                TGAG     CTTTTAGGTGT
                                ||||     ||||||||||
                                ACTC     GAGGGTCCGTA
                                  TA____
GAM264  LOC220021 5'  GCACTTGGAGTTCTGCT     93395     AA    T
                                AGCA  AGCTTT AGGTGT
                                ||||  |||||| ||||||
                                TCGT  TTGAGG TTCACG
                                  C_    _
GAM264  LOC220058 5'  ACATCTGGGACTGTTGTTC    91723       A  C
                                GAGCAA AG TTTTAGGTGT
                                |||||| || ||||||||||
                                CTTGTT TC AGGGTCTACA
                                   G  _
GAM264  LOC220549 5'  ATGCCTAGATCTTTTGGTTA   92915     G     CT
                                TGA CAAAAG  TTTAGGTGT
                                ||| ||||||  |||||||||
                                ATT GTTTTC  AGATCCGTA
                                  G     T_
GAM264  LOC220573 3'  ATACTTGAAGGAAATGTTT    69600      AAAG
                                GAGCA    CTTTTAGGTGT
                                |||||    ||||||||||
                                TTTGT    GGAAGTTCATA
                                   AAA_
GAM264  LOC220595 5'  CACCTGACGTTTGTCA      91139     G    AGCTT
                                TGA CAAA     TTAGGTG
                                ||| ||||     |||||||
                                ACT GTTT     AGTCCAC
                                  _   GC___
GAM264  LOC220758 3'  ATACCTTGCCCCGTTTTTGCCC 90782    A       TTTT__
           A                     TG GCAAAAGC      AGGTGT
                                || ||||||||      ||||||
                                AC CGTTTTTG      TCCATA
                                 C       CCCCGT
GAM264  LOC220763 5'  ATGCTTGGGAGTCTTCTGCT   73345      A  _
                                AGCA AAG CTTTTAGGTGT
                                |||| ||| ||||||||||
                                TCGT TTC GAGGGTTCGTA
                                  C  T
GAM264  LOC220776 3'  GGCCAAAGTTTTGCTT      68393        G    TA  TG
                                GAGCAAAA CTTT  GG  T
                                |||||||| ||||  ||  |
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                                TTCGTTTT GAAA  CC  G
                                   _   __  GT
GAM264   LOC220963 3'  GCACCTAGAGAGACTGCTC   91450      AAAG    _
                                GAGCA   CTTTT AGGTGT
                                |||||   ||||| ||||||
                                CTCGT   GAGAG TCCACG
                                  CA__    A
GAM264   LOC220992 5'  ACACCTGGATGCTGCTCA    91467      AAA  T
                                TGAGCA  GC TTTAGGTGT
                                ||||||  || |||||||||
                                ACTCGT  CG AGGTCCACA
                                   ___  T
GAM264   LOC221002 3'  GCACTTACAAAGTTTTTTTT  91477    C       _
                                GAG AAAAGCTTT TAGGTGT
                                ||| ||||||||| |||||||
                                TTT TTTTTGAAA ATTCACG
                                  _       C
GAM264   LOC221037 3'  GCATCTGGGAAATTGCT     93155     AAGC
                                AGCAA   TTTTAGGTGT
                                |||||   ||||||||||
                                TCGTT   AGGGTCTACG
                                  AA__
GAM264   LOC221037 3'  ACATTGGCTTGCTTTTGTT   93154       TTTTA
                                AGCAAAAGC    GGTGT
                                |||||||||    |||||
                                TTGTTTTCG    TTACA
                                     TTCGG
GAM264   LOC221042 3'  ACACCTAGGAGAAGCTCA    93179     AAAAG
                                TGAGC    CTTTTAGGTGT
                                |||||    ||||||||||
                                ACTCG    GAGGATCCACA
                                  AA___
GAM264   LOC221272 5'  GTGCTTGAGGGCTTACTGC   93608    A_       TG
                                GCA  AAGCTTTTAGG  T
                                |||  ||||||||||  |
                                CGT  TTCGGGAGTTC  G
                                  CA         GT
GAM264   LOC221337 3'  GGCTTGTTGCTTTGCTT     92113      A  TTT   TG
                                GAGCAAA GC   TAGG  T
                                |||||||  ||   ||||  |
                                TTCGTTT CG   GTTC  G
                                   _  TT_    GT
GAM264   LOC221362 3'  ATAATGAAAGCTTTTGGTTA  93756    G         GGTGT
                                TGA CAAAAGCTTTTA
                                ||| ||||||||||||
                                ATT GTTTTCGAAAGT
                                  G          AATA
GAM264   LOC221370 5'  ATGCCTGAAAGGCGACTC    92009    CAAAA  _
                                GAG    GC TTTTAGGTGT
                                |||    || ||||||||||
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                                CTC    CG AAAGTCCGTA
                                  AG___  G
GAM264  LOC221415 5'  GCGCCTGGGCTCTGC      93875    AA   TT
                                GCA  AGCT  TAGGTGT
                                |||  ||||  |||||||
                                CGT  TCGG  GTCCGCG
                                  C_   __
GAM264  LOC221477 3'  GCACTTGAATGGCCTGTTT   92153     AAA  _
                                GAGCA   GCT TTTAGGTGT
                                |||||   ||| |||||||||
                                TTTGT   CGG AAGTTCACG
                                   C__   T
GAM264  LOC221490 5'  GCACTTGAGGCCTTGCTT    93660      AA    T
                                GAGCAA  GCTTT AGGTGT
                                ||||||  ||||| ||||||
                                TTCGTT  CGGAG TTCACG
                                   C_    _
GAM264  LOC221683 3'  ACTCTTTGTAGGTTTTTGTTT  93709          TT_   T
                                GAGCAAAAGCTT   AGG GT
                                ||||||||||||   ||| ||
                                TTTGTTTTTTGGA   TTC CA
                                      TGT   T
GAM264  LOC221688 3'  ACACTTATGTTCCTTTGCTTA  93673        AGCTTT
                                TGAGCAAA     TAGGTGT
                                ||||||||     |||||||
                                ATTCGTTT     ATTCACA
                                     CCTTGT
GAM264  LOC221713 5'  TAGGAGTTTTTGTTCA      92040
                                TGAGCAAAAGCTTTTA
                                ||||||||||||||||
                                ACTTGTTTTTGAGGAT

GAM264  LOC221751 3'  GCATCTGGAAGACGGGCT    92049     AAAAG
                                AGC    CTTTTAGGTGT
                                |||    ||||||||||
                                TCG    GAAGGTCTACG
                                  GGCA_
GAM264  LOC221751 5'  ACATGAATTTGGCTTTTGCT   92045         TTTAG_
                                AGCAAAAGCT     GTGT
                                ||||||||||     ||||
                                TCGTTTTCGG     TACA
                                      TTTAAG
GAM264  LOC221763 3'  ACACTTAAGCAGTAATTGCT   93795      AA   _
                                AGCAA  GCT TTTAGGTGT
                                |||||  ||| |||||||||
                                TCGTT  TGA GAATTCACA
                                   AA   C
GAM264  LOC221787 3'  ACGCTTAAAAGGAAATGTT    92466     AAAG
                                AGCA    CTTTTAGGTGT
                                ||||    ||||||||||
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                                TTGT    GAAAATTCGCA
                                  AAAG
GAM264   LOC221810 3'  ACATTTAGGGGATGCTCA    93929       AAAG
                                TGAGCA    CTTTTAGGTGT
                                ||||||    ||||||||||
                                ACTCGT    GGGGATTTACA
                                   A___
GAM264   LOC221931 5'  GCACCTGGGGGCTGATGC    93994     AA
                                GCA  AGCTTTTAGGTGT
                                |||  ||||||||||||
                                CGT  TCGGGGGTCCACG
                                  AG
GAM264   LOC221935 3'  ATAACTGAGCTGAAGTTTTTGT 92618           TA___   GT
           TTA                    TGAGCAAAAGCTTT     GGT
                                ||||||||||||||     |||
                                ATTTGTTTTTGAAG     TCA
                                        TCGAG   ATA
GAM264   LOC221964 3'  ATATTTGAGAGGATGTTCA    93978       AAAG
                                TGAGCA    CTTTTAGGTGT
                                ||||||    ||||||||||
                                ACTTGT    GAGAGTTTATA
                                   AG__
GAM264   LOC221975 3'  ACACCTGAAGACATGCTC    92601      AAAG    T
                                GAGCA    CTTT AGGTGT
                                |||||    |||| ||||||
                                CTCGT    GAAG TCCACA
                                   ACA_   _
GAM264   LOC222008 3'  GCATCTGAGAGCTGGACTC    94010     CAAA
                                GAG    AGCTTTTAGGTGT
                                |||    ||||||||||||
                                CTC    TCGAGAGTCTACG
                                  AGG_
GAM264   LOC222031 3'  GCATCTAGGGGAGGAGTGCT   94023      AAAG_
                                AGCA    CTTTTAGGTGT
                                ||||    ||||||||||
                                TCGT    GGGGATCTACG
                                   GAGGA
GAM264   LOC222159 5'  GCACTGTTGGCTTTGTTTA    94079        A   TTTA
                                TGAGCAAA GCT    GGTGT
                                |||||||| |||    |||||
                                ATTTGTTT CGG    TCACG
                                     _   TTG_
GAM264   LOC222166 3'  ATATCTGTGATGAGCTTTGCTC 94090         A    T___
           A                     TGAGCAAA GCTT    TAGGTGT
                                ||||||||| ||||    |||||||
                                ACTCGTTT CGAG    GTCTATA
                                     _   TAGT
GAM264   LOC222166 3'  CCGTAAGTGAAAGGTTTTGCTT 94093         G     GGTGT
           A                     TGAGCAAAA CTTTTA
                                |||||||| ||||||
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                                ATTCGTTTT GAAAGT
                                     G     GAATGCCT
GAM264   LOC222166 3'  ACACCTGGGTTCTAGTTCA   94088      AAA  CT
                                TGAGC   AG  TTTAGGTGT
                                |||||   ||  |||||||||
                                ACTTG   TC  GGGTCCACA
                                   A__  TT
GAM264   LOC222190 3'  GCACCTGGGAGTTCAGTT    94218     AAA
                                AGC   AGCTTTTAGGTGT
                                |||   ||||||||||||
                                TTG   TTGAGGGTCCACG
                                  AC_
GAM264   LOC222256 3'  CACCTTCTTTTGTTT       94260         CTTTT
                                GAGCAAAAG    AGGTG
                                |||||||||    |||||
                                TTTGTTTTC    TCCAC
                                     T____
GAM264   LOC222662 5'  GCACCTGGCAAGCTTTCCTT   92843     CA     _
                                GAG  AAAGCTT TTAGGTGT
                                |||  ||||||| ||||||||
                                TTC  TTTCGAA GGTCCACG
                                  C_     C
GAM264   LOC253187 3'  ACATCTAGAGGATGTCCA    97108    AG  AAAG
                                TG  CA    CTTTTAGGTGT
                                ||  ||    ||||||||||
                                AC  GT    GGAGATCTACA
                                 CT  A___
GAM264   LOC253258 3'  GCACTTAGAAGAACGATCA   96474     GCAAAAG
                                TGA      CTTTTAGGTGT
                                |||      ||||||||||
                                ACT      GAAGATTCACG
                                  AGCAA__
GAM264   LOC253286 5'  ACACCTGGAGGCAGCCAGCT   97562     AAAA_
                                AGC    GCTTTTAGGTGT
                                |||    ||||||||||
                                TCG    CGGAGGTCCACA
                                  ACCGA
GAM264   LOC253350 5'  GCATCTGGAGGAAGCTT     97563      AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                TTCG    GGAGGTCTACG
                                  AA___
GAM264   LOC253443 5'  GCATTTTTTATGCTTTTGTGCA 95870    A       TTTT_
                                TG GCAAAAGC     AGGTGT
                                || ||||||||     ||||||
                                AC TGTTTTCG     TTTACG
                                 G       TATTT
GAM264   LOC253531 5'  GCACCATGCTAAAAGCTTTTAT 96470     C         ____
            TTA                    GAG AAAAGCTTTTA    GGTGT
                                ||| ||||||||||    |||||
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                                TTT TTTTCGAAAAT   CCACG
                                  A         CGTA
GAM264  LOC253532 5'  GCACCTGGGAGTTCAGTT    96028     AAA
                                AGC   AGCTTTTAGGTGT
                                |||   ||||||||||||
                                TTG   TTGAGGGTCCACG
                                  AC_
GAM264  LOC253626 5'  GTGTCTGGAAGTGTCTGTTT   97219      AAA       TG
                                GAGCA   GCTTTTAGG  T
                                |||||   |||||||||  |
                                TTTGT   TGAAGGTCT  G
                                   CTG       GT
GAM264  LOC253758 3'  GCTCCGGAGAGGGCTTTGTTC  96971       A     A__  T
                                GAGCAAA GCTTTT   GG GT
                                |||||||  ||||||   || ||
                                CTTGTTT CGGGAG   CC CG
                                    _     AGG  T
GAM264  LOC253912 5'  GCGCCTGGAGGGGGCGCT    97358     AAAAG
                                AGC    CTTTTAGGTGT
                                |||    ||||||||||
                                TCG    GGAGGTCCGCG
                                  CGGG_
GAM264  LOC253955 5'  ATACTTAAAAGTTGATGC    94421     AA
                                GCA  AGCTTTTAGGTGT
                                |||  ||||||||||||
                                CGT  TTGAAAATTCATA
                                  AG
GAM264  LOC253981 3'  ATACTTGAGCGGTTTTTGT   95828         _
                                GCAAAAGCT TTTAGGTGT
                                |||||||| |||||||||
                                TGTTTTTGG GAGTTCATA
                                      C
GAM264  LOC254016 3'  GCACTTGGGGGTGGGTG     96923     AAA
                                CA   GCTTTTAGGTGT
                                ||   ||||||||||||
                                GT   TGGGGGTTCACG
                                  GGG
GAM264  LOC254045 3'  ACACCTAGAGGCTGGGC     96501     AAA
                                GC   AGCTTTTAGGTGT
                                ||   ||||||||||||
                                CG   TCGGAGATCCACA
                                  GG_
GAM264  LOC254295 5'  GCGCTTAGAAGCCGCCCA    96177     A  AAAA
                                TG GC    GCTTTTAGGTGT
                                || ||    ||||||||||||
                                AC CG    CGAAGATTCGCG
                                 C  C___
GAM264  LOC254295 5'  GCACCTGGAGGCCGCGCTTA   96176       AAAA
                                TGAGC    GCTTTTAGGTGT
                                |||||    ||||||||||||
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                                ATTCG    CGGAGGTCCACG
                                   CGC_
GAM264   LOC254394 3'  ACACTTAAAAGCCTTTGC    95983       A
                                GCAAA GCTTTTAGGTGT
                                ||||| ||||||||||||
                                CGTTT CGAAAATTCACA
                                   C
GAM264   LOC254440 5'  GCACCTTTACCTGTGTTTTGCT 97066        _  TTTT__
            C                    GAGCAAAA GC     AGGTGT
                                ||||||||| ||     ||||||
                                CTCGTTTT TG     TCCACG
                                     G  TCCATT
GAM264   LOC254440 3'  GTGCCTGGGAGGGCGGGGCTC  97071      AAAA     __   TG
                                GAGC    GCTTTT  AGG  T
                                ||||    ||||||  |||  |
                                CTCG    CGGGAG  TCC  G
                                  GGG_     GG   GT
GAM264   LOC254485 5'  ACACCTGAGAGATGAAGGTTTA 95011       AAAAG_
                                TGAGC     CTTTTAGGTGT
                                |||||     ||||||||||||
                                ATTTG     GAGAGTCCACA
                                   GAAGTA
GAM264   LOC254531 5'  ACAAGAAGGCTTTGCTTA    94978         A     AG
                                TGAGCAAA GCTTTT  GT
                                |||||||| ||||||  ||
                                ATTCGTTT CGGAAG  CA
                                     _     AA
GAM264   LOC254532 5'  GTGTCTGGGAGGGTTTTGCCCG 96644    A     G    _   TG
                                TG GCAAAA CTTTT AGG  T
                                || |||||| ||||| |||  |
                                GC CGTTTT GGAGG TCT  G
                                 C     G    G   GT
GAM264   LOC254559 3'  ACACCTAGTCAGGTCTGTTT   96592       AAA   __
                                GAGCA   GCTT  TTAGGTGT
                                |||||   ||||  ||||||||
                                TTTGT   TGGA  GATCCACA
                                   C__    CT
GAM264   LOC254672 3'  ATGCCTGGCTGGTTTTTG    94640         T_
                                CAAAAGCT  TTAGGTGT
                                ||||||||  ||||||||
                                GTTTTTGG  GGTCCGTA
                                     TC
GAM264   LOC254746 3'  GCGCCTGAGGGGTGGCT     95141     AAAAG
                                AGC    CTTTTAGGTGT
                                |||    ||||||||||||
                                TCG    GGGAGTCCGCG
                                  GTG__
GAM264   LOC254778 3'  ATATCTGAAAGTGATTTG    96127      A_
                                CAAA  GCTTTTAGGTGT
                                ||||  ||||||||||||
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                                GTTT  TGAAAGTCTATA
                                  AG
GAM264   LOC254875 5'  GCACCTGGGAGTTCAGTT    96058     AAA
                                AGC   AGCTTTTAGGTGT
                                |||   ||||||||||||
                                TTG   TTGAGGGTCCACG
                                  AC_
GAM264   LOC254896 5'  GTGCTTGGAAGTGACTGCT    96148      AAA        TG
                                AGCA   GCTTTTAGG  T
                                ||||   |||||||||  |
                                TCGT   TGAAGGTTC  G
                                  CAG        GT
GAM264   LOC254978 5'  GTGCCTGGAAGTGGTCA     95944     G AAAA        TG
                                TGA C    GCTTTTAGG  T
                                ||| |    |||||||||  |
                                ACT G    TGAAGGTCC  G
                                  G _____        GT
GAM264   LOC255096 3'  ACATCTAGGGAGATTGTGC    97621     AAAG   _
                                GCA    CTTT TAGGTGT
                                |||    |||| |||||||
                                CGT    GAGG ATCTACA
                                  GTTA    G
GAM264   LOC255131 3'  ATGCCTGAAGAGCTGTATCA   95999     GCAAA     _
                                TGA     AGCTTT TAGGTGT
                                |||     |||||| |||||||
                                ACT     TCGAGA GTCCGTA
                                  ATG__      A
GAM264   LOC255152 5'  GCATCTGAGGAGAAAAGCTC   97438      AAAAG   _
                                GAGC     CTT TTAGGTGT
                                ||||     ||| ||||||||
                                CTCG     GAG AGTCTACG
                                  AAAA_   G
GAM264   LOC255196 5'  GTGCCTAAGAGAATCATGCTTA 97175       AAAG_       TG
                                TGAGCA     CTTTTAGG  T
                                ||||||     ||||||||  |
                                ATTCGT     GAGAATCC  G
                                    ACTAA       GT
GAM264   LOC255252 3'  ACAGCTTGAGATTTTGTTTA   95005         G   TT  G
                                TGAGCAAAA CTT  AG TGT
                                ||||||||| |||  || |||
                                ATTTGTTTT GAG  TC ACA
                                      A   T_  G
GAM264   LOC255299 5'  GCACCTGAAGCCAAGCCCA    97467    A  AAAA     T
                                TG GC    GCTTT AGGTGT
                                || ||    ||||| ||||||
                                AC CG    CGAAG TCCACG
                                 C  AAC_     _
GAM264   LOC255328 3'  GCTGGGCCTTTGCTCA      96561         A    TTA
                                TGAGCAAA GCTT   GGT
                                ||||||| ||||   |||
```

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                                ACTCGTTT CGGG   TCG
                                    C   ___
GAM264   LOC255332 3'  GCATCTAGAACAATGCTCA   96210      AAAGC
                                TGAGCA    TTTTAGGTGT
                                ||||||    ||||||||||
                                ACTCGT    AAGATCTACG
                                   AAC__
GAM264   LOC255515 5'  ACACCTGGAAGCTGACTGGTC  96089    G  AA_
                                GA CA   AGCTTTTAGGTGT
                                || ||   ||||||||||||
                                CT GT   TCGAAGGTCCACA
                                 G  CAG
GAM264   LOC255520 3'  ACATTTAAAGTGCTTGC     95851     AA  _
                                GCA  AGC TTTTAGGTGT
                                |||  ||| ||||||||||
                                CGT  TCG GAAATTTACA
                                  __  T
GAM264   LOC255520 3'  GTATCATTCTGTTTTTGCTTA 95862          TTTTA   GT
                                TGAGCAAAAGC    GGT
                                ||||||||||    |||
                                ATTCGTTTTTG    CTA
                                      TCTTA   TG
GAM264   LOC255570 3'  GGCTAGAGCTTTTGTGCA    97035    A        TA  TG
                                TG GCAAAAGCTTT  GG  T
                                || ||||||||||  ||  |
                                AC TGTTTTCGAGA  TC  G
                                 G         __ GT
GAM264   LOC255862 3'  ACGTCTGAAATTGCTC      94485       AAGC     GT
                                GAGCAA   TTTTAG  GT
                                ||||||   ||||||  ||
                                CTCGTT   AAAGTC  CA
                                   ____     TG
GAM264   LOC256078 5'  GTGCCTGGGAGTCGCGTGCCA 95845    A   AAA_       TG
                                TG GCA   GCTTTTAGG  T
                                || |||   |||||||||  |
                                AC CGT   TGAGGGTCC  G
                                 _  GCGC       GT
GAM264   LOC256207 5'  ACATCTGAAGGTGTTATCTTA  95164     CAAAA
                                TGAG    GCTTTTAGGTGT
                                ||||    ||||||||||||
                                ATTC    TGGAAGTCTACA
                                  TATTG
GAM264   LOC256221 3'  ACACCTGGGGGACCTCA     95208     CAAAAG
                                TGAG     CTTTTAGGTGT
                                ||||     ||||||||||
                                ACTC     GGGGGTCCACA
                                  CA____
GAM264   LOC256286 3'  TACCTGGAGCGCCTGCGTC   95203    _  AAA    T   GT
                                GA GCA   GCTTT AGGT
                                || |||   ||||| ||||
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                                CT CGT   CGAGG TCCA
                                 G  CCG    _   TG
GAM264  LOC256300 5' CACCTAACTCTTCTCA     97592     CAA  CTT
                                TGAG  AAG  TTAGGTG
                                ||||  |||  |||||||
                                ACTC  TTC  AATCCAC
                                  ___  TC_
GAM264  LOC256416 3' ATATTTAAGCTGCTGCTC    94408     AA   TT
                                GAGCA  AGCT  TAGGTGT
                                |||||  ||||  |||||||
                                CTCGT  TCGA  ATTTATA
                                  CG   __
GAM264  LOC256476 5' GGCTTAAGAGCTCTTCA     96820     CAAA       TG
                                TGAG   AGCTTTTAGG  T
                                ||||   ||||||||||  |
                                ACTT   TCGAGAATTC  G
                                  C___        GT
GAM264  LOC256530 3' ACATCTGGAAAGCAGGCCCA  96812    A  AAAA    _
                                TG GC   GCTTTT AGGTGT
                                || ||   |||||| ||||||
                                AC CG   CGAAAG TCTACA
                                 C  GA__     G
GAM264  LOC256642 3' ACACCTAACAATTGCTT     96305       AAGCTT
                                GAGCAA     TTAGGTGT
                                ||||||     ||||||||
                                TTCGTT     AATCCACA
                                   AAC___
GAM264  LOC256642 3' ATGTTGAAAGTTTTGCTTA   96306         G     GTGT
                                TGAGCAAAA CTTTTAG
                                ||||||||| |||||||
                                ATTCGTTTT GAAAGTT
                                      _     GTAT
GAM264  LOC256658 3' GCACCTGGGAGACAGAGGTT  97325     AAAAG_
                                AGC     CTTTTAGGTGT
                                |||     ||||||||||
                                TTG     GAGGGTCCACG
                                  GAGACA
GAM264  LOC256686 3' GCGCCTGGGGTCAAGCTCA   96825      AAAA    T
                                TGAGC   GCTTT AGGTGT
                                |||||   ||||| ||||||
                                ACTCG   TGGGG TCCGCG
                                  AAC_    _
GAM264  LOC257095 5' ACACTTGGGAGAGGGGCCCG  96934    A  AAAAG
                                TG GC    CTTTTAGGTGT
                                || ||    ||||||||||
                                GC CG    GAGGGTTCACA
                                 C  GGGA_
GAM264  LOC257282 5' AGCTCCTGGAAGCTTTTTCTCA 96398     C          T
                                TGAG AAAAGCTTTTAGG GT
                                |||| |||||||||||| ||
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                                ACTC TTTTCGAAGGTCC CG
                                  T          T  AC
GAM264  LOC257395 3'  GCACTTGGAAGAAGCT     95419     AAAAG
                                AGC    CTTTTAGGTGT
                                |||    ||||||||||
                                TCG    GAAGGTTCACG
                                  AA___
GAM264  LOC257407 3'  GCGCCTACTATTTGCTC     96988       _ CTTT
                                GAGCAAA AG    TAGGTGT
                                ||||||| ||    |||||||
                                CTCGTTT TC    ATCCGCG
                                    A ____
GAM264  LOC257465 3'  GCATTTGGAGTGGCGTTTGC   81593      A  __
                                GCAAA GCT  TTTAGGTGT
                                ||||| |||  |||||||||
                                CGTTT CGG  AGGTTTACG
                                   G   TG
GAM264  LOC257484 3'  ATACCTGGGGGCGGGTTG    88814     AA_
                                CAA   GCTTTTAGGTGT
                                |||   ||||||||||||
                                GTT   CGGGGGTCCATA
                                  GGG
GAM264  LOC257494 3'  ACGCCTAAGATCATTTTGCT   97788       GC_
                                AGCAAAA   TTTTAGGTGT
                                |||||||   ||||||||||
                                TCGTTTT   AGAATCCGCA
                                    ACT
GAM264  LOC51003  5'  GCGTCTCTGGGCTTTTGCTC   32148          TT  GT
                                GAGCAAAAGCTT  AG  GT
                                ||||||||||||  ||  ||
                                CTCGTTTTCGGG  TC  CG
                                       TC  TG
GAM264  LOC51054  5'  ATGCCTGGAAAGGTTGC     31906     AAGC
                                GCAA    TTTTAGGTGT
                                ||||    ||||||||||
                                CGTT    AAGGTCCGTA
                                  GGA_
GAM264  LOC51096  3'  ACATGTGGCAGCTTTTGTTT   32047          T   G
                                GAGCAAAAGCT TTA GTGT
                                |||||||||||| ||| ||||
                                TTTGTTTTCGA GGT TACA
                                      C   G
GAM264  LOC51096  3'  ATGTGGCAGCTTTTGTTT    32048          T   G  GT
                                GAGCAAAAGCT TTA GT
                                |||||||||||| ||| ||
                                TTTGTTTTCGA GGT TA
                                      C   G
GAM264  LOC51097  3'  GCACTTTTTGCTGTTTTTGC   32049        TTTT__
                                GCAAAAGC     AGGTGT
                                ||||||||     ||||||
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                              CGTTTTTG     TTCACG
                                   TCGTTT
GAM264  LOC51131  3' CACCTAGTATGCTCA      32278       AAA   TTT
                              TGAGCA   GCT   AGGTG
                              ||||||   |||   |||||
                              ACTCGT   TGA   TCCAC
                                 A__   ___
GAM264  LOC51131  3' ACACTCTTGTGTTTTTTGCTCA 32276          CTTTT _
                              TGAGCAAAAG    AG GTGT
                              ||||||||||    || ||||
                              ACTCGTTTTT    TC CACA
                                    TGTGT  T
GAM264  LOC51291  3' ACACCTGGGACAGGGGTGCTT  33362       AAAGC_
                              GAGCA     TTTTAGGTGT
                              |||||     ||||||||||
                              TTCGT     AGGGTCCACA
                                 GGGGAC
GAM264  LOC51580  3' ACACAGTGCTTTTGTTCA    31858          TTTTAG
                              TGAGCAAAAGC     GTGT
                              ||||||||||     ||||
                              ACTTGTTTTCG     CACA
                                    TGA___
GAM264  LOC51611  3' ATACCTGGATGCATGC     31984     AAA  T
                              GCA   GC TTTAGGTGT
                              |||   || |||||||||
                              CGT   CG AGGTCCATA
                                A__  T
GAM264  LOC51659  3' ACACTTGGGCAGGTGTTCA   32239       AAA   TT
                              TGAGCA   GCT  TAGGTGT
                              ||||||   |||  |||||||
                              ACTTGT   CGG  GTTCACA
                                 GGA   __
GAM264  LOC51659  3' ACACTTGGGCAGGTGTTCA   94575       AAA   TT
                              TGAGCA   GCT  TAGGTGT
                              ||||||   |||  |||||||
                              ACTTGT   CGG  GTTCACA
                                 GGA   __
GAM264  LOC51673  3' ATATTTAAGCTGCTGCTC    94567      AA    TT
                              GAGCA  AGCT  TAGGTGT
                              |||||  ||||  |||||||
                              CTCGT  TCGA  ATTTATA
                                 CG   __
GAM264  LOC51696  3' GCATCTAGGTCGGTGTTTGATC 32547     G    A  __
          A                    TGA CAAA GCT  TTTAGGTGT
                              ||| |||| |||  |||||||||
                              ACT GTTT TGG  GGATCTACG
                                A   G   CT
GAM264  LOC51754  5' GGCCTGGGGTTTTCTCA     71030      CA       T   TG
                              TGAG  AAAGCTTT AGG  T
                              ||||  |||||||| |||  |
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                                ACTC  TTTTGGGG TCC  G
                                  __      _  GT
GAM264  LOC51762  3' TTTATTTAAGGGCTTTTTCTTA 33272     C          T
                                TGAG AAAAGCTTTTAGGTG
                                |||| ||||||||||||||
                                ATTC TTTTCGGGAATTTAT
                                  T           TTA
GAM264  LOC54505  5' ACATTTAGGAAGCTCTCA    67836     CAAA    _
                                TGAG   AGCTTT TAGGTGT
                                ||||   |||||| |||||||
                                ACTC   TCGAAG ATTTACA
                                  ____     G
GAM264  LOC54516  3' ACACCTAGAATAATGTTT    38756      AAAGC
                                GAGCA    TTTTAGGTGT
                                |||||    ||||||||||
                                TTTGT    AAGATCCACA
                                   AAT__
GAM264  LOC56961  5' CACCTGATCTTTCTCA      62904     CA   CTT
                                TGAG  AAAG   TTAGGTG
                                ||||  ||||   |||||||
                                ACTC  TTTC   AGTCCAC
                                  __   T__
GAM264  LOC58486  5' GCCTCGGTGAAGGCTTTTGGTT 41082     G        ____   GT
          A                      TGA CAAAAGCTTTT    AGGT
                                ||| ||||||||||    ||||
                                ATT GTTTTCGGAAG    TCCG
                                  G         TGGC
GAM264  LOC63929  3' ACACTTCTGAGCTTTTCTT    42039     C      TT
                                GAG AAAAGCTT  AGGTGT
                                ||| ||||||||  ||||||
                                TTC TTTTCGAG  TTCACA
                                  _       TC
GAM264  LOC64116  5' GCGTTTGAGGGCTACTGCCA   42202    A   AA      GG
                                TG GCA  AGCTTTTA  TGT
                                || |||  ||||||||  |||
                                AC CGT  TCGGGAGT  GCG
                                  _  CA       TT
GAM264  LOC64146  3' ATACCTGAAAGCTGTCTT    42275     CAAA
                                GAG    AGCTTTTAGGTGT
                                |||    ||||||||||||
                                TTC    TCGAAAGTCCATA
                                  TG__
GAM264  LOC64150  5' ACACCTGGAGGAGAGTGCT    67280      AAAG
                                AGCA    CTTTTAGGTGT
                                ||||    ||||||||||
                                TCGT    GGAGGTCCACA
                                   GAGA
GAM264  LOC84549  3' ACACCTCCAGTTTTTGCTC    50698          TTT
                                GAGCAAAAGCT   AGGTGT
                                ||||||||||   ||||||
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                              CTCGTTTTTGA  TCCACA
                                    CC_
GAM264  LOC85414  3' ACACCTAGAGAAGGGTTTTTG  52391       ____
                              CAAAAGCT   TTTAGGTGT
                              ||||||||   |||||||||
                              GTTTTTGG   AGATCCACA
                                  GAAG
GAM264  LOC85569  3' ACATTTAAAGGAATTGTGTTC  52406     AAAG_
                              GAGCA    CTTTTAGGTGT
                              |||||    ||||||||||
                              CTTGT    GGAAATTTACA
                                 GTTAA
GAM264  LOC90092  3' ACCAGCCTTTTGCTTA     61398        _ TTTA
                              TGAGCAAAAG CT    GGT
                              |||||||||| ||   |||
                              ATTCGTTTTC GA    CCA
                                    C ____
GAM264  LOC90141  3' ACACTTAGCCATGTGTGTTCA  61620      AAAGCTT
                              TGAGCA     TTAGGTGT
                              ||||||     ||||||||
                              ACTTGT     GATTCACA
                                 GTGTACC
GAM264  LOC90148  3' TAAATGGCTTGTGCTCA     61664      A   _
                              TGAGCA AAGCT TTTA
                              |||||| ||||| ||||
                              ACTCGT TTCGG AAAT
                                 G    T
GAM264  LOC90170  5' GCGTTTGGCTGTGTTGTTTGCT 61707       _  TT__  GG
          CA                    TGAGCAAA AGC    TTA  TGT
                              |||||||| |||    |||  |||
                              ACTCGTTT TTG    GGT  GCG
                                   G   TGTC   TT
GAM264  LOC90183  3' GCAAGCTGAGGGTCTTTGTTT  61732      AG     G_
                              GAGCAAA  CTTTTAG  TGT
                              |||||||  |||||||  |||
                              TTTGTTT  GGGAGTC  ACG
                                   CT      GA
GAM264  LOC90249  3' ACGTCTGAGGGGCCCTGCTC  61922     AAAG     GT
                              GAGCA    CTTTTAG  GT
                              |||||    |||||||  ||
                              CTCGT    GGGAGTC  CA
                                 CCCG      TG
GAM264  LOC90288  3' ACATCTAAGGTACAGCTTA   62073     AAAA    T
                              TGAGC    GCTTT AGGTGT
                              |||||    ||||| ||||||
                              ATTCG    TGGAA TCTACA
                                 ACA_    _
GAM264  LOC90333  5' ATGCCTGGACCCTGCTCA    62282      AAA CT
                              TGAGCA   G  TTTAGGTGT
                              ||||||   |  |||||||||
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                                ACTCGT  C  AGGTCCGTA
                                   ___ CC
GAM264  LOC90509  3' TGTTTAGAGGCTTTTGTCA   63107    G         GT T
                                TGA CAAAAGCTTTTAG  G
                                ||| ||||||||||||  |
                                ACT GTTTTCGGAGATT  T
                                  _         TG T
GAM264  LOC90550  3' TTGTCTGGAGGCTTTGTTCA  73096       A      GT T
                                TGAGCAAA GCTTTTAG  G
                                |||||||| ||||||||  |
                                ACTTGTTT CGGAGGTC  T
                                     _      TG TC
GAM264  LOC90591  3' CCTAATTTTTTGTTCA     63420        CTT
                                TGAGCAAAAG  TTAGG
                                ||||||||||  |||||
                                ACTTGTTTTT  AATCC
                                      T__
GAM264  LOC90639  3' GCATCTGGCTGTTTTTCTTA  63658    C    TT
                                TGAG AAAAGC  TTAGGTGT
                                |||| ||||||  ||||||||
                                ATTC TTTTTG  GGTCTACG
                                  _     TC
GAM264  LOC90719  3' ACATTTGAGAGAGATTTGT   63879     AG_
                                GCAAA  CTTTTAGGTGT
                                |||||  ||||||||||
                                TGTTT  GAGAGTTTACA
                                   AGA
GAM264  LOC90750  5' ATGTTTTTGGCTATTTGCTCA 63915       _  TTT  TG
                                TGAGCAAA AGCT  AGG  T
                                |||||||| ||||  |||  |
                                ACTCGTTT TCGG  TTT  A
                                     A   TT_  GT
GAM264  LOC90784  5' ACACTTAGGGAGCTTTTTA   63996   C      _
                                G AAAAGCTTT TAGGTGT
                                | |||||||||  |||||||
                                A TTTTCGAGG ATTCACA
                                 T       G
GAM264  LOC90829  5' ATGCCTCCAGTTTTGTTC    64097       G  TTT
                                GAGCAAAA CT  AGGTGT
                                |||||||| ||  ||||||
                                CTTGTTTT GA  TCCGTA
                                     _ CC_
GAM264  LOC90835  5' GCACCTAGGGCCTGCT     64130     AAA    T
                                AGCA  GCTTT AGGTGT
                                ||||  ||||| ||||||
                                TCGT  CGGGA TCCACG
                                  C__    _
GAM264  LOC90906  5' GCACTTTGGTTTTTGTTT    64303         TTT
                                GAGCAAAAGCT  AGGTGT
                                ||||||||||  ||||||
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                                TTTGTTTTTGG  TTCACG
                                      T__
GAM264  LOC90917  3' ATGCCTGGATCTTGCTC    64336      AAGCT
                                GAGCAA    TTTAGGTGT
                                ||||||    |||||||||
                                CTCGTT    AGGTCCGTA
                                   CT___
GAM264  LOC91138  5' TTTTCAGGAAGTTTTTCTCA  65033    C       TA  TGT
                                TGAG AAAAGCTTT  GG
                                |||| |||||||||  ||
                                ACTC TTTTTGAAG  CT
                                  _       GA  TTTA
GAM264  LOC91149  3' ACATAGCATGCTTTTGCTCA  65065          TTTTAG
                                TGAGCAAAAGC     GTGT
                                ||||||||||      ||||
                                ACTCGTTTTCG     TACA
                                      TACGA_
GAM264  LOC91149  3' GCACTTGAGAGCCACTGT    65078    AAA
                                GCA   GCTTTTAGGTGT
                                |||   ||||||||||||
                                TGT   CGAGAGTTCACG
                                  CAC
GAM264  LOC91170  3' ACATCTGGAGTGTGCGTGCTT  65133      AAA  _
                                GAGCA   GC TTTTAGGTGT
                                |||||   || ||||||||||
                                TTCGT   TG GAGGTCTACA
                                   GCG  T
GAM264  LOC91291  5' ACGTTTGAGAGCTGTGTT    65475    AA      GG
                                AGCA  AGCTTTTA  TGT
                                ||||  ||||||||  |||
                                TTGT  TCGAGAGT  GCA
                                  G_       TT
GAM264  LOC91308  3' ATACCTAGGTGCTTTTTA    65556   C     T
                                G AAAAGC TTTAGGTGT
                                | |||||| |||||||||
                                A TTTTCG GGATCCATA
                                 T     T
GAM264  LOC91464  3' GCCAAGGAGAGGTTGTTTGTTC 66139        _     A___   GT
          A                      TGAGCAAA AGCTTTT    GGT
                                 ||||||||| |||||||    |||
                                 ACTTGTTT TTGGAGA    CCG
                                      G      GGAA
GAM264  LOC91523  3' ATGCCTCGTCTTCCTTTTGTTC 56393         CTTTT__
          A                      TGAGCAAAAG      AGGTGT
                                 ||||||||||      ||||||
                                 ACTTGTTTTC      TCCGTA
                                       CTTCTGC
GAM264  LOC91565  3' GCATTTACAAGTTTTTGTTT   66461          T
                                GAGCAAAAGCTT TAGGTGT
                                |||||||||||| |||||||
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                                TTTGTTTTTGAA ATTTACG
                                       C
GAM264  LOC91565  5' ACTAAAAGGCTTTGGTTCA   66458      A       A
                                TGAGC AAAGCTTTT GGT
                                ||||| ||||||||| |||
                                ACTTG TTTCGGAAA TCA
                                   G        A
GAM264  LOC91574  3' GCACTTGGAGGGGTTC      66520     AAAAG
                                GAGC    CTTTTAGGTGT
                                ||||    ||||||||||
                                CTTG    GGAGGTTCACG
                                  G____
GAM264  LOC91660  5' ATACCTAAAGTCTCTGCTCA  66867       AA  C
                                TGAGCA  AG TTTTAGGTGT
                                ||||||  || ||||||||||
                                ACTCGT  TC GAAATCCATA
                                    C_  T
GAM264  LOC91661  3' ACATCAGAGGGTTTTTGTTT  56396           A
                                GAGCAAAAGCTTTT GGTGT
                                |||||||||||||| |||||
                                TTTGTTTTTGGGAG CTACA
                                         A
GAM264  LOC91748  3' ACGCCTAAGAGTGCCCATC   67053    GCAAAA
                                GA     GCTTTTAGGTGT
                                ||     ||||||||||||
                                CT     TGAGAATCCGCA
                                 ACCCG_
GAM264  LOC91947  3' ATACCTAAGAGAATGTCA    67611     G  AAAG
                                TGA CA    CTTTTAGGTGT
                                ||| ||    ||||||||||
                                ACT GT    GAGAATCCATA
                                  _  AA__
GAM264  LOC92017  5' GCATCTAGGGAGCTGCT     67891      AAA    _
                                AGCA   GCTTT TAGGTGT
                                ||||   ||||| |||||||
                                TCGT   CGAGG ATCTACG
                                  ___    G
GAM264  LOC92017  5' ACGTCTAAAAGCTCAATCTGC  67884     AA___       GT
                                GCA    AGCTTTTAG  GT
                                |||    |||||||||  ||
                                CGT    TCGAAAATC  CA
                                  CTAAC        TG
GAM264  LOC92080  3' ACATCTGGAGGTGAGC      68037    AAAA
                                GC    GCTTTTAGGTGT
                                ||    ||||||||||||
                                CG    TGGAGGTCTACA
                                 AG__
GAM264  LOC92181  3' CATCAAAGTTTTTGTTCA    68404           TA   T
                                TGAGCAAAAGCTTT  GGTG
                                ||||||||||||||  ||||
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                                ACTTGTTTTTGAAA  CTAC
                                      __    T
GAM264  LOC92283  5' ATGTTGGAAGGCCTTTGTTCA  68745        A     AG TG
                                TGAGCAAA GCTTTT  G  T
                                |||||||| ||||||  | |
                                ACTTGTTT CGGAAG  T  A
                                     C     GT GT
GAM264  LOC92336  3' ACATTTGAGGGTTACTTTTG   68973       ___
                                CAAAAG   CTTTTAGGTGT
                                ||||||   ||||||||||
                                GTTTTC   GGGAGTTTACA
                                   ATT
GAM264  LOC92360  3' GCACCTGGAACTGTTTGTTT   69075        AGC
                                GAGCAAA   TTTTAGGTGT
                                |||||||   ||||||||||
                                TTTGTTT   AAGGTCCACG
                                    GTC
GAM264  LOC92539  5' GCACTTAGTCTGTTTTGCTTA  69636         GCTT
                                TGAGCAAAA    TTAGGTGT
                                |||||||||    ||||||||
                                ATTCGTTTT    GATTCACG
                                      GTCT
GAM264  LOC92661  5' ACACCTGAGGTGAGGCCCA    70075    A  AAAA    T
                                TG GC    GCTTT AGGTGT
                                || ||    ||||| ||||||
                                AC CG    TGGAG TCCACA
                                 C  GAG_    _
GAM264  LOC92689  3' ACCTTAGACTTTTGTTTA     70210         C   T
                                TGAGCAAAAG TTT AGGT
                                |||||||||| ||| ||||
                                ATTTGTTTTC AGA TCCA
                                      _   T
GAM264  LOC92697  5' ACGCCTGACTGGTTTT       70260        T_
                                AAAGCT  TTAGGTGT
                                ||||||  ||||||||
                                TTTTGG  AGTCCGCA
                                   TC
GAM264  LOC92710  3' AAGGGATTTTTGCTCA       70352          _
                                TGAGCAAAAG CTTTT
                                |||||||||| |||||
                                ACTCGTTTTT GGGAA
                                      A
GAM264  LOC92719  3' GCCAGGGGGCTTTGCTCA     70382         A     TA
                                TGAGCAAA GCTTT  GGT
                                |||||||| |||||  |||
                                ACTCGTTT CGGGG  CCG
                                     _    GA
GAM264  LOC92912  3' ACATCTGAGAGACTTGTCA    70843     G   AAG
                                TGA CAA   CTTTTAGGTGT
                                ||| |||   ||||||||||
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                                ACT GTT   GAGAGTCTACA
                                  _  CA_
GAM264  LOC92997  3' GCGCCTACTATTTGCTC     71089       _ CTTT
                                GAGCAAA AG    TAGGTGT
                                ||||||| ||    |||||||
                                CTCGTTT TC    ATCCGCG
                                   A ____
GAM264  LOC93052  5' TACCTGAGGGCTGGGGTTT   71266     AAA        GT
                                GAGC   AGCTTTTAGGT
                                ||||   ||||||||||
                                TTTG   TCGGGAGTCCA
                                  GGG         TG
GAM264  LOC93082  3' ACATCTGAGGGAGTTCA     56439      AAAAG
                                TGAGC    CTTTTAGGTGT
                                |||||    ||||||||||
                                ACTTG    GGGAGTCTACA
                                  A____
GAM264  LOC93109  3' TTCACAGAAGCTTTTGCTT   71419           AG   T
                                GAGCAAAAGCTTTT  GTG
                                |||||||||||||  |||
                                TTCGTTTTCGAAGA  CAC
                                        __  TTG
GAM264  LOC93444  5' ACACTTAGGGAAGCTGTTC   72384      AAA    __
                                GAGCA   GCTTT  TAGGTGT
                                |||||   |||||  |||||||
                                CTTGT   CGAAG  ATTCACA
                                   ___    GG
GAM265  EDNRA     3' TAAGAGAAAAAGATCGA     64112    A    A
                                TC ATCTT TTTCTCTTA
                                || ||||| |||||||||
                                AG TAGAA AAAGAGAAT
                                 C    _
GAM265  cerk      3' AGATAGTAAAAACTTAGGAT   42841       TTTCTC
                                ATCTTA     TTACTATCT
                                ||||||     |||||||||
                                TAGGAT     AATGATAGA
                                   TCAAA_
GAM265  DIO2      5' AGATAGCAAGAAGGGAAAGACA 5825     AA   A  TC    A
              GA                  TC  TCTT TT  TCTT CTATCT
                                ||  |||| ||  |||| ||||||
                                AG  AGAA GG  AGAA GATAGA
                                 AC    A  GA    C
GAM265  DIO2      5' AGATAGCAAGAAGGGAAAGACA 25677    AA   A  TC    A
              GA                  TC  TCTT TT  TCTT CTATCT
                                ||  |||| ||  |||| ||||||
                                AG  AGAA GG  AGAA GATAGA
                                 AC    A  GA    C
GAM265  TIGD4     5' AAGAGAAAAAGACTGA      89067     A    A
                                TCA TCTT TTTCTCTT
                                ||| |||| ||||||||
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                                AGT AGAA AAAGAGAA
                                  C   _
GAM265  WAC      3'  AGGGGAAAGATACAAGATTGA  33550        A____
                                TCAATCTT    TTTCTCTT
                                ||||||||    ||||||||
                                AGTTAGAA    AAAGGGGA
                                    CATAG
GAM265  WAC      3'  AGGGGAAAGATACAAGATTGA  55190        A____
                                TCAATCTT    TTTCTCTT
                                ||||||||    ||||||||
                                AGTTAGAA    AAAGGGGA
                                    CATAG
GAM265  WAC      3'  AGGGGAAAGATACAAGATTGA  55184        A____
                                TCAATCTT    TTTCTCTT
                                ||||||||    ||||||||
                                AGTTAGAA    AAAGGGGA
                                    CATAG
GAM265  ZNF271   5'  AGATGGTGAGAACAAGA     95248      ATTTC
                                TCTT    TCTTACTATCT
                                ||||    ||||||||||
                                AGAA    AGAGTGGTAGA
                                  CA___
GAM265  LOC144321 3'  ATAGTAAGGTGCTTAAGAT   83062       TTTC
                                ATCTTA   TCTTACTAT
                                ||||||   |||||||||
                                TAGAAT   GGAATGATA
                                   TCGT
GAM265  LOC219902 5'  AGATAAGGAAAATAAGAT    91498        CT   _
                                ATCTTATTT  CTTA CT
                                |||||||||  |||| ||
                                TAGAATAAA  GAAT GA
                                     AG   A
GAM265  LOC91694  5'  GATGGAAGAAATAAGCTGA   66961     AT       CTTA
                                TCA  CTTATTTCT   CTATC
                                |||  |||||||||   |||||
                                AGT  GAATAAAGA   GGTAG
                                  C_       A___
GAM266  ATRN     3'  CAACACTAACCCCACTCC    57796      AGATT
                                GGAGT    GTTAGTGTTG
                                |||||    ||||||||||
                                CCTCA    CAATCACAAC
                                  CCC__
GAM266  CSAGE    3'  CAACACTATCCAGCCACTCTGA 86860     G   AGA   T_
                                TCAG AGT   TTG  TAGTGTTG
                                |||| |||   |||  ||||||||
                                AGTC TCA   GAC  ATCACAAC
                                  _  CC_   CT
GAM266  DPP8     3'  CATGTAACATCTACTCCTGA   55233          T   _
                                TCAGGAGTAGAT GTTA GTG
                                ||||||||||| |||| |||
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                                AGTCCTCATCTA CAAT TAC
                                      _   G
GAM266  FLJ13197  5'  CAACACCAGCGCTGCACC    44847    A   AT   A
                                GG GTAG  TGTT GTGTTG
                                || ||||  |||| ||||||
                                CC CGTC  GCGA CACAAC
                                 A   __   C
GAM266  TRAG3     3'  CAACACTATCCAGCCACTCTGA 67525     G   AGA   T_
                                TCAG AGT   TTG  TAGTGTTG
                                |||| |||   |||  ||||||||
                                AGTC TCA   GAC  ATCACAAC
                                   _   CC_   CT
GAM266  TRAG3     3'  CAACACTATCCAGCCACTCTGA 16932     G   AGA   T_
                                TCAG AGT   TTG  TAGTGTTG
                                |||| |||   |||  ||||||||
                                AGTC TCA   GAC  ATCACAAC
                                   _   CC_   CT
GAM266  LOC196890 3'  AACAACCTGCTCCTGA      89642          A
                                TCAGGAGTAG TTGTT
                                |||||||||| |||||
                                AGTCCTCGTC AACAA
                                      C
GAM266  LOC92017  5'  AACCATCCACTCCTGA      67883         A   T
                                TCAGGAGT GAT GTT
                                |||||||| ||| |||
                                AGTCCTCA CTA CAA
                                     C   C
GAM267  PPEF1     5'  AAACAGAATCTATGACTGAAGA 20679     _   GGACT  A
                                TCT CAGT     GA TTCTGTTT
                                ||| ||||     || ||||||||
                                AGA GTCA     CT AAGACAAA
                                  A    GTAT_  _
GAM267  CYLD      3'  AACATACAGTCCATAAGAA    30880      CA       AATTC
                                TTCT  GTGGACTG     TGTT
                                ||||  ||||||||     ||||
                                AAGA  TACCTGAC     ACAA
                                   A_       AT___
GAM267  DKFZP564B1162 5'  TCAGTCCAGCTGAGAA      48532         _
                                TTCTCAG TGGACTGA
                                ||||||| ||||||||
                                AAGAGTC ACCTGACT
                                    G
GAM267  FLJ10884  5'  AAACAGAATCCAGTCTTGA    38835     GT     A
                                TCA  GGACTG ATTCTGTTT
                                |||  |||||| |||||||||
                                AGT  TCTGAC TAAGACAAA
                                  __     C
GAM267  FLJ10997  3'  AAACAGAATCAGGACA      36955     GA    A
                                TG  CTGA TTCTGTTT
                                ||  |||| ||||||||
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                                AC  GACT AAGACAAA
                                 AG   _
GAM267  FLJ12643  3'  AATCCAGTCCACTAGAA     82784      C        A
                                TTCT AGTGGACTG ATT
                                |||| ||||||||| |||
                                AAGA TCACCTGAC TAA
                                  _        C
GAM267  KIAA0073  5'  AAACAGAACTCAGCGAAAGAGA 67801       AGTGGA    A
           G                     TTCTC     CTGA TTCTGTTT
                                |||||      |||| ||||||||
                                GAGAG     GACT AAGACAAA
                                   AAAGC_    C
GAM267  KIAA1344  5'  AAACAGAACACAGCAGTGA   72443     G  GA   AA
                                TCA TG  CTG  TTCTGTTT
                                ||| ||  |||  ||||||||
                                AGT AC  GAC  AAGACAAA
                                  G  __   AC
GAM267  LOC112703 3'  AGGTCAGTCCATTAAGAA    73499      C        AT
                                TTCT AGTGGACTGA  TCT
                                |||| ||||||||||  |||
                                AAGA TTACCTGACT  GGA
                                  A         __
GAM267  LOC143888 3'  AAACAGAATTTTTTGACTAAG  76658    C   G  CT
                                CT AGT GA  GAATTCTGTTT
                                || ||| ||  ||||||||||
                                GA TCA TT  TTTAAGACAAA
                                 A   G  T_
GAM267  LOC220980 5'  CAGATCAATTCACTGA      93148         C   AT
                                TCAGTGGA TGA  TCTG
                                |||||||| |||  ||||
                                AGTCACTT ACT  AGAC
                                     A   __
GAM268  ALDH8A1   3'  CTTGGGAATCTCCAGAT     42608         AAATCTG
                                ATCTGGG      TCTCAAG
                                |||||||      |||||||
                                TAGACCT      AGGGTTC
                                    CTA____
GAM268  APOL1     3'  TGAGAACCCAAACTTCCCAGAG 13354     A       ATCTG___
           A                     TC TCTGGGAA       TCTCA
                                || ||||||||       |||||
                                AG AGACCCTT       AGAGT
                                 _       CAAACCCA
GAM268  ATM       5'  TTGAGACAGAATTCCCA     56297       A
                                TGGGAA TCTGTCTCAA
                                |||||| ||||||||||
                                ACCCTT AGACAGAGTT
                                   A
GAM268  ATM       5'  TTGAGACAGAATTCCCA     56309       A
                                TGGGAA TCTGTCTCAA
                                |||||| ||||||||||
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                                ACCCTT AGACAGAGTT
                                   A
GAM268  CLNS1A   3'  TCTTGAGACAGACTATACTGAG 7098     G  AAA__
           A                    TCT GG    TCTGTCTCAAGA
                                ||| ||    ||||||||||||
                                AGA TC    AGACAGAGTTCT
                                  G  ATATC
GAM268  HOXC13   3'  CTTAGGCAAGATTTCCCAG   59683          _   C
                                CTGGGAAATCT GTCT AAG
                                |||||||||| |||| |||
                                GACCCTTTAGA CGGA TTC
                                      A   _
GAM268  STK38    3'  AGACAGATCTTGCCGTGG    23441     CT  G  _
                                TCAT  GG AA ATCTGTCT
                                ||||  || || ||||||||
                                GGTG  CC TT TAGACAGA
                                  __  G  C
GAM268  ZNF256   5'  CTTGAGACAGATTTTGCA    19318    G
                                TG GAAATCTGTCTCAAG
                                || ||||||||||||||
                                AC TTTTAGACAGAGTTC
                                 G
GAM268  acmsd    5'  TGAGACAAGGATTCAGATG   56356        AAA  _
                                CATCTGGG   TCT GTCTCA
                                ||||||||   ||| ||||||
                                GTAGACTT   GGA CAGAGT
                                     A__   A
GAM268  APOL2    3'  TGAGAACCCAAACTTCCCAGAG 48056    A      ATCTG___
           A                    TC TCTGGGAA       TCTCA
                                || ||||||||       |||||
                                AG AGACCCTT       AGAGT
                                 _       CAAACCCA
GAM268  ATP6V1G3 3'  TCTCAGAATAATCTCTCAGATG 55820         A  CTG   CA
           A                    TCATCTGGGA AT   TCT  AGA
                                |||||||||| ||   |||  |||
                                AGTAGACTCT TA   AGA  TCT
                                      C  ATA   C_
GAM268  DKFZp434A171 3'  TAGATTCCCCAGATGA      50011         A
                                TCATCTGGG AATCTG
                                ||||||||| ||||||
                                AGTAGACCC TTAGAT
                                     C
GAM268  DKFZP762D096 3'  TCTTGAGGTTTACTTCTCAAAT 65581      C     ATCTG
           GA                     TCAT TGGGAA    TCTCAAGA
                                |||| ||||||    ||||||||
                                AGTA ACTCTT    GGAGTTCT
                                  A     CATTT
GAM268  FLJ10665 3'  GGACCACATTTCCCAAAGGA  36393    ATC      CT_
                                TC   TGGGAAAT   GTCT
                                ||   ||||||||   ||||
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                                AG   ACCCTTTA   CAGG
                                 GAA       CAC
GAM268  FLJ13117  3'  CTTGATCTTTCCCAGTGA    43540     T      TCTGTC
                                TCA CTGGGAAA     TCAAG
                                ||| ||||||||     |||||
                                AGT GACCCTTT     AGTTC
                                  _       CT____
GAM268  FLJ20716  3'  CTAAGGACAATTTCCCAGCTGA 35603     T       C    CA
                                TCA CTGGGAAAT TGTCT  AG
                                ||| ||||||||| |||||  ||
                                AGT GACCCTTTA ACAGG  TC
                                  C        _    AA
GAM268  GBA2      5'  AGACAGATTTATGGTTG     71021    T   GG
                                CA CTG  AAATCTGTCT
                                || |||  ||||||||||
                                GT GGT  TTTAGACAGA
                                 T   A_
GAM268  KIAA0215  3'  TGAGGCAGTTTCCCA       28422        T
                                TGGGAAA CTGTCTCA
                                ||||||| ||||||||
                                ACCCTTT GACGGAGT
                                      _
GAM268  KIAA0318  3'  CTCGAGACAGAGAAACGGA   68954      GGAAA       A
                                TCTG    TCTGTCTC AG
                                ||||    |||||||| ||
                                AGGC    AGACAGAG TC
                                  AAAG_       C
GAM268  KIAA1128  3'  CAAATTCCCCAGACTGA     68473     _     A   C
                                TCA TCTGGG AAT TG
                                ||| |||||| ||| ||
                                AGT AGACCC TTA AC
                                  C     C   A
GAM268  LNX       3'  CTTGACCTTTTCTCAGAT     50919          TCTGTC
                                ATCTGGGAAA     TCAAG
                                ||||||||||     |||||
                                TAGACTCTTT     AGTTC
                                      TCC___
GAM268  NAV3      3'  CTTAAAACAGATTTCTATGA   29771      CTG        CTC
                                TCAT   GGAAATCTGT   AAG
                                ||||   ||||||||||   |||
                                AGTA   TCTTTAGACA   TTC
                                  ___         AAA
GAM268  PALM      3'  CTTGATTTTCCCAGAGA     10412    A       TCTGTC
                                TC TCTGGGAAA     TCAAG
                                || |||||||||     |||||
                                AG AGACCCTTT     AGTTC
                                 _       T_____
GAM268  ROBO4     3'  TGAGACTTCCCAGACGG     38792    A       ATCT
                                TC TCTGGGAA    GTCTCA
                                || ||||||||    ||||||
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                                GG AGACCCTT    CAGAGT
                                 C       ____
GAM268  STAF65(gamma) 3'  TGAACAATTCCCCAGATGA    29448         A   C   C
                                TCATCTGGG AAT TGT TCA
                                ||||||||| ||| ||| |||
                                AGTAGACCC TTA ACA AGT
                                     C   _   _
GAM268  TCL6     5'  TCTTGAGACACTCCAGATGA   40149         AAATC
                                TCATCTGGG    TGTCTCAAGA
                                |||||||||    ||||||||||
                                AGTAGACCT    ACAGAGTTCT
                                     C____
GAM268  TCL6     5'  TCTTGAGACACTCCAGATGA   40164         AAATC
                                TCATCTGGG    TGTCTCAAGA
                                |||||||||    ||||||||||
                                AGTAGACCT    ACAGAGTTCT
                                     C____
GAM268  TTTY2    5'  CTCGAATTTGATTCCCAGAGGA 87003    A       A  TGTC  A
                                TC TCTGGGAA TC    TC AG
                                || |||||||| ||    || ||
                                AG AGACCCTT AG    AG TC
                                 G       _  TTTA  C
GAM268  LOC135818 3'  CTTGAGACAAACTGAGGGA    75236    A   G  AAATC
                                TC TCT GG     TGTCTCAAG
                                || ||| ||     |||||||||
                                AG GGA TC     ACAGAGTTC
                                 _   G  AA___
GAM268  LOC145497 5'  TGGGATGCCCCCAGATGA     77218         AAATCT
                                TCATCTGGG     GTCTCA
                                |||||||||     ||||||
                                AGTAGACCC     TAGGGT
                                     CCG___
GAM268  LOC150482 3'  TAGATTCCCCAGATGA      63075         A
                                TCATCTGGG AATCTG
                                ||||||||| ||||||
                                AGTAGACCC TTAGAT
                                     C
GAM268  LOC151568 5'  TCTTTGGAAATCTCCCAGGTGA 56704          AATCTG   C
                                TCATCTGGGA     TCT AAGA
                                ||||||||||     ||| ||||
                                AGTGGACCCT     AGG TTCT
                                      CTAA__   T
GAM268  LOC158327 3'  GACTTTCCCAGAAGA      81881    A       TCT
                                TC TCTGGGAAA   GTC
                                || |||||||||   |||
                                AG AGACCCTTT   CAG
                                 A       ___
GAM268  LOC159148 5'  CTCGAATTTGATTCCCAGAGGA 87012    A       A  TGTC  A
                                TC TCTGGGAA TC    TC AG
                                || |||||||| ||    || ||
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                                AG AGACCCTT AG    AG TC
                                 G       _ TTTA  C
GAM268  LOC169426 5'  AGGCAGAGATTTCCCAGAT   87285          __
                                ATCTGGGAAA  TCTGTCT
                                ||||||||||  |||||||
                                TAGACCCTTT  AGACGGA
                                      AG
GAM268  LOC200014 5'  TGAGACAGACCCTCCAG     88544       AAA
                                CTGGG   TCTGTCTCA
                                |||||   |||||||||
                                GACCT   AGACAGAGT
                                   CCC
GAM268  LOC202986 5'  TCCTGAGAACATCCCGGATGA  90445          AATC  _   A
                                TCATCTGGGA    TGT CTCA GA
                                ||||||||||    ||| |||| ||
                                AGTAGGCCCT    ACA GAGT CT
                                      _____  A   C
GAM268  LOC220115 5'  TCTTAAGGATATTCCCAGATGG 91745          ATC    C_
                                TCATCTGGGAA   TGTCT  AAGA
                                ||||||||||   |||||  ||||
                                GGTAGACCCTT   ATAGG  TTCT
                                      ___     AA
GAM268  LOC221756 5'  CTCTGGACTCCTCAGATGA    92139       _  AATCT   CA
                                TCATCTG GGA    GTCT  AG
                                |||||||  |||    ||||  ||
                                AGTAGAC CCT    CAGG  TC
                                     T  ______   TC
GAM268  LOC254228 3'  TTTGGGACCTCCCAAGTGA    95962    TC    AATCT
                                TCA  TGGGA    GTCTCAAG
                                |||  |||||    ||||||||
                                AGT  ACCCT    CAGGGTTT
                                  GA    C_____
GAM268  LOC51145  3'  TCTTAAGCTGATTTCCCA     32399        T T  C
                                TGGGAAATC G CT AAGA
                                |||||||||  |  ||  ||||
                                ACCCTTTAG C GA TTCT
                                      T _  A
GAM268  LOC90322  3'  CTTGAGGCCTGCCAAATGA    62266     C   GAAATCT
                                TCAT TGG      GTCTCAAG
                                ||||  |||      ||||||||
                                AGTA ACC      CGGAGTTC
                                   A   GTC_____
GAM268  LOC90632  5'  GAGACCCCCAGATGG       63647         AAATCT
                                TCATCTGGG     GTCTC
                                |||||||||     |||||
                                GGTAGACCC     CAGAG
                                      C_____
GAM269  A1BG      3'  ACTCACCTCTACCTC       55410           T C
                                GAGGTAGAGGT G AGT
                                ||||||||||  |  |||
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                                CTCCATCTCCA C TCA
                                      _ _
GAM269  A1BG    3'  GCTCACAGCAACCTCTACCTC  55422          A
                                GAGGTAGAGGTTGC GTGAGC
                                |||||||||||||| ||||||
                                CTCCATCTCCAACG CACTCG
                                       A
GAM269  A1BG    3'  GCTCACTGCAGTTTTGACCTC  55423     A  GG
                                GAGGT GA  TTGCAGTGAGC
                                ||||| ||  ||||||||||
                                CTCCA TT  GACGTCACTCG
                                   G  TT
GAM269  ACPT    3'  GCCCACCTGCCCCTGCCTCT  54983       A  TT   _  A
                                AGAGGTAG GG  GCAG TG GC
                                |||||||| ||  |||| || ||
                                TCTCCGTC CC  CGTC AC CG
                                     _ __   C  C
GAM269  ACPT    3'  GCCCACCTGCCCCTGCCTCT  54989       A  TT   _  A
                                AGAGGTAG GG  GCAG TG GC
                                |||||||| ||  |||| || ||
                                TCTCCGTC CC  CGTC AC CG
                                     _ __   C  C
GAM269  ACVR1   5'  GCCCACTGCAGCCTCCACCTC  6608      A        A
                                GAGGT GAGGTTGCAGTG GC
                                ||||| |||||||||||| ||
                                CTCCA CTCCGACGTCAC CG
                                   C         C
GAM269  ADAMTS4  3'  GCTCACTGCAACCTTCGCC   17511   TA
                                GG  GAGGTTGCAGTGAGC
                                ||  ||||||||||||||
                                CC  TTCCAACGTCACTCG
                                 GC
GAM269  ADAMTS4  3'  GCTCACTGCATCCTCCGCCTC  17512     TA   T
                                GAGG  GAGG TGCAGTGAGC
                                ||||  |||| ||||||||||
                                CTCC  CTCC ACGTCACTCG
                                   GC   T
GAM269  ADCY6   5'  GCTCACTGCAACCTCTGCC   30932
                                GGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||
                                CCGTCTCCAACGTCACTCG

GAM269  ADRB3   3'  CTTTCCACAACCTCTACCTT  3434          CAGT
                                GAGGTAGAGGTTG   GAG
                                ||||||||||||   |||
                                TTCCATCTCCAAC   TTC
                                       ACCT
GAM269  AHR     3'  GCTCACTGCAACCTCTACCTC  7879
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
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                                CTCCATCTCCAACGTCACTCG

GAM269  AIM1     3'  GCTCACTGCAGCCTCTACCTC  91824
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCATCTCCGACGTCACTCG

GAM269  ALDH1B1  3'  ACTGCAACCTCCGCCTC     5486      TA
                                GAGG  GAGGTTGCAGT
                                ||||  ||||||||||
                                CTCC  CTCCAACGTCA
                                  GC
GAM269  APM1     3'  CTCACTGCTACCTCTA      16589       T
                                TAGAGGT GCAGTGAG
                                |||||||  ||||||||
                                ATCTCCA CGTCACTC
                                     T
GAM269  APOL1    3'  GCTCACTGCAAGCTCTGCCTC  13349         G
                                GAGGTAGAG TTGCAGTGAGC
                                |||||||||  ||||||||||
                                CTCCGTCTC AACGTCACTCG
                                      G
GAM269  APPBP2   3'  GCTCACTGCAACCTCCGCCTC  21077      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  AQP6     3'  GCTCACTGCAACCTCTACCTC  7954
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCATCTCCAACGTCACTCG

GAM269  AQP6     3'  GCTCACTGCAACCTCTACCTC  53930
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCATCTCCAACGTCACTCG

GAM269  ARCN1    3'  GCTCACTGCAACCTCCGCCTC  7981      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  ATM      3'  GCTCACTGCATCCTCAACCTC  56307     A   T
                                GAGGT GAGG TGCAGTGAGC
                                |||||  ||||  ||||||||||
                                CTCCA CTCC ACGTCACTCG
                                   A   T
GAM269  ATP1B2   3'  CTCACTGCAACTTCCGC     8046    TA
                                G  GAGGTTGCAGTGAG
                                |  |||||||||||||
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                                C  CTTCAACGTCACTC
                                 GC
GAM269  ATP7A    3'  GCTCACTGCAACCTCTGCCT  3525
                                AGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                TCCGTCTCCAACGTCACTCG

GAM269  ATP8B2   3'  GCTCACTGCAACCTCCACCTC  65228      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  B4GALT5  3'  GCTCACTGCAGCCTCCATCTC  16505      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCTA CTCCGACGTCACTCG
                                   C
GAM269  BAZ2A    5'  ACTCAACCTCTGCCTCT     25590           C
                                AGAGGTAGAGGTTG AGT
                                |||||||||||||| |||
                                TCTCCGTCTCCAAC TCA
                                          _
GAM269  BCL10    3'  GCTCACTGCAACTTCTGCCTC  14059
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTTCAACGTCACTCG

GAM269  BRIP1    3'  GCTCACTGCAACCTTCACCTC  49398      AG
                                GAGGT  AGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCCA  TCCAACGTCACTCG
                                   CT
GAM269  C7       3'  CTGCAACCTCCGCCTC      5163       TA
                                GAGG  GAGGTTGCAG
                                ||||  ||||||||||
                                CTCC  CTCCAACGTC
                                  GC
GAM269  CACNA1S  3'  CGCAGCAGCCTCCCTC      3565       TA       A
                                GAGG  GAGGTTGC GTG
                                ||||  |||||||| |||
                                CTCC  CTCCGACG CGC
                                  __       A
GAM269  CACNA2D2 3'  CTCACCACCTGCCTCT      20084       AG    TGCA
                                AGAGGT  AGGT    GTGAG
                                ||||||  ||||    |||||
                                TCTCCG  TCCA    CACTC
                                   __    C___
GAM269  CAMLG    3'  GCTCACCGCAACCTCCACCTT  8240       A       A
                                GAGGT GAGGTTGC GTGAGC
                                ||||| |||||||| ||||||
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                                TTCCA CTCCAACG CACTCG
                                  C       C
GAM269  CAPNS1   3'  CACTCCGTAACCTCTCCCCT  8249     A  T       __
                                AG GG AGAGGTTGC  AGTG
                                || || |||||||||  ||||
                                TC CC TCTCCAATG  TCAC
                                 _ C        CC
GAM269  CASP10   3'  GCTCACTGTAGTCTCGACCTC  52120      A   GT
                                GAGGT GAG  TGCAGTGAGC
                                ||||| |||  ||||||||||
                                CTCCA CTC  ATGTCACTCG
                                  G   TG
GAM269  CASP10   3'  GCTCACTGTAGTCTCGACCTC  52104      A   GT
                                GAGGT GAG  TGCAGTGAGC
                                ||||| |||  ||||||||||
                                CTCCA CTC  ATGTCACTCG
                                  G   TG
GAM269  CASP2    3'  GCTCACTGCAAGCTCCAACTC  52171     GTA   G
                                GAG   GAG TTGCAGTGAGC
                                |||   ||| ||||||||||
                                CTC   CTC AACGTCACTCG
                                  AAC   G
GAM269  CASP2    3'  GCTCACTGCAAGCTCCAACTC  52143     GTA   G
                                GAG   GAG TTGCAGTGAGC
                                |||   ||| ||||||||||
                                CTC   CTC AACGTCACTCG
                                  AAC   G
GAM269  CASP2    3'  GCTCACTGCAAGCTCCAACTC  52156     GTA   G
                                GAG   GAG TTGCAGTGAGC
                                |||   ||| ||||||||||
                                CTC   CTC AACGTCACTCG
                                  AAC   G
GAM269  CASP2    3'  GCTCACTGCAAGCTCCAACTC  6901      GTA   G
                                GAG   GAG TTGCAGTGAGC
                                |||   ||| ||||||||||
                                CTC   CTC AACGTCACTCG
                                  AAC   G
GAM269  CBFA2T2  3'  GCTCACGGTAACCTCTGCCTC  17470           A
                                GAGGTAGAGGTTGC GTGAGC
                                |||||||||||||| ||||||
                                CTCCGTCTCCAATG CACTCG
                                       G
GAM269  CCNF     3'  CTCACTGTAACCTCCGCCTC  8318       TA
                                GAGG  GAGGTTGCAGTGAG
                                ||||  ||||||||||||||
                                CTCC  CTCCAATGTCACTC
                                  GC
GAM269  CDH17    3'  GCTCACTGCAACCTCCGCCTC  14506      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
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                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  CIAS1    5'  GCTCACTGCAGCCTCCACCTC  16901      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM269  CLASP2   3'  GCTCAAATTCTCTACCTCT   64594          TTGCAG
                                AGAGGTAGAGG    TGAGC
                                ||||||||||     |||||
                                TCTCCATCTCT    ACTCG
                                      TAA___
GAM269  CLECSF12 3'  CTCACTGCAGCTATCTCT   76689       AGA
                                AGAGGT  GGTTGCAGTGAG
                                ||||||  ||||||||||||
                                TCTCTA  TCGACGTCACTC
                                  ___
GAM269  CLECSF12 3'  GCTCACCGCAACCTCCGCC  76692    TA      A
                                GG  GAGGTTGC GTGAGC
                                ||  |||||||| ||||||
                                CC  CTCCAACG CACTCG
                                 GC       C
GAM269  CMAR     5'  GCTCACTGCAACCACCATCTC  17776      AGA
                                GAGGT  GGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCTA  CCAACGTCACTCG
                                   CCA
GAM269  CNGA1    5'  GCTCACTGCAGTCTTCACCTC  59510      AG  GT
                                GAGGT  AG  TGCAGTGAGC
                                |||||  ||  ||||||||||
                                CTCCA  TC  ACGTCACTCG
                                   CT  TG
GAM269  CNN2     3'  GCTCACTGCACCTCCACCTT   15176      A    T
                                GAGGT GAGGT GCAGTGAGC
                                ||||| ||||| |||||||||
                                TTCCA CTCCA CGTCACTCG
                                   C    _
GAM269  COL6A2   3'  GCTCACTGCCCCCACGCCT   54169     AGA  TT
                                AGGT   GG  GCAGTGAGC
                                ||||   ||  |||||||||
                                TCCG   CC  CGTCACTCG
                                  CA_  CC
GAM269  CORO2B   5'  GCTCACTGCAACCTCTGCC   64575
                                GGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||
                                CCGTCTCCAACGTCACTCG

GAM269  COX15    3'  GCTCACTCTGCAACCTCCACTT 54317      A       __
            C                    GAGGT GAGGTTGCA  GTGAGC
                                ||||| |||||||||  ||||||
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                                CTTCA CTCCAACGT  CACTCG
                                   C       CT
GAM269  CPS1    3' GCTCACTGCAATTTGCGTCT  8530     G   AG
                                AGA GTAG  GTTGCAGTGAGC
                                ||| ||||  ||||||||||||
                                TCT CGTT  TAACGTCACTCG
                                  G   __
GAM269  CR1     3' GCTCACTGCAACGTCCGCCTC 5135      TA  G
                                GAGG  GA GTTGCAGTGAGC
                                ||||  || ||||||||||||
                                CTCC  CT CAACGTCACTCG
                                  GC  G
GAM269  CRMP1   3' CTCATTGCCCCCACCTCT    7152       AGA  TT
                                AGAGGT   GG  GCAGTGAG
                                ||||||   ||  ||||||||
                                TCTCCA   CC  CGTTACTC
                                   ___  CC
GAM269  CRTAP   3' GCTCACTGCAACCTCCGCCTCT 21037      TA
                                AGAGG  GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                TCTCC  CTCCAACGTCACTCG
                                   GC
GAM269  CSNK2A2 5' GCTCACTGCAACCTCCACCTC  8565       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  CXCL13  5' GCTCAAGTCTGAACTCTACCTC 21198        GTTG  ___
                                GAGGTAGAG   CAG   TGAGC
                                |||||||||   |||   |||||
                                CTCCATCTC   GTC   ACTCG
                                     AA__   TGA
GAM269  CXCL16  3' GCTCACTGCAACCCCCATCTC  41920      AGA
                                GAGGT   GGTTGCAGTGAGC
                                |||||   ||||||||||||
                                CTCTA   CCAACGTCACTCG
                                   CCC
GAM269  CYP1A2  3' GCTCACTGCAACCTCCACCTC  5694       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  CYP1A2  3' GCTCACTGCAACCTCTGCCTC  5696
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  CYP1A2  3' GCTCACTGCAACCTCCACCTC  69114      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
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                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  CYP1A2   3' GCTCACTGCAACCTCTGCCTC 69116
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  CYP2B6   3' ACTGCAACCTCCACATC    5719    G A
                                GA GT GAGGTTGCAGT
                                || || ||||||||||
                                CT CA CTCCAACGTCA
                                 A  C
GAM269  CYP2B6   3' GCTCACTGCAACCTCCACC   5733     A
                                GGT GAGGTTGCAGTGAGC
                                ||| ||||||||||||||
                                CCA CTCCAACGTCACTCG
                                  C
GAM269  CYP4F3   3' ATTGCAACCTCCGCCTC    6108     TA
                                GAGG  GAGGTTGCAGT
                                ||||  ||||||||||
                                CTCC  CTCCAACGTTA
                                   GC
GAM269  CYP51    3' GCTCACTGCATCCTCTGCCTC 5784         T
                                GAGGTAGAGG TGCAGTGAGC
                                |||||||||| ||||||||||
                                CTCCGTCTCC ACGTCACTCG
                                      T
GAM269  CYP8B1   3' GCTCACTACAACCTCTGCCTC 15265          C
                                GAGGTAGAGGTTG AGTGAGC
                                |||||||||||| |||||||
                                CTCCGTCTCCAAC TCACTCG
                                       A
GAM269  CYP8B1   3' GCTCACTGCAACCTCTGCCTC 15267
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  DAB2     3' ACTGAACCCTACCTCT     7196        A  G
                                AGAGGTAG GGTT CAGT
                                |||||||| |||| ||||
                                TCTCCATC CCAA GTCA
                                      _  _
GAM269  DFFB     3' GCTCACTGCAACCTCCGCCTCT 87386     TA
                                AGAGG  GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                TCTCC  CTCCAACGTCACTCG
                                   GC
GAM269  DISC1    3' GCTCACTGCAACCTCTACCTC 37881
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
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                                CTCCATCTCCAACGTCACTCG

GAM269  DSC3    3' GCTCACTGAAAGCTCCGCCTC 8677      TA  G  G
                                GAGG  GAG TT CAGTGAGC
                                ||||  ||| || ||||||||
                                CTCC  CTC AA GTCACTCG
                                  GC   G  A
GAM269  DSC3    3' GCTCACTGAAAGCTCCGCCTC 44342     TA  G  G
                                GAGG  GAG TT CAGTGAGC
                                ||||  ||| || ||||||||
                                CTCC  CTC AA GTCACTCG
                                  GC   G  A
GAM269  DSCR3   3' GCTCACGGCAGCCTCAACCTC 20183      A      A
                                GAGGT GAGGTTGC GTGAGC
                                ||||| |||||||| ||||||
                                CTCCA CTCCGACG CACTCG
                                   A       G
GAM269  DSCR3   3' GCTCACTGCAACCTCCACCTC 20186      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                  C
GAM269  DUOX1   3' CCACACCTCACCTCT      33830      A    TGCA  A
                                AGAGGT GAGGT   GTG G
                                |||||| |||||   ||| |
                                TCTCCA CTCCA   CAC C
                                  _    _____  C
GAM269  EFNB2   3' GCTCACTGCTGCTGCCTCT   14574       AGGTT
                                AGAGGTAG    GCAGTGAGC
                                ||||||||    |||||||||
                                TCTCCGTC    CGTCACTCG
                                    GT___
GAM269  EHD2    3' GCTCACTGCAACCTCCACCTC 27497      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                  C
GAM269  ELMO1   3' GCTCAAATCTCCTCCCACCTCT 55283      A_   TTGCAG
                                AGAGGT  GAGG     TGAGC
                                ||||||  ||||     |||||
                                TCTCCA  CTCC     ACTCG
                                   CC   TCTAA_
GAM269  EPB72   3' GCTCACTGCAACCTCCGCCTC 14606     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  EPS8    3' GCTCACTGTAGGCTAGCCTCT 15469      AG  G
                                AGAGGT  AG TTGCAGTGAGC
                                ||||||  || ||||||||||
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                                TCTCCG  TC GATGTCACTCG
                                   A_  G
GAM269  F2RL2    3'  GCTCATTGCAACCTCTGCCTC  14624
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTTACTCG

GAM269  F2RL3    3'  CACCGCAACCTCATCCCCT   14172    A  TA      A
                                AG GG  GAGGTTGC GTG
                                || ||  |||||||| |||
                                TC CC  CTCCAACG CAC
                                 C  TA       C
GAM269  F2RL3    3'  CTCACTGCAAGTTCCTGCC   14177      _  G
                                GGTAG AG TTGCAGTGAG
                                ||||| || ||||||||||
                                CCGTC TT AACGTCACTC
                                   C  G
GAM269  FANCE    3'  GCTCACTGTAACCTCTGCCTC  41612
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAATGTCACTCG

GAM269  FANCF    3'  GCTCAGTGCAACCTCTGCCTC  42675             G
                                GAGGTAGAGGTTGCA TGAGC
                                |||||||||||||| |||||
                                CTCCGTCTCCAACGT ACTCG
                                         G
GAM269  FCAR     3'  CTCACTGCAACCTTCGCCTC  55794     TA
                                GAGG  GAGGTTGCAGTGAG
                                ||||  ||||||||||||||
                                CTCC  TTCCAACGTCACTC
                                  GC
GAM269  FCAR     3'  CTCACTGCAACCTTCGCCTC  55812     TA
                                GAGG  GAGGTTGCAGTGAG
                                ||||  ||||||||||||||
                                CTCC  TTCCAACGTCACTC
                                  GC
GAM269  FCGR2A   3'  GCTCACTGCAAACCCGCCTC  79262      AGA   _
                                GAGGT   GGTT GCAGTGAGC
                                |||||   |||| |||||||||
                                CTCCG   CCAA CGTCACTCG
                                   C__   A
GAM269  FEZ1     3'  GCTCACTGCAACCTCCACCTC  42573      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  FGF5     3'  GCTCACTGCAACCTCCAACTC  52488     GTA
                                GAG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
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                                CTC   CTCCAACGTCACTCG
                                  AAC
GAM269   FGF5     3'  GCTCACTGCAACCTCCAACTC  15542     GTA
                                GAG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||||
                                CTC   CTCCAACGTCACTCG
                                  AAC
GAM269   FHL1     3'  CTCACTGCTCACCCTCT     7558       TA  GGTT
                                AGAGG  GA    GCAGTGAG
                                |||||  ||    ||||||||
                                TCTCC  CT    CGTCACTC
                                   CA  _____
GAM269   FHL2     5'  GCTCACTGCAAGCTCTACCTCT 7566           G
                                AGAGGTAGAG TTGCAGTGAGC
                                |||||||||| ||||||||||
                                TCTCCATCTC AACGTCACTCG
                                      G
GAM269   FOS      3'  CTCAAGTCCTTACCTCT     17905       A    TTGCAG
                                AGAGGT GAGG     TGAG
                                |||||| ||||     ||||
                                TCTCCA TTCC     ACTC
                                   _    TGA___
GAM269   FUT1     3'  GCTCACTGCAACTTCCGCCTC  3792       TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTTCAACGTCACTCG
                                  GC
GAM269   FUT1     3'  GCTCACTGCAAGCTCTGCCTC  3794           G
                                GAGGTAGAG TTGCAGTGAGC
                                |||||||||| ||||||||||
                                CTCCGTCTC AACGTCACTCG
                                      G
GAM269   FXYD6    3'  GCTCTGGGACCCTACCCCT   41839    A    A    G  GT
                                AG GGTAG GGTT CA  GAGC
                                || ||||| |||| ||  ||||
                                TC CCATC CCAG GT  CTCG
                                 C     _    G  __
GAM269   FZD4     3'  GCTCACTGCAACCTCTGCCTC  24142
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   G6PC     3'  GCTCACTGCAACCTCTTCCTC  3829       T
                                GAGG AGAGGTTGCAGTGAGC
                                |||| ||||||||||||||||
                                CTCC TCTCCAACGTCACTCG
                                  T
GAM269   GAB2     3'  CACTTCCAGCTCCACTTCT   54446       A  G   C_
                                AGAGGT GAG TTG  AGTG
                                |||||| ||| |||  ||||
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                                TCTTCA CTC GAC  TCAC
                                   C   _   CT
GAM269  GAB2    3'  CACTTCCAGCTCCACTTCT   24489       A  G  C_
                                AGAGGT GAG TTG  AGTG
                                |||||| ||| |||  ||||
                                TCTTCA CTC GAC  TCAC
                                   C   _   CT
GAM269  GFPT2   3'  GCCCACATCCCTCCACTTCT  17577       A   TTGCA  A
                                AGAGGT GAGG    GTG GC
                                |||||| ||||    ||| ||
                                TCTTCA CTCC    CAC CG
                                   C   CTA__   C
GAM269  GHR     3'  CTCACTGCAATCTCCACCTC  3881        A
                                GAGGT GAGGTTGCAGTGAG
                                ||||| ||||||||||||||
                                CTCCA CTCTAACGTCACTC
                                   C
GAM269  GM2A    3'  ACTGCAACCTCCGCCTC    67767      TA
                                GAGG  GAGGTTGCAGT
                                ||||  ||||||||||
                                CTCC  CTCCAACGTCA
                                  GC
GAM269  GNE     3'  GCTCAATGCAACCTCTGCC   18480           G
                                GGTAGAGGTTGCA TGAGC
                                |||||||||||| |||||
                                CCGTCTCCAACGT ACTCG
                                      A
GAM269  GPR4    3'  GCTCACTGCAGCCTCCACCTC  59905      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM269  GPR56   5'  GCTCATCGTAACCTCCACCTC  19070      A      A
                                GAGGT GAGGTTGC GTGAGC
                                ||||| |||||||| ||||||
                                CTCCA CTCCAATG TACTCG
                                   C       C
GAM269  GPR81   3'  GCTCACTGCAACCTCTGCCTC  50762
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  GPT     5'  CACTGCCTCTGCCTC       17963         GTT
                                GAGGTAGAG   GCAGTG
                                |||||||||   ||||||
                                CTCCGTCTC   CGTCAC
                                      ___
GAM269  GRAF    3'  GCTCACTGCAACCTCCGCCTC  30564     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
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                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  HCS     3'  GCTCACCGCAACCTCCGCCTT  38474     TA      A
                                GAGG  GAGGTTGC GTGAGC
                                ||||  |||||||| ||||||
                                TTCC  CTCCAACG CACTCG
                                  GC       C
GAM269  HIF1A   5'  CTCGCACCCCCACCTCT     7734       AGA   TGCA
                                AGAGGT   GGT   GTGAG
                                ||||||   |||   |||||
                                TCTCCA   CCA   CGCTC
                                   CCC  ____
GAM269  HLCS    5'  GCTCACCACAACCTCTGCCT   4668          CA
                                AGGTAGAGGTTG  GTGAGC
                                ||||||||||||  ||||||
                                TCCGTCTCCAAC  CACTCG
                                      AC
GAM269  HMGA2   5'  CACTACTCTGTCCTCT      12994      _    GTTGC
                                AGAGG TAGAG    AGTG
                                ||||| |||||    ||||
                                TCTCC GTCTC    TCAC
                                   T    A____
GAM269  HMMR    3'  GCTCACTTGGTCCTACCT    25029       A  TT C
                                AGGTAG GG  G AGTGAGC
                                |||||| ||  | |||||||
                                TCCATC CT  T TCACTCG
                                   _  GG _
GAM269  HMMR    3'  GCTCACTTGGTCCTACCT    25030       A  TT C
                                AGGTAG GG  G AGTGAGC
                                |||||| ||  | |||||||
                                TCCATC CT  T TCACTCG
                                   _  GG _
GAM269  HTR1D   3'  GCTCACTGCAACCTCCGCATC  5999     G TA
                                GA G  GAGGTTGCAGTGAGC
                                || |  ||||||||||||||
                                CT C  CTCCAACGTCACTCG
                                 A GC
GAM269  HTR1E   5'  ATTGCAACCTCCGCCTC     6009      TA
                                GAGG  GAGGTTGCAGT
                                ||||  ||||||||||
                                CTCC  CTCCAACGTTA
                                  GC
GAM269  IFNAR2  3'  GCTCACTGCAACATCCGCCTC  6042      TA  G
                                GAGG  GA GTTGCAGTGAGC
                                ||||  || ||||||||||||
                                CTCC  CT CAACGTCACTCG
                                  GC  A
GAM269  IL11    3'  TCACTGCAAGCTCCACCTC   5336       A   G
                                GAGGT GAG TTGCAGTGA
                                ||||| ||| |||||||||
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                                CTCCA CTC AACGTCACT
                                   C   G
GAM269  INMT    3'  CTCACTGCAAGCTCCGCCTC  22270     TA   G
                                GAGG  GAG TTGCAGTGAG
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTC
                                  GC   G
GAM269  ITGAM   3'  GCTCACTGCAACCTCCGCCTC  71841     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  JRK     3'  GCTCACTGCAGCCTCGACCTC  86531     A
                                GAGGT GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   G
GAM269  KLK2    3'  GCCCCTGTCCCACCCCTACCTC 18690       A  T__   TGA
            T                    AGAGGTAG GGT   GCAG   GC
                                |||||||| |||   ||||   ||
                                TCTCCATC CCA   TGTC   CG
                                     C   CCC    CC_
GAM269  KMO     3'  ACTGCAACCTCTGCCTC     13440
                                GAGGTAGAGGTTGCAGT
                                |||||||||||||||||
                                CTCCGTCTCCAACGTCA

GAM269  KRT6A   3'  GCTCACCATCAGATCAACCTCT 18694      A  GG   CA_
                                AGAGGT GA  TTG   GTGAGC
                                ||||||  ||  |||   ||||||
                                TCTCCA CT  GAC   CACTCG
                                   A  A_   TAC
GAM269  LANCL1  3'  CTCACTGCATGACCCT     20213    A  __
                                AG GGT  TGCAGTGAG
                                ||  |||  |||||||||
                                TC CCA  ACGTCACTC
                                 _   GT
GAM269  LILRA3  3'  GCTCACTGCAACCTCCGCCTCT 95309      TA
                                AGAGG  GAGGTTGCAGTGAGC
                                |||||  |||||||||||||||
                                TCTCC  CTCCAACGTCACTCG
                                   GC
GAM269  LLGL1   3'  GCTCACTGCAAGCCCCGCC   66879     AGA   _
                                GGT   GGTT GCAGTGAGC
                                |||   |||| |||||||||
                                CCG   CCGA CGTCACTCG
                                  CC_    A
GAM269  LNK     3'  GCTCACTGCAACCTCCACCTT  18465      A
                                GAGGT GAGGTTGCAGTGAGC
                                |||||  |||||||||||||||
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                                TTCCA CTCCAACGTCACTCG
                                   C
GAM269  LRP1    5'  CTCGGAACTCTACCTCT    9801          GTTGCAG
                                AGAGGTAGAG     TGAG
                                ||||||||||     ||||
                                TCTCCATCTC     GCTC
                                     AAG____
GAM269  LTB4R   5'  GCTCACTGCAGCCTCCACTTC  5647       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTTCA CTCCGACGTCACTCG
                                   C
GAM269  LYZ     3'  GCTCACTGCAACCTCCACCTC  4103       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  MADH7   3'  CAGTGCCCTCTCCCCT     19743    A T    TT   G
                                AG GG AGAGG  GCA TG
                                || || |||||  ||| ||
                                TC CC TCTCC  CGT AC
                                 _ C    __   G
GAM269  MAK     3'  GCTTACTGCAACCTCCACCTC  19764      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCATTCG
                                   C
GAM269  MEF2A   5'  ACTGCAACCTCCGCCTC     18777     TA
                                GAGG  GAGGTTGCAGT
                                ||||  ||||||||||
                                CTCC  CTCCAACGTCA
                                  GC
GAM269  MEFV    3'  GCTCACTGCAACCTCCACCTC  4143       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  MEFV    3'  GCTCACTGCAACCTCCGCCTC  4145      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  MHC2TA  3'  ACTGCAACCTCCGCCTCT    4161       TA
                                AGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                TCTCC  CTCCAACGTCA
                                   GC
GAM269  MHC2TA  3'  GCTCACTGCAGCCTCAACCTC  4177       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
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                                CTCCA CTCCGACGTCACTCG
                                   A
GAM269  MICB    3'  GCTCACTGCAACCTCTGCCTC  19829
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  MPL     3'  GCTCACTGCAACCTCCACCTC  18146      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  MPL     3'  GCTCACTGCAACCTCTGCCTC  18148
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  MRPL49  3'  GCTCACTGCAACTTCCACCTCT 69571       A
                                AGAGGT GAGGTTGCAGTGAGC
                                |||||| ||||||||||||||
                                TCTCCA CTTCAACGTCACTCG
                                    C
GAM269  MYCL2   3'  GCTCACTGCAACCTCTGCCTC  18183
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  MYO1C   3'  GCCCACTGCTGACACTTCT   61206      AGAG  _    A
                                AGAGGT   GTT GCAGTG GC
                                ||||||   ||| |||||| ||
                                TCTTCA   CAG CGTCAC CG
                                   ____  T    C
GAM269  NAGA    3'  ACCCCAACCCCTACTTCT    4232        A    CA
                                AGAGGTAG GGTTG  GT
                                |||||||| |||||  ||
                                TCTTCATC CCAAC  CA
                                     C    CC
GAM269  NCOA3   3'  CTTTTAAACCCCTCCCTCT   21529      T  A   GCAGT
                                AGAGG AG GGTT    GAG
                                ||||| || ||||    |||
                                TCTCC TC CCAA    TTC
                                   C  C   ATT__
GAM269  NCOA6   5'  GCTCACTGCAGCCTCAACCTC  25971      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   A
GAM269  NDRG3   3'  GCTCACTGCAACCTCTGCC   49299
                                GGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
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                                CCGTCTCCAACGTCACTCG

GAM269  NONO     3'  GCTCACTGCAATCTCTGCCTC  82019
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCTAACGTCACTCG

GAM269  NOTCH3   3'  GCCCACTGCCAACTCCCTCT  4747      TA  GTT    A
                                AGAGG  GAG   GCAGTG GC
                                |||||  |||   |||||| ||
                                TCTCC  CTC   CGTCAC CG
                                   __  AAC     C
GAM269  NPR2L    3'  GCTCACTGTAGGCTCTATCTC  21560       G
                                GAGGTAGAG TTGCAGTGAGC
                                |||||||||| ||||||||||
                                CTCTATCTC GATGTCACTCG
                                      G
GAM269  NQO1     3'  GCTCACTGCAACCTCTGCCTC  6161
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  PCDHA9   3'  GCTCACTGCAACGTCTGCCTC  25764       G
                                GAGGTAGA GTTGCAGTGAGC
                                |||||||| ||||||||||||
                                CTCCGTCT CAACGTCACTCG
                                      G
GAM269  PCDHB11  3'  GCTCACTGCAACCTCTGCCTC  38417
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  PCDHB11  3'  GCTCACTGCACCCTCCGCCTCT 38419      TA   T
                                AGAGG  GAGG TGCAGTGAGC
                                |||||  |||| ||||||||||
                                TCTCC  CTCC ACGTCACTCG
                                   GC   C
GAM269  PCDHB16  3'  GCTCACTGCAACCTCTGCCTC  40552
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  PCDHB9   3'  GCTCACTGCAACCTCCGCCTC  38941     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  PDCL     3'  GCTCACTGCAACCTCCACCTC  18214     A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
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                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  PDE6B    3'  GCTCACTGCAACCTCCACCTC  4284       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  PER2     3'  GCTCACTGCAACCTCTGCCTC  43036
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  PHGDH    3'  GCTCACTGGTCCCTGCCTCT   64261        A  TTG
                                AGAGGTAG GG   CAGTGAGC
                                |||||||| ||   ||||||||
                                TCTCCGTC CC   GTCACTCG
                                     _  TG_
GAM269  PIGR     3'  GCTCACTGCAACCTCCGCCTC  72602      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269  PIK3C2B  3'  CTCACTGCAAAATCTGCCTC   10565        GG
                                GAGGTAGA  TTGCAGTGAG
                                ||||||||  |||||||||
                                CTCCGTCT  AACGTCACTC
                                     AA
GAM269  PIK3CD   3'  GCTCACTGTAACCTCCGCCTC  17246      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAATGTCACTCG
                                   GC
GAM269  PLA2G2D  3'  CCACACCCTCTACCCT      24789    A      TTGCA   A
                                AG GGTAGAGG     GTG G
                                || ||||||||     ||| |
                                TC CCATCTCC     CAC C
                                 _       CA___   C
GAM269  PLEK     3'  GCTCACTGCAGCCCCTCTGCCC 10632    A     __
           CT                     AG GGTAGA  GGTTGCAGTGAGC
                                || ||||||  ||||||||||||||
                                TC CCGTCT  CCGACGTCACTCG
                                 C     CC
GAM269  PMCHL1   3'  GCTCACTGAAACCTCTGCCTC  49074           G
                                GAGGTAGAGGTT CAGTGAGC
                                |||||||||||| ||||||||
                                CTCCGTCTCCAA GTCACTCG
                                       A
GAM269  PON1     3'  GCTCACTGCAACTTCTACCTC  4803
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
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                                CTCCATCTTCAACGTCACTCG

GAM269  PPID     3'  GCTCACTGCATCCTCTGCCTC  87433          T
                                GAGGTAGAGG TGCAGTGAGC
                                |||||||||| ||||||||||
                                CTCCGTCTCC ACGTCACTCG
                                      T
GAM269  PRKAB1   3'  GCTCAGGACCTCTGCCCCT   20737    A        GCAG
                                AG GGTAGAGGTT   TGAGC
                                || ||||||||||   |||||
                                TC CCGTCTCCAG   ACTCG
                                 C        G___
GAM269  PRKR     3'  GCTCACTGCAACTTCTGCCTCT 10883
                                AGAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                TCTCCGTCTTCAACGTCACTCG

GAM269  PRKWNK3  3'  GCTCACTGCTGCAACCTCCCCC 61553     TA         ___
           T                     AGG  GAGGTTGCAGT   GAGC
                                |||  ||||||||||   ||||
                                TCC  CTCCAACGTCG   CTCG
                                  CC         TCA
GAM269  PRKWNK3  3'  TGCTGCAACCTCCCCCTC    61558     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCGT
                                   CC
GAM269  PRODH    3'  GCCCAAGGCCCCCACCTCT   32926       AGA  TT  AG  A
                                AGAGGT   GG  GC  TG GC
                                ||||||   ||  ||  || ||
                                TCTCCA   CC  CG  AC CG
                                   ___  CC  GA  C
GAM269  PSMB2    3'  GCTCACTGCAACCTCCGCCTC  10951     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269  PTGES    3'  GCTCACTGCAGCCTCCGCCTC  16861     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCGACGTCACTCG
                                   GC
GAM269  PTGIS    3'  GCTCACTGCAAGCTCTGCCTC  6336          G
                                GAGGTAGAG TTGCAGTGAGC
                                ||||||||| ||||||||||
                                CTCCGTCTC AACGTCACTCG
                                      G
GAM269  PTPN1    3'  CACTGTCCGCCTCT       11047       AGA  TT
                                AGAGGT   GG  GCAGTG
                                ||||||   ||  ||||||
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                                TCTCCG  CC  TGTCAC
                                   ___  __
GAM269  RAB36   3' CTCACTGCAAGCTTCC     16958    TA  G
                                GG  GAG TTGCAGTGAG
                                ||  ||| ||||||||||
                                CC  TTC AACGTCACTC
                                 __  G
GAM269  RAB36   3' GCTCAGTGCAACCTCTGCCTC 16966           G
                                GAGGTAGAGGTTGCA TGAGC
                                ||||||||||||||| |||||
                                CTCCGTCTCCAACGT ACTCG
                                        G
GAM269  RAB6A   3' GCTCACTGCTTTGGCCCCCT  11197    TAGA  ___
                                AGG   GGTT  GCAGTGAGC
                                |||   ||||  |||||||||
                                TCC   CCGG  CGTCACTCG
                                 C___   TTT
GAM269  RAD52   3' GCCCAAGTGATACTCCCACCTC 11241      A_  _ TG AG  A
          T                      AGAGGT  GAG GT  C  TG GC
                                 ||||||  ||| ||  |  || ||
                                 TCTCCA  CTC TA  G  AC CG
                                    CC   A  GT A_  C
GAM269  RAD52   3' GCCCAAGTGATACTCCCACCTC 56196      A_  _ TG AG  A
          T                      AGAGGT  GAG GT  C  TG GC
                                 ||||||  ||| ||  |  || ||
                                 TCTCCA  CTC TA  G  AC CG
                                    CC   A  GT A_  C
GAM269  RAD52   3' GCCCAAGTGATACTCCCACCTC 56203      A_  _ TG AG  A
          T                      AGAGGT  GAG GT  C  TG GC
                                 ||||||  ||| ||  |  || ||
                                 TCTCCA  CTC TA  G  AC CG
                                    CC   A  GT A_  C
GAM269  RAD52   3' GCCCAAGTGATACTCCCACCTC 56212      A_  _ TG AG  A
          T                      AGAGGT  GAG GT  C  TG GC
                                 ||||||  ||| ||  |  || ||
                                 TCTCCA  CTC TA  G  AC CG
                                    CC   A  GT A_  C
GAM269  RALBP1  3' GCTCACTTTGTACCCCTCACCT 22297      A   T_  __
          CT                     AGAGGT GAGG  TGCA  GTGAGC
                                 |||||| ||||  ||||  ||||||
                                 TCTCCA CTCC  ATGT  CACTCG
                                    _   CC   TT
GAM269  RHD     3' GCTCACTGCAACCTCTACCTC  32617
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCATCTCCAACGTCACTCG

GAM269  RHD     3' GCTCACTGCAACCTCCGCCTC  32307     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
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                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  RHD     3'  GCTCACTGCAACCTCTACCTC  32308
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCATCTCCAACGTCACTCG

GAM269  RHD     3'  GCTCACTGCAACCTCCGCCTC  32616     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  RPH3AL  3'  GCTCACTGCAACCTCCACCTC  22748      A
                                GAGGT GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  RPP30   3'  GCTCACTGCAACCTCAATCCT  21168     TA_
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                TCC   CTCCAACGTCACTCG
                                  TAA
GAM269  RPP30   3'  GCTCACTGCAAGCTCCGCCTC  21169     TA  G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC  G
GAM269  SAS     3'  GCTCACCGCAACCTCTGCCTC  19955          A
                                GAGGTAGAGGTTGC GTGAGC
                                |||||||||||||| ||||||
                                CTCCGTCTCCAACG CACTCG
                                        C
GAM269  SCML2   3'  GCTCACTGCAACCTCGCCTC   20319      A
                                GAGGT GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCCG CTCCAACGTCACTCG
                                  _
GAM269  SEDL    3'  ACCGTAACCTCTGCCTC     27312          A
                                GAGGTAGAGGTTGC GT
                                |||||||||||||| ||
                                CTCCGTCTCCAATG CA
                                        C
GAM269  SEDL    3'  GCTCACTGCAACCTCCACCTC  27342      A
                                GAGGT GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  SEDL    3'  GCTCACTGCAACCTCCACCTC  27343      A
                                GAGGT GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
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                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  SEDL    3' GCTCACTGCAACCTCCGCCTC 27346     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  SEPN1   3' GCTCACTGCAACCTCCACCTC 66371      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  SERPINB9 3' GCTCACTGCAAGCTCCGCCTC 14758     TA  G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC  G
GAM269  SERPINB9 3' GCTCACTGCAACCTCCTCCTC 14757     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  TC
GAM269  SH3BP2  3' GCTCACTGCCACCTCCGCCTCT 11605     TA   T
                                AGAGG  GAGGT GCAGTGAGC
                                |||||  ||||| |||||||||
                                TCTCC  CTCCA CGTCACTCG
                                  GC    C
GAM269  SHOX    3' CTCACTGCAACCTCCGCCTC  22534     TA
                                GAGG  GAGGTTGCAGTGAG
                                ||||  |||||||||||||
                                CTCC  CTCCAACGTCACTC
                                  GC
GAM269  SIL     3' ACTGCAACCTCTGCCTC     11679
                                GAGGTAGAGGTTGCAGT
                                |||||||||||||||||
                                CTCCGTCTCCAACGTCA

GAM269  SLA2    3' GCTCACTGCAACCTCCATCTC 49900      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCTA CTCCAACGTCACTCG
                                   C
GAM269  SLC13A1 3' GCTCACTGCAAGCTCCGCCTC 42380     TA  G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC  G
GAM269  SLC14A2 5' GCTCACTGCAACCTCCACCTC 23134      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
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                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  SLC15A1  3'  GCTCACTGCAACCTCCGCCTC  17405     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  SLC7A6   5'  GCTCACTGCAACCTCCGACTC  14310    GTA
                                GAG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||||
                                CTC   CTCCAACGTCACTCG
                                 AGC
GAM269  SMAC     5'  GCTCACTGCAACCTCTGCCTC  57213
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  SMAC     5'  GCTCACTGCAACCTGTGCCTC  57215      G
                                GAGGTA AGGTTGCAGTGAGC
                                ||||||| ||||||||||||||
                                CTCCGT TCCAACGTCACTCG
                                   G
GAM269  SMARCD1  3'  CTCACTCCACCCTGCCTCT   57432       A  T C
                                AGAGGTAG GGT G AGTGAG
                                |||||||| ||| | ||||||
                                TCTCCGTC CCA C TCACTC
                                   _  _ C
GAM269  SMARCD1  3'  CTCACTCCACCCTGCCTCT   11814       A  T C
                                AGAGGTAG GGT G AGTGAG
                                |||||||| ||| | ||||||
                                TCTCCGTC CCA C TCACTC
                                   _  _ C
GAM269  SNAP23   3'  GCTCACTGCAACCTCCGCCTC  13811     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  SNAP23   3'  GCTCACTGCAACCTCCGCCTC  55464     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  SNX15    3'  GCTCACTGCAACCTCCACCTC  73742     A
                                GAGGT GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  SPN      3'  ACTGCAACCTCTGCCTC     11912
                                GAGGTAGAGGTTGCAGT
                                |||||||||||||||||
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                                CTCCGTCTCCAACGTCA

GAM269  SREBF2   3'  GCCCACCCCTCCACCTCT    15991       A   TTGCA  A
                                AGAGGT GAGG    GTG GC
                                |||||| ||||    ||| ||
                                TCTCCA CTCC    CAC CG
                                   C   C____   C
GAM269  SS18     3'  GCTCACTGCAACCTCCGCCTC  18887     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  STAU     5'  GCTCACTGCAACCTCCACCTC  16005      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  STIM1    3'  CTCCCAGCTCCACCTCT     60148       A  G  CAGT
                                AGAGGT GAG TTG   GAG
                                |||||| ||| |||   |||
                                TCTCCA CTC GAC   CTC
                                   C   _  C___
GAM269  SULT2B1  5'  GCTCACTGCAACCTCCGCCTC  16027     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  SYNGR1   3'  GCCCACTGTGGAGCCAGCCTC  16317      AGA  __    A
                                GAGGT  GGTT  GCAGTG GC
                                |||||  ||||  |||||| ||
                                CTCCG  CCGA  TGTCAC CG
                                   A__   GG    C
GAM269  TAPBP    3'  ACTGCAACCTCCGCCTC     12117     TA
                                GAGG  GAGGTTGCAGT
                                ||||  ||||||||||
                                CTCC  CTCCAACGTCA
                                  GC
GAM269  TAPBP    3'  GCTCACTGCAAGCTCCGCCTCT 12128      TA  G
                                AGAGG  GAG TTGCAGTGAGC
                                |||||  ||| ||||||||||
                                TCTCC  CTC AACGTCACTCG
                                   GC  G
GAM269  TAT      3'  GCTCACTGCAACCTCCACCTC  4470       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  TBXA2R   3'  GCTCACTGCAACCTCCACCTC  6497       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
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                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  TBXA2R   3'  GCTCACTGCAACCTCCGCCTC  6499      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  TCN2     5'  GCTCACTGCTCACCCACCTGCT 4481    _   AGA   T_
                                AG AGGT   GGT  GCAGTGAGC
                                || ||||   |||  |||||||||
                                TC TCCA   CCA  CGTCACTCG
                                 G   C__   CT
GAM269  TERF1    3'  GCTCACTGAACCTCTGCCTC  33973          G
                                GAGGTAGAGGTT CAGTGAGC
                                |||||||||||| ||||||||
                                CTCCGTCTCCAA GTCACTCG

                                          _
GAM269  TIM3     3'  GCTCACTGCAAGCTCCGCCTC  51346     TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269  TLR9     3'  ACTCACCTCACCTCT      33848       A    T C
                                AGAGGT GAGGT G AGT
                                |||||| ||||| | |||
                                TCTCCA CTCCA C TCA

                                     _    _ _
GAM269  TMC1     5'  GCTCTCTGCAACCTCCGCCTC  56904     TA       T
                                GAGG  GAGGTTGCAG GAGC
                                ||||  |||||||||| ||||
                                CTCC  CTCCAACGTC CTCG
                                  GC        T
GAM269  TNFRSF10B 3'  GCTCAGTGCAACCTCCGCCTC  13871     TA       G
                                GAGG  GAGGTTGCA TGAGC
                                ||||  ||||||||| |||||
                                CTCC  CTCCAACGT ACTCG
                                  GC        G
GAM269  TPMT     3'  GCTCACTGCAACCTCTGCCTC  4542
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  TRAF5    3'  GCTCACTGCAAACTCTGCCTC  16081         G
                                GAGGTAGAG TTGCAGTGAGC
                                |||||||||  ||||||||||
                                CTCCGTCTC AACGTCACTCG
                                      A
GAM269  TRIM9    5'  GCTCACTGCAACCTCCGCCTC  30762     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
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                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  TRPM6   3' ACTGCAACCTCTGCCTC    34528
                                GAGGTAGAGGTTGCAGT
                                |||||||||||||||||
                                CTCCGTCTCCAACGTCA

GAM269  TRPV1   3' GCTCACTGCAACCTCTGCCTC  38086
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  TRPV1   3' GCTCCCTGCAACCTCCGCCTC  38087     TA       T
                                GAGG  GAGGTTGCAG GAGC
                                ||||  |||||||||| ||||
                                CTCC  CTCCAACGTC CTCG
                                  GC         C
GAM269  TRPV1   3' GCTCACTGCAACCTCTGCCTC  54804
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  TRPV1   3' GCTCCCTGCAACCTCCGCCTC  54805     TA       T
                                GAGG  GAGGTTGCAG GAGC
                                ||||  |||||||||| ||||
                                CTCC  CTCCAACGTC CTCG
                                  GC         C
GAM269  TRPV1   3' GCTCACTGCAACCTCTGCCTC  54837
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  TRPV1   3' GCTCCCTGCAACCTCCGCCTC  54838     TA       T
                                GAGG  GAGGTTGCAG GAGC
                                ||||  |||||||||| ||||
                                CTCC  CTCCAACGTC CTCG
                                  GC         C
GAM269  TRPV1   3' GCTCACTGCAACCTCTGCCTC  54870
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  TRPV1   3' GCTCCCTGCAACCTCCGCCTC  54871     TA       T
                                GAGG  GAGGTTGCAG GAGC
                                ||||  |||||||||| ||||
                                CTCC  CTCCAACGTC CTCG
                                  GC         C
GAM269  TUBA3   5' GCAACAACCTCTCCTCT    20025      T      CA
                                AGAGG AGAGGTTG  GT
                                |||||  ||||||||  ||
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                                TCTCC TCTCCAAC  CG
                                  _       AA
GAM269  TUFT1    3'  GCTCACTGCAACCTCTGCCTC  39262
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  VENTX2   3'  GCTCACTGCAACCTCCGCCTC  27114      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  VENTX2   3'  CTCACCTGTCCCCCTCC     27111    T  A  TT   _
                                GG AG GG  GCAG TGAG
                                || || ||  |||| ||||
                                CC TC CC  TGTC ACTC
                                 _ _ CC    C
GAM269  VHL      3'  GCTCACTACAAGCTCTGCCTC  5073          G   C
                                GAGGTAGAG TTG AGTGAGC
                                ||||||||| ||| |||||||
                                CTCCGTCTC AAC TCACTCG
                                     G   A
GAM269  VHL      3'  GCTCACTGCAACCTCTGCCTC  5074
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  YES1     3'  GCTCACTGCAAGCTCTGCCTC  18354         G
                                GAGGTAGAG TTGCAGTGAGC
                                ||||||||| ||||||||||
                                CTCCGTCTC AACGTCACTCG
                                     G
GAM269  ZNF133   5'  CTCACTGCAACCTCCACC    12835     A
                                GGT GAGGTTGCAGTGAG
                                ||| ||||||||||||
                                CCA CTCCAACGTCACTC
                                  C
GAM269  ZNF144   5'  GCCCACTGCAGCCCTCCAGCCT 23080       A_   _      A
           CT                     AGAGGT  GAGG TTGCAGTG GC
                                ||||||  |||| |||||||| ||
                                TCTCCG  CTCC GACGTCAC CG
                                   AC    C       C
GAM269  ZNF261   3'  GCCCACTCCCTTCTCTACTCT  17495      G     TTGC    A
                                AGAG TAGAGG    AGTG GC
                                |||| ||||||    |||| ||
                                TCTC ATCTCT    TCAC CG
                                  _     TCCC    C
GAM269  ZNF264   3'  GCTCACTGCAACCTCCGCCTC  12758      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
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                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  ZNF264   3'  GCTCTCTGCAACCTCTGCCTC  12759            T
                                GAGGTAGAGGTTGCAG GAGC
                                |||||||||||||||| ||||
                                CTCCGTCTCCAACGTC CTCG
                                         T
GAM269  ZNF74    5'  GCTCACTGCAACCTCTGCTTC  12798
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTTCGTCTCCAACGTCACTCG

GAM269  20D7-FC4 5'  GCTCACTGCAGCCTCCACCTC  60903      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM269  AAK1     3'  GCTCACTGCAGCCTCCATCTC  29848      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCTA CTCCGACGTCACTCG
                                   C
GAM269  AP3S2    3'  GCTCACTGCAACCTCTGCTTC  19520
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTTCGTCTCCAACGTCACTCG

GAM269  APCL     3'  GCCCACTGCAAGGCCTCCCTC  19676     TA   __     A
                                GAGG  GAGGT  TGCAGTG GC
                                ||||  |||||  ||||||| ||
                                CTCC  CTCCG  ACGTCAC CG
                                  __    GA      C
GAM269  APOL2    3'  GCTCACTGCAAACTCCGCCTC  48049     TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC   A
GAM269  ARHF     3'  GCTCACTGCAAGCTCCACCTC  38745      A   G
                                GAGGT GAG TTGCAGTGAGC
                                ||||| ||| ||||||||||
                                CTCCA CTC AACGTCACTCG
                                   C   G
GAM269  ARPP-19  3'  GCTCACTGCAACCTCTGCCTC  21798
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  ARPP-19  3'  GCTCACTGCAACCTTACTCCT  21800     TA_
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
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                                TCC  TTCCAACGTCACTCG
                                  TCA
GAM269  ASB16    3'  GCTCACTGCAACTTCTACC   55108
                                GGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||
                                CCATCTTCAACGTCACTCG

GAM269  ASB16    5'  GCTCACTGCAACCTCCGCCTC  69939     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  ASE-1    3'  GCTCACTGCAACCTCCGCCTC  23950     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  ASE-1    3'  GCTCACTGCAAGCTCCGCCTC  23951     TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269  ATP1B4   3'  GCTCACTGCAACCTCCACCTC  23821      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  BA108L7.2 3'  GCTCACTGCAACCTCTGCCTC  48265
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  BAG5     3'  GCTCACTGCAACCTCCACCTC  16846      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  BNIP-S   3'  GCTCACTGCAACCTCCGCCTC  56261     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  BPES     3'  GCTCACCTCCCTGACCTCT   43532      AG   TTGCA
                                AGAGGT  AGG    GTGAGC
                                ||||||  |||    ||||||
                                TCTCCA  TCC    CACTCG
                                   G_   CTC__
GAM269  BTN3A1   3'  GCTCCCTGCAACCTCCACCTC  22921      A       T
                                GAGGT GAGGTTGCAG GAGC
                                ||||| |||||||||| ||||
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                                CTCCA CTCCAACGTC CTCG
                                   C         C
GAM269  BTN3A3    3'  GCTCACCACTGTATCCCCTCT  22771       TAGA  T     ___
                                AGAGG    GG TGCAGT   GAGC
                                |||||    || ||||||   ||||
                                TCTCC    CC ATGTCA   CTCG
                                   _____ T     CCA
GAM269  C(27)-3BETA-HSD 3'  GCTCACTGCACCCTCAACCTC  47273       A    T
                                GAGGT GAGG TGCAGTGAGC
                                ||||| |||| ||||||||||
                                CTCCA CTCC ACGTCACTCG
                                   A    C
GAM269  C11orf17  3'  GCTCACTGCAAGTTCCGCCTC  40212      TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTT AACGTCACTCG
                                   GC   G
GAM269  C13orf1   3'  GCTCACTGCAACCTCTGCTTC  39971
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTTCGTCTCCAACGTCACTCG

GAM269  C1orf24   3'  GCTCACTGCAACCTCCGCCTC  53722      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269  C1QTNF6   3'  ACTGCAACCTCTGCCTC     49134
                                GAGGTAGAGGTTGCAGT
                                |||||||||||||||||
                                CTCCGTCTCCAACGTCA

GAM269  C20orf103 5'  GCTCACCCCGGCCCACTC    24327     GTAGA    CA
                                GAG    GGTTG  GTGAGC
                                |||    |||||  ||||||
                                CTC    CCGGC  CACTCG
                                  AC___     CC
GAM269  C20orf27  3'  GCCCACGCCTCTCACCTCT    35385       _     TGCA   A
                                AGAGGT AGAGGT    GTG GC
                                |||||| ||||||    ||| ||
                                TCTCCA TCTCCG    CAC CG
                                   C     ____   C
GAM269  C21orf25  3'  GCTTACTGCAACCTCCACCTC  63553       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCATTCG
                                   C
GAM269  C21orf93  5'  CACCTTGGCTCTCTGCCCCT   59084    A      _   CA
                                AG GGTAGAG GTTG  GTG
                                || ||||||| ||||  |||
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                                TC CCGTCTC CGGT  CAC
                                 C      T   TC
GAM269  C22orf19  3'  GCTCACTGCCGCCTCAACCTCT 13425       A    T
                                AGAGGT GAGGT GCAGTGAGC
                                |||||| ||||| |||||||||
                                TCTCCA CTCCG CGTCACTCG
                                   A    C
GAM269  C3F       3'  GCTCACCGCAACCTCCACCTC  19294      A      A
                                GAGGT GAGGTTGC GTGAGC
                                ||||| |||||||| ||||||
                                CTCCA CTCCAACG CACTCG
                                   C       C
GAM269  C6orf33   3'  GCTCACTGCAGCCTCGACCTC  55882      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   G
GAM269  C6orf5    3'  GCTCACTGCAACCTGCGCCTC  31353      AG
                                GAGGT  AGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCCG  TCCAACGTCACTCG
                                   CG
GAM269  C8orf13   5'  GCTCACTGCGCGGTCCCTCT   81574      TA  GGT
                                AGAGG  GA   TGCAGTGAGC
                                |||||  ||   ||||||||||
                                TCTCC  CT   GCGTCACTCG
                                   __  GGC
GAM269  C9orf9    3'  GCTCACTGCAACCTCCACCTC  38516      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  C9orf9    3'  GCTCACTGCAACCTCCGCCTC  38518      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269  CARD6     3'  GCTCACCGCAACCTCTGCTTC  50857           A
                                GAGGTAGAGGTTGC GTGAGC
                                |||||||||||||| ||||||
                                CTTCGTCTCCAACG CACTCG
                                         C
GAM269  CCRN4L    3'  GCTCACTGCAAGATCCGCCTC  24009      TA  GG
                                GAGG  GA  TTGCAGTGAGC
                                ||||  ||  ||||||||||
                                CTCC  CT  AACGTCACTCG
                                   GC  AG
GAM269  CDC14B    3'  GCTCACTGCAACCTCCTTCTC  52856      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
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                                CTCT  CTCCAACGTCACTCG
                                  TC
GAM269  CDC14B   3'  GCCCACTGCAAGTTCTCTC   52853    GT   G      A
                                GAG  AGAG TTGCAGTG GC
                                |||  |||| |||||||| ||
                                CTC  TCTT AACGTCAC CG
                                 __   G       C
GAM269  CEACAM8  3'  CTCACTGCAAGCTCCGCCTC  8423      TA  G
                                GAGG  GAG TTGCAGTGAG
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTC
                                  GC   G
GAM269  CECR1    3'  GCTCACTGCAACTTCCACTC  33816    GTA
                                GAG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                CTC   CTTCAACGTCACTCG
                                 AC_
GAM269  CENPH    3'  GCTCACTGCAACCTCTGCCTC  43275
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  CHRAC1   3'  GCTCACTGCAACCTCCGCCTC  33873     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  CLSTN2   3'  CTCACTGTGCGTCTCCTC    42131     T   G  T
                                GAGG AGA GT GCAGTGAG
                                |||| ||| || ||||||||
                                CTCC TCT CG TGTCACTC
                                  _  G  _
GAM269  COLEC12  3'  GCTCACTGCAACCCCC     47869    TAGA
                                GG    GGTTGCAGTGAGC
                                ||    ||||||||||||
                                CC    CCAACGTCACTCG
                                 C___
GAM269  COPS7B   3'  CCATTTCCTCCCCTCT     42692      TA   TTGC   A
                                AGAGG  GAGG    AGTG G
                                |||||  ||||    |||| |
                                TCTCC  CTCC    TTAC C
                                  C_    T___    C
GAM269  CPSF2    3'  GCTCACCGCAACCTCTGCCTC  61588           A
                                GAGGTAGAGGTTGC GTGAGC
                                |||||||||||||| ||||||
                                CTCCGTCTCCAACG CACTCG
                                         C
GAM269  CPSF2    3'  GCTCACTATAACCTCTTCCTC  61589     T      C
                                GAGG AGAGGTTG AGTGAGC
                                |||| |||||||| |||||||
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                                CTCC TCTCCAAT TCACTCG
                                  T       A
GAM269  DAPK2     3'  GCCCATGCTCCCTCTACCTC  26739          TT  G  A
                                GAGGTAGAGG  GCA TG GC
                                ||||||||||  ||| || ||
                                CTCCATCTCC  CGT AC CG
                                     CT   _  C
GAM269  DBR1      3'  GCTCACCGCAACCTCCGCCTC  32534      TA       A
                                GAGG  GAGGTTGC GTGAGC
                                ||||  |||||||| ||||||
                                CTCC  CTCCAACG CACTCG
                                  GC       C
GAM269  DCOHM     3'  GCTCACTGCAGTCTCCACCTC  49605       A   GT
                                GAGGT GAG  TGCAGTGAGC
                                ||||| |||  ||||||||||
                                CTCCA CTC  ACGTCACTCG
                                   C   TG
GAM269  DKFZp434A2417 3'  GCTCACTGCAACTTCCACCTC  66104       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTTCAACGTCACTCG
                                   C
GAM269  DKFZP434C212 3'  GCTCACTGCAACCTCCACCTC  68913       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  DKFZP434D146 3'  GCCCACTGCAACCTCTGCTTC  31525                 A
                                GAGGTAGAGGTTGCAGTG GC
                                |||||||||||||||||  ||
                                CTTCGTCTCCAACGTCAC CG
                                          C
GAM269  DKFZp434E2220 5'  GCTCACTGCAACCTCCGCCTC  34297       TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  |||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269  DKFZP434F0318 3'  GCTCACTGCAACCTCCGACTC  48012     GTA
                                GAG   GAGGTTGCAGTGAGC
                                |||   |||||||||||||||
                                CTC   CTCCAACGTCACTCG
                                  AGC
GAM269  DKFZp434F1719 3'  GCTCACTGCAGGCTCTGCCTC  50001          G
                                GAGGTAGAG TTGCAGTGAGC
                                |||||||||  ||||||||||
                                CTCCGTCTC GACGTCACTCG
                                      G
GAM269  DKFZp547H025 3'  GCTCACTGCAACCTCCACCTC  39360       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
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                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  DKFZP564O0523 3'  GCTCACTGCAACCTCCACCTC  49516      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  DKFZP564O1664 5'  GCTCAGCTCCCCTCTGCC    47938       TT_ AG
                                GGTAGAGG  GC  TGAGC
                                ||||||||  ||  |||||
                                CCGTCTCC  CG  ACTCG
                                     CCT  __
GAM269  DKFZp586H0623 3'  CTCACTGCAGACTTCCTCT   34069      TA  G
                                AGAGG  GAG TTGCAGTGAG
                                |||||  ||| ||||||||||
                                TCTCC  TTC GACGTCACTC
                                   __  A
GAM269  DKFZp761D112 3'  GCTCACCAAGCTACTATCTCT  50191       A   GCA
                                AGAGGTAG GGTT  GTGAGC
                                |||||||| ||||  ||||||
                                TCTCTATC TCGA  CACTCG
                                     A   AC_
GAM269  DKFZp761J139 5'  GCTCACTGCAACGTCCACCTCT 50112      A  G
                                AGAGGT GA GTTGCAGTGAGC
                                |||||| || ||||||||||||
                                TCTCCA CT CAACGTCACTCG
                                   C  G
GAM269  DKFZp761N1114 3'  GCTCACTGCAACCTCCGCCTC  79019     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  DKFZp761O0113 5'  GCTCACCGCAGCCTCCGCCTC  37279     TA      A
                                GAGG  GAGGTTGC GTGAGC
                                ||||  |||||||| ||||||
                                CTCC  CTCCGACG CACTCG
                                  GC      C
GAM269  DKFZp762L0311 3'  GCTCACTGCAACCTTTGCCTC  38057
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTTTCCAACGTCACTCG

GAM269  DKFZp762P2111 3'  GCTCACTGCAACCTCCGCCTCT 86357      TA
                                AGAGG  GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||||
                                TCTCC  CTCCAACGTCACTCG
                                   GC
GAM269  DKK3    3'  GCTCAGCTCCTACCTCT    25132        AG   C
                                AGAGGTAG  GTTG AGT
                                ||||||||  |||| |||
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                                TCTCCATC  CGAC TCG
                                    CT   _
GAM269  DSCR6    3'  GCTCACTGCAACCTCCACTTCT 38549       A
                                AGAGGT GAGGTTGCAGTGAGC
                                |||||| ||||||||||||||||
                                TCTTCA CTCCAACGTCACTCG
                                   C
GAM269  EREG     3'  GCTCACTGCAACCTCACCTC  7503       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                  _
GAM269  EVI5     3'  GCTCACTGCAACTTCCACTTC  19001      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTTCA CTTCAACGTCACTCG
                                   C
GAM269  FBXL6    3'  CCACCCTCCACCTTT      24077       A   TTGCA   A
                                AGAGGT GAGG    GTG G
                                |||||| ||||    ||| |
                                TTTCCA CTCC    CAC C
                                   C   _____  C
GAM269  FBXL6    3'  CCACCCTCCACCTTT      44645       A   TTGCA   A
                                AGAGGT GAGG    GTG G
                                |||||| ||||    ||| |
                                TTTCCA CTCC    CAC C
                                   C   _____  C
GAM269  FER1L4   3'  GCTGACTGCAACCTCCACCTC  47350      A        G
                                GAGGT GAGGTTGCAGT AGC
                                ||||| |||||||||| |||
                                CTCCA CTCCAACGTCA TCG
                                   C         G
GAM269  FER1L4   3'  GCTGACTGCAACCTCCACCTC  47351      A        G
                                GAGGT GAGGTTGCAGT AGC
                                ||||| |||||||||| |||
                                CTCCA CTCCAACGTCA TCG
                                   C         G
GAM269  FKBP9    3'  GCTCACTGCAGCCTCCGCCTC  94065     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCGACGTCACTCG
                                  GC
GAM269  FLJ00024 5'  GCTCACTGCAACCTCTGCCTC  63763
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  FLJ00060 5'  GCTCACTGCAAGCTCTGCCTC  61099        G
                                GAGGTAGAG TTGCAGTGAGC
                                |||||||| ||||||||||
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                                CTCCGTCTC AACGTCACTCG
                                     G
GAM269  FLJ10043 3' CTCTTCCACCCTCTACCCCT  35757    A      T  CAGT
                                AG GGTAGAGG TG    GAG
                                || |||||||| ||    |||
                                TC CCATCTCC AC    CTC
                                 C       C  CTT_
GAM269  FLJ10232 3' GCTCACTGCAACCTCCGCCTC  35927     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  FLJ10346 5' GCTCACTGCAAGCTCCACCTC  36045     A  G
                                GAGGT GAG TTGCAGTGAGC
                                ||||| ||| ||||||||||
                                CTCCA CTC AACGTCACTCG
                                   C  G
GAM269  FLJ10535 3' GCTCACTGCAACCTCTGCCTC  36242
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  FLJ10560 3' GCTCACTGCAAGCTCTGCCTC  36280        G
                                GAGGTAGAG TTGCAGTGAGC
                                ||||||||| ||||||||||
                                CTCCGTCTC AACGTCACTCG
                                     G
GAM269  FLJ10583 3' GCCCACTGCAGCCCTGACC   36309    _ A       A
                                GGT AG GGTTGCAGTG GC
                                ||| || |||||||||| ||
                                CCA TC CCGACGTCAC CG
                                  G _       C
GAM269  FLJ10716 5' GCTCACTGCAGCCTCAACCTC  36484     A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   A
GAM269  FLJ10761 3' CTCAACAGCCTCCACCTC    36579     A     CAG
                                GAGGT GAGGTTG   TGAG
                                ||||| |||||||   ||||
                                CTCCA CTCCGAC   ACTC
                                   C      A__
GAM269  FLJ10901 3' GCTCACTGCAACCCCCGTCTC  36828     TAGA
                                GAGG    GGTTGCAGTGAGC
                                ||||    ||||||||||||
                                CTCT    CCAACGTCACTCG
                                  GCCC
GAM269  FLJ10922 3' GCTCACTGCAACCTCCGCCTC  36877     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
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                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  FLJ11004  5' GCTCACTGCAACCTCTACCTC  36969
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCATCTCCAACGTCACTCG

GAM269  FLJ11117  3' TTGAAATCTCCACCTCT    37076      A    G
                                AGAGGT GAGGTT CAG
                                |||||| |||||| |||
                                TCTCCA CTCTAA GTT
                                   C     A
GAM269  FLJ11996  3' GCTTCTCAAACCTCTACCTTT  46437          GC  T
                                AGAGGTAGAGGTT  AG GAGC
                                ||||||||||||  || ||||
                                TTTCCATCTCCAA  TC TTCG
                                       AC  _
GAM269  FLJ12363  3' GCTCACTGCAACCTCCACCTC  49685      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                  C
GAM269  FLJ12409  3' CTCACTGCAACCTCCGCCTC  47047     TA
                                GAGG  GAGGTTGCAGTGAG
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTC
                                  GC
GAM269  FLJ12572  5' GCTCACTGCAACCTCTGCCTC  43253
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  FLJ12581  3' GCTCACTGCAAGCTCCGCCTC  45879     TA  G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC  G
GAM269  FLJ12586  3' CTCACAGCAACCTCTGCCTC  44876          A
                                GAGGTAGAGGTTGC GTGAG
                                |||||||||||||| |||||
                                CTCCGTCTCCAACG CACTC
                                       A
GAM269  FLJ12649  3' GCTCACTGCAACCTCCGCCTC  44780     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  FLJ12668  3' TCACTGCAACCTCCATCTC   46523      A
                                GAGGT GAGGTTGCAGTGA
                                ||||| ||||||||||||
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                                CTCTA CTCCAACGTCACT
                                   C
GAM269  FLJ12687  3'  GCTCACTGCAACCTCCGCCTC  46198     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  FLJ12747  3'  ACTGCAACCTCTGCCTC     49707
                                GAGGTAGAGGTTGCAGT
                                |||||||||||||||||
                                CTCCGTCTCCAACGTCA

GAM269  FLJ12876  3'  GCTCACTGCAAGCTCCGCCTC  42788     TA  G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC  G
GAM269  FLJ12960  3'  GCTCTATGCAACCTCCACCTC  44951      A       GT
                                GAGGT GAGGTTGCA  GAGC
                                ||||| |||||||||  ||||
                                CTCCA CTCCAACGT  CTCG
                                   C        AT
GAM269  FLJ12973  3'  GCTCACCGCAACCTCCGCCTC  46106     TA       A
                                GAGG  GAGGTTGC GTGAGC
                                ||||  |||||||| ||||||
                                CTCC  CTCCAACG CACTCG
                                  GC       C
GAM269  FLJ12975  3'  GCTCACTGCAATCTCTGCCTC  69587
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCTAACGTCACTCG

GAM269  FLJ13072  5'  GCTCACTGCAACCTCTGCCTC  89816
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  FLJ13188  3'  GCTCACTGCAACCACTGCTTC  41939       A
                                GAGGTAG GGTTGCAGTGAGC
                                ||||||| ||||||||||||
                                CTTCGTC CCAACGTCACTCG
                                    A
GAM269  FLJ13197  3'  GCTCACTGCAACCTCTACCTC  44856
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCATCTCCAACGTCACTCG

GAM269  FLJ13590  5'  GCTCACTGCAGCCTCCATCTC  45786      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
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                                CTCTA CTCCGACGTCACTCG
                                   C
GAM269  FLJ13984  5'  GCTCACTGCAGTTTCAACCTC  45450      A  GG
                                GAGGT GA  TTGCAGTGAGC
                                ||||| ||  ||||||||||
                                CTCCA CT  GACGTCACTCG
                                   A  TT
GAM269  FLJ14442  3'  GCTCACTGCAACTTCTGCCTC  51370
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTTCAACGTCACTCG

GAM269  FLJ14803  3'  GCTCACTACAACTTCTGCCTC  51617           C
                                GAGGTAGAGGTTG AGTGAGC
                                |||||||||||| |||||||
                                CTCCGTCTTCAAC TCACTCG
                                         A
GAM269  FLJ14950  3'  GCTCACTGCAACCTCCACCTC  51721      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  FLJ14957  3'  GCTCACTGCAACCTCTGCCTC  51752
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  FLJ20004  3'  GCTCATTGCAACCTCCGCCTC  95294     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTTACTCG
                                   GC
GAM269  FLJ20034  3'  GCTCACTGCAACCTCTGCCTC  34375
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  FLJ20045  3'  GCTCACTGCAACCTCTGCCTC  34422
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  FLJ20079  3'  GCTCACCGCAACCTCCACCTC  34496      A      A
                                GAGGT GAGGTTGC GTGAGC
                                ||||| |||||||| ||||||
                                CTCCA CTCCAACG CACTCG
                                   C       C
GAM269  FLJ20136  3'  GCTCACTGCAATCTCTGCCTCT 34614
                                AGAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||||
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                                TCTCCGTCTCTAACGTCACTCG

GAM269  FLJ20342 3' ACTGCAACCTCTGCCTC    34983
                                GAGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                CTCCGTCTCCAACGTCA

GAM269  FLJ20344 3' GCTCACTGCAACCTCCGCCTCT 35013      TA
                                AGAGG  GAGGTTGCAGTGAGC
                                |||||  |||||||||||||||
                                TCTCC  CTCCAACGTCACTCG
                                   GC
GAM269  FLJ20507 3' GCTCACTGCAACCTCTGCCTC  35294
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  FLJ20507 3' GCTCACTGCAACCTCTGCCTC  60229
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  FLJ20511 3' GCTCACTGCAAGCTCCACCTC  35327      A  G
                                GAGGT GAG TTGCAGTGAGC
                                ||||| ||| ||||||||||
                                CTCCA CTC AACGTCACTCG
                                   C  G
GAM269  FLJ20542 3' CTCACCCAGCCGCCACCTCT   49784      AGA    CA
                                AGAGGT   GGTTG  GTGAG
                                ||||||   |||||  |||||
                                TCTCCA   CCGAC  CACTC
                                   CCG    C_
GAM269  FLJ20619 3' CTCACTGCAGGAATCCCT    35463    TA  GG_
                                AGG  GA   TTGCAGTGAG
                                |||  ||   ||||||||||
                                TCC  CT   GACGTCACTC
                                  __  AAG
GAM269  FLJ20671 3' GCTCACCGTAATCTCCGCCTC  35527     TA      A
                                GAGG  GAGGTTGC GTGAGC
                                ||||  |||||||| ||||||
                                CTCC  CTCTAATG CACTCG
                                   GC       C
GAM269  FLJ20700 3' GCTCACTGCAACCTCTGTCTC  35578    GT
                                GAG  AGAGGTTGCAGTGAGC
                                |||  ||||||||||||||||
                                CTC  TCTCCAACGTCACTCG
                                  TG
GAM269  FLJ20813 3' GCTCACTGCAACTCCACCTC   35686      A  G
                                GAGGT GAG TTGCAGTGAGC
                                ||||| ||| ||||||||||
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                                CTCCA CTC AACGTCACTCG
                                  C  _
GAM269  FLJ21126 3' ACTCACCTCTACCTTT     90325          T C
                                AGAGGTAGAGGT G AGT
                                |||||||||||| | |||
                                TTTCCATCTCCA C TCA
                                     _ _
GAM269  FLJ21135 5' GCTCACCGCCCCCTCCCCT   45885    TA   TT  A
                                AGG  GAGG  GC GTGAGC
                                |||  ||||  || ||||||
                                TCC  CTCC  CG CACTCG
                                 C_   CC  C
GAM269  FLJ21276 3' CACTGTCTGTCTACCTT    44918       GGTT
                                GAGGTAGA   GCAGTG
                                ||||||||   ||||||
                                TTCCATCT   TGTCAC
                                    GTC_
GAM269  FLJ21302 3' ACTGCAACCTCCGCCTC    43208     TA
                                GAGG  GAGGTTGCAGT
                                ||||  ||||||||||
                                CTCC  CTCCAACGTCA
                                  GC
GAM269  FLJ21459 3' GCTCACTGCAAACTCCGCCTC 44517     TA  G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC  A
GAM269  FLJ21603 3' GCTCACTGCAAGCCCTGCCTC 45424       A  _
                                GAGGTAG GGTT GCAGTGAGC
                                ||||||| |||| |||||||||
                                CTCCGTC CCGA CGTCACTCG
                                   _  A
GAM269  FLJ22002 3' GCTCACTGCAACCTCCGCCTC 45775     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  FLJ22167 5' GCTCACTGCCACCTCTGCCTC 44577         T
                                GAGGTAGAGGT GCAGTGAGC
                                |||||||||| |||||||||
                                CTCCGTCTCCA CGTCACTCG
                                      C
GAM269  FLJ22341 3' GCCCACCATGCCCCTTCCTCT 44803     T  A  TGCA  A
                                AGAGG AG GGT   GTG GC
                                ||||| || |||   ||| ||
                                TCTCC TC CCG   CAC CG
                                  T  C  TAC_  C
GAM269  FLJ22529 3' GCTCACTGAAACCACCACC   45573    AGA   G
                                GGT  GGTT CAGTGAGC
                                |||  |||| ||||||||
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                                CCA   CCAA GTCACTCG
                                  CCA    A
GAM269  FLJ22531  5' GCTCACTGCAACCTCCACCTC  45031      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  FLJ22582  3' CTCTTGCCCCCTAACCTCT   46779      AG   TT    T
                                AGAGGT  AGG  GCAG GAG
                                ||||||  |||  |||| |||
                                TCTCCA  TCC  CGTT CTC
                                   A_   CC   _
GAM269  FLJ22684  3' GCTCACTGCAACCCTGCAACCT 46796      ___  A
           CT                     AGAGGT   AG GGTTGCAGTGAGC
                                ||||||   || ||||||||||||
                                TCTCCA   TC CCAACGTCACTCG
                                   ACG  _
GAM269  FLJ22794  3' GCTCACTGCAACTTCCACCTC  91609      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTTCAACGTCACTCG
                                   C
GAM269  FLJ22965  3' GCTCACTGCAACCTCCGCCTC  42051     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  FLJ22969  3' GCTCACTGCAACCTCTGCCTC  68654
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  FLJ23024  3' GCTCACTGCAACCTCTGCCTC  46270
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  FLJ23185  3' CACTTCCTGCCTCT       46829        A  TTGC
                                AGAGGTAG GG    AGTG
                                |||||||| ||    ||||
                                TCTCCGTC CT    TCAC
                                     _ _____
GAM269  FLJ23189  3' CACCTTCTACCCTATCCTCT   46838      _   A   TGCA_
                                AGAGG TAG GGT     GTG
                                ||||| ||| |||     |||
                                TCTCC ATC CCA     CAC
                                   T   _   TCTTC
GAM269  FLJ23263  5' GCTCACTGCAAACTCCGCCTC  47082     TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
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                                CTCC  CTC AACGTCACTCG
                                  GC   A
GAM269   FLJ23356  3' GCTCACTGCAGCCTCTGCCTC  49940
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCGACGTCACTCG

GAM269   FLJ23392  3' GCTCACTGCAACCTCTGCCTC  45539
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   FLJ23392  3' GCTCACTGCAAGCTCAGCCTC  45540      A   G
                                GAGGT GAG TTGCAGTGAGC
                                ||||| ||| ||||||||||
                                CTCCG CTC AACGTCACTCG
                                   A   G
GAM269   FLJ23519  3' GCTCACTGCAAGCTCCGCCTC  49967     TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269   FLJ23556  3' GCTCACTGCACCTCTGCCTC   45951          T
                                GAGGTAGAGGT GCAGTGAGC
                                |||||||||| |||||||||
                                CTCCGTCTCCA CGTCACTCG
                                          _
GAM269   FLJ23563  3' ACTGCAACCTCTGCCTC     67583
                                GAGGTAGAGGTTGCAGT
                                |||||||||||||||||
                                CTCCGTCTCCAACGTCA

GAM269   FLJ25416  5' GCTCACTGCAACCTCCGCATC  58811    G TA
                                GA G  GAGGTTGCAGTGAGC
                                || |  ||||||||||||||||
                                CT C  CTCCAACGTCACTCG
                                 A GC
GAM269   FLJ25449  5' CATTCACCTCTACCTC      58513          T C
                                GAGGTAGAGGT G AGTG
                                |||||||||| | ||||
                                CTCCATCTCCA C TTAC
                                          _ _
GAM269   FLJ30532  3' GCTCACTGCAGCCTCTGCCTC  58549
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCGACGTCACTCG

GAM269   FLJ31101  3' GCTCACTGCAACCTCTGCCTC  35713
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
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                                CTCCGTCTCCAACGTCACTCG

GAM269  FLJ31153  3'  GCTCACTGCAATCTCTGCCTC  58125
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCTAACGTCACTCG

GAM269  FLJ31168  3'  GCTCACTCCATCCCCTACCTTT 58504        A  T  C
                                AGAGGTAG GG TG AGTGAGC
                                |||||||| || || |||||||
                                TTTCCATC CC AC TCACTCG
                                     C  T  C
GAM269  FLJ31812  3'  CTCACCATCTCTGCCTC    58649          TGCA
                                GAGGTAGAGGT   GTGAG
                                ||||||||||    |||||
                                CTCCGTCTCTA   CACTC
                                       C___
GAM269  FLJ32865  3'  GCTCACTGCAACCTCTGCCTC  58177
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  GAL3ST-4  3'  GCTCACTGCAACCTCTGCCTC  44938
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  GFRA4     3'  CATTGTAGCCACCT       42156     AGA
                                AGGT   GGTTGCAGTG
                                ||||   ||||||||||
                                TCCA   CCGATGTTAC
                                        ___
GAM269  GMPPB     5'  GCTCACTGCAACCTCCACCTC  95743      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  GNG4      3'  GCTCACTGCGACCTCCACCTC  15619      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAGCGTCACTCG
                                   C
GAM269  GOLGA3    3'  GCTCACTGCAAGCTCCGCCTC  19719     TA  G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC  G
GAM269  GR6       5'  GCTCACTGAAACCTCTGCCTC  23730         G
                                GAGGTAGAGGTT CAGTGAGC
                                |||||||||||| ||||||||
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                                CTCCGTCTCCAA GTCACTCG
                                      A
GAM269  GREB1   3'  GCTCACTGCAACCTCTGCCTC  27877
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  GREB1   3'  GCTCACTGCAAGCTCCGCCTC  27878     TA  G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC  G
GAM269  GRWD    3'  GCTCACTGCAACCTCCGCCTC  48968     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  GTF2E1  3'  GCTCACTGCAACCTCTGCCTC  18615
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  GTPBG3  3'  GCTCACTGCAACCTCCATCTC  50901      A
                                GAGGT GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCTA CTCCAACGTCACTCG
                                   C
GAM269  GTPBG3  3'  GCTTACTGCAACCTCCACCTC  50905      A
                                GAGGT GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCCA CTCCAACGTCATTCG
                                   C
GAM269  H-plk   5'  CTCACTGCAACCTCCACCTC   31807      A
                                GAGGT GAGGTTGCAGTGAG
                                |||||  |||||||||||||
                                CTCCA CTCCAACGTCACTC
                                   C
GAM269  H2AFY   5'  CTCACTGATCCGCCTC      16890      AGA  TTG
                                GAGGT   GG   CAGTGAG
                                |||||   ||   |||||||
                                CTCCG   CC   GTCACTC
                                   ___  TA_
GAM269  H2AFY   5'  CTCACTGATCCGCCTC      56810      AGA  TTG
                                GAGGT   GG   CAGTGAG
                                |||||   ||   |||||||
                                CTCCG   CC   GTCACTC
                                   ___  TA_
GAM269  H2AFY   5'  CTCACTGATCCGCCTC      56813      AGA  TTG
                                GAGGT   GG   CAGTGAG
                                |||||   ||   |||||||
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                                CTCCG  CC  GTCACTC
                                   ___ TA_
GAM269  H2AV    3' GCTCACTGCAACCCTCCCTC  56855     T  A
                                GAGG AG GGTTGCAGTGAGC
                                |||| || ||||||||||||
                                CTCC TC CCAACGTCACTCG
                                  C  _
GAM269  HEMK    3' GCCCACTGCCCGTGCAGCCTC 32433      AGA__ TT    A
                                GAGGT   GG  GCAGTG GC
                                |||||    ||  |||||| ||
                                CTCCG    CC  CGTCAC CG
                                   ACGTG __     C
GAM269  HML2    5' CTCCAGTCACCTCTACC    20951        T  AGT
                                GGTAGAGGT GC   GAG
                                ||||||||| ||   |||
                                CCATCTCCA TG   CTC
                                     C  AC_
GAM269  HRH4    3' ACTGCAACCTCTGCCTC    41244
                                GAGGTAGAGGTTGCAGT
                                |||||||||||||||||
                                CTCCGTCTCCAACGTCA

GAM269  HSJ1    3' GCCCACTCCTCCTCCCTCT   22131      TA   TTGC   A
                                AGAGG  GAGG   AGTG GC
                                |||||  ||||   |||| ||
                                TCTCC  CTCC   TCAC CG
                                   __   TCC_   C
GAM269  HSMPP8  3' GCTCACTGCAAGCTCTGCCTC 93479        G
                                GAGGTAGAG TTGCAGTGAGC
                                ||||||||| ||||||||||
                                CTCCGTCTC AACGTCACTCG
                                     G
GAM269  HSNOV1  3' ACTGTAACCTCTGCCTC    34002
                                GAGGTAGAGGTTGCAGT
                                |||||||||||||||||
                                CTCCGTCTCCAATGTCA

GAM269  HSPC065 3' GCTCACTGCAACCTCCACCTCT 26308      A
                                AGAGGT GAGGTTGCAGTGAGC
                                |||||| ||||||||||||||
                                TCTCCA CTCCAACGTCACTCG
                                   C
GAM269  HSPC065 3' GCTGCAACCTCCTCCTC    26311     TA
                                GAGG  GAGGTTGCAGT
                                ||||  ||||||||||
                                CTCC  CTCCAACGTCG
                                  TC
GAM269  HU-K4   3' GCTCTCCCACCTCTACCTC   24368         TGCAGT
                                GAGGTAGAGGT    GAGC
                                ||||||||||     ||||
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                                CTCCATCTCCA     CTCG
                                      CCCT__
GAM269  humNRDR  3'  CACTGGCCTTTCCCACCTCT  40662       ___     TG
                                AGAGGT  AGAGGT  CAGTG
                                ||||||  ||||||  |||||
                                TCTCCA  TTTCCG  GTCAC
                                   CCC     __
GAM269  ICK      3'  GCTCTCTGCAACCTCTGCCTC  29933            T
                                GAGGTAGAGGTTGCAG GAGC
                                |||||||||||||||| ||||
                                CTCCGTCTCCAACGTC CTCG
                                          T
GAM269  JAM1     3'  GCTCACTGTAACCTCCGCCTC  33762     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAATGTCACTCG
                                  GC
GAM269  JAM1     3'  GCTCACTGTAACCTCCGCCTC  57900     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAATGTCACTCG
                                  GC
GAM269  JAM1     5'  GCTCACTGCAACCTCCTCCTC  57928     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  TC
GAM269  JAM1     3'  GCTCACTGTAACCTCCGCCTC  57929     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAATGTCACTCG
                                  GC
GAM269  JAM1     3'  GCTCACTGTAACCTCCGCCTC  57955     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAATGTCACTCG
                                  GC
GAM269  JM11     3'  GCTCACTGCAACCTCTGCCTC  53263
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  KCNMB3L  5'  CACGGTGGCCTCTCCTCT    26959      T     TG A
                                AGAGG AGAGGT  C GTG
                                ||||| ||||||  | |||
                                TCTCC TCTCCG  G CAC
                                   _     GT G
GAM269  KIAA0063 3'  GCTCACTGCAACCTCCACCTC  29631       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
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                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  KIAA0140 3' GCCCACAAACCCTGCCTCT   27809        A   GCA  A
                                AGAGGTAG GGTT  GTG GC
                                |||||||| ||||  ||| ||
                                TCTCCGTC CCAA  CAC CG
                                     _   A__  C
GAM269  KIAA0161 3' GCTCACTGCAAGCTCTGCCTC 28508         G
                                GAGGTAGAG TTGCAGTGAGC
                                ||||||||| ||||||||||
                                CTCCGTCTC AACGTCACTCG
                                     G
GAM269  KIAA0186 3' GCTCACTGCAATCTCTATC   40755
                                GGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||
                                CTATCTCTAACGTCACTCG

GAM269  KIAA0205 3' GCTCACTGCAGTCTCTGCCTC 29587         GT
                                GAGGTAGAG  TGCAGTGAGC
                                |||||||||  ||||||||||
                                CTCCGTCTC  ACGTCACTCG
                                     TG
GAM269  KIAA0210 5' GCTCACCGCAATCTCCGCCTC 28479     TA       A
                                GAGG  GAGGTTGC GTGAGC
                                ||||  |||||||| ||||||
                                CTCC  CTCTAACG CACTCG
                                  GC       C
GAM269  KIAA0391 3' ACTGCAACCTCTGCCTC     27900
                                GAGGTAGAGGTTGCAGT
                                |||||||||||||||||
                                CTCCGTCTCCAACGTCA

GAM269  KIAA0426 3' GCTCACTGCAACCTCCGCCTC 28259     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  KIAA0441 3' ACTCACCTCTACTCT       28951      G      T C
                                AGAG TAGAGGT G AGT
                                |||| ||||||| | |||
                                TCTC ATCTCCA C TCA
                                   _      _ _
GAM269  KIAA0449 3' CTCACTGCACAAGCACCCT   34200    A  AGAG  T
                                AG GGT    GT GCAGTGAG
                                || |||    || ||||||||
                                TC CCA    CA CGTCACTC
                                 _  CGAA  _
GAM269  KIAA0450 5' TTGCAGCCTCCACCCCT     27656    A  A
                                AG GGT GAGGTTGCAG
                                || ||| ||||||||||
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                                TC CCA CTCCGACGTT
                                 C   C
GAM269  KIAA0459 3' GCTCACTGCAACCTCCACCTC 60999      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  KIAA0469 3' GCTCACTGCAAGCTCCATCTC 29338      A   G
                                GAGGT GAG TTGCAGTGAGC
                                ||||| ||| ||||||||||
                                CTCTA CTC AACGTCACTCG
                                   C   G
GAM269  KIAA0469 3' GCTCACTGCAGCCTCCACCTC 29339      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM269  KIAA0472 5' GCTCACTGCAACCTCCTCCTT 71867     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                TTCC  CTCCAACGTCACTCG
                                   TC
GAM269  KIAA0475 3' GCTCACTGCAACCTCCGTCTC 29496     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCT  CTCCAACGTCACTCG
                                   GC
GAM269  KIAA0478 3' GCTCACTGCAACCTCTGC    29551
                                GTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||
                                CGTCTCCAACGTCACTCG

GAM269  KIAA0495 3' GCTCACTGCAACCTCCGTCTC 62592      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCT  CTCCAACGTCACTCG
                                   GC
GAM269  KIAA0513 5' ACTGCAGCCTCCACCTC     28334      A
                                GAGGT GAGGTTGCAGT
                                ||||| ||||||||||
                                CTCCA CTCCGACGTCA
                                   C
GAM269  KIAA0513 3' CTCACTGCAACCTCCACCTC  28352      A
                                GAGGT GAGGTTGCAGTGAG
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTC
                                   C
GAM269  KIAA0527 3' GCTCACTGCAACCTCTGCCTC 95802
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
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                                CTCCGTCTCCAACGTCACTCG

GAM269  KIAA0544 3' ACTGCAACCTCCGCCTC    70884     TA
                                GAGG  GAGGTTGCAGT
                                ||||  ||||||||||
                                CTCC  CTCCAACGTCA
                                  GC
GAM269  KIAA0561 3' CTCAGTGTCCCCTCCCCT    65880     TA   TT   G
                                AGG  GAGG  GCA TGAG
                                |||  ||||  ||| ||||
                                TCC  CTCC  TGT ACTC
                                 C_   CC   G
GAM269  KIAA0561 3' GCTCACTGCAACCTCCGCCTC 65892     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  |||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  KIAA0562 3' GCCCCCTGCAACCTCCGCCTC 28155     TA        TGA
                                GAGG  GAGGTTGCAG   GC
                                ||||  |||||||||   ||
                                CTCC  CTCCAACGTC   CG
                                  GC        CCC
GAM269  KIAA0563 5' GCTCACTGCAACCTCTGCCTC 29190
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  KIAA0594 3' ACTGCAACCTCCGCCTC    64891     TA
                                GAGG  GAGGTTGCAGT
                                ||||  ||||||||||
                                CTCC  CTCCAACGTCA
                                  GC
GAM269  KIAA0599 3' ACTGCAACCTCCGCCTC    77161     TA
                                GAGG  GAGGTTGCAGT
                                ||||  ||||||||||
                                CTCC  CTCCAACGTCA
                                  GC
GAM269  KIAA0599 3' GCTCACTGCAACCTCCGCCTC 77182     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  |||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  KIAA0663 5' CTGCAACCTCCGCCTC     29127     TA
                                GAGG  GAGGTTGCAG
                                ||||  |||||||||
                                CTCC  CTCCAACGTC
                                  GC
GAM269  KIAA0720 3' GCTCACTGCAACCTCTGCCTC 62323
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
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                                CTCCGTCTCCAACGTCACTCG

GAM269  KIAA0737 3' GCTCACTGAAACCTCTGCCTC 29141          G
                                GAGGTAGAGGTT CAGTGAGC
                                |||||||||||| ||||||||
                                CTCCGTCTCCAA GTCACTCG
                                      A
GAM269  KIAA0753 3' GCCAAACCTCTCCTCT     28998      T     __
                                AGAGG AGAGGTT  GC
                                ||||| |||||||  ||
                                TCTCC TCTCCAA  CG
                                   _     AC
GAM269  KIAA0798 3' GCTCACTGCAACCCCGCCTC  27723      AGA
                                GAGGT  GGTTGCAGTGAGC
                                |||||  ||||||||||||
                                CTCCG  CCAACGTCACTCG
                                   CC_
GAM269  KIAA0841 3' GCTCACTGCAACCTCCGCCTC 71388     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  KIAA0841 3' GCTCACTGCAACCTCTGCCTC 71390
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  KIAA0861 3' GCTCACTGCAAACCGCCTC   88928      AGA   _
                                GAGGT  GGTT GCAGTGAGC
                                |||||  |||| |||||||||
                                CTCCG  CCAA CGTCACTCG
                                   ___   A
GAM269  KIAA0889 3' GCTCACTGTAACCTCCGCCTC 31141     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAATGTCACTCG
                                  GC
GAM269  KIAA0924 3' GCTCACTGCAACCCCCGCC   29717    AGA
                                GGT  GGTTGCAGTGAGC
                                |||  ||||||||||||
                                CCG  CCAACGTCACTCG
                                 CCC
GAM269  KIAA0961 3' GCTCACTGCAAGCTCTGCCTC 29735         G
                                GAGGTAGAG TTGCAGTGAGC
                                ||||||||| ||||||||||
                                CTCCGTCTC AACGTCACTCG
                                      G
GAM269  KIAA1026 3' GCTCACTGCAACCAACACCTT 71200      AGA
                                GAGGT  GGTTGCAGTGAGC
                                |||||  ||||||||||||
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                              TTCCA  CCAACGTCACTCG
                                 CAA
GAM269  KIAA1040 3' GCTCACTGCAACCTCTGCTTC 72230
                              GAGGTAGAGGTTGCAGTGAGC
                              |||||||||||||||||||||
                              CTTCGTCTCCAACGTCACTCG

GAM269  KIAA1041 3' GCTCACTGCAACCTCCGCCTC 30134    TA
                              GAGG GAGGTTGCAGTGAGC
                              ||||  ||||||||||||||
                              CTCC CTCCAACGTCACTCG
                                GC
GAM269  KIAA1054 3' GCTCACTGCAACCTCCGCCTC 68441    TA
                              GAGG GAGGTTGCAGTGAGC
                              ||||  ||||||||||||||
                              CTCC CTCCAACGTCACTCG
                                GC
GAM269  KIAA1100 3' GCCCAATCTCCTCTCCCTCT  29754    T   TTGCAG A
                              AGAGG AGAGG    TG GC
                              ||||| |||||    || ||
                              TCTCC TCTCC    AC CG
                                 C   TCTA__ C
GAM269  KIAA1128 3' GCTCACTGCAACTTCTGCCTC 68480
                              GAGGTAGAGGTTGCAGTGAGC
                              |||||||||||||||||||||
                              CTCCGTCTTCAACGTCACTCG

GAM269  KIAA1143 3' GCTCACTGCAAGCTCCGCCTC 68683    TA  G
                              GAGG GAG TTGCAGTGAGC
                              ||||  ||| ||||||||||
                              CTCC CTC AACGTCACTCG
                                GC  G
GAM269  KIAA1161 5' CTCCCAGGAACCTCCCACCTCT 81747     A_    GCAGT
                              AGAGGT GAGGTT   GAG
                              ||||||  ||||||   |||
                              TCTCCA CTCCAA   CTC
                                 CC    GGACC
GAM269  KIAA1161 5' GCTCACTGCAACCCCTCCTC  81756    T A
                              GAGG AG GGTTGCAGTGAGC
                              |||| || ||||||||||||
                              CTCC TC CCAACGTCACTCG
                                _ C
GAM269  KIAA1169 5' GCTCACTGTAGCCTCCAACC  35450    A_
                              GGT GAGGTTGCAGTGAGC
                              |||  ||||||||||||||
                              CCA CTCCGATGTCACTCG
                               AC
GAM269  KIAA1170 3' GCTCACTGCAACCTCCGCCTC 69854    TA
                              GAGG GAGGTTGCAGTGAGC
                              ||||  ||||||||||||||
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                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  KIAA1184  3'  CACTGGCCTCTGCCTCT    42610          TG
                                AGAGGTAGAGGT  CAGTG
                                ||||||||||||  |||||
                                TCTCCGTCTCCG  GTCAC
                                      ___
GAM269  KIAA1193  3'  GCTCACTGCAACCTCCGCCTC  67642     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  KIAA1198  3'  GCTCACTGCAACCTCCACTTCT 63315      A
                                AGAGGT GAGGTTGCAGTGAGC
                                ||||||| ||||||||||||||
                                TCTTCA CTCCAACGTCACTCG
                                   C
GAM269  KIAA1198  3'  GCTCACTGCAAGCTCCGCCTC  63317     TA  G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC  G
GAM269  KIAA1198  3'  GCTCACTGCAATCTCTGCCTC  63318
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
                                CTCCGTCTCTAACGTCACTCG

GAM269  KIAA1198  3'  GCTCACCGCAACCTCCGCCTC  63314     TA      A
                                GAGG  GAGGTTGC GTGAGC
                                ||||  |||||||| ||||||
                                CTCC  CTCCAACG CACTCG
                                  GC       C
GAM269  KIAA1209  3'  GCTCACTGCAGCCTCCACCTC  60758      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM269  KIAA1210  3'  GCTCACTGCAAGCTCCGCCTC  96333     TA  G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC  G
GAM269  KIAA1254  3'  GCTCACTGCAACCTCTGTCTC  70020     GT
                                GAG  AGAGGTTGCAGTGAGC
                                |||  ||||||||||||||
                                CTC  TCTCCAACGTCACTCG
                                  TG
GAM269  KIAA1257  3'  GCTCACCGCAACCTCCGCCTC  62745     TA      A
                                GAGG  GAGGTTGC GTGAGC
                                ||||  |||||||| ||||||
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                                CTCC  CTCCAACG CACTCG
                                  GC       C
GAM269  KIAA1257 3' GCTCACTACAGCCTCTGCC   62746          C
                                GGTAGAGGTTG AGTGAGC
                                |||||||||||  |||||||
                                CCGTCTCCGAC TCACTCG
                                      A
GAM269  KIAA1271 3' GCTCACTGTGGCCCCACC    69549    AGA   TG
                                GGT   GGT  CAGTGAGC
                                |||   |||  ||||||||
                                CCA   CCG  GTCACTCG
                                  CC_   GT
GAM269  KIAA1280 5' GCTCACTGCAGCCTCAACCTC  69723      A
                                GAGGT GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   A
GAM269  KIAA1287 3' GCTCACTGCAACTTCTGCC   78327
                                GGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||
                                CCGTCTTCAACGTCACTCG

GAM269  KIAA1305 5' CTCACTGCAACTGGATCTT   46931      AGA
                                GAGGT   GGTTGCAGTGAG
                                |||||   ||||||||||||
                                TTCTA   TCAACGTCACTC
                                   GG_
GAM269  KIAA1320 5' GCTCACTGCAACCTCTGCCTC  69304
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  KIAA1373 3' GCTCACTGCAACCTCCACCTC  70943      A
                                GAGGT GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  KIAA1434 3' GCTCACTTTCTGTCCTATCTCT 69614        A  TTGC_
                                AGAGGTAG GG    AGTGAGC
                                ||||||||  ||    |||||||
                                TCTCTATC CT    TCACTCG
                                     _  GTCTT
GAM269  KIAA1443 3' GCTCACTGCAAGCTCCGCCTC  63833     TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  |||  ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269  KIAA1456 3' GCTCACTGTAAGCTCCGCCTC  66999     TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  |||  ||||||||||
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                                CTCC  CTC AATGTCACTCG
                                  GC   G
GAM269  KIAA1465 3' GCTCACTGCATCTTCCGCCTC  60831     TA   T
                                GAGG  GAGG TGCAGTGAGC
                                ||||  |||| ||||||||||
                                CTCC  CTTC ACGTCACTCG
                                  GC    T
GAM269  KIAA1467 3' GCTCACTGCAACCTTCGCCTC  71610     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  TTCCAACGTCACTCG
                                  GC
GAM269  KIAA1473 3' GCTCACTGCAACCTCCGTCTC  70670     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCT  CTCCAACGTCACTCG
                                  GC
GAM269  KIAA1497 5' GCTCACTGCAACCTCTGCCTC  67511
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  KIAA1508 3' GCTCACTGCAACCTCCGCCTC  61885     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  KIAA1530 3' GCTCACTGCAACTACCACCTC  67954      AGA
                                GAGGT   GGTTGCAGTGAGC
                                |||||   ||||||||||||
                                CTCCA   TCAACGTCACTCG
                                   CCA
GAM269  KIAA1571 3' GCTCACCGCAACCTCCACCTC  60956      A      A
                                GAGGT GAGGTTGC GTGAGC
                                ||||| |||||||| ||||||
                                CTCCA CTCCAACG CACTCG
                                   C       C
GAM269  KIAA1573 5' GCTCACCTAACCTCTCCCCT   62688    A  T      CA
                                AG GG AGAGGTTG  GTGAGC
                                || || ||||||||  ||||||
                                TC CC TCTCCAAT  CACTCG
                                 _  C       C_
GAM269  KIAA1602 3' GCCCACCAGCCGTGCCATCT   64632    _   GA    CA   A
                                AGA GGTA  GGTTG  GTG GC
                                ||| ||||  |||||  ||| ||
                                TCT CCGT  CCGAC  CAC CG
                                  A   G_    __   C
GAM269  KIAA1615 3' TCACTGCAACCTCCACCTC   68728      A
                                GAGGT GAGGTTGCAGTGA
                                ||||| ||||||||||||
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                                CTCCA CTCCAACGTCACT
                                   C
GAM269  KIAA1615 3' GCTCACCTCAACCTCTGCCTC 68718          CA
                                GAGGTAGAGGTTG GTGAGC
                                |||||||||||| ||||||
                                CTCCGTCTCCAAC CACTCG
                                      TC
GAM269  KIAA1617 3' GCTCACTGCAACCTCTCTCTC 91430    GT
                                GAG AGAGGTTGCAGTGAGC
                                ||| ||||||||||||||||
                                CTC TCTCCAACGTCACTCG
                                  TC
GAM269  KIAA1649 3' GCTCACTGCAACCTCCGC   50271   TA
                                G GAGGTTGCAGTGAGC
                                | ||||||||||||||
                                C CTCCAACGTCACTCG
                                 GC
GAM269  KIAA1655 3' GCTCACTGTAACCTCCACCTC 66616     A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAATGTCACTCG
                                   C
GAM269  KIAA1655 3' GCTCATTGCAACCTCCGCCTC 66617     TA
                                GAGG GAGGTTGCAGTGAGC
                                |||| ||||||||||||||||
                                CTCC CTCCAACGTTACTCG
                                  GC
GAM269  KIAA1668 3' GCTCACTGCAAGCTCCGCCTC 66476     TA  G
                                GAGG GAG TTGCAGTGAGC
                                |||| ||| ||||||||||
                                CTCC CTC AACGTCACTCG
                                  GC  G
GAM269  KIAA1671 5' GCTCACCACATAACCTCTG   65679       CA__
                                TAGAGGTTG   GTGAGC
                                |||||||||   ||||||
                                GTCTCCAAT   CACTCG
                                     ACAC
GAM269  KIAA1712 3' GCTCACCGCAACCTCTGCCT  67539         A
                                AGGTAGAGGTTGC GTGAGC
                                |||||||||||| ||||||
                                TCCGTCTCCAACG CACTCG
                                      C
GAM269  KIAA1727 3' GCTCACTGCAGCTTTGACCTC 64057     A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA TTTCGACGTCACTCG
                                   G
GAM269  KIAA1737 3' GCTCACTGCAACCTCCGCCTC 67358     TA
                                GAGG GAGGTTGCAGTGAGC
                                |||| ||||||||||||||||
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                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  KIAA1751  3'  GCTCACTGCAGCCTCGACCTC  71699      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   G
GAM269  KIAA1754  3'  GCTCAGCAGCCCCCCACCTCT  63238      AGA_    AG
                                AGAGGT   GGTTGC  TGAGC
                                ||||||   ||||||  |||||
                                TCTCCA   CCGACG  ACTCG
                                   CCCC    __
GAM269  KIAA1775  3'  CTCACACACCTCTACTTCT   52380         TGCA
                                AGAGGTAGAGGT   GTGAG
                                ||||||||||||   |||||
                                TCTTCATCTCCA   CACTC
                                      CA__
GAM269  KIAA1784  3'  GCTCACTGCAACCTCCGCCTC  65151     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  KIAA1786  3'  GCTCACTGTAGTCTCCACC   66034    A  GT
                                GGT GAG  TGCAGTGAGC
                                ||| |||  ||||||||||
                                CCA CTC  ATGTCACTCG
                                  C   TG
GAM269  KIAA1829  3'  GCTCACTGCAGCCTCTGCCTC  61951
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCGACGTCACTCG

GAM269  KIAA1887  5'  GCCCACCCTGGTCCTGCCTCT  76776       A  TT CA   A
                                AGAGGTAG GG  G  GTG GC
                                |||||||| ||  |  ||| ||
                                TCTCCGTC CT  T  CAC CG
                                     _  GG CC   C
GAM269  KIAA1922  5'  GCTCACTGCAACCTCCGCCTC  73630     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  KIAA1924  3'  GCTCACTGCAAGCTCCGCCTC  73682     TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269  KIAA1956  3'  GCTCACTGCAGCCTCCACCTC  78437      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
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                                CTCCA CTCCGACGTCACTCG
                                   C
GAM269  KIAA1971 3' GCTCACTGCAAGCTCCGCCTC 74221     TA  G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269  KIAA1971 3' GCTTACTGCAACCTCCACCTC 74223      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCATTCG
                                   C
GAM269  KIAA1975 5' GCTCACTGCAAGCTCCGCCTC 73975     TA  G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269  KIAA1987 5' GCTCACTGCAATCTCCGCCTC 88018     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCTAACGTCACTCG
                                  GC
GAM269  KLK7     3' GCTCACTGCAACCTCCGCCTC 57732     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  KLK7     3' GCTCACTGCAACCTCCGCCTC 17292     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  KRTAP9-4 5' CCACCCTCTACCCCT      52598    A      TTGCA  A
                                AG GGTAGAGG    GTG G
                                || ||||||||    ||| |
                                TC CCATCTCC    CAC C
                                 C      _____  C
GAM269  KRTAP9-8 5' ACTCCACCCTCTACCCCT    49234    A      T  C
                                AG GGTAGAGG TG AGT
                                || |||||||| || |||
                                TC CCATCTCC AC TCA
                                 C       C  C
GAM269  LAMP3    3' GCTTATGGCAACCTCCGCCTC 59492     TA      A
                                GAGG  GAGGTTGC GTGAGC
                                ||||  |||||||| ||||||
                                CTCC  CTCCAACG TATTCG
                                  GC       G
GAM269  LRP1B    5' GCTCACACACGCTCTGCCTC  37670        _  TGCA
                                GAGGTAGAG GT    GTGAGC
                                |||||||| ||    ||||||
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                                CTCCGTCTC CA    CACTCG
                                     G  CA__
GAM269  LY75     3'  CTCACTGCAAATCTCC      9838     T   GG
                                GG AGA  TTGCAGTGAG
                                || |||  ||||||||||
                                CC TCT  AACGTCACTC
                                 _   A_
GAM269  MAP4K1   3'  GCTCCCAGCAACCTCTACATC  23207    G         AGT
                                GA GTAGAGGTTGC   GAGC
                                || ||||||||||   ||||
                                CT CATCTCCAACG   CTCG
                                 A          ACC
GAM269  MCLC     3'  GCTCACTGCAACCTCCACCTC  30686      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  MEF-2    3'  GCTCACTGCAACCTCCGCCTC  64388     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  MESDC2   3'  GCTCACTGAAGTCTCTACCT   72493        GT G
                                AGGTAGAG  T CAGTGAGC
                                ||||||||  | ||||||||
                                TCCATCTC  A GTCACTCG
                                     TG A
GAM269  MGC10200 3'  GCTCACTGCAGCCTCAACCTC  58989      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   A
GAM269  MGC10818 3'  CTCAGCCACCTGCTACCTCT   47540        _   T  AG
                                AGAGGTAG AGGT GC  TGAG
                                |||||||| |||| ||  ||||
                                TCTCCATC TCCA CG  ACTC
                                     G   C __
GAM269  MGC10966 5'  CACCTGCAGCCCCCAGCCCT   48893    A  AGA_      _
                                AG GGT    GGTTGCAG TG
                                || |||    |||||||| ||
                                TC CCG    CCGACGTC AC
                                 _   ACCC       C
GAM269  MGC1127  3'  GCTCACTGCCAGGCTCCTCTCC 53216    A  T    TT____
           CCT                    AG GG AGAGG     GCAGTGAGC
                                || || |||||     |||||||||
                                TC CC TCTCC     CGTCACTCG
                                 _ C     TCGGAC
GAM269  MGC12518 3'  ACTGCAACCTCTGCCCCT    64077    A
                                AG GGTAGAGGTTGCAGT
                                || ||||||||||||||
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                                TC CCGTCTCCAACGTCA
                                 C
GAM269  MGC13138 3' GCTCACTGCAACCTCTGCCTC  53020
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  MGC13198 5' GCTCACTGCAACCTCCGTCTCT 51096      TA
                                AGAGG  GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                TCTCT  CTCCAACGTCACTCG
                                   GC
GAM269  MGC14836 3' GCTCACTGCAACCTCCGCCTC  53038     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269  MGC16025 3' GCCCACTGTGGGCCCTTCCCCT 51921     TA   __ TG    A
                                AGG  GAGG  T  CAGTG GC
                                |||  ||||  |  ||||| ||
                                TCC  TTCC  G  GTCAC CG
                                  CC    CG GT    C
GAM269  MGC2474  3' CTCACTGCAACTTCCACCTC  43722      A
                                GAGGT GAGGTTGCAGTGAG
                                ||||| ||||||||||||||
                                CTCCA CTTCAACGTCACTC
                                   C
GAM269  MGC2477  5' GCTCACTGCAAGCTCTGCCTC  44066        G
                                GAGGTAGAG TTGCAGTGAGC
                                ||||||||| ||||||||||
                                CTCCGTCTC AACGTCACTCG
                                      G
GAM269  MGC2488  3' GCTCACTGCAACCTCTGTGTC  43873    GG
                                GA  TAGAGGTTGCAGTGAGC
                                ||  ||||||||||||||||
                                CT  GTCTCCAACGTCACTCG
                                 GT
GAM269  MGC2574  3' GCTCTGAGCACCTCCACACC  44053    A__    T  AGT
                                GGT   GAGGT GC   GAGC
                                |||   ||||| ||   ||||
                                CCA   CTCCA CG   CTCG
                                  CAC    _ AGT
GAM269  MGC29891 3' GCTCACTGCAACCTCCGCCTC  58207     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269  MGC3113  3' GCTCACTGCAGCCTCCACCTC  43848      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
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                                CTCCA CTCCGACGTCACTCG
                                   C
GAM269  MGC3329  3' GCTCACTGCAACCCCCGCCTC 44017      AGA
                                GAGGT  GGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCCG  CCAACGTCACTCG
                                   CCC
GAM269  MGC4604  3' GCTCACTGCATGCAGCCCCT  48980   A  AGAGGT
                                AG GGT     TGCAGTGAGC
                                || |||     ||||||||||
                                TC CCG     ACGTCACTCG
                                 C  ACGT__
GAM269  MGC4638  3' GCTCACTGCAACCTCCGTCTC 48943     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCT  CTCCAACGTCACTCG
                                   GC
GAM269  MGC5149  3' GCTCACTGCAACCTCTGCCTC 72293
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  MGC9912  3' GCTCACTGCAACCTCCACCTC 54719      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  MIDORI   3' GCCCACCAGCACCTGCCTCT  73788       AG   CA  A
                                AGAGGTAG  GTTG  GTG GC
                                ||||||||  ||||  ||| ||
                                TCTCCGTC  CGAC  CAC CG
                                     CA   __  C
GAM269  MKRN4    3' GCTCACTGCAACCTCCGTCTT 47750     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                TTCT  CTCCAACGTCACTCG
                                   GC
GAM269  MLZE     5' GCTCACTGCAACCTCTGCCTC 48622
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  MMPL1    3' ACTGCAGCCTCCACCTC     14714      A
                                GAGGT GAGGTTGCAGT
                                ||||| ||||||||||
                                CTCCA CTCCGACGTCA
                                   C
GAM269  moblak   3' GCTCACTGCATCCTCCACCTC 55504      A   T
                                GAGGT GAGG TGCAGTGAGC
                                ||||| |||| ||||||||||
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                                CTCCA CTCC ACGTCACTCG
                                   C    T
GAM269  moblak   3'  GCTCACTGCAAGCTCCGCCTC  55503     TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                   GC   G
GAM269  MOCS3    3'  GCTCACTGCAACCTCCGCCTC  27153      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269  MRPL44   3'  GCTCACTGCAACCTCCACCTC  43321      A
                                GAGGT GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  MRPS27   3'  GCTCACTGCAACCTCCGACTC  30638     GTA
                                GAG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                CTC   CTCCAACGTCACTCG
                                  AGC
GAM269  MtFMT    3'  GCTCACTGCAACCTCCGCCTC  57655     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269  MYT1     3'  GCCCACCACACCGTTTACCTC  15775        _   T CA   A
                                GAGGTAGA GGT G  GTG GC
                                |||||||| ||| |  ||| ||
                                CTCCATTT CCA C  CAC CG
                                     G   _ AC   C
GAM269  N4BP3    3'  CTCCTGTCTGCCTC       66261        AGGTT    T
                                GAGGTAG    GCAG GAG
                                |||||||    |||| |||
                                CTCCGTC    TGTC CTC
                                     _____   _
GAM269  NDP52    3'  CTCACTACAGCCTCTGCCTC   19528           C
                                GAGGTAGAGGTTG AGTGAG
                                |||||||||||| ||||||
                                CTCCGTCTCCGAC TCACTC
                                        A
GAM269  NDUFB1   5'  GCTCACTGCAACCTCTGCCTC  15818
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  NDUFC2   3'  GCTCACTGCAACCTCCACCTC  15836      A
                                GAGGT GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
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                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  NINJ2    3'  GCTCACTGCACCTCCGCCTC  33286     TA    T
                                GAGG  GAGGT GCAGTGAGC
                                ||||  ||||| |||||||||
                                CTCC  CTCCA CGTCACTCG
                                  GC    _
GAM269  Nup43    3'  GCTCACTGCAACCTCCACCTC  45003      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  OR51E2   3'  GCTCACTGCAACCTCCACATC  47794    G  A
                                GA GT GAGGTTGCAGTGAGC
                                || || ||||||||||||||
                                CT CA CTCCAACGTCACTCG
                                 A  C
GAM269  OS-9     3'  ACTCAATCCTCTTCCTCT    22342      T    _  C
                                AGAGG AGAGG TTG AGT
                                ||||| ||||| ||| |||
                                TCTCC TCTCC AAC TCA
                                   T    T  _
GAM269  OS4      3'  GCCCACCTGCAACTCCCCC   19184    TA  G    _  A
                                GG  GAG TTGCAG TG GC
                                ||  ||| |||||| || ||
                                CC  CTC AACGTC AC CG
                                 CC  _     C  C
GAM269  OSBPL2   3'  GCTCACCGCAACCTCCGCCTC  29215     TA      A
                                GAGG  GAGGTTGC GTGAGC
                                ||||  |||||||| ||||||
                                CTCC  CTCCAACG CACTCG
                                  GC       C
GAM269  OSBPL2   3'  GCTCACCGCAACCTCCGCCTC  57866     TA      A
                                GAGG  GAGGTTGC GTGAGC
                                ||||  |||||||| ||||||
                                CTCC  CTCCAACG CACTCG
                                  GC       C
GAM269  p25      3'  CACTCGGCTCCCATCTCT    22846      AGA    C
                                AGAGGT   GGTTG AGTG
                                ||||||   ||||| ||||
                                TCTCTA   TCGGC TCAC
                                   CCC    _
GAM269  P66      3'  CTCAGTTCCCCTACTCT     40364     G   A  TT  AG
                                AGAG TAG GG  GC  TGAG
                                |||| ||| ||  ||  ||||
                                TCTC ATC CC  TG  ACTC
                                  _  _ CT  __
GAM269  PASK     5'  ACTGCAACCTCTGCCTC     30708
                                GAGGTAGAGGTTGCAGT
                                |||||||||||||||||
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                                CTCCGTCTCCAACGTCA

GAM269  PELI1    5'  GCTCACTGCAACCTCCTCCTC  40271      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  TC
GAM269  PELI1    5'  GCTCACTGCAAGCTCTGCCTC  40272         G
                                GAGGTAGAG TTGCAGTGAGC
                                |||||||| ||||||||||
                                CTCCGTCTC AACGTCACTCG
                                      G
GAM269  PELI1    5'  ACTGCAACCTCTGCCTC     40249
                                GAGGTAGAGGTTGCAGT
                                |||||||||||||||||
                                CTCCGTCTCCAACGTCA

GAM269  PIP3-E   3'  GCTCACTGCAACCTCTGCCTC  66806
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  POLD4    5'  GCCCACTGGCCGGTCTCTCCTC 40986      T   GT __    A
          T                      AGAGG AGAG  TG  CAGTG GC
                                 ||||| ||||  ||  ||||| ||
                                 TCTCC TCTC  GC  GTCAC CG
                                   _   TG  CG    C
GAM269  PPIL2    3'  GCTCACTGCAGCCTCGACCTC  26767      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   G
GAM269  PRO0365  5'  GCTCACTGCAACCTCTGTCTC  26165     GT
                                GAG  AGAGGTTGCAGTGAGC
                                |||  ||||||||||||||
                                CTC  TCTCCAACGTCACTCG
                                  TG
GAM269  PRO0365  5'  GCTCACTGCAACCTCCACCTC  26163      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  PRO0529  5'  GCTCACTGCAGTCTCCACCTCT 25994       A   GT
                                AGAGGT GAG  TGCAGTGAGC
                                |||||| |||  ||||||||||
                                TCTCCA CTC  ACGTCACTCG
                                    C   TG
GAM269  PRO1048  3'  GCTCACTGAAGTCTCGACCTC  37519      A   GT G
                                GAGGT GAG  T CAGTGAGC
                                ||||| |||  | ||||||||
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                                CTCCA CTC  A GTCACTCG
                                   G   TG A
GAM269  PRO1992  5'  GCTCACTGCAACCTCTGCCTC  26058
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  PRO2955  3'  GCTCACTGCAACCTCTGCCTC  37640
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  PRSS22   3'  GCTCATCTACCTCTACCTCT   42091          TGCA
                                AGAGGTAGAGGT   GTGAGC
                                ||||||||||||   ||||||
                                TCTCCATCTCCA   TACTCG
                                      TC__
GAM269  PSPH     3'  GCTCACTGCAAGCTCTGCCTC  15916        G
                                GAGGTAGAG TTGCAGTGAGC
                                ||||||||| ||||||||||
                                CTCCGTCTC AACGTCACTCG
                                     G
GAM269  PSTPIP2  3'  GCTCACTGCAACCTCTGCCTC  44392
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  RAB21    3'  GCTCACTGCAAGCTCCACCTC  30388      A  G
                                GAGGT GAG TTGCAGTGAGC
                                ||||| ||| ||||||||||
                                CTCCA CTC AACGTCACTCG
                                   C   G
GAM269  RAB24    3'  GCCAAACCCCTACTTCT     55389        A   __
                                AGAGGTAG GGTT  GC
                                |||||||| ||||  ||
                                TCTTCATC CCAA  CG
                                     C    AC
GAM269  RAB33B   3'  GCTCACTGCAACCTCCGCCTC  48496     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  RAI      5'  GCTCACTGCAACCTCCGCCTC  21883     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  RAI16    3'  CTCAGTGACCTCTGCCTCT    42754          TG AG
                                AGAGGTAGAGGT  C  TGAG
                                ||||||||||||  |  ||||
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                                TCTCCGTCTCCA G ACTC
                                      GT __
GAM269  RASGRP4  3' GCTGAACAACCTCTACCT   53656          __
                                AGGTAGAGGTTG CAGT
                                |||||||||||| ||||
                                TCCATCTCCAAC GTCG
                                      AA
GAM269  RASSF2   3' GCTCACTGCAACATCCGCCTCT 28439      TA G
                                AGAGG GA GTTGCAGTGAGC
                                ||||| || ||||||||||||
                                TCTCC CT CAACGTCACTCG
                                   GC A
GAM269  RI58     5' GCCCACCGCGCGGCTTCCCCC 24847    TA      A__  A
                                GG GAGGTTGC  GTG GC
                                || |||||||  ||| ||
                                CC CTTCGGCG  CAC CG
                                 CC      CGC  C
GAM269  RILP     3' GCCCACCTCCCTCTCTACGTCT 48693    G     TTGCA  A
                                AGA GTAGAGG    GTG GC
                                ||| |||||||    ||| ||
                                TCT CATCTCT    CAC CG
                                  G     CCCTC  C
GAM269  RNF8     3' GCTCACTGCAACCTCCACCTC  14231      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  RNF9     3' CTCACTGCCTCCTTCCTC    53412     TA   TT
                                GAGG GAGG GCAGTGAG
                                |||| |||| ||||||||
                                CTCC TTCC CGTCACTC
                                   __  TC
GAM269  RNO2     5' GCTCACTGCAACCTCCACCTT  52772      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
                                TTCCA CTCCAACGTCACTCG
                                   C
GAM269  SC4MOL   3' GCTCACTGCAACCTCTGCCTC  22158
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  SCAMP-4  3' GCTCACTGCAACCTCTGCCTC  54396
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  SCAND2   3' CTCACTGCAACATCTGCCTC   41887        G
                                GAGGTAGA GTTGCAGTGAG
                                |||||||| ||||||||||
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                                CTCCGTCT CAACGTCACTC
                                    A
GAM269  SCYA16   3' GCTCACTGTAACCTCCACCTC 15961      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAATGTCACTCG
                                   C
GAM269  SERF1B   3' GCTCACTGCAACCTCCGCCTC 43416     TA
                                GAGG GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  SERF1B   3' GCTCCATGCAACCTCTGCCTC 43418           GT
                                GAGGTAGAGGTTGCA GAGC
                                |||||||||||||| ||||
                                CTCCGTCTCCAACGT CTCG
                                        AC
GAM269  SFXN2    3' GCTCACTGCAAACTCTGCCTC 73949        G
                                GAGGTAGAG TTGCAGTGAGC
                                ||||||||| ||||||||||
                                CTCCGTCTC AACGTCACTCG
                                    A
GAM269  SIRPB1   3' GCTCACTGCAACCCCCGCCTC 20255      AGA
                                GAGGT  GGTTGCAGTGAGC
                                |||||  ||||||||||||
                                CTCCG  CCAACGTCACTCG
                                   CCC
GAM269  SLC11A1  3' CTCATTGCAACCTCCACCTT  59455      A
                                GAGGT GAGGTTGCAGTGAG
                                ||||| |||||||||||||
                                TTCCA CTCCAACGTTACTC
                                   C
GAM269  SLC12A8  3' GCTCACTGCAACCTCTGCTTC 44901
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTTCGTCTCCAACGTCACTCG

GAM269  SLC16A4  3' GCTCACTGTAATCTCCGCCTC 16281     TA
                                GAGG GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCTAATGTCACTCG
                                  GC
GAM269  SLC19A3  3' GCTCACTGCAGACTTCACCTC 47492      A   _
                                GAGGT GAGGT TGCAGTGAGC
                                ||||| ||||| ||||||||||
                                CTCCA CTTCA ACGTCACTCG
                                   _   G
GAM269  SLC2A10  3' GCTCACTGCAACCTCCACTTC 47822      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
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                                CTTCA CTCCAACGTCACTCG
                                   C
GAM269  SLC6A14  3'  GCTCACTGCAACCTCTGCCTT  23353
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                TTCCGTCTCCAACGTCACTCG

GAM269  SP2      3'  GCCACAACCTCTCCTC      11890      T       CA
                                GAGG AGAGGTTG  GT
                                |||| ||||||||  ||
                                CTCC TCTCCAAC  CG
                                   _       AC
GAM269  SQV7L    5'  GCTCACTGCAACCACTGCCTC  70576        A
                                GAGGTAG GGTTGCAGTGAGC
                                ||||||| |||||||||||||
                                CTCCGTC CCAACGTCACTCG
                                     A
GAM269  SREC     3'  GCTCACTGCAAGCTCTGCCTC  13503         G
                                GAGGTAGAG TTGCAGTGAGC
                                ||||||||| ||||||||||
                                CTCCGTCTC AACGTCACTCG
                                      G
GAM269  SS-56    3'  GCTCACTGCAGGCTCTGCCTC  59606         G
                                GAGGTAGAG TTGCAGTGAGC
                                ||||||||| ||||||||||
                                CTCCGTCTC GACGTCACTCG
                                      G
GAM269  SSI-1    3'  CTCGCACCTCCTACCTCT     13628         _    TGCA
                                AGAGGTAG AGGT    GTGAG
                                |||||||| ||||    |||||
                                TCTCCATC TCCA    CGCTC
                                     C    ____
GAM269  STAF65(gamma) 3'  CTCACTGCAACCTCTGCCTC   29432
                                GAGGTAGAGGTTGCAGTGAG
                                |||||||||||||||||||
                                CTCCGTCTCCAACGTCACTC

GAM269  SUN1     3'  GCTCACTGCAGCCTCCACCTC  47158       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM269  SYT13    3'  GCTCACTGCAACCTCCGCCTC  93456      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269  TADA3L   3'  GCTCACTGCAAGCTCCGCCTC  55996      TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
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                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269  TCL6    5'  GCTCACTGCAGCCTTCACCTC  40084      AG
                                GAGGT  AGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCCA  TCCGACGTCACTCG
                                   CT
GAM269  TCL6    5'  GCTCACTGCAGCCTTCACCTC  40106      AG
                                GAGGT  AGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCCA  TCCGACGTCACTCG
                                   CT
GAM269  TCL6    5'  GCTCACTGTAGTCTCAACCTC  40138      A   GT
                                GAGGT GAG  TGCAGTGAGC
                                |||||  |||  ||||||||||
                                CTCCA CTC  ATGTCACTCG
                                   A   TG
GAM269  TCL6    5'  GCTCACTGTAGTCTCAACCTC  40160      A   GT
                                GAGGT GAG  TGCAGTGAGC
                                |||||  |||  ||||||||||
                                CTCCA CTC  ATGTCACTCG
                                   A   TG
GAM269  TCL6    5'  GCTCACTGCAGCCTTCACCTC  26998      AG
                                GAGGT  AGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCCA  TCCGACGTCACTCG
                                   CT
GAM269  TCL6    5'  GCTCACTGCAGCCTTCACCTC  24982      AG
                                GAGGT  AGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCCA  TCCGACGTCACTCG
                                   CT
GAM269  TERA    3'  GCTCACTGCAACTTCCGTCT  41135     TA
                                AGG  GAGGTTGCAGTGAGC
                                |||  ||||||||||||||
                                TCT  CTTCAACGTCACTCG
                                  GC
GAM269  THEA    3'  GCTCACTGCAACCTCGGCCTC  66288      A
                                GAGGT GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                CTCCG CTCCAACGTCACTCG
                                   G
GAM269  TJP4    3'  GCCCTTGACCTCTCCTCT    54610      T     ____
                                AGAGG AGAGGTT    GC
                                |||||  |||||||    ||
                                TCTCC TCTCCAG    CG
                                   _      TTCC
GAM269  TNRC4   3'  GCTCACCCTCACCCCAGCCTCT 23223       AGA   TGCA
                                AGAGGT   GGT    GTGAGC
                                ||||||   |||    ||||||
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                                TCTCCG  CCA   CACTCG
                                   ACC  CTCC
GAM269  TOR1B    3'  CTCACTGCAACCTCCGCT    27199    TA
                                GG  GAGGTTGCAGTGAG
                                ||  ||||||||||||||
                                TC  CTCCAACGTCACTC
                                 GC
GAM269  TRIM16   3'  GCTCACTGCAAGCTCCGCCTC  21341     TA  G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC  G
GAM269  TRIM26   3'  GCCCACGGACCCAACCTCT   12889      AGA   GCA  A
                                AGAGGT  GGTT  GTG GC
                                ||||||  ||||  ||| ||
                                TCTCCA  CCAG  CAC CG
                                   AC_   G__  C
GAM269  TRIM5    3'  GTTCACTGCAACCTCCACCTCT 52302       A
                                AGAGGT GAGGTTGCAGTGAGC
                                |||||| ||||||||||||||
                                TCTCCA CTCCAACGTCACTTG
                                   C
GAM269  TRIM6    3'  GCTCACTGCAACCTCTGCCTC  54140
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  TTYH2    3'  CTCACCACGCGGGCCAGCCTCT 50994       AGA   _  A__
                                AGAGGT  GGTT GC  GTGAG
                                ||||||  |||| ||  |||||
                                TCTCCG  CCGG CG  CACTC
                                   A__   G  CAC
GAM269  TU12B1-TY 3'  GCTCACTGCAACCTCTGCCTC  33389
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  TU12B1-TY 3'  GCTCACTGCAACCTCTTGCCTC 33390       _
                                GAGGTA GAGGTTGCAGTGAGC
                                |||||| ||||||||||||||
                                CTCCGT CTCCAACGTCACTCG
                                   T
GAM269  TUCAN    3'  GCTCACTGCAACCTCTGCCTC  30277
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  UBF-fl   3'  GCTCACTGCAACCTCTGCCTC  51566
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
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                                CTCCGTCTCCAACGTCACTCG

GAM269  USP22    3'  GCTCACTGCAACCTCCACCTC  68015      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  VDU1     3'  GCTCACTGCAGCCTCCACCTC  30422      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM269  VPS33A   3'  CTCACTGCAACCTCCACCTC   43339      A
                                GAGGT GAGGTTGCAGTGAG
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTC
                                   C
GAM269  WBSCR20A 5'  GCTCACCGCAACCTCTGCCTC  49653            A
                                GAGGTAGAGGTTGC GTGAGC
                                |||||||||||||| ||||||
                                CTCCGTCTCCAACG CACTCG
                                         C
GAM269  WBSCR23  3'  GCTCACTGCTTGGGCCCCCT   46764     TAGA   ___
                                AGG   GGTT   GCAGTGAGC
                                |||   ||||   |||||||||
                                TCC   CCGG   CGTCACTCG
                                  C___   GTT
GAM269  WIT-1    5'  CACCACCCCTCTACCTCT    31819          TTGCA
                                AGAGGTAGAGG    GTG
                                ||||||||||     |||
                                TCTCCATCTCC    CAC
                                      CCAC_
GAM269  ZNF338   3'  GCTCACTGCAACGTCCGCCTC  42012      TA  G
                                GAGG  GA GTTGCAGTGAGC
                                ||||  || ||||||||||||
                                CTCC  CT CAACGTCACTCG
                                   GC  G
GAM269  ZNF339   3'  GCTCACTGCAACCTTGACCTC  41121      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA TTCCAACGTCACTCG
                                   G
GAM269  ZTL1     3'  ACTGCAACCTCTGCCTC     43908
                                GAGGTAGAGGTTGCAGT
                                |||||||||||||||||
                                CTCCGTCTCCAACGTCA

GAM269  LOC112687 3'  GCTCACTGCAACCTCTGCC   72862
                                GGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
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                                CCGTCTCCAACGTCACTCG

GAM269   LOC112724 5'  GCTCACTGCAACCTCCACCTC  56499      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269   LOC113675 5'  GCTCACTGCAACCTCCGCCTC  56571      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC115219 5'  GCTCACTGCAACCTCCGCCTC  73310      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC116068 3'  CTTTAACCTCACCTCT      73726      A      C
                                AGAGGT GAGGTTG AG
                                |||||| ||||||| ||
                                TCTCCA CTCCAAT TC
                                   _      T
GAM269   LOC116411 5'  GCTCACTGCAACCTCCCTGCCT 73868      __
                                AGGTA  GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||||
                                TCCGT  CTCCAACGTCACTCG
                                   CC
GAM269   LOC119392 3'  CTCACTGCAACCTCTGCCTCT  59133
                                AGAGGTAGAGGTTGCAGTGAG
                                |||||||||||||||||||||
                                TCTCCGTCTCCAACGTCACTC

GAM269   LOC120114 3'  GCTCACTGCAATCTCCACCTC  75532      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCTAACGTCACTCG
                                   C
GAM269   LOC120224 5'  GCTCACTGCAACCTCCCTCT   57101      TA
                                AGAGG  GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||||
                                TCTCC  CTCCAACGTCACTCG
                                   __
GAM269   LOC120939 3'  GCTCACTGTAACCTCCACCTC  76258      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAATGTCACTCG
                                   C
GAM269   LOC121219 5'  CTCAGGCCCTCAACCTCT    74045      A    TT  AG
                                AGAGGT GAGG  GC  TGAG
                                |||||| ||||  ||  ||||
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                                TCTCCA CTCC  CG  ACTC
                                   A   __  G_
GAM269   LOC122728 3'  CTCACTTCCCGCCTCT     74151       AGA  TTGC
                                AGAGGT   GG   AGTGAG
                                ||||||   ||   ||||||
                                TCTCCG   CC   TCACTC
                                   ___  CT__
GAM269   LOC124369 3'  GCTCACTGCAAGCACTGCCTC  74278       AG  _
                                GAGGTAG  GTT GCAGTGAGC
                                |||||||  ||| |||||||||
                                CTCCGTC  CGA CGTCACTCG
                                   A_  A
GAM269   LOC126133 3'  GCCCACTGCAGCCTCGACCTCT 74443       A         A
                                AGAGGT GAGGTTGCAGTG GC
                                |||||| |||||||||||| ||
                                TCTCCA CTCCGACGTCAC CG
                                   G          C
GAM269   LOC126364 3'  GCTCACTGCAACCTCCGCCTC  75691     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC126526 3'  CACTTTTCTACCTCT       74533          TTGC
                                AGAGGTAGAGG    AGTG
                                ||||||||||    ||||
                                TCTCCATCTTT    TCAC
                                      ____
GAM269   LOC126661 3'  GCTCACTGCAACCTCCGCCTC  74555     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC126669 3'  GCTCACTGCAACATCTGACTC  75409     G   G
                                GAG TAGA GTTGCAGTGAGC
                                ||| |||| ||||||||||||
                                CTC GTCT CAACGTCACTCG
                                  A   A
GAM269   LOC127002 3'  GCCCACTGCAACGGAGCC    74633     AGAG       A
                                GGT    GTTGCAGTG GC
                                |||    ||||||||| ||
                                CCG    CAACGTCAC CG
                                  AGG_        C
GAM269   LOC128077 3'  GCTCACTGCAACCTCCGCCTC  74713     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC128077 3'  GCTCACTGCAACCTCTGCCTC  74714
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
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                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC128387 3'  GCTCACTGCAACCTCCACTTC  74749      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTTCA CTCCAACGTCACTCG
                                   C
GAM269   LOC128989 3'  GCTCACTGCAACCTCCGCCTC  74814      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC129676 3'  CTCACTGCCTTTACCTACT    75733    _       GTT
                                AG AGGTAGAG   GCAGTGAG
                                || ||||||||   ||||||||
                                TC TCCATTTC   CGTCACTC
                                 A      ___
GAM269   LOC129880 3'  GCTCACTGCAACCTCCCTGCCT 74903       __
                                AGGTA  GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||||
                                TCCGT  CTCCAACGTCACTCG
                                   CC
GAM269   LOC130813 3'  GCTCACCGCAACCTCCGCCTC  75772      TA       A
                                GAGG  GAGGTTGC GTGAGC
                                ||||  |||||||| ||||||
                                CTCC  CTCCAACG CACTCG
                                  GC       C
GAM269   LOC131308 3'  GCTCACTGCAACCTCTGCTTC  75004
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTTCGTCTCCAACGTCACTCG

GAM269   LOC132625 3'  GCTCACTGCAACCTCCACCTC  75909      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269   LOC135154 3'  CTCACTGCAACTTCCGCC    75215    TA
                                GG  GAGGTTGCAGTGAG
                                ||  ||||||||||||||
                                CC  CTTCAACGTCACTC
                                 GC
GAM269   LOC135293 3'  GCTCACTGCAACCTCTGCCTC  76184
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC135763 3'  GCTCACTGCAACCTCCGCCTC  56791      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
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                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC138399 5'  CACTGCGGGTCTCCTCT     75325      T  GG
                                AGAGG AGA  TTGCAGTG
                                ||||| |||  ||||||||
                                TCTCC TCT  GGCGTCAC
                                  _  G_
GAM269   LOC142913 5'  ACTGCAGCCTCCACCTC     76411      A
                                GAGGT GAGGTTGCAGT
                                ||||| ||||||||||
                                CTCCA CTCCGACGTCA
                                  C
GAM269   LOC143187 3'  GCTCACTGCAACCTCCACCTC  59098       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                  C
GAM269   LOC143241 5'  GCTCACTGCAACCTCTGCCTC  57178
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC143920 3'  CTTCTTGCAACCTCTTCCCCT  76625    A  T         T
                                AG GG AGAGGTTGCAG GAG
                                || || ||||||||||| |||
                                TC CC TCTCCAACGTT TTC
                                 C  T         C
GAM269   LOC144248 5'  GCTCACTGCAACCTCCACCTC  76739       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                  C
GAM269   LOC144317 5'  CTCACTGCAACCTCTTCCTC   76788      T
                                GAGG AGAGGTTGCAGTGAG
                                |||| |||||||||||||
                                CTCC TCTCCAACGTCACTC
                                  T
GAM269   LOC144524 5'  GCTCACTGCAACCTCCACCTC  83131       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                  C
GAM269   LOC144594 3'  ACTGTGAAATACCTCTACCTC  76897            ____
                                GAGGTAGAGGT    TGCAGT
                                ||||||||||    ||||||
                                CTCCATCTCCA    GTGTCA
                                      TAAA
GAM269   LOC145009 3'  GCTCACTGCATCCTCCGCCTC  60349      TA   T
                                GAGG  GAGG TGCAGTGAGC
                                ||||  |||| ||||||||||
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                                CTCC  CTCC ACGTCACTCG
                                  GC    T
GAM269   LOC145268 5'  GCTCACTGCAACCTCCACC   77059     A
                                GGT GAGGTTGCAGTGAGC
                                ||| ||||||||||||||
                                CCA CTCCAACGTCACTCG
                                  C
GAM269   LOC145368 3'  CTCACTTCCCGCCTCT      77094       AGA  TTGC
                                AGAGGT   GG    AGTGAG
                                ||||||   ||    ||||||
                                TCTCCG   CC    TCACTC
                                   ____  CT__
GAM269   LOC145371 3'  GCTCATCTTGCCCTCTACCTC  77156          TT   __
                                GAGGTAGAGG  GCA  GTGAGC
                                ||||||||||  |||  ||||||
                                CTCCATCTCC  CGT  TACTCG
                                      __   TC
GAM269   LOC145622 3'  GCTCACTGCAACTTCTGCCTC  77303
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTTCAACGTCACTCG

GAM269   LOC145725 3'  GCTCACTGCAGCCTCCACCTC  77410       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM269   LOC145732 3'  GCTCACTGCAGCCTCCACCTC  77432       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM269   LOC145757 5'  GCTCACTACAACCTCTGCCTC  77464            C
                                GAGGTAGAGGTTG AGTGAGC
                                |||||||||||| |||||||
                                CTCCGTCTCCAAC TCACTCG
                                        A
GAM269   LOC145757 5'  GCTCACTGCAAGCTCCGCCTC  77466     TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269   LOC145813 5'  GCTCACTGCAACCTTGACGTC  83511    G  A
                                GA GT GAGGTTGCAGTGAGC
                                || || ||||||||||||||
                                CT CA TTCCAACGTCACTCG
                                 G  G
GAM269   LOC145864 3'  GCCCACCTCTACTTCT      77557           T_
                                AGAGGTAGAGGT  GC
                                ||||||||||||  ||
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                                TCTTCATCTCCA  CG
                                       CC
GAM269   LOC145955 5'  CTCACTGCCACCCTCC      83591    T  A   T
                                GG AG GGT GCAGTGAG
                                || || ||| ||||||||
                                CC TC CCA CGTCACTC
                                 _ _  C
GAM269   LOC146050 3'  GCTCACTGCAACCTCTGCCTT  77640
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                TTCCGTCTCCAACGTCACTCG

GAM269   LOC146050 3'  GCTCACTGCAACCTCTGCTTC  77642
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTTCGTCTCCAACGTCACTCG

GAM269   LOC146092 5'  ACTCAGCCTCTACCCT      83612    A        C
                                AG GGTAGAGGTTG AGT
                                || ||||||||||| |||
                                TC CCATCTCCGAC TCA
                                 _         _
GAM269   LOC146229 3'  GCTCACTGCAACCTCCACCTC  77754      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269   LOC146229 3'  GCTCCCTGCAACCTCCACCTC  77756      A        T
                                GAGGT GAGGTTGCAG GAGC
                                ||||| |||||||||| ||||
                                CTCCA CTCCAACGTC CTCG
                                   C         C
GAM269   LOC146346 5'  GCTCACTGCAACTTCTGCCTC  77844
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTTCAACGTCACTCG

GAM269   LOC146429 5'  GCTCACTGCAGCCTCCAACTCT 83672      GTA
                                AGAG   GAGGTTGCAGTGAGC
                                ||||   ||||||||||||||
                                TCTC   CTCCGACGTCACTCG
                                  AAC
GAM269   LOC146455 3'  GCTCACTGCAATCTCTGCCTCT 77905
                                AGAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                TCTCCGTCTCTAACGTCACTCG

GAM269   LOC146603 5'  GCTCACTGCAAGCTCCGCCTC  78018      TA  G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
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                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269   LOC146784 5'  GCTCACTGCAACCTCCACCTC  78119      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269   LOC146820 5'  GCTCACTGCAACCTCCGCATC  78149    G TA
                                GA G  GAGGTTGCAGTGAGC
                                || |  ||||||||||||||||
                                CT C  CTCCAACGTCACTCG
                                 A GC
GAM269   LOC146901 3'  GCTCATTGCAACCTCCACCTT  83842      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                TTCCA CTCCAACGTTACTCG
                                   C
GAM269   LOC146909 3'  GCTCACTGCAACCTCCGCCTC  78176     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC146909 3'  GCTCACTGCAAGCTCCGCCTC  78177     TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269   LOC146952 5'  GCTCACTGCAACCTCCACCTCT 83870       A
                                AGAGGT GAGGTTGCAGTGAGC
                                |||||| ||||||||||||||||
                                TCTCCA CTCCAACGTCACTCG
                                   C
GAM269   LOC147071 5'  GCTCACTGCAACCTCTGCCTC  73001
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC147080 5'  GCTCACTGCAAGCTCCGCCTCT 83935      TA   G
                                AGAGG  GAG TTGCAGTGAGC
                                |||||  ||| ||||||||||
                                TCTCC  CTC AACGTCACTCG
                                  GC   G
GAM269   LOC147166 3'  GCTCACTGCAAGCTCCGCCTC  78288     TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269   LOC147276 3'  GCTCACTGCAACGTCTGCCTC  78336       G
                                GAGGTAGA GTTGCAGTGAGC
                                |||||||| ||||||||||||
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                                CTCCGTCT CAACGTCACTCG
                                     G
GAM269   LOC147407 3'  GCTCACTGCAACCTCCGCCTC  76325     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC147429 5'  GCTCACTGCAATCTCCATCTC  78362      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCTA CTCTAACGTCACTCG
                                   C
GAM269   LOC147660 3'  CTCACAGCAACCTCCGCCTC   78391     TA       A
                                GAGG  GAGGTTGC GTGAG
                                ||||  |||||||| |||||
                                CTCC  CTCCAACG CACTC
                                  GC       A
GAM269   LOC147694 3'  GCTCACTGCAAGCTCCGCCTC  78452     TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269   LOC147817 3'  GCTCACTGCAACCTCCACCTC  78500      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269   LOC147841 3'  GCTCACAGCAACCTCTGCCTC  78531           A
                                GAGGTAGAGGTTGC GTGAGC
                                |||||||||||||| ||||||
                                CTCCGTCTCCAACG CACTCG
                                        A
GAM269   LOC147990 3'  GCTCACTACAACCTCTGCCTC  84095          C
                                GAGGTAGAGGTTG AGTGAGC
                                |||||||||||| |||||||
                                CTCCGTCTCCAAC TCACTCG
                                        A
GAM269   LOC148137 3'  GCTCACGGCAACCTCCACCTC  58434      A       A
                                GAGGT GAGGTTGC GTGAGC
                                ||||| |||||||| ||||||
                                CTCCA CTCCAACG CACTCG
                                   C       G
GAM269   LOC148137 3'  GCTCACTGCAAGCTTCGCCTC  58435     TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  TTC AACGTCACTCG
                                  GC   G
GAM269   LOC148147 3'  GCTCACTGCAATCTCTGCCTC  78684
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
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                                CTCCGTCTCTAACGTCACTCG

GAM269   LOC148189 5'  GCTCACTGCAACCTCCACCTC  78712      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269   LOC148195 3'  GCTCACTGCAGGCTCTGCCTC  84131        G
                                GAGGTAGAG TTGCAGTGAGC
                                ||||||||| ||||||||||
                                CTCCGTCTC GACGTCACTCG
                                      G
GAM269   LOC148198 3'  GCTCACTGCAACCTCCATCTC  70684      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCTA CTCCAACGTCACTCG
                                   C
GAM269   LOC148760 3'  GCCCACCAGCTTCTCCTCT    84206      T      CA   A
                                AGAGG AGAGGTTG  GTG GC
                                ||||| ||||||||  ||| ||
                                TCTCC TCTTCGAC  CAC CG
                                   _      __   C
GAM269   LOC148887 5'  GCTCACTGCAACATCTGCCTC  84242        G
                                GAGGTAGA GTTGCAGTGAGC
                                |||||||| ||||||||||||
                                CTCCGTCT CAACGTCACTCG
                                      A
GAM269   LOC148918 5'  CTCAGCTTCTTCTACCTC    79067         TT  AG
                                GAGGTAGAGG  GC  TGAG
                                ||||||||||  ||  ||||
                                CTCCATCTTC  CG  ACTC
                                      TT  __
GAM269   LOC148918 5'  GCTCACTGCAGCCTCCACCTC  79074      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM269   LOC148932 3'  CTCATCCCTCTGCCTC      79108        TTGCA
                                GAGGTAGAGG    GTGAG
                                ||||||||||    |||||
                                CTCCGTCTCC    TACTC
                                      C____
GAM269   LOC149171 5'  GCTCACTGCAACCTCTGTCTC  79219     GT
                                GAG  AGAGGTTGCAGTGAGC
                                |||  ||||||||||||||||
                                CTC  TCTCCAACGTCACTCG
                                  TG
GAM269   LOC149421 3'  GCTCACTGCAAGCCCCACCTT  79360      AGA   _
                                GAGGT   GGTT GCAGTGAGC
                                |||||   |||| |||||||||
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                                TTCCA   CCGA CGTCACTCG
                                   CC_    A
GAM269   LOC149506 3'  GCTCACTGCAACCTCTGCCTC  84472
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC149506 3'  GCTCACTGCAACTTCCACCTC  84473      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTTCAACGTCACTCG
                                   C
GAM269   LOC149692 3'  GCTCACTGTAACCTCTGCCTC  84589
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAATGTCACTCG

GAM269   LOC149703 5'  GCTTAATGCAACCTCTACCTC  84657            G
                                GAGGTAGAGGTTGCA TGAGC
                                |||||||||||||| |||||
                                CTCCATCTCCAACGT ATTCG
                                          A
GAM269   LOC149711 3'  GCTCACTGCAACCTCTGCTTC  84684
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTTCGTCTCCAACGTCACTCG

GAM269   LOC149821 5'  GCCCACTGCAAGCTCCGCCTC  84763     TA  G      A
                                GAGG  GAG TTGCAGTG GC
                                ||||  ||| |||||||| ||
                                CTCC  CTC AACGTCAC CG
                                  GC  G       C
GAM269   LOC150054 5'  GCTCACTGCAACCTTCGCCTCT 84835      TA
                                AGAGG  GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                TCTCC  TTCCAACGTCACTCG
                                   GC
GAM269   LOC150166 5'  GCTCACTGCAGCCTCGACCTC  84886      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   G
GAM269   LOC150166 5'  GCTCACTGGATCCTTCCTCT   84887      T A   G
                                AGAGG AG GGTT CAGTGAGC
                                ||||| || |||| ||||||||
                                TCTCC TC CTAG GTCACTCG
                                   T _   _
GAM269   LOC150225 3'  CTCACTGCAACTTCCGCCTC   84992     TA
                                GAGG  GAGGTTGCAGTGAG
                                ||||  ||||||||||||||
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                                CTCC  CTTCAACGTCACTC
                                  GC
GAM269   LOC150397 3'  GCTCATTGCAACCTCCGCCTC  79847     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTTACTCG
                                  GC
GAM269   LOC150407 3'  GCTCACTGCAACCTCAAACTC  79827     GTA
                                GAG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                CTC   CTCCAACGTCACTCG
                                 AAA
GAM269   LOC150423 3'  CTCACTTTCCGCCTCT      79865      TA   GTTGC
                                AGAGG  GAG    AGTGAG
                                |||||  |||    ||||||
                                TCTCC  CTT    TCACTC
                                  GC  _____
GAM269   LOC150519 3'  CTGCAACCTGCCACCTC     79918      AG_
                                GAGGT   AGGTTGCAG
                                |||||   |||||||||
                                CTCCA   TCCAACGTC
                                  CCG
GAM269   LOC150696 3'  GCTCACTGCAGCCTCCACCTC  58483      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                  C
GAM269   LOC150960 3'  GCTGCAACCTCCGCCTC     80066     TA
                                GAGG  GAGGTTGCAGT
                                ||||  ||||||||||
                                CTCC  CTCCAACGTCG
                                  GC
GAM269   LOC151057 3'  GCTCACTGCAACCTCTGCCTC  85213
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC151201 3'  GCTCACTGCAACCTCCACCTC  85284      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                  C
GAM269   LOC151414 3'  GCTGAAACCCCAACCTCT    80240      AGA   G
                                AGAGGT   GGTT CAGT
                                ||||||   |||| ||||
                                TCTCCA   CCAA GTCG
                                   ACC   A
GAM269   LOC151475 5'  GCTCACTGCAACCTCCACCTC  85409      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
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                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269   LOC151475 5'  GCTCACTGCAACCTCTGCCTC  85412
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC151521 5'  GCCCAACATCCCTTTACCTCT  85437          TTGCAG  A
                                AGAGGTAGAGG     TG GC
                                ||||||||||      || ||
                                TCTCCATTTCC     AC CG
                                      CTACA_  C
GAM269   LOC151602 3'  GCTCACTGCAACCTGGAACTC  80297     GTAG
                                GAG    AGGTTGCAGTGAGC
                                |||    |||||||||||||||
                                CTC    TCCAACGTCACTCG
                                  AAGG
GAM269   LOC151826 3'  GCTCACTGCAACCTCCGCCTC  80359      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  |||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269   LOC152137 3'  GCTCACTGCAACCTCCGCC    80481    TA
                                GG  GAGGTTGCAGTGAGC
                                ||  |||||||||||||||
                                CC  CTCCAACGTCACTCG
                                 GC
GAM269   LOC152220 3'  GCTCACTGCAACCTCCGCTTC  85584      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  |||||||||||||||
                                CTTC  CTCCAACGTCACTCG
                                   GC
GAM269   LOC152245 3'  GCTCACTGCAACCTCCGCCTT  85603      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  |||||||||||||||
                                TTCC  CTCCAACGTCACTCG
                                   GC
GAM269   LOC152300 3'  GCTCACTGCAAGCTCTGCCTCT 80546          G
                                AGAGGTAGAG TTGCAGTGAGC
                                |||||||||| ||||||||||
                                TCTCCGTCTC AACGTCACTCG
                                      G
GAM269   LOC152343 3'  CTCAGTGCAACCTCCGCCTC   80563      TA        G
                                GAGG  GAGGTTGCA TGAG
                                ||||  ||||||||| ||||
                                CTCC  CTCCAACGT ACTC
                                   GC        G
GAM269   LOC152445 3'  ACTGCAACCTCTGCCTC     85739
                                GAGGTAGAGGTTGCAGT
                                |||||||||||||||||
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                                CTCCGTCTCCAACGTCA

GAM269   LOC152582 5'  GCTCACCGCAACCTCTGCCTC  85792            A
                                GAGGTAGAGGTTGC GTGAGC
                                |||||||||||||| ||||||
                                CTCCGTCTCCAACG CACTCG
                                      C
GAM269   LOC152620 3'  GCTCACTACAACCTCTGCCTC  60082            C
                                GAGGTAGAGGTTG AGTGAGC
                                |||||||||||| |||||||
                                CTCCGTCTCCAAC TCACTCG
                                      A
GAM269   LOC152719 5'  ACTGCAACCTCTGCCTC     85844
                                GAGGTAGAGGTTGCAGT
                                |||||||||||||||||
                                CTCCGTCTCCAACGTCA

GAM269   LOC152719 5'  GCTCACTGCAAGCTCCGCCTC  85851      TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269   LOC152794 5'  CTCACTGCAACCTCTACCTC   80676
                                GAGGTAGAGGTTGCAGTGAG
                                |||||||||||||||||||
                                CTCCATCTCCAACGTCACTC

GAM269   LOC152804 3'  GCTCACTGCAACCTCAAACTC  85885     GTA
                                GAG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                CTC   CTCCAACGTCACTCG
                                  AAA
GAM269   LOC152925 3'  ACTCCAACCTCTGCCTC     80733            C
                                GAGGTAGAGGTTG AGT
                                |||||||||||| |||
                                CTCCGTCTCCAAC TCA
                                      C
GAM269   LOC153077 3'  GCTCACTGCAACCTCCGCCTC  85911      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC153338 5'  GCCCACTTGGTTCTCTATCCCT 85995    A       TTGC    A
                                AG GGTAGAGG    AGTG GC
                                || ||||||||    |||| ||
                                TC CTATCTCT    TCAC CG
                                 C       TGGT    C
GAM269   LOC153688 3'  GCTCACTGCAACCTCCACCTC  86113      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
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                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269   LOC153811 3'  GCTCACTGCAAGCTCCGCCTC  80952      TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269   LOC153883 5'  ACTGCAACCTCCACCCT     80977    A   A
                                AG GGT GAGGTTGCAGT
                                || ||| ||||||||||
                                TC CCA CTCCAACGTCA
                                 _  C
GAM269   LOC154075 3'  GCTCACTGCAACCTCCGCCTC  81047      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC154282 5'  GCTCACTGCAACCTCCACCTC  86202       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269   LOC154822 3'  GCTCACTGCAACCTCTGTCTC  86262     GT
                                GAG  AGAGGTTGCAGTGAGC
                                |||  ||||||||||||||
                                CTC  TCTCCAACGTCACTCG
                                  TG
GAM269   LOC154834 3'  CTCACTGCCACCCCTCT     86265       TAGA   T
                                AGAGG    GGT GCAGTGAG
                                |||||    ||| ||||||||
                                TCTCC    CCA CGTCACTC
                                   _____  C
GAM269   LOC154877 3'  GCTCACTGCAACCTCTACCTC  86299
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCATCTCCAACGTCACTCG

GAM269   LOC155100 5'  CACGGTGGCCTCTCCTCT    73025       T     TG A
                                AGAGG AGAGGT  C GTG
                                ||||| ||||||  | |||
                                TCTCC TCTCCG  G CAC
                                   _     GT G
GAM269   LOC157247 5'  GCTCACTGCAACCTCCACC    81369     A
                                GGT GAGGTTGCAGTGAGC
                                ||| ||||||||||||||
                                CCA CTCCAACGTCACTCG
                                  C
GAM269   LOC157506 3'  GCTCACTGCAATCTCTGCCTC  81443
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
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                                CTCCGTCTCTAACGTCACTCG

GAM269  LOC157507 5' GCTCACTGCAACGTCCGCCTC 81458     TA  G
                                GAGG  GA GTTGCAGTGAGC
                                ||||  || ||||||||||||
                                CTCC  CT CAACGTCACTCG
                                  GC  G
GAM269  LOC157798 5' ACTGCAACCTCCGCCTC    86544     TA
                                GAGG  GAGGTTGCAGT
                                ||||  ||||||||||
                                CTCC  CTCCAACGTCA
                                  GC
GAM269  LOC157858 5' GCTCACTGCAACCTCTGCCTC 86593
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  LOC158014 5' GCTCACTGCAATCTCCGCCTC 81651     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCTAACGTCACTCG
                                  GC
GAM269  LOC158263 3' CTCATTCCCCCACCTTT    81845      AGA  TTGC
                                AGAGGT   GG   AGTGAG
                                ||||||   ||   ||||||
                                TTTCCA   CC   TTACTC
                                   CCC  _____
GAM269  LOC158288 5' CTCACCTCTCTGCCTCT    86711         TTGCA
                                AGAGGTAGAGG    GTGAG
                                ||||||||||    |||||
                                TCTCCGTCTCT    CACTC
                                      C_____
GAM269  LOC158310 5' GCTCACTGCAACCTTGGCCTC 86757      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCG TTCCAACGTCACTCG
                                   G
GAM269  LOC158402 5' GCTCACTGTAACCTCTGCCTC 86809
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAATGTCACTCG

GAM269  LOC158476 3' GCTCACTGCAACCTCCGCC   86848    TA
                                GG  GAGGTTGCAGTGAGC
                                ||  ||||||||||||||
                                CC  CTCCAACGTCACTCG
                                 GC
GAM269  LOC158549 5' GCTCACTGTGACCTCCGCCTC 86867     TA    TG
                                GAGG  GAGGT  CAGTGAGC
                                ||||  |||||  ||||||||
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                                CTCC  CTCCA  GTCACTCG
                                  GC    GT
GAM269   LOC158668 3'  GCTCACTGCAACCTCTGCCTC  69371
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC158865 5'  GCTCACTGCAACCTCTGCCTC  86937
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC159121 5'  CTCCTTCATCCCCTACCTC   86994       A  T  C  T
                                GAGGTAG GG TG AG GAG
                                ||||||| || || || |||
                                CTCCATC CC AC TC CTC
                                    C  T  T  _
GAM269   LOC161829 3'  GCTCACTGCAACCTCCGCCTC  82316     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC162461 3'  CTCACTGCACCCACC      82360     AGA  T
                                GGT   GG TGCAGTGAG
                                |||   || |||||||||
                                CCA   CC ACGTCACTC
                                  ___  C
GAM269   LOC165140 5'  GCTCACTGCCTTCCTACACTC  82464     _   A  TT
                                GAG GTAG GG  GCAGTGAGC
                                ||| |||| ||  |||||||||
                                CTC CATC CT  CGTCACTCG
                                  A   _  TC
GAM269   LOC169611 3'  GCTCACTGCAATCTCCGCCTC  82769     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCTAACGTCACTCG
                                  GC
GAM269   LOC196047 5'  GCTCACTGCAACCTCCGCCTC  89604     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC196264 3'  GCTCACTGCAACCTCTGCCTC  87607
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC196411 3'  GCTCACTGCAACCTCCGCCTC  87674     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
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                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC196529 3'  GCTCACTGCAACCTCCACCTC  87776      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269   LOC196759 3'  CACTGCAGTTCTCCTCT     87515      T   GGT
                                AGAGG AGA   TGCAGTG
                                ||||| |||   |||||||
                                TCTCC TCT   ACGTCAC
                                   _   TG_
GAM269   LOC196761 3'  CACAACACCTCTGCCCCT    89553    A       T CA
                                AG GGTAGAGGT G  GTG
                                || |||||||| |  |||
                                TC CCGTCTCCA C  CAC
                                 C        _ AA
GAM269   LOC196957 3'  GCTCACTGCAGCCTCCACCTC  87826      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM269   LOC196961 3'  GCTCACTGCAGCCTCCACCTC  87847      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM269   LOC197138 3'  GCTCACTGCAGCCTCCACCTC  87920      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM269   LOC197358 3'  GCTCACTGTAGGCTCTACCTC  88040        G
                                GAGGTAGAG TTGCAGTGAGC
                                ||||||||| ||||||||||
                                CTCCATCTC GATGTCACTCG
                                      G
GAM269   LOC197358 3'  GCTCCCTGCAACCTCCGCCTC  88042     TA       T
                                GAGG  GAGGTTGCAG GAGC
                                ||||  |||||||||| ||||
                                CTCC  CTCCAACGTC CTCG
                                  GC         C
GAM269   LOC199699 3'  GCTCACTGCAAGCTCCACCTC  88310      A   G
                                GAGGT GAG TTGCAGTGAGC
                                ||||| ||| ||||||||||
                                CTCCA CTC AACGTCACTCG
                                   C   G
GAM269   LOC199786 3'  GCTCACTGCAACCTCCGCCTC  88387     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
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                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC199864 3'  CACTGCAGGTCTCCTCT     89864      T   GG
                                AGAGG AGA  TTGCAGTG
                                ||||| |||  ||||||||
                                TCTCC TCT  GACGTCAC
                                  _  G_
GAM269   LOC200014 3'  GCTCGCTGCAACCCCCACCTC  88532      AGA
                                GAGGT   GGTTGCAGTGAGC
                                |||||   ||||||||||||||
                                CTCCA   CCAACGTCGCTCG
                                  CCC
GAM269   LOC200107 3'  GCTCACCGCAACCTCCTCTTCT 88575      TA       A
                                AGAGG  GAGGTTGC GTGAGC
                                |||||  |||||||| ||||||
                                TCTTC  CTCCAACG CACTCG
                                  TC       C
GAM269   LOC200169 5'  GCTCACTGCAACCTCTGCCTC  89951
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC200268 3'  GCTCACTGCAACCTCTGCCTC  88684
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC200301 5'  GCTCACTGCAAGCTCCGCCTC  88746     TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269   LOC200310 3'  GCTCACTACAACCTCTGCCTC  65739           C
                                GAGGTAGAGGTTG AGTGAGC
                                |||||||||||| |||||||
                                CTCCGTCTCCAAC TCACTCG
                                        A
GAM269   LOC200314 3'  GCTCACTGCAACCTCCACCTC  90011      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                  C
GAM269   LOC200339 3'  GCTCACTGCAACCTCTGCCTC  90036
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC200845 5'  GCTCACTGCAACCTCCGCCTCT 88901      TA
                                AGAGG  GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
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                                TCTCC  CTCCAACGTCACTCG
                                   GC
GAM269   LOC200860 3'  GTTCACTGCAACCTCCACCTC  90170      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTTG
                                   C
GAM269   LOC201164 3'  GCTCACTGCATCCTCTGCCTC  88118          T
                                GAGGTAGAGG TGCAGTGAGC
                                |||||||||| ||||||||||
                                CTCCGTCTCC ACGTCACTCG
                                      T
GAM269   LOC201173 5'  GCTCACTGCAACCTCTGCCTC  87331
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC201220 5'  GCTCACTGCAACCTCTGCCTC  87352
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC201294 3'  GCTCACTGCAACCTCCGCCTC  88213     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269   LOC201294 3'  GCTCACTGCAACCTCCGCCTC  88214     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269   LOC201411 3'  GCTCACTGCAACCTCTGCCTC  62958
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC201626 3'  GCTCACTGCAACCTCCGCC   88992    TA
                                GG  GAGGTTGCAGTGAGC
                                ||  ||||||||||||||||
                                CC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC201627 3'  GCTGACTGCAACCTCCACCTC  89016      A         G
                                GAGGT GAGGTTGCAGT AGC
                                ||||| |||||||||| |||
                                CTCCA CTCCAACGTCA TCG
                                   C         G
GAM269   LOC201696 3'  GCTCACTGCAGCCACTGCCTC  63134       A
                                GAGGTAG GGTTGCAGTGAGC
                                ||||||| ||||||||||||
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                                CTCCGTC CCGACGTCACTCG
                                    A
GAM269   LOC201702 5'  GCTCACTGCAACCTCTGACTC  89032     G
                                GAG TAGAGGTTGCAGTGAGC
                                ||| ||||||||||||||||
                                CTC GTCTCCAACGTCACTCG
                                  A
GAM269   LOC202025 3'  GCTCACTGCAACCTCCGCCTC  90293      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269   LOC202908 5'  GCTCACTGCAACGTCTGCCTC  89238         G
                                GAGGTAGA GTTGCAGTGAGC
                                |||||||| ||||||||||||
                                CTCCGTCT CAACGTCACTCG
                                     G
GAM269   LOC202908 5'  GCTCACTGCAGCCTCCACCT   89239      A
                                AGGT GAGGTTGCAGTGAGC
                                |||| ||||||||||||||||
                                TCCA CTCCGACGTCACTCG
                                   C
GAM269   LOC202908 5'  GCTCACTGCAGCTTCCACTTC  89241       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTTCA CTTCGACGTCACTCG
                                   C
GAM269   LOC202934 3'  GCTCACTACAACCTCTGCCTC  90416            C
                                GAGGTAGAGGTTG AGTGAGC
                                |||||||||||| |||||||
                                CTCCGTCTCCAAC TCACTCG
                                        A
GAM269   LOC203197 3'  GCTCACTGCAACCCCCGCC    89291     AGA
                                GGT   GGTTGCAGTGAGC
                                |||   ||||||||||||||
                                CCG   CCAACGTCACTCG
                                  CCC
GAM269   LOC203297 5'  GCTCACTGCAACCTCTGCCTC  75351
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC203350 3'  ACTGCAACCTCCGCCTC     90558      TA
                                GAGG  GAGGTTGCAGT
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCA
                                   GC
GAM269   LOC203369 3'  GCTCACTGCAAGCTCCGCCTC  89343      TA  G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||||
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                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269   LOC203378 3'  GCTCACGGCAACCTCTGCCTC  90608          A
                                GAGGTAGAGGTTGC GTGAGC
                                |||||||||||||| ||||||
                                CTCCGTCTCCAACG CACTCG
                                       G
GAM269   LOC204804 3'  GCTCACTGCAACCTCGACCTC  89476      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                  G
GAM269   LOC204804 3'  GCTCACTGCCACCTCCACCTC  89478      A    T
                                GAGGT GAGGT GCAGTGAGC
                                ||||| ||||| |||||||||
                                CTCCA CTCCA CGTCACTCG
                                  C    C
GAM269   LOC219445 5'  GCTCACTGCAGCCTCCGCCTC  91575     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCGACGTCACTCG
                                  GC
GAM269   LOC219673 5'  GCTCACTGTAGCCTCTGCCTC  93033
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCGATGTCACTCG

GAM269   LOC219735 3'  GCTCACTGCAACCTCTGCCTC  93111
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC219894 3'  GTTCACTGCAAGCTCCACCTC  93286      A  G
                                GAGGT GAG TTGCAGTGAGC
                                ||||| ||| ||||||||||
                                CTCCA CTC AACGTCACTTG
                                  C  G
GAM269   LOC220064 3'  GCTCACTGTAACCTCCGCCTC  93427     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAATGTCACTCG
                                  GC
GAM269   LOC220074 3'  GCTCACTGCAACCTCAGCCTC  59276      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCG CTCCAACGTCACTCG
                                  A
GAM269   LOC220074 3'  GCTCACTGCAACCTCCGCCT   59278     TA
                                AGG  GAGGTTGCAGTGAGC
                                |||  ||||||||||||||||
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                                TCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC220575 3'  GCTCACTGCAACCTCAACCTT  76315      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                TTCCA CTCCAACGTCACTCG
                                   A
GAM269   LOC220662 3'  GTTCACTGCAACCTCCACCTC  91176      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTTG
                                   C
GAM269   LOC220662 3'  ACTGCAACCTCCACTTC     91161      A
                                GAGGT GAGGTTGCAGT
                                ||||| ||||||||||
                                CTTCA CTCCAACGTCA
                                   C
GAM269   LOC220846 3'  CTTTCCACAACCTCTACCTT   90815           CAGT
                                GAGGTAGAGGTTG   GAG
                                ||||||||||||    |||
                                TTCCATCTCCAAC   TTC
                                      ACCT
GAM269   LOC221035 3'  GCTCACTACAACCTCTGCCTC  93165           C
                                GAGGTAGAGGTTG AGTGAGC
                                ||||||||||||| |||||||
                                CTCCGTCTCCAAC TCACTCG
                                      A
GAM269   LOC221174 5'  GCTCACTGCGACCTCCACCTC  93504      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAGCGTCACTCG
                                   C
GAM269   LOC221271 3'  GCTCACTGCAACCTCTGCCTC  91864
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC221296 3'  GCTCACTGCAACCTCCACCTC  91965      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269   LOC221463 3'  CATTAACACCCTACCTCT     92067        A   TGC
                                AGAGGTAG GGT   AGTG
                                |||||||| |||   ||||
                                TCTCCATC CCA   TTAC
                                     _  CAA
GAM269   LOC221466 5'  GCTCCTTCCACCCCTACCTCT  93689        A   TGC  T
                                AGAGGTAG GGT   AG GAGC
                                |||||||| |||   || ||||
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                                TCTCCATC CCA   TC CTCG
                                    C   CCT  _
GAM269   LOC221489 3'  CTCACTGCAGACTCTCT     93640    T   G
                                GG AGAG TTGCAGTGAG
                                || |||| ||||||||||
                                TC TCTC GACGTCACTC
                                 _   A
GAM269   LOC221608 3'  GCTCACCACTGTATCCCCTCT  92187      TAGA  T    ___
                                AGAGG   GG TGCAGT   GAGC
                                |||||   || ||||||  ||||
                                TCTCC   CC ATGTCA   CTCG
                                  _____ T     CCA
GAM269   LOC221663 5'  GCTCACTGCAACCTCCACCTC  93818      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269   LOC221715 5'  CAAATGCCTCTACCTTT     93749          TGCAG
                                AGAGGTAGAGGT    TG
                                ||||||||||||    ||
                                TTTCCATCTCCG    AC
                                      TAA__
GAM269   LOC221760 5'  GCTCACTGCAACCTCAAATTC  93788     GTA
                                GAG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||||
                                CTT   CTCCAACGTCACTCG
                                  AAA
GAM269   LOC221773 3'  GCTCACTGTGACCTCCGCCTC  91047     TA    TG
                                GAGG  GAGGT  CAGTGAGC
                                ||||  |||||  ||||||||
                                CTCC  CTCCA  GTCACTCG
                                  GC    GT
GAM269   LOC221960 3'  GCTCACTGCAGCCTCAACCTC  91084      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   A
GAM269   LOC222070 5'  GCTCACTGCAACCTCTGCCTC  94156
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269   LOC222224 5'  GCTCACTGCAACCTCAGCCTC  94199      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCG CTCCAACGTCACTCG
                                   A
GAM269   LOC245771 5'  GCTCACTGCAACCCCCGTCTC  92894     TAGA
                                GAGG   GGTTGCAGTGAGC
                                ||||   ||||||||||||
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                                CTCT    CCAACGTCACTCG
                                  GCCC
GAM269   LOC253612 5'  GCTCACTGCAACCTCCGCCTC  96752     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC253664 3'  GCTCATTGCAACCTCTGCCTC  94812
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTTACTCG

GAM269   LOC253666 5'  GCTCACTGCAACCTCCGCCTC  95064     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269   LOC254013 3'  GCTCACTGTAGCCTCCACCTC  94879      A
                                GAGGT GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||||
                                CTCCA CTCCGATGTCACTCG
                                   C
GAM269   LOC254268 3'  GCTCACTGCAACCTTTGTCTC  95410     GT
                                GAG  AGAGGTTGCAGTGAGC
                                |||  ||||||||||||||||
                                CTC  TTTCCAACGTCACTCG
                                  TG
GAM269   LOC254351 3'  GCCCACCGCAACCTCGGCCTC  94993      A       A  A
                                GAGGT GAGGTTGC GTG GC
                                |||||  ||||||||  |||  ||
                                CTCCG CTCCAACG CAC CG
                                   G       C   C
GAM269   LOC254655 3'  GCTCACTGCAACCTCTGCCTT  95472
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                TTCCGTCTCCAACGTCACTCG

GAM269   LOC254672 3'  GCTCACTGAAACCTCTGCCTC  94647           G
                                GAGGTAGAGGTT CAGTGAGC
                                ||||||||||||  ||||||||
                                CTCCGTCTCCAA GTCACTCG
                                       A
GAM269   LOC254755 3'  CTCAGTGACCTCTGCCTCT    97367           TG AG
                                AGAGGTAGAGGT  C  TGAG
                                ||||||||||||  |  ||||
                                TCTCCGTCTCCA  G  ACTC
                                       GT __
GAM269   LOC255196 5'  GCTCACTGCAGTCTCGACCTC  97170      A   GT
                                GAGGT GAG  TGCAGTGAGC
                                |||||  |||  ||||||||||
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                                CTCCA CTC  ACGTCACTCG
                                   G   TG
GAM269   LOC255465 3'  GCTCACTGTATCCTCTGCCTC  97293         T
                                GAGGTAGAGG TGCAGTGAGC
                                |||||||||| ||||||||||
                                CTCCGTCTCC ATGTCACTCG
                                      T
GAM269   LOC255497 3'  GCTCACTGCAACCTCCGCCTC  97192      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269   LOC255743 5'  GCTCAGAACACCTCTACC    95918         TGCAG
                                GGTAGAGGT    TGAGC
                                |||||||||    |||||
                                CCATCTCCA    ACTCG
                                     CAAG_
GAM269   LOC255870 3'  GCTCACTGTGACCCACTCT   94659      GTAGA   TG
                                AGAG    GGT  CAGTGAGC
                                ||||    |||  ||||||||
                                TCTC    CCA  GTCACTCG
                                   AC___   GT
GAM269   LOC255919 3'  GCTTTCTGCAACCTCTGCCTC  95038             T
                                GAGGTAGAGGTTGCAG GAGC
                                |||||||||||||| ||||
                                CTCCGTCTCCAACGTC TTCG
                                          T
GAM269   LOC256267 3'  GCTCACTGCAACCTCCGCCTC  96805      TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269   LOC256306 3'  GCTCACTGCAACCTCCACCTC  96693       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269   LOC256476 5'  GCTCACTGCAGCCTCGACCTC  96819       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   G
GAM269   LOC257054 5'  GCTCACTGCAGCCTCGACCTC  95665       A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   G
GAM269   LOC257334 3'  GCTCACTGCAACCTCCGCCT   97276      TA
                                AGG  GAGGTTGCAGTGAGC
                                |||  ||||||||||||||
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                                TCC  CTCCAACGTCACTCG
                                  GC
GAM269  LOC257465 3'  GCTCACTGCAGCCTCCGCCTC  81595     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCGACGTCACTCG
                                  GC
GAM269  LOC257486 3'  GCTCACTGCAAGCTCCGCCTC  69248     TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                  GC   G
GAM269  LOC257494 3'  GCCCACGGACCCAACCTCT   97793      AGA   GCA   A
                                AGAGGT   GGTT   GTG GC
                                ||||||   ||||   ||| ||
                                TCTCCA   CCAG   CAC CG
                                   AC_   G__   C
GAM269  LOC51008  5'  GCTCACAGCAACCTCTGCCTC  31965          A
                                GAGGTAGAGGTTGC GTGAGC
                                |||||||||||||| ||||||
                                CTCCGTCTCCAACG CACTCG
                                       A
GAM269  LOC51200  3'  GCTCACCACAACCTCTGCCTC  32998         CA
                                GAGGTAGAGGTTG  GTGAGC
                                ||||||||||||  ||||||
                                CTCCGTCTCCAAC  CACTCG
                                       AC
GAM269  LOC51219  5'  GCTCACCGCAACCTCCGCCTC  33122     TA      A
                                GAGG  GAGGTTGC GTGAGC
                                ||||  |||||||| ||||||
                                CTCC  CTCCAACG CACTCG
                                  GC       C
GAM269  LOC51279  3'  GCTCCTCCTCACCCTCTACCTC 33315         T  C__  T
                                GAGGTAGAGG TG   AG GAGC
                                |||||||||| ||   || ||||
                                CTCCATCTCC AC   TC CTCG
                                      C  TCC  _
GAM269  LOC51622  3'  GCTCACTGCAGCCTCAACCTC  31569      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   A
GAM269  LOC51696  3'  GCTCACTGCAACCTCTGCCTC  32551
                                GAGGTAGAGGTTGCAGTGAGC
                                ||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  LOC56181  5'  GCTCACTGCAAGCTCTGCCTC  95538         G
                                GAGGTAGAG TTGCAGTGAGC
                                |||||||| ||||||||||
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                                CTCCGTCTC AACGTCACTCG
                                     G
GAM269  LOC57107  3' CTCACTGCAACCTCCGCCTC  39833    TA
                                GAGG  GAGGTTGCAGTGAG
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTC
                                  GC
GAM269  LOC57146  3' GCTCACTGCAACCTCCAACTC  39923    GTA
                                GAG   GAGGTTGCAGTGAGC
                                |||   |||||||||||||||
                                CTC   CTCCAACGTCACTCG
                                 AAC
GAM269  LOC64102  5' CTCACTTGCAACTCCACCTC  42172    A  G   _
                                GAGGT GAG TTGCA GTGAG
                                ||||| ||| ||||| |||||
                                CTCCA CTC AACGT CACTC
                                   C  _   T
GAM269  LOC81034  3' GCTCACTGCAACCTCCACCTC  47854     A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  LOC89231  3' GCTCACCGCAACCTTCCTCT  92732     TA     A
                                AGAGG  GAGGTTGC GTGAGC
                                |||||  |||||||| ||||||
                                TCTCC  TTCCAACG CACTCG
                                  __       C
GAM269  LOC89932  3' GCTCACTGCAACCTCCACCTC  60804     A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  LOC89932  3' GCTCACTGCAACCTCCGTCTC  60807    TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCT  CTCCAACGTCACTCG
                                   GC
GAM269  LOC90141  3' GCTCACTGCAACTTCCGCCTC  61629    TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTTCAACGTCACTCG
                                   GC
GAM269  LOC90288  3' CTCACTGCAACCTCCACCTC  62091     A
                                GAGGT GAGGTTGCAGTGAG
                                ||||| |||||||||||||
                                CTCCA CTCCAACGTCACTC
                                   C
GAM269  LOC90333  5' GCTCACTGCAACCTCCACTTC  62290     A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
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                                CTTCA CTCCAACGTCACTCG
                                   C
GAM269  LOC90333 3' GCTCACTGCAACCTCCTCCTC 62292     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  TC
GAM269  LOC90371 5' GCTCACTGCAACCTCCACCTC 62500      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  LOC90408 5' GCTCACTGCAACCTCTACCTC 62661
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCATCTCCAACGTCACTCG

GAM269  LOC90459 3' GCTCACTGCAACCTCCGCCTC 62890     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269  LOC90485 3' GCTCACTGCAACCTCCGCCTC 63020     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269  LOC90591 3' GCTCACTGCAAGCTCCACCTC 63434      A  G
                                GAGGT GAG TTGCAGTGAGC
                                ||||| ||| ||||||||||
                                CTCCA CTC AACGTCACTCG
                                   C  G
GAM269  LOC91035 5' ACTCAGCCTCCGACCCCT    64664    A  A_     C
                                AG GGT  GAGGTTG AGT
                                || |||  ||||||| |||
                                TC CCA  CTCCGAC TCA
                                 C  GC     _
GAM269  LOC91115 3' GCTCACTGCAACCTCCACCTC 64940      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  LOC91115 3' GCTCACTGCAACCTCCGCCTC 64942     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269  LOC91115 3' GCTCACTGCAACTTCTGCCTC 64944
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
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                                CTCCGTCTTCAACGTCACTCG

GAM269  LOC91291  5' GCTCACTGCAACCTCGACCTCT 65482       A
                                AGAGGT GAGGTTGCAGTGAGC
                                |||||| ||||||||||||||||
                                TCTCCA CTCCAACGTCACTCG
                                   G
GAM269  LOC91308  3' CTGCAACCTCCACCTC      65559      A
                                GAGGT GAGGTTGCAG
                                ||||| ||||||||||
                                CTCCA CTCCAACGTC
                                   C
GAM269  LOC91373  3' GCTCACTGCAACCTCCAGGCC  65841     A__
                                GGT   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||||
                                CCG   CTCCAACGTCACTCG
                                  GAC
GAM269  LOC91561  5' GCTCACTGCAAGCTCCGCCTC  66452     TA   G
                                GAGG  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCG
                                   GC   G
GAM269  LOC92267  3' GCTCACTGCAACCTCCACCTC  68618      A
                                GAGGT GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM269  LOC92283  3' GCTCACTGCAACCTCCGCC   68747    TA
                                GG  GAGGTTGCAGTGAGC
                                ||  ||||||||||||||
                                CC  CTCCAACGTCACTCG
                                  GC
GAM269  LOC92303  3' CTCACTGCAACCTCTGCCCT   68824    A
                                AG GGTAGAGGTTGCAGTGAG
                                || ||||||||||||||||||
                                TC CCGTCTCCAACGTCACTC
                                   _
GAM269  LOC92466  3' GCTCACTGCAACCTCCGCCTC  69430     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                   GC
GAM269  LOC92661  5' GCTCACTGCAAGCTCCACCTC  70082      A   G
                                GAGGT GAG TTGCAGTGAGC
                                ||||| ||| ||||||||||
                                CTCCA CTC AACGTCACTCG
                                   C   G
GAM269  LOC92689  3' GCTCACTGCAACCTCCGCCTC  70224     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
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                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  LOC92697  5'  GCTCACCGCAACCTCCGCCTC  70275     TA       A
                                GAGG  GAGGTTGC GTGAGC
                                ||||  |||||||| ||||||
                                CTCC  CTCCAACG CACTCG
                                  GC       C
GAM269  LOC92841  3'  GCTCACCGCAACCTCCTCCTC  70711     TA       A
                                GAGG  GAGGTTGC GTGAGC
                                ||||  |||||||| ||||||
                                CTCC  CTCCAACG CACTCG
                                  TC       C
GAM269  LOC92841  3'  GCTCACTGCAAGCTCTGCCTC  70712         G
                                GAGGTAGAG TTGCAGTGAGC
                                |||||||||  ||||||||||
                                CTCCGTCTC AACGTCACTCG
                                     G
GAM269  LOC93129  3'  GCTCACTGCAAGCACTGCCTC  71465        AG  _
                                GAGGTAG  GTT GCAGTGAGC
                                |||||||  ||| |||||||||
                                CTCCGTC  CGA CGTCACTCG
                                   A_  A
GAM269  LOC93132  5'  GCTCACTGCAACCTCCGCCTC  71491     TA
                                GAGG  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                CTCC  CTCCAACGTCACTCG
                                  GC
GAM269  LOC93320  3'  GCCCACTGCAGCTGCC      72052     AGA        A
                                GGT   GGTTGCAGTG GC
                                |||   |||||||||| ||
                                CCG   TCGACGTCAC CG
                                  ____         C
GAM269  LOC93349  3'  GCTCACTGCAACCTCTGCCTC  56461
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM269  LOC93408  5'  GCTCACTGCAACCTCTGCCTC  56480
                                GAGGTAGAGGTTGCAGTGAGC
                                |||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCG

GAM270  AMPD3     3'  CTGGATTTCCTTATTCC     4897      CTA   A
                                GGA   GAG GAAATCCAG
                                |||   ||| |||||||||
                                CCT   TTC CTTTAGGTC
                                  TA_  _
GAM270  CDK10     3'  CTGAGCTGGATCCCTGCTC    13401     _  AA
                                GAG AG  ATCCAGCTCAG
                                ||| ||  ||||||||||
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                                CTC TC  TAGGTCGAGTC
                                  G  CC
GAM270  CDK10   3'  CTGAGCTGGATCCCTGCTC   53768    _ AA
                                GAG AG  ATCCAGCTCAG
                                ||| ||  ||||||||||
                                CTC TC  TAGGTCGAGTC
                                  G  CC
GAM270  CDK10   3'  CTGAGCTGGATCCCTGCTC   53777    _ AA
                                GAG AG  ATCCAGCTCAG
                                ||| ||  ||||||||||
                                CTC TC  TAGGTCGAGTC
                                  G  CC
GAM270  CLTCL1  3'  CTGAGCTGGCCATCCTCTACTC 63671    C    A  AAT
            C                    GGA TAGAG GA   CCAGCTCAG
                                ||| ||||| ||   ||||||||
                                CCT ATCTC CT   GGTCGAGTC
                                  C    _ ACC
GAM270  MCL1    3'  CTGAACTCTTTCTAGCC    41717    A       AATC
                                GG CTAGAGAGA    CAG
                                || |||||||||    |||
                                CC GATCTTTCT    GTC
                                 _       CAA_
GAM270  MDM1    3'  CTGAGCTGACTTCTACCTAGCC 39271    A   AG   ATC
                                GG CTAG  AGAA   CAGCTCAG
                                || ||||  ||||   ||||||||
                                CC GATC  TCTT   GTCGAGTC
                                 _   CA   CA_
GAM270  PML     3'  CTGAGCTGCCTCCTCCAGCCC  52661    A  A   A  AATC
                                GG CT GAG GA    CAGCTCAG
                                || || ||| ||    ||||||||
                                CC GA CTC CT    GTCGAGTC
                                 C  C   _ CC__
GAM270  PML     3'  CTGAGCTGCCTCCTCCAGCCC  52667    A  A   A  AATC
                                GG CT GAG GA    CAGCTCAG
                                || || ||| ||    ||||||||
                                CC GA CTC CT    GTCGAGTC
                                 C  C   _ CC__
GAM270  PML     3'  CTGAGCTGCCTCCTCCAGCCC  52673    A  A   A  AATC
                                GG CT GAG GA    CAGCTCAG
                                || || ||| ||    ||||||||
                                CC GA CTC CT    GTCGAGTC
                                 C  C   _ CC__
GAM270  SHOX    3'  TGAGCTGAACTGTAGATCC   4839     _  G  AGAAATC
                                GGA CTA AG      CAGCTCA
                                ||| ||| ||      |||||||
                                CCT GAT TC      GTCGAGT
                                  A  G  AA_____
GAM270  TRPM1   5'  CTGAGCTGTGCCCTCTCCATTC 10057    CTA    AAATC
            C                    GGA   GAGAG    CAGCTCAG
                                |||   |||||    ||||||||
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                                CCT   CTCTC    GTCGAGTC
                                  TAC    CCGT_
GAM270  ELOVL1    5' GGACTTCTCTCTGGCC     43062    A        A
                                GG CTAGAGAGAA TCC
                                || |||||||||| |||
                                CC GGTCTCTCTT AGG
                                  _        C
GAM270  FLJ20296  5' CTGACGCGTTTCTCTCCATTCC 34890     CTA       CCA _
                                GGA   GAGAGAAAT   GC TCAG
                                |||   |||||||||   || ||||
                                CCT   CTCTCTTTG   CG AGTC
                                  TAC        ___ C
GAM270  FLJ20721  3' GACTTCTCTCTAGTGC     35609   G        A
                                G ACTAGAGAGAA TC
                                | ||||||||||| ||
                                C TGATCTCTCTT AG
                                 G          C
GAM270  KIAA0265  3' AGCGACCTCTTCTCTAGTCC   69874          _ AA  CA
                                GGACTAGAGA GA  TC  GCT
                                |||||||||| ||  ||  |||
                                CCTGATCTCT CT  AG  CGA
                                      T  CC  __
GAM270  KIAA0285  3' GCTAGATGCCCTCTCTAGTCC  29018          AA_   C
                                GGACTAGAGAG   ATC AGC
                                ||||||||||   ||| |||
                                CCTGATCTCTC   TAG TCG
                                       CCG   A
GAM270  KIAA0820  3' CTGAGCTGAATCTTAAAAAGCC 69023    ACTAGA    AATC
                                GG     GAGA    CAGCTCAG
                                ||     ||||   ||||||||
                                CC     TTCT    GTCGAGTC
                                 GAAAAA    AA__
GAM270  KIAA1274  3' GGCATCTCTCTCTGTCC     91367      T      A _
                                GGAC AGAGAGA AT CC
                                |||| ||||||| || ||
                                CCTG TCTCTCT TA GG
                                  _      C  C
GAM270  KIAA1831  3' CTGAGCTGCTGTGGCTCCCTAG 63782    A   A   AA  C_
           CC                     GG CTAG GAG  AT  CAGCTCAG
                                || |||| |||  ||  ||||||||
                                CC GATC CTC  TG  GTCGAGTC
                                 _   C   GG  TC
GAM270  MGC2560   5' CTGAGCTGGATTGACATAGCC  48781    A   GAGAGA
                                GG CTA     AATCCAGCTCAG
                                || |||     ||||||||||||
                                CC GAT     TTAGGTCGAGTC
                                 _  ACAG__
GAM270  Rab11-FIP3 3' CTGAGCTGGATTCGGGACTC   28125     AGA__
                                GAG    AATCCAGCTCAG
                                |||    ||||||||||||
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                                CTC    TTAGGTCGAGTC
                                  AGGGC
GAM270  UGT2B10  3' CTGAGCTGGAGCCTCCATGCC 6541    ACTAGA  AAA
                                GG    GAG  TCCAGCTCAG
                                ||    |||  ||||||||||
                                CC    CTC  AGGTCGAGTC
                                 GTAC__  CG_
GAM270  LOC145815 5' GGATTTCTCCCTGACCC    83519   AC  A
                                GG  TAG GAGAAATCC
                                ||  ||| |||||||||
                                CC  GTC CTCTTTAGG
                                 CA  C
GAM270  LOC146745 5' TGAGCTGAGGCTGCAGTCC   78091     AG  AGAAATC
                                GGACT  AG     CAGCTCA
                                |||||  ||     |||||||
                                CCTGA  TC     GTCGAGT
                                   CG  GGA____
GAM270  LOC201243 5' TGAGCTGAGGCTGCAGTCC   88163     AG  AGAAATC
                                GGACT  AG     CAGCTCA
                                |||||  ||     |||||||
                                CCTGA  TC     GTCGAGT
                                   CG  GGA____
GAM270  LOC221929 3' CTGAGCTGGACTTCCTCCTCC 92675    CTA  A  A
                                GGA  GAG GAA TCCAGCTCAG
                                |||  ||| ||| ||||||||||
                                CCT  CTC CTT AGGTCGAGTC
                                  C__  _  C
GAM270  LOC51042  5' GAGCGCACTCTCTAGCC    31854    A      AAATCCA
                                GG CTAGAGAG     GCTC
                                || ||||||||     ||||
                                CC GATCTCTC     CGAG
                                 _      ACG____
GAM270  LOC56912  3' TGAGCTGGCCCCTCTGCC   39337    AC    AGAAAT
                                GG  TAGAG    CCAGCTCA
                                ||  |||||    ||||||||
                                CC  GTCTC    GGTCGAGT
                                 __    CCC___
GAM271  ADH1B    3' CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||  ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM271  ADH1B    3' CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||  ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM271  AHR      3' ATCTCAGATGTTAAAATAAATG 7875       CAC  C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
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                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM271  AHR     3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM271  FDFT1   3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM271  FDFT1   3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM271  JTB     3'  ATCTCAGACAGTGAAAGTGAAA 21959
           TG                     CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM271  JTB     3'  ATCTCAGACAGTGAAAGTGAAA 21959
           TG                     CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM271  KLF4    3'  TCCCAGACAGTGGATATG    14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM271  KLF4    3'  TCCCAGACAGTGGATATG    14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM271  PHYH    3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM271  PHYH    3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM271  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
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                                AAAGTGAAAGT  GGAC CT
                                     T__   _
GAM271  PKD2    3'  TCCAGGTTGAAAGTGAAA   60096        CTG   A
                                TTTCACTTTCA  TCTG GA
                                ||||||||||  |||| ||
                                AAAGTGAAAGT  GGAC CT
                                     T__   _
GAM271  WRN     3'  GGGCAGTGAAAATGAAA    5098      C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM271  WRN     3'  GGGCAGTGAAAATGAAA    5098      C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM271  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017       CA   CTG
                                TTTCACTTT  CTGT  AGAT
                                |||||||||  ||||  ||||
                                AAAGTGAAA  GACA  TCTA
                                     C_   CG_
GAM271  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017       CA   CTG
                                TTTCACTTT  CTGT  AGAT
                                |||||||||  ||||  ||||
                                AAAGTGAAA  GACA  TCTA
                                     C_   CG_
GAM271  CG012   5'  CTCACTCTGAAAGTGAA    83218       CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                     CT  __
GAM271  CG012   5'  CTCACTCTGAAAGTGAA    83218       CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                     CT  __
GAM271  EIF2C2  3'  ATCTTCTGAGAGTGAAAG   71946       G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM271  EIF2C2  3'  ATCTTCTGAGAGTGAAAG   71946       G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM271  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802      ACTTTCACT
           G                     CATTTC       GTCTGAGAT
                                ||||||       |||||||||
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                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM271  FLJ23462  3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
            G                    CATTTC       GTCTGAGAT
                                 ||||||       |||||||||
                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM271  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   |||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM271  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   |||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM271  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM271  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM271  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM271  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM271  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM271  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM271  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
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                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM271  PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                |||||||| || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM271  PP35     3' ATCTCAGACTGAAA      22814      CT
                                TTTCA  GTCTGAGAT
                                ||||| |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM271  PP35     3' ATCTCAGACTGAAA      22814      CT
                                TTTCA  GTCTGAGAT
                                ||||| |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM271  PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148       TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                |||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM271  PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148       TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                |||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM271  SEP15    3' TCCTACAGTAAGAGTGAAA   14934       C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM271  SEP15    3' TCCTACAGTAAGAGTGAAA   14934       C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM271  SFXN2    3' CTCAGGGGAAAAAAGTGAAA  73941       CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM271  SFXN2    3' CTCAGGGGAAAAAAGTGAAA  73941       CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM271  LOC149703 3' ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
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                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM271   LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM271   LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM271   LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM271   LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226     A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM271   LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226     A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM271   LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM271   LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM272   CHRNE    3'  CAAACACCTTCAGTGCTGG    3583     T        CA
                                CC GCACTGAAGG  TTTG
                                || ||||||||||  ||||
                                GG CGTGACTTCC  AAAC
                                  T         AC
GAM272   COG3     3'  GATTACAATAAGTAGTGCA    48698        AAGGCAT
                                TGCACTG      TTGTAATC
                                |||||||      ||||||||
                                ACGTGAT      AACATTAG
                                    GAAT___
GAM272   FANCC    5'  ACCATTTCCTTCAGTGCTGG   70517    T        CATTT
                                CC GCACTGAAGG     GT
                                || ||||||||||     ||
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                                GG CGTGACTTCC    CA
                                 T        TTTAC
GAM272  GABRP    3'  ATTACAAATGTACTCAG     26398     AG
                                CTGA  GCATTTGTAAT
                                ||||  ||||||||||
                                GACT  TGTAAACATTA
                                  CA
GAM272  JAG2     3'  ACAAGTGCCTTCACACAG    9466     CAC
                                CTG   TGAAGGCATTTGT
                                |||   |||||||||||||
                                GAC   ACTTCCGTGAACA
                                 AC_
GAM272  KIF3B    3'  TGCCTGCCTTCAGCAG      16613     AC      TTT
                                CTGC  TGAAGGCA   GTA
                                ||||  ||||||||   |||
                                GACG  ACTTCCGT   CGT
                                  __       C__
GAM272  MAML1    3'  ATTATTTCCCTAAGTGCAGG  28588        GA   CATTT
                                CCTGCACT  AGG    GTAAT
                                ||||||||  |||    |||||
                                GGACGTGA  TCC    TATTA
                                    A_   CTT__
GAM272  MATN2    3'  GATTACAATGAACGCAGTGCAG 9931         AAGG    T
                                CTGCACTG    CATT GTAATC
                                ||||||||    |||| ||||||
                                GACGTGAC    GTAA CATTAG
                                    GCAA    _
GAM272  MITF     3'  TACAAATGCCTCCAAAGTA   4199     AC  A
                                TGC  TG AGGCATTTGTA
                                |||  || ||||||||||
                                ATG  AC TCCGTAAACAT
                                 AA  C
GAM272  MSR1     3'  TGCAAACATCTTCAGTGCAG  56954          CA
                                CTGCACTGAAGG  TTTGTA
                                ||||||||||||  ||||||
                                GACGTGACTTCT  AAACGT
                                      AC
GAM272  MSR1     3'  TGCAAACATCTTCAGTGCAG  56962          CA
                                CTGCACTGAAGG  TTTGTA
                                ||||||||||||  ||||||
                                GACGTGACTTCT  AAACGT
                                      AC
GAM272  NR3C2    3'  ACACCTGCCTTAGTGCA     6130         A    TT
                                TGCACTGA GGCA  TGT
                                ||||||||  ||||  |||
                                ACGTGATT CCGT  ACA
                                    _    CC
GAM272  NR5A2    3'  TACAAACTTTCAAAGCA     13791     AC     CA
                                TGC  TGAAGG  TTTGTA
                                |||  ||||||  ||||||
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                                ACG  ACTTTC  AAACAT
                                  AA     __
GAM272  PIN1L    3'  TGGGTGCCTTCAGCAAAGG   20625     GCA        TT
                                CCT   CTGAAGGCAT  G
                                |||   ||||||||||  |
                                GGA   GACTTCCGTG  T
                                  AAC         GG
GAM272  RAI3     3'  ATCACAGCCCAGTGCAG     14282         AA   ATT   A
                                CTGCACTG  GGC   TGT AT
                                ||||||||  |||   ||| ||
                                GACGTGAC  CCG   ACA TA
                                    __   ___   C
GAM272  UBE2B    3'  TACATAACTTCAGTGCA     12476          GCATT
                                TGCACTGAAG    TGTA
                                ||||||||||    ||||
                                ACGTGACTTC    ACAT
                                      AAT__
GAM272  UBL3     3'  ATTACAAATATGTGTAG     23030       TGAAGGC
                                CTGCAC      ATTTGTAAT
                                ||||||      |||||||||
                                GATGTG      TAAACATTA
                                   TA_____
GAM272  UPF3B    3'  AGGTGCCTTCAGGGCA      43452     A
                                TGC CTGAAGGCATTT
                                ||| ||||||||||||
                                ACG GACTTCCGTGGA
                                  G
GAM272  UPF3B    3'  AGGTGCCTTCAGGGCA      54660     A
                                TGC CTGAAGGCATTT
                                ||| ||||||||||||
                                ACG GACTTCCGTGGA
                                  G
GAM272  XK       3'  AAATGCCTTCAGCTCAGG    40796     CA
                                CCTG  CTGAAGGCATTT
                                ||||  ||||||||||||
                                GGAC  GACTTCCGTAAA
                                  TC
GAM272  AQP9     3'  TGCACCTTCAGTCA        40609    C      CATT
                                TG ACTGAAGG    TGTA
                                || ||||||||    ||||
                                AC TGACTTCC    ACGT
                                _      _____
GAM272  b5&b5R   3'  CAAATGTTCCTTCAGTACAGG  32649      C       __
                                CCTG ACTGAAGG  CATTTG
                                |||| ||||||||  ||||||
                                GGAC TGACTTCC  GTAAAC
                                  A       TT
GAM272  C1orf34  3'  ATTCAGCTGCCTTCAG      60663         T   T
                                CTGAAGGCA TTG AAT
                                ||||||||| ||| |||
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                                GACTTCCGT GAC TTA
                                     C  _
GAM272  C1QR1    3' ATTACAAGATTTCTATGCAGG 23836      CT   GCAT
                                CCTGCA GAAG   TTGTAAT
                                |||||| ||||   |||||||
                                GGACGT CTTT   AACATTA
                                   AT   AG__
GAM272  C5orf6   3' GATTACAAATACAAAAAGTG  33481     GAAGGC
                                CACT     ATTTGTAATC
                                ||||     ||||||||||
                                GTGA     TAAACATTAG
                                  AAAACA
GAM272  DKFZP566K0524 3' GATTACAGAGCCCAATAAAGG 69352     GCAC  AA  A
                                CCT   TG  GGC TTTGTAATC
                                |||   ||  ||| |||||||||
                                GGA   AC  CCG AGACATTAG
                                 AATA  __  _
GAM272  FLJ13491 3' ACACTTACCTCCAGGGCAGG  44883      A  A  CATT
                                CCTGC CTG AGG   TGT
                                ||||| ||| |||   |||
                                GGACG GAC TCC   ACA
                                   G  C  ATTC
GAM272  FLJ14251 3' TGCGTTGCCTGCAGTGCAG   45978       A   TT
                                CTGCACTG AGGCA  TGTA
                                |||||||| |||||  ||||
                                GACGTGAC TCCGT  GCGT
                                     G   T_
GAM272  GADD45A  3' ATTACAAAGAACCATGCAGG  8627       CTGAA  CA_
                                CCTGCA   GG  TTTGTAAT
                                ||||||   ||  ||||||||
                                GGACGT   CC  AAACATTA
                                   A____  AAG
GAM272  HSPC023  3' ACGCTGGCCCCAGTGCAGG   25907       AA  ATT
                                CCTGCACTG  GGC  TGT
                                |||||||||  |||  |||
                                GGACGTGAC  CCG  GCA
                                     C_  GTC
GAM272  HT002    3' TACAAATGCGGGGGCCAGG   25946     CA  GAAG
                                CCTG  CT   GCATTTGTA
                                ||||  ||   |||||||||
                                GGAC  GG   CGTAAACAT
                                  CG  GG__
GAM272  IDI2     3' AATGCCCTCAGTGCAGG     52694         A
                                CCTGCACTGA GGCATT
                                |||||||||| ||||||
                                GGACGTGACT CCGTAA
                                      C
GAM272  KIAA0052 3' TACAAATGCCTGCAAGT    67834     GA_
                                ACT   AGGCATTTGTA
                                |||   ||||||||||
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                              TGA   TCCGTAAACAT
                                ACG
GAM272  KIAA0471 3' ATTACAAATGAGTGT      29386      GAAGG
                              GCACT    CATTTGTAAT
                              |||||    ||||||||||
                              TGTGA    GTAAACATTA
                                  _____
GAM272  KIAA1946 3' GATTACAAATGTTGAGG     82471    GAA
                              CT   GGCATTTGTAATC
                              ||   |||||||||||||
                              GG   TTGTAAACATTAG
                               AG_
GAM272  MGC10818 3' ACAAGTGCCCTCAGCAAG    47533    GCA   A
                              CT   CTGA GGCATTTGT
                              ||   |||| |||||||||
                              GA   GACT CCGTGAACA
                               AC_   C
GAM272  MGC11257 3' AGTGCCTTCAGCGCAG      50370     A
                              CTGC CTGAAGGCATT
                              |||| ||||||||||
                              GACG GACTTCCGTGA
                                C
GAM272  MGC11324 3' ATTACACATCAGTGCA      51165       AGGCATT
                              TGCACTGA     TGTAAT
                              ||||||||     ||||||
                              ACGTGACT     ACATTA
                                   AC_____
GAM272  MGC11386 3' ACACTGCTTTCAGTGCA     51946          TT
                              TGCACTGAAGGCA  TGT
                              ||||||||||||  |||
                              ACGTGACTTTCGT  ACA
                                     C_
GAM272  MGC14433 3' TACAAAGCCAGTGCAG      51869       GAA   A
                              CTGCACT   GGC TTTGTA
                              |||||||   ||| ||||||
                              GACGTGA   CCG AAACAT
                                  ___   _
GAM272  MGC3207  3' ACACTTGTTCCTAGTGCAGG  62556        AA   TT
                              CCTGCACTG  GGCA  TGT
                              |||||||||  ||||  |||
                              GGACGTGAT  TTGT  ACA
                                   CC    TC
GAM272  MGC4268  3' TATATGGCCTTCAGTGCA    48747          ATT
                              TGCACTGAAGGC   TGTA
                              ||||||||||||   ||||
                              ACGTGACTTCCG   ATAT
                                     GT_
GAM272  OSBPL5   3' GCCCATGCCCTCGGTGCAGG  72686         A    TT
                              CCTGCACTGA GGCAT  GT
                              |||||||||| |||||  ||
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                                GGACGTGGCT CCGTA  CG
                                      C    CC
GAM272  SLC11A2   3'  ATGGGTGTCTTCAGCACA    5233    CA       TG
                                TG  CTGAAGGCATT  T
                                ||  ||||||||||  |
                                AC  GACTTCTGTGG  A
                                 AC        GT
GAM272  LOC144559 5'  AATGCCACTCAGTGCA     76878       A_
                                TGCACTGA  GGCATT
                                ||||||||  ||||||
                                ACGTGACT  CCGTAA
                                    CA
GAM272  LOC154792 3'  ATATACTCCTTCAGTGCAGG  86248         CATT
                                CCTGCACTGAAGG   TGT
                                ||||||||||||   |||
                                GGACGTGACTTCC   ATA
                                       TCAT
GAM272  LOC157292 5'  ATTACAAAGTATCAGCCAGG  86410    CA   AG  A
                                CCTG  CTGA  GC TTTGTAAT
                                ||||  ||||  || ||||||||
                                GGAC  GACT  TG AAACATTA
                                  C_   A_  _
GAM272  LOC164832 3'  ACACCATTGTTCAGTGCAGG  82452       AG   TT__
                                CCTGCACTGA  GCA   TGT
                                ||||||||||  |||   |||
                                GGACGTGACT  TGT   ACA
                                      __   TACC
GAM272  LOC200014 5'  ACACTGAACCTCCAGTGCAG  88514       A   CATT_
                                CTGCACTG AGG    TGT
                                ||||||||| |||    |||
                                GACGTGAC TCC    ACA
                                    C   AAGTC
GAM272  LOC200830 3'  TACAAATGACCTATACAG    90149    A__  _
                                CTG   AGG CATTTGTA
                                |||   ||| ||||||||
                                GAC   TCC GTAAACAT
                                  ATA   A
GAM272  LOC206327 5'  ACTCTGCCTCTAGTGCAG    90716       A    TTT
                                CTGCACTG AGGCA   GT
                                |||||||| |||||   ||
                                GACGTGAT TCCGT   CA
                                    C    CT_
GAM272  LOC221895 3'  AAATACTTCAGTGCA      92520        GC
                                TGCACTGAAG  ATTT
                                ||||||||||  ||||
                                ACGTGACTTC  TAAA
                                      A_
GAM272  LOC254531 5'  CAGGAGCCTTCATCGCAGG   94983      AC     A
                                CCTGC  TGAAGGC TTTG
                                |||||  ||||||| ||||
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                                GGACG  ACTTCCG GGAC
                                  CT       A
GAM272  LOC91801  3'  ACAGTGATACCTCAGTGCAG   57073         A  C   __
                                CTGCACTGA GG ATT  TGT
                                ||||||||| || |||  |||
                                GACGTGACT CC TAG  ACA
                                     _  A   TG
GAM273  AOAH      5'  ACAGACTCCCTCCAGCTCT   91114     AA    A  A  A
                                AGA  TGGAG GA GT TGT
                                |||  ||||| || || |||
                                TCT  ACCTC CT CA ACA
                                  CG    C  _  G
GAM273  AOAH      5'  ACAGACTCCCTCCAGCTCT   91114     AA    A  A  A
                                AGA  TGGAG GA GT TGT
                                |||  ||||| || || |||
                                TCT  ACCTC CT CA ACA
                                  CG    C  _  G
GAM273  CCND2     3'  ATACTCCTCCCCTCTTCT    8286      AT  A   A
                                AGAA  GG GAG AGTAT
                                ||||  || ||| |||||
                                TCTT  CC CTC TCATA
                                  CT  C   C
GAM273  CCND2     3'  ATACTCCTCCCCTCTTCT    8286      AT  A   A
                                AGAA  GG GAG AGTAT
                                ||||  || ||| |||||
                                TCTT  CC CTC TCATA
                                  CT  C   C
GAM273  CD209     3'  ACAGTTCCTTCTCTCCAT    40956         TA__
                                ATGGAGAGAAG   TGT
                                ||||||||||    |||
                                TACCTCTCTTC   ACA
                                     CTTG
GAM273  CD209     3'  ACAGTTCCTTCTCTCCAT    40956         TA__
                                ATGGAGAGAAG   TGT
                                ||||||||||    |||
                                TACCTCTCTTC   ACA
                                     CTTG
GAM273  CD209L    3'  GCGCTTCTTCTCTCCAT     26520         TATGTA
                                ATGGAGAGAAG    CGC
                                ||||||||||     |||
                                TACCTCTCTTC    GCG
                                     TTC___
GAM273  CD209L    3'  GCGCTTCTTCTCTCCAT     26520         TATGTA
                                ATGGAGAGAAG    CGC
                                ||||||||||     |||
                                TACCTCTCTTC    GCG
                                     TTC___
GAM273  CHRNB4    3'  CATCTCTCTCCACTTC      5628      A      A T
                                GAA TGGAGAGA G ATG
                                ||| |||||||| | |||
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                                CTT ACCTCTCT C TAC
                                  C       _ _
GAM273  CHRNB4   3'  CATCTCTCTCCACTTC      5628      A       A T
                                GAA TGGAGAGA G ATG
                                ||| |||||||| | |||
                                CTT ACCTCTCT C TAC
                                  C       _ _
GAM273  CXCR4    3'  GCATAGATAATCTCTCCATT   12951          AG   G  C
                                AATGGAGAGA  TAT TA GC
                                ||||||||||  ||| || ||
                                TTACCTCTCT  ATA AT CG
                                      A_   G  A
GAM273  CXCR4    3'  GCATAGATAATCTCTCCATT   12951          AG   G  C
                                AATGGAGAGA  TAT TA GC
                                ||||||||||  ||| || ||
                                TTACCTCTCT  ATA AT CG
                                      A_   G  A
GAM273  DDOST    3'  ACTCCTCTCATTTCT       17815        G    A
                                AGAAATG AGAG AGT
                                ||||||| |||| |||
                                TCTTTAC TCTC TCA
                                   _    C
GAM273  DDOST    3'  ACTCCTCTCATTTCT       17815        G    A
                                AGAAATG AGAG AGT
                                ||||||| |||| |||
                                TCTTTAC TCTC TCA
                                   _    C
GAM273  DTNB     3'  GCACATTCCTCTCCATCTTT   52502      A       A   A
                                AGA ATGGAGAG AGT TGT
                                ||| |||||||| ||| |||
                                TTT TACCTCTC TTA ACG
                                  C       C   C
GAM273  DTNB     3'  GCACATTCCTCTCCATCTTT   52502      A       A   A
                                AGA ATGGAGAG AGT TGT
                                ||| |||||||| ||| |||
                                TTT TACCTCTC TTA ACG
                                  C       C   C
GAM273  DTNB     3'  GCACATTCCTCTCCATCTTT   41580      A       A   A
                                AGA ATGGAGAG AGT TGT
                                ||| |||||||| ||| |||
                                TTT TACCTCTC TTA ACG
                                  C       C   C
GAM273  DTNB     3'  GCACATTCCTCTCCATCTTT   41580      A       A   A
                                AGA ATGGAGAG AGT TGT
                                ||| |||||||| ||| |||
                                TTT TACCTCTC TTA ACG
                                  C       C   C
GAM273  GCK      3'  ACATGCCACCCTCTCCAT     53170        AA__
                                ATGGAGAG    GTATGT
                                ||||||||    ||||||
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                              TACCTCTC  CGTACA
                                  CCAC
GAM273  GCK     3'  ACATGCCACCCTCTCCAT  53170      AA__
                              ATGGAGAG  GTATGT
                              ||||||||  ||||||
                              TACCTCTC  CGTACA
                                  CCAC
GAM273  GCK     3'  ACATGCCACCCTCTCCAT  53175      AA__
                              ATGGAGAG  GTATGT
                              ||||||||  ||||||
                              TACCTCTC  CGTACA
                                  CCAC
GAM273  GCK     3'  ACATGCCACCCTCTCCAT  53175      AA__
                              ATGGAGAG  GTATGT
                              ||||||||  ||||||
                              TACCTCTC  CGTACA
                                  CCAC
GAM273  GCK     3'  ACATGCCACCCTCTCCAT  3863       AA__
                              ATGGAGAG  GTATGT
                              ||||||||  ||||||
                              TACCTCTC  CGTACA
                                  CCAC
GAM273  GCK     3'  ACATGCCACCCTCTCCAT  3863       AA__
                              ATGGAGAG  GTATGT
                              ||||||||  ||||||
                              TACCTCTC  CGTACA
                                  CCAC
GAM273  GORASP1  3'  GTGTACTTGCCCCCATCTCC  49113     GAA__  T
                              GGAGA   GTA GTACGC
                              |||||   ||| ||||||
                              CCTCT   CGT CATGTG
                                 ACCCC  T
GAM273  GORASP1  3'  GTGTACTTGCCCCCATCTCC  49113     GAA__  T
                              GGAGA   GTA GTACGC
                              |||||   ||| ||||||
                              CCTCT   CGT CATGTG
                                 ACCCC  T
GAM273  GSPT1    5'  CGCCCCTGCCTCCATTTCT  9141       AGAA  TGTA
                              AGAAATGGAG  GTA  CG
                              ||||||||||  |||  ||
                              TCTTTACCTC  CGT  GC
                                    ____  CCCC
GAM273  GSPT1    5'  CGCCCCTGCCTCCATTTCT  9141       AGAA  TGTA
                              AGAAATGGAG  GTA  CG
                              ||||||||||  |||  ||
                              TCTTTACCTC  CGT  GC
                                    ____  CCCC
GAM273  HCN4     3'  ACGTTCTCTCTCCAGTCCT  18487   AAA     A T
                              AG  TGGAGAGA G ATGT
                              ||  |||||||| | ||||
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                                TC   ACCTCTCT C TGCA
                                 CTG       _ T
GAM273   HCN4     3'  ACGTTCTCTCTCCAGTCCT   18487    AAA       A T
                                AG   TGGAGAGA G ATGT
                                ||   |||||||| | ||||
                                TC   ACCTCTCT C TGCA
                                 CTG       _ T
GAM273   HRB      3'  ACATTACATCTCTCCACCTCT  15703     AA       A  _
                                AGA  TGGAGAGA GTA TGT
                                |||  |||||||| ||| |||
                                TCT  ACCTCTCT CAT ACA
                                  CC       A   T
GAM273   HRB      3'  ACATTACATCTCTCCACCTCT  15703     AA       A  _
                                AGA  TGGAGAGA GTA TGT
                                |||  |||||||| ||| |||
                                TCT  ACCTCTCT CAT ACA
                                  CC       A   T
GAM273   IL2RB    3'  GCACACTTGGTCCATCCATTTC 6071         GA ___   A
                                GAAATGGA  GA   AGT TGT
                                ||||||||  ||   ||| |||
                                CTTTACCT  CT   TCA ACG
                                     AC  GGT   C
GAM273   IL2RB    3'  GCACACTTGGTCCATCCATTTC 6071         GA ___   A
                                GAAATGGA  GA   AGT TGT
                                ||||||||  ||   ||| |||
                                CTTTACCT  CT   TCA ACG
                                     AC  GGT   C
GAM273   KCNJ5    3'  GCATCTGTTCTCTCCAT     6092          GT_
                                ATGGAGAGAA   ATGT
                                ||||||||||   ||||
                                TACCTCTCTT   TACG
                                      GTC
GAM273   KCNJ5    3'  GCATCTGTTCTCTCCAT     6092          GT_
                                ATGGAGAGAA   ATGT
                                ||||||||||   ||||
                                TACCTCTCTT   TACG
                                      GTC
GAM273   KLF7     5'  GCTGGATGCCTCTCTCCAT   13542         A   G  C
                                ATGGAGAGA GTAT TA GC
                                ||||||||| |||| || ||
                                TACCTCTCT CGTA GT CG
                                     C   G  _
GAM273   KLF7     5'  GCTGGATGCCTCTCTCCAT   13542         A   G  C
                                ATGGAGAGA GTAT TA GC
                                ||||||||| |||| || ||
                                TACCTCTCT CGTA GT CG
                                     C   G  _
GAM273   LRP1     3'  GCACAGTATTATTTCTCCAT  9803          _   GTAC
                                ATGGAGAGA AGTAT   GC
                                |||||||| |||||   ||
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                                TACCTCTTT TTATG   CG
                                     A    ACA_
GAM273  LRP1    3'  GCACAGTATTATTTCTCCAT  9803        _   GTAC
                                ATGGAGAGA AGTAT   GC
                                ||||||||| |||||   ||
                                TACCTCTTT TTATG   CG
                                     A    ACA_
GAM273  MAP1A   3'  GCACCCTTTCCTCCATTTC   9898       AG  TA
                                GAAATGGAG  AAG  TGT
                                |||||||||  |||  |||
                                CTTTACCTC  TTC  ACG
                                     CT   CC
GAM273  MAP1A   3'  GCACCCTTTCCTCCATTTC   9898       AG  TA
                                GAAATGGAG  AAG  TGT
                                |||||||||  |||  |||
                                CTTTACCTC  TTC  ACG
                                     CT   CC
GAM273  MYD88   3'  ACAGCTGTTCTCTCCCTCTCT  10160    AAT     GTA_
                                AGA  GGAGAGAA   TGT
                                |||  ||||||||   |||
                                TCT  CCTCTCTT   ACA
                                  CTC      GTCG
GAM273  MYD88   3'  ACAGCTGTTCTCTCCCTCTCT  10160    AAT     GTA_
                                AGA  GGAGAGAA   TGT
                                |||  ||||||||   |||
                                TCT  CCTCTCTT   ACA
                                  CTC      GTCG
GAM273  MYL3    5'  GCATTCTTCTCTCCACATC   63900    AA      T
                                GA  TGGAGAGAAG ATGT
                                ||  |||||||||| ||||
                                CT  ACCTCTCTTC TACG
                                  AC       T
GAM273  MYL3    5'  GCATTCTTCTCTCCACATC   63900    AA      T
                                GA  TGGAGAGAAG ATGT
                                ||  |||||||||| ||||
                                CT  ACCTCTCTTC TACG
                                  AC       T
GAM273  OPRM1   3'  GCATCATTTTCACCTCCATTTC 6202        A_  T  TAC
          T                      AGAAATGGAG  GAAG ATG  GC
                                 |||||||||  |||| |||  ||
                                 TCTTTACCTC  CTTT TAC  CG
                                      CA   _  TA_
GAM273  OPRM1   3'  GCATCATTTTCACCTCCATTTC 6202        A_  T  TAC
          T                      AGAAATGGAG  GAAG ATG  GC
                                 |||||||||  |||| |||  ||
                                 TCTTTACCTC  CTTT TAC  CG
                                      CA   _  TA_
GAM273  PLP2    3'  GCGAACTTCCCTCATTTCT   10652      G  A   A
                                AGAAATG AG GAAGT TGT
                                ||||||| || ||||| |||
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                                TCTTTAC TC CTTCA GCG
                                   _ C    A
GAM273  PLP2    3'  GCGAACTTCCCTCATTTCT   10652       G  A    A
                                AGAAATG AG GAAGT TGT
                                ||||||| || ||||| |||
                                TCTTTAC TC CTTCA GCG
                                   _ C    A
GAM273  POLG    5'  ACGTGTCTCTCTCCACGTCT  10677    AA      AG
                                AGA  TGGAGAGA  TATGT
                                |||  ||||||||  |||||
                                TCT  ACCTCTCT  GTGCA
                                  GC       CT
GAM273  POLG    5'  ACGTGTCTCTCTCCACGTCT  10677    AA      AG
                                AGA  TGGAGAGA  TATGT
                                |||  ||||||||  |||||
                                TCT  ACCTCTCT  GTGCA
                                  GC       CT
GAM273  PTTG1IP  3'  GCTGCAGCTCTCTCCAGCCCT  15092   AAA      A  A   C
                                AG   TGGAGAGA GT TGTA GC
                                ||   |||||||| || |||| ||
                                TC   ACCTCTCT CG ACGT CG
                                 CCG       _ _   _
GAM273  PTTG1IP  3'  GCTGCAGCTCTCTCCAGCCCT  15092   AAA      A  A   C
                                AG   TGGAGAGA GT TGTA GC
                                ||   |||||||| || |||| ||
                                TC   ACCTCTCT CG ACGT CG
                                 CCG       _ _   _
GAM273  SERPINB6 3'  GCAGCCCCTCTCCTCTCT   15878    AAT    AA  A
                                AGA   GGAGAG  GT TGT
                                |||   ||||||  || |||
                                TCT   CCTCTC  CG ACG
                                  CT_     CC  _
GAM273  SERPINB6 3'  GCAGCCCCTCTCCTCTCT   15878    AAT    AA  A
                                AGA   GGAGAG  GT TGT
                                |||   ||||||  || |||
                                TCT   CCTCTC  CG ACG
                                  CT_     CC  _
GAM273  SFN     3'  GCTACTTCTCCCCTCCTCT   74561    AAT  A      T
                                AGA   GG GAGAAGTA GT
                                |||   || ||||||||  ||
                                TCT   CC CTCTTCAT CG
                                  CCT  C       _
GAM273  SFN     3'  GCTACTTCTCCCCTCCTCT   74561    AAT  A      T
                                AGA   GG GAGAAGTA GT
                                |||   || ||||||||  ||
                                TCT   CC CTCTTCAT CG
                                  CCT  C       _
GAM273  SLC16A2  3'  ACTTCTCTCCATACTCT    21499    A_
                                AGA  ATGGAGAGAAGT
                                |||  ||||||||||||
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                                TCT  TACCTCTCTTCA
                                  CA
GAM273  SLC16A2  3'  ACTTCTCTCCATACTCT     21499     A_
                                AGA  ATGGAGAGAAGT
                                |||  ||||||||||||
                                TCT  TACCTCTCTTCA
                                  CA
GAM273  SLC7A8   3'  ACACACCCCTCTCTCTGCTTTT 24273      AT      A__  A
                                AGAA  GGAGAGA   GT TGT
                                ||||  |||||||   || |||
                                TTTT  TCTCTCT   CA ACA
                                  CG      CCC  C
GAM273  SLC7A8   3'  ACACACCCCTCTCTCTGCTTTT 24273      AT      A__  A
                                AGAA  GGAGAGA   GT TGT
                                ||||  |||||||   || |||
                                TTTT  TCTCTCT   CA ACA
                                  CG      CCC  C
GAM273  ACAS2L   3'  GCATTGCCATCTCCATTCCT   68075    A      GAAGT
                                AG AATGGAGA     ATGT
                                || ||||||||     ||||
                                TC TTACCTCT     TACG
                                 C       ACCGT
GAM273  ACAS2L   3'  GCATTGCCATCTCCATTCCT   68075    A      GAAGT
                                AG AATGGAGA     ATGT
                                || ||||||||     ||||
                                TC TTACCTCT     TACG
                                 C       ACCGT
GAM273  APOA5    3'  GCATACTGTGTGCTCTCCCCAT 53729    A   A   _______
           CTC                    GA ATGG GAGA      AGTATGT
                                || |||| ||||      |||||||
                                CT TACC CTCT      TCATACG
                                 C   C    CGTGTG
GAM273  APOA5    3'  GCATACTGTGTGCTCTCCCCAT 53729    A   A   _______
           CTC                    GA ATGG GAGA      AGTATGT
                                || |||| ||||      |||||||
                                CT TACC CTCT      TCATACG
                                 C   C    CGTGTG
GAM273  ATP9A    3'  TATTTCTCCCCCTTCT      62051      AT  A
                                AGAA  GG GAGAAGTA
                                ||||  || ||||||||
                                TCTT  CC CTCTTTAT
                                  CC  _
GAM273  ATP9A    3'  TATTTCTCCCCCTTCT      62051      AT  A
                                AGAA  GG GAGAAGTA
                                ||||  || ||||||||
                                TCTT  CC CTCTTTAT
                                  CC  _
GAM273  BBX      5'  GCGAGCTTCTCTCCACTTTC   39589      _         A
                                GAAA TGGAGAGAAGT TGT
                                |||| |||||||||| |||
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                                CTTT ACCTCTCTTCG GCG
                                  C         A
GAM273  BBX      5'  GCGAGCTTCTCTCCACTTTC  39589     _         A
                                GAAA TGGAGAGAAGT TGT
                                |||| |||||||||| |||
                                CTTT ACCTCTCTTCG GCG
                                  C         A
GAM273  CLSTN3   5'  ACTTCTCTCCTTTCT      28203      T
                                AGAAA GGAGAGAAGT
                                ||||| ||||||||||
                                TCTTT CCTCTCTTCA

                                  _
GAM273  CLSTN3   5'  ACTTCTCTCCTTTCT      28203      T
                                AGAAA GGAGAGAAGT
                                ||||| ||||||||||
                                TCTTT CCTCTCTTCA

                                  _
GAM273  CYP2S1   3'  ACACGCCCTCTCCATTC    47611     A     AA TA
                                GAA TGGAGAG  G  TGT
                                ||| |||||||  |  |||
                                CTT ACCTCTC  C  ACA
                                  _     C_ GC
GAM273  CYP2S1   3'  ACACGCCCTCTCCATTC    47611     A     AA TA
                                GAA TGGAGAG  G  TGT
                                ||| |||||||  |  |||
                                CTT ACCTCTC  C  ACA
                                  _     C_ GC
GAM273  DKFZP564F0522 3'  ACATAACATCTCTCCTTTCT  68584      T     AG_
                                AGAAA GGAGAGA   TATGT
                                ||||| |||||||   |||||
                                TCTTT CCTCTCT   ATACA
                                  _     ACA
GAM273  DKFZP564F0522 3'  ACATAACATCTCTCCTTTCT  68584      T     AG_
                                AGAAA GGAGAGA   TATGT
                                ||||| |||||||   |||||
                                TCTTT CCTCTCT   ATACA
                                  _     ACA
GAM273  DKFZP761E1824 3'  GCAACTTTCTCCATT      66439         A  A
                                AATGGAGAGA GT TGT
                                |||||||||| || |||
                                TTACCTCTTT CA ACG

                                    _ _
GAM273  DKFZP761E1824 3'  GCAACTTTCTCCATT      66439         A  A
                                AATGGAGAGA GT TGT
                                |||||||||| || |||
                                TTACCTCTTT CA ACG

                                    _ _
GAM273  EPB41L1  3'  ACACCCTTCTCTCCTTTCT   70586      T       TA
                                AGAAA GGAGAGAAG  TGT
                                ||||| |||||||||  |||
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                                TCTTT CCTCTCTTC  ACA
                                  _       CC
GAM273  EPB41L1  3' ACACCCTTCTCTCCTTTCT   70586     T      TA
                                AGAAA GGAGAGAAG  TGT
                                ||||| |||||||||  |||
                                TCTTT CCTCTCTTC  ACA
                                  _       CC
GAM273  FLJ10525 5' ACGTTTTCTCTCCCCTTTCT  36222     T_      T
                                AGAAA  GGAGAGAAG ATGT
                                |||||  ||||||||| ||||
                                TCTTT  CCTCTCTTT TGCA
                                  CC       _
GAM273  FLJ10525 5' ACGTTTTCTCTCCCCTTTCT  36222     T_      T
                                AGAAA  GGAGAGAAG ATGT
                                |||||  ||||||||| ||||
                                TCTTT  CCTCTCTTT TGCA
                                  CC       _
GAM273  FLJ10853 3' GCATTGAACTCCTCTCATTTCT 36769      G   A  ___
                                AGAAATG AGAG AGT   ATGT
                                ||||||| |||| |||   ||||
                                TCTTTAC TCTC TCA   TACG
                                   _   C   AGT
GAM273  FLJ10853 3' GCATTGAACTCCTCTCATTTCT 36769      G   A  ___
                                AGAAATG AGAG AGT   ATGT
                                ||||||| |||| |||   ||||
                                TCTTTAC TCTC TCA   TACG
                                   _   C   AGT
GAM273  FLJ13154 3' GCATCAGTTTTCTCCACTTCT  44798     A      GT_
                                AGAA TGGAGAGAA   ATGT
                                |||| |||||||||   ||||
                                TCTT ACCTCTTTT   TACG
                                  C       GAC
GAM273  FLJ13154 3' GCATCAGTTTTCTCCACTTCT  44798     A      GT_
                                AGAA TGGAGAGAA   ATGT
                                |||| |||||||||   ||||
                                TCTT ACCTCTTTT   TACG
                                  C       GAC
GAM273  FLJ13848 3' ACATCCATCTTTCTCCACTTC  45458     A      AG __
                                GAA TGGAGAGA  T  ATGT
                                ||| ||||||||  |  ||||
                                CTT ACCTCTTT  A  TACA
                                  C       CT CC
GAM273  FLJ13848 3' ACATCCATCTTTCTCCACTTC  45458     A      AG __
                                GAA TGGAGAGA  T  ATGT
                                ||| ||||||||  |  ||||
                                CTT ACCTCTTT  A  TACA
                                  C       CT CC
GAM273  FLJ22169 3' GCTCACCTCTCTCCGCTTCT   44005     A      A  AT
                                AGAA TGGAGAGA GT  GT
                                |||| |||||||| ||  ||
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                                TCTT GCCTCTCT CA  CG
                                  C       C  CT
GAM273  FLJ22169  3'  GCTCACCTCTCTCCGCTTCT   44005      A       A  AT
                                AGAA TGGAGAGA GT  GT
                                |||| |||||||| ||  ||
                                TCTT GCCTCTCT CA  CG
                                  C       C  CT
GAM273  FLJ22644  3'  ACCTCTGCTCCATTTCT     47000          _   A
                                AGAAATGGAG AGA GT
                                |||||||||| ||| ||
                                TCTTTACCTC TCT CA
                                     G   C
GAM273  FLJ22644  3'  ACCTCTGCTCCATTTCT     47000          _   A
                                AGAAATGGAG AGA GT
                                |||||||||| ||| ||
                                TCTTTACCTC TCT CA
                                     G   C
GAM273  GOLGB1    3'  ACAGGTCTTCTCTCCAACTCT  15631     AA        TA_
                                AGA  TGGAGAGAAG   TGT
                                |||  ||||||||||   |||
                                TCT  ACCTCTCTTC   ACA
                                  CA         TGG
GAM273  GOLGB1    3'  ACAGGTCTTCTCTCCAACTCT  15631     AA        TA_
                                AGA  TGGAGAGAAG   TGT
                                |||  ||||||||||   |||
                                TCT  ACCTCTCTTC   ACA
                                  CA         TGG
GAM273  HBOA      3'  ACGAACTCCTCCTCCATTTC   22963         _  A   A
                                GAAATGGAG AG AGT TGT
                                ||||||||| || ||| |||
                                CTTTACCTC TC TCA GCA
                                     C  C   A
GAM273  HBOA      3'  ACGAACTCCTCCTCCATTTC   22963         _  A   A
                                GAAATGGAG AG AGT TGT
                                ||||||||| || ||| |||
                                CTTTACCTC TC TCA GCA
                                     C  C   A
GAM273  ING4      3'  ACACTTTTCTTCTCCATT     59702         _   TA
                                AATGGAGA GAAG  TGT
                                |||||||| ||||  |||
                                TTACCTCT CTTT  ACA
                                    T    TC
GAM273  ING4      3'  ACACTTTTCTTCTCCATT     59702         _   TA
                                AATGGAGA GAAG  TGT
                                |||||||| ||||  |||
                                TTACCTCT CTTT  ACA
                                    T    TC
GAM273  ITGA10    5'  CATCACTCCTCCCATTCCT    59376    A    A  A  _
                                AG AATGG GAG AGT ATG
                                || ||||| ||| ||| |||
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                                TC TTACC CTC TCA TAC
                                 C    _  C  C
GAM273  ITGA10   5' CATCACTCCTCCCATTCCT   59376   A   A  A  _
                                AG AATGG GAG AGT ATG
                                || ||||| ||| ||| |||
                                TC TTACC CTC TCA TAC
                                 C    _  C  C
GAM273  ITM3     3' ACATGTCTCTCCATTCCT    48161   A      AG
                                AG AATGGAGAGA  TATGT
                                || ||||||||||  |||||
                                TC TTACCTCTCT  GTACA
                                 C       __
GAM273  ITM3     3' ACATGTCTCTCCATTCCT    48161   A      AG
                                AG AATGGAGAGA  TATGT
                                || ||||||||||  |||||
                                TC TTACCTCTCT  GTACA
                                 C       __
GAM273  KIAA0247 3' ACATAACAATGTCGCCTCCATT 28390       A_  AG____
           TC                    GAAATGGAG  GA    TATGT
                                |||||||||  ||    |||||
                                CTTTACCTC  CT    ATACA
                                     CG  GTAACA
GAM273  KIAA0247 3' ACATAACAATGTCGCCTCCATT 28390       A_  AG____
           TC                    GAAATGGAG  GA    TATGT
                                |||||||||  ||    |||||
                                CTTTACCTC  CT    ATACA
                                     CG  GTAACA
GAM273  KIAA0254 3' GCTCACTTCTCTCCCACTTCT  28598    AT_      AT
                                AGAA   GGAGAGAAGT  GT
                                ||||   ||||||||||  ||
                                TCTT   CCTCTCTTCA  CG
                                  CAC        CT
GAM273  KIAA0254 3' GCTCACTTCTCTCCCACTTCT  28598    AT_      AT
                                AGAA   GGAGAGAAGT  GT
                                ||||   ||||||||||  ||
                                TCTT   CCTCTCTTCA  CG
                                  CAC        CT
GAM273  KIAA0286 3' ACATGCTCTGTCCATTCCT    68316   A    G  A
                                AG AATGGA AGA GTATGT
                                || |||||| ||| ||||||
                                TC TTACCT TCT CGTACA
                                 C     G  _
GAM273  KIAA0286 3' ACATGCTCTGTCCATTCCT    68316   A    G  A
                                AG AATGGA AGA GTATGT
                                || |||||| ||| ||||||
                                TC TTACCT TCT CGTACA
                                 C     G  _
GAM273  KIAA0431 3' CGACATGCTCCTTTCT       30891      A     A
                                GGAGAG AGTATGT CG
                                |||||| ||||||| ||
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                                TCTTTC TCGTACA GC
                                   C      _
GAM273  KIAA0431  3'  CGACATGCTCCTTTCT     30891       A      A
                                GGAGAG AGTATGT CG
                                |||||| ||||||| ||
                                TCTTTC TCGTACA GC
                                   C      _
GAM273  KIAA0523  3'  ACATTCATTCCTCCATTTC   67725        A   GT_
                                GAAATGGAG GAA   ATGT
                                ||||||||| |||   ||||
                                CTTTACCTC CTT   TACA
                                      _  ACT
GAM273  KIAA0523  3'  ACATTCATTCCTCCATTTC   67725        A   GT_
                                GAAATGGAG GAA   ATGT
                                ||||||||| |||   ||||
                                CTTTACCTC CTT   TACA
                                      _  ACT
GAM273  KIAA0748  3'  ACATCTCTTCATTTCT     28931          A
                                AGAAATGGAGAGA GT
                                |||||||||||| ||
                                TCTTTACTTCTCT CA
                                        A
GAM273  KIAA0748  3'  ACATCTCTTCATTTCT     28931          A
                                AGAAATGGAGAGA GT
                                |||||||||||| ||
                                TCTTTACTTCTCT CA
                                        A
GAM273  KIAA1029  3'  GCACACACACTCTCTCTTTCT  23475     AT     A  A   AC
                                AGAA  GGAGAGA GT TGT  GC
                                ||||  ||||||| || |||  ||
                                TCTT  TCTCTCT CA ACA  CG
                                  __      _  C   CA
GAM273  KIAA1029  3'  GCACACACACTCTCTCTTTCT  23475     AT     A  A   AC
                                AGAA  GGAGAGA GT TGT  GC
                                ||||  ||||||| || |||  ||
                                TCTT  TCTCTCT CA ACA  CG
                                  __      _  C   CA
GAM273  KIAA1305  3'  ACCCACATTCTCTCCAACTCT  46926     AA       _  AT
                                AGA  TGGAGAGAA GT  GT
                                |||  ||||||||| ||  ||
                                TCT  ACCTCTCTT CA  CA
                                  CA        A  CC
GAM273  KIAA1305  3'  ACCCACATTCTCTCCAACTCT  46926     AA       _  AT
                                AGA  TGGAGAGAA GT  GT
                                |||  ||||||||| ||  ||
                                TCT  ACCTCTCTT CA  CA
                                  CA        A  CC
GAM273  KIAA1317  5'  ACATCTCTCCATCTTT      86028     A       A
                                AGA ATGGAGAGA GT
                                ||| ||||||||| ||
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                                TTT TACCTCTCT CA
                                  C       A
GAM273  KIAA1317 5' ACATCTCTCCATCTTT     86028    A      A
                                AGA ATGGAGAGA GT
                                ||| ||||||||| ||
                                TTT TACCTCTCT CA
                                  C       A
GAM273  KIAA1319 3' GCATGGCTCTACCCATTTCT  40407      AG  AG
                                AGAAATGG  AGA  TATGT
                                ||||||||  |||  |||||
                                TCTTTACC  TCT  GTACG
                                    CA   CG
GAM273  KIAA1319 3' GCATGGCTCTACCCATTTCT  40407      AG  AG
                                AGAAATGG  AGA  TATGT
                                ||||||||  |||  |||||
                                TCTTTACC  TCT  GTACG
                                    CA   CG
GAM273  KIAA1915 3' GCATTACCTTCCTCCCATTTCT 73282      _ A   T__
                                AGAAATGG AG GAAG   ATGT
                                |||||||| || ||||   ||||
                                TCTTTACC TC CTTC   TACG
                                    C _    CAT
GAM273  KIAA1915 3' GCATTACCTTCCTCCCATTTCT 73282      _ A   T__
                                AGAAATGG AG GAAG   ATGT
                                |||||||| || ||||   ||||
                                TCTTTACC TC CTTC   TACG
                                    C _    CAT
GAM273  LASP1    3' GCATATGTTTCCCCATCTCT  20457    A   A   A
                                AGA ATGG GAGA GTATGT
                                ||| |||| |||| ||||||
                                TCT TACC CTTT TATACG
                                  C   C   G
GAM273  LASP1    3' GCATATGTTTCCCCATCTCT  20457    A   A   A
                                AGA ATGG GAGA GTATGT
                                ||| |||| |||| ||||||
                                TCT TACC CTTT TATACG
                                  C   C   G
GAM273  MGC13053 3' ACTCAATTCTCTCCAATTCT  51130     A      GTAT
                                AGAA TGGAGAGAA   GT
                                |||| |||||||||   ||
                                TCTT ACCTCTCTT   CA
                                  A       AACT
GAM273  MGC13053 3' ACTCAATTCTCTCCAATTCT  51130     A      GTAT
                                AGAA TGGAGAGAA   GT
                                |||| |||||||||   ||
                                TCTT ACCTCTCTT   CA
                                  A       AACT
GAM273  MGC2477  5' ACATACACATCCCTCTCCAT  44056      AA____
                                ATGGAGAG    GTATGT
                                ||||||||    ||||||
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                                TACCTCTC     CATACA
                                    CCTACA
GAM273  MGC2477   5' ACATACACATCCCTCTCCAT   44056        AA____
                                ATGGAGAG     GTATGT
                                ||||||||     ||||||
                                TACCTCTC     CATACA
                                    CCTACA
GAM273  MGC26988  5' GCAGTTACCTTCTCTCCGTCTC 55654     A        TA___
          T                      AGA ATGGAGAGAAG     TGT
                                ||| ||||||||||     |||
                                TCT TGCCTCTCTTC     ACG
                                  C         CATTG
GAM273  MGC26988  5' GCAGTTACCTTCTCTCCGTCTC 55654     A        TA___
          T                      AGA ATGGAGAGAAG     TGT
                                ||| ||||||||||     |||
                                TCT TGCCTCTCTTC     ACG
                                  C         CATTG
GAM273  MGC33182  3' GCATTTGTTTCTCCCCACATCT 75577     AA  A    T__
                                AGA  TGG GAGAAG   ATGT
                                |||  ||| ||||||   ||||
                                TCT  ACC CTCTTT   TACG
                                  AC   C     GTT
GAM273  MGC33182  3' GCATTTGTTTCTCCCCACATCT 75577     AA  A    T__
                                AGA  TGG GAGAAG   ATGT
                                |||  ||| ||||||   ||||
                                TCT  ACC CTCTTT   TACG
                                  AC   C     GTT
GAM273  P66       3' GCATAACCCTTCTCTCCA    40366        ___
                                TGGAGAGAAG   TATGT
                                ||||||||||   |||||
                                ACCTCTCTTC   ATACG
                                      CCA
GAM273  P66       3' GCATAACCCTTCTCTCCA    40366        ___
                                TGGAGAGAAG   TATGT
                                ||||||||||   |||||
                                ACCTCTCTTC   ATACG
                                      CCA
GAM273  PRDM15    3' ACATTTTCTCCTCACTTCT   61711     A  GA    T
                                AGAA TG  GAGAAG ATGT
                                ||||  ||  ||||||  ||||
                                TCTT AC  CTCTTT TACA
                                  C  TC     _
GAM273  PRDM15    3' ACATTTTCTCCTCACTTCT   61711     A  GA    T
                                AGAA TG  GAGAAG ATGT
                                ||||  ||  ||||||  ||||
                                TCTT AC  CTCTTT TACA
                                  C  TC     _
GAM273  PRO1580   5' ACTTCTCTTCACTTCT     37529     A
                                AGAA TGGAGAGAAGT
                                ||||  ||||||||||
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                                TCTT ACTTCTCTTCA
                                  C
GAM273  PRO1580  5' ACTTCTCTTCACTTCT     37529     A
                                AGAA TGGAGAGAAGT
                                |||| ||||||||||
                                TCTT ACTTCTCTTCA
                                  C
GAM273  SEPT3    3' ACATTGCTTTCTCTCC     38881       _  _
                                GGAGAGAA GTA TGT
                                |||||||| ||| |||
                                CCTCTCTT CGT ACA
                                     T  T
GAM273  SEPT3    3' ACATTGCTTTCTCTCC     38881       _  _
                                GGAGAGAA GTA TGT
                                |||||||| ||| |||
                                CCTCTCTT CGT ACA
                                     T  T
GAM273  SFRS6    3' GCATGAAGACCCTCTCCCTTCT 20782     AT    AAG___
                                AGAA  GGAGAG     TATGT
                                ||||  ||||||     |||||
                                TCTT  CCTCTC     GTACG
                                  C_     CCAGAA
GAM273  SFRS6    3' GCATGAAGACCCTCTCCCTTCT 20782     AT    AAG___
                                AGAA  GGAGAG     TATGT
                                ||||  ||||||     |||||
                                TCTT  CCTCTC     GTACG
                                  C_     CCAGAA
GAM273  SOX17    3' ACAGCTTCCTCCATTTC     42395       A   A
                                GAAATGGAG GAAGT TGT
                                ||||||||| ||||| |||
                                CTTTACCTC CTTCG ACA
                                     _    _
GAM273  SOX17    3' ACAGCTTCCTCCATTTC     42395       A   A
                                GAAATGGAG GAAGT TGT
                                ||||||||| ||||| |||
                                CTTTACCTC CTTCG ACA
                                     _    _
GAM273  STAG2    5' GCATCGATCTCTCCATCCCT  70566    AA      AGT
                                AG  ATGGAGAGA   ATGT
                                ||  |||||||||   ||||
                                TC  TACCTCTCT   TACG
                                 CC        AGC
GAM273  STAG2    5' GCATCGATCTCTCCATCCCT  70566    AA      AGT
                                AG  ATGGAGAGA   ATGT
                                ||  |||||||||   ||||
                                TC  TACCTCTCT   TACG
                                 CC        AGC
GAM273  SUPT4H1  3' GCATCTTTGCTCTCCACCTC  12062    AA     _  T
                                GA  TGGAGAG AAG ATGT
                                ||  ||||||| ||| ||||
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                                CT  ACCTCTC TTT TACG
                                 CC      G   C
GAM273  SUPT4H1   3'  GCATCTTTGCTCTCCACCTC   12062    AA      _   T
                                GA  TGGAGAG AAG ATGT
                                ||  ||||||| ||| ||||
                                CT  ACCTCTC TTT TACG
                                 CC      G   C
GAM273  ZNF333    3'  ACATCTCTCCACTTCT      50567     A       A
                                AGAA TGGAGAGA GT
                                |||| |||||||| ||
                                TCTT ACCTCTCT CA
                                  C       A
GAM273  ZNF333    3'  ACATCTCTCCACTTCT      50567     A       A
                                AGAA TGGAGAGA GT
                                |||| |||||||| ||
                                TCTT ACCTCTCT CA
                                  C       A
GAM273  LOC116349 5'  GCATTTTCTCTCCTTTC     73833     T       T
                                GAAA GGAGAGAAG ATGT
                                |||| ||||||||| ||||
                                CTTT CCTCTCTTT TACG
                                  _       _
GAM273  LOC116349 5'  GCATTTTCTCTCCTTTC     73833     T       T
                                GAAA GGAGAGAAG ATGT
                                |||| ||||||||| ||||
                                CTTT CCTCTCTTT TACG
                                  _       _
GAM273  LOC121506 3'  ACACACAGAGCTTCATTTC    74093         AGAA  A
                                GAAATGGAG    GT TGT
                                |||||||||    || |||
                                CTTTACTTC    CA ACA
                                     GAGA  C
GAM273  LOC121506 3'  ACACACAGAGCTTCATTTC    74093         AGAA  A
                                GAAATGGAG    GT TGT
                                |||||||||    || |||
                                CTTTACTTC    CA ACA
                                     GAGA  C
GAM273  LOC143451 3'  ACAGCTCTTCTCTCCTTCTCT  76561     AAT       TA_
                                AGA   GGAGAGAAG   TGT
                                |||   |||||||||   |||
                                TCT   CCTCTCTTC   ACA
                                  CTT       TCG
GAM273  LOC143451 3'  ACAGCTCTTCTCTCCTTCTCT  76561     AAT       TA_
                                AGA   GGAGAGAAG   TGT
                                |||   |||||||||   |||
                                TCT   CCTCTCTTC   ACA
                                  CTT       TCG
GAM273  LOC145125 3'  ACAGCTCTTCTCTCCTTCTCT  77003     AAT       TA_
                                AGA   GGAGAGAAG   TGT
                                |||   |||||||||   |||
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                                TCT  CCTCTCTTC  ACA
                                  CTT       TCG
GAM273  LOC145125 3' ACAGCTCTTCTCTCCTTCTCT 77003    AAT      TA_
                                AGA  GGAGAGAAG  TGT
                                |||  |||||||||  |||
                                TCT  CCTCTCTTC  ACA
                                  CTT       TCG
GAM273  LOC145547 3' ACCCACATTCTCTCCAACTCT 77262    AA       _ AT
                                AGA TGGAGAGAA GT GT
                                ||| ||||||||| || ||
                                TCT ACCTCTCTT CA CA
                                  CA       A CC
GAM273  LOC145547 3' ACCCACATTCTCTCCAACTCT 77262    AA       _ AT
                                AGA TGGAGAGAA GT GT
                                ||| ||||||||| || ||
                                TCT ACCTCTCTT CA CA
                                  CA       A CC
GAM273  LOC145601 3' ACATTCTCTCTCCATCTC   83360    A       A T
                                GA ATGGAGAGA G ATGT
                                || ||||||||| | ||||
                                CT TACCTCTCT C TACA
                                 C       _ T
GAM273  LOC145601 3' ACATTCTCTCTCCATCTC   83360    A       A T
                                GA ATGGAGAGA G ATGT
                                || ||||||||| | ||||
                                CT TACCTCTCT C TACA
                                 C       _ T
GAM273  LOC145845 3' ACATCTGTCTCCATTCCT   83549    A      GA  T
                                AG AATGGAGA  AG ATGT
                                || ||||||||  || ||||
                                TC TTACCTCT  TC TACA
                                 C       G_ _
GAM273  LOC145845 3' ACATCTGTCTCCATTCCT   83549    A      GA  T
                                AG AATGGAGA  AG ATGT
                                || ||||||||  || ||||
                                TC TTACCTCT  TC TACA
                                 C       G_ _
GAM273  LOC145955 5' ACAGACCTCTCTCCAGCCCT  83583    AAA      A  A
                                AG  TGGAGAGA GT TGT
                                ||  |||||||| || |||
                                TC  ACCTCTCT CA ACA
                                 CCG       C  G
GAM273  LOC145955 5' ACAGACCTCTCTCCAGCCCT  83583    AAA      A  A
                                AG  TGGAGAGA GT TGT
                                ||  |||||||| || |||
                                TC  ACCTCTCT CA ACA
                                 CCG       C  G
GAM273  LOC148137 3' GCGTGCCTCTCCCCAGCTTCT 58433     A_  A   A
                                AGAA  TGG GAGA GTATGT
                                ||||  ||| |||| ||||||
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                                TCTT  ACC CTCT CGTGCG
                                  CG   C    C
GAM273   LOC148137 3'  GCGTGCCTCTCCCCAGCTTCT  58433      A_   A    A
                                AGAA  TGG GAGA GTATGT
                                ||||  ||| |||| ||||||
                                TCTT  ACC CTCT CGTGCG
                                  CG   C    C
GAM273   LOC148764 5'  ATTTCTCCCACTTCT       78981      A   A
                                AGAA TGG GAGAAGT
                                |||| ||| |||||||
                                TCTT ACC CTCTTTA
                                  C   _
GAM273   LOC148764 5'  ATTTCTCCCACTTCT       78981      A   A
                                AGAA TGG GAGAAGT
                                |||| ||| |||||||
                                TCTT ACC CTCTTTA
                                  C   _
GAM273   LOC149506 3'  ACCTGCTTCCCCCCATTTTT   84443        AGA     T
                                AGAAATGG   GAAGTA GT
                                ||||||||   |||||| ||
                                TTTTTACC   CTTCGT CA
                                     CCC     C
GAM273   LOC149506 3'  ACCTGCTTCCCCCCATTTTT   84443        AGA     T
                                AGAAATGG   GAAGTA GT
                                ||||||||   |||||| ||
                                TTTTTACC   CTTCGT CA
                                     CCC     C
GAM273   LOC154739 5'  ACATACATTTTCTCCACTTCT  86222      A       _
                                AGAA TGGAGAGAA GTATGT
                                |||| ||||||||| ||||||
                                TCTT ACCTCTTTT CATACA
                                  C        A
GAM273   LOC154739 5'  ACATACATTTTCTCCACTTCT  86222      A       _
                                AGAA TGGAGAGAA GTATGT
                                |||| ||||||||| ||||||
                                TCTT ACCTCTTTT CATACA
                                  C        A
GAM273   LOC158364 5'  ACTTCTCTCCACCCTCT     81872     AA_
                                AGA   TGGAGAGAAGT
                                |||   ||||||||||
                                TCT   ACCTCTCTTCA
                                  CCC
GAM273   LOC158364 5'  ACTTCTCTCCACCCTCT     81872     AA_
                                AGA   TGGAGAGAAGT
                                |||   ||||||||||
                                TCT   ACCTCTCTTCA
                                  CCC
GAM273   LOC169181 5'  GCATTCCCTCCTCTCCAT     82734        A  T__
                                ATGGAGAG AG   ATGT
                                |||||||| ||   ||||
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                                TACCTCTC TC   TACG
                                    C  CCT
GAM273   LOC169181 5'  GCATTCCCTCCTCTCCAT    82734        A  T__
                                ATGGAGAG AG   ATGT
                                |||||||| ||   ||||
                                TACCTCTC TC   TACG
                                    C  CCT
GAM273   LOC170221 3'  GCCTCATTTTCTTTCCAT    82578          T   TAC
                                ATGGAGAGAAG ATG   GC
                                |||||||||||| |||   ||
                                TACCTTTCTTT TAC   CG
                                      _   TC_
GAM273   LOC170221 3'  GCCTCATTTTCTTTCCAT    82578          T   TAC
                                ATGGAGAGAAG ATG   GC
                                |||||||||||| |||   ||
                                TACCTTTCTTT TAC   CG
                                      _   TC_
GAM273   LOC196860 3'  ACATGCTTCTCTCCACTTCT   89640      A
                                AGAA TGGAGAGAAGTATGT
                                |||| ||||||||||||||||
                                TCTT ACCTCTCTTCGTACA
                                  C
GAM273   LOC196860 3'  ACATGCTTCTCTCCACTTCT   89640      A
                                AGAA TGGAGAGAAGTATGT
                                |||| ||||||||||||||||
                                TCTT ACCTCTCTTCGTACA
                                  C
GAM273   LOC200197 3'  ACGCCCTTCTCTCCACTTT    88611     A        TA
                                GAA TGGAGAGAAG  TGT
                                ||| ||||||||||  |||
                                TTT ACCTCTCTTC  GCA
                                  C         CC
GAM273   LOC200197 3'  ACGCCCTTCTCTCCACTTT    88611     A        TA
                                GAA TGGAGAGAAG  TGT
                                ||| ||||||||||  |||
                                TTT ACCTCTCTTC  GCA
                                  C         CC
GAM273   LOC203276 3'  ACATATATTTTCTCCACTTCT  90470      A       _
                                AGAA TGGAGAGAA GTATGT
                                |||| ||||||||| ||||||
                                TCTT ACCTCTTTT TATACA
                                  C         A
GAM273   LOC203276 3'  ACATATATTTTCTCCACTTCT  90470      A       _
                                AGAA TGGAGAGAA GTATGT
                                |||| ||||||||| ||||||
                                TCTT ACCTCTTTT TATACA
                                  C         A
GAM273   LOC203305 3'  ACATATATTTTCTCCACTTCT  90514      A       _
                                AGAA TGGAGAGAA GTATGT
                                |||| ||||||||| ||||||
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                                TCTT ACCTCTTTT TATACA
                                  C        A
GAM273   LOC203305 3'  ACATATATTTTCTCCACTTCT  90514      A       _
                                AGAA TGGAGAGAA GTATGT
                                |||| ||||||||| ||||||
                                TCTT ACCTCTTTT TATACA
                                  C        A
GAM273   LOC219653 3'  ACGTGTTTCCCCTCTCCTTTCT 91289      T    ___
                                AGAAA GGAGA   GAAGTATGT
                                ||||| |||||   |||||||||
                                TCTTT CCTCT   CTTTGTGCA
                                  _    CCC
GAM273   LOC219653 3'  ACGTGTTTCCCCTCTCCTTTCT 91289      T    ___
                                AGAAA GGAGA   GAAGTATGT
                                ||||| |||||   |||||||||
                                TCTTT CCTCT   CTTTGTGCA
                                  _    CCC
GAM273   LOC221656 3'  CAAGCCCCTCTCCACTTCT   92227      A      AA  A
                                AGAA TGGAGAG  GT TG
                                |||| |||||||  || ||
                                TCTT ACCTCTC  CG AC
                                  C      CC  A
GAM273   LOC221656 3'  CAAGCCCCTCTCCACTTCT   92227      A      AA  A
                                AGAA TGGAGAG  GT TG
                                |||| |||||||  || ||
                                TCTT ACCTCTC  CG AC
                                  C      CC  A
GAM273   LOC221882 5'  ACATCCTCTCCTCTCTCCTTCT 92499     AAT     ____  T
           CT                     AGA   GGAGAGA    AG ATGT
                                |||   |||||||    || ||||
                                TCT   CCTCTCT    TC TACA
                                  CTT      CCTC  C
GAM273   LOC221882 5'  ACATCCTCTCCTCTCTCCTTCT 92499     AAT     ____  T
           CT                     AGA   GGAGAGA    AG ATGT
                                |||   |||||||    || ||||
                                TCT   CCTCTCT    TC TACA
                                  CTT      CCTC  C
GAM273   LOC222899 5'  ACATCCTGCTTCTCCATCTC   94364    A      A_  T
                                GA ATGGAGAG  AG ATGT
                                || ||||||||  || ||||
                                CT TACCTCTT  TC TACA
                                  C       CG  C
GAM273   LOC222899 5'  ACATCCTGCTTCTCCATCTC   94364    A      A_  T
                                GA ATGGAGAG  AG ATGT
                                || ||||||||  || ||||
                                CT TACCTCTT  TC TACA
                                  C       CG  C
GAM273   LOC254243 3'  ACATATATTTTCTCCACTTCT  97399      A       _
                                AGAA TGGAGAGAA GTATGT
                                |||| |||||||| ||||||
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                                TCTT ACCTCTTTT TATACA
                                  C       A
GAM273  LOC254243 3'  ACATATATTTTCTCCACTTCT  97399     A      _
                                AGAA TGGAGAGAA GTATGT
                                |||| ||||||||| ||||||
                                TCTT ACCTCTTTT TATACA
                                  C       A
GAM273  LOC254440 3'  ACAGCTCTTCTCTCCTTCTCT  97063    AAT      TA_
                                AGA  GGAGAGAAG  TGT
                                |||  |||||||||  |||
                                TCT  CCTCTCTTC  ACA
                                  CTT       TCG
GAM273  LOC254440 3'  ACAGCTCTTCTCTCCTTCTCT  97063    AAT      TA_
                                AGA  GGAGAGAAG  TGT
                                |||  |||||||||  |||
                                TCT  CCTCTCTTC  ACA
                                  CTT       TCG
GAM273  LOC51125  3'  ACATACCATTGGTTCTCTTCAT 32246    A       _______
            TCCT                  AG AATGGAGAGAA    GTATGT
                                || ||||||||||     ||||||
                                TC TTACTTCTCTT     CATACA
                                 C         GGTTAC
GAM273  LOC51125  3'  ACATACCATTGGTTCTCTTCAT 32246    A       _______
            TCCT                  AG AATGGAGAGAA    GTATGT
                                || ||||||||||     ||||||
                                TC TTACTTCTCTT     CATACA
                                 C         GGTTAC
GAM273  LOC51195  3'  GCGGGGTGCTTTCTCCA    32946       A   GTA
                                TGGAGAGA GTAT   CGC
                                |||||||| ||||   |||
                                ACCTCTTT CGTG   GCG
                                    _   GG_
GAM273  LOC51195  3'  GCGGGGTGCTTTCTCCA    32946       A   GTA
                                TGGAGAGA GTAT   CGC
                                |||||||| ||||   |||
                                ACCTCTTT CGTG   GCG
                                    _   GG_
GAM273  LOC90038  3'  ACATATATTTTCTCCACTTCT  61143     A      _
                                AGAA TGGAGAGAA GTATGT
                                |||| ||||||||| ||||||
                                TCTT ACCTCTTTT TATACA
                                  C       A
GAM273  LOC90038  3'  ACATATATTTTCTCCACTTCT  61143     A      _
                                AGAA TGGAGAGAA GTATGT
                                |||| ||||||||| ||||||
                                TCTT ACCTCTTTT TATACA
                                  C       A
GAM274  BTG2     3'  GCAAGGTTAGCAACTGTGAA  22214       _ __  A
                                TTCACAGT GC  GCC TGT
                                |||||||| ||  ||| |||
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                                AAGTGTCA CG  TGG ACG
                                    A  AT   A
GAM274  IGJ     3'  GTAGAGAACATATATGCAT   58316      CC_      C
                                GTGCG   ATGTTCTC AC
                                ||||||  |||||||| ||
                                TACGT   TACAAGAG TG
                                   ATA       A
GAM274  IL6R    3'  GAACTTGGGCCACTGTGAA   5120         C   AT_
                                TTCACAGTG GCC   GTTC
                                ||||||||| |||   ||||
                                AAGTGTCAC CGG   CAAG
                                    _  GTT
GAM274  ISL1    3'  ATGGTAGCAACACTGTGAA   9361         C____
                                TTCACAGTG    GCCAT
                                |||||||||    |||||
                                AAGTGTCAC    TGGTA
                                     AACGA
GAM274  OLR1    3'  GTGGAGAACATGCATACT    10338     C  C
                                AGTG GC ATGTTCTCCAC
                                |||| || ||||||||||
                                TCAT CG TACAAGAGGTG
                                  A  _
GAM274  TPX1    3'  AGATGATGACAACTGTGAA   12378       GCGC   GT
                                TTCACAGT   CAT  TCT
                                ||||||||   |||  |||
                                AAGTGTCA   GTA  AGA
                                    ACA_   GT
GAM274  BTN2A1  3'  TGAAGAACATGGATGCACGTGG 54343      A    _      C
           A                     TTCAC GTGCG CCATGTTCT CA
                                |||||| ||||| |||||||| ||
                                AGGTG CACGT GGTACAAGA GT
                                  _    A       A
GAM274  BTN2A2  3'  TGAAGAACATGGACTCATGTGG 22782       GTGCG       C
           A                     TTCACA    CCATGTTCT CA
                                ||||||    ||||||||| ||
                                AGGTGT    GGTACAAGA GT
                                   ACTCA       A
GAM274  BZW1    3'  GGAGAACAGACTTGAA     27891     C   GCGCCA
                                TTCA AGT     TGTTCTCC
                                |||| |||     ||||||||
                                AAGT TCA     ACAAGAGG
                                  _  G_____
GAM274  C20orf151 3'  GGAGAATAAACACTTGAA    88701     C   CGCCA
                                TTCA AGTG    TGTTCTCC
                                |||| ||||    ||||||||
                                AAGT TCAC    ATAAGAGG
                                  _   AA___
GAM274  C2F     3'  GGAGAAGAACTGTGAA     20931        GCGCCATG
                                TTCACAGT      TTCTCC
                                ||||||||      ||||||
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                                AAGTGTCA       AAGAGG
                                    AG_______
GAM274  DHODH    3'  GGCATGGCTGCACTGT      7240         _
                                ACAGTGC GCCATGTT
                                ||||||| ||||||||
                                TGTCACG CGGTACGG
                                    T
GAM274  FLJ12800 3'  AGAAGCAGAGCCACTGTGAA  43226         C  CA   _
                                TTCACAGTG GC  TGTT CT
                                ||||||||| ||  |||| ||
                                AAGTGTCAC CG  ACGA GA
                                    _ AG   A
GAM274  GC20     3'  GAAAACATGGGGTATGT     68899     G  G      C
                                ACA TGC CCATGTT TC
                                ||| ||| ||||||| ||
                                TGT ATG GGTACAA AG
                                  _  G      A
GAM274  KIAA0773 5'  GGCATCAACGCACTGTGAG   28057          CC_
                                TTCACAGTGCG   ATGTT
                                ||||||||||   |||||
                                GAGTGTCACGC   TACGG
                                     AAC
GAM274  MGC12466 5'  TGGAGAAAAGCCCTATGAA   79036     C  T  GCCATG
                                TTCA AG GC     TTCTCCA
                                |||| || ||     |||||||
                                AAGT TC CG     AAGAGGT
                                  A  C  AA____
GAM274  MGC14801 3'  GGAGCCCAGCACTGTGAA    51119         GCCA  TT
                                TTCACAGTGC    TG  CTCC
                                ||||||||||    ||  ||||
                                AAGTGTCACG    AC  GAGG
                                     _____  CC
GAM274  MGC35558 3'  AGAAACACCGACTGTGAA    58772         G  CCATG
                                TTCACAGT CG    TTCT
                                |||||||| ||    ||||
                                AAGTGTCA GC    AAGA
                                    _  CACA_
GAM274  PRDM8    5'  TGAGAATTGAACTGTGAA    39572        GCGCCAT     C
                                TTCACAGT      GTTCTC A
                                ||||||||      |||||| |
                                AAGTGTCA      TAAGAG T
                                    AGT_____     A
GAM274  PTBP2    3'  AGAAAGTGTACTGCGAA     41031     A      CATG
                                TTC CAGTGCGC    TTCT
                                ||| ||||||||    ||||
                                AAG GTCATGTG    AAGA
                                  C       A___
GAM274  RBMS1    5'  ATGGCAAACACTGTGAA     33704         C__
                                TTCACAGTG   GCCAT
                                |||||||||   |||||
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                                AAGTGTCAC   CGGTA
                                     AAA
GAM274  SLAC2-B   3'  GAATTACCCAGCACAACTGTGA 30512        _ C  CAT___
           A                    TTCACAGT G GC     GTTC
                                |||||||| | ||     ||||
                                AAGTGTCA C CG     TAAG
                                    A A  ACCCAT
GAM274  TUBGCP2   5'  GGAGAACATATTGTGA     21855       GCGCC
                                TCACAGT    ATGTTCTCC
                                |||||||    |||||||||
                                AGTGTTA    TACAAGAGG
                                     _____
GAM274  LOC146506 3'  TGGCCCAGCAGCACACTGTGAA 77937        C  CA   CT_
                                TTCACAGTG GC  TGTT   CCA
                                ||||||||| ||  ||||   |||
                                AAGTGTCAC CG  ACGA   GGT
                                     A __    CCC
GAM274  LOC151579 3'  GGAGAACAGACTTGAA     69457     C   GCGCCA
                                TTCA AGT     TGTTCTCC
                                |||| |||     ||||||||
                                AAGT TCA     ACAAGAGG
                                  _  G_____
GAM274  LOC153546 5'  GAAAGGAGCGACTGTGAA    80885       G   CATG
                                TTCACAGT CGC    TTC
                                |||||||| |||    |||
                                AAGTGTCA GCG    AAG
                                     _  AGGA
GAM274  LOC200531 5'  TGGAGACTCACACTGTGA    88824       CGCCA  T_
                                TCACAGTG    TG  TCTCCA
                                ||||||||    ||  ||||||
                                AGTGTCAC    AC  AGAGGT
                                     _____  TC
GAM274  LOC202309 5'  AGAATTACACTGTGAA      90334       CGCCAT
                                TTCACAGTG     GTTCT
                                |||||||||     |||||
                                AAGTGTCAC     TAAGA
                                     AT____
GAM274  LOC253792 3'  TGAAGAACATGCTCCTG     97228     TGC  C      C
                                CAG   GC ATGTTCT CA
                                |||   || |||||||  ||
                                GTC   CG TACAAGA GT
                                  CT_  _      A
GAM274  LOC91548  3'  AGAAAAGCACTGTGAA      66409         GCCATG
                                TTCACAGTGC     TTCT
                                ||||||||||     ||||
                                AAGTGTCACG     AAGA
                                     AA____
GAM275  ADH4      3'  TAAAAAGATTTTTACTGGA    5408        CGT
                                TCCAGTGG   TCTTTTTA
                                ||||||||   ||||||||
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                                AGGTCATT  AGAAAAAT
                                    TTT
GAM275  B4GALT2  3'  AGTAAAAAACGTGAATGGA  47580     GTG   CT
                                TCCA  GCGTT  TTTTACT
                                ||||  |||||  |||||||
                                AGGT  TGCAA  AAAATGA
                                  AAG   __
GAM275  CTBP1    3'  AAAAAGAAAACCTGAAGGAG  67941     AGT_  CG
                                CTCC   GG  TTCTTTTT
                                ||||   ||  ||||||||
                                GAGG   CC  AAGAAAAA
                                  AAGT  AA
GAM275  ENPP3    3'  TAAAAAGAACAGCAGAGAG   17226     CAGTG  _
                                CTC    GC GTTCTTTTTA
                                |||    || ||||||||||
                                GAG    CG CAAGAAAAAT
                                  AGA__  A
GAM275  F8       3'  TAAAAAAATAAGTCAGGAGGA  3732       AG   GTTC_
                                TCCTCC  TGGC    TTTTTA
                                ||||||  ||||    ||||||
                                AGGAGG  ACTG    AAAAAT
                                   __   AATAA
GAM275  GK       3'  AGCAAAAAGAATGCTAT     3911          A
                                GTGGCGTTCTTTTT CT
                                |||||||||||||| ||
                                TATCGTAAGAAAAA GA
                                      C
GAM275  ID4      3'  GAAAAAAAGCCACCGGAGGA   7755       A    GTTC
                                TCCTCC GTGGC    TTTTT
                                |||||| |||||    |||||
                                AGGAGG CACCG    AAAAG
                                   C    AAA_
GAM275  PITX1    3'  GAAAAAGACGTCGGAG      10599     AGT    T     A
                                CTCC   GGCGT CTTTTT C
                                ||||   ||||| |||||| |
                                GAGG   CTGCA GAAAAA G
                                  ___    _     C
GAM275  TDG      3'  GAAAAAGATGCTGGAG      12191        GCGT     A
                                CTCCAGTG    TCTTTTT C
                                ||||||||    ||||||| |
                                GAGGTCGT    AGAAAAA G
                                     ____       C
GAM275  XRCC2    3'  AGCAAAAAGAACAAAGCTGGAG 18318         GGC       A
          G                      CCTCCAGT   GTTCTTTTT CT
                                ||||||||   ||||||||| ||
                                GGAGGTCG   CAAGAAAAA GA
                                     AAA        C
GAM275  DKFZP727M111 5'  AAAAGGAAAAGCCCTGAAG   31401    C   T   G_
                                CT CAG GGC  TTCTTTTT
                                || ||| |||  ||||||||
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                                GA GTC CCG  AAGGAAAA
                                 A  _  AA
GAM275  ELKS     3'  AGTGGTCAACGCCCTGGAAGA  30501    C    T    CTTT
                                TC TCCAG GGCGTT   TTACT
                                || ||||| ||||||   |||||
                                AG AGGTC CCGCAA   GGTGA
                                 A    _     CT__
GAM275  FLJ10648  3'  AGCAAAAAGAACAAAGTCCTGG 36378        T  ___       A
           AGGA                    TCCTCCAG GGC   GTTCTTTTT CT
                                ||||||||| |||   ||||||||| ||
                                AGGAGGTC CTG   CAAGAAAAA GA
                                     _  AAA       C
GAM275  FLJ20151  3'  AAAGACCCTGGAGGA      34648        T  CGT
                                TCCTCCAG GG   TCTTT
                                |||||||| ||   |||||
                                AGGAGGTC CC   AGAAA

                                   _  ___
GAM275  FLJ20435  3'  TAAAAAGAGCCATCTGGAGGA  35162        _   GT
                                TCCTCCAG TGGC  TCTTTTTA
                                |||||||| ||||  ||||||||
                                AGGAGGTC ACCG  AGAAAAAT
                                     T   __
GAM275  MDS024    3'  AAAAAGAATTGCCAAGGA    41522     AG    _
                                TCC  TGGCG TTCTTTTT
                                |||  ||||| ||||||||
                                AGG  ACCGT AAGAAAAA
                                  A_    T
GAM275  ShrmL     5'  AGAGCGCCACTGAAGGA     40463      C
                                TCCT CAGTGGCGTTCT
                                |||| ||||||||||||
                                AGGA GTCACCGCGAGA
                                   A
GAM275  SIAT8C    5'  TAAAAAAGCCCCACAGAGGA   31883      CA    C   C
                                TCCTC  GTGG GTT TTTTTA
                                |||||  |||| ||| ||||||
                                AGGAG  CACC CGA AAAAAT
                                   A_    C   _
GAM275  VEST1     5'  AAAAAGATGCACTGGGGA    53678     T     G   T
                                TCC CCAGTG CGT CTTTTT
                                ||| |||||| ||| ||||||
                                AGG GGTCAC GTA GAAAAA

                                  _     _  _
GAM275  ZFD25     5'  AAAAAGAGCCCTGGA       32573       T   GT
                                TCCAG GGC  TCTTTTT
                                ||||| |||  |||||||
                                AGGTC CCG  AGAAAAA

                                   _  __
GAM275  LOC124626 3'  AGTAAGACCAAACCACTGGA   74313         CGTTCT
                                TCCAGTGG     TTTTACT
                                ||||||||     |||||||
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                                AGGTCACC     AGAATGA
                                     AAACC_
GAM275  LOC144577 3'  TAAAAAGAAGCCACAAAGAG  76902     CA_    G
                                CTC   GTGGC TTCTTTTTA
                                |||   ||||| |||||||||
                                GAG   CACCG AAGAAAAAT
                                  AAA    _
GAM275  LOC145837 5'  AGCAAAAAGAACCAAAGAGGA  83542      CAG   CG      A
                                TCCTC   TGG  TTCTTTTT CT
                                |||||   |||  |||||||| ||
                                AGGAG   ACC  AAGAAAAA GA
                                   AA_  __       C
GAM275  LOC151194 3'  TAAAAAAACTGGGGA      59215     T    GGCGTTC
                                TCC CCAGT      TTTTTA
                                ||| |||||      ||||||
                                AGG GGTCA      AAAAAT
                                  _    A_______
GAM275  LOC154789 5'  AGTAAAATCTCAGGCCACTAGA 81131     C     GTTCT_
          G                      CTC AGTGGC     TTTTACT
                                |||  ||||||     |||||||
                                GAG TCACCG     AAAATGA
                                  A     GACTCT
GAM275  LOC197322 3'  AAAGACTCCACTGGAGGA    89736          C  T
                                TCCTCCAGTGG GT CTTT
                                |||||||||||  ||  ||||
                                AGGAGGTCACC CA GAAA
                                       T  _
GAM275  LOC221596 3'  TAAAAACCTCACACTGGAGAGA 91980    _      GCGTTC
                                TC CTCCAGTG     TTTTTA
                                ||  ||||||||     ||||||
                                AG GAGGTCAC     AAAAAT
                                  A       ACTCC_
GAM275  LOC91796  3'  AGCAAAAAGAACAAGGCTGGA  67208       GGC       A
                                TCCAGT   GTTCTTTTT CT
                                ||||||   |||||||||  ||
                                AGGTCG   CAAGAAAAA GA
                                    GAA       C
GAM275  LOC92539  5'  TAAAAAGTGTCACTG       69638         TT
                                CAGTGGCG  CTTTTTA
                                ||||||||  |||||||
                                GTCACTGT  GAAAAAT
                                          __
GAM276  CABC1     5'  GCACAAACAGACGCTC      39654      CTGGC
                                GAGC    TCTGTTTGTGC
                                ||||    ||||||||||
                                CTCG    AGACAAACACG
                                  C_____
GAM276  CEACAM5   3'  AACAGAGCAAGACTCCA     15153       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  A
GAM276  F2R     3'  AACAGAGCAAGACTCCA     8831       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM276  FGFR2   3'  GACAGAGCGAGACTCCA     43377      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM276  FGFR2   3'  GACAGAGCGAGACTCCA     43383      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM276  FUT6    3'  GACAGAGCAAGACTCCA     3812       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM276  GCLM    5'  GGCGCAGACCAGGCTCCA    9026          C    TTGT  _
                                TGGAGCCTGG TCTGT   GC C
                                |||||||||| |||||   || |
                                ACCTCGGACC AGACG   CG G
                                      _   _____  A
GAM276  GPC1    3'  GGCTGCAGAGCCCGGCCCCA  9103     A  T      TTGT
                                TGG GCC GGCTCTGT   GCC
                                ||| ||| ||||||||   |||
                                ACC CGG CCGAGACG   CGG
                                  C  C      T____
GAM276  HPSE    3'  CAAACAGGCCAGGCTCCA    21890          T
                                TGGAGCCTGGC CTGTTTG
                                |||||||||| |||||||
                                ACCTCGGACCG GACAAAC
                                      _
GAM276  IFIT4   3'  AACAGAGCAAGACTCCA     70918      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM276  KCNJ5   3'  GACAGAGCGAGACTCCA     6091       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM276  LY94    3'  GACAGAGCGAGACTCCA     16705      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAG
                                   A  G
GAM276  LZTS1    3' ACAGAGCCTGGCCCCA     40676     A  T
                                TGG GCC GGCTCTGT
                                ||| ||| ||||||||
                                ACC CGG CCGAGACA
                                  C  T
GAM276  MSH3     3' AACAGAGCAAGACTCCA     10116      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM276  POLH     3' AACAGAGCGAGACTCCA     21461      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM276  PRKAB1   3' GCACACCACCAGGCTCCA    20736         CTC  TT
                                TGGAGCCTGG  TG  TGTGC
                                ||||||||||  ||  |||||
                                ACCTCGGACC  AC  ACACG
                                      ___  C_
GAM276  SIGLEC6  3' AACAGAGCGAGACTCCA     59925      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM276  SLC10A2  5' AGCAGAGCCAGGGCCCA     4840      AG
                                TGG  CCTGGCTCTGTT
                                |||  ||||||||||||
                                ACC  GGACCGAGACGA
                                  CG
GAM276  SNRPN    5' CAAGCAAAAACCAGGCTCCA  42998         CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM276  SNRPN    5' CAAGCAAAAACCAGGCTCCA  43005         CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM276  SNRPN    5' CAAGCAAAAACCAGGCTCCA  43013         CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM276  SNRPN    5' CAAGCAAAAACCAGGCTCCA  42991         CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
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                                ACCTCGGACC    ACGAAC
                                      AAAA
GAM276  TNFSF11   5'  CAGGAGCCAAAGCCGGGCTCCA 13512          CT_   G
                                TGGAGCCTGGCT   GTTT TG
                                ||||||||||||   |||| ||
                                ACCTCGGGCCGA   CGAG AC
                                       AAC    G
GAM276  TSNAX     3'  GGTAACAGAGCAAGACTCCA   20002      C  G     TTG
                                TGGAG CT GCTCTGT   TGCC
                                ||||| || |||||||   ||||
                                ACCTC GA CGAGACA   ATGG
                                   A  A     ___
GAM276  UBE2L3    3'  GCCTTTGCAGAGTCAAGCTCCA 12503       C       TTGT
                                TGGAGC TGGCTCTGT    GC
                                |||||| |||||||||    ||
                                ACCTCG ACTGAGACG    CG
                                    A        TTTC
GAM276  ZNF264    3'  AACAGAGCGAGACTCCA     12738      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM276  ARNTL2    3'  GACAGAGCGAGACTCCA     39466      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM276  C22orf5   3'  GGATCAGAGCCAGACACCA   24344     AGC       TTTGTG
                                TGG   CTGGCTCTG     CC
                                |||   |||||||||     ||
                                ACC   GACCGAGAC     GG
                                  ACA        TA____
GAM276  DKFZp547C176 3'  GACAGAGCAAGACTCCA     67223      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM276  DKFZp564K142 3'  AACAGAGCGAGACTCCA     49522      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM276  FADS1     3'  GACAGAGCAAGACTCCA     25477      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM276  FLJ12298  3'  AACAGAGCGAGACTCCA     49664      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  G
GAM276  FLJ14117  3'  AACAGAGCAAGACTCCA     42896      C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM276  FLJ14251  3'  GGTAACAGAGCGAGACTCCA   45977      C  G      TTG
                                TGGAG CT GCTCTGT   TGCC
                                |||||| || |||||||   ||||
                                ACCTC GA CGAGACA   ATGG
                                   A  G      ___
GAM276  FLJ14327  3'  AACAGAGCTAGACTCCA     46127      C
                                TGGAG CTGGCTCTGTT
                                ||||| ||||||||||
                                ACCTC GATCGAGACAA
                                   A
GAM276  FLJ14566  5'  GGCCACAGAGCCAGCCCCA    51446     A  C       TT T
                                TGG GC TGGCTCTGT  G GCC
                                ||| || |||||||||  | |||
                                ACC CG ACCGAGACA  C CGG
                                  C  _       __ _
GAM276  FLJ20084  3'  AACAGAGCGAGACTCCA     34511      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM276  FLJ20306  3'  GACAGAGCAAGACTCCA     34917      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM276  FLJ20456  3'  GGTAACAGAGCTAGACTCCA   35215      C        TTG
                                TGGAG CTGGCTCTGT   TGCC
                                ||||| ||||||||||   ||||
                                ACCTC GATCGAGACA   ATGG
                                   A        ___
GAM276  FLJ22054  3'  AACAGAGCAAGACTCCA     94391      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM276  FLJ22393  5'  AGCAGGAACCAGGCTCCA    47058          C_
                                TGGAGCCTGG  TCTGTT
                                ||||||||||  ||||||
                                ACCTCGGACC  GGACGA
                                      AA
GAM276  FLJ23598  3'  GCCAAGAGCCAGCTCCA     45522       C      GTT  T
                                TGGAGC TGGCTCT   TG GC
                                |||||| |||||||   || ||
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                                ACCTCG ACCGAGA   AC CG
                                _     ____  _
GAM276  FLJ31168  3'  GACAGAGCGAGACTCCA     58502      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM276  GP5       3'  GACAGAGCGAGACTCCA     15646      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM276  GTPBP5    3'  GACAGAGCAAGACTCCA     65357      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM276  HIC       3'  AACAGAGCGAGACTCCA     67444      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM276  ING1-like 3'  GACAGAGCGAGACTCCA     54156      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM276  KBRAS2    3'  AACAGAGCAAGACTCCA     34191      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM276  KIAA0189  3'  CAGGAGCAGAGCCAGGCCCA  28273      A          G
                                TGG GCCTGGCTCTGTTT TG
                                ||| |||||||||||||| ||
                                ACC CGGACCGAGACGAG AC
                                _           G
GAM276  KIAA0472  3'  AGCAGAGCAAGACTCCA     71853      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACGA
                                   A  A
GAM276  KIAA0563  3'  GACAGAGCAAGACTCCA     29188      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM276  KIAA0565  3'  GACAGAGCAAGACTCCA     66890      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAG
                                   A  A
GAM276  KIAA0648  3'  CAAACAGAAGCAGGCTCCA   82651        GC
                                TGGAGCCTG  TCTGTTTG
                                |||||||||  ||||||||
                                ACCTCGGAC  AGACAAAC
                                     GA
GAM276  KIAA0924  3'  AACAGAGCGAGACTCCA    29712      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM276  KIAA1028  3'  CAGAGCACAGGCTCCA     91934        _
                                TGGAGCCTG GCTCTG
                                ||||||||| ||||||
                                ACCTCGGAC CGAGAC
                                     A
GAM276  KIAA1719  3'  GGCCAGGGCCAGGCCCCA   68169    A        TTTGT
                                TGG GCCTGGCTCTG    GCC
                                ||| ||||||||||     |||
                                ACC CGGACCGGGAC    CGG
                                  C        _____
GAM276  KIAA1940  3'  GGTCTCAGAACCAAGGCTCCA  79988       _ C    TTTGT
                                TGGAGCCT GG TCTG    GCC
                                |||||||| || ||||    |||
                                ACCTCGGA CC AGAC    TGG
                                     A  A   TC___
GAM276  LGI2      3'  CAAATCAAAGCCAGGCTC    36397         C _
                                GAGCCTGGCT TG TTTG
                                |||||||||| || ||||
                                CTCGGACCGA AC AAAC
                                     A  T
GAM276  MGC10200  3'  AACAGAGCGAGACTCCA     58980      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM276  MGC2705   5'  GCACCAAGCCAGGCTCC     51113         C  TTT
                                GGAGCCTGGCT TG  GTGC
                                |||||||||| ||  ||||
                                CCTCGGACCGA AC  CACG
                                     _  ___
GAM276  MGC4562   3'  AACAGAGCGAGACTCCA     55908      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM276  MGC4663   3'  AACAGAGCCAGACTCC      44501      C
                                GGAG CTGGCTCTGTT
                                |||| ||||||||||
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                                CCTC GACCGAGACAA
                                  A
GAM276  NPTXR    3'  AACAGAGCAAGACTCCA     26635      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM276  NPTXR    3'  AACAGAGCAAGACTCCA     54171      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM276  OR7C1    5'  AACAGAGCCAAGTCCA      82428      G C
                                TGGA C TGGCTCTGTT
                                |||| | ||||||||||
                                ACCT G ACCGAGACAA
                                  _ A
GAM276  POFUT1   3'  AACAGAGCGAGACTCCA     70462      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM276  PTK6     3'  GACAGAGCGAGACTCCA     19936      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM276  RASGRF2  3'  GCACGAAGCCAGGCTCC     61042          CTGT
                                GGAGCCTGGCT   TTGTGC
                                ||||||||||    ||||||
                                CCTCGGACCGA   AGCACG
                                     ____
GAM276  SC65     3'  GACAGAGCGAGACTCCA     21289      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM276  SNURF    3'  CAAGCAAAAACCAGGCTCCA  19052          CTC_
                                TGGAGCCTGG    TGTTTG
                                ||||||||||    ||||||
                                ACCTCGGACC    ACGAAC
                                      AAAA
GAM276  TMG4     3'  GACAGAGCAAGACTCCA     43989      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM276  WBSCR23  3'  GACAGAGCAAGACTCCA     46762      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAG
                                   A  A
GAM276  WIRE      3'  GACAGAGCCAGACTCC      78305      C
                                GGAG CTGGCTCTGTT
                                |||| ||||||||||
                                CCTC GACCGAGACAG
                                   A
GAM276  WSB1      3'  AACAGAGCGAGACTCCA     56144      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM276  WSB1      3'  AACAGAGCGAGACTCCA     56138      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM276  LOC115704 3'  CAGCCAGAGCCAGGCCCC    73541    A         T
                                GG GCCTGGCTCTG TTG
                                || |||||||||| |||
                                CC CGGACCGAGAC GAC
                                 C          C
GAM276  LOC124220 5'  GGCACAACCAGACGCC      59146    _    T
                                GGC TCTG TTGTGCC
                                ||| |||| |||||||
                                CCG AGAC AACACGG
                                  C    C
GAM276  LOC127262 3'  GACAGAGCGAGACTCCA     76110      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM276  LOC129563 3'  AGCAGAGCAGGCCCCA      74878     A    G
                                TGG GCCTG CTCTGTT
                                ||| ||||| |||||||
                                ACC CGGAC GAGACGA
                                  C    _
GAM276  LOC129880 3'  AACAGAGCAAGACTCCA     74900      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM276  LOC143196 3'  AACAGAGCGAGACTCCA     82903      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM276  LOC144319 3'  GGCACAAACAGGCGCCCC    83057    A  CTG  T
                                GG GC   GC CTGTTTGTGCC
                                || ||   || ||||||||||
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                                CC CG   CG GACAAACACGG
                                 C ___  _
GAM276  LOC145216 3'  GACAGAGCAAGACTCCA     83267      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM276  LOC145820 3'  GACAGAGCAAGACTCCA     77514      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM276  LOC146227 3'  GGTCAGAGCCAGACCCC     77711    AGC       TTTGT
                                GG   CTGGCTCTG    GCC
                                ||   |||||||||    |||
                                CC   GACCGAGAC    TGG
                                 CCA       _____
GAM276  LOC146713 3'  AACAGAGCAAGACTCCA     83720      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM276  LOC147071 3'  GACAGAGCAAGACTCCA     72999      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM276  LOC147649 3'  GACAGAGCGAGACTCCA     78414      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM276  LOC148936 3'  AACAGAGCAAGACTCCA     84286      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM276  LOC149803 5'  CAGGCAGAGCAAGCTCCA    79538       CTG
                                TGGAGC   GCTCTGTTTG
                                ||||||   ||||||||||
                                ACCTCG   CGAGACGGAC
                                   AA_
GAM276  LOC150299 3'  GACAGAGCAAGACTCCA     84970      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM276  LOC151429 3'  GACAGAGCAAGACTCCA     85353      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAG
                                   A  A
GAM276  LOC151904 3'  AACAGAGCGAGACTCCA     80382      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM276  LOC158292 5'  GACAGAGCGAGACTCCA     86730      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM276  LOC162137 5'  CAAGCAGGCCAAGCCCCA    87111     A  C   T
                                TGG GC TGGC CTGTTTG
                                ||| || |||| |||||||
                                ACC CG ACCG GACGAAC
                                  C  A   _
GAM276  LOC163033 5'  CGACCAGGACCAAGCCCCA   82396     A  C   CT   T
                                TGG GC TGG  CTG TTG
                                ||| || |||  ||| |||
                                ACC CG ACC  GAC AGC
                                  C  A   AG   C
GAM276  LOC163682 3'  ACACTCAAAGCCGGGCTCCA  87020           C  TT
                                TGGAGCCTGGCT TG  TGT
                                |||||||||||| ||  |||
                                ACCTCGGGCCGA AC  ACA
                                       A  TC
GAM276  LOC200261 3'  GCACAAACCTCTGGAGGCCCA 88655     A   GGCTCT
                                TGG GCCT     GTTTGTGC
                                ||| ||||     ||||||||
                                ACC CGGA     CAAACACG
                                  _   GGTCTC
GAM276  LOC201173 3'  GACAGAGCAAGACTCCA     87329      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM276  LOC201182 5'  AACAGAGCAAGACTCCA     89760      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM276  LOC219627 3'  GACAGAGCGAGACTCCA     92178      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM276  LOC221543 5'  GACAGAGCAAGACTCCA     93742      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAG
                                   A  A
GAM276  LOC221943 5'  GACAGAGCAAGACTCCA     93989      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM276  LOC222160 5'  GACAGAGCAAGACTCCA     94127      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM276  LOC253039 5'  GGCTCCAAAACCAGGCTCTA   96159          CTCTG   T_
                                TGGAGCCTGG    TTTG  GCC
                                ||||||||||    ||||  |||
                                ATCTCGGACC    AAAC  CGG
                                      A____   CT
GAM276  LOC254659 3'  AAACAGAGCAAGACTCCA     95109      C  G
                                TGGAG CT GCTCTGTTT
                                ||||| || |||||||||
                                ACCTC GA CGAGACAAA
                                   A  A
GAM276  LOC256158 5'  AACATCGAGCCAGGCCCA     97639      A       __
                                TGG GCCTGGCTC  TGTT
                                ||| |||||||||  ||||
                                ACC CGGACCGAG  ACAA
                                  _       CT
GAM276  LOC256207 3'  GACAGAGCAAGACTCCA     95169      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM276  LOC257596 5'  GACAGAGCAAGACTCCA     97935      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM276  LOC56963  3'  GCACAAAGCCAGGCTTCA    71455          CTGT
                                TGGAGCCTGGCT   TTGTGC
                                ||||||||||||   ||||||
                                ACTTCGGACCGA   AACACG
                                       ____
GAM276  LOC91149  3'  GCTGAACCAGAGCCAGACTCCA 65079      C       _   T
                                TGGAG CTGGCTCTG TTTG GC
                                ||||| ||||||||| |||| ||
                                ACCTC GACCGAGAC AAGT CG
                                   A       C   _
GAM276  LOC91409  3'  AGGCAAGGCCAGGCCCCA    65951      A      TC
                                TGG GCCTGGC  TGTTT
                                ||| |||||||  |||||
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                                ACC CGGACCG  ACGGA
                                  C      GA
GAM276  LOC91862 3' GGTGACAGAGCGAGACTCCA  53470      C  G      TGT
                                TGGAG CT GCTCTGTT   GCC
                                ||||| || ||||||||   |||
                                ACCTC GA CGAGACAG   TGG
                                   A  G      ___
GAM276  LOC92482 3' AACAGAGCAAGACTCCA     69485      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM277  BAZ1A    3' TTCAGCTTTACAGAACTGT    25584      _      AAA
                                ACAGT CTGTGAA   CTGAA
                                ||||| |||||||   |||||
                                TGTCA GACATTT   GACTT
                                   A      C__
GAM277  BAZ2A    3' CAGCCTCTTCAGACTGTG     25596        T_  AAAA
                                CACAGTCTG  GA    CTG
                                |||||||||  ||    |||
                                GTGTCAGAC  CT    GAC
                                     TT  CC__
GAM277  CNR1     3' TTTTCACAGCTATGA       32218     C  T
                                TCA AG CTGTGAAAA
                                ||| || |||||||||
                                AGT TC GACACTTTT
                                  A  _
GAM277  CPA3     3' TCAGTTTCTCACAGATT      8522          A
                                AGTCTGTGA AAACTGA
                                ||||||||| |||||||
                                TTAGACACT TTTGACT
                                     C
GAM277  CX3CR1   3' TTCAGTTTCCTGGTCTGTAGA  70647    _   T   T   AA
                                TC ACAG CTG GAA  ACTGAA
                                || |||| ||| |||  ||||||
                                AG TGTC GGT CTT  TGACTT
                                 A    T   C   __
GAM277  DIAPH2   3' TTCAACTTTTCACACTACTGT  22072      C_      AC
                                ACAGT  TGTGAAAA  TGAA
                                |||||  ||||||||  ||||
                                TGTCA  ACACTTTT  ACTT
                                   TC       CA
GAM277  DNMT2    3' TTCAGTTTATACAGCAGACTG  15332        GAA__
                                CAGTCTGT    AAACTGAA
                                ||||||||    ||||||||
                                GTCAGACG    TTTGACTT
                                     ACATA
GAM277  EDNRA    3' CAGATGTTTACAGACTGTGA   64105           AAA
                                TCACAGTCTGTGAA   CTG
                                ||||||||||||||   |||
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                                AGTGTCAGACATTT  GAC
                                        GTA
GAM277  EVA1    3'  TTCAGTTTTTAATCGACTGGA  19399    A    T  G
                                TC CAGTC GT AAAAACTGAA
                                || ||||| || ||||||||||
                                AG GTCAG TA TTTTTGACTT
                                 _    C  A
GAM277  FCMD    3'  CAGTTTTTCAGTCTGTTGA   22089    _  T  GT
                                TCA CAG CT  GAAAAACTG
                                ||| ||| ||  |||||||||
                                AGT GTC GA  CTTTTTGAC
                                  T  T  __
GAM277  GALR1   3'  TTCAACTCTTCATAGATTGTGA 7620            AAAC
                                TCACAGTCTGTGAA   TGAA
                                ||||||||||||||   ||||
                                AGTGTTAGATACTT   ACTT
                                        CTCA
GAM277  GCH1    3'  TTCAATTGTTACAGATGTGA  3861      G     AAAAC
                                TCACA TCTGTGA    TGAA
                                ||||| |||||||    ||||
                                AGTGT AGACATT    ACTT
                                   _      GTTA_
GAM277  GPR85   3'  TCAGTTTTAACTTGTGA    38580      TCT  GA
                                TCACAG   GT  AAAACTGA
                                ||||||   ||  ||||||||
                                AGTGTT   CA  TTTTGACT
                                    ___  A_
GAM277  HAX1    5'  TCAATTTCTCACAGGGCTG   20384     _    A  C
                                CAGTC TGTGA AAA TGA
                                ||||| ||||| ||| |||
                                GTCGG ACACT TTT ACT
                                   G    C  A
GAM277  HSPA9B  3'  TTCAGTCTTTTTACTGTG   14704      CTGT   A
                                CACAGT   GAAA ACTGAA
                                ||||||   |||| ||||||
                                GTGTCA   TTTT TGACTT
                                    T___   C
GAM277  IL18R1  3'  TTCAGTTTCCTCATCTGTGA  13910      TCT   A_
                                TCACAG   GTGA  AAACTGAA
                                ||||||   ||||  ||||||||
                                AGTGTC   TACT  TTTGACTT
                                    ___   CC
GAM277  LFG     3'  TTCAGTTTTTCCATCTG    76730    TC  T
                                CAG  TG GAAAAACTGAA
                                |||  || ||||||||||
                                GTC  AC CTTTTTGACTT
                                  T_ _
GAM277  P2RY6   5'  CAGCACTTCACGGACTG    14740         AAA
                                CAGTCTGTGAA   CTG
                                ||||||||||   |||
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                                GTCAGGCACTT  GAC
                                      CAC
GAM277  PLAG1   3'  TTCAGTTTTTTAAAACT    10612    CTG
                                AGT  TGAAAAACTGAA
                                |||  ||||||||||||
                                TCA  ATTTTTTGACTT
                                  AA_
GAM277  PLAUR   3'  TCAGTTTTCCCAGCTATGA   10618    C  T  T   A
                                TCA AG CTG GAAAA CTGA
                                ||| || ||| ||||| ||||
                                AGT TC GAC CTTTT GACT
                                  A  _  C   _
GAM277  PLCB2   3'  CAGCCTTCTGAGGCTGTGG   15890       GT  AAA
                                TCACAGTCT  GAA  CTG
                                |||||||||  |||  |||
                                GGTGTCGGA  CTT  GAC
                                     GT  CC_
GAM277  POU2AF1  3'  TCAGCCTCTCAGAGTGCTGG  20659    _  G   T  AAAA
                                TCA CA TCTG GA   CTGA
                                ||| || |||| ||   ||||
                                GGT GT AGAC CT   GACT
                                  C  G   T  CC__
GAM277  PPP1R14B 3'  TCAGTTTTCCACTTTTG    56896    TCT  A
                                CAG  GTG AAAACTGA
                                |||  ||| ||||||||
                                GTT  CAC TTTTGACT
                                  TT_  C
GAM277  PPT2    3'  TTCAGTTTTTTTGCTGT    57234     CTGT
                                ACAGT   GAAAAACTGAA
                                |||||   ||||||||||
                                TGTCG   TTTTTTGACTT
                                  T___
GAM277  PTPRO   3'  TTCAGTAAACAGACTGT    47719       GAAAA
                                ACAGTCTGT   ACTGAA
                                |||||||||   ||||||
                                TGTCAGACA   TGACTT
                                     AA___
GAM277  RNMT    3'  CAGTTATCAAGATTGTGA    13714       G  AA
                                TCACAGTCT TGA  AACTG
                                ||||||||| |||  |||||
                                AGTGTTAGA ACT  TTGAC
                                     _  A_
GAM277  SHANK2  3'  TTCAGTTTTTCCATCATGAGA  24590   A  GTC  T
                                TC CA  TG GAAAAACTGAA
                                || ||  || ||||||||||
                                AG GT  AC CTTTTTGACTT
                                 A  ACT  _
GAM277  SIT     3'  TCAGGAGTCCACAGACTGGA  27079   A      AAAAA
                                TC CAGTCTGTG   CTGA
                                || |||||||||   ||||
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                                AG GTCAGACAC    GACT
                                 _       CTGAG
GAM277  STAM     3'  TTCAGTTTCACATTAAACTG  12963     C___     AA
                                CAGT   TGTGAA  ACTGAA
                                ||||   ||||||  ||||||
                                GTCA   ACACTT  TGACTT
                                  AATT     __
GAM277  TMPRSS3  3'  TTCAGCCTCCCACAGTGCTGGG 43801    A   _    AAAAA
           A                     TC CAGT CTGTG    CTGAA
                                || |||| |||||    |||||
                                AG GTCG GACAC    GACTT
                                 G   T    CCTCC
GAM277  TMPRSS3  3'  TTCAGCCTCCCACAGTGCTGGG 50512    A   _    AAAAA
           A                     TC CAGT CTGTG    CTGAA
                                || |||| |||||    |||||
                                AG GTCG GACAC    GACTT
                                 G   T    CCTCC
GAM277  TMPRSS3  3'  TTCAGCCTCCCACAGTGCTGGG 50533    A   _    AAAAA
           A                     TC CAGT CTGTG    CTGAA
                                || |||| |||||    |||||
                                AG GTCG GACAC    GACTT
                                 G   T    CCTCC
GAM277  UBE2A    3'  TTCAGTTTTTCTGTTGT    12471     TCTGT
                                ACAG    GAAAAACTGAA
                                ||||    ||||||||||
                                TGTT    CTTTTTGACTT
                                  GT___
GAM277  UMPS     3'  TCAGTCTCTCAAAGTGCTGGGA 4558     A   _ G   AAA
                                TC CAGT CT TGA   ACTGA
                                || |||| || |||   |||||
                                AG GTCG GA ACT   TGACT
                                 G   T  A   CTC
GAM277  XKRY     3'  TTCAGTTTTTAGAAAATGTGA  60020      GTCTGTG
                                TCACA      AAAAACTGAA
                                |||||      ||||||||||
                                AGTGT      TTTTTGACTT
                                   AAAAGA_
GAM277  ZFP36    3'  CAGTTTTTATAGACCTG     12711     _       A
                                CAG TCTGTGAAAA CTG
                                ||| |||||||||| |||
                                GTC AGATATTTTT GAC
                                  C        _
GAM277  ZFP93    3'  TCATATTTCACAGATGCGA   14888    A  G       AAC
                                TC CA TCTGTGAAA   TGA
                                || || |||||||||   |||
                                AG GT AGACACTTT   ACT
                                 C  _       AT_
GAM277  ASAH     3'  TTCAGTTTTTCACTTCT     15051     TCT
                                AG   GTGAAAAACTGAA
                                ||   ||||||||||||
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                              TC  CACTTTTTGACTT
                               TT_
GAM277  ASE-1    5' CAGTTTTTCCTGCAGA     23947      __
                              TCTGT  GAAAAACTG
                              |||||  |||||||||
                              AGACG  CTTTTTGAC
                                 TC
GAM277  ATP1B4   3' TCAGCCTCCCACAGTGCTGGGA 23828    A  _    AAAAA
                              TC CAGT CTGTG    CTGA
                              || |||| |||||    ||||
                              AG GTCG GACAC    GACT
                               G   T    CCTCC
GAM277  B3GNT1   3' TTCAGTTTTTCAATTGTGG   21663       CTG
                              TCACAGT   TGAAAAACTGAA
                              |||||||   ||||||||||||
                              GGTGTTA   ACTTTTTGACTT
                                  ___
GAM277  B3GNT1   3' TTCAGTTTTTCAATTGTGG   52687       CTG
                              TCACAGT   TGAAAAACTGAA
                              |||||||   ||||||||||||
                              GGTGTTA   ACTTTTTGACTT
                                  ___
GAM277  C11orf9  3' TCAGCCCTTCACAGGCCTG   25214    _      AAA
                              CAG TCTGTGAA   CTGA
                              ||| ||||||||   ||||
                              GTC GGACACTT   GACT
                                C       CCC
GAM277  C21orf41 3' TCAGCTTCGTGGACCCTGA   56360    CA   TG   AAA
                              TCA  GTC  TGAA   CTGA
                              |||  |||  ||||   ||||
                              AGT  CAG  GCTT   GACT
                                CC   GT   C__
GAM277  C9orf12  3' TTCAGTTTTTTATTCTATG   42797    GTCT
                              CA   GTGAAAAACTGAA
                              ||   ||||||||||||
                              GT   TATTTTTTGACTT
                               ATCT
GAM277  CLL-1    3' TTCAGAGAGAATAGACTGTGA  56369          GAAAAA
                              TCACAGTCTGT     CTGAA
                              ||||||||||      |||||
                              AGTGTCAGATA     GACTT
                                    AGAGA_
GAM277  COQ7     3' CAGCCTCTAGGACTGTGA    32329        GT  AAAA
                              TCACAGTCT  GA   CTG
                              |||||||||  ||   |||
                              AGTGTCAGG  CT   GAC
                                   AT  CC__
GAM277  CRNKL1   3' TTCAGAGTCACAGACTTGA   33602     C       AAAA
                              TCA AGTCTGTGA   CTGAA
                              ||| |||||||||   |||||
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                                AGT TCAGACACT    GACTT
                                  _       GA__
GAM277   CYorf15B  3'  TTCAGTTTCTCATAGAGCT    50821    _      A
                                AG TCTGTGA AAACTGAA
                                || ||||||| ||||||||
                                TC AGATACT TTTGACTT
                                 G      C
GAM277   DKFZP434B103 3'  TTCAAGGCCAGACTGTGA    31593          ____
                                TCACAGTCTG    TGAA
                                ||||||||||    ||||
                                AGTGTCAGAC    ACTT
                                      CGGA
GAM277   DKFZP434G1415 3'  TTCAGTTTCAACATCTGT    48446      TC   GAA
                                ACAG  TGT   AAACTGAA
                                ||||  |||   ||||||||
                                TGTC  ACA   TTTGACTT
                                  T_  AC_
GAM277   DKFZp547H236 3'  CAGCCTCCGGCTGTGA      78540       T   T  AAAA
                                TCACAG CTG GA    CTG
                                |||||| ||| ||    |||
                                AGTGTC GGC CT    GAC
                                   _   _  CC__
GAM277   DKFZP564M182 3'  TCAGCTTTTCGCAAC       78042     C       A
                                GT TGTGAAAA CTGA
                                || |||||||| ||||
                                CA ACGCTTTT GACT
                                 _       C
GAM277   DKFZp761D081 3'  TTCAGTTTTTGCTGCTGTGA   34284        CT  G
                                TCACAGT  GT AAAAACTGAA
                                |||||||  || ||||||||||
                                AGTGTCG  CG TTTTTGACTT
                                    T_  _
GAM277   DREV1    3'  TTCAGTTTTGTCTACTGAC    32072     T  _  _
                                GTC GT GA AAAACTGAA
                                ||| || || |||||||||
                                CAG CA CT TTTTGACTT
                                  T  T  G
GAM277   ESDN     3'  TTCAGTTTTCCATAAACTGT   55180      C    A
                                ACAGT TGTG AAAACTGAA
                                ||||| |||| |||||||||
                                TGTCA ATAC TTTTGACTT
                                   A    C
GAM277   FBP17    3'  TCAGCCTCCCAAATAGCTGTGA 72806        T    GAAAAA__
                                TCACAG CTGT       CTGA
                                |||||| ||||       ||||
                                AGTGTC GATA       GACT
                                   _    AACCCTCC
GAM277   FKBP14   3'  TTCACTTTCACAGATATGA   35630     CA        AAC
                                TCA  GTCTGTGAAA   TGAA
                                |||  ||||||||||   ||||
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                                AGT  TAGACACTTT   ACTT
                                  A_         C__
GAM277  FLJ10853  3'  TTCAGTTTCAACACTCTG    36773     TC   GAA
                                CAG  TGT   AAACTGAA
                                |||  |||   ||||||||
                                GTC  ACA   TTTGACTT
                                  TC   AC_
GAM277  FLJ11850  3'  TTCAGTTTTTCCTAACCTGT   42724      TC  T
                                ACAG  TG GAAAAACTGAA
                                ||||  || ||||||||||
                                TGTC  AT CTTTTTGACTT
                                  CA  C
GAM277  FLJ14668  3'  TTCAGCCTGGAGACTGTG    51517         G GAAAAA
                                CACAGTCT T      CTGAA
                                ||||||||  |     |||||
                                GTGTCAGA G      GACTT
                                     G TCC___
GAM277  FLJ20113  3'  TCAGCCCCCAGGCTGTGA    34578          TGAAAAA
                                TCACAGTCTG       CTGA
                                ||||||||||       ||||
                                AGTGTCGGAC       GACT
                                     CCCC___
GAM277  FLJ20195  3'  CAGGAGCACAGACTGGA     34707     A        AAAAA
                                TC CAGTCTGTG     CTG
                                || |||||||||     |||
                                AG GTCAGACAC     GAC
                                 _        GAG__
GAM277  FLJ20449  3'  TCAGTTTTCACCCTG       35188     TCT      A
                                CAG   GTGAAAA CTGA
                                |||   ||||||| ||||
                                GTC   CACTTTT GACT
                                  C__       _
GAM277  FLJ20637  3'  TCAGTCTCTAATTGGCTGTGA  35483         T  GAAAA
                                TCACAGTC GT     ACTGA
                                |||||||| ||     |||||
                                AGTGTCGG TA     TGACT
                                     T  ATCTC
GAM277  FLJ21324  5'  TTCAGTTTCTCATCCAGG    91214      __   A
                                TCTG  TGA AAACTGAA
                                ||||  ||| ||||||||
                                GGAC  ACT TTTGACTT
                                   CT   C
GAM277  FLJ21870  3'  TTCAGTTTTAATCACTGA    43469    T    __
                                TC GTGA  AAAACTGAA
                                || ||||  |||||||||
                                AG CACT  TTTTGACTT
                                 T    AA
GAM277  FLJ23042  3'  TCAGTTTTCTCATCTGT     47176      TCT    _
                                ACAG   GTGA AAAACTGA
                                ||||   |||| ||||||||
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                                TGTC   TACT TTTTGACT
                                  ___    C
GAM277  FLJ23598  5'  TTCAGTTTCCATATGACCAGGA 45523    ACA  _   AA
                                TC   GTC TGTG  AAACTGAA
                                ||   ||| ||||  ||||||||
                                AG   CAG ATAC  TTTGACTT
                                 GAC   T   C_
GAM277  FREQ      3'  TTCAGTTTCCTGTGGCTGGTGA 26594     _   TGTGAA
                                TCAC AGTC     AAACTGAA
                                |||| ||||     ||||||||
                                AGTG TCGG     TTTGACTT
                                  G   TGTCC_
GAM277  GMPPB     5'  CAGGATGGCACAGGCTGTGA  95726          AAAAA
                                TCACAGTCTGTG    CTG
                                ||||||||||||    |||
                                AGTGTCGGACAC    GAC
                                       GGTAG
GAM277  GRIN3A    3'  TTCAGTTTCTATGACTGTGG  55975       TGT   AA
                                TCACAGTC   GAA  ACTGAA
                                ||||||||   |||  ||||||
                                GGTGTCAG   CTT  TGACTT
                                     TAT   __
GAM277  HXCP2     3'  TCAGTTTTGTGACCATGA    50837     CA   TGTGA
                                TCA  GTC    AAAACTGA
                                |||  |||    ||||||||
                                AGT  CAG    TTTTGACT
                                  AC   TG___
GAM277  KIAA0285  3'  TCAGTTTTCTCATCTGT     29022     TCT   _
                                ACAG   GTGA AAAACTGA
                                ||||   |||| ||||||||
                                TGTC   TACT TTTTGACT
                                  ___    C
GAM277  KIAA0534  3'  TTCAGTTTAGAATGACTTTGA  71439     C    TGTGAA
                                TCA AGTC     AAACTGAA
                                ||| ||||     ||||||||
                                AGT TCAG     TTTGACTT
                                  T   TAAGA_
GAM277  KIAA0819  3'  CAGCCTTCTGCTCCCGACTGTG 63576        T___  GA  AA
          A                      TCACAGTC    GT  AA  CTG
                                ||||||||   ||  ||  |||
                                AGTGTCAG    CG  TT  GAC
                                     CCCT  TC  CC
GAM277  KIAA1026  3'  TCAGAGGACAGACTGGGA    71208    A      GAAAAA
                                TC CAGTCTGT     CTGA
                                || ||||||||     ||||
                                AG GTCAGACA     GACT
                                 G       GGA___
GAM277  KIAA1155  3'  TTCAGTTTCTCCAGGCCTTTGA 62245     CA_    T  A
                                TCA   GTCTG GA AAACTGAA
                                |||   ||||| || ||||||||
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                              AGT   CGGAC CT TTTGACTT
                                TTC    _ C
GAM277  KIAA1327 3'  TCAGTTTTTCATAAGA     72269    _
                              TCT GTGAAAAACTGA
                              ||| ||||||||||||
                              AGA TACTTTTTGACT
                                A
GAM277  KIAA1354 3'  TCAGTTTTTTATTACT     60917    CT
                              AGT  GTGAAAAACTGA
                              |||  ||||||||||||
                              TCA  TATTTTTTGACT
                                T_
GAM277  KIAA1596 3'  CAGCCATGCAGGACTGTGA   70914        G  AAAAA
                              TCACAGTCT TG    CTG
                              ||||||||| ||    |||
                              AGTGTCAGG AC    GAC
                                    _ GTACC
GAM277  KIAA1615 3'  TTCAGTTTTTTAATTGT     68740     CTG
                              ACAGT   TGAAAAACTGAA
                              |||||   ||||||||||||
                              TGTTA   ATTTTTTGACTT
                                 ___
GAM277  KIAA1795 5'  TCAGTTTATTTAAAGACTGTGA 72156        G   _
                              TCACAGTCT TGAA AAACTGA
                              ||||||||| |||| |||||||
                              AGTGTCAGA ATTT TTTGACT
                                    A   A
GAM277  KIAA1877 3'  CAGTTTTTCTTATAGA     66169     __
                              TCTGT  GAAAAACTG
                              |||||  |||||||||
                              AGATA  CTTTTTGAC
                                 TT
GAM277  MCM10    3'  TTCAGTTTTCTCATCTGT    37577     TCT   _
                              ACAG   GTGA AAAACTGAA
                              ||||   |||| |||||||||
                              TGTC   TACT TTTTGACTT
                                ___   C
GAM277  MEIS3    3'  CAGCCTCCGGCTGTGA     78277      T   T  AAAA
                              TCACAG CTG GA   CTG
                              |||||| ||| ||   |||
                              AGTGTC GGC CT   GAC
                                 _  _ CC__
GAM277  MGC10334 5'  TTAGGAACCACAGACTGTGA  47559          AAAAA
                              TCACAGTCTGTG    CTGA
                              ||||||||||||    ||||
                              AGTGTCAGACAC    GATT
                                     CAAG_
GAM277  MGC2474  3'  CAGCCTCTCAGATGGCTGTGA 43715        TG_  AAAA
                              TCACAGTC   TGA   CTG
                              ||||||||   |||   |||
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                                AGTGTCGG  ACT   GAC
                                    TAG  CTCC
GAM277  MY014   3' TTCAGTTTTCTCTTCTGTGA  48145      TCTGT _
                                TCACAG    GA AAAACTGAA
                                ||||||    || |||||||||
                                AGTGTC    CT TTTTGACTT
                                   TT___  C
GAM277  NMT1    3' TTTTCACACACGTGA      40793     A  C
                                TCAC GT TGTGAAAA
                                |||| || ||||||||
                                AGTG CA ACACTTTT
                                  _ C
GAM277  NMT2    3' TTCAGTTTCTTCTCAGC    16670   T  T  _
                                G CTG GAA AAACTGAA
                                | ||| ||| ||||||||
                                C GAC CTT TTTGACTT
                                _  T  C
GAM277  NUP133  3' TCAGTTTTCTGCGACTATGA  36689    C   T GA
                                TCA AGTC GT  AAAACTGA
                                ||| |||| ||  ||||||||
                                AGT TCAG CG  TTTTGACT
                                  A   _ TC
GAM277  ORC6L   3' CAGCTCCTCAGTAGGCTGAGA  26723    A     _  AAAA
                                TC CAGTCTG TGA   CTG
                                || ||||||| |||   |||
                                AG GTCGGAT ACT   GAC
                                 A      G  CCTC
GAM277  PAK7    3' TTCAGTTTTCTTTCAAACTGGA 69651    A   C  T  _
                                TC CAGT TG GA AAAACTGAA
                                || |||| || || |||||||||
                                AG GTCA AC TT TTTTGACTT
                                 _   A  T  C
GAM277  PARG1   5' TTCAGTTTTTCTGACTGT    16684      TGT
                                ACAGTC   GAAAAACTGAA
                                ||||||   ||||||||||||
                                TGTCAG   CTTTTTGACTT
                                   T__
GAM277  PDZD2   5' CAGTGGCTCACAGACAGTGA  80864     A      AAA
                                TCAC GTCTGTGA  ACTG
                                |||| ||||||||  ||||
                                AGTG CAGACACT  TGAC
                                  A       CGG
GAM277  PEG10   3' TTCAGTCCCCTCATTAGACTGT 30534       _  AAA_
                                ACAGTCTG TGA   ACTGAA
                                |||||||| |||   ||||||
                                TGTCAGAT ACT   TGACTT
                                     T  CCCC
GAM277  PLAGL2  3' TCAGTTTTTGGCTCTGT    70458     TCT  G
                                ACAG  GT AAAAACTGA
                                ||||  || |||||||||
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                                TGTC  CG TTTTTGACT
                                  T__  G
GAM277  PP1057   3'  TTCAGTTTCTCCTGACTGTGA  48436       TGT  A
                                TCACAGTC  GA AAACTGAA
                                ||||||||  || ||||||||
                                AGTGTCAG  CT TTTGACTT
                                    TC_  C
GAM277  RAB40A   3'  TTCAGTTTCTCACGGG     55149       A
                                TCTGTGA AAACTGAA
                                ||||||| ||||||||
                                GGGCACT TTTGACTT
                                    C
GAM277  RAB40A   3'  TTCAGTTTCTCACGGG     82074       A
                                TCTGTGA AAACTGAA
                                ||||||| ||||||||
                                GGGCACT TTTGACTT
                                    C
GAM277  RNF38    3'  CAGTCAGGACTGTGA      42935       G  AAAA
                                TCACAGTCT TGA   CTG
                                ||||||||| |||   |||
                                AGTGTCAGG ACT   GAC
                                    _  ____
GAM277  RNO2     5'  CAGCTTCTCAGTAGGCTG    52766       _  A  A
                                CAGTCTG TGA AA CTG
                                ||||||| ||| || |||
                                GTCGGAT ACT TT GAC
                                    G  C  C
GAM277  RoXaN    3'  TTCAGTTTCTGCATTCTG    46660    TC  GAA
                                CAG  TGT  AAACTGAA
                                |||  |||  ||||||||
                                GTC  ACG  TTTGACTT
                                  TT  TC_
GAM277  SHARP    3'  CAGTGAAGACAGGCTGTGA   30396        GAAAA
                                TCACAGTCTGT   ACTG
                                ||||||||||   ||||
                                AGTGTCGGACA   TGAC
                                      GAAG_
GAM277  SLC2A13  3'  TCAGTTTTCCTACAGA     53549       A_
                                TCTGTG  AAAACTGA
                                ||||||  ||||||||
                                AGACAT  TTTTGACT
                                   CC
GAM277  SMCR5    3'  TTCAGTTTCCCCACTGGC    58597    T  AA_
                                GTC GTG  AAACTGAA
                                ||| |||  ||||||||
                                CGG CAC  TTTGACTT
                                  T  CCC
GAM277  SUN1     3'  CAGTTTCTACAGACTG      47156       AA
                                CAGTCTGTG  AAACTG
                                |||||||||  ||||||
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                                GTCAGACAT  TTTGAC
                                     C_
GAM277  TCEB1    3'  TTTTCACAAACTGAGA      18942    A   C
                                TC CAGT TGTGAAAA
                                || |||| ||||||||
                                AG GTCA ACACTTTT
                                 A   A
GAM277  THEA     3'  TCAGCTCTGAAGGCTGTGA   66297        GT_  AAAA
                                TCACAGTCT  GA   CTGA
                                |||||||||  ||   ||||
                                AGTGTCGGA  CT   GACT
                                     AGT  C___
GAM277  TOSO     5'  CAGTTCCAGATTGTGA      18388         T  AAA
                                TCACAGTCTG GA  ACTG
                                |||||||||| ||  ||||
                                AGTGTTAGAC CT  TGAC
                                     _  ___
GAM277  TRIM15   5'  CAGTTCTCCCCAGCCACTGTGG 52653       __  TGAAA
                                TCACAGT  CTG    AACTG
                                |||||||  |||    |||||
                                GGTGTCA  GAC    TTGAC
                                    CC   CCCTC
GAM277  WNT10A   5'  CAGTCCCACTGGGCTGTGA   47401        _  AAAA
                                TCACAGTCT GTG   ACTG
                                |||||||| |||   ||||
                                AGTGTCGGG CAC   TGAC
                                     T  CC__
GAM277  LOC126074 3'  TTCAGTTTCCCATGGCTGGA  74436    A    T  AA
                                TC CAGTC GTG  AAACTGAA
                                || ||||| |||  ||||||||
                                AG GTCGG TAC  TTTGACTT
                                 _    _  CC
GAM277  LOC126302 3'  TTCAGCCTGCAGAGACTGTGG  74496        G  AAAAA
                                TCACAGTCT TG    CTGAA
                                ||||||||| ||    |||||
                                GGTGTCAGA AC    GACTT
                                     G  GTCC_
GAM277  LOC138429 3'  TTTTTACAGACCATGA     75343     CA
                                TCA  GTCTGTGAAAA
                                |||  ||||||||||
                                AGT  CAGACATTTTT
                                  AC
GAM277  LOC145566 5'  TCAGTTTTTCTTTCTGT     77279     TCTGT
                                ACAG    GAAAAACTGA
                                ||||    ||||||||||
                                TGTC    CTTTTTGACT
                                  TTT__
GAM277  LOC145678 5'  CAGTTTTTCAACATTTTG    83420     TC  _
                                CAG  TGT GAAAAACTG
                                |||  ||| |||||||||
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                                GTT  ACA CTTTTTGAC
                                  TT   A
GAM277   LOC149267 3'  TCAGTCTGGTATCCAGACTGTG 56679          T  AAA___
             A                    TCACAGTCTG GA      ACTGA
                                  |||||||||| ||      |||||
                                  AGTGTCAGAC CT      TGACT
                                        _  ATGGTC
GAM277   LOC150280 3'  TTCAGTTTATCAGTCTGT    79713      T   TGAA
                                  ACAG CTG    AAACTGAA
                                  |||| |||    ||||||||
                                  TGTC GAC    TTTGACTT
                                    T   TA__
GAM277   LOC150421 3'  TTCAGTTTTTCTCTCTG     85040     TCTGT
                                  CAG     GAAAAACTGAA
                                  |||     ||||||||||
                                  GTC     CTTTTTGACTT
                                    TCT__
GAM277   LOC151174 5'  TTCAGTTCCTCATGGGCT    85255          AA
                                  AGTCTGTGA  AACTGAA
                                  |||||||||  |||||||
                                  TCGGGTACT  TTGACTT
                                       CC
GAM277   LOC152845 3'  TCAGTTTTTGGCTCTGT     60335      TCT  G
                                  ACAG   GT AAAAACTGA
                                  ||||   || |||||||||
                                  TGTC   CG TTTTTGACT
                                    T__  G
GAM277   LOC157621 3'  TCAGTTCATAGGATGT      86496     GT     AAA
                                  ACA  CTGTGA   ACTGA
                                  |||  ||||||   |||||
                                  TGT  GATACT   TGACT
                                    AG     ____
GAM277   LOC158527 5'  TTCAATTTTTTACTTCTGTG   81947       TCT       C
                                  CACAG   GTGAAAAA TGAA
                                  |||||   |||||||| ||||
                                  GTGTC   CATTTTTT ACTT
                                     TT_       A
GAM277   LOC165741 3'  CAGCTTTTCTGAGGCTGTG    87254         GT    A
                                  CACAGTCT  GAAAA CTG
                                  ||||||||  ||||| |||
                                  GTGTCGGA  CTTTT GAC
                                       GT    C
GAM277   LOC169611 3'  TCAGCCTCCCAGACTGTTGG   82778     _      T  AAAA
                                  TCA CAGTCTG GA    CTGA
                                  ||| ||||||| ||    ||||
                                  GGT GTCAGAC CT    GACT
                                    T      C  CC__
GAM277   LOC200830 3'  TTCAGTTTTAACACACAG     90151       A___
                                  CTGTG    AAAACTGAA
                                  |||||    |||||||||
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                                GACAC    TTTTGACTT
                                   ACAA
GAM277   LOC221495 3'  TCAGTTTTTTCATCCTG     93864     TC  T
                                CAG  TG GAAAAACTGA
                                |||  || ||||||||||
                                GTC  AC TTTTTTGACT
                                  CT  _
GAM277   LOC221752 3'  TCAGACATGACTGTGA      93781         _  GAAAAA
                                TCACAGTC TGT     CTGA
                                |||||||| |||     ||||
                                AGTGTCAG ACA     GACT
                                     T  _______
GAM277   LOC221876 5'  TCAGTTTTGCACCGGG      93925      _ A
                                TCTG TG AAAACTGA
                                |||| || ||||||||
                                GGGC AC TTTTGACT
                                   C  G
GAM277   LOC253955 5'  TCAGTTTTCCATAGC       94432    T    A
                                G CTGTG AAAACTGA
                                | ||||| ||||||||
                                C GATAC TTTTGACT
                                _    C
GAM277   LOC254249 5'  TCAGTTTTTCTCATAT      95448    C  T
                                GT TG GAAAAACTGA
                                || || ||||||||||
                                TA AC CTTTTTGACT
                                 T  T
GAM277   LOC255446 5'  CAGAACTTCACAGACTGT    97152           AAA
                                ACAGTCTGTGAA   CTG
                                ||||||||||||   |||
                                TGTCAGACACTT   GAC
                                       CAA
GAM277   LOC256372 5'  CAGTTTGGCACTGTGA      95270        CTGT AA
                                TCACAGT    G  AAACTG
                                |||||||    |  ||||||
                                AGTGTCA    C  TTTGAC
                                    ____ GG
GAM277   LOC257106 3'  CAGCTTCTCTCTTTGACTGTGG 95385         TGT__  A  A
                                TCACAGTC     GA AA CTG
                                ||||||||     || || |||
                                GGTGTCAG     CT TT GAC
                                     TTTCT  C  C
GAM277   LOC257468 3'  CAGCCTCCGGCTGTGA      95184       T   T  AAAA
                                TCACAG CTG GA    CTG
                                |||||| ||| ||    |||
                                AGTGTC GGC CT    GAC
                                   _  _  CC__
GAM277   LOC51029  3'  CAGTTTTTCAGCTCAGG     32181      ___
                                TCTG   TGAAAAACTG
                                ||||   ||||||||||
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                                GGAC   ACTTTTTGAC
                                  TCG
GAM277  LOC54518  3' TTCAGTTTGAGACCAGACTGGA 38774    A      TGAA_
                                TC CAGTCTG    AAACTGAA
                                || |||||||    ||||||||
                                AG GTCAGAC    TTTGACTT
                                 _      CAGAG
GAM277  LOC57826  3' TTCAGTTTTAACATCGTGA   41020     AGTC   GA
                                TCAC   TGT  AAAACTGAA
                                ||||   |||  |||||||||
                                AGTG   ACA  TTTTGACTT
                                  CT__   A_
GAM277  LOC90957  5' TCAGCCACCAGACTGT     64466        _ AAAAA
                                ACAGTCTG TG    CTGA
                                |||||||| ||    ||||
                                TGTCAGAC AC    GACT
                                     C  C____
GAM277  LOC91097  3' TTCAGTTTCTCATCCAGG    64841     __   A
                                TCTG  TGA AAACTGAA
                                ||||  ||| ||||||||
                                GGAC  ACT TTTGACTT
                                  CT   C
GAM277  LOC91115  3' TCAGTTTTTGAGACGTGA    64953     A   GTG
                                TCAC GTCT   AAAAACTGA
                                |||| ||||   |||||||||
                                AGTG CAGA   TTTTTGACT
                                  _   G__
GAM277  LOC91351  3' CAGCCTCCAGGATTGTGA    65706        GT  AAAA
                                TCACAGTCT  GA    CTG
                                |||||||||  ||    |||
                                AGTGTTAGG  CT    GAC
                                     AC  CC__
GAM277  LOC91464  3' TCAGTTTTCTCATCTGT     66144     TCT   _
                                ACAG   GTGA AAAACTGA
                                ||||   |||| ||||||||
                                TGTC   TACT TTTTGACT
                                  ___    C
GAM277  LOC92223  5' TCAGTTTTTCTCCTGTTGA   68525     _  TCTGT
                                TCA CAG    GAAAAACTGA
                                ||| |||    ||||||||||
                                AGT GTC    CTTTTTGACT
                                  T   CT___
GAM278  ESRRG     3' GTAGTAAAAATAATAATA    66393        C
                                TATTATTA TTTTGCTAC
                                |||||||| |||||||||
                                ATAATAAT AAAATGATG
                                     A
GAM278  PBX2      3' AGATGTGGGGAAAAGTAA    10443        G  AC
                                TTACTTTT CT  CATCT
                                |||||||| ||  |||||
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                                AATGAAAA GG  GTAGA
                                     G  GT
GAM278  SIP      3'  AGATGGTTTATAAAAGTAATAA 26974          CT_
                                TTATTACTTTTG   ACCATCT
                                ||||||||||||  |||||||
                                AATAATGAAAAT   TGGTAGA
                                      ATT
GAM278  TRIM8    3'  AGCAAAAGCAAATAATA     48113        A_
                                TATTATT  CTTTTGCT
                                |||||||  ||||||||
                                ATAATAA  GAAAACGA
                                     AC
GAM278  FAF1     3'  TGCTGGAAAAAGTAATAATA   22932          G   C
                                TATTATTACTTTT CTA CA
                                |||||||||||| ||| ||
                                ATAATAATGAAAA GGT GT
                                       A   C
GAM278  KIAA1466 3'  TAGCATAAGTAATAATAG    71916          T
                                CTATTATTACTT TGCTA
                                |||||||||||| |||||
                                GATAATAATGAA ACGAT
                                       T
GAM278  LAMP3    3'  AGATGGTAGAACTAAACAATAA 59485       ACTTTTG_
                                TTATT       CTACCATCT
                                |||||       |||||||||
                                AATAA       GATGGTAGA
                                   CAAATCAA
GAM278  LAMP3    3'  AGCAAGAGACAATAATA     59486        A_
                                TATTATT  CTTTTGCT
                                |||||||  ||||||||
                                ATAATAA  GAGAACGA
                                     CA
GAM278  MAP2K1IP1 3'  ATGGCTTGGTAAAAGTAATAA  41743            __
                                TTATTACTTTTGCTA  CCAT
                                ||||||||||||||  ||||
                                AATAATGAAAATGGT  GGTA
                                       TC
GAM278  MGC23980 3'  TGGCAATAATAGTAATAG    58761         CTT
                                CTATTATTA   TTGCTA
                                |||||||||   ||||||
                                GATAATGAT   AACGGT
                                      AAT
GAM278  ZNF238   5'  GGTAGCAAAAGTAATAA     20965
                                TTATTACTTTTGCTACC
                                |||||||||||||||||
                                AATAATGAAAACGATGG

GAM278  LOC146988 5'  GGGAATAATAGTAATAATAG  83894          T   CTA
                                CTATTATTACT TTG   CC
                                ||||||||||| |||   ||
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                                GATAATAATGA AAT   GG
                                      T   AAG
GAM278  LOC149420 3'  AGTACTGGTAATAATA      79366          TT
                                TATTATTACT  TGCT
                                ||||||||||  ||||
                                ATAATAATGG  ATGA
                                      TC
GAM278  LOC221405 3'  TAGCAAAAGTAATAATTA    93887    T
                                C ATTATTACTTTTGCTA
                                | ||||||||||||||||
                                A TAATAATGAAAACGAT
                                 T
GAM278  LOC255158 3'  TAGCAAATATTATAATAG    96172        TACT
                                CTATTAT    TTTGCTA
                                |||||||    |||||||
                                GATAATA    AAACGAT
                                     TTAT
GAM278  LOC91660  5'  GTGGCAATAATAATAATAG   66869         CTT
                                CTATTATTA   TTGCTAC
                                |||||||||   |||||||
                                GATAATAAT   AACGGTG
                                      AAT
GAM279  BAZ1A     3'  TTCAGCTTTACAGAACTGT    25584      _      AAA
                                ACAGT CTGTGAA   CTGAA
                                ||||| |||||||   |||||
                                TGTCA GACATTT   GACTT
                                   A      C__
GAM279  BAZ2A     3'  CAGCCTCTTCAGACTGTG     25596         T_  AAAA
                                CACAGTCTG  GA    CTG
                                |||||||||  ||    |||
                                GTGTCAGAC  CT    GAC
                                      TT  CC__
GAM279  CNR1      3'  TTTTCACAGCTATGA       32218     C  T
                                TCA AG CTGTGAAAA
                                ||| || |||||||||
                                AGT TC GACACTTTT
                                  A  _
GAM279  CPA3      3'  TCAGTTTCTCACAGATT      8522          A
                                AGTCTGTGA AAACTGA
                                |||||||| |||||||
                                TTAGACACT TTTGACT
                                      C
GAM279  CX3CR1    3'  TTCAGTTTCCTGGTCTGTAGA  70647    _   T   T   AA
                                TC ACAG CTG GAA  ACTGAA
                                || |||| ||| |||  ||||||
                                AG TGTC GGT CTT  TGACTT
                                 A    T   C   __
GAM279  DIAPH2    3'  TTCAACTTTTCACACTACTGT  22072      C_      AC
                                ACAGT  TGTGAAAA  TGAA
                                |||||  ||||||||  ||||
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                                TGTCA  ACACTTTT  ACTT
                                  TC       CA
GAM279  DNMT2    3'  TTCAGTTTATACAGCAGACTG  15332        GAA__
                                CAGTCTGT    AAACTGAA
                                ||||||||    ||||||||
                                GTCAGACG    TTTGACTT
                                    ACATA
GAM279  EDNRA    3'  CAGATGTTTACAGACTGTGA  64105           AAA
                                TCACAGTCTGTGAA  CTG
                                ||||||||||||||  |||
                                AGTGTCAGACATTT  GAC
                                        GTA
GAM279  EVA1     3'  TTCAGTTTTTAATCGACTGGA  19399    A    T  G
                                TC CAGTC GT AAAAACTGAA
                                || ||||| || ||||||||||
                                AG GTCAG TA TTTTTGACTT
                                 _    C  A
GAM279  FCMD     3'  CAGTTTTTCAGTCTGTTGA   22089    _  T  GT
                                TCA CAG CT  GAAAAACTG
                                ||| ||| ||  |||||||||
                                AGT GTC GA  CTTTTTGAC
                                  T   T  __
GAM279  GALR1    3'  TTCAACTCTTCATAGATTGTGA 7620           AAAC
                                TCACAGTCTGTGAA   TGAA
                                ||||||||||||||   ||||
                                AGTGTTAGATACTT   ACTT
                                        CTCA
GAM279  GCH1     3'  TTCAATTGTTACAGATGTGA  3861      G     AAAAC
                                TCACA TCTGTGA    TGAA
                                ||||| |||||||    ||||
                                AGTGT AGACATT    ACTT
                                   _     GTTA_
GAM279  GPR85    3'  TCAGTTTTAACTTGTGA    38580      TCT  GA
                                TCACAG   GT  AAAACTGA
                                ||||||   ||  ||||||||
                                AGTGTT   CA  TTTTGACT
                                    ___  A_
GAM279  HAX1     5'  TCAATTTCTCACAGGGCTG   20384     _    A  C
                                CAGTC TGTGA AAA TGA
                                ||||| ||||| ||| |||
                                GTCGG ACACT TTT ACT
                                   G    C  A
GAM279  HSPA9B   3'  TTCAGTCTTTTTACTGTG    14704      CTGT   A
                                CACAGT    GAAA ACTGAA
                                ||||||    |||| ||||||
                                GTGTCA    TTTT TGACTT
                                   T___    C
GAM279  IL18R1   3'  TTCAGTTTCCTCATCTGTGA  13910      TCT   A_
                                TCACAG   GTGA  AAACTGAA
                                ||||||   ||||  ||||||||
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                                AGTGTC  TACT  TTTGACTT
                                   ___   CC
GAM279  LFG     3'  TTCAGTTTTTCCATCTG    76730    TC  T
                                CAG  TG GAAAAACTGAA
                                |||  || ||||||||||
                                GTC  AC CTTTTTGACTT
                                  T_  _
GAM279  P2RY6   5'  CAGCACTTCACGGACTG    14740         AAA
                                CAGTCTGTGAA  CTG
                                ||||||||||  |||
                                GTCAGGCACTT  GAC
                                      CAC
GAM279  PLAG1   3'  TTCAGTTTTTTAAAACT    10612    CTG
                                AGT  TGAAAAACTGAA
                                |||  ||||||||||||
                                TCA  ATTTTTTGACTT
                                  AA_
GAM279  PLAUR   3'  TCAGTTTTCCCAGCTATGA   10618    C  T  T   A
                                TCA AG CTG GAAAA CTGA
                                ||| || ||| ||||| ||||
                                AGT TC GAC CTTTT GACT
                                  A  _  C    _
GAM279  PLCB2   3'  CAGCCTTCTGAGGCTGTGG   15890       GT  AAA
                                TCACAGTCT  GAA  CTG
                                |||||||||  |||  |||
                                GGTGTCGGA  CTT  GAC
                                     GT  CC_
GAM279  POU2AF1 3'  TCAGCCTCTCAGAGTGCTGG  20659    _  G   T  AAAA
                                TCA CA TCTG GA   CTGA
                                ||| || |||| ||   ||||
                                GGT GT AGAC CT   GACT
                                  C  G   T  CC__
GAM279  PPP1R14B 3' TCAGTTTTCCACTTTTG    56896    TCT  A
                                CAG  GTG AAAACTGA
                                |||  ||| ||||||||
                                GTT  CAC TTTTGACT
                                  TT_  C
GAM279  PPT2    3'  TTCAGTTTTTTTGCTGT    57234     CTGT
                                ACAGT   GAAAAACTGAA
                                |||||   ||||||||||
                                TGTCG   TTTTTTGACTT
                                  T___
GAM279  PTPRO   3'  TTCAGTAAACAGACTGT    47719       GAAAA
                                ACAGTCTGT   ACTGAA
                                |||||||||   ||||||
                                TGTCAGACA   TGACTT
                                     AA___
GAM279  RNMT    3'  CAGTTATCAAGATTGTGA   13714       G  AA
                                TCACAGTCT TGA  AACTG
                                ||||||||| |||  |||||
```

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                                AGTGTTAGA ACT  TTGAC
                                      _  A_
GAM279  SHANK2   3'  TTCAGTTTTTCCATCATGAGA  24590    A  GTC  T
                                TC CA   TG GAAAAACTGAA
                                || ||   || ||||||||||
                                AG GT   AC CTTTTTGACTT
                                 A  ACT  _
GAM279  SIT      3'  TCAGGAGTCCACAGACTGGA   27079    A       AAAAA
                                TC CAGTCTGTG    CTGA
                                || |||||||||    ||||
                                AG GTCAGACAC    GACT
                                 _       CTGAG
GAM279  STAM     3'  TTCAGTTTCACATTAAACTG   12963     C___     AA
                                CAGT   TGTGAA  ACTGAA
                                ||||   ||||||  ||||||
                                GTCA   ACACTT  TGACTT
                                  AATT     __
GAM279  TMPRSS3  3'  TTCAGCCTCCCACAGTGCTGGG 50512    A   _    AAAAA
           A                     TC CAGT CTGTG    CTGAA
                                || |||| |||||    |||||
                                AG GTCG GACAC    GACTT
                                 G   T    CCTCC
GAM279  TMPRSS3  3'  TTCAGCCTCCCACAGTGCTGGG 50533    A   _    AAAAA
           A                     TC CAGT CTGTG    CTGAA
                                || |||| |||||    |||||
                                AG GTCG GACAC    GACTT
                                 G   T    CCTCC
GAM279  TMPRSS3  3'  TTCAGCCTCCCACAGTGCTGGG 43801    A   _    AAAAA
           A                     TC CAGT CTGTG    CTGAA
                                || |||| |||||    |||||
                                AG GTCG GACAC    GACTT
                                 G   T    CCTCC
GAM279  UBE2A    3'  TTCAGTTTTTCTGTTGT     12471      TCTGT
                                ACAG    GAAAAACTGAA
                                ||||    ||||||||||
                                TGTT    CTTTTTGACTT
                                  GT___
GAM279  UMPS     3'  TCAGTCTCTCAAAGTGCTGGGA 4558     A   _ G   AAA
                                TC CAGT CT TGA   ACTGA
                                || |||| || |||   |||||
                                AG GTCG GA ACT   TGACT
                                 G   T A   CTC
GAM279  XKRY     3'  TTCAGTTTTTAGAAAATGTGA  60020      GTCTGTG
                                TCACA      AAAAACTGAA
                                |||||      ||||||||||
                                AGTGT      TTTTTGACTT
                                   AAAAGA_
GAM279  ZFP36    3'  CAGTTTTTATAGACCTG     12711     _        A
                                CAG TCTGTGAAAA CTG
                                ||| |||||||||| |||
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                                GTC AGATATTTTT GAC
                                  C       _
GAM279  ZFP93    3' TCATATTTCACAGATGCGA   14888    A  G       AAC
                                TC CA TCTGTGAAA   TGA
                                || || |||||||||   |||
                                AG GT AGACACTTT   ACT
                                 C  _       AT_
GAM279  ASAH     3' TTCAGTTTTTCACTTCT     15051    TCT
                                AG   GTGAAAAACTGAA
                                ||   ||||||||||||
                                TC   CACTTTTTGACTT
                                 TT_
GAM279  ASE-1    5' CAGTTTTTCCTGCAGA      23947      __
                                TCTGT  GAAAAACTG
                                |||||  |||||||||
                                AGACG  CTTTTTGAC
                                   TC
GAM279  ATP1B4   3' TCAGCCTCCCACAGTGCTGGGA 23828    A   _    AAAAA
                                TC CAGT CTGTG    CTGA
                                || |||| |||||    ||||
                                AG GTCG GACAC    GACT
                                 G   T    CCTCC
GAM279  B3GNT1   3' TTCAGTTTTTCAATTGTGG   21663       CTG
                                TCACAGT   TGAAAAACTGAA
                                |||||||   ||||||||||||
                                GGTGTTA   ACTTTTTGACTT
                                    ___
GAM279  B3GNT1   3' TTCAGTTTTTCAATTGTGG   52687       CTG
                                TCACAGT   TGAAAAACTGAA
                                |||||||   ||||||||||||
                                GGTGTTA   ACTTTTTGACTT
                                    ___
GAM279  C11orf9  3' TCAGCCCTTCACAGGCCTG   25214    _      AAA
                                CAG TCTGTGAA   CTGA
                                ||| ||||||||   ||||
                                GTC GGACACTT   GACT
                                  C       CCC
GAM279  C21orf41 3' TCAGCTTCGTGGACCCTGA   56360    CA   TG   AAA
                                TCA  GTC  TGAA   CTGA
                                |||  |||  ||||   ||||
                                AGT  CAG  GCTT   GACT
                                  CC   GT   C__
GAM279  C9orf12  3' TTCAGTTTTTTATTCTATG   42797    GTCT
                                CA   GTGAAAAACTGAA
                                ||   ||||||||||||
                                GT   TATTTTTTGACTT
                                 ATCT
GAM279  CLL-1    3' TTCAGAGAGAATAGACTGTGA  56369          GAAAAA
                                TCACAGTCTGT     CTGAA
                                ||||||||||      |||||
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                                AGTGTCAGATA     GACTT
                                      AGAGA_
GAM279  COQ7     3'  CAGCCTCTAGGACTGTGA    32329         GT  AAAA
                                TCACAGTCT  GA    CTG
                                |||||||||  ||    |||
                                AGTGTCAGG  CT    GAC
                                     AT  CC__
GAM279  CRNKL1   3'  TTCAGAGTCACAGACTTGA   33602     C       AAAA
                                TCA AGTCTGTGA    CTGAA
                                ||| |||||||||    |||||
                                AGT TCAGACACT    GACTT
                                  _       GA__
GAM279  CYorf15B 3'  TTCAGTTTCTCATAGAGCT   50821    _      A
                                AG TCTGTGA AAACTGAA
                                || ||||||| ||||||||
                                TC AGATACT TTTGACTT
                                 G      C
GAM279  DKFZP434B103 3'  TTCAAGGCCAGACTGTGA    31593          ____
                                TCACAGTCTG    TGAA
                                ||||||||||    ||||
                                AGTGTCAGAC    ACTT
                                      CGGA
GAM279  DKFZP434G1415 3'  TTCAGTTTCAACATCTGT    48446      TC   GAA
                                ACAG  TGT   AAACTGAA
                                ||||  |||   ||||||||
                                TGTC  ACA   TTTGACTT
                                  T_  AC_
GAM279  DKFZp547H236 3'  CAGCCTCCGGCTGTGA      78540       T   T  AAAA
                                TCACAG CTG GA    CTG
                                |||||| ||| ||    |||
                                AGTGTC GGC CT    GAC
                                   _   _  CC__
GAM279  DKFZP564M182 3'  TCAGCTTTTCGCAAC       78042     C       A
                                GT TGTGAAAA CTGA
                                || |||||||| ||||
                                CA ACGCTTTT GACT
                                 _       C
GAM279  DKFZp761D081 3'  TTCAGTTTTTGCTGCTGTGA   34284        CT  G
                                TCACAGT  GT AAAAACTGAA
                                |||||||  || ||||||||||
                                AGTGTCG  CG TTTTTGACTT
                                     T_  _
GAM279  DREV1    3'  TTCAGTTTTGTCTACTGAC    32072     T  _  _
                                GTC GT GA AAAACTGAA
                                ||| || || |||||||||
                                CAG CA CT TTTTGACTT
                                  T  T  G
GAM279  ESDN     3'  TTCAGTTTTCCATAAACTGT   55180       C    A
                                ACAGT TGTG AAAACTGAA
                                ||||| |||| |||||||||
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                                TGTCA ATAC TTTTGACTT
                                  A   C
GAM279  FBP17    3'  TCAGCCTCCCAAATAGCTGTGA 72806      T   GAAAAA__
                                TCACAG CTGT      CTGA
                                |||||| ||||      ||||
                                AGTGTC GATA      GACT
                                   _   AACCCTCC
GAM279  FKBP14   3'  TTCACTTTCACAGATATGA   35630    CA       AAC
                                TCA  GTCTGTGAAA  TGAA
                                |||  ||||||||||  ||||
                                AGT  TAGACACTTT  ACTT
                                  A_       C__
GAM279  FLJ10853 3'  TTCAGTTTCAACACTCTG    36773    TC   GAA
                                CAG  TGT   AAACTGAA
                                |||  |||   ||||||||
                                GTC  ACA   TTTGACTT
                                  TC   AC_
GAM279  FLJ11850 3'  TTCAGTTTTTCCTAACCTGT   42724     TC  T
                                ACAG  TG GAAAAACTGAA
                                ||||  || ||||||||||
                                TGTC  AT CTTTTTGACTT
                                  CA  C
GAM279  FLJ14668 3'  TTCAGCCTGGAGACTGTG    51517       G GAAAAA
                                CACAGTCT T     CTGAA
                                |||||||| |     |||||
                                GTGTCAGA G     GACTT
                                     G TCC___
GAM279  FLJ20113 3'  TCAGCCCCCAGGCTGTGA    34578         TGAAAAA
                                TCACAGTCTG      CTGA
                                ||||||||||      ||||
                                AGTGTCGGAC      GACT
                                     CCCC___
GAM279  FLJ20195 3'  CAGGAGCACAGACTGGA     34707    A       AAAAA
                                TC CAGTCTGTG    CTG
                                || |||||||||    |||
                                AG GTCAGACAC    GAC
                                 _       GAG__
GAM279  FLJ20449 3'  TCAGTTTTCACCCTG       35188    TCT     A
                                CAG   GTGAAAA CTGA
                                |||   ||||||| ||||
                                GTC   CACTTTT GACT
                                  C__      _
GAM279  FLJ20637 3'  TCAGTCTCTAATTGGCTGTGA  35483       T  GAAAA
                                TCACAGTC GT    ACTGA
                                |||||||| ||    |||||
                                AGTGTCGG TA    TGACT
                                     T  ATCTC
GAM279  FLJ21324 5'  TTCAGTTTCTCATCCAGG    91214     __  A
                                TCTG  TGA AAACTGAA
                                ||||  ||| ||||||||
```

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                                GGAC  ACT TTTGACTT
                                  CT   C
GAM279  FLJ21870  3'  TTCAGTTTTAATCACTGA    43469    T   __
                                TC GTGA  AAAACTGAA
                                || ||||  |||||||||
                                AG CACT  TTTTGACTT
                                 T    AA
GAM279  FLJ23042  3'  TCAGTTTTCTCATCTGT     47176     TCT   _
                                ACAG   GTGA AAAACTGA
                                ||||   |||| ||||||||
                                TGTC   TACT TTTTGACT
                                  ___    C
GAM279  FLJ23598  5'  TTCAGTTTCCATATGACCAGGA 45523    ACA   _    AA
                                TC   GTC TGTG  AAACTGAA
                                ||   ||| ||||  ||||||||
                                AG   CAG ATAC  TTTGACTT
                                 GAC   T    C_
GAM279  FREQ     3'  TTCAGTTTCCTGTGGCTGGTGA 26594      _    TGTGAA
                                TCAC AGTC     AAACTGAA
                                |||| ||||     ||||||||
                                AGTG TCGG     TTTGACTT
                                  G    TGTCC_
GAM279  GMPPB    5'  CAGGATGGCACAGGCTGTGA   95726           AAAAA
                                TCACAGTCTGTG    CTG
                                ||||||||||||    |||
                                AGTGTCGGACAC    GAC
                                       GGTAG
GAM279  GRIN3A   3'  TTCAGTTTCTATGACTGTGG   55975        TGT   AA
                                TCACAGTC   GAA  ACTGAA
                                ||||||||   |||  ||||||
                                GGTGTCAG   CTT  TGACTT
                                     TAT   __
GAM279  HXCP2    3'  TCAGTTTTGTGACCATGA    50837     CA   TGTGA
                                TCA  GTC    AAAACTGA
                                |||  |||    ||||||||
                                AGT  CAG    TTTTGACT
                                  AC   TG___
GAM279  KIAA0285 3'  TCAGTTTTCTCATCTGT     29022     TCT   _
                                ACAG   GTGA AAAACTGA
                                ||||   |||| ||||||||
                                TGTC   TACT TTTTGACT
                                  ___    C
GAM279  KIAA0534 3'  TTCAGTTTAGAATGACTTTGA  71439     C    TGTGAA
                                TCA AGTC     AAACTGAA
                                ||| ||||     ||||||||
                                AGT TCAG     TTTGACTT
                                  T    TAAGA_
GAM279  KIAA0819 3'  CAGCCTTCTGCTCCCGACTGTG 63576        T___  GA  AA
           A                     TCACAGTC    GT  AA  CTG
                                ||||||||    ||  ||  |||
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                              AGTGTCAG   CG  TT  GAC
                                   CCCT  TC  CC
GAM279  KIAA1026 3' TCAGAGGACAGACTGGGA    71208    A      GAAAAA
                              TC CAGTCTGT     CTGA
                              || ||||||||     ||||
                              AG GTCAGACA     GACT
                               G       GGA___
GAM279  KIAA1155 3' TTCAGTTTCTCCAGGCCTTTGA 62245     CA_    T  A
                              TCA   GTCTG GA AAACTGAA
                              |||   ||||| || ||||||||
                              AGT   CGGAC CT TTTGACTT
                                TTC    _  C
GAM279  KIAA1327 3' TCAGTTTTTCATAAGA      72269     _
                              TCT GTGAAAAACTGA
                              ||| ||||||||||||
                              AGA TACTTTTTGACT
                                A
GAM279  KIAA1354 3' TCAGTTTTTTATTACT      60917     CT
                              AGT  GTGAAAAACTGA
                              |||  ||||||||||||
                              TCA  TATTTTTTGACT
                                T_
GAM279  KIAA1596 3' CAGCCATGCAGGACTGTGA   70914         G  AAAAA
                              TCACAGTCT TG    CTG
                              |||||||| ||    |||
                              AGTGTCAGG AC    GAC
                                   _ GTACC
GAM279  KIAA1615 3' TTCAGTTTTTTAATTGT     68740      CTG
                              ACAGT   TGAAAAACTGAA
                              |||||   ||||||||||||
                              TGTTA   ATTTTTTGACTT
                                 ___
GAM279  KIAA1795 5' TCAGTTTATTTAAAGACTGTGA 72156         G   _
                              TCACAGTCT TGAA AAACTGA
                              |||||||| |||| |||||||
                              AGTGTCAGA ATTT TTTGACT
                                   A   A
GAM279  KIAA1877 3' CAGTTTTTCTTATAGA      66169       __
                              TCTGT  GAAAAACTG
                              |||||  |||||||||
                              AGATA  CTTTTTGAC
                                 TT
GAM279  MCM10    3' TTCAGTTTTCTCATCTGT    37577      TCT   _
                              ACAG   GTGA AAAACTGAA
                              ||||   |||| |||||||||
                              TGTC   TACT TTTTGACTT
                                ___    C
GAM279  MEIS3    3' CAGCCTCCGGCTGTGA      78277       T   T  AAAA
                              TCACAG CTG GA    CTG
                              |||||| ||| ||    |||
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                                AGTGTC GGC CT   GAC
                                   _  _  CC__
GAM279  MGC10334  5'  TTAGGAACCACAGACTGTGA  47559          AAAAA
                                TCACAGTCTGTG   CTGA
                                ||||||||||||   ||||
                                AGTGTCAGACAC   GATT
                                      CAAG_
GAM279  MGC2474   3'  CAGCCTCTCAGATGGCTGTGA  43715       TG_  AAAA
                                TCACAGTC  TGA  CTG
                                ||||||||  |||  |||
                                AGTGTCGG  ACT  GAC
                                    TAG  CTCC
GAM279  MY014     3'  TTCAGTTTTCTCTTCTGTGA  48145      TCTGT  _
                                TCACAG    GA AAAACTGAA
                                ||||||    || |||||||||
                                AGTGTC    CT TTTTGACTT
                                   TT___  C
GAM279  NMT1      3'  TTTTCACACACGTGA      40793     A  C
                                TCAC GT TGTGAAAA
                                |||| || ||||||||
                                AGTG CA ACACTTTT
                                  _ C
GAM279  NMT2      3'  TTCAGTTTCTTCTCAGC    16670   T  T  _
                                G CTG GAA AAACTGAA
                                | ||| ||| ||||||||
                                C GAC CTT TTTGACTT
                                 _  T  C
GAM279  NUP133    3'  TCAGTTTTCTGCGACTATGA  36689    C   T  GA
                                TCA AGTC GT  AAAACTGA
                                ||| |||| ||  ||||||||
                                AGT TCAG CG  TTTTGACT
                                  A   _  TC
GAM279  ORC6L     3'  CAGCTCCTCAGTAGGCTGAGA  26723    A     _  AAAA
                                TC CAGTCTG TGA   CTG
                                || ||||||| |||   |||
                                AG GTCGGAT ACT   GAC
                                 A      G  CCTC
GAM279  PAK7      3'  TTCAGTTTTCTTTCAAACTGGA 69651    A   C  T  _
                                TC CAGT TG GA AAAACTGAA
                                || |||| || || |||||||||
                                AG GTCA AC TT TTTTGACTT
                                 _   A  T  C
GAM279  PARG1     5'  TTCAGTTTTTCTGACTGT    16684      TGT
                                ACAGTC  GAAAAACTGAA
                                ||||||  ||||||||||
                                TGTCAG  CTTTTTGACTT
                                   T__
GAM279  PDZD2     5'  CAGTGGCTCACAGACAGTGA  80864     A      AAA
                                TCAC GTCTGTGA  ACTG
                                |||| ||||||||  ||||
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                                AGTG CAGACACT   TGAC
                                  A       CGG
GAM279  PEG10    3'  TTCAGTCCCCTCATTAGACTGT 30534        _  AAA_
                                ACAGTCTG TGA    ACTGAA
                                |||||||| |||    ||||||
                                TGTCAGAT ACT    TGACTT
                                    T   CCCC
GAM279  PLAGL2   3'  TCAGTTTTTGGCTCTGT     70458      TCT  G
                                ACAG   GT AAAAACTGA
                                ||||   || |||||||||
                                TGTC   CG TTTTTGACT
                                  T__  G
GAM279  PP1057   3'  TTCAGTTTCTCCTGACTGTGA  48436        TGT  A
                                TCACAGTC   GA AAACTGAA
                                ||||||||   || ||||||||
                                AGTGTCAG   CT TTTGACTT
                                    TC_  C
GAM279  RAB40A   3'  TTCAGTTTCTCACGGG      55149        A
                                TCTGTGA AAACTGAA
                                ||||||| ||||||||
                                GGGCACT TTTGACTT
                                    C
GAM279  RAB40A   3'  TTCAGTTTCTCACGGG      82074        A
                                TCTGTGA AAACTGAA
                                ||||||| ||||||||
                                GGGCACT TTTGACTT
                                    C
GAM279  RNF38    3'  CAGTCAGGACTGTGA       42935        G   AAAA
                                TCACAGTCT TGA    CTG
                                ||||||||| |||    |||
                                AGTGTCAGG ACT    GAC
                                      _  ____
GAM279  RNO2     5'  CAGCTTCTCAGTAGGCTG    52766        _   A  A
                                CAGTCTG TGA AA CTG
                                ||||||| ||| || |||
                                GTCGGAT ACT TT GAC
                                    G   C  C
GAM279  RoXaN    3'  TTCAGTTTCTGCATTCTG    46660     TC   GAA
                                CAG  TGT   AAACTGAA
                                |||  |||   ||||||||
                                GTC  ACG   TTTGACTT
                                  TT   TC_
GAM279  SHARP    3'  CAGTGAAGACAGGCTGTGA   30396          GAAAA
                                TCACAGTCTGT    ACTG
                                ||||||||||    ||||
                                AGTGTCGGACA    TGAC
                                      GAAG_
GAM279  SLC2A13  3'  TCAGTTTTCCTACAGA      53549        A_
                                TCTGTG  AAAACTGA
                                ||||||  ||||||||
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                                AGACAT  TTTTGACT
                                   CC
GAM279  SMCR5    3'  TTCAGTTTCCCCACTGGC    58597     T   AA_
                                GTC GTG   AAACTGAA
                                ||| |||   ||||||||
                                CGG CAC   TTTGACTT
                                  T   CCC
GAM279  SUN1     3'  CAGTTTCTACAGACTG      47156         AA
                                CAGTCTGTG  AAACTG
                                |||||||||  ||||||
                                GTCAGACAT  TTTGAC
                                     C_
GAM279  TCEB1    3'  TTTTCACAAACTGAGA      18942    A    C
                                TC CAGT TGTGAAAA
                                || |||| ||||||||
                                AG GTCA ACACTTTT
                                 A   A
GAM279  THEA     3'  TCAGCTCTGAAGGCTGTGA   66297         GT_  AAAA
                                TCACAGTCT   GA   CTGA
                                |||||||||   ||   ||||
                                AGTGTCGGA   CT   GACT
                                     AGT  C___
GAM279  TOSO     5'  CAGTTCCAGATTGTGA      18388          T  AAA
                                TCACAGTCTG GA   ACTG
                                |||||||||| ||   ||||
                                AGTGTTAGAC CT   TGAC
                                     _  ___
GAM279  TRIM15   5'  CAGTTCTCCCCAGCCACTGTGG 52653        __   TGAAA
                                TCACAGT  CTG    AACTG
                                |||||||  |||    |||||
                                GGTGTCA  GAC    TTGAC
                                   CC   CCCTC
GAM279  WNT10A   5'  CAGTCCCACTGGGCTGTGA   47401         _   AAAA
                                TCACAGTCT GTG   ACTG
                                ||||||||| |||   ||||
                                AGTGTCGGG CAC   TGAC
                                     T   CC__
GAM279  LOC126074 3'  TTCAGTTTCCCATGGCTGGA  74436    A    T   AA
                                TC CAGTC GTG  AAACTGAA
                                || ||||| |||  ||||||||
                                AG GTCGG TAC  TTTGACTT
                                 _    _   CC
GAM279  LOC126302 3'  TTCAGCCTGCAGAGACTGTGG  74496         G  AAAAA
                                TCACAGTCT TG    CTGAA
                                ||||||||| ||    |||||
                                GGTGTCAGA AC    GACTT
                                     G  GTCC_
GAM279  LOC138429 3'  TTTTTACAGACCATGA      75343     CA
                                TCA  GTCTGTGAAAA
                                |||  ||||||||||
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                                AGT  CAGACATTTTT
                                  AC
GAM279   LOC145566 5'  TCAGTTTTTCTTTCTGT     77279      TCTGT
                                ACAG     GAAAAACTGA
                                ||||     ||||||||||
                                TGTC     CTTTTTGACT
                                  TTT__
GAM279   LOC145678 5'  CAGTTTTTCAACATTTTG     83420     TC  _
                                CAG  TGT GAAAAACTG
                                |||  ||| |||||||||
                                GTT  ACA CTTTTTGAC
                                  TT   A
GAM279   LOC149267 3'  TCAGTCTGGTATCCAGACTGTG 56679          T  AAA___
           A                     TCACAGTCTG GA      ACTGA
                                ||||||||||| ||      |||||
                                AGTGTCAGAC CT      TGACT
                                      _  ATGGTC
GAM279   LOC150280 3'  TTCAGTTTATCAGTCTGT     79713      T   TGAA
                                ACAG CTG    AAACTGAA
                                |||| |||    ||||||||
                                TGTC GAC    TTTGACTT
                                  T   TA__
GAM279   LOC150421 3'  TTCAGTTTTTCTCTCTG     85040     TCTGT
                                CAG     GAAAAACTGAA
                                |||     ||||||||||
                                GTC     CTTTTTGACTT
                                  TCT__
GAM279   LOC151174 5'  TTCAGTTCCTCATGGGCT    85255         AA
                                AGTCTGTGA  AACTGAA
                                |||||||||  |||||||
                                TCGGGTACT  TTGACTT
                                     CC
GAM279   LOC152845 3'  TCAGTTTTTGGCTCTGT     60335      TCT  G
                                ACAG   GT AAAAACTGA
                                ||||   || |||||||||
                                TGTC   CG TTTTTGACT
                                  T__  G
GAM279   LOC157621 3'  TCAGTTCATAGGATGT      86496     GT     AAA
                                ACA  CTGTGA   ACTGA
                                |||  ||||||   |||||
                                TGT  GATACT   TGACT
                                  AG     ___
GAM279   LOC158527 5'  TTCAATTTTTTACTTCTGTG   81947      TCT      C
                                CACAG   GTGAAAAA TGAA
                                |||||   |||||||| ||||
                                GTGTC   CATTTTTT ACTT
                                   TT_       A
GAM279   LOC165741 3'  CAGCTTTTCTGAGGCTGTG    87254         GT    A
                                CACAGTCT  GAAAA CTG
                                ||||||||  ||||| |||
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                                GTGTCGGA  CTTTT GAC
                                     GT    C
GAM279   LOC169611 3'  TCAGCCTCCCAGACTGTTGG  82778    _     T  AAAA
                                TCA CAGTCTG GA    CTGA
                                ||| ||||||| ||    ||||
                                GGT GTCAGAC CT    GACT
                                  T      C  CC__
GAM279   LOC200830 3'  TTCAGTTTTAACACACAG    90151      A___
                                CTGTG    AAAACTGAA
                                |||||    |||||||||
                                GACAC    TTTTGACTT
                                   ACAA
GAM279   LOC221495 3'  TCAGTTTTTTCATCCTG     93864     TC  T
                                CAG  TG GAAAAACTGA
                                |||  || ||||||||||
                                GTC  AC TTTTTTGACT
                                  CT  _
GAM279   LOC221752 3'  TCAGACATGACTGTGA      93781         _  GAAAAA
                                TCACAGTC TGT     CTGA
                                |||||||| |||     ||||
                                AGTGTCAG ACA     GACT
                                     T  _______
GAM279   LOC221876 5'  TCAGTTTTGCACCGGG      93925     _ A
                                TCTG TG AAAACTGA
                                |||| || ||||||||
                                GGGC AC TTTTGACT
                                  C  G
GAM279   LOC253955 5'  TCAGTTTTCCATAGC       94432    T    A
                                G CTGTG AAAACTGA
                                | ||||| ||||||||
                                C GATAC TTTTGACT
                                 _    C
GAM279   LOC254249 5'  TCAGTTTTTTCTCATAT      95448    C  T
                                GT TG GAAAAACTGA
                                || || ||||||||||
                                TA AC CTTTTTGACT
                                 T  T
GAM279   LOC255446 5'  CAGAACTTCACAGACTGT     97152           AAA
                                ACAGTCTGTGAA   CTG
                                ||||||||||||   |||
                                TGTCAGACACTT   GAC
                                       CAA
GAM279   LOC256372 5'  CAGTTTGGCACTGTGA      95270        CTGT AA
                                TCACAGT    G  AAACTG
                                |||||||    |  ||||||
                                AGTGTCA    C  TTTGAC
                                    ____ GG
GAM279   LOC257106 3'  CAGCTTCTCTCTTTGACTGTGG 95385         TGT__  A  A
                                TCACAGTC     GA AA CTG
                                ||||||||     || || |||
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                                GGTGTCAG    CT TT GAC
                                    TTTCT  C  C
GAM279  LOC257468 3'  CAGCCTCCGGCTGTGA     95184       T   T  AAAA
                                TCACAG CTG GA    CTG
                                |||||| ||| ||    |||
                                AGTGTC GGC CT    GAC
                                   _   _  CC__
GAM279  LOC51029  3'  CAGTTTTTCAGCTCAGG     32181      ___
                                TCTG   TGAAAAACTG
                                ||||   ||||||||||
                                GGAC   ACTTTTTGAC
                                  TCG
GAM279  LOC54518  3'  TTCAGTTTGAGACCAGACTGGA 38774    A      TGAA_
                                TC CAGTCTG    AAACTGAA
                                || |||||||    ||||||||
                                AG GTCAGAC    TTTGACTT
                                 _      CAGAG
GAM279  LOC57826  3'  TTCAGTTTTAACATCGTGA   41020     AGTC   GA
                                TCAC    TGT  AAAACTGAA
                                ||||    |||  |||||||||
                                AGTG    ACA  TTTTGACTT
                                  CT__   A_
GAM279  LOC90957  5'  TCAGCCACCAGACTGT      64466        _  AAAAA
                                ACAGTCTG TG    CTGA
                                |||||||| ||    ||||
                                TGTCAGAC AC    GACT
                                    C  C_____
GAM279  LOC91097  3'  TTCAGTTTCTCATCCAGG    64841      __   A
                                TCTG  TGA AAACTGAA
                                ||||  ||| ||||||||
                                GGAC  ACT TTTGACTT
                                  CT   C
GAM279  LOC91115  3'  TCAGTTTTTGAGACGTGA    64953      A   GTG
                                TCAC GTCT   AAAAACTGA
                                |||| ||||   |||||||||
                                AGTG CAGA   TTTTTGACT
                                  _   G__
GAM279  LOC91351  3'  CAGCCTCCAGGATTGTGA    65706         GT  AAAA
                                TCACAGTCT  GA    CTG
                                |||||||||  ||    |||
                                AGTGTTAGG  CT    GAC
                                    AC  CC__
GAM279  LOC91464  3'  TCAGTTTTCTCATCTGT     66144      TCT   _
                                ACAG   GTGA AAAACTGA
                                ||||   |||| ||||||||
                                TGTC   TACT TTTTGACT
                                  ___    C
GAM279  LOC92223  5'  TCAGTTTTTCTCCTGTTGA   68525     _  TCTGT
                                TCA CAG    GAAAAACTGA
                                ||| |||    ||||||||||
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                                AGT GTC    CTTTTTGACT
                                  T  CT___
GAM280  KHK     3'  CTGGATTCAAATCTGCCA    4032      CA
                                TGGCA  ATTTGAATTCAG
                                |||||  ||||||||||||
                                ACCGT  TAAACTTAGGTC
                                   C_
GAM280  KHK     3'  CTGGATTCAAATCTGCCA    21402     CA
                                TGGCA  ATTTGAATTCAG
                                |||||  ||||||||||||
                                ACCGT  TAAACTTAGGTC
                                   C_
GAM280  NRXN3   5'  GCTGGAATTCAAACTGCC    57280     CAA       _
                                GGCA   TTTGAATTC AGT
                                ||||   ||||||||| |||
                                CCGT   AAACTTAAG TCG
                                   C__       G
GAM280  PRSS16  3'  CTGGTTCAAATTCTGCCA    19629     C       T
                                TGGCA AATTTGAAT CAG
                                |||||  ||||||||| |||
                                ACCGT TTAAACTTG GTC
                                   C       _
GAM280  PXF     3'  ATTCAAGATTGTGCCA      11149         _
                                TGGCACAATTT GAAT
                                |||||||||||  ||||
                                ACCGTGTTAGA CTTA
                                      A
GAM280  RAG1    3'  TTACTGAAACATTTTGCCA   4819      C   TTGAA
                                TGGCA AAT    TTCAGTAA
                                |||||  |||    ||||||||
                                ACCGT TTA    AAGTCATT
                                   T  CA___
GAM280  SLC25A15 3' ACTGAAATTGTGCCA       26507         TGAAT
                                TGGCACAATT    TCAGT
                                ||||||||||    |||||
                                ACCGTGTTAA    AGTCA
                                      _____
GAM280  TPM1    3'  CTGGTTCAAATGTGCCA     4526       A     T
                                TGGCACA TTTGAAT CAG
                                |||||||  |||||||  |||
                                ACCGTGT AAACTTG GTC
                                      _     _
GAM280  DKFZP434E2135 5' TTACTGAGATCAGCCA     47959     ACAATT  A
                                TGGC     TGA TTCAGTAA
                                ||||     ||| ||||||||
                                ACCG     ACT GAGTCATT
                                   ______  A
GAM280  FLJ10824 3' ACTGAATTCTGAGGGTGCC   72574      AA  T
                                GGCAC  TT GAATTCAGT
                                |||||  || |||||||||
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                                CCGTG  AG CTTAAGTCA
                                   GG  T
GAM280  FLJ22282  3'  TGGACCAAATTGTGCC      45594          AA
                                GGCACAATTTG  TTCA
                                ||||||||||  ||||
                                CCGTGTTAAAC  AGGT
                                      C_
GAM280  H2AV     3'  CTAGATTCAAATTATGC     56848     C       TC
                                GCA AATTTGAAT  AG
                                ||| |||||||||  ||
                                CGT TTAAACTTA  TC
                                  A       GA
GAM280  HPCL2    3'  TACTGTTAAAATTGTGC     24323         GAATT
                                GCACAATTT    CAGTA
                                |||||||||    |||||
                                CGTGTTAAA    GTCAT
                                      ATT__
GAM280  KIAA0256  3'  TTTACTGAACTCATTGGGACTA 64425     CA_   TT   A
                                TGG   CAA  TGA TTCAGTAAA
                                |||   |||  ||| |||||||||
                                ATC   GTT  ACT AAGTCATTT
                                  AGG   __   C
GAM280  KIAA0265  3'  TTAGGTTCAAATTATGCCA    69888       C       TC
                                TGGCA AATTTGAAT  AG
                                ||||| |||||||||  ||
                                ACCGT TTAAACTTG  TT
                                   A       GA
GAM280  KRTAP2-4  3'  TTTTACTGCTCAAACTGTCACC 52592     C_   A    ATT
            A                    TGG  ACA TTTGA   CAGTAAAA
                                |||  ||| |||||   ||||||||
                                ACC  TGT AAACT   GTCATTTT
                                  AC   C    C__
GAM280  SGKL     3'  ACTGAAATTGTGCCA       25139          TGAAT
                                TGGCACAATT    TCAGT
                                ||||||||||    |||||
                                ACCGTGTTAA    AGTCA
                                      _____
GAM280  Spir-1    5'  TACTGAATCAGATGCACCA   64702     CACA     A
                                TGG    ATTTGA TTCAGTA
                                |||    |||||| |||||||
                                ACC    TAGACT AAGTCAT
                                  ACG_     _
GAM280  LOC149566 3'  TTGGTTTAAATTATGCCA    84498       C       T
                                TGGCA AATTTGAAT CAG
                                ||||| ||||||||| |||
                                ACCGT TTAAATTTG GTT
                                   A       _
GAM280  LOC158490 3'  TTTACTGAAAATCCTGCCA   81936       CA   GAAT
                                TGGCA  ATTT   TCAGTAAA
                                |||||  ||||   ||||||||
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                                ACCGT  TAAA    AGTCATTT
                                  CC    ____
GAM280  LOC201183 5'  TTTACTGCTGAATTGTCCA   89759     C       AATT
                                TGG ACAATTTG    CAGTAAA
                                ||| ||||||||    |||||||
                                ACC TGTTAAGT    GTCATTT
                                  _       C___
GAM280  LOC253725 3'  ACTGAATTCTGAGGGTGCC    94700       AA  T
                                GGCAC  TT GAATTCAGT
                                |||||  || |||||||||
                                CCGTG  AG CTTAAGTCA
                                  GG  T
GAM280  LOC254268 3'  GAATTCAAATTAACCA      95408     CAC
                                TGG   AATTTGAATTC
                                |||   ||||||||||
                                ACC   TTAAACTTAAG
                                  AA_
GAM280  LOC51133  3'  TTTACTGAATTTCAGT      32286     T
                                ATT GAATTCAGTAAA
                                ||| ||||||||||||
                                TGA TTTAAGTCATTT
                                  C
GAM280  LOC54466  3'  TTACTGAACTCAGGTACAGC   38656    ACA     A
                                GC   ATTTGA TTCAGTAA
                                ||   |||||| ||||||||
                                CG   TGGACT AAGTCATT
                                  ACA     C
GAM281  AQP3      3'  TTCACGATCCACCCTTTC     59593      T_   _
                                GAAA  GTGG TCGTGAA
                                ||||  |||| |||||||
                                CTTT  CACC AGCACTT
                                  CC    T
GAM281  ARSB      3'  TCACGACTCTTGTC        3502         AATGTG
                                GACAAGA     GTCGTGA
                                |||||||     |||||||
                                CTGTTCT     CAGCACT
                                      _______
GAM281  B4GALT5   3'  TTTTCACAAAAATAGTCCTTTG 16519        AAA_   GGTC
            TCA                   TGACAAG    TGT    GTGAAAA
                                |||||||    |||    |||||||
                                ACTGTTT    ATA    CACTTTT
                                    CCTG   AAAA
GAM281  CHRNA3    3'  TCGTTACCCATTTCTT      5610         T   CG
                                AAGAAATG GGT  TGA
                                |||||||| |||  |||
                                TTCTTTAC CCA  GCT
                                    _  TT
GAM281  DRD1      3'  TTACAACCACATTTCTGGCCA  5840     ACA         C
                                TG   AGAAATGTGGT GTGA
                                ||   |||||||||| ||||
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                                AC   TCTTTACACCA CATT
                                 CGG         A
GAM281  FUT1     3'  TCTGATCACATCCCCTGTC   3798      AGAA       T
                                GACA    ATGTGGTCG GA
                                ||||    |||||||||| ||
                                CTGT    TACACTAGT CT
                                  CCCC        _
GAM281  IRF1     3'  GCCACATTTCTGATCA      64345     CA
                                TGA  AGAAATGTGGT
                                |||  ||||||||||
                                ACT  TCTTTACACCG
                                  AG
GAM281  MAP3K8   5'  TCACGACCACCTCATG      17791     A  AAT
                                CA GA   GTGGTCGTGA
                                || ||   ||||||||||
                                GT CT   CACCAGCACT
                                 A  C__
GAM281  NGFR     3'  TTCTGACCACACTTCCTGTC   10231      A   A       T
                                GACA GAA TGTGGTCG GAA
                                |||| ||| |||||||| |||
                                CTGT CTT ACACCAGT CTT
                                  C   C       _
GAM281  OLR1     3'  TTCACAACAGTTCTTGTTA    10341          ATGTG  C
                                TGACAAGAA     GT GTGAA
                                |||||||||     || |||||
                                ATTGTTCTT     CA CACTT
                                      GA___  A
GAM281  POU4F1   3'  CACTGAAAACATTTTTGTCA   20660          A   GG  _
                                TGACAAGAA TGT  TC GTG
                                ||||||||| |||  || |||
                                ACTGTTTTT ACA  AG CAC
                                      _   AA  T
GAM281  SMP1     3'  TTTCACATGAATAATTTTTGTC 26705          A   GGTC
           A                     TGACAAGAA TGT    GTGAAA
                                |||||||||| |||    ||||||
                                ACTGTTTTT ATA    CACTTT
                                      A   AGTA
GAM281  ZNF264   3'  TTCTATTAACATTTCTTTTCA  12769     C        GGTCGT
                                TGA AAGAAATGT      GAA
                                ||| |||||||||      |||
                                ACT TTCTTTACA      CTT
                                  T         ATTAT_
GAM281  C20orf175 3'  CGAGCTCCACGTTTCCTGCCA  55063     A  A        ___
                                TG CA GAAATGTGG   TCG
                                || || |||||||||   |||
                                AC GT CTTTGCACC   AGC
                                 C  C        TCG
GAM281  CAPNS2   3'  TTTCACAACCCTACATATTTCT 50323     CA       ____   C
           GATCA                    TGA  AGAAATGT    GGT GTGAAA
                                |||  ||||||||    ||| ||||||
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                                ACT  TCTTTATA    CCA CACTTT
                                  AG       CATC   A
GAM281  CLDN6    3'  TTTACACTCACATTTTTATCA  41041     CA       _  C
                                TGA  AGAAATGTG GT GTGAA
                                |||  |||||||||| || |||||
                                ACT  TTTTTACAC CA CATTT
                                  A_       T  _
GAM281  DKFZP564L0864 3'  GCACCAATTTCTTGCCA     72555    A      G    C
                                TG CAAGAAAT TGGT GT
                                || |||||||| |||| ||
                                AC GTTCTTTA ACCA CG
                                 C       _   _
GAM281  DKFZP566B183 3'  TTTCCATAAACATTTCTTTTCA 31330     C       GGTCGT
                                TGA AAGAAATGT     GAAA
                                ||| |||||||||      ||||
                                ACT TTCTTTACA     CTTT
                                  T       AATAC_
GAM281  GTF2E1    3'  TACAGACCTCTTGTCA      18616        AATGT    _
                                TGACAAGA    GGTC GTG
                                ||||||||    |||| |||
                                ACTGTTCT    CCAG CAT
                                     _____   A
GAM281  KIAA0089  3'  TTTTAATTCACATTTCTT    69967          TCG
                                AAGAAATGTGG   TGAAA
                                ||||||||||   |||||
                                TTCTTTACACT   ATTTT
                                      TA_
GAM281  KIAA0373  5'  TTTTCAAAGTAACATTTCTT   28015         GGTCG
                                AAGAAATGT    TGAAAA
                                |||||||||    ||||||
                                TTCTTTACA    ACTTTT
                                     ATGAA
GAM281  KIAA1813  3'  TTTTCACACTGTAAATTTCTTG 70314         __ TG  C
           T                     ACAAGAAAT  G  GT GTGAAAA
                                |||||||||  |  || |||||||
                                TGTTCTTTA  T  CA CACTTTT
                                     AA GT  _
GAM281  KIAA1951  3'  TTCCAGGCTTCTCTTGTCA   73766        AATGT   GT
                                TGACAAGA    GGTC  GAA
                                ||||||||    ||||  |||
                                ACTGTTCT    TCGG  CTT
                                    CT___    AC
GAM281  MGC4170   3'  TTCACCATTTCTTGTC     44227          TGGTC
                                GACAAGAAATG    GTGAA
                                ||||||||||    |||||
                                CTGTTCTTTAC    CACTT
                                      _____
GAM281  NRN1     3'  CACTGCACATTTCTCCTCA   33432     CA       GTC
                                TGA  AGAAATGTG   GTG
                                |||  |||||||||   |||
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                                ACT  TCTTTACAC   CAC
                                  CC        GT_
GAM281   PLA2G12   3'  TTTTCACAACCACATTT     48028          C
                                AAATGTGGT GTGAAAA
                                ||||||||| |||||||
                                TTTACACCA CACTTTT
                                     A
GAM281   PPY2      3'  CACTCCACATTCCTGGCCA    40819    ACA  A      TC
                                TG   AG AATGTGG  GTG
                                ||   || |||||||  |||
                                AC   TC TTACACC  CAC
                                 CGG  C      T_
GAM281   ZNF31     3'  TTTGTAGACCACATTTCCTGTT 64992       A          _ TG
            A                    TGACA GAAATGTGGTC G  AA
                                ||||| |||||||||||  |  ||
                                ATTGT CTTTACACCAG T  TT
                                   C          A GT
GAM281   LOC115219 3'  CACGACAACGGGTCCTCA    73295     CAA  AA   G
                                TGA   GA  TGT GTCGTG
                                |||   ||  ||| ||||||
                                ACT   CT  GCA CAGCAC
                                  C__  GG   A
GAM281   LOC120376 5'  TTCAGAGCATTTCTTTCA    75986     C        GG  G
                                TGA AAGAAATGT  TC TGAA
                                ||| |||||||||  || ||||
                                ACT TTCTTTACG  AG ACTT
                                  _        __  _
GAM281   LOC133418 3'  TTTCATATACATTTTTTGCCA  75094    A         GTC
                                TG CAAGAAATGTG   GTGAAA
                                || ||||||||||   ||||||
                                AC GTTTTTTACAT   TACTTT
                                 C          A__
GAM281   LOC151199 3'  TTAAAACCACAGCTCTTGCCA  80174    A    AA     CG
                                TG CAAGA  TGTGGT  TGA
                                || |||||  ||||||  |||
                                AC GTTCT  ACACCA  ATT
                                 C    CG     AA
GAM281   LOC152317 5'  TCACACTGACTTTTGTCA    85649         AATG   C
                                TGACAAGA    TGGT GTGA
                                ||||||||    |||| ||||
                                ACTGTTTT    GTCA CACT
                                     CA__    _
GAM281   LOC152674 3'  TTCAACCCACCCTCTTGTCA   85841         AAT    TCG
                                TGACAAGA   GTGG   TGAA
                                ||||||||   ||||   ||||
                                ACTGTTCT   CACC   ACTT
                                     CC_    CA_
GAM281   LOC152845 5'  CATGACCACATTTTTCA     60330     CAA
                                TGA   GAAATGTGGTCGTG
                                |||   ||||||||||||||
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                                ACT   TTTTACACCAGTAC
                                  ___
GAM281  LOC154743 3'  TTTAGTCCACATTGTCTTGTCA 81118        _      TCG
                                TGACAAGA AATGTGG   TGAA
                                |||||||| |||||||   ||||
                                ACTGTTCT TTACACC   ATTT
                                     G      TG_
GAM281  LOC165476 5'  TTCACGGCACCTTCT      87201      AT   G
                                AGAA  GTG TCGTGAA
                                ||||  ||| |||||||
                                TCTT  CAC GGCACTT
                                  C_  _
GAM281  LOC254266 5'  TTTTCGGTCACACATCTTATCA 97356     C    AA    GT  T
                                TGA AAGA  TGTG  CG GAA
                                ||| ||||  ||||  || |||
                                ACT TTCT  ACAC  GC TTT
                                  A   AC    TG  T
GAM281  LOC255919 3'  TTTCATTCTTACATTTCTAATC 95043     CA        TC
           A                     TGA  AGAAATGTGG  GTGAAA
                                |||  ||||||||||  ||||||
                                ACT  TCTTTACATT  TACTTT
                                  AA         CT
GAM281  LOC51754  5'  CACGGCCACATCTCTGTCA    71027      A  A
                                TGACA GA ATGTGGTCGTG
                                ||||| || ||||||||||
                                ACTGT CT TACACCGGCAC
                                  _  C
GAM281  LOC55862  3'  ACCTCATTTCTTGCCA      37485    A       T
                                TG CAAGAAATG GGT
                                || |||||||| |||
                                AC GTTCTTTAC CCA
                                 C        T
GAM281  LOC55954  3'  CACGTGGTCACTTTTCTCATCA 38877     CA    T   GT __
                                TGA  AGAAA GTG  C  GTG
                                |||  ||||| |||  |  |||
                                ACT  TCTTT CAC  G  CAC
                                  AC    T   TG TG
GAM282  CYP24    3'  ACAAGTGTAAAGCATGCA    5766      _  GATGG
                                TGC TGT    ACACTTGT
                                ||| |||    ||||||||
                                ACG ACG    TGTGAACA
                                  T   AAA__
GAM282  CYP4F3   3'  ACAAGTGTTCAAACAG      6104      GA
                                CTGT  TGGACACTTGT
                                ||||  ||||||||||
                                GACA  ACTTGTGAACA
                                  A_
GAM282  DAZL     3'  ACAAGTACCTGTGAACAGTA   68137       G_   AC
                                TGCTGT  ATGG  ACTTGT
                                ||||||  ||||  ||||||
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                                ATGACA  TGTC  TGAACA
                                   AG    CA
GAM282  DLEC1    3'  ACAGGCCACACCACAGCAGA  94628        A  GACA
                                TCTGCTGTG TG    CTTGT
                                |||||||||  ||    |||||
                                AGACGACAC AC    GGACA
                                     C  ACC_
GAM282  DLEC1    3'  ACAGGCCACACCACAGCAGA  23684        A  GACA
                                TCTGCTGTG TG    CTTGT
                                |||||||||  ||    |||||
                                AGACGACAC AC    GGACA
                                     C  ACC_
GAM282  DLEC1    3'  ACAGGCCACACCACAGCAGA  23692        A  GACA
                                TCTGCTGTG TG    CTTGT
                                |||||||||  ||    |||||
                                AGACGACAC AC    GGACA
                                     C  ACC_
GAM282  DLEC1    3'  ACAGGCCACACCACAGCAGA  23694        A  GACA
                                TCTGCTGTG TG    CTTGT
                                |||||||||  ||    |||||
                                AGACGACAC AC    GGACA
                                     C  ACC_
GAM282  DUSP3    3'  ACAAGTGTGTCCCAACACA   14561      A  ___
                                TGTG TGG   ACACTTGT
                                ||||  |||   ||||||||
                                ACAC ACC   TGTGAACA
                                  A  CTG
GAM282  HYAL1    3'  ACAAGTCATGGTCACAGTA   23605        GGAC
                                TGCTGTGAT    ACTTGT
                                |||||||||    ||||||
                                ATGACACTG    TGAACA
                                     GTAC
GAM282  HYAL1    3'  ACAAGTCATGGTCACAGTA   52534        GGAC
                                TGCTGTGAT    ACTTGT
                                |||||||||    ||||||
                                ATGACACTG    TGAACA
                                     GTAC
GAM282  IFRD2    3'  ACAAATGCCACCACAGCAGG  22220        A  A  C
                                TCTGCTGTG TGG CA TTGT
                                ||||||||| ||| || ||||
                                GGACGACAC ACC GT AACA
                                     C   _  A
GAM282  IL21R    3'  ACAAGTGTGCACAGTA      41421       ATGG
                                TGCTGTG    ACACTTGT
                                |||||||    ||||||||
                                ATGACAC    TGTGAACA
                                   G___
GAM282  IRS1     3'  TGGACATCACAGCAGA      18667          GA
                                TCTGCTGTGATG  CA
                                ||||||||||||  ||
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                                AGACGACACTAC  GT
                                      AG
GAM282  KAL1     3'  ACAAGTGAGAAACAGTAGA   4009        GATGGA
                                TCTGCTGT     CACTTGT
                                ||||||||     |||||||
                                AGATGACA     GTGAACA
                                     AAGA__
GAM282  PPL      3'  ACAAGCCAACCACAGCAG    10703       A_  ACA
                                CTGCTGTG  TGG   CTTGT
                                ||||||||  |||   |||||
                                GACGACAC  ACC   GAACA
                                     CA   ___
GAM282  PPP2R5D  5'  ACAAATATTCATGCAGCGGA  20713       G    CAC
                                TCTGCTGT ATGGA   TTGT
                                |||||||| |||||   ||||
                                AGGCGACG TACTT   AACA
                                     _    ATA
GAM282  SERPINB9 3'  ACAAACTGTTTTCCACAGCAG  14743       AT    C_
                                CTGCTGTG  GGACA  TTGT
                                ||||||||  |||||  ||||
                                GACGACAC  TTTGT  AACA
                                     CT    CA
GAM282  UBQLN2   3'  ACAAGTGTTGTCCTACAGA   25563     C  T  TG A
                                TCTG TG GA  G CACTTGT
                                |||| || ||  | |||||||
                                AGAC AT CT  T GTGAACA
                                  _ C  GT _
GAM282  B3GNT1   5'  ACAAGTGCCGGAGTAGCAGA  21656       GA   A
                                TCTGCTGT  TGG CACTTGT
                                ||||||||  ||| |||||||
                                AGACGATG  GCC GTGAACA
                                     AG   _
GAM282  B3GNT1   5'  ACAAGTGCCGGAGGTAGCAGA  52681       TGA_   A
                                TCTGCTG    TGG CACTTGT
                                |||||||    ||| |||||||
                                AGACGAT    GCC GTGAACA
                                     GGAG   _
GAM282  BTN3A3   3'  CAAGTGAACAGCAGA      22770       GATGGA
                                TCTGCTGT     CACTTG
                                ||||||||     ||||||
                                AGACGACA     GTGAAC
                                     A_____
GAM282  C20orf42 5'  ACAAGTGTCCAAAGGC     34580     GTGA
                                GCT    TGGACACTTGT
                                |||    ||||||||||
                                CGG    ACCTGTGAACA
                                  AA__
GAM282  CBX3     3'  TGCCATCACAGCAGG       33429           A
                                TCTGCTGTGATGG CA
                                |||||||||||| ||
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                                GGACGACACTACC GT
                                              _
GAM282  CBX3     3'  TGCCATCACAGCAGG       23456            A
                                TCTGCTGTGATGG CA
                                |||||||||||| ||
                                GGACGACACTACC GT
                                              _
GAM282  CYP4F2   3'  ACAAGTGTTCAAACAG      6552       GA
                                CTGT  TGGACACTTGT
                                ||||  ||||||||||
                                GACA  ACTTGTGAACA
                                  A_
GAM282  DKFZP434N1511 3'  TGACCAGCCACAGCAGA     91423          A_   A
                                TCTGCTGTG  TGG CA
                                |||||||||  ||| ||
                                AGACGACAC  ACC GT
                                      CG   A
GAM282  DKFZP761L0424 3'  ACAAGTTTGCACAGCTAGA   91335     _     ATGGAC
                                TCT GCTGTG     ACTTGT
                                ||| ||||||     ||||||
                                AGA CGACAC     TGAACA
                                  T     GTT___
GAM282  FLJ20048  3'  ACAAGTAACACCACAGCAGA   34435          A  GAC
                                TCTGCTGTG TG   ACTTGT
                                ||||||||| ||   ||||||
                                AGACGACAC AC   TGAACA
                                      C  AA_
GAM282  FLJ21709  3'  ACAAATGTCCATGTCACAG    49842       __     C
                                CTGTGA  TGGACA TTGT
                                ||||||  |||||| ||||
                                GACACT  ACCTGT AACA
                                   GT     A
GAM282  KCNS1    3'  TGCCCATCACACAGA       9584       C       A
                                TCTG TGTGATGG CA
                                |||| |||||||| ||
                                AGAC ACACTACC GT
                                  _       C
GAM282  KIAA0285  3'  ACAAGTGTCCAGGAAGCAGA   29010       GTGA
                                TCTGCT    TGGACACTTGT
                                ||||||    ||||||||||
                                AGACGA    ACCTGTGAACA
                                   AGG_
GAM282  KIAA0342  3'  TGTCCTCACAGCAGA       70622          T
                                TCTGCTGTGA GGACA
                                |||||||||| |||||
                                AGACGACACT CCTGT
                                              _
GAM282  KIAA1028  3'  ACAGGCGCCCCCACCACAGCAG 91932          A   ACA__
            A                    TCTGCTGTG TGG     CTTGT
                                ||||||||| |||     |||||
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                                AGACGACAC ACC    GGACA
                                     C   CCCGC
GAM282  MGC10818 3'  ACAAGTGCCCTCAGCAAGA   47534    _   TGAT  A
                                TCT GCTG   GG CACTTGT
                                ||| ||||   || |||||||
                                AGA CGAC   CC GTGAACA
                                  A   TC__  _
GAM282  MGC20255 3'  CAAGTGTGCATGCAGA     53438     TGTG   G
                                TCTGC   ATG ACACTTG
                                |||||   ||| |||||||
                                AGACG   TAC TGTGAAC
                                   _____  G
GAM282  NINJ2    3'  ACAAGTGTTGGAGCTGCAGA  33278     T  GATG
                                TCTGC GT   GACACTTGT
                                ||||| ||   |||||||||
                                AGACG CG   TTGTGAACA
                                   T  AGG_
GAM282  NR6A1    3'  ACAAATGTTTGCAGCAGA    7640       GAT    C
                                TCTGCTGT   GGACA TTGT
                                ||||||||   ||||| ||||
                                AGACGACG   TTTGT AACA
                                     ___    A
GAM282  NR6A1    3'  ACAAATGTTTGCAGCAGA    52877      GAT    C
                                TCTGCTGT   GGACA TTGT
                                ||||||||   ||||| ||||
                                AGACGACG   TTTGT AACA
                                     ___    A
GAM282  NR6A1    3'  ACAAATGTTTGCAGCAGA    52865      GAT    C
                                TCTGCTGT   GGACA TTGT
                                ||||||||   ||||| ||||
                                AGACGACG   TTTGT AACA
                                     ___    A
GAM282  NYD-SP18 5'  CAAATGTGCAGCAGG      50875      GATGG  C
                                TCTGCTGT    ACA TTG
                                ||||||||    ||| |||
                                GGACGACG    TGT AAC
                                     _____  A
GAM282  TA-LRRP  5'  ACAAACATCCAAACCATAGCAG 31066       A__   CAC
                                CTGCTGTG   TGGA   TTGT
                                ||||||||   ||||   ||||
                                GACGATAC   ACCT   AACA
                                     CAA    ACA
GAM282  TBC1D2   5'  TGTCCATCCCAGCAGA     37327      T
                                TCTGCTG GATGGACA
                                ||||||| ||||||||
                                AGACGAC CTACCTGT
                                     C
GAM282  VPS33A   3'  CAAGTGTACTGCAGA      43334      T  GATGG
                                TCTGC GT    ACACTTG
                                ||||| ||    |||||||
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                                AGACG CA     TGTGAAC
                                  T ______
GAM282   LOC144486 3'  ACAAGTGTCCATCACTAGGA   83078     GCT
                                TCT   GTGATGGACACTTGT
                                |||   ||||||||||||||||
                                AGG   CACTACCTGTGAACA
                                  AT_
GAM282   LOC145815 5'  AGTGCCCATCATAGCA      83517          A
                                TGCTGTGATGG CACT
                                |||||||||| ||||
                                ACGATACTACC GTGA
                                       C
GAM282   LOC150819 5'  GTGTCCATTACAGCAGA     85121
                                TCTGCTGTGATGGACAC
                                ||||||||||||||||
                                AGACGACATTACCTGTG

GAM282   LOC151614 3'  CAAGCACTGCAGCAGA      80301        GA  GACA
                                TCTGCTGT  TG    CTTG
                                ||||||||  ||    ||||
                                AGACGACG  AC    GAAC
                                     TC  _____
GAM282   LOC200339 3'  ACAAATGTCCATAGCAGC    90024       G      C
                                GCTGT ATGGACA TTGT
                                ||||| ||||||| ||||
                                CGACG TACCTGT AACA
                                   A      A
GAM282   LOC203429 3'  ATAGGTGTCCCACAGCA     89363        AT
                                TGCTGTG  GGACACTTGT
                                |||||||  ||||||||||
                                ACGACAC  CCTGTGGATA
                                   __
GAM282   LOC205327 3'  ACAAAACTGCCATCATAGCA   89497           A  C__
                                TGCTGTGATGG CA   TTGT
                                |||||||||| ||   ||||
                                ACGATACTACC GT   AACA
                                       _  CAA
GAM282   LOC220758 3'  ACAAGTGCCCACATGGCAGG   90780         A   A
                                TCTGCTGTG TGG CACTTGT
                                ||||||||| ||| |||||||
                                GGACGGTAC ACC GTGAACA
                                      _   C
GAM282   LOC221490 5'  ACAAGTGTCCACCACTCCA    93654     CT   A
                                TG  GTG TGGACACTTGT
                                ||  ||| ||||||||||
                                AC  CAC ACCTGTGAACA
                                 CT   C
GAM282   LOC221954 3'  ACAAGTGTGGGCAACACA     93996      A  G__
                                TGTG TG   ACACTTGT
                                |||| ||   ||||||||
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                                ACAC AC   TGTGAACA
                                  A  GGG
GAM282  LOC222166 3'  ACAAGCAGTAGCAGCAGA    94087       GA_  GACA
                                TCTGCTGT   TG    CTTGT
                                ||||||||   ||    |||||
                                AGACGACG   AC    GAACA
                                    ATG  ____
GAM282  LOC223009 5'  ACATCTGTCTCACAGCAGA   94369        TG    CT
                                TCTGCTGTGA  GACA  TGT
                                ||||||||||  ||||  |||
                                AGACGACACT  CTGT  ACA
                                      __    CT
GAM282  LOC255987 5'  ACATCTGCCTCACAGCAGA   96063        T  A  CT
                                TCTGCTGTGA GG CA  TGT
                                |||||||||| || ||  |||
                                AGACGACACT CC GT  ACA
                                      _ _  CT
GAM282  LOC91138  5'  ACAAAAGTTCATCAGCA     65026     GT      AC
                                TGCT  GATGGAC  TTGT
                                ||||  |||||||  ||||
                                ACGA  CTACTTG  AACA
                                  __       AA
GAM283  ABCA2     3'  AGGGAGGTGGCTGTCCTG    96168    T      CTGAGT
                                CA GACGGCT     TCTTCCT
                                || |||||||     |||||||
                                GT CTGTCGG     GGAGGGA
                                 C      T_____
GAM283  ACVR1B    3'  GGGGGTGTGGTCGTCATG    15035         CTGAGTT
                                CATGACGGCT      CTTCC
                                ||||||||||      |||||
                                GTACTGCTGG      GGGGG
                                      TGT____
GAM283  ADAM19    3'  CAGGAAGAAGACTGGCCATTAT 52703      C    CTGAG
          G                      CATGA GGCT     TTCTTCCTG
                                |||||  ||||    |||||||||
                                GTATT CCGG     AAGAAGGAC
                                   A    TCAG_
GAM283  ADAMTS3   3'  AATTTGCAGCTGTTGTG     26477    TG     C
                                CA  ACGGCT TGAGTT
                                ||  |||||| ||||||
                                GT  TGTCGA GTTTAA
                                 GT     C
GAM283  ADH7      3'  CAGGAGGTCTGTGTTGTCATG  5419         TCT  GTT
                                CATGACGGC   GA   CTTCCTG
                                |||||||||   ||   |||||||
                                GTACTGTTG   CT   GGAGGAC
                                      TGT  ____
GAM283  AK1       3'  GAACAGTTGGGGCTGTTATG   4884          TG __
                                CATGACGGCTC  A  GTTC
                                ||||||||||  |  ||||
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                                GTATTGTCGGG  T  CAAG
                                      GT GA
GAM283  ALDH3A2  5'  CGGGGAGAGGGCGGGGGCCGCG 69272      A      _ AG
           TG                   CATG CGGCTCT G  TTCTTCCTG
                                |||| ||||||| |  |||||||||
                                GTGC GCCGGGG C  GAGAGGGGC
                                  _      G GG
GAM283  ALEX1    5'  CAGGAAGAAACGCAAAGTTGTC 33500        C  AG_
           A                    TGACGGCT TG   TTCTTCCTG
                                |||||||| ||   |||||||||
                                ACTGTTGA AC   AAGAAGGAC
                                    A  GCA
GAM283  ARAF1    5'  CAGGATCTCTTGGACTGTCGTG 63938        C  TG  TTCT
                                CATGACGG TC  AG    TCCTG
                                |||||||| ||  ||    |||||
                                GTGCTGTC AG  TC    AGGAC
                                    _  GT  TCT_
GAM283  ARHC     5'  TGGGAGGAGTTTATGGGTATGT 17709     _   _  GT
                                ACG GCTC TGA  TCTTCCTG
                                ||| |||| |||  ||||||||
                                TGT TGGG ATT  AGGAGGGT
                                  A   T   TG
GAM283  ATF7     3'  TGGGGGGAATTGTGTGTTGTG  22468    TG   G TCTG
                                CA  ACG C    AGTTCTTCCTG
                                ||  ||| |    ||||||||||
                                GT  TGT G    TTAAGGGGGGT
                                 GT   _ TG__
GAM283  ATP11A   3'  AGGGCACGGAGCCGTCA     77019          A
                                TGACGGCTCTG GTTCT
                                |||||||||| |||||
                                ACTGCCGAGGC CGGGA
                                      A
GAM283  BCL11B   3'  CAGGAGAAAAAGGGTTGTTTG  43184    T       GAG    T
                                A GACGGCTCT   TTCT CCTG
                                | |||||||||   |||| ||||
                                G TTGTTGGGA   AAGA GGAC
                                 T       AA_   _
GAM283  C21orf2  3'  TGGGAAGAGTCGCAAGTCTTAT 17018      C   C_  G
           G                    CATGA GGCT  TGA TTCTTCCTG
                                ||||| ||||  ||| |||||||||
                                GTATT CTGA  GCT GAGAAGGGT
                                  _   AC  _
GAM283  C8A      3'  CAGGGAGAACTTACAGGATGTT 5113       G_  C
           A                    TGACG  CT TGAGTTCTTCCTG
                                |||||  || ||||||||||||
                                ATTGT  GA ATTCAAGAGGGAC
                                  AG  C
GAM283  CACNA1S  3'  CAGCATGGGCTTAGAGCTGGCA 3564       A          TTC
           TG                   CATG CGGCTCTGAGTTC   CTG
                                |||| ||||||||||||   |||
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                                GTAC GTCGAGATTCGGG   GAC
                                  G          TAC
GAM283  CALCB    3'  AGGAAGAAGGTTATCATG    87570      CG   CTGAG
                                CATGA  GCT    TTCTTCCT
                                |||||  |||    ||||||||
                                GTACT  TGG    AAGAAGGA
                                  AT  _____
GAM283  CARKL    3'  TGGGGAGAATTCGTAGATC   25191    _  C
                                GG CT TGAGTTCTTCCTG
                                || || ||||||||||||
                                CT GA GCTTAAGAGGGGT
                                 A  T
GAM283  CCR2     3'  CAGGAACCTCAGGGCTGTGTG  5387      G         TTC
                                CAT ACGGCTCTGAG   TTCCTG
                                ||| ||||||||||   ||||||
                                GTG TGTCGGGACTC   AAGGAC
                                  _         C__
GAM283  CDK9     3'  CAGGAGGGCACTGGAGCTGTC  7002          G  _
                                GACGGCTCT AGT TCTTCCTG
                                ||||||||| ||| ||||||||
                                CTGTCGAGG TCA GGGAGGAC
                                     _  C
GAM283  CDKN2C   5'  CGGGACCTGGCGGGGCCGGCAT 7003       A       AGTTCT
           G                    CATG CGGCTCTG     TCCTG
                                |||| ||||||||     |||||
                                GTAC GCCGGGGC     AGGGC
                                  G       GGTCC_
GAM283  CENTD2   5'  GGGTCGGGGCTGTGTG     30873     G        G
                                CAT ACGGCTCTGA TT
                                ||| |||||||||| ||
                                GTG TGTCGGGGCT GG
                                  _         G
GAM283  CRY1     5'  GGCTCGGGCCGTCGTG      14522          T
                                CATGACGGC CTGAGTT
                                ||||||||| |||||||
                                GTGCTGCCG GGCTCGG
                                          _
GAM283  CTSL     3'  GGGAGGAATTCATCTTCA    8589      C  CTC
                                TGA GG   TGAGTTCTTCCT
                                |||  ||   ||||||||||||
                                ACT CT   ACTTAAGGAGGG
                                  T  ____
GAM283  CYP21A2  3'  GGGAAAGGGGTTGTCA      4949           GAG
                                TGACGGCTCT   TTCT
                                ||||||||||   ||||
                                ACTGTTGGGG   AGGG
                                     AA_
GAM283  DBN1     5'  GGGGCCCGGGGCCGCGTG    55151      A       A
                                CATG CGGCTCTG GTTCT
                                |||| |||||||| |||||
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                                GTGC GCCGGGGC CGGGG
                                  _      C
GAM283  DBP     3'  GGGGAGGGTTCTCTGTGTG   7217     G   CTCT  TT
                                CAT ACGG   GAG  CTTCCT
                                ||| ||||   |||  ||||||
                                GTG TGTC   CTT  GAGGGG
                                  _   T___  GG
GAM283  DEK     3'  GATTCTTGAGCTGTTGTG    12957    TG     T_
                                CA  ACGGCTC  GAGTT
                                ||  |||||||  |||||
                                GT  TGTCGAG  CTTAG
                                 GT      TT
GAM283  DHCR7   3'  TGGGGAGAAAGGGGCTTTCATG 7238       C     GAG
                                CATGA GGCTCT   TTCTTCCTG
                                ||||| ||||||   |||||||||
                                GTACT TCGGGG   AAGAGGGGT
                                   T     A__
GAM283  DHCR7   3'  TAGGGAGAAGCCCTGTGGGGCT 7237          _ ___
            GTCA                   ACGGCTCTG AG   TTCTTCCTG
                                |||||||||  ||   |||||||||
                                TGTCGGGGT TC   AAGAGGGAT
                                     G  CCG
GAM283  DIO1    3'  TGGGAAGAATTCCAGTTGTTA  5821          CT
                                TGACGGCT  GAGTTCTTCCTG
                                ||||||||  ||||||||||||
                                ATTGTTGA  CTTAAGAAGGGT
                                    C_
GAM283  DOK1    3'  TGGGAGGGGCCATGCTGTGTG  7275     G    TC  A
                                CAT ACGGC  TG GTTCTTCCTG
                                |||  |||||  ||  ||||||||||
                                GTG TGTCG  AC CGGGGAGGGT
                                  _    T_  _
GAM283  DYRK1B  5'  GGGGGGGCCGGTTTGTTGTG  16330    TG   CT   A
                                CA  ACGG  CTG GTTCTTCC
                                ||  ||||  ||| ||||||||
                                GT  TGTT  GGC CGGGGGGG
                                 GT   T_  _
GAM283  EMD     3'  AGGGGCAGGGGCTTTATG    3679       C     GA
                                CATGA GGCTCT  GTTCTT
                                ||||| ||||||  ||||||
                                GTATT TCGGGG  CGGGGA
                                   _     A_
GAM283  ENO2    3'  GGGAGCGTCAGGGTTGGTGTG  8777     GA       _
                                CAT  CGGCTCTGA GTTCTT
                                |||  ||||||||| ||||||
                                GTG  GTTGGGACT CGAGGG
                                  TG       G
GAM283  EPB41   5'  CAGGAAGAACTCAGAG      15428
                                CTCTGAGTTCTTCCTG
                                ||||||||||||||||
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                                GAGACTCAAGAAGGAC

GAM283  EPB41L2  3'  AGAGGGGGAGGGGGCTGTGGTG 7479      G       GAG       G
                                CAT ACGGCTCT   TTCTTCCT
                                ||| ||||||||   ||||||||
                                GTG TGTCGGGG   GAGGGGGA
                                  G       ___       GAG
GAM283  FACL4    3'  TGGGAAGAGCTTAGAAACTG   15513     C_
                                CGG  TCTGAGTTCTTCCTG
                                |||  ||||||||||||||
                                GTC  AGATTCGAGAAGGGT
                                  AA
GAM283  FACL4    3'  TGGGAAGAGCTTAGAAACTG   43403     C_
                                CGG  TCTGAGTTCTTCCTG
                                |||  ||||||||||||||
                                GTC  AGATTCGAGAAGGGT
                                  AA
GAM283  FACL5    5'  CAGGAAGAACTCAGAGCCG   64186
                                CGGCTCTGAGTTCTTCCTG
                                ||||||||||||||||||
                                GCCGAGACTCAAGAAGGAC

GAM283  FANCC    3'  CGGGAGGTGGGAGTTGTAGTG  70520     G       GAGTT
                                CAT ACGGCTCT    CTTCCTG
                                ||| ||||||||    |||||||
                                GTG TGTTGAGG    GGAGGGC
                                  A       GT___
GAM283  FLRT2    3'  CAGGGAGGACAACATCTTCATG 25058       C  CTCTGA
                                CATGA GG     GTTCTTCCTG
                                |||||  ||     ||||||||||
                                GTACT CT     CAGGAGGGAC
                                   T  ACAA__
GAM283  FRAT2    3'  AGCCCTTGGGGGCGTCGTG   23879        G   TG  TT
                                CATGACG CTC  AG  CT
                                |||||||  |||  ||  ||
                                GTGCTGC GGG  TC  GA
                                    G   GT  CC
GAM283  FUS2     3'  TGGCTCTGGCTCAGAGCCGTCA 24118             CTT_  TG
                                TGACGGCTCTGAGTT    CC
                                ||||||||||||||    ||
                                ACTGCCGAGACTCGG    GG
                                          TCTC  T
GAM283  FZD1     3'  TGGGAAGAAGCATGAAGCTTTG 13040    TG C    _ _  AG
          TG                    CA  A GGCT C TG  TTCTTCCTG
                                ||  | |||| | ||  |||||||||
                                GT  T TCGA G AC  AAGAAGGGT
                                 GT _    A T  G_
GAM283  GAK      3'  AGGTTGGGAGCCGTCGTG    17909          G  TTCTT
                                CATGACGGCTCT AG     CCT
                                ||||||||||| ||     |||
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                                GTGCTGCCGAGG TT    GGA
                                       G _____
GAM283  GGA1    3'  TGGGGAGGAAGCACAGCTGTT  25346       C  AG
                                GACGGCT TG  TTCTTCCTG
                                ||||||| ||  |||||||||
                                TTGTCGA AC  AGGAGGGGT
                                    C  GA
GAM283  GOLGA4  3'  TGGGAAGAGTTTTATGTTGTT  60071       TCT  GT
                                GACGGC   GA  TCTTCCTG
                                ||||||   ||  ||||||||
                                TTGTTG   TT  AGAAGGGT
                                   TAT  TG
GAM283  GPC1    3'  GGGGTCCAGGGCTGTT      9106          AG
                                GACGGCTCTG  TTCT
                                ||||||||||  ||||
                                TTGTCGGGAC  GGGG
                                      CT
GAM283  GPR4    3'  TAGGAAGAGTGAGGTTGGTGTG 59906     GA    T  GA
                                CAT  CGGC CT  GTTCTTCCTG
                                |||  |||| ||  ||||||||||
                                GTG  GTTG GA  TGAGAAGGAT
                                  TG   _  G_
GAM283  GRB10   3'  AGCTCAGGGTTGTTTTG     17972    T
                                CA GACGGCTCTGAGTT
                                || ||||||||||||||
                                GT TTGTTGGGACTCGA
                                 T
GAM283  H1F0    3'  CGGGGGGGGCTTGTGTGTTTTG 18016    T    G TCT
                                CA GACG C   GAGTTCTTCCTG
                                || |||| |   ||||||||||||
                                GT TTGT G   TTCGGGGGGGGC
                                 T   _ TG_
GAM283  HDAC4   3'  AGGGAGGGTTCCTTCATG    20105      C  CTCT   TT
                                CATGA GG    GAG  CTTCCT
                                ||||| ||    |||  ||||||
                                GTACT TC    CTT  GAGGGA
                                   _ ____   GG
GAM283  HOXD4   3'  TGGGAAGGGTTCAAAGTTCAT  27533     CG   C    TT
                                ATGA  GCT TGAG  CTTCCTG
                                ||||  ||| ||||  |||||||
                                TACT  TGA ACTT  GAAGGGT
                                  __  A   GG
GAM283  IER3    3'  TGGGGAGGACTCGGGT     53386    T
                                GC CTGAGTTCTTCCTG
                                || ||||||||||||||
                                TG GGCTCAGGAGGGGT
                                 _
GAM283  IER3    3'  TGGGGAGGACTCGGGT     13998    T
                                GC CTGAGTTCTTCCTG
                                || ||||||||||||||
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                                TG GGCTCAGGAGGGGT
                                  _
GAM283  IFRD1   3'  AGGGAGACAAAGCTTTATG   60122      C   C  AGT
                                CATGA GGCT TG   TCTTCCT
                                ||||| |||| ||   |||||||
                                GTATT TCGA AC   AGAGGGA
                                  _   A  ___
GAM283  IL10RA  3'  TGGGGCTTTCTGGAGTTGTGGT 59646   G      ___      TCCTG
          G                      AT ACGGCTCT   GAGTTCT
                                || ||||||||   |||||||
                                TG TGTTGAGG   TTCGGGG
                                 G       TCT      T  G
GAM283  IMPA2   3'  GGGGAGGTGGCCCTCGTG    95241      C   CTGAGT
                                CATGA GGCT     TCTTCCT
                                ||||| ||||     |||||||
                                GTGCT CCGG     GGAGGGG
                                  C   T_____
GAM283  KCNF1   3'  CAGGAGCCGCAGGGCCGTGTG  9520      G       AGTTC
                                CAT ACGGCTCTG    TTCCTG
                                ||| |||||||||    ||||||
                                GTG TGCCGGGAC    GAGGAC
                                  _       GCC__
GAM283  LAD1    3'  GGGGAGAAGGAGCTGCCGTG   18701      A      GAG
                                CATG CGGCTCT   TTCTTCCT
                                |||| |||||||   ||||||||
                                GTGC GTCGAGG   AAGAGGGG
                                  C      ___
GAM283  LDLR    3'  CAGGCATTTGAGGCTGTCGTG  4983          CT   TCTT
                                CATGACGGCT  GAGT   CCTG
                                ||||||||||  ||||   ||||
                                GTGCTGTCGG  TTTA   GGAC
                                      AG   C___
GAM283  LOR     3'  GATGGGCTTAGAGCTCTCATG  4719       C          T
                                CATGA GGCTCTGAGTTC TC
                                ||||| |||||||||||| ||
                                GTACT TCGAGATTCGGG AG
                                  C          T
GAM283  LRP1    3'  CAGGGAGGGCTTGGGGCTGCA  9797     A     TG
                                TG CGGCTC  AGTTCTTCCTG
                                || ||||||  ||||||||||
                                AC GTCGGG  TCGGGAGGGAC
                                  _     GT
GAM283  MADD    5'  CAGGAAGAGAAGAGCCGTGTG  55332     G      GAGT
                                CAT ACGGCTCT    TCTTCCTG
                                ||| ||||||||    ||||||||
                                GTG TGCCGAGA    AGAAGGAC
                                  _       AG__
GAM283  MADH6   5'  GGGGGGCTGGAGTTGTT     18766         G
                                GACGGCTCT AGTTCTTC
                                ||||||||| ||||||||
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                                TTGTTGAGG TCGGGGGG

                                        _
GAM283  MAN2A2   3'  CAGGAAGGACTCGCTAGAGATT 20392     _   ___
           GTCATG                 ACGG CTCT   GAGTTCTTCCTG
                                |||| ||||  ||||||||||||
                                TGTT GAGA   CTCAGGAAGGAC
                                  A   TCG
GAM283  MAP3K11  5'  GGGGTCGGAGCCGTCG     10054          G
                                TGACGGCTCTGA TTC
                                |||||||||||| |||
                                GCTGCCGAGGCT GGG
                                       G
GAM283  MAX     5'  TGGGGGGGACTCGGCTTGTTGT 9943    TG    T__
           TGT                   A  ACGGC   CTGAGTTCTTCCTG
                                | |||||  ||||||||||||||
                                T  TGTTG   GGCTCAGGGGGGGT
                                 GT    TTC
GAM283  MAX     5'  TGGGGGGGACTCGGCTTGTTGT 59036   TG    T__
           TGT                   A  ACGGC   CTGAGTTCTTCCTG
                                | |||||  ||||||||||||||
                                T  TGTTG   GGCTCAGGGGGGGT
                                 GT    TTC
GAM283  MAX     5'  TGGGGGGGACTCGGCTTGTTGT 59039   TG    T__
           TGT                   A  ACGGC   CTGAGTTCTTCCTG
                                | |||||  ||||||||||||||
                                T  TGTTG   GGCTCAGGGGGGGT
                                 GT    TTC
GAM283  MAX     5'  TGGGGGGGACTCGGCTTGTTGT 59046   TG    T__
           TGT                   A  ACGGC   CTGAGTTCTTCCTG
                                | |||||  ||||||||||||||
                                T  TGTTG   GGCTCAGGGGGGGT
                                 GT    TTC
GAM283  MBTPS1   3'  CAGGAGGGACTTAGTGGCT   13702     _
                                GGCT CTGAGTTCTTCCTG
                                |||| ||||||||||||||
                                TCGG GATTCAGGGAGGAC
                                  T
GAM283  MEF2C    3'  GGGAAGGGGGGGTCGATATG   9990      A     GAGT
                                CATG CGGCTCT    TCTTCCT
                                |||| |||||||    |||||||
                                GTAT GCTGGGG    GGAAGGG
                                  A     _____
GAM283  MEOX2    5'  GGCCTTTGGAACCGTCGTG   19805        C  TG  TT
                                CATGACGG TC  AG  CT
                                |||||||| ||  ||  ||
                                GTGCTGCC AG  TT  GG
                                     A  GT  CC
GAM283  MFGE8    3'  CAGGGTGGGCGTTTGGGGCCCT 19810     C    TG __   T
           CATG                   ATGA GGCTC  A  GTTC TCCTG
                                |||| |||||  |  |||| |||||
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                                TACT CCGGG  T  CGGG GGGAC
                                  C     GT TG    T
GAM283  MLLT2    3'  TAGGAGGAGAATTTGGCTGTC  19852        CTGAG
                                GACGGCT     TTCTTCCTG
                                |||||||     |||||||||
                                CTGTCGG     GAGGAGGAT
                                    TTTAA
GAM283  MLLT2    3'  TGGAACTGCAACTTGGGGCTTT 19854   TG C     TG    C___    TG
            GTG                     A GGCTC  AGTT    TTCC
                                 | |||||  ||||    ||||
                                 T TCGGG  TCAA    AAGG
                                GT _     GT    CGTC    T
GAM283  MTMR3    3'  GGGAGTGGGTAGCCGTCATG   40815          _  GAGTT
                                CATGACGGCT CT     CTTCC
                                |||||||||| ||     |||||
                                GTACTGCCGA GG     GAGGG
                                      T  GT___
GAM283  MYCL2    5'  CGGGTCGCGCGCTCGGTGGCCG 18181   G     _     TCTT__
            TTGTG                   ACGGCT CTGAGT     CCTG
                                 |||||| ||||||      ||||
                                 TGCCGG GGCTCG     GGGC
                                T     T     CGCGCT
GAM283  MYO9A    3'  TAGGGGGGATATTGCTGTCCTG 22583    T     TCTGA
                                CA GACGGC     GTTCTTCCTG
                                || ||||||     ||||||||||
                                GT CTGTCG     TAGGGGGGAT
                                 C     TTA__
GAM283  NDRG2    3'  CAGGAAGGGGCCTGGGGCCGTT 32717    T       GA    _
            TG                    A GACGGCTCT  GTTC TTCCTG
                                | |||||||||  |||| ||||||
                                G TTGCCGGGG  CGGG AAGGAC
                                 T       TC    G
GAM283  NOL3     3'  TAGGGAGGGCTTAGAGCTCACA 14157    AC
                                TG  GGCTCTGAGTTCTTCCTG
                                ||  ||||||||||||||||||
                                AC  TCGAGATTCGGGAGGGAT
                                 AC
GAM283  NOS1     3'  TGGGAAGAACTTGTCCCTCA   5255      C  CTC
                                TGA GG   TGAGTTCTTCCTG
                                ||| ||   ||||||||||||
                                ACT CC   GTTCAAGAAGGGT
                                  C  T__
GAM283  NOTCH2   3'  TGGGGAGAACCTATCTGCATG  44316      A   CTC  A
                                CATG CGG   TG GTTCTTCCTG
                                |||| |||   || ||||||||||
                                GTAC GTC   AT CAAGAGGGGT
                                   _   T__  C
GAM283  NPM3     3'  TGGGAGGGACTTGGGTC     22769     T TG
                                GGC C  AGTTCTTCCTG
                                ||| |  ||||||||||
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                                CTG G  TCAGGGAGGGT
                                  _ GT
GAM283  NPTX1    3'  CAGCCATCTCGGAGCCCTTGTG 10259    TG C       TTCTTC
                                CA  A GGCTCTGAG     CTG
                                ||  | |||||||||     |||
                                GT  T CCGAGGCTC     GAC
                                 GT C       TACC__
GAM283  NR4A1    3'  GGGAGGGGGATGCCTTCATG  9240      C  _  GAGT
                                CATGA GGC TCT   TCTTCCT
                                ||||| ||| |||   |||||||
                                GTACT CCG AGG   GGGAGGG
                                   T  T  ____
GAM283  OLIG2    3'  CGGGGGGGGGAGGGGGTGTTATG 19410       G   GAGT
                                CATGACG CTCT   TCTTCCTG
                                ||||||| ||||   ||||||||
                                GTATTGT GGGG   GGGGGGGC
                                    G   AG__
GAM283  PACE     3'  GGGGATCTCAGGGGCTGTTTG  10396   T      _   T
                                A GACGGCTC TGAG TCTTC
                                | |||||||| |||| |||||
                                G TTGTCGGG ACTC AGGGG
                                 T      G   T
GAM283  PES1     3'  AGGGGGAGCATTTGTTAT    26670       CTCTGA
                                ATGACGG     GTTCTTCCT
                                |||||||     |||||||||
                                TATTGTT     CGAGGGGGA
                                    TA____
GAM283  PFKL     3'  GGGGCCTGGGCTGTTGTG    10521    TG     TGA
                                CA  ACGGCTC   GTTCT
                                ||  |||||||   |||||
                                GT  TGTCGGG   CGGGG
                                 GT      TC_
GAM283  PKDREJ   3'  GGGCTTAGGGCCTCGTG     20278      C
                                CATGA GGCTCTGAGTTC
                                ||||| ||||||||||||
                                GTGCT CCGGGATTCGGG
                                  _
GAM283  PODXL    3'  GGGGGACAGACTGTTGTG    18236    TG   C   AGT
                                CA  ACGG TCTG   TCTTCC
                                ||  |||| ||||   ||||||
                                GT  TGTC AGAC   AGGGGG
                                 GT   _   ____
GAM283  POU4F1   5'  GGGGCTAGAGCTGTCG      20665         G
                                TGACGGCTCT AGTTCT
                                |||||||||| ||||||
                                GCTGTCGAGA TCGGGG
                                    _
GAM283  PPIF     3'  AACTCAGGGCTTTTGTG     19169    TG C
                                CA  A GGCTCTGAGTT
                                ||  | ||||||||||
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                                GT  T TCGGGACTCAA
                                 GT T
GAM283  PPP1R2   5'  TGGCTCTGGCGTCGGGGTCGTT 20697   TG       _  CTT_  TG
            GTG                   A  ACGGCTCTGA GTT    CC
                                |  |||||||||| |||    ||
                                T  TGCTGGGGCT CGG    GG
                                 GT        G   TCTC  T
GAM283  PPT2     3'  GGGAGGGAAGCACTGTCATG  57230        CTC  AG
                                CATGACGG   TG  TTCTTCCT
                                ||||||||   ||  ||||||||
                                GTACTGTC   AC  AGGGAGGG
                                     ___  GA
GAM283  PTGFRN   3'  AGGGCTGGAGTTGTTA      67182         G
                                TGACGGCTCT AGTTCT
                                |||||||||| ||||||
                                ATTGTTGAGG TCGGGA

                                     _
GAM283  PTPN11   3'  TAGGAAGAATTTAATATCTGTT 54596   T    CTC_
            TG                    A GACGG    TGAGTTCTTCCTG
                                | |||||    ||||||||||||
                                G TTGTC    ATTTAAGAAGGAT
                                 T     TATA
GAM283  PUM2     3'  AGGATCAAAGCTGTCATG    31014         C   GTTCT
                                CATGACGGCT TGA     TCCT
                                |||||||||| |||     ||||
                                GTACTGTCGA ACT     AGGA
                                      A  _____
GAM283  RERE     3'  CAGGGAGGCAAAGCTGACATG  23964      A    C  AGT
                                CATG CGGCT TG   TCTTCCTG
                                |||| ||||| ||   ||||||||
                                GTAC GTCGA AC   GGAGGGAC
                                  A    A  ___
GAM283  RNMT     3'  CAGGAAGAGCACCTGTTGCTG  13713      TCTGA__
                                CGGC      GTTCTTCCTG
                                ||||      ||||||||||
                                GTCG      CGAGAAGGAC
                                  TTGTCCA
GAM283  RS1      3'  GGGAAGGACTCACATCAT    4397       CGGCTC
                                ATGA     TGAGTTCTTCCT
                                ||||     ||||||||||||
                                TACT     ACTCAGGAAGGG
                                  AC____
GAM283  RXRB     3'  GGGGTGCTGGGGCTGCATG   41761      A      G   T
                                CATG CGGCTCT AGT CTTC
                                |||| ||||||| ||| ||||
                                GTAC GTCGGGG TCG GGGG
                                  _      _  T
GAM283  S100A9   3'  AGGGCCCCGGGGCCTGTTATG  11429       _      A_
                                CATGAC GGCTCTG  GTTCT
                                |||||| |||||||  |||||
```

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                                GTATTG CCGGGGC  CGGGA
                                   T      CC
GAM283  SACS     3'  TTCTTGGAGAATTCTGGAGTTG 94917          _       CTG
            TTATG                   ATGACGGCTCT GAGTTCTTC
                                ||||||||||| |||||||||
                                TATTGTTGAGG CTTAAGAGG
                                      T       TTCTTG
GAM283  SIX2     5'  CGGGCCGTTGGGGTTCGGAGCT 33723    C       TT  T____
            TCGTG                   A GGCTCTGAG  CT    CCTG
                                | |||||||||  ||    ||||
                                T TCGAGGCTT  GG    GGGC
                                _       GG  TTGCC
GAM283  SLC10A2  5'  TAGGAGGGGTTTAAAAGTT   4842      C_   TT
                                GGCT  TGAG  CTTCCTG
                                ||||  ||||  |||||||
                                TTGA  ATTT  GGAGGAT
                                  AA    GG
GAM283  SLC16A2  3'  CAGGAGGATGAGGTTGTCCTG  21500    T     T  GAGT
                                CA GACGGC CT    TCTTCCTG
                                || |||||| ||    ||||||||
                                GT CTGTTG GA    AGGAGGAC
                                 C     _  GT__
GAM283  SLC7A6   3'  CAGGAAGAGCTTGGTACTTGTG 14299      AC  CT TG
                                CATG  GG  C  AGTTCTTCCTG
                                ||||  ||  |  ||||||||||
                                GTGT  TC  G  TCGAGAAGGAC
                                  __  AT GT
GAM283  SLC9A3R1  3'  CGGGGAGGGTTTGGCT      70421      CT   TT
                                GGCT  GAG  CTTCCTG
                                ||||  |||  |||||||
                                TCGG  TTT  GAGGGGC
                                  __   GG
GAM283  SMARCA3  3'  GACTTGGAGTTTTATG      11790      C    TG
                                CATGA GGCTC  AGTT
                                ||||| |||||  ||||
                                GTATT TTGAG  TCAG
                                  _    GT
GAM283  SMURF1   3'  TAGGAAGGAAACCAGGGTCTCA 92459       C      AG_
            TG                    CATGA GGCTCTG   TTCTTCCTG
                                ||||| |||||||   |||||||||
                                GTACT CTGGGAC   AGGAAGGAT
                                  _      CAA
GAM283  SNL      3'  GGGAAGGGAAGCTGTCG     11853        CTGAG
                                TGACGGCT    TTCTTCCT
                                ||||||||    ||||||||
                                GCTGTCGA    GGGAAGGG
                                   A_____
GAM283  SNRPA    3'  TGGGGGCCTTCTTGGAGCCGTG 15987     G      TG  TT__    TG
            TG                    CAT ACGGCTC  AG   CTTCC
                                ||| |||||||  ||   |||||
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                                GTG TGCCGAG  TC    GGGGG
                                  _      GT  TTCC     T
GAM283  SNTB2    3'  CAGGATACTTGTTCAGGGTTGC 55610     A        TTCT__
             CATG                    ATG CGGCTCTGAG     TCCTG
                                |||  ||||||||||      |||||
                                TAC GTTGGGACTT      AGGAC
                                  C         GTTCAT
GAM283  SOST     3'  CTTCCAGAATTCAGAGTTGTGA 47469     G           TCCTG
             TG                    CAT ACGGCTCTGAGTTCT
                                |||  ||||||||||||||||
                                GTA TGTTGAGACTTAAGA
                                  G             CCTTCA
GAM283  SOX12    3'  TGGGGAGAACGCTGCTGTTA   22700        TCTGA
                                TGACGGC    GTTCTTCCTG
                                |||||||     ||||||||||
                                ATTGTCG    CAAGAGGGGT
                                     TCG__
GAM283  SPOCK    3'  GGGAGAAAGGGTGTTGTG    62819    TG   G    GAG
                                CA  ACG CTCT   TTCTTCC
                                ||  |||  ||||   |||||||
                                GT  TGT GGGA   AAGAGGG
                                 GT   _   ____
GAM283  SPON1    3'  TGGGGGGAAAAAAGTCCTCATG 62458       C    CTGAG
                                CATGA GGCT     TTCTTCCTG
                                |||||  ||||     |||||||||
                                GTACT CTGA     AAGGGGGGT
                                   C    AAA__
GAM283  SRRM1    3'  TAGGGGGAAATGTTTGTTATG  19554         CTCTGAG
                                CATGACGG      TTCTTCCTG
                                |||||||       |||||||||
                                GTATTGTT      AAGGGGGAT
                                     TGTA____
GAM283  STARD5   3'  ACTCAGGGTTGGCGTG      47556      A
                                CATG CGGCTCTGAGT
                                ||||  ||||||||||
                                GTGC GTTGGGACTCA
                                  G
GAM283  STK19    3'  CGGGAGGGGACTAGAAGAGCTG 50594     A      G__     _
             CATG                    TG CGGCTCT   AGTTCT TCCTG
                                ||  |||||||   ||||||  |||||
                                AC GTCGAGA   TCAGGG AGGGC
                                  _      AGA      G
GAM283  STK19    3'  CGGGAGGGGACTAGAAGAGCTG 14837     A      G__     _
             CATG                    TG CGGCTCT   AGTTCT TCCTG
                                ||  |||||||   ||||||  |||||
                                AC GTCGAGA   TCAGGG AGGGC
                                  _      AGA      G
GAM283  STK24    5'  TAGGGAGAGTGCTTTCGTTTG  13118    T    CTCT    __
                                A GACGG    GAGT  TCTTCCTG
                                |  |||||    ||||  ||||||||
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                                G TTGCT   TTCG  AGAGGGAT
                                 T    ____   TG
GAM283  TAL1    5'  CGGGAGGGGTTGTTGTT    12102      TCTG  TT
                                GACGGC   AG  CTTCCTG
                                ||||||   ||  |||||||
                                TTGTTG   TT  GGAGGGC
                                   ____  GG
GAM283  TBX1    3'  GGGCACATGGAGTTGTCGTG  54670          A  T
                                CATGACGGCTCTG GT CTT
                                |||||||||||| || |||
                                GTGCTGTTGAGGT CA GGG
                                       A  C
GAM283  TCF2    3'  TGGGAAGACAATGGCCATTGTG 21388    TG C   CTGAGT
                                CA  A GGCT    TCTTCCTG
                                ||  | ||||    ||||||||
                                GT  T CCGG    AGAAGGGT
                                 GT A   TAAC__
GAM283  TCF20   3'  GGGAGGGACTGTCGCTGT    66957      TCTG
                                ACGGC   AGTTCTTCCT
                                |||||   ||||||||||
                                TGTCG   TCAGGGAGGG
                                  CTG_
GAM283  TCF4    5'  CGGGGGGATCTTGGCTGTGTG  12149    G     CT   T
                                CAT ACGGCT  GAG TCTTCCTG
                                ||| ||||||  ||| ||||||||
                                GTG TGTCGG  TTC AGGGGGGC
                                 _     __   T
GAM283  THPO    5'  CAGGAAGGATTCAGGG      4862
                                CTCTGAGTTCTTCCTG
                                ||||||||||||||||
                                GGGACTTAGGAAGGAC

GAM283  TIF1    5'  CAGGAGGAGGAGGAGGTCGTCG 60378        _  GAG
                                TGACGGC TCT   TTCTTCCTG
                                ||||||| |||   |||||||||
                                GCTGCTG AGG   GAGGAGGAC
                                    G   AG_
GAM283  TIMM44  3'  CGGGAGGGGACAACGGGCTGTT 71420        TGAG_
                                GACGGCTC    TTCTTCCTG
                                ||||||||    |||||||||
                                TTGTCGGG    GGGGAGGGC
                                     CAACA
GAM283  TIMP3   5'  GGGGGCAAGGGCTTTGTG    4513     TG C     GA
                                CA  A GGCTCT  GTTCTT
                                ||  | ||||||  ||||||
                                GT  T TCGGGA  CGGGGG
                                 GT _     A_
GAM283  TNFSF11 3'  AGTTTTTGGAGTGTTATG    52238       G   TG  TT
                                CATGACG CTC  AG  CT
                                ||||||| |||  ||  ||
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                                GTATTGT GAG  TT  GA
                                   _  GT  TT
GAM283  TNFSF11  3'  AGTTTTTGGAGTGTTATG    13510       G   TG  TT
                                CATGACG CTC  AG  CT
                                ||||||| |||  ||  ||
                                GTATTGT GAG  TT  GA
                                   _  GT  TT
GAM283  TNR      3'  GGGGTGCAGATTGTTATG    12356       C    A TT
                                CATGACGG TCTG G  CT
                                |||||||| |||| |  ||
                                GTATTGTT AGAC T  GG
                                   _   G GG
GAM283  TRIM34   5'  TGGGAGGAAAAAGCAGCTGTCC 55226    T     _  GAG
           TG                     CA GACGGCT CT   TTCTTCCTG
                                || ||||||| ||   |||||||||
                                GT CTGTCGA GA   AAGGAGGGT
                                 C      C  AA_
GAM283  UC28     3'  CAGGAAGAGGGAAGGCTGTTTG 41289    T     T  GAG
                                A GACGGC CT   TTCTTCCTG
                                | |||||| ||   |||||||||
                                G TTGTCG GA   GAGAAGGAC
                                 T     _  AGG
GAM283  YWHAE    3'  GGGAGGGACTTCGTTGTAATG  22196     G     TCT        G
                                CAT ACGGC   GAGTTCTTCCT
                                ||| |||||   ||||||||||
                                GTA TGTTG   TTCAGGGAGGG
                                  A    C__         G
GAM283  ZNF134   5'  CAGGAGGGGCTTGGACAGGCC  12845     ___  TG
                                GGC   TC  AGTTCTTCCTG
                                |||   ||  ||||||||||
                                CCG   AG  TCGGGGAGGAC
                                  GAC  GT
GAM283  ZNF144   5'  CAGGAAGAGGGTACAGCTTTGT 23077    TG C    C  AG
           G                     CA  A GGCT TG  TTCTTCCTG
                                ||  | |||| ||  |||||||||
                                GT  T TCGA AT  GAGAAGGAC
                                 GT _    C  GG
GAM283  ZNF165   5'  TGGGAAGAGTAACCGCCGTTTT 12883    T     TCTGAG
           G                     CA GACGGC     TTCTTCCTG
                                || ||||||     |||||||||
                                GT TTGCCG     GAGAAGGGT
                                 T     CCAAT_
GAM283  ZNF175   5'  GGGAAAAGTGGAGTTGTCA    23094          AG  C
                                TGACGGCTCTG  TT TTCC
                                ||||||||||  || ||||
                                ACTGTTGAGGT  AA AGGG
                                       GA  _
GAM283  ZNF239   5'  CAGGAAGCTGTGCGGAGCTGTG 19038     G        AGTT_
           ATG                     CAT ACGGCTCTG    CTTCCTG
                                ||| |||||||||    |||||||
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                                GTA TGTCGAGGC    GAAGGAC
                                  G       GTGTC
GAM283  ZNF41    5'  GGGAAGAGTGGGGTTGTCA   63941          AG
                                TGACGGCTCTG  TTCTTCCT
                                ||||||||||  ||||||||
                                ACTGTTGGGGT  GAGAAGGG
                                           __
GAM283  20D7-FC4 3'  AGGAATTGGGGGCTGTCA    60895          G
                                TGACGGCTCT AGTTCTT
                                |||||||||| |||||||
                                ACTGTCGGGG TTAAGGA
                                      G
GAM283  AMOTL1   3'  GGGAGATGGGAGCTGTTTTG  73654    T       GAGT
                                CA GACGGCTCT   TCTTCC
                                || |||||||||   ||||||
                                GT TTGTCGAGG   AGAGGG
                                 T       GT__
GAM283  APCL     3'  GTCCTCAACTCAGGGCCGCTGT 19683    GA         CTTCCTG
           G                     CAT  CGGCTCTGAGTT
                                |||  ||||||||||||
                                GTG  GCCGGGACTCAA
                                  TC          CTCCTGT
GAM283  ARHGDIG  3'  GCTCAGGGCTTCGTG       6778       C
                                CATGA GGCTCTGAGT
                                ||||| ||||||||||
                                GTGCT TCGGGACTCG
                                          _
GAM283  ARHU     3'  TAGGAGGAGCTCTCAATTTTAT 41078      CGGCTCT
           G                     CATGA      GAGTTCTTCCTG
                                |||||      ||||||||||||
                                GTATT      CTCGAGGAGGAT
                                   TTAACT_
GAM283  BCAA     5'  CGGGGGGGATTTTTCGTCGTC  33047       TCT
                                GACGGC   GAGTTCTTCCTG
                                ||||||   ||||||||||||
                                CTGCTG   TTTAGGGGGGGC
                                    CTT
GAM283  BFAR     3'  AGGGAGGATTGTCTGTTTG   60768   T   CTCTG
                                A GACGG    AGTTCTTCCT
                                | |||||    ||||||||||
                                G TTGTC    TTAGGAGGGA
                                 T    TG___
GAM283  BM045    3'  CGGGGGGGGCTTGGAATGTT   37458     GC  TG
                                GACG  TC  AGTTCTTCCTG
                                ||||  ||  ||||||||||||
                                TTGT  AG  TCGGGGGGGGC
                                  A_  GT
GAM283  C11orf16 3'  AGGAAGGCACCTGTTGTG    40215    TG   CTCTGA _
                                CA  ACGG     GT TCTTCCT
                                ||  ||||     || |||||||
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                                GT  TGTC     CA GGAAGGA
                                 GT   _______  C
GAM283   C20orf102 3'  AGGGCCTGGGGCTGTT      54614          GA
                                GACGGCTCT  GTTCT
                                |||||||||  |||||
                                TTGTCGGGG  CGGGA
                                     TC
GAM283   C20orf116 3'  GGACTCAGAGTTGGTGTG     43738     GA
                                CAT  CGGCTCTGAGTTC
                                |||  ||||||||||||
                                GTG  GTTGAGACTCAGG
                                  TG
GAM283   C20orf139 3'  AGGGAACAGAATTGTCATG    84752         C    AGTTC
                                CATGACGG TCTG     TTCCT
                                |||||||| ||||     |||||
                                GTACTGTT AGAC     AGGGA
                                     A    A_____
GAM283   C20orf29  3'  CAGGGAGAGAAGTTGCTGTCA  37124         TCTGAG
                                TGACGGC      TTCTTCCTG
                                |||||||      |||||||||
                                ACTGTCG      GAGAGGGAC
                                     TTGAA_
GAM283   C20orf60  5'  GGGGCTGGAGCTGTCG       53736          G
                                TGACGGCTCT AGTTCT
                                |||||||||| ||||||
                                GCTGTCGAGG TCGGGG
                                                _
GAM283   C22orf5   3'  TGGGGGGAGCTCAGTGGC     24349     _
                                GCT CTGAGTTCTTCCTG
                                ||| ||||||||||||||
                                CGG GACTCGAGGGGGGT
                                  T
GAM283   CAGE      5'  GGGAAAATGTGGTTGTCATG   82696          CTGA   C
                                CATGACGGCT    GTT TTCC
                                ||||||||||    ||| ||||
                                GTACTGTTGG    TAA AGGG
                                      TG__   A
GAM283   CAMKK2    3'  CAGGAAAGGAGGTGCTGTTATG 21578          T  GAG    _
                                CATGACGGC CT   TTCTT CCTG
                                ||||||||| ||   ||||| ||||
                                GTATTGTCG GG   AGGAA GGAC
                                      T ____     A
GAM283   CAMTA2    3'  AGGGGGAGCCCCTGTCG      61219       CTCTGA
                                TGACGG      GTTCTTCCT
                                ||||||      |||||||||
                                GCTGTC      CGAGGGGGA
                                   CC_____
GAM283   CARD9     3'  GGGCATTGGGGCCGTTTG     53377    T       TG _
                                A GACGGCTC  A GTTC
                                | ||||||||  | ||||
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                                G TTGCCGGG  T CGGG
                                 T       GT A
GAM283  CARD9    3'  GGGCATTGGGGCCGTTTG    42290   T      TG _
                                A GACGGCTC  A GTTC
                                | ||||||||  | ||||
                                G TTGCCGGG  T CGGG
                                 T       GT A
GAM283  CBX6     3'  TGGGAGGGTGGGGGTTGTCA  26631         GA TT    TG
                                TGACGGCTCT  G  CTTCC
                                ||||||||||  |  |||||
                                ACTGTTGGGG  T  GAGGG
                                      G_ GG    T
GAM283  CCR6     3'  GGAAGGTACTGTCATG     15170        CTCTGAGT
                                CATGACGG      TCTTCC
                                ||||||||      ||||||
                                GTACTGTC      GGAAGG
                                    AT_______
GAM283  CCR6     3'  GGAAGGTACTGTCATG     48586        CTCTGAGT
                                CATGACGG      TCTTCC
                                ||||||||      ||||||
                                GTACTGTC      GGAAGG
                                    AT_______
GAM283  CDC14B   3'  TGGAATTCTGACTTAGAGTCGT 52839   TG         C___   TG
          TGT                     ACGGCTCTGAGTT   TTCC
                                  ||||||||||||   ||||
                                  TGCTGAGATTCAG   AAGG
                                GT          TCTT   T
GAM283  CNNM3    3'  GGGAGGAAGGGATCGTCATG   34342       _   GAG
                                CATGACGG CTCT   TTCTTCC
                                |||||||| ||||  |||||||
                                GTACTGCT GGGA   AGGAGGG
                                    A   ___
GAM283  CSRP2BP  3'  GGGATTGGGGTTGTT      70114        G
                                GACGGCTCT AGTTCT
                                ||||||||| ||||||
                                TTGTTGGGG TTAGGG
                                          _
GAM283  CTCF     3'  TGGGAAGGACTTAGAGTT    21637
                                GGCTCTGAGTTCTTCCTG
                                ||||||||||||||||||
                                TTGAGATTCAGGAAGGGT

GAM283  DCNP1    3'  GGGAGGAACTGAATGCATG   55623     A  GC  TG
                                CATG CG  TC  AGTTCTTCCT
                                |||| ||  ||  ||||||||||
                                GTAC GT  AG  TCAAGGAGGG
                                  _ A_  __
GAM283  DDX33    3'  AGTGTTTAGGGCTGTC      39368          TT
                                GACGGCTCTGAG  CT
                                ||||||||||||  ||
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                                CTGTCGGGATTT  GA
                                      GT
GAM283  Di-Ras2  3'  GGGGGGGTGGGGGCTGCATG  34189     A     GA TT
                                CATG CGGCTCT  G  CTTCC
                                |||| |||||||  |  |||||
                                GTAC GTCGGGG  T  GGGGG
                                  _     G_ GG
GAM283  DKFZp434A171 5'  CAGGAGGAGTCTTGTGCCGTTA 70797        TCT  _
          T                      ATGACGGC   GAG TTCTTCCTG
                                 ||||||||   ||| |||||||||
                                 TATTGCCG   TTC GAGGAGGAC
                                      TG_   T
GAM283  DKFZp434I1930 3'  CAGGAGGAGCTCAGTTGTCG   50032     T_
                                CGGC  CTGAGTTCTTCCTG
                                ||||  ||||||||||||||
                                GCTG  GACTCGAGGAGGAC
                                  TT
GAM283  DKFZP434N014 3'  GGGGTTGGGGCTGCATG     60600     A     TG G
                                CATG CGGCTC  A TTC
                                |||| ||||||  | |||
                                GTAC GTCGGG  T GGG
                                  _     GT G
GAM283  DKFZP564C186 3'  CGGGGGGAGGCAGGGCCATTGT 72407    TG C     AG
          G                      CA  A GGCTCTG  TTCTTCCTG
                                 ||  | |||||||  |||||||||
                                 GT  T CCGGGAC  GAGGGGGGC
                                  GT A      G_
GAM283  DKFZP564I1171 5'  AGGAGGAGACGCCGCTGTG   71582    GA   TCTGAG
                                CAT  CGGC     TTCTTCCT
                                |||  ||||     ||||||||
                                GTG  GCCG     GAGGAGGA
                                  TC   CA____
GAM283  DKFZP564I1171 3'  CAGGAGGAGTTCTTAAAGAGTT 71584   C     _____  GT
          TTATG                    A GGCTCT    GA  TCTTCCTG
                                | ||||||    ||  ||||||||
                                T TTGAGA    CT  AGGAGGAC
                                _     AATT  TG
GAM283  DKFZP566J091 3'  GGGGACAAGGCTGTCGTG    48125        T  GA
                                CATGACGGC CT  GTTCTT
                                |||||||| ||  ||||||
                                GTGCTGTCG GA  CAGGGG
                                      _ A_
GAM283  DKFZP586J1624 3'  GGATGGGCTGTCGTG      31394          TGAGTTCT
                                CATGACGGCTC       TCC
                                ||||||||||       |||
                                GTGCTGTCGGG       AGG
                                       T_______
GAM283  DKFZP761G1913 3'  GGGAGATGGGGGTTGTAGTG  48917     G      GAGT
                                CAT ACGGCTCT    TCTTCC
                                ||| ||||||||    ||||||
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                                GTG TGTTGGGG   AGAGGG
                                  A       GT__
GAM283  DRF1     3'  CAGGAGGGGTACATGGCTGTGA 47026     G     C  A TT
              TG                   CAT ACGGCT TG G  CTTCCTG
                                   ||| |||||| || |  |||||||
                                   GTA TGTCGG AC T  GGAGGAC
                                     G     T  A GG
GAM283  DXS1357E 5'  GGGGCCGGGGCTGCTGTG    19232     GA       A
                                   CAT  CGGCTCTG GTTCT
                                   |||  |||||||| |||||
                                   GTG  GTCGGGGC CGGGG
                                     TC       _
GAM283  ENAH     3'  GCTTGAGTTGTTATG       36616           T
                                   CATGACGGCTC GAGT
                                   |||||||||| ||||
                                   GTATTGTTGAG TTCG
                                              _
GAM283  ERp44    3'  TAGGGAGGACTTAGGGATGTT  81699      G
                                   GACG CTCTGAGTTCTTCCTG
                                   |||| ||||||||||||||||
                                   TTGT GGGATTCAGGAGGGAT
                                     A
GAM283  EVI5     3'  ACAGGAGTTTGGGGCTGTAGTG 18986     G      TG  TTC
                                   CAT ACGGCTC  AG   TTCCTG
                                   ||| |||||||  ||   ||||||
                                   GTG TGTCGGG  TT   GAGGAC
                                     A      GT ____     AT
GAM283  EZF-2    3'  CAGGAGGAGCTTGGGCGC    37096    _  TG
                                   GC TC  AGTTCTTCCTG
                                   || ||  ||||||||||
                                   CG GG  TCGAGGAGGAC
                                    C  GT
GAM283  FADS1    3'  TAGGAGGGAAGGAGCTGTT   25484         GAG
                                   GACGGCTCT   TTCTTCCTG
                                   |||||||||   |||||||||
                                   TTGTCGAGG   AGGGAGGAT
                                         A__
GAM283  FENS-1   3'  TAGGGGGCCTTCCAGGGTTCTT 40444    TG CG     _  TT
              GTG                    CA  A  GCTCTG AG  CTTCCTG
                                   ||  |  |||||| ||  |||||||
                                   GT  T  TGGGAC TT  GGGGGAT
                                    GT CT     C  CC
GAM283  FER1L4   3'  CAGCTATGAGCTCAGAGTTGTC 47334              TTC_
              AT                     ATGACGGCTCTGAGTTC   CTG
                                   ||||||||||||||||   |||
                                   TACTGTTGAGACTCGAG   GAC
                                              TATC
GAM283  FLJ10097 5'  GGCGTCAGAGCCGTCGTG    68511            _
                                   CATGACGGCTCTGA GTT
                                   |||||||||||||| |||
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                                GTGCTGCCGAGACT CGG
                                       G
GAM283  FLJ10292  3' GGGAGGGGTTATTTGTCAT   35975       CTC   G
                                ATGACGG   TGA TTCTTCC
                                |||||||   ||| |||||||
                                TACTGTT   ATT GGGAGGG
                                    T__   G
GAM283  FLJ10702  3' AGCTAGAGTTGTCATG     36436          G
                                CATGACGGCTCT AGTT
                                |||||||||||| ||||
                                GTACTGTTGAGA TCGA
                                         _
GAM283  FLJ10826  5' CAGGAAGAAGTCATTGTCATG  36701        CTC   G
                                CATGACGG   TGA TTCTTCCTG
                                |||||||   ||| |||||||||
                                GTACTGTT   ACT AAGAAGGAC
                                    ___   G
GAM283  FLJ10971  3' CAGGGCATTTTAGGGCTGTC   36925          TTCT
                                GACGGCTCTGAG   TCCTG
                                ||||||||||||   |||||
                                CTGTCGGGATTT   GGGAC
                                       TAC_
GAM283  FLJ11017  3' CAGGGAGGTAAGCTGGTGTCAT 36986      ___   CTGAGT
          G                     ATGAC   GGCT    TCTTCCTG
                                |||||   ||||    ||||||||
                                TACTG   TCGA    GGAGGGAC
                                  TGG   AT____
GAM283  FLJ11526  5' CGGGGGGAGCGAACTGTTGTGG 44910    G    TCTGA
          TG                    CAT ACGGC    GTTCTTCCTG
                                ||| |||||    ||||||||||
                                GTG TGTTG    CGAGGGGGGC
                                  G    TCAAG
GAM283  FLJ11939  3' AGGCCTCAGAGCTGTGTG    45172    G        TT
                                CAT ACGGCTCTGAG  CT
                                ||| ||||||||||  ||
                                GTG TGTCGAGACTC  GA
                                  _        CG
GAM283  FLJ12387  3' CAGGAGGGGCTCCCCCTGTT   43066      CTCT
                                GACGG   GAGTTCTTCCTG
                                |||||   ||||||||||||
                                TTGTC   CTCGGGGAGGAC
                                  CCC_
GAM283  FLJ12443  3' CAGGGGCCTCGGGGGCTGTTTG 45726   T      _   TT TT
                                A GACGGCTCT GAG  C  CCTG
                                | |||||||| |||  |  ||||
                                G TTGTCGGGG CTC  G  GGAC
                                 T       G   CG __
GAM283  FLJ12800  3' GGGAGGGGTGTTTTCATG    43235      CG  TCTGA TT
                                CATGA  GC    G  CTTCCT
                                |||||  ||    |  ||||||
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                                GTACT  TG    T  GGAGGG
                                   TT  _____ GG
GAM283  FLJ12800  3'  GGGAGGGGTGTTTTCATG    88961      CG  TCTGA TT
                                CATGA  GC    G  CTTCCT
                                ||||||  ||    |  ||||||
                                GTACT  TG    T  GGAGGG
                                   TT  _____ GG
GAM283  FLJ13072  3'  AGGGAGGACAACTGCATG    89802      A   CTCTGA
                                CATG CGG     GTTCTTCCT
                                ||||| |||     |||||||||
                                GTAC GTC     CAGGAGGGA
                                   _   AA____
GAM283  FLJ13162  5'  CAGGAAGAGTGGCCCTGTGTG  46551      AC_   CTGAG
                                CATG   GGCT    TTCTTCCTG
                                ||||   ||||    |||||||||
                                GTGT   CCGG    GAGAAGGAC
                                   GTC   T____
GAM283  FLJ13197  3'  GCTCAGAGCTGCTGTG      44858     GA
                                CAT  CGGCTCTGAGT
                                |||  ||||||||||
                                GTG  GTCGAGACTCG
                                  TC
GAM283  FLJ13265  3'  GGGAGCCGGGTCGTCGTG    45930        T   A
                                CATGACGGC CTG GTTCTT
                                ||||||||| ||| ||||||
                                GTGCTGCTG GGC CGAGGG
                                          _   _
GAM283  FLJ14106  3'  AGGAAAAGGAGCTGTTTTG   46864    T       GAGTTC
                                CA GACGGCTCT     TTCCT
                                || |||||||||     |||||
                                GT TTGTCGAGG     AAGGA
                                 T       AA____
GAM283  FLJ20374  5'  TGGGAAGGGCTCGGATACCG   35082     C_
                                CGG  TCTGAGTTCTTCCTG
                                |||  ||||||||||||||
                                GCC  AGGCTCGGGAAGGGT
                                  AT
GAM283  FLJ20489  3'  GGGAGGGAAGGGGCTGTT    35253        GAG
                                GACGGCTCT   TTCTTCC
                                |||||||||   |||||||
                                TTGTCGGGG   GGGAGGG
                                     AA_
GAM283  FLJ20507  3'  AGGAGGGACTTGGCATG     35273     ACGGCT TG
                                CATG     C  AGTTCTTCCT
                                ||||     |  ||||||||||
                                GTAC     G  TCAGGGAGGA
                                  _______ GT
GAM283  FLJ20546  3'  CAGGGAAAACTCGGGGCTTTGT 35365    TG C         C
          G                      CA  A GGCTCTGAGTT TTCCTG
                                ||  | ||||||||||| ||||||
```

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                                GT  T TCGGGGCTCAA AGGGAC
                                 GT _         A
GAM283  FLJ20574  3' CGGGAAGGGGAAGAGCGTGTTG 35420    TG  _    GAG
             TG                   CA  ACG GCTCT   TTCTTCCTG
                                  ||  ||| |||||   |||||||||
                                GT  TGT CGAGA   GGGAAGGGC
                                 GT   G    AG_
GAM283  FLJ20584  3' GGGAGAAAGGCGCCGTCGTG   35431         T  GAG
                                CATGACGGC CT   TTCTTCC
                                |||||||||  ||   |||||||
                                GTGCTGCCG GG   AAGAGGG
                                      C  A__
GAM283  FLJ20619  3' GACTGGAGTTGTTATG      35464           G
                                CATGACGGCTCT AGTT
                                |||||||||||| ||||
                                GTATTGTTGAGG TCAG
                                          _
GAM283  FLJ21777  5' GGGAGGGGTCAGCCGTCCTG   49865    T     CT  G
                                CA GACGGCT  GA TTCTTCC
                                ||  |||||||  ||  |||||||
                                GT CTGCCGA  CT GGGAGGG
                                 C      __  G
GAM283  FLJ22693  3' GGTTTCTCAGAGTCTCATG    42762      C       TTCTT
                                CATGA GGCTCTGAG    CC
                                |||||  |||||||||    ||
                                GTACT CTGAGACTC    GG
                                   _       TTT__
GAM283  FLJ22795  3' AGGGAGGGAAGGGGGCTGTGTG 46940     G      GAG      G
                                CAT ACGGCTCT   TTCTTCCT
                                |||  ||||||||   ||||||||
                                GTG TGTCGGGG   AGGGAGGG
                                  _      GA_       AG
GAM283  FLJ22833  5' GGGAGCGGGGTTGGTGTG    43107     GA      AGTT
                                CAT  CGGCTCTG    CTTCC
                                |||  ||||||||   |||||
                                GTG  GTTGGGGC    GAGGG
                                  TG      ____
GAM283  FLJ23017  3' GGGAATATTTGGAGTTGTTTG  43124   T      TG   TC    G
                                A GACGGCTC  AGT  TTCCT
                                |  ||||||||  |||  |||||
                                G TTGTTGAG  TTA  AAGGG
                                 T      GT   T_    G
GAM283  FLJ23022  5' TGGGAGGGGCTCAGGCC     46815     T
                                GGC CTGAGTTCTTCCTG
                                |||  ||||||||||||||
                                CCG GACTCGGGGAGGGT
                                  _
GAM283  FLJ23420  3' TGGGGAGACAGACAGGATGTTG 46850    TG   GC    AGT_
             TG                   CA  ACG  TCTG   TCTTCCTG
                                  ||  |||  ||||   ||||||||
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                                GT  TGT  GGAC   AGAGGGGT
                                 GT   A_   AGAC
GAM283   FLJ23556  3'  CAGGTGACTCGGGCTGTTGTG  45944    TG    T     CTT
                                CA  ACGGC CTGAGTT   CCTG
                                ||  ||||| |||||||   ||||
                                GT  TGTCG GGCTCAG   GGAC
                                 GT    _     T__
GAM283   FLJ32356  3'  TGGGAGGGGTTCAGAGCTTC   58370    C       TT
                                GA GGCTCTGAG  CTTCCTG
                                || |||||||||  |||||||
                                CT TCGAGACTT  GGAGGGT
                                  _       GG
GAM283   FLJ32940  5'  CAGGAGTTTCAGGTTTGGAGTG 58220     G   TG  TTC____
            TTATG                   ACG CTC  AG      TTCCTG
                                ||| |||  ||      ||||||
                                TGT GAG  TT      GAGGAC
                                  _  GT  GGACTTT
GAM283   G2       3'  GGCTTGGGGCCTTATG      66661       C     TG
                                CATGA GGCTC  AGTT
                                ||||| |||||  ||||
                                GTATT CCGGG  TCGG
                                   _    GT
GAM283   GIOT-3    5'  GGGAGGGACGCCCCGTC     32752       CTCTGA
                                GACGG     GTTCTTCCT
                                |||||     |||||||||
                                CTGCC     CAGGGAGGG
                                   CCG___
GAM283   GMFB     5'  CAGGAAGGGAGGCGGCCGCCGT 14665      A     CTGAG
            G                    CATG CGGCT     TTCTTCCTG
                                |||| |||||     |||||||||
                                GTGC GCCGG     GGGAAGGAC
                                  C    CGGA_
GAM283   GMPPB    3'  AGGGCCAGGGCTGTATG      25301      A       A
                                CATG CGGCTCTG GTTCT
                                |||| |||||||| |||||
                                GTAT GTCGGGAC CGGGA
                                  _      _
GAM283   GMPPB    3'  AGGGCCAGGGCTGTATG      41745      A       A
                                CATG CGGCTCTG GTTCT
                                |||| |||||||| |||||
                                GTAT GTCGGGAC CGGGA
                                  _      _
GAM283   GMPPB    5'  AGGGCCAGGGCTGTATG      95721      A       A
                                CATG CGGCTCTG GTTCT
                                |||| |||||||| |||||
                                GTAT GTCGGGAC CGGGA
                                  _      _
GAM283   GPA33    3'  GGGGGGTGGGGGCTGTCCTG   19457    T       GAGT
                                CA GACGGCTCT    TCTTCC
                                || |||||||||    ||||||
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                                GT CTGTCGGGG   GGGGGG
                                 C       GT__
GAM283  GPS2    5'  GGGGGTGGGGAGCCGTGTG   15669    G      GAGTT
                                CAT ACGGCTCT    CTTCC
                                ||| ||||||||    |||||
                                GTG TGCCGAGG    GGGGG
                                  _      GGT__
GAM283  HAGE    5'  GGGGGGGCTAGCCTCGTG    37900     C   CTG
                                CATGA GGCT   AGTTCTTCC
                                ||||| ||||  |||||||||
                                GTGCT CCGA   TCGGGGGGG
                                  _   ____
GAM283  HM74    3'  TGGGGGGGGCTCAGCTCCTCG  20058    C  CT
                                TGA GG  CTGAGTTCTTCCTG
                                ||| ||  ||||||||||||||
                                GCT CC  GACTCGGGGGGGGT
                                  _ TC
GAM283  HN1L    3'  TGGGAAGAGGGTTAGTCTTATG 58007     C   CTGAG
                                CATGA GGCT    TTCTTCCTG
                                ||||| ||||    |||||||||
                                GTATT CTGA    GAGAAGGGT
                                  _   TTGG_
GAM283  HSPC055  5'  CAGGGAAACAGGAGCTGTCA  26267        GA  C
                                TGACGGCTCT  GTT TTCCTG
                                ||||||||||  ||| ||||||
                                ACTGTCGAGG  CAA AGGGAC
                                     A_  _
GAM283  HSPC156  5'  TAGGAGGAAAGGTGCTTTGTG  26356   TG C   T  GAG
                                CA  A GGC CT   TTCTTCCTG
                                ||  | ||| ||   |||||||||
                                GT  T TCG GG   AAGGAGGAT
                                 GT _   T  A__
GAM283  HT002    3'  CAGGGAGAAGGCAGCCGTGTG  25933    G     CT AG
                                CAT ACGGCT  G  TTCTTCCTG
                                ||| ||||||  |  |||||||||
                                GTG TGCCGA  C  AAGAGGGAC
                                  _     __ GG
GAM283  HUMZD58C02 3'  CGGGAAGGGCCCATCCCGTT   79765      CTC  A
                                GACGG   TG GTTCTTCCTG
                                |||||   || ||||||||||
                                TTGCC   AC CGGGAAGGGC
                                   CT_  C
GAM283  IAN4L1   3'  GACTTGGAGCTGTGTG     37224     G      TG
                                CAT ACGGCTC  AGTT
                                ||| |||||||  ||||
                                GTG TGTCGAG  TCAG
                                  _      GT
GAM283  IBTK     3'  AAGATTTGGAGTCATTGTG   67485    TG C    TG   T
                                CA  A GGCTC  AGT CTT
                                ||  | |||||  ||| |||
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                                GT  T CTGAG  TTA GAA
                                 GT A    GT  _
GAM283  IGF2AS   3'  TAGGGGGGACATGGAGGGCCGT 33101   TG      GA__
            TGT                   A  ACGGCTCT   GTTCTTCCTG
                                | ||||||||   ||||||||||
                                T  TGCCGGGA   CAGGGGGGAT
                                 GT       GGTA
GAM283  IGSF2    3'  CAGGGGGAGCTATAGCTTCATG 14922      C   CTG
                                CATGA GGCT   AGTTCTTCCTG
                                ||||| ||||  ||||||||||
                                GTACT TCGA   TCGAGGGGGAC
                                   _   TA_
GAM283  IL-17RC  3'  AGACCTGTGGAGCCGTCGTG   51198          _ T
                                CATGACGGCTCTG AG TCT
                                |||||||||||| || |||
                                GTGCTGCCGAGGT TC AGA
                                       G  C
GAM283  ING3     3'  ACTCCAGAGCTGTTATG     38830          _
                                CATGACGGCTCTG AGT
                                |||||||||||| |||
                                GTATTGTCGAGAC TCA
                                       C
GAM283  JAM1     5'  CAGGAGTCCTTCGGCGGCTGTT 33751    TG    _    TTC
            GTG                   CA  ACGGCT CTGAG   TTCCTG
                                || ||||| |||||   ||||||
                                GT  TGTCGG GGCTT   GAGGAC
                                 GT     C    CCT
GAM283  JAM1     5'  CAGGAGTCCTTCGGCGGCTGTT 57878    TG    _    TTC
            GTG                   CA  ACGGCT CTGAG   TTCCTG
                                || ||||| |||||   ||||||
                                GT  TGTCGG GGCTT   GAGGAC
                                 GT     C    CCT
GAM283  JAM1     5'  CAGGAGTCCTTCGGCGGCTGTT 57889    TG    _    TTC
            GTG                   CA  ACGGCT CTGAG   TTCCTG
                                || ||||| |||||   ||||||
                                GT  TGTCGG GGCTT   GAGGAC
                                 GT     C    CCT
GAM283  JAM1     5'  CAGGAGTCCTTCGGCGGCTGTT 57944    TG    _    TTC
            GTG                   CA  ACGGCT CTGAG   TTCCTG
                                || ||||| |||||   ||||||
                                GT  TGTCGG GGCTT   GAGGAC
                                 GT     C    CCT
GAM283  KHSRP    3'  TGGGGGGGACTTGGGGGCATG  13485     ACGG   TG
                                CATG   CTC  AGTTCTTCCTG
                                ||||   |||  ||||||||||
                                GTAC   GGG  TCAGGGGGGGT
                                  G___   GT
GAM283  KIAA0100 3'  TGGGAGGGGCTTCCCGTTAT   27974        CTCT
                                ATGACGG   GAGTTCTTCCTG
                                |||||||   ||||||||||
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                                TATTGCC    TTCGGGGAGGGT
                                   C___
GAM283  KIAA0232  3'  GGGGTGTGGGGTCGTATG    72752      A       A TT
                                CATG CGGCTCTG G  CT
                                |||| |||||||| |  ||
                                GTAT GCTGGGGT T  GG
                                  _       G GG
GAM283  KIAA0237  3'  GGGATGATAGGGTTGTTA    28531          AGT  T
                                TGACGGCTCTG   TC TCCT
                                ||||||||||   || ||||
                                ATTGTTGGGAT   AG AGGG
                                      ___  T
GAM283  KIAA0255  3'  AGTTCCTCAGGGCTGTT     28463          TT_
                                GACGGCTCTGAG   CT
                                ||||||||||||   ||
                                TTGTCGGGACTC   GA
                                      CTT
GAM283  KIAA0265  3'  GGGAAGGAAAAGCTGTGTG    69881     G     CTGAG
                                CAT ACGGCT    TTCTTCCT
                                ||| ||||||    ||||||||
                                GTG TGTCGA    AGGAAGGG
                                  _     AA___
GAM283  KIAA0275  3'  GACTTGGGGCTGTGATG     28679     G      TG
                                CAT ACGGCTC  AGTT
                                ||| |||||||  ||||
                                GTA TGTCGGG  TCAG
                                  G      GT
GAM283  KIAA0275  3'  GGGGGTGGGGGTTGTTA     28683          GAGTT
                                TGACGGCTCT    CTTCC
                                ||||||||||    |||||
                                ATTGTTGGGG    GGGGG
                                      GT___
GAM283  KIAA0349  3'  GGTTTTTCAGGGCTGTTA    92307           TTCTT
                                TGACGGCTCTGAG    CC
                                ||||||||||||    ||
                                ATTGTCGGGACTT    GG
                                      TTT__
GAM283  KIAA0356  3'  TGGGGAGGGCTTGGGCC     66198     T TG
                                GGC C  AGTTCTTCCTG
                                ||| |  ||||||||||||
                                CCG G  TCGGGAGGGGT
                                  _ GT
GAM283  KIAA0379  5'  CAGGGAGGACTGCATTACATCA 68149       CGGCTC  _
          TG                     CATGA     TG AGTTCTTCCTG
                                |||||     || ||||||||||||
                                GTACT     AC TCAGGAGGGAC
                                   ACATT_  G
GAM283  KIAA0435  3'  GGACACTCTCGGGGTTGTC    28978           TTCT
                                GACGGCTCTGAG    TCC
                                ||||||||||||    |||
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                                CTGTTGGGGCTC   AGG
                                       TCAC
GAM283  KIAA0450 5' TGGGAGGAGACCCTGGTTTTCA 27653     CG  CTGAG
            TG                  CATGA  GCT    TTCTTCCTG
                                ||||| |||    |||||||||
                                GTACT  TGG    GAGGAGGGT
                                  TT   TCCCA
GAM283  KIAA0469 3' GGGTTCTGGGCTGTCATG    29343         T   TT
                                CATGACGGCTC GAG  C
                                |||||||||| ||| |
                                GTACTGTCGGG CTT  G
                                       T   GG
GAM283  KIAA0475 3' GGACTCAGAGCTGTGTG     29498     G
                                CAT ACGGCTCTGAGTTC
                                ||| ||||||||||||||
                                GTG TGTCGAGACTCAGG
                                 _
GAM283  KIAA0494 3' TAGGGAGAATTCAGGGTTTCCA 28747     AC
            TG                  CATG  GGCTCTGAGTTCTTCCTG
                                |||| ||||||||||||||||||
                                GTAC  TTGGGACTTAAGAGGGAT
                                  CT
GAM283  KIAA0514 3' GGGATTCTGGGGCTGTCA    28092         _
                                TGACGGCTCT GAGTTCT
                                |||||||||| |||||||
                                ACTGTCGGGG CTTAGGG
                                       T
GAM283  KIAA0522 3' TGGGGGGGGCTCAGGTCTG   71971     CT
                                CGG  CTGAGTTCTTCCTG
                                |||  ||||||||||||||
                                GTC  GACTCGGGGGGGGT
                                  TG
GAM283  KIAA0599 3' CAGGAAGGATGCTCCCGTGTG 77170     G   CTCT   __
                                CAT ACGG   GAGT  TCTTCCTG
                                ||| ||||   ||||  ||||||||
                                GTG TGCC   CTCG  GGAAGGAC
                                  _  _____   TA
GAM283  KIAA0599 3' CAGGTACTTTTGAGGGTTGTTG 77171    TG      G  TTCTT
            TG                  CA  ACGGCTCT AG    CCTG
                                ||  |||||||| ||    ||||
                                GT  TGTTGGGA TT    GGAC
                                 GT       G  TTCAT
GAM283  KIAA0848 5' AGGAGGAGACGTTGTTTTG   29987    T     TCTGAG
                                CA GACGGC     TTCTTCCT
                                || ||||||     ||||||||
                                GT TTGTTG     GAGGAGGA
                                 T     CA____
GAM283  KIAA0869 3' TGGGGGGGATTCAGAGGTGCAT 70857     A  G
                                ATG CG CTCTGAGTTCTTCCTG
                                ||| || ||||||||||||||||
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                                TAC GT GAGACTTAGGGGGGGT
                                  _ G
GAM283  KIAA0931  3'  TGGGAAGAAAGCAGCTGTTCTG 67427    T      CT AG
                                CA GACGGCT  G  TTCTTCCTG
                                || |||||||  |  |||||||||
                                GT TTGTCGA  C  AAGAAGGGT
                                 C      __ GA
GAM283  KIAA0964  5'  CAGGAACCTTGGGGCCTTGTG  29757    TG C    TG  TTC
                                CA  A GGCTC  AG   TTCCTG
                                ||  | |||||  ||   ||||||
                                GT  T CCGGG  TC   AAGGAC
                                 GT _    GT  C__
GAM283  KIAA0979  3'  AGTATTTTAGGTGCTGTTATG  30442          _     TT_
                                CATGACGGC TCTGAG   CT
                                |||||||||| ||||||   ||
                                GTATTGTCG GGATTT   GA
                                      T     TAT
GAM283  KIAA0982  3'  CAGGAAGGTAATATTTACAGCT 25845       C    _____
            GTCATG                  ACGGCT TGAGT    TCTTCCTG
                                |||||| |||||    ||||||||
                                TGTCGA ATTTA    GGAAGGAC
                                   C     TAAT
GAM283  KIAA1029  3'  CAGGGGGGACTCAGGGAGGAAT 23471      ACGG_
            ATG                   CATG    CTCTGAGTTCTTCCTG
                                ||||    ||||||||||||||||
                                GTAT    GGGACTCAGGGGGGAC
                                  AAGGA
GAM283  KIAA1041  3'  TGGGGAGAAAGGAAGAGCTTTA 30145      C     GAG_
            TG                    CATGA GGCTCT    TTCTTCCTG
                                ||||| ||||||    |||||||||
                                GTATT TCGAGA    AAGAGGGGT
                                  _     AGGA
GAM283  KIAA1053  3'  GGCTGGAGTCGTTGTG     94924    TG      G
                                CA  ACGGCTCT AGTT
                                ||  |||||||| ||||
                                GT  TGCTGAGG TCGG
                                 GT       _
GAM283  KIAA1086  3'  GGGAGGGGCCGCCGTC      70752       TCT A
                                GACGGC   G GTTCTTCCT
                                ||||||   | |||||||||
                                CTGCCG   C CGGGGAGGG
                                   ___ _
GAM283  KIAA1110  3'  CAGGAGGGACTTGGGTGC    61842    _  TG
                                GC TC  AGTTCTTCCTG
                                || ||  ||||||||||
                                CG GG  TCAGGGAGGAC
                                 T  GT
GAM283  KIAA1297  3'  AGGACCTCAGGGCTGTCG    72167           TTCT
                                TGACGGCTCTGAG    TCCT
                                ||||||||||||    ||||
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                                GCTGTCGGGACTC   AGGA
                                      C___
GAM283  KIAA1377 5' GGGAGCTAGGGCTGTCG    67178         G
                                TGACGGCTCT AGTTCTT
                                |||||||||| |||||||
                                GCTGTCGGGA TCGAGGG
                                          _
GAM283  KIAA1399 3' CAGGGAGGGATATGCTGGTGTG 70249    GA   TCTGAG
                                CAT  CGGC    TTCTTCCTG
                                |||  ||||    |||||||||
                                GTG  GTCG    GGGAGGGAC
                                  TG   TATA__
GAM283  KIAA1399 3' TGGGAGGAGCTTGACCAGTGTG 70255     AC  C  T
                                CATG  GG TC GAGTTCTTCCTG
                                ||||  || || ||||||||||||
                                GTGT  CC AG TTCGAGGAGGGT
                                   GA  _  _
GAM283  KIAA1503 5' TAGGAAGGGACAGTTGTT    68352       CTGAG
                                GACGGCT    TTCTTCCTG
                                |||||||    |||||||||
                                TTGTTGA    GGGAAGGAT
                                    CA___
GAM283  KIAA1503 5' TGGGGAGAAGAGGCAGTTGT   68353      _ GAG
                                ACGGCT CT   TTCTTCCTG
                                |||||| ||   |||||||||
                                TGTTGA GG   AAGAGGGGT
                                   C  AG_
GAM283  KIAA1649 3' GGGAGGGGGCTGTGTTG    66981    TG      GAGTT
                                CA  ACGGCTCT    CTTCC
                                ||  ||||||||    |||||
                                GT  TGTCGGGG    GAGGG
                                 TG      ______
GAM283  KIAA1715 3' AGGAAGAACTTTGGTT     68116     CT
                                GGCT  GAGTTCTTCCT
                                ||||  ||||||||||
                                TTGG  TTCAAGAAGGA
                                  T_
GAM283  KIAA1755 5' AGGAGGAGCAGTCTGTC    61337      _ CTGA
                                GACGG CT    GTTCTTCCT
                                |||||  ||   |||||||||
                                CTGTC GA    CGAGGAGGA
                                   T _____
GAM283  KIAA1813 5' AGAGGCTAGGAGTTGTCATG  70288          G  _
                                CATGACGGCTCT AGT TCT
                                |||||||||||| ||| |||
                                GTACTGTTGAGG TCG AGA
                                       A   G
GAM283  KIAA1904 3' GGAGGCCAGGAGCTTGGGGCTT 73492    C    TG     __  G
             CGTG                  TGA GGCTC  AGTTCTT  CCT
                                ||| |||||  |||||||  |||
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                                GCT TCGGG  TCGAGGA  GGA
                                  _    GT      CC   GGA
GAM283  KIAA1904  3'  GGGAAAAGGGCTGTCA      73495          GAG
                                TGACGGCTCT   TTCT
                                ||||||||||   ||||
                                ACTGTCGGGA   AGGG
                                     AA_
GAM283  KIAA1909  5'  AGGGACCCGAGACCGTCATG   73836        _   T A
                                CATGACGG CTC G GTTCTT
                                |||||||| ||| | ||||||
                                GTACTGCC GAG C CAGGGA
                                    A   _ C
GAM283  KIAA1941  3'  CAGATCCTGGACTCAGAGCTGT 74837    T            TTC__
            TTG                   A GACGGCTCTGAGTTC     CTG
                                | ||||||||||||||     |||
                                G TTGTCGAGACTCAGG     GAC
                                 T            TCCTA
GAM283  KLK7      3'  ACTGGGGTCGTCATG       57725           G
                                CATGACGGCTCT AGT
                                |||||||||||| |||
                                GTACTGCTGGGG TCA
                                          _
GAM283  KLK7      3'  ACTGGGGTCGTCATG       17285           G
                                CATGACGGCTCT AGT
                                |||||||||||| |||
                                GTACTGCTGGGG TCA
                                          _
GAM283  LAT1-3TM  3'  CAGGAGGGAGCTTGCTGTC   48313       TCT      _
                                GACGGC   GAGTTCT TCCTG
                                ||||||   ||||||| |||||
                                CTGTCG   TTCGAGG AGGAC
                                   ___       G
GAM283  LGALS12   5'  GGGAGTGGGGCTGGTGTG    52390     GA       AGTT
                                CAT  CGGCTCTG    CTTCC
                                |||  ||||||||    |||||
                                GTG  GTCGGGGT    GAGGG
                                  TG      _____
GAM283  LIMK2     5'  GGGAGCCCCGGGCCTGTCATG  33627       _     TGA
                                CATGAC GGCTC   GTTCTT
                                |||||| |||||   ||||||
                                GTACTG CCGGG   CGAGGG
                                    T    CCC
GAM283  LIN-7-C   3'  CAGGAAGAATAGAATTGTATG  37164      A   C   GA
                                CATG CGG TCT  GTTCTTCCTG
                                |||| ||| |||  ||||||||||
                                GTAT GTT AGA  TAAGAAGGAC
                                  _  A  __
GAM283  LSM4      3'  AGGGGGAACCCCCTTCGTG    24637       C  CTCTGA
                                CATGA GG     GTTCTTCCT
                                ||||| ||     |||||||||
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                              GTGCT CC     CAAGGGGGA
                                 T  CC____
GAM283  LYPLA3   3' GGCCTCTGGGGCTGTCATG   24632          _  TT
                              CATGACGGCTCT GAG  C
                              |||||||||||| |||  |
                              GTACTGTCGGGG CTC  G
                                     T   CG
GAM283  MAFB     3' TAGGAAGAGTTCTTGGTGGT   18415    G   CT  GT
                              AC GCT  GA  TCTTCCTG
                              || |||  ||  ||||||||
                              TG TGG  CT  AGAAGGAT
                               G   TT  TG
GAM283  MGC10818 3' CAGGAGGAGCTCATCTTTG   47535     CTC
                              CGG   TGAGTTCTTCCTG
                              |||   ||||||||||||
                              GTT   ACTCGAGGAGGAC
                                TCT
GAM283  MGC12921 3' GGGGGAAAGGGGTTTTGTG   63778    TG C     GAG
                              CA  A GGCTCT   TTCTTCC
                              ||  | ||||||   |||||||
                              GT  T TTGGGG   AAGGGGG
                               GT _     A__
GAM283  MGC13053 5' GAAGGAGGGAGAGGGTCGTTGT 51132    TG       GAG       G
           G                   CA  ACGGCTCT   TTCTTCCT
                              ||  ||||||||   |||||||
                              GT  TGCTGGGA   AGGGAGGA
                               GT       G__       AGG
GAM283  MGC14258 5' TGGTGTCAATTTGGGGCCTTGT 51862    TG C    TG    CTT_  TG
           G                   CA  A GGCTC  AGTT    CC
                              ||  | |||||  ||||    ||
                              GT  T CCGGG  TTAA    GG
                               GT _    GT    CTGT  T
GAM283  MGC17330 3' TAGGAGGAACTACCACTTTGT  53532      CTCTG_
                              ACGG     AGTTCTTCCTG
                              ||||     ||||||||||
                              TGTT     TCAAGGAGGAT
                                TCACCA
GAM283  MGC20481 3' CAGGGACTTACCTGGGGCTGGC 62712      A      GA  TC_
           ATG                   CATG CGGCTCT  GT   TTCCTG
                              |||| |||||||  ||   ||||||
                              GTAC GTCGGGG  CA   AGGGAC
                                G      TC  TTC
GAM283  MGC2555  3' GGGGAGGACTCGGGCC      51316     T
                              GGC CTGAGTTCTTCCT
                              ||| ||||||||||||
                              CCG GGCTCAGGAGGGG
                                _
GAM283  MGC34923 3' GGAAGAGCCTGTTGTC      58521        TCTGA
                              GACGGC    GTTCTTCC
                              ||||||    ||||||||
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                                CTGTTG    CGAGAAGG
                                   TC___
GAM283  MGC4281  3' AGGGGCCGGGGCTCTCATG   54709      C      A
                                CATGA GGCTCTG GTTCTT
                                ||||| ||||||| ||||||
                                GTACT TCGGGGC CGGGGA
                                   C     _
GAM283  MGC4293  3' TGGGAAGAGGCTGACGTTATG  48524       GCTCTG  _
                                CATGACG     AGT TCTTCCTG
                                |||||||     ||| ||||||||
                                GTATTGC     TCG AGAAGGGT
                                    AG____  G
GAM283  MGC4771  3' CAGTTCTGGATTCAGGCTGTTG 51030    TG    T      TTC_
           TG                     CA  ACGGC CTGAGTTC   CTG
                                ||  ||||| ||||||||   |||
                                GT  TGTCG GACTTAGG   GAC
                                 GT    _      TCTT
GAM283  MIG-6    3' GGAAGGTTTAGAGCAGTTGTG  38488    TG  G     AGT
                                CA  AC GCTCTG   TCTTCC
                                ||  || ||||||   ||||||
                                GT  TG CGAGAT   GGAAGG
                                 GT  A     TT_
GAM283  moblak   3' TGGGGAGCCCCCAGGGCTGCTG 55518     GA      A__     CTG
           TG                     CAT  CGGCTCTG   GTTCTTC
                                |||  ||||||||   |||||||
                                GTG  GTCGGGAC   CGAGGGG
                                  TC       CCC      T
GAM283  MOST2    3' CAGGGGGAGTTCAAGGTC    39678     TC   GT
                                GGC  TGA  TCTTCCTG
                                |||  |||  ||||||||
                                CTG  ACT  AGGGGGAC
                                  GA   TG
GAM283  MRVI1    3' AGGAAGAATTTGCTTAATG   55218     GAC   TCT
                                CAT   GGC   GAGTTCTTCCT
                                |||   |||   ||||||||||
                                GTA   TCG   TTTAAGAAGGA
                                  AT_   ___
GAM283  MRVI1    3' AGGAAGAATTTGCTTAATG   20271     GAC   TCT
                                CAT   GGC   GAGTTCTTCCT
                                |||   |||   ||||||||||
                                GTA   TCG   TTTAAGAAGGA
                                  AT_   ___
GAM283  MYH10    3' AGGAAGAATTTGTCCTGT    69138     CTC
                                ACGG   TGAGTTCTTCCT
                                ||||   ||||||||||||
                                TGTC   GTTTAAGAAGGA
                                  CT_
GAM283  MYT1     3' GGCTTGGGGCCGTGGTG     15778     G      TG
                                CAT ACGGCTC  AGTT
                                ||| |||||||  ||||
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                                GTG TGCCGGG  TCGG
                                  G      GT
GAM283  NASP     3'  CAGGAGGAGACTAAGCTGTC  67968        CTGAG
                                GACGGCT    TTCTTCCTG
                                |||||||    |||||||||
                                CTGTCGA    GAGGAGGAC
                                    ATCA_
GAM283  NIN283   3'  GGGATTGGGGCTGTC       50073         G
                                GACGGCTCT AGTTCT
                                ||||||||| ||||||
                                CTGTCGGGG TTAGGG
                                          _
GAM283  NISCH    3'  CGGGCCCCTCAGGGCTGTCG  23212           TTCTT
                                TGACGGCTCTGAG    CCTG
                                ||||||||||||    ||||
                                GCTGTCGGGACTC    GGGC
                                      CCC__
GAM283  OAZ2     3'  CAGGGAGGCAAGTGTGTTGTG  10305    TG   G T  GA  T
                                CA  ACG C CT  GT CTTCCTG
                                ||  ||| | ||  || |||||||
                                GT  TGT G GA  CG GAGGGAC
                                 GT   _ T  A_  _
GAM283  OR51E2   3'  AGGGAGAATGTTGTTGTC    47789       TCTGA
                                GACGGC    GTTCTTCCT
                                ||||||    |||||||||
                                CTGTTG    TAAGAGGGA
                                   TTG__
GAM283  P5326    3'  CAGCCCTTCTTGGAGCCTTCAT 48771      C    TG  TTCTTC
          G                      CATGA GGCTC  AG     CTG
                                |||||  |||||  ||     |||
                                GTACT CCGAG  TC     GAC
                                   T    GT  TTCCC_
GAM283  POFUT1   3'  GGGAAATAGGAGCTGTCAT   70474          GAG
                                ATGACGGCTCT   TTCTT
                                ||||||||||   |||||
                                TACTGTCGAGG   AAGGG
                                      ATA
GAM283  PP5395   5'  GGACCAGTTTGGGGCTGCGTG  72108     A     TG GT CT
                                CATG CGGCTC  A  T  TCC
                                ||||  ||||||  |  |  |||
                                GTGC GTCGGG  T  A  AGG
                                  _     GT TG CC
GAM283  PRO1777  5'  GGGCCTTAGGGCCGCTGTG   37764    GA        TT
                                CAT  CGGCTCTGAG  CT
                                |||  ||||||||||  ||
                                GTG  GCCGGGATTC  GG
                                  TC        CG
GAM283  PRO2289  3'  TGGGGAGAACTTAGAAGATTAT 37796      CGGC
          G                      CATGA   TCTGAGTTCTTCCTG
                                |||||   ||||||||||||||
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                                GTATT   AGATTCAAGAGGGGT
                                   AGA_
GAM283  PRO2533  3'  TAGGACCCTATGGAGCTGTTGT 37801   TG       _ TTCT
                                A  ACGGCTCTG AG   TCCTG
                                |  ||||||||| ||   |||||
                                T  TGTCGAGGT TC   AGGAT
                                 GT       A  CC__
GAM283  PTK9    3'  AGGAAGACTACCTGTCATG   11025       CTCTG  T
                                CATGACGG    AGT CTTCCT
                                ||||||||    ||| ||||||
                                GTACTGTC    TCA GAAGGA
                                     CA___  _
GAM283  PTRF    3'  AGTCTTAGAGCTGTTA     63496           TT
                                TGACGGCTCTGAG  CT
                                ||||||||||||  ||
                                ATTGTCGAGATTC  GA
                                       T_
GAM283  R32184_3  3'  GGGGGCTTTCAGGGTTTCGTG  53070      C       TT
                                CATGA GGCTCTGAG  CTTCC
                                |||||  |||||||||  |||||
                                GTGCT TTGGGACTT  GGGGG
                                   _       TC
GAM283  RAB22A   3'  TAGGGAGGACAATTATTGTC   59931      CTCTGA
                                GACGG     GTTCTTCCTG
                                |||||     ||||||||||
                                CTGTT     CAGGAGGGAT
                                   ATTAA_
GAM283  RBBP4    3'  AGGGGGAGTTCAAGTCGT    18823       C   GT
                                ACGGCT TGA  TCTTCCT
                                ||||||  |||  |||||||
                                TGCTGA ACT  AGGGGGA
                                   _  TG
GAM283  RBM7    3'  TAGGAGGGGGTGAAGTTGTATG 32236      A    CT AG
                                CATG CGGCT  G  TTCTTCCTG
                                ||||  |||||  |  |||||||||
                                GTAT GTTGA  T  GGGGAGGAT
                                   _    AG G_
GAM283  RIP60    5'  AGCTTCTCAGAGTTGCTGTG   25454     GA       TT_
                                CAT  CGGCTCTGAG   CT
                                |||  ||||||||||   ||
                                GTG  GTTGAGACTC   GA
                                  TC        TTC
GAM283  RLUCL    5'  CGGGAGGGGCTCGGAGCCAGGG 54217     ___
           TCG                    TGAC   GGCTCTGAGTTCTTCCTG
                                ||||   ||||||||||||||||||
                                GCTG   CCGAGGCTCGGGGAGGGC
                                  GGA
GAM283  SBB103   5'  AGGGGGTTGGAGCCTTGTG   19356    TG C    TG GTT
                                CA  A GGCTC  A   CTTCCT
                                ||  | |||||  |   ||||||
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                                GT  T CCGAG  T   GGGGGA
                                 GT _    GT ___
GAM283  SCDGF-B  5'  TGGGGAGAGCTCGGCGATTA  52454    _ GCT
                                TGA CG   CTGAGTTCTTCCTG
                                ||| ||   ||||||||||||||
                                ATT GC   GGCTCGAGAGGGGT
                                  A ___
GAM283  SCDGF-B  5'  TGGGGAGAGCTCGGCGATTA  47382    _ GCT
                                TGA CG   CTGAGTTCTTCCTG
                                ||| ||   ||||||||||||||
                                ATT GC   GGCTCGAGAGGGGT
                                  A ___
GAM283  SEPW1    3'  TAGGAAGGACTGAAAAGTCTTG 11541    TG C    CTG_
            TG                    CA  A GGCT    AGTTCTTCCTG
                                || | ||||   ||||||||||
                                GT  T CTGA    TCAGGAAGGAT
                                 GT _   AAAG
GAM283  SNPH     5'  CAGTGGACTCAGGGTTGTT   28239            TTC
                                GACGGCTCTGAGTTC   CTG
                                ||||||||||||||   |||
                                TTGTTGGGACTCAGG   GAC
                                          T__
GAM283  SNURF    3'  TGGGGAGAACTTGGTATCCATG 19055      AC  CT TG
                                CATG  GG  C  AGTTCTTCCTG
                                ||||  ||  |  ||||||||||
                                GTAC  CT  G  TCAAGAGGGGT
                                  __  AT GT
GAM283  SPRY1    3'  GATTTAGAGTTGTTTTG     65005    T
                                CA GACGGCTCTGAGTT
                                || ||||||||||||||
                                GT TTGTTGAGATTTAG
                                 T
GAM283  ST6GalNAcl 3'  GGGGCCAGGGCTGCCATG    37287      A       A
                                CATG CGGCTCTG GTTCT
                                |||| |||||||| |||||
                                GTAC GTCGGGAC CGGGG
                                  C      _
GAM283  STRAIT11499 3'  CAGGAGGCGCGGTGGGGCTGCG 41140      A       A_  T
            TG                    CATG CGGCTCTG  GT CTTCCTG
                                |||| ||||||||  || |||||||
                                GTGC GTCGGGGT  CG GGAGGAC
                                  _       GG  C
GAM283  SULT4A1  3'  GGGGACCGGGGTTGTC      68493          A
                                GACGGCTCTG GTTCTT
                                |||||||||| ||||||
                                CTGTTGGGGC CAGGGG
                                          _
GAM283  SUPT4H1  3'  TGGGAGGGATTTGGGTTGGTG  12065     GA    T TG
                                CAT  CGGC C  AGTTCTTCCTG
                                |||  |||| |  ||||||||||
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                                GTG  GTTG G  TTAGGGAGGGT
                                  __   _ GT
GAM283  TED      3'  GAGGGCGGGCCTGGAGCTGCGT 31637      A      GA   T   G
              G                   CATG CGGCTCT  GTTC TCCT
                                  |||| |||||||  |||| ||||
                                  GTGC GTCGAGG  CGGG GGGA
                                    _      TC   C   GG
GAM283  TGOLN2   5'  GGGGGGCCAGACTGTTGTG   64049    TG   C   A
                                  CA  ACGG TCTG GTTCTTC
                                  ||  |||| |||| |||||||
                                  GT  TGTC AGAC CGGGGGG
                                   GT   _   _
GAM283  TOB2     5'  CGGGAAGGTGCGGGTTGTT   95622       T   AGT
                                  GACGGC CTG   TCTTCCTG
                                  |||||| |||   ||||||||
                                  TTGTTG GGC   GGAAGGGC
                                     _   GT_
GAM283  TRIP10   3'  CGGGAAGAGGGGGGCTGTCG   14899          GAG
                                  TGACGGCTCT   TTCTTCCTG
                                  ||||||||||   |||||||||
                                  GCTGTCGGGG   GAGAAGGGC
                                       G__
GAM283  TSLRP    5'  GGGAGGGAAAGCTGTTA     25007        CTGAG
                                  TGACGGCT    TTCTTCCT
                                  ||||||||    ||||||||
                                  ATTGTCGA    AGGGAGGG
                                      A____
GAM283  TUB      3'  AGCTCTCAGGGCTGTC      12424          TT
                                  GACGGCTCTGAG  CT
                                  ||||||||||||  ||
                                  CTGTCGGGACTC  GA
                                         TC
GAM283  UBP1     3'  GGGGGACAGTGCTGTTGTG   27226    TG    T   AGT
                                  CA  ACGGC CTG   TCTTCC
                                  ||  ||||| |||   ||||||
                                  GT  TGTCG GAC   AGGGGG
                                   GT    T  ___
GAM283  ZDHHC4   3'  CAGGAGGGGCTTGCGGCCGT   36155       C
                                  ACGGCT TGAGTTCTTCCTG
                                  |||||| ||||||||||||
                                  TGCCGG GTTCGGGGAGGAC
                                     C
GAM283  LOC112885 3'  CGGGAGGGGTAGCTGCCGATGT 56524      A    TCTGA TT
              G                   CATG CGGC     G  CTTCCTG
                                  |||| ||||     |  |||||||
                                  GTGT GCCG     T  GGAGGGC
                                    A    TCGA_ GG
GAM283  LOC113444 3'  AGGAGGGATACCTGCATG    56556      A   CTCTGA
                                  CATG CGG     GTTCTTCCT
                                  |||| |||     |||||||||
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                                GTAC GTC     TAGGGAGGA
                                  _  CA____
GAM283  LOC115114 3'  AGGAAGGGCTTTATTCATG   68757      CGGCTCT
                                CATGA      GAGTTCTTCCT
                                |||||      ||||||||||
                                GTACT      TTCGGGAAGGA
                                  TAT____
GAM283  LOC115219 5'  CAGGGAGGGCTCAGAGGAGCC  73300       ___
                                GGCTCT   GAGTTCTTCCTG
                                ||||||   ||||||||||||
                                CCGAGG   CTCGGGAGGGAC
                                   AGA
GAM283  LOC116228 3'  TAGGAAGGATGCAGAGGCTGTG 73803     G    _   A
          TG                     CAT ACGGC TCTG GTTCTTCCTG
                                ||| ||||| |||| ||||||||||
                                GTG TGTCG AGAC TAGGAAGGAT
                                  _    G   G
GAM283  LOC119369 3'  AGGGATAGTAGCTTGGAGTCTC 75509     C    TG   _ _   G
          ATG                     ATGA GGCTC  AGTT CT TCCT
                                |||| |||||  |||| || ||||
                                TACT CTGAG  TCGA GA AGGG
                                  _    GT   T T   AC
GAM283  LOC120376 5'  CGGGGAGAATTTTCCAGTTGT  75985       CT_
                                ACGGCT   GAGTTCTTCCTG
                                ||||||   ||||||||||||
                                TGTTGA   TTTAAGAGGGGC
                                   CCT
GAM283  LOC121219 5'  TGGGGGGAGCTTGGAGCTGTC  74051         TG
                                GACGGCTC  AGTTCTTCCTG
                                ||||||||  ||||||||||
                                CTGTCGAG  TCGAGGGGGGT
                                     GT
GAM283  LOC124369 3'  CAGGGGGAGCTGCAGGCTGTGT 74277     G    T  _
          G                      CAT ACGGC CTG AGTTCTTCCTG
                                ||| ||||| ||| ||||||||||
                                GTG TGTCG GAC TCGAGGGGGAC
                                  _    _  G
GAM283  LOC124512 5'  CGGGGGCCGACGGGGCTGTCCT 74299    T        AGTT    TG
          G                      CA GACGGCTCTG    CTTCC
                                || ||||||||||    |||||
                                GT CTGTCGGGGC    GGGGG
                                 C         AGCC     C
GAM283  LOC124801 3'  CAGGAAGAACTCTCTTGCATG  74336      A   CTCT
                                CATG CGG    GAGTTCTTCCTG
                                ||||  |||    ||||||||||||
                                GTAC GTT    CTCAAGAAGGAC
                                  _   CT__
GAM283  LOC125228 3'  TGGGAGGAACATCTGTCA     74403       CTCTGA
                                TGACGG     GTTCTTCCTG
                                ||||||     ||||||||||
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                                ACTGTC     CAAGGAGGGT
                                   TA____
GAM283  LOC132927 5'  GGGGGGGAAGGCGGGAGCTGTT 75920   T       _ AG       G
            TG                    A GACGGCTCT G  TTCTTCCT
                                | |||||||||  |  ||||||||
                                G TTGTCGAGG C  AAGGGGGG
                                 T        G GG       GT
GAM283  LOC133688 3'  ATTCAGGGCTGTTGTG      75113    TG
                                CA  ACGGCTCTGAGT
                                ||  ||||||||||||
                                GT  TGTCGGGACTTA
                                 GT
GAM283  LOC136345 3'  GGGATTTTGGAGTTGTTTG   76208   T      TG  T
                                A GACGGCTC  AG TCTT
                                | ||||||||  || ||||
                                G TTGTTGAG  TT AGGG
                                 T       GT  T
GAM283  LOC139728 5'  CAGGGTGGCAGAGCTGTGGTG  75385     G       AGTTCT
                                CAT ACGGCTCTG     TCCTG
                                ||| |||||||||     ||||||
                                GTG TGTCGAGAC     GGGAC
                                  G        GGT___
GAM283  LOC143310 5'  CAGGAAGAACTCCCAGGTGT   76527     G  CT
                                ACG CT  GAGTTCTTCCTG
                                ||| ||  ||||||||||||
                                TGT GA  CTCAAGAAGGAC
                                  G  CC
GAM283  LOC144308 3'  AGGGAGGGCTCAGCCCG     83041     CT
                                CGG  CTGAGTTCTTCCT
                                |||  ||||||||||||
                                GCC  GACTCGGGAGGGA
                                  C_
GAM283  LOC144512 3'  CAGGGGCTTCAAGAGTTGTTGT 83114   TG      __       CCTG
                                A  ACGGCTCT  GAGTTCTT
                                |  ||||||||  ||||||||
                                T  TGTTGAGA  TTCGGGGA
                                 GT       AC       C
GAM283  LOC144559 3'  AGAACCCTTAGAGTTGTCA   76879           __
                                TGACGGCTCTGA  GTTCT
                                ||||||||||||  ||||||
                                ACTGTTGAGATT  CAAGA
                                       CC
GAM283  LOC145135 5'  CGGGAGGCCGGCTCAGAGCTGT 83252   T          __
            TCTG                    A GACGGCTCTGAGTT  CTTCCTG
                                | ||||||||||||||  |||||||
                                T TTGTCGAGACTCGG  GGAGGGC
                                 C            CC
GAM283  LOC145482 3'  AGGGGGAGGTTGCCGT      77228       TCT  G
                                ACGGC   GA TTCTTCCT
                                |||||   || ||||||||
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                                TGCCG   TT GAGGGGGA
                                   ___  G
GAM283   LOC145717 3'  AAGGAGGGAAGGGGGCTGTGTG 66826     G       GAG       G
                                CAT ACGGCTCT   TTCTTCCT
                                ||| ||||||||   ||||||||
                                GTG TGTCGGGG   AGGGAGGA
                                  _       GA_       AG
GAM283   LOC145748 3'  GGGAAGAGCTCGTCCTCA    83469     C   TCT
                                TGA GGC   GAGTTCTTCCT
                                ||| |||   ||||||||||
                                ACT CTG   CTCGAGAAGGG
                                  C  ___
GAM283   LOC145853 5'  CGGGAGGCCACGGGGCCGCTGT 83558     GA       AGTT
            G                    CAT  CGGCTCTG    CTTCCTG
                                |||  ||||||||    |||||||
                                GTG  GCCGGGGC    GGAGGGC
                                  TC       ACC_
GAM283   LOC145989 3'  GGGAAGGGAAGCCGTCA     59547         CTGAG
                                TGACGGCT     TTCTTCCT
                                ||||||||     ||||||||
                                ACTGCCGA     GGGAAGGG
                                     A_____
GAM283   LOC146243 3'  AGGAACCCAGGGCTGTTCTG   83640    T        A
                                CA GACGGCTCTG GTTCTT
                                || ||||||||| ||||||
                                GT TTGTCGGGAC CAAGGA
                                 C         C
GAM283   LOC146520 5'  GGGGGGGACAAGCTGTT     77957         CTGA
                                GACGGCT    GTTCTTCCT
                                |||||||    |||||||||
                                TTGTCGA    CAGGGGGGG
                                     A___
GAM283   LOC147299 5'  AGGAAGGTGGCTGTGCATG    78342      _     CTGAGT
                                CATG ACGGCT     TCTTCCT
                                |||| ||||||     |||||||
                                GTAC TGTCGG     GGAAGGA
                                  G     T_____
GAM283   LOC147524 5'  AGCTTCAGATTGTTATG     78373         C    _
                                CATGACGG TCTGA GTT
                                |||||||| ||||| |||
                                GTATTGTT AGACT CGA
                                     _     T
GAM283   LOC147650 5'  TGGGAGGGACTCAGGAAGC    78388     __
                                GCT  CTGAGTTCTTCCTG
                                |||  |||||||||||||
                                CGA  GACTCAGGGAGGGT
                                  AG
GAM283   LOC147942 3'  ATTCTGAGTTGTTATG      78577           T
                                CATGACGGCTC GAGT
                                |||||||||| ||||
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                                GTATTGTTGAG CTTA
                                       T
GAM283  LOC148046 5'  GGGGGGGGCTGGCTGTCA    84107        CTG        G
                                TGACGGCT   AGTTCTTCCT
                                ||||||||   ||||||||||
                                ACTGTCGG   TCGGGGGGGG
                                    ___         G
GAM283  LOC148078 3'  CGGGGGGCAGCTGGGGTCGTTG 84111    TG       G   _
          T                      A  ACGGCTCT AGTT CTTCCTG
                                |  |||||||| |||| |||||||
                                T  TGCTGGGG TCGA GGGGGGC
                                 GT       _    C
GAM283  LOC148114 5'  AGGAGGTGAGCTGTTCTG    78658    T      TGAGTT
                                CA GACGGCTC     CTTCCT
                                || ||||||||     ||||||
                                GT TTGTCGAG     GGAGGA
                                 C       T_____
GAM283  LOC148166 5'  TGGGAAGTCCCTAGAGTCGTCA 78697          AGTT
                                TGACGGCTCTG    CTTCCTG
                                ||||||||||    |||||||
                                ACTGCTGAGAT    GAAGGGT
                                       CCCT
GAM283  LOC148231 3'  TGGGGACCCAGGGAGCCGTCG  78753         __ A     CCTG
                                TGACGGCTCT  G GTTCTT
                                ||||||||||  | ||||||
                                GCTGCCGAGG  C CAGGGG
                                      GA C     T
GAM283  LOC148413 3'  AGGGCGTAGTGGCTGTCATG   78827         _  A
                                CATGACGGCT CTG GTTCT
                                |||||||||| ||| |||||
                                GTACTGTCGG GAT CGGGA
                                      T   G
GAM283  LOC148443 3'  AGGAAGAGTTCATCATG     78854      CGGCTC   GT
                                CATGA     TGA  TCTTCCT
                                |||||     |||  |||||||
                                GTACT     ACT  AGAAGGA
                                   _______  TG
GAM283  LOC149319 5'  CAGGGAGGATTTGGGAGGGC   79290      ___
                                GCTCT   GAGTTCTTCCTG
                                |||||   ||||||||||||
                                CGGGA   TTTAGGAGGGAC
                                   GGG
GAM283  LOC149319 5'  CGGGAAGGAGACACAGGCCTTG 79294    TG C   T   A   __
          TG                     CA  A GGC CTG GTT  CTTCCTG
                                ||  | ||| ||| |||  |||||||
                                GT  T CCG GAC CAG  GAAGGGC
                                 GT _   _   A   AG
GAM283  LOC149319 5'  GGGAGGAGGGCTGTCG      79300          GAGT
                                TGACGGCTCT    TCTTCC
                                ||||||||||    ||||||
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                                GCTGTCGGGA   GGAGGG
                                     ____
GAM283  LOC149657 3'  GGGTCGGGGCTGACGTG    84575     A       G
                                CATG CGGCTCTGA TT
                                |||| ||||||||| ||
                                GTGC GTCGGGGCT GG
                                  A       G
GAM283  LOC149911 5'  CAGCCCTCACTCAGGGCTTCAT 84705      C        TCTTC
          G                      CATGA GGCTCTGAGT    CTG
                                ||||| ||||||||||    |||
                                GTACT TCGGGACTCA    GAC
                                  _       CTCCC
GAM283  LOC150095 5'  AGGGACTTGGGGCTGTT    84854        TG
                                GACGGCTC  AGTTCTT
                                ||||||||  |||||||
                                TTGTCGGG  TCAGGGA
                                    GT
GAM283  LOC150271 3'  CAGGGAGAATTCAGTGAGATTG 84949     _  __
          T                      ACGG CTC  TGAGTTCTTCCTG
                                |||| |||  ||||||||||||
                                TGTT GAG  ACTTAAGAGGGAC
                                  A  TG
GAM283  LOC150282 5'  GGGATCAGGGCTGTCAT    79731           G
                                ATGACGGCTCTGA TTCT
                                |||||||||||| ||||
                                TACTGTCGGGACT AGGG
                                          _
GAM283  LOC151124 5'  TAGGGAGGGCGGGGGTTGTGGT 85232    G      GA
          G                      CAT ACGGCTCT  GTTCTTCCTG
                                ||| ||||||||  ||||||||||
                                GTG TGTTGGGG  CGGGAGGGAT
                                  G       G_
GAM283  LOC151162 5'  AGCACTTAGGGTTTTGTG    85238    TG C        T
                                CA  A GGCTCTGAGT CT
                                ||  | ||||||||||| ||
                                GT  T TTGGGATTCA GA
                                 GT _         C
GAM283  LOC151162 5'  TAGGAAGCTGGGAGTTTCGTG  85247      C     G  TT
                                CATGA GGCTCT AG  CTTCCTG
                                ||||| ||||||  ||  |||||||
                                GTGCT TTGAGG TC  GAAGGAT
                                  _     G  __
GAM283  LOC151516 3'  TGGGGGGGGTTGCATATCCTCA 80271      C  CTC  _  TT
          TG                     CATGA GG   TG AG  CTTCCTG
                                ||||| ||   || ||  |||||||
                                GTACT CC   AC TT  GGGGGGT
                                  _  TAT  G  GG
GAM283  LOC153474 5'  AGGAGGAGACGCCGCTGTG   80843     GA   TCTGAG
                                CAT  CGGC     TTCTTCCT
                                |||  ||||     ||||||||
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                                GTG  GCCG     GAGGAGGA
                                  TC    CA____
GAM283   LOC153727 3'  TAGGGAGGCAGAGGTTGTAGTG 86154     G    _   AGT
                                CAT ACGGC TCTG   TCTTCCTG
                                ||| ||||| ||||   ||||||||
                                GTG TGTTG AGAC   GGAGGGAT
                                  A    G   ___
GAM283   LOC154222 3'  CAGGGAGAATGTCTGGTTGT   86189       CTGA
                                ACGGCT    GTTCTTCCTG
                                ||||||    ||||||||||
                                TGTTGG    TAAGAGGGAC
                                    TCTG
GAM283   LOC154877 5'  GGGAAGAGCTCACTTCTG    86304     CTC
                                CGG   TGAGTTCTTCCT
                                |||   ||||||||||||
                                GTC   ACTCGAGAAGGG
                                  TTC
GAM283   LOC155032 5'  GGGATTTTGGAGTTGTTTG    86323    T       TG  T
                                A GACGGCTC  AG TCTT
                                | ||||||||  || ||||
                                G TTGTTGAG  TT AGGG
                                 T       GT  T
GAM283   LOC157254 5'  TGGGAGGAGGCGGGAGCCGTGT 81391     G       GA  _
   G                             CAT ACGGCTCT  GT TCTTCCTG
                                ||| ||||||||  || ||||||||
                                GTG TGCCGAGG  CG AGGAGGGT
                                  _       G_  G
GAM283   LOC157349 3'  AGGGGCTCTGGGGCTGTTTG   81409    T       _
                                A GACGGCTCT GAGTTCTT
                                | |||||||||| ||||||||
                                G TTGTCGGGG CTCGGGGA
                                 T       T
GAM283   LOC158292 5'  AGGAGGAGCTTGGACTG     86727     C  TG
                                CGG TC  AGTTCTTCCT
                                ||| ||  ||||||||||
                                GTC AG  TCGAGGAGGA
                                  _  GT
GAM283   LOC160130 5'  TGGGGAGAAGAAAGGCAGTTAT 82207       G  T  GAG
   G                             CATGAC GC CT   TTCTTCCTG
                                ||||||| || ||   |||||||||
                                GTATTG CG GA   AAGAGGGGT
                                    A  _  AAG
GAM283   LOC165693 5'  AGGGAGGCCCAGCGTTGT    82593      T   A  T
                                ACGGC CTG GT CTTCCT
                                ||||| ||| || ||||||
                                TGTTG GAC CG GAGGGA
                                   C   C  _
GAM283   LOC168448 3'  GGGCATTAGGGCCATTATG    82700      C       _
                                CATGA GGCTCTGA GTTC
                                ||||| |||||||| ||||
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                                GTATT CCGGGATT CGGG
                                   A       A
GAM283  LOC169426 5'  TGGGAGGAAAGGGGCTGTC   87287         GAG      TG
                                GACGGCTCT   TTCTTCC
                                |||||||||   |||||||
                                CTGTCGGGG   AGGAGGG
                                     AA_      T
GAM283  LOC169611 3'  ACTTGTGAGCTGTCATG     82753          _
                                CATGACGGCTC TGAGT
                                |||||||||||| |||||
                                GTACTGTCGAG GTTCA
                                       T
GAM283  LOC196403 3'  GGAGGAGCACCGTGTG      89629     G    CTCTGA
                                CAT ACGG     GTTCTTCC
                                ||| ||||     ||||||||
                                GTG TGCC     CGAGGAGG
                                  _   A_____
GAM283  LOC196411 5'  GGGGAGACGAGTTGCATG    87677     A     TGAGT
                                CATG CGGCTC    TCTTCCT
                                |||| ||||||    |||||||
                                GTAC GTTGAG    AGAGGGG
                                  _     C____
GAM283  LOC197201 3'  CAGGGAGGCAGAGGTTGTGGTG 87934     G    _    AGT
                                CAT ACGGC TCTG   TCTTCCTG
                                ||| ||||| ||||   ||||||||
                                GTG TGTTG AGAC   GGAGGGAC
                                  G    G   ___
GAM283  LOC199986 5'  AGGAGGAACTCAAGCT      89897     C
                                GGCT TGAGTTCTTCCT
                                |||| ||||||||||||
                                TCGA ACTCAAGGAGGA
                                  _
GAM283  LOC200197 3'  AGGGATGGGGAGCCTCATG   88612      C     GA
                                CATGA GGCTCT  GTTCTT
                                ||||| ||||||  ||||||
                                GTACT CCGAGG  TAGGGA
                                   _     GG
GAM283  LOC200197 3'  TGGGGCTCCATCAGGGCTGTTT 88623   T        GTTCT
          G                      A GACGGCTCTGA    TCCTG
                                | ||||||||||    |||||
                                G TTGTCGGGACT    GGGGT
                                 T         ACCTC
GAM283  LOC200488 5'  CAGGGAGGATTTAGTTATTC   90083    CGGCT
                                GA    CTGAGTTCTTCCTG
                                ||    ||||||||||||||
                                CT    GATTTAGGAGGGAC
                                 TATT_
GAM283  LOC200953 5'  GGGGGTGGCAGAGCCGTGTG   90209     G       AGTT
                                CAT ACGGCTCTG    CTTCC
                                ||| |||||||||    |||||
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                                GTG TGCCGAGAC    GGGGG
                                  _       GGT_
GAM283   LOC201176 3'  GGGAGGGGGTGGCCATTATG   88133      C    CTGAG
                                CATGA GGCT     TTCTTCCT
                                ||||| ||||     ||||||||
                                GTATT CCGG     GGGGAGGG
                                   A    TG___
GAM283   LOC201305 3'  GGGAATGGAGCTGTCA      88236          GA
                                TGACGGCTCT  GTTCTT
                                ||||||||||  ||||||
                                ACTGTCGAGG  TAAGGG
                                      __
GAM283   LOC201514 3'  CAGGGAGAGTTCCCGTGTG   88253     G    CTCT  GT
                                CAT ACGG    GA  TCTTCCTG
                                ||| ||||    ||  ||||||||
                                GTG TGCC    CT  AGAGGGAC
                                  _   ____  TG
GAM283   LOC202052 3'  AGGAAGAATTCAGTCACTG    90305     CT_
                                CGG   CTGAGTTCTTCCT
                                |||   ||||||||||||
                                GTC   GACTTAAGAAGGA
                                  ACT
GAM283   LOC203078 3'  AGGAGCTCAAGGGCTGTTTG   89272    T       _
                                A GACGGCTCT GAGTTCTT
                                | |||||||| ||||||||
                                G TTGTCGGGA CTCGAGGA
                                 T        A
GAM283   LOC203377 5'  AGCACTTAGGGTTTTGTG     90576    TG C        T
                                CA  A GGCTCTGAGT CT
                                ||  | ||||||||| ||
                                GT  T TTGGGATTCA GA
                                  GT _         C
GAM283   LOC203377 5'  TAGGAAGCTGGGAGTTTCGTG  90585       C     G  TT
                                CATGA GGCTCT AG  CTTCCTG
                                ||||| |||||| ||  |||||||
                                GTGCT TTGAGG TC  GAAGGAT
                                   _     G  __
GAM283   LOC219940 3'  AGGAGGGACTTTGATCATG    93354       CGGC  T
                                CATGA    TC GAGTTCTTCCT
                                |||||    || ||||||||||
                                GTACT    AG TTCAGGGAGGA
                                   _____  T
GAM283   LOC220020 5'  AGGAGGAGTTTGAGTGGT     93417     G    T  GT
                                AC GCTC GA  TCTTCCT
                                || |||| ||  |||||||
                                TG TGAG TT  AGGAGGA
                                 G    _  TG
GAM283   LOC220071 3'  AGACCCCTTAGAGTTGTCA    93433           T__
                                TGACGGCTCTGAG   TCT
                                ||||||||||||   |||
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                                ACTGTTGAGATTC   AGA
                                      CCC
GAM283  LOC220537 3'  AGGGAGGGAAGGGGGCTGTGTG 90726     G       GAG       G
                                CAT ACGGCTCT   TTCTTCCT
                                ||| ||||||||   ||||||||
                                GTG TGTCGGGG   AGGGAGGG
                                  _       GA_       AG
GAM283  LOC220565 5'  CAGGAGGGAGCTTGCTGTC    90746       TCT      _
                                GACGGC   GAGTTCT TCCTG
                                ||||||   ||||||| |||||
                                CTGTCG   TTCGAGG AGGAC
                                   ___       G
GAM283  LOC220776 3'  CAGGCCCGTTCTGCAGGGCTGT 68386    TG       _  TTCTT_
          TGTG                    A  ACGGCTCTG AG     CCTG
                                |  ||||||||| ||      ||||
                                T  TGTCGGGAC TC     GGAC
                                 GT        G  TTGCCC
GAM283  LOC221421 3'  CAGTAAGGAGCTCACAGCTGTC 92276          C        C_
          ATG                     CATGACGGCT TGAGTTCTT  CTG
                                |||||||||| |||||||||  |||
                                GTACTGTCGA ACTCGAGGA  GAC
                                      C        AT
GAM283  LOC221477 3'  GGGAAAGAGGGTTGTCA     92160          GAG
                                TGACGGCTCT   TTCTT
                                ||||||||||   |||||
                                ACTGTTGGGA   AAGGG
                                      GA_
GAM283  LOC221496 3'  CGGGGAGAAGGGTTGAGTTTTC 91999      CG    TGAG_
          ATG                     CATGA  GCTC    TTCTTCCTG
                                |||||  ||||    |||||||||
                                GTACT  TGAG    AAGAGGGGC
                                   TT    TTGGG
GAM283  LOC221550 5'  GGCTTAGGGCTTTATG      92120       C
                                CATGA GGCTCTGAGTT
                                ||||| ||||||||||
                                GTATT TCGGGATTCGG
                                   _
GAM283  LOC221583 5'  CAGGGAGGACGTGGTTGTTGT  92143    TG     CTGA
                                A  ACGGCT    GTTCTTCCTG
                                |  ||||||    ||||||||||
                                T  TGTTGG    CAGGAGGGAC
                                 GT     TG__
GAM283  LOC221787 5'  GGAGATTCGGAGCCGTCA    92468            CT
                                TGACGGCTCTGAGTT  TCC
                                ||||||||||||||  |||
                                ACTGCCGAGGCTTAG  AGG
                                         __
GAM283  LOC221876 5'  TGGGAGGAACTCGGGTGGGCGT 93927      ACG  T
          G                      CATG   GC CTGAGTTCTTCCTG
                                ||||   || ||||||||||||||
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                                GTGC   TG GGCTCAAGGAGGGT
                                  GGG  _
GAM283   LOC221922 5'  CAGGGTCTCAGGGTCCTCATG  92687      C       TTCT
                                CATGA GGCTCTGAG    TCCTG
                                ||||| |||||||||    |||||
                                GTACT CTGGGACTC    GGGAC
                                   C       T___
GAM283   LOC222193 3'  TGGGAAGAATTTGGATACC    94183    C_  TG
                                GG  TC  AGTTCTTCCTG
                                ||  ||  ||||||||||
                                CC  AG  TTAAGAAGGGT
                                 AT  GT
GAM283   LOC254057 3'  ACCAGAGTTGTCATG       96995            A
                                CATGACGGCTCTG GT
                                |||||||||||| ||
                                GTACTGTTGAGAC CA

                                          _
GAM283   LOC254110 3'  GGGGGTAGGGCTGCCATG    95107      A       AGTT
                                CATG CGGCTCTG    CTTCC
                                |||| ||||||||    |||||
                                GTAC GTCGGGAT    GGGGG
                                  C      ____
GAM283   LOC254143 3'  CAGGGGCTTCAAGAGTTGTTGT 96496    TG      __       CCTG
                                A  ACGGCTCT  GAGTTCTT
                                |  ||||||||  ||||||||
                                T  TGTTGAGA  TTCGGGGA
                                 GT       AC       C
GAM283   LOC254532 3'  GGCTCAGAGTCCTCATG     96641      C
                                CATGA GGCTCTGAGTT
                                ||||| ||||||||||
                                GTACT CTGAGACTCGG
                                   C
GAM283   LOC254962 5'  GGGGCCGGAGTCGCGTG     96615      A       A
                                CATG CGGCTCTG GTTCT
                                |||| |||||||| |||||
                                GTGC GCTGAGGC CGGGG

                                  _       _
GAM283   LOC255328 3'  TGGGCCTTTGCTCAGGGCTGTC 96567            TCTT_
                                GACGGCTCTGAGT     CCTG
                                ||||||||||||     ||||
                                CTGTCGGGACTCG     GGGT
                                        TTTCC
GAM283   LOC255481 3'  GGAATTTGGGGTTGTCCTG    94440    T       TG
                                CA GACGGCTC  AGTTCT
                                || ||||||||  ||||||
                                GT CTGTTGGG  TTAAGG
                                 C       GT
GAM283   LOC255515 3'  AGAACCCTTAGAGTTGTCA    96090           __
                                TGACGGCTCTGA  GTTCT
                                ||||||||||||  |||||
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                                ACTGTTGAGATT  CAAGA
                                      CC
GAM283   LOC256021 3'  GGGGATGGGGCTGGCATG    96515      A      GA
                                CATG CGGCTCT  GTTCTT
                                |||| |||||||  ||||||
                                GTAC GTCGGGG  TAGGGG
                                  G      __
GAM283   LOC256158 5'  TGGGGAGAGCACGGCTGTCG   97683         CT A
                                TGACGGCT  G GTTCTTCCTG
                                ||||||||  | ||||||||||
                                GCTGTCGG  C CGAGAGGGGT
                                     __ A
GAM283   LOC256250 5'  CGGGAAGAGCTTCTTATTCATG 97210       CGGCTCT
                                CATGA      GAGTTCTTCCTG
                                |||||      ||||||||||||
                                GTACT      TTCGAGAAGGGC
                                   TATTC__
GAM283   LOC256310 5'  CGGGGAGAACGGCTCCGTCCTG 96345    T    CT  GA
                                CA GACGG  CT  GTTCTTCCTG
                                || |||||  ||  ||||||||||
                                GT CTGCC  GG  CAAGAGGGGC
                                 C    TC  __
GAM283   LOC256401 3'  GGGCATTAGGGCCATTATG    96020       C       _
                                CATGA GGCTCTGA GTTC
                                ||||| |||||||| ||||
                                GTATT CCGGGATT CGGG
                                   A       A
GAM283   LOC256781 5'  GATTCAGGGCTGTGATG     97603     G
                                CAT ACGGCTCTGAGTT
                                ||| ||||||||||||
                                GTA TGTCGGGACTTAG
                                  G
GAM283   LOC256790 5'  AGGGCTGGAGCTGTGTG     94832     G       G
                                CAT ACGGCTCT AGTTCT
                                ||| |||||||| ||||||
                                GTG TGTCGAGG TCGGGA
                                  _      _
GAM283   LOC257495 5'  GGCTTAGGGCTTTATG      97726       C
                                CATGA GGCTCTGAGTT
                                ||||| ||||||||||
                                GTATT TCGGGATTCGG
                                  _
GAM283   LOC257576 5'  GGCTTAGGGCTTTATG      97883       C
                                CATGA GGCTCTGAGTT
                                ||||| ||||||||||
                                GTATT TCGGGATTCGG
                                  _
GAM283   LOC51077  3'  AGGAAGAATATGTTTTATG   31993       C   TCTGA
                                CATGA GGC    GTTCTTCCT
                                ||||| |||    |||||||||
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                                GTATT TTG    TAAGAAGGA
                                  _  TA___
GAM283  LOC51152  3' GGGGAGGGCTCACCTGT    32453     CTC
                                ACGG  TGAGTTCTTCCT
                                ||||  ||||||||||||
                                TGTC  ACTCGGGAGGGG
                                  C__
GAM283  LOC51195  3' AGGAGCTAGGGTTGTC     32935        G
                                GACGGCTCT AGTTCTT
                                ||||||||| |||||||
                                CTGTTGGGA TCGAGGA
                                    _
GAM283  LOC51601  5' GGTTGCTCGGGGTCGTATG   31936     A        TCTT
                                CATG CGGCTCTGAGT   CC
                                |||| ||||||||||   ||
                                GTAT GCTGGGGCTCG   GG
                                  _        TT__
GAM283  LOC51696  3' TAGCCAAATTTGGGGTTGATGT 32555     A    TG   CTTCCTG
          G                      CATG CGGCTC  AGTT
                                |||| ||||||  ||||
                                GTGT GTTGGG  TTAA
                                  A    GT   ACCGAT
GAM283  LOC51701  3' TTGGGAGTTTGGGGTTTTATG  32654     C    TG  TT    TG
                                CATGA GGCTC  AG  CTTCC
                                ||||| |||||  ||  |||||
                                GTATT TTGGG  TT  GAGGG
                                  _    GT  __    TTT
GAM283  LOC56891  5' TGGGAGGGGCTTGGAATC    39278   GC  TG
                                G  TC  AGTTCTTCCTG
                                |  ||  ||||||||||
                                C  AG  TCGGGGAGGGT
                                 TA  GT
GAM283  LOC58525  3' TGGGAAGAGCTCAGAGCTGACA 78653    A
                                TG CGGCTCTGAGTTCTTCCTG
                                || ||||||||||||||||||
                                AC GTCGAGACTCGAGAAGGGT
                                 A
GAM283  LOC84570  5' GGGAGTCGGAAGAGCTGTC   50712        GAGTT
                                GACGGCTCT    CTTCC
                                |||||||||    |||||
                                CTGTCGAGA    GAGGG
                                     AGGCT
GAM283  LOC85414  3' CAGGGGGGGTTTAAGTGCCGTT 52394   T    T  _  TT
          TG                     A GACGGC CT GAG  CTTCCTG
                                | |||||| || |||  |||||||
                                G TTGCCG GA TTT  GGGGGAC
                                 T    T  A   GG
GAM283  LOC90288  3' GGGAGGCAGAGTTGCGTG    62102     A      AGT
                                CATG CGGCTCTG   TCTTCC
                                |||| ||||||||   ||||||
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                                GTGC GTTGAGAC   GGAGGG
                                  _     ____
GAM283  LOC90352  3' GGGAGGGGTTATTTGTCAT   62401       CTC   G
                                ATGACGG   TGA TTCTTCC
                                |||||||   ||| |||||||
                                TACTGTT   ATT GGGAGGG
                                   T__   G
GAM283  LOC90630  3' CAGGGAGAACAGCATGCTGTGT 63628    G    TCTGA
           G                     CAT ACGGC    GTTCTTCCTG
                                ||| |||||    ||||||||||
                                GTG TGTCG    CAAGAGGGAC
                                  _    TACGA
GAM283  LOC90850  5' CGGGAAGGCGGGAGCTGCGTG  64212     A     GA  T
                                CATG CGGCTCT  GT CTTCCTG
                                |||| |||||||  || |||||||
                                GTGC GTCGAGG  CG GAAGGGC
                                  _     G_ _
GAM283  LOC90925  3' CGGGGAGGAAACACTGGCTGTT 64427   T     C_  AG
           TG                    A GACGGCT  TG  TTCTTCCTG
                                | |||||||  ||  |||||||||
                                G TTGTCGG  AC  AGGAGGGGC
                                 T      TC  AA
GAM283  LOC91179  3' CGGGAAGGGCCCATCCCGTT   65169      CTC  A
                                GACGG   TG GTTCTTCCTG
                                |||||   || ||||||||||
                                TTGCC   AC CGGGAAGGGC
                                   CT_  C
GAM283  LOC91208  3' CAGGGAGAACAGCATGCTGTGT 65243    G    TCTGA
           G                     CAT ACGGC    GTTCTTCCTG
                                ||| |||||    ||||||||||
                                GTG TGTCG    CAAGAGGGAC
                                  _    TACGA
GAM283  LOC92689  3' AGGAGGGGCATTGTCA      70216       CTCTGA
                                TGACGG     GTTCTTCCT
                                ||||||     |||||||||
                                ACTGTT     CGGGGAGGA
                                   A_____
GAM283  LOC93017  3' TGTCCGGGCCCAGAGTTGTCAT 71155           A   TTCCTG
           G                     CATGACGGCTCTG GTTC
                                ||||||||||||| ||||
                                GTACTGTTGAGAC CGGG
                                        C   CCTGT
GAM283  LOC93129  3' CAGGGGGAGCTGCAGGCTGTGT 71463    G    T  _
           G                     CAT ACGGC CTG AGTTCTTCCTG
                                ||| ||||| ||| ||||||||||
                                GTG TGTCG GAC TCGAGGGGGAC
                                  _    _  G
GAM283  LOC93259  5' AGCCCTCAGGGCCTTCATG   71803      C       TT
                                CATGA GGCTCTGAG  CT
                                ||||| |||||||||  ||
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                                GTACT CCGGGACTC  GA
                                   T       CC
GAM284  ARHGEF6  3'  CAAACTTGAAGCCAGGC    68197       ACCA
                                GCCTGG   CAAGTTTG
                                ||||||   ||||||||
                                CGGACC   GTTCAAAC
                                   GAA_
GAM284  CNTN2    3'  GTCACAACCCAGGTGA     17411       ACCACAA  _
                                TCGCCTGG     GTT TGAC
                                ||||||||     ||| ||||
                                AGTGGACC     CAA ACTG
                                     ________  C
GAM284  CORO2A   3'  AAACTGTGGTCCAGAGA    12642   GC       A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_       _
GAM284  CORO2A   3'  AAACTGTGGTCCAGAGA    53398   GC       A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_       _
GAM284  GRLF1    3'  AGGTCAGAAAGTGGCCCAGG  78551     A   AAG
                                CCTGG CCAC   TTTGACCT
                                ||||| ||||   ||||||||
                                GGACC GGTG   AGACTGGA
                                   C   AA_
GAM284  LAPTM5   3'  AGGCTTGTGGTCAAGC     22199   CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCGGA
                                 AA_
GAM284  POU2AF1  3'  AGATTTACAGTCCAGGC     20647       CAC
                                GCCTGGAC   AAGTTT
                                ||||||||   ||||||
                                CGGACCTG   TTTAGA
                                     ACA
GAM284  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  6355        C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM284  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  54574       C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM284  TRIM34   5'  AGGTCAAGTTGAGCCCAG    55224     ACCA   G
                                CTGG    CAA TTTGACCT
                                ||||    ||| ||||||||
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                                GACC    GTT GAACTGGA
                                  CGA_  _
GAM284  TRIM9    5'  AGGCCAGGCAAGTCCAGGC   30749        CACAA    A
                                GCCTGGAC    GTTTG CCT
                                ||||||||    ||||| |||
                                CGGACCTG    CGGAC GGA
                                    AA___    C
GAM284  ABLIM    5'  GATATGTAACCCAGGCGG    22030        ACC   A
                                TCGCCTGG   ACA GTT
                                ||||||||   ||| |||
                                GGCGGACC   TGT TAG
                                    CAA   A
GAM284  AMOT     3'  AGGCATCTTCATGGTCCAGGGA 55716    G       C_   TT  A
                                TC CCTGGACCA  AAG  TG CCT
                                || |||||||||  |||  || |||
                                AG GGACCTGGT  TTC  AC GGA
                                 _       AC   T_ _
GAM284  DKFZp434D177 5'  TTAGACCCAGGCGA       50056        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                              _______
GAM284  DKFZp434D177 5'  TTAGACCCAGGCGA       79443        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                              _______
GAM284  FLJ23420  3'  CAAGTGGGTCCAGGC       46845         A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                              _ __
GAM284  HSA249128 5'  GGCGCGGTCCAGGCGG      34152          ACAA
                                TCGCCTGGACC    GTT
                                ||||||||||    |||
                                GGCGGACCTGG    CGG
                                      CG__
GAM284  MGC15668  5'  AGACCCGGTGGTCCAGACG   51277    C       AA_
                                CG CTGGACCAC   GTTT
                                || |||||||||   ||||
                                GC GACCTGGTG   CAGA
                                 A        GCC
GAM284  MGC22014  3'  AGGTCCCGAGTGTAACCCAGGT 64486        ACC   AGTTT
           GA                    TCGCCTGG   ACA    GACCT
                                ||||||||   |||    |||||
                                AGTGGACC   TGT    CTGGA
                                    CAA   GAGCC
GAM284  SDCCAG10  5'  AGAGTTGTGGTCCAAAGA    19641    GCC        G
                                TC   TGGACCACAA TTT
                                ||   |||||||||| |||
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                                AG   ACCTGGTGTT AGA
                                 AA_         G
GAM284   LOC115442 3'  AGGTCAGGGATGGTCCAG    72676         CAAG
                                CTGGACCA    TTTGACCT
                                ||||||||    ||||||||
                                GACCTGGT    GGACTGGA
                                     AG__
GAM284   LOC129011 5'  AGACCTGCGGTCCAGGC     74862          A  A
                                GCCTGGACC CA GTTT
                                ||||||||| || ||||
                                CGGACCTGG GT CAGA
                                      C  C
GAM284   LOC130536 5'  GCAAAGTCCAGGCG        75746          CACAAG    A
                                CGCCTGGAC     TTTG C
                                |||||||||     |||| |
                                GCGGACCTG     AAAC G
                                     _______   C
GAM284   LOC149108 3'  AGACTTCACTGTGGTCCA    84357          _____
                                TGGACCACA    AGTTT
                                |||||||||    |||||
                                ACCTGGTGT    TCAGA
                                      CACT
GAM284   LOC221688 5'  AGACTCGGGCCCAGACGA    93674     C    A  ACA
                                TCG CTGG CC   AGTTT
                                ||| |||| ||   |||||
                                AGC GACC GG   TCAGA
                                  A   C  GC_
GAM284   LOC256228 5'  AGACTTGTGGTCAAAGC     96233     CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCAGA
                                 AAA
GAM284   LOC257441 5'  TTAGACCCAGGCGA        95566          ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                     _______
GAM284   LOC91960  3'  AGGTGCCTCTCGTGGTCCAAGC 67657     C       A  TTTG
                                GC TGGACCAC AG    ACCT
                                || |||||||| ||    ||||
                                CG ACCTGGTG TC    TGGA
                                 A       C  TCCG
GAM284   LOC92840  3'  GTCCCTCGGGTCCAGGC     56435          ACA  TTT
                                GCCTGGACC   AG   GAC
                                |||||||||   ||   |||
                                CGGACCTGG   TC   CTG
                                      GC_  C__
GAM285   DISC1     3'  ACTCATGGCCACTGTGGA    37867          _
                                TTCACAGTGGCCA GAGT
                                |||||||||||| ||||
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                                AGGTGTCACCGGT CTCA
                                      A
GAM285  EGFL3    3'  GGTATTTATGGGCCACTG    62617        A__
                                CAGTGGCC   GAGTACC
                                ||||||||   |||||||
                                GTCACCGG   TTTATGG
                                     GTA
GAM285  EPHB1    3'  AGAGGTTGACCACTGTGGA   15438          C  GAGT   C
                                TTCACAGTGG CA    ACC CT
                                |||||||||| ||    ||| ||
                                AGGTGTCACC GT    TGG GA
                                      A _____   A
GAM285  FADD     3'  AGGAAGGTAGCCCAGCACTGTG 13795         G CAGAG   __
             AA                   TTCACAGTG C    TACC  CCT
                                |||||||||| |    ||||  |||
                                AAGTGTCAC G    ATGG  GGA
                                     _ ACCCG    AA
GAM285  GYS1     3'  TGCTCTGCCCACTGTGAA    88402          C
                                TTCACAGTGG CAGAGTA
                                |||||||||| |||||||
                                AAGTGTCACC GTCTCGT
                                      C
GAM285  SELPLG   3'  GGGAAGGAACTCTGGCCAC   59690          A __
                                GTGGCCAGAGT CC  CCT
                                |||||||||| ||  |||
                                CACCGGTCTCA GG  GGG
                                      A  AA
GAM285  WNT3A    3'  CTCTGCCACTGTGAA      52429          C
                                TTCACAGTGGC AGAG
                                |||||||||| ||||
                                AAGTGTCACCG TCTC
                                      _
GAM285  ADIR     3'  TAGGAGCACCCCGTTTGGGACT 42332        GG    _____ ACC
             GTGAG                TCACAGT  CCAGA   GT   CCTA
                                |||||||  |||||   ||   ||||
                                AGTGTCA  GGTTT    CA   GGAT
                                     G_    GCCC  CGA
GAM285  ARHGEF4  5'  CTGACAGCCACTGTGAG    52213          ___
                                TTCACAGTGGC   CAG
                                ||||||||||   |||
                                GAGTGTCACCG   GTC
                                      ACA
GAM285  DSCR1L1  3'  AGGGAACCTCCTAGCACTGTGA 19493         GCCA   TAC
             A                    TTCACAGTG   GAG   CCCT
                                |||||||||   |||   ||||
                                AAGTGTCAC   CTC   GGGA
                                     GATC   CAA
GAM285  DVL2     3'  AGGAGATTGTGGCCACTGTGA  15359          G   ACC
                                TCACAGTGGCCA AGT   CCT
                                |||||||||||| |||   |||
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                                AGTGTCACCGGT TTA  GGA
                                      G  GA_
GAM285  FLJ12586 3' ATTCAGCCACTGTGAA     44875         CA
                                TTCACAGTGGC  GAGT
                                ||||||||||  ||||
                                AAGTGTCACCG  CTTA
                                      A_
GAM285  FLJ20436 3' AGAGTGGATTGGCTACTG    35166        AG  CC
                                CAGTGGCCAG  TAC  CT
                                |||||||||  |||  ||
                                GTCATCGGTT  GTG  GA
                                      AG  A_
GAM285  FLJ22054 3' GGGTACTCTAGTTTTATGT   94398    GT_  C
                                ACA  GGC AGAGTACCC
                                |||  ||| |||||||||
                                TGT  TTG TCTCATGGG
                                  ATT  A
GAM285  KIAA0404 3' AGGGGATGGCCACTGTGAA   69623          GAGTA
                                TTCACAGTGGCCA    CCCCT
                                ||||||||||||    |||||
                                AAGTGTCACCGGT    GGGGA
                                      A____
GAM285  KIAA0972 3' AGAAGTAAACCCTCACTGTGAA 30006        CCAGAG  CC
                                TTCACAGTGG     TAC  CT
                                |||||||||     |||  ||
                                AAGTGTCACT     ATG  GA
                                      CCCAA_  AA
GAM285  KIAA1199 3' GGGTCTCACACTGTGAA    72518        GCCA  T
                                TTCACAGTG   GAG ACCC
                                |||||||||   ||| ||||
                                AAGTGTCAC   CTC TGGG
                                     A___  _
GAM285  LYPLA3   3' GTACTCTGGATGCTGT     24634      GG
                                ACAGT  CCAGAGTAC
                                |||||  |||||||||
                                TGTCG  GGTCTCATG
                                   TA
GAM285  PDZD2    5' AGGAATACCACATTGTGAA   80858        GCCAGA  CC
                                TTCACAGTG     GTA  CCT
                                |||||||||     |||  |||
                                AAGTGTTAC     CAT  GGA
                                     AC____   AA
GAM285  RNF24    3' AGGGAGCCACTGTGAA      23314         CAGAGTAC
                                TTCACAGTGGC       CCCT
                                ||||||||||       ||||
                                AAGTGTCACCG       GGGA
                                      A_______
GAM285  SPANXB1  5' GCTCTGGGCCACTGCGAA    50607     A      _
                                TTC CAGTGGCC AGAGT
                                ||| |||||||| |||||
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                                AAG GTCACCGG TCTCG
                                  C       G
GAM285  ZFP106    3'  TGCCTGGCCACTGAGAA     42481     A        A
                                TTC CAGTGGCCAG GTA
                                ||| |||||||||| |||
                                AAG GTCACCGGTC CGT
                                  A        _
GAM285  LOC144970 5'  ACTTGACCACTGTGAA      76980          CCA
                                TTCACAGTGG   GAGT
                                ||||||||||   ||||
                                AAGTGTCACC   TTCA
                                      AG_
GAM285  LOC152048 3'  TAGGAGCTGGAACTACTGTGAA 85549          __    AGTACC
                                TTCACAGTGG  CCAG     CCTA
                                ||||||||||  ||||     ||||
                                AAGTGTCATC  GGTC     GGAT
                                      AA    GA_____
GAM285  LOC157867 5'  TGGTTTGGCCACTTTGAA    86561      C        G
                                TTCA AGTGGCCAGA TA
                                |||| |||||||||| ||
                                AAGT TCACCGGTTT GT
                                   T         G
GAM285  LOC220018 5'  GCTCTGGCCACCAAGAA     93403     ACA
                                TTC   GTGGCCAGAGT
                                |||   ||||||||||
                                AAG   CACCGGTCTCG
                                  AAC
GAM285  LOC220587 3'  AGGAGATTGTGGCCACTGTGA  90762           G   ACC
                                TCACAGTGGCCA AGT   CCT
                                |||||||||||| |||   |||
                                AGTGTCACCGGT TTA   GGA
                                      G   GA_
GAM285  LOC221088 5'  GGTGCTGGCCACTCGAA     93266     AC       GA
                                TTC  AGTGGCCA  GTACC
                                |||  ||||||||  |||||
                                AAG  TCACCGGT  CGTGG
                                  C_       __
GAM285  LOC255242 5'  TGCATTGCCACTGTGAA     95929          C  A
                                TTCACAGTGGC AG GTA
                                |||||||||| || |||
                                AAGTGTCACCG TT CGT
                                      _ A
GAM285  LOC51285  3'  AGGGAAACAGCCACTGTGA   33344          CAGA  AC
                                TCACAGTGGC   GT  CCCT
                                ||||||||||   ||  ||||
                                AGTGTCACCG   CA  GGGA
                                      A___  AA
GAM286  ADH4      3'  TAAAAAGATTTTTACTGGA   5409         CGT
                                TCCAGTGG   TCTTTTTA
                                ||||||||   ||||||||
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                                AGGTCATT  AGAAAAAT
                                    TTT
GAM286  ADRA2B   3'  GGGGGAACACACTAGAG    5465     C   GC
                                CTC AGTG  GTTCTTTT
                                ||| ||||  ||||||||
                                GAG TCAC  CAAGGGGG
                                  A   A_
GAM286  CTBP1    3'  AAAAAGAAAACCTGAAGGAG  67942     AGT_  CG
                                CTCC   GG  TTCTTTTT
                                ||||   ||  ||||||||
                                GAGG   CC  AAGAAAAA
                                  AAGT  AA
GAM286  EGFL5    5'  GTAAAAAGAAAAATATGGGGA  86626    T  GTGGCG
                                TCC CCA    TTCTTTTTAC
                                ||| |||    ||||||||||
                                AGG GGT    AAGAAAAATG
                                  _  ATAAA_
GAM286  ENPP3    3'  TAAAAAGAACAGCAGAGAG   17227    CAGTG  _
                                CTC    GC GTTCTTTTTA
                                |||    || ||||||||||
                                GAG    CG CAAGAAAAAT
                                  AGA__  A
GAM286  F8       3'  TAAAAAAATAAGTCAGGAGGA  3733       AG   GTTC_
                                TCCTCC  TGGC    TTTTTA
                                ||||||  ||||    ||||||
                                AGGAGG  ACTG    AAAAAT
                                    __   AATAA
GAM286  ID4      3'  AAAAAAAGCCACCGGAGGA   7752       A    GTTC
                                TCCTCC GTGGC   TTTTT
                                |||||| |||||   |||||
                                AGGAGG CACCG   AAAAA
                                   C    AA__
GAM286  PITX1    3'  AAAAAGACGTCGGAG      10596     AGT    T
                                CTCC   GGCGT CTTTTT
                                ||||   ||||| ||||||
                                GAGG   CTGCA GAAAAA
                                  ___    _
GAM286  TDG      3'  AAAAAGATGCTGGAG      12184       GCGT
                                CTCCAGTG   TCTTTTT
                                ||||||||   |||||||
                                GAGGTCGT   AGAAAAA
                                    _____
GAM286  XRCC2    3'  AAAAAGAACAAAGCTGGAGG  18314       GGC
                                CCTCCAGT   GTTCTTTTT
                                ||||||||   |||||||||
                                GGAGGTCG   CAAGAAAAA
                                    AAA
GAM286  ABCA10   5'  AAAAAGAGACCAGTGGA    54406     G  CG
                                TCCA TGG  TTCTTTTT
                                |||| |||  ||||||||
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                                AGGT ACC  GAGAAAAA
                                  G  A_
GAM286  ABCC13   3'  AAAAGTTTTCCACTGGGGA   56988     T      CGTT
                                TCC CCAGTGG   CTTTT
                                ||| |||||||   |||||
                                AGG GGTCACC   GAAAA
                                  _     TTTT
GAM286  ARFGAP1  3'  GGAACACCCTGGAAGA     36593    C    T  C
                                TC TCCAG GG GTTCT
                                || ||||| || |||||
                                AG AGGTC CC CAAGG
                                 A    _ A
GAM286  BA526D8.4 5'  TAAAAAAATTCATACTGGAGGG 70385          GCGTTC
                                TCCTCCAGTG     TTTTTA
                                ||||||||||     ||||||
                                GGGAGGTCAT     AAAAAT
                                      ACTTAA
GAM286  DKFZP727M111 5'  AAAAGGAAAAGCCCTGAAG   31402    C  T  G_
                                CT CAG GGC  TTCTTTTT
                                || ||| |||  ||||||||
                                GA GTC CCG  AAGGAAAA
                                 A  _  AA
GAM286  DKFZp761H079 3'  AAAAAGAGCCAATGGA     58727     G   GT
                                TCCA TGGC  TCTTTTT
                                |||| ||||  |||||||
                                AGGT ACCG  AGAAAAA
                                  A  __
GAM286  FLJ10648  3'  AAAAAGAACAAAGTCCTGGAGG 36377        T  ___
           A                     TCCTCCAG GGC   GTTCTTTTT
                                ||||||||| |||   |||||||||
                                AGGAGGTC CTG   CAAGAAAAA
                                     _  AAA
GAM286  FLJ20151  3'  AAAGACCCTGGAGGA      34649        T  CGT
                                TCCTCCAG GG   TCTTT
                                |||||||| ||   |||||
                                AGGAGGTC CC   AGAAA
                                     _ ____
GAM286  FLJ20190  5'  AAAGGACACCATTGGAG     34702         C
                                CTCCAGTGG GTTCTTT
                                ||||||||| |||||||
                                GAGGTTACC CAGGAAA
                                      A
GAM286  FLJ20435  3'  TAAAAAGAGCCATCTGGAGGA  35163        _   GT
                                TCCTCCAG TGGC  TCTTTTTA
                                |||||||| ||||  ||||||||
                                AGGAGGTC ACCG  AGAAAAAT
                                     T   __
GAM286  FLJ22477  5'  GACACCATCTGGAGGA     45343        _  C
                                TCCTCCAG TGG GTT
                                |||||||| ||| |||
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                                AGGAGGTC ACC CAG
                                     T   A
GAM286  HNRPA3    3' GTAAAAATCTGTCACAGAAGGA 19256      CCA     TTC
                                TCCT   GTGGCG   TTTTTAC
                                ||||   ||||||   |||||||
                                AGGA   CACTGT   AAAAATG
                                  AGA     CT_
GAM286  KIAA1091  3' GTAAAAAGAAAACTAGAGGA   69685      CAG   CG
                                TCCTC   TGG  TTCTTTTTAC
                                |||||   |||  ||||||||||
                                AGGAG   ATC  AAGAAAAATG
                                   ___   AA
GAM286  KIAA1546  3' AAAAAGAAGGTGGGGA      67900       CAGTG  G
                                TCCTC     GC TTCTTTTT
                                |||||     || ||||||||
                                AGGGG     TG AAGAAAAA
                                   _____  G
GAM286  KIAA1956  3' GTAAAACATAACACTGGAGGA  78439          GC  TCT
                                TCCTCCAGTG  GT   TTTTAC
                                ||||||||||  ||   ||||||
                                AGGAGGTCAC  TA   AAAATG
                                      AA  C__
GAM286  MDS024    3' AAAAAGAATTGCCAAGGA    41523     AG    _
                                TCC  TGGCG TTCTTTTT
                                |||  ||||| ||||||||
                                AGG  ACCGT AAGAAAAA
                                  A_    T
GAM286  MEGF11    3' AAAAGGAGACTGGGGA      50576     T    GGCG
                                TCC CCAGT    TTCTTTTT
                                ||| |||||    ||||||||
                                AGG GGTCA    GAGGAAAA
                                  _    _____
GAM286  MGC11082  5' AAAAAAAAGGCGGAGGG     51098       AGTG  G  C
                                TCCTCC    GC TT TTTTT
                                ||||||    || || |||||
                                GGGAGG    CG AA AAAAA
                                   _____  G  A
GAM286  MGC13105  3' AAAAAGTCACACTAGAGGA   71477      C    GCGTT
                                TCCTC AGTG    CTTTTT
                                ||||| ||||    ||||||
                                AGGAG TCAC    GAAAAA
                                   A    ACT__
GAM286  RPL13     3' AAAAAGAGCCAAGGA      78080     AG    GT
                                TCC  TGGC  TCTTTTT
                                |||  ||||  |||||||
                                AGG  ACCG  AGAAAAA
                                  A_    __
GAM286  ShrmL     5' AGAGCGCCACTGAAGGA     40464      C
                                TCCT CAGTGGCGTTCT
                                |||| ||||||||||||
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                                AGGA GTCACCGCGAGA
                                  A
GAM286  SIAT8C   5'  TAAAAAAGCCCCACAGAGGA  31884      CA   C  C
                                TCCTC  GTGG GTT TTTTTA
                                |||||  |||| ||| ||||||
                                AGGAG  CACC CGA AAAAAT
                                  A_   C  _
GAM286  VEST1    5'  AAAAAGATGCACTGGGGA    53679     T    G  T
                                TCC CCAGTG CGT CTTTTT
                                ||| |||||| ||| ||||||
                                AGG GGTCAC GTA GAAAAA
                                  _    _  _
GAM286  ZFD25    5'  AAAAAGAGCCCTGGA       32574      T  GT
                                TCCAG GGC  TCTTTTT
                                ||||| |||  |||||||
                                AGGTC CCG  AGAAAAA
                                  _  __
GAM286  LOC124626 3'  GTAAGACCAAACCACTGGA   74315        CGTTCT
                                TCCAGTGG     TTTTAC
                                ||||||||     ||||||
                                AGGTCACC     AGAATG
                                    AAACC_
GAM286  LOC126302 3'  AAAAAGAAGCAGGAGGA     74486       AGTG  G
                                TCCTCC    GC TTCTTTTT
                                ||||||    || ||||||||
                                AGGAGG    CG AAGAAAAA
                                  A___  _
GAM286  LOC132332 5'  AAAAAGAAGGCTGGA       76159      GTG  G
                                TCCA   GC TTCTTTTT
                                ||||   || ||||||||
                                AGGT   CG AAGAAAAA
                                  ___  G
GAM286  LOC144577 3'  TAAAAAGAAGCCACAAAGAG  76903     CA_    G
                                CTC   GTGGC TTCTTTTTA
                                |||   ||||| |||||||||
                                GAG   CACCG AAGAAAAAT
                                  AAA    _
GAM286  LOC145078 3'  GTAAAAATCTGCCACAGAAGGA 60292      CCA     TTC
                                TCCT   GTGGCG   TTTTTAC
                                ||||   ||||||   |||||||
                                AGGA   CACCGT   AAAAATG
                                  AGA     CT_
GAM286  LOC145837 5'  AAAAAGAACCAAAGAGGA    83540      CAG   CG
                                TCCTC   TGG  TTCTTTTT
                                |||||   |||  ||||||||
                                AGGAG   ACC  AAGAAAAA
                                  AA_   __
GAM286  LOC148753 3'  AAAAGGAGCACCAGGGA     84207     AG   C
                                TCC  TGG GTTCTTTTT
                                |||  ||| |||||||||
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                                AGG  ACC CGAGGAAAA
                                  G_  A
GAM286  LOC148981 3'  GTAAAAATCTGCCACAGAAGGA 84317     CCA     TTC
                                TCCT  GTGGCG  TTTTTAC
                                ||||  ||||||  |||||||
                                AGGA  CACCGT  AAAAATG
                                  AGA     CT_
GAM286  LOC153711 5'  AAAAGCGTCCCGCCAGAGGA  86129     CA   C TT
                                TCCTC  GTGG G  CTTTT
                                |||||  |||| |  |||||
                                AGGAG  CGCC T  GAAAA
                                   AC    C GC
GAM286  LOC154789 5'  GTAAAATCTCAGGCCACTAGAG 81140    C     GTTCT_
                                CTC AGTGGC     TTTTAC
                                ||| ||||||     ||||||
                                GAG TCACCG     AAAATG
                                  A     GACTCT
GAM286  LOC197322 3'  AAAGACTCCACTGGAGGA    89737          C  T
                                TCCTCCAGTGG GT CTTT
                                |||||||||| || ||||
                                AGGAGGTCACC CA GAAA
                                       T  _
GAM286  LOC220988 3'  GTAAAAATCTGCCACAGAAGGA 90848     CCA     TTC
                                TCCT  GTGGCG  TTTTTAC
                                ||||  ||||||  |||||||
                                AGGA  CACCGT  AAAAATG
                                  AGA     CT_
GAM286  LOC221596 3'  TAAAAACCTCACACTGGAGAGA 91981    _      GCGTTC
                                TC CTCCAGTG     TTTTTA
                                || ||||||||     ||||||
                                AG GAGGTCAC     AAAAAT
                                 A       ACTCC_
GAM286  LOC255190 3'  GTAAAAATCTGCCACAGAAGGA 97689     CCA     TTC
                                TCCT  GTGGCG  TTTTTAC
                                ||||  ||||||  |||||||
                                AGGA  CACCGT  AAAAATG
                                  AGA     CT_
GAM286  LOC91796  3'  AAAAAGAACAAGGCTGGA    67207       GGC
                                TCCAGT  GTTCTTTTT
                                ||||||  |||||||||
                                AGGTCG  CAAGAAAAA
                                   GAA
GAM286  LOC92539  5'  TAAAAAGTGTCACTG       69639        TT
                                CAGTGGCG  CTTTTTA
                                ||||||||  |||||||
                                GTCACTGT  GAAAAAT
                                          __
GAM286  LOC93444  3'  GAACCCACTGGAAGA       72387    C       C
                                TC TCCAGTGG GTTC
                                || |||||||| ||||
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                                AG AGGTCACC CAAG
                                 A      _
GAM286  LOC93538  5'  GTAAAGCTTCAGCGACTGAAGG 72562     C    G  GTTCT
              A                   TCCT CAGT GC    TTTTAC
                                  |||| |||| ||    ||||||
                                  AGGA GTCA CG    GAAATG
                                    A   G  ACTTC
GAM287  ADCY2    3'  TGGTCAAACTTGTTTTCT    65022          GGCATA
                                  AGGAAGCAGGTT     GCCA
                                  ||||||||||||     ||||
                                  TCTTTTGTTCAA     TGGT
                                        AC____
GAM287  ADCY9    3'  CTGGCTAATACCCTGTTTTT   6657         T  GCA
                                  GGAAGCAGG TG   TAGCCAG
                                  |||||||||  ||   |||||||
                                  TTTTTGTCC AT   ATCGGTC
                                       C  A__
GAM287  ADK      3'  TGCCCTAATTGCTTCCTG    6662          GTT_
                                  CAGGAAGCAG   GGCA
                                  ||||||||||   ||||
                                  GTCCTTCGTT   CCGT
                                       AATC
GAM287  ADK      3'  TGCCCTAATTGCTTCCTG    22046         GTT_
                                  CAGGAAGCAG   GGCA
                                  ||||||||||   ||||
                                  GTCCTTCGTT   CCGT
                                       AATC
GAM287  AP2B1    3'  TTGGATTTTCAGTTTGCTTTTT 7067        GG   CATAG
                                  AGGAAGCA  TTGG    CCAG
                                  ||||||||  ||||    ||||
                                  TTTTTCGT  GACT    GGTT
                                      TT   TTTA_
GAM287  APOH     3'  TAAAATGTCACACTTGTTTCTT 3486          _    AGCCAG
              G                    CAGGAAGCAGGT TGGCAT
                                   ||||||||||| ||||||
                                   GTTCTTTGTTCA ACTGTA
                                         C     AAAT
GAM287  APTX     3'  CTGGTTATACATTTCTGTTTCT 34657         T_ GC
              T                    AGGAAGCAGG  TG  ATAGCCAG
                                   |||||||||  ||  ||||||||
                                   TTCTTTGTCT  AC  TATTGGTC
                                        TT  A_
GAM287  ATP2A3   3'  TGCTGACCTGCTGTTTG     17725     A     TG
                                  CAGG AGCAGGT  GCA
                                  |||| |||||||  |||
                                  GTTT TCGTCCA  CGT
                                    G      GT
GAM287  ATP6IP1  3'  CTGGCTGTGGATAGTGCTTTT  6790        G_  GG
                                  GGAAGCA  GTT  CATAGCCAG
                                  |||||||  |||  |||||||||
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                                TTTTCGT  TAG  GTGTCGGTC
                                   GA  __
GAM287  ATP6IP1  3'  TTGGCTGTCGTTATCGTTTTCT 6792        A  T  _
            G                   CAGGAAGC GGT GGC ATAGCCAG
                                |||||||| ||| ||| ||||||||
                                GTCTTTTG CTA TTG TGTCGGTT
                                   _  _  C
GAM287  ATRN    3'  CTGGTTATGTCTTATTTTTTTC 57800     C   T_
                                GAAG AGGT  GGCATAGCCAG
                                |||| ||||  ||||||||||
                                CTTT TTTA  CTGTATTGGTC
                                  T   TT
GAM287  ATRN    3'  TGGCAATCTGCTTTTT     57805          G
                                AGGAAGCAGGTTG CA
                                |||||||||||| ||
                                TTTTTCGTCTAAC GT
                                      G
GAM287  BACH2   3'  GGCCTCGGCTTGCTCTTG    41490      A       CATA
                                CAGGA GCAGGTTGG   GCC
                                ||||| |||||||||   |||
                                GTTCT CGTTCGGCT   CGG
                                  _       C___
GAM287  BACH2   3'  TTGAGCATTGTAGGTTTGTTTT 41493        GG TG  TA  _
            TTG                   CAGGAAGCA  T  GCA  GC CAG
                                |||||||||  |  |||  || |||
                                GTTTTTTGT  G  TGT  CG GTT
                                     TT GA   TA  A
GAM287  BCL9    3'  TGCCCCACCTTGTTTTCTG   15070        _  T_
                                CAGGAAGCA GGT  GGCA
                                ||||||||| |||  ||||
                                GTCTTTTGT CCA  CCGT
                                     T   CC
GAM287  BTEB1   3'  TGTTGGTCTCCTTCCTG    6853        C   TT
                                CAGGAAG AGG  GGCA
                                ||||||| |||  ||||
                                GTCCTTC TCT  TTGT
                                   C   GG
GAM287  C4BPA   3'  TGCTGGCTTGCCTCTTG    5551       A     TG
                                CAGGA GCAGGT  GCA
                                ||||| ||||||  |||
                                GTTCT CGTTCG  CGT
                                  C     GT
GAM287  CALCRL  3'  TGTCAACCTCTTCCTG     19390       C
                                CAGGAAG AGGTTGGCA
                                ||||||| |||||||||
                                GTCCTTC TCCAACTGT
                                   _
GAM287  CARD15  3'  GGCTGAACTTGTTTTCTG   42217          GGCA
                                CAGGAAGCAGGTT   TAGCC
                                ||||||||||||   |||||
```

```
                              GTCTTTTGTTCAA   GTCGG
                                      ____
GAM287  CASP8    3'  TTGGCTAACTATATTTGCTTTT 52940          _  CA
           TG                  CAGGAAGCAGGT TGG  TAGCCAG
                               |||||||||||| |||  |||||||
                               GTTTTTCGTTTA ATC  ATCGGTT
                                     T   A_
GAM287  CASP8    3'  TTGGCTAACTATATTTGCTTTT 52957          _  CA
           TG                  CAGGAAGCAGGT TGG  TAGCCAG
                               |||||||||||| |||  |||||||
                               GTTTTTCGTTTA ATC  ATCGGTT
                                     T   A_
GAM287  CASP8    3'  TTGGCTAACTATATTTGCTTTT 52929          _  CA
           TG                  CAGGAAGCAGGT TGG  TAGCCAG
                               |||||||||||| |||  |||||||
                               GTTTTTCGTTTA ATC  ATCGGTT
                                     T   A_
GAM287  CASP8    3'  TTGGCTAACTATATTTGCTTTT 6923           _  CA
           TG                  CAGGAAGCAGGT TGG  TAGCCAG
                               |||||||||||| |||  |||||||
                               GTTTTTCGTTTA ATC  ATCGGTT
                                     T   A_
GAM287  CDC27    3'  GTGCTGACGTGTTTCTTG    6990         G  TG
                               CAGGAAGCA GT  GCAT
                               ||||||||| ||  ||||
                               GTTCTTTGT CA  CGTG
                                     G  GT
GAM287  CISH     3'  CTGCAGTTCTGCTAGGTCTGCT 25278         _    T  __
           TCCTG                  GAAGCAGGT TGGCA AGC  CAG
                               ||||||||| ||||| |||  |||
                               CTTCGTCTG ATCGT TTG  GTC
                                     G    C   AC
GAM287  CISH     3'  CTGCAGTTCTGCTAGGTCTGCT 59015         _    T  __
           TCCTG                  GAAGCAGGT TGGCA AGC  CAG
                               ||||||||| ||||| |||  |||
                               CTTCGTCTG ATCGT TTG  GTC
                                     G    C   AC
GAM287  CKTSF1B1 3'  TTGGATTTGGTTAACCTGTTTT 25373            ATAG_
           CT                  AGGAAGCAGGTTGGC    CCAG
                               ||||||||||||||    ||||
                               TCTTTTGTCCAATTG    GGTT
                                     GTTTA
GAM287  CLASP1   3'  TTGAGCACCAACTTGTTTCCT  65315           CATA  _
                               AGGAAGCAGGTTGG   GC CAG
                               ||||||||||||||   || |||
                               TCCTTTGTTCAACC   CG GTT
                                     A___  A
GAM287  CLCN4    3'  CTGTTCTCAGCCTGTTATCTG  8443       A       _ C
                               CAGG AGCAGGTTG G ATAG
                               |||| ||||||||| | ||||
```

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                                GTCT TTGTCCGAC C TGTC
                                  A       T T
GAM287  CLCN5    5'  GCTCCAACCTCCTTTTTG    3594        C     CAT
                                CAGGAAG AGGTTGG   AGC
                                ||||||| |||||||   |||
                                GTTTTTC TCCAACC   TCG
                                   C      ___
GAM287  COX15    3'  GGGTTTTTGTTTTGCTTTTTG  15196         TTG   T_   AG
                                CAGGAAGCAGG   GCA  AGCC
                                ||||||||||   |||  ||||
                                GTTTTTCGTTT   TGT  TTGG
                                      ___   TT   GT
GAM287  CPS1     3'  CTGGTTTGCAGTTTTGTTTTCT 8529          TTG   T
           G                     CAGGAAGCAGG   GCA AGCCAG
                                ||||||||||   ||| ||||||
                                GTCTTTTGTTT   CGT TTGGTC
                                      TGA   _
GAM287  CPSF6    3'  TGTCCAGCAGTTTGCTTCTTG  22804         ___    _
                                CAGGAAGCAG   GTTGG CA
                                |||||||||   ||||| ||
                                GTTCTTCGTT   CGACC GT
                                     TGA    T
GAM287  CRAT     3'  CTGGTTCCACTCAGCTTGGTTC 14353       G      CAT_
           CTG                    CAGGAA CAGGTTGG   AGCCAG
                                ||||||  ||||||||   ||||||
                                GTCCTT GTTCGACT   TTGGTC
                                   G       CACC
GAM287  CRAT     3'  CTGGTTCCACTCAGCTTGGTTC 5661        G      CAT_
           CTG                    CAGGAA CAGGTTGG   AGCCAG
                                ||||||  ||||||||   ||||||
                                GTCCTT GTTCGACT   TTGGTC
                                   G       CACC
GAM287  CRKL     3'  GCTGTTGCCCTGTTTCCTG   17795         TTG   _
                                CAGGAAGCAGG   GCA TAGC
                                ||||||||||   ||| ||||
                                GTCCTTTGTCC   CGT GTCG
                                      ___   T
GAM287  CSK      3'  TGGCGGGCCTTTTTCCTG    15220       CAGGTT   ATA
                                CAGGAAG     GGC   GCCA
                                |||||||     |||   ||||
                                GTCCTTT     CCG   CGGT
                                   TT____   GG_
GAM287  CYP1A2   3'  CTGGCAACTGCTAATCTACTTT 69111       C       TA_
           CTG                    CAGGAAG AGGTTGGCA   GCCAG
                                |||||||  |||||||||   |||||
                                GTCTTTC TCTAATCGT   CGGTC
                                   A       CAA
GAM287  CYP1A2   3'  CTGGCAACTGCTAATCTACTTT 5691        C       TA_
           CTG                    CAGGAAG AGGTTGGCA   GCCAG
                                |||||||  |||||||||   |||||
```

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                                GTCTTTC TCTAATCGT   CGGTC
                                    A       CAA
GAM287  CYP2B6   3'  TGTCAATCTGGTTTTTG    5744       G
                                CAGGAA CAGGTTGGCA
                                ||||||| ||||||||||
                                GTTTTT GTCTAACTGT
                                   G
GAM287  CYP8B1   3'  TTGCCCAGCTAATTTAGTTTCC 15277        _      ATA  CAG
           TG                     CAGGAAGC AGGTTGGC   GC
                                ||||||||| ||||||||  ||
                                GTCCTTTG TTTAATCG   CG
                                    A       ACC  TT
GAM287  DAB2     5'  CTGGTACTGAGGTTTGCTGCCT 7197      A   GG  GG  TA
           G                     CAGG AGCA  TT  CA  GCCAG
                                |||| ||||  ||  ||  |||||
                                GTCC TCGT  GG  GT  TGGTC
                                  G   TT  A_  CA
GAM287  DCK      3'  TGCCTCAGTCTGCTTTCT    5795         GT __
                                AGGAAGCAG  T  GGCA
                                |||||||||  |  ||||
                                TCTTTCGTC  A  CCGT
                                     TG CT
GAM287  DDX9     3'  TTGGTTATGTCAGTTCCTGT   88550      __
                                GCAGG  TTGGCATAGCCAG
                                |||||  ||||||||||||
                                TGTCC  GACTGTATTGGTT
                                   TT
GAM287  DPYSL2   3'  CTGAATACCAAATCTGCTTTTT 7296           _  CA  GC
           G                     CAGGAAGCAGGTT GG  TA  CAG
                                |||||||||||| ||  ||  |||
                                GTTTTTCGTCTAA CC  AT  GTC
                                       A  __  AA
GAM287  DPYSL2   3'  TGTTGGCTTGCTTTGTG     7305     G       TG
                                CA GAAGCAGGT  GCA
                                || |||||||||  |||
                                GT TTTCGTTCG  TGT
                                 G       GT
GAM287  DUSP5    3'  CTGGTTGTTGTTGTTGTTCTTG 15352       G   GT    _
                                CAGGAA CAG  TGGCA TAGCCAG
                                |||||| |||  ||||| |||||||
                                GTTCTT GTT  GTTGT GTTGGTC
                                   _  __    T
GAM287  DYRK1A   3'  CTGACTAGGTCAATTTTTTTTC 55203        C      A   C
           TG                     CAGGAAG AGGTTGGC TAG CAG
                                ||||||| |||||||| ||| |||
                                GTCTTTT TTTAACTG ATC GTC
                                   T       G   A
GAM287  DYRK1A   3'  CTGACTAGGTCAATTTTTTTTC 55243        C      A   C
           TG                     CAGGAAG AGGTTGGC TAG CAG
                                ||||||| |||||||| ||| |||
```

```
                                GTCTTTT TTTAACTG ATC GTC
                                    T       G   A
GAM287  DYRK1A   3'  CTGACTAGGTCAATTTTTTTTC 7352         C       A   C
            TG                    CAGGAAG AGGTTGGC TAG CAG
                                  ||||||| |||||||| ||| |||
                                GTCTTTT TTTAACTG ATC GTC
                                    T       G   A
GAM287  ED1      3'  CTGGGCTCAGCCTGGTTTCTG  7370        G      _ ATAG
                                CAGGAA CAGGTTG GC    CCAG
                                |||||| ||||||| ||    ||||
                                GTCTTT GTCCGAC CG    GGTC
                                   G      T ____
GAM287  EHD2     3'  CTGGAACTGCCCAGCCTGCTCC 27493       A       _  TAG
            TG                    CAGGA GCAGGTTGG CA   CCAG
                                  ||||| ||||||||| ||   ||||
                                GTCCT CGTCCGACC GT   GGTC
                                  _       C  CAA
GAM287  EIF2C1   3'  CTGTGTACCTGATTTGTTCTCT 24173    GA      TG ___    CCAG
            G                     AG  AGCAGGT  G   CATAG
                                  ||  |||||||  |   |||||
                                TC  TTGTTTA  C   GTGTC
                                 TC      GT CAT       G
GAM287  ELAVL2   3'  TGGTTGTGTCTTTTTTTTC   15418     C   TT
                                GAAG AGG  GGCATAGCCA
                                |||| |||  ||||||||||
                                CTTT TTT  CTGTGTTGGT
                                  _  TT
GAM287  EMR1     3'  CTGGCTACCATTTTGTTTTCT  8774          T   CA
                                AGGAAGCAGG TGG  TAGCCAG
                                |||||||||| |||  |||||||
                                TCTTTTGTTT ACC  ATCGGTC
                                      T  __
GAM287  EPHA2    3'  TTGGTTGTGTTGAGGTTTTT   15411       AGG TG
                                GGAAGC   T  GCATAGCCAG
                                ||||||   |  ||||||||||
                                TTTTTG   A  TGTGTTGGTT
                                   G__ GT
GAM287  EPHB2    3'  GTTTGTTGGGTTGTTTTTTG   15446         G TG   T
                                CAGGAAGCAG T  GCA AGC
                                |||||||||| |  ||| |||
                                GTTTTTTGTT G  TGT TTG
                                      G GT  _
GAM287  EPHB2    3'  GTTTGTTGGGTTGTTTTTTG   33888         G TG   T
                                CAGGAAGCAG T  GCA AGC
                                |||||||||| |  ||| |||
                                GTTTTTTGTT G  TGT TTG
                                      G GT  _
GAM287  FBLN5    3'  CTGGGAGTAGCTAGTTTGCTTT 20915         GG    _  AG
            TTG                   CAGGAAGCA  TTGGC AT  CCAG
                                  |||||||||  ||||| ||  ||||
```

```
                                GTTTTTCGT  GATCG TG  GGTC
                                     TT    A  AG
GAM287  FBXL11   3'  TTGGTTTTTATGTTTGTTTTTT 24579        GTTG    ___
           G                    AGGAAGCAG   GCATA   GCCAG
                                |||||||||   |||||  |||||
                                TTTTTTGTT   TGTAT   TGGTT
                                     ____    TTT
GAM287  FLRT2    3'  GAACCATATGCTGATTTGCTTC 25061         TG    GCCAG
           T                    GGAAGCAGGT  GCATA
                                ||||||||||  |||||
                                TCTTCGTTTA  CGTAT
                                     GT    ACCAAGT
GAM287  FUS1     3'  CTGGTTCCTTGCCTGGTCTGCT 23449       GT _   T__
           TTCT                   GAAGCAG  T GGCA   AGCCAG
                                |||||||  | ||||  ||||||
                                TTTCGTC  G CCGT   TTGGTC
                                    TG T   TCC
GAM287  FZD10    3'  TTGGTTGTGTTTTTCTTTCTT  23243      GC   TT
                                AGGAA  AGG  GGCATAGCCAG
                                |||||  |||  ||||||||||
                                TTCTT  TCT  TTGTGTTGGTT
                                   __  TT
GAM287  GALNT7   3'  TTGAATTGTCAATTTGTATTTT 33803      A        TAGCCAG
           G                    CAGGA GCAGGTTGGCA
                                |||||  ||||||||||
                                GTTTT TGTTTAACTGT
                                   A         TAAGTT
GAM287  GDI1     3'  TTGATTTGCTGTTTTGTTTCTT 59983         TT    TAGCCAG
           G                    CAGGAAGCAGG  GGCA
                                ||||||||||  ||||
                                GTTCTTTGTTT  TCGT
                                     TG    TTAGTT
GAM287  GDI1     3'  TTGGAGGTTGATTTGCTGTTTT 59984      _     TG  ATAG
           G                    CAGGA AGCAGGT  GC    CCAG
                                |||||  |||||||  ||    ||||
                                GTTTT TCGTTTA  TG    GGTT
                                   G      GT  GA__
GAM287  GNAL     3'  GGTTGTGTAGCTTCT       9060        AGGTTG
                                GGAAGC     GCATAGCC
                                ||||||     ||||||||
                                TCTTCG     TGTGTTGG
                                   A_____
GAM287  GOCAP1   3'  TTGGCTAGTGATTCTTGTTTTC 42705         TTGG  _
                                GGAAGCAGG    CAT AGCCAG
                                |||||||||    ||| ||||||
                                CTTTTGTTC    GTG TCGGTT
                                     TTA_   A
GAM287  GPRC5B   3'  TGGCTGTGTCTTTCTTG     32666      TT_
                                CAGG   GGCATAGCCA
                                ||||   ||||||||||
```

```
                                GTTC  CTGTGTCGGT
                                  TTT
GAM287  GRF2    3'  CTGGAGCCTGCCAGCCGCTTCC 17991       A      TAG_
           TG                    CAGGAAGC GGTTGGCA   CCAG
                                 |||||||| ||||||||   ||||
                                 GTCCTTCG CCGACCGT   GGTC
                                     _      CCGA
GAM287  GRF2    3'  CTGGTTTGGTTTTGTTTTCTG  17992         TTG  AT
                                 CAGGAAGCAGG  GC  AGCCAG
                                 ||||||||||  ||  ||||||
                                 GTCTTTTGTTT  TG  TTGGTC
                                       ___  GT
GAM287  GRP     3'  CTGGTTTAAACTTGTTTGCTG  9137     G      GGCAT
                                 CAG AAGCAGGTT    AGCCAG
                                 ||| |||||||||    ||||||
                                 GTC TTTGTTCAA    TTGGTC
                                   G       AT___
GAM287  GTF2E2  3'  CTGTCTTCCTATCTGCTTCTTG 9146          T  CAT  C
                                 CAGGAAGCAGGT GG   AG CAG
                                 |||||||||||| ||   || |||
                                 GTTCTTCGTCTA CC   TC GTC
                                       T  T__  T
GAM287  HCS     3'  TGGCGTTTAGTTTGTTTTTTG  38483        GG   CATA   G
                                 CAGGAAGCA  TTGG   GCCA
                                 |||||||||  ||||   ||||
                                 GTTTTTTGT  GATT   CGGT
                                      TT   TG__   G
GAM287  HGF     3'  CTGTCTAAGCTGCTTTCTG   94234         G   C
                                 CAGGAAGCAG TTGG ATAG
                                 |||||||||| |||| ||||
                                 GTCTTTCGTC AATC TGTC
                                       G   _
GAM287  HNRPD   3'  ATGTCAATTTGTTTGTTG   48574    G
                                 CAG AAGCAGGTTGGCAT
                                 ||| ||||||||||||||
                                 GTT TTTGTTTAACTGTA
                                   G
GAM287  HNRPD   3'  ATGTCAATTTGTTTGTTG   9243     G
                                 CAG AAGCAGGTTGGCAT
                                 ||| ||||||||||||||
                                 GTT TTTGTTTAACTGTA
                                   G
GAM287  HPS3    3'  TTACAAAGCTAACTTTCTTCTT 50483       C      ATAGCCAG
           G                     CAGGAAG AGGTTGGC
                                 |||||||| ||||||||
                                 GTTCTTC TTCAATCG
                                     T       AAACATT
GAM287  HSPA4   3'  TTGGTGTAAAGATTTGTATCCT 89174      A     GGCATA
           G                     CAGGA GCAGGTT     GCCAG
                                 ||||| |||||||     |||||
```

```
                                GTCCT TGTTTAG     TGGTT
                                  A      AAATG_
GAM287  ID4     3'  CTGGCTCTTAATTTGCTTTT  7753           CAT
                                GGAAGCAGGTTGG  AGCCAG
                                ||||||||||||  ||||||
                                TTTTCGTTTAATT  TCGGTC
                                    C__
GAM287  IL17    3'  CTGAGTACCAATTTGCTTCTTG 9330            CATA  _
                                CAGGAAGCAGGTTGG   GC CAG
                                ||||||||||||||   || |||
                                GTTCTTCGTTTAACC   TG GTC
                                     A___  A
GAM287  IL24    3'  CTGGCACTGGTTTGTTCCCTG  22443     A   GG TG CATA
                                CAGG AGCA  T  G   GCCAG
                                |||| ||||  |  |   |||||
                                GTCC TTGT  G  C   CGGTC
                                  C   TT GT A___
GAM287  ILF1    3'  CTGGCTATTTTTTGTTGTTTG  15718     A    TTGGC
                                CAGG AGCAGG    ATAGCCAG
                                |||| ||||||    ||||||||
                                GTTT TTGTTT    TATCGGTC
                                  G     TT___
GAM287  INHBB   3'  CTGGCTCGATGTCTGCTTCTT  9339        GTTG   __
                                AGGAAGCAG   GCAT  AGCCAG
                                |||||||||   ||||  ||||||
                                TTCTTCGTC   TGTA  TCGGTC
                                     ____   GC
GAM287  ITGAM   3'  CTGGGATGGGCCTGCTTCCTG  71839          GG   AG
                                CAGGAAGCAGGTT  CAT  CCAG
                                ||||||||||||  |||  ||||
                                GTCCTTCGTCCGG  GTA  GGTC
                                     __  G_
GAM287  JAM3    3'  GGGTTCCTAATCTGTTTCT   51424          CAT   AG
                                GGAAGCAGGTTGG  AGCC
                                ||||||||||||  ||||
                                TCTTTGTCTAATC  TTGG
                                     C__   GT
GAM287  KCNA5   3'  TTGGTATGGGCTGTTCTGTTTC 59710         TT   ATA_
          CTG                   CAGGAAGCAGG  GGC   GCCAG
                                ||||||||||  |||   |||||
                                GTCCTTTGTCT  TCG   TGGTT
                                     TG   GGTA
GAM287  KCNA6   3'  CTGGCCCTCTACCTTGCTTCCT 9512          T   CATA
          G                    CAGGAAGCAGG TGG   GCCAG
                                ||||||||||| |||   |||||
                                GTCCTTCGTTC ATC   CGGTC
                                     C   TCC_
GAM287  KCNA6   3'  TGCCATTTGTTTTTTG     9519           T
                                CAGGAAGCAGGT GGCA
                                |||||||||||| ||||
```

```
                                GTTTTTTGTTTA CCGT
                                          _
GAM287  KCNS2    3'  CTGGAGATGACTTGTTTCC   68303          TGG  AG
                                GGAAGCAGGT  CAT  CCAG
                                ||||||||||  |||  ||||
                                CCTTTGTTCA  GTA  GGTC
                                     ____  GA
GAM287  KCNS2    3'  TTGGTTATAGGTTTGTGTTTTC 68314        GGTT  __
            TG                   CAGGAAGCA   GGC  ATAGCCAG
                                ||||||||||  |||  ||||||||
                                GTCTTTTGT   TTG  TATTGGTT
                                     GT__  GA
GAM287  KIAA0442 5'  GTGTCAATTTTTTTTTG    31473        C
                                CAGGAAG AGGTTGGCAT
                                ||||||| ||||||||||
                                GTTTTTT TTTAACTGTG
                                          _
GAM287  KLHL2    5'  CTGGCTGTGTTGGTCGGTGCCT 23385     AA  A  TT
            G                    CAGG  GC GG  GGCATAGCCAG
                                ||||  || ||  ||||||||||
                                GTCC  TG CT  TTGTGTCGGTC
                                  G_  G  GG
GAM287  KLHL3    3'  CTAGCCAGTCATGTTTTCTG   87455         _ GT   A
                                CAGGAAGCA G  TGGC TAG
                                ||||||||| |  |||| |||
                                GTCTTTTGT C  ACCG ATC
                                     A TG   _
GAM287  LAMC1    3'  TTGGTTTCCTTTTAACTTTCTT 9682        C      CAT__
            TTTG                   AGGAAG AGGTTGG    AGCCAG
                                ||||||| |||||||    ||||||
                                TTTTTC TTCAATT    TTGGTT
                                   T      TTCCT
GAM287  LIFR     3'  TTGGTTGGTTGTTTGTTTTTT  9751         GG T   A
                                AGGAAGCA  T GGC TAGCCAG
                                ||||||||  | ||| |||||||
                                TTTTTTGT  G TTG GTTGGTT
                                     TT _  _
GAM287  LRP4     3'  TGCCTAATTTGCTTTTT     64447          _
                                AGGAAGCAGGTT GGCA
                                |||||||||||| ||||
                                TTTTTCGTTTAA CCGT
                                       T
GAM287  LSP1     3'  CTGGCTAAGAAGTTGCTTCCTG 9809          G  GGCA
                                CAGGAAGCAG TT    TAGCCAG
                                |||||||||| ||    |||||||
                                GTCCTTCGTT AA    ATCGGTC
                                     G  GA__
GAM287  MAK      3'  TTGGCTTAAGAGGTTTGTCTTT 19771      AG  GG  GGCAT
            TG                   CAGGA  CA  TT    AGCCAG
                                |||||  ||  ||    ||||||
```

```
                              GTTTT  GT  GG    TCGGTT
                                CT  TT  AGAAT
GAM287  MAPRE1   3'  TTGTATTGATTTGTTTCT    24662        TG C
                              GGAAGCAGGT  G ATAG
                              ||||||||||  | ||||
                              TCTTTGTTTA  T TGTT
                                   GT A
GAM287  MAPT     3'  TTGGTTAATCACTTAACCTGCT 33694          CA___
           TTT                 GGAAGCAGGTTGG    TAGCCAG
                              ||||||||||||||    |||||||
                              TTTTCGTCCAATT    ATTGGTT
                                    CACTA
GAM287  MAPT     3'  TTGGTTAATCACTTAACCTGCT 33703          CA___
           TTT                 GGAAGCAGGTTGG    TAGCCAG
                              ||||||||||||||    |||||||
                              TTTTCGTCCAATT    ATTGGTT
                                    CACTA
GAM287  MAPT     3'  TTGGTTAATCACTTAACCTGCT 33713          CA___
           TTT                 GGAAGCAGGTTGG    TAGCCAG
                              ||||||||||||||    |||||||
                              TTTTCGTCCAATT    ATTGGTT
                                    CACTA
GAM287  MAPT     3'  TTGGTTAATCACTTAACCTGCT 19783          CA___
           TTT                 GGAAGCAGGTTGG    TAGCCAG
                              ||||||||||||||    |||||||
                              TTTTCGTCCAATT    ATTGGTT
                                    CACTA
GAM287  MBD1     5'  TGGCTACTGCTGCTTCCTG   31791        GGTTG  _
                              CAGGAAGCA    GCA TAGCCA
                              |||||||||    ||| ||||||
                              GTCCTTCGT    CGT ATCGGT
                                   _____  C
GAM287  MBD1     5'  TGGCTACTGCTGCTTCCTG   31776        GGTTG  _
                              CAGGAAGCA    GCA TAGCCA
                              |||||||||    ||| ||||||
                              GTCCTTCGT    CGT ATCGGT
                                   _____  C
GAM287  MBD1     5'  TGGCTACTGCTGCTTCCTG   31777        GGTTG  _
                              CAGGAAGCA    GCA TAGCCA
                              |||||||||    ||| ||||||
                              GTCCTTCGT    CGT ATCGGT
                                   _____  C
GAM287  MBD1     5'  TGGCTACTGCTGCTTCCTG   31784        GGTTG  _
                              CAGGAAGCA    GCA TAGCCA
                              |||||||||    ||| ||||||
                              GTCCTTCGT    CGT ATCGGT
                                   _____  C
GAM287  MBD1     5'  TGGCTACTGCTGCTTCCTG   9950         GGTTG  _
                              CAGGAAGCA    GCA TAGCCA
                              |||||||||    ||| ||||||
```

```
                                GTCCTTCGT    CGT ATCGGT
                                     _____  C
GAM287  MBNL    3'  GGCTGCAATTTGTTTT     40730          GCA
                                GAAGCAGGTTG   TAGCC
                                ||||||||||   |||||
                                TTTTGTTTAAC   GTCGG
                                     ___
GAM287  MCM2    3'  TTGTGCATTCGGTTTGGTTTCT 67932      G  GG  ___     CCAG
          G                      AGGAA CA  TTG   GCATAG
                                |||||  ||  |||   ||||||
                                TCTTT GT  GGC   CGTGTT
                                   G  TT   TTA       G
GAM287  MCM3    3'  TTGGGGGCACAACTGTTTTCTG 9964          G  _  ATAG
                                CAGGAAGCAG TTG GC    CCAG
                                |||||||||| ||| ||    ||||
                                GTCTTTTGTC AAC CG    GGTT
                                     _  A  GG__
GAM287  MGEA5   3'  GGGCAGTTATTCTGCTTTTTG  24216        GT   ATA   AG
                                CAGGAAGCAG  TGGC   GCC
                                ||||||||||  ||||   |||
                                GTTTTTCGTC  ATTG   CGG
                                     TT   A__   GG
GAM287  MKPX    3'  TTGGCGCTCGTGATTGCTTCCT 39487         GT_  _  ATA
          G                      CAGGAAGCAG   TG GC   GCCAG
                                ||||||||||   || ||   |||||
                                GTCCTTCGTT   GC CG   CGGTT
                                     AGT  T  ___
GAM287  MLC1    3'  TGGCGGGGTCTGCTCCTG    30787      A   GTTG  ATA
                                CAGGA GCAG    GC   GCCA
                                |||||  ||||    ||   ||||
                                GTCCT CGTC    TG   CGGT
                                   _   ____  GGG
GAM287  MLC1    3'  TGGCGGGGTCTGCTCCTG    57599      A   GTTG  ATA
                                CAGGA GCAG    GC   GCCA
                                |||||  ||||    ||   ||||
                                GTCCT CGTC    TG   CGGT
                                   _   ____  GGG
GAM287  MLLT3   3'  TTGGTTGTGATTTTTTGTTCTT 15760       G   TTGG
          G                      CAGGAA CAGG    CATAGCCAG
                                ||||||  ||||    |||||||||
                                GTTCTT GTTT    GTGTTGGTT
                                   _   TTTA
GAM287  MOV10L1 3'  TTGGCATATGCCAGCCTGTTCC 38637       G         _
          TG                      CAGGAA CAGGTTGGCATA GCCAG
                                ||||||  |||||||||||| |||||
                                GTCCTT GTCCGACCGTAT CGGTT
                                   _         A
GAM287  MSL3L1  3'  GTCATGCTGCCTGCTTTCTG   54369          T    AG
                                CAGGAAGCAGGT GGCAT  C
                                ||||||||||| |||||  |
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                                GTCTTTCGTCCG TCGTA  G
                                      _    CT
GAM287  MYBL1   3'  CTAGAAGCCAATGTTGTTTCCT 64072        _    ATAGCCAG
            G                  CAGGAAGCAG GTTGGC
                               |||||||||| ||||||
                               GTCCTTTGTT TAACCG
                                     G     AAGATC
GAM287  MYH3    5'  TGGCTGTTGCTGTCTTCTG   10171     AG  GGTTG  _
                               CAGGA  CA    GCA TAGCCA
                               |||||  ||    ||| ||||||
                               GTCTT  GT    CGT GTCGGT
                                  CT _____  T
GAM287  NCOA6   5'  CTGGCCCACGATCTGTTTTT  25962         GCATA
                               GGAAGCAGGTTG    GCCAG
                               ||||||||||||    |||||
                               TTTTTGTCTAGC    CGGTC
                                     ACC__
GAM287  NDUFV3  5'  TGGTAGGATGTGTTTCCTG   40779       G   GGCATA
                               CAGGAAGCA GTT     GCCA
                               ||||||||| |||     ||||
                               GTCCTTTGT TAG     TGGT
                                     G  GA____
GAM287  NEO1    3'  CTGGGGTTGGCTTGTTTTTTG  10202         TG  ATAG
                               CAGGAAGCAGGT  GC   CCAG
                               ||||||||||||  ||   ||||
                               GTTTTTTGTTCG  TG   GGTC
                                     GT  G___
GAM287  NEU3    3'  CTGGCTCTGCCACTGGCTTGCT 21848        ___    T
            TTT                  GAAGCAGGT   TGGCA AGCCAG
                               |||||||||   ||||| ||||||
                               TTTCGTTCG   ACCGT TCGGTC
                                     GTC    C
GAM287  NFKB1   3'  CTGGATCACAGCTGCTTTCTG  14341        G   GCATAG
                               CAGGAAGCAG TTG     CCAG
                               |||||||||| |||     ||||
                               GTCTTTCGTC GAC     GGTC
                                     _  ACTA__
GAM287  NOVA1   3'  TGTTCATTTGTTTCTTG    21413          TG
                               CAGGAAGCAGGT  GCA
                               ||||||||||||  |||
                               GTTCTTTGTTTA  TGT
                                     CT
GAM287  NPPB    3'  CTGGCTGCAGACACCTGCTTCT 10253        TG__   TA
                               GGAAGCAGGT   GCA  GCCAG
                               ||||||||||   |||  |||||
                               TCTTCGTCCA   CGT  CGGTC
                                     CAGA  __
GAM287  NR4A2   3'  TAGAGATGCTGATTTTTTTTCT 20534       C   TG   AGCCAG
            G                  CAGGAAG AGGT  GCAT
                               |||||||  ||||  ||||
```

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                                GTCTTTT TTTA  CGTA
                                    T   GT   GAGATT
GAM287  OCLN    3'  TGGTTAAGTCTGTTTT     10318       GT GGCA
                                GAAGCAG  T   TAGCCA
                                |||||||  |   ||||||
                                TTTTGTC  A   ATTGGT
                                    TG ____
GAM287  ORC2L   3'  TTGGTTTTGTTTGCTATTCTG  20551     _   GTTG  T
                                CAGGA AGCAG   GCA AGCCAG
                                ||||| |||||   ||| ||||||
                                GTCTT TCGTT   TGT TTGGTT
                                  A    _____  T
GAM287  OTOF    3'  TTGGCTGTTTTTCTTTTCTTG  16647       C  TT   TA
                                CAGGAAG AGG  GGCA  GCCAG
                                ||||||| |||  ||||  |||||
                                GTTCTTT TCT  TTGT  CGGTT
                                    _  TT   __
GAM287  P4HB    3'  TGGTGGGGCTTGTTTCCTG   6221           GGCATA
                                CAGGAAGCAGGTT     GCCA
                                ||||||||||||     ||||
                                GTCCTTTGTTCGG     TGGT
                                      GG____
GAM287  PAX7    3'  CTGGCTAAGCCTCTGCTTCC   25638        TT  A
                                GGAAGCAGG  GGC TAGCCAG
                                |||||||||  ||| |||||||
                                CCTTCGTCT  CCG ATCGGTC
                                    __  A
GAM287  PAX7    3'  CTGGCTAAGCCTCTGCTTCC   10434        TT  A
                                GGAAGCAGG  GGC TAGCCAG
                                |||||||||  ||| |||||||
                                CCTTCGTCT  CCG ATCGGTC
                                    __  A
GAM287  PEA15   3'  TACTCCTGTGCTGGACTGTTTC 13654         G TG    CCAG
          CTG                   CAGGAAGCAG T  GCATAG
                                ||||||||||  |  ||||||
                                GTCCTTTGTC G  CGTGTC
                                    A GT     CTCATG
GAM287  PFKFB3  3'  GCTTAGCTTGTGTCCTG     82874      A      _
                                CAGGA GCAGGTTG GC
                                ||||| ||||||||  ||
                                GTCCT TGTTCGAT CG
                                  G       T
GAM287  PLA2G5  3'  TTGGCTGTGTCTCTTTTCTTC  6251      C   TT
                                GAAG AGG  GGCATAGCCAG
                                ||||  |||  ||||||||||
                                CTTC TTT  CTGTGTCGGTT
                                  T   CT
GAM287  PLCB2   5'  TGGCTGGCCTCCTTCCTG    15896      AGC   TT   A
                                CAGGA   AGG  GGC TAGCCA
                                |||||   |||  ||| ||||||
```

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                                GTCCT   TCC  CCG GTCGGT
                                   ___   T_   _
GAM287  PMM2     3'  CTGGTTGCCCCTGGCTGGCTTC 72090        A   TG CA_
              CTG                    CAGGAAGC GGT  G   TAGCCAG
                                |||||||| |||  |   |||||||
                                GTCCTTCG TCG  C   GTTGGTC
                                    G   GT CCC
GAM287  PPP1R12A  3'  TTGTTGTTGTTGGTTTGTTTTT 10182         GG TG   _    CAG
              TG                    CAGGAAGCA  T  GCA TAGC
                                |||||||||  |  ||| ||||
                                GTTTTTTGT  G  TGT GTTG
                                     TT GT   T    TT
GAM287  PPY      3'  CTGGCCAAAGCTTGCTCCCTG  10769      A       GGCATA
                                CAGG AGCAGGTT     GCCAG
                                |||| ||||||||      |||||
                                GTCC TCGTTCGA     CGGTC
                                  C       AAC___
GAM287  PRPS2    3'  CTGACTTCTGACTTGTTTTT   10902          TG CAT  C
                                GGAAGCAGGT  G   AG CAG
                                ||||||||||  |   || |||
                                TTTTTGTTCA  C   TC GTC
                                     GT T__  A
GAM287  PRSS8    3'  CTGGCTCCCACCTGTTTCT    10917          T  CAT
                                GGAAGCAGGT GG   AGCCAG
                                |||||||||| ||   ||||||
                                TCTTTGTCCA CC   TCGGTC
                                     C  ___
GAM287  PYGO2    3'  TGGTTATGGCAGTTTCTTG    63993        AGGT  G
                                CAGGAAGC    TG CATAGCCA
                                ||||||||    || ||||||||
                                GTTCTTTG    AC GTATTGGT
                                    _____  G
GAM287  RAD21    3'  TGTTAGTCTGGTTTTTG     20762       G   GT
                                CAGGAA CAG  TGGCA
                                ||||||  |||  |||||
                                GTTTTT GTC  ATTGT
                                    G   TG
GAM287  RAMP3    3'  GCCAGCCTGCTCCCTG      19590      A
                                CAGG AGCAGGTTGGC
                                |||| ||||||||||
                                GTCC TCGTCCGACCG
                                  C
GAM287  RERE     3'  CTGCCCTCTGTCGGCCCTGCTT 23966          _     T  C_
              CCTG                    AGGAAGCAGG TTGGCA AG  CAG
                                |||||||||| |||||| ||  |||
                                TCCTTCGTCC GGCTGT TC  GTC
                                     C     C  CC
GAM287  RET      3'  TGGAGCAGTTGCTTTTTG    40185          GTTG  ATAG
                                CAGGAAGCAG    GC    CCA
                                ||||||||||    ||    |||
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                                GTTTTTCGTT   CG   GGT
                                     GA__  A___
GAM287  RRM2B    3'  CCATCTATGTTGATTTGCTTTT 67825        TG    CCAG
                                GGAAGCAGGT  GCATAG
                                ||||||||||  ||||||
                                TTTTCGTTTA  TGTATC
                                     GT     TACCA
GAM287  SDC4     3'  CTGGTGTTCTTTGGTTTGCTTT 11477       GG TG CATA_
           CT                    AGGAAGCA  T  G    GCCAG
                                ||||||||  |  |    |||||
                                TCTTTCGT  G  T    TGGTC
                                    TT GT TCTTG
GAM287  SELP     3'  CTGGACCAACCCTGTTTCCTG  11536         _   CATAG
                                CAGGAAGCAGG TTGG    CCAG
                                ||||||||||| ||||    ||||
                                GTCCTTTGTCC AACC    GGTC
                                      C   A____
GAM287  SFRS2    3'  TTGGCTGTTTCCTGTTTTCT   65190        TTGGC
                                AGGAAGCAGG    ATAGCCAG
                                ||||||||||    ||||||||
                                TCTTTTGTCC    TGTCGGTT
                                     TT___
GAM287  SH3GL3   3'  TTGGTTAAATGTATTTGCTTCC 11638          TG  __
           TG                    CAGGAAGCAGGT  GCA  TAGCCAG
                                ||||||||||||  |||  |||||||
                                GTCCTTCGTTTA  TGT  ATTGGTT
                                     __   AA
GAM287  SHMT2    3'  AGGCAGCCAGTTGCTTCCTG   18261       GGT   ATA   AG
                                CAGGAAGCA   TGGC   GCC
                                |||||||||   ||||   |||
                                GTCCTTCGT   ACCG   CGG
                                     TG_   A__   AC
GAM287  SLC16A1  5'  TTGGATTTGACCTGCATTTTG  11745      A     TG CATAG
                                CAGGA GCAGGT  G    CCAG
                                ||||| ||||||  |    ||||
                                GTTTT CGTCCA  T    GGTT
                                   A     GT TA___
GAM287  SLC17A4  3'  TGCCCCACATCTGCTTTTTG   18527          T___
                                CAGGAAGCAGGT   GGCA
                                ||||||||||||   ||||
                                GTTTTTCGTCTA   CCGT
                                      CACC
GAM287  SLC22A5  3'  CTGTGTCTGACTTGCTCCTG   11763      A     TG _
                                CAGGA GCAGGT  G CATAG
                                ||||| ||||||  | |||||
                                GTCCT CGTTCA  C GTGTC
                                   _     GT T
GAM287  SORBS1   3'  GCTAATGTGTTTCCTG      31157         G
                                CAGGAAGCA GTTGGC
                                ||||||||| ||||||
```

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                                GTCCTTTGT TAATCG
                                     G
GAM287  SOX4    3'  TTGGTTTTGTTTTATTTTGCTT 11882          TT__   T
            CTTG                    AGGAAGCAGG   GGCA AGCCAG
                                ||||||||||   |||| ||||||
                                TTCTTCGTTT   TTGT TTGGTT
                                     TATT   T
GAM287  SPG4    3'  CTAGTCTGTTGATCTGCCTTTT 30117      A     TG   TAGCCAG
            G                    CAGGA GCAGGT  GCA
                                ||||| ||||||  |||
                                GTTTT CGTCTA  TGT
                                   C     GT   CTGATC
GAM287  SPG4    3'  GTAGACTGTTAACTTCTTCCTG 30118       C       TAGCCAG
                                CAGGAAG AGGTTGGCA
                                ||||||| |||||||||
                                GTCCTTC TTCAATTGT
                                   _       CAGATGT
GAM287  SPON1   3'  GCCAGCCTCTTCCTG      62450       C
                                CAGGAAG AGGTTGGC
                                ||||||| ||||||||
                                GTCCTTC TCCGACCG
                                   _
GAM287  SRP46   3'  GTGCTGAGCTGCTTCCTG    49464         G TG
                                CAGGAAGCAG T  GCAT
                                |||||||||| |  ||||
                                GTCCTTCGTC A  CGTG
                                     G GT
GAM287  SULT1C1  5'  CTGCAATTGCCGTCTGCTTCCT 6465           T   TA_  CAG
            G                    CAGGAAGCAGGT GGCA   GC
                                ||||||||||| ||||   ||
                                GTCCTTCGTCTG CCGT   CG
                                      _   TAA  TC
GAM287  SYN2    3'  CTGGTTGTTTACCTGTTCCTG  12073      G    TG   TA
                                CAGGAA CAGGT  GCA  GCCAG
                                |||||| |||||  |||  |||||
                                GTCCTT GTCCA  TGT  TGGTC
                                   _    TT   __
GAM287  SYN3    3'  TGCCAGCCTGTTCTCTG    56095    GA
                                CAG  AGCAGGTTGGCA
                                |||  ||||||||||||
                                GTC  TTGTCCGACCGT
                                  TC
GAM287  SYN3    3'  TGCCAGCCTGTTCTCTG    56099    GA
                                CAG  AGCAGGTTGGCA
                                |||  ||||||||||||
                                GTC  TTGTCCGACCGT
                                  TC
GAM287  TACC1   3'  TGTGAGCTTGCTTTCTG    20803          G
                                CAGGAAGCAGGTT GCA
                                |||||||||||| |||
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                                GTCTTTCGTTCGA TGT
                                      G
GAM287  TCFL1    3'  TGCCTAATCTGTTTCTT     19996          _
                                AGGAAGCAGGTT GGCA
                                |||||||||||| ||||
                                TTCTTTGTCTAA CCGT
                                      T
GAM287  TCOF1    3'  TTGGTTGTGTTTTTTGTTTTTT 4487          TT
                                AGGAAGCAGG  GGCATAGCCAG
                                ||||||||||  ||||||||||
                                TTTTTTGTTT  TTGTGTTGGTT
                                      T_
GAM287  TCTE1L   3'  CTGGTGAACTTGCTATCTG   70972     A      G  A
                                CAGG AGCAGGTT GC TAG
                                |||| |||||||| || |||
                                GTCT TCGTTCAA TG GTC
                                  A      G  _
GAM287  TDG      5'  TTGGTTATAAGGTTTGCTTCT  12196       GG  GGC
                                GGAAGCA  TT   ATAGCCAG
                                |||||||  ||   ||||||||
                                TCTTCGT  GG   TATTGGTT
                                    TT  AA_
GAM287  TEM1     3'  TTGGCTCTCAGGAACTCTGCTT 39878         _  GGCAT_
           CCTG                   AGGAAGCAG GTT     AGCCAG
                                |||||||| |||     ||||||
                                TCCTTCGTC CAA     TCGGTT
                                      T   GGACTC
GAM287  TIMP4    3'  TGGCTTAGTCTGTTTTCT    12292         GT  GCAT
                                AGGAAGCAG  TG    AGCCA
                                |||||||||  ||   |||||
                                TCTTTTGTC  AT    TCGGT
                                      TG  _____
GAM287  TLX1     5'  TGGGAATGGTCGCTTCCTG   18634         AGGTT   ATAG_
                                CAGGAAGC    GGC    CCA
                                ||||||||    |||    |||
                                GTCCTTCG    CTG    GGT
                                    ______  GTAAG
GAM287  TNFRSF9  3'  ATGCAGGTTTGTTTTTTG    7786          GG TG
                                CAGGAAGCA  T  GCAT
                                |||||||||  |  ||||
                                GTTTTTTGT  G  CGTA
                                      TT GA
GAM287  TRAM     3'  GCTGTTAACCTACTTCCTG   26657        C       TA
                                CAGGAAG AGGTTGGCA  GC
                                |||||||  |||||||||  ||
                                GTCCTTC TCCAATTGT  CG
                                    A       __
GAM287  UNRIP    5'  GTCGACTGTTTCTTG       23202          G
                                CAGGAAGCAG TTGGC
                                |||||||||| |||||
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                                GTTCTTTGTC AGCTG
                                      _
GAM287  VAT1    3'  GTGCTGTCTGTTTCTTG    21047        GTT
                                CAGGAAGCAG  GGCAT
                                ||||||||||  |||||
                                GTTCTTTGTC  TCGTG
                                     TG_
GAM287  VPS41   3'  TGGGTTTGGCTTTTTTCTG   54659      C   TG C  AG
                                CAGGAAG AGGT  G AT  CCA
                                ||||||| ||||  | ||  |||
                                GTCTTTT TTCG  T TG  GGT
                                    _   GT _ __
GAM287  VPS41   3'  TGGGTTTGGCTTTTTTCTG   26929      C   TG C  AG
                                CAGGAAG AGGT  G AT  CCA
                                ||||||| ||||  | ||  |||
                                GTCTTTT TTCG  T TG  GGT
                                    _   GT _ __
GAM287  WNT5A   3'  GGGCTGCTAGCTTGCTTTCTG  12671            TA  AG
                                CAGGAAGCAGGTTGGCA  GCC
                                ||||||||||||||||  |||
                                GTCTTTCGTTCGATCGT  CGG
                                          __  GA
GAM287  WRB     3'  TTGTGCTCAACTTGTGTTTTG  16127      A      _
                                CAGGA GCAGGTTG GCATAG
                                ||||| |||||||| ||||||
                                GTTTT TGTTCAAC CGTGTT
                                   G       T
GAM287  XYLB    3'  CTGGTGGACGTGCTTCCTG   17560        G  G  A
                                CAGGAAGCA GTT GC TAG
                                ||||||||| ||| || |||
                                GTCCTTCGT CAG TG GTC
                                     G  G  _
GAM287  ABCA5   3'  TGTTCGGTCTGCTTACTG   37918    G    GT  _
                                CAG AAGCAG  TGG CA
                                ||| ||||||  ||| ||
                                GTC TTCGTC  GCT GT
                                  A     TG  T
GAM287  ABT1    3'  CTGGCCCTGCTCTGCTTCCTG  25375        GTT   TA
                                CAGGAAGCAG  GGCA  GCCAG
                                ||||||||||  ||||  |||||
                                GTCCTTCGTC  TCGT  CGGTC
                                     ____  CC
GAM287  ADAMTSL1 3'  CTGGTCATTCAATCTGTTTTTT 57687          C  AG
                                AGGAAGCAGGTTGG AT  CCAG
                                |||||||||||||| ||  ||||
                                TTTTTTGTCTAACT TA  GGTC
                                      _ CT
GAM287  ADNP    3'  CTGGTATTTCAGATCTGTTTTC 31045          GGCATA
           TG                  CAGGAAGCAGGTT    GCCAG
                               ||||||||||||     |||||
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                                GTCTTTTGTCTAG     TGGTC
                                      ACTTTA
GAM287  AGS3    3'  CTGGTGAGGTGACCTGCTTCT  73113          G ATA
                                GGAAGCAGGTTG C   GCCAG
                                |||||||||||| |   |||||
                                TCTTCGTCCAGT G   TGGTC
                                      _ GAG
GAM287  AP3M2   3'  GTTGTGTTGGTTTCTTTCTG   22315       C GG TG
                                CAGGAAG A  T  GCATAGC
                                ||||||| |  |  |||||||
                                GTCTTTC T  G  TGTGTTG
                                    _ TT GT
GAM287  API5    3'  GCAATCTTGACTTGTTTTT    21688         TG C  A
                                GGAAGCAGGT  G AT GC
                                ||||||||||  | || ||
                                TTTTTGTTCA  T TA CG
                                      GT C  A
GAM287  ARHGEF2  3'  CTGGGAGATAACCTGGCTTCCT 16361        _     GCATAG
           G                     CAGGAAGC AGGTTG     CCAG
                                ||||||||| ||||||     ||||
                                GTCCTTCG TCCAAT     GGTC
                                    G     AGAG__
GAM287  ARPC5   3'  TGTTGGCTGGTTTTTTG     19140        A   TG
                                CAGGAAGC GGT  GCA
                                |||||||| |||  |||
                                GTTTTTTG TCG  TGT
                                    G   GT
GAM287  ARPP-19  3'  GCCAACCTGCCTTCTG     21796      A
                                CAGGA GCAGGTTGGC
                                ||||| ||||||||||
                                GTCTT CGTCCAACCG
                                  C
GAM287  ATP9A   3'  GGGTTTTCAAGTTGCTTCTTG  62050         G   CAT   AG
                                CAGGAAGCAG TTGG   AGCC
                                |||||||||| ||||   ||||
                                GTTCTTCGTT AACT   TTGG
                                      G   T__   GT
GAM287  BIVM    3'  TGCCTCATTTGTTTCCTG    34668          T_
                                CAGGAAGCAGGT  GGCA
                                ||||||||||||  ||||
                                GTCCTTTGTTTA  CCGT
                                      CT
GAM287  BMF     3'  CTGGAATTCAGCTTGTGTTCTG 53156      A       CATAG
                                CAGGA GCAGGTTGG    CCAG
                                ||||| |||||||||    ||||
                                GTCTT TGTTCGACT    GGTC
                                  G       TAA__
GAM287  BPES    3'  CTGGTTGTACTGTAGCTTGTTG 43531     A      __  C
           TTTG                   AGG AGCAGGTT  GG ATAGCCAG
                                ||| ||||||||  || ||||||||
```

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                                TTT TTGTTCGA  TC TGTTGGTC
                                  G       TG  A
GAM287  C11orf14  3'  CTGGTTATGGCCATTGTTTTTT 40228         GT   _
                                AGGAAGCAG  TGGC ATAGCCAG
                                |||||||||  |||| ||||||||
                                TTTTTTGTT  ACCG TATTGGTC
                                     __    G
GAM287  C13orf1   3'  TGCTTTTGATTTGCTTTGTG   39980    G       ___
                                CA GAAGCAGGTT   GGCA
                                || ||||||||||   ||||
                                GT TTTCGTTTAG   TCGT
                                 G         TTT
GAM287  C1orf35   3'  TGGAGCAGCCGGCTTCCTG    44235        A    GCATAG
                                CAGGAAGC GGTTG     CCA
                                |||||||| |||||     |||
                                GTCCTTCG CCGAC     GGT
                                     G    GA____
GAM287  C1orf8    3'  CTGTAGCTATTTTGTTTTTTG  16831          T   _
                                CAGGAAGCAGG TGGC ATAG
                                |||||||||||| |||| ||||
                                GTTTTTTGTTT ATCG TGTC
                                       T    A
GAM287  C1QR1     3'  TTGTGTTTTGGTCTGTTCTTG  23847       G    TT __
                                CAGGAA CAGG  G  GCATAG
                                |||||| ||||  |  ||||||
                                GTTCTT GTCT  T  TGTGTT
                                    _    GG TT
GAM287  C20orf164 3'  CTGGTAAAAGGGCCTGTTTTC  79479          GGCATA
                                GGAAGCAGGTT     GCCAG
                                ||||||||||      |||||
                                CTTTTGTCCGG     TGGTC
                                       GAAAA_
GAM287  C20orf30  3'  TGCCAATTTGTTCTTG      26252       G
                                CAGGAA CAGGTTGGCA
                                |||||| ||||||||||
                                GTTCTT GTTTAACCGT

                                    _
GAM287  C20orf35  3'  TGCTAATTTTTTCCTG      37484        C
                                CAGGAAG AGGTTGGCA
                                ||||||| |||||||||
                                GTCCTTT TTTAATCGT

                                    _
GAM287  C6orf37   3'  TTGGCAGTATAATTTGTTTGTT 67482    G        GC  A
                                AG AAGCAGGTTG  AT GCCAG
                                || ||||||||||  || |||||
                                TT TTTGTTTAAT  TG CGGTT
                                 G         A_  A
GAM287  C9orf12   3'  TGGTTGTGAATGTTTTT     42795        GGTTGG
                                GGAAGCA     CATAGCCA
                                |||||||     ||||||||
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                                TTTTTGT     GTGTTGGT
                                    AA____
GAM287  C9orf5   3'  CTGGTTTCTTACTAGCTTTTTG 49274        A   T  CAT
                                CAGGAAGC GGT GG   AGCCAG
                                |||||||| ||| ||   ||||||
                                GTTTTTCG TCA TC   TTGGTC
                                    A   T  T__
GAM287  C9orf7   3'  GGCTTGCCTGCTTCT      34178          TGGCAT
                                GGAAGCAGGT     AGCC
                                ||||||||||     ||||
                                TCTTCGTCCG     TCGG
                                     T_____
GAM287  CACNG4   3'  CTGGCTATCCTCTTTGCTTCT  26953         TT  C
                                GGAAGCAGG  GG ATAGCCAG
                                |||||||||  || ||||||||
                                TCTTCGTTT  CC TATCGGTC
                                    CT  _
GAM287  caspr5   3'  TTGGTTTGTGGTGGTTTGCTTT 55384          TT G    _
            CT                    AGGAAGCAGG  G CATAG CCAG
                                |||||||||||  | ||||| ||||
                                TCTTTCGTTT  T GTGTT GGTT
                                     GG G    T
GAM287  CAT56    3'  TGGCACTGGTTGTTTTCTG   47520         G TT  CATA
                                CAGGAAGCA G  GG   GCCA
                                |||||||||  |  ||   ||||
                                GTCTTTTGT T  TC   CGGT
                                    _ GG  A___
GAM287  CBX6     3'  CTGTCTCTCTAGCTTGCTTCCT 26613             CAT  C
            G                     CAGGAAGCAGGTTGG   AG CAG
                                ||||||||||||||   || |||
                                GTCCTTCGTTCGATC   TC GTC
                                      TC_  T
GAM287  CGGBP1   3'  TGTTGGCTTTCTTCTTG     13365        C    TG
                                CAGGAAG AGGT  GCA
                                |||||||  ||||  |||
                                GTTCTTC TTCG  TGT
                                    T   GT
GAM287  COLEC12  3'  CTGTGCCTGCCCTGCTTCTTG  47866          TT_
                                CAGGAAGCAGG   GGCATAG
                                ||||||||||   |||||||
                                GTTCTTCGTCC   CCGTGTC
                                     CGT
GAM287  CPEB1    5'  ATGTCAATATGTTTTCTG    47596         G
                                CAGGAAGCA GTTGGCAT
                                |||||||||  ||||||||
                                GTCTTTTGT TAACTGTA
                                    A
GAM287  CRA      3'  TTGGTCTTGATTTGTTTT    21976         TG CATA
                                GAAGCAGGT  G   GCCAG
                                |||||||||  |   |||||
```

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                                TTTTGTTTA  T    TGGTT
                                     GT C___
GAM287  CREG     3'  TGGTTTGTTTGCTTGCTT    13897        TG   T
                                AAGCAGGT  GCA AGCCA
                                ||||||||  ||| |||||
                                TTCGTTCG  TGT TTGGT
                                     TT   _
GAM287  CREG     3'  TGTCACATGCTGGTTTGTTTGC 13898     _    GG TG    AGCCAG
           TTG                    CAGG AAGCA  T  GCAT
                                ||||| |||||  |  ||||
                                GTTC TTTGT  G  CGTA
                                  G    TT GT    CACTGTC
GAM287  D4ST-1   3'  CTGGTTTCAACGCCAGCTTTCT 55324        A   T GCAT
           G                     CAGGAAGC GGT G    AGCCAG
                                |||||||| ||| |    ||||||
                                GTCTTTCG CCG C    TTGGTC
                                     A   _ AACT
GAM287  DKFZP434B044 3'  TGGCCCACCTGTTTTCTG    48931          T  CATA
                                CAGGAAGCAGGT GG    GCCA
                                ||||||||||| ||    ||||
                                GTCTTTTGTCCA CC    CGGT
                                     _ _____
GAM287  DKFZp434J0226 5'  CTGGCTGTCTTGGCCGCTTTCT 72334        A   TG C
           G                     CAGGAAGC GGT  G ATAGCCAG
                                |||||||| |||  | ||||||||
                                GTCTTTCG CCG  T TGTCGGTC
                                     _  GT C
GAM287  DKFZP434O125 3'  TTGGGACTAGTCTGTATCTTG  64964      A    GT   CATAG
                                CAGGA GCAG  TGG     CCAG
                                ||||| ||||  |||     ||||
                                GTTCT TGTC  ATC     GGTT
                                   A    TG   AG___
GAM287  DKFZp547C176 3'  TGACTAGTTTGTTTTCT     67232        GG   _
                                AGGAAGCA  TTGG CA
                                ||||||||  |||| ||
                                TCTTTTGT  GATC GT
                                     TT    A
GAM287  DKFZp547D155 3'  TTGGCCCCAGTTTGCATTCTG  70440      A   GG    CATA
                                CAGGA GCA  TTGG    GCCAG
                                ||||| |||  ||||    |||||
                                GTCTT CGT  GACC    CGGTT
                                   A   TT    C___
GAM287  DKFZp547I224 5'  CTGGCTCAGCATCTGCTTCT   39557         TG  AT
                                GGAAGCAGGT  GC  AGCCAG
                                ||||||||||  ||  ||||||
                                TCTTCGTCTA  CG  TCGGTC
                                     __  AC
GAM287  DKFZp564A176 3'  TGCCGCCACTTGCTTCCTG    49973           __
                                CAGGAAGCAGGT  TGGCA
                                ||||||||||||  |||||
```

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                                GTCCTTCGTTCA  GCCGT
                                      CC
GAM287  DKFZP564C1940 5'  CTGGTGCCACAGCCTGCTACCT 25901      A       GCATA
          G                    CAGG AGCAGGTTG     GCCAG
                               |||| |||||||||     |||||
                               GTCC TCGTCCGAC     TGGTC
                                 A        ACCG_
GAM287  DKFZp761N0624 3'  TGGCACAACCAGCTTCCTG    50183        A     GCATA
                               CAGGAAGC GGTTG     GCCA
                               |||||||| |||||     ||||
                               GTCCTTCG CCAAC     CGGT
                                    A     A____
GAM287  DKFZp762K222 5'  CTGGGCGGCTGTCCTGCTTCCT 71117          T    ATAG
          G                    CAGGAAGCAGG TGGC    CCAG
                               |||||||||| ||||    ||||
                               GTCCTTCGTCC GTCG    GGTC
                                      T    GCG_
GAM287  DKK2     3'  TTGGCCATAACCTGTATTTTG  27020       A       GCATA
                               CAGGA GCAGGTTG     GCCAG
                               ||||| ||||||||     |||||
                               GTTTT TGTCCAAT     CGGTT
                                  A       AC___
GAM287  DNAJC6   3'  ATTCCAATTGCTTTTTG     28844          G    C
                               CAGGAAGCAG TTGG AT
                               |||||||||| |||| ||
                               GTTTTTCGTT AACC TA
                                     _    T
GAM287  DNAL4    5'  TGGCAGGGCCTGCTTCCTG    19220            GGCATA
                               CAGGAAGCAGGTT      GCCA
                               ||||||||||||      ||||
                               GTCCTTCGTCCGG     CGGT
                                      GA____
GAM287  DOK4     3'  TTGGTTGTGTGGGGTTTTTTG  36185         AGG  G
                               CAGGAAGC   TT GCATAGCCAG
                               ||||||||   || ||||||||||
                               GTTTTTTG   GG TGTGTTGGTT
                                    ___  G
GAM287  EFS2     3'  AGCTGCCTCCCTGACTCTGCTT 19618       _  _____    TAGCCAG
          CTTG                   AAGCAG GTT     GGCA
                               |||||| |||     ||||
                               TTCGTC CAG     CCGT
                                  T   TCCCT    C   GAC
GAM287  EML4     3'  TTGGTTTCCATGTGATTTGTTT 38815           G  ___
          TCT                    GGAAGCAGGTTG CAT   AGCCAG
                               |||||||||||| |||   ||||||
                               CTTTTGTTTAGT GTA   TTGGTT
                                     _  CCT
GAM287  FBXL9    3'  CTGGCCTTGACCCGGGTTGCTT 24082         G   __ TA
          TTTG                   AGGAAGCAG TTGG  CA  GCCAG
                               |||||||| ||||  ||  |||||
```

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                                TTTTTCGTT GGCC  GT  CGGTC
                                     G   CA  TC
GAM287  FHX     3'  TTGGCCCTAAATTGTTTTTTG  37312         G   CATA
                                CAGGAAGCAG TTGG   GCCAG
                                |||||||||| ||||   |||||
                                GTTTTTTGTT AATC   CGGTT
                                     A   C___
GAM287  FKBP9   3'  TGCCGGCCTGATTCCTG    94072       G
                                CAGGAA CAGGTTGGCA
                                |||||| ||||||||||
                                GTCCTT GTCCGGCCGT
                                   A
GAM287  FLJ00024  5'  TCCTTATGCAAGTTTGCTTCCT 63770         GG  G     CCAG
           G                     CAGGAAGCA  TT GCATAG
                                |||||||||  || ||||||
                                GTCCTTCGT  GA CGTATT
                                     TT  A     CCTT
GAM287  FLJ10346  5'  TGGCTAATTTTGTTTTT     36051         TTGGCA
                                GGAAGCAGG     TAGCCA
                                |||||||||     ||||||
                                TTTTTGTTT     ATCGGT
                                     TA____
GAM287  FLJ10407  3'  CTGTACCGATTGCTTTTTG   36090         G   C
                                CAGGAAGCAG TTGG ATAG
                                |||||||||| |||| ||||
                                GTTTTTCGTT AGCC TGTC
                                     _   A
GAM287  FLJ10618  5'  GAGGGCTGTGCCGGTTGCTTTC 36346         G TT       AG
           TG                    CAGGAAGCA G  GGCATAGCC
                                ||||||||| |  |||||||||
                                GTCTTTCGT T  CCGTGTCGG
                                     _ GG       GAGG
GAM287  FLJ11274  5'  TGGTGGGCTGGTTTCCTG    37201         AGGT   ATA
                                CAGGAAGC   TGGC   GCCA
                                ||||||||   ||||  ||||
                                GTCCTTTG   GTCG   TGGT
                                     _____   GG_
GAM287  FLJ12581  3'  TTGGTTGTGCTAATCT     45882
                                AGGTTGGCATAGCCAG
                                ||||||||||||||||
                                TCTAATCGTGTTGGTT

GAM287  FLJ12700  3'  GGAGGATTGCTGGCTGGTTTCC 46119         A  TG   TAG  AG
           TG                    CAGGAAGC GGT  GCA   CC
                                ||||||||| |||  |||   ||
                                GTCCTTTG TCG  CGT   GG
                                     G   GT   TA_  AGGG
GAM287  FLJ12787  3'  CTGGGCCCTTGCTTAGCTTGCT 49748           _   TA_   AG
           TCCTG                   GGAAGCAGGTTG GCA   GCC
                                ||||||||||| |||   |||
```

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                                CCTTCGTTCGAT CGT   CGG
                                      T   TCC   GTC
GAM287  FLJ13263  3' CTGGAGGACTGCCTGCTTGCTT 47092          T    TAG__
             TCTG                 AGGAAGCAGGT GGCA     CCAG
                                  |||||||||| ||||     ||||
                                  TCTTTCGTTCG CCGT     GGTC
                                        T    CAGGA
GAM287  FLJ13456  3' CTTTTGTGTTAATCTGTTTTCT 65938               CCAG
                                  AGGAAGCAGGTTGGCATAG
                                  ||||||||||||||||||
                                  TCTTTTGTCTAATTGTGTT
                                              TTC
GAM287  FLJ13456  3' TGTTGACCTGATTTCTG     65947       G     TG
                                  CAGGAA CAGGT  GCA
                                  |||||| |||||  |||
                                  GTCTTT GTCCA  TGT
                                     A     GT
GAM287  FLJ13769  3' CCATAAATGTTGATTTCCTTTC 46607        C    TG    AGCCAG
             TG                    CAGGAAG AGGT  GCAT
                                   ||||||| ||||  ||||
                                   GTCTTTC TTTA  TGTA
                                      C    GT    AATACCT
GAM287  FLJ13910  3' GTTGGGTTTTTGTTTGTTTGTT 42929          TT    T_    AG
             TTTTG                 AGGAAGCAGG  GGCA  AGCC
                                   ||||||||||  ||||  ||||
                                   TTTTTTGTTT  TTGT  TTGG
                                         GT    TT    GTTGG
GAM287  FLJ14007  3' TTGGCTGTGACACTGCTTTGTG 45212     G      GTTGG
                                  CA GAAGCAG     CATAGCCAG
                                  || |||||||     |||||||||
                                  GT TTTCGTC     GTGTCGGTT
                                   G      ACA__
GAM287  FLJ14107  5' TTGGCTAGAATGGCTTGTTCCT 46702        G      GCA
             G                     CAGGAA CAGGTTG   TAGCCAG
                                   |||||| |||||||   |||||||
                                   GTCCTT GTTCGGT   ATCGGTT
                                      _      AAG
GAM287  FLJ14251  3' TTGGTTCCCTGACCTGTTTTT  45981          TG CAT
                                  GGAAGCAGGT  G   AGCCAG
                                  ||||||||||  |   ||||||
                                  TTTTTGTCCA  C   TTGGTT
                                        GT CC_
GAM287  FLJ14280  3' TGCCGGCCAGTTTCCTG     46000         A
                                  CAGGAAGC GGTTGGCA
                                  |||||||| ||||||||
                                  GTCCTTTG CCGGCCGT
                                     A
GAM287  FLJ14549  3' CTGGCCGAGGCATTGCTTTCTG 51442          GGTTG  ATA_
                                  CAGGAAGCA    GC    GCCAG
                                  |||||||||    ||    |||||
```

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                                GTCTTTCGT    CG   CGGTC
                                     TA___  GAGC
GAM287  FLJ20040  3' TTGGCTGTGAGAAGAAACCTGC 38635        GG____
             TTTT                 AAGCAGGTT     CATAGCCAG
                                |||||||||     |||||||||
                                TTCGTCCAA     GTGTCGGTT
                                     AGAAGA
GAM287  FLJ20208  3' ATGCCAGCTTTTTTTTTG    34742        C
                                CAGGAAG AGGTTGGCAT
                                ||||||| ||||||||||
                                GTTTTTT TTCGACCGTA
                                     T
GAM287  FLJ20275  3' TGGCTGTGTTTGTCTTCTG   34828      AG   GTTG
                                CAGGA  CAG   GCATAGCCA
                                |||||  |||   |||||||||
                                GTCTT  GTT   TGTGTCGGT
                                   CT  _____
GAM287  FLJ20298  3' CTGTAGCTGTCAGTTTGATTCC 34901       G  GG     TA __
             TG                   CAGGAA CA  TTGGCA  GC  CAG
                                |||||| ||  ||||||  ||  |||
                                GTCCTT GT  GACTGT  CG  GTC
                                   A  TT      __  AT
GAM287  FLJ20716  3' CTGGCTAAGATTTTGTTTGCTT 35604      _      TTGGCA
             G                    CAGG AAGCAGG     TAGCCAG
                                |||| |||||||     |||||||
                                GTTC TTTGTTT     ATCGGTC
                                  G      TAGA__
GAM287  FLJ21736  5' GTTTGTGTGTTTGTTTGTTTTT 46232          TT     GCCAG
             TG                   CAGGAAGCAGG  GGCATA
                                ||||||||||  ||||||
                                GTTTTTTGTTT  TTGTGT
                                      GT     GTTTGT
GAM287  FLJ21918  3' TGGTAGCTTCTTTCTG      46291        C     G
                                CAGGAAG AGGTTG CA
                                ||||||| |||||| ||
                                GTCTTTC TTCGAT GT
                                   _     G
GAM287  FLJ21934  3' TGGCTCATCTGGCTTTTTG    45362        A  T  GCAT
                                CAGGAAGC GG TG    AGCCA
                                |||||||| || ||    |||||
                                GTTTTTCG TC AC    TCGGT
                                     G  T  _____
GAM287  FLJ21939  5' CTGGCGACCCGGTTTGTTTTC  42411       GG   CATA
                                GGAAGCA  TTGG   GCCAG
                                |||||||  ||||   |||||
                                CTTTTGT  GGCC   CGGTC
                                     TT   CAG_
GAM287  FLJ22127  3' CTGGTGCCCAGCTTGCTTCT   42885           CATA
                                GGAAGCAGGTTGG   GCCAG
                                ||||||||||||   |||||
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                                TCTTCGTTCGACC   TGGTC
                                      CG__
GAM287  FLJ22283  5' CTGGCTGTGCTGTGGTTTCT  49916      AGGT
                                GGAAGC   TGGCATAGCCAG
                                ||||||   ||||||||||||
                                TCTTTG   GTCGTGTCGGTC
                                   GT__
GAM287  FLJ22479  3' CTGGCCCCCACTTTGTTTCTTG 46073         T  CATA
                                CAGGAAGCAGG TGG   GCCAG
                                |||||||||||| |||   |||||
                                GTTCTTTGTTT ACC   CGGTC
                                      C  CC__
GAM287  FLJ23091  3' TGTCAGTTTGCCTTCTG    46126      A  GG
                                CAGGA GCA  TTGGCA
                                ||||| |||  ||||||
                                GTCTT CGT  GACTGT
                                   C  TT
GAM287  FLJ23360  3' GCTCTAAGCTGCTTTCTG    43570        G   CAT
                                CAGGAAGCAG TTGG   AGC
                                |||||||||| ||||   |||
                                GTCTTTCGTC AATC   TCG
                                      G   ___
GAM287  FLJ23560  3' TTGGCTAAGTGTGTCTGTTTTT 45194        TTG  A
           T                     AGGAAGCAGG   GC TAGCCAG
                                ||||||||||   || |||||||
                                TTTTTTGTCT   TG ATCGGTT
                                      GTG  A
GAM287  FLJ23563  3' TAAAATTGCTAGTTTCTTTCTG 67597       C GG     TAGCCAG
                                CAGGAAG A  TTGGCA
                                ||||||| |  ||||||
                                GTCTTTC T  GATCGT
                                   _ TT     TAAAATT
GAM287  FLJ23590  5' GGGCTGCTGGTCTGCTTCCTG  45021        TT   TA  AG
                                CAGGAAGCAGG  GGCA  GCC
                                ||||||||||  ||||  |||
                                GTCCTTCGTCT  TCGT  CGG
                                      GG   __  GG
GAM287  FXYD3    3' CTGGCACTGAGCCTGCTTGTTG 41585    G       GG  TA
                                CAG AAGCAGGTT  CA  GCCAG
                                ||| |||||||||  ||  |||||
                                GTT TTCGTCCGA  GT  CGGTC
                                  G        __  CA
GAM287  FXYD3    3' CTGGCACTGAGCCTGCTTGTTG 19925    G       GG  TA
                                CAG AAGCAGGTT  CA  GCCAG
                                ||| |||||||||  ||  |||||
                                GTT TTCGTCCGA  GT  CGGTC
                                  G        __  CA
GAM287  GMPPB    3' TGGTCCCCAACCTGCCTTCTG  95756      A       CATA   G
                                CAGGA GCAGGTTGG   GCCA
                                ||||| |||||||||   ||||
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                                GTCTT CGTCCAACC    TGGT
                                   C       CC__    G
GAM287  GOLGB1   3'  CTGGCGAGTCTGCTTTCT    15632         GT G  A
                                AGGAAGCAG  T GC TAG
                                |||||||||  | || |||
                                TCTTTCGTC  A CG GTC
                                     TG G  _
GAM287  GPA33    3'  TTGGTTGTGCCTTCCCTTCTCT 19460    _    CA  TT
           G                     CAG GAAG  GG  GGCATAGCCAG
                                |||  ||||  ||  ||||||||||
                                GTC CTTC  CC  CCGTGTTGGTT
                                  T    __  TT
GAM287  GRWD     3'  CTGGCTCTGATCTTGCTTCCTG 48964          TTGG  T
                                CAGGAAGCAGG    CA AGCCAG
                                ||||||||||    || ||||||
                                GTCCTTCGTTC    GT TCGGTC
                                       TA__  C
GAM287  H17      3'  CTGGCTCCACTGGCTTGCATCC 34088       A     TG CAT
           TG                    CAGGA GCAGGT  G   AGCCAG
                                ||||| ||||||  |   ||||||
                                GTCCT CGTTCG  C   TCGGTC
                                   A     GT ACC
GAM287  H17      3'  CTGGCTGTGTTCACAGCCTTGT 34089      _    ____
           TTGCTG                 AAGCA GGTTG   GCATAGCCAG
                                ||||| |||||   ||||||||||
                                TTTGT CCGAC   TGTGTCGGTC
                                   T     ACT
GAM287  H2AV     3'  TGGCATGGCCCTGTTTCCTG   56861          TTG  ATA   G
                                CAGGAAGCAGG   GC   GCCA
                                ||||||||||   ||   ||||
                                GTCCTTTGTCC   CG   CGGT
                                      ___  GTA   G
GAM287  HOOK3    3'  GCCAGCTTATTTTTTG      50549        C
                                CAGGAAG AGGTTGGC
                                ||||||| ||||||||
                                GTTTTTT TTCGACCG
                                     A
GAM287  HSNOV1   3'  CTGTGCCTGGCCTGTTTGTT   34008    G       _
                                AG AAGCAGGTT GGCATAG
                                || |||||||| |||||||
                                TT TTTGTCCGG CCGTGTC
                                  G       T
GAM287  HSPC129  3'  TGGTGAAATTTGCATTTTG    33074      A      GGCATA
                                CAGGA GCAGGTT     GCCA
                                ||||| |||||||     ||||
                                GTTTT CGTTTAA     TGGT
                                   A      AG____
GAM287  HSRNAFEV 3'  CTGGTACTAGATTTGCTCCTG  34022      A      GGCATA
                                CAGGA GCAGGTT     GCCAG
                                ||||| |||||||     |||||
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                                GTCCT CGTTTAG     TGGTC
                                  _      ATCA__
GAM287  HT002    3'  TTGGACTGTCCAACTTGCTTCC 25951           C   _
                                GGAAGCAGGTTGG ATAG CCAG
                                |||||||||||| |||| ||||
                                CCTTCGTTCAACC TGTC GGTT
                                       _   A
GAM287  HTCD37   3'  CTGGTATTCTGTGATCTGCCTC 67675     A      G  TA__
           TTG                   AGGA GCAGGTTG CA   GCCAG
                                |||| |||||||| ||   |||||
                                TTCT CGTCTAGT GT   TGGTC
                                  C       _ CTTA
GAM287  HUMGT198A 3'  TGGCTACCTTGTTTTT     33334         TTGGCA
                                GGAAGCAGG     TAGCCA
                                |||||||||     ||||||
                                TTTTTGTTC     ATCGGT
                                     C_____
GAM287  HUMGT198A 3'  TGGCTACCTTGTTTTT     25238         TTGGCA
                                GGAAGCAGG     TAGCCA
                                |||||||||     ||||||
                                TTTTTGTTC     ATCGGT
                                     C_____
GAM287  HUMNPIIY20 3'  CTGGTGGTGGCCTGCTACCTG  83345     A      TGG   A
                                CAGG AGCAGGT   CAT GCCAG
                                |||| |||||||   ||| |||||
                                GTCC TCGTCCG   GTG TGGTC
                                  A      ___   G
GAM287  HZFW1    3'  CTGGCCCTGCAGCTGCTTTTTG 47461         GTTG   TA
                                CAGGAAGCAG    GCA  GCCAG
                                ||||||||||    |||  |||||
                                GTTTTTCGTC    CGT  CGGTC
                                     GA__   CC
GAM287  KIAA0057 3'  TGCTTGCTCTGTTTCTTG    24443          _  T
                                CAGGAAGCAG GT GGCA
                                |||||||||| || ||||
                                GTTCTTTGTC CG TCGT
                                     T  T
GAM287  KIAA0186 3'  TTGGCTATGTTAAGTCCTTTGC 40767      __ __
           TTTT                   AAGCA  GG  TTGGCATAGCCAG
                                |||||  ||  ||||||||||||||
                                TTCGT  CC  AATTGTATCGGTT
                                   TT  TG
GAM287  KIAA0226 3'  GTTAACCTGGCTTTTTG     63522        _
                                CAGGAAGC AGGTTGGC
                                |||||||| ||||||||
                                GTTTTTCG TCCAATTG
                                     G
GAM287  KIAA0232 3'  TTGGCTGCTGCAGCTAGCCGCT 72765      A      A____
           TCTTG                   AAGC GGTTGGC     TAGCCAG
                                |||| |||||||     |||||||
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                                TTCG CCGATCG    GTCGGTT
                                  _     ACGTC
GAM287  KIAA0237  3'  GTGGTCTCTGCTTTGTTTTCTG 28536        GTT   T _  G
                                CAGGAAGCAG  GGCA AG CCA
                                ||||||||||  |||| || |||
                                GTCTTTTGTT  TCGT TC GGT
                                      ___   C  T   GG
GAM287  KIAA0265  3'  CTGGTTTGTTTGATTTGTTTTT 69878         TG _  T
          T                      AGGAAGCAGGT  G CA AGCCAG
                                ||||||||||  | || ||||||
                                TTTTTTGTTTA  T GT TTGGTC
                                      GT T  _
GAM287  KIAA0295  3'  TGCCCAGCATTGTTTTCTG   68110         _    _
                                CAGGAAGCAG GTTGG CA
                                |||||||||| ||||| ||
                                GTCTTTTGTT CGACC GT
                                      A    C
GAM287  KIAA0332  3'  TTGGAAATGCGATTTGTTTTGT 62708   G       G   AG
          G                     CA GAAGCAGGTTG CAT  CCAG
                                || |||||||||| |||  ||||
                                GT TTTTGTTTAGC GTA  GGTT
                                 G        _  AA
GAM287  KIAA0427  3'  GTCCCAGTCTGTTTTCTG    28722        GT   C
                                CAGGAAGCAG  TGG AT
                                |||||||||  ||| ||
                                GTCTTTTGTC  ACC TG
                                      TG   C
GAM287  KIAA0444  3'  CTGGTTCCTGTCCTGTTTTCTG 62340        TT_  CAT
                                CAGGAAGCAGG   GG   AGCCAG
                                ||||||||||   ||   ||||||
                                GTCTTTTGTCC   CC   TTGGTC
                                      TGT  ___
GAM287  KIAA0444  3'  TGCTGCCTTGTTTCCTG     62349         TT
                                CAGGAAGCAGG  GGCA
                                ||||||||||  ||||
                                GTCCTTTGTTC  TCGT
                                      CG
GAM287  KIAA0446  5'  TGCCCTTTGGCCTGTTCCTG   68881       G    ____
                                CAGGAA CAGGTT    GGCA
                                ||||||  ||||||    ||||
                                GTCCTT GTCCGG    CCGT
                                  _     TTTC
GAM287  KIAA0478  5'  TCCATGTGCCACTTGTTTCTTG 29558          T    GCCAG
                                CAGGAAGCAGGT GGCATA
                                |||||||||||| ||||||
                                GTTCTTTGTTCA CCGTGT
                                      _     ACCTT
GAM287  KIAA0483  3'  GTTAACTTTTTTCTG       30792        C
                                CAGGAAG AGGTTGGC
                                ||||||| ||||||||
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                                GTCTTTT TTCAATTG
                                     _
GAM287  KIAA0543 3' GTGCATGACCTGTTTCCTG   68939          _
                                CAGGAAGCAGGTTG GCAT
                                |||||||||||||| ||||
                                GTCCTTTGTCCAGT CGTG
                                      A
GAM287  KIAA0546 3' CTGTTTGGCCTGCTTCT    71309        TG C
                                GGAAGCAGGT  G ATAG
                                ||||||||||  | ||||
                                TCTTCGTCCG  T TGTC
                                     GT _
GAM287  KIAA0747 3' CTGAGCTGGCTGTTTCCTG   30964        G TG  A
                                CAGGAAGCAG T  GC TAG
                                |||||||||| |  || |||
                                GTCCTTTGTC G  CG GTC
                                     _ GT  A
GAM287  KIAA0759 3' CTGGTAGATTTGACTTGCTCTT 67322     A     TG CATA
          G                      CAGGA GCAGGT  G   GCCAG
                                ||||| ||||||  |   |||||
                                GTTCT CGTTCA  T   TGGTC
                                   _    GT TAGA
GAM287  KIAA0779 3' CTGGCTGCTGCTGCTGCTTTTT 85726        GTT   _
          G                      CAGGAAGCAG   GGCA TAGCCAG
                                ||||||||||   |||| |||||||
                                GTTTTTCGTC   TCGT GTCGGTC
                                     G__   C
GAM287  KIAA0819 3' TGGCTGTGCCCCTTTTTTC   63582     C   TT
                                GGAAG AGG  GGCATAGCCA
                                ||||| |||  ||||||||||
                                CTTTT TCC  CCGTGTCGGT
                                   T  __
GAM287  KIAA0937 3' TGCCTCAGCCGGCTTCTTG   91593       A   __
                                CAGGAAGC GGTT  GGCA
                                |||||||| ||||  ||||
                                GTTCTTCG CCGA  CCGT
                                     G   CT
GAM287  KIAA0964 5' CTGTCCCAAGCTGCTTCCTG  29762        G   C
                                CAGGAAGCAG TTGG ATAG
                                |||||||||| |||| ||||
                                GTCCTTCGTC AACC TGTC
                                     G   C
GAM287  KIAA0976 3' CTAGCTTACCTGTTTCCTG   29890         T  A
                                CAGGAAGCAGGT GGC TAG
                                |||||||||||| ||| |||
                                GTCCTTTGTCCA TCG ATC
                                     T  _
GAM287  KIAA1026 3' TTGGTTCGTCGGTTTGTTTTT 71218      GG    AT
                                GGAAGCA  TTGGC  AGCCAG
                                |||||||  |||||  ||||||
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                              TTTTTGT  GGCTG  TTGGTT
                                 TT    C_
GAM287  KIAA1034 3' TGTTAGTTTGTTTTTTG    62472        GG
                              CAGGAAGCA  TTGGCA
                              |||||||||  ||||||
                              GTTTTTTGT  GATTGT
                                 TT
GAM287  KIAA1034 3' TGTTAGTTTGTTTTTTG    62473        GG
                              CAGGAAGCA  TTGGCA
                              |||||||||  ||||||
                              GTTTTTTGT  GATTGT
                                 TT
GAM287  KIAA1091 3' TGCTGATTTGCTTTTT     69688         TG
                              AGGAAGCAGGT  GCA
                              ||||||||||  |||
                              TTTTTCGTTTA  CGT
                                  GT
GAM287  KIAA1128 3' TGCCAATTTGTTTCTT     68488
                              AGGAAGCAGGTTGGCA
                              ||||||||||||||||
                              TTCTTTGTTTAACCGT

GAM287  KIAA1165 3' TGGTTATTCCTGTTTTCT    67409         TTGGC
                              AGGAAGCAGG    ATAGCCA
                              |||||||||    |||||||
                              TCTTTTGTCC    TATTGGT
                                 T____
GAM287  KIAA1198 3' CTGGTTATTTTGTTTGTTTGTT 63306    G     TT  C
           G                   CAG AAGCAGG  GG ATAGCCAG
                              ||| |||||||  || ||||||||
                              GTT TTTGTTT  TT TATTGGTC
                                G      GT  _
GAM287  KIAA1223 3' TTGTAGTGTATGGCCTGTTTCT 71149          TG_   A  CAG
           TG                    CAGGAAGCAGGT   GCAT GC
                              ||||||||||||  |||| ||
                              GTTCTTTGTCCG   TGTG TG
                                    GTA    A  TT
GAM287  KIAA1228 3' TTGGAGCTTTTAGCTTGTTTC  65053          CATAG
                              GAAGCAGGTTGG    CCAG
                              ||||||||||||    ||||
                              CTTTGTTCGATT    GGTT
                                    TTCGA
GAM287  KIAA1254 3' GCCAAGTTTGTTTCTT      70018         _
                              AGGAAGCAGG TTGGC
                              |||||||||| |||||
                              TTCTTTGTTT AACCG
                                    G
GAM287  KIAA1254 3' TGCTGACTTGTTTTCT      70027          TG
                              AGGAAGCAGGT  GCA
                              ||||||||||  |||
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                                TCTTTTGTTCA  CGT
                                      GT
GAM287  KIAA1257 3' CTGGCTATTTTTTTTATTTTCT 62738       C   TT  C
            G                  CAGGAAG AGG  GG ATAGCCAG
                               ||||||| |||  || ||||||||
                               GTCTTTT TTT  TT TATCGGTC
                                   A   TT  _
GAM287  KIAA1280 5' TTGGGGCTGGTTTGGTTTTTG  69734       G  GG TG  ATAG
                               CAGGAA CA  T  GC    CCAG
                               |||||| ||  |  ||    ||||
                               GTTTTT GT  G  CG    GGTT
                                  G  TT GT  G___
GAM287  KIAA1372 3' TGGCTGTCCTGTTTGTTT    91654        TT  C
                               AAGCAGG  GG ATAGCCA
                               |||||||  || |||||||
                               TTTGTTT  CC TGTCGGT
                                   GT  _
GAM287  KIAA1391 3' TTGGTTGTATTTGTCGGTTTGT 67267      GG    _____
            TTTTT                  AAGCA  TTGGCA    TAGCCAG
                               |||||  ||||||   |||||||
                               TTTGT  GGCTGT    GTTGGTT
                                  TT     TTAT
GAM287  KIAA1416 3' CTGGTGAACAGCCTGTTTGCTG 86458     G        GCATA
                               CAG AAGCAGGTTG    GCCAG
                               ||| ||||||||||    |||||
                               GTC TTTGTCCGAC    TGGTC
                                 G        AAG__
GAM287  KIAA1443 3' GCTGTCAATTTGTTTCC     63836             TA
                               GGAAGCAGGTTGGCA  GC
                               ||||||||||||||  ||
                               CCTTTGTTTAACTGT  CG
                                          __
GAM287  KIAA1456 3' TTGGTTGTTTTTGTTTTC    67010         TTGGC
                               GGAAGCAGG    ATAGCCAG
                               |||||||||    ||||||||
                               CTTTTGTTT    TGTTGGTT
                                    T____
GAM287  KIAA1466 3' TTGCTTCTGTAAGCCTGCTTCC 71920           G  T_  CAG
            TG                   CAGGAAGCAGGTT GCA  AGC
                               |||||||||||| |||  |||
                               GTCCTTCGTCCGA TGT  TCG
                                       A   CT   TT
GAM287  KIAA1535 3' CTGGTTATCTTCCTGTTCCTG  79411       G   TT  C
                               CAGGAA CAGG  GG ATAGCCAG
                               |||||| ||||  || ||||||||
                               GTCCTT GTCC  TC TATTGGTC
                                  _   T_  _
GAM287  KIAA1549 3' TGCTGCTTTGTTTTCTG     69348          TT
                               CAGGAAGCAGG  GGCA
                               ||||||||||  ||||
```

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                                GTCTTTTGTTT  TCGT
                                      CG
GAM287  KIAA1553  3'  TTGGTTTTTAGTTGTTTGTTTT 91923        GG TGGCAT_
              TTG                  CAGGAAGCA  T      AGCCAG
                                   |||||||||  |      ||||||
                                   GTTTTTTGT  G      TTGGTT
                                        TT TTGATTT
GAM287  KIAA1554  3'  GTGTCAGTCTCTTTCTG     95154        C  GT
                                   CAGGAAG AG  TGGCAT
                                   |||||||  ||  ||||||
                                   GTCTTTC TC  ACTGTG
                                       _  TG
GAM287  KIAA1608  3'  TTGGTTGGTTGGTTTGTTGTTT 45690      A    GG TG  A
              G                     CAGG AGCA  T  GC TAGCCAG
                                   ||||  ||||  |  ||  |||||||
                                   GTTT TTGT  G  TG GTTGGTT
                                     G    TT GT  _
GAM287  KIAA1706  3'  GCCAGATTGCTTTTTG      92788          G
                                   CAGGAAGCAG TTGGC
                                   ||||||||||  |||||
                                   GTTTTTCGTT GACCG
                                         A
GAM287  KIAA1729  3'  TGCTTTAATTTGTGTTCTG    89133       A      __
                                   CAGGA GCAGGTT  GGCA
                                   |||||  |||||||  ||||
                                   GTCTT TGTTTAA  TCGT
                                      G      TT
GAM287  KIAA1786  3'  CTGGGAGGGGTTGATTTCTTCT 66027        C    TG  ATAG_
              TG                     CAGGAAG AGGT  GC     CCAG
                                   |||||||  ||||  ||     ||||
                                   GTTCTTC TTTA  TG     GGTC
                                       _    GT  GGGAG
GAM287  KIAA1805  3'  TTGGTTGTCCTTTCCTTCCTG  79971        CA  TT  C
                                   CAGGAAG  GG  GG ATAGCCAG
                                   |||||||  ||  ||  ||||||||
                                   GTCCTTC  CT  CC TGTTGGTT
                                       __  TT  _
GAM287  KIAA1956  3'  CTGAACCCCTGGCCTGTTCCT  78434       G     TG CATAGC
                                   AGGAA CAGGT  G      CAG
                                   |||||  |||||  |      |||
                                   TCCTT GTCCG  C      GTC
                                      _     GT CCCAA_
GAM287  LIMK2     3'  TGGCTGGTTGTTTCCTG     33630          GGTTG  A
                                   CAGGAAGCA     GC TAGCCA
                                   |||||||||     || ||||||
                                   GTCCTTTGT     TG GTCGGT
                                                 ______  _
GAM287  LIMK2     3'  TGGCTGGTTGTTTCCTG     18730          GGTTG  A
                                   CAGGAAGCA     GC TAGCCA
                                   |||||||||     || ||||||
```

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                              GTCCTTTGT    TG GTCGGT
                                    _____ _
GAM287  LRP1B    3' GGTTAATTGTTTTCTG     37672         GTTGGCA
                              CAGGAAGCAG     TAGCC
                              ||||||||||     |||||
                              GTCTTTTGTT     ATTGG
                                   A_______
GAM287  LRP1B    5' GGTTGTTTTGCTTTCTG    37673          TTGGC
                              CAGGAAGCAGG    ATAGCC
                              ||||||||||    ||||||
                              GTCTTTCGTTT    TGTTGG
                                    _____
GAM287  MGC10986 3' GCCCACCACCCTGCTTCCTG  47563          T  CATA
                              CAGGAAGCAGG TGG   GC
                              |||||||||| |||   ||
                              GTCCTTCGTCC ACC   CG
                                    C  ACC_
GAM287  MGC11316 3' GCCTCCAACCTGCTTCT    51941           CATA
                              GGAAGCAGGTTGG   GC
                              ||||||||||||    ||
                              TCTTCGTCCAACC   CG
                                     TC__
GAM287  MGC13090 3' TGCCTCTGGCCTGTGTCCTG  51142      A     ___
                              CAGGA GCAGGTT  GGCA
                              ||||| |||||||  ||||
                              GTCCT TGTCCGG  CCGT
                                 G      TCT
GAM287  MGC15429 3' GCCAAGCTTGTTTCCTG    51250           _
                              CAGGAAGCAGGTT GGC
                              |||||||||||| |||
                              GTCCTTTGTTCGA CCG
                                     A
GAM287  MGC16943 3' CTGGCAAAATCTGACTTGCCTC 54710      A     TG CATA_
           TTG                  CAGGA GCAGGT  G    GCCAG
                              ||||| ||||||  |    |||||
                              GTTCT CGTTCA  C    CGGTC
                                 C     GT TAAAA
GAM287  MGC20235 3' TTGGTTAGTTTTTTGTTTTTT  58905         TT  A
                              AGGAAGCAGG  GGC TAGCCAG
                              ||||||||||  ||| |||||||
                              TTTTTTGTTT  TTG ATTGGTT
                                    T_  _
GAM287  MGC21621 3' CTGGTTATGTCAAGGCTCTG  58795    GA  AGG
                              CAG  AGC   TTGGCATAGCCAG
                              |||  |||   ||||||||||||
                              GTC  TCG   AACTGTATTGGTC
                                __   G__
GAM287  MGC2747  3' GGGTTTCTGAGTCTGCTTTTTG 44087          _ TG CAT   AG
                              CAGGAAGCAGG T  G   AGCC
                              |||||||||| |  |   ||||
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                                GTTTTTCGTCT A  C   TTGG
                                      G GT T__   GT
GAM287  MGC29956 3'  CTGGGGTTGGTCTGCTTTGTG  58280    G      TT   ATAG
                                CA GAAGCAGG  GGC   CCAG
                                || ||||||||  |||   ||||
                                GT TTTCGTCT  TTG   GGTC
                                 G      GG   G___
GAM287  MGC4172  3'  TGTTAACTTGTTCTTG     44205      G
                                CAGGAA CAGGTTGGCA
                                |||||| ||||||||||
                                GTTCTT GTTCAATTGT
                                   _
GAM287  MGC4268  5'  GCCGATTTTTTCTTG      48744       C
                                CAGGAAG AGGTTGGC
                                ||||||| ||||||||
                                GTTCTTT TTTAGCCG
                                   _
GAM287  MGC4643  3'  CTGGCCCTCATAACTTGTTTCC 51153          GCATA
                                GGAAGCAGGTTG    GCCAG
                                ||||||||||||    |||||
                                CCTTTGTTCAAT    CGGTC
                                      ACTCC
GAM287  MKRN1    3'  TTGTGTTTTGTTGCTCTGTTTC 25579          TT   T  _
           CTG                    CAGGAAGCAGG  GGCA AGC CAG
                                ||||||||||  |||| ||| |||
                                GTCCTTTGTCT  TTGT TTG GTT
                                      CG   T  T
GAM287  MKRN4    3'  CTGGCTTTAAAGTTCGTTTTTT 47745        _  G  GGCAT
           G                     CAGGAAGC AG TT    AGCCAG
                                |||||||| || ||    ||||||
                                GTTTTTTG TT AA    TCGGTC
                                    C  G  ATT__
GAM287  MVD     3'  CTGGCTATGCCCAGTTCTCTG  10141    GA   AGGTT
                                CAG  AGC    GGCATAGCCAG
                                |||  |||    ||||||||||
                                GTC  TTG    CCGTATCGGTC
                                  TC   AC___
GAM287  MYH10    5'  GTCTGATTTGCTTCTTG     69143          TG _
                                CAGGAAGCAGGT  G C
                                ||||||||||  | |
                                GTTCTTCGTTTA  C G
                                      GT T
GAM287  NCKX3    5'  CTGAGCCAGCTCTGCTTCCTG  40351         _     A
                                CAGGAAGCAG GTTGGC TAG
                                |||||||||| |||||| |||
                                GTCCTTCGTC CGACCG GTC
                                      T     A
GAM287  NDST4    5'  CTGTACTCGGTCTGCTCCCTG  42609     A    GT  _ C
                                CAGG AGCAG  TG G ATAG
                                |||| |||||  || | ||||
```

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                                GTCC TCGTC  GC C TGTC
                                  C    TG  T A
GAM287  NEK11    3'  CTGTCTTAGCTGACCTGTTTTT 45624         TG  AT  C
                                GGAAGCAGGT  GC  AG CAG
                                ||||||||||  ||  || |||
                                TTTTTGTCCA  CG  TC GTC
                                     GT  AT  T
GAM287  NLI-IF   3'  TTGGCCCCTTCCGGTTCTGCTT 41054         _ TT  CATA_
           CCTG                   AGGAAGCAG G  GG    GCCAG
                                ||||||||| |  ||    |||||
                                TCCTTCGTC T  CC    CGGTT
                                     T GG  TTCCC
GAM287  NPC1L1   3'  CTGGAGGATGGCCTGCTCTTG  25414      A    TGG   AG_
                                CAGGA GCAGGT   CAT   CCAG
                                ||||| ||||||   |||   ||||
                                GTTCT CGTCCG   GTA   GGTC
                                  _    ___   GGA
GAM287  NSBP1    5'  TGCCTTCGGCTTTTTTTCTG   47773       C    ___
                                CAGGAAG AGGTT   GGCA
                                ||||||| |||||   ||||
                                GTCTTTT TTCGG   CCGT
                                    T    CTT
GAM287  NXP-2    3'  TTGGTATGAAGCTGGTTTTCTG 71111        A   GG   G
                                CAGGAAGC GGTT  CATA CCAG
                                |||||||| ||||  |||| ||||
                                GTCTTTTG TCGA  GTAT GGTT
                                     G   A_   _
GAM287  NY-REN-41 3'  CTGTGGTCAATTTGTCTTCTG  54686      AG       _
                                CAGGA  CAGGTTGGC ATAG
                                |||||  ||||||||| ||||
                                GTCTT  GTTTAACTG TGTC
                                   CT       G
GAM287  p47      3'  TTGGTTGGACGTTTGTTTTCT  32344        GG T GCA
                                AGGAAGCA  T G   TAGCCAG
                                ||||||||  | |   |||||||
                                TCTTTTGT  G C   GTTGGTT
                                     TT _ AG_
GAM287  PANK     3'  CTGGTTGAAATAAAGCCTGTTT 56333         GGCA__
           CT                    GGAAGCAGGTT     TAGCCAG
                                ||||||||||      |||||||
                                TCTTTGTCCGA     GTTGGTC
                                     AATAAA
GAM287  PASK     3'  TGTCTTGATCTGTTTCGTG   30729    G       __
                                CA GAAGCAGGTT  GGCA
                                || ||||||||||  ||||
                                GT CTTTGTCTAG  CTGT
                                 G         TT
GAM287  PCDH20   3'  CTGTGTACTCGAATTGCTTTCT 43129         G  ___     CCAG
           G                     AGGAAGCAG TTG   GCATAG
                                |||||||| |||   ||||||
```

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                                TCTTTCGTT AGC   TGTGTC
                                    A   TCA       G
GAM287  PDCD7    3'  TTGGTTCTGTTTTGGTTTGGTT 72144      G    TT __   T
            TTTG                    AGGAA CAGG  G  GCA AGCCAG
                                |||||| ||||  |  ||| |||||||
                                TTTTT GTTT  T  TGT TTGGTT
                                   G    GG TT   C
GAM287  PDZ-GEF1 3'  TGCCAGCCTGGTTTCTG     26496       G
                                CAGGAA CAGGTTGGCA
                                |||||| ||||||||||
                                GTCTTT GTCCGACCGT
                                   G
GAM287  PLXNC1   3'  CTGTGTCGTTAATTTGTTGTTT 19266     A       ___      CCAG
            G                     AGG AGCAGGTT   GGCATAG
                                ||| ||||||||   |||||||
                                TTT TTGTTTAA   CTGTGTC
                                  G       TTG        G
GAM287  PME-1    3'  CTGGGACCTACTTTGTTTTTTG 32353          _  T  CATAG
                                CAGGAAGCAG GT GG     CCAG
                                |||||||||| || ||     ||||
                                GTTTTTTGTT CA CC     GGTC
                                      T  T  AG___
GAM287  POLE3    3'  TTGGCCTTTCTTAGCCTTTTTC 33861        C      CATA_
            TG                    CAGGAAG AGGTTGG     GCCAG
                                ||||||| |||||||     |||||
                                GTCTTTT TCCGATT     CGGTT
                                   _      CTTTC
GAM287  PPFIA4   3'  CTGGCTGTGCCAAATGGTCTG  70322      AAG  GG
                                CAGG   CA  TTGGCATAGCCAG
                                ||||   ||  ||||||||||||||
                                GTCT   GT  AACCGTGTCGGTC
                                  G__  A_
GAM287  PPM1G    3'  AGCTGCCCACCTAGACTGTTTT 10708       _____   T    TAGCCAG
            CTG                     GAAGCA     GGT GGCA
                                ||||||     ||| ||||
                                TTTTGT     CCA CCGT
                                   CAGAT   C    C   GAC
GAM287  PPP1R16B 3'  TTGGTCATGGGATCTGCTCTTT 61395     GA       GG   AG
            G                     CAG  AGCAGGTT  CAT  CCAG
                                |||  ||||||||  |||  ||||
                                GTT  TCGTCTAG  GTA  GGTT
                                  TC       G_   CT
GAM287  PRO0456  5'  CTAGCAACTGCTAATTTGCTTT 26175              TA_  CAG
            TTG                     CAGGAAGCAGGTTGGCA   GC
                                ||||||||||||||||   ||
                                GTTTTTCGTTTAATCGT   CG
                                         CAA  ATC
GAM287  PRO1584  3'  CTGGCTCTCGCCTGTTTCC   37725          T  CAT
                                GGAAGCAGGT GG   AGCCAG
                                |||||||||| ||   ||||||
```

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                                CCTTTGTCCG TC   TCGGTC
                                      C  ___
GAM287  PRO1635  3'  TTCAAAAGCCAATTTTTTTTCT 37732       C       ATAGCCAG
            G                   CAGGAAG AGGTTGGC
                                ||||||| ||||||||
                                GTCTTTT TTTAACCG
                                    T       AAAACTT
GAM287  PRO2958  3'  TGCTAGCTTCTTTTTG      37653       C
                                CAGGAAG AGGTTGGCA
                                ||||||| |||||||||
                                GTTTTTC TTCGATCGT
                                  _
GAM287  PSMD3    3'  TGGCTTGTATGTTTTTTG    10975         GGTTG   T
                                CAGGAAGCA    GCA AGCCA
                                |||||||||    ||| |||||
                                GTTTTTTGT    TGT TCGGT
                                    A____   _
GAM287  RAB1B    3'  TGGCACAGCTGCTTCCTG    48290         G   GCATA
                                CAGGAAGCAG TTG    GCCA
                                |||||||||| |||    ||||
                                GTCCTTCGTC GAC    CGGT
                                      _   A____
GAM287  RHOBTB3  3'  TTGGCTCAAGAATTTGTTTTT  29746          GGCAT
                                GGAAGCAGGTT    AGCCAG
                                ||||||||||    ||||||
                                TTTTTGTTTAA    TCGGTT
                                      GAAC_
GAM287  S164     3'  TTGTTCTGCTGATTTGTTTCTT 60785          TG   T   CAG
            G                   CAGGAAGCAGGT  GCA AGC
                                ||||||||||||  ||| |||
                                GTTCTTTGTTTA  CGT TTG
                                      GT   C   TT
GAM287  SCYB5    3'  TCCAGTAGTTAGCTTTCTTCCT 11469       C       ATAGCCAG
            G                   CAGGAAG AGGTTGGC
                                ||||||| ||||||||
                                GTCCTTC TTCGATTG
                                    T       ATGACCTT
GAM287  SEC15L   3'  ATGATAATCTGTTTTTTG    72271           G
                                CAGGAAGCAGGTTG CAT
                                |||||||||||||| |||
                                GTTTTTTGTCTAAT GTA
                                      A
GAM287  SH3BP1   3'  TGCCGACATGTTTTTTG     38535         G
                                CAGGAAGCA GTTGGCA
                                ||||||||| |||||||
                                GTTTTTTGT CAGCCGT
                                    A
GAM287  SIAT9    3'  TGTTGGTCTGCCTTCTG     13992       A    TT
                                CAGGA GCAGG  GGCA
                                ||||| |||||  ||||
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                                GTCTT CGTCT  TTGT
                                  C    GG
GAM287  SLC5A6   3'  TGCCAATCTGTTTTTT     40834
                                AGGAAGCAGGTTGGCA
                                ||||||||||||||||
                                TTTTTTGTCTAACCGT

GAM287  SLK      3'  CTGGCCAAGTTTGTTTTTT   28224          _    A
                                AGGAAGCAGG TTGGC TAG
                                |||||||||| ||||| |||
                                TTTTTTGTTT AACCG GTC
                                      G    _
GAM287  SMOC2    3'  TGGGCTGGTTTGTTTCTTG   72379         GG TG  ATAG
                                CAGGAAGCA  T  GC   CCA
                                |||||||||  |  ||   |||
                                GTTCTTTGT  G  CG   GGT
                                      TT GT  _____
GAM287  SRPK1    3'  TTGGTCTTGTTTTGTTTTGTTT 11968          TT__   TA
            TTTG                   AGGAAGCAGG   GGCA  GCCAG
                                |||||||||||   ||||  |||||
                                TTTTTTGTTT   TTGT  TGGTT
                                      TGTT   TC
GAM287  SRPK2    5'  TGGTTGTGAATATTTTCTG   11973       CAGGTTGG
                                CAGGAAG      CATAGCCA
                                |||||||      ||||||||
                                GTCTTTT      GTGTTGGT
                                    ATAA_____
GAM287  SYNPO2   3'  TTGTGTTTGCTTTGCTTTTTG  71898         _ TG
                                CAGGAAGCAG GT  GCATAG
                                |||||||||| ||  ||||||
                                GTTTTTCGTT CG  TGTGTT
                                      T  TT
GAM287  TGIF2    3'  TGCTGTTTTGTTTTTTG     41460          TT
                                CAGGAAGCAGG  GGCA
                                ||||||||||  ||||
                                GTTTTTTGTTT  TCGT
                                       TG
GAM287  TGIF2    3'  TTGTTCCAGCCTGGTTTCCTG 41462        _     C
                                CAGGAAGC AGGTTGG ATAG
                                |||||||| ||||||| ||||
                                GTCCTTTG TCCGACC TGTT
                                    G      T
GAM287  TIEG     3'  TATACCAATGTGTTTTCTG   18959         G    C
                                CAGGAAGCA GTTGG ATA
                                ||||||||| ||||| |||
                                GTCTTTTGT TAACC TAT
                                      G    A
GAM287  TRAD     3'  GCCAATGCTGCTTTCTG     22953          _
                                CAGGAAGCAG GTTGGC
                                |||||||||| ||||||
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                                GTCTTTCGTC TAACCG
                                      G
GAM287  TSGA14   3'  CTGTTCTAATCTGCGTTTTG  38045      A       C
                                CAGGA GCAGGTTGG ATAG
                                ||||| ||||||||| ||||
                                GTTTT CGTCTAATC TGTC
                                   G        T
GAM287  TUCAN    3'  GTTGACATTGTTTTCTG     30279          _  TG
                                CAGGAAGCAG GT  GC
                                |||||||||| ||  ||
                                GTCTTTTGTT CA  TG
                                      A  GT
GAM287  UBE3B    5'  GGGTGATTTGTTCCTG      76925       G     GGCAT G
                                CAGGAA CAGGTT     A CC
                                |||||| ||||||     | ||
                                GTCCTT GTTTAG     T GG
                                  _     _____ G
GAM287  UPLC1    3'  CTGTAGCTGGCCTTCTTCCTG  34724       C    TG  _
                                CAGGAAG AGGT  GC ATAG
                                ||||||| ||||  || ||||
                                GTCCTTC TCCG  CG TGTC
                                    T   GT  A
GAM287  USP20    5'  ATGCTGGCCGCTTCCTG     21924        A   TG
                                CAGGAAGC GGT  GCAT
                                |||||||| |||  ||||
                                GTCCTTCG CCG  CGTA
                                     _  GT
GAM287  UST      3'  TTGGCTGTGTTTTCTCTGCTCT 19137      A   _ TT
            TG                    CAGGA GCAG G  GGCATAGCCAG
                                ||||| |||| |  ||||||||||
                                GTTCT CGTC C  TTGTGTCGGTT
                                   _   T TT
GAM287  ZDHHC9   5'  TGGGACGGTCCGTTTCCTG   61683        A GT  GCATAG
                                CAGGAAGC G  TG     CCA
                                |||||||| |  ||     |||
                                GTCCTTTG C  GC     GGT
                                     C TG  AG____
GAM287  ZF5128   3'  CTGGGGGCCATTTGCTTCCTG  26803          T   ATAG
                                CAGGAAGCAGGT GGC    CCAG
                                |||||||||||| |||    ||||
                                GTCCTTCGTTTA CCG    GGTC
                                      _  GG__
GAM287  ZID      3'  TTATAAGTGTTAACCTTTTTTT 21779        C        AGCCAG
            G                     CAGGAAG AGGTTGGCAT
                                ||||||| ||||||||||
                                GTTTTTT TCCAATTGTG
                                   _        AATATTG
GAM287  ZNF238   3'  TTGGGATATTAACTTGTTTTT  20974           C  AG
                                GGAAGCAGGTTGG AT  CCAG
                                |||||||||||| ||  ||||
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                                TTTTTGTTCAATT TA  GGTT
                                      A  G_
GAM287  ZWINT    3'  CTGAGTTCAGCTTGATTTCTG  22935       G       CATA  _
                                CAGGAA CAGGTTGG    GC CAG
                                |||||| ||||||||    || |||
                                GTCTTT GTTCGACT    TG GTC
                                   A       ____  A
GAM287  ZWINT    3'  CTGAGTTCAGCTTGATTTCTG  52221       G       CATA  _
                                CAGGAA CAGGTTGG    GC CAG
                                |||||| ||||||||    || |||
                                GTCTTT GTTCGACT    TG GTC
                                   A       ____  A
GAM287  LOC113146 3'  TGGTATAACTTCTTTCCTG   72974        C     GCATA
                                CAGGAAG AGGTTG     GCCA
                                ||||||| ||||||     ||||
                                GTCCTTT TTCAAT     TGGT
                                    C     A____
GAM287  LOC114928 3'  TTGGTGTTCACAGTCTGTTTTT 56591          GT  GCATA
          T                      AGGAAGCAG  TG    GCCAG
                                |||||||||  ||     |||||
                                TTTTTTGTC  AC     TGGTT
                                     TG  ACTTG
GAM287  LOC114932 3'  TTGTGACCTGATTGTTTTTTG  72716          GTT  _
                                CAGGAAGCAG   GG CATAG
                                ||||||||||   || |||||
                                GTTTTTTGTT   CC GTGTT
                                      AGT  A
GAM287  LOC116113 3'  CTGGCTCTGGCCGTGTTTTCTG 92215          _   TG CAT
                                CAGGAAGCA GGT  G   AGCCAG
                                ||||||||| |||  |   ||||||
                                GTCTTTTGT CCG  C   TCGGTC
                                     G   GT ___
GAM287  LOC120114 3'  CTGGTTGGTTTTGTGTTTTCTG 75526          GGTT   A
                                CAGGAAGCA    GGC TAGCCAG
                                |||||||||    ||| |||||||
                                GTCTTTTGT    TTG GTTGGTC
                                     GTT_  _
GAM287  LOC126913 3'  CCAAGTCTGTTTCTTG      74601           _
                                CAGGAAGCAGG TTGG
                                |||||||||| ||||
                                GTTCTTTGTCT AACC
                                      G
GAM287  LOC127428 3'  TGGCTGTGCTAGATTTTC    74674      CAGG
                                GAAG    TTGGCATAGCCA
                                ||||    ||||||||||||
                                CTTT    GATCGTGTCGGT
                                  TA__
GAM287  LOC130327 3'  CTGACTCCACCCTGTTTCTTG  74917          T   CAT  C
                                CAGGAAGCAGG TGG   AG CAG
                                |||||||||| |||   || |||
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                                GTTCTTTGTCC ACC   TC GTC
                                      C   ___  A
GAM287   LOC132671 3'  CTGGTCATCAGCTTGCTTTGTG 59168    G         CATA
                                CA GAAGCAGGTTGG    GCCAG
                                || ||||||||||||    |||||
                                GT TTTCGTTCGACT    TGGTC
                                 G          AC__
GAM287   LOC135293 3'  GGCTATGTTAAATTTG      76188       _
                                CAGGTT GGCATAGCC
                                |||||| |||||||||
                                GTTTAA TTGTATCGG
                                   A
GAM287   LOC139202 3'  CTGAGTCTGGCCTCCTTTCTG  76239       C    TG CATA  _
                                CAGGAAG AGGT  G    GC CAG
                                ||||||| ||||  |    || |||
                                GTCTTTC TCCG  C    TG GTC
                                    C    GT _____  A
GAM287   LOC143437 3'  CTGGCTTCTAGCCCAGTGTGCT 82954       GG    _ AT__
            TTCTG                GAAGCA  TTGG C    AGCCAG
                                ||||||  |||| |    ||||||
                                TTTCGT  GACC G    TCGGTC
                                   GT    C ATCT
GAM287   LOC144262 5'  TGTCGGACTTGCTTTCTG     76754           _
                                CAGGAAGCAGGTT GGCA
                                |||||||||||||| ||||
                                GTCTTTCGTTCAG CTGT
                                       G
GAM287   LOC144473 5'  TTGGAATGTGATCTTGCTTTCT 83077          TTG    AG
            G                    CAGGAAGCAGG   GCAT  CCAG
                                |||||||||||   ||||  ||||
                                GTCTTTCGTTC   TGTA  GGTT
                                      TAG    A_
GAM287   LOC144871 5'  CTGGCTATGTCAGCAATATCTT 83199       CAG__
            TTT                   AGGAAG    GTTGGCATAGCCAG
                                ||||||    ||||||||||||||
                                TTTTTC    CGACTGTATCGGTC
                                   TATAA
GAM287   LOC144997 3'  TGGTTGTGCCAATGTGT     83211     G
                                GCA GTTGGCATAGCCA
                                ||| ||||||||||||
                                TGT TAACCGTGTTGGT
                                  G
GAM287   LOC145241 5'  CTGGTTGTGTTCAGTGCTTGTT 62868     G    GG   _
            G                    CAG AAGCA  TTGG CATAGCCAG
                                ||| |||||  |||| |||||||||
                                GTT TTCGT  GACT GTGTTGGTC
                                  G    __   T
GAM287   LOC145815 5'  CTGGCCTCTCCTGGCCTGTTTC 83518          TG CATA_
            TT                   AGGAAGCAGGT  G    GCCAG
                                ||||||||||  |    |||||
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                                TTCTTTGTCCG  C    CGGTC
                                      GT CTCTC
GAM287   LOC146268 5'  GTCGGCTTGCTGCCTG     77813     A
                                CAGG AGCAGGTTGGC
                                |||| ||||||||||
                                GTCC TCGTTCGGCTG
                                  G
GAM287   LOC146823 3'  TGGTTTATATGCTTCCTG    83804        GGTTGGCAT
                                CAGGAAGCA       AGCCA
                                |||||||||       |||||
                                GTCCTTCGT       TTGGT
                                     ATAT_____
GAM287   LOC147160 5'  TTGAGCTCCTGACCTGTTTCT  83977         TG CAT  _
                                GGAAGCAGGT  G   AGC CAG
                                ||||||||||  |   ||| |||
                                TCTTTGTCCA  C   TCG GTT
                                      GT C__   A
GAM287   LOC147396 5'  CTAAGCTGATCTGGTTCCTG   78352      G    TG  A
                                CAGGAA CAGGT  GC TAG
                                |||||| |||||  || |||
                                GTCCTT GTCTA  CG ATC
                                   G    GT  A
GAM287   LOC147649 3'  TGGGCAGTATGTTTTCTG    78417        GGTTG  ATAG
                                CAGGAAGCA    GC    CCA
                                |||||||||    ||    |||
                                GTCTTTTGT    CG    GGT
                                     ATGA_  _____
GAM287   LOC148229 5'  GCCAGTTCTGCTTCCTG     78748         TT_
                                CAGGAAGCAGG   GGC
                                ||||||||||   |||
                                GTCCTTCGTCT   CCG
                                      TGA
GAM287   LOC148293 3'  TGGTTGGTCTGTTGCTT     78786       GTT   A
                                AAGCAG   GGC TAGCCA
                                ||||||   ||| ||||||
                                TTCGTT   CTG GTTGGT
                                   GT_   _
GAM287   LOC148760 3'  CTGGTTGTTCCTTGCCTTCTG  84205      A   GTT  C
                                CAGGA GCAG   GG ATAGCCAG
                                ||||| ||||   || ||||||||
                                GTCTT CGTT   CC TGTTGGTC
                                   C    ___  T
GAM287   LOC148805 3'  CTGGCTAGTGGTTTGTTACTTG 78993      A     TT G A
                                CAGG AGCAGG  G C TAGCCAG
                                |||| ||||||  | | |||||||
                                GTTC TTGTTT  T G ATCGGTC
                                  A     GG _ _
GAM287   LOC148902 3'  AGCTGCCTCTCTGGATCTGCTT 84264         _______   TAGCCAG
            CCTG                   AAGCAGGTT     GGCA
                                |||||||||     ||||
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                                TTCGTCTAG     CCGT
                                     GTCTCT    C   GAC
GAM287   LOC148932 3'  TGGCTGGGGTTGTTTCCTG    79114          G  GGCA
                                CAGGAAGCAG TT    TAGCCA
                                |||||||||| ||    ||||||
                                GTCCTTTGTT GG    GTCGGT
                                     G  ____
GAM287   LOC149076 3'  TTGGCTTCTCAGTCTGCATCTT 79155       A    GT   CAT
           G                     CAGGA GCAG  TGG   AGCCAG
                                ||||| ||||  |||   ||||||
                                GTTCT CGTC  ACT   TCGGTT
                                   A    TG   CT_
GAM287   LOC149086 3'  CTGGATGAGTTAACCTCTTCCT 84337        C       A  G
           G                     CAGGAAG AGGTTGGC TA CCAG
                                ||||||| |||||||| || ||||
                                GTCCTTC TCCAATTG GT GGTC
                                   _       A  A
GAM287   LOC149149 3'  CTGTTTGGTCTTGCTTCTTG   84365          _ TG C
                                CAGGAAGCAGG T  G ATAG
                                |||||||||||  |  | ||||
                                GTTCTTCGTTC G  T TGTC
                                     T GT _
GAM287   LOC149351 3'  TTGGCTATTGTACTTATTTCTT 79311        C    TG  _
           G                     CAGGAAG AGGT  GCA TAGCCAG
                                ||||||| ||||  ||| |||||||
                                GTTCTTT TTCA  TGT ATCGGTT
                                   A   __  T
GAM287   LOC149420 3'  TGCTGGTCTGTTTTTT      79373          TT
                                AGGAAGCAGG  GGCA
                                ||||||||||  ||||
                                TTTTTTGTCT  TCGT
                                     GG
GAM287   LOC149837 3'  GCAGTTTAATCTGCTCTTG    84741       A       C  A
                                CAGGA GCAGGTTGG AT GC
                                ||||| ||||||||| || ||
                                GTTCT CGTCTAATT TG CG
                                   _       _  A
GAM287   LOC149912 3'  GTGGCGGCCTGCTTTCTG     84718            G
                                CAGGAAGCAGGTTG CAT
                                |||||||||||||| |||
                                GTCTTTCGTCCGGC GTG
                                       G
GAM287   LOC150082 5'  TTGTTTCAATCTGCTTTT     79569            C
                                GGAAGCAGGTTGG ATAG
                                |||||||||||| ||||
                                TTTTCGTCTAACT TGTT
                                       T
GAM287   LOC150142 5'  CTGGAGGCCGGCTCTGCTTCCT 79577          _     ATAG
           G                     CAGGAAGCAG GTTGGC    CCAG
                                ||||||||| ||||||    ||||
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                                GTCCTTCGTC CGGCCG    GGTC
                                      T     GA__
GAM287   LOC150225 3'  GGCGACAATTTGTTTTCT    85003           GCATA
                                AGGAAGCAGGTTG    GCC
                                ||||||||||||     |||
                                TCTTTTGTTTAAC    CGG
                                      AG___
GAM287   LOC150519 3'  TGGCAGGATTTGTTTTT     79927          GGCATA
                                GGAAGCAGGTT     GCCA
                                ||||||||||      ||||
                                TTTTTGTTTAG     CGGT
                                      GA____
GAM287   LOC150696 3'  CTGGCTAATTTTTGTGTTTTTT 58480         GGTTGGCA
              G                  CAGGAAGCA       TAGCCAG
                                |||||||||       |||||||
                                GTTTTTTGT       ATCGGTC
                                      GTTTTTA_
GAM287   LOC150848 5'  TGGCTATTTCTCTTTTCTG   85135       C   TTGGC
                                CAGGAAG AGG    ATAGCCA
                                ||||||| |||    |||||||
                                GTCTTTT TCT    TATCGGT
                                    C   T____
GAM287   LOC151040 3'  CTGGTTGTCTTTTCTTTCCTG  80102      GC   TT  C
                                CAGGAA  AGG  GG ATAGCCAG
                                ||||||  |||  || ||||||||
                                GTCCTT  TCT  TC TGTTGGTC
                                   __   TT  _
GAM287   LOC151162 5'  ATATCGGTTTGCTTTTTG    85240        GG   GC
                                CAGGAAGCA  TTG  AT
                                |||||||||  |||  ||
                                GTTTTTCGT  GGC  TA
                                      TT   TA
GAM287   LOC151201 5'  GCTATTTGCTTCCTG       85281          T
                                CAGGAAGCAGGT GGC
                                |||||||||||| |||
                                GTCCTTCGTTTA TCG
                                                _
GAM287   LOC152018 3'  TGGCTATACTGTTTCTT     85547         GTTGGC
                                AGGAAGCAG     ATAGCCA
                                |||||||||     |||||||
                                TTCTTTGTC     TATCGGT
                                      A_____
GAM287   LOC152275 3'  GTTCTCTGATCTGTTGTCTG   85621     GA      TG CAT
                                CAG  AGCAGGT  G   AGC
                                |||  |||||||  |   |||
                                GTC  TTGTCTA  C   TTG
                                  TG      GT TC_
GAM287   LOC152286 3'  GCCCCAGCCTGCTTCTTG    85631           CATA
                                CAGGAAGCAGGTTGG    GC
                                ||||||||||||||    ||
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                                GTTCTTCGTCCGACC   CG
                                      C___
GAM287  LOC152426 5'  TGGCTCTCACCTTTTCCTG   85720       C   T  CAT
                                CAGGAAG AGGT GG   AGCCA
                                ||||||| |||| ||   |||||
                                GTCCTTT TCCA TC   TCGGT
                                   _   C  ___
GAM287  LOC152519 3'  TTGGTTTATATTTCAATCTGTT 80611     G      C  ___
          CCT                    GAA CAGGTTGG ATA   GCCAG
                                ||| |||||||| |||   |||||
                                CTT GTCTAACT TAT   TGGTT
                                  _      T  ATT
GAM287  LOC153163 3'  TTGGACTCCTGGCTTGCTTTT  80772         TG CAT  _
                                GGAAGCAGGT  G   AG CCAG
                                ||||||||||  |   || ||||
                                TTTTCGTTCG  C   TC GGTT
                                      GT C__  A
GAM287  LOC153505 3'  CTGGTCTGCCTGGTCTGCTTCC 80849         GT _   TA
          T                     AGGAAGCAG  T GGCA  GCCAG
                                |||||||||  | ||||  |||||
                                TCCTTCGTC  G CCGT  TGGTC
                                     TG T   C_
GAM287  LOC153743 3'  TGTTGATTTGTTTTTT      60513          TG
                                AGGAAGCAGGT  GCA
                                ||||||||||  |||
                                TTTTTTGTTTA  TGT
                                      GT
GAM287  LOC153931 3'  TTGGCTCCTTCTGACTTCTTTT 81003       C   TG CAT_
          TG                     CAGGAAG AGGT  G   AGCCAG
                                ||||||| ||||  |   ||||||
                                GTTTTTC TTCA  C   TCGGTT
                                   _   GT TTCC
GAM287  LOC154562 3'  TGCCTCTATCTTGTTTTTTG   81095         TT___
                                CAGGAAGCAGG    GGCA
                                ||||||||||    ||||
                                GTTTTTTGTTC    CCGT
                                      TATCT
GAM287  LOC155438 3'  TTGGTTGTTACTCTCTGTTTCC 86399         TTGGC
                                GGAAGCAGG    ATAGCCAG
                                |||||||||    ||||||||
                                CCTTTGTCT    TGTTGGTT
                                     CTCAT
GAM287  LOC157421 5'  TGACCACTGCCAGCCTCGCTTC 86446        _       TAGCCAG
          CTG                    CAGGAAGC AGGTTGGCA
                                ||||||||| |||||||||
                                GTCCTTCG TCCGACCGT
                                     C        CACCAGTC
GAM287  LOC158230 3'  CTGGCTTTGGTTTGGTTTTTG  81798       G  GG TG CAT
                                CAGGAA CA  T  G   AGCCAG
                                |||||| ||  |  |  ||||||
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                                GTTTTT GT  G  T   TCGGTC
                                   G  TT GT ___
GAM287   LOC164386 5'  TTGGCTGTGTTGACTGAGCT   87208    A_   TG
                                AGC  GGT  GCATAGCCAG
                                |||  |||  ||||||||||
                                TCG  TCA  TGTGTCGGTT
                                  AG   GT
GAM287   LOC164397 3'  TTGGCTGTGTTCTTTGTCCTG  82534     AGC   TT
                                CAGGA   AGG  GGCATAGCCAG
                                |||||   |||  ||||||||||
                                GTCCT   TTC  TTGTGTCGGTT
                                   GT_  __
GAM287   LOC166765 3'  TGTTAATTTGTTTTTT      82664
                                AGGAAGCAGGTTGGCA
                                ||||||||||||||||
                                TTTTTTGTTTAATTGT

GAM287   LOC169693 3'  TTGTTTTGTTAGCTTGTTTCCT 87295            T   CAG
                                AGGAAGCAGGTTGGCA AGC
                                |||||||||||||||| |||
                                TCCTTTGTTCGATTGT TTG
                                          T   TT
GAM287   LOC196529 5'  TGTTGATCTGTTTTTT      87785          TG
                                AGGAAGCAGGT  GCA
                                ||||||||||  |||
                                TTTTTTGTCTA  TGT
                                      GT
GAM287   LOC199678 3'  TGTGAACCTGCTTCCTG     89795           G
                                CAGGAAGCAGGTT GCA
                                |||||||||||| |||
                                GTCCTTCGTCCAA TGT
                                       G
GAM287   LOC200138 5'  CTGGCCGGCTCCGGTCTGCTTC 89933        GT   CATA_
            T                    GGAAGCAG  TGG    GCCAG
                                ||||||||  |||    |||||
                                TCTTCGTC  GCC    CGGTC
                                     TG   TCGGC
GAM287   LOC200169 3'  TGGGGTGTTCTGTTTCTTG    89960          TTG    AG
                                CAGGAAGCAGG   GCAT  CCA
                                ||||||||||   ||||  |||
                                GTTCTTTGTCT   TGTG  GGT
                                      ___    G_
GAM287   LOC201965 3'  GTGGTTGTATTGGTTTGTTTTT 89115         GG TG C      G
            TG                    CAGGAAGCA  T  G ATAGCCA
                                |||||||||  |  | |||||||
                                GTTTTTTGT  G  T TGTTGGT
                                     TT GT A      GT
GAM287   LOC202934 5'  TGTGTTTGATTTGTTCTTG   90434       G    TG _
                                CAGGAA CAGGT  G CATA
                                ||||||  |||||  |  ||||
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                                GTTCTT GTTTA  T GTGT
                                   _    GT T
GAM287   LOC203068 3'  TGCCTCTATCTTGTTTTTTG  89257          TT___
                                CAGGAAGCAGG    GGCA
                                ||||||||||    ||||
                                GTTTTTTGTTC    CCGT
                                     TATCT
GAM287   LOC203286 5'  AGGTTTTGTGCCTGCTTTTTG 90493           TG  T   AG
                                CAGGAAGCAGGT  GCA AGCC
                                ||||||||||||  ||| ||||
                                GTTTTTCGTCCG  TGT TTGG
                                      __  T   AG
GAM287   LOC203350 3'  TGTCTACCTGCTTCCTG    90573          T
                                CAGGAAGCAGGT GGCA
                                ||||||||||||| ||||
                                GTCCTTCGTCCA CTGT
                                      T
GAM287   LOC203377 5'  ATATCGGTTTGCTTTTTG   90578        GG  GC
                                CAGGAAGCA  TTG  AT
                                |||||||||  |||  ||
                                GTTTTTCGT  GGC  TA
                                     TT   TA
GAM287   LOC203562 5'  TTGGTTGGCAGTCTGCTTTTT 90644        GT  G  TA
                                AGGAAGCAG  TG CA  GCCAG
                                |||||||||  || ||  |||||
                                TTTTTCGTC  AC GT  TGGTT
                                     TG  G  __
GAM287   LOC204084 5'  CTGGCTCTGGGATCTGTTTCCT 89446          GG  T
                                AGGAAGCAGGTT  CA AGCCAG
                                ||||||||||||  || ||||||
                                TCCTTTGTCTAG  GT TCGGTC
                                      G_  C
GAM287   LOC206962 3'  CTGGACGTGGCCTGTTTTCT   89548          TGG   AG
                                AGGAAGCAGGT   CAT  CCAG
                                ||||||||||   |||  ||||
                                TCTTTTGTCCG   GTG  GGTC
                                     ___   CA
GAM287   LOC219397 3'  GGGTAATGAGCTTGTTTCTTG 93471           GG   A   AG
                                CAGGAAGCAGGTT  CAT GCC
                                ||||||||||||  ||| |||
                                GTTCTTTGTTCGA  GTA TGG
                                      __  A   GG
GAM287   LOC219673 5'  CTGACTCTCAACTTTGTTTTTT 93030          _    CAT  C
           G                     CAGGAAGCAG GTTGG   AG CAG
                                ||||||||||  |||||   || |||
                                GTTTTTTGTT CAACT   TC GTC
                                      T    C__  A
GAM287   LOC219735 3'  ATGCCAATTTACTTCCTG    93106        C
                                CAGGAAG AGGTTGGCAT
                                |||||||  ||||||||||
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                                GTCCTTC TTTAACCGTA
                                    A
GAM287  LOC220097 5'  TGGCAGGCTGGTTTCCTG    93469        AGGT    ATA
                                CAGGAAGC    TGGC   GCCA
                                ||||||||    ||||   ||||
                                GTCCTTTG    GTCG   CGGT
                                     _____    GA_
GAM287  LOC220763 5'  TGGTGTTGGCTTTTTTCTG    73349        C    TG  ATA
                                CAGGAAG AGGT  GC   GCCA
                                ||||||| ||||  ||   ||||
                                GTCTTTT TTCG  TG   TGGT
                                    _   GT  ___
GAM287  LOC221103 5'  TGGCAACCTGCCTTCTG     93246       A       G
                                CAGGA GCAGGTTG CA
                                ||||| |||||||| ||
                                GTCTT CGTCCAAC GT
                                   C       G
GAM287  LOC221405 5'  TTGGCTATGTGTTGTTTTCT   93890         GTTG
                                AGGAAGCAG    GCATAGCCAG
                                |||||||||    ||||||||||
                                TCTTTTGTT    TGTATCGGTT
                                     G___
GAM287  LOC221751 5'  CTGGCTTTCCACCCGGCCTGCT 92047    A        CAT___
           GCTTG                   G AGCAGGTTGG     AGCCAG
                                | ||||||||||     ||||||
                                C TCGTCCGGCC     TCGGTC
                                 G         CACCTT
GAM287  LOC222488 3'  TGGCTATGATGCTTACTG    94347     G    GGTTGG
                                CAG AAGCA     CATAGCCA
                                ||| |||||     ||||||||
                                GTC TTCGT     GTATCGGT
                                  A    A_____
GAM287  LOC253220 5'  CTGGTCAGCCCTGCTTTCTG   96369          _    A
                                CAGGAAGCAGG TTGGC TAG
                                |||||||||| ||||| |||
                                GTCTTTCGTCC GACTG GTC
                                     C    _
GAM287  LOC253296 3'  CTGGCTGCAGCTGATCTGTTTC 94489          TG  A_
           CT                     AGGAAGCAGGT  GC  TAGCCAG
                                |||||||||||  ||  |||||||
                                TCCTTTGTCTA  CG  GTCGGTC
                                     GT  AC
GAM287  LOC253298 5'  CTGGCTGCAGCTGATCTGTTTC 97214          TG  A_
           CT                     AGGAAGCAGGT  GC  TAGCCAG
                                |||||||||||  ||  |||||||
                                TCCTTTGTCTA  CG  GTCGGTC
                                     GT  AC
GAM287  LOC253531 3'  CTGGCTTCTAGCCCAGTGTGCT 96469       GG   _ AT__
           TTCTG                   GAAGCA  TTGG C    AGCCAG
                                ||||||  |||| |   ||||||
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                                TTTCGT  GACC G    TCGGTC
                                   GT    C ATCT
GAM287   LOC253664 3'  TTGTTTTGTTGTTTTGTTTTTT 94818          TT    T   CAG
             G                      CAGGAAGCAGG  GGCA AGC
                                    |||||||||||  |||| |||
                                    GTTTTTTGTTT  TTGT TTG
                                          TG    T   TT
GAM287   LOC253769 5'  CTGGCTGTCCAGAGTTGCTTCC 97226          G_    C
             TG                      CAGGAAGCAG  TTGG ATAGCCAG
                                    ||||||||||  |||| ||||||||
                                    GTCCTTCGTT  GACC TGTCGGTC
                                          GA    _
GAM287   LOC253955 5'  CTGAGCCCCCTCGTCTGCTTCT 94428          TT  CATA  _
             TG                      CAGGAAGCAGG  GG    GC CAG
                                    ||||||||||  ||    || |||
                                    GTTCTTCGTCT  TC    CG GTC
                                          GC  CCC_  A
GAM287   LOC253971 3'  TGCCCGGCTCTGCTTTCTG    96141          _    _
                                    CAGGAAGCAG GTTGG CA
                                    ||||||||| ||||| ||
                                    GTCTTTCGTC CGGCC GT
                                          T     C
GAM287   LOC254182 5'  TGTCAATCTGCTCCTG      96037       A
                                    CAGGA GCAGGTTGGCA
                                    ||||| ||||||||||
                                    GTCCT CGTCTAACTGT
                                      _
GAM287   LOC254704 5'  GTTAATATGTTTTCTG      95653          G
                                    CAGGAAGCA GTTGGC
                                    |||||||| ||||||
                                    GTCTTTTGT TAATTG
                                          A
GAM287   LOC255465 5'  TGTGTTTGATTTGTTCTTG   97305       G    TG _
                                    CAGGAA CAGGT  G CATA
                                    |||||| |||||  | ||||
                                    GTTCTT GTTTA  T GTGT
                                       _    GT T
GAM287   LOC256273 3'  TTATCAGCTGGTGCTGCTTCCT 96410          _ TT   ATAGCCAG
             G                      CAGGAAGCAG G  GGC
                                    ||||||||||  |  |||
                                    GTCCTTCGTC T  TCG
                                          G GG   ACTATT
GAM287   LOC256295 3'  CTGGCTGTGCGCTGCTGTGTTC 96590       A   GTTG
             TG                      CAGGA GCAG    GCATAGCCAG
                                    ||||| ||||    ||||||||||
                                    GTCTT TGTC    CGTGTCGGTC
                                       G    GTCG
GAM287   LOC256302 3'  CTAGAGCCAGCCTGCATCCTG  95192       A        A_
                                    CAGGA GCAGGTTGGC  TAG
                                    ||||| ||||||||||  |||
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                                GTCCT CGTCCGACCG  ATC
                                   A         AG
GAM287  LOC256730 3'  GCTAACCTCCTTCTTG      95231         C
                                CAGGAAG AGGTTGGC
                                ||||||| ||||||||
                                GTTCTTC TCCAATCG
                                    C
GAM287  LOC257451 3'  TGGTTATGGCAGTTTCTTG   95563         AGGT  G
                                CAGGAAGC   TG CATAGCCA
                                ||||||||   || ||||||||
                                GTTCTTTG   AC GTATTGGT
                                     ____  G
GAM287  LOC257570 3'  CTGGCTGCAGCTGATCTGTTTC 97832          TG  A_
           CT                    AGGAAGCAGGT  GC  TAGCCAG
                                ||||||||||  ||  |||||||
                                TCCTTTGTCTA  CG  GTCGGTC
                                      GT  AC
GAM287  LOC257571 5'  CTGGCTGCAGCTGATCTGTTTC 97944          TG  A_
           CT                    AGGAAGCAGGT  GC  TAGCCAG
                                ||||||||||  ||  |||||||
                                TCCTTTGTCTA  CG  GTCGGTC
                                      GT  AC
GAM287  LOC51049  3'  TTGGCACAGGCCTGCTTTGTG  31890    G        GGCATA
                                CA GAAGCAGGTT     GCCAG
                                || ||||||||||     |||||
                                GT TTTCGTCCGG     CGGTT
                                 G        ACA___
GAM287  LOC51097  3'  TGGCCTAACCTGTTTCTTG   32052           CATA   G
                                CAGGAAGCAGGTTGG   GCCA
                                ||||||||||||||   ||||
                                GTTCTTTGTCCAATC   CGGT
                                      ____   G
GAM287  LOC51170  3'  TGCCACTCTGTTTCCTG     32695          GT
                                CAGGAAGCAG  TGGCA
                                ||||||||||  |||||
                                GTCCTTTGTC  ACCGT
                                      TC
GAM287  LOC51312  5'  TGGCTTTTATTGTTTCTTG   37716          GTTGGCAT
                                CAGGAAGCAG       AGCCA
                                ||||||||||       |||||
                                GTTCTTTGTT       TCGGT
                                      ATTT____
GAM287  LOC51315  3'  TGCACAATCTGTTTCTTG    33531            _
                                CAGGAAGCAGGTTG GCA
                                ||||||||||||| |||
                                GTTCTTTGTCTAAC CGT
                                       A
GAM287  LOC90333  3'  CACTGTGCCTGGCCTGTTTTTT 62285            _      CCAG
           G                     CAGGAAGCAGGTT GGCATAG
                                ||||||||||||| |||||||
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                                GTTTTTTGTCCGG CCGTGTC
                                       T      AC
GAM287  LOC90333  3'  CTGTGCCTGGCCTGTTTTTTG  62288          _
                                CAGGAAGCAGGTT GGCATAG
                                ||||||||||||| |||||||
                                GTTTTTTGTCCGG CCGTGTC
                                       T
GAM287  LOC90378  3'  TGGCTGTATTGCTTTTT     62524         GTTGGC
                                AGGAAGCAG     ATAGCCA
                                |||||||||     |||||||
                                TTTTTCGTT     TGTCGGT
                                     A_____
GAM287  LOC90538  3'  GCTGGCTTAGATATTCTGGTTT 63192     GG TG C _____
           GTTTCTTG                GCA  T  G AT    AGCCAG   C
                                |||  |  | ||    ||||||  |
                                TGT  G  C TA    TCGGTC   G
                                  TT GT T  TAGAT
GAM287  LOC90550  3'  TGCTAATCTGCTTTGTG     73095    G
                                CA GAAGCAGGTTGGCA
                                || ||||||||||||||
                                GT TTTCGTCTAATCGT
                                 G
GAM287  LOC90826  3'  CTGCTGCAGATTTGCTTTCTG  64092          G  _
                                CAGGAAGCAGGTT GCA TAG
                                ||||||||||||| ||| |||
                                GTCTTTCGTTTAG CGT GTC
                                       A   C
GAM287  LOC91050  3'  CTGGGAGCCAGTCTAGTTTCCT 64745        _ GT    ATAG
           G                     CAGGAAGC AG  TGGC    CCAG
                                ||||||||  ||  ||||    ||||
                                GTCCTTTG TC  ACCG    GGTC
                                     A  TG    AG__
GAM287  LOC91145  3'  CTAAAGCAGCAATCTGCTTCTT 65057           __  ATAGCCAG
           G                     CAGGAAGCAGGTTG  GC
                                ||||||||||||||  ||
                                GTTCTTCGTCTAAC  CG
                                       GA  AAATC
GAM287  LOC91496  5'  TGTCTCCAGCTGTTTCTTG   66226         G    CAT  C
                                CAGGAAGCAG TTGG   AG CA
                                |||||||||| ||||   || ||
                                GTTCTTTGTC GACC   TC GT
                                     _   ____  T
GAM287  LOC91960  3'  ATGTCAGTTTGCTTCTT     67658        GG
                                AGGAAGCA  TTGGCAT
                                ||||||||  |||||||
                                TTCTTCGT  GACTGTA
                                     TT
GAM287  LOC92539  5'  TTGGTTATTTTACTGTTCTTG  69645       G   GTTGGC
                                CAGGAA CAG     ATAGCCAG
                                ||||||  |||     ||||||||
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                                GTTCTT GTC     TATTGGTT
                                   _  ATTT__
GAM287  LOC92755  3'  TGCCTCTATCTTGTTTTTTG  70503          TT___
                                CAGGAAGCAGG    GGCA
                                ||||||||||    ||||
                                GTTTTTTGTTC    CCGT
                                    TATCT
GAM287  LOC92912  3'  TTGGCTGGGCTGAATCTGCTGC 70849     A      _  A
          TTG                    CAGG AGCAGGTT GGC TAGCCAG
                                |||| |||||||| ||| |||||||
                                GTTC TCGTCTAA TCG GTCGGTT
                                  G       G  G
GAM287  LOC93356  5'  TGGTTTAAATTGTTTTCTG   72081         GTTGGCAT
                                CAGGAAGCAG      AGCCA
                                ||||||||||      |||||
                                GTCTTTTGTT      TTGGT
                                    AAAT_____
GAM288  ADH7     5'  GGCACAAGCTGCTGTTATA   5420          CAC   ACA
                                TATAACAGC   CTTG   GTC
                                |||||||||   ||||   |||
                                ATATTGTCG   GAAC   CGG
                                    TC_    A__
GAM288  BACH2    3'  ACTAGTTTGGTAACTGTTA   41481       CC   TT   _
                                TAACAG  ACC  GAC AGT
                                ||||||  |||  ||| |||
                                ATTGTC  TGG  TTG TCA
                                   AA   T_   A
GAM288  G6PT1    3'  AAGGTGACTTGTTATA      7596         _ C
                                TATAACA G CACCTT
                                ||||||| | ||||||
                                ATATTGT C GTGGAA
                                    T A
GAM288  H3F3B    3'  GACTTGTTGGGTAGCTATTA  18021     C   C    T   _
                                TAA AGC ACCT GACA GTC
                                ||| ||| |||| |||| |||
                                ATT TCG TGGG TTGT CAG
                                  A   A    _    T
GAM288  MNT      3'  ACTGTATTCTAGTGGCTGTTCA 39701    T       CTTG__
                                A AACAGCCAC     ACAGT
                                | |||||||||     |||||
                                A TTGTCGGTG     TGTCA
                                 C       ATCTTA
GAM288  PHEMX    3'  GACCATTCAGGCTGTTG     19120        ACCT   CA_
                                TAACAGCC    TGA   GTC
                                ||||||||    |||   |||
                                GTTGTCGG    ACT   CAG
                                    _____   TAC
GAM288  PHEMX    3'  GACCATTCAGGCTGTTG     57365        ACCT   CA_
                                TAACAGCC    TGA   GTC
                                ||||||||    |||   |||
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                                GTTGTCGG   ACT  CAG
                                    ____  TAC
GAM288  PHEMX    3'  GACCATTCAGGCTGTTG    57369       ACCT  CA_
                                TAACAGCC   TGA  GTC
                                ||||||||   |||  |||
                                GTTGTCGG   ACT  CAG
                                    ____  TAC
GAM288  PHEMX    3'  GACCATTCAGGCTGTTG    57360       ACCT  CA_
                                TAACAGCC   TGA  GTC
                                ||||||||   |||  |||
                                GTTGTCGG   ACT  CAG
                                    ____  TAC
GAM288  RFXAP    3'  GACTTAATCATGGCTGTT    5014       CCT  C__
                                AACAGCCA   TGA  AGTC
                                ||||||||   |||  ||||
                                TTGTCGGT   ACT  TCAG
                                    ___  AAT
GAM288  SMN1     3'  ACTGGTGGACATGGCTGTTCA  4429    T     ___ TTGA
                                A AACAGCCA   CC   CAGT
                                | ||||||||   ||   ||||
                                A TTGTCGGT   GG   GTCA
                                 C       ACA  TG__
GAM288  SMN1     3'  ACTGGTGGACATGGCTGTTCA  43153   T     ___ TTGA
                                A AACAGCCA   CC   CAGT
                                | ||||||||   ||   ||||
                                A TTGTCGGT   GG   GTCA
                                 C       ACA  TG__
GAM288  SMT3H1   3'  GACTGTCACTTGCTGTTA    59959       CACCT
                                TAACAGC    TGACAGTC
                                |||||||    ||||||||
                                ATTGTCG    ACTGTCAG
                                    TTC__
GAM288  SNAI1    3'  GACTGTGAGTAATGGCTGT    19969       CC_  G
                                ACAGCCA   TT ACAGTC
                                |||||||   || ||||||
                                TGTCGGT   GA TGTCAG
                                    AAT  G
GAM288  SS18     3'  ACTGTGTTTCAAATGGACTGTT 18881       _  CC   ____
          A                      TAACAG CCA  TTGA   CAGT
                                ||||||  |||  ||||   ||||
                                ATTGTC GGT  AACT   GTCA
                                   A  A_   TTGT
GAM288  UPK1B    3'  CAAGGTGCCTGTTATA      22716        C
                                TATAACAG CACCTTG
                                |||||||| |||||||
                                ATATTGTC GTGGAAC
                                     C
GAM288  DKFZP434A0225 3'  ACTGTTGGAATGGCTGTT    93904        CC TG
                                AACAGCCA  T  ACAGT
                                ||||||||  |  |||||
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                                TTGTCGGT  G  TGTCA
                                    AA GT
GAM288  FLJ10462  3'  ACTGTCAAATGTCACCTGTTAT 36138       CC_  C_
            G                    TATAACAG   AC  TTGACAGT
                                 ||||||||   ||  ||||||||
                                 GTATTGTC   TG  AACTGTCA
                                    CAC  TA
GAM288  FLJ11175  3'  GACCAATGTTATGGCTGTT   37134       CCT   ___
                                 AACAGCCA   TGACA   GTC
                                 ||||||||   |||||   |||
                                 TTGTCGGT   ATTGT   CAG
                                    ___     AAC
GAM288  FLJ13491  5'  GACTTCCAGCAGCTGTTA    44885       CAC  T  C
                                 TAACAGC   CT GA AGTC
                                 |||||||   || || ||||
                                 ATTGTCG   GA CT TCAG
                                    AC_  C  _
GAM288  FLJ20079  3'  GTTAAGATGGCTGATATA    34498     A     C
                                 TATA CAGCCA CTTGAC
                                 |||| |||||| ||||||
                                 ATAT GTCGGT GAATTG
                                   A     A
GAM288  FLJ23518  3'  CGACTGTCAAGTGAATGAGCTG 45306       _  C___       III
            TTG                    AACAGC CA    CTTGACAGTC   G
                                 ||||||  ||    ||||||||||   |
                                 TTGTCG GT    GAACTGTCAG   C
                                    A  AAGT        III
GAM288  FLJ32334  3'  ACTGCCCTCAGGGTGGCTGTTA 57980            ___
                                 TAACAGCCACCTTGA   CAGT
                                 ||||||||||||||||   ||||
                                 ATTGTCGGTGGGACT   GTCA
                                          CCC
GAM288  KIAA0418  5'  GACCACAGTGTGGCTGT     27556        C   ACA
                                 ACAGCCAC TTG   GTC
                                 |||||||| |||   |||
                                 TGTCGGTG GAC   CAG
                                    T   AC_
GAM288  KIAA0438  3'  TTAAGATAGCTGTTGTA     29075        CAC
                                 TATAACAGC   CTTGA
                                 |||||||||   |||||
                                 ATGTTGTCG   GAATT
                                    ATA
GAM288  KIAA0459  3'  GACTGTTGTCAGCAGCTGTTA  60996       CACCT_
                                 TAACAGC     TGACAGTC
                                 |||||||     ||||||||
                                 ATTGTCG     GTTGTCAG
                                    ACGACT
GAM288  KIAA1280  5'  GACTGTCCGTGGTGGCTGT    69716        TT_
                                 ACAGCCACC   GACAGTC
                                 |||||||||   |||||||
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                                TGTCGGTGG   CTGTCAG
                                      TGC
GAM288  KIAA1376  3'  GACTGTCAAGATTGT      63622      CCAC
                                ACAG    CTTGACAGTC
                                ||||    ||||||||||
                                TGTT    GAACTGTCAG
                                  A___
GAM288  KIAA1962  3'  ACAGTTAAAAGCTGTTATA   81915         CACC    A
                                TATAACAGC    TTGAC GT
                                |||||||||    ||||| ||
                                ATATTGTCG    AATTG CA
                                      AA__     A
GAM288  MGC19606  3'  TCAGGATGGGGCTGTCATA   53042     A     AC__
                                TAT ACAGCC    CTTGA
                                ||| ||||||    |||||
                                ATA TGTCGG    GGACT
                                  C      GGTA
GAM288  MGC3178   3'  ACTGTCAAGAGTCTTGT     47981      CC  _
                                ACAG  AC CTTGACAGT
                                ||||  || |||||||||
                                TGTT  TG GAACTGTCA
                                  C_  A
GAM288  MPPE1     5'  AAGCATGGCTGTTATA      43559          C_
                                TATAACAGCCA  CTT
                                ||||||||||  |||
                                ATATTGTCGGT  GAA
                                       AC
GAM288  NMP200    3'  GACGTGGTGGTGGCTGTT    27174          TTGA  _
                                AACAGCCACC    CA GTC
                                ||||||||||    || |||
                                TTGTCGGTGG    GT CAG
                                      TG__  G
GAM288  NUDT13    3'  ACTGCCAAAATGTGCCTGTTGT 63212        C   C__   A
            A                    TATAACAG CAC   TTG CAGT
                                ||||||||| |||   ||| ||||
                                ATGTTGTC GTG   AAC GTCA
                                     C   TAA   C
GAM288  NYD-SP25  5'  ACTGTCAAGGTGTCCATTGTA  53183      CAGC
                                TATAA    CACCTTGACAGT
                                |||||    ||||||||||||
                                ATGTT    GTGGAACTGTCA
                                   ACCT
GAM288  PC4       3'  ACTGTCAAAATGTTAT      22011       GCCACC
                                ATAACA     TTGACAGT
                                ||||||     ||||||||
                                TATTGT     AACTGTCA
                                   AA_____
GAM288  PDE1C     3'  GACTGTCAATGCCGTTA     17220      A  CACC
                                TAAC GC    TTGACAGTC
                                |||| ||    |||||||||
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                                ATTG CG    AACTGTCAG
                                  C  T___
GAM288  PEPP3     3'  GACTGCCTGGGAGATGGCTGTT 30040         ___   TGA
              A                    TAACAGCCA   CCT   CAGTC
                                   |||||||||   |||   |||||
                                   ATTGTCGGT   GGG   GTCAG
                                        AGA   TCC
GAM288  PRO1992   5'  TAAGGTGGCTAGTATA      26060      AC
                                   TATA  AGCCACCTTG
                                   ||||  ||||||||||
                                   ATAT  TCGGTGGAAT
                                     GA
GAM288  PTGES2    3'  GACCCTCAGTGGCTGT      46881        CT   CA
                                   ACAGCCAC  TGA  GTC
                                   ||||||||  |||  |||
                                   TGTCGGTG  ACT  CAG
                                        __  CC
GAM288  SRP9      3'  GACTGTCACAACTGTTATG   79192        CCACCT
                                   TATAACAG     TGACAGTC
                                   ||||||||     ||||||||
                                   GTATTGTC     ACTGTCAG
                                        AAC___
GAM288  SYNE-1    5'  GACCATCAAGGTGCTG      30968      C      CA
                                   CAGC ACCTTGA  GTC
                                   |||| |||||||  |||
                                   GTCG TGGAACT  CAG
                                     _      AC
GAM288  ZNF185    3'  ACTCAGAGAGGTGGCTATTG   23105     C       GAC_
                                   TAA AGCCACCTT    AGT
                                   ||| |||||||||    |||
                                   GTT TCGGTGGAG    TCA
                                     A        AGAC
GAM288  LOC130507 3'  GACTTCCATGGCTTGTTATA   74951        _   CCT  AC
                                   TATAACA GCCA   TG  AGTC
                                   ||||||| ||||   ||  ||||
                                   ATATTGT CGGT   AC  TCAG
                                        T   ___  CT
GAM288  LOC134359 5'  ACTGTCAGGTTGCCGT      75182     A  C    T
                                   AC GC ACCT GACAGT
                                   || || |||| ||||||
                                   TG CG TGGA CTGTCA
                                    C  T   _
GAM288  LOC143914 5'  GACTGTCAAAGTGGTTGT    76612         C
                                   ACAGCCAC TTGACAGTC
                                   |||||||| |||||||||
                                   TGTTGGTG AACTGTCAG
                                        A
GAM288  LOC144465 5'  ACTATCAAGTGAACCACTGTTA 76851         C____   C    C
              TG                     TATAACAG     CAC TTGA AGT
                                   ||||||||     ||| |||| |||
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                                GTATTGTC    GTG AACT TCA
                                     ACCAA  _   A
GAM288  LOC148078 3'  GACCCGTAAGTGGCTGT    84112        C  ACA
                                ACAGCCAC TTG  GTC
                                |||||||| |||  |||
                                TGTCGGTG AAT  CAG
                                     _  GCC
GAM288  LOC150378 5'  GACTGATGTGAGGTGGCT    79745         A__
                                AGCCACCTTG  CAGTC
                                ||||||||||  |||||
                                TCGGTGGAGT  GTCAG
                                      GTA
GAM288  LOC153727 5'  GACTGTCAAAACTTGTT    86152      CCACC
                                AACAG    TTGACAGTC
                                |||||    |||||||||
                                TTGTT    AACTGTCAG
                                   CAA__
GAM288  LOC163231 5'  TCAGCAGGTGGCTGTTA    82443          __
                                TAACAGCCACCT  TGA
                                ||||||||||||  |||
                                ATTGTCGGTGGA  ACT
                                      CG
GAM288  LOC201931 3'  ACTTCTGTGGCTGTTTA    89108   T      CTT  C
                                A AACAGCCAC   GA AGT
                                | |||||||||   || |||
                                A TTGTCGGTG   CT TCA
                                 T       T__  _
GAM288  LOC253698 3'  ACTGTCAAGAGCCGTGTTA   94887      __  CAC
                                TAACA  GC   CTTGACAGT
                                |||||  ||   |||||||||
                                ATTGT  CG   GAACTGTCA
                                   GC  A__
GAM288  LOC256158 5'  GACAGGCGAGGTGGCCGTCATG 97665    A  A       ACA
                                TAT AC GCCACCTTG   GTC
                                ||| || |||||||||   |||
                                GTA TG CGGTGGAGC   CAG
                                  C  C        GGA
GAM288  LOC90906  3'  CAAGGTGGCTGTTATA     64293
                                TATAACAGCCACCTTG
                                ||||||||||||||||
                                ATATTGTCGGTGGAAC

GAM288  LOC91012  3'  TAAGGTGGTTGCTATA     64643     A
                                TATA CAGCCACCTTG
                                |||| ||||||||||
                                ATAT GTTGGTGGAAT
                                   C
GAM289  AXIN1     3'  CGAGTGCCTTCAACACAGCTT  60850       A       AA_
                                AAGCTG GTTGAAGG   TTG
                                |||||| ||||||||   |||
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                                TTCGAC CAACTTCC   AGC
                                   A       GTG
GAM289  CNTN1    3'  ACAATTCCTTCCAATTT     8457       _
                                GAGTTG AAGGAATTGT
                                |||||| ||||||||||
                                TTTAAC TTCCTTAACA
                                   C
GAM289  CSF1R    3'  CACAGACCACACTCAGCT    17802        TGAA  AA
                                AGCTGAGT   GG  TTGTG
                                ||||||||   ||  |||||
                                TCGACTCA   CC  GACAC
                                    CA__  A_
GAM289  CYP1A1   5'  CACCCTTCCCAGCTCAGCT   4941          AA   TT
                                AGCTGAGTTG  GGAA  GTG
                                ||||||||||  ||||  |||
                                TCGACTCGAC  CCTT  CAC
                                     __   CC
GAM289  EPB49    3'  CAGGCCCCAGCTCAGC      8783         AA  AA
                                GCTGAGTTG  GG  TTG
                                |||||||||  ||  |||
                                CGACTCGAC  CC  GAC
                                     __ CG
GAM289  FZD4     3'  CAGTGACCTTCAATCAACT   24130    C  G      A_
                                AG TGA TTGAAGG  ATTG
                                || ||| |||||||  ||||
                                TC ACT AACTTCC  TGAC
                                 A  _      AG
GAM289  GCN5L2   3'  CACGGACCCGACTCAGCTT   59839          AA  AA
                                AAGCTGAGTTG  GG  TTGTG
                                ||||||||||  ||  |||||
                                TTCGACTCAGC  CC  GGCAC
                                     __ A_
GAM289  HLA-G    3'  CACAATTCCTCCTCTGGC    9223      _  TTGA
                                GCT GAG   AGGAATTGTG
                                ||| |||   ||||||||||
                                CGG CTC   TCCTTAACAC
                                  T  C___
GAM289  IHH      3'  GCGACTCCCAACTCAGC     72113         AA  A
                                GCTGAGTTG  GGA TTGT
                                |||||||||  ||| ||||
                                CGACTCAAC  CCT AGCG
                                     __  C
GAM289  IHPK3    5'  ACAGGCCATCTCAGCTT     54021        TTGAA  AA
                                AAGCTGAG    GG  TTGT
                                ||||||||    ||  ||||
                                TTCGACTC    CC  GACA
                                    TA___  G_
GAM289  PCDH9    5'  CAATTTTCAACCAGC       82793      A    AG
                                GCTG GTTGA  GAATTG
                                |||| |||||  ||||||
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                                CGAC CAACT  TTTAAC
                                  _    __
GAM289  PIN1L    3'  CACAATTCAGCGACTGCAGCT  20619      _    AAG
                                AGCTG AGTTG   GAATTGTG
                                ||||| |||||   ||||||||
                                TCGAC TCAGC   CTTAACAC
                                   G    GA_
GAM289  RFPL2    5'  TTCCTCCACCTCAGCT      21729       T  A
                                AGCTGAG TG AGGAA
                                ||||||| || |||||
                                TCGACTC AC TCCTT
                                    C  C
GAM289  RFPL3    5'  TTCCTCCACCTCAGCT      21724       T  A
                                AGCTGAG TG AGGAA
                                ||||||| || |||||
                                TCGACTC AC TCCTT
                                    C  C
GAM289  SCG3     3'  CAGGTCCCTGCAACTCAGC   25097        AA_  A
                                GCTGAGTTG   GGA TTG
                                |||||||||   ||| |||
                                CGACTCAAC   CCT GAC
                                     GTC   G
GAM289  SLC1A1   3'  CACGATTCCAACCCAG      14792     A   GAA
                                CTG GTT   GGAATTGTG
                                ||| |||   |||||||||
                                GAC CAA   CCTTAGCAC
                                  C  ___
GAM289  SLC22A7  3'  CAGGCCCTTCAACTCAGGCT  21911     _        AA
                                AGC TGAGTTGAAGG  TTG
                                ||| ||||||||||  |||
                                TCG ACTCAACTTCC  GAC
                                  G         CG
GAM289  SLC2A4   3'  CACCTTCCCCAGACTCAGCT  6439         GAA   TT
                                AGCTGAGTT   GGAA  GTG
                                |||||||||   ||||  |||
                                TCGACTCAG   CCTT  CAC
                                     ACC   C_
GAM289  TCF7     3'  CACAATTCCATTTCCAGTT   12157      AGTT  A
                                AGCTG   GA GGAATTGTG
                                |||||   || |||||||||
                                TTGAC   TT CCTTAACAC
                                   CT__  A
GAM289  TFF3     3'  ACTGTTCATCTCAGCTT     63564        TTGAAG   T
                                AAGCTGAG     GAAT GT
                                ||||||||     |||| ||
                                TTCGACTC     CTTG CA
                                     TA____   T
GAM289  TIMP3    3'  ACAATTCCCCAGCCCA      4500     A   AA
                                TG GTTG  GGAATTGT
                                || ||||  ||||||||
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                                AC CGAC  CCTTAACA
                                 C   C_
GAM289  FBXO27   3'  GAAGCCCTCAACTCATCT    74510    C      A  AA
                                AG TGAGTTGA GG  TT
                                || |||||||| ||  ||
                                TC ACTCAACT CC  AG
                                 T       C  GA
GAM289  FLJ10853 3'  CATTTCCTAACTCAGCTT    36766         GA    T
                                AAGCTGAGTT  AGGAA TG
                                ||||||||||  ||||| ||
                                TTCGACTCAA  TCCTT AC
                                      __    T
GAM289  FLJ12409 3'  CCTTCTCAACTCACCTT     47046     C      __
                                AAG TGAGTTGA  AGG
                                ||| ||||||||  |||
                                TTC ACTCAACT  TCC
                                  C       CT
GAM289  FYCO1    3'  CAAAATCATCAACTCAGC    44487         A  AA
                                GCTGAGTTGA GG  TTG
                                |||||||||| ||  |||
                                CGACTCAACT CT  AAC
                                      A  AA
GAM289  HEMK     3'  CACAATTCCCTGGCCAAGC   32428     GA   GAA
                                GCT  GTT   GGAATTGTG
                                |||  |||   |||||||||
                                CGA  CGG   CCTTAACAC
                                  AC   TC_
GAM289  KIAA0056 3'  CACAACTTTAAAACTGCAGCTT 91554       _   GAA   A
                                AAGCTG AGTT   GGA TTGTG
                                |||||| ||||   ||| |||||
                                TTCGAC TCAA   TTT AACAC
                                   G   AA_   C
GAM289  KIAA0323 3'  CAGCCGCCTCCAGCTCAGC   63258         A   AA_
                                GCTGAGTTG AGG   TTG
                                ||||||||| |||   |||
                                CGACTCGAC TCC   GAC
                                      C   GCC
GAM289  KIAA0522 3'  CAGCTCCTCACTCAGCT     71966        T  A   A
                                AGCTGAGT GA GGA TTG
                                |||||||| || ||| |||
                                TCGACTCA CT CCT GAC
                                     _ _   C
GAM289  KIAA0820 3'  CACATATGGCTCAACTCAAGT  69021     _      AGGAAT
                                GCT GAGTTGA      TGTG
                                ||| |||||||      ||||
                                TGA CTCAACT      ACAC
                                  A      CGGTAT
GAM289  KIAA0914 5'  CATGCCCCCAACCCAGCTT    29677       A    AA  AAT
                                AAGCTG GTTG  GG   TG
                                |||||| ||||  ||   ||
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                                TTCGAC CAAC  CC   AC
                                   C   CC  GT_
GAM289  KIAA1032  5'  ACAATTCCTCCGACCGC     66148    T A    A
                                GC G GTTG AGGAATTGT
                                || | |||| |||||||||
                                CG C CAGC TCCTTAACA
                                 _ _   C
GAM289  KIAA1303  3'  CAGTCCTTCAACTCA       65999           A
                                TGAGTTGAAGGA TTG
                                |||||||||||| |||
                                ACTCAACTTCCT GAC
                                          _
GAM289  KIAA1321  3'  CACAATTCCTTACAGAGCACTT 62224     C  AG  _
                                AAG TG  TTG AAGGAATTGTG
                                ||| ||  ||| ||||||||||
                                TTC AC  GAC TTCCTTAACAC
                                  _ GA   A
GAM289  KIAA1441  3'  ACAATTCCTTCAGGC       88409     GAGT
                                GCT    TGAAGGAATTGT
                                |||    ||||||||||||
                                CGG    ACTTCCTTAACA
                                 _____
GAM289  KIAA1449  3'  CACAATTTGAGAACCAGC    40449      A  GAAG
                                GCTG GTT    GAATTGTG
                                |||| |||    ||||||||
                                CGAC CAA    TTTAACAC
                                  _   GAG_
GAM289  LPAAT-delta 5'  CGGCTCCATCTCAGCTT     39288         TTGAA   A
                                AAGCTGAG     GGA TTG
                                ||||||||     ||| |||
                                TTCGACTC     CCT GGC
                                     TA___   C
GAM289  QKI       3'  TCCTCCAACTCAGCTT      65447           A
                                AAGCTGAGTTG AGGA
                                |||||||||| ||||
                                TTCGACTCAAC TCCT
                                      C
GAM289  TReP-132  5'  CAGGCCCCCAACTCAGC     37290         AA  AA
                                GCTGAGTTG  GG  TTG
                                |||||||||  ||  |||
                                CGACTCAAC  CC  GAC
                                     C_  CG
GAM289  TReP-132  5'  CAGGCCCCCAACTCAGC     53146         AA  AA
                                GCTGAGTTG  GG  TTG
                                |||||||||  ||  |||
                                CGACTCAAC  CC  GAC
                                     C_  CG
GAM289  TReP-132  5'  CAGGCCCCCAACTCAGC     53137         AA  AA
                                GCTGAGTTG  GG  TTG
                                |||||||||  ||  |||
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                                CGACTCAAC CC GAC
                                     C_ CG
GAM289  TSGA14   3' CATTTTTCCACACTCAGCTT 38042       TGAA  TT
                                AAGCTGAGT  GGAA GTG
                                |||||||||  |||| |||
                                TTCGACTCA  CCTT TAC
                                     CA__  TT
GAM289  ZNF302   3' TCCTTCAACCAGCTT     37929     A
                                AAGCTG GTTGAAGGA
                                |||||| |||||||||
                                TTCGAC CAACTTCCT
                                   _
GAM289  LOC120772 5' CACTTGTGCCCCCAGCTCAGC 74022       AA AATT_
                                GCTGAGTTG GG   GTG
                                ||||||||| ||   |||
                                CGACTCGAC CC   CAC
                                     CC GTGTT
GAM289  LOC254873 3' CACCTTCCCCAGACTCAGCT  94569       GAA  TT
                                AGCTGAGTT  GGAA GTG
                                |||||||||  |||| |||
                                TCGACTCAG  CCTT CAC
                                     ACC   C_
GAM289  LOC256867 5' CACTTGTGCCCCCAGCTCAGC 94861       AA AATT_
                                GCTGAGTTG GG   GTG
                                ||||||||| ||   |||
                                CGACTCGAC CC   CAC
                                     CC GTGTT
GAM289  LOC92249  5' TTCCTTCAAACTCAGCT    68568       _
                                AGCTGAGTT GAAGGAA
                                ||||||||| |||||||
                                TCGACTCAA CTTCCTT
                                     A
GAM290  AQP3     3' TTGCCCAAATAGCACCTTA  59594       C_  A
                                TAAGGTGC  TTTG GCAG
                                ||||||||  |||| ||||
                                ATTCCACG  AAAC CGTT
                                     AT   C
GAM290  NRL      3' ATCTCGCCAAAGGCACCT   20514        A _
                                AGGTGCCTTTG GC AGAT
                                |||||||||| || ||||
                                TCCACGGAAAC CG TCTA
                                      _ C
GAM290  KIAA0022 3' TCTATAACAGGCACCTTA   29673       TTGAGCAG
                                TAAGGTGCCT     ATAGA
                                ||||||||||     |||||
                                ATTCCACGGA     TATCT
                                     CAA_____
GAM290  KIAA1077 5' ATCTTCAAAGGACCCT    72902    TG    GC
                                AGG CCTTTGA AGAT
                                |||  ||||||| ||||
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                                TCC  GGAAACT  TCTA
                                  CA      __
GAM290  LOC124152 3'  CTATCTGCCCATGCTTTA    74257        CCTT  A
                                TAAGGTG    TG GCAGATAG
                                |||||||    || ||||||||
                                ATTTCGT    AC CGTCTATC
                                    _____  C
GAM290  LOC126549 5'  CTATCTGCTGCTGGACC     75709     G  TTTG
                                GGT CC    AGCAGATAG
                                ||| ||    |||||||||
                                CCA GG    TCGTCTATC
                                  _  TCG_
GAM290  LOC145845 3'  ATCTATCTAGAGACAAACCCTT 83550       ___  C    GAGC
           A                     TAAGG   TG CTTT    AGATAGAT
                                |||||   || ||||    ||||||||
                                ATTCC   AC GAGA    TCTATCTA
                                   CAA  A   _____
GAM290  LOC149401 3'  CTGCTCAAAAGTCACCTTA    79334        _ C
                                TAAGGTG C TTTGAGCAG
                                ||||||| | |||||||||
                                ATTCCAC G AAACTCGTC
                                    T A
GAM290  LOC159989 3'  TGACTCAAAGGCAGCT      82205     G        _
                                AG TGCCTTTGAG CA
                                || ||||||||| ||
                                TC ACGGAAACTC GT
                                 G         A
GAM291  ACCN1    3'  TATTAAAAGCTGGTCTTGTGGA 6584         __     TA    CC
           AA                     TTTTCAC  GGCCA  GCTT  AATA
                                |||||||  |||||  ||||  ||||
                                AAAGGTG  CTGGT  CGAA  TTAT
                                    TT     __    AA
GAM291  IRF2     5'  TTGGTAGCGTGAAAA      9358         GGCCATA   T
                                TTTTCAC      GCT CCAA
                                |||||||      ||| ||||
                                AAAAGTG      CGA GGTT
                                    ________  T
GAM291  PABPN1   5'  ATTGGAAGCTGTCCAGGAAAA  16174      AC  CC
                                TTTTC  GG  ATAGCTTCCAAT
                                |||||  ||  ||||||||||||
                                AAAAG  CC  TGTCGAAGGTTA
                                   GA  __
GAM291  TPO      5'  GAGTTACAGCCGTGAAAA    5046          CA
                                TTTTCACGGC  TAGCTT
                                ||||||||||  ||||||
                                AAAAGTGCCG  ATTGAG
                                      AC
GAM291  ARHU     3'  TATTAGAAGCTATATTAGCTG  41079      C___       C
                                CGGC    ATAGCTTC AATA
                                ||||    |||||||| ||||
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                                GTCG    TATCGAAG TTAT
                                  ATTA       A
GAM291  FLJ12998  3'  ATTGGTTTTGCCGTGAAAA   42835          CATAGCTT
                                TTTTCACGGC       CCAAT
                                ||||||||||       |||||
                                AAAAGTGCCG       GGTTA
                                     TTTT_____
GAM291  GNB4      3'  AGCCTATAGCTGTGAAAA    41267          C   _
                                TTTTCACGGC ATAG CT
                                |||||||||| |||| ||
                                AAAAGTGTCG TATC GA
                                     A   C
GAM291  LOC150418 3'  GAGTCGGCCGTGAAGA      65509          ATA
                                TTTTCACGGCC   GCTT
                                ||||||||||   ||||
                                AGAAGTGCCGG   TGAG
                                     C__
GAM291  LOC199957 3'  GAGTCGGCCGTGAAGA      88505          ATA
                                TTTTCACGGCC   GCTT
                                ||||||||||   ||||
                                AGAAGTGCCGG   TGAG
                                     C__
GAM291  LOC91431  5'  ATTGGAAATGCAAGGCCGTGGA 56922          ATA  __
          AA                    TTTTCACGGCC   GC  TTCCAAT
                                ||||||||||   ||  |||||||
                                AAAGGTGCCGG   CG  AAGGTTA
                                     AA_  TA
GAM292  A1BG      3'  GCAACCTCTACCTCCT      55419    A
                                AG AGGTAGAGGTTGC
                                || ||||||||||||
                                TC TCCATCTCCAACG
                                 C
GAM292  ACVR1     5'  AGCCCACTGCAGCCTCCACCT  6601       A          T
                                AGGT GAGGTTGCAGTG GCT
                                |||| |||||||||||| |||
                                TCCA CTCCGACGTCAC CGA
                                  C          C
GAM292  ADRB3     3'  AGCCTTTCCACAACCTCTACCT 3430             CAGTGT_
          TC                    GAAGGTAGAGGTTG      GCT
                                ||||||||||||||      |||
                                CTTCCATCTCCAAC      CGA
                                     ACCTTTC
GAM292  AHR       3'  ACTGCAACCTCTACCTCCT    7874     A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCATCTCCAACGTCA
                                 C
GAM292  AIM1      3'  ACTGCAGCCTCTACCT       91811
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
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                                TCCATCTCCGACGTCA

GAM292  AKAP1    3'  AGCACACACACCCTACCTTC   57707        A   TGCA
                                GAAGGTAG GGT    GTGTGCT
                                |||||||| |||    |||||||
                                CTTCCATC CCA    CACACGA
                                     _   CA__
GAM292  ALDH1B1  3'  ACTGCAACCTCCGCCT      5484      TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  APPBP2   3'  ACTGCAACCTCCGCCT      21067     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  AQP6     3'  ACTGCAACCTCTACCTCCT    53907    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCATCTCCAACGTCA
                                 C
GAM292  AQP6     3'  ACTGCAACCTCTACCTCCT    7938     A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCATCTCCAACGTCA
                                 C
GAM292  ARCN1    3'  AGCTCACTGCAACCTCCGCCTC 7971     A   TA         T
            CT                    AG AGG  GAGGTTGCAGTG GCT
                                || |||  |||||||||||| |||
                                TC TCC  CTCCAACGTCAC CGA
                                 C   GC          T
GAM292  ATP8B2   3'  AGCTCACTGCAACCTCCACCTC 65211    A    A         T
            CT                    AG AGGT GAGGTTGCAGTG GCT
                                || |||| |||||||||||| |||
                                TC TCCA CTCCAACGTCAC CGA
                                 C    C          T
GAM292  B4GALT5  3'  ACCCTGCAACCCCCATC     16493    A  TAGA      T
                                GA GG    GGTTGCAG GT
                                || ||    |||||||| ||
                                CT CC    CCAACGTC CA
                                 A  C___       C
GAM292  BCL2L2   3'  AGCACACTCTTCACCCTACCCT 14462    A    A   TGC_
            CT                    AGA GGTAG GGT    AGTGTGCT
                                ||| ||||| |||    ||||||||
                                TCT CCATC CCA    TCACACGA
                                  C     _   CTTC
GAM292  BSN      3'  CACACTGCCACCATCT      12917     _   T
                                AGA GGT GCAGTGTG
                                ||| ||| ||||||||
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                                TCT CCA CGTCACAC
                                  A   C
GAM292  C7      3'  CTGCAACCTCCGCCTCCT    5164     A   TA
                                AG AGG  GAGGTTGCAG
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTC
                                 C   GC
GAM292  CAMLG   3'  ACCGCAACCTCCACCTTC    8230       A      A
                                GAAGGT GAGGTTGC GT
                                |||||| |||||||| ||
                                CTTCCA CTCCAACG CA
                                   C       C
GAM292  CDH17   3'  AGCTCACTGCAACCTCCGCCTC 14500    A   TA         T
            CT                    AG AGG  GAGGTTGCAGTG GCT
                                || |||  |||||||||||| |||
                                TC TCC  CTCCAACGTCAC CGA
                                 C   GC          T
GAM292  CIAS1   5'  ACTGCAGCCTCCACCT      16894      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCGACGTCA
                                  C
GAM292  CLECSF12 3'  ACCGCAACCTCCGCCCCCT   76682    AA  TA      A
                                AG  GG  GAGGTTGC GT
                                ||  ||  |||||||| ||
                                TC  CC  CTCCAACG CA
                                 CC  GC       C
GAM292  COX15   3'  ACTCTGCAACCTCCACTTC    54309      GTA        T
                                GAAG   GAGGTTGCAG GT
                                ||||   |||||||||| ||
                                CTTC   CTCCAACGTC CA
                                  AC_         T
GAM292  CSNK2A2  5'  AGCTCACTGCAACCTCCACCT  8558       A          T
                                AGGT GAGGTTGCAGTG GCT
                                |||| |||||||||||| |||
                                TCCA CTCCAACGTCAC CGA
                                  C          T
GAM292  CXCL16   3'  ACTGCAACCCCCATCTCC    41913    T  ____
                                GG AGA    GGTTGCAGT
                                || |||    |||||||||
                                CC TCT    CCAACGTCA
                                 _   ACCC
GAM292  CYP1A2   3'  AGCTCACTGCAACCTCCACCTC 5674     A   A          T
                                GA GGT GAGGTTGCAGTG GCT
                                || ||| |||||||||||| |||
                                CT CCA CTCCAACGTCAC CGA
                                 _  C          T
GAM292  CYP1A2   3'  AGCTCACTGCAACCTCTGCCT  5675               T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
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                                TCCGTCTCCAACGTCAC CGA
                                           T
GAM292  CYP1A2   3'  AGCTCACTGCAACCTCCACCTC 69093    A   A         T
                                GA GGT GAGGTTGCAGTG GCT
                                || ||| ||||||||||||| |||
                                CT CCA CTCCAACGTCAC CGA
                                 _  C          T
GAM292  CYP1A2   3'  AGCTCACTGCAACCTCTGCCT  69094              T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                           T
GAM292  CYP2B6   3'  ACTGCAACCTCTGCCTTC    5722
                                GAAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CTTCCGTCTCCAACGTCA

GAM292  CYP4F3   3'  ATTGCAACCTCCGCCTCCT   6109     A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTTA
                                 C   GC
GAM292  CYP8B1   3'  ACTACAACCTCTGCCT      15249           C
                                AGGTAGAGGTTG AGT
                                |||||||||||| |||
                                TCCGTCTCCAAC TCA
                                      A
GAM292  CYP8B1   3'  ACTGCAACCTCTGCCTCCT   15255    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  DHFR     3'  ACTGCAACCTCCGCCTTC    5798       TA
                                GAAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CTTCC  CTCCAACGTCA
                                   GC
GAM292  DISC1    3'  ACTGCAACCTCTACCT      37868
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCATCTCCAACGTCA

GAM292  DSCR3    3'  AGCTCACTGCAACCTCCACCT  20170      A         T
                                AGGT GAGGTTGCAGTG GCT
                                |||| |||||||||||| |||
                                TCCA CTCCAACGTCAC CGA
                                   C          T
GAM292  EHD2     3'  AGCTCACTGCAACCTCCACCTC 27486    A   A         T
             CT                   AG AGGT GAGGTTGCAGTG GCT
                                || |||| |||||||||||| |||
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                                TC TCCA CTCCAACGTCAC CGA
                                 C   C          T
GAM292  EPB72   3' ACTGCAACCTCCGCCTCCT  14598   A  TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||||
                                TC TCC  CTCCAACGTCA
                                 C  GC
GAM292  F2RL2   3' ATTGCAACCTCTGCCT     14616
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTTA

GAM292  FEZ1    3' ACTGCAACCTCCACCT     42562     A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  FGF5    3' ACTGCAACCTCCAACT     52474     A_
                                GGT  GAGGTTGCAGT
                                |||  ||||||||||||
                                TCA  CTCCAACGTCA
                                  AC
GAM292  FGF5    3' ACTGCAACCTCCAACT     15528     A_
                                GGT  GAGGTTGCAGT
                                |||  ||||||||||||
                                TCA  CTCCAACGTCA
                                  AC
GAM292  FZD4    3' ACTGCAACCTCTGCCTCCT  24123    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  G6PC    3' ACTGCAACCTCTTCCTCCT  3819     A  T
                                AG AGG AGAGGTTGCAGT
                                || ||| ||||||||||||
                                TC TCC TCTCCAACGTCA
                                 C  T
GAM292  GHR     3' ACTGCAATCTCCACCT     3874      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||||
                                TCCA CTCTAACGTCA
                                  C
GAM292  GM2A    3' ACTGCAACCTCCGCCTCCT  67769    A  TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||||
                                TC TCC  CTCCAACGTCA
                                 C  GC
GAM292  GPR4    3' ACTGCAGCCTCCACCTCCT  59900    A  A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||||
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                                TC TCCA CTCCGACGTCA
                                 C   C
GAM292  GPR81    3'  ACTGCAACCTCTGCCT      50748
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  GRAF     3'  ACTGCAACCTCCGCCT      30546     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  HCS      3'  ACCGCAACCTCCGCCTTC    38453       TA       A
                                GAAGG  GAGGTTGC GT
                                |||||  |||||||| ||
                                CTTCC  CTCCAACG CA
                                   GC       C
GAM292  HCS      3'  ACTGCAACCTCCGCCTTC    38457       TA
                                GAAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CTTCC  CTCCAACGTCA
                                   GC
GAM292  HTR1E    5'  ATTGCAACCTCCGCCT      6007      TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTTA
                                  GC
GAM292  IL11     3'  GGTCACTGCAAGCTCCACCT   5332       A   G       T
                                AGGT GAG TTGCAGTG GCT
                                |||| ||| |||||||| |||
                                TCCA CTC AACGTCAC TGG
                                  C   G       _
GAM292  IRF1     5'  ACCCGGCAACCTCTGCCTTCT  64344              AGT
                                AGAAGGTAGAGGTTGC   GT
                                ||||||||||||||||   ||
                                TCTTCCGTCTCCAACG   CA
                                          GCC
GAM292  IRF2     3'  AGCACACTCAGCACCCCCTTCT 9354         TAGAG    C
                                AGAAGG    GTTG AGTGTGCT
                                ||||||    |||| ||||||||
                                TCTTCC    CGAC TCACACGA
                                   CCCA_   _
GAM292  ITGAM    3'  ACTGCAACCTCCGCCT      71831     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  KCNA3    3'  AGCACACTTCATTCTCCCTCT  9505      A  TA   GT  C
                                AGA GG  GAG  TG AGTGTGCT
                                ||| ||  |||  || ||||||||
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                                TCT CC  CTC  AC TCACACGA
                                  _ __   TT  T
GAM292  KLK5    3'  AGCACACCGGCATCCCCACCTG 24859    A   AGA  T  A_
            CT                    AG AGGT   GG TGC  GTGTGCT
                                || ||||   || |||  |||||||
                                TC TCCA   CC ACG  CACACGA
                                 G    CC_  T   GC
GAM292  KMO     3'  ACTGCAACCTCTGCCTCCT    13442    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  LNK     3'  ACTGCAACCTCCACCTTC     18455       A
                                GAAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CTTCCA CTCCAACGTCA
                                    C
GAM292  LYZ     3'  ACTGCAACCTCCACCT      4094       A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  LZTS1   3'  ACCTTGCAACCTCACCTTC   40677       A        T
                                GAAGGT GAGGTTGCAG GT
                                |||||| |||||||||| ||
                                CTTCCA CTCCAACGTT CA
                                   _         C
GAM292  MAK     3'  ACTGCAACCTCCACCTCCT   19754    A   A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||
                                TC TCCA CTCCAACGTCA
                                 C   C
GAM292  MEFV    3'  ACTGCAACCTCCGCCT      4120      TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  MEFV    3'  AGCTCACTGCAACCTCCACCT  4124       A         T
                                AGGT GAGGTTGCAGTG GCT
                                |||| |||||||||||| |||
                                TCCA CTCCAACGTCAC CGA
                                  C          T
GAM292  MICB    3'  AGCTCACTGCAACCTCTGCCT  19819              T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                            T
GAM292  MPL     3'  AGCTCACTGCAACCTCCACCT  18130      A         T
                                AGGT GAGGTTGCAGTG GCT
                                |||| |||||||||||| |||
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                                TCCA CTCCAACGTCAC CGA
                                  C          T
GAM292  MPL      3'  ACTGCAACCTCTGCCT      18126
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  MYCL2    3'  ACTGCAACCTCTGCCT      18169
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  NDRG3    3'  ACTGCAACCTCTGCCCCCT   49289    AA
                                AG  GGTAGAGGTTGCAGT
                                ||  ||||||||||||||
                                TC  CCGTCTCCAACGTCA
                                 CC
GAM292  NQO1     3'  ACTGCAACCTCTGCCT      6147
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  NR1I2    5'  AGCACACTGTTCAGGCTACTTC 13962      G   AGGTT
                                GAAG TAG    GCAGTGTGCT
                                |||| |||    ||||||||||
                                CTTC ATC    TGTCACACGA
                                  _  GGACT
GAM292  NSF      3'  CACATTTCCTTTACCCTC    63070    A      TTGC
                                GA GGTAGAGG    AGTGTG
                                || ||||||||    ||||||
                                CT CCATTTCC    TTACAC
                                 C       T___
GAM292  PCDHB11  3'  AGCTCACTGCAACCTCTGCCTC 38410    A             T
            CT                    AG AGGTAGAGGTTGCAGTG GCT
                                || |||||||||||||||| |||
                                TC TCCGTCTCCAACGTCAC CGA
                                 C              T
GAM292  PCDHB16  3'  ACTGCAACCTCTGCCTCCT   40548    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  PCDHB9   3'  AGCTCACTGCAACCTCCGCCT  38935     TA          T
                                AGG  GAGGTTGCAGTG GCT
                                |||  |||||||||||| |||
                                TCC  CTCCAACGTCAC CGA
                                  GC          T
GAM292  PDCL     3'  ACTGCAACCTCCACCTCCT   18207    A    A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||
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                                TC TCCA CTCCAACGTCA
                                 C   C
GAM292  PDE6B   3'  AGCTCACTGCAACCTCCACCT  4270      A         T
                                AGGT GAGGTTGCAGTG GCT
                                |||| |||||||||||| |||
                                TCCA CTCCAACGTCAC CGA
                                  C          T
GAM292  PER2    3'  ACTGCAACCTCTGCCT     43023
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  PIGR    3'  ACTGCAACCTCCGCCT     72587     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  PRKWNK3 3'  TGCTGCAACCTCCCCCTCCT  61560    A   TA
                                AG AGG  GAGGTTGCAGTG
                                || |||  ||||||||||||
                                TC TCC  CTCCAACGTCGT
                                 C   CC
GAM292  PSMB2   3'  ACTGCAACCTCCGCCT     10943     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  RASA1   3'  GCACACTTTTCCACATTC    42636     G  A    TTGC
                                GAA GT GAGG    AGTGTGC
                                ||| || ||||    |||||||
                                CTT CA CTTT    TCACACG
                                  A  C   ____
GAM292  RHD     3'  ACTGCAACCTCCGCCT     32289     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  RHD     3'  ACTGCAACCTCTACCTCCT   32294    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCATCTCCAACGTCA
                                 C
GAM292  RHD     3'  ACTGCAACCTCCGCCT     32598     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  RHD     3'  ACTGCAACCTCTACCTCCT   32603    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
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                                TC TCCATCTCCAACGTCA
                                 C
GAM292  RPH3AL   3'  ACTGCAACCTCCACCT      22738      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  RS1      3'  AGCTTCTCACCCTCCACCCTCT 4387      A   A    T  C  TGT
                                AGA GGT GAGG TG AG   GCT
                                ||| ||| |||| || ||   |||
                                TCT CCA CTCC AC TC   CGA
                                  C   C    C  _  TT_
GAM292  SACM2L   3'  ACACTAACCTCTCCCCTC    42588    A  T     GC
                                GA GG AGAGGTT  AGTGT
                                || || |||||||  |||||
                                CT CC TCTCCAA  TCACA
                                 C  C      __
GAM292  SACM2L   3'  ACACTAACCTCTCCCCTC    54542    A  T     GC
                                GA GG AGAGGTT  AGTGT
                                || || |||||||  |||||
                                CT CC TCTCCAA  TCACA
                                 C  C      __
GAM292  SAS      3'  ACCGCAACCTCTGCCT      19945            A
                                AGGTAGAGGTTGC GT
                                |||||||||||| ||
                                TCCGTCTCCAACG CA
                                        C
GAM292  SEDL     3'  ACTGCAACCTCCACCT      27314      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  SEDL     3'  ACTGCAACCTCCACCTCCT   27317    A   A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||
                                TC TCCA CTCCAACGTCA
                                 C    C
GAM292  SEDL     3'  ACTGCAACCTCCGCCT      27318     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  SEPN1    3'  ACTGCAACCTCCACCT      66357      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  SERPINB9 3'  ACTGCAACCTCCTCCTCCT   14747    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
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                                TC TCC  CTCCAACGTCA
                                 C   TC
GAM292  SHOX    3'  ACTGCAACCTCCGCCT     22525     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  SIL     3'  ACTGCAACCTCTGCCTCCT   11681    A
                                AG AGGTAGAGGTTGCAGT
                                ||  ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  SLA2    3'  AGCTCACTGCAACCTCCATCTC 49890    A   A          T
            CT                    AG AGGT GAGGTTGCAGTG GCT
                                ||  ||||  |||||||||||| |||
                                TC TCTA CTCCAACGTCAC CGA
                                 C   C          T
GAM292  SLC14A2  5'  ACTGCAACCTCCACCT     23127     A
                                AGGT GAGGTTGCAGT
                                ||||  ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  SLC15A1  3'  AGCTCACTGCAACCTCCGCCT  17396    TA         T
                                AGG  GAGGTTGCAGTG GCT
                                |||  ||||||||||| |||
                                TCC  CTCCAACGTCAC CGA
                                  GC          T
GAM292  SMAC    5'  ACTGCAACCTCTGCCT     57199
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  SNAP23  3'  ACTGCAACCTCCGCCT     13800     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  SNAP23  3'  ACTGCAACCTCCGCCT     55453     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  SNX15   3'  ACTGCAACCTCCACCT     73731     A
                                AGGT GAGGTTGCAGT
                                ||||  ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  SPN     3'  ACTGCAACCTCTGCCTCCT   11914    A
                                AG AGGTAGAGGTTGCAGT
                                ||  ||||||||||||||||
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                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  SS18     3'  AGCTCACTGCAACCTCCGCCT  18882     TA         T
                                AGG  GAGGTTGCAGTG GCT
                                |||  |||||||||||| |||
                                TCC  CTCCAACGTCAC CGA
                                  GC          T
GAM292  STAU     5'  ACTGCAACCTCCACCT      15992      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  SULT2B1  5'  ACTGCAACCTCCGCCTCCT   16020    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292  TAPBP    3'  ACTGCAACCTCCGCCTCCT   12119    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292  TAT      3'  ACTGCAACCTCCACCTCCT   4460     A   A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||
                                TC TCCA CTCCAACGTCA
                                 C   C
GAM292  TBXA2R   3'  ACTGCAACCTCCGCCT      6473      TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  TBXA2R   3'  AGCTCACTGCAACCTCCACCT  6479       A         T
                                AGGT GAGGTTGCAGTG GCT
                                |||| |||||||||||| |||
                                TCCA CTCCAACGTCAC CGA
                                  C          T
GAM292  TNFRSF10B 3'  TGCAACCTCCGCCTCCT     13883    A   TA
                                AG AGG  GAGGTTGCA
                                || |||  |||||||||
                                TC TCC  CTCCAACGT
                                 C   GC
GAM292  TPMT     3'  ACTGCAACCTCTGCCT      4529
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  TRIM9    5'  ACTGCAACCTCCGCCT      30743     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
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                                TCC  CTCCAACGTCA
                                  GC
GAM292  TRPM6   3' ACTGCAACCTCTGCCT     34526
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  TRPV1   3' ACTGCAACCTCTGCCT     38067
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  TRPV1   3' CTGCAACCTCCGCCTCCT    38082    A   TA
                                AG AGG  GAGGTTGCAG
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTC
                                 C   GC
GAM292  TRPV1   3' CTGCAACCTCCGCCTCCT    54868    A   TA
                                AG AGG  GAGGTTGCAG
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTC
                                 C   GC
GAM292  TRPV1   3' ACTGCAACCTCTGCCT     54786
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  TRPV1   3' CTGCAACCTCCGCCTCCT    54803    A   TA
                                AG AGG  GAGGTTGCAG
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTC
                                 C   GC
GAM292  TRPV1   3' ACTGCAACCTCTGCCT     54821
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  TRPV1   3' CTGCAACCTCCGCCTCCT    54836    A   TA
                                AG AGG  GAGGTTGCAG
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTC
                                 C   GC
GAM292  TRPV1   3' ACTGCAACCTCTGCCT     54853
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  TUFT1   3' AGCTCACTGCAACCTCTGCCT 39250            T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
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                                TCCGTCTCCAACGTCAC CGA
                                           T
GAM292  VENTX2   3' ACTGCAACCTCCGCCTCCT   27106    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||||
                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292  VHL     3' ACTGCAACCTCTGCCTCCT   5055     A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  ZNF133  5' CACTGCAACCTCCACCCCCT  12832    AA  A
                                AG  GGT GAGGTTGCAGTG
                                ||  ||| ||||||||||||
                                TC  CCA CTCCAACGTCAC
                                 CC   C
GAM292  ZNF264  3' ACTGCAACCTCCGCCTCCT   12744    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||||
                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292  20D7-FC4 5' AGCTCACTGCAGCCTCCACCTC 60894    A   A         T
           CT                    AG AGGT GAGGTTGCAGTG GCT
                                || |||| |||||||||||| |||
                                TC TCCA CTCCGACGTCAC CGA
                                 C   C          T
GAM292  ARHF    3' ACTGCAAGCTCCACCTCCT   38736    A   A   G
                                AG AGGT GAG TTGCAGT
                                || |||| ||| |||||||
                                TC TCCA CTC AACGTCA
                                 C   C   G
GAM292  ARPP-19 3' ACTGCAACCTCTGCCTCCT   21786    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  ASB16   5' ACTGCAACCTCCGCCT     69927     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  ASE-1   3' ACTGCAACCTCCGCCTCCT   23943    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||||
                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292  ATIP1   3' GCAAACCTTCTACCTCCT    40393    A     _   _
                                AG AGGTAGA GGTT GC
                                || ||||||| |||| ||
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                                TC TCCATCT CCAA CG
                                 C      T   A
GAM292  ATP1B4   3'  ACTGCAACCTCCACCT      23811      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  BA108L7.2 3'  ACTGCAACCTCTGCCTCCT   48252    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  BAG5     3'  AGCTCACTGCAACCTCCACCT  16836      A          T
                                AGGT GAGGTTGCAGTG GCT
                                |||| |||||||||||| |||
                                TCCA CTCCAACGTCAC CGA
                                  C          T
GAM292  BNIP-S   3'  ACTGCAACCTCCGCCT      56252     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  BTN3A1   3'  AGCTCCCTGCAACCTCCACCTC 22914    A    A        TGT
           CT                     AG AGGT GAGGTTGCAG   GCT
                                || |||| |||||||||   |||
                                TC TCCA CTCCAACGTC   CGA
                                 C   C         CCT
GAM292  C1orf24  3'  ACTGCAACCTCCGCCTCCT   53705    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTCA
                                 C  GC
GAM292  C1QTNF6  3'  ACTGCAACCTCTGCCT      49133
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  C21orf25  3'  AGCTTACTGCAACCTCCACCTC 63541    A    A          T
           CT                     AG AGGT GAGGTTGCAGTG GCT
                                || |||| |||||||||||| |||
                                TC TCCA CTCCAACGTCAT CGA
                                 C   C          T
GAM292  C3F      3'  AGCTCACCGCAACCTCCACCTC 19284    A   A      A   T
           CT                     AG AGGT GAGGTTGC GTG GCT
                                || |||| |||||||| ||| |||
                                TC TCCA CTCCAACG CAC CGA
                                 C   C       C  T
GAM292  C9orf9   3'  ACTGCAACCTCCACCT      38497      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
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                                TCCA CTCCAACGTCA
                                  C
GAM292  C9orf9    3'  ACTGCAACCTCCGCCT      38499     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  CENPH     3'  ACTGCAACCTCTGCCT      43266
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  CHRAC1    3'  AGCTCACTGCAACCTCCGCCT  33864     TA          T
                                AGG  GAGGTTGCAGTG GCT
                                |||  |||||||||||| |||
                                TCC  CTCCAACGTCAC CGA
                                  GC           T
GAM292  CPSF2     3'  ACCGCAACCTCTGCCTCCT    61569     A           A
                                AG AGGTAGAGGTTGC GT
                                || |||||||||||| ||
                                TC TCCGTCTCCAACG CA
                                 C            C
GAM292  DKFZp434A2417 3'  ACTGCAACTTCCACCTCCT    66094     A    A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||
                                TC TCCA CTTCAACGTCA
                                 C    C
GAM292  DKFZP434C212 3'  ACTGCAACCTCCACCT      68902      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  DKFZp434E2220 5'  ACTGCAACCTCCGCCT      34289     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  DKFZp547H025 3'  AGCTCACTGCAACCTCCACCTC 39350     A    A          T
           CT                     AG AGGT GAGGTTGCAGTG GCT
                                || |||| |||||||||||| |||
                                TC TCCA CTCCAACGTCAC CGA
                                 C    C           T
GAM292  DKFZP564O0523 3'  ACTGCAACCTCCACCT      49509      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  DKFZp761N1114 3'  ACTGCAACCTCCGCCT      79009     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
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                                TCC  CTCCAACGTCA
                                  GC
GAM292  DSCR6    3' ACTGCAACCTCCACTTCT    38541      GTA
                                AGAAG   GAGGTTGCAGT
                                |||||   ||||||||||||
                                TCTTC   CTCCAACGTCA
                                  AC_
GAM292  EREG     3' ACTGCAACCTCACCT       7487       A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||||
                                TCCA CTCCAACGTCA
                                  _
GAM292  FER1L4   3' ACTGCAACCTCCACCTCCT   47329    A   A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||||
                                TC TCCA CTCCAACGTCA
                                 C   C
GAM292  FER1L4   3' ACTGCAACCTCCACCTCCT   47330    A   A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||||
                                TC TCCA CTCCAACGTCA
                                 C   C
GAM292  FLJ00001 3' AGCACACTGTCCCCACCGCCT 81810      AGA  TT
                                AGGT   GG  GCAGTGTGCT
                                ||||   ||  ||||||||||
                                TCCG   CC  TGTCACACGA
                                  CCA  CC
GAM292  FLJ00024 5' ACTGCAACCTCTGCCT      63743
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  FLJ10232 3' ACTGCAACCTCCGCCT      35916     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  FLJ10346 5' ACTGCAAGCTCCACCT      36038      A  G
                                AGGT GAG TTGCAGT
                                |||| ||| |||||||
                                TCCA CTC AACGTCA
                                  C   G
GAM292  FLJ10535 3' ACTGCAACCTCTGCCT      36229
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  FLJ10922 3' ACTGCAACCTCCGCCTCCT   36867    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||||
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                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292  FLJ11004  5' ACTGCAACCTCTACCTCCT   36965    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCATCTCCAACGTCA
                                 C
GAM292  FLJ12363  3' AGCTCACTGCAACCTCCACCT  49668      A          T
                                AGGT GAGGTTGCAGTG GCT
                                |||| |||||||||||| |||
                                TCCA CTCCAACGTCAC CGA
                                  C           T
GAM292  FLJ12572  5' ACTGCAACCTCTGCCT      43241
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  FLJ12649  3' ACTGCAACCTCCGCCTCCT   44774    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292  FLJ12668  3' ACTGCAACCTCCATCT      46509      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCTA CTCCAACGTCA
                                  C
GAM292  FLJ12687  3' ACTGCAACCTCCGCCT      46181     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  FLJ12747  3' ACTGCAACCTCTGCCT      49705
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  FLJ12787  3' ACTGCAACCTCTGCCCTC    49744    A
                                GA GGTAGAGGTTGCAGT
                                || ||||||||||||||
                                CT CCGTCTCCAACGTCA
                                 C
GAM292  FLJ12960  3' TGCAACCTCCACCTCCT     44955    A   A
                                AG AGGT GAGGTTGCA
                                || |||| |||||||||
                                TC TCCA CTCCAACGT
                                 C   C
GAM292  FLJ13197  3' ACTGCAACCTCTACCTCCT   44846    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
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                                TC TCCATCTCCAACGTCA
                                 C
GAM292  FLJ14950 3' ACTGCAACCTCCACCT      51710      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  FLJ14957 3' ACTGCAACCTCTGCCT      51733
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  FLJ20004 3' ATTGCAACCTCCGCCT      95286     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTTA
                                  GC
GAM292  FLJ20034 3' AGCTCACTGCAACCTCTGCCT  34356              T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                           T
GAM292  FLJ20045 3' ACTGCAACCTCTGCCTCCT    34412    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  FLJ20079 3' ACCGCAACCTCCACCTCCT    34485    A   A      A
                                AG AGGT GAGGTTGC GT
                                || |||| |||||||| ||
                                TC TCCA CTCCAACG CA
                                 C   C       C
GAM292  FLJ20342 3' ACTGCAACCTCTGCCTCCT    34985    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  FLJ20507 3' AGCTCACTGCAACCTCTGCCTC 35272    A            T
           CT                     AG AGGTAGAGGTTGCAGTG GCT
                                || |||||||||||||||| |||
                                TC TCCGTCTCCAACGTCAC CGA
                                 C             T
GAM292  FLJ20507 3' AGCTCACTGCAACCTCTGCCTC 60208    A            T
           CT                     AG AGGTAGAGGTTGCAGTG GCT
                                || |||||||||||||||| |||
                                TC TCCGTCTCCAACGTCAC CGA
                                 C             T
GAM292  FLJ20511 3' ACTGCAAGCTCCACCTCCT    35317    A   A  G
                                AG AGGT GAG TTGCAGT
                                || |||| ||| |||||||
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                                TC TCCA CTC AACGTCA
                                 C   C  G
GAM292  FLJ20813 3' ACTGCAACTCCACCT      35675     A  G
                                AGGT GAG TTGCAGT
                                |||| ||| |||||||
                                TCCA CTC AACGTCA
                                  C  _
GAM292  FLJ21302 3' ACTGCAACCTCCGCCTCCT   43210    A  TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTCA
                                 C  GC
GAM292  FLJ22002 3' AGCTCACTGCAACCTCCGCCT 45767    TA        T
                                AGG  GAGGTTGCAGTG GCT
                                |||  |||||||||||| |||
                                TCC  CTCCAACGTCAC CGA
                                  GC         T
GAM292  FLJ22531 5' ACTGCAACCTCCACCT      45025     A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  FLJ22794 3' AGCTCACTGCAACTTCCACCT 91601     A         T
                                AGGT GAGGTTGCAGTG GCT
                                |||| |||||||||||| |||
                                TCCA CTTCAACGTCAC CGA
                                  C          T
GAM292  FLJ22965 3' ACTGCAACCTCCGCCT      42044     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  FLJ22969 3' ACTGCAACCTCTGCCTCCT   68644    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  FLJ23024 3' AGCTCACTGCAACCTCTGCCT 46265             T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                           T
GAM292  FLJ23392 3' AGCTCACTGCAACCTCTGCCT 45526             T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                           T
GAM292  FLJ23563 3' ACTGCAACCTCTGCCT      67581
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
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                                TCCGTCTCCAACGTCA

GAM292  FLJ23563  3'  AGCACACTACAGGTACTACC  67585      AGG  C
                                GGTAG  TTG AGTGTGCT
                                |||||  ||| ||||||||
                                CCATC  GAC TCACACGA
                                   ATG  A
GAM292  FLJ30058  3'  CACACTGCCAGCCCCT     58638     TAGA    _
                                AGG   GGTTG CAGTGTG
                                |||   ||||| |||||||
                                TCC   CCGAC GTCACAC
                                  ____   C
GAM292  FLJ30213  5'  ACGAGAGACAACCTCTGCC   58766          CAG__
                                GGTAGAGGTTG    TGT
                                ||||||||||    |||
                                CCGTCTCCAAC    GCA
                                      AGAGA
GAM292  FLJ31101  3'  AGCTCACTGCAACCTCTGCCTC 35705    A            T
            CT                    AG AGGTAGAGGTTGCAGTG GCT
                                || ||||||||||||||| |||
                                TC TCCGTCTCCAACGTCAC CGA
                                 C             T
GAM292  FLJ32865  3'  AGCTCACTGCAACCTCTGCCT  58166             T
                                AGGTAGAGGTTGCAGTG GCT
                                ||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                       T
GAM292  FLJ32942  3'  AGCACACTTTTTTCCTCCCCC  58097    TA   TTGC_
                                GG  GAGG    AGTGTGCT
                                ||  ||||    ||||||||
                                CC  CTCC    TCACACGA
                                 CC   TTTTT
GAM292  GAL3ST-4  3'  ACTGCAACCTCTGCCT     44928
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  GMPPB    5'  ACTGCAACCTCCACCT     95718     A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  GNG4     3'  AGCTCACTGCGACCTCCACCTC 15608    A   A        T
            CT                    AG AGGT GAGGTTGCAGTG GCT
                                || |||| |||||||||||| |||
                                TC TCCA CTCCAGCGTCAC CGA
                                 C   C          T
GAM292  GREB1    3'  ACTGCAACCTCTGCCTCCT   27862    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
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                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  GRWD     3'  ACTGCAACCTCCGCCTCCT   48961    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292  GTF2E1   3'  ACTGCAACCTCTGCCTCCT   18609    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  GTPBG3   3'  ACTGCAACCTCCACCT      50892      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                   C
GAM292  H-plk    5'  ACTGCAACCTCCACCT      31801      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                   C
GAM292  HRH4     3'  ACTGCAACCTCTGCCTCCT   41246    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  HSPC065  3'  ACTGCAACCTCCACCTCT    26287     A   A
                                AGA GGT GAGGTTGCAGT
                                ||| ||| ||||||||||
                                TCT CCA CTCCAACGTCA
                                  _  C
GAM292  HSPC065  3'  GCTGCAACCTCCTCCTCCT   26314    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTCG
                                 C   TC
GAM292  ICK      3'  AGCTCTCTGCAACCTCTGCCT  29923            TGT
                                AGGTAGAGGTTGCAG   GCT
                                ||||||||||||||   |||
                                TCCGTCTCCAACGTC   CGA
                                          TCT
GAM292  IL18BP   3'  CACACCCCCTCCTTCT      19104       T  A  TTGCA
                                AGAAGG AG GG     GTGTG
                                |||||| || ||    |||||
                                TCTTCC TC CC     CACAC
                                   _  C  _____
GAM292  JAM1     5'  ACTGCAACCTCCTCCT      57908     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
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                                TCC  CTCCAACGTCA
                                  TC
GAM292  JM11     3'  AGCTCACTGCAACCTCTGCCTC 53251    A           T
              CT                  AG AGGTAGAGGTTGCAGTG GCT
                                  || |||||||||||||||| |||
                                  TC TCCGTCTCCAACGTCAC CGA
                                   C             T
GAM292  KIAA0063 3'  ACTGCAACCTCCACCTCCT   29615    A   A
                                  AG AGGT GAGGTTGCAGT
                                  || |||| ||||||||||
                                  TC TCCA CTCCAACGTCA
                                   C   C
GAM292  KIAA0391 3'  ACTGCAACCTCTGCCTCCT   27902    A
                                  AG AGGTAGAGGTTGCAGT
                                  || ||||||||||||||
                                  TC TCCGTCTCCAACGTCA
                                   C
GAM292  KIAA0426 3'  ACTGCAACCTCCGCCT      28250     TA
                                  AGG  GAGGTTGCAGT
                                  |||  ||||||||||
                                  TCC  CTCCAACGTCA
                                    GC
GAM292  KIAA0459 3'  ACTGCAACCTCCACCT      60980      A
                                  AGGT GAGGTTGCAGT
                                  |||| ||||||||||
                                  TCCA CTCCAACGTCA
                                    C
GAM292  KIAA0469 3'  ACTGCAGCCTCCACCTCCT   29320    A   A
                                  AG AGGT GAGGTTGCAGT
                                  || |||| ||||||||||
                                  TC TCCA CTCCGACGTCA
                                   C   C
GAM292  KIAA0472 5'  AGCTCACTGCAACCTCCTCCTT 71854       TA          T
              CT                  AGAAGG  GAGGTTGCAGTG GCT
                                  ||||||  |||||||||||| |||
                                  TCTTCC  CTCCAACGTCAC CGA
                                     TC          T
GAM292  KIAA0513 3'  ACTGCAACCTCCACCT      28329      A
                                  AGGT GAGGTTGCAGT
                                  |||| ||||||||||
                                  TCCA CTCCAACGTCA
                                    C
GAM292  KIAA0513 5'  ACTGCAGCCTCCACCT      28332      A
                                  AGGT GAGGTTGCAGT
                                  |||| ||||||||||
                                  TCCA CTCCGACGTCA
                                    C
GAM292  KIAA0527 3'  AGCTCACTGCAACCTCTGCCT  95791              T
                                  AGGTAGAGGTTGCAGTG GCT
                                  |||||||||||||||| |||
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                                TCCGTCTCCAACGTCAC CGA
                                          T
GAM292  KIAA0544 3' ACTGCAACCTCCGCCT     70882     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  KIAA0561 3' AGCTCACTGCAACCTCCGCCT 65872     TA          T
                                AGG  GAGGTTGCAGTG GCT
                                |||  |||||||||||| |||
                                TCC  CTCCAACGTCAC CGA
                                  GC          T
GAM292  KIAA0563 5' ACTGCAACCTCTGCCT     29178
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  KIAA0594 3' ACTGCAACCTCCGCCT     64890     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  KIAA0599 3' ACTGCAACCTCCGCCT     77159     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  KIAA0599 3' ACTGCAACCTCCGCCT     77160     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  KIAA0720 3' ACTGCAACCTCTGCCT     62313
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  KIAA0841 3' AGCTCACTGCAACCTCCGCCT 71372     TA          T
                                AGG  GAGGTTGCAGTG GCT
                                |||  |||||||||||| |||
                                TCC  CTCCAACGTCAC CGA
                                  GC          T
GAM292  KIAA0841 3' AGCTCACTGCAACCTCTGCCTC 71374    A             T
          CT                      AG AGGTAGAGGTTGCAGTG GCT
                                || |||||||||||||||| |||
                                TC TCCGTCTCCAACGTCAC CGA
                                 C             T
GAM292  KIAA1041 3' ACTGCAACCTCCGCCT     30120     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
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                                TCC  CTCCAACGTCA
                                  GC
GAM292  KIAA1054  3' ACTGCAACCTCCGCCT     68423     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  KIAA1161  5' AGCTCACTGCAACCCCTCCTCC 81733    A   T  A        T
             T                   AG AGG AG GGTTGCAGTG GCT
                                || ||| || |||||||||| |||
                                TC TCC TC CCAACGTCAC CGA
                                 C   _  C         T
GAM292  KIAA1170  3' ACTGCAACCTCCGCCT     69839     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  KIAA1193  3' ACTGCAACCTCCGCCTCCT   67627    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292  KIAA1198  3' ACTGCAACCTCCACTTCT    63285      GTA
                                AGAAG   GAGGTTGCAGT
                                |||||   ||||||||||
                                TCTTC   CTCCAACGTCA
                                   AC_
GAM292  KIAA1209  3' ACTGCAGCCTCCACCT      60744      A
                                AGGT GAGGTTGCAGT
                                ||||| ||||||||||
                                TCCA CTCCGACGTCA
                                  C
GAM292  KIAA1257  3' AGCTCACCGCAACCTCCGCCT  62726     TA       A   T
                                AGG  GAGGTTGC GTG GCT
                                |||  |||||||| ||| |||
                                TCC  CTCCAACG CAC CGA
                                  GC       C   T
GAM292  KIAA1320  5' AGCTCACTGCAACCTCTGCCTC 69294    A            T
             CT                   AG AGGTAGAGGTTGCAGTG GCT
                                || |||||||||||||||| |||
                                TC TCCGTCTCCAACGTCAC CGA
                                 C              T
GAM292  KIAA1373  3' AGCTCACTGCAACCTCCACCT  70926      A         T
                                AGGT GAGGTTGCAGTG GCT
                                |||| |||||||||||| |||
                                TCCA CTCCAACGTCAC CGA
                                  C          T
GAM292  KIAA1497  5' ACTGCAACCTCTGCCT      67499
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
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                                TCCGTCTCCAACGTCA

GAM292  KIAA1508 3' AGCTCACTGCAACCTCCGCCTC 61874    A   TA         T
            CT                    AG AGG  GAGGTTGCAGTG GCT
                                  || |||  |||||||||||| |||
                                  TC TCC  CTCCAACGTCAC CGA
                                   C   GC          T
GAM292  KIAA1571 3' AGCTCACCGCAACCTCCACCT  60949     A      A   T
                                  AGGT GAGGTTGC GTG GCT
                                  |||| |||||||| ||| |||
                                  TCCA CTCCAACG CAC CGA
                                    C       C   T
GAM292  KIAA1615 3' AGATCACTGCAACCTCCACCT  68697     A          TG
                                  AGGT GAGGTTGCAGTG  CT
                                  |||| ||||||||||||  ||
                                  TCCA CTCCAACGTCAC  GA
                                    C          TA
GAM292  KIAA1655 3' AGCTCACTGTAACCTCCACCT  66588     A          T
                                  AGGT GAGGTTGCAGTG GCT
                                  |||| |||||||||||| |||
                                  TCCA CTCCAATGTCAC CGA
                                    C          T
GAM292  KIAA1655 3' ATTGCAACCTCCGCCT     66592     TA
                                  AGG  GAGGTTGCAGT
                                  |||  ||||||||||
                                  TCC  CTCCAACGTTA
                                    GC
GAM292  KIAA1737 3' ACTGCAACCTCCGCCTCCT   67348    A   TA
                                  AG AGG  GAGGTTGCAGT
                                  || |||  ||||||||||
                                  TC TCC  CTCCAACGTCA
                                   C  GC
GAM292  KIAA1784 3' ACTGCAACCTCCGCCT      65139     TA
                                  AGG  GAGGTTGCAGT
                                  |||  ||||||||||
                                  TCC  CTCCAACGTCA
                                    GC
GAM292  KIAA1922 5' AGCTCACTGCAACCTCCGCCT 73615     TA          T
                                  AGG  GAGGTTGCAGTG GCT
                                  |||  |||||||||||| |||
                                  TCC  CTCCAACGTCAC CGA
                                    GC          T
GAM292  KIAA1971 3' ACTGCAACCTCCACCT      74212      A
                                  AGGT GAGGTTGCAGT
                                  |||| ||||||||||
                                  TCCA CTCCAACGTCA
                                    C
GAM292  KLK7     3' ACTGCAACCTCCGCCTCCT   17284    A   TA
                                  AG AGG  GAGGTTGCAGT
                                  || |||  ||||||||||
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                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292  KLK7     3'  ACTGCAACCTCCGCCTCCT   57724    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292  MCLC     3'  ACTGCAACCTCCACCT      30676      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  MEF-2    3'  ACTGCAACCTCCGCCTCCT   64377    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292  MGC2474  3'  ACTGCAACTTCCACCTCCT   43711    A    A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||
                                TC TCCA CTTCAACGTCA
                                 C    C
GAM292  MGC3113  3'  AGCTCACTGCAGCCTCCACCTC 43839    A    A         T
          CT                      AG AGGT GAGGTTGCAGTG GCT
                                || |||| |||||||||||| |||
                                TC TCCA CTCCGACGTCAC CGA
                                 C    C          T
GAM292  MGC3329  3'  AGCTCACTGCAACCCCCGCCT  44012      AGA        T
                                AGGT   GGTTGCAGTG GCT
                                ||||   |||||||||| |||
                                TCCG   CCAACGTCAC CGA
                                  CCC         T
GAM292  MGC5149  3'  AGCTCACTGCAACCTCTGCCT  72285              T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                           T
GAM292  MGC9912  3'  ACTGCAACCTCCACCTCCT   54713    A    A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||
                                TC TCCA CTCCAACGTCA
                                 C    C
GAM292  MLZE     5'  AGCTCACTGCAACCTCTGCCT  48614              T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                           T
GAM292  MMPL1    3'  ACTGCAGCCTCCACCT      14712      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
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                                TCCA CTCCGACGTCA
                                  C
GAM292  MOCS3    3'  AGCTCACTGCAACCTCCGCCT  27148     TA          T
                                AGG  GAGGTTGCAGTG GCT
                                |||  |||||||||||| |||
                                TCC  CTCCAACGTCAC CGA
                                  GC           T
GAM292  MR       3'  GCACACCACAGCACCTTT    48320       AGAG    CA
                                GAAGGT    GTTG  GTGTGC
                                ||||||    ||||  ||||||
                                TTTCCA    CGAC  CACACG
                                    ____    AC
GAM292  MRPL44   3'  ACTGCAACCTCCACCTC     43313     A   A
                                GA GGT GAGGTTGCAGT
                                || ||| ||||||||||
                                CT CCA CTCCAACGTCA
                                 _  C
GAM292  MtFMT    3'  AGCTCACTGCAACCTCCGCCT  57648     TA          T
                                AGG  GAGGTTGCAGTG GCT
                                |||  |||||||||||| |||
                                TCC  CTCCAACGTCAC CGA
                                  GC           T
GAM292  NDUFB1   5'  AGCTCACTGCAACCTCTGCCT  15814                 T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                       T
GAM292  NDUFC2   3'  ACTGCAACCTCCACCTCCT    15824     A   A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||
                                TC TCCA CTCCAACGTCA
                                 C   C
GAM292  Nup43    3'  ACTGCAACCTCCACCT       44992       A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  PARVA    3'  ACATAACCTCTCCCTTCT     36649       T      GCA
                                AGAAGG AGAGGTT   GTGT
                                |||||| |||||||   ||||
                                TCTTCC TCTCCAA   TACA
                                   C     ___
GAM292  PASK     5'  ACTGCAACCTCTGCCTCCT    30710     A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  PELI1    5'  ACTGCAACCTCCTCCT       40244     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
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                                TCC  CTCCAACGTCA
                                  TC
GAM292  PIP3-E   3'  AGCTCACTGCAACCTCTGCCT  66796             T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                           T
GAM292  PLAGL2   3'  ACACACTTCTACCTCT      70441     A       TGCA
                                AGA GGTAGAGGT    GTGT
                                ||| |||||||||    ||||
                                TCT CCATCTTCA    CACA
                                  _      ____
GAM292  PLAGL2   3'  GGTTCCCTGCAACCCCCGCCCT 70454    A   AGA      TGT
           C                     GA GGT   GGTTGCAG   GCT
                                || |||   ||||||||   |||
                                CT CCG   CCAACGTC   TGG
                                 C   CCC       CCT
GAM292  PRO0365  5'  AGCTCACTGCAACCTCCACCT  26147     A         T
                                AGGT GAGGTTGCAGTG GCT
                                |||| |||||||||||| |||
                                TCCA CTCCAACGTCAC CGA
                                  C          T
GAM292  PRO1992  5'  ACTGCAACCTCTGCCTCCT    26051    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  PRO2955  3'  AGCTCACTGCAACCTCTGCCT  37630             T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                           T
GAM292  PSTPIP2  3'  AGCTCACTGCAACCTCTGCCT  44381             T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                           T
GAM292  RAB21    3'  ACTGCAAGCTCCACCT      30380     A   G
                                AGGT GAG TTGCAGT
                                |||| ||| |||||||
                                TCCA CTC AACGTCA
                                  C   G
GAM292  RAB33B   3'  ACTGCAACCTCCGCCT      48482     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  RAI      5'  ACTGCAACCTCCGCCTCCT    21871    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
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                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292  RNF8     3'  AGCTCACTGCAACCTCCACCT  14214      A          T
                                AGGT GAGGTTGCAGTG GCT
                                |||| |||||||||||| |||
                                TCCA CTCCAACGTCAC CGA
                                  C           T
GAM292  RNO2     5'  AGCTCACTGCAACCTCCACCTT 52761       A          T
                                AAGGT GAGGTTGCAGTG GCT
                                ||||| |||||||||||| |||
                                TTCCA CTCCAACGTCAC CGA
                                   C           T
GAM292  SC4MOL   3'  AGCTCACTGCAACCTCTGCCT  22150              T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                           T
GAM292  SCAMP-4  3'  ACTGCAACCTCTGCCT      54385
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  SCYA16   3'  ACTGTAACCTCCACCT      15950      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAATGTCA
                                  C
GAM292  SERF1B   3'  AGCTCCATGCAACCTCTGCCTC 43408    A          GTGT
           CT                     AG AGGTAGAGGTTGCA   GCT
                                || ||||||||||||||   |||
                                TC TCCGTCTCCAACGT   CGA
                                 C            ACCT
GAM292  SERF1B   3'  ACTGCAACCTCCGCCT      43404      TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  SLC11A1  3'  CATTGCAACCTCCACCTTCT   59454        A
                                AGAAGGT GAGGTTGCAGTG
                                ||||||| ||||||||||||
                                TCTTCCA CTCCAACGTTAC
                                    C
GAM292  SLC2A10  3'  ACTGCAACCTCCACTTC     47814      GTA
                                GAAG   GAGGTTGCAGT
                                ||||   ||||||||||
                                CTTC   CTCCAACGTCA
                                  AC_
GAM292  SLC6A14  3'  AGCTCACTGCAACCTCTGCCTT 23345              T
           CT                     AGAAGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||||| |||
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                                TCTTCCGTCTCCAACGTCAC CGA
                                             T
GAM292  STAF65(gamma) 3'  ACTGCAACCTCTGCCT      29420
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  SYT13    3'  ACTGCAACCTCCGCCT      93444     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  TRIM5    3'  ACTGCAACCTCCACCTCT    52292     A   A
                                AGA GGT GAGGTTGCAGT
                                ||| ||| ||||||||||
                                TCT CCA CTCCAACGTCA
                                  _  C
GAM292  TRIM6    3'  ACTGCAACCTCTGCCTCCT   54130    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  TU12B1-TY 3'  AGCTCACTGCAACCTCTGCCT  33369              T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                             T
GAM292  TUCAN    3'  AGCTCACTGCAACCTCTGCCTC 30268    A             T
           CT                     AG AGGTAGAGGTTGCAGTG GCT
                                || ||||||||||||||| |||
                                TC TCCGTCTCCAACGTCAC CGA
                                 C              T
GAM292  UBF-fl   3'  ACTGCAACCTCTGCCT      51544
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  USP22    3'  ACTGCAACCTCCACCTCCT   67998    A   A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||
                                TC TCCA CTCCAACGTCA
                                 C   C
GAM292  VDU1     3'  AGCTCACTGCAGCCTCCACCTC 30409    A   A         T
           CT                     AG AGGT GAGGTTGCAGTG GCT
                                || |||| |||||||||||| |||
                                TC TCCA CTCCGACGTCAC CGA
                                 C   C          T
GAM292  VPS33A   3'  ACTGCAACCTCCACCTCCT   43332    A   A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||
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                                TC TCCA CTCCAACGTCA
                                 C    C
GAM292  WBSCR20A  5'  ACCGCAACCTCTGCCTCCT   49647    A          A
                                AG AGGTAGAGGTTGC GT
                                || |||||||||||| ||
                                TC TCCGTCTCCAACG CA
                                 C           C
GAM292  ZTL1      3'  ACTGCAACCTCTGCCT      43906
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  LOC112724 5'  ACTGCAACCTCCACCT      56489      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                   C
GAM292  LOC113675 5'  ACTGCAACCTCCGCCT      56565     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  LOC115219 5'  ACTGCAACCTCCGCCTCCT   73294    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292  LOC120114 3'  AGCTCACTGCAATCTCCACCTC 75519    A    A          T
           CT                     AG AGGT GAGGTTGCAGTG GCT
                                || |||| |||||||||||| |||
                                TC TCCA CTCTAACGTCAC CGA
                                 C    C           T
GAM292  LOC120939 3'  AGCTCACTGTAACCTCCACCT  76245      A          T
                                AGGT GAGGTTGCAGTG GCT
                                |||| |||||||||||| |||
                                TCCA CTCCAATGTCAC CGA
                                   C           T
GAM292  LOC126364 3'  AGCTCACTGCAACCTCCGCCTC 75681    A   TA          T
           CT                     AG AGG  GAGGTTGCAGTG GCT
                                || |||  |||||||||||| |||
                                TC TCC  CTCCAACGTCAC CGA
                                 C   GC           T
GAM292  LOC126661 3'  AGCTCACTGCAACCTCCGCCT  74543     TA          T
                                AGG  GAGGTTGCAGTG GCT
                                |||  |||||||||||| |||
                                TCC  CTCCAACGTCAC CGA
                                  GC           T
GAM292  LOC128077 3'  ACTGCAACCTCCGCCT      74698     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
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                                TCC  CTCCAACGTCA
                                  GC
GAM292   LOC128387 3'  ACTGCAACCTCCACTTC     74745      GTA
                                GAAG   GAGGTTGCAGT
                                ||||   ||||||||||
                                CTTC   CTCCAACGTCA
                                  AC_
GAM292   LOC128989 3'  ACTGCAACCTCCGCCT      74800     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292   LOC130813 3'  ACCGCAACCTCCGCCTCCT    75761    A   TA       A
                                AG AGG  GAGGTTGC GT
                                || |||  |||||||| ||
                                TC TCC  CTCCAACG CA
                                 C   GC       C
GAM292   LOC132625 3'  ACTGCAACCTCCACCT      75894      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292   LOC135293 3'  ACTGCAACCTCTGCCT      76170
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292   LOC135763 3'  ACTGCAACCTCCGCCTCCT    56785    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292   LOC142913 5'  ACTGCAGCCTCCACCTCCT    76413    A    A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||
                                TC TCCA CTCCGACGTCA
                                 C    C
GAM292   LOC143187 3'  ACTGCAACCTCCACCT      59093      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292   LOC143241 5'  AGCTCACTGCAACCTCTGCCT  57173                T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                            T
GAM292   LOC144248 5'  ACTGCAACCTCCACCTCCT    76733    A    A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||
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                                TC TCCA CTCCAACGTCA
                                 C    C
GAM292   LOC144317 5'  CACTGCAACCTCTTCCT     76785     T
                                AGG AGAGGTTGCAGTG
                                ||| ||||||||||||
                                TCC TCTCCAACGTCAC
                                  T
GAM292   LOC144524 5'  AGCTCACTGCAACCTCCACCTC 83119     A    A          T
                  CT                    AG AGGT GAGGTTGCAGTG GCT
                                || |||| |||||||||||| |||
                                TC TCCA CTCCAACGTCAC CGA
                                 C    C           T
GAM292   LOC145725 3'  ACTGCAGCCTCCACCTCCT    77399     A    A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||
                                TC TCCA CTCCGACGTCA
                                 C    C
GAM292   LOC145732 3'  ACTGCAGCCTCCACCTCCT    77421     A    A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||
                                TC TCCA CTCCGACGTCA
                                 C    C
GAM292   LOC145757 5'  ACTACAACCTCTGCCT      77447            C
                                AGGTAGAGGTTG AGT
                                |||||||||||| |||
                                TCCGTCTCCAAC TCA
                                       A
GAM292   LOC146050 3'  AGCTCACTGCAACCTCTGCCTT 77624                  T
                  CT                    AGAAGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||||||| |||
                                TCTTCCGTCTCCAACGTCAC CGA
                                          T
GAM292   LOC146229 3'  ACTGCAACCTCCACCTCCT    77727     A    A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||
                                TC TCCA CTCCAACGTCA
                                 C    C
GAM292   LOC146784 5'  ACTGCAACCTCCACCT      78102      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292   LOC146901 3'  ATTGCAACCTCCACCTTC     83832       A
                                GAAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CTTCCA CTCCAACGTTA
                                    C
GAM292   LOC146909 3'  ACTGCAACCTCCGCCTCCT    78165     A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
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                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292   LOC146952 5'  AGCTCACTGCAACCTCCACCTC 83857     A   A         T
              T                   AGA GGT GAGGTTGCAGTG GCT
                                  ||| ||| |||||||||||| |||
                                  TCT CCA CTCCAACGTCAC CGA
                                   _   C           T
GAM292   LOC147071 5'  ACTGCAACCTCTGCCT      72989
                                  AGGTAGAGGTTGCAGT
                                  ||||||||||||||||
                                  TCCGTCTCCAACGTCA

GAM292   LOC147407 3'  ACTGCAACCTCCGCCT      76318     TA
                                  AGG  GAGGTTGCAGT
                                  |||  ||||||||||
                                  TCC  CTCCAACGTCA
                                    GC
GAM292   LOC147817 3'  ACTGCAACCTCCACCT      78487      A
                                  AGGT GAGGTTGCAGT
                                  |||| ||||||||||
                                  TCCA CTCCAACGTCA
                                    C
GAM292   LOC147841 3'  AGCTCACAGCAACCTCTGCCTC 78524     A          A   T
              CT                    AG AGGTAGAGGTTGC GTG GCT
                                  || |||||||||||| ||| |||
                                  TC TCCGTCTCCAACG CAC CGA
                                   C           A   T
GAM292   LOC148137 3'  ACGGCAACCTCCACCT      58416      A       A
                                  AGGT GAGGTTGC GT
                                  |||| |||||||| ||
                                  TCCA CTCCAACG CA
                                    C       G
GAM292   LOC148189 5'  ACTGCAACCTCCACCTCCT    78704     A    A
                                  AG AGGT GAGGTTGCAGT
                                  || |||| ||||||||||
                                  TC TCCA CTCCAACGTCA
                                   C    C
GAM292   LOC148918 5'  ACTGCAGCCTCCACCT      79055      A
                                  AGGT GAGGTTGCAGT
                                  |||| ||||||||||
                                  TCCA CTCCGACGTCA
                                    C
GAM292   LOC149421 3'  ACTGCAAGCCCCACCTTCT    79354         AGA    _
                                  AGAAGGT   GGTT GCAGT
                                  |||||||   |||| |||||
                                  TCTTCCA   CCGA CGTCA
                                      CC_    A
GAM292   LOC149506 3'  ACTGCAACTTCCACCT      84446      A
                                  AGGT GAGGTTGCAGT
                                  |||| ||||||||||
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                                TCCA CTTCAACGTCA
                                  C
GAM292  LOC149506 3'  AGCTCACTGCAACCTCTGCCTC 84450    A            T
                CT                AG AGGTAGAGGTTGCAGTG GCT
                                  || |||||||||||||||| |||
                                  TC TCCGTCTCCAACGTCAC CGA
                                   C              T
GAM292  LOC149773 3'  AGCACATTTCAGCCCCCACCCC 79473    AA   AGA    C
                CT                AG  GGT   GGTTG AGTGTGCT
                                  ||  |||   ||||| ||||||||
                                  TC  CCA   CCGAC TTACACGA
                                   CC   CCC    T
GAM292  LOC150397 3'  ATTGCAACCTCCGCCT     79838     TA
                                  AGG  GAGGTTGCAGT
                                  |||  ||||||||||
                                  TCC  CTCCAACGTTA
                                    GC
GAM292  LOC150519 3'  CTGCAACCTGCCACCTCCT   79919    A   AG_
                                  AG AGGT   AGGTTGCAG
                                  || ||||   |||||||||
                                  TC TCCA   TCCAACGTC
                                   C   CCG
GAM292  LOC150696 3'  ACTGCAGCCTCCACCTCCT   58477    A   A
                                  AG AGGT GAGGTTGCAGT
                                  || |||| ||||||||||
                                  TC TCCA CTCCGACGTCA
                                   C   C
GAM292  LOC150960 3'  GCTGCAACCTCCGCCT     80064     TA
                                  AGG  GAGGTTGCAGT
                                  |||  ||||||||||
                                  TCC  CTCCAACGTCG
                                    GC
GAM292  LOC151057 3'  ACTGCAACCTCTGCCTCCT   85205    A
                                  AG AGGTAGAGGTTGCAGT
                                  || ||||||||||||||||
                                  TC TCCGTCTCCAACGTCA
                                   C
GAM292  LOC151201 3'  AGCTCACTGCAACCTCCACCT  85270     A          T
                                  AGGT GAGGTTGCAGTG GCT
                                  |||| |||||||||||| |||
                                  TCCA CTCCAACGTCAC CGA
                                    C           T
GAM292  LOC151475 5'  ACTGCAACCTCCACCT     85383     A
                                  AGGT GAGGTTGCAGT
                                  |||| ||||||||||
                                  TCCA CTCCAACGTCA
                                    C
GAM292  LOC151475 5'  AGCTCACTGCAACCTCTGCCTC 85389    A            T
                CT                AG AGGTAGAGGTTGCAGTG GCT
                                  || |||||||||||||||| |||
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                                TC TCCGTCTCCAACGTCAC CGA
                                 C              T
GAM292   LOC151701 3'  CTGCAACCTCCACTTTC     85485       A
                                GAAGGT GAGGTTGCAG
                                |||||| ||||||||||
                                CTTTCA CTCCAACGTC
                                   C
GAM292   LOC151826 3'  AGCTCACTGCAACCTCCGCCTC 80353    A   TA          T
           CT                    AG AGG  GAGGTTGCAGTG GCT
                                || |||  |||||||||||| |||
                                TC TCC  CTCCAACGTCAC CGA
                                 C  GC          T
GAM292   LOC152445 3'  ACTGCAACCTCTGCCTCCT   85741    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292   LOC152582 5'  ACCGCAACCTCTGCCT      85784            A
                                AGGTAGAGGTTGC GT
                                |||||||||||| ||
                                TCCGTCTCCAACG CA
                                        C
GAM292   LOC152719 5'  ACTGCAACCTCTGCCT      85843
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292   LOC152794 5'  ACTGCAACCTCTACCT      80669
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCATCTCCAACGTCA

GAM292   LOC153077 3'  ACTGCAACCTCCGCCTCCT   85904    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTCA
                                 C  GC
GAM292   LOC153387 5'  GGCACACTACCCCCACC     86038     AGA   TGC
                                GGT   GGT   AGTGTGCT
                                |||   |||   ||||||||
                                CCA   CCA   TCACACGG
                                  CCC   ___
GAM292   LOC153688 3'  ACTGCAACCTCCACCT      86091      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292   LOC153883 5'  AGTTCACTGCAACCTCCACC   80978     A          T
                                GGT GAGGTTGCAGTG GCT
                                ||| |||||||||||| |||
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                                CCA CTCCAACGTCAC TGA
                                  C           T
GAM292   LOC154075 3'  AGCTCACTGCAACCTCCGCCTC 81043    A   TA          T
                CT                  AG AGG  GAGGTTGCAGTG GCT
                                    || |||  |||||||||||| |||
                                    TC TCC  CTCCAACGTCAC CGA
                                     C   GC           T
GAM292   LOC154282 5'  ACTGCAACCTCCACCT      86191      A
                                    AGGT GAGGTTGCAGT
                                    |||| ||||||||||
                                    TCCA CTCCAACGTCA
                                      C
GAM292   LOC154877 3'  AGCTCACTGCAACCTCTACCTC 86279    A              T
                CT                  AG AGGTAGAGGTTGCAGTG GCT
                                    || ||||||||||||||| |||
                                    TC TCCATCTCCAACGTCAC CGA
                                     C              T
GAM292   LOC154877 3'  ATTGCAACCTCCGCCTTC    86282       TA
                                    GAAGG  GAGGTTGCAGT
                                    |||||  ||||||||||
                                    CTTCC  CTCCAACGTTA
                                       GC
GAM292   LOC157247 5'  AGCTCACTGCAACCTCCACC   81357     A          T
                                    GGT GAGGTTGCAGTG GCT
                                    ||| |||||||||||| |||
                                    CCA CTCCAACGTCAC CGA
                                      C           T
GAM292   LOC157798 5'  ACTGCAACCTCCGCCT      86542     TA
                                    AGG  GAGGTTGCAGT
                                    |||  ||||||||||
                                    TCC  CTCCAACGTCA
                                      GC
GAM292   LOC157858 5'  ACTGCAACCTCTGCCT      86577
                                    AGGTAGAGGTTGCAGT
                                    ||||||||||||||||
                                    TCCGTCTCCAACGTCA

GAM292   LOC158476 3'  AGCTCACTGCAACCTCCGCCCC 86836    AA  TA          T
                CT                  AG  GG  GAGGTTGCAGTG GCT
                                    ||  ||  |||||||||||| |||
                                    TC  CC  CTCCAACGTCAC CGA
                                     CC  GC           T
GAM292   LOC158668 3'  AGCTCACTGCAACCTCTGCCT  69363              T
                                    AGGTAGAGGTTGCAGTG GCT
                                    |||||||||||||||| |||
                                    TCCGTCTCCAACGTCAC CGA
                                                 T
GAM292   LOC158865 5'  ACTGCAACCTCTGCCTCCT    86930    A
                                    AG AGGTAGAGGTTGCAGT
                                    || ||||||||||||||||
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                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  LOC161829 3' ACTGCAACCTCCGCCT     82307     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  LOC196047 5' ACTGCAACCTCCGCCT     89586     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  LOC196264 3' ACTGCAACCTCTGCCTCCT   87601    A
                                AG AGGTAGAGGTTGCAGT
                                ||  ||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  LOC196411 3' ACTGCAACCTCCGCCT     87661     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  LOC196529 3' ACTGCAACCTCCACCTC     87768    A  A
                                GA GGT GAGGTTGCAGT
                                ||  ||| ||||||||||
                                CT CCA CTCCAACGTCA
                                 _  C
GAM292  LOC196957 3' ACTGCAGCCTCCACCTCCT   87816    A   A
                                AG AGGT GAGGTTGCAGT
                                ||  |||| ||||||||||
                                TC TCCA CTCCGACGTCA
                                 C   C
GAM292  LOC196961 3' ACTGCAGCCTCCACCTCCT   87837    A   A
                                AG AGGT GAGGTTGCAGT
                                ||  |||| ||||||||||
                                TC TCCA CTCCGACGTCA
                                 C   C
GAM292  LOC197138 3' ACTGCAGCCTCCACCTCCT   87910    A   A
                                AG AGGT GAGGTTGCAGT
                                ||  |||| ||||||||||
                                TC TCCA CTCCGACGTCA
                                 C   C
GAM292  LOC197358 3' AGCTCCCTGCAACCTCCGCCT 88024     TA       TGT
                                AGG  GAGGTTGCAG   GCT
                                |||  ||||||||||   |||
                                TCC  CTCCAACGTC   CGA
                                  GC        CCT
GAM292  LOC199699 3' AGCTCACTGCAAGCTCCACCT  88297     A  G      T
                                AGGT GAG TTGCAGTG GCT
                                ||||  ||| ||||||||  |||
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                                TCCA CTC AACGTCAC CGA
                                  C  G       T
GAM292  LOC199786 3'  ACTGCAACCTCCGCCT     88361     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  LOC200010 3'  CACACTGTTTCCACCCTCT   89920     A   AGA  TT
                                AGA GGT   GG  GCAGTGTG
                                ||| |||   ||  ||||||||
                                TCT CCA   CC  TGTCACAC
                                  C  ___  TT
GAM292  LOC200014 3'  AGCTCGCTGCAACCCCCACCT 88515     AGA        T
                                AGGT   GGTTGCAGTG GCT
                                ||||   |||||||||| |||
                                TCCA   CCAACGTCGC CGA
                                   CCC         T
GAM292  LOC200169 5'  ACTGCAACCTCTGCCTCCT   89941    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  LOC200268 3'  ACTGCAACCTCTGCCTCCT   88674    A
                                AG AGGTAGAGGTTGCAGT
                                || ||||||||||||||||
                                TC TCCGTCTCCAACGTCA
                                 C
GAM292  LOC200310 3'  ACTACAACCTCTGCCT      65725           C
                                AGGTAGAGGTTG AGT
                                ||||||||||| |||
                                TCCGTCTCCAAC TCA
                                        A
GAM292  LOC200314 3'  ACTGCAACCTCCACCT      90000     A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  LOC200339 3'  ACTGCAACCTCTGCCT      90025
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292  LOC200860 3'  ACTGCAACCTCCACCT      90154     A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  LOC201173 5'  ACTGCAACCTCTGCCT      87319
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
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                                TCCGTCTCCAACGTCA

GAM292   LOC201220 5' ACTGCAACCTCTGCCT     87339
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292   LOC201294 3' ACTGCAACCTCCGCCTCCT   88201    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292   LOC201411 3' AGCTCACTGCAACCTCTGCCT 62951              T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                           T
GAM292   LOC201626 3' ACTGCAACCTCCGCCCCCT   88986    AA  TA
                                AG  GG  GAGGTTGCAGT
                                ||  ||  ||||||||||
                                TC  CC  CTCCAACGTCA
                                 CC  GC
GAM292   LOC201627 3' ACTGCAACCTCCACCT     89002      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                   C
GAM292   LOC202025 3' ACTGCAACCTCCGCCT     90276     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292   LOC202934 3' AGCTCACTACAACCTCTGCCT 90400           C    T
                                AGGTAGAGGTTG AGTG GCT
                                |||||||||||| |||| |||
                                TCCGTCTCCAAC TCAC CGA
                                       A    T
GAM292   LOC203297 5' ACTGCAACCTCTGCCT     75344
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292   LOC203350 3' ACTGCAACCTCCGCCT     90556     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292   LOC204804 3' ACTGCAACCTCGACCTCCT   89468    A   A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||
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                                TC TCCA CTCCAACGTCA
                                 C    G
GAM292   LOC219735 3'  ACTGCAACCTCTGCCT      93101
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292   LOC219894 3'  ACTGCAAGCTCCACCT      93274      A   G
                                AGGT GAG TTGCAGT
                                |||| ||| |||||||
                                TCCA CTC AACGTCA
                                  C   G
GAM292   LOC220575 3'  ACTGCAACCTCAACCTTCT    76305        A
                                AGAAGGT GAGGTTGCAGT
                                ||||||| ||||||||||
                                TCTTCCA CTCCAACGTCA
                                    A
GAM292   LOC220662 3'  ACTGCAACCTCCACCT      91156      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292   LOC220662 3'  ACTGCAACCTCCACTTC     91161      GTA
                                GAAG   GAGGTTGCAGT
                                ||||   ||||||||||
                                CTTC   CTCCAACGTCA
                                  AC_
GAM292   LOC220846 3'  AGCCTTTCCACAACCTCTACCT 90811             CAGTGT_
           TC                     GAAGGTAGAGGTTG      GCT
                                ||||||||||||||      |||
                                CTTCCATCTCCAAC      CGA
                                       ACCTTTC
GAM292   LOC221035 3'  ACTACAACCTCTGCCT      93158           C
                                AGGTAGAGGTTG AGT
                                |||||||||||| |||
                                TCCGTCTCCAAC TCA
                                       A
GAM292   LOC221174 5'  AGCTCACTGCGACCTCCACCT  93497      A          T
                                AGGT GAGGTTGCAGTG GCT
                                |||| |||||||||||| |||
                                TCCA CTCCAGCGTCAC CGA
                                  C          T
GAM292   LOC221271 3'  AGCTCACTGCAACCTCTGCCT  91843              T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                          T
GAM292   LOC221296 3'  ACTGCAACCTCCACCT      91953      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||
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                                TCCA CTCCAACGTCA
                                  C
GAM292   LOC221663 5'  ACTGCAACCTCCACCTCCT   93808    A   A
                                AG AGGT GAGGTTGCAGT
                                || |||| ||||||||||
                                TC TCCA CTCCAACGTCA
                                 C   C
GAM292   LOC222070 5'  ACTGCAACCTCTGCCT     94145
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTCA

GAM292   LOC253612 5'  ACTGCAACCTCCGCCT     96735    TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292   LOC253664 3'  ATTGCAACCTCTGCCT     94805
                                AGGTAGAGGTTGCAGT
                                ||||||||||||||||
                                TCCGTCTCCAACGTTA

GAM292   LOC253666 5'  AGCTCACTGCAACCTCCGCCT  95059    TA         T
                                AGG  GAGGTTGCAGTG GCT
                                |||  |||||||||||| |||
                                TCC  CTCCAACGTCAC CGA
                                  GC          T
GAM292   LOC254655 3'  ACTGCAACCTCTGCCTTCT   95467
                                AGAAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                TCTTCCGTCTCCAACGTCA

GAM292   LOC255497 3'  ACTGCAACCTCCGCCTCCT   97186    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||
                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292   LOC256267 3'  AGCTCACTGCAACCTCCGCCTC 96796    A   TA         T
           CT                     AG AGG  GAGGTTGCAGTG GCT
                                || |||  |||||||||||| |||
                                TC TCC  CTCCAACGTCAC CGA
                                 C   GC          T
GAM292   LOC256306 3'  AGCTCACTGCAACCTCCACCT  96676     A         T
                                AGGT GAGGTTGCAGTG GCT
                                |||| |||||||||||| |||
                                TCCA CTCCAACGTCAC CGA
                                  C          T
GAM292   LOC51200  3'  ACCACAACCTCTGCCTCCT   32988    A         CA
                                AG AGGTAGAGGTTG  GT
                                || ||||||||||||  ||
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                                TC TCCGTCTCCAAC  CA
                                 C          AC
GAM292  LOC51696  3' AGCTCACTGCAACCTCTGCCTC 32542    A             T
             CT                  AG AGGTAGAGGTTGCAGTG GCT
                                 || |||||||||||||||| |||
                                 TC TCCGTCTCCAACGTCAC CGA
                                  C             T
GAM292  LOC57107  3' ACTGCAACCTCCGCCTCCT   39826    A   TA
                                 AG AGG  GAGGTTGCAGT
                                 || |||  ||||||||||
                                 TC TCC  CTCCAACGTCA
                                  C   GC
GAM292  LOC57146  3' ACTGCAACCTCCAACT     39908     A_
                                 GGT  GAGGTTGCAGT
                                 |||  ||||||||||
                                 TCA  CTCCAACGTCA
                                   AC
GAM292  LOC81034  3' AGCTCACTGCAACCTCCACCT  47842      A          T
                                 AGGT GAGGTTGCAGTG GCT
                                 |||| |||||||||||| |||
                                 TCCA CTCCAACGTCAC CGA
                                   C          T
GAM292  LOC89932  3' ACTGCAACCTCCACCTCCT   60787    A   A
                                 AG AGGT GAGGTTGCAGT
                                 || |||| ||||||||||
                                 TC TCCA CTCCAACGTCA
                                  C   C
GAM292  LOC90288  3' ACTGCAACCTCCACCT     62074     A
                                 AGGT GAGGTTGCAGT
                                 |||| ||||||||||
                                 TCCA CTCCAACGTCA
                                   C
GAM292  LOC90333  5' ACTGCAACCTCCACTTC     62276     GTA
                                 GAAG   GAGGTTGCAGT
                                 ||||   ||||||||||
                                 CTTC   CTCCAACGTCA
                                   AC_
GAM292  LOC90333  3' AGCTCACTGCAACCTCCTCCT  62281     TA          T
                                 AGG  GAGGTTGCAGTG GCT
                                 |||  |||||||||||| |||
                                 TCC  CTCCAACGTCAC CGA
                                   TC          T
GAM292  LOC90371  5' ACTGCAACCTCCACCT     62490     A
                                 AGGT GAGGTTGCAGT
                                 |||| ||||||||||
                                 TCCA CTCCAACGTCA
                                   C
GAM292  LOC90408  5' ACTGCAACCTCTACCTCCT   62654    A
                                 AG AGGTAGAGGTTGCAGT
                                 || ||||||||||||||||
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                                TC TCCATCTCCAACGTCA
                                 C
GAM292  LOC90459 3' ACTGCAACCTCCGCCTCCT   62880    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||||
                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292  LOC90485 3' ACTGCAACCTCCGCCT     63003     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||||
                                TCC  CTCCAACGTCA
                                 GC
GAM292  LOC90591 3' AGCTCACTGCAAGCTCCACCTC 63413    A    A  G      T
             CT                   AG AGGT GAG TTGCAGTG GCT
                                || |||| ||| |||||||| |||
                                TC TCCA CTC AACGTCAC CGA
                                 C    C   G       T
GAM292  LOC91115 3' ACTGCAACCTCCACCT      64915      A
                                AGGT GAGGTTGCAGT
                                |||| ||||||||||||
                                TCCA CTCCAACGTCA
                                  C
GAM292  LOC91115 3' ACTGCAACCTCCGCCT      64917     TA
                                AGG  GAGGTTGCAGT
                                |||  ||||||||||||
                                TCC  CTCCAACGTCA
                                  GC
GAM292  LOC92267 3' AGCTCACTGCAACCTCCACCT  68602      A         T
                                AGGT GAGGTTGCAGTG GCT
                                |||| |||||||||||| |||
                                TCCA CTCCAACGTCAC CGA
                                  C          T
GAM292  LOC92303 3' CACTGCAACCTCTGCCCTC    68821    A
                                GA GGTAGAGGTTGCAGTG
                                || ||||||||||||||||
                                CT CCGTCTCCAACGTCAC
                                 C
GAM292  LOC92466 3' AGCTCACTGCAACCTCCGCCTC 69421    A   TA         T
             CT                   AG AGG  GAGGTTGCAGTG GCT
                                || |||  |||||||||||| |||
                                TC TCC  CTCCAACGTCAC CGA
                                 C   GC          T
GAM292  LOC92661 5' ACTGCAAGCTCCACCT      70077      A   G
                                AGGT GAG TTGCAGT
                                |||| ||| |||||||
                                TCCA CTC AACGTCA
                                  C   G
GAM292  LOC92689 3' ACTGCAACCTCCGCCTCCT    70214    A   TA
                                AG AGG  GAGGTTGCAGT
                                || |||  ||||||||||||
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                                TC TCC  CTCCAACGTCA
                                 C   GC
GAM292  LOC93132  5'  AGCTCACTGCAACCTCCGCCT  71480     TA          T
                                AGG  GAGGTTGCAGTG GCT
                                |||  |||||||||||| |||
                                TCC  CTCCAACGTCAC CGA
                                  GC          T
GAM292  LOC93349  3'  AGCTCACTGCAACCTCTGCCT  56450               T
                                AGGTAGAGGTTGCAGTG GCT
                                |||||||||||||||| |||
                                TCCGTCTCCAACGTCAC CGA
                                           T
GAM293  EIF4G2    3'  ATTAGCAGCATGCAAT      7422        CA
                                ATTGCA  TTGCTAAT
                                ||||||  ||||||||
                                TAACGT  GACGATTA
                                    AC
GAM293  KIAA0268  3'  CTTTGAAATGTGCAAT      70003          GCTAA TG
                                ATTGCACATT    T  AAG
                                ||||||||||    |  |||
                                TAACGTGTAA    A  TTC
                                      _____ GT
GAM293  KIAA1673  3'  ACTTCAAGTTATGTGCAAT    70780         T   AAT
                                ATTGCACAT GCT   TGAAGT
                                |||||||| |||   ||||||
                                TAACGTGTA TGA   ACTTCA
                                      T  ___
GAM293  SE57-1    3'  ACTTCAATTAAATGTATAATGA 47394       C    GC
                                TCATTG ACATT  TAATTGAAGT
                                ||||||| |||||  ||||||||||
                                AGTAAT TGTAA  ATTAACTTCA
                                   A    __
GAM293  LOC158117 3'  CTTCAATCAGTAGCAAGA    81705    A   ACAT   A
                                TC TTGC    TGCT ATTGAAG
                                || ||||    |||| |||||||
                                AG AACG    ATGA TAACTTC
                                 _   _____    C
GAM293  LOC203275 3'  CTTCAATCAGTAGCAAGA    89321    A   ACAT   A
                                TC TTGC    TGCT ATTGAAG
                                || ||||    |||| |||||||
                                AG AACG    ATGA TAACTTC
                                 _   _____    C
GAM293  LOC90333  3'  TTACAAGTGCAATGA       62308         A  C
                                TCATTGCAC TTG TAA
                                ||||||||| ||| |||
                                AGTAACGTG AAC ATT
                                      _  _
GAM294  ARCN1     3'  AGACTGCACTCTCTGTCA     7970          CA_
                                TGACAGAGA   CAGTTT
                                |||||||||   ||||||
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                                ACTGTCTCT   GTCAGA
                                     CAC
GAM294  CBFA2T2  3'  GAGCAAAACTCTGTCT      17466       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                   C
GAM294  CTLA4    3'  CAGAGCTGGGATGTTTCTGTCA 17807          CAGTTTT
                                TGACAGAGACA      GCTCTG
                                ||||||||||       ||||||
                                ACTGTCTTTGT      CGAGAC
                                      AGGGT__
GAM294  ITK      3'  CAGAACAGGAGTGATGTCTCTG 18674         _ G    C
                                CAGAGACA CA TTTTG TCTG
                                |||||||| || ||||| ||||
                                GTCTCTGT GT AGGAC AGAC
                                     A G    A
GAM294  LAMP2    3'  GGTGAAACCCCATCTCTATCA  25716    C    CACA    TG
                                TGA AGAGA    GTTT  CT
                                ||| |||||    ||||  ||
                                ACT TCTCT    CAAA  GG
                                  A    ACCC    GT
GAM294  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   52963        A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM294  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   52960        A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM294  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   40865        A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM294  PDGFRB   5'  CAGAGCCTGGAACTGTG     65969          __
                                CACAGTTTT  GCTCTG
                                |||||||||  ||||||
                                GTGTCAAGG  CGAGAC
                                      TC
GAM294  PTPRA    3'  AGAGCGGTATCTCTG       11088       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM294  PTPRA    3'  AGAGCGGTATCTCTG       55079       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
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                                GTCTCT TG    GCGAGA
                                   A _____
GAM294  PTPRA    3'  AGAGCGGTATCTCTG      55087      C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM294  RAD51L3  3'  CAAAACTCAGGTATGTCTCTGT 56065        C_____
                                ACAGAGACA    AGTTTTG
                                |||||||||    |||||||
                                TGTCTCTGT    TCAAAAC
                                     ATGGAC
GAM294  TBL2     3'  CAGAACTGTGTTCCATCA    24924    CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM294  TBL2     3'  CAGAACTGTGTTCCATCA    52178    CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM294  AGTRL2   5'  CAGAGCAAGAACTGTTC    17691    C     _
                                GA ACAGTTTT GCTCTG
                                || |||||||| ||||||
                                CT TGTCAAGA CGAGAC
                                  _      A
GAM294  CABP5    3'  AGAGCGGTATCTTTGCCA    39079    A    C  AGTTT
                                TG CAGAGA AC    TGCTCT
                                || |||||| ||    ||||||
                                AC GTTTCT TG    GCGAGA
                                  C    A _____
GAM294  CUL4A    5'  AGAGCAGCACCTCCATCA    13149    CA  ACACA  T
                                TGA  GAG    GT TTGCTCT
                                |||  |||    || |||||||
                                ACT  CTC    CA GACGAGA
                                  AC  _____  C
GAM294  DKFZp761O17121 3'  CAGACAGCCCCTGTGTCTCTGT 50136          TT_  C
           C                    GACAGAGACACAG   TTG TCTG
                                ||||||||||||   ||| ||||
                                CTGTCTCTGTGTC   GAC AGAC
                                     CCC  _
GAM294  FLJ10375 3'  CAGAGGCCTGTGTCTGTGCCA  36073    A  G      TTTTG
                                TG CA AGACACAG    CTCTG
                                || || ||||||||    |||||
                                AC GT TCTGTGTC    GAGAC
                                  C  G      CG___
GAM294  FLJ10738 5'  CAAAGCCAGCCCTCTGTCA   36527        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
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                                ACTGTCTC    CGAAAC
                                    CCGAC
GAM294  FLJ10803  3' CAAAACAAAACTCTGTCA    36660       ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
                                ACTGTCTC    CAAAAC
                                    AAAA_
GAM294  FLJ10842  3' AAAGTGTGCTCTGTCA     36723       A   G
                                TGACAGAG CACA TTT
                                |||||||| |||| |||
                                ACTGTCTC GTGT AAA
                                    _   G
GAM294  FLJ13153  3' CAGAGCCCAGCATCCATCTCTG 45555       CACA_  TT
          TCA                     TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                    ACCTA   CC
GAM294  FLJ20035  3' CAAACCTGCCATGTTCTGTCA  34395       A ___   T
                                TGACAGAG CA   CAG TTTG
                                |||||||| ||   ||| ||||
                                ACTGTCTT GT   GTC AAAC
                                    _ ACC   C
GAM294  FLJ22195  5' CAGAGCAGAGGGAAGTCTCTGC 42800    A     ACAG
          CA                      TG CAGAGAC    TTTTGCTCTG
                                || |||||||    ||||||||||
                                AC GTCTCTG    GAGACGAGAC
                                 C      AAGG
GAM294  FLJ32191  5' GAACTGCACCTCTGTCA     58411       ACA
                                TGACAGAG   CAGTTT
                                ||||||||   ||||||
                                ACTGTCTC   GTCAAG
                                    CAC
GAM294  KIAA1023  3' CAAAGCTGTATCTGCTATCA   34255     C  _   C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM294  KIAA1586  5' AGTGTGATGTGTCTCTG     92326       GTT TG T
                                CAGAGACACA   T  C CT
                                ||||||||||   |  | ||
                                GTCTCTGTGT   A  G GA
                                    ___ GT T
GAM294  KIAA1754  3' GACTAACGTCTCTGTCA     63236       AC_
                                TGACAGAGAC   AGTT
                                ||||||||||   ||||
                                ACTGTCTCTG   TCAG
                                    CAA
GAM294  LANCL2    3' CAGAGTGCACTGCAGCTCTGTC 37995       ACA    TTT
          A                      TGACAGAG   CAGT   GCTCTG
                                ||||||||   ||||   ||||||
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                                ACTGTCTC  GTCA  TGAGAC
                                    GAC   CG_
GAM294  LIG-1    3'  CAGAGCAGGCCTGTCCATGCCA 63893    A  GAGAC   TT
                                TG CA    ACAG  TTGCTCTG
                                || ||    ||||  ||||||||
                                AC GT    TGTC  GACGAGAC
                                 C  ACC__   CG
GAM294  MGC5242  3'  AGAGTACATGTCTCTG     43823       CAGTTT
                                CAGAGACA     TGCTCT
                                ||||||||     ||||||
                                GTCTCTGT     ATGAGA
                                    AC____
GAM294  OSMR     3'  CAGAGCTGGCACCCTGTCA   14345      AGACA
                                TGACAG    CAGTTTTG
                                ||||||    ||||||||
                                ACTGTC    GTCGAGAC
                                   CCACG
GAM294  RAB21    3'  CAGAACAAAACTGTGGATC   30383    GA       C
                                GA  CACAGTTTTG TCTG
                                ||  |||||||||| ||||
                                CT  GTGTCAAAAC AGAC
                                 AG        A
GAM294  SPTLC2   3'  CAGAGCAAAACTGTGTCTC   16799
                                GAGACACAGTTTTGCTCTG
                                ||||||||||||||||||
                                CTCTGTGTCAAAACGAGAC

GAM294  TGIF2    3'  GAGTCATGCTCTGTCA     41454       A  CAGTTT  _
                                TGACAGAG CA     TG CTC
                                |||||||| ||     || |||
                                ACTGTCTC GT     AC GAG
                                    _  _______  T
GAM294  WBSCR23  5'  GCTGACTGTGTCTCCATCA   46765    CA       TT
                                TGA  GAGACACAGTT  GC
                                |||  ||||||||||  ||
                                ACT  CTCTGTGTCAG  CG
                                  AC         T_
GAM294  LOC115129 3'  GGCAAAACCCCGTCTCT    73235      ACA
                                AGAGAC   GTTTTGCT
                                ||||||   ||||||||
                                TCTCTG   CAAAACGG
                                   CCC
GAM294  LOC129198 3'  AGCAAGCTGTGCCTC      76117    A      T
                                GAG CACAGTTT GCT
                                ||| |||||||| |||
                                CTC GTGTCGAA CGA
                                  C       _
GAM294  LOC145231 3'  GGTGAAACTATGTCTCT    83293       C    TG
                                AGAGACA AGTTT  CT
                                ||||||| |||||  ||
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                                TCTCTGT TCAAA  GG
                                    A    GT
GAM294   LOC145483 3'  GAGCAAAACTCTGTCT     77243      C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                   C
GAM294   LOC146713 3'  GAGCAAAACTCCGTCT     83726     AC
                                AGAC  AGTTTTGCTC
                                ||||  ||||||||||
                                TCTG  TCAAAACGAG
                                  CC
GAM294   LOC149175 3'  CAGGGTGAAACCACGTCTCT  79208       ACA   TG
                                AGAGAC   GTTT  CTCTG
                                ||||||   ||||  |||||
                                TCTCTG   CAAA  GGGAC
                                    CAC    GT
GAM294   LOC150299 3'  CAGAACCTGCATCTTTGTCA  84968        CA  _
                                TGACAGAGA  CAG TTTTG
                                |||||||||  ||| |||||
                                ACTGTTTCT  GTC AAGAC
                                     AC   C
GAM294   LOC153277 3'  TAAAACTGTGCCTGTGCCA   85990    A  G  A
                                TG CA AG CACAGTTTTG
                                || || || ||||||||||
                                AC GT TC GTGTCAAAAT
                                 C  G  C
GAM294   LOC155179 3'  CAAAGCTGTATCTGCTATCA  81312     C  _  C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM294   LOC221074 3'  AAAGTGTGTCTCTTTCA     93177     C       G
                                TGA AGAGACACA TTT
                                ||| ||||||||| |||
                                ACT TCTCTGTGT AAA
                                  T       G
GAM294   LOC221103 5'  AGTTTATGTGTGCTCTGTCA  93244        _    GTTTT
                                TGACAGAG ACACA    GCT
                                |||||||| |||||    |||
                                ACTGTCTC TGTGT    TGA
                                    G    ATT__
GAM294   LOC255988 5'  CAGAGCCCAGCATCCATCTCTG 97608        CACA_  TT
           TCA                    TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                     ACCTA   CC
GAM295   CCR9     3'  CTCCATGCACTGTGAA      48297         G
                                TTCACAGTG CATGGAG
                                ||||||||| |||||||
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                                AAGTGTCAC GTACCTC
                                        _
GAM295  CCR9     3'  CTCCATGCACTGTGAA      21813          G
                                TTCACAGTG CATGGAG
                                ||||||||| |||||||
                                AAGTGTCAC GTACCTC
                                        _
GAM295  MDH2     3'  TGAAGGCATCATGTCACTG   19796          GA  CC
                                CAGTGGCATG  GTC  CA
                                ||||||||||  |||  ||
                                GTCACTGTAC  CGG  GT
                                      TA  AA
GAM295  MFRP     5'  GGGACTCCAGAAAGCCAT    48706       A___
                                GTGGC   TGGAGTCCC
                                |||||   |||||||||
                                TACCG   ACCTCAGGG
                                   AAAG
GAM295  MIP      5'  GGGACCCAGGCACTGTGA    23803         G A  A
                                TCACAGTG C TGG GTCCC
                                |||||||| | ||| |||||
                                AGTGTCAC G ACC CAGGG
                                     _ G  _
GAM295  RFC2     3'  GACTCCATCTGGGGAA      11305     A_  TGGC
                                TTC  CAG   ATGGAGTC
                                |||  |||   ||||||||
                                AAG  GTC   TACCTCAG
                                  GG  ____
GAM295  SIRT4    3'  GGGACTTTCACTTGAA      24269     C    CATG
                                TTCA AGTGG   GAGTCCC
                                |||| |||||   |||||||
                                AAGT TCACT   TTCAGGG
                                  _   _____
GAM295  VSX1     3'  GTGAAGACTCCATACAGACAC  27468     GC___      CC
                                GTG    ATGGAGTC  CAC
                                |||    ||||||||  |||
                                CAC    TACCTCAG  GTG
                                  AGACA       AA
GAM295  ARHGEF4  5'  GACTGACAGCCACTGTGAG   52215          A  G_
                                TTCACAGTGGC TG  AGTC
                                |||||||||| ||  ||||
                                GAGTGTCACCG AC  TCAG
                                      _ AG
GAM295  C2orf9   3'  GACTCTGTATACTGGGAA    50233     A    GC
                                TTC CAGTG  ATGGAGTC
                                ||| |||||  ||||||||
                                AAG GTCAT  TGTCTCAG
                                  G    A_
GAM295  DRIL2    3'  ACACCACCACTGTGA       21321          CA  A
                                TCACAGTGG  TGG GT
                                |||||||||  ||| ||
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                                AGTGTCACC  ACC CA
                                    __   A
GAM295  FBP17    3'  GTGAGGCCGATCGCCACTGT   72802        A__   AGT  C
                                ACAGTGGC   TGG   CC CAC
                                ||||||||   |||   || |||
                                TGTCACCG   GCC   GG GTG
                                    CTA   ___  A
GAM295  FLJ13153 3'  TGGGGGCTCACAGCACTG    45560      G A  _
                                CAGTG C TG GAGTCCCCA
                                ||||| | || |||||||||
                                GTCAC G AC CTCGGGGGT
                                  _ _  A
GAM295  FLJ20373 3'  GAAACATGCCACAGTGAA    35071      A      GAG
                                TTCAC GTGGCATG   TC
                                ||||| ||||||||   ||
                                AAGTG CACCGTAC   AG
                                  A       AA_
GAM295  FLJ20825 3'  GGACTCCATGACCTGCTGTG   35700      _  _
                                CACAGT GG CATGGAGTCC
                                |||||| || ||||||||||
                                GTGTCG CC GTACCTCAGG
                                  T  A
GAM295  KIAA0774 5'  GGGAAGAGGCAACTGTGAA   91755        G  ATGGAG
                                TTCACAGT GC     TCCC
                                |||||||| ||     ||||
                                AAGTGTCA CG     AGGG
                                    A  GAGA__
GAM295  KIAA1814 3'  GGGAGCTCCACTGTGAA     70364        GGCAT    TC
                                TTCACAGT    GGAG  CCC
                                ||||||||    ||||  |||
                                AAGTGTCA    CCTC  GGG
                                    ______   GA
GAM295  MGC14801 3'  GGAGCCCAGCACTGTGAA    51119        G A   A TC
                                TTCACAGTG C TGG G  CC
                                ||||||||| | ||| |  ||
                                AAGTGTCAC G ACC C  GG
                                    _ _  _ GA
GAM295  MGC26684 3'  GTGGGGACAGTGACACTACGAA 57991     AC   G   GGA
                                TTC  AGTG CAT   GTCCCCAC
                                |||  |||| |||   ||||||||
                                AAG  TCAC GTG   CAGGGGTG
                                  CA   A  A__
GAM295  SEMA7A   3'  TGAGGGCACCGACTGTGAA   13219        GGCA  A   C
                                TTCACAGT   TGG GTCC CA
                                ||||||||   ||| |||| ||
                                AAGTGTCA   GCC CGGG GT
                                    _____  A   A
GAM295  STAM2    3'  TCATGCCAACTGTGAA      19568        _
                                TTCACAGT GGCATGG
                                |||||||| |||||||
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                                AAGTGTCA CCGTACT
                                    A
GAM295  TCL6     5'  GTGGGGACCAGGCAGCCACTGT 27005        A  GA__
            G                    CACAGTGGC TG   GTCCCCAC
                                 ||||||||| ||   ||||||||
                                 GTGTCACCG AC   CAGGGGTG
                                     _ GGAC
GAM295  TCL6     5'  GTGGGGACCAGGCAGCCACTGT 40111        A  GA__
            G                    CACAGTGGC TG   GTCCCCAC
                                 ||||||||| ||   ||||||||
                                 GTGTCACCG AC   CAGGGGTG
                                     _ GGAC
GAM295  TCL6     5'  GTGGGGACCAGGCAGCCACTGT 40088        A  GA__
            G                    CACAGTGGC TG   GTCCCCAC
                                 ||||||||| ||   ||||||||
                                 GTGTCACCG AC   CAGGGGTG
                                     _ GGAC
GAM295  TCL6     5'  GTGGGGACCAGGCAGCCACTGT 24989        A  GA__
            G                    CACAGTGGC TG   GTCCCCAC
                                 ||||||||| ||   ||||||||
                                 GTGTCACCG AC   CAGGGGTG
                                     _ GGAC
GAM295  LOC129198 5'  GGAACTGAGTGCCACTGGAA  76120    A      GG  C
                                 TTC CAGTGGCAT  AGT CC
                                 ||| |||||||||  ||| ||
                                 AAG GTCACCGTG  TCA GG
                                   _       AG  A
GAM295  LOC148189 5'  GGGACGCTGCTGCCACTGT   78718        _  A
                                 ACAGTGGCA TGG GTCCC
                                 ||||||||| ||| |||||
                                 TGTCACCGT GTC CAGGG
                                     C  G
GAM295  LOC155006 3'  GGACGTTGCACATCACTGTGAA 81239        ____  TGGA
                                 TTCACAGTG   GCA   GTCC
                                 |||||||||   |||   ||||
                                 AAGTGTCAC   CGT   CAGG
                                     TACA  TG__
GAM295  LOC163231 3'  TGGGAACCTGTTCACTGTGAG  82446        C   A  C
                                 TTCACAGTGG ATGG GT CCCA
                                 |||||||||| |||| || ||||
                                 GAGTGTCACT TGTC CA GGGT
                                     _   _ A
GAM295  LOC166929 5'  GACCATCTGTACATCCACTGTG 82668        C___   __
            AA                    TTCACAGTGG   ATGGA  GTC
                                  ||||||||||   |||||  |||
                                  AAGTGTCACC   TGTCT  CAG
                                     TACA    AC
GAM295  LOC200531 5'  TGGAGACTCACACTGTGA    88824       GCATG   C
                                 TCACAGTG    GAGTC CCA
                                 ||||||||    ||||| |||
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                                AGTGTCAC    CTCAG GGT
                                   A____    A
GAM295  LOC255452 3'  GACCGACAGCCACTGTGAG   97536         A  GA_
                                TTCACAGTGGC TG   GTC
                                |||||||||| ||   |||
                                GAGTGTCACCG AC   CAG
                                      _ AGC
GAM295  LOC93134  3'  TGGAAACTCTGTGACTGT    71522      GG      CC
                                ACAGT  CATGGAGT  CCA
                                |||||  ||||||||  |||
                                TGTCA  GTGTCTCA  GGT
                                  __       AA
GAM296  ADAM19    3'  CAGACCCATTTTCTGGGAGCTG 52702      GTT___      C
          C                      GCAGT     AAAATGGG CTG
                                |||||     |||||||| |||
                                CGTCG     TTTTACCC GAC
                                   AGGGTC       A
GAM296  ADORA2A   3'  CAGGCCCAGCCCTCCACTGC   5432       TTAAAA
                                GCAGTG     TGGGCCTG
                                ||||||     ||||||||
                                CGTCAC     ACCCGGAC
                                   CTCCCG
GAM296  ATP8B2    5'  TCCTCAACACCGTTGTG     65239       A    AAAAT
                                CACAGC GTGTT    GGG
                                |||||| |||||    |||
                                GTGTTG CACAA    CCT
                                   C    CT___
GAM296  CEACAM6   3'  GCATCTTTAACACAGCCGTG   10187     A  A      ATGG
                                CAC GC GTGTTAAA   GC
                                ||| || ||||||||   ||
                                GTG CG CACAATTT   CG
                                  C  A       CTA_
GAM296  CLN6      3'  CAGGCCCACCCTGACCCT    35401    T   AAA
                                AG GTTA   TGGGCCTG
                                || ||||   ||||||||
                                TC CAGT   ACCCGGAC
                                 C   CCC
GAM296  DDX11     3'  CAGGCCCATTCCCAGCTGCTG  47649       GTTAA
                                CAGCAGT    AATGGGCCTG
                                |||||||    ||||||||||
                                GTCGTCG    TTACCCGGAC
                                    ACCC_
GAM296  DHCR24    3'  CAGGCCCACCCCAGCCACCACT 28626     CA   TTAAAA_
          G                      CAG  GTG     TGGGCCTG
                                |||  |||     ||||||||
                                GTC  CAC     ACCCGGAC
                                  AC   CGACCCC
GAM296  EGLN2     5'  AGTTCTTAACATTGCTG     34097          AAAT  GC
                                CAGCAGTGTTA   GG  CT
                                ||||||||||   ||  ||
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                                GTCGTTACAAT   TC  GA
                                      ____  TT
GAM296  ESRRB   5'  CAGGCCCACCTTAGTCACTGT  67318      _   AA
                                GCAGTG TTAA  TGGGCCTG
                                |||||| ||||  ||||||||
                                TGTCAC GATT  ACCCGGAC
                                   T   CC
GAM296  GYG     3'  CTATCTCAACACTGCTG    14689        AAA
                                CAGCAGTGTT   ATGG
                                ||||||||||   ||||
                                GTCGTCACAA   TATC
                                      CTC
GAM296  LIF     3'  CAGGCCCACCTTGCGGCCCTG  9731     T   A_  A_
                                CAG GTT  AA  TGGGCCTG
                                ||| |||  ||  ||||||||
                                GTC CGG  TT  ACCCGGAC
                                  C   CG  CC
GAM296  MCCC2   3'  CAGTAATTTTTTTAACACTGT  42136          TG GC_
                                GCAGTGTTAAAA  G   CTG
                                ||||||||||||  |   |||
                                TGTCACAATTTT  T   GAC
                                      TT AAT
GAM296  MYO7A   3'  CAGGCCCATCAGCTACCCCTGC 4228      T_  TAAA_
                                GCAG  GT    ATGGGCCTG
                                ||||  ||    |||||||||
                                CGTC  CA    TACCCGGAC
                                  CC  TCGAC
GAM296  PPP1R8  5'  AGAGTTCAACACTGC      10721       TAAAA    _
                                GCAGTGT    TGGGC CT
                                |||||||    ||||| ||
                                CGTCACA    ACTTG GA
                                     _____    A
GAM296  PPP2R4  3'  CAGGCCCATTGAGGGCCACCGC 60556    A   _  AA_
                                GC GTG TT   AATGGGCCTG
                                || ||| ||   ||||||||||
                                CG CAC GG   TTACCCGGAC
                                 C   C  GAG
GAM296  PTPN7   5'  AGCTCCAACACTGCTG     54544        TAAAA   GC
                                CAGCAGTGT    TGG  CT
                                |||||||||    |||  ||
                                GTCGTCACA    ACC  GA
                                     _____   TC
GAM296  RANBP3  5'  CAGCATCCCCTGACACTGCTG  23630          AAAT   C__
                                CAGCAGTGTTA   GGG   CTG
                                ||||||||||    |||   |||
                                GTCGTCACAGT   CCC   GAC
                                      C___   TAC
GAM296  ATE1    3'  CAGGCCCATTTTAAACTG    72612      G
                                CAGT TTAAAATGGGCCTG
                                |||| ||||||||||||||
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                                GTCA AATTTTACCCGGAC
                                   _
GAM296  C11orf11  5'  CAGGCCCACTGAGCCTCTGC  93251     T_  AAAA
                                GCAG  GTT   TGGGCCTG
                                ||||  |||   ||||||||
                                CGTC  CGA   ACCCGGAC
                                  TC  GTC_
GAM296  C1orf19   3'  CTTGTCAACACTGCTGT     68192         AAA TG
                                ACAGCAGTGTT   A  GG
                                ||||||||||  |  ||
                                TGTCGTCACAA   T  TC
                                      C__ GT
GAM296  C20orf130 3'  GCCTTGCTTTTAACACCCCTG  61757     CA       T__
                                CAG  GTGTTAAAA   GGGC
                                |||  |||||||||   ||||
                                GTC  CACAATTTT   TCCG
                                  CC        CGT
GAM296  C20orf162 5'  GCCCACCTATGCTGCTG     54601         TAAAA
                                CAGCAGTGT    TGGGC
                                |||||||||    |||||
                                GTCGTCGTA    ACCCG
                                     TCC__
GAM296  C22orf4   3'  CAGGCCCTAGGACACTGC    60640        AAAAT
                                GCAGTGTT    GGGCCTG
                                ||||||||    |||||||
                                CGTCACAG    CCCGGAC
                                     GAT__
GAM296  CDC14B    3'  AGGCCCACTGCTGCTG      52843       GTTAAAA
                                CAGCAGT      TGGGCCT
                                |||||||      |||||||
                                GTCGTCG      ACCCGGA
                                    TC_____
GAM296  DKFZP564O0423 5'  CAGGCGCCTTCTACACACTGCT 91681         TAAAAT  _
          G                      CAGCAGTGT     GG GCCTG
                                |||||||||     || |||||
                                GTCGTCACA     CC CGGAC
                                     CATCTT  G
GAM296  ERO1L     3'  CAGTTTACACTGCTGT      27430         T   A
                                ACAGCAGTGT AAA TG
                                |||||||||| ||| ||
                                TGTCGTCACA TTT AC
                                     _   G
GAM296  FLJ10846  3'  CAGTACTTCCTACCACTGCTG  36736       T  AAAT  GC
                                CAGCAGTG TA   GG  CTG
                                |||||||| ||   ||  |||
                                GTCGTCAC AT   TC  GAC
                                     C  CCT_  AT
GAM296  FLJ12294  3'  CAGGCCCACCAGCCACTCGC   47009    _   TTAAAA
                                GC AGTG     TGGGCCTG
                                || ||||     ||||||||
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                                CG TCAC     ACCCGGAC
                                 C   CGACC_
GAM296  FLJ12765  3'  AGAAACCAACACTGTGTG    45846     G     TAAAA  GC_
                                CACA CAGTGT    TGG  CT
                                |||| ||||||    |||  ||
                                GTGT GTCACA    ACC  GA
                                  _    _____  AAA
GAM296  FLJ20079  3'  CTGATTTTAACCCGCTGC    34492      __      G
                                GCAGT  GTTAAAAT GG
                                |||||  |||||||| ||
                                CGTCG  CAATTTTA TC
                                   CC       G
GAM296  FLJ22615  3'  CAGGCCCATCCCAGAGCACTG  68515       AAA__
                                CAGTGTT    ATGGGCCTG
                                |||||||    |||||||||
                                GTCACGA    TACCCGGAC
                                    GACCC
GAM296  FLJ32452  3'  CAGGCCCATCGTAGGAGCAC   58017      AAA___
                                GTGTT     ATGGGCCTG
                                |||||     |||||||||
                                CACGA     TACCCGGAC
                                   GGATGC
GAM296  G0S2      3'  CATTTCCAACACTGTGTG    31681     G     A_
                                CACA CAGTGTT  AAATG
                                |||| |||||||  |||||
                                GTGT GTCACAA  TTTAC
                                  _      CC
GAM296  KIAA0339  3'  CAGATTCATCAACCACTGCTG  71473       TTAAA   GC
                                CAGCAGTG    ATGG  CTG
                                ||||||||    ||||  |||
                                GTCGTCAC    TACT  GAC
                                    CAAC_   TA
GAM296  KIAA0513  3'  CAGACCCAGCCACACTGCTCA  28344   C      TAAAA   C
                                A AGCAGTGT    TGGG CTG
                                | ||||||||    |||| |||
                                A TCGTCACA    ACCC GAC
                                 C       CCG__   A
GAM296  KIAA0515  3'  CAGGCCCATCCCAGGCCCCGTG 63804    A__  AG  TTAAA
                                CAC   GC  TG    ATGGGCCTG
                                |||   ||  ||    |||||||||
                                GTG   CG  AC    TACCCGGAC
                                  CCC  G_  CC___
GAM296  KIAA0523  3'  CAGGAGTTTCCACACTGCTGTG 67730         TA   GGG
                                CACAGCAGTGT  AAAT   CCTG
                                ||||||||||  ||||   ||||
                                GTGTCGTCACA  TTTG   GGAC
                                      CC    A__
GAM296  KIAA0981  3'  GTTTTAATACTGCTGTG    61424
                                CACAGCAGTGTTAAAAT
                                |||||||||||||||||
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                                GTGTCGTCATAATTTTG

GAM296  KIAA1084  3'  CTGATTTTGACACCACTGT   29836     CA       G
                                ACAG  GTGTTAAAAT GG
                                ||||  |||||||||| ||
                                TGTC  CACAGTTTTA TC
                                  AC        G
GAM296  KIAA1573  5'  CAATTCAAGACTGCTGT    62683       G  A  A
                                ACAGCAGT TT AA TG
                                |||||||| || || ||
                                TGTCGTCA AA TT AC
                                     G  C  A
GAM296  KIAA1656  5'  CAGGCCCACCTTGAGGCCACCC 65782    CA__  G   AA
           TG                     CAG   GT TTAA  TGGGCCTG
                                |||   || ||||  ||||||||
                                GTC   CG AGTT  ACCCGGAC
                                  CCAC  G   CC
GAM296  KIAA1673  3'  GCCCCAGCACTGCTGTG    70782          AAAAT
                                CACAGCAGTGTT    GGGC
                                ||||||||||||    ||||
                                GTGTCGTCACGA    CCCG
                                       C____
GAM296  MAP4K3    3'  CATTTAACACTATTGT     13239     C       A
                                ACAG AGTGTTAAA TG
                                |||| |||||||| ||
                                TGTT TCACAATTT AC
                                  A       _
GAM296  MGC3020   3'  CAGGCCCACCTGGCTCCTGCTG 43892      T_   AAA
                                CAGCAG  GTTA   TGGGCCTG
                                ||||||  ||||   ||||||||
                                GTCGTC  CGGT   ACCCGGAC
                                   CT   CC_
GAM296  MGC5601   5'  CAGGCCCATTGGAACTACT   47506    _  AA
                                AGT GTT  AATGGGCCTG
                                ||| |||  ||||||||||
                                TCA CAA  TTACCCGGAC
                                  T   GG
GAM296  P66       3'  TTTATTTCACACTGCTG     40370        TA
                                CAGCAGTGT  AAATGGG
                                |||||||||  |||||||
                                GTCGTCACA  TTTATTT
                                     C_
GAM296  PPP4R2    3'  CAGTTCTGGTTTTAACACTGT  39070          G  C_
                                GCAGTGTTAAAAT GG  CTG
                                |||||||||||| ||  |||
                                TGTCACAATTTTG TC  GAC
                                       G  TT
GAM296  PRO2900   5'  CAGGCCCATTCAGGGCTGC   37805      G  AA
                                GCAGT TT  AATGGGCCTG
                                ||||| ||  ||||||||||
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                                CGTCG GA  TTACCCGGAC
                                   G  C_
GAM296  RPH3A    3'  AGACCCGGACAATGCTGTG   30240       G   AAAA   C
                                CACAGCA TGTT   TGGG CT
                                ||||||| ||||   |||| ||
                                GTGTCGT ACAG   GCCC GA
                                    A   ____   A
GAM296  SDF1     3'  GCCCAGCACTGCTTG      90858   C      TAAAA
                                A AGCAGTGT    TGGGC
                                | ||||||||    |||||
                                G TCGTCACG    ACCCG
                                 T     _____
GAM296  SDNSF    3'  CATTTCCAACTACTGCTG    57751       _  A_
                                CAGCAGT GTT  AAATG
                                ||||||| |||  |||||
                                GTCGTCA CAA  TTTAC
                                    T  CC
GAM296  SEMA4G   5'  CAGAACTACTCAACACTGCTG  94673        AAAA  GC
                                CAGCAGTGTT   TGG  CTG
                                ||||||||||   |||  |||
                                GTCGTCACAA   ATC  GAC
                                     CTC_  AA
GAM296  LOC124045 3'  CAGGCCCACCCCACCCTGTG  76032     CA  TTAAAA
                                CACAG  GTG    TGGGCCTG
                                |||||  |||    ||||||||
                                GTGTC  CAC    ACCCGGAC
                                   C_  CCC___
GAM296  LOC124045 3'  CAGGCCCACCCCACCCTGTG  76033     CA  TTAAAA
                                CACAG  GTG    TGGGCCTG
                                |||||  |||    ||||||||
                                GTGTC  CAC    ACCCGGAC
                                   C_  CCC___
GAM296  LOC129305 5'  CAGGCGACCTCAAACTGCTGT  75723       GTTAAAAT __
                                ACAGCAGT      GG  GCCTG
                                ||||||||      ||  |||||
                                TGTCGTCA      CC  CGGAC
                                    AACT____  AG
GAM296  LOC145623 3'  GCCCCAACACTGCTGT     83397         AAAAT
                                ACAGCAGTGTT    GGGC
                                ||||||||||    ||||
                                TGTCGTCACAA    CCCG
                                     C____
GAM296  LOC148046 3'  CAGGCCCATTCTTTCTGATCTG 84104     T   A____
          C                      GCAG GTTA    AATGGGCCTG
                                 |||| ||||    ||||||||||
                                 CGTC TAGT    TTACCCGGAC
                                   _   CTTTC
GAM296  LOC151987 3'  CAGTTCTGGTTTTAACACTGT  67465          G  C_
                                GCAGTGTTAAAAT GG  CTG
                                |||||||||||| ||  |||
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                                TGTCACAATTTTG TC  GAC
                                       G  TT
GAM296  LOC196489 3'  CAGGCCCAAGGCCACACCCTGC 87735     __    TAAAA
                                GCA  GTGT     TGGGCCTG
                                |||  ||||     ||||||||
                                CGT  CACA     ACCCGGAC
                                  CC    CCGGA
GAM296  LOC196955 5'  CAGACCCACCTTTAATACTGGT 77367    G        A_    C
          G                      CA CAGTGTTAAA  TGGG CTG
                                || ||||||||||  |||| |||
                                GT GTCATAATTT  ACCC GAC
                                 G        CC    A
GAM296  LOC197342 3'  AGGCCCATTTGGTGACAC    87988       __
                                GTGTTA  AAATGGGCCT
                                ||||||  ||||||||||
                                CACAGT  TTTACCCGGA
                                    GG
GAM296  LOC200609 5'  GCCCATTTCTGCTCA       90101    C     TGTTA
                                A AGCAG     AAATGGGC
                                | |||||     ||||||||
                                A TCGTC     TTTACCCG
                                 C    _____
GAM296  LOC200854 3'  CAGTTCTGGTTTTAACACTGT  87421            G  C_
                                GCAGTGTTAAAAT GG  CTG
                                |||||||||||| ||  |||
                                TGTCACAATTTTG TC  GAC
                                       G  TT
GAM296  LOC219445 3'  TAGGTCCTCCAACACCACTGT  91578      CA     AAAAT
                                ACAG  GTGTT    GGGCCTG
                                ||||  |||||    |||||||
                                TGTC  CACAA    CCTGGAT
                                  AC    CCT__
GAM296  LOC221550 5'  AGGCCCAGCCACTCTGTG    92118      C    TTAAAA
                                CACAG AGTG     TGGGCCT
                                ||||| ||||     |||||||
                                GTGTC TCAC     ACCCGGA
                                   _   CG____
GAM296  LOC222057 3'  CAGGCCCACCTCTTCCTCACCC 92765     CA   TTAAAA___
          TG                      CAG  GTG       TGGGCCTG
                                |||  |||       ||||||||
                                GTC  CAC       ACCCGGAC
                                  C_   TCCTTCTCC
GAM296  LOC253517 3'  CAGGCCCACCCCACCCTGTG   95104      CA   TTAAAA
                                CACAG  GTG     TGGGCCTG
                                |||||  |||     ||||||||
                                GTGTC  CAC     ACCCGGAC
                                   C_   CCC___
GAM296  LOC255057 3'  CAGGCCCAGACCAGCTACCGC  95350    A  _   AAAA
                                GC GT GTT    TGGGCCTG
                                || || |||    ||||||||
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                                CG CA CGA    ACCCGGAC
                                 C  T   CCAG
GAM296   LOC255320 5'  CCCATTTTGGCTTTGT      95004      T
                                GCAG GTTAAAATGGG
                                |||| ||||||||||
                                TGTT CGGTTTTACCC
                                  T
GAM296   LOC256849 5'  CAGGCCCATCCTGGGTCTTGCT 96947        TG  AAA_
           GT                    ACAGCAG  TT    ATGGGCCTG
                                |||||||  ||    |||||||||
                                TGTCGTT  GG    TACCCGGAC
                                   CT  GTCC
GAM296   LOC257495 5'  AGGCCCAGCCACTCTGTG    97724      C    TTAAAA
                                CACAG AGTG     TGGGCCT
                                ||||| ||||     |||||||
                                GTGTC TCAC     ACCCGGA
                                  _   CG____
GAM296   LOC257576 5'  AGGCCCAGCCACTCTGTG    97881      C    TTAAAA
                                CACAG AGTG     TGGGCCT
                                ||||| ||||     |||||||
                                GTGTC TCAC     ACCCGGA
                                  _   CG____
GAM296   LOC91266  5'  AGGCCCACCTTAGGCT      65407     AGTG    AA
                                AGC    TTAA  TGGGCCT
                                |||    ||||  |||||||
                                TCG    GATT  ACCCGGA
                                  _____   CC
GAM297   ADH1B     3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM297   ADH1B     3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM297   AHR       3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                  TA_   T  _
GAM297   AHR       3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                  TA_   T  _
GAM297   FDFT1     3'  TAGGAAAGTGAAATG       15518            A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
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                                GTAAAGTGAAAG GAT
                                              _
GAM297  FDFT1    3'  TAGGAAAGTGAAATG       15518          A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                              _
GAM297  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
                TG                  CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM297  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
                TG                  CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM297  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||  ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM297  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||  ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM297  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM297  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM297  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM297  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM297  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
```

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                                AAAGT AAAGTGACGGG
                                   A
GAM297  WRN     3' GGGCAGTGAAAATGAAA    5098      C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM297  ZNF216  3' ATCTGCACAGCAAAGTGAAA  20017       CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_    CG_
GAM297  ZNF216  3' ATCTGCACAGCAAAGTGAAA  20017       CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_    CG_
GAM297  CG012   5' CTCACTCTGAAAGTGAA    83218       CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                     CT   __
GAM297  CG012   5' CTCACTCTGAAAGTGAA    83218       CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                     CT   __
GAM297  EIF2C2  3' ATCTTCTGAGAGTGAAAG   71946       G  T_
                                CTTTCACT TC  GAGAT
                                |||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM297  EIF2C2  3' ATCTTCTGAGAGTGAAAG   71946       G  T_
                                CTTTCACT TC  GAGAT
                                |||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM297  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802      ACTTTCACT
           G                     CATTTC       GTCTGAGAT
                                 ||||||       |||||||||
                                 GTAAAG       CAGACTCTA
                                    AAACATTT_
GAM297  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802      ACTTTCACT
           G                     CATTTC       GTCTGAGAT
                                 ||||||       |||||||||
                                 GTAAAG       CAGACTCTA
                                    AAACATTT_
GAM297  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
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                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM297  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM297  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM297  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM297  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM297  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM297  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM297  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM297  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM297  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM297  PP35      3'  ATCTCAGACTGAAA        22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
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                              AAAGT  CAGACTCTA
                                   __
GAM297  PP35     3'  ATCTCAGACTGAAA      22814      CT
                              TTTCA  GTCTGAGAT
                              |||||  |||||||||
                              AAAGT  CAGACTCTA
                                   __
GAM297  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG 48148        TCAC  C_
                              CATTTCACTT   TGT  TGAG
                              ||||||||||   |||  ||||
                              GTAAAGTGAA   ACG  ACTC
                                   TA__   TT
GAM297  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG 48148        TCAC  C_
                              CATTTCACTT   TGT  TGAG
                              ||||||||||   |||  ||||
                              GTAAAGTGAA   ACG  ACTC
                                   TA__   TT
GAM297  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                              TTTCACTTT ACTGT  GA
                              ||||||||| |||||  ||
                              AAAGTGAGA TGACA  CT
                                   A    TC
GAM297  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                              TTTCACTTT ACTGT  GA
                              ||||||||| |||||  ||
                              AAAGTGAGA TGACA  CT
                                   A    TC
GAM297  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941        CACTG
                              TTTCACTTT    TCTGAG
                              |||||||||    ||||||
                              AAAGTGAAA    GGACTC
                                   AAAGG
GAM297  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941        CACTG
                              TTTCACTTT    TCTGAG
                              |||||||||    ||||||
                              AAAGTGAAA    GGACTC
                                   AAAGG
GAM297  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                              TTTC      CTGTCTGAGAT
                              ||||      ||||||||||
                              AAAG      GACAGACTCTA
                                GTTTGCC
GAM297  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                              TTTC      CTGTCTGAGAT
                              ||||      ||||||||||
                              AAAG      GACAGACTCTA
                                GTTTGCC
GAM297  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015      TTCACT  C
                              TTTCACT     GT TGAGAT
                              |||||||     || ||||||
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                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM297  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM297  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226     A      GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM297  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226     A      GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM297  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM297  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM298  ARCN1    3'  AGACTGCACTCTCTGTCA    7970          CA_
                                TGACAGAGA   CAGTTT
                                |||||||||   ||||||
                                ACTGTCTCT   GTCAGA
                                      CAC
GAM298  CBFA2T2  3'  GAGCAAAACTCTGTCT      17466      C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                   C
GAM298  CTLA4    3'  CAGAGCTGGGATGTTTCTGTCA 17807          CAGTTTT
                                TGACAGAGACA      GCTCTG
                                ||||||||||       ||||||
                                ACTGTCTTTGT      CGAGAC
                                      AGGGT__
GAM298  ITK      3'  CAGAACAGGAGTGATGTCTCTG 18674        _ G    C
                                CAGAGACA CA TTTTG TCTG
                                |||||||| || ||||| ||||
                                GTCTCTGT GT AGGAC AGAC
                                     A G    A
GAM298  LAMP2    3'  GGTGAAACCCCATCTCTATCA  25716    C    CACA    TG
                                TGA AGAGA    GTTT  CT
                                ||| |||||    ||||  ||
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                                ACT TCTCT   CAAA  GG
                                  A    ACCC   GT
GAM298  MRPS12   3' CAAAGGGTGCCCCTCTGTCA  40865       A__  AG
                                TGACAGAG  CAC  TTTTG
                                ||||||||  |||  |||||
                                ACTGTCTC  GTG  GAAAC
                                    CCC   G_
GAM298  MRPS12   3' CAAAGGGTGCCCCTCTGTCA  52963       A__  AG
                                TGACAGAG  CAC  TTTTG
                                ||||||||  |||  |||||
                                ACTGTCTC  GTG  GAAAC
                                    CCC   G_
GAM298  MRPS12   3' CAAAGGGTGCCCCTCTGTCA  52960       A__  AG
                                TGACAGAG  CAC  TTTTG
                                ||||||||  |||  |||||
                                ACTGTCTC  GTG  GAAAC
                                    CCC   G_
GAM298  PDGFRB   5' CAGAGCCTGGAACTGTG    65969       __
                                CACAGTTTT  GCTCTG
                                |||||||||  ||||||
                                GTGTCAAGG  CGAGAC
                                     TC
GAM298  PTPRA    3' AGAGCGGTATCTCTG      55079      C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A  _____
GAM298  PTPRA    3' AGAGCGGTATCTCTG      55087      C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A  _____
GAM298  PTPRA    3' AGAGCGGTATCTCTG      11088      C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A  _____
GAM298  RAD51L3  3' CAAAACTCAGGTATGTCTCTGT 56065       C_____
                                ACAGAGACA     AGTTTTG
                                |||||||||     |||||||
                                TGTCTCTGT     TCAAAAC
                                     ATGGAC
GAM298  TBL2     3' CAGAACTGTGTTCCATCA    52178    CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM298  TBL2     3' CAGAACTGTGTTCCATCA    24924    CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
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                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM298  AGTRL2   5'  CAGAGCAAGAACTGTTC     17691    C      _
                                GA ACAGTTTT GCTCTG
                                || |||||||| ||||||
                                CT TGTCAAGA CGAGAC
                                 _       A
GAM298  CABP5    3'  AGAGCGGTATCTTTGCCA    39079    A    C  AGTTT
                                TG CAGAGA AC    TGCTCT
                                || |||||| ||    ||||||
                                AC GTTTCT TG    GCGAGA
                                 C     A _____
GAM298  CUL4A    5'  AGAGCAGCACCTCCATCA    13149    CA   ACACA  T
                                TGA  GAG    GT TTGCTCT
                                |||  |||    || |||||||
                                ACT  CTC    CA GACGAGA
                                  AC  _____  C
GAM298  DKFZp761O17121 3'  CAGACAGCCCCTGTGTCTCTGT 50136           TT_  C
          C                      GACAGAGACACAG   TTG TCTG
                                |||||||||||||   ||| ||||
                                CTGTCTCTGTGTC   GAC AGAC
                                       CCC  _
GAM298  FLJ10375 3'  CAGAGGCCTGTGTCTGTGCCA  36073    A  G      TTTTG
                                TG CA AGACACAG    CTCTG
                                || || ||||||||    |||||
                                AC GT TCTGTGTC    GAGAC
                                 C  G       CG___
GAM298  FLJ10738 5'  CAAAGCCAGCCCTCTGTCA   36527        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
                                ACTGTCTC    CGAAAC
                                     CCGAC
GAM298  FLJ10803 3'  CAAAACAAAACTCTGTCA    36660        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
                                ACTGTCTC    CAAAAC
                                     AAAA_
GAM298  FLJ10842 3'  AAAGTGTGCTCTGTCA      36723        A   G
                                TGACAGAG CACA TTT
                                |||||||| |||| |||
                                ACTGTCTC GTGT AAA
                                     _   G
GAM298  FLJ13153 3'  CAGAGCCCAGCATCCATCTCTG 45555         CACA_  TT
          TCA                    TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                      ACCTA   CC
GAM298  FLJ20035 3'  CAAACCTGCCATGTTCTGTCA  34395        A ___  T
                                TGACAGAG CA   CAG TTTG
                                |||||||| ||   ||| ||||
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                                ACTGTCTT GT   GTC AAAC
                                    _ ACC   C
GAM298  FLJ22195  5'  CAGAGCAGAGGGAAGTCTCTGC 42800    A      ACAG
           CA                    TG CAGAGAC    TTTTGCTCTG
                                || |||||||    ||||||||||
                                AC GTCTCTG    GAGACGAGAC
                                 C      AAGG
GAM298  FLJ32191  5'  GAACTGCACCTCTGTCA     58411         ACA
                                TGACAGAG   CAGTTT
                                ||||||||   ||||||
                                ACTGTCTC   GTCAAG
                                     CAC
GAM298  KIAA1023  3'  CAAAGCTGTATCTGCTATCA   34255     C _   C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM298  KIAA1586  5'  AGTGTGATGTGTCTCTG     92326          GTT TG T
                                CAGAGACACA   T  C CT
                                ||||||||||   |  | ||
                                GTCTCTGTGT   A  G GA
                                     ___ GT T
GAM298  KIAA1754  3'  GACTAACGTCTCTGTCA     63236          AC_
                                TGACAGAGAC   AGTT
                                ||||||||||   ||||
                                ACTGTCTCTG   TCAG
                                     CAA
GAM298  LANCL2    3'  CAGAGTGCACTGCAGCTCTGTC 37995         ACA    TTT
           A                     TGACAGAG   CAGT   GCTCTG
                                ||||||||   ||||   ||||||
                                ACTGTCTC   GTCA   TGAGAC
                                     GAC    CG_
GAM298  LIG-1     3'  CAGAGCAGGCCTGTCCATGCCA 63893    A  GAGAC    TT
                                TG CA    ACAG  TTGCTCTG
                                || ||    ||||  ||||||||
                                AC GT    TGTC  GACGAGAC
                                 C  ACC__    CG
GAM298  MGC5242   3'  AGAGTACATGTCTCTG      43823         CAGTTT
                                CAGAGACA     TGCTCT
                                ||||||||     ||||||
                                GTCTCTGT     ATGAGA
                                     AC_____
GAM298  OSMR      3'  CAGAGCTGGCACCCTGTCA    14345       AGACA
                                TGACAG    CAGTTTTG
                                ||||||    ||||||||
                                ACTGTC    GTCGAGAC
                                    CCACG
GAM298  RAB21     3'  CAGAACAAAACTGTGGATC    30383    GA        C
                                GA  CACAGTTTTG TCTG
                                ||  |||||||||| ||||
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                                CT  GTGTCAAAAC AGAC
                                 AG         A
GAM298  SPTLC2    3'  CAGAGCAAAACTGTGTCTC   16799
                                GAGACACAGTTTTGCTCTG
                                ||||||||||||||||||
                                CTCTGTGTCAAAACGAGAC

GAM298  TGIF2     3'  GAGTCATGCTCTGTCA      41454         A  CAGTTT  _
                                TGACAGAG CA     TG CTC
                                |||||||| ||     || |||
                                ACTGTCTC GT     AC GAG
                                     _ _______  T
GAM298  WBSCR23   5'  GCTGACTGTGTCTCCATCA   46765     CA         TT
                                TGA  GAGACACAGTT  GC
                                |||  ||||||||||  ||
                                ACT  CTCTGTGTCAG  CG
                                  AC          T_
GAM298  LOC115129 3'  GGCAAAACCCCGTCTCT     73235       ACA
                                AGAGAC   GTTTTGCT
                                ||||||   ||||||||
                                TCTCTG   CAAAACGG
                                   CCC
GAM298  LOC129198 3'  AGCAAGCTGTGCCTC       76117     A       T
                                GAG CACAGTTT GCT
                                ||| |||||||| |||
                                CTC GTGTCGAA CGA
                                  C       _
GAM298  LOC145231 3'  GGTGAAACTATGTCTCT     83293        C     TG
                                AGAGACA AGTTT  CT
                                |||||||  |||||  ||
                                TCTCTGT TCAAA  GG
                                    A    GT
GAM298  LOC145483 3'  GAGCAAAACTCTGTCT      77243       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                   C
GAM298  LOC146713 3'  GAGCAAAACTCCGTCT      83726      AC
                                AGAC  AGTTTTGCTC
                                ||||  ||||||||||
                                TCTG  TCAAAACGAG
                                  CC
GAM298  LOC149175 3'  CAGGGTGAAACCACGTCTCT   79208        ACA    TG
                                AGAGAC   GTTT  CTCTG
                                ||||||   ||||  |||||
                                TCTCTG   CAAA  GGGAC
                                   CAC    GT
GAM298  LOC150299 3'  CAGAACCTGCATCTTTGTCA   84968         CA   _
                                TGACAGAGA  CAG TTTTG
                                |||||||||  ||| |||||
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                                ACTGTTTCT  GTC AAGAC
                                     AC   C
GAM298  LOC153277 3'  TAAAACTGTGCCTGTGCCA   85990    A  G  A
                                TG CA AG CACAGTTTTG
                                || || || ||||||||||
                                AC GT TC GTGTCAAAAT
                                 C  G  C
GAM298  LOC155179 3'  CAAAGCTGTATCTGCTATCA  81312     C  _  C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM298  LOC221074 3'  AAAGTGTGTCTCTTTCA     93177     C        G
                                TGA AGAGACACA TTT
                                ||| ||||||||| |||
                                ACT TCTCTGTGT AAA
                                  T        G
GAM298  LOC221103 5'  AGTTTATGTGTGCTCTGTCA  93244         _    GTTTT
                                TGACAGAG ACACA    GCT
                                |||||||| |||||    |||
                                ACTGTCTC TGTGT    TGA
                                     G    ATT__
GAM298  LOC255988 5'  CAGAGCCCAGCATCCATCTCTG 97608          CACA_  TT
           TCA                    TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                     ACCTA   CC
GAM299  ADCY8    5'  CCACTCTGACAGGTCTCCA   6650          A  TTT
                                TGGAGGCCTG TC   GTGG
                                |||||||||| ||   ||||
                                ACCTCTGGAC AG   CACC
                                     _ TCT
GAM299  ANK1     3'  GGCCACCCCGGCCCGGCCTCCA 3474         TGATCTTT
                                TGGAGGCC       GTGGCC
                                ||||||||       ||||||
                                ACCTCCGG       CACCGG
                                     CCCGGCCC
GAM299  ANK1     3'  GGCCACCCCGGCCCGGCCTCCA 40028        TGATCTTT
                                TGGAGGCC       GTGGCC
                                ||||||||       ||||||
                                ACCTCCGG       CACCGG
                                     CCCGGCCC
GAM299  BMP6     3'  GGCCACAGCCAGGGCTCCA   8165       G   ATCT
                                TGGAG CCTG    TTGTGGCC
                                ||||| ||||    ||||||||
                                ACCTC GGAC    GACACCGG
                                   G   C___
GAM299  CHST2    3'  GCCACAAAATACACACCCC   62695    A  CC  ATC
                                GG GG  TG   TTTGTGGC
                                || ||  ||   ||||||||
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                                CC CC  AC   AAACACCG
                                 _ AC  ATA
GAM299  COL1A1   5'  GCCACAAAGAGTCTACA     3606     G   CTGA
                                TG AGGC   TCTTTGTGGC
                                || ||||   ||||||||||
                                AC TCTG   AGAAACACCG
                                 A  _____
GAM299  COL4A3   3'  GGCCTCCACTCAGGCCTCCA  3623          TCTTTGT
                                TGGAGGCCTGA     GGCC
                                ||||||||||      ||||
                                ACCTCCGGACT     CCGG
                                      CACCT__
GAM299  COL4A3   3'  GGCCTCCACTCAGGCCTCCA  48558         TCTTTGT
                                TGGAGGCCTGA     GGCC
                                ||||||||||      ||||
                                ACCTCCGGACT     CCGG
                                      CACCT__
GAM299  COL4A3   3'  GGCCTCCACTCAGGCCTCCA  48569         TCTTTGT
                                TGGAGGCCTGA     GGCC
                                ||||||||||      ||||
                                ACCTCCGGACT     CCGG
                                      CACCT__
GAM299  DBY      3'  GCAGTGACCAGGCCTC      16228        A  T
                                GAGGCCTG TC TTGT
                                |||||||| || ||||
                                CTCCGGAC AG GACG
                                     C  T
GAM299  DIA1     3'  GCCAGGCCCAGGCCTC      23645        AT  TTG
                                GAGGCCTG  CT   TGGC
                                ||||||||  ||   ||||
                                CTCCGGAC  GG   ACCG
                                     CC  ___
GAM299  DPYSL3   3'  ACCTGGGATCAGACTTCCA   7309         C       T_
                                TGGAGG CTGATCTT  GT
                                |||||| ||||||||  ||
                                ACCTTC GACTAGGG  CA
                                    A       TC
GAM299  FANCC    3'  GGCCACTGGGACCAGGCCTCC  70524         A   TT
                                GGAGGCCTG TCT  GTGGCC
                                ||||||||| |||  ||||||
                                CCTCCGGAC AGG  CACCGG
                                     C   GT
GAM299  GNAS     3'  GGCCACAAAAGTTCCCTCT    54424      CCT  TC
                                GGAGG   GA  TTTGTGGCC
                                |||||   ||  |||||||||
                                TCTCC   TT  AAACACCGG
                                   C__  GA
GAM299  GNAS     3'  GGCCACAAAAGTTCCCTCT    33441      CCT  TC
                                GGAGG   GA  TTTGTGGCC
                                |||||   ||  |||||||||
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                                TCTCC  TT  AAACACCGG
                                  C__  GA
GAM299  GNAS    3'  GGCCACAAAAGTTCCCTCT   54426     CCT  TC
                                GGAGG  GA  TTTGTGGCC
                                |||||  ||  |||||||||
                                TCTCC  TT  AAACACCGG
                                  C__  GA
GAM299  GNAS    3'  GGCCACAAAAGTTCCCTCT   4968      CCT  TC
                                GGAGG  GA  TTTGTGGCC
                                |||||  ||  |||||||||
                                TCTCC  TT  AAACACCGG
                                  C__  GA
GAM299  HNRPF   5'  GCCACAAAAAAGCCACACCCA  17120    A___  CTGATC
                                TGG   GGC    TTTGTGGC
                                |||   |||    ||||||||
                                ACC   CCG    AAACACCG
                                  CACA  AAA___
GAM299  IL2RB   3'  CCACAAGGGGCTCCA     6070      G  GATCT
                                TGGAG CCT    TTGTGG
                                ||||| |||    ||||||
                                ACCTC GGG    AACACC
                                  G  _____
GAM299  IRAK1   3'  GGCCACAAGCTCAGCCTC   7810      C  T  T
                                GAGGC TGA CTT GTGGCC
                                ||||| ||| ||| ||||||
                                CTCCG ACT GAA CACCGG
                                  _  C  _
GAM299  LFNG    3'  GCCCCACGAAGCCCCCA    92640    A  CTGATC   __
                                TGG GGC    TTTGT  GGC
                                ||| |||    |||||  |||
                                ACC CCG    AAGCA  CCG
                                  C  _______   CC
GAM299  MMP15   3'  ACAGGGAATTAGGCCCCCA  10071    A     _
                                TGG GGCCTGAT CTTTGT
                                ||| |||||||| ||||||
                                ACC CCGGATTA GGGACA
                                  C      A
GAM299  MS4A4A  3'  GTTAAAATGAGGCCTCCA   43784       G  CTTTG
                                TGGAGGCCT AT   TGGC
                                ||||||||| ||   ||||
                                ACCTCCGGA TA   ATTG
                                     G  AA___
GAM299  MUC4    3'  CCAACTCAGGCCTCCA     56322         TCTTTG
                                TGGAGGCCTGA    TGG
                                ||||||||||     |||
                                ACCTCCGGACT    ACC
                                      CA____
GAM299  NESG1   5'  GGCCAGGGACCAGGCCTTCA  24703        A   TG
                                TGGAGGCCTG TCTT  TGGCC
                                |||||||||| ||||  |||||
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                                ACTTCCGGAC AGGG  ACCGG
                                      C   __
GAM299  PFKL    3'  GGCCACCTGCCAGGCCTCC   10519        ATCTTT
                                GGAGGCCTG    GTGGCC
                                |||||||||    ||||||
                                CCTCCGGAC    CACCGG
                                     CGTC__
GAM299  PLAUR   5'  GGCCACAAAACTGCCTCC    10617      CTGATC
                                GGAGGC    TTTGTGGCC
                                ||||||    |||||||||
                                CCTCCG    AAACACCGG
                                   TCA___
GAM299  PODXL   5'  GCCACCCACAGGCCTCC     18234        ATCTTT
                                GGAGGCCTG    GTGGC
                                |||||||||    |||||
                                CCTCCGGAC    CACCG
                                     ACC___
GAM299  RAB36   3'  GCCACCGCGTCCGGCCTCCA  16963       T  CTTT
                                TGGAGGCC GAT   GTGGC
                                |||||||| |||   |||||
                                ACCTCCGG CTG   CACCG
                                     C  CGC_
GAM299  RAD17   3'  GAAGATCAAGCCTTCA     55870       C
                                TGGAGGC TGATCTTT
                                ||||||| ||||||||
                                ACTTCCG ACTAGAAG
                                     A
GAM299  RAD17   3'  GAAGATCAAGCCTTCA     55865       C
                                TGGAGGC TGATCTTT
                                ||||||| ||||||||
                                ACTTCCG ACTAGAAG
                                     A
GAM299  RAD17   3'  GAAGATCAAGCCTTCA     55863       C
                                TGGAGGC TGATCTTT
                                ||||||| ||||||||
                                ACTTCCG ACTAGAAG
                                     A
GAM299  RAD17   3'  GAAGATCAAGCCTTCA     55872       C
                                TGGAGGC TGATCTTT
                                ||||||| ||||||||
                                ACTTCCG ACTAGAAG
                                     A
GAM299  RAD17   3'  GAAGATCAAGCCTTCA     11212       C
                                TGGAGGC TGATCTTT
                                ||||||| ||||||||
                                ACTTCCG ACTAGAAG
                                     A
GAM299  RAD17   3'  GAAGATCAAGCCTTCA     55876       C
                                TGGAGGC TGATCTTT
                                ||||||| ||||||||
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                                ACTTCCG ACTAGAAG
                                    A
GAM299  RAD17   3'  GAAGATCAAGCCTTCA      55868       C
                                TGGAGGC TGATCTTT
                                ||||||| ||||||||
                                ACTTCCG ACTAGAAG
                                    A
GAM299  RAD17   3'  GAAGATCAAGCCTTCA      55874       C
                                TGGAGGC TGATCTTT
                                ||||||| ||||||||
                                ACTTCCG ACTAGAAG
                                    A
GAM299  SYN3    3'  CCCAAACCAGGCCTCCA      56092         ATC   T
                                TGGAGGCCTG   TTTG GG
                                ||||||||||   |||| ||
                                ACCTCCGGAC   AAAC CC
                                      C__   _
GAM299  TNFRSF13C 3'  CCACAGCATTCAGCCCCCA   53640     A  C   TCT
                                TGG GGC TGA   TTGTGG
                                ||| ||| |||   ||||||
                                ACC CCG ACT   GACACC
                                  C   _   TAC
GAM299  XRCC3   3'  GGCCACAGACTGACCCCCA   18340     A  CCTGATC
                                TGG GG      TTTGTGGCC
                                ||| ||      |||||||||
                                ACC CC      AGACACCGG
                                  _  CAGTC__
GAM299  AF9Q34  3'  GCCACAAAGCCCCCCA      50738     A  CCTGAT
                                TGG GG     CTTTGTGGC
                                ||| ||     |||||||||
                                ACC CC     GAAACACCG
                                  _  CC_____
GAM299  ARNTL2  3'  CATAGAGATCAAACCTCC    39458      CC
                                GGAGG  TGATCTTTGTG
                                |||||  ||||||||||
                                CCTCC  ACTAGAGATAC
                                   AA
GAM299  C20orf59  5'  GCCTCCATCGGCCTCCA     41996        T   CTTTGT
                                TGGAGGCC GAT     GGC
                                |||||||| |||     |||
                                ACCTCCGG CTA     CCG
                                     _   CCT___
GAM299  CBX6    3'  GGAGATCAGCCTCCA       26619       C
                                TGGAGGC TGATCTTT
                                ||||||| ||||||||
                                ACCTCCG ACTAGAGG
                                     _
GAM299  CECR6   3'  GCAGATATCAGGCCCCCA    49089     A      C
                                TGG GGCCTGAT TTTGT
                                ||| |||||||| |||||
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                                ACC CCGGACTA AGACG
                                  C       T
GAM299  CINP     3'  GCCTGGATCAGACCCCA     50938     A  C      TTGT
                                TGG GG CTGATCT    GGC
                                ||| || |||||||    |||
                                ACC CC GACTAGG    CCG
                                  _ A      T___
GAM299  DCAMKL1   5'  GCCACAAAGACCCCC       16410    A  CCTGA
                                GG GG    TCTTTGTGGC
                                || ||    ||||||||||
                                CC CC    AGAAACACCG
                                 C _____
GAM299  DKFZp434I099 5'  CCACATCACGGCCTCCA     50080         _  TCTT
                                TGGAGGCC TGA    TGTGG
                                |||||||| |||    |||||
                                ACCTCCGG ACT    ACACC
                                     C  ____
GAM299  DKFZP434O047 5'  CCACAAAGCCCAGCACCCA    31508     AG  C  AT
                                TGG  GC TG  CTTTGTGG
                                |||  || ||  ||||||||
                                ACC  CG AC  GAAACACC
                                  CA  _  CC
GAM299  DKFZP564C1940 3'  GGCCATGGCCAGACACCCCA   25904     A  C__   AT TTT
                                TGG GG   CTG  C   GTGGCC
                                ||| ||   |||  |   ||||||
                                ACC CC   GAC  G   TACCGG
                                  _  ACA   CG ___
GAM299  DKFZP564K1964 5'  GCCACAGCCTGAGGCCCTCA   31422    GA    GATCT
                                TG  GGCCT    TTGTGGC
                                ||  |||||    |||||||
                                AC  CCGGA    GACACCG
                                 TC    GTCC_
GAM299  DKFZP566G1424 5'  CCTCAGCAGGCCCCCA      84783     A     ATCT   T
                                TGG GGCCTG    TTG GG
                                ||| ||||||    ||| ||
                                ACC CCGGAC    GAC CC
                                  C     _____  T
GAM299  DKFZP586B2420 3'  GCCACAAAGAGGGCCTCC    74997        GA
                                GGAGGCCT  TCTTTGTGGC
                                ||||||||  ||||||||||
                                CCTCCGGG  AGAAACACCG
                                          __
GAM299  FLJ10432  3'  GCCACAAGGGGCGTCCA     38828     G   TGAT
                                TGGA GCC    CTTTGTGGC
                                |||| |||    |||||||||
                                ACCT CGG    GGAACACCG
                                  G  _____
GAM299  FLJ13154  3'  AAAGCCAGGCCTCCA       44788          AT
                                TGGAGGCCTG  CTTT
                                ||||||||||  ||||
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                                ACCTCCGGAC  GAAA
                                      C_
GAM299  FLJ20277  3'  CACTGGACCAGGCCTCC     34833         A   TT
                                GGAGGCCTG TCT  GTG
                                ||||||||| |||  |||
                                CCTCCGGAC AGG  CAC
                                     C   T_
GAM299  FLJ20637  3'  GGCCATGGGCCAGACCTGCA  35482    G   C   AT  TT
                                TG AGG CTG  CT  GTGGCC
                                || ||| |||  ||  ||||||
                                AC TCC GAC  GG  TACCGG
                                 G   A   CG  __
GAM299  FLJ20671  3'  CCACAAGGAACCTACA      35518    G   CCTGA
                                TG AGG    TCTTTGTGG
                                || |||    |||||||||
                                AC TCC    AGGAACACC
                                 A   A____
GAM299  FLJ23584  5'  GCCTACCATGGCCTCCA     44740        _  ATCTTT  _
                                TGGAGGCC TG     GT GGC
                                |||||||| ||     || |||
                                ACCTCCGG AC     CA CCG
                                     T  _______  T
GAM299  FLJ32356  3'  GCTCCTGACCAGGCCTTCA   58363         A  TTTGT
                                TGGAGGCCTG TC    GGC
                                |||||||||| ||    |||
                                ACTTCCGGAC AG    TCG
                                      C  TCC__
GAM299  FREQ      3'  GCAAGCAGGCCTCCA      26577         ATC
                                TGGAGGCCTG   TTTGT
                                ||||||||||   |||||
                                ACCTCCGGAC   GAACG
                                          ___
GAM299  GLE1L     3'  TCATAACCAGGCCTC      7678         ATCT
                                GAGGCCTG   TTGTGG
                                ||||||||   ||||||
                                CTCCGGAC   AATACT
                                     C___
GAM299  GMEB2     3'  GCCAGCCCAGGCCTCC     24734         AT  TTGT
                                GGAGGCCTG  CT   GGC
                                |||||||||  ||   |||
                                CCTCCGGAC  GA   CCG
                                     CC  ____
GAM299  GPR9      3'  GCCACAGCCCAGGCCTCCA  7687          ATCT
                                TGGAGGCCTG   TTGTGGC
                                ||||||||||   |||||||
                                ACCTCCGGAC   GACACCG
                                      CC__
GAM299  HIG2      3'  GGCCACAGTGCAAGACTCCA  25294       GC  GATCT
                                TGGAG  CT    TTGTGGCC
                                |||||  ||    ||||||||
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                                ACCTC  GA    GACACCGG
                                  A_  ACGT_
GAM299  HMP19    3'  GCCTTGACCAGGCCTCC     87473         A  TTTGT
                                GGAGGCCTG TC    GGC
                                ||||||||| ||    |||
                                CCTCCGGAC AG    CCG
                                    C  TT___
GAM299  HTATIP   3'  GGCCACAGCCCAGGCCTCC   21108         ATCT
                                GGAGGCCTG   TTGTGGCC
                                |||||||||   ||||||||
                                CCTCCGGAC   GACACCGG
                                    CC__
GAM299  KIAA0125 5'  GGCCAGCTGCCATCAGGCCCCA 28899     A       CTTT _
                                TGG GGCCTGAT   G TGGCC
                                ||| ||||||||   | |||||
                                ACC CCGGACTA   C ACCGG
                                  _      CCGT G
GAM299  KIAA0426 3'  ACAGAGATCAGACCTC      28249      C
                                GAGG CTGATCTTTGT
                                |||| ||||||||||
                                CTCC GACTAGAGACA
                                  A
GAM299  KIAA0560 3'  GCCACAAGGAGACCTTCA    61505       CCTGA
                                TGGAGG    TCTTTGTGGC
                                ||||||    ||||||||||
                                ACTTCC    AGGAACACCG
                                   AG___
GAM299  KIAA0599 3'  GCTCTGCTCAGGCCTCCA    77183          TCTTTGT
                                TGGAGGCCTGA     GGC
                                ||||||||||      |||
                                ACCTCCGGACT     TCG
                                    CGTC___
GAM299  KIAA0638 3'  GAGGACCAGGCCTCCA     72397          A
                                TGGAGGCCTG TCTTT
                                |||||||||| |||||
                                ACCTCCGGAC AGGAG
                                    C
GAM299  KIAA0652 3'  CCCAAGATCAGAACTCCA    28460      GC       T T
                                TGGAG  CTGATCTT G GG
                                |||||  |||||||| | ||
                                ACCTC  GACTAGAA C CC
                                  AA      _ _
GAM299  KIAA0662 3'  GGCCACAGGCTGGCAGCCTCCA 81857        C  ATC_
                                TGGAGGC TG    TTTGTGGCC
                                ||||||| ||    |||||||||
                                ACCTCCG AC    GGACACCGG
                                   _ GGTC
GAM299  KIAA1036 5'  ACAGAACAAGGCCTCCA     29809         GATC
                                TGGAGGCCT    TTTGT
                                |||||||||    |||||
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                                ACCTCCGGA   AGACA
                                    ACA_
GAM299  KIAA1196  3'  GCCACATAGGCCTCCA     61467        ATCTT   _
                                TGGAGGCCTG   TGTGG C
                                ||||||||||   ||||| |
                                ACCTCCGGAT   ACACC G
                                     _____   C
GAM299  KIAA1280  5'  GCCACAAAGAGCCCATCCA  69719    __  CTGA
                                TGGA GGC   TCTTTGTGGC
                                ||||  |||  ||||||||||
                                ACCT CCG   AGAAACACCG
                                  AC  ____
GAM299  KIAA1437  3'  GGAGAGCAGGCCTCCA     60588        A
                                TGGAGGCCTG TCTTT
                                |||||||||| |||||
                                ACCTCCGGAC AGAGG
                                      G
GAM299  KIAA1679  5'  GCAACAGGCCTCCA       70152        ATCT
                                TGGAGGCCTG   TTGT
                                ||||||||||   ||||
                                ACCTCCGGAC   AACG
                                     _____
GAM299  KIAA1706  3'  CCATTCAGGACCTCCA     92786      _   TCTTT
                                TGGAGG CCTGA   GTGG
                                |||||| |||||   ||||
                                ACCTCC GGACT   TACC
                                   A   ______
GAM299  KIAA1784  3'  GCGTGGGTCAGGCCTCCA   65150          T
                                TGGAGGCCTGATCT TGT
                                |||||||||||||| |||
                                ACCTCCGGACTGGG GCG
                                        T
GAM299  KIAA1798  5'  GGCCACAAACTCCATCCTCCA 60621      CCT  TC
                                TGGAGG   GA  TTTGTGGCC
                                ||||||   ||  |||||||||
                                ACCTCC   CT  AAACACCGG
                                   TAC  C_
GAM299  KIAA1979  3'  GTCGCAAATCAAACCTC    88289     CC   CT
                                GAGG  TGAT  TTGTGGC
                                ||||  ||||  |||||||
                                CTCC  ACTA  AACGCTG
                                  AA   __
GAM299  LYPLA3    3'  GCCACAGATAGGCCTGCCA   24630    _    ATC
                                TGG AGGCCTG   TTTGTGGC
                                ||| |||||||   ||||||||
                                ACC TCCGGAT   AGACACCG
                                  G     ___
GAM299  MGC3036   5'  GGCATCGGAACCAGGCCTCC  43748        ATC   TG
                                GGAGGCCTG   TTTG  GCC
                                |||||||||   ||||  |||
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                                CCTCCGGAC  AGGC  CGG
                                     CA_   TA
GAM299  NDUFC2   5' GGTCTGAGACCAGGCCTC   15842       A   TGT
                                GAGGCCTG TCTT  GGCC
                                |||||||| ||||  ||||
                                CTCCGGAC AGAG  CTGG
                                    C   T__
GAM299  p25      3' GGCCAGGCCCAGGCCTCC   22854       AT  TTG
                                GGAGGCCTG  CT  TGGCC
                                |||||||||  ||  |||||
                                CCTCCGGAC  GG  ACCGG
                                     CC  ___
GAM299  RAI1     5' GCCACCCAGGCCTCC      60325       ATCTTT
                                GGAGGCCTG    GTGGC
                                |||||||||    |||||
                                CCTCCGGAC    CACCG
                                     C_____
GAM299  RALGPS1A 3' GTCAATCAGCCCTCCA     27609      C    CTTTG
                                TGGAGG CTGAT   TGGC
                                |||||| |||||    ||||
                                ACCTCC GACTA   ACTG
                                   C    _____
GAM299  RIN3     3' AGAGACAGGCCTCCA      45742       A
                                TGGAGGCCTG TCTTT
                                |||||||||| |||||
                                ACCTCCGGAC AGAGA
                                          _
GAM299  SIAT4B   5' CCACAAGGACCCCG       22653    A  CCTGA
                                TGG GG    TCTTTGTGG
                                ||| ||    |||||||||
                                GCC CC    AGGAACACC
                                  _ _____
GAM299  SIAT8D   5' GCCACAGAAGACCCCA     19030    A  C  GATC
                                TGG GG CT   TTTGTGGC
                                ||| || ||   ||||||||
                                ACC CC GA   AGACACCG
                                  _ A ____
GAM299  Spir-2   3' GCCCCAGGTGGCCAGGCCTCCA 70629        AT _   T
                                TGGAGGCCTG  C TTTG GGC
                                ||||||||||  | |||| |||
                                ACCTCCGGAC  G GGAC CCG
                                     CG T   C
GAM299  STRAIT11499 5' GGCTATAGCCAGGCCCCCA  41146    A    ATCT
                                TGG GGCCTG   TTGTGGCC
                                ||| ||||||   ||||||||
                                ACC CCGGAC   GATATCGG
                                  C    C___
GAM299  SV2      5' ACCTAGACCAGGTCTCCA   29301       A   TT
                                TGGAGGCCTG TCT  GT
                                |||||||||| |||  ||
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                                ACCTCTGGAC AGA  CA
                                      C   TC
GAM299  TReP-132  5'  ACAGGACCAGGCCTCC      53144         A   T
                                GGAGGCCTG TCTT GT
                                ||||||||| |||| ||
                                CCTCCGGAC AGGA CA
                                      C   _
GAM299  TReP-132  5'  GCAGTCGACCAGGCCTCC    53140         A  T_
                                GGAGGCCTG TC  TTGT
                                ||||||||| ||  ||||
                                CCTCCGGAC AG  GACG
                                      C  CT
GAM299  TReP-132  5'  GCAGTCGACCAGGCCTCC    37293         A  T_
                                GGAGGCCTG TC  TTGT
                                ||||||||| ||  ||||
                                CCTCCGGAC AG  GACG
                                      C  CT
GAM299  TRIP-Br2  3'  GGTCCAAGCCAGGCCCCCA   28586    A     ATC   T
                                TGG GGCCTG   TTTG GGCC
                                ||| ||||||   |||| ||||
                                ACC CCGGAC   GAAC CTGG
                                  C     C__   _
GAM299  ZNF11B    3'  GCCACAAGTCAGCCTCCA    73985       C   CT
                                TGGAGGC TGAT  TTGTGGC
                                ||||||| ||||  |||||||
                                ACCTCCG ACTG  AACACCG
                                      _   __
GAM299  LOC115708 3'  GGCCACAGCAAAGGCCTGCA  73555    G     GATCT
                                TG AGGCCT    TTGTGGCC
                                || ||||||    ||||||||
                                AC TCCGGA    GACACCGG
                                 G     AAC__
GAM299  LOC116113 3'  GCTGAGCCAGGCCTCCA     92218         AT   TGT
                                TGGAGGCCTG  CTT   GGC
                                ||||||||||  |||   |||
                                ACCTCCGGAC  GAG   TCG
                                      C_  ____
GAM299  LOC120224 3'  CAGGAAATCAGGCCTACA    57094    G       C  G
                                TG AGGCCTGAT TTT TG
                                || |||||||| ||| ||
                                AC TCCGGACTA AAG AC
                                 A       _  G
GAM299  LOC123591 3'  GGCCACAAGCTTCAGACCTC  75613     C   TC
                                GAGG CTGA  TTTGTGGCC
                                |||| ||||  |||||||||
                                CTCC GACT  GAACACCGG
                                  A   TC
GAM299  LOC133362 5'  GCAGGGGTCAGGCCCCCA    75923     A
                                TGG GGCCTGATCTTTGT
                                ||| |||||||||||||
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                                ACC CCGGACTGGGGACG
                                  C
GAM299  LOC139522 5'  GCCACAAGCCTTGGTCCCCA  75850    A   TGATC
                                TGG GGCC    TTTGTGGC
                                ||| ||||    ||||||||
                                ACC CTGG    GAACACCG
                                  C   TTCC_
GAM299  LOC145447 3'  CCACAAAGTAGCCCTC     77202     C  AT
                                GAGG CTG  CTTTGTGG
                                |||| |||  ||||||||
                                CTCC GAT  GAAACACC
                                  C  __
GAM299  LOC145547 3'  GGCCATCCTCCCAGGCCTC  77266       ATCTTT
                                GAGGCCTG    GTGGCC
                                ||||||||    ||||||
                                CTCCGGAC    TACCGG
                                     CCTCC_
GAM299  LOC145601 3'  GCAGAGATCAGGCCACCA   83366    A
                                TGG GGCCTGATCTTTGT
                                ||| ||||||||||||||
                                ACC CCGGACTAGAGACG
                                  A
GAM299  LOC146953 5'  GCTACCAAATCGGCCTCCA  78214       T  C  T
                                TGGAGGCC GAT TT GTGGC
                                |||||||| ||| || |||||
                                ACCTCCGG CTA AA CATCG
                                     _  _  C
GAM299  LOC148089 3'  CCACAGGGATGGCCCCCA   78627    A   TG
                                TGG GGCC  ATCTTTGTGG
                                ||| ||||  ||||||||||
                                ACC CCGG  TAGGGACACC
                                  C   __
GAM299  LOC148397 3'  GCCGTAGAGACAAACCCCCA  78818    A  CC  A
                                TGG GG  TG TCTTTGTGGC
                                ||| ||  || ||||||||||
                                ACC CC  AC AGAGATGCCG
                                  C  AA  _
GAM299  LOC148930 3'  ACAGTGCGACAGACCTCCA   79090      C   A  T__
                                TGGAGG CTG TC   TTGT
                                |||||| ||| ||   ||||
                                ACCTCC GAC AG   GACA
                                   A   _  CGT
GAM299  LOC150319 3'  GGCCACAGCCCAGGCCCCA   79658    A     ATCT
                                TGG GGCCTG    TTGTGGCC
                                ||| ||||||    ||||||||
                                ACC CCGGAC    GACACCGG
                                  _     CC__
GAM299  LOC150368 3'  GCCACAGAGCAAGACCCCA   79700    A  C  GAT
                                TGG GG CT   CTTTGTGGC
                                ||| || ||   |||||||||
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                                ACC CC GA   GAGACACCG
                                  _ A  AC_
GAM299  LOC150481 3'  GCCTCATAGGCCTCCA      79887          ATCTT  T
                                TGGAGGCCTG    TG GGC
                                ||||||||||    || |||
                                ACCTCCGGAT    AC CCG
                                      _____  T
GAM299  LOC150622 5'  GCCCAGGCACCAGGCATCCA  79961     G    ATC    T
                                TGGA GCCTG   TTTG GGC
                                |||| |||||   |||| |||
                                ACCT CGGAC   GGAC CCG
                                  A    CAC   _
GAM299  LOC152860 5'  GGCCGTAGGGACCAGACCCCA 80702    A  C   A
                                TGG GG CTG TCTTTGTGGCC
                                ||| || ||| ||||||||||
                                ACC CC GAC AGGGATGCCGG
                                  _ A  C
GAM299  LOC153910 3'  GGCCACAGAGAGGCCCCCA   80998    A   TGA
                                TGG GGCC   TCTTTGTGGCC
                                ||| ||||   ||||||||||
                                ACC CCGG   AGAGACACCGG
                                  C   ___
GAM299  LOC155032 3'  GCAGGAACAAGGCCTCCA    86322        GA_   T
                                TGGAGGCCT   TCTT GT
                                |||||||||   |||| ||
                                ACCTCCGGA   AGGA CG
                                      ACA   _
GAM299  LOC157273 3'  GCCACAGCTAAGCTCCA     86431      GC  GATCT
                                TGGAG  CT    TTGTGGC
                                |||||  ||    |||||||
                                ACCTC  GA    GACACCG
                                   ___ ATC__
GAM299  LOC196955 3'  GGCCACAATGGCAGCCTC    77384      C  A  T
                                GAGGC TG TC TTGTGGCC
                                ||||| || || ||||||||
                                CTCCG AC GG AACACCGG
                                   _ _  T
GAM299  LOC200170 3'  GGCCACAGGCAAGATCCCC   88591    CCT    ___
                                GG   GATCTT   TGTGGCC
                                ||   ||||||   |||||||
                                CC   CTAGAA   ACACCGG
                                  C__     CGG
GAM299  LOC221143 3'  CCACAAATTGGCCCCA      93565     A   TGATC
                                TGG GGCC    TTTGTGG
                                ||| ||||    |||||||
                                ACC CCGG    AAACACC
                                  _   TT___
GAM299  LOC253461 5'  GCCAGATGGAACCAAGCCTGCA 96283    G   C  A_  TTG
                                TG AGGC TG  TCT   TGGC
                                || |||| ||  |||   ||||
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                                AC TCCG AC  AGG   ACCG
                                 G   A  CA   TAG
GAM299  LOC253549 3'  ACACTGATCAGGCCTCCA    96776          TT
                                TGGAGGCCTGATC  TGT
                                |||||||||||||  |||
                                ACCTCCGGACTAG  ACA
                                       TC
GAM299  LOC254826 3'  GCAAATCAACCTCCA      97242      CC    CT
                                TGGAGG  TGAT  TTGT
                                ||||||  ||||  ||||
                                ACCTCC  ACTA  AACG
                                   A_   __
GAM299  LOC256113 5'  GCCACAAACACATCCA     96771     GGCC  ATC
                                TGGA   TG   TTTGTGGC
                                ||||   ||   ||||||||
                                ACCT   AC   AAACACCG
                                  AC__  ____
GAM299  LOC257371 5'  ACTGAGGATCAGGCCCACA   97509    GA        _
                                TG  GGCCTGATCTTT GT
                                ||  ||||||||||||  ||
                                AC  CCGGACTAGGAG CA
                                 AC          T
GAM299  LOC89958  3'  CCACGACAGGCCTC       60919        ATCT
                                GAGGCCTG    TTGTGG
                                ||||||||    ||||||
                                CTCCGGAC    AGCACC
                                      _____
GAM299  LOC90019  5'  CCGCAGAGATGAGACCCCCA   56759     A  C  G
                                TGG GG CT ATCTTTGTGG
                                ||| || || ||||||||||
                                ACC CC GA TAGAGACGCC
                                  C  A  G
GAM299  LOC90979  3'  GGCCACAAAGCAAGACTCCA   64530      GC  GAT
                                TGGAG  CT   CTTTGTGGCC
                                |||||  ||   ||||||||||
                                ACCTC  GA   GAAACACCGG
                                   A_  AC_
GAM299  LOC93496  3'  GCCACATTTGGCCAGGCCTCC  72434         AT TT_
                                GGAGGCCTG  C   TGTGGC
                                |||||||||  |   ||||||
                                CCTCCGGAC  G   ACACCG
                                     CG TTT
GAM299  LOC93613  5'  GCAAGACCAGGCCTCC      72699         A    TGTG
                                GGAGGCCTG TCTT    GC
                                |||||||||  ||||    ||
                                CCTCCGGAC AGAA    CG
                                     C    _____
GAM300  EGFL5     3'  TAGCCATGGACACAAGAA     86628         G    A
                                TTCTTGTG CCAT GCTG
                                ||||||||  ||||  ||||
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                                AAGAACAC GGTA CGAT
                                    A   C
GAM300  NDRG3    3' ACATCCACATATCCACAAGAA 49287       CC  GC  TC
                                TTCTTGTGG ATA TG ATGT
                                ||||||||| ||| || ||||
                                AAGAACACC TAT AC TACA
                                    __  AC C_
GAM300  NR3C1    3' ACATATTTACTAAGCCACAAGA 3919       CA  CTGTC
          A                      TTCTTGTGGC TAG   ATGT
                                ||||||||||  |||   ||||
                                AAGAACACCG ATC   TACA
                                    A_  ATTTA
GAM300  DKFZP434D193 3' ACACCTGTATGACACAAGAA  88875      GCC_  C
                                TTCTTGTG   ATAG TGT
                                ||||||||   |||| |||
                                AAGAACAC   TGTC ACA
                                    AGTA   C
GAM300  FLJ11016  3' ACAGACAACAGCCATAAGAA  36983       CATAG_
                                TTCTTGTGGC    CTGT
                                ||||||||||    ||||
                                AAGAATACCG    GACA
                                    ACAACA
GAM300  FLJ20151  3' ACACTATAACTACAAGAA   34650       CC  C
                                TTCTTGTGG ATAG TGT
                                ||||||||| |||| |||
                                AAGAACATC TATC ACA
                                    AA  _
GAM300  FLJ20671  3' GCAGCTATAACCACAAGGA  35526       CC
                                TTCTTGTGG ATAGCTGT
                                ||||||||| ||||||||
                                AGGAACACC TATCGACG
                                    AA
GAM300  FLJ21080  3' ACATGGTTTGCAAACCACAAGA 42726       CCATA TG_
          A                      TTCTTGTGG   GC  TCATGT
                                |||||||||   ||  ||||||
                                AAGAACACC   CG  GGTACA
                                    AAA__ TTT
GAM300  KIAA0261  3' ATAGCTATAGGCACAAGAA   68178       G _
                                TTCTTGTG CC ATAGCTGT
                                |||||||| || ||||||||
                                AAGAACAC GG TATCGATA
                                    _ A
GAM300  KIAA0788  3' ACATCAGCACTACCACAAGAA 71335       CCATA   TC
                                TTCTTGTGG   GCTG ATGT
                                |||||||||   |||| ||||
                                AAGAACACC   CGAC TACA
                                    ATCA_  __
GAM300  WWP1     3' ACATGACAGCCATTCATTCATA 22812      CC__ A
          A                      TTGTGG   AT GCTGTCATGT
                                ||||||   || ||||||||||
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                                AATACT    TA CGACAGTACA
                                   TACT  C
GAM300  LOC148738 3'  ACATGATCATTAGCCATAAGAA 59200         CA   CT
                                TTCTTGTGGC  TAG  GTCATGT
                                ||||||||||  |||  |||||||
                                AAGAATACCG  ATT  TAGTACA
                                      __  AC
GAM300  LOC254312 3'  ACATGACAAAATAAGCCAAAGA 96391      G   CATAGC
          A                      TTCTT TGGC     TGTCATGT
                                ||||| ||||     ||||||||
                                AAGAA ACCG     ACAGTACA
                                   _   AATAAA
GAM301  BAZ2A    3'  AAAATGTTCAGAGGTCCCTGTC 25587      AA   GAGTA_
                                GACAG  GGA     AACATTTT
                                |||||  |||     ||||||||
                                CTGTC  CCT     TTGTAAAA
                                   __  GGAGAC
GAM301  FGF5     3'  AAAATGTTTAAATTCTCTTTC  52473         __
                                GAAGGAGAGT  AAACATTTT
                                ||||||||||  |||||||||
                                CTTTCTCTTA  TTTGTAAAA
                                      AA
GAM301  FGF5     3'  AAAATGTTTAAATTCTCTTTC  15527         __
                                GAAGGAGAGT  AAACATTTT
                                ||||||||||  |||||||||
                                CTTTCTCTTA  TTTGTAAAA
                                      AA
GAM301  LGI1     3'  AAAATGTTTACATTTTCTTTC  17500        __
                                GAAGGAGA  GTAAACATTTT
                                ||||||||  ||||||||||
                                CTTTCTTT  CATTTGTAAAA
                                     TA
GAM301  PRCC     3'  AAAATGTTGAACCCTCC     19929      A  A_
                                GGAG GT  AACATTTT
                                ||||  ||  ||||||||
                                CCTC CA  TTGTAAAA
                                  C  AG
GAM301  SHMT2    3'  GTCTGCTCTCCCTCTGTCA    18270        A       A
                                TGACAGA GGAGAGTA AC
                                |||||||  |||||||  ||
                                ACTGTCT CCTCTCGT TG
                                     C       C
GAM301  C6orf5   3'  AAAATGTTTACTCTTTT     31335
                                AGGAGAGTAAACATTTT
                                |||||||||||||||||
                                TTTTCTCATTTGTAAAA

GAM301  CECR6    3'  AAAATGTTTACACTCC      49080      A
                                GGAG GTAAACATTTT
                                |||| ||||||||||
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                                CCTC CATTTGTAAAA
                                  A
GAM301  DKFZP564O0463 3'  AAAATACTTACTCTCT     26275        AC
                                GGAGAGTAA  ATTTT
                                |||||||||  |||||
                                TCTCTCATT  TAAAA
                                     CA
GAM301  FLJ12443  3'  AAAATGTTTACTAACTTCCTCA 45724    CA   GAG
                                TGA  GAAG   AGTAAACATTTT
                                |||  ||||   ||||||||||||
                                ACT  CTTC   TCATTTGTAAAA
                                  C_   AA_
GAM301  HEYL    3'  AAAATGCAGAAACCCTTCTGT  27387       AGAGTAAA
                                ACAGAAGG       CATTTT
                                ||||||||       ||||||
                                TGTCTTCC       GTAAAA
                                     CAAAGAC_
GAM301  HOOK3    3'  AATGTCCTCTTCTTC       50545         TAA
                                GAAGGAGAG   ACATT
                                |||||||||   |||||
                                CTTCTTCTC   TGTAA
                                     C__
GAM301  KIAA0318 3'  AAAATGTTTACTCAATCATTC  68942     G  __
                                GAA GA  GAGTAAACATTTT
                                ||| ||  ||||||||||||||
                                CTT CT  CTCATTTGTAAAA
                                  A  AA
GAM301  KIAA0599 3'  GTTTATTCCCCTCCTGTCA   77187       A   A
                                TGACAG AGG GAGTAAAC
                                |||||| ||| ||||||||
                                ACTGTC TCC CTTATTTG
                                   C   C
GAM301  KIAA1396 3'  AAATGTTCCACTTCTTTC    62982       G   A_
                                GAAGGA AGT  AACATTT
                                |||||| |||  |||||||
                                CTTTCT TCA  TTGTAAA
                                   _  CC
GAM301  KIAA1918 3'  AAAATGTTTATTGCACTCATGT 73157      GA  GAG
           CA                     TGACA  AG   AGTAAACATTTT
                                |||||  ||   ||||||||||||
                                ACTGT  TC   TTATTTGTAAAA
                                  AC  ACG
GAM301  MKP-7    5'  GTTTAACTCTCCTTTTGCCA   66421    A         _
                                TG CAGAAGGAGAGT AAAC
                                || ||||||||||| ||||
                                AC GTTTTCCTCTCA TTTG
                                 C          A
GAM301  ORCTL4   3'  AAAATGCCCCCTCCTTCTGCA  16648    A       AGTAAA
                                TG CAGAAGGAG     CATTTT
                                || |||||||||     ||||||
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                                AC GTCTTCCTC     GTAAAA
                                 _       CCCC__
GAM301  SV2B    3'  AAAATGTTTACTCTCCTTCTGT 29288
              CA                  TGACAGAAGGAGAGTAAACATTTT
                                  ||||||||||||||||||||||||
                                  ACTGTCTTCCTCTCATTTGTAAAA

GAM301  TNRC6   3'  AAAATGTTTACTCTTCCATC  70504   A  _
                                  GA GGA GAGTAAACATTTT
                                  || ||| ||||||||||||
                                  CT CCT CTCATTTGTAAAA
                                   A  T
GAM301  LOC135818 3'  AAAATGTTTACAGCTCC    75228     A_
                                  GGAG  GTAAACATTTT
                                  ||||  ||||||||||
                                  CCTC  CATTTGTAAAA
                                    GA
GAM301  LOC150960 3'  AAAATGTTTACCTTTACCT   80052    _  _
                                  AGG AGAG TAAACATTTT
                                  ||| |||| ||||||||||
                                  TCC TTTC ATTTGTAAAA
                                    A   C
GAM301  LOC157660 3'  AAAATGTTTTACTGTCTATC  86504   A  G    _
                                  GA GGA AGTAAA CATTTT
                                  || ||| |||||| ||||||
                                  CT TCT TCATTT GTAAAA
                                   A  G    T
GAM301  LOC221849 3'  AAAATGCCTATTACTTTTGTCA 92489        GAGA  AA
                                  TGACAGAAG   GTA  CATTTT
                                  |||||||||   |||  ||||||
                                  ACTGTTTTC   TAT  GTAAAA
                                        AT__  CC
GAM302  HAP1    3'  AATATGCACATGAAAGATGACC 14163         AT_______  GATA
              TTG                   AGGTCATCTT       GCA   T
                                  ||||||||||       |||   |
                                  TCCAGTAGAA       CGT   A
                                       AGTACAIII   ATAG
GAM302  PRKAR2B  3'  CATACTGATAAAATGACTTTG  10805        C   G   A
                                  CAAGGTCAT TTAT CAG TATG
                                  ||||||||| |||| ||| ||||
                                  GTTTCAGTA AATA GTC ATAC
                                        A   _  _
GAM302  TP53    3'  GCACATCTGCATTTTCACC   5040     CATCTT      A
                                  GGT     ATGCAGAT TGC
                                  |||     |||||||| |||
                                  CCA     TACGTCTA ACG
                                    CTTT__       C
GAM302  DKFZp434E169 3'  TGCATAAGATGACTTTG     50064
                                  CAAGGTCATCTTATGCA
                                  |||||||||||||||||
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                                GTTTCAGTAGAATACGT

GAM302  KIAA0329  3'  CAAATCTGCATAAAATACCTCA 29269   A   C  C       A
                                C AGGT AT TTATGCAGAT TG
                                | |||| || |||||||||| ||
                                A TCCA TA AATACGTCTA AC
                                 C   _ A       A
GAM302  PRO2012   3'  CATATCTGTAGGAATAAACCT  37779     CATCTTA
                                AGGT      TGCAGATATG
                                ||||      ||||||||||
                                TCCA      ATGTCTATAC
                                  AATAAGG
GAM302  RA-GEF-2  3'  CATACCCATTTGGATGACC   32953       T_  CAGA
                                GGTCATCT  ATG   TATG
                                ||||||||  |||   ||||
                                CCAGTAGG  TAC   ATAC
                                     TT  CC__
GAM302  RENT2     3'  GCACATCTGTATGCGACAACTT 54591     CA  T       A
                                AGGT  TC TATGCAGAT TGC
                                ||||  || |||||||||| |||
                                TTCA  AG GTATGTCTA ACG
                                  AC  C       C
GAM302  RENT2     3'  GCACATCTGTATGCGACAACTT 31420     CA  T       A
                                AGGT  TC TATGCAGAT TGC
                                ||||  || |||||||||| |||
                                TTCA  AG GTATGTCTA ACG
                                  AC  C       C
GAM302  SARCOSIN  3'  TGCCATAAGATGACTTCA    20235   A         _
                                C AGGTCATCTTATG CA
                                | |||||||||||| ||
                                A TTCAGTAGAATAC GT
                                 C          C
GAM302  TIGA1     5'  CACATCCGCAGAGGTGACTCG  53800   A       A  A  A
                                A GGTCATCTT TGC GAT TG
                                | ||||||||| ||| ||| ||
                                G TCAGTGGAG ACG CTA AC
                                 C       _  C  C
GAM302  VAV3      3'  CAGATATGCACACACAAAGATG 20363       AT_________  GATA
            ACCT                  GTCATCTT       GCA   TG
                                ||||||||        |||   ||
                                CAGTAGAA        CGT   AC
                                     ACACACAIII  ATAG
GAM302  LOC221755 3'  TATGTCTTCAAGATGACC    92397       TA  C
                                GGTCATCT  TG AGATATG
                                ||||||||  || |||||||
                                CCAGTAGA  AC TCTGTAT
                                     __ T
GAM302  LOC255330 3'  GCATATCTTTAAGACAACC   95813    CA    TGC
                                GGT  TCTTA   AGATATGC
                                |||  |||||   ||||||||
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                                CCA  AGAAT   TCTATACG
                                  AC    T__
GAM302  LOC51071  3'  CACATCTGAAATGATCTT    31977        CTTATG    A
                                AAGGTCAT     CAGAT TG
                                ||||||||     ||||| ||
                                TTCTAGTA     GTCTA AC
                                    AA____    C
GAM303  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM303  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM303  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM303  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
           TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM303  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||  ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM303  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM303  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM303  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM303  ZNF216   3'  ATCTGCACAGCAAAGTGAAA   20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
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                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM303  CG012    5' CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                     CT  __
GAM303  EIF2C2   3' ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM303  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC       GTCTGAGAT
                                ||||||       |||||||||
                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM303  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM303  KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM303  KLHL6    3' ATCTCAGAGCAGGAAA      55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM303  NIR3     3' GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM303  PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM303  PP35     3' ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM303  PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148         TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
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                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM303  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM303  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941        CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM303  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM303  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM303  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226     A      GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _      ATTT
GAM303  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                       _
GAM304  APM1     3'  ACTCCAGTGATGTTTTTCA   16583       A  GGGTTG
                                TGAAAGA CAT     TGGAGT
                                ||||||| |||     ||||||
                                ACTTTTT GTA     ACCTCA
                                    _  GTG___
GAM304  IL1RAP   3'  CAACCCACATTTTTTCA     9310         CA
                                TGAAAGAA  TGGGTTG
                                ||||||||  |||||||
                                ACTTTTTT  ACCCAAC
                                     AC
GAM304  MDFI     3'  CCCACCCATGTCCTCTCA     18769     A  A      T T
                                TGA AG ACATGGGT G GG
                                ||| || |||||||| | ||
                                ACT TC TGTACCCA C CC
                                  C  C       _ _
GAM304  PROK1    3'  ACCCAGCTCCCATGACTCTCCC 50553    AA  A_     TTG   A
            A                    TG  AGA  CATGGG   TGG GT
                                ||  |||  ||||||   ||| ||
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                                AC  TCT  GTACCC   ACC CA
                                 CC   CA     TCG  _
GAM304  SH3BP4   3' ACTCCACCCCATAATTTC    27231     GAAC    TT
                                GAAA   ATGGG  GTGGAGT
                                ||||   |||||  |||||||
                                CTTT   TACCC  CACCTCA
                                  AA__    __
GAM304  USP11    5' ACAATCCACACTCTTTCA    16200       ACA
                                TGAAAGA   TGGGTTGT
                                |||||||   ||||||||
                                ACTTTCT   ACCTAACA
                                    CAC
GAM304  XYLB     3' ACCCCACAGTCTCTTCTCTC   17555    A   CAT  GT    A
                                GA AGAA   GG  TGTGG GT
                                || ||||   ||  ||||| ||
                                CT TCTT   TC  ACACC CA
                                 C   C__  TG    C
GAM304  CXorf9   3' ACCCTGCCCATGTCCCTCA   38622     AA  A     TGT  A
                                TGA  GA CATGGGT   GG GT
                                |||  || |||||||   || ||
                                ACT  CT GTACCCG   CC CA
                                  CC  _      T__  _
GAM304  DKFZP761L0424 3' GACCTGGTAACCCACGCTCTTG 91337    A   ACA     TGGA
           CA                    TG AAGA   TGGGTTG    GTC
                                || ||||   |||||||   |||
                                AC TTCT   ACCCAAT    CAG
                                 G   CGC      GGTC
GAM304  FLJ10803 3' ACTCCACAGTGGCCTCTCA   36659    A  AA   GGGT
                                TGA AG  CAT    TGTGGAGT
                                ||| ||  |||    ||||||||
                                ACT TC  GTG    ACACCTCA
                                  C  CG  ____
GAM304  KIAA0100 5' ACTCCTTAGCCATGATCTTCCA 27970    A   A    G   T
                                TG AAGA CATGG TTG GGAGT
                                || |||| ||||| ||| |||||
                                AC TTCT GTACC GAT CCTCA
                                 C   A    _  T
GAM304  KIAA0121 3' ACTCCACAGCGCTTTCTCA   72653   A   CAT  _
                                A AGAA   GG GTTGTGGAGT
                                | ||||   || ||||||||||
                                A TCTT   TC CGACACCTCA
                                 C   ___  G
GAM304  KIAA0453 3' ACTCATGACCCAAATCCTTC   69042    A  ACA    TG  G
                                GAA GA   TGGGT  TG AGT
                                ||| ||   |||||  || |||
                                CTT CT   ACCCA  AC TCA
                                  C  AA_    GT  _
GAM304  KIAA1598 3' GACTGTTTCCATGTTCTCCCA  37078    AA       TTGTGG
                                TG  AGAACATGGG     AGTC
                                ||  ||||||||||     ||||
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                                AC  TCTTGTACCT     TCAG
                                 CC         TTG___
GAM304  KIAA1975  5'  GACCCCATGAGTCATGCTCTTT 73972    _    A    G TG   A
            ACA                    TG AAAGA CATGG T  TGG GTC
                                || ||||| ||||| |  ||| |||
                                AC TTTCT GTACT A  ACC CAG
                                 A    C    G GT   C
GAM304  PF1      3'  GACTCCATCCCATACCTTCCA  95121    A   AAC    TT
                                TG AAG   ATGGG  GTGGAGTC
                                || |||   |||||  ||||||||
                                AC TTC   TACCC  TACCTCAG
                                 C   CA_    __
GAM304  PRO0899   5'  GACCCCAGTCCATGCTCCTTC  37695     A  A    GT  T  A
                                GAA GA CATGG  TG GG GTC
                                ||| || |||||  || || |||
                                CTT CT GTACC  AC CC CAG
                                  C  C    TG  _  _
GAM304  PRO1331   3'  ATAACCCACCTCTCTCA     47833     A   ACA
                                TGA AGA   TGGGTTGT
                                ||| |||   ||||||||
                                ACT TCT   ACCCAATA
                                  C   CC_
GAM304  SDOS     3'  CCCAGCCCATCCTCTCA     50367    A   AC       T
                                A AGA  ATGGGTTG GG
                                | |||  |||||||| ||
                                A TCT  TACCCGAC CC
                                 C   CC       _
GAM304  STX6     3'  GACCCCACAATTGACATGGCTC 19488    A_   __      A
                                GA  CATG  GGTTGTGG GTC
                                ||  ||||  |||||||| |||
                                CT  GTAC  TTAACACC CAG
                                 CG    AG       C
GAM304  LOC145815 3'  ACTCCACAATATCTCTATCA   83515     A   ACATGG
                                TGA AGA     GTTGTGGAGT
                                ||| |||     ||||||||||
                                ACT TCT     TAACACCTCA
                                  A   CTA___
GAM304  LOC158819 5'  GACTCCACAATGCCCCTTTC   86906      AACAT   __
                                GAAAG    GGGT  TGTGGAGTC
                                |||||    ||||  |||||||||
                                CTTTC    CCCG  ACACCTCAG
                                   _____    TA
GAM304  LOC200169 3'  ACTCCATCCAGTACATTCTTTC 89937       CA___   GTT
                                GAAAGAA    TGG   GTGGAGT
                                |||||||    |||   |||||||
                                CTTTCTT    ACC   TACCTCA
                                    ACATG   ___
GAM304  LOC205327 3'  ACTCCTTGACTCATTCTTTCA  89499       AC       T
                                TGAAAGA  ATGGGTTG GGAGT
                                |||||||  |||||||| |||||
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                                ACTTTCT  TACTCAGT CCTCA
                                   __       T
GAM304  LOC253584 5'  ACTCTGTGCCACATCCTCTTCA 96972     A  AC  _  TGT
                                TGAA GA  ATG GGT   GGAGT
                                |||| ||  ||| |||   |||||
                                ACTT CT  TAC CCG   TCTCA
                                  _ CC   A   TG_
GAM304  LOC90494  5'  ACTCCATCCATGTCCCT    63050    A_    GTT
                                AG  ACATGG   GTGGAGT
                                ||  ||||||   |||||||
                                TC  TGTACC   TACCTCA
                                 CC     ___
GAM305  ANGPT2   5'  TGTTCTTCCCACTGCAATCTG  6707     CTGC    T_
                                CAGG   GCAGT  GAAGAACA
                                ||||   |||||  ||||||||
                                GTCT   CGTCA  CTTCTTGT
                                  AA__    CC
GAM305  BCAT1    3'  CTTCACCCTGCAGTCTG     66202        CA  T
                                CAGGCTGCG  GT GAAG
                                |||||||||  || ||||
                                GTCTGACGT  CA CTTC
                                     CC  _
GAM305  DVL1     3'  TCTGCCCTGGCAGCCTG     59339        G   TTGA
                                CAGGCTGC CAG   AGA
                                |||||||| |||   |||
                                GTCCGACG GTC   TCT
                                    _  CCG_
GAM305  EGFL4    3'  TGTCCTCTTTGGCGTGCAGCC  61822        A  TG   __
                                GGCTGCGC GT  AAGA  ACA
                                |||||||| ||  ||||  |||
                                CCGACGTG CG  TTCT  TGT
                                    _ GT   CC
GAM305  GRM4     3'  TCACTGCTGGCAGCCTG     5922         __    T
                                CAGGCTGC  GCAGT GA
                                ||||||||  ||||| ||
                                GTCCGACG  CGTCA CT
                                     GT    _
GAM305  HOXB13   3'  TGTTCCTCAGGAGCGGCCTG  21015        GCAG   A
                                CAGGCTGC   TTGA GAACA
                                ||||||||   |||| |||||
                                GTCCGGCG   GACT CTTGT
                                    AG__   C
GAM305  MYO10    3'  TCTTCAACAGCTGGCTCC    24701   A    C  A
                                C GGCTG GC GTTGAAGA
                                | ||||| || ||||||||
                                C TCGGT CG CAACTTCT
                                 C    _ A
GAM305  PABPN1   3'  TCTCAACTGCGCAAGCT     16184     _       A
                                GGCT GCGCAGTTGA GA
                                |||| ||||||||| ||
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                                TCGA CGCGTCAACT CT
                                  A       _
GAM305  SLC6A8   5'  CTTCTGACTGCGCCGCC    18849    T      _
                                GGC GCGCAGTT GAAG
                                ||| |||||||| ||||
                                CCG CGCGTCAG CTTC
                                  C       T
GAM305  BTBD1    5'  TGGGCAACCGCGCAGCT    47477        A   AAGAA
                                GGCTGCGC GTTG    CA
                                |||||||| ||||    ||
                                TCGACGCG CAAC    GT
                                    C   GG___
GAM305  C20orf80 5'  CTTCCTGGCGCCTG       65286      T  G   TT
                                CAGGC GC CAG  GAAG
                                ||||| || |||  ||||
                                GTCCG CG GTC  CTTC

                                  _ _  __
GAM305  DKFZp434O0320 3'  ATTGCTCTTGGCTGAAGCAGCC 83693        G_   TG A  A
           TG                     CAGGCTGC  CAGT  A GA CAAT
                                ||||||||  ||||  | || ||||
                                GTCCGACG  GTCG  T CT GTTA
                                    AA   GT _  C
GAM305  DKFZP434P0721 3'  CTTCAGCTGTACCACCTG    63716     C  C_
                                CAGG TG  GCAGTTGAAG
                                |||| ||  ||||||||||
                                GTCC AC  TGTCGACTTC
                                  _  CA
GAM305  EPI64    3'  TCACTCCCTGCGCAGCCT    95633          T___
                                AGGCTGCGCAG   TGA
                                ||||||||||   |||
                                TCCGACGCGTC   ACT
                                      CCTC
GAM305  FBXO27   3'  CTTCTTGCAAGACAGCCTG   74509       C___   TT
                                CAGGCTG   GCAG  GAAG
                                |||||||   ||||  ||||
                                GTCCGAC   CGTT  CTTC
                                    AGAA   __
GAM305  FLJ20489 3'  TGCCCTTCAACTAGAGCTT   35255      GCGC      AA
                                AGGCT   AGTTGAAG  CA
                                |||||   ||||||||  ||
                                TTCGA   TCAACTTC  GT
                                  GA__      CC
GAM305  IMP-2    3'  TCAACTGCCAGCCTG      21573       C
                                CAGGCTG GCAGTTGA
                                ||||||| ||||||||
                                GTCCGAC CGTCAACT
                                  _
GAM305  NXPH3    3'  TGCCCTTCAAGGCAGTCTG   65771        GCAG     AA
                                CAGGCTGC   TTGAAG  CA
                                ||||||||   ||||||  ||
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                                GTCTGACG   AACTTC  GT
                                    G___     CC
GAM305  PI4KII   3'  TGTCCCAGGTCCTGCGCAGCTC 37350   A       TTGAAGA_
           A                     C GGCTGCGCAG       ACA
                                 | ||||||||||       |||
                                 A TCGACGCGTC       TGT
                                  C         CTGGACCC
GAM305  POLD4    3'  ATTGCTCCTGCTCAGCTCAGCC 40984      CGC     A___  A
                                 GGCTG   AGTTGA   GA CAAT
                                 |||||   ||||||   || ||||
                                 CCGAC   TCGACT   CT GTTA
                                    ___     CGTC  C
GAM305  SDF1     3'  TGTTCCCCCTGTGCAGCC    90864          TTGAA
                                 GGCTGCGCAG    GAACA
                                 ||||||||||    |||||
                                 CCGACGTGTC    CTTGT
                                       CCC__
GAM305  SIRPB1   3'  ATTGCAAAAAGACTGTGCAACC 20241      C       GAAGAA
           TG                      CAGG TGCGCAGTT     CAAT
                                 |||| |||||||||     ||||
                                 GTCC ACGTGTCAG     GTTA
                                   A        AAAAAC
GAM306  AGRN     3'  TCACCCTCGCTCCGTCA     78839       A       CACT
                                 TGGCG AGCGAGGG    TGA
                                 ||||| ||||||||    |||
                                 ACTGC TCGCTCCC    ACT
                                   C       _____
GAM306  PER2     5'  TCGAACCCCCCGCTTCGC     13988         A   CAC
                                 GCGAAGCG GGG   TTGA
                                 |||||||| |||   ||||
                                 CGCTTCGC CCC   AGCT
                                       _   CA_
GAM306  PER2     5'  TCGAACCCCCCGCTTCGC     43046         A   CAC
                                 GCGAAGCG GGG   TTGA
                                 |||||||| |||   ||||
                                 CGCTTCGC CCC   AGCT
                                       _   CA_
GAM306  RASGRP2  5'  TTTCATTCCTCGCTCCCCA    19512     C  A      CACT
                                 TGG GA GCGAGGG    TGAAA
                                 ||| || |||||||    |||||
                                 ACC CT CGCTCCT    ACTTT
                                   C  _       T___
GAM306  CNNM4    3'  CAAGTGCCCTGCTCTCCA    39476     C  A  G
                                 TGG GA GC AGGGCACTTG
                                 ||| || || ||||||||||
                                 ACC CT CG TCCCGTGAAC
                                   T  _  _
GAM306  DKFZP434C131 3'  TGCCCTCGCCCTGCCA      69079       AA
                                 TGGCG  GCGAGGGCA
                                 |||||  |||||||||
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                                ACCGT  CGCTCCCGT
                                   CC
GAM306  FLJ23469  5'  GGGTGCCCCCGCCTCACC    45247    C  A   A
                                GG GA GCG GGGCACTT
                                || || ||| |||||||||
                                CC CT CGC CCCGTGGG
                                 A  C   C
GAM306  GBTS1     3'  TGGGTGCCCCCACTCCCCCA   59061     CGA  CGA
                                TGG   AG   GGGCACTTG
                                |||   ||   |||||||||
                                ACC   TC   CCCGTGGGT
                                  CCC  ACC
GAM306  KIAA0821  5'  AGGCCGCCCTCGTCCCGCCA   29939      AA      A_
                                TGGCG  GCGAGGGC  CTT
                                |||||  ||||||||  |||
                                ACCGC  TGCTCCCG  GGA
                                   CC       CC
GAM306  KIAA1344  3'  TTTCAAGTGTTCCTTGC     72454        _
                                GCGAGGG CACTTGAAA
                                ||||||| |||||||||
                                CGTTCCT GTGAACTTT
                                     T
GAM306  NSE1      5'  TCCTGGCCCTCGCCTCGCCA   59076       A       ACTT
                                TGGCGA GCGAGGGC   GA
                                |||||| ||||||||   ||
                                ACCGCT CGCTCCCG   CT
                                    C       GTC_
GAM306  PDE3A     3'  CAAATGCCCTCGTCG       6226     AA       C
                                CG  GCGAGGGCA TTG
                                ||  ||||||||| |||
                                GC  TGCTCCCGT AAC
                                  __       A
GAM306  TRIM26    3'  CAAGTGCTCTGCCA        12887      GAAGCG
                                TGGC     AGGGCACTTG
                                ||||     ||||||||||
                                ACCG     TCTCGTGAAC
                                  _______
GAM306  LOC146310 5'  TCAACCTCTTCGCCA       77819        GC    GCAC
                                TGGCGAA  GAGG   TTGA
                                |||||||  ||||   ||||
                                ACCGCTT  CTCC   AACT
                                     __   ____
GAM306  LOC196707 3'  ATTTCAAATGCCCCCCTTTC  87525      CGA    C
                                GAAG   GGGCA TTGAAAT
                                ||||   ||||| |||||||
                                CTTT   CCCGT AACTTTA
                                   CCC    A
GAM306  LOC257494 3'  CAAGTGCTCTGCCA        97791      GAAGCG
                                TGGC     AGGGCACTTG
                                ||||     ||||||||||
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                                ACCG     TCTCGTGAAC
                                  ______
GAM307  GAK      3'  CACTTTGTAATCAGTCC     17910      AC       T
                                GGAC  GATTACGG GTG
                                ||||  |||||||| |||
                                CCTG  CTAATGTT CAC
                                  A_       T
GAM307  GAS7     3'  GCGCTGAATCGTGTCC      13322          A
                                GGACACGATT CGGTGT
                                |||||||||| ||||||
                                CCTGTGCTAA GTCGCG
                                     _
GAM307  LOH11CR2A 3'  CTCCCCGTAATCGTTCCTG   27539       C        TGT  C
                                CAGGA ACGATTACGG   GA G
                                ||||| ||||||||||   || |
                                GTCCT TGCTAATGCC   CT C
                                  _        C__  _
GAM307  RAD51L3   3'  CATCACCATTGTGTCCTG    56067          TAC   _
                                CAGGACACGAT   GGTG TG
                                ||||||||||   |||| ||
                                GTCCTGTGTTA   CCAC AC
                                     ___    T
GAM307  RAD51L3   3'  CATCACCATTGTGTCCTG    56074          TAC   _
                                CAGGACACGAT   GGTG TG
                                ||||||||||   |||| ||
                                GTCCTGTGTTA   CCAC AC
                                     ___    T
GAM307  RAD51L3   3'  CATCACCATTGTGTCCTG    56080          TAC   _
                                CAGGACACGAT   GGTG TG
                                ||||||||||   |||| ||
                                GTCCTGTGTTA   CCAC AC
                                     ___    T
GAM307  RAD51L3   3'  CATCACCATTGTGTCCTG    11234          TAC   _
                                CAGGACACGAT   GGTG TG
                                ||||||||||   |||| ||
                                GTCCTGTGTTA   CCAC AC
                                     ___    T
GAM307  TRPC1     5'  CGCCACACTGTCGTCCCC    12386    AC   TTA      A
                                GG  ACGA   CGGTGTG CG
                                ||  ||||   ||||||| ||
                                CC  TGCT   GTCACAC GC
                                 CC    ___      C
GAM307  CAMKK1    3'  GCACCACATCGTCCCTG     50171     AC    TAC
                                CAGG  ACGAT   GGTGT
                                ||||  |||||   |||||
                                GTCC  TGCTA   CCACG
                                  C_    CA_
GAM307  DKFZp434J0226 5'  ACGTCCTAATCTGTGTCCTG   72329         _    C  _
                                CAGGACAC GATTA GG TGT
                                |||||||| ||||| || |||
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                                GTCCTGTG CTAAT CC GCA
                                     T    _ T
GAM307  FLJ13815  5'  TGTGACGCGCGTGAAAACCGTG 78843      A___    ____  TGA
          TCCTG                  GACACG   TTACG   GTG  CG
                                 ||||||   |||||   |||  ||
                                 CTGTGC   AGTGC   CGC  GT
                                    CAAA    GIII  AGT
GAM307  FLJ20378  3'  ACACTCAATCATATCGTGCCCT 35088    A    TAC____
                                 AGG CACGAT     GGTGT
                                 ||| ||||||     |||||
                                 TCC GTGCTA     TCACA
                                   C    TACTAAC
GAM307  FLJ22174  3'  CGTCACACCGCCCGGCCC   41675   ACA  ATTA
                                 GG  CG   CGGTGTGACG
                                 ||  ||   ||||||||||
                                 CC  GC   GCCACACTGC
                                  CG_  CC__
GAM307  KATII     3'  CGTCACACCTATAATCCC   32645   ACAC   C_
                                 GG   GATTA  GGTGTGACG
                                 ||   |||||  |||||||||
                                 CC   CTAAT  CCACACTGC
                                  ____    AT
GAM307  KIAA0193  3'  GCACCACAATTGTGATGTCCT  28654     ___    AC
                                 AGGAC   ACGATT  GGTGT
                                 |||||   ||||||  |||||
                                 TCCTG   TGTTAA  CCACG
                                    TAG     CA
GAM307  KIAA0430  3'  GCATCTTTTAATCGTGTCT   38841        C__
                                 GGACACGATTA   GGTGT
                                 ||||||||||   |||||
                                 TCTGTGCTAAT   CTACG
                                       TTT
GAM307  LOC151877 3'  CGTCACTGGATGTGTCCTG   85505       G   ACGGT
                                 CAGGACAC ATT    GTGACG
                                 |||||||| |||    ||||||
                                 GTCCTGTG TAG    CACTGC
                                     _   GT___
GAM307  LOC151996 5'  GCGTCACAAATATCCCCCATCC 85535     CAC__   TACGG
          TG                     CAGGA    GAT    TGTGACGC
                                 |||||    |||    ||||||||
                                 GTCCT    CTA    ACACTGCG
                                    ACCCC   TAA__
GAM307  LOC202134 3'  ACATAGAAAATAATGTGTCCTG 90318       G   CG____
                                 CAGGACAC ATTA     GTGT
                                 |||||||| ||||     ||||
                                 GTCCTGTG TAAT     TACA
                                     _   AAAAGA
GAM308  BMP4      3'  ACATACACCACACACACACGT  6828    _      TAAG_
                                 AC TGTGTGTGT    ATGT
                                 || |||||||||    ||||
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                                TG ACACACACA    TACA
                                 C       CCACA
GAM308  BMP4    3'  ACATACACCACACACACACGT  55632   _      TAAG_
                                AC TGTGTGTGT    ATGT
                                || |||||||||    ||||
                                TG ACACACACA    TACA
                                 C       CCACA
GAM308  BMP4    3'  ACATACACCACACACACACGT  55636   _      TAAG_
                                AC TGTGTGTGT    ATGT
                                || |||||||||    ||||
                                TG ACACACACA    TACA
                                 C       CCACA
GAM308  CACNG6  5'  ACATCTCCTCCAAACACACACA 49099         A_____
            G                    CTGTGTGTGTT    AGATGT
                                ||||||||||     ||||||
                                GACACACACAA    TCTACA
                                       ACCTCC
GAM308  DYRK1A  3'  ACATCTTAGCAAGCAC     55196     G
                                GTGT TGTTAAGATGT
                                |||| ||||||||||
                                CACG ACGATTCTACA
                                  A
GAM308  DYRK1A  3'  ACATCTTAGCAAGCAC     55238     G
                                GTGT TGTTAAGATGT
                                |||| ||||||||||
                                CACG ACGATTCTACA
                                  A
GAM308  DYRK1A  3'  ACATCTTAGCAAGCAC     7347      G
                                GTGT TGTTAAGATGT
                                |||| ||||||||||
                                CACG ACGATTCTACA
                                  A
GAM308  GALNT1  3'  TTACATGTGCACACACA    40022        TAAG
                                TGTGTGTGT   ATGTAA
                                |||||||||   ||||||
                                ACACACACG   TACATT
                                      TG__
GAM308  LAMC1   3'  TACATCCTAACATATGCATTG  9679    C        A
                                CA TGTGTGTGTTA GATGTA
                                || ||||||||||| ||||||
                                GT ACGTATACAAT CTACAT
                                 T         C
GAM308  MNT     3'  CACCTGGACACACACA     39704         A  A
                                TGTGTGTGTT AG TG
                                |||||||||| || ||
                                ACACACACAG TC AC
                                       G  C
GAM308  MYH11   3'  ACACCTCAGACACGCACAGTTC 10172   C        A_  A
                                A ACTGTGTGTGTT  AG TGT
                                | ||||||||||||  || |||
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                                C TGACACGCACAG  TC ACA
                                 T          AC  C
GAM308  MYH11    3'  ACACCTCAGACACGCACAGTTC 43133    C          A_  A
                                A ACTGTGTGTGTT  AG TGT
                                | ||||||||||||  || |||
                                C TGACACGCACAG  TC ACA
                                 T          AC  C
GAM308  MYH11    3'  ACACCTCAGACACGCACAGTTC 43147    C          A_  A
                                A ACTGTGTGTGTT  AG TGT
                                | ||||||||||||  || |||
                                C TGACACGCACAG  TC ACA
                                 T          AC  C
GAM308  PBX2     3'  ACACCTCACACACACA      10440          TA  A
                                TGTGTGTGT  AG TGT
                                |||||||||  || |||
                                ACACACACA  TC ACA
                                      C_  C
GAM308  QDPR     3'  ACATCTTATATACAGCAGT    4354       _      T
                                ACTG TGTGTGT AAGATGT
                                |||| ||||||| |||||||
                                TGAC ACATATA TTCTACA
                                  G      _
GAM308  SCD      3'  TTACATCTTTTCTAATCACAGT 17352          TGTGTT_
            GTT                   AACACTGTG      AAGATGTAA
                                |||||||||      |||||||||
                                TTGTGACAC      TTCTACATT
                                     TAATCTT
GAM308  SHOC2    3'  TTACATATAAACACACACA    23767          AAG
                                TGTGTGTGTT   ATGTAA
                                ||||||||||   ||||||
                                ACACACACAA   TACATT
                                      ATA
GAM308  SIP1     3'  ACATCTTAACCTGTGCA     13231    TG  T
                                TG  TG GTTAAGATGT
                                ||  || ||||||||||
                                AC  GT CAATTCTACA
                                 GT  C
GAM308  SLC15A1  3'  ACGTACACACACTGT       17393    T      TAAG
                                AC GTGTGTGT    ATGT
                                || ||||||||    ||||
                                TG CACACACA    TGCA
                                 T      ____
GAM308  SMTN     3'  ACATACACACGCAGCGTT    22668     A        TAAG
                                AAC CTGTGTGTGT    ATGT
                                ||| ||||||||||    ||||
                                TTG GACGCACACA    TACA
                                  C        ____
GAM308  SMTN     3'  ACATACACACGCAGCGTT    56153     A        TAAG
                                AAC CTGTGTGTGT    ATGT
                                ||| ||||||||||    ||||
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                                TTG GACGCACACA    TACA
                                  C       ____
GAM308  SMTN     3'  ACATACACACGCAGCGTT    56157     A       TAAG
                                AAC CTGTGTGTGT    ATGT
                                ||| ||||||||||    ||||
                                TTG GACGCACACA    TACA
                                  C       ____
GAM308  TLX1     3'  TACACCACACACAACAG     18632     _     TAAGA
                                CTGT GTGTGT    TGTA
                                |||| ||||||    ||||
                                GACA CACACA    ACAT
                                  A     CC___
GAM308  TLX1     3'  ACACTGTGACACACTACA    18630     _      AGA
                                TGT GTGTGTTA   TGT
                                ||| ||||||||   |||
                                ACA CACACAGT   ACA
                                  T       GTC
GAM308  ZNF274   3'  TTACATCCACAGTACCACAGT  32884       T   TTAA_
                                ACTGTG GTG    GATGTAA
                                |||||| |||    |||||||
                                TGACAC CAT    CTACATT
                                   _  GACAC
GAM308  ZNF274   3'  TTACATCCACAGTACCACAGT  56058       T   TTAA_
                                ACTGTG GTG    GATGTAA
                                |||||| |||    |||||||
                                TGACAC CAT    CTACATT
                                   _  GACAC
GAM308  DKFZP434C212 5'  CAGGAGAACACACAAAGTGTT  68907       G       AAGA
                                AACACT TGTGTGTT    TG
                                |||||| ||||||||    ||
                                TTGTGA ACACACAA    AC
                                   A       GAGG
GAM308  DKFZP564O0463 3'  ACATGCTCACACACACA     26276         TA  _
                                TGTGTGTGT  AG ATGT
                                |||||||||  || ||||
                                ACACACACA  TC TACA
                                     C_  G
GAM308  FLJ11383  3'  ACATACACATACAG       46279          TAAG
                                CTGTGTGTGT    ATGT
                                ||||||||||    ||||
                                GACATACACA    TACA
                                              ____
GAM308  FLJ12704  3'  TTACGTGAACACACA      46538         AAG
                                TGTGTGTT   ATGTAA
                                ||||||||   ||||||
                                ACACACAA   TGCATT
                                     G__
GAM308  FLJ14871  3'  ACAAATACACACACACTG    51664     C       TAAGA
                                CA TGTGTGTGT    TGT
                                || |||||||||    |||
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```
                                GT ACACACACA     ACA
                                 C        TAA__
GAM308  FLJ20695  3'  ACATACACTACACACACTGTG  35554     T       TAAG_
                                CAC GTGTGTGT     ATGT
                                ||| ||||||||     ||||
                                GTG CACACACA     TACA
                                  T       TCACA
GAM308  FLJ21156  3'  GTCTCAACACACAAAGTG    44811      G       A
                                CACT TGTGTGTT AGAT
                                |||| |||||||| ||||
                                GTGA ACACACAA TCTG
                                  A       C
GAM308  GABARAPL1 3'  TACACCACACACACCGT     48603     T       TAAGA
                                AC GTGTGTGT     TGTA
                                || ||||||||     ||||
                                TG CACACACA     ACAT
                                 C       CC___
GAM308  GABARAPL3 3'  TACACCGCACACACCGT     50803     T       TAAGA
                                AC GTGTGTGT     TGTA
                                || ||||||||     ||||
                                TG CACACACG     ACAT
                                 C       CC___
GAM308  HLA-DOA   3'  CATTCAACACACACA       9209           AA
                                TGTGTGTGTT  GATG
                                ||||||||||  ||||
                                ACACACACAA  TTAC
                                      C_
GAM308  KIAA0367  3'  TTACACCTCTCCCAGAACACAG 67303          GTGTTA  __
           TGTT                    AACACTGTGT     AGA  TGTAA
                                ||||||||||     |||  |||||
                                TTGTGACACA     TCT  ACATT
                                     AGACCC   CC
GAM308  KIAA0748  3'  ACATCCTAATGCTGCCACA   28930      T__     A
                                TGTG   GTGTTA GATGT
                                ||||   |||||| |||||
                                ACAC   CGTAAT CTACA
                                  CGT     C
GAM308  KIAA0960  3'  TTACACCTGCTGTACACACAC  92657         TA___  A
                                GTGTGTGT     AG TGTAA
                                ||||||||     || |||||
                                CACACACA     TC ACATT
                                     TGTCG  C
GAM308  KIAA1061  3'  ACTCTCAACACACACAG     71172           A   T
                                CTGTGTGTGTT AGA GT
                                |||||||||||| ||| ||
                                GACACACACAA TCT CA
                                      C   _
GAM308  KIAA1130  3'  TTACATAGGAACACACAG    62431         GTTAAG
                                CTGTGTGT     ATGTAA
                                ||||||||     ||||||
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                                GACACACA     TACATT
                                     AGGA__
GAM308  KIAA1550 3'  ACATTCGTACACACACA     66539         TAA
                                TGTGTGTGT   GATGT
                                |||||||||   |||||
                                ACACACACA   TTACA
                                     TGC
GAM308  KIAA1676 3'  ATCAAGACACACAGTGTT    93121           G  AA
                                AACACTGTGTGT TT  GAT
                                |||||||||||| ||  |||
                                TTGTGACACACA AA  CTA
                                      G  __
GAM308  KIAA1950 3'  ACATGCACACACACACTGT   92587     C       TAAG
                                ACA TGTGTGTGT    ATGT
                                ||| |||||||||    ||||
                                TGT ACACACACA    TACA
                                  C       CG__
GAM308  RNF11    3'  TACATACAAAACACAGTGT   26874         G_  TAAG
                                ACACTGTGT  TGT    ATGTA
                                |||||||||  |||    |||||
                                TGTGACACA  ACA    TACAT
                                     AA  _____
GAM308  SEPT3    3'  CACTTCACACACACA       38885         T   A
                                TGTGTGTGT AAG TG
                                ||||||||| ||| ||
                                ACACACACA TTC AC
                                     C   _
GAM308  SSX5     3'  TTACACAAACACACACA     40673          AAGA
                                TGTGTGTGTT    TGTAA
                                ||||||||||    |||||
                                ACACACACAA    ACATT
                                     AC__
GAM308  STRN3    3'  ACATCTTAATGTCAAGC     27405    G  _
                                GT TG TGTTAAGATGT
                                || || ||||||||||
                                CG AC GTAATTCTACA
                                  A  T
GAM308  TGFB1I1  3'  TACATAAACACACGCA      31932          AAG
                                TGTGTGTGTT   ATGTA
                                ||||||||||   |||||
                                ACGCACACAA   TACAT
                                     A__
GAM308  TRIM2    3'  TACATACGTACCACAGT     30945       T   TTAAG
                                ACTGTG GTG    ATGTA
                                |||||| |||    |||||
                                TGACAC CAT    TACAT
                                   _  GCA__
GAM308  TRIP-Br2 3'  CATAAACACACACACAGTG   28579           TAAG
                                CACTGTGTGTGT   ATG
                                ||||||||||||   |||
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                                GTGACACACACA    TAC
                                      CAAA
GAM308   LOC120856 3'  TTACACTGTCACACACA     74033        TTA  A
                                TGTGTGTG   AG TGTAA
                                ||||||||   || |||||
                                ACACACAC   TC ACATT
                                     TG_  _
GAM308   LOC128989 3'  ACATGGCACACACA       74799         AAG
                                TGTGTGTGTT   ATGT
                                ||||||||||   ||||
                                ACACACACGG   TACA
                                      ___
GAM308   LOC150630 5'  TACACCGAGGGAACACACAGCA 85112     _      AAGA___
              G                  CTG TGTGTGTT      TGTA
                                ||| ||||||||      ||||
                                GAC ACACACAA      ACAT
                                  G       GGGAGCC
GAM308   LOC152274 3'  TGTCAACACACACAGT      80512          AA
                                ACTGTGTGTGTT  GATG
                                ||||||||||||  ||||
                                TGACACACACAA  CTGT
                                      __
GAM308   LOC154789 5'  ACATCTTCAGTGCACTGTG    81129     T   TG GTT
                                CAC GTG  T   AAGATGT
                                ||| |||  |   |||||||
                                GTG CAC  G   TTCTACA
                                  T   GT AC_
GAM308   LOC154930 3'  TACATCTTAGAAAACAC     81181      GTG
                                GTGT   TTAAGATGTA
                                ||||   ||||||||||
                                CACA   GATTCTACAT
                                   AAA
GAM308   LOC199775 3'  ACATCTTAACATCACAGAGTT  88354     A    T
                                AAC CTGTG GTGTTAAGATGT
                                ||| ||||| ||||||||||||
                                TTG GACAC TACAATTCTACA
                                  A    _
GAM308   LOC203536 3'  TTACACACACACACACACA    89382         TAAGA
                                TGTGTGTGT     TGTAA
                                |||||||||     |||||
                                ACACACACA     ACATT
                                      CACAC
GAM308   LOC221178 3'  ACATCTTGCCCACATGC     93523        T_
                                GTGTGTG  TAAGATGT
                                |||||||  ||||||||
                                CGTACAC  GTTCTACA
                                     CC
GAM308   LOC221751 5'  ACACCTTGAGCACACAC     92044        _    A
                                GTGTGTG TTAAG TGT
                                ||||||| ||||| |||
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                                CACACAC AGTTC ACA
                                    G    C
GAM308  LOC51246  3'  ACATGCACACACAG       33214         TAAG
                                CTGTGTGTGT   ATGT
                                ||||||||||   ||||
                                GACACACACG   TACA
                                     _____
GAM308  LOC51287  3'  ACATCTTAAGTCAGTGT     33348       TGTGTG
                                ACACTG     TTAAGATGT
                                ||||||     |||||||||
                                TGTGAC     AATTCTACA
                                   TG____
GAM308  LOC51701  5'  ACACCCTTCCACACACGC    32650        T_  A_
                                GTGTGTGT  AAG  TGT
                                ||||||||  |||  |||
                                CGCACACA  TTC  ACA
                                     CC   CC
GAM309  ALDOA     5'  GGAACTTGCTACTACCAGCA   3468      A       ATGAT
                                TGC GGTAGTAG    GGTTCC
                                ||| ||||||||    ||||||
                                ACG CCATCATC    TCAAGG
                                  A       GT___
GAM309  FBN2      3'  GGAACCATATGTGCTACCCACA 8847      CA      G   A
                                TG  GGTAGTA ATG TGGTTCC
                                ||  ||||||| ||| |||||||
                                AC  CCATCGT TAT ACCAAGG
                                 AC      G  _
GAM309  GOT2      3'  GAACCACCATCTGCTCT     92902     T       A
                                GG AGTAGATG TGGTTC
                                || |||||||| ||||||
                                TC TCGTCTAC ACCAAG
                                 _       C
GAM309  KCNJ5     3'  GAACCATCACCTTGTCCCCTCA 6090     C   TAGT_  A
                                TG AGG     AG TGATGGTTC
                                || |||     || |||||||||
                                AC TCC     TC ACTACCAAG
                                 _  CCTGT  C
GAM309  M6PR      3'  AACCATCACCTTTTGTA     9860        TAGT  A
                                TGCAGG    AG TGATGGTT
                                ||||||    || ||||||||
                                ATGTTT    TC ACTACCAA
                                    _____  C
GAM309  ODF2      5'  AACCATCAGCGACCAGCA    10323     A   A  AGA
                                TGC GGT GT   TGATGGTT
                                ||| ||| ||   ||||||||
                                ACG CCA CG   ACTACCAA
                                  A  G  ___
GAM309  TACR1     3'  GGAACCATCAGAAACACCCTCA 6472     C   TA  AGA
                                TG AGG  GT   TGATGGTTCC
                                || |||  ||   ||||||||||
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                                AC TCC  CA   ACTACCAAGG
                                 _   CA  AAG
GAM309  TGFB3    3'  GAACCACCACTGCCTG      12261         AGAT A
                                CAGGTAGT    G TGGTTC
                                ||||||||    | ||||||
                                GTCCGTCA    C ACCAAG
                                     _____ C
GAM309  ABCA9    3'  AACCATCATCCTCAGCA     54407     A  TAGTA
                                TGC GG     GATGATGGTT
                                ||| ||     ||||||||||
                                ACG CT     CTACTACCAA
                                  A  C_____
GAM309  ARL8     3'  AACCATCAGGTACTGCCTGCA  93194           GA
                                TGCAGGTAGTA  TGATGGTT
                                ||||||||||  ||||||||
                                ACGTCCGTCAT  ACTACCAA
                                       GG
GAM309  ASB16    5'  GGAACCATCATATGCACCAGCA 69941     A   A   G
                                TGC GGT GTA ATGATGGTTCC
                                ||| ||| ||| ||||||||||
                                ACG CCA CGT TACTACCAAGG
                                  A   _   A
GAM309  CAMTA2   3'  AACCCGCGCCCCACATACCTGC 61218         _  AGA_  AT
           A                     TGCAGGTA GT    TG  GGTT
                                ||||||||  ||    ||  ||||
                                ACGTCCAT CA    GC  CCAA
                                     A  CCCC  GC
GAM309  CBARA1   3'  GGAACCATCCACACACCTGC   20292       A  AGAT
                                GCAGGT GT    GATGGTTCC
                                ||||||  ||    |||||||||
                                CGTCCA CA    CTACCAAGG
                                   _  CAC_
GAM309  CTPS2    3'  AACCCATACTACTACCTCA    39082     C       _   AT
                                TG AGGTAGTAG ATG  GGTT
                                ||  |||||||||  |||  ||||
                                AC TCCATCATC TAC  CCAA
                                 _        A   __
GAM309  FLJ13220 3'  ATTATACTACTACCTACA     41633     C       _
                                TG AGGTAGTAG ATGAT
                                ||  |||||||||  |||||
                                AC TCCATCATC TATTA
                                 A        A
GAM309  FLJ20257 5'  ACCACCCACTGCCTGCA      38989          AGATGA
                                TGCAGGTAGT     TGGT
                                ||||||||||     ||||
                                ACGTCCGTCA     ACCA
                                      CCC____
GAM309  FLJ20847 3'  GAAATGTCCACTACCTG      94829         A   GATGG
                                CAGGTAGT GAT     TTC
                                ||||||||  |||    |||
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                                GTCCATCA CTG    AAG
                                    C  TA___
GAM309  GIT1    3'  ACCATCACTACCTGCA     25862        AGAT
                                TGCAGGTAGT   GATGGT
                                ||||||||||   ||||||
                                ACGTCCATCA   CTACCA
                                     _____
GAM309  HHLA2   3'  GACCCACTACCTGCA      22985        AGATGAT
                                TGCAGGTAGT     GGTT
                                ||||||||||     ||||
                                ACGTCCATCA     CCAG
                                    C_______
GAM309  HSPC157  5' AATTGTCCTACTACCTGC    26357         AT  TG
                                GCAGGTAGTAG  GA  GTT
                                ||||||||||  ||  |||
                                CGTCCATCATC  CT  TAA
                                     __  GT
GAM309  KIAA0596 3' GGCCTTCACCTCTACCTGCA  62834        T  A   T
                                TGCAGGTAG AG TGA GGTT
                                |||||||| || ||| ||||
                                ACGTCCATC TC ACT CCGG
                                     _ C   T
GAM309  KIAA1853 3' GAACCATCATCTTGTGGCA   69392    AGGTAGT
                                TGC      AGATGATGGTTC
                                |||      ||||||||||||
                                ACG      TCTACTACCAAG
                                  GTGT___
GAM309  KIAA1937 3' ATCATCCACTCCTGCA     73693       T   A
                                TGCAGG AGT GATGAT
                                |||||| ||| ||||||
                                ACGTCC TCA CTACTA
                                    _  C
GAM309  MGC19780 3' AATATGTATTACTACCTGCA  58706         A   ATG
                                TGCAGGTAGT GATG   GTT
                                |||||||||| ||||   |||
                                ACGTCCATCA TTAT   TAA
                                     _   GTA
GAM309  POF1B   3'  GGAACCATGCTGCTACC     46221        ATG
                                GGTAGTAG   ATGGTTCC
                                ||||||||   ||||||||
                                CCATCGTC   TACCAAGG
                                    G__
GAM309  POLM    3'  GAACCATGCATACCTGCA    91088        _  AGATG
                                TGCAGGTA GT    ATGGTTC
                                |||||||| ||    |||||||
                                ACGTCCAT CG    TACCAAG
                                    A _____
GAM309  PRO1635  3' GGAAGGCATCCATACCTGCA  37729        GTA   ATGG
                                TGCAGGTA   GATG   TTCC
                                ||||||||   ||||   ||||
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                                ACGTCCAT  CTAC   AAGG
                                   AC_   GG__
GAM309  PRPF8    3'  AACCTCAACTACCTGCA    61179        AGA  T
                                TGCAGGTAGT  TGA GGTT
                                ||||||||||  ||| ||||
                                ACGTCCATCA  ACT CCAA
                                    ____  _
GAM309  LOC128387 3'  GAACCACCACCTGAACTG    74748    GTAG  A  A
                                CAG   TAG TG TGGTTC
                                |||   ||| || ||||||
                                GTC   GTC AC ACCAAG
                                  AA__  C  C
GAM309  LOC154222 3'  AACCATCCATTCACTGC     86184      AG  _
                                GTAGT  ATG ATGGTT
                                |||||  ||| ||||||
                                CGTCA  TAC TACCAA
                                   CT  C
GAM309  LOC169611 3'  AACCATCATCATTAACTG    82751    G   A
                                CAG TAGT GATGATGGTT
                                ||| |||| ||||||||||
                                GTC ATTA CTACTACCAA
                                  A  _
GAM309  LOC221755 3'  AACCATACTACCTGTA      92391         GATGA
                                TGCAGGTAGTA    TGGTT
                                ||||||||||    |||||
                                ATGTCCATCAT    ACCAA
                                      _____
GAM309  LOC90288  3'  GAACCATTACAACCACC     62095    A  AGA
                                GGT GT  TGATGGTTC
                                ||| ||  |||||||||
                                CCA CA  ATTACCAAG
                                  C  AC_
GAM310  BTG2     3'  ACAGGCCACCACATACCTCA  22207        ATA__
                                TGAGGTATGT    TTTGT
                                ||||||||||    |||||
                                ACTCCATACA    GGACA
                                      CCACC
GAM310  DRG2     3'  TACAAATACACGTACCCCA   7323    A     A
                                TG GGTATGT TATTTGTG
                                || ||||||| ||||||||
                                AC CCATGCA ATAAACAT
                                 C      C
GAM310  KIAA0442  3'  GTGACTTCACACACACCTCA  31472      A  ATATTT  G
                                TGAGGT TGT     GT CAC
                                |||||| |||     || |||
                                ACTCCA ACA     CA GTG
                                   C  CACTT_ _
GAM310  STMN1    3'  GCACAAATGACCGCA      18718    A  ATGTA
                                TG GGT    TATTTGTGC
                                || |||    |||||||||
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                                AC CCA    GTAAACACG
                                 G  _____
GAM310  FLJ10244  3'  AATATACAAATACCTCA     35939       __
                                TGAGGTA  TGTATATT
                                |||||||  ||||||||
                                ACTCCAT  ACATATAA
                                    AA
GAM310  FLJ32499  3'  CGGTACACTTCACACACCTGCA 58156   _   A   ATATTT   C
                                TG AGGT TGT     GTG ACCG
                                || |||| |||     ||| ||||
                                AC TCCA ACA     CAC TGGC
                                 G   C   CTT___   A
GAM310  KIAA0057  3'  GCCAAGGACACCATACCTCA   24430        TATA_   T
                                TGAGGTATG    TTTG GC
                                |||||||||    |||| ||
                                ACTCCATAC    GAAC CG
                                     CACAG   _
GAM310  KIAA1169  5'  CGGTGTGTGTACACATACTCA  35447     G    A   TT TG
                                TGAG TATGT TAT  G  CACCG
                                |||| ||||| |||  |  |||||
                                ACTC ATACA ATG  T  GTGGC
                                  _    C   __ GT
GAM310  KIAA1364  3'  TGCAATACATGCCTCA      63599          ATTTG
                                TGAGGTATGTAT    TGCA
                                ||||||||||||    ||||
                                ACTCCGTACATA    ACGT
                                          _____
GAM310  KIAA1656  3'  GTGCAAGTGGATACATACCTC  65805         ATTTG
                                GAGGTATGTAT    TGCAC
                                ||||||||||    |||||
                                CTCCATACATA    ACGTG
                                      GGTGA
GAM310  KIAA1750  3'  GTGCATGAGACACACACCT   68251     A   ATA  TG
                                AGGT TGT   TT  TGCAC
                                |||| |||   ||  |||||
                                TCCA ACA   GA  ACGTG
                                  C   CA_  GT
GAM310  NESCA     3'  GTACAATACATGCCTCA     26744          ATT
                                TGAGGTATGTAT   TGTGC
                                ||||||||||||   |||||
                                ACTCCGTACATA   ACATG
                                          ___
GAM310  LOC147694 3'  ATCTATATACATCCTCA     78450      T      TT
                                TGAGG ATGTATAT  GT
                                ||||| ||||||||  ||
                                ACTCC TACATATA  TA
                                   _       TC
GAM311  TNFAIP1   3'  CATCAGCTGAGGACAGCAAACT 40917     AG     G
             CC                   GGA  TTGCTG CTTCAGCTGATG
                                  |||  |||||| ||||||||||||
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                                CCT  AACGAC GGAGTCGACTAC
                                  CA     A
GAM311  C1orf2   3'  CAGCTGGTTGGGACCAGCAGCC 21681    AA      _ ___
           CCC                    GG  GTTGCTGG CT   TCAGCTG
                                || ||||||| ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM311  C1orf2   3'  CAGCTGGTTGGGACCAGCAGCC 94622    AA      _ ___
           CCC                    GG  GTTGCTGG CT   TCAGCTG
                                || ||||||| ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM311  C20orf59  3'  CATCCCTAGCCAGCAGCTCC   41992     A       TC  CT
                                GGA GTTGCTGGCT  AG  GATG
                                ||| ||||||||||  ||  ||||
                                CCT CGACGACCGA  TC  CTAC
                                 _       __ C_
GAM311  FLJ20079  3'  CATTCTGGTAAACCAGCAGCCT 34490     A      CT__   CT
           CC                     GGA GTTGCTGG   TCAG  GATG
                                ||| ||||||||   ||||  ||||
                                CCT CGACGACC   GGTC  TTAC
                                  C       AAAT   __
GAM311  SSAT2    3'  CATCAGCTGAAGCACTCTTC   56041     TTGCTG
                                GAAG     GCTTCAGCTGATG
                                ||||     ||||||||||||
                                CTTC     CGAAGTCGACTAC
                                  TCA___
GAM311  SYNJ2    3'  ATCAGCTTAAGCAATTCC    61763     GTTGCTG   C
                                GGAA      GCTT AGCTGAT
                                ||||      |||| |||||||
                                CCTT      CGAA TCGACTA
                                  AA_____   T
GAM311  LOC162333 5'  CTGAAGCCAGCAATTCC     87131     G
                                GGAA TTGCTGGCTTCAG
                                |||| ||||||||||||
                                CCTT AACGACCGAAGTC
                                  _
GAM311  LOC222060 5'  CACCTCCCACCAGCAACCCCC  94104    AA      CTTC  C
                                GG  GTTGCTGG   AG TG
                                ||  ||||||||   || ||
                                CC  CAACGACC   TC AC
                                 CC       ACCC  C
GAM311  LOC255650 3'  CATCAGCCCCAGGCAACTTCC  96711        _  CTTCA
                                GGAAGTTGC TGG    GCTGATG
                                |||||||||  |||    |||||||
                                CCTTCAACG ACC    CGACTAC
                                     G  C____
GAM312  ADAM19   3'  CAGGAAGAAGACTGGCCATTAT 52703      C   CTGAG
           G                     CATGA GGCT    TTCTTCCTG
                                |||||  ||||    |||||||||
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                                GTATT CCGG    AAGAAGGAC
                                   A   TCAG_
GAM312  FACL5    5'  CAGGAAGAACTCAGAGCCG   64186
                                CGGCTCTGAGTTCTTCCTG
                                ||||||||||||||||||
                                GCCGAGACTCAAGAAGGAC

GAM312  GNAL     5'  CAGGAAAGAGAGGAGCCGTCG  9058          GAG TC
                                TGACGGCTCT   T  TTCCTG
                                ||||||||||   |  ||||||
                                GCTGCCGAGG   A  AAGGAC
                                      AG_ GA
GAM312  KAL1     3'  CAGGAAGAACTTCTGTCA    4013        CTCT
                                TGACGG   GAGTTCTTCCTG
                                ||||||   ||||||||||||
                                ACTGTC   TTCAAGAAGGAC
                                     ____
GAM312  MYO1E    3'  CAGGAGGACAAAACCACCATG  17187      AC  CTC  AGT
                                CATG  GG   TG   TCTTCCTG
                                ||||  ||   ||   ||||||||
                                GTAC  CC   AC   AGGAGGAC
                                  CA  AAA  ___
GAM312  PRKAR2B  3'  CAGAAAGAACTCAGATGT    10804   _         C
                                GC TCTGAGTTCTT CTG
                                || ||||||||||| |||
                                TG AGACTCAAGAA GAC
                                 T          A
GAM312  PUM2     3'  AGGATCAAAGCTGTCATG    31014          C   GTTCT
                                CATGACGGCT TGA    TCCT
                                |||||||||| |||    ||||
                                GTACTGTCGA ACT    AGGA
                                      A  _____
GAM312  SKI      3'  CAGGAAGTGCAGAGCCGCA   11701    A       AGTT
                                TG CGGCTCTG   CTTCCTG
                                || ||||||||   |||||||
                                AC GCCGAGAC   GAAGGAC
                                 _      GT__
GAM312  TEM8     3'  AGGAAGATGCAACCCCATG   36326     AC  CTC  AGT
                                CATG  GG   TG   TCTTCCT
                                ||||  ||   ||   |||||||
                                GTAC  CC   AC   AGAAGGA
                                  C_  A__  GT_
GAM312  ARHGEF4  5'  AGAAAAAACTCAGGGC      52207          C  C
                                GCTCTGAGTT TT CT
                                |||||||||| || ||
                                CGGGACTCAA AA GA
                                      A  A
GAM312  FLJ31978 3'  CAGGAAGGAACAAGCGCC    58348     T  GAG
                                GGC CT   TTCTTCCTG
                                ||| ||   |||||||||
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                                CCG GA   AGGAAGGAC
                                  C  ACA
GAM312  HSU24186  5'  AGAACTCAAAGCCGTC      25324        C
                                GACGGCT TGAGTTCT
                                ||||||| ||||||||
                                CTGCCGA ACTCAAGA
                                    A
GAM312  KCNT1     3'  AGCTCCCAGGGCCGCCA     61825     A      __
                                TG CGGCTCT  GAGTT
                                || |||||||  |||||
                                AC GCCGGGA  CTCGA
                                 C      CC
GAM312  KIAA1867  3'  CAGGAAGAACCCAAGAGCTCAT 94822      CG     GA_
                                ATGA  GCTCT   GTTCTTCCTG
                                ||||  |||||   ||||||||||
                                TACT  CGAGA   CAAGAAGGAC
                                  __    ACC
GAM312  KIAA1878  3'  AATTCAGAGAATCGTCATG    91707         __
                                CATGACGG  CTCTGAGTT
                                ||||||||  |||||||||
                                GTACTGCT  GAGACTTAA
                                    AA
GAM312  MFN1      3'  CAGGAAGAACTCATGA      35541     _
                                TC TGAGTTCTTCCTG
                                || ||||||||||||
                                AG ACTCAAGAAGGAC
                                 T
GAM312  MIDORI    3'  CAGGGCCCTTCCAGAGCCTGTC 73784        _      AGTTCT
            ATG                   CATGAC GGCTCTG     TCCTG
                                ||||||| |||||||      |||||
                                GTACTG CCGAGAC      GGGAC
                                   T      CTTCCC
GAM312  MYH7B     3'  CAGGAAGAACCTGGCTCGCATG 70530      A  _   CTGA
                                CATG CG GCT    GTTCTTCCTG
                                |||| || |||    ||||||||||
                                GTAC GC CGG    CAAGAAGGAC
                                  _  T   TC__
GAM312  RNAHP     3'  AGAAAGCAGCAGCCGTCAT    23761          _   AG
                                ATGACGGCT CTG  TTCT
                                ||||||||| |||  ||||
                                TACTGCCGA GAC  AAGA
                                    C   GA
GAM312  SLC37A1   3'  AGACGGAGCTCAGACCC      38561     C        TC
                                GG TCTGAGTTCT  CT
                                || ||||||||||  ||
                                CC AGACTCGAGG  GA
                                 C         CA
GAM312  LOC116236 3'  CAGGAAAAGCACAAACCTCAT  73809      C  CTC  A   C
                                ATGA GG   TG GTT TTCCTG
                                |||| ||   || ||| ||||||
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                                TACT CC   AC CGA AAGGAC
                                  _ AA_ A   A
GAM312  LOC124801 3'  CAGGAAGAACTCTCTTGCATG  74336     A   CTCT
                                CATG CGG    GAGTTCTTCCTG
                                |||| |||    ||||||||||||
                                GTAC GTT    CTCAAGAAGGAC
                                  _   CT__
GAM312  LOC222160 5'  AGGAAGAACTCACCCC      94117     CTC
                                GG   TGAGTTCTTCCT
                                ||   ||||||||||||
                                CC   ACTCAAGAAGGA
                                 CC_
GAM312  LOC51094  3'  CAGGAAGAATAAAGCC      32045      CTGA
                                GGCT    GTTCTTCCTG
                                ||||    ||||||||||
                                CCGA    TAAGAAGGAC
                                  AA__
GAM312  LOC92078  3'  CAGGAAGAAGAATCGACCGTC  67977      C  T  G__
                                GACGG TC GA   TTCTTCCTG
                                ||||| || ||   |||||||||
                                CTGCC AG CT   AAGAAGGAC
                                  _ _  AAG
GAM313  ABCC3     3'  CAGGCATGGATCCAGAACTGCA 39153          AGT  G   T
          C                      GTGCAGTTCT   TT CAT CCTG
                                ||||||||||   || ||| ||||
                                CACGTCAAGA   AG GTA GGAC
                                     CCT  _   C
GAM313  CFTR      3'  AGGAACCACAAGACTGCAC    4926         T  A  TTGCA
                                GTGCAGT CT GT     TTCCT
                                ||||||| || ||     |||||
                                CACGTCA GA CA     AAGGA
                                   _  A  CC___
GAM313  MAN1A2    5'  AGGAATGGAAGAACCCAC     21981      CA     AGTT G
                                GTG  GTTCT    T CATTCCT
                                |||  |||||    | |||||||
                                CAC  CAAGA    A GTAAGGA
                                  C_    _____ G
GAM313  HS6ST     3'  AGGAACAGCAGAACTGC      62023         A   TGCA
                                GCAGTTCT GTT    TTCCT
                                |||||||| |||    |||||
                                CGTCAAGA CGA    AAGGA
                                     _   C___
GAM313  TU3A      5'  CAGGAATGCAAAGGCTGT     23184       CTAG
                                GCAGTT    TTTGCATTCCTG
                                ||||||    ||||||||||||
                                TGTCGG    AAACGTAAGGAC
                                           ____
GAM313  LOC115051 3'  AGGAACAGCAGAACTGC      60034         A   TGCA
                                GCAGTTCT GTT    TTCCT
                                |||||||| |||    |||||
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                                CGTCAAGA CGA    AAGGA
                                    _  C___
GAM313  LOC143279 5'  GAATGTGAGAGAACCAC     76509     CA    AG  TG
                                GTG  GTTCT  TT  CATTC
                                |||  |||||  ||  |||||
                                CAC  CAAGA  GA  GTAAG
                                  __    __ GT
GAM313  LOC253017 3'  CAGAAATGCAAATCAAAACCAC 95841     CA   CTA       C
                                GTG  GTT   GTTTGCATT CTG
                                |||  |||   ||||||||| |||
                                CAC  CAA   TAAACGTAA GAC
                                  __  AAC       A
GAM314  CCND1    5'  CACACGGACTACAGGGG     53885       CAA    AATT
                                TCCCTG   TCCG    TGTG
                                ||||||   ||||    ||||
                                GGGGAC   AGGC    ACAC
                                   ATC   _____
GAM314  FANCE    3'  AATTCTCAGGCTGCAGGGA    41609        AT C__
                                TCCCTGCA  C   GAATT
                                ||||||||  |   |||||
                                AGGGACGT  G   CTTAA
                                    CG ACT
GAM314  IFIT4    5'  GCTTTTCAGAACTGCAGGGA   70923        A_  C   TTT
                                TCCCTGCA  TC GAA   GT
                                ||||||||  || |||   ||
                                AGGGACGT  AG CTT   CG
                                    CA  A   TT_
GAM314  LDHB     5'  CACACAAATTCAGGTAGCAGG  9702       A   C
                                CCTGC ATC GAATTTGTGTG
                                ||||| ||| ||||||||||
                                GGACG TGG CTTAAACACAC
                                  A   A
GAM314  LILRA1   3'  CAGTGTTGGATTGCAGAGA    22487    C         AT
                                TC CTGCAATCCGA  TTG
                                || ||||||||||  |||
                                AG GACGTTAGGTT  GAC
                                 A          GT
GAM314  MAP1B    5'  CACACAAACCCAGCCTGGGGA  49269       __  AATCCGAA
                                TCCCT  GC       TTTGTGTG
                                |||||  ||       ||||||||
                                AGGGG  CG       AAACACAC
                                  TC  ACCC_____
GAM314  MGAM     3'  CAGTTTCTCCAGGCTGCAGGGA 72361         AT C___   T
                                TCCCTGCA  C    GAA TTG
                                ||||||||  |    ||| |||
                                AGGGACGT  G    CTT GAC
                                    CG ACCT   T
GAM314  OXCT     3'  CACACAAGATTTAATTGAAAGG 4751      CTG    CC  A
            A                    TCC   CAAT  GA TTTGTGTG
                                |||   ||||  || ||||||||
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                                AGG   GTTA  TT GAACACAC
                                  AAA    AT  A
GAM314  PDGFRA   5'  CACTGGGAGATTCGGAGCGCAG 20593        AA       GT__
            GGA                    TCCCTGC  TCCGAATTT    GTG
                                |||||||  |||||||||    |||
                                AGGGACG  AGGCTTAGA    CAC
                                    CG        GGGT
GAM314  PSEN2    3'  CACAGGCTGCAAGCTGCAGGGA 25031         ATCCGAA_
                                TCCCTGCA       TTTGTG
                                ||||||||       ||||||
                                AGGGACGT       GGACAC
                                    CGAACGTC
GAM314  PSEN2    3'  CACAGGCTGCAAGCTGCAGGGA 4807          ATCCGAA_
                                TCCCTGCA       TTTGTG
                                ||||||||       ||||||
                                AGGGACGT       GGACAC
                                    CGAACGTC
GAM314  SPS2     3'  CACACAAAGTAAATTGCA    24287       CCGAA
                                TGCAAT    TTTGTGTG
                                ||||||    ||||||||
                                ACGTTA    AAACACAC
                                   AATG_
GAM314  WSX1     3'  CAGGAGTTCGAAGCTGCAGGGA 16731         ATC_     G
                                TCCCTGCA   CGAATTT TG
                                ||||||||   ||||||| ||
                                AGGGACGT   GCTTGAG AC
                                    CGAA     G
GAM314  ATP6M8-9 3'  CACACAAAAATCCCTGAGGGA  19273      G  ATCCGAA
                                TCCCT CA      TTTGTGTG
                                ||||| ||      ||||||||
                                AGGGA GT      AAACACAC
                                  _  CCCTAA_
GAM314  C6orf31  5'  CACTCCGGCTGCAGGGA     47640         AT   AATTT
                                TCCCTGCA  CCG    GTG
                                |||||||  |||    |||
                                AGGGACGT  GGC    CAC
                                    C_   CT___
GAM314  DGS-A    3'  CACACAAGAGGTACTGGAGGGA 84894       G  AT_  GAAT
                                TCCCT CA   CC    TTGTGTG
                                ||||| ||   ||    |||||||
                                AGGGA GT   GG    AACACAC
                                  G  CAT  AG__
GAM314  FLJ13102 3'  ACACAGAATTTCAGGGA     46001       C   CCGAA
                                TCCCTG AAT    TTTGTGT
                                |||||| |||    |||||||
                                AGGGAC TTA    AGACACA
                                   T  _____
GAM314  FLJ13204 3'  CACGTTCTAACTGCAGGGA   45415         ATCC    TT
                                TCCCTGCA   GAAT  GTG
                                ||||||||   ||||  |||
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                                AGGGACGT   CTTG  CAC
                                    CAAT   __
GAM314  FLJ20413  3'  CACACTGGCGCAGCTGCAGGGA 35129       ATC_  AATTT
                                TCCCTGCA   CG    GTGTG
                                ||||||||   ||    |||||
                                AGGGACGT   GC    CACAC
                                    CGAC  GGT__
GAM314  FLJ22649  5'  CAGACGGCGCGGATCGCAGGGA 41635       A    AAT   G
                                TCCCTGC ATCCG   TTGT TG
                                ||||||| |||||   |||| ||
                                AGGGACG TAGGC   GGCA AC
                                    C    GC_   G
GAM314  FLJ30707  3'  CACACAAACTCAGAGACACAG  58816     CAA_  C  A
                                CTG   TC GA TTTGTGTG
                                |||   || || ||||||||
                                GAC   AG CT AAACACAC
                                  ACAG  A  C
GAM314  FLJ30791  5'  CAGGCTCGGAGCTGCAGGGA   58445       A_    A
                                TCCCTGCA  TCCGA TTTG
                                ||||||||  ||||| ||||
                                AGGGACGT  AGGCT GGAC
                                    CG    C
GAM314  GENX-3414 3'  CACAGCCCGACTGCAGGGA   14146       A  CGAAT
                                TCCCTGCA TC    TTGTG
                                |||||||| ||    |||||
                                AGGGACGT AG    GACAC
                                    C  CCC__
GAM314  HOOK3     3'  CACACAAGAACATTTCAGG   50546     C   CCGAA
                                CCTG AAT    TTTGTGTG
                                |||| |||    ||||||||
                                GGAC TTA    GAACACAC
                                  T   CAA__
GAM314  HRMT1L3   3'  CACACGTGGGAAGCTGCAGAGA 39072    C    A__   GAATT
                                TC CTGCA   TCC    TGTGTG
                                || |||||   |||    ||||||
                                AG GACGT   AGG    GCACAC
                                 A    CGA   GT___
GAM314  KIAA0332  3'  CATGGTCTTCCAGTTGCAGG   62698       CC   T_ TG
                                CCTGCAAT  GAA  T  TG
                                ||||||||  |||  |  ||
                                GGACGTTG  CTT  G  AC
                                    AC   CT GT
GAM314  KIAA1655  5'  CACACAGAATGATTACAG    66595     C   CGAA
                                CTG AATC    TTTGTGTG
                                ||| ||||    ||||||||
                                GAC TTAG    AGACACAC
                                  A   TA__
GAM314  KIAA1904  3'  CAGACTCTCTGACTGCAGGGA  73479       A  C  ATTT  G
                                TCCCTGCA TC GA    GT TG
                                |||||||| || ||    || ||
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                                AGGGACGT AG CT    CA AC
                                    C  T  CT__  G
GAM314  MGC1842   3'  ACACCAGATTGCACAGGA    65635     C_      CGAATTT
                                TCC  TGCAATC      GTGT
                                |||  |||||||      ||||
                                AGG  ACGTTAG      CACA
                                  AC      AC_____
GAM314  MGC22014  3'  CACACAGCAGTAGATGTGCAAG 64490     C   _   CGAAT
           GA                     TCC TGCA ATC     TTGTGTG
                                |||  |||| |||     |||||||
                                AGG ACGT TAG     GACACAC
                                  A   G   ATGAC
GAM314  PP1057    5'  CACACAAATCGGGAACAGG    48432      CAA     A
                                CCTG   TCCGA TTTGTGTG
                                ||||   ||||| ||||||||
                                GGAC   GGGCT AAACACAC
                                  AA_    _
GAM314  ROBO4     3'  CACCATTTGGATCACAGG     38790      CA       TT
                                CCTG  ATCCGAAT  GTG
                                ||||  ||||||||  |||
                                GGAC  TAGGTTTA  CAC
                                  AC       C_
GAM314  SE57-1    3'  ACACAAACGCACAGGGA      47393       CAATC  AA
                                TCCCTG    CG  TTTGTGT
                                ||||||    ||  |||||||
                                AGGGAC    GC  AAACACA
                                   AC___  __
GAM314  LOC132228 3'  CACACAAATCCATTCCAGG    75043      C   CCGA
                                CCTG AAT    ATTTGTGTG
                                |||| |||    |||||||||
                                GGAC TTA    TAAACACAC
                                  C   CC__
GAM314  LOC148645 3'  CACACACGGAGATGCACAGA   84178    CC    A_    AATT
                                TC  TGCA  TCCG    TGTGTG
                                ||  ||||  ||||    ||||||
                                AG  ACGT  AGGC    ACACAC
                                 AC    AG    _____
GAM314  LOC150035 5'  CACACATGGGGTGGAGCCACAA 84807     C  CAA_    AATT_
           GGA                    TCC TG    TCCG     TGTGTG
                                |||  ||    ||||     ||||||
                                AGG AC    AGGT     ACACAC
                                  A  ACCG    GGGGT
GAM314  LOC153222 3'  CACACAAAAAAATTGAGG    80783     G    CCGAA
                                CCT CAAT     TTTGTGTG
                                |||  ||||     ||||||||
                                GGA GTTA     AAACACAC
                                  _    AAA__
GAM314  LOC196205 3'  CATGGAAATTCGGACTCAGGGA 87589       CAA       G
                                TCCCTG   TCCGAATTT TGTG
                                ||||||   ||||||||| ||||
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                                AGGGAC   AGGCTTAAA GTAC
                                   TC_       G
GAM314  LOC221692 3'  CACACAAAACATGACCACAGG  92236     CAA  CGAA
                                CCTG   TC    TTTGTGTG
                                ||||   ||    ||||||||
                                GGAC   AG    AAACACAC
                                  ACC  TACA
GAM315  MAP3K7    3'  ACTTCAAAACAGATGCAGTGAA 12098         GACGAAC
                                TTCATTGCAT      TTGAAGT
                                ||||||||||      |||||||
                                AAGTGACGTA      AACTTCA
                                      GACAA__
GAM315  NR2E1     3'  CTTCAAGGAGATGAATGAA    12325       G   GACGAA
                                TTCATT CAT     CTTGAAG
                                |||||| |||     |||||||
                                AAGTAA GTA     GAACTTC
                                   _   GAG___
GAM315  ZNF18     3'  CTCAAGTTCATAATGTA     78139      GAC       A
                                TGCAT   GAACTTGA G
                                |||||   |||||||| |
                                ATGTA   CTTGAACT C
                                   ATA       C
GAM315  AFAP      3'  CTTCAAGTCCATGACA      41302    _    ACGA
                                TG CATG    ACTTGAAG
                                || ||||    ||||||||
                                AC GTAC    TGAACTTC
                                 A    C___
GAM315  CHODL     3'  ACTTCAAACTTCAAGCAAATGA 46309       _  A   CGAAC
           A                     TTCATT GC TGA     TTGAAGT
                                |||||| || |||     |||||||
                                AAGTAA CG ACT     AACTTCA
                                   A  A   TCA__
GAM315  DCNP1     3'  ACCTCAAGTTCCTTGCAG     55618       TGAC       A
                                TTGCA    GAACTTGA GT
                                |||||    |||||||| ||
                                GACGT    CTTGAACT CA
                                   TC__       C
GAM315  FLJ20281  3'  GCTGCATTCATCAGCAATGAA  90982         A   C   CT  A
                                TTCATTGC TGA GAA  TG AGT
                                |||||||| ||| |||  || |||
                                AAGTAACG ACT CTT  AC TCG
                                     _   A   __  G
GAM315  LOC158450 3'  ACTTCAAGCCCATTGTGACAG  81929     _  TG CGAA
                                TTG CA  A    CTTGAAGT
                                ||| ||  |    ||||||||
                                GAC GT  T    GAACTTCA
                                  A  GT ACCC
GAM315  LOC158504 3'  ACTTCAAGCCCATTGTGACAG  81937     _  TG CGAA
                                TTG CA  A    CTTGAAGT
                                ||| ||  |    ||||||||
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                                GAC GT  T    GAACTTCA
                                  A  GT ACCC
GAM315  LOC51313  3'  ACCTCAAGCCCGTTTAGCAATG 33508         AT    AA    A
              AG                    TTCATTGC  GACG  CTTGA GT
                                    ||||||||  ||||  ||||| ||
                                    GAGTAACG  TTGC  GAACT CA
                                        AT    CC    C
GAM316  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                    ATTT ACTTT   TGTCTGAG
                                    |||| |||||   ||||||||
                                    TAAA TGAAA   ACAGATTC
                                      A    T__
GAM316  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875        CAC   C  T
                                    CATTT   TTT AC GTCTGAGAT
                                    |||||   ||| || |||||||||
                                    GTAAA   AAA TG TAGACTCTA
                                       TA_   T  _
GAM316  FDFT1    3'  TAGGAAAGTGAAATG       15518            A
                                    CATTTCACTTTC CTG
                                    |||||||||||| |||
                                    GTAAAGTGAAAG GAT
                                                _
GAM316  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                    CATTTCACTTTCACTGTCTGAGAT
                                    ||||||||||||||||||||||||
                                    GTAAAGTGAAAGTGACAGACTCTA

GAM316  KLF4     3'  TCCCAGACAGTGGATATG     14891     CT         A
                                    CA  TTCACTGTCTG GA
                                    ||  |||||||||| ||
                                    GT  AGGTGACAGAC CT
                                     AT          C
GAM316  PHYH     3'  ACAGTAAAAGTGAAAT      20608           C
                                    ATTTCACTTT ACTGT
                                    |||||||||| |||||
                                    TAAAGTGAAA TGACA
                                          A
GAM316  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096           CTG    A
                                    TTTCACTTTCA   TCTG GA
                                    ||||||||||   |||| ||
                                    AAAGTGAAAGT   GGAC CT
                                          T__    _
GAM316  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                    TTTCA TTTCACTGTCT
                                    ||||| ||||||||||
                                    AAAGT AAAGTGACGGG
                                       A
GAM316  ZNF216   3'  ATCTGCACAGCAAAGTGAAA   20017          CA    CTG
                                    TTTCACTTT  CTGT   AGAT
                                    |||||||||  ||||   ||||
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                                AAAGTGAAA  GACA   TCTA
                                    C_   CG_
GAM316  CG012    5' CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                    CT  __
GAM316  EIF2C2   3' ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                    G  TC
GAM316  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM316  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM316  KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM316  KLHL6    3' ATCTCAGAGCAGGAAA      55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM316  NIR3     3' GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM316  PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM316  PP35     3' ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM316  PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148         TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
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                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM316  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM316  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941        CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM316  LOC149703 3' ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM316  LOC154007 3' ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM316  LOC155004 3' TCATTTAAGTGAAAGGAAA   81226     A      GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||   |||
                                AAAG GAAAGTGA    ACT
                                  _      ATTT
GAM316  LOC222134 5' ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                       _
GAM317  CCR2     3'  CAATCTCTGATTCTGTCA    5386         CG   GG
                                TGACAGAA  AGAG  TG
                                |||||||  ||||  ||
                                ACTGTCTT  TCTC  AC
                                     AG    TA
GAM317  CYP51    5'  AGCTTCTCTCGTTCCGTC    5779     A        T
                                GAC GAACGAGAGGG GCT
                                ||| ||||||||||| |||
                                CTG CTTGCTCTCTT CGA
                                  C         _
GAM317  GABRP    3'  TCAGAGAGTCGCTGTCATTCTG 26402        C  G  _  TG
            TCA                   TGACAGAA GA AG GG  CTCTGA
                                |||||||| || || ||  ||||||
                                ACTGTCTT CT TC CT  GAGACT
                                     A  G  G  GA
GAM317  GMPS     5'  GGCACCCTCCCGCCCCGTC   13918     AGAA  A
                                GAC    CG GAGGGTGCT
                                |||    || |||||||||
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                                CTG    GC CTCCCACGG
                                  CCCC  C
GAM317  LIMD1    3'  GGGGACCCTCTCTTCCCATCA  26463     CA_  C      G
                                TGA   GAA GAGAGGGT CTC
                                |||   ||| |||||||| |||
                                ACT   CTT CTCTCCCA GGG
                                  ACC  _      G
GAM317  OCRL     3'  CACTCCCCTCGTTCTGTCA   7825           A  _
                                TGACAGAACGAG GG GTG
                                |||||||||||| || |||
                                ACTGTCTTGCTC CC CAC
                                       C  T
GAM317  OCRL     3'  CACTCCCCTCGTTCTGTCA   4259           A  _
                                TGACAGAACGAG GG GTG
                                |||||||||||| || |||
                                ACTGTCTTGCTC CC CAC
                                       C  T
GAM317  PYGO2    3'  GCTCCCTCTCGCTCTCTCA   63987    C   A      T
                                TGA AGA CGAGAGGG GC
                                ||| ||| |||||||| ||
                                ACT TCT GCTCTCCC CG
                                  C   C       T
GAM317  TCFL4    3'  TCAAAATCACCCTTTCTGTCA  63465       ACGA     CTC_
                                TGACAGA    GAGGGTG    TGA
                                |||||||    |||||||    |||
                                ACTGTCT    TTCCCAC    ACT
                                    _____      TAAA
GAM317  BIRC1    3'  CAGTCTCTCCCATTCTGT    15787      C__     G
                                ACAGAA   GAGAGG TG
                                ||||||   |||||| ||
                                TGTCTT   CTCTCT AC
                                   ACC     G
GAM317  CHERP    3'  AGCGCCTTCCACTCCATCA   21096     CA  ACGA
                                TGA  GA    GAGGGTGCT
                                |||  ||    |||||||||
                                ACT  CT    CTTCCGCGA
                                  AC  CAC_
GAM317  DKFZP564K2062 3'  TCAGAAGTCTCAGTTCTGTCA  31238        GA   GTGC
                                TGACAGAAC  GAGG    TCTGA
                                |||||||||  ||||    |||||
                                ACTGTCTTG  CTCT    AGACT
                                     A_    GA__
GAM317  FLJ10482  3'  TCAGAGTGATCTGTCCTGCCA  36165    A   AAC  G  GG
                                TG CAG   GA AG  TGCTCTGA
                                || |||   || ||  ||||||||
                                AC GTC   CT TC  GTGAGACT
                                 C   ___  G  TA
GAM317  FLJ13848  3'  CAGAAGGACTTCTCGTTCCTCA 45461     CA        GTGC
                                TGA  GAACGAGAGG    TCTG
                                |||  ||||||||||    ||||
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                                ACT  CTTGCTCTTC   AGAC
                                  C_       AGGA
GAM317  FLJ21802  3'  CAGAGCACCAACTTCATC   44980   AC  AG
                                GA  GAG  GGTGCTCTG
                                ||  |||  |||||||||
                                CT  TTC  CCACGAGAC
                                 AC   AA
GAM317  KIAA1458  3'  CAGGACCTCCATTCTGTCA   69002       CGA   GTGC
                                TGACAGAA   GAGG   TCTG
                                ||||||||   ||||   ||||
                                ACTGTCTT   CTCC   GGAC
                                     AC_   A___
GAM317  MGC10500  3'  GTCCCCCTCGTTCTGT     48935        A   TG
                                ACAGAACGAG GGG  C
                                |||||||||| |||  |
                                TGTCTTGCTC CCC  G
                                      _  CT
GAM317  NDP52     3'  CATCCTCTCACCTGTCA     19526      AAC
                                TGACAG   GAGAGGGTG
                                ||||||   |||||||||
                                ACTGTC   CTCTCCTAC
                                   CA_
GAM317  SEC24C    3'  TCAAGTATCCTGCCACTCTGTC 17000       ACGAG      C
           A                     TGACAGA    AGGGTGCT TGA
                                |||||||    |||||||| |||
                                ACTGTCT    TCCTATGA ACT
                                    CACCG      _
GAM317  SNRPD3    5'  CAGAGCCGAACTCTCTTCCTGC 14800    A   AAC      ___
           CA                     TG CAG   GAGAGGGT   GCTCTG
                                ||  |||   ||||||||   ||||||
                                AC GTC   TTCTCTCA   CGAGAC
                                 C   C__       AGC
GAM317  LOC152328 3'  CAAGTGCCCTCCCCTATCA   80523     C  AACGA    TG  C
                                TGA AG    GAGGG  CT TG
                                ||| ||    |||||  || ||
                                ACT TC    CTCCC  GA AC
                                  A  CC___    GT  _
GAM317  LOC158835 3'  CATCCCTCTCATTCCATC    82009    CA   C     _
                                GA  GAA GAGAGGG TG
                                ||  ||| ||||||| ||
                                CT  CTT CTCTCCC AC
                                 AC   A      T
GAM317  LOC197003 3'  CAGACCTTCTCACACTGCCA   87871    A   AAC     TGC
                                TG CAG   GAGAGGG   TCTG
                                || |||   |||||||   ||||
                                AC GTC   CTCTTCC   AGAC
                                 C   ACA      ___
GAM317  LOC257443 3'  CAGGACCTCCATTCTGTCA   95846       CGA   GTGC
                                TGACAGAA   GAGG   TCTG
                                ||||||||   ||||   ||||
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                                ACTGTCTT  CTCC   GGAC
                                    AC_   A___
GAM317  LOC257451 3'  GCTCCCTCTCGCTCTCTCA  95557    C  A     T
                                TGA AGA CGAGAGGG GC
                                ||| ||| |||||||| ||
                                ACT TCT GCTCTCCC CG
                                  C  C      T
GAM317  LOC92609  5'  CAAAGTCTCTCGTTC      72844        GGT  C
                                GAACGAGAG  GCT TG
                                |||||||||  ||| ||
                                CTTGCTCTC  TGA AC
                                     ___  A
GAM318  GDF5    3'  GCTTTCCGATGAGACTCA   5107      AC
                                TGAGT  CATCGGAAAGC
                                |||||  ||||||||||
                                ACTCA  GTAGCCTTTCG
                                   GA
GAM318  LZTS1   3'  CACACAGCCCCTATAGCACT  40680    ACC  C  AAA
                                AGT  AT GG  GCTGTGTG
                                |||  || ||  ||||||||
                                TCA  TA CC  CGACACAC
                                  CGA  T  C__
GAM318  POLR2E  3'  CACACAGCCCTGTGGGCACCA  59912   A  A_   C  AAA
                                TG GT  CCAT GG  GCTGTGTG
                                || ||  |||| ||  ||||||||
                                AC CA  GGTG CC  CGACACAC
                                 _ CG   T ___
GAM318  SNRPA   3'  CACAGCATTGTACCCA     15986    A   C  CGGAAA
                                TG GTAC AT     GCTGTG
                                || |||| ||     ||||||
                                AC CATG TA     CGACAC
                                 C   T _______
GAM318  ZNF14   3'  CACACAGCCTTTTGAGCACAC  40714    ACCA     A
                                GT   TCGGAA GCTGTGTG
                                ||   |||||| ||||||||
                                CA   AGTTTT CGACACAC
                                 CACG     C
GAM318  FLJ00024  3'  CACACAGCCTCAATGTTAGTCT 63749     T  CAT  GAAA_
          CA                     TGAG AC  CG    GCTGTGTG
                                |||| ||  ||    ||||||||
                                ACTC TG  GT    CGACACAC
                                  _ ATT  AACTC
GAM318  FLJ31978  3'  CACACAGCTCTGGGTGC    58347      AT   AA
                                GTACC  CGGA  GCTGTGTG
                                |||||  ||||  ||||||||
                                CGTGG  GTCT  CGACACAC
                                   __   __
GAM318  LOC144871 3'  CACAGCAATGGTATCA     83197     G     CGGAAA
                                TGA TACCAT     GCTGTG
                                ||| ||||||     ||||||
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                                ACT ATGGTA     CGACAC
                                  _     A_____
GAM318  LOC253181 3'  CACACGGCAACGACCCTCA   97556     TACCA   GAAA
                                TGAG    TCG   GCTGTGTG
                                ||||    |||   ||||||||
                                ACTC    AGC   CGGCACAC
                                  CC___   AA__
GAM319  CYP4A11   5'  CTGGCACACAGTAAATGCTCA  5755     A      AC  T
                                TGA CATTTACT  GT CCAG
                                ||| ||||||||  || ||||
                                ACT GTAAATGA  CA GGTC
                                  C       CA  C
GAM319  GJB3      5'  CTGGTACATAGTAAATGCTCAA 43767      A       C  T
              TA                  TATTGA CATTTACTA GT CCAG
                                ||||||| |||||||| || ||||
                                ATAACT GTAAATGAT CA GGTC
                                   C        A  T
GAM319  GPR81     3'  TGGCAGTAAGTGCTCAATA   50769      A      ACGTT
                                TATTGA CATTTACT    CCA
                                |||||| ||||||||    |||
                                ATAACT GTGAATGA    GGT
                                   C       C____
GAM319  PODXL     3'  TGCAGTGAATGTTCAA      18242           A
                                TTGAACATTTACT CG
                                |||||||||||| ||
                                AACTTGTAAGTGA GT
                                      C
GAM319  GOA       3'  CTGGCATGTAGTAGATGCTCAA 78075      A         T
              TA                  TATTGA CATTTACTACGT CCAG
                                |||||| |||||||||||| ||||
                                ATAACT GTAGATGATGTA GGTC
                                   C          C
GAM319  KIAA0747  3'  CTGCATGTAGCAAATGTTCAG  30965         A     TC
                                TTGAACATTT CTACGT  CAG
                                |||||||||| ||||||  |||
                                GACTTGTAAA GATGTA  GTC
                                      C     C_
GAM319  KIAA1130  3'  ACATAGTAGATGTTCAATA   62409            C
                                TATTGAACATTTACTA GT
                                |||||||||||||||| ||
                                ATAACTTGTAGATGAT CA
                                         A
GAM319  MDS018    3'  CTGGAACGTAGTAAATGTCAA  41532      A
                                TTGA CATTTACTACGTTCCAG
                                |||| ||||||||||||||||
                                AACT GTAAATGATGCAAGGTC
                                  _
GAM319  MGC4170   3'  TGGAACGCAGTCTTCA      44226      CATTT   A
                                TGAA    ACT CGTTCCA
                                ||||    ||| |||||||
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                                ACTT     TGA GCAAGGT
                                  C____   C
GAM319  NTSR2     3'  CTGGTGCGTAGTAGATGCTCAA 24717        A          T
                TA                  TATTGA CATTTACTACGT CCAG
                                    |||||| |||||||||||| ||||
                                    ATAACT GTAGATGATGCG GGTC
                                       C          T
GAM319  LOC135818 3'  CTGGAAACAAGCTAAATGTTCA 75234          _ ACG
                                    TGAACATTTA CT   TTCCAG
                                    |||||||||| ||   ||||||
                                    ACTTGTAAAT GA   AAGGTC
                                          C  ACA
GAM319  LOC151162 5'  TAGTAAATGTTAAATA      85248      G
                                    TATT AACATTTACTA
                                    |||| ||||||||||
                                    ATAA TTGTAAATGAT
                                      A
GAM319  LOC158191 3'  CTGGCTCAGAGTAAGTGCTCAA 81774       A       ACGTT
                TA                  TATTGA CATTTACT     CCAG
                                    |||||| ||||||||     ||||
                                    ATAACT GTGAATGA     GGTC
                                       C       GACTC
GAM319  LOC203377 5'  TAGTAAATGTTAAATA      90586      G
                                    TATT AACATTTACTA
                                    |||| ||||||||||
                                    ATAA TTGTAAATGAT
                                      A
GAM319  LOC91628  3'  TAGTAAGTGCTCAATA      66762       A
                                    TATTGA CATTTACTA
                                    |||||| |||||||||
                                    ATAACT GTGAATGAT
                                       C
GAM320  ADAMTS4   5'  GTCCCTCCCAGCTGCAGTA   17517         GA_   C
                                    TACTGCAGT   GAGG AT
                                    |||||||||   |||| ||
                                    ATGACGTCG   CTCC TG
                                          ACC    C
GAM320  ATP11B    3'  AACCATTATTTACTGCAGTA   80312           AGGC
                                    TACTGCAGTGAG    ATGGTT
                                    ||||||||||||    ||||||
                                    ATGACGTCATTT    TACCAA
                                           AT__
GAM320  FGA       3'  GCCTCTCACTAAGTA       4961       GC
                                    TACT  AGTGAGAGGC
                                    ||||  ||||||||||
                                    ATGA  TCACTCTCCG
                                      A_
GAM320  HIF1A     3'  ACCATTGCATTGCAGTA     7733           AGAGGC
                                    TACTGCAGTG     ATGGT
                                    ||||||||||     |||||
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                                ATGACGTTAC     TACCA
                                    GT____
GAM320  HIS1    3'  ATGTCCCCTCACTGCAG    21313        A _
                                CTGCAGTGAG GG CAT
                                |||||||||| || |||
                                GACGTCACTC CC GTA
                                    C  T
GAM320  SEDL    5'  GCCTCCCACTGCAGTA     27338        A
                                TACTGCAGTG GAGGC
                                |||||||||| |||||
                                ATGACGTCAC CTCCG
                                    C
GAM320  SLC30A3  3'  AACTTGTGTCTCACTGCA    12932         G  T
                                TGCAGTGAGA GCA GGTT
                                |||||||||| ||| ||||
                                ACGTCACTCT TGT TCAA
                                    G  _
GAM320  TBL1X   3'  AACCATAAGGTACTGCAG    18922        AGAGGC
                                CTGCAGTG     ATGGTT
                                ||||||||     ||||||
                                GACGTCAT     TACCAA
                                    GGAA__
GAM320  TJP1    5'  AACCTCAGCTCACTGCAG    12294         AGGCAT
                                CTGCAGTGAG     GGTT
                                ||||||||||     ||||
                                GACGTCACTC     CCAA
                                    GACT__
GAM320  AP1S3   3'  ATCCTCTCACCGCAG      74918     A      C
                                CTGC GTGAGAGG AT
                                |||| |||||||| ||
                                GACG CACTCTCC TA
                                  C      _
GAM320  ARHF    3'  ACTGTTCCCCCCACTGCGG   38737        AGA  C
                                CTGCAGTG   GG ATGGT
                                ||||||||   || |||||
                                GGCGTCAC   CC TGTCA
                                    CCC  T
GAM320  C6orf9  5'  AACCATGCCCCTCCCAGT    42073     CAGT   A
                                ACTG    GAG GGCATGGTT
                                ||||    ||| |||||||||
                                TGAC    CTC CCGTACCAA
                                  C___   C
GAM320  CHERP   3'  AACCACACCAGGAGGCGCTGCA 21095       AGA___  CA
                                TGCAGTG     GG  TGGTT
                                |||||||     ||  |||||
                                ACGTCGC     CC  ACCAA
                                    GGAGGA  AC
GAM320  CPR2    3'  AACCATGATAGCACCACTGCAG 48084         AGAGG__
            T                    ACTGCAGTG      CATGGTT
                                |||||||||      |||||||
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                                TGACGTCAC      GTACCAA
                                     CACGATA
GAM320  DKFZP434L0117 5'  AACCACCGCTCACCGCAG    42917      A    A  CA
                                CTGC GTGAG GG  TGGTT
                                |||| ||||| ||  |||||
                                GACG CACTC CC  ACCAA
                                  C    G __
GAM320  DKFZP564B1162 3'  AACCATGCCCACGTGAG     48525    G _   AGA
                                CT CA GTG   GGCATGGTT
                                || || |||   |||||||||
                                GA GT CAC   CCGTACCAA
                                 _ G  ___
GAM320  FLJ11286  3'  ATGTCCTCTCACCAG       37216     CA       _
                                CTG  GTGAGAGG CAT
                                |||  |||||||| |||
                                GAC  CACTCTCC GTA
                                 __       T
GAM320  FLJ14957  3'  AACCTTGGCTCACTGCA     51731          AGG  T
                                TGCAGTGAG   CA GGTT
                                |||||||||   || ||||
                                ACGTCACTC   GT CCAA
                                     G__  T
GAM320  FLJ20729  3'  AATGGTCCTCTCACTGCAG    35645            C  G
                                CTGCAGTGAGAGG AT GTT
                                |||||||||||| || |||
                                GACGTCACTCTCC TG TAA
                                       _ G
GAM320  FLJ21820  3'  ACCACATACTGCAGTG      41621          AGAGGCA
                                TACTGCAGTG      TGGT
                                ||||||||||      ||||
                                GTGACGTCAT      ACCA
                                     AC_____
GAM320  FLJ21841  3'  CCATCTCACTGCAGTA      44832            _
                                TACTGCAGTGAGA GG
                                |||||||||||| ||
                                ATGACGTCACTCT CC
                                       A
GAM320  FLJ21841  3'  GCCACCTCACTGCAGTA     44833           A_
                                TACTGCAGTGAG  GGC
                                |||||||||||  |||
                                ATGACGTCACTC  CCG
                                      CA
GAM320  GGA2      3'  ACCTCCTCTCACCACAG     56868     CA       CAT
                                CTG  GTGAGAGG   GGT
                                |||  ||||||||   |||
                                GAC  CACTCTCC   CCA
                                  AC       T__
GAM320  HSPC019   3'  ACCCCCCCATTGCAGTA      25854          AGA  CAT
                                TACTGCAGTG   GG   GGT
                                |||||||||   ||   |||
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                                ATGACGTTAC   CC   CCA
                                     ____  C__
GAM320  KIAA1854  3'  AATTGTGCTCCCACTGCA    71735       A   G  TG
                                TGCAGTG GAG CA  GTT
                                ||||||| ||| ||  |||
                                ACGTCAC CTC GT  TAA
                                    C   _  GT
GAM320  MESDC2    3'  AACCACTGTTTCACTGCA    72488        AG  _
                                TGCAGTGAG  GCA TGGTT
                                |||||||||  ||| |||||
                                ACGTCACTT  TGT ACCAA
                                     __   C
GAM320  SEC14L2   3'  ACCGGCCTCTCACCAAGCA   24870     A__       A
                                TGC   GTGAGAGGC TGGT
                                |||   ||||||||| ||||
                                ACG   CACTCTCCG GCCA
                                  AAC        _
GAM320  LOC113675 5'  AACCTTGGCTCACTGCA     56564        AGG  T
                                TGCAGTGAG   CA GGTT
                                |||||||||   || ||||
                                ACGTCACTC   GT CCAA
                                     G__  T
GAM320  LOC135892 3'  ACCATGCTATCTGCGC      75242     _  _
                                GTG AGA GGCATGGT
                                ||| ||| ||||||||
                                CGC TCT TCGTACCA
                                  G   A
GAM320  LOC142779 5'  CCTGCTCTCACTGCA       76394         G  T
                                TGCAGTGAGAG CA GG
                                |||||||||||| || ||
                                ACGTCACTCTC GT CC
                                      _  _
GAM320  LOC146443 5'  AACCACATTCACTGCAG     77879         AGGCA
                                CTGCAGTGAG    TGGTT
                                ||||||||||    |||||
                                GACGTCACTT    ACCAA
                                     AC___
GAM320  LOC148932 3'  ACCGACCCACTGCAG       79101        AGA  CA
                                CTGCAGTG   GG  TGGT
                                ||||||||   ||  ||||
                                GACGTCAC   CC  GCCA
                                     ___  A_
GAM320  LOC150142 5'  AACCATGTTGGCACCACTGCA  79573       AGA__
                                TGCAGTG    GGCATGGTT
                                |||||||    |||||||||
                                ACGTCAC    TTGTACCAA
                                    CACGG
GAM320  LOC152106 3'  AACCATGCCTCTACT       70059     G
                                AGT AGAGGCATGGTT
                                ||| ||||||||||||
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                                TCA TCTCCGTACCAA
                                  _
GAM320  LOC154222 3'  AACCATCCATTCACTGCA    86185        A  C
                                TGCAGTGAG GG ATGGTT
                                ||||||||| || ||||||
                                ACGTCACTT CC TACCAA
                                     A  _
GAM320  LOC158056 5'  AACCATGCCTCTGTCCAG    81680    CAGTG
                                CTG    AGAGGCATGGTT
                                |||    ||||||||||||
                                GAC    TCTCCGTACCAA
                                  CTG__
GAM320  LOC158308 3'  AACCAGGCCTCTCACTCCAG  86738    C        A
                                CTG AGTGAGAGGC TGGTT
                                ||| |||||||||| |||||
                                GAC TCACTCTCCG ACCAA
                                  C        G
GAM320  LOC196812 3'  AACCATGCCCCATCTTTAC   89559    _ ____
                                GTGA GA   GGCATGGTT
                                |||| ||   |||||||||
                                CATT CT   CCGTACCAA
                                   T  ACC
GAM320  LOC202908 5'  AACCTCTGCTCACTGCAG    89223        _  CAT
                                CTGCAGTGAG AGG   GGTT
                                |||||||||| |||   ||||
                                GACGTCACTC TCT   CCAA
                                     G  ____
GAM320  LOC255820 3'  GCCTCTCGCTGCAGTA      95708
                                TACTGCAGTGAGAGGC
                                ||||||||||||||||
                                ATGACGTCGCTCTCCG

GAM320  LOC257369 5'  ACTGGCCTCTCACAGCAG    95924     A       A
                                CTGC GTGAGAGGC TGGT
                                |||| ||||||||| ||||
                                GACG CACTCTCCG GTCA
                                   A       _
GAM320  LOC55885  3'  AACCATATTTTCACTACAG   37812    C      GC
                                CTG AGTGAGAG  ATGGTT
                                ||| ||||||||  ||||||
                                GAC TCACTTTT  TACCAA
                                  A       A_
GAM320  LOC87769  5'  AACCTGGGTTCTCACTGCAG  71319          G AT_
                                CTGCAGTGAGAG C   GGTT
                                |||||||||||| |   ||||
                                GACGTCACTCTT G   CCAA
                                       _ GGT
GAM321  ARCN1     3'  AGACTGCACTCTCTGTCA    7970         CA_
                                TGACAGAGA   CAGTTT
                                |||||||||   ||||||
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                                ACTGTCTCT   GTCAGA
                                     CAC
GAM321  CBFA2T2  3'  GAGCAAAACTCTGTCT      17466       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                   C
GAM321  CTLA4    3'  CAGAGCTGGGATGTTTCTGTCA 17807           CAGTTTT
                                TGACAGAGACA      GCTCTG
                                ||||||||||       ||||||
                                ACTGTCTTTGT      CGAGAC
                                      AGGGT__
GAM321  ITK      3'  CAGAACAGGAGTGATGTCTCTG 18674         _ G    C
                                CAGAGACA CA TTTTG TCTG
                                |||||||| || ||||| ||||
                                GTCTCTGT GT AGGAC AGAC
                                     A G    A
GAM321  LAMP2    3'  GGTGAAACCCCATCTCTATCA  25716    C    CACA    TG
                                TGA AGAGA    GTTT  CT
                                ||| |||||    ||||  ||
                                ACT TCTCT    CAAA  GG
                                  A    ACCC    GT
GAM321  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   40865        A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM321  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   52960        A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM321  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   52963        A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM321  PDGFRB   5'  CAGAGCCTGGAACTGTG     65969          __
                                CACAGTTTT  GCTCTG
                                |||||||||  ||||||
                                GTGTCAAGG  CGAGAC
                                     TC
GAM321  PTPRA    3'  AGAGCGGTATCTCTG       55079       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM321  PTPRA    3'  AGAGCGGTATCTCTG       55087       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
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                                GTCTCT TG    GCGAGA
                                   A _____
GAM321  PTPRA    3'  AGAGCGGTATCTCTG      11088      C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM321  RAD51L3  3'  CAAAACTCAGGTATGTCTCTGT 56065        C_____
                                ACAGAGACA    AGTTTTG
                                |||||||||    |||||||
                                TGTCTCTGT    TCAAAAC
                                     ATGGAC
GAM321  TBL2     3'  CAGAACTGTGTTCCATCA    24924    CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM321  TBL2     3'  CAGAACTGTGTTCCATCA    52178    CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM321  AGTRL2   5'  CAGAGCAAGAACTGTTC    17691    C     _
                                GA ACAGTTTT GCTCTG
                                || |||||||| ||||||
                                CT TGTCAAGA CGAGAC
                                  _      A
GAM321  CABP5    3'  AGAGCGGTATCTTTGCCA    39079    A    C  AGTTT
                                TG CAGAGA AC    TGCTCT
                                || |||||| ||    ||||||
                                AC GTTTCT TG    GCGAGA
                                 C    A _____
GAM321  CUL4A    5'  AGAGCAGCACCTCCATCA    13149    CA  ACACA  T
                                TGA  GAG    GT TTGCTCT
                                |||  |||    || |||||||
                                ACT  CTC    CA GACGAGA
                                  AC  _____  C
GAM321  DKFZp761O17121 3'  CAGACAGCCCCTGTGTCTCTGT 50136          TT_  C
           C                    GACAGAGACACAG   TTG TCTG
                                ||||||||||||   ||| ||||
                                CTGTCTCTGTGTC   GAC AGAC
                                     CCC  _
GAM321  FLJ10375 3'  CAGAGGCCTGTGTCTGTGCCA  36073    A  G      TTTTG
                                TG CA AGACACAG    CTCTG
                                || || ||||||||    |||||
                                AC GT TCTGTGTC    GAGAC
                                 C  G      CG___
GAM321  FLJ10738 5'  CAAAGCCAGCCCTCTGTCA   36527        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
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                                ACTGTCTC    CGAAAC
                                    CCGAC
GAM321  FLJ10803  3'  CAAAACAAAACTCTGTCA    36660       ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
                                ACTGTCTC    CAAAAC
                                    AAAA_
GAM321  FLJ10842  3'  AAAGTGTGCTCTGTCA     36723       A   G
                                TGACAGAG CACA TTT
                                |||||||| |||| |||
                                ACTGTCTC GTGT AAA
                                    _   G
GAM321  FLJ13153  3'  CAGAGCCCAGCATCCATCTCTG 45555       CACA_  TT
          TCA                     TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                     ACCTA   CC
GAM321  FLJ20035  3'  CAAACCTGCCATGTTCTGTCA  34395       A ___   T
                                TGACAGAG CA   CAG TTTG
                                |||||||| ||   ||| ||||
                                ACTGTCTT GT   GTC AAAC
                                    _ ACC   C
GAM321  FLJ22195  5'  CAGAGCAGAGGGAAGTCTCTGC 42800    A     ACAG
          CA                      TG CAGAGAC    TTTTGCTCTG
                                || |||||||    ||||||||||
                                AC GTCTCTG    GAGACGAGAC
                                 C      AAGG
GAM321  FLJ32191  5'  GAACTGCACCTCTGTCA     58411       ACA
                                TGACAGAG   CAGTTT
                                ||||||||   ||||||
                                ACTGTCTC   GTCAAG
                                    CAC
GAM321  KIAA1023  3'  CAAAGCTGTATCTGCTATCA   34255     C _   C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM321  KIAA1586  5'  AGTGTGATGTGTCTCTG     92326       GTT TG T
                                CAGAGACACA   T  C CT
                                ||||||||||   |  | ||
                                GTCTCTGTGT   A  G GA
                                     ___ GT T
GAM321  KIAA1754  3'  GACTAACGTCTCTGTCA     63236       AC_
                                TGACAGAGAC   AGTT
                                ||||||||||   ||||
                                ACTGTCTCTG   TCAG
                                     CAA
GAM321  LANCL2    3'  CAGAGTGCACTGCAGCTCTGTC 37995       ACA    TTT
          A                      TGACAGAG   CAGT   GCTCTG
                                ||||||||   ||||   ||||||
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                                ACTGTCTC  GTCA  TGAGAC
                                    GAC   CG_
GAM321  LIG-1    3'  CAGAGCAGGCCTGTCCATGCCA 63893    A  GAGAC   TT
                                TG CA    ACAG  TTGCTCTG
                                || ||    ||||  ||||||||
                                AC GT    TGTC  GACGAGAC
                                 C  ACC__   CG
GAM321  MGC5242  3'  AGAGTACATGTCTCTG     43823       CAGTTT
                                CAGAGACA     TGCTCT
                                ||||||||     ||||||
                                GTCTCTGT     ATGAGA
                                    AC____
GAM321  OSMR     3'  CAGAGCTGGCACCCTGTCA   14345      AGACA
                                TGACAG    CAGTTTTG
                                ||||||    ||||||||
                                ACTGTC    GTCGAGAC
                                   CCACG
GAM321  RAB21    3'  CAGAACAAAACTGTGGATC   30383    GA       C
                                GA  CACAGTTTTG TCTG
                                ||  |||||||||| ||||
                                CT  GTGTCAAAAC AGAC
                                 AG        A
GAM321  SPTLC2   3'  CAGAGCAAAACTGTGTCTC   16799
                                GAGACACAGTTTTGCTCTG
                                ||||||||||||||||||
                                CTCTGTGTCAAAACGAGAC

GAM321  TGIF2    3'  GAGTCATGCTCTGTCA     41454       A  CAGTTT  _
                                TGACAGAG CA     TG CTC
                                |||||||| ||     || |||
                                ACTGTCTC GT     AC GAG
                                    _  _______  T
GAM321  WBSCR23  5'  GCTGACTGTGTCTCCATCA   46765    CA       TT
                                TGA  GAGACACAGTT  GC
                                |||  ||||||||||  ||
                                ACT  CTCTGTGTCAG  CG
                                  AC         T_
GAM321  LOC115129 3'  GGCAAAACCCCGTCTCT    73235      ACA
                                AGAGAC   GTTTTGCT
                                ||||||   ||||||||
                                TCTCTG   CAAAACGG
                                   CCC
GAM321  LOC129198 3'  AGCAAGCTGTGCCTC      76117    A      T
                                GAG CACAGTTT GCT
                                ||| |||||||| |||
                                CTC GTGTCGAA CGA
                                  C       _
GAM321  LOC145231 3'  GGTGAAACTATGTCTCT    83293       C    TG
                                AGAGACA AGTTT  CT
                                ||||||| |||||  ||
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                                TCTCTGT TCAAA  GG
                                    A    GT
GAM321   LOC145483 3'  GAGCAAAACTCTGTCT     77243      C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                   C
GAM321   LOC146713 3'  GAGCAAAACTCCGTCT     83726     AC
                                AGAC  AGTTTTGCTC
                                ||||  ||||||||||
                                TCTG  TCAAAACGAG
                                  CC
GAM321   LOC149175 3'  CAGGGTGAAACCACGTCTCT  79208       ACA   TG
                                AGAGAC   GTTT  CTCTG
                                ||||||   ||||  |||||
                                TCTCTG   CAAA  GGGAC
                                    CAC    GT
GAM321   LOC150299 3'  CAGAACCTGCATCTTTGTCA  84968        CA  _
                                TGACAGAGA  CAG TTTTG
                                |||||||||  ||| |||||
                                ACTGTTTCT  GTC AAGAC
                                     AC   C
GAM321   LOC153277 3'  TAAAACTGTGCCTGTGCCA   85990    A  G  A
                                TG CA AG CACAGTTTTG
                                || || || ||||||||||
                                AC GT TC GTGTCAAAAT
                                 C  G  C
GAM321   LOC155179 3'  CAAAGCTGTATCTGCTATCA  81312     C  _  C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM321   LOC221074 3'  AAAGTGTGTCTCTTTCA     93177     C       G
                                TGA AGAGACACA TTT
                                ||| ||||||||| |||
                                ACT TCTCTGTGT AAA
                                  T       G
GAM321   LOC221103 5'  AGTTTATGTGTGCTCTGTCA  93244        _    GTTTT
                                TGACAGAG ACACA    GCT
                                |||||||| |||||    |||
                                ACTGTCTC TGTGT    TGA
                                    G    ATT__
GAM321   LOC255988 5'  CAGAGCCCAGCATCCATCTCTG 97608        CACA_  TT
           TCA                    TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                     ACCTA   CC
GAM322   ARCN1    3'  AGACTGCACTCTCTGTCA    7970         CA_
                                TGACAGAGA   CAGTTT
                                |||||||||   ||||||
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                                ACTGTCTCT   GTCAGA
                                     CAC
GAM322  CBFA2T2  3'  GAGCAAAACTCTGTCT      17466       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                   C
GAM322  CTLA4    3'  CAGAGCTGGGATGTTTCTGTCA 17807          CAGTTTT
                                TGACAGAGACA      GCTCTG
                                ||||||||||       ||||||
                                ACTGTCTTTGT      CGAGAC
                                      AGGGT__
GAM322  ITK      3'  CAGAACAGGAGTGATGTCTCTG 18674         _ G    C
                                CAGAGACA CA TTTTG TCTG
                                |||||||| || ||||| ||||
                                GTCTCTGT GT AGGAC AGAC
                                     A G    A
GAM322  LAMP2    3'  GGTGAAACCCCATCTCTATCA  25716    C    CACA    TG
                                TGA AGAGA    GTTT  CT
                                ||| |||||    ||||  ||
                                ACT TCTCT    CAAA  GG
                                  A    ACCC    GT
GAM322  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   40865        A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM322  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   52960        A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM322  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   52963        A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM322  PDGFRB   5'  CAGAGCCTGGAACTGTG     65969          __
                                CACAGTTTT  GCTCTG
                                |||||||||  ||||||
                                GTGTCAAGG  CGAGAC
                                     TC
GAM322  PTPRA    3'  AGAGCGGTATCTCTG       55079       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM322  PTPRA    3'  AGAGCGGTATCTCTG       55087       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
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                                GTCTCT TG    GCGAGA
                                   A _____
GAM322  PTPRA    3'  AGAGCGGTATCTCTG      11088      C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM322  RAD51L3  3'  CAAAACTCAGGTATGTCTCTGT 56065        C_____
                                ACAGAGACA    AGTTTTG
                                |||||||||    |||||||
                                TGTCTCTGT    TCAAAAC
                                     ATGGAC
GAM322  TBL2     3'  CAGAACTGTGTTCCATCA    52178    CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM322  TBL2     3'  CAGAACTGTGTTCCATCA    24924    CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM322  AGTRL2   5'  CAGAGCAAGAACTGTTC    17691    C     _
                                GA ACAGTTTT GCTCTG
                                || |||||||| ||||||
                                CT TGTCAAGA CGAGAC
                                  _      A
GAM322  CABP5    3'  AGAGCGGTATCTTTGCCA    39079    A    C  AGTTT
                                TG CAGAGA AC    TGCTCT
                                || |||||| ||    ||||||
                                AC GTTTCT TG    GCGAGA
                                  C    A _____
GAM322  CUL4A    5'  AGAGCAGCACCTCCATCA    13149    CA  ACACA  T
                                TGA  GAG    GT TTGCTCT
                                |||  |||    || |||||||
                                ACT  CTC    CA GACGAGA
                                  AC  _____  C
GAM322  DKFZp761O17121 3'  CAGACAGCCCCTGTGTCTCTGT 50136          TT_  C
           C                    GACAGAGACACAG   TTG TCTG
                                ||||||||||||   ||| ||||
                                CTGTCTCTGTGTC   GAC AGAC
                                     CCC  _
GAM322  FLJ10375 3'  CAGAGGCCTGTGTCTGTGCCA  36073    A  G      TTTTG
                                TG CA AGACACAG    CTCTG
                                || || ||||||||    |||||
                                AC GT TCTGTGTC    GAGAC
                                  C  G      CG___
GAM322  FLJ10738 5'  CAAAGCCAGCCCTCTGTCA   36527        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
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                                ACTGTCTC    CGAAAC
                                    CCGAC
GAM322  FLJ10803  3'  CAAAACAAAACTCTGTCA    36660       ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
                                ACTGTCTC    CAAAAC
                                    AAAA_
GAM322  FLJ10842  3'  AAAGTGTGCTCTGTCA     36723       A   G
                                TGACAGAG CACA TTT
                                |||||||| |||| |||
                                ACTGTCTC GTGT AAA
                                    _   G
GAM322  FLJ13153  3'  CAGAGCCCAGCATCCATCTCTG 45555       CACA_  TT
          TCA                     TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                     ACCTA   CC
GAM322  FLJ20035  3'  CAAACCTGCCATGTTCTGTCA  34395       A ___   T
                                TGACAGAG CA   CAG TTTG
                                |||||||| ||   ||| ||||
                                ACTGTCTT GT   GTC AAAC
                                    _ ACC   C
GAM322  FLJ22195  5'  CAGAGCAGAGGGAAGTCTCTGC 42800    A     ACAG
          CA                      TG CAGAGAC    TTTTGCTCTG
                                || |||||||    ||||||||||
                                AC GTCTCTG    GAGACGAGAC
                                 C      AAGG
GAM322  FLJ32191  5'  GAACTGCACCTCTGTCA     58411       ACA
                                TGACAGAG   CAGTTT
                                ||||||||   ||||||
                                ACTGTCTC   GTCAAG
                                    CAC
GAM322  KIAA1023  3'  CAAAGCTGTATCTGCTATCA   34255     C _   C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM322  KIAA1586  5'  AGTGTGATGTGTCTCTG     92326       GTT TG T
                                CAGAGACACA   T  C CT
                                ||||||||||   |  | ||
                                GTCTCTGTGT   A  G GA
                                     ___ GT T
GAM322  KIAA1754  3'  GACTAACGTCTCTGTCA     63236       AC_
                                TGACAGAGAC   AGTT
                                ||||||||||   ||||
                                ACTGTCTCTG   TCAG
                                     CAA
GAM322  LANCL2    3'  CAGAGTGCACTGCAGCTCTGTC 37995       ACA    TTT
          A                      TGACAGAG   CAGT   GCTCTG
                                ||||||||   ||||   ||||||
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                                ACTGTCTC  GTCA  TGAGAC
                                    GAC   CG_
GAM322  LIG-1    3'  CAGAGCAGGCCTGTCCATGCCA 63893    A  GAGAC   TT
                                TG CA    ACAG  TTGCTCTG
                                || ||    ||||  ||||||||
                                AC GT    TGTC  GACGAGAC
                                 C  ACC__   CG
GAM322  MGC5242  3'  AGAGTACATGTCTCTG     43823       CAGTTT
                                CAGAGACA     TGCTCT
                                ||||||||     ||||||
                                GTCTCTGT     ATGAGA
                                    AC____
GAM322  OSMR     3'  CAGAGCTGGCACCCTGTCA   14345      AGACA
                                TGACAG    CAGTTTTG
                                ||||||    ||||||||
                                ACTGTC    GTCGAGAC
                                   CCACG
GAM322  RAB21    3'  CAGAACAAAACTGTGGATC   30383    GA       C
                                GA  CACAGTTTTG TCTG
                                ||  |||||||||| ||||
                                CT  GTGTCAAAAC AGAC
                                 AG        A
GAM322  SPTLC2   3'  CAGAGCAAAACTGTGTCTC   16799
                                GAGACACAGTTTTGCTCTG
                                ||||||||||||||||||
                                CTCTGTGTCAAAACGAGAC

GAM322  TGIF2    3'  GAGTCATGCTCTGTCA     41454       A  CAGTTT  _
                                TGACAGAG CA     TG CTC
                                |||||||| ||     || |||
                                ACTGTCTC GT     AC GAG
                                    _  _______  T
GAM322  WBSCR23  5'  GCTGACTGTGTCTCCATCA   46765    CA       TT
                                TGA  GAGACACAGTT  GC
                                |||  ||||||||||  ||
                                ACT  CTCTGTGTCAG  CG
                                  AC         T_
GAM322  LOC115129 3'  GGCAAAACCCCGTCTCT    73235      ACA
                                AGAGAC   GTTTTGCT
                                ||||||   ||||||||
                                TCTCTG   CAAAACGG
                                   CCC
GAM322  LOC129198 3'  AGCAAGCTGTGCCTC      76117    A      T
                                GAG CACAGTTT GCT
                                ||| |||||||| |||
                                CTC GTGTCGAA CGA
                                  C       _
GAM322  LOC145231 3'  GGTGAAACTATGTCTCT    83293       C    TG
                                AGAGACA AGTTT  CT
                                ||||||| |||||  ||
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                                TCTCTGT TCAAA  GG
                                    A    GT
GAM322  LOC145483 3'  GAGCAAAACTCTGTCT     77243      C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                   C
GAM322  LOC146713 3'  GAGCAAAACTCCGTCT     83726     AC
                                AGAC  AGTTTTGCTC
                                ||||  ||||||||||
                                TCTG  TCAAAACGAG
                                  CC
GAM322  LOC149175 3'  CAGGGTGAAACCACGTCTCT  79208       ACA   TG
                                AGAGAC   GTTT  CTCTG
                                ||||||   ||||  |||||
                                TCTCTG   CAAA  GGGAC
                                    CAC    GT
GAM322  LOC150299 3'  CAGAACCTGCATCTTTGTCA  84968        CA  _
                                TGACAGAGA  CAG TTTTG
                                |||||||||  ||| |||||
                                ACTGTTTCT  GTC AAGAC
                                     AC   C
GAM322  LOC153277 3'  TAAAACTGTGCCTGTGCCA   85990    A  G  A
                                TG CA AG CACAGTTTTG
                                || || || ||||||||||
                                AC GT TC GTGTCAAAAT
                                 C  G  C
GAM322  LOC155179 3'  CAAAGCTGTATCTGCTATCA  81312     C  _  C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM322  LOC221074 3'  AAAGTGTGTCTCTTTCA     93177     C       G
                                TGA AGAGACACA TTT
                                ||| ||||||||| |||
                                ACT TCTCTGTGT AAA
                                  T       G
GAM322  LOC221103 5'  AGTTTATGTGTGCTCTGTCA  93244        _    GTTTT
                                TGACAGAG ACACA    GCT
                                |||||||| |||||    |||
                                ACTGTCTC TGTGT    TGA
                                     G    ATT__
GAM322  LOC255988 5'  CAGAGCCCAGCATCCATCTCTG 97608        CACA_  TT
          TCA                     TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                     ACCTA   CC
GAM323  GP9     3'  CAGAATAAACTGGCAGCTC   3918            ACGAA
                                GAGCTGCCAGTTTG    TCTG
                                ||||||||||||||    ||||
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                                CTCGACGGTCAAAT    AGAC
                                      A_____
GAM323  ITGBL1   5'  CCAAATCCTCGCAGGCAGCTC  16574       A  TT  C  ATC
                                GAGCTGCC GT  GA GA   TGG
                                |||||||| ||  || ||   |||
                                CTCGACGG CG  CT CT   ACC
                                    A  __  C  AA_
GAM323  LIF      3'  CCAGATCCCGTCCGGCAGCTT  9732        AGTTT   A_
                                GAGCTGCC    GACG  ATCTGG
                                ||||||||    ||||  ||||||
                                TTCGACGG    CTGC  TAGACC
                                    C_____   CC
GAM323  PLXNA2   3'  CCAGACCAGACACCTGGCAGC  47208       TT  ACGAA
                                GCTGCCAG  TG    TCTGG
                                ||||||||  ||    |||||
                                CGACGGTC  AC    AGACC
                                    C_  AGACC
GAM323  DKFZp547I224 3'  CAGATTCATAAGGCAAGT    39553    _   AGT   AC
                                GC TGCC   TTG  GAATCTG
                                || ||||   |||  |||||||
                                TG ACGG   AAT  CTTAGAC
                                 A   ____  A_
GAM323  HSJ1     3'  CCAGATTCAGAACTGGAGC    22128     G     GAC
                                GCT CCAGTTT   GAATCTGG
                                ||| |||||||   ||||||||
                                CGA GGTCAAG   CTTAGACC
                                  _      A__
GAM323  KIAA0321  5'  CAGAGAGACTGGCAGC      62389         TGACGAA
                                GCTGCCAGTT      TCTG
                                ||||||||||      ||||
                                CGACGGTCAG      AGAC
                                     AG_____
GAM323  KIAA1464  3'  CCAGAGCAAAAACTGGCACTC  68263     C       GACGAA
                                GAG TGCCAGTTT     TCTGG
                                ||| |||||||||     |||||
                                CTC ACGGTCAAA     AGACC
                                  _       AACG__
GAM323  P2RX1    3'  CCAGACCTCCTGAACCAAAAGC 67168      GCCA   GAC  A_
           TC                    GAGCT   GTTT   GA  TCTGG
                                |||||   ||||  ||  |||||
                                CTCGA   CAAG   CT  AGACC
                                   AAAC   TC_  CC
GAM323  PASK     3'  CCAGATTCATCAGGACCTGCTC 30715     TGCCAG    C
                                GAGC     TTTGA GAATCTGG
                                ||||     ||||| ||||||||
                                CTCG     GGACT CTTAGACC
                                  TCCA__     A
GAM323  LOC115051 3'  CGTGGGCCAACTGGCAGC    60038         ___ G
                                GCTGCCAGTT   T ACG
                                ||||||||||   | |||
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                                CGACGGTCAA   G TGC
                                     CCG G
GAM323  LOC145355 5'  CCAGATTCATCTCAGCAGCTT  77097        CAGTTT  C
                                GAGCTGC     GA GAATCTGG
                                |||||||     || ||||||||
                                TTCGACG     CT CTTAGACC
                                   ACT___  A
GAM323  LOC146220 3'  CCAGACCATCACTGGCAGCT   83627          TT  CGAA
                                AGCTGCCAGT  GA   TCTGG
                                ||||||||||  ||   |||||
                                TCGACGGTCA  CT   AGACC
                                     __  ACC_
GAM323  LOC157421 5'  CCAGATTCAGGAGCTAACATGC 86444    _  CC    GAC
                                GC TG  AGTTT   GAATCTGG
                                || ||  |||||   ||||||||
                                CG AC  TCGAG   CTTAGACC
                                 T  AA    GA_
GAM324  ADCY7    3'  GAGACAACTTGGACAACCTGTG 6639         _____ TG  __
           AG                    CTCACAGG   C  AGT  TCTT
                                |||||||   |  |||  ||||
                                GAGTGTCC   G  TCA  AGAG
                                    AACA GT   AC
GAM324  AES      3'  GAGGCAAGCTAAGGCCTGGAGG 6676       A     GAGTT
                                CCTC CAGGCT    CTTGCCTC
                                |||| ||||||    ||||||||
                                GGAG GTCCGG    GAACGGAG
                                  _     AATC_
GAM324  C21orf2  3'  GGGCCCTCAGCTGTGAGG    17016        G    TTCTT
                                CCTCACAG CTGAG    GCCT
                                |||||||| |||||    ||||
                                GGAGTGTC GACTC    CGGG
                                    _    C_____
GAM324  CASP3    3'  GAGCACTCAGCCCGGGAGG   52196      ACA       T
                                CCTC   GGCTGAGT CTT
                                ||||   |||||||| |||
                                GGAG   CCGACTCA GAG
                                  GGC       C
GAM324  CASP3    3'  GAGCACTCAGCCCGGGAGG   15102      ACA       T
                                CCTC   GGCTGAGT CTT
                                ||||   |||||||| |||
                                GGAG   CCGACTCA GAG
                                  GGC       C
GAM324  CELSR3   3'  GAGGACCCACCTGTGAGG    7400          C  A
                                CCTCACAGG TG GTTCTT
                                ||||||||| || ||||||
                                GGAGTGTCC AC CAGGAG
                                     _ C
GAM324  DMD      5'  CAGCCACTCAGCCAGTGA    14394      A       TC
                                TCAC GGCTGAGT  TTG
                                |||| ||||||||  |||
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                                AGTG CCGACTCA  GAC
                                  A       CC
GAM324  DMD     5'  CAGCCACTCAGCCAGTGA    14417     A       TC
                                TCAC GGCTGAGT  TTG
                                |||| ||||||||  |||
                                AGTG CCGACTCA  GAC
                                  A       CC
GAM324  DMD     5'  CAGCCACTCAGCCAGTGA    14424     A       TC
                                TCAC GGCTGAGT  TTG
                                |||| ||||||||  |||
                                AGTG CCGACTCA  GAC
                                  A       CC
GAM324  DYRK2   3'  AGGTTCTCTCAGCCTGGGA   21389    A       TTCTT
                                TC CAGGCTGAG    GCCT
                                || |||||||||    ||||
                                AG GTCCGACTC    TGGA
                                 G       TCT__
GAM324  DYRK2   3'  AGGTTCTCTCAGCCTGGGA   13125    A       TTCTT
                                TC CAGGCTGAG    GCCT
                                || |||||||||    ||||
                                AG GTCCGACTC    TGGA
                                 G       TCT__
GAM324  FHIT    5'  AAGACTTCAACTGTGAGG    8895        GC    T
                                CCTCACAG  TGAG TCTT
                                ||||||||  |||| ||||
                                GGAGTGTC  ACTT AGAA
                                    A_    C
GAM324  GPR56   3'  AGCAAGAACTCCTGGAG     19063     A   CTG       C
                                CTC CAGG   AGTTCTTGC T
                                ||| ||||   ||||||||| |
                                GAG GTCC   TCAAGAACG A
                                  _    ___       A
GAM324  HP      3'  GCAAGATTTCAGCCTGGAAG   17639    CA       T
                                CT  CAGGCTGAG TCTTGC
                                ||  ||||||||| ||||||
                                GA  GTCCGACTT AGAACG
                                 AG       T
GAM324  ITCH    5'  AAGTGACTCAAACTGTGAG    48947       GC     _
                                CTCACAG  TGAGTT CTT
                                |||||||  |||||| |||
                                GAGTGTC  ACTCAG GAA
                                    AA     T
GAM324  LAMC2   3'  AAGATTTTCCCAGTCTGTGA   38145        AGT___
                                TCACAGGCTG     TCTT
                                ||||||||||     ||||
                                AGTGTCTGAC     AGAA
                                      CCTTTT
GAM324  LPP     5'  AGACAAGATCGGCCTG      18743        GT    C
                                CAGGCTGA  TCTTG CT
                                ||||||||  ||||| ||
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                                GTCCGGCT  AGAAC GA
                                   __     A
GAM324  MASP1    3'  GCAATCTTTCAGCCTTGA    57472     C       TTC
                                TCA AGGCTGAG   TTGC
                                ||| ||||||||   ||||
                                AGT TCCGACTT   AACG
                                  _       TCT
GAM324  PDGFRB   3'  AGGCAAGAAAACTGCAGGG   65967     CA   GCTGAG
                                CCT  CAG     TTCTTGCCT
                                |||  |||     |||||||||
                                GGG  GTC     AAGAACGGA
                                  AC   AA____
GAM324  PMP2     3'  AGGCAAGAAAGAACCATGTG   10670     _  CTGAG
                                CACA GG     TTCTTGCCT
                                ||||  ||    |||||||||
                                GTGT CC     AAGAACGGA
                                  A  AAGA_
GAM324  RNMT     3'  GCTTGCTCAGCCATGAG     13722      CA       TCTT
                                CTCA  GGCTGAGT    GC
                                ||||  ||||||||    ||
                                GAGT  CCGACTCG    CG
                                  A_       TT__
GAM324  SULT1A3  5'  GGAACTCAGCCTGTGAG     12053
                                CTCACAGGCTGAGTTCT
                                |||||||||||||||||
                                GAGTGTCCGACTCAAGG

GAM324  TBL1X    3'  AAGATGGCCCAGCCCGTGGGG  18923       A     A  __
                                CCTCAC GGCTG GT  TCTT
                                |||||| ||||| ||  ||||
                                GGGGTG CCGAC CG  AGAA
                                   C     C  GT
GAM324  TNFAIP2  3'  GTTCCTTCTCAGCCTGAGAGG  20832      A        TTCTT
                                CCTC CAGGCTGAG     GC
                                |||| |||||||||     ||
                                GGAG GTCCGACTC     TG
                                  A        TTCCT
GAM324  TRPM1    5'  GAGACTCAGCCTGAGA      10059     A        T
                                TC CAGGCTGAGT CTT
                                || ||||||||||  |||
                                AG GTCCGACTCA GAG
                                 A        _
GAM324  ZNF91    5'  GGCCCAGCCTGTGTGG      12822     T        AGTTCTT
                                CC CACAGGCTG       GCC
                                || |||||||||       |||
                                GG GTGTCCGAC       CGG
                                 T        C_______
GAM324  acmsd    5'  CAGGGCAGCCAGTGA       56355      A     AGT
                                TCAC GGCTG   TCTTG
                                ||||  |||||   |||||
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                                AGTG CCGAC   GGGAC
                                  A    ___
GAM324  BICD2    5'  GAGGGCCCGGCCTGCGAG    70394     A      A
                                CTC CAGGCTG GTTCTT
                                ||| ||||||| ||||||
                                GAG GTCCGGC CGGGAG
                                  C      C
GAM324  C9orf14  5'  GAGGCAAGATTTTCCTG     86674      CT    T
                                CAGG  GAGT CTTGCCTC
                                ||||  |||| ||||||||
                                GTCC  TTTA GAACGGAG
                                  T_   _
GAM324  CPSF2    3'  GAGGCCTCCCCAGCCTGTGGG  61585           AGTTCTT
                                CTCACAGGCTG      GCCTC
                                ||||||||||       |||||
                                GGGTGTCCGAC      CGGAG
                                       CCCTC__
GAM324  CTCFL    3'  AGGCAAATGTGTACCTGTAAGG 82502     C     C  AG TC
                                CCT ACAGG TG  T  TTGCCT
                                ||| ||||| ||  |  ||||||
                                GGA TGTCC AT  G  AACGGA
                                  A    _  GT TA
GAM324  D2S448   3'  GAGGCAGCATTTCAGCTGTGAG 73523         G     TTC
           G                     CCTCACAG CTGAG   TTGCCTC
                                ||||||||| |||||   |||||||
                                GGAGTGTC GACTT   GACGGAG
                                     _    TAC
GAM324  DDM36    3'  GAGGCCCTTCCCACCCTGTGAG 40572          C  AGTTCTT
           G                     CCTCACAGG TG       GCCTC
                                |||||||||  ||       |||||
                                GGAGTGTCC AC       CGGAG
                                      C  CCTTCC_
GAM324  DKFZp434G171 5'  AGGCAGGCCAACCTGGAG    79429     A    C  A TT
                                CTC CAGG TG G  CTTGCCT
                                ||| |||| ||  |  |||||||
                                GAG GTCC AC C  GGACGGA
                                  _    A  _ __
GAM324  DKFZP434K1772 5'  AGGCCCCACCACCCAGCCTGTG 67708           A  TCTT__
           G                     TCACAGGCTG GT      GCCT
                                ||||||||||  ||      ||||
                                GGTGTCCGAC CA      CGGA
                                      C  CCACCC
GAM324  FLJ10688  3'  GAAGCAAAATAAACTCAGCC   36415         C___    C
                                GGCTGAGTT    TTGC TC
                                |||||||||    |||| ||
                                CCGACTCAA    AACG AG
                                      ATAA    A
GAM324  FLJ12960  3'  AGACAAAAGCTTTAACTGTGAG 44945         GCT    C   C
           G                     CCTCACAG   GAGTT TTG CT
                                ||||||||   ||||| ||| ||
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                                GGAGTGTC   TTCGA AAC GA
                                     AAT    A  A
GAM324  FLJ20487  3'  AGGCAAGTCTGCCACGAG    35245     ACA   T  GTT
                                CTC   GGC GA   CTTGCCT
                                |||   ||| ||   |||||||
                                GAG   CCG CT   GAACGGA
                                  CA_   T  ___
GAM324  FLJ20694  3'  GAGACAAGAACTGAGTT     35548      G       C
                                GGCT AGTTCTTG CTC
                                |||| |||||||| |||
                                TTGA TCAAGAAC GAG
                                  G       A
GAM324  FLJ22362  5'  GAGGCCTGACCAACCGCGAGG  43076      ACA  C  A   CTT
                                CCTC   GG TG GTT   GCCTC
                                ||||   || || |||   |||||
                                GGAG   CC AC CAG   CGGAG
                                  CG_  A  _   TC_
GAM324  ICB-1     3'  AAGTTACCAGCCTGTGAG    16756          A  T_
                                CTCACAGGCTG GT  CTT
                                ||||||||||| ||  |||
                                GAGTGTCCGAC CA  GAA
                                       _  TT
GAM324  KIAA0372  3'  GAAGCAAAGAAAAAGCTGTAAG 27664    C    G  GAG    _  C
                                CT ACAG CT   TTCTT GC TC
                                || |||| ||   ||||| || ||
                                GA TGTC GA   AAGAA CG AG
                                 A   _  AA_    A  A
GAM324  KIAA0557  3'  AGGCCGCCAGGCTGCGAGG   77987      A   G   A  TCTT
                                CCTC CAG CTG GT    GCCT
                                |||| ||| ||| ||    ||||
                                GGAG GTC GAC CG    CGGA
                                  C   G   _  C___
GAM324  KIAA0599  3'  GAGACAATTTCCCACTCACCTG 77179         C    TC____   C
           TGAGG                  CTCACAGG TGAGT     TTG CTC
                                |||||||| |||||     ||| |||
                                GAGTGTCC ACTCA     AAC GAG
                                     _    CCCTTT   A
GAM324  KIAA0601  3'  GAGGCAAGCAAGTGCTGTGA   62511       _  GAGTT
                                TCACAG GCT    CTTGCCTC
                                |||||| |||    ||||||||
                                AGTGTC TGA    GAACGGAG
                                   G   AC___
GAM324  KIAA0809  5'  AGGCAAGAACCTAGCCTCCGAG 80576      AC     A
           G                    CCTC  AGGCTG GTTCTTGCCT
                                ||||  |||||| ||||||||||
                                GGAG  TCCGAT CAAGAACGGA
                                  CC     C
GAM324  KIAA1468  5'  AACTCCCCAGCCTGCAGAG   91772     A_     ___
                                CTC  CAGGCT   GAGTT
                                |||  ||||||   |||||
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                                GAG  GTCCGA   CTCAA
                                  AC     CCC
GAM324  KIAA1904  3'  AGCTCAGCCCTGAGG      73477      CA
                                CCTCA  GGCTGAGTT
                                |||||  |||||||||
                                GGAGT  CCGACTCGA
                                   C_
GAM324  KIAA1956  3'  AGGCAAGAACATCCTGGAGG   78430     A   CTGA
                                CCTC CAGG    GTTCTTGCCT
                                |||| ||||    ||||||||||
                                GGAG GTCC    CAAGAACGGA
                                   _    TA__
GAM324  KRTHB2    3'  GTTGAACCCAAACTGTGAG    52287       GC  A    TT
                                CTCACAG  TG GTTC  GC
                                |||||||  || ||||  ||
                                GAGTGTC  AC CAAG  TG
                                    AA  C    T_
GAM324  MGC27382  3'  GAGATGGACTCAGCTCATGAGG 58453      CA        TTGC
                                CCTCA  GGCTGAGTTC    CTC
                                |||||  ||||||||||    |||
                                GGAGT  TCGACTCAGG    GAG
                                   AC         TA__
GAM324  MOST2     5'  AGACAAGAACTCCCTGAGG    39673      CA  CT       C
                                CCTCA  GG  GAGTTCTTG CT
                                |||||  ||  |||||||| ||
                                GGAGT  CC  CTCAAGAAC GA
                                   __  __        A
GAM324  NYD-SP26  5'  AGCAAGACCTGTGAG       52420        CTGAGT     C
                                CTCACAGG     TCTTGC T
                                ||||||||     |||||| |
                                GAGTGTCC     AGAACG A
                                    _______     A
GAM324  PGDS      3'  AGACAGCTACATCAGCCTGCCA 27162    CA      _  TC   C
           G                     CT  CAGGCTGA GT  TTG CT
                                ||  |||||||| ||  ||| ||
                                GA  GTCCGACT CA  GAC GA
                                 CC       A  TC   A
GAM324  PHYHIP    3'  GCAAACAGAGAGCCTGTGGG   28610          GAGTTC
                                CTCACAGGCT     TTGC
                                ||||||||||     ||||
                                GGGTGTCCGA     AACG
                                     GAGACA
GAM324  PP3501    3'  GAGACTCAGCCACAAGG     41370     CACA      T
                                CCT    GGCTGAGT CTT
                                |||    |||||||| |||
                                GGA    CCGACTCA GAG
                                  ACA_       _
GAM324  PPP1R1A   3'  GAGGCAAGAGCAGAGCCTGAGA 22147    A     GA
                                TC CAGGCT  GTTCTTGCCTC
                                || ||||||  ||||||||||
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                                AG GTCCGA  CGAGAACGGAG
                                 A     GA
GAM324  PRDM9    3'  AGGCAAGAAGAGTCCAGAAGG  39574     CACA   GAG
                                CCT   GGCT   TTCTTGCCT
                                |||   ||||  |||||||||
                                GGA   CTGA   AAGAACGGA
                                  AGAC   G__
GAM324  RNF8     3'  AAGGGCTCAGCCTGTGA     14212
                                TCACAGGCTGAGTTCTT
                                |||||||||||||||||
                                AGTGTCCGACTCGGGAA

GAM324  SUCLG2   3'  AGGCAAGAATCACTG       65607     GC   G
                                CAG  TGA TTCTTGCCT
                                |||  ||| |||||||||
                                GTC  ACT AAGAACGGA
                                  __   _
GAM324  SV2B     3'  GAACATCAGCCTGCAAG     29297    CA      _
                                CT  CAGGCTGA GTTC
                                ||  |||||||| ||||
                                GA  GTCCGACT CAAG
                                 AC       A
GAM324  TIP120B  3'  AGGCCCCCAGCCCAAGCTGTGA 72416        GC  A   CTT_
           GG                     CCTCACAG  TG GTT    GCCT
                                |||||||  || |||   ||||
                                GGAGTGTC  AC CGA    CGGA
                                     GA  C   CCCC
GAM324  TIX1     3'  AGGCAAGAATGCCCATGTAAGG 61737     C   __   TGA
                                CCT ACA  GGC   GTTCTTGCCT
                                ||| |||  |||   ||||||||||
                                GGA TGT  CCG   TAAGAACGGA
                                  A   AC   ___
GAM324  VPS39    3'  GAGACTCTGCTCAGGCCTGTGA 62845          _    ____
           GG                     CCTCACAGGC TGAGT    TCTT
                                |||||||||| |||||    ||||
                                GGAGTGTCCG ACTCG    AGAG
                                     G     TCTC
GAM324  ZNF17    5'  AGGCCCAGCCCTGTGAG     82384         _  AGTTCTT
                                CTCACAGG CTG      GCCT
                                |||||||| |||      ||||
                                GAGTGTCC GAC      CGGA
                                     C   C_______
GAM324  LOC120103 3'  GAGACCACTCAGCCTTGAG    74005      C       __
                                CTCA AGGCTGAGT  TCTT
                                |||| |||||||||  ||||
                                GAGT TCCGACTCA  AGAG
                                  _       CC
GAM324  LOC123096 3'  GAGGCACCATATCAGCCTGCGG 74202     A       GTTCT
           G                     CTC CAGGCTGA     TGCCTC
                                ||| ||||||||     ||||||
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                                GGG GTCCGACT    ACGGAG
                                  C       ATACC
GAM324   LOC123905 5'  GAGGACGCACTCAGCCTG    74249         TCTTG
                                CAGGCTGAGT    CCTC
                                ||||||||||    ||||
                                GTCCGACTCA    GGAG
                                     CGCA_
GAM324   LOC124989 5'  GAGGCAAGAACTATTGGGC   74385    G___
                                GCT   AGTTCTTGCCTC
                                |||   ||||||||||||
                                CGG   TCAAGAACGGAG
                                  GTTA
GAM324   LOC125704 5'  GAGGCAAGAAGGTGCTGCAGG 74409    CACA  TGAG
                                CCT   GGC   TTCTTGCCTC
                                |||   |||   ||||||||||
                                GGA   TCG   AAGAACGGAG
                                  CG__  TGG_
GAM324   LOC125929 3'  GAGGCTTACTCAGCCTGTGGG 75674          TCTT
                                CTCACAGGCTGAGT   GCCTC
                                ||||||||||||||   |||||
                                GGGTGTCCGACTCA   CGGAG
                                       TT__
GAM324   LOC145864 5'  GAGGCAAGGGAGGCCTGCCAGG 77556    CA    GAGT
                                CCT  CAGGCT   TCTTGCCTC
                                |||  ||||||   |||||||||
                                GGA  GTCCGG   GGAACGGAG
                                  CC    AG__
GAM324   LOC148085 3'  AGACAAAAATGTCAGGCCTGTG 84114        GA__  C  C
           AG                     CTCACAGGCT   GTT TTG CT
                                ||||||||||   ||| ||| ||
                                GAGTGTCCGG   TAA AAC GA
                                     ACTG  A  A
GAM324   LOC148356 3'  AGACAAAAATATGCCTGTGA  74565       TGA  C  C
                                TCACAGGC  GTT TTG CT
                                ||||||||  ||| ||| ||
                                AGTGTCCG  TAA AAC GA
                                    TA_  A  A
GAM324   LOC150279 3'  AGGCAAGGAATTGCCCTGAGG 79664     CA  TGAG
                                CCTCA GGC   TTCTTGCCT
                                |||||  |||  |||||||||
                                GGAGT  CCG   AGGAACGGA
                                  C_  TTA_
GAM324   LOC150299 3'  AAGTTTCTCAACCTGTGGG   84964       C   TT_
                                CTCACAGG TGAG  CTT
                                |||||||| ||||  |||
                                GGGTGTCC ACTC  GAA
                                    A   TTT
GAM324   LOC150372 5'  GAGAACCAGCCTGTGAGG    79800          A
                                CCTCACAGGCTG GTTCTT
                                |||||||||||| ||||||
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                                GGAGTGTCCGAC CAAGAG
                                          _
GAM324  LOC150837 5'  AGACAAGGCGAGCCTGTGA   80016        GA  T   C
                                TCACAGGCT  GT CTTG CT
                                |||||||||  || |||| ||
                                AGTGTCCGA  CG GAAC GA
                                     G_ _   A
GAM324  LOC150838 5'  AGACAAGGCGAGCCTGTGA   85123        GA  T   C
                                TCACAGGCT  GT CTTG CT
                                |||||||||  || |||| ||
                                AGTGTCCGA  CG GAAC GA
                                     G_ _   A
GAM324  LOC151878 3'  GCAAGACTTGTAAGG      80376    C    CTGAGT
                                CCT ACAGG     TCTTGC
                                ||| |||||     ||||||
                                GGA TGTTC     AGAACG
                                  A   _______
GAM324  LOC152271 3'  GAGACAGCTTCAGCCTGTGTAG 80519   _        TTC  C
                                CT CACAGGCTGAG   TTG CTC
                                || ||||||||||   ||| |||
                                GA GTGTCCGACTT   GAC GAG
                                 T         C__   A
GAM324  LOC157860 3'  GAGATAAACTCAGCCACAAGG  86568    CACA      ___
                                CCT   GGCTGAGT   TCTT
                                |||   ||||||||   ||||
                                GGA   CCGACTCA   AGAG
                                  ACA_       AAT
GAM324  LOC158292 5'  AAGCTGTTCAGCCTGGAG    86726    A       TT_
                                CTC CAGGCTGAG   CTT
                                ||| |||||||||   |||
                                GAG GTCCGACTT   GAA
                                  _       GTC
GAM324  LOC162137 5'  AGGCAAGGCGAGGCCCGCAGAG 87110    ACA_   GA  T
                                CTC   GGCT  GT CTTGCCT
                                |||   ||||  || |||||||
                                GAG   CCGG  CG GAACGGA
                                  ACGC   AG  _
GAM324  LOC197117 3'  GCCCTGAACTCAGCCTGGAGG  89719     A         TT_
                                CCTC CAGGCTGAGTTC   GC
                                |||| ||||||||||||   ||
                                GGAG GTCCGACTCAAG   CG
                                  _          TCC
GAM324  LOC199883 3'  AGACAAGAAAAATCCTGTGAG  89869       CTGAG     C
                                CTCACAGG     TTCTTG CT
                                ||||||||     |||||| ||
                                GAGTGTCC     AAGAAC GA
                                     TAAA_     A
GAM324  LOC200020 3'  AGACAAGAAAAATCCTGTGAG  89927       CTGAG     C
                                CTCACAGG     TTCTTG CT
                                ||||||||     |||||| ||
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                                GAGTGTCC    AAGAAC GA
                                    TAAA_     A
GAM324  LOC200862 5'  AGACAGGACCCTCAGCCTCGAG 90179     AC      T_    C
           G                     CCTC  AGGCTGAG  TCTTG CT
                                 ||||  ||||||||  ||||| ||
                                 GGAG  TCCGACTC  AGGAC GA
                                   C_      CC     A
GAM324  LOC202915 3'  GAGAGCCCACCTGTGAGG    90391        C  A
                                 CCTCACAGG TG GTTCTT
                                 |||||||||  || ||||||
                                 GGAGTGTCC AC CGAGAG
                                       _ C
GAM324  LOC219295 5'  GGCAAACTCGCCTGTGA     92994        T    CT
                                 TCACAGGC GAGTT  TGCC
                                 ||||||||  |||||  ||||
                                 AGTGTCCG CTCAA  ACGG
                                    _    __
GAM324  LOC219731 5'  AGACAAGGGAGGAGCCTGTGAG 93088         GAG     C
                                 CTCACAGGCT   TTCTTG CT
                                 ||||||||||   |||||| ||
                                 GAGTGTCCGA   GGGAAC GA
                                      GGA     A
GAM324  LOC221794 5'  AGCTTCAGCCTGTGTAG     93912    _       _
                                 CT CACAGGCTGA GTT
                                 || ||||||||||  |||
                                 GA GTGTCCGACT CGA
                                  T         T
GAM324  LOC256987 3'  GAGGACAGGACTCAGCCTGCAG 95947     CA          TG
           GG                     CCT  CAGGCTGAGTTCT  CCTC
                                  |||  ||||||||||||  ||||
                                  GGG  GTCCGACTCAGGA  GGAG
                                    AC           CA
GAM324  LOC257489 3'  AGGCAAGAATCACTG       65611     GC   G
                                  CAG  TGA TTCTTGCCT
                                  |||  ||| |||||||||
                                  GTC  ACT AAGAACGGA
                                     __   _
GAM324  LOC51015  5'  AAGTTCCTCAGCCTGTACGG   32117    TC        TT_
                                  CC  ACAGGCTGAG   CTT
                                  ||  ||||||||||   |||
                                  GG  TGTCCGACTC   GAA
                                   CA         CTT
GAM324  LOC90288  3'  GCAAGAAAATGCGCTTTAAGG  62096     CAC  _  TGAG
                                  CCT   AG GC    TTCTTGC
                                  |||   || ||    |||||||
                                  GGA   TC CG    AAGAACG
                                    ATT  G  TAA_
GAM324  LOC90906  3'  GAGGCAAGACCAAGCC      64299      GA  T
                                  GGCT  GT CTTGCCTC
                                  ||||  || ||||||||
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                                CCGA  CA GAACGGAG
                                  AC  _
GAM324  LOC91355  5'  AGACAAGGGGGACTGTGAGG  65710        G  GAG     C
                                CCTCACAG CT   TTCTTG CT
                                |||||||| ||   |||||| ||
                                GGAGTGTC GG   GGGAAC GA
                                    A ____     A
GAM324  LOC92080  3'  GACTCAGCCCTGAGG       68049       CA
                                CCTCA  GGCTGAGTT
                                |||||  |||||||||
                                GGAGT  CCGACTCAG
                                  C_
GAM325  ADH1B     3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM325  AHR       3'  ATCTCAGATGTTAAAATAAATG 7875        CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM325  FDFT1     3'  TAGGAAAGTGAAATG        15518            A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                                _
GAM325  JTB       3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM325  KLF4      3'  TCCCAGACAGTGGATATG     14891     CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM325  PHYH      3'  ACAGTAAAAGTGAAAT       20608           C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                     A
GAM325  PKD2      3'  TCCAGGTTGAAAGTGAAA     60096           CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM325  WRN       3'  GGGCAGTGAAAATGAAA      5098        C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
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                                AAAGT AAAGTGACGGG
                                   A
GAM325  ZNF216   3' ATCTGCACAGCAAAGTGAAA  20017        CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM325  CG012    5' CTCACTCTGAAAGTGAA    83218        CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM325  EIF2C2   3' ATCTTCTGAGAGTGAAAG   71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM325  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||         |||||||||
                                GTAAAG         CAGACTCTA
                                   AAACATTT_
GAM325  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM325  KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM325  KLHL6    3' ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM325  NIR3     3' GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM325  PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM325  PP35     3' ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
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                                AAAGT  CAGACTCTA
                                  __
GAM325  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148          TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM325  SEP15     3'  TCCTACAGTAAGAGTGAAA   14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM325  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM325  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM325  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM325  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226     A      GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _      ATTT
GAM325  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM326  ADSS      3'  GAACTTATTTCTGTCA      71759         CAC
                                TGACAGAGA   AGTTT
                                |||||||||   |||||
                                ACTGTCTTT   TCAAG
                                     AT_
GAM326  APM1      3'  CAGGAAGGACTGTGCTTCCGTC 16585     A  GA      AG T
          A                   TGAC GA  CACAGTTT  C CTG
                              |||| ||  ||||||||  | |||
                              ACTG CT  GTGTCAGG  G GAC
                                C  TC       AA _
GAM326  ARCN1     3'  AGACTGCACTCTCTGTCA    7970          CA_
                                TGACAGAGA   CAGTTT
                                |||||||||   ||||||
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                                ACTGTCTCT  GTCAGA
                                     CAC
GAM326  ASB2    5' AGAGCCCTGTGTCTGTCA   32354     GA    TTTA
                                TGACA GACACAG  GCTCT
                                ||||| |||||||  |||||
                                ACTGT CTGTGTC  CGAGA
                                   __    C___
GAM326  CADPS   3' AAACTACTGTCTTCTGTCA  65204      _  C_
                                TGACAGA GACA AGTTT
                                ||||||| |||| |||||
                                ACTGTCT CTGT TCAAA
                                    T  CA
GAM326  CTLA4   3' CAGAGCTGGGATGTTTCTGTCA 17807        CAG
                                TGACAGAGACA  TTTAGCTCTG
                                |||||||||||  ||||||||||
                                ACTGTCTTTGT  GGGTCGAGAC
                                      A__
GAM326  KNSL1   3' AAACCTCGTCTCTGTTA    15745        ACA
                                TGACAGAGAC  GTTT
                                ||||||||||  ||||
                                ATTGTCTCTG  CAAA
                                     CTC
GAM326  MRPS12  3' AAAGGGTGCCCCTCTGTCA  52962      A__  AG
                                TGACAGAG  CAC  TTT
                                ||||||||  |||  |||
                                ACTGTCTC  GTG  AAA
                                    CCC  GG
GAM326  MRPS12  3' AAAGGGTGCCCCTCTGTCA  52959      A__  AG
                                TGACAGAG  CAC  TTT
                                ||||||||  |||  |||
                                ACTGTCTC  GTG  AAA
                                    CCC  GG
GAM326  MRPS12  3' AAAGGGTGCCCCTCTGTCA  40864      A__  AG
                                TGACAGAG  CAC  TTT
                                ||||||||  |||  |||
                                ACTGTCTC  GTG  AAA
                                    CCC  GG
GAM326  PDGFRB  5' CAGAGCCTGGAACTGTG    65969      A__
                                CACAGTTT  GCTCTG
                                ||||||||  ||||||
                                GTGTCAAG  CGAGAC
                                    GTC
GAM326  PKIA    3' CAGACTTTTCCCTACCTCTGTC 22382      ACACAGTTT  C
          A                  TGACAGAG      AG TCTG
                             ||||||||      || ||||
                             ACTGTCTC      TC AGAC
                                CATCCCTTT  _
GAM326  TBL2    3' GAACTGTGTTCCATCA    24927    CA  A
                                TGA  GAG CACAGTTT
                                |||  ||| ||||||||
```

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                                ACT  CTT GTGTCAAG
                                  AC   _
GAM326  TBL2     3'  GAACTGTGTTCCATCA      52184     CA   A
                                TGA  GAG CACAGTTT
                                |||  ||| ||||||||
                                ACT  CTT GTGTCAAG
                                  AC   _
GAM326  DKFZp761O17121 3'  CAGACAGCCCCTGTGTCTCTGT 50136           TTTA  __
          C                      GACAGAGACACAG    GC  TCTG
                                ||||||||||||    ||  ||||
                                CTGTCTCTGTGTC    CG  AGAC
                                       CC__  AC
GAM326  FLJ10375  3'  CAGAGGCCTGTGTCTGTGCCA  36073    A  G      TTTAG
                                TG CA AGACACAG     CTCTG
                                || || ||||||||     |||||
                                AC GT TCTGTGTC     GAGAC
                                 C  G       CG___
GAM326  FLJ10842  3'  AAAGTGTGCTCTGTCA      36723        A    G
                                TGACAGAG CACA TTT
                                |||||||| |||| |||
                                ACTGTCTC GTGT AAA
                                     _   G
GAM326  FLJ13153  3'  CAGAGCCCAGCATCCATCTCTG 45555         CACA_   TA
          TCA                     TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                     ACCTA   CC
GAM326  FLJ13984  5'  GAGCCTCACTCTGTCA      45449        ACAC  TTTA
                                TGACAGAG    AG    GCTC
                                ||||||||    ||    ||||
                                ACTGTCTC    TC    CGAG
                                     AC__  _____
GAM326  FLJ20281  3'  CAGAGCTATGGGTTTCT     90980       A  GTT
                                AGAGAC CA   TAGCTCTG
                                ||||||  ||   ||||||||
                                TCTTTG GT   ATCGAGAC
                                   G  ___
GAM326  FLJ32191  5'  CTGAACTGCACCTCTGTCA    58410        ACA
                                TGACAGAG   CAGTTTAG
                                ||||||||   ||||||||
                                ACTGTCTC   GTCAAGTC
                                     CAC
GAM326  FPGT     3'  CAGAGGATGTTATGTCTTTGTC 13846          CAGTTTAG
          A                      TGACAGAGACA       CTCTG
                                ||||||||||        |||||
                                ACTGTTTCTGT       GAGAC
                                       ATTGTAG_
GAM326  H2AFZ    3'  AGTGGACTGTATCTCTGT    9171         C       G
                                ACAGAGA ACAGTTTA CT
                                ||||||| |||||||| ||
```

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                                TGTCTCT TGTCAGGT GA
                                   A      _
GAM326  KIAA0210  3'  CAGAGCTGTATATACCTGTCA  28470       AGACACAGTT
                                TGACAG        TAGCTCTG
                                ||||||        ||||||||
                                ACTGTC        GTCGAGAC
                                   CATATAT___
GAM326  KIAA0368  3'  CAGAACTAAACTGACCCTT   65163    ACA      C
                                GAG   CAGTTTAG TCTG
                                |||   |||||||| ||||
                                TTC   GTCAAATC AGAC
                                  CCA       A
GAM326  KIAA0628  3'  CAGAACCAAAAACGTTTCTGTC 28865          ACA   AGC__
          A                      TGACAGAGAC   GTTT    TCTG
                                ||||||||||   ||||    ||||
                                ACTGTCTTTG   CAAA    AGAC
                                      ___    AACCA
GAM326  KIAA0894  3'  CAGAGCTGAGATCACACCTCTG 29703    A    ACACAG_
          CA                     TG CAGAG      TTTAGCTCTG
                                || |||||      ||||||||||
                                AC GTCTC      GAGTCGAGAC
                                 _    CACACTA
GAM326  KIAA1198  3'  AAGCTGTGCTAATATCTCTGTC 63279        _______
                                GACAGAGA     CACAGTTT
                                ||||||||     ||||||||
                                CTGTCTCT     GTGTCGAA
                                     ATAATC
GAM326  KIAA1754  3'  GACTAACGTCTCTGTCA     63236          AC_
                                TGACAGAGAC   AGTT
                                ||||||||||   ||||
                                ACTGTCTCTG   TCAG
                                      CAA
GAM326  LANCL2    3'  CAGAGTGCACTGCAGCTCTGTC 37995        ACA   TTA
          A                      TGACAGAG   CAGT   GCTCTG
                                ||||||||   ||||   ||||||
                                ACTGTCTC   GTCA   TGAGAC
                                     GAC    CG_
GAM326  MBLL39    5'  CAGAGCTAAACAAGGTTT    19250     ACA
                                AGAC   GTTTAGCTCTG
                                ||||   ||||||||||||
                                TTTG   CAAATCGAGAC
                                  GAA
GAM326  MBLL39    5'  CAGAGCTAAACAAGGTTT    58607     ACA
                                AGAC   GTTTAGCTCTG
                                ||||   ||||||||||||
                                TTTG   CAAATCGAGAC
                                  GAA
GAM326  MGC5242   3'  AGAGTACATGTCTCTG     43823        CA  TTA
                                CAGAGACA  GT   GCTCT
                                ||||||||  ||   |||||
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                                GTCTCTGT  CA   TGAGA
                                    A_ ___
GAM326  OSMR     3'  AGAGCTGGCACCCTGTC     14344      CA  _
                                GACA  GT TTAGCTCT
                                |||| || ||||||||
                                CTGT  CA GGTCGAGA
                                  CC  C
GAM326  OSTF1    3'  AAACTTTGTCTTTGCCA     24723    A       C
                                TG CAGAGACA AGTTT
                                || |||||||| |||||
                                AC GTTTCTGT TCAAA
                                 C       T
GAM326  TGIF2    3'  GAGTCATGCTCTGTCA      41454         A  CAGTTTA
                                TGACAGAG CA      GCTC
                                |||||||| ||      ||||
                                ACTGTCTC GT      TGAG
                                    _  AC_____
GAM326  WBSCR23  5'  GCTGACTGTGTCTCCATCA   46765     CA         T
                                TGA  GAGACACAGTT AGC
                                |||  |||||||||||| |||
                                ACT  CTCTGTGTCAG TCG
                                  AC         _
GAM326  LOC129198 3'  AGCAAGCTGTGCCTC       76117     A       A
                                GAG CACAGTTT GCT
                                ||| |||||||| |||
                                CTC GTGTCGAA CGA
                                  C       _
GAM326  LOC146839 5'  TTAAACTGTCCTCTATCA    83817     C    AC
                                TGA AGAG  ACAGTTTAG
                                ||| ||||  |||||||||
                                ACT TCTC  TGTCAAATT
                                  A   C_
GAM326  LOC146961 5'  AGAGCCTGCCGCTCTGTCA   78217         ACA   TTTA
                                TGACAGAG   CAG    GCTCT
                                ||||||||   |||    |||||
                                ACTGTCTC   GTC    CGAGA
                                    GCC  _____
GAM326  LOC150299 3'  GAACCTGCATCTTTGTCA    84969         CA  _
                                TGACAGAGA  CAG TTT
                                |||||||||  ||| |||
                                ACTGTTTCT  GTC AAG
                                    AC   C
GAM326  LOC153277 3'  AAACTGTGCCTGTGCCA     85988    A  G  A
                                TG CA AG CACAGTTT
                                || || || ||||||||
                                AC GT TC GTGTCAAA
                                 C  G  C
GAM326  LOC157918 3'  CAGAGCTACGTTATCTC     86643      CAC  TT
                                GAGA   AG  TAGCTCTG
                                ||||   ||  ||||||||
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                                CTCT   TT  ATCGAGAC
                                  A__  GC
GAM326  LOC157919 5'  CAGAGCTACGTTATCTC     81632      CAC  TT
                                GAGA   AG  TAGCTCTG
                                ||||   ||  ||||||||
                                CTCT   TT  ATCGAGAC
                                  A__  GC
GAM326  LOC203339 3'  GAGCTCTGTCTCTGT       90545         CAGTTT
                                ACAGAGACA     AGCTC
                                |||||||||     |||||
                                TGTCTCTGT     TCGAG
                                     C_____
GAM326  LOC221074 3'  AAAGTGTGTCTCTTTCA     93177     C       G
                                TGA AGAGACACA TTT
                                ||| ||||||||| |||
                                ACT TCTCTGTGT AAA
                                  T       G
GAM326  LOC221103 5'  AGTTTATGTGTGCTCTGTCA  93244        _    GTTT
                                TGACAGAG ACACA    AGCT
                                |||||||| |||||    ||||
                                ACTGTCTC TGTGT    TTGA
                                     G    AT__
GAM326  LOC221641 5'  CAGGTTGGACTGTACCTCCTTC 93726     CA   AC       T
          A                      TGA  GAG  ACAGTTTAGC CTG
                                |||  |||  ||||||||||| |||
                                ACT  CTC  TGTCAGGTTG GAC
                                  TC   CA       _
GAM326  LOC255988 5'  CAGAGCCCAGCATCCATCTCTG 97608        CACA_   TA
          TCA                    TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                     ACCTA   CC
GAM326  LOC96597  3'  CAGGGCTACTGGGCCCCTGTCA 66907       AGACA    TT
                                TGACAG    CAGT  AGCTCTG
                                ||||||    ||||  |||||||
                                ACTGTC    GTCA  TCGGGAC
                                   CCCGG   __
GAM327  CDH6      3'  ACACTTGAACCTAATACC     17026         TG   T_
                                GGTATTAGGT  TCA  TGT
                                ||||||||||  |||  |||
                                CCATAATCCA  AGT  ACA
                                     __   TC
GAM327  SH3BP2    3'  CATAAATGCACAACCTAACAC  11597    A       _   G
                                GT TTAGGTTGT CATT TATG
                                || |||||||| |||| ||||
                                CA AATCCAACA GTAA ATAC
                                  C       C   _
GAM327  DKFZP434I116 5'  CATACAATGATCCAACAACCT  31322     ATTA  TT
                                AGGT    GG  GTCATTGTATG
                                ||||    ||  ||||||||||
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                                TCCA   CC  TAGTAACATAC
                                  ACAA  __
GAM327  LOC145844 3'  ATAGGTACAACCTAACAC    77537    A       CA
                                GT TTAGGTTGT  TTGT
                                || |||||||||  ||||
                                CA AATCCAACA  GATA
                                 C        TG
GAM327  LOC146952 5'  CATATGCCTCAACCTAACACTT 83863      A       TCATT
                                AGGT TTAGGTTG    GTATG
                                |||| ||||||||    |||||
                                TTCA AATCCAAC    TATAC
                                  C       TCCG_
GAM328  ACN       5'  AACACCCAAGCGCCCC      30367      AAA T  ATCA
                                GGGGC   G CT   GGTGTT
                                |||||   | ||   ||||||
                                CCCCG   C GA   CCACAA
                                  ____ _  AC__
GAM328  CLCN6     3'  AAACACCTCTCTCTCCCC    41379     CAA  TCTATC
                                GGGG   AG     AGGTGTTT
                                ||||   ||     ||||||||
                                CCCC   TC     TCCACAAA
                                  ___  TCTC__
GAM328  CLCN6     3'  AAACACCTCTCTCTCCCC    41394     CAA  TCTATC
                                GGGG   AG     AGGTGTTT
                                ||||   ||     ||||||||
                                CCCC   TC     TCCACAAA
                                  ___  TCTC__
GAM328  CLCN6     3'  AAACACCTCTCTCTCCCC    7072      CAA  TCTATC
                                GGGG   AG     AGGTGTTT
                                ||||   ||     ||||||||
                                CCCC   TC     TCCACAAA
                                  ___  TCTC__
GAM328  CNTN3     3'  TATCTGATCAGACTTTGCCCC  66698          _
                                GGGGCAAAGTCT ATCAGGTG
                                |||||||||||| ||||||||
                                CCCCGTTTCAGA TAGTCTAT
                                       C
GAM328  CSRP1     3'  CAAACACCTTTCCCTTTGCCCT 14526         TCTATC
                                GGGGCAAAG     AGGTGTTTG
                                |||||||||     |||||||||
                                TCCCGTTTC     TCCACAAAC
                                    CCTT__
GAM328  MYCL2     3'  TGATAGATTTTGCCCC      18191
                                GGGGCAAAGTCTATCA
                                ||||||||||||||||
                                CCCCGTTTTAGATAGT

GAM328  NTSR1     3'  ACTTCCTGCCAAACTTTGCCCC 10284         CTAT   T_
                                GGGGCAAAGT   CAGG  GT
                                ||||||||||   ||||  ||
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                                CCCCGTTTCA   GTCC  CA
                                     AACC   TT
GAM328  RAB26    3'  CAAGTGGACAGACTTTGCC   26822        A  AGG_
                                GGCAAAGTCT TC   TG
                                |||||||||| ||   ||
                                CCGTTTCAGA AG   AC
                                     C  GTGA
GAM328  STK10    3'  CCTGATAGACCTGCCCC    19984      AA
                                GGGGCA  GTCTATCAGG
                                ||||||  ||||||||||
                                CCCCGT  CAGATAGTCC
                                   C_
GAM328  TCTA     3'  CAAACACCCACATACCTGGCCC 42234    AAA  CTATCA
                                GGGC   GT    GGTGTTTG
                                ||||   ||    ||||||||
                                CCCG   CA    CCACAAAC
                                  GTC  TACAC_
GAM328  ELKS     3'  CAAACACTACAAACTTCATCCC 30502    CA   CTATCA
                                GGGG  AAGT    GGTGTTTG
                                ||||  ||||    ||||||||
                                CCCT  TTCA    TCACAAAC
                                  AC   AACA__
GAM328  FLJ23537 3'  CAAACACCTGCCTCTCTTCAAC 46023    GCA   TCTAT
           CC                   GGG   AAG    CAGGTGTTTG
                                |||   |||    ||||||||||
                                CCC   TTC    GTCCACAAAC
                                  AAC   TCTCC
GAM328  KIAA0433 5'  CAAACACCTCACCCCTGCCTC  30835      AAGTCTATC
                                GGGGCA       AGGTGTTTG
                                ||||||       |||||||||
                                CTCCGT       TCCACAAAC
                                   CCCCAC___
GAM328  KIAA0450 3'  CACTGCTGATGACTTTGCCCC  27620         T   __
                                GGGGCAAAGTC ATCAG  GTG
                                |||||||||| |||||  |||
                                CCCCGTTTCAG TAGTC  CAC
                                     _    GT
GAM328  LEAP-2   5'  AAATATAAACTTTGCCCC    53739         CTATCAG
                                GGGGCAAAGT     GTGTTT
                                ||||||||||     ||||||
                                CCCCGTTTCA     TATAAA
                                     AA_____
GAM328  LOC147077 3'  CACCTCCTAATAGACTTAGCCC 78249      A      C___
           C                    GGGGC AAGTCTAT   AGGTG
                                ||||| ||||||||   |||||
                                CCCCG TTCAGATA   TCCAC
                                  A       ATCC
GAM329  FLT1     3'  AACTAAAGCAAATTTTAGACCT 8909         CAGCCA__   C
           TTA                  TAAAGGTC       GCTT AGTT
                                ||||||||       |||| ||||
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                                ATTTCCAG       CGAA TCAA
                                    ATTTTAAA    A
GAM329  PDE6B    3'  AACTGAAGCCAACTGTGA    4268     _  CCA
                                TC CAG   GCTTCAGTT
                                || |||   |||||||||
                                AG GTC   CGAAGTCAA
                                 T   AAC
GAM329  PLCB4    3'  AACTGAAGCAGCAAACC     6254      CCA  CA
                                GGT   GC  GCTTCAGTT
                                |||   ||  |||||||||
                                CCA   CG  CGAAGTCAA
                                  AA_  A_
GAM329  SCN3A    5'  AACTGAAGCCAAGCCACATC   22626     CCA  CA_
                                GGT   GC   GCTTCAGTT
                                |||   ||   |||||||||
                                CTA   CG   CGAAGTCAA
                                  CAC  AAC
GAM329  GW112    3'  AACTGAAGCCAGCACTGG    21183     __  CA
                                CCA  GC  GCTTCAGTT
                                |||  ||  |||||||||
                                GGT  CG  CGAAGTCAA
                                  CA  AC
GAM329  KIAA0527 3'  AACTTCGAGGCCAGCTGAAGCC 95786     C_   CA    __
                                GGT  CAGC  GCTTC  AGTT
                                |||  ||||  |||||  ||||
                                CCG  GTCG  CGGAG  TCAA
                                  AA    AC    CT
GAM329  TADA3L   3'  CTGGCTGGCCTCTAA      55992     A   T
                                TTA AGG CCAGCCAG
                                ||| ||| ||||||||
                                AAT TCC GGTCGGTC
                                  C  _
GAM329  TADA3L   3'  CTGGCTGGCCTCTAA      56002     A   T
                                TTA AGG CCAGCCAG
                                ||| ||| ||||||||
                                AAT TCC GGTCGGTC
                                  C  _
GAM329  LOC115219 3'  ACCAGAGCTGGCCTTTAA    73290       GTCCA       CA
                                TTAAAG    GCCAGCTT  GT
                                ||||||    ||||||||  ||
                                AATTTC    CGGTCGAG  CA
                                    _____       AC
GAM329  LOC151199 5'  AGCTGGCTAAGCCTTTAA    80172        CC
                                TTAAAGGT  AGCCAGCT
                                ||||||||  ||||||||
                                AATTTCCG  TCGGTCGA
                                    AA
GAM329  LOC153684 5'  AACTGGTCATCGCTAAACCTTT 86080        CC   CAGCT
            AA                    TTAAAGGT  AGC    TCAGTT
                                ||||||||  |||    ||||||
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                                AATTTCCA  TCG    GGTCAA
                                    AA   CTACT
GAM330  ASB1     3'  GCTGTGCTGCTGCTGGTC    32268        _ T     A
                                GACCAGT GC GGCATA GC
                                ||||||| || ||||||| ||
                                CTGGTCG CG TCGTGT CG
                                   T _     _
GAM330  B3GAT1   3'  TTCAGAATATAGCATTGGTT   37834          GCATAAG
                                GACCAGTGCTG      CTGAA
                                ||||||||||       |||||
                                TTGGTTACGAT      GACTT
                                      ATAA___
GAM330  B3GAT1   3'  TTCAGAATATAGCATTGGTT   53982          GCATAAG
                                GACCAGTGCTG      CTGAA
                                ||||||||||       |||||
                                TTGGTTACGAT      GACTT
                                      ATAA___
GAM330  BLTR2    5'  TTCAGCTTGTGCTGTTTCCTGG 39045      T__  T
                                CCAG   GC GGCATAAGCTGAA
                                ||||   || ||||||||||||
                                GGTC   TG TCGTGTTCGACTT
                                  CTT  _
GAM330  C4B      3'  TGGCAGCAAAGTGTCAGTGTTG 5173       TG      AA_   AA
           G                     CCAG  CTGGCAT   GCTG
                                ||||  |||||||   ||||
                                GGTT  GACTGTG   CGAC
                                  GT      AAA    GGTT
GAM330  CAPN1    3'  TTCAGGGACTTGTGTACTGGTT 17752        GCTG      ___
                                GACCAGT    GCATAAG   CTGAA
                                |||||||    |||||||   |||||
                                TTGGTCA    TGTGTTC   GACTT
                                    ____      AGG
GAM330  CASP8AP2 3'  TTCAGCTTGTGCTAGTCAT   24005     _
                                GTG CTGGCATAAGCTGAA
                                ||| ||||||||||||||
                                TAC GATCGTGTTCGACTT
                                  T
GAM330  COL1A2   3'  TCAGATTCAGCATTTGTT    3613      C       CATAAG
                                GAC AGTGCTGG     CTGA
                                ||| ||||||||     ||||
                                TTG TTACGACT     GACT
                                  T       TA____
GAM330  COX7A2   5'  TTCAGTTGTGGCGGTTGCTGGT 8518         _  G    G
           C                     GACCAGTG CTG CATAA CTGAA
                                ||||||||| ||| ||||| |||||
                                CTGGTCGT GGC GTGTT GACTT
                                     T  G    _
GAM330  CRYGB    3'  TTAGCTTGTGTTTCTGG     94626      TGCT
                                CCAG    GGCATAAGCTGA
                                ||||    ||||||||||||
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                                GGTC   TTGTGTTCGATT
                                  T___
GAM330  CRYGB   3'  TTAGCTTGTGTTTCTGG    17799     TGCT
                                CCAG   GGCATAAGCTGA
                                ||||   ||||||||||||
                                GGTC   TTGTGTTCGATT
                                  T___
GAM330  CSE1L   3'  TTCAGTGTATGGCGTTGGTT  61859        TGG   A
                                GACCAGTGC  CATA GCTGAA
                                |||||||||  |||| ||||||
                                TTGGTTGCG  GTAT TGACTT
                                     ___   G
GAM330  CUL4B   3'  GAGATTCTGTGTCATGCTGGTT 13141       C     AGCTGAA
                                GACCAGTG TGGCATA
                                |||||||| |||||||
                                TTGGTCGT ACTGTGT
                                    _     CTTAGAGT
GAM330  CXCL6   3'  TTCCTGTGTGTCATGTTGGTT  11466     GT C     AGCT
                                GACCA  G TGGCATA   GAA
                                |||||  | |||||||   |||
                                TTGGT  T ACTGTGT   CTT
                                   TG _     GTC_
GAM330  DUSP11   5'  TTTGGCCGGCTTGGCATTGG  13134       _ ATAA  TG
                                CCAGTGCTG GC   GC  AA
                                |||||||| ||   ||  ||
                                GGTTACGGT CG   CG  TT
                                     T  GC__  GT
GAM330  DUSP4   5'  TGAGCTTGTCGGCGCTGGT   54057         TA   GAA
                                ACCAGTGCTGGCA  AGCT
                                ||||||||||||  ||||
                                TGGTCGCGGCTGT  TCGA
                                       __   GTT
GAM330  DYRK1A   3'  TTCAGATGTTGGTCTTGGTC  55208      T  TG   AAG
                                GACCAG GC  GCAT   CTGAA
                                ||||||  ||  ||||   |||||
                                CTGGTT TG  TGTA   GACTT
                                   C  GT   ___
GAM330  DYRK1A   3'  TTCAGATGTTGGTCTTGGTC  55251      T  TG   AAG
                                GACCAG GC  GCAT   CTGAA
                                ||||||  ||  ||||   |||||
                                CTGGTT TG  TGTA   GACTT
                                   C  GT   ___
GAM330  DYRK1A   3'  TTCAGATGTTGGTCTTGGTC  7357       T  TG   AAG
                                GACCAG GC  GCAT   CTGAA
                                ||||||  ||  ||||   |||||
                                CTGGTT TG  TGTA   GACTT
                                   C  GT   ___
GAM330  EFNB2   3'  TTTGGTTTATGCGGTGCTG   14581    TG  G     TG
                                CAG  CTG CATAAGC  AA
                                |||  ||| |||||||  ||
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                                GTC  GGC GTATTTG  TT
                                  GT  _     GT
GAM330  ESRRG    3'  TTTATGTTGTGTGCCAGTCTGG 66398       T      _  _
              TC                  GACCAG GCTGGCATA AGC TGAA
                                  |||||| ||||||||| ||| ||||
                                  CTGGTC TGACCGTGT TTG ATTT
                                     _       G   T
GAM330  ETV3     3'  TTTGGTTTATTTGGTTGGTT   17883      GT  TG C     TG
                                  GACCA  GC  G ATAAGC  AA
                                  |||||  ||  | ||||||  ||
                                  TTGGT  TG  T TATTTG  TT
                                     __ GT _     GT
GAM330  FGF5     3'  TTCAGCTGAATTATATTGGTC  15551        C   CATA
                                  GACCAGTG TGG    AGCTGAA
                                  |||||||| |||    |||||||
                                  CTGGTTAT ATT    TCGACTT
                                       _  AAG_
GAM330  FGF5     3'  TTCAGCTGAATTATATTGGTC  52496        C   CATA
                                  GACCAGTG TGG    AGCTGAA
                                  |||||||| |||    |||||||
                                  CTGGTTAT ATT    TCGACTT
                                       _  AAG_
GAM330  FMOD     3'  TTTGGCTTGATGGTTTGGTT   8934       T   GCA    TG
                                  GACCAG GCTG   TAAGC  AA
                                  |||||| ||||   |||||  ||
                                  TTGGTT TGGT   GTTCG  TT
                                     _   A__    GT
GAM330  FOXG1B   3'  TCAGTTTGTGTTGTGTAT    17902     _
                                  GTGC TGGCATAAGCTGA
                                  |||| ||||||||||||
                                  TATG GTTGTGTTTGACT
                                    T
GAM330  GCH1     3'  TTCAGTGTGTGTGCGTTGGTT  3862         TG    A
                                  GACCAGTGC  GCATA GCTGAA
                                  |||||||||  ||||| ||||||
                                  TTGGTTGCG  TGTGT TGACTT
                                       __    G
GAM330  GCK      3'  TTCAGCTCCCATAGCGCTGG   3872         GCATA
                                  CCAGTGCTG    AGCTGAA
                                  |||||||||    |||||||
                                  GGTCGCGAT    TCGACTT
                                       ACCC_
GAM330  GCK      3'  TTCAGCTCCCATAGCGCTGG   53174        GCATA
                                  CCAGTGCTG    AGCTGAA
                                  |||||||||    |||||||
                                  GGTCGCGAT    TCGACTT
                                       ACCC_
GAM330  GCK      3'  TTCAGCTCCCATAGCGCTGG   53180        GCATA
                                  CCAGTGCTG    AGCTGAA
                                  |||||||||    |||||||
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                                GGTCGCGAT    TCGACTT
                                     ACCC_
GAM330  GLI3    3'  TTCAGTTTTGAATCAGTATTG  3912         CAT_
                                CAGTGCTGG   AAGCTGAA
                                |||||||||   ||||||||
                                GTTATGACT   TTTGACTT
                                     AAGT
GAM330  GPR85   3'  TTTACAAATGCTAGATATTGGT 38582        _     AAGCTGAA
          C                      GACCAGTG CTGGCAT
                                |||||||| |||||||
                                CTGGTTAT GATCGTA
                                     A      AACATTT
GAM330  H3F3B   5'  TTCGTTGGGCGGTGCTGGTT   18026      TG   G ATA   T
                                GACCAG  CTG C   AGC GAA
                                ||||||  ||| |   ||| |||
                                TTGGTC  GGC G   TTG CTT
                                   GT   _ GG_   _
GAM330  HRASLS  5'  TTCAGCGTGGCGGCGCTGGT   39855        G   AA
                                ACCAGTGCTG CAT  GCTGAA
                                ||||||||||| |||  ||||||
                                TGGTCGCGGC GTG  CGACTT
                                     G   __
GAM330  HYOU1   3'  TTCAGTAGCTGTTGATGCTGGT 59653        CT    TAA
          T                     GACCAGTG  GGCA   GCTGAA
                                ||||||||  ||||   ||||||
                                TTGGTCGT  TTGT   TGACTT
                                     AG    CGA
GAM330  JRK     3'  GCCCAGTGTCAGCATGGTC   86529      G       AA_
                                GACCA TGCTGGCAT   GC
                                ||||| |||||||||   ||
                                CTGGT ACGACTGTG   CG
                                   _       ACC
GAM330  KCNJ1   5'  TCAGCTTGGGGCTTGGTC    4027       T   GGCA
                                GACCAG GCT    TAAGCTGA
                                |||||| |||    ||||||||
                                CTGGTT CGG    GTTCGACT
                                   _   G___
GAM330  KLF8    3'  TTTGGTTTTCAGACAGTGCTGG 23407      TG   GCAT_   TG
          T                     ACCAG  CTG    AAGC  AA
                                |||||  |||    ||||  ||
                                TGGTC  GAC    TTTG  TT
                                   GT   AGACT    GT
GAM330  MEN1    5'  AGTTGTTAGTGTTGGTT    93367       TG     TAA
                                GACCAG  CTGGCA   GCT
                                ||||||  ||||||   |||
                                TTGGTT  GATTGT   TGA
                                   GT     ___
GAM330  MPZ     3'  TCAGTATAGCATTGGTT     4999          GCATAA
                                GACCAGTGCTG     GCTGA
                                ||||||||||      |||||
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                                TTGGTTACGAT     TGACT
                                      A_____
GAM330  MTNR1A   3'  TTCAGCTGGCAGAGTTAGCATT 19893          ATA___
             GG                   CCAGTGCTGGC     AGCTGAA
                                  ||||||||||      |||||||
                                  GGTTACGATTG     TCGACTT
                                        AGACGG
GAM330  MYCBP    3'  TTAGGAATGATGGCACTGGTT  24697         GG   AAG
                                  GACCAGTGCT  CAT   CTGA
                                  ||||||||||  |||   ||||
                                  TTGGTCACGG  GTA   GATT
                                        TA   AG_
GAM330  NAV2     3'  TTTGGTCCTGCTCAGTTTTGGT 60163       T   _   TAA  TG
             T                    GACCAG GCTG GCA   GC  AA
                                  ||||||  |||| |||   ||  ||
                                  TTGGTT TGAC CGT   TG  TT
                                     T    T   CC_  GT
GAM330  NCAM2    3'  TTTAGTTTATGTTTGTCTG   15807     T  TG
                                  CAG GC  GCATAAGCTGAA
                                  |||  ||  ||||||||||||
                                  GTC TG  TGTATTTGATTT
                                    _  TT
GAM330  NEURL    3'  TTTGGTTTGTGGTTTTGG    14868     T  TGG      TG
                                  CCAG GC   CATAAGC  AA
                                  ||||  ||   |||||||  ||
                                  GGTT TG   GTGTTTG  TT
                                    T  ____       GT
GAM330  NRG1     5'  TTCAGTTTGGGCTACTGGTT   25652       GCT   A
                                  GACCAGT   GGC TAAGCTGAA
                                  |||||||   |||  |||||||||
                                  TTGGTCA   TCG GTTTGACTT
                                      ____   G
GAM330  NUP98    3'  TGGTTTGGTCCCTGGTT     32864       TGCT   A    TG
                                  GACCAG    GGC TAAGC  A
                                  ||||||    |||  |||||  |
                                  TTGGTC    CTG GTTTG  T
                                     C____   _     GT
GAM330  OLFM1    3'  TTCAGTTTATGCGATGATTG   26557     GCTG
                                  CAGT    GCATAAGCTGAA
                                  ||||    ||||||||||||
                                  GTTA    CGTATTTGACTT
                                    GTAG
GAM330  PCDHGA11 3'  TTCAACTATGCTGGTTTGGTT  49456       T  TG    A C
                                  GACCAG GC  GCATA G TGAA
                                  ||||||  ||  |||||  |  ||||
                                  TTGGTT TG  CGTAT C ACTT
                                     _  GT    _ A
GAM330  PCSK1    3'  TGGCTTGAAGTATGGTT     4777       G   GGCA    TG
                                  GACCA TGCT    TAAGC  A
                                  |||||  ||||   |||||  |
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                                TTGGT ATGA   GTTCG  T
                                  _   A___    GT
GAM330  PER2    3'  TGGCTTCTGGTGTGGTC    43049     G  TG CAT   TG
                                GACCA TGC  G   AAGC  A
                                ||||| |||  |  ||||  |
                                CTGGT GTG  C   TTCG  T
                                  _  GT ___   GT
GAM330  PER2    3'  TTCAGAAAATTTAATATTGGTC 43050       C   CATAAG
                                GACCAGTG TGG     CTGAA
                                |||||||| |||     |||||
                                CTGGTTAT ATT     GACTT
                                    A  TAAAA_
GAM330  PIGH    3'  TTCAGAAGGCCAGCATTG    15880         ATAAG
                                CAGTGCTGGC    CTGAA
                                ||||||||||    |||||
                                GTTACGACCG    GACTT
                                     GAA__
GAM330  PIGN    3'  TCAGCTTTCAGCACTGGTT   24673          CAT     A
                                GACCAGTGCTGG   AAGCTGA
                                ||||||||||||   |||||||
                                TTGGTCACGACT   TTCGACT
                                       ___      A
GAM330  PPP2R5E  3'  TTCAGTACCTGACCAGTATTAG 20730    C      _  TAA
          TT                     GAC AGTGCTGG CA   GCTGAA
                                ||| |||||||| ||   ||||||
                                TTG TTATGACC GT   TGACTT
                                  A       A  CCA
GAM330  PRPS2   3'  GCAGTGCTTGTATTGGTT    10903         T    AA
                                GACCAGTGC GGCAT  GC
                                |||||||||  |||||  ||
                                TTGGTTATG TCGTG  CG
                                     T    A_
GAM330  PTPRK   3'  TTCAGCCTGTGGCCCAGCACTG 11125          __   A
          GTC                     GACCAGTGCTGG  CATA GCTGAA
                                ||||||||||||  ||||  ||||||
                                CTGGTCACGACC  GTGT CGACTT
                                      CG   C
GAM330  PTX3    3'  TCAGTTTAATGCTGTGT     11144   TG T    _
                                G  C GGCAT AAGCTGA
                                |  | |||||  |||||||
                                T  G TCGTA TTTGACT
                                 GT _    A
GAM330  QPCT    3'  TTTAGTTTAGGATAATTGGTT  24837       GCTGGCA
                                GACCAGT      TAAGCTGAA
                                |||||||      |||||||||
                                TTGGTTA      ATTTGATTT
                                   ATAGG__
GAM330  RAB6A   3'  TCAGGCTGGTTTTGGTT     11199       T  TG  ATAAG
                                GACCAG GC  GC    CTGA
                                ||||||  ||  ||    ||||
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                                TTGGTT TG  CG    GACT
                                   T  GT  _____
GAM330  RAD18    3'  TTTGGTTTGGTTTGGTTTGGTT 39399      T  TG CA    TG
                                GACCAG GC  G  TAAGC  AA
                                |||||| ||  |  |||||  ||
                                TTGGTT TG  T  GTTTG  TT
                                   _  GT TG    GT
GAM330  RAD50    3'  TTCAGTCACATGGCATGGTT   56010      G    GCATAA
                                GACCA TGCTG     GCTGAA
                                ||||| |||||     ||||||
                                TTGGT ACGGT     TGACTT
                                   _    ACAC__
GAM330  RAD50    3'  TTCAGTCACATGGCATGGTT   19196      G    GCATAA
                                GACCA TGCTG     GCTGAA
                                ||||| |||||     ||||||
                                TTGGT ACGGT     TGACTT
                                   _    ACAC__
GAM330  RALBP1   3'  TTACAAATGTCTCAGCATTGGT 22300          __   AAGCTGAA
           T                     GACCAGTGCTG  GCAT
                                ||||||||||  ||||
                                TTGGTTACGAC  TGTA
                                      TC    AACATT
GAM330  RANBP2L1 3'  TTTGGTTACACAGAACATTGGT 17317        __  GCATA   TG
           T                     GACCAGTG  CTG    AGC  AA
                                |||||||  |||    |||  ||
                                TTGGTTAC  GAC    TTG  TT
                                     AA   ACA__   GT
GAM330  RB1      3'  TTTAAGTCAGTATGGTC     90917      G      A
                                GACCA TGCTGGC TAAG
                                ||||| ||||||| ||||
                                CTGGT ATGACTG ATTT
                                   _      A
GAM330  RDS      3'  TTTGGACACCCTGTCAGACGTT 4367       _     TAAG__ TG
              GGTC                  CCAGTG CTGGCA     C  AA
                                |||||| ||||||     |  ||
                                GGTTGC GACTGT     G  TT
                                   A     CCCACA GT
GAM330  SERPINB9 3'  TTCAGTGCCACTTAGTATTG   14772        CATAA
                                CAGTGCTGG    GCTGAA
                                |||||||||    ||||||
                                GTTATGATT    TGACTT
                                     CACCG
GAM330  SIAT7D   3'  TGACCTTGTGCCAGTCCTGGTC 26950       TG        CTGAA
                                GACCAG  CTGGCATAAG
                                ||||||  ||||||||||
                                CTGGTC  GACCGTGTTC
                                   CT        CAGT
GAM330  SLC19A2  3'  TTTGGTTTTCATGTTGGCACTG 68983    C     TG   __   TG
              CTC                   GA CAGTGC  GCAT  AAGC  AA
                                || ||||||  ||||  ||||  ||
```

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                                CT GTCACG  TGTA  TTTG  TT
                                 C     GT    CT    GT
GAM330  SLC5A1   3'  CGGGTGTCAGTGTGGTT     4428       G       AAG
                                GACCA TGCTGGCAT   CTG
                                ||||| |||||||||   |||
                                TTGGT GTGACTGTG   GGC
                                  _       ___
GAM330  SMURF1   3'  TTTAGCCTTTGGCTTTGGTC   92462       T  TG CATAA
                                GACCAG GC  G    GCTGAA
                                |||||| ||  |    ||||||
                                CTGGTT CG  T    CGATTT
                                   T  GT TC___
GAM330  SPAP1    3'  TTCAGCGCTTGATATTGGTC   47775        CT_   ATAA
                                GACCAGTG   GGC    GCTGAA
                                ||||||||   |||    ||||||
                                CTGGTTAT   TCG    CGACTT
                                     AGT   ____
GAM330  SRGAP1   3'  TTGGAGTATAGCCAGTGTTGGT 72268       TG    _   AG TG A
            C                    GACCAG  CTGGC ATA  C  A
                                ||||||  ||||| |||  |  |
                                CTGGTT  GACCG TAT  G  T
                                   GT    A   GA GT
GAM330  STAU2    3'  TTCTGTTGCTAGTATTG     26911          TAA  T
                                CAGTGCTGGCA   GC GAA
                                ||||||||||   || |||
                                GTTATGATCGT   TG CTT
                                      ___  T
GAM330  STK24    3'  TTTGGAATCGTGCCACTGCTGG 13119       GC     AAG_ TG
            TC                    GACCAGT  TGGCAT    C  AA
                                |||||||  ||||||   |  ||
                                CTGGTCG  ACCGTG   G  TT
                                   TC     CTAA GT
GAM330  TAF7     3'  TCAGTCTTCAGACTGGTC    18913       G    CATAA
                                GACCAGT CTGG    GCTGA
                                ||||||| ||||    |||||
                                CTGGTCA GACT    TGACT
                                   _   TC___
GAM330  TCF7     3'  TTTAGTTCCTACTTTAGCCACT 12165       _   CA __
            GGTT                   CCAGTG CTGG  TA  AGCTGAA
                                |||||| ||||  ||  |||||||
                                GGTCAC GATT  AT  TTGATTT
                                   C   TC  CC
GAM330  TEX15    3'  TGGTTTATGTTTGGTT     48391       TGCTG       TG
                                GACCAG    GCATAAGC  A
                                ||||||    ||||||||  |
                                TTGGTT    TGTATTTG  T
                                   _____      GT
GAM330  TIA1     3'  TTCAGCTTGTGCACAATTCTG  41852     TGC  _
                                CAG   TG GCATAAGCTGAA
                                |||   || ||||||||||||
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                                GTC   AC CGTGTTCGACTT
                                  TTA  A
GAM330  TIA1     3'  TTCAGCTTGTGCACAATTCTG  42249     TGC  _
                                CAG   TG GCATAAGCTGAA
                                |||   || ||||||||||||
                                GTC   AC CGTGTTCGACTT
                                  TTA  A
GAM330  TIMELESS 3'  TCAGCAGCAGTATTGG      14053         G ATAA
                                CCAGTGCTG C    GCTGA
                                |||||||||  |    |||||
                                GGTTATGAC G    CGACT
                                     _ A___
GAM330  TRPM7    3'  TTCAGTGATGATATCACTGGTT 62132         C  G   AA
                                GACCAGTG TG CAT  GCTGAA
                                |||||||| || |||  ||||||
                                TTGGTCAC AT GTA  TGACTT
                                     T  A   G_
GAM330  TRPS1    3'  TTTGGTTTTTCAGTACTG    26088         CAT    TG
                                CAGTGCTGG   AAGC  AA
                                |||||||||   ||||  ||
                                GTCATGACT   TTTG  TT
                                     T__    GT
GAM330  TXNRD1   3'  TTTAGTTTATTGTGTGCTGGTC 12463        TG TG  _
                                GACCAG  C  GCA TAAGCTGAA
                                ||||||  |  ||| |||||||||
                                CTGGTC  G  TGT ATTTGATTT
                                   GT __   T
GAM330  UBL3     3'  TTCAAATGGTCAGCGTTG    23035          ATAAGC
                                CAGTGCTGGC     TGAA
                                ||||||||||     ||||
                                GTTGCGACTG     ACTT
                                     GTAA__
GAM330  USP6     3'  TGTGATTTGTGTTATACTGGTT 91150         C        CTGAA
                                GACCAGTG TGGCATAAG
                                |||||||| |||||||||
                                TTGGTCAT ATTGTGTTT
                                     _       AGTGTG
GAM330  VDR      3'  TTTAGCTGCAGAACTGTATTGG 4576          TGGCATA_
           TC                     GACCAGTGC       AGCTGAA
                                |||||||||       |||||||
                                CTGGTTATG       TCGATTT
                                     TCAAGACG
GAM330  YES1     3'  TTCATGCAAGTTGGCAGTGGTT 18359       G   TG  ATAA  _
                                GACCA TGC  GC    GC TGAA
                                ||||| |||  ||    || ||||
                                TTGGT ACG  TG    CG ACTT
                                   G   GT  AA__  T
GAM330  ZNF265   3'  TTAGTTTGTTTTCTGGTT    18399       TGCT    TA
                                GACCAG   GGCA  AGCTGA
                                ||||||   ||||  ||||||
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                                TTGGTC   TTGT  TTGATT
                                   TT__   __
GAM330  ACAS2    3'  TTGTGCCAGATGCCAGTACTG  37934          AA_  TGAA
                                CAGTGCTGGCAT   GC
                                ||||||||||||  ||
                                GTCATGACCGTA  CG
                                      GAC  TGTTT
GAM330  ACAS2    3'  TTGTGCCAGATGCCAGTACTG  57704          AA_  TGAA
                                CAGTGCTGGCAT   GC
                                ||||||||||||  ||
                                GTCATGACCGTA  CG
                                      GAC  TGTTT
GAM330  AMOT     3'  TTTGGTTTAAAATGTATGTGGT 55732      _   TGGCA    TG
          C                      GACCA GTGC    TAAGC  AA
                                |||||  ||||    |||||  ||
                                CTGGT TATG    ATTTG  TT
                                   G   TAAA_    GT
GAM330  BIRC2    5'  TTTAGCTATCAAACAGTACTG  67205        GCATA_
                                CAGTGCTG     AGCTGAA
                                ||||||||     |||||||
                                GTCATGAC     TCGATTT
                                     AAACTA
GAM330  BM-002   3'  TTCAGTTTACATGCATTATTGG 33528        CTG  __
          TT                    GACCAGTG   GCA  TAAGCTGAA
                                ||||||||   |||  |||||||||
                                TTGGTTAT   CGT  ATTTGACTT
                                     TA_   AC
GAM330  BMF      3'  TCAGCTTGTGTTCTGC     53164    T_
                                GC  GGCATAAGCTGA
                                ||  ||||||||||||
                                CG  TTGTGTTCGACT
                                 TC
GAM330  BS69     3'  TTCAGCTTAATTTACTGTTC  21769    C    CTGGCA
                                GA CAGTG     TAAGCTGAA
                                || |||||     |||||||||
                                CT GTCAT     ATTCGACTT
                                 T    TTA___
GAM330  C19orf7  3'  TTCAGCCACCAGTGTTGG    61133     TG   CATAA
                                CCAG  CTGG    GCTGAA
                                ||||  ||||    ||||||
                                GGTT  GACC    CGACTT
                                  GT   AC___
GAM330  C20orf164 3'  TTAGCTGAAGCATTGG      79480        GGCATA
                                CCAGTGCT     AGCTGA
                                ||||||||     ||||||
                                GGTTACGA     TCGATT
                                     AG____
GAM330  CGGBP1   3'  TTTAGCTTCTGGTCAGCACTG  13366         AT_
                                CAGTGCTGGC   AAGCTGAA
                                |||||||||   ||||||||
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                                GTCACGACTG   TTCGATTT
                                     GTC
GAM330  COLEC12  3' TTCGGCTTGTGCTCTGCAGTC  47877    CAG   T_
                                GAC   TGC  GGCATAAGCTGAA
                                |||   |||  ||||||||||||
                                CTG   ACG  TCGTGTTCGGCTT
                                  ___   TC
GAM330  DKFZp564A176 5' TTCAGTAGCCCCTAGCATTGG  49974         CATAA
                                CCAGTGCTGG    GCTGAA
                                ||||||||||    ||||||
                                GGTTACGATC    TGACTT
                                      CCCGA
GAM330  DKFZP586D0623 3'  TTCAGTTTATGTTAGAC     71978    G
                                GT CTGGCATAAGCTGAA
                                || ||||||||||||||
                                CA GATTGTATTTGACTT
                                 _
GAM330  DKFZp761D0614 3'  TTGTGTTGGCTTGGTC      87558       T  TG
                                GACCAG GC  GCATAA
                                |||||| ||  ||||||
                                CTGGTT CG  TGTGTT
                                   _ GT
GAM330  DMRTB1    3'  TTCAGCCATTATGGGCACTGGT 66247          GG    __
           T                     GACCAGTGCT  CATAA  GCTGAA
                                |||||||||  |||||  ||||||
                                TTGGTCACGG  GTATT  CGACTT
                                     __     AC
GAM330  FLJ10330  3' TTTGGCATGGTTGCCATGTTGG 36033      GT C    TAA__  TG
           TT                    GACCA  G TGGCA    GC  AA
                                |||||  | |||||    ||  ||
                                TTGGT  T ACCGT    CG  TT
                                   TG _    TGGTA  GT
GAM330  FLJ10701  3' GTTAGATGTACAGCATTGGTT  36431          _   AAG   A
                                GACCAGTGCTG GCAT   CTGA
                                |||||||||| ||||  ||||
                                TTGGTTACGAC TGTA   GATT
                                      A   ___   GT
GAM330  FLJ10803  3' TTTGGTTTATTGCAGTGGTC   36673      G   TGGC     TG
                                GACCA TGC    ATAAGC  AA
                                ||||| |||   ||||||  ||
                                CTGGT ACG    TATTTG  TT
                                   G   T___     GT
GAM330  FLJ10971  3' TTTAGCTTGTGTATATAATTGT 36932    _   GCTG_
           GTT                    GAC CAGT    GCATAAGCTGAA
                                ||| ||||    ||||||||||||
                                TTG GTTA    TGTGTTCGATTT
                                  T   ATATA
GAM330  FLJ12587  3' TCAGCTTTGCAGTGGTT    42499      G   TGGCAT
                                GACCA TGC     AAGCTGA
                                ||||| |||     |||||||
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                                TTGGT ACG     TTCGACT
                                  G   T_____
GAM330  FLJ13153  5'  TGGCTGTCAGTGCTGGTC    45559      TG     TAA  TG
                                GACCAG  CTGGCA   GC  A
                                ||||||  ||||||   ||  |
                                CTGGTC  GACTGT   CG  T
                                   GT     ___  GT
GAM330  FLJ14075  3'  TTCGGCTTGTTTATGTATTAGT 46051     C     TGGC
          T                      GAC AGTGC    ATAAGCTGAA
                                 |||  |||||    ||||||||||
                                 TTG TTATG    TGTTCGGCTT
                                   A     TATT
GAM330  FLJ20070  5'  TCGGCGACGCCGCTGGTC    34477       GCT   ATAA
                                GACCAGT   GGC    GCTGA
                                |||||||   |||    |||||
                                CTGGTCG   CCG    CGGCT
                                   ___   CAG_
GAM330  FLJ20701  3'  TTCAGCAAAGGCAGCATTGGTC 35592          G ATAA
                                GACCAGTGCTG C    GCTGAA
                                ||||||||||| |    ||||||
                                CTGGTTACGAC G    CGACTT
                                      _ GAAA
GAM330  FOXN4     3'  TTCAGCTTGGACACACTGG    75574       C  GCA
                                CCAGTG TG   TAAGCTGAA
                                |||||| ||   |||||||||
                                GGTCAC AC   GTTCGACTT
                                   _  AG_
GAM330  GL004     3'  TTAGTTTTGCACTTGGTT     65996      _   TGGCAT
                                GACCA GTGC     AAGCTGA
                                |||||  ||||     |||||||
                                TTGGT CACG     TTTGATT
                                   T    T_____
GAM330  GRWD      3'  TTTAGAGGCTGGTGCTGTGTC  48974     _   TG TG  ATAAG
                                GAC CAG  C  GC    CTGAA
                                |||  |||  |  ||    |||||
                                CTG GTC  G  CG    GATTT
                                  T   GT GT  GA___
GAM330  GW112     3'  TTCAACTGAAGCCAGCACTGGT 21194           ATA  C
          T                      GACCAGTGCTGGC   AG TGAA
                                 ||||||||||||   || ||||
                                 TTGGTCACGACCG   TC ACTT
                                       AAG  A
GAM330  IRAK3     3'  TTTAGCTTGCTTGCACGGGTT  23245     A   T   TA
                                GACC GTGC GGCA  AGCTGAA
                                ||||  |||| ||||  |||||||
                                TTGG CACG TCGT  TCGATTT
                                  G   T   __
GAM330  KIAA0057  3'  TCAGCCCCATGCTGGTC     24441        C   CATAA
                                GACCAGTG TGG    GCTGA
                                ||||||||  |||    |||||
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                                CTGGTCGT ACC    CGACT
                                    _  C____
GAM330  KIAA0205 3' TTTGGTTTGGGTACTGGTT  29594       GGCA   TG
                                GACCAGTGCT   TAAGC  AA
                                ||||||||||   |||||  ||
                                TTGGTCATGG   GTTTG  TT
                                     ____    GT
GAM330  KIAA0212 3' TTTGGTTTGGGGCACTGG   27947      GGCA   TG
                                CCAGTGCT   TAAGC  AA
                                ||||||||   |||||  ||
                                GGTCACGG   GTTTG  TT
                                    G___   GT
GAM330  KIAA0336 3' TTTGGTTACACAGAACATTGGT 27592      __  GCATA  TG
          T                      GACCAGTG  CTG   AGC  AA
                                ||||||||  |||   |||  ||
                                TTGGTTAC  GAC   TTG  TT
                                    AA  ACA__  GT
GAM330  KIAA0410 3' TTAGCTTAGTGTAGGTT    28781     A TG  GCATA
                                GACC G  CTG    AGCTGA
                                ||||  |  |||    ||||||
                                TTGG T  GAT    TCGATT
                                  A GT  _____
GAM330  KIAA0459 3' TTTAGTAATTTTACTACTGGTT 61013       C  CATAA
                                GACCAGTG TGG    GCTGAA
                                |||||||| |||    ||||||
                                TTGGTCAT ATT    TGATTT
                                    C  TTAA_
GAM330  KIAA0534 5' TTCAGTTCTCTTAGCATTG   71438       CATA
                                CAGTGCTGG   AGCTGAA
                                |||||||||   |||||||
                                GTTACGATT   TTGACTT
                                     CTC_
GAM330  KIAA0630 3' TCAGCACTATATTGGTC    89397       C  CATAA
                                GACCAGTG TGG    GCTGA
                                |||||||| |||    |||||
                                CTGGTTAT ATC    CGACT
                                    _  A____
GAM330  KIAA0801 5' GTGTTTAGCGCTGGTC     29151         _
                                GACCAGTGCTGG CAT
                                |||||||||||| |||
                                CTGGTCGCGATT GTG
                                       T
GAM330  KIAA0923 3' TCAGCTTGATGCATGGTC   25838      G  TGGCA
                                GACCA TGC    TAAGCTGA
                                |||||  |||    ||||||||
                                CTGGT ACG    GTTCGACT
                                   _  TA___
GAM330  KIAA1000 3' TTCAGCTTTGCAAAGTACTGG  65281       G_  T
                                CCAGTGCT  GCA AAGCTGAA
                                ||||||||  ||| ||||||||
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                                GGTCATGA  CGT TTCGACTT
                                    AA  _
GAM330  KIAA1068 3' TTCAGCTGCCACCGGCACTG  31044        CATA
                                CAGTGCTGG   AGCTGAA
                                |||||||||   |||||||
                                GTCACGGCC   TCGACTT
                                    ACCG
GAM330  KIAA1089 3' TGGCCTGTGCCAGCACGGTC  68848     A        A
                                GACC GTGCTGGCATA GCTG
                                |||| |||||||||| ||||
                                CTGG CACGACCGTGT CGGT
                                  _        C
GAM330  KIAA1189 3' TATGCTAACGCTGGTC      72047        C
                                GACCAGTG TGGCATA
                                |||||||| |||||||
                                CTGGTCGC ATCGTAT
                                    A
GAM330  KIAA1383 3' TCAGTTTGTTCAATGGTT    69785      GTGC  C
                                GACCA   TGG ATAAGCTGA
                                |||||   ||| |||||||||
                                TTGGT   ACT TGTTTGACT
                                  A___  _
GAM330  KIAA1467 3' TTTAGCTTGTGTTAGTAAAAGG 71620    AG_
                                CC  TGCTGGCATAAGCTGAA
                                ||  ||||||||||||||||
                                GG  ATGATTGTGTTCGATTT
                                 AAA
GAM330  KIAA1508 5' TTGCTCTGTGCCAGTGCTGG  61895     TG      _  TGAA
                                CCAG  CTGGCATA AGC
                                ||||  |||||||| |||
                                GGTC  GACCGTGT TCG
                                  GT      C  TT
GAM330  KIAA1608 3' TTTAGTTTTGTTGGTTGGTT  45691     GT  TG  T
                                GACCA  GC  GCA AAGCTGAA
                                |||||  ||  ||| ||||||||
                                TTGGT  TG  TGT TTTGATTT
                                  __  GT  _
GAM330  KIAA1813 5' TCAGACCAGCATTGG       70308         CATAAG
                                CCAGTGCTGG     CTGA
                                ||||||||||     ||||
                                GGTTACGACC     GACT
                                    A_____
GAM330  MGC12217 3' TTTAGCAGCAGACATTGGTT  51314       _  G ATAA
                                GACCAGTG CTG C   GCTGAA
                                |||||||| ||| |   ||||||
                                TTGGTTAC GAC G   CGATTT
                                    A  _ A___
GAM330  MGC12972 3' TTCAGCTCCGGAGCATTGG   51079       __ CATA
                                CCAGTGCT  GG   AGCTGAA
                                ||||||||  ||   |||||||
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                                GGTTACGA  CC    TCGACTT
                                    GG  ____
GAM330  MGC3047  3'  TGGCTTCTGTACTGG      50365       T  CAT    TG
                                CCAGTGC GG   AAGC  A
                                ||||||| ||   ||||  |
                                GGTCATG TC   TTCG  T
                                   _ ___    GT
GAM330  MGC4161  3'  TTTGGTTTGTGTTGCTGTTC  44192    C    GCT       TG
                                GA CAGT   GGCATAAGC  AA
                                || ||||   |||||||||  ||
                                CT GTCG   TTGTGTTTG  TT
                                 T   ___       GT
GAM330  MGC5469  3'  TTCATGTGGTTAGTTTGGTC  50398      T     ATAAGC
                                GACCAG GCTGGC     TGAA
                                |||||| ||||||      ||||
                                CTGGTT TGATTG     ACTT
                                   _     GTGT__
GAM330  NPEPL1   3'  TTTGGTTTGTCTTTCTGGTC  45093      TGCT  C     TG
                                GACCAG    GG ATAAGC  AA
                                ||||||    || ||||||  ||
                                CTGGTC    TC TGTTTG  TT
                                   TT__ _     GT
GAM330  ORCTL3   3'  AGCTGCTGCTGGTT       14917       GCT    TAA
                                GACCAGT   GGCA   GCT
                                |||||||   ||||   |||
                                TTGGTCG   TCGT   CGA
                                    ___   ___
GAM330  PANK     3'  TATGTAAGCGCTGGTC      56335          G
                                GACCAGTGCT GCATA
                                |||||||||| |||||
                                CTGGTCGCGA TGTAT
                                      A
GAM330  PDCD7    3'  TTTGGTTCTGTTTTGGTTTGGT 72145       T  TG C  _   TG
           T                     GACCAG GC  G ATA AGC  AA
                                ||||||  ||  | ||| |||  ||
                                TTGGTT TG  T TGT TTG  TT
                                   _  GT T   C   GT
GAM330  PIGM     3'  TTTAAGCCAGTATTTGTT    59048     C       A
                                GAC AGTGCTGGC TAAG
                                ||| ||||||||| ||||
                                TTG TTATGACCG ATTT
                                  T       A
GAM330  PPIL3    5'  TGTGTTGCTACTGGTT      55662        _  T
                                GACCAGT GC GGCATA
                                ||||||| || ||||||
                                TTGGTCA CG TTGTGT
                                    T  _
GAM330  PRO0800  3'  TGGCTTTTGTCTGGTT      37743       TGCTG   T    TG
                                GACCAG    GCA AAGC  A
                                ||||||    ||| ||||  |
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                                TTGGTC    TGT TTCG  T
                                   _____  T   GT
GAM330  PRO2831  5'  TCAGTATGGTTGCTGGTC    37602       GCT   ATAA
                                GACCAGT   GGC   GCTGA
                                |||||||   |||   |||||
                                CTGGTCG   TTG   TGACT
                                   ___  GTA_
GAM330  PSMA4    5'  TTCGGTGAGCGGTGGTGGTT   10942      G    G ATAA
                                GACCA TGCTG C   GCTGAA
                                ||||| ||||| |   ||||||
                                TTGGT GTGGC G   TGGCTT
                                  G    _ AG__
GAM330  RAB6C    3'  TCAGGCTGGTTTTGGTT     49571       T  TG  ATAAG
                                GACCAG GC  GC    CTGA
                                ||||||  ||  ||    ||||
                                TTGGTT TG  CG    GACT
                                   T  GT  _____
GAM330  RAI17    3'  TTTAGCTTCAGTGTACTAGTC  91288     C    TG  AT
                                GAC AGTGC  GC  AAGCTGAA
                                |||  |||||  ||  ||||||||
                                CTG TCATG  TG  TTCGATTT
                                 A    __  AC
GAM330  RGS18    3'  TTGGGCATCTGCCACATTGGTT 55395        C    TAA  G
                                GACCAGTG TGGCA   GCT AA
                                |||||||| |||||   ||| ||
                                TTGGTTAC ACCGT   CGG TT
                                   _    CTA   G
GAM330  SAE1     3'  TCAGGGCTATGTTGGTC     18534      GT C    ATAAG
                                GACCA  G TGGC    CTGA
                                |||||  | ||||    ||||
                                CTGGT  T ATCG    GACT
                                  TG _   G____
GAM330  TBCC     3'  TTCAGCTTCCCAAAGTGCTGG  12144     TG  GGCAT
                                CCAG  CT    AAGCTGAA
                                ||||  ||    ||||||||
                                GGTC  GA    TTCGACTT
                                  GT  AACCC
GAM330  TERA     3'  TGGCTGCAGTATTGGT      41137         G  TAA  TG
                                ACCAGTGCTG CA   GC  A
                                ||||||||||  ||   ||  |
                                TGGTTATGAC GT   CG  T
                                   _  ___  GT
GAM330  TRIM4    3'  TTTGGTTTTCTGTTCATGTGTT 52258     TG _   _  T_   TG
           GGTT                   CCAG  C TGG CA  AAGC  AA
                                ||||  | ||| ||  ||||  ||
                                GGTT  G ACT GT  TTTG  TT
                                  GT T   T  CT    GT
GAM330  TSPAN-2  3'  TGGCTCATTACTGGTT      19167        C  GCATA   TG
                                GACCAGTG TG    AGC  A
                                ||||||||  ||    |||  |
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                                TTGGTCAT AC    TCG  T
                                    T _____  GT
GAM330  WBP4     3'  TTTAGTTTGAACCAGGCATTGT 23233    _    _  CA
            GTT                   GAC CAGTGC TGG  TAAGCTGAA
                                ||| |||||| |||  |||||||||
                                TTG GTTACG ACC  GTTTGATTT
                                  T    G   AA
GAM330  X123     5'  TTCAGCCCTGTAGTGCTGTTC  69926    C   TG   G  TAA
                                GA CAG  CTG CA   GCTGAA
                                || |||  ||| ||   ||||||
                                CT GTC  GAT GT   CGACTT
                                 T  GT   _ CC_
GAM330  ZNF340   5'  TTAGCTTGTGCTCAAGT     84565     __
                                GCT  GGCATAAGCTGA
                                |||  ||||||||||||
                                TGA  TCGTGTTCGATT
                                  AC
GAM330  LOC144486 3'  TTTAGCAAGTACAGTGCTG   83089     TG   GC  AA
                                CAG  CTG  AT  GCTGAA
                                |||  |||  ||  ||||||
                                GTC  GAC  TG  CGATTT
                                  GT   A_  AA
GAM330  LOC147077 3'  TTTAGGGTGATCAGTGCTGG   78251      TG   _  AAG
                                CCAG  CTGG CAT   CTGAA
                                ||||  |||| |||   |||||
                                GGTC  GACT GTG   GATTT
                                  GT    A   G__
GAM330  LOC148734 5'  TTCAGCTTTTGTGCTCTGGTT  78959       T  TG   T
                                GACCAG GC  GCA AAGCTGAA
                                |||||| ||  ||| ||||||||
                                TTGGTC CG  TGT TTCGACTT
                                   T __   T
GAM330  LOC150311 5'  TTCAGCCATGGTAGTGCTGGTT 79760       TG   G   AA
                                GACCAG  CTG CAT  GCTGAA
                                ||||||  ||| |||  ||||||
                                TTGGTC  GAT GTA  CGACTT
                                   GT   G   C_
GAM330  LOC150406 3'  TTGTGTGGGCATTGGTT     79860          G
                                GACCAGTGCT GCATAA
                                |||||||||| ||||||
                                TTGGTTACGG TGTGTT
                                     G
GAM330  LOC150862 3'  TGTGCCATACTGGTC       80021         C
                                GACCAGTG TGGCATA
                                |||||||| |||||||
                                CTGGTCAT ACCGTGT
                                          _
GAM330  LOC151201 5'  TTTAGTTTATACCATTGG    85299      TGC   C
                                CCAG   TGG ATAAGCTGAA
                                ||||   ||| ||||||||||
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                                GGTT   ACC TATTTGATTT
                                  ___  A
GAM330   LOC151518 3'  TCAGCTTACTATTGGTT     85435        CTGGCA
                                GACCAGTG     TAAGCTGA
                                ||||||||     ||||||||
                                TTGGTTAT     ATTCGACT
                                    C_____
GAM330   LOC155038 3'  GCGTGTTATGCTGGTT      81258        C     AA
                                GACCAGTG TGGCAT  GC
                                |||||||| ||||||  ||
                                TTGGTCGT ATTGTG  CG
                                  _     __
GAM330   LOC157660 3'  TTTAGTTTATGCCTTGTGTT   86514    TG T_
                                AG  C  GGCATAAGCTGAA
                                ||  |  ||||||||||||||
                                TT  G  CCGTATTTGATTT
                                 GT TT
GAM330   LOC158187 3'  TTTGGCTTGTGCTAGAAC     86698    G         TG
                                GT CTGGCATAAGC  AA
                                || ||||||||||  ||
                                CA GATCGTGTTCG  TT
                                 A          GT
GAM330   LOC158332 3'  GCTGTGCTAGTATCGGTT     81889      A         A
                                GACC GTGCTGGCATA GC
                                |||| |||||||||| ||
                                TTGG TATGATCGTGT CG
                                  C          _
GAM330   LOC158337 5'  TTAGCTGACAGCACTGG      86775         GCATA
                                CCAGTGCTG     AGCTGA
                                |||||||||     ||||||
                                GGTCACGAC     TCGATT
                                     AG___
GAM330   LOC163882 3'  TTTGGTTTACACTTGTTGGGTC 82170      AGT  T  CA     TG
                                GACC   GC GG  TAAGC  AA
                                ||||   || ||  |||||  ||
                                CTGG   TG TC  ATTTG  TT
                                  GT_  T  AC     GT
GAM330   LOC166754 5'  TTTGTAGCCAGCGCTGG      82662          _
                                CCAGTGCTGGC ATAAG
                                |||||||||| |||||
                                GGTCGCGACCG TGTTT
                                       A
GAM330   LOC168448 3'  TTCAGCTTGTGACCCTGTGTC  82701     _   TGCT  _
                                GAC CAG    GG CATAAGCTGAA
                                ||| |||    || ||||||||||
                                CTG GTC    CC GTGTTCGACTT
                                  T  _____  A
GAM330   LOC199692 3'  TTGTGTTATGTCAGTGTTGGT  59244       TG        GCTGAA
                                ACCAG  CTGGCATAA
                                |||||  |||||||||
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                                TGGTT  GACTGTATT
                                  GT       GTGTT
GAM330  LOC200734 3'  TTTGGTTTGTGAAGGCATCGGT 88867     A    GG      TG
          T                     GACC GTGCT  CATAAGC  AA
                                |||| |||||  |||||||  ||
                                TTGG TACGG  GTGTTTG  TT
                                  C    AA      GT
GAM330  LOC201965 3'  TTTGTGGTTGTATTGGTT    89116        TGG
                                GACCAGTGC   CATAAG
                                |||||||||   ||||||
                                TTGGTTATG   GTGTTT
                                     TTG
GAM330  LOC220692 3'  TTTGGTTACACAGAACATTGGT 91224       __   GCATA   TG
          T                     GACCAGTG  CTG    AGC  AA
                                ||||||||  |||    |||  ||
                                TTGGTTAC  GAC    TTG  TT
                                    AA   ACA__   GT
GAM330  LOC221596 3'  TTCAGTGATTGGTTAGCACTTG 91985     C       ATAA_
          TT                     GAC AGTGCTGGC    GCTGAA
                                 ||| |||||||||    ||||||
                                 TTG TCACGATTG    TGACTT
                                   T       GTTAG
GAM330  LOC221830 3'  TTTAGTACCAGACATAGTGCTG 92515      TG   GCATAA__
          GTC                    GACCAG  CTG      GCTGAA
                                 ||||||  |||      ||||||
                                 CTGGTC  GAT      TGATTT
                                    GT   ACAGACCA
GAM330  LOC221882 3'  TTTGTGTTTGCTTGGTGCTGGT 92503      TG   _   TAA  TGAA
          T                      GACCAG  CTG GCA   GC
                                 ||||||  ||| |||   ||
                                 TTGGTC  GGT CGT   TG
                                    GT   T   TTG  TTT
GAM330  LOC221975 5'  TTCGTCCGGGTGCCAGCGCTGG 92611          AAGC_
                                 CCAGTGCTGGCAT    TGAA
                                 ||||||||||||    ||||
                                 GGTCGCGACCGTG    GCTT
                                       GGCCT
GAM330  LOC253891 3'  TTCCACGTGTGTTGTGTTGGTT 94418      TG T     AGCT
                                 GACCAG  C GGCATA    GAA
                                 ||||||  | ||||||    |||
                                 TTGGTT  G TTGTGT    CTT
                                    GT _     GCAC
GAM330  LOC254251 3'  TTTGGTTTAAATGTGCTGGTT  95915      TG TGGCA    TG
                                 GACCAG  C    TAAGC  AA
                                 ||||||  |    |||||  ||
                                 TTGGTC  G    ATTTG  TT
                                    GT TAA__     GT
GAM330  LOC255242 3'  TTCATGTGGTTAGTTTGGTC   95930      T     ATAAGC
                                 GACCAG GCTGGC     TGAA
                                 |||||| ||||||     ||||
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                                CTGGTT TGATTG     ACTT
                                   _     GTGT__
GAM330  LOC255870 5'  TTTGGCAAGGCATGTTGGTT  94660      __    GGCATAA  TG
                                GACCA  GTGCT     GC  AA
                                |||||  |||||      ||  ||
                                TTGGT  TACGG     CG  TT
                                   TG    AA_____  GT
GAM330  LOC63920  5'  TCAGTTAGCCACTGGTT    42025       GCT   ATA
                                GACCAGT   GGC   AGCTGA
                                |||||||   |||   ||||||
                                TTGGTCA   CCG   TTGACT
                                   ___   A__
GAM330  LOC84570  5'  TTCGGCTTCGCGAGTAGCATTG 50713         ___  AT
           GTT                    ACCAGTGCTG   GC  AAGCTGAA
                                ||||||||||   ||  ||||||||
                                TGGTTACGAT   CG  TTCGGCTT
                                     GAG  C_
GAM330  LOC90826  5'  TTTGGTTTGTGCTCCAGC    64096     __      TG
                                GCTG  GCATAAGC  AA
                                ||||  ||||||||  ||
                                CGAC  CGTGTTTG  TT
                                  CT      GT
GAM330  LOC91694  3'  GCACATCTAGTGCTGGTT    66962       TG    C  AA
                                GACCAG  CTGG AT  GC
                                ||||||  |||| ||  ||
                                TTGGTC  GATC TA  CG
                                   GT   _  CA
GAM331  CMAR     3'  ATGAAAGGACCCTGTGAGCC   17771       TGTCT    CC
                                GGCTCG    GTCCT  CAT
                                ||||||    |||||  |||
                                CCGAGT    CAGGA  GTA
                                   GTCC_    AA
GAM331  GARP     3'  GGAAGTGGCCCCACATAGCCCG 18596        C    CT_  _  C
           A                    TCGGGCT GTGT   GTC CT CC
                                |||||||  ||||   ||| || ||
                                AGCCCGA TACA   CGG GA GG
                                   _   CCC   T  A
GAM331  LTBP1    3'  ATGAGAGGATTTAGGATGAGCC 5274          G   __     C
           CGA                    TCGGGCTCGT TCT  GTCCTC CAT
                                ||||||||||  |||  ||||||  |||
                                AGCCCGAGTA GGA  TAGGAG GTA
                                     _  TT     A
GAM331  SPG7     3'  ATGAAAGGACCCTGTGAGCC   11902       TGTCT    CC
                                GGCTCG    GTCCT  CAT
                                ||||||    |||||  |||
                                CCGAGT    CAGGA  GTA
                                   GTCC_    AA
GAM331  B3GAT3   3'  AGGACAGATGGACCC       24187     C  G
                                GGG TC TGTCTGTCCT
                                |||  ||  ||||||||||
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                                CCC AG GTAGACAGGA
                                  _ _
GAM331  KIAA0185  3'  GGAGGACAAATTCAGAGCCC  62972      GT_  C
                                GGGCTC  GT TGTCCTCC
                                |||||||  || ||||||||
                                CCCGAG  TA ACAGGAGG
                                   ACT  A
GAM331  LOC146328 5'  AGGAAAGAGGAGCCCGA    77830       GTG  G
                                TCGGGCTC  TCT TCCT
                                ||||||||  ||| ||||
                                AGCCCGAG  AGA AGGA
                                    G__  A
GAM331  LOC201304 3'  GGAAAAACTGAAGCCCGA   88232       _  T  CTG
                                TCGGGCT CG GT  TCC
                                ||||||| || ||  |||
                                AGCCCGA GT CA  AGG
                                    A  _  AAA
GAM332  ASTN    3'  TCCTACTTACATTC      69337       AACA   A
                                GAATGTA   AGTA GGA
                                |||||||   |||| |||
                                CTTACAT   TCAT CCT
                                   ____   _
GAM332  BCRP2   3'  TCTCACCCTGTTTACATGCC  62407   A      A_  A
                                GG ATGTAAACA  GT AGG
                                || |||||||||  || |||
                                CC TACATTTGT  CA TCT
                                 G       CC  C
GAM332  CLTC    3'  CCTTATTTCACATTCC     16780       AAAC
                                GGAATGT   AAGTAAGG
                                |||||||   ||||||||
                                CCTTACA   TTTATTCC
                                   C___
GAM332  CYP3A4  3'  GTTTCCCTACACCTCTTGCATT 33925        ACAA_  A
           CC                     GGAATGTAA    GTA GGAAAC
                                |||||||||    ||| ||||||
                                CCTTACGTT    CAT CCTTTG
                                     CTCCA  C
GAM332  DFNA5   3'  TCTGTCACTTGCATTCC    15306      TAAA   AA_
                                GGAATG   CAAGT  GGA
                                ||||||   |||||  |||
                                CCTTAC   GTTCA  TCT
                                   ____   CTG
GAM332  ENAM    3'  TCCCCTACTGCTTACATTCC  49079       ACA   A_
                                GGAATGTAA  AGTA  GGA
                                |||||||||  ||||  |||
                                CCTTACATT  TCAT  CCT
                                     CG_   CC
GAM332  EXTL2   3'  TTTTATTGTTTACATCC    7523     A      G
                                GGA TGTAAACAA TAAGG
                                ||| ||||||||| |||||
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                                CCT ACATTTGTT ATTTT
                                  _       _
GAM332  GAS2     3'  TTCCGAAAAGTTTACATTC   17913         AAGTAA
                                GAATGTAAAC     GGAA
                                ||||||||||     ||||
                                CTTACATTTG     CCTT
                                     AAAAG_
GAM332  HHEX     3'  TCCAGAGCTGCCTACATTTC  10785        AACA  AA_
                                GGAATGTA   AGT  GGA
                                ||||||||   |||  |||
                                CTTTACAT   TCG  CCT
                                    CCG_   AGA
GAM332  HOXA3    3'  TTCCTTGCTGCTCACATTCTG 47692        AAACA
                                CGGAATGT    AGTAAGGAA
                                ||||||||    |||||||||
                                GTCTTACA    TCGTTCCTT
                                    CTCG_
GAM332  IL1F5    3'  TCCTCGTGTTTACATTCTG   24384          AGTA
                                CGGAATGTAAACA   AGGA
                                ||||||||||||    ||||
                                GTCTTACATTTGT   TCCT
                                      GC__
GAM332  INHBC    3'  CCCAGCTCTGCCTACATTCTG 18653         AA _  AA
                                CGGAATGTA  CA AGT  GG
                                |||||||||  || |||  ||
                                GTCTTACAT  GT TCG  CC
                                    CC  C   AC
GAM332  ITGB4BP  3'  CCTTCTCCACATTCCG      9403         AAACA  T
                                CGGAATGT    AG AAGG
                                ||||||||    || ||||
                                GCCTTACA    TC TTCC
                                    CC___  _
GAM332  MEA      3'  CCTTATATTCCTACATTCC   27544         AACAA
                                GGAATGTA    GTAAGG
                                ||||||||    ||||||
                                CCTTACAT    TATTCC
                                    CCTTA
GAM332  MGAT5    5'  TTTTTGCTGACATTCCG     10031         AAA  A
                                CGGAATGT   CA GTAAGGA
                                ||||||||   || |||||||
                                GCCTTACA   GT CGTTTTT
                                     ___  _
GAM332  PINX1    3'  TTTCCCCCAAGTTACATTCC  35414         ACAAGTAA
                                GGAATGTAA       GGAAA
                                |||||||||       |||||
                                CCTTACATT       CCTTT
                                    GAACCC__
GAM332  PRex1    3'  GTTTCCTTCAACGTCCACATTC 40434        AA  AAGT
          C                      GGAATGT  AC    AAGGAAAC
                                 |||||||  ||    ||||||||
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                                CCTTACA TG   TTCCTTTG
                                   CC CAAC
GAM332  PTPRN    3' CCTTCTCCTGCCTACATTCC  11129       AA __ T
                                GGAATGTA CA AG AAGG
                                |||||||| || || ||||
                                CCTTACAT GT TC TTCC
                                   CC CC _
GAM332  SFRS1    3' TCCTAACATCTACATTCC    22641       AACAA A
                                GGAATGTA   GT AGGA
                                ||||||||   || ||||
                                CCTTACAT   CA TCCT
                                   CTA__ A
GAM332  SHANK2   3' TTCCTGTAACTTGTTCTACATT 24591       _     A__
           CC                    GGAATGTA AACAAGT  AGGAA
                                ||||||||| |||||||  |||||
                                CCTTACAT TTGTTCA  TCCTT
                                   C     ATG
GAM332  SLC38A2  3' TTACTTGTTTACATCC     38594    A
                                GGA TGTAAACAAGTAA
                                ||| ||||||||||||
                                CCT ACATTTGTTCATT
                                 _
GAM332  SLC9A1   3' TTTTGTTTGTTCACACTCC   70416    A  A
                                GGA TGT AACAAGTAAGG
                                ||| ||| ||||||||||
                                CCT ACA TTGTTTGTTTT
                                  C  C
GAM332  SOCS5    3' GTTTCCTTACCTGCTGCTACA 25799    AA__ A
                                TGTA   CA GTAAGGAAAC
                                ||||   || ||||||||||
                                ACAT   GT CATTCCTTTG
                                  CGTC C
GAM332  SRR      3' GTTTCCTTACCTAAAGGTTCC 41688     GTAAACAA
                                GGAAT      GTAAGGAAAC
                                |||||      ||||||||||
                                CCTTG      CATTCCTTTG
                                   GAAATC__
GAM332  TEM8     3' TCCAAAATTGCCTATATTCC  36332      AA  GTAA
                                GGAATGTA CAA   GGA
                                |||||||| |||   |||
                                CCTTATAT GTT   CCT
                                   CC  AAAA
GAM332  TFDP1    3' GTTTCCTTTTGGCCTACTCCC 23049   AAT  AA_  GT
                                GG  GTA  CAA  AAGGAAAC
                                ||  |||  |||  ||||||||
                                CC  CAT  GTT  TTCCTTTG
                                 CT_  CCG  __
GAM332  YWHAZ    3' TTCCTTTGCTTGCATCCC   12710   A    A  GTA
                                GG ATGTAA CAA  AGGAA
                                || |||||| |||  |||||
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                                CC TACGTT GTT   TCCTT
                                 C     C  ___
GAM332  ZNF26    5'  TCTCCTTGTTCACATCCG    72983      A  A     TAA
                                CGGA TGT AACAAG   GGA
                                |||| ||| ||||||   |||
                                GCCT ACA TTGTTC   TCT
                                  _  C     C__
GAM332  ABLIM    3'  TTCCTTACCTGTCAATA     9781      AA  A
                                TGT  ACA GTAAGGAA
                                |||  ||| ||||||||
                                ATA  TGT CATTCCTT
                                  AC   C
GAM332  ABLIM    3'  TTCCTTACCTGTCAATA     22043     AA  A
                                TGT  ACA GTAAGGAA
                                |||  ||| ||||||||
                                ATA  TGT CATTCCTT
                                  AC   C
GAM332  ARHGAP5  3'  TTCCTTATTCACTTACATT   6757        ACA
                                AATGTAA   AGTAAGGAA
                                |||||||   |||||||||
                                TTACATT   TTATTCCTT
                                    CAC
GAM332  ARHGAP5  3'  TTCCTTATTCACTTACATT   77084       ACA
                                AATGTAA   AGTAAGGAA
                                |||||||   |||||||||
                                TTACATT   TTATTCCTT
                                    CAC
GAM332  ATP6V1B2 3'  TTCCCTACCCCGTGCATTCC  8088        AACAA  A
                                GGAATGTA    GTA GGAA
                                ||||||||    ||| ||||
                                CCTTACGT    CAT CCTT
                                     GCCC_  C
GAM332  C1orf10  5'  CCACTTGTTTCATCCC     32465    A  T      AA
                                GG ATG AAACAAGT  GG
                                || ||| ||||||||  ||
                                CC TAC TTTGTTCA  CC
                                 C  _       __
GAM332  CTCFL    3'  TTGCCCTGGTTACATTCC    82504        A  A_
                                GGAATGTAA CA  GTAA
                                ||||||||| ||  ||||
                                CCTTACATT GT  CGTT
                                     G  CC
GAM332  FLJ10081 5'  TTTCCTCACCTGTTTACA    35805        A  A
                                TGTAAACA GT AGGAAA
                                |||||||| || ||||||
                                ACATTTGT CA TCCTTT
                                    C  C
GAM332  FLJ10618 3'  CCTTTGTTTAATTCC       36344       G      GTA
                                GGAAT TAAACAA   AGG
                                ||||| |||||||   |||
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                                CCTTA ATTTGTT   TCC
                                  _     ___
GAM332  FLJ13072  3'  CCTGCTGTTTACACCC      89808    AA       A   A
                                GG  TGTAAACA GTA GG
                                ||  |||||||| ||| ||
                                CC  ACATTTGT CGT CC
                                 C_       _  _
GAM332  FLJ13449  3'  TTCTTGATCCACTTGCATTCC  44621          ACAAG_
                                GGAATGTAA     TAAGGA
                                |||||||||     ||||||
                                CCTTACGTT     GTTCTT
                                      CACCTA
GAM332  FLJ13657  3'  TTTCATTTACATTCC       45722          CAAGTAA
                                GGAATGTAAA      GGAA
                                ||||||||||      ||||
                                CCTTACATTT      CTTT
                                      A_______
GAM332  FLJ14393  3'  GTTTCCTTACCTGCGTATCT   51321     _    AACAA
                                GGA ATGTA     GTAAGGAAAC
                                ||| |||||     ||||||||||
                                TCT TGCGT     CATTCCTTTG
                                  A    C____
GAM332  FLJ21459  5'  TTTCTTATTTACATCCC     44522     A     ACAA
                                GG ATGTAA    GTAAGGAA
                                || ||||||    ||||||||
                                CC TACATT    TATTCTTT
                                 C     _____
GAM332  FLJ23189  3'  TTTCTACTGCACTTACATTC   46843        ACA_   A
                                GAATGTAA    AGTA GGAA
                                ||||||||    |||| ||||
                                CTTACATT    TCAT CTTT
                                     CACG    _
GAM332  GAS2L1    3'  CCTCTGTTGTACATTCCG    21361          _   AGTA
                                CGGAATGTA AACA    AGG
                                ||||||||| ||||    |||
                                GCCTTACAT TTGT    TCC
                                      G    C___
GAM332  GMFB      3'  TTCCAGTTTTTACATTCCG    14672          CAAGTAA
                                CGGAATGTAAA      GGAA
                                ||||||||||      ||||
                                GCCTTACATTT      CCTT
                                       TTGA___
GAM332  GPA33     3'  TCCTTTGCTTCATTCC      19459       TAAAC     _
                                GGAATG     AAGTAA GGA
                                ||||||     |||||| |||
                                CCTTAC     TTCGTT CCT
                                   _____      T
GAM332  HRIHFB2436 3'  TTTACTGTTTACACCCC     26799     AA       A
                                GG  TGTAAACA GTAAG
                                ||  |||||||| |||||
```

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                                CC  ACATTTGT CATTT
                                 CC       _
GAM332  HSPC117  3' GCTCTGTTTACATTCCG     26677           _
                                CGGAATGTAAACA AGT
                                |||||||||||| |||
                                GCCTTACATTTGT TCG
                                       C
GAM332  HYA22    3' CCTTATTTGACCACACTCC    19424     A   AAA
                                GGA TGT   CAAGTAAGG
                                ||| |||   |||||||||
                                CCT ACA   GTTTATTCC
                                  C   CCA
GAM332  KIAA0087 3' TCCTTGGCATTTTACTTCC    28705     T    CAAG
                                GGAA GTAAA    TAAGGA
                                |||| |||||    ||||||
                                CCTT CATTT    GTTCCT
                                  _    TACG
GAM332  KIAA0202 3' TCCTTACTCACTATAGTC    64371    A    AACA
                                GA TGTA    AGTAAGGA
                                || ||||    ||||||||
                                CT ATAT    TCATTCCT
                                 G   CAC_
GAM332  KIAA0493 3' CCTTCAAAACCTCTTACATTCC 64273         ACAA ____
                                GGAATGTAA    GT    AAGG
                                |||||||||    ||    ||||
                                CCTTACATT    CA    TTCC
                                      CTC_  AAAC
GAM332  KIAA0643 3' TCCTATGTTTGCATTCC     45602           AGTA
                                GGAATGTAAACA    AGGA
                                ||||||||||||    ||||
                                CCTTACGTTTGT    TCCT
                                       A___
GAM332  KIAA0895 3' TTCCATTGCTGTTCAGACTCC  92727     ATGTA    A   _
                                GGA     AACA GTAA GGAA
                                |||     |||| |||| ||||
                                CCT     TTGT CGTT CCTT
                                  CAGAC    _    A
GAM332  KIAA0914 3' CTCTACTGTTTACATT      29678          A   AG
                                AATGTAAACA GTA  G
                                |||||||||| |||  |
                                TTACATTTGT CAT  C
                                      _  CT
GAM332  KIAA0970 3' CCTCATATACTGTACATTCC  29956        AA   A  ____
                                GGAATGT  ACA GTA    AGG
                                |||||||  ||| |||    |||
                                CCTTACA  TGT CAT    TCC
                                    __  _  ATAC
GAM332  KIAA0997 3' TTTCCTCCTCTATATTCC    30195         AACA  TA
                                GGAATGTA    AG  AGGAAA
                                ||||||||    ||  ||||||
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                                CCTTATAT   TC  TCCTTT
                                    C___  C_
GAM332  KIAA1061  3'  TTTTCTTACCCACATTCC    71180       AAACAA
                                GGAATGT     GTAAGGAAA
                                |||||||     |||||||||
                                CCTTACA     CATTCTTTT
                                    CC____
GAM332  KIAA1265  3'  CTTTCTGTTTACATCC      70789     A      A T
                                GGA TGTAAACA G AAGG
                                ||| |||||||| | ||||
                                CCT ACATTTGT C TTTC
                                  _      _ _
GAM332  KIAA1416  3'  TCCTACTGTTTACACTC     86463    A      A   A
                                GA TGTAAACA GTA GGA
                                || |||||||| ||| |||
                                CT ACATTTGT CAT CCT
                                 C      _  _
GAM332  LANO      3'  CCCTGCTTACATTCC       36620        AACA    A
                                GGAATGTA    AGTA GG
                                ||||||||    |||| ||
                                CCTTACAT    TCGT CC
                                    _____   C
GAM332  MGC10526  5'  TTTCCTTACTAGATGACATTTC 50969        AAACA
                                GGAATGT     AGTAAGGAAA
                                |||||||     ||||||||||
                                CTTTACA     TCATTCCTTT
                                    GTAGA
GAM332  MGC23937  3'  TCCTGGAATTTTACATTCC    58956         CAAGTA
                                GGAATGTAAA      AGGA
                                ||||||||||      ||||
                                CCTTACATTT      TCCT
                                     TAAGG_
GAM332  MGC5560   3'  TCCCTGCTACATTCC       38787        AAACA    A
                                GGAATGT     AGTA GGA
                                |||||||     |||| |||
                                CCTTACA     TCGT CCT
                                    ______   C
GAM332  MRPL56    3'  TTTTCTTTGTTTCCATTCC    51691       T     GTA
                                GGAATG AAACAA   AGGAAA
                                |||||| ||||||   ||||||
                                CCTTAC TTTGTT   TCTTTT
                                   C     ___
GAM332  NR6A1     3'  GTTTCCTTACCTGGATCTCC   52875     ATGTAAA  A
                                GGA      CA GTAAGGAAAC
                                |||      || ||||||||||
                                CCT      GT CATTCCTTTG
                                  CTAG___  C
GAM332  NR6A1     3'  GTTTCCTTACCTGGATCTCC   52887     ATGTAAA  A
                                GGA      CA GTAAGGAAAC
                                |||      || ||||||||||
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                                CCT      GT CATTCCTTTG
                                  CTAG___  C
GAM332  NR6A1    3'  GTTTCCTTACCTGGATCTCC   7650     ATGTAAA  A
                                GGA      CA GTAAGGAAAC
                                |||      || ||||||||||
                                CCT      GT CATTCCTTTG
                                  CTAG___  C
GAM332  NY-REN-25 3'  TTTCTGTGTTTGCATTCC    60638          AGTA
                                GGAATGTAAACA   AGGAA
                                ||||||||||||   |||||
                                CCTTACGTTTGT   TCTTT
                                       G___
GAM332  OS4      5'  TTTCCTCCTCTTGTTTTCACTC 19188     A  T      TA_
            CG                    CGGA TG AAACAAG   AGGAAA
                                |||| || |||||||   ||||||
                                GCCT AC TTTGTTC   TCCTTT
                                  C  T      TCC
GAM332  PP1628   5'  TCCCCAGTAGTTTACATTCC   47308          AAGTAA
                                GGAATGTAAAC     GGA
                                ||||||||||      |||
                                CCTTACATTTG     CCT
                                      ATGACC
GAM332  PRKRIR   3'  TCGTTGCTGTTTACATTCC   16297          A   G
                                GGAATGTAAACA GTAA GA
                                |||||||||||| |||| ||
                                CCTTACATTTGT CGTT CT
                                      _   G
GAM332  SH3BGRL2  3'  TACTTGTTCTCATTCCG     48889        TA
                                CGGAATG  AACAAGTA
                                |||||||  ||||||||
                                GCCTTAC  TTGTTCAT
                                    TC
GAM332  SLC16A6  3'  TCTTTGGTTCACATTCCG    16276        A  AAG
                                CGGAATGT AAC   TAAGGA
                                |||||||| |||   ||||||
                                GCCTTACA TTG   GTTTCT
                                    C  ___
GAM332  SLC2A11  5'  TCCTACCCGCATTCCG      47966        AAACAA  A
                                CGGAATGT     GTA GGA
                                ||||||||     ||| |||
                                GCCTTACG     CAT CCT
                                    CC_____  _
GAM332  SLK      3'  TTCCCAGCTTGCATTCC     28230       TAAA    AA
                                GGAATG   CAAGT  GGAA
                                ||||||   |||||  ||||
                                CCTTAC   GTTCG  CCTT
                                   _____    AC
GAM332  TA-PP2C  3'  GTTTCCTTACAAAACTACCCCG 57760     AAT   AACAA
                                CGG  GTA    GTAAGGAAAC
                                |||  |||    ||||||||||
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                                GCC   CAT    CATTCCTTTG
                                  C__   CAAAA
GAM332   TDRKH    3'  TCTTACCTGTTTACAGCCC   22484    AA      A
                                GG  TGTAAACA GTAAGG
                                ||  |||||||| ||||||
                                CC  ACATTTGT CATTCT
                                  CG       C
GAM332   TLE4     3'  TCCTTTTTGTTCACCCCC    67923    AAT  A     T
                                GG   GT AACAAG AAGGA
                                ||   || |||||| |||||
                                CC   CA TTGTTT TTCCT
                                  CC_  C     _
GAM332   LOC143310 5'  TCCTTTGTTTGCACCCC     76541    AA       GTA
                                GG  TGTAAACAA   AGGA
                                ||  |||||||||   ||||
                                CC  ACGTTTGTT   TCCT
                                  CC        ___
GAM332   LOC144308 3'  TTTCCATAGAGTTTACATCC   83054     A      AAG  A
                                GGA TGTAAAC   TA GGAAA
                                |||  |||||||   || |||||
                                CCT ACATTTG   AT CCTTT
                                  _      AG_  A
GAM332   LOC147229 5'  TCCTTACCTGCGTTCTG     78323         AACAA
                                CGGAATGTA    GTAAGGA
                                |||||||||    |||||||
                                GTCTTGCGT    CATTCCT
                                     C____
GAM332   LOC150848 3'  TCTTTACCTCTACATTCC    85131        AACAA
                                GGAATGTA    GTAAGGA
                                ||||||||    |||||||
                                CCTTACAT    CATTTCT
                                     CTC__
GAM332   LOC157922 3'  CCTTACTTGAAGTTCT      86632       GTAAA
                                GGAAT    CAAGTAAGG
                                |||||    |||||||||
                                TCTTG    GTTCATTCC
                                   AA___
GAM332   LOC168448 3'  TTCCTTGCCCTCATTCCG    82702        TAAACAA
                                CGGAATG      GTAAGGAA
                                |||||||      ||||||||
                                GCCTTAC      CGTTCCTT
                                    TCC____
GAM332   LOC200107 3'  TACCTGTTTACATTCC      88577           A
                                GGAATGTAAACA GTA
                                |||||||||||| |||
                                CCTTACATTTGT CAT
                                         C
GAM332   LOC204161 5'  CCTTTGTTTACTCTCC      90658     AT       GTA
                                GGA  GTAAACAA   AGG
                                |||  ||||||||   |||
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                                CCT  CATTTGTT   TCC
                                  CT       ___
GAM332  LOC219855 3'  TCTTGCTTGTTCAGATTCC   91518      GTA
                                GGAAT   AACAAGTAAGG
                                |||||   ||||||||||
                                CCTTA   TTGTTCGTTCT
                                   GAC
GAM332  LOC255147 5'  GTTTCTTTCTGCCTCCATTCC  95702       TAAACA  T
                                GGAATG     AG AAGGAAAC
                                ||||||     || ||||||||
                                CCTTAC     TC TTTCTTTG
                                   CTCCG_  _
GAM332  LOC256401 3'  TTCCTTGCCCTCATTCCG    96021       TAAACAA
                                CGGAATG      GTAAGGAA
                                |||||||      ||||||||
                                GCCTTAC      CGTTCCTT
                                    TCC____
GAM332  LOC90643  3'  TCCTTACTTTCATCC       63692     A  TAAAC
                                GGA TG     AAGTAAGGA
                                ||| ||     |||||||||
                                CCT AC     TTCATTCCT
                                  _  T____
GAM332  LOC90750  3'  TTCCTTACTCGCATCTG     63928      A   AAACA
                                CGGA TGT     AGTAAGGAA
                                |||| |||     |||||||||
                                GTCT ACG     TCATTCCTT
                                  _   C____
GAM332  LOC91818  3'  TCCTTACTTTCATCC       67272     A  TAAAC
                                GGA TG     AAGTAAGGA
                                ||| ||     |||||||||
                                CCT AC     TTCATTCCT
                                  _  T____
GAM332  LOC92181  3'  TCCTTATTTACATTC       68408        ACAA
                                GAATGTAA    GTAAGGA
                                ||||||||    |||||||
                                CTTACATT    TATTCCT
                                            ____
GAM333  HTR4      3'  ATGGAAGACACAGGGTCA    6029        C       A
                                TGACTC GTGTCTTC CAT
                                |||||| |||||||| |||
                                ACTGGG CACAGAAG GTA
                                   A       _
GAM333  MBP       3'  TGGATGTGATGGCGTCA     89782      T   TGTCT
                                TGAC CCG     TCACATCCA
                                |||| |||     |||||||||
                                ACTG GGT     AGTGTAGGT
                                  C  _____
GAM333  NEDD4L    3'  CTGGATGTAAAGCTGAG     30949     CGT T   C
                                CTC   G CTT ACATCCAG
                                |||   | ||| ||||||||
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                                GAG   C GAA TGTAGGTC
                                  T__ _   A
GAM333  PES1     3'  TGGATGTGGCAGAGGC      26673     G  _
                                GT TCT TCACATCCA
                                || ||| |||||||||
                                CG AGA GGTGTAGGT
                                 G   C
GAM333  CASKIN1  3'  TGAAAGGACACGAAGTC     40402      C       CA
                                GACT CGTGTCTT  CA
                                |||| ||||||||  ||
                                CTGA GCACAGGA  GT
                                  A       AA
GAM333  CHDH     5'  CTGGATGTGAGGGAGAAGT   80578     CCGTG
                                ACT    TCTTCACATCCAG
                                |||    ||||||||||||
                                TGA    GGGAGTGTAGGTC
                                  AGA__
GAM333  DIS3     3'  GTGAGGACACAGAGCCA     30234     A   C
                                TG CTC GTGTCTTCAC
                                || ||| ||||||||||
                                AC GAG CACAGGAGTG
                                 C   A
GAM333  EREG     3'  GATGTGAGGAGAGTC       7498       CGTG
                                GACTC    TCTTCACATC
                                |||||    ||||||||||
                                CTGAG    AGGAGTGTAG
                                   ____
GAM333  FLJ11362 3'  GGATGTGAAATCCAGGCGTCA 41682      T  GTGTC
                                TGAC CC     TTCACATCC
                                ||||  ||    |||||||||
                                ACTG GG     AAGTGTAGG
                                  C  ACCTA
GAM333  FLJ20551 3'  CTGGATGTGAGGAGAGGAGTCA 35387        GTG
                                TGACTCC   TCTTCACATCCAG
                                |||||||   ||||||||||||
                                ACTGAGG   AGGAGTGTAGGTC
                                    AG_
GAM333  FOXP1    5'  TGGAGGACACAGAGCCA     51072     A   C       A
                                TG CTC GTGTCTTC CA
                                || ||| |||||||| ||
                                AC GAG CACAGGAG GT
                                 C   A       _
GAM333  GPS2     5'  GGATGTGACGCAGGGGCCA   15668     A   G   CT
                                TG CTCC TGT  TCACATCC
                                || |||| |||  ||||||||
                                AC GGGG ACG  AGTGTAGG
                                 C    _   C_
GAM333  HARSL    3'  TGGATGTGAAAGAGAC      24202     G   _
                                GT TCTT CACATCCA
                                || |||| ||||||||
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                                CA AGAA GTGTAGGT
                                 G   A
GAM333  KIAA1161  3'  CTGGATGTGAGACATGGAGTCA 81749          T
                                TGACTCCGTGTCT CACATCCAG
                                |||||||||||| |||||||||
                                ACTGAGGTACAGA GTGTAGGTC
                                          _
GAM333  KIAA1719  3'  TGAAGACAGGAGCCA      68174    A   G
                                TG CTCC TGTCTTCA
                                || |||| ||||||||
                                AC GAGG ACAGAAGT
                                 C   _
GAM333  KIAA1817  3'  CTGGGAGTGAAGACACGGAGTC 68228            AT
                                GACTCCGTGTCTTCAC  CCAG
                                ||||||||||||||||  ||||
                                CTGAGGCACAGAAGTG  GGTC
                                          AG
GAM333  MGC27434  5'  GGAGAGAAGACACATAGTCA  58949     CC      ACA
                                TGACT  GTGTCTTC   TCC
                                |||||  ||||||||   |||
                                ACTGA  CACAGAAG   AGG
                                   TA       AG_
GAM333  NESHBP    3'  CTGAATGTGAAGTCAAGTC   31251     CCG  T      C
                                GACT   TG CTTCACAT CAG
                                ||||   || |||||||| |||
                                CTGA   AC GAAGTGTA GTC
                                  ___  T       A
GAM333  TBDN100   3'  CTGGATATGAAGAGGA     46951     GTG     C
                                TCC   TCTTCA ATCCAG
                                |||   |||||| ||||||
                                AGG   AGAAGT TAGGTC
                                  ___      A
GAM333  ZNF286    3'  CTGAATGTGAAGAAATG     40295     G       C
                                CGT TCTTCACAT CAG
                                ||| ||||||||| |||
                                GTA AGAAGTGTA GTC
                                  A        A
GAM333  LOC151124 5'  CTGGATGTTGGAACAGGA    85229     G   C   _
                                TCC TGT TTCA CATCCAG
                                ||| ||| |||| |||||||
                                AGG ACA AGGT GTAGGTC
                                  _   _    T
GAM333  LOC152275 3'  TGAATGTGAGGAAGCCGA    85622     C  G       C
                                TC GT TCTTCACAT CA
                                || || ||||||||| ||
                                AG CG AGGAGTGTA GT
                                 C  A        A
GAM333  LOC153810 3'  CTGGATGTGAGACATGGAATCA 80933     C       T
                                TGA TCCGTGTCT CACATCCAG
                                ||| ||||||||| |||||||||
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                                ACT AGGTACAGA GTGTAGGTC
                                  A       _
GAM333  LOC165693 3'  CTGGGGGCGAAGACACGAAGCA 82596    A  C       ACA
                                TG CT CGTGTCTTC   TCCAG
                                || || |||||||||   |||||
                                AC GA GCACAGAAG   GGGTC
                                 _ A       CGG
GAM333  LOC197322 5'  GGATATGACATGGGGCCA    89740    A       TTCAC
                                TG CTCCGTGTC    ATCC
                                || |||||||||    ||||
                                AC GGGGTACAG    TAGG
                                 C       TA___
GAM333  LOC254065 5'  GTGAAGACTCGGAGCCA     97428    A    T
                                TG CTCCG GTCTTCAC
                                || ||||| ||||||||
                                AC GAGGC CAGAAGTG
                                 C    T
GAM333  LOC254471 3'  GATGAGACACGAAATCA     97207     CTC      TCA
                                TGA   CGTGTCT   CATC
                                |||   |||||||   ||||
                                ACT   GCACAGA   GTAG
                                  AAA     ___
GAM333  LOC254559 5'  TGAGGGAAACGCGGAGCCA   96598    A      ___
                                TG CTCCGTGT   CTTCA
                                || ||||||||   |||||
                                AC GAGGCGCA   GGAGT
                                 C       AAG
GAM333  LOC91266  5'  TGGATGTTCACGGGATCA    65417     CT    TCTTC
                                TGA  CCGTG    ACATCCA
                                |||  |||||    |||||||
                                ACT  GGCAC    TGTAGGT
                                  AG    T____
GAM334  ADH1B     3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM334  AHR       3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM334  FDFT1     3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                                _
GAM334  JTB       3'  ATCTCAGACAGTGAAAGTGAAA 21959
                TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
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                                GTAAAGTGAAAGTGACAGACTCTA

GAM334  KLF4    3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM334  PHYH    3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM334  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM334  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM334  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_   CG_
GAM334  CG012   5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM334  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM334  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                 ||||||        |||||||||
                                 GTAAAG        CAGACTCTA
                                    AAACATTT_
GAM334  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                    C__
GAM334  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
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                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM334  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM334  NIR3     3'  GCAGTGAAAGTGCAAT      66242      T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM334  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598         CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM334  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM334  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__   TT
GAM334  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM334  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                      AAAGG
GAM334  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC       CTGTCTGAGAT
                                ||||       ||||||||||||
                                AAAG       GACAGACTCTA
                                  GTTTGCC
GAM334  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM334  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
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                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM334   LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                      _
GAM335   ABCA1     5'  TCAGGGCGCTTTGCTCCTTGTT 18551       AAC  _
                                GACAG   GAG AGGGTGCTCTGA
                                |||||   ||| ||||||||||||
                                TTGTT   CTC TTTCGCGGGACT
                                   C__   G
GAM335   ABCB7     3'  AAGACATTTTCTTTTTTTGTT  63509        C       C   GA
                                GACAGAA GAGAGGGTG TCT
                                ||||||| ||||||||| |||
                                TTGTTTT TTCTTTTAC AGA
                                    T       _  AT
GAM335   ADAM19    3'  TTGGAGTGTTTTTTTGTATTGC 52714    A   A       TG   TG
             CA                   TG CAG ACGAGAGGG  CTC  A
                                || ||| |||||||||  |||  |
                                AC GTT TGTTTTTTT  GAG  T
                                 C   A        GT   GT
GAM335   ADAMTS3   3'  TCCTTTTGTTCTGCA       26480    A
                                TG CAGAACGAGAGGG
                                || ||||||||||||
                                AC GTCTTGTTTTCCT
                                      _
GAM335   ANKH      3'  CCCTTTTTTTTTGTTTTGTT    39062          ____
                                GACAGAACGA    GAGGG
                                ||||||||||    |||||
                                TTGTTTTGTT    TTCCC
                                      TTTT
GAM335   ANKH      3'  CCCTTTTTTTTTGTTTTGTT    53988          ____
                                GACAGAACGA    GAGGG
                                ||||||||||    |||||
                                TTGTTTTGTT    TTCCC
                                      TTTT
GAM335   APM1      3'  CTCTTTAGTTCTGTCA       16590          G
                                TGACAGAAC AGAGGG
                                ||||||||| ||||||
                                ACTGTCTTG TTTCTC
                                     A
GAM335   APPL      3'  TATTTTTTCATTTTGTCA     23930         C
                                TGACAGAA GAGAGGGTG
                                |||||||| |||||||||
                                ACTGTTTT CTTTTTTAT
                                     A
GAM335   APTX      5'  TCTAGTGATTCTTTTGTTTTGT 34661              _  CTGA
             C                    GACAGAACGAGAGGGT GCT
                                |||||||||||||||| |||
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                                CTGTTTTGTTTTCTTA TGA
                                       G   TCT
GAM335  AR      5'  TCAGAGCGCTTTTTGCGTGGTT 3495      A_  _
             G                   CAG  ACG AGAGGGTGCTCTGA
                                 |||  ||| ||||||||||||||
                                 GTT  TGC TTTTTCGCGAGACT
                                   GG   G
GAM335  ASH1    5'  GAGATCCTTGTTTT       37500       GA     G
                                 AGAAC  GAGGGT CTC
                                 |||||  |||||| |||
                                 TTTTG  TTCCTA GAG
                                    __     _
GAM335  ASPH    3'  TAGGGGTAGCTCTTGATTTTGT 50633         _    G G     GA
             TA                   TGACAGAA CGAGA G TGCTCT
                                 ||||||||| ||||| | ||||||
                                 ATTGTTTT GTTCT C ATGGGG
                                      A    _ G     ATT
GAM335  ASPH    5'  TTGAGTTTTTTTTTTGTTTTGT 50635             T_   TGA
             T                    GACAGAACGAGAGGG  GCTC
                                 ||||||||||||||  ||||
                                 TTGTTTTGTTTTTTT  TGAG
                                        TT   TT
GAM335  ASPH    3'  TAGGGGTAGCTCTTGATTTTGT 50621         _    G G     GA
             TA                   TGACAGAA CGAGA G TGCTCT
                                 ||||||||| ||||| | ||||||
                                 ATTGTTTT GTTCT C ATGGGG
                                      A    _ G     ATT
GAM335  ATP8A2  3'  CACCGCCCTTCTCGTTCTGT   93509           T  TC  A
                                 ACAGAACGAGAGGG GC  TG
                                 |||||||||||||| ||  ||
                                 TGTCTTGCTCTTCC CG  AC
                                        _ CC  C
GAM335  ATP8B2  3'  GGTTCTCTCTCGTTTT      65232           T
                                 AGAACGAGAGGG GCT
                                 |||||||||||| |||
                                 TTTTGCTCTCTC TGG
                                        T
GAM335  BDP1    3'  TTGGAGACAGTCTTGTTCTGTT 37368          GG  G   TG
                                 GACAGAACGAGA  GT CTC  A
                                 ||||||||||||  || |||  |
                                 TTGTCTTGTTCT  CA GAG  T
                                        GA  _   GT
GAM335  BHLHB3  3'  TCAGATTTACACCTTTTTTTTG 47766       AC       C___
             TCA                   ACAGA  GAGAGGGTG    TCTGA
                                 |||||  |||||||||    |||||
                                 TGTTT  TTTTTCCAC    AGACT
                                    __        ATTT
GAM335  CACNA1C  3'  CGCTGAGCGCTCTTTTGTTTTG 5560                TGA
             T                    ACAGAACGAGAGGGTGCTC
                                 |||||||||||||||||||
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                                TGTTTTGTTTTCTCGCGAG
                                      TCGCC
GAM335  CALM3    3'  GGTTTGTTTCCTCTTGTTTGTC 17745       A      T  TCTGA
            A                    TGACAGA CGAGAGGG GC
                                 ||||||| |||||||| ||
                                 ACTGTTT GTTCTCCT TG
                                    _      T  TTTGGT
GAM335  CASP10   3'  TTGGAGATAGTCTCATTCTGTC 52110       C   GG  G   TG
            A                    TGACAGAA GAGA  GT CTC  A
                                 |||||||| ||||  || |||  |
                                 ACTGTCTT CTCT  TA GAG  T
                                      A   GA  _   GT
GAM335  CASP10   3'  TTGGAGATAGTCTCATTCTGTC 52126       C   GG  G   TG
            A                    TGACAGAA GAGA  GT CTC  A
                                 |||||||| ||||  || |||  |
                                 ACTGTCTT CTCT  TA GAG  T
                                      A   GA  _   GT
GAM335  CCND2    3'  GCTCTTTTTGTTGTTGTT    8294       _       T
                                 GACAG AACGAGAGGG GC
                                 ||||| |||||||||| ||
                                 TTGTT TTGTTTTTCT CG
                                   G       _
GAM335  CDH1     3'  AGCTACTCTAGTTCTGTT    15139       G   GGT
                                 GACAGAAC AGAG   GCT
                                 |||||||| ||||   |||
                                 TTGTCTTG TCTC   CGA
                                      A   AT_
GAM335  CHC1L    3'  TAGAATTCTTGTTCTG     7017          GGTGC
                                 CAGAACGAGAG    TCTG
                                 ||||||||||     ||||
                                 GTCTTGTTCTT    AGAT
                                       A____
GAM335  CLECSF5  3'  GGGTACCCTGGCTGTT     25128      AACGAG
                                 GACAG     AGGGTGCTC
                                 |||||     |||||||||
                                 TTGTC     TCCCATGGG
                                   GG____
GAM335  CLN5     3'  TTGGAGTGTTTTTGTTTCTGTT 21434       CGA   TG  TG
                                 GACAGAA   GAGGG  CTC  A
                                 |||||||   |||||  |||  |
                                 TTGTCTT   TTTTT  GAG  T
                                      TG_    GT   GT
GAM335  COL19A1  3'  CATTTTCTTGTTTTATTA    8508     C
                                 TGA AGAACGAGAGGGTG
                                 ||| ||||||||||||||
                                 ATT TTTTGTTCTTTTAC
                                   A
GAM335  COL4A4   3'  TCAGTGGTTCCTTCTGTTTTGT 3629        G     T   _
            C                    GACAGAAC AGAGGG GCT CTGA
                                 |||||||| |||||| ||| ||||
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                                CTGTTTTG TCTTCC TGG GACT
                                    _     T  T
GAM335  CREB1    3'  ACAAAACATTTTTTTGTTCTCT 15200    C          CTCTGA
              T                  GA AGAACGAGAGGGTG
                                 || |||||||||||||
                                 TT TCTTGTTTTTTTAC
                                  C           AAAACAT
GAM335  CREB1    3'  TTGGAGTGCTTTTTATGTATGT 15205     GA  _    TG  TG
              T                  GACA  ACG AGAGGG  CTC  A
                                 ||||  ||| ||||||  |||  |
                                 TTGT  TGT TTTTTC  GAG  T
                                   A_  A     GT   GT
GAM335  DDEF2    3'  GTACTTTTTGTTTTTGTTA   13955        CG
                                 TGACAGAA  AGAGGGTGC
                                 ||||||||  |||||||||
                                 ATTGTTTT  TTTTTCATG
                                       TG
GAM335  DDX11    3'  TCAGAGCACCCTGAAGTTTTTG 47662   C    GAG
                                 A AGAAC   AGGGTGCTCTGA
                                 | |||||   ||||||||||||
                                 G TTTTG   TCCCACGAGACT
                                  T    AAG
GAM335  DNMT3B   3'  TTAGAGTATTTTCCACAATG   22565    GAACGA
                                 CA     GAGGGTGCTCTGA
                                 ||     ||||||||||||
                                 GT     CTTTTATGAGATT
                                  AACAC_
GAM335  DUSP5    3'  TCTTTTTGTCTGTTA       15356        A
                                 TGACAGA CGAGAGGG
                                 |||||||  ||||||||
                                 ATTGTCT GTTTTTCT
                                    _
GAM335  E48      3'  CACTCCTTCTGTTTTGTT    13505         AG  _
                                 GACAGAACG  AGG GTG
                                 |||||||||  ||| |||
                                 TTGTTTTGT  TCC CAC
                                       CT   T
GAM335  EFNB2    3'  TTACTGTCTCACTCGTTCTGTT 14580          A   T  TC
              A                  TGACAGAACGAG GGG GC  TGA
                                 ||||||||||||| ||| ||  |||
                                 ATTGTCTTGCTC CTC TG  ATT
                                        A   _  TC
GAM335  EGR4     3'  TTGGGTTTTTTTTCCTTTTGTT 8747         C      T    TGA
                                 GACAGAA GAGAGGG GCTC
                                 |||||||  |||||||  ||||
                                 TTGTTTT CTTTTTT TGGG
                                     C      T   TT
GAM335  EHF      3'  TCAGAGGAATTTTTTTTGTTTT 24064             TG__
              GTT                   GACAGAACGAGAGGG    CTCTGA
                                    ||||||||||||||    ||||||
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                                TTGTTTTGTTTTTTT   GAGACT
                                      TAAG
GAM335  EIF4EL3  3'  TCGGAGTCTGTTGTTCTGTT  16752        G  GGT
                                GACAGAACGA AG   GCTCTGA
                                |||||||||| ||   |||||||
                                TTGTCTTGTT TC   TGAGGCT
                                     G  ___
GAM335  ELAVL2   5'  GCCCCTTTTTGTTTAGTT    15414    A        T
                                GAC GAACGAGAGGG GC
                                ||| |||||||||| ||
                                TTG TTTGTTTTTCC CG
                                  A         C
GAM335  ELOVL4   3'  CACCTTTGTTTTGTT      42685         GA
                                GACAGAACGA  GGGTG
                                |||||||||  |||||
                                TTGTTTTGTT  TCCAC

                                     __
GAM335  ERBB2    3'  TACTTTTTTTGTTTTGTT    15475          _
                                GACAGAACGAGAGG GTG
                                |||||||||||||| |||
                                TTGTTTTGTTTTTT CAT
                                      T
GAM335  EVA1     3'  TAGATTTTTGTTGTTTTGTTA  19397         G   TGC
                                TGACAGAACGA AGGG   TCTG
                                |||||||||| ||||   ||||
                                ATTGTTTTGTT TTTT   AGAT
                                     G   T__
GAM335  FBP1     5'  TCGGGGCGGCAGTCGGTCTGTC 4959        A  GAGG  _
           A                    TGACAGA CGA    GT GCTCTGA
                                ||||||| |||    || |||||||
                                ACTGTCT GCT    CG CGGGGCT
                                    G  GA__  G
GAM335  FBXL2    3'  CACCTTTTTGTTTCTGTCA   24065        _
                                TGACAGAA CGAGAGGGTG
                                |||||||| ||||||||||
                                ACTGTCTT GTTTTTCCAC
                                     T
GAM335  FEZ1     3'  GGGGGATGTGTTTTTTTGTTTT 42578            TG _  GA
           GTT                    GACAGAACGAGAGGG  C TCT
                                |||||||||||||  | |||
                                TTGTTTTGTTTTTTT  G AGG
                                      GT T   GGGC
GAM335  FGF2     3'  TTTTCTTGTTTGTCA      8879        A
                                TGACAGA CGAGAGGG
                                ||||||| ||||||||
                                ACTGTTT GTTCTTTT
                                    _
GAM335  FGF7     3'  ACTTTATTGTTTTGTTA     8882          G
                                TGACAGAACGA AGGGT
                                |||||||||| |||||
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                                ATTGTTTTGTT TTTCA
                                      A
GAM335  FGF7    3'  GGCATGTTTTTGTTTT     8885          G
                                AGAACGAGAG GTGCT
                                |||||||||| |||||
                                TTTTGTTTTT TACGG
                                      G
GAM335  FIGF    5'  TTAGAGTGCTTTCTAATTTC  15558    CG_    TG
                                GAA  AGAGGG  CTCTGA
                                |||  ||||||  ||||||
                                CTT  TCTTTC  GAGATT
                                  TAA    GT
GAM335  FMO2    3'  CAGTTTCTTTTCTGTT     7585        C    G
                                GACAGAA GAGAGG TG
                                ||||||| |||||| ||
                                TTGTCTT TTCTTT AC
                                   _    G
GAM335  FZD4    3'  TTGGAAGGAACCTTTTTTTTGT 24158      AC      G_ _ TG
            T                    GACAGA  GAGAGGGT  CT C  A
                                |||||| ||||||||  || |  |
                                TTGTTT  TTTTTCCA  GA G  T
                                   __       AG  A GT
GAM335  GM2A    3'  CACTCTTTTTTTTTTTGTCA  67772       C__
                                TGACAGAA   GAGAGGGTG
                                ||||||||   |||||||||
                                ACTGTTTT   TTTTCTCAC
                                     TTT
GAM335  GNB5    3'  TCAGAGCACTTTAAAGTCTG  21665    A GAG
                                CAGA C   AGGGTGCTCTGA
                                |||| |   ||||||||||||
                                GTCT G   TTTCACGAGACT
                                  _ AAA
GAM335  GNB5    3'  TCAGAGCACTTTAAAGTCTG  32469    A GAG
                                CAGA C   AGGGTGCTCTGA
                                |||| |   ||||||||||||
                                GTCT G   TTTCACGAGACT
                                  _ AAA
GAM335  HAKAI   3'  CAGAAGTATTGTTTTGTT   45672      G    _
                                AACGAGA GGTGCT CTG
                                ||||||| |||||| |||
                                TTGTTTT TTATGA GAC
                                     G     A
GAM335  HCS     5'  TCGGAGCGGGAGTGTTCGTT  38480    A    AGAGGG
                                GAC GAACG     TGCTCTGA
                                ||| |||||     ||||||||
                                TTG CTTGT     GCGAGGCT
                                  _    GAGG__
GAM335  HDAC4   3'  TGGAGGAATTTTGTTTTGTT  20119         GGGTG  TG
                                GACAGAACGAGA    CTC  A
                                ||||||||||||    |||  |
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                                TTGTTTTGTTTT    GAG  T
                                      AAG__   GT
GAM335  HOXA3    5'  TCAGAGCACTCTCAGAAGTTC  47691     GA__
                                GAAC   GAGGGTGCTCTGA
                                ||||   ||||||||||||
                                CTTG   CTCTCACGAGACT
                                  AAGA
GAM335  HUS1     3'  ATCTTTTGTTTTCTTGTTTTGT 91100          GG  CTCTGA
              T                  GACAGAACGAGAG  TG
                                ||||||||||||  ||
                                TTGTTTTGTTCTT  GT
                                      TT  TTTCTAT
GAM335  HUS1     5'  TCAGGGCGCGACGCTTTTCTGT 91102       C   AGG_
              TA                   TGACAGAA GAG   GTGCTCTGA
                                ||||||||| |||   |||||||||
                                ATTGTCTT TTC   CGCGGGACT
                                    _  GCAG
GAM335  IDS      3'  TTAGAGCTGGTCGTTTTGT   3978         GAGGGT
                                ACAGAACGA    GCTCTGA
                                |||||||||    |||||||
                                TGTTTTGCT    CGAGATT
                                     GGT___
GAM335  IL13RA1  3'  TATTCTTTCGTTCAGTTA   7777      A
                                TGAC GAACGAGAGGGTG
                                |||| ||||||||||||
                                ATTG CTTGCTTTCTTAT
                                  A
GAM335  JUND     3'  CCCTTTTTTTGTTCTGTT    18084         ___
                                GACAGAACGA   GAGGG
                                ||||||||||   |||||
                                TTGTCTTGTT   TTCCC
                                      TTT
GAM335  KCNS2    3'  GCTCCTCTTGTTCGGTTA    68309     A        T
                                TGAC GAACGAGAGGG GC
                                |||| |||||||||| ||
                                ATTG CTTGTTCTCCT CG
                                  G        _
GAM335  KRT6B    3'  GCCTTCTTTTGTTCTGTT    18696            T
                                GACAGAACGAGAGGG GC
                                |||||||||||||| ||
                                TTGTCTTGTTTTCTT CG
                                       C
GAM335  LDB3     3'  TGGAGCATTCTGTTATTTTTG  76408   C   CG G       TG
                                A AGAA  A AGGGTGCTC  A
                                | ||||  | |||||||||  |
                                G TTTT  T TCTTACGAG  T
                                 T   AT G       GT
GAM335  LEP      3'  TCAGGGCATCTTAGCTTCTATT 4058     C   CGAG
              A                   TGA AGAA   AGGGTGCTCTGA
                                ||| ||||   ||||||||||||
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                                ATT TCTT    TTCTACGGGACT
                                  A    CGA_
GAM335  LPXN     3'  TCAGTGTATTTTTGTTTTTCA  16677     C       GG    T
                                TGA AGAACGAGA  GTGC CTGA
                                ||| |||||||||  |||| ||||
                                ACT TTTTGTTTT  TATG GACT
                                  _       ___    T
GAM335  LRP8     3'  TGGGGCATTTGTTTTTTGT    16149       CGAGA       TG
                                ACAGAA    GGGTGCTC  A
                                ||||||    |||||||| |
                                TGTTTT    TTTACGGG  T
                                   TTG__       GT
GAM335  LRP8     3'  TGGGGCATTTGTTTTTTGT    52781       CGAGA       TG
                                ACAGAA    GGGTGCTC  A
                                ||||||    |||||||| |
                                TGTTTT    TTTACGGG  T
                                   TTG__       GT
GAM335  LTA4H    3'  GGCTTTTTATTGTTTTGTT    6102          G    T
                                GACAGAACGA AGGG GCT
                                |||||||||| |||| |||
                                TTGTTTTGTT TTTT CGG
                                     A    T
GAM335  MAB21L1  5'  TCAGCGCAACTTTTGTTTT    18761         GG   T
                                AGAACGAGAG  TGC CTGA
                                |||||||||  ||| ||||
                                TTTTGTTTTC  ACG GACT
                                     A_   C
GAM335  MBNL     3'  TAGAGTATTATTTCTTC     40731     C    GG
                                GAA GAGA  GTGCTCTG
                                ||| ||||  ||||||||
                                CTT CTTT  TATGAGAT
                                  _    AT
GAM335  MCM3     3'  GCTGTTTTTTTGTTTTGTT    9963            GG _
                                GACAGAACGAGAG  T GC
                                ||||||||||||  | ||
                                TTGTTTTGTTTTT  G CG
                                       TT T
GAM335  MINPP1   3'  TTAGCTAACTTTTTCATTCTGT 16909         C       GCT
           CA                     TGACAGAA GAGAGGGT   CTGA
                                ||||||| ||||||||   ||||
                                ACTGTCTT CTTTTTCA   GATT
                                   A       ATC
GAM335  MLLT3    3'  TTGGTTGTGATTTTTTGTTCTT 15761     _        GT  T_ TG
           GTT                      GACA GAACGAGAGG  GC  C  A
                                |||| ||||||||||  ||  |  |
                                TTGT CTTGTTTTTT  TG  G  T
                                  T        AG  TT GT
GAM335  MME      5'  GGAGTTATGTTTTGTTA     23511          AGAGGGT
                                TGACAGAACG      GCTCT
                                ||||||||||      |||||
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                                ATTGTTTTGT      TGAGG
                                      AT_____
GAM335  MTL5    3'  GACGCTTTTGGTTCTGTT    17001        GA      C
                                GACAGAAC  GAGGGTG TC
                                |||||||| ||||||| ||
                                TTGTCTTG  TTTTCGC AG
                                    G_      _
GAM335  MX2     3'  TGGGGCCAAACTCTTCTGTCA  10150       ACG    GG  _   TG
                                TGACAGA   AGAG  TG CTC  A
                                |||||||   ||||  || |||  |
                                ACTGTCT   TCTC  AC GGG  T
                                    ___    AA  C   GT
GAM335  MYO1B   5'  GGGTGCTTCTCTGTCA     24235       ACGA   G TG
                                TGACAGA    GAG G  CTC
                                |||||||    ||| |  |||
                                ACTGTCT    CTT C  GGG
                                    _____   _ GT
GAM335  MYOG    3'  GGGGTGATTTCTTTTGTTA    59346        C    GGGT
                                TGACAGAA GAGA    GCTCT
                                |||||||| ||||    |||||
                                ATTGTTTT CTTT    TGGGG
                                    _    AG__
GAM335  NAB1    3'  TTAGTTGATTTTTTCATTTTGT 19912        C       GCT
          TA                      TGACAGAA GAGAGGGT   CTGA
                                |||||||| ||||||||   ||||
                                ATTGTTTT CTTTTTTA   GATT
                                    A       GTT
GAM335  NLGN2   5'  TGGGGTGCTCGGTTTTCTCA   88159     C    GAGA   TG   TG
                                TGA AGAAC    GGG  CTC  A
                                ||| |||||    |||  |||  |
                                ACT TTTTG    CTC  GGG  T
                                  C    G___   GT   GT
GAM335  NONO    3'  GAGTATTTTTTGTTTTTCA    82018     C        G
                                TGA AGAACGAGAGG TGCTC
                                ||| ||||||||||| |||||
                                ACT TTTTGTTTTTT ATGAG
                                  _       _
GAM335  NRIP1   3'  AGGGTACTTTATTTTG      59949       CGAG
                                CAGAA    AGGGTGCTCT
                                |||||    ||||||||||
                                GTTTT    TTTCATGGGA
                                   A___
GAM335  NRIP1   3'  ATTTTTTTGTTTTGTT      59951
                                GACAGAACGAGAGGGT
                                ||||||||||||||||
                                TTGTTTTGTTTTTTTA

GAM335  OCRL    3'  CACTCCCCTCGTTCTGTCA    4258            A  _
                                TGACAGAACGAG GG GTG
                                |||||||||||| || |||
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                                ACTGTCTTGCTC CC CAC
                                      C  T
GAM335  OCRL     3'  CACTCCCCTCGTTCTGTCA   7824          A  _
                                TGACAGAACGAG GG GTG
                                |||||||||||| || |||
                                ACTGTCTTGCTC CC CAC
                                      C  T
GAM335  ORC3L    3'  TTAGAGGAGCCTGTTTTGTT  24722       GAGA   G_
                                GACAGAAC   GGGT  CTCTGA
                                ||||||||   ||||  ||||||
                                TTGTTTTG   TCCG  GAGATT
                                     ____   AG
GAM335  PCDHA9   3'  AGATGAGAATTCACTTGTTCTG 25754          A   G   TGA
            TCA                    TGACAGAACGAG GGGT CTC
                                |||||||||||| |||| |||
                                ACTGTCTTGTTC CTTA GAG
                                      A   A   TAGAT
GAM335  PCDHA9   3'  TATTTTTTTTTTTTTGTCA    25768       C
                                TGACAGAA GAGAGGGTG
                                |||||||| |||||||||
                                ACTGTTTT TTTTTTTAT
                                     T
GAM335  PELO     5'  GGTTCCTTTGGTTCTGTCA   31956       G     T
                                TGACAGAAC AGAGGG GCT
                                ||||||||| |||||| |||
                                ACTGTCTTG TTTCCT TGG
                                     G    _
GAM335  PIK3R3   3'  TGGGGTTTTTGTTTTGTT    61066         GGGT   TG
                                GACAGAACGAGA   GCTC  A
                                ||||||||||||   ||||  |
                                TTGTTTTGTTTT   TGGG  T
                                     ____   GT
GAM335  PLS1     3'  TTAGGGTGTTCTTTTTCTC   10664    AC     TG
                                GA  GAGAGGG  CTCTGA
                                ||  |||||||  ||||||
                                CT  TTTTCTT  GGGATT
                                 CT     GT
GAM335  PMP22    3'  CAGTATTTTTGTTTTGTT    4323          GGTGCT
                                GACAGAACGAGAG     CTG
                                ||||||||||||     |||
                                TTGTTTTGTTTTT     GAC
                                      AT____
GAM335  PPP2R2B  3'  TTAGACAAATTCTTCTTGTTTT 15911          ___  C
            GT                   ACAGAACGAGAGGG   TG TCTGA
                                ||||||||||||||   || |||||
                                TGTTTTGTTCTTCT   AC AGATT
                                      TAA  _
GAM335  PRKCB1   3'  GGGTTTTGTTTCTGTT     70514       _   AGGGT
                                GACAGAA CGAG    GCTC
                                |||||||  ||||    ||||
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                                TTGTCTT GTTT    TGGG
                                   T  _____
GAM335  PRNP    3'  GCATGTTCTTGTTTTGTTA  4336          G
                                TGACAGAACGAGAG GTGC
                                |||||||||||||| ||||
                                ATTGTTTTGTTCTT TACG
                                      G
GAM335  PTEN    3'  TCCTTTTGTGTTCTGTCA   4345        __
                                TGACAGAAC  GAGAGGG
                                |||||||||  |||||||
                                ACTGTCTTG  TTTTCCT
                                     TG
GAM335  PTGS2   3'  TTTTTTTGTTATGTCA     6363      G
                                TGACA AACGAGAGGG
                                ||||| ||||||||||
                                ACTGT TTGTTTTTTT
                                   A
GAM335  PTK2    3'  TTGGGTTCATTTTTTGTTTTGT 18817         GT_   TGA
            T                    GACAGAACGAGAGG  GCTC
                                ||||||||||||||  ||||
                                TTGTTTTGTTTTTT  TGGG
                                       ACT   TT
GAM335  PTPRF   3'  TTGGGGTTTATTTTGTTTTGTT 55270         GGGT   TG
                                GACAGAACGAGA   GCTC  A
                                ||||||||||||   ||||  |
                                TTGTTTTGTTTT   TGGG  T
                                      ATT_   GT
GAM335  PTPRF   3'  TTGGGGTTTATTTTGTTTTGTT 11108         GGGT   TG
                                GACAGAACGAGA   GCTC  A
                                ||||||||||||   ||||  |
                                TTGTTTTGTTTT   TGGG  T
                                      ATT_   GT
GAM335  PTPRO   3'  GCATTCCTTGTTCTGTT    11134         A
                                GACAGAACGAG GGGTGC
                                |||||||||| ||||||
                                TTGTCTTGTTC CTTACG
                                     _
GAM335  PTPRO   3'  TCTTTTTGTTTTGTTA     11135
                                TGACAGAACGAGAGGG
                                ||||||||||||||||
                                ATTGTTTTGTTTTTCT

GAM335  PTPRO   3'  GCATTCCTTGTTCTGTT    47698         A
                                GACAGAACGAG GGGTGC
                                |||||||||| ||||||
                                TTGTCTTGTTC CTTACG
                                     _
GAM335  PTPRO   3'  TCTTTTTGTTTTGTTA     47699
                                TGACAGAACGAGAGGG
                                ||||||||||||||||
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                                ATTGTTTTGTTTTTCT

GAM335  PTPRO    3'  GCATTCCTTGTTCTGTT     47702          A
                                GACAGAACGAG GGGTGC
                                |||||||||| ||||||
                                TTGTCTTGTTC CTTACG
                                         _
GAM335  PTPRO    3'  TCTTTTTGTTTTGTTA      47703
                                TGACAGAACGAGAGGG
                                ||||||||||||||||
                                ATTGTTTTGTTTTTCT

GAM335  PTPRO    3'  TCTTTTTGTTTTGTTA      47717
                                TGACAGAACGAGAGGG
                                ||||||||||||||||
                                ATTGTTTTGTTTTTCT

GAM335  PTPRO    3'  GCATTCCTTGTTCTGTT     47707          A
                                GACAGAACGAG GGGTGC
                                |||||||||| ||||||
                                TTGTCTTGTTC CTTACG
                                         _
GAM335  PTPRO    3'  TCTTTTTGTTTTGTTA      47708
                                TGACAGAACGAGAGGG
                                ||||||||||||||||
                                ATTGTTTTGTTTTTCT

GAM335  PTPRO    3'  GCATTCCTTGTTCTGTT     47715          A
                                GACAGAACGAG GGGTGC
                                |||||||||| ||||||
                                TTGTCTTGTTC CTTACG
                                         _
GAM335  PUM1     3'  TGTAGTATTTTCTTGTTTTG  27961              CTGA
                                CAGAACGAGAGGGTGCT
                                |||||||||||||||||
                                GTTTTGTTCTTTTATGA
                                          TGTT
GAM335  RAB18    3'  CATTTTGTTGTTTTGTT     41166          G
                                GACAGAACGA AGGGTG
                                |||||||||| ||||||
                                TTGTTTTGTT TTTTAC
                                      G
GAM335  RBM6     3'  TGTCTCTCCTTTTCTTTTGTTA 19329        C      TGCTCTGA
                                TGACAGAA GAGAGGG
                                |||||||| |||||||
                                ATTGTTTT CTTTTCC
                                     _     TCTCTGTT
GAM335  RCN1     3'  TTGGGGTATAAAAATTGTTTTT 59630    C      GAGG_     TG
              C                  GA AGAACGA    GTGCTC  A
                                || |||||||    ||||||  |
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                                CT TTTTGTT    TATGGG  T
                                 _     AAAAA    GT
GAM335  RCN1    3'  TTGGGGTATAAAAATTGTTTTT 11273    C     GAGG_    TG
              C                  GA AGAACGA    GTGCTC  A
                                 || |||||||    ||||||  |
                                CT TTTTGTT    TATGGG  T
                                 _     AAAAA    GT
GAM335  RECK    3'  TTAGTAGGATTTTTGTTTTGTT 40874          GG_   CTGA
                                GACAGAACGAGAG   TGCT
                                ||||||||||||||  ||||
                                TTGTTTTGTTTTT   ATGA
                                       AGG    TT
GAM335  RERE    5'  TTAGAGCATTTTTGAAACGTT  23970     A___
                                AACG    GAGGGTGCTCTGA
                                ||||    ||||||||||||||
                                TTGC    TTTTTACGAGATT
                                  AAAG
GAM335  RHEB2   3'  CTTTTTTCTTCTGTTA      18832        C
                                TGACAGAA GAGAGGG
                                ||||||||| |||||||
                                ATTGTCTT TTTTTTC
                                     C
GAM335  RIG     3'  ACTGTCTTTGTTTTGTCA    21127          _ G
                                TGACAGAACGA GA GGT
                                |||||||||||| || |||
                                ACTGTTTTGTT CT TCA
                                       T  G
GAM335  RP42    3'  TACTTTTTTTTTGTCA      40205        AC
                                TGACAGA  GAGAGGGTG
                                |||||||  |||||||||
                                ACTGTTT  TTTTTTCAT
                                   __
GAM335  RTN3    3'  AGTTCTTTTCTTTTGTT     73897        C      T
                                GACAGAA GAGAGGG GCT
                                ||||||| ||||||| |||
                                TTGTTTT CTTTTCT TGA
                                   _     _
GAM335  RUNX1   3'  GTTTTTTTTTGTTTTGTT    8267             T
                                GACAGAACGAGAGGG GC
                                |||||||||||||| ||
                                TTGTTTTGTTTTTTT TG
                                       T
GAM335  S100A2  3'  TCAATAAACTTTTTTTGTCTGT 88490       AC       GCTC
              T                  GACAGA  GAGAGGGT   TGA
                                 ||||||  ||||||||   |||
                                TTGTCT  TTTTTTCA   ACT
                                   GT       AATA
GAM335  S100A2  3'  TCAATAAACTTTTTTTGTCTGT 19944       AC       GCTC
              T                  GACAGA  GAGAGGGT   TGA
                                 ||||||  ||||||||   |||
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                                TTGTCT  TTTTTTCA   ACT
                                   GT       AATA
GAM335  SALL1    3'  ACCTTTTTTTTGTC       11431       AC
                                GACAGA  GAGAGGGT
                                ||||||  ||||||||
                                CTGTTT  TTTTTCCA
                                   __
GAM335  SCML2    3'  AGCAGTTTTTGTTTTGT     20310          G G
                                ACAGAACGAGA G TGCT
                                |||||||||||| | ||||
                                TGTTTTGTTTT T ACGA
                                      _ G
GAM335  SERPINE2  3'  TCAGGAATTTTTGTTTTGTT   74923           GGTG T
                                GACAGAACGAGAG   C CTGA
                                ||||||||||||    | ||||
                                TTGTTTTGTTTTT   G GACT
                                      AA__ _
GAM335  SH3BP5   3'  TTAGAGCACTGTATTTTTGTCT 16744    GA     ___
           TGTTA                   CA  ACGAGAG   GGTGCTCTGA
                                ||  |||||||   ||||||||||
                                GT  TGTTTTT   TCACGAGATT
                                 TC      ATG
GAM335  SIP1     3'  GTTTTTTGTTGTTTTGTTA   13233          G   T
                                TGACAGAACGA AGGG GC
                                |||||||||||| |||| ||
                                ATTGTTTTGTT TTTT TG
                                      G   T
GAM335  SLC17A5  3'  TCAGAGTGCCCAGCGTTTATCA 24897    CA    AGA   TG
                                TGA  GAACG   GGG  CTCTGA
                                |||  |||||   |||  ||||||
                                ACT  TTTGC   CCC  GAGACT
                                  A_    GA_   GT
GAM335  SLC22A1LS 5'  TCGGAGAGACCTTTTTTTTTGT 23027       C     GTG
           CA                    TGACAGAA GAGAGG   CTCTGA
                                ||||||||  ||||||   ||||||
                                ACTGTTTT TTTTCC   GAGGCT
                                     T     AGA
GAM335  SLC22A3  3'  CTTTCTTTTTTTGTTA     41763        C
                                TGACAGAA GAGAGGG
                                ||||||||  |||||||
                                ATTGTTTT TTCTTTC
                                     T
GAM335  SLC38A2  3'  ACTTTTTTGTTTTGTT     38585
                                GACAGAACGAGAGGGT
                                ||||||||||||||||
                                TTGTTTTGTTTTTTCA

GAM335  SLC7A5   3'  GTCGTTGTGCTTTTTTGTTTTG 13014            TG TC
           T                     ACAGAACGAGAGGG  C  TGA
                                ||||||||||||||  |  |||
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                                TGTTTTGTTTTTTC  G  GCT
                                        GT TT   GA
GAM335  SLC9A1   3' CAGAGTGTCCCTTTTTGCA   70406    A   AC   A   TG
                                TG CAGA  GAG GGG  CTCTG
                                || ||||  ||| |||  |||||
                                AC GTTT  TTC CCT  GAGAC
                                 _   __  _   GT
GAM335  SMCY     5' TATCTTGCTTTTTCGTTCTGTC 16209              CTCTGA
                                GACAGAACGAGAGGGTG
                                |||||||||||||||||
                                CTGTCTTGCTTTTTCGT
                                          TCTATT
GAM335  SMS      3' TAGGGTGTTTTTTTTTTG    15985     AC      TG
                                CAGA  GAGAGGG  CTCTG
                                ||||  |||||||  |||||
                                GTTT  TTTTTTT  GGGAT
                                  __      GT
GAM335  SPON1    3' GGGTGGCTTTTGTTCTTTCA  62454     C        GGT
                                TGA AGAACGAGAG   GCTC
                                ||| ||||||||||   ||||
                                ACT TCTTGTTTTC   TGGG
                                  T        GG_
GAM335  SRD5A1   3' AGTTTTTTTGTTCTGTT     6455            GT
                                GACAGAACGAGAGG  GCT
                                ||||||||||||||  |||
                                TTGTCTTGTTTTTT  TGA
                                                __
GAM335  STARD4   3' TTTTTTTGTTCTGCA       57522    A
                                TG CAGAACGAGAGGG
                                || ||||||||||||
                                AC GTCTTGTTTTTTT
                                 _
GAM335  TARDBP   3' GTTCTTTTGTTTTGTT      23773           GG
                                GACAGAACGAGAG  T
                                ||||||||||||  |
                                TTGTTTTGTTTTC  G
                                       TT
GAM335  TBX5     3' ACTTTCTTGTTTTGTC      54887
                                GACAGAACGAGAGGGT
                                ||||||||||||||||
                                CTGTTTTGTTCTTTCA

GAM335  TBX5     3' ACTTTCTTGTTTTGTC      3955
                                GACAGAACGAGAGGGT
                                ||||||||||||||||
                                CTGTTTTGTTCTTTCA

GAM335  TCERG1   3' GGGTTTGTTTTGTT        21996          GAGGGT
                                GACAGAACGA     GCTC
                                ||||||||||     ||||
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                                TTGTTTTGTT     TGGG
                                       _______
GAM335  TCF1     3'  TCAGCGTGGCCTTGTTCTGTCA 5037          GA   G   T
                                TGACAGAAC  GAGG TGC CTGA
                                |||||||||  |||| ||| ||||
                                ACTGTCTTG  TTCC GTG GACT
                                      __   G   C
GAM335  TCF19    3'  CAGAGCACCTATCAGTT     97733     _  GA
                                AAC GA  GGGTGCTCTG
                                ||| ||  ||||||||||
                                TTG CT  TCCACGAGAC
                                  A  A_
GAM335  TCF19    3'  CAGAGCACCTATCAGTT     97863     _  GA
                                AAC GA  GGGTGCTCTG
                                ||| ||  ||||||||||
                                TTG CT  TCCACGAGAC
                                  A  A_
GAM335  TCF3     3'  TTGGGGGTTCTCTTGGTTTTGT 70737         _    GG G   TGA
              CA                  TGACAGAAC GAGAG  T CTC
                                |||||||||  |||||  | |||
                                ACTGTTTTG TTCTC  G GGG
                                     G    TT G   TT
GAM335  TCFL4    3'  TTGGGGTATCCTTCAAGTATTG 63467    A   A  GA_       TG
              CA                  TG CAG AC   GAGGGTGCTC  A
                                || ||| ||   ||||||||||  |
                                AC GTT TG   TTCCTATGGG  T
                                  _  A  AAC        GT
GAM335  TMPO     3'  TGCCAACATTTTCTTTTCTGTT 12344        C       CTCTGA
              A                   TGACAGAA GAGAGGGTG
                                ||||||||  |||||||||
                                ATTGTCTT TTCTTTTAC
                                     _       AACCGTA
GAM335  TNFAIP2  3'  TTAGAGTACTGCTTTTGT    20836       _
                                ACGAGAG GGTGCTCTGA
                                |||||||  ||||||||||
                                TGTTTTC TCATGAGATT
                                    G
GAM335  TNFSF11  3'  GTACCTTTTTTGTTTTTTCA   52241     C       _
                                TGA AGAACGAGAG GGTGC
                                |||  ||||||||||  |||||
                                ACT TTTTGTTTTT CCATG
                                  T        T
GAM335  TRAP240  3'  TAGAGTATTATTTTTTTG    17602     AC   GG
                                CAGA  GAGA  GTGCTCTG
                                ||||  ||||  ||||||||
                                GTTT  TTTT  TATGAGAT
                                  __   AT
GAM335  TRIM39   5'  CTTTCTTGTCTGTTA      41171       A
                                TGACAGA CGAGAGGG
                                |||||||  ||||||||
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                                ATTGTCT GTTCTTTC
                                      _
GAM335  TRIM9    3'  TCATAGTTCCTCTTGTTCT   30767          T   C
                                AGAACGAGAGGG GCT TGA
                                |||||||||||| ||| |||
                                TCTTGTTCTCCT TGA ACT
                                      _  T
GAM335  TSNAX    3'  AGCAATTTTTGTTTTTGTTA  19997       _     GG
                                TGACAGAA CGAGAG  TGCT
                                |||||||| ||||||  ||||
                                ATTGTTTT GTTTTT  ACGA
                                     T     A_
GAM335  TSPY     3'  TTGGGGCATCTTTTTG     82110          TG
                                CGAGAGGGTGCTC  A
                                |||||||||||||  |
                                GTTTTTCTACGGG  T
                                       GT
GAM335  VASP     5'  TGGGGCATCCCCTTTCTGCTG  12569    AAC     __    TG
                                CAG   GAGAGGG  TGCTC  A
                                |||   |||||||  ||||||  |
                                GTC   CTTTCCC  ACGGG  T
                                  GT_     CT    GT
GAM335  WASF3    3'  TTGGTTTTTCCTTTTGTTTTTT 21831    C         TGCT TG
           TA                     TGA AGAACGAGAGGG    C  A
                                ||| ||||||||||||   |  |
                                ATT TTTTGTTTTCCT    G  T
                                  T          TTTT GT
GAM335  XPR1     3'  GAGGTTTTTTTGTTTTGTT   16428          GG G
                                GACAGAACGAGAG  T CTC
                                ||||||||||||||  | |||
                                TTGTTTTGTTTTT  G GAG
                                       TT _
GAM335  XPR1     3'  GCTTTTTTGTGTTTTGTTA   16429         A    T
                                TGACAGAACG GAGGG GC
                                |||||||||| ||||| ||
                                ATTGTTTTGT TTTTT CG
                                      G    T
GAM335  ZNF189   3'  TGGGAGTGCCTTTTTTGTTTTT 12905    C       _ TG   GA
           CA                     TGA AGAACGAGAG GG  CTCT
                                ||| |||||||||| ||  ||||
                                ACT TTTTGTTTTT CC  GAGG
                                  _        T  GT   GTT
GAM335  ZNF198   3'  GGGTTTTGTTTTGTT      12907          AGGGT
                                GACAGAACGAG    GCTC
                                ||||||||||     ||||
                                TTGTTTTGTTT    TGGG
                                       _____
GAM335  ZNF2     3'  TTGGGGCACTAATCTTGTTCTC 40810    C       G_     TG
           TT                     GA AGAACGAGA  GGTGCTC  A
                                || |||||||||  |||||||  |
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                                TT TCTTGTTCT  TCACGGG  T
                                 C        AA      GT
GAM335  ZNF215   3'  TGAAAAATGTTTTTGTTTTGTT 25118           G  GCTCTGA
            A                    TGACAGAACGAGAG GT
                                 ||||||||||||| ||
                                 ATTGTTTTGTTTTT TA
                                        G  AAAAGTT
GAM335  ZNF22    3'  CCCTTTTTTTGTTTTGTT    91463         ___
                                 GACAGAACGA   GAGGG
                                 ||||||||||   |||||
                                 TTGTTTTGTT   TTCCC
                                       TTT
GAM335  ACTR2    3'  TAGGGCATTTCCTCTGT     19152    G    __
                                 AC AGAGG  GTGCTCTG
                                 || |||||  ||||||||
                                 TG TCTCC  TACGGGAT
                                  _    TT
GAM335  AKR7A2   3'  CACCTCTTTTGTTCTCTCA   13492     C       _
                                 TGA AGAACGAGAG GGTG
                                 ||| |||||||||| ||||
                                 ACT TCTTGTTTTC CCAC
                                   C        T
GAM335  ALS2CR2  3'  CCCTTTTTCTTCTGTTA     37704        C_
                                 TGACAGAA  GAGAGGG
                                 ||||||||  |||||||
                                 ATTGTCTT  TTTTCCC
                                      CT
GAM335  AQP10    3'  TTAGGGCACTCTCTTGTTACTG 54434     _
                                 CAG AACGAGAGGGTGCTCTGA
                                 ||| ||||||||||||||||||
                                 GTC TTGTTCTCTCACGGGATT
                                   A
GAM335  ARHE     3'  TTGGGTTTTTTTTTTTTTGTT 17715        C      T    TGA
            A                    TGACAGAA GAGAGGG GCTC
                                 |||||||| ||||||| ||||
                                 ATTGTTTT TTTTTTT TGGG
                                      T      T    TT
GAM335  ARPC5    3'  TTGGCTGGTTTTTTGTTCTGTT 19141           G _   CTGA
                                 GACAGAACGAGAGG T GCT
                                 |||||||||||||| | |||
                                 TTGTCTTGTTTTTT G CGG
                                       G T   TT
GAM335  ATE1     3'  TTGTGCATTTTTTTTGGTTCTG 72614         __        TCTGA
            TTA                    GACAGAAC  GAGAGGGTGC
                                   ||||||||  ||||||||||
                                   TTGTCTTG  TTTTTTTACG
                                      GT         TGTT
GAM335  BAG4     3'  TTGGACTTCTGTTTTGTTTTGT 16856           G  TGC  TG
            TA                     TGACAGAACGAGA GG   TC  A
                                   |||||||||||| ||   ||  |
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                                ATTGTTTTGTTTT TC   AG  T
                                       G  TTC  GT
GAM335  BICD2    3'  TAGGGTGTTCTCTTTC      70402    AC      TG
                                GA  GAGAGGG  CTCTG
                                ||  |||||||  |||||
                                CT  TTCTCTT  GGGAT
                                 __      GT
GAM335  BOP      5'  GAGTTTCTTTTTCTGTCA    85051         C     GGT
                                TGACAGAA GAGAG   GCTC
                                ||||||||| |||||   ||||
                                ACTGTCTT TTCTT   TGAG
                                     T    ___
GAM335  BPES     3'  TGTTGTGTTTTTTTGTTTTGTT 43537              TG TCTGA
                                GACAGAACGAGAGGG  C
                                ||||||||||||||  |
                                TTGTTTTGTTTTTTT  G
                                          GT TTGTT
GAM335  BTN2A2   3'  TCAGTGGGAAATTCTCTCCTTC 22781       C       GCT___
           TGTT                    CAGAA GAGAGGGT     CTGA
                                ||||| ||||||||     ||||
                                GTCTT CTCTCTTA     GACT
                                   C       AAGGGT
GAM335  C11orf23 3'  TTGGGGCATCATTTTGTTTTGT 37017           G      TG
           C                     GACAGAACGAGA GGTGCTC  A
                                ||||||||||| |||||||  |
                                CTGTTTTGTTTT CTACGGG  T
                                       A      GT
GAM335  C11orf25 3'  GCATTTTTTTTTTTTGTTA   48642         C
                                TGACAGAA GAGAGGGTGC
                                |||||||| ||||||||||
                                ATTGTTTT TTTTTTTACG
                                     T
GAM335  C1orf16  3'  GTGGTTTTTTGTTTTGTT    29234             G
                                GACAGAACGAGAGG TGC
                                |||||||||||||| |||
                                TTGTTTTGTTTTTT GTG
                                          G
GAM335  C1orf34  3'  TGCTCTTTCATTTTGTTA    60683         C
                                TGACAGAA GAGAGGGTG
                                |||||||| |||||||||
                                ATTGTTTT CTTTCTCGT
                                     A
GAM335  C20orf80 3'  ATGCTTTCATTTTCTTGTTTTC 65285    C           CTCTGA
           TT                     GA AGAACGAGAGGGTG
                                || ||||||||||||||
                                TT TTTTGTTCTTTTAC
                                 C            TTTCGTAT
GAM335  C6orf5   3'  GGGGCCCTTGTTCTG       31359       GA     G
                                CAGAAC  GAGGGT CT
                                ||||||  |||||| ||
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                                GTCTTG  TTCCCG GG
                                   __     G
GAM335  C8orf4   3'  CAAGCTTCTCTTCTGTCA    39280        C     G_
                                TGACAGAA GAGAGG  TG
                                |||||||| ||||||  ||
                                ACTGTCTT CTCTTC  AC
                                   _     GA
GAM335  C9orf14  3'  AGCTTTTCTCGTTTTGTT    86671             T
                                GACAGAACGAGAGGG GCT
                                |||||||||||||| |||
                                TTGTTTTGCTCTTTT CGA
                                                _
GAM335  CCR1     3'  TCTTTTTGTTCTTCA      7109      C
                                TGA AGAACGAGAGGG
                                ||| ||||||||||||
                                ACT TCTTGTTTTTCT
                                 _
GAM335  CHORDC1  3'  GCTGCTGTAATCTTTTGTTTTG 24018           GG   TCTGA
           TT                    GACAGAACGAGAG  TGC
                                ||||||||||||  |||
                                TTGTTTTGTTTTC  ATG
                                      TA   TCGTCGT
GAM335  CL25084  3'  CAGAGTATCTATCTG      31657      ACGAGA
                                CAGA     GGGTGCTCTG
                                ||||     ||||||||||
                                GTCT     TCTATGAGAC
                                  A_____
GAM335  COL12A1  3'  TCAGGGCATCTGTCTTTTTGTT 15185        C  GA
           A                     TGACAGAA GA  GGGTGCTCTGA
                                |||||||| ||  ||||||||||
                                ATTGTTTT CT  TCTACGGGACT
                                     T  G_
GAM335  COL12A1  3'  TCAGGGCATCTGTCTTTTTGTT 54667        C  GA
           A                     TGACAGAA GA  GGGTGCTCTGA
                                |||||||| ||  ||||||||||
                                ATTGTTTT CT  TCTACGGGACT
                                     T  G_
GAM335  COVA1    3'  TTGGAGTGTTTTCAGTGTCTGT 73262      _ GA    TG   TG
                                ACAGA AC  GAGGG  CTC  A
                                ||||| ||  |||||  |||  |
                                TGTCT TG  CTTTT  GAG  T
                                   G  A_    GT   GT
GAM335  CPEB1    5'  TGGAGCACTCATCTCTATC   47602    AC   _      TG
                                GA  GAGA GGGTGCTC  A
                                ||  |||| ||||||||  |
                                CT  CTCT CTCACGAG  T
                                 AT   A      GT
GAM335  CTAGE-1  3'  TATGCTTCTGTTCTGTTA    42650          AG  G
                                TGACAGAACG  AG GTG
                                ||||||||||  || |||
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                                ATTGTCTTGT  TC TAT
                                      CT  G
GAM335  DCAMKL1   3'  TCAGAGTGTTTTTTCTGTC   16416      ACGA    TG
                                GACAGA   GAGGG  CTCTGA
                                ||||||   |||||  ||||||
                                CTGTCT   TTTTT  GAGACT
                                   ____    GT
GAM335  DDX36    3'  TTGAGAAATTCCTTTGTTCTGT 40484        G     TG__  TGA
           TA                    TGACAGAAC AGAGGG   CTC
                                |||||||||  ||||||   |||
                                ATTGTCTTG TTTCCT   GAG
                                   _     TAAA   TT
GAM335  DGS-A    3'  TCAGTCTCTTTTTTGTTTTTTT 84902    C         TGCT
                                GA AGAACGAGAGGG   CTGA
                                || ||||||||||||   ||||
                                TT TTTTGTTTTTTC   GACT
                                 T         TCT_
GAM335  Di-Ras2   3'  AGAGTATTTATCTTC      34186     C  GA
                                GAA GA  GGGTGCTCT
                                ||| ||  |||||||||
                                CTT CT  TTTATGAGA
                                  _ A_
GAM335  DKFZP434E2135 5'  TTAGAATTTTTTTTTTGTTTTG 47960             TGC_
           TT                    GACAGAACGAGAGGG   TCTGA
                                ||||||||||||||   |||||
                                TTGTTTTGTTTTTTT   AGATT
                                      TTTA
GAM335  DKFZp434I1916 3'  TGAATTTGCCTTTTTGTTGTTG 49977      _         CTCTGA
           TT                    GACAG AACGAGAGGGTG
                                |||||  ||||||||||||
                                TTGTT TTGTTTTTCCGT
                                   G         TTAAGTT
GAM335  DKFZp547I224 5'  GGAGTGTTTTGTTTTGT     39560          GGG
                                ACAGAACGAGA   TGCTCT
                                ||||||||||   ||||||
                                TGTTTTGTTTT   GTGAGG
                                      ___
GAM335  DKFZp547O146 3'  TCAAAGCTTTTTTGTTTGGTT  39568     A         GCTC
                                GAC GAACGAGAGGGT   TGA
                                ||| ||||||||||||   |||
                                TTG TTTGTTTTTTCG   ACT
                                  G         AA__
GAM335  DKFZP564D166 3'  TTAGAGACAAAGTCTTGTTCTG 47681          GGG  _
           TT                    GACAGAACGAGA   TG CTCTGA
                                ||||||||||||   || ||||||
                                TTGTCTTGTTCT   AC GAGATT
                                      GAA  A
GAM335  DKFZP564K2062 3'  TTGGAGTCAGAAGTCTCAGTTC 31240       _   GGG_ _   TG
           TGTCA                    CAGAAC GAGA   TG CTC  A
                                ||||||  ||||   ||  |||  |
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                                GTCTTG CTCT    AC GAG  T
                                   A    GAAG  T   GT
GAM335  DKFZp566H0824 5'  GCTGTTTTGTTCTGTT      34054           G
                                GACAGAACGAGA GGT
                                |||||||||||| |||
                                TTGTCTTGTTTT TCG
                                      G
GAM335  DKFZP586A0522 3'  TGGGGGGCGGTTTTTTTGGTTT 25873       AC_     G     GA
           GTT                    GACAGA   GAGAGG TGCTCT
                                |||||||   |||||| ||||||
                                TTGTTT   TTTTTT GCGGGG
                                   GGT     G     GGTT
GAM335  DKFZP586M0622 5'  TAGAGCATCCATCTGGT     31486    G  _
                                AC AGA GGGTGCTCTG
                                || ||| ||||||||||
                                TG TCT CCTACGAGAT
                                 G   A
GAM335  DKFZP667C165 3'  TTAGAGTGCCCAACTTATTGTC 67896       AAC   A_   TG
           A                     TGACAG   GAG  GGG  CTCTGA
                                |||||||   |||  |||  |||||||
                                ACTGTT   TTC  CCC  GAGATT
                                   A__   AA   GT
GAM335  DNAJA4    3'  CGGAGTGTCTTCCTGGTC    37754    A  A    TG
                                GA CG GAGGG  CTCTG
                                || || |||||  |||||
                                CT GT CTTCT  GAGGC
                                 G  C    GT
GAM335  DVS27     3'  TTTCATTGTTCTGTCA      53084           _
                                TGACAGAACGA GAGG
                                |||||||||||| ||||
                                ACTGTCTTGTT CTTT
                                      A
GAM335  EDR1      3'  TCAGAGTTTTTTCTTTTTGTT  15384       AC      T
                                GACAGA  GAGAGGG GCTCTGA
                                ||||||  ||||||| |||||||
                                TTGTTT  TTCTTTT TGAGACT
                                   __      T
GAM335  EKN1      3'  AGTACTTTAGTTCTGTT     55524         GAGA
                                GACAGAAC    GGGTGCT
                                ||||||||    |||||||
                                TTGTCTTG    TTCATGA
                                   AT__
GAM335  ELL2      3'  CTGTAGGGTGTTTTTTTGTTTT 23870    C          TG    A
           TTT                    GA AGAACGAGAGGG  CTCTG
                                || ||||||||||||  |||||
                                TT TTTTGTTTTTTT  GGGAT
                                 T          GT    GTCA
GAM335  ENAH      3'  TCAGCAACCTCTTTTGATTTTG 36618        _     _  GCT
           TT                     GACAGAA CGAGAG GGT   CTGA
                                |||||||  |||||| |||   ||||
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                                TTGTTTT GTTTTC CCA   GACT
                                    A     T   AC_
GAM335  FBXO30   3'  GCAGCTTTCTTTTTTGTTA   49577        C      _
                                TGACAGAA GAGAGGG TGC
                                |||||||| ||||||| |||
                                ATTGTTTT TTCTTTC ACG
                                    _      G
GAM335  FBXO30   3'  GCTGTTCTCTTTTTTGTTA   49578        C    GG _
                                TGACAGAA GAGAG  T GC
                                |||||||| |||||  | ||
                                ATTGTTTT TTCTC  G CG
                                    _    TT T
GAM335  FIGN     5'  TCGGAGCATCCTTTTATTTG  95644      AC
                                CAGA  GAGAGGGTGCTCTGA
                                ||||  ||||||||||||||
                                GTTT  TTTTCCTACGAGGCT
                                  A_
GAM335  FKSG14   5'  CATTTTCTGGTTCTGTT     67807        G
                                GACAGAAC AGAGGGTG
                                |||||||| ||||||||
                                TTGTCTTG TCTTTTAC
                                     G
GAM335  FLJ00007 3'  TACCTTCTCTTCTGTCA     71280        C
                                TGACAGAA GAGAGGGTG
                                |||||||| |||||||||
                                ACTGTCTT CTCTTCCAT
                                    _
GAM335  FLJ10099 3'  AGTTTTTTTTGTTTTGTT    35812            T
                                GACAGAACGAGAGGG GCT
                                |||||||||||||| |||
                                TTGTTTTGTTTTTTT TGA
                                       _
GAM335  FLJ10483 3'  TCGGGGTGTCTTTGAGGTTGTT 36175      AACGA    TG
                                GACAG    GAGGG  CTCTGA
                                |||||    |||||  ||||||
                                TTGTT    TTTCT  GGGGCT
                                   GGAG_    GT
GAM335  FLJ10687 3'  TCAGTTAACATTTTTTTGTTTT 36413    C          CT__
            TCA                   GA AGAACGAGAGGGTG   CTGA
                                || ||||||||||||||   ||||
                                CT TTTTGTTTTTTTAC   GACT
                                  _           AATT
GAM335  FLJ10769 3'  TTAGGGTGTTCTCTTATACTTT 36600    C  AAC      TG
            CA                   TGA AG   GAGAGGG  CTCTGA
                                ||| ||   |||||||  ||||||
                                ACT TC   TTCTCTT  GGGATT
                                  T  ATA      GT
GAM335  FLJ10781 3'  TCAGGGCGTCTTTTCCGACTTC 36636    C  AAC     GT
            A                    TGA AG   GAGAGG  GCTCTGA
                                ||| ||   ||||||  |||||||
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                                ACT TC   CTTTTC  CGGGACT
                                  _ AGC     TG
GAM335  FLJ10856  3'  TCGGAGTATTTGGTGTGTTCT  36776       AGA_
                                AGAACG    GGGTGCTCTGA
                                ||||||    ||||||||||
                                TCTTGT    TTTATGAGGCT
                                   GTGG
GAM335  FLJ10971  3'  TCAGGGCATTTTAGGGCTGTC  36930       AACGAG
                                GACAG     AGGGTGCTCTGA
                                |||||     ||||||||||||
                                CTGTC     TTTTACGGGACT
                                  GGGA__
GAM335  FLJ11021  3'  TAGACTTCTTGTTCTG      66443           GTGC
                                CAGAACGAGAGG    TCTG
                                ||||||||||||    ||||
                                GTCTTGTTCTTC    AGAT
                                        ____
GAM335  FLJ11383  3'  AGAGTAGTTTTTGTCA      46280         CGAGAG G
                                TGACAGAA     G TGCTCT
                                ||||||||     | ||||||
                                ACTGTTTT     T ATGAGA
                                     _______ G
GAM335  FLJ12389  3'  TTCTCTGTTTTGTTA       60268         G
                                TGACAGAAC AGAGGG
                                ||||||||| ||||||
                                ATTGTTTTG TCTCTT
                                        _
GAM335  FLJ12787  3'  TCAGGGTTTTTTTTTGTTTTTT 49751    C          T
          T                      GA AGAACGAGAGGG GCTCTGA
                                || ||||||||||| |||||||
                                TT TTTTGTTTTTTT TGGGACT
                                 T          T
GAM335  FLJ12888  3'  CAGGGTATTGCTCTGTT     46317     G   _
                                AAC AGAG GGTGCTCTG
                                ||| |||| |||||||||
                                TTG TCTC TTATGGGAC
                                  _   G
GAM335  FLJ13842  3'  TCAGAGCATAATTATTCTGTTA 44988         CG GAGG
                                TGACAGAA  A    GTGCTCTGA
                                ||||||||  |    |||||||||
                                ATTGTCTT  T    TACGAGACT
                                     AT AA__
GAM335  FLJ13902  3'  CACCCTTGCGTTTTGTT     45040          AG
                                GACAGAACG  AGGGTG
                                |||||||||  ||||||
                                TTGTTTTGC  TCCCAC
                                      GT
GAM335  FLJ14251  3'  CAGAGCACTTGTGTCTGCA   45968    A   ACGAGA
                                TG CAGA     GGGTGCTCTG
                                || ||||     ||||||||||
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                                AC GTCT     TTCACGAGAC
                                 _   GTG___
GAM335  FLJ20489  3' CAGAGTGCCCTTGCTGCA    35248    A   AACGA    TG
                                TG CAG    GAGGG  CTCTG
                                || |||    |||||  |||||
                                AC GTC    TTCCC  GAGAC
                                 _  G____    GT
GAM335  FLJ21415  3' CCTTCTCGTGTTGTCA      45353       A
                                TGACAG ACGAGAGGG
                                |||||| |||||||||
                                ACTGTT TGCTCTTCC
                                   G
GAM335  FLJ21439  3' TGTTTTCTTGTACTGTTA    89727       A      GG
                                TGACAG ACGAGAG  TG
                                |||||| |||||||  ||
                                ATTGTC TGTTCTT  GT
                                   A      TT
GAM335  FLJ22202  3' TTAGGGAATTTTTGTTTTGCA  45992    A        GGTG
                                TG CAGAACGAGAG   CTCTGA
                                || ||||||||||   ||||||
                                AC GTTTTGTTTTT   GGGATT
                                 _         AA__
GAM335  FLJ22501  5' TCAGGGCACTCTGGCCTGT   45370     AA GAG
                                ACAG  C   AGGGTGCTCTGA
                                ||||  |   ||||||||||||
                                TGTC  G   TCTCACGGGACT
                                  CG ___
GAM335  FLJ22800  3' CGGAGCATTCTGGATTTTG   45604      CGAG
                                CAGAA   AGGGTGCTCTG
                                |||||   ||||||||||
                                GTTTT   TCTTACGAGGC
                                   AGG_
GAM335  FLJ23017  3' TCTAAGTCATTTTTTTATTTTG 43125        CG      _  CT
           TTA                    TGACAGAA  AGAGGGTG CT  GA
                                |||||||  |||||||  ||  ||
                                ATTGTTTT  TTTTTTAC GA  CT
                                     AT       T  AT
GAM335  FLJ23563  5' TTAGATACGATCTTTTTTGTTC 67606   A         TGC___
           TGCG                    CAGAACGAGAGGG     TCTGA
                                 ||||||||||||     |||||
                                 GTCTTGTTTTTTC     AGATT
                                _           TAGCAT
GAM335  FLJ30525  3' ACTTTTTTGTTTTCTCA     58064     C
                                TGA AGAACGAGAGGGT
                                ||| ||||||||||||
                                ACT TTTTGTTTTTTCA
                                  C
GAM335  FLJ31153  3' GGGTATCTTTTGTC       58128       ACGAGA
                                GACAGA     GGGTGCTC
                                ||||||     ||||||||
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                                CTGTTT     TCTATGGG
                                       _______
GAM335  GOLPH3   3'  TAGAGATTTTTTTTGTT     42115          TG
                                AACGAGAGGG  CTCTG
                                ||||||||||  |||||
                                TTGTTTTTTT  GAGAT
                                      TA
GAM335  GP5      3'  TCCTCTTTTTTGATTTGTCA   15658        A ____
                                TGACAGA C    GAGAGGG
                                ||||||| |    |||||||
                                ACTGTTT G    TTCTCCT
                                    A TTTT
GAM335  H2AV     3'  CAGAGCACTTTTCCTTG     56846      __
                                CGAG  AGGGTGCTCTG
                                ||||  ||||||||||
                                GTTC  TTTCACGAGAC
                                  CT
GAM335  HN1L     3'  TCAGAGTGCTTAGTCTGCTCA  58002     _   ACGAGA   TG
                                TGA CAGA     GGG  CTCTGA
                                ||| ||||     |||  ||||||
                                ACT GTCT     TTC  GAGACT
                                  C    GA____   GT
GAM335  HSH2     3'  CCATATCATCTGTTTGTTCTGT 51672          A    CTC  A
             T                   GACAGAACGAG GGGTG   TG
                                ||||||||||| |||||   ||
                                TTGTCTTGTTT TCTAC   AC
                                      G    TAT  CC
GAM335  HYPH     3'  TTAGAAAAAATTTTCTTTTTGT 94901        C    GGTGC
             TA                   TGACAGAA GAGAG    TCTGA
                                ||||||||| |||||    |||||
                                ATTGTTTT CTTTT    AGATT
                                     T    AAAAA
GAM335  IMP-2    3'  TTGGAGCATTTTTTTATTTTTT 21574    C   CG        TG
             TA                   TGA AGAA  AGAGGGTGCTC  A
                                ||| ||||  ||||||||||  |
                                ATT TTTT  TTTTTTACGAG  T
                                  T   AT        GT
GAM335  KIAA0084 3'  TTCTCTTGTTTAGTTA     68145     A
                                TGAC GAACGAGAGGG
                                |||| ||||||||||
                                ATTG TTTGTTCTCTT
                                  A
GAM335  KIAA0121 3'  ATCTTTTTTTTTGTC      72654       C
                                GACAGAA GAGAGGGT
                                ||||||| ||||||||
                                CTGTTTT TTTTTCTA
                                      _
GAM335  KIAA0164 3'  GGTTACTTTTATTCTGTTA   28451        CG   GGT
                                TGACAGAA  AGAG   GCT
                                ||||||||  ||||   |||
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                                ATTGTCTT  TTTC   TGG
                                    AT    AT_
GAM335  KIAA0173  3'  TCAGAGTATTTTTTGAAGTGGT 27671     AGAACG
            T                    GAC     AGAGGGTGCTCTGA
                                 |||     ||||||||||||||
                                 TTG     TTTTTTATGAGACT
                                   GTGAAG
GAM335  KIAA0227  3'  TCAGAGCACTTTCATGTATTTT 60703    C  _  A
            TC                   GA AGA ACG GAGGGTGCTCTGA
                                 || ||| ||| ||||||||||||||
                                 CT TTT TGT CTTTCACGAGACT
                                  T  A  A
GAM335  KIAA0232  3'  TGGAGCATTTAGGCTTTGTTC  72759       A___      TG
                                 GAACGAG   GGGTGCTC  A
                                 |||||||   ||||||||  |
                                 CTTGTTT   TTTACGAG  T
                                     CGGA      GT
GAM335  KIAA0237  3'  CAGAGCGTCTGTCTTTGT    28522     GAAC   G  _
                                 ACA   GAGA GG TGCTCTG
                                 |||   |||| || |||||||
                                 TGT   TTCT TC GCGAGAC
                                   _____   G  T
GAM335  KIAA0261  3'  CAGTTTTTTGTTTTGTT     68179           G
                                 GACAGAACGAGAGG TG
                                 |||||||||||||| ||
                                 TTGTTTTGTTTTTT AC
                                         G
GAM335  KIAA0352  3'  TTGGAGTGCCTGGCTCTCTG  29159     AC  A_  TG  TG
                                 CAGA  GAG  GGG  CTC  A
                                 ||||  |||  |||  |||  |
                                 GTCT  CTC  TCC  GAG  T
                                   __   GG   GT   GT
GAM335  KIAA0376  3'  ACATTTTTGTTTTGTTA     65595           G
                                 TGACAGAACGAGAG GT
                                 |||||||||||||| ||
                                 ATTGTTTTGTTTTT CA
                                         A
GAM335  KIAA0377  3'  TGGGGTGGGTTGGTCTGTCA  27798       A G  AGGG    TG
                                 TGACAGA C AG    TGCTC  A
                                 ||||||| | ||    |||||  |
                                 ACTGTCT G TT    GTGGG  T
                                     _ G  GG__     GT
GAM335  KIAA0410  3'  TTAGAAAAATCTTATGTTCTGT 28780        A    GTGC
            C                    GACAGAACG GAGG    TCTGA
                                 |||||||||  ||||    |||||
                                 CTGTCTTGT TTCT    AGATT
                                       A    AAAA
GAM335  KIAA0418  3'  GTTTCCTTTTGTTTTGT     27563           T
                                 ACAGAACGAGAGGG GC
                                 |||||||||||||| ||
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                                TGTTTTGTTTTCCT TG
                                        T
GAM335  KIAA0433  3'  TCAGGAAAACTTTTGTTTTGT  30839          GGTG T
                                ACAGAACGAGAG   C CTGA
                                ||||||||||||   | ||||
                                TGTTTTGTTTTC   G GACT
                                      AAAA _
GAM335  KIAA0446  5'  AGTGCCCTCTCTTCTGTT    68853       C      TG
                                GACAGAA GAGAGGG  CT
                                ||||||| |||||||  ||
                                TTGTCTT CTCTCCC  GA
                                    _     GT
GAM335  KIAA0447  3'  TGCCTGCGGCTTTCTCGGTTTG 71678       A       _  TCTGA
            TC                    GACAGA CGAGAGGGT GC
                                ||||||| ||||||||| ||
                                CTGTTT GCTCTTTCG CG
                                   G       G  TCCGTT
GAM335  KIAA0469  3'  TTAGGGTACCTTCAGTACTTTT 29360     ____  GA
            TGCA                  CAGA   AC  GAGGGTGCTCTGA
                                ||||   ||  ||||||||||||||
                                GTTT   TG  CTTCCATGGGATT
                                  TTCA  A_
GAM335  KIAA0478  3'  ATCCTTGTTTTGTT       29541        GA
                                GACAGAAC  GAGGGT
                                ||||||||  ||||||
                                TTGTTTTG  TTCCTA
                                      __
GAM335  KIAA0555  3'  ACTTTCTTGTGTTGTT      28878      A
                                GACAG ACGAGAGGGT
                                ||||| ||||||||||
                                TTGTT TGTTCTTTCA
                                  G
GAM335  KIAA0557  3'  TTAGTCTCCTTTTTTTGTTTTG 78013         ___   GT   CTGA
            TT                    ACAGAACGA   GAGG  GCT
                                |||||||||   ||||  |||
                                TGTTTTGTT   TTCC  TGA
                                     TTT    TC   TT
GAM335  KIAA0757  3'  ATTGGGGTTTTGTTTTGTTTTG 20127          G  T    TG
            TT                    GACAGAACGAGA GG GCTC  A   T
                                ||||||||||||| || ||||  |   |
                                TTGTTTTGTTTT TT TGGG  T   A
                                      G  T    GT
GAM335  KIAA0769  3'  GTGCCTTTTTTTTTTGTT    29098       C      TG
                                GACAGAA GAGAGGG  C
                                ||||||| |||||||  |
                                TTGTTTT TTTTTCC  G
                                   T      GT
GAM335  KIAA0779  3'  GGGTTCTTTTGTCTTGTCA   85730       GA       GT
                                TGACA  ACGAGAGG  GCTC
                                |||||  ||||||||  ||||
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                                ACTGT  TGTTTTCT  TGGG
                                  TC      __
GAM335  KIAA0876 3' TCAGAGCATCTCGCTGTTTTTT 64683      C  G  ___
             TGTT                  CAGAA GA AG   GGTGCTCTGA
                                |||||  ||  ||   ||||||||||
                                GTTTT TT TC   CTACGAGACT
                                  T  G  GCT
GAM335  KIAA0916 5' TGGAGCGTTCTCAGTTTCTCA 30493     CA    GA   GG    TG
                                TGA  GAAC  GAG  TGCTC  A
                                |||  ||||  |||  |||||  |
                                ACT  TTTG  CTC  GCGAG  T
                                  C_    A_   TT    GT
GAM335  KIAA0940 3' ATTCTTTTGTTTGTT      29866       A
                                GACAGA CGAGAGGGT
                                ||||||  |||||||||
                                TTGTTT GTTTTCTTA

                                  _
GAM335  KIAA1091 3' TCAGTCCCACGTATTTTCTTTT 69687     C        T_____
             TTGTCA                  GAA GAGAGGGTGC     CTGA
                                |||  ||||||||||      ||||
                                TTT TTCTTTTATG     GACT
                                  _        CACCCT
GAM335  KIAA1165 3' TTAGGGTATCTAAACATTTTTG 67410      CGAGA_
                                CAGAA     GGGTGCTCTGA
                                |||||     ||||||||||
                                GTTTT     TCTATGGGATT
                                  TACAAA
GAM335  KIAA1170 3' TTAGAGCACCTGCACCTTCT   69862     CGAGA
                                AGAA    GGGTGCTCTGA
                                ||||    ||||||||||
                                TCTT    TCCACGAGATT
                                  CCACG
GAM335  KIAA1193 3' TCTGCATTGTTTTTTTGTTTTG 67652          ___   TCTGA
             TT                   ACAGAACGAGAGG   GTGC
                                ||||||||||||   ||||
                                TGTTTTGTTTTTT   TACG
                                       TGT   TCT
GAM335  KIAA1237 3' GGGCATCCTGGTTTTG      80474       GAG
                                CAGAAC   AGGGTGCTC
                                ||||||   |||||||||
                                GTTTTG   TCCTACGGG
                                  G__
GAM335  KIAA1240 3' GGCCATTTTTTCTTCTGTCA   66735       C      _
                                TGACAGAA GAGAGGGTG CT
                                ||||||||  |||||||| ||
                                ACTGTCTT CTTTTTTAC GG
                                     _       C
GAM335  KIAA1247 3' TATTCTTTTGGTTTGTCA    61855       A
                                TGACAGA CGAGAGGGTG
                                |||||||  ||||||||||
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                                ACTGTTT GTTTTCTTAT
                                   G
GAM335  KIAA1265 3' ATTGGGGTGTTCTTTCTGTTTT 70787       _     TG  TG
             GTT                  ACAGAAC GAGAGGG  CTC  A   T
                                  ||||||| |||||||  |||  |   |
                                  TGTTTTG CTTTCTT  GGG  T   A
                                     T     GT   GT
GAM335  KIAA1321 3' GGGTTTTCTTGTTTTGTT    62227           GT
                                  GACAGAACGAGAGG  GCTC
                                  ||||||||||||||  ||||
                                  TTGTTTTGTTCTTT  TGGG
                                                  __
GAM335  KIAA1322 3' TTGGCAAATTTTTTGTTCTGTC 72744          GG_   CTGA
                                  GACAGAACGAGAG   TGCT
                                  ||||||||||||   ||||
                                  CTGTCTTGTTTTT   ACGG
                                         TAA   TT
GAM335  KIAA1350 3' TTAGAGCATCCTTCCCTTTT  72705     CGA
                                  AGAA   GAGGGTGCTCTGA
                                  ||||   ||||||||||||||
                                  TTTT   TTCCTACGAGATT
                                    CCC
GAM335  KIAA1371 3' TTAGGGTGTTTTTTTTTTTT  89048     C      TG
                                  AGAA GAGAGGG  CTCTGA
                                  |||| |||||||  ||||||
                                  TTTT TTTTTTT  GGGATT
                                    T     GT
GAM335  KIAA1430 3' TTAGGCCAGATTCTTGTTCAGT 80769     A       GG  CT
             TA                    TGAC GAACGAGAG  TG  CTGA
                                  |||| |||||||||  ||  ||||
                                  ATTG CTTGTTCTT  AC  GATT
                                    A       AG  CG
GAM335  KIAA1450 3' TCATTCCACCTTTTTGTTTTGT 65828            CTC
                                  ACAGAACGAGAGGGTG   TGA
                                  ||||||||||||||||   |||
                                  TGTTTTGTTTTTCCAC   ACT
                                           CTT
GAM335  KIAA1492 3' TCAGTCACCCTCCTGTTTTGTT 64508         A     CT
                                  GACAGAACG GAGGGTG  CTGA
                                  |||||||| |||||||  ||||
                                  TTGTTTTGT CTCCCAC  GACT
                                       C      T_
GAM335  KIAA1492 3' TTCTCTTGTTTTATTA     64512     C
                                  TGA AGAACGAGAGGG
                                  ||| ||||||||||||
                                  ATT TTTTGTTCTCTT
                                    A
GAM335  KIAA1608 3' CACTTTTAGTTTTGTT     45689         GA
                                  GACAGAAC  GAGGGTG
                                  ||||||||  |||||||
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                                TTGTTTTG  TTTTCAC
                                    A_
GAM335  KIAA1691  3'  TCGCTGTGTTTTTTTGTTTTTT 92565     C          TG TC
              TA                  TGA AGAACGAGAGGG  C  TGA
                                  ||| |||||||||||  |  |||
                                  ATT TTTTGTTTTTTT  G  GCT
                                    T          GT TC
GAM335  KIAA1728  3'  GTTACTTTTGTTTTGTT     68418            GGT
                                  GACAGAACGAGAG   GC
                                  ||||||||||||   ||
                                  TTGTTTTGTTTTC   TG
                                        AT_
GAM335  KIAA1750  3'  TACCTTCTCTTTTGTTA     68252         C
                                  TGACAGAA GAGAGGGTG
                                  |||||||| |||||||||
                                  ATTGTTTT CTCTTCCAT
                                    _
GAM335  KIAA1804  3'  TAATACGTTTTCTTGTTTTATC 69792     C         GG  CTCTGA
              A                    TGA AGAACGAGAG  TG
                                  ||| ||||||||||  ||
                                  ACT TTTTGTTCTT  GC
                                    A         TT  ATAATT
GAM335  KIAA1867  3'  CAGGGCACGTTCTGGTT     94823     G    G
                                  AAC AGAG GTGCTCTG
                                  ||| |||| ||||||||
                                  TTG TCTT CACGGGAC
                                    G    G
GAM335  KIAA1889  3'  TTAGGGTGTCTTGATGGCGTT  73504      AG___    TG
                                  AACG    AGGG  CTCTGA
                                  ||||    ||||  ||||||
                                  TTGC    TTCT  GGGATT
                                     GGTAG    GT
GAM335  KIAA1900  3'  TAGAGCATTCTTTGT       73249     G
                                  AC AGAGGGTGCTCTG
                                  || ||||||||||||
                                  TG TTTCTTACGAGAT
                                    _
GAM335  KIAA1915  3'  CCTTTTTCTTTTGTCA      73280         C
                                  TGACAGAA GAGAGGG
                                  |||||||| |||||||
                                  ACTGTTTT TTTTTCC
                                      C
GAM335  KIAA1958  3'  TTGATGCGCCTTTTTTTTCTGT 81913        C        _  TGA
              T                    GACAGAA GAGAGGGTGC TC
                                  ||||||| |||||||||| ||
                                  TTGTCTT TTTTTCCGCG AG
                                      T        T  TT
GAM335  KIAA1975  5'  GTTTTTTTTTTGTTTTGTTA  73977              T_
                                  TGACAGAACGAGAGGG  GC
                                  ||||||||||||||||  ||
```

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                                ATTGTTTTGTTTTTTT  TG
                                      TT
GAM335  LANCL2   3'  GAGGTTCTTTGGTTTTGTTA  37997        G   GG G
                                TGACAGAAC AGAG  T CTC
                                ||||||||| ||||  | |||
                                ATTGTTTTG TTTC  G GAG
                                     G   TT _
GAM335  LCE     3'  TATCCTTTTGTTCAGTT    44029    A
                                GAC GAACGAGAGGGTG
                                ||| ||||||||||||
                                TTG CTTGTTTTCCTAT
                                  A
GAM335  LRBA    5'  AAGAGGGACCCTTTCGTTTTGC 22050    A          G   GA
            A                    TG CAGAACGAGAGGGT CTCT
                                || ||||||||||||| ||||
                                AC GTTTTGCTTTCCCA GGGA
                                 _          _   GAAG
GAM335  LSFR2   3'  TATTTTTTGGTTTTGTCA   60569        G
                                TGACAGAAC AGAGGGTG
                                ||||||||| ||||||||
                                ACTGTTTTG TTTTTTAT
                                     G
GAM335  LSM5    3'  TTATATGCTTATTTGTTTTGTC 24641          AG   CTCTGA
            A                    TGACAGAACGAG  GGTG
                                ||||||||||||  ||||
                                ACTGTTTTGTTT  TCGT
                                       AT   ATATT
GAM335  LUC7A   3'  TTGTGTATCTTTTTTGTTCT  33138         _    TCTGA
                                AGAACGAGAG GGTGC
                                |||||||||| |||||
                                TCTTGTTTTT CTATG
                                      T    TGTT
GAM335  M96     3'  TTGGAGAAACGTTGTTTGTTTT 23741         _ G  G_  TG
            GTTA                  GACAGAACGAG AG GT  CTC  A
                                |||||||||| || ||  |||  |
                                TTGTTTTGTTT TT CA  GAG  T
                                      G  G  AA   GT
GAM335  MAL2    3'  TTAGTATCCCTTTTGTTTGGTT 53560    A        _   CTGA
                                GAC GAACGAGAGGG TGCT
                                ||| ||||||||||| ||||
                                TTG TTTGTTTTCCC ATGA
                                  G         T   TT
GAM335  MAN1    3'  TCAGTTTCCTTTTTGTTTT   26715          TGCT
                                AGAACGAGAGGG   CTGA
                                ||||||||||||   ||||
                                TTTTGTTTTTCC   GACT
                                       TTT_
GAM335  MAPK6   5'  GAGTTTCTTGTTTTCGTTA   10835     _       GGT
                                TGAC AGAACGAGAG   GCTC
                                |||| ||||||||||  ||||
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                                ATTG TTTTGTTCTT   TGAG
                                  C       ___
GAM335  MGC10765  3'  TGCCTTTGTGTTTTGTTA    44304          A
                                TGACAGAACG GAGGGTG
                                |||||||||| |||||||
                                ATTGTTTTGT TTTCCGT
                                     G
GAM335  MGC10848  3'  CCAACCTGCTTTTCTGTTCTGT 47544          AG     CTCTGA
          TA                      TGACAGAACG  AGGGTG
                                |||||||||  ||||||
                                ATTGTCTTGT  TTTCGT
                                     CT     CCAACCC
GAM335  MGC13017  3'  TCAGGGTTTTTTGTTTTTTGTT 54693          GT____
          TTGTT                     AGAACGAGAGG     GCTCTGA
                                ||||||||||      |||||||
                                TTTTGTTTTTT     TGGGACT
                                     GTTTTT
GAM335  MGC15606  3'  TCAGGTGTTTTTTTTTTTGTT  58879        C      TG T
                                GACAGAA GAGAGGG  C CTGA
                                ||||||| |||||||  | ||||
                                TTGTTTT TTTTTTT  G GACT
                                   _      GT _
GAM335  MGC16186  3'  TCCTCTTGTTTTATCA      50432     C
                                TGA AGAACGAGAGGG
                                ||| ||||||||||||
                                ACT TTTTGTTCTCCT
                                  A
GAM335  MGC2477   5'  TTGGGTTTTTTTTTGGTTTTGT 44076         G     T_    TGA
          T                      GACAGAAC AGAGGG  GCTC
                                |||||||| ||||||  ||||
                                TTGTTTTG TTTTTT  TGGG
                                     G     TT    TT
GAM335  MGC27434  3'  CTTTTTTATTCTGTTA      58948         CG
                                TGACAGAA  AGAGGG
                                ||||||||  ||||||
                                ATTGTCTT  TTTTTC
                                     AT
GAM335  MGC29937  3'  ACACCTTTCATTCTGTT     58109         C     _
                                GACAGAA GAGAGG GT
                                ||||||| |||||| ||
                                TTGTCTT CTTTCC CA
                                     A     A
GAM335  MGC3040   3'  TTGGGGTTCAGCTTTGTTTTCT 66847     C       AGGGT    TG
          CA                      TGA AGAACGAG    GCTC  A
                                ||| ||||||||    ||||  |
                                ACT TTTTGTTT    TGGG  T
                                  C       CGACT    GT
GAM335  MGC3251   3'  TTTTCTTGTTTTGCA      49315    A
                                TG CAGAACGAGAGGG
                                || ||||||||||||
```

```
                                AC GTTTTGTTCTTTT
                                  _
GAM335  MGC34923  3'  GTGCTCCTTTTTTCTGTT    58524       C    _ TG
                                GACAGAA GAGAGG G  C
                                ||||||| |||||| |  |
                                TTGTCTT TTTTCC C  G
                                   _     T GT
GAM335  MGC4268   5'  GGGTTCCTCTTGCTTTGTCA  48746       A      T
                                TGACAGA CGAGAGGG GCTC
                                ||||||| |||||||| ||||
                                ACTGTTT GTTCTCCT TGGG
                                    C      _
GAM335  MIDORI    3'  TCAGGGTATCTTCTCCTTC   73793     C
                                GAA GAGAGGGTGCTCTGA
                                ||| ||||||||||||||
                                CTT CTCTTCTATGGGACT
                                  C
GAM335  MKRN1     3'  TTGGAAATTGTACCTTTGTGTT 25577       A      ____ TG
            TTGTT                  AGAACG GAGGGTGC   TC  A
                                |||||| ||||||||   ||  |
                                TTTTGT TTTCCATG   AG  T
                                   G       TTAA  GT
GAM335  MO25      3'  TCATTTTACCCTTTTGTTTTTC 32814     C          CTC
            A                   TGA AGAACGAGAGGGTG   TGA
                                ||| ||||||||||||||   |||
                                ACT TTTTGTTTTCCCAT   ACT
                                  _           TTT
GAM335  MRPL15    5'  TCAGGGCGCCCTTGAAAGTTCT 26348   C    GA__
            TG                   A AGAAC    GAGGGTGCTCTGA
                                | |||||    ||||||||||||||
                                G TCTTG    TTCCCGCGGGACT
                                 T    AAAG
GAM335  MUF1      3'  CTTTCTCTTTCTGTCA      95489        C
                                TGACAGAA GAGAGGG
                                |||||||| |||||||
                                ACTGTCTT CTCTTTC
                                    T
GAM335  MY050     5'  TCTGAGCCTTTTTTTTTTGTCA 50926       C      T   T
                                TGACAGAA GAGAGGG GCTC GA
                                |||||||| ||||||| |||| ||
                                ACTGTTTT TTTTTTC CGAG CT
                                   _      _   T
GAM335  NCOA5     3'  ATTGGGGCTGTATCTTTTTTTG 40583       __   ___   TG
            TTTTGTT                AACGAGA  GGGT   GCTC  A   T
                                |||||||  ||||  |||| |  |
                                TTGTTTT  TCTA  CGGG  T   A
                                   TT   TGT   GT
GAM335  NETO2     3'  TTCTTTCCTTTTGTTA      36117        C
                                TGACAGAA GAGAGGG
                                |||||||| |||||||
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                                ATTGTTTT CTTTCTT
                                     C
GAM335  NICE-3   3'  TTAGGGCATCTTAGAGTT    31277     GAG
                                AAC   AGGGTGCTCTGA
                                |||   ||||||||||||
                                TTG   TTCTACGGGATT
                                  AGA
GAM335  NKX2B    3'  TTGGGTTTGTTTTTTGTTTTGT 10237            GT_   TGA
             T                   GACAGAACGAGAGG   GCTC
                                 ||||||||||||||   ||||
                                 TTGTTTTGTTTTTT   TGGG
                                          GTT    TT
GAM335  OLIG1    3'  TTAGGGCGCCTTGCCGTGGTTG 95593     A_   AG
                                 CAG  ACG  AGGGTGCTCTGA
                                 |||  |||  ||||||||||||
                                 GTT  TGC  TTCCGCGGGATT
                                   GG   CG
GAM335  P2RX1    3'  TCGGGGCATTTTCACTGTCA   67173       AACGA
                                 TGACAG    GAGGGTGCTCTGA
                                 ||||||    ||||||||||||
                                 ACTGTC    CTTTTACGGGGCT
                                    A____
GAM335  PARVA    3'  TCTTTTCTTTTCTGTTA     36655        C_
                                 TGACAGAA  GAGAGGG
                                 ||||||||  |||||||
                                 ATTGTCTT  CTTTTCT
                                      TT
GAM335  PDE11A   3'  CATCCTTTTGTTCTTTTA    33776     C
                                 TGA AGAACGAGAGGGTG
                                 ||| ||||||||||||||
                                 ATT TCTTGTTTTCCTAC
                                   T
GAM335  PER3     3'  TTAGCCTCATTTATTTTGTTCT 33684         _____   T   CTGA
             GTTA                    AGAACGAGA    GGG GCT
                                 |||||||||    ||| |||
                                 TCTTGTTTT    CTC CGA
                                      ATTTA  _   TT
GAM335  PF1      3'  GCCTGTTTTGTTCTGTCA    95122           G  T
                                 TGACAGAACGAGA GG GC
                                 |||||||||||||| || ||
                                 ACTGTCTTGTTTT TC CG
                                        G  _
GAM335  PHCA     3'  GAAGACCTTTTTTTCTGTT   37177        C       GC
                                 GACAGAA GAGAGGGT  TC
                                 |||||||| ||||||||  ||
                                 TTGTCTT TTTTTCCA  AG
                                    _       GA
GAM335  PISD     3'  GGCCCCTTTTGTTTT       26773           T
                                 AGAACGAGAGGG GCT
                                 ||||||||||||| |||
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                                TTTTGTTTTCCC CGG
                                          _
GAM335  PLP1     3'  TGGATAGCATGTCTTTTTTTCT 5012        C     _    CTGA
             GTTA                    GACAGAA GAGAGG GTGCT
                                     ||||||| |||||| |||||
                                     TTGTCTT TTTTCT TACGA
                                        T     G     TAGGTT
GAM335  PLPL     3'  TTAGGGTATCCTTGGCTG    39436     AACGA
                                     CAG    GAGGGTGCTCTGA
                                     |||    ||||||||||||||
                                     GTC    TTCCTATGGGATT
                                       GG___
GAM335  PPFIA4   3'  TCAGAGCACCTTGAGAAGTGTT 70331      GAACGAG
                                     GACA      AGGGTGCTCTGA
                                     ||||      ||||||||||||
                                     TTGT      TTCCACGAGACT
                                       GAAGAG_
GAM335  PPP4R1L  3'  TAGAGTGTTCTGCTGTTC    79504      AG   TG
                                     GAACG  AGGG  CTCTG
                                     |||||  ||||  |||||
                                     CTTGT  TCTT  GAGAT
                                        CG   GT
GAM335  PRO0899  5'  TTGTTTTGTTTTGTTA     37698           G
                                     TGACAGAACGAGA GG
                                     |||||||||||||| ||
                                     ATTGTTTTGTTTT TT
                                              G
GAM335  PRO1600  5'  TACTATTTCTCTTTTGTTA   26034        C    __
                                     TGACAGAA GAGAG  GGTG
                                     |||||||| |||||  ||||
                                     ATTGTTTT CTCTT  TCAT
                                          _    TA
GAM335  PTK9     3'  TTAGAGTATTTGGGGTTTTGTT 11029        GAGA
                                     GACAGAAC   GGGTGCTCTGA
                                     ||||||||   ||||||||||||
                                     TTGTTTTG   TTTATGAGATT
                                          GGG_
GAM335  PTP4A1   5'  TCAGTGCACTTCTTTTCTGTT  12942       C     G   T
                                     GACAGAA GAGAGG TGC CTGA
                                     ||||||| |||||| ||| ||||
                                     TTGTCTT TTCTTC ACG GACT
                                          _     _   T
GAM335  RAB10    3'  TTGGTTTTCCTTTTTTGTTCTG 85182        __    T_   CTGA
                                     CAGAACGA  GAGGG  GCT
                                     ||||||||  |||||  |||
                                     GTCTTGTT  TTCCT  TGG
                                          TT    TT   TT
GAM335  RAB40A   5'  TACATATTTTTTCAGTTTTGTT 82072          _       CTCTGA
             A                        TGACAGAAC GAGAGGGTG
                                     |||||||||| |||||||||
```

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                                ATTGTTTTG CTTTTTTAT
                                    A       ACAT
GAM335  RABEX5   3'  TCAGAGCATTTTTTAAAGGTAC 27189    _ AGAACG
          A                      TG AC     AGAGGGTGCTCTGA
                                 || ||     ||||||||||||||
                                 AC TG     TTTTTTACGAGACT
                                  A  GAAA__
GAM335  RACGAP1  3'  GAGCTTTTTCTTCTGTTA    25197       C     GT
                                 TGACAGAA GAGAGG  GCTC
                                 |||||||| ||||||  ||||
                                 ATTGTCTT CTTTTT  CGAG
                                    _     __
GAM335  RAD51    3'  TGCACAGATTCTTTTTTTCTGT 11227      C     ____   TCTGA
          CA                     ACAGAA GAGAGG   GTGC
                                 ||||||| ||||||   ||||
                                 TGTCTT TTTTCT    CACG
                                    T     TAGA    T   A
GAM335  RAD51    3'  TGCACAGATTCTTTTTTTCTGT 56021      C     ____   TCTGA
          CA                     ACAGAA GAGAGG   GTGC
                                 ||||||| ||||||   ||||
                                 TGTCTT TTTTCT    CACG
                                    T     TAGA    T   A
GAM335  RBBP1    3'  CAGAGTTTTTATTTTGTTA   11258       CG   GGGT
                                 TGACAGAA  AGA   GCTCTG
                                 |||||||| |||   ||||||
                                 ATTGTTTT  TTT   TGAGAC
                                     AT  ____
GAM335  RBBP1    3'  CAGAGTTTTTATTTTGTTA   43429       CG   GGGT
                                 TGACAGAA  AGA   GCTCTG
                                 |||||||| |||   ||||||
                                 ATTGTTTT  TTT   TGAGAC
                                     AT  ____
GAM335  RERG     3'  ATTTTCTCATTCTGTCA    51895       C
                                 TGACAGAA GAGAGGGT
                                 |||||||| ||||||||
                                 ACTGTCTT CTCTTTTA
                                     A
GAM335  RNPC1    3'  AGAGACTTGCTTTTGTT    33985       __  G
                                 AACGAGAG  GGT CTCT
                                 |||||||| |||  ||||
                                 TTGTTTTC  TCA GAGA
                                     GT  _
GAM335  RPL26L1  3'  CATTTCCTGTTTTGTTA    32238       G  AG
                                 TGACAGAAC AG  GGTG
                                 ||||||||| ||  ||||
                                 ATTGTTTTG TC  TTAC
                                     _ CT
GAM335  RYK      3'  CAGGGCATTCTTATTTC    82618    CGA
                                 GAA   GAGGGTGCTCTG
                                 |||   ||||||||||||
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                                CTT   TTCTTACGGGAC
                                  TA_
GAM335  S100Z    3'  GCATCTTTTTGGTTTGTCA   55377        A
                                TGACAGA CGAGAGGGTGC
                                ||||||| ||||||||||
                                ACTGTTT GTTTTTCTACG
                                    G
GAM335  SAP18    5'  CATCCTTTTGTTTGTCA     19645        A
                                TGACAGA CGAGAGGGTG
                                ||||||| |||||||||
                                ACTGTTT GTTTTCCTAC
                                    _
GAM335  SDFR1    3'  AGTGATTATCTTTTCTTCTGTT 24864        C       C  TGA
            A                    TGACAGAA GAGAGGGTG TC
                                ||||||||| ||||||||| ||
                                ATTGTCTT CTTTTCTAT AG
                                    _       T  TGAA
GAM335  SDFR1    3'  AGTGATTATCTTTTCTTCTGTT 33914        C       C  TGA
            A                    TGACAGAA GAGAGGGTG TC
                                ||||||||| ||||||||| ||
                                ATTGTCTT CTTTTCTAT AG
                                    _       T  TGAA
GAM335  SEC24A   3'  GGGTTTTTTGTTTTGTT    82682           GGT
                                GACAGAACGAGAG  GCTC
                                |||||||||||||  ||||
                                TTGTTTTGTTTTT  TGGG
                                    ___
GAM335  SEF      3'  TTAGGGTATTCAGCTTTGTTC 69468        A__
                                GAACGAG  GGGTGCTCTGA
                                |||||||  ||||||||||
                                CTTGTTT  CTTATGGGATT
                                    CGA
GAM335  SFRS5    3'  TAGAGCAGCTGTTTGTT     22645        A  G
                                AACGAG GG TGCTCTG
                                |||||| || |||||||
                                TTGTTT TC ACGAGAT
                                    G  G
GAM335  SNRK     5'  CTAAATATTTTTTCTTCTGTT  34765        C       CTCTGA
                                GACAGAA GAGAGGGTG
                                ||||||| |||||||||
                                TTGTCTT CTTTTTTAT
                                    _       AAATCT
GAM335  SNRK     3'  TAGATTATCTCTTTTGTT    34769        _   C
                                AACGAGAG GGTG TCTG
                                |||||||| |||| ||||
                                TTGTTTTC CTAT AGAT
                                    T   T
GAM335  SOX7     3'  TTAAAGCAGTTCTTTTTTTTTG 48726        C     _   CTGA
            TTA                    TGACAGAA GAGAGGG TGCT
                                ||||||||| ||||||| ||||
```

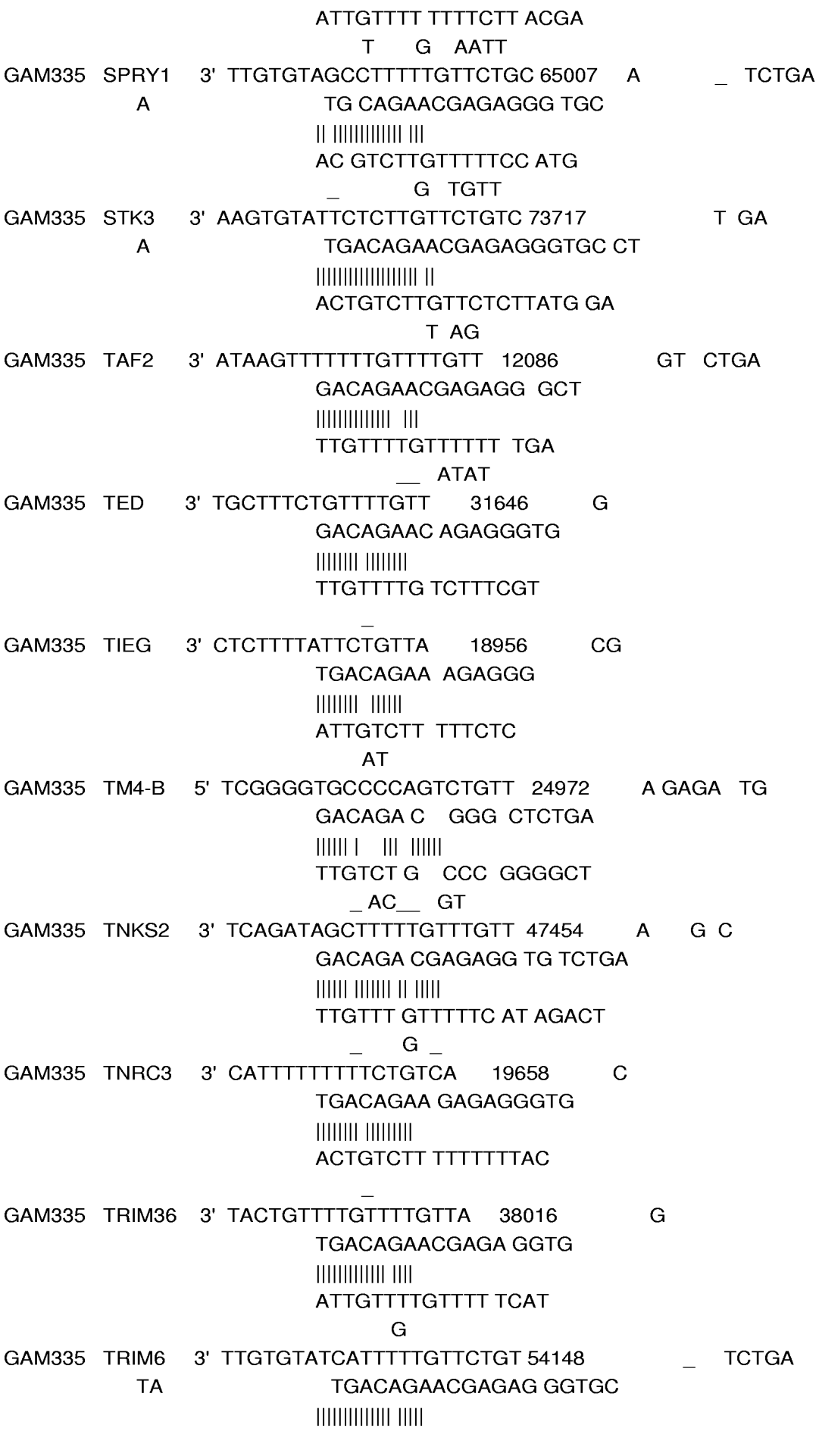
ATTGTTTT TTTTCTT ACGA
T G AATT
GAM335 SPRY1 3' TTGTGTAGCCTTTTTGTTCTGC 65007 A _ TCTGA
A TG CAGAACGAGAGGG TGC
|| |||||||||||| |||
AC GTCTTGTTTTTCC ATG
_ G TGTT
GAM335 STK3 3' AAGTGTATTCTCTTGTTCTGTC 73717 T GA
A TGACAGAACGAGAGGGTGC CT
|||||||||||||||||| ||
ACTGTCTTGTTCTCTTATG GA
T AG
GAM335 TAF2 3' ATAAGTTTTTTTGTTTTGTT 12086 GT CTGA
GACAGAACGAGAGG GCT
|||||||||||| |||
TTGTTTTGTTTTTT TGA
__ ATAT
GAM335 TED 3' TGCTTTCTGTTTTGTT 31646 G
GACAGAAC AGAGGGTG
|||||||| ||||||||
TTGTTTTG TCTTTCGT
_
GAM335 TIEG 3' CTCTTTTATTCTGTTA 18956 CG
TGACAGAA AGAGGG
|||||||| ||||||
ATTGTCTT TTTCTC
AT
GAM335 TM4-B 5' TCGGGGTGCCCCAGTCTGTT 24972 A GAGA TG
GACAGA C GGG CTCTGA
|||||| | ||| ||||||
TTGTCT G CCC GGGGCT
_ AC__ GT
GAM335 TNKS2 3' TCAGATAGCTTTTTGTTTGTT 47454 A G C
GACAGA CGAGAGG TG TCTGA
|||||| ||||||| || |||||
TTGTTT GTTTTTC AT AGACT
_ G _
GAM335 TNRC3 3' CATTTTTTTTTCTGTCA 19658 C
TGACAGAA GAGAGGGTG
|||||||| |||||||||
ACTGTCTT TTTTTTTAC
_
GAM335 TRIM36 3' TACTGTTTTGTTTTGTTA 38016 G
TGACAGAACGAGA GGTG
|||||||||||| ||||
ATTGTTTTGTTTT TCAT
G
GAM335 TRIM6 3' TTGTGTATCATTTTTGTTCTGT 54148 _ TCTGA
TA TGACAGAACGAGAG GGTGC
|||||||||||||| |||||

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                                ATTGTCTTGTTTTT CTATG
                                       A    TGTT
GAM335  TRPC4    3'  TCAAAAACCTTTTTGTTTTGT 32450          GCTC
                                ACAGAACGAGAGGGT   TGA
                                |||||||||||||||   |||
                                TGTTTTGTTTTTCCA   ACT
                                       AAA_
GAM335  TSGA14   3'  AGTTTTTTTGTTTTGTT    38041          GT
                                GACAGAACGAGAGG GCT
                                |||||||||||||| |||
                                TTGTTTTGTTTTTT TGA
                                       __
GAM335  TTC2     3'  TTAGAGCAGTTTCGTTTTCTCA 12410    C      GGG
                                TGA AGAACGAGA  TGCTCTGA
                                ||| |||||||||  ||||||||
                                ACT TTTTGCTTT  ACGAGATT
                                  C       G__
GAM335  UMP-CMPK 3'  TACTTTTTTTTCTTCTGTCA  32844       C__
                                TGACAGAA  GAGAGGGTG
                                ||||||||  |||||||||
                                ACTGTCTT  TTTTTTCAT
                                     CTT
GAM335  UREB1    3'  TATTTTTTTGTTCTGTT    48580
                                GACAGAACGAGAGGGTG
                                |||||||||||||||||
                                TTGTCTTGTTTTTTTAT

GAM335  VDU1     3'  TAGGGCACTTTTTATTTTG   30424     CG
                                CAGAA  AGAGGGTGCTCTG
                                |||||  ||||||||||||
                                GTTTT  TTTTTCACGGGAT
                                   A_
GAM335  WBP11    3'  TCAGGGTATTTTCTAATTTC  32849    CG_
                                GAA  AGAGGGTGCTCTGA
                                |||  ||||||||||||||
                                CTT  TCTTTTATGGGACT
                                  TAA
GAM335  WS-3     3'  TAGCTTTTCTTTTGTTA    21647       C    G
                                TGACAGAA GAGAGG TG
                                |||||||| |||||| ||
                                ATTGTTTT CTTTTC AT
                                     _    G
GAM335  YF13H12  5'  TGGAACTCTTTTGTTCTG   26663          GC  TG
                                CAGAACGAGAGGGT  TC  A
                                |||||||||||||  ||  |
                                GTCTTGTTTTCTCA  AG  T
                                       __ GT
GAM335  ZDHHC2   3'  TAGAGCACGTTTTGGTC    33011    A G   G
                                GA C AGAG GTGCTCTG
                                || | |||| ||||||||
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                                CT G TTTT CACGAGAT
                                 _ G   G
GAM335  ZNF262   3'  CAGGGTATCTCATTTTTT    17484     C  GA
                                GAA GA  GGGTGCTCTG
                                ||| ||  ||||||||||
                                TTT TT  TCTATGGGAC
                                  T  AC
GAM335  ZNRD1    5'  TTCTCTCTTTTGTTA       96001         C
                                TGACAGAA GAGAGGG
                                |||||||| |||||||
                                ATTGTTTT CTCTCTT
                                        _
GAM335  LOC120105 3'  TCCTGGTTTGTTTTGTTTTGTT 75515            G  T   CT
          A                      TGACAGAACGAGA GG GCT  GA
                                ||||||||||||| || |||  ||
                                ATTGTTTTGTTTT TT TGG  CT
                                       G  _   TC
GAM335  LOC121536 3'  GTGTTTTCTTTTTTTGTT    74089        C      TG
                                GACAGAA GAGAGGG  C
                                ||||||| |||||||  |
                                TTGTTTT TTCTTTT  G
                                    T      GT
GAM335  LOC121838 5'  TAGAGTTATTTTCTGTT     76004     G       _
                                AAC AGAGGGTG CTCTG
                                ||| |||||||| |||||
                                TTG TCTTTTAT GAGAT
                                  _       T
GAM335  LOC126669 3'  TAGTTTCTGTTCTGTCA     75417         G    G
                                TGACAGAAC AGAGG TG
                                ||||||||| ||||| ||
                                ACTGTCTTG TCTTT AT
                                      _    G
GAM335  LOC129831 3'  TGGGGTTGTTTTGTTTTG    74896          G GT    TG
                                CAGAACGAGA G  GCTC  A
                                |||||||||| |  ||||  |
                                GTTTTGTTTT T  TGGG  T
                                       G __    GT
GAM335  LOC131308 3'  TTTTCTTGTATTGTTA      75008       A
                                TGACAG ACGAGAGGG
                                |||||| |||||||||
                                ATTGTT TGTTCTTTT
                                   A
GAM335  LOC134111 3'  TTTTCTCTTCTGTTA       75142         C
                                TGACAGAA GAGAGGG
                                |||||||| |||||||
                                ATTGTCTT CTCTTTT
                                        _
GAM335  LOC134218 3'  TGCTTTTGTGTTTTGTTA    75159          A
                                TGACAGAACG GAGGGTG
                                ||||||||| |||||||
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                                ATTGTTTTGT TTTTCGT
                                      G
GAM335  LOC136442 3'  TCAGGGCACCTTTTCCTC    54287    AC
                                GA  GAGAGGGTGCTCTGA
                                ||  ||||||||||||||
                                CT  CTTTTCCACGGGACT
                                 C_
GAM335  LOC139410 5'  GGGGTACTGTTTGTT      75834      AG
                                AACGAG  GGTGCTCT
                                |||||||  ||||||||
                                TTGTTT  TCATGGGG
                                   G_
GAM335  LOC144453 3'  TCCTTTTATTCTGTCA     76848       CG
                                TGACAGAA  AGAGGG
                                ||||||||  ||||||
                                ACTGTCTT  TTTCCT
                                      AT
GAM335  LOC145047 3'  ACTCTTTTTTTTGTT      60515       C
                                GACAGAA GAGAGGGT
                                ||||||| ||||||||
                                TTGTTTT TTTTCTCA
                                      _
GAM335  LOC145082 5'  TTAGGGTATCTAGCTTCTG   83250      CGAGA
                                CAGAA    GGGTGCTCTGA
                                |||||    ||||||||||||
                                GTCTT    TCTATGGGATT
                                   CGA__
GAM335  LOC145439 5'  CCTTTTCTTTCTGTCA     77207       C
                                TGACAGAA GAGAGGG
                                |||||||| |||||||
                                ACTGTCTT CTTTTCC
                                      T
GAM335  LOC145547 3'  TTGGGGTACTTGGAGAATTTGC 77269    A   ACGAGA      TG
           CA                   TG CAGA     GGGTGCTC  A
                                || ||||     ||||||||  |
                                AC GTTT     TTCATGGG  T
                                 C   AAGAGG       GT
GAM335  LOC145844 3'  TTGTAAACTTTTTTTCTTCTGT 77539       C___    GG   TCTGA
           TA                   GACAGAA    GAGAG  TGC
                                |||||||    |||||  |||
                                TTGTCTT    TTTTC  ATG
                                   CTTT    AA   TT
GAM335  LOC146287 3'  ATCTTCTTGTTCCGTCA     83650     A
                                TGAC GAACGAGAGGGT
                                |||| ||||||||||||
                                ACTG CTTGTTCTTCTA
                                  C
GAM335  LOC146435 3'  TGGATTTTCTTTCTTTTGTCA  77899       C      TGC  TG
                                TGACAGAA GAGAGGG   TC  A
                                |||||||| |||||||   ||  |
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                                ACTGTTTT CTTTCTT   AG  T
                                    _      TT_  GT
GAM335  LOC146723 3'  CATCTTTGTTTTGTT       78082          GA
                                GACAGAACGA  GGGTG
                                ||||||||||  |||||
                                TTGTTTTGTT  TCTAC
                                   __
GAM335  LOC146839 3'  TTATATACCTTTTTTGTTTTGT 83818           _   CTCTGA
                                ACAGAACGAGAG GGTG
                                |||||||||||| ||||
                                TGTTTTGTTTTT CCAT
                                      T    ATATT
GAM335  LOC146894 3'  CATTATTTCGTTTTGTT     59188           GG
                                GACAGAACGAGA  GTG
                                ||||||||||||  |||
                                TTGTTTTGCTTT  TAC
                                      AT
GAM335  LOC146975 3'  TTAGGGTGGCTGTTGTTGCTGT 78225       _    GA  G
          TA                     TGACAG AACGA  GG TGCTCTGA
                                |||||| |||||  || ||||||||
                                ATTGTC TTGTT  TC GTGGGATT
                                   G    G_  G
GAM335  LOC147341 3'  TTGTACGCTGCTTTTGTTCTGT 83998           _   CTCTGA
          T                     GACAGAACGAGAG GGTG
                                |||||||||||| ||||
                                TTGTCTTGTTTTC TCGC
                                      G    ATGTT
GAM335  LOC147694 3'  TGCTTTTTCGCTCTGTT     78457       A
                                GACAGA CGAGAGGGTG
                                |||||| ||||||||||
                                TTGTCT GCTTTTTCGT
                                   C
GAM335  LOC148189 3'  TCAATGTTTCTTTTATTTTGTT 78721        CG     T  TC
          A                     TGACAGAA  AGAGGG GC  TGA
                                |||||||  |||||| ||  |||
                                ATTGTTTT  TTTCTT TG  ACT
                                     AT     _  TA
GAM335  LOC150142 5'  TTAGGGCACAGACTTGTTCTGT 79582          AGG
                                ACAGAACGAG   GTGCTCTGA
                                |||||||||   |||||||||
                                TGTCTTGTTC   CACGGGATT
                                     AGA
GAM335  LOC150166 5'  CTTTCTTGCTTTTGTT      84884       _
                                GACAGAA CGAGAGGG
                                ||||||| ||||||||
                                TTGTTTT GTTCTTTC
                                   C
GAM335  LOC150960 3'  AGTCTTTTTGTTTTGTT     80054           GT
                                GACAGAACGAGAGG  GCT
                                ||||||||||||||  |||
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                                TTGTTTTGTTTTTC  TGA
                                    __
GAM335  LOC151126 3'  TAGAGCATCTATATCTGCA   80129    A   ACGAGA
                                TG CAGA     GGGTGCTCTG
                                || ||||     ||||||||||
                                AC GTCT     TCTACGAGAT
                                 _   ATA___
GAM335  LOC151201 3'  GCGTCTTTTATTCTGTCA    85279       CG    GT
                                TGACAGAA  AGAGG  GC
                                ||||||||  |||||  ||
                                ACTGTCTT  TTTTC  CG
                                     A_    TG
GAM335  LOC151414 3'  TTAGAGTGTTTGCAATTTGTTC 80243      GA___  TG
                                GAACGA    GGG  CTCTGA
                                ||||||    |||  ||||||
                                CTTGTT    TTT  GAGATT
                                    TAACG   GT
GAM335  LOC151643 3'  GCAACTCTCTCCTTTTGTTA   80325       C      _
                                TGACAGAA GAGAGGGT GC
                                |||||||| ||||||||  ||
                                ATTGTTTT CTCTCTCA CG
                                     C       A
GAM335  LOC152275 3'  TGTTTTCTCGTTTTGTT     85624          GG
                                GACAGAACGAGAG  TG
                                ||||||||||||  ||
                                TTGTTTTGCTCTT  GT
                                       TT
GAM335  LOC152328 3'  TCAGGGTATCCGGTATTTTGT  80528      CGAGA
                                ACAGAA    GGGTGCTCTGA
                                ||||||    ||||||||||
                                TGTTTT    CCTATGGGACT
                                   ATGG_
GAM335  LOC153222 3'  TCAGAAATGTCTGCGTTTTGTC 80789        _  GG  GC
          A                      TGACAGAACG AGA  GT  TCTGA
                                ||||||||| |||  ||  |||||
                                ACTGTTTTGC TCT  TA  AGACT
                                      G   G_  A_
GAM335  LOC153606 5'  GGGTTTTTTGTTTTGTT     86075          GGT
                                GACAGAACGAGAG   GCTC
                                ||||||||||||   ||||
                                TTGTTTTGTTTTT   TGGG
                                       ___
GAM335  LOC155061 3'  TCAGGGCGTGCATTTCTGTCA  81269       CGAGAGGG
                                TGACAGAA       TGCTCTGA
                                ||||||||       ||||||||
                                ACTGTCTT       GCGGGACT
                                     TACGT___
GAM335  LOC155072 5'  GTCCTTGTGTTTTCTTGTTTTG 86385            TG TCTGA
          TT                     GACAGAACGAGAGGG  C
                                ||||||||||||||  |
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                                TTGTTTTGTTCTTTT  G
                                       GT TTCCTGT
GAM335  LOC157503 3'  ATTTTTTTGTTTTGTT      86468
                                GACAGAACGAGAGGGT
                                ||||||||||||||||
                                TTGTTTTGTTTTTTTA

GAM335  LOC157860 5'  TTAGGGTGTCTTTTTAGATG   86574    GAAC      TG
                                CA   GAGAGGG  CTCTGA
                                ||   |||||||  ||||||
                                GT   TTTTTCT  GGGATT
                                 AGA_     GT
GAM335  LOC157922 3'  GGATACTTTTGTTTTGTT    86636           GGTG
                                GACAGAACGAGAG   CT
                                ||||||||||||   ||
                                TTGTTTTGTTTTC   GG
                                       ATA_
GAM335  LOC158116 3'  GCATTTTTTTGTTTTTTTA   60322     C
                                TGA AGAACGAGAGGGTGC
                                ||| ||||||||||||||
                                ATT TTTTGTTTTTTTACG
                                  T
GAM335  LOC158357 3'  TCAGAGTACTCTACAAATTTTT 81884       CGAG__
          G                      CAGAA     AGGGTGCTCTGA
                                |||||     ||||||||||||
                                GTTTT     TCTCATGAGACT
                                   TAAACA
GAM335  LOC169286 5'  TGGAGCACTCTTTAAGATTC   82736     CG__         TG
                                GAA   AGAGGGTGCTC  A
                                |||   ||||||||||| |
                                CTT   TTTCTCACGAG  T
                                  AGAA         GT
GAM335  LOC169693 3'  TTGTTCAGCCTTTTGTTTTGTT 87294             G  CTCTGA
          A                      TGACAGAACGAGAGG TG
                                |||||||||||||| ||
                                ATTGTTTTGTTTTCC AC
                                       G  TTGTT
GAM335  LOC169933 5'  TCAGAGCATTTAAGGAATCTGC 82553    A   ACGAGA
          A                      TG CAGA     GGGTGCTCTGA
                                || ||||     ||||||||||||
                                AC GTCT     TTTACGAGACT
                                 _   AAGGAA
GAM335  LOC169961 5'  TGGAGTGTTCAGCTCTTTGT   82554      AC   A_   TG   TG
                                ACAGA  GAG  GGG  CTC  A
                                |||||  |||  |||  |||  |
                                TGTTT  CTC  CTT  GAG  T
                                   __   GA   GT   GT
GAM335  LOC170394 3'  TCCTCTTTTTTGTCA       82857         C
                                TGACAGAA GAGAGGG
                                |||||||| |||||||
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                                ACTGTTTT TTCTCCT
                                      _
GAM335  LOC196027 3'  TGGGGCATTATCGGTTTTTCA  87553     C    GA  GG     TG
                                TGA AGAAC  GA  GTGCTC  A
                                ||| |||||  ||  ||||||  |
                                ACT TTTTG  CT  TACGGG  T
                                  _    G_  AT     GT
GAM335  LOC196478 5'  TTGCACTTTCTATTGTTTTGTC 87728          __       TCTGA
          A                      TGACAGAACG  AGAGGGTGC
                                ||||||||||  |||||||||
                                ACTGTTTTGT  TCTTTCACG
                                      TA        TT
GAM335  LOC196529 3'  TGGGGGGCGGTTTTTTTGGTTT 87784       AC_     G     GA
          GTT                     GACAGA   GAGAGG TGCTCT
                                ||||||   |||||| ||||||
                                TTGTTT   TTTTTT GCGGGG
                                   GGT     G     GGTT
GAM335  LOC196529 3'  TTAAGGTTTTTTTGTTTTGTT  87786           GT  TC
                                GACAGAACGAGAGG  GC  TGA
                                ||||||||||||||  ||  |||
                                TTGTTTTGTTTTTT  TG  ATT
                                        __  GA
GAM335  LOC197342 3'  TCGGGTAGAATCTCTTGTTCTG 88007    A         G__   T
          CA                      TG CAGAACGAGAGG   TGC CTGA
                                || ||||||||||||   ||| ||||
                                AC GTCTTGTTCTCT   ATG GGCT
                                _          AAG   _
GAM335  LOC197414 3'  TCAGAGTGCCCTGCGCCTG   88069     AA  AG    TG
                                CAG  CG  AGGG  CTCTGA
                                |||  ||  ||||  ||||||
                                GTC  GC  TCCC  GAGACT
                                  C_  G_    GT
GAM335  LOC199906 3'  ATTACCCTTTTTTTTGTTTTGT 88474          _____      CTCTGA
          T                       ACAGAACGA    GAGGGTG
                                |||||||||    |||||||
                                TGTTTTGTT    TTCCCAT
                                      TTTT      T   AG
GAM335  LOC199907 3'  TTCTTTTGTGCTGTTA      88471        A
                                TGACAG ACGAGAGGG
                                |||||| |||||||||
                                ATTGTC TGTTTTCTT
                                   G
GAM335  LOC200035 3'  TTGGAGTATTTTGGTTTTTC   73256    C    G   GG     TG
                                GA AGAAC AGA  GTGCTC  A
                                || ||||| |||  ||||||  |
                                CT TTTTG TTT  TATGAG  T
                                  _    G   __      GT
GAM335  LOC200132 3'  CACTTTTTTTTTTTCTGTTA   88582         C_
                                TGACAGAA  GAGAGGGTG
                                ||||||||  |||||||||
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                                ATTGTCTT  TTTTTTCAC
                                    TT
GAM335  LOC200933 3'  GTCTCTTTTGTCTTGTTA    90200      GA       T
                                TGACA  ACGAGAGGG GC
                                |||||  ||||||||| ||
                                ATTGT  TGTTTTCTC TG
                                   TC       _
GAM335  LOC202868 5'  GTCCTTGTGTTTTCTTGTTTTG 90383             TG TCTGA
          TT                     GACAGAACGAGAGGG  C
                                |||||||||||||||  |
                                TTGTTTTGTTCTTTT  G
                                         GT TTCCTGT
GAM335  LOC202934 3'  GACTGCAGTATTTTTTTTTTTT 90412        C         CTGA
          GTC                     GACAGAA GAGAGGGTGCT
                                |||||||  ||||||||||
                                CTGTTTT TTTTTTTATGA
                                    T         CGTCAGA
GAM335  LOC202934 5'  GGGTCTCTTTTTTTGTT     90423        C    GGT
                                GACAGAA GAGAG   GCTC
                                |||||||  |||||   ||||
                                TTGTTTT TTCTC   TGGG
                                    T    ___
GAM335  LOC219688 3'  TGCTTTTTTGTTGTTGTT    93055      _
                                GACAG AACGAGAGGGTG
                                |||||  ||||||||||||
                                TTGTT TTGTTTTTTCGT
                                   G
GAM335  LOC219790 3'  TGGGGTGTTCTTTTTCT     91361     AC      TG   TG
                                AGA  GAGAGGG  CTC  A
                                |||  |||||||  |||  |
                                TCT  TTTTCTT  GGG  T
                                  __      GT   GT
GAM335  LOC219920 3'  GCAAAACTTTCTGTTCTGTTA  93313         _    GG_
                                TGACAGAAC GAGAG   TGC
                                |||||||||  |||||   |||
                                ATTGTCTTG CTTTC   ACG
                                     T    AAA
GAM335  LOC220595 5'  TTGGAGCACCTGACGTTTGTCA 91142        A  AGA       TG
                                TGACAGA CG   GGGTGCTC  A
                                |||||||  ||   ||||||||  |
                                ACTGTTT GC   TCCACGAG  T
                                    _ AG_       GT
GAM335  LOC221061 3'  TTGGGGTTTGCCTTTTTTTGTT 93223        CGA     __   TG
                                GACAGAA   GAGGGT  GCTC  A
                                |||||||   ||||||  ||||  |
                                TTGTTTT   TTTCCG  TGGG  T
                                    ___     TT   GT
GAM335  LOC221271 3'  TGCCTTTTTTTTCTGTCA    91880        C
                                TGACAGAA GAGAGGGTG
                                ||||||||  |||||||||
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                                ACTGTCTT TTTTTCCGT
                                    T
GAM335  LOC221489 3'  TCACTGCAGACTCTCTTGTTTT 93643          __ TC
                                AGAACGAGAGGGT  GC  TGA
                                ||||||||||||  ||  |||
                                TTTTGTTCTCTCA  CG  ACT
                                    GA  TC
GAM335  LOC221550 5'  TGGGGTATTTTTTTTTTTG   92122      C        TG
                                CAGAA GAGAGGGTGCTC  A
                                |||||  ||||||||||||  |
                                GTTTT TTTTTTTATGGG  T
                                  _         GT
GAM335  LOC221830 3'  GCCATTCTAGTTTTGTT     92510       G   _
                                GACAGAAC AGAG GGT
                                ||||||||  ||||  |||
                                TTGTTTTG TCTT CCG
                                    A   A
GAM335  LOC221833 3'  ATTTTTTTTTTTTGTCA     92539       C
                                TGACAGAA GAGAGGGT
                                ||||||||  ||||||||
                                ACTGTTTT TTTTTTTA
                                    T
GAM335  LOC222160 3'  TCAGAGTGTTAACTTCTTTTG  94134      C   AG  TG
                                CAGAA GAG  GG  CTCTGA
                                |||||  |||  ||  ||||||
                                GTTTT TTC  TT  GAGACT
                                  C   AA  GT
GAM335  LOC222803 5'  TGCGGTGTCATTCTGTCGTTCT 94356         G    _ T   A
          GTTA                    GACAGAACGA AGGGTG C CTG
                                ||||||||||  ||||||  |  |||
                                TTGTCTTGCT TCTTAC G GGC
                                    G     T T   GTT
GAM335  LOC253664 3'  TACTGTTTTTTGTTTTGTT   94814          __
                                GACAGAACGAGAG  GGTG
                                ||||||||||||  ||||
                                TTGTTTTGTTTTT  TCAT
                                    TG
GAM335  LOC254826 3'  CAGTAGTTCTCTTTTGTT    97240         T  _
                                AACGAGAGGG GCT CTG
                                ||||||||||  |||  |||
                                TTGTTTTCTC TGA GAC
                                    T   T
GAM335  LOC255533 5'  TTAGGGTAGTTTGTTTTGTTTT 96982          __ G
          GTT                     GACAGAACGAGA  GG TGCTCTGA
                                ||||||||||||  ||  ||||||||
                                TTGTTTTGTTTT  TT ATGGGATT
                                    GT  G
GAM335  LOC255925 3'  TCTGTGGCTTTCTAGTTCTGTT 96480        G      GCTCTGA
                                GACAGAAC AGAGGGT
                                ||||||||  |||||||
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                                TTGTCTTG TCTTTCG
                                    A      GTGTCT
GAM335  LOC256642 3'  TGGGAGCATCTCTCTCTTTTTG 96309        C    _      GA
          TCA                    TGACAGAA GAGAG GGTGCTCT
                                 |||||||| ||||| ||||||||
                                 ACTGTTTT CTCTC CTACGAGG
                                     T    T       GTT
GAM335  LOC256691 3'  AGAGCACCCTCCTTC       96195     CGA
                                 GAA   GAGGGTGCTCT
                                 |||   ||||||||||
                                 CTT   CTCCCACGAGA
                                   C__
GAM335  LOC257042 3'  CAGATTTTCTTATTCTGTT    96897       CG     TGC    A
                                 GACAGAA  AGAGGG   TCTG
                                 |||||||  ||||||   ||||
                                 TTGTCTT  TCTTTT   AGAC
                                     AT     ___    G
GAM335  LOC257495 5'  TGGGGTATTTTTTTTTTTG   97728      C         TG
                                 CAGAA GAGAGGGTGCTC  A
                                 ||||| |||||||||||  |
                                 GTTTT TTTTTTTATGGG  T
                                    _          GT
GAM335  LOC257576 5'  TGGGGTATTTTTTTTTTTG   97885      C         TG
                                 CAGAA GAGAGGGTGCTC  A
                                 ||||| |||||||||||  |
                                 GTTTT TTTTTTTATGGG  T
                                    _          GT
GAM335  LOC51193  3'  TTAGAGATGGTCTCGTTCTGTT 32913           GG  G
                                 GACAGAACGAGA  GT CTCTGA
                                 ||||||||||||  || ||||||
                                 TTGTCTTGCTCT  TA GAGATT
                                        GG  _
GAM335  LOC51219  3'  CCCTCTCTTTTTTTGTCA    33114        C__
                                 TGACAGAA   GAGAGGG
                                 ||||||||   |||||||
                                 ACTGTTTT   CTCTCCC
                                     TTT
GAM335  LOC51314  5'  AGGAGGACCTGTTTTGTTA   33519         GAGA   G   GA
                                 TGACAGAAC    GGGT CTCT
                                 |||||||||    |||| ||||
                                 ATTGTTTTG    TCCA GAGG
                                      ____    G   AG
GAM335  LOC51580  3'  AGTTTTTTTGTTTTGTT     31860           GT
                                 GACAGAACGAGAGG  GCT
                                 ||||||||||||||  |||
                                 TTGTTTTGTTTTTT  TGA
                                                __
GAM335  LOC51631  3'  ATTTTTCTGTTCTGTT      68081         AG
                                 GACAGAACG  AGGGT
                                 |||||||||  |||||
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                                TTGTCTTGT  TTTTA
                                     CT
GAM335  LOC54499  3' GTAACTGTTTGTTTTGTT    70633          A  G
                                GACAGAACGAG GG TGC
                                |||||||||| || |||
                                TTGTTTTGTTT TC ATG
                                      G  A
GAM335  LOC64116  3' CAGCTTTTTGTTCTGTT     42197            G
                                GACAGAACGAGAGG TG
                                |||||||||||||| ||
                                TTGTCTTGTTTTTC AC
                                        G
GAM335  LOC84524  3' TCAGAGTGCCCTCTTGTGTG  50672    GA       TG
                                CA  ACGAGAGGG  CTCTGA
                                ||  |||||||||  ||||||
                                GT  TGTTCTCCC  GAGACT
                                 G_       GT
GAM335  LOC90378  3' CCCTCTTTTCTTTCTGTT    62521       C___
                                GACAGAA   GAGAGGG
                                |||||||   |||||||
                                TTGTCTT   TTCTCCC
                                    TCTT
GAM335  LOC91355  5' TGGGGCACTTTCTGAGTGCTG  65723     A  G_        TG
                                CAG AC  AGAGGGTGCTC  A
                                ||| ||  ||||||||||  |
                                GTC TG  TCTTTCACGGG  T
                                  G  AG         GT
GAM335  LOC92181  3' ACCTTTTTGTTTTGTT      68400
                                GACAGAACGAGAGGGT
                                ||||||||||||||||
                                TTGTTTTGTTTTTCCA

GAM335  LOC92305  3' TCAGAGCGCCCTCATTTGT   56419      ACGA
                                ACAGA   GAGGGTGCTCTGA
                                |||||   ||||||||||||
                                TGTTT   CTCCCGCGAGACT
                                   A___
GAM335  LOC92465  5' TCAGAGACAGGTCTCATTCTGT 69414       C   GG_  G
          T                     GACAGAA GAGA   GT CTCTGA
                                ||||||| ||||   || ||||||
                                TTGTCTT CTCT   CA GAGACT
                                    A   GGA  _
GAM335  LOC93132  5' GGGGGTTTTGTTCTGT      71497          GGG G
                                ACAGAACGAGA   T CTC
                                ||||||||||   | |||
                                TGTCTTGTTTT   G GGG
                                       ___ G
GAM336  CCKBR     3' AAACACAAACCACAACTGACA  5586     CA   C    AT
                                TG  AGT TGTG  TTTGTGTTT
                                ||  ||| ||||  |||||||||
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                                AC  TCA ACAC  AAACACAAA
                                 AG  _   C_
GAM336  GAC1     5'  AAACACAAAGAGCAGGACT   20939     _  GA
                                AGTC TGT  TTTTGTGTTT
                                |||| |||  ||||||||||
                                TCAG ACG  GAAACACAAA
                                  G  A_
GAM336  KCNMB3   5'  ACAGATCTCTACAGACTTGCA  26961          _  T_
                                TGCAAGTCTGT GA  TTTGT
                                |||||||||| ||  |||||
                                ACGTTCAGACA CT  AGACA
                                       T  CT
GAM336  SLC25A4  3'  AAACACAAGTTCACAGATTTAC 59522    C        T
           A                     TG AAGTCTGTGA TTTGTGTTT
                                || |||||||||| |||||||||
                                AC TTTAGACACT GAACACAAA
                                 A         T
GAM336  CHERP    3'  AAACACAAAACTTTGACTTG   21094       TGTGA
                                CAAGTC    TTTTGTGTTT
                                ||||||    ||||||||||
                                GTTCAG    AAAACACAAA
                                   TTTC_
GAM336  CHL1     3'  AAACACAAAACAAATCCTGCA  21742      AGTCTG  A
                                TGCA     TG TTTTGTGTTT
                                ||||     || ||||||||||
                                ACGT     AC AAAACACAAA
                                  CCTAA_  _
GAM336  FLJ21596 3'  AGAACCACAGACTTGCA     45698           A
                                TGCAAGTCTGTG TTTT
                                |||||||||||| ||||
                                ACGTTCAGACAC AAGA
                                       C
GAM336  UHRF1    3'  AAATCACATACCTGCA      25217      A  C
                                TGCA GT TGTGATTT
                                |||| || ||||||||
                                ACGT CA ACACTAAA
                                  C  T
GAM336  ZDHHC7   3'  ACTTGCTCACAGACTTCCA   34838    C        TTTT
                                TG AAGTCTGTGA   GT
                                || ||||||||||   ||
                                AC TTCAGACACT   CA
                                 C         CGTT
GAM336  LOC147958 5'  AATTCAGAAACACAGACCTGCA 87176      A      A    T
                                TGCA GTCTGTG TTTTG GTT
                                |||| ||||||| ||||| |||
                                ACGT CAGACAC AAGAC TAA
                                  C      A    T
GAM336  LOC158377 3'  GAAATCACAGAACTGCA     86794      AG
                                TGCA  TCTGTGATTTT
                                ||||  ||||||||||
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                                ACGT  AGACACTAAAG
                                  CA
GAM336  LOC200918 3'  ACTAAATACAGACTTACA    88937    C       A   T
                                TG AAGTCTGTG TTT GT
                                || ||||||||| ||| ||
                                AC TTCAGACAT AAA CA
                                 A       _  T
GAM337  ERBB4    3'  GCTCCAATTTCCCCA      17876     AA      A
                                TGGG  GAATTGGA GT
                                ||||  |||||||| ||
                                ACCC  TTTAACCT CG
                                  C_      _
GAM337  FLOT1    3'  GCATGTAACCCACTGGCCTCCC 19407     AGAAT_  AA
                                GGGA     TGG  GTTACATGC
                                ||||     |||  |||||||||
                                CCCT     ACC  CAATGTACG
                                  CCGGTC  __
GAM337  IRTA2    3'  TCCCAAGTTCTTCCCA     48410          __
                                TGGGAAGAATT  GGA
                                ||||||||||  |||
                                ACCCTTCTTGA  CCT
                                      AC
GAM337  SGCB     3'  GCATGTTTATATCCCCAATTCT 4066     GA      AAGTT___
           CACCA                  TGG  AGAATTGG      ACATGC
                                |||  ||||||||      ||||||
                                ACC  TCTTAACC      TGTACG
                                  AC       CCTATATT
GAM337  WDR3     3'  GCATATAACTTTTGATTCCCCA 22290     AA    TG     C
                                TGGG  GAAT  GAAGTTA ATGC
                                ||||  ||||  ||||||| ||||
                                ACCC  CTTA  TTTCAAT TACG
                                  __   GT     A
GAM337  CCR6     5'  GCAAACGTTCCCAAATCTTCCC 48584        A   AA__  ACA
           A                     TGGGAAGA TTGG   GTT   TGC
                                |||||||| ||||   |||   |||
                                ACCCTTCT AACC   CAA   ACG
                                     A   CTTG  ___
GAM337  DKFZP434O125 3'  CTTCCAATCTCCCCA      64960     A   A
                                TGGG AGA TTGGAAG
                                |||| ||| |||||||
                                ACCC TCT AACCTTC
                                  C  _
GAM337  KIAA0632  3'  TATGTGGCAACCCTCCCA    31427     A AATT  AA
                                TGGGA G   GG  GTTACATG
                                ||||| |   ||  ||||||||
                                ACCCT C   CC  CGGTGTAT
                                  _ _____  AA
GAM337  SNAP91   3'  AACCCCAAACTCTTCCCA    29264       A_   AA
                                TGGGAAGA  TTGG  GTT
                                ||||||||  ||||  |||
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                                ACCCTTCT  AACC  CAA
                                    CA    C_
GAM337  TUSP     3'  ACTCCCAATTCTCTCCA     39622     GA       A
                                TGG  AGAATTGG AGT
                                |||  |||||||| |||
                                ACC  TCTTAACC TCA
                                  TC       C
GAM337  ZNF333   3'  CATGTAACCACCACCCCA    50570     AAGAAT   AA
                                TGGG     TGG  GTTACATG
                                ||||     |||  ||||||||
                                ACCC     ACC  CAATGTAC
                                  C_____   AC
GAM337  LOC153688 3'  TTTCCACTCTTCCCA      86128        AT
                                TGGGAAGA  TGGAAG
                                ||||||||  ||||||
                                ACCCTTCT  ACCTTT
                                    C_
GAM337  LOC196955 5'  AACTTCCAACTCCTCC      77357     A  A
                                GGA GA TTGGAAGTT
                                ||| || |||||||||
                                CCT CT AACCTTCAA
                                  C  C
GAM337  LOC219818 3'  CTCCCAACTCTTCCCA      90890        A    A
                                TGGGAAGA TTGG AG
                                |||||||| |||| ||
                                ACCCTTCT AACC TC
                                    C    C
GAM337  LOC91923  5'  GCATATGGATATCCAATCTTCC 67552        A    A   AC_
           CA                     TGGGAAGA TTGGA GTT   ATGC
                                |||||||| ||||| |||   ||||
                                ACCCTTCT AACCT TAG   TACG
                                    _    A   GTA
GAM337  LOC93259  5'  CACCTGGCTTCCACCCTCCCCA 71806      A  AAT       CA
                                TGGG AG   TGGAAGTTA  TG
                                |||| ||   |||||||||  ||
                                ACCC TC   ACCTTCGGT  AC
                                  C  CC_       CC
GAM338  ADCY7    3'  AGGCATGCAGATGGCTGTG    6636         AC     GC
                                CACAGCCA  TTTGTG  GCCT
                                ||||||||  ||||||  ||||
                                GTGTCGGT  AGACGT  CGGA
                                    __     A_
GAM338  APXL     3'  GGTGAAGCTGGCTGTG      7930         ACTTT  GG
                                CACAGCCA    GT  CGCC
                                ||||||||    ||  ||||
                                GTGTCGGT    CG  GTGG
                                    _____  AA
GAM338  INPPL1   3'  GGCACCACGAAGCTGTG     7803         CAAC      C
                                CACAGC    TTTGTGG GCC
                                ||||||    ||||||| |||
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                                GTGTCG    AAGCACC CGG
                                   ____       A
GAM338  LGR6     5'  AGGCGCCAACACCTTGACTG   84199     C   CTTTG
                                CAG CAA     TGGCGCCT
                                ||| |||     ||||||||
                                GTC GTT     ACCGCGGA
                                  A   CCACA
GAM338  SH3GL3   5'  GTTCCACAAAGCCAGCCAGTA  11636     ACA  CAA       C
                                TAC   GC   CTTTGTGG GC
                                |||   ||   |||||||| ||
                                ATG   CG   GAAACACC TG
                                  AC_  ACC       T
GAM338  SIAT8E   5'  AGGCGCCAAGTCGGC       59857     A   TTG
                                GCC ACT   TGGCGCCT
                                ||| |||   ||||||||
                                CGG TGA   ACCGCGGA
                                  C  ___
GAM338  SRM      3'  GCCTATACCAGCTGTGTA     11956        CAACTT     C
                                TACACAGC     TGTGG GC
                                ||||||||     ||||| ||
                                ATGTGTCG     ATATC CG
                                     ACC___     _
GAM338  WISP2    5'  AGGCTCAAAGCTGGCTCTG    13932    C     A     TGGC
                                CA AGCCA CTTTG    GCCT
                                || ||||| |||||    ||||
                                GT TCGGT GAAAC    CGGA
                                 C     C     T___
GAM338  ACAS2    3'  CAGGGAGGCAGCTGTGTA     57702        CAA    G
                                TACACAGC   CTTT TG
                                ||||||||   |||| ||
                                ATGTGTCG   GAGG AC
                                     ACG    G
GAM338  ACAS2    3'  CAGGGAGGCAGCTGTGTA     37932        CAA    G
                                TACACAGC   CTTT TG
                                ||||||||   |||| ||
                                ATGTGTCG   GAGG AC
                                     ACG    G
GAM338  BRD1     3'  ATAAAGTTATGCTGTGTA     27414        C_
                                TACACAGC  AACTTTGT
                                ||||||||  ||||||||
                                ATGTGTCG  TTGAAATA
                                     TA
GAM338  CARD9    3'  AGGCGCAGCTACTGGCCGTG   42283     A    ACTTT  G
                                CAC GCCA     GT GCGCCT
                                ||| ||||     || ||||||
                                GTG CGGT     CG CGCGGA
                                  C    CAT__  A
GAM338  CASKIN1  3'  AGGCGCTGCCGTCGGCTGTCA  40397   C     A  TTT TG
                                A ACAGCC AC   G  GCGCCT
                                | ||||||  ||   |  ||||||
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                                A TGTCGG TG   C  CGCGGA
                                 C     C  C__ GT
GAM338  CNOT7    3'  CAGGAAAATTGGTTGTG     53983         C_   G
                                CACAGCCAA  TTT TG
                                |||||||||  ||| ||
                                GTGTTGGTT  AAG AC
                                     AA   G
GAM338  EHM2     3'  ACAAGTTGGCTGTTA       38910    C         T
                                A ACAGCCAACTT GT
                                | ||||||||||| ||
                                A TGTCGGTTGAA CA
                                 T         _
GAM338  FLJ10508 3'  ACTGAGAAATGGCTGTGTA   36198          A__   T
                                TACACAGCCA   CTT GT
                                ||||||||||   ||| ||
                                ATGTGTCGGT   GAG CA
                                     AAA   T
GAM338  FLJ14721 3'  GGCACCACAGGGGCT       51585      AAC      C
                                AGCC   TTTGTGG GCC
                                ||||   ||||||| |||
                                TCGG   GGACACC CGG
                                  ___      A
GAM338  FLJ22004 3'  TGCTATGTAGCTGTGTA     47214         CA  TTT
                                TACACAGC  AC   GTGGCG
                                ||||||||  ||   ||||||
                                ATGTGTCG  TG   TATCGT
                                     A_  ___
GAM338  HCBP6    3'  GTTGGAAAGTTGGCTG       80902          G
                                CAGCCAACTTT TGGC
                                |||||||||| ||||
                                GTCGGTTGAAA GTTG
                                      G
GAM338  KIAA0527 3'  ACAAAGTTAGCTTTGTA     95787      C   C
                                TACA AGC AACTTTGT
                                |||| ||| ||||||||
                                ATGT TCG TTGAAACA
                                  T   A
GAM338  KIAA0648 3'  TCAAGAGTTGGCTGTGTA    82657             G
                                TACACAGCCAACTTT TGG
                                |||||||||||||| |||
                                ATGTGTCGGTTGAGA ACT
                                                _
GAM338  KIAA1157 3'  AGGCTTTGTGAAGTCAGCTGTG 72238        CA     TG C
                                CACAGC  ACTTTG  G GCCT
                                ||||||  ||||||  | ||||
                                GTGTCG  TGAAGT  T CGGA
                                   AC     GT T
GAM338  KIAA1979 3'  CGCATTGGTTGGCTGTGT    88276           T_
                                ACACAGCCAACT  TGTG
                                ||||||||||  ||||
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                                TGTGTCGGTTGG  ACGC
                                      TT
GAM338  KIAA1987  3'  GGAGCCAGGCTGTGTA     88019        AACTTTG   G
                                TACACAGCC     TGGC CC
                                |||||||||     |||| ||
                                ATGTGTCGG     ACCG GG
                                    _______   A
GAM338  MAPK8IP3  3'  GCCAGTATAAGTCAGCTGTG  52985      CA   TG__
                                CACAGC  ACTT   TGGC
                                ||||||  ||||   ||||
                                GTGTCG  TGAA   ACCG
                                   AC   TATG
GAM338  MCM10     3'  GCAAAGGATTGGCTGTGTA   37573         __
                                TACACAGCCAA  CTTTGT
                                ||||||||||  ||||||
                                ATGTGTCGGTT  GAAACG
                                      AG
GAM338  PSR       3'  CCACAGAGCCAGCTGTGTA   65179       CAA
                                TACACAGC   CTTTGTGG
                                ||||||||   ||||||||
                                ATGTGTCG   GAGACACC
                                     ACC
GAM338  TRIM28    5'  GGCAGCAGTTGGCCGTG     19267     A     TTGTG _
                                CAC GCCAACT    GC GCC
                                ||| |||||||    || |||
                                GTG CGGTTGA    CG CGG
                                  C      _____ A
GAM338  ZNF263    5'  AGGCGCCGGAGCCGGC      19222     AA   TG
                                GCC  CTT  TGGCGCCT
                                |||  |||  ||||||||
                                CGG  GAG  GCCGCGGA
                                  CC   __
GAM338  LOC118672 5'  AGGCGCCAATCCTACTGGCTG  73922       ACTTTG_
                                CAGCCA      TGGCGCCT
                                ||||||      ||||||||
                                GTCGGT      ACCGCGGA
                                   CATCCTA
GAM338  LOC149997 5'  GCCATAAAACTGGCTG      76341       AC
                                CAGCCA  TTTGTGGC
                                ||||||  ||||||||
                                GTCGGT  AAATACCG
                                   CA
GAM338  LOC151126 3'  CATTTTTAGTTGCTGTGTA   80125        C   TT__
                                TACACAGC AACT   GTG
                                |||||||| ||||   |||
                                ATGTGTCG TTGA   TAC
                                     _   TTTT
GAM338  LOC158852 5'  AGGCGCCACAACTTCACTG   82032     CCAACT
                                CAG     TTGTGGCGCCT
                                |||     ||||||||||
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                                GTC     AACACCGCGGA
                                  ACTTC_
GAM338  LOC170221 3'  AGGCGCCGCTCCCTGGCT    82576      ACTTT
                                AGCCA    GTGGCGCCT
                                |||||    |||||||||
                                TCGGT    CGCCGCGGA
                                   CCCT_
GAM338  LOC201292 5'  GCAGTTGCTAAGCCGGCTGTGT 88188         AA   T TG  _
          G                      TACACAGCC  CTT G  GC GC
                                |||||||||  ||| |  || ||
                                GTGTGTCGG  GAA C  TG CG
                                     CC   T GT  A
GAM338  LOC221154 5'  GCGCCGCCTAGCTGCGCT    93546     _  A  TT
                                AGC CA CT  GTGGCGC
                                ||| || ||  |||||||
                                TCG GT GA  CGCCGCG
                                  C  C  TC
GAM338  LOC221296 3'  AGGCAAAGAAGTTGGCCTGT   91955      _       GTGGC
                                ACAG CCAACTTT     GCCT
                                |||| ||||||||     ||||
                                TGTC GGTTGAAG     CGGA
                                  C       AAA__
GAM338  LOC221576 3'  GGGCATGCAAAGCCGGCTGTGT 93705         AA      GC
          G                      TACACAGCC  CTTTGTG  GCCT
                                |||||||||  |||||||  ||||
                                GTGTGTCGG  GAAACGT  CGGG
                                     CC      A_
GAM338  LOC257122 5'  AGGCGCCACAACTTCACTG   96212     CCAACT
                                CAG     TTGTGGCGCCT
                                |||     ||||||||||||
                                GTC     AACACCGCGGA
                                  ACTTC_
GAM338  LOC257515 3'  GGGCATGCAAAGCCGGCTGTGT 97785         AA      GC
          G                      TACACAGCC  CTTTGTG  GCCT
                                |||||||||  |||||||  ||||
                                GTGTGTCGG  GAAACGT  CGGG
                                     CC      A_
GAM338  LOC257572 3'  GGGCATGCAAAGCCGGCTGTGT 97914         AA      GC
          G                      TACACAGCC  CTTTGTG  GCCT
                                |||||||||  |||||||  ||||
                                GTGTGTCGG  GAAACGT  CGGG
                                     CC      A_
GAM339  ARHGEF7   3'  ACAATGTTGATGCTACACTGT  14000      C_   __
                                ACAG  TAGC  CAACATTGT
                                ||||  ||||  |||||||||
                                TGTC  ATCG  GTTGTAACA
                                  AC    TA
GAM339  BACE      3'  ACAATGTTGGCCTGT       57282      CTA
                                ACAG   GCCAACATTGT
                                ||||   ||||||||||||
```

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                              TGTC  CGGTTGTAACA
                                    ___
GAM339  BACE    3'  ACAATGTTGGCCTGT      23972     CTA
                              ACAG  GCCAACATTGT
                              ||||  ||||||||||
                              TGTC  CGGTTGTAACA
                                    ___
GAM339  BCL11B  3'  ACAATGTTGAGTTCAGC     43181    _  _
                              GCT AGC CAACATTGT
                              ||| ||| |||||||||
                              CGA TTG GTTGTAACA
                                C   A
GAM339  CD28    3'  ACAATGTTAGCTATTG      20433    C   C
                              CAG TAGC AACATTGT
                              ||| |||| ||||||||
                              GTT ATCG TTGTAACA
                                _   A
GAM339  JUNB    5'  ACAGCTGCCGGCTGGCTG    9481         AA  _
                              CAGCTAGCC  CA TTGT
                              |||||||||  || ||||
                              GTCGGTCGG  GT GACA
                                   CC  C
GAM339  LATS2   3'  ACAAATCATGCTGCTGTTAT  27402        T   CAACA
                              ATAACAGC AGC    TTGT
                              |||||||| |||    ||||
                              TATTGTCG TCG    AACA
                                   _  TACTA
GAM339  PDZK1   3'  ACAATGTTGTGGTTG       10506       GC
                              CAGCTA  CAACATTGT
                              ||||||  |||||||||
                              GTTGGT  GTTGTAACA
                                      __
GAM339  PKHD1   3'  ACAATGTTAAGGGGTTGTTGT  56912         AGCC
                              ATAACAGCT   AACATTGT
                              |||||||||   ||||||||
                              TGTTGTTGG   TTGTAACA
                                   GGAA
GAM339  DKFZP564B1162 3'  ACAATTTGCCAGCTGTTA    48526        A  C  C
                              TAACAGCT GC AA ATTGT
                              |||||||| || || |||||
                              ATTGTCGA CG TT TAACA
                                   C  _  _
GAM339  FLJ14082  3'  ACAATGTTGATGCTACTG    46665     C   __
                              CAG TAGC  CAACATTGT
                              ||| ||||  |||||||||
                              GTC ATCG  GTTGTAACA
                                _   TA
GAM339  FLJ25348  3'  ACAATGTTTGCTGTTG      57992     T   C
                              CAGC AGC AACATTGT
                              |||| ||| ||||||||
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                                GTTG TCG TTGTAACA
                                  _  T
GAM339  KIAA1372  5'  AGTGTTAGCTGCTGTTAT    91649        T  C
                                ATAACAGC AGC AACATT
                                |||||||| ||| ||||||
                                TATTGTCG TCG TTGTGA
                                    _  A
GAM339  KIAA1913  3'  ACAATGTTGACTAATG      73882    GC  C
                                CA  TAG CAACATTGT
                                ||  ||| |||||||||
                                GT  ATC GTTGTAACA
                                 A_  A
GAM339  MGC16733  3'  TGTGGTAGCTGTTA        53211         G  A
                                TAACAGCTA CCA CA
                                ||||||||| ||| ||
                                ATTGTCGAT GGT GT
                                    _  _
GAM339  NSBP1     3'  ACAATGTTGTGTCCACTGTT  47770      CTA  _
                                AACAG   GC CAACATTGT
                                |||||   || |||||||||
                                TTGTC   TG GTTGTAACA
                                   ACC  T
GAM339  PRO0159   5'  ACAGGTCTGGCTAGCTGT    26107          ACA
                                ACAGCTAGCCA   TTGT
                                ||||||||||   ||||
                                TGTCGATCGGT   GACA
                                      CTG
GAM339  SLC19A3   3'  ACAATGTTGGCCAGGCTG    47480      A_
                                CAGCT  GCCAACATTGT
                                |||||  ||||||||||
                                GTCGG  CGGTTGTAACA
                                   AC
GAM339  TPD52     3'  ACAATGTTGTATTTGTTAT    17420       C  GC
                                ATAACAG TA  CAACATTGT
                                ||||||| ||  |||||||||
                                TATTGTT AT  GTTGTAACA
                                    T  __
GAM339  TRAD      3'  CAATATTAGCTGTTA       22950          CCAAC
                                TAACAGCTAG    ATTG
                                ||||||||||    ||||
                                ATTGTCGATT    TAAC
                                      A_____
GAM339  LOC151414 3'  ACAATGTTAGGAGGCT      80232      AG  _
                                AGCT  CC AACATTGT
                                ||||  || ||||||||
                                TCGG  GG TTGTAACA
                                  A_  A
GAM339  LOC153222 3'  ACAATGTTGCTTACCTG     80780     C  C
                                CAG TAG CAACATTGT
                                ||| ||| |||||||||
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                                GTC ATT GTTGTAACA
                                  C   C
GAM339  LOC158310 5'  ACAATGTTGACCAGGCTG    86747      AGC_
                                CAGCT    CAACATTGT
                                |||||    |||||||||
                                GTCGG    GTTGTAACA
                                   ACCA
GAM339  LOC199232 3'  ACAATGTTGGAGCTGT      88970       AG
                                ACAGCT  CCAACATTGT
                                ||||||  ||||||||||
                                TGTCGA  GGTTGTAACA
                                   __
GAM339  LOC255252 3'  CAGTAGCTAGCTGCTAT     95007     A       CAAC
                                ATA CAGCTAGC    ATTG
                                ||| ||||||||    ||||
                                TAT GTCGATCG    TGAC
                                  C       A___
GAM339  LOC91947  3'  ATGTAGCTGCTGTTAT      67612        T   CA
                                ATAACAGC AGC  ACAT
                                |||||||| |||  ||||
                                TATTGTCG TCG  TGTA
                                    _   A_
GAM340  ARHGEF6   3'  CAAACTTGAAGCCAGGC     68197       ACCA
                                GCCTGG    CAAGTTTG
                                ||||||    ||||||||
                                CGGACC    GTTCAAAC
                                   GAA_
GAM340  CNTN2     3'  GTCACAACCCAGGTGA      17411        ACCACAA   _
                                TCGCCTGG      GTT TGAC
                                ||||||||      ||| ||||
                                AGTGGACC      CAA ACTG
                                    ________   C
GAM340  CORO2A    3'  AAACTGTGGTCCAGAGA     12642    GC        A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_         _
GAM340  CORO2A    3'  AAACTGTGGTCCAGAGA     53398    GC        A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_         _
GAM340  GRLF1     3'  AGGTCAGAAAGTGGCCCAGG   78551      A   AAG
                                CCTGG CCAC   TTTGACCT
                                ||||| ||||   ||||||||
                                GGACC GGTG   AGACTGGA
                                   C    AA_
GAM340  LAPTM5    3'  AGGCTTGTGGTCAAGC      22199    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
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                                CG  CTGGTGTTCGGA
                                 AA_
GAM340  POU2AF1  3' AGATTTACAGTCCAGGC    20647       CAC
                                GCCTGGAC  AAGTTT
                                ||||||||  ||||||
                                CGGACCTG  TTTAGA
                                    ACA
GAM340  PTGS1    3' GTCTCCTGTCTTATGGTCCAG 54574       C  TTT___
                                CTGGACCA AAG    GAC
                                |||||||| |||    |||
                                GACCTGGT TTC    CTG
                                    A  TGTCCT
GAM340  PTGS1    3' GTCTCCTGTCTTATGGTCCAG 6355        C  TTT___
                                CTGGACCA AAG    GAC
                                |||||||| |||    |||
                                GACCTGGT TTC    CTG
                                    A  TGTCCT
GAM340  TRIM34   5' AGGTCAAGTTGAGCCCAG   55224    ACCA  G
                                CTGG   CAA TTTGACCT
                                ||||   ||| ||||||||
                                GACC   GTT GAACTGGA
                                  CGA_  _
GAM340  TRIM9    5' AGGCCAGGCAAGTCCAGGC   30749       CACAA   A
                                GCCTGGAC    GTTTG CCT
                                ||||||||    ||||| |||
                                CGGACCTG    CGGAC GGA
                                    AA___    C
GAM340  ABLIM    5' GATATGTAACCCAGGCGG    22030       ACC  A
                                TCGCCTGG  ACA GTT
                                ||||||||  ||| |||
                                GGCGGACC  TGT TAG
                                    CAA  A
GAM340  AMOT     3' AGGCATCTTCATGGTCCAGGGA 55716   G       C_  TT  A
                                TC CCTGGACCA  AAG  TG CCT
                                || |||||||||  |||  || |||
                                AG GGACCTGGT  TTC  AC GGA
                                 _       AC  T_ _
GAM340  DKFZp434D177 5'  TTAGACCCAGGCGA       50056       ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                          _______
GAM340  DKFZp434D177 5'  TTAGACCCAGGCGA       79443       ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                          _______
GAM340  FLJ23420 3'  CAAGTGGGTCCAGGC       46845        A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
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                                CGGACCTGG GT  GAAC
                                      _  __
GAM340  HSA249128 5'  GGCGCGGTCCAGGCGG      34152          ACAA
                                TCGCCTGGACC    GTT
                                ||||||||||    |||
                                GGCGGACCTGG    CGG
                                     CG__
GAM340  MGC15668  5'  AGACCCGGTGGTCCAGACG    51277    C       AA_
                                CG CTGGACCAC   GTTT
                                || |||||||||   ||||
                                GC GACCTGGTG   CAGA
                                 A        GCC
GAM340  MGC22014  3'  AGGTCCCGAGTGTAACCCAGGT 64486        ACC   AGTTT
           GA                     TCGCCTGG   ACA    GACCT
                                ||||||||   |||    |||||
                                AGTGGACC   TGT    CTGGA
                                     CAA   GAGCC
GAM340  SDCCAG10  5'  AGAGTTGTGGTCCAAAGA    19641    GCC        G
                                TC   TGGACCACAA TTT
                                ||   |||||||||| |||
                                AG   ACCTGGTGTT AGA
                                 AA_         G
GAM340  LOC115442 3'  AGGTCAGGGATGGTCCAG    72676        CAAG
                                CTGGACCA    TTTGACCT
                                ||||||||    ||||||||
                                GACCTGGT    GGACTGGA
                                     AG__
GAM340  LOC129011 5'  AGACCTGCGGTCCAGGC     74862         A  A
                                GCCTGGACC CA GTTT
                                ||||||||| || ||||
                                CGGACCTGG GT CAGA
                                     C  C
GAM340  LOC130536 5'  GCAAAGTCCAGGCG        75746         CACAAG    A
                                CGCCTGGAC      TTTG C
                                |||||||||      |||| |
                                GCGGACCTG      AAAC G
                                     _______   C
GAM340  LOC149108 3'  AGACTTCACTGTGGTCCA    84357          _____
                                TGGACCACA    AGTTT
                                |||||||||    |||||
                                ACCTGGTGT    TCAGA
                                     CACT
GAM340  LOC221688 5'  AGACTCGGGCCCAGACGA    93674     C    A  ACA
                                TCG CTGG CC   AGTTT
                                ||| |||| ||   |||||
                                AGC GACC GG   TCAGA
                                  A   C  GC_
GAM340  LOC256228 5'  AGACTTGTGGTCAAAGC     96233    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
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                                CG   CTGGTGTTCAGA
                                 AAA
GAM340  LOC257441 5'  TTAGACCCAGGCGA       95566        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                              _______
GAM340  LOC91960  3'  AGGTGCCTCTCGTGGTCCAAGC 67657    C       A  TTTG
                                GC TGGACCAC AG    ACCT
                                || |||||||| ||    ||||
                                CG ACCTGGTG TC    TGGA
                                 A       C  TCCG
GAM340  LOC92840  3'  GTCCCTCGGGTCCAGGC     56435         ACA  TTT
                                GCCTGGACC   AG   GAC
                                |||||||||   ||   |||
                                CGGACCTGG   TC   CTG
                                      GC_  C__
GAM341  DDEF1     3'  GAGCTTTAGCAGCCTC      59564    A   AGATAC      A
                                GA GCT     CTAAAGCT C
                                || |||      |||||||| |
                                CT CGA     GATTTCGA G
                                 C   C_____       C
GAM341  DDX3      3'  GAGCCTTAGGTATTTG      43759          A   A
                                TAGATACCTAA GCT C
                                |||||||||||| ||| |
                                GTTTATGGATT CGA G
                                      C   C
GAM341  GRAF      3'  GGTAACTCCCTCCCTAGCTTC  30573        ATACCTAA  C
                                GAAGCTAG       AG TACC
                                ||||||||       || ||||
                                CTTCGATC       TC ATGG
                                    CCTCCC__  A
GAM341  MAT1A     3'  AGCTTTAGAATCCCAGC     90825     A_   AC
                                GCT  GAT  CTAAAGCT
                                |||  |||  ||||||||
                                CGA  CTA  GATTTCGA
                                  CC   A_
GAM341  MYLK      3'  AGCTTCAGACATTTGGTT    97018        AC  A
                                AGCTAGAT  CT AAGCT
                                ||||||||  || |||||
                                TTGGTTTA  GA TTCGA
                                    CA  C
GAM341  RGL       3'  GTAGCTAAAACTTAGCTTCA  30736         ATACCTAA
                                TGAAGCTAG       AGCTAC
                                |||||||||       ||||||
                                ACTTCGATT       TCGATG
                                     CAAAA___
GAM341  ZFP93     3'  GTAGCCTTAATAACGTTAGTTT 14887         ATACC_   A
            CA                    TGAAGCTAG     TAA GCTAC
                                |||||||||     ||| |||||
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                                ACTTTGATT     ATT CGATG
                                      GCAATA   C
GAM341  C3orf4   3'  AGCATTGACACATAGCTTCA  39118        GATACC   A
                                TGAAGCTA     TAA GCT
                                ||||||||     ||| |||
                                ACTTCGAT     GTT CGA
                                     ACACA_   A
GAM341  D2S448   3'  GGCAGGAGTCCTAGCTTCA   73527         _  A   AAA
                                TGAAGCTAG AT CCT   GCT
                                ||||||||| || |||   |||
                                ACTTCGATC TG GGA   CGG
                                      C  A   ___
GAM341  FLJ12604 3'  AGCTTTAGTATTGACTTCA   64436      CTA    C
                                TGAAG   GATAC TAAAGCT
                                |||||   ||||| |||||||
                                ACTTC   TTATG ATTTCGA
                                   AG_    _
GAM341  FLJ14280 5'  GGTAGCTCCTGGCCAGCTCA   45999     A   AGATA  TAA
                                TGA GCT    CC   AGCTACC
                                ||| |||    ||   |||||||
                                ACT CGA    GG   TCGATGG
                                  _   CC___  TCC
GAM341  H2AFJ    3'  GTTGTCAAGTTTCTAGCTTCA  36842         T  CTAA_
                                TGAAGCTAGA AC     AGC
                                |||||||||| ||     |||
                                ACTTCGATCT TG     TTG
                                      T  AACTG
GAM341  KIAA0441 3'  TAGCTTTGTTAATCTAGCCTC  28960    A      ACC
                                GA GCTAGAT   TAAAGCTA
                                || |||||||   ||||||||
                                CT CGATCTA   GTTTCGAT
                                 C      ATT
GAM341  KIAA1128 3'  TAGCTTTATGTGCAGCTTGCA  68483    _    AGA   C
                                TG AAGCT   TAC TAAAGCTA
                                || |||||   ||| ||||||||
                                AC TTCGA   GTG ATTTCGAT
                                 G    C__   T
GAM341  KIAA1750 3'  TAGCCCCAGGAGTGGGCTTTA  68254       AG  A   AAA
                                TGAAGCT  AT CCT   GCTA
                                |||||||  || |||   ||||
                                ATTTCGG  TG GGA   CGAT
                                     G_  A   CCC
GAM341  KPNA5    3'  GGTAGCTTCAGGTAACT     9629     A    A
                                AG TACCT AAGCTACC
                                || ||||| ||||||||
                                TC ATGGA TTCGATGG
                                 A    C
GAM341  MAGEH1   5'  GGTAGCTTCAGCGGCAGCAGCT 25924       AGATAC_  A
           TC                     GAAGCT      CT AAGCTACC
                                ||||||      || ||||||||
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                                CTTCGA      GA TTCGATGG
                                   CGACGGC  C
GAM341  MGC12921  3'  AGCCCTATTTAGCTTC      63774          CCTAAA
                                GAAGCTAGATA     GCT
                                ||||||||||      |||
                                CTTCGATTTAT     CGA
                                      CC____
GAM341  MGC30052  3'  AGCTTTAGAATAGCTTC     58532        GATAC
                                GAAGCTA    CTAAAGCT
                                |||||||    ||||||||
                                CTTCGAT    GATTTCGA
                                   AA___
GAM341  RNF34     3'  AGCAAGGGCTGCATCTAGCTTC 47094         A___   AAA
                                GAAGCTAGAT   CCT   GCT
                                ||||||||||   |||  |||
                                CTTCGATCTA   GGG   CGA
                                      CGTC   AA_
GAM341  TNFRSF19L 3'  GTAGCTTTTATCCCAGC     51779     A_   CCT
                                GCT  GATA   AAAGCTAC
                                |||  ||||   ||||||||
                                CGA  CTAT   TTTCGATG
                                  CC   ___
GAM341  LOC121536 3'  AGCAAATCACATTTAGCTTCA  74082          ACCTAAA
                                TGAAGCTAGAT      GCT
                                ||||||||||       |||
                                ACTTCGATTTA      CGA
                                      CACTAAA
GAM341  LOC255452 3'  TAGGTACCTACCTTCA      97544       C   A
                                TGAAG TAG TACCTA
                                |||||  |||  ||||||
                                ACTTC ATC ATGGAT
                                   C   C
GAM341  LOC257396 3'  GGCAGCTTTAGGCTTAACTT   97139     C   ATA       A
                                AAG TAG   CCTAAAGCT CC
                                |||  |||   |||||||||  ||
                                TTC ATT   GGATTTCGA GG
                                  A   C__        C
GAM341  LOC92710  3'  GTACAAGGCATCTAGCTT     70359         A   AAAGC
                                AAGCTAGAT CCT     TAC
                                |||||||||  |||     |||
                                TTCGATCTA GGA     ATG
                                      C   AC___
GAM342  ACTR1B    3'  GGCAGCCAGCAGCTCC      70823     A        ACA
                                GGA GTTGCTGGCT   GCT
                                |||  ||||||||||   |||
                                CCT CGACGACCGA   CGG
                                  _        ___
GAM342  AMFR      3'  CATTACGCAGGCCAGCAACTCC 57243     A        ACA  _
                                GGA GTTGCTGGCT   GC TGATG
                                |||  ||||||||||   ||  |||||
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                                CCT CAACGACCGG   CG ATTAC
                                  _        A__  C
GAM342  TNFAIP1   3'  CATCAGCTGAGGACAGCAAACT 40917     AG     G  A
            CC                    GGA  TTGCTG CT CAGCTGATG
                                  |||  |||||| || |||||||||
                                  CCT  AACGAC GG GTCGACTAC
                                    CA     A  A
GAM342  C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 21681    AA      _  A___
            CCC                    GG  GTTGCTGG CT    CAGCTG
                                  ||  |||||||| ||    ||||||
                                  CC  CGACGACC GG    GTCGAC
                                   CC       A  GTTG
GAM342  C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 94622    AA      _  A___
            CCC                    GG  GTTGCTGG CT    CAGCTG
                                  ||  |||||||| ||    ||||||
                                  CC  CGACGACC GG    GTCGAC
                                   CC       A  GTTG
GAM342  C20orf59  3'  CATCCCTAGCCAGCAGCTCC   41992     A        CAGCT
                                  GGA GTTGCTGGCTA     GATG
                                  ||| ||||||||||     ||||
                                  CCT CGACGACCGAT     CTAC
                                    _         CC___
GAM342  C9orf7    3'  GCTGCCAGCAACCTCC      34176     A        TAC
                                  GGA GTTGCTGGC   AGC
                                  ||| |||||||||   |||
                                  CCT CAACGACCG   TCG
                                    C       ___
GAM342  KIAA0057  3'  TGTTCAGCCAGCAGCCTCC    24444     A        __
                                  GGA GTTGCTGGCT  ACA
                                  ||| ||||||||||  |||
                                  CCT CGACGACCGA  TGT
                                    C         CT
GAM342  KIAA0542  3'  CATGGCTCAGCCAGCAGCCCCC 66083    AA        AC    G
                                  GG  GTTGCTGGCT  AGCT ATG
                                  ||  ||||||||||  |||| |||
                                  CC  CGACGACCGA  TCGG TAC
                                   CC         C_   _
GAM342  KIAA1209  5'  CATCAGCTGTAACCAAAGTTCC 60752      G  GC   C
                                  GGAA TT  TGG TACAGCTGATG
                                  |||| ||  ||| ||||||||||
                                  CCTT AA  ACC ATGTCGACTAC
                                    G  __   A
GAM342  RAB14     5'  CAGCCACCAGCAACCCCC    32868     AA       CTACA
                                  GG  GTTGCTGG    GCTG
                                  ||  ||||||||    ||||
                                  CC  CAACGACC    CGAC
                                   CC       AC___
GAM342  SYNJ2     3'  ATCAGCTTAAGCAATTCC    61763      G    GGCTAC
                                  GGAA TTGCT     AGCTGAT
                                  |||| |||||     |||||||
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                                CCTT AACGA     TCGACTA
                                  _    AT____
GAM342  LOC155032 3'  TAGCAACCAGCAACTCC     86324     A       CTACA
                                GGA GTTGCTGG    GCTG
                                ||| ||||||||    ||||
                                CCT CAACGACC    CGAT
                                  _      AA___
GAM342  LOC200958 3'  CATCAGCTGCAGCCAGGCATGT 65923     AGT  _    A
          CC                      GGA  TGC TGGCT CAGCTGATG
                                ||| ||| ||||| |||||||||
                                CCT  ACG ACCGA GTCGACTAC
                                  GT_  G    C
GAM342  LOC222060 5'  CACCTCCCACCAGCAACCCCC  94104    AA       CTAC  C
                                GG  GTTGCTGG    AG TG
                                ||  ||||||||    || ||
                                CC  CAACGACC    TC AC
                                 CC       ACCC  C
GAM342  LOC255650 3'  CATCAGCCCCAGGCAACTTCC  96711          _  CTACA
                                GGAAGTTGC TGG    GCTGATG
                                ||||||||| |||    |||||||
                                CCTTCAACG ACC    CGACTAC
                                     G  C____
GAM343  ABCB1    5'  CCAGAACATTCCTCCTGGAA  6247      CTGT  CT
                                TTCC   GG  ATGTTCTGG
                                ||||   ||  |||||||||
                                AAGG   CC  TACAAGACC
                                  TCCT  T_
GAM343  AGT      3'  CCAGAACACAGTGCCTGGCA  3454     __  TA__
                                TGT  GGC   TGTTCTGG
                                |||  |||   ||||||||
                                ACG  CCG   ACAAGACC
                                  GT   TGAC
GAM343  ALDOB    3'  CCAGAATACCCACCCAAGAA  68087    CCT_   CTA
                                TTC   GTGG   TGTTCTGG
                                |||   ||||   ||||||||
                                AAG   CACC   ATAAGACC
                                  AACC   C__
GAM343  ARL4     3'  CCAGAACACAGTTGTGGGAA  19198      T TG   A
                                TTCCC G  GCT TGTTCTGG
                                ||||| |  ||| ||||||||
                                AAGGG T  TGA ACAAGACC
                                  _ GT   C
GAM343  B3GAT1   3'  CCAGAACAAAGGACAGAGAA  37827    C   GG  A
                                TTC CTGT  CT TGTTCTGG
                                ||| ||||  || ||||||||
                                AAG GACA  GA ACAAGACC
                                  A   G_  A
GAM343  B3GAT1   3'  CCAGAACAAAGGACAGAGAA  53972    C   GG  A
                                TTC CTGT  CT TGTTCTGG
                                ||| ||||  || ||||||||
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                                AAG GACA  GA ACAAGACC
                                  A   G_  A
GAM343  CD79B   3'  CCAGAAGAGCCACAGG      41207          ATG
                                CCTGTGGCT   TTCTGG
                                |||||||||   ||||||
                                GGACACCGA   AAGACC
                                     G__
GAM343  CD79B   3'  CCAGAAGAGCCACAGG      5271           ATG
                                CCTGTGGCT   TTCTGG
                                |||||||||   ||||||
                                GGACACCGA   AAGACC
                                     G__
GAM343  CDH3    3'  CCAAACGTCAGGCCACAG    8380           __    C
                                CTGTGGCT  ATGTT TGG
                                ||||||||  ||||| |||
                                GACACCGG  TGCAA ACC
                                     AC   _
GAM343  COL5A1  5'  GCCAGAACAGCCGCCGCCACAA 3634    CC     TA____      III
            AGAA                  C  TGTGGC     TGTTCTGG   C
                                |  ||||||     ||||||||  |
                                G  ACACCG     ACAAGACC   G
                                 AA     CCGCCG       III
GAM343  CRIM1   3'  CCAGAACAAAGGCAG      33173      GG  A
                                CTGT  CT TGTTCTGG
                                ||||  || ||||||||
                                GACG  GA ACAAGACC
                                  __  A
GAM343  DIAPH2  3'  CCAAAACAAGTCTAGCAGGGAA 22063        __    A    C
                                TTCCCTGT  GGCT TGTT TGG
                                ||||||||  |||| |||| |||
                                AAGGGACG  CTGA ACAA ACC
                                     AT   _   A
GAM343  DMD     3'  AGAAAATATAGTCACAGG    14414           __
                                CCTGTGGCTATGT  TCT
                                ||||||||||||  |||
                                GGACACTGATATA  AGA
                                       AA
GAM343  ED1     3'  TTGGAACAATCACAGGGAA   7376           CTA    TG
                                TTCCCTGTGG   TGTTC  G
                                |||||||||   |||||  |
                                AAGGGACACT   ACAAG  T
                                     A__     GT
GAM343  EXTL3   3'  CCAAAACATGCCGCAGGGAG  7528            T    C
                                TTCCCTGTGGC ATGTT TGG
                                |||||||||| ||||| |||
                                GAGGGACGCCG TACAA ACC
                                       _    A
GAM343  FCRH3   3'  CCAGAGTGGCCCACAGG     53630        _   GT
                                CCTGTGG CTAT  TCTGG
                                |||||| ||||  |||||
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                                GGACACC GGTG  AGACC
                                   C   __
GAM343  FECH    3'  CGTGGTGCCACAGGGAA    3753          __
                                TTCCCTGTGGC  TATG
                                ||||||||||  ||||
                                AAGGGACACCG  GTGC
                                      TG
GAM343  FGFRL1  3'  CCAGAACATACAAGGA     41619    C   GGCT
                                TCC TGT   ATGTTCTGG
                                ||| |||   |||||||||
                                AGG ACA   TACAAGACC
                                  A  ____
GAM343  GATA4   3'  CCAGAACAACAACTGGGAA   9004      T  GGCTA
                                TTCCC GT    TGTTCTGG
                                ||||| ||    ||||||||
                                AAGGG CA    ACAAGACC
                                   T  ACA__
GAM343  GNRH1   5'  CCATCACCAGCCACAGAGA   5883    C      AT  TC
                                TC CTGTGGCT  GT  TGG
                                || ||||||||  ||  |||
                                AG GACACCGA  CA  ACC
                                 A       C_  CT
GAM343  HAMP    3'  CCAGAACATAGGTCTTGGAA  40991     CTGT  _
                                TTCC    GGC TATGTTCTGG
                                ||||    ||| ||||||||||
                                AAGG    CTG ATACAAGACC
                                  TT__   G
GAM343  IPP     3'  TAGTTTGAGCCACAGAGAA   19729    C      ATGTT
                                TTC CTGTGGCT    CTG
                                ||| ||||||||    |||
                                AAG GACACCGA    GAT
                                  A       GTTT_
GAM343  ITGB1   3'  CCAGTGTGGCCCAGGGAA    53369       T     GTT
                                TTCCCTG GGCTAT   CTGG
                                ||||||| ||||||   ||||
                                AAGGGAC CCGGTG   GACC
                                     _     T__
GAM343  KCNQ1   3'  CCAGCTGCTGAGCCGCAGAGAA 4021      C      AT  T_
                                TTC CTGTGGCT  GT  CTGG
                                ||| ||||||||  ||  ||||
                                AAG GACGCCGA  CG  GACC
                                  A       GT  TC
GAM343  KDR     3'  CAGAATACCACAAAGAA     9591     CC    CTA
                                TTC  TGTGG   TGTTCTG
                                |||  |||||   |||||||
                                AAG  ACACC   ATAAGAC
                                  AA    ____
GAM343  LEP     3'  CCAGGGGCCCACAGGGAA    4047          _  ATGT
                                TTCCCTGTGG CT    TCTGG
                                |||||||||| ||    |||||
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                                AAGGGACACC GG    GGACC
                                      C _____
GAM343  MKI67    3'  CCAGTGACCAGCCACAGGAGA  10041    _       AT  _
                                TC CCTGTGGCT  GTT CTGG
                                || |||||||||  ||| ||||
                                AG GGACACCGA  CAG GACC
                                 A        C_  T
GAM343  NEFH     3'  CCGGAACAGCCAAAG      40780    G    AT
                                CT TGGCT  GTTCTGG
                                || |||||  |||||||
                                GA ACCGA  CAAGGCC
                                 A    __
GAM343  NXF2     5'  CCAGAACATCACCAAG      35136    G   CT
                                CT TGG  ATGTTCTGG
                                || |||  |||||||||
                                GA ACC  TACAAGACC
                                 _  AC
GAM343  PDE6D    3'  CCAGCATACACACAGGGAA   10489        GC   TT
                                TTCCCTGTG  TATG  CTGG
                                |||||||||  ||||  ||||
                                AAGGGACAC  ATAC  GACC
                                      AC   __
GAM343  PHEMX    5'  CCAGCTGGAAACCACAGGGAG  57359         CTATGTT
                                TTCCCTGTGG      CTGG
                                ||||||||||      ||||
                                GAGGGACACC      GACC
                                      AAAGGTC
GAM343  PHEMX    5'  CCAGCTGGAAACCACAGGGAG  57364         CTATGTT
                                TTCCCTGTGG      CTGG
                                ||||||||||      ||||
                                GAGGGACACC      GACC
                                      AAAGGTC
GAM343  PODXL    3'  CCAGAATGACACAAAGGA    18230     C_   GCTAT
                                TCC  TGTG    GTTCTGG
                                |||  ||||    |||||||
                                AGG  ACAC    TAAGACC
                                  AA   AG___
GAM343  PRODH    3'  CTGGGACAGCCACTGGAA    32925     CT    AT   TG
                                TTCC  GTGGCT  GTTC  G
                                ||||  ||||||  ||||  |
                                AAGG  CACCGA  CAGG  C
                                  T_     __    GT
GAM343  RANBP2L1 3'  CCAGAATAAAACCACCAGGAA  17313     CT   CTA
                                TTCC  GTGG   TGTTCTGG
                                ||||  ||||   ||||||||
                                AAGG  CACC   ATAAGACC
                                  AC   AAA
GAM343  REGL     3'  CCAGAACATGAATTCAGG    21486     TGGC
                                CCTG    TATGTTCTGG
                                ||||    ||||||||||
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                              GGAC   GTACAAGACC
                                TTAA
GAM343  SLC19A1  5' CCAGAATGCATCCAGAGGGAA 11755      G  CTA
                              TTCCCT TGG  TGTTCTGG
                              ||||||| |||  ||||||||
                              AAGGGA ACC  GTAAGACC
                                 G  TAC
GAM343  ST14    3' CCAGAACATACACTGTGAA   41765    CCT  GC
                              TTC  GTG  TATGTTCTGG
                              |||  |||  ||||||||||
                              AAG  CAC  ATACAAGACC
                                TGT  __
GAM343  TBL2    3' CCAGAACAACCTAGAGAA    52182    C  T  CTA
                              TTC CTG GG  TGTTCTGG
                              ||| ||| ||  ||||||||
                              AAG GAT CC  ACAAGACC
                                A  _ A__
GAM343  TBL2    3' CCAGAACAACCTAGAGAA    24926    C  T  CTA
                              TTC CTG GG  TGTTCTGG
                              ||| ||| ||  ||||||||
                              AAG GAT CC  ACAAGACC
                                A  _ A__
GAM343  TCFL4   3' CCAGGATAAGACCACAGGGAA  63461        _ A
                              TTCCCTGTGG CT TGTTCTGG
                              |||||||||| || ||||||||
                              AAGGGACACC GA ATAGGACC
                                    A  _
GAM343  TFAP4   3' CCGGGGCAGCCACAGGGAG   12237         AT
                              TTCCCTGTGGCT  GTTCTGG
                              ||||||||||||  |||||||
                              GAGGGACACCGA  CGGGGCC
                                       __
GAM343  UBE2L6  3' CCAGGGGGAGCCACGG     14873       ATG
                              CTGTGGCT   TTCTGG
                              ||||||||   ||||||
                              GGCACCGA   GGGACC
                                   GG_
GAM343  UBQLN3  3' CAAAACATAGTGGAG      33926     CTGTG      C
                              TTCC    GCTATGTT TG
                              ||||    |||||||| ||
                              GAGG    TGATACAA AC
                                ______      A
GAM343  UMOD    3' CCAGTGCTCCAGCCACAG    12548       AT_  T
                              CTGTGGCT   GT CTGG
                              ||||||||   || ||||
                              GACACCGA   CG GACC
                                   CCT  T
GAM343  WBSCR5  3' CCAGAACAGGGCAGAG     26256    G  G  A
                              CT TG CT TGTTCTGG
                              || || || ||||||||
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                                GA AC GG ACAAGACC
                                 G  G  _
GAM343  WBSCR5   3'  CCAGAACAGGGCAGAG     41856    G  G  A
                                CT TG CT TGTTCTGG
                                || || || ||||||||
                                GA AC GG ACAAGACC
                                 G  G  _
GAM343  WBSCR5   3'  CCAGAACAGGGCAGAG     50610    G  G  A
                                CT TG CT TGTTCTGG
                                || || || ||||||||
                                GA AC GG ACAAGACC
                                 G  G  _
GAM343  ZNF134   3'  CAGTTTAAGCCACAGGGAA   12846          A  TT
                                TTCCCTGTGGCT TG  CTG
                                |||||||||||| ||  |||
                                AAGGGACACCGA AT  GAC
                                       _  TT
GAM343  ZNF36    3'  CCTTCGTAGCCACAAGG     93960    C       TTCT
                                CC TGTGGCTATG    GG
                                || ||||||||||    ||
                                GG ACACCGATGC    CC
                                 A        TT__
GAM343  ABCA9    5'  CAGAACATGCAGAGA       54410    C   GGCT
                                TC CTGT    ATGTTCTG
                                || ||||    ||||||||
                                AG GACG    TACAAGAC
                                 A   _____
GAM343  ADAMTSL1 3'  CCTCAAATAGCACAGGGAA   57686        G   GTTCT
                                TTCCCTGTG CTAT     GG
                                ||||||||| ||||     ||
                                AAGGGACAC GATA     CC
                                      _    AACT_
GAM343  BAIAP1   3'  CCAGAACGGCAGCAGG      16449      G   AT
                                CCTGT GCT  GTTCTGG
                                ||||| |||  |||||||
                                GGACG CGG  CAAGACC
                                   A  __
GAM343  BCKDK    3'  CCAGAACTTGGAGCAGGGAA  59793        GG   T
                                TTCCCTGT  CTA GTTCTGG
                                ||||||||  ||| |||||||
                                AAGGGACG  GGT CAAGACC
                                     A_   T
GAM343  C11orf25 3'  CCAAATTAGGGCCACAG     48639        AT_  C
                                CTGTGGCT   GTT TGG
                                ||||||||   ||| |||
                                GACACCGG   TAA ACC
                                     GAT   _
GAM343  C20orf112 3' CCAGTGCTGCCACAGGGA    54640         TAT  T
                                TCCCTGTGGC   GT CTGG
                                ||||||||||   || ||||
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                                AGGGACACCG   CG GACC
                                     T__  T
GAM343  C6orf26   3'  CCAAAACACAGAGCAGG     47509      GG  A    C
                                CCTGT  CT TGTT TGG
                                |||||  || |||| |||
                                GGACG  GA ACAA ACC
                                   A_  C    A
GAM343  CGGBP1    5'  CTGGCACCACAGGGAA      13362          CTA    CT
                                TTCCCTGTGG   TGTT  G
                                ||||||||||   ||||  |
                                AAGGGACACC   ACGG  C
                                     ____   T_
GAM343  DKFZP566G1424 5'  CCAGTGCTGCCACAGGGA    84779          TAT  T
                                TCCCTGTGGC   GT CTGG
                                ||||||||||   || ||||
                                AGGGACACCG   CG GACC
                                     T__  T
GAM343  DKFZp586I021 5'  CCAGACGTCACCACAGGGA    50088         CT    T
                                TCCCTGTGG  ATGT CTGG
                                |||||||||  |||| ||||
                                AGGGACACC  TGCA GACC
                                     AC   _
GAM343  DKFZP727M111 5'  CCAATCTGGTCACAGGGAA    31407           T  TC
                                TTCCCTGTGGCTA GT  TGG
                                |||||||||||| ||  |||
                                AAGGGACACTGGT TA  ACC
                                       C  __
GAM343  ELF4      3'  CCGTGGATCAGCCACAGGGA   7431           AT   _
                                TCCCTGTGGCT  GTTC TGG
                                ||||||||||  |||| |||
                                AGGGACACCGA  TAGG GCC
                                     C_   T
GAM343  ERG-1     3'  CCAGGATGCCAAAGG      41842     G    TAT
                                CCT TGGC   GTTCTGG
                                ||| ||||   |||||||
                                GGA ACCG   TAGGACC
                                  A   ___
GAM343  FLJ00058  5'  CCAGAAATGCCAGCAGGGAA   78765        _    TATG
                                TTCCCTG TGGC    TTCTGG
                                ||||||| ||||    ||||||
                                AAGGGAC ACCG    AAGACC
                                    G    TA__
GAM343  FLJ12816  3'  CCAGAACAGGACGACAGTGAA  41932     C    GGCTA
                                TTC CTGT     TGTTCTGG
                                ||| ||||     ||||||||
                                AAG GACA     ACAAGACC
                                  T    GCAGG
GAM343  FLJ13315  3'  CCAGAACATAATACA       46568      GC
                                TGTG  TATGTTCTGG
                                ||||  ||||||||||
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                                ACAT  ATACAAGACC
                                  A_
GAM343  FLJ20010  3'  CCAGAACGATTGGAACAGG   38716      GG  __
                                CCTGT  CTA  TGTTCTGG
                                |||||  |||  ||||||||
                                GGACA  GGT  GCAAGACC
                                   A_   TA
GAM343  FLJ22369  5'  ATGGCGCGACAGGGAA     49918        _ _
                                TTCCCTGT G GCTAT
                                |||||||| | |||||
                                AAGGGACA C CGGTA
                                     G G
GAM343  FLJ23563  3'  CCAGAATGCTACAAAAGAA   67593    CC_     TAT
                                TTC   TGTGGC   GTTCTGG
                                |||   ||||||   |||||||
                                AAG   ACATCG   TAAGACC
                                  AAA     ___
GAM343  FLJ32332  3'  CACAGCACACAGGGAA     58299         _  A
                                TTCCCTGTG GCT TG
                                |||||||| ||| ||
                                AAGGGACAC CGA AC
                                     A   C
GAM343  GRIN3A    3'  CCAAGTGAAGCAGCCACAGGGA 55968          ATG  ___
                                TCCCTGTGGCT   TTC   TGG
                                ||||||||||   |||   |||
                                AGGGACACCGA   AAG   ACC
                                      CG_   TGA
GAM343  HSPC166   3'  CCAGAACACATGGAGGGAA   26366       G  GCTA
                                TTCCCT TG    TGTTCTGG
                                ||||||  ||    ||||||||
                                AAGGGA GT    ACAAGACC
                                   G  AC__
GAM343  HSPC251   3'  CCAGGCTAGAGCCACAGAGA  33249    C       A  TT
                                TC CTGTGGCT TG  CTGG
                                || ||||||||  ||  ||||
                                AG GACACCGA AT  GACC
                                 A       G  CG
GAM343  IGF2AS    3'  CCAGGGTGCAACAGAGAA    33095    C    G  TAT TT
                                TTC CTGT GC   G  CTGG
                                ||| |||| ||   |  ||||
                                AAG GACA CG   T  GACC
                                  A   A  ___ GG
GAM343  ILF3      3'  CCAAAACACGCTGGGAA     15722      T   GCTA   C
                                TTCCC GTG    TGTT TGG
                                ||||| |||    |||| |||
                                AAGGG CGC    ACAA ACC
                                   T  _____   A
GAM343  KIAA0040  3'  CCAAAGTTTCCAGCAGGGAA  27780        _  CT  GTTC
                                TTCCCTG TGG  AT    TGG
                                ||||||| |||  ||    |||
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                                AAGGGAC ACC  TG    ACC
                                    G   TT  AA__
GAM343  KIAA0254  3'  CAGACAGTCACAGGGAA     28596          ATGT
                                TTCCCTGTGGCT    TCTG
                                ||||||||||||   ||||
                                AAGGGACACTGA    AGAC
                                      C___
GAM343  KIAA0336  3'  CCAGAATAAAACCACCAGGAA 27589      CT    CTA
                                TTCC  GTGG   TGTTCTGG
                                ||||  ||||   ||||||||
                                AAGG  CACC   ATAAGACC
                                  AC    AAA
GAM343  KIAA0494  3'  CCAGAACACATTTGGG      28740     T_   GCTA
                                CCC  GTG    TGTTCTGG
                                |||  |||    ||||||||
                                GGG  TAC    ACAAGACC
                                  TT  _____
GAM343  KIAA0537  3'  CCAGAACAGCCTACAGGGGA   29244        _    AT
                                TTCCCTGT GGCT  GTTCTGG
                                |||||||| ||||  |||||||
                                AGGGGACA CCGA  CAAGACC
                                     T   __
GAM343  KIAA0774  5'  CGGGATGCCACAAGGAA     91752      C     TAT    TG
                                TTCC TGTGGC   GTTC  G
                                |||| ||||||   ||||  |
                                AAGG ACACCG   TAGG  C
                                  A     ___    GT
GAM343  KIAA0828  3'  CCATGAAAGCCACAGAGGA   81194     _      ATG   _
                                TCC CTGTGGCT   TTC TGG
                                ||| ||||||||   ||| |||
                                AGG GACACCGA   AAG ACC
                                  A       ___   T
GAM343  KIAA1118  3'  CCAGAGGCCCACAGGGA     69606         _ ATGT
                                TCCCTGTGG CT    TCTGG
                                |||||||||  ||    |||||
                                AGGGACACC GG    AGACC
                                     C  _____
GAM343  KIAA1742  3'  CAGATCCACAGGGAG       77657          CTATGT
                                TTCCCTGTGG     TCTG
                                ||||||||||     ||||
                                GAGGGACACC     AGAC
                                      T_____
GAM343  KIAA1944  5'  CCAACCTAGCCACAGGGA    75558           T  TC
                                TCCCTGTGGCTA GT  TGG
                                ||||||||||||  ||  |||
                                AGGGACACCGAT CA  ACC
                                      C  __
GAM343  KIAA1981  3'  CGGAACAGCACAAGGAA     88342      C    G  AT    TG
                                TTCC TGTG CT  GTTC  G
                                |||| |||| ||  ||||  |
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                                AAGG ACAC GA  CAAG  C
                                  A   _ __   GT
GAM343  NXPH3   3'  ACGGAGCCACAGAGAG     65747    C      A
                                TTC CTGTGGCT TGT
                                ||| |||||||| |||
                                GAG GACACCGA GCA
                                  A       G
GAM343  PP5395  3'  TCAGGATAGCACAGGGAA    72110        G  AT
                                TTCCCTGTG CT  GTTCTGG
                                ||||||||| ||  |||||||
                                AAGGGACAC GA  TAGGACT
                                    _ __
GAM343  PRDM7   3'  CCAGAAGGGCCACAGAGAA   53788    C      ATG
                                TTC CTGTGGCT   TTCTGG
                                ||| ||||||||   ||||||
                                AAG GACACCGG   AAGACC
                                  A       G__
GAM343  PRDM9   3'  CCAGAAGGGCCACAGAGAA   39575    C      ATG
                                TTC CTGTGGCT   TTCTGG
                                ||| ||||||||   ||||||
                                AAG GACACCGG   AAGACC
                                  A       G__
GAM343  PXR2b   3'  ATATAGCCCAAGGAA      33337     C  T
                                TTCC TG GGCTATGT
                                |||| || ||||||||
                                AAGG AC CCGATATA
                                  A _
GAM343  RAB33B  3'  CCAGCTTAGCCACAAAGAA   48490    CC      TGTT
                                TTC  TGTGGCTA   CTGG
                                |||  ||||||||   ||||
                                AAG  ACACCGAT   GACC
                                  AA       TC__
GAM343  SH120   3'  CCAGAACATGAGAGGGAG    32920      GTGGC
                                TTCCCT    TATGTTCTGG
                                ||||||    ||||||||||
                                GAGGGA    GTACAAGACC
                                   GA___
GAM343  SH120   3'  CCAGAACATGAGAGGGAG    94606      GTGGC
                                TTCCCT    TATGTTCTGG
                                ||||||    ||||||||||
                                GAGGGA    GTACAAGACC
                                   GA___
GAM343  SLC2A12 3'  CCAGAACACACAGTGTGGA   59078    ___    GCTA
                                TCC   CTGTG   TGTTCTGG
                                |||   |||||   ||||||||
                                AGG   GACAC   ACAAGACC
                                  TGT    ____
GAM343  SP329   3'  CCAGAGTGCTCCACAGGGA   47924        CTA GT
                                TCCCTGTGG   T  TCTGG
                                |||||||||   |  |||||
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                                AGGGACACC   G  AGACC
                                     TC_ TG
GAM343  SSH2     3'  TCAGTAAGCCCACAGGGAA   62213         _  ATGTT
                                TTCCCTGTGG CT    CTGG
                                |||||||||| ||    ||||
                                AAGGGACACC GA    GACT
                                      C  AT___
GAM343  SYTL4    5'  CCAGTCAGCCACAGGGAA    54939          ATGTT
                                TTCCCTGTGGCT    CTGG
                                ||||||||||||    ||||
                                AAGGGACACCGA    GACC
                                       CT___
GAM343  TNRC4    3'  CCAGTCAGCCACAGAGA     23221    C      ATGTT
                                TC CTGTGGCT    CTGG
                                || ||||||||    ||||
                                AG GACACCGA    GACC
                                 A       CT___
GAM343  UBE3B    3'  CCAGACTGTCAGCACAGGGAA  76919        G  _  GT
                                TTCCCTGTG CT AT  TCTGG
                                ||||||||| || ||  |||||
                                AAGGGACAC GA TG  AGACC
                                      _  C  TC
GAM343  VPS4A    3'  CCTTGCAGCCACAGAGA     25102    C      AT  TCT
                                TC CTGTGGCT  GT   GG
                                || ||||||||  ||   ||
                                AG GACACCGA  CG   CC
                                 A       __  TT_
GAM343  XYLT1    5'  CCAACAGCAGCCACGGGAA   77847      T     A_  TC
                                TTCCC GTGGCT  TGT  TGG
                                ||||| ||||||  |||  |||
                                AAGGG CACCGA  ACA  ACC
                                   _     CG  __
GAM343  ZFP100   3'  CCAGAAAGCCAAAAAGAA    70050     CCTG    ATG
                                TTC    TGGCT   TTCTGG
                                |||    |||||   ||||||
                                AAG    ACCGA   AAGACC
                                  AAAA    ____
GAM343  ZNF213   5'  CAGCTACCACAGGGGA      65091          C  TGTT
                                TTCCCTGTGG TA    CTG
                                |||||||||| ||    |||
                                AGGGGACACC AT    GAC
                                      _  C___
GAM343  LOC112609 3'  CCAGTGTGGCACAGGGAA    72837         G   GTT
                                TTCCCTGTG CTAT   CTGG
                                ||||||||| ||||   ||||
                                AAGGGACAC GGTG   GACC
                                      _   T__
GAM343  LOC115073 5'  CCAGGCGTCAAACCACAGGGA  73204         CT__   T
                                TCCCTGTGG    ATGT CTGG
                                |||||||||    |||| ||||
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                                AGGGACACC    TGCG GACC
                                     AAAC    _
GAM343   LOC122962 5'  CCAGACAGTGGCCACTGAGAA  75587     CCT      GT
                                TTC   GTGGCTAT  TCTGG
                                |||   ||||||||  |||||
                                AAG   CACCGGTG  AGACC
                                  AGT       AC
GAM343   LOC124044 3'  CCAGAACACTCAGAGGGA    76025      G   CTA
                                TCCCT TGG   TGTTCTGG
                                ||||| |||   ||||||||
                                AGGGA ACT   ACAAGACC
                                   G   C__
GAM343   LOC143308 5'  CCAAATTTGGCCACAG      82936         T   C
                                CTGTGGCTA GTT TGG
                                ||||||||| ||| |||
                                GACACCGGT TAA ACC
                                     T   _
GAM343   LOC145314 3'  CCAGAACACATCACCTGAG   77086     CCT    CTA
                                TTC   GTGG   TGTTCTGG
                                |||   ||||   ||||||||
                                GAG   CACT   ACAAGACC
                                  TC_   AC_
GAM343   LOC146420 3'  CCAGAACCAGTTACAG      83667         AT
                                CTGTGGCT  GTTCTGG
                                ||||||||  |||||||
                                GACATTGA  CAAGACC
                                     C_
GAM343   LOC146445 3'  CCAGAGCCACCACAGGGA    83678          CTAT
                                TCCCTGTGG    GTTCTGG
                                |||||||||    |||||||
                                AGGGACACC    CGAGACC
                                     AC__
GAM343   LOC147178 3'  CCAGCCAGCCACGGAGAA    61323     C       ATGTT
                                TTC CTGTGGCT     CTGG
                                ||| ||||||||     ||||
                                AAG GGCACCGA     GACC
                                  A       CC___
GAM343   LOC148529 5'  CACAGCCACAGGAGAA      84166     _       A
                                TTC CCTGTGGCT TG
                                ||| ||||||||| ||
                                AAG GGACACCGA AC
                                  A        C
GAM343   LOC148930 5'  CCAGGGGCAGACCACGGGGAA  79093          CTA    _
                                TTCCCTGTGG   TGTTC TGG
                                ||||||||||   ||||| |||
                                AAGGGGCACC   ACGGG ACC
                                     AG_     G
GAM343   LOC149950 5'  CCAGAACATGATCTCAGG     79551      T GC
                                CCTG G  TATGTTCTGG
                                |||| |  ||||||||||
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                                GGAC C  GTACAAGACC
                                  T TA
GAM343  LOC150378 5'  CCAGAAACAAGCCACGGGAA  79742      T     ATG
                                TTCCC GTGGCT   TTCTGG
                                ||||| ||||||   ||||||
                                AAGGG CACCGA   AAGACC
                                   _     ACA
GAM343  LOC150951 5'  CCAGGGCCACACAGGGAA    85167        GCTAT
                                TTCCCTGTG    GTTCTGG
                                |||||||||    |||||||
                                AAGGGACAC    CGGGACC
                                     AC___
GAM343  LOC151429 3'  CCAGGAGACCACAGGGA     85347        _ ATGT
                                TCCCTGTGG CT    TCTGG
                                ||||||||| ||    |||||
                                AGGGACACC GA    GGACC
                                     A ____
GAM343  LOC158434 3'  CCAGAATAAACCACTGGGAA  86819      T   CTA
                                TTCCC GTGG   TGTTCTGG
                                ||||| ||||   ||||||||
                                AAGGG CACC   ATAAGACC
                                   T   AA_
GAM343  LOC170106 5'  CCAAGGCAGTCAGCCACAGG  82571        A__  TC
                                CCTGTGGCT   TGT  TGG
                                |||||||||   |||  |||
                                GGACACCGA   ACG  ACC
                                     CTG   GA
GAM343  LOC196446 3'  CGGAAAGCCACAGAGAA     87708     C      ATG   TG
                                TTC CTGTGGCT   TTC  G
                                ||| ||||||||   |||  |
                                AAG GACACCGA   AAG  C
                                  A       ___   GT
GAM343  LOC197136 3'  CCAGAACACTCAGAGGGA    89728      G   CTA
                                TCCCT TGG   TGTTCTGG
                                ||||| |||   ||||||||
                                AGGGA ACT   ACAAGACC
                                   G   C__
GAM343  LOC197342 3'  CCAGGAGAAGCCACAGGGGA  87993          ATG
                                TTCCCTGTGGCT   TTCTGG
                                ||||||||||||   ||||||
                                AGGGGACACCGA   AGGACC
                                     AG_
GAM343  LOC200734 3'  CCATCCGCAGCCACAGGGGA  88860          A  TTC
                                TTCCCTGTGGCT TG   TGG
                                |||||||||||| ||   |||
                                AGGGGACACCGA GC   ACC
                                     C  CT_
GAM343  LOC201102 3'  CCTGACCAGCCACAGGAGA   88090    _       AT   CT
                                TC CCTGTGGCT  GTT  GG
                                || |||||||||  |||  ||
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                                AG GGACACCGA  CAG  CC
                                 A        C_   T_
GAM343   LOC201283 3'  CCAGAACACAGTCGTGAGGA   60413     CT     A
                                TCC  GTGGCT TGTTCTGG
                                |||  |||||| ||||||||
                                AGG  TGCTGA ACAAGACC
                                  AG     C
GAM343   LOC202915 3'  CCACACGCCAGCCACAGGGGA  90388           A_   TC
                                TTCCCTGTGGCT  TGT  TGG
                                ||||||||||||  |||  |||
                                AGGGGACACCGA  GCA  ACC
                                       CC   C_
GAM343   LOC204965 5'  CAGAGTGCACAGAGAA      90647     C     G TATG
                                TTC CTGTG C    TTCTG
                                ||| ||||| |    |||||
                                AAG GACAC G    GAGAC
                                  A    _ T___
GAM343   LOC205418 3'  CACAGCCAGCAGGGAA      90681        _     A
                                TTCCCTG TGGCT TG
                                ||||||| ||||| ||
                                AAGGGAC ACCGA AC
                                    G    C
GAM343   LOC220692 3'  CCAGAATAAAACCACCAGGAA  91220      CT    CTA
                                TTCC  GTGG   TGTTCTGG
                                ||||  ||||   ||||||||
                                AAGG  CACC   ATAAGACC
                                  AC    AAA
GAM343   LOC222631 5'  CCAGAACACAGCTGGAA     92838      CTGT    A
                                TTCC    GGCT TGTTCTGG
                                ||||    |||| ||||||||
                                AAGG    TCGA ACAAGACC
                                  _____    C
GAM343   LOC253039 3'  CCAAATACATCTACAGGGAA   96153         CT    TC_
                                TTCCCTGTGG  ATGT   TGG
                                ||||||||||  ||||   |||
                                AAGGGACATC  TACA   ACC
                                      __    TAA
GAM343   LOC253841 5'  CCAGAATGTAGCCACAG     96342
                                CTGTGGCTATGTTCTGG
                                ||||||||||||||||
                                GACACCGATGTAAGACC

GAM343   LOC254028 3'  CCAGAACAGAAGCACCAAGAA  96539     CC  TG   A_
                                TTC  TG  GCT  TGTTCTGG
                                |||  ||  |||  ||||||||
                                AAG  AC  CGA  ACAAGACC
                                  A_  CA   AG
GAM343   LOC257449 3'  CAGATCCACAGGGAG       62718          CTATGT
                                TTCCCTGTGG     TCTG
                                ||||||||||     ||||
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                                GAGGGACACC     AGAC
                                      T_____
GAM343  LOC89231  3'  GGACAGCACAGGGAA      92733        G  AT
                                TTCCCTGTG CT  GTTC
                                ||||||||| ||  ||||
                                AAGGGACAC GA  CAGG
                                      _  __
GAM343  LOC90550  3'  CCAGAACACAAATCAGAGGGA  73090      G   CTA_
                                TCCCT TGG    TGTTCTGG
                                ||||| |||    ||||||||
                                AGGGA ACT    ACAAGACC
                                   G   AAAC
GAM343  LOC91373  3'  CCAGCAAGGCCACAG      65834        A  TT
                                CTGTGGCT TG  CTGG
                                |||||||| ||  ||||
                                GACACCGG AC  GACC
                                     A  __
GAM343  LOC91445  3'  CCAGAACCTGCCACAGG     60547        TAT
                                CCTGTGGC   GTTCTGG
                                ||||||||   |||||||
                                GGACACCG   CAAGACC
                                     TC_
GAM344  ADAMTS5   3'  GCTTCACGTGACAGTGGTGAC  22893     _  TGAG   C
                                GTC CC    ACT TCATGTGAAGC
                                ||| ||    ||| ||||||||||
                                CAG GG    TGA AGTGCACTTCG
                                  T  _____   C
GAM344  ADCY2     3'  GTTTTACATATCTGTTTAGG   65021       ACTCTC
                                CCTGAG     ATGTGAAGC
                                ||||||     |||||||||
                                GGATTT     TACATTTTG
                                   GTCTA_
GAM344  ALP       3'  GTTTTGCAACTCTTTTTGGGGC 27127      T    CTCTCA  TG
                                GTCCC GAGA     TG  AAGC
                                ||||| ||||     ||  ||||
                                CGGGG TTTT     AC  TTTG
                                   T    CTCA__  GT
GAM344  ANKH      3'  GCTTTGCAGTGGTTTCAGAGGC 53990     C       CTCA  TG
                                GTC CTGAGACT    TG  AAGC
                                ||| ||||||||    ||  ||||
                                CGG GACTTTGG    AC  TTCG
                                  A       TG__  GT
GAM344  APP       3'  GCTTCATGTGAACGTGGGA   4908       TGAG  TC
                                TCCC    AC  TCATGTGAAGC
                                ||||    ||  ||||||||||
                                AGGG    TG  AGTGTACTTCG
                                  _____  CA
GAM344  BCL2L2    3'  TTTGGCAAGTTTAGGGGC    14472         A  CTCA   G
                                GTCCCTGAG CT    TGT AAG
                                ||||||||| ||    ||| |||
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                                CGGGGATTT GA   ACG TTT
                                   _ _____  G
GAM344  BCL7A   3'  TTTTGTTGTTTTTGGGGGC   40648     TG  CTCT  T TG
                                GTCCC  AGA   CA G  AAG
                                |||||  |||   || |  |||
                                CGGGG  TTT   GT T  TTT
                                   GT  T___  _ GT
GAM344  BNC     3'  TTTCATATCATTTGGGGC    8162      T  GACTCTC
                                GTCCC GA     ATGTGAAG
                                ||||| ||     ||||||||
                                CGGGG TT     TATACTTT
                                   T  AC_____
GAM344  CANX    3'  GCTTCATGTGGCACTTGGG   87482    TG  ACTC
                                CC  AG   TCATGTGAAGC
                                ||  ||   ||||||||||
                                GG  TC   GGTGTACTTCG
                                 GT  AC__
GAM344  COL4A2  3'  GCTCGAGGGGCTCAGGGGC   8469        A    AT
                                GTCCCTGAG CTCTC  GT
                                ||||||||| |||||  ||
                                CGGGGACTC GGGAG  CG
                                     G    CT
GAM344  COX7A2L 3'  GCTGAGGACCTCAGGGAC    16352       AC    T
                                GTCCCTGAG  TCTCA GT
                                |||||||||  ||||| ||
                                CAGGGACTC  GGAGT CG
                                     CA    _
GAM344  CSK     5'  GCTTTACTGTGACTCGGGGAC  15219       AC  T  T
                                GTCCCTGAG  TC CA GTGAAGC
                                |||||||||  || || |||||||
                                CAGGGGCTC  AG GT CATTTCG
                                     __  T  _
GAM344  CYP39A1 3'  CTTCACTTTGTTTTAGG     33445       TCTCAT
                                CCTGAGAC     GTGAAG
                                ||||||||     ||||||
                                GGATTTTG     CACTTC
                                     TTT___
GAM344  DNM2    3'  GCGGGGGGTCTTGGGGGC    17055      TG      A
                                GTCCC  AGACTCTC TGT
                                |||||  |||||||| |||
                                CGGGG  TCTGGGGG GCG
                                   GT       _
GAM344  DRIL1   3'  GTTTTTAAGAGGTTTCGGGGG  17832        T   ATGT
                                TCCCTGAGAC CTC    GAAGC
                                |||||||||| |||    |||||
                                GGGGGCTTTG GAG    TTTTG
                                     _   AAT_
GAM344  EHD1    3'  GCTTTCCCGCGGGGGTCTCAGG 69624           A  T_
            GA                    TCCCTGAGACTCTC TG  GAAGC
                                ||||||||||||| ||  |||||
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                                AGGGACTCTGGGGG GC  TTTCG
                                      C  CC
GAM344  EMD     3'  GCTTTATGTGTTTTTGCTTGGG 3681      TG  ACTCT_
          GG                  TCCC  AG     CATGTGAAGC
                              ||||  ||     ||||||||||
                              GGGG  TC     GTGTATTTCG
                                GT  GTTTTT
GAM344  ETF1    3'  GTTTCACATGATACATTTAGGG 16399       ACTC
                              CCCTGAG    TCATGTGAAGC
                              |||||||    ||||||||||
                              GGGATTT    AGTACACTTTG
                                 ACAT
GAM344  FGFR2   3'  GTTCTGCTGATAGTTTTGGGGA 43360      TG    C   T  GA
          T                   GTCCC  AGACT TCA GT  AGC
                              |||||  ||||| ||| ||  |||
                              TAGGG  TTTGA AGT CG  TTG
                                 GT    T  _  TC
GAM344  FGFR2   3'  GTTCTGCTGATAGTTTTGGGGA 43372      TG    C   T  GA
          T                   GTCCC  AGACT TCA GT  AGC
                              |||||  ||||| ||| ||  |||
                              TAGGG  TTTGA AGT CG  TTG
                                 GT    T  _  TC
GAM344  FGFR2   3'  GTTCTGCTGATAGTTTTGGGGA 43483      TG    C   T  GA
          T                   GTCCC  AGACT TCA GT  AGC
                              |||||  ||||| ||| ||  |||
                              TAGGG  TTTGA AGT CG  TTG
                                 GT    T  _  TC
GAM344  FGFR2   3'  GTTCTGCTGATAGTTTTGGGGA 43493      TG    C   T  GA
          T                   GTCCC  AGACT TCA GT  AGC
                              |||||  ||||| ||| ||  |||
                              TAGGG  TTTGA AGT CG  TTG
                                 GT    T  _  TC
GAM344  FGFR2   3'  GTTCTGCTGATAGTTTTGGGGA 43503      TG    C   T  GA
          T                   GTCCC  AGACT TCA GT  AGC
                              |||||  ||||| ||| ||  |||
                              TAGGG  TTTGA AGT CG  TTG
                                 GT    T  _  TC
GAM344  FGFR2   3'  GTTCTGCTGATAGTTTTGGGGA 3764       TG    C   T  GA
          T                   GTCCC  AGACT TCA GT  AGC
                              |||||  ||||| ||| ||  |||
                              TAGGG  TTTGA AGT CG  TTG
                                 GT    T  _  TC
GAM344  FRAT2   3'  TTTAAGGAGGGCTCAGGGG   23883        A    ATG
                              TCCCTGAG CTCTC   TGAA
                              ||||||||  |||||  ||||
                              GGGGACTC GGGAG   ATTT
                                 _    GA_
GAM344  FZD1    3'  GCTTTGTGTGGGTTGGAAGAGA 13036     C  GAGACT     TG
          C                   GTC CT     CTCATG  AAGC
                              |||  ||     ||||||  ||||
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                                CAG GA     GGGTGT  TTCG
                                  A  AGGTT_     GT
GAM344  FZD4     3'  CATGAGATCTTGGGGAC     24131       TG   C
                                GTCCC  AGA TCTCATG
                                |||||  ||| |||||||
                                CAGGG  TCT AGAGTAC
                                   GT   _
GAM344  GARP     3'  TGGGCGGTTTCAGGGAC     18603            _
                                GTCCCTGAGACT CTCA
                                |||||||||||| ||||
                                CAGGGACTTTGG GGGT
                                       C
GAM344  GATA6    5'  GCTTCGCATCCCTTCGGGGC   17917       T   ACTCTC
                                GTCCC GAG     ATGTGAAGC
                                ||||| |||     |||||||||
                                CGGGG TTC     TACGCTTCG
                                   C   CC____
GAM344  GLDC     3'  GTTTTGCGTAGAAAGTTTTAGG 64240         C  _   TG
                                CCTGAGACT TC ATG  AAGC
                                ||||||||| || |||  ||||
                                GGATTTTGA AG TGC  TTTG
                                     A  A   GT
GAM344  GNRHR    5'  ACATTAAGTATCTCAGGGAC   4640          CT  C_
                                GTCCCTGAGA  CT  ATGT
                                ||||||||||  ||  ||||
                                CAGGGACTCT  GA  TACA
                                      AT  AT
GAM344  GP1BA    3'  GTGGGAGGTTTGGGGAC     3916       TG  A
                                GTCCC  AG CTCTCAT
                                |||||  || |||||||
                                CAGGG  TT GAGGGTG
                                   GT  G
GAM344  GRM1     5'  GCTGGGCGTCTTGGGGG     5916       TG   T   T
                                TCCC  AGAC CTCA GT
                                ||||  |||| |||| ||
                                GGGG  TCTG GGGT CG
                                   GT   C   _
GAM344  HDAC5    3'  GTTTCCTGGGTTCTCAGGGGC  57612          CT   TGT
                                GTCCCTGAGA  CTCA   GAAGC
                                ||||||||||  ||||   |||||
                                CGGGGACTCT  GGGT   CTTTG
                                     T_   C__
GAM344  HOXB9    3'  GTTTCGTGATTTCTTTGGGG   43779     T   CTC   GT
                                TCCC GAGA   TCAT  GAAGC
                                |||| ||||   ||||  |||||
                                GGGG TTCT   AGTG  CTTTG
                                  T   TT_   __
GAM344  IL12RB2  3'  GCTCTGGGGGAGTCTTAGG   7771           ATGT  A
                                CCTGAGACTCTC   GA GC
                                ||||||||||||   || ||
```

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                                GGATTCTGAGGG   CT CG
                                      GGT_ _
GAM344  JUP     3'  CTTCTCTTGAAAAGTTCAGGGA 9487        ACTC  TGT
           C                   GTCCCTGAG   TCA  GAAG
                               |||||||||   |||  ||||
                               CAGGGACTT   AGT  CTTC
                                   GAAA  TCT
GAM344  KIAA0857 3'  GTTTCAGTCATGCTTTTGGGGG 66678    TG  CTCT  __
                               TCCC  AGA   CATG  TGAAGC
                               ||||  |||   ||||  ||||||
                               GGGG  TTT   GTAC  ACTTTG
                                 GT  C___   TG
GAM344  LAMP1   3'  GTTTTGCCGTGGCTTGGGGAT  18707     TG  ACTC  _ TG
                               GTCCC  AG   TCAT G  AAGC
                               |||||  ||   |||| |  ||||
                               TAGGG  TC   GGTG C  TTTG
                                 GT  ____   C GT
GAM344  LILRA2  3'  GCGTGGTGGAGCCTCAGGGAC  22489       A  __
                               GTCCCTGAG CTCT  CATGT
                               ||||||||| ||||  |||||
                               CAGGGACTC GAGG  GTGCG
                                   C   TG
GAM344  LIMD1   3'  GCTTCTGCAAGGCAAGTCTCAG 26462       C_  A  _
           G                   CCTGAGACT  TC TGT GAAGC
                               |||||||||  || ||| |||||
                               GGACTCTGA  GG ACG CTTCG
                                   AC  A   T
GAM344  MARS    3'  GCGGTGTGGGAGTGTTTGGGGA 94895     TG  _     TG GAAGC
           C                   GTCCC  AG ACTCTCA  T
                               |||||  || |||||||  |
                               CAGGG  TT TGAGGGT  G
                                 GT  G     GT GCG
GAM344  MCL1    3'  GTTTTATCCTGTCTTTGGGGGC 41719     TG _  TCTCAT
                               GTCCC  A GAC     GTGAAGC
                               |||||  | |||     |||||||
                               CGGGG  T CTG     TATTTTG
                                 GT T   TCC___
GAM344  MEF2D   3'  GCTTCTAGACGGAGTTTCA   96913       CATGT
                               TGAGACTCT    GAAGC
                               |||||||||    |||||
                               ACTTTGAGG    CTTCG
                                   CAGAT
GAM344  MLLT2   3'  GTTTCGCCATGGCTTCAGGGAT 19850       ACTC   _
                               GTCCCTGAG   TCATG TGAAGC
                               |||||||||   ||||| ||||||
                               TAGGGACTT   GGTAC GCTTTG
                                   C___    C
GAM344  MLLT4   3'  GCTTTGTGTGCATTTCAAGGG  72485    _  CTCT   TG
                               CCCT GAGA   CATG  AAGC
                               |||| ||||   ||||  ||||
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                                GGGA CTTT   GTGT  TTCG
                                  A   AC__   GT
GAM344  MTMR8   3'  GTTTCATGTGGCCTGTTAGGG  31297      GACTC
                                CCCTGA    TCATGTGAAGC
                                ||||||    ||||||||||
                                GGGATT    GGTGTACTTTG
                                   GTCC_
GAM344  MYBL2   3'  TTTACAGGGGTTGTGGGGGC  10156      A    CA
                                GTCCCTG GACTCT  TGTGAA
                                ||||||| ||||||  ||||||
                                CGGGGGT TTGGGG  ACATTT
                                    G    __
GAM344  PACE    3'  GCTTTCCCCTGTGGGGATCTCA 10392      CT    T___
          GGGGC                  CCTGAGA  CTCATG   GAAGC
                                |||||||  ||||||   |||||
                                GGACTCT  GGGTGT   TTTCG
                                    AG    CCCC
GAM344  PDGFB   5'  CTTTCCGATTTTGGGGGC   10501      TG   C  TCAT TG
                                GTCCC  AGA TC   G  AAG
                                |||||  ||| ||   |  |||
                                CGGGG  TTT AG   C  TTC
                                  GT  _  _____ CT
GAM344  POLS    3'  GCTTCGGTCAGTTTTAGTGAC  22792    C      CTCATG
                                GTC CTGAGACT     TGAAGC
                                ||| ||||||||     ||||||
                                CAG GATTTTGA     GCTTCG
                                  T       CTG___
GAM344  POU5F1  3'  GTTTGTGCCAGGGTTTTTGGGA 97769      T      CA  TG  GC
          T                     GTCCC GAGACTCT  TG  AA
                                |||||  ||||||||  ||  ||
                                TAGGG TTTTGGGA  GT  TT
                                  T       CC  GT  G
GAM344  PRDM1   5'  CACTGTGAGGTTTCAGGGAT   6825          T    _
                                GTCCCTGAGAC CTCAT GTG
                                |||||||||||  |||||  |||
                                TAGGGACTTTG GAGTG CAC
                                      _    T
GAM344  PRDM2   3'  TTTGTTGTAGGTTTCAGGGAT  31853          CT  T TG
                                GTCCCTGAGACT  CA G  AA
                                ||||||||||||  || |  ||
                                TAGGGACTTTGG  GT T  TT
                                     AT  _ GT
GAM344  PYCS    3'  GCTTTGTGTCACCTCAGTGAC  11167    C    ACTCTC   TG
                                GTC CTGAG     ATG  AAGC
                                ||| |||||     |||  ||||
                                CAG GACTC     TGT  TTCG
                                  T    CAC___   GT
GAM344  ROBO1   5'  CTTCATACATTTGGGGAC    56087      TG  ACTCTCA
                                GTCCC  AG      TGTGAAG
                                |||||  ||      |||||||
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                                CAGGG  TT      ATACTTC
                                  GT  AC_____
GAM344  RTN2     3'  GCTTTGCATGGGGCCCAGGGG  18834       AGAC      TG
                                TCCCTG   TCTCATG  AAGC
                                ||||||   |||||||  ||||
                                GGGGAC   GGGGTAC  TTCG
                                   CC__     GT
GAM344  SCN8A    3'  CTTCACGTGGTTTGGAGAT   26383     C TG  ACTC
                                GTC C  AG   TCATGTGAAG
                                ||| |  ||   ||||||||||
                                TAG G  TT   GGTGCACTTC
                                 A GT  ____
GAM344  SHC1     3'  GTTTTATATGCATATATTTTAG 11653   T       CTCT__
            GGC                   CCCTGAGA     CATGTGAAGC
                                 ||||||||     ||||||||||
                                 GGGATTTT     GTATATTTTG
                                _      ATATAC
GAM344  SNCA     3'  GCTTTATGTATTTTGGGGA   4431       TG   CTCTC
                                TCCC  AGA    ATGTGAAGC
                                ||||  |||    |||||||||
                                AGGG  TTT    TGTATTTCG
                                  GT   A____
GAM344  SULT2B1  5'  GCTTTATAAAGTTTATAGGGAC 16029        _    CTCA
                                GTCCCTG AGACT    TGTGAAGC
                                ||||||| |||||   ||||||||
                                CAGGGAT TTTGA    ATATTTCG
                                    A    A___
GAM344  TIA1     3'  TTTTATATGAGAAGGTGC    41853   TC   GAGAC
                                G  CCT    TCTCATGTGAAG
                                |  |||    ||||||||||||
                                C  GGA    AGAGTATATTTT
                                 GT  _____
GAM344  TIA1     3'  TTTTATATGAGAAGGTGC    42250   TC   GAGAC
                                G  CCT    TCTCATGTGAAG
                                |  |||    ||||||||||||
                                C  GGA    AGAGTATATTTT
                                 GT  _____
GAM344  TMEPAI   3'  GCTTTGCGTGAGAAAGGGGA  39448       GAGAC      TG
                                TCCCT    TCTCATG  AAGC
                                |||||    |||||||  ||||
                                AGGGG    AGAGTGC  TTCG
                                   AA___      GT
GAM344  VCL      3'  CTTCACATAAGCTCAG      25735       A  CTC
                                CTGAG CT   ATGTGAAG
                                ||||| ||   ||||||||
                                GACTC GA   TACACTTC
                                   _ A__
GAM344  VCL      3'  CTTCACATAAGCTCAG      12576       A  CTC
                                CTGAG CT   ATGTGAAG
                                ||||| ||   ||||||||
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                                GACTC GA   TACACTTC
                                  _ A__
GAM344  WHSC1    3'  TTTCCTGATTTTTAGGGAT   23674         C  TCATGT
                                GTCCCTGAGA TC     GAAG
                                |||||||||| ||     ||||
                                TAGGGATTTT AG     CTTT
                                     T  TC____
GAM344  XPR1     3'  TTTTAAAATTTTAGGGAT    16431         CTCTCATG
                                GTCCCTGAGA      TGAAG
                                ||||||||||      |||||
                                TAGGGATTTT      ATTTT
                                     AAA_____
GAM344  ZNF85    5'  GCTTTGTGTTTTCTGCTCGTGG 12819     C   ACTCTC   TG
           AC                     GTCC TGAG     ATG  AAGC
                                |||| ||||     |||  ||||
                                CAGG GCTC     TGT  TTCG
                                  T   GTCTTT   GT
GAM344  7h3      3'  GCCTGGGGATTTTAGGGAC   52274         CT   T
                                GTCCCTGAGA  CTCA GT
                                ||||||||||  |||| ||
                                CAGGGATTTT  GGGT CG
                                     AG   C
GAM344  AGTRL2   5'  GCTTTACAAATCATCAGGGG   17693       GACTCTCA
                                TCCCTGA       TGTGAAGC
                                |||||||       ||||||||
                                GGGGACT       ACATTTCG
                                    ACTAA___
GAM344  APOL3    5'  GTTTTGCATGTTTGATCAGGAG 26816   TC    GACTCT   TG
           C                     G  CCTGA     CATG  AAGC
                                |  |||||     ||||  ||||
                                C  GGACT     GTAC  TTTG
                                 GA    AGTTT_   GT
GAM344  ARFGAP3  3'  GCTTCATGTGGGGGAGGAGGA  27386     _  GAGA
                                TCC CT    CTCTCATGTGAAGC
                                ||| ||    ||||||||||||||
                                AGG GG    GGGGGTGTACTTCG
                                  A  A___
GAM344  ATF3     3'  GTTTCTAAGAGTTTTGGGGG   14435     TG      CATGT
                                TCCC  AGACTCT    GAAGC
                                ||||  |||||||    |||||
                                GGGG  TTTGAGA    CTTTG
                                  GT      AT___
GAM344  C11orf11 3'  CAGGACGAGCCATCAGGGAC   93250        GA_  _  A
                                GTCCCTGA   CTC TC TG
                                ||||||||   ||| || ||
                                CAGGGACT   GAG AG AC
                                     ACC   C  G
GAM344  C11orf24 5'  GCTGGCTGGGAGCCTCGGGGAC 42274         A     T  GA
                                GTCCCTGAG CTCTCA GT  AGC
                                ||||||||| |||||| ||  |||
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                                CAGGGGCTC GAGGGT CG  TCG
                                     C     _ G_
GAM344  C1orf35  3'  TTCGCATACCAGGGAT     44236        AGACTCTC
                                GTCCCTG       ATGTGAA
                                |||||||       |||||||
                                TAGGGAC       TACGCTT
                                   CA_______
GAM344  CAMKK1   3'  TCATTTGGGGTCTTGGGGGC   50177      TG     T  T
                                GTCCC  AGACTC CA GTGA
                                |||||  |||||| || ||||
                                CGGGG  TCTGGG GT TACT
                                   GT     _ T
GAM344  CDC14A   3'  TTTTGCATCCTGGGGGGC    13396       G  ACTCTC   TG
                                GTCCCT AG     ATG  AAG
                                |||||| ||     |||  |||
                                CGGGGG TC     TAC  TTT
                                   G  C_____   GT
GAM344  CGBP     5'  GCCTGAGGGGTCTTGGGGGC   27471      TG     _   T
                                GTCCC  AGACTC TCA GT
                                |||||  |||||| ||| ||
                                CGGGG  TCTGGG AGT CG
                                   GT     G   C
GAM344  DKFZP434B044 3'  CTTTGCATGAACAGGGGC    48924        AGACTC    TG
                                GTCCCTG     TCATG  AAG
                                |||||||     |||||  |||
                                CGGGGAC     AGTAC  TTC
                                   A_____     GT
GAM344  DKFZP586C1619 3'  GTTTTGCTGCTGGTTTTAGGGG 61936           CT  T TG
           C                     GTCCCTGAGACT  CA G  AAGC
                                ||||||||||||  || |  ||||
                                CGGGGATTTTGG  GT C  TTTG
                                      TC  _ GT
GAM344  DKFZP586M1120 3'  CGTCTGAGAGCATCAGGGAC   48455        GA     TG
                                GTCCCTGA  CTCTCA  TG
                                ||||||||  ||||||  ||
                                CAGGGACT  GAGAGT  GC
                                   AC     CT
GAM344  DKFZP586M1120 3'  GTTTTGTGTGCGTTCCCAGGGG 48469        A  CTCT    TG
           C                     GTCCCTG GA    CATG  AAGC
                                |||||||  ||    ||||  ||||
                                CGGGGAC CT    GTGT  TTTG
                                   C  TGC_    GT
GAM344  DKK2     5'  GCTTTGCGTCTTCCTGGGGAC  27017       GA  CTCTC   TG
                                GTCCCT  GA    ATG  AAGC
                                ||||||  ||    |||  ||||
                                CAGGGG  CT    TGC  TTCG
                                   TC  TC___   GT
GAM344  FLJ00024  5'  GCCTGGGAGTTTCAGG      63762            T
                                CCTGAGACTCTCA GT
                                |||||||||||| ||
```

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                                GGACTTTGAGGGT CG
                                       C
GAM344  FLJ10375  3'  CACCATGGCCCAGGGAC     36072        AGACTC    _
                                GTCCCTG     TCATG TG
                                |||||||     ||||| ||
                                CAGGGAC     GGTAC AC
                                    CC____     C
GAM344  FLJ10521  3'  GTTTTGGGGAGGAGTTTTAGGG 36220    T         _ ATG
          C                      G CCCTGAGACTC TC   TGAAGC
                                | ||||||||||| ||   ||||||
                                C GGGATTTTGAG AG   GTTTTG
                                 _         G  GG_
GAM344  FLJ10619  3'  CTTCTGAGTCTCAAGG      36351    C       TCATGT
                                CC TGAGACTC     GAAG
                                || ||||||||     ||||
                                GG ACTCTGAG     CTTC
                                 A       T_____
GAM344  FLJ10748  5'  CTCCTGGAACTCAGGGAC    36556         AC  T  TGT  A
                                GTCCCTGAG  TC CA   GA G
                                |||||||||  || ||   || |
                                CAGGGACTC  AG GT   CT C
                                      A_  _  C__  C
GAM344  FLJ11198  3'  GTGGGGGTCTGGGGGG      37159       G
                                TCCCT AGACTCTCAT
                                ||||| ||||||||||
                                GGGGG TCTGGGGGTG
                                   G
GAM344  FLJ11526  5'  CTGCGGGGGTCTCAGCGAC    44911     C         ATGTGA
                                GTC CTGAGACTCTC     AG
                                ||| ||||||||||     ||
                                CAG GACTCTGGGGG     TC
                                  C         CG____
GAM344  FLJ11850  3'  GCTGTGAGTTTCGGGGG     42723           T  T
                                TCCCTGAGACTC CA GT
                                |||||||||||| || ||
                                GGGGGCTTTGAG GT CG
                                       T  _
GAM344  FLJ13052  3'  ATGAGGGTTTCCGGGGC     43471       T
                                GTCCC GAGACTCTCAT
                                ||||| ||||||||||
                                CGGGG CTTTGGGAGTA
                                   C
GAM344  FLJ13241  3'  GCTTTGTAAGATGGTCTTGGGA 46967    TC  TG    C  A  TG
          GC                     G  CC  AGACT TC TG  AAGC
                                |  ||  ||||| || ||  ||||
                                C  GG  TCTGG AG AT  TTCG
                                 GA  GT    T  A  GT
GAM344  FLJ14356  5'  GCCTCCATGAGAGGTTTGGGGA 48032       TG  A       T  A
          T                      GTCCC  AG CTCTCATG GA GC
                                |||||  || |||||||| || ||
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                                TAGGG  TT GAGAGTAC CT CG
                                  GT  G       _  C
GAM344  FLJ14356  5'  TTTGGGGATGGGGGGTGTTTAGG 48035         _       GTGAAGC
            GG                    TCCCTGAG ACTCTCAT
                                  |||||||| ||||||||
                                  GGGGATTT TGGGGGTA
                                     G       GGGGTTTG
GAM344  FLJ14547  3'  GTTTCATATTCTCTCAGG    51439        CTCTC
                                  CCTGAGA    ATGTGAAGC
                                  |||||||    |||||||||
                                  GGACTCT    TATACTTTG
                                     CT___
GAM344  FLJ20013  3'  TCACAGTCTTGGGGAC      34337       TG    CTCAT
                                  GTCCC  AGACT    GTGA
                                  |||||  |||||    ||||
                                  CAGGG  TCTGA    CACT
                                    GT    _____
GAM344  FLJ20275  3'  GTTTTATGAGAAGTTTTATGGG 34824      C      _     TGAAGC
            C                      GTCC TGAGACT CTCATG
                                  |||| ||||||| ||||||
                                  CGGG ATTTTGA GAGTAT
                                    T      A      TTTG
GAM344  FLJ20297  3'  GTTTTCGGTGTGGGGTTTTGGG 34898      TG      _  GT
            GG                    TCCC  AGACTCT CAT  GAAGC
                                  ||||  ||||||| |||  |||||
                                  GGGG  TTTGGGG GTG  TTTTG
                                    GT      T   GC
GAM344  FLJ20297  3'  GTTTTCGGTGTGGGGTTTTGGG 35638      TG      _  GT
            GG                    TCCC  AGACTCT CAT  GAAGC
                                  ||||  ||||||| |||  |||||
                                  GGGG  TTTGGGG GTG  TTTTG
                                    GT      T   GC
GAM344  FLJ20330  3'  CAGATTGAGAACCTCGGGGAC  38618          AC    _ G
                                  GTCCCTGAG  TCTCA T TG
                                  |||||||||  ||||| | ||
                                  CAGGGGCTC  AGAGT A AC
                                       CA     T G
GAM344  FLJ20436  5'  TCCAGTGCCCAGGTCTCAGG   35172         CT__  GT
                                  CCTGAGACT    CAT  GA
                                  |||||||||    |||  ||
                                  GGACTCTGG    GTG  CT
                                       ACCC   AC
GAM344  FLJ20450  3'  CTTTACGGTTCTAGGGAC    35193        AG   CTCAT
                                  GTCCCTG  ACT    GTGAAG
                                  |||||||  |||    ||||||
                                  CAGGGAT  TGG    CATTTC
                                     CT  _____
GAM344  FLJ20643  5'  TTTCCCACGTTGAGGGTCTCGA 35491     C         _    AAGC
            GGAC                     TCC TGAGACTCTCA TGTG
                                  ||| ||||||||||| ||||
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                                AGG GCTCTGGGAGT GCAC
                                  A         T    CCTTTG
GAM344  FLJ22692  3'  GCATAAAGAGGGAGTTTTGGGG 46803      TG       A___    AAGC
              GC                  TCCC  AGACTCTC    TGTG
                                  ||||  ||||||||    ||||
                                  GGGG  TTTGAGGG    ATAC
                                    GT       AGAA    G
GAM344  FLJ22969  3'  CTTCACATTGCTCAGTGGAC   68651      _    ACTCTC
                                  GTCC CTGAG     ATGTGAAG
                                  |||| |||||     ||||||||
                                  CAGG GACTC     TACACTTC
                                    T    GT____
GAM344  FLJ23056  3'  GTTTTACATGACAGTGGGTAC  44724    _  TGAG   C
                                  GT CCC    ACT TCATGTGAAGC
                                  || |||    ||| ||||||||||
                                  CA GGG    TGA AGTACATTTTG
                                   T  _____  C
GAM344  FLJ23251  5'  TGTGGGAGTCTCGGAGAC    45688     C
                                  GTC CTGAGACTCTCATG
                                  ||| ||||||||||||||
                                  CAG GGCTCTGAGGGTGT
                                    A
GAM344  FLJ23590  5'  CTTTGTGGAGAGTCTCAGTAAC 45019    CC         A  TG
                                  GT  CTGAGACTCTC TG  AAG
                                  ||  ||||||||||| ||  |||
                                  CA  GACTCTGAGAG GT  TTC
                                   AT          _  GT
GAM344  FLJ31455  3'  GCTTCACAATAATGTCAGGGAC 58627        GACTCTCA
                                  GTCCCTGA       TGTGAAGC
                                  ||||||||       ||||||||
                                  CAGGGACT       ACACTTCG
                                       GTAATA__
GAM344  FLJ31455  3'  GCTTCACAATAATGTCAGGGAC 58627        GACTCTCA
                                  GTCCCTGA       TGTGAAGC
                                  ||||||||       ||||||||
                                  CAGGGACT       ACACTTCG
                                       GTAATA__
GAM344  FLJ31709  5'  GCTTCTGCAAGGTCTCAGGGAC 58272          T  CA  _
                                  GTCCCTGAGAC CT  TGT GAAGC
                                  |||||||||| ||  ||| |||||
                                  CAGGGACTCTG GA  ACG CTTCG
                                         _  __   T
GAM344  FLJ31709  5'  GCTTCTGCAAGGTCTCAGGGAC 58272          T  CA  _
                                  GTCCCTGAGAC CT  TGT GAAGC
                                  |||||||||| ||  ||| |||||
                                  CAGGGACTCTG GA  ACG CTTCG
                                         _  __   T
GAM344  FLJ32818  5'  GCCTGGGGGTTTGGGGG     58408      G        T
                                  CCCT AGACTCTCA GT
                                  |||| ||||||||| ||
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                                GGGG TTTGGGGGT CG
                                  G       C
GAM344  GL009    5'  GTCCGCGTGAGGGGTTCGGGGG 72636        A        AAGC
                                TCCCTGAG CTCTCATGTG
                                |||||||| ||||||||||
                                GGGGGCTT GGGAGTGCGC
                                    G        CTG
GAM344  HMT-1    3'  GCTTCTTCTTGGAGTCTCAGGG 38900          CATGT
                                CCCTGAGACTCT    GAAGC
                                ||||||||||||    |||||
                                GGGACTCTGAGG    CTTCG
                                       TTCTT
GAM344  HSPC054  3'  GCTTCATGCTATTTTTAGG   26262       CTCTCAT
                                CCTGAGA     GTGAAGC
                                |||||||     |||||||
                                GGATTTT     TACTTCG
                                    TATCG__
GAM344  HSPC065  3'  GCTTTTGTTGGGTTTCAGGGA  26316          TCATGT
                                TCCCTGAGACTC    GAAGC
                                ||||||||||||    |||||
                                AGGGACTTTGGG    TTTCG
                                       TTGT__
GAM344  IRF5     3'  CTTCTTGAGAGTCCAAG    50973    GA      TGT
                                CT  GACTCTCA   GAAG
                                ||  ||||||||   ||||
                                GA  CTGAGAGT   CTTC
                                  AC       T__
GAM344  IRF5     5'  CTTCTTGAGAGTCCAAG    97251    GA      TGT
                                CT  GACTCTCA   GAAG
                                ||  ||||||||   ||||
                                GA  CTGAGAGT   CTTC
                                  AC       T__
GAM344  KIAA0247 3'  GCTTCACAGCTTAATGCCAAGG 28404     C  AGACTCTCA
                AC                GTCC TG       TGTGAAGC
                                |||| ||       ||||||||
                                CAGG AC       ACACTTCG
                                  A  CGTAATTCG
GAM344  KIAA0376 3'  TTTTCCCTCTGGGAGTCTCATG 65605    _        TGT_   C
                GG                CCC TGAGACTCTCA   GAAG
                                ||| ||||||||||   ||||
                                GGG ACTCTGAGGGT   CTTT
                                  T        CTCC   TG
GAM344  KIAA0420 3'  CATGTGGAGGTCTCGGGGAC  63354          CT
                                GTCCCTGAGACT  CATGTG
                                ||||||||||||  ||||||
                                CAGGGGCTCTGG  GTGTAC
                                       AG
GAM344  KIAA0543 3'  GTTTCAGCCCCTGAGTTTTGGT 68940    C TG     TCATG_
                GGC                GTC C  AGACTC     TGAAGC
                                ||| |  ||||||     ||||||
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                                CGG G  TTTGAG     ACTTTG
                                  T GT     TCCCCG
GAM344  KIAA0546 5' TTTTGCATGGTCAGGAGAT   71315    _    GACTC    TG
                                GTC CCTGA    TCATG  AAG
                                ||| |||||    |||||  |||
                                TAG GGACT    GGTAC  TTT
                                  A    _____    GT
GAM344  KIAA0555 3' ATATGAGAATCCAGG      60113     A  C
                                CCTG GA TCTCATGT
                                |||| || ||||||||
                                GGAC CT AGAGTATA
                                  _ A
GAM344  KIAA0565 3' GTTTTATACATTTTAGGGG   66895         CTCTCA
                                TCCCTGAGA     TGTGAAGC
                                |||||||||     ||||||||
                                GGGGATTTT     ATATTTTG
                                     AC____
GAM344  KIAA0630 3' GTTTTATGTGATTTGTTTGGGG 89396     TG  ACTC
            A                    TCCC  AG   TCATGTGAAGC
                                ||||  ||   ||||||||||
                                AGGG  TT   AGTGTATTTTG
                                  GT  GTTT
GAM344  KIAA0711 3' CTTCGAAGGAGCCCCGAGGAC  29518     C  AGA   CATG
                                GTCC TG   CTCT    TGAAG
                                |||| ||   ||||   |||||
                                CAGG GC   GAGG    GCTTC
                                  A  CCC    AA__
GAM344  KIAA1024 3' GCTTGGGGTCTTGGGAT     69061      T      T  T
                                GTCCC GAGACTC CA GT
                                ||||| ||||||| || ||
                                TAGGG TTCTGGG GT CG
                                  _      _  T
GAM344  KIAA1223 3' GCATGAAAATTCTCAGGGAC   71147          CTC_
                                GTCCCTGAGA    TCATGT
                                ||||||||||    ||||||
                                CAGGGACTCT    AGTACG
                                     TAAA
GAM344  KIAA1443 3' CTTTGTGTTCTTCAGGG     63829       _ CTCTC   TG
                                CCCTGA GA     ATG  AAG
                                ||||||  ||     |||  |||
                                GGGACT CT     TGT  TTC
                                   T  _____   GT
GAM344  KIAA1543 3' GCTGAGCTGGGAGGTTCAGGGA 70986          A     T  GA
            C                    GTCCCTGAG CTCTCA GT  AGC
                                |||||||||  ||||||  ||  |||
                                CAGGGACTT GAGGGT CG  TCG
                                     G     _  AG
GAM344  KIAA1577 3' GTTTTGTATGAGAGAGAGG   64480     GAGA       TG
                                CCT    CTCTCATG  AAGC
                                |||    ||||||||  ||||
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                                GGA   GAGAGTAT  TTTG
                                  GA__      GT
GAM344  KIAA1674  3'  GCTTCCTGGTGAGCCTCAGGGA 68784       A  _  TGT
                                TCCCTGAG CTC TCA  GAAGC
                                |||||||| ||| |||  |||||
                                AGGGACTC GAG GGT  CTTCG
                                    C  T  C__
GAM344  KIAA1674  3'  GTTTTGTGTGTGTCAGGTGAC  68793    _   G  TCTC  TG
                                GTC CCTGA AC   ATG  AAGC
                                ||| ||||| ||   |||  ||||
                                CAG GGACT TG   TGT  TTTG
                                  T   G ____  GT
GAM344  KIAA1677  3'  GCTTTATGTGGGGAGAAGTGG  67069   _ GAGAC
                                CC CT    TCTCATGTGAAGC
                                || ||    ||||||||||||
                                GG GA    GGGGTGTATTTCG
                                 T  AGA__
GAM344  KIAA1877  3'  GTTTCAATGACAGGTTTTGGTG 66176    C TG   C_   G
            AT                   GTC C  AGACT  TCAT TGAAGC
                                ||| |  |||||  |||| ||||||
                                TAG G  TTTGG  AGTA ACTTTG
                                  T GT    AC   _
GAM344  KIAA1979  3'  GCTTTATAAAAAGGTTATGGGG 88284       A   CTCA
            AC                   GTCCCTG GACT   TGTGAAGC
                                ||||||| ||||   ||||||||
                                CAGGGGT TTGG   ATATTTCG
                                    A   AAAA
GAM344  KREMEN   3'  GCTTTGTGTGACTTGCTCAGG  49407      ACTC   TG
                                CCTGAG   TCATG  AAGC
                                ||||||   |||||  ||||
                                GGACTC   AGTGT  TTCG
                                   GTTC    GT
GAM344  LIN-28   3'  CAAGTGAGGGTTCTGGGGGC  45146      GA      G
                                GTCCCT  GACTCTCAT TG
                                ||||||  ||||||||| ||
                                CGGGGG  TTGGGAGTG AC
                                    TC       A
GAM344  MCLC     3'  GCTTTATATCCATTTGGGGAT  30690      TG  ACTCTC
                                GTCCC  AG    ATGTGAAGC
                                |||||  ||    |||||||||
                                TAGGG  TT    TATATTTCG
                                  GT  ACC___
GAM344  MGC10715  3'  GCTTTACATGGGTGGGGAGGGA 44249      GAGA  _
                                TCCCT   CT CTCATGTGAAGC
                                |||||   || ||||||||||||
                                AGGGA   GG GGGTACATTTCG
                                  GG__  T
GAM344  MGC13040  5'  TACTGGGGAGCTCGGGGAC   51940        A    AT
                                GTCCCTGAG CTCTC  GTG
                                ||||||||| |||||  |||
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                                CAGGGGCTC GAGGG  CAT
                                      _    GT
GAM344  MGC25056 3'  GCTTCATGTGACACAGGGG   79116      AGACTC
                                TCCCTG     TCATGTGAAGC
                                ||||||     ||||||||||
                                GGGGAC     AGTGTACTTCG
                                   AC____
GAM344  MGC2721  3'  GCTAGCGAGGGTTCTGGGGG  51220      GA     AT  GA
                                TCCCT  GACTCTC  GT  AGC
                                |||||  |||||||  ||  |||
                                GGGGG  TTGGGAG  CG  TCG
                                   TC      __  A_
GAM344  MGC5508  3'  TGTGGGGGTTTCAGAGAC    44041     C
                                GTC CTGAGACTCTCATG
                                ||| ||||||||||||||
                                CAG GACTTTGGGGGTGT
                                  A
GAM344  MIL1     3'  GCTAAATTGAGAATCTTAGGGG 31092         C    T  GA
                                TCCCTGAGA TCTCA GT  AGC
                                |||||||||  |||||  ||  |||
                                GGGGATTCT AGAGT TA  TCG
                                      A    _  AA
GAM344  MTHFS    3'  TTTTATATGAGAGTAAAG    21238    GAG
                                CT   ACTCTCATGTGAAG
                                ||   ||||||||||||||
                                GA   TGAGAGTATATTTT
                                  AA_
GAM344  NYD-SP29  3'  GCTTCCTGAAGGGGTGTTTTGG 74571     TG   T   ATGT__
           GGAC                    TCCC  AGAC CTC     GAAGC
                                ||||  |||| |||     |||||
                                AGGG  TTTG GGG     CTTCG
                                  GT    T   GAAGTC
GAM344  P24B     3'  GCTGAAGGTCTCAGAGAC    23751     C      TC   T
                                GTC CTGAGAC  TCA GT
                                ||| |||||||  ||| ||
                                CAG GACTCTG  AGT CG
                                  A      GA   _
GAM344  P450RAI-2 3'  GCTGGGAGGTCTCAGGGGC    39104          _    T
                                GTCCCTGAGAC TCTCA GT
                                ||||||||||| ||||| ||
                                CGGGGACTCTG AGGGT CG
                                      G    _
GAM344  PPP1R12C  3'  GCTCCGGGGGGAAGTCTCAGAGA 34280    C      _  A  T  A
                                TC CTGAGACT CTC TG GA GC
                                || |||||||| ||| || || ||
                                AG GACTCTGA GGG GC CT CG
                                 A       A   G  _  _
GAM344  PRDM7    3'  GTGAGTGTGGGGGGTTTCAAGGG 53791      _        TG GAA
                                CCCT GAGACTCTCA  T   GC
                                |||| ||||||||||  |   ||
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                                GGGA CTTTGGGGGT  G   TG
                                  A        GT AG_
GAM344  PRO0800   3'  CTTCACATGAGGTCAGGGAC  37739        GAC
                                GTCCCTGA   TCTCATGTGAAG
                                ||||||||   ||||||||||||
                                CAGGGACT   GGAGTACACTTC
                                          ___
GAM344  PXR2b     3'  GTTTTGTATGTGTTTGGGGC  33340      TG   TCT   TG
                                GTCCC  AGAC   CATG  AAGC
                                |||||  ||||   ||||  ||||
                                CGGGG  TTTG   GTAT  TTTG
                                   __   T__   GT
GAM344  R32184_3  3'  GCTTTCAGGGTTTCGTGGGG  53067     _       CATGT
                                TCCC TGAGACTCT    GAAGC
                                |||| |||||||||    |||||
                                GGGG GCTTTGGGA    TTTCG
                                  T       C____
GAM344  RPL39L    5'  GCGTCTCGGAGTCTCAGAGAC  53733    C        C__
                                GTC CTGAGACTCT   ATGT
                                ||| ||||||||||   ||||
                                CAG GACTCTGAGG   TGCG
                                  A        CTC
GAM344  SKD3      3'  TTTCGTCAGCCTTGGGGAC   47996      TG  ACTCTCA  _
                                GTCCC  AG      TG TGAAG
                                |||||  ||      || |||||
                                CAGGG  TC      AC GCTTT
                                   GT  CG_____  T
GAM344  SLC11A1   3'  GCCAACCTGGGGGCTTTAGGGA 59457        GA     T  GAA
          C                      GTCCCTGA  CTCTCA GT   GC
                                ||||||||  |||||| ||   ||
                                CAGGGATT  GGGGGT CA   CG
                                     TC     C  AC_
GAM344  SNRPD1    3'  GTTTTACTCCACGGAGTCTTAG 22678    C        CAT__
          GTAC                    T CCTGAGACTCT    GTGAAGC
                                | ||||||||||    |||||||
                                A GGATTCTGAGG    CATTTTG
                                 T         CACCT
GAM344  Spir-1    3'  TTGTGTGGGAGTTTCAGG    64704            TG
                                CCTGAGACTCTCATG  A
                                ||||||||||||||  |
                                GGACTTTGAGGGTGT  T
                                          GT
GAM344  STC2      3'  CGTGGGGTCTCAGGGG      13549           T
                                TCCCTGAGACTC CATG
                                |||||||||||| ||||
                                GGGGACTCTGGG GTGC
                                          _
GAM344  STOML2    3'  GCTTGGCCAGGGAGTCTGGGGA 25557       G       AT  G
          C                      GTCCCT AGACTCTC  GT AAGC
                                ||||||  ||||||||  || ||||
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                                CAGGGG TCTGAGGG  CG TTCG
                                   _       AC  G
GAM344  TIMM13   3'  GCTTGGATCTCGGGGG      24941          C  T  T
                                TCCCTGAGA TC CA GT
                                ||||||||| || || ||
                                GGGGGCTCT AG GT CG
                                   _ _ T
GAM344  TMLHE    3'  CACGAAAAGGGTCTCAGGGAC  36514             CA_
                                GTCCCTGAGACTCT   TGTG
                                ||||||||||||||   ||||
                                CAGGGACTCTGGGA   GCAC
                                      AAA
GAM344  UHRF2    3'  GTTTTACATCTGCAGAGTTTTG 73451    CT       _ __
           AGGGC                    C  GAGACTCT CA  TGTGAAGC
                                |  |||||||| ||  ||||||||
                                G  TTTTGAGA GT  ACATTTTG
                                 AG       C  CT
GAM344  ZNF11B   5'  GTTTTGCGTGGGAGGCGGTCCC 73987    T_ GA__      TG
           GGGAT                    CC  GA   CTCTCATG  AAGC
                                ||  ||   ||||||||  ||||
                                GG  CT   GAGGGTGC  TTTG
                                 CC  GGCG       GT
GAM344  ZNF238   5'  GCCTGATTAAAATTCAGGGAC  20963          ACTC__   T
                                GTCCCTGAG     TCA GT
                                |||||||||     ||| ||
                                CAGGGACTT     AGT CG
                                      AAAATT   C
GAM344  LOC112473 5'  GCTTCGGAACAAGCTCTCGGGG 73202          _  CTCATG
           AC                     GTCCCTGAGA CT     TGAAGC
                                ||||||||||  ||      ||||||
                                CAGGGGCTCT GA     GCTTCG
                                      C  ACAAG_
GAM344  LOC116238 3'  GCTTCATATGGACACTGGGAC  56644       TGAGAC  T
                                GTCCC     TC CATGTGAAGC
                                |||||     || ||||||||||
                                CAGGG     AG GTATACTTCG
                                   TCAC__  _
GAM344  LOC124599 3'  GCTTCACCAGCTGGACTCAGGG 75654          A  CTCAT
           GC                     GTCCCTGAG CT     GTGAAGC
                                |||||||||  ||    |||||||
                                CGGGGACTC GG     CACTTCG
                                      A  TCGAC
GAM344  LOC126917 3'  GTATGGGAGTTTCGTGGGC    74593      C
                                GTCC TGAGACTCTCATGT
                                ||||  ||||||||||||||
                                CGGG GCTTTGAGGGTATG
                                   T
GAM344  LOC129868 5'  GCTTTGCAACTGGCTTTGGGGA 57129       TG GA  CTCA  TG
           C                      GTCCC  A  CT    TG  AAGC
                                |||||  |  ||    ||  ||||
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                                CAGGG  T  GG    AC  TTCG
                                   GT TC  TCA_  GT
GAM344   LOC130633 5'  GCTTTGCAACTGGCTTTGGGGA 74965       TG GA  CTCA  TG
            C                    GTCCC  A  CT    TG  AAGC
                                |||||  |  ||    ||  ||||
                                CAGGG  T  GG    AC  TTCG
                                   GT TC  TCA_  GT
GAM344   LOC132422 5'  TGGGGGTCTGGGGGGC      75888       G
                                GTCCCT AGACTCTCA
                                |||||| |||||||||
                                CGGGGG TCTGGGGGT
                                   G
GAM344   LOC143425 3'  GTTTCATATGAAGCCCTTGGTG 87640     C TG  A_  C
            AT                    GTC C  AG  CT TCATGTGAAGC
                                ||| |  ||  || ||||||||||
                                TAG G  TC  GA AGTATACTTTG
                                  T GT  CC  _
GAM344   LOC145098 5'  GTTTCATATACAAGTTTGGGA  76995      TG    CTC
                                TCCC  AGACT   ATGTGAAGC
                                ||||  |||||   |||||||||
                                AGGG  TTTGA   TATACTTTG
                                  __    ACA
GAM344   LOC145197 3'  ACTGTGGGAGTTTTGGCGGC   83276     C TG        _
                                GTC C  AGACTCTCAT GT
                                ||| |  |||||||||| ||
                                CGG G  TTTGAGGGTG CA
                                  C GT         T
GAM344   LOC145757 3'  GTGAGAAGTGGGGATCTTGGGG 77472      TG   CT    GTGAA
            G                     TCCC  AGA  CTCAT    GC
                                ||||  |||  |||||    ||
                                GGGG  TCT  GGGTG    TG
                                  GT   AG    AAGAG
GAM344   LOC147396 5'  TGAGGGTTCAGGGAT       78353          A
                                GTCCCTGAG CTCTCA
                                ||||||||| ||||||
                                TAGGGACTT GGGAGT
                                      _
GAM344   LOC148183 3'  GCAGTGAGAGTTTCAGG     84120           _
                                CCTGAGACTCTCA TGT
                                |||||||||||| |||
                                GGACTTTGAGAGT ACG
                                      G
GAM344   LOC150372 3'  CTCTGGGATTTCAGGGAT    79798          C    TGT  A
                                GTCCCTGAGA TCTCA   GA G
                                |||||||||| |||||   || |
                                TAGGGACTTT AGGGT   CT C
                                      _    ___  C
GAM344   LOC150776 3'  GTTTTCGGTGTGGGGTTTTGGG 63226      TG      _  GT
            GG                    TCCC  AGACTCT CAT  GAAGC
                                ||||  ||||||| |||  |||||
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                                GGGG  TTTGGGG GTG  TTTTG
                                  GT      T  GC
GAM344  LOC151009 5'  GCTTTGGCAGGTGTCGGGGGC  85197       G  CTCA  _
                                GTCCCTGA ACT    TGT GAAGC
                                ||||||| |||    ||| |||||
                                CGGGGGCT TGG    ACG TTTCG
                                   G  _____  G
GAM344  LOC152765 3'  TTTTATACATTTTAGGGA    80664        CTCTCA
                                TCCCTGAGA     TGTGAAG
                                |||||||||     |||||||
                                AGGGATTTT     ATATTTT
                                     AC____
GAM344  LOC153027 3'  CAAGTGAGGCTCTTGGGGG   67431     TG  CT    G
                                TCCC  AGA  CTCAT TG
                                ||||  |||  ||||| ||
                                GGGG  TCT  GAGTG AC
                                  GT  CG    A
GAM344  LOC157589 3'  TCAGATGAGAATTTTAGGGGC  59561         C     G
                                GTCCCTGAGA TCTCAT TGA
                                |||||||||| |||||| |||
                                CGGGGATTTT AGAGTA ACT
                                     A     G
GAM344  LOC158427 3'  GCTTCATATAAGCTCGGTGAC  57679    C    A  CTC
                                GTC CTGAG CT   ATGTGAAGC
                                ||| ||||| ||   |||||||||
                                CAG GGCTC GA   TATACTTCG
                                  T    _  A__
GAM344  LOC159090 5'  GCAGTGAGAGTCTTGGGA    82089     T       _
                                TCCC GAGACTCTCA TGT
                                |||| |||||||||| |||
                                AGGG TTCTGAGAGT ACG
                                  _        G
GAM344  LOC159121 3'  GCTTCTCCGGGGGTTTTAAGGG 86996     _       ATGT
                                CCCT GAGACTCTC    GAAGC
                                |||| |||||||||    |||||
                                GGGA TTTTGGGGG    CTTCG
                                  A        CCT_
GAM344  LOC162617 5'  GCTTGGACAGAGCTCAGGGGC  82373        A   CATGTG
                                GTCCCTGAG CTCT     AAGC
                                ||||||||| ||||     ||||
                                CGGGGACTC GAGA     TTCG
                                     _   CAGG__
GAM344  LOC164397 5'  CAAGTGGGAGTCCAGGGAC    82519       A       G
                                GTCCCTG GACTCTCAT TG
                                ||||||| ||||||||| ||
                                CAGGGAC CTGAGGGTG AC
                                     _       A
GAM344  LOC197202 5'  GCTTCGGAACAAGCTCTCGGGG 87960         _ CTCATG
           AC                     GTCCCTGAGA CT     TGAAGC
                                ||||||||| ||     ||||||
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                                CAGGGGCTCT GA     GCTTCG
                                      C  ACAAG_
GAM344   LOC200014 3'  GCTTTGTATGTGTCCTTTTGGG 88537     TG   CTCT_   TG
            GG                    TCCC  AGA    CATG  AAGC
                                  ||||  |||    ||||  ||||
                                  GGGG  TTT    GTAT  TTCG
                                    GT   CCTGT    GT
GAM344   LOC200125 5'  GTTTTGTGGGCTGTCTCAAGGA 89930     C     T_    GT
            T                     GTCC TGAGAC  CTCAT  GAAGC
                                  |||| ||||||  |||||  |||||
                                  TAGG ACTCTG  GGGTG  TTTTG
                                    A     TC    __
GAM344   LOC200609 5'  CTTCATATGCTTTAGTGG    90097    _    ACTCT
                                  CC CTGAG    CATGTGAAG
                                  || |||||    |||||||||
                                  GG GATTT    GTATACTTC
                                   T    C_____
GAM344   LOC200609 5'  GCTTGGTATGAGAGTCTTAGGG 90102             TG
            A                     TCCCTGAGACTCTCATG  AAGC
                                  ||||||||||||||||  ||||
                                  AGGGATTCTGAGAGTAT  TTCG
                                            GG
GAM344   LOC201229 5'  GCTGGACAGAGGGTCTCACGGA 88145     C        A   GA
            T                     GTCC TGAGACTCTC TGT  AGC
                                  |||| ||||||||| |||  |||
                                  TAGG ACTCTGGGAG ACA  TCG
                                    C         _   GG
GAM344   LOC201895 3'  GTTTTCTGTAGTTTTGGGGAC  89092      TG    CT  TGT
                                  GTCCC  AGACT  CA   GAAGC
                                  |||||  |||||  ||   |||||
                                  CAGGG  TTTGA  GT   TTTTG
                                     GT    T_  C__
GAM344   LOC202754 3'  GCTGTGGGTTTTGGGGGC    82707      TG     T  T
                                  GTCCC  AGACTC CA GT
                                  |||||  |||||| || ||
                                  CGGGG  TTTGGG GT CG
                                     GT     T  _
GAM344   LOC219540 5'  GCTTCATATGAGGGTCCAGG   93600     A
                                  CCTG GACTCTCATGTGAAGC
                                  |||| ||||||||||||||||
                                  GGAC CTGGGAGTATACTTCG
                                    _
GAM344   LOC219908 5'  GCTTCACACAGTTCCCCAGGG  94317      A__    CTCA
                                  CCCTG   GACT    TGTGAAGC
                                  |||||   ||||    ||||||||
                                  GGGAC   TTGA    ACACTTCG
                                     CCC    C___
GAM344   LOC220758 3'  GTTTTGCATAGAAAGTTTTAGG 90786         C  _   TG
                                  CCTGAGACT TC ATG  AAGC
                                  ||||||||| || |||  ||||
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                                GGATTTTGA AG TAC  TTTG
                                     A  A   GT
GAM344   LOC220766 5'  TTCAGGGAGTCTTGGGCAC   90801    C  TG       ATG
                                GT CC  AGACTCTC   TGAA
                                || ||  ||||||||   ||||
                                CA GG  TCTGAGGG   ACTT
                                 C  GT       ___
GAM344   LOC221683 5'  GCCTGAAAGTTTTAGGGAT   93714           C   T
                                GTCCCTGAGACT TCA GT
                                |||||||||||| ||| ||
                                TAGGGATTTTGA AGT CG
                                       A   C
GAM344   LOC221683 5'  GCTTCGCCCAAGTTTGGGGAC  93715       G    CTCAT
                                GTCCCT AGACT    GTGAAGC
                                |||||| |||||    |||||||
                                CAGGGG TTTGA    CGCTTCG
                                   _    ACC__
GAM344   LOC221692 3'  GCTTCATGTCTGTCTCTCAGG  92242       CTCTC
                                CCTGAGA    ATGTGAAGC
                                |||||||    |||||||||
                                GGACTCT    TGTACTTCG
                                     CTGTC
GAM344   LOC253955 3'  TATGAAGTCCCAGGGAC     94431        A   C
                                GTCCCTG GACT TCATG
                                ||||||| |||| |||||
                                CAGGGAC CTGA AGTAT
                                     C   _
GAM344   LOC254186 5'  GCTTGGACAGAGCTCAGGGGC  96262         A   CATGTG
                                GTCCCTGAG CTCT     AAGC
                                ||||||||| ||||     ||||
                                CGGGGACTC GAGA     TTCG
                                      _   CAGG__
GAM344   LOC254387 3'  CCCACATGGGCCAGGGGC    94908       AGACT      AA
                                GTCCCTG    CTCATGTG  G
                                |||||||    |||||||| |
                                CGGGGAC    GGGTACAC  C
                                     C____       CC
GAM344   LOC256207 3'  TTTTATACATTTTAGGGA    95180         CTCTCA
                                TCCCTGAGA     TGTGAAG
                                |||||||||     |||||||
                                AGGGATTTT     ATATTTT
                                      AC____
GAM344   LOC256849 5'  TGGGAGTTTCGAGGAC      96952      C
                                GTCC TGAGACTCTCA
                                |||| ||||||||||
                                CAGG GCTTTGAGGGT
                                  A
GAM344   LOC257354 3'  CATGTGGAGGTCTCGGGGAC   95087           CT
                                GTCCCTGAGACT  CATGTG
                                ||||||||||  ||||||
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                                CAGGGGCTCTGG  GTGTAC
                                      AG
GAM344  LOC89919  3' GCTATAGAGTTTCAGGGAT   60725          CAT
                                GTCCCTGAGACTCT   GT
                                ||||||||||||||   ||
                                TAGGGACTTTGAGA   CG
                                      TAT
GAM344  LOC90829  5' GTTTTGTTCTTTTGGCTTAGGG 64099        ACTCTCAT TG
          AT                    GTCCCTGAG       G  AAGC
                                |||||||||       |  ||||
                                TAGGGATTC       T  TTTG
                                   GGTTTTCT GT
GAM344  LOC90982  5' CTGGCAGGGTCTCGGGGGC   64538          CAT  GA
                                GTCCCTGAGACTCT   GT  AG
                                ||||||||||||||   ||  ||
                                CGGGGGCTCTGGGA   CG  TC
                                      ___  G_
GAM344  LOC92305  3' GCTTTGAACTGAGTTTCAAGGG 56417     C       TCATG
          C                     GTCC TGAGACTC     TGAAGC
                                |||| ||||||||     ||||||
                                CGGG ACTTTGAG     GTTTCG
                                  A       TCAA_
GAM344  LOC92568  3' GTTTTAAGCCCAGTTTTAGG   69776        CTCATG
                                CCTGAGACT     TGAAGC
                                |||||||||     ||||||
                                GGATTTTGA     ATTTTG
                                   CCCGA_
GAM344  LOC93259  3' CTTCATGTGCTAGGGGGC    71818       G  ACTCT
                                GTCCCT AG     CATGTGAAG
                                |||||| ||     |||||||||
                                CGGGGG TC     GTGTACTTC
                                  A  _____
GAM344  LOC93268  5' GCTTCCTATGAGGAGTTCAGGG 71883        AC      T
          G                     TCCCTGAG  TCTCATG GAAGC
                                ||||||||  ||||||| |||||
                                GGGGACTT  GGAGTAT CTTCG
                                     GA      C
GAM345  ABR     3'  CGGCAGGAGTCAGGAGCCAGGG 6571       A       TA___
          A                     TCCC GGCTCCTG     TGCCG
                                |||| ||||||||     |||||
                                AGGG CCGAGGAC     ACGGC
                                  A       TGAGG
GAM345  ABR     3'  CGGCAGGAGTCAGGAGCCAGGG 41723      A       TA___
          A                     TCCC GGCTCCTG     TGCCG
                                |||| ||||||||     |||||
                                AGGG CCGAGGAC     ACGGC
                                  A       TGAGG
GAM345  ADAMTS13  3' CGGCGGTGGCCTGGGA      57374        TC  GTAT
                                TCCCAGGC  CT    GCCG
                                ||||||||  ||    ||||
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                                AGGGTCCG  GG    CGGC
                                    GT  ____
GAM345  ADORA1   3'  TGCAGGAGGCCTGGGA     5430         _
                                TCCCAGGC TCCTGTA
                                |||||||| |||||||
                                AGGGTCCG AGGACGT
                                    G
GAM345  AIRE     3'  GCTACATGGGAGCCTGAGG   4602     _        AT_
                                CC CAGGCTCCTGT   GC
                                || ||||||||||   ||
                                GG GTCCGAGGGTA   CG
                                 A          CAT
GAM345  ALPI     3'  GGGAGCAGGAGCCCAGGG    7897      A_       ATG
                                CCC  GGCTCCTGT   CC
                                |||  |||||||||   ||
                                GGG  CCGAGGACG   GG
                                  AC        AG_
GAM345  ANK1     3'  TCGGAGGCGGAGAGCCTGG   60392        _   ATG
                                CCAGGCTC CTGT   CCGA
                                |||||||| ||||   ||||
                                GGTCCGAG GGCG   GGCT
                                    A   GA_
GAM345  ANK1     3'  TCGGAGGCGGAGAGCCTGG   40030        _   ATG
                                CCAGGCTC CTGT   CCGA
                                |||||||| ||||   ||||
                                GGTCCGAG GGCG   GGCT
                                    A   GA_
GAM345  ANK1     3'  TCGGAGGCGGAGAGCCTGG   3476         _   ATG
                                CCAGGCTC CTGT   CCGA
                                |||||||| ||||   ||||
                                GGTCCGAG GGCG   GGCT
                                    A   GA_
GAM345  AOC3     5'  CGCCAGAGTCCGGGA       13586      A    C  TAT  C
                                TCCC GGCTC TG   GC G
                                |||| ||||| ||   || |
                                AGGG CTGAG AC   CG C
                                  C    _ ____  A
GAM345  BCL11B   3'  CGAATGCGAGGGCCTGGGA   43188          C    GC
                                TCCCAGGCTC TGTAT  CG
                                |||||||||| |||||  ||
                                AGGGTCCGGG GCGTA  GC
                                    A    A_
GAM345  CACNB1   3'  TCAGCGTAGGCACCTGGGA   5575        CT   GT   C
                                TCCCAGG  CCT  ATGC GA
                                |||||||  |||  |||| ||
                                AGGGTCC  GGA  TGCG CT
                                    AC   __   A
GAM345  CELL     3'  CATGAAGCGGAGCCTGAGA   8408     C      TG__
                                TC CAGGCTCC    TATG
                                || ||||||||    ||||
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                                AG GTCCGAGG   GTAC
                                 A       CGAA
GAM345  CTSZ    5'  CGGAGCGGGACCCAGGA    62115    CA  C    ATG
                                TCC  GG TCCTGT   CCG
                                |||  || ||||||   |||
                                AGG  CC AGGGCG   GGC
                                  AC  _     A__
GAM345  CYBB    3'  TCAGTTATAAGGAGTCTGAGA  76357    C       GTAT  C
                                TC CAGGCTCCT   GC GA
                                || |||||||||   || ||
                                AG GTCTGAGGA   TG CT
                                 A        ATAT  A
GAM345  DIAPH2   5'  CGGGGGTGCCTGGGA      22065        T   GTATG
                                TCCCAGGC CCT    CCG
                                |||||||| |||    |||
                                AGGGTCCG GGG    GGC
                                     T  ______
GAM345  DIAPH2   5'  CGGGGGTGCCTGGGA      23600        T   GTATG
                                TCCCAGGC CCT    CCG
                                |||||||| |||    |||
                                AGGGTCCG GGG    GGC
                                     T  ______
GAM345  EFNB1    5'  CAGTCGGGAGCCCGGGG     15394     A       TA
                                TCCC GGCTCCTG  TG
                                |||| ||||||||  ||
                                GGGG CCGAGGGC  AC
                                  C       TG
GAM345  EGR4     5'  CGAAGCCAGGAGCCCGGGG   8744      A       TAT  __
                                TCCC GGCTCCTG   GC  CG
                                |||| ||||||||   ||  ||
                                GGGG CCGAGGAC   CG  GC
                                  C       ___  AA
GAM345  EMX2     5'  GCCAGGAGCTGGGA       87566       G     TAT
                                TCCCAG CTCCTG   GC
                                ||||||  ||||||   ||
                                AGGGTC GAGGAC   CG
                                     _    ____
GAM345  EPHA8    3'  GGGGTCAGGCGCCTGGGA    40063        T   T  G
                                TCCCAGGC CCTG AT CC
                                |||||||| |||| || ||
                                AGGGTCCG GGAC TG GG
                                     C    _  G
GAM345  F2RL3    3'  GGAGACAGGCCTGGGA      14187        TC    ATG
                                TCCCAGGC  CTGT   CC
                                ||||||||  ||||   ||
                                AGGGTCCG  GACA   GG
                                     __    GA_
GAM345  FBXL7    5'  TCGAGCCGCGGAGCCCAGGG   24556     A_     T  AT  _
                                CCC  GGCTCC GT  GC CGA
                                |||  ||||||  ||  || |||
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                                GGG  CCGAGG CG  CG GCT
                                  AC     _ C_  A
GAM345  FUT5    3'  CGGCATGGGGCCTGGG      8965          TGT
                                CCCAGGCTCC   ATGCCG
                                ||||||||||   ||||||
                                GGGTCCGGGG   TACGGC
                                             ___
GAM345  GAA     3'  CGAGCAAGCCTGGGA       3841          CCTGTA  _
                                TCCCAGGCT     TGC CG
                                |||||||||      ||| ||
                                AGGGTCCGA     ACG GC
                                     _______  A
GAM345  GARP    3'  GTGGGGGAGCCTGAGG      18600    _       G
                                CC CAGGCTCCT TAT
                                || |||||||||  |||
                                GG GTCCGAGGG GTG
                                 A        G
GAM345  GCN1L1  3'  TCAGCAAATGGCAGCCCAGGA  69758     CA    C    A   C
                                TCC  GGCT CTGT TGC GA
                                |||  ||||  ||||  ||| ||
                                AGG  CCGA GGTA ACG CT
                                  AC    C    A   A
GAM345  GJB5    5'  CGGCTGCTGGGAGCCAGG    17947    A      _  T
                                CC GGCTCCT GTA GCCG
                                || |||||||  |||  ||||
                                GG CCGAGGG CGT CGGC
                                 A      T  _
GAM345  GYPC    5'  GGTCAGGAGCCCGGGA      33654      A       TAT
                                TCCC GGCTCCTG   GCC
                                ||||  ||||||||   |||
                                AGGG CCGAGGAC   TGG
                                  C       ___
GAM345  GYPC    5'  GGTCAGGAGCCCGGGA      9164       A       TAT
                                TCCC GGCTCCTG   GCC
                                ||||  ||||||||   |||
                                AGGG CCGAGGAC   TGG
                                  C       ___
GAM345  HMOX1   3'  GCAGCAGAGCCTGG        9234          C   A
                                CCAGGCTC TGT TGC
                                ||||||||  |||  |||
                                GGTCCGAG ACG ACG
                                         _   _
GAM345  ICMT    3'  TGTGCAGCCTGGGA        24821          CCT
                                TCCCAGGCT   GTATG
                                |||||||||   |||||
                                AGGGTCCGA   CGTGT
                                            ___
GAM345  ITPKB   3'  GTACAGGAGCTGGGA       9436         G
                                TCCCAG CTCCTGTAT
                                ||||||  |||||||||
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                                AGGGTC GAGGACATG
                                      _
GAM345  JUNB     5'  GCAGGGAGCTGGGA       9484        G    GTA
                                TCCCAG CTCCT   TGC
                                |||||| |||||   |||
                                AGGGTC GAGGG   ACG
                                      _   ___
GAM345  KCNAB2   3'  GCGGGGAGAGCCTGGGG     13305         ___
                                TCCCAGGCT   CCTGT
                                |||||||||   |||||
                                GGGGTCCGA   GGGCG
                                     GAG
GAM345  KCNAB2   3'  GGCCAAGGCCTGGGA       13307         CC  TAT
                                TCCCAGGCT  TG   GCC
                                |||||||||  ||   |||
                                AGGGTCCGG  AC   CGG
                                     A_  ___
GAM345  KCNH3    3'  GGCAGGGAGCCTGG        64607         GTA
                                CCAGGCTCCT   TGCC
                                ||||||||||   ||||
                                GGTCCGAGGG   ACGG
                                     ___
GAM345  KCNJ4    3'  GCACCCAGGCCTGGGA      17147         TC   TA
                                TCCCAGGC  CTG  TGC
                                ||||||||  |||  |||
                                AGGGTCCG  GAC  ACG
                                     __  CC
GAM345  KCNQ1    3'  CGGCAATAAAAGCCCAGGA   4022      CA   CC   A
                                TCC  GGCT  TGT TGCCG
                                |||  ||||  ||| |||||
                                AGG  CCGA  ATA ACGGC
                                  AC   AA  _
GAM345  KIF1B    3'  GCTGCTTGGGAGCCTGAGG   30589    _       __   T
                                CC CAGGCTCCT  GTA GC
                                || |||||||||  ||| ||
                                GG GTCCGAGGG  CGT CG
                                 A       TT  _
GAM345  LATS2    5'  CGGCGCGAGAGGCCCGGGA   27403      A   TC  GTA
                                TCCC GGC  CT   TGCCG
                                |||| |||  ||   |||||
                                AGGG CCG  GA   GCGGC
                                  C   GA  GC_
GAM345  LLGL1    3'  GGTGTGGGCCTGGGA       66880         CTGT
                                TCCCAGGCTC   ATGCC
                                ||||||||||   |||||
                                AGGGTCCGGG   TGTGG
                                     ____
GAM345  MAP3K14  5'  GGATGAGCACAAGCCTGGGA  14207         CC   ATG_
                                TCCCAGGCT  TGT   CC
                                |||||||||  |||   ||
```

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                                AGGGTCCGA ACG   GG
                                     AC  AGTA
GAM345  MLLT7   3' GGCTAGCTGGAGCCTGGGA  19863        T AT
                                TCCCAGGCTCC GT GCC
                                |||||||||| || |||
                                AGGGTCCGAGG CG CGG
                                      T AT
GAM345  NR2C2   5' CGACACCGGGAGCCCGGG   12381    A     TA C
                                CCC GGCTCCTG TG CG
                                ||| |||||||| || ||
                                GGG CCGAGGGC AC GC
                                  C      C_ A
GAM345  NTRK2   5' CGGCGGTAGCAGGAGCCTGG  20522         A__
                                CCAGGCTCCTGT  TGCCG
                                ||||||||||||  |||||
                                GGTCCGAGGACG  GCGGC
                                       ATG
GAM345  NTSR1   3' CAGCCAGGAGCTGGGA     10289      G    TA
                                TCCCAG CTCCTG TG
                                |||||| |||||| ||
                                AGGGTC GAGGAC AC
                                   _     CG
GAM345  PCDH7   5' CGGAGCAGAGCCTGGG     50597       C  ATG
                                CCCAGGCTC TGT  CCG
                                ||||||||| |||  |||
                                GGGTCCGAG ACG  GGC
                                     _  A__
GAM345  PCDH7   5' CGGAGCAGAGCCTGGG     50602       C  ATG
                                CCCAGGCTC TGT  CCG
                                ||||||||| |||  |||
                                GGGTCCGAG ACG  GGC
                                     _  A__
GAM345  PCDH7   5' CGGAGCAGAGCCTGGG     10459       C  ATG
                                CCCAGGCTC TGT  CCG
                                ||||||||| |||  |||
                                GGGTCCGAG ACG  GGC
                                     _  A__
GAM345  PCTK3   3' CGGCATACGCTTTGCTGG   72965    G TCC_
                                CCAG C   TGTATGCCG
                                |||| |   |||||||||
                                GGTC G   GCATACGGC
                                  _ TTTC
GAM345  PCTK3   3' CGGGGGCTGGAAGCCTGGG  72966       _ T ATG
                                CCCAGGCT CC GT  CCG
                                |||||||| || ||  |||
                                GGGTCCGA GG CG  GGC
                                     A  T  GG_
GAM345  PER2    5' GCAGCTCAGGAGCCTGAGG  13987   _       TA_
                                CC CAGGCTCCTG  TGC
                                || ||||||||||  |||
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                                GG GTCCGAGGAC   ACG
                                 A         TCG
GAM345  PER2     5'  GCAGCTCAGGAGCCTGAGG   43034    _        TA_
                                CC CAGGCTCCTG   TGC
                                || ||||||||||   |||
                                GG GTCCGAGGAC   ACG
                                 A         TCG
GAM345  PPP1R12B 5'  TCAGCAAGTGCTGGGCCTGG   49473       T  T   __   C
                                CCAGGC CC GTA  TGC GA
                                |||||| || |||  ||| ||
                                GGTCCG GG CGT  ACG CT
                                   _ T   GA   A
GAM345  PPP1R12B 5'  TCAGCAAGTGCTGGGCCTGG   49484       T  T   __   C
                                CCAGGC CC GTA  TGC GA
                                |||||| || |||  ||| ||
                                GGTCCG GG CGT  ACG CT
                                   _ T   GA   A
GAM345  PTGFR    5'  CGGCTGGCGGCCTGGGA     6317          _  TGTAT
                                TCCCAGGCT CC    GCCG
                                |||||||||  ||    ||||
                                AGGGTCCGG GG    CGGC
                                     C  T_____
GAM345  RAP1GA1  3'  CGGCACAGCTGCTGGGA     11251       G TC    AT
                                TCCCAG C  CTGT  GCCG
                                ||||||  |  ||||  ||||
                                AGGGTC G  GACA  CGGC
                                   _ TC    __
GAM345  RASGRP2  3'  GCAGGGAGCCTGGGG       19509           GTA
                                TCCCAGGCTCCT   TGC
                                ||||||||||||   |||
                                GGGGTCCGAGGG   ACG
                                       ____
GAM345  RGS3     5'  CGGCTAGACAGGAGCCAAGGA  56221     CA       AT_
                                TCC  GGCTCCTGT   GCCG
                                |||  |||||||||   ||||
                                AGG  CCGAGGACA   CGGC
                                  AA        GAT
GAM345  SERPINA4 3'  GGTCCAGGAGTCCAGGA     20613     CA      TAT
                                TCC  GGCTCCTG   GCC
                                |||  ||||||||   |||
                                AGG  CTGAGGAC   TGG
                                  AC       C__
GAM345  SH3BP4   5'  CGACGAGCGGAGCCTCAGGA  27233     C_     T  A  C
                                TCC  AGGCTCC GT TG CG
                                |||  ||||||| || || ||
                                AGG  TCCGAGG CG GC GC
                                  AC      _  A  A
GAM345  SIM2     3'  CGCGCCAGGAGCCTGG       17385           TAT  _
                                CCAGGCTCCTG   GC CG
                                ||||||||||   || ||
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                                GGTCCGAGGAC  CG GC
                                     ___  C
GAM345  SLC15A1  5'  CGGCAGTCGCAGGAGCCCTGGG 17401       _     A__
            A                    TCCCAGG CTCCTGT  TGCCG
                                 ||||||| |||||||  |||||
                                 AGGGTCC GAGGACG  ACGGC
                                    C      CTG
GAM345  SLC22A12 5'  GGCCACACAGCCTGGGA    58073        CC  AT
                                 TCCCAGGCT  TGT  GCC
                                 |||||||||  |||  |||
                                 AGGGTCCGA  ACA  CGG
                                      C_  C_
GAM345  SLC6A8   5'  GCGGGCAGGAGCCTCGGGA   18851    _       A
                                 TCCC AGGCTCCTGT TGC
                                 |||| |||||||||| |||
                                 AGGG TCCGAGGACG GCG
                                   C        G
GAM345  SNAI1    3'  ACAGGTGGGCCTGGGA     19966        __
                                 TCCCAGGCT  CCTGT
                                 |||||||||  |||||
                                 AGGGTCCGG  GGACA
                                      GT
GAM345  SOD3     5'  CGGCATACAGCATGGTGA    11862   _  GGCTC
                                 TC CCA    CTGTATGCCG
                                 || |||    ||||||||||
                                 AG GGT    GACATACGGC
                                  T  AC___
GAM345  TNFRSF8  3'  GGCCTAGGGGCCCAGGA    6961    CA      TAT
                                 TCC  GGCTCCTG  GCC
                                 |||  ||||||||  |||
                                 AGG  CCGGGGAT  CGG
                                   AC      C__
GAM345  TNNT1    3'  CGGACAGTGGCACCTGGGA   12351       CT  TGTA  _
                                 TCCCAGG  CC   TG CCG
                                 |||||||  ||   || |||
                                 AGGGTCC  GG   AC GGC
                                     AC  TG__  A
GAM345  TRPM2    3'  CGGATGGAGCCTGGGG     12399         TGTATG
                                 TCCCAGGCTCC    CCG
                                 ||||||||||     |||
                                 GGGGTCCGAGG    GGC
                                       TA_____
GAM345  UCP3     3'  TCAGCCACGGAGCCTGG     12537        T  AT  C
                                 CCAGGCTCC GT  GC GA
                                 |||||||| ||  || ||
                                 GGTCCGAGG CA  CG CT
                                      _ C_  A
GAM345  WBSCR1   3'  CGGCAGCAGGAGCCTGGGA   49259           A
                                 TCCCAGGCTCCTGT TGCCG
                                 |||||||||||||| |||||
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                                AGGGTCCGAGGACG ACGGC
                                                _
GAM345  WBSCR1   3'  CGGCAGCAGGAGCCTGGGA   42227          A
                                TCCCAGGCTCCTGT TGCCG
                                ||||||||||||| |||||
                                AGGGTCCGAGGACG ACGGC
                                                _
GAM345  XRCC3    3'  GGCTGGAGCCTGGGG      18342         TGTAT
                                TCCCAGGCTCC    GCC
                                ||||||||||     |||
                                GGGGTCCGAGG    CGG
                                       T____
GAM345  ZNF26    5'  CGGTCAGGAGCCTGGGG    72980          TAT
                                TCCCAGGCTCCTG   GCCG
                                ||||||||||||   ||||
                                GGGGTCCGAGGAC   TGGC
                                                ___
GAM345  ZNF74    5'  TCAGCCGTGAGCCTGG     12803       C  TAT  C
                                CCAGGCTC TG   GC GA
                                |||||||| ||   || ||
                                GGTCCGAG GC   CG CT
                                     T ___  A
GAM345  A        5'  CGGCAGGCAGCGGGAGCC   27075        A___
                                GGCTCCTGT    TGCCG
                                |||||||||    |||||
                                CCGAGGGCG    ACGGC
                                     ACGG
GAM345  A        5'  CGGCAGGCAGCGGGAGCC   39095        A___
                                GGCTCCTGT    TGCCG
                                |||||||||    |||||
                                CCGAGGGCG    ACGGC
                                     ACGG
GAM345  AMOTL1   3'  GGCCAGGAGCCTCAGA     73652    CC       TAT
                                TC  AGGCTCCTG   GCC
                                ||  |||||||||   |||
                                AG  TCCGAGGAC   CGG
                                 AC       ___
GAM345  ARPP-21  5'  GCAACTGACAGGAGCTTGGGA  32828           A___
                                TCCCAGGCTCCTGT    TGC
                                ||||||||||||||    |||
                                AGGGTTCGAGGACA    ACG
                                       GTCA
GAM345  ASB10    5'  TCAGCCTCGGAGCGTGGGA   55128      G    T TAT  C
                                TCCCA GCTCC G   GC GA
                                ||||| ||||| |   || ||
                                AGGGT CGAGG C   CG CT
                                   G    _ TC_  A
GAM345  C20orf28 3'  GGTAAAGAAGCTGGGA     31229       G  C  GTA
                                TCCCAG CT CT   TGCC
                                |||||| || ||   ||||
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                                AGGGTC GA GA   ATGG
                                   _  A  A__
GAM345  CGI-85   5'  GGCAGCGGGGCCTGGGA     32081        T    A
                                TCCCAGGC CCTGT TGCC
                                |||||||| ||||| ||||
                                AGGGTCCG GGGCG ACGG
                                   _    _
GAM345  CLSTN1   5'  CGGCCTTAGGAGCCCGGGA   30105     A      TAT
                                TCCC GGCTCCTG   GCCG
                                |||| ||||||||   ||||
                                AGGG CCGAGGAT   CGGC
                                  C       TC_
GAM345  CXYorf1  5'  TCGGCTCGGGAGGCCTGGGA  82053        _    TAT
                                TCCCAGGC TCCTG   GCCGA
                                |||||||| |||||   |||||
                                AGGGTCCG AGGGC   CGGCT
                                     G    T__
GAM345  DHRS2    3'  GCCCAGGAGCCTGAGG      19382    _       TAT
                                CC CAGGCTCCTG   GC
                                || ||||||||||   ||
                                GG GTCCGAGGAC   CG
                                 A        C__
GAM345  DKFZP434B195 5'  CGGTTGGCGGCAGCCTGGGA   48428         C   AT
                                TCCCAGGCT CTGT  GCCG
                                |||||||| ||||  ||||
                                AGGGTCCGA GGCG  TGGC
                                     C   GT
GAM345  DKFZP434P0111 3'  TCGGCAGTGCTGAAGGAGCCTG 67374          ___  _
           GGA                   TCCCAGGCTCCT   GTA TGCCGA
                                ||||||||||||   ||| ||||||
                                AGGGTCCGAGGA   CGT ACGGCT
                                       AGT   G
GAM345  DKFZP586J1624 3'  GCACACAGGCCTGGGG      31392        TC   A
                                TCCCAGGC  CTGT TGC
                                ||||||||  |||| |||
                                GGGGTCCG  GACA ACG
                                   __    C
GAM345  DOK4     3'  TCGGCCAAGAGCCTGG      36181        C  TAT
                                CCAGGCTC TG   GCCGA
                                |||||||| ||   |||||
                                GGTCCGAG AC   CGGCT
                                   A  ___
GAM345  ENDO180  3'  GGAGCAGGAGTCTGGGA     20146           ATG
                                TCCCAGGCTCCTGT   CC
                                ||||||||||||||   ||
                                AGGGTCTGAGGACG   GG
                                       A__
GAM345  FLJ10751  3'  CATGTAGGAGCCCGAGG     36567    CA_
                                CC   GGCTCCTGTATG
                                ||   ||||||||||||
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                              GG   CCGAGGATGTAC
                               AGC
GAM345  FLJ10751  3' CATGTAGGAGCCCGAGG     36728    CA_
                              CC   GGCTCCTGTATG
                              ||   ||||||||||||
                              GG   CCGAGGATGTAC
                               AGC
GAM345  FLJ10901  3' TCAGCTACAGAGCTGG      36832     G   C    T  C
                              CCAG CTC TGTA GC GA
                              |||| ||| |||| || ||
                              GGTC GAG ACAT CG CT
                                _  _   _ A
GAM345  FLJ12154  3' CGGAGAAGCCTGGGA       41669         C  GTATG
                              TCCCAGGCT CT    CCG
                              |||||||| ||    |||
                              AGGGTCCGA GA    GGC
                                   A _____
GAM345  FLJ12178  3' GCACTTTGGGAGCCTGAGG   47101    _        TA_
                              CC CAGGCTCCTG   TGC
                              || ||||||||||   |||
                              GG GTCCGAGGGT   ACG
                               A         TTC
GAM345  FLJ13162  3' TGGCTGGGCCTGGGA       46562          CTGTAT
                              TCCCAGGCTC     GCCG
                              |||||||||      ||||
                              AGGGTCCGGG     CGGT
                                   T_____
GAM345  FLJ13798  3' GCGCAGGAGCCGGGA       87108      A       AT
                              TCCC GGCTCCTGT  GC
                              |||| |||||||||  ||
                              AGGG CCGAGGACG  CG
                                _       __
GAM345  FLJ13909  5' TCGGCTGCTGCATGCCTGGGA  47069         TCCT_  T
                              TCCCAGGC    GTA GCCGA
                              ||||||||    ||| |||||
                              AGGGTCCG    CGT CGGCT
                                   TACGT  _
GAM345  FLJ14129  3' TCAGCTACTTGGGAGCCTGGGG 48071           __  T  C
                              TCCCAGGCTCCT  GTA GC GA
                              ||||||||||||  ||| || ||
                              GGGGTCCGAGGG  CAT CG CT
                                     TT   _ A
GAM345  FLJ20034  3' TGGGGCAGGAGCATGG      34390     G      ATG
                              CCA GCTCCTGT   CCG
                              ||| ||||||||   |||
                              GGT CGAGGACG   GGT
                                A       G__
GAM345  FLJ20275  3' TCAGCACCTCAGTCTGGGA   34825         CCTGTA   C
                              TCCCAGGCT     TGC GA
                              |||||||||     ||| ||
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                                AGGGTCTGA     ACG CT
                                     CTCC__   A
GAM345  FLJ20509  3' CAGCCAGGTTGAGCCTAGGG  35311    _    ___   TA
                                CCC AGGCT   CCTG  TG
                                ||| |||||   ||||  ||
                                GGG TCCGA   GGAC  AC
                                  A    GTT    CG
GAM345  FLJ20627  5' CGGCGGAGAGCTTGGGA    35472         CTGTA
                                TCCCAGGCTC    TGCCG
                                ||||||||||    |||||
                                AGGGTTCGAG    GCGGC
                                     AG___
GAM345  FLJ21156  3' GCAGGGAGCCTGGGA      44810          GTA
                                TCCCAGGCTCCT   TGC
                                ||||||||||||   |||
                                AGGGTCCGAGGG   ACG
                                      ___
GAM345  FLJ21865  3' CAAGCAGAGACTGGGA     42804       G   C   A
                                TCCCAG CTC TGT TG
                                |||||| ||| ||| ||
                                AGGGTC GAG ACG AC
                                   A   _   A
GAM345  FLJ22649  5' CGGAACGGGAGCCTGGG     41636           ATG
                                CCCAGGCTCCTGT   CCG
                                ||||||||||||   |||
                                GGGTCCGAGGGCA   GGC
                                      A__
GAM345  FLJ22795  3' TCGGCACTCCCAGGCTGGGA  46945       GCT    TA__
                                TCCCAG   CCTG    TGCCGA
                                ||||||   ||||    ||||||
                                AGGGTC   GGAC    ACGGCT
                                   ___    CCTC
GAM345  FLJ22865  5' TGGAGCAGGAGCTGGGA     47072       G      ATG
                                TCCCAG CTCCTGT   CCG
                                |||||| |||||||   |||
                                AGGGTC GAGGACG   GGT
                                   _      A__
GAM345  FLJ23584  3' CGGCAGCGGAGTCCAGGA    44737     CA     T  A
                                TCC  GGCTCC GT TGCCG
                                |||  |||||| || |||||
                                AGG  CTGAGG CG ACGGC
                                  AC     _ _
GAM345  FLJ30681  5' TCGGCGCTGGGAAGAAGCCGGG 91791      A  _____   GTA
          A                      TCCC GGC    TCCT   TGCCGA
                                 |||| |||    ||||   ||||||
                                 AGGG CCG    AGGG   GCGGCT
                                   _  AAGA    TC_
GAM345  FLJ31168  3' GGTACGTGGACCTGGGA     58509        C   T TA
                                TCCCAGG TCC G  TGCC
                                ||||||| ||| |  ||||
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                                AGGGTCC AGG T  ATGG
                                    _  _ GC
GAM345  GHITM    5'  CGACGCTAGGGGCCCGG     26916    A      TA  C
                                CC GGCTCCTG  TG CG
                                || ||||||||  || ||
                                GG CCGGGGAT  GC GC
                                 C       C_  A
GAM345  GMEB2    5'  TCGGAACCAGAGCCTGG     24738        C  TATG
                                CCAGGCTC TG    CCGA
                                ||||||||| ||    ||||
                                GGTCCGAG AC    GGCT
                                    _ CAA_
GAM345  GPS2     5'  CGGCAGGGGAAGGCCTGGGA  87157        __    GTA
                                TCCCAGGC  TCCT   TGCCG
                                ||||||||  ||||   |||||
                                AGGGTCCG  AGGG   ACGGC
                                     GA   G__
GAM345  H11      5'  GCCTGGGCAGCCTGGGA     26849         _    TAT
                                TCCCAGGCT CCTG   GC
                                |||||||||| ||||   ||
                                AGGGTCCGA GGGT   CG
                                     C    C__
GAM345  HSH2     3'  GCTACTTGGGAGCCTGAGG   51676    _       __   T
                                CC CAGGCTCCT  GTA GC
                                || |||||||||  ||| ||
                                GG GTCCGAGGG  CAT CG
                                 A        TT  _
GAM345  HSRNAFEV 3'  CGGGGAGGGCCCGGGA      34021     A    _  GTATG
                                TCCC GGCTC CT    CCG
                                |||| ||||| ||    |||
                                AGGG CCGGG GG    GGC
                                  C    A _____
GAM345  KCNK13   5'  CGGCGGTGGGGCGCCCGGGA  41907     A   T   GTA
                                TCCC GGC CCT   TGCCG
                                |||| ||| |||   |||||
                                AGGG CCG GGG   GCGGC
                                  C   C   GTG
GAM345  KIAA0033 5'  TCGGCGTAGTAAGGAGCCTG  76586         G__
                                CAGGCTCCT   TATGCCGA
                                |||||||||   ||||||||
                                GTCCGAGGA   ATGCGGCT
                                     ATG
GAM345  KIAA0057 3'  CGGTCAGAAGCCTGGGG     24421         C   TAT
                                TCCCAGGCT CTG   GCCG
                                |||||||||| |||   ||||
                                GGGGTCCGA GAC   TGGC
                                     A  ___
GAM345  KIAA0229 3'  GCAGGTTGGGGCCTGGGA    92427          TGTA
                                TCCCAGGCTCC    TGC
                                ||||||||||    |||
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                                AGGGTCCGGGG   ACG
                                      TTGG
GAM345  KIAA0370  5' GCAAATAGGAGCCTGG     73208          A
                                CCAGGCTCCTGT TGC
                                |||||||||||| |||
                                GGTCCGAGGATA ACG
                                      A
GAM345  KIAA0450  5' CATGCCAGTGCCTGGGA    27624       TC  _
                                TCCCAGGC  CTG TATG
                                ||||||||  ||| ||||
                                AGGGTCCG  GAC GTAC
                                     T_  C
GAM345  KIAA0514  3' TCTGCACCTAGGAGCCCAGGA 28097    CA      TA  C
                                TCC  GGCTCCTG  TGC GA
                                |||  ||||||||  ||| ||
                                AGG  CCGAGGAT  ACG CT
                                  AC       CC  T
GAM345  KIAA0556  3' TCAGTCCCAGGAGCTGG    69087    G     TAT  C
                                CCAG CTCCTG   GC GA
                                |||| ||||||   || ||
                                GGTC GAGGAC   TG CT
                                  _     CC_  A
GAM345  KIAA0618  3' GCAGTGGGAGCCTGGG     29164         TG A
                                CCCAGGCTCC  T TGC
                                ||||||||||  | |||
                                GGGTCCGAGG  G ACG
                                      GT _
GAM345  KIAA0793  3' TCGGACCAAAGCCTGGG    29027       CC  TATG
                                CCCAGGCT  TG   CCGA
                                ||||||||  ||   ||||
                                GGGTCCGA  AC   GGCT
                                     A_  CA__
GAM345  KIAA0836  3' CGCATCACTTGGGA       64561       CTCC  T   C
                                TCCCAGG   TG ATGC G
                                |||||||   || |||| |
                                AGGGTTC   AC TACG C
                                    ____  _   A
GAM345  KIAA1023  3' GGCGTGCGGAGCCTGTGGA  34264    _      T
                                TCC CAGGCTCC GTATGCC
                                ||| |||||||| |||||||
                                AGG GTCCGAGG CGTGCGG
                                  T      _
GAM345  KIAA1045  3' ACAAGGAGAAGCCCTGGGA  71045       ____   _
                                TCCCAGG   CTCCT GT
                                |||||||   ||||| ||
                                AGGGTCC   GAGGA CA
                                     CGAA    A
GAM345  KIAA1091  3' TGGCATACAAGAGCCCGG   69690    A   C
                                CC GGCTC TGTATGCCG
                                || ||||| |||||||||
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                                GG CCGAG ACATACGGT
                                 C    A
GAM345  KIAA1126 3' TCAGTGTGCAGAGCC      71940      C     C
                                GGCTC TGTATGC GA
                                ||||| ||||||| ||
                                CCGAG ACGTGTG CT
                                  _     A
GAM345  KIAA1297 5' TCAGCACGGGGGCCCAGGA   72186    CA       AT  C
                                TCC  GGCTCCTGT  GC GA
                                |||  |||||||||  || ||
                                AGG  CCGGGGGCA  CG CT
                                 AC        __ A
GAM345  KIAA1510 5' TGTGCCAGGAGCCAGG     61359    A      TAT  _
                                CC GGCTCCTG   GC CG
                                || ||||||||   || ||
                                GG CCGAGGAC   CG GT
                                 A       ___ T
GAM345  KIAA1607 3' GCATCACCACAGCCTGGGG   63799        CCT  _
                                TCCCAGGCT   GT ATGC
                                |||||||||   || ||||
                                GGGGTCCGA   CA TACG
                                     CAC  C
GAM345  KIAA1768 5' TCAGCGAGCAGGAAGCCTGGG 87508        _    A   C
                                CCCAGGCT CCTGT TGC GA
                                |||||||| ||||| ||| ||
                                GGGTCCGA GGACG GCG CT
                                     A    A  A
GAM345  KIAA1796 5' CGGCAGAGAGAGCCTGG     91454        _ GTA
                                CCAGGCTC CT   TGCCG
                                |||||||| ||   |||||
                                GGTCCGAG GA   ACGGC
                                     A  G__
GAM345  KIAA1822 3' CGGCGGGGGAGCCTGG      67564         GTA
                                CCAGGCTCCT   TGCCG
                                ||||||||||   |||||
                                GGTCCGAGGG   GCGGC
                                      G__
GAM345  KIAA1858 3' GGAGCAAGAGCCTGGGA     67135         C   ATG
                                TCCCAGGCTC TGT   CC
                                |||||||||| |||   ||
                                AGGGTCCGAG ACG   GG
                                      A   A__
GAM345  KIAA1870 5' TCAGCTGGACGAAGGCCGGGA 51833     A   CC   AT_  C
                                TCCC GGCT  TGT   GC GA
                                |||| ||||  |||   || ||
                                AGGG CCGG  GCA   CG CT
                                  _   AA   GGT  A
GAM345  KIAA1884 3' TGGCCAGGAGCCCAAGG     73343    CA_      TAT
                                CC   GGCTCCTG   GCCG
                                ||   ||||||||   ||||
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                                GG  CCGAGGAC  CGGT
                                 AAC      ___
GAM345  KIAA1904  3'  GCACAGGGCTGGGA      73488      G T   AT
                                TCCCAG C CCTGT  GC
                                |||||| | |||||  ||
                                AGGGTC G GGACA  CG
                                  _ _   __
GAM345  KIAA1922  5'  GGAGGCGGGCCTGGGA     73636       T  T  ATG
                                TCCCAGGC CC GT  CC
                                |||||||| || ||  ||
                                AGGGTCCG GG CG  GG
                                    _ _ GA_
GAM345  LCHN    5'  CGGAGGCGGGAGCCCGAGG   86255   CA_      ATG
                                CC  GGCTCCTGT  CCG
                                ||  |||||||||  |||
                                GG  CCGAGGGCG  GGC
                                 AGC       GA_
GAM345  LSFR2   3'  TCGGCATGGGCACCTGGG   60570     CT  GT
                                CCCAGG  CCT  ATGCCGA
                                ||||||  |||  |||||||
                                GGGTCC  GGG  TACGGCT
                                   AC  __
GAM345  LXN     5'  TCGGATGCAGGGAGCCTGGG  39413        _   G
                                CCCAGGCTCC TGTAT CCGA
                                |||||||||| ||||| ||||
                                GGGTCCGAGG ACGTA GGCT
                                     G   _
GAM345  MAPKAPK2  3'  TCAGCTGCATGGAGCCTGG   51985       _  T  C
                                CCAGGCTCC TGTA GC GA
                                ||||||||| |||| || ||
                                GGTCCGAGG ACGT CG CT
                                     T   _ A
GAM345  MAPKAPK2  3'  TCAGCTGCATGGAGCCTGG   16474       _  T  C
                                CCAGGCTCC TGTA GC GA
                                ||||||||| |||| || ||
                                GGTCCGAGG ACGT CG CT
                                     T   _ A
GAM345  MGC15438  5'  GGCTGGGAGCTGGGA     51793      G    TAT
                                TCCCAG CTCCTG  GCC
                                |||||| ||||||  |||
                                AGGGTC GAGGGT  CGG
                                  _    ____
GAM345  MGC2574   3'  CAGAGGGGGCCTGGGA    44051         GTA
                                TCCCAGGCTCCT  TG
                                ||||||||||||  ||
                                AGGGTCCGGGGG  AC
                                    AG_
GAM345  MGC2603   3'  CGCCTAAGCTTGGGA     43859       CCTG  T  C
                                TCCCAGGCT   TA GC G
                                |||||||||   || || |
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                                AGGGTTCGA   AT CG C
                                     ____  C  A
GAM345  MGC4655  3'  CATATAGGAGCCTGAGA    52800   C
                                TC CAGGCTCCTGTATG
                                || ||||||||||||||
                                AG GTCCGAGGATATAC
                                 A
GAM345  MP1      3'  TCGACTGCACAGGAGCC     30358       AT ___
                                GGCTCCTGT  GC  CGA
                                |||||||||  ||  |||
                                CCGAGGACA  CG  GCT
                                     __ TCA
GAM345  MYBPC3   3'  CGTGCCAGGAGCCTGG      4226         TAT _
                                CCAGGCTCCTG  GC CG
                                ||||||||||  || ||
                                GGTCCGAGGAC  CG GC
                                     ___ T
GAM345  NET-7    3'  GGGAGCAGAGCCTGGG      24711       C  ATG
                                CCCAGGCTC TGT  CC
                                ||||||||| |||  ||
                                GGGTCCGAG ACG  GG
                                     _  AG_
GAM345  NIN283   3'  TCGGTGGTTCAGAGCCTGGG  50076       C  TA_
                                CCCAGGCTC TG  TGCCGA
                                ||||||||| ||  ||||||
                                GGGTCCGAG AC  GTGGCT
                                     _ TTG
GAM345  OS4      3'  CGGCTGAGTGCCTGGGA     19181       TC  GTAT
                                TCCCAGGC  CT   GCCG
                                ||||||||  ||   ||||
                                AGGGTCCG  GA   CGGC
                                    T_  GT__
GAM345  P4HA2    5'  GCAGCAGGAGCCTGG       14840         A
                                CCAGGCTCCTGT TGC
                                |||||||||||| |||
                                GGTCCGAGGACG ACG
                                          _
GAM345  PMF1     3'  GCATGCCTGGCCTGGG      23325       CCT
                                CCCAGGCT  GTATGC
                                ||||||||  ||||||
                                GGGTCCGG  CGTACG
                                    TC_
GAM345  PPP1R10  3'  CGGCGTGCTGGGCCTG      10731      T  T
                                CAGGC CC GTATGCCG
                                ||||| || ||||||||
                                GTCCG GG CGTGCGGC
                                   _ T
GAM345  PRO2949  5'  TCAGCATACAGTTTCTG     37624     CTC      C
                                CAGG  CTGTATGC GA
                                ||||  |||||||| ||
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                                GTCT   GACATACG CT
                                  TT_       A
GAM345  PTD012   3'  GCACACTGGAGCCCAGGA    25892     CA     T  A
                                TCC  GGCTCC GT TGC
                                |||  |||||| || |||
                                AGG  CCGAGG CA ACG
                                  AC     T  C
GAM345  PTK9     5'  TCAGCGCCGGAGCCGGGA    11028      A     T  AT  C
                                TCCC GGCTCC GT  GC GA
                                |||| |||||| ||  || ||
                                AGGG CCGAGG CG  CG CT
                                  _     C  __  A
GAM345  RAB11B   3'  CGGGCCGGGGCCCAGGA     73904     CA     T  ATG
                                TCC  GGCTCC GT   CCG
                                |||  |||||| ||   |||
                                AGG  CCGGGG CG   GGC
                                  AC     C  ____
GAM345  RAB3D    3'  GCCAGGAGCCTGGGG       15009           TAT
                                TCCCAGGCTCCTG   GC
                                ||||||||||||   ||
                                GGGGTCCGAGGAC   CG
                                       ___
GAM345  RAB3IL1  3'  CGACACACAGGGAGACGGGG   25463     AGG   _   A  C
                                CCC   CTCC TGT TG CG
                                |||   |||| ||| || ||
                                GGG   GAGG ACA AC GC
                                  GCA    G   C  A
GAM345  SAMP14   3'  GGAGGACAGGGCCTGGGA    56053        T    ATG
                                TCCCAGGC CCTGT   CC
                                ||||||||  |||||   ||
                                AGGGTCCG GGACA   GG
                                     _    GGA
GAM345  SCYA14   5'  GGAAGCAGTGAGCCCAGGA    52000     CA    _   ATG
                                TCC  GGCTC CTGT   CC
                                |||  |||||  ||||   ||
                                AGG  CCGAG GACG   GG
                                  AC     T    AA_
GAM345  SCYA14   5'  GGAAGCAGTGAGCCCAGGA    14788     CA    _   ATG
                                TCC  GGCTC CTGT   CC
                                |||  |||||  ||||   ||
                                AGG  CCGAG GACG   GG
                                  AC     T    AA_
GAM345  SCYA15   5'  GGAAGCAGTGAGCCCAGGA    52001     CA    _   ATG
                                TCC  GGCTC CTGT   CC
                                |||  |||||  ||||   ||
                                AGG  CCGAG GACG   GG
                                  AC     T    AA_
GAM345  SCYA23   5'  GGAAGCAGTGAGCCCAGGA    17355     CA    _   ATG
                                TCC  GGCTC CTGT   CC
                                |||  |||||  ||||   ||
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                                AGG  CCGAG GACG   GG
                                  AC    T   AA_
GAM345  SHANK3   5'  CGGCCCGAGCCTGGGG     65493         CTGTAT
                                TCCCAGGCTC     GCCG
                                ||||||||||     ||||
                                GGGGTCCGAG     CGGC
                                     CC____
GAM345  SLC2A10  3'  TGGTCCAGGGCCTGGGA     47830        T   TAT
                                TCCCAGGC CCTG   GCCG
                                |||||||| ||||   ||||
                                AGGGTCCG GGAC   TGGT
                                     _   C__
GAM345  STAM2    5'  CATACAAAAGTCTGGGA     19560         CC
                                TCCCAGGCT  TGTATG
                                |||||||||  ||||||
                                AGGGTCTGA  ACATAC
                                     AA
GAM345  STAM2    5'  TGGGACAGGAGCGCGGGA    19569     AG      ATG
                                TCCC  GCTCCTGT   CCG
                                ||||  ||||||||   |||
                                AGGG  CGAGGACA   GGT
                                  CG       G__
GAM345  TRAF3    3'  TGGGCAGCAGCCTGGGA     59746         C   ATG
                                TCCCAGGCT CTGT   CCG
                                ||||||||| ||||   |||
                                AGGGTCCGA GACG   GGT
                                     C   ___
GAM345  TSPAN-1  5'  TGGCAACACCCGGGA      19168     A  CTCC   A
                                TCCC GG    TGT TGCCG
                                |||| ||    ||| |||||
                                AGGG CC    ACA ACGGT
                                  C _____  _
GAM345  VI       3'  GTGCGGAGTCTGAGA      25559    C       T
                                TC CAGGCTCC GTAT
                                || |||||||| ||||
                                AG GTCTGAGG CGTG
                                 A       _
GAM345  VPS18    5'  CGGCTGAAGGGAGCCTGTGA  54438    C       GTAT
                                TC CAGGCTCCT    GCCG
                                || |||||||||    ||||
                                AG GTCCGAGGG    CGGC
                                  T        AAGT
GAM345  ZDHHC2   5'  GGCTGAGGAGCCGGGA     33010     A     GTAT
                                TCCC GGCTCCT    GCC
                                |||| |||||||    |||
                                AGGG CCGAGGA    CGG
                                  _      GT__
GAM345  ZNF263   5'  CGGCGTGGCGGCGCCTGGGA  19226        T  TG
                                TCCCAGGC CC  TATGCCG
                                |||||||| ||  |||||||
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                                AGGGTCCG GG  GTGCGGC
                                     C  CG
GAM345  ZNF297B  3'  GGCAGCCAGAGCCTGGGA    25786          C  TA
                                TCCCAGGCTC TG  TGCC
                                |||||||||| ||  ||||
                                AGGGTCCGAG AC  ACGG
                                      _  CG
GAM345  ZNF339   5'  CGAGCCGGGAGGCTGGGA    41118       G     TAT  _
                                TCCCAG CTCCTG   GC CG
                                |||||| ||||||   || ||
                                AGGGTC GAGGGC   CG GC
                                   G     ___  A
GAM345  LOC112609 5'  TCGGAGGAGCCAGGAGCCGG   72841    A       TATG__
                                CC GGCTCCTG     CCGA
                                || ||||||||     ||||
                                GG CCGAGGAC     GGCT
                                 _       CGAGGA
GAM345  LOC124602 3'  CGGCAGAGGACCCAGGA     74307     CA  C    GTA
                                TCC  GG TCCT   TGCCG
                                |||  || ||||   |||||
                                AGG  CC AGGA   ACGGC
                                  AC  _   G__
GAM345  LOC124935 5'  GCAGCAGGAGCCAGGA      74371     CA        A
                                TCC  GGCTCCTGT TGC
                                |||  ||||||||| |||
                                AGG  CCGAGGACG ACG
                                  A_       _
GAM345  LOC125206 3'  GCAAAGCGGGAGCCCTG     75664      _      A_
                                CAGG CTCCTGT  TGC
                                |||| |||||||  |||
                                GTCC GAGGGCG  ACG
                                  C      AA
GAM345  LOC131870 3'  GGATTCAGGAGCTGGGA     75022       G     TATG
                                TCCCAG CTCCTG    CC
                                |||||| ||||||    ||
                                AGGGTC GAGGAC    GG
                                   _     TTA_
GAM345  LOC143310 5'  CATGGAAGGAGACCCAGGA   76529     CA  _    G_
                                TCC  GG CTCCT  TATG
                                |||  || |||||  ||||
                                AGG  CC GAGGA  GTAC
                                  AC  A     AG
GAM345  LOC143425 3'  CGCATATCCTGGGA        87634        CTCCT     C
                                TCCCAGG     GTATGC G
                                |||||||     |||||| |
                                AGGGTCC     TATACG C
                                    _____      A
GAM345  LOC143524 5'  CGGCATACAAGCTTATGGA   76595     C_    CC
                                TCC  AGGCT  TGTATGCCG
                                |||  |||||  |||||||||
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                                AGG  TTCGA  ACATACGGC
                                  TA    __
GAM345  LOC144559 5'  CGGCATACAAGCTTATGGA   76882    C_    CC
                                TCC  AGGCT  TGTATGCCG
                                |||  |||||  |||||||||
                                AGG  TTCGA  ACATACGGC
                                  TA    __
GAM345  LOC145693 5'  CGGCAGGGAGCCTGG      77351         GTA
                                CCAGGCTCCT   TGCCG
                                ||||||||||   |||||
                                GGTCCGAGGG   ACGGC
                                      ___
GAM345  LOC145717 3'  TCGGCACTCCCAGGCTGGGA  66834      GCT   TA__
                                TCCCAG   CCTG   TGCCGA
                                ||||||   ||||   ||||||
                                AGGGTC   GGAC   ACGGCT
                                   ___   CCTC
GAM345  LOC145725 3'  CGGCAGGAGGAAGCCCAGGA  77406    CA   _  GTA
                                TCC  GGCT CCT   TGCCG
                                |||  |||| |||   |||||
                                AGG  CCGA GGA   ACGGC
                                  AC   A   GG_
GAM345  LOC145732 3'  CGGCAGGAGGAAGCCCAGGA  77428    CA   _  GTA
                                TCC  GGCT CCT   TGCCG
                                |||  |||| |||   |||||
                                AGG  CCGA GGA   ACGGC
                                  AC   A   GG_
GAM345  LOC146669 3'  TCAGCCCTGCAGCCTGGGA   78060        CCT   T_  C
                                TCCCAGGCT   GTA  GC GA
                                |||||||||   |||  || ||
                                AGGGTCCGA   CGT  CG CT
                                     ___   CC  A
GAM345  LOC147515 3'  TGGTAGGAGCCTTGGA     84029     C      GTAT
                                TCC AGGCTCCT    GCCG
                                ||| ||||||||    ||||
                                AGG TCCGAGGA    TGGT
                                  T       _____
GAM345  LOC148137 3'  GCCTAAGAGCCTGGGG      58431         CTG  T
                                TCCCAGGCTC   TA GC
                                ||||||||||   || ||
                                GGGGTCCGAG   AT CG
                                     A__  C
GAM345  LOC148223 3'  TGGCCAGGAGCCCAGGG     78746     A_      TAT
                                CCC  GGCTCCTG   GCCG
                                |||  ||||||||   ||||
                                GGG  CCGAGGAC   CGGT
                                  AC       ___
GAM345  LOC149372 3'  CAGTCAGGAGCTGGGA      79321       G     TA
                                TCCCAG CTCCTG  TG
                                |||||| ||||||  ||
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                                AGGGTC GAGGAC  AC
                                   _     TG
GAM345  LOC149501 3'  CGGCTGGAGTCTGGGA      75273          TGTAT
                                TCCCAGGCTCC    GCCG
                                ||||||||||    ||||
                                AGGGTCTGAGG    CGGC
                                      T_____
GAM345  LOC149995 3'  TGGTAGGAGCCTTGGA      84851     C      GTAT
                                TCC AGGCTCCT   GCCG
                                ||| ||||||||   ||||
                                AGG TCCGAGGA   TGGT
                                  T      _____
GAM345  LOC150157 5'  CGGCAGGGCTGGAGGCCTGGGA 84876         _   T  A_
                                TCCCAGGC TCC GT  TGCCG
                                |||||||| ||| ||  |||||
                                AGGGTCCG AGG CG  ACGGC
                                     G   T  GG
GAM345  LOC150538 3'  GCATAGGAGCTGAGCATAGGA  79936     CA_____      GT
                                TCC      GGCTCCT  ATGC
                                |||      |||||||  ||||
                                AGG      TCGAGGA  TACG
                                  ATACGAG      __
GAM345  LOC150935 3'  CGTGGAGGAGCCTTGGGA     80033      _      G
                                TCCCA GGCTCCT TATG
                                ||||| ||||||| ||||
                                AGGGT CCGAGGA GTGC
                                   T      G
GAM345  LOC151009 5'  CGGCAGCACAGTCTGGGA     85195         CC   A
                                TCCCAGGCT  TGT TGCCG
                                |||||||||  ||| |||||
                                AGGGTCTGA  ACG ACGGC
                                     C_   _
GAM345  LOC151102 3'  GCTCCCAGGGCCTGGGA      85221         T    TAT
                                TCCCAGGC CCTG   GC
                                |||||||| ||||   ||
                                AGGGTCCG GGAC   CG
                                     _    CCT
GAM345  LOC151162 5'  CATTTAGGAAGCTGGGA      85241       GC     T
                                TCCCAG  TCCTG ATG
                                ||||||  ||||| |||
                                AGGGTC  AGGAT TAC
                                   GA     T
GAM345  LOC151963 5'  GGCCAAAGCCTGGGA        80403         CC  TAT
                                TCCCAGGCT  TG   GCC
                                |||||||||  ||   |||
                                AGGGTCCGA  AC   CGG
                                     A_  ___
GAM345  LOC153243 3'  CGGCTGGAGTCTGGGA       80795          TGTAT
                                TCCCAGGCTCC    GCCG
                                ||||||||||     ||||
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                                AGGGTCTGAGG    CGGC
                                      T____
GAM345  LOC153711 5'  TCAGCTCTCTGGACCTGGGA  86137       C  TGTAT  C
                                TCCCAGG TCC    GC GA
                                ||||||| |||    || ||
                                AGGGTCC AGG    CG CT
                                   _  TCTCT  A
GAM345  LOC155061 5'  CAGGAAGGAGCCTGGGA    81265         GTA
                                TCCCAGGCTCCT  TG
                                ||||||||||||  ||
                                AGGGTCCGAGGA  AC
                                      AGG
GAM345  LOC155179 3'  GGCGTGCGGAGCCTGTGGA  81318    _      T
                                TCC CAGGCTCC GTATGCC
                                ||| |||||||| |||||||
                                AGG GTCCGAGG CGTGCGG
                                  T      _
GAM345  LOC157623 5'  TCAGCCACTATGAGCCTGGGA 81501        CT_ AT  C
                                TCCCAGGCTC  GT  GC GA
                                ||||||||||  ||  || ||
                                AGGGTCCGAG  CA  CG CT
                                      TAT  C_  A
GAM345  LOC157860 3'  TCAGCAGAAAGAGACCCTGAGA 86570   C   C  _  GTA   C
                                TC CAGG TC CT   TGC GA
                                || |||| || ||   ||| ||
                                AG GTCC AG GA   ACG CT
                                 A   C  A  AAG   A
GAM345  LOC160646 3'  TCGACAGGGAGCCTGGG    82231         GTA  C
                                CCCAGGCTCCT   TG CGA
                                ||||||||||   || |||
                                GGGTCCGAGGG   AC GCT
                                      ___  A
GAM345  LOC161528 3'  TCGGCACTCCCAGGCTGGGA  82280      GCT   TA__
                                TCCCAG   CCTG    TGCCGA
                                ||||||   ||||    ||||||
                                AGGGTC   GGAC    ACGGCT
                                   ___    CCTC
GAM345  LOC164714 3'  GTGTGGGGGAGCCTGG     87238         G
                                CCAGGCTCCT TATGC
                                |||||||||| |||||
                                GGTCCGAGGG GTGTG
                                      G
GAM345  LOC165741 3'  ACAGGAAAGCTTGGGA     87253        __
                                TCCCAGGC  TCCTGT
                                ||||||||  ||||||
                                AGGGTTCG  AGGACA
                                     AA
GAM345  LOC196707 3'  GCAGCAGAGAGCCTGGGA   87528         _   A
                                TCCCAGGCTC CTGT TGC
                                |||||||||| |||| |||
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                                AGGGTCCGAG GACG ACG
                                     A   _
GAM345  LOC196890 5'  CGGCGGGGCTGGAGGCCTGGGA 89646        _  T A_
                                TCCCAGGC TCC GT  TGCCG
                                ||||||| ||| ||  |||||
                                AGGGTCCG AGG CG  GCGGC
                                     G  T  GG
GAM345  LOC197201 3'  GGCTTGGGAGCCTGGGG    87945          GTAT
                                TCCCAGGCTCCT   GCC
                                ||||||||||||   |||
                                GGGGTCCGAGGG   CGG
                                      TT__
GAM345  LOC197257 5'  GGTCTGCAACCTGGGA     87963       CTCC   T
                                TCCCAGG   TGTA GCC
                                |||||||   |||| |||
                                AGGGTCC   ACGT TGG
                                     A___   C
GAM345  LOC200093 5'  TCGGCTCGGGAGGCCTGGGA  63101        _    TAT
                                TCCCAGGC TCCTG  GCCGA
                                |||||||| |||||  |||||
                                AGGGTCCG AGGGC  CGGCT
                                     G    T__
GAM345  LOC201304 3'  TGGGACAGAACCTGGGA    88233       CTC   ATG
                                TCCCAGG  CTGT  CCG
                                |||||||  ||||  |||
                                AGGGTCC  GACA  GGT
                                     AA_   G__
GAM345  LOC203377 5'  CATTTAGGAAGCTGGGA    90579       GC    T
                                TCCCAG  TCCTG ATG
                                ||||||  ||||| |||
                                AGGGTC  AGGAT TAC
                                    GA    T
GAM345  LOC203397 3'  CGGCAGAGGACCCAGGA    89351     CA  C   GTA
                                TCC  GG TCCT   TGCCG
                                |||  || ||||  |||||
                                AGG  CC AGGA   ACGGC
                                  AC  _   G__
GAM345  LOC203542 5'  CGGCGCGGAGAGCGCGGGA  89383     AG   _   AT
                                TCCC  GCTC CTGT  GCCG
                                ||||  |||| ||||  ||||
                                AGGG  CGAG GGCG  CGGC
                                  CG   A   __
GAM345  LOC203668 5'  TCAGCACCTGAAGCCTGGGG  89437        CCTGTA  C
                                TCCCAGGCT     TGC GA
                                |||||||||     ||| ||
                                GGGGTCCGA     ACG CT
                                     AGTCC_  A
GAM345  LOC219654 3'  GGCCAGGAGCCCAGGG     91307     A_      TAT
                                CCC  GGCTCCTG   GCC
                                |||  ||||||||   |||
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                                GGG  CCGAGGAC   CGG
                                  AC       ___
GAM345  LOC219918 5'  CGGCATACAAGCTTATGGA   91540    C_    CC
                                TCC  AGGCT  TGTATGCCG
                                |||  |||||  |||||||||
                                AGG  TTCGA  ACATACGGC
                                  TA    __
GAM345  LOC220071 5'  CGGCATACAAGCTTATGGA   93436    C_    CC
                                TCC  AGGCT  TGTATGCCG
                                |||  |||||  |||||||||
                                AGG  TTCGA  ACATACGGC
                                  TA    __
GAM345  LOC220537 3'  TCGGCACTCCCAGGCTGGGA  90731      GCT   TA__
                                TCCCAG   CCTG   TGCCGA
                                ||||||   ||||   ||||||
                                AGGGTC   GGAC   ACGGCT
                                   ___   CCTC
GAM345  LOC221463 3'  TCAGCATCAGCCTGGGA    92076       CCT T   C
                                TCCCAGGCT   G ATGC GA
                                |||||||||   | |||| ||
                                AGGGTCCGA   C TACG CT
                                    ___ _   A
GAM345  LOC245727 5'  TCGGCACTCCCAGGCTGGGA  91130      GCT   TA__
                                TCCCAG   CCTG   TGCCGA
                                ||||||   ||||   ||||||
                                AGGGTC   GGAC   ACGGCT
                                   ___   CCTC
GAM345  LOC245771 3'  TCAGCTACAGAGCTGG     92897     G   C   T  C
                                CCAG CTC TGTA GC GA
                                |||| ||| |||| || ||
                                GGTC GAG ACAT CG CT
                                  _  _   _ A
GAM345  LOC253609 5'  GGCCAGGAGCCCGGG      96761     A      TAT
                                CCC GGCTCCTG   GCC
                                |||  ||||||||   |||
                                GGG CCGAGGAC   CGG
                                  C       ___
GAM345  LOC253731 5'  CATTAGAAGTCTGGGA     97488        C   T
                                TCCCAGGCT CTG ATG
                                ||||||||| ||| |||
                                AGGGTCTGA GAT TAC
                                    A  _
GAM345  LOC254102 5'  CGGGTCGGAGCCTGGGA    94743         T T  G
                                TCCCAGGCTCC G AT CCG
                                |||||||||||  | || |||
                                AGGGTCCGAGG C TG GGC
                                     _ _  _
GAM345  LOC254532 3'  GGAATGAGGAGCCTTGGA   96639     C      G   G
                                TCC AGGCTCCT TAT CC
                                |||  |||||||| ||| ||
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                                AGG TCCGAGGA GTA GG
                                  T       _  A
GAM345  LOC254552 5'  GGCTACAGGAGCCCGGGG    94776     A       T
                                TCCC GGCTCCTGTA GCC
                                |||| |||||||||| |||
                                GGGG CCGAGGACAT CGG
                                  C        _
GAM345  LOC255042 3'  GCTACTCGGGAGCCTGAGG   95320    _       TAT_
                                CC CAGGCTCCTG   GC
                                || ||||||||||   ||
                                GG GTCCGAGGGC   CG
                                 A        TCAT
GAM345  LOC255189 5'  CGGCACCAGGCTCGGGA     96588     AG  TC   TA
                                TCCC  GC  CTG  TGCCG
                                ||||  ||  |||  |||||
                                AGGG  CG  GAC  ACGGC
                                  CT  __   C_
GAM345  LOC255452 3'  GGCCGCAGAGCTTGGGA     97540        C   AT
                                TCCCAGGCTC TGT  GCC
                                |||||||||| |||  |||
                                AGGGTTCGAG ACG  CGG
                                      _  C_
GAM345  LOC255515 5'  CGGCATACAAGCTTATGGA   96095    C_    CC
                                TCC  AGGCT  TGTATGCCG
                                |||  |||||  |||||||||
                                AGG  TTCGA  ACATACGGC
                                  TA    __
GAM345  LOC256041 5'  GTGGAAGGAGCCTTGGA     97607    C      GTA
                                TCC AGGCTCCT   TGC
                                ||| ||||||||   |||
                                AGG TCCGAGGA   GTG
                                  T       AG_
GAM345  LOC256273 3'  TGGGAAGGAGCCTGGGA     96409         GTATG
                                TCCCAGGCTCCT    CCG
                                ||||||||||||    |||
                                AGGGTCCGAGGA    GGT
                                      AG___
GAM345  LOC55971  3'  CGGCCAGGAGCCTGG       38128         TAT
                                CCAGGCTCCTG   GCCG
                                ||||||||||   ||||
                                GGTCCGAGGAC   CGGC
                                      ___
GAM345  LOC90288  3'  CACACAGGAGCCCTGG      62083      _     A
                                CCAGG CTCCTGT TG
                                ||||| ||||||| ||
                                GGTCC GAGGACA AC
                                   C      C
GAM345  LOC91252  3'  GCACAGGGGCCAGGGA      65340     A       AT
                                TCCC GGCTCCTGT  GC
                                |||| |||||||||  ||
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                                AGGG CCGGGGACA  CG
                                  A       __
GAM345  LOC91828  3'  TCAGCCAGGAGCCCAGGG    67278    A_      TAT  C
                                CCC  GGCTCCTG   GC GA
                                |||  ||||||||   || ||
                                GGG  CCGAGGAC   CG CT
                                  AC       ____  A
GAM345  LOC92095  3'  GGGTGCAGGAGCCTGGG     68095           G
                                CCCAGGCTCCTGTAT CC
                                |||||||||||||| ||
                                GGGTCCGAGGACGTG GG
                                                _
GAM345  LOC92096  3'  GGCACAGGAGCCTGGG      68100          AT
                                CCCAGGCTCCTGT  GCC
                                ||||||||||||  |||
                                GGGTCCGAGGACA  CGG
                                                __
GAM345  LOC92997  5'  GTGGAAGGAGCCTGGGA     71091          GTA
                                TCCCAGGCTCCT   TGC
                                ||||||||||||   |||
                                AGGGTCCGAGGA   GTG
                                       AG_
GAM345  LOC93109  3'  TCAGCTCAGAGCCCAGGG    71418    A_    C  TAT  C
                                CCC  GGCTC TG   GC GA
                                |||  ||||| ||   || ||
                                GGG  CCGAG AC   CG CT
                                  AC     _ T__  A
GAM345  LOC93259  5'  CATGCCAACAGCCTGGGA    71809        CCT_
                                TCCCAGGCT    GTATG
                                |||||||||    |||||
                                AGGGTCCGA    CGTAC
                                      CAAC
GAM346  ACOX1     5'  GGCCACTGCCTATGCCTTCCA  87367    A  A      TGTGA
                                TG AAG CATGGGT    TGGCC
                                || ||| |||||||     |||||
                                AC TTC GTATCCG    ACCGG
                                 C   C      TC____
GAM346  ADAM8     3'  GCCATGCGTTCCAGCCTTCCA  6616     A  ACA  GT   G
                                TG AAG   TGG  TGT ATGGC
                                || |||   |||  ||| |||||
                                AC TTC   ACC  GCG TACCG
                                 C   CG_   TT   _
GAM346  ARHGEF6   3'  CCATCACATGCCTCCCCTC   68200    CAT_   _
                                GA    GGGT TGTGATGG
                                ||    |||| ||||||||
                                CT    TCCG ACACTACC
                                 CCCC    T
GAM346  CHGB      3'  GCCATCACATGATCTGTTTTTC 8429         T  GT_
          A                      TGAAAGACA GG   TGTGATGGC
                                |||||||||  ||   |||||||||
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                                ACTTTTTGT CT   ACACTACCG
                                     _ AGT
GAM346  CXCL16   3' GGCTCACTGCAACCCCCATCTC 41924    AA  CAT     GA _
           CCA                  TG  AGA   GGGTTGT  TG GCC
                                || |||   ||||||| || |||
                                AC  TCT   CCCAACG  AC CGG
                                 CC   ACC      TC  T
GAM346  EPHA3    3' CAAAACCCATGCATTTCA    17867      GA      G
                                TGAAA  CATGGGTT TG
                                ||||| |||||||| ||
                                ACTTT  GTACCCAA AC
                                   AC       A
GAM346  FGFR2    3' GCCACCATGTAACCCCTCTC   43357    CAT    __  A
                                GA   GGGTT  GTG TGGC
                                ||   |||||  ||| ||||
                                CT   CCCAA  TAC ACCG
                                 CTC    TG   C
GAM346  FGFR2    3' GCCACCATGTAACCCCTCTC   43369    CAT    __  A
                                GA   GGGTT  GTG TGGC
                                ||   |||||  ||| ||||
                                CT   CCCAA  TAC ACCG
                                 CTC    TG   C
GAM346  FGFR2    3' GCCACCATGTAACCCCTCTC   43480    CAT    __  A
                                GA   GGGTT  GTG TGGC
                                ||   |||||  ||| ||||
                                CT   CCCAA  TAC ACCG
                                 CTC    TG   C
GAM346  FGFR2    3' GCCACCATGTAACCCCTCTC   43490    CAT    __  A
                                GA   GGGTT  GTG TGGC
                                ||   |||||  ||| ||||
                                CT   CCCAA  TAC ACCG
                                 CTC    TG   C
GAM346  FGFR2    3' GCCACCATGTAACCCCTCTC   43500    CAT    __  A
                                GA   GGGTT  GTG TGGC
                                ||   |||||  ||| ||||
                                CT   CCCAA  TAC ACCG
                                 CTC    TG   C
GAM346  FGFR2    3' GCCACCATGTAACCCCTCTC   3761     CAT    __  A
                                GA   GGGTT  GTG TGGC
                                ||   |||||  ||| ||||
                                CT   CCCAA  TAC ACCG
                                 CTC    TG   C
GAM346  LAMC2    3' CCCACAACCCACAACCTTCCA  38147    A   ACA_      AT
                                TG AAG   TGGGTTGTG  GG
                                || |||   ||||||||| ||
                                AC TTC   ACCCAACAC  CC
                                 C  CAAC      __
GAM346  MMP1     5' GCCATCACTTACCTTG     10061    T   T_
                                CA GGGT  GTGATGGC
                                || ||||  ||||||||
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                                GT TCCA  CACTACCG
                                 _   TT
GAM346  PFN1     3'  GGCCATTACCCCAT       17229      TT
                                ATGGG  GTGATGGCC
                                |||||  |||||||||
                                TACCC  CATTACCGG
                                  __
GAM346  PPP1R3C  3'  CACAACTCACATCCTTCA    18248     A  CA
                                TGAA GA  TGGGTTGTG
                                ||||  ||  |||||||||
                                ACTT CT  ACTCAACAC
                                  C  AC
GAM346  SELENBP1 3'  TCGTAACCCTGTCCTTCA    14154     A    T
                                TGAA GACA GGGTTGTGA
                                |||| |||| |||||||||
                                ACTT CTGT CCCAATGCT
                                  C   _
GAM346  SNX5     3'  GCCATCACCTGGCCCATGTC   27034          __
                                GACATGGGTT  GTGATGGC
                                ||||||||||  ||||||||
                                CTGTACCCGG  CACTACCG
                                      TC
GAM346  TEM7     3'  GGCCACAAGACCCATGTCT    39889          G  A
                                AGACATGGGTT TG TGGCC
                                ||||||||||| || |||||
                                TCTGTACCCAG AC ACCGG
                                      A  _
GAM346  TSN      3'  GGCCATTTGGCATACCTTTCA  16109       AC   GGTTGT
                                TGAAAG  ATG     GATGGCC
                                ||||||  |||     |||||||
                                ACTTTC  TAC     TTACCGG
                                   CA   GGT___
GAM346  WARS     5'  GGCCACCTCTGCAGTGTCTTCC 67287    A      GG  TGTGA
           A                     TG AAGACAT  GT     TGGCC
                                || |||||||  ||    |||||
                                AC TTCTGTG  CG     ACCGG
                                 C      A_  TCTCC
GAM346  DKFZP761I2123 5'  GCAACCATGTCTTCCA      48764    A       G
                                TG AAGACATGG TTGT
                                || |||||||| ||||
                                AC TTCTGTACC AACG
                                 C       _
GAM346  FLJ10103  5'  ACCATCCATGTCTTCCA     35815    A        T
                                TG AAGACATGGGT GT
                                || |||||||||| ||
                                AC TTCTGTACCTA CA
                                 C         C
GAM346  FLJ13782  3'  GGCCACCACGTTTATCTC    46170    C   GG T   A
                                GA ATG  T GTG TGGCC
                                || |||  | ||| |||||
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                                CT TAT  G CAC ACCGG
                                 C   TT _   C
GAM346  FLJ14326  3'  GGCCATCACGGCTCTCCTC   49812    CAT
                                GA   GGGTTGTGATGGCC
                                ||   ||||||||||||||
                                CT   CTCGGCACTACCGG
                                 CCT
GAM346  FLJ14525  3'  CAGAAGCCATGTCTCTCA    51413     A      G  G
                                TGA AGACATGG TT TG
                                ||| |||||||| || ||
                                ACT TCTGTACC AA AC
                                  C       G  G
GAM346  FLJ20644  5'  CATTTTCCATCTCTTTCA    35492       C    TT
                                TGAAAGA ATGGG  GTG
                                |||||||  |||||  |||
                                ACTTTCT TACCT  TAC
                                    C    TT
GAM346  FLJ21324  5'  CACGTTCCTGCCTTTCA     91191       A  T  GT
                                TGAAAG CA GG  TGTG
                                ||||||  || ||  ||||
                                ACTTTC GT CC  GCAC
                                   C  _  TT
GAM346  HIF1AN    3'  GGCCATCATTCACATCTATTCA 61976     _  CA   GTT
                                TGAA AGA  TGG   GTGATGGCC
                                ||||  |||  |||   |||||||||
                                ACTT TCT  ACT   TACTACCGG
                                  A   AC  ___
GAM346  KIAA1303  3'  GCCAGGCCCACCACCTCTCA   66002     A  ACA_     GTGA
                                TGA AG    TGGGTT    TGGC
                                |||  ||    ||||||    ||||
                                ACT TC    ACCCGG    ACCG
                                  C  CACC     ____
GAM346  KIAA1764  3'  GCCATCTCCACATCACTCA    69289     AA  CA    TTGT
                                TGA  GA  TGGG    GATGGC
                                |||   ||  ||||    ||||||
                                ACT  CT  ACCT    CTACCG
                                  CA  AC   ____
GAM346  MFN2      3'  GCCATCACTCATCTTTG     29601     T   T_
                                CA GGGT  GTGATGGC
                                ||  ||||  ||||||||
                                GT TCTA  CACTACCG
                                 T   CT
GAM346  NPD009    5'  GCCATCGCATCATGTTTCCCA  95050     AA      GT
                                TG  AGACATGG  TGTGATGGC
                                ||  ||||||||  |||||||||
                                AC  TTTGTACT  ACGCTACCG
                                 CC       __
GAM346  SAMHD1    3'  GGCCATCACAGGCATCATCCTC 61316    C_   _ _
                                GA  ATGG GT TGTGATGGCC
                                ||  ||||  || ||||||||||
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                                CT  TACT CG ACACTACCGG
                                 CC    A  G
GAM346  SV2      3'  CACAACCCTGCCTCCCA     29306    AA  A  T
                                TG  AG CA GGGTTGTG
                                ||  || || ||||||||
                                AC  TC GT CCCAACAC
                                 CC  C  _
GAM346  TSPEAR   3'  CCACACCTGCCACGGTCTTCCA 58718    A    ATG   T_  A
                                TG AAGAC   GGT  GTG TGG
                                || |||||   |||  ||| |||
                                AC TTCTG   CCG  CAC ACC
                                 C    GCA   TC   _
GAM346  UBE3B    3'  GGCCACCCGTCTCCACAGTCCT 76922      A   A  _  TTG  A_
           TCA                    TGAA GAC TG GG   TG  TGGCC
                                |||| ||| || ||   ||  |||||
                                ACTT CTG AC CC   GC  ACCGG
                                  C   _  A  TCT  CC
GAM346  LOC120973 5'  GCCATCACCAATCTTTCA    75554       CA   GTTG
                                TGAAAGA  TGG    TGATGGC
                                |||||||  |||    |||||||
                                ACTTTCT  ACC    ACTACCG
                                   A_  _____
GAM346  LOC145813 3'  GCCATCACGTATCCCTG     83509    T   _
                                CA GGGT TGTGATGGC
                                || |||| |||||||||
                                GT CCTA GCACTACCG
                                 C    T
GAM346  LOC146337 3'  GCCATCACCCCATGCCGTC   83660    AAGA     TT
                                GA    CATGGG  GTGATGGC
                                ||    ||||||  ||||||||
                                CT    GTACCC  CACTACCG
                                 GCC_     __
GAM346  LOC146774 3'  GGCCATCAGAAATGTCTTTT   78096         GGG  G
                                GAAAGACAT   TT TGATGGCC
                                |||||||||   || ||||||||
                                TTTTCTGTA   AA ACTACCGG
                                     ___  G
GAM346  LOC149111 3'  CCATCACAGAGTCTTT      79180       ATGGG
                                AAAGAC    TTGTGATGG
                                ||||||    |||||||||
                                TTTCTG    GACACTACC
                                   A_____
GAM346  LOC151405 5'  CCATCACCAAACATCTTATCA  85336     _   CA  GGTT
                                TGA AAGA  TG    GTGATGG
                                ||| ||||  ||    |||||||
                                ACT TTCT  AC    CACTACC
                                  A    __  AAAC
GAM346  LOC157858 3'  CCACCACCCTCCATGCCT    86585    A     TT   A
                                AG CATGGG  GTG TGG
                                || ||||||  ||| |||
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                                TC GTACCT  CAC ACC
                                 C     CC   C
GAM346  LOC222234 3'  GGCCACCCACATGCCTTCTC   94246    CAT   _   A_
                                GA   GGGT TGTG  TGGCC
                                ||   |||| ||||  |||||
                                CT   TCCG ACAC  ACCGG
                                 CT_    T    CC
GAM346  LOC92609  5'  GCAACCCATCCCTTCA      72846      A AC
                                TGAA G  ATGGGTTGT
                                |||| |  |||||||||
                                ACTT C  TACCCAACG
                                  _ CC
GAM347  GRID1     3'  CTTCAGACACTGCAAATAATAA 68497         CT     C__
           TC                     GATTATTA  TTTGTA   TCTGAAG
                                |||||||  ||||||   |||||||
                                CTAATAAT  AAACGT   AGACTTC
                                     __      CAC
GAM347  LOC255294 5'  CTTCAGAGGAGAATAATGA    94473       C    GTA
                                TTATTA TTTT   CTCTGAAG
                                ||||||| ||||   ||||||||
                                AGTAAT AGAG   GAGACTTC
                                   A   ___
GAM348  DFFB      3'  ACCCCCCAATGTCTGTTGA    87372      _        CA
                                TCAA AGACATTGGG  GT
                                |||| ||||||||||  ||
                                AGTT TCTGTAACCC  CA
                                  G         CC
GAM348  KLRD1     3'  GAGTCTATAAAATGTTTTT    9620          GGGCA
                                AAAGACATT    GTAGACTC
                                |||||||||    ||||||||
                                TTTTTGTAA    TATCTGAG
                                     AA___
GAM348  KLRD1     3'  GAGTCTATAAAATGTTTTT    23679         GGGCA
                                AAAGACATT    GTAGACTC
                                |||||||||    ||||||||
                                TTTTTGTAA    TATCTGAG
                                     AA___
GAM348  PCTP      3'  ACCACCCAATGTCTCTGG     41093     A        CA
                                TCA AGACATTGGG  GT
                                ||| ||||||||||  ||
                                GGT TCTGTAACCC  CA
                                  C         AC
GAM348  PIGA      3'  GAATCTAAATCATGTCTTTGA  40005          T  GCAG   C
                                TCAAAGACAT GG    TAGA TC
                                |||||||||| ||    |||| ||
                                AGTTTCTGTA CT    ATCT AG
                                     _  AA__    A
GAM348  PIGA      3'  GAATCTAAATCATGTCTTTGA  40014          T  GCAG   C
                                TCAAAGACAT GG    TAGA TC
                                |||||||||| ||    |||| ||
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                                AGTTTCTGTA CT    ATCT AG
                                      _ AA__    A
GAM348  PIGA     3'  GAATCTAAATCATGTCTTTGA  10553         T  GCAG    C
                                TCAAAGACAT GG    TAGA TC
                                |||||||||| ||    |||| ||
                                AGTTTCTGTA CT    ATCT AG
                                      _ AA__    A
GAM348  PXMP3    5'  CTAACCTGCAGTGTCTCTGA  4347     A     GG   __
                                TCA AGACATT  GCAG  TAG
                                ||| |||||||  ||||  |||
                                AGT TCTGTGA  CGTC  ATC
                                  C      __    CA
GAM348  TNC      5'  AGTCTACTCTGTGCTT     9286     A   TG  C
                                AAG CAT  GG AGTAGACT
                                ||| |||  || ||||||||
                                TTC GTG  TC TCATCTGA
                                  _  __  _
GAM348  UBE2A    3'  TTAAAGCCAATGTCTGCGA   12470    AA       G AG
                                TC  AGACATTGG C  TAG
                                ||  |||||||||  |  |||
                                AG  TCTGTAACC G  ATT
                                 CG        _ AA
GAM348  UBE4A    3'  AGTCTACTGGGTGCCTTT    16558     A   GGG
                                AAAG CATT   CAGTAGACT
                                |||| ||||   |||||||||
                                TTTC GTGG   GTCATCTGA
                                  C   ____
GAM348  DKFZP586F1318 3'  AGTCTGACTACCATGTCTTT   31618        T  GC  _
                                AAAGACAT GG  AGT AGACT
                                |||||||| ||  ||| |||||
                                TTTCTGTA CC  TCA TCTGA
                                     _ A_   G
GAM348  FLJ20085  3'  GAGTCTACAAAAATGTTTTT   34517         GGGCA
                                AAAGACATT    GTAGACTC
                                |||||||||    ||||||||
                                TTTTTGTAA    CATCTGAG
                                     AAA__
GAM348  FLJ25179  5'  CTGCCCAATGTCCCTGG     58355     AA
                                TCA  GACATTGGGCAG
                                |||  ||||||||||||
                                GGT  CTGTAACCCGTC
                                  CC
GAM348  HYA22    3'  ACTGCCTTAAATGTCTTGA    19417     A    __
                                TCAA GACATT  GGGCAGT
                                |||| ||||||  |||||||
                                AGTT CTGTAA  TCCGTCA
                                  _     AT
GAM348  KIAA0329  3'  GAGTCTACTAATTATTGCCTTT 29275      A  T   GC
          G                      CAAAG CA TGG  AGTAGACTC
                                |||||  || |||  |||||||||
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                                GTTTC GT ATT  TCATCTGAG
                                   C  T   AA
GAM348  KIAA0685  3'  GAGTCCATTTTTAATGTTCTGA 27963     AA       C   A
                                TCA  GACATTGGG AGT GACTC
                                |||  ||||||||| ||| |||||
                                AGT  TTGTAATTT TTA CTGAG
                                  C_       _   C
GAM348  KIAA0918  3'  AGTCTCTATACAATGTCTTT   73132         GGC  T
                                AAAGACATTG   AG AGACT
                                ||||||||||   || |||||
                                TTTCTGTAAC   TC TCTGA
                                      ATA  _
GAM348  KIAA1157  3'  CTCCCATGTCTTTGA      72241          T   C
                                TCAAAGACAT GGG AG
                                |||||||||| ||| ||
                                AGTTTCTGTA CCC TC

                                      _  _
GAM348  MAPKAP1   3'  GCCCACCCGGTGTCCTGA    44141     AA       CA_
                                TCA  GACATTGGG   GT
                                |||  |||||||||   ||
                                AGT  CTGTGGCCC   CG
                                  C_       ACC
GAM348  SURB7     3'  GAGTCTACTGATAATCTC    14947    C    GG
                                GA ATTG  CAGTAGACTC
                                || ||||  ||||||||||
                                CT TAAT  GTCATCTGAG
                                 C   A_
GAM348  TRIM6     3'  GCCACCAATGTCTGTTGA    54139     _       GCA
                                TCAA AGACATTGG   GT
                                |||| |||||||||   ||
                                AGTT TCTGTAACC   CG
                                   G       AC_
GAM348  LOC129080 3'  GCTGCCCAATCCTCTGA     55979     A  AC
                                TCA AG  ATTGGGCAGT
                                ||| ||  ||||||||||
                                AGT TC  TAACCCGTCG
                                  C  C_
GAM348  LOC129831 3'  ACAACCCCAATGTCCATGA   74890     AA       CA_
                                TCA  GACATTGGG   GT
                                |||  |||||||||   ||
                                AGT  CTGTAACCC   CA
                                  AC       CAA
GAM348  LOC149773 5'  GAGTCTACCGACTGTCTGTCTC 79477   AA    TTG    ____
          AGA                     C  AGACA   GGCAGT    AGACTC
                                |  |||||   ||||||   ||||||
                                G  TCTGT   CTGTCA    TCTGAG
                                 AC    ___     GCCA
GAM348  LOC222160 3'  CTGCCCAATATGTTTGA     94124       GAC
                                TCAAA   ATTGGGCAG
                                |||||   |||||||||
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                                AGTTT  TAACCCGTC
                                   GTA
GAM349  CA12     3'  CAGACAAGAATGTGCACTC   6876     C        AAG
                                GA TGCACATTCT  TTG
                                || ||||||||||  |||
                                CT ACGTGTAAGA  GAC
                                 C         ACA
GAM349  DNASE1L1 5'  TAACTCAGAAGTGTGCAG    22079          _  A
                                CTGCACATT CT AGTTG
                                ||||||||| || |||||
                                GACGTGTGA GA TCAAT
                                      A  C
GAM349  GAS1     3'  GTCAACTTGGTGTAG       8993        ATTC
                                CTGCAC   TAAGTTGAC
                                ||||||   |||||||||
                                GATGTG   GTTCAACTG
                                  ____
GAM349  GHR      3'  CAGATCAACTTACCAGGCA   3878     ACATTC      C
                                TGC     TAAGTTGA CTG
                                |||     |||||||| |||
                                ACG     ATTCAACT GAC
                                  GACC__       A
GAM349  KIAA0442 3'  AGGTCAACCTTGTGGAG    31467    G   TTCTAA
                                CT CACA     GTTGACCT
                                || ||||     ||||||||
                                GA GTGT     CAACTGGA
                                 G   TC____
GAM349  RASGRP1  3'  CAGGTCAACTTATAGTTGTAG  19204      C  C
                                CTGCA ATT TAAGTTGACCTG
                                ||||| ||| ||||||||||||
                                GATGT TGA ATTCAACTGGAC
                                   _  T
GAM349  TSN      3'  ACTTAAAATGTGCAGT      16100          C
                                ACTGCACATT TAAGT
                                |||||||||| |||||
                                TGACGTGTAA ATTCA
                                      A
GAM349  FLJ10702 3'  TTAACTTAAAATGTGCA     36443         C
                                TGCACATT TAAGTTGA
                                |||||||| ||||||||
                                ACGTGTAA ATTCAATT
                                    A
GAM349  RPL13A   3'  CAGCTGTTAGAATGTGCA    24852          __
                                TGCACATTCTA  AGTTG
                                ||||||||||  |||||
                                ACGTGTAAGAT  TCGAC
                                       TG
GAM349  LOC169026 3'  CAGGTCAACTTTACCACCAG  82722     CACATTCT
                                CTG       AAGTTGACCTG
                                |||       ||||||||||
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                                GAC       TTCAACTGGAC
                                  CACCAT__
GAM349  LOC221178 3'  CAGATCAACTTGGTGTCCCAGT 93530      C_   TT       C
            C                      GACTG  ACA  CTAAGTTGA CTG
                                   |||||  |||  ||||||||| |||
                                   CTGAC  TGT  GGTTCAACT GAC
                                     CC   __       A
GAM349  LOC256307 3'  GTCATTGGAATGGCAG      97055      A      GT
                                   CTGC CATTCTAA  TGAC
                                   |||| ||||||||  ||||
                                   GACG GTAAGGTT  ACTG
                                     _      __
GAM349  LOC51231  3'  AGCCCTGGAATGTGCATTC    33170    C        A_
                                   GA TGCACATTCTA  GTT
                                   || ||||||||||  |||
                                   CT ACGTGTAAGGT  CGA
                                    T         CC
GAM350  DEC1      3'  CTGTGTCCCTGAGGCAC     33798         TGCA
                                   GTGCCTTAG    GACACAG
                                   |||||||||    |||||||
                                   CACGGAGTC    CTGTGTC
                                        C___
GAM350  PXN       3'  CTGTGTCTGATTTTGGC     11161     TT   G
                                   GCC  AGT CAGACACAG
                                   |||  ||| |||||||||
                                   CGG  TTA GTCTGTGTC
                                     TT   _
GAM350  ARHGEF10  3'  CTGTGTCTGCTTTAGCACG   60421      CT   T
                                   CGTGC  TAG GCAGACACAG
                                   |||||  ||| ||||||||||
                                   GCACG  ATT CGTCTGTGTC
                                      __   T
GAM350  COTL1     3'  CTGCGTCTGCACCACAC     87954     CCTTA      A
                                   GTG    GTGCAGAC CAG
                                   |||    |||||||| |||
                                   CAC    CACGTCTG GTC
                                     AC___       C
GAM350  DKFZp761N0624 3'  CTGTGTCTGATCTAAACGT    50180     GCC    TG
                                   ACGT   TTAG  CAGACACAG
                                   ||||   ||||  |||||||||
                                   TGCA   AATC  GTCTGTGTC
                                      ___    TA
GAM350  KIAA1938  5'  CTGTGCGGCTGAAAGCACGTTA 92196        C  AGT  AGA
                                   TAACGTGC TT   GC   CACAG
                                   |||||||| ||   ||   |||||
                                   ATTGCACG AA   CG   GTGTC
                                        A  GT_  GC_
GAM350  PAIP1     3'  CTGTGTCTGCTAATACAGTTA  66924      G  CC   GT
                                   TAAC TG  TTA  GCAGACACAG
                                   |||| ||  |||  ||||||||||
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                                ATTG AC  AAT  CGTCTGTGTC
                                  _ AT   __
GAM350  RAB20     3'  TGCGTCTGCACCTGCAC     35157      CTTA       A
                                GTGC    GTGCAGAC CA
                                ||||    |||||||| ||
                                CACG    CACGTCTG GT
                                  TC__       C
GAM350  LOC143677 3'  GTGTCTGCAGCACG        82980      CTTAG
                                CGTGC    TGCAGACAC
                                ||||||    |||||||||
                                GCACG    ACGTCTGTG
                                  _____
GAM350  LOC145813 5'  CTGCGTGACCTAAGGCACGT   83506          ____
                                ACGTGCCTTAG    TGCAG
                                ||||||||||    |||||
                                TGCACGGAATC    GCGTC
                                       CAGT
GAM350  LOC254430 5'  CTGCGTCTGCACTACGGAGC   97579    G  T        A
                                GT CC TAGTGCAGAC CAG
                                || || |||||||||| |||
                                CG GG ATCACGTCTG GTC
                                 A  C         C
GAM351  FCN2      3'  AACAACCAGTCCTTCTCCACCA 31729    A      _   TA
                                TG TGGAGGAG ATTG  TGTT
                                || |||||||| ||||  ||||
                                AC ACCTCTTC TGAC  ACAA
                                 C       C    CA
GAM351  SCA1      5'  ACAGCAATCTCCTCCTCCA    4400     AT         A
                                TG  GGAGGAGATTGT TGT
                                ||  ||||||||||| |||
                                AC  CCTCCTCTAACG ACA
                                 CT          _
GAM351  STS       5'  TGCAATCTCCTCCATCA     4456
                                TGATGGAGGAGATTGTA
                                ||||||||||||||||
                                ACTACCTCCTCTAACGT

GAM351  TNFRSF4   3'  ATAACATACAGTGCCGCCACCA 12450    A   A  AG
                                TG TGG GG  ATTGTATGTTAT
                                || ||| ||  ||||||||||||
                                AC ACC CC  TGACATACAATA
                                 C  G  G_
GAM351  CAPN6     3'  TATAAATGCCACCTCCTCCAT  26607         ATT    G
                                ATGGAGGAG   GTAT TTATA
                                |||||||||   |||| |||||
                                TACCTCCTC   CGTA AATAT
                                      CAC   _
GAM351  KIAA1671  3'  TATAACCTTGTCTCCTCCAGCA 65690    A         TGTAT
                                TG TGGAGGAGAT    GTTATA
                                || ||||||||||    ||||||
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                                AC ACCTCCTCTG    CAATAT
                                 G        TTC__
GAM351  SP2     3'  ACAACCTCTCCTCCAGCA    11884    A      __
                                TG TGGAGGAGA  TTGT
                                || |||||||||  ||||
                                AC ACCTCCTCT  AACA
                                 G        CC
GAM351  LOC149271 3'  TACAACCTCCCCATCA     79247       A   A
                                TGATGG GGAG TTGTA
                                |||||| |||| |||||
                                ACTACC CCTC AACAT
                                   _   C
GAM351  LOC51651  3'  TATGACAACAACCCCTCCATCA 32183         AGA   A
                                TGATGGAGG   TTGT TGTTATA
                                |||||||||   |||| |||||||
                                ACTACCTCC   AACA ACAGTAT
                                      CC_   _
GAM352  CAPZA1    3'  ACCAAAGTGAAAGGATAACT   72622         GTTA   C
                                AGTTATCCTT    GCTT GGT
                                ||||||||||    |||| |||
                                TCAATAGGAA    TGAA CCA
                                      AG__    A
GAM352  LOC136288 3'  ACTTGGCTAACAAACACAACTA 75249       ATCC       TC
                                TAGTT    TTGTTAGCT  GGT
                                |||||    |||||||||  |||
                                ATCAA    AACAATCGG  TCA
                                   CACA        T_
GAM353  ARCN1     3'  AGACTGCACTCTCTGTCA    7970          CA_
                                TGACAGAGA   CAGTTT
                                |||||||||   ||||||
                                ACTGTCTCT   GTCAGA
                                      CAC
GAM353  CBFA2T2   3'  GAGCAAAACTCTGTCT      17466       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                   C
GAM353  CTLA4     3'  CAGAGCTGGGATGTTTCTGTCA 17807          CAGTTTT
                                TGACAGAGACA      GCTCTG
                                ||||||||||       ||||||
                                ACTGTCTTTGT      CGAGAC
                                      AGGGT__
GAM353  ITK       3'  CAGAACAGGAGTGATGTCTCTG 18674         _  G    C
                                CAGAGACA CA TTTTG TCTG
                                |||||||| || ||||| ||||
                                GTCTCTGT GT AGGAC AGAC
                                     A  G    A
GAM353  LAMP2     3'  GGTGAAACCCCATCTCTATCA  25716     C    CACA    TG
                                TGA AGAGA    GTTT  CT
                                ||| |||||    ||||  ||
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                                ACT TCTCT   CAAA  GG
                                  A    ACCC   GT
GAM353  MRPS12   3' CAAAGGGTGCCCCTCTGTCA  40865       A__  AG
                                TGACAGAG  CAC  TTTTG
                                ||||||||  |||  |||||
                                ACTGTCTC  GTG  GAAAC
                                    CCC   G_
GAM353  MRPS12   3' CAAAGGGTGCCCCTCTGTCA  52960       A__  AG
                                TGACAGAG  CAC  TTTTG
                                ||||||||  |||  |||||
                                ACTGTCTC  GTG  GAAAC
                                    CCC   G_
GAM353  MRPS12   3' CAAAGGGTGCCCCTCTGTCA  52963       A__  AG
                                TGACAGAG  CAC  TTTTG
                                ||||||||  |||  |||||
                                ACTGTCTC  GTG  GAAAC
                                    CCC   G_
GAM353  PDGFRB   5' CAGAGCCTGGAACTGTG    65969        __
                                CACAGTTTT  GCTCTG
                                |||||||||  ||||||
                                GTGTCAAGG  CGAGAC
                                     TC
GAM353  PTPRA    3' AGAGCGGTATCTCTG      55079       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A  _____
GAM353  PTPRA    3' AGAGCGGTATCTCTG      55087       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A  _____
GAM353  PTPRA    3' AGAGCGGTATCTCTG      11088       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A  _____
GAM353  RAD51L3  3' CAAAACTCAGGTATGTCTCTGT 56065        C_____
                                ACAGAGACA     AGTTTTG
                                |||||||||     |||||||
                                TGTCTCTGT     TCAAAAC
                                     ATGGAC
GAM353  TBL2     3' CAGAACTGTGTTCCATCA    52178     CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM353  TBL2     3' CAGAACTGTGTTCCATCA    24924     CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
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                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM353  AGTRL2   5'  CAGAGCAAGAACTGTTC     17691    C      _
                                GA ACAGTTTT GCTCTG
                                || |||||||| ||||||
                                CT TGTCAAGA CGAGAC
                                 _       A
GAM353  CABP5    3'  AGAGCGGTATCTTTGCCA    39079    A    C  AGTTT
                                TG CAGAGA AC    TGCTCT
                                || |||||| ||    ||||||
                                AC GTTTCT TG    GCGAGA
                                 C     A _____
GAM353  CUL4A    5'  AGAGCAGCACCTCCATCA    13149    CA   ACACA  T
                                TGA  GAG    GT TTGCTCT
                                |||  |||    || |||||||
                                ACT  CTC    CA GACGAGA
                                  AC  _____  C
GAM353  DKFZp761O17121 3'  CAGACAGCCCCTGTGTCTCTGT 50136           TT_  C
            C                    GACAGAGACACAG   TTG TCTG
                                |||||||||||||   ||| ||||
                                CTGTCTCTGTGTC   GAC AGAC
                                       CCC  _
GAM353  FLJ10375 3'  CAGAGGCCTGTGTCTGTGCCA  36073    A  G      TTTTG
                                TG CA AGACACAG    CTCTG
                                || || ||||||||    |||||
                                AC GT TCTGTGTC    GAGAC
                                 C  G       CG___
GAM353  FLJ10738 5'  CAAAGCCAGCCCTCTGTCA   36527        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
                                ACTGTCTC    CGAAAC
                                     CCGAC
GAM353  FLJ10803 3'  CAAAACAAAACTCTGTCA    36660        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
                                ACTGTCTC    CAAAAC
                                     AAAA_
GAM353  FLJ10842 3'  AAAGTGTGCTCTGTCA      36723        A   G
                                TGACAGAG CACA TTT
                                |||||||| |||| |||
                                ACTGTCTC GTGT AAA
                                     _   G
GAM353  FLJ13153 3'  CAGAGCCCAGCATCCATCTCTG 45555         CACA_  TT
            TCA                   TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                      ACCTA   CC
GAM353  FLJ20035 3'  CAAACCTGCCATGTTCTGTCA  34395        A ___  T
                                TGACAGAG CA   CAG TTTG
                                |||||||| ||   ||| ||||
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                                ACTGTCTT GT   GTC AAAC
                                     _ ACC   C
GAM353  FLJ22195  5'  CAGAGCAGAGGGAAGTCTCTGC 42800    A      ACAG
            CA                    TG CAGAGAC    TTTTGCTCTG
                                || |||||||    ||||||||||
                                AC GTCTCTG    GAGACGAGAC
                                 C      AAGG
GAM353  FLJ32191  5'  GAACTGCACCTCTGTCA     58411         ACA
                                TGACAGAG   CAGTTT
                                ||||||||   ||||||
                                ACTGTCTC   GTCAAG
                                     CAC
GAM353  KIAA1023  3'  CAAAGCTGTATCTGCTATCA   34255     C _   C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM353  KIAA1586  5'  AGTGTGATGTGTCTCTG     92326          GTT TG T
                                CAGAGACACA   T  C CT
                                ||||||||||   |  | ||
                                GTCTCTGTGT   A  G GA
                                     ___ GT T
GAM353  KIAA1754  3'  GACTAACGTCTCTGTCA     63236          AC_
                                TGACAGAGAC   AGTT
                                ||||||||||   ||||
                                ACTGTCTCTG   TCAG
                                     CAA
GAM353  LANCL2    3'  CAGAGTGCACTGCAGCTCTGTC 37995         ACA    TTT
            A                    TGACAGAG   CAGT   GCTCTG
                                ||||||||   ||||   ||||||
                                ACTGTCTC   GTCA   TGAGAC
                                     GAC    CG_
GAM353  LIG-1     3'  CAGAGCAGGCCTGTCCATGCCA 63893    A  GAGAC    TT
                                TG CA    ACAG  TTGCTCTG
                                || ||    ||||  ||||||||
                                AC GT    TGTC  GACGAGAC
                                 C  ACC__    CG
GAM353  MGC5242   3'  AGAGTACATGTCTCTG      43823         CAGTTT
                                CAGAGACA     TGCTCT
                                ||||||||     ||||||
                                GTCTCTGT     ATGAGA
                                     AC_____
GAM353  OSMR      3'  CAGAGCTGGCACCCTGTCA    14345       AGACA
                                TGACAG    CAGTTTTG
                                ||||||    ||||||||
                                ACTGTC    GTCGAGAC
                                    CCACG
GAM353  RAB21     3'  CAGAACAAAACTGTGGATC    30383    GA        C
                                GA  CACAGTTTTG TCTG
                                ||  |||||||||| ||||
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                                CT  GTGTCAAAAC AGAC
                                 AG         A
GAM353  SPTLC2    3'  CAGAGCAAAACTGTGTCTC   16799
                                GAGACACAGTTTTGCTCTG
                                ||||||||||||||||||
                                CTCTGTGTCAAAACGAGAC

GAM353  TGIF2     3'  GAGTCATGCTCTGTCA      41454         A  CAGTTT  _
                                TGACAGAG CA     TG CTC
                                |||||||| ||     || |||
                                ACTGTCTC GT     AC GAG
                                     _ _______  T
GAM353  WBSCR23   5'  GCTGACTGTGTCTCCATCA   46765     CA         TT
                                TGA  GAGACACAGTT  GC
                                |||  ||||||||||  ||
                                ACT  CTCTGTGTCAG  CG
                                  AC          T_
GAM353  LOC115129 3'  GGCAAAACCCCGTCTCT     73235       ACA
                                AGAGAC   GTTTTGCT
                                ||||||   ||||||||
                                TCTCTG   CAAAACGG
                                   CCC
GAM353  LOC129198 3'  AGCAAGCTGTGCCTC       76117     A       T
                                GAG CACAGTTT GCT
                                ||| |||||||| |||
                                CTC GTGTCGAA CGA
                                  C       _
GAM353  LOC145231 3'  GGTGAAACTATGTCTCT     83293        C     TG
                                AGAGACA AGTTT  CT
                                |||||||  |||||  ||
                                TCTCTGT TCAAA  GG
                                    A    GT
GAM353  LOC145483 3'  GAGCAAAACTCTGTCT      77243       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                   C
GAM353  LOC146713 3'  GAGCAAAACTCCGTCT      83726      AC
                                AGAC  AGTTTTGCTC
                                ||||  ||||||||||
                                TCTG  TCAAAACGAG
                                  CC
GAM353  LOC149175 3'  CAGGGTGAAACCACGTCTCT   79208        ACA    TG
                                AGAGAC   GTTT  CTCTG
                                ||||||   ||||  |||||
                                TCTCTG   CAAA  GGGAC
                                   CAC    GT
GAM353  LOC150299 3'  CAGAACCTGCATCTTTGTCA   84968         CA   _
                                TGACAGAGA  CAG TTTTG
                                |||||||||  ||| |||||
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                                ACTGTTTCT  GTC AAGAC
                                     AC   C
GAM353  LOC153277 3'  TAAAACTGTGCCTGTGCCA   85990    A  G  A
                                TG CA AG CACAGTTTTG
                                || || || ||||||||||
                                AC GT TC GTGTCAAAAT
                                 C  G  C
GAM353  LOC155179 3'  CAAAGCTGTATCTGCTATCA  81312     C  _  C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM353  LOC221074 3'  AAAGTGTGTCTCTTTCA     93177     C        G
                                TGA AGAGACACA TTT
                                ||| ||||||||| |||
                                ACT TCTCTGTGT AAA
                                  T        G
GAM353  LOC221103 5'  AGTTTATGTGTGCTCTGTCA  93244         _    GTTTT
                                TGACAGAG ACACA    GCT
                                |||||||| |||||    |||
                                ACTGTCTC TGTGT    TGA
                                     G    ATT__
GAM353  LOC255988 5'  CAGAGCCCAGCATCCATCTCTG 97608          CACA_  TT
           TCA                    TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                     ACCTA   CC
GAM354  TNFAIP1   3'  CATCAGCTGAGGACAGCAAACT 40917     AG     G
           CC                     GGA  TTGCTG CTTCAGCTGATG
                                |||  |||||| ||||||||||||
                                CCT  AACGAC GGAGTCGACTAC
                                  CA     A
GAM354  C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 21681    AA       _ ___
           CCC                    GG  GTTGCTGG CT   TCAGCTG
                                ||  |||||||| ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM354  C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 94622    AA       _ ___
           CCC                    GG  GTTGCTGG CT   TCAGCTG
                                ||  |||||||| ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM354  C20orf59  3'  CATCCCTAGCCAGCAGCTCC   41992     A        TC  CT
                                GGA GTTGCTGGCT  AG  GATG
                                ||| ||||||||||  ||  ||||
                                CCT CGACGACCGA  TC  CTAC
                                  _         __ C_
GAM354  FLJ20079  3'  CATTCTGGTAAACCAGCAGCCT 34490     A       CT__    CT
           CC                     GGA GTTGCTGG    TCAG  GATG
                                ||| ||||||||    ||||  ||||
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                                CCT CGACGACC    GGTC  TTAC
                                  C       AAAT   __
GAM354  SSAT2    3'  CATCAGCTGAAGCACTCTTC   56041      TTGCTG
                                GAAG     GCTTCAGCTGATG
                                ||||     ||||||||||||
                                CTTC     CGAAGTCGACTAC
                                  TCA___
GAM354  SYNJ2    3'  ATCAGCTTAAGCAATTCC     61763      GTTGCTG    C
                                GGAA      GCTT AGCTGAT
                                ||||      |||| |||||||
                                CCTT      CGAA TCGACTA
                                  AA_____    T
GAM354  LOC162333 5'  CTGAAGCCAGCAATTCC     87131      G
                                GGAA TTGCTGGCTTCAG
                                |||| ||||||||||||
                                CCTT AACGACCGAAGTC
                                  _
GAM354  LOC222060 5'  CACCTCCCACCAGCAACCCCC  94104    AA       CTTC  C
                                GG  GTTGCTGG    AG TG
                                ||  ||||||||    || ||
                                CC  CAACGACC    TC AC
                                 CC       ACCC  C
GAM354  LOC255650 3'  CATCAGCCCCAGGCAACTTCC  96711          _   CTTCA
                                GGAAGTTGC TGG     GCTGATG
                                ||||||||| |||     |||||||
                                CCTTCAACG ACC     CGACTAC
                                     G   C____
GAM355  ADAMTS4   5'  AGTCCCTCCCAGCTGCAGTA   17502         _   A  A_
                                TACTGCAG TGG AG  ACT
                                |||||||| ||| ||  |||
                                ATGACGTC ACC TC  TGA
                                     G   C  CC
GAM355  COL2A1    3'  ACACAATCCGTTGCA       52504          AGAAC
                                TGCAGTGGA     TGTGT
                                |||||||||     |||||
                                ACGTTGCCT     ACACA
                                     A____
GAM355  COL2A1    3'  ACACAATCCGTTGCA       8458           AGAAC
                                TGCAGTGGA     TGTGT
                                |||||||||     |||||
                                ACGTTGCCT     ACACA
                                     A____
GAM355  LPIN2     3'  AACACAGTTCTCAGTGGCA    27701      AGTG  A
                                TGC    GA GAACTGTGTT
                                |||    || ||||||||||
                                ACG    CT CTTGACACAA
                                  GTGA  _
GAM355  MNAT1     3'  AACACAGTCCTTCCACTAGCAG 10099       _       A
                                CTGC AGTGGAAG ACTGTGTT
                                |||| |||||||| ||||||||
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                                GACG TCACCTTC TGACACAA
                                  A       C
GAM355  PRG1     3'  AACACAGTTGTGCTGT      10774       G AGA
                                GCAGTG A   ACTGTGTT
                                |||||| |   ||||||||
                                TGTCGT T   TGACACAA
                                   G ___
GAM355  BCMP1    3'  AACACAGTTCTTCTTTCAG    48727     CAGT
                                CTG    GGAAGAACTGTGTT
                                |||    ||||||||||||||
                                GAC    TCTTCTTGACACAA
                                  TT__
GAM355  CASPR3   3'  AACACAGTCCTCCAC       53349       A  A
                                GTGGA GA CTGTGTT
                                ||||| || |||||||
                                CACCT CT GACACAA
                                   C  _
GAM355  CHST4    5'  AGGTCTTCCACTTCAG      19302     C       A
                                CTG AGTGGAAGA CT
                                ||| ||||||||| ||
                                GAC TCACCTTCT GA
                                  T        G
GAM355  EIF3S1   3'  AACACAGCTCTTGGGAGTACAG 63167    T    CAGTGG_    A
           TTC                    A ACTG       AAGA CTGTGTT
                                | ||||       |||| |||||||
                                C TGAC       TTCT GACACAA
                                 T    ATGAGGG    C
GAM355  HSPC065  3'  AACACAGTTAATGCCTGTA    26285       TGGAAG
                                TGCAG      AACTGTGTT
                                |||||      |||||||||
                                ATGTC      TTGACACAA
                                   CGTAA_
GAM355  KIAA0056 3'  AACACAACTTTAAAACTGCAG  91552        GGA   AC
                                CTGCAGT   AGA  TGTGTT
                                |||||||   |||  ||||||
                                GACGTCA   TTT  ACACAA
                                     AAA   CA
GAM355  KIAA0441 3'  AACACAGTTGTTACCAC      28947      _  G
                                GTGG AA AACTGTGTT
                                |||| || |||||||||
                                CACC TT TTGACACAA
                                  A  G
GAM355  KIAA0483 3'  ACATCTTCCACCGCA       30788      A       AC
                                TGC GTGGAAGA  TGT
                                ||| ||||||||  |||
                                ACG CACCTTCT  ACA
                                  C       __
GAM355  KIAA0905 3'  TCTTCCACTCAATAT       30031      C  C
                                ATA TG AGTGGAAGA
                                ||| || |||||||||
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                                TAT AC TCACCTTCT
                                  A  _
GAM355  KIAA1416  5'  ACCTGTCCTCCACTGCAG    86454          A  ACT
                                CTGCAGTGGA GA   GT
                                |||||||||| ||   ||
                                GACGTCACCT CT   CA
                                      C  GTC
GAM355  NAV3      3'  AACACAGTCCAAACATGAGCA  29770     A_   GAAGA
                                TGC  GTG    ACTGTGTT
                                |||  |||    ||||||||
                                ACG  TAC    TGACACAA
                                  AG   AAACC
GAM355  LOC132864 3'  ACACAGTCTGCTGCTATAT    75066     CT    TG  AGAA
                                ATA  GCAG  GA    CTGTGT
                                |||  ||||  ||    ||||||
                                TAT  CGTC  CT    GACACA
                                  AT    GT  _____
GAM355  LOC199918 3'  AACACAGGTATCACTGCA     89874         AAGAA
                                TGCAGTGG     CTGTGTT
                                ||||||||     |||||||
                                ACGTCACT     GACACAA
                                     ATG__
GAM355  LOC202860 3'  ACAAGCTTCCATTGCA       89220           AAC
                                TGCAGTGGAAG   TGT
                                ||||||||||   |||
                                ACGTTACCTTC   ACA
                                      GA_
GAM355  LOC92568  3'  AAGGCTCCCTCCTCCACTGCAG 69769           A  ACT_  G
                                CTGCAGTGGA GA    GT TT
                                |||||||||| ||    || ||
                                GACGTCACCT CT    CG AA
                                      C  CCCT  G
GAM356  ADAMTS4   5'  AGTCCCTCCCAGCTGCAGTA   17502         _   A  A_
                                TACTGCAG TGG AG  ACT
                                |||||||| ||| ||  |||
                                ATGACGTC ACC TC  TGA
                                     G   C  CC
GAM356  COL2A1    3'  ACACAATCCGTTGCA       8458          AGAAC
                                TGCAGTGGA     TGTGT
                                |||||||||     |||||
                                ACGTTGCCT     ACACA
                                     A_____
GAM356  COL2A1    3'  ACACAATCCGTTGCA       52504         AGAAC
                                TGCAGTGGA     TGTGT
                                |||||||||     |||||
                                ACGTTGCCT     ACACA
                                     A_____
GAM356  LPIN2     3'  AACACAGTTCTCAGTGGCA   27701     AGTG  A
                                TGC    GA GAACTGTGTT
                                |||    || ||||||||||
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                                ACG    CT CTTGACACAA
                                  GTGA  _
GAM356  MNAT1    3'  AACACAGTCCTTCCACTAGCAG 10099      _       A
                                CTGC AGTGGAAG ACTGTGTT
                                |||| |||||||| ||||||||
                                GACG TCACCTTC TGACACAA
                                   A       C
GAM356  PRG1     3'  AACACAGTTGTGCTGT      10774        G AGA
                                GCAGTG A   ACTGTGTT
                                |||||| |   ||||||||
                                TGTCGT T   TGACACAA
                                   G ___
GAM356  BCMP1    3'  AACACAGTTCTTCTTTCAG    48727     CAGT
                                CTG    GGAAGAACTGTGTT
                                |||    ||||||||||||||
                                GAC    TCTTCTTGACACAA
                                  TT__
GAM356  CASPR3   3'  AACACAGTCCTCCAC       53349       A  A
                                GTGGA GA CTGTGTT
                                ||||| || |||||||
                                CACCT CT GACACAA
                                   C  _
GAM356  CHST4    5'  AGGTCTTCCACTTCAG      19302      C        A
                                CTG AGTGGAAGA CT
                                ||| ||||||||| ||
                                GAC TCACCTTCT GA
                                  T        G
GAM356  EIF3S1   3'  AACACAGCTCTTGGGAGTACAG 63167    T    CAGTGG_    A
            TTC                   A ACTG       AAGA CTGTGTT
                                | ||||       |||| |||||||
                                C TGAC       TTCT GACACAA
                                 T    ATGAGGG    C
GAM356  HSPC065  3'  AACACAGTTAATGCCTGTA    26285       TGGAAG
                                TGCAG      AACTGTGTT
                                |||||      |||||||||
                                ATGTC      TTGACACAA
                                   CGTAA_
GAM356  KIAA0056 3'  AACACAACTTTAAAACTGCAG  91552         GGA   AC
                                CTGCAGT   AGA  TGTGTT
                                |||||||   |||  ||||||
                                GACGTCA   TTT  ACACAA
                                    AAA   CA
GAM356  KIAA0441 3'  AACACAGTTGTTACCAC     28947      _  G
                                GTGG AA AACTGTGTT
                                |||| || |||||||||
                                CACC TT TTGACACAA
                                  A  G
GAM356  KIAA0483 3'  ACATCTTCCACCGCA       30788      A       AC
                                TGC GTGGAAGA  TGT
                                ||| ||||||||  |||
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                                ACG CACCTTCT  ACA
                                  C       __
GAM356  KIAA0905  3'  TCTTCCACTCAATAT      30031     C  C
                                ATA TG AGTGGAAGA
                                ||| || |||||||||
                                TAT AC TCACCTTCT
                                  A  _
GAM356  KIAA1416  5'  ACCTGTCCTCCACTGCAG    86454          A  ACT
                                CTGCAGTGGA GA   GT
                                |||||||||| ||   ||
                                GACGTCACCT CT   CA
                                      C  GTC
GAM356  NAV3      3'  AACACAGTCCAAACATGAGCA  29770     A_   GAAGA
                                TGC  GTG    ACTGTGTT
                                |||  |||    ||||||||
                                ACG  TAC    TGACACAA
                                  AG   AAACC
GAM356  LOC132864 3'  ACACAGTCTGCTGCTATAT    75066     CT    TG  AGAA
                                ATA  GCAG  GA    CTGTGT
                                |||  ||||  ||    ||||||
                                TAT  CGTC  CT    GACACA
                                  AT    GT  _____
GAM356  LOC199918 3'  AACACAGGTATCACTGCA     89874         AAGAA
                                TGCAGTGG     CTGTGTT
                                ||||||||     |||||||
                                ACGTCACT     GACACAA
                                     ATG__
GAM356  LOC202860 3'  ACAAGCTTCCATTGCA       89220           AAC
                                TGCAGTGGAAG   TGT
                                ||||||||||   |||
                                ACGTTACCTTC   ACA
                                      GA_
GAM356  LOC92568  3'  AAGGCTCCCTCCTCCACTGCAG 69769          A  ACT_  G
                                CTGCAGTGGA GA    GT TT
                                |||||||||| ||    || ||
                                GACGTCACCT CT    CG AA
                                      C  CCCT  G
GAM357  ACTB      3'  GAGATTGGCATGGCTTTAT    6589           A   GATAGA
                                ATAAAGCTATG CAA     TC
                                |||||||||| |||     ||
                                TATTTCGGTAC GTT     AG
                                      G   AG_____
GAM357  ACTB      3'  GAGATTGGCATGGCTTTAT    6589           A   GATAGA
                                ATAAAGCTATG CAA     TC
                                |||||||||| |||     ||
                                TATTTCGGTAC GTT     AG
                                      G   AG_____
GAM357  ALDH1A1   3'  ATCTCTCTAGCTTTGT      5480          ATGACA   T
                                ATAAAGCT     AGA AGAT
                                ||||||||     ||| ||||
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                                TGTTTCGA     TCT TCTA
                                       _______  C
GAM357  ALDH1A1   3' ATCTCTCTAGCTTTGT      5480          ATGACA   T
                                TATAAAGCT     AGA AGAT
                                ||||||||      ||| ||||
                                TGTTTCGA     TCT TCTA
                                       _______  C
GAM357  AMD1      3' GTTTTTGTTTTGTTTTGGTTTT 7901          T         TCA
           GT                     ATAAAGCTA GACAAGATAGA
                                  |||||||||  ||||||||||
                                  TGTTTTGGT TTGTTTTGTTT
                                        T          TTGT
GAM357  AMD1      3' GTTTTTGTTTTGTTTTGGTTTT 7901          T         TCA
           GT                     ATAAAGCTA GACAAGATAGA
                                  |||||||||  ||||||||||
                                  TGTTTTGGT TTGTTTTGTTT
                                        T          TTGT
GAM357  ARHGAP6   3' TTTTGCCATAGCTTTAT     6771           A
                                  ATAAAGCTATG CAAGA
                                  ||||||||||| |||||
                                  TATTTCGATAC GTTTT
                                        C
GAM357  ARHGAP6   3' TTTTGCCATAGCTTTAT     6771           A
                                  ATAAAGCTATG CAAGA
                                  ||||||||||| |||||
                                  TATTTCGATAC GTTTT
                                        C
GAM357  ARHGAP6   3' TTTTGCCATAGCTTTAT     25522          A
                                  ATAAAGCTATG CAAGA
                                  ||||||||||| |||||
                                  TATTTCGATAC GTTTT
                                        C
GAM357  ARHGAP6   3' TTTTGCCATAGCTTTAT     25522          A
                                  ATAAAGCTATG CAAGA
                                  ||||||||||| |||||
                                  TATTTCGATAC GTTTT
                                        C
GAM357  ARHGEF12  3' TGATTTGTCTTGTCCAAGTTAT 31005     A    AT
           AT                     ATA AGCT  GACAAGATAGATCA
                                  ||| ||||  ||||||||||||||
                                  TAT TTGA  CTGTTCTGTTTAGT
                                    A    AC
GAM357  ARHGEF12  3' TGATTTGTCTTGTCCAAGTTAT 31005     A    AT
           AT                     ATA AGCT  GACAAGATAGATCA
                                  ||| ||||  ||||||||||||||
                                  TAT TTGA  CTGTTCTGTTTAGT
                                    A    AC
GAM357  CACNB2    3' TGATCTGTCTTGTAATATTTTG 5580        C   G
           T                      ATAAAG TAT ACAAGATAGATCA
                                  ||||||  ||| ||||||||||||
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                                TGTTTT ATA TGTTCTGTCTAGT
                                   _  A
GAM357  CACNB2   3'  TGATCTGTCTTGTAATATTTTG 5580       C   G
           T                    ATAAAG TAT ACAAGATAGATCA
                                |||||| ||| ||||||||||||
                                TGTTTT ATA TGTTCTGTCTAGT
                                   _  A
GAM357  CPSF6    3'  TGATTTAAAAAGTTATAGCTTT 22803         AAGA
                                AAAGCTATGAC   TAGATCA
                                ||||||||||   |||||||
                                TTTCGATATTG   ATTTAGT
                                      AAAA
GAM357  CPSF6    3'  TGATTTAAAAAGTTATAGCTTT 22803         AAGA
                                AAAGCTATGAC   TAGATCA
                                ||||||||||   |||||||
                                TTTCGATATTG   ATTTAGT
                                      AAAA
GAM357  CRK      3'  TGATTTATTCAGTGGTTTTGT  59854         GACAA
                                ATAAAGCTAT    GATAGATCA
                                ||||||||||    |||||||||
                                TGTTTTGGTG    TTATTTAGT
                                      AC___
GAM357  CRK      3'  TGATTTATTCAGTGGTTTTGT  59854         GACAA
                                ATAAAGCTAT    GATAGATCA
                                ||||||||||    |||||||||
                                TGTTTTGGTG    TTATTTAGT
                                      AC___
GAM357  CXADR    3'  TGAAAAAGTTTGTCTTAGTTTT 7193         T     ATAGA
           GT                     ATAAAGCTA GACAAG     TCA
                                |||||||||  ||||||     |||
                                TGTTTTGAT CTGTTT     AGT
                                     T     GAAAA
GAM357  CXADR    3'  TGAAAAAGTTTGTCTTAGTTTT 7193         T     ATAGA
           GT                     ATAAAGCTA GACAAG     TCA
                                |||||||||  ||||||     |||
                                TGTTTTGAT CTGTTT     AGT
                                     T     GAAAA
GAM357  EIF1AY   3'  TGATTTATTTTCATTGTTTTA  16261       T   CA
                                TAAAGC ATGA  AGATAGATCA
                                ||||||  ||||  ||||||||||
                                ATTTTG TACT  TTTATTTAGT
                                   T   __
GAM357  EIF1AY   3'  TGATTTATTTTCATTGTTTTA  16261       T   CA
                                TAAAGC ATGA  AGATAGATCA
                                ||||||  ||||  ||||||||||
                                ATTTTG TACT  TTTATTTAGT
                                   T   __
GAM357  FAT      3'  ATTTTTCATAGTTTTA      17890          C
                                TAAAGCTATGA AAGAT
                                ||||||||||| |||||
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                                ATTTTGATACT TTTTA
                                          _
GAM357  FAT      3' ATTTTTCATAGTTTTA      17890          C
                                TAAAGCTATGA AAGAT
                                |||||||||| |||||
                                ATTTTGATACT TTTTA
                                          _
GAM357  FOXO1A   3' TGATTTATTTTCTCTGGTTT  8907        T  C
                                AAGCTA GA AAGATAGATCA
                                |||||| || ||||||||||
                                TTTGGT CT TTTTATTTAGT
                                   _ C
GAM357  FOXO1A   3' TGATTTATTTTCTCTGGTTT  8907        T  C
                                AAGCTA GA AAGATAGATCA
                                |||||| || ||||||||||
                                TTTGGT CT TTTTATTTAGT
                                   _ C
GAM357  GRF2     3' TGGTTTTCTGGTTTGGTTTTGT 17997         T  A  T
                                ATAAAGCTA GAC AGA AGATCA
                                ||||||||| ||| ||| ||||||
                                TGTTTTGGT TTG TCT TTTGGT
                                     _  G  _
GAM357  GRF2     3' TGGTTTTCTGGTTTGGTTTTGT 17997         T  A  T
                                ATAAAGCTA GAC AGA AGATCA
                                ||||||||| ||| ||| ||||||
                                TGTTTTGGT TTG TCT TTTGGT
                                     _  G  _
GAM357  NCKAP1   3' TGATCTGTACCTATGGTTCTTA 25539      _     ACAAG
           T                     ATAA AGCTATG    ATAGATCA
                                |||| |||||||    ||||||||
                                TATT TTGGTAT    TGTCTAGT
                                  C     CCA__
GAM357  NCKAP1   3' TGATCTGTACCTATGGTTCTTA 25539      _     ACAAG
           T                     ATAA AGCTATG    ATAGATCA
                                |||| |||||||    ||||||||
                                TATT TTGGTAT    TGTCTAGT
                                  C     CCA__
GAM357  NEUROD1  3' TGAATTATTTTGTTGTGATTTT 10212       C  TG       A
           GT                    ATAAAG TA  ACAAGATAG TCA
                                |||||| ||  |||||||||| |||
                                TGTTTT GT  TGTTTTATT AGT
                                   A  GT       A
GAM357  NEUROD1  3' TGAATTATTTTGTTGTGATTTT 10212       C  TG       A
           GT                    ATAAAG TA  ACAAGATAG TCA
                                |||||| ||  |||||||||| |||
                                TGTTTT GT  TGTTTTATT AGT
                                   A  GT       A
GAM357  NIPSNAP1 3' TGGTCCTGCTGTCTTGGTTTTG 13295         T   A ATA
           T                     ATAAAGCTA GACA G   GATCA
                                ||||||||| |||| |   |||||
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                                TGTTTTGGT CTGT C   CTGGT
                                     T   _ GTC
GAM357  NIPSNAP1  3'  TGGTCCTGCTGTCTTGGTTTTG 13295        T   A ATA
           T                     ATAAAGCTA GACA G   GATCA
                                 ||||||||| |||| |   |||||
                                 TGTTTTGGT CTGT C   CTGGT
                                     T   _ GTC
GAM357  PABPN1    3'  TGATCTATTTTGTTTCCTTTTG 16185      CTAT
           T                     ATAAAG   GACAAGATAGATCA
                                 ||||||   ||||||||||||||
                                 TGTTTT   TTGTTTTATCTAGT
                                    CCT_
GAM357  PABPN1    3'  TGATCTATTTTGTTTCCTTTTG 16185      CTAT
           T                     ATAAAG   GACAAGATAGATCA
                                 ||||||   ||||||||||||||
                                 TGTTTT   TTGTTTTATCTAGT
                                    CCT_
GAM357  PCDH15    3'  TTTTGATCGTAGTTTTAT    52339         _
                                 ATAAAGCTATGA CAAGA
                                 |||||||||||| |||||
                                 TATTTTGATGCT GTTTT
                                       A
GAM357  PCDH15    3'  TTTTGATCGTAGTTTTAT    52339         _
                                 ATAAAGCTATGA CAAGA
                                 |||||||||||| |||||
                                 TATTTTGATGCT GTTTT
                                       A
GAM357  PPARGC1   3'  TACATGTATTGTTGTGGTTTTA 25162       TG   G   GATCA
           T                     ATAAAGCTA  ACAA ATA
                                 |||||||||  |||| |||
                                 TATTTTGGT  TGTT TGT
                                      GT   A   ACAT
GAM357  PPARGC1   3'  TACATGTATTGTTGTGGTTTTA 25162       TG   G   GATCA
           T                     ATAAAGCTA  ACAA ATA
                                 |||||||||  |||| |||
                                 TATTTTGGT  TGTT TGT
                                      GT   A   ACAT
GAM357  PRex1     3'  TGGTTTATTTTGGGATTTTTTG 40435      CT  GA
           T                     ATAAAG  AT  CAAGATAGATCA
                                 ||||||  ||  ||||||||||||
                                 TGTTTT  TA  GTTTTATTTGGT
                                    T_  GG
GAM357  PRex1     3'  TGGTTTATTTTGGGATTTTTTG 40435      CT  GA
           T                     ATAAAG  AT  CAAGATAGATCA
                                 ||||||  ||  ||||||||||||
                                 TGTTTT  TA  GTTTTATTTGGT
                                    T_  GG
GAM357  PRKWNK3   3'  TGGTTTGTCTTGCATTCTTTTG 61561      CT   A
                                 TAAAG  ATG CAAGATAGATCA
                                 |||||  ||| ||||||||||||
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```
                                GTTTT  TAC GTTCTGTTTGGT
                                   CT  _
GAM357  PRKWNK3  3'  TGGTTTGTCTTGCATTCTTTTG 61561      CT  A
                                TAAAG  ATG CAAGATAGATCA
                                |||||  ||| ||||||||||||
                                GTTTT  TAC GTTCTGTTTGGT
                                   CT  _
GAM357  RASA1    3'  TGATCTATTGCTCATCAGCTTT 42638        _   CAA
           AT                    ATAAAGCT ATGA   GATAGATCA
                                |||||||| ||||  |||||||||
                                TATTTCGA TACT   TTATCTAGT
                                    C   CG_
GAM357  RASA1    3'  TGATCTATTGCTCATCAGCTTT 42638        _   CAA
           AT                    ATAAAGCT ATGA   GATAGATCA
                                |||||||| ||||  |||||||||
                                TATTTCGA TACT   TTATCTAGT
                                    C   CG_
GAM357  RNF7     3'  TGGTTTAGCATTTTGTCAGTTT 26482       AT    ___
           TAT                   AAAGCT  GACAAGA   TAGATCA
                                ||||||  |||||||  |||||||
                                TTTTGA  CTGTTTT   ATTTGGT
                                  __      ACG
GAM357  RNF7     3'  TGGTTTAGCATTTTGTCAGTTT 26482       AT    ___
           TAT                   AAAGCT  GACAAGA   TAGATCA
                                ||||||  |||||||  |||||||
                                TTTTGA  CTGTTTT   ATTTGGT
                                  __      ACG
GAM357  RPS6KA2  3'  TTATTTTGTTGGGTTTTGT   40909        A
                                ATAAAGCT TGACAAGATAG
                                ||||||||| ||||||||||
                                TGTTTTGG GTTGTTTTATT
                                  _
GAM357  RPS6KA2  3'  TTATTTTGTTGGGTTTTGT   40909        A
                                ATAAAGCT TGACAAGATAG
                                ||||||||| ||||||||||
                                TGTTTTGG GTTGTTTTATT
                                  _
GAM357  RS1      3'  GGAAACTTTTGTCACGGCTTTA 4396        TA      TAGATCA
           T                     ATAAAGC  TGACAAGA
                                |||||||  ||||||||
                                TATTTCG  ACTGTTTT
                                    GC       CAAAGGT
GAM357  RS1      3'  GGAAACTTTTGTCACGGCTTTA 4396        TA      TAGATCA
           T                     ATAAAGC  TGACAAGA
                                |||||||  ||||||||
                                TATTTCG  ACTGTTTT
                                    GC       CAAAGGT
GAM357  SERPINB13 3'  TATCTTGTAGTTTTGT     24773        ATG
                                ATAAAGCT   ACAAGATA
                                ||||||||   ||||||||
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                              TGTTTTGA  TGTTCTAT
                                        ___
GAM357  SERPINB13 3'  TATCTTGTAGTTTTGT     24773        ATG
                              ATAAAGCT  ACAAGATA
                              ||||||||  ||||||||
                              TGTTTTGA  TGTTCTAT
                                        ___
GAM357  SRP14    3'  TGGTCTGTGCTGCATGGTTATA 11958    A     A  AG
           T                   ATA AGCTATG CA  ATAGATCA
                              ||| ||||||| ||  ||||||||
                              TAT TTGGTAC GT  TGTCTGGT
                                A     _ CG
GAM357  SRP14    3'  TGGTCTGTGCTGCATGGTTATA 11958    A     A  AG
           T                   ATA AGCTATG CA  ATAGATCA
                              ||| ||||||| ||  ||||||||
                              TAT TTGGTAC GT  TGTCTGGT
                                A     _ CG
GAM357  TIM3     3'  GATCTGTCTTGCTTATTGT   51343    T  _
                              GC ATGA CAAGATAGATC
                              || |||| ||||||||||
                              TG TATT GTTCTGTCTAG
                               T   C
GAM357  TIM3     3'  GATCTGTCTTGCTTATTGT   51343    T  _
                              GC ATGA CAAGATAGATC
                              || |||| ||||||||||
                              TG TATT GTTCTGTCTAG
                               T   C
GAM357  TIMELESS  3'  TGGTCTGTTCCTTTGGCTTT   14054       TGACAA
                              AAAGCTA    GATAGATCA
                              |||||||    |||||||||
                              TTTCGGT    TTGTCTGGT
                                  TTCC__
GAM357  TIMELESS  3'  TGGTCTGTTCCTTTGGCTTT   14054       TGACAA
                              AAAGCTA    GATAGATCA
                              |||||||    |||||||||
                              TTTCGGT    TTGTCTGGT
                                  TTCC__
GAM357  TMEM2    3'  GGTTTTTTGTTATTGTTTTGT  25424       T      TA   A
                              ATAAAGC ATGACAAGA  GATC
                              ||||||| |||||||||  ||||
                              TGTTTTG TATTGTTTT  TTGG
                                  T       __   G
GAM357  TMEM2    3'  GGTTTTTTGTTATTGTTTTGT  25424       T      TA   A
                              ATAAAGC ATGACAAGA  GATC
                              ||||||| |||||||||  ||||
                              TGTTTTG TATTGTTTT  TTGG
                                  T       __   G
GAM357  TOP1     3'  TGATTTGTTTTGAATTTTGTTT 12359   T    TATGA_
           TTA                   A AAAGC    CAAGATAGATCA
                              | |||||    ||||||||||||
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                                A TTTTG     GTTTTGTTTAGT
                                 T    TTTTAA
GAM357  TOP1    3'  TGATTTGTTTTGAATTTTGTTT 12359   T    TATGA_
            TTA                   A AAAGC     CAAGATAGATCA
                                | |||||     ||||||||||||
                                A TTTTG     GTTTTGTTTAGT
                                 T    TTTTAA
GAM357  TP53BP1  3'  ATCTTGTATATAGTTTTAT   18969          _
                                ATAAAGCTATG ACAAGAT
                                |||||||||||  |||||||
                                TATTTTGATAT TGTTCTA
                                      A
GAM357  TP53BP1  3'  ATCTTGTATATAGTTTTAT   18969          _
                                ATAAAGCTATG ACAAGAT
                                |||||||||||  |||||||
                                TATTTTGATAT TGTTCTA
                                      A
GAM357  UGDH    3'  GTCTCTTGTTGAGTTTTAT   12545        A      TA
                                ATAAAGCT TGACAAGA  GAT
                                ||||||||  ||||||||  |||
                                TATTTTGA GTTGTTCT  CTG
                                     _      __
GAM357  UGDH    3'  GTCTCTTGTTGAGTTTTAT   12545        A      TA
                                ATAAAGCT TGACAAGA  GAT
                                ||||||||  ||||||||  |||
                                TATTTTGA GTTGTTCT  CTG
                                     _      __
GAM357  UROD    3'  TGAACTATTGTGTAGTTTTGT  70145         G  AG   A
                                ATAAAGCTAT ACA  ATAG TCA
                                ||||||||||  |||  ||||  |||
                                TGTTTTGATG TGT  TATC AGT
                                     _  __    A
GAM357  UROD    3'  TGAACTATTGTGTAGTTTTGT  70145         G  AG   A
                                ATAAAGCTAT ACA  ATAG TCA
                                ||||||||||  |||  ||||  |||
                                TGTTTTGATG TGT  TATC AGT
                                     _  __    A
GAM357  VCP     3'  TGATTTATTTTACATGCTTT   75371      T  AC
                                AAAGC ATG  AAGATAGATCA
                                |||||  |||  ||||||||||
                                TTTCG TAC  TTTTATTTAGT
                                   _  A_
GAM357  VCP     3'  TGATTTATTTTACATGCTTT   75371      T  AC
                                AAAGC ATG  AAGATAGATCA
                                |||||  |||  ||||||||||
                                TTTCG TAC  TTTTATTTAGT
                                   _  A_
GAM357  ZNF24   3'  GTCTGTCATGGCTTT      22728          A
                                AAAGCTATGACA GAT
                                ||||||||||||  |||
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                                TTTCGGTACTGT CTG
                                           _
GAM357  ZNF24    3'  GTCTGTCATGGCTTT      22728          A
                                AAAGCTATGACA GAT
                                |||||||||||| |||
                                TTTCGGTACTGT CTG
                                           _
GAM357  AF15Q14  3'  TGATTTGTCAATTTGGCTTTAT 39822        TGACAA
                                ATAAAGCTA    GATAGATCA
                                |||||||||    |||||||||
                                TATTTCGGT    CTGTTTAGT
                                     TTAA__
GAM357  AF15Q14  3'  TGATTTGTCAATTTGGCTTTAT 39822        TGACAA
                                ATAAAGCTA    GATAGATCA
                                |||||||||    |||||||||
                                TATTTCGGT    CTGTTTAGT
                                     TTAA__
GAM357  AKAP11   3'  TATTTTGTCATAGTTT     57834
                                AAGCTATGACAAGATA
                                ||||||||||||||||
                                TTTGATACTGTTTTAT

GAM357  AKAP11   3'  TATTTTGTCATAGTTT     57834
                                AAGCTATGACAAGATA
                                ||||||||||||||||
                                TTTGATACTGTTTTAT

GAM357  ARNTL2   3'  TGATTTATAATAGTAGGTTTGT 39470      G   GACAAG
                                ATAAA CTAT    ATAGATCA
                                ||||| ||||    ||||||||
                                TGTTT GATG    TATTTAGT
                                   G   ATAA__
GAM357  ARNTL2   3'  TGATTTATAATAGTAGGTTTGT 39470      G   GACAAG
                                ATAAA CTAT    ATAGATCA
                                ||||| ||||    ||||||||
                                TGTTT GATG    TATTTAGT
                                   G   ATAA__
GAM357  AWP1     3'  TTTTGTTTTGGTTTTGT     38665        T
                                ATAAAGCTA GACAAGA
                                ||||||||| |||||||
                                TGTTTTGGT TTGTTTT
                                     T
GAM357  AWP1     3'  TTTTGTTTTGGTTTTGT     38665        T
                                ATAAAGCTA GACAAGA
                                ||||||||| |||||||
                                TGTTTTGGT TTGTTTT
                                     T
GAM357  BRIX     3'  TGATTTGTTTTTCAGTTACTTT 87478      CTA_  C
           AT                    ATAAAG   TGA AAGATAGATCA
                                ||||||   ||| ||||||||||
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                                TATTTC   ACT TTTTGTTTAGT
                                   ATTG  _
GAM357  BRIX     3'  TGATTTGTTTTTCAGTTACTTT 87478       CTA_  C
              AT                   ATAAAG   TGA AAGATAGATCA
                                |||||||   ||| ||||||||||
                                TATTTC   ACT TTTTGTTTAGT
                                   ATTG  _
GAM357  C20orf46 3'  TGATCTGTTTTGTAGCTGAGGT 37150      ATG___
              TTTG                 AAGCT    ACAAGATAGATCA
                                |||||     ||||||||||||
                                TTTGG     TGTTTTGTCTAGT
                                   AGTCGA
GAM357  C20orf46 3'  TGATCTGTTTTGTAGCTGAGGT 37150      ATG___
              TTTG                 AAGCT    ACAAGATAGATCA
                                |||||     ||||||||||||
                                TTTGG     TGTTTTGTCTAGT
                                   AGTCGA
GAM357  CPEB1    3'  GTTTTGTCAGGTTTTGT     47600        A
                                ATAAAGCT TGACAAGAT
                                |||||||| |||||||||
                                TGTTTTGG ACTGTTTTG
                                      _
GAM357  CPEB1    3'  GTTTTGTCAGGTTTTGT     47600        A
                                ATAAAGCT TGACAAGAT
                                |||||||| |||||||||
                                TGTTTTGG ACTGTTTTG
                                      _
GAM357  DC6      3'  TTAGATTGTGTTGTTGTGGTTT 39490        TG   G   A A
              TAT                  ATAAAGCTA  ACAA ATAG TC
                                |||||||||  |||| |||| ||
                                TATTTTGGT  TGTT TGTT AG
                                     GT   G   _ ATTA
GAM357  DC6      3'  TTAGATTGTGTTGTTGTGGTTT 39490        TG   G   A A
              TAT                  ATAAAGCTA  ACAA ATAG TC
                                |||||||||  |||| |||| ||
                                TATTTTGGT  TGTT TGTT AG
                                     GT   G   _ ATTA
GAM357  DKFZP434N178 3'  TGATCTATGTTTTTATGGTTTT 71911         C  G
                                AAAGCTATGA AA ATAGATCA
                                |||||||||| || ||||||||
                                TTTTGGTATT TT TATCTAGT
                                      T  G
GAM357  DKFZP434N178 3'  TGATCTATGTTTTTATGGTTTT 71911         C  G
                                AAAGCTATGA AA ATAGATCA
                                |||||||||| || ||||||||
                                TTTTGGTATT TT TATCTAGT
                                      T  G
GAM357  DKFZP564K0322 3'  TCTTGTTAAAGTTTTGT     49365        A
                                ATAAAGCT TGACAAGA
                                |||||||| ||||||||
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                                TGTTTTGA ATTGTTCT
                                     A
GAM357  DKFZP564K0322 3'  TCTTGTTAAAGTTTTGT     49365         A
                                ATAAAGCT TGACAAGA
                                |||||||| ||||||||
                                TGTTTTGA ATTGTTCT
                                     A
GAM357  DKFZP564M182 3'  TGATTTATCTTCCATAAGCCTT 78045      A  _  AC
           AT                    ATAA GCT ATG  AAGATAGATCA
                                |||| ||| |||  ||||||||||
                                TATT CGA TAC  TTCTATTTAGT
                                  C   A   C_
GAM357  DKFZP564M182 3'  TGATTTATCTTCCATAAGCCTT 78045      A  _  AC
           AT                    ATAA GCT ATG  AAGATAGATCA
                                |||| ||| |||  ||||||||||
                                TATT CGA TAC  TTCTATTTAGT
                                  C   A   C_
GAM357  DKFZp761N1114 3'  TGGTCTAGGAGTATAGTTTTA  79029          ACAAGA
                                TAAAGCTATG     TAGATCA
                                ||||||||||     |||||||
                                ATTTTGATAT     ATCTGGT
                                     GAGG__
GAM357  DKFZp761N1114 3'  TGGTCTAGGAGTATAGTTTTA  79029          ACAAGA
                                TAAAGCTATG     TAGATCA
                                ||||||||||     |||||||
                                ATTTTGATAT     ATCTGGT
                                     GAGG__
GAM357  DSCR1L1   3'  TGAGGGATTGTTGTGGTTTT   19500        TG   GATAGA
                                AAAGCTA  ACAA     TCA
                                |||||||  ||||     |||
                                TTTTGGT  TGTT     AGT
                                   GT   AGGG__
GAM357  DSCR1L1   3'  TGAGGGATTGTTGTGGTTTT   19500        TG   GATAGA
                                AAAGCTA  ACAA     TCA
                                |||||||  ||||     |||
                                TTTTGGT  TGTT     AGT
                                   GT   AGGG__
GAM357  ERp44     3'  GTAGAGTCTTGTTATAGTTGTA 81695     A          AGATCA
           T                     ATA AGCTATGACAAGAT
                                ||| ||||||||||||||
                                TAT TTGATATTGTTCTG
                                  G           AGATGT
GAM357  ERp44     3'  GTAGAGTCTTGTTATAGTTGTA 81695     A          AGATCA
           T                     ATA AGCTATGACAAGAT
                                ||| ||||||||||||||
                                TAT TTGATATTGTTCTG
                                  G           AGATGT
GAM357  FLJ11011  3'  GGTTTAATCAAGGCTTTAT    36978         A   CAAGA
                                ATAAAGCT TGA    TAGATC
                                |||||||| |||    ||||||
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                              TATTTCGG ACT    ATTTGG
                                  A  A____
GAM357  FLJ11011  3' GGTTTAATCAAGGCTTTAT   36978       A  CAAGA
                              ATAAAGCT TGA    TAGATC
                              |||||||| |||    ||||||
                              TATTTCGG ACT    ATTTGG
                                  A  A____
GAM357  FLJ11036  3' TGATCTGTCTGGGTTCATGGTT 36999        _ A_
           TT                  AAAGCTATGA C  AGATAGATCA
                              |||||||||| |  ||||||||||
                              TTTTGGTACT G  TCTGTCTAGT
                                   T GG
GAM357  FLJ11036  3' TGATCTGTCTGGGTTCATGGTT 36999        _ A_
           TT                  AAAGCTATGA C  AGATAGATCA
                              |||||||||| |  ||||||||||
                              TTTTGGTACT G  TCTGTCTAGT
                                   T GG
GAM357  FLJ12750  3' TGGTCCTTCTGTTGCAGCTTTA 45126       AT   A  TA
           T                   ATAAAGCT  GACA GA  GATCA
                              ||||||||  |||| ||  |||||
                              TATTTCGA  TTGT CT  CTGGT
                                  CG   _  TC
GAM357  FLJ12750  3' TGGTCCTTCTGTTGCAGCTTTA 45126       AT   A  TA
           T                   ATAAAGCT  GACA GA  GATCA
                              ||||||||  |||| ||  |||||
                              TATTTCGA  TTGT CT  CTGGT
                                  CG   _  TC
GAM357  FLJ13057  3' CTTGTCATGTTTTAT      42455       T
                              ATAAAGC ATGACAAG
                              ||||||| ||||||||
                              TATTTTG TACTGTTC
                                  _
GAM357  FLJ13057  3' CTTGTCATGTTTTAT      42455       T
                              ATAAAGC ATGACAAG
                              ||||||| ||||||||
                              TATTTTG TACTGTTC
                                  _
GAM357  FLJ13449  3' GTTTTGTTTTTGGTTTTGT   44618        T_
                              ATAAAGCTA  GACAAGAT
                              |||||||||  ||||||||
                              TGTTTTGGT  TTGTTTTG
                                   TT
GAM357  FLJ13449  3' GTTTTGTTTTTGGTTTTGT   44618        T_
                              ATAAAGCTA  GACAAGAT
                              |||||||||  ||||||||
                              TGTTTTGGT  TTGTTTTG
                                   TT
GAM357  FLJ20546  3' TCTTGTCCTGGTTTTAT     35371        T
                              ATAAAGCTA GACAAGA
                              ||||||||| |||||||
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                                TATTTTGGT CTGTTCT
                                     C
GAM357  FLJ20546 3'  TCTTGTCCTGGTTTTAT    35371        T
                                ATAAAGCTA GACAAGA
                                ||||||||| |||||||
                                TATTTTGGT CTGTTCT
                                     C
GAM357  FLJ21103 3'  TCTTGTTGCAGTTTTGT    44647       AT
                                ATAAAGCT  GACAAGA
                                ||||||||  |||||||
                                TGTTTTGA  TTGTTCT
                                     CG
GAM357  FLJ21103 3'  TCTTGTTGCAGTTTTGT    44647       AT
                                ATAAAGCT  GACAAGA
                                ||||||||  |||||||
                                TGTTTTGA  TTGTTCT
                                     CG
GAM357  FLJ23516 3'  TGATTTGTCAACCATAGTTT  44590       ACAA
                                AAGCTATG   GATAGATCA
                                ||||||||   |||||||||
                                TTTGATAC   CTGTTTAGT
                                     CAA_
GAM357  FLJ23516 3'  TGATTTGTCAACCATAGTTT  44590       ACAA
                                AAGCTATG   GATAGATCA
                                ||||||||   |||||||||
                                TTTGATAC   CTGTTTAGT
                                     CAA_
GAM357  FLJ32430 3'  GATCTAGCTAGGGCTTTGT   58323       ATGACA  A
                                ATAAAGCT    AG TAGATC
                                ||||||||    || ||||||
                                TGTTTCGG    TC ATCTAG
                                     GA____  G
GAM357  FLJ32430 3'  GATCTAGCTAGGGCTTTGT   58323       ATGACA  A
                                ATAAAGCT    AG TAGATC
                                ||||||||    || ||||||
                                TGTTTCGG    TC ATCTAG
                                     GA____  G
GAM357  GBTS1    3'  TGGTTTATCTGAGAGCATTTAT 59062     _  ATGACA
                                ATAAA GCT    AGATAGATCA
                                ||||| |||    ||||||||||
                                TATTT CGA    TCTATTTGGT
                                   A  GAG___
GAM357  GBTS1    3'  TGGTTTATCTGAGAGCATTTAT 59062     _  ATGACA
                                ATAAA GCT    AGATAGATCA
                                ||||| |||    ||||||||||
                                TATTT CGA    TCTATTTGGT
                                   A  GAG___
GAM357  HARS2    3'  TGATTTGTCTTGTTACCTGT   55040   TA_
                                GC  TGACAAGATAGATCA
                                ||  ||||||||||||||
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                              TG  ATTGTTCTGTTTAGT
                               TCC
GAM357  HARS2    3' TGATTTGTCTTGTTACCTGT  55040    TA_
                              GC  TGACAAGATAGATCA
                              ||  ||||||||||||||
                              TG  ATTGTTCTGTTTAGT
                               TCC
GAM357  HNRPA3   3' GTTCTTTTATCTGTTGTAGCTT 19259        TG  A    TCA
           TGT                  ATAAAGCTA  ACA GATAGA
                              |||||||||  ||| ||||||
                              TGTTTCGAT  TGT CTATTT
                                   GT  _    TCTTGG
GAM357  HNRPA3   3' GTTCTTTTATCTGTTGTAGCTT 19259        TG  A    TCA
           TGT                  ATAAAGCTA  ACA GATAGA
                              |||||||||  ||| ||||||
                              TGTTTCGAT  TGT CTATTT
                                   GT  _    TCTTGG
GAM357  KIAA0121 3' TGATCTTTTTTTTTGTCGTAGA 72663    G       T___
           TTTGT                AA CTATGACAAGA   AGATCA
                              || ||||||||||   ||||||
                              TT GATGCTGTTTT   TCTAGT
                               A        TTTT
GAM357  KIAA0121 3' TGATCTTTTTTTTTGTCGTAGA 72663    G       T___
           TTTGT                AA CTATGACAAGA   AGATCA
                              || ||||||||||   ||||||
                              TT GATGCTGTTTT   TCTAGT
                               A        TTTT
GAM357  KIAA0349 3' TGATTTGTTCCGCATGTTTTAT 92308       T  ACAA
                              ATAAAGC ATG   GATAGATCA
                              ||||||| |||   |||||||||
                              TATTTTG TAC   TTGTTTAGT
                                  _  GCC_
GAM357  KIAA0349 3' TGATTTGTTCCGCATGTTTTAT 92308       T  ACAA
                              ATAAAGC ATG   GATAGATCA
                              ||||||| |||   |||||||||
                              TATTTTG TAC   TTGTTTAGT
                                  _  GCC_
GAM357  KIAA0373 5' TTTTGTTAGAGTTTTAT    28016        A
                              ATAAAGCT TGACAAGA
                              |||||||| ||||||||
                              TATTTTGA ATTGTTTT
                                   G
GAM357  KIAA0373 5' TTTTGTTAGAGTTTTAT    28016        A
                              ATAAAGCT TGACAAGA
                              |||||||| ||||||||
                              TATTTTGA ATTGTTTT
                                   G
GAM357  KIAA0451 3' TTTATTTTGTTTGGTTTTAT  29122        T
                              ATAAAGCTA GACAAGATAGA
                              ||||||||| ||||||||||
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                                TATTTTGGT TTGTTTTATTT
                                          _
GAM357  KIAA0451  3'  TTTATTTTGTTTGGTTTTAT  29122        T
                                ATAAAGCTA GACAAGATAGA
                                ||||||||| ||||||||||
                                TATTTTGGT TTGTTTTATTT
                                          _
GAM357  KIAA0861  5'  GTTTTGTTTGGCTTTAT    88933        T
                                ATAAAGCTA GACAAGAT
                                ||||||||| ||||||||
                                TATTTCGGT TTGTTTTG
                                          _
GAM357  KIAA0861  5'  GTTTTGTTTGGCTTTAT    88933        T
                                ATAAAGCTA GACAAGAT
                                ||||||||| ||||||||
                                TATTTCGGT TTGTTTTG
                                          _
GAM357  KIAA0931  3'  TGGAATCTTTTTCATGGCTTTG 67426          C_    AGATCA
          T                      ATAAAGCTATGA  AAGAT
                                ||||||||||||  |||||
                                TGTTTCGGTACT  TTCTA
                                      TT    AGGT
GAM357  KIAA0931  3'  TGGAATCTTTTTCATGGCTTTG 67426          C_    AGATCA
          T                      ATAAAGCTATGA  AAGAT
                                ||||||||||||  |||||
                                TGTTTCGGTACT  TTCTA
                                      TT    AGGT
GAM357  KIAA0937  3'  TGGTCTTCTCTGTGGTTTTAT  91594         ACA   T
                                ATAAAGCTATG   AGA AGATCA
                                ||||||||||   ||| ||||||
                                TATTTTGGTGT   TCT TCTGGT
                                      C__   _
GAM357  KIAA0937  3'  TGGTCTTCTCTGTGGTTTTAT  91594         ACA   T
                                ATAAAGCTATG   AGA AGATCA
                                ||||||||||   ||| ||||||
                                TATTTTGGTGT   TCT TCTGGT
                                      C__   _
GAM357  KIAA0971  3'  TGATTTATAAAGTAGCCTTGT  30004     A    GACAAG
                                ATAA GCTAT     ATAGATCA
                                |||| |||||     ||||||||
                                TGTT CGATG     TATTTAGT
                                  C    AAA___
GAM357  KIAA0971  3'  TGATTTATAAAGTAGCCTTGT  30004     A    GACAAG
                                ATAA GCTAT     ATAGATCA
                                |||| |||||     ||||||||
                                TGTT CGATG     TATTTAGT
                                  C    AAA___
GAM357  KIAA1013  3'  TGGTTTATTGTAGGGTTTTGT  88891        ATG   AG
                                ATAAAGCT   ACA  ATAGATCA
                                ||||||||   |||  ||||||||
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                                TGTTTTGG  TGT  TATTTGGT
                                   GA_  __
GAM357  KIAA1013 3' TGGTTTATTGTAGGGTTTTGT 88891       ATG  AG
                                ATAAAGCT  ACA  ATAGATCA
                                ||||||||  |||  ||||||||
                                TGTTTTGG  TGT  TATTTGGT
                                   GA_  __
GAM357  KIAA1126 3' TGGTCTCATTTGTGGTGGTTTT 71944        G   AT
           GT                  ATAAAGCTAT ACAAG  AGATCA
                               ||||||||||| |||||  ||||||
                               TGTTTTGGTG TGTTT  TCTGGT
                                    G    AC
GAM357  KIAA1126 3' TGGTCTCATTTGTGGTGGTTTT 71944        G   AT
           GT                  ATAAAGCTAT ACAAG  AGATCA
                               ||||||||||| |||||  ||||||
                               TGTTTTGGTG TGTTT  TCTGGT
                                    G    AC
GAM357  KIAA1240 3' TGGTCTATTTTGGGTTTGTAGT 66741      TG ___
           TTTA                  AAGCTA  A   CAAGATAGATCA
                               ||||||  |   ||||||||||||
                               TTTGAT  T   GTTTTATCTGGT
                                  GT TGG
GAM357  KIAA1240 3' TGGTCTATTTTGGGTTTGTAGT 66741      TG ___
           TTTA                  AAGCTA  A   CAAGATAGATCA
                               ||||||  |   ||||||||||||
                               TTTGAT  T   GTTTTATCTGGT
                                  GT TGG
GAM357  KIAA1318 3' TGATCTGTTGTTTATGGCCTTT 67309      _    CAA
           GT                  ATAAAG CTATGA   GATAGATCA
                               ||||||| ||||||   |||||||||
                               TGTTTC GGTATT   TTGTCTAGT
                                  C     TG_
GAM357  KIAA1318 3' TGATCTGTTGTTTATGGCCTTT 67309      _    CAA
           GT                  ATAAAG CTATGA   GATAGATCA
                               ||||||| ||||||   |||||||||
                               TGTTTC GGTATT   TTGTCTAGT
                                  C     TG_
GAM357  KIAA1328 3' TGATCTGGAGGGTGTGGCTTT  61658       G  AAGA
                               AAAGCTAT AC    TAGATCA
                               ||||||||  ||    |||||||
                               TTTCGGTG TG    GTCTAGT
                                   _  GGAG
GAM357  KIAA1328 3' TGATCTGGAGGGTGTGGCTTT  61658       G  AAGA
                               AAAGCTAT AC    TAGATCA
                               ||||||||  ||    |||||||
                               TTTCGGTG TG    GTCTAGT
                                   _  GGAG
GAM357  KIAA1557 3' TCTTCTTATAGCTTTAT     61138          C
                               ATAAAGCTATGA AAGA
                               |||||||||||| ||||
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                                TATTTCGATATT TTCT
                                      C
GAM357  KIAA1557  3'  TCTTCTTATAGCTTTAT     61138          C
                                ATAAAGCTATGA AAGA
                                |||||||||||| ||||
                                TATTTCGATATT TTCT
                                      C
GAM357  KIAA1623  3'  TTTAATTTATTTTGTCATATTT 72070       C          CA
          TTGT                    ATAAAG TATGACAAGATAGAT
                                |||||| ||||||||||||||
                                TGTTTT ATACTGTTTTATTTA
                                   T          ATTTT
GAM357  KIAA1623  3'  TTTAATTTATTTTGTCATATTT 72070       C          CA
          TTGT                    ATAAAG TATGACAAGATAGAT
                                |||||| ||||||||||||||
                                TGTTTT ATACTGTTTTATTTA
                                   T          ATTTT
GAM357  KIAA1950  3'  TGATCTGTCTCCCTTTAGTTTT 92599        TGACA
          G                      TAAAGCTA    AGATAGATCA
                                ||||||||    ||||||||||
                                GTTTTGAT    TCTGTCTAGT
                                     TTCCC
GAM357  KIAA1950  3'  TGATCTGTCTCCCTTTAGTTTT 92599        TGACA
          G                      TAAAGCTA    AGATAGATCA
                                ||||||||    ||||||||||
                                GTTTTGAT    TCTGTCTAGT
                                     TTCCC
GAM357  LNX       5'  TGATTTATTAACGTGGCTT    50921        ACAA
                                AAGCTATG    GATAGATCA
                                ||||||||    |||||||||
                                TTCGGTGC    TTATTTAGT
                                     AA__
GAM357  LNX       5'  TGATTTATTAACGTGGCTT    50921        ACAA
                                AAGCTATG    GATAGATCA
                                ||||||||    |||||||||
                                TTCGGTGC    TTATTTAGT
                                     AA__
GAM357  MESDC2    3'  TGTCTGTCAGGTTTTAT     72504         A    A
                                ATAAAGCT TGACA GATA
                                |||||||| ||||| ||||
                                TATTTTGG ACTGT CTGT
                                     _    _
GAM357  MESDC2    3'  TGTCTGTCAGGTTTTAT     72504         A    A
                                ATAAAGCT TGACA GATA
                                |||||||| ||||| ||||
                                TATTTTGG ACTGT CTGT
                                     _    _
GAM357  MGC14433  3'  TCAAGTGTTTTGTTGTAGCTT  51870        TG       GATCA
                                AAGCTA  ACAAGATA
                                ||||||  ||||||||
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                                TTCGAT  TGTTTTGT
                                   GT       GAACTG
GAM357  MGC14433  3'  TCAAGTGTTTTGTTGTAGCTT  51870       TG       GATCA
                                AAGCTA  ACAAGATA
                                ||||||  ||||||||
                                TTCGAT  TGTTTTGT
                                   GT       GAACTG
GAM357  MGC5528   3'  TGATTTATTTAAAGTTTGGCTT 44046       T   A__
          T                     AAAGCTA GAC   AGATAGATCA
                                |||||||  |||   ||||||||||
                                TTTCGGT TTG   TTTATTTAGT
                                   _   AAA
GAM357  MGC5528   3'  TGATTTATTTAAAGTTTGGCTT 44046       T   A__
          T                     AAAGCTA GAC   AGATAGATCA
                                |||||||  |||   ||||||||||
                                TTTCGGT TTG   TTTATTTAGT
                                   _   AAA
GAM357  MO25      3'  TGATGTGGTGTCCTGGCTTTGT 32815        T   AGA  G
                                ATAAAGCTA GACA   TA ATCA
                                |||||||||  ||||   ||  ||||
                                TGTTTCGGT CTGT   GT TAGT
                                     C    G__  G
GAM357  MO25      3'  TGATGTGGTGTCCTGGCTTTGT 32815        T   AGA  G
                                ATAAAGCTA GACA   TA ATCA
                                |||||||||  ||||   ||  ||||
                                TGTTTCGGT CTGT   GT TAGT
                                     C    G__  G
GAM357  NUDT4     3'  TGGTTTATTTTGTCATCAG   38867    _
                                CT ATGACAAGATAGATCA
                                ||  ||||||||||||||||
                                GA TACTGTTTTATTTGGT
                                 C
GAM357  NUDT4     3'  TGGTTTATTTTGTCATCAG   38867    _
                                CT ATGACAAGATAGATCA
                                ||  ||||||||||||||||
                                GA TACTGTTTTATTTGGT
                                 C
GAM357  PALMD     5'  GATTTATGGTAGCTTTG     34812         GACAAG
                                TAAAGCTAT     ATAGATC
                                |||||||||     |||||||
                                GTTTCGATG     TATTTAG
                                     G_____
GAM357  PALMD     5'  GATTTATGGTAGCTTTG     34812         GACAAG
                                TAAAGCTAT     ATAGATC
                                |||||||||     |||||||
                                GTTTCGATG     TATTTAG
                                     G_____
GAM357  PEG10     3'  TGATTTATTTTGTTGT      30533    TG
                                A  ACAAGATAGATCA
                                |  ||||||||||||||
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                              T  TGTTTTATTTAGT
                               GT
GAM357  PEG10    3'  TGATTTATTTTGTTGT     30533    TG
                              A  ACAAGATAGATCA
                              |  ||||||||||||
                              T  TGTTTTATTTAGT
                               GT
GAM357  PPP1R3B  3'  TTGTTTTGTTTTGGTTTTGT   44827         T
                              ATAAAGCTA GACAAGATAG
                              ||||||||| ||||||||||
                              TGTTTTGGT TTGTTTTGTT
                                    T
GAM357  PPP1R3B  3'  TTGTTTTGTTTTGGTTTTGT   44827         T
                              ATAAAGCTA GACAAGATAG
                              ||||||||| ||||||||||
                              TGTTTTGGT TTGTTTTGTT
                                    T
GAM357  RIP60    3'  GTCTGTCTCGCTTTAT     25459        TATGACA
                              ATAAAGC     AGATAGAT
                              |||||||     ||||||||
                              TATTTCG     TCTGTCTG
                                 C_______
GAM357  RIP60    3'  GTCTGTCTCGCTTTAT     25459        TATGACA
                              ATAAAGC     AGATAGAT
                              |||||||     ||||||||
                              TATTTCG     TCTGTCTG
                                 C_______
GAM357  RPIA     3'  TGATTTGTTTTTAGTTAGTTTT 57970        TGAC
                              AAAGCTA    AAGATAGATCA
                              |||||||    ||||||||||
                              TTTTGAT    TTTTGTTTAGT
                                 TGAT
GAM357  RPIA     3'  TGATTTGTTTTTAGTTAGTTTT 57970        TGAC
                              AAAGCTA    AAGATAGATCA
                              |||||||    ||||||||||
                              TTTTGAT    TTTTGTTTAGT
                                 TGAT
GAM357  SEC15B   3'  GTCATTTTGTCTAGCTTTAT   66686         T      A
                              ATAAAGCTA GACAAGAT GAT
                              ||||||||| |||||||| |||
                              TATTTCGAT CTGTTTTA CTG
                                       _      _
GAM357  SEC15B   3'  GTCATTTTGTCTAGCTTTAT   66686         T      A
                              ATAAAGCTA GACAAGAT GAT
                              ||||||||| |||||||| |||
                              TATTTCGAT CTGTTTTA CTG
                                       _      _
GAM357  SLC38A4  3'  TCTTGTCATACTTTTGT     35878        C
                              ATAAAG TATGACAAGA
                              |||||| ||||||||||
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                                TGTTTT ATACTGTTCT
                                   C
GAM357  SLC38A4  3'  TCTTGTCATACTTTTGT     35878       C
                                ATAAAG TATGACAAGA
                                |||||| ||||||||||
                                TGTTTT ATACTGTTCT
                                   C
GAM357  TA-PP2C  3'  TGATGATTGGTGTGGCTTTAT  57761         GA   GATAG
                                ATAAAGCTAT  CAA    ATCA
                                ||||||||||  |||    ||||
                                TATTTCGGTG  GTT    TAGT
                                      TG   AG___
GAM357  TA-PP2C  3'  TGATGATTGGTGTGGCTTTAT  57761         GA   GATAG
                                ATAAAGCTAT  CAA    ATCA
                                ||||||||||  |||    ||||
                                TATTTCGGTG  GTT    TAGT
                                      TG   AG___
GAM357  TM9SF2   5'  TGGTTTATCTCTGGCGGCCTTG 16629      A   ATGA  _
          T                     ATAA GCT    CA AGATAGATCA
                                |||| |||    || ||||||||||
                                TGTT CGG    GT TCTATTTGGT
                                  C   CG__  C
GAM357  TM9SF2   5'  TGGTTTATCTCTGGCGGCCTTG 16629      A   ATGA  _
          T                     ATAA GCT    CA AGATAGATCA
                                |||| |||    || ||||||||||
                                TGTT CGG    GT TCTATTTGGT
                                  C   CG__  C
GAM357  TNFAIP3  3'  TTTTGTGATGGTTTTAT     20827          G
                                ATAAAGCTAT ACAAGA
                                |||||||||| ||||||
                                TATTTTGGTA TGTTTT
                                      G
GAM357  TNFAIP3  3'  TTTTGTGATGGTTTTAT     20827          G
                                ATAAAGCTAT ACAAGA
                                |||||||||| ||||||
                                TATTTTGGTA TGTTTT
                                      G
GAM357  TP53TG3  3'  CTTGGTATGGTTTTAT      31105          A
                                ATAAAGCTATG CAAG
                                |||||||||||  ||||
                                TATTTTGGTAT GTTC
                                       G
GAM357  TP53TG3  3'  CTTGGTATGGTTTTAT      31105          A
                                ATAAAGCTATG CAAG
                                |||||||||||  ||||
                                TATTTTGGTAT GTTC
                                       G
GAM357  TReP-132 5'  ATGGTTTATTTACCTTTTTTAT 37289       CA_____
          GGTTTTGT                CTATGA      AGATAGATCA   T
                                ||||||      ||||||||||   |
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                              GGTATT     TTTATTTGGT  A
                                 TTTTCCA
GAM357  TReP-132  5'  ATGGTTTATTTACCTTTTTTAT 37289      CA_____
           GGTTTTGT              CTATGA     AGATAGATCA  T
                              ||||||     ||||||||||  |
                              GGTATT     TTTATTTGGT  A
                                 TTTTCCA
GAM357  TReP-132  5'  ATGGTTTATTTACCTTTTTTAT 53136      CA_____
           GGTTTTGT              CTATGA     AGATAGATCA  T
                              ||||||     ||||||||||  |
                              GGTATT     TTTATTTGGT  A
                                 TTTTCCA
GAM357  TReP-132  5'  ATGGTTTATTTACCTTTTTTAT 53136      CA_____
           GGTTTTGT              CTATGA     AGATAGATCA  T
                              ||||||     ||||||||||  |
                              GGTATT     TTTATTTGGT  A
                                 TTTTCCA
GAM357  TUSP    5'  TGGTCTGTTTTGCACGGTTT  39644     TA  A
                              AAGC  TG CAAGATAGATCA
                              ||||  || ||||||||||||
                              TTTG  AC GTTTTGTCTGGT
                                GC  _
GAM357  TUSP    5'  TGGTCTGTTTTGCACGGTTT  39644     TA  A
                              AAGC  TG CAAGATAGATCA
                              ||||  || ||||||||||||
                              TTTG  AC GTTTTGTCTGGT
                                GC  _
GAM357  UBAP    3'  TGGTTTGTTTTGTATTATGTT  76352    TATG_
                              AGC    ACAAGATAGATCA
                              |||    ||||||||||||
                              TTG    TGTTTTGTTTGGT
                                TATTA
GAM357  UBAP    3'  TGGTTTGTTTTGTATTATGTT  76352    TATG_
                              AGC    ACAAGATAGATCA
                              |||    ||||||||||||
                              TTG    TGTTTTGTTTGGT
                                TATTA
GAM357  LOC120105 3'  TGGTTTGTTTTGTTTTGTT   75517    TAT
                              AGC   GACAAGATAGATCA
                              |||   ||||||||||||||
                              TTG   TTGTTTTGTTTGGT
                                TT_
GAM357  LOC120105 3'  TGGTTTGTTTTGTTTTGTT   75517    TAT
                              AGC   GACAAGATAGATCA
                              |||   ||||||||||||||
                              TTG   TTGTTTTGTTTGGT
                                TT_
GAM357  LOC120114 3'  GTCTTGTATGGCTTTGT    75536         A
                              ATAAAGCTATG CAAGAT
                              |||||||||| ||||||
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                                TGTTTCGGTAT GTTCTG
                                          _
GAM357  LOC120114 3'  GTCTTGTATGGCTTTGT     75536          A
                                ATAAAGCTATG CAAGAT
                                |||||||||| ||||||
                                TGTTTCGGTAT GTTCTG
                                          _
GAM357  LOC126669 3'  TGATTTGTTTTGTTTTGTTT   75422     TAT
                                AAGC   GACAAGATAGATCA
                                ||||   ||||||||||||||
                                TTTG   TTGTTTTGTTTAGT
                                  TT_
GAM357  LOC126669 3'  TGATTTGTTTTGTTTTGTTT   75422     TAT
                                AAGC   GACAAGATAGATCA
                                ||||   ||||||||||||||
                                TTTG   TTGTTTTGTTTAGT
                                  TT_
GAM357  LOC130413 5'  ATCCTGTTGAGCTTTAT     75742        A    A
                                ATAAAGCT TGACA GAT
                                |||||||| ||||| |||
                                TATTTCGA GTTGT CTA
                                     _    C
GAM357  LOC130413 5'  ATCCTGTTGAGCTTTAT     75742        A    A
                                ATAAAGCT TGACA GAT
                                |||||||| ||||| |||
                                TATTTCGA GTTGT CTA
                                     _    C
GAM357  LOC145078 3'  GAGGTCTTTTATCTGTTGTAGC 60291       TG  A  ___    A
          TTTGT                   AAGCTA  ACA GAT   AGATC
                                |||||| ||| |||  |||||
                                TTCGAT  TGT CTA   TCTGG
                                   GT  _  TTT    AGT
GAM357  LOC145078 3'  GAGGTCTTTTATCTGTTGTAGC 60291       TG  A  ___    A
          TTTGT                   AAGCTA  ACA GAT   AGATC
                                |||||| ||| |||  |||||
                                TTCGAT  TGT CTA   TCTGG
                                   GT  _  TTT    AGT
GAM357  LOC157567 3'  TGATTAGTTTTTGTTGGTGGTT 81485        _     TA_
          TTGT                    TAAAGCTAT GACAAGA   GATCA
                                ||||||||| |||||||  |||||
                                GTTTTGGTG TTGTTTT   TTAGT
                                     G      TGA
GAM357  LOC157567 3'  TGATTAGTTTTTGTTGGTGGTT 81485        _     TA_
          TTGT                    TAAAGCTAT GACAAGA   GATCA
                                ||||||||| |||||||  |||||
                                GTTTTGGTG TTGTTTT   TTAGT
                                     G      TGA
GAM357  LOC200282 3'  TGATTTATTTTGTTTGCT    88708     TAT
                                AGC   GACAAGATAGATCA
                                |||   ||||||||||||||
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                              TCG   TTGTTTTATTTAGT
                                T__
GAM357   LOC200282 3'  TGATTTATTTTGTTTGCT    88708     TAT
                              AGC   GACAAGATAGATCA
                              |||   ||||||||||||||
                              TCG   TTGTTTTATTTAGT
                                T__
GAM357   LOC200609 5'  TGATCTGTTTTGTCCTTATGGT 90105        ___
            TTTG                  AAGCTAT   GACAAGATAGATCA
                              |||||||   ||||||||||||||
                              TTTGGTA   CTGTTTTGTCTAGT
                                  TTC
GAM357   LOC200609 5'  TGATCTGTTTTGTCCTTATGGT 90105        ___
            TTTG                  AAGCTAT   GACAAGATAGATCA
                              |||||||   ||||||||||||||
                              TTTGGTA   CTGTTTTGTCTAGT
                                  TTC
GAM357   LOC220988 3'  GAGGTCTTTTATCTGTTGTAGC 90847       TG   A  ___    A
            TTTGT                 AAGCTA  ACA GAT   AGATC
                              ||||||  ||| |||   |||||
                              TTCGAT  TGT CTA   TCTGG
                                 GT   _   TTT    AGT
GAM357   LOC220988 3'  GAGGTCTTTTATCTGTTGTAGC 90847       TG   A  ___    A
            TTTGT                 AAGCTA  ACA GAT   AGATC
                              ||||||  ||| |||   |||||
                              TTCGAT  TGT CTA   TCTGG
                                 GT   _   TTT    AGT
GAM357   LOC221968 3'  TGAACATTTTGTAGTAGTTTTG 92569          G      AGATCA
            T                  ATAAAGCTAT ACAAGAT
                              ||||||||||| |||||||
                              TGTTTTGATG TGTTTTA
                                    A      CAAGT
GAM357   LOC221968 3'  TGAACATTTTGTAGTAGTTTTG 92569          G      AGATCA
            T                  ATAAAGCTAT ACAAGAT
                              ||||||||||| |||||||
                              TGTTTTGATG TGTTTTA
                                    A      CAAGT
GAM357   LOC222028 3'  CTTGGTATGGTTTTAT      94057          A
                              ATAAAGCTATG CAAG
                              ||||||||||| ||||
                              TATTTTGGTAT GTTC
                                     G
GAM357   LOC222028 3'  CTTGGTATGGTTTTAT      94057          A
                              ATAAAGCTATG CAAG
                              ||||||||||| ||||
                              TATTTTGGTAT GTTC
                                     G
GAM357   LOC253634 5'  GGTCTGGGCATAGCTT      96618        ACAAGA
                              AAGCTATG     TAGATC
                              ||||||||     ||||||
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                                TTCGATAC     GTCTGG
                                     GG____
GAM357  LOC253634 5'  GGTCTGGGCATAGCTT      96618         ACAAGA
                                AAGCTATG     TAGATC
                                ||||||||     ||||||
                                TTCGATAC     GTCTGG
                                     GG____
GAM357  LOC255190 3'  GAGGTCTTTTATCTGTTGTAGC 97688       TG   A  ___    A
           TTTGT                  AAGCTA  ACA GAT   AGATC
                                ||||||  ||| |||   |||||
                                TTCGAT  TGT CTA   TCTGG
                                   GT   _   TTT     AGT
GAM357  LOC255190 3'  GAGGTCTTTTATCTGTTGTAGC 97688       TG   A  ___    A
           TTTGT                  AAGCTA  ACA GAT   AGATC
                                ||||||  ||| |||   |||||
                                TTCGAT  TGT CTA   TCTGG
                                   GT   _   TTT     AGT
GAM357  LOC51031  3'  TGAAAATGTTTTCTTGTAGTTT 32200        TG C     GA_
           TGT                    ATAAAGCTA  A AAGATA   TCA
                                |||||||||  | ||||||   |||
                                TGTTTTGAT  T TTTTGT   AGT
                                     GT C     AAA
GAM357  LOC51031  3'  TGAAAATGTTTTCTTGTAGTTT 32200        TG C     GA_
           TGT                    ATAAAGCTA  A AAGATA   TCA
                                |||||||||  | ||||||   |||
                                TGTTTTGAT  T TTTTGT   AGT
                                     GT C     AAA
GAM357  LOC51315  3'  TGATTGGGTTTGTTATAGTTTT 33530            ATA
           G                     TAAAGCTATGACAAG   GATCA
                                ||||||||||||||   |||||
                                GTTTTGATATTGTTT   TTAGT
                                        GGG
GAM357  LOC51315  3'  TGATTGGGTTTGTTATAGTTTT 33530            ATA
           G                     TAAAGCTATGACAAG   GATCA
                                ||||||||||||||   |||||
                                GTTTTGATATTGTTT   TTAGT
                                        GGG
GAM357  LOC51580  3'  TGGTTGGTTTTTGTTTGGTTTT 31867         T      TA_
           GT                     ATAAAGCTA GACAAGA   GATCA
                                |||||||| |||||||   |||||
                                TGTTTTGGT TTGTTTT   TTGGT
                                     _      TGG
GAM357  LOC51580  3'  TGGTTGGTTTTTGTTTGGTTTT 31867         T      TA_
           GT                     ATAAAGCTA GACAAGA   GATCA
                                |||||||| |||||||   |||||
                                TGTTTTGGT TTGTTTT   TTGGT
                                     _      TGG
GAM357  LOC57826  3'  GATCATTGTTATTAGCTTTGT  41018         _     GATA    A
                                ATAAAGCTA TGACAA    GATC
                                |||||||| ||||||    ||||
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                                TGTTTCGAT ATTGTT   CTAG
                                     T    A___   G
GAM357  LOC57826  3'  GATCATTGTTATTAGCTTTGT  41018       _    GATA   A
                                ATAAAGCTA TGACAA   GATC
                                ||||||||| ||||||   ||||
                                TGTTTCGAT ATTGTT   CTAG
                                     T    A___   G
GAM358  C5R1      3'  CCCAGCCTCCCCCAATGGCA  8202       AA_  T_
                                TGCCATTG  GA  CTGGG
                                ||||||||  ||  |||||
                                ACGGTAAC  CT  GACCC
                                    CCC  CC
GAM358  CALM3     3'  TCCCCAGATCCCCTTGGAGC  17747    G  TTGAA
                                GCT CCA   GATCTGGGGA
                                ||| |||   ||||||||||
                                CGA GGT   CTAGACCCCT
                                  _  TCCC_
GAM358  EVPL      3'  TCCCCAGACCAGGACAGCAGC  8807     CA__  AAGA
                                GCTGC   TTG   TCTGGGGA
                                |||||   |||   ||||||||
                                CGACG   GAC   AGACCCCT
                                  ACAG  C___
GAM358  EZH1      3'  TCCCAGGCCCCAACGGCAGC  8829      A  AAGA
                                GCTGCC TTG   TCTGGGG
                                |||||| |||   |||||||
                                CGACGG AAC   GGACCCT
                                   C  CCC_
GAM358  GORASP1   3'  CCTGTATCCCCAGTGGCAACT  49109   C     AA  CT
                                AG TGCCATTG  GAT  GGG
                                || ||||||||  |||  |||
                                TC ACGGTGAC  CTA  TCC
                                 A      CC  TG
GAM358  GPR62     5'  CCCCAAGAGGATGGCAGC   89518       GAAGA  _
                                GCTGCCATT    TCT GGGG
                                |||||||||    ||| ||||
                                CGACGGTAG    AGA CCCC
                                     G____  A
GAM358  KIP2      3'  TCCCCAGGAAAGCAGTGGCAGC 21092       AAGA
                                GCTGCCATTG   TCTGGGGA
                                ||||||||||   ||||||||
                                CGACGGTGAC   GGACCCCT
                                      GAAA
GAM358  MHC2TA    3'  TCCTGTGTCTTGCAATGGCAGC 4193        _   CT
                                GCTGCCATTG AAGAT  GGGG
                                |||||||||| |||||  ||||
                                CGACGGTAAC TTCTG  TCCT
                                      G    TG
GAM358  MMP15     3'  TCCCCAGGGAAGCAGCAGC   10077     CAT  AAGA
                                GCTGC   TG   TCTGGGGA
                                |||||   ||   ||||||||
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                              CGACG  AC   GGACCCCT
                                 ___ GAAG
GAM358  MTERF    3' TCCCCAGAAAGGAATGCAGC  22734     C  GAAGA
                              GCTGC ATT   TCTGGGGA
                              ||||| |||   ||||||||
                              CGACG TAA   AGACCCCT
                                 _  GGAA_
GAM358  POLS     3' TCCATCTTCAAGAACAGCT   22794     CCA     TC
                              AGCTG  TTGAAGA  TGGG
                              |||||  |||||||  ||||
                              TCGAC  AACTTCT  ACCT
                                 AAG     __
GAM358  SERPINB9 3' TCCCCAGATCCCCACTACAGCT 14768     CCAT  AA
                              AGCTG   TG  GATCTGGGGA
                              |||||   ||  ||||||||||
                              TCGAC   AC  CTAGACCCCT
                                 ATC_  CC
GAM358  SLC1A5   5' CCCCAGATTCTGGCA      18845     TTGAA
                              TGCCA    GATCTGGGG
                              |||||    |||||||||
                              ACGGT    TTAGACCCC
                                 C____
GAM358  SLC1A5   5' CCCCAGATTCTGGCA      78536     TTGAA
                              TGCCA    GATCTGGGG
                              |||||    |||||||||
                              ACGGT    TTAGACCCC
                                 C____
GAM358  TCF3     3' TCCCCAGACTGGCTTGGGAGC  70734    G   TTGA  A
                              GCT CCA   AG TCTGGGGA
                              ||| |||   || ||||||||
                              CGA GGT   TC AGACCCCT
                                G  TCGG  _
GAM358  TCTA     3' TCCCCAGACCTCAGGGACAACT 42242    C  _  A   A A
                              AG TG CC TTGA G TCTGGGGA
                              || || || |||| | ||||||||
                              TC AC GG GACT C AGACCCCT
                               A  A  _   _ C
GAM358  TGFB1    5' TCCCCAGACCTCGGGCGC    5404     T   AT   A A
                              GC GCC  TGA G TCTGGGGA
                              || |||  ||| | ||||||||
                              CG CGG  GCT C AGACCCCT
                               _  __  _ C
GAM358  TK2      3' TCCCCAGAGGTCACACAGC   16061     CCAT   AGA
                              GCTG   TGA   TCTGGGGA
                              ||||   |||   ||||||||
                              CGAC   ACT   AGACCCCT
                                AC__   GG_
GAM358  ABLIM    3' CCCTCCTGCAATGGCAGC    9762          A  ATCT
                              GCTGCCATTG AG   GGGG
                              |||||||||| ||   ||||
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                                CGACGGTAAC TC    TCCC
                                      G  C___
GAM358  ABLIM    3'  CCCTCCTGCAATGGCAGC    22023          A  ATCT
                                GCTGCCATTG AG    GGGG
                                |||||||||| ||    ||||
                                CGACGGTAAC TC    TCCC
                                      G  C___
GAM358  APH2     3'  TCAAGGGCCTCCAAGGGCAGCT 50319        A   A  AT  GG
          T                      AAGCTGCC TTG AG  CT  GG
                                |||||||| ||| ||  ||  ||
                                TTCGACGG AAC TC  GG  CT
                                     G   C  CG  AA
GAM358  C11orf9  3'  CCCCAGATGGTATTGCAGCTT  25209       CAT  AAG
                                AAGCTGC   TG   ATCTGGGG
                                |||||||   ||   ||||||||
                                TTCGACG   AT   TAGACCCC
                                    TT_  GG_
GAM358  C20orf139 3'  CCCCAAACTTGGCAGCT     84755        TTGA  ATC
                                AGCTGCCA    AG   TGGGG
                                ||||||||    ||   |||||
                                TCGACGGT    TC   ACCCC
                                     _____  AA_
GAM358  C6orf28  5'  TCCCCAGACCTGCTCGCAGC   40995      CATTGA  A
                                GCTGC     AG TCTGGGGA
                                |||||     || ||||||||
                                CGACG     TC AGACCCCT
                                   CTCG__  C
GAM358  DEPP     5'  CCCCAGACCTCCTCAGCT    22820      CCATT  A A
                                AGCTG     GA G TCTGGGG
                                |||||     || | |||||||
                                TCGAC     CT C AGACCCC
                                   TC___  _ C
GAM358  DKFZp547E052 3'  CCCCTTCCCAGTGGCAGCTT   50096          AA  TCT
                                AAGCTGCCATTG  GA   GGGG
                                ||||||||||||  ||   ||||
                                TTCGACGGTGAC  CT   CCCC
                                       C_  T__
GAM358  DKFZp761H2121 5'  TCCCCAGGGGAAAATGGC    56372       GAAGA
                                GCCATT    TCTGGGGA
                                ||||||    ||||||||
                                CGGTAA    GGACCCCT
                                    AAGG_
GAM358  ELSPBP1  5'  TCCCCAGATAATCCAGAGCT   42158     GCCATT  AG
                                AGCT     GA  ATCTGGGGA
                                ||||     ||  |||||||||
                                TCGA     CT  TAGACCCCT
                                  GAC___  AA
GAM358  FLJ10209  5'  TCCCCAGATCTGGGCCACAGC  35899     CCATTGA
                                GCTG      AGATCTGGGGA
                                ||||      ||||||||||
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                                CGAC      TCTAGACCCCT
                                  ACCGGG_
GAM358  FLJ10774  3'  TCCCGGCATCCATGGCAGC   45086        TGAA  _
                                GCTGCCAT   GAT CTGGGG
                                ||||||||   ||| ||||||
                                CGACGGTA   CTA GGCCCT
                                    C___  C
GAM358  FLJ12783  3'  TCCCCAGATCTCTCAG     48683     _
                                TTGA AGATCTGGGGA
                                |||| ||||||||||
                                GACT TCTAGACCCCT
                                  C
GAM358  FLJ12788  3'  CCCCAGATTACTCACAGCT   42542     CCAT  A_
                                AGCTG   TGA  GATCTGGGG
                                |||||   |||  |||||||||
                                TCGAC   ACT  TTAGACCCC
                                  _____  CA
GAM358  FLJ22582  3'  TCCCCAGACCACCCCGGCAGC  46781      ATTGAAGA
                                GCTGCC      TCTGGGGA
                                ||||||      ||||||||
                                CGACGG      AGACCCCT
                                   CCCCACC_
GAM358  FLJ32332  3'  CCATCTTCAAGACAGC     58301     CCA     TC
                                GCTG  TTGAAGA  TGG
                                ||||  |||||||  |||
                                CGAC  AACTTCT  ACC
                                  AG_     __
GAM358  ITGA10    3'  CCCCAGACCAGCAGC      59377     CAT  AAGA
                                GCTGC  TG   TCTGGGG
                                |||||  ||   |||||||
                                CGACG  AC   AGACCCC
                                  ____ C___
GAM358  KIAA1538  3'  CCCCAAATCCAGTGAGCT   71536     GC    AA  C
                                AGCT  CATTG  GAT TGGGG
                                ||||  |||||  ||| |||||
                                TCGA  GTGAC  CTA ACCCC
                                  __    __  A
GAM358  MEIS3     3'  CCCCAGAAGATGGCAGCT   78279        GAAGA
                                AGCTGCCATT    TCTGGGG
                                ||||||||||    |||||||
                                TCGACGGTAG    AGACCCC
                                    A_____
GAM358  MGC2941   3'  CCCCAAATCTGGAGAGC    44158    G_  TTGAA  C
                                GCT  CCA    GAT TGGGG
                                |||  |||    ||| |||||
                                CGA  GGT    CTA ACCCC
                                  GA  ______  A
GAM358  PALM      3'  CCCCATGTCACGGCAGCTT   10411       ATTGAA  C
                                AAGCTGCC     GAT TGGGG
                                ||||||||     ||| |||||
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                                TTCGACGG     CTG ACCCC
                                     CA____   T
GAM358  PRO2730   5'  TTCCACCAACGGCAGCTT    47422        A   AAGATC   GG
                                AAGCTGCC TTG     TGG  A
                                |||||||| |||     |||  |
                                TTCGACGG AAC     ACC  T
                                     C   C_____   TT
GAM358  RPS6KC1   3'  TCTGTGTCTTCAACAGC     24853      CCA      CT
                                GCTG   TTGAAGAT  GGG
                                ||||   ||||||||  |||
                                CGAC   AACTTCTG  TCT
                                   ___       TG
GAM358  TRAD      3'  TCCCCGCAAATTCACTGGCAGC 22955        T    GATC
              T                  AGCTGCCA TGAA    TGGGGA
                                ||||||||| ||||    ||||||
                                TCGACGGT ACTT    GCCCCT
                                     C    AAAC
GAM358  LOC130813 3'  CCCCACACAAGGCAGCTT    75767        A   AAGATC
                                AAGCTGCC TTG     TGGGG
                                |||||||| |||     |||||
                                TTCGACGG AAC     ACCCC
                                     _   AC____
GAM358  LOC138835 5'  CCATCTCCACGGCAGCTT    75954        AT  A   TC
                                AAGCTGCC  TG AGA  TGG
                                |||||||| || |||  |||
                                TTCGACGG  AC TCT  ACC
                                     C_  C   __
GAM358  LOC144577 3'  TCAGAAGATCCTCATGGCAGCT 76904         T  A    GGG
              T                   AAGCTGCCAT GA GATCT   GA
                                ||||||||||| || |||||   ||
                                TTCGACGGTA CT CTAGA   CT
                                     _  C    AGA
GAM358  LOC146268 3'  CCCCAGACCTGCAGCTT     77804        CATTGA  A
                                AAGCTGC     AG TCTGGGG
                                |||||||     || |||||||
                                TTCGACG     TC AGACCCC
                                    _______  C
GAM358  LOC151996 3'  CCCAGATCCCACAGT       85531      CCAT  AA
                                GCTG    TG  GATCTGGG
                                ||||    ||  ||||||||
                                TGAC    AC  CTAGACCC
                                   _____  C_
GAM358  LOC154403 3'  TCCCCAGAAGGAATGCAGC   81076       C   GAAGA
                                GCTGC ATT    TCTGGGGA
                                ||||| |||    ||||||||
                                CGACG TAA    AGACCCCT
                                   _   GGA__
GAM358  LOC158809 3'  TCAGATCCTCAACAG       86898     CCA    A
                                CTG   TTGA GATCTGG
                                |||   |||| |||||||
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                                GAC   AACT CTAGACT
                                  ___    C
GAM358  LOC161244 3'  CCCCAGATCTCCCCGTCAGC   87081     CCATT  A
                                GCTG    GA GATCTGGGG
                                ||||    || |||||||||
                                CGAC    CT CTAGACCCC
                                  TGCCC  _
GAM358  LOC161244 3'  CCCCAGATCTCCCCGTCAGC   87082     CCATT  A
                                GCTG    GA GATCTGGGG
                                ||||    || |||||||||
                                CGAC    CT CTAGACCCC
                                  TGCCC  _
GAM358  LOC170063 3'  TCAGTTTCAATGGCA       87247          AT
                                TGCCATTGAAG  CTGG
                                ||||||||||  ||||
                                ACGGTAACTTT  GACT
                                      __
GAM358  LOC196955 5'  CCCCACCCTCAATGGCAGCT   77370          A ATC
                                AGCTGCCATTGA G   TGGGG
                                ||||||||||| |   |||||
                                TCGACGGTAACT C   ACCCC
                                      _ CC_
GAM358  LOC200186 3'  TCCCCAGATCCTCTTTCTAGC  89964     CCATT  A
                                GCTG    GA GATCTGGGGA
                                ||||    || ||||||||||
                                CGAT    CT CTAGACCCCT
                                  CTTT_  C
GAM358  LOC221405 5'  CCCAAGGCCCCACTGGCAGCTT 93881         T  AAGA   G
                                AAGCTGCCA TG    TCT GGG
                                |||||||| ||    ||| |||
                                TTCGACGGT AC    GGA CCC
                                     C  CCC_   A
GAM358  LOC254105 3'  TCCCCAGATGGAGGCAGTCA   94771    A     A  GAAG
                                A GCTGCC TT    ATCTGGGGA
                                | |||||| ||    |||||||||
                                A TGACGG AG    TAGACCCCT
                                 C      _  G___
GAM358  LOC257468 3'  CCCCAGAAGATGGCAGCT    95186         GAAGA
                                AGCTGCCATT    TCTGGGG
                                ||||||||||    |||||||
                                TCGACGGTAG    AGACCCC
                                     A_____
GAM359  MMP20    3'  TCCAAATCAACACAATGCAC   16484           CAGGA
                                GTGCATTGTGTTG    TTGGG
                                ||||||||||||    |||||
                                CACGTAACACAAC    AACCT
                                      TA___
GAM359  PIM2     3'  TCCCAATCCTACAAAGGAGC   59991    A  GTG   C
                                GC TT   TTG AGGATTGGGA
                                || ||   ||| ||||||||||
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                                CG AG   AAC TCCTAACCCT
                                 _ GA_   A
GAM359  RXRA     3'  CCCAATCCTTAGCAATGC    11405       GTTGC
                                GCATTGT    AGGATTGGG
                                |||||||    |||||||||
                                CGTAACG    TCCTAACCC
                                   AT___
GAM359  BRAG     3'  TCCCAATTCCAAAACACAATGC 29477          GCA
              AC                  GTGCATTGTGTT   GGATTGGGA
                                |||||||||||  |||||||||
                                CACGTAACACAA   CTTAACCCT
                                      AAC
GAM359  DKFZp547O146 5'  CCCAATCCCCCAACAC      39564       CA
                                GTGTTG  GGATTGGG
                                ||||||  ||||||||
                                CACAAC  CCTAACCC
                                   CC
GAM359  KIAA1762  3'  TCCCAATCCCCACAGACACACA 63792     CAT     GCA__
              C                   GTG   TGTGTT    GGATTGGGA
                                |||   ||||||    |||||||||
                                CAC   ACACAG    CCTAACCCT
                                 ___     ACACC
GAM359  LOC145820 3'  CCCAATCCTTAAGCAATCAC   77512     C    GTTGC
                                GTG ATTGT    AGGATTGGG
                                ||| |||||    |||||||||
                                CAC TAACG    TCCTAACCC
                                  _    AAT__
GAM359  LOC253980 3'  TCCCAACCCCATTGCTAACAA  95076      GTT  ___  A
                                TTGT   GCA   GG TTGGGA
                                ||||   |||   || ||||||
                                AACA   CGT   CC AACCCT
                                  AT_   TAC  C
GAM360  ACCN1    3'  TATTAAAAGCTGGTCTTGTGGA 6584         __    TA   CC
              AA                  TTTTCAC  GGCCA  GCTT  AATA
                                |||||||  |||||  ||||  ||||
                                AAAGGTG  CTGGT  CGAA  TTAT
                                   TT    __   AA
GAM360  IRF2     5'  TTGGTAGCGTGAAAA      9358        GGCCATA   T
                                TTTTCAC      GCT CCAA
                                |||||||      ||| ||||
                                AAAAGTG      CGA GGTT
                                   ________  T
GAM360  PABPN1   5'  ATTGGAAGCTGTCCAGGAAAA  16174      AC  CC
                                TTTTC  GG  ATAGCTTCCAAT
                                |||||  ||  ||||||||||||
                                AAAAG  CC  TGTCGAAGGTTA
                                  GA  __
GAM360  TPO      5'  GAGTTACAGCCGTGAAAA    5046          CA
                                TTTTCACGGC  TAGCTT
                                ||||||||||  ||||||
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                                AAAAGTGCCG  ATTGAG
                                      AC
GAM360  ARHU     3'  TATTAGAAGCTATATTAGCTG  41079     C___      C
                                CGGC    ATAGCTTC AATA
                                ||||    |||||||| ||||
                                GTCG    TATCGAAG TTAT
                                  ATTA       A
GAM360  FLJ12998  3'  ATTGGTTTTGCCGTGAAAA   42835         CATAGCTT
                                TTTTCACGGC       CCAAT
                                ||||||||||       |||||
                                AAAAGTGCCG       GGTTA
                                      TTTT____
GAM360  GNB4     3'  AGCCTATAGCTGTGAAAA    41267         C   _
                                TTTTCACGGC ATAG CT
                                |||||||||| |||| ||
                                AAAAGTGTCG TATC GA
                                      A   C
GAM360  LOC150418 3'  GAGTCGGCCGTGAAGA      65509          ATA
                                TTTTCACGGCC   GCTT
                                ||||||||||   ||||
                                AGAAGTGCCGG   TGAG
                                      C__
GAM360  LOC199957 3'  GAGTCGGCCGTGAAGA      88505          ATA
                                TTTTCACGGCC   GCTT
                                ||||||||||   ||||
                                AGAAGTGCCGG   TGAG
                                      C__
GAM360  LOC91431  5'  ATTGGAAATGCAAGGCCGTGGA 56922          ATA __
           AA                    TTTTCACGGCC   GC  TTCCAAT
                                ||||||||||   ||  |||||||
                                AAAGGTGCCGG   CG  AAGGTTA
                                      AA_  TA
GAM361  CSNK1G2   3'  GGCCCAGCCCTGCAGGT     7170        AAC   ACTT
                                ACCTGTAG   CTG    GGCC
                                ||||||||   |||    ||||
                                TGGACGTC   GAC    CCGG
                                     CC_   _____
GAM361  PCDH11X   3'  CAATCATATTCTACAG      27238        CC   C
                                CTGTAGAA  TGA TTG
                                ||||||||  ||| |||
                                GACATCTT  ACT AAC
                                     AT   _
GAM361  SFTPA2    3'  GGTCAGGCTCTCCAGGTG    22650       T   A
                                CACCTG AGA CCTGACT
                                |||||| ||| |||||||
                                GTGGAC TCT GGACTGG
                                   C   C
GAM361  TBX5      5'  CCAAGTCCTATAGGTG      54888         AACCT
                                CACCTGTAG    GACTTGG
                                |||||||||    |||||||
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                              GTGGATATC    CTGAACC
                                    _____
GAM361  TBX5     5'  CCAAGTCCTATAGGTG     3956         AACCT
                              CACCTGTAG    GACTTGG
                              |||||||||    |||||||
                              GTGGATATC    CTGAACC
                                    _____
GAM361  ZNF132   3'  GCCAAGTCAAACTTCATGCAG  12826      _  CC_
                              CTGTA GAA   TGACTTGGC
                              ||||| |||   |||||||||
                              GACGT CTT   ACTGAACCG
                                 A   CAA
GAM361  C9orf14  5'  GCCAAGTCCATCTAAAGTG   86676    CTG   ACCT
                              CAC   TAGA   GACTTGGC
                              |||   ||||   ||||||||
                              GTG   ATCT   CTGAACCG
                                AA_    AC__
GAM361  DKFZP434J037 3'  GCCCGGTCAGGCTCTCAG    48213     T  A     T
                              CTG AGA CCTGACT GGC
                              ||| ||| ||||||| |||
                              GAC TCT GGACTGG CCG
                                _  C      C
GAM361  ELOVL2   3'  GCCTAGGTTATACAG      34959      G     ACTT
                              CTGTA AACCTG    GGC
                              ||||| ||||||    |||
                              GACAT TTGGAT    CCG
                                 A     ____
GAM361  FLJ11996 3'  TTAGGTGCCTACAGGT     46447        A_
                              ACCTGTAG  ACCTGA
                              ||||||||  ||||||
                              TGGACATC  TGGATT
                                   CG
GAM361  FLJ13265 3'  GCCAGAACTTTACAGGTG    45926         ACCTGAC
                              CACCTGTAGA      TTGGC
                              ||||||||||      |||||
                              GTGGACATTT      GACCG
                                    CAA____
GAM361  FLJ20038 5'  CCAAGTCAGAACTGCG      34402      AAC
                              TGTAG   CTGACTTGG
                              |||||   |||||||||
                              GCGTC   GACTGAACC
                                 AA_
GAM361  FLJ20972 3'  GCCAAGTCAGTTCCTGGTG   46725     TGTA   C
                              CACC    GAAC TGACTTGGC
                              ||||    |||| |||||||||
                              GTGG    CTTG ACTGAACCG
                                TC__    _
GAM361  KIAA0061 3'  GCCAAGTTCTACATGTG     68292     C     ACCTG
                              CAC TGTAGA    ACTTGGC
                              ||| ||||||    |||||||
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                                GTG ACATCT    TGAACCG
                                  T    _____
GAM361  KIAA0141  3'  CGGGAGTTCAGGTTCCCAAG  28732   GTA     _  GG
                                CT  GAACCTGA CTT  CCG
                                ||  |||||||| |||  |||
                                GA  CTTGGACT GAG  GGC
                                 ACC      T  __
GAM361  KIAA1260  3'  GTCAGGTTGCACAGGTG    60029      AG
                                CACCTGT  AACCTGAC
                                |||||||  ||||||||
                                GTGGACA  TTGGACTG
                                    CG
GAM361  KIAA1301  3'  GCCTATGGGTTTACAGG    66342      A   ACTT
                                CCTGTAGA CCTG   GGC
                                |||||||| ||||   |||
                                GGACATTT GGGT   CCG
                                   _   AT__
GAM361  KIAA1485  3'  GGCTGCCAGGCTCTGCAGG  89262      A   ACT
                                CCTGTAGA CCTG  TGGCC
                                |||||||| ||||  |||||
                                GGACGTCT GGAC  GTCGG
                                    C   C__
GAM361  KIAA1546  3'  CAGGCAAACACCTACAGGT  67904      AACC_  A
                                ACCTGTAG    TG CTTG
                                ||||||||    || ||||
                                TGGACATC    AC GGAC
                                    CACAA  _
GAM361  KIAA1643  3'  CACCTCAGGTTCCCAGGTG  64548      TA     CT
                                CACCTG  GAACCTGA  TG
                                ||||||  ||||||||  ||
                                GTGGAC  CTTGGACT  AC
                                   C_      CC
GAM361  MGC10981  3'  CTGAGTCGATCCCACAGGTG  51017      A_  ACC   TG
                                CACCTGT  GA  TGACT  G
                                |||||||  ||  |||||  |
                                GTGGACA  CT  GCTGA  C
                                    CC  A__   GT
GAM361  MGC11324  3'  AGGCAGAACCTACAGGTG   51164      AAC  A
                                CACCTGTAG  CTG CTT
                                |||||||||  ||| |||
                                GTGGACATC  GAC GGA
                                    CAA  _
GAM361  MOST2     5'  CGGCCAAGCCTGTGCCTACGGT 39682    T   A_  CTGA
          G                  CACC GTAG  AC   CTTGGCCG
                             |||| ||||  ||   ||||||||
                             GTGG CATC  TG   GAACCGGC
                               _   CG  TCC_
GAM361  PADI3     3'  CGGCCAAGCTCCTGC     32657     AACCT  _
                                GTAG    GA CTTGGCCG
                                ||||    || ||||||||
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                                CGTC    CT GAACCGGC
                                  _____ C
GAM361  phospho1  5'  CAGAGTCCCTACAGGTG    82367        A_ _
                                CACCTGTAG  AC CTG
                                |||||||||  || |||
                                GTGGACATC  TG GAC
                                     CC  A
GAM361  RAB3D     3'  TGGCTGCCAGGTTCCTCAGG  15010     TA     ACT
                                CCTG  GAACCTG   TGGCCG
                                ||||  |||||||   ||||||
                                GGAC  CTTGGAC   GTCGGT
                                  TC      C__
GAM361  LOC122955 5'  GCTGTCAGTTCTACAG     75585        C    TT
                                CTGTAGAAC TGAC  GGC
                                ||||||||| ||||  |||
                                GACATCTTG ACTG  TCG
                                      _   __
GAM361  LOC149386 5'  CAAGTCAGGTCCACA      84404     A  A
                                TGT GA CCTGACTTG
                                ||| || |||||||||
                                ACA CT GGACTGAAC
                                  C  _
GAM361  LOC150197 5'  GCCAGGTCCTACGG       79598       AACCT
                                CTGTAG    GACTTGGC
                                ||||||    ||||||||
                                GGCATC    CTGGACCG
                                     _____
GAM361  LOC151878 5'  CTAGTTCAGACTCTAAGG    80374     G    AC    C
                                CCT TAGA  CTGA TTGG
                                ||| ||||  |||| ||||
                                GGA ATCT  GACT GATC
                                  _   CA   T
GAM361  LOC153146 5'  GCCAGAGCCTACAGGT      85929        AAC  GAC
                                ACCTGTAG   CT   TTGGC
                                ||||||||   ||   |||||
                                TGGACATC   GA   GACCG
                                     C__  ___
GAM361  LOC221931 3'  AAGTTGCAGGTTCTTCAG    93992     T       __
                                CTG AGAACCTG  ACTT
                                ||| ||||||||  ||||
                                GAC TCTTGGAC  TGAA
                                  T       GT
GAM361  LOC254848 5'  CGGCAGGCACAGGTTCTCCA  97090    T      A_   G
                                TG AGAACCTG  CTTG CCG
                                || ||||||||  |||| |||
                                AC TCTTGGAC  GGAC GGC
                                 C       AC   _
GAM362  BTN2A1    3'  ACAATCCCCAGGGTTCCTGAGA 54336    C       GTCTATTT
                                TC CAGGAACCC       TTGT
                                || |||||||||       ||||
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                                AG GTCCTTGGG       AACA
                                 A        ACCCCT__
GAM362  DKFZP564K0822 3'  CAAAACAGACACCCTGGGA   94042        AACCC   AT
                                TCCCAGG    GTCT  TTTTG
                                |||||||    ||||  |||||
                                AGGGTCC    CAGA  AAAAC
                                    CA___    C_
GAM362  DKK2     3'  AAAATGGACTCCTG       27013      ACCC
                                CAGGA    GTCTATTTT
                                |||||    |||||||||
                                GTCCT    CAGGTAAAA
                                   _____
GAM362  FLJ14213  3'  CAAGCAGAGCTCCTGGGA    45793        ACCC T  ATT
                                TCCCAGGA    G CT   TTTG
                                ||||||||    | ||   ||||
                                AGGGTCCT    C GA   GAAC
                                    _____ _  GAC
GAM362  FLJ21458  3'  ACAAAAATAGGGGTCTTCCTGG 45844       __    GT
                                CCAGGA  ACCC  CTATTTTTGT
                                ||||||  ||||  ||||||||||
                                GGTCCT  TGGG  GATAAAAACA
                                    TC   __
GAM362  FLJ21615  3'  AAGTGGACAAATTTCTG     49834       CCC
                                CAGGAA   GTCTATTT
                                ||||||   ||||||||
                                GTCTTT   CAGGTGAA
                                    AAA
GAM362  FLJ22729  5'  CGGAAAACCGGTTCCTGAGA   45188    C       C  CTA
                                TC CAGGAACC GT   TTTTTG
                                || ||||||||  ||   ||||||
                                AG GTCCTTGG CA   AAAGGC
                                 A       C  ___
GAM362  HTMP10    5'  AGAAGGTTCCTGGGA      52604          CG
                                TCCCAGGAACC  TCT
                                ||||||||||  |||
                                AGGGTCCTTGG  AGA
                                      A_
GAM362  KIAA0447  3'  ACAAAAATAGCCCCTCCTG   71663      ACCC T
                                CAGGA    G CTATTTTTGT
                                |||||    | ||||||||||
                                GTCCT    C GATAAAAACA
                                   CCC_ _
GAM362  KIAA0459  3'  ACAGGAGACGAACTCCTGGGG  60979        ACC    ATT
                                TCCCAGGA   CGTCT   TTTGT
                                ||||||||   |||||   |||||
                                GGGGTCCT   GCAGA   GGACA
                                     CAA    ___
GAM362  KIAA0871  3'  CAAAAATAGATTCC       30300     ACCC
                                GGA    GTCTATTTTTG
                                |||    ||||||||||
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                                CCT    TAGATAAAAAC
                                  ____
GAM362  MGC21688  3'  ACAGCCTAGAGGGCTCCTGGGA 58263         A   G    TTT
                                TCCCAGGA CCC TCTA   TTGT
                                |||||||| ||| ||||   ||||
                                AGGGTCCT GGG AGAT   GACA
                                     C   _    CC_
GAM362  MGC2668   3'  AGATGGGCTCCTGAGA      60573     C     A
                                TC CAGGA CCCGTCT
                                || ||||| |||||||
                                AG GTCCT GGGTAGA
                                 A     C
GAM362  LOC125228 3'  AAAGATAGACTCACTG      74400      _  ACCC
                                CAG GA    GTCTATTTTT
                                ||| ||    ||||||||||
                                GTC CT    CAGATAGAAA
                                  A  _____
GAM362  LOC152426 5'  CAAAAGAAGGCTCCCTGG     85710       AACCC    A
                                CCAGG     GTCT TTTTTG
                                |||||     |||| ||||||
                                GGTCC     CGGA GAAAAC
                                   CT___    A
GAM362  LOC254007 3'  ACAAAAATGATGAGTCCTTGGA 96707     C    A C    T
                                TCC AGGA C CGTC ATTTTTGT
                                ||| |||| | |||| ||||||||
                                AGG TCCT G GTAG TAAAAACA
                                  T    _ A    _
GAM362  LOC91628  3'  ACAAAAATAAGATAGAATTTCC 66756    A    CCC__    _
            AGG                    CC GGAA     GTCT ATTTTTGT
                                || ||||     |||| ||||||||
                                GG CCTT     TAGA TAAAAACA
                                 A    TAAGA    A
GAM362  LOC92293  3'  TAGATAGGTTCCTAGGA     68764     C       CG
                                TCC AGGAACC  TCTA
                                ||| |||||||  ||||
                                AGG TCCTTGG  AGAT
                                  A       AT
GAM362  LOC92710  3'  AGTGGCCAGCAGGTTCCTGGGA 70353           C  ___
                                TCCCAGGAACC GT   CTATT
                                |||||||||| ||   |||||
                                AGGGTCCTTGG CG   GGTGA
                                       A  ACC
GAM363  ALDH1B1   3'  CACCTTGACCAATGCTTGCCA  5489     A      GC   G __
                                TG CAAGCAT  GGT A  GTG
                                || |||||||  ||| |  |||
                                AC GTTCGTA  CCA T  CAC
                                 C       A_   G TC
GAM363  AMPH      3'  TCACTCATTCCCATGTTGTCA  7907        G    C  __
                                TGACAA CATG GG  TGAGTGA
                                |||||| |||| ||  |||||||
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                                ACTGTT GTAC CC  ACTCACT
                                   _   _  TT
GAM363  APG5L   3'  TCACTGTAAGCCTGTCA    16763      A  A
                                TGACA GC TGCGGTGA
                                ||||| || ||||||||
                                ACTGT CG ATGTCACT
                                   C  A
GAM363  ATP7B   3'  CACTCACCACAAGCTGAGCA  3540     ACA  A  C
                                TG  AGC TG GGTGAGTG
                                ||  ||| || ||||||||
                                AC  TCG AC CCACTCAC
                                 GAG  A  A
GAM363  CSRP1   3'  CACTCCTGCGCTTTTCA    14528    C   AT   T
                                TGA AAGC  GCGG GAGTG
                                ||| ||||  |||| |||||
                                ACT TTCG  CGTC CTCAC
                                  T   __   _
GAM363  CTPS    3'  TCACTTGCATGTCCCATCA   88595    CAA_     _
                                TGA   GCATGCG GTGA
                                |||   ||||||| ||||
                                ACT   TGTACGT CACT
                                  ACCC      T
GAM363  DGAT2   3'  CACTACCCCACGCTCGTC    50788    A  A C  G
                                GAC AGC TG GGT AGTG
                                ||| ||| || ||| ||||
                                CTG TCG AC CCA TCAC
                                  C  C C  _
GAM363  EPB41L2 3'  CACAGTGCCAATGCTTGTCA  7481         GC   A_
                                TGACAAGCAT  GGTG  GTG
                                ||||||||||  ||||  |||
                                ACTGTTCGTA  CCGT  CAC
                                     A_   GA
GAM363  FLNA    3'  CTGGCCGCCCGCCTGTCA    7579      A  AT   G
                                TGACA GC  GCGGT AG
                                ||||| ||  ||||| ||
                                ACTGT CG  CGCCG TC
                                   C  CC    G
GAM363  FLRT2   3'  TCAAACATGCACATGCTTGT  25066       CG_  AG
                                ACAAGCATG  GTG  TGA
                                |||||||||  |||  |||
                                TGTTCGTAC  TAC  ACT
                                     ACG  AA
GAM363  GPC1    3'  TCACTCACTGAGGCCATCA   9107     CAA  ATG
                                TGA  GC  CGGTGAGTGA
                                |||  ||  ||||||||||
                                ACT  CG  GTCACTCACT
                                  AC_  GA_
GAM363  HAX1    3'  TCACTCACCCAAACTGACCA  20385    ACA  CA  C
                                TG  AG  TG GGTGAGTGA
                                ||  ||  || |||||||||
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                                AC   TC  AC CCACTCACT
                                 CAG  AA  _
GAM363  HOXC13   3'  CACCCACCCGCTGCTTG     59681       T   _  A
                                CAAGCA GCGG TG GTG
                                |||||| |||| || |||
                                GTTCGT CGCC AC CAC
                                   _   C  C
GAM363  IGFBP4   3'  TCACTCACTCATTCCTTCA   7763    C   C_  C
                                A AAG  ATG GGTGAGTGA
                                | |||  ||| |||||||||
                                A TTC  TAC TCACTCACT
                                 C   CT  _
GAM363  INHBB    3'  CACTCACCTGCCCGCCTG    9338     A  AT  _
                                CA GC  GC GGTGAGTG
                                || ||  || ||||||||
                                GT CG  CG CCACTCAC
                                 C  CC  T
GAM363  LAPTM5   3'  TCAAAAACCCACTTGTCA    22204       CA  C   GAG
                                TGACAAG  TG GGT   TGA
                                |||||||  || |||   |||
                                ACTGTTC  AC CCA   ACT
                                   __  _   AAA
GAM363  LRP4     3'  TCACTTGGTTCATGCTCATTCA 64445     CA_     CGG
                                TGA   AGCATG   TGAGTGA
                                |||   ||||||   |||||||
                                ACT   TCGTAC   GTTCACT
                                  TAC     TTG
GAM363  MASP1    3'  TCACTCCTGACCACTTATCA  57474    C   CATG   T
                                TGA AAG    CGG GAGTGA
                                ||| |||    ||| ||||||
                                ACT TTC    GTC CTCACT
                                  A   ACCA  _
GAM363  MBNL     5'  CACGTTTTCATGCTTGCA    40727    A      CG TGA
                                TG CAAGCATG  G   GTG
                                || ||||||||  |   |||
                                AC GTTCGTAC  T   CAC
                                 _       TT TG_
GAM363  MCM2     3'  CACTCGCCACAGTTATCA    67928     CA   A  C
                                TGA  AGC TG GGTGAGTG
                                |||  ||| || ||||||||
                                ACT  TTG AC CCGCTCAC
                                  A_   _ A
GAM363  MYCL2    3'  TCACCAACCCGCAGCTTGTCA  18187        A    __  A
                                TGACAAGC TGCGG  TG GTGA
                                |||||||| |||||  || ||||
                                ACTGTTCG ACGCC  AC CACT
                                     _    CA  _
GAM363  NFATC1   3'  TCATAGTCGCATGCTCGCA   20487    ACA       TGA
                                TG   AGCATGCGG   GTGA
                                ||   |||||||||   ||||
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                                AC   TCGTACGCT   TACT
                                 GC_        GA_
GAM363  PLS1     3'  TCACCCAGCTTTTCA       10662     C    A  C
                                TGA AAGC TG GGTGA
                                ||| |||| || |||||
                                ACT TTCG AC CCACT
                                  T   _ _
GAM363  PRDM4    3'  TCACCCATGCACCTGGTCA    24827      AA___     C
                                TGAC    GCATG GGTGA
                                ||||    ||||| |||||
                                ACTG    CGTAC CCACT
                                  GTCCA    _
GAM363  PSMD7    3'  TCACTTGACATGCTTATTA    10977     C      CGG
                                TGA AAGCATG   TGAGTGA
                                ||| |||||||   |||||||
                                ATT TTCGTAC   GTTCACT
                                  A      A__
GAM363  RANBP2L1 5'  CGCCGCACGCTCGTCA      50043      A   A
                                TGAC AGC TGCGGTG
                                |||| ||| |||||||
                                ACTG TCG ACGCCGC
                                  C   C
GAM363  SDHC     3'  TCACCCATCTTTCTGTTTGTCA 69386         TGC_    A
                                TGACAAGCA    GGTG GTGA
                                |||||||||    |||| ||||
                                ACTGTTTGT    CTAC CACT
                                     CTTT    C
GAM363  SLC13A4  5'  TCACAAAACGATGCTCATCA   24922     CA    G  GTGA
                                TGA  AGCAT CG    GTGA
                                |||  ||||| ||    ||||
                                ACT  TCGTA GC    CACT
                                  AC     _  AAAA
GAM363  SMARCD1  3'  TCACTCACTCCACCCTGC    57438     ___  C
                                GCA   TG GGTGAGTGA
                                |||   || |||||||||
                                CGT   AC TCACTCACT
                                  CCC  C
GAM363  SMARCD1  3'  TCACTCACTCCACCCTGC    11820     ___  C
                                GCA   TG GGTGAGTGA
                                |||   || |||||||||
                                CGT   AC TCACTCACT
                                  CCC  C
GAM363  SPTAN1   3'  TCACCCACCCCTCGCTGCTTG  11938       T ____    A
                                CAAGCA GC    GGTG GTGA
                                |||||| ||    |||| ||||
                                GTTCGT CG    CCAC CACT
                                   _ CTCC    C
GAM363  SRD5A1   3'  TCACTCACCGTGAGCCATCA   6458      CAA  A
                                TGA   GC TGCGGTGAGTGA
                                |||   || ||||||||||||
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                                ACT   CG GTGCCACTCACT
                                  AC_  A
GAM363  UBE2L3   3'  TCACTGCACTCTGCTCATCA  12506    CA   ___
                                TGA  AGCA   TGCGGTGA
                                |||  ||||   ||||||||
                                ACT  TCGT   ACGTCACT
                                  AC    CTC
GAM363  ZNF216   3'  TCACTGATGCTTGTC      20022        G
                                GACAAGCAT CGGTGA
                                ||||||||| ||||||
                                CTGTTCGTA GTCACT
                                      _
GAM363  ABLIM    3'  TCAGCATGCTTGTC       9776          GG
                                GACAAGCATGC  TGA
                                ||||||||||  |||
                                CTGTTCGTACG  ACT
                                      __
GAM363  ABLIM    3'  TCAGCATGCTTGTC       22037         GG
                                GACAAGCATGC  TGA
                                ||||||||||  |||
                                CTGTTCGTACG  ACT
                                      __
GAM363  AK5      3'  TCACCCATGTATTTGTT    23912      __   C
                                GACAA  GCATG GGTGA
                                |||||  ||||| |||||
                                TTGTT  TGTAC CCACT
                                   TA    _
GAM363  BRD4     3'  CACAGCATGCTTCTCA     26665    C      G
                                TGA AAGCATGC GTG
                                |||  |||||||| |||
                                ACT TTCGTACG CAC
                                  C       A
GAM363  CNNM4    3'  CACCCACTGTGTCTT      39477    C      A
                                AAG ATGCGGTG GTG
                                |||  |||||||| |||
                                TTC TGTGTCAC CAC
                                  _       C
GAM363  CREG     3'  TCACTCACCACAGCT      13895    A  C
                                AGC TG GGTGAGTGA
                                |||  ||  |||||||||
                                TCG AC CCACTCACT
                                  _  A
GAM363  DCNP1    3'  TCACTCCGTGCCTGTC     55627    A    C
                                GACA GCATG GGTGA
                                ||||  ||||| |||||
                                CTGT CGTGC TCACT
                                  C    C
GAM363  DEFB118  3'  TCACTCACCCCTGTCCTCA  54028    CAA  TGC
                                TGA   GCA   GGTGAGTGA
                                |||   |||   |||||||||
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                                ACT   TGT   CCACTCACT
                                  CC_   CC_
GAM363  DEGS     3'  TCACTCATGTCTGTCA      13414       AG    C
                                TGACA  CATG GGTGA
                                |||||  |||| |||||
                                ACTGT  GTAC TCACT
                                   CT    _
GAM363  ELF2     3'  TCACTCACTTAGCCTTG     22500      CAT  __
                                CAAG   GC  GGTGAGTGA
                                ||||   ||  |||||||||
                                GTTC   CG  TCACTCACT
                                  ___  AT
GAM363  EZFIT    3'  CAGATGCAGCTTGTCA      41105        A    G_
                                TGACAAGC TGCG  TG
                                |||||||| ||||  ||
                                ACTGTTCG ACGT  AC
                                     _   AG
GAM363  FLJ00001 3'  TCACTCACCACGGAGTCA    81821      AAGCA  C
                                TGAC    TG GGTGAGTGA
                                ||||    || |||||||||
                                ACTG    GC CCACTCACT
                                  AG___  A
GAM363  FLJ10346 5'  CACTCCTGCTCACTCACTCA   36039     CA_  CAT    T
                                TGA   AG   GCGG GAGTG
                                |||   ||   |||| |||||
                                ACT   TC   CGTC CTCAC
                                  CAC  ACT   _
GAM363  FLJ11017 3'  CATGCTGCTTGTCA       36987         T   G
                                TGACAAGCA GCG TG
                                ||||||||| ||| ||
                                ACTGTTCGT CGT AC
                                     _  _
GAM363  FLJ11110 3'  CACTCACTTATTCTTGCA    37061    A    C   C
                                TG CAAG ATG GGTGAGTG
                                || |||| ||| ||||||||
                                AC GTTC TAT TCACTCAC
                                 _    T   _
GAM363  FLJ22021 3'  TCAGCTGCTGCTCATCA     44588     CA    T    _
                                TGA  AGCA GCGG TGA
                                |||  |||| |||| |||
                                ACT  TCGT CGTC ACT
                                  AC    _    G
GAM363  FLJ22476 3'  TCACTCTAGCACTTGCCA    46775    A    CA   GGT
                                TG CAAG  TGC   GAGTGA
                                || ||||  |||   ||||||
                                AC GTTC  ACG   CTCACT
                                 C    __   AT_
GAM363  GFR      3'  TCACTCTTCCTGCCTGTTCA  24475   A    T    T__
                                C AGCA GCGG   GAGTGA
                                | |||| ||||   ||||||
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                                A TTGT CGTC   CTCACT
                                 C   C   CTT
GAM363  GPR105   3'  CACGTGTGCATGTTGTCA    29653       G     GTGA
                                TGACAA CATGCG   GTG
                                |||||| ||||||   |||
                                ACTGTT GTACGT   CAC
                                   _     GTG_
GAM363  H-L(3)MBT 3'  CACTCATTTGCTTGCCA     49487    A     TGC
                                TG CAAGCA   GGTGAGTG
                                || ||||||   ||||||||
                                AC GTTCGT   TTACTCAC
                                 C     ___
GAM363  HOMER-2B  3'  CACTCACTCCTTTTCA      16720     C   CATGC
                                TGA AAG    GGTGAGTG
                                ||| |||    ||||||||
                                ACT TTC    TCACTCAC
                                  T   C____
GAM363  KIAA0218  3'  TCACCCGCCTACTTGTC     28624      CAT    TGA
                                GACAAG   GCGG   GTGA
                                ||||||   ||||   ||||
                                CTGTTC   CGCC   CACT
                                   ATC    ___
GAM363  KIAA0515  3'  CACTCACTTTTGCCTGTTA    63803      A   TGC
                                TGACA GCA   GGTGAGTG
                                ||||| |||   ||||||||
                                ATTGT CGT   TCACTCAC
                                   C   TT_
GAM363  KIAA0544  3'  CACCCACCCTGCGTGTCA    70892      A   TGC    A
                                TGACA GCA   GGTG GTG
                                ||||| |||   |||| |||
                                ACTGT CGT   CCAC CAC
                                   G   C__    C
GAM363  KIAA0694  3'  TCACCAATATTTGTCA      72583       C  GC
                                TGACAAG AT  GGTGA
                                ||||||| ||  |||||
                                ACTGTTT TA  CCACT
                                    A  A_
GAM363  KIAA0825  3'  TCACCCACCTGCTGCT      61031      T  _   A
                                AGCA GC GGTG GTGA
                                |||| || |||| ||||
                                TCGT CG CCAC CACT
                                  _ T   C
GAM363  KIAA0870  3'  TCACTCACCCAGTCCTT     81473     CA_  C
                                AAG   TG GGTGAGTGA
                                |||   || |||||||||
                                TTC   AC CCACTCACT
                                  CTG  _
GAM363  KIAA1091  3'  TCAAAGACCATACACTTGTCA  69686       CA  C   GAG
                                TGACAAG  TG GGT   TGA
                                |||||||  || |||   |||
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                                ACTGTTC  AT CCA   ACT
                                    AC  A   GAA
GAM363  KIAA1655  3'  CACTCATCACGTGCTT      66596        C
                                AAGCATG GGTGAGTG
                                ||||||| ||||||||
                                TTCGTGC CTACTCAC
                                    A
GAM363  KIAA1750  3'  TCACCTAGCTGCATCACTTATC 68255     C   C_      GA_
          A                      TGA AAG  ATGCGGT   GTGA
                                ||| |||  |||||||   ||||
                                ACT TTC  TACGTCG   CACT
                                  A   AC      ATC
GAM363  KIAA1813  5'  CACTCACCTTCCTAGTCA    70292      A  CATGC
                                TGAC AG    GGTGAGTG
                                |||| ||    ||||||||
                                ACTG TC    CCACTCAC
                                  A  CTT__
GAM363  KIAA1937  3'  CACTCTCGCTGTCGTCA     73694      AA   T    T
                                TGAC  GCA GCGG GAGTG
                                ||||  ||| |||| |||||
                                ACTG  TGT CGCT CTCAC
                                  C_  _   _
GAM363  LGI2      3'  TCATATGAATGCTTGTCA    36400         GCG_
                                TGACAAGCAT    GTGA
                                ||||||||||    ||||
                                ACTGTTCGTA    TACT
                                      AGTA
GAM363  LGI3      3'  CACCCCGTCTGCATGCT     57741         _  A_
                                AGCATGCGG TG  GTG
                                ||||||||| ||  |||
                                TCGTACGTC GC  CAC
                                     T  CC
GAM363  LMOD1     3'  CACCCACTTGCCTGTCA     24039      A   TGC    A
                                TGACA GCA   GGTG GTG
                                ||||| |||   |||| |||
                                ACTGT CGT   TCAC CAC
                                   C   ___    C
GAM363  MACF1     3'  TCACCAGCACACTTGTTA    23893        CA   _
                                TGACAAG  TGC GGTGA
                                |||||||  ||| |||||
                                ATTGTTC  ACG CCACT
                                    AC   A
GAM363  MBLL39    5'  TCACTCACCTTCAGACTT    19252     CA  C_
                                AAG  TG  GGTGAGTGA
                                |||  ||  |||||||||
                                TTC  AC  CCACTCACT
                                  AG  TT
GAM363  MBLL39    5'  TCACTCACCTTCAGACTT    58611     CA  C_
                                AAG  TG  GGTGAGTGA
                                |||  ||  |||||||||
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                                TTC  AC  CCACTCACT
                                  AG  TT
GAM363  MGC19595 3'  TCACTCACTGCCCTGTC     53041      A CAT
                                GACA G   GCGGTGAGTGA
                                |||| |   ||||||||||
                                CTGT C   CGTCACTCACT
                                  _ C__
GAM363  MGC4170  3'  TCACTCTTGCTGCTT       44225       T   T
                                AAGCA GCGG GAGTGA
                                ||||| |||| ||||||
                                TTCGT CGTT CTCACT
                                  _   _
GAM363  MGC5306  3'  TCACTCACTGTACACTCATC   44139    CA  CA
                                GA  AG  TGCGGTGAGTGA
                                ||  ||  ||||||||||||
                                CT  TC  ATGTCACTCACT
                                 AC  AC
GAM363  MIDORI   3'  TCACTCACTCGCCTGCTTCCCA 73791    AC    T  _
                                TG  AAGCA GCG GTGAGTGA
                                ||  |||||| ||| ||||||||
                                AC  TTCGT CGC CACTCACT
                                 CC    C   T
GAM363  MIL1     3'  ATCACCCACCACCATGGTTACT 31091      _____   C_   A   III
           TGCCA                  CAAG    CATG  GGTG GTGA   T
                                ||||   ||||  |||| ||||   |
                                GTTC   GTAC  CCAC CACT   A
                                  ATTG   CA   C   III
GAM363  MOCS3    3'  TCACCATGTTTGTCA      27157          GC
                                TGACAAGCAT  GGTGA
                                ||||||||||  |||||
                                ACTGTTTGTA  CCACT
                                     __
GAM363  P15-2    3'  TCACCTCATACTTATCA     38010     C   C   C
                                TGA AAG ATG GGTGA
                                ||| ||| ||| |||||
                                ACT TTC TAC CCACT
                                  A   A   T
GAM363  PABPC5   5'  CACTCACTGCGCGTTTGCCA   55071    A    A
                                TG CAAGC TGCGGTGAGTG
                                || ||||| ||||||||||
                                AC GTTTG GCGTCACTCAC
                                 C    C
GAM363  PC4      3'  TCACTTATTAAACATGTTCA   22014     CAA    C__
                                TGA   GCATG   GGTGAGTGA
                                |||   |||||   |||||||||
                                ACT   TGTAC   TTATTCACT
                                  ____    AAA
GAM363  PCDH20   3'  TCACTGAAGTGCCTGTCA     43131      A   G_
                                TGACA GCAT  CGGTGA
                                ||||| ||||  ||||||
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                                ACTGT CGTG  GTCACT
                                  C    AA
GAM363  PDCD7    3'  TCACTCATATAACATGTCA   72143   A    CG__
                                A GCATG   GTGAGTGA
                                | |||||   ||||||||
                                A TGTAC   TACTCACT
                                 C    AATA
GAM363  PDZD2    5'  TCATAGCACGCAGCACTTATCA 80881    C   CA_   _ GA
                                TGA AAG   TGCG GT  GTGA
                                ||| |||   |||| ||  ||||
                                ACT TTC   ACGC CG  TACT
                                  A   ACG   A  A_
GAM363  PILR(BETA) 5'  CACTCACCTCAGCCCTCA    25552    CAA  A  C
                                TGA   GC TG GGTGAGTG
                                |||   || || ||||||||
                                ACT   CG AC CCACTCAC
                                  CC_  _  T
GAM363  PPFIA4   3'  CACTCTCTTGCTTGTC      70321        TGC  T
                                GACAAGCA   GG GAGTG
                                ||||||||   || |||||
                                CTGTTCGT   TC CTCAC
                                     ___  T
GAM363  PPP1R3B  5'  TCACGTAGTCGCGCTTGCCA  44825    A    AT    GA_
                                TG CAAGC  GCGGT   GTGA
                                || |||||  |||||   ||||
                                AC GTTCG  CGCTG   CACT
                                 C     __     ATG
GAM363  PRRG1    3'  TATCACATGCTTGCCA     6287     A      C
                                TG CAAGCATG GGTG
                                || |||||||| ||||
                                AC GTTCGTAC CTAT
                                 C       A
GAM363  RRN3     3'  TCACTTGTCATGCCCTCA    37359     CAA    CG TG
                                TGA   GCATG  G  AGTGA
                                |||   |||||  |  |||||
                                ACT   CGTAC  T  TCACT
                                  CC_    __ GT
GAM363  SDCCAG1  3'  TCATTGATACTTGTCA      16327        C  G
                                TGACAAG AT CGGTGA
                                ||||||| || ||||||
                                ACTGTTC TA GTTACT
                                    A  _
GAM363  SLC2A10  3'  ACAAACCTGCTTGTCA      47812        TGC   GA
                                TGACAAGCA   GGT  GT
                                |||||||||   |||  ||
                                ACTGTTCGT   CCA  CA
                                     ___   AA
GAM363  SUN1     3'  CACTCACTGCCTGTCA      47154       AGCAT
                                TGACA    GCGGTGAGTG
                                |||||    ||||||||||
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                                ACTGT    CGTCACTCAC
                                  C____
GAM363  SYT6     3'  TCAAAGCTGAGACACTTGTCA 78774       CATG_   GAG
                                TGACAAG    CGGT   TGA
                                |||||||    ||||  |||
                                ACTGTTC    GTCG   ACT
                                    ACAGA    AA_
GAM363  TReP-132 5'  TCACCCAGGTGTTTGCCA    53143    A      GC_
                                TG CAAGCAT   GGTGA
                                || |||||||  |||||
                                AC GTTTGTG   CCACT
                                 C      GAC
GAM363  TReP-132 5'  TCACCCAGGTGTTTGCCA    37296    A      GC_
                                TG CAAGCAT   GGTGA
                                || |||||||  |||||
                                AC GTTTGTG   CCACT
                                 C      GAC
GAM363  UBCE7IP5 3'  TCACTGCAGCTTGCCA      30159    A    A
                                TG CAAGC TGCGGTGA
                                || ||||| ||||||||
                                AC GTTCG ACGTCACT
                                 C    _
GAM363  UBE2D3   3'  TCATTCACATGCTCATC     12480    CA    GCG
                                GA  AGCAT   GTGAGTGA
                                ||  |||||   ||||||||
                                CT  TCGTA   CACTTACT
                                 AC    ____
GAM363  WDR7     3'  TCACTTGTGCATGCTTCTCA   30960     C       G TG
                                TGA AAGCATGC G  AGTGA
                                ||| |||||||| |  |||||
                                ACT TTCGTACG T  TCACT
                                 C       _ GT
GAM363  ZMPSTE24 3'  TCACTCACTGATAATGCTTATT 19595     C      G__
           A                     TGA AAGCAT   CGGTGAGTGA
                                |||| ||||||  ||||||||||
                                ATT TTCGTA   GTCACTCACT
                                  A     ATA
GAM363  LOC115110 3' CACTGATTTGCACACTTGCCA  71713    A   CA    _ G
                                TG CAAG  TGCGG T AGTG
                                || ||||  ||||| | ||||
                                AC GTTC  ACGTT A TCAC
                                 C    AC     T G
GAM363  LOC120224 5' TCACCATGTTTGTCA       57104          GC
                                TGACAAGCAT  GGTGA
                                ||||||||||  |||||
                                ACTGTTTGTA  CCACT
                                          __
GAM363  LOC124460 3' CAAGGACCCACACTTGTCA    76039        CA  C   GAG
                                TGACAAG  TG GGT   TG
                                |||||||  || |||   ||
```

```
                                ACTGTTC  AC CCA   AC
                                    AC  _  GGA
GAM363  LOC124470 3'  TCACTCTGGTGCATGCTGTCA  75642      A     G _
                                TGACA GCATGCG T GAGTGA
                                ||||| ||||||| | ||||||
                                ACTGT CGTACGT G CTCACT
                                   _      G T
GAM363  LOC128338 3'  TCATACACATGCTTGCA     74743    A      CG_
                                TG CAAGCATG   GTGA
                                || ||||||||   ||||
                                AC GTTCGTAC   TACT
                                 _       ACA
GAM363  LOC129446 3'  CACCCATGTTTGTCA       76122          C
                                TGACAAGCATG GGTG
                                |||||||||| ||||
                                ACTGTTTGTAC CCAC
                                          _
GAM363  LOC142937 3'  CTGGCCTCATACTTGTCA    56655       C   C   G
                                TGACAAG ATG GGT AG
                                ||||||| ||| ||| ||
                                ACTGTTC TAC CCG TC
                                    A   T   G
GAM363  LOC144308 3'  CTTGTCTGCACACTTGTCA   83046       CA    _
                                TGACAAG  TGCGG TGAG
                                |||||||  ||||| ||||
                                ACTGTTC  ACGTC GTTC
                                    AC    T
GAM363  LOC145980 3'  CACTCCTCATGCTCGTCA    83601     A     C  T
                                TGAC AGCATG GG GAGTG
                                |||| |||||| || |||||
                                ACTG TCGTAC TC CTCAC
                                  C     _ _
GAM363  LOC146337 5'  TCAAGCAGCTGCTTGTCA    83664         T  GG  AG
                                TGACAAGCA GC  TG  TGA
                                ||||||||| ||  ||  |||
                                ACTGTTCGT CG  AC  ACT
                                     _ __  GA
GAM363  LOC147160 5'  CACTCACTCCTTCTCA      83960     C   CATGC
                                TGA AAG    GGTGAGTG
                                ||| |||    ||||||||
                                ACT TTC    TCACTCAC
                                  C  C_____
GAM363  LOC149018 5'  TCACTCAACTGCTTGTCA    79134         TGCGG
                                TGACAAGCA    TGAGTGA
                                |||||||||    |||||||
                                ACTGTTCGT    ACTCACT
                                     CA___
GAM363  LOC149111 3'  TCACCCTGTTTGTCA       79187         TGC
                                TGACAAGCA   GGTGA
                                |||||||||   |||||
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                                ACTGTTTGT   CCACT
                                     C__
GAM363   LOC149566 3'  TCACCCAACTTGTCA      84494       CA  C
                                TGACAAG  TG GGTGA
                                |||||||  || |||||
                                ACTGTTC  AC CCACT
                                   A_  _
GAM363   LOC150166 3'  TCATAACATGCTTGCTCA    84889    _      CG
                                TGA CAAGCATG  GTGA
                                ||| ||||||||  ||||
                                ACT GTTCGTAC  TACT
                                  C       AA
GAM363   LOC200197 3'  TCACTCACCGACTCTCATCA  88622    CA  CATG
                                TGA  AG   CGGTGAGTGA
                                |||  ||   ||||||||||
                                ACT  TC   GCCACTCACT
                                  AC  TCA_
GAM363   LOC200448 5'  TCACACAGCTTGTCA       88818       A  CG
                                TGACAAGC TG  GTGA
                                |||||||| ||  ||||
                                ACTGTTCG AC  CACT
                                     _ A_
GAM363   LOC200860 5'  TCACTCATTCATCCACTCGTC  90174    A  C__   C
                                GAC AG   ATG GGTGAGTGA
                                ||| ||   ||| |||||||||
                                CTG TC   TAC TTACTCACT
                                  C  ACC   _
GAM363   LOC203339 3'  TCACCATGTTTGCCA      90549    A     GC
                                TG CAAGCAT  GGTGA
                                || |||||||  |||||
                                AC GTTTGTA  CCACT
                                 C      __
GAM363   LOC203378 3'  CACTCACCCACTGTGCATCA  90595    CAA  _  C
                                TGA   GCA TG GGTGAGTG
                                |||   ||| || ||||||||
                                ACT   TGT AC CCACTCAC
                                  ACG   C  _
GAM363   LOC204285 5'  TCATTGACATGCTCTTCA    89461    CA    _
                                TGA  AGCATG CGGTGA
                                |||  |||||| ||||||
                                ACT  TCGTAC GTTACT
                                  TC     A
GAM363   LOC205418 5'  CACCACGCATGCTGACCA    90682    ACA      G  A
                                TG   AGCATGCG TG GTG
                                ||   |||||||| || |||
                                AC   TCGTACGC AC CAC
                                 CAG       _ _
GAM363   LOC220763 5'  TCACTGTGCATGCTGATCA   73348    CA      GTG
                                TGA  AGCATGCG   AGTGA
                                |||  ||||||||   |||||
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                                ACT  TCGTACGT   TCACT
                                  AG       G__
GAM363  LOC221468 3'  TCACTTACGAGCTCATCA    59291     CA   ATGCG
                                TGA  AGC    GTGAGTGA
                                |||  |||    ||||||||
                                ACT  TCG    CATTCACT
                                  AC   AG___
GAM363  LOC253868 3'  CACTCACCACAGTGAGTT    95577     AA  A  C
                                GAC  GC TG GGTGAGTG
                                |||  || || ||||||||
                                TTG  TG AC CCACTCAC
                                  AG  _  A
GAM363  LOC253955 5'  GCTCGATGCTTGCCA       94429     A      GCGG
                                TG CAAGCAT    TGAGT
                                || |||||||    |||||
                                AC GTTCGTA    GCTCG
                                 C      _____
GAM363  LOC51285  3'  TCAAGACCACATGCTTGCA    33346     A      C   GAG
                                TG CAAGCATG GGT   TGA
                                || |||||||| |||   |||
                                AC GTTCGTAC CCA   ACT
                                 _       A   GA_
GAM363  LOC51713  5'  CACTCACCGGTGTCCCCGTC   32760     AA__    G
                                GAC    GCAT CGGTGAGTG
                                |||    |||| |||||||||
                                CTG    TGTG GCCACTCAC
                                  CCCC   _
GAM363  LOC90133  5'  TCACTACTGTATACTCAGCA   61608     ACA  C      G
                                TG   AG ATGCGGT AGTGA
                                ||   || ||||||| |||||
                                AC   TC TATGTCA TCACT
                                 GAC  A      _
GAM363  LOC90317  3'  CAATCACTACTTGTCA       62249        CATGC    G
                                TGACAAG     GGTGA TG
                                |||||||     ||||| ||
                                ACTGTTC     TCACT AC
                                    A_____     A
GAM363  LOC90362  3'  TCAAGTTGCATGCTTGTCA    62445             TGAG
                                TGACAAGCATGCGG    TGA
                                ||||||||||||||    |||
                                ACTGTTCGTACGTT    ACT
                                        GA__
GAM363  LOC94976  3'  CACTCACCTCGCTCTTCTCA   71749     C   CA  C
                                TGA AAG  TG GGTGAGTG
                                ||| |||  || ||||||||
                                ACT TTC  GC CCACTCAC
                                  C   TC  T
GAM364  AXIN1     3'  GAGTGCCTTCAACACAGC     60853      AGC
                                GCTG   TGAAGGCACTT
                                ||||   ||||||||||
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                                CGAC   ACTTCCGTGAG
                                  ACA
GAM364  BAI2    3'  TGGAACCCCATCTTCAGCCCAG 8122      A      CACTTAG
             C                   GCTG GCTGAAGG      TCCA
                                 |||| ||||||||      ||||
                                 CGAC CGACTTCT      AGGT
                                   C       ACCCCA_
GAM364  BCAT1   5'  GGATCTGCCCTCCGCTCAGC   66204       T  A   CTTA
                                 GCTGAGC GA GGCA    GTCC
                                 ||||||| || ||||    ||||
                                 CGACTCG CT CCGT    TAGG
                                     C  C    C___
GAM364  CKM     5'  GACAGCCCCCCTTCAGCCCAGC 8435      A      CACTTA
                                 GCTG GCTGAAGG      GTC
                                 |||| ||||||||      |||
                                 CGAC CGACTTCC      CAG
                                   C       CCCCGA
GAM364  HIP12   3'  AGGCCCTCCAGCTCAGC     66229         A   CA
                                 GCTGAGCTG AGG  CT
                                 ||||||||| |||  ||
                                 CGACTCGAC TCC  GA
                                      C   CG
GAM364  LIFR    3'  TGATTGCCTTCAGCACAGC    9748       A        C
                                 GCTG GCTGAAGGCA TTA
                                 |||| |||||||||| |||
                                 CGAC CGACTTCCGT AGT
                                   A         T
GAM364  MAN2B1  5'  AGTGTCACCTTTAGCCCA    4994     A      ___
                                 TG GCTGAAGG   CACT
                                 || ||||||||   ||||
                                 AC CGATTTCC   GTGA
                                  C       ACT
GAM364  PSD     5'  GGACCCCCCCAGCTCAG      10931         AA  CACTTA
                                 CTGAGCTG  GG     GTCC
                                 ||||||||  ||     ||||
                                 GACTCGAC  CC     CAGG
                                      CC  C_____
GAM364  PTPRCAP  3'  TGGACTGGACCCCCAGCCCA   18819    A   AA  CAC
                                 TG GCTG  GG   TTAGTCCA
                                 || ||||  ||   ||||||||
                                 AC CGAC  CC   GGTCAGGT
                                  C   CC  A__
GAM364  RFPL2   5'  TGGACGCTTCCTCCACCTCAGC 21728       C  A   CACTTA
                                 GCTGAG TG AGG      GTCCA
                                 |||||| || |||      |||||
                                 CGACTC AC TCC      CAGGT
                                    C  C   TTCG__
GAM364  RFPL3   5'  TGGACCCTTCCTCCACCTCAGC 21723       C  A   CACTTA
                                 GCTGAG TG AGG      GTCCA
                                 |||||| || |||      |||||
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                                CGACTC AC TCC      CAGGT
                                   C  C   TTCC__
GAM364  SLC35A2  3'  GACCCACCTCAGCTCAGC    18978          A  CACTTA
                                GCTGAGCTGA GG      GTC
                                |||||||||| ||      |||
                                CGACTCGACT CC      CAG
                                      _  ACC___
GAM364  TNFSF4   3'  AGGAGCCTCCCAGCTCAGC    12442          A_   A
                                GCTGAGCTG  AGGC CTT
                                |||||||||  |||| |||
                                CGACTCGAC  TCCG GGA
                                     CC    A
GAM364  WFDC1    3'  AGTTCACATTCAGCTCAGC    41042          GGC__
                                GCTGAGCTGAA     ACT
                                ||||||||||     |||
                                CGACTCGACTT     TGA
                                      ACACT
GAM364  CNNM1    3'  GAACTTTCAGCCCAGC       39772      A       CACTTAG
                                GCTG GCTGAAGG       TC
                                |||| ||||||||       ||
                                CGAC CGACTTTC       AG
                                  C       A_______
GAM364  CSRP2BP  3'  GAGATGCCTTCAGCCAGC     70112      A        _
                                GCTG GCTGAAGGCA CTT
                                |||| |||||||||| |||
                                CGAC CGACTTCCGT GAG
                                  _         A
GAM364  DKFZp434C0328 3'  TGAACTAAGATTGGCTTCAGCT 34138            G __     C
           TAGC                     GCTGAGCTGAAG CA  CTTAGT CA
                                |||||||||||| ||  |||||| ||
                                CGATTCGACTTC GT  GAATCA GT
                                      G  TA     A
GAM364  DKFZP434P211 5'  GGGCGTCCTCCAGCTCAGC    27266          A   C  TTA
                                GCTGAGCTG AGG AC   GTCC
                                ||||||||| ||| ||   ||||
                                CGACTCGAC TCC TG   CGGG
                                     C   _  ___
GAM364  DKFZp586H0623 3'  GTGTCCCTCAGCTCAGC     34073          A  _
                                GCTGAGCTGA GG CAC
                                |||||||||| || |||
                                CGACTCGACT CC GTG
                                     C  T
GAM364  ERN1     3'  ACCAAGTGCCTTGAGCT      7516       G        A
                                AGCT AAGGCACTT GT
                                |||| ||||||||| ||
                                TCGA TTCCGTGAA CA
                                  G        C
GAM364  FLJ12425  3'  TGGACTAAGTACTATCAGACCA 85894      AG    A  C
           GC                     GCTG  CTGA GG ACTTAGTCCA
                                ||||  |||| || ||||||||||
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                                CGAC  GACT TC TGAATCAGGT
                                  CA   A  A
GAM364  FLJ14327  3'  GAGACCTTCAGCTCCGC    46138    T       CA
                                GC GAGCTGAAGG  CTT
                                || ||||||||||  |||
                                CG CTCGACTTCC  GAG
                                 C        A_
GAM364  FLJ14596  3'  ACTTTGCCTTCAGTTCA    51456           CTT
                                TGAGCTGAAGGCA   AGT
                                ||||||||||||   |||
                                ACTTGACTTCCGT   TCA
                                       T__
GAM364  FLJ22031  3'  ACTAAGTGCTCTGCCCA    46884    A  TGAA
                                TG GC    GGCACTTAGT
                                || ||    ||||||||||
                                AC CG    TCGTGAATCA
                                 C  TC__
GAM364  FLJ22056  3'  TGCCCTTCAGCCCAGC     42536     A      _
                                GCTG GCTGAAGG CA
                                |||| |||||||| ||
                                CGAC CGACTTCC GT
                                  C       C
GAM364  FLJ22938  5'  GACATGCCTTCAGTCAGC    45160      G       CTTA
                                GCTGA CTGAAGGCA    GTC
                                ||||| |||||||||    |||
                                CGACT GACTTCCGT    CAG
                                   _       A___
GAM364  FLJ31762  3'  GGCTTGCCCCTCAGCTCAGC  58143         A_   CTT
                                GCTGAGCTGA  GGCA   AGTC
                                ||||||||||  ||||   ||||
                                CGACTCGACT  CCGT   TCGG
                                      CC   ___
GAM364  GPR9      3'  GCCCAGGCCTCCAGCTCAGC  7688          A   A  TA
                                GCTGAGCTG AGGC CT  GT
                                ||||||||| |||| ||  ||
                                CGACTCGAC TCCG GA  CG
                                     C   _  CC
GAM364  KIAA0574  3'  GAGGCCTTCAGGCCCAGC    69281     A  _     A
                                GCTG GC TGAAGGC CTT
                                |||| || ||||||| |||
                                CGAC CG ACTTCCG GAG
                                  C  G     _
GAM364  KIAA1671  3'  GGACACCCCTCAGCCCGC    65683    T A    A  CACTTA
                                GC G GCTGA GG     GTCC
                                || | ||||| ||     ||||
                                CG C CGACT CC     CAGG
                                 _ C    C  CA____
GAM364  MGC15854  5'  GATCCAGGCCCTCAGCTCAGC  58848          A   A  TA
                                GCTGAGCTGA GGC CT  GTC
                                |||||||||| ||| ||  |||
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                                CGACTCGACT CCG GA  TAG
                                      C   _  CC
GAM364  MO25     3'  GACTAAGTAACCCAGT     32809      AA  C_
                                GCTG  GG  ACTTAGTC
                                ||||  ||  ||||||||
                                TGAC  CC  TGAATCAG
                                  __  AA
GAM364  NEUROG3  5'  GGGCGCCTGCAGCTCAGC    40657         A    ACTTA
                                GCTGAGCTG AGGC    GTCC
                                ||||||||| ||||    ||||
                                CGACTCGAC TCCG    CGGG
                                      G   _____
GAM364  PCSK7    3'  GGTCTGCCTCCAGCCA      16337    A    A    CTTA T
                                TG GCTG AGGCA   G CC
                                || |||| |||||   | ||
                                AC CGAC TCCGT   C GG
                                 _   C    ____ T
GAM364  PHCA     3'  GCTGCACCTTCAGCCAGC    37178      A       CACT
                                GCTG GCTGAAGG   TAGT
                                |||| ||||||||   ||||
                                CGAC CGACTTCC   GTCG
                                  _       AC__
GAM364  PLAGL2   3'  GAGGCCCTCAGCTCAGT     70449          A   A
                                GCTGAGCTGA GGC CTT
                                |||||||||| ||| |||
                                TGACTCGACT CCG GAG
                                      C   _
GAM364  PPP1R16B 3'  AGCTGCCTTCAGCCAGC     61377      A        _
                                GCTG GCTGAAGGCA CT
                                |||| |||||||||| ||
                                CGAC CGACTTCCGT GA
                                  _        C
GAM364  PRAM-1   3'  AAGCGCCCTCAGTTCAGC    69378          A   A
                                GCTGAGCTGA GGC CTT
                                |||||||||| ||| |||
                                CGACTTGACT CCG GAA
                                      C   C
GAM364  RCD-8    3'  ACTGACCTCAAGCTCAGC    26748         GA   CAC
                                GCTGAGCT  AGG   TTAGT
                                ||||||||  |||   |||||
                                CGACTCGA  TCC   AGTCA
                                    AC   ___
GAM364  REG1B    3'  GACTATGTCTCCAACTCAGT   21482       C  A    CT
                                GCTGAG TG AGGCA  TAGTC
                                ||||||  || |||||  |||||
                                TGACTC AC TCTGT  ATCAG
                                   A  C    __
GAM364  TRAF4    3'  TGAGTGCTTCAGCCCAGC    62631      A      G
                                GCTG GCTGAAG CACTTA
                                |||| ||||||| ||||||
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                                CGAC CGACTTC GTGAGT
                                  C      _
GAM364  LOC116411 5'  GGTGCCTCCACTCAGC      73869       C  A
                                GCTGAG TG AGGCACT
                                ||||||| || |||||||
                                CGACTC AC TCCGTGG
                                   _  C
GAM364  LOC120772 5'  ACTTGTGCCCCCAGCTCAGC   74021         AA    TT
                                GCTGAGCTG  GGCAC  AGT
                                |||||||||  |||||  |||
                                CGACTCGAC  CCGTG  TCA
                                     CC    T_
GAM364  LOC145622 5'  GGAGAGGGTTCCTTCAGCCCA  77307    A       C    AG
                                TG GCTGAAGG ACTT  TCC
                                || |||||||| ||||  |||
                                AC CGACTTCC TGGG  AGG
                                 C       T    AG
GAM364  LOC145622 3'  GGAAAGGGTTCCTTCAGCCCA  77306    A       C    AG
                                TG GCTGAAGG ACTT  TCC
                                || |||||||| ||||  |||
                                AC CGACTTCC TGGG  AGG
                                 C       T    AA
GAM364  LOC146733 3'  GGACCACCTCAGCTCAGC     83767          A  CACTTA
                                GCTGAGCTGA GG     GTCC
                                |||||||||| ||     ||||
                                CGACTCGACT CC     CAGG
                                     _  AC_____
GAM364  LOC149267 3'  ACTAAGCCAGCTCAGC      56674        GAA   AC
                                GCTGAGCT   GGC  TTAGT
                                ||||||||   |||  |||||
                                CGACTCGA   CCG  AATCA
                                    ____   __
GAM364  LOC150174 5'  GGGCATCCTCCAGCTCAGC    79609         A   CACTTA
                                GCTGAGCTG AGG     GTCC
                                ||||||||| |||     ||||
                                CGACTCGAC TCC     CGGG
                                     C   TA_____
GAM364  LOC150213 5'  GGGCGTCCTCCAGCTCAGC    74857         A   C  TTA
                                GCTGAGCTG AGG AC   GTCC
                                ||||||||| ||| ||   ||||
                                CGACTCGAC TCC TG   CGGG
                                     C   _  ____
GAM364  LOC151174 5'  GGCTCACCCCACAGCTCAGC   85252         AA  CACTT
                                GCTGAGCTG  GG    AGTC
                                |||||||||  ||    ||||
                                CGACTCGAC  CC    TCGG
                                     AC  CAC__
GAM364  LOC157273 5'  GCTGTGCCTTCAACTTAGC    86432       C        TT
                                GCTGAG TGAAGGCAC  AGT
                                |||||| |||||||||  |||
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                                CGATTC ACTTCCGTG  TCG
                                   A       __
GAM364  LOC195977 3'  GAGCTGCCTTCAACCCAGC   87538     AGC      _
                                GCTG   TGAAGGCA CTT
                                ||||   |||||||| |||
                                CGAC   ACTTCCGT GAG
                                  CCA       C
GAM364  LOC196266 3'  GGTCTGCCTCCAGCCA     87305    A   A    CTTA T
                                TG GCTG AGGCA    G CC
                                || |||| |||||    | ||
                                AC CGAC TCCGT    C GG
                                 _   C     _____ T
GAM364  LOC221463 3'  AGAGCCCTCAGCCCAGC     92063     A    A  A
                                GCTG GCTGA GGC CT
                                |||| ||||| ||| ||
                                CGAC CGACT CCG GA
                                  C    C  A
GAM364  LOC253782 3'  ACTAAATGCCTTCATCTTAG   95692      C       C
                                CTGAG TGAAGGCA TTAGT
                                ||||| |||||||| |||||
                                GATTC ACTTCCGT AATCA
                                   T       A
GAM364  LOC254295 5'  TGGACTGGGACTCAGCCCAGC  96179     A    A GCA
                                GCTG GCTGA G   CTTAGTCCA
                                |||| ||||| |   |||||||||
                                CGAC CGACT C   GGGTCAGGT
                                  C    _ A__
GAM364  LOC256158 5'  GTGGCCTTCAGCCCAGC     97680     A       _
                                GCTG GCTGAAGGC AC
                                |||| ||||||||| ||
                                CGAC CGACTTCCG TG
                                  C       G
GAM364  LOC256867 5'  ACTTGTGCCCCCAGCTCAGC   94860        AA    TT
                                GCTGAGCTG  GGCAC  AGT
                                |||||||||  |||||  |||
                                CGACTCGAC  CCGTG  TCA
                                     CC    T_
GAM364  LOC90917  3'  GACCCAGCCTGCAGCTCAGC   64338        A   ACTTA
                                GCTGAGCTG AGGC    GTC
                                |||||||| ||||    |||
                                CGACTCGAC TCCG    CAG
                                     G   ACC__
GAM365  ARCN1     3'  AGACTGCACTCTCTGTCA    7970         CA_
                                TGACAGAGA   CAGTTT
                                |||||||||   ||||||
                                ACTGTCTCT   GTCAGA
                                     CAC
GAM365  CBFA2T2   3'  GAGCAAAACTCTGTCT     17466      C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
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                                TCTGT TCAAAACGAG
                                   C
GAM365  CTLA4    3'  CAGAGCTGGGATGTTTCTGTCA 17807          CAGTTTT
                                TGACAGAGACA      GCTCTG
                                ||||||||||       ||||||
                                ACTGTCTTTGT      CGAGAC
                                     AGGGT__
GAM365  ITK      3'  CAGAACAGGAGTGATGTCTCTG 18674        _ G    C
                                CAGAGACA CA TTTTG TCTG
                                |||||||| || ||||| ||||
                                GTCTCTGT GT AGGAC AGAC
                                     A G    A
GAM365  LAMP2    3'  GGTGAAACCCCATCTCTATCA 25716    C    CACA    TG
                                TGA AGAGA    GTTT  CT
                                ||| |||||    ||||  ||
                                ACT TCTCT    CAAA  GG
                                  A    ACCC    GT
GAM365  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA  40865       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM365  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA  52960       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM365  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA  52963       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM365  PDGFRB   5'  CAGAGCCTGGAACTGTG    65969         __
                                CACAGTTTT  GCTCTG
                                |||||||||  ||||||
                                GTGTCAAGG  CGAGAC
                                     TC
GAM365  PTPRA    3'  AGAGCGGTATCTCTG      55079       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM365  PTPRA    3'  AGAGCGGTATCTCTG      55087       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM365  PTPRA    3'  AGAGCGGTATCTCTG      11088       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
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                                GTCTCT TG    GCGAGA
                                   A _____
GAM365  RAD51L3  3'  CAAAACTCAGGTATGTCTCTGT 56065        C_____
                                ACAGAGACA    AGTTTTG
                                |||||||||    |||||||
                                TGTCTCTGT    TCAAAAC
                                     ATGGAC
GAM365  TBL2     3'  CAGAACTGTGTTCCATCA    52178    CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM365  TBL2     3'  CAGAACTGTGTTCCATCA    24924    CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM365  AGTRL2   5'  CAGAGCAAGAACTGTTC    17691    C     _
                                GA ACAGTTTT GCTCTG
                                || |||||||| ||||||
                                CT TGTCAAGA CGAGAC
                                 _      A
GAM365  CABP5    3'  AGAGCGGTATCTTTGCCA    39079    A    C  AGTTT
                                TG CAGAGA AC    TGCTCT
                                || |||||| ||    ||||||
                                AC GTTTCT TG    GCGAGA
                                 C     A _____
GAM365  CUL4A    5'  AGAGCAGCACCTCCATCA    13149    CA  ACACA  T
                                TGA  GAG    GT TTGCTCT
                                |||  |||    || |||||||
                                ACT  CTC    CA GACGAGA
                                  AC  _____  C
GAM365  DKFZp761O17121 3'  CAGACAGCCCCTGTGTCTCTGT 50136          TT_  C
           C                    GACAGAGACACAG   TTG TCTG
                                ||||||||||||   ||| ||||
                                CTGTCTCTGTGTC   GAC AGAC
                                       CCC  _
GAM365  FLJ10375 3'  CAGAGGCCTGTGTCTGTGCCA  36073    A  G      TTTTG
                                TG CA AGACACAG    CTCTG
                                || || ||||||||    |||||
                                AC GT TCTGTGTC    GAGAC
                                 C  G       CG___
GAM365  FLJ10738 5'  CAAAGCCAGCCCTCTGTCA   36527        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
                                ACTGTCTC    CGAAAC
                                     CCGAC
GAM365  FLJ10803 3'  CAAAACAAAACTCTGTCA    36660        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
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                                ACTGTCTC    CAAAAC
                                    AAAA_
GAM365  FLJ10842  3'  AAAGTGTGCTCTGTCA     36723        A   G
                                TGACAGAG CACA TTT
                                |||||||| |||| |||
                                ACTGTCTC GTGT AAA
                                    _   G
GAM365  FLJ13153  3'  CAGAGCCCAGCATCCATCTCTG 45555        CACA_  TT
          TCA                    TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                    ACCTA   CC
GAM365  FLJ20035  3'  CAAACCTGCCATGTTCTGTCA  34395        A ___  T
                                TGACAGAG CA   CAG TTTG
                                |||||||| ||   ||| ||||
                                ACTGTCTT GT   GTC AAAC
                                    _ ACC   C
GAM365  FLJ22195  5'  CAGAGCAGAGGGAAGTCTCTGC 42800    A     ACAG
          CA                     TG CAGAGAC    TTTTGCTCTG
                                || |||||||    ||||||||||
                                AC GTCTCTG    GAGACGAGAC
                                 C      AAGG
GAM365  FLJ32191  5'  GAACTGCACCTCTGTCA     58411        ACA
                                TGACAGAG   CAGTTT
                                ||||||||   ||||||
                                ACTGTCTC   GTCAAG
                                    CAC
GAM365  KIAA1023  3'  CAAAGCTGTATCTGCTATCA   34255    C  _   C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM365  KIAA1586  5'  AGTGTGATGTGTCTCTG     92326         GTT TG T
                                CAGAGACACA   T  C CT
                                ||||||||||   |  | ||
                                GTCTCTGTGT   A  G GA
                                    ___ GT T
GAM365  KIAA1754  3'  GACTAACGTCTCTGTCA     63236         AC_
                                TGACAGAGAC   AGTT
                                ||||||||||   ||||
                                ACTGTCTCTG   TCAG
                                    CAA
GAM365  LANCL2    3'  CAGAGTGCACTGCAGCTCTGTC 37995        ACA    TTT
          A                     TGACAGAG   CAGT   GCTCTG
                                ||||||||   ||||   ||||||
                                ACTGTCTC   GTCA   TGAGAC
                                    GAC    CG_
GAM365  LIG-1     3'  CAGAGCAGGCCTGTCCATGCCA 63893    A  GAGAC    TT
                                TG CA    ACAG  TTGCTCTG
                                || ||    ||||  ||||||||
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                                AC GT    TGTC  GACGAGAC
                                 C  ACC__   CG
GAM365  MGC5242  3'  AGAGTACATGTCTCTG     43823        CAGTTT
                                CAGAGACA    TGCTCT
                                ||||||||    ||||||
                                GTCTCTGT    ATGAGA
                                    AC____
GAM365  OSMR     3'  CAGAGCTGGCACCCTGTCA   14345       AGACA
                                TGACAG    CAGTTTTG
                                ||||||    ||||||||
                                ACTGTC    GTCGAGAC
                                   CCACG
GAM365  RAB21    3'  CAGAACAAAACTGTGGATC   30383    GA        C
                                GA  CACAGTTTTG TCTG
                                ||  |||||||||| ||||
                                CT  GTGTCAAAAC AGAC
                                 AG         A
GAM365  SPTLC2   3'  CAGAGCAAAACTGTGTCTC   16799
                                GAGACACAGTTTTGCTCTG
                                |||||||||||||||||||
                                CTCTGTGTCAAAACGAGAC

GAM365  TGIF2    3'  GAGTCATGCTCTGTCA      41454        A  CAGTTT  _
                                TGACAGAG CA     TG CTC
                                |||||||| ||     || |||
                                ACTGTCTC GT     AC GAG
                                    _ _______  T
GAM365  WBSCR23  5'  GCTGACTGTGTCTCCATCA   46765     CA        TT
                                TGA  GAGACACAGTT  GC
                                |||  ||||||||||  ||
                                ACT  CTCTGTGTCAG  CG
                                  AC         T_
GAM365  LOC115129 3' GGCAAAACCCCGTCTCT     73235       ACA
                                AGAGAC   GTTTTGCT
                                ||||||   ||||||||
                                TCTCTG   CAAAACGG
                                   CCC
GAM365  LOC129198 3' AGCAAGCTGTGCCTC       76117     A       T
                                GAG CACAGTTT GCT
                                ||| |||||||| |||
                                CTC GTGTCGAA CGA
                                  C       _
GAM365  LOC145231 3' GGTGAAACTATGTCTCT     83293        C     TG
                                AGAGACA AGTTT  CT
                                ||||||| |||||  ||
                                TCTCTGT TCAAA  GG
                                    A    GT
GAM365  LOC145483 3' GAGCAAAACTCTGTCT      77243       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
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                                TCTGT TCAAAACGAG
                                   C
GAM365  LOC146713 3'  GAGCAAAACTCCGTCT      83726      AC
                                AGAC  AGTTTTGCTC
                                ||||  ||||||||||
                                TCTG  TCAAAACGAG
                                  CC
GAM365  LOC149175 3'  CAGGGTGAAACCACGTCTCT   79208       ACA    TG
                                AGAGAC   GTTT  CTCTG
                                ||||||   ||||  |||||
                                TCTCTG   CAAA  GGGAC
                                   CAC    GT
GAM365  LOC150299 3'  CAGAACCTGCATCTTTGTCA   84968         CA   _
                                TGACAGAGA  CAG TTTTG
                                |||||||||  ||| |||||
                                ACTGTTTCT  GTC AAGAC
                                      AC   C
GAM365  LOC153277 3'  TAAAACTGTGCCTGTGCCA    85990    A  G  A
                                TG CA AG CACAGTTTTG
                                || || || ||||||||||
                                AC GT TC GTGTCAAAAT
                                 C  G  C
GAM365  LOC155179 3'  CAAAGCTGTATCTGCTATCA   81312     C  _   C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM365  LOC221074 3'  AAAGTGTGTCTCTTTCA     93177     C        G
                                TGA AGAGACACA TTT
                                ||| ||||||||| |||
                                ACT TCTCTGTGT AAA
                                  T        G
GAM365  LOC221103 5'  AGTTTATGTGTGCTCTGTCA   93244         _     GTTTT
                                TGACAGAG ACACA     GCT
                                |||||||| |||||     |||
                                ACTGTCTC TGTGT     TGA
                                     G     ATT__
GAM365  LOC255988 5'  CAGAGCCCAGCATCCATCTCTG 97608          CACA_   TT
           TCA                    TGACAGAGA     GTT  GCTCTG
                                |||||||||     |||  ||||||
                                ACTGTCTCT     CGA  CGAGAC
                                     ACCTA   CC
GAM366  ARCN1    3'  AGACTGCACTCTCTGTCA    7970          CA_
                                TGACAGAGA   CAGTTT
                                |||||||||   ||||||
                                ACTGTCTCT   GTCAGA
                                     CAC
GAM366  CBFA2T2   3'  GAGCAAAACTCTGTCT      17466       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
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                                TCTGT TCAAAACGAG
                                   C
GAM366  CTLA4    3'  CAGAGCTGGGATGTTTCTGTCA 17807          CAGTTTT
                                TGACAGAGACA      GCTCTG
                                ||||||||||       ||||||
                                ACTGTCTTTGT      CGAGAC
                                     AGGGT__
GAM366  ITK      3'  CAGAACAGGAGTGATGTCTCTG 18674        _ G    C
                                CAGAGACA CA TTTTG TCTG
                                |||||||| || ||||| ||||
                                GTCTCTGT GT AGGAC AGAC
                                     A G    A
GAM366  LAMP2    3'  GGTGAAACCCCATCTCTATCA  25716    C    CACA    TG
                                TGA AGAGA    GTTT  CT
                                ||| |||||    ||||  ||
                                ACT TCTCT    CAAA  GG
                                  A    ACCC    GT
GAM366  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   40865       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM366  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   52960       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM366  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   52963       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM366  PDGFRB   5'  CAGAGCCTGGAACTGTG     65969         __
                                CACAGTTTT  GCTCTG
                                |||||||||  ||||||
                                GTGTCAAGG  CGAGAC
                                     TC
GAM366  PTPRA    3'  AGAGCGGTATCTCTG       55079       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM366  PTPRA    3'  AGAGCGGTATCTCTG       55087       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM366  PTPRA    3'  AGAGCGGTATCTCTG       11088       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
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                                GTCTCT TG    GCGAGA
                                   A _____
GAM366  RAD51L3  3'  CAAAACTCAGGTATGTCTCTGT 56065         C_____
                                ACAGAGACA     AGTTTTG
                                |||||||||     |||||||
                                TGTCTCTGT     TCAAAAC
                                     ATGGAC
GAM366  TBL2     3'  CAGAACTGTGTTCCATCA    52178     CA   A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM366  TBL2     3'  CAGAACTGTGTTCCATCA    24924     CA   A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM366  AGTRL2   5'  CAGAGCAAGAACTGTTC     17691     C      _
                                GA ACAGTTTT GCTCTG
                                || |||||||| ||||||
                                CT TGTCAAGA CGAGAC
                                 _       A
GAM366  CABP5    3'  AGAGCGGTATCTTTGCCA    39079     A     C  AGTTT
                                TG CAGAGA AC     TGCTCT
                                || |||||| ||     ||||||
                                AC GTTTCT TG     GCGAGA
                                 C     A _____
GAM366  CUL4A    5'  AGAGCAGCACCTCCATCA    13149     CA   ACACA  T
                                TGA  GAG     GT TTGCTCT
                                |||  |||     || |||||||
                                ACT  CTC     CA GACGAGA
                                  AC  _____  C
GAM366  DKFZp761O17121 3'  CAGACAGCCCCTGTGTCTCTGT 50136            TT_  C
           C                     GACAGAGACACAG   TTG TCTG
                                ||||||||||||   ||| ||||
                                CTGTCTCTGTGTC   GAC AGAC
                                       CCC  _
GAM366  FLJ10375 3'  CAGAGGCCTGTGTCTGTGCCA  36073    A  G      TTTTG
                                TG CA AGACACAG    CTCTG
                                || || ||||||||    |||||
                                AC GT TCTGTGTC    GAGAC
                                 C  G       CG___
GAM366  FLJ10738 5'  CAAAGCCAGCCCTCTGTCA   36527        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
                                ACTGTCTC    CGAAAC
                                     CCGAC
GAM366  FLJ10803 3'  CAAAACAAAACTCTGTCA    36660        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
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                                ACTGTCTC    CAAAAC
                                    AAAA_
GAM366  FLJ10842  3'  AAAGTGTGCTCTGTCA     36723        A   G
                                TGACAGAG CACA TTT
                                |||||||| |||| |||
                                ACTGTCTC GTGT AAA
                                    _   G
GAM366  FLJ13153  3'  CAGAGCCCAGCATCCATCTCTG 45555        CACA_  TT
          TCA                    TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                    ACCTA   CC
GAM366  FLJ20035  3'  CAAACCTGCCATGTTCTGTCA  34395        A ___  T
                                TGACAGAG CA   CAG TTTG
                                |||||||| ||   ||| ||||
                                ACTGTCTT GT   GTC AAAC
                                    _ ACC   C
GAM366  FLJ22195  5'  CAGAGCAGAGGGAAGTCTCTGC 42800    A     ACAG
          CA                     TG CAGAGAC    TTTTGCTCTG
                                || |||||||    ||||||||||
                                AC GTCTCTG    GAGACGAGAC
                                 C      AAGG
GAM366  FLJ32191  5'  GAACTGCACCTCTGTCA     58411        ACA
                                TGACAGAG   CAGTTT
                                ||||||||   ||||||
                                ACTGTCTC   GTCAAG
                                    CAC
GAM366  KIAA1023  3'  CAAAGCTGTATCTGCTATCA   34255    C  _   C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM366  KIAA1586  5'  AGTGTGATGTGTCTCTG     92326         GTT TG T
                                CAGAGACACA   T  C CT
                                ||||||||||   |  | ||
                                GTCTCTGTGT   A  G GA
                                    ___ GT T
GAM366  KIAA1754  3'  GACTAACGTCTCTGTCA     63236         AC_
                                TGACAGAGAC   AGTT
                                ||||||||||   ||||
                                ACTGTCTCTG   TCAG
                                    CAA
GAM366  LANCL2    3'  CAGAGTGCACTGCAGCTCTGTC 37995        ACA    TTT
          A                     TGACAGAG   CAGT   GCTCTG
                                ||||||||   ||||   ||||||
                                ACTGTCTC   GTCA   TGAGAC
                                    GAC    CG_
GAM366  LIG-1     3'  CAGAGCAGGCCTGTCCATGCCA 63893    A  GAGAC    TT
                                TG CA    ACAG  TTGCTCTG
                                || ||    ||||  ||||||||
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                                AC GT    TGTC  GACGAGAC
                                 C  ACC__   CG
GAM366  MGC5242  3'  AGAGTACATGTCTCTG     43823        CAGTTT
                                CAGAGACA    TGCTCT
                                ||||||||    ||||||
                                GTCTCTGT    ATGAGA
                                    AC____
GAM366  OSMR     3'  CAGAGCTGGCACCCTGTCA   14345       AGACA
                                TGACAG    CAGTTTTG
                                ||||||    ||||||||
                                ACTGTC    GTCGAGAC
                                   CCACG
GAM366  RAB21    3'  CAGAACAAAACTGTGGATC   30383    GA        C
                                GA  CACAGTTTTG TCTG
                                ||  |||||||||| ||||
                                CT  GTGTCAAAAC AGAC
                                 AG         A
GAM366  SPTLC2   3'  CAGAGCAAAACTGTGTCTC   16799
                                GAGACACAGTTTTGCTCTG
                                |||||||||||||||||||
                                CTCTGTGTCAAAACGAGAC

GAM366  TGIF2    3'  GAGTCATGCTCTGTCA      41454        A  CAGTTT  _
                                TGACAGAG CA     TG CTC
                                |||||||| ||     || |||
                                ACTGTCTC GT     AC GAG
                                    _ _______  T
GAM366  WBSCR23  5'  GCTGACTGTGTCTCCATCA   46765     CA        TT
                                TGA  GAGACACAGTT  GC
                                |||  ||||||||||  ||
                                ACT  CTCTGTGTCAG  CG
                                  AC         T_
GAM366  LOC115129 3' GGCAAAACCCCGTCTCT     73235       ACA
                                AGAGAC   GTTTTGCT
                                ||||||   ||||||||
                                TCTCTG   CAAAACGG
                                   CCC
GAM366  LOC129198 3' AGCAAGCTGTGCCTC       76117     A       T
                                GAG CACAGTTT GCT
                                ||| |||||||| |||
                                CTC GTGTCGAA CGA
                                  C       _
GAM366  LOC145231 3' GGTGAAACTATGTCTCT     83293        C     TG
                                AGAGACA AGTTT  CT
                                ||||||| |||||  ||
                                TCTCTGT TCAAA  GG
                                    A    GT
GAM366  LOC145483 3' GAGCAAAACTCTGTCT      77243       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
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                                TCTGT TCAAAACGAG
                                   C
GAM366  LOC146713 3'  GAGCAAAACTCCGTCT     83726      AC
                                AGAC  AGTTTTGCTC
                                ||||  ||||||||||
                                TCTG  TCAAAACGAG
                                  CC
GAM366  LOC149175 3'  CAGGGTGAAACCACGTCTCT   79208       ACA    TG
                                AGAGAC   GTTT  CTCTG
                                ||||||   ||||  |||||
                                TCTCTG   CAAA  GGGAC
                                   CAC    GT
GAM366  LOC150299 3'  CAGAACCTGCATCTTTGTCA   84968         CA   _
                                TGACAGAGA  CAG TTTTG
                                |||||||||  ||| |||||
                                ACTGTTTCT  GTC AAGAC
                                      AC   C
GAM366  LOC153277 3'  TAAAACTGTGCCTGTGCCA    85990    A  G  A
                                TG CA AG CACAGTTTTG
                                || || || ||||||||||
                                AC GT TC GTGTCAAAAT
                                 C  G  C
GAM366  LOC155179 3'  CAAAGCTGTATCTGCTATCA   81312     C  _   C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM366  LOC221074 3'  AAAGTGTGTCTCTTTCA     93177     C        G
                                TGA AGAGACACA TTT
                                ||| ||||||||| |||
                                ACT TCTCTGTGT AAA
                                  T        G
GAM366  LOC221103 5'  AGTTTATGTGTGCTCTGTCA   93244         _     GTTTT
                                TGACAGAG ACACA     GCT
                                |||||||| |||||     |||
                                ACTGTCTC TGTGT     TGA
                                     G     ATT__
GAM366  LOC255988 5'  CAGAGCCCAGCATCCATCTCTG 97608          CACA_   TT
           TCA                    TGACAGAGA     GTT  GCTCTG
                                |||||||||     |||  ||||||
                                ACTGTCTCT     CGA  CGAGAC
                                      ACCTA   CC
GAM367  ARCN1    3'  AGACTGCACTCTCTGTCA    7970          CA_
                                TGACAGAGA   CAGTTT
                                |||||||||   ||||||
                                ACTGTCTCT   GTCAGA
                                      CAC
GAM367  CBFA2T2   3'  GAGCAAAACTCTGTCT      17466       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
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                                TCTGT TCAAAACGAG
                                   C
GAM367  CTLA4    3'  CAGAGCTGGGATGTTTCTGTCA 17807          CAGTTTT
                                TGACAGAGACA      GCTCTG
                                ||||||||||       ||||||
                                ACTGTCTTTGT      CGAGAC
                                     AGGGT__
GAM367  ITK      3'  CAGAACAGGAGTGATGTCTCTG 18674        _ G    C
                                CAGAGACA CA TTTTG TCTG
                                |||||||| || ||||| ||||
                                GTCTCTGT GT AGGAC AGAC
                                     A G    A
GAM367  LAMP2    3'  GGTGAAACCCCATCTCTATCA 25716    C    CACA    TG
                                TGA AGAGA    GTTT  CT
                                ||| |||||    ||||  ||
                                ACT TCTCT    CAAA  GG
                                  A    ACCC    GT
GAM367  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA  52963       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM367  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA  52960       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM367  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA  40865       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM367  PDGFRB   5'  CAGAGCCTGGAACTGTG     65969        __
                                CACAGTTTT  GCTCTG
                                |||||||||  ||||||
                                GTGTCAAGG  CGAGAC
                                     TC
GAM367  PTPRA    3'  AGAGCGGTATCTCTG       55087       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM367  PTPRA    3'  AGAGCGGTATCTCTG       11088       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM367  PTPRA    3'  AGAGCGGTATCTCTG       55079       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
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                                GTCTCT TG    GCGAGA
                                   A _____
GAM367  RAD51L3  3'  CAAAACTCAGGTATGTCTCTGT 56065        C_____
                                ACAGAGACA    AGTTTTG
                                |||||||||    |||||||
                                TGTCTCTGT    TCAAAAC
                                     ATGGAC
GAM367  TBL2     3'  CAGAACTGTGTTCCATCA    52178    CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM367  TBL2     3'  CAGAACTGTGTTCCATCA    24924    CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM367  AGTRL2   5'  CAGAGCAAGAACTGTTC    17691    C     _
                                GA ACAGTTTT GCTCTG
                                || |||||||| ||||||
                                CT TGTCAAGA CGAGAC
                                 _      A
GAM367  CABP5    3'  AGAGCGGTATCTTTGCCA    39079    A    C  AGTTT
                                TG CAGAGA AC    TGCTCT
                                || |||||| ||    ||||||
                                AC GTTTCT TG    GCGAGA
                                 C     A _____
GAM367  CUL4A    5'  AGAGCAGCACCTCCATCA    13149    CA  ACACA  T
                                TGA  GAG    GT TTGCTCT
                                |||  |||    || |||||||
                                ACT  CTC    CA GACGAGA
                                  AC  _____  C
GAM367  DKFZp761O17121 3'  CAGACAGCCCCTGTGTCTCTGT 50136           TT_  C
           C                    GACAGAGACACAG   TTG TCTG
                                ||||||||||||   ||| ||||
                                CTGTCTCTGTGTC   GAC AGAC
                                       CCC  _
GAM367  FLJ10375 3'  CAGAGGCCTGTGTCTGTGCCA  36073    A  G      TTTTG
                                TG CA AGACACAG    CTCTG
                                || || ||||||||    |||||
                                AC GT TCTGTGTC    GAGAC
                                 C  G       CG___
GAM367  FLJ10738 5'  CAAAGCCAGCCCTCTGTCA   36527        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
                                ACTGTCTC    CGAAAC
                                     CCGAC
GAM367  FLJ10803 3'  CAAAACAAAACTCTGTCA    36660        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
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                                ACTGTCTC    CAAAAC
                                    AAAA_
GAM367  FLJ10842  3'  AAAGTGTGCTCTGTCA     36723        A   G
                                TGACAGAG CACA TTT
                                |||||||| |||| |||
                                ACTGTCTC GTGT AAA
                                    _   G
GAM367  FLJ13153  3'  CAGAGCCCAGCATCCATCTCTG 45555        CACA_  TT
          TCA                    TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                    ACCTA   CC
GAM367  FLJ20035  3'  CAAACCTGCCATGTTCTGTCA  34395        A ___  T
                                TGACAGAG CA   CAG TTTG
                                |||||||| ||   ||| ||||
                                ACTGTCTT GT   GTC AAAC
                                    _ ACC   C
GAM367  FLJ22195  5'  CAGAGCAGAGGGAAGTCTCTGC 42800    A     ACAG
          CA                     TG CAGAGAC    TTTTGCTCTG
                                || |||||||    ||||||||||
                                AC GTCTCTG    GAGACGAGAC
                                 C      AAGG
GAM367  FLJ32191  5'  GAACTGCACCTCTGTCA     58411        ACA
                                TGACAGAG   CAGTTT
                                ||||||||   ||||||
                                ACTGTCTC   GTCAAG
                                    CAC
GAM367  KIAA1023  3'  CAAAGCTGTATCTGCTATCA   34255    C  _   C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM367  KIAA1586  5'  AGTGTGATGTGTCTCTG     92326         GTT TG T
                                CAGAGACACA   T  C CT
                                ||||||||||   |  | ||
                                GTCTCTGTGT   A  G GA
                                    ___ GT T
GAM367  KIAA1754  3'  GACTAACGTCTCTGTCA     63236         AC_
                                TGACAGAGAC   AGTT
                                ||||||||||   ||||
                                ACTGTCTCTG   TCAG
                                    CAA
GAM367  LANCL2    3'  CAGAGTGCACTGCAGCTCTGTC 37995        ACA    TTT
          A                     TGACAGAG   CAGT   GCTCTG
                                ||||||||   ||||   ||||||
                                ACTGTCTC   GTCA   TGAGAC
                                    GAC    CG_
GAM367  LIG-1     3'  CAGAGCAGGCCTGTCCATGCCA 63893    A  GAGAC    TT
                                TG CA    ACAG  TTGCTCTG
                                || ||    ||||  ||||||||
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                                AC GT    TGTC  GACGAGAC
                                 C  ACC__   CG
GAM367  MGC5242  3'  AGAGTACATGTCTCTG     43823        CAGTTT
                                CAGAGACA    TGCTCT
                                ||||||||    ||||||
                                GTCTCTGT    ATGAGA
                                    AC____
GAM367  OSMR     3'  CAGAGCTGGCACCCTGTCA   14345       AGACA
                                TGACAG    CAGTTTTG
                                ||||||    ||||||||
                                ACTGTC    GTCGAGAC
                                   CCACG
GAM367  RAB21    3'  CAGAACAAAACTGTGGATC   30383    GA        C
                                GA  CACAGTTTTG TCTG
                                ||  |||||||||| ||||
                                CT  GTGTCAAAAC AGAC
                                 AG         A
GAM367  SPTLC2   3'  CAGAGCAAAACTGTGTCTC   16799
                                GAGACACAGTTTTGCTCTG
                                |||||||||||||||||||
                                CTCTGTGTCAAAACGAGAC

GAM367  TGIF2    3'  GAGTCATGCTCTGTCA      41454        A  CAGTTT  _
                                TGACAGAG CA     TG CTC
                                |||||||| ||     || |||
                                ACTGTCTC GT     AC GAG
                                    _  _______  T
GAM367  WBSCR23  5'  GCTGACTGTGTCTCCATCA   46765     CA        TT
                                TGA  GAGACACAGTT  GC
                                |||  ||||||||||  ||
                                ACT  CTCTGTGTCAG  CG
                                  AC         T_
GAM367  LOC115129 3' GGCAAAACCCCGTCTCT     73235       ACA
                                AGAGAC   GTTTTGCT
                                ||||||   ||||||||
                                TCTCTG   CAAAACGG
                                   CCC
GAM367  LOC129198 3' AGCAAGCTGTGCCTC       76117     A       T
                                GAG CACAGTTT GCT
                                ||| |||||||| |||
                                CTC GTGTCGAA CGA
                                  C       _
GAM367  LOC145231 3' GGTGAAACTATGTCTCT     83293        C     TG
                                AGAGACA AGTTT  CT
                                ||||||| |||||  ||
                                TCTCTGT TCAAA  GG
                                    A    GT
GAM367  LOC145483 3' GAGCAAAACTCTGTCT      77243       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
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                                TCTGT TCAAAACGAG
                                  C
GAM367  LOC146713 3'  GAGCAAAACTCCGTCT     83726     AC
                                AGAC  AGTTTTGCTC
                                ||||  ||||||||||
                                TCTG  TCAAAACGAG
                                  CC
GAM367  LOC149175 3'  CAGGGTGAAACCACGTCTCT  79208      ACA   TG
                                AGAGAC  GTTT  CTCTG
                                ||||||  ||||  |||||
                                TCTCTG  CAAA  GGGAC
                                   CAC   GT
GAM367  LOC150299 3'  CAGAACCTGCATCTTTGTCA  84968       CA  _
                                TGACAGAGA  CAG TTTTG
                                |||||||||  ||| |||||
                                ACTGTTTCT  GTC AAGAC
                                     AC  C
GAM367  LOC153277 3'  TAAAACTGTGCCTGTGCCA   85990    A  G  A
                                TG CA AG CACAGTTTTG
                                || || || ||||||||||
                                AC GT TC GTGTCAAAAT
                                 C  G  C
GAM367  LOC155179 3'  CAAAGCTGTATCTGCTATCA  81312     C  _  C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G  A
GAM367  LOC221074 3'  AAAGTGTGTCTCTTTCA     93177     C       G
                                TGA AGAGACACA TTT
                                ||| ||||||||| |||
                                ACT TCTCTGTGT AAA
                                  T       G
GAM367  LOC221103 5'  AGTTTATGTGTGCTCTGTCA  93244        _    GTTTT
                                TGACAGAG ACACA    GCT
                                |||||||| |||||    |||
                                ACTGTCTC TGTGT    TGA
                                    G    ATT__
GAM367  LOC255988 5'  CAGAGCCCAGCATCCATCTCTG 97608        CACA_  TT
           TCA                    TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                     ACCTA   CC
GAM368  FCMD    3'  ACAACTATTCACCCTACCT   22086    C    GTTAGT
                                AG TAGGG     ATAGTTGT
                                || |||||     ||||||||
                                TC ATCCC     TATCAACA
                                 C    ACT___
GAM368  MPDZ    3'  CAACCCAACCCCTAGCT     13817          AGTATA
                                AGCTAGGGGTT     GTTG
                                ||||||||||     ||||
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                                TCGATCCCCAA     CAAC
                                      CC____
GAM368  C12orf4   3'  ACTGGTGATCAACCCCTAACTT 39809     C      AGTA__
            A                    TAAG TAGGGGTT     TAGT
                                 |||| ||||||||     ||||
                                 ATTC ATCCCCAA     GTCA
                                   A       CTAGTG
GAM368  DKFZP434F0318 3'  CAACCATTCCCTAACTCC    48005        T__  A
                                 GGGGTTAG   AT GTTG
                                 ||||||||   || ||||
                                 CCTCAATC   TA CAAC
                                      CCT  C
GAM368  U5-100K   3'  ACAATCCAACTCCCTAGC    59678       GTT   ATA
                                 GCTAGGG   AGT   GTTGT
                                 |||||||   |||   |||||
                                 CGATCCC   TCA   TAACA
                                     ___   ACC
GAM369  CFL1      3'  CCTTTTCCCCTGGTCA      18572       AGTTCACA
                                 TGACTA       GGAAAAGG
                                 ||||||       ||||||||
                                 ACTGGT       CCTTTTCC
                                    CC_______
GAM369  LMCD1     5'  TCCCTCCCAGGCCCGCGAACTT 27427    A       ACA  AAA___
            GGCCA                    TG CTAAGTTC   GG     AGGGA
                                 || ||||||||   ||     |||||
                                 AC GGTTCAAG   CC     TCCCT
                                  C       CGC  GGACCC
GAM369  NAV2      3'  CCCTTCCCCTCTTGGTCA    60158        TTCAC   AA
                                 TGACTAAG    AGG  AAGGG
                                 ||||||||    |||  |||||
                                 ACTGGTTC    TCC  TTCCC
                                      _____  CC
GAM369  NOTCH3    3'  TCCCTCCCCCTGTGAAC     4750         AAA
                                 GTTCACAGG   AGGGA
                                 |||||||||   |||||
                                 CAAGTGTCC   TCCCT
                                       CCC
GAM369  NR4A1     5'  CCCCCCTCCTGTGAGGCT    9235     _      AAA
                                 AGT TCACAGGA   GGG
                                 ||| ||||||||   |||
                                 TCG AGTGTCCT   CCC
                                   G       CCC
GAM369  SUV39H1   3'  CCCTTTCCCTGTCCCAGC    12068     C__    A
                                 GTT   ACAGG AAAGGG
                                 |||   ||||| ||||||
                                 CGA   TGTCC TTTCCC
                                   CCC    C
GAM369  ZNF133    5'  TCCCTTTTCCTAACCTAG    12843     A   CAC
                                 CTA GTT   AGGAAAAGGGA
                                 ||| |||   ||||||||||
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                                GAT CAA   TCCTTTTCCCT
                                  C  ___
GAM369  ARHGEF9  3' TCCCTTTTCCTCAACTCAGT  30822    A   CAC
                                ACT AGTT   AGGAAAAGGGA
                                ||| ||||   ||||||||||
                                TGA TCAA   TCCTTTTCCCT
                                  C   C__
GAM369  BRPF3    3' CCCTCTCCCCAGGTAGTTGGTC 92315       GT_ ACA  AA
           A                     TGACTAA   TC   GGA  AGGG
                                |||||||   ||   |||  ||||
                                ACTGGTT   GG   CCT  TCCC
                                    GAT  ACC   C_
GAM369  CSR1     3' CCCTCTCCTGTGACTGAG    32685    A  T     AA
                                CT AGT CACAGGA  AGGG
                                || ||| |||||||  ||||
                                GA TCA GTGTCCT  TCCC
                                 G  _      C_
GAM369  FLJ12787 3' TCCCTGAGTAATTATGAACTTA 49752          C  GAAA__
           GTCA                   TGACTAAGTTCA AG     AGGGA
                                ||||||||||| ||     |||||
                                ACTGATTCAAGT TT     TCCCT
                                      A  AATGAG
GAM369  FLJ14775 3' TCCTACAAACTTGGTCA     51605         CAC
                                TGACTAAGTT   AGGA
                                |||||||||   ||||
                                ACTGGTTCAA   TCCT
                                      ACA
GAM369  KIAA0322 3' CCCTTTTCCCTTTCCCTTAATC 92751     C    TTCACA
           A                     TGA TAAG     GGAAAAGGG
                                ||| ||||     |||||||||
                                ACT ATTC     CCTTTTCCC
                                  A   CCTTTC
GAM369  KIAA0495 5' CCCTTCTCCTGTGGGAC     62575     _     A
                                GTTC ACAGGA AAGGG
                                |||| |||||| |||||
                                CAGG TGTCCT TTCCC
                                  G     C
GAM369  KIAA0794 3' TCCCTTTTCCTGTGAG      80414
                                TTCACAGGAAAAGGGA
                                ||||||||||||||||
                                GAGTGTCCTTTTCCCT

GAM369  KRTAP4-2 3' TCCACCTGTGAACTGAATCA  52344     CTA        AAAA
                                TGA   AGTTCACAGG   GGG
                                |||   ||||||||||   |||
                                ACT   TCAAGTGTCC   CCT
                                  AAG        A___
GAM369  MGC16153 3' CCCTTTTCAGACTCAG      51297    A   CACAG
                                CT AGTT    GAAAAGGG
                                || ||||    ||||||||
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                                GA TCAG    CTTTTCCC
                                 C   A____
GAM369  PSKH1    3'  CCCTCCCTGGAACTTAGCCA  68237    A      A   AAA
                                TG CTAAGTTC CAGG   AGGG
                                || |||||||| ||||   ||||
                                AC GATTCAAG GTCC   TCCC
                                 C       _   C__
GAM369  SEC15B   3'  CCCTTTTAGAATTTGAACTTA  66685        CAGG__
                                TAAGTTCA     AAAAGGG
                                ||||||||     |||||||
                                ATTCAAGT     TTTTCCC
                                     TTAAGA
GAM369  SNPH     3'  TCCCTTCTCCCATGGGC     28245      CA  A
                                GTTCA  GGA AAGGGA
                                |||||  ||| ||||||
                                CGGGT  CCT TTCCCT
                                   AC   C
GAM369  LOC145375 3'  CCGCCCCTTAAACTTAGTCA  59968         CAC   AAAA
                                TGACTAAGTT   AGG   GG
                                ||||||||||   |||   ||
                                ACTGATTCAA   TCC   CC
                                      AT_   CCG_
GAM369  LOC148003 3'  CCCTTCCCCTACACTTGGTCA  78614         TCAC   AA
                                TGACTAAGT    AGG  AAGGG
                                |||||||||    |||  |||||
                                ACTGGTTCA    TCC  TTCCC
                                     CA__   CC
GAM369  LOC148525 3'  CCCTTTTCCTGCAGAT     78892     CA
                                GTT  CAGGAAAAGGG
                                |||  ||||||||||
                                TAG  GTCCTTTTCCC
                                  AC
GAM369  LOC221405 5'  CCCTTTTCCCACTGAAC     93882      CA_
                                GTTCA   GGAAAAGGG
                                |||||   |||||||||
                                CAAGT   CCTTTTCCC
                                   CAC
GAM369  LOC257355 3'  CCCTTTTCTACAGACCTCATCA 94406     CTA  T  ACA
                                TGA   AG TC   GGAAAAGGG
                                |||   || ||   |||||||||
                                ACT   TC AG   TCTTTTCCC
                                  AC_  C  ACA
GAM369  LOC51172  3'  CCCTTTTCTACAGACCTCATCA 63348     CTA  T  ACA
                                TGA   AG TC   GGAAAAGGG
                                |||   || ||   |||||||||
                                ACT   TC AG   TCTTTTCCC
                                  AC_  C  ACA
GAM370  ABCF1    3'  ATTCAGGCACATGAAGGTGGAG 6566           C_      AT
           TG                    CATTTCACTTTCA  TGTCTGAG
                                |||||||||||||  ||||||||
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                                GTGAGGTGGAAGT  ACGGACTT
                                      AC       A
GAM370  ACVRL1   5'  GCGGTGGAGGGGAGGTG     3418        A
                                CATTTC CTTTCACTGT
                                |||||| ||||||||||
                                GTGGAG GGAGGTGGCG
                                   G
GAM370  ADRA1A   3'  TCTTGATGGAAGTGAGG     5448          CTG  T
                                TTTCACTTTCA   TC GAGA
                                ||||||||||   || ||||
                                GGAGTGAAGGT   AG TTCT
                                      ___ _
GAM370  AGT      3'  ATTTTAGAGAATGGGGGTGGGG 3453    TT   TT  CTG
                                T  CACT  CA   TCTGAGAT
                                |  ||||  ||   ||||||||
                                G  GTGG  GT   AGATTTTA
                                 GG    GG  AAG
GAM370  AIM1     3'  ATCTCAGGCTGGAGTGCAGTG  91816     T     CACT
                                CATT CACTTT    GTCTGAGAT
                                |||| ||||||    |||||||||
                                GTGA GTGAGG    CGGACTCTA
                                  C     T___
GAM370  AKAP13   3'  GTTTTGGGCATGGATAAAGTGA 22144        ___    C    TG
           AG                     TTTCACT   TTCA TGTC  AGAT
                                |||||||   |||| ||||  ||||
                                GAAGTGA   AGGT ACGG  TTTG
                                    AAT   _   GT
GAM370  AKAP13   3'  GTTTTGGGCATGGATAAAGTGA 23248        ___    C    TG
           AG                     TTTCACT   TTCA TGTC  AGAT
                                |||||||   |||| ||||  ||||
                                GAAGTGA   AGGT ACGG  TTTG
                                    AAT   _   GT
GAM370  AKAP13   3'  GTTTTGGGCATGGATAAAGTGA 58580        ___    C    TG
           AG                     TTTCACT   TTCA TGTC  AGAT
                                |||||||   |||| ||||  ||||
                                GAAGTGA   AGGT ACGG  TTTG
                                    AAT   _   GT
GAM370  ATP11B   3'  ATTTCAGGTGTGGCTGTGGAAT 80315        TT    TGT
           G                      CATTTCAC  TCAC   CTGAGAT
                                |||||||  ||||   |||||||
                                GTAAGGTG  GGTG   GACTTTA
                                    TC    TG_
GAM370  B4GALT4  3'  TAGCAGGAGGGTGGAGTG    13674          A   T
                                CATTTCACTTTC CTG CTG
                                |||||||||||| ||| |||
                                GTGAGGTGGGAG GAC GAT
                                      _  _
GAM370  BLAME    3'  ATCTGGGAGTGAGGGTGGAG  39239          TG   G
                                TTTCACTTTCAC  TCT AGAT
                                ||||||||||||  ||| ||||
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                                GAGGTGGGAGTG  AGG TCTA
                                      __  G
GAM370  C20orf1  5' ATTTCAGAAAAGGGGTGAAA  23999        CACTG
                                TTTCACTTT   TCTGAGAT
                                |||||||||   ||||||||
                                AAAGTGGGG   AGACTTTA
                                     AAA__
GAM370  C21orf5  3' TTTCAGGCTAGGTGCGGTG   17614     TT   __
                                CACT  CACT  GTCTGAGA
                                ||||  ||||  ||||||||
                                GTGG  GTGG  CGGACTTT
                                  C_   AT
GAM370  CAPN10   3' GTCTCAGAACCGAGTGAGGTG 43604         TCACTG
                                CATTTCACTT    TCTGAGAT
                                ||||||||||    ||||||||
                                GTGGAGTGAG    AGACTCTG
                                      CCA___
GAM370  CARPX    3' ATTTCAGATAGTGTCCTAGGA  39415    A  TT__
                                TC CT   CACTGTCTGAGAT
                                || ||   ||||||||||||
                                AG GA   GTGATAGACTTTA
                                 _ TCCT
GAM370  CARPX    5' TCGGGTGGGAGTGCGAGTG   39426     _   TT  TGT
                                CATTT CACT  CAC   CTGA
                                ||||| ||||  |||   ||||
                                GTGAG GTGA  GTG   GGCT
                                   C   GG  ___
GAM370  CASP10   3' TTTTGGACTGGGTGCGGTG   52111     TT   __  TG
                                CACT  CACT  GTC  AGA
                                ||||  ||||  |||  |||
                                GTGG  GTGG  CAG  TTT
                                  C_   GT  GT
GAM370  CASP10   3' TTTTGGACTGGGTGCGGTG   52127     TT   __  TG
                                CACT  CACT  GTC  AGA
                                ||||  ||||  |||  |||
                                GTGG  GTGG  CAG  TTT
                                  C_   GT  GT
GAM370  CCND1    3' GTGGTGGCAGTGGAGGTGGGGT 53891     TT         TGAGAT
           G                     CAT  CACTTTCACTGTC
                                 |||  ||||||||||||
                                 GTG  GTGGAGGTGACGG
                                   GG          TGGTG
GAM370  CDK4     5' GTCACATGGTGAGGGTGGGG   53763   TT        C   GAT
                                T  CACTTTCACTGT TGA
                                |  |||||||||||| |||
                                G  GTGGGAGTGGTA ACT
                                 GG         C   G
GAM370  CDK4     5' GTCACATGGTGAGGGTGGGG   3573    TT        C   GAT
                                T  CACTTTCACTGT TGA
                                |  |||||||||||| |||
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                              G  GTGGGAGTGGTA ACT
                               GG         C   G
GAM370  CDKN2A   5'  GTCCGGGTGGGAGTGGGGGTGG 54229   TT   TT   G___   A
           GGTG                  T  CACT  CACT   TCTG GAT
                              |  ||||  ||||   |||| |||
                              G  GTGG  GTGA   GGGC CTG
                               GG   GG   GGGT   _
GAM370  CDKN2A   5'  TATCTTGGAGGTCCGGGTGGGA 54230    TT   G_____ TG
           GTGGGG                ACT  CACT    TC  AGAT   A
                              |||  ||||    ||  ||||  |
                              TGA  GTGG    AG  TCTA   T
                                GG   GCCTGG  GT
GAM370  CDKN2B   3'  AGGTGGTGGAGTGGAGTG   54353         T   TG
                              CATTTCACTT CAC  TCT
                              ||||||||||  |||  |||
                              GTGAGGTGAG GTG  GGA
                                    _  GT
GAM370  CERD4    3'  ATCTCAGAGCAGAGGAGGTGGG 23849   TT     A  _
           G                   T  CACTTTC CTG TCTGAGAT
                              |  |||||||  ||| ||||||||
                              G  GTGGAGG GAC AGACTCTA
                               GG     A   G
GAM370  CHRM1    3'  TTTTCCTGGGAGTGGGAGTCAA 94794      C   TT   G  T_   T
           GTG                   CATTT ACT  CACT TC  GAGA
                              |||||  |||  ||||  ||  ||||
                              GTGAA TGA  GTGA GG  CTTT
                                 C   GG   G  TC   TA
GAM370  CLASP1   3'  GGGGGTGGGGTGGGGTG    65305    TT    T   G
                              CAT  CACTT CACT TC
                              |||  |||||  ||||  ||
                              GTG  GTGGG GTGG GG
                                GG    _   G
GAM370  CMAR     5'  ATTTTGGACGGTGCTCTGA   17772    CTTT     TG
                              TCA   CACTGTC  AGAT
                              |||   |||||||  ||||
                              AGT   GTGGCAG  TTTA
                                CTC_     GT
GAM370  COL1A1   3'  ATCTATGTGATGGGTGGGGTG  3601     TT    _   TGTCTG
                              CAT  CACTT TCAC     AGAT
                              |||  |||||  ||||     ||||
                              GTG  GTGGG AGTG     TCTA
                                GG    T   TA____
GAM370  COL4A4   5'  CAGGCGGGGAAGTGGGGTG   3626     TT     A
                              CAT  CACTTTC CTGTCTG
                              |||  |||||||  |||||||
                              GTG  GTGAAGG GGCGGAC
                                GG     _
GAM370  COL4A6   3'  GTCTTAGGCAGGCAAGAGAATT 8473     ___    CA_
           GAAATG                TCA   CTTT   CTGTCTGAGAT
                              |||   ||||   ||||||||||
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                                AGT  GAGA  GACGGATTCTG
                                  TAA   ACG
GAM370  CPT1B   3'  GCCCAGGTGGTGGAGGTGGGGT 15199   TT      TG   AGAT
                                AT  CACTTTCAC  TCTG
                                ||  |||||||||  ||||
                                TG  GTGGAGGTG  GGAC
                                  GG       GT   CCG
GAM370  D10S170  3'  GTTTTGTACTTTGGTAGTGAAG 18367       T  CT  CT
           TG                     CATTTCACT TCA  GT  GAGAT
                                |||||||||  |||  ||  |||||
                                GTGAAGTGA GGT  CA  TTTTG
                                      T  TT  TG
GAM370  DDEF2   3'  ATTTTAGGCGGCCAGTGAACTG 13952   T    TTCA
                                CA TTCACT   CTGTCTGAGAT
                                || ||||||   ||||||||||
                                GT AAGTGA   GGCGGATTTTA
                                 C    CC__
GAM370  DES     3'  TCTCAGGCTGGTGGGAG    72132   TT  _
                                CT  CACT GTCTGAGA
                                ||  ||||  ||||||||
                                GA  GTGG CGGACTCT
                                 GG   T
GAM370  DLEC1   3'  TAGAGAGAGTGAGGTG     23706          A
                                CATTTCACTTTC CTG
                                ||||||||||||  |||
                                GTGGAGTGAGAG GAT
                                       A
GAM370  DPYSL3  3'  ATCTCAGCTTATATGAAAGTCA 7311     C     C  ___
           AGTG                    TTT ACTTTCA TGT   CTGAGAT
                                |||  |||||||  |||   |||||||
                                GAA TGAAAGT ATA   GACTCTA
                                  C      _  TTC
GAM370  DRIL1   3'  GTTTTGGACATTCAGAGAGATG 17831      A  TTCAC   TG
                                CATTTC CT    TGTC  AGAT
                                ||||||  ||    ||||  ||||
                                GTAGAG GA    ACAG  TTTG
                                   A  CTT__   GT
GAM370  DXS1283E  3'  GTTTTAGATAGTTTTTGATGGA 70836      CTTTC_
           A                     TTTCA     ACTGTCTGAGAT
                                |||||     ||||||||||||
                                AAGGT     TGATAGATTTTG
                                   AGTTTT
GAM370  EHF     3'  GTCTCAGATGGTTAGGACAAAG 24063      __  ___
           TGGA                    CACTT  TC   ACTGTCTGAGAT
                                |||||  ||   ||||||||||||
                                GTGAA  AG   TGGTAGACTCTG
                                   AC  GAT
GAM370  EIF2B1  5'  CTGCGGAAGTGGAGTG     59658      T   G   _
                                CACTT CACT TCTG AG
                                ||||| |||| |||| ||
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                                GTGAG GTGA AGGC TC
                                  _   _    G
GAM370  EPHA1    3'  GTTTTAAAAGGGAGGTGGGG  17861   TT      A  GTC
                                T  CACTTTC CT   TGAGAT
                                |  ||||||| ||   ||||||
                                G  GTGGAGG GA   ATTTTG
                                 GG       _  AA_
GAM370  ESRRA    3'  ATCTCAGGGAGGGAAGGGGATG 15479     TT A     A  G
                                CAT  C CTTTC CT TCTGAGAT
                                |||  | ||||| || ||||||||
                                GTA  G GAAGG GA GGACTCTA
                                  GG _     _  G
GAM370  FCAR     3'  GCACTGAGAGTGAAGTG     55798            C
                                CATTTCACTTTCA TGT
                                |||||||||||| |||
                                GTGAAGTGAGAGT ACG
                                        C
GAM370  FCAR     3'  GCACTGAGAGTGAAGTG     55814            C
                                CATTTCACTTTCA TGT
                                |||||||||||| |||
                                GTGAAGTGAGAGT ACG
                                        C
GAM370  FGF2     3'  GTCTCAGATACTTGGGAGGCTG 8873       _    AC__
            AGGTG                   TTCA CTTTC    TGTCTGAGAT
                                |||| |||||   ||||||||||
                                GAGT GGAGG    ATAGACTCTG
                                  C    GTTC
GAM370  FRAT2    3'  GGCTGGTGAAGGTGGGA     23881    TT       _
                                T  CACTTTCACT GTC
                                |  |||||||||| |||
                                A  GTGGAAGTGG CGG
                                 GG        T
GAM370  GCKR     3'  ATTTCAGAAATAAAATGAAATG 7635        C   CACTG
                                CATTTCA TTT     TCTGAGAT
                                ||||||| |||    ||||||||
                                GTAAAGT AAA     AGACTTTA
                                    A   TAA__
GAM370  GNPI     3'  GTCTTAGGCCTTCATGGAGTGG 18448        CACT__
            A                    TTCACTTT     GTCTGAGAT
                                ||||||||     |||||||||
                                AGGTGAGG     CGGATTCTG
                                     TACTTC
GAM370  GPR61    3'  TGGGCTGGTGGGAGTGGGAT   78914    TT    TT   _
                                AT  CACT  CACT GTCTG
                                ||  ||||  |||| |||||
                                TA  GTGA  GTGG CGGGT
                                 GG    GG    T
GAM370  GUCY1B3  3'  ATCTTGGATTATGGGGTGAAG  5963         T  CT   TG
                                TTTCACTT CA  GTC  AGAT
                                |||||||| ||  |||  ||||
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                                GAAGTGGG GT  TAG  TCTA
                                     _ AT   GT
GAM370  GYG2     3'  ATTTCAGGTGAGTCAGGGTTGG 14047      TC     C  _ GT
             ATG                    CATT  ACTTT AC T  CTGAGAT
                                |||| |||||  || |  |||||||
                                GTAG  TGGGA TG G  GACTTTA
                                  GT    C  A TG
GAM370  HHEX     3'  ATTTCAGGCAGCCTTGGAGT   10784      CA__
                                ACTTT    CTGTCTGAGAT
                                |||||    ||||||||||
                                TGAGG    GACGGACTTTA
                                   TTCC
GAM370  HMGA2    3'  TCTGGGGTGGGGTGGGGTG    13004     TT    TTCA TG   G
                                CAT  CACT    C  TCT AGA
                                |||  ||||    |  ||| |||
                                GTG  GTGG    G  GGG TCT
                                  GG    ____ GT   G
GAM370  HOXD4    5'  TTTTGGGGTACTAGGGAGTGAG 27534         TT AC_ GT  G   T
             GT                     ATTTCACT  C   T  CT AGA
                                |||||||| |   |  || |||
                                TGGAGTGA  G   A  GG TTT
                                     GG ATC TG  G   TG
GAM370  HPCAL1   5'  GTGGTGACAGGTGAAATG     56190          _    TG
                                CATTTCACTT TCAC  T
                                |||||||||| ||||  |
                                GTAAAGTGGA AGTG  G
                                      C    GT
GAM370  HPCAL1   3'  TTATGTATGGTGAAGTGGAGTG 56191          T     CTGAGAT
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTGAGGTGAA GTGGTA
                                      _      TGTATTA
GAM370  HPCAL1   3'  TTATGTATGGTGAAGTGGAGTG 9272           T     CTGAGAT
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTGAGGTGAA GTGGTA
                                      _      TGTATTA
GAM370  IGF1R    3'  TTCTCTCAGTGAAGGTGGGG   6049     TT         TCT    T
                                T  CACTTTCACTG   GAGA
                                |  ||||||||||   ||||
                                G  GTGGAAGTGAC   CTCT
                                 GG         T__    TT
GAM370  IL11     3'  ATTTCAGGAGCAGGGGTGGGA  5324     TT     CA  G
                                T  CACTTT  CT TCTGAGAT
                                |  ||||||  || ||||||||
                                A  GTGGGG  GA GGACTTTA
                                 GG     AC  _
GAM370  IL13RA1  3'  TTAGGGGCAGTGGAGGTAGAAT 7782       TC           GAGAT
             G                      CATT  ACTTTCACTGTCT
                                ||||  ||||||||||||
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                                GTAA  TGGAGGTGACGGG
                                  GA          GATTG
GAM370  IL1F5    3'  ATTTCTGTGGGGGTGGGGTG  24377    TT   TT   TGTCT
                                CAT  CACT  CAC    GAGAT
                                |||  ||||  |||    |||||
                                GTG  GTGG  GTG    CTTTA
                                  GG   GG  T____
GAM370  IL1RN    3'  GATGGTGAAAGTAAGTG     5143       C
                                CATTT ACTTTCACTGTC
                                ||||| ||||||||||||
                                GTGAA TGAAAGTGGTAG
                                  _
GAM370  IL24     3'  TTGGGGTGGGGGTAAGGTG   22447      C   TT   GT TG
                                CATTT ACT  CACT  C  A
                                ||||| |||  ||||  |  |
                                GTGGA TGG  GTGG  G  T
                                   A   GG   __ GT
GAM370  IRS1     3'  ATCTTTTTTTTGGATGTGGGAT 18662    TT   T   CTGTCT
            G                    CAT  CAC TTCA     GAGAT
                                |||  ||| ||||     |||||
                                GTA  GTG AGGT     TTCTA
                                  GG   T   TTTTT_
GAM370  IRS2     3'  TCTCAATGGAAGTGAAAT    59723          CTGTC
                                ATTTCACTTTCA    TGAGA
                                ||||||||||||    |||||
                                TAAAGTGAAGGT    ACTCT
                                      A____
GAM370  JTB      3'  CTATCTCAGACAGTGAAAGTGA 21961
            AATG                   CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA
                                              TCC
GAM370  KCNA7    3'  TCTCAGAGCAGGGGAGTG    49061      TT A  _
                                CACT  C CTG TCTGAGA
                                ||||  | ||| |||||||
                                GTGA  G GAC AGACTCT
                                  GG _   G
GAM370  KCNK6    3'  ATGGAGGAGGTGAGGTG     16690           A
                                CATTTCACTTTC CTGT
                                |||||||||||| ||||
                                GTGGAGTGGAGG GGTA
                                      A
GAM370  KCNK6    3'  TTTCAGGCTGAGTGTGGTG   16699      TT   __
                                CACT  CACT  GTCTGAGA
                                ||||  ||||  ||||||||
                                GTGG  GTGA  CGGACTTT
                                  T_   GT
GAM370  LAMC1    3'  GTCTCAGGCCACAATGGGGTG  9677      TT  CTTTCACT
                                CAT  CA       GTCTGAGAT
                                |||  ||       |||||||||
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                                GTG  GT       CGGACTCTG
                                  GG  AACAC___
GAM370  MALT1    3'  ATTTTAGATGCCTGTGAAAT   22291        TTTCACT
                                ATTTCAC      GTCTGAGAT
                                |||||||      |||||||||
                                TAAAGTG      TAGATTTTA
                                   TCCG___
GAM370  MAPK14   3'  TCCTCCATGGTGGAAGGGGGTG 7161      TT A        CT   AT
                                CAT  C CTTTCACTGT  GAG
                                |||  | ||||||||||  |||
                                GTG  G GAAGGTGGTA  CTC
                                  GG _        C_   CTT
GAM370  MAPK14   3'  TCCTCCATGGTGGAAGGGGGTG 57335     TT A        CT   AT
                                CAT  C CTTTCACTGT  GAG
                                |||  | ||||||||||  |||
                                GTG  G GAAGGTGGTA  CTC
                                  GG _        C_   CTT
GAM370  MAPK14   3'  TCCTCCATGGTGGAAGGGGGTG 57346     TT A        CT   AT
                                CAT  C CTTTCACTGT  GAG
                                |||  | ||||||||||  |||
                                GTG  G GAAGGTGGTA  CTC
                                  GG _        C_   CTT
GAM370  MAPRE1   3'  ATTTTTTGGGGAAGTGAGGTG  24661           A  GTCT
                                CATTTCACTTTC CT    GAGAT
                                ||||||||||||  ||    |||||
                                GTGGAGTGAAGG GG    TTTTA
                                      _  TT__
GAM370  MBP      5'  TTTTGGAAGGTGGAGTG     89783       T    G  TG
                                CACTT CACT TC  AGA
                                |||||  |||| ||  |||
                                GTGAG GTGG AG  TTT
                                   _    A  GT
GAM370  MGAT5    5'  TGCCTCATGGTGGGAGTGAAA  10030        TT    TC    AT
                                TTTCACT  CACTG  TGAG
                                |||||||  |||||  ||||
                                AAAGTGA  GTGGT  ACTC
                                    GG    __    CGTT
GAM370  MGEA5    3'  GTTTCAGAAGTGTCAGGGTGGA 24218          __    G
              GTG                  ATTTCACTTT  CACT TCTGAGAT
                                ||||||||||  ||||  ||||||||
                                TGAGGTGGGA  GTGA AGACTTTG
                                     CT   _
GAM370  MMP19    3'  TCAATGGTGGAGGGAGATG   42975       A        C
                                CATTTC CTTTCACTGT TGA
                                ||||||  |||||||||| |||
                                GTAGAG GGAGGTGGTA ACT
                                   _        _
GAM370  MMP19    3'  TCAATGGTGGAGGGAGATG   42981       A        C
                                CATTTC CTTTCACTGT TGA
                                ||||||  |||||||||| |||
```

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                                GTAGAG GGAGGTGGTA ACT
                                  _      _
GAM370  MMP19   3'  TCAATGGTGGAGGGAGATG   42985      A       C
                                CATTTC CTTTCACTGT TGA
                                |||||| |||||||||| |||
                                GTAGAG GGAGGTGGTA ACT
                                  _      _
GAM370  MMP19   3'  TCAATGGTGGAGGGAGATG   10086      A       C
                                CATTTC CTTTCACTGT TGA
                                |||||| |||||||||| |||
                                GTAGAG GGAGGTGGTA ACT
                                  _      _
GAM370  MOG     3'  TCTTGGCAGGGGTGGAG     10107       TCA   T TG
                                TTTCACTT   CTG C  AGA
                                ||||||||   ||| |  |||
                                GAGGTGGG   GAC G  TCT
                                   ___   _ GT
GAM370  MPP4    5'  TATCGGGAGCAGTGAGGTG   52347      T    __   GAT
                                CACTT CACTGT  CTGA
                                ||||| ||||||  ||||
                                GTGGA GTGACG  GGCT
                                  _     AG    ATT
GAM370  MS4A1   3'  ATTTTGGGGAGACAAAGGGAAA 3748       A   CA  G  TG
          TG                    CATTTC CTTT  CT TC  AGAT
                                |||||| ||||  || ||  ||||
                                GTAAAG GAAA  GA GG  TTTA
                                   G    CA  G  GT
GAM370  MTNR1A  3'  ACAATGAAAGTGGGGTG     19887     TT      C
                                CAT  CACTTTCA TGT
                                |||  |||||||| |||
                                GTG  GTGAAAGT ACA
                                  GG       A
GAM370  MYOZ1   5'  ATCTCAGGCTCTAGGTGCAATG 41149     T    TCACT
                                CATT CACTT    GTCTGAGAT
                                |||| |||||    |||||||||
                                GTAA GTGGA    CGGACTCTA
                                  C    TCT__
GAM370  NAV2    3'  TTTCATTAGGGGTGGGGTG   60162     TT    TCA   TC
                                CAT  CACTT   CTG  TGAGA
                                |||  |||||   |||  |||||
                                GTG  GTGGG   GAT  ACTTT
                                  GG    ___   T_
GAM370  NDST2   3'  ATCTTGGGAGGTGGGGAGGAAT 13296       AC TT   GT TG
          G                     CATTTC  T  CACT  C  AGAT
                                ||||||  |  ||||  |  ||||
                                GTAAGG  G  GTGG  G  TCTA
                                   A_ GG    AG GT
GAM370  NEBL    3'  TTTTTGTGGTAGGGAAGTGGGA 21126    TT      A  GT _    T
          TG                    CAT  CACTTTC CT  C TGAGA
                                |||  ||||||| ||  | |||||
```

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                                GTA  GTGAAGG GA  G GTTTT
                                  GG      _ TG T    TA
GAM370  NEU1     3'  GTCTTGGGCAGGTCTAGTGAGC 4742     T     TTCA    TG
            TG                   CA TTCACT   CTGTC  AGAT
                                || ||||||   |||||  ||||
                                GT GAGTGA   GACGG  TCTG
                                 C     TCTG    GT
GAM370  NEUROD2  3'  ATTTTGGCGGGAGGGGAAGTG  20478       A    A   T TG
                                CATTTC CTTTC CTG C  AGAT
                                |||||| ||||| ||| |  ||||
                                GTGAAG GGGAG GGC G  TTTA
                                   _    _  _ GT
GAM370  NFE2L1   3'  TGTCTGCCCCAGACAAGTGGGA 12177     TT   _    ____
            GTGAAATG                ACT  CACT GTCTG   AGAT   G
                                ||| |||| |||||   ||||  |
                                TGA  GTGA CAGAC   TCTG   T
                                  GG   A    CCCG
GAM370  NFRKB    5'  GTCTTAAGGGAAGTGAAAGAGG 20497      A      G_  _
            AGTG                  ATTTC CTTTCACT  TCT GAGAT
                                ||||| ||||||||  ||| |||||
                                TGAGG GAAAGTGA  GGA TTCTG
                                   A       AG   A
GAM370  NGB      3'  GTTTTGGTGGCAGAGGTGGGAT 41188     TT     CA   T TG
            G                    CAT  CACTTT  CTG C  AGAT
                                |||  ||||||  ||| |  ||||
                                GTA  GTGGAG  GGT G  TTTG
                                  GG     AC   _ GT
GAM370  NLGN1    3'  CCTTTTGGTAAGGTGAAGTG   30024          C   GTCT   AT
                                CATTTCACTTT ACT    GAG
                                |||||||||| |||    |||
                                GTGAAGTGGAA TGG    TTC
                                      _  TT__   CT
GAM370  NPC2     3'  GTCTTAGGTGGTTTCATTAAAT 21223      CACTTTC  TG
            G                    CATTT      AC  TCTGAGAT
                                |||||      ||  ||||||||
                                GTAAA      TG  GGATTCTG
                                   TTACTT_  GT
GAM370  OCRL     3'  GTTTCTTGGTGGGGGTGGGG   7830    TT    TT    GTCT
                                T  CACT  CACT    GAGAT
                                |  ||||  ||||    |||||
                                G  GTGG  GTGG    CTTTG
                                 GG    GG    TT__
GAM370  OCRL     3'  GTTTCTTGGTGGGGGTGGGG   4264    TT    TT    GTCT
                                T  CACT  CACT    GAGAT
                                |  ||||  ||||    |||||
                                G  GTGG  GTGG    CTTTG
                                 GG    GG    TT__
GAM370  PER2     3'  TTTTTGATGGAGGTGAAAT    43051          CTG  T
                                ATTTCACTTTCA   TC GAGA
                                ||||||||||||   || ||||
```

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                                TAAAGTGGAGGT   AG TTTT
                                       ____  T
GAM370  PGAM1    3'  TTTCATGGCAGTGAAA      76276          _
                                TTTCACTGTC TGAGA
                                |||||||||| |||||
                                AAAGTGACGG ACTTT
                                       T
GAM370  PIGN     5'  GTCTCAGTCCTGTGCAAAGTGA 24672          _  TGT_
             GATG                   ATTTCACTTT CAC    CTGAGAT
                                |||||||||| |||   |||||||
                                TAGAGTGAAA GTG    GACTCTG
                                      C   TCCT
GAM370  PKP4     3'  GAAATGTGAAAGTGAAGTG    13266            TG_
                                CATTTCACTTTCAC   TC
                                ||||||||||||||   ||
                                GTGAAGTGAAAGTG   AG
                                         TAA
GAM370  PRDM2    3'  GTCTCGGAGAAACGGGTGAGCT 24250    T      TCACTG
             G                   CA TTCACTT     TCTGAGAT
                                || |||||||     |||||||||
                                GT GAGTGGG     AGGCTCTG
                                 C      CAAAG_
GAM370  PSEN1    5'  ATAGTGGAGGCTGGGATG    23621     TT  _
                                CAT  CA CTTTCACTGT
                                |||  || ||||||||||
                                GTA  GT GGAGGTGATA
                                  GG  C
GAM370  RALB     3'  GTTTTGGAGGAGGGAGTGGAGT 11245         TT A  G  TG
                                ATTTCACT  C CT TC  AGAT
                                ||||||||  | || ||  ||||
                                TGAGGTGA  G GG AG  TTTG
                                     GG A  _  GT
GAM370  RAMP3    3'  CGGTGAGATGGAGTG       19589         C
                                CATTTCA TTTCACTG
                                ||||||| ||||||||
                                GTGAGGT AGAGTGGC
                                       _
GAM370  RANBP7   3'  ATTTTGGGGGTGGGGGGGA   21113     A  TT   G  TG
                                TTC CT  CACT TC  AGAT
                                ||| ||  |||| ||  ||||
                                AGG GG  GTGG GG  TTTA
                                  _  GG   _  GT
GAM370  RGS19IP1 3'  GATGGTGAGGGGAGGTG     62509       A
                                CATTTC CTTTCACTGTC
                                |||||| ||||||||||
                                GTGGAG GGGAGTGGTAG
                                       _
GAM370  RNASE1   3'  ATTTTGGGGGTGAAGAGTGGGT 63875    T      _   G  TG
             TG                    CA TTCACTTT CACT TC  AGAT
                                || |||||||| |||| ||  ||||
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                                GT GGGTGAGA GTGG GG  TTTA
                                 T       A   _ GT
GAM370  RNGTT    3' ATTTTGGACATTGTGAAGGAAA 13729       A  T  __   TG
           TG                    CATTTC CTT CAC  TGTC  AGAT
                                 |||||| ||| |||  ||||  ||||
                                 GTAAAG GAA GTG  ACAG  TTTA
                                    _  _  TT   GT
GAM370  RXRB     3' CAGTGGTGGAGGTGGG      41758           T
                                 TTCACTTTCACTG CTG
                                 |||||||||||| |||
                                 GGGTGGAGGTGGT GAC
                                          _
GAM370  SEDL     3' ATTCTGCAGTTGGGAGTGAAAT 27322         TT  _   CT   AT
           G                     CATTTCACT  CA CTGT  GAG
                                 |||||||||  || ||||  |||
                                 GTAAAGTGA  GT GACG  CTT
                                       GG  T    T_  A
GAM370  SH3BP4   3' CAGTAGAGTGAGGTG      27232          C
                                 CATTTCACTTT ACTG
                                 |||||||||| ||||
                                 GTGGAGTGAGA TGAC
                                          _
GAM370  SIGLEC6  3' ATTTTAAGACTGAAAGTGAAAT 59926           CT   _
                                 ATTTCACTTTCA  GTCT GAGAT
                                 |||||||||||  |||| |||||
                                 TAAAGTGAAAGT  CAGA TTTTA
                                       __   A
GAM370  SLC17A2  5' TTTAATGGTGAAGGTAAGTG   19546      C         C
                                 CATTT ACTTTCACTGT TGAG
                                 ||||| |||||||||| ||||
                                 GTGAA TGGAAGTGGTA ATTT
                                    _         _
GAM370  SLC19A1  5' GTCTCGGGGCCCTGGGGTGAG  11758        T  CT   _
                                 TTCACTT CA  GTCT GAGAT
                                 ||||||| ||  |||| |||||
                                 GAGTGGG GT  CGGG CTCTG
                                    _ CC    G
GAM370  SLC38A2  3' TCTCGGGTTAAGGGAAGTG   38593        A  G__
                                 CACTTTC CT   TCTGAGA
                                 ||||||| ||   |||||||
                                 GTGAAGG GA   GGGCTCT
                                    _ ATT
GAM370  SLC6A4   3' TTTTGGACGTGTGAGGATG   6452     CT    _   TG
                                 CA  TTCAC TGTC  AGA
                                 ||  ||||| ||||  |||
                                 GT  GAGTG GCAG  TTT
                                  AG    T   GT
GAM370  SLC7A8   3' GTCTTGGGGCAGGGTGAAA   24282        TTCA   _ TG
                                 TTTCACT    CTGT C  AGAT
                                 |||||||    |||| |  ||||
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                                AAAGTGG   GACG G  TCTG
                                    ____   G GT
GAM370  SMARCB1  3'  TCGGGTGGGGGTGGAGTG   65586        TT   TGT
                                CATTTCACT  CAC   CTGA
                                |||||||||  |||   ||||
                                GTGAGGTGG  GTG   GGCT
                                     GG   ___
GAM370  SNCA     3'  TTAATTATTGAAAGTGGGGTG  4433     TT      C  TC
                                CAT  CACTTTCA TG  TGA
                                |||  |||||||| ||  |||
                                GTG  GTGAAAGT AT  ATT
                                  GG       T  TA
GAM370  SRRM2    3'  TTTGGGGTGGGAGGGAATG   32918      A  TT   GT TG
                                CATTTC CT  CACT  C  AG
                                ||||||  ||  ||||  |  ||
                                GTAAGG GA  GTGG  G  TT
                                   _  GG   __ GT
GAM370  SSPN     3'  GTCTTAGAAGAAAGTGGAAT   17445         ACTG
                                ATTTCACTTTC   TCTGAGAT
                                ||||||||||   ||||||||
                                TAAGGTGAAAG   AGATTCTG
                                      A___
GAM370  STAR     3'  ATCTCCATCTGGTGACAGTGGG 4443     TT   T   GTCT_
           ATG                    CAT  CACT TCACT    GAGAT
                                |||  |||| |||||    |||||
                                GTA  GTGA AGTGG    CTCTA
                                  GG   C    TCTAC
GAM370  T        3'  GTCTCAGGTTAAGAAGGAAATG 12077       A   CACTG
                                CATTTC CTTT    TCTGAGAT
                                ||||||  ||||    ||||||||
                                GTAAAG GAAG    GGACTCTG
                                   _   AATT_
GAM370  TAF1C    3'  TGGTGAGGGTGGAGTG      19060
                                CATTTCACTTTCACTG
                                ||||||||||||||||
                                GTGAGGTGGGAGTGGT

GAM370  TIMP3    3'  GTTTTAGTGTCAAAAGTGAGAT 4517          CACTGT
           G                     CATTTCACTTT     CTGAGAT
                                ||||||||||     |||||||
                                GTAGAGTGAAA     GATTTTG
                                      ACTGT_
GAM370  TMOD4    5'  TACCACACAGTGGGAGGGGGTG 25331     TT A  TT     C  AGAT
                                CAT  C CT  CACTGT TG
                                |||  | ||  |||||| ||
                                GTG  G GA  GTGACA AC
                                  GG _  GG     C  CATG
GAM370  TNFRSF4  3'  ATCTTGGCCAGGGTGGAGTG   12451        TTCA   T TG
                                CATTTCACT    CTG C  AGAT
                                |||||||||    ||| |  ||||
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                                GTGAGGTGG   GAC G  TCTA
                                     ____   C GT
GAM370  TRH     3'  CAGCCAGTGAGGGTGGGGTG  23051    TT        T
                                CAT  CACTTTCACTG CTG
                                |||  ||||||||||| |||
                                GTG  GTGGGAGTGAC GAC
                                  GG         C
GAM370  TRHDE   3'  TTTTGGGCAATGTGAGAG    25393       __   TG
                                CTTTCAC  TGTC  AGA
                                |||||||  ||||  |||
                                GAGAGTG  ACGG  TTT
                                    TA   GT
GAM370  TRIM9   3'  GTTTCAAATGGGTGGTGGGGTG 53761    TT   TTCA   C
                                CAT  CACT   CTGT TGAGAT
                                |||  ||||   |||| ||||||
                                GTG  GTGG   GGTA ACTTTG
                                  GG   TG__   A
GAM370  TSG     3'  ATTTCCTACTGTGAGTGGAGTG 40231       TT   T  CT
                                CATTTCAC  TCAC GT  GAGAT
                                ||||||||  |||| ||  |||||
                                GTGAGGTG  AGTG CA  CTTTA
                                     __   T  TC
GAM370  TSLP    5'  TTTAGTGTGAAACTGGGGTG  52310    TT  C    TGT
                                CAT  CA TTTCAC   CTGAG
                                |||  || ||||||   |||||
                                GTG  GT AAAGTG   GATTT
                                  GG  C    T__
GAM370  VDAC1   3'  TTTGGGGTGGAGAAGGTGGA  12583       A TG   G   T
                                TTCACTTTC C  TCT AGA
                                |||||||||  |  ||| |||
                                AGGTGGAAG G  GGG TTT
                                     A GT   G   T
GAM370  VDR     3'  TCTTTGTGAGAGTGAGCTG   4571    T       TGTCT
                                CA TTCACTTTCAC    GAGA
                                || ||||||||||    ||||
                                GT GAGTGAGAGTG    TTCT
                                 C         T____
GAM370  WNT10B  3'  GGGTGGTGGGGGTCAGGTG   12675     C   TT   TG
                                CATTT ACT  CAC  TCT
                                |||||  |||  |||  |||
                                GTGGA TGG  GTG  GGG
                                   C   GG   GT
GAM370  ZNF239  5'  GTCAGGATAATGGTGGGAATGG 19042   TT  C TT    ____   GAT
          GGTG                    CA T  CACTGT   CTGA
                                 || |  ||||||   ||||
                                 GT A  GTGGTA   GACT
                                GG  A GG    ATAG   G
GAM370  AKAP6   5'  GTTTTGGAAAGAAGTGAGGT  14996       CACTG  TG
                                ATTTCACTTT    TC  AGAT
                                ||||||||||    ||  ||||
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                                TGGAGTGAAG    AG  TTTG
                                      AA___  GT
GAM370  APXL2    3'  TAGGTGGAGAGGGTGGGGTG  75196    TT     A TG
                                CAT  CACTTTC C  TCTG
                                |||  ||||||| |  ||||
                                GTG  GTGGGAG G  GGAT
                                  GG      A GT
GAM370  ARFGAP3  3'  ATCTCAGGCGGCAGTGAAGT  27385       TTCA
                                ATTTCACT   CTGTCTGAGAT
                                ||||||||   ||||||||||
                                TGAAGTGA   GGCGGACTCTA
                                     C___
GAM370  ARHGEF9  3'  TTTTAGGTACTGTGAAGG   30827       __ GT
                                CTTTCAC  T  CTGAGA
                                |||||||  |  ||||||
                                GGAAGTG  A  GATTTT
                                    TC TG
GAM370  ARHGEF9  3'  TTTTGGGGAAGTGAAAT    30829         ACTGT TG
                                ATTTCACTTTC    C  AGA
                                ||||||||||    |  |||
                                TAAAGTGAAGG    G  TTT
                                      _____ GT
GAM370  BCL2L1   3'  GTCTGTGTGAAGGTGAAA   56807         TGTCTG
                                TTTCACTTTCAC    AGAT
                                ||||||||||    ||||
                                AAAGTGGAAGTG    TCTG
                                      TG____
GAM370  C19orf7  3'  AGACAGTGAGAGTGAAA    61124
                                TTTCACTTTCACTGTCT
                                |||||||||||||||||
                                AAAGTGAGAGTGACAGA

GAM370  C1orf17  3'  TTTCAGAGTGGGGAAGTG   68219       A  _
                                CACTTTC CTG TCTGAGA
                                ||||||| ||| |||||||
                                GTGAAGG GGT AGACTTT
                                    _  G
GAM370  C1orf34  3'  GCAGTGAGGGTGAGCTG    60673   T
                                CA TTCACTTTCACTGT
                                || ||||||||||||||
                                GT GAGTGGGAGTGACG
                                 C
GAM370  C20orf151 3'  TCTGGCAGTGAGGGTGGAG   88703            T
                                TTTCACTTTCACTGTC GA
                                |||||||||||||||| ||
                                GAGGTGGGAGTGACGG CT
                                          T
GAM370  C20orf21  3'  TCTCAGGACAAGTGGAAG    35117       _  _
                                CTTTCACT GTC TGAGA
                                |||||||| ||| |||||
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                                GAAGGTGA CAG ACTCT
                                    A   G
GAM370  C20orf29  3'  GTCTCAGACTCCCCTGAGGGTG 37129          CT___
            GAG                   TTTCACTTTCA    GTCTGAGAT
                                  ||||||||||    |||||||||
                                  GAGGTGGGAGT    CAGACTCTG
                                       CCCCT
GAM370  C20orf60  3'  TAGGGGTGGGGGTGGGATG   53738    TT   TT   G
                                  CAT  CACT  CACT TCTG
                                  |||  ||||  |||| ||||
                                  GTA  GTGG  GTGG GGAT
                                    GG   GG   _
GAM370  C22orf5   5'  GACAGTGAGGGGGGATG    24342    TT A
                                  CAT  C CTTTCACTGTC
                                  |||  | ||||||||||
                                  GTA  G GGGAGTGACAG
                                    GG _
GAM370  C8orf2    3'  ATAGTGAAAGTAAGATG    23157     C
                                  CATTT ACTTTCACTGT
                                  ||||| ||||||||||
                                  GTAGA TGAAAGTGATA
                                     A
GAM370  CCR5      3'  ATTTCAGACTGAATGGGGGTGG 5147   TT   TT  CT__
            GG                    T  CACT  CA   GTCTGAGAT
                                  |  ||||  ||   |||||||||
                                  G  GTGG  GT   CAGACTTTA
                                   GG   GG  AAGT
GAM370  CCR6      3'  TCTCTTCAGGGTGGGGTG   15173    TT   TTCA   TCT
                                  CAT  CACT   CTG   GAGA
                                  |||  ||||   |||   ||||
                                  GTG  GTGG   GAC   CTCT
                                    GG   ____   TT_
GAM370  CCR6      3'  TCTCTTCAGGGTGGGGTG   48589    TT   TTCA   TCT
                                  CAT  CACT   CTG   GAGA
                                  |||  ||||   |||   ||||
                                  GTG  GTGG   GAC   CTCT
                                    GG   ____   TT_
GAM370  CECR7     5'  ATAGTGGGAATGAAATG    79615      C TT
                                  CATTTCA T  CACTGT
                                  |||||||  |  ||||||
                                  GTAAAGT A  GTGATA
                                      A GG
GAM370  CENTA2    3'  TCTCAGATGGCTGAAATGT   37269    _    _
                                  AC TTTCA CTGTCTGAGA
                                  ||  ||||| ||||||||||
                                  TG AAAGT GGTAGACTCT
                                   T    C
GAM370  CEP3      3'  ATCTTGGCAAAAAAAGGAAGTG 21247      A   CAC  T TG
                                  CATTTC CTTT   TG C  AGAT
                                  ||||||  ||||   ||  |  ||||
```

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                                GTGAAG GAAA   AC G  TCTA
                                   _    AAA  _ GT
GAM370  CHSY1    3'  TTGGGGACAAAAGTGAAATG  29905          CAC    GA  T
                                CATTTCACTTT  TGTCT  GA
                                ||||||||||  |||||  ||
                                GTAAAGTGAAA  ACAGG  TT
                                      ___    GG  T
GAM370  CNNM2    3'  GGACAGTGAGGGAGGAATG   34461       A
                                CATTTC CTTTCACTGTCT
                                |||||| ||||||||||||
                                GTAAGG GGGAGTGACAGG
                                   A
GAM370  COLEC10  3'  TTTCAGACCATGTGGAATG   21230        TTTCACT
                                CATTTCAC      GTCTGAGA
                                ||||||||      ||||||||
                                GTAAGGTG      CAGACTTT
                                     TAC____
GAM370  CRR9     3'  ATTTCAGGTGGTTTTCTAAGTG 47878      TC___  TG
                                CACTT    AC  TCTGAGAT
                                |||||    ||  ||||||||
                                GTGAA    TG  GGACTTTA
                                   TCTTT  GT
GAM370  CYYR1    3'  ATTTTAGGTGGGTGTGAAGTG  53670        TTTCA TG
                                CATTTCAC    C  TCTGAGAT
                                ||||||||    |  ||||||||
                                GTGAAGTG    G  GGATTTTA
                                     TG___ GT
GAM370  DAPK3    3'  GTCGTGGGACGGGGAGGGTGGG 7211     TT      A     GA_
           ATG                    CAT  CACTTTC CTGTCT   GAT
                                |||  ||||||| ||||||   |||
                                GTA  GTGGGAG GGCAGG   CTG
                                  GG      G     GTG
GAM370  DDX8     3'  GGATGGGAAGGTGGAGTG    17053          A
                                CATTTCACTTTC CTGTCT
                                |||||||||||| ||||||
                                GTGAGGTGGAAG GGTAGG
                                                _
GAM370  DKFZp434B217 3'  GGGTTTGGGCGGGAGTGGGCTG 70701    T      TCA    TG  AT
                                CA TTCACTT   CTGTC  AG
                                || |||||||   |||||  ||
                                GT GGGTGAG   GGCGG  TT
                                 C      ___     GT  GGGT
GAM370  DKFZP434K028 3'  CTTACAGTGGAGGTAAAGTG   93231       C         CT
                                CATTT ACTTTCACTGT  GAG
                                ||||| ||||||||||  |||
                                GTGAA TGGAGGTGACA  TTC
                                   A         __
GAM370  DKFZp434O0320 3'  GGTGGCAGGTGGAGTG      83696          _
                                CATTTCACTT TCACT
                                |||||||||| |||||
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                                GTGAGGTGGA GGTGG
                                      C
GAM370  DKFZP434O047 5'  ATTTTGGACAAGGTGCTGAAGT 31503       CTTT   __   TG
           G                     CATTTCA   CACT  GTC  AGAT
                                 |||||||   ||||  |||  ||||
                                 GTGAAGT   GTGG  CAG  TTTA
                                     C___   AA   GT
GAM370  DKFZp547F072 5'  TCCATGGGCGGGGGTGGGGTG  50094    TT   TT A  GTC  A  T
                                 CAT  CACT  C CT   TG GA
                                 |||  ||||  | ||   || ||
                                 GTG  GTGG  G GG   AC CT
                                   GG   GG C  GT_  _  T
GAM370  DKFZP564C103 3'  TCTTAGATAAGTAAGGTG    31612       C   _
                                 CACTTT ACT GTCTGAGA
                                 ||||||  ||| ||||||||
                                 GTGGAA TGA TAGATTCT
                                    _   A
GAM370  DKFZP564I052 3'  GTTTTAGGTGGTGATCTTAAAT 66718      CACTT    TG
           G                     CATTT    TCAC  TCTGAGAT
                                 |||||    ||||  ||||||||
                                 GTAAA    AGTG  GGATTTTG
                                    TTCT_   GT
GAM370  DKFZP564I052 3'  GTTTTGAGAGGGGAGTAGAAGT 66719       _   TT A  G  T
           G                     CATTTC ACT  C CT TC GAGAT
                                 ||||||  |||  | || || |||||
                                 GTGAAG TGA  G GA AG TTTTG
                                    A   GG _  G  _
GAM370  DKFZP566G1424 3'  ATTTTGGACTCAGTGAAAGTG  84773          __   TG
                                 CACTTTCACT  GTC  AGAT
                                 ||||||||||  |||  ||||
                                 GTGAAAGTGA  CAG  TTTA
                                       CT   GT
GAM370  DKFZp761N1114 3'  GTTTCAGAAAGCTGGGTGGTGG 79022      _   _  G
                                 TCACT TTCA CT TCTGAGAT
                                 |||||  |||| ||  ||||||||
                                 GGTGG GGGT GA AGACTTTG
                                    T   C  A
GAM370  DKFZp762P2111 3'  GTCTCAGGTGTTCTGGGGATG  86361    TT ACTTT   TGT
                                 CAT  C    CAC   CTGAGAT
                                 |||  |    |||   |||||||
                                 GTA  G    GTG   GACTCTG
                                   GG GTCTT   ___
GAM370  DKFZp762P2111 3'  TGAGAAACAGTGGAGTGGAGTG 86365          T     CTGAGAT
                                 CATTTCACTT CACTGT
                                 ||||||||||  ||||||
                                 GTGAGGTGAG GTGACA
                                       _     AAGAGTA
GAM370  DMRTA2   3'  GTTTTGTTTAGGAGGGTGGG   60660         A   TC
                                 TTCACTTTC CTG  TGAGAT
                                 |||||||||  |||  ||||||
```

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                                GGGTGGGAG GAT  GTTTTG
                                      _  TT
GAM370  DRIL2    3'  ATCGTGGGGGCGGGGAGGTGGA 21322          A     GA__
            GTG                    ATTTCACTTTC CTGTCT    GAT
                                |||||||||| ||||||   |||
                                TGAGGTGGAGG GGCGGG    CTA
                                      _    GGTG
GAM370  EAT2     3'  TCAGGTGAAGGTGAGG      79281           TGT
                                TTTCACTTTCAC   CTGA
                                ||||||||||||  ||||
                                GGAGTGGAAGTG   GACT
                                      ____
GAM370  EPS8R1   5'  TAGAACATGAAGGTGGGATG   34803     TT      C  _
                                CAT  CACTTTCA TGT CTG
                                |||  |||||||| ||| |||
                                GTA  GTGGAAGT ACA GAT
                                  GG       _  A
GAM370  FBXL3B   5'  ATCTTCTGTATGTAGGAGGTGG 24070          _  TGTCT_
            AATG                   ATTTCACTTTC AC     GAGAT
                                |||||||||| ||     |||||
                                TAAGGTGGAGG TG     TTCTA
                                      A  TATGTC
GAM370  FHX      3'  TCAAGGGTGAAAGTGATGATG  37307      _        GTC
                                CATT TCACTTTCACT   TGA
                                |||| ||||||||||   |||
                                GTAG AGTGAAAGTGG   ACT
                                   T         GA_
GAM370  FKSG42   3'  GTCTCAGGGTGGGAAGTGGGA  49335   TT      _  GT
                                T  CACTTTC ACT  CTGAGAT
                                |  ||||||| |||  |||||||
                                A  GTGAAGG TGG  GACTCTG
                                 GG      G  __
GAM370  FLJ00024 3'  GTCTTGGGAGAAGGGTGAGG   63765         CA  G  TG
                                TTTCACTTT  CT TC  AGAT
                                |||||||||  || ||  ||||
                                GGAGTGGGA  GA GG  TCTG
                                      A_  _  GT
GAM370  FLJ10052 3'  ATCTCAGGCTCCACAGTGAGG  35771        TTCACT
                                TTTCACT     GTCTGAGAT
                                |||||||     |||||||||
                                GGAGTGA     CGGACTCTA
                                    CACCT_
GAM370  FLJ11506 3'  TGGGTGGGGAAGTGAAATG   45115           A TG
                                CATTTCACTTTC C  TCTG
                                |||||||||||| |  ||||
                                GTAAAGTGAAGG G  GGGT
                                      _ GT
GAM370  FLJ12056 3'  TTTGGGGGCAGGGAGGTTGGGT 46258      TC     A     GA  T
            G                    CATT  ACTTTC CTGTCT  GA
                                ||||  |||||| ||||||  ||
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                                GTGG  TGGAGG GACGGG  TT
                                  GT     _     GG  TT
GAM370  FLJ12121  3' GTTTTGGACAGTCATTTGGAAT 46458       CTTTC     TG
                                ATTTCA    ACTGTC  AGAT
                                ||||||    ||||||  ||||
                                TAAGGT    TGACAG  TTTG
                                   TTAC_     GT
GAM370  FLJ12547  3' ATCTCAGCCAGAGAGAGTGAAC 46489    T       A   T
           TG                    CA TTCACTTTC CTG CTGAGAT
                                 || |||||||| ||| |||||||
                                 GT AAGTGAGAG GAC GACTCTA
                                  C        A   C
GAM370  FLJ12581  3' TCTCATGGAGGGTGGAGT    45881          ACTGTC
                                ATTTCACTTTC     TGAGA
                                ||||||||||      |||||
                                TGAGGTGGGAG     ACTCT
                                      GT____
GAM370  FLJ12787  3' TTTCAGGTCAGAGGAA      49756      A  _
                                TTTC CTG TCTGAGA
                                |||| ||| |||||||
                                AAGG GAC GGACTTT
                                  A   T
GAM370  FLJ12891  3' ACTGTGGAGGTGGAGTG     46335            T
                                CATTTCACTTTCAC GT
                                |||||||||||||| ||
                                GTGAGGTGGAGGTG CA
                                       T
GAM370  FLJ13072  5' GACAGTGAGAGTGAAA      89814
                                TTTCACTTTCACTGTC
                                ||||||||||||||||
                                AAAGTGAGAGTGACAG

GAM370  FLJ13852  3' TGGGCAGTGGTAGGTGGGGTG  43579     TT    _
                                CAT  CACTT TCACTGTCTG
                                |||  ||||| ||||||||||
                                GTG  GTGGA GGTGACGGGT
                                  GG    T
GAM370  FLJ14107  3' GCAGGGGAGGTGAAATG     46693           A
                                CATTTCACTTTC CTGT
                                |||||||||||| ||||
                                GTAAAGTGGAGG GACG
                                       G
GAM370  FLJ14346  3' GGCAGGGAAGTGAGATG     46714           A
                                CATTTCACTTTC CTGTC
                                |||||||||||| |||||
                                GTAGAGTGAAGG GACGG
                                          _
GAM370  FLJ14502  3' GTTTTGGGCTTAATAAATGGGG 62717     TT  C  TCACT   TG
           TG                    CAT  CA TT    GTC  AGAT
                                 |||  || ||    |||  ||||
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                                GTG  GT AA    CGG  TTTG
                                  GG  A  TAATT   GT
GAM370   FLJ14641  5' CGGGGAAGTGGAATG      51483          A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAGGTGAAGG GGC
                                          _
GAM370   FLJ14743  3' GCTCTGGGGTGGGGGTGGGGTG 68064     TT   TT   G  T  AT
                                CAT  CACT  CACT TC GAG
                                |||  ||||  |||| || |||
                                GTG  GTGG  GTGG GG CTC
                                  GG   GG   _  T  GT
GAM370   FLJ20034  3' TTTGTACGTGAGGGTGGA    34392          T  CT
                                TTCACTTTCAC GT  GAG
                                |||||||||| ||  |||
                                AGGTGGGAGTG CA  TTT
                                       _ TG
GAM370   FLJ20043  3' GTTTTGGGAAAGGAGTGGGAT  34406    TT    CACTG  TG
                                AT  CACTTT    TC  AGAT
                                ||  ||||||    ||  ||||
                                TA  GTGAGG    GG  TTTG
                                 GG     AAA__  GT
GAM370   FLJ20306  3' GAAGGTGGAGGTGGAA      34916          G
                                TTTCACTTTCACT TC
                                |||||||||||| ||
                                AAGGTGGAGGTGG AG
                                         A
GAM370   FLJ20340  3' TTGGAGTGGAGTGGGGTG    34980    TT    T  TG  TG
                                CAT  CACTT CAC  TC  A
                                |||  ||||| |||  ||  |
                                GTG  GTGAG GTG  AG  T
                                  GG    _  __  GT
GAM370   FLJ20400  3' TTCTTGACTGAAGGTGAGATG  66514          CT  T   T
                                CATTTCACTTTCA  GTC GAGA
                                ||||||||||||  ||| ||||
                                GTAGAGTGGAAGT  CAG TTCT
                                       __  _   TT
GAM370   FLJ20729  3' GTCTTGGAGTGCAAGTGGTATG 35649     T    T  TG  TG
                                CAT TCACTT CAC  TC  AGAT
                                ||| |||||| |||  ||  ||||
                                GTA GGTGAA GTG  AG  TCTG
                                  T    C  __  GT
GAM370   FLJ21125  3' GTTTGGATGCAGGAAGGTGGGA 44892     TT     A   __ TG  AT
           TG                   CAT  CACTTTC CTGT  C  AG
                                |||  ||||||| ||||  |  ||
                                GTA  GTGGAAG GACG  G  TT
                                  GG     _   TA GT  G
GAM370   FLJ21162  3' TCTTGGGCTGGGTGCAGTG   45896     TT   __  TG
                                CACT  CACT  GTC  AGA
                                ||||  ||||  |||  |||
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                                GTGA  GTGG  CGG  TCT
                                  C_   GT   GT
GAM370  FLJ21324  5'  ATCTGCAGGTGGAAGGAGGTG  91189      A     TGT  _
                                CATTTC CTTTCAC   CTG AGAT
                                |||||| |||||||   ||| ||||
                                GTGGAG GAAGGTG   GAC TCTA
                                   _     ___  G
GAM370  FLJ21736  3'  TTTCAGATGGAAGTGAGA    46234          CTG
                                TTTCACTTTCA   TCTGAGA
                                ||||||||||   |||||||
                                AGAGTGAAGGT   AGACTTT
                                      ___
GAM370  FLJ22378  3'  GTCTCGGGTCCAGGGAGTGGAG 46905        TT ACTG
                                TTTCACT  C    TCTGAGAT
                                |||||||  |   ||||||||
                                GAGGTGA  G   GGGCTCTG
                                    GG ACCT
GAM370  FLJ22659  5'  GTGGTGAAGGTTAAATG     46261      C       TG
                                CATTT ACTTTCAC  T
                                ||||| ||||||||  |
                                GTAAA TGGAAGTG  G
                                   T       GT
GAM370  FLJ23059  3'  ATCTCAGAACAGAAGGGTGGGA 49933   TT     CA   _
                                T  CACTTT  CTGT CTGAGAT
                                |  ||||||  |||| |||||||
                                A  GTGGGA  GACA GACTCTA
                                 GG     A_   A
GAM370  FLJ23091  3'  ACCTCATGTGGGGGTGGGGTG  46124    TT   TT   TGTC   AT
                                CAT  CACT  CAC   TGAG
                                |||  ||||  |||   ||||
                                GTG  GTGG  GTG   ACTC
                                  GG   GG  T___   CAA
GAM370  FLJ23185  3'  TTTCAGGCAGGTGGAG     46837     CA
                                CTTT  CTGTCTGAGA
                                ||||  ||||||||||
                                GAGG  GACGGACTTT
                                  TG
GAM370  FLJ23309  3'  ATCTTGGGTGATGGAGGAAATG 46061       A  T  C GT TG
                                CATTTC CTT CA T  C  AGAT
                                |||||| ||| || |  |  ||||
                                GTAAAG GAG GT G  G  TCTA
                                   _  _  A TG GT
GAM370  FLJ23476  3'  GTCTCAGGTGGCTGCGTGTGGT 44962    TT   TTT  _ TG
          G                    CAT  CAC   CA C  TCTGAGAT
                               |||  |||   || |  ||||||||
                               GTG  GTG   GT G  GGACTCTG
                                 GT   C__  C GT
GAM370  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
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                                GTAAAGT  AGTGACAGACTCTA
                                   C__
GAM370  FLJ23556 3' GTTTTAATAAGGGAGGTGGAA 45956        A  GTC
                                TTTCACTTTC CT  TGAGAT
                                |||||||||| ||  ||||||
                                AAGGTGGAGG GA  ATTTTG
                                      _ ATA
GAM370  FLJ31762 3' TCTTCTGGGGGTGAGATG   58145        TT  CTGTCT
                                CATTTCACT  CA    GAGA
                                |||||||||  ||    ||||
                                GTAGAGTGG  GT    TTCT
                                     GG  C_____
GAM370  FTSJ3   3' GTCTGAAGAACAGTGAGGTGGA 34455        T    _  G_
           GTG                    ATTTCACTT CACTGT CT  AGAT
                                |||||||||  ||||||  ||  ||||
                                TGAGGTGGA GTGACA GA  TCTG
                                     _    A  AG
GAM370  G4      5' ATCTCAGATTGTGGGGGTGTGG 90991      _   TT   T
           ATG                    CATTT CACT  CAC GTCTGAGAT
                                |||||  ||||  |||  |||||||||
                                GTAGG GTGG  GTG TAGACTCTA
                                   T   GG   T
GAM370  GBTS1   3' ATTTTGGGGAGTGGGTGATATG 59050    T    TT   G  TG
                                CAT TCACT  CACT TC  AGAT
                                |||  |||||  ||||  ||  ||||
                                GTA AGTGG  GTGA GG  TTTA
                                  T   __   G  GT
GAM370  GBTS1   3' TTAGTGAGGGAAGGTGAGATG  59064         A  GT_
                                CATTTCACTTTC CT  CTGA
                                ||||||||||||  ||  ||||
                                GTAGAGTGGAAG GG  GATT
                                      _ AGT
GAM370  GK001   3' TTTCTGGTGGGAGTGGGGTG  39503    TT   TT   TCT   T
                                CAT  CACT  CACTG  GAGA
                                |||  ||||  |||||  ||||
                                GTG  GTGA  GTGGT  CTTT
                                  GG   GG   ___   T
GAM370  GPS2    5' GTCTTTGAGGTGAAAGTGGAA  15671         G  T
                                TTTCACTTTCACT TC GAGAT
                                ||||||||||||| || |||||
                                AAGGTGAAAGTGG AG TTCTG
                                      _ T
GAM370  GPT2    3' TTTCAGATCTGGAGAAATG   55962      ACT   CT
                                CATTTC   TTCA  GTCTGAGA
                                ||||||   ||||  ||||||||
                                GTAAAG   AGGT  TAGACTTT
                                   ___   C_
GAM370  GRSF1   3' ATTTTAGAACAAGTAGGGGTG  9139      TC  _ _
                                CACTT  ACT GT CTGAGAT
                                |||||  ||| ||  |||||||
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                                GTGGG  TGA CA GATTTTA
                                   GA   A  A
GAM370  HBXAP    5'  CAGTGAAATGAAGTG       33420        C
                                CATTTCA TTTCACTG
                                ||||||| ||||||||
                                GTGAAGT AAAGTGAC
                                   _
GAM370  HIC      5'  GTTTCAGGATTGTAGGAGTGGA 67452         TC  TG_
             A                   TTTCACTT  AC   TCTGAGAT
                                ||||||||  ||   ||||||||
                                AAGGTGAG  TG   GGACTTTG
                                    GA  TTA
GAM370  HIF1AN   3'  ATCTATTCAGTGGGAGTGGGGT 61968    TT    TT     TCTG
                                AT  CACT  CACTG    AGAT
                                ||  ||||  |||||    ||||
                                TG  GTGA  GTGAC    TCTA
                                 GG    GG    TTA_
GAM370  HSF2     3'  TCGGGGGTGGGATGGGATG    15710     TT  C TT    G
                                CAT  CA T  CACT TCTGA
                                |||  || |  |||| |||||
                                GTA  GT A  GTGG GGGCT
                                  GG  _ GG   _
GAM370  HSPC054  3'  TTTTACAGCTGTGGAAAGTGAA 26264           _  T T   _   T
             GTG                   ATTTCACTTTC AC G CTG AGA
                                ||||||||||| || | ||| |||
                                TGAAGTGAAAG TG C GAC TTT
                                      G  T _   A   TG
GAM370  HXCP2    3'  ATCTCAGTTTGGGAAGTGGGAT 50832     TT      ACTGT
             G                    CAT  CACTTTC     CTGAGAT
                                |||  |||||||    |||||||
                                GTA  GTGAAGG    GACTCTA
                                  GG      GTTT_
GAM370  HYPK     3'  TCTTGGGTCAAGTAGAGTG    33080       C   _ _  TG
                                CACTTT ACT G TC  AGA
                                |||||| ||| | ||  |||
                                GTGAGA TGA C GG  TCT
                                   _   A T  GT
GAM370  IL18BP   3'  TCTTGGGCAGAGGAGGTG    19113        A    TG
                                CACTTTC CTGTC  AGA
                                |||||||  |||||  |||
                                GTGGAGG GACGG  TCT
                                    A    GT
GAM370  IL22R    3'  GTGGTGAAGATGAAATG     41192        C     TG
                                CATTTCA TTTCAC  T
                                |||||||  ||||||  |
                                GTAAAGT GAAGTG  G
                                    A     GT
GAM370  IMAGE3451454 3'  GTTTTAGCCAAAAGTGAAAT   53873          CAC  T
                                ATTTCACTTT   TG CTGAGAT
                                ||||||||||   || |||||||
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                                TAAAGTGAAA   AC GATTTTG
                                     ___  C
GAM370  KIAA0092 3' ATTTTGGAATAAAGTGAGA   27967        CACTG  TG
                                TTTCACTTT    TC  AGAT
                                |||||||||    ||  ||||
                                AGAGTGAAA    AG  TTTA
                                     TA___  GT
GAM370  KIAA0174 5' ATTTTGGATGGTGAACCCTGAA 78592       CT_       TG
          GT                      ATTTCA   TTCACTGTC  AGAT
                                |||||||  |||||||||  ||||
                                TGAAGT   AAGTGGTAG  TTTA
                                   CCC       GT
GAM370  KIAA0212 3' GTGAGACCGTGGTGAAAGGGGG 27940   TT A      ___    GAGAT
          ATG                     T  C CTTTCACT   GTCT
                                |  | ||||||||   ||||
                                A  G GAAAGTGG   CAGA
                                 GG G       TGC    GTG
GAM370  KIAA0284 3' TGGTGGGGGTGGACGTG     63119     _     TT
                                CAT TTCACT  CACTG
                                |||  ||||||  |||||
                                GTG AGGTGG  GTGGT
                                  C     GG
GAM370  KIAA0285 5' GGCAGTGGAGGTGAGA      29020
                                TTTCACTTTCACTGTC
                                ||||||||||||||||
                                AGAGTGGAGGTGACGG

GAM370  KIAA0419 5' ATTTCAGATAGTGTGTGA    28187      TTT
                                TCAC   CACTGTCTGAGAT
                                ||||   ||||||||||||
                                AGTG   GTGATAGACTTTA
                                  T__
GAM370  KIAA0426 3' GTTTTAGATGGTGTTACTGAGA 28261      CTTT
                                TTTCA    CACTGTCTGAGAT
                                |||||    ||||||||||||
                                AGAGT    GTGGTAGATTTTG
                                   CATT
GAM370  KIAA0453 3' GTCTTGCTGGGGGGGTGGTGATG 69049      _    TT ACT  CT
                                CATT TCACT  C   GT  GAGAT
                                |||| |||||  |   ||  |||||
                                GTAG GGTGG  G   CG  TTCTG
                                   T    GG GT_  __
GAM370  KIAA0459 3' ATTTCAGATGGGATGCAGGTG  60983      T  __
                                CACTT CA  CTGTCTGAGAT
                                ||||| ||  ||||||||||
                                GTGGA GT  GGTAGACTTTA
                                   C  AG
GAM370  KIAA0523 3' ATCTTGGGCTCACAAGTGAGG  67728        TCACT   TG
                                TTTCACTT    GTC  AGAT
                                ||||||||    |||  ||||
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                                GGAGTGAA    CGG  TCTA
                                    CACT_   GT
GAM370  KIAA0552 3' GTTTTGGGGGGCAAGGTGGAG 28320        CA  G  TG
                                TTTCACTTT  CT TC  AGAT
                                |||||||||  || ||  ||||
                                GAGGTGGAA  GG GG  TTTG
                                    C_  G  GT
GAM370  KIAA0660 3' GTTTCAGGCAGGAGTGGGGT  24515    TT    TCA
                                AT  CACTT   CTGTCTGAGAT
                                ||  |||||   ||||||||||
                                TG  GTGAG   GACGGACTTTG
                                 GG    ___
GAM370  KIAA0759 3' GTTTCTGTTTTGAAAGTGAAAT 67329          CTGTCT
            G                    CATTTCACTTTCA     GAGAT
                                ||||||||||||      |||||
                                GTAAAGTGAAAGT     CTTTG
                                       TTTGT_
GAM370  KIAA0795 3' ATTTCAGGGAAGAGGTGGGAT  46588    TT     CA  GT
                                AT  CACTTT  CT  CTGAGAT
                                ||  ||||||  ||  |||||||
                                TA  GTGGAG  GG  GACTTTA
                                 GG     AA  __
GAM370  KIAA0830 3' ATTTCAGCAGTGTGAAGGTAAA 69694      CA   _    T
            TG                   CATTT  CTTT CACTG CTGAGAT
                                |||||  |||| ||||| |||||||
                                GTAAA  GAAG GTGAC GACTTTA
                                   TG   T    _
GAM370  KIAA0871 3' ATTTCAGAATAGGAAGTAAATG 30299      C     ACTG
                                CATTT ACTTTC    TCTGAGAT
                                ||||| ||||||    ||||||||
                                GTAAA TGAAGG    AGACTTTA
                                   _     ATA_
GAM370  KIAA0893 3' GTTTCAGGCTAAAAGGTAAATG 30360      C    CACT
                                CATTT ACTTT    GTCTGAGAT
                                ||||| |||||    |||||||||
                                GTAAA TGGAA    CGGACTTTG
                                   _    AAT_
GAM370  KIAA0918 3' GTTTCAACGTTTAGGGTGAAGT 73134          CAC   C
            G                    CATTTCACTTT   TGT TGAGAT
                                ||||||||||   ||| ||||||
                                GTGAAGTGGGA   GCA ACTTTG
                                      TTT   _
GAM370  KIAA0931 3' ATCTCAGACTAATGGGGTGTGA 67412     _ TT  CT_
                                TCAC T  CA   GTCTGAGAT
                                ||||  |  ||   |||||||||
                                AGTG G  GT   CAGACTCTA
                                  T GG  AAT
GAM370  KIAA0934 3' GGCATGGGGGGTGAAATG     64223         TT  C
                                CATTTCACT  CA TGTC
                                |||||||||  || ||||
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                                GTAAAGTGG  GT ACGG
                                     GG  _
GAM370  KIAA0978 3' CTCGACGTGAGGGTGAAATG  70480          T  T
                                CATTTCACTTTCAC GTC GAG
                                |||||||||||||| ||| |||
                                GTAAAGTGGGAGTG CAG CTC
                                          _  _
GAM370  KIAA1036 3' TGATGGGGGGGTGGGGGTGGGGT 29831    TT   TT   G   AGAT
           G                     CAT  CACT  CACT TCTG
                                |||  ||||  |||| ||||
                                GTG  GTGG  GTGG GGGT
                                  GG   GG   G   AGTG
GAM370  KIAA1046 3' ATCTTAGAAGAGGGGTGGG   29990       CACTG
                                TTCACTTT    TCTGAGAT
                                ||||||||    ||||||||
                                GGGTGGGG    AGATTCTA
                                     AGA__
GAM370  KIAA1046 3' TTTCAGATGTTGGAAATG    30002    C    CT
                                CA TTTCA  GTCTGAGA
                                || |||||  ||||||||
                                GT AAGGT  TAGACTTT
                                 A    TG
GAM370  KIAA1237 3' TTTTGGATGAAGTGAGGG    80476       __  TG
                                CTTTCACT  GTC  AGA
                                ||||||||  |||  |||
                                GGGAGTGA  TAG  TTT
                                     AG   GT
GAM370  KIAA1257 3' GTTGGCACGACTGAGAGTGGGA 62755    TT      CT  _  A_
           TG                     CAT  CACTTTCA  GTC TG  GAT
                                |||  ||||||||  ||| ||  |||
                                GTA  GTGAGAGT  CAG AC  TTG
                                  GG       __   C  GG
GAM370  KIAA1456 3' GTTTTGGAGGAAGGAGGAAATG 67006      A_    A TG  TG
                                CATTTC  CTTTC C  TC  AGAT
                                ||||||  ||||| |  ||  ||||
                                GTAAAG  GGAAG G  AG  TTTG
                                   GA    _ __  GT
GAM370  KIAA1538 3' GTTTTAGACAGGCTCCCTGAA  71556     CTTTCA
                                TTCA     CTGTCTGAGAT
                                ||||     ||||||||||
                                AAGT     GACAGATTTTG
                                  CCCTCG
GAM370  KIAA1559 3' TTGGAGACAGTGAGGGAAGTG  73078      A  T      GAGAT
                                CATTTC CTT CACTGTCT
                                |||||| ||| ||||||||
                                GTGAAG GGA GTGACAGA
                                   _  _      GGTTT
GAM370  KIAA1560 3' TTTGGGAGAGGGAGGGA    64183    A    A  G  G
                                TC CTTTC CT TCT AGA
                                || ||||| || ||| |||
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                                AG GGAGG GA AGG TTT
                                 _    _ G   G
GAM370  KIAA1655 5' ATCTCACCTCCAGTGGGAGGGA 66590      A  TT    TC__
             AGTG                   ATTTC CT  CACTG    TGAGAT
                                |||||  ||  |||||    ||||||
                                TGAAG GA  GTGAC    ACTCTA
                                   G  GG    CTCC
GAM370  KIAA1655 5' TCTCACTGAGAGTGAGA     66634          CTGTC
                                TTTCACTTTCA    TGAGA
                                ||||||||||    |||||
                                AGAGTGAGAGT    ACTCT
                                      C____
GAM370  KIAA1729 3' GTCTTAGGCGATTTGTGGGGTG 89130     TT   TTTCAC
                                CAT  CAC     TGTCTGAGAT
                                |||  |||     ||||||||||
                                GTG  GTG     GCGGATTCTG
                                  GG   TTTA__
GAM370  KIAA1799 5' ATCTTATTTCCGGTGGCGGTGA 74634        T     TC__
             GGTG                   ATTTCACT TCACTG    TGAGAT
                                |||||||| ||||||    ||||||
                                TGGAGTGG GGTGGC    ATTCTA
                                    C     CTTT
GAM370  KIAA1808 5' CATTGAGGGTGAGGTG      85861           C
                                CATTTCACTTTCA TG
                                |||||||||||| ||
                                GTGGAGTGGGAGT AC
                                       T
GAM370  KIAA1811 3' ATCTCTCTGCGGGGTGGGGTG  64793     TT   TTCA   CT_
                                CAT  CACT   CTGT   GAGAT
                                |||  ||||   ||||  |||||
                                GTG  GTGG   GGCG   CTCTA
                                  GG   ____   TCT
GAM370  KIAA1821 3' GGGCAGTGAGGGTGAGG     71790
                                TTTCACTTTCACTGTCT
                                |||||||||||||||||
                                GGAGTGGGAGTGACGGG

GAM370  KIAA1893 3' GTCTCGGGCAGCACGTGAGGT  73217        TTTCA
                                ATTTCAC    CTGTCTGAGAT
                                |||||||    ||||||||||
                                TGGAGTG    GACGGGCTCTG
                                    CAC__
GAM370  KPNA6    3' GCAGAGGAGGGTGGAGTG    24609           A_
                                CATTTCACTTTC  CTGT
                                ||||||||||||  ||||
                                GTGAGGTGGGAG  GACG
                                       GA
GAM370  LMOD1    3' ATCTTTGAGGTGAGGGTGGGGT 24038     TT        G  T
             G                    CAT  CACTTTCACT TC GAGAT
                                |||  |||||||||| || |||||
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                                GTG  GTGGGAGTGG AG TTCTA
                                  GG        _ T
GAM370  LY6G5B   5'  TTTCAGGCTCAGAGAAGTG   41131       CACT_
                                CACTTT    GTCTGAGA
                                ||||||    ||||||||
                                GTGAAG    CGGACTTT
                                   AGACT
GAM370  MAGE-E1  3'  GATTGGACGGTGGAGCTGGGAT 47945     TT  C        TG GAT
           G                     CAT  CA TTTCACTGTC  A
                                |||  || ||||||||||  |
                                GTA  GT GAGGTGGCAG  T
                                  GG  C        GT AG
GAM370  MGC10960 3'  ATCTCCCCAGGAGGGTGAGATG 51003          A   TCT
                                CATTTCACTTTC CTG   GAGAT
                                |||||||||||| |||   |||||
                                GTAGAGTGGGAG GAC   CTCTA
                                       _  CC_
GAM370  MGC2628  3'  ATTTCCGGGTTAGGGTGGAATG 43968          C   GT T
                                CATTTCACTTT ACT  C GAGAT
                                |||||||||| |||  | |||||
                                GTAAGGTGGGA TGG  G CTTTA
                                      T  __ C
GAM370  MGC27044 5'  CTTGGTGTTGAAAGTGAAATG  58673          CTGT TG
                                CATTTCACTTTCA    C  AG
                                ||||||||||||    |  ||
                                GTAAAGTGAAAGT    G  TC
                                       TGT_ GT
GAM370  MGC35558 3'  TCTCAGGTGGGTGAGGG     58787       _ TG
                                CTTTCA C  TCTGAGA
                                ||||||  |  |||||||
                                GGGAGT G  GGACTCT
                                   G GT
GAM370  MGC4251  3'  GTTGGCCTGGTGGGGGTGGAGT 50460        TT   __   TGAGAT
                                ATTTCACT  CACT  GTC
                                ||||||||  ||||  |||
                                TGAGGTGG  GTGG  CGG
                                     GG   TC   TTG
GAM370  MLLT10   5'  AGGCGGTGGAGGGGAGGTG   16166       A
                                CATTTC CTTTCACTGTCT
                                ||||||  ||||||||||||
                                GTGGAG GGAGGTGGCGGA
                                   G
GAM370  MOCS3    3'  TCTTGGACATGTGAGATGT   27161   _    _   TG
                                AC TTTCAC TGTC  AGA
                                ||  ||||||  ||||  |||
                                TG AGAGTG ACAG  TCT
                                 T     T   GT
GAM370  NR6A1    3'  ATTTTGAGGGAGAGGGTGGGAT 7642      TT      A  G  T
           G                     CAT  CACTTTC CT TC GAGAT
                                |||  |||||||  ||  ||  |||||
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                                GTA  GTGGGAG GG AG TTTTA
                                  GG      A  G  _
GAM370  NR6A1    3'  ATTTTGAGGGAGAGGGTGGGAT 52867     TT      A  G  T
           G                     CAT  CACTTTC CT TC GAGAT
                                 |||  ||||||| || || |||||
                                GTA  GTGGGAG GG AG TTTTA
                                  GG      A  G  _
GAM370  NR6A1    3'  ATTTTGAGGGAGAGGGTGGGAT 52879     TT      A  G  T
           G                     CAT  CACTTTC CT TC GAGAT
                                 |||  ||||||| || || |||||
                                GTA  GTGGGAG GG AG TTTTA
                                  GG      A  G  _
GAM370  P450RAI-2 3'  TGGTGGAGATGGAATG      39107        C
                                CATTTCA TTTCACTG
                                ||||||| ||||||||
                                GTAAGGT GAGGTGGT
                                    A
GAM370  PALM     3'  TCTCAGGCAGTTGGGGTGA    10417       TC
                                TCACTT  ACTGTCTGAGA
                                ||||||  ||||||||||
                                AGTGGG  TGACGGACTCT
                                   GT
GAM370  PB1      3'  ATTTTAGTTACTGGGGGTGGGG 36368    TT    TT  C  T
                                T  CACT  CA TG CTGAGAT
                                |  ||||  || || |||||||
                                G  GTGG  GT AT GATTTTA
                                 GG    GG  C  T
GAM370  pcnp     3'  GTTTTGAAATTGGGGTGTGGGG 39789     TT   _ TT  CTG  T
           TG                    CAT  CAC T  CA   TC GAGAT
                                 |||  ||| |  ||   || |||||
                                GTG  GTG G  GT   AG TTTTG
                                  GG   T GG  TAA  _
GAM370  PEF      3'  TCTGTGGAGAGTGGAGTG    24754       T    G    _
                                CACTT CACT TCTG AGA
                                ||||| |||| |||| |||
                                GTGAG GTGA AGGT TCT
                                   _   G   G
GAM370  PGGT1B   3'  ATTTTAGATTGGGAGGGTGGGG 17231    TT      ACT
                                T  CACTTTC   GTCTGAGAT
                                |  |||||||   |||||||||
                                G  GTGGGAG   TAGATTTTA
                                 GG      GGT
GAM370  PINK1    3'  GTCTGTGAATGGTGAGGGTGGG 50543    TT          _ TG
           A                     T  CACTTTCACTGT C  AGAT
                                 |  ||||||||||| |  ||||
                                A  GTGGGAGTGGTA G  TCTG
                                 GG          A TG
GAM370  PP1057   5'  GTTTTGTGGGGGTGGGAGTGGA 48435         TT    G  _
           G                     TTTCACT  CACT TC TGAGAT
                                 |||||||  |||| || ||||||
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                                GAGGTGA  GTGG GG GTTTTG
                                   GG   G  T
GAM370  PRMT3    3'  GTTTTTAATGTGGGGGTAGAGT 65025     TC   TT   TGTCT
           G                    CATT  ACT  CAC    GAGAT
                                |||| ||| |||    |||||
                                GTGA  TGG  GTG    TTTTG
                                  GA   GG   TAAT_
GAM370  PRMT6    3'  GTTTCGCGGGGGAGTGAGG   36272       TT A    CT
                                TTTCACT  C CTGT  GAGAT
                                |||||||  | ||||  |||||
                                GGAGTGA  G GGCG  CTTTG
                                   GG _   __
GAM370  PRO2900  5'  TTCAACTGAGAGTGAGGTG   37809          CT  C
                                CATTTCACTTTCA  GT TGAG
                                ||||||||||||  || ||||
                                GTGGAGTGAGAGT  CA ACTT

                                      __  _
GAM370  PSMF1    3'  GTCTTAGGTGTTCTATGGGAGG 22354    A  TT  C____ GT
           AAGTG                   TC CT  CA    T  CTGAGAT
                                || ||  ||    |  |||||||
                                AG GA  GT    G  GATTCTG
                                 _  GG  ATCTT TG
GAM370  PXR2b    3'  ATTTTTAACTTGGGGGTGAAA  33338       TT  CT  CT
                                TTTCACT  CA  GT  GAGAT
                                |||||||  ||  ||  |||||
                                AAAGTGG  GT  CA  TTTTA
                                   GG  T_  AT
GAM370  RAB6B    3'  GTCTTTAGGAGTAGGGTGGGAT 33414    TT     C   G    _
           G                    CAT  CACTTT ACT TCTGA GAT
                                |||  |||||| ||| ||||| |||
                                GTA  GTGGGA TGA GGATT CTG
                                  GG     _  _    T
GAM370  RACGAP1  3'  GTCTCAGGGTGGGAAGTGGGA  25200   TT     _   GT
                                T  CACTTTC ACT  CTGAGAT
                                |  ||||||| |||  |||||||
                                A  GTGAAGG TGG  GACTCTG
                                 GG      G  __
GAM370  RAD51    3'  TTTCAGGCCAGTGTGGTG    56023     TT    _
                                CACT  CACTG TCTGAGA
                                ||||  ||||| |||||||
                                GTGG  GTGAC GGACTTT
                                  T_    C
GAM370  RAD51    3'  TTTCAGGCCAGTGTGGTG    11229     TT    _
                                CACT  CACTG TCTGAGA
                                ||||  ||||| |||||||
                                GTGG  GTGAC GGACTTT
                                  T_    C
GAM370  RASSF2   3'  GTTTCAGGTTGAAGGGAAATG  28443      A     CTG
                                CATTTC CTTTCA   TCTGAGAT
                                |||||| ||||||   ||||||||
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                                GTAAAG GGAAGT   GGACTTTG
                                  _     T__
GAM370  RBM7    3'  ATTTTAGACACTTTAGGAGGGG 32235    TT A   CAC__
           GTG                    AT  C CTTT    TGTCTGAGAT
                                || | ||||    ||||||||||
                                TG  G GAGG    ACAGATTTTA
                                 GG _   ATTTC
GAM370  RIL     3'  GGGGGTGGTGGTGGGGTG    13488    TT   T    G
                                CAT  CACT TCACT TC
                                |||  |||| ||||| ||
                                GTG  GTGG GGTGG GG
                                  GG   T    G
GAM370  RILP    5'  GTCCCAGTGGAGGGTGGGGTG  48694    TT     ACTGT   A
                                CAT  CACTTTC    CTG GAT
                                |||  |||||||    ||| |||
                                GTG  GTGGGAG    GAC CTG
                                  GG     GT___   C
GAM370  RNO2    5'  ATTTTTTTAGTGGAGATGGGGT 52762    TT  C      TCT
           G                     CAT  CA TTTCACTG   GAGAT
                                |||  || ||||||||   |||||
                                GTG  GT GAGGTGAT   TTTTA
                                  GG  A      TT_
GAM370  RoXaN   3'  ACAGTGGGTGTGAGATG    46627        T
                                CATTTCAC TTCACTGT
                                |||||||| ||||||||
                                GTAGAGTG GGGTGACA
                                     T
GAM370  SAE1    3'  TTTTGGGAGAAAGGAGATG   18537      A    ACTG  TG
                                CATTTC CTTTC    TC  AGA
                                |||||| |||||    ||  |||
                                GTAGAG GAAAG    GG  TTT
                                   _    A___  GT
GAM370  SDS3    3'  ATTTTTCCATTGAAGGTGGAGT 69223          C  TCT
                                ATTTCACTTTCA TG   GAGAT
                                ||||||||||| ||   |||||
                                TGAGGTGGAAGT AC   TTTTA
                                       T  CT_
GAM370  SEMA4C  3'  ACATATGGAGGTGGGGTG    35052    TT      C_
                                CAT  CACTTTCA  TGT
                                |||  ||||||||  |||
                                GTG  GTGGAGGT  ACA
                                  GG       AT
GAM370  SFXN5   3'  TCTTAGGGTAGGGGAAGTG   58040       A  GT _
                                CACTTTC CT  C TGAGA
                                |||||||  ||  | |||||
                                GTGAAGG GA  G ATTCT
                                    G  TG G
GAM370  SGT1    3'  ATTTCAGACATGGTGAAACTG  21992    C      __
                                CA TTTCACT  GTCTGAGAT
                                ||  |||||||  |||||||||
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                                GT AAAGTGG  CAGACTTTA
                                 C      TA
GAM370  SH3BGRL2  3'  ATCTCAGACAGTGATCAGGA   48883    ACTT
                                TC    TCACTGTCTGAGAT
                                ||    ||||||||||||||
                                AG    AGTGACAGACTCTA
                                 GACT
GAM370  SMC1L1    3'  GTCTTAGGCAGTTACCTGAAA  71960      CTTTC
                                TTTCA     ACTGTCTGAGAT
                                ||||||    ||||||||||||
                                AAAGT     TGACGGATTCTG
                                   CCAT_
GAM370  SPTLC2    5'  GTTTCGGGGAGGTGGGTGGGGT 16809     TT    TCA  G
           G                     CAT  CACTT   CT TCTGAGAT
                                |||  |||||   || ||||||||
                                GTG  GTGGG   GA GGGCTTTG
                                  GG    TG_  G
GAM370  STK29     3'  GTCTCAGGCAGTGGGGG     87579    TT
                                CT  CACTGTCTGAGAT
                                ||  ||||||||||||||
                                GG  GTGACGGACTCTG
                                 GG
GAM370  TA-PP2C   3'  GTAGACGCGGTGGGGGCGGGGT 57759     TT A  TT   __    AGAT
           G                     CAT  C CT  CACT  GTCTG
                                |||  | ||  ||||  |||||
                                GTG  G GG  GTGG  CAGAT
                                  GG C  GG    CG    G
GAM370  THEA      3'  TTTTAGGCCAGGTGTGGTG   66305     TT   __
                                CACT  CACT  GTCTGAGA
                                ||||  ||||  ||||||||
                                GTGG  GTGG  CGGATTTT
                                  T_   AC
GAM370  TIAM2     3'  ATCTTGGGCTGTATCAAGGGAG 24931      A   TC_  T   TG
           TG                     CATTTC CTT   AC GTC  AGAT
                                ||||||  |||   ||  |||  ||||
                                GTGAGG  GAA   TG CGG  TCTA
                                   _   CTA  T   GT
GAM370  TP53TG3   3'  ATCTTGGACATCTTGGAGATG  31102      ACTTTCAC    TG
                                CATTTC       TGTC  AGAT
                                ||||||       ||||  ||||
                                GTAGAG       ACAG  TCTA
                                   GTTCT___    GT
GAM370  TRIP3     3'  GTTTCAGGCAGACTTGGGGT   78220    TT  CTTTCA
                                AT  CA     CTGTCTGAGAT
                                ||  ||     ||||||||||||
                                TG  GT     GACGGACTTTG
                                 GG  TCA___
GAM370  VIAAT     3'  GTTTTGGGGGGAGGCGGGGTG  54541     TT A    A  GT TG
                                CAT  C CTTTC CT  C  AGAT
                                |||  | ||||| ||  |  ||||
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                                GTG  G GGAGG GG  G  TTTG
                                  GG C     _  __ GT
GAM370  VPS39    3'  GTCTTTGATGGTGGTGAGGGTG 62849          ___   T
           GG                    TTCACTTTCACT   GTC GAGAT
                                 ||||||||||||   ||| |||||
                                 GGGTGGGAGTGG   TAG TTCTG
                                       TGG   T
GAM370  ZAP3     3'  GTTTTGGGGAGGGAGGGAG   77224     A    A  G  TG
                                 TTC CTTTC CT TC  AGAT
                                 ||| ||||| || ||  ||||
                                 GAG GGAGG GA GG  TTTG
                                   _    _  G  GT
GAM370  ZNF297B  3'  ATTTCAGTACTAAGGTGGTGA  25775      T  ACT  _
                                 TCACT TC   GT CTGAGAT
                                 ||||| ||   || |||||||
                                 AGTGG GG   CA GACTTTA
                                    T  AAT  T
GAM370  ZNF323   5'  ATCTTAAGATTGTGAAAGTGGA 48077          T   _
           G                     TTTCACTTTCAC GTCT GAGAT
                                 ||||||||||||| |||| |||||
                                 GAGGTGAAAGTG TAGA TTCTA
                                       T    A
GAM370  ZNF84    3'  TCTTGGACTTCAGGAAATG    12817       A  TTCACT   TG
                                 CATTTC CT     GTC  AGA
                                 |||||| ||     |||  |||
                                 GTAAAG GA     CAG  TCT
                                    _ CTT___   GT
GAM370  LOC114987 3'  TCTTGAGGGGAGTGGGATG   59124     TT    TT A  GTC
                                 CAT  CACT  C CT   TGAGA
                                 |||  ||||  | ||   |||||
                                 GTA  GTGA  G GA   GTTCT
                                   GG   GG _  ___
GAM370  LOC115219 5'  GGCGGTGGAGGGGAGATG    73312       A
                                 CATTTC CTTTCACTGTC
                                 |||||| ||||||||||
                                 GTAGAG GGAGGTGGCGG
                                    G
GAM370  LOC115297 3'  ATCTCAGATATCCTACGGTGAG 72884        TTCAC_
           A                      TTTCACT     TGTCTGAGAT
                                  |||||||     ||||||||||
                                  AGAGTGG     ATAGACTCTA
                                     CATCCT
GAM370  LOC116150 3'  TCTTACTTGAGAGTGAG     56638          CT  CT
                                 TTCACTTTCA  GT  GAGA
                                 ||||||||||  ||  ||||
                                 GAGTGAGAGT  CA  TTCT
                                       T_  __
GAM370  LOC124446 3'  TTTTAGAAAAAGTGAAG     74293          CACTG
                                 TTTCACTTT    TCTGAGA
                                 |||||||||    |||||||
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                                GAAGTGAAA    AGATTTT
                                     A____
GAM370  LOC126964 3'  GTTTTGGTGGGATGGGGGGAGG 74622       A  TT  _  GT TG
            TG                    CATTTC CT  CA CT  C  AGAT
                                  ||||||  ||  ||  ||  |  ||||
                                  GTGGAG GG  GT GG  G  TTTG
                                     _  GG  A  GT GT
GAM370  LOC128977 3'  GTCTGTGAACAGTGGGGGTGGG 74827    TT    TT     _ TG
            G                     T  CACT  CACTGT C  AGAT
                                  |  ||||  ||||||  |  ||||
                                  G  GTGG  GTGACA G  TCTG
                                   GG    GG     A TG
GAM370  LOC130940 5'  GTCTCGGGCGCGGGAGGGGGTG 57139     TT A  TT AC
                                  CAT  C CT  C  TGTCTGAGAT
                                  |||  | ||  |  ||||||||||
                                  GTG  G GA  G  GCGGGCTCTG
                                    GG _  GG C_
GAM370  LOC131368 3'  ATTTCAGATACTTTAAGTGAAT 75858    T      TCAC
            TG                    CA TTCACTT    TGTCTGAGAT
                                  ||  |||||||    ||||||||||
                                  GT AAGTGAA    ATAGACTTTA
                                   T      TTTC
GAM370  LOC134288 3'  TCCACAGAGGTGAGAGTCGGGT 75178      TC        G    AGAT
            G                     CATT  ACTTTCACT TCTG
                                  ||||  |||||||||  ||||
                                  GTGG  TGAGAGTGG AGAC
                                    GC        _    ACCTT
GAM370  LOC142948 3'  GTCTTGGCAGCATGGAAGTGAG 82891           __   T TG
            A                     TTTCACTTTCA  CTG C  AGAT
                                  ||||||||||  |||  |  ||||
                                  AGAGTGAAGGT  GAC G  TCTG
                                        AC   _ GT
GAM370  LOC143279 5'  GTCCTGGTGGTGGAGGTGGGG  76511    TT        TG  TGA
                                  T  CACTTTCAC  TC   GAT
                                  |  |||||||||  ||   |||
                                  G  GTGGAGGTG  GG   CTG
                                   GG        GT  TC_
GAM370  LOC144483 3'  TTTCATGGCAGTGAAA      60179           _
                                  TTTCACTGTC TGAGA
                                  ||||||||||  |||||
                                  AAAGTGACGG ACTTT
                                        T
GAM370  LOC144486 3'  TTTTGGTGTGAAGGTGAAAT   83090           TGT TG   T
                                  ATTTCACTTTCAC   C  AGA
                                  ||||||||||||||  |  |||
                                  TAAAGTGGAAGTG   G  TTT
                                          T__ GT   T
GAM370  LOC144845 5'  GTGGGGCAAGGTGGGGGTGAAG 56664         TT   __   GAGAT
            TG                    CATTTCACT  CACT  GTCT
                                  |||||||||  ||||  ||||
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                                GTGAAGTGG  GTGG  CGGG
                                     GG    AA    GTG
GAM370   LOC144845 5'  TCGCTCAGGGAGGTGGAGTG   56665          A   TC
                                CATTTCACTTTC CTG  TGA
                                |||||||||||| |||  |||
                                GTGAGGTGGAGG GAC  GCT
                                       _   TC
GAM370   LOC145828 5'  GTTTTGGAAGGGAGAGGAGGTG 83538       A    A  G  TG
                                CATTTC CTTTC CT TC  AGAT
                                |||||| ||||| || ||  ||||
                                GTGGAG GAGAG GG AG  TTTG
                                   _    _ A  GT
GAM370   LOC146050 3'  ATCTCAGATGATTTAGGAAGTG 77625        ACT___
                                CACTTTC     GTCTGAGAT
                                |||||||     |||||||||
                                GTGAAGG     TAGACTCTA
                                     ATTTAG
GAM370   LOC146229 3'  GTGGTAGAGTGGAATG      77769          C  TG
                                CATTTCACTTT AC  T
                                |||||||||||  ||  |
                                GTAAGGTGAGA TG  G
                                       _  GT
GAM370   LOC146336 3'  GACAGTGAGGCTGAAATG     77832        C
                                CATTTCA TTTCACTGTC
                                ||||||| ||||||||||
                                GTAAAGT GGAGTGACAG
                                     C
GAM370   LOC146728 5'  TCGGAGTGGGGTGGAGTG     83753          T   TG
                                CATTTCACTT CAC  TCTGA
                                |||||||||| |||  |||||
                                GTGAGGTGGG GTG  AGGCT
                                       _  __
GAM370   LOC146990 5'  ATCTCGGGCGGCTGGAGGGGTG 83884        __   _
            AGG                    TTCACT  TTCA CTGTCTGAGAT
                                |||||| |||| ||||||||||
                                GAGTGG  AGGT GGCGGGCTCTA
                                   GG    C
GAM370   LOC147632 5'  TGGTGGAATGAGATG       56670        C
                                CATTTCA TTTCACTG
                                ||||||| ||||||||
                                GTAGAGT AAGGTGGT
                                       _
GAM370   LOC148413 3'  GCAGTGAGGATGGAGTG     78830        CT
                                CATTTCA  TTCACTGT
                                |||||||  ||||||||
                                GTGAGGT  GAGTGACG
                                     AG
GAM370   LOC148479 3'  GTTCCCTGCAGTGGAGGTGGAC 78879    T          CT_  AT
            TG                     CA TTCACTTTCACTGT   GAG
                                || ||||||||||||||   |||
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                                GT AGGTGGAGGTGACG   CTT
                                 C           TCC   G
GAM370   LOC148529 5'  TCTTAGGCGAGTGGGAG     84172    TT   _
                                CT  CACT GTCTGAGA
                                ||  |||| ||||||||
                                GA  GTGA CGGATTCT
                                 GG    G
GAM370   LOC149076 3'  ATCTTGGAGGCAGGGAGGTGAG 79148          A     __
           G                     TTTCACTTTC CTGTCT  GAGAT
                                ||||||||||  ||||||  |||||
                                GGAGTGGAGG GACGGA  TTCTA
                                      _     GG
GAM370   LOC149182 5'  TCTTGTGCAGGGTGAGATG    84379         TTCA    CT
                                CATTTCACT    CTGT  GAGA
                                |||||||||    ||||  ||||
                                GTAGAGTGG    GACG  TTCT
                                     ____    TG
GAM370   LOC149711 3'  ATTTCACCTGCTTGGAAAGTGA 84673          ACT  C__
           GATG                    ATTTCACTTTC   GT   TGAGAT
                                ||||||||||   ||   ||||||
                                TAGAGTGAAAG   CG   ACTTTA
                                      GTT  TCC
GAM370   LOC149837 5'  GTTTTGAGGGTGGAATGAGGTG 84745        C      G  T
                                CATTTCA TTTCACT TC GAGAT
                                ||||||| ||||||| || |||||
                                GTGGAGT AAGGTGG AG TTTTG
                                     _      G  _
GAM370   LOC149844 5'  GGTGGTGGGGGTGGTGGTG    79519     _    TT   TG
                                CATT TCACT  CAC  TC
                                ||||  |||||  |||  ||
                                GTGG GGTGG  GTG  GG
                                  T    GG   GT
GAM370   LOC149844 3'  TGGTGAGTGAGATG        79521         TT
                                CATTTCAC  TCACTG
                                ||||||||  ||||||
                                GTAGAGTG  AGTGGT
                                     __
GAM370   LOC150225 3'  GTCTTTTGCAGGTGAAGGTGGG 85009    TT       _  CT
           A                     T  CACTTTCAC TGT  GAGAT
                                |  |||||||| |||  |||||
                                A  GTGGAAGTG ACG  TTCTG
                                 GG        G   TT
GAM370   LOC150351 5'  TTTTAGATAGTACGAAGT    60249      C_
                                ACTTT  ACTGTCTGAGA
                                |||||  ||||||||||
                                TGAAG  TGATAGATTTT
                                   CA
GAM370   LOC150358 3'  TCTCAGAGAGTGAAGTGA    84928       T   G
                                TCACTT CACT TCTGAGA
                                ||||||  |||| |||||||
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                                AGTGAA GTGA AGACTCT
                                   _   G
GAM370  LOC150819 5'  GTTAGGGAGCAGTGAAAGTGAG 85122            ___   GAT
          G                    TTTCACTTTCACTGT  CTGA
                               ||||||||||||||  ||||
                               GGAGTGAAAGTGACG  GATT
                                       AGG   G
GAM370  LOC150933 3'  ATTTCAGTCACAGGAAATGGGG 85156    TT  C   A   __
          TG                   CAT  CA TTTC CTGT  CTGAGAT
                               |||  || |||| ||||  |||||||
                               GTG  GT AAAG GACA  GACTTTA
                                 GG  _   _   CT
GAM370  LOC151056 3'  ATCTTTTTTGGGAGTGAACTG  80106    T    TT  CTGTCT
                               CA TTCACT  CA     GAGAT
                               || ||||||  ||     |||||
                               GT AAGTGA  GT     TTCTA
                                C     GG  TTT___
GAM370  LOC151176 3'  GTTTTGATAAGGGGGTGATGTG 85263    T    TT AC   T
                               CAT TCACT  C  TGTC GAGAT
                               ||| |||||  |  |||| |||||
                               GTG AGTGG  G  ATAG TTTTG
                                 T    GG A_   _
GAM370  LOC151194 3'  ATTTTAGATGGTGAAATTAGAA 59213      AC_
          GT                   ATTTC   TTTCACTGTCTGAGAT
                               |||||   ||||||||||||||||
                               TGAAG   AAAGTGGTAGATTTTA
                                  ATT
GAM370  LOC151414 3'  ATTTTGGCATATGGGGGTGGAG 80235       TT  C   _ TG
                               TTTCACT  CA TGT C  AGAT
                               |||||||  || ||| |  ||||
                               GAGGTGG  GT ATA G  TTTA
                                   GG  _   C GT
GAM370  LOC151438 5'  TTTTCGGTGTGAAGGTGGGATG 85373    TT       TGT     T
                               CAT  CACTTTCAC   CTGAGA
                               |||  |||||||||   ||||||
                               GTA  GTGGAAGTG   GGCTTT
                                 GG       T__     TT
GAM370  LOC151610 3'  GGATGGTGGGAGTGAAG    80288       TT
                               TTTCACT  CACTGTCT
                               |||||||  ||||||||
                               GAAGTGA  GTGGTAGG
                                  GG
GAM370  LOC151658 5'  GTGGTGGAGTGGAGTG     85481         T   TG
                               CATTTCACTT CAC  T
                               |||||||||| |||  |
                               GTGAGGTGAG GTG  G
                                     _  GT
GAM370  LOC151826 3'  TTTTAGGCTAGTGAAA     80370       _
                               TTTCACT GTCTGAGA
                               ||||||| ||||||||
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                                AAAGTGA CGGATTTT
                                    T
GAM370  LOC151904 5'  CCCTGCGTGGTGGAGGGAGGTG 80387       A      TG CTGAGAT
                                CATTTC CTTTCAC  T
                                |||||| |||||||  |
                                GTGGAG GGAGGTG  G
                                   _      GT CGTCCCT
GAM370  LOC152274 3'  TCTTGGATTGGATGAGATG   80509       CT   CT   TG
                                CATTTCA  TTCA  GTC  AGA
                                |||||||  ||||  |||  |||
                                GTAGAGT  AGGT  TAG  TCT
                                   __   __  GT
GAM370  LOC152275 3'  GGGGGCGACAGGGAGGTGGGAT 85620     TT     A    TGAGAT
          G                      CAT  CACTTTC CTGTC
                                |||  ||||||| |||||
                                GTA  GTGGAGG GACAG
                                  GG     _    CGGGGGT
GAM370  LOC152633 5'  GTCTTGCTGTGCTGGGGGTGGG 85817     TT   TT  CTGTCT_
          GTG                    CAT  CACT  CA      GAGAT
                                |||  ||||  ||      |||||
                                GTG  GTGG  GT      TTCTG
                                  GG   GG  CGTGTCG
GAM370  LOC152805 5'  TCTCAGGATGAGTGAGG     80689         TCACTG
                                TTTCACTT     TCTGAGA
                                ||||||||     |||||||
                                GGAGTGAG     GGACTCT
                                    TA____
GAM370  LOC153196 5'  GTCTTAGAGCTAGAGATGAGGT 85975       C    ACTG
          G                      CATTTCA TTTC    TCTGAGAT
                                |||||||| ||||    ||||||||
                                GTGGAGT AGAG    AGATTCTG
                                   _    ATCG
GAM370  LOC153222 3'  TTTTGGAGGAGTGAAAT     80791         CACTG  TG
                                ATTTCACTTT    TC  AGA
                                ||||||||||    ||  |||
                                TAAAGTGAGG    AG  TTT
                                    _____  GT
GAM370  LOC153339 5'  GTTTTGGTGGGGTGGTGGGATG 86012     TT   T  A   T TG
                                CAT  CACT TC CTG C  AGAT
                                |||  |||| || ||| |  ||||
                                GTA  GTGG GG GGT G  TTTG
                                  GG   T  _   _ GT
GAM370  LOC153651 3'  TTTTAGATGGTGATTGT     80918     TT
                                AC  TCACTGTCTGAGA
                                ||  ||||||||||||
                                TG  AGTGGTAGATTTT
                                 TT
GAM370  LOC153711 3'  TCGGGTGGGAGAGGGA      86138     A    A TG
                                TTC CTTTC C  TCTGA
                                ||| ||||| |  |||||
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                                AGG GAGAG G  GGGCT
                                  _    _ GT
GAM370  LOC153811 3'  GCAGTGGGGGTAAGGTG     80950      C   TT
                                CATTT ACT  CACTGT
                                ||||| |||  ||||||
                                GTGGA TGG  GTGACG
                                   A   GG
GAM370  LOC154386 3'  GTTTCAGTTCTGGAAGGTGAAA 81084          ACTGT
                                TTTCACTTTC     CTGAGAT
                                ||||||||||     |||||||
                                AAAGTGGAAG     GACTTTG
                                      GTCTT
GAM370  LOC154792 3'  TTTTGGATATGTGAGAG     86250        _    TG
                                CTTTCAC TGTC  AGA
                                ||||||| ||||  |||
                                GAGAGTG ATAG  TTT
                                    T    GT
GAM370  LOC154877 3'  GTCTTTACTGAGGGTGGCAGTG 86306      T    G  T___
                                CACT TCACT TC    GAGAT
                                |||| ||||| ||    |||||
                                GTGA GGTGG AG    TTCTG
                                  C     G  TCAT
GAM370  LOC157623 5'  CAACGAGGCGGTGTGGGTGGAG 81493         TT       GAGAT
          TG                     CATTTCACT  CACTGTCT
                                |||||||||  ||||||||
                                GTGAGGTGG  GTGGCGGA
                                     GT       GCAACT
GAM370  LOC157693 3'  TCTTGGACGCAGTGAAGT    81558        TTCAC    TG
                                ATTTCACT     TGTC  AGA
                                ||||||||     ||||  |||
                                TGAAGTGA     GCAG  TCT
                                    C____    GT
GAM370  LOC157918 3'  GTCTTGGGCACAGGTGGGGT   86649    TT    TCAC    TG
                                AT  CACTT    TGTC  AGAT
                                ||  |||||    ||||  ||||
                                TG  GTGGA    ACGG  TCTG
                                 GG    C___    GT
GAM370  LOC157919 3'  GTTTCAGACAGTGGAA      81637
                                TTTCACTGTCTGAGAT
                                ||||||||||||||||
                                AAGGTGACAGACTTTG

GAM370  LOC158117 3'  GGCGTGGTGGAATGGAATG    81709        C      __
                                CATTTCA TTTCACT  GTC
                                ||||||| |||||||  |||
                                GTAAGGT AAGGTGG  CGG
                                    _      TG
GAM370  LOC158382 5'  ACGGGGGAAGTGAGGTG     86782           A
                                CATTTCACTTTC CTGT
                                |||||||||||| ||||
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                                GTGGAGTGAAGG GGCA
                                      G
GAM370  LOC158382 5'  GTGGTGGAAGATGAAGTG    86789        _     TG
                                CATTTCA CTTTCAC  T
                                ||||||| |||||||  |
                                GTGAAGT GAAGGTG  G
                                    A      GT
GAM370  LOC158954 3'  TTTTGGGTGGGGGGGGAAGTG   60437       A  TT   TGT TG
                                CATTTC CT  CAC   C  AGA
                                |||||| ||  |||   |  |||
                                GTGAAG GG  GTG   G  TTT
                                   G  GG   ___ GT
GAM370  LOC159184 5'  TCAATGGTGAAGGTGAAGT   60051             C
                                ATTTCACTTTCACTGT TGA
                                |||||||||||||||| |||
                                TGAAGTGGAAGTGGTA ACT
                                                 _
GAM370  LOC163882 3'  ATGCTGGCAGTGAGAGTGAAA  82163             TGAGAT
                                TTTCACTTTCACTGTC
                                ||||||||||||||||
                                AAAGTGAGAGTGACGG
                                      TCGTA
GAM370  LOC166983 5'  GTCTGGCCCAAGGGGAGGTGGA 87266         A  ___   T  GAT
           GTG                    TTTCACTTTC CT   GTC GA
                                ||||||||| ||   ||| ||
                                GAGGTGGAGG GA   CGG CT
                                     G  ACC   T  G
GAM370  LOC169436 5'  GGGGTAGATGTGGGGGTGGAAT 82743        TT   T    AGAT
           G                     CATTTCACT  CAC GTCTG
                                |||||||||  ||| |||||
                                GTAAGGTGG  GTG TAGAT
                                     GG  _    GGGGT
GAM370  LOC196761 3'  GTTTTGGGCAGTGGAG      89556          TG
                                TTTCACTGTC  AGAT
                                ||||||||||  ||||
                                GAGGTGACGG  TTTG
                                      GT
GAM370  LOC197379 3'  GATGGTGAGGGTGGGGT     89742    TT
                                AT  CACTTTCACTGTC
                                ||  ||||||||||||
                                TG  GTGGGAGTGGTAG
                                 GG
GAM370  LOC197414 3'  ATTTTGGGCAGGCGCTGAGTGG 88061   TT    TCA__    TG
           GG                    T  CACTT    CTGTC  AGAT
                                |  |||||    |||||  ||||
                                G  GTGAG    GACGG  TTTA
                                 GG    TCGCG    GT
GAM370  LOC201203 3'  ATCTCAGATTGTGAGGTAAATG 88140      C   T   T
                                CATTT ACTT CAC GTCTGAGAT
                                ||||| |||| ||| |||||||||
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                                GTAAA TGGA GTG TAGACTCTA
                                  _   _  T
GAM370  LOC201895 3'  TCTTAGGCCAGTGCAGTG    89094     TT   _
                                CACT  CACTG TCTGAGA
                                ||||  ||||| |||||||
                                GTGA  GTGAC GGATTCT
                                  C_    C
GAM370  LOC202152 3'  ATCTCAGATTTAAAAACGTGGG 89157    TT  _  CACT
          ATG                     CAT  CAC TTT   GTCTGAGAT
                                ||| ||| |||   |||||||||
                                GTA  GTG AAA   TAGACTCTA
                                  GG   C   AATT
GAM370  LOC203275 3'  GGCGTGGTGGAATGGAATG   89325       C     __
                                CATTTCA TTTCACT  GTC
                                ||||||| |||||||  |||
                                GTAAGGT AAGGTGG  CGG
                                   _      TG
GAM370  LOC203317 5'  GTCTTGCCAATGGAAGTTGGAG 89333       _    C  TC
          TG                      CATTTCA CTTTCA TG  TGAGAT
                                ||||||| ||||||  ||  ||||||
                                GTGAGGT GAAGGT AC  GTTCTG
                                   T     A  C_
GAM370  LOC219333 3'  GTCAGGGCAGTGGAAGTGGA  93542            GA
                                TTCACTTTCACTGTCT  GAT
                                ||||||||||||||||  |||
                                AGGTGAAGGTGACGGG  CTG
                                      A_
GAM370  LOC219529 3'  GTCTCAGGTGAGTGGAGG    92972       _ GT
                                CTTTCAC T  CTGAGAT
                                ||||||| |  |||||||
                                GGAGGTG G  GACTCTG
                                   A TG
GAM370  LOC220143 5'  GCGGGAGGGTGAAATG      93589          A
                                CATTTCACTTTC CTGT
                                |||||||||||| ||||
                                GTAAAGTGGGAG GGCG
                                      _
GAM370  LOC220549 5'  GCGGTGAGAGAGAGGTG     92919       A
                                CATTTC CTTTCACTGT
                                |||||| ||||||||||
                                GTGGAG GAGAGTGGCG
                                   A
GAM370  LOC220739 5'  ATTTCCCATGGGAGTGGAGT  92925       TT  C  TCT
                                ATTTCACT  CA TG   GAGAT
                                ||||||||  || ||   |||||
                                TGAGGTGA  GT AC   CTTTA
                                   GG  _  C__
GAM370  LOC221400 3'  GTCTCAGGTTGATGGTGGGGTG 92299    TT   T  CTG
                                CAT  CACT TCA   TCTGAGAT
                                |||  |||| |||   ||||||||
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                                GTG  GTGG AGT   GGACTCTG
                                  GG   T  T__
GAM370   LOC221405 3'  TTTTAGATTAGTGGAA     93892        _
                                TTTCACTG TCTGAGA
                                |||||||| |||||||
                                AAGGTGAT AGATTTT
                                     T
GAM370   LOC221415 3'  TTTCCTGGGGGTTGAGGTG   93878      C   G  T_
                                CACTTT ACT TC  GAGA
                                |||||| ||| ||  ||||
                                GTGGAG TGG GG  CTTT
                                   T   G  TC
GAM370   LOC221584 3'  TCTCGAGAGAAAGGGAGTG   93833      A    A  GTC
                                CATTTC CTTTC CT   TGAGA
                                |||||| ||||| ||   |||||
                                GTGAGG GAAAG GA   GCTCT
                                   _    A  ___
GAM370   LOC221683 5'  GTCTTAGGTTTTGGTGTGA   93717     TT   CT
                                TCAC  TCA  GTCTGAGAT
                                ||||  |||  |||||||||
                                AGTG  GGT  TGGATTCTG
                                  T_   TT
GAM370   LOC221865 3'  ATTTTGGGTATATGGGGTGAAA 92486          CAC GT TG
           T                     ATTTCACTTT   T  C  AGAT
                                ||||||||||  |  |  ||||
                                TAAAGTGGGG   A  G  TTTA
                                      TAT TG GT
GAM370   LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                      _
GAM370   LOC245728 5'  TTCAGGCAATGAAGTG      91135       T  C
                                CACTT CA TGTCTGAG
                                ||||| || ||||||||
                                GTGAA GT ACGGACTT
                                   _  A
GAM370   LOC253115 3'  ATTTTTATTGTGGGGTGGGATG 94494     TT    T   TGTCT
                                CAT  CACTT CAC    GAGAT
                                |||  ||||| |||    |||||
                                GTA  GTGGG GTG    TTTTA
                                  GG    _   TTAT_
GAM370   LOC254485 3'  CTGGGAAGTGAGGTG       95013      T   G   G
                                CACTT CACT TCT AG
                                ||||| |||| ||| ||
                                GTGGA GTGA AGG TC
                                   _   _  G
GAM370   LOC254755 3'  GCAGGGAGGTGGGGTG      97369     TT      A
                                CAT  CACTTTC CTGT
                                |||  ||||||| ||||
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                                GTG  GTGGAGG GACG
                                  GG      _
GAM370   LOC254756 3'  GCAGGGAGGTGGGGTG      97363     TT      A
                                CAT  CACTTTC CTGT
                                |||  ||||||| ||||
                                GTG  GTGGAGG GACG
                                  GG      _
GAM370   LOC255391 5'  TCTCTGGGGGTGCGGTG     97614      TT    G  T
                                CACT  CACT TC GAGA
                                ||||  |||| || ||||
                                GTGG  GTGG GG CTCT
                                  C_    G  T
GAM370   LOC255394 3'  GTTTCAGACACTGCTTAGGTGC 94886     T     T__  C
            AGTG                   ATT CACTT   CA TGTCTGAGAT
                                ||| |||||   || ||||||||||
                                TGA GTGGA   GT ACAGACTTTG
                                  C     TTC  C
GAM370   LOC255452 5'  GTCTCTATCCGAGAGGGTGGAG 97543           ACTGTCT
            TG                   CATTTCACTTTC      GAGAT
                                ||||||||||||      |||||
                                GTGAGGTGGGAG      CTCTG
                                      AGCCTAT
GAM370   LOC255480 3'  TCTTGAGGAGGTGAAGG     96521         GT  _
                                CTTTCACT  CT GAGA
                                ||||||||  || ||||
                                GGAAGTGG  GA TTCT
                                     AG  G
GAM370   LOC255779 3'  ATTTCCCCATGCAAAGTGGGAT 96013     TT     _  C  TCT
            G                    CAT  CACTTT CA TG   GAGAT
                                |||  |||||| || ||   |||||
                                GTA  GTGAAA GT AC   CTTTA
                                  GG     C  _  CC_
GAM370   LOC256145 5'  GTCTCGGGCATCGTGGG     96543       __
                                TTCAC  TGTCTGAGAT
                                |||||  ||||||||||
                                GGGTG  ACGGGCTCTG
                                   CT
GAM370   LOC256405 5'  ATCTCAGGACCAGATAGTGGAG 95872          T  ACTG
            TG                   CATTTCACT TC    TCTGAGAT
                                |||||||| ||    ||||||||
                                GTGAGGTGA AG    GGACTCTA
                                     T  ACCA
GAM370   LOC256639 5'  GTCTTGCTTCAGGAAGGTGAAG 96219           A   TC_
            TG                   CATTTCACTTTC CTG   TGAGAT
                                |||||||||||| |||   ||||||
                                GTGAAGTGGAAG GAC   GTTCTG
                                      _  TTC
GAM370   LOC257048 3'  TATGTAGGTAGTGGGGGGAAAT 96216       A  TT    GT   AGAT
            G                    CATTTC CT  CACT  CTG
                                ||||||  ||  ||||  |||
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                                GTAAAG GG  GTGA  GAT
                                   _ GG   TG   GTATT
GAM370  LOC257554 5'  ATCTCAGATTGTGGGGGTGTGG 97691      _   TT  T
            ATG                    CATTT CACT  CAC GTCTGAGAT
                                |||||| ||||  ||| |||||||||
                                GTAGG GTGG  GTG TAGACTCTA
                                   T   GG   T
GAM370  LOC257556 3'  ATTTTTATTGTGGGGTGGGATG 97707    TT    T  TGTCT
                                CAT  CACTT CAC    GAGAT
                                |||  ||||| |||    |||||
                                GTA  GTGGG GTG    TTTTA
                                  GG    _  TTAT_
GAM370  LOC257617 3'  ATTTTTATTGTGGGGTGGGATG 97813    TT    T  TGTCT
                                CAT  CACTT CAC    GAGAT
                                |||  ||||| |||    |||||
                                GTA  GTGGG GTG    TTTTA
                                  GG    _  TTAT_
GAM370  LOC51107  3'  TTTCTGCTGAGGGTGGAGTG   32064          CT  CT
                                CATTTCACTTTCA  GT  GAGA
                                ||||||||||||  ||  ||||
                                GTGAGGTGGGAGT  CG  CTTT
                                      __  T_
GAM370  LOC51152  3'  GTCTCAAAGGAGAAAGTGAGGT 32454          A  GTC
            G                   CATTTCACTTTC CT   TGAGAT
                                ||||||||||| ||   ||||||
                                GTGGAGTGAAAG GG   ACTCTG
                                      A  AA_
GAM370  LOC51716  3'  GCAGTGAAGGTGAGGT     32792
                                ATTTCACTTTCACTGT
                                ||||||||||||||||
                                TGGAGTGGAAGTGACG

GAM370  LOC56912  5'  CTCACGAGAGTGGAAG      39336        G  _
                                CTTTCACT TC TGAG
                                |||||||| || ||||
                                GAAGGTGA AG ACTC
                                     G  C
GAM370  LOC56959  5'  TCTTGACCGGAGGTGGAA    81927         ACT   T
                                TTTCACTTTC   GTC GAGA
                                |||||||||   ||| ||||
                                AAGGTGGAGG   CAG TTCT
                                     C__  _
GAM370  LOC89135  3'  TGGTGAGTGAGATG       60319        TT
                                CATTTCAC  TCACTG
                                ||||||||  ||||||
                                GTAGAGTG  AGTGGT
                                     __
GAM370  LOC90170  5'  GGTGGTGAGGGTTAAATG    61710      C      TG
                                CATTT ACTTTCAC  TC
                                ||||| ||||||||  ||
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                                GTAAA TGGGAGTG  GG
                                   T       GT
GAM370  LOC90826  5' GTCTTGGGTTTGGAATGTGAAA 64095        _    CTG  TG
             TG                   CATTTCAC TTTCA   TC  AGAT
                                  |||||||| |||||   ||  ||||
                                  GTAAAGTG AAGGT   GG  TCTG
                                     T    TT_  GT
GAM370  LOC91363  3' ATCTCAGAACAGAAGGGTGGGA 65776   TT     CA   _
                                  T  CACTTT  CTGT CTGAGAT
                                  |  ||||||  |||| |||||||
                                  A  GTGGGA  GACA GACTCTA
                                   GG     A_    A
GAM370  LOC91450  3' GTTTTGGGCAGAGGAGTGGGG  66076   TT     CA    TG
                                  T  CACTTT  CTGTC  AGAT
                                  |  ||||||  |||||  ||||
                                  G  GTGAGG  GACGG  TTTG
                                   GG     A_    GT
GAM370  LOC91628  3' GCAGTGGATGTGGGATG     66760     TT   T
                                  CAT  CAC TTCACTGT
                                  |||  ||| ||||||||
                                  GTA  GTG AGGTGACG
                                    GG   T
GAM370  LOC92305  3' GTCTCAGACTCCTGGGTAGGGG 56418     TT _   TCACT
             TG                   CAT  C ACTT    GTCTGAGAT
                                  |||  | ||||    |||||||||
                                  GTG  G TGGG    CAGACTCTG
                                    GG A    TCCT_
GAM370  LOC93349  3' CTTAGGCGGATGGAGG      56457       _
                                  CTTTCA CTGTCTGAG
                                  |||||| |||||||||
                                  GGAGGT GGCGGATTC
                                     A
GAM370  LOC93587  3' TAGGAGAAAGTGAGGTG     72648           A_
                                  CATTTCACTTTC  CTG
                                  ||||||||||||  |||
                                  GTGGAGTGAAAG  GAT
                                        AG
GAM371  GGA3     3'  CATTAGAAGAGGACAAG     56826       T     C
                                  CTTGTT CTCTTC AATG
                                  |||||| |||||| ||||
                                  GAACAG GAGAAG TTAC
                                     _     A
GAM371  GGA3     3'  CATTAGAAGAGGACAAG     25742       T     C
                                  CTTGTT CTCTTC AATG
                                  |||||| |||||| ||||
                                  GAACAG GAGAAG TTAC
                                     _     A
GAM371  NYX      3'  CATTGGAAAAGAGAAGCAAGAA 42597     GC          __
             TGA                    TCA  TCTTGTTTCTCT  TCCAATG
                                  |||  ||||||||||||  |||||||
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                                AGT  AGAACGAAGAGA  AGGTTAC
                                  A_          AA
GAM371  PTX3     3'  CATTGGAAGAATAACAA     11143       TC
                                TTGTT  TCTTCCAATG
                                |||||  ||||||||||
                                AACAA  AGAAGGTTAC
                                   TA
GAM371  RFXANK   5'  CATTGGAAGAGAAAAGTTTGT  13560    TCTTG
                                GC    TTTCTCTTCCAATG
                                ||    ||||||||||||||
                                TG    AAAGAGAAGGTTAC
                                 TTTGA
GAM371  RFXANK   5'  CATTGGAAGAGAAAAGTTTGT  56238    TCTTG
                                GC    TTTCTCTTCCAATG
                                ||    ||||||||||||||
                                TG    AAAGAGAAGGTTAC
                                 TTTGA
GAM371  SLC26A4  3'  CATTGAAAGAGAAGCA      4784          C
                                TGTTTCTCTT CAATG
                                |||||||||| |||||
                                ACGAAGAGAA GTTAC
                                      A
GAM371  VCAM1    3'  GAGAAAAACAATGAGCTGA    6547        _     C
                                TCAGCTC TTGTTT TCTT
                                ||||||| |||||| ||||
                                AGTCGAG AACAAA AGAG
                                    T     A
GAM371  VCAM1    3'  GAGAAAAACAATGAGCTGA    54771       _     C
                                TCAGCTC TTGTTT TCTT
                                ||||||| |||||| ||||
                                AGTCGAG AACAAA AGAG
                                    T     A
GAM371  DKFZP434A0225 3'  AAGAGAAACAAAAATGA     93902     GCTC
                                TCA    TTGTTTCTCTT
                                |||    ||||||||||
                                AGT    AACAAAGAGAA
                                  AAA_
GAM371  DNAH8    5'  CATTAAAAGAGAGACAGGC    7259      CT        CC
                                GCT  TGTTTCTCTT  AATG
                                |||  ||||||||||  ||||
                                CGG  ACAGAGAGAA  TTAC
                                  __         AA
GAM371  FLJ10201 3'  CATTGGAAAAAGGAGAGC    35892       G   CTC
                                GCTCTT TTT   TTCCAATG
                                |||||| |||   ||||||||
                                CGAGAG AAA   AAGGTTAC
                                   G  ___
GAM371  FLJ20004 3'  ATTGGGCAACAAGAGC      95289         TCTCT
                                GCTCTTGTT    TCCAAT
                                |||||||||    ||||||
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                                CGAGAACAA    GGGTTA
                                     C____
GAM371  FLJ20281  5'  AGAGAAAAAGAGCTGA      90979         G
                                TCAGCTCTT TTTCTCT
                                ||||||||| |||||||
                                AGTCGAGAA AAAGAGA
                                          _
GAM371  FLJ20315  3'  GAGTGGACAAGAGCTGA     34935          _
                                TCAGCTCTTGTTT CTC
                                |||||||||||| |||
                                AGTCGAGAACAGG GAG
                                         T
GAM371  FLJ20758  5'  ATTGGAAGAGGAAAATGA    35642    TTG
                                TC   TTTCTCTTCCAAT
                                ||   ||||||||||||
                                AG   AAGGAGAAGGTTA
                                 TAA
GAM371  KIAA0643  3'  AAGAAGAAATAAGAGCTGA   45596           _
                                TCAGCTCTTGTTTCT CTT
                                |||||||||||||| |||
                                AGTCGAGAATAAAGA GAA
                                          A
GAM371  PDCD10    5'  TGGAAGAAGGAAGAG       23310       G    CT
                                CTCTT TTTCT  TCCA
                                ||||| |||||  ||||
                                GAGAA GAAGA  AGGT
                                   G    __
GAM371  PIP5K2B   3'  GAAAGAGACTTTAGCTGA    13072       CTT     C
                                TCAGCT   GTTTCT TTC
                                ||||||   |||||| |||
                                AGTCGA   CAGAGA AAG
                                    TTT    _
GAM371  ZNF185    3'  CATTGAAAGAAATCTTGCAAGA 23109        TTC___    C
           GC                     GCTCTTGT     TCTT CAATG
                                ||||||||     |||| |||||
                                CGAGAACG     AGAA GTTAC
                                     TTCTAA    A
GAM371  LOC116068 3'  ATTGGGAAACAAAGGC      73724    TC      TCTT
                                GC  TTGTTTC    CCAAT
                                ||  |||||||    |||||
                                CG  AACAAAG    GGTTA
                                 GA      _____
GAM371  LOC127255 3'  ATTGGAAATGAAAAACAA    59161       C __
                                TTGTTT TC  TTCCAAT
                                |||||| ||  |||||||
                                AACAAA AG  AAGGTTA
                                   A  TA
GAM371  LOC127703 3'  TTGGAAAAGGAGCTG       74685        GTTTCTC
                                CAGCTCTT      TTCCAA
                                ||||||||      ||||||
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                                GTCGAGGA      AAGGTT
                                    A_______
GAM371  LOC146485 5'  GAGAAAGACAAGAACTGA    59788      C       C
                                TCAG TCTTGTTT TCTT
                                |||| |||||||| ||||
                                AGTC AGAACAGA AGAG
                                  A       A
GAM371  LOC147004 3'  TGGAAGAGTTGAAAGAGCTGG  83907         GTTT
                                TCAGCTCTT   CTCTTCCA
                                |||||||||   ||||||||
                                GGTCGAGAA   GAGAAGGT
                                      AGTT
GAM371  LOC150082 5'  ATCAGAAGAGAAGGCTGG    79568       CTTGT      CA
                                TCAGCT    TTCTCTTC  AT
                                ||||||    ||||||||  ||
                                GGTCGG    AAGAGAAG  TA
                                   ______       AC
GAM371  LOC196797 3'  TGGAAGAGTGGCTGA       87523       CTTGTTT
                                TCAGCT      CTCTTCCA
                                ||||||      ||||||||
                                AGTCGG      GAGAAGGT
                                   T_______
GAM371  LOC220164 3'  CATTGGAAGGTTAAAAACTGGA 91796     T   C___
                                TCT GTTT    TCTTCCAATG
                                ||| ||||    ||||||||||
                                AGG CAAA    GGAAGGTTAC
                                  T   AATT
GAM371  LOC220595 5'  AAGAAAAAACAAGAGCTGG    91138           C_
                                TCAGCTCTTGTTT  TCTT
                                ||||||||||||  ||||
                                GGTCGAGAACAAA  AGAA
                                       AA
GAM371  LOC90120  3'  TGGAAGAGAAACTTTTTGA    61543      CTCTT
                                TCAG    GTTTCTCTTCCA
                                ||||    ||||||||||||
                                AGTT    CAAAGAGAAGGT
                                  TTT__
GAM372  NCALD     3'  TGCTTTTCTGAGCAGATCAATA 49380          CC   CCTGT
                                TATTGATCTGT  CAG    GCA
                                ||||||||||  |||    |||
                                ATAACTAGACG  GTC    CGT
                                      A_   TTTT_
GAM372  FLJ10242  5'  TACTTCCTGAAGCAGATCAA   35934        CC   CCT
                                TTGATCTGT  CAG   GTG
                                |||||||||  |||   |||
                                AACTAGACG  GTC   CAT
                                      AA   CTT
GAM372  FLJ13842  3'  TGCACAGAACTGGAACAGATCA 44990        C    C_
                                TGATCTGT CCAG  CTGTGCA
                                ||||||||  ||||  |||||||
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                                ACTAGACA GGTC  GACACGT
                                    A   AA
GAM372  GPR88    3'  CACAGTCAAGACGGATCAATA  41878          CCAGC
                                TATTGATCTGTC    CTGTG
                                ||||||||||||    |||||
                                ATAACTAGGCAG    GACAC
                                      AACT_
GAM372  KIAA0415 3'  TGCACCGTGGAGCAGATCAA   92582        TC   GCCT
                                TTGATCTG  CCA   GTGCA
                                ||||||||  |||   |||||
                                AACTAGAC  GGT   CACGT
                                    GA   GC__
GAM372  KIAA0513 3'  GCACAGGCTAAGACCACAGA   28359       CCC___
                                TCTGT     AGCCTGTGC
                                |||||     |||||||||
                                AGACA     TCGGACACG
                                   CCAGAA
GAM372  TCL6     3'  GCACAGGCTGGTCTCAA     40135      TCTGTC
                                TTGA     CCAGCCTGTGC
                                ||||     ||||||||||
                                AACT     GGTCGGACACG
                                  CT_____
GAM372  TCL6     3'  GCACAGGCTGGTCTCAA     40103      TCTGTC
                                TTGA     CCAGCCTGTGC
                                ||||     ||||||||||
                                AACT     GGTCGGACACG
                                  CT_____
GAM372  LOC219529 5'  TGCAACAGAAGACAGATTAA   92975          CCAGC   _
                                TTGATCTGTC    CTGT GCA
                                ||||||||||    |||| |||
                                AATTAGACAG    GACA CGT
                                      AA___    A
GAM372  LOC253281 5'  CACAGGCTGGAGGTGCTCA   97343     TC GT _
                                TGA  T  C CCAGCCTGTG
                                |||  |  | ||||||||||
                                ACT  G  G GGTCGGACAC
                                  C_ TG A
GAM373  ARCN1    3'  AGACTGCACTCTCTGTCA    7970          CA_
                                TGACAGAGA   CAGTTT
                                |||||||||   ||||||
                                ACTGTCTCT   GTCAGA
                                     CAC
GAM373  CBFA2T2  3'  GAGCAAAACTCTGTCT      17466       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                   C
GAM373  CTLA4    3'  CAGAGCTGGGATGTTTCTGTCA 17807          CAGTTTT
                                TGACAGAGACA      GCTCTG
                                ||||||||||       ||||||
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                                ACTGTCTTTGT      CGAGAC
                                     AGGGT__
GAM373  ITK      3'  CAGAACAGGAGTGATGTCTCTG 18674        _ G    C
                                CAGAGACA CA TTTTG TCTG
                                |||||||| || ||||| ||||
                                GTCTCTGT GT AGGAC AGAC
                                     A G    A
GAM373  LAMP2    3'  GGTGAAACCCCATCTCTATCA  25716    C    CACA    TG
                                TGA AGAGA    GTTT  CT
                                ||| |||||    ||||  ||
                                ACT TCTCT    CAAA  GG
                                  A    ACCC    GT
GAM373  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   40865       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM373  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   52963       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM373  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   52960       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM373  PDGFRB   5'  CAGAGCCTGGAACTGTG     65969         __
                                CACAGTTTT  GCTCTG
                                |||||||||  ||||||
                                GTGTCAAGG  CGAGAC
                                      TC
GAM373  PTPRA    3'  AGAGCGGTATCTCTG       55079       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM373  PTPRA    3'  AGAGCGGTATCTCTG       55087       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM373  PTPRA    3'  AGAGCGGTATCTCTG       11088       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM373  RAD51L3  3'  CAAAACTCAGGTATGTCTCTGT 56065         C_____
                                ACAGAGACA     AGTTTTG
                                |||||||||     |||||||
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                                TGTCTCTGT     TCAAAAC
                                      ATGGAC
GAM373  TBL2    3'  CAGAACTGTGTTCCATCA    24924     CA   A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC   _
GAM373  TBL2    3'  CAGAACTGTGTTCCATCA    52178     CA   A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC   _
GAM373  AGTRL2  5'  CAGAGCAAGAACTGTTC     17691    C       _
                                GA ACAGTTTT GCTCTG
                                || |||||||| ||||||
                                CT TGTCAAGA CGAGAC
                                 _       A
GAM373  CABP5   3'  AGAGCGGTATCTTTGCCA    39079    A     C  AGTTT
                                TG CAGAGA AC     TGCTCT
                                || |||||| ||     ||||||
                                AC GTTTCT TG     GCGAGA
                                 C     A _____
GAM373  CUL4A   5'  AGAGCAGCACCTCCATCA    13149     CA   ACACA  T
                                TGA  GAG     GT TTGCTCT
                                |||  |||     || |||||||
                                ACT  CTC     CA GACGAGA
                                  AC   _____  C
GAM373  DKFZp761O17121 3'  CAGACAGCCCCTGTGTCTCTGT 50136            TT_   C
           C                     GACAGAGACACAG   TTG TCTG
                                ||||||||||||   ||| ||||
                                CTGTCTCTGTGTC   GAC AGAC
                                       CCC   _
GAM373  FLJ10375 3'  CAGAGGCCTGTGTCTGTGCCA  36073    A  G       TTTTG
                                TG CA AGACACAG     CTCTG
                                || || ||||||||     |||||
                                AC GT TCTGTGTC     GAGAC
                                 C  G       CG___
GAM373  FLJ10738 5'  CAAAGCCAGCCCTCTGTCA    36527         ACACA
                                TGACAGAG     GTTTTG
                                ||||||||     ||||||
                                ACTGTCTC     CGAAAC
                                     CCGAC
GAM373  FLJ10803 3'  CAAAACAAAACTCTGTCA     36660         ACACA
                                TGACAGAG     GTTTTG
                                ||||||||     ||||||
                                ACTGTCTC     CAAAAC
                                     AAAA_
GAM373  FLJ10842 3'  AAAGTGTGCTCTGTCA       36723         A   G
                                TGACAGAG CACA TTT
                                |||||||| |||| |||
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                                ACTGTCTC GTGT AAA
                                    _   G
GAM373  FLJ13153  3'  CAGAGCCCAGCATCCATCTCTG 45555        CACA_  TT
           TCA                   TGACAGAGA    GTT  GCTCTG
                                 |||||||||    |||  ||||||
                                 ACTGTCTCT    CGA  CGAGAC
                                     ACCTA   CC
GAM373  FLJ20035  3'  CAAACCTGCCATGTTCTGTCA  34395        A  ___  T
                                 TGACAGAG CA   CAG TTTG
                                 |||||||| ||   ||| ||||
                                 ACTGTCTT GT   GTC AAAC
                                     _ ACC   C
GAM373  FLJ22195  5'  CAGAGCAGAGGGAAGTCTCTGC 42800    A      ACAG
           CA                    TG CAGAGAC    TTTTGCTCTG
                                 || |||||||    ||||||||||
                                 AC GTCTCTG    GAGACGAGAC
                                  C      AAGG
GAM373  FLJ32191  5'  GAACTGCACCTCTGTCA     58411        ACA
                                 TGACAGAG   CAGTTT
                                 ||||||||   ||||||
                                 ACTGTCTC   GTCAAG
                                     CAC
GAM373  KIAA1023  3'  CAAAGCTGTATCTGCTATCA   34255     C  _  C
                                 TGA AG AGA ACAGTTTTG
                                 ||| || ||| |||||||||
                                 ACT TC TCT TGTCGAAAC
                                   A  G   A
GAM373  KIAA1586  5'  AGTGTGATGTGTCTCTG     92326         GTT TG T
                                 CAGAGACACA   T  C CT
                                 ||||||||||   |  | ||
                                 GTCTCTGTGT   A  G GA
                                     ___ GT T
GAM373  KIAA1754  3'  GACTAACGTCTCTGTCA     63236         AC_
                                 TGACAGAGAC   AGTT
                                 ||||||||||   ||||
                                 ACTGTCTCTG   TCAG
                                     CAA
GAM373  LANCL2    3'  CAGAGTGCACTGCAGCTCTGTC 37995        ACA    TTT
           A                     TGACAGAG   CAGT   GCTCTG
                                 ||||||||   ||||   ||||||
                                 ACTGTCTC   GTCA   TGAGAC
                                     GAC    CG_
GAM373  LIG-1     3'  CAGAGCAGGCCTGTCCATGCCA 63893    A  GAGAC    TT
                                 TG CA    ACAG  TTGCTCTG
                                 || ||    ||||  ||||||||
                                 AC GT    TGTC  GACGAGAC
                                  C  ACC__    CG
GAM373  MGC5242   3'  AGAGTACATGTCTCTG     43823         CAGTTT
                                 CAGAGACA     TGCTCT
                                 ||||||||     ||||||
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                                GTCTCTGT     ATGAGA
                                   AC____
GAM373  OSMR     3'  CAGAGCTGGCACCCTGTCA   14345       AGACA
                                TGACAG    CAGTTTTG
                                ||||||    ||||||||
                                ACTGTC    GTCGAGAC
                                   CCACG
GAM373  RAB21    3'  CAGAACAAAACTGTGGATC   30383    GA        C
                                GA  CACAGTTTTG TCTG
                                ||  |||||||||| ||||
                                CT  GTGTCAAAAC AGAC
                                 AG         A
GAM373  SPTLC2   3'  CAGAGCAAAACTGTGTCTC   16799
                                GAGACACAGTTTTGCTCTG
                                |||||||||||||||||||
                                CTCTGTGTCAAAACGAGAC

GAM373  TGIF2    3'  GAGTCATGCTCTGTCA      41454        A  CAGTTT  _
                                TGACAGAG CA     TG CTC
                                |||||||| ||     || |||
                                ACTGTCTC GT     AC GAG
                                   _ _______ T
GAM373  WBSCR23  5'  GCTGACTGTGTCTCCATCA   46765     CA        TT
                                TGA  GAGACACAGTT  GC
                                |||  ||||||||||  ||
                                ACT  CTCTGTGTCAG  CG
                                  AC         T_
GAM373  LOC115129 3' GGCAAAACCCCGTCTCT     73235       ACA
                                AGAGAC   GTTTTGCT
                                ||||||   ||||||||
                                TCTCTG   CAAAACGG
                                   CCC
GAM373  LOC129198 3' AGCAAGCTGTGCCTC       76117     A       T
                                GAG CACAGTTT GCT
                                ||| |||||||| |||
                                CTC GTGTCGAA CGA
                                  C       _
GAM373  LOC145231 3' GGTGAAACTATGTCTCT     83293       C     TG
                                AGAGACA AGTTT  CT
                                ||||||| |||||  ||
                                TCTCTGT TCAAA  GG
                                   A     GT
GAM373  LOC145483 3' GAGCAAAACTCTGTCT      77243       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                  C
GAM373  LOC146713 3' GAGCAAAACTCCGTCT      83726      AC
                                AGAC  AGTTTTGCTC
                                ||||  ||||||||||
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                                TCTG  TCAAAACGAG
                                  CC
GAM373  LOC149175 3'  CAGGGTGAAACCACGTCTCT   79208       ACA   TG
                                AGAGAC   GTTT  CTCTG
                                ||||||   ||||  |||||
                                TCTCTG   CAAA  GGGAC
                                   CAC    GT
GAM373  LOC150299 3'  CAGAACCTGCATCTTTGTCA   84968        CA  _
                                TGACAGAGA  CAG TTTTG
                                |||||||||  ||| |||||
                                ACTGTTTCT  GTC AAGAC
                                     AC   C
GAM373  LOC153277 3'  TAAAACTGTGCCTGTGCCA    85990    A  G  A
                                TG CA AG CACAGTTTTG
                                || || || ||||||||||
                                AC GT TC GTGTCAAAAT
                                 C  G  C
GAM373  LOC155179 3'  CAAAGCTGTATCTGCTATCA   81312     C  _   C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM373  LOC221074 3'  AAAGTGTGTCTCTTTCA     93177     C        G
                                TGA AGAGACACA TTT
                                ||| |||||||| |||
                                ACT TCTCTGTGT AAA
                                  T        G
GAM373  LOC221103 5'  AGTTTATGTGTGCTCTGTCA   93244         _    GTTTT
                                TGACAGAG ACACA     GCT
                                |||||||| |||||     |||
                                ACTGTCTC TGTGT     TGA
                                     G    ATT__
GAM373  LOC255988 5'  CAGAGCCCAGCATCCATCTCTG 97608          CACA_   TT
           TCA                    TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                     ACCTA   CC
GAM374  ARCN1    3'  AGACTGCACTCTCTGTCA    7970          CA_
                                TGACAGAGA   CAGTTT
                                |||||||||   ||||||
                                ACTGTCTCT   GTCAGA
                                     CAC
GAM374  CBFA2T2   3'  GAGCAAAACTCTGTCT      17466       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                  C
GAM374  CTLA4    3'  CAGAGCTGGGATGTTTCTGTCA 17807           CAGTTTT
                                TGACAGAGACA      GCTCTG
                                ||||||||||      ||||||
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                                ACTGTCTTTGT      CGAGAC
                                     AGGGT__
GAM374  ITK      3'  CAGAACAGGAGTGATGTCTCTG 18674        _ G    C
                                CAGAGACA CA TTTTG TCTG
                                |||||||| || ||||| ||||
                                GTCTCTGT GT AGGAC AGAC
                                     A G    A
GAM374  LAMP2    3'  GGTGAAACCCCATCTCTATCA  25716    C    CACA    TG
                                TGA AGAGA    GTTT  CT
                                ||| |||||    ||||  ||
                                ACT TCTCT    CAAA  GG
                                  A    ACCC    GT
GAM374  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   52963        A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM374  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   52960        A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM374  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   40865        A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM374  PDGFRB   5'  CAGAGCCTGGAACTGTG     65969         __
                                CACAGTTTT  GCTCTG
                                |||||||||  ||||||
                                GTGTCAAGG  CGAGAC
                                      TC
GAM374  PTPRA    3'  AGAGCGGTATCTCTG       11088       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM374  PTPRA    3'  AGAGCGGTATCTCTG       55079       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM374  PTPRA    3'  AGAGCGGTATCTCTG       55087       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM374  RAD51L3  3'  CAAAACTCAGGTATGTCTCTGT 56065         C_____
                                ACAGAGACA     AGTTTTG
                                |||||||||     |||||||
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                                TGTCTCTGT     TCAAAAC
                                      ATGGAC
GAM374  TBL2    3'  CAGAACTGTGTTCCATCA    24924     CA   A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC   _
GAM374  TBL2    3'  CAGAACTGTGTTCCATCA    52178     CA   A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC   _
GAM374  AGTRL2  5'  CAGAGCAAGAACTGTTC     17691    C       _
                                GA ACAGTTTT GCTCTG
                                || |||||||| ||||||
                                CT TGTCAAGA CGAGAC
                                 _       A
GAM374  CABP5   3'  AGAGCGGTATCTTTGCCA    39079    A     C  AGTTT
                                TG CAGAGA AC     TGCTCT
                                || |||||| ||     ||||||
                                AC GTTTCT TG     GCGAGA
                                 C     A _____
GAM374  CUL4A   5'  AGAGCAGCACCTCCATCA    13149     CA   ACACA  T
                                TGA  GAG    GT TTGCTCT
                                |||  |||    || |||||||
                                ACT  CTC    CA GACGAGA
                                  AC   _____  C
GAM374  DKFZp761O17121 3'  CAGACAGCCCCTGTGTCTCTGT 50136            TT_   C
            C                    GACAGAGACACAG   TTG TCTG
                                ||||||||||||   ||| ||||
                                CTGTCTCTGTGTC   GAC AGAC
                                       CCC   _
GAM374  FLJ10375 3'  CAGAGGCCTGTGTCTGTGCCA  36073    A  G       TTTTG
                                TG CA AGACACAG     CTCTG
                                || || ||||||||     |||||
                                AC GT TCTGTGTC     GAGAC
                                 C  G       CG___
GAM374  FLJ10738 5'  CAAAGCCAGCCCTCTGTCA    36527         ACACA
                                TGACAGAG     GTTTTG
                                ||||||||     ||||||
                                ACTGTCTC     CGAAAC
                                     CCGAC
GAM374  FLJ10803 3'  CAAAACAAAACTCTGTCA     36660         ACACA
                                TGACAGAG     GTTTTG
                                ||||||||     ||||||
                                ACTGTCTC     CAAAAC
                                     AAAA_
GAM374  FLJ10842 3'  AAAGTGTGCTCTGTCA       36723         A   G
                                TGACAGAG CACA TTT
                                |||||||| |||| |||
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                                ACTGTCTC GTGT AAA
                                    _   G
GAM374  FLJ13153  3'  CAGAGCCCAGCATCCATCTCTG 45555        CACA_  TT
           TCA                   TGACAGAGA    GTT  GCTCTG
                                 |||||||||    |||  ||||||
                                 ACTGTCTCT    CGA  CGAGAC
                                     ACCTA   CC
GAM374  FLJ20035  3'  CAAACCTGCCATGTTCTGTCA  34395        A ___  T
                                 TGACAGAG CA   CAG TTTG
                                 |||||||| ||   ||| ||||
                                 ACTGTCTT GT   GTC AAAC
                                     _ ACC   C
GAM374  FLJ22195  5'  CAGAGCAGAGGGAAGTCTCTGC 42800    A      ACAG
           CA                    TG CAGAGAC    TTTTGCTCTG
                                 || |||||||    ||||||||||
                                 AC GTCTCTG    GAGACGAGAC
                                  C      AAGG
GAM374  FLJ32191  5'  GAACTGCACCTCTGTCA     58411        ACA
                                 TGACAGAG   CAGTTT
                                 ||||||||   ||||||
                                 ACTGTCTC   GTCAAG
                                     CAC
GAM374  KIAA1023  3'  CAAAGCTGTATCTGCTATCA   34255     C  _   C
                                 TGA AG AGA ACAGTTTTG
                                 ||| || ||| |||||||||
                                 ACT TC TCT TGTCGAAAC
                                   A  G   A
GAM374  KIAA1586  5'  AGTGTGATGTGTCTCTG     92326         GTT TG T
                                 CAGAGACACA   T  C CT
                                 ||||||||||   |  | ||
                                 GTCTCTGTGT   A  G GA
                                     ___ GT T
GAM374  KIAA1754  3'  GACTAACGTCTCTGTCA     63236         AC_
                                 TGACAGAGAC   AGTT
                                 ||||||||||   ||||
                                 ACTGTCTCTG   TCAG
                                     CAA
GAM374  LANCL2    3'  CAGAGTGCACTGCAGCTCTGTC 37995        ACA    TTT
           A                     TGACAGAG   CAGT   GCTCTG
                                 ||||||||   ||||   ||||||
                                 ACTGTCTC   GTCA   TGAGAC
                                     GAC    CG_
GAM374  LIG-1     3'  CAGAGCAGGCCTGTCCATGCCA 63893    A  GAGAC    TT
                                 TG CA    ACAG  TTGCTCTG
                                 || ||    ||||  ||||||||
                                 AC GT    TGTC  GACGAGAC
                                  C  ACC__    CG
GAM374  MGC5242   3'  AGAGTACATGTCTCTG     43823         CAGTTT
                                 CAGAGACA     TGCTCT
                                 ||||||||     ||||||
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                                GTCTCTGT     ATGAGA
                                   AC____
GAM374  OSMR     3'  CAGAGCTGGCACCCTGTCA   14345       AGACA
                                TGACAG    CAGTTTTG
                                ||||||    ||||||||
                                ACTGTC    GTCGAGAC
                                   CCACG
GAM374  RAB21    3'  CAGAACAAAACTGTGGATC   30383    GA        C
                                GA  CACAGTTTTG TCTG
                                ||  |||||||||| ||||
                                CT  GTGTCAAAAC AGAC
                                 AG         A
GAM374  SPTLC2   3'  CAGAGCAAAACTGTGTCTC   16799
                                GAGACACAGTTTTGCTCTG
                                |||||||||||||||||||
                                CTCTGTGTCAAAACGAGAC

GAM374  TGIF2    3'  GAGTCATGCTCTGTCA      41454        A  CAGTTT  _
                                TGACAGAG CA     TG CTC
                                |||||||| ||     || |||
                                ACTGTCTC GT     AC GAG
                                   _ _______ T
GAM374  WBSCR23  5'  GCTGACTGTGTCTCCATCA   46765     CA        TT
                                TGA  GAGACACAGTT  GC
                                |||  ||||||||||  ||
                                ACT  CTCTGTGTCAG  CG
                                  AC         T_
GAM374  LOC115129 3' GGCAAAACCCCGTCTCT     73235       ACA
                                AGAGAC   GTTTTGCT
                                ||||||   ||||||||
                                TCTCTG   CAAAACGG
                                   CCC
GAM374  LOC129198 3' AGCAAGCTGTGCCTC       76117     A       T
                                GAG CACAGTTT GCT
                                ||| |||||||| |||
                                CTC GTGTCGAA CGA
                                  C       _
GAM374  LOC145231 3' GGTGAAACTATGTCTCT     83293       C     TG
                                AGAGACA AGTTT  CT
                                ||||||| |||||  ||
                                TCTCTGT TCAAA  GG
                                   A     GT
GAM374  LOC145483 3' GAGCAAAACTCTGTCT      77243       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                  C
GAM374  LOC146713 3' GAGCAAAACTCCGTCT      83726      AC
                                AGAC  AGTTTTGCTC
                                ||||  ||||||||||
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                                TCTG  TCAAAACGAG
                                  CC
GAM374  LOC149175 3'  CAGGGTGAAACCACGTCTCT   79208       ACA   TG
                                AGAGAC   GTTT  CTCTG
                                ||||||   ||||  |||||
                                TCTCTG   CAAA  GGGAC
                                   CAC    GT
GAM374  LOC150299 3'  CAGAACCTGCATCTTTGTCA   84968        CA  _
                                TGACAGAGA  CAG TTTTG
                                |||||||||  ||| |||||
                                ACTGTTTCT  GTC AAGAC
                                     AC   C
GAM374  LOC153277 3'  TAAAACTGTGCCTGTGCCA    85990    A  G  A
                                TG CA AG CACAGTTTTG
                                || || || ||||||||||
                                AC GT TC GTGTCAAAAT
                                 C  G  C
GAM374  LOC155179 3'  CAAAGCTGTATCTGCTATCA   81312     C  _   C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM374  LOC221074 3'  AAAGTGTGTCTCTTTCA     93177     C        G
                                TGA AGAGACACA TTT
                                ||| ||||||||| |||
                                ACT TCTCTGTGT AAA
                                  T        G
GAM374  LOC221103 5'  AGTTTATGTGTGCTCTGTCA   93244         _    GTTTT
                                TGACAGAG ACACA     GCT
                                |||||||| |||||     |||
                                ACTGTCTC TGTGT     TGA
                                     G    ATT__
GAM374  LOC255988 5'  CAGAGCCCAGCATCCATCTCTG 97608          CACA_   TT
           TCA                    TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                     ACCTA   CC
GAM375  ARCN1    3'  AGACTGCACTCTCTGTCA    7970          CA_
                                TGACAGAGA   CAGTTT
                                |||||||||   ||||||
                                ACTGTCTCT   GTCAGA
                                     CAC
GAM375  CBFA2T2   3'  GAGCAAAACTCTGTCT      17466       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                  C
GAM375  CTLA4    3'  CAGAGCTGGGATGTTTCTGTCA 17807           CAGTTTT
                                TGACAGAGACA      GCTCTG
                                ||||||||||      ||||||
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                                ACTGTCTTTGT      CGAGAC
                                     AGGGT__
GAM375  ITK      3'  CAGAACAGGAGTGATGTCTCTG 18674        _ G    C
                                CAGAGACA CA TTTTG TCTG
                                |||||||| || ||||| ||||
                                GTCTCTGT GT AGGAC AGAC
                                     A G    A
GAM375  LAMP2    3'  GGTGAAACCCCATCTCTATCA  25716    C    CACA    TG
                                TGA AGAGA    GTTT  CT
                                ||| |||||    ||||  ||
                                ACT TCTCT    CAAA  GG
                                  A    ACCC    GT
GAM375  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   40865       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM375  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   52960       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM375  MRPS12   3'  CAAAGGGTGCCCCTCTGTCA   52963       A__   AG
                                TGACAGAG   CAC  TTTTG
                                ||||||||   |||  |||||
                                ACTGTCTC   GTG  GAAAC
                                     CCC   G_
GAM375  PDGFRB   5'  CAGAGCCTGGAACTGTG     65969         __
                                CACAGTTTT  GCTCTG
                                |||||||||  ||||||
                                GTGTCAAGG  CGAGAC
                                      TC
GAM375  PTPRA    3'  AGAGCGGTATCTCTG       55079       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM375  PTPRA    3'  AGAGCGGTATCTCTG       55087       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM375  PTPRA    3'  AGAGCGGTATCTCTG       11088       C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM375  RAD51L3  3'  CAAAACTCAGGTATGTCTCTGT 56065         C_____
                                ACAGAGACA     AGTTTTG
                                |||||||||     |||||||
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                                TGTCTCTGT     TCAAAAC
                                      ATGGAC
GAM375  TBL2    3'  CAGAACTGTGTTCCATCA    52178    CA   A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC   _
GAM375  TBL2    3'  CAGAACTGTGTTCCATCA    24924    CA   A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC   _
GAM375  AGTRL2  5'  CAGAGCAAGAACTGTTC     17691    C      _
                                GA ACAGTTTT GCTCTG
                                || |||||||| ||||||
                                CT TGTCAAGA CGAGAC
                                 _      A
GAM375  CABP5   3'  AGAGCGGTATCTTTGCCA    39079    A    C  AGTTT
                                TG CAGAGA AC    TGCTCT
                                || |||||| ||    ||||||
                                AC GTTTCT TG    GCGAGA
                                 C     A _____
GAM375  CUL4A   5'  AGAGCAGCACCTCCATCA    13149    CA   ACACA  T
                                TGA  GAG    GT TTGCTCT
                                |||  |||    || |||||||
                                ACT  CTC    CA GACGAGA
                                  AC   _____  C
GAM375  DKFZp761O17121 3'  CAGACAGCCCCTGTGTCTCTGT 50136          TT_  C
          C                      GACAGAGACACAG   TTG TCTG
                                ||||||||||||   ||| ||||
                                CTGTCTCTGTGTC   GAC AGAC
                                       CCC   _
GAM375  FLJ10375 3'  CAGAGGCCTGTGTCTGTGCCA  36073    A  G      TTTTG
                                TG CA AGACACAG    CTCTG
                                || || ||||||||    |||||
                                AC GT TCTGTGTC    GAGAC
                                 C  G       CG___
GAM375  FLJ10738 5'  CAAAGCCAGCCCTCTGTCA   36527        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
                                ACTGTCTC    CGAAAC
                                     CCGAC
GAM375  FLJ10803 3'  CAAAACAAAACTCTGTCA    36660        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
                                ACTGTCTC    CAAAAC
                                     AAAA_
GAM375  FLJ10842 3'  AAAGTGTGCTCTGTCA      36723        A   G
                                TGACAGAG CACA TTT
                                |||||||| |||| |||
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                                ACTGTCTC GTGT AAA
                                    _   G
GAM375  FLJ13153  3'  CAGAGCCCAGCATCCATCTCTG 45555        CACA_  TT
            TCA                   TGACAGAGA    GTT  GCTCTG
                                  |||||||||    |||  ||||||
                                  ACTGTCTCT    CGA  CGAGAC
                                       ACCTA   CC
GAM375  FLJ20035  3'  CAAACCTGCCATGTTCTGTCA  34395        A  ___   T
                                  TGACAGAG CA   CAG TTTG
                                  ||||||||  ||   |||  ||||
                                  ACTGTCTT GT   GTC AAAC
                                       _  ACC   C
GAM375  FLJ22195  5'  CAGAGCAGAGGGAAGTCTCTGC 42800    A      ACAG
            CA                    TG CAGAGAC    TTTTGCTCTG
                                  ||  |||||||    ||||||||||
                                  AC GTCTCTG    GAGACGAGAC
                                   C      AAGG
GAM375  FLJ32191  5'  GAACTGCACCTCTGTCA     58411         ACA
                                  TGACAGAG   CAGTTT
                                  ||||||||   ||||||
                                  ACTGTCTC   GTCAAG
                                       CAC
GAM375  KIAA1023  3'  CAAAGCTGTATCTGCTATCA   34255     C  _   C
                                  TGA AG AGA ACAGTTTTG
                                  |||  ||  |||  |||||||||
                                  ACT TC TCT TGTCGAAAC
                                    A  G   A
GAM375  KIAA1586  5'  AGTGTGATGTGTCTCTG     92326          GTT TG T
                                  CAGAGACACA   T  C CT
                                  ||||||||||   |  | ||
                                  GTCTCTGTGT   A  G GA
                                       ___ GT T
GAM375  KIAA1754  3'  GACTAACGTCTCTGTCA     63236          AC_
                                  TGACAGAGAC   AGTT
                                  ||||||||||   ||||
                                  ACTGTCTCTG   TCAG
                                       CAA
GAM375  LANCL2    3'  CAGAGTGCACTGCAGCTCTGTC 37995        ACA    TTT
            A                     TGACAGAG   CAGT   GCTCTG
                                  ||||||||   ||||   ||||||
                                  ACTGTCTC   GTCA   TGAGAC
                                       GAC    CG_
GAM375  LIG-1     3'  CAGAGCAGGCCTGTCCATGCCA 63893    A  GAGAC    TT
                                  TG CA     ACAG  TTGCTCTG
                                  ||  ||    ||||  ||||||||
                                  AC GT     TGTC  GACGAGAC
                                   C  ACC__    CG
GAM375  MGC5242   3'  AGAGTACATGTCTCTG      43823         CAGTTT
                                  CAGAGACA     TGCTCT
                                  ||||||||     ||||||
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                                GTCTCTGT     ATGAGA
                                   AC____
GAM375  OSMR     3'  CAGAGCTGGCACCCTGTCA   14345       AGACA
                                TGACAG    CAGTTTTG
                                ||||||    ||||||||
                                ACTGTC    GTCGAGAC
                                   CCACG
GAM375  RAB21    3'  CAGAACAAAACTGTGGATC   30383    GA        C
                                GA  CACAGTTTTG TCTG
                                ||  |||||||||| ||||
                                CT  GTGTCAAAAC AGAC
                                 AG         A
GAM375  SPTLC2   3'  CAGAGCAAAACTGTGTCTC   16799
                                GAGACACAGTTTTGCTCTG
                                |||||||||||||||||||
                                CTCTGTGTCAAAACGAGAC

GAM375  TGIF2    3'  GAGTCATGCTCTGTCA      41454        A  CAGTTT  _
                                TGACAGAG CA     TG CTC
                                |||||||| ||     || |||
                                ACTGTCTC GT     AC GAG
                                   _ _______ T
GAM375  WBSCR23  5'  GCTGACTGTGTCTCCATCA   46765     CA        TT
                                TGA  GAGACACAGTT  GC
                                |||  ||||||||||  ||
                                ACT  CTCTGTGTCAG  CG
                                  AC         T_
GAM375  LOC115129 3' GGCAAAACCCCGTCTCT     73235       ACA
                                AGAGAC   GTTTTGCT
                                ||||||   ||||||||
                                TCTCTG   CAAAACGG
                                   CCC
GAM375  LOC129198 3' AGCAAGCTGTGCCTC       76117     A       T
                                GAG CACAGTTT GCT
                                ||| |||||||| |||
                                CTC GTGTCGAA CGA
                                  C       _
GAM375  LOC145231 3' GGTGAAACTATGTCTCT     83293        C     TG
                                AGAGACA AGTTT  CT
                                ||||||| |||||  ||
                                TCTCTGT TCAAA  GG
                                   A     GT
GAM375  LOC145483 3' GAGCAAAACTCTGTCT      77243       C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                  C
GAM375  LOC146713 3' GAGCAAAACTCCGTCT      83726      AC
                                AGAC  AGTTTTGCTC
                                ||||  ||||||||||
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                                TCTG  TCAAAACGAG
                                  CC
GAM375  LOC149175 3'  CAGGGTGAAACCACGTCTCT   79208       ACA    TG
                                AGAGAC   GTTT  CTCTG
                                ||||||   ||||  |||||
                                TCTCTG   CAAA  GGGAC
                                   CAC    GT
GAM375  LOC150299 3'  CAGAACCTGCATCTTTGTCA   84968         CA   _
                                TGACAGAGA  CAG TTTTG
                                |||||||||  ||| |||||
                                ACTGTTTCT  GTC AAGAC
                                     AC   C
GAM375  LOC153277 3'  TAAAACTGTGCCTGTGCCA    85990     A  G  A
                                TG CA AG CACAGTTTTG
                                || || || ||||||||||
                                AC GT TC GTGTCAAAAT
                                 C  G  C
GAM375  LOC155179 3'  CAAAGCTGTATCTGCTATCA   81312      C  _   C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM375  LOC221074 3'  AAAGTGTGTCTCTTTCA     93177     C        G
                                TGA AGAGACACA TTT
                                ||| |||||||| |||
                                ACT TCTCTGTGT AAA
                                  T        G
GAM375  LOC221103 5'  AGTTTATGTGTGCTCTGTCA   93244         _     GTTTT
                                TGACAGAG ACACA     GCT
                                |||||||| |||||     |||
                                ACTGTCTC TGTGT     TGA
                                     G     ATT__
GAM375  LOC255988 5'  CAGAGCCCAGCATCCATCTCTG 97608          CACA_   TT
           TCA                    TGACAGAGA     GTT  GCTCTG
                                |||||||||     |||  ||||||
                                ACTGTCTCT     CGA  CGAGAC
                                     ACCTA   CC
GAM376  ABCC11    3'  GTGGGGATTGCTGGATGGA    52506     _     TG CGTTC
                                TCC TCCAG  G     TTTTTAC
                                ||| |||||  |    |||||||
                                AGG AGGTC  T     AGGGGTG
                                  T    GT _____
GAM376  ABCD1     5'  CCCCGGGGAGGGGCGCCACCGG 3462        A           ACT
           GGGA                    TCCTCC GTGGCGTTCTTTTT
                                |||||| ||||||||||||||
                                AGGGGG CACCGCGGGGAGGG
                                   C           GCCCCG
GAM376  ACVR1     5'  GTGAGAGCTGCTGGAG      6611        TG  GTTCT
                                CTCCAG  GC     TTTTAC
                                ||||||  ||     ||||||
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                                GAGGTC  CG    AGAGTG
                                   GT _____
GAM376  ADCY8    5'  AGTAAAGAGGCTCCTGTAGGA  6649      C   TG  GTT
                                TCCT CAG  GC   CTTTTTACT
                                |||| |||  ||   |||||||||
                                AGGA GTC  CG   GAGAAATGA
                                  T  CT  ___
GAM376  ADRA2B   3'  AGTGGGGCCTGCTGCTGAGGGG 5458      _   TG  __    TTTTACT
           G                     CCTC CAG  GC  GTTCT
                                |||| |||  ||  |||||
                                GGGG GTC  CG  CGGGG
                                  A  GT  TC    TGA   T
GAM376  AGPAT2   3'  GGTGGAAGCCGATGGCTGGAGG 65825       ____  G   TTTTACT
           A                     CTCCAGT    GGC TTCT
                                |||||||    ||| ||||
                                GAGGTCG    CCG AAGG
                                   GTAG  _   TGG   T
GAM376  AGPAT2   3'  GGTGGAAGCCGATGGCTGGAGG 21157       ____  G   TTTTACT
           A                     CTCCAGT    GGC TTCT
                                |||||||    ||| ||||
                                GAGGTCG    CCG AAGG
                                   GTAG  _   TGG   T
GAM376  AMFR     3'  AGTGGGAAGAGTGTGGGGGAGG 6694       AGTG
                                CCTCC    GCGTTCTTTTTACT
                                |||||    ||||||||||||||
                                GGAGG    TGTGAGAAGGGTGA
                                  GGG_
GAM376  AMFR     3'  AGTGGGAAGAGTGTGGGGGAGG 57241      AGTG
                                CCTCC    GCGTTCTTTTTACT
                                |||||    ||||||||||||||
                                GGAGG    TGTGAGAAGGGTGA
                                  GGG_
GAM376  AMN      3'  GTGAGGGGAGGGTGAGGA    48193      CAGTG  G
                                TCCTC    GC TTCTTTTTAC
                                |||||    || ||||||||||
                                AGGAG    TG GAGGGGAGTG
                                  _____  G
GAM376  ANK1     3'  AGGAGCCGTTAGGGGA     60386      C     G
                                TCCTC AGTGGC TTCT
                                ||||| |||||| ||||
                                AGGGG TTGCCG AGGA
                                  A    _
GAM376  ANK1     3'  AGGAGCCGTTAGGGGA     3470       C     G
                                TCCTC AGTGGC TTCT
                                ||||| |||||| ||||
                                AGGGG TTGCCG AGGA
                                  A    _
GAM376  ANK1     3'  AGGAGCCGTTAGGGGA     40024      C     G
                                TCCTC AGTGGC TTCT
                                ||||| |||||| ||||
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                                AGGGG TTGCCG AGGA
                                  A    _
GAM376  ANKRA2   5'  AGTAGGAGGTGTGACCGGAGGG 43525      A  G   TT
                                TCCTCC GT GCG  CTTTTTACT
                                |||||| || |||  |||||||||
                                GGGAGG CA TGT  GGAGGATGA
                                   C  G  __
GAM376  AQP2     3'  GGTAAGAGGGAAACTCTGGAG  4910       T  CG
                                CTCCAG GG  TTCTTTTTACT
                                |||||| ||  ||||||||||
                                GAGGTC TC  AGGGAGAATGG
                                   _ AA
GAM376  ARHGEF5  3'  GGTGGGGGGGATTTCGAGGGA  18364     AG   C
                                TCC  TGG GTTCTTTTTACT
                                |||  ||| ||||||||||
                                AGG  GCT TAGGGGGGGTGG
                                  GA   T
GAM376  ASB2     3'  GGTAGGGGGAGCCTGGGTCTTG 32358      T  _____
           GAGGG                  CCAG GGC    GTTCTTTTTACT
                                |||| |||    ||||||||||
                                GGTT CTG    CGAGGGGGATGG
                                  _  GGTC
GAM376  ATP1A2   3'  AGGGCTGGCTGGAGGA      5520          GGC
                                TCCTCCAGT   GTTCT
                                |||||||||   |||||
                                AGGAGGTCG   CGGGA
                                     GT_
GAM376  ATP1B1   3'  GGTGGGGGTTTGTCATGGGGGA 8042         G    TT    T
                                TCCTCCA TGGCG  CTTTT ACT
                                ||||||| |||||  ||||| |||
                                AGGGGGT ACTGT  GGGGG TGG
                                   _    TT    _
GAM376  ATP2B2   5'  GAGGGTGTGCTGAGGA      8066        C    G  TT
                                TCCTC AGTG CG  CTT
                                ||||| |||| ||  |||
                                AGGAG TCGT GT  GAG
                                   _   _  GG
GAM376  ATP5G3   5'  GGTGGGAAGAACAGGCCCCTGG 8075         T  __
           AGGG                   CCTCCAG GGC  GTTCTTTTTACT
                                ||||||| |||  ||||||||||||
                                GGAGGTC CCG  CAAGAAGGGTGG
                                   C   GA
GAM376  ATP6V1A1 3'  GGCCTGCTATTGAGGA      8081        C      TT
                                TCCTC AGTGGCG  CT
                                ||||| |||||||  ||
                                AGGAG TTATCGT  GG
                                   _      CC
GAM376  AXL      5'  GGAGTTCTGGAGGA       8104          T   G
                                TCCTCCAG GGC TTC
                                |||||||| ||| |||
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                                AGGAGGTC TTG AGG
                                   _  _
GAM376  AXL     5'  GGAGTTCTGGAGGA       41601        T  G
                                TCCTCCAG GGC TTC
                                |||||||| ||| |||
                                AGGAGGTC TTG AGG
                                   _  _
GAM376  BAIAP3   3'  AGTGAAAAGGGTGCCACTGG   14122         TT
                                CCAGTGGCG  CTTTTTACT
                                |||||||||  |||||||||
                                GGTCACCGT  GAAAAGTGA
                                     GG
GAM376  BAK1     3'  AGTAGGGAGTTCATCTGGAGGG 91987         _  CGTT
                                TCCTCCAG TGG    CTTTTTACT
                                |||||||| |||    |||||||||
                                GGGAGGTC ACT    GAGGGATGA
                                     T  T___
GAM376  BAT5     3'  GTGAGAGGAGACATGAGGA   40967      CA  GCGT
                                TCCTC  GTG    TCTTTTTAC
                                |||||  |||    |||||||||
                                AGGAG  TAC    AGGAGAGTG
                                   __  AG__
GAM376  BAZ1B    3'  AGTGGTCAGTGTCGGTGGGGGG 50537       G    TT  TT
                                TCCTCCA TGGCG  CT  TTACT
                                ||||||| |||||  ||  |||||
                                GGGGGGT GCTGT  GA  GGTGA
                                    G    __ CT
GAM376  BMP1     3'  GGAGTCCCTGGGGGA      20424        T  G
                                TCCTCCAG GGC TTC
                                |||||||| ||| |||
                                AGGGGGTC CTG AGG
                                     C  _
GAM376  BRCA2    3'  GGTGGGAGGAGTGCTTGAGG   3551      CAGT
                                CCTC    GGCGTTCTTTTTACT
                                ||||    ||||||||||||||||
                                GGAG    TCGTGAGGAGGGTGG
                                  T___
GAM376  BTEB1    3'  GGTAGGGAGTGGGTGGGGGG   6849        GTGGCGTT
                                TCCTCCA       CTTTTTACT
                                |||||||       |||||||||
                                GGGGGGT       GAGGGATGG
                                    GGGT____
GAM376  CALM2    5'  AGTGGAGAGAGCGAGCTGAGTG 8226     TC_   GG
           G                     CC   CAGT  CGTTCTTTTTACT
                                ||   ||||  ||||||||||||
                                GG   GTCG  GCGAGAGAGGTGA
                                 TGA   A_
GAM376  CARP     3'  AGTGAAGAGAACGTCATGAG   26898     CA
                                CTC  GTGGCGTTCTTTTTACT
                                |||  |||||||||||||||||
```

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                              GAG  TACTGCAAGAGAAGTGA
                                ___
GAM376  CARPX    5'  GGTGAGGGGGGCGGACTTCGAG 39424      C_  GG
            GG                  TCCTC  AGT  CGTTCTTTTTACT
                              |||||  |||  ||||||||||||
                              GGGAG  TCA  GCGGGGGGAGTGG
                                CT   G_
GAM376  CCNG1    3'  TGGTATTGAAAATGCTATTGGA 14486            C  TT
            GGA                 TCCTCCAGTGGCGTT TT  TACT
                              |||||||||||||| ||  ||||
                              AGGAGGTTATCGTAA AG  ATGG
                                      A  TT   TG
GAM376  CDC6     5'  GGTGGAAAGAAGAGGATTGCTC 6985     C  TG CG___
            GAGGA                 TC AG  G    TTCTTTTTACT
                              || ||  |    ||||||||||
                              AG TC  T    AAGAAAGGTGG
                               C  GT AGGAG
GAM376  CDH7     5'  GGGCTGTGATTGGAGGA     15152         G  _
                              TCCTCCAGT GC GTTC
                              |||||||| || ||||
                              AGGAGGTTA TG CGGG
                                   G  T
GAM376  CDX2     5'  AGTGGGAAGGAGGTGGGAGGA  7009        AGTG  G
                              TCCTCC    GC TTCTTTTTACT
                              ||||||    || ||||||||||
                              AGGAGG    TG AGGAAGGGTGA
                                 G___  G
GAM376  CFTR     3'  TAAGGGGAATTGAGGA      4929       CAGTGGC
                              TCCTC      GTTCTTTTTA
                              |||||      ||||||||||
                              AGGAG      TAAGGGGAAT
                                 T_______
GAM376  CGB      5'  AGTGAGAGGAGAGGGCTGGGG  5599        GGCG
                              CTCCAGT    TTCTTTTTACT
                              |||||||    ||||||||||
                              GGGGTCG    GAGGAGAGTGA
                                  GGA_
GAM376  CHC1     3'  GGTGGGGAGAGAGGGTGGAGGG 7023         GTGGCG
                              TCCTCCA     TTCTTTTTACT
                              |||||||     ||||||||||
                              GGGAGGT     GAGAGGGGTGG
                                  GGGA__
GAM376  CHST5    3'  GGTGGAGAGGGAGCTGGGG   24030        GGCGT
                              CTCCAGT     TCTTTTTACT
                              |||||||     ||||||||||
                              GGGGTCG     GGAGAGGTGG
                                  AG___
GAM376  CHST6    3'  GGTAGGAGGAGAGAAGGCTGGG 41232     T    GGCG_
            GA                  TCC CCAGT    TTCTTTTTACT
                              ||| |||||     ||||||||||
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                                AGG GGTCG    GAGGAGGATGG
                                  _    GAAGA
GAM376  CHST6    3'  GGTGAGAAGGAGGATGAAGGG  41233     C  GTGGCG
                                TCCT CA     TTCTTTTTACT
                                |||| ||     ||||||||||
                                GGGA GT     AGGAAGAGTGG
                                  A  AGG___
GAM376  CKTSF1B1 3'  TGAAAAATCTGGAGGA     25371        TGGCGTTC
                                TCCTCCAG       TTTTTA
                                ||||||||       ||||||
                                AGGAGGTC       AAAAGT
                                    TA_______
GAM376  CLN5     5'  GGTAAAAGTTCGGTGTTGGGAG 21431       _ GT G  TT    T
            GA                    TCCTCC A  G CG  CTTTT ACT
                                ||||||  |  | ||  ||||| |||
                                AGGAGG T  T GC  GAAAA TGG
                                   G TG G  TT    _
GAM376  CLN6     3'  GGTGGGAGGGTGGGCCATGGAG 35410       G    GT_
            GG                    TCCTCCA TGGC   TCTTTTTACT
                                ||||||| ||||  ||||||||||
                                GGGAGGT ACCG   GGGAGGGTGG
                                   _   GGT
GAM376  CLN6     3'  GTAGGGGGGGTGTGGG     35411     AGTG   TT
                                TCC    GCG  CTTTTTAC
                                |||    |||  ||||||||
                                GGG    TGT  GGGGGATG
                                  _____  GG
GAM376  CNN1     3'  GGGGGGCCCATTGGGGGG    7116           C
                                TCCTCCAGTGG GTTCTTT
                                |||||||||| |||||||
                                GGGGGGTTACC CGGGGGG
                                        _
GAM376  CNN2     3'  AGTGGAGAGAGTGCTAGGA   15174     AG
                                TCC  TGGCGTTCTTTTTACT
                                |||  ||||||||||||||||
                                AGG  ATCGTGAGAGAGGTGA
                                  __
GAM376  COL4A6   3'  AGTAGAGGGGGTGGGTGCGTAG 53317      CCA  GG_  TT
            GA                    TCCT   GT   CG  CTTTTTACT
                                ||||   ||   ||  |||||||||
                                AGGA   CG   GT  GGGAGATGA
                                  TG_  TGG  GG
GAM376  COL5A3   3'  GGTGGGAGGGACCGTGAGGG   31696      CAGTG  _
                                TCCTC     GCG TTCTTTTTACT
                                |||||     ||| ||||||||||
                                GGGAG     TGC AGGGAGGGTGG
                                  ______  C
GAM376  COMP     3'  AGTGAGAAGGGCTCAGAGAGGA 3635       CAG   C
                                TCCTC   TGG GTTCTTTTTACT
                                |||||   ||| ||||||||||
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                                AGGAG   ACT CGGGAAGAGTGA
                                  AG_  _
GAM376  CRYZL1   5'  GGTGAAGGTGCAGGCCGTTGGG 17580          __  TC
            G                    CTCCAGTGGC  GT  TTTTTACT
                                 ||||||||||  ||  ||||||||
                                 GGGGTTGCCG  CG  GGAAGTGG
                                      GA  T_
GAM376  CSF1R    5'  GTGAGGAGAAGGTGGAG     17803      AGTG  G
                                 CTCC    GC TTCTTTTTAC
                                 ||||    || ||||||||||
                                 GAGG    TG AAGAGGAGTG
                                   ____  G
GAM376  CST      3'  GGTGAGGGGGGGCTCCCTGGGG 16791         T  C      _
            GG                    TCCTCCAG GG GTTCTTT TTACT
                                  |||||||| || ||||||| |||||
                                  GGGGGGTC CC CGGGGGG AGTGG
                                      _ T      G
GAM376  CTSH     3'  GGTGGAAATCCTGCCCTGGAGG 15248         T    TTC
            A                     TCCTCCAG GGCG   TTTTTACT
                                  |||||||| ||||   ||||||||
                                  AGGAGGTC CCGT   AAAGGTGG
                                      _   CCT
GAM376  CYP19    5'  GGAGTGTTCTTGGGGGGG     48336         TG
                                 TCCTCCAG  GCGTTCT
                                 ||||||||  |||||||
                                 GGGGGGTT  TGTGAGG
                                      CT
GAM376  CYP51    3'  GGTGAAACAATTGTTGAGGGGG 5786        AG     TTCT
                                 CCTCC  TGGCG    TTTTACT
                                 |||||  |||||    |||||||
                                 GGGGG  GTTGT    AAAGTGG
                                   A_    TAAC
GAM376  DAXX     5'  AGTGGGAAGGAAGGCGGAGGG  7212        AGTG  G_
                                 TCCTCC    GC  TTCTTTTTACT
                                 ||||||    ||  ||||||||||
                                 GGGAGG    CG  AGGAAGGGTGA
                                     ____  GA
GAM376  DDAH2    5'  AGTGGGGGTGGCCGCTGGAG   25661          _ TT  TTT
                                 CTCCAGTGGC G  CT   TACT
                                 |||||||||| |  ||   ||||
                                 GAGGTCGCCG T  GG   GTGA
                                      G GG  ___
GAM376  DGAT2    5'  ACCTAGAGGATGCCACTAGAGG 50786       C           TTACT
            A                     TCCTC AGTGGCGTTCTTT
                                  ||||| ||||||||||||
                                  AGGAG TCACCGTAGGAGA
                                    A           TCCA
GAM376  DLG4     5'  GGTGAGAGGAGGCCCAGGAGGA 7256        AGT   G
                                 TCCTCC   GGC TTCTTTTTACT
                                 ||||||   ||| ||||||||||
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                                AGGAGG   CCG GAGGAGAGTGG
                                   AC_   _
GAM376  DPYS     5'  GGTGGGGACCTTGCAGGAGGG  7285        A TG C     TTT
                                TCCTCC G  G GTTCT   TACT
                                |||||| |  | |||||   ||||
                                GGGAGG C  T CAGGG   GTGG
                                   A GT C    ____
GAM376  DPYSL3   3'  AGTGGAAAGGGTGTTTGGGA   7310      AGT    TT
                                TCC   GGCG  CTTTTTACT
                                |||   ||||  |||||||||
                                AGG   TTGT  GAAAGGTGA
                                  GT_   GG
GAM376  DSCR1    3'  GGTAAGAGGGAGCCGGTTTGGG 15336    CT   __    G
            AGA                    C  CCAG  TGGC TTCTTTTTACT
                                |  ||||  |||| ||||||||||
                                G  GGTT  GCCG AGGGAGAATGG
                                 AG    TG   _
GAM376  DTR      3'  AGAGTGCCACTGCGGGA     8688       C
                                TCCT CAGTGGCGTTCT
                                |||| ||||||||||||
                                AGGG GTCACCGTGAGA
                                   C
GAM376  ELK1     3'  GGTGGGAAGGAAGGGATTTGGG 17844         TGGCG_
            GGG                    TCCTCCAG     TTCTTTTTACT
                                ||||||||     ||||||||||
                                GGGGGGTT     AGGAAGGGTGG
                                     TAGGGA
GAM376  EPB49    3'  GTGAGAGGAATGAGGGG     8790       AGTGG
                                CTCC     CGTTCTTTTTAC
                                ||||     ||||||||||||
                                GGGG    GTAAGGAGAGTG
                                  A____
GAM376  EPHA1    3'  AGTAAAAGGATGATCATGGGAG 17858        A   _   T
            GG                    TCCTCC GTGG CGT CTTTTTACT
                                |||||| |||| ||| |||||||||
                                GGGAGG TACT GTA GGAAAATGA
                                   G   A   _
GAM376  EPHB2    3'  AGTAAAAGGGATACAGGGGA   15441      CAG  GC
                                TCCTC   TG  GTTCTTTTTACT
                                |||||   ||  ||||||||||||
                                AGGGG   AC  TAGGGAAAATGA
                                   ___  A_
GAM376  EPHB6    5'  AGAAAAAGGGGTGGCTGTTGGA 15464         TG  _ TT     ACT
            GGA                    TCCTCCAG  GC G  CTTTTT
                                |||||||  || |  ||||||
                                AGGAGGTT  CG T  GGAAAA
                                     GT  G GG     AGA
GAM376  ERBB2IP  3'  GGTGAAGGTGGTGCTGGTGGG  37986     T     G  TTC
                                TCC CCAGTG CG   TTTTTACT
                                ||| |||||| ||   ||||||||
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                                GGG GGTCGT GT   GGAAGTGG
                                  T     G ___
GAM376  EXTL3    3'  GAATGTCACTGGTGGA      7531      T
                                TCC CCAGTGGCGTTC
                                ||| ||||||||||||
                                AGG GGTCACTGTAAG
                                  T
GAM376  EZH1     3'  AGTAGAAAGGGTGTGGGCGGG  8812      T  AGTG   TT
                                TCC CC    GCG  CTTTTTACT
                                ||| ||    |||  |||||||||
                                GGG GG    TGT  GAAAGATGA
                                  C  G___   GG
GAM376  F2RL3    3'  TGGTGGGGGTGGACAGTGTGTG 14196      ___ _   _
           CTGGGGGG                  AGTG   GC GTTC TTTTTACT   G
                                ||||   || |||| ||||||||   |
                                TCGT   TG CAGG GGGGGTGG   T
                                  GTG  A    T
GAM376  FCN2     3'  GGTAAAAGTCCAGGCCTTTGGG 31733         T   GTTC_
           GGA                     TCCTCCAG GGC     TTTTTACT
                                |||||||| |||     ||||||||
                                AGGGGGTT CCG     GAAAATGG
                                     T   GACCT
GAM376  FCN2     3'  GGTAAAAGTCCAGGCCTTTGGG 31743         T   GTTC_
           GGA                     TCCTCCAG GGC     TTTTTACT
                                |||||||| |||     ||||||||
                                AGGGGGTT CCG     GAAAATGG
                                     T   GACCT
GAM376  FCN2     3'  GGTGGGGGGTGACACTGGGAGG  31744       _   G  TT  TTT
                                CCTCC AGTG CG  CT   TACT
                                ||||| |||| ||  ||   ||||
                                GGAGG TCAC GT  GG   GTGG
                                  G    A  GG  ___
GAM376  FGF2     5'  AGTAGGGGGCGGCGCGCAGGAG 8867         A   G   _
           GG                      TCCTCC GTG CGTT CTTTTTACT
                                |||||| ||| |||| |||||||||
                                GGGAGG CGC GCGG GGGGGATGA
                                   A   _   C
GAM376  FOSB     3'  GGTGGGAGGTAGGCTGTGGGG  22109       G    GTT
                                CTCCA TGGC   CTTTTTACT
                                ||||| ||||   |||||||||
                                GGGGT GTCG   GGAGGGTGG
                                   _   GAT
GAM376  FRZB     5'  TGGTAAAGCTCGTGGGACCCCA 7593        C    _____
           TTGGGGGA                 AGTGG GTTCT     TTTTACT   G
                                ||||| |||||     |||||||   |
                                TTACC CAGGG     GAAATGG   T
                                  C     TGCTC
GAM376  GEM      5'  AGTAAGGGGGACGGCCCGAG   17928     CAGT   _
                                CTC    GGC GTTCTTTTTACT
                                |||    ||| ||||||||||||
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                                GAG   CCG CAGGGGGAATGA
                                  C___  G
GAM376  GJB1     3'  GGTAAGAGGAGCAGAGGGCAGG 59972     _  AGTGGC
                G                  TCCT CC     GTTCTTTTTACT
                                   |||| ||     ||||||||||||
                                   GGGA GG     CGAGGAGAATGG
                                     C  GAGA__
GAM376  GLUL     3'  AGTGGGGAGGAGGGTGGGGAG  9040      AGTG  G     _
                                   CTCC    GC TTCTTTTT ACT
                                   ||||    || |||||||| |||
                                   GAGG    TG GAGGAGGG TGA
                                     GG__  G       G
GAM376  GNPI     3'  AGTGGGAGGTCCACTGGGG    18444        CGTT
                                   CTCCAGTGG    CTTTTTACT
                                   |||||||||    |||||||||
                                   GGGGTCACC    GGAGGGTGA
                                        T___
GAM376  GPT      3'  GTGGGGGGGGTGCTGGG     17966      GTG   TT
                                   TCCA   GCG  CTTTTTAC
                                   ||||   |||  ||||||||
                                   GGGT   CGT  GGGGGGTG
                                     ___   GG
GAM376  GSS      3'  GGTAGGAGGAGGGGGAGTGGAG 3931        GTGGCG
                GG                   TCCTCCA     TTCTTTTTACT
                                     |||||||     ||||||||||
                                     GGGAGGT     GAGGAGGATGG
                                        GAGGGG
GAM376  GTF2IRD1  5'  GGGGCGCCGCTGGCAGGA    32894     _
                                   TCCT CCAGTGGCGTTCT
                                   |||| ||||||||||||
                                   AGGA GGTCGCCGCGGGG
                                     C
GAM376  GZMM     3'  GGTGGGAGGGACAGGGAGGG   18012       AGTGGC
                                   TCCTCC     GTTCTTTTTACT
                                   ||||||     ||||||||||||
                                   GGGAGG     CAGGGAGGGTGG
                                      GA____
GAM376  HDGF     3'  GGTGGGGGCAGCACAGGAGGG  15684       A   GC    TTT
                                   TCCTCC GTG  GTTCT   TACT
                                   |||||| |||  |||||   ||||
                                   GGGAGG CAC  CGGGG   GTGG
                                      A   GA    ___
GAM376  HK2      3'  GGTGGAGGGGTGACAGTGGAGG 3953        G  GCGT
                A                   TCCTCCA TG    TCTTTTTACT
                                    |||||||  ||    ||||||||||
                                    AGGAGGT AC    GGGGAGGTGG
                                       G  AGT_
GAM376  HKE4     3'  GGTGCTGGGGCTGCTGGGGGG  22731        TG  GTT   TT
                                   TCCTCCAG  GC   CTT  TACT
                                   ||||||||  ||   |||  ||||
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                                GGGGGGTC  CG   GGG  GTGG
                                    GT  ___   TC
GAM376  HOXB13   3'  GGTGGGAGGAGCGAAAGTGGGG 21013       GTGG
            G                    CCTCCA   CGTTCTTTTTACT
                                 ||||||   ||||||||||||
                                 GGGGGT   GCGAGGAGGGTGG
                                    GAAA
GAM376  HOXB13   5'  GGTGGGGAGAGCGAGCTGGG  21014       GG
                                 TCCAGT  CGTTCTTTTTACT
                                 ||||||  ||||||||||||
                                 GGGTCG  GCGAGAGGGGTGG
                                    A_
GAM376  HOXB9    3'  GTGGGGAGGGCGAGGGG    43778      AGTGG
                                 CTCC    CGTTCTTTTTAC
                                 ||||    ||||||||||||
                                 GGGG    GCGGGAGGGGTG
                                   A____
GAM376  HPCA     5'  GGTGTCTCCGCGTCGCTGGGTG 9256     _         TCTTTT
            G                    CC TCCAGTGGCGT     TACT
                                 || ||||||||||      ||||
                                 GG GGGTCGCTGCG     GTGG
                                  T         CCTCT_
GAM376  HSD17B1  5'  GGTGGGGAGAGCGGGCCAGGGA 4689      AG   __
                                 TCC  TGGC  GTTCTTTTTACT
                                 |||  ||||  ||||||||||||
                                 AGG  ACCG  CGAGAGGGGTGG
                                   G_   GG
GAM376  IER3     3'  GGTAGAGGGGTGGGGGTTGGTG 13997     T    TGGCGT
            GG                     TCC CCAG     TCTTTTTACT
                                 ||| ||||     ||||||||||
                                 GGG GGTT     GGGGAGATGG
                                   T   GGGGGT
GAM376  IFNW1    5'  AGTAAGGAGGGTAAAAATGGAG 9299        GTGGC TT
            G                    CCTCCA    G  CTTTTTACT
                                 ||||||    |  |||||||||
                                 GGAGGT    T  GAGGAATGA
                                    AAAAA GG
GAM376  IL1F5    3'  GTGAGGGGTGAGTGGAGGA   24383       GTGG  TT  TT
                                 TCCTCCA   CG  CT  TTAC
                                 |||||||   ||  ||  ||||
                                 AGGAGGT   GT  GG  AGTG
                                     GA__  GG  __
GAM376  IL1RAP   3'  GTAAAAAGAACAAGGGG    9314      AGTGGC
                                 CTCC     GTTCTTTTTAC
                                 ||||     ||||||||||
                                 GGGG     CAAGAAAAATG
                                   AA____
GAM376  INHBA    3'  AGTGAAGAGACAGATTGGGAGG 9337        AGTGGCGT
            G                    TCCTCC       TCTTTTTACT
                                 ||||||       ||||||||||
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                                GGGAGG       AGAGAAGTGA
                                   GTTAGAC_
GAM376  JAM3     3'  GGTAAATTGGTTGCTGGAAGA  51425    C    TG  GTT TT
                                TC TCCAG  GC   C  TTTACT
                                || |||||  ||   |  ||||||
                                AG AGGTC  TG   G  AAATGG
                                 A    GT  ___ TT
GAM376  JUN      5'  GGTGAGGAGGGCGCAGCGGGGA 9480      T  A  G
                                TCC CC GT GCGTTCTTTTTACT
                                ||| || || ||||||||||||||
                                AGG GG CG CGCGGGAGGAGTGG
                                  _ _ A
GAM376  KCNA7    3'  GGTGGAGGGCAAGGCTGGGGGG 49059       AGT   G  _
           A                     TCCTCC   GGC TT CTTTTTACT
                                ||||||   ||| || |||||||||
                                AGGGGG   TCG AA GGGAGGTGG
                                   G__   G  C
GAM376  KCND2    5'  AGTGAAGGGGCGATTGGGCGA  24392    C     G  GTT
                                TC TCCAGT GC   CTTTTTACT
                                || ||||||| ||   |||||||||
                                AG GGGTTA CG   GGGAAGTGA
                                 C     G  ___
GAM376  KCNH2    3'  AGTGAGAGGGGCAGGGGCAGGG 4093       _  AGTGGC
                                TCCT CC      GTTCTTTTTACT
                                |||| ||      ||||||||||||
                                GGGA GG     CGGGGAGAGTGA
                                  C  GGA___
GAM376  KCNK4    5'  GTAAGGGGAAGGCTGGAG    52808       GTG  G
                                CTCCA   GC TTCTTTTTAC
                                |||||   || ||||||||||
                                GAGGT   CG AAGGGGAATG
                                   ___  G
GAM376  KCNN3    5'  GGGGGCTTGTGCTGCAGGG   9562       C   ___   G
                                TCCT CAGT   GGC TTC
                                |||| ||||   ||| |||
                                GGGA GTCG   TCG GGG
                                  C    TGT   G
GAM376  KISS1    3'  GTGGGGGGGACGTAGGG     9613     AGTG
                                CC    GCGTTCTTTTTAC
                                ||    ||||||||||||
                                GG    TGCAGGGGGGGTG
                                 GA__
GAM376  KITLG    5'  AGTGGAGAGGGCGCTGCGCTCG 6128      TCCA TG
             GG                   TCC    G  GCGTTCTTTTTACT
                                |||    |  ||||||||||||||
                                GGG    C  CGCGGGAGAGGTGA
                                  CTCG GT
GAM376  KITLG    5'  AGTGGAGAGGGCGCTGCGCTCG 14340     TCCA TG
             GG                   TCC    G  GCGTTCTTTTTACT
                                |||    |  ||||||||||||||
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                                GGG   C  CGCGGGAGAGGTGA
                                  CTCG GT
GAM376  KLF8    5'  GTAAAAGGGGAACGGAGGA   23406       A  GGCGT
                                TCCTCC GT    TCTTTTTAC
                                ||||||  ||    |||||||||
                                AGGAGG CA    GGGAAAATG
                                   _  AG___
GAM376  KNSL2   3'  GGTGAGGGGTGGGAGGGTTGCT 73850     TG  G    ____
           GGAGGG                  CCAG  GC TTCTT   TTTACT
                                ||||  || |||||   ||||||
                                GGTC  TG GAGGG   GAGTGG
                                  GT  G    TGGG
GAM376  KNSL2   3'  GGTGGGAGGGTTGCTGGAGGG  73851        TG  G   TTT
                                TCCTCCAG  GC TTCT   TACT
                                ||||||||  || ||||   ||||
                                GGGAGGTC  TG GAGG   GTGG
                                     GT  G   ___
GAM376  KRT16   5'  GGTGCGTGCTCTGGAGGA    95199        TG_   T
                                TCCTCCAG   GCGT CT
                                ||||||||   |||| ||
                                AGGAGGTC   TGCG GG
                                     TCG   T
GAM376  LAMC2   3'  GTGGGAATTGCTGGAGGA    18714        TG CGTTC
                                TCCTCCAG  G    TTTTTAC
                                ||||||||  |    |||||||
                                AGGAGGTC  T    AAGGGTG
                                     GT _____
GAM376  LANGERIN 3' AGTGGGAGGGGTGGGTAGAGAG 31689      CAGTGG  TT
           GA                    TCCTC     CG  CTTTTTACT
                                |||||     ||  |||||||||
                                AGGAG     GT  GGAGGGTGA
                                   AGATGG  GG
GAM376  LFG     3'  GGATGTTCTGGGGGA       76725         T
                                TCCTCCAG GGCGTTC
                                |||||||| |||||||
                                AGGGGGTC TTGTAGG
                                        _
GAM376  LFG     3'  GTAGGAAGGGCAGGGGA     76726       CAGTGGC
                                TCCTC      GTTCTTTTTAC
                                |||||      ||||||||||
                                AGGGG      CGGGAAGGATG
                                   A_______
GAM376  LIMK1   3'  GGTGAAGGGGGTCCCTTGAGGG 33650       C  T  C TT
                                TCCTC AG GG G  CTTTTTACT
                                ||||| || || |  |||||||||
                                GGGAG TC CC T  GGGAAGTGG
                                   T  _  _ GG
GAM376  LIMK1   3'  GGTGAAGGGGGTCCCTTGAGGG 9788        C  T  C TT
                                TCCTC AG GG G  CTTTTTACT
                                ||||| || || |  |||||||||
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                                GGGAG TC CC T  GGGAAGTGG
                                   T  _  _ GG
GAM376  LPL     3'  GGTGGAGAGGTTCCTGGGGTGG 4090     _     TG  GTT
                                TC CTCCAG  GC   CTTTTTACT
                                || ||||||  ||   |||||||||
                                GG GGGGTC  TG   GAGAGGTGG
                                 T     CT  ___
GAM376  MADH6   5'  AGTAAGAAGGGAGCTGGGGG   18764        GGCGT
                                CCTCCAGT    TCTTTTTACT
                                ||||||||    ||||||||||
                                GGGGGTCG    GGAAGAATGA
                                     AG___
GAM376  MAFF    3'  GGCTTAGAGAACAGCTGTTGGG 24652        TG  _      TTACT
           GGA                     TCCTCCAG  GC GTTCTTT
                                ||||||||  || |||||||
                                AGGGGGTT  CG CAAGAGA
                                     GT  A      TTCGG
GAM376  MAGEA8  3'  GGGGCAGGTTGTGGGAGGG   18106       A TG  __
                                TCCTCC G  GC  GTTCT
                                ||||||  |  ||  |||||
                                GGGAGG T  TG  CGGGG
                                   G GT  GA
GAM376  MAGEB3  3'  AGTGAAGGACTGGGTGTTACTG 9886          TT ___
           GAGGG                   TCCAGTGGCG  C   TTTTTACT
                                |||||||||| |   ||||||||
                                AGGTCATTGT  G   GGAAGTGA
                                     GG TCA
GAM376  MAGEB3  3'  GGGTGTTACTGGAGGG      9887            TT
                                TCCTCCAGTGGCG  C
                                ||||||||||||  |
                                GGGAGGTCATTGT  G
                                       GG
GAM376  MAP3K12  3'  GGTGGGGGGAGGGGCGGTGGGA 20863       AG G  G _
           GGG                     TCCTCC  T GC T TCTTTTTACT
                                ||||||  | || | ||||||||||
                                GGGAGG  G CG G AGGGGGGTGG
                                   GT G  G G
GAM376  MAP3K12  3'  GTGGGAGGGGCAGGAGAGA   20864    _   AGTGGC
                                TC CTCC     GTTCTTTTTAC
                                || ||||     ||||||||||||
                                AG GAGG     CGGGGAGGGTG
                                 A   A_____
GAM376  MBP     3'  GGTGAACTCAGCCATTAGAGGA 89781       C     GTTCTT
                                TCCTC AGTGGC     TTTACT
                                ||||| ||||||     ||||||
                                AGGAG TTACCG     AAGTGG
                                   A     ACTC__
GAM376  MEN1    5'  TGAGACCTCTGGAGGA      93381         T  CGTTCT
                                TCCTCCAG GG     TTTTA
                                |||||||| ||     |||||
```

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                                AGGAGGTC CC     AGAGT
                                    T _______
GAM376  METTL1   3'  AGTGAAGACCCCGTTGTGGGA  43508    TC     C  CTT
                                TCC  CAGTGG GTT   TTTACT
                                |||  |||||| |||   ||||||
                                AGG  GTTGCC CAG   AAGTGA
                                  GT     C  ___
GAM376  METTL1   3'  AGTGAAGACCCCGTTGTGGGA  43514    TC     C  CTT
                                TCC  CAGTGG GTT   TTTACT
                                |||  |||||| |||   ||||||
                                AGG  GTTGCC CAG   AAGTGA
                                  GT     C  ___
GAM376  MGAT4B   5'  GGTAGCCCACCCGCTGGAGGG  53951          C  TCTTT
                                TCCTCCAGTGG GT    TTACT
                                ||||||||||| ||    |||||
                                GGGAGGTCGCC CA    GATGG
                                      _  CCC__
GAM376  MLLT7    3'  GTGGGGAGAGGTGGGGAG    19869      AGTG  G
                                CTCC    GC TTCTTTTTAC
                                ||||    || ||||||||||
                                GAGG    TG GAGAGGGGTG
                                  GG__  _
GAM376  MMP14    3'  AGTGGAGGGAGCAAGAGGAGAG 17168       CAGTGGC
          GG                    TCCTC      GTTCTTTTTACT
                                |||||      ||||||||||||
                                GGGAG      CGAGGGAGGTGA
                                   AGGAGAA
GAM376  MMP25    3'  GGTGGAATCAGTGGCTGGAGGG 42445         G  GTTCT
                                TCCTCCAGT GC     TTTTACT
                                |||||||||  ||    |||||||
                                GGGAGGTCG TG     AAGGTGG
                                     G  ACT__
GAM376  MMP26    3'  AGGGAGTTTATTGGAGGA    41437          CG
                                TCCTCCAGTGG  TTCTT
                                ||||||||||  |||||
                                AGGAGGTTATT  AGGGA
                                      TG
GAM376  MPDU1    3'  TGGAGGGACTGGGAGG      16828      AGTGG  T
                                CCTCC    CG TCTTTTTA
                                |||||    || ||||||||
                                GGAGG    GT AGGGAGGT
                                   _____  C
GAM376  MPP2     3'  GTGGGAAGGAAATGGGG     59828      GTGGCG
                                CTCCA     TTCTTTTTAC
                                |||||     ||||||||||
                                GGGGT     AGGAAGGGTG
                                   AA____
GAM376  MRC1     5'  GGTGGAGAGGCAGTTGGGGGG  10114        TG  GTT
                                TCCTCCAG  GC   CTTTTTACT
                                ||||||||  ||   |||||||||
```

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                              GGGGGGTT  CG   GAGAGGTGG
                                  GA  ___
GAM376  MTA1L1   3'  AGTGAGTGTGTGTCCCTGGAGG 16443        T   TTCTT
          G                    TCCTCCAG GGCG    TTTACT
                               |||||||| ||||    ||||||
                               GGGAGGTC CTGT    GAGTGA
                                  C   GTGT_
GAM376  MTR      3'  GTGGAAGGGACAGGAG     4214      AGTGGC
                               CTCC     GTTCTTTTTAC
                               ||||     ||||||||||
                               GAGG     CAGGGAAGGTG
                                 A_____
GAM376  MYCL2    3'  GGTGGTGGATGTTGTTGGGGG  18186       TG     TTT
                               CCTCCAG  GCGTTC   TTACT
                               |||||||  ||||||   |||||
                               GGGGGTT  TGTAGG   GGTGG
                                  GT     T__
GAM376  MYO10    3'  AGTGGGAAGGGGGATGGAG   24700      GTGGCG
                               CTCCA     TTCTTTTTACT
                               |||||     ||||||||||
                               GAGGT     GGGAAGGGTGA
                                 AGG___
GAM376  NCOA6    5'  AGTGAAAGGAAAATGAGGGGA  25954      _  GTGGCG
                               TCCTC CA     TTCTTTTTACT
                               ||||| ||     ||||||||||
                               AGGGG GT     AAGGAAAGTGA
                                 A  AA____
GAM376  NDRG3    3'  AGACAGAGAGTATTGCTGGAGG 49290        TG CG     TTACT
          G                    TCCTCCAG  G  TTCTTT
                               ||||||||  |  ||||||
                               GGGAGGTC  T  GAGAGA
                                  GT AT     CAGA
GAM376  NDST2    3'  GTGGGGAGGAATGAGAGGG   13297      CA  GGCG
                               TCCTC  GT   TTCTTTTTAC
                               |||||  ||   ||||||||||
                               GGGAG  TA   AGGAGGGGTG
                                 AG  _____
GAM376  NGFRAP1  5'  GGTAAGGGGAGAAAGCTGGAGG 26884         GGCG
          G                    TCCTCCAGT    TTCTTTTTACT
                               |||||||||    ||||||||||
                               GGGAGGTCG    GAGGGGAATGG
                                  AAA_
GAM376  NPTX1    3'  GGTGGGAAGGTCCTTTTTGGGG 10265        TGGCGT
          GA                    TCCTCCAG     TCTTTTTACT
                               ||||||||     ||||||||||
                               AGGGGGTT     GGAAGGGTGG
                                  TTTCCT
GAM376  NR0B2    3'  GGTGACCCAATGCTCCTGGAGG 41741        TG    CTTT
          G                    TCCTCCAG  GCGTT    TTACT
                               ||||||||  |||||    |||||
```

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                                GGGAGGTC  CGTAA   AGTGG
                                    CT    CCC_
GAM376  NRXN2   3'  GGGGAAGCTGCTGGAGGA   57016       TG  G
                                TCCTCCAG  GC TTCTTT
                                |||||||  || ||||||
                                AGGAGGTC  CG AAGGGG
                                    GT  _
GAM376  NRXN2   3'  GGTGGGAAGGAAGGCTGGGGG  57017       GGCG
                                CCTCCAGT   TTCTTTTTACT
                                |||||||   ||||||||||
                                GGGGGTCG   AGGAAGGGTGG
                                    GA__
GAM376  NRXN2   3'  GGGGAAGCTGCTGGAGGA   57027       TG  G
                                TCCTCCAG  GC TTCTTT
                                |||||||  || ||||||
                                AGGAGGTC  CG AAGGGG
                                    GT  _
GAM376  NRXN2   3'  GGTGGGAAGGAAGGCTGGGGG  57028       GGCG
                                CCTCCAGT   TTCTTTTTACT
                                |||||||   ||||||||||
                                GGGGGTCG   AGGAAGGGTGG
                                    GA__
GAM376  NRXN2   3'  GGGGAAGCTGCTGGAGGA   30630       TG  G
                                TCCTCCAG  GC TTCTTT
                                |||||||  || ||||||
                                AGGAGGTC  CG AAGGGG
                                    GT  _
GAM376  NRXN2   3'  GGTGGGAAGGAAGGCTGGGGG  30631       GGCG
                                CCTCCAGT   TTCTTTTTACT
                                |||||||   ||||||||||
                                GGGGGTCG   AGGAAGGGTGG
                                    GA__
GAM376  NUP98   3'  AGTGAATGCCTGTCACGGAGGG 32859      A    TTCTT
                                TCCTCC GTGGCG   TTTACT
                                |||||| ||||||   ||||||
                                GGGAGG CACTGT   AAGTGA
                                   _    CCGT_
GAM376  NYX     3'  GGTGAAAATCCCAGTGGAGGG  42604       G  CGTTC
                                TCCTCCA TGG   TTTTTACT
                                ||||||| |||   ||||||||
                                GGGAGGT ACC   AAAAGTGG
                                    G  CT___
GAM376  OASL    3'  GTGGGAGGAGCGCTTGAG   13581    CAGT
                                CTC   GGCGTTCTTTTTAC
                                |||   ||||||||||||||
                                GAG   TCGCGAGGAGGGTG
                                  T___
GAM376  OLIG2   3'  GGGGAGGGGGTGTTATGGGAGG 19413      A    TT    ACT
          G                      TCCTCC GTGGCG  CTTTTT
                                |||||| ||||||  ||||||
```

```
                                GGGAGG TATTGT  GGGAGG
                                   G     GG     GG
GAM376  OXTR     3'  GGTAGAAATTTAAATTGTTGGT 6214      _    TG CGTTC_
            GGGA                    CCT CCAG  G     TTTTTACT
                                ||| |||| |     ||||||||
                                GGG GGTT  T     AAAGATGG
                                  T   GT AAATTT
GAM376  PACSIN1  3'  AGTGAAAGGACCTTTGGGGG  92254       T  CGT
                                CCTCCAG GG   TCTTTTTACT
                                ||||||| ||   ||||||||||
                                GGGGGTT CC   AGGAAAGTGA
                                   T ___
GAM376  PAX2     3'  GCGCCAGGAGCTTCGCTGGAGG 14324          C     TTTACT
            G                    TCCTCCAGTGG GTTCTT
                                ||||||||||| ||||||
                                GGGAGGTCGCT CGAGGA
                                      T     CCGCGG
GAM376  PAX2     3'  GCGCCAGGAGCTTCGCTGGAGG 14333          C     TTTACT
            G                    TCCTCCAGTGG GTTCTT
                                ||||||||||| ||||||
                                GGGAGGTCGCT CGAGGA
                                      T     CCGCGG
GAM376  PAX7     5'  GGTAGGGAGTGTGTGTGGAGGG 10435       GTG   TT
                                TCCTCCA   GCG  CTTTTTACT
                                |||||||   |||  |||||||||
                                GGGAGGT   TGT  GAGGGATGG
                                   G__   GT
GAM376  PAX7     5'  GGTGAAGGGAGCGGACGGGA   10436     A  GG
                                TCC GT  CGTTCTTTTTACT
                                ||| ||  ||||||||||||
                                AGG CA  GCGAGGGAAGTGG
                                  G  G_
GAM376  PAX7     5'  GGTAGGGAGTGTGTGTGGAGGG 25639       GTG   TT
                                TCCTCCA   GCG  CTTTTTACT
                                |||||||   |||  |||||||||
                                GGGAGGT   TGT  GAGGGATGG
                                   G__   GT
GAM376  PAX7     5'  GGTGAAGGGAGCGGACGGGA   25640     A  GG
                                TCC GT  CGTTCTTTTTACT
                                ||| ||  ||||||||||||
                                AGG CA  GCGAGGGAAGTGG
                                  G  G_
GAM376  PBX2     3'  GGTGGGAGGCATGGGCCGGGGG 10447       A  GG   T
            G                    TCCTCC GT  CGT CTTTTTACT
                                ||||||| ||  ||| |||||||||
                                GGGGGG CG  GTA GGAGGGTGG
                                   C  G_   C
GAM376  PCTK1    5'  AGTAGGGGGAACGAGTGGTGA  52259    CT   GTGG
                                TC  CCA    CGTTCTTTTTACT
                                ||  |||    ||||||||||||
```

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                                AG  GGT   GCAAGGGGGATGA
                                 T_   GA__
GAM376  PDE4A    3'  GGTGGGGGGGCAGTCACTGTGGG 20587     TC      GTT
             A                   TCC  CAGTGGC   CTTTTTACT
                                 |||  |||||||   |||||||||
                                 AGG  GTCACTG   GGGGGGTGG
                                   GT      AC_
GAM376  PDGFRB   5'  AGTAAGGAGGACTTCCTGGAGG 65968         T  C
             G                   TCCTCCAG GG GTTCTTTTTACT
                                 ||||||||  ||  ||||||||||||
                                 GGGAGGTC CT CAGGAGGAATGA
                                      _  T
GAM376  PIK3C2B  3'  AGTAGGAGGCTGGATTGGAGTG 10560   _      __  G   TTTTACT
             G                   C CTCCAGT  GGC TTCT
                                 |  |||||||  |||  ||||
                                 G GAGGTTA  TCG AGGA
                                 T      GG   G    TGA   T
GAM376  PIN1     3'  GGTGGGAGGGGTGTTCCAAAGA 20616     CAG   __  TT
             G                   CTC   TGG  CG  CTTTTTACT
                                 |||   |||  ||  |||||||||
                                 GAG   ACC  GT  GGAGGGTGG
                                   AA_   TT  GG
GAM376  PIN1L    3'  GGTGGGAGGAGTGTTCCAAAGA 20624     CAG   __
             G                   CTC   TGG  CGTTCTTTTTACT
                                 |||   |||  ||||||||||||
                                 GAG   ACC  GTGAGGAGGGTGG
                                   AA_   TT
GAM376  PIP5K1A  3'  GGTGGGAGGGAATATTTGAGGG 13057     TC   TGGCG
             A                   TCC  CAG     TTCTTTTTACT
                                 |||  |||     ||||||||||
                                 AGG  GTT     AGGGAGGGTGG
                                   GA   TATA_
GAM376  PML      3'  AGTGAAAGGTTGGACTGGGTGG 52664     _     GGCGTT
                                 CC TCCAGT      CTTTTTACT
                                 ||  ||||||     |||||||||
                                 GG GGGTCA      GGAAAGTGA
                                  T     GGTT__
GAM376  PML      3'  AGTGAAAGGTTGGACTGGGTGG 52670     _     GGCGTT
                                 CC TCCAGT      CTTTTTACT
                                 ||  ||||||     |||||||||
                                 GG GGGTCA      GGAAAGTGA
                                  T     GGTT__
GAM376  PODXL    3'  GGTAGGGGGAGGGGCTGGGGA  18237     T    GGCG
                                 TCC CCAGT    TTCTTTTTACT
                                 |||  |||||    ||||||||||
                                 AGG GGTCG    GAGGGGGATGG
                                   _     GG__
GAM376  POLR2E   3'  GGTGCAGGGGACGTGCTGGAGG 59921          G       T
             G                   TCCTCCAGTG CGTTCTTT TACT
                                 ||||||||||  ||||||||  ||||
```

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                                GGGAGGTCGT GCAGGGGA GTGG
                                      _      C
GAM376  PPARBP   3' GGTGGGAGGGGTGTAGGGAG  16491     AGTG  TT
                                CTCC   GCG  CTTTTTACT
                                ||||   |||  |||||||||
                                GAGG   TGT  GGAGGGTGG
                                  GA__  GG
GAM376  PPFIA3   3' GGTGAGGACCGTGCTGGGCGA  61016   C     G  T  TT
                                TC TCCAGTG CG TCT  TTACT
                                || ||||||| || |||  |||||
                                AG GGGTCGT GC AGG  AGTGG
                                 C      _ C  __
GAM376  PPT2     5' AGTGGGGAGAATCAAGGCGGGG 57228      CAG_  GC
           A                     TCCTC   TG  GTTCTTTTTACT
                                 |||||   ||  ||||||||||||
                                 AGGGG   AC  TAAGAGGGGTGA
                                   CGGA  __
GAM376  PPT2     3' GGTGAGAGGCTGTCATCTGGAG 57233        _    TT
           GG                      TCCTCCAG TGGCG  CTTTTTACT
                                 |||||||| |||||  |||||||||
                                 GGGAGGTC ACTGT  GGAGAGTGG
                                     T    C_
GAM376  PPT2     5' AGTGGGGAGAATCAAGGCGGGG 17668      CAG_  GC
           A                     TCCTC   TG  GTTCTTTTTACT
                                 |||||   ||  ||||||||||||
                                 AGGGG   AC  TAAGAGGGGTGA
                                   CGGA  __
GAM376  PRPS1    3' GGTGGGGGGGTGGTTGAGGGGG  10899     AG   GTT
                                CCTCC  TGGC   CTTTTTACT
                                |||||  ||||   |||||||||
                                GGGGG  GTTG   GGGGGGGTGG
                                   A_   GT_
GAM376  PTGFRN   3' AGTAAGAAGGGCTGCAAGGAAG 67184     _ AGTG  _
           GG                      TCCT CC   GC GTTCTTTTTACT
                                 |||| ||   || ||||||||||||
                                 GGGA GG   CG CGGGAAGAATGA
                                   A  AA__  T
GAM376  RAB13    3' GTAAAGAGAATGAGGAG     11203     AGTGG
                                CTCC    CGTTCTTTTTAC
                                ||||    ||||||||||||
                                GAGG    GTAAGAGAAATG
                                  A____
GAM376  RAB27A   3' GGTGGGAAGGGGATTGGGGTGG 15926    _     GGCG
                                TC CTCCAGT   TTCTTTTTACT
                                || |||||||   ||||||||||
                                GG GGGGTTA   GGGAAGGGTGG
                                 T     G___
GAM376  RAB33A   5' TGCAAGGAGGGTGCGCTGGAGG 16578         G  TT    ACT
           A                     TCCTCCAGTG CG  CTTTTT
                                 |||||||||| ||  ||||||
```

```
                                AGGAGGTCGC GT  GAGGAA
                                      _ GG     CGTC
GAM376  RAB5C    3'  GGTAAGGGGGGGAGTGGGAGGG 59835       AGTG  G_
                                TCCTCC    GC  TTCTTTTTACT
                                ||||||    ||  ||||||||||
                                GGGAGG    TG  GGGGGGAATGG
                                   G___   AG
GAM376  RDS      5'  GGTGGGAGCTGTGCTGTGGGA  4362      TC    GC    TTT
                                TCC  CAGTG  GTTCT   TACT
                                |||  |||||  |||||   ||||
                                AGG  GTCGT  CGAGG   GTGG
                                  GT    GT    ___
GAM376  RNF28    3'  GGTGGGAGGGGTCGGGGCCCCT 50862      T  _____ TT
           GGAGGG                  CCAG GGC    G  CTTTTTACT
                                ||||  |||    |  |||||||||
                                GGTC CCG    T  GGAGGGTGG
                                  C   GGGC GG
GAM376  RNH      5'  GGTGGGGAGGGTGCTGAAGAGG 59623      CAG    TT
           A                     TCCTC   TGGCG  CTTTTTACT
                                |||||   |||||  |||||||||
                                AGGAG   GTCGT  GAGGGGTGG
                                   AA_    GG
GAM376  RNH      5'  GGTGGGGAGGGTGCTGAAGAGG 11368      CAG    TT
           A                     TCCTC   TGGCG  CTTTTTACT
                                |||||   |||||  |||||||||
                                AGGAG   GTCGT  GAGGGGTGG
                                   AA_    GG
GAM376  RS1      3'  GGTGGGGGGGGGGGTGGGGGGA  4398       AGTG  G
                                TCCTCC    GC TTCTTTTTACT
                                ||||||    || ||||||||||
                                AGGGGG    TG GGGGGGGGTGG
                                   G___   G
GAM376  RTKN     5'  AGTGGGAGGAGGAACTGTGGGA 52324     TC    GGCG
                                TCC  CAGT    TTCTTTTTACT
                                |||  ||||    ||||||||||
                                AGG  GTCA    GAGGAGGGTGA
                                  GT   AG__
GAM376  SALL2    5'  GTGATTTGCGCTGGGGGA    63862         G  TTCTTT
                                TCCTCCAGTG CG     TTAC
                                |||||||||| ||     ||||
                                AGGGGGTCGC GT     AGTG
                                      _ TT_____
GAM376  SDC4     3'  GGTAGGGGGGGGGGGAATGGGGG 11481       GTGGCG
           A                     TCCTCCA     TTCTTTTTACT
                                |||||||     ||||||||||
                                AGGGGGT     GGGGGGGATGG
                                    AAGGG_
GAM376  SEMA3F   3'  GGGGGGTGATTGGAAGGG    14821      _    G  G
                                TCCT CCAGT GC TTCT
                                |||| ||||| || ||||
```

```
                                GGGA GGTTA TG GGGG
                                  A    G G
GAM376  SERPINA5  3'  AGTAGGAGGGATGTTCCAGTGG 5268      G  __
            A                    TCCA TGG  CGTTCTTTTTACT
                                 |||| |||  ||||||||||||
                                 AGGT ACC  GTAGGGAGGATGA
                                   G   TT
GAM376  SERPINF2  3'  GGTGGGGGGGGGGCGCGGCTGGG 6258       _  G        _
            AGGA                   CCTCC AGT GCGTTCTTTTT ACT
                                   ||||| ||| |||||||||| |||
                                   GGAGG TCG CGCGGGGGGGG TGG
                                     G  G         G
GAM376  SFRS1    3'  GGTAAAAGGAGCAAAGCGAGGA 22639      CA  GGC
                                   TCCTC  GT   GTTCTTTTTACT
                                   |||||  ||   ||||||||||||
                                   AGGAG  CG   CGAGGAAAATGG
                                     __  AAA
GAM376  SLC19A2  3'  AGTAGAAAAGTGCTGTTTGAGG 68977      C  TG    C
            G                    TCCTC AG  GCGTT TTTTTACT
                                 |||||| ||  ||||| ||||||||
                                 GGGAG TT  CGTGA AAAGATGA
                                   T  GT    _
GAM376  SLC1A2   3'  TTGAATGGATGCTGCTGGAGGA 61931        TG     TT    CT
                                 TCCTCCAG  GCGTTC  TTTA
                                 ||||||||  ||||||  ||||
                                 AGGAGGTC  CGTAGG  AAGT
                                      GT     T_    TT
GAM376  SLC22A2  5'  AAGAATTTGTTGGGCGGA    59529     _    TG C
                                 TCC TCCAG  G GTTCTT
                                 ||| |||||  | ||||||
                                 AGG GGGTT  T TAAGAA
                                   C    GT _
GAM376  SLC5A5   5'  AGTGAGAGGGGAGGTGGCAGGA 4844      A  G  G_
                                 TCC GT GC  TTCTTTTTACT
                                 ||| || ||  ||||||||||
                                 AGG CG TG  GGGGAGAGTGA
                                   A  G  GA
GAM376  SLC7A6   3'  GGTGGGGGGAAGATTGGGGA   14313     T    GGCG
                                 TCC CCAGT    TTCTTTTTACT
                                 ||| |||||    ||||||||||
                                 AGG GGTTA    AAGGGGGGTGG
                                   _    G___
GAM376  SLIT2    5'  GGTGGAGAGGGCGGTGGGAGG  16553      AGTGG
                                 CCTCC    CGTTCTTTTTACT
                                 |||||    ||||||||||||
                                 GGAGG    GCGGGAGAGGTGG
                                   GTG__
GAM376  SNAI2    3'  TATGTGCCTTGGGGGA      11777         T   TTCTTTT
                                 TCCTCCAG GGCG      TA
                                 |||||||| ||||      ||
```

```
                                AGGGGGTT CCGT      AT
                                    _   GT_____
GAM376  SOST    3'  ACTAAAAGAATATTATTGGGGG 47465          CG      TACT
            A                    TCCTCCAGTGG  TTCTTTT
                                 ||||||||||  |||||||
                                 AGGGGGTTATT  AAGAAAA
                                       AT      TCA
GAM376  SOX9    3'  AGTGAGGGAGGCTACCTGGAGG 4436         _   G   TT
            G                    TCCTCCAG TGGC TTCT  TTACT
                                 ||||||||| |||| ||||  |||||
                                 GGGAGGTC ATCG AGGG  AGTGA
                                     C   G   __
GAM376  SPAG8   3'  GGTGAGGAGGGAAGTGGGG   24903      GTGGCG
                                 CTCCA     TTCTTTTTACT
                                 |||||     ||||||||||
                                 GGGGT     GGGAGGAGTGG
                                    GAA___
GAM376  STAC    3'  AGTGGGGAGGAGAAGTGGGGA  11988     T  GTGGCG
                                 TCC CCA     TTCTTTTTACT
                                 ||| |||     ||||||||||
                                 AGG GGT     AGGAGGGGTGA
                                   _  GAAG__
GAM376  STAT6   3'  GGGAGCATAGGAGGG       12023       A  G G
                                 TCCTCC GTG C TTCT
                                 |||||| ||| | ||||
                                 GGGAGG TAC G AGGG
                                    A  _ _
GAM376  SYBL1   3'  AGTAGAGGGGGTGGGGAGG   18891      AGTGG  TT
                                 CCTCC    CG  CTTTTTACT
                                 |||||    ||  |||||||||
                                 GGAGG    GT  GGGAGATGA
                                   G_____  GG
GAM376  TBX5    5'  TGGGATAGTTGGAGGG      54894       GTG  GTTCT
                                 TCCTCCA  GC    TTTTA
                                 |||||||  ||    |||||
                                 GGGAGGT  TG    AGGGT
                                     ___  AT___
GAM376  TCF20   3'  AGTGGGAAGGTTTTGGGGGA  66953        TGGCGT
                                 TCCTCCAG     TCTTTTTACT
                                 ||||||||     ||||||||||
                                 AGGGGGTT     GGAAGGGTGA
                                     TT_____
GAM376  TCF20   3'  GGTGGGGGGAATTAAAAGGGAG 66958       AGTGGC
            GG                   TCCTCC     GTTCTTTTTACT
                                 ||||||     ||||||||||||
                                 GGGAGG     TAAGGGGGGTGG
                                    GAAAAT
GAM376  TFEB    3'  AGTGAAGGACATGCTTGAGGG  92124      C   GC    TT
                                 TCCTC AGTG  GTTCT  TTACT
                                 ||||| ||||  |||||  |||||
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                                GGGAG TCGT  CAGGA  AGTGA
                                  T   A_    __
GAM376  TFEB    3'  GGTGAGAAGAGGGCCTGGTGGA 92128    T  GT   G
                                TCC CCA  GGC TTCTTTTTACT
                                ||| |||  ||| ||||||||||
                                AGG GGT  CCG GAGAAGAGTGG
                                  T  __  G
GAM376  TGM2    3'  GGTAGAGAGGGGACTGGGGGA  16056        GGCG
                                TCCTCCAGT   TTCTTTTTACT
                                |||||||||   ||||||||||
                                AGGGGGTCA   GGGAGAGATGG
                                     G___
GAM376  THY1    3'  GGTGGGGTACCAGCCACTGGAG 20813          GTTCT
           GG                     TCCTCCAGTGGC    TTTTACT
                                |||||||||||    |||||||
                                GGGAGGTCACCG    GGGGTGG
                                       ACCAT
GAM376  TM7SF3  3'  AAGGGTGTACTAGGGGA    59664      C   G  TT
                                TCCTC AGTG CG  CTT
                                ||||| |||| ||  |||
                                AGGGG TCAT GT  GAA
                                  A   _ GG
GAM376  TMEPAI  3'  GTGAGAGGAAGGCGGGGGG   39449      AGTG  G
                                TCCTCC   GC TTCTTTTTAC
                                ||||||   || ||||||||||
                                GGGGGG   CG AAGGAGAGTG
                                   ____  G
GAM376  TNFRSF14 3'  GGGGCCCCTGCTGGGG     13784       _  C
                                CTCCAGT GG GTTCT
                                ||||||| || |||||
                                GGGGTCG CC CGGGG
                                    T  C
GAM376  TNFSF11  3'  AGTGGAGAGGGTGTCAT    13509       TT
                                GTGGCG  CTTTTTACT
                                ||||||  |||||||||
                                TACTGT  GAGAGGTGA
                                   GG
GAM376  TNFSF11  3'  AGTGGAGAGGGTGTCAT    52237       TT
                                GTGGCG  CTTTTTACT
                                ||||||  |||||||||
                                TACTGT  GAGAGGTGA
                                   GG
GAM376  TPSB1    5'  GGTAGAAGGAACAGGGAGCGG  12376   _   AGTGGC
                                TC CTCC     GTTCTTTTTACT
                                || ||||     ||||||||||||
                                GG GAGG     CAAGGAAGATGG
                                 C   GA____
GAM376  TPX1    5'  GGTGAGAGGGGCGCGCA     12379   _
                                TG GCGTTCTTTTTACT
                                || ||||||||||||||
```

```
                                AC CGCGGGGAGAGTGG
                                 G
GAM376  TRADD    3'  GGTGGGGGGGGACCTGCTTTGGA 13700      __ TG C
             G                   CTCCA  G  G GTTCTTTTTACT
                                 ||||||  |  | ||||||||||||
                                 GAGGT  C  C CAGGGGGGGTGG
                                   TT GT _
GAM376  TRPC1    3'  GGTGGGAAGAAAATATGGAGGA 12391       GTGGCG
                                 TCCTCCA     TTCTTTTTACT
                                 |||||||     ||||||||||
                                 AGGAGGT     AAGAAGGGTGG
                                     ATAA__
GAM376  TRPC5    5'  GGTGGGGAGGATAAAGGGAG   25001     AGTGGC
                                 CTCC     GTTCTTTTTACT
                                 ||||     ||||||||||||
                                 GAGG     TAGGAGGGGTGG
                                   GAAA__
GAM376  TSPY     3'  GTGGAAGGAAGATGGTGGG    82108     T   GTGGCG
                                 TCC CCA     TTCTTTTTAC
                                 ||| |||     ||||||||||
                                 GGG GGT     AAGGAAGGTG
                                   T  AG____
GAM376  TUFT1    3'  AGTGATTGGAGAATGTCCTGGG 39251        T        __
             GGA                   CCTCCAG GGCGTTCTTT  TTACT
                                 |||||||  |||||||||  |||||
                                 GGGGGTC CTGTAAGAGG  AGTGA
                                     _        TT
GAM376  USP11    5'  GGGAGGCATACTGCAGGG    16204     C    _  G
                                 TCCT CAGTG GC TTCT
                                 |||| ||||| || ||||
                                 GGGA GTCAT CG AGGG
                                   C    A  G
GAM376  VANGL2   3'  GGGAAACTCTGGGGGG      71652         T  CG
                                 TCCTCCAG GG  TTCT
                                 ||||||||  ||  ||||
                                 GGGGGGTC TC  AGGG
                                     _  AA
GAM376  VAPB     3'  GGTGAACTGGTATTGCTGCTGG 16440        TG   TT_  T_
             AGGG                  CCTCCAG  GCG   CT  TTTACT
                                 |||||||  |||   ||  ||||||
                                 GGAGGTC  CGT   GG  AAGTGG
                                     GT   TAT  TC
GAM376  VPS26    5'  AGTAGGGGGGGACGCGGCGGCGG 16906    T  A  G
                                 CC CC GT GCGTTCTTTTTACT
                                 || || || ||||||||||||||
                                 GG GG CG CGCAGGGGGGATGA
                                  C  _  G
GAM376  WASF3    5'  AGTGGTGATGCTACTTGAGGG  21825      C       CTTT
                                 TCCTC AGTGGCGTT    TTACT
                                 ||||| |||||||||    |||||
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                                GGGAG TCATCGTAG   GGTGA
                                  T       T___
GAM376  WNT15   3'  GTGAGAAAGACATGGAGGG   12679       GTGGC  TC
                                TCCTCCA    GT  TTTTTAC
                                |||||||    ||  |||||||
                                GGGAGGT    CA  AAGAGTG
                                   A____  GA
GAM376  WRN     5'  GGGGACGGCGCTGGAGGG    5099         G
                                TCCTCCAGTG CGTTCTT
                                |||||||||| |||||||
                                GGGAGGTCGC GCAGGGG
                                     G
GAM376  ZIC1    5'  GGTGGGGGGGGGCGGGGGAGG  12723      AGTGG
                                CCTCC    CGTTCTTTTTACT
                                |||||    ||||||||||||
                                GGAGG    GCGGGGGGGGGTGG
                                  GG___
GAM376  ZNF278  3'  GTGGAAGGGAACAGGAGGG   49440      A  GGCG
                                TCCTCC GT   TTCTTTTTAC
                                |||||| ||   ||||||||||
                                GGGAGG CA   AGGGAAGGTG
                                   A  _____
GAM376  ZNF35   3'  GGTAATGATGCTATTTGGGGA  12780      C       CTTT
                                TCCTC AGTGGCGTT   TTACT
                                ||||| |||||||||   |||||
                                AGGGG TTATCGTAG   AATGG
                                  T       T___
GAM376  ZRF1    5'  AGTGAGAGGTAGAGCTGGAGGG 94288        GGCGTT
                                TCCTCCAGT    CTTTTTACT
                                |||||||||    |||||||||
                                GGGAGGTCG    GGAGAGTGA
                                     AGAT__
GAM376  ABCA9   3'  GGGGCCTGTTGGGGGG     54411        TG C
                                TCCTCCAG  G GTTCT
                                ||||||||  | |||||
                                GGGGGGTT  C CGGGG
                                     GT _
GAM376  ABIN-2  5'  AGTGGACGCGCTGCTGGAG   44206      TG   TCTT
                                CTCCAG  GCGT   TTTACT
                                ||||||  ||||   ||||||
                                GAGGTC  CGCG   AGGTGA
                                   GT   C___
GAM376  ACTR2   3'  GGTGGGTTTTGTTGCGGGGGGG 19151      A TG   TTCTT
                                TCCTCC G  GCG    TTTACT
                                |||||| |  |||    ||||||
                                GGGGGG C  TGT    GGGTGG
                                   G GT   TTT__
GAM376  AF9Q34  3'  GGATGTGCTGGAGGG      50739         G
                                TCCTCCAGTG CGTTC
                                |||||||||| |||||
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                                GGGAGGTCGT GTAGG
                                      _
GAM376  AF9Q34   3'  GGTAAGAAGGGTGGGAGTGGGG 50740      GTGG  TT
                                CTCCA   CG  CTTTTTACT
                                ||||||   ||  |||||||||
                                GGGGT   GT  GAAGAATGG
                                   GAGG  GG
GAM376  AGS3     3'  GGTGAGGTGACCTGCTTCTGGA 73114        T   T_  T
           GGG                    TCCTCCAG GGCG  TC TTTTACT
                                ||||||||| ||||  || |||||||
                                GGGAGGTC TCGT  AG GGAGTGG
                                     T   CC  T
GAM376  ALS2CR19 3'  GGTGGAAGGGGCGCTGCCGCGA 54113     CA_ TG
           G                     CTC   G  GCGTTCTTTTTACT
                                |||   |  ||||||||||||||
                                GAG   C  CGCGGGGAAGGTGG
                                  CGC GT
GAM376  AMOTL1   3'  AGTGAGAAGAAGCATCGAGGG  73647      CAGTG  G
                                TCCTC    GC TTCTTTTTACT
                                ||||||    || ||||||||||
                                GGGAG    CG AAGAAGAGTGA
                                   CTA__  _
GAM376  ARF6     5'  GTGAGAGGAAGGCGGAGGA   8013        AGTG  G
                                TCCTCC   GC TTCTTTTTAC
                                ||||||   || ||||||||||
                                AGGAGG   CG AAGGAGAGTG
                                   _____  G
GAM376  ARHGAP11A 5'  GGTAGAGGCAGGCTGATGGGGG 28797        GT   G  C
           A                     TCCTCCA  GGC TT TTTTTACT
                                |||||||  ||| || ||||||||
                                AGGGGGT  TCG GA GGAGATGG
                                    AG   _  C
GAM376  ARHGEF15  5'  AGTGGAGGGGATTCAAGGGGGA 30256       AG   C
                                TCCTCC  TGG GTTCTTTTTACT
                                ||||||  ||| ||||||||||||
                                AGGGGG  ACT TAGGGGAGGTGA
                                   A_  _
GAM376  ARHGEF9   5'  GTAAAGGGAGTAGGGGAG    30817     AGTG  GT
                                CTCC   GC  TCTTTTTAC
                                ||||   ||  |||||||||
                                GAGG   TG  AGGGAAATG
                                  GGA_ ___
GAM376  ASP      5'  GGTCTAGGGTGTTGTTGGAG   49167       TG   TT  TTTT
                                CTCCAG  GCG  CT   ACT
                                ||||||  |||  ||   |||
                                GAGGTT  TGT  GA   TGG
                                   GT   GG  TC__
GAM376  BATF     5'  GTGAGGAGGACGCAGGGG    21131      AGTG
                                CTCC   GCGTTCTTTTTAC
                                ||||   ||||||||||||
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                                GGGG   CGCAGGAGGAGTG
                                  A___
GAM376  BDH      5'  GCCGCAGGAGTGCTGGTGGAGG 14476       G        TTTACT
                G                  TCCTCCA TGGCGTTCTT
                                   ||||||| |||||||||
                                   GGGAGGT GTCGTGAGGA
                                      G        CGCCGG
GAM376  BET3     3'  GGTGGAGGGAGGAAGGGCTGGG 26965      _  GGCG_
                AGGG                  CCTCC AGT    TTCTTTTTACT
                                   ||||| |||    ||||||||||
                                   GGAGG TCG    GAGGGAGGTGG
                                     G  GGAAG
GAM376  BICD2    3'  GGTAAAGAGTCACATTGGTAGG 70400     _     GCGTT
                A                   TCCT CCAGTG    CTTTTTACT
                                   |||| ||||||    |||||||||
                                   AGGA GGTTAC    GAGAAATGG
                                     T     ACT__
GAM376  C11orf21 3'  GGAAGCCATTGGGGTGA     26242    _       G
                                   TC CTCCAGTGGC TTCT
                                   || |||||||||| ||||
                                   AG GGGGTTACCG AAGG
                                    T        _
GAM376  C11orf9  3'  GTTCAGGTGCCCTGGAGGG    25213        T   TT   TTT
                                   TCCTCCAG GGCG  CTT   AC
                                   |||||||| ||||  |||   ||
                                   GGGAGGTC CCGT  GGA   TG
                                      _   ___  CT_
GAM376  C12orf22 3'  AGTGAAAAACTGTGTTGGGGGG 47976       GT G  TTC
                                   TCCTCCA  G CG   TTTTTACT
                                   |||||||  | ||   ||||||||
                                   GGGGGGT  T GT   AAAAGTGA
                                      TG _  CA_
GAM376  C14orf4  3'  GGTAAGGGGGTGTCGGGGGGG  67340      AG    TT    T
                                   CCTCC  TGGCG  CTTTT ACT
                                   |||||  |||||  ||||| |||
                                   GGGGG  GCTGT  GGGAA TGG
                                     G_    GG    _
GAM376  C1orf25  3'  AGTGGGGGGAAGGGGGTGGAGG 72531       GTGGCG
                G                   TCCTCCA     TTCTTTTTACT
                                   |||||||     ||||||||||
                                   GGGAGGT     AAGGGGGGTGA
                                      GGGGG_
GAM376  C1QR1    3'  AGTGAAAGGAAAGATGGAGG   23835       GTGGCG
                                   CCTCCA     TTCTTTTTACT
                                   ||||||     ||||||||||
                                   GGAGGT     AAGGAAAGTGA
                                     AGA___
GAM376  C20orf141 5'  GGTGAGGAGGGTTTGCTGGGTG 54949     _    TG C TT
                GG                   TCC TCCAG  G G  CTTTTTACT
                                   ||| |||||  | |  |||||||||
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                                GGG GGGTC  T T  GAGGAGTGG
                                  T    GT _ GG
GAM376  C20orf151 3'  GGTGGAGGGAGACAGTGGGCGG 88702    _   G  GCGT
                                CC TCCA TG   TCTTTTTACT
                                || |||| ||   ||||||||||
                                GG GGGT AC   AGGGAGGTGG
                                 C   G  AG__
GAM376  C20orf188 3'  AGTGGGGAGGAAGATATGGGTG 31576    C    GTGGCG
           A                     TC TCCA     TTCTTTTTACT
                                || ||||     ||||||||||
                                AG GGGT     AGGAGGGGTGA
                                 T   ATAGA_
GAM376  C20orf35  3'  GTGGGAAGGATGGTGGGA    37481      CCAGT G
                                TCCT    G CGTTCTTTTTAC
                                ||||    | ||||||||||||
                                AGGG    T GTAGGAAGGGTG
                                  _____ G
GAM376  C20orf7   3'  GTGAGAAGAACATAGAGGA   44144      CAG  GC
                                TCCTC   TG  GTTCTTTTTAC
                                |||||   ||  ||||||||||
                                AGGAG   AT  CAAGAAGAGTG
                                  ___  A_
GAM376  C22orf5   3'  GGTGGGGGGGAGCTCAGTGGCAG 24347      _  G   C
           GG                    TCCT CCA TGG GTTCTTTTTACT
                                |||| ||| ||| ||||||||||||
                                GGGA GGT ACT CGAGGGGGGTGG
                                  C   G   _
GAM376  C5orf7    5'  GGTGGTTGGTGGTGGCTGTTGG 63870        TG  GTT__  TT
           GGGG                   CCTCCAG  GC    CT  TTACT
                                |||||||  ||    ||  |||||
                                GGGGGTT  CG    GG  GGTGG
                                   GT  GTGGT  TT
GAM376  C6orf9    3'  AGTAAGAAGGGAAGGTGGGTGG 42075     T  AGTGGCG
           G                     TCC CC      TTCTTTTTACT
                                ||| ||      ||||||||||
                                GGG GG      GGGAAGAATGA
                                  T  GTGGAA_
GAM376  CAT56     3'  GTGAGAGCTGTTGGAG      47519       TG  GTTCT
                                CTCCAG  GC    TTTTAC
                                ||||||  ||    ||||||
                                GAGGTT  CG    AGAGTG
                                   GT  _____
GAM376  CBCIP2    3'  AGTGGGGTCAGGCCCTGGGGGA 51587        T   G  CT
                                TCCTCCAG GGC TT  TTTTACT
                                |||||||| ||| ||  |||||||
                                AGGGGGTC CCG GA  GGGGTGA
                                     _   _  CT
GAM376  CCR5      3'  GGTGGGGGGGGGCGCCTTAGG   5150     AGT
                                CC   GGCGTTCTTTTTACT
                                ||   ||||||||||||||
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                                GG  CCGCGGGGGGGGTGG
                                 ATT
GAM376  CDCA4   3'  AGTAGCATTGCTGCTGGATGA  35655   C   TG  TTCTTT
                                TC TCCAG  GCG    TTACT
                                || |||||  |||    |||||
                                AG AGGTC  CGT    GATGA
                                 T   GT  TAC___
GAM376  CECR2   3'  AGTGGGAAGGGTGGGTGGGGA  48607    T  GTGG  TT
                                TCC CCA   CG  CTTTTTACT
                                ||| |||   ||  |||||||||
                                AGG GGT   GT  GAAGGGTGA
                                  _  GG__  GG
GAM376  CECR6   3'  GAGGACGGCTTGGAGGG    49087       GT  _
                                TCCTCCA  GGC GTTCTT
                                |||||||  ||| ||||||
                                GGGAGGT  TCG CAGGAG
                                    __  G
GAM376  CG018   3'  GGTGGAGAGAAGTGGTGGGGGG 53395       G G  G
                                TCCTCCA T GC TTCTTTTTACT
                                ||||||| | || ||||||||||
                                GGGGGGT G TG AAGAGAGGTGG
                                    _ G  _
GAM376  CGB5    5'  AGTGAGAGGAGAGGGCTGGGG  52314       GGCG
                                CTCCAGT   TTCTTTTTACT
                                |||||||   ||||||||||
                                GGGGTCG   GAGGAGAGTGA
                                    GGA_
GAM376  CGB8    5'  AGTGAGAGGAGAGGGCTGGGG  52589       GGCG
                                CTCCAGT   TTCTTTTTACT
                                |||||||   ||||||||||
                                GGGGTCG   GAGGAGAGTGA
                                    GGA_
GAM376  CGI-01  3'  GTGGAGGGAGTGTATGGA   31944     GTG
                                TCCA  GCGTTCTTTTTAC
                                ||||  ||||||||||||
                                AGGT  TGTGAGGGAGGTG
                                  A__
GAM376  CLDN7   3'  GGTGGGGGGGGTGCCGTTGGTGG 7141      _       TT    T
            GA                    TCCT CCAGTGGCG  CTTTT ACT
                                ||||  |||||||||  |||||  |||
                                AGGG GGTTGCCGT  GGGGG TGG
                                  T       GG    _
GAM376  CLDN7   3'  GGTGGGGGGGGTGCCGTTGGTGG 94585     _       TT    T
            GA                    TCCT CCAGTGGCG  CTTTT ACT
                                ||||  |||||||||  |||||  |||
                                AGGG GGTTGCCGT  GGGGG TGG
                                  T       GG    _
GAM376  CLIC4   5'  AGAGTGCCGCGGGGGGG     25628       A
                                TCCTCC GTGGCGTTCT
                                ||||||  ||||||||||
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                                GGGGGG CGCCGTGAGA
                                      _
GAM376  CLTH     5'  GGTAGGGGGTGCGGTGGGGGG  23146       G G   TT  TT
                                TCCTCCA T GCG  CT  TTACT
                                ||||||| | |||  ||  |||||
                                GGGGGGT G CGT  GG  GATGG
                                   _ G   GG  __
GAM376  CMRF-35H 3'  AGTGAAGAGAGTGCCAAAGCGG 70417     AG__
           AG                    CTCC   TGGCGTTCTTTTTACT
                                ||||   ||||||||||||||||
                                GAGG   ACCGTGAGAGAAGTGA
                                  CGAA
GAM376  CNNM4    3'  AGTGGAGGCTTATCTGTTGGGA 39473       _  TG CGTTC
           GGA                   TCCTCC AG  G    TTTTTACT
                                ||||||  ||  |    ||||||||
                                AGGAGG TT  C    GGAGGTGA
                                   G  GT TATTC
GAM376  CTCF     5'  GGGCGCCGCGGGGGGG      21635       A
                                TCCTCC GTGGCGTTC
                                ||||||| |||||||||
                                GGGGGG CGCCGCGGG
                                      _
GAM376  DDR1     3'  GGTGAGGAGGACAAGAAGGAG  25697      AGTGGC
                                CTCC     GTTCTTTTTACT
                                ||||     ||||||||||||
                                GAGG     CAGGAGGAGTGG
                                  AAGAA_
GAM376  DDR1     3'  GGTGAGGAGGACAAGAAGGAG  25706      AGTGGC
                                CTCC     GTTCTTTTTACT
                                ||||     ||||||||||||
                                GAGG     CAGGAGGAGTGG
                                  AAGAA_
GAM376  DDR1     3'  GGTGAGGAGGACAAGAAGGAG  8724       AGTGGC
                                CTCC     GTTCTTTTTACT
                                ||||     ||||||||||||
                                GAGG     CAGGAGGAGTGG
                                  AAGAA_
GAM376  DDX34    3'  GTAGGAGGGGCGTTAGAG    27988     CAG
                                CTC   TGGCGTTCTTTTTAC
                                |||   |||||||||||||||
                                GAG   ATTGCGGGGAGGATG
                                     ____
GAM376  DGKD     3'  GGTGGGGAGGGGACATGAGGA  59409      CA   GCG
                                TCCTC  GTG   TTCTTTTTACT
                                |||||  |||   ||||||||||
                                AGGAG  TAC   GGGAGGGGTGG
                                   __  AG_
GAM376  DGKZ     3'  GGGACGGCCACGGGGGGA    13324       A    _
                                TCCTCC GTGGC GTTCT
                                |||||| ||||| |||||
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                                AGGGGG CACCG CAGGG
                                   G    G
GAM376  DKFZp434A1520 3'  AGTGAGGAATTTTATTGGTGGA 61113    T     C    TT
                                TCC CCAGTGG GTTCT  TTACT
                                ||| ||||||| |||||  |||||
                                AGG GGTTATT TAAGG  AGTGA
                                  T     T   __
GAM376  DKFZP434D146 3'  AGTAGAAAGCCTTACTGTAGGA 31520     C     CGTT
                                TCCT CAGTGG   CTTTTTACT
                                |||| ||||||   |||||||||
                                AGGA GTCATT   GAAAGATGA
                                  T     CC__
GAM376  DKFZP434F1735 5'  AGTGAAGAGATGAGGCTGGAG  31495       GG   T
                                CTCCAGT  CGT CTTTTTACT
                                |||||||  ||| |||||||||
                                GAGGTCG  GTA GAGAAGTGA
                                   GA  _
GAM376  DKFZP434H0820 3'  GGTGGAGAGATGAGATTTAGGG 63853      __   GG   T
           GG                    CCTCC  AGT  CGT CTTTTTACT
                                |||||  |||  ||| |||||||||
                                GGGGG  TTA  GTA GAGAGGTGG
                                  AT   GA  _
GAM376  DKFZP434I0714 5'  GGTGAGAGGGGCAAAGGAGGA  85800       AGTGGC
                                TCCTCC     GTTCTTTTTACT
                                ||||||     ||||||||||||
                                AGGAGG     CGGGGAGAGTGG
                                   AAA___
GAM376  DKFZP434N178 3'  GTGGGGGGGCCTTGGGAGG   71910      AGT   G   TTT
                                CCTCC   GGC TTCT   TAC
                                |||||   ||| ||||   |||
                                GGAGG   CCG GGGG   GTG
                                   GTT   G   ___
GAM376  DKFZp547J036 5'  GGTGGGGGGGGGCCCAGGGAG   50129     AG   C
                                CTCC  TGG GTTCTTTTTACT
                                ||||  ||| ||||||||||||
                                GAGG  ACC CGGGGGGGGTGG
                                  G_  _
GAM376  DKFZP564B1162 3'  AGTGGGAGGGGGCCAGGCTGCA 48528     C   __   G
           GGA                   CCT CAGT  GGC TTCTTTTTACT
                                ||| ||||  ||| ||||||||||
                                GGA GTCG  CCG GGGGAGGGTGA
                                  C   GA  _
GAM376  DKFZp566D234 3'  CTTGAAGGGAATGTCACAGGAG 61863       A            CT
           GA                    TCCTCC GTGGCGTTCTTTTTA
                                ||||||| |||||||||||||||
                                AGGAGG CACTGTAAGGGAAGT
                                   A            TCC
GAM376  DKFZP566J091 3'  GGAGCCTGCTGGGGGG      48123         TG C
                                TCCTCCAG  G GTTCT
                                ||||||||  | |||||
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                                GGGGGGTC  C CGAGG
                                     GT _
GAM376  DKFZP586N0721 3'  AGTTCTGAATGTTGGTGGAGGG 31201        G       TTTTT
                                TCCTCCA TGGCGTTC     ACT
                                ||||||| ||||||||     |||
                                GGGAGGT GTTGTAAG     TGA
                                     G       TCT__
GAM376  DKFZP667O116 3'  GTGAGAGGGAGTGGGGAGG    94286       AGTG  G
                                CCTCC    GC TTCTTTTTAC
                                |||||    || ||||||||||
                                GGAGG    TG AGGGAGAGTG
                                   GG__  _
GAM376  DKFZP727G051 5'  GTGGAGAGCATGTGGAGGG    69477       AGTG    T
                                TCCTCC    GCGT CTTTTTAC
                                ||||||    |||| ||||||||
                                GGGAGG    TGTA GAGAGGTG
                                     ____    C
GAM376  DKFZp761H079 5'  GGTGGGAGGAGCGACCCGGGA  58736     AGT  _
                                TCC   GG CGTTCTTTTTACT
                                |||   || ||||||||||||
                                AGG   CC GCGAGGAGGGTGG
                                  GC_  A
GAM376  DKFZP762N2316 3'  GGTAGAAGACTTCTCATTGGGG 67129     T      CGTTC
           A                     TCC CCAGTGG     TTTTTACT
                                ||| |||||||     ||||||||
                                AGG GGTTACT     GAAGATGG
                                  _       CTTCA
GAM376  DNAJB5    3'  AGTGGGAGGGAGGTGGGGAG   24353      AGTG  G
                                CTCC    GC TTCTTTTTACT
                                ||||    || ||||||||||
                                GAGG    TG AGGGAGGGTGA
                                  GG__  G
GAM376  DNAJC5    3'  AGGCTGCCACTGGAGGG      61446            TT
                                TCCTCCAGTGGCG  CT
                                ||||||||||||  ||
                                GGGAGGTCACCGT  GA
                                        CG
GAM376  DOCK3     3'  AGTGGAGAGGAGGGAACTGGTG 66496     T    GGCG
           GA                     TCC CCAGT    TTCTTTTTACT
                                ||| |||||    ||||||||||
                                AGG GGTCA    AGGAGAGGTGA
                                  T    AGGG
GAM376  DOCK3     3'  GGTAAAGAGGGTGGGAGGG    66506       AGTGG  TT
                                TCCTCC     CG  CTTTTTACT
                                ||||||     ||  |||||||||
                                GGGAGG     GT  GAGAAATGG
                                     _____  GG
GAM376  DT1P1A10  3'  AGTGAGTGTGGGTGTGGCTGGA 61564         G   TT TT_
           GGA                      TCCTCCAGT GCG  C   TTTACT
                                ||||||||| |||  |   ||||||
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                                AGGAGGTCG TGT  G   GAGTGA
                                     G   GG TGT
GAM376  EBF2     5'  AGTGAAGGCTGGACCACAGGAG 42643       A    CGTTC
             GA                    TCCTCC GTGG     TTTTTACT
                                   ||||||| ||||     ||||||||
                                   AGGAGG CACC     GGAAGTGA
                                      A    AGGTC
GAM376  ELF2     3'  AGTGGGAGGGGTTGGGATGGG  22497     _  AGTGGC TT
                                   TCC TCC     G  CTTTTTACT
                                   ||| |||     |  |||||||||
                                   GGG AGG     T  GGAGGGTGA
                                     T   GT____ GG
GAM376  ERF      3'  TGGTGGGGGGGAGTAGAGGGGCC 21440       G _______
             GCTGGAG                   GTGGC T     TCTTTTTACT   G
                                   ||||| |     ||||||||||   |
                                   CGCCG G     AGGGGGGTGG   T
                                      G GAGATG
GAM376  EZF-2    5'  AGTGAGGACAGGCTGCGGGAGG 37095       A TG  G  C
             A                     TCCTCC G  GC TT TTTTTACT
                                   ||||||| |  || || ||||||||
                                   AGGAGG C  CG GA AGGAGTGA
                                      G GT  _  C
GAM376  EZFIT    3'  GGAGCTGGTGGAGGG       41110        G    G
                                   TCCTCCA TGGC TTC
                                   ||||||| |||| |||
                                   GGGAGGT GTCG AGG
                                      G   _
GAM376  FER1L4   5'  AGTACTATGCGTCGCTGCAGGA 47332      C        TCTTTT
                                   TCCT CAGTGGCGT      TACT
                                   |||| |||||||||      ||||
                                   AGGA GTCGCTGCG      ATGA
                                     C        TATC__
GAM376  FKBP8    5'  AGTGAGCTGCCACCGCTGGAGG 24099          C_  TCTT
             A                     TCCTCCAGTGG  GT    TTTACT
                                   ||||||||||  ||    ||||||
                                   AGGAGGTCGCC  CG    GAGTGA
                                         AC  TC__
GAM376  FLJ10315 3'  GGTAGAAGTGGTGGTGGGGGG  36021        G  G  TTC
                                   TCCTCCA TG CG   TTTTTACT
                                   ||||||| || ||   ||||||||
                                   GGGGGGT GT GT   GAAGATGG
                                      G  G  ___
GAM376  FLJ10483 5'  GAGGGCGCCGCTGGGCGG    36170    _
                                   CC TCCAGTGGCGTTCTT
                                   || ||||||||||||||
                                   GG GGGTCGCCGCGGGAG
                                    C
GAM376  FLJ10525 3'  GGTAGGGGGAGGAGTTGTGGGG 36225       A TG  G_
             GA                    TCCTCC G  GC  TTCTTTTTACT
                                   |||||| |  ||  ||||||||||
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                                AGGGGG T  TG  GAGGGGGATGG
                                   _ GT  AG
GAM376  FLJ10702  5'  GCACCAAGGAGCCGTTGGAGGG 36441          G    TTTACT
                                TCCTCCAGTGGC TTCTT
                                |||||||||||| |||||
                                GGGAGGTTGCCG AGGAA
                                       _    CCACGG
GAM376  FLJ10898  5'  GGTGAAGGGCAGACTGCTAGAG 59437      C  TG CGTT
          GA                     TCCTC AG  G   CTTTTTACT
                                ||||| ||  |   |||||||||
                                AGGAG TC  C   GGGAAGTGG
                                  A  GT AGAC
GAM376  FLJ10933  3'  GTAAGACATTGTTGGTGGA   36903    T   TG C   CTTT
                                TCC CCAG  G GTT   TTAC
                                ||| ||||  | |||   ||||
                                AGG GGTT  T CAG   AATG
                                  T   GT A  _____
GAM376  FLJ11017  5'  AGAGAAGGAATGTTGCTGGGGA 36985    T   TG        ACT
                                TCC CCAG  GCGTTCTTTTT
                                ||| ||||  ||||||||||
                                AGG GGTC  TGTAAGGAAGA
                                  _   GT         GA
GAM376  FLJ11186  5'  GTTAGAGAACGTCGCGGAGGA  37144       A         TT
                                TCCTCC GTGGCGTTCTTT  AC
                                |||||| ||||||||||||  ||
                                AGGAGG CGCTGCAAGAGA  TG
                                   _          T_
GAM376  FLJ11996  3'  GTGGAAAGGGTGGGTGGA   46444    T  AGTGG  TT
                                TCC CC    CG  CTTTTTAC
                                ||| ||    ||  ||||||||
                                AGG GG    GT  GAAAGGTG
                                  T  _____  GG
GAM376  FLJ12294  3'  AGTGGAAGGCCACAGCTGGAG  47006       ___  G   TTTTACT
                                CTCCAGT   GGC TTCT
                                |||||||   ||| ||||
                                GAGGTCG   CCG AAGG
                                     ACA   G   TGA   T
GAM376  FLJ12377  5'  GGTAGAGGGGGCGGCGGCGGCG 46485    T  AG  G
          G                     CC CC  TG CGTTCTTTTTACT
                                || ||  || ||||||||||||
                                GG GG  GC GCGGGGGAGATGG
                                 C  CG  G
GAM376  FLJ12572  3'  GTAGGAGGGGCAGGAGG    43254      AGTGGC
                                CCTCC     GTTCTTTTTAC
                                |||||     ||||||||||
                                GGAGG     CGGGGAGGATG
                                  A_____
GAM376  FLJ12770  5'  GGGGCCCGTTGGGGGG      49742          C
                                TCCTCCAGTGG GTTCT
                                |||||||||| |||||
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                                GGGGGGTTGCC CGGGG
                                      _
GAM376  FLJ12973  3' AGTAAGGGAGAAGTCTTGGAGG 46101        T  G    _
             G                  TCCTCCAG GGC TTCTTT TTACT
                                |||||||| ||| |||||| |||||
                                GGGAGGTT CTG AAGAGG AATGA
                                   _  _    G
GAM376  FLJ13181  5' GTGGAGGGAGCGAGAGG    47241     CAGTGG
                                CCTC    CGTTCTTTTTAC
                                ||||    ||||||||||||
                                GGAG    GCGAGGGAGGTG
                                  A_____
GAM376  FLJ13291  3' AGTGAAAACTTATGTTAGGGGA 49778      CAG    TC_
                                TCCTC  TGGCGT  TTTTTACT
                                |||||  ||||||  ||||||||
                                AGGGG  ATTGTA  AAAAGTGA
                                   ___    TTC
GAM376  FLJ13639  3' GGGACTGTCCCCTGGGGGG   45235       T  _ _
                                TCCTCCAG GG C GTTCT
                                |||||||| || | |||||
                                GGGGGGTC CC G CAGGG
                                     C  T T
GAM376  FLJ13769  3' GAGAATGACATGGGGGA    46612       G  G
                                TCCTCCA TG CGTTCTT
                                ||||||| || |||||||
                                AGGGGGT AC GTAAGAG
                                   _ A
GAM376  FLJ13769  3' TAAGGGGGACAGAGGG     46625      CAGTGGC
                                TCCTC     GTTCTTTTTA
                                |||||     ||||||||||
                                GGGAG     CAGGGGGAAT
                                  A_______
GAM376  FLJ13798  3' GGTGGGGAGAGCCCAGAAGGA  87109     CCAG  C
                                TCCT   TGG GTTCTTTTTACT
                                ||||   ||| ||||||||||||
                                AGGA   ACC CGAGAGGGGTGG
                                  AG__  _
GAM376  FLJ14326  3' GTGGAGGGGGTGTTCTG    49818    T   TT
                                CAG GGCG  CTTTTTAC
                                ||| ||||  ||||||||
                                GTC TTGT  GGGAGGTG
                                  _   GG
GAM376  FLJ14346  3' GTGGAGAGGGGCTGAGGGA   46720    TC   GGCG
                                TCC  CAGT   TTCTTTTTAC
                                |||  ||||   ||||||||||
                                AGG  GTCG   GGGAGAGGTG
                                  GA   _____
GAM376  FLJ14827  5' GGTGGGAAGAAGGTGCGGGGA  51653    T  A   G G
                                TCC CC GTG C TTCTTTTTACT
                                ||| || ||| | ||||||||||
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                                AGG GG CGT G AAGAAGGGTGG
                                  _ _  _ G
GAM376  FLJ14855  3'  TAGAGTTCCTGGAGGG     52620        TG  GTTCTT
                                TCCTCCAG  GC     TTTA
                                ||||||||  ||     ||||
                                GGGAGGTC  TG     AGAT
                                    CT  _______
GAM376  FLJ14927  3'  AGTAGCCTTGCTGTTGGGTGA  51704    C    TG   TTCTTT
                                TC TCCAG  GCG     TTACT
                                || |||||  |||     |||||
                                AG GGGTT  CGT     GATGA
                                 T    GT   TCC___
GAM376  FLJ20036  5'  CCTGCGGAGGGGCGTTATCTGG 34397        _          TACT
           AGGG                    CCTCCAG TGGCGTTCTTTT
                                ||||||| ||||||||||||
                                GGAGGTC ATTGCGGGGAGG
                                    T          CGTCCG
GAM376  FLJ20040  5'  GGTGGAAGGGAGCTGTTGCGGG 38634      _  TG  G
           G                     CCTC CAG  GC TTCTTTTTACT
                                |||| |||  || ||||||||||
                                GGGG GTT  CG AGGGAAGGTGG
                                  C   GT  _
GAM376  FLJ20311  3'  GGGGGTTATGGAGGA      34924        G   G
                                TCCTCCA TGGC TTC
                                ||||||| |||| |||
                                AGGAGGT ATTG GGG
                                    _   G
GAM376  FLJ20321  3'  GGTGGAAGGGACCCTCCTCACT 34950        C____
           GGATGG                  CCAGTGG    GTTCTTTTTACT
                                |||||||    ||||||||||||
                                GGTCACT    CAGGGAAGGTGG
                                    CCTCC
GAM376  FLJ20464  5'  TGGGGGTGCCGGAGGA     35236       AGT   TT  TTT
                                TCCTCC   GGCG  CT   TA
                                ||||||   ||||  ||   ||
                                AGGAGG   CCGT  GG   GT
                                   ___    GG  ___
GAM376  FLJ20583  5'  GGTGGAGGGGACGCGGCGG   35425    A  G
                                CC GT GCGTTCTTTTTACT
                                || || ||||||||||||||
                                GG CG CGCAGGGGAGGTGG
                                 _ G
GAM376  FLJ20967  5'  GGTGGAGGGACACCTGGAGG   41964       GT  C  T
                                CCTCCA  GG GT CTTTTTACT
                                ||||||  || || |||||||||
                                GGAGGT  CC CA GGGAGGTGG
                                   __  A  _
GAM376  FLJ21438  5'  GGTGGGGAGAAGGCGGCTGGAG 61526         G  G
           GG                     TCCTCCAGT GC TTCTTTTTACT
                                |||||||||  || ||||||||||
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                                GGGAGGTCG CG AAGAGGGGTGG
                                     G  G
GAM376  FLJ21870  3'  GGACCCAGAGCAGCCGCTGGAG 43461          _    TTTTACT
            GG                    TCCTCCAGTGGC GTTCT
                                  |||||||||||| |||||
                                  GGGAGGTCGCCG CGAGA
                                        A    CCCAGG
GAM376  FLJ21924  5'  TAGTGGAGAGAGTGCTACATCA 45479    CA__
            GAG                   TC   GTGGCGTTCTTTTTACT  A
                                  ||   ||||||||||||||||  |
                                  AG   CATCGTGAGAGAGGTGA  T
                                   ACTA
GAM376  FLJ21945  3'  GGTTGAGGAGTCTGCTGGGGGG 47318        TG C     TT
                                  TCCTCCAG  G GTTCTTT  ACT
                                  ||||||||  | |||||||  |||
                                  GGGGGGTC  C TGAGGAG  TGG
                                       GT _     T_
GAM376  FLJ22054  5'  GGTAGAAAATCCATTAGAGGA  94399      C    CGTTC
                                  TCCTC AGTGG    TTTTTACT
                                  ||||| |||||    ||||||||
                                  AGGAG TTACC    AAAGATGG
                                     A    TA___
GAM376  FLJ22167  3'  GGTGGAGAGGGAGCTGGGG   44582       GGCGT
                                  CTCCAGT    TCTTTTTACT
                                  |||||||    ||||||||||
                                  GGGGTCG    GGAGAGGTGG
                                       AG___
GAM376  FLJ22378  3'  AGTGGGGAGGACGAGGATGTGG 46894    TC  GTGG
            GA                    TCC  CA   CGTTCTTTTTACT
                                  |||  ||   ||||||||||||
                                  AGG  GT   GCAGGAGGGGTGA
                                    GT  AGGA
GAM376  FLJ22386  5'  GGTGGGGAGGGCGCTCGGCGGC 44744    T  A  __
            GG                    CC CC GT  GGCGTTCTTTTTACT
                                  || || ||  ||||||||||||||
                                  GG GG CG  TCGCGGGAGGGGTGG
                                   C  _  GC
GAM376  FLJ22405  5'  GGGGAGCTGCTGGAGGA    42522        TG  G
                                  TCCTCCAG  GC TTCTT
                                  ||||||||  || |||||
                                  AGGAGGTC  CG AGGGG
                                       GT  _
GAM376  FLJ22596  5'  GTAGAAAGGATGTCGGGG    46963     AGT
                                  CTCC   GGCGTTCTTTTTAC
                                  ||||   ||||||||||||||
                                  GGGG   CTGTAGGAAAGATG
                                         ___
GAM376  FLJ22655  3'  GGTAAAAAGAATTCTCTTGGAG 45312       T  C
                                  CTCCAG GG GTTCTTTTTACT
                                  |||||| || ||||||||||||
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                                GAGGTT TC TAAGAAAAATGG
                                   C  T
GAM376  FLJ22679  3' AGTGAAGAGAATGTGATAGG   49920    A  G
                                CC GT GCGTTCTTTTTACT
                                || || ||||||||||||||
                                GG TA TGTAAGAGAAGTGA
                                 A  G
GAM376  FLJ22679  3' AGTGAAGAGAATGTGATAGG   34678    A  G
                                CC GT GCGTTCTTTTTACT
                                || || ||||||||||||||
                                GG TA TGTAAGAGAAGTGA
                                 A  G
GAM376  FLJ22690  3' GGTGGAGACAGTGCTGGGAG   45249     AGT     C
                                CTCC   GGCGTT TTTTTACT
                                ||||   |||||| ||||||||
                                GAGG   TCGTGA AGAGGTGG
                                   G__     C
GAM376  FLJ23091  3' GGTGGGGGGTGTATTCCTTGGGG 46125        T  C  TC_
           GA                     TCCTCCAG GG GT   TTTTTACT
                                ||||||||| || ||   ||||||||
                                AGGGGGTT CC TA   GGGGGGTGG
                                     _  T  TGT
GAM376  FLJ23185  3' AGTGATCAGGCCACTGGAGGA  46825          GTT  TT
                                TCCTCCAGTGGC   CT  TTACT
                                ||||||||||||   ||  |||||
                                AGGAGGTCACCG   GA  AGTGA
                                       ____  CT
GAM376  FLJ23185  3' GGTGGAGAGGATGAGGTTTGAG 46832      CAGTGG
           GA                     TCCTC     CGTTCTTTTTACT
                                |||||      ||||||||||||||
                                AGGAG     GTAGGAGAGGTGG
                                   TTTGGA
GAM376  FLJ23231  3' GGTGGGGAGGGAGGTGGGGG   46914       GTGGCG
                                CCTCCA     TTCTTTTTACT
                                ||||||     ||||||||||
                                GGGGGT     GGGAGGGGTGG
                                    GGA___
GAM376  FLJ23375  3' GGTGGAGGGCCAGGATTGGTGG 46358    T   ___    G   TTTTACT
           G                      CC CCAG   TGGC TTCT
                                || ||||   |||| ||||
                                GG GGTT   ACCG GAGG
                                 T   AGG   G   TGG  T
GAM376  FLJ23510  3' GGTGGAATGGTGTATGCTGTTG 45288   T   TG   ___  T
           GTGGA                    CCAG  GCGT   TC TTTTACT
                                 ||||  ||||   || |||||||
                                 GGTT  CGTA   GG AAGGTGG
                                T   GT    TGT  T
GAM376  FLJ23519  5' GGTGGGGAGGGTGCTGAAGAGG 69206      CAG    TT
           A                      TCCTC   TGGCG  CTTTTTACT
                                |||||   |||||  |||||||||
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                                AGGAG  GTCGT  GAGGGGTGG
                                  AA_    GG
GAM376  FLJ30567  3'  GGATGTTACTGGAGGG     58828
                                TCCTCCAGTGGCGTTC
                                ||||||||||||||||
                                GGGAGGTCATTGTAGG

GAM376  FLJ31455  5'  GGTGAGGGGATCAGTCTGGTGG 58631    T   TG  GT_
          A                    TCC CCAG  GC   TCTTTTTACT
                               ||| ||||  ||   ||||||||||
                               AGG GGTC  TG   AGGGGAGTGG
                                 T   __  ACT
GAM376  FLJ31455  5'  TGGAAAGGACAGAGGA     58632      CAGTGGC
                               TCCTC      GTTCTTTTTA
                               |||||      ||||||||||
                               AGGAG      CAGGAAAGGT
                                  A_______
GAM376  FOXO3A    5'  GGGGGGTGACGGGGGG      7577       A  G  G
                               TCCTCC GT GC TTCT
                               |||||| || || ||||
                               GGGGGG CA TG GGGG
                                  _  G  G
GAM376  GALNT6    3'  AGTAGGGAAGGCAGCTGGGGGA 23289        G  G   TT
                               TCCTCCAGT GC TTCT  TTACT
                               ||||||||| || ||||  |||||
                               AGGGGGTCG CG AAGG  GATGA
                                    A  G   __
GAM376  GIT2      3'  GGTGGAATGACGTGGCCATTGG 28762         GT__  T
          AGGG                   CCTCCAGTGGC   TC TTTTACT
                               ||||||||||||   || |||||||
                               GGAGGTTACCG   AG AAGGTGG
                                     GTGC  T
GAM376  GIT2      3'  GGTGGAATGACGTGGCCATTGG 54084         GT__  T
          AGGG                   CCTCCAGTGGC   TC TTTTACT
                               ||||||||||||   || |||||||
                               GGAGGTTACCG   AG AAGGTGG
                                     GTGC  T
GAM376  GIT2      3'  GGTGGAATGACGTGGCCATTGG 54097         GT__  T
          AGGG                   CCTCCAGTGGC   TC TTTTACT
                               ||||||||||||   || |||||||
                               GGAGGTTACCG   AG AAGGTGG
                                     GTGC  T
GAM376  GPA33     5'  GGTGAGAAGAGGGAAAATTGCA 19458     C   GGCG_
          GGG                    TCCT CAGT    TTCTTTTTACT
                               ||||  ||||    ||||||||||
                               GGGA GTTA    GAGAAGAGTGG
                                 C   AAAGG
GAM376  GPS2      5'  GGGGGCTCTGGGGGA      87161       T  G
                               TCCTCCAG GGC TTC
                               |||||||| ||| |||
```

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                                AGGGGGTC TCG GGG
                                    _  G
GAM376  GTF3C4   3'  TGAAGAGAAGGATGCACTGGAG 24195         G       ACT
            GA                   TCCTCCAGTG CGTTCTTTTT
                                 |||||||||| ||||||||||
                                 AGGAGGTCAC GTAGGAAGAG
                                     _        AAGTC
GAM376  H2AFY    5'  GGTGAGGAGGATTAACTGAAGG 16891     C   GGC
            A                    TCCT CAGT   GTTCTTTTTACT
                                 |||| ||||  ||||||||||||
                                 AGGA GTCA   TAGGAGGAGTGG
                                   A   AT_
GAM376  HAPIP    3'  AGTGAAGAGGTTAATTAGAGGG 14159      C   GGCGT
                                 TCCTC AGT    TCTTTTTACT
                                 ||||| |||    ||||||||||
                                 GGGAG TTA    GGAGAAGTGA
                                    A  ATT__
GAM376  HEMK     3'  GGTGGGGAGGGCGAAGGGGG  32438      AGTGG
                                 CCTCC    CGTTCTTTTTACT
                                 |||||    ||||||||||||
                                 GGGGG    GCGGGAGGGGTGG
                                   AA___
GAM376  HES2     3'  TGGGAAGAATGGGGAG     38857      AGTGG
                                 CTCC    CGTTCTTTTTA
                                 ||||    ||||||||||
                                 GAGG    GTAAGAAGGGT
                                   G____
GAM376  HNRPA3   3'  GGTGGATATGGTGGCGGTGTTG 19255     GT G   _  T__
            GAGGA                  TCCA  G CGTT CT   TTTACT
                                   ||||  | |||| ||   ||||||
                                   AGGT  T GCGG GG   AGGTGG
                                     TG G    T  TAT
GAM376  HTATIP   3'  AGTGAGAAGGGATCCGGATGGG 21105       G_  CG
            GGA                    TCCTCCA  TGG  TTCTTTTTACT
                                   |||||||  |||  ||||||||||
                                   AGGGGGT  GCC  GGGAAGAGTGA
                                      AG   TA
GAM376  IMPACT   3'  GGATGCTGTTTGGAGGA     37392        _ TG
                                   TCCTCCA G  GCGTTC
                                   |||||||  |  ||||||
                                   AGGAGGT T  CGTAGG
                                      T GT
GAM376  INSM2    3'  GGTGGGGAGGATGCTACTTTAC 50869      _____
            TGGAG                   CAGT    GGCGTTCTTTTTACT
                                    ||||    ||||||||||||||
                                    GTCA    TCGTAGGAGGGGTGG
                                      TTTCA
GAM376  KCNJ9    3'  GTGGAGGGGGTGTCTGGA    17156      TG   TT
                                    TCCAG  GCG  CTTTTTAC
                                    |||||  |||  ||||||||
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                                AGGTC  TGT  GGGAGGTG
                                  __   GG
GAM376  KCNK16   3'  GTAGAGGGATTTCGGGGG    49507      AGT  CGT
                                CCTCC   GG   TCTTTTTAC
                                |||||   ||   |||||||||
                                GGGGG   CT   AGGGAGATG
                                  ____  TT_
GAM376  KCNV1    5'  GGTGGAGAGGGTGCGCCAAGGA 26883      AG     __
           G                     CTCC  TGGCGT  TCTTTTTACT
                                ||||  ||||||  ||||||||||
                                GAGG  ACCGCG  GGAGAGGTGG
                                  A_     TG
GAM376  KIAA0089 3'  AGTGAATCATGCAACGTGTTGG 69963      GT G    CTT___
           GGGA                    CTCCA  G CGTT     TTTACT
                                |||||  | ||||     ||||||
                                GGGGT  T GCAA     AAGTGA
                                   TG _    CGTACT
GAM376  KIAA0100 3'  TGAAAGGGTAGGGGGA     27973       AGTGGCGT
                                TCCTCC       TCTTTTTA
                                ||||||       ||||||||
                                AGGGGG       GGGAAAGT
                                   AT_______
GAM376  KIAA0143 3'  AGTGGAGTCGTTACCGCTGGAG 64779          CGTTCT
           GA                    TCCTCCAGTGG     TTTTACT
                                ||||||||||     |||||||
                                AGGAGGTCGCC     GAGGTGA
                                      ATTGCT
GAM376  KIAA0247 3'  GGTAGGGAGCTGGTTGGAG    28408       TGGC    TT
                                CTCCAG    GTTCT  TTACT
                                ||||||    |||||  |||||
                                GAGGTT    CGAGG  GATGG
                                   GGT_    __
GAM376  KIAA0247 3'  GTAGAAGGGGATGCAGGG    28409    AGTG     _
                                CC    GCGTTCT TTTTAC
                                ||    ||||||| ||||||
                                GG    CGTAGGG AAGATG
                                 GA__      G
GAM376  KIAA0261 3'  GGTGGGGGGGAGGTGGTGGGGGA 68182        G G  G
                                TCCTCCA T GC TTCTTTTTACT
                                ||||||| | || ||||||||||
                                AGGGGGT G TG GAGGGGGGTGG
                                   _ G  _
GAM376  KIAA0323 3'  GGTAAAAATACCTGTTGGGAGG 63269       _  TG C  TC
           A                     TCCTCC AG  G GT  TTTTTACT
                                ||||||  ||  | ||  ||||||||
                                AGGAGG TT  C CA  AAAAATGG
                                   G  GT _  T_
GAM376  KIAA0352 3'  CCTCCAGGGGGGCGCTATTGGAT 29154    _            TTACT
           GG                      CC TCCAGTGGCGTTCTTT
                                || ||||||||||||||||
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```
                                GG AGGTTATCGCGGGGGA
                                 T            CCTCCA
GAM376  KIAA0354  3'  TGTGGGAAAGAGCCCATTGGAG 29573          C       ACT
          GA                     TCCTCCAGTGG GTTCTTTTT
                                 |||||||||| |||||||||
                                 AGGAGGTTACC CGAGAAAGG
                                        _       GTGTA
GAM376  KIAA0367  3'  AGTGAGAAAGTTTGTTTGAGGG 67291      CAGT   TT  _
                                 TCCTC   GGCG  CTT TTTACT
                                 |||||   ||||  ||| ||||||
                                 GGGAG   TTGT  GAA GAGTGA
                                    T___   TT   A
GAM376  KIAA0367  3'  GGTGGAAAATTCATTGGGGA  67301     T      CGTTC
                                 TCC CCAGTGG    TTTTTACT
                                 ||| |||||||    ||||||||
                                 AGG GGTTACT    AAAGGTGG
                                   _      TA___
GAM376  KIAA0431  3'  GGTGAGAGGATCACTCGAGGA  30894      C    CGT
                                 TCCTC AGTGG   TCTTTTTACT
                                 ||||| |||||   ||||||||||
                                 AGGAG TCACT   AGGAGAGTGG
                                    C    ___
GAM376  KIAA0446  5'  AGTGAGGGACAATTTCTGGAGG 68852        TGGC_    TT
          A                      TCCTCCAG    GTTCT  TTACT
                                 ||||||||    |||||  |||||
                                 AGGAGGTC    CAGGG  AGTGA
                                      TTTAA    __
GAM376  KIAA0472  3'  AGTGGGGAGGGTGGAAGGGAGG 71855       AGTGG  TT
          G                      TCCTCC    CG  CTTTTTACT
                                 ||||||    ||  |||||||||
                                 GGGAGG    GT  GAGGGGTGA
                                    GAAG_  GG
GAM376  KIAA0472  3'  GAGATTGTGGCTGGAGGA    71864         G   T
                                 TCCTCCAGT GCG TCTT
                                 ||||||||| ||| ||||
                                 AGGAGGTCG TGT AGAG
                                      G   T
GAM376  KIAA0495  5'  GGTGGAGACCCTTTACTGCAGG 62598      C     CGTTC
          G                      TCCT CAGTGG    TTTTTACT
                                 |||| ||||||    ||||||||
                                 GGGA GTCATT    AGAGGTGG
                                   C     TCCC_
GAM376  KIAA0522  3'  AGTGGGAGGGGCTGTATGGAG  71964      GTGGC
                                 CTCCA    GTTCTTTTTACT
                                 |||||    ||||||||||||
                                 GAGGT    CGGGGAGGGTGA
                                    ATGT_
GAM376  KIAA0557  3'  AGTGGAGGGGGCAGGGGAGGG  77988       AGTGGC
                                 TCCTCC     GTTCTTTTTACT
                                 ||||||     ||||||||||||
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                                GGGAGG     CGGGGGAGGTGA
                                   GGA___
GAM376  KIAA0563  5'  AAGAACGGCTGTGGGGGA    29177        G   _
                                TCCTCCA TGGC GTTCTT
                                ||||||| |||| ||||||
                                AGGGGGT GTCG CAAGAA
                                   _   G
GAM376  KIAA0596  3'  AGCTGTGGGATGTTGCTGCAGG 62824     C   TG      TTTTACT
          A                      TCCT CAG  GCGTTCT
                                 |||| |||  |||||||
                                 AGGA GTC  TGTAGGG
                                   C   GT      TGTCGA
GAM376  KIAA0620  3'  GGTGGAGGGGAGGGATGGGGGG 62122        GTGGCG
                                TCCTCCA     TTCTTTTTACT
                                |||||||     ||||||||||
                                GGGGGGT     AGGGGAGGTGG
                                   AGGG__
GAM376  KIAA0664  3'  GTGGGGAGGGGTGGGGAG    64287     AGTG  G
                                CTCC    GC TTCTTTTTAC
                                ||||    || ||||||||||
                                GAGG    TG GGGAGGGGTG
                                  GG__ _
GAM376  KIAA0677  3'  GGTGGGGGGGTGGGACTAGAGGG 27830      C   GG  TT   TT
                                TCCTC AGT  CG  CTT  TACT
                                ||||| |||  ||  |||  ||||
                                GGGAG TCA  GT  GGG  GTGG
                                  A   GG  GG  __
GAM376  KIAA0767  3'  GGTGCCGGGGGGTGCTTTGGGGG 60630        T    TT   TT
          G                      TCCTCCAG GGCG  CTT  TACT
                                 |||||||| ||||  |||  ||||
                                 GGGGGGTT TCGT  GGG  GTGG
                                    _   GG   CC
GAM376  KIAA0773  3'  AGTGAGAAGGTTGAGAGTTGGG 28045        GG_  TT
          G                      CTCCAGT   CG  CTTTTTACT
                                 |||||||   ||  |||||||||
                                 GGGGTTG   GT  GAAGAGTGA
                                    AGA  TG
GAM376  KIAA0773  3'  AGTGGGAGGGATGTGATGCTGG 28046         __
          AG                      CTCCAGTG  GCGTTCTTTTTACT
                                  ||||||||  ||||||||||||||
                                  GAGGTCGT  TGTAGGGAGGGTGA
                                     AG
GAM376  KIAA0773  3'  GGTGGGGAGGGGCATGTGCAGG 28060     C  GTG  G
          A                      TCCT CA   GC TTCTTTTTACT
                                 |||| ||   || ||||||||||
                                 AGGA GT   CG GGGAGGGGTGG
                                   C  GTA  _
GAM376  KIAA0774  5'  GGATGTCATTGAGGA      91754       C
                                TCCTC AGTGGCGTTC
                                ||||| ||||||||||
```

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                                AGGAG TTACTGTAGG
                                  _
GAM376  KIAA0775 3' GGTGGGGGGGAAGGTGTTAGAGG 28283      CAGTG  G
            A                    TCCTC    GC TTCTTTTTACT
                                 |||||    || ||||||||||
                                 AGGAG    TG AAGGGGGGTGG
                                   ATTG_  G
GAM376  KIAA0794 3' AGTAAGGAGGATGGCGGAGG   80407      AGT G
                                 CCTCC   G CGTTCTTTTTACT
                                 |||||   | ||||||||||||
                                 GGAGG   C GTAGGAGGAATGA
                                   ___ G
GAM376  KIAA0821 3' AGTGAGGAGGGAGAACTTGGAA 29940     _  _  GGCG
            GGG                    CCT CCA GT    TTCTTTTTACT
                                 ||| ||| ||    ||||||||||
                                 GGA GGT CA    GGGAGGAGTGA
                                   A  T  AGA_
GAM376  KIAA0841 3' AGTGATGTAATGTCATTGGGGA 71375     T        CTTT
                                 TCC CCAGTGGCGTT    TTACT
                                 ||| ||||||||||    |||||
                                 AGG GGTTACTGTAA    AGTGA
                                   _         TGT_
GAM376  KIAA0863 3' GTAGAAATATTTGGAGGA    95247        TGGCGTTC
                                 TCCTCCAG       TTTTTAC
                                 ||||||||       |||||||
                                 AGGAGGTT       AAAGATG
                                      TAT_____
GAM376  KIAA0869 3' AGTGAGGGGAGGGCTGTGGGGA 70855     T   G    G
                                 TCC CCA TGGC TTCTTTTTACT
                                 ||| ||| |||| ||||||||||
                                 AGG GGT GTCG GAGGGGAGTGA
                                   _  _    G
GAM376  KIAA0888 3' GTAAACTGCCTTTGGGGGA    63231        T    TTCTT
                                 TCCTCCAG GGCG     TTTAC
                                 |||||||| ||||     |||||
                                 AGGGGGTT CCGT     AAATG
                                      T    C____
GAM376  KIAA0903 3' AGTGGGAGGGGTACAAGGGGA  71405     T  AG  GC TT
                                 TCC CC  TG  G  CTTTTTACT
                                 ||| ||  ||  |  |||||||||
                                 AGG GG  AC  T  GGAGGGTGA
                                   _ A_  A_ GG
GAM376  KIAA0960 3' AGTGAAAATCATACTGCCACTG 92654          _  TC__
            GAG                    CTCCAGTGGC GT    TTTTTACT
                                 ||||||||||  ||    ||||||||
                                 GAGGTCACCG CA    AAAAGTGA
                                       T  TACT
GAM376  KIAA0972 3' GTGGAAAGAGCACGAGGA    30015       CAGT GC
                                 TCCTC    G  GTTCTTTTTAC
                                 |||||    |  ||||||||||
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                                AGGAG   C  CGAGAAAGGTG
                                  _____ A_
GAM376  KIAA0992  3'  AGTAGGGAGGAGAATGAAGGA  32203     C  GTGGCG
                                TCCT CA     TTCTTTTTACT
                                |||| ||     ||||||||||
                                AGGA GT     AGGAGGGATGA
                                  A  AAG___
GAM376  KIAA1032  3'  GGACCAGGATGCTGGTTGGAGG 66157       GT_      TTTTACT
            G                    TCCTCCA   GGCGTTCT
                                |||||||   ||||||||
                                GGGAGGT   TCGTAGGA
                                    TGG       CCAGG
GAM376  KIAA1036  3'  AGTAGAGAGAGCTCGTGCTGGG 29812     T     GC_
            GA                    TCC CCAGTG   GTTCTTTTTACT
                                ||| ||||||   ||||||||||||
                                AGG GGTCGT   CGAGAGAGATGA
                                  _     GCT
GAM376  KIAA1036  3'  GGTGAGAAGGAGGCCTGAAGGG 29828     C  GT   G
                                TCCT CA  GGC TTCTTTTTACT
                                |||| ||  ||| ||||||||||
                                GGGA GT  CCG AGGAAGAGTGG
                                  A  __   G
GAM376  KIAA1056  3'  AGTGGGGGTACATGCTGGAAGG 29691      _     GC  TC
            A                    TCCT CCAGTG  GT  TTTTTACT
                                |||| ||||||  ||  ||||||||
                                AGGA GGTCGT  CA  GGGGGTGA
                                  A     A_  T_
GAM376  KIAA1077  3'  AGTAGAAAGAAAGGCTGGGGA  72901     T    GGCG
                                TCC CCAGT    TTCTTTTTACT
                                ||| |||||    ||||||||||
                                AGG GGTCG    AAGAAAGATGA
                                  _    GA__
GAM376  KIAA1110  3'  GGTGGGAGGAGTGAGGAGGG   61848       AGTGG
                                TCCTCC    CGTTCTTTTTACT
                                ||||||    ||||||||||||
                                GGGAGG    GTGAGGAGGGTGG
                                   A____
GAM376  KIAA1130  3'  AGTGAGAATCCCGCTGTTTGGG 62411      ___     C     TTTACT
            GA                    CCTC   CAGTGG GTTCTT
                                ||||   |||||| ||||||
                                GGGG   GTCGCC TAAGAG
                                  TTT     C     TGA
GAM376  KIAA1130  3'  GTGAGGAGGGTGCCTGGG    62426     GT   TT
                                TCCA  GGCG  CTTTTTAC
                                ||||  ||||  ||||||||
                                GGGT  CCGT  GAGGAGTG
                                  __    GG
GAM376  KIAA1181  3'  GTGGGGGGAAAGTAGAGGA   68377      CAGTG  G
                                TCCTC    GC TTCTTTTTAC
                                |||||    || ||||||||||
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                                AGGAG    TG AAGGGGGGTG
                                  A____ A
GAM376  KIAA1190 3' GGTGAGGGGGGTGCTGGGGG  71103      GTG  TT
                                CCTCCA  GCG  CTTTTTACT
                                ||||||  |||  |||||||||
                                GGGGGT  CGT  GGGGAGTGG
                                   ___  GG
GAM376  KIAA1196 3' GCTCTGAGTGGCCACTGGGGGA 61470          GTT  TTTACT
                                TCCTCCAGTGGC  CTT
                                ||||||||||||  |||
                                AGGGGGTCACCG  GAG
                                      GT_  TCTCGG
GAM376  KIAA1219 3' AGAATAGCACTGGAGGA    61364         GC
                                TCCTCCAGTG  GTTCT
                                ||||||||||  |||||
                                AGGAGGTCAC  TAAGA
                                      GA
GAM376  KIAA1244 3' AGTACTCCACAGTTTACTGGGG 71987          _ GTTCTTTT
           GA                   TCCTCCAGTGG C       TACT
                                |||||||||||  |       ||||
                                AGGGGGTCATT G       ATGA
                                      T ACACCTC_
GAM376  KIAA1259 3' GGTGAAGAGGGCGGAGAGAGGG 49831      AGTGG_
           GG                   CCTCC     CGTTCTTTTTACT
                                |||||     |||||||||||||
                                GGGGG     GCGGGAGAAGTGG
                                  AGAGAG
GAM376  KIAA1277 3' GAGAACGCTGGGGCGG     64457    T  AG
                                CC CC  TGGCGTTCTT
                                || ||  ||||||||||
                                GG GG  GTCGCAAGAG
                                 C  G_
GAM376  KIAA1297 3' GGACCAGGTGCTGCTGGAGGG  72183        TG _____
                                TCCTCCAG  GC    GTTC
                                ||||||||  ||    ||||
                                GGGAGGTC  CG    CAGG
                                     GT  TGGAC
GAM376  KIAA1319 3' GGTGAGGGGAATGTTATGGG   40408      G
                                TCCA TGGCGTTCTTTTTACT
                                |||| ||||||||||||||||
                                GGGT ATTGTAAGGGGAGTGG
                                  _
GAM376  KIAA1337 3' GGATGTTTTGGGGGA       72681         T
                                TCCTCCAG GGCGTTC
                                |||||||| |||||||
                                AGGGGGTT TTGTAGG
                                   _
GAM376  KIAA1344 3' AGTGGGGAGAGGAATCTTGAGG 72446       C  TGGCG
           G                    TCCTC AG    TTCTTTTTACT
                                ||||| ||    ||||||||||
```

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                                GGGAG TC    GAGAGGGGTGA
                                  T  TAAG_
GAM376  KIAA1416 5' AAAGGAGCGCCGCGGAGGA   86452       A
                                TCCTCC GTGGCGTTCTTTT
                                |||||| ||||||||||||
                                AGGAGG CGCCGCGAGGAAA
                                  _
GAM376  KIAA1456 3' AGTTTGGGGGTTTATTGGAGGA 66987          C TT   TTT
                                TCCTCCAGTGG G  CTT   ACT
                                |||||||||||  |  |||   |||
                                AGGAGGTTATT T  GGG   TGA
                                      _ GG   TT_
GAM376  KIAA1463 3' GGTAAAGCATCCTGTGGAGGG  72278       GT  CGTTCT
                                TCCTCCA  GG     TTTTACT
                                |||||||  ||     |||||||
                                GGGAGGT  CC     GAAATGG
                                    GT  TAC___
GAM376  KIAA1464 3' AGTGGGAAAGGCACCTGGGGGA 68260       GT  C  TC
                                TCCTCCA  GG GT  TTTTTACT
                                |||||||  || ||  ||||||||
                                AGGGGGT  CC CG  AAGGGTGA
                                   __  A  GA
GAM376  KIAA1497 3' GTGGAGAGGACGGGTGGA    67517     T  AGTGG
                                TCC CC     CGTTCTTTTTAC
                                ||| ||     ||||||||||||
                                AGG GG     GCAGGAGAGGTG
                                  T  ______
GAM376  KIAA1503 5' GGTAGGAAGGGACAGTTGTTGG 68351    T    TG _       _
           GGA                    CC CCAG  GC GTTCTTTT TACT
                                || ||||  || |||||||| ||||
                                GG GGTT  TG CAGGGAAG ATGG
                                 _   GT  A       G
GAM376  KIAA1538 3' GGTGAGGGGGACCGGATGGAGG 71554        GTGGC
           G                     TCCTCCA    GTTCTTTTTACT
                                |||||||    ||||||||||||
                                GGGAGGT    CAGGGGGAGTGG
                                    AGGC_
GAM376  KIAA1538 3' GGTGGGGAGGACCAGCTCTGGA 71555        T  __
           GG                     CCTCCAG GGC  GTTCTTTTTACT
                                ||||||| |||  ||||||||||||
                                GGAGGTC TCG  CAGGAGGGGTGG
                                   _  AC
GAM376  KIAA1582 5' AGTGGGGGCAGTGCTGAAGGA  65367     C    GC    TTT
                                TCCT CAGTG  GTTCT   TACT
                                |||| |||||  |||||   ||||
                                AGGA GTCGT  CGGGG   GTGA
                                  A    GA    ___
GAM376  KIAA1614 3' GGTGGGGAGTGTGCGGGAGGG  70123       AGTG   TT
                                TCCTCC    GCG  CTTTTTACT
                                ||||||    |||  |||||||||
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                                GGGAGG   CGT  GAGGGGTGG
                                   G___   GT
GAM376  KIAA1622  3'  AGTAAGAAGATATGAAGTTGGA 40558       GG  _
            G                   CTCCAGT  CGT TCTTTTTACT
                                |||||||  ||| ||||||||||
                                GAGGTTG  GTA AGAAGAATGA
                                    AA   T
GAM376  KIAA1712  5'  GGACTGGCCATTGAGGA     67541      C     __
                                TCCTC AGTGGC  GTTC
                                ||||| ||||||  ||||
                                AGGAG TTACCG  CAGG
                                   _     GT
GAM376  KIAA1755  3'  GTGGGGGTGCATTTGGGGA   61353    T   TG   TT  TTT
                                TCC CCAG  GCG  CT   TAC
                                ||| ||||  |||  ||   |||
                                AGG GGTT  CGT  GG   GTG
                                  _   TA   GG  ___
GAM376  KIAA1821  3'  GGTGAGGAGAGGGGATCTGGGG 71793     T   TGGCG
            A                    TCC CCAG    TTCTTTTTACT
                                 ||| ||||    ||||||||||
                                 AGG GGTC    GAGAGGAGTGG
                                   _   TAGGG
GAM376  KIAA1831  3'  GGTGGGAGGAGGCACTTCTGGG 63785       TG__  G
            GGA                    CCTCCAG   GC TTCTTTTTACT
                                   |||||||   || ||||||||||
                                   GGGGGTC   CG GAGGAGGGTGG
                                       TTCA  _
GAM376  KIAA1857  3'  GGTGAGAAGGGTGCGGCCCGAG 50720     CA  G   TT
            G                    CCTC  GT GCG  CTTTTTACT
                                 ||||  || |||  |||||||||
                                 GGAG  CG CGT  GAAGAGTGG
                                   CC  G   GG
GAM376  KIAA1889  5'  AGTGGGGAGAATGACAGATGGA 73501       G_  G
            GG                     CCTCCA  TG CGTTCTTTTTACT
                                   ||||||  || ||||||||||||
                                   GGAGGT  AC GTAAGAGGGGTGA
                                      AG  A
GAM376  KIAA1906  3'  GGTAGGGGGGTGTAACTGGGGA  73196    T    G   TT  TT
                                TCC CCAGT GCG  CT  TTACT
                                ||| ||||| |||  ||  |||||
                                AGG GGTCA TGT  GG  GATGG
                                  _    A   GG  __
GAM376  KIAA1906  3'  GTAGGAAGGATCTGCAGGG   73197     C   TGGC
                                TCCT CAG    GTTCTTTTTAC
                                |||| |||    ||||||||||
                                GGGA GTC    TAGGAAGGATG
                                  C   ____
GAM376  KIAA1938  3'  GGTGGAGGGGGCCACCGGGG   92199     A    GT
                                CTCC GTGGC  TCTTTTTACT
                                |||| |||||  ||||||||||
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                                GGGG CACCG  GGGGAGGTGG
                                  C    __
GAM376  KIAA1938  3'  GGTGGGGGGGACCTGTGTTGGAG 92200       __ TG C  T
              GA                   CCTCCA  G  G GT CTTTTTACT
                                |||||| |  | || |||||||||
                                GGAGGT  T  C CA GGGGGGTGG
                                   TG GT _  _
GAM376  KIAA1938  3'  GGTGGGTAGGCCATGGGAGGG  92201       A    GTT  T
                                TCCTCC GTGGC   CT TTTACT
                                |||||| |||||   || ||||||
                                GGGAGG TACCG   GA GGGTGG
                                   G    ___  T
GAM376  KIAA1941  3'  GGTGGAGGTTGTTGGTGGAGGA 74843       G    TT   TT
                                TCCTCCA TGGCG  CTT  TACT
                                ||||||| |||||  |||  ||||
                                AGGAGGT GTTGT  GAG  GTGG
                                    G    TG  __
GAM376  KIAA1952  5'  GTGGAAACTGCTGGAG      73173       TG CGTTC
                                CTCCAG  G    TTTTTAC
                                ||||||  |    |||||||
                                GAGGTC  C    AAAGGTG
                                   GT _____
GAM376  LENG1     5'  GGGAGCTGCTGGAGGA      84075        TG  G
                                TCCTCCAG  GC TTCT
                                ||||||||  || ||||
                                AGGAGGTC  CG AGGG
                                    GT  _
GAM376  LGI3      3'  GTCTCCTCAGGGTGGCCACTGG 57748          _ TT  TTTTACT
              AGGA                   CCTCCAGTGGC G  CT
                                ||||||||||| |  ||
                                GGAGGTCACCG T  GA
                                      G GG  CTCCTCTGG
GAM376  LGI4      5'  TGGGGGGGGCAGGAG       57766      AGTGGC
                                CTCC     GTTCTTTTTA
                                ||||     ||||||||||
                                GAGG     CGGGGGGGGT
                                  A_____
GAM376  LIN-28    3'  AGTAAAGAGATGCAATTGGGGG 45145        G    T
                                CCTCCAGT GCGT CTTTTTACT
                                |||||||| |||| |||||||||
                                GGGGGTTA CGTA GAGAAATGA
                                    A   _
GAM376  LSM1      5'  GTAAGGGTAATATGGAGGA   27096        GTG_  GTTCT
                                TCCTCCA   GC    TTTTAC
                                |||||||   ||    ||||||
                                AGGAGGT   TG    GGAATG
                                    ATAA  _____
GAM376  MAD4      3'  GGTGAGGGGGGCGTGCGCTAGA 21281      C   _
              GGG                   CCTC AGTG GCGTTCTTTTTACT
                                |||| |||| ||||||||||||||
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                                GGAG TCGC TGCGGGGGGAGTGG
                                  A   G
GAM376  MAD4     3'  GGTGAGGGGTTGCCCACTGGGT 21282    _      C  T_
              GG                  CC TCCAGTGG GT  CTTTTTACT
                                || |||||||| ||  |||||||||
                                GG GGGTCACC CG  GGGGAGTGG
                                 T      _  TT
GAM376  MADHIP   3'  GGTGGGAAAGGGTGGTTGGGGG 23639        TG  G  C
              G                   TCCTCCAG  GC TT TTTTTACT
                                ||||||||  || || ||||||||
                                GGGGGGTT  TG GA AAGGGTGG
                                    GG  G  _
GAM376  MADHIP   3'  GGTGGGAAAGGGTGGTTGGGGG 16621        TG  G  C
              G                   TCCTCCAG  GC TT TTTTTACT
                                ||||||||  || || ||||||||
                                GGGGGGTT  TG GA AAGGGTGG
                                    GG  G  _
GAM376  MANBAL   3'  AGTGAGAGGGTTCCTGGGGGA  41977        TG  GTT
                                TCCTCCAG  GC   CTTTTTACT
                                ||||||||  ||   |||||||||
                                AGGGGGTC  TG   GGAGAGTGA
                                    CT  ___
GAM376  MAPK8    3'  TGGGAGGGATGGGGAG     57393     AGTGG
                                CTCC    CGTTCTTTTTA
                                ||||    ||||||||||
                                GAGG    GTAGGGAGGGT
                                  G____
GAM376  MAPK8    3'  TGGGAGGGATGGGGAG     57394     AGTGG
                                CTCC    CGTTCTTTTTA
                                ||||    ||||||||||
                                GAGG    GTAGGGAGGGT
                                  G____
GAM376  MAPK8    3'  TGGGAGGGATGGGGAG     57399     AGTGG
                                CTCC    CGTTCTTTTTA
                                ||||    ||||||||||
                                GAGG    GTAGGGAGGGT
                                  G____
GAM376  MAPK8    3'  TGGGAGGGATGGGGAG     10843     AGTGG
                                CTCC    CGTTCTTTTTA
                                ||||    ||||||||||
                                GAGG    GTAGGGAGGGT
                                  G____
GAM376  MESDC2   3'  GTGACGCGCTGTGGGGGGA   72497      A TG   TCTTT
                                TCCTCC G  GCGT    TTAC
                                |||||| |  ||||    ||||
                                AGGGGG T  CGCG    AGTG
                                   G GT   C____
GAM376  MFN2     3'  GGTAGAAAGGATGCTGCTGAGG 29604     C  TG
                                CCTC AG  GCGTTCTTTTTACT
                                |||| ||  ||||||||||||||
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                                GGAG TC  CGTAGGAAAGATGG
                                  _ GT
GAM376  MGC10966 5' GGGACCTGCTGCTGGAGGA   48897       TG __
                                TCCTCCAG  GC  GTTCT
                                ||||||||  ||  |||||
                                AGGAGGTC  CG  CAGGG
                                    GT  TC
GAM376  MGC12335 3' GGTGGAGGGAGGTGGTGGAGGA 51238       G G  G
                                TCCTCCA T GC TTCTTTTTACT
                                ||||||| | || ||||||||||
                                AGGAGGT G TG GAGGGAGGTGG
                                   _ G  _
GAM376  MGC14258 3' AGATAGAACCTGTTGGGGGA   51859       TG C    T
                                TCCTCCAG  G GTTCT TTT
                                ||||||||  | ||||| |||
                                AGGGGGTT  C CAAGA AGA
                                    GT _    T
GAM376  MGC16384 5' GTAGAAATTTGTGGAGGA    53867      AGTG   TTC
                                TCCTCC   GCG   TTTTTAC
                                ||||||   |||   |||||||
                                AGGAGG   TGT   AAAGATG
                                   _____  TT_
GAM376  MGC17303 5' GGTAGGAGGGGCGAGCGCGAG  57502    CA   G_
                                CTC  GTG  CGTTCTTTTTACT
                                |||  |||  ||||||||||||
                                GAG  CGC  GCGGGGAGGATGG
                                  __  GA
GAM376  MGC20255 3' GTGAGACAGCATTGGAGGG   53445        G GTTCT
                                TCCTCCAGTG C    TTTTAC
                                |||||||||| |    ||||||
                                GGGAGGTTAC G    AGAGTG
                                     _ AC___
GAM376  MGC20496 3' GGGAGCTTGGAGGA       53434       GT   G
                                TCCTCCA  GGC TTCT
                                |||||||  ||| ||||
                                AGGAGGT  TCG AGGG
                                   __  _
GAM376  MGC20647 3' AGTGAGGGGGGAGGGTGGGGAG 95605     AGTGGCG
                                CTCC      TTCTTTTTACT
                                ||||      ||||||||||
                                GAGG      GGGGGGAGTGA
                                  GGTGGGA
GAM376  MGC2477  5' GTGGGATTGCTAGGGGGA    44068      AG    T  TTT
                                TCCTCC  TGGCG TCT   TAC
                                ||||||  ||||| |||   |||
                                AGGGGG  ATCGT AGG   GTG
                                   __    T  ___
GAM376  MGC2668  3' AGAAGCCTGGGGGGG       60572       GT   G
                                TCCTCCA  GGC TTCT
                                |||||||  ||| ||||
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                              GGGGGGT  CCG AAGA
                                 __  _
GAM376  MGC2705  3' GGTGGGGGGAAGGTTGGGGGG 51117       GTG  G
                              TCCTCCA   GC TTCTTTTTACT
                              |||||||   || ||||||||||
                              GGGGGGT   TG AAGGGGGGTGG
                                 ___  G
GAM376  MGC3123  3' GGTGGAAAGGATGTGATGGA   44099     G G
                              TCCA T GCGTTCTTTTTACT
                              |||| | ||||||||||||||
                              AGGT A TGTAGGAAAGGTGG
                                _ G
GAM376  MGC4415  3' GTAGGGGGAGATGGGGAG    48953     AGTGGCG
                              CTCC      TTCTTTTTAC
                              ||||      ||||||||||
                              GAGG      GAGGGGGATG
                                GGTA___
GAM376  MGC5508  3' TAAGGGGACCTGAGGA     44040      CAGT  CGT
                              TCCTC   GG   TCTTTTTA
                              |||||   ||   ||||||||
                              AGGAG   CC   AGGGGAAT
                                 T___  ___
GAM376  MGC8407  3' AGTGGAGAGAATGAGTAGGAGG 43888       AG GG
           G                   TCCTCC  T  CGTTCTTTTTACT
                              ||||||  |  |||||||||||||
                              GGGAGG  G  GTAAGAGAGGTGA
                                 AT A_
GAM376  MGC9753  5' GGTGGTCTTGCTGCTGCAGGG  53057     C   TG   TTCTTT
                              TCCT CAG  GCG     TTACT
                              |||| |||  |||     |||||
                              GGGA GTC  CGT     GGTGG
                                C   GT   TCT___
GAM376  MLLT10   5' GGTGGAGGGGAGGTGGGGGGA  16169       AGTG  G
                              TCCTCC    GC TTCTTTTTACT
                              ||||||    || ||||||||||
                              AGGGGG    TG AGGGGAGGTGG
                                 G___  G
GAM376  MLLT10   5' GGTGGGGAGGGAAGACGCTGAG 16170      C    GCG_
           GA                   TCCTC AGTG    TTCTTTTTACT
                              |||||  ||||    ||||||||||
                              AGGAG TCGC    GGGAGGGGTGG
                                _    AGAA
GAM376  MRPL16   5' GGAGTCGCTGGGGGA      35244           G
                              TCCTCCAGTGGC TTC
                              |||||||||||| |||
                              AGGGGGTCGCTG AGG
                                        _
GAM376  MRPS7    3' GTGAAACTGGCTGGAGGA    31997         GGC   CTTT
                              TCCTCCAGT   GTT    TTAC
                              |||||||||   |||    ||||
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                                AGGAGGTCG  CAA   AGTG
                                    GT_  ____
GAM376  MRVI1   3'  AGTGACTTGATGTTCTTGGAGG 20272       TG   CTTT
          A                  TCCTCCAG  GCGTT   TTACT
                             ||||||||  |||||   |||||
                             AGGAGGTT  TGTAG   AGTGA
                                 CT    TTC_
GAM376  MRVI1   3'  AGTGACTTGATGTTCTTGGAGG 55219       TG   CTTT
          A                  TCCTCCAG  GCGTT   TTACT
                             ||||||||  |||||   |||||
                             AGGAGGTT  TGTAG   AGTGA
                                 CT    TTC_
GAM376  MYLE    3'  GAGGAAGCTGTTGGGGGG    25814       TG  G
                             TCCTCCAG  GC TTCTTT
                             ||||||||  || ||||||
                             GGGGGGTT  CG AAGGAG
                                 GT  _
GAM376  MYT1    3'  GGTGGAGTCCTGTTGCTGTGAG 15780      _  TG   TTCT
          GG                   TCCTC CAG  GCG   TTTTACT
                             |||||  |||  |||   |||||||
                             GGGAG GTC  TGT   GAGGTGG
                                T   GT   CCT_
GAM376  NAF1    5'  GCCCTAGGAGTGCTACGGGGGG 20224       A        TTTACT
                             TCCTCC GTGGCGTTCTT
                             ||||||  ||||||||||
                             GGGGGG CATCGTGAGGA
                                _         TCCCGA
GAM376  NASP    3'  AGTGGAGGGGACAGTGGAGG   67967       G GGC
                             CCTCCA T   GTTCTTTTTACT
                             ||||||  |   ||||||||||||
                             GGAGGT A   CAGGGGAGGTGA
                                G ___
GAM376  NCOR1    3'  AGTGAGGGGAACAGGGTGCAGG 20878      C  GTGGC
          A                  TCCT CA    GTTCTTTTTACT
                             ||||  ||    ||||||||||||
                             AGGA GT    CAAGGGGAGTGA
                               C  GGGA_
GAM376  NFAT5   5'  GGTAGGAGGGGAGTGTTAGGGG 56948      CAG   __
          A                  TCCTC   TGGCG  TTCTTTTTACT
                             |||||   |||||  ||||||||||||
                             AGGGG   ATTGT  GGGGAGGATGG
                                ___    GA
GAM376  NFKBIE   3'  GGTGGAAAGGGCCTGAGGGGTG 92023    _   AGT   GT
          A                  TC CTCC   GGC  TCTTTTTACT
                             ||  ||||   |||  ||||||||||
                             AG GGGG   CCG  GGAAAGGTGG
                              T   AGT   __
GAM376  NMP200   3'  GGTGGGGGGGAATCTATGGGGGG 27175       A   C
          A                  TCCTCC GTGG GTTCTTTTTACT
                             ||||||  |||| ||||||||||||
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                                AGGGGG TATC TAAGGGGGGTGG
                                   G   _
GAM376  NMT1     3'  GTGGGAGGAGTCGGAGAGG   40790     CAG   GT
                                CCTC   TGGC  TCTTTTTAC
                                ||||   ||||  |||||||||
                                GGAG   GCTG  AGGAGGGTG
                                  AG_   __
GAM376  NPFF     5'  AGTCCTGGGGGGCGCCATGGGAG 13553       A        TTT
           GA                     TCCTCC GTGGCGTTCTT   ACT
                                ||||||| ||||||||||   |||
                                AGGAGG TACCGCGGGGG   TGA
                                   G         TCC
GAM376  NSG-X    3'  GGTAGAAATGTACCATGGGGGA 26972       G   CG TC
                                TCCTCCA TGG  T  TTTTTACT
                                ||||||| |||  |  ||||||||
                                AGGGGGT ACC  G  AAAGATGG
                                   _   AT T_
GAM376  NXPH2    5'  AGTGGTGCATGCCACGGAGGG  72718       A      TCTTT
                                TCCTCC GTGGCGT    TTACT
                                |||||| |||||||    |||||
                                GGGAGG CACCGTA    GGTGA
                                   _      CGT__
GAM376  OS-9     3'  GGTAGAGAGAGCAAGGAGGG   22343       AGTGGC
                                TCCTCC     GTTCTTTTTACT
                                ||||||     ||||||||||||
                                GGGAGG     CGAGAGAGATGG
                                   AA_____
GAM376  OS4      5'  AGCCCGGAGCTGCCGCTGGGGG 19175          _    TTTTACT
           A                     TCCTCCAGTGGC GTTCT
                                ||||||||||||| |||||
                                AGGGGGTCGCCG CGAGG
                                      T    CCCGA
GAM376  OSBPL5   3'  GTGGGAGGGCCTGTGGGGG   72692       GT   G   TTT
                                CCTCCA  GGC TTCT   TAC
                                ||||||  ||| ||||   |||
                                GGGGGT  CCG GAGG   GTG
                                   GT   G   ____
GAM376  P2RXL1   3'  GGTAGAAAGAGGAGTGATGGGG 18384       G G  G_
           GA                     TCCTCCA T GC  TTCTTTTTACT
                                ||||||| | ||  ||||||||||
                                AGGGGGT A TG  GAGAAAGATGG
                                   _ G  AG
GAM376  P450RAI-2 3'  GGTAGAAACCTGTGTGTGGGAG 39105       AGTG_   TTC
           GG                     TCCTCC    GCG   TTTTTACT
                                ||||||    |||   ||||||||
                                GGGAGG    TGT   AAAGATGG
                                   GTGTG   CC_
GAM376  P66      3'  GCTGCCAGAGTGCACTGGGGGG 40367         G     TTTTACT
                                TCCTCCAGTG CGTTCT
                                |||||||||| ||||||
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                                GGGGGGTCAC GTGAGA
                                      _    CCGTCGA
GAM376  P8      3'  AGTGAGAGGCTGGGAATGGAGG 24742       GTGGCGTT
             G                   TCCTCCA      CTTTTTACT
                                 |||||||      |||||||||
                                 GGGAGGT      GGAGAGTGA
                                    AAGGGTC_
GAM376  PASK    5'  GGGAGCTGTTGGAGGG     30722       TG  G
                                 TCCTCCAG  GC TTCT
                                 ||||||||  || ||||
                                 GGGAGGTT  CG AGGG
                                     GT  _
GAM376  PCL1    5'  TGGGAGGACTGCGGGG     32826     AGTG   T
                                 CTCC    GCG TCTTTTTA
                                 ||||    ||| ||||||||
                                 GGGG    CGT AGGAGGGT
                                   _____  C
GAM376  PCQAP   3'  AGTGGAGCGGGTTGCTTGGGGG 31895       _ TG __    TTTTACT
             G                   CCTCCA G  GC  GTTCT
                                 |||||| |  ||  |||||
                                 GGGGGT C  TG  CGAGG
                                    T GT  GG    TGA   T
GAM376  PDZD2   5'  AGTGGGAAGGTCCGACTGCGGG 80861     C   _  CGT
             A                   TCCT CAGT GG   TCTTTTTACT
                                 |||| |||| ||   ||||||||||
                                 AGGG GTCA CC   GGAAGGGTGA
                                   C   G  T__
GAM376  PDZD2   5'  GTGAAAAGCGCAGGGGGG    80877      AGTG   TT
                                 CCTCC    GCG  CTTTTTAC
                                 |||||    |||  ||||||||
                                 GGGGG    CGC  GAAAAGTG
                                   GA__   __
GAM376  PHRET1  3'  GTGGGGAGAACAGGAG     41063     AGTGGC
                                 CTCC     GTTCTTTTTAC
                                 ||||     ||||||||||
                                 GAGG     CAAGAGGGGTG
                                   A_____
GAM376  PI4KII  3'  AGTAAAAAGGGTGCCATCTG   37340     _    TT
                                 CAG TGGCG  CTTTTTACT
                                 ||| |||||  |||||||||
                                 GTC ACCGT  GAAAAATGA
                                   T    GG
GAM376  PI4KII  3'  GGTGGGAGGAAGCCTGGGGAG  37346     AGT   G
                                 CTCC   GGC TTCTTTTTACT
                                 ||||   ||| ||||||||||
                                 GAGG   CCG AAGGAGGGTGG
                                   GGT  _
GAM376  PIP5K2A 5'  GGTGGAGGGGACATAGGAGG   17262      A  GGC
                                 CCTCC GT   GTTCTTTTTACT
                                 ||||| ||   ||||||||||||
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                                GGAGG TA   CAGGGGAGGTGG
                                  A ___
GAM376  PMF1     3'  AGTGATGGAATTTGCTGGAGGA 23324        TG C    TT
                                TCCTCCAG  G GTTCT  TTACT
                                ||||||||  | |||||  |||||
                                AGGAGGTC  T TAAGG  AGTGA
                                    GT _    T_
GAM376  PNMA5    3'  GGTGGGGGGGGGCCACACTGAGG 73599     TC    GC
           GA                    TCC  CAGTG  GTTCTTTTTACT
                                |||  |||||  ||||||||||||
                                AGG  GTCAC  CGGGGGGGGTGG
                                  GA    AC
GAM376  POR1     3'  GGTGGGAAGAGTGCCTGGAGG  24805      GT
                                CCTCCA  GGCGTTCTTTTTACT
                                ||||||  ||||||||||||||
                                GGAGGT  CCGTGAGAAGGGTGG
                                   __
GAM376  PP1628   5'  GGTGGAGACCCCTGTGGGGGA  47305       GT  C   CTT
                                TCCTCCA  GG GTT   TTTACT
                                |||||||  || |||   ||||||
                                AGGGGGT  CC CAG   AGGTGG
                                    GT  C  ___
GAM376  PP591    5'  GGTCTGGGTGGCTACTGGAGGG 47373          GT   TTTT
                                TCCTCCAGTGGC  TCT    ACT
                                ||||||||||||  |||    |||
                                GGGAGGTCATCG  GGG    TGG
                                      GT   TC__
GAM376  PRAC     5'  AGAGCGCCACTGGGAGG     50499      _
                                CCTCC AGTGGCGTTCT
                                ||||| ||||||||||
                                GGAGG TCACCGCGAGA
                                  G
GAM376  PRIC285  3'  TCCTTCAGGGGCTGCTGGAGGG 61438        TG  G    TTTTACT
                                TCCTCCAG  GC TTCT
                                ||||||||  || ||||
                                GGGAGGTC  CG GGGA
                                    GT _    CTTCCTG
GAM376  PRKWNK2  3'  GGAGCTCGCGGAGGA      90538       A    C
                                TCCTCC GTGG GTTCT
                                |||||| |||| |||||
                                AGGAGG CGCT CGAGG
                                   _   _
GAM376  PRO0132  5'  AGTGAAAAAGGTCCTTGGAGGA 26100        T   G  CT
                                TCCTCCAG GGC TT  TTTTACT
                                |||||||| ||| ||  |||||||
                                AGGAGGTT CTG AA  AAAGTGA
                                    C   G  __
GAM376  PRTD-NY3 5'  GGTAGAAGGCCTGTTGTGGAGG 48149       A TG   TT
           G                     TCCTCC G  GCG  CTTTTTACT
                                ||||||  |  |||  |||||||||
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                                GGGAGG T  TGT  GGAAGATGG
                                   _ GT   CC
GAM376  PSKH1    3'  GGTAGGAGTTGCCGCCCTGGGG 68242        T   _ TC
                GA                  TCCTCCAG GGCG T  TTTTTACT
                                    |||||||| |||| |  ||||||||
                                    AGGGGGTC CCGC G  GAGGATGG
                                       _   C TT
GAM376  RAB11B   3'  GGTGGGGAGGGCGGCAGGATGG 73906    _  AG  G
                A                    TCC TCC  TG CGTTCTTTTTACT
                                     ||| |||  || ||||||||||||
                                     AGG AGG  AC GCGGGAGGGGTGG
                                      T  __  G
GAM376  RAB35    3'  GGTGGGAAGGAATGGCTGGGGC 22482    _     GGCG
                GG                   TC CTCCAGT    TTCTTTTTACT
                                     || |||||||    ||||||||||
                                     GG GGGGTCG    AGGAAGGGTGG
                                      C      GTA_
GAM376  RAB35    3'  TGGGAAGGAGGGTGCTGTGGAG 22483       G    TT     ACT
                GG                   TCCTCCA TGGCG  CTTTTT
                                     ||||||| |||||  ||||||
                                     GGGAGGT GTCGT  GAGGAA
                                        _    GG     GGGTC
GAM376  RAD52B   5'  GTGAAGGGAGGATGGCGGA   88227     T   GTGGCG
                                     TCC CCA     TTCTTTTTAC
                                     ||| |||     ||||||||||
                                     AGG GGT     GAGGGAAGTG
                                      C   AG____
GAM376  RAI17    3'  GGTAGGGAGGGTGCACCAGTG  91283    G  __  TT
                                     CA TG  GCG  CTTTTTACT
                                     || ||  |||  |||||||||
                                     GT AC  CGT  GAGGGATGG
                                      G  CA   GG
GAM376  RBM12    3'  AGAACTCATTGAGGG      20158      C    C
                                     TCCTC AGTGG GTTCT
                                     ||||| ||||| |||||
                                     GGGAG TTACT CAAGA
                                        _    _
GAM376  RELB     3'  GGTGGGGAGGGAGGTGGAGGA  21488       GTGGCG
                                     TCCTCCA     TTCTTTTTACT
                                     |||||||     ||||||||||||
                                     AGGAGGT     GGGAGGGGTGG
                                         GGA___
GAM376  REM      3'  GCTCCAGGGACGCCACTGCGGG 25808     _          TTTACT
                G                     CCTC CAGTGGCGTTCTT
                                      |||| ||||||||||||
                                      GGGG GTCACCGCAGGGA
                                        C          CCTCGG
GAM376  REPRIMO  3'  GGTGGAGAGGGCGGGCAGGGGA 39054   _   AG  G_
                GAGA                    C CTCC  TG  CGTTCTTTTTACT
                                        | ||||  ||  ||||||||||||
```

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                                G GAGG  AC  GCGGGAGAGGTGG
                                 A   GG  GG
GAM376  RICH1    3'  AGTGAAAAGCTTTCAGTGGAGG 36007       G   CGTT
             A                    TCCTCCA TGG    CTTTTTACT
                                  ||||||| |||    |||||||||
                                  AGGAGGT ACT    GAAAAGTGA
                                     G   TTC_
GAM376  RILP     5'  AGTGGAGGGTGGGGTGGGGGG 48691       GTGG  TT   TT
                                  TCCTCCA   CG  CTT  TACT
                                  |||||||   ||  |||  ||||
                                  GGGGGGT   GT  GAG  GTGA
                                     GGG_  GG  __
GAM376  RODH-4   3'  GTGGAAATGGCCTGGAGGA   13539       TGGC  TC
                                  TCCTCCAG   GT  TTTTTAC
                                  ||||||||   ||  |||||||
                                  AGGAGGTC   CG  AAAGGTG
                                      ____  GT
GAM376  RPIA     3'  GGTGGGGGGAAGAGTGGGAGGG 57969      AGTG  G_
                                  TCCTCC   GC  TTCTTTTTACT
                                  ||||||   ||  ||||||||||
                                  GGGAGG   TG  AAGGGGGGTGG
                                     G___  AG
GAM376  RTN4IP1  5'  AGTGGAGGGGGTGAAAGTGAGG 51191      CAGTGG  TT
             G                    TCCTC    CG  CTTTTTACT
                                  |||||    ||  |||||||||
                                  GGGAG    GT  GGGAGGTGA
                                    TGAAA_  GG
GAM376  SBB103   3'  GGTAGGGGTTAATCTGTTGGGG 19361       TG CGTTC
             G                    CCTCCAG  G    TTTTTACT
                                  |||||||  |    ||||||||
                                  GGGGGTT  C    GGGGATGG
                                     GT TAATT
GAM376  SDC3     5'  GGTAAAGAGAGGGGGTTGGGAG 27760     AGTGGCG
                                  CTCC      TTCTTTTTACT
                                  ||||      ||||||||||
                                  GAGG      GAGAGAAATGG
                                    GTTGGGG
GAM376  SDF1     3'  GGTGGGGAGACTGGGCTGAGGG 90859     TC   GG  T
             A                    TCC  CAGT  CG TCTTTTTACT
                                  |||  ||||  || ||||||||||
                                  AGG  GTCG  GT AGAGGGGTGG
                                    GA   G_  C
GAM376  SDNSF    5'  GGTGAGGCCCGAGGCGTTGGAG 57752     GTG   T  ____
             GG                     CTCCA  GCGT CTT   TTTACT
                                    |||||  |||| |||   ||||||
                                    GAGGT  TGCG GAG   GAGTGG
                                      ___   _  CCCG
GAM376  SEC14L1  3'  GTGGGGGTGCTGGGGGGA   11507      AGT   TT  TTT
                                  TCCTCC  GGCG  CT   TAC
                                  ||||||  ||||  ||   |||
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                                AGGGGG  TCGT  GG  GTG
                                   G__   GG  ___
GAM376  SEC63L   5'  GGTGAGAAGAGCGAGGCGGAGG 23304      A  GG
           A                    TCCTCC GT  CGTTCTTTTTACT
                                ||||||  ||  ||||||||||||
                                AGGAGG CG  GCGAGAAGAGTGG
                                   _  GA
GAM376  SEMA5A   3'  GGTGAGGGCATCCCTGCTGGGG 14260   T   TG C___    TTTACT
           A                    C CCAG  G   GTTCTT
                                | ||||  |   ||||||
                                G GGTC  C   CGGGAG
                                _   GT CCTA    TGG  T
GAM376  SHANK3   3'  GGTGAATCCCTGCTGCTTGGGG 65503     C  TG  TTCTT
           A                    TCCTC AG  GCG    TTTACT
                                |||||  ||  |||    ||||||
                                AGGGG TC  CGT    AAGTGG
                                   T  GT  CCCT_
GAM376  ShrmL    5'  ATCTTCAGAGCGCCACTGAAGG 40465     C         TTTTACT
           A                    TCCT CAGTGGCGTTCT
                                ||||  ||||||||||||
                                AGGA GTCACCGCGAGA
                                  A         CTTCTA
GAM376  SLC19A3  3'  AGTGAGAGGTTAATTTGAGGG  47481     C  GGCGTT
                                TCCTC AGT     CTTTTTACT
                                |||||  |||     |||||||||
                                GGGAG TTA     GGAGAGTGA
                                   T  ATT___
GAM376  SLC26A10 5'  GGGGCTGTTGCCTGGAGGG   56032       _ TG  _
                                TCCTCCA G  GC GTTCT
                                |||||||  |  ||  |||||
                                GGGAGGT C  TG CGGGG
                                    C GT  T
GAM376  SLC37A1  3'  GGTGGGGGGGGGTGCACAGG   38568   A  G  TT
                                CC GTG CG  CTTTTTACT
                                ||  |||  ||  |||||||||
                                GG CAC GT  GGGGGGTGG
                                 A  _  GG
GAM376  SMARCF1  5'  GGTGGGGAGGGCAGCCCGGGGG 20043      AGT  _
           A                    TCCTCC   GGC GTTCTTTTTACT
                                ||||||   ||| ||||||||||||
                                AGGGGG   CCG CGGGAGGGGTGG
                                   C__   A
GAM376  SMARCF1  5'  GGTGGGGAGGGCAGCCCGGGGG 37440      AGT  _
           A                    TCCTCC   GGC GTTCTTTTTACT
                                ||||||   ||| ||||||||||||
                                AGGGGG   CCG CGGGAGGGGTGG
                                   C__   A
GAM376  SMARCF1  5'  GGTGGGGAGGGCAGCCCGGGGG 57489      AGT  _
           A                    TCCTCC   GGC GTTCTTTTTACT
                                ||||||   ||| ||||||||||||
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                                AGGGGG  CCG CGGGAGGGGTGG
                                   C__  A
GAM376  SPIB    3'  GGTAAGGGGAGTGCTGC    11911   TG
                                G  GCGTTCTTTTTACT
                                |  ||||||||||||||
                                C  CGTGAGGGGAATGG
                                 GT
GAM376  SR-A1   3'  GGGATGACTGGGGGA      70047       GG
                                TCCTCCAGT  CGTTCT
                                |||||||||  ||||||
                                AGGGGGTCA  GTAGGG
                                     __
GAM376  STIM2   3'  GGTGAGAAGGGAGCTCTGGAG  40478      T   G
                                CTCCAG GGC TTCTTTTTACT
                                ||||||| ||| ||||||||||
                                GAGGTC TCG GGGAAGAGTGG
                                   _  A
GAM376  SWAP2   3'  GGTGGGGAGGACAAGGGGG   22933     AGTGGC
                                CCTCC     GTTCTTTTTACT
                                |||||     ||||||||||||
                                GGGGG     CAGGAGGGGTGG
                                  AA____
GAM376  SYNCOILIN 3'  AGTGAAAAACATACTGGGGA  47894    T    GC   CT
                                TCC CCAGTG  GTT  TTTTACT
                                ||| ||||||  |||  |||||||
                                AGG GGTCAT  CAA  AAAGTGA
                                  _     A_  __
GAM376  SYT12   3'  GGTAGGAGCTGTGCTTGGAGGG 94735      GT    TC
                                TCCTCCA  GGCGT  TTTTTACT
                                |||||||  |||||  ||||||||
                                GGGAGGT  TCGTG  GAGGATGG
                                   __    TC
GAM376  SYT12   3'  GGTGGAAGGGCGGCTTGAGGG  94737     C   G  GTT
                                TCCTC AGT GC   CTTTTTACT
                                ||||| ||| ||   |||||||||
                                GGGAG TCG CG   GGAAGGTGG
                                   T   G  ___
GAM376  TAO1    3'  GGAGCCTGACCCTGGAGGG   16547       T  _ __
                                TCCTCCAG GG C  GTTCT
                                |||||||| || |  |||||
                                GGGAGGTC CC G  CGAGG
                                   _  A TC
GAM376  TBX21   3'  GGTGGGAGGGGTCAGGTGTGGG 25327    TC  G_   GT
          A                      TCC  CA  TGGC  TCTTTTTACT
                                 |||  ||  ||||  ||||||||||
                                 AGG  GT  ACTG  GGGAGGGTGG
                                   GT  GG   __
GAM376  TBX4    3'  GGTGGGAAGATTCTCGCTGCTG 37495     TG   T___
          GGG                     TCCAG  GCG   TCTTTTTACT
                                  |||||  |||   ||||||||||
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                                GGGTC  CGC    AGAAGGGTGG
                                   GT   TCTT
GAM376  TCL6     3'  AGTGGGAAGGGGTGATGGATGA 40093    C    G G  G
                                TC TCCA T GC TTCTTTTTACT
                                || |||| | || ||||||||||
                                AG AGGT A TG GGGAAGGGTGA
                                 T    _ G  _
GAM376  TCL6     3'  AGTGGGAAGGGGTGATGGATGA 40122    C    G G  G
                                TC TCCA T GC TTCTTTTTACT
                                || |||| | || ||||||||||
                                AG AGGT A TG GGGAAGGGTGA
                                 T    _ G  _
GAM376  THTPA    5'  AGTGGAAGGGATTTTACTGGAG 44259          C
                                CTCCAGTGG GTTCTTTTTACT
                                ||||||||| ||||||||||
                                GAGGTCATT TAGGGAAGGTGA
                                      T
GAM376  TLK1     5'  GGAAGTTTGGAGGG       24455        TG  G
                                TCCTCCAG  GC TTCT
                                ||||||||  || ||||
                                GGGAGGTT  TG AAGG
                                      __  _
GAM376  TMG3     3'  GGTGGGGAGGGTGGGGGTAGGG 43994      _  AGTGG  TT
                                TCCT CC     CG  CTTTTTACT
                                |||| ||     ||  |||||||||
                                GGGA GG     GT  GAGGGGTGG
                                  T  GG___  GG
GAM376  TMLHE    3'  AGTAAGGGAGACTTGTTGGAG  36510       TG C  TC
                                CTCCAG  G GT  TTTTTACT
                                ||||||  | ||  ||||||||
                                GAGGTT  T CA  GGGAATGA
                                   GT _  GA
GAM376  TOLLIP   3'  AGTGGGGGCCAGCCTCGCTGGA 38678         __  GTTC
           GGG                    CCTCCAGT  GGC    TTTTTACT
                                ||||||||  |||   ||||||||
                                GGAGGTCG  CCG    GGGGGTGA
                                     CT   ACC_
GAM376  TRAF2    3'  AGTGAAGGGAGAGGCCCTGGGT 40927    _    T  G_
           GGG                    CC TCCAG GGC  TTCTTTTTACT
                                || ||||| |||  ||||||||||
                                GG GGGTC CCG  GAGGGAAGTGA
                                 T     _  GA
GAM376  TREX1    5'  AGTGGGAGGGGTGGAGCAGGA  53277     A  GG  TT
                                TCC GT  CG  CTTTTTACT
                                ||| ||  ||  |||||||||
                                AGG CG  GT  GGAGGGTGA
                                  A  AG  GG
GAM376  TREX1    5'  AGTGGGAGGGGTGGAGCAGGA  53287     A  GG  TT
                                TCC GT  CG  CTTTTTACT
                                ||| ||  ||  |||||||||
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                                AGG CG  GT  GGAGGGTGA
                                  A  AG  GG
GAM376  TREX1    5'  AGTGGGAGGGGTGGAGCAGGA  33057     A  GG  TT
                                TCC GT  CG  CTTTTTACT
                                ||| ||  ||  |||||||||
                                AGG CG  GT  GGAGGGTGA
                                  A  AG  GG
GAM376  TUSP     5'  GAAAAGGGGAGTGCTAACTGGG 39634          _          ACT
           GGA                    TCCTCCAGT GGCGTTCTTTTT
                                ||||||||| ||||||||||||
                                AGGGGGTCA TCGTGAGGGGAA
                                     A          AAGA
GAM376  UGT2B10  3'  GAGAACTTGGAGGA       6542          TGGC
                                TCCTCCAG   GTTCTT
                                ||||||||   ||||||
                                AGGAGGTT   CAAGAG
                                    ____
GAM376  UPB1     3'  GTGGGAAGAGGGTGAGGG    32890       CAGTG  G
                                TCCTC    GC TTCTTTTTAC
                                |||||    || ||||||||||
                                GGGAG    TG GAGAAGGGTG
                                   _____ G
GAM376  VPS33B   5'  GGAGTGCTGCTGAGGA     37904       C  TG
                                TCCTC AG  GCGTTCT
                                ||||| ||  |||||||
                                AGGAG TC  CGTGAGG
                                   _  GT
GAM376  VPS4A    3'  GGGAGGTTGATTGGGG      25104        _  G
                                CTCCAGT GGC TTCT
                                ||||||| ||| ||||
                                GGGGTTA TTG AGGG
                                    G  G
GAM376  VPS4B    3'  AGTAAAAAGGATGTCA      16820
                                TGGCGTTCTTTTTACT
                                ||||||||||||||||
                                ACTGTAGGAAAAATGA

GAM376  VPS4B    5'  GGTGGAGAGAGTGTTGT     16824    TG
                                G  GCGTTCTTTTTACT
                                |  |||||||||||||
                                T  TGTGAGAGAGGTGG
                                 GT
GAM376  WFDC2    5'  GTGAGGGGCAGTGGGGGG    54937        G  GCGTT
                                TCCTCCA TG    CTTTTTAC
                                ||||||| ||    ||||||||
                                GGGGGGT AC    GGGGAGTG
                                    G  _____
GAM376  ZAP3     3'  GGGGGTCTGCTGGAGGA     77223          _  G
                                TCCTCCAGT GGC TTC
                                ||||||||| ||| |||
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                                AGGAGGTCG CTG GGG
                                      T   G
GAM376  ZF5128    3'  GGTGAGAGGGATGCAGGCATGG 26808     _ G_
                                CCA GT  GCGTTCTTTTTACT
                                ||| ||  ||||||||||||||
                                GGT CG  CGTAGGGAGAGTGG
                                  A  GA
GAM376  ZNF282    3'  GGTGGACCCAGCTGCTGGGGA  89218     T    TG  GTTCTT
                                TCC CCAG  GC      TTTACT
                                ||| ||||  ||      ||||||
                                AGG GGTC  CG      AGGTGG
                                  _    GT  ACCC__
GAM376  ZNF384    3'  GGTAGAAGGAGATTTGGGG    55986       TGGCG
                                CTCCAG     TTCTTTTTACT
                                ||||||     ||||||||||
                                GGGGTT     GAGGAAGATGG
                                    TA___
GAM376  LOC115207 3'  GGTAGGAAGGGTGGGAAGGGAG 56602      AGTGG  TT
                                CTCC     CG  CTTTTTACT
                                ||||     ||  |||||||||
                                GAGG     GT  GAAGGATGG
                                   GAAGG  GG
GAM376  LOC115207 3'  GTTTGGATCTATTGGGGGA    56605          C    TTTTT
                                TCCTCCAGTGG GTTC     AC
                                |||||||||| ||||     ||
                                AGGGGGTTATC TAGG     TG
                                       _    TT___
GAM376  LOC115219 5'  GGTGGAGGGGAGATGGGGG    73316       GTGGCG
                                CCTCCA      TTCTTTTTACT
                                ||||||      ||||||||||
                                GGGGGT      AGGGGAGGTGG
                                   AG____
GAM376  LOC115399 3'  GTGGAAGGAGTGCCTGG     73437     GT
                                CCA  GGCGTTCTTTTTAC
                                |||  |||||||||||||
                                GGT  CCGTGAGGAAGGTG
                                  __
GAM376  LOC116150 5'  AGTGGAAAGGGGTTCGGGCTCG 56629    _  ___   G
           GGGGG                   CC AGT   GGC TTCTTTTTACT
                                || |||   ||| ||||||||||
                                GG TCG   TTG GGGAAAGGTGA
                                 C   GGC   _
GAM376  LOC116173 3'  AGAGGAGGGGAACTTATTGGGG 56640           C        ACT
           GA                    TCCTCCAGTGG GTTCTTTTT
                                |||||||||| |||||||||
                                AGGGGGTTATT CAAGGGGAG
                                       _       GAGAC
GAM376  LOC118668 5'  GGGATGCTGCTGGCGGG     75483     T    TG
                                TCC CCAG  GCGTTCT
                                ||| ||||  |||||||
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                                GGG GGTC  CGTAGGG
                                  C    GT
GAM376  LOC118812 5'  GGGGCAATCGCTGGTGGA    73933     T      C_
                                TCC CCAGTGG  GTTCT
                                ||| |||||||  |||||
                                AGG GGTCGCT  CGGGG
                                  T      AA
GAM376  LOC121219 5'  AGTGGAAGGAGCAGAACGTGAG 74041       CA  GGC
              GG                  TCCTC  GT   GTTCTTTTTACT
                                ||||||  ||   ||||||||||||
                                GGGAG  CA   CGAGGAAGGTGA
                                   TG  AGA
GAM376  LOC123591 5'  GAGAGCGTCGTGGAGGA     75611        G
                                TCCTCCA TGGCGTTCTT
                                ||||||| ||||||||||
                                AGGAGGT GCTGCGAGAG
                                   _
GAM376  LOC123591 3'  GTGGGAGGGTCCTAGAGGG    75614      C  T   G    TTT
                                TCCTC AG GGC TTCT   TAC
                                ||||| || ||| ||||   |||
                                GGGAG TC CTG GAGG   GTG
                                   A  _   G    ___
GAM376  LOC124222 3'  GAAGGCCTGCAGGAGGG     74272       A  _   G
                                TCCTCC GT GGC TTC
                                |||||| || ||| |||
                                GGGAGG CG CCG AAG
                                    A  T   G
GAM376  LOC124402 3'  AGGGGTGCCGTGGAGGA     59148       G    TT
                                TCCTCCA TGGCG  CTT
                                ||||||| |||||  |||
                                AGGAGGT GCCGT  GGA
                                   _    GG
GAM376  LOC124446 3'  AGTGAAGAGCTGGAATGTGGGG 74286      AGTG     ____
              GA                  CTCC    GCGTTCT    TTTTACT
                                ||||    |||||||    |||||||
                                GGGG    TGTAAGG    GAAGTGA
                                  ____       TCGA
GAM376  LOC125268 3'  TGGAGACCTGGGGGG       76082         TGGCGTTC
                                TCCTCCAG       TTTTTA
                                ||||||||       ||||||
                                GGGGGGTC       AGAGGT
                                    C_______
GAM376  LOC125875 5'  AGTAAGGGGAACGAGGTCTGGA 74416         TGG_
              GGG                   TCCTCCAG    CGTTCTTTTTACT
                                ||||||||    ||||||||||||
                                GGGAGGTC    GCAAGGGGAATGA
                                    TGGA
GAM376  LOC125943 5'  TAGTGGGAAGGGCCGGGGTTCG 74422      _ ____
              TTGGGG                AGTGG C    GTTCTTTTTACT   A
                                |||||  |    ||||||||||||   |
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                                TTGCT G    CGGGAAGGGTGA   T
                                   T GGGC
GAM376   LOC126208 3'  GTGGGGGGTGCTGCGAGGA    74464      CA TG   TT   TT
                                TCCTC  G  GCG  CTT  TAC
                                ||||||  |  |||  |||  |||
                                AGGAG  C  CGT  GGG  GTG
                                   __ GT   GG   __
GAM376   LOC126299 3'  GGTGGGAGGAGGGGGCTGAGGA 74485       C   GGCG
                                TCCTC AGT    TTCTTTTTACT
                                ||||| |||    ||||||||||
                                AGGAG TCG    GAGGAGGGTGG
                                   _  GGG_
GAM376   LOC126917 3'  TGGGGAGTCTGGAGGG      74596         TGGCGTT
                                TCCTCCAG      CTTTTTA
                                ||||||||      |||||||
                                GGGAGGTC      GAGGGGT
                                     T_______
GAM376   LOC126964 3'  TGAGAAGTGTGGAGGG      74624         GTGGCGTT
                                TCCTCCA       CTTTTTA
                                |||||||       |||||||
                                GGGAGGT       GAAGAGT
                                    GT_______
GAM376   LOC127255 3'  GGTAAAGAGGATGTCGC     59164
                                GTGGCGTTCTTTTTACT
                                |||||||||||||||||
                                CGCTGTAGGAGAAATGG

GAM376   LOC127294 5'  GGAAGGTCACGGAGGA      74656        A     G
                                TCCTCC GTGGC TTCT
                                |||||| ||||| ||||
                                AGGAGG CACTG AAGG
                                   _    G
GAM376   LOC127534 3'  GGTGAGGAGGGTGGCTGTGGGG 75440        G    _ TT
            G                    CCTCCA TGGC G  CTTTTTACT
                                ||||||  |||| |  |||||||||
                                GGGGGT GTCG T  GAGGAGTGG
                                   _   G GG
GAM376   LOC128665 5'  AAGAGGGACGCCGCTGAGGG   74791       C
                                TCCTC AGTGGCGTTCTTTTT
                                ||||| |||||||||||||||
                                GGGAG TCGCCGCAGGGAGAA
                                   _
GAM376   LOC128954 5'  GGTGGAGGGAATGCCAGCCGG  75802     A _
                                CC G TGGCGTTCTTTTTACT
                                || | |||||||||||||||
                                GG C ACCGTAAGGGAGGTGG
                                 C G
GAM376   LOC129198 5'  GTGGAAAGAGGATGGGCGA    76121     C    GTGGCG
                                TC TCCA      TTCTTTTTAC
                                || ||||      ||||||||||
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                                AG GGGT     GAGAAAGGTG
                                 C    AG____
GAM376   LOC130951 3'  AGTGTGTGTGCTGGGGGG    57141          _   TT
                                TCCTCCAGTG GCG  CT
                                |||||||||| |||  ||
                                GGGGGGTCGT TGT  GA
                                      G   GT
GAM376   LOC131478 5'  AGTGGGAAGGGGCACCGGGGGG 75863       A   G G
                                TCCTCC GTG C TTCTTTTTACT
                                |||||| ||| | ||||||||||
                                GGGGGG CAC G GGGAAGGGTGA
                                   C   _ _
GAM376   LOC132228 3'  GTGTGTGTTGGTGGGGGA    75045        G     TTCTTTT
                                TCCTCCA TGGCG       TAC
                                ||||||| |||||       |||
                                AGGGGGT GTTGT       GTG
                                    G     GT_____
GAM376   LOC132617 5'  AGTGATAAGTGCTGCTGCAGGA 75890      C   TG   TT   T
                                TCCT CAG  GCG  CTT TTACT
                                |||| |||  |||  ||| |||||
                                AGGA GTC  CGT  GAA AGTGA
                                  C   GT   __   T
GAM376   LOC132927 5'  AGTGTCGGGTTCTGCTGGGGGG 75919         TG C TT TTTT
                                TCCTCCAG  G G  C    TACT
                                ||||||||  | |  |   ||||
                                GGGGGGTC  C T  G    GTGA
                                     GT T GG CT__
GAM376   LOC138639 5'  GTGGAGAGGCTGGGAGGG    75364       AGT   GTT
                                TCCTCC   GGC   CTTTTTAC
                                ||||||   |||   ||||||||
                                GGGAGG   TCG   GAGAGGTG
                                   G__   ____
GAM376   LOC138729 3'  TGGGAGGGTGGGAGGG      76238       AGTGGCGT
                                TCCTCC       TCTTTTTA
                                ||||||       ||||||||
                                GGGAGG       GGGAGGGT
                                   GT_______
GAM376   LOC139904 5'  GGTGGATGCGCTGCTGGAG    75852       TG    TCTT
                                CTCCAG  GCGT    TTTACT
                                ||||||  ||||    ||||||
                                GAGGTC  CGCG    AGGTGG
                                   GT    T___
GAM376   LOC142893 5'  GGTGGGAAGGATGGGTTGGGTG 82877    C     TGG
           A                     TC TCCAG   CGTTCTTTTTACT
                                || |||||   ||||||||||||
                                AG GGGTT   GTAGGAAGGGTGG
                                 T    GG_
GAM376   LOC143287 5'  GGTGGAGGGAACTGGGGAGGA  82932       AGTGGC
                                TCCTCC     GTTCTTTTTACT
                                ||||||     ||||||||||||
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                                AGGAGG     CAAGGGAGGTGG
                                   GGT___
GAM376  LOC144473 3'  AGGATGTTGTTGGGGA     83067     T    TG
                                TCC CCAG  GCGTTCT
                                ||| ||||  |||||||
                                AGG GGTT  TGTAGGA
                                  _   GT
GAM376  LOC144486 5'  AGTGATGCGCGTCGTTGGAG   83080          TCTTT
                                CTCCAGTGGCGT    TTACT
                                ||||||||||||    |||||
                                GAGGTTGCTGCG    AGTGA
                                      CGT__
GAM376  LOC144486 3'  GGTAATGGAATGTTGCTGGATG 83087    _    TG      TT
           G                     CC TCCAG  GCGTTCT  TTACT
                                || |||||  |||||||  |||||
                                GG AGGTC  TGTAAGG  AATGG
                                 T    GT      T_
GAM376  LOC144509 5'  GAAGGTGTATTGGGGA     76860     T    _ G
                                TCC CCAGTG GC TTC
                                ||| ||||||  || |||
                                AGG GGTTAT TG AAG
                                  _     G  G
GAM376  LOC144587 3'  GGTGGAAAGGATGTGATGGA   67029      G G
                                TCCA T GCGTTCTTTTTACT
                                |||| | ||||||||||||||
                                AGGT A TGTAGGAAAGGTGG
                                  _ G
GAM376  LOC144603 5'  ATGTGGAGGACGTCACGGAGGA 60366       A          TTACT
                                TCCTCC GTGGCGTTCTTT
                                ||||||  ||||||||||||
                                AGGAGG CACTGCAGGAGG
                                   _          TGTAG
GAM376  LOC144893 5'  GGTAGAGGGGATGGCTGGTGA  83189    CT    GG
                                TC  CCAGT  CGTTCTTTTTACT
                                ||  |||||  ||||||||||||
                                AG  GGTCG  GTAGGGGAGATGG
                                 T_    __
GAM376  LOC145483 3'  AGTGGGGAGGCTCAGGTGGAGG 77239        G_   C  T
           G                     TCCTCCA  TGG GT CTTTTTACT
                                |||||||  ||| || |||||||||
                                GGGAGGT  ACT CG GAGGGGTGA
                                    GG  _ _
GAM376  LOC145601 3'  GGTGGGGAGGGGGCTGGTTGGG 83368      AG__   G
           AG                     CTCC    TGGC TTCTTTTTACT
                                ||||    |||| ||||||||||
                                GAGG    GTCG GGGAGGGGTGG
                                  GTTG    G
GAM376  LOC145624 5'  GTAGGATTTCCTTGGAGGA   83409         T  CGTTCT
                                TCCTCCAG GG      TTTTAC
                                |||||||| ||      ||||||
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                                AGGAGGTT CC     AGGATG
                                    _ TTT___
GAM376  LOC145786 5' AGTGGTTATGTTGCTGGGGA  83489    T   TG   TCTTT
                                TCC CCAG  GCGT    TTACT
                                ||| ||||  ||||    |||||
                                AGG GGTC  TGTA    GGTGA
                                  _   GT   TT___
GAM376  LOC145980 5' GGACTGTCGCTGGCGGG    83606    T      _
                                TCC CCAGTGGC GTTC
                                ||| |||||||| ||||
                                GGG GGTCGCTG CAGG
                                  C       T
GAM376  LOC146071 5' GGTAAGGGGCACTGCCACTGTG 77662     _     _ T
           GGG                    CCTC CAGTGGC GT CTTTTTACT
                                ||||| ||||||| || |||||||||
                                GGGG GTCACCG CA GGGGAATGG
                                  T      T  C
GAM376  LOC146138 3' AGTGAGAGGGGCACCTGAAGGA 83614     C  GT  C
                                TCCT CA  GG GTTCTTTTTACT
                                ||||  ||  || ||||||||||||
                                AGGA GT  CC CGGGGAGAGTGA
                                  A  __  A
GAM376  LOC146174 5' GGTGGGGGGGAGCGGGGCGGGGA 77703     A_  GG
           G                    CTCC  GT  CGTTCTTTTTACT
                                ||||  ||  ||||||||||||
                                GAGG  CG  GCGAGGGGGGTGG
                                  GG  GG
GAM376  LOC146224 5' AGTGGGAAGCTTCCTGGGGGA  77706       T  CGTT
                                TCCTCCAG GG    CTTTTTACT
                                |||||||| ||    |||||||||
                                AGGGGGTC CT    GAAGGGTGA
                                    _ TC__
GAM376  LOC146517 3' GGTATGAAATGCTGCTGGTGGG 77946     T    TG    CTTTT
                                TCC CCAG  GCGTT    TACT
                                ||| ||||  |||||    ||||
                                GGG GGTC  CGTAA    ATGG
                                  T   GT    AGT__
GAM376  LOC146909 3' GGTGGGAGGTGGGCTGGAGGA  78181        GGCGTT
                                TCCTCCAGT     CTTTTTACT
                                |||||||||     |||||||||
                                AGGAGGTCG     GGAGGGTGG
                                    GGT___
GAM376  LOC147071 5' AAGAACGGCTGTGGGGGA    72988       G   _
                                TCCTCCA TGGC GTTCTT
                                ||||||| |||| ||||||
                                AGGGGGT GTCG CAAGAA
                                    _   G
GAM376  LOC147160 5' GGTGGGGAGAGAGAAAGTGGGG 83969       GTGGCG
           GG                     TCCTCCA     TTCTTTTTACT
                                |||||||     ||||||||||
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                                GGGGGGT     GAGAGGGGTGG
                                    GAAAGA
GAM376  LOC147160 5'  TAGTGGGGGGCAAAAGGCGCCA 83971         _____
            TTGGGCGG                AGTGGCGTT    CTTTTTACT   A
                                ||||||||||  ||||||||||  |
                                TTACCGCGG    GGGGGGTGA   T
                                    AAAAC
GAM376  LOC147515 3'  AGGAGCCTTGGAGGG       84019        T   G
                                TCCTCCAG GGC TTCT
                                |||||||| ||| ||||
                                GGGAGGTT CCG AGGA
                                    _  _
GAM376  LOC147965 5'  GTGAAGGGGTAGTGGAGGG    78600        G  GCGT
                                TCCTCCA TG    TCTTTTTAC
                                ||||||| ||    |||||||||
                                GGGAGGT AT    GGGGAAGTG
                                    G  _____
GAM376  LOC148147 3'  AGAGTCCCACTGGAGGA     78671          CG
                                TCCTCCAGTGG  TTCT
                                ||||||||||  ||||
                                AGGAGGTCACC  GAGA
                                      CT
GAM376  LOC148354 3'  GGTGGAGGGAACTGTGTGGGG  78802       GTG  _
                                CTCCA   GC GTTCTTTTTACT
                                |||||   || ||||||||||||
                                GGGGT   TG CAAGGGAGGTGG
                                   G__  T
GAM376  LOC148426 5'  GGTAGGGCACAGGTCTTGGGGG 84151         T   GTTCT
            A                    TCCTCCAG GGC     TTTTACT
                                ||||||||| |||     |||||||
                                AGGGGGTT CTG     GGGATGG
                                    _   GACAC
GAM376  LOC148529 5'  GGTGGGGAGAGGGATGGGGGG  84170        GTGGCG
                                TCCTCCA     TTCTTTTTACT
                                |||||||     ||||||||||||
                                GGGGGGT     GAGAGGGGTGG
                                    AGG___
GAM376  LOC148697 5'  GGTAAGAAGAGTGTGACCAGGA 78929      A_  G
            G                    CTCC  GT GCGTTCTTTTTACT
                                ||||  || ||||||||||||||
                                GAGG  CA TGTGAGAAGAATGG
                                  AC  G
GAM376  LOC148709 3'  GGTGAGGACATGCTTGTGGGAG 78948       AGT_    TC
            GG                   TCCTCC    GGCGT  TTTTTACT
                                ||||||    |||||  ||||||||
                                GGGAGG    TCGTA  AGGAGTGG
                                   GTGT     C_
GAM376  LOC148753 3'  AGGGTGCCGCTGGGGGA     84210           TT
                                TCCTCCAGTGGCG  CT
                                ||||||||||||  ||
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                                AGGGGGTCGCCGT  GA
                                      GG
GAM376  LOC148758 5'  GGTGGGGAGTGTGCGGGAGGG  78975       AGTG   TT
                                TCCTCC   GCG  CTTTTTACT
                                ||||||   |||  |||||||||
                                GGGAGG   CGT  GAGGGGTGG
                                   G___  GT
GAM376  LOC148930 3'  GGTGGAGGGGGTGGGAATGGGG 79099       GTGG  TT
          GA                     TCCTCCA   CG  CTTTTTACT
                                ||||||||  ||  |||||||||
                                AGGGGGT   GT  GGGAGGTGG
                                    AAGG  GG
GAM376  LOC148981 5'  GGTGGAAACTTTGGTGGAGGA  84316       G   C   CTT
                                TCCTCCA TGG GTT   TTTACT
                                ||||||| ||| |||   ||||||
                                AGGAGGT GTT CAA   AGGTGG
                                    G   T  ___
GAM376  LOC149111 3'  GGTGGGAGTTATGCTGGGGG   79186      GTG    TC
                                CCTCCA   GCGT  TTTTTACT
                                ||||||   ||||  ||||||||
                                GGGGGT   CGTA  GAGGGTGG
                                   ___    TT
GAM376  LOC149420 3'  AGTGAAATTCTTTCATTGGGGG 79367         CGTTCT
                                CCTCCAGTGG     TTTTACT
                                ||||||||||     |||||||
                                GGGGGTTACT     AAAGTGA
                                     TTCTT_
GAM376  LOC149498 3'  TGGGAAGGTGGGAGGG      79408       AGTGGCGT
                                TCCTCC       TCTTTTTA
                                ||||||       ||||||||
                                GGGAGG       GGAAGGGT
                                   GT_______
GAM376  LOC149501 3'  AGGAAGCTACTGGAGGG     75272           G
                                TCCTCCAGTGGC TTCTT
                                |||||||||||| |||||
                                GGGAGGTCATCG AAGGA
                                             _
GAM376  LOC149657 3'  GTCCCACGGGCCTACTGGGGGG 84577           C    TTTTTACT
                                TCCTCCAGTGG GTTC
                                |||||||||||| ||||
                                GGGGGGTCATC CGGG
                                     _   CACCCTGA
GAM376  LOC149668 5'  GGTGAGGGGGACTCTAGTGCTG 84549       ___  C
          GAGG                    TCCAGT   GG GTTCTTTTTACT
                                ||||||   || ||||||||||||
                                AGGTCG   TC CAGGGGGAGTGG
                                   TGA  T
GAM376  LOC149706 5'  AGGGGCCACTGGGGGG      84636           G
                                TCCTCCAGTGGC TTCT
                                |||||||||||| ||||
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                                GGGGGGTCACCG GGGA
                                        _
GAM376  LOC149706 5'  GGTGGAAGGAGCAGGGCTCTGG 84645      T  ___
            AGGG                  TCCAG GGC   GTTCTTTTTACT
                                  ||||| |||   ||||||||||||
                                  AGGTC TCG   CGAGGAAGGTGG
                                    _  GGA
GAM376  LOC149722 3'  GGGGCCTCACTGGGGA     84604    T     C
                                  TCC CCAGTGG GTTCT
                                  ||| ||||||| |||||
                                  AGG GGTCACT CGGGG
                                    _     C
GAM376  LOC149840 5'  AGTTTTCTGGAGTGCTTTGGAG 79524       T      TTTT_
            GA                    TCCTCCAG GGCGTTCT    ACT
                                  |||||||| ||||||||    |||
                                  AGGAGGTT TCGTGAGG    TGA
                                     _       TCTTT
GAM376  LOC149995 3'  AGGAGCCTTGGAGGG      84841       T  G
                                  TCCTCCAG GGC TTCT
                                  |||||||| ||| ||||
                                  GGGAGGTT CCG AGGA
                                     _  _
GAM376  LOC150271 5'  AGTGGGAGGGGAAATGGGTGA  84948    C   GTGGCG
                                  TC TCCA     TTCTTTTTACT
                                  || ||||     ||||||||||
                                  AG GGGT     GGGGAGGGTGA
                                   T   AAA___
GAM376  LOC150279 5'  AGTGGAAGGAGATGTGGGGTGG 79665    T  AGTG   _
                                  CC CC    GCGT TCTTTTTACT
                                  || ||   |||| ||||||||||
                                  GG GG    TGTA AGGAAGGTGA
                                   T  GG__    G
GAM376  LOC150370 3'  GGATTGTCTCTGGAGGG     84942       T   T
                                  TCCTCCAG GGCG TCT
                                  |||||||| |||| |||
                                  GGGAGGTC CTGT AGG
                                     T   T
GAM376  LOC150605 5'  TCCTGAGTGGGAATGTTGCTGG 85085       TG      TTTACT
            AGGG                  TCCTCCAG  GCGTTCTT
                                  ||||||||  ||||||||
                                  GGGAGGTC  TGTAAGGG
                                     GT       TGAGTCCTT
GAM376  LOC150759 3'  GGTAGAGGGAGGAATGATGGAG 80008       GTGGCG
            GG                    TCCTCCA     TTCTTTTTACT
                                  |||||||     ||||||||||
                                  GGGAGGT     GAGGGAGATGG
                                     AGTAAG
GAM376  LOC150935 3'  GGTGAGAAGAAGCGTGAAGGG  80036     C  GTG  G
                                  TCCT CA   GC TTCTTTTTACT
                                  |||| ||   || ||||||||||
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                                GGGA GT   CG AAGAAGAGTGG
                                  A  G__  _
GAM376  LOC150951 5'  AGTGGAGGGGTCCCTGCGGGA  85166     C   T  CGT
                                TCCT CAG GG   TCTTTTTACT
                                |||| ||| ||   ||||||||||
                                AGGG GTC CC   GGGGAGGTGA
                                  C   _  T__
GAM376  LOC151031 5'  GGTGGAAGTCTTCGCCGGAGGA 87189       AGT    TTC_
                                TCCTCC   GGCG    TTTTTACT
                                ||||||   ||||    ||||||||
                                AGGAGG   CCGC    GAAGGTGG
                                   ___    TTCT
GAM376  LOC151040 3'  GGTGGGGGGGAGCGGGGAGGG   80103       AGTGG
                                TCCTCC     CGTTCTTTTTACT
                                ||||||     ||||||||||||
                                GGGAGG     GCGAGGGGGGTGG
                                   G____
GAM376  LOC151188 5'  GGTAGAGAGGTGCCCTTAATGG 80161       GT__  C  _
           GGGA                    CTCCA    GG GT TCTTTTTACT
                                ||||||    || || ||||||||||
                                GGGGT    CC CG GGAGAGATGG
                                  AATT  _  T
GAM376  LOC151273 3'  AGTGGGAGGGGTTGGGATGGG  67015     _   AGTGGC TT
                                TCC TCC      G  CTTTTTACT
                                ||| |||      |  |||||||||
                                GGG AGG      T  GGAGGGTGA
                                  T   GT____ GG
GAM376  LOC151323 3'  GGTAGAGGGAGGAATGATGGAG 80220       GTGGCG
           GG                     TCCTCCA     TTCTTTTTACT
                                |||||||      ||||||||||
                                GGGAGGT      GAGGGAGATGG
                                   AGTAAG
GAM376  LOC151360 3'  GGTGGGGAGGGTCCGAGGGGA  85314     T  AG   C TT
                                TCC CC  TGG G  CTTTTTACT
                                ||| ||  ||| |  |||||||||
                                AGG GG  GCC T  GAGGGGTGG
                                  _  A_   _ GG
GAM376  LOC151361 3'  GGTGGGGAGGGTCCGAGGGGA  85328     T  AG   C TT
                                TCC CC  TGG G  CTTTTTACT
                                ||| ||  ||| |  |||||||||
                                AGG GG  GCC T  GAGGGGTGG
                                  _  A_   _ GG
GAM376  LOC151429 3'  GGTGGGGGCCCGCACTCGGGGA 85360       C    G  TT    T
                                TCCTC AGTG CG  CTTTT ACT
                                ||||| |||| ||  ||||| |||
                                AGGGG TCAC GC  GGGGG TGG
                                  C    _  CC    _
GAM376  LOC151438 5'  GGTGGAAGGGGTGTGCCAGGAG 85368       AG    __ TT
           GG                     CCTCC  TGGC  G  CTTTTTACT
                                |||||  ||||  |  |||||||||
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                                GGAGG  ACCG  T  GGAAGGTGG
                                  __    TG GG
GAM376  LOC151475 3'  GAGTATGTGTGCTGGGGGG   85404          _   T
                                TCCTCCAGTG GCGT CTT
                                |||||||||| |||| |||
                                GGGGGGTCGT TGTA GAG
                                     G    T
GAM376  LOC151701 3'  GGAAAGCGACTGGAGG      85487        G  G
                                CCTCCAGT GC TTCT
                                |||||||| || ||||
                                GGAGGTCA CG AAGG
                                    G  A
GAM376  LOC151742 5'  GTAGGAGGGATGCTGGTG    57670    G
                                CA TGGCGTTCTTTTTAC
                                || ||||||||||||||
                                GT GTCGTAGGGAGGATG
                                 G
GAM376  LOC151878 3'  GAGAATGTGGGAGGA       80375       AGTG
                                TCCTCC    GCGTTCTT
                                ||||||    ||||||||
                                AGGAGG    TGTAAGAG
                                   G___
GAM376  LOC152008 3'  AGTGAAAAGGATGTGTAGTGG  80433     G  _
                                CCA TG GCGTTCTTTTTACT
                                ||| || ||||||||||||||
                                GGT AT TGTAGGAAAAGTGA
                                  G  G
GAM376  LOC152110 3'  GGATTGGGTGCTGCTAGAGGG  80456      C  TG   TT TT
                                TCCTC AG  GCG  C  TTT
                                ||||| ||  |||  |  |||
                                GGGAG TC  CGT  G  AGG
                                   A  GT   GG TT
GAM376  LOC152185 5'  GTGGGGAGAACGGTGGTGG    58526     G  G
                                CCA TG CGTTCTTTTTAC
                                ||| || ||||||||||||
                                GGT GT GCAAGAGGGGTG
                                  G  G
GAM376  LOC152502 3'  AGTGAAGAGGCTTATGCTGAGG 59313      C    GCGT
          A                      TCCTC AGTG    TCTTTTTACT
                                ||||| ||||    ||||||||||
                                AGGAG TCGT    GGAGAAGTGA
                                   _    ATTC
GAM376  LOC152579 3'  AGTGGGAAGGTGGTTGATTGGA 80622          _  GT
          GGG                     TCCTCCAGT GGC  TCTTTTTACT
                                |||||||||| |||  ||||||||||
                                GGGAGGTTA TTG  GGAAGGGTGA
                                     G   GT
GAM376  LOC153114 5'  GCTCATGGAATGTGTTGGAGGA 85921        GT G     TTTTACT
                                TCCTCCA  G CGTTCT
                                |||||||  | ||||||
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                                AGGAGGT  T GTAAGG
                                   TG _     TACTCGA
GAM376  LOC153196 5'  AGTGAGGGGACTGGGCTGCGGG 85955     C    GG  T
          A                     TCCT CAGT  CG TCTTTTTACT
                                |||| ||||  || ||||||||||
                                AGGG GTCG  GT AGGGGAGTGA
                                  C   G_  C
GAM376  LOC153196 3'  GGGGGGCACACTGGGGA     85969     T     _ G
                                TCC CCAGTG GC TTCT
                                ||| |||||| || ||||
                                AGG GGTCAC CG GGGG
                                  _     A  G
GAM376  LOC153196 5'  GGTGGAGCATCCTGCTGCTTGG 85971       _ TG   TTCT_
          AGGA                    CCTCCA G  GCG    TTTTACT
                                |||||| |  |||    |||||||
                                GGAGGT C  CGT    GAGGTGG
                                   T GT   CCTAC
GAM376  LOC153196 3'  GGTGGGGAGAGTGGGGAGAGGG 85973      AGTGG_
          GG                    CCTCC     CGTTCTTTTTACT
                                ||||||     ||||||||||||||
                                GGGGG     GTGAGAGGGGTGG
                                  AGAGGG
GAM376  LOC153243 3'  AAGAAGCTGCTGGAGGG     80792        TG  G
                                TCCTCCAG  GC TTCTT
                                ||||||||  || |||||
                                GGGAGGTC  CG AAGAA
                                    GT  _
GAM376  LOC155036 5'  GAGAGGTCGGTGGAGGA     86341        G   G
                                TCCTCCA TGGC TTCTT
                                ||||||| |||| |||||
                                AGGAGGT GCTG GAGAG
                                   G   _
GAM376  LOC155038 3'  GGAGGGTGGCAGGAGGG     81259       A  G  G
                                TCCTCC GT GC TTCT
                                |||||| || || ||||
                                GGGAGG CG TG GAGG
                                   A  G  G
GAM376  LOC155063 3'  GGTGAAGAGGTAGCTTGGGAG  86369     AGT   GT
                                CTCC   GGC  TCTTTTTACT
                                ||||   |||  ||||||||||
                                GAGG   TCG  GGAGAAGTGG
                                  GT_   AT
GAM376  LOC155064 3'  GGTGGAAAGAAAGTGCTTGGGG 81250       TG  G
          G                     CCTCCAG  GC TTCTTTTTACT
                                |||||||  || ||||||||||
                                GGGGGTT  TG AAGAAAGGTGG
                                   CG  A
GAM376  LOC155066 5'  AGTGAGGAGAACGCGTGCTGAG 81278      C   _
          GA                      TCCTC AGTG GCGTTCTTTTTACT
                                ||||| |||| ||||||||||||||
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                                AGGAG TCGT CGCAAGAGGAGTGA
                                  _   G
GAM376  LOC155072 5'  GTGGAAGGGGTGAGGGG    86386     AGTGG  TT
                                CTCC    CG  CTTTTTAC
                                ||||    ||  ||||||||
                                GGGG    GT  GGAAGGTG
                                  A____  GG
GAM376  LOC157349 5'  GGTAAAAACATGCTGGGGAGG  81421      AG     TC
                                CCTCC  TGGCGT  TTTTTACT
                                |||||  ||||||  ||||||||
                                GGAGG  GTCGTA  AAAAATGG
                                  G_     C_
GAM376  LOC157693 5'  GGGGAGAGTCTGCTGGAGGA   81557         _  G
                                TCCTCCAGT GGC TTCTTT
                                ||||||||| ||| ||||||
                                AGGAGGTCG CTG GAGGGG
                                     T   A
GAM376  LOC157848 3'  ACAGGAAGGGTCCCACTGGAGG 81615          C TT     ACT
            G                    TCCTCCAGTGG G  CTTTTT
                                ||||||||||| |  ||||||
                                GGGAGGTCACC T  GAAGGA
                                     C GG     CA
GAM376  LOC157848 3'  GGTAGGGGGTGGGCTGGGGGA  81623        GG  TT  TT
                                TCCTCCAGT  CG  CT  TTACT
                                |||||||||  ||  ||  |||||
                                AGGGGGTCG  GT  GG  GATGG
                                     G_  GG  __
GAM376  LOC157860 3'  AGTGAAGGGGTGGAGGGGCTGG 86564        GGCGT__
            AGGA                   CCTCCAGT      TCTTTTTACT
                                ||||||||      ||||||||||
                                GGAGGTCG      GGGGAAGTGA
                                     GGGAGGT
GAM376  LOC158046 5'  GGGGCGCAGTTGGGGGA     59216        TG
                                TCCTCCAG  GCGTTCT
                                ||||||||  |||||||
                                AGGGGGTT  CGCGGGG
                                     GA
GAM376  LOC158107 5'  AGTTGCCGGGGTCTGCTGGGGG 86684        TG C TT  TTTT
            A                    TCCTCCAG  G G  CT    ACT
                                ||||||||  | |  ||    |||
                                AGGGGGTC  C T  GG    TGA
                                     GT _ GG  CCGT
GAM376  LOC158187 3'  AGTAGAGAGAACTGAATTAGAG 86686      C   GGC
            GA                     TCCTC AGT   GTTCTTTTTACT
                                |||||  |||   ||||||||||||
                                AGGAG TTA   CAAGAGAGATGA
                                  A   AGT
GAM376  LOC158288 5'  GGTGGCTGTGCCATGGGAGGA  86720       A     TTCTTT
                                TCCTCC GTGGCG     TTACT
                                ||||||  ||||||      |||||
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                                AGGAGG TACCGT     GGTGG
                                   G     GTC___
GAM376  LOC158431 5'  AGTAGAGGGGGCGCAGCTGGGG 86830        G
                                CTCCAGT GCGTTCTTTTTACT
                                ||||||| |||||||||||||
                                GGGGTCG CGCGGGGGAGATGA
                                    A
GAM376  LOC158434 3'  GTGAAGGGCAATTGGGAGA   86823   CT    G  GTTC
                                TC  CCAGT GC    TTTTTAC
                                ||  ||||| ||    |||||||
                                AG  GGTTA CG    GGAAGTG
                                 AG    A _____
GAM376  LOC158535 5'  GGTAAAAAGGAATTTGAGAGGA 87242       _   TGGCG
                                TCCTC CAG     TTCTTTTTACT
                                ||||| |||     ||||||||||
                                AGGAG GTT     AGGAAAAATGG
                                   A   TA___
GAM376  LOC159036 3'  AGTAGGAAGAATGCAGGAGGA  86968       AGTG
                                TCCTCC    GCGTTCTTTTTACT
                                ||||||    ||||||||||||||
                                AGGAGG    CGTAAGAAGGATGA
                                   A___
GAM376  LOC159199 5'  GTGGAGGGAGCGCCAGG     82186    AG
                                CC  TGGCGTTCTTTTTAC
                                ||  ||||||||||||||
                                GG  ACCGCGAGGGAGGTG
                                 __
GAM376  LOC161734 3'  AGTAAAGATCCCTGTTATTGGA 87096           TTC_
           GG                     CCTCCAGTGGCG    TTTTTACT
                                ||||||||||||    ||||||||
                                GGAGGTTATTGT    AGAAATGA
                                      CCCT
GAM376  LOC162333 5'  GGGACCCGCTGGAGGA      87136          C
                                TCCTCCAGTGG GTTCT
                                |||||||||| |||||
                                AGGAGGTCGCC CAGGG
                                      _
GAM376  LOC162461 3'  AGTAGAATGGGCTACTGTGAGG 82357       _      GT  T
           G                     TCCTC CAGTGGC  TC TTTTACT
                                ||||| |||||||  || |||||||
                                GGGAG GTCATCG  GG AAGATGA
                                   T      __  T
GAM376  LOC164397 5'  GATGCCATTGTGGGGG      82526       _
                                TCCTC CAGTGGCGTT
                                ||||| ||||||||||
                                GGGGG GTTACCGTAG
                                   T
GAM376  LOC195977 5'  TGAAAGGGCAGGAGGA      87541        AGTG  GTT
                                TCCTCC    GC   CTTTTTA
                                ||||||    ||   |||||||
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                                AGGAGG   CG  GGAAAGT
                                  A___  ___
GAM376  LOC196047 5'  GGTGAGAAGGAGCCTTCGGAGG 89607       AGT  G
          G                     TCCTCC  GGC TTCTTTTTACT
                                |||||||  ||| ||||||||||
                                GGGAGG  CCG AGGAAGAGTGG
                                  CTT  _
GAM376  LOC196205 3'  GGGGGCCACTGGAGGG     87591          G
                                TCCTCCAGTGGC TTC
                                |||||||||||| |||
                                GGGAGGTCACCG GGG
                                      G
GAM376  LOC196283 3'  GAGAAGCTGCTGGAGGA    87619        TG  G
                                TCCTCCAG  GC TTCTT
                                ||||||||  || |||||
                                AGGAGGTC  CG AAGAG
                                    GT  _
GAM376  LOC196500 3'  GGTGGGAGGTGAGCTGGGGG  87743        GGCGTT
                                CCTCCAGT    CTTTTTACT
                                ||||||||    |||||||||
                                GGGGGTCG    GGAGGGTGG
                                    AGT___
GAM376  LOC196549 3'  GGTGGGGACAGACTTGCTGGAG 59233        TG C  C_
          GA                    TCCTCCAG  G GTT  TTTTTACT
                                ||||||||  | |||  ||||||||
                                AGGAGGTC  T CAG  AGGGGTGG
                                    GT _  AC
GAM376  LOC197117 3'  GGTAAAGGGGTGACTGGGGA  89721    T    G  GTT
                                TCC CCAGT GC   CTTTTTACT
                                ||| ||||| ||   |||||||||
                                AGG GGTCA TG   GGGAAATGG
                                  _    G  ___
GAM376  LOC197363 3'  GGTGGGAGGGTAATTGGAGGG  88057        GGCGT
                                TCCTCCAGT    TCTTTTTACT
                                |||||||||    ||||||||||
                                GGGAGGTTA    GGGAGGGTGG
                                    AT___
GAM376  LOC199678 3'  GTGACTTGCTTTGGGGGA    89793        T   TTCTTT
                                TCCTCCAG GGCG    TTAC
                                |||||||| ||||    ||||
                                AGGGGGTT TCGT    AGTG
                                    _   TC_____
GAM376  LOC199787 3'  GGTGAGGACCATGTCGCTGGAT 88397    _        TC
          GG                    CC TCCAGTGGCGT  TTTTTACT
                                || ||||||||||  ||||||||
                                GG AGGTCGCTGTA  AGGAGTGG
                                 T         CC
GAM376  LOC200125 5'  GTAGTACTGTTATTGGAG    89929          TTCTTT
                                CTCCAGTGGCG    TTAC
                                ||||||||||    ||||
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                                GAGGTTATTGT     GATG
                                      CAT___
GAM376  LOC200197 3'  GGATGCCCCTGGAGGG      88619        T
                                TCCTCCAG GGCGTTC
                                |||||||| |||||||
                                GGGAGGTC CCGTAGG
                                     C
GAM376  LOC200312 3'  GTGGGAGGAAGGATGAGGG   89997      CAGTGGCG
                                TCCTC       TTCTTTTTAC
                                |||||       ||||||||||
                                GGGAG       AAGGAGGGTG
                                   TAGG____
GAM376  LOC200399 3'  GGTAGAGGGAGGAATGATGGAG 88811        GTGGCG
           GG                     TCCTCCA     TTCTTTTTACT
                                |||||||     ||||||||||
                                GGGAGGT     GAGGGAGATGG
                                     AGTAAG
GAM376  LOC200982 3'  GGTGAAGAGGAGATGCTGGGGA 90224     T     GCG
                                TCC CCAGTG   TTCTTTTTACT
                                ||| ||||||   ||||||||||
                                AGG GGTCGT   AGGAGAAGTGG
                                  _     AG_
GAM376  LOC201102 3'  GGTGGAGGGGCAATTGGAAGG  88096     _    G  GTT
                                CCT CCAGT GC   CTTTTTACT
                                ||| ||||| ||   |||||||||
                                GGA GGTTA CG   GGGAGGTGG
                                  A    A ___
GAM376  LOC201139 3'  GGTGCGTGCTCTGGAGGA     88132        TG_    T
                                TCCTCCAG   GCGT CT
                                ||||||||   |||| ||
                                AGGAGGTC   TGCG GG
                                     TCG    T
GAM376  LOC201173 5'  AAGAACGGCTGTGGGGGA     87318        G    _
                                TCCTCCA TGGC GTTCTT
                                ||||||| |||| ||||||
                                AGGGGGT GTCG CAAGAA
                                     _    G
GAM376  LOC201220 5'  AAGAACGGCTGTGGGGGA     87338        G    _
                                TCCTCCA TGGC GTTCTT
                                ||||||| |||| ||||||
                                AGGGGGT GTCG CAAGAA
                                     _    G
GAM376  LOC201705 3'  AGTGAGGAGGCCAGTGCTGCTG 90251       TG   T___
           GAG                     TCCAG  GCG    TCTTTTTACT
                                |||||  |||    ||||||||||
                                AGGTC  CGT    GGAGGAGTGA
                                   GT   GACC
GAM376  LOC201910 3'  AGTGGGAGTCAGTTATGGGAGG 89098       A     GTTC
           A                      TCCTCC GTGGC    TTTTTACT
                                ||||||| |||||    ||||||||
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                                AGGAGG TATTG    GAGGGTGA
                                   G    ACT_
GAM376  LOC202781 5'  GGGGACGTGCTGGGGGG     90368          G
                                TCCTCCAGTG CGTTCTT
                                |||||||||| |||||||
                                GGGGGGTCGT GCAGGGG
                                          _
GAM376  LOC202868 5'  GTGGAAGGGGTGAGGGG     90384      AGTGG  TT
                                CTCC    CG  CTTTTTAC
                                ||||    ||  ||||||||
                                GGGG    GT  GGAAGGTG
                                  A____  GG
GAM376  LOC203197 3'  GGTGAGGAGAGAAGCATCTGGG 89294        TG  G_
           GG                     CCTCCAG  GC  TTCTTTTTACT
                                |||||||  ||  ||||||||||
                                GGGGGTC  CG  GAGAGGAGTGG
                                    TA  AA
GAM376  LOC203668 5'  GGTGGGGAGCCGGAGCTGGAAG 89436    C     GG  TT
           A                     TC TCCAGT  CG  CTTTTTACT
                                || ||||||  ||  |||||||||
                                AG AGGTCG  GC  GAGGGGTGG
                                 A     AG  C_
GAM376  LOC204689 5'  GGTGCCTGTGAGTGATGCTGGG 90662         GG    TTTT_
           GGA                     TCCTCCAGT  CGTTC    TACT
                                |||||||||  |||||    ||||
                                AGGGGGTCG  GTGAG    GTGG
                                      TA    TGTCC
GAM376  LOC204820 5'  GTGGGGAGGGCGAGTGGA    90664     GTGG
                                TCCA    CGTTCTTTTTAC
                                ||||    ||||||||||||
                                AGGT    GCGGGAGGGGTG
                                  GA__
GAM376  LOC219513 3'  GAGGACGACTACTGGGGGG    94328          _
                                TCCTCCAGTGG CGTTCTT
                                |||||||||| |||||||
                                GGGGGGTCATC GCAGGAG
                                       A
GAM376  LOC219842 5'  GGTAGAGAGAGCCAACAAGGTG 93269     T  AG__   GT
           GA                     TCC CC    TGGC  TCTTTTTACT
                                ||| ||    ||||  ||||||||||
                                AGG GG    ACCG  AGAGAGATGG
                                  T  AACA   __
GAM376  LOC219920 5'  AGAGGGCCTGGGGGA      93298       GT   G
                                TCCTCCA  GGC TTCT
                                |||||||  ||| ||||
                                AGGGGGT  CCG GAGA
                                    __  G
GAM376  LOC220038 5'  AGTGGGGGGCAGGGTTAGAGGG 91718      CAG   G  _
                                TCCTC   TGGC TT CTTTTTACT
                                |||||   |||| || |||||||||
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                                GGGAG   ATTG GA GGGGGGTGA
                                  ___   G  C
GAM376  LOC220058 3'  AGTGACACTGCTTTACTGGAGG 91724         C  TCTTT
          A                    TCCTCCAGTGG GT    TTACT
                               ||||||||||| ||    |||||
                               AGGAGGTCATT CG    AGTGA
                                     T  TCAC_
GAM376  LOC220070 3'  GGTAAAAGCAGCCGTATTGGGG 59261         __  GTTC
          GA                   TCCTCCAGT  GGC   TTTTTACT
                               |||||||||  |||   ||||||||
                               AGGGGGTTA  CCG   GAAAATGG
                                    TG   AC__
GAM376  LOC220549 5'  AGTCATTAGGAGTACCACTGGA 92914         CG    TTT_
          GGA                   TCCTCCAGTGG  TTCTT   ACT
                               ||||||||||  |||||   |||
                               AGGAGGTCACC  GAGGA   TGA
                                     AT    TTAC
GAM376  LOC220705 3'  AGAGTGTGCTGGAGGA      91225         G
                               TCCTCCAGTG CGTTCT
                               |||||||||| ||||||
                               AGGAGGTCGT GTGAGA
                                     _
GAM376  LOC221088 5'  AGTGGAAGGAGACCTCGGGGA  93264      CAGT  CG
                               TCCTC   GG  TTCTTTTTACT
                               |||||   ||  ||||||||||
                               AGGGG   CC  GAGGAAGGTGA
                                  CT__  A_
GAM376  LOC221312 3'  GTGAAGAGATTTTGAAGGG   91908      C   TGGCGT
                               TCCT CAG     TCTTTTTAC
                               |||| |||     |||||||||
                               GGGA GTT     AGAGAAGTG
                                 A  TT____
GAM376  LOC221466 5'  GATGGGGGGATGCTGCTGGAGG 93688        TG        TACT
                               CCTCCAG  GCGTTCTTTT
                               |||||||  ||||||||||
                               GGAGGTC  CGTAGGGGGG
                                    GT        TAGG
GAM376  LOC221466 5'  GGTGAAAAGGACTCCGGGGG   93691      AGT  C
                               CCTCC   GG GTTCTTTTTACT
                               |||||   || ||||||||||||
                               GGGGG   CC CAGGAAAAGTGG
                                  ___  T
GAM376  LOC221466 5'  GGTGGAGGGGGGGATGGGGGG   93692       GTGGCG
                               TCCTCCA     TTCTTTTTACT
                               |||||||     ||||||||||
                               GGGGGGT     GGGGGAGGTGG
                                  AG_____
GAM376  LOC221773 3'  AGTAGAGGGGACGTGAGAGAAG 91036      CCAGTG
          GG                   TCCT     GCGTTCTTTTTACT
                               ||||     ||||||||||||||
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                                GGGA     TGCAGGGGAGATGA
                                  AGAGAG
GAM376  LOC221833 3'  GGTGGAGAGGGAGAGGCTGGAG 92541        GGCG
            G                      CCTCCAGT    TTCTTTTTACT
                                   ||||||||    ||||||||||
                                   GGAGGTCG    GGGAGAGGTGG
                                       GAGA
GAM376  LOC221876 5'  TGGGAGGGGCGGTGGA      93928      GTGG
                                   TCCA    CGTTCTTTTTA
                                   ||||    ||||||||||
                                   AGGT    GCGGGGAGGGT
                                     G___
GAM376  LOC221922 5'  GGTGAAGGGGGGGCTGGAGGG  92699        GTG  G
                                   TCCTCCA   GC TTCTTTTTACT
                                   |||||||   || ||||||||||
                                   GGGAGGT   CG GGGGGAAGTGG
                                       ___  G
GAM376  LOC221922 5'  GGTGAGGAGAGCAAGAGGGCAG 92700      _  AGTGGC
            GG                     TCCT CC     GTTCTTTTTACT
                                   |||| ||     ||||||||||||
                                   GGGA GG     CGAGAGGAGTGG
                                     C  GAGAA_
GAM376  LOC221922 5'  GGTGAGGAGGGAGCAGGAGGG  92701        AGTG  G
                                   TCCTCC    GC TTCTTTTTACT
                                   ||||||    || ||||||||||
                                   GGGAGG    CG GGGAGGAGTGG
                                      A___  A
GAM376  LOC221922 5'  GGTGGAGGCCCCATGCCGGAGG 92702        AGT     TC__
            G                      TCCTCC   GGCGT    TTTTTACT
                                   ||||||   |||||    ||||||||
                                   GGGAGG   CCGTA    GGAGGTGG
                                      ___     CCCC
GAM376  LOC221922 5'  GTGAGGAGAGCAGGAG      92703      AGTGGC
                                   CTCC     GTTCTTTTTAC
                                   ||||     ||||||||||
                                   GAGG     CGAGAGGAGTG
                                     A_____
GAM376  LOC221922 5'  GTGAGGGGGAGCAGGAGGG    92704        AGTG  G
                                   TCCTCC    GC TTCTTTTTAC
                                   ||||||    || ||||||||||
                                   GGGAGG    CG AGGGGGAGTG
                                      A___  _
GAM376  LOC222112 5'  GTGGGAGGGGCGCCAGG     92806     AG
                                   CC  TGGCGTTCTTTTTAC
                                   ||  ||||||||||||||
                                   GG  ACCGCGGGGAGGGTG
                                     __
GAM376  LOC222178 3'  GGTGAGAAGGCGTGGCTGAGGG 94173     TC    G    T
            A                      TCC  CAGT GCGT CTTTTTACT
                                   |||  |||| |||| |||||||||
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                                AGG  GTCG TGCG GAAGAGTGG
                                  GA   G   _
GAM376   LOC245728 5'  GGTGGGCAGCTTGATGGCTGCT 91134      TG  _  ___  T
             GGAGGG                 CCAG  GC GTT   CT TTTACT
                                ||||  || |||   || |||||||
                                GGTC  CG TAG   GA GGGTGG
                                  GT  G   TTC  C
GAM376   LOC253001 3'  GAAGGGTGCTGCTGGGGTGG   96256    _     TG   TT
                                TC CTCCAG  GCG  CTTT
                                || ||||||  |||  ||||
                                GG GGGGTC  CGT  GAAG
                                 T     GT   GG
GAM376   LOC253150 3'  GGTGAAGGGGGCGCCCAGGG   95518    AGT
                                CC   GGCGTTCTTTTTACT
                                ||   ||||||||||||||
                                GG   CCGCGGGGGAAGTGG
                                 GAC
GAM376   LOC253299 5'  AGTGAGAGGGACATGGTGGCAG 96452      _  G  GC
             GG                   TCCT CCA TG  GTTCTTTTTACT
                                |||| ||| ||  ||||||||||||
                                GGGA GGT GT  CAGGGAGAGTGA
                                  C   G  A_
GAM376   LOC253893 3'  ACAGGAAGGGTCCCACTGGAGG 96109          C TT     ACT
             G                    TCCTCCAGTGG G  CTTTTT
                                |||||||||||  |  ||||||
                                GGGAGGTCACC T  GAAGGA
                                       C GG     CA
GAM376   LOC253893 3'  GGTAGGGGGTGGGCTGGGGGA  96117         GG  TT  TT
                                TCCTCCAGT  CG  CT  TTACT
                                |||||||||  ||  ||  |||||
                                AGGGGGTCG  GT  GG  GATGG
                                     G_  GG  __
GAM376   LOC253962 5'  GGTGTGCTGGGCGCCGGTGGAG 96658        G       TTTT
             GG                   TCCTCCA TGGCGTTC    TACT
                                ||||||| ||||||||    ||||
                                GGGAGGT GCCGCGGG    GTGG
                                   G       TCGT
GAM376   LOC254266 5'  TGAGGGGGTAGGGGGA      97355        AGTGGCGT
                                TCCTCC       TCTTTTTA
                                ||||||       ||||||||
                                AGGGGG       GGGGGAGT
                                   AT_______
GAM376   LOC254559 5'  AGTAGGAGGGCCCGCCGGAGGA 96594        A   C  T
                                TCCTCC GTGG GT CTTTTTACT
                                |||||| |||| || |||||||||
                                AGGAGG CGCC CG GGAGGATGA
                                   C   _ _
GAM376   LOC254835 3'  AGTGGAGAGGAAATTGGAGGG  96929          GGCG
                                TCCTCCAGT    TTCTTTTTACT
                                |||||||||    ||||||||||
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                                GGGAGGTTA   AGGAGAGGTGA
                                     A___
GAM376  LOC254901 5'  TGGGAGGAGCGGGGAG     96264     AGTGG
                                CTCC    CGTTCTTTTTA
                                ||||    ||||||||||
                                GAGG    GCGAGGAGGGT
                                  G____
GAM376  LOC254944 3'  GGTGGAGGGGGCATGTCTGGAG 97209       TGGC
          GG                     TCCTCCAG   GTTCTTTTTACT
                                 ||||||||   ||||||||||||
                                 GGGAGGTC   CGGGGGAGGTGG
                                     TGTA
GAM376  LOC255043 3'  GTGGGGGGATTCGGGGGGA   95331      AGTGG  T_
                                TCCTCC    CG  TCTTTTTAC
                                ||||||    ||  |||||||||
                                AGGGGG    GC  AGGGGGGTG
                                   _____  TT
GAM376  LOC255328 3'  AGCAGAGGGGGCCCATTGGAGG 96556          C       A
          G                      TCCTCCAGTGG GTTCTTTTT CT
                                 ||||||||||| ||||||||| ||
                                 GGGAGGTTACC CGGGGGAGA GA
                                       _       C
GAM376  LOC255461 5'  AGTGGCACACATGCCGTTGGGG 97316     T       TCTTT
          A                      TCC CCAGTGGCGT    TTACT
                                 ||| ||||||||||    |||||
                                 AGG GGTTGCCGTA    GGTGA
                                   _       CACAC
GAM376  LOC255465 3'  GTGAGGCTTTGCTGAGGA    97299      C  TG C  TCTT
                                TCCTC AG  G GT    TTTAC
                                ||||| ||  | ||    |||||
                                AGGAG TC  T CG    GAGTG
                                   _ GT T  ____
GAM376  LOC255480 3'  GGTGAAGGGAGGTAGGTGGGGG 96520       GTG  G
                                CCTCCA   GC TTCTTTTTACT
                                ||||||   || ||||||||||
                                GGGGGT   TG GAGGGAAGTGG
                                    GGA  _
GAM376  LOC255516 5'  AGTGGCACACATGCCGTTGGGG 97329     T       TCTTT
          A                      TCC CCAGTGGCGT    TTACT
                                 ||| ||||||||||    |||||
                                 AGG GGTTGCCGTA    GGTGA
                                   _       CACAC
GAM376  LOC255650 3'  GGAGCTCTGGGGGGG       96713        T   G
                                TCCTCCAG GGC TTC
                                |||||||| ||| |||
                                GGGGGGTC TCG AGG
                                     _  _
GAM376  LOC256273 3'  GGGACACAGCTGGGGGA     96406         GGC
                                TCCTCCAGT   GTTCT
                                |||||||||   |||||
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                                AGGGGGTCG   CAGGG
                                     ACA
GAM376  LOC256598 5'  GACCGCTACTTGGAGGA     96351        _     T
                                TCCTCCA GTGGCG TC
                                ||||||| |||||| ||
                                AGGAGGT CATCGC AG
                                    T     C
GAM376  LOC256867 5'  GGAGCCTCCTGGGGGG      94865         TG C
                                TCCTCCAG  G GTTCT
                                ||||||||  | |||||
                                GGGGGGTC  C CGAGG
                                     CT _
GAM376  LOC257127 3'  GGTGAAGGGAGCCCACGTGGAG 96673       _   C
                                CTCCA GTGG GTTCTTTTTACT
                                ||||| |||| ||||||||||||
                                GAGGT CACC CGAGGGAAGTGG
                                   G   _
GAM376  LOC51136  3'  AGTGAAGATTAATTTACTGAGG 32323       C    CGTTC
           A                     TCCTC AGTGG     TTTTTACT
                                ||||| |||||     ||||||||
                                AGGAG TCATT     AGAAGTGA
                                   _     TAATT
GAM376  LOC51146  5'  GGTGAGGAAAGCACTGCAGGA  32402      C    G G    TT
                                TCCT CAGTG C TTCT  TTACT
                                |||| ||||| | ||||  |||||
                                AGGA GTCAC G AAGG  AGTGG
                                  C    _ A   __
GAM376  LOC51161  3'  AGTGGGAGGGATTGGGGGAGGA 32507       AGTGGC
                                TCCTCC     GTTCTTTTTACT
                                ||||||     ||||||||||||
                                AGGAGG     TAGGGAGGGTGA
                                   GGGT__
GAM376  LOC51182  5'  GGTAGCTGTTGCTGTTGGGGGA 32827        TG   TTCTTT
                                TCCTCCAG  GCG     TTACT
                                ||||||||  |||     |||||
                                AGGGGGTT  CGT     GATGG
                                     GT   TGTC__
GAM376  LOC51279  3'  AGTGAGGACTGAACACTGGGG  33306        GC__     TTTACT
                                CTCCAGTG    GTTCTT
                                ||||||||    ||||||
                                GGGGTCAC    CAGGAG
                                     AAGT     TGA
GAM376  LOC51725  3'  GGTGAAGGGAACAAAGCTGGAG 69867        GGC
           G                     CCTCCAGT   GTTCTTTTTACT
                                ||||||||   ||||||||||||
                                GGAGGTCG   CAAGGGAAGTGG
                                     AAA
GAM376  LOC55908  5'  GGGATCCACTGGGGA      37954     T      C
                                TCC CCAGTGG GTTCT
                                ||| ||||||| |||||
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                                AGG GGTCACC TAGGG
                                  _     _
GAM376  LOC56959  5' AGTAAAAGTCCATTGTGAGGA  81925      _     CGTTC
                                TCCTC CAGTGG     TTTTTACT
                                ||||| ||||||     ||||||||
                                AGGAG GTTACC     GAAAATGA
                                   T     T____
GAM376  LOC57019  3' GAAGCTGGCTGGGGGG      39724         _  G
                                TCCTCCAGT GGC TTC
                                ||||||||| ||| |||
                                GGGGGGTCG TCG AAG
                                      G  _
GAM376  LOC57105  3' AGTAGGAGGAGGATCTGGGG   39817       TGGCG
                                CTCCAG     TTCTTTTTACT
                                ||||||     ||||||||||
                                GGGGTC     GAGGAGGATGA
                                   TAG__
GAM376  LOC58525  5' AGGATGATACTGGAGGG     78642          G
                                TCCTCCAGTG CGTTCT
                                |||||||||| ||||||
                                GGGAGGTCAT GTAGGA
                                      A
GAM376  LOC64182  5' GGTGGAGAGAGAATGGGGA    42298     T   GTGGCG
                                TCC CCA      TTCTTTTTACT
                                ||| |||      ||||||||||
                                AGG GGT      GAGAGAGGTGG
                                  _   AA____
GAM376  LOC85569  3' AGTGAGGAGAGGCAGTTTGGAG 52408       TG_  G
                                CTCCAG   GC TTCTTTTTACT
                                ||||||   || ||||||||||
                                GAGGTT   CG GAGAGGAGTGA
                                   TGA  _
GAM376  LOC89919  3' AGTAAAGGGAATGTATCATGTG 60717    _  GTG_
           A                     TC CA    GCGTTCTTTTTACT
                                 || ||    ||||||||||||||
                                 AG GT    TGTAAGGGAAATGA
                                  T  ACTA
GAM376  LOC90050  3' AGTGGAGGGCAGGATTGGGG   56379       GGC     TT
                                CTCCAGT   GTTCTT  TACT
                                |||||||   ||||||  ||||
                                GGGGTTA   CGGGAG  GTGA
                                    GGA     __
GAM376  LOC90190  3' GTGGGAAGAGGATGAGGA    61781      CAGTGGCG
                                TCCTC       TTCTTTTTAC
                                |||||       ||||||||||
                                AGGAG       GAGAAGGGTG
                                   TAG_____
GAM376  LOC90309  5' GGTAATTATGGTACTGGGGGA  62183          G   TCTTT
                                TCCTCCAGTG CGT     TTACT
                                |||||||||| |||     |||||
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                                AGGGGGTCAT GTA    AATGG
                                     G  TT___
GAM376  LOC90317  3' GGGGCCCATTGGGAGG     62250      _   C
                                CCTCC AGTGG GTTCT
                                ||||| ||||| |||||
                                GGAGG TTACC CGGGG
                                   G   _
GAM376  LOC90378  5' AGGGGCTGCTGGAGGA     62520       TG  G
                                TCCTCCAG  GC TTCT
                                ||||||||  || ||||
                                AGGAGGTC  CG GGGA
                                     GT  _
GAM376  LOC90408  5' GTCGGAGGGATGACTGCTGGAG 62665       TG _      TT  T
           GA                     TCCTCCAG  G CGTTCTTT  AC
                                ||||||||  | ||||||||  ||
                                AGGAGGTC  C GTAGGGAG  TG
                                     GT A       GC
GAM376  LOC90719  3' GTGGAGGGGGGGGTGGGGA   63887    T   GTGGCG
                                TCC CCA     TTCTTTTTAC
                                ||| |||     ||||||||||
                                AGG GGT     GGGGGAGGTG
                                  _  GGG___
GAM376  LOC90784  5' AGTGGAGAGGACAGTGGGGAGG 63997      AGTG  _
                                CCTCC    GC GTTCTTTTTACT
                                |||||    || ||||||||||||
                                GGAGG    TG CAGGAGAGGTGA
                                   GG__  A
GAM376  LOC91064  5' GGTGGGGAGGGTGGCAGCGGG  64766    AG  G  TT
                                TCC  TG CG  CTTTTTACT
                                |||  || ||  |||||||||
                                GGG  AC GT  GAGGGGTGG
                                  CG  G  GG
GAM376  LOC91149  3' AGTATGCTTGGTGTGTTGGAGG 65068       GTG   TT  TTT__
           A                     TCCTCCA   GCG  CT    TACT
                                |||||||   |||  ||    ||||
                                AGGAGGT   TGT  GG    ATGA
                                     ___   GT  TTCGT
GAM376  LOC91266  5' AGTAAGGAGGATGCTACAGAAA 65408     CCA_
           GGA                     TCCT    GTGGCGTTCTTTTTACT
                                ||||    ||||||||||||||||
                                AGGA    CATCGTAGGAGGAATGA
                                  AAGA
GAM376  LOC91300  3' GTAATTGTGTTTTGGGGGA   57071        T   TTCTTT
                                TCCTCCAG GGCG     TTAC
                                |||||||| ||||     ||||
                                AGGGGGTT TTGT     AATG
                                     _   GTT___
GAM376  LOC91300  3' GTAATTGTGTTTTGGGGGA   94598        T   TTCTTT
                                TCCTCCAG GGCG     TTAC
                                |||||||| ||||     ||||
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                                AGGGGGTT TTGT     AATG
                                    _   GTT___
GAM376  LOC91301  5' AGTAAAGGGAGGACCTGCGGGG 65538      A TG C    __
             G                   CCTCC G  G GTTCTT  TTTACT
                                 ||||| |  | ||||||  ||||||
                                 GGGGG C  C CAGGAG  AAATGA
                                   _ GT _     GG
GAM376  LOC91308  3' GTGGAAAGAATGCTTTG     65562     T
                                 CAG GGCGTTCTTTTTAC
                                 ||| ||||||||||||||
                                 GTT TCGTAAGAAAGGTG
                                  _
GAM376  LOC91565  5' GGGAGGCTGGGCTGGGAGA    66464    CT    __   G
                                 TC  CCAGT  GGC TTCT
                                 ||  |||||  ||| ||||
                                 AG  GGTCG  TCG AGGG
                                  AG    GG   G
GAM376  LOC91689  5' GGTGAGGGGCGGAGCTGGGGG  52823        GG     TT
                                 CCTCCAGT  CGTTCT  TTACT
                                 ||||||||  ||||||  |||||
                                 GGGGGTCG  GCGGGG  AGTGG
                                     AG     __
GAM376  LOC91812  5' AGGGAGGAGAAGGCAGGAGGA  67237       AGTG  G      TA
                                 TCCTCC    GC TTCTTTT  CT
                                 ||||||    || |||||||  ||
                                 AGGAGG    CG AAGAGGA  GA
                                    A___  G      GG  A
GAM376  LOC91813  5' AGGGAGGAGAAGGCAGGAGGA  67244       AGTG  G      TA
                                 TCCTCC    GC TTCTTTT  CT
                                 ||||||    || |||||||  ||
                                 AGGAGG    CG AAGAGGA  GA
                                    A___  G      GG  A
GAM376  LOC91907  3' GTGGAGAGGACGGGTGGA    67495     T  AGTGG
                                 TCC CC    CGTTCTTTTTAC
                                 ||| ||    ||||||||||||
                                 AGG GG    GCAGGAGAGGTG
                                   T  _____
GAM376  LOC91974  5' AGTGAGAAGGTAGATGCCAACT 67750      _    ___
             GGAGGG                CCAGT GGCGTT   CTTTTTACT
                                 ||||| ||||||   |||||||||
                                 GGTCA CCGTAG   GAAGAGTGA
                                    A     ATG
GAM376  LOC92017  5' GTGGAGAGGAGGATGGGGA   67894     T  GTGGCG
                                 TCC CCA     TTCTTTTTAC
                                 ||| |||     ||||||||||
                                 AGG GGT     AGGAGAGGTG
                                   _  AGG___
GAM376  LOC92270  5' AGTGAAGAGAAAGAGTGGGAG  68628     AGTGGCG
                                 CTCC      TTCTTTTTACT
                                 ||||      ||||||||||
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                                GAGG      AAGAGAAGTGA
                                  GTGAGA_
GAM376  LOC92578  3' AGTGAGGAGAGAGCCTGGGGG  69822       GT   G
                                CCTCCA  GGC TTCTTTTTACT
                                ||||||  ||| ||||||||||
                                GGGGGT  CCG GAGAGGAGTGA
                                   __   A
GAM376  LOC92912  5' GGTGAGGGGGACGGGGGCGGGG 70846      A  GG_
                                CTCC GT   CGTTCTTTTTACT
                                |||| ||   ||||||||||||
                                GGGG CG   GCAGGGGGAGTGG
                                  _ GGG
GAM376  LOC92997  5' AGTGGAAGGAGCCTGGGAG   71085      AGT   GT
                                CTCC   GGC  TCTTTTTACT
                                ||||   |||  ||||||||||
                                GAGG   CCG  AGGAAGGTGA
                                  GT_  __
GAM376  LOC93109  3' GGGCCCTGTGCTGGGGGG    71416         ___  C
                                TCCTCCAGT   GG GTTC
                                |||||||||   || ||||
                                GGGGGGTCG   CC CGGG
                                     TGT  _
GAM376  LOC93109  3' GGTGGGAGTGAACACTGGGGTG 71417    _      GGC   _
          A                      TC CTCCAGT   GTTC TTTTTACT
                                 || |||||||   |||| ||||||||
                                 AG GGGGTCA   CAAG GAGGGTGG
                                  T       ___    T
GAM376  LOC93132  5' GGTAACAGTAGATGCCTTGGGG 71498         T     CT  _
          GA                     TCCTCCAG GGCGTT  TT TTACT
                                 |||||||| ||||||  || |||||
                                 AGGGGGTT CCGTAG  GA AATGG
                                      _     AT  C
GAM376  LOC96810  3' GTGAGGAGAGCAAGAGGA    70564       CAGTGGC
                                 TCCTC      GTTCTTTTTAC
                                 |||||      ||||||||||
                                 AGGAG      CGAGAGGAGTG
                                   AA_____
GAM377  ARHGEF6   3' CAAACTTGAAGCCAGGC     68197       ACCA
                                 GCCTGG    CAAGTTTG
                                 ||||||    ||||||||
                                 CGGACC    GTTCAAAC
                                    GAA_
GAM377  CNTN2     3' GTCACAACCCAGGTGA      17411         ACCACAA  _
                                 TCGCCTGG      GTT TGAC
                                 ||||||||      ||| ||||
                                 AGTGGACC      CAA ACTG
                                      ________  C
GAM377  CORO2A    3' AAACTGTGGTCCAGAGA     12642    GC        A
                                 TC  CTGGACCACA GTTT
                                 ||  |||||||||| ||||
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                                AG  GACCTGGTGT CAAA
                                 A_       _
GAM377  CORO2A   3'  AAACTGTGGTCCAGAGA    53398    GC       A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_       _
GAM377  GRLF1    3'  AGGTCAGAAAGTGGCCCAGG   78551      A   AAG
                                CCTGG CCAC   TTTGACCT
                                ||||| ||||   ||||||||
                                GGACC GGTG   AGACTGGA
                                   C   AA_
GAM377  LAPTM5   3'  AGGCTTGTGGTCAAGC     22199    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCGGA
                                 AA_
GAM377  POU2AF1  3'  AGATTTACAGTCCAGGC     20647       CAC
                                GCCTGGAC   AAGTTT
                                ||||||||   ||||||
                                CGGACCTG   TTTAGA
                                     ACA
GAM377  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  6355        C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM377  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  54574       C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM377  TRIM34   5'  AGGTCAAGTTGAGCCCAG    55224     ACCA   G
                                CTGG    CAA TTTGACCT
                                ||||    ||| ||||||||
                                GACC    GTT GAACTGGA
                                  CGA_   _
GAM377  TRIM9    5'  AGGCCAGGCAAGTCCAGGC   30749       CACAA    A
                                GCCTGGAC    GTTTG CCT
                                ||||||||    ||||| |||
                                CGGACCTG    CGGAC GGA
                                     AA___    C
GAM377  ABLIM    5'  GATATGTAACCCAGGCGG    22030       ACC   A
                                TCGCCTGG   ACA GTT
                                ||||||||   ||| |||
                                GGCGGACC   TGT TAG
                                     CAA   A
GAM377  AMOT     3'  AGGCATCTTCATGGTCCAGGGA 55716    G       C_   TT  A
                                TC CCTGGACCA  AAG  TG CCT
                                || |||||||||  |||  || |||
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                                AG GGACCTGGT  TTC  AC GGA
                                 _       AC   T_ _
GAM377  DKFZp434D177 5'  TTAGACCCAGGCGA       79443        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                          ________
GAM377  DKFZp434D177 5'  TTAGACCCAGGCGA       50056        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                          ________
GAM377  FLJ23420  3'  CAAGTGGGTCCAGGC       46845         A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                          _  __
GAM377  HSA249128 5'  GGCGCGGTCCAGGCGG      34152          ACAA
                                TCGCCTGGACC    GTT
                                ||||||||||    |||
                                GGCGGACCTGG    CGG
                                       CG__
GAM377  MGC15668  5'  AGACCCGGTGGTCCAGACG    51277    C       AA_
                                CG CTGGACCAC   GTTT
                                || |||||||||   ||||
                                GC GACCTGGTG   CAGA
                                 A        GCC
GAM377  MGC22014  3'  AGGTCCCGAGTGTAACCCAGGT 64486        ACC   AGTTT
           GA                     TCGCCTGG   ACA    GACCT
                                ||||||||   |||    |||||
                                AGTGGACC   TGT    CTGGA
                                     CAA   GAGCC
GAM377  SDCCAG10  5'  AGAGTTGTGGTCCAAAGA    19641    GCC        G
                                TC   TGGACCACAA TTT
                                ||   |||||||||| |||
                                AG   ACCTGGTGTT AGA
                                 AA_         G
GAM377  LOC115442 3'  AGGTCAGGGATGGTCCAG    72676        CAAG
                                CTGGACCA    TTTGACCT
                                ||||||||    ||||||||
                                GACCTGGT    GGACTGGA
                                     AG__
GAM377  LOC129011 5'  AGACCTGCGGTCCAGGC     74862         A  A
                                GCCTGGACC CA GTTT
                                ||||||||| || ||||
                                CGGACCTGG GT CAGA
                                       C  C
GAM377  LOC130536 5'  GCAAAGTCCAGGCG        75746         CACAAG    A
                                CGCCTGGAC     TTTG C
                                |||||||||     |||| |
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                                GCGGACCTG     AAAC G
                                      _____   C
GAM377  LOC149108 3'  AGACTTCACTGTGGTCCA    84357        ____
                                TGGACCACA   AGTTT
                                |||||||||   |||||
                                ACCTGGTGT   TCAGA
                                     CACT
GAM377  LOC221688 5'  AGACTCGGGCCCAGACGA    93674    C   A  ACA
                                TCG CTGG CC   AGTTT
                                ||| |||| ||   |||||
                                AGC GACC GG   TCAGA
                                  A   C  GC_
GAM377  LOC256228 5'  AGACTTGTGGTCAAAGC     96233    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCAGA
                                 AAA
GAM377  LOC257441 5'  TTAGACCCAGGCGA        95566        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                      _______
GAM377  LOC91960  3'  AGGTGCCTCTCGTGGTCCAAGC 67657    C      A  TTTG
                                GC TGGACCAC AG    ACCT
                                || |||||||| ||    ||||
                                CG ACCTGGTG TC    TGGA
                                 A       C  TCCG
GAM377  LOC92840  3'  GTCCCTCGGGTCCAGGC     56435        ACA  TTT
                                GCCTGGACC   AG   GAC
                                |||||||||   ||   |||
                                CGGACCTGG   TC   CTG
                                     GC_  C__
GAM378  ABCB1     5'  AGCGCCGGGGCGTGGG      6246         TATCCT
                                CCCGTGTTCC     TGTT
                                ||||||||||     ||||
                                GGGTGCGGGG     GCGA
                                     CC_____
GAM378  ABCB10    5'  CGGCGGGCTGAGGCGTACGGGT 23887       TT   ATC
                                ACCCGTG  CCT   CTTGTTG
                                |||||||  |||   |||||||
                                TGGGCAT  GGA   GGGCGGC
                                   GC   GTC
GAM378  ABCB9     5'  AGCGGCGCAGCGCGGGT     39032        CCTAT  TT
                                ACCCGTGTT    CC  GTT
                                |||||||||    ||  |||
                                TGGGCGCGA    GG  CGA
                                     CGC__  __
GAM378  ACE       3'  GAGACTGGGATGGGAACACTGG 5796      C          T   G
           T                     ACC GTGTTCCTATCCT GTT
                                 ||| |||||||||||| |||
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                                TGG CACAAGGGTAGGG CAG
                                  T          T  AGA
GAM378  ACK1     5'  AGGATGTAGGGGCATGGG    19341          __
                                CCCGTGTTCCTA  TCCT
                                ||||||||||||  ||||
                                GGGTACGGGGAT  AGGA
                                      GT
GAM378  ACOX3    5'  TGGCAGGGGTTGAACTGTGG   13026    _ T   CT
                                CC CG GTTC  ATCCTTGTTG
                                || || ||||  ||||||||||
                                GG GT CAAG  TGGGGACGGT
                                 T _   T_
GAM378  ACP2     3'  TAGCTCAGAGGGACACGG    7854          ATCCTT
                                CCGTGTTCCT     GTTG
                                ||||||||||     ||||
                                GGCACAGGGA     CGAT
                                      GACT__
GAM378  ADAM10   5'  CGGGAGGTAGGGGCGCGG    6618           _
                                CCGTGTTCCTATC CTTG
                                |||||||||||| ||||
                                GGCGCGGGGATGG GGGC
                                       A
GAM378  ADAMTS8  5'  TGGTAGGGGTTAACGTGGGT  22887        CCT     TT
                                ACCCGTGTT   ATCCTTG  G
                                |||||||||   |||||||  |
                                TGGGTGCAA   TGGGGAT  T
                                      T__      GG
GAM378  AGRN     3'  GGCGGTGGGGCTGGGT      78837      T  T     _
                                ACCCG GT CCTATC CT
                                ||||| || |||||| ||
                                TGGGT CG GGGTGG GG
                                   _ _     C
GAM378  AGTR1    5'  CAGCGCCCGGGGCGCGGGT   23778          TATCCT
                                ACCCGTGTTCC     TGTTG
                                ||||||||||      |||||
                                TGGGCGCGGGG     GCGAC
                                      CCC___
GAM378  AGTR1    5'  CAGCGCCCGGGGCGCGG     16708         TATCCT
                                CCGTGTTCC     TGTTG
                                |||||||||     |||||
                                GGCGCGGGG     GCGAC
                                     CCC___
GAM378  AGTR1    5'  CAGCGCCCGGGGCGCGGGT   5472           TATCCT
                                ACCCGTGTTCC     TGTTG
                                ||||||||||      |||||
                                TGGGCGCGGGG     GCGAC
                                      CCC___
GAM378  AGTR1    5'  CAGCGCCCGGGGCGCGGGT   49007          TATCCT
                                ACCCGTGTTCC     TGTTG
                                ||||||||||      |||||
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                                TGGGCGCGGGG     GCGAC
                                      CCC___
GAM378  AKAP2    3'  TAACAAGGTATTTGCATGAGT  23268    C    TCCTAT
                                AC CGTGT     CCTTGTTG
                                || |||||     ||||||||
                                TG GTACG     GGAACAAT
                                 A    TTTAT_
GAM378  AKT2     5'  GGCGATGGGCGGGGGT      7888      G  TT    _
                                ACCC TG  CCTATC CT
                                |||| ||  |||||| ||
                                TGGG GC  GGGTAG GG
                                  G __     C
GAM378  ALDH3A2  5'  CAATAGGGGTGAGGCTTTGGGT 69271      TGTT  _
                                ACCCG    CCT ATCCTTGTTG
                                |||||    ||| ||||||||||
                                TGGGT    GGA TGGGGATAAC
                                   TTC_  G
GAM378  ALX3     3'  CAGCAGGGGGCGCACTGGT    21421     C    T  TAT
                                ACC GTGT CC   CCTTGTTG
                                ||| |||| ||   ||||||||
                                TGG CACG GG   GGGACGAC
                                  T   C ___
GAM378  AMPD3    5'  CGACGGGGGCTGCACGCGG    4896     _    TCCTA
                                CC CGTGT     TCCTTGTTG
                                || |||||    |||||||||
                                GG GCACG     GGGGGCAGC
                                 C    TC___
GAM378  APTX     3'  TGGTGAGGGTGGCTGGG     34662     TGTTC      TG
                                CCCG    CTATCCT  TTG
                                ||||    |||||||  |||
                                GGGT    GGTGGGA  GGT
                                  C____      GT
GAM378  APXL     3'  CGGTGGAGGAGGGGCACGGG   7926          A_  TTGTTG
                                CCCGTGTTCCT  TCC
                                ||||||||||  |||
                                GGGCACGGGGA  AGG
                                      GG   TGGC
GAM378  ARAF1    5'  AATAAGGGTGGAAGGC      63934    G   T
                                GT TTCC ATCCTTGTT
                                || |||| |||||||||
                                CG AAGG TGGGAATAA
                                 G   _
GAM378  ARCN1    5'  CAGTGGAGCCGGAGTGCGGG   7975      TG   TA_  _  TTG
                                CCCG  TTCC   TCC TTG
                                ||||  ||||   ||| |||
                                GGGC  GAGG   AGG GAC
                                  GT   CCG   T
GAM378  ARHGEF12 3'  TGGCAGGGGTGGGGGTTGCTAA 31006    GT____ TT
           GG                   CC     G  CCTATCCTTGTTG
                                ||     |  ||||||||||||
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                                GG     T  GGGTGGGGACGGT
                                 AATCGT GG
GAM378  ARNT2    3'  AACAGGGGTCCAGGGT      29451      G  TTCCT
                                ACCC TG    ATCCTTGTT
                                |||| ||    |||||||||
                                TGGG AC    TGGGGACAA
                                  _  C____
GAM378  ASNS     3'  TGTTGGATGGGGACTGTGGGT  8034      GT_       TTGTTG
                                ACCC   GTTCCTATCC
                                ||||   ||||||||||
                                TGGG   CAGGGGTAGG
                                  TGT        TTGT
GAM378  ASNS     3'  TGTTGGATGGGGACTGTGGGT  55944     GT_       TTGTTG
                                ACCC   GTTCCTATCC
                                ||||   ||||||||||
                                TGGG   CAGGGGTAGG
                                  TGT        TTGT
GAM378  ATF4     5'  CGGCAGGGCGGCGGCGCGGG   8036       TC  AT
                                CCCGTGT  CT  CCTTGTTG
                                |||||||  ||  ||||||||
                                GGGCGCG  GG  GGGACGGC
                                    GC  C_
GAM378  ATF7     3'  GGACATGGCAATATGGGT    22467        _  TA_
                                ACCCGTGTT CC   TCC
                                |||||||||  ||   |||
                                TGGGTATAA GG   AGG
                                     C  TAC
GAM378  ATP11A   3'  GTGACGGGGGTGGCACACAGGA 77033      _______
           CACGGGT                 TGTTC     CTATCCTTGTTG   T
                                |||||     ||||||||||||   |
                                ACAGG     GGTGGGGGCAGT   G
                                  ACACAC
GAM378  ATP5G2   3'  CAGCCTGGGGAACGTGG     17727        TAT  TT
                                CCGTGTTCC   CC  GTTG
                                |||||||||   ||  ||||
                                GGTGCAAGG   GG  CGAC
                                     ___  TC
GAM378  ATP6IP1  3'  CAATAAGCAGTACACGGGT   6788        TC  ATC
                                ACCCGTGT  CT   CTTGTTG
                                ||||||||  ||   |||||||
                                TGGGCACA  GA   GAATAAC
                                    T_  C__
GAM378  ATP8B2   3'  CAGTGAGGTGGGGGCGGGT   65216       GT    T  TG
                                ACCCGT  TCCTA CCT  TTG
                                ||||||  ||||| |||  |||
                                TGGGCG  GGGGT GGA  GAC
                                  __    _  GT
GAM378  AXIN1    3'  TGCGATGGGGAACAGTGTTGGG 60859      _____     _  CTTGTTG
           T                     CCCG    TGTTCCT ATC
                                ||||    ||||||| |||
```

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                                GGGT   ACAAGGG TAG
                                  TGTG     G  C  GTT
GAM378  B3GAT1   5'  TAATGAGGAGCCGTGGGT   37832      TTCCTA   TG
                                ACCCGTG    TCCT  TTG
                                |||||||    ||||  |||
                                TGGGTGC    AGGA  AAT
                                   CG____   GT
GAM378  B3GAT1   5'  TAATGAGGAGCCGTGGGT   53978      TTCCTA   TG
                                ACCCGTG    TCCT  TTG
                                |||||||    ||||  |||
                                TGGGTGC    AGGA  AAT
                                   CG____   GT
GAM378  BAZ2A    3'  TGTAGGGATAGGGCATG    25613     T       TT
                                CGTGT CCTATCCTTG  G
                                |||||  ||||||||||  |
                                GTACG GGATAGGGAT  T
                                  _       GG
GAM378  BCL2     3'  CGGTAAGGATACTTTACATGG  5301      TCC_     TT
                                CCGTGT   TATCCTTG  G
                                ||||||   ||||||||  |
                                GGTACA   ATAGGAAT  C
                                   TTTC      GG
GAM378  BCL2     3'  AGATCGGGGGTTGGAGTGCGGG 5396      TG   T     TTG
          T                      ACCCG  TTCC ATCCTTG
                                 |||||  ||||  |||||||
                                 TGGGC  GAGG TGGGGGC
                                   GT   T     TAGAG
GAM378  BCL7A    3'  GGGGTGGGGTGGGGTCATGGGT 40643       TT      TGTTG
                                ACCCGTG  CCTATCCT
                                |||||||  ||||||||
                                TGGGTAC  GGGTGGGG
                                   TG      TGGGGG
GAM378  BCR      5'  TGGTAAGGGCGATGAGTGTGGG 15075     TG   CTA_    TT
                                CCCG  TTC   TCCTTG  G
                                ||||  |||   ||||||  |
                                GGGT  GAG   GGGAAT  T
                                  GT   TAGC     GG
GAM378  BLAME    3'  AGGATCTGGGAGTGAGGGT   39238     G GT   __
                                ACCC T  TCCT  ATCCT
                                ||||  |  ||||  |||||
                                TGGG G  AGGG  TAGGA
                                  A TG    TC
GAM378  BLTR2    5'  GGGAAGGAGCAGGGT      39043     G     A
                                ACCC TGTTCCT TCCT
                                |||| ||||||| ||||
                                TGGG ACGAGGA AGGG
                                  _     _
GAM378  BMP4     5'  TGGCGGGGGAAGGAGTGTGG   55640    TG    A
                                CCG  TTCCT TCCTTGTTG
                                |||  ||||| |||||||||
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                                GGT  GAGGA GGGGGCGGT
                                  GT    A
GAM378  BMPR1B   5'  CGGCGGGGCCTCGCGGGACGCG 6834          TAT___
            GG                    CCCGTGTTCC     CCTTGTTG
                                  ||||||||||     ||||||||
                                  GGGCGCAGGG     GGGGCGGC
                                       CGCTCC
GAM378  BRF1     3'  TGGCAGGGGGCCTCGCGGGT   7716        TTCCTA
                                  ACCCGTG     TCCTTGTTG
                                  |||||||     |||||||||
                                  TGGGCGC     GGGGACGGT
                                     TCCG__
GAM378  BTAF1    3'  TGGTGAGGGTAGGTATATG    72457       T       TG
                                  CGTGT CCTATCCT  TTG
                                  ||||| ||||||||  |||
                                  GTATA GGATGGGA  GGT
                                     T       GT
GAM378  BTEB1    3'  GGGGAGGGTAGGGAGTGGGT   6848       GTG         G  G
                                  ACCC   TTCCTATCCTT TT
                                  ||||   |||||||||||| ||
                                  TGGG   AGGGATGGGAG GG
                                    TG_         G  G
GAM378  CA3      5'  GCAGGGAGGGGCGTGGGT    17736          TA
                                  ACCCGTGTTCC  TCCTTGT
                                  ||||||||||  |||||||
                                  TGGGTGCGGGG  AGGGACG
                                              __
GAM378  CABC1    3'  CAGTGAGGGTGGGAGCAGCGG  39653     _          TG
                                  CCG TGTTCCTATCCT  TTG
                                  ||| ||||||||||||  |||
                                  GGC ACGAGGGTGGGA  GAC
                                    G          GT
GAM378  CACNA1S  3'  GCAATGGGGGTGGGGAAGTTGC 3566     TG____        TG
            TGGG                    CG     TTCCTATCCT  TTG   C
                                  ||     ||||||||||  |||  |
                                  GT     AGGGGTGGGG  AAC   G
                                   CGTTGA         GT
GAM378  CACNG6   3'  TGATGGGGTAGCTGGGGTGTGG 49105      TG    TAT__   TG
            G                     CCCG  TTCC     CCT  TTG
                                  ||||  ||||     |||  |||
                                  GGGT  GGGG     GGG  AGT
                                    GT    TCGAT   GT
GAM378  CALB2    3'  TGGAAGGTGATGGGGGCATGGG 8211             _   GTTG
            T                      ACCCGTGTTCCTATC CTT
                                  |||||||||||||||  |||
                                  TGGGTACGGGGGTAG GGA
                                            T   AGGT
GAM378  CALM3    3'  CAGCAGCCTGTTGGGGCAGGGG 17740      G     TATCC_
            T                      ACCC TGTTCC     TTGTTG
                                  |||| ||||||     ||||||
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                                TGGG ACGGGG     GACGAC
                                  G     TTGTCC
GAM378  CARKL    3'  TGGTAGGGATGGCTGTGGGGT  25192     GTGTTC       TT
                                ACCC     CTATCCTTG  G
                                ||||     |||||||||  |
                                TGGG     GGTAGGGAT  T
                                  GTGTC_       GG
GAM378  CARP     5'  TAATGGGGGTGGGAGTGT    26900    TG       TG
                                G  TTCCTATCCT  TTG
                                |  ||||||||||  |||
                                T  GAGGGTGGGG  AAT
                                 GT        GT
GAM378  CARPX    5'  CAGCGAGGCATCGGACATGTGT 39418    C      CTAT
                                AC CGTGTTC    CCTTGTTG
                                || |||||||    ||||||||
                                TG GTACAGG    GGAGCGAC
                                 T      CTAC
GAM378  CARPX    5'  CGGCTGTCGGGTGGGAGTGCGA 39419    C  TG       TT__
            GT                    AC CG  TTCCTATCC    GTTG
                                || ||  |||||||||    ||||
                                TG GC  GAGGGTGGG    CGGC
                                 A  GT       CTGT
GAM378  CASP8    3'  TGACAAGAAAAAACATGGG    52955        CCTATC
                                CCCGTGTT     CTTGTTG
                                ||||||||     |||||||
                                GGGTACAA     GAACAGT
                                     AAA___
GAM378  CCNH     5'  TAACGAACCCGGGATACGG    6953         TATCC
                                CCGTGTTCC    TTGTTG
                                |||||||||    ||||||
                                GGCATAGGG    AGCAAT
                                     CCCA_
GAM378  CD244    3'  TGGCAGGTTCTGCACGTGG    33064    _    TCCTAT   T
                                CC CGTGT     CCT GTTG
                                || |||||     ||| ||||
                                GG GCACG     GGA CGGT
                                 T    TCTT__   _
GAM378  CDC27    3'  TGACAATTTATGGGGGGTAGGG 6991      GTG      CC_
            T                    ACCC   TTCCTAT   TTGTTG
                                ||||   |||||||   ||||||
                                TGGG   GGGGGTA   AACAGT
                                  ATG      TTT
GAM378  CDK2     3'  ATTGAGTGAGGGCATGGGT    8392         T   ATC    TTG
                                ACCCGTGT CCT   CTTG
                                |||||||| |||   ||||
                                TGGGTACG GGA   GAGT
                                     _  GT_    TAG
GAM378  CDK4     5'  TGGTGAGGGTGGGGGTGAGGG  53764     GT TT       TG
                                CCC  G  CCTATCCT  TTG
                                |||  |  ||||||||  |||
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                                GGG  T  GGGTGGGA  GGT
                                  AG GG       GT
GAM378  CDK4     5'  TGGTGAGGGTGGGGGTGAGGG  3574      GT TT       TG
                                CCC  G  CCTATCCT  TTG
                                |||  |  ||||||||  |||
                                GGG  T  GGGTGGGA  GGT
                                  AG GG       GT
GAM378  CDKN1C   5'  CAGCAGGCATCGAGGGGGCGCG 3575          ___  C
           G                     CCGTGTTCCT   AT CTTGTTG
                                ||||||||||   || |||||||
                                GGCGCGGGGG   TA GGACGAC
                                      AGC  C
GAM378  CDKN2A   5'  GGGAGTGGGGGTGGGGT     54225      G  TT   _
                                ACCC TG  CCTA TCCT
                                ||||  ||  ||||  ||||
                                TGGG GT  GGGT AGGG
                                  _  GG   G
GAM378  CDKN2A   5'  GGGGTGGGGTGGGGGTGGGGGT 54226      G  TT       TGTTG
                                ACCC TG  CCTATCCT
                                ||||  ||  ||||||||
                                TGGG GT  GGGTGGGG
                                  G  GG       TGGGGG
GAM378  CENTD2   3'  CAGCGGGGGGGTGCATGGG    30867        T  TAT
                                CCCGTGT CC   CCTTGTTG
                                |||||||  ||   ||||||||
                                GGGTACG GG   GGGGCGAC
                                     T  ___
GAM378  CENTD2   3'  CGGCAGGGGTGGGAGGCAGCAG 30868    G  _____
           GGGT                    CC TGT    TCCTATCCTTGTTG
                                ||  |||    ||||||||||||||
                                GG ACG    AGGGTGGGGACGGC
                                 G   ACGG
GAM378  CENTD2   3'  CAGCGGGGGGGTGCATGGG    57552        T  TAT
                                CCCGTGT CC   CCTTGTTG
                                |||||||  ||   ||||||||
                                GGGTACG GG   GGGGCGAC
                                     T  ___
GAM378  CENTD2   3'  CGGCAGGGGTGGGAGGCAGCAG 57554    G  _____
           GGGT                    CC TGT    TCCTATCCTTGTTG
                                ||  |||    ||||||||||||||
                                GG ACG    AGGGTGGGGACGGC
                                 G   ACGG
GAM378  CERD4    3'  TGATGAGATGAAGAATGTGGG  23854      TG   C_   C TG
                                CCCG  TTC  TATC T  TTG
                                ||||  |||  ||||  |  |||
                                GGGT  AAG  GTAG A  AGT
                                  GT   AA    _ GT
GAM378  CHRNA10  3'  CAGTGGGGAGCACATGGGT   39875        TCCTA    TG
                                ACCCGTGT    TCCT  TTG
                                ||||||||    ||||  |||
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                                TGGGTACA    AGGG  GAC
                                    CG___   GT
GAM378  CHRNA4   3'  CAGCCAGGGGTGGGGATGGGGT 5613      G          _
                                ACCC TGTTCCTATCCTTG TTG
                                |||| |||||||||||||| |||
                                TGGG GTAGGGGTGGGGAC GAC
                                  _          C
GAM378  CHST2    3'  TAATTTGGATGTGGGGGTGGGG 62696     G  TT  __   TT
            GT                   ACCC TG  CCT  ATCC  GTTG
                                |||| ||  |||  ||||  ||||
                                TGGG GT  GGG  TAGG  TAAT
                                  G  GG   TG   TT
GAM378  CISH     3'  CAGCAAGAGCAAGGCATGGG   59013       CCTATC
                                CCCGTGTT    CTTGTTG
                                ||||||||    |||||||
                                GGGTACGG    GAACGAC
                                    AACGA_
GAM378  CISH     3'  CAGCAAGAGCAAGGCATGGG   25276       CCTATC
                                CCCGTGTT    CTTGTTG
                                ||||||||    |||||||
                                GGGTACGG    GAACGAC
                                    AACGA_
GAM378  CLASP1   3'  TAACATATTTGGGGGTGGGGT  65310     G  TT   TCCT
                                ACCC TG  CCTA   TGTTG
                                |||| ||  ||||   |||||
                                TGGG GT  GGGT   ACAAT
                                  _ GG   TTAT   A
GAM378  CLN6     3'  CAGGAGTAGGGGGGGGTGTGGGT 35400      TG   A____   TGTTG
                                ACCCG  TTCCT    TCCT
                                |||||  |||||    ||||
                                TGGGT  GGGGG    AGGA
                                   GT   GGATG   C  G
GAM378  COL1A1   3'  GGGCGGGGATGGGGGCAGGGT  3607      G          G
                                ACCC TGTTCCTATCCTTGTT
                                |||| ||||||||||||||||
                                TGGG ACGGGGGTAGGGGCGG
                                  _           GG
GAM378  CR1L     3'  AACCTCATGGGAATGGGGT   89403     G      CCTT  G
                                ACCC TGTTCCTAT   GTT
                                |||| |||||||||   |||
                                TGGG GTAAGGGTA   CAA
                                  _       CTC_  G
GAM378  CRACC    3'  CAGTGAGACTGGTGGGGCACGG 41004       T    ___  TG
            G                    CCCGTGT CCTATC  CT  TTG
                                ||||||| ||||||  ||  |||
                                GGGCACG GGGTGG  GA  GAC
                                   _    TCA  GT
GAM378  CRIM1    3'  TGAGTTTGGATGGGGAAATGGG 33181      G       TTGTTG
            T                    ACCCGT TTCCTATCC
                                ||||||| |||||||||
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                                TGGGTA AGGGGTAGG
                                   A       TTTGAGTG
GAM378  CRSP9   3'  TAGCAAAGTGGGGTATGGG   14961       TT  TATCC
                                CCCGTG  CC    TTGTTG
                                ||||||  ||    ||||||
                                GGGTAT  GG    AACGAT
                                   GG  TGA__
GAM378  CTNS    3'  TGGCAGGAGGGGTGGGGGT   17046     G  TT   ATC
                                ACCC TG  CCT   CTTGTTG
                                ||||  ||  |||   |||||||
                                TGGG GT  GGA   GGACGGT
                                  G  GG  ___
GAM378  CTPS    3'  TGCGATGGGAACCGATGGT   88597     __  T       CTTGTTG
                                ACC  CG GTTCCTATC
                                |||  || |||||||||
                                TGG  GC CAAGGGTAG
                                  TA  _       C   GTT
GAM378  CXCL16  5'  AGCAGGGCCGGTGGGT     41914      TGTT  TAT
                                ACCCG   CC   CCTTGTT
                                |||||   ||   |||||||
                                TGGGT   GG   GGGACGA
                                   _____  CC_
GAM378  CYB561  3'  CAGCAGGCGGGCGCGTGGGT   8597         T   ATC
                                ACCCGTGT CCT   CTTGTTG
                                |||||||| |||   |||||||
                                TGGGTGCG GGG   GGACGAC
                                     C   C__
GAM378  CYLN2   3'  AACGGGGGCTGGGGGT     12627     GTGTT  TA
                                ACCC    CC  TCCTTGTT
                                ||||    ||  ||||||||
                                TGGG    GG  GGGGGCAA
                                   ______  TC
GAM378  DCTN1   3'  CAGCCCCCAGGTAGAAACGTGG 43476         C   T   T___
          GT                      ACCCGTGTT CTA CCT    GTTG
                                |||||||||| ||| |||   ||||
                                TGGGTGCAA GAT GGA    CGAC
                                     A   _   CCCC
GAM378  DCTN1   3'  CAGCCCCCAGGTAGAAACGTGG 14553         C   T   T___
          GT                      ACCCGTGTT CTA CCT    GTTG
                                |||||||||| ||| |||   ||||
                                TGGGTGCAA GAT GGA    CGAC
                                     A   _   CCCC
GAM378  DDAH2   5'  CAGCGCGACAGGAGTGGGGGT  25662      G GT    A  CT
                                ACCC T  TCCT TC  TGTTG
                                ||||  |  ||||  ||  |||||
                                TGGG G  AGGA AG  GCGAC
                                  G TG    C  C_
GAM378  DDX11   3'  TGGCAAGGATGTTCGGCTGGT  47664     C  GTTCC
                                ACC GT    TATCCTTGTTG
                                |||  ||    ||||||||||
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                              TGG CG    GTAGGAACGGT
                                T  GCTT_
GAM378  DDX15   5' TAGCGGGAGGGGTGGGGGT   7232      G  TT   ATC
                              ACCC TG  CCT   CTTGTTG
                              |||| ||  |||   |||||||
                              TGGG GT  GGA   GGGCGAT
                                G  GG  ___
GAM378  DDX3    5' CGACAGGGAATTGCGGTGT   7224    _    TTCCTA
                              AC CCGTG     TCCTTGTTG
                              || |||||     |||||||||
                              TG GGCGT     AGGGACAGC
                               T    TA____
GAM378  DDX3    5' CGACAGGGAATTGCGGTGT   43758   _    TTCCTA
                              AC CCGTG     TCCTTGTTG
                              || |||||     |||||||||
                              TG GGCGT     AGGGACAGC
                               T    TA____
GAM378  DGAT1   5' CGACGGGCCTGACGCGGG    64541       CCTATC
                              CCCGTGTT     CTTGTTG
                              ||||||||     |||||||
                              GGGCGCAG     GGGCAGC
                                   TCC___
GAM378  DGCR2   3' AGTGAGGAAACGGGGT     17626     G   CCTA   TG
                              ACCC TGTT    TCCT  TT
                              |||| ||||    ||||  ||
                              TGGG GCAA    AGGA  GA
                                _   ____   GT
GAM378  DPP6    3' TAATGAGGACGTTCAACATGG  55452       CCTA_   TG
                              CCGTGTT    TCCT  TTG
                              |||||||    ||||  |||
                              GGTACAA    AGGA  AAT
                                  CTTGC   GT
GAM378  DRP2    3' AGCAGGGATCTGGTGG     8660     TGTT  T_
                              CCG   CC  ATCCTTGTT
                              |||   ||  |||||||||
                              GGT   GG  TAGGGACGA
                                ____  TC
GAM378  DRPLA   3' TGGCGAGGATGGGGACA    8670
                              TGTTCCTATCCTTGTTG
                              |||||||||||||||||
                              ACAGGGGTAGGAGCGGT

GAM378  DUSP4   3' CAGCAAGGGTAGGACGGG    7335      TGT
                              CCCG   TCCTATCCTTGTTG
                              ||||   ||||||||||||||
                              GGGC   AGGATGGGAACGAC
                                ___
GAM378  DUSP4   3' CAGCAAGGGTAGGACGGG    54053     TGT
                              CCCG   TCCTATCCTTGTTG
                              ||||   ||||||||||||||
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                              GGGC  AGGATGGGAACGAC
                                ___
GAM378  DUSP4   5' CAGCAGGGCTGGGACTGGGT  54054     T   TAT
                              ACCCG GTTCC  CCTTGTTG
                              ||||| |||||  ||||||||
                              TGGGT CAGGG  GGGACGAC
                                 _   TC_
GAM378  DUSP6   3' TGATAGGGTAGGAGCATGTGT 65965   C         TGTTG
                              AC CGTGTTCCTATCCT
                              || ||||||||||||||
                              TG GTACGAGGATGGGA
                               T          TAGT
GAM378  EGLN2   3' AGGAGGAGCATGGGT     53851         TA
                              ACCCGTGTTCC  TCCT
                              ||||||||||  ||||
                              TGGGTACGAGG  AGGA
                                   __
GAM378  EGLN2   3' AGGAGGAGCATGGGT     54925         TA
                              ACCCGTGTTCC  TCCT
                              ||||||||||  ||||
                              TGGGTACGAGG  AGGA
                                   __
GAM378  EGLN2   3' AGGAGGAGCATGGGT     34094         TA
                              ACCCGTGTTCC  TCCT
                              ||||||||||  ||||
                              TGGGTACGAGG  AGGA
                                   __
GAM378  EGR2    5' AGCGAGGGAGTTGGGT     4625      TGTTC  A
                              ACCCG    CT TCCTTGTT
                              |||||    || ||||||||
                              TGGGT    GA GGGAGCGA
                                 T____  _
GAM378  EIF5A   3' GGTGGGGGAGAAGGGGGTGGGT 8770      TGT   A_   GTTG
                              ACCCG   TCCT  TCCTT
                              |||||  ||||  |||||
                              TGGGT  GGGA  AGGGG
                                 GG_   AG    GTGGT
GAM378  EMD     3' GGGGGTGGGGGTGGGGGCAGGG 3684     G        TG  G
          G                    CCC TGTTCCTATCCT  TT
                              ||| ||||||||||||  ||
                              GGG ACGGGGGTGGGG  GG
                                G         GT  GGGT
GAM378  EN1     5' GAAGGAGGGGGAGGGACGCGGG 7450          A_   G  G
          T                    ACCCGTGTTCCT  TCCTT TT
                              ||||||||||||  ||||| ||
                              TGGGCGCAGGGA  GGGAG AA
                                     GG    G  GT
GAM378  EN2     5' CGACAGGGAAAGCGCGGG    7458        CCTA
                              CCCGTGTT   TCCTTGTTG
                              ||||||||   |||||||||
```

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                                GGGCGCGA   AGGGACAGC
                                    A___
GAM378  ENG     3'  CAGTGGGTCTGGGATATGG   3689        T_   _  TTG
                                CCGTGTTCC  ATCC TTG
                                |||||||||  |||| |||
                                GGTATAGGG  TGGG GAC
                                    TC   T
GAM378  EPB41   5'  CGGCGACCGAGAACGCGG    15431       CTATCC
                                CCGTGTTC    TTGTTG
                                ||||||||    ||||||
                                GGCGCAAG    AGCGGC
                                    AGCC__
GAM378  EPHA2   5'  CGGCGTGCAGGCGTGCGGGT  15405     TG T  ATCCT
                                ACCCG  T CCT    TGTTG
                                |||||  | |||    |||||
                                TGGGC  G GGA    GCGGC
                                   GT C  CGT__
GAM378  ERBB2IP 3'  TGGTAAGGATTAATGCATGG  37987     TCCT     TT
                                CCGTGT   ATCCTTG  G
                                ||||||   |||||||  |
                                GGTACG   TAGGAAT  T
                                   TAAT     GG
GAM378  ERCC3   5'  CGGCGGGCCTGTGGGAGCGGGG 3695     G       C__
          T                      ACCC TGTTCCTAT  CTTGTTG
                                |||| |||||||||  |||||||
                                TGGG GCGAGGGTG  GGGCGGC
                                  _       TCC
GAM378  ESR1    3'  CAGCACCCTGGGGCACGGG   3700        TATCCT
                                CCCGTGTTCC    TGTTG
                                ||||||||||    |||||
                                GGGCACGGGG    ACGAC
                                     TCCC__
GAM378  EXO1    5'  TGATAAGGTGTCAACAGGGT  55232     G   CCTAT
                                ACCC TGTT    CCTTGTTG
                                |||| ||||    ||||||||
                                TGGG ACAA    GGAATAGT
                                  _   CTGT_
GAM378  EYA2    3'  TGATGAGGAGGGGATGGGT   17887     TGT   A   TG
                                ACCCG   TCCT TCCT  TTG
                                |||||   |||| ||||  |||
                                TGGGT   AGGG AGGA  AGT
                                  ___   G   GT
GAM378  FADD    3'  TGGTGGGGAGAGGCATGG    13799     TT   A   TG
                                CCGTG  CCT TCCT  TTG
                                |||||  ||| ||||  |||
                                GGTAC  GGA AGGG  GGT
                                  __  G   GT
GAM378  FANCF   3'  TGGCAGTGTCAGGAATATTGGT 42682    C      ATCC
                                ACC GTGTTCCT   TTGTTG
                                ||| ||||||||   ||||||
```

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                                TGG TATAAGGA   GACGGT
                                  T      CTGT
GAM378  FLNB    3'  AACAAGGACGGCACGG     62169       CCTA
                                CCGTGTT   TCCTTGTT
                                |||||||   ||||||||
                                GGCACGG   AGGAACAA
                                   C___
GAM378  FLOT1   5'  CAACGGGGTGCGGCAGGGT   19405     G   CCTAT
                                ACCC TGTT    CCTTGTTG
                                |||| ||||    ||||||||
                                TGGG ACGG    GGGGCAAC
                                  _   CGT__
GAM378  FLOT1   5'  CGGCAGGGTGGGGAACGCGGG  19406         AT
                                CCCGTGTTCCT  CCTTGTTG
                                ||||||||||  ||||||||
                                GGGCGCAAGGG  GGGACGGC
                                      GT
GAM378  FOLH1   5'  CAGCAGCACAGGCGCGGGT   15578       TT  ATCC
                                ACCCGTG  CCT   TTGTTG
                                |||||||  |||   ||||||
                                TGGGCGC  GGA   GACGAC
                                   __  CAC_
GAM378  FOXG1B  3'  CAGCGAGGTGCAATGTGGG   17900     TG  CCTAT
                                CCCG  TT    CCTTGTTG
                                ||||  ||    ||||||||
                                GGGT  AA    GGAGCGAC
                                  GT  CGT__
GAM378  FPGS    3'  CAGCCTCCTGGGGGATACGG   17083        ATCCTT
                                CCGTGTTCCT     GTTG
                                ||||||||||     ||||
                                GGCATAGGGG     CGAC
                                      GTCCTC
GAM378  FRAP1   3'  TAACTTTAGAAATACGGGT   17099        C   TCCTT
                                ACCCGTGTT CTA    GTTG
                                |||||||| |||    ||||
                                TGGGCATAA GAT    CAAT
                                     A   TT___
GAM378  FUS1    3'  TGATAGGAGTGGGGACTGGGT  23452      T     TC
                                ACCCG GTTCCTA  CTTGTTG
                                ||||| |||||||  |||||||
                                TGGGT CAGGGGT  GGATAGT
                                  _      GA
GAM378  G6PD    5'  GGCGATGGGGATGCGGG     4635           _
                                CCCGTGTTCCTATC CT
                                |||||||||||||| ||
                                GGGCGTAGGGGTAG GG
                                      C
GAM378  GABRP   3'  ACGGGAATGGGTGGGAGTGCTG 26394     C TG       _  G
          GT                    ACC G  TTCCTATCC TT TTG
                                ||| |  |||||||| || |||
```

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                                TGG C  GAGGGTGGG AA GGC
                                  T GT       T  G   AA
GAM378  GAS1    3'  CAGTGACGTGGGGGTGAGGGT  8992      GT TT    CC TG
                                ACCC  G  CCTAT  T  TTG
                                ||||  |  |||||  |  |||
                                TGGG  T  GGGTG  A  GAC
                                  AG GG    C_ GT
GAM378  GBF1    3'  GGCAGGTGGGGGGCTGGGT    14835      T     T   T
                                ACCCG GTTCCTA CCT GTT
                                ||||| ||||||| ||| |||
                                TGGGT CGGGGGT GGA CGG
                                  _     _  _
GAM378  GCN1L1  3'  TAGCAGGGTCAGACTGTGGGT  69757     GT T  CTAT
                                ACCC  G TC    CCTTGTTG
                                ||||  | ||   ||||||||
                                TGGG  T AG    GGGACGAT
                                  TG C  ACT_
GAM378  GFPT2   3'  CAGCAGGGATGCTACATGGG   17574       TCC
                                CCCGTGT   TATCCTTGTTG
                                |||||||   ||||||||||
                                GGGTACA   GTAGGGACGAC
                                   TC_
GAM378  GJB1    3'  CAGTGAGGAGGGATGTGGGT   59969      TG   TA   TG
                                ACCCG  TTCC  TCCT  TTG
                                |||||  ||||  ||||  |||
                                TGGGT  AGGG  AGGA  GAC
                                  GT   __   GT
GAM378  GLI2    3'  GGTAGGGAGCATTTGGGT    47526     __      AT
                                ACCC  GTGTTCCT  CC
                                ||||  ||||||||  ||
                                TGGG  TACGAGGG  GG
                                  TT      AT
GAM378  GPR44   3'  CAGCAGGGGATGGCGTGGT   16524     _  GT   TATC
                                ACC CGT  TCC   CTTGTTG
                                ||| |||  |||   |||||||
                                TGG GCG  AGG   GGACGAC
                                  T  GT  ____
GAM378  GPX3    3'  AGGCATGTGGGTGTGGGT    9118      TG   C  _
                                ACCCG  TTC TAT CCT
                                |||||  ||| ||| |||
                                TGGGT  GGG GTA GGA
                                  GT   T   C
GAM378  GRAF    3'  TAGCAGGGGTTTGTCATGG   30575      TTCCT
                                CCGTG    ATCCTTGTTG
                                |||||    ||||||||||
                                GGTAC    TGGGGACGAT
                                  TGTT_
GAM378  GRIN2B  3'  TGACGGGGGTGAACTTGG    5907     T   CT
                                CCG GTTC  ATCCTTGTTG
                                ||| ||||  ||||||||||
```

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                                GGT CAAG  TGGGGGCAGT
                                  T   __
GAM378  GRLF1    3'  AGAATGGGGACGTGGG      78550           C
                                CCCGTGTTCCTAT CT
                                |||||||||||| ||
                                GGGTGCAGGGGTA GA
                                       A
GAM378  GRM1     5'  CGGGACCAGCGTGGGAACGCGG 5913          C  T   G
                                CCGTGTTCCTAT CT GTT
                                |||||||||||| || |||
                                GGCGCAAGGGTG GA CAG
                                       C  C   GGCG
GAM378  GRM3     3'  TGACAGGGTCTGACATGG    5920        CCTAT
                                CCGTGTT    CCTTGTTG
                                |||||||    ||||||||
                                GGTACAG    GGGACAGT
                                    TCT__
GAM378  GSTM4    5'  CAGCGGGGCCGAGGGGGCGGGT 5952       G    AT_
                                ACCCGT TTCCT   CCTTGTTG
                                |||||| |||||   ||||||||
                                TGGGCG GGGGA   GGGGCGAC
                                   _    GCC
GAM378  GUCY2D   3'  GGGTCCTGGGAGGGTGGGT   3935      TG     T__
                                ACCCG  TTCCTA   CCT
                                |||||  ||||||   |||
                                TGGGT  GAGGGT   GGG
                                   GG     CCT
GAM378  GZMM     3'  CAGTGGGGTGGGTGAGGACGGG 18011      G  _ AT   TG
           T                     ACCCGT TTC CT  CCT  TTG
                                |||||| ||| ||  |||  |||
                                TGGGCA GAG GG  GGG  GAC
                                   G   T  GT   GT
GAM378  HBQ1     5'  CGGCGGGTTCCAGCGCGGG   18045       CCT   TT
                                CCCGTGTT   ATCC  GTTG
                                ||||||||   ||||  ||||
                                GGGCGCGA   TGGG  CGGC
                                     CCT   __
GAM378  HCR      5'  CAGTAGGGGGCTCTCGCGG   90997      TTCCTA
                                CCGTG     TCCTTGTTG
                                |||||     |||||||||
                                GGCGC     GGGGATGAC
                                   TCTCG_
GAM378  HDAC4    3'  CAGCCTCACAGGGAACACGGG  20107         ATCCTT
                                CCCGTGTTCCT     GTTG
                                ||||||||||     ||||
                                GGGCACAAGGG     CGAC
                                       ACACTC
GAM378  HDAC4    3'  CGGCGGGGGGTCTGCACCCGGG 20108     __   TCCTA
           T                     ACCC  GTGT    TCCTTGTTG
                                ||||  ||||    ||||||||
```

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                                TGGG  CACG    GGGGGCGGC
                                  CC    TCTG_
GAM378  HDAC5    3'  CAACAAGGTGTGCCGTGTGGGT 57604      TG TCCTAT
                                ACCCG  T     CCTTGTTG
                                |||||  |     ||||||||
                                TGGGT  G     GGAACAAC
                                   GT CCGTGT
GAM378  HEM1     3'  GGGGGTGGGAATGGGGT     18053      G
                                ACCC TGTTCCTATCCTT
                                |||| ||||||||||||
                                TGGG GTAAGGGTGGGGG
                                  _
GAM378  HIRA     5'  CGGCGGAGGGGGGCGCGGG    12434          A   TT
                                CCCGTGTTCCT TCC  GTTG
                                |||||||||| |||  ||||
                                GGGCGCGGGGG AGG  CGGC
                                      G  __
GAM378  HIRA     5'  CGGCGGCCGGAGGGCGGGT    12435       G   TAT  TT
                                ACCCGT TTCC   CC  GTTG
                                ||||||| ||||   ||  ||||
                                TGGGCG GAGG   GG  CGGC
                                   G   CC_ __
GAM378  HIRA     5'  GGCGGCCGAGCGCGGGT     12438         CTAT  TT
                                ACCCGTGTTC    CC  GTT
                                |||||||||    ||  |||
                                TGGGCGCGAG    GG  CGG
                                     CC__ __
GAM378  HLCS     3'  TAACAGGCAGAACATGGG    4675          CTATC
                                CCCGTGTTC     CTTGTTG
                                |||||||||     |||||||
                                GGGTACAAG     GGACAAT
                                     AC___
GAM378  HMGCS1   3'  GGGCATGGGGTGGGGGTATGGG 9232        TT      _   G
                                CCCGTG  CCTATCCT TGTT
                                ||||||  |||||||| ||||
                                GGGTAT  GGGTGGGG ACGG
                                   GG       T   GT
GAM378  HOXC10   3'  AGATGGGGGTGGGAGTGTGG   61266     TG       TG  G
                                CCG  TTCCTATCCT  TT
                                |||  ||||||||||  ||
                                GGT  GAGGGTGGGG  AG
                                  GT        GT  AT
GAM378  HS2ST1   3'  TAGTGAGCTGTGGTATGGGT   24336       TT  TATC  TG
                                ACCCGTG  CC    CT  TTG
                                |||||||  ||    ||  |||
                                TGGGTAT  GG    GA  GAT
                                   __ TGTC  GT
GAM378  HSPA4    3'  GGTGTGGGGATGGGGT     89171      G       _
                                ACCC TGTTCCTAT CC
                                |||| ||||||||| ||
```

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                                TGGG GTAGGGGTG GG
                                  _       T
GAM378  HTR1D    3'  TAGCGGGGGTAGGATGGTTGGG 6001      TGT_
                                CCCG   TCCTATCCTTGTTG
                                ||||   ||||||||||||||
                                GGGT   AGGATGGGGGCGAT
                                  TGGT
GAM378  ID3      3'  TGGCAAAGTAGACATGGGT   79049       TC   CC
                                ACCCGTGT  CTAT  TTGTTG
                                ||||||||  ||||  ||||||
                                TGGGTACA  GATG  AACGGT
                                    __    A_
GAM378  IL1RAP   3'  CAATAGGGATAAATTTAGGGT  9311      GT_  CC
                                ACCC   GTT  TATCCTTGTTG
                                ||||   |||  ||||||||||
                                TGGG   TAA  ATAGGGATAAC
                                  ATT   __
GAM378  IMPDH1   5'  CGGCAGGGAAGGGGACGGGGT  6081      G     A
                                ACCC TGTTCCT TCCTTGTTG
                                |||| ||||||| |||||||||
                                TGGG GCAGGGG AGGGACGGC
                                  _      A
GAM378  INSR     3'  TGGCGGGGGCGGGCAGGGGT   70983     G  TT   AT
                                ACCC TG  CCT  CCTTGTTG
                                |||| ||  |||  ||||||||
                                TGGG AC  GGG  GGGGCGGT
                                  G  __   CG
GAM378  IQGAP2   5'  CAGCGAGGGTAGCCGCGGG   21811       TTC
                                CCCGTG   CTATCCTTGTTG
                                ||||||   ||||||||||||
                                GGGCGC   GATGGGAGCGAC
                                   C__
GAM378  IRAK1    3'  CAGTGGGGGTGGGGGC      7807          TG
                                GTTCCTATCCT  TTG
                                ||||||||||  |||
                                CGGGGGTGGGG  GAC
                                      GT
GAM378  ISL1     3'  GACAAGGTGATATGG       9365        CCTAT
                                CCGTGTT    CCTTGTT
                                |||||||    |||||||
                                GGTATAG    GGAACAG
                                   T_____
GAM378  ITGA11   3'  CAGCAGGGGTAGGGGTAGGG   24204     G  TT
                                CCC TG  CCTATCCTTGTTG
                                ||| ||  ||||||||||||
                                GGG AT  GGATGGGGACGAC
                                  _ GG
GAM378  ITGB2    3'  TGGTGAGGTTAGGTGCGTG    3992       T   T   TG
                                CGTGT CCTA CCT  TTG
                                ||||| |||| |||  |||
```

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                                GTGCG GGAT GGA  GGT
                                  T   T  GT
GAM378  ITIH3   3' GGCATCTGGAACATGGG    9414          T_ _
                                CCCGTGTTCC  AT CC
                                ||||||||||  || ||
                                GGGTACAAGG  TA GG
                                     TC  C
GAM378  JUN     5' CGACAAGTAAGAGTGCGGG   9476      TG  C  TC
                                CCCG  TTC TA  CTTGTTG
                                ||||  ||| ||  |||||||
                                GGGC  GAG AT  GAACAGC
                                  GT   A  __
GAM378  JUP     3' AGCTTCTGGGGATGCAGGT   9486     C       TCCTT  G
                                ACC GTGTTCCTA    GTT
                                ||| |||||||||    |||
                                TGG CGTAGGGGT    CGA
                                  A       CTT__  G
GAM378  JUP     3' TGGTGGGGATGGGGAGGC    9491    G       TG
                                GT TTCCTATCCT  TTG
                                || ||||||||||  |||
                                CG AGGGGTAGGG  GGT
                                 G        GT
GAM378  KCNA6   3' GGATGGCAGCATGGGT      9514         C
                                ACCCGTGTT CTATCC
                                ||||||||| ||||||
                                TGGGTACGA GGTAGG
                                     C
GAM378  KCNA7   3' CAGCCTGCTGGGACACACGGGT 49050        _    TCCTT
                                ACCCGTGT TCCTA    GTTG
                                |||||||| |||||    ||||
                                TGGGCACA AGGGT    CGAC
                                    C    CGTC_
GAM378  KCNF1   5' CGGCGGCTGCAGGGGGCGCGGG 9522          ATCC_
                                CCCGTGTTCCT    TTGTTG
                                ||||||||||    ||||||
                                GGGCGCGGGGG    GGCGGC
                                       ACGTC
GAM378  KCNJ10  3' TGGTAAGGAATACTACCCGGGT 9539      T  TCCTA    TT
                                ACCCG GT    TCCTTG  G
                                ||||| ||    ||||||  |
                                TGGGC CA    AGGAAT  T
                                  C  TCATA     GG
GAM378  KCNK3   3' AGGGGTGGGGGCTGGGT     9547      T
                                ACCCG GTTCCTATCCTT
                                ||||| ||||||||||||
                                TGGGT CGGGGGTGGGGA
                                  _
GAM378  KCNK7   3' GGTGAGGGTGGGCGGG      53093     TGTT      TG
                                CCCG   CCTATCCT  TT
                                ||||   ||||||||  ||
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                              GGGC   GGGTGGGA  GG
                                _____      GT
GAM378  KCNK7   3'  GGTGAGGGTGGGCGGG    52916    TGTT     TG
                              CCCG   CCTATCCT  TT
                              ||||   ||||||||  ||
                              GGGC   GGGTGGGA  GG
                                _____      GT
GAM378  KCNK7   3'  GGTGAGGGTGGGCGGG    52917    TGTT     TG
                              CCCG   CCTATCCT  TT
                              ||||   ||||||||  ||
                              GGGC   GGGTGGGA  GG
                                _____      GT
GAM378  KCNK7   3'  GGTGAGGGTGGGCGGG    19131    TGTT     TG
                              CCCG   CCTATCCT  TT
                              ||||   ||||||||  ||
                              GGGC   GGGTGGGA  GG
                                _____      GT
GAM378  KCNMB1  5'  GGGGTGGGGGCGGGGGT    14709    G
                              ACCC TGTTCCTATCCT
                              |||| ||||||||||||
                              TGGG GCGGGGGTGGGG
                                G
GAM378  KCNS2   3'  GATGGGGAACCTGGGT     68306     T    _
                              ACCCG GTTCCT ATC
                              ||||| |||||| |||
                              TGGGT CAAGGG TAG
                                 C     G
GAM378  KHK     3'  TGACAGGCCAGTGGGGGGCAGG 21405    G     ATC___
          GGT                   CCC TGTTCCT     CTTGTTG
                              ||| |||||||     |||||||
                              GGG ACGGGGG     GGACAGT
                                G      GTGACC
GAM378  KHK     3'  TGACAGGCCAGTGGGGGGCAGG 4035     G     ATC___
          GGT                   CCC TGTTCCT     CTTGTTG
                              ||| |||||||     |||||||
                              GGG ACGGGGG     GGACAGT
                                G      GTGACC
GAM378  KLHL3   3'  TGATGGGGATGAGGCTGGG   87469     T   CC     TG
                              CCCG GTT  TATCCT  TTG
                              |||| |||  ||||||  |||
                              GGGT CGG  GTAGGG  AGT
                                _  A_     GT
GAM378  KMO     3'  TAGCAGGTGTGGATGTGGG   13453     TG T  T TC
                              CCCG  T CC A  CTTGTTG
                              ||||  | || |  |||||||
                              GGGT  A GG T  GGACGAT
                                GT _  _ GT
GAM378  LAD1    5'  CGGCGGCCGGCGGGGCGCGGG  18700         TAT  __
                              CCCGTGTTCC   CC  TTGTTG
                              ||||||||||   ||  ||||||
```

```
                                GGGCGCGGGG  GG  GGCGGC
                                      C__  CC
GAM378  LANCL1   5'  GGGCGTGGGAACGGGGT    20215     G      _
                                ACCC TGTTCCTAT CCT
                                |||| ||||||||| |||
                                TGGG GCAAGGGTG GGG
                                  _       C
GAM378  LASS1    3'  CGGCAGTATGAGGACATGG   41196      T   ATCC
                                CCGTGT CCT   TTGTTG
                                |||||| |||   ||||||
                                GGTACA GGA   GACGGC
                                   _  GTAT
GAM378  LASS2    5'  TGACGGGCGTGGACGCGG    67686      T  T  C
                                CCGTGT CC AT CTTGTTG
                                |||||| || || |||||||
                                GGCGCA GG TG GGGCAGT
                                   _ _  C
GAM378  LCP2     5'  CAACAGGGGTGTTCCACAGGGT 18719     _  TTCC
                                ACCC GTG   TATCCTTGTTG
                                |||| |||   ||||||||||
                                TGGG CAC   GTGGGGACAAC
                                  A  CTT_
GAM378  LFG      3'  CAGCAAAGGCATTGGGGGCACG 76715          T__   _
           GGT                    CCCGTGTTCCTA   CCTT GTTG
                                ||||||||||   |||| ||||
                                GGGCACGGGGGT   GGAA CGAC
                                      TAC   A
GAM378  LHX5     3'  AGACGCGGTGGGAGACGTGGGT 42302        _    T  T   G
                                ACCCGTGT TCCTA CC TGTT
                                |||||||| ||||| || ||||
                                TGGGTGCA AGGGT GG GCAG
                                    G    _ C   AC
GAM378  LIF      3'  CAGCAGGGGTTTGTGGAGGTGG 9729       TG   CT__
           GT                     ACCCG  TTC   ATCCTTGTTG
                                |||||  |||   ||||||||||
                                TGGGT  AGG   TGGGGACGAC
                                  GG   TGTT
GAM378  LIF      3'  CAGCAAGACGAGGATGTGG   9728     TG T   ATC
                                CCG  T CCT   CTTGTTG
                                |||  | |||   |||||||
                                GGT  A GGA   GAACGAC
                                  GT _   GCA
GAM378  LRP4     3'  TGGGACATGGGGGTGTGGGT  64448      TG    __   TGTTG
                                ACCCG  TTCCTA  TCCT
                                |||||  ||||||  ||||
                                TGGGT  GGGGGT  AGGG
                                  GT    AC   T  G
GAM378  LRP8     5'  CGGCGGCGCGGGGAGCGCGGG  52780         ATCC
                                CCCGTGTTCCT   TTGTTG
                                ||||||||||   ||||||
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                                GGGCGCGAGGG  GGCGGC
                                      GCGC
GAM378  LRP8    5'  CGGCGGCGCGGGGAGCGCGGG  34027        ATCC
                                CCCGTGTTCCT  TTGTTG
                                ||||||||||  ||||||
                                GGGCGCGAGGG  GGCGGC
                                      GCGC
GAM378  LRP8    5'  CGGCGGCGCGGGGAGCGCGGG  16148        ATCC
                                CCCGTGTTCCT  TTGTTG
                                ||||||||||  ||||||
                                GGGCGCGAGGG  GGCGGC
                                      GCGC
GAM378  LSS     3'  AGGCAGGGATGGGGACAGGGT  9812     G          G
                                ACCC TGTTCCTATCCTTGTT
                                |||| ||||||||||||||||
                                TGGG ACAGGGGTAGGGACGG
                                  _           AG
GAM378  LTB     3'  TGGTGGGGTGAGGGAATATGAG  23792   C      AT_  TG
            T                    AC CGTGTTCCT  CCT  TTG
                                || |||||||||  |||  |||
                                TG GTATAAGGG  GGG  GGT
                                 A       AGT  GT
GAM378  LTB4R   5'  AGTGAAGGGAGTGGGT    5640      TG   A  _
                                ACCCG  TTCCT TC CT
                                |||||  ||||| || ||
                                TGGGT  GAGGG AG GA
                                   __    A  T
GAM378  LTB4R   5'  CAGCAGGGTAACCACATGGG  5642       TCCTAT
                                CCCGTGT    CCTTGTTG
                                |||||||    ||||||||
                                GGGTACA    GGGACGAC
                                    CCAAT_
GAM378  LTBR    3'  TAACAACTAGGGGGTTGGGT  9824      TG    TCC
                                ACCCG  TTCCTA  TTGTTG
                                |||||  ||||||  ||||||
                                TGGGT  GGGGAT  AACAAT
                                   TG    C__
GAM378  MADH7   3'  CAGCAGCTGCCAGGAGCACGG  19742        ATCC_
                                CCGTGTTCCT   TTGTTG
                                ||||||||||   ||||||
                                GGCACGAGGA   GACGAC
                                      CCGTC
GAM378  MAFG    3'  CGATCGTAGGGACGCGCGT   70094   C       CC
                                AC CGTGTTCCTAT  TTG
                                || ||||||||||  |||
                                TG GCGCAGGGATG  AGC
                                 C         CT
GAM378  MAN2B1  5'  GATAGGCCCGGCCGGGT    4995      T  ___
                                ACCCG GTT  CCTATC
                                ||||| |||  ||||||
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                                TGGGC CGG   GGATAG
                                  _  CCC
GAM378  MAP2K2   3'  CAGCGCATGCAGGAACGGGGGT 47693     G     ATCCT
                                ACCC TGTTCCT    TGTTG
                                |||| |||||||    |||||
                                TGGG GCAAGGA    GCGAC
                                  G     CGTAC
GAM378  MAP3K11  5'  CAGCGGGGGTGGGGACCACGGG 10053      _
                                CCCGTG TTCCTATCCTTGTTG
                                |||||| ||||||||||||||
                                GGGCAC AGGGGTGGGGGCGAC
                                   C
GAM378  MAPK14   5'  GCAGCAAGGGCCGGGGAGAGGG 57332  TG ____   A__
           TGCGGGT                T   TCCT  TCCTTGTTG  C
                                |   ||||  |||||||||  |
                                G   AGGG  GGGAACGAC  G
                                GT GGAG   GCC
GAM378  MAPK14   5'  GCAGCAAGGGCCGGGGAGAGGG 57338  TG ____   A__
           TGCGGGT                T   TCCT  TCCTTGTTG  C
                                |   ||||  |||||||||  |
                                G   AGGG  GGGAACGAC  G
                                GT GGAG   GCC
GAM378  MAPK14   5'  GCAGCAAGGGCCGGGGAGAGGG 57343  TG ____   A__
           TGCGGGT                T   TCCT  TCCTTGTTG  C
                                |   ||||  |||||||||  |
                                G   AGGG  GGGAACGAC  G
                                GT GGAG   GCC
GAM378  MAPK14   5'  GCAGCAAGGGCCGGGGAGAGGG 7158   TG ____   A__
           TGCGGGT                T   TCCT  TCCTTGTTG  C
                                |   ||||  |||||||||  |
                                G   AGGG  GGGAACGAC  G
                                GT GGAG   GCC
GAM378  MAPK4    3'  CAGCAAGGGCTCTTAGGGGT  10824     G  TTCCTA
                                ACCC TG     TCCTTGTTG
                                |||| ||     |||||||||
                                TGGG AT     GGGAACGAC
                                  G  TCTC__
GAM378  MATN4    3'  CGGCGTCAGGGGGATAGCGGGT 47586      _     ATCCT
                                ACCCG TGTTCCT    TGTTG
                                ||||| |||||||    |||||
                                TGGGC ATAGGGG    GCGGC
                                   G     GACT_
GAM378  MATN4    3'  CGGCGTCAGGGGGGATAGCGGGT 13821      _     ATCCT
                                ACCCG TGTTCCT    TGTTG
                                ||||| |||||||    |||||
                                TGGGC ATAGGGG    GCGGC
                                   G     GACT_
GAM378  MBD3     3'  CAGTGAGGGCTCCTACGGGT  14094       TTCCTA   TG
                                ACCCGTG     TCCT  TTG
                                |||||||     ||||  |||
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                                TGGGCAT     GGGA  GAC
                                   CCTC__    GT
GAM378  MEIS1    3'  CAATGGGTGTGAGTATGGG   9994          C    _
                                CCCGTGTTC TATCC TTG
                                ||||||||| ||||| |||
                                GGGTATGAG GTGGG AAC
                                     T    T
GAM378  MGAT3    3'  GGAGTGGGGGTGGGGGTAGGGT 10017     G  TT      TG  G
                                ACCC TG  CCTATCCT  TT
                                |||| ||  ||||||||  ||
                                TGGG AT  GGGTGGGG  GA
                                  _ GG       GT  GGG
GAM378  MLLT2    5'  CGGCGGTCTTCGAGCGTGGG   19845         CTAT_  TT
                                CCCGTGTTC    CC  GTTG
                                |||||||||    ||  ||||
                                GGGTGCGAG    GG  CGGC
                                     CTTCT  __
GAM378  MLLT4    3'  CAGCAAGGACTCTCATTGGGT  72483      _  TTCCTA
                                ACCCG TG     TCCTTGTTG
                                ||||| ||     |||||||||
                                TGGGT AC     AGGAACGAC
                                   T  TCTC__
GAM378  MME      3'  CAGCAAGAGAAGGAGTATGTGT 23486    C       A  _
                                AC CGTGTTCCT TC CTTGTTG
                                || ||||||||| || |||||||
                                TG GTATGAGGA AG GAACGAC
                                 T       _  A
GAM378  MME      3'  CAGCAAGAGAAGGAGTATGTGT 23496    C       A  _
                                AC CGTGTTCCT TC CTTGTTG
                                || ||||||||| || |||||||
                                TG GTATGAGGA AG GAACGAC
                                 T       _  A
GAM378  MME      3'  CAGCAAGAGAAGGAGTATGTGT 23507    C       A  _
                                AC CGTGTTCCT TC CTTGTTG
                                || ||||||||| || |||||||
                                TG GTATGAGGA AG GAACGAC
                                 T       _  A
GAM378  MME      3'  CAGCAAGAGAAGGAGTATGTGT 6139     C       A  _
                                AC CGTGTTCCT TC CTTGTTG
                                || ||||||||| || |||||||
                                TG GTATGAGGA AG GAACGAC
                                 T       _  A
GAM378  MMP19    3'  GAGGTGGGGGTGGGGGT     42973     G  TT   T
                                ACCC TG  CCTA CCTT
                                |||| ||  |||| ||||
                                TGGG GT  GGGT GGAG
                                  G  GG   _
GAM378  MMP19    3'  GAGGTGGGGGTGGGGGT     10085     G  TT   T
                                ACCC TG  CCTA CCTT
                                |||| ||  |||| ||||
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                                TGGG GT  GGGT GGAG
                                  G  GG   _
GAM378  MMP2     5'  CGGCGGGGGCTGGGGCGCGGG  15764          TA
                                CCCGTGTTCC  TCCTTGTTG
                                ||||||||||  |||||||||
                                GGGCGCGGGG  GGGGGCGGC
                                     TC
GAM378  MN1      5'  TGACAACCGCCCGGGGCATGGG 10098          TATCC_
                                CCCGTGTTCC     TTGTTG
                                ||||||||||     ||||||
                                GGGTACGGGG     AACAGT
                                     CCCGCC
GAM378  MSF      3'  CGGCGGGGTGGGGTGGGGGT   88082      G  TT  TAT
                                ACCC TG  CC   CCTTGTTG
                                ||||  ||  ||   ||||||||
                                TGGG GT  GG   GGGGCGGC
                                  G  GG  T__
GAM378  MTCP1    5'  TGGCAGGAGAGGATGTGGG    26435      TG T   A    T
                                CCCG  T CCT TCCT GTTG
                                ||||  | ||| |||| ||||
                                GGGT  A GGA AGGA CGGT
                                  GT _   G   _
GAM378  MTMR3    5'  TGGCAGGGAGCCTGGTGGGGT  40816      GTGTT  TA__
                                ACCC    CC    TCCTTGTTG
                                ||||    ||    |||||||||
                                TGGG    GG    AGGGACGGT
                                  GT___  TCCG
GAM378  MUCDHL   3'  CGATGAGGGCGAGGGCGCGGG  48368        T   A_   TG
                                CCCGTGT CCT  TCCT  TTG
                                |||||||  |||  ||||  |||
                                GGGCGCG GGA  GGGA  AGC
                                    _  GC   GT
GAM378  MYCL1    3'  TGATAGGGAACTGGGGAATGGG 18167       G     __
                                CCCGT TTCCTA  TCCTTGTTG
                                |||||  ||||||  |||||||||
                                GGGTA AGGGGT  AGGGATAGT
                                   _     CA
GAM378  MYO1C    3'  GGCATGGGAGCGTGGG      61209           _
                                CCCGTGTTCCTAT CC
                                ||||||||||||| ||
                                GGGTGCGAGGGTA GG
                                      C
GAM378  MYO1E    5'  CAGCCAGAGGAGTACGG     17186          ATC  T
                                CCGTGTTCCT   CT GTTG
                                ||||||||||   || ||||
                                GGCATGAGGA   GA CGAC
                                     ____  C
GAM378  MYOM2    3'  GGGTGTGGGCACATGGGT    14267         T    _
                                ACCCGTGT CCTAT CCT
                                |||||||| ||||| |||
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                                TGGGTACA GGGTG GGG
                                    C    T
GAM378  NEURL   3'  TGGCAGGCAGGGCATGGGT   14865       T  ATC
                                ACCCGTGT CCT   CTTGTTG
                                |||||||| |||   |||||||
                                TGGGTACG GGA   GGACGGT
                                   _   C__
GAM378  NFYC    5'  CGACTCCGTAGGAGCGCGGG   26440          CCTT
                                CCCGTGTTCCTAT   GTTG
                                ||||||||||||   ||||
                                GGGCGCGAGGATG   CAGC
                                      CCT_
GAM378  NMB     5'  CGGCGGGCGCGGGGCACGG   73781        TATC
                                CCGTGTTCC   CTTGTTG
                                |||||||||   |||||||
                                GGCACGGGG   GGGCGGC
                                    CGC_
GAM378  NONO    3'  GTACAATCTTGGGAACAGGGT  82020     G      TCC   TG
                                ACCC TGTTCCTA   TTGT
                                |||| ||||||||   ||||
                                TGGG ACAAGGGT   AACA
                                  _      TCT   TGA
GAM378  NOS1    3'  CGACAAGGGCAACTCACGGGT  5249        TTCCTA
                                ACCCGTG    TCCTTGTTG
                                |||||||    |||||||||
                                TGGGCAC    GGGAACAGC
                                    TCAAC_
GAM378  NQO2    5'  GCGGTCCTTGGGGAGACGCGGG 6173        _   AT____  TTGTTG
          T                      CCCGTGT TCCT     CC
                                |||||||| ||||     ||
                                GGGCGCA AGGG     GG
                                   G   GTTCCT  C   GT
GAM378  NRIP1   3'  CAGTAATAGGAGTGGGT    59952      TG     CC
                                ACCCG  TTCCTAT  TTG
                                |||||  |||||||  |||
                                TGGGT  GAGGATA  GAC
                                  __      AT
GAM378  NRXN2   3'  CAGTGGGTGGGTGGGGTGGGGT 57009     GTGT     __ TG
                                ACCC   TCCTATCC  T  TTG
                                ||||   ||||||||  |  |||
                                TGGG   GGGGTGGG  G  GAC
                                  GT__       TG GT
GAM378  NRXN2   3'  CAGTGGGTGGGTGGGGTGGGGT 57020     GTGT     __ TG
                                ACCC   TCCTATCC  T  TTG
                                ||||   ||||||||  |  |||
                                TGGG   GGGGTGGG  G  GAC
                                  GT__       TG GT
GAM378  NRXN2   3'  CAGTGGGTGGGTGGGGTGGGGT 30623     GTGT     __ TG
                                ACCC   TCCTATCC  T  TTG
                                ||||   ||||||||  |  |||
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                                TGGG   GGGGTGGG  G  GAC
                                  GT__       TG GT
GAM378  NT5C3    5'  TGGCGGGGGTGGTGCTGG    33237     T  TC
                                CCG GT  CTATCCTTGTTG
                                ||| ||  ||||||||||||
                                GGT CG  GGTGGGGGCGGT
                                  _  T_
GAM378  NTSR1    3'  AGGTAGGGACACGTGT      10286    C        T
                                AC CGTGTTCCTA CCT
                                || ||||||||| |||
                                TG GCACAGGGAT GGA
                                 T        _
GAM378  OCRL     5'  GGGTGTGGGGACGCGGG     4262              _
                                CCCGTGTTCCTAT CCT
                                |||||||||||| |||
                                GGGCGCAGGGGTG GGG
                                         T
GAM378  OCRL     5'  GGGTGTGGGGACGCGGG     7828              _
                                CCCGTGTTCCTAT CCT
                                |||||||||||| |||
                                GGGCGCAGGGGTG GGG
                                         T
GAM378  OGT      5'  CAGTGGGGGTAGGAAAACTCGG 13201     TG__        TG
                                CCG    TTCCTATCCT  TTG
                                |||    ||||||||||  |||
                                GGC    AAGGATGGGG  GAC
                                  TCAA         GT
GAM378  OXCT     3'  GACAGGGGCCCATGGG      4753         TTCCTA
                                CCCGTG     TCCTTGTT
                                ||||||     ||||||||
                                GGGTAC     GGGGACAG
                                   CC_____
GAM378  PABPN1   5'  CGATAGGAGGTGGGACGCGTGT 16177    C    T    _
                                AC CGTGT CCTATC CTTGTTG
                                || ||||| |||||| |||||||
                                TG GCGCA GGGTGG GGATAGC
                                 T    _     A
GAM378  PAP      5'  CAGCAAGGGTGTCCTGGG    57239      TGTTCC
                                CCCG     TATCCTTGTTG
                                ||||     ||||||||||
                                GGGT     GTGGGAACGAC
                                  CCT___
GAM378  PAX5     5'  CGGCGCGCTGGGGGCGCGGCGT 33634    _         TCCT
                                AC CCGTGTTCCTA    TGTTG
                                || ||||||||||    |||||
                                TG GGCGCGGGGGT    GCGGC
                                 C         CGC_
GAM378  PCDH1    3'  AAGGTGGGGTAGGGACGGGGGT 50560      G          TGTTG
                                ACCC TGTTCCTATCCT
                                |||| ||||||||||||
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                                TGGG GCAGGGATGGGG
                                  G          TGGAAA
GAM378  PCDHB16  5'  AAGTGGGATGGGAGAACGGGT  40543       G        TGTTG
                                ACCCGT TTCCTATCCT
                                |||||| ||||||||||
                                TGGGCA GAGGGTAGGG
                                   A         TGAAT
GAM378  PCOLCE2  5'  GGCGGTGTGAGCGCGG      25341        C   _
                                CCGTGTTC TATC CT
                                |||||||| |||| ||
                                GGCGCGAG GTGG GG
                                     T   C
GAM378  PDE1B    3'  AGGATCTGGGAATGGGGT    6240       G     __
                                ACCC TGTTCCT  ATCCT
                                |||| |||||||  |||||
                                TGGG GTAAGGG  TAGGA
                                  _      TC
GAM378  PDGFRB   3'  CAGCGCTCCATGGGGGTATGG  65971      TT    CCT_
                                CCGTG  CCTAT   TGTTG
                                |||||  |||||   |||||
                                GGTAT  GGGTA   GCGAC
                                   GG    CCTC
GAM378  PGF      3'  CAAAAGTAGGGATGCGG     10533          CC
                                CCGTGTTCCTAT  TTG
                                ||||||||||||  |||
                                GGCGTAGGGATG  AAC
                                       AA
GAM378  PHB      3'  TGATGGACTGGGGAGCACAGGT 10540     C       A__   TTGTTG
                                ACC GTGTTCCT   TCC
                                ||| ||||||||   |||
                                TGG CACGAGGG   AGG
                                  A       GTC   TAGT
GAM378  PHLDA3   3'  GGCTTGTGGGGGCACGG     24765          ___
                                CCGTGTTCCTAT   CC
                                ||||||||||||   ||
                                GGCACGGGGGTG   GG
                                       TTC
GAM378  PHLDA3   3'  TGGTGGGGGTGAGGGGGGGT   24768     GTG    _    TG
                                ACCC   TTCCT ATCCT  TTG
                                ||||   ||||| |||||  |||
                                TGGG   GGGGA TGGGG  GGT
                                  ___    G    GT
GAM378  PIK3C2B  3'  TAGCATTTTGGGGGTGGGT   10575     GT TT   TCCT
                                ACCC  G  CCTA   TGTTG
                                ||||  |  ||||   |||||
                                TGGG  T  GGGT   ACGAT
                                  __ GG   TTT_
GAM378  PIK3R3   3'  TGACGAGGATAGAAAGGG    61065     GTGTTC
                                CCC     CTATCCTTGTTG
                                |||     ||||||||||||
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                                GGG     GATAGGAGCAGT
                                  AAA___
GAM378  PIN1     3'  CAGCAGGGGTGGGAGGC     20615    G
                                GT TTCCTATCCTTGTTG
                                || ||||||||||||||
                                CG GAGGGTGGGGACGAC
                                 _
GAM378  PKD1     3'  TGGCGGGGGTGGGCCGTGGAGT 4313     _    TT
                                AC CCGTG  CCTATCCTTGTTG
                                || |||||  ||||||||||||
                                TG GGTGC  GGGTGGGGGCGGT
                                 A    C_
GAM378  PKDREJ   3'  CAGCAGGATCACAGTGTGGG   20276     TG  CCT    T
                                CCCG  TT   ATCCT GTTG
                                ||||  ||   ||||| ||||
                                GGGT  GA   TAGGA CGAC
                                  GT  CAC    _
GAM378  PKIA     5'  TGGCAGGTGGGGCGCGGG    22387         TATC
                                CCCGTGTTCC    CTTGTTG
                                ||||||||||    |||||||
                                GGGCGCGGGG    GGACGGT
                                      T___
GAM378  PLAG1    3'  GTTGGGGATGGGGGCAAGGGT  10609      G           TTG
                                ACCC TGTTCCTATCCTTG
                                |||| ||||||||||||||
                                TGGG ACGGGGGTAGGGGT
                                  A            TGC
GAM378  PNUTL2   5'  TGACAGGGAGTCTGAAGCGTGG 15897        _ CTA_
           G                     CCCGTGTT C    TCCTTGTTG
                                ||||||||| |    |||||||||
                                GGGTGCGA G    AGGGACAGT
                                     A TCTG
GAM378  PNUTL2   3'  TGACAAGGAGTATGTGGG    54421      TG TCCTA
                                CCCG  T     TCCTTGTTG
                                ||||  |     |||||||||
                                GGGT  A     AGGAACAGT
                                  GT TG___
GAM378  PNUTL2   5'  TGACAGGGAGTCTGAAGCGTGG 54422        _ CTA_
           G                     CCCGTGTT C    TCCTTGTTG
                                ||||||||| |    |||||||||
                                GGGTGCGA G    AGGGACAGT
                                     A TCTG
GAM378  POLL     3'  TGGTGGTGCTGGGAATGGGGT  25181      G       T__  TTGTTG
                                ACCC TGTTCCTA   CC
                                |||| ||||||||   ||
                                TGGG GTAAGGGT   GG
                                  _       CGT  TGGT
GAM378  POLR2C   3'  AGCAGCTGGATATGGG      10683        T  TATCC
                                CCCGTGT CC     TTGTT
                                ||||||| ||     |||||
```

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                                GGGTATA GG    GACGA
                                   _ TC___
GAM378  POU2AF1  3' GTAAGGGGTGGGAAGTGGGT  20658     GTG       GTTG
                                ACCC  TTCCTATCCTT
                                ||||  ||||||||||
                                TGGG  AAGGGTGGGGA
                                  TG_       ATGA
GAM378  POU5F1   5' AACAGGGAATGGGT      10693      GTTCCTA
                                ACCCGT    TCCTTGTT
                                ||||||    ||||||||
                                TGGGTA    AGGGACAA
                                  _______
GAM378  PPFIA3   3' CGACCTTGGGGGTGCGGG   61015     TG    TCCTT
                                CCCG  TTCCTA   GTTG
                                ||||  ||||||   ||||
                                GGGC  GGGGGT   CAGC
                                  GT    TC___
GAM378  PPIC     3' TGGCAGGGGTGTGTGTGTGTGT 6268    C  TG TCC
                                AC CG  T  TATCCTTGTTG
                                || ||  |  ||||||||||
                                TG GT  G  GTGGGGACGGT
                                 T  GT TGT
GAM378  PPP1R8   3' GATTGGGTGGGAATGGGGT   26067     G       TT  G
                                ACCC TGTTCCTATCC  GTT
                                |||| ||||||||||  |||
                                TGGG GTAAGGGTGGG  TAG
                                  _       T_  G
GAM378  PPP1R8   3' TGACAATTGGGGGTGGGGT   26068     G  TT   TCC
                                ACCC TG  CCTA   TTGTTG
                                |||| ||  ||||   ||||||
                                TGGG GT  GGGT   AACAGT
                                  _ GG   T__
GAM378  PPP1R8   3' GATTGGGTGGGAATGGGGT   56741     G       TT  G
                                ACCC TGTTCCTATCC  GTT
                                |||| ||||||||||  |||
                                TGGG GTAAGGGTGGG  TAG
                                  _       T_  G
GAM378  PPP1R8   3' TGACAATTGGGGGTGGGGT   56743     G  TT   TCC
                                ACCC TG  CCTA   TTGTTG
                                |||| ||  ||||   ||||||
                                TGGG GT  GGGT   AACAGT
                                  _ GG   T__
GAM378  PPP1R8   3' GATTGGGTGGGAATGGGGT   10724     G       TT  G
                                ACCC TGTTCCTATCC  GTT
                                |||| ||||||||||  |||
                                TGGG GTAAGGGTGGG  TAG
                                  _       T_  G
GAM378  PPP1R8   3' TGACAATTGGGGGTGGGGT   10727     G  TT   TCC
                                ACCC TG  CCTA   TTGTTG
                                |||| ||  ||||   ||||||
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                                TGGG GT  GGGT   AACAGT
                                  _ GG   T__
GAM378  PPP2R1A  3'  CAACGGGCTAGGGGAGCACGGG 26441          ATC_
                                CCCGTGTTCCT   CTTGTTG
                                ||||||||||   |||||||
                                GGGCACGAGGG   GGGCAAC
                                      GATC
GAM378  PPP2R2C  5'  GACAAGGGCGGCCGGGT    61761      T  CCTA
                                ACCCG GTT   TCCTTGTT
                                ||||| |||   ||||||||
                                TGGGC CGG   GGGAACAG
                                  _  C___
GAM378  PSCD4    5'  CGGCAAGCGACAGGAGCACGGG 25405          A  _
          T                      ACCCGTGTTCCT TC CTTGTTG
                                ||||||||||| || |||||||
                                TGGGCACGAGGA AG GAACGGC
                                      C  C
GAM378  PSME3    5'  AGCAAGGGCGGTCGGGT    19368      TGTTC  AT
                                ACCCG    CT  CCTTGTT
                                |||||    ||  |||||||
                                TGGGC    GG  GGAACGA
                                  T_____  CG
GAM378  PTPN2    5'  CGACAGGGCTTGGCGTGGG   11054      TT  TAT
                                CCCGTG  CC   CCTTGTTG
                                ||||||  ||   ||||||||
                                GGGTGC  GG   GGGACAGC
                                   __  TTC
GAM378  PTPRJ    5'  CAGCGGGACGAGCGCGGG    11117       CTA   T
                                CCCGTGTTC   TCCT GTTG
                                |||||||||   |||| ||||
                                GGGCGCGAG   AGGG CGAC
                                      C__   _
GAM378  QDPR     5'  CAACGGGTAACGGGGAATAAGG 4356      G      ATC__
          GT                      ACCC TGTTCCT    CTTGTTG
                                |||| |||||||    |||||||
                                TGGG ATAAGGG    GGGCAAC
                                  A      GCAAT
GAM378  RAB3B    3'  TAACAGGTCACTACACGGGT   11187       TCCTAT   T
                                ACCCGTGT     CCT GTTG
                                ||||||||     ||| ||||
                                TGGGCACA     GGA CAAT
                                     TCACT_  _
GAM378  RAB5C    3'  TGATGAGTATTTGGGGGTGGGT 59836     GT TT   TC__  TG
                                ACCC  G  CCTA   CT  TTG
                                ||||  |  ||||   ||  |||
                                TGGG  T  GGGT   GA  AGT
                                  __ GG   TTAT  GT
GAM378  RANBP3   3'  CGGCGGGGGCTGTGGCCGGGT  23632      T   CCTA
                                ACCCG GTT   TCCTTGTTG
                                ||||| |||   |||||||||
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                                TGGGC CGG   GGGGGCGGC
                                  _  TGTC
GAM378  RAP1B   5'  CGACCCGGGGGGAGCGCGGG  31599         A  TT
                                CCCGTGTTCCT TCC  GTTG
                                |||||||||| |||  ||||
                                GGGCGCGAGGG GGG  CAGC
                                      _  CC   G
GAM378  RASD1   3'  TAAGCGGGGGGGCGTGGGT   32224          ATC
                                ACCCGTGTTCCT  CTTG
                                ||||||||||||  ||||
                                TGGGTGCGGGGG  GAAT
                                       GGC
GAM378  RASGRP1  5'  CGGCACCGGGAGCGCGGG   19205         ATCCT
                                CCCGTGTTCCT   TGTTG
                                ||||||||||    |||||
                                GGGCGCGAGGG   ACGGC
                                       CC___
GAM378  RBBP2   3'  TAACAGGGCATATAGGATGTGG 17324    TG T   ___
                                CCG  T CCTAT  CCTTGTTG
                                |||  | |||||  ||||||||
                                GGT  A GGATA  GGGACAAT
                                  GT _   TAC
GAM378  RBM10   5'  AGCGGGGGTGGCTGGG     19044     TGTTC
                                CCCG   CTATCCTTGTT
                                ||||   ||||||||||
                                GGGT   GGTGGGGGCGA
                                  C____
GAM378  RDS     5'  GTGGGACTCGACATGGGT   4363        ____
                                ACCCGTGT   TCCTAT
                                ||||||||   ||||||
                                TGGGTACA   AGGGTG
                                     GCTC
GAM378  REPS2   5'  CGGCAGCTGCGGGGCGTGGG  16372         TATCC
                                CCCGTGTTCC    TTGTTG
                                ||||||||||    ||||||
                                GGGTGCGGGG    GACGGC
                                       CGTC_
GAM378  RGS14   3'  CGTAGGGGTGGAAAGGGG   21369    GTG   T     TT
                                CCC  TTCC ATCCTTG  G
                                |||  |||| |||||||  |
                                GGG  AAGG TGGGGAT  C
                                  GA_  _     GG
GAM378  RGS6    3'  TGTGGTGGGGAGACTCGGTGGG 15029    _____ G      CTTGTTG
          T                      CCC    GT TTCCTATC
                                 |||    || ||||||||
                                 GGG    CA AGGGGTGG
                                   TGGCT  G      T   GTT
GAM378  RNMT    3'  CGATGATTGATCTGGGAACATG 13719         __  C_ TG
          G                      CCGTGTTCCT  ATC  T  TTG
                                 |||||||||  |||  |  |||
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                                GGTACAAGGG TAG A AGC
                                     TC  TT GT
GAM378 RPA2    3' TGACAGGGATGCAATCCAGGGT 11379    GTGTTCC
                                ACCC     TATCCTTGTTG
                                ||||     ||||||||||
                                TGGG     GTAGGGACAGT
                                  ACCTAAC
GAM378 RPS6KA1 5' GGAGGAGCGCGGGT      59318        TA
                                ACCCGTGTTCC TCC
                                |||||||||| |||
                                TGGGCGCGAGG AGG
                                        __
GAM378 RUNX3   3' CGAGAGGATGGAGCTGGGT  15113    T   T    GTTG
                                ACCCG GTTCC ATCCTT
                                ||||| ||||| ||||||
                                TGGGT CGAGG TAGGAG
                                  _   _    AGCG
GAM378 S100A5  5' GGGATTGGGGACGTGTGT   11427   C       _
                                AC CGTGTTCCTA TCCT
                                || |||||||||| ||||
                                TG GTGCAGGGGT AGGG
                                 T       T
GAM378 SALL2   3' AGCTGGTGGGTATGGGT    63856      TT   T TT
                                ACCCGTG CCTA CC GTT
                                ||||||| |||| ||  |||
                                TGGGTAT GGGT GG CGA
                                   __   _ T_
GAM378 SDC1    5' CGGCGGGAGAGGTGCGGG   11472     GTT  A   T
                                CCCGT  CCT TCCT GTTG
                                |||||  ||| |||| ||||
                                GGGCG  GGA AGGG CGGC
                                  T__  G   _
GAM378 SET     3' AGCTGGGAAACGTGGGT    11554       CCTA   T
                                ACCCGTGTT   TCCT GTT
                                |||||||||   |||| |||
                                TGGGTGCAA   AGGG CGA
                                    ____   T
GAM378 SFN     3' TGGCAGGGGCTGGAGATGGGT 74563     G   TA
                                ACCCGT TTCC TCCTTGTTG
                                |||||| ||||  |||||||||
                                TGGGTA GAGG GGGGACGGT
                                   _   TC
GAM378 SFPQ    3' TGGTAGGGGGTGAAAGTGGGT 17372     TG  CTA    TT
                                ACCCG TTC  TCCTTG G
                                |||||  |||  |||||| |
                                TGGGT AAG  GGGGAT T
                                  GA  TG_    GG
GAM378 SFRS1   3' TAATAGGGACTAATGTGGG  22640     TG CCTA
                                CCCG TT   TCCTTGTTG
                                ||||  ||  |||||||||
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                              GGGT  AA   AGGGATAAT
                                GT  TC__
GAM378  SH3BP5   3'  CAGTGGGGATGCGGGGGGATGA 16740   GT    ____    TG
            GGGT                 CC  GTTCCT   ATCCT  TTG
                              ||  ||||||   |||||  |||
                              GG  TAGGGG   TAGGG  GAC
                               AG    GGCG    GT
GAM378  SIP1     3'  GATACTCAGAATATGGGT    13232        C___
                              ACCCGTGTTC   TATC
                              ||||||||||   ||||
                              TGGGTATAAG   ATAG
                                    ACTC
GAM378  SIX2     5'  CGGTGAGGGCGCGCGCGGG   33724      TCCTA   TG
                              CCCGTGT    TCCT  TTG
                              |||||||    ||||  |||
                              GGGCGCG    GGGA  GGC
                                  CGC__   GT
GAM378  SIX3     5'  GTGGATGTGTGTGGGGTGTGGG 18276     TG   _____    TTGTTG
            T                  CCCG  TTCC    TATCC
                              ||||  ||||    |||||
                              GGGT  GGGG    GTAGG
                                GT   TGTGT    T  GT
GAM378  SLC10A2  3'  AGCAGGGGTTTACGG      4841      TTCCT
                              CCGTG    ATCCTTGTT
                              |||||    |||||||||
                              GGCAT    TGGGGACGA
                                T____
GAM378  SLC12A4  5'  CGGCGGGCGGCTGGGACGGCGG 17390      _    TA  _
            GT                  ACCCGT GTTCC  TC CTTGTTG
                              ||||||| |||||  || |||||||
                              TGGGCG CAGGG  GG GGGCGGC
                                 G    TC  C
GAM378  SLC1A2   5'  CGGGCGGAGGGGAGCGCGGGT  61929          A   TTGTTG
                              ACCCGTGTTCCT TCC
                              |||||||||||| |||
                              TGGGCGCGAGGG AGG
                                     G   CGGGC
GAM378  SLC21A2  3'  GGGACTGGGGGTGTGGG     18864     TG    _
                              CCCG  TTCCTA TCCT
                              ||||  |||||| ||||
                              GGGT  GGGGGT AGGG
                                GT     C
GAM378  SLC29A1  3'  GTGGGGACATTGTGGGT     17076     ___
                              ACCC   GTGTTCCTAT
                              ||||   ||||||||||
                              TGGG   TACAGGGGTG
                                TGT
GAM378  SLC2A6   3'  TGTGATGGGGCCTCAGCAGCGG 34161     _  _____     CTTGTTG
            GT                  CCG TGT    TCCTATC
                              ||| |||    |||||||
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                                GGC ACG    GGGGTAG
                                  G   ACTCC      T  GTT
GAM378  SLC7A5   3' CAACGAAGCCGGACACGG    13009        CTATCC
                                CCGTGTTC     TTGTTG
                                ||||||||     ||||||
                                GGCACAGG     AGCAAC
                                    CCGA__
GAM378  SLC8A2   3' ATGGGGGGTGGGGATGGGT   66327     GT         GTTG
                                ACCC  GTTCCTATCCTT
                                ||||  ||||||||||||
                                TGGG  TAGGGGTGGGGG
                                  __          GTAG
GAM378  SMARCD1  3' CAGCAAGGGTGGGAGAC     57430    G
                                GT TTCCTATCCTTGTTG
                                || ||||||||||||||
                                CA GAGGGTGGGAACGAC
                                 _
GAM378  SMARCD1  3' CAGCAAGGGTGGGAGAC     11812    G
                                GT TTCCTATCCTTGTTG
                                || ||||||||||||||
                                CA GAGGGTGGGAACGAC
                                 _
GAM378  SNX6     5' CGGTGGGGGCAGCGGGCGCGGG 41159         _ AT   TG
                                CCCGTGTTC CT  CCT  TTG
                                |||||||| ||  |||  |||
                                GGGCGCGGG GA  GGG  GGC
                                     C  CG   GT
GAM378  SORD     3' CAATGGCTGGACATGGGT    11868        T  TAT  _
                                ACCCGTGT CC   CC TTG
                                |||||||| ||   || |||
                                TGGGTACA GG   GG AAC
                                    _  TC_  T
GAM378  SPINT2   3' TGGCAGGGATGGGTTTGC    63151     TT
                                GTG  CCTATCCTTGTTG
                                |||  ||||||||||||
                                CGT  GGGTAGGGACGGT
                                  TT
GAM378  SPTBN4   3' TGATGGGGGTGGGCAGGGG   47392     G  TT      TG
                                CCC TG  CCTATCCT  TTG
                                ||| ||  ||||||||  |||
                                GGG AC  GGGTGGGG  AGT
                                  G  __       GT
GAM378  STAT5B   3' CAGCGAAGGGAGTGCGAGT   24914    C  TG    ATCC
                                AC CG  TTCCT    TTGTTG
                                || ||  |||||    ||||||
                                TG GC  GAGGG    AGCGAC
                                 A  GT    A___
GAM378  STK11    3' TGGCAGGGGGGGCTGTGGG    4849     GT TT  TAT
                                CCC  G  CC   CCTTGTTG
                                |||  |  ||   ||||||||
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                                GGG  T  GG   GGGACGGT
                                  TG CG  ___
GAM378  SURF4    3'  CAATGGCTTCAGGACATGGGT  52541        T   ATCC TG
                                ACCCGTGT CCT    T  TTG
                                |||||||| |||    |  |||
                                TGGGTACA GGA    G  AAC
                                     _   CTTC GT
GAM378  SURF5    3'  CAGTCATGGGAATGTGGG    22181      TG      CC
                                CCCG  TTCCTAT  TTG
                                ||||  |||||||  |||
                                GGGT  AAGGGTA  GAC
                                  GT      CT
GAM378  SYNGR1   3'  CAACAAGGCACAGATGAGGGT  16310      GTGT  CTAT
                                ACCC    TC    CCTTGTTG
                                ||||    ||    ||||||||
                                TGGG    AG    GGAACAAC
                                  AGT_  ACAC
GAM378  TACSTD2  3'  CGGCGGGGCAGGGGATGGGGT  9856       G      AT
                                ACCC TGTTCCT  CCTTGTTG
                                |||| |||||||  ||||||||
                                TGGG GTAGGGG  GGGGCGGC
                                  _       AC
GAM378  TBX3     3'  CAGCAAGGCTGGTCTGGGT   33352       TGTT  TAT
                                ACCCG    CC   CCTTGTTG
                                |||||    ||   ||||||||
                                TGGGT    GG   GGAACGAC
                                   CT__  TC_
GAM378  TCF19    3'  GAGGTAGGAATACAGGT     97736     C       T
                                ACC GTGTTCCTA CCTT
                                ||| ||||||||| ||||
                                TGG CATAAGGAT GGAG
                                  A       _
GAM378  TCF19    3'  GAGGTAGGAATACAGGT     97866     C       T
                                ACC GTGTTCCTA CCTT
                                ||| ||||||||| ||||
                                TGG CATAAGGAT GGAG
                                  A       _
GAM378  TCFL4    3'  AGGACTTGGGGGTGGGGT    63455      G  TT   __
                                ACCC TG  CCTA  TCCT
                                |||| ||  ||||  ||||
                                TGGG GT  GGGT  AGGA
                                  _ GG    TC
GAM378  TMC2     3'  AGTTTAGGACACGGGT      54960        T    TC
                                ACCCGTGT CCTA  CT
                                |||||||| ||||  ||
                                TGGGCACA GGAT  GA
                                     _    TT
GAM378  TNFRSF1B 3'  TAGCAGAGCAGGGGCAGGGT  6526       G      A_  CT
                                ACCC TGTTCCT  TC  TGTTG
                                |||| |||||||  ||  |||||
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                                TGGG ACGGGGA  AG  ACGAT
                                  _      CG  __
GAM378  TNFRSF6B  5'  GACAGCTGGGGACGGGT     33166       GT    TCC
                                ACCCGT  TCCTA   TTGTT
                                ||||||  |||||   |||||
                                TGGGCA  GGGGT   GACAG
                                   __     C__
GAM378  TNFSF6    3'  GTGCAATTGTAGGGGTGTGTGT 5320     C  TG      CC    TG
                                AC CG  TTCCTAT  TTGT
                                || ||  |||||||  ||||
                                TG GT  GGGGATG  AACG
                                 T  GT      TT    TGA
GAM378  TRAP240   3'  TAACGGGGATAGAGGGGG    17601     GTG TC
                                CCC   T  CTATCCTTGTTG
                                |||   |  ||||||||||||
                                GGG   G  GATAGGGGCAAT
                                  ___ GA
GAM378  TRH       3'  CAGTGAGGGTGGGGTGGG    23052      TGT       TG
                                CCCG   TCCTATCCT  TTG
                                ||||   |||||||||  |||
                                GGGT   GGGGTGGGA  GAC
                                   ___         GT
GAM378  TRPC5     5'  AGAACAGGGTAGGGACATTGGT 24995     C          T   G
                                ACC GTGTTCCTATCCT GTT
                                ||| ||||||||||||| |||
                                TGG TACAGGGATGGGA CAA
                                  T           _   GAG
GAM378  TRPS1     5'  TAATAAGGGTGGGGGAGGG    26078     GTGT
                                CCC    TCCTATCCTTGTTG
                                |||    ||||||||||||||
                                GGG    GGGGTGGGAATAAT
                                  AG__
GAM378  TRPV1     5'  TGGCAAGGAGGGCAGGTGGG   54886      TGTT   A
                                CCCG    CCT TCCTTGTTG
                                ||||    ||| |||||||||
                                GGGT    GGG AGGAACGGT
                                   GGAC   _
GAM378  TSG       5'  GGCGGGGATCTAGGGGT     40236      G  TTCCT
                                ACCC TG     ATCCTTGTT
                                |||| ||     |||||||||
                                TGGG AT     TAGGGGCGG
                                  G  C_____
GAM378  TSPY      5'  CGGCAGGGTTTCTGTGGCGTGG 82105         CCTAT__
              GT                  ACCCGTGTT      CCTTGTTG
                                  |||||||||      ||||||||
                                  TGGGTGCGG      GGGACGGC
                                       TGTCTTT
GAM378  TTYH1     3'  AAGCTGGGGGTGGGGACATGAG 40320    C           _   G
              T                   AC CGTGTTCCTATCCTT GTT
                                  || |||||||||||||| |||
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                                TG GTACAGGGGTGGGGG CGA
                                 A           T  AT
GAM378  UBE3A   3'  GATAAGGTAACATGGG     55578        _  _
                                CCCGTGTT CCT ATC
                                |||||||| ||| |||
                                GGGTACAA GGA TAG
                                    T  A
GAM378  UBE3A   3'  GATAAGGTAACATGGG     55590        _  _
                                CCCGTGTT CCT ATC
                                |||||||| ||| |||
                                GGGTACAA GGA TAG
                                    T  A
GAM378  UBE3A   3'  GATAAGGTAACATGGG     4866         _  _
                                CCCGTGTT CCT ATC
                                |||||||| ||| |||
                                GGGTACAA GGA TAG
                                    T  A
GAM378  UBTF    3'  CGGTGGGGGTAGGGGGCTGG  26448   C  G       TG
                                CC GT TTCCTATCCT  TTG
                                || || ||||||||||  |||
                                GG CG GGGGATGGGG  GGC
                                 T  _       GT
GAM378  VIPR2   3'  TGATGGGGTTACGTGGGGTGCG 12618     TG   TAT___  TG
          GG                    CCCG  TTCC    CCT  TTG
                                ||||  ||||    |||  |||
                                GGGC  GGGG    GGG  AGT
                                  GT   TGCATT  GT
GAM378  WISP1   3'  CAGGTTCAGGTAGGGGTGTGGG 13942     TG      ____   TTG
          T                     CCCG  TTCCTATC   CTTG
                                ||||  ||||||||   ||||
                                GGGT  GGGGATGG   GGAC
                                  GT      ACTT     G
GAM378  WISP2   3'  GGGAATGGGGACACGGTGT   13937   _        _
                                AC CCGTGTTCCTAT CCT
                                || ||||||||||| |||
                                TG GGCACAGGGGTA GGG
                                 T         A
GAM378  WNT5A   3'  TAATGGGGGTGGGAACCACG  12672     _       TG
                                CGTG TTCCTATCCT  TTG
                                |||| ||||||||||  |||
                                GCAC AAGGGTGGGG  AAT
                                  C       GT
GAM378  XBP1    3'  AGTGACTGTGGATACGGG    17429        C  _  _
                                CCCGTGTTC TA TC CT
                                ||||||||| || || ||
                                GGGCATAGG GT AG GA
                                    T  C  T
GAM378  ZFP103  5'  TGGCGGGGGTGTTGGGGACGGG 19027       G   __
          T                     ACCCGT TTCC  TATCCTTGTTG
                                ||||||  ||||  ||||||||||
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                                TGGGCA GGGG  GTGGGGGCGGT
                                   _    TT
GAM378  ZIC1     5'  TGGCGAGGGTGGGGGGGGCGGG 12727       G    _
                                CCCGT TTCCT ATCCTTGTTG
                                ||||| ||||| ||||||||||
                                GGGCG GGGGG TGGGAGCGGT
                                   G    G
GAM378  ZNF144   3'  CCTTGGGGGTGGGGGGCGGGT  23078       G         TTG
                                ACCCGT TTCCTATCCTTG
                                |||||| ||||||||||||
                                TGGGCG GGGGGTGGGGGT
                                   _         TCCA
GAM378  ZNF147   5'  CGGCGGCCTCGGAGCGCGGGT  17434          TATCC
                                ACCCGTGTTCC    TTGTTG
                                ||||||||||     ||||||
                                TGGGCGCGAGG    GGCGGC
                                      CTCC_
GAM378  ZNF175   5'  GTGATGAGGGGCTTGTTGGGGG 23095    TT   _______   TG
           TGGGGGT                 TG  CCTA     TCCT  TTG   T
                                ||  ||||     ||||  |||  |
                                GT  GGGT     GGGA  AGT   G
                                 GG    TGTTCG    GT
GAM378  ZNF179   3'  GGGAACTGGGGGGTGCGGG    23103      TG     __
                                CCCG  TTCCTA  TCCT
                                ||||  ||||||  ||||
                                GGGC  GGGGGT  AGGG
                                  GT     CA
GAM378  ZNF180   5'  CAGGTTGGTAGGGGCGTGGG   25137            __   TTG
                                CCCGTGTTCCTATC  CTTG
                                ||||||||||||||  ||||
                                GGGTGCGGGGATGG  GGAC
                                      TT
GAM378  ZNF219   3'  CAGCAGGGGGCAGCGTGGG    33132         _ TAT
                                CCCGTGTT CC   CCTTGTTG
                                |||||||| ||   ||||||||
                                GGGTGCGA GG   GGGACGAC
                                     C ___
GAM378  ZNF239   5'  TAATGGTGGGAATGGGGT     19043      G        C
                                ACCC TGTTCCTATC TTG
                                |||| |||||||||| |||
                                TGGG GTAAGGGTGG AAT
                                  _        T
GAM378  ABT1     3'  AATGGGGTGGACTGGGT     25374       T   CTAT   TG
                                ACCCG GTTC    CCT  TT
                                ||||| ||||    |||  ||
                                TGGGT CAGG    GGG  AA
                                   _   T___   GT
GAM378  AGS3     5'  TGGCAGGGCTGACACAGGGT   73115      _    CCTAT
                                ACCC GTGTT    CCTTGTTG
                                |||| |||||    ||||||||
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                                TGGG CACAG    GGGACGGT
                                  A    TC___
GAM378  AKAP11   3'  CAATGGGGGTGGGGGTGG    57830    GT TT      TG
                                CC  G  CCTATCCT  TTG
                                ||  |  ||||||||  |||
                                GG  T  GGGTGGGG  AAC
                                 __ GG       GT
GAM378  AKL3L    3'  CAGCATTGTGGAACATGG    32804         TATCCT
                                CCGTGTTCC     TGTTG
                                |||||||||     |||||
                                GGTACAAGG     ACGAC
                                     TGTT__
GAM378  AP3M2    3'  TGATGGGGGTAGGAAGCTTGG  22316     T  _      TG
                                CCG GTT CCTATCCT  TTG
                                ||| ||| ||||||||  |||
                                GGT CGA GGATGGGG  AGT
                                  T  A       GT
GAM378  AP3S2    3'  ATAAGCACAGAGATGGGCAGTG 19518      TG _     _ _   G
           TGGGT                   CCCG  TT CCTATC CT TGTT
                                ||||  || ||||||  || ||||
                                GGGT  GA GGGTAG GA ACGA
                                  GT  C     A  C    ATAG
GAM378  APCL     3'  CAGCAAGGTGCGCAACATGG   19664        CCTAT
                                CCGTGTT    CCTTGTTG
                                |||||||    ||||||||
                                GGTACAA    GGAACGAC
                                    CGCGT
GAM378  APCL     3'  CAGCTGTGGGAGTGCGGGT    19666      TG      CCTT
                                ACCCG  TTCCTAT    GTTG
                                |||||  |||||||    ||||
                                TGGGC  GAGGGTG    CGAC
                                  GT      T___
GAM378  APM2     3'  AGCAGGGAGACTTGGGT     22404      T   CCTA
                                ACCCG GTT    TCCTTGTT
                                ||||| |||    ||||||||
                                TGGGT CAG    AGGGACGA
                                  T  _____
GAM378  APM2     3'  AGCAGGGAGACTTGGGT     22405      T   CCTA
                                ACCCG GTT    TCCTTGTT
                                ||||| |||    ||||||||
                                TGGGT CAG    AGGGACGA
                                  T  _____
GAM378  APXL2    5'  GGGGAGGAAAGGAACATGGGT  75193           A    GTTG
                                ACCCGTGTTCCT TCCTT
                                |||||||||||| |||||
                                TGGGTACAAGGA AGGAG
                                       A    GGGT
GAM378  ARHF     3'  GGACATGGTGGTGATGTGGGT  38747      TG TC    CT    G
                                ACCCG  T  CTATC  TGTT
                                |||||  |  |||||  ||||
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                                TGGGT  A  GGTGG  ACAG
                                   GT GT    T_   GG
GAM378  ARHGAP11A 5'  GGTGGCGAACGAGGGT     28799     G    _
                                ACCC TGTTC CTATC
                                |||| ||||| |||||
                                TGGG GCAAG GGTGG
                                  A    C
GAM378  ARHGEF15  3'  CAGTGGGGAGAGATTGGAGAGC 30258     G   TA____   TG
           GGGT                   CCGT TTCC     TCCT  TTG
                                |||| ||||     ||||  |||
                                GGCG GAGG     AGGG  GAC
                                  A   TTAGAG   GT
GAM378  ARPC4    3'  CGGCAGGGAGTTGGGT     19142      TGTTCCTA
                                ACCCG       TCCTTGTTG
                                |||||       |||||||||
                                TGGGT       AGGGACGGC
                                   TG_______
GAM378  ASTN2    3'  CAGTGAGGAAGCATGGGT    73183        CCTA   TG
                                ACCCGTGTT    TCCT  TTG
                                |||||||||    ||||  |||
                                TGGGTACGA    AGGA  GAC
                                      ____    GT
GAM378  ATP6V0A1  3'  TAGCAGGGGTGGGTCCAGG    17731    G  TT
                                CC TG  CCTATCCTTGTTG
                                || ||  ||||||||||||||
                                GG AC  GGGTGGGGACGAT
                                 _  CT
GAM378  BC022889  3'  AAGCAAAGGAGCGTGGG     83643         ATCC    G
                                CCCGTGTTCCT    TTGTT
                                ||||||||||    |||||
                                GGGTGCGAGGA    AACGA
                                      ____    AA
GAM378  BC022889  5'  GGTGGGGAGATGCGGG      83648        __
                                CCCGTGTT  CCTATC
                                ||||||||  ||||||
                                GGGCGTAG  GGGTGG
                                     AG
GAM378  BDG-29    5'  TAACGAGGGCCGCACGGG    72356       TCCTA
                                CCCGTGT    TCCTTGTTG
                                |||||||    |||||||||
                                GGGCACG    GGGAGCAAT
                                    CC___
GAM378  BG1       3'  AGGCTGTGGAGCGGGT      87306       GT  _  T
                                ACCCGT  TCC TA CCT
                                ||||||  ||| || |||
                                TGGGCG  AGG GT GGA
                                   __   T  C
GAM378  BIK       3'  TAGCAGGGGGAGTGCTGGT    6823      C TG    TAT
                                ACC G  TTCC   CCTTGTTG
                                ||| |  ||||   ||||||||
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                                TGG C  GAGG   GGGACGAT
                                  T GT   ___
GAM378  BIRC3    3'  TGACATTTTAGGGACATGG    67199          TCCT
                                CCGTGTTCCTA    TGTTG
                                ||||||||||    |||||
                                GGTACAGGGAT    ACAGT
                                      TTT_
GAM378  BPES     5'  AGCAAGCAAGCGCGGG      43530        CCTATC
                                CCCGTGTT     CTTGTT
                                ||||||||     ||||||
                                GGGCGCGA     GAACGA
                                    AC____
GAM378  BPNT1    5'  AACGAGGGACCTGGGT      64755       T   CCTAT
                                ACCCG GTT    CCTTGTT
                                ||||| |||    |||||||
                                TGGGT CAG    GGAGCAA
                                  C  _____
GAM378  BRD1     5'  GTGTGTGGTGGTAGGGACGCAG 27417     C         _  TGTTG
              GT                  ACC GTGTTCCTATC CT
                                ||| ||||||||||| ||
                                TGG CGCAGGGATGG GG
                                  A         T  TGTGTGG
GAM378  BTN3A1   3'  CGAGTACTGGGAATATAGGT   22916     CG       TC_
                                ACC  TGTTCCTA   CTTG
                                |||  ||||||||   ||||
                                TGG  ATAAGGGT   GAGC
                                  AT       CAT
GAM378  C12orf2  3'  TAGCAAGTGTCAGCAAGGGT   82788     G    CCT TC
                                ACCC TGTT   A  CTTGTTG
                                |||| ||||   |  |||||||
                                TGGG ACGA   T  GAACGAT
                                  A    C__ GT
GAM378  C12orf8  3'  TGGTGGGGGTAGGGAGGGG    22364     GTG        TG
                                CCC   TTCCTATCCT  TTG
                                |||   ||||||||||  |||
                                GGG   AGGGATGGGG  GGT
                                  G__         GT
GAM378  C14orf4  5'  TGGCAGAGGTGGGCGTGGGT   67341        TT     C
                                ACCCGTG  CCTATC TTGTTG
                                |||||||  ||||||  ||||||
                                TGGGTGC  GGGTGG GACGGT
                                    __     A
GAM378  C15orf15 5'  TGTGGTGGGGTTACACGCGGGT 32833         ____      CTTGTTG
                                ACCCGTGT    TCCTATC
                                ||||||||    |||||||
                                TGGGCGCA    GGGGTGG
                                     CATT      T  GTT
GAM378  C1orf17  3'  CAGTAGGGGTGGGTATTTGGGT 68211       T  T
                                ACCCG GT CCTATCCTTGTTG
                                ||||| || |||||||||||||
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                                TGGGT TA GGGTGGGGATGAC
                                  T  T
GAM378  C1orf17   3'  CGGCACCCGGGGGAGTGGTGGG 68212      TG_    ATCCT
           T                     ACCCG   TTCCT    TGTTG
                                 |||||   |||||    |||||
                                 TGGGT   GAGGG    ACGGC
                                   GGT    GGCCC
GAM378  C1orf34   3'  CAGCAAGGAGAACTGCTGGT   60666    C  _   CTA
                                 ACC GT GTTC   TCCTTGTTG
                                 ||| || ||||   |||||||||
                                 TGG CG CAAG   AGGAACGAC
                                  T  T   ___
GAM378  C20orf108 3'  CAGCAAGGCATCGGAGATGGGT 55043       G   T  _
                                 ACCCGT TTCC AT CCTTGTTG
                                 |||||| |||| || ||||||||
                                 TGGGTA GAGG TA GGAACGAC
                                    _   C  C
GAM378  C20orf108 3'  TGGCGAGGGTCTGTGGGT    55051      TGTTCCT
                                 ACCCG      ATCCTTGTTG
                                 |||||      ||||||||||
                                 TGGGT      TGGGAGCGGT
                                   GTC____
GAM378  C20orf183 3'  GGCATGGGGATGGGT      47807      GT      _
                                 ACCC  GTTCCTAT CC
                                 ||||  |||||||| ||
                                 TGGG  TAGGGGTA GG
                                   __       C
GAM378  C20orf188 3'  GGGTGAGCGTGGGT       31580          CT
                                 ACCCGTGTTC  ATCC
                                 ||||||||||  ||||
                                 TGGGTGCGAG  TGGG
                                       __
GAM378  C20orf60  3'  GCCGAGTAGGGGTGGGGGT   53735     G  TT   TC   TTG
                                 ACCC TG  CCTA  CTTG
                                 |||| ||  ||||  ||||
                                 TGGG GT  GGAT  GAGC
                                   G  GG   __   CGG
GAM378  C20orf60  3'  TAAGGTCATGGGAGAGTGGGT  53737      TG     __    TTG
                                 ACCCG  TTCCTAT  CCTTG
                                 |||||  |||||||  |||||
                                 TGGGT  GAGGGTA  GGAAT
                                   GA      CT
GAM378  C21orf61  5'  TAATGGGGAGGCTATGCAGGT  88710    C   T_  TA   TG
                                 ACC GTGT  CC  TCCT  TTG
                                 ||| ||||  ||  ||||  |||
                                 TGG CGTA  GG  AGGG  AAT
                                   A   TC  __   GT
GAM378  C21orf93  3'  CAGCGAGGGTGAGGTGGG    59085     TGTT  _
                                 CCCG   CCT ATCCTTGTTG
                                 ||||   ||| ||||||||||
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                                GGGT   GGA TGGGAGCGAC
                                  ____  G
GAM378  C22orf20  3'  TGACAGGTGTTTGGATGGGT  47436     TGT  T_ TC
                                ACCCG  TCC  A  CTTGTTG
                                |||||  |||  |  |||||||
                                TGGGT  AGG  T  GGACAGT
                                  ___  TT GT
GAM378  C22orf5   3'  CAGGAGTGGGGATGTGGG   24340     TG    TC
                                CCCG  TTCCTA  CTTG
                                ||||  ||||||  ||||
                                GGGT  AGGGGT  GGAC
                                  GT    GA
GAM378  C5orf6    3'  CGAGCCTGGGAATGGGGGT   33480     G     TC
                                ACCC TGTTCCTA  CTTG
                                |||| ||||||||  ||||
                                TGGG GTAAGGGT  GAGC
                                  G      CC
GAM378  C5orf7    5'  CGGCGGGCGGGAGCGCGGGT  63868         AT  TT
                                ACCCGTGTTCCT  CC  GTTG
                                ||||||||||||  ||  ||||
                                TGGGCGCGAGGG  GG  CGGC
                                       CG  __
GAM378  C9orf12   5'  TGGCAGGCGCCGGGGGCGTGG  42794        ATC_
                                CCGTGTTCCT   CTTGTTG
                                ||||||||||   |||||||
                                GGTGCGGGGG   GGACGGT
                                     CCGC
GAM378  C9orf7    3'  GGTGGGCTGGGCGTGGG    34179        ___
                                CCCGTGTT   CCTATC
                                ||||||||   ||||||
                                GGGTGCGG   GGGTGG
                                    GTC
GAM378  CACNA1H   5'  GGGCTGGGGACGCGGG     40843         T
                                CCCGTGTTCCTA CCT
                                |||||||||||| |||
                                GGGCGCAGGGGT GGG
                                       C
GAM378  CAM-KIIN  3'  CAGCGGCCAGGAGCGCGGG   52691         AT  TT
                                CCCGTGTTCCT  CC  GTTG
                                ||||||||||  ||  ||||
                                GGGCGCGAGGA  GG  CGAC
                                       CC  __
GAM378  CAP       3'  TGACAAGCGAGGCAAGGGT   21025     G  TT  ATC
                                ACCC TG  CCT   CTTGTTG
                                |||| ||  |||  |||||||
                                TGGG AC  GGA   GAACAGT
                                  A  __  GC_
GAM378  CAPN6     3'  AGCAGCTGGACATGGG      26600       T  TATCC
                                CCCGTGT CC    TTGTT
                                |||||||  ||    |||||
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                                GGGTACA GG    GACGA
                                   _ TC___
GAM378  CASKIN1  3' GGGTTTGGTGAATGTGGGT   40400     TG  _  T_
                                ACCCG  TTC CTA  CCT
                                |||||  ||| |||  |||
                                TGGGT  AAG GGT  GGG
                                   GT   T   TT
GAM378  CCR7     3' CAACAGGGGAGAGTGTGGTGT  8451    _  TG   CTA
                                AC CCG  TTC   TCCTTGTTG
                                || |||  |||   |||||||||
                                TG GGT  GAG   GGGGACAAC
                                 T   GT   A__
GAM378  CDC14B   5' TAGCGAGGGCTGCGGCGCCGGT 13388    C    CCTA
                                ACC GTGTT    TCCTTGTTG
                                ||| |||||    |||||||||
                                TGG CGCGG    GGGAGCGAT
                                  C    CGTC
GAM378  CDC14B   5' TAGCGAGGGCTGCGGCGCCGGT 52837    C    CCTA
                                ACC GTGTT    TCCTTGTTG
                                ||| |||||    |||||||||
                                TGG CGCGG    GGGAGCGAT
                                  C    CGTC
GAM378  CDC14B   5' TAGCGAGGGCTGCGGCGCCGGT 52860    C    CCTA
                                ACC GTGTT    TCCTTGTTG
                                ||| |||||    |||||||||
                                TGG CGCGG    GGGAGCGAT
                                  C    CGTC
GAM378  CDC16    5' GGGGCCTGGGTGGGGGGTGCGG 14019     TG    _   TT   G
           GT                     ACCCG  TTCCT ATCC  GTT
                                |||||  ||||| ||||  |||
                                TGGGC  GGGGG TGGG  CGG
                                   GT    G    TC   GGC
GAM378  CDC16    5' TGTGGGTGGGGGGGTGCGGGT   14021     TG    _   TTGTTG
                                ACCCG  TTCCT ATCC
                                |||||  ||||| ||||
                                TGGGC  GGGGG TGGG
                                   GT    G    T   GTT
GAM378  CDH22    5' GGCGACGGGGGCGCGGG     41157        TA  _
                                CCCGTGTTCC  TC CT
                                ||||||||||  || ||
                                GGGCGCGGGG  AG GG
                                      GC  C
GAM378  CDIPT    5' CGGCGGGGTCCAGGGCGCAGGT 20887    C    T   AT_
                                ACC GTGT CCT   CCTTGTTG
                                ||| |||| |||   ||||||||
                                TGG CGCG GGA   GGGGCGGC
                                  A    _   CCT
GAM378  CECR2    5' CGGCGGGCAGAGCGCGGG    48608        CTATC
                                CCCGTGTTC    CTTGTTG
                                |||||||||    |||||||
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                                GGGCGCGAG    GGGCGGC
                                     AC___
GAM378  CENTG2   5' CGGCGGGGGGCGCGCGG    29879      T  TAT
                                CCGTGT CC   CCTTGTTG
                                |||||| ||   ||||||||
                                GGCGCG GG   GGGGCGGC
                                   C  ___
GAM378  CFLAR    5' AACAAGGACCACGGG      13926      TTCCTA
                                CCCGTG     TCCTTGTT
                                ||||||     ||||||||
                                GGGCAC     AGGAACAA
                                   C_____
GAM378  CFLAR    3' TAGCTGGGTGTGGGTGTGGGT 13931      TG   C    TT
                                ACCCG  TTC TATCC  GTTG
                                |||||  ||| |||||  ||||
                                TGGGT  GGG GTGGG  CGAT
                                   GT   T    T_
GAM378  CGI-96   3' GGGCTGGGAGCATGTGT    31663    C       T
                                AC CGTGTTCCTA CCT
                                || |||||||||| |||
                                TG GTACGAGGGT GGG
                                 T        C
GAM378  CHERP    3' GGCGTGGAGGGCACGGGT    21102         _   _
                                ACCCGTGTTC CTAT CC
                                |||||||||| |||| ||
                                TGGGCACGGG GGTG GG
                                      A   C
GAM378  CHST3    5' CGGCGGCCGGGGACAAGGGT  14972     G     AT  TT
                                ACCC TGTTCCT  CC  GTTG
                                |||| |||||||  ||  ||||
                                TGGG ACAGGGG  GG  CGGC
                                  A      CC  __
GAM378  CIP29    3' AGGTGTGGGAACTGGGT     50399      T      _
                                ACCCG GTTCCTAT CCT
                                ||||| |||||||| |||
                                TGGGT CAAGGGTG GGA
                                   _       T
GAM378  CL24751  3' TGGTGGGGGTATTGCTACGG  64689     _ TCC     TG
                                CCGT GT   TATCCT  TTG
                                |||| ||   ||||||  |||
                                GGCA CG   ATGGGG  GGT
                                  T  TT_     GT
GAM378  CLDN6    3' CAACAGCTTTGGGATGGGT   41039      TGT    TCC
                                ACCCG   TCCTA   TTGTTG
                                |||||   |||||   ||||||
                                TGGGT   AGGGT   GACAAC
                                   ___    TTC
GAM378  CLTH     5' CGGTGGGGGTAGGGGGTGCGG 23145     TG   _     TG
                                CCG  TTCC TATCCT  TTG
                                |||  |||| ||||||  |||
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                                GGC  GGGG ATGGGG  GGC
                                  GT   G    GT
GAM378  CNTNAP1   3'  CAGCAGGGACAGATGTGTGGG  13276     TG TC  A
                                CCCG  T  CT TCCTTGTTG
                                |||| |  || |||||||||
                                GGGT  G  GA AGGGACGAC
                                  GT TA  C
GAM378  CPLX1     3'  TAGCAGACGGGGGGGTGCGGG  21837     TG    ATCC
                                CCCG  TTCCT   TTGTTG
                                ||||  |||||   ||||||
                                GGGC  GGGGG   GACGAT
                                  GT    GGCA
GAM378  D13S106E  5'  TCCGAGGGGAACGTGGGT    19400         TAT    TTG
                                ACCCGTGTTCC   CCTTG
                                ||||||||||   |||||
                                TGGGTGCAAGG   GGAGC
                                      ___    CTG
GAM378  DAMS      5'  AACAAAGATACATGGGT     41821        TCCT   C
                                ACCCGTGT    ATC TTGTT
                                ||||||||    ||| |||||
                                TGGGTACA    TAG AACAA
                                    ____   A
GAM378  DDX34     3'  TGATGAGGTATCAGGTGGGT   27990      TGTT  _ _  TG
                                ACCCG    CCT AT CCT  TTG
                                |||||    ||| || |||  |||
                                TGGGT    GGA TA GGA  AGT
                                  ____   C  T   GT
GAM378  DIO2      3'  TGGCAAGGAGAATATGCGGG   5836        TCCTA
                                CCCGTGT    TCCTTGTTG
                                |||||||    |||||||||
                                GGGCGTA    AGGAACGGT
                                   TAAG_
GAM378  DIO2      3'  TGGCAAGGAGAATATGCGGG   25688       TCCTA
                                CCCGTGT    TCCTTGTTG
                                |||||||    |||||||||
                                GGGCGTA    AGGAACGGT
                                   TAAG_
GAM378  DKFZP434B103 5'  CAATGGGGGCTGTGGCATGCG  31587      T  TA__   TG
                                CGTGT CC    TCCT  TTG
                                ||||| ||    ||||  |||
                                GCGTA GG    GGGG  AAC
                                  C  TGTC    GT
GAM378  DKFZP434B205 3'  CGGCAGGGCCCGTGCTGGGT   75319      T  TCCTAT
                                ACCCG GT     CCTTGTTG
                                ||||| ||     ||||||||
                                TGGGT CG     GGGACGGC
                                  _ TGCCC_
GAM378  DKFZP434C128 3'  TGACAGGCAGTGGGGAGTGGGT 64846      GTG      C_
                                ACCC   TTCCTAT  CTTGTTG
                                ||||   |||||||  |||||||
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                                TGGG  AGGGGTG  GGACAGT
                                  TG_     AC
GAM378  DKFZP434C1715 3'  CAGTAAGGGGGTATGTGGG   86147     TG T   AT
                                CCCG  T CCT  CCTTGTTG
                                |||| | |||  ||||||||
                                GGGT  A GGG  GGAATGAC
                                  GT T  __
GAM378  DKFZP434C212 3'  TAACAAATTGCATAGGAGTGTG 68917     TG      CC___
          GG                    CCCG  TTCCTAT    TTGTTG
                                |||| |||||||    ||||||
                                GGGT  GAGGATA    AACAAT
                                  GT      CGTTA
GAM378  DKFZp434E0519 3'  CAACAAGGCCAGGCATGG    49981      TT   AT
                                CCGTG  CCT  CCTTGTTG
                                |||||  |||  ||||||||
                                GGTAC  GGA  GGAACAAC
                                  __   CC
GAM378  DKFZP434H0820 3'  AGGCTGGGGGTGCTGGGT    63845     _ TG     T
                                ACCC G  TTCCTA CCT
                                |||| |  |||||| |||
                                TGGG C  GGGGGT GGA
                                  T GT     C
GAM378  DKFZp434J0226 5'  CAGCTCCTCTAGGAATATGGG  72330           TCCTT
                                CCCGTGTTCCTA    GTTG
                                ||||||||||||    ||||
                                GGGTATAAGGAT    CGAC
                                       CTCCT
GAM378  DKFZp434K1815 3'  CGATGGGGGTGGGGGGGGGT   94264     GTG        TG
                                ACCC   TTCCTATCCT  TTG
                                ||||   ||||||||||  |||
                                TGGG   GGGGGTGGGG  AGC
                                  G__         GT
GAM378  DKFZP434N178 3'  CAACAAAGATGGGGGGTAGGGT 71902      GTG       C
                                ACCC   TTCCTATC TTGTTG
                                ||||   |||||||| ||||||
                                TGGG   GGGGGTAG AACAAC
                                  ATG       A
GAM378  DKFZP434N178 3'  GGTGGACAGAGCGAGGGT    71909      G    ___
                                ACCC TGTTC   CTATC
                                |||| |||||   |||||
                                TGGG GCGAG   GGTGG
                                  A     ACA
GAM378  DKFZp547H236 5'  CGGCGGGGGTGGGGGGGCG    78542     G
                                CGT TTCCTATCCTTGTTG
                                ||| ||||||||||||||
                                GCG GGGGGTGGGGGCGGC
                                  G
GAM378  DKFZp547M072 3'  CAGCGAGGATGGGAGGGGGT   61077      GTG
                                ACCC   TTCCTATCCTTGTTG
                                ||||   ||||||||||||||
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                                TGGG  GAGGGTAGGAGCGAC
                                  G__
GAM378  DKFZP564I052 5'  GTAGCTGAAAATGGGGATACGG 66716          CCTT_
                                CCGTGTTCCTAT    GTTG
                                ||||||||||||   ||||
                                GGCATAGGGGTA    CGAT
                                       AAAGT   GA
GAM378  DKFZP564K2062 3'  TGGGCCCCTGGGAACATGTGT  31239   C       T___  TGTTG
                                AC CGTGTTCCTA   CCT
                                || ||||||||||   |||
                                TG GTACAAGGGT   GGG
                                 T       CCCC  T  G
GAM378  DKFZP566J091 3'  CAGCAGCCATGGGTACATGGGT 48119       T    CC
                                ACCCGTGT CCTAT  TTGTTG
                                |||||||| |||||  ||||||
                                TGGGTACA GGGTA  GACGAC
                                     T    CC
GAM378  DKFZP586H2123 3'  CAGCAGAGCTGGGATGTGG   61925    TG   TA_  CT
                                CCG  TTCC   TC  TGTTG
                                |||  ||||   ||  |||||
                                GGT  AGGG   AG  ACGAC
                                  GT   TCG  __
GAM378  DKFZp761B0514 5'  CGGCACCTGAAGGGACGCGGG  50154         A  CT_
                                CCCGTGTTCCT TC   TGTTG
                                |||||||||| ||   |||||
                                GGGCGCAGGGA AG   ACGGC
                                       _  TCC
GAM378  DKFZp761F2014 3'  CAAAGTGGATGGGAGTGTGGG  39533     TG       TTG
                                CCCG  TTCCTATCC   TTG
                                ||||  |||||||||   |||
                                GGGT  GAGGGTAGG   AAC
                                  GT       TGA
GAM378  DKFZp761H2121 5'  GACTCTTAGGAAAATGGGT    56370      G     TCCTT   G
                                ACCCGT TTCCTA    GTT
                                ||||||  ||||||    |||
                                TGGGTA AAGGAT    CAG
                                   A     TCT__   A
GAM378  DMTF1    5'  GGAGATAGGAACATGGG     40941           _
                                CCCGTGTTCCTATC CT
                                |||||||||||||| ||
                                GGGTACAAGGATAG GG
                                       A
GAM378  DOCK3    3'  GAGGTAGGGAGGGGAGTATGGG 66502          A       G
          T                     ACCCGTGTTCCT TCCTTGTT
                                |||||||||||| ||||||||
                                TGGGTATGAGGG AGGGATGG
                                       G       AGA
GAM378  DT1P1A10  3'  TGATAGGGGGCTGGCTGGGT   61565      T   CCTA
                                ACCCG GTT    TCCTTGTTG
                                ||||| |||    |||||||||
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                                TGGGT CGG   GGGGATAGT
                                  _  TCG_
GAM378  DUSP9   3'  GGGATGGGGGTGGGGGT    7342      G  TT
                                ACCC TG  CCTATCCT
                                |||| ||  ||||||||
                                TGGG GT  GGGTAGGG
                                  G  GG
GAM378  E1B-AP5  3'  GGTGCTGGGGATGGGGT    22903     G      T__
                                ACCC TGTTCCTA   CC
                                |||| ||||||||   ||
                                TGGG GTAGGGGT   GG
                                  _      CGT
GAM378  E1B-AP5  3'  GGTGCTGGGGATGGGGT    58569     G      T__
                                ACCC TGTTCCTA   CC
                                |||| ||||||||   ||
                                TGGG GTAGGGGT   GG
                                  _      CGT
GAM378  E2IG4   3'  CAATGGGCAGAGGGTGGGT   90907     TGT   ATC  TG
                                ACCCG   TCCT   CT  TTG
                                |||||   ||||   ||  |||
                                TGGGT   GGGA   GG  AAC
                                  ___   GAC  GT
GAM378  EDG2    5'  GGTTGGGGGGCGCGCGT     7383     C       T
                                AC CGTGTTCCTA CC
                                || ||||||||| ||
                                TG GCGCGGGGGT GG
                                 C        T
GAM378  EDR1    3'  TGGTAAGGCAAGGAACTGGGT  15386     T     AT    TT
                                ACCCG GTTCCT  CCTTG  G
                                ||||| ||||||  |||||  |
                                TGGGT CAAGGA  GGAAT  T
                                  _    AC    GG
GAM378  EPB41L1  3'  GTAGGGGCTGACGGGT     70596      __
                                ACCCGT  GTTCCTAT
                                ||||||  ||||||||
                                TGGGCA  CGGGGATG
                                   GT
GAM378  EREG    3'  TAGTGAGGATGGTGCTGAGT   7509    C  T  TC     TG
                                AC CG GT  CTATCCT  TTG
                                || || ||  |||||||  |||
                                TG GT CG  GGTAGGA  GAT
                                 A  _  T_     GT
GAM378  ERF     3'  TGGTGGGGGTGGGTGGGT    21441     TGTT      TG
                                ACCCG   CCTATCCT  TTG
                                |||||   ||||||||  |||
                                TGGGT   GGGTGGGG  GGT
                                  _____      GT
GAM378  ERG-1   5'  TGACGAGGGTAGGTGGAGGTGG 41844     TG  __
            G                    CCCG  TT  CCTATCCTTGTTG
                                ||||  ||  ||||||||||||
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                                GGGT  AG  GGATGGGAGCAGT
                                  GG  GT
GAM378  ESDN     5'  TGGTGAGGAGCGCGGCGCGGG  55179        CCTA   TG
                                CCCGTGTT   TCCT  TTG
                                ||||||||   ||||  |||
                                GGGCGCGG   AGGA  GGT
                                    CGCG   GT
GAM378  ET(B)R-LP-2 3'  CAGTAGGGGTGGGGAGGGAGGG 16482     GTG_
                                CCC   TTCCTATCCTTGTTG
                                |||   ||||||||||||||
                                GGG   AGGGGTGGGGATGAC
                                  AGGG
GAM378  FBXO6    5'  CGGCCCTGCGTAGGAGGCGGGT 37382       G      CCTT_
                                ACCCGT TTCCTAT    GTTG
                                |||||| |||||||    ||||
                                TGGGCG GAGGATG    CGGC
                                   _      CGTCC
GAM378  FEM-2    3'  CAGCAGGGATGCTGCTGGG   27570      T  TCC
                                CCCG GT   TATCCTTGTTG
                                |||| ||   ||||||||||
                                GGGT CG   GTAGGGACGAC
                                  _ TC_
GAM378  FEM-2    3'  CGGCAGGGCCAGTATGGG    27575       TTC  AT
                                CCCGTG   CT  CCTTGTTG
                                ||||||   ||  ||||||||
                                GGGTAT   GA  GGGACGGC
                                   ____  CC
GAM378  FEM-2    3'  GAACCCAGGATAGGAAATGGGT 27579       G        T_  G
                                ACCCGT TTCCTATCCT  GTT
                                |||||| ||||||||||  |||
                                TGGGTA AAGGATAGGA  CAA
                                   _        CC   GA
GAM378  FEM-2    3'  TAGTGGGGAAAGGGACGGGGT  27583      G      A   TG
                                ACCC TGTTCCT TCCT  TTG
                                |||| ||||||| ||||  |||
                                TGGG GCAGGGA AGGG  GAT
                                  _      A   GT
GAM378  FHOD2    5'  CAACGCAGGGAGCATGG     73823          ATCCT
                                CCGTGTTCCT    TGTTG
                                ||||||||||    |||||
                                GGTACGAGGG    GCAAC
                                     AC____
GAM378  FHX      5'  TAACAAGCAGGGTGTGGG    37305      TG T   ATC
                                CCCG  T CCT   CTTGTTG
                                ||||  | |||   |||||||
                                GGGT  G GGA   GAACAAT
                                  GT _   C__
GAM378  FKBP9    3'  AGTGAGGGTGCAAGGGT     94061      G   TCCT    TG
                                ACCC TGT    ATCCT  TT
                                |||| |||    |||||  ||
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                                TGGG ACG   TGGGA  GA
                                  A  ____    GT
GAM378  FKSG28   3' CAGTAGGGATGATCATGGG   48175      T  CT
                                CCCGTG TC  ATCCTTGTTG
                                |||||| ||  ||||||||||
                                GGGTAC AG  TAGGGATGAC
                                   T  __
GAM378  FKSG42   3' AGTGATGGGAGTATGTGT    49332    C        _
                                AC CGTGTTCCTATC CT
                                || ||||||||||||  ||
                                TG GTATGAGGGTAG GA
                                 T         T
GAM378  FLJ00007 3' CAGCAGGGAGGAGGGGAGTGAG 71272    GTG__    A_
           GGT                    CCC    TTCCT  TCCTTGTTG
                                |||    |||||  |||||||||
                                GGG    GGGGA  AGGGACGAC
                                  AGTGA    GG
GAM378  FLJ00026 3' GGGATGGAGGATGGGT     64995      G   T
                                ACCCGT TTCC ATCCT
                                |||||| |||| |||||
                                TGGGTA GAGG TAGGG
                                   G   _
GAM378  FLJ10006 5' TGACGGGGGCGGCGCGGG    80094       CCTA
                                CCCGTGTT   TCCTTGTTG
                                ||||||||   |||||||||
                                GGGCGCGG   GGGGGCAGT
                                    C___
GAM378  FLJ10058 3' TAGTGAGGATATGGATGAGGGT 35787     GTGT  _    TG
                                ACCC   TCC TATCCT  TTG
                                ||||   ||| ||||||  |||
                                TGGG   AGG ATAGGA  GAT
                                  AGT_  T    GT
GAM378  FLJ10110 5' CGGCGAGGGCTGAGCGCGGG   35822       CTA
                                CCCGTGTTC   TCCTTGTTG
                                |||||||||   |||||||||
                                GGGCGCGAG   GGGAGCGGC
                                     TC_
GAM378  FLJ10276 3' CAATGAGTGAAAGGGATCGTGG 35962       _    A  _  TG
           GT                    ACCCGTG TTCCT TC CT  TTG
                                ||||||| ||||| || ||  |||
                                TGGGTGC AGGGA AG GA  AAC
                                   T    A  T  GT
GAM378  FLJ10315 3' TGGCAAGGGGCTGTTGGGT   36022     TGTT  TAT
                                ACCCG   CC   CCTTGTTG
                                |||||   ||  ||||||||
                                TGGGT   GG   GGAACGGT
                                  TGTC  ___
GAM378  FLJ10375 3' AGGTTGGGGATGGGGT     36069     G      T
                                ACCC TGTTCCTA CCT
                                |||| |||||||| |||
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                                TGGG GTAGGGGT GGA
                                  _      T
GAM378  FLJ10607  3'  GGTAGTCAAGAGTATGGGT   77123          ____
                                ACCCGTGTTC   CTATC
                                ||||||||||   |||||
                                TGGGTATGAG   GATGG
                                     AACT
GAM378  FLJ10716  5'  AGTGGTGTGAACACGG     36481        C   _
                                CCGTGTTC TATC CT
                                |||||||| |||| ||
                                GGCACAAG GTGG GA
                                     T   T
GAM378  FLJ10769  3'  CGGCAGGGAGCTGGGCAGGGGT 36596     G    CTA
                                ACCC TGTTC   TCCTTGTTG
                                |||| |||||   |||||||||
                                TGGG ACGGG   AGGGACGGC
                                  G    TCG
GAM378  FLJ10769  3'  TAGCGGGGCATGGTACGG    36599      TTC   _
                                CCGTG   CTAT CCTTGTTG
                                |||||   |||| ||||||||
                                GGCAT   GGTA GGGGCGAT
                                   ___   C
GAM378  FLJ10891  3'  CAATAGGGGTTTTTATAGGT   36805    CG  TTCCT
                                ACC  TG    ATCCTTGTTG
                                |||  ||    ||||||||||
                                TGG  AT    TGGGGATAAC
                                  AT  TTT__
GAM378  FLJ10891  3'  GACAAGGATTTCGGGT     36806      TGTTCCT
                                ACCCG      ATCCTTGTT
                                |||||      |||||||||
                                TGGGC      TAGGAACAG
                                  TT_____
GAM378  FLJ10900  3'  AACACAGGGACACGGG     36814          ATCCT   G
                                CCCGTGTTCCT    TGTT
                                ||||||||||    ||||
                                GGGCACAGGGA    ACAA
                                     C____   A
GAM378  FLJ10979  5'  CGGCGGGGGTCGGCAGGGGGCC 36933    T    _____
          GGGT                    CG GTTCCT    ATCCTTGTTG
                                || ||||||    ||||||||||
                                GC CGGGGG    TGGGGGCGGC
                                 _     ACGGC
GAM378  FLJ11016  3'  TGGGTTTATATAGGAATAGGGT 36984    G      _____  TGTTG
                                CCC TGTTCCTAT    CCT
                                ||| |||||||||    |||
                                GGG ATAAGGATA    GGG
                                  _      TATTT  T  G
GAM378  FLJ11240  3'  CAAAAATGGGAGCATGG    37183          CC
                                CCGTGTTCCTAT  TTG
                                ||||||||||||  |||
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                                GGTACGAGGGTA  AAC
                                      AA
GAM378  FLJ11320 3' CAGTGGCCTGGGAATGGGGT  37242     G      T_ _
                                ACCC TGTTCCTA  CC TTG
                                |||| ||||||||  || |||
                                TGGG GTAAGGGT  GG GAC
                                  _       CC  T
GAM378  FLJ11413 3' CAGCAATCTGGGACGTGG    44643        TATCC
                                CCGTGTTCC    TTGTTG
                                |||||||||    ||||||
                                GGTGCAGGG    AACGAC
                                     TCT__
GAM378  FLJ11700 3' CAGCCTTTGGGAACAGGGT   46036     G      TCCTT
                                ACCC TGTTCCTA    GTTG
                                |||| ||||||||    ||||
                                TGGG ACAAGGGT    CGAC
                                  _       TTC__
GAM378  FLJ12229 3' TGGAGAGGTAGGGGTGCGGG  45919     TG     _  GTTG
                                CCCG  TTCCTATC CTT
                                ||||  |||||||| |||
                                GGGC  GGGGATGG GAG
                                  GT       A  GT
GAM378  FLJ12242 3' CAGGTATTGGGGATGCAGGT  45179    C       TC_
                                ACC GTGTTCCTA   CTTG
                                ||| |||||||||   ||||
                                TGG CGTAGGGGT   GGAC
                                  A        TAT
GAM378  FLJ12587 3' TGACAGGGACTGGGCAGGGT  42500     G  T  TA
                                ACCC TGT CC  TCCTTGTTG
                                |||| ||| ||  |||||||||
                                TGGG ACG GG  AGGGACAGT
                                  _  _ TC
GAM378  FLJ12671 3' GGCAATGGGGACGCTGGT    48280    C       __
                                ACC GTGTTCCTAT  CC
                                ||| ||||||||||  ||
                                TGG CGCAGGGGTA  GG
                                  T        AC
GAM378  FLJ12691 3' AGCAAGGGCCATGGG      44701       TTCCTA
                                CCCGTG     TCCTTGTT
                                ||||||     ||||||||
                                GGGTAC     GGGAACGA
                                   C_____
GAM378  FLJ12761 3' TGACAAGGATGGCTGGCTGGT 44613    C  GTTC
                                ACC GT    CTATCCTTGTTG
                                ||| ||    ||||||||||||
                                TGG CG    GGTAGGAACAGT
                                  T  GTC_
GAM378  FLJ12761 3' TGGTGGGGGTGGGGGGAGGGT 44614     GTG       TG
                                ACCC   TTCCTATCCT  TTG
                                ||||   ||||||||||  |||
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                                TGGG  GGGGGTGGGG  GGT
                                  AG_       GT
GAM378  FLJ12788  3'  GTGGTGGGGGACATAGTGTGGT 42550    _ ___     AT  TTGTTG
                                ACC C  GTGTTCCT  CC
                                ||| |  |||||||| ||
                                TGG G  TACAGGGG  GG
                                  T TGA      GT  T  GT
GAM378  FLJ12998  3'  TGGCAGGGACTGGATGCTGGGT 42839     T  _  TA
                                ACCCG GT TCC  TCCTTGTTG
                                ||||| || |||  |||||||||
                                TGGGT CG AGG  AGGGACGGT
                                  _ T  TC
GAM378  FLJ13072  5'  AGCCTGAGGACACGGGT    89800       T  ATCCTT
                                ACCCGTGT CCT    GTT
                                |||||||| |||    |||
                                TGGGCACA GGA    CGA
                                    _  GTC___
GAM378  FLJ13158  3'  AGCAGGGATGTCAGGGT    46109    G  TTCC
                                ACCC TG   TATCCTTGTT
                                |||| ||   ||||||||||
                                TGGG AC   GTAGGGACGA
                                  _ T___
GAM378  FLJ13241  3'  TAGGGACATGGAGGCATGGGT  46968      TC  __    TTG
                                ACCCGTGT  CTA  TCCTTG
                                ||||||||  |||  ||||||
                                TGGGTACG  GGT  AGGGAT
                                    GA  AC
GAM378  FLJ13456  3'  AATAGGCCGGGCGCGG    65930       CTATC
                                CCGTGTTC    CTTGTT
                                ||||||||    ||||||
                                GGCGCGGG    GGATAA
                                    CC___
GAM378  FLJ13639  3'  CAGCAGGGATGGGGGT    45232   TT
                                G  CCTATCCTTGTTG
                                |  |||||||||||||
                                T  GGGTAGGGACGAC
                                 GG
GAM378  FLJ13639  3'  CAGCAGGGATGGGGGTCTAAC  45233   ___ TT
                                GT   G  CCTATCCTTGTTG
                                ||   |  |||||||||||||
                                CA   T  GGGTAGGGACGAC
                                 ATC GG
GAM378  FLJ13639  5'  CGGTGGGGCTAGGCGTGGG   45234     TT   T  TG
                                CCCGTG  CCTA CCT  TTG
                                ||||||  |||| |||  |||
                                GGGTGC  GGAT GGG  GGC
                                   __   C  GT
GAM378  FLJ13646  3'  TAACAGGGGTCCTCTATGGG  44728     TTCCT
                                CCCGTG    ATCCTTGTTG
                                ||||||    ||||||||||
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                                GGGTAT    TGGGGACAAT
                                   CTCC_
GAM378  FLJ13852  3'  CAGCGAGGCTGGGCGGCGGGT  43574      GTT   T
                                ACCCGT   CCTA CCTTGTTG
                                ||||||   |||| ||||||||
                                TGGGCG   GGGT GGAGCGAC
                                   GC_   C
GAM378  FLJ14249  3'  TAGCGAGGTGTCACATGGG   42408      TCCTAT
                                CCCGTGT    CCTTGTTG
                                |||||||    ||||||||
                                GGGTACA    GGAGCGAT
                                   CTGT__
GAM378  FLJ14249  3'  TAGCGAGGTGTCACATGGG   55215      TCCTAT
                                CCCGTGT    CCTTGTTG
                                |||||||    ||||||||
                                GGGTACA    GGAGCGAT
                                   CTGT__
GAM378  FLJ14486  5'  CAATGGAGCAGAGTATGGG   51395       CTA  _
                                CCCGTGTTC   TCC TTG
                                |||||||||   ||| |||
                                GGGTATGAG   AGG AAC
                                     ACG   T
GAM378  FLJ14547  3'  CAGCAGCCGCCGGGCACGG   51432       CTATCC
                                CCGTGTTC    TTGTTG
                                ||||||||    ||||||
                                GGCACGGG    GACGAC
                                   CCGCC_
GAM378  FLJ14547  3'  GGTTATGGGGGCGGGGT    51436    G      __
                                ACCC TGTTCCTAT  CC
                                |||| |||||||||  ||
                                TGGG GCGGGGGTA  GG
                                  _       TT
GAM378  FLJ14564  3'  GTGGGGGGTGGGTGCTGG   76505    T  T      GTTG
                                CCG GT CCTATCCTT
                                ||| || |||||||||
                                GGT CG GGGTGGGGG
                                  _ T       GTGG
GAM378  FLJ14594  3'  CGATGGGGGTGGGAGCCTG   51453   T       TG
                                CG GTTCCTATCCT  TTG
                                || ||||||||||  |||
                                GT CGAGGGTGGGG  AGC
                                 C         GT
GAM378  FLJ14596  3'  TGACAAGGGTGCTGGGAGGGT  51465    GTG   __
                                ACCC   TTCC  TATCCTTGTTG
                                ||||   ||||  ||||||||||
                                TGGG   AGGG  GTGGGAACAGT
                                  ___    TC
GAM378  FLJ14743  3'  CTCTGGGGTGGGGGTGGGGT   68063    G  TT     TGTTG
                                ACCC TG  CCTATCCT
                                |||| ||  ||||||||
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                                TGGG GT  GGGTGGGG
                                  _ GG       TCTCG
GAM378  FLJ14834  3'  TAATGAGGAAGAGTTATGGGT  51656       TTC  A    TG
                                ACCCGTG   CT TCCT  TTG
                                |||||||   || ||||  |||
                                TGGGTAT   GA AGGA  AAT
                                    TGA  _    GT
GAM378  FLJ14888  3'  TGGGTCTCATGGGAACACAGGT 51687     C        ____   TGTTG
                                ACC GTGTTCCTAT    CCT
                                ||| ||||||||||    |||
                                TGG CACAAGGGTA    GGG
                                  A        CTCT   T   G
GAM378  FLJ14917  5'  CGACGAGCAGTTGGGCACGGG  51696         CTATC
                                CCCGTGTTC    CTTGTTG
                                |||||||||    |||||||
                                GGGCACGGG    GAGCAGC
                                     TTGAC
GAM378  FLJ20208  3'  AGTTTGGGAACGGGGT      34741      G       TC
                                ACCC TGTTCCTA  CT
                                |||| ||||||||  ||
                                TGGG GCAAGGGT  GA
                                  _       TT
GAM378  FLJ20232  3'  TAACAAGGATTTCTTATGG    38675      TTCCT
                                CCGTG    ATCCTTGTTG
                                |||||    ||||||||||
                                GGTAT    TAGGAACAAT
                                   TCTT_
GAM378  FLJ20257  5'  CGGCGGGACGGAGCGTGG    38995         TA    T
                                CCGTGTTCC  TCCT GTTG
                                |||||||||  |||| ||||
                                GGTGCGAGG  AGGG CGGC
                                     C_   _
GAM378  FLJ20257  3'  TGGCAGGGAGGCACGCAGGT   39001     C    T  TA
                                ACC GTGT CC  TCCTTGTTG
                                ||| |||| ||  |||||||||
                                TGG CGCA GG  AGGGACGGT
                                  A   C  __
GAM378  FLJ20374  5'  TGGCGAGGCTGAAGTCTGGGT  35081      TG_  CTAT
                                ACCCG   TTC    CCTTGTTG
                                |||||   |||    ||||||||
                                TGGGT   AAG    GGAGCGGT
                                   CTG   TC__
GAM378  FLJ20378  3'  CGACAGGTGTGGACGTGGGT   35090        T  T TC
                                ACCCGTGT CC A  CTTGTTG
                                |||||||| || |  |||||||
                                TGGGTGCA GG T  GGACAGC
                                     _ _ GT
GAM378  FLJ20378  3'  TGACAGATGTGGACGTGGGT   35098         C    CT
                                ACCCGTGTTC TATC  TGTTG
                                |||||||||| ||||  |||||
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                                TGGGTGCAGG GTAG  ACAGT
                                      T   __
GAM378  FLJ20378 3' TGACAGGTGTGGACGTGGGT  35099       T  T TC
                                ACCCGTGT CC A  CTTGTTG
                                |||||||| || |  |||||||
                                TGGGTGCA GG T  GGACAGT
                                    _ _ GT
GAM378  FLJ20378 3' TGACAGGTGTGGACGTGGGT  35100       T  T TC
                                ACCCGTGT CC A  CTTGTTG
                                |||||||| || |  |||||||
                                TGGGTGCA GG T  GGACAGT
                                    _ _ GT
GAM378  FLJ20378 3' TGACAGGTGTGGACGTGGGT  35101       T  T TC
                                ACCCGTGT CC A  CTTGTTG
                                |||||||| || |  |||||||
                                TGGGTGCA GG T  GGACAGT
                                    _ _ GT
GAM378  FLJ20378 3' TGACAGGTGTGGACGTGGGT  35102       T  T TC
                                ACCCGTGT CC A  CTTGTTG
                                |||||||| || |  |||||||
                                TGGGTGCA GG T  GGACAGT
                                    _ _ GT
GAM378  FLJ20401 3' TGGGACGGTGGGAGCATGGG  35126         ___   TGTTG
                                CCCGTGTTCCTA   TCCT
                                ||||||||||||   ||||
                                GGGTACGAGGGT   AGGG
                                      GGC   T   G
GAM378  FLJ20413 3' TGACAAACCAGGAGCACGAGT 35135   C       ATCC
                                AC CGTGTTCCT    TTGTTG
                                || |||||||||    ||||||
                                TG GCACGAGGA    AACAGT
                                 A       CCA_
GAM378  FLJ20420 3' TAACAAAGTAGGATGGGGT   35143     GTGT     CC
                                ACCC    TCCTAT  TTGTTG
                                ||||    ||||||  ||||||
                                TGGG    AGGATG  AACAAT
                                  GT__      A_
GAM378  FLJ20511 5' CAGTGAGGATTCACATTTGGGT 35320      __   TCCT    TG
                                ACCC  GTGT    ATCCT  TTG
                                ||||  ||||    |||||  |||
                                TGGG  TACA    TAGGA  GAC
                                  TT    CT__     GT
GAM378  FLJ20531 5' CAGTGGGGGTGAGGGCGCGTGG 35355    _      C     TG
                                CC CGTGTTC TATCCT  TTG
                                || ||||||| ||||||  |||
                                GG GCGCGGG GTGGGG  GAC
                                 T      A     GT
GAM378  FLJ20568 3' GGGAGGGGTGGGAGCATGGG  35417             GTTG
                                CCCGTGTTCCTATCCTT
                                |||||||||||||||||
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                                GGGTACGAGGGTGGGGA
                                     GGGT
GAM378  FLJ20644  5' TGTAGGGGTGGAGCAGG    35493   G    T     TT
                                CC TGTTCC ATCCTTG  G
                                || |||||| |||||||  |
                                GG ACGAGG TGGGGAT  T
                                 _    _      GG
GAM378  FLJ20701  3' TGTGAGGAGGGTGGGAGTGTGG 35591    TG        G TG
                                CCG  TTCCTATCCTT T
                                |||  |||||||||||  |
                                GGT  GAGGGTGGGAG A
                                  GT         G GTGTC
GAM378  FLJ21162  3' CAACAGGCAACGAGGGAGCGTG 45893         A ____
          G                      CCGTGTTCCT TC    CTTGTTG
                                ||||||||||  ||    |||||||
                                GGTGCGAGGG AG    GGACAAC
                                      _  CAAC
GAM378  FLJ21324  5' CAGTGAGTCAGACACGGGT   91193        CCTATC  TG
                                ACCCGTGTT     CT  TTG
                                |||||||||     ||  |||
                                TGGGCACAG     GA  GAC
                                     ACT___  GT
GAM378  FLJ21432  3' CAGTAGGTGTTTGGGAATATGG 44632          TC__
          G                      CCCGTGTTCCTA    CTTGTTG
                                ||||||||||||    |||||||
                                GGGTATAAGGGT    GGATGAC
                                      TTGT
GAM378  FLJ21870  3' TGACGGGGAAAGCGCCGCGGGT 43466       TTC  A
                                ACCCGTG   CT TCCTTGTTG
                                |||||||   || |||||||||
                                TGGGCGC   GA AGGGGCAGT
                                    CGC  A
GAM378  FLJ21870  5' TGGCGGGGGAGCAGCGCGG   43467       C  A
                                CCGTGTT CT TCCTTGTTG
                                ||||||| || |||||||||
                                GGCGCGA GA GGGGGCGGT
                                    C  _
GAM378  FLJ21870  3' TTGTGGTGGGAGCCCTGGACGA 43470  _  _____      CTTGTTG
          GG                     CGT    GTTCCTATC
                                 |||    |||||||||
                                 GCA    CGAGGGTGG
                                A  GGTCC       T  GTTG
GAM378  FLJ21877  3' TGGGGGATTGGGATGGGGGT  41944     G    T    GTTG
                                ACCC TGTTCC ATCCTT
                                |||| |||||| ||||||
                                TGGG GTAGGG TAGGGG
                                  G    T    GT  G
GAM378  FLJ21916  3' CAGTGAGGCCCTGGGTGGGT  43641     TGTT   T__  TG
                                ACCCG   CCTA   CCT  TTG
                                |||||   ||||   |||  |||
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                                TGGGT   GGGT  GGA  GAC
                                  _____   CCC   GT
GAM378  FLJ21977  3' CAGTGGGGGTAGGGCAAGG   49882   G  T     TG
                                CC TGT CCTATCCT  TTG
                                || ||| ||||||||  |||
                                GG ACG GGATGGGG  GAC
                                 A  _      GT
GAM378  FLJ22160  3' CAACATAAGGAGCGTGGG    44730         ATCCT
                                CCCGTGTTCCT    TGTTG
                                ||||||||||    |||||
                                GGGTGCGAGGA    ACAAC
                                      AT___
GAM378  FLJ22167  5' CAGTAATTGGGGCATGGG    44567         T  CC
                                CCCGTGTTCC AT  TTG
                                |||||||||| ||  |||
                                GGGTACGGGG TA  GAC
                                      T  AT
GAM378  FLJ22362  3' CAACTGGGGATAGGGATGGGGT 43070     G         _
                                ACCC TGTTCCTATCCTT GTTG
                                |||| |||||||||||| ||||
                                TGGG GTAGGGATAGGGG CAAC
                                  _          T
GAM378  FLJ22378  3' CAGTGGGGAGGACGAGGATGTG 46895     TG  CTA___   TG
           GG                   CCCG  TTC     TCCT  TTG
                                ||||  |||     ||||  |||
                                GGGT  AGG     AGGG  GAC
                                  GT   AGCAGG   GT
GAM378  FLJ22378  3' CAGTGGGGGTGGGGCTGGG   46896     T  T      TG
                                CCCG GT CCTATCCT  TTG
                                |||| || ||||||||  |||
                                GGGT CG GGGTGGGG  GAC
                                  _ _      GT
GAM378  FLJ22378  3' TGGCAGAGATGGGGCACGGG   46911       T     C
                                CCCGTGT CCTATC TTGTTG
                                ||||||| |||||| ||||||
                                GGGCACG GGGTAG GACGGT
                                   _     A
GAM378  FLJ22578  5' CAGCAAGTCCAGCGCGGG    45873        CCTATC
                                CCCGTGTT     CTTGTTG
                                ||||||||     |||||||
                                GGGCGCGA     GAACGAC
                                     CCT___
GAM378  FLJ22593  3' TAGCAGGGGTGGGCACACGGGT 45228         T
                                ACCCGTGT CCTATCCTTGTTG
                                |||||||| ||||||||||||
                                TGGGCACA GGGTGGGGACGAT
                                     C
GAM378  FLJ22693  5' GGCGAGGGCGCACAGGT     42761     C   TCCTA
                                ACC GTGT    TCCTTGTT
                                ||| ||||    ||||||||
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                              TGG CACG    GGGAGCGG
                                A   C____
GAM378  FLJ22724  3' CAACAAGAAGGGAATGCAGGT  44563    C      ATC
                              ACC GTGTTCCT   CTTGTTG
                              ||| ||||||||   |||||||
                              TGG CGTAAGGG   GAACAAC
                                A       AA_
GAM378  FLJ22833  5' GGTTGGGAGCGGGGT      43108     G      T
                              ACCC TGTTCCTA CC
                              |||| |||||||| ||
                              TGGG GCGAGGGT GG
                                _       T
GAM378  FLJ22969  3' TGACAGGCTCAGCATGGG    68666       CCTATC
                              CCCGTGTT     CTTGTTG
                              ||||||||     |||||||
                              GGGTACGA     GGACAGT
                                   CTC___
GAM378  FLJ23306  5' CAGTGGGGCACAGGTTGGGT  44556     TGTT  AT_  TG
                              ACCCG   CCT   CCT  TTG
                              |||||   |||   |||  |||
                              TGGGT   GGA   GGG  GAC
                                 T___   CAC   GT
GAM378  FLJ23436  3' CAGCAGGGGTGGGAGGTGTGGG 45141     TG _
                              CCCG  T TCCTATCCTTGTTG
                              ||||  | ||||||||||||||
                              GGGT  G AGGGTGGGGACGAC
                                GT G
GAM378  FLJ23447  3' GATGAGGAGGCTGGGT     45712      T  CCTA   TG
                              ACCCG GTT    TCCT  TT
                              ||||| |||    ||||  ||
                              TGGGT CGG    AGGA  AG
                                _  _____   GT
GAM378  FLJ23510  3' GGGTTGAGAACATGGGT     45287        CT_
                              ACCCGTGTTC   ATCC
                              ||||||||||   ||||
                              TGGGTACAAG   TGGG
                                    AGT
GAM378  FLJ23594  3' GGTGGGGATGGCAGGT     45508     C  _
                              ACC GT GTTCCTATC
                              ||| || |||||||||
                              TGG CG TAGGGGTGG
                                A  G
GAM378  FLJ25416  5' CGGCGGAAAAGGACGCGGG   58806       CTA   TT
                              CCCGTGTTC   TCC  GTTG
                              |||||||||   |||  ||||
                              GGGCGCAGG   AGG  CGGC
                                    AAA   __
GAM378  FLJ31168  3' GGACCTGGGATGGGAGTGGGGT 58505     G GT       T_  G
                              ACCC T  TCCTATCCT  GTT
                              |||| |  |||||||||  |||
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                                TGGG G  AGGGTAGGG  CAG
                                  _ TG       TC   GT
GAM378  FLJ31762  3'  GGCGGGGGTCGGGGGT     58142     GTGTT  T
                                ACCC    CC ATCCTTGTT
                                ||||    || |||||||||
                                TGGG    GG TGGGGGCGG
                                  _____  C
GAM378  FLJ31978  3'  CGACAATGGGGAACGCGGTGT  58349    _       ATCC
                                AC CCGTGTTCCT    TTGTTG
                                || ||||||||||   ||||||
                                TG GGCGCAAGGG    AACAGC
                                 T        GT__
GAM378  FLJ32356  3'  AGTGACTGGGGACACAGGT   58358    C       _ _
                                ACC GTGTTCCTA TC CT
                                ||| |||||||| || ||
                                TGG CACAGGGGT AG GA
                                  A        C  T
GAM378  FLJ32356  3'  TGAGTGGTGTGGGTGTGGGT   58369      TG   C   _
                                ACCCG  TTC TATC CTTG
                                |||||  ||| |||| ||||
                                TGGGT  GGG GTGG GAGT
                                   GT   T    T
GAM378  FLJ32752  5'  TGGGGAATGGGGATCATGGGT  58336       _     _    TTG
                                ACCCGTG TTCCTAT CCTTG
                                ||||||| ||||||| |||||
                                TGGGTAC AGGGGTA GGGGT
                                    T      A
GAM378  FLJ32783  3'  CAGCAAGGAGCTCAGTGTGG   58641    TG  CCTA
                                CCG  TT    TCCTTGTTG
                                |||  ||    |||||||||
                                GGT  GA    AGGAACGAC
                                  GT  CTCG
GAM378  FUK       3'  TGAGCGTGGGAGTGAGGGT    58977     G GT     C
                                ACCC T  TCCTAT CTTG
                                |||| |  |||||| ||||
                                TGGG G  AGGGTG GAGT
                                  A TG     C
GAM378  GAPCENA   3'  TAGTGGGGGGTGGGGCAAGGG   24162     G   T      TG
                                CCC TGT CCTATCCT  TTG
                                ||| ||| ||||||||  |||
                                GGG ACG GGGTGGGG  GAT
                                  A  _       GT
GAM378  GMPPB     5'  TAGTGGGGGGGCTATGGGACGCG 95752         TA___    TG
            G                    CCGTGTTCC     TCCT  TTG
                                |||||||||     ||||  |||
                                GGCGCAGGG     GGGG  GAT
                                     TATCG    GT
GAM378  GOLGA1    5'  CGGTGGGGGGTTGGTGACGCGGG 9090         _ T     TG
                                CCCGTGTT CC ATCCT  TTG
                                |||||||| || |||||  |||
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                                GGGCGCAG GG TGGGG  GGC
                                     T T    GT
GAM378  GRASP1   3'  GGGATTGGGGATGCTGGGT   39302     _       _
                                ACCC GTGTTCCTA TCCT
                                |||| ||||||||| ||||
                                TGGG CGTAGGGGT AGGG
                                  T       T
GAM378  GRIN3A   3'  CAGCAAGGGAAAGGAATATGGG 55967          A_
           T                     ACCCGTGTTCCT  TCCTTGTTG
                                ||||||||||||  |||||||||
                                TGGGTATAAGGA  GGGAACGAC
                                       AA
GAM378  HAPIP    3'  TGGCAGGGCTGGTGTGGG    14160     TGTT  TAT
                                CCCG   CC   CCTTGTTG
                                ||||   ||   ||||||||
                                GGGT   GG   GGGACGGT
                                  GT__  TC_
GAM378  HEMK     3'  AGCACTGGGGCAAGGGT    32425     G     TATCCT
                                ACCC TGTTCC     TGTT
                                |||| ||||||     ||||
                                TGGG ACGGGG     ACGA
                                  A     TC____
GAM378  HNK-1ST  3'  GCCCAGGAATGGGGGCGCTGGT 16770     C        C    TTG
                                ACC GTGTTCCTAT CTTG
                                ||| |||||||||| ||||
                                TGG CGCGGGGGTA GGAC
                                  T        A    CCGG
GAM378  HPCAL4   3'  AGCAAGGCCACTGGGT     32729     _   TTCCTAT
                                ACCC GTG      CCTTGTT
                                |||| |||      |||||||
                                TGGG CAC      GGAACGA
                                  T  C_______
GAM378  HPIP     3'  TAGCAAATTGAGTGTGGGT   40051      TG   CTATCC
                                ACCCG  TTC     TTGTTG
                                |||||  |||     ||||||
                                TGGGT  GAG     AACGAT
                                   GT   TTA___
GAM378  HS6ST    3'  GGGGTGGAGACGTGGGT     62030        TC
                                ACCCGTGT  CTATCCT
                                ||||||||  |||||||
                                TGGGTGCA  GGTGGGG
                                     GA
GAM378  HSA277841 3'  TGCTGGGGTGGGATTATGGGT  37659        T       T  TG
                                ACCCGTG TCCTATCCT GT
                                ||||||| ||||||||| ||
                                TGGGTAT AGGGTGGGG CG
                                     T       T  T
GAM378  HSJ1     3'  GGGTGGGGGCCGGGT      22135       T
                                ACCCG GTTCCTATCC
                                ||||| ||||||||||
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                                TGGGC CGGGGGTGGG
                                     _
GAM378  HSPBP1   3'  GGGAGGAGGGGCACGGGT    24363          A_
                                ACCCGTGTTCCT  TCCT
                                ||||||||||||  ||||
                                TGGGCACGGGGA  AGGG
                                      GG
GAM378  HSPC156  5'  CAGCAGGAGCCGGCGCGGG   26354        CCTA   T
                                CCCGTGTT   TCCT GTTG
                                ||||||||   |||| ||||
                                GGGCGCGG   AGGA CGAC
                                    CCG_   _
GAM378  HSPC251  3'  CAGCAGGAGGGGGGAACATGG  33248         AT _
                                CCGTGTTCCT  C CTTGTTG
                                ||||||||||  | |||||||
                                GGTACAAGGG  G GGACGAC
                                      GG A
GAM378  HT002    5'  CGAGCTGGGGGTGTGGG     25936     TG     TC
                                CCCG  TTCCTA  CTTG
                                ||||  ||||||  ||||
                                GGGT  GGGGGT  GAGC
                                  GT     C_
GAM378  HT002    3'  TGGCGAGGAAACAGTACAGGGT 25948      G   TCCTA_
                                ACCC TGT     TCCTTGTTG
                                |||| |||     |||||||||
                                TGGG ACA     AGGAGCGGT
                                  _  TGACAA
GAM378  HTCD37   3'  TAGCACGAATAGGGGTGTGG   67679     TG      CCT
                                CCG  TTCCTAT   TGTTG
                                |||  |||||||   |||||
                                GGT  GGGGATA   ACGAT
                                  GT      AGC
GAM378  IL-17RE  3'  CAGTGGGGGTTGGGGGTGGGGT 58289      G  TT   _   TG
                                ACCC TG  CCTA TCCT  TTG
                                |||| ||  |||| ||||  |||
                                TGGG GT  GGGT GGGG  GAC
                                  _ GG   T   GT
GAM378  IL18BP   3'  CGGCAGCATCGGGGACACAGGT 19107     C       ATCC
                                ACC GTGTTCCT    TTGTTG
                                ||| ||||||||    ||||||
                                TGG CACAGGGG    GACGGC
                                  A       CTAC
GAM378  ING1-like 3'  TAACAGGTAGTTTGGGGACATG 54160    C        TC___
            CGT                   C CGTGTTCCTA     CTTGTTG
                                | ||||||||||    |||||||
                                G GTACAGGGGT    GGACAAT
                                 C         TTGAT
GAM378  IR1899308 3'  CGACGGGGGCATTCCTGCGGGT 37908       GTTCCTA
                                ACCCGT      TCCTTGTTG
                                ||||||      |||||||||
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                                TGGGCG      GGGGGCAGC
                                   TCCTTAC
GAM378  IRX1     5' CGGCGGGGCAGGCGCGG     85937      TT   AT
                                CCGTG  CCT  CCTTGTTG
                                |||||  |||  ||||||||
                                GGCGC  GGA  GGGGCGGC
                                  __   C_
GAM378  JM5      5' CGACAGCTGGGGCCCGGGT    22990      T    TATCC
                                ACCCG GTTCC    TTGTTG
                                ||||| |||||    ||||||
                                TGGGC CGGGG    GACAGC
                                  C    TC___
GAM378  KCNT1    3' CGACGAGGGGCTCTCCGTGGT  61830     _  TGTTCCTA
                                ACC CG       TCCTTGTTG
                                ||| ||       |||||||||
                                TGG GC       GGGAGCAGC
                                 T  CTCTCG__
GAM378  KIAA0062 3' CAGTGAGGCAGGGACAGGGGT  70236     G      AT   TG
                                ACCC TGTTCCT  CCT  TTG
                                |||| |||||||  |||  |||
                                TGGG ACAGGGA  GGA  GAC
                                  G      C_   GT
GAM378  KIAA0169 3' TGGCAGGGGTGCTGCTGG    72821     T  TCC
                                CCG GT   TATCCTTGTTG
                                ||| ||   ||||||||||
                                GGT CG   GTGGGGACGGT
                                 _  TC_
GAM378  KIAA0170 3' CAACTTGTCCTGGAACATGGGT 27673          TATCCTT
                                ACCCGTGTTCC      GTTG
                                ||||||||||       ||||
                                TGGGTACAAGG      CAAC
                                      TCCTGTT
GAM378  KIAA0194 5' CGACAGCGGGGAGCGCGAGT   65985    C       ATCC
                                AC CGTGTTCCT    TTGTTG
                                || |||||||||    ||||||
                                TG GCGCGAGGG    GACAGC
                                 A        GC__
GAM378  KIAA0202 3' CAATAAGGATTGTGTGTAGGT  64368     C TG TCCT
                                ACC G  T    ATCCTTGTTG
                                ||| |  |    ||||||||||
                                TGG T  G    TAGGAATAAC
                                 A GT TGT_
GAM378  KIAA0226 3' TAACATAAAAGGAGTGCGAGT  63523    C  TG    ATCCT
                                AC CG  TTCCT    TGTTG
                                || ||  |||||    |||||
                                TG GC  GAGGA    ACAAT
                                 A  GT    AAAT_
GAM378  KIAA0227 5' CAGCGGGGAGAATGGGAGTGCG 60696      TG     ___
           GG                    CCCG  TTCCTA   TCCTTGTTG
                                ||||  ||||||   |||||||||
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                                GGGC  GAGGGT   AGGGGCGAC
                                  GT     AAG
GAM378  KIAA0258 3' CAATAGGGGGCGGATGTGAGT  28808    C  TG   CTA
                                AC CG  TTC   TCCTTGTTG
                                || ||  |||   |||||||||
                                TG GT  AGG   GGGGATAAC
                                 A  GT   CG_
GAM378  KIAA0258 3' CAGTGGGGATTGGTGCGTG   28811      T  T    TG
                                CGTGT CC ATCCT  TTG
                                ||||| || |||||  |||
                                GTGCG GG TAGGG  GAC
                                   T  T    GT
GAM378  KIAA0258 3' GGGTCCTGGGGGCGCGG     28820          T__
                                CCGTGTTCCTA   CCT
                                ||||||||||   |||
                                GGCGCGGGGGT   GGG
                                      CCT
GAM378  KIAA0266 3' CGACAGTTAAGGGCTGGGT   41330      T  T   ATCC
                                ACCCG GT CCT    TTGTTG
                                ||||| || |||    ||||||
                                TGGGT CG GGA    GACAGC
                                  _ _   ATT_
GAM378  KIAA0275 3' CAGCAGGCAAGGAGCCTGGGT  28673      T     ATC
                                ACCCG GTTCCT   CTTGTTG
                                ||||| ||||||   |||||||
                                TGGGT CGAGGA   GGACGAC
                                   C     AC_
GAM378  KIAA0275 3' GGGGTGGGGGTGGGGGT     28684     G  TT
                                ACCC TG  CCTATCCT
                                ||||  ||  ||||||||
                                TGGG GT  GGGTGGGG
                                  G  GG
GAM378  KIAA0284 3' TGGTGGGGGTGGACGTGGG   63120       T  T    TG
                                CCCGTGT CC ATCCT  TTG
                                ||||||| || |||||  |||
                                GGGTGCA GG TGGGG  GGT
                                    _ _    GT
GAM378  KIAA0296 3' CAGCACGTGGGGGCGTGG    28110          CCT
                                CCGTGTTCCTAT   TGTTG
                                ||||||||||||   |||||
                                GGTGCGGGGGTG   ACGAC
                                      C__
GAM378  KIAA0310 3' GATGAGGACCATGGGT      81678        T   _
                                ACCCGTG TCCT ATC
                                ||||||| |||| |||
                                TGGGTAC AGGA TAG
                                    C   G
GAM378  KIAA0321 3' GCGGTGGGGGGGTGGTGGGGGGA 62396    G_     ____   TG
           GCGGGT                GT  TTCCTAT    CCT  TTG   C
                                ||  |||||||    |||  |||   |
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                                CG  GGGGGTG   GGG  GGC   G
                                 AG      GTGG   GT
GAM378  KIAA0326  3'  GGTGTGGGAACTGGGT      64331       T      _
                                ACCCG GTTCCTAT CC
                                ||||| |||||||| ||
                                TGGGT CAAGGGTG GG
                                  _       T
GAM378  KIAA0352  3'  AGATTGGGGACAGGGT      29152      G       TC
                                ACCC TGTTCCTA  CT
                                |||| ||||||||  ||
                                TGGG ACAGGGGT  GA
                                  _       TA
GAM378  KIAA0415  3'  AGCAGTGGGTGTGGG       92572      TGTTCC    _
                                CCCG     TATCC TTGTT
                                ||||     ||||| |||||
                                GGGT     GTGGG GACGA
                                  _______    T
GAM378  KIAA0415  3'  TGGCCTGGATGGGGATGGGGT  92583      G         TT
                                ACCC TGTTCCTATCC  GTTG
                                |||| ||||||||||  ||||
                                TGGG GTAGGGGTAGG  CGGT
                                  _         TC
GAM378  KIAA0418  5'  CAGCGCTGGGTAGGGGCCGGGT 27552       T        T_
                                ACCCG GTTCCTATCC  TGTTG
                                ||||| ||||||||||  |||||
                                TGGGC CGGGGATGGG  GCGAC
                                  _         TC
GAM378  KIAA0441  5'  CAGCGGGCCCCGGCGTGGGT   28953         CCTATC
                                ACCCGTGTT     CTTGTTG
                                |||||||||     |||||||
                                TGGGTGCGG     GGGCGAC
                                     CCCC__
GAM378  KIAA0446  3'  TGGTGGGGATGGGACGG     68886     TGT       TG
                                CCG   TCCTATCCT  TTG
                                |||   |||||||||  |||
                                GGC   AGGGTAGGG  GGT
                                  ___       GT
GAM378  KIAA0450  5'  CGGCTCGTCATGGGGGCGCGG  27636           CCTT_
                                CCGTGTTCCTAT    GTTG
                                ||||||||||||    ||||
                                GGCGCGGGGGTA    CGGC
                                       CTGCT
GAM378  KIAA0472  3'  AAGGTGGGAGGCGGGT      71849       G     T
                                ACCCGT TTCCTA CCTT
                                |||||| |||||| ||||
                                TGGGCG GAGGGT GGAA
                                  _     _
GAM378  KIAA0493  5'  TGGTGAGGGTCGCTCGTGGGT  64283        TTCCT    TG
                                ACCCGTG    ATCCT  TTG
                                |||||||    |||||  |||
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                                TGGGTGC    TGGGA  GGT
                                    TCGC_    GT
GAM378  KIAA0513 3' GCAGGGGCTGGGGGTGGGGGT 28361     G  TT   _     TTG
                                ACCC TG  CCTA TCCTTG
                                |||| ||  |||| ||||||
                                TGGG GT  GGGT GGGGAC
                                  G  GG   C       GT
GAM378  KIAA0513 3' GTGGCGAGGGTGGGGGTGGGCA 28369   G  ____
           AGGG                  C TGT   TCCTATCCTTGTTG  T
                                | |||   ||||||||||||||  |
                                G ACG   GGGGTGGGAGCGGT  G
                                 A  GGTG
GAM378  KIAA0513 3' TGACATGAGGAATGCAGGT   28381     C      ATCCT
                                ACC GTGTTCCT    TGTTG
                                ||| ||||||||    |||||
                                TGG CGTAAGGA    ACAGT
                                  A       GT___
GAM378  KIAA0514 3' CAGCAGGGATGGGGCATCGGT  28080     C   T
                                ACC GTGT CCTATCCTTGTTG
                                ||| |||| ||||||||||||
                                TGG TACG GGGTAGGGACGAC
                                  C   _
GAM378  KIAA0523 3' CAGGGAGGTGGGAAGGTGGGT  67731      TG    T   G
                                ACCCG  TTCCTA CCTT TG
                                |||||  |||||| |||| |||
                                TGGGT  AAGGGT GGAG GAC
                                   GG     _   G
GAM378  KIAA0523 3' TAAGCATGGGGGCGTGGG    67742          C
                                CCCGTGTTCCTAT CTTG
                                |||||||||||| ||||
                                GGGTGCGGGGGTA GAAT
                                        C
GAM378  KIAA0537 3' GGGGGGGGGTGGGGGTGTGGGT 29255      TG        G  G
                                ACCCG  TTCCTATCCTT TT
                                |||||  |||||||||| ||
                                TGGGT  GGGGGTGGGGG GG
                                   GT         G  GT
GAM378  KIAA0542 3' CAGCGGGCGACAGTGCGGG   66082     TG  CCTA  _
                                CCCG  TT   TC CTTGTTG
                                ||||  ||   || |||||||
                                GGGC  GA   AG GGGCGAC
                                  GT  C___  C
GAM378  KIAA0542 5' TGCGGTGGGGATGCCCAGAGGG 66088    _____       CTTGTTG
           T                   CCC    GTGTTCCTATC
                               |||    ||||||||||
                               GGG    CGTAGGGGTGG
                                 AGACC         C   GTT
GAM378  KIAA0552 5' TGGTGGGAATAGGAGTAGGGT  28323     GTG     _  TGTTG
                                ACCC   TTCCTAT CCT
                                ||||   ||||||| |||
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                                TGGG  GAGGATA GGG
                                  AT_     A  TGGT
GAM378  KIAA0555  3'  CAACATCTATAGGGAACATGGG 28879          ATCCT_
                                CCCGTGTTCCT    TGTTG
                                ||||||||||    |||||
                                GGGTACAAGGG    ACAAC
                                      ATATCT
GAM378  KIAA0594  3'  AAGTGTGGGGGCAGGGGT   64889     G      TC
                                ACCC TGTTCCTA  CTT
                                |||| ||||||||  |||
                                TGGG ACGGGGGT  GAA
                                  G      GT
GAM378  KIAA0599  3'  AGCAGGGCTGCTGGGT     77166      T  TCCTAT
                                ACCCG GT     CCTTGTT
                                ||||| ||     |||||||
                                TGGGT CG     GGGACGA
                                  _ TC____
GAM378  KIAA0607  3'  GATGGGGGTTGGGGGGT    72570     GTGT  T    TG
                                ACCC   TCC ATCCT  TT
                                ||||   ||| |||||  ||
                                TGGG   GGG TGGGG  AG
                                  ____  T    GT
GAM378  KIAA0682  3'  CAAAGTGTGGGGATTACGGGT  29363       _    TC  GTTG
                                ACCCGTG TTCCTA  CTT
                                ||||||| ||||||  |||
                                TGGGCAT AGGGGT  GAA
                                    T    GT  AC
GAM378  KIAA0711  5'  CGGCGAGGAACAAGAGTGTGG  29516    TG  CTA_
                                CCG  TTC   TCCTTGTTG
                                |||  |||   |||||||||
                                GGT  GAG   AGGAGCGGC
                                 GT  AACA
GAM378  KIAA0711  3'  GGCAGGGGTTTGCGGG     29525      GTTCCT
                                CCCGT     ATCCTTGTT
                                |||||     |||||||||
                                GGGCG     TGGGGACGG
                                  TT____
GAM378  KIAA0711  3'  TGGTGGATGTTGGATGGGGGT  29529     G   C_   TTGTTG
                                ACCC TGTTC  TATCC
                                |||| |||||  |||||
                                TGGG GTAGG  GTAGG
                                  G    TT    TGGT
GAM378  KIAA0773  3'  GGTGCTGGGGGGCAGGGT    28059     G      T__
                                ACCC TGTTCCTA   CC
                                |||| ||||||||   ||
                                TGGG ACGGGGGT   GG
                                  _      CGT
GAM378  KIAA0788  5'  GGTAGGGAGGCGTGGT     71338    _  G
                                ACC CGT TTCCTATC
                                ||| ||| ||||||||
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                                TGG GCG AGGGATGG
                                  T  G
GAM378  KIAA0790 5' AGCGCGGGGGCGCGG      68693         ATCCT
                                CCGTGTTCCT    TGTT
                                ||||||||||    ||||
                                GGCGCGGGGG    GCGA
                                     C____
GAM378  KIAA0792 3' CAGTAGGGGCGGGATGGGGGT 28104     G  T  AT
                                ACCC TGT CCT  CCTTGTTG
                                |||| ||| |||  ||||||||
                                TGGG GTA GGG  GGGATGAC
                                  G  _  CG
GAM378  KIAA0826 3' AGTATGTGGGATAAGGGT    82635     G    _  C
                                ACCC TGTTCC TAT CT
                                |||| |||||| ||| ||
                                TGGG ATAGGG GTA GA
                                  A    T  T
GAM378  KIAA0830 3' AGTAAGGATAGGTGGC      69693     _
                                GTT CCTATCCTTGTT
                                ||| ||||||||||||
                                CGG GGATAGGAATGA
                                  T
GAM378  KIAA0863 3' CAGTGAGTGTTCAGAGACGTGG 29875       TC __ TC  TG
          GT                    ACCCGTGT  CT  A  CT  TTG
                                ||||||||  ||  |  ||  |||
                                TGGGTGCA  GA  T  GA  GAC
                                    GA  CT GT  GT
GAM378  KIAA0863 3' CAGTGAGTGTTCAGAGACGTGG 95244       TC __ TC  TG
          GT                    ACCCGTGT  CT  A  CT  TTG
                                ||||||||  ||  |  ||  |||
                                TGGGTGCA  GA  T  GA  GAC
                                    GA  CT GT  GT
GAM378  KIAA0907 3' TGGCGGGGATGGGGTTGGGGT 30183     GTGT
                                ACCC   TCCTATCCTTGTTG
                                ||||   ||||||||||||||
                                TGGG   GGGGTAGGGGCGGT
                                  GTT_
GAM378  KIAA0978 3' CAATGGGGTTGGGGAATAGGGT 70477     G     AT_  TG
                                ACCC TGTTCCT   CCT  TTG
                                |||| |||||||   |||  |||
                                TGGG ATAAGGG   GGG  AAC
                                  _     GTT   GT
GAM378  KIAA1036 3' AACAAGGAGGTGCAGG     29808    G  T  TA
                                CC TGT CC  TCCTTGTT
                                || ||| ||  ||||||||
                                GG ACG GG  AGGAACAA
                                  _  T  __
GAM378  KIAA1036 3' ATGGGGGGTGGGGGTGGGGT  29813     G  TT       GTTG
                                ACCC TG  CCTATCCTT
                                |||| ||  |||||||||
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                                TGGG GT  GGGTGGGGG
                                  _ GG       GTAG
GAM378  KIAA1036 3' CAGCGGGGGTGGCGCATGGAGT 29815   _    T  T
                                AC CCGTGT CC ATCCTTGTTG
                                || |||||| || ||||||||||
                                TG GGTACG GG TGGGGGCGAC
                                 A     C  _
GAM378  KIAA1036 3' GACTAATAGGGGCATGG     29821          CCTT
                                CCGTGTTCCTAT    GTT
                                ||||||||||||    |||
                                GGTACGGGGATA    CAG
                                       AT__
GAM378  KIAA1036 3' TGACAAGAGAGAAGAAACATGG 29830        C  A_  _
           GT                     ACCCGTGTT CT  TC CTTGTTG
                                |||||||||  ||  || |||||||
                                TGGGTACAA GA  AG GAACAGT
                                      A  AG  A
GAM378  KIAA1075 3' CGGCAGGGATGGGAGAGGGGT  61716     GTG
                                ACCC   TTCCTATCCTTGTTG
                                ||||   ||||||||||||||||
                                TGGG   GAGGGTAGGGACGGC
                                  GA_
GAM378  KIAA1078 3' TGCAGAAGGAATATGG      65124          A  CT   TG
                                CCGTGTTCCT TC  TGT
                                ||||||||||  ||  |||
                                GGTATAAGGA AG  ACG
                                      _  __   TA
GAM378  KIAA1126 3' CAAGGCGGGGCTGGGGACGCCG 71924     C        T      G
           GT                     ACC GTGTTCCTA CCTTGTT
                                ||| |||||||||  |||||||
                                TGG CGCAGGGGT GGGGCGG
                                  C        C       AACA
GAM378  KIAA1163 3' TGGCGGGGGATGAGCAGGGT   78907     G    CTA
                                ACCC TGTTC   TCCTTGTTG
                                |||| |||||   |||||||||
                                TGGG ACGAG   GGGGGCGGT
                                  _     TA_
GAM378  KIAA1165 5' CGACGGGGGTGGCCGTGGG    67405       TTC
                                CCCGTG   CTATCCTTGTTG
                                ||||||   ||||||||||||
                                GGGTGC   GGTGGGGGCAGC
                                   C__
GAM378  KIAA1181 3' CAGTGGCAGGGAGTGGGGGT   68373     G GT    AT  _
                                ACCC T  TCCT  CC TTG
                                |||| |  ||||  || |||
                                TGGG G  AGGG  GG GAC
                                  G TG    AC  T
GAM378  KIAA1193 3' CAGCAACCCCAGGCGTGGGT   67633       TT   ATCC
                                ACCCGTG  CCT    TTGTTG
                                |||||||  |||   ||||||
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                                TGGGTGC  GGA    AACGAC
                                   __   CCCC
GAM378  KIAA1193  3'  GGTGATGGGATATGGG      67646        T     _
                                CCCGTGT CCTATC CT
                                ||||||| |||||| ||
                                GGGTATA GGGTAG GG
                                   _     T
GAM378  KIAA1198  3'  CAGCAGGGATGGGTCAGG    63294    G  TT
                                CC TG  CCTATCCTTGTTG
                                || ||  |||||||||||||
                                GG AC  GGGTAGGGACGAC
                                 _ T_
GAM378  KIAA1198  3'  GGCACGATAGGGGTCGGGT    63326      T TT     CT    G
                                ACCCG G  CCTATC  TGTT
                                ||||| |  ||||||  ||||
                                TGGGC T  GGATAG  ACGG
                                   _ GG     C_    A
GAM378  KIAA1199  3'  CAGTGGGGGATGGCTGGGT    72512      TGTT  TA    TG
                                ACCCG    CC  TCCT  TTG
                                |||||    ||  ||||  |||
                                TGGGT    GG  GGGG  GAC
                                   C___  TA    GT
GAM378  KIAA1228  3'  CAGCGGTGGGGGATGGGGGT   65038      G      AT  TT
                                ACCC TGTTCCT  CC  GTTG
                                |||| |||||||  ||  ||||
                                TGGG GTAGGGG  GG  CGAC
                                  G      GT  __
GAM378  KIAA1265  3'  TGGCGGGGGTAGGTGAGGGT   70794      GTGTT
                                ACCC    CCTATCCTTGTTG
                                ||||    |||||||||||||
                                TGGG    GGATGGGGGCGGT
                                  AGT__
GAM378  KIAA1280  5'  GGCAAGACGGATGCGG      69726        CTATC
                                CCGTGTTC    CTTGTT
                                ||||||||    ||||||
                                GGCGTAGG    GAACGG
                                     CA___
GAM378  KIAA1318  3'  CAGGTGGTGGGGTTATGGGT   67306        TT     _
                                ACCCGTG  CCTATC CTTG
                                |||||||  |||||| ||||
                                TGGGTAT  GGGTGG GGAC
                                   TG     T
GAM378  KIAA1332  3'  CAATGAGGAAACAACATGTGT  71160    C     CCTA    TG
                                AC CGTGTT    TCCT  TTG
                                || ||||||    ||||  |||
                                TG GTACAA    AGGA  AAC
                                 T     CAA_    GT
GAM378  KIAA1376  3'  AATAAGGAAATGGGGGT     63620      G    CCTA
                                ACCC TGTT    TCCTTGTT
                                |||| ||||    ||||||||
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                                TGGG GTAA    AGGAATAA
                                  G   ____
GAM378  KIAA1388 3' TGGCAGGGGAGATGTGCAGGGT 93584     _ TG TC  A
                                ACCC G  T  CT TCCTTGTTG
                                |||| |  |  || |||||||||
                                TGGG C  G  GA GGGGACGGT
                                  A GT TA  _
GAM378  KIAA1416 5' TGGCGAGGATGGGAATAT    86465
                                GTGTTCCTATCCTTGTTG
                                ||||||||||||||||||
                                TATAAGGGTAGGAGCGGT

GAM378  KIAA1432 3' CAAGTCATTGGGGGTGTGGG  66747     TG     TC__   TTG
                                CCCG  TTCCTA   CTTG
                                ||||  ||||||   ||||
                                GGGT  GGGGGT   GAAC
                                  GT     TACT
GAM378  KIAA1434 3' GGGACTAGGATGTGGGT     69616      TG T   _
                                ACCCG  T CCTA TCCT
                                |||||  | |||| ||||
                                TGGGT  A GGAT AGGG
                                   GT _   C
GAM378  KIAA1443 3' TAGTGAGGGTGGACCAGGG   63841     G  T   T    TG
                                CCC TG TCC ATCCT  TTG
                                ||| || ||| |||||  |||
                                GGG AC AGG TGGGA  GAT
                                  _ C  _    GT
GAM378  KIAA1443 3' TGTGGCAGGGGGATATAGTGAG 63843   _____      AT_  TTGTTG
           GGT                    C    GTGTTCCT   CC
                                |    ||||||||   ||
                                G    TATAGGGG   GG
                                 AGTGA       GAC  T   GTT
GAM378  KIAA1456 3' TGGTGGGGGAGGGCACAGGT  67008    C    T   A    TG
                                ACC GTGT CCT TCCT  TTG
                                ||| |||| ||| ||||  |||
                                TGG CACG GGA GGGG  GGT
                                  A   _  _   GT
GAM378  KIAA1473 3' TAACAAGGCCGGGCACGG    70672        CTAT
                                CCGTGTTC   CCTTGTTG
                                ||||||||   ||||||||
                                GGCACGGG   GGAACAAT
                                     CC__
GAM378  KIAA1493 3' GCAACATGATGGGGACATGAGG 64162    _         CT
           T                    ACC CGTGTTCCTATC  TGTTG
                                ||| ||||||||||||  |||||
                                TGG GTACAGGGGTAG  ACAAC
                                  A          T_    GA
GAM378  KIAA1522 3' TGACAAGGATGGGAAGCCAC  64979    __
                                GTG  TTCCTATCCTTGTTG
                                |||  ||||||||||||||
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                                CAC  AAGGGTAGGAACAGT
                                  CG
GAM378  KIAA1530 3' CAGCAGAGTGGGCGTGGGT   67945       TT   TC  T
                                ACCCGTG  CCTA  CT GTTG
                                |||||||  ||||  || ||||
                                TGGGTGC  GGGT  GA CGAC
                                   __    GA  _
GAM378  KIAA1538 5' CACACGGGGGAGCGCAGGT   71532    C      AT  T   TG
                                ACC GTGTTCCT  CC TGT
                                ||| ||||||||  || |||
                                TGG CGCGAGGG  GG ACA
                                  A       __ C   CG
GAM378  KIAA1538 5' CGACGAGGGGCCAGCACGCGGG 71539       TCCTA_
                                CCCGTGT     TCCTTGTTG
                                |||||||     |||||||||
                                GGGCGCA     GGGAGCAGC
                                    CGACCG
GAM378  KIAA1538 3' TGATAGGGGTCGGATGGGT   71559      TGT   T
                                ACCCG   TCC ATCCTTGTTG
                                |||||   ||| ||||||||||
                                TGGGT   AGG TGGGGATAGT
                                   ____  C
GAM378  KIAA1553 3' CGGCGGGGCAGCCTGAGTGTGG 91917     TG   CTAT__
          G                      CCCG  TTC     CCTTGTTG
                                ||||  |||     ||||||||
                                GGGT  GAG     GGGGCGGC
                                  GT   TCCGAC
GAM378  KIAA1573 5' CAGTAAGGGTAGTGTGGG    62685     TG TCC
                                CCCG  T   TATCCTTGTTG
                                ||||  |   ||||||||||
                                GGGT  G   ATGGGAATGAC
                                  GT ____
GAM378  KIAA1580 5' TAGCGGGGGGAGGAATGGGT   69449      GT    AT
                                ACCCGT  TCCT  CCTTGTTG
                                ||||||  ||||  ||||||||
                                TGGGTA  AGGA  GGGGCGAT
                                   __    GG
GAM378  KIAA1596 3' TGGTAAGGTGTGGGTGATGGGT 70917      GTT    _    TT
                                ACCCGT   CCTAT CCTTG  G
                                ||||||   ||||| |||||  |
                                TGGGTA   GGGTG GGAAT  T
                                   GT_    T    GG
GAM378  KIAA1604 5' GGAGTGGGGGTGGCGGGT    64237       _ TT   _
                                ACCCGT G  CCTA TCC
                                |||||| |  |||| |||
                                TGGGCG T  GGGT AGG
                                   G GG   G
GAM378  KIAA1614 3' GGTGGGGAGTGTGCGGG     70122       ____
                                CCCGTG   TTCCTATC
                                ||||||   ||||||||
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                                GGGCGT   AGGGGTGG
                                   GTG
GAM378  KIAA1655 5' AGGTAGGAGCACAGGT     66589     C       T
                                ACC GTGTTCCTA CCT
                                ||| ||||||||| |||
                                TGG CACGAGGAT GGA
                                  A       _
GAM378  KIAA1656 5' TAGCAAGGCCGGGCGCGG    65806        CTAT
                                CCGTGTTC   CCTTGTTG
                                ||||||||   ||||||||
                                GGCGCGGG   GGAACGAT
                                     CC__
GAM378  KIAA1715 5' TGGCGGGGGTGGACGCCCGGG 68131     T  TC
                                CCCG GT  CTATCCTTGTTG
                                |||| ||  ||||||||||||
                                GGGC CG  GGTGGGGGCGGT
                                  C  CA
GAM378  KIAA1735 3' TGGCAGGGATCATTCTGGGT   87630      TGTTCCT
                                ACCCG      ATCCTTGTTG
                                |||||      ||||||||||
                                TGGGT      TAGGGACGGT
                                   CTTAC__
GAM378  KIAA1750 3' AGTGATAGAGTATGGG      68246         C   _
                                CCCGTGTTC TATC CT
                                ||||||||| |||| ||
                                GGGTATGAG ATAG GA
                                     _   T
GAM378  KIAA1750 3' TAGCAAGGGTGTGCTAGGT   68253    CGT  TCC
                                ACC   GT   TATCCTTGTTG
                                |||   ||   ||||||||||
                                TGG   CG   GTGGGAACGAT
                                  AT_  T__
GAM378  KIAA1751 3' CAGCAGGCCCAGCACGGG    71689        CCTATC
                                CCCGTGTT     CTTGTTG
                                ||||||||     |||||||
                                GGGCACGA     GGACGAC
                                     CCC___
GAM378  KIAA1754 3' TAACAGGGACAGATATGGG   63241        TC  A
                                CCCGTGT  CT TCCTTGTTG
                                |||||||  || |||||||||
                                GGGTATA  GA AGGGACAAT
                                   __  C
GAM378  KIAA1821 3' CAGCCCCTTAGGACGCGGGT  71779         T   TCCTT
                                ACCCGTGT CCTA    GTTG
                                |||||||| ||||    ||||
                                TGGGCGCA GGAT    CGAC
                                     _   TCCC_
GAM378  KIAA1822 3' AAGGTGGGAGCAGGGT      67558      G      T
                                ACCC TGTTCCTA CCTT
                                |||| |||||||| ||||
```

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                                TGGG ACGAGGGT GGAA
                                  _     _
GAM378  KIAA1822 3' CAGCCTCGGATGGGAGCACGGG 67562            TT_
             T                   ACCCGTGTTCCTATCC  GTTG
                                 ||||||||||||||||  ||||
                                 TGGGCACGAGGGTAGG  CGAC
                                       CTC
GAM378  KIAA1822 3' TAGAGTGAAGGGGGTGCGGGT 67574     TG   A _  GTTG
                                 ACCCG  TTCCT TC CTT
                                 |||||  ||||| || |||
                                 TGGGC  GGGGG AG GAG
                                    GT    A T  AT
GAM378  KIAA1858 3' TAATGGGGGTATTGGGTGGG  67137     TGT  __    TG
                                 CCCG  TCC  TATCCT  TTG
                                 ||||  |||  ||||||  |||
                                 GGGT  GGG  ATGGGG  AAT
                                   ___  TT    GT
GAM378  KIAA1863 3' CGATGGTGGGGTGTGGG    64869     TG T    C
                                 CCCG  T CCTATC TTG
                                 ||||  | ||||||  |||
                                 GGGT  G GGGTGG AGC
                                   GT _    T
GAM378  KIAA1871 3' TGACAAGTTTAAATGTGGG   61237     TG  CC  TC
                                 CCCG  TT  TA  CTTGTTG
                                 ||||  ||  ||  |||||||
                                 GGGT  AA  AT  GAACAGT
                                   GT  __  TT
GAM378  KIAA1877 3' CAGCAACTCTGGAATGTGGGT  66168     TG   TATCC
                                 ACCCG  TTCC    TTGTTG
                                 |||||  ||||    ||||||
                                 TGGGT  AAGG    AACGAC
                                    GT   TCTC_
GAM378  KIAA1904 3' GAGCGAGGGATGTGTGGGT   73486     TG TCCTA      G
                                 ACCCG  T    TCCTTGTT
                                 |||||  |    ||||||||
                                 TGGGT  G    GGGAGCGA
                                    GT TA___       GG
GAM378  KIAA1906 3' CAGCAAGGACCACAGAGCGTGG 73190        CTA__
                                 CCGTGTTC    TCCTTGTTG
                                 ||||||||    |||||||||
                                 GGTGCGAG    AGGAACGAC
                                      ACACC
GAM378  KIAA1940 3' CAGTGGGGGTGGCCACTTGGT  79977    C_  TTC     TG
                                 ACC  GTG   CTATCCT  TTG
                                 |||  |||   |||||||  |||
                                 TGG  CAC   GGTGGGG  GAC
                                   TT   C__      GT
GAM378  KIAA1940 3' CAGTGGGGTAGTGGGGGTGGGT 79978     GT TT    __   TG
                                 ACCC  G  CCTAT  CCT  TTG
                                 ||||  |  |||||  |||  |||
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                              TGGG T GGGTG GGG GAC
                                __ GG   AT  GT
GAM378  KIAA1940 3' TAGTGGGGGTGGGTTTGG   79990   TGTT    TG
                              CCG  CCTATCCT TTG
                              |||  |||||||| |||
                              GGT  GGGTGGGG GAT
                                TT__     GT
GAM378  KIAA1949 5' GGTGACAGGACAGGGT    92086    G  T  A _
                              ACCC TGT CCT TC CT
                              |||| ||| ||| || ||
                              TGGG ACA GGA AG GG
                                _  _  C  T
GAM378  KIAA1949 5' TGACAGGACAGGGTGGGGGT  92089    GTGT   A   T
                              ACCC   TCCT TCCT GTTG
                              ||||   |||| |||| ||||
                              TGGG   GGGA AGGA CAGT
                                GGT_   C   _
GAM378  KIAA1949 5' GGTGACAGGACAGGGT    97754    G  T  A _
                              ACCC TGT CCT TC CT
                              |||| ||| ||| || ||
                              TGGG ACA GGA AG GG
                                _  _  C  T
GAM378  KIAA1949 5' TGACAGGACAGGGTGGGGGT  97757    GTGT   A   T
                              ACCC   TCCT TCCT GTTG
                              ||||   |||| |||| ||||
                              TGGG   GGGA AGGA CAGT
                                GGT_   C   _
GAM378  KIAA1949 5' GGTGACAGGACAGGGT    97876    G  T  A _
                              ACCC TGT CCT TC CT
                              |||| ||| ||| || ||
                              TGGG ACA GGA AG GG
                                _  _  C  T
GAM378  KIAA1949 5' TGACAGGACAGGGTGGGGGT  97879    GTGT   A   T
                              ACCC   TCCT TCCT GTTG
                              ||||   |||| |||| ||||
                              TGGG   GGGA AGGA CAGT
                                GGT_   C   _
GAM378  KIAA1950 3' TAACGGGGAAGTGACGGGGT  92597    G  TC A
                              ACCC TGT  CT TCCTTGTTG
                              |||| |||  || |||||||||
                              TGGG GCA  GA AGGGGCAAT
                                _  GT _
GAM378  KIAA1957 3' TGACGAGGGTGGGCGCGG   75722    TT
                              CCGTG CCTATCCTTGTTG
                              |||||  ||||||||||||
                              GGCGC GGGTGGGAGCAGT
                                __
GAM378  KIAA1979 3' TGATAGGGATTTTTATGGGT  88294     TTCCT
                              ACCCGTG   ATCCTTGTTG
                              |||||||   ||||||||||
```

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                                TGGGTAT    TAGGGATAGT
                                   TTT__
GAM378  KIF13B   3'  TGGCGGACGGGCAGCGTGGGT  82827        _ TA  TTGTTG
                                ACCCGTGTT CC  TCC
                                ||||||||| ||  |||
                                TGGGTGCGA GG  AGG
                                     C  GC   CGGT
GAM378  KIF13B   3'  TGGCGGACGGGCAGCGTGGGT  30914        _ TA  TTGTTG
                                ACCCGTGTT CC  TCC
                                ||||||||| ||  |||
                                TGGGTGCGA GG  AGG
                                     C  GC   CGGT
GAM378  KLK6     3'  TGATGAGTGAGGACTTGGGT   10923      T  T   ATC  TG
                                ACCCG GT CCT   CT  TTG
                                ||||| || |||   ||  |||
                                TGGGT CA GGA   GA  AGT
                                   T  _   GT_  GT
GAM378  KPTN     5'  AGGTTGGGTAGTGCGGGT    73408      TG  _    T
                                ACCCG  TT CCTA CCT
                                |||||  || |||| |||
                                TGGGC  GA GGGT GGA
                                   GT  T    T
GAM378  LANO     3'  TGATGAGAATAGGAATGTGG   36626     TG      C  TG
                                CCG  TTCCTAT CT  TTG
                                |||  ||||||| ||  |||
                                GGT  AAGGATA GA  AGT
                                  GT      A  GT
GAM378  LGI3     3'  TGATAAGGATGAGAATGGT    57749     CGT    C
                                ACC   GTTC TATCCTTGTTG
                                |||   |||| ||||||||||
                                TGG   TAAG GTAGGAATAGT
                                  ___    A
GAM378  LGI4     3'  CAACGGGACTCTGGGCATGG   57764        CTA_   T
                                CCGTGTTC    TCCT GTTG
                                ||||||||    |||| ||||
                                GGTACGGG    AGGG CAAC
                                     TCTC   _
GAM378  LIMK2    3'  TAATAAATTGGGAATGGGT    33629      GT    TCC
                                ACCCGT  TCCTA   TTGTTG
                                ||||||  |||||   ||||||
                                TGGGTA  AGGGT   AATAAT
                                   __     TA_
GAM378  LIMK2    3'  TAATAAATTGGGAATGGGT    18729      GT    TCC
                                ACCCGT  TCCTA   TTGTTG
                                ||||||  |||||   ||||||
                                TGGGTA  AGGGT   AATAAT
                                   __     TA_
GAM378  LRRFIP1  3'  TAGGCTGATAGGAATGTGGGT  16418      TG      __   TTG
                                ACCCG  TTCCTATC  CTTG
                                |||||  ||||||||  ||||
```

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                                TGGGT  AAGGATAG  GGAT
                                  GT       TC
GAM378  LUC7L    3'  TGGTGGGGATGGGGCTGGG   35915     T  T      TG
                                CCCG GT CCTATCCT  TTG
                                |||| || ||||||||  |||
                                GGGT CG GGGTAGGG  GGT
                                  _ _       GT
GAM378  MACF1    3'  TAATAGGGTTTCTGCGCGG   23892      TCCTAT
                                CCGTGT     CCTTGTTG
                                ||||||     ||||||||
                                GGCGCG     GGGATAAT
                                   TCTTT_
GAM378  MACF1    3'  TAATAGGGTTTCTGCGCGG   52270      TCCTAT
                                CCGTGT     CCTTGTTG
                                ||||||     ||||||||
                                GGCGCG     GGGATAAT
                                   TCTTT_
GAM378  MADHIP   3'  GGAATAGGGTGGGAGTGGGGGT 16620      G GT       T   G
                                ACCC T  TCCTATCCT GTT
                                |||| |  ||||||||| |||
                                TGGG G  AGGGTGGGA TAA
                                  G TG        _   GGG
GAM378  MADHIP   3'  TAATGGGGTGGGGAATAGGGT  16624      GTG        TGTTG
                                ACCC   TTCCTATCCT
                                ||||   ||||||||||
                                TGGG   AGGGGTGGGG
                                  ATA         TAAT
GAM378  MADHIP   3'  GGAATAGGGTGGGAGTGGGGGT 23637      G GT       T   G
                                ACCC T  TCCTATCCT GTT
                                |||| |  ||||||||| |||
                                TGGG G  AGGGTGGGA TAA
                                  G TG        _   GGG
GAM378  MADHIP   3'  TAATGGGGTGGGGAATAGGGT  23640      GTG        TGTTG
                                ACCC   TTCCTATCCT
                                ||||   ||||||||||
                                TGGG   AGGGGTGGGG
                                  ATA         TAAT
GAM378  MARCKS   3'  GATAGGGGTCACAATGGG    9867      ___   _
                                CCC   GTG TTCCTATC
                                |||   ||| ||||||||
                                GGG   CAC GGGGATAG
                                  TAA   T
GAM378  MARKL1   3'  CGGTGGGGGTGGGAAGGTAAGG 48634    CG_ G        TG
                                CC   T TTCCTATCCT  TTG
                                ||   | ||||||||||  |||
                                GG   G AAGGGTGGGG  GGC
                                 AAT G         GT
GAM378  MFN2     3'  GTGGAAGGTGGGGACGTTGGT  29605     CG       T    GTTG
                                ACC  TGTTCCTA CCTT
                                |||  |||||||| ||||
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                                TGG  GCAGGGGT GGAA
                                  TT       _   GGTGG
GAM378  MGC10814 3' TAATGGGGCCGGGCACGG    51043        CTAT   TG
                                CCGTGTTC    CCT  TTG
                                ||||||||    |||  |||
                                GGCACGGG    GGG  AAT
                                    CC__    GT
GAM378  MGC10966 3' GGCCAGGGATGGGGGTGGGGGT 48895      G  TT        TTG
                                ACCC TG  CCTATCCTTG
                                |||| ||  ||||||||||
                                TGGG GT  GGGTAGGGAC
                                  G  GG        CGGA
GAM378  MGC10992 3' TGGCAGATGTGGGCGGGGGT   52628     G    C    CT
                                ACCC TGTTC TATC  TGTTG
                                |||| ||||| ||||  |||||
                                TGGG GCGGG GTAG  ACGGT
                                  G    T   __
GAM378  MGC11257 3' GGCGGTGGGGGGCCGGGT     50372      T       _
                                ACCCG GTTCCTATC CT
                                ||||| |||||||||  ||
                                TGGGC CGGGGGTGG GG
                                  _       C
GAM378  MGC1127  3' AACAGGTCTGCATGGGT     53213        TCCTAT   T
                                ACCCGTGT     CCT GTT
                                ||||||||     ||| |||
                                TGGGTACG     GGA CAA
                                    TCT___   _
GAM378  MGC1127  3' CAGCACTTGGGGGGGTGGGT   53214      TG   TATCCT
                                ACCCG  TTCC     TGTTG
                                |||||  ||||     |||||
                                TGGGT  GGGG     ACGAC
                                  GG   TTC___
GAM378  MGC11352 3' CAGCTGTACTGGTAGGGGGTGG 64800      TGT     CTT___
          GT                    ACCCG   TCCTATC     GTTG
                                |||||   |||||||     ||||
                                TGGGT   GGGATGG     CGAC
                                  GG_      TCATGT
GAM378  MGC12921 3' TGGCGAGGTGGCGGGCGTGGGT 63779          _  T
                                ACCCGTGTTC CTA CCTTGTTG
                                |||||||||| ||| ||||||||
                                TGGGTGCGGG GGT GGAGCGGT
                                    C  _
GAM378  MGC13272 3' CAGCGGGCAGGGACTGTGGGT  50384     GT_    AT  TT
                                ACCC   GTTCCT  CC  GTTG
                                ||||   ||||||  ||  ||||
                                TGGG   CAGGGA  GG  CGAC
                                  TGT     CG  __
GAM378  MGC14141 3' GGTGCTAGGGGCGTGGG     51934          T__
                                CCCGTGTTCCTA   CC
                                ||||||||||||   ||
```

```
                                GGGTGCGGGGAT  GG
                                      CGT
GAM378  MGC14161  5'  CAGCAGGAGCCTGGAGCGCGAG 51840   C      TA__   T
             T                  AC CGTGTTCC   TCCT GTTG
                                || ||||||||   |||| ||||
                                TG GCGCGAGG   AGGA CGAC
                                 A      TCCG  _
GAM378  MGC14258  3'  AGCGAGGAGGTGTGGG     51860     TG  CCTA
                                CCCG  TT   TCCTTGTT
                                ||||  ||   ||||||||
                                GGGT  GG   AGGAGCGA
                                  GT  ____
GAM378  MGC14289  3'  GGTTGGGGATGGGGT      54705     G      T
                                ACCC TGTTCCTA CC
                                |||| |||||||| ||
                                TGGG GTAGGGGT GG
                                  _      T
GAM378  MGC14859  3'  GCGGTGGGGATGGGGGGGGAGAG 61920    ______      TG
             CACGGGT               TGT    TCCTATCCT  TTG  C
                                |||    |||||||||  |||  |
                                ACG    GGGGTAGGG  GGC  G
                                 AGAGGG       GT
GAM378  MGC15416  5'  CGGTGGGGAGTGGGCGAGGGT  56540     G    CTA   TG
                                ACCC TGTTC   TCCT  TTG
                                |||| |||||  ||||  |||
                                TGGG GCGGG   AGGG  GGC
                                  A    TG_   GT
GAM378  MGC15634  5'  CAACAATAAGGGACATGAGT   51272    C      ATCC
                                AC CGTGTTCCT   TTGTTG
                                || |||||||||   ||||||
                                TG GTACAGGGA   AACAAC
                                 A       AT__
GAM378  MGC16279  5'  TAGCTGTCTAGGCGTGTGGGT  51889      TG T   TCCTT
                                ACCCG  T CCTA    GTTG
                                |||||  | ||||    ||||
                                TGGGT  G GGAT    CGAT
                                   GT C   CTGT_
GAM378  MGC16279  3'  TAGCTGTCTAGGCGTGTGGGT  62875      TG T   TCCTT
                                ACCCG  T CCTA    GTTG
                                |||||  | ||||    ||||
                                TGGGT  G GGAT    CGAT
                                   GT C   CTGT_
GAM378  MGC1842   3'  CAGCAGCTGTGGGGTGTGGG   65645     TG T    CC
                                CCCG  T CCTAT  TTGTTG
                                ||||  | |||||  ||||||
                                GGGT  G GGGTG  GACGAC
                                  GT _    TC
GAM378  MGC19764  3'  AGCAAGGCAGGGCGGGT     58662      GTT   AT
                                ACCCGT   CCT  CCTTGTT
                                ||||||   |||  |||||||
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                                TGGGCG  GGA  GGAACGA
                                   ___  C_
GAM378  MGC20258  3'  CAGCAGGGATGGGAGGGG   58148    GTG
                                CCC  TTCCTATCCTTGTTG
                                |||  ||||||||||||||
                                GGG  GAGGGTAGGGACGAC
                                  ___
GAM378  MGC21854  3'  TGATGAGTCCCAGGGGCACTGG 53492    C      ATC_  TG
          T                      ACC GTGTTCCT   CT  TTG
                                ||| ||||||||   ||  |||
                                TGG CACGGGGA   GA  AGT
                                  T      CCCT  GT
GAM378  MGC23937  5'  CAGCGGGGATAGCCCGGG   58954     T TTC
                                CCCG G  CTATCCTTGTTG
                                ||||  |  ||||||||||||
                                GGGC C  GATAGGGGCGAC
                                  C ___
GAM378  MGC2452   5'  GGGACTGGGAGCACGGG    50988          _
                                CCCGTGTTCCTA TCCT
                                |||||||||||| ||||
                                GGGCACGAGGGT AGGG
                                       C
GAM378  MGC2541   3'  TGATGAAAGTGGGGTGTGGG  54753     TG T    CC TG
                                CCCG  T CCTAT  T  TTG
                                ||||  | |||||  |  |||
                                GGGT  G GGGTG  A  AGT
                                  GT _    AA GT
GAM378  MGC2714   5'  GACGAGGATACCTGGG     50200     T  TCCT
                                CCCG GT   ATCCTTGTT
                                ||||  ||   |||||||||
                                GGGT CA   TAGGAGCAG
                                  C _____
GAM378  MGC2721   3'  TAGCGAGGGTTCTGGGGGTGGG 51223     GT TT  ___
          T                      ACCC  G  CCT   ATCCTTGTTG
                                ||||  |  |||  ||||||||||
                                TGGG  T  GGG   TGGGAGCGAT
                                  __ GG   TCT
GAM378  MGC2821   5'  CGGCGGGGCTCGCGCGGGT   43905       TCCTAT
                                ACCCGTGT    CCTTGTTG
                                ||||||||    ||||||||
                                TGGGCGCG    GGGGCGGC
                                    CTC___
GAM378  MGC29654  5'  CGGCGGCACGTGGCGCGGGT  66637       CCTAT  TT
                                ACCCGTGTT   CC  GTTG
                                |||||||||   ||  ||||
                                TGGGCGCGG   GG  CGGC
                                     TGCAC  __
GAM378  MGC29654  5'  TGGCGGGGTCTCGCGGCGCGGG 66639       CCTAT_
                                CCCGTGTT    CCTTGTTG
                                ||||||||    ||||||||
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                                GGGCGCGG     GGGGCGGT
                                     CGCTCT
GAM378  MGC29891  5'  AGAATGGGAGCATGAGT     58197    C         C
                                AC CGTGTTCCTAT CT
                                || |||||||||| ||
                                TG GTACGAGGGTA GA
                                 A          A
GAM378  MGC32043  3'  TAATGGGAAGGGGGCAGGGGT  58056     G      A    TGTTG
                                ACCC TGTTCCT TCCT
                                |||| ||||||| ||||
                                TGGG ACGGGGG AGGG
                                  G      A    TAAT
GAM378  MGC35570  3'  TGGTGGATAGCGGGGAGCATGG 58118          ____    TTGTTG
                                CCGTGTTCCT    ATCC
                                ||||||||||    ||||
                                GGTACGAGGG    TAGG
                                      GCGA    TGGT
GAM378  MGC4251   3'  TGGCAGGGCTGGGATGCGG    50462         TAT
                                CCGTGTTCC   CCTTGTTG
                                |||||||||   ||||||||
                                GGCGTAGGG   GGGACGGT
                                      TC_
GAM378  MGC4293   3'  AGGCCTGGGTAGGGACAGGGT  48521      G         TT   G
                                ACCC TGTTCCTATCC  GTT
                                |||| ||||||||||  |||
                                TGGG ACAGGGATGGG  CGG
                                  _         TC   AG
GAM378  MGC4365   5'  TGGAGTGGTGGGGGCCTGGGT  44274      T       _   GTTG
                                ACCCG GTTCCTATC CTT
                                ||||| ||||||||| |||
                                TGGGT CGGGGGTGG GAG
                                   C        T   GT
GAM378  MGC4737   5'  CAGCAAGTATAAGAATGCGGG  48845         C   C
                                CCCGTGTTC TAT CTTGTTG
                                ||||||||| ||| |||||||
                                GGGCGTAAG ATA GAACGAC
                                      A   T
GAM378  MGC4796   3'  TAGCAAGGGTCCTCCATGG    61496       TTCCT
                                CCGTG    ATCCTTGTTG
                                |||||    ||||||||||
                                GGTAC    TGGGAACGAT
                                   CTCC_
GAM378  MGC5508   3'  CAGTAGGGAGGGGCAGGGGT   44034      G     TA
                                ACCC TGTTCC  TCCTTGTTG
                                |||| ||||||  |||||||||
                                TGGG ACGGGG  AGGGATGAC
                                  G     __
GAM378  MGC5560   3'  TAATGAGGAAGTATGGCGTGGT 38786     _   GTTC  A    TG
                                ACC CGT    CT TCCT  TTG
                                ||| |||    || ||||  |||
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                                TGG GCG   GA AGGA  AAT
                                  T  GTAT  _   GT
GAM378  MGC5627  3'  CAGCAGGTGATGACGGGGGT  44047     G   CCT  _
                                ACCC TGTT  ATC CTTGTTG
                                |||| ||||  ||| |||||||
                                TGGG GCAG  TAG GGACGAC
                                  G   ___  T
GAM378  MGC5627  3'  TGACGGGGGTACCAGGGGT   44048     G  TTCC
                                ACCC TG   TATCCTTGTTG
                                |||| ||   ||||||||||
                                TGGG AC   ATGGGGGCAGT
                                  G  C___
GAM378  MIC2L1   3'  TAGTAAGGGTGGGGTGGC    48826    GT
                                GT  TCCTATCCTTGTTG
                                ||  ||||||||||||||
                                CG  GGGGTGGGAATGAT
                                 GT
GAM378  MKRN4    5'  CGGCAGGGACCGAGCGGGT   47741      GT  CTA
                                ACCCGT  TC  TCCTTGTTG
                                ||||||  ||  |||||||||
                                TGGGCG  AG  AGGGACGGC
                                   __  CC_
GAM378  MMD      3'  TGGCACTTGGGAGTGGGGT   59811     G GT    TCCT
                                ACCC T  TCCTA   TGTTG
                                |||| |  |||||   |||||
                                TGGG G  AGGGT   ACGGT
                                  _ TG    TC__
GAM378  MMPL1    3'  TGGCAAGGGGGAGACGGGT   14726      G   TAT
                                ACCCGT TTCC  CCTTGTTG
                                |||||| ||||  ||||||||
                                TGGGCA AGGG  GGAACGGT
                                   G   ___
GAM378  MOST2    5'  TAGCAAGGACTGGCCGGGT   39692     T TT  TA
                                ACCCG G  CC  TCCTTGTTG
                                ||||| |  ||  ||||||||||
                                TGGGC C  GG  AGGAACGAT
                                  _ __  TC
GAM378  MRPL1    5'  CGGCGGCCGTAAGGTGCATGGG 39591       T  _  CC
           T                    ACCCGTGT CCT AT  TTGTTG
                                |||||||| ||| ||  ||||||
                                TGGGTACG GGA TG  GGCGGC
                                    T   A  CC
GAM378  MYO18B   3'  TGATGGGGTGCAGATAGGGGT  50890     G   CC    TGTTG
                                ACCC TGTT  TATCCT
                                |||| ||||  ||||||
                                TGGG ATAG  GTGGGG
                                  G   AC     TAGT
GAM378  N4BP3    3'  CAGCCAGTGGGGAGTGGGT   66252     TG    ATC  T
                                ACCCG  TTCCT   CT GTTG
                                |||||  |||||   || ||||
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                                TGGGT  GAGGG   GA CGAC
                                  __    GT_  C    A
GAM378  N4BP3    3'  CAGTGGGGCCGTGGGCTGGGT  66255      T   CTAT   TG
                                ACCCG GTTC    CCT  TTG
                                ||||| ||||    |||  |||
                                TGGGT CGGG    GGG  GAC
                                  _   TGCC   GT
GAM378  NAG73    5'  TGGTAGGGGTTTTCCAGAGTGT 50807     TG   CT____     TT
           GGG                    CCG  TTC     ATCCTTG  G
                                |||  |||     |||||||  |
                                GGT  GAG     TGGGGAT  T
                                 GT   ACCTTT      GG
GAM378  NAP1L1   3'  CAGTGAGGGTGGATTATTGG  57618    C   T   T    TG
                                CC GTG TCC ATCCT  TTG
                                || ||| ||| |||||  |||
                                GG TAT AGG TGGGA  GAC
                                 T   T  _    GT
GAM378  NAT5     5'  CGGCAGGGCGGGCGCGGG    32252        CTAT
                                CCCGTGTTC   CCTTGTTG
                                |||||||||   ||||||||
                                GGGCGCGGG   GGGACGGC
                                     C___
GAM378  NEU4     3'  GGCAGGGTGGGGGGCAGGGT   54953     G         T   G
                                ACCC TGTTCCTATCCT GTT
                                |||| ||||||||||| |||
                                TGGG ACGGGGGTGGGA CGG
                                  _         _  G
GAM378  NFASC    3'  TAACAAGGGTACGATATGGG   70348       T C
                                CCCGTGT C TATCCTTGTTG
                                ||||||| | ||||||||||
                                GGGTATA G ATGGGAACAAT
                                    _ C
GAM378  NICN1    3'  CAACCGTGGTGGGGAGTGGGT  50289     GTG      CTT
                                ACCC   TTCCTATC   GTTG
                                ||||   ||||||||   ||||
                                TGGG   AGGGGTGG   CAAC
                                  TG_       TGC
GAM378  NIN283   3'  GGTGGTTCAGAGCCTGGGT   50075      T   _____
                                ACCCG GTTC    CTATC
                                ||||| ||||    |||||
                                TGGGT CGAG    GGTGG
                                  C    ACTT
GAM378  NKIR     3'  GGAAGTGGACGTGGGT      57356          _  A
                                ACCCGTGTTC CT TCC
                                |||||||||| || |||
                                TGGGTGCAGG GA AGG
                                      T  _
GAM378  NKX2C    3'  GGTAGGGACGGGGCGGGT    59221       ___
                                ACCCGT   GTTCCTATC
                                ||||||   |||||||||
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                                TGGGCG  CAGGGATGG
                                   GGG
GAM378  NOL4    5'  AGCGGCCGAGCGCGGG     13693        CTAT  TT
                                CCCGTGTTC   CC  GTT
                                |||||||||   ||  |||
                                GGGCGCGAG   GG  CGA
                                   CC__  __
GAM378  NP220   3'  TGATGGGGAAAGTATGATGGGT 27172      GTTC  A   TG
                                ACCCGT   CT TCCT  TTG
                                ||||||   || ||||  |||
                                TGGGTA   GA AGGG  AGT
                                   GTAT  A   GT
GAM378  NRM     3'  CAGCAAGGAAGAGTGGGGT   92024     G GT  CTA
                                ACCC T  TC   TCCTTGTTG
                                |||| |  ||   |||||||||
                                TGGG G  AG   AGGAACGAC
                                  _ TG  A__
GAM378  NRM     3'  CAGCAAGGAAGAGTGGGGT   97889     G GT  CTA
                                ACCC T  TC   TCCTTGTTG
                                |||| |  ||   |||||||||
                                TGGG G  AG   AGGAACGAC
                                  _ TG  A__
GAM378  NRM     3'  CAGCAAGGAAGAGTGGGGT   97763     G GT  CTA
                                ACCC T  TC   TCCTTGTTG
                                |||| |  ||   |||||||||
                                TGGG G  AG   AGGAACGAC
                                  _ TG  A__
GAM378  NSAP1   5'  CGGTGGGGCGGGGACGCGAGGT 21041     _       AT   TG
                                ACC CGTGTTCCT  CCT  TTG
                                ||| |||||||||  |||  |||
                                TGG GCGCAGGGG  GGG  GGC
                                  A       C_  GT
GAM378  NUDT3   3'  ATTGAGGGTGGGGGTTGGGT   21988      T TT        TTG
                                ACCCG G  CCTATCCTTG
                                |||||  |  ||||||||||
                                TGGGT T  GGGTGGGAGT
                                   _ GG        TAT
GAM378  NXPH3   3'  AGCAGCGGGCACGGGT      65748        TCCTAT  _
                                ACCCGTGT     CC TTGTT
                                ||||||||     || |||||
                                TGGGCACG     GG GACGA
                                     _______  C
GAM378  NXPH3   3'  CAATGAGGGTGTTCCTTGGTGT 65751    _  TGTTCC     TG
                                AC CCG     TATCCT  TTG
                                || |||     ||||||  |||
                                TG GGT     GTGGGA  AAC
                                 T  TCCTT_     GT
GAM378  OBTP    5'  GGGGTGGGGACCGGGT      34247      T
                                ACCCG GTTCCTATCCT
                                ||||| ||||||||||
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                                TGGGC CAGGGGTGGGG
                                  _
GAM378  OLIG1    3'  GCTGGGTTGGGACGTGGGT   95591          T   TT
                                ACCCGTGTTCC ATCC  GT
                                |||||||||| ||||  ||
                                TGGGTGCAGGG TGGG  CG
                                      T   T_
GAM378  ORCTL4   3'  AGTTTGGGGGCAGGGT     16649     G      TC
                                ACCC TGTTCCTA  CT
                                |||| ||||||||  ||
                                TGGG ACGGGGGT  GA
                                  _      TT
GAM378  ORMDL3   3'  TGGCAGGGGAGGGGTAGGGT   74312     G  TT   A
                                ACCC TG  CCT TCCTTGTTG
                                |||| ||  ||| |||||||||
                                TGGG AT  GGA GGGGACGGT
                                  _ GG  _
GAM378  P2RXL1   3'  CAGTGGGGTGGTGCAGGGT   18380     G   T  TAT   TG
                                ACCC TGT CC   CCT  TTG
                                |||| ||| ||   |||  |||
                                TGGG ACG GG   GGG  GAC
                                  _  T  T__   GT
GAM378  PACSIN2  3'  CGGCGGGGGTGGGGGGAACGTG 23340          ___
           GG                   CCCGTGTTCCT   ATCCTTGTTG
                                ||||||||||   ||||||||||
                                GGGTGCAAGGG   TGGGGGCGGC
                                      GGG
GAM378  PALM     3'  ACCTCGGATGGGAGCCTGGGT  10410      T       TTGTTG
                                ACCCG GTTCCTATCC
                                ||||| ||||||||||
                                TGGGT CGAGGGTAGG
                                   C        CTCCAC
GAM378  PARD6A   3'  TGGCAGGGACTTCACAGTGGG  33770     _  TCCTA
                                CCCG TGT    TCCTTGTTG
                                |||| |||    |||||||||
                                GGGT ACA    AGGGACGGT
                                  G  CTTC_
GAM378  PCANAP7  5'  CGGTGGGCCGAGGGCCGGGT   93365     T  T   ATC  TG
                                ACCCG GT CCT   CT  TTG
                                ||||| || |||   ||  |||
                                TGGGC CG GGA   GG  GGC
                                  _ _  GCC  GT
GAM378  PCDH10   5'  TGGTGGGGGAGGTGATTGGGT  40429     TGTT   A   TG
                                ACCCG   CCT TCCT  TTG
                                |||||   ||| ||||  |||
                                TGGGT   GGA GGGG  GGT
                                   TAGT  _   GT
GAM378  PCDH10   5'  TGGTGGGGGAGGTGATTGGGT  51997     TGTT   A   TG
                                ACCCG   CCT TCCT  TTG
                                |||||   ||| ||||  |||
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                                TGGGT   GGA GGGG  GGT
                                  TAGT  _   GT
GAM378  PCDH19   3'  CAGTAGGGATGGGGTTAGG   63700   GTGT
                                CC   TCCTATCCTTGTTG
                                ||   ||||||||||||||
                                GG   GGGGTAGGGATGAC
                                 ATT_
GAM378  PCDH19   3'  TAAGGCAGTAGGGATGGGGT  63708     G      __
                                ACCC TGTTCCTAT  CCTTG
                                |||| |||||||||  |||||
                                TGGG GTAGGGATG  GGAAT
                                  _       AC
GAM378  PDE11A   5'  TGGCGCTGAACTGGGAATACTG 33778    C      __ CT
           GT                    ACC GTGTTCCTA  TC  TGTTG
                                ||| |||||||||  ||  |||||
                                TGG CATAAGGGT  AG  GCGGT
                                  T       CA  TC
GAM378  PDE4DIP  3'  TGGCACTTGGGGACATGAGT  27691   C       TCCT
                                AC CGTGTTCCTA   TGTTG
                                || ||||||||||   |||||
                                TG GTACAGGGGT   ACGGT
                                 A        TC__
GAM378  PDE8B    5'  AGCGGTAGCAGCGCGGGT   67577        C   _
                                ACCCGTGTT CTATC CT
                                ||||||||| ||||| ||
                                TGGGCGCGA GATGG GA
                                     C   C
GAM378  PDEF     3'  CAACTGCCCCAGGGGGATATGG 24746          ATCCTT__
           GT                    ACCCGTGTTCCT      GTTG
                                ||||||||||||      ||||
                                TGGGTATAGGGG      CAAC
                                      GACCCCGT
GAM378  PEPP3    3'  GGTGTGGGGATCTGGGT    30042      T     _
                                ACCCG GTTCCTAT CC
                                ||||| ||||||| ||
                                TGGGT TAGGGGTG GG
                                  C       T
GAM378  PGCP     3'  GGTAGGGATTACAGTGGG    32326     _  ___
                                CCCG TGT   TCCTATC
                                |||| |||   |||||||
                                GGGT ACA   GGGATGG
                                  G   TTA
GAM378  PI4KII   3'  TGGCAGGCAAGAGTGTGGG   37349     TG   CTATC
                                CCCG  TTC    CTTGTTG
                                ||||  |||    |||||||
                                GGGT  GAG    GGACGGT
                                  GT   AAC__
GAM378  PIF1     3'  TGTGGTGGGGACTCAGGCTGGG 61023    _ ____       CTTGTTG
           T                     CCC GT    GTTCCTATC
                                ||| ||    |||||||||
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                                GGG CG    CAGGGGTGG
                                  T  GACT       T   GTT
GAM378  PINK1    3'  TGGTGAGGGTGGGAGTCAGG   50544    G  _       TG
                                CC TG TTCCTATCCT  TTG
                                || || ||||||||||  |||
                                GG AC GAGGGTGGGA  GGT
                                 _  T        GT
GAM378  PIP5K2A  5'  CGGCGGGCGCAGGATACGGG   17261       T   ATC
                                CCCGTGT CCT   CTTGTTG
                                ||||||| |||   |||||||
                                GGGCATA GGA   GGGCGGC
                                    _  CGC
GAM378  PKNOX2   3'  CAGCAACCATGGACATGGG    90875       T  TATCC
                                CCCGTGT CC    TTGTTG
                                ||||||| ||    ||||||
                                GGGTACA GG    AACGAC
                                    _  TACC_
GAM378  PLCL2    5'  GGCGGCGGGGACGCGGG     68136         AT  _
                                CCCGTGTTCCT  C CT
                                ||||||||||  | ||
                                GGGCGCAGGGG  G GG
                                      CG C
GAM378  PMX2B    3'  TAATAAGGTTCTCACGGG    14087       TTCCTAT
                                CCCGTG      CCTTGTTG
                                ||||||      ||||||||
                                GGGCAC      GGAATAAT
                                   TCTT___
GAM378  PNMA5    5'  CAGCAAGGAGGGTGCTGGGT   73593      T  T   A
                                ACCCG GT CCT TCCTTGTTG
                                ||||| || ||| |||||||||
                                TGGGT CG GGG AGGAACGAC
                                  _  T   _
GAM378  POLA2    3'  TGACAAGGTGAACAGTTGGGT  10676      __    CTAT
                                ACCCG  TGTTC   CCTTGTTG
                                |||||  |||||   ||||||||
                                TGGGT  ACAAG   GGAACAGT
                                   TG    T___
GAM378  POMT2    3'  CAGCGCAGGGGAGGATGGGT   25394      G   TAT  _
                                ACCCGT TTCC   CCT TGTTG
                                |||||| ||||   ||| |||||
                                TGGGTA GAGG   GGA GCGAC
                                   G    ___   C
GAM378  PORIMIN  3'  TGGCTGGGGTGGGGGCATTGGT 53609    C          T
                                ACC GTGTTCCTATCCT GTTG
                                ||| |||||||||||| ||||
                                TGG TACGGGGGTGGGG CGGT
                                  T          T
GAM378  PPFIA4   3'  AGGAATGGGTGTATGGGT    70319       TT    _
                                ACCCGTG  CCTAT CCT
                                |||||||  ||||| |||
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                                TGGGTAT  GGGTA GGA
                                   GT    A
GAM378  PPP1R16B  3'  TGGCAGGGGTGGATTCGGG   61392     TGT   T
                                CCCG   TCC ATCCTTGTTG
                                ||||   ||| ||||||||||
                                GGGC   AGG TGGGGACGGT
                                  TT_  _
GAM378  PPP1R16B  3'  TGTAGGGCTAGAGTTGGGT   61393     TGTTC   T    TT
                                ACCCG    CTA CCTTG  G
                                |||||    ||| |||||  |
                                TGGGT    GAT GGGAT  T
                                   TGA__   C    GG
GAM378  PRO1584   5'  GGTGGTGGGGGGGTGGGGT   37726     GTG      _
                                ACCC   TTCCTATC CT
                                ||||   |||||||| ||
                                TGGG   GGGGGTGG GG
                                  GTG       T
GAM378  PRO1584   5'  GTGGGGGGTGGGGTGGGGT   37727     GTGT       GTTG
                                ACCC    TCCTATCCTT
                                ||||    ||||||||||
                                TGGG    GGGGTGGGGG
                                  GT__        GTGG
GAM378  PRO2015   3'  AAGTGAGGGTAGGAGCTGGGT  37554      T        TG  G
                                ACCCG GTTCCTATCCT  TT
                                ||||| ||||||||||  ||
                                TGGGT CGAGGATGGGA  GA
                                  _         GT  AG
GAM378  PRO2389   3'  GTCTCTAGGGGAGGGGCATGGG 63738          A     TTG
          T                      ACCCGTGTTCCT TCCTTG
                                ||||||||||| ||||||
                                TGGGTACGGGGA GGGGAT
                                       _     CTCTGG
GAM378  QSCN6     3'  TGGCATGGGAAGGATGTGGGT  11042      TG T   A   T   TG
                                ACCCG  T CCT TCC TGT
                                |||||  | ||| ||| |||
                                TGGGT  A GGA GGG ACG
                                   GT _   A   T   GTG
GAM378  R32184_3  3'  CAGCAAGGAGAGGGGGTGGGGT 53063     G  TT   A_
                                ACCC TG  CCT  TCCTTGTTG
                                |||| ||  |||  |||||||||
                                TGGG GT  GGG  AGGAACGAC
                                  _ GG   AG
GAM378  R32184_3  3'  GGGCATAGGGACGTGGG     53068          _
                                CCCGTGTTCCTAT CCT
                                ||||||||||||| |||
                                GGGTGCAGGGATA GGG
                                         C
GAM378  Rab11-FIP3 3'  TGGTGGGGGGAAGGACGGGT   28128      TGT    A    TG
                                ACCCG   TCCT TCCT  TTG
                                |||||   |||| ||||  |||
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                                TGGGC  AGGA GGGG  GGT
                                  ___   A   GT
GAM378  RAB24    5'  AGCGGGGGCACACGGG     55386       TCCTA
                                CCCGTGT    TCCTTGTT
                                |||||||    ||||||||
                                GGGCACA    GGGGGCGA
                                   C____
GAM378  RAB33B   5'  GGCGGGGCGGGCGGGT     48499      GTT  TAT
                                ACCCGT  CC  CCTTGTT
                                ||||||  ||  |||||||
                                TGGGCG  GG  GGGGCGG
                                   ___ C__
GAM378  RAB3GAP  3'  CAGCGAGGATGGGCTTGAGC  66948    GTT__
                                GT    CCTATCCTTGTTG
                                ||    |||||||||||||
                                CG    GGGTAGGAGCGAC
                                 AGTTC
GAM378  RACGAP1  3'  AGTGATGGGAGTATGCGT    25194    C        _
                                AC CGTGTTCCTATC CT
                                || |||||||||||| ||
                                TG GTATGAGGGTAG GA
                                 C         T
GAM378  RAI      3'  CAGCAGTCTTGGGGTCTGGGT  21875      TGT    TCC
                                ACCCG  TCCTA  TTGTTG
                                |||||  |||||  ||||||
                                TGGGT  GGGGT  GACGAC
                                   CT_    TCT
GAM378  RAI17    3'  CAGCGACTCAAGGGACGTGTGT 91276    C       ATCC
                                AC CGTGTTCCT    TTGTTG
                                || |||||||||    ||||||
                                TG GTGCAGGGA    AGCGAC
                                 T       ACTC
GAM378  RANBP8   5'  TGGCGGGGGGGTGGGGTGTGAGG 21112     _ TG    TA
           T                     ACC CG  TTCC  TCCTTGTTG
                                ||| ||  ||||  |||||||||
                                TGG GT  GGGG  GGGGGCGGT
                                  A  GT   TG
GAM378  RCD-8    5'  GGCGGAACGAACGCGG      26751        CTA   TT
                                CCGTGTTC   TCC  GTT
                                ||||||||   |||  |||
                                GGCGCAAG   AGG  CGG
                                    CA_  __
GAM378  RHOBTB2  3'  TGAGAATGGGGACACAGGT   60945     C        C
                                ACC GTGTTCCTAT CTTG
                                ||| |||||||||| ||||
                                TGG CACAGGGGTA GAGT
                                  A        A
GAM378  RIP60    3'  CGGCAAGGACTGCCGCATTGGT 25456     C    TCCTA
                                ACC GTGT    TCCTTGTTG
                                ||| ||||    |||||||||
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                                TGG TACG    AGGAACGGC
                                  T   CCGTC
GAM378  RLUCL    5'  CGGGCCTGTGCGGGGCGCGGGT 54218          _  ___  TGTTG
                                ACCCGTGTTCC TAT  CCT
                                |||||||||| |||  |||
                                TGGGCGCGGGG GTG  GGG
                                      C  TCC  C  G
GAM378  RNF38    5'  AGCGAGGATCCGCGGG     42932      TTCCT
                                CCCGTG    ATCCTTGTT
                                ||||||    |||||||||
                                GGGCGC    TAGGAGCGA
                                   C____
GAM378  RNF8     3'  TGAGGCAGTAGGAGTGTGGG  14245     TG     __    TTG
                                CCCG  TTCCTAT  CCTTG
                                ||||  |||||||  |||||
                                GGGT  GAGGATG  GGAGT
                                  GT      AC
GAM378  RPH3A    3'  CAATGGGGATGGGGTTGGG   30241     TGT      TG
                                CCCG   TCCTATCCT  TTG
                                ||||   |||||||||  |||
                                GGGT   GGGGTAGGG  AAC
                                  T__       GT
GAM378  RTP801   5'  GGTGGTTGGCACGGGT     38799        C_
                                ACCCGTGTT  CTATC
                                |||||||||  |||||
                                TGGGCACGG  GGTGG
                                     TT
GAM378  SAE1     3'  GACAAGGGGCGCAGGGT     18531     G  T  TAT
                                ACCC TGT CC   CCTTGTT
                                |||| ||| ||   |||||||
                                TGGG ACG GG   GGAACAG
                                  _  C  ___
GAM378  SAMHD1   3'  CAGTGGGGATGGGAGCCATG   61309     _       TG
                                CGTG TTCCTATCCT  TTG
                                |||| ||||||||||  |||
                                GTAC GAGGGTAGGG  GAC
                                  C        GT
GAM378  SARM     3'  CAATATCCAGGGACATGG    30598         ATCCT
                                CCGTGTTCCT    TGTTG
                                ||||||||||    |||||
                                GGTACAGGGA    ATAAC
                                     CCT__
GAM378  SCAMP5   3'  GGTGGTGGGTGGGAGGGTGGGT 57261      TG       TTGTTG
                                ACCCG  TTCCTATCC
                                |||||  |||||||||
                                TGGGT  GAGGGTGGG
                                  GG       TGGTGGT
GAM378  SCYA3    3'  TGAGCCTTGGGAACATGCGT   59848    C        TC_
                                AC CGTGTTCCTA   CTTG
                                || ||||||||||   ||||
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                                TG GTACAAGGGT   GAGT
                                 C        TCC
GAM378  SDS3     5'  CGGCGAGTACCGAGCGCGGGT  69228         CTATC
                                ACCCGTGTTC    CTTGTTG
                                ||||||||||    |||||||
                                TGGGCGCGAG    GAGCGGC
                                     CCAT_
GAM378  SEC14L2  3'  CAATGAGGAGTAGCAGGGT   24872     G   CCTA   TG
                                ACCC TGTT    TCCT  TTG
                                |||| ||||    ||||  |||
                                TGGG ACGA    AGGA  AAC
                                  _   TG__    GT
GAM378  SELB     3'  TGGTGAGGAGCTGAGGGGGATG 61916      G    A___    TG
             GGT                   CCCGT TTCCT    TCCT  TTG
                                ||||| |||||    ||||  |||
                                GGGTA GGGGA    AGGA  GGT
                                   G    GTCG    GT
GAM378  SELM     3'  CAGCAGGGATGGGGTTGGG    54435     TGT
                                CCCG   TCCTATCCTTGTTG
                                ||||   ||||||||||||||
                                GGGT   GGGGTAGGGACGAC
                                  T__
GAM378  SENP7    3'  GGAATGGGAATGGGGGT     40301      G       _
                                ACCC TGTTCCTAT CC
                                |||| ||||||||| ||
                                TGGG GTAAGGGTA GG
                                  G        A
GAM378  SES2     3'  GGCATGGGGATCTGGGT     48812      T      _
                                ACCCG GTTCCTAT CC
                                ||||| |||||||| ||
                                TGGGT TAGGGGTA GG
                                  C       C
GAM378  SGKL     3'  TAACAGGCCGGGCGCGGGT   25146         CTATC
                                ACCCGTGTTC    CTTGTTG
                                ||||||||||    |||||||
                                TGGGCGCGGG    GGACAAT
                                     CC___
GAM378  SLC16A3  3'  TGACTTTAATGGGAGGGTGGGT 14854      TG      CCTT
                                ACCCG  TTCCTAT    GTTG
                                |||||  |||||||    ||||
                                TGGGT  GAGGGTA    CAGT
                                   GG      ATTT
GAM378  SLC1A7   3'  CGGTGAGGGCGGCAGGCAGGGG 21907     G   C_  AT   TG
             T                   ACCC TGTT  CT  CCT  TTG
                                |||| ||||  ||  |||  |||
                                TGGG ACGG  GG  GGA  GGC
                                  G   AC  CG   GT
GAM378  SLC39A3  3'  CAGCAGCCCAGAGTGTGGGT  57973      TG   CTATCC
                                ACCCG  TTC     TTGTTG
                                |||||  |||     ||||||
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                                TGGGT  GAG     GACGAC
                                  GT   ACCC__
GAM378  SLIT1    3'  CAGCGGGGGTGGGCGAGG    11765    _  TGTT
                                CC CG    CCTATCCTTGTTG
                                || ||    ||||||||||||
                                GG GC    GGGTGGGGGCGAC
                                 A _____
GAM378  SMC1L1   3'  TAGTAAGGAGATACAGTGGGT  71962      _   TCCTA
                                ACCCG TGT    TCCTTGTTG
                                ||||| |||    |||||||||
                                TGGGT ACA    AGGAATGAT
                                  G   TAG__
GAM378  SMCR5    3'  CAGCGGGTCAGGTGGGACAGGG 58592      G   T     ___
              GT                  ACCC TGT CCTATC   CTTGTTG
                                ||||| ||| ||||||   |||||||
                                TGGG ACA GGGTGG   GGGCGAC
                                  G   _     ACT
GAM378  SNPH     5'  CAGCAAGGGGGTGTGTGGGT   28238      TG T   AT
                                ACCCG  T CCT  CCTTGTTG
                                |||||  | |||  ||||||||
                                TGGGT  G GGG  GGAACGAC
                                  GT T  __
GAM378  SOX17    5'  CGACAGGCCAGAACACGGG   42397        CTATC
                                CCCGTGTTC    CTTGTTG
                                |||||||||    |||||||
                                GGGCACAAG    GGACAGC
                                     ACC__
GAM378  Spir-2   3'  AGGTGGGGACAGGGT      70628      G      T
                                ACCC TGTTCCTA CCT
                                |||| |||||||| |||
                                TGGG ACAGGGGT GGA
                                  _      _
GAM378  SSBP4    5'  CGGTGAGGCCCGGGGCGCGGG  50934         TAT   TG
                                CCCGTGTTCC   CCT  TTG
                                ||||||||||   |||  |||
                                GGGCGCGGGG   GGA  GGC
                                     CCC   GT
GAM378  SSTK     5'  TGGGCACATGGGGGTGCGGG   49347     TG      ___   TGTTG
                                CCCG  TTCCTAT   CCT
                                ||||  |||||||   |||
                                GGGC  GGGGGTA   GGG
                                  GT      CAC   T   G
GAM378  STK16    3'  TGGTGGGATATGGAACATGG   72119         _     TGTTG
                                CCGTGTTCC TATCCT
                                ||||||||| ||||||
                                GGTACAAGG ATAGGG
                                     T     TGGT
GAM378  STOML1   3'  GGGATTGGGCATGGG      16674         CT
                                CCCGTGTTC  ATCCT
                                |||||||||  |||||
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                                GGGTACGGG  TAGGG
                                     T_
GAM378  STRBP    5'  CGGCGGAGCGGGAGCGGGT   37231      GT   A_  TT
                                ACCCGT  TCCT  TCC  GTTG
                                ||||||  ||||  |||  ||||
                                TGGGCG  AGGG  AGG  CGGC
                                   __   CG   __
GAM378  SYNE-2   3'  GCGGCGGGGGTGGGGGCGGGGG 30801    G
                                CCC TGTTCCTATCCTTGTTG  C
                                ||| ||||||||||||||||  |
                                GGG GCGGGGGTGGGGGCGGC  G
                                  G
GAM378  SYT12    5'  AGTGAGTAGGGCATGG     94724       T   TC  TG
                                CCGTGT CCTA  CT  TT
                                |||||| ||||  ||  ||
                                GGTACG GGAT  GA  GA
                                   _   __  GT
GAM378  SYT12    3'  CAGCCGTGGTGGGGACCGGGT  94725     T       CTT
                                ACCCG GTTCCTATC   GTTG
                                ||||| |||||||||   ||||
                                TGGGC CAGGGGTGG   CGAC
                                   _       TGC
GAM378  SYT12    3'  TGGCAGGGGTGGGGCA     94742     T
                                TGT CCTATCCTTGTTG
                                ||| ||||||||||||
                                ACG GGGTGGGGACGGT
                                  _
GAM378  TA-PP2C  3'  AGACGCGGTGGGGGCGGGGT  57754     G      T  T   G
                                ACCC TGTTCCTA CC TGTT
                                |||| |||||||| || ||||
                                TGGG GCGGGGGT GG GCAG
                                  _      _ C   AT
GAM378  TEB4     3'  AGCATTGGGAGTTGGGT     60654      TGT    TCCT
                                ACCCG   TCCTA   TGTT
                                |||||   |||||   ||||
                                TGGGT   AGGGT   ACGA
                                   TG_    T___
GAM378  TGIF2    3'  CAGTGGGGAAGAATGAACATGG 41449        ___  A   TG
                                CCGTGTTC   CT TCCT  TTG
                                ||||||||   || ||||  |||
                                GGTACAAG   GA AGGG  GAC
                                     TAA  _   GT
GAM378  THG-1    5'  AGCAGGGTCACGCGGG      48181       TCCTAT
                                CCCGTGT     CCTTGTT
                                |||||||     |||||||
                                GGGCGCA     GGGACGA
                                    CT_____
GAM378  TIAF1    3'  GGTGAGGAGAGCCGGGT     54330      T   CTA   TG
                                ACCCG GTTC   TCCT  TT
                                ||||| ||||   ||||  ||
```

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                                TGGGC CGAG   AGGA  GG
                                  _   ___    GT
GAM378  TIP-1    5'  CAGCGAGGGCGCGACCGCGGGT 27503       T  CTA
                                ACCCGTG TC   TCCTTGTTG
                                ||||||| ||   |||||||||
                                TGGGCGC AG   GGGAGCGAC
                                   C  CGC
GAM378  TIX1     3'  TGGCAGTGGGGGATGTGGG   61750     TG    ATCC
                                CCCG  TTCCT    TTGTTG
                                ||||  |||||    ||||||
                                GGGT  AGGGG    GACGGT
                                  GT    GT__
GAM378  TMEM8    5'  CGGCGGCGCGGGACGCGGG   41193         TAT  TT
                                CCCGTGTTCC   CC  GTTG
                                ||||||||||   ||  ||||
                                GGGCGCAGGG   GG  CGGC
                                     CGC  __
GAM378  TMEM8    5'  CGGCGGGGGCCGGCGGCGCGGG 41194        _  TA
                                CCCGTGTT CC  TCCTTGTTG
                                ||||||||| ||  |||||||||
                                GGGCGCGG GG  GGGGGCGGC
                                    C  CC
GAM378  TNKS2    5'  CAGCGAGGGGCGCGCGTGG   47451   _    T  TAT
                                CC CGTGT CC   CCTTGTTG
                                || ||||| ||   ||||||||
                                GG GCGCG GG   GGAGCGAC
                                 T    C  ___
GAM378  TOB2     5'  CAGCGAGCTGAGGCGCGGG   95619      TT   ATC
                                CCCGTG  CCT   CTTGTTG
                                ||||||  |||   |||||||
                                GGGCGC  GGA   GAGCGAC
                                   __  GTC
GAM378  TOR2A    3'  AGCGGGGAAGCGAGGGT    55312     G   CCTA
                                ACCC TGTT    TCCTTGTT
                                |||| ||||    ||||||||
                                TGGG GCGA    AGGGGCGA
                                  A   _____
GAM378  TOR2A    3'  GGTTTTAGCAACACGGGT    55316        C   T__
                                ACCCGTGTT CTA   CC
                                ||||||||| |||   ||
                                TGGGCACAA GAT   GG
                                    C   TTT
GAM378  TP53INP1 3'  TAATGAGGCCAGGGTGCAGGGT 72955     G  _   AT   TG
                                ACCC TGT TCCT  CCT  TTG
                                |||| ||| ||||  |||  |||
                                TGGG ACG GGGA  GGA  AAT
                                  _  T   CC   GT
GAM378  TP53INP1 3'  TAATGAGGCCAGGGTGCAGGGT 52728     G  _   AT   TG
                                ACCC TGT TCCT  CCT  TTG
                                |||| ||| ||||  |||  |||
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                                TGGG ACG GGGA  GGA  AAT
                                  _  T   CC   GT
GAM378  TPC2     3'  AGGTGGGGATGCTGGT      57444     C       T
                                ACC GTGTTCCTA CCT
                                ||| ||||||||| |||
                                TGG CGTAGGGGT GGA
                                  T       _
GAM378  TRAP150  3'  GTGTGTGGGGTGGGGGCAGGGG 17599      G          TGTTG
           T                     ACCC TGTTCCTATCCT
                                ||||| |||||||||||
                                TGGG ACGGGGGTGGGG
                                  G          TGTGTGG
GAM378  TRIM15   5'  TGATAGGTGGTGGGCAGGGT   52654     G  TT     _
                                ACCC TG  CCTATC CTTGTTG
                                |||| ||  |||||| |||||||
                                TGGG AC  GGGTGG GGATAGT
                                  _ __     T
GAM378  TRIM31   3'  GGAGATGGGGGCGGGGGT    91001     G        _
                                ACCC TGTTCCTATC CT
                                |||| |||||||||| ||
                                TGGG GCGGGGGTAG GG
                                  G        A
GAM378  TSPEAR   3'  CAGTGAGGATGAGAGGGGGT   58715     GTG   C     TG
                                ACCC   TTC TATCCT  TTG
                                ||||   ||| ||||||  |||
                                TGGG   GAG GTAGGA  GAC
                                  G__   A     GT
GAM378  TTTY2    5'  CAATAAGGTCAGATAGGGGT   87001     G   CCTAT
                                ACCC TGTT    CCTTGTTG
                                |||| ||||    ||||||||
                                TGGG ATAG    GGAATAAC
                                  G   ACT__
GAM378  UBF-fl   3'  AGCAGGGATTACCGG      51548     T  TCCT
                                CCG GT    ATCCTTGTT
                                ||| ||    |||||||||
                                GGC CA    TAGGGACGA
                                  _ T___
GAM378  UGTREL1  3'  GACTTAATAGGAATATGGG    19514          CCTT   G
                                CCCGTGTTCCTAT    GTT
                                ||||||||||||    |||
                                GGGTATAAGGATA    CAG
                                       ATT_   G
GAM378  UPB1     3'  CAGCAAGGCTGTGGTGGGT    32886      TGTT  _  T
                                ACCCG    CC TA CCTTGTTG
                                |||||    || || ||||||||
                                TGGGT    GG GT GGAACGAC
                                   _____  T  C
GAM378  USP8     5'  CGGCGTCACGGTGAGTGCGGGT 17665      TG   _  ATCCT
                                ACCCG  TTC CT    TGTTG
                                |||||  ||| ||    |||||
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                                TGGGC  GAG GG    GCGGC
                                  GT   T  CACT_
GAM378  ust3    3'  TAACAAGGCTGGGTGCGG    93230     GTT    T
                                CCGT   CCTA CCTTGTTG
                                ||||   |||| ||||||||
                                GGCG   GGGT GGAACAAT
                                  T__    C
GAM378  UXS1    5'  TAGTGAGGAAGGCATGTGT    46891    C    TT   A    TG
                                AC CGTG  CCT TCCT  TTG
                                || ||||  ||| ||||  |||
                                TG GTAC  GGA AGGA  GAT
                                 T   __  _   GT
GAM378  VEST1   5'  CAGTAGGGGTGGGGGAGG    53686    GTGT
                                CC   TCCTATCCTTGTTG
                                ||   ||||||||||||||
                                GG   GGGGTGGGGATGAC
                                 AG__
GAM378  VPS39   3'  TGGTGAGGGTGGGTGATGG    62852     GTT      TG
                                CCGT   CCTATCCT  TTG
                                ||||   ||||||||  |||
                                GGTA   GGGTGGGA  GGT
                                  GT_      GT
GAM378  VRP     5'  CAACACCTGCGAGGAGTGTGGG 22945     TG    ATCCT_
                                CCCG  TTCCT     TGTTG
                                ||||  |||||     |||||
                                GGGT  GAGGA     ACAAC
                                  GT    GCGTCC
GAM378  WBSCR22  3'  TGGTGAGGAAGAGTCGGGCATG 34037         __ A_   TG
           GGT                   CCCGTGTTC  CT  TCCT  TTG
                                |||||||||  ||  ||||  |||
                                GGGTACGGG  GA  AGGA  GGT
                                     CT  GA   GT
GAM378  WDR13   5'  CGGCGGGGACAAGATGGGT   35413       G  CCTA
                                ACCCGT TT    TCCTTGTTG
                                |||||| ||    |||||||||
                                TGGGTA AA    AGGGGCGGC
                                   G  C___
GAM378  XRN2    3'  TGATGGAATAGGAGTACTGGT  24301     C        _  TTGTTG
                                ACC GTGTTCCTAT CC
                                ||| ||||||||| ||
                                TGG CATGAGGATA GG
                                  T        A  TAGT
GAM378  ZAK     3'  CAGCAAGTGGGGTATGTGT   56123    C    TT  TATC
                                AC CGTG  CC    CTTGTTG
                                || ||||  ||    |||||||
                                TG GTAT  GG    GAACGAC
                                 T   GG  T___
GAM378  ZBRK1   3'  TAATGGTGGAATGTGGG     60246     TG    T   C
                                CCCG  TTCC ATC TTG
                                ||||  |||| ||| |||
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                                GGGT  AAGG TGG AAT
                                  GT   _  T
GAM378  ZNF213   3'  GGCAGGGACAGCAGGGT     65104      G    CCTA
                                ACCC TGTT    TCCTTGTT
                                |||| ||||    ||||||||
                                TGGG ACGA    AGGGACGG
                                  _    C___
GAM378  ZNF300   5'  CAATAGGGATGTGACAGCGG   53474      GT  C
                                CCGT  TC TATCCTTGTTG
                                ||||  || ||||||||||
                                GGCG  AG GTAGGGATAAC
                                  AC  T
GAM378  ZNF313   3'  GACAGGGGAAGTGGGT      37940       TGTTC  A
                                ACCCG     CT TCCTTGTT
                                |||||     || ||||||||
                                TGGGT     GA GGGGACAG
                                  _____  A
GAM378  LOC113828 3'  GGTGGCTGGGCAGGGGT     56586      G    __
                                ACCC TGTTC  CTATC
                                |||| |||||  |||||
                                TGGG ACGGG  GGTGG
                                  G     TC
GAM378  LOC114971 3'  TGGAGAAGTGGGAGCATGGG   73155           C_  GTTG
                                CCCGTGTTCCTAT  CTT
                                ||||||||||||  |||
                                GGGTACGAGGGTG  GAG
                                       AA   GT
GAM378  LOC115004 3'  CGGCGGGGATGGTGAAAGGGGT 73175      GTG  _
                                ACCC   TTC CTATCCTTGTTG
                                ||||   ||| ||||||||||||
                                TGGG   AAG GGTAGGGGCGGC
                                  GA_   T
GAM378  LOC115051 3'  GGGGTGGAGACGTGGGT     60041         TC
                                ACCCGTGT  CTATCCT
                                ||||||||  |||||||
                                TGGGTGCA  GGTGGGG
                                     GA
GAM378  LOC115110 3'  GGCCGTGGGAACGTGAGT    71718    C         __
                                AC CGTGTTCCTAT  CC
                                || ||||||||||  ||
                                TG GTGCAAGGGTG  GG
                                 A          CC
GAM378  LOC115219 5'  TAGCGGGGATTACTGGTGCG   73317    TG  CCT_
                                CG  TT    ATCCTTGTTG
                                ||  ||    ||||||||||
                                GC  GG    TAGGGGCGAT
                                 GT  TCAT
GAM378  LOC115330 3'  AGCAAGGCCTGCCGGGT     56607       T  TCCTAT
                                ACCCG GT     CCTTGTT
                                ||||| ||     |||||||
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                                TGGGC CG     GGAACGA
                                   _ TCC___
GAM378  LOC115399 5'  CAATTTGGGGAGCATGGG    73423          TAT  TT
                                CCCGTGTTCC   CC  GTTG
                                ||||||||||   ||  ||||
                                GGGTACGAGG   GG  TAAC
                                     ___  TT
GAM378  LOC115574 5'  TGGCGAGGGGGCGCGGCGCGGG 73469         ___  AT
                                CCCGTGTT   CCT  CCTTGTTG
                                ||||||||   |||  ||||||||
                                GGGCGCGG   GGG  GGAGCGGT
                                     CGC  __
GAM378  LOC116150 3'  TAGCACATTTTAGGGGCATGG  56637          TCCT_
                                CCGTGTTCCTA     TGTTG
                                ||||||||||     |||||
                                GGTACGGGGAT    ACGAT
                                       TTTAC
GAM378  LOC116166 3'  CAATGGCTGGACATGGGT    59762        T  TAT  _
                                ACCCGTGT CC   CC TTG
                                |||||||| ||   || |||
                                TGGGTACA GG   GG AAC
                                     _ TC_  T
GAM378  LOC118471 3'  AGCAGGCCGGGCGCGG      73914        CTATC
                                CCGTGTTC    CTTGTT
                                ||||||||    ||||||
                                GGCGCGGG    GGACGA
                                     CC___
GAM378  LOC120526 5'  CAGCAGGCGAGGAGTGGGT   74014      TG    ATC
                                ACCCG  TTCCT   CTTGTTG
                                |||||  |||||   |||||||
                                TGGGT  GAGGA   GGACGAC
                                   __    GC_
GAM378  LOC121536 5'  CAGCGGGGATGGGGACGGCAAG 74085    C_  _
           G                     CC  GT GTTCCTATCCTTGTTG
                                 ||  || ||||||||||||||||
                                 GG  CG CAGGGGTAGGGGCGAC
                                  AA  G
GAM378  LOC121536 5'  GACGAGGGCTACGGG       74087       TTCCTA
                                CCCGTG     TCCTTGTT
                                ||||||     ||||||||
                                GGGCAT     GGGAGCAG
                                   C_____
GAM378  LOC122830 5'  CGGCGGGGACCCGTGCGGG   74165      TG TCCTA
                                CCCG  T    TCCTTGTTG
                                ||||  |    |||||||||
                                GGGC  G    AGGGGCGGC
                                  GT CCC__
GAM378  LOC123242 5'  AGCAGGCTGGCATGGG      75590       TT  TATC
                                CCCGTG  CC    CTTGTT
                                ||||||  ||    ||||||
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                                GGGTAC  GG    GGACGA
                                   __ TC__
GAM378  LOC123745 3'  CAGCAGGGAGTGGTGTGGGT   75621      TG TC TA
                                ACCCG  T  C  TCCTTGTTG
                                |||||  |  |  |||||||||
                                TGGGT  G  G  AGGGACGAC
                                   GT GT __
GAM378  LOC123879 5'  CGGCGGGGGTAGGGAGCCTGG  75631     T    _
                                CCG GTTCC TATCCTTGTTG
                                ||| ||||| ||||||||||
                                GGT CGAGG ATGGGGGCGGC
                                  C    G
GAM378  LOC124044 3'  CGGCGGGGTCTTGGTGGGT    76026      TGTT  TAT_
                                ACCCG    CC    CCTTGTTG
                                |||||    ||    ||||||||
                                TGGGT    GG    GGGGCGGC
                                   _____ TTCT
GAM378  LOC124044 3'  TGGCGAGGGAGAGGGCAGGGT  76028     G    _  A
                                ACCC TGTTC CT TCCTTGTTG
                                |||| ||||| || |||||||||
                                TGGG ACGGG GA GGGAGCGGT
                                  _    A  _
GAM378  LOC124222 5'  CAGCGCCGGAGGGGCGCGGG   74270         TA   T_
                                CCCGTGTTCC  TCC  TGTTG
                                ||||||||||  |||  |||||
                                GGGCGCGGGG  AGG  GCGAC
                                      __  CC
GAM378  LOC124460 5'  GGGCCTAGGGGTGCAGGGT    76047     _ TG     T_
                                ACCC G  TTCCTA  CCT
                                ||||  |  ||||||  |||
                                TGGG C  GGGGAT  GGG
                                  A GT     CC
GAM378  LOC124602 5'  CGGAGGCGGTGGGGGTGCGG   74306     TG       _   GTTG
                                CCG  TTCCTATC CTT
                                |||  |||||||| |||
                                GGC  GGGGGTGG GGA
                                  GT       C   GGC
GAM378  LOC124976 3'  ACAAGAGGATGGGGTGGGGGT  74377     G  TT  T     GTTG
                                ACCC TG  CC ATCCTT
                                |||| ||  || ||||||
                                TGGG GT  GG TAGGAG
                                  G  GG  _     AACAG
GAM378  LOC124977 5'  CGATGGGGAAATCGCACTGGT  76059     C    TCCTA    TG
                                ACC GTGT    TCCT  TTG
                                ||| ||||    ||||  |||
                                TGG CACG    AGGG  AGC
                                  T   CTAA_   GT
GAM378  LOC126299 3'  CAGTGGTCATGGGGGATGGG   74484      G      CC TG
                                CCCGT TTCCTAT  T  TTG
                                ||||| |||||||  |  |||
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                                GGGTA GGGGGTA  G  GAC
                                  _      CT GT
GAM378  LOC126328 5'  TGGCGGGGTCCGTGGTGCGGG  74497     TG  CCTAT
                                CCCG  TT    CCTTGTTG
                                ||||  ||    ||||||||
                                GGGC  GG    GGGGCGGT
                                  GT  TGCCT
GAM378  LOC126520 5'  TGGCGGGGCTGGGGCCGGGT   74526      T    TAT
                                ACCCG GTTCC   CCTTGTTG
                                ||||| |||||   ||||||||
                                TGGGC CGGGG   GGGGCGGT
                                  _    TC_
GAM378  LOC126917 3'  CAGCACTGACTGGGTAGTGTGG 74579      TG _   _ CT
          GT                    ACCCG  TT CCTA TC  TGTTG
                                |||||  || |||| ||  |||||
                                TGGGT  GA GGGT AG  ACGAC
                                  GT  T    C  TC
GAM378  LOC127703 3'  TGGTGGGGATGGGGACAGAGG  74683    CG         TG
                                CC  TGTTCCTATCCT  TTG
                                ||  ||||||||||||  |||
                                GG  ACAGGGGTAGGG  GGT
                                 AG          GT
GAM378  LOC128344 3'  TGATGGGGGTGGAGGTGGG    74738     TG TC      TG
                                CCCG  T  CTATCCT  TTG
                                ||||  |  |||||||  |||
                                GGGT  G  GGTGGGG  AGT
                                  __ GA      GT
GAM378  LOC128844 5'  TGGCAGGAGCCCAGCGCGGG   75787        CCTA    T
                                CCCGTGTT    TCCT GTTG
                                ||||||||    |||| ||||
                                GGGCGCGA    AGGA CGGT
                                    CCCG    _
GAM378  LOC128977 3'  CAGTGGGGGTGGGGGTGGGGGT 74822      G  TT       TG
                                ACCC TG  CCTATCCT  TTG
                                |||| ||  ||||||||  |||
                                TGGG GT  GGGTGGGG  GAC
                                  G  GG       GT
GAM378  LOC130074 3'  CAGCAGGTGGCAGGGGTGTGG  76127     TG    AT _
                                CCG  TTCCT  C CTTGTTG
                                |||  |||||  | |||||||
                                GGT  GGGGA  G GGACGAC
                                  GT    CG T
GAM378  LOC130074 3'  CAGTGAGGGTCAGAGTGGGGGT 76130      G GT  CT    TG
                                ACCC T  TC  ATCCT  TTG
                                |||| |  ||  |||||  |||
                                TGGG G  AG  TGGGA  GAC
                                  G TG  AC    GT
GAM378  LOC130595 5'  TAATAAGGAAGAAGAATATGG  75751        CTA_
                                CCGTGTTC    TCCTTGTTG
                                ||||||||    |||||||||
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                                GGTATAAG   AGGAATAAT
                                    AAGA
GAM378  LOC131377 5'  AGCAGGAAAGCAGGGGT    76268     G   CCTA   T
                                ACCC TGTT   TCCT GTT
                                |||| ||||   |||| |||
                                TGGG ACGA   AGGA CGA
                                  G   A___   _
GAM378  LOC131870 3'  TGGCGAGGCTGGAGGGCAGGGT 75026     G   _  T
                                ACCC TGTTC CTA CCTTGTTG
                                |||| ||||| ||| ||||||||
                                TGGG ACGGG GGT GGAGCGGT
                                  _   A  C
GAM378  LOC132660 5'  GGGAACAGGGAATGTGGGT   75061      TG   A__
                                ACCCG  TTCCT   TCCT
                                |||||  |||||   ||||
                                TGGGT  AAGGG   AGGG
                                   GT    ACA
GAM378  LOC132880 5'  TGGCAAGGATAACCTGGG    75068     T  TCC
                                CCCG GT   TATCCTTGTTG
                                |||| ||   ||||||||||
                                GGGT CA   ATAGGAACGGT
                                  C  ___
GAM378  LOC134121 3'  AGTAAGGATGGGTGG      75150     TGTT
                                CCG   CCTATCCTTGTT
                                |||   ||||||||||||
                                GGT   GGGTAGGAATGA
                                  _____
GAM378  LOC135293 3'  TGATAAGTGAGGACAGGGT   76194     G  T  ATC
                                ACCC TGT CCT   CTTGTTG
                                |||| ||| |||   |||||||
                                TGGG ACA GGA   GAATAGT
                                  _  _  GT_
GAM378  LOC135892 5'  GATGGGGCACGCGCGGT     75246    _   _
                                ACC CGTGT TCCTATC
                                ||| ||||| |||||||
                                TGG GCGCA GGGGTAG
                                  C   C
GAM378  LOC135892 5'  TGATGAGGCACGGACGTGGG   75247        CTAT   TG
                                CCCGTGTTC   CCT  TTG
                                |||||||||   |||  |||
                                GGGTGCAGG   GGA  AGT
                                    CAC_   GT
GAM378  LOC138389 3'  GACTCCGGTGGGACGTGGGT   76226       T    CTT   G
                                ACCCGTGT CCTATC   GTT
                                |||||||| ||||||   |||
                                TGGGTGCA GGGTGG   CAG
                                    _    CCT   G
GAM378  LOC138389 5'  GTGGCGAGGAGGCTGGCGGGAC 76230       TA_____
            ACGGGT                GTGTTCC     TCCTTGTTG   T
                                |||||||     |||||||||  |
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                                CACAGGG      AGGAGCGGT   G
                                    CGGTCGG
GAM378   LOC138649 5'  GGATTTGGGGCTGGGT      75356       T    T_
                                ACCCG GTTCC  ATCC
                                ||||| |||||  ||||
                                TGGGT CGGGG  TAGG
                                  _    TT
GAM378   LOC138649 3'  GGCAGGGATTCACGGG      75357       TTCCT
                                CCCGTG    ATCCTTGTT
                                ||||||    |||||||||
                                GGGCAC    TAGGGACGG
                                   T____
GAM378   LOC138724 5'  TGGCAGGGCGGAACAAGGGT   75368      G     TAT
                                ACCC TGTTCC   CCTTGTTG
                                |||| ||||||   ||||||||
                                TGGG ACAAGG   GGGACGGT
                                  A     C__
GAM378   LOC139673 5'  GGCTGAGGATGGGGGTACTGGT 75978     C   TT        TTG
                                ACC GTG  CCTATCCTTG
                                ||| |||  ||||||||||
                                TGG CAT  GGGTAGGAGT
                                  T  GG        CGGT
GAM378   LOC143153 3'  AGTAAGGGGTGGTGGCATGG   76461       TC      GTTG
                                CCGTGT  CTATCCTT
                                ||||||  ||||||||
                                GGTACG  GGTGGGGA
                                   GT       ATGAT
GAM378   LOC143154 3'  AGTAAGGGGTGGTGGCATGG   76477       TC      GTTG
                                CCGTGT  CTATCCTT
                                ||||||  ||||||||
                                GGTACG  GGTGGGGA
                                   GT       ATGAT
GAM378   LOC143243 3'  GGTGGGGGAGAAGGGGGTGGGT 60309       TGT   A_    GTTG
                                ACCCG   TCCT  TCCTT
                                |||||   ||||  |||||
                                TGGGT   GGGA  AGGGG
                                   GG_    AG    GTGGT
GAM378   LOC143282 3'  GAATGGGGGTGGGGGCAAGGGT 76515     G         TG  G
                                ACCC TGTTCCTATCCT  TT
                                |||| ||||||||||||  ||
                                TGGG ACGGGGGTGGGG  AA
                                  A          GT  GC
GAM378   LOC143282 3'  GATGGGGGAGGCGTGGG     76516       ____
                                CCCGTGT   TCCTATC
                                |||||||   |||||||
                                GGGTGCG   GGGGTAG
                                   GAG
GAM378   LOC143308 5'  AGACACAGGATGGGAAATGGGT 82933       G        _   G
                                ACCCGT TTCCTATCCT TGTT
                                |||||| |||||||||| ||||
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                                TGGGTA AAGGGTAGGA ACAG
                                  _       C   AA
GAM378  LOC143916 5'  TGACAGGGGCAGTAGAGTAGGG 76648     G   __ AT
          GT                    ACCC TGTTC  CT  CCTTGTTG
                                |||| |||||  ||  ||||||||
                                TGGG ATGAG  GA  GGGACAGT
                                  G    AT  CG
GAM378  LOC144266 5'  CAATAAGAGCAGACATGGGT   76761        CCTATC
                                ACCCGTGTT     CTTGTTG
                                |||||||||     |||||||
                                TGGGTACAG     GAATAAC
                                    ACGA__
GAM378  LOC144453 3'  TAATGGGGATCGGATGTTGG   76847     TGT   T    TG
                                CCG   TCC ATCCT  TTG
                                |||   ||| |||||  |||
                                GGT   AGG TAGGG  AAT
                                  TGT   C    GT
GAM378  LOC145047 3'  TAGTGGGGGTGGCAGAGGT   60516     CG  TTC     TG
                                ACC  TG   CTATCCT  TTG
                                |||  ||   |||||||  |||
                                TGG  AC   GGTGGGG  GAT
                                  AG  ___      GT
GAM378  LOC145371 3'  AGGACTTAGGGACAGGGT    77149     G      __
                                ACCC TGTTCCTA  TCCT
                                |||| ||||||||  ||||
                                TGGG ACAGGGAT  AGGA
                                  _       TC
GAM378  LOC145375 3'  CAGCGAGGATGCAGACG     59967     CC
                                TGTT  TATCCTTGTTG
                                ||||  ||||||||||
                                GCAG  GTAGGAGCGAC
                                  AC
GAM378  LOC145748 3'  CAGCAGGGATGACCCGGG    83464     T   CCT
                                CCCG GTT   ATCCTTGTTG
                                |||| |||   ||||||||||
                                GGGC CAG   TAGGGACGAC
                                  C  ___
GAM378  LOC145758 5'  GGATAGGAACGGGT       83485       GT
                                ACCCGT  TCCTATCC
                                ||||||  ||||||||
                                TGGGCA  AGGATAGG
                                    __
GAM378  LOC145758 5'  TAGCACTGTTAGGGACATGG   83486          TCCT
                                CCGTGTTCCTA    TGTTG
                                ||||||||||    |||||
                                GGTACAGGGAT    ACGAT
                                      TGTC
GAM378  LOC145783 5'  CGGGCCTCCTGGGAGCGGGGT  77480     G      T____   TGTTG
                                ACCC TGTTCCTA    CCT
                                |||| ||||||||    |||
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                                TGGG GCGAGGGT    GGG
                                  _      CCTCC  C  G
GAM378  LOC145858 3'  CGACGAGGCCCTAGGAATGGGT 77544      GT    T__
                                ACCCGT  TCCTA  CCTTGTTG
                                ||||||  |||||  ||||||||
                                TGGGTA  AGGAT  GGAGCAGC
                                   __    CCC
GAM378  LOC145871 5'  CGACGGGGGCATTCCTGCGGGT 83563      GTTCCTA
                                ACCCGT      TCCTTGTTG
                                ||||||      |||||||||
                                TGGGCG      GGGGGCAGC
                                   TCCTTAC
GAM378  LOC145873 3'  CAGGGACAGGTGGGAGAATGGG 77552      G    ____     TTG
          T                      CCCGT TTCCTA    TCCTTG
                                |||||  ||||||    ||||||
                                GGGTA GAGGGT    AGGGAC
                                   A     GGAC       G
GAM378  LOC145955 3'  CAACAAGTGCTCAGCAGGGT   83589     G   CCTATC
                                ACCC TGTT     CTTGTTG
                                ||||  ||||     |||||||
                                TGGG ACGA     GAACAAC
                                  _   CTCGT_
GAM378  LOC145989 3'  GCGGGGGGGGTAGGGGTGTGGG  59546     TG        GTTG
                                CCCG  TTCCTATCCTT
                                ||||  ||||||||||
                                GGGT  GGGGATGGGGG
                                  GT         GGCGG
GAM378  LOC146226 5'  AGCTGGTGGGGGGCAGGGGT    83621     G      T  TT   G
                                ACCC TGTTCCTA CC  GTT
                                |||| |||||||| ||  |||
                                TGGG ACGGGGGT GG  CGA
                                  G       _ T_  G
GAM378  LOC146433 3'  CAGTGAGGGCACAGCTGTGGGT 77872     GT_  CCTA   TG
                                ACCC   GTT   TCCT  TTG
                                ||||   |||   ||||  |||
                                TGGG   CGA   GGGA  GAC
                                  TGT   CAC_   GT
GAM378  LOC146455 3'  GTACAATCTTGGGAACAGGGT  77906     G      TCC   TG
                                ACCC TGTTCCTA   TTGT
                                |||| ||||||||   ||||
                                TGGG ACAAGGGT   AACA
                                  _      TCT   TGA
GAM378  LOC146506 3'  GGCAGGGCCGGTGGGT     77934      TGTT  TAT
                                ACCCG   CC   CCTTGTT
                                |||||   ||   |||||||
                                TGGGT   GG   GGGACGG
                                   _____ CC_
GAM378  LOC146714 5'  TGGCAAGGAAAGACAGGGT   83742     G   TC  A
                                ACCC TGT  CT TCCTTGTTG
                                |||| |||  || |||||||||
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                                TGGG ACA  GA AGGAACGGT
                                  _  __ A
GAM378  LOC146733 5'  GTGGATTCTCTGGGGACATGGG 83770          _____   TTGTTG
                                CCCGTGTTCCT    ATCC
                                ||||||||||    ||||
                                GGGTACAGGGG    TAGG
                                      TCTCT   T  GT
GAM378  LOC146756 3'  CAGTGAGGAGGGGGGCTTGGGT 83773      T    A   TG
                                ACCCG GTTCCT TCCT  TTG
                                ||||| |||||| ||||  |||
                                TGGGT CGGGGG AGGA  GAC
                                   T    G   GT
GAM378  LOC146783 5'  CGACGGAGATAGGAGTGCGG  83789    TG      CT
                                CCG  TTCCTATC  TGTTG
                                |||  ||||||||  |||||
                                GGC  GAGGATAG  GCAGC
                                  GT       AG
GAM378  LOC146784 5'  CGACAAGGGTAGGAGTGC    78107   TG
                                G  TTCCTATCCTTGTTG
                                |  ||||||||||||||
                                C  GAGGATGGGAACAGC
                                 GT
GAM378  LOC146953 3'  GGAGAAGGGGTGGGAAGATGGG 78215       G        GTTG
          T                      ACCCGT TTCCTATCCTT
                                ||||||  ||||||||||
                                TGGGTA AAGGGTGGGGA
                                   G         AGAGGA
GAM378  LOC146957 3'  CAGCAGGGGTGGGGTTACG   78201     TT
                                CGTG  CCTATCCTTGTTG
                                ||||  ||||||||||||
                                GCAT  GGGTGGGGACGAC
                                  TG
GAM378  LOC147515 5'  GGTCCGGGTGGGGGGCGGGT  84027       G       TTGTTG
                                ACCCGT TTCCTATCC
                                ||||||  |||||||||
                                TGGGCG GGGGGTGGG
                                   _       CCTGGT
GAM378  LOC147515 5'  TGGCAGGGATGGGTTGTGG   84028    TGTT
                                CCG   CCTATCCTTGTTG
                                |||   ||||||||||||
                                GGT   GGGTAGGGACGGT
                                  GTT_
GAM378  LOC147664 3'  CAGCAAAAGGAGGAGCGTGG  78405        TA  __
                                CCGTGTTCC  TCCT  TGTTG
                                |||||||||  ||||  |||||
                                GGTGCGAGG  AGGA  ACGAC
                                      __   AA
GAM378  LOC147669 5'  TGGCAGGGATCAAGCAGG    84067   G   CCT
                                CC TGTT   ATCCTTGTTG
                                || ||||   ||||||||||
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                                GG ACGA   TAGGGACGGT
                                 _   AC_
GAM378  LOC147837 3'  TAATATTTGCAGGAGCGTGG   78519         ATCCT
                                CCGTGTTCCT    TGTTG
                                ||||||||||    |||||
                                GGTGCGAGGA    ATAAT
                                     CGTTT
GAM378  LOC147965 5'  CGGCGGGGATGGCGCGG     78598      TTC
                                CCGTG   CTATCCTTGTTG
                                |||||  ||||||||||||
                                GGCGC   GGTAGGGGCGGC
                                  ___
GAM378  LOC148022 3'  TGGTGGGGGTATTGCTACGG   78617     _ TCC     TG
                                CCGT GT   TATCCT  TTG
                                |||| ||   ||||||  |||
                                GGCA CG   ATGGGG  GGT
                                  T  TT_     GT
GAM378  LOC148198 3'  TAGCAAGGCCAGGCGCGG    70688      TT   AT
                                CCGTG  CCT  CCTTGTTG
                                |||||  |||  ||||||||
                                GGCGC  GGA  GGAACGAT
                                   __  CC
GAM378  LOC148413 3'  AGTGAGGATGGAGTGG     78828     TG   T    TG
                                CCG  TTCC ATCCT  TT
                                |||  |||| |||||  ||
                                GGT  GAGG TAGGA  GA
                                  __   _    GT
GAM378  LOC148479 3'  GATAGGGTAACATGGG     78869       __
                                CCCGTGT  TCCTATC
                                |||||||  |||||||
                                GGGTACA  GGGATAG
                                    AT
GAM378  LOC148758 5'  GGTGGGGAGTGTGCGGG     78974       ___
                                CCCGTG   TTCCTATC
                                ||||||   ||||||||
                                GGGCGT   AGGGGTGG
                                   GTG
GAM378  LOC148758 5'  TGGTATAGACAGGAGTGTGGG  78977     TG    A  CT  TT
                                CCCG  TTCCT TC  TG  G
                                ||||  ||||| ||  ||  |
                                GGGT  GAGGA AG  AT  T
                                  GT    C  AT  GG
GAM378  LOC149134 5'  AAATGGGATGGGAGTGTGTGT  84359    C  TG       TGTTG
                                AC CG  TTCCTATCCT
                                || ||  ||||||||||
                                TG GT  GAGGGTAGGG
                                 T  GT        TAAAC
GAM378  LOC149297 5'  CAGCGGGGACCCCGCGCGG   84392      TCCTA
                                CCGTGT    TCCTTGTTG
                                ||||||    |||||||||
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                                GGCGCG    AGGGGCGAC
                                   CCCC_
GAM378  LOC149297 3'  CAGTGAGGGTGCCAGGGGT   84393     G  TTCC     TG
                                ACCC TG   TATCCT  TTG
                                |||| ||   ||||||  |||
                                TGGG AC   GTGGGA  GAC
                                  G  C___     GT
GAM378  LOC149464 3'  TAACAGGGCAGAGTGACGGGT  84433      GTTC  AT_
                                ACCCGT   CT   CCTTGTTG
                                ||||||   ||  ||||||||
                                TGGGCA   GA   GGGACAAT
                                   GT__  GAC
GAM378  LOC149483 3'  TGGCAGGGGCTAGCATGGG   79389       CCTA
                                CCCGTGTT   TCCTTGTTG
                                ||||||||   |||||||||
                                GGGTACGA   GGGGACGGT
                                     TC__
GAM378  LOC149668 3'  TGGTGGGGGTGGGAGTGC    84552   TG       TG
                                G  TTCCTATCCT  TTG
                                |  ||||||||||  |||
                                C  GAGGGTGGGG  GGT
                                 GT        GT
GAM378  LOC149711 5'  GGGATGGGGGTGGGGT     84686     G  TT
                                ACCC TG  CCTATCCT
                                |||| ||  ||||||||
                                TGGG GT  GGGTAGGG
                                  _  GG
GAM378  LOC149832 5'  TAACGAGGCAAGAGGACATGGG 84703         _  AT
                                CCCGTGTTC CT  CCTTGTTG
                                |||||||||  ||  ||||||||
                                GGGTACAGG GA  GGAGCAAT
                                     A  AC
GAM378  LOC149837 3'  GCCAAGGGGAATGGGGGT    84742     G     TAT    TTG
                                ACCC TGTTCC   CCTTG
                                |||| ||||||   |||||
                                TGGG GTAAGG   GGAAC
                                  G     ___     CGT
GAM378  LOC149837 5'  TGGTGGGGGGTAGACAGGGGT   84748     G   TC     TG
                                ACCC TGT  CTATCCT  TTG
                                |||| |||  |||||||  |||
                                TGGG ACA  GATGGGG  GGT
                                  G   __      GT
GAM378  LOC149844 5'  TGGTGGGGGGTGGTGGTGGGGGT 79523     G   TC     TG
                                ACCC TGT  CTATCCT  TTG
                                |||| |||  |||||||  |||
                                TGGG GTG  GGTGGGG  GGT
                                  G   GT     GT
GAM378  LOC149995 5'  TGGCAGGGATGGGTTATGG   84850      TT
                                CCGTG  CCTATCCTTGTTG
                                |||||  |||||||||||||
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                                GGTAT  GGGTAGGGACGGT
                                  T_
GAM378  LOC150185 3'  CAGTGGGGCTGGGCGCGG    84906      TT   T  TG
                                CCGTG  CCTA CCT  TTG
                                |||||  |||| |||  |||
                                GGCGC  GGGT GGG  GAC
                                  __   C   GT
GAM378  LOC150225 3'  GGTGGGTGATAGTGGG      85008     _   _
                                CCCG TGTT CCTATC
                                |||| |||| ||||||
                                GGGT ATAG GGGTGG
                                  G   T
GAM378  LOC150245 5'  TGCGATGGCACCAGGGCACGGG 84939         _____    CTTGTTG
                                CCCGTGTTC    CTATC
                                |||||||||    |||||
                                GGGCACGGG    GGTAG
                                     ACCAC    C  GTT
GAM378  LOC150275 5'  GGGCCTGGGGACGCGGG     79709          T_
                                CCCGTGTTCCTA  CCT
                                ||||||||||||  |||
                                GGGCGCAGGGGT  GGG
                                      CC
GAM378  LOC150295 5'  CAGCGGTTTGGAACATGGGT   84960         TAT  TT
                                ACCCGTGTTCC   CC  GTTG
                                ||||||||||   ||  ||||
                                TGGGTACAAGG   GG  CGAC
                                      TTT  __
GAM378  LOC150358 3'  TGTGATGAGGGGCCAGGCGTGG 84930    _  ___     _  CTTGTTG
          T                    CC CGT   GTTCCT ATC
                               || |||   |||||| |||
                               GG GCG   CGGGGA TAG
                                T  GAC     G  T  GTT
GAM378  LOC150368 3'  TTTTGGGAGGGGACATGGGT   79705          A   TGTTG
                                ACCCGTGTTCCT TCCT
                                |||||||||||| ||||
                                TGGGTACAGGGG AGGG
                                      _   TTTTG
GAM378  LOC150372 3'  CAAGGAGGTGGGGGCAAGGGT  79788     G      T   G
                                ACCC TGTTCCTA CCTT TTG
                                |||| |||||||| |||| |||
                                TGGG ACGGGGGT GGAG AAC
                                  A       _   G
GAM378  LOC150397 3'  CAGCCTTCAGGGATATGAGGT  79841     _       ATCCTT
                                ACC CGTGTTCCT     GTTG
                                ||| |||||||||     ||||
                                TGG GTATAGGGA     CGAC
                                  A       CTTC__   G
GAM378  LOC150407 3'  TGGCGAGGGAGAGATGGGT    79835       G  CTA
                                ACCCGT TTC   TCCTTGTTG
                                |||||| |||   |||||||||
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                                TGGGTA GAG   GGGAGCGGT
                                   _   A__
GAM378  LOC150481 3'  GAGGTGGGGACATGG       79886          T
                                CCGTGTTCCTA CCTT
                                |||||||||| ||||
                                GGTACAGGGGT GGAG
                                          _
GAM378  LOC150696 3'  CAGCAATCTGCAGGTAGGGAGT 58479    GTG       C_____
           GGGT                  C   TTCCTATC     TTGTTG
                                |  ||||||||     ||||||
                                G   AGGGATGG     AACGAC
                                 TG_       ACGTCT
GAM378  LOC150933 3'  TAATAAGGAAGCAGAGAGTATG 85164          _  A__
           GG                    CCCGTGTTC CT   TCCTTGTTG
                                ||||||||| ||   |||||||||
                                GGGTATGAG GA   AGGAATAAT
                                      A  CGA
GAM378  LOC151009 5'  CAGGGGTGGGCAGGGGCGCGGG 85193           ____      TTG
           T                     CCCGTGTTCCT    ATCCTTG
                                ||||||||||    |||||||
                                GGGCGCGGGGA    TGGGGAC
                                      CGGG         G
GAM378  LOC151438 5'  TAGCAATGGAGAACGTGGGT   85369          CTA   _
                                ACCCGTGTTC   TCC TTGTTG
                                ||||||||||   ||| ||||||
                                TGGGTGCAAG   AGG AACGAT
                                      ___   T
GAM378  LOC151438 3'  TGACAGGACACAGAGGAGCGTG 85371          ATC___
           G                     CCGTGTTCCT      CTTGTTG
                                ||||||||||      |||||||
                                GGTGCGAGGA      GGACAGT
                                      GACACA
GAM378  LOC151475 3'  CAGTGGGGTGTCCAGCAAGGGT 85397      G    CCTAT   TG
                                ACCC TGTT     CCT  TTG
                                |||| ||||     |||  |||
                                TGGG ACGA     GGG  GAC
                                  A    CCTGT   GT
GAM378  LOC151571 5'  CAGCAGGTCCTCAGCCGGGT   85443      T   CCTAT   T
                                ACCCG GTT     CCT GTTG
                                ||||| |||     ||| ||||
                                TGGGC CGA     GGA CGAC
                                  _   CTCCT   _
GAM378  LOC151610 3'  CAGCAAGGACTGCTGTGTGTGG 80285       TG TCCTA__
           GT                    ACCCG  T      TCCTTGTTG
                                |||||  |      |||||||||
                                TGGGT  G      AGGAACGAC
                                   GT TGTCGTC
GAM378  LOC151610 3'  CAGCAGGGGTTTAGATGG     80286      GTTCCT
                                CCGT      ATCCTTGTTG
                                ||||      ||||||||||
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                                GGTA     TGGGGACGAC
                                  GATT__
GAM378  LOC151904 5'  TGATGAGGATAGAGAGGG    80395    GTGT _     TG
                                CCC    TC CTATCCT  TTG
                                |||    || |||||||  |||
                                GGG    AG GATAGGA  AGT
                                 _____ A      GT
GAM378  LOC151979 3'  TGTAAGGATTCAGAGGGGT   80428     GTG   CT_     TT
                                ACCC   TTC   ATCCTTG  G
                                ||||   |||   |||||||  |
                                TGGG   GAG   TAGGAAT  T
                                  ___  ACT      GG
GAM378  LOC151996 5'  AGCAGGCGACACGGG      85528        CCTATC
                                CCCGTGTT     CTTGTT
                                ||||||||     ||||||
                                GGGCACAG     GGACGA
                                    C_____
GAM378  LOC152059 3'  TGACAAGCGAGGCAGGGGT   80451     G  TT   ATC
                                ACCC TG  CCT   CTTGTTG
                                |||| ||  |||   |||||||
                                TGGG AC  GGA   GAACAGT
                                  G  __  GC_
GAM378  LOC152245 3'  TAGCAGCCGGGAGCGCTGGT  85605     C       ATCC
                                ACC GTGTTCCT    TTGTTG
                                ||| ||||||||    ||||||
                                TGG CGCGAGGG    GACGAT
                                  T       CC__
GAM378  LOC152275 3'  TGGCAGGTAGAGGATGGGGT  85623     GTGT    ATC
                                ACCC    TCCT   CTTGTTG
                                ||||    ||||   |||||||
                                TGGG    AGGA   GGACGGT
                                  GT__    GAT
GAM378  LOC152283 5'  CAGCGGGGCACATGAGG     85680    _    TCCTAT
                                CC CGTGT     CCTTGTTG
                                || |||||     ||||||||
                                GG GTACA     GGGGCGAC
                                 A    C_____
GAM378  LOC152313 5'  TGGTGGGGCGGGGAACAAGGGT 85670      G      AT   TG
                                ACCC TGTTCCT  CCT  TTG
                                |||| |||||||  |||  |||
                                TGGG ACAAGGG  GGG  GGT
                                  A      GC   GT
GAM378  LOC152441 5'  GGTGAGGATGTGGGGGT     85734      GTGTT _     TG
                                ACCC     CC TATCCT  TT
                                ||||     || ||||||  ||
                                TGGG     GG GTAGGA  GG
                                  _____  T     GT
GAM378  LOC152464 5'  CGACAGCTGGGGCCTGGGT    59986      T    TATCC
                                ACCCG GTTCC     TTGTTG
                                ||||| |||||     ||||||
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                                TGGGT CGGGG    GACAGC
                                  C    TC___
GAM378  LOC152762 3'  CCCCGGGGTGGGGTGTGGGT  80649      TG T      TGTTG
                                ACCCG  T CCTATCCT
                                |||||  | ||||||||
                                TGGGT  G GGGTGGGG
                                  GT _       CCCCA
GAM378  LOC153196 5'  CAGCCTGTGGGGGCCTGGGT  85956      T      CCTT
                                ACCCG GTTCCTAT   GTTG
                                ||||| ||||||||   ||||
                                TGGGT CGGGGGTG   CGAC
                                  C      TC__
GAM378  LOC153205 3'  CAAGCGTGTGGGACATGGGT  85941          _  C
                                ACCCGTGTTCC TAT CTTG
                                |||||||||||| ||| ||||
                                TGGGTACAGGG GTG GAAC
                                       T  C
GAM378  LOC153243 5'  TGGTGGGGCCAGCGGCATGGG  80801       TC  AT   TG
                                CCCGTGT  CT  CCT  TTG
                                |||||||  ||  |||  |||
                                GGGTACG  GA  GGG  GGT
                                    GC  CC   GT
GAM378  LOC153688 3'  TGGTGGGGTAAGTGGAATGGGG 86126     G     ___     TGTTG
          T                      ACCC TGTTCC   TATCCT
                                |||| ||||||   ||||||
                                TGGG GTAAGG   ATGGGG
                                  _     TGA     TGGT
GAM378  LOC153711 3'  TGTAAGGGAGAGTGCTGGT   86140     C TG   CTA     TT
                                ACC G  TTC   TCCTTG  G
                                ||| |  |||   ||||||  |
                                TGG C  GAG   GGGAAT  T
                                  T GT   A__     GG
GAM378  LOC153769 3'  CAGCAGGGGTGTGACAACGG   80925     GT  C
                                CCGT  TC TATCCTTGTTG
                                ||||  || ||||||||||
                                GGCA  AG GTGGGGACGAC
                                  AC  T
GAM378  LOC153785 5'  AGCCGGGTAGGAGTCGGGT   80931      TGT      TT   G
                                ACCCG   TCCTATCC  GTT
                                |||||   ||||||||  |||
                                TGGGC   AGGATGGG  CGA
                                  TG_      C_   G
GAM378  LOC154101 5'  CGGCGGGGACCCGGCACGG   82687       CCTA
                                CCGTGTT    TCCTTGTTG
                                |||||||    |||||||||
                                GGCACGG    AGGGGCGGC
                                    CCC_
GAM378  LOC155004 5'  TAATAGGGAAGGCGTGCG    81225    TG T   A
                                CG  T CCT TCCTTGTTG
                                ||  | ||| |||||||||
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                                GC  G GGA AGGGATAAT
                                 GT C   _
GAM378   LOC157254 5'  CAGCCTGGGGGATGTTGGT   81383    C TG   TAT  TT
                                ACC G  TTCC   CC  GTTG
                                ||| |  ||||   ||  ||||
                                TGG T  AGGG   GG  CGAC
                                  T GT    ___  TC
GAM378   LOC157623 5'  CAACGAGGCGGTGTGGGT    81492      TG  CCTAT
                                ACCCG  TT    CCTTGTTG
                                |||||  ||    ||||||||
                                TGGGT  GG    GGAGCAAC
                                   GT  C____
GAM378   LOC157651 3'  CAGTAATAATGGGTATGCGGGT 81539        T    CC
                                ACCCGTGT CCTAT  TTGTTG
                                |||||||| |||||  ||||||
                                TGGGCGTA GGGTA  AATGAC
                                     T    AT
GAM378   LOC158014 5'  TGGTGGGGATGGGAGGCAGGT  81661     C  G        TG
                                ACC GT TTCCTATCCT  TTG
                                ||| || ||||||||||  |||
                                TGG CG GAGGGTAGGG  GGT
                                  A  _        GT
GAM378   LOC158187 3'  AATAGGCCGGGCACGG      86685        CTATC
                                CCGTGTTC    CTTGTT
                                ||||||||    ||||||
                                GGCACGGG    GGATAA
                                     CC___
GAM378   LOC158191 3'  GAGGTGGGGACACGG       81776          T
                                CCGTGTTCCTA CCTT
                                |||||||||| ||||
                                GGCACAGGGGT GGAG
                                          _
GAM378   LOC158236 5'  CAACGAGGATCACAGCCCGGGT 86705      T   CCT
                                ACCCG GTT   ATCCTTGTTG
                                ||||| |||   ||||||||||
                                TGGGC CGA   TAGGAGCAAC
                                   C   CAC
GAM378   LOC158314 3'  CGACACTTAGGGGTATGGGT   86768       TT   TCCT
                                ACCCGTG  CCTA    TGTTG
                                |||||||  ||||   |||||
                                TGGGTAT  GGAT    ACAGC
                                    GG   TC__
GAM378   LOC158856 5'  CGGCGGGGCCTGCGCGGG    86915       TCCTAT
                                CCCGTGT     CCTTGTTG
                                |||||||     ||||||||
                                GGGCGCG     GGGGCGGC
                                    TCC___
GAM378   LOC158856 5'  GGCCTTGGGAACACGGG     86917          T__
                                CCCGTGTTCCTA   CC
                                ||||||||||||   ||
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                                GGGCACAAGGGT  GG
                                      TCC
GAM378  LOC159121 3' CAGCAGGGTCCACGTGG    86991   _   TTCCTAT
                                CC CGTG     CCTTGTTG
                                || ||||     ||||||||
                                GG GCAC     GGGACGAC
                                 T   CT_____
GAM378  LOC159148 5' CAATAAGGTCAGATAGGGGT  87010    G   CCTAT
                                ACCC TGTT   CCTTGTTG
                                |||| ||||   ||||||||
                                TGGG ATAG   GGAATAAC
                                  G   ACT__
GAM378  LOC159199 5' CAGCAGAGTGAGCAGGGGT   82181    G   _ ATCC
                                ACCC TGTTC CT   TTGTTG
                                |||| ||||| ||   ||||||
                                TGGG ACGAG GA   GACGAC
                                  G    T ____
GAM378  LOC159723 5' GGCGAGGCTGGTGGGT     82194     TGTT  TAT
                                ACCCG   CC  CCTTGTT
                                |||||   ||  |||||||
                                TGGGT   GG  GGAGCGG
                                   _____ TC_
GAM378  LOC160646 3' AGGATTAGGGATGTGGG    82223     TG    _
                                CCCG  TTCCTA TCCT
                                ||||  |||||| ||||
                                GGGT  AGGGAT AGGA
                                  GT    T
GAM378  LOC161482 3' GGCAAGAGAGGGTGGGT    87090     TGT   ATC
                                ACCCG  TCCT  CTTGTT
                                |||||  ||||  ||||||
                                TGGGT  GGGA  GAACGG
                                   ___   GA_
GAM378  LOC162239 3' CAGTATTGAGGGAACATGGG  82340        A  CT
                                CCCGTGTTCCT TC  TGTTG
                                |||||||||| ||  |||||
                                GGGTACAAGGG AG  ATGAC
                                      _ TT    A
GAM378  LOC164397 5' CAATGGGGATGTTGTCGTGGGT 82521       TTCC    TG
                                ACCCGTG   TATCCT  TTG
                                |||||||   ||||||  |||
                                TGGGTGC   GTAGGG  AAC
                                    TGTT    GT
GAM378  LOC165254 5' TATTGAGGGCGGGTGCGGGT  87193      GTT  AT   TTG
                                ACCCGT  CCT  CCTTG
                                ||||||  |||  |||||
                                TGGGCG  GGG  GGAGT
                                   T__  CG   TATG
GAM378  LOC165693 3' CAGTGGGGAGAAGTGCTGGGT 82594     T  TCCTA   TG
                                ACCCG GT   TCCT  TTG
                                ||||| ||   ||||  |||
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                              TGGGT CG    AGGG  GAC
                                _ TGAAG   GT
GAM378  LOC166341 3'  CGGCAGGACGGGGGGTATGG  82631     TT  ATC
                              CCGTG  CCT   CTTGTTG
                              |||||  |||   |||||||
                              GGTAT  GGG   GGACGGC
                                 GG   GCA
GAM378  LOC169693 5'  CAGCAGGGTCAGGGTGCTGGGT 87290     T _   AT
                              ACCCG GT TCCT  CCTTGTTG
                              ||||| || ||||  ||||||||
                              TGGGT CG GGGA  GGGACGAC
                                 _ T    CT
GAM378  LOC170261 3'  GGGGTGGGGGGTGGGGGT    82585     G  TT
                              ACCC TG  CCTATCCT
                              ||||  ||  ||||||||
                              TGGG GT  GGGTGGGG
                                G  GG
GAM378  LOC170394 5'  GTGGTGGGGGGAGCTGAACGGGT 82856      ___     AT_  TTGTTG
                              ACCCGT   GTTCCT   CC
                              ||||||   ||||||   ||
                              TGGGCA   CGAGGG   GG
                                 AGT     GGT  T   GT
GAM378  LOC196214 5'  CAGTCATGGGGGGTGCCGGT   89618    C TG     CC
                              ACC G  TTCCTAT  TTG
                              ||| |  |||||||  |||
                              TGG C  GGGGGGTA  GAC
                                C GT      CT
GAM378  LOC196264 3'  TAGTGGGGGGGCTTATGGAGT   87612    _    TT  TAT   TG
                              AC CCGTG  CC   CCT  TTG
                              || |||||  ||   |||  |||
                              TG GGTAT  GG   GGG  GAT
                               A    TC  ___   GT
GAM378  LOC196707 3'  CGACAAGGACAGTGTGGG    87527     TG  CCTA
                              CCCG  TT    TCCTTGTTG
                              ||||  ||    |||||||||
                              GGGT  GA    AGGAACAGC
                                GT  C___
GAM378  LOC196955 5'  AGCAGGCTGGCATGGG      77360      TT  TATC
                              CCCGTG  CC    CTTGTT
                              ||||||  ||    ||||||
                              GGGTAC  GG    GGACGA
                                 __  TC__
GAM378  LOC197003 5'  CGGTGAGGATGGGATGG     87873     TGT      TG
                              CCG   TCCTATCCT  TTG
                              |||   |||||||||  |||
                              GGT   AGGGTAGGA  GGC
                                ___       GT
GAM378  LOC197135 5'  CGAGCTGGGAGGGTGGGT    87891      TG     TC
                              ACCCG  TTCCTA  CTTG
                              |||||  ||||||  ||||
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                                TGGGT  GAGGGT  GAGC
                                  GG     C_
GAM378  LOC197136 3'  CGGCGGGGTCTTGGTGGGT   89729      TGTT  TAT_
                                ACCCG   CC   CCTTGTTG
                                |||||   ||   ||||||||
                                TGGGT   GG   GGGGCGGC
                                  ____  TTCT
GAM378  LOC197136 3'  TGGCGAGGGAGGGGGCAGGGT  89730      G      A
                                ACCC TGTTCCT TCCTTGTTG
                                |||| ||||||| |||||||||
                                TGGG ACGGGGG GGGAGCGGT
                                  _      A
GAM378  LOC197273 5'  CGACGGGGGAAGATGTGTCGGT 67398     C TG TC  A
                                ACC G  T  CT TCCTTGTTG
                                ||| |  |  || |||||||||
                                TGG T  G  GA GGGGGCAGC
                                  C GT TA  A
GAM378  LOC197379 3'  TGGTGAGGGTGGGGTCGTAGGG 89745     GTGT_       TG
                                CCC    TCCTATCCT  TTG
                                |||    |||||||||  |||
                                GGG    GGGGTGGGA  GGT
                                  ATGCT       GT
GAM378  LOC197408 5'  TAACAGGATGAGGCAGGGGT   89752     G   CC     T
                                ACCC TGTT  TATCCT GTTG
                                |||| ||||  |||||| ||||
                                TGGG ACGG  GTAGGA CAAT
                                  G   A_    _
GAM378  LOC199725 3'  TGACAATCAGAGGGACACGG   89842         ATCC
                                CCGTGTTCCT   TTGTTG
                                ||||||||||   ||||||
                                GGCACAGGGA   AACAGT
                                     GACT
GAM378  LOC199848 5'  CGGCGGGGGACGGTGCGG    89861     GTT  TA
                                CCGT   CC  TCCTTGTTG
                                ||||   ||  |||||||||
                                GGCG   GG  GGGGGCGGC
                                  T__  CA
GAM378  LOC199848 5'  CGGCGGGGGATGGTGCGG    89862     GTT  TA
                                CCGT   CC  TCCTTGTTG
                                ||||   ||  |||||||||
                                GGCG   GG  GGGGGCGGC
                                  T__  TA
GAM378  LOC199907 3'  AACATCGGGACATGGGT     88457          TATCCT
                                ACCCGTGTTCC     TGTT
                                ||||||||||     ||||
                                TGGGTACAGGG     ACAA
                                     CT_____
GAM378  LOC199964 5'  CGGCGGAGAGGGCGCGG     89890       T   A   TT
                                CCGTGT CCT TCC  GTTG
                                |||||| ||| |||  ||||
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                                GGCGCG GGA AGG  CGGC
                                   _  G  __
GAM378  LOC200169 5'  GGCATTTGGGGACGGGT    89954      GT    TCCT
                                ACCCGT  TCCTA   TGTT
                                ||||||  |||||   ||||
                                TGGGCA  GGGGT   ACGG
                                   __    TT__
GAM378  LOC200301 3'  CAGCAGCGGGGCACGTGGT   88738    _      TATCC
                                ACC CGTGTTCC    TTGTTG
                                ||| ||||||||    ||||||
                                TGG GCACGGGG    GACGAC
                                  T      C____
GAM378  LOC200312 3'  CAATAAGGAAAGAGAATATGGG 89991         _  A
                                CCCGTGTTC CT TCCTTGTTG
                                ||||||||| || |||||||||
                                GGGTATAAG GA AGGAATAAC
                                      A  A
GAM378  LOC200339 3'  AGCAGGGATTACAGGT     90029    C   TTCCT
                                ACC GTG    ATCCTTGTT
                                ||| |||    |||||||||
                                TGG CAT    TAGGGACGA
                                  A  _____
GAM378  LOC200953 5'  TGGTGGGGATGGGAGTAGC   90213   GT_      TG
                                GT   TCCTATCCT  TTG
                                ||   |||||||||  |||
                                CG   AGGGTAGGG  GGT
                                  ATG       GT
GAM378  LOC200982 3'  CAGTGGGGATGGGGGAAGG   90217   GTG       TG
                                CC   TTCCTATCCT  TTG
                                ||   ||||||||||  |||
                                GG   GGGGGTAGGG  GAC
                                  AA_       GT
GAM378  LOC201102 3'  CGGTGAGGGTAAGGTTGGTGGG 88092     TGTT  _    TG
                                CCCG    CCT ATCCT  TTG
                                ||||    ||| |||||  |||
                                GGGT    GGA TGGGA  GGC
                                   GGTT   A    GT
GAM378  LOC201102 3'  CTCTCAAGGGGTGGGGGTGGGG 88093     G  TT       GTTG
           T                     ACCC TG  CCTATCCTT
                                ||||  ||  |||||||||
                                TGGG GT  GGGTGGGGA
                                   _  GG       ACTCTCC
GAM378  LOC201102 3'  TAGTGAGGGTTCCCCGGTGAGG 88098     GTGTT  T____    TG
           GT                     CCC    CC    ATCCT  TTG
                                |||    ||    |||||  |||
                                GGG    GG    TGGGA  GAT
                                  AGT__  CCCCT    GT
GAM378  LOC201252 5'  CAGCACCCTGAGGAGCATGG   88166         ATCCT
                                CCGTGTTCCT    TGTTG
                                ||||||||||    |||||
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                                GGTACGAGGA    ACGAC
                                      GTCCC
GAM378  LOC201522 3'  CAACCCCATCGGGAACGAGGGT 88254     G     ATCCTT
                                ACCC TGTTCCT    GTTG
                                |||| |||||||    ||||
                                TGGG GCAAGGG    CAAC
                                  A     CTACCC
GAM378  LOC201689 5'  TAGCAGGGGCAGGGTGTGTGT  67152    C  TG T   AT
                                AC CG  T CCT  CCTTGTTG
                                || ||  | |||  ||||||||
                                TG GT  G GGA  GGGACGAT
                                 T  GT _   CG
GAM378  LOC202038 5'  GGCGAGGGCTGGGGGT     89148     GTGTT  TA
                                ACCC    CC  TCCTTGTT
                                ||||    ||  ||||||||
                                TGGG    GG  GGGAGCGG
                                  _____  TC
GAM378  LOC202134 3'  TAACAGGCAAGGCAAGGGT   90323     G  TT   ATC
                                ACCC TG  CCT   CTTGTTG
                                |||| ||  |||   |||||||
                                TGGG AC  GGA   GGACAAT
                                  A  __   AC_
GAM378  LOC202451 3'  AGCCAGTGGGTGGTATGGGT   90351       TTC    _   TTG
                                ACCCGTG   CTATCC TTG
                                |||||||   |||||| |||
                                TGGGTAT   GGTGGG GAC
                                   ___     T   CGAA
GAM378  LOC202785 5'  TGACGAGAGTTGGGAGTGTGG  89201    TG    TC_
                                CCG  TTCCTA   CTTGTTG
                                |||  ||||||   |||||||
                                GGT  GAGGGT   GAGCAGT
                                  GT     TGA
GAM378  LOC202908 5'  CAGTCAAGGTGGGAGCAGGGT  89230     G      T    _
                                ACCC TGTTCCTA CCTTG TTG
                                |||| |||||||| ||||| |||
                                TGGG ACGAGGGT GGAAC GAC
                                  _      _    T
GAM378  LOC203042 3'  GGATTTGGGAGCGCGGG     90448          __
                                CCCGTGTTCCT  ATCC
                                ||||||||||  ||||
                                GGGCGCGAGGG  TAGG
                                      TT
GAM378  LOC203350 3'  CAGTGAGGTGCTGGGACATGG  90565        TAT_  TG
                                CCGTGTTCC   CCT  TTG
                                |||||||||   |||  |||
                                GGTACAGGG   GGA  GAC
                                     TCGT   GT
GAM378  LOC203397 5'  CGGAGGCGGTGGGGGTGCGG  89350    TG      _  GTTG
                                CCG  TTCCTATC CTT
                                |||  |||||||| |||
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                                GGC  GGGGGTGG GGA
                                  GT       C   GGC
GAM378   LOC203636 3'  TGACAGAAGCCGAGCGTGGG   89433         CTATCC
                                CCCGTGTTC     TTGTTG
                                |||||||||     ||||||
                                GGGTGCGAG     GACAGT
                                    CCGAA_
GAM378   LOC204970 3'  TGACGAGGGTGGGAGATGC    89419     _
                                GTGT TCCTATCCTTGTTG
                                |||| ||||||||||||||
                                CGTA AGGGTGGGAGCAGT
                                  G
GAM378   LOC205095 3'  CAACGAGGGGGCCCACGGG    90696       TT   AT
                                CCCGTG  CCT  CCTTGTTG
                                ||||||  |||  ||||||||
                                GGGCAC  GGG  GGAGCAAC
                                   CC  __
GAM378   LOC219294 3'  AGTAAGGGGTGGTGGCATGG   93003       TC      GTTG
                                CCGTGT  CTATCCTT
                                ||||||  ||||||||
                                GGTACG  GGTGGGGA
                                   GT       ATGAT
GAM378   LOC219295 3'  AGTAAGGGGTGGTGGCATGG   92988       TC      GTTG
                                CCGTGT  CTATCCTT
                                ||||||  ||||||||
                                GGTACG  GGTGGGGA
                                   GT       ATGAT
GAM378   LOC219376 5'  AGCTTTTGGGGCGCGGGT     93896          TATCCTT
                                ACCCGTGTTCC      GTT
                                ||||||||||       |||
                                TGGGCGCGGGG      CGA
                                     TTTT___
GAM378   LOC219376 5'  GGGCGCGGGTGGGAGCGCGGG  93899             T   G
                                CCCGTGTTCCTATCC TGTT
                                ||||||||||||||| ||||
                                GGGCGCGAGGGTGGG GCGG
                                       C   GG
GAM378   LOC219397 3'  AGTGTTGGGGGTGGGGGGTGGG 93470       TGT         TTG
           T                     ACCCG   TCCTATCCTTG
                                 |||||   ||||||||||
                                 TGGGT   GGGGTGGGGGT
                                   GG_         TGTGAA
GAM378   LOC219513 5'  CAGCAAGGATGGGAGACGG    94326      G
                                CCGT TTCCTATCCTTGTTG
                                |||| ||||||||||||||
                                GGCA GAGGGTAGGAACGAC
                                  _
GAM378   LOC219529 5'  TGGCAGCCAGGGGCGGGGGT   92976      G      ATCC
                                ACCC TGTTCCT    TTGTTG
                                |||| |||||||    ||||||
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                                TGGG GCGGGGA   GACGGT
                                  G     CC__
GAM378  LOC219667 3'  GGGATGGGCATGTGGT     91313    _   TT
                                ACC CGTG  CCTATCCT
                                ||| ||||  ||||||||
                                TGG GTAC  GGGTAGGG
                                  T   __
GAM378  LOC219686 5'  CAATGGGGATGTGGGCGCGGG  90840        C     TG
                                CCCGTGTTC TATCCT  TTG
                                ||||||||| ||||||  |||
                                GGGCGCGGG GTAGGG  AAC
                                      T     GT
GAM378  LOC219686 5'  CGAGACAATGGGGATGTGGG   90841     TG     C__   TTG
                                CCCG  TTCCTAT   CTTG
                                ||||  |||||||   ||||
                                GGGT  AGGGGTA   GAGC
                                  GT      ACA
GAM378  LOC220001 3'  GGTGGGGATGCCTGGG     91636    __
                                CCC  GTGTTCCTATC
                                |||  ||||||||||
                                GGG  CGTAGGGGTGG
                                  TC
GAM378  LOC220514 3'  CGGCGGGGGTGGGGGGAACGTG 60445          ___
           GG                     CCCGTGTTCCT   ATCCTTGTTG
                                ||||||||||   ||||||||||
                                GGGTGCAAGGG   TGGGGGCGGC
                                      GGG
GAM378  LOC220705 3'  TGGTAGGGCAGTAACATTGGGT 91231      _   C  AT   TGTTG
                                ACCCG TGTT CT  CCT
                                ||||| |||| ||  |||
                                TGGGT ACAA GA  GGA
                                  T    T  CG   TGGT
GAM378  LOC220753 3'  TAATAAGAAAGCTGAGAATGTG 92943     TG   CTATC___
           GGT                    CCCG  TTC       CTTGTTG
                                ||||  |||      |||||||
                                GGGT  AAG       GAATAAT
                                  GT   AGTCGAAA
GAM378  LOC220758 3'  TGGCAGGGACCCTCATGG    90787      TTCCTA
                                CCGTG     TCCTTGTTG
                                |||||     |||||||||
                                GGTAC     AGGGACGGT
                                  TCCC__
GAM378  LOC220776 3'  CAGCAAGGGTCTCTCATGG    68385      TTCCT
                                CCGTG    ATCCTTGTTG
                                |||||    ||||||||||
                                GGTAC    TGGGAACGAC
                                  TCTC_
GAM378  LOC220790 5'  TAGCGACCCGCGGGGAGCGCGG 91234          ATCC__
           G                     CCCGTGTTCCT     TTGTTG
                                ||||||||||     ||||||
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                                GGGCGCGAGGG     AGCGAT
                                      GCGCCC
GAM378  LOC220963 3'  CAGTGGGGATGGGCTGCA    91446     T_      TG
                                TGT  CCTATCCT  TTG
                                |||  ||||||||  |||
                                ACG  GGGTAGGG  GAC
                                  TC       GT
GAM378  LOC220992 5'  TGACATTTGGGGATGTGG    91472     TG     TCCT
                                CCG  TTCCTA    TGTTG
                                |||  ||||||    |||||
                                GGT  AGGGGT    ACAGT
                                  GT     TT__
GAM378  LOC221002 3'  AATGGGGAAGCCTGGGT     91473      T   CCTA    TG
                                ACCCG GTT    TCCT  TT
                                ||||| |||    ||||  ||
                                TGGGT CGA    AGGG  AA
                                   C  _____   GT
GAM378  LOC221288 5'  AGCAGGGGTAGAGGG      93613     GTGTTC
                                CCC     CTATCCTTGTT
                                |||     ||||||||||
                                GGG     GATGGGGACGA
                                  A_____
GAM378  LOC221393 3'  GGGGTGGGAGTGGGAGTGTGGG 92296      TG     TC  TG  G
          T                      ACCCG  TTCCTA  CT  TT
                                |||||  ||||||  ||  ||
                                TGGGT  GAGGGT  GG  GG
                                   GT     GA  GT  GGG
GAM378  LOC221466 5'  CAGCAGGTGGGTGGGGGATGTG 93683      TG    _    __
          GGT                     CCCG  TTCCT ATCC  TTGTTG
                                ||||  ||||| ||||  ||||||
                                GGGT  AGGGG TGGG  GACGAC
                                  GT    G   TG
GAM378  LOC221474 5'  AAGGAGGGACATGGGT      92374          TA
                                ACCCGTGTTCC  TCCTT
                                ||||||||||  |||||
                                TGGGTACAGGG  AGGAA
                                          __
GAM378  LOC221474 5'  TGGTGGGGATGGTGTGGG    92388      TG TCC     TG
                                CCCG  T   TATCCT  TTG
                                ||||  |   ||||||  |||
                                GGGT  G   GTAGGG  GGT
                                  GT ___     GT
GAM378  LOC221474 3'  TTCCCCAGGTGGGGGTATGGTG 92390    _    TT    T   TGTTG
          T                      AC CCGTG  CCTA CCT
                                ||  |||||  |||| |||
                                TG GGTAT  GGGT GGA
                                 T    GG   _   CCCCTTG
GAM378  LOC221687 3'  CGGCAGGGGTGTGGTGTGT   92248   TG T  _
                                G  T CC TATCCTTGTTG
                                |  | || ||||||||||
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                                T  G GG GTGGGGACGGC
                                 GT T  T
GAM378  LOC221833 3'  ACTTACGGGGTGGGGGCGGGGG 92538      G          TGTTG
           T                      ACCC TGTTCCTATCCT
                                  ||||| ||||||||||||
                                  TGGG GCGGGGGTGGGG
                                    G          CATTCAA
GAM378  LOC221882 5'  GGCGGGCGGGCGCGGGT     92501          _ AT
                                  ACCCGTGTTC CT  CC
                                  |||||||||| ||  ||
                                  TGGGCGCGGG GG  GG
                                        C  GC
GAM378  LOC221922 5'  GAGGACAGGTGGGGGCGTGGG  92693           T  T  G
                                  CCCGTGTTCCTA CCT GTT
                                  |||||||||||| ||| |||
                                  GGGTGCGGGGGT GGA CAG
                                        _  _  GAGA
GAM378  LOC221922 5'  TGATGGGGAATAGGAGGGCAGG 92706     G  __     _  TG
           GGT                     CCC TGT  TCCTAT CCT  TTG
                                  ||| |||  |||||| |||  |||
                                  GGG ACG  AGGATA GGG  AGT
                                    G  GG     A  GT
GAM378  LOC221960 3'  CTTGCTGGATGGGGACACGG   91082           TT  TG
                                  CCGTGTTCCTATCC  GT
                                  ||||||||||||||  ||
                                  GGCACAGGGGTAGG  CG
                                        T_  TTCT
GAM378  LOC222031 3'  GGGTTGGGGGGCGTGGG      94027          T
                                  CCCGTGTTCCTA CCT
                                  |||||||||||| |||
                                  GGGTGCGGGGGT GGG
                                        T
GAM378  LOC222060 5'  TGGTGAGGTAAAGGTGGGT   94112      TGTT   AT_  TG
                                  ACCCG   CCT   CCT  TTG
                                  |||||   |||   |||  |||
                                  TGGGT   GGA   GGA  GGT
                                     _____  AAT   GT
GAM378  LOC222189 3'  TAGCAAGGACTTTGGGTGGGT  94171      TGTT   ___
                                  ACCCG   CCTA   TCCTTGTTG
                                  |||||   ||||   |||||||||
                                  TGGGT   GGGT   AGGAACGAT
                                     _____   TTC
GAM378  LOC245771 5'  CGGCGGGGCGGTACGTGGT   92884     _   TT  TAT
                                  ACC CGTG  CC   CCTTGTTG
                                  ||| ||||  ||   ||||||||
                                  TGG GCAT  GG   GGGGCGGC
                                    T   __  C__
GAM378  LOC253039 5'  CGGCGAGGGTGGGGACTCACGG 96155       __
           G                       CCCGT  GTTCCTATCCTTGTTG
                                  |||||  ||||||||||||||||
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                                GGGCA  CAGGGGTGGGAGCGGC
                                   CT
GAM378  LOC253489 5'  CGGCGGGCTGGGCGCGGG    95493       TT   T  T
                                CCCGTG  CCTA CCT GTTG
                                ||||||  |||| ||| ||||
                                GGGCGC  GGGT GGG CGGC
                                   __   C  _
GAM378  LOC253912 3'  GGGCTTAGGGACGCTGGT    97359    C       T_
                                ACC GTGTTCCTA  CCT
                                ||| |||||||||  |||
                                TGG CGCAGGGAT  GGG
                                  T       TC
GAM378  LOC253912 3'  GGTGAAATGGAGCGTGGGT   97360          TA_ _
                                ACCCGTGTTCC   TC CT
                                ||||||||||   || ||
                                TGGGTGCGAGG   AG GG
                                      TAA  T
GAM378  LOC253955 5'  CGGCGGGGGTGGGCAGGG    94427    G  TT
                                CCC TG  CCTATCCTTGTTG
                                ||| ||  |||||||||||||
                                GGG AC  GGGTGGGGGCGGC
                                 _ __
GAM378  LOC254015 3'  CAGTGAGGAGGGGGGCTTGGGT 96701      T    A   TG
                                ACCCG GTTCCT TCCT  TTG
                                ||||| |||||| ||||  |||
                                TGGGT CGGGGG AGGA  GAC
                                   T     G   GT
GAM378  LOC254107 5'  CAGCGGGACCCCAGCGCGGG   94383       CCTA   T
                                CCCGTGTT    TCCT GTTG
                                ||||||||    |||| ||||
                                GGGCGCGA    AGGG CGAC
                                     CCCC   _
GAM378  LOC254120 3'  CGGCAGGGGTGGGGCAGGGGT  97395     G   T
                                ACCC TGT CCTATCCTTGTTG
                                |||| ||| ||||||||||||
                                TGGG ACG GGGTGGGGACGGC
                                  G  _
GAM378  LOC254124 3'  CGACAGCGCCCGGGAACACGG  96649         ATCC_
                                CCGTGTTCCT    TTGTTG
                                ||||||||||    ||||||
                                GGCACAAGGG    GACAGC
                                      CCCGC
GAM378  LOC254413 5'  CGATAAGGATCAAGCAGG    97122    G   CCT
                                CC TGTT   ATCCTTGTTG
                                || ||||   ||||||||||
                                GG ACGA   TAGGAATAGC
                                 _   AC_
GAM378  LOC254428 3'  GGAATCTGGGGACATGGG    95460          ___
                                CCCGTGTTCCTA   TCC
                                ||||||||||||   |||
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                                GGGTACAGGGGT  AGG
                                      CTA
GAM378  LOC254753 3'  CAACAGGGGTGTTGCGGG   96145      TTCC
                                CCCGTG   TATCCTTGTTG
                                ||||||   ||||||||||
                                GGGCGT   GTGGGGACAAC
                                   T___
GAM378  LOC254755 3'  AGCAGGGAGGTGGGGT     97365     GTGTT  TA
                                ACCC    CC  TCCTTGTT
                                ||||    ||  ||||||||
                                TGGG    GG  AGGGACGA
                                  GT___  __
GAM378  LOC254756 3'  AGCAGGGAGGTGGGGT     97362     GTGTT  TA
                                ACCC    CC  TCCTTGTT
                                ||||    ||  ||||||||
                                TGGG    GG  AGGGACGA
                                  GT___  __
GAM378  LOC254808 3'  TGGTGAGGGCATCAGCATGGGT 97025        CCTA   TG
                                ACCCGTGTT   TCCT  TTG
                                |||||||||   ||||  |||
                                TGGGTACGA   GGGA  GGT
                                     CTAC   GT
GAM378  LOC254866 5'  CGGCAGGGCGTGCGCAGGGT  96766     _   TCCTAT
                                ACCC GTGT     CCTTGTTG
                                |||| ||||     ||||||||
                                TGGG CGCG     GGGACGGC
                                  A   TGC___
GAM378  LOC254890 3'  CAACCTGAATTGGGAACATGGG 95159          TCCTT_
                                CCCGTGTTCCTA     GTTG
                                ||||||||||||     ||||
                                GGGTACAAGGGT     CAAC
                                      TAAGTC
GAM378  LOC255031 5'  CAACAGGAGCAGGGTGCGG   97230     TG T   A_   T
                                CCG  T CCT  TCCT GTTG
                                |||  | |||  |||| ||||
                                GGC  G GGA  AGGA CAAC
                                  GT _   CG   _
GAM378  LOC255042 5'  GGTGGGGATGAGGCGGG     95323      ___
                                CCCGT   GTTCCTATC
                                |||||   |||||||||
                                GGGCG   TAGGGGTGG
                                   GAG
GAM378  LOC255082 5'  TGGCGGGTCCTAGGGACGTGGG 96397          TC_
          T                      ACCCGTGTTCCTA   CTTGTTG
                                ||||||||||||||   |||||||
                                TGGGTGCAGGGAT   GGGCGGT
                                      CCT
GAM378  LOC255158 3'  CAATGAGGTATAGCATGTGT   96170    C    TTC   _   TG
                                AC CGTG   CTAT CCT  TTG
                                || ||||   ||||  |||  |||
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                                TG GTAC   GATA GGA  AAC
                                 T   ___   T  GT
GAM378  LOC255170 3'  CAGCGGGATAAAGGGGTGTGGG 97516     TG   __    T
                                CCCG  TTCCT  ATCCT GTTG
                                ||||  |||||  ||||| ||||
                                GGGT  GGGGA  TAGGG CGAC
                                  GT    AA   _
GAM378  LOC255242 5'  AACAAGGATGATGTGG     95925     TG  CCT
                                CCG  TT   ATCCTTGTT
                                |||  ||   |||||||||
                                GGT  AG   TAGGAACAA
                                 GT  ___
GAM378  LOC255270 5'  GGGATTGGGGACGTGTGT    94605    C       _
                                AC CGTGTTCCTA TCCT
                                || ||||||||||  ||||
                                TG GTGCAGGGGT AGGG
                                 T        T
GAM378  LOC255452 3'  CAGCAGGAGCAATGCGGG    97527        CCTA   T
                                CCCGTGTT    TCCT GTTG
                                ||||||||    |||| ||||
                                GGGCGTAA    AGGA CGAC
                                    CG__   _
GAM378  LOC255480 3'  AGGTGGGGGTGTGGGT      96519      TG     T
                                ACCCG  TTCCTA CCT
                                |||||  ||||||  |||
                                TGGGT  GGGGGT GGA
                                  GT    _
GAM378  LOC255671 3'  GATGGTGGCACATGGGT     97257        _ _
                                ACCCGTGT TC CTATC
                                |||||||| || |||||
                                TGGGTACA GG GGTAG
                                    C  T
GAM378  LOC255749 3'  ACAGGGTGGGAATGGGGGT   96446     G         T
                                ACCC TGTTCCTATCCT GT
                                |||| ||||||||||| ||
                                TGGG GTAAGGGTGGGA CA
                                  G         _
GAM378  LOC255971 3'  TGGCAAGGTGCCGGGCGCGG  96537        CTAT
                                CCGTGTTC   CCTTGTTG
                                ||||||||   ||||||||
                                GGCGCGGG   GGAACGGT
                                    CCGT
GAM378  LOC256158 5'  GATGTGTGGGATGCGGG     97667         ___
                                CCCGTGTTCC   TATC
                                ||||||||||   ||||
                                GGGCGTAGGG   GTAG
                                     TGT
GAM378  LOC256524 5'  CGGCGGGACTGGCGCGGG    95576       TT  TA   T
                                CCCGTG  CC  TCCT GTTG
                                ||||||  ||  |||| ||||
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                                GGGCGC  GG  AGGG CGGC
                                   __ TC   _
GAM378  LOC256790 5'  ATGAAGTTTGGGACAGGGGT  94833     G  T   TC  GTTG
                                ACCC TGT CCTA  CTT
                                |||| ||| ||||  |||
                                TGGG ACA GGGT  GAA
                                  G  _   TT  GTAA
GAM378  LOC256830 3'  TGGCAAGGATGTTCGGCTGGT  94554    C  GTTCC
                                ACC GT    TATCCTTGTTG
                                ||| ||    ||||||||||
                                TGG CG    GTAGGAACGGT
                                  T  GCTT_
GAM378  LOC256923 5'  CGGCGGGTCGGGGCGAGGGT  95138     G    T   TT
                                ACCC TGTTCC ATCC  GTTG
                                |||| |||||| ||||  ||||
                                TGGG GCGGGG TGGG  CGGC
                                  A     C   __
GAM378  LOC257051 3'  GGGGTGGGGGTGGGGGT    96319     G  TT
                                ACCC TG  CCTATCCT
                                |||| ||  ||||||||
                                TGGG GT  GGGTGGGG
                                  G  GG
GAM378  LOC257054 3'  CAGCGGGGGGCATGCGTGGG  95655       TCCTA
                                CCCGTGT    TCCTTGTTG
                                |||||||    |||||||||
                                GGGTGCG    GGGGGCGAC
                                    TACG_
GAM378  LOC257104 5'  TGCGGTGGGGGCACCCCGTGG  97496   _ ___        CTTGTTG
                                CC C   GTGTTCCTATC
                                || |   ||||||||||
                                GG G   CACGGGGGTGG
                                 T CCC         C   GTT
GAM378  LOC257160 3'  GAACAGGAAGCGCGGGT    94847        CCTA   T   G
                                ACCCGTGTT    TCCT GTT
                                |||||||||    |||| |||
                                TGGGCGCGA    AGGA CAA
                                     ____   _  GT
GAM378  LOC257203 5'  CGGCAGGGATTCCGGCGG    96930     GTTCCT
                                CCGT     ATCCTTGTTG
                                ||||     ||||||||||
                                GGCG     TAGGGACGGC
                                  GCCT__
GAM378  LOC257478 5'  CAACAGCGCGGAGTGCGAGT  73107    C  TG   TATCC
                                AC CG  TTCC    TTGTTG
                                || ||  ||||    ||||||
                                TG GC  GAGG    GACAAC
                                 A  GT   CGC__
GAM378  LOC257547 5'  CAGTAGGGGGCTCTCGCGG   97698     TTCCTA
                                CCGTG     TCCTTGTTG
                                |||||     |||||||||
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                                GGCGC     GGGGATGAC
                                   TCTCG_
GAM378  LOC257607 5'  CAGTAGGGGGCTCTCGCGG   97818      TTCCTA
                                CCGTG     TCCTTGTTG
                                |||||     |||||||||
                                GGCGC     GGGGATGAC
                                   TCTCG_
GAM378  LOC257608 3'  GGAGATGGGGGCGGGGGT    97829      G        _
                                ACCC TGTTCCTATC CT
                                |||| |||||||||| ||
                                TGGG GCGGGGGTAG GG
                                  G         A
GAM378  LOC51112  5'  CAGCGAGGGCGACGCGGG    32083        CCTA
                                CCCGTGTT    TCCTTGTTG
                                ||||||||    |||||||||
                                GGGCGCAG    GGGAGCGAC
                                     C___
GAM378  LOC51112  5'  CGGCGAGGCTACGCGTGG    32087    _    TCCTAT
                                CC CGTGT     CCTTGTTG
                                || |||||     ||||||||
                                GG GCGCA     GGAGCGGC
                                 T    TC_____
GAM378  LOC51161  3'  CAAGTTATAGGGACAGGGT    32508     G        C_
                                ACCC TGTTCCTAT  CTTG
                                |||| |||||||||  ||||
                                TGGG ACAGGGATA  GAAC
                                  _        TT
GAM378  LOC51161  3'  GAGAGTGGGGAGATGGGT    32513       G     TC
                                ACCCGT TTCCTA  CTT
                                ||||||| ||||||  |||
                                TGGGTA AGGGGT  GAG
                                   G     GA
GAM378  LOC51194  3'  TAATAGGGGTATACCTGGG    32934      T  TCC
                                CCCG GT   TATCCTTGTTG
                                |||| ||   ||||||||||
                                GGGT CA   ATGGGGATAAT
                                  C  T__
GAM378  LOC51291  3'  TGACACCTGGGACAGGGGT    33365      G     TATCCT
                                ACCC TGTTCC      TGTTG
                                |||| ||||||      |||||
                                TGGG ACAGGG      ACAGT
                                  G     TCC___
GAM378  LOC51301  3'  AGGAAGGGGGTGAGGATGTGGG 33438       TG   C     TG  G
          T                      ACCCG  TTC TATCCT  TT
                                |||||  ||| ||||||  ||
                                TGGGT  AGG GTGGGG  AG
                                   GT   A     GA  GAA
GAM378  LOC51622  3'  CTTGCTGGATGGGGACACGG   31567            TT  TG
                                CCGTGTTCCTATCC  GT
                                ||||||||||||||  ||
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                                GGCACAGGGGTAGG  CG
                                      T_  TTCT
GAM378  LOC54518  5' CAGCGACCTGGAGCCCGGGT  38770     T    TATCC
                                ACCCG GTTCC    TTGTTG
                                ||||| |||||    ||||||
                                TGGGC CGAGG    AGCGAC
                                   C    TCC__
GAM378  LOC57406  3' AGCAGGGTACATGGGT     40343       TCCTAT
                                ACCCGTGT     CCTTGTT
                                ||||||||     |||||||
                                TGGGTACA     GGGACGA
                                    T_____
GAM378  LOC63923  3' TGGCAGCTTGGGGCGGG    67124     GTT   TCC
                                CCCGT   CCTA   TTGTTG
                                |||||   ||||   ||||||
                                GGGCG   GGGT   GACGGT
                                   ___   TC_
GAM378  LOC64182  3' GATAGAAGAGCATGGG     42296       __
                                CCCGTGTTC  CTATC
                                |||||||||  |||||
                                GGGTACGAG  GATAG
                                     AA
GAM378  LOC83985  5' CGGTGGGACCGGAGCGCGGG  49349        TA   TGTTG
                                CCCGTGTTCC  TCCT
                                ||||||||||  ||||
                                GGGCGCGAGG  AGGG
                                      CC   TGGC
GAM378  LOC84548  5' CAGCAGCGTGGACGCGG    71251      T  TATCC
                                CCGTGT CC    TTGTTG
                                |||||| ||    ||||||
                                GGCGCA GG    GACGAC
                                   _  TGC__
GAM378  LOC85414  5' CAGCAGGTGTTGAGCATGGG  52393       CT TC
                                CCCGTGTTC  A  CTTGTTG
                                |||||||||  |  |||||||
                                GGGTACGAG  T  GGACGAC
                                     T_ GT
GAM378  LOC89919  5' TAACAGGGTAACATACGG    60729      TCCTAT
                                CCGTGT     CCTTGTTG
                                ||||||     ||||||||
                                GGCATA     GGGACAAT
                                   CAAT__
GAM378  LOC89944  3' CAGTGAGGAGGACATG     91544       CTA   TG
                                CGTGTTC   TCCT  TTG
                                |||||||   ||||  |||
                                GTACAGG   AGGA  GAC
                                   ___   GT
GAM378  LOC90024  5' CGGCGGGGCGCTGTGGAACGCG 61111         TAT___
           GG                   CCCGTGTTCC     CCTTGTTG
                                ||||||||||     ||||||||
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                              GGGCGCAAGG     GGGGCGGC
                                    TGTCGC
GAM378  LOC90148  3' TAACACTTGGGGAATATGAGT  61665    C       ATCCT
                              AC CGTGTTCCT    TGTTG
                              || |||||||||    |||||
                              TG GTATAAGGG    ACAAT
                                A       GTTC_
GAM378  LOC90167  3' GGCAAGGCAAGGTGGGT     61704      TGTT   AT
                              ACCCG   CCT  CCTTGTT
                              |||||   |||  |||||||
                              TGGGT   GGA  GGAACGG
                                 _____  AC
GAM378  LOC90342  5' CAGTAAGGGCTGGGAGTATGGA 62356    _        _
           GT                   AC CCGTGTTCCTA TCCTTGTTG
                              || |||||||||| |||||||||
                              TG GGTATGAGGGT GGGAATGAC
                               A         C
GAM378  LOC90362  3' GGAAAGGAGGGAGCGTGGGT   62443          A    GTTG
                              ACCCGTGTTCCT TCCTT
                              |||||||||||| |||||
                              TGGGTGCGAGGG AGGAA
                                     _    AGGT
GAM378  LOC90381  3' CAGAAGTGGGGGGCGGGT    62543       G      CC
                              ACCCGT TTCCTAT  TTG
                              |||||| |||||||  |||
                              TGGGCG GGGGGTG  GAC
                                 _      AA
GAM378  LOC90415  3' TGACAAGGATGGGCTATAGGG  62711     G   T_
                              CCC TGT  CCTATCCTTGTTG
                              ||| |||  ||||||||||||
                              GGG ATA  GGGTAGGAACAGT
                                _  TC
GAM378  LOC90499  3' GGACTACTGTGGGAATAGGGGT 63064      G       CCTT   G
                              ACCC TGTTCCTAT    GTT
                              |||| |||||||||    |||
                              TGGG ATAAGGGTG    CAG
                                G       TCAT   GT
GAM378  LOC90625  3' TAGCAGAAGAGGGTGCGGG    63614     TG T   ATCC
                              CCCG  T CCT    TTGTTG
                              ||||  | |||    ||||||
                              GGGC  G GGA    GACGAT
                                GT _   GAA_
GAM378  LOC90639  3' AGCCTGGGCAACATGGGT     63650         _   TC
                              ACCCGTGTT CCTA  CT
                              ||||||||| ||||  ||
                              TGGGTACAA GGGT  GA
                                   C   CC
GAM378  LOC90668  3' CGGCAGGACCAGGCATGGG    82269       TT  A_   T
                              CCCGTG  CCT  TCCT GTTG
                              ||||||  |||  |||| ||||
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                                GGGTAC  GGA  AGGA CGGC
                                   __   CC   _
GAM378  LOC90750  5' CGATAGGTATTTGGAGCATGAG 63920    C      T_  C
             T                   AC CGTGTTCC  AT CTTGTTG
                                 || ||||||||  || |||||||
                                 TG GTACGAGG  TA GGATAGC
                                  A       TT  T
GAM378  LOC90784  5' CAGTGGGGAGGTACTTGGGT   64000      T  T  TA    TG
                                 ACCCG GT CC  TCCT  TTG
                                 ||||| || ||  ||||  |||
                                 TGGGT CA GG  AGGG  GAC
                                    T  T __   GT
GAM378  LOC90784  5' GGCAGGGTACCTGGGT      64003      T  TCCTAT
                                 ACCCG GT     CCTTGTT
                                 ||||| ||     |||||||
                                 TGGGT CA     GGGACGG
                                    C  T_____
GAM378  LOC90841  3' CAGCATGAAGGAGGGTGGGT   64195      TG    A  CT
                                 ACCCG  TTCCT TC  TGTTG
                                 |||||  ||||| ||  |||||
                                 TGGGT  GAGGA AG  ACGAC
                                    GG    _  T_
GAM378  LOC90982  3' TGACAGGGGTAGAAATTGGG   64539     T   C
                                 CCCG GTT CTATCCTTGTTG
                                 |||| ||| ||||||||||||
                                 GGGT TAA GATGGGGACAGT
                                    _   A
GAM378  LOC91010  3' TGGCAGGGGACAAGGAGCATGG 64618          A__
                                 CCGTGTTCCT   TCCTTGTTG
                                 ||||||||||   |||||||||
                                 GGTACGAGGA   GGGGACGGT
                                       ACA
GAM378  LOC91064  5' CGGTGGGGAGGGTGGCAGCGGG 64762       _   TC  A    TG
             T                   ACCCG TGT  CT TCCT  TTG
                                 ||||| |||  || ||||  |||
                                 TGGGC ACG  GG AGGG  GGC
                                    G   GT  G   GT
GAM378  LOC91263  5' TGATGGGGGAAAAACACAGGT  65384     C    CCTA    TG
                                 ACC GTGTT    TCCT  TTG
                                 ||| |||||    ||||  |||
                                 TGG CACAA    GGGG  AGT
                                   A    AAA_   GT
GAM378  LOC91461  3' GGTGGGGGCTGCGTGG      66135    _  _
                                 CC CGT GTTCCTATC
                                 || ||| |||||||||
                                 GG GCG CGGGGGTGG
                                  T  T
GAM378  LOC91828  5' CGGCGGCCGGGCGCGGG     67276         CTAT  TT
                                 CCCGTGTTC    CC  GTTG
                                 |||||||||    ||  ||||
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                              GGGCGCGGG   GG  CGGC
                                   CC__  __
GAM378  LOC91875  3' CAGCAGGGATGGGAGGAATG  67437    G_
                              CGT  TTCCTATCCTTGTTG
                              |||  ||||||||||||||
                              GTA  GAGGGTAGGGACGAC
                                AG
GAM378  LOC92235  5' TGATGAGGACAGCGTGGG   68558       CCTA   TG
                              CCCGTGTT   TCCT  TTG
                              ||||||||   ||||  |||
                              GGGTGCGA   AGGA  AGT
                                   C___   GT
GAM378  LOC92270  5' TAGTGACTTGGGGATGGGGGT 68635    G      TCC TG
                              ACCC TGTTCCTA   T  TTG
                              |||| ||||||||   |  |||
                              TGGG GTAGGGGT   A  GAT
                                G       TC_ GT
GAM378  LOC92305  3' CAGACTCCTGGGTAGGGGTGGG 56414    G  TT     TT__   G
          GGT                   ACCC TG  CCTATCC    GTT
                              ||||  ||  |||||||    |||
                              TGGG GT  GGATGGG    CAG
                                G  GG      TCCT   AC
GAM378  LOC92539  5' TAACGAGGGTGGTCACGG    69640      TT  T
                              CCGTG  CC ATCCTTGTTG
                              |||||  ||  ||||||||||
                              GGCAC  GG TGGGAGCAAT
                                T_  _
GAM378  LOC92552  3' TGACGAGAGAGATGTGGG    69666     TG TC  ATC
                              CCCG  T  CT   CTTGTTG
                              ||||  |  ||   |||||||
                              GGGT  A  GA   GAGCAGT
                                GT GA  ____
GAM378  LOC92578  3' TGGCAGCTAGGACACGGG    69832       T    TCC
                              CCCGTGT CCTA   TTGTTG
                              |||||||  ||||   ||||||
                              GGGCACA GGAT   GACGGT
                                   _    C__
GAM378  LOC92661  5' TGGCGGGGAGGCCCATG     70089     TT  TA
                              CGTG  CC  TCCTTGTTG
                              ||||  ||  |||||||||
                              GTAC  GG  AGGGGCGGT
                                CC  __
GAM378  LOC92689  3' CAGCAGGGGGTGAGCGGTGGGT 70220       _    CTA
                              ACCCGT GTTC   TCCTTGTTG
                              ||||||  ||||   |||||||||
                              TGGGTG CGAG   GGGGACGAC
                                 G    TG_
GAM378  LOC93132  5' TGGCAAGGGTGGGAAT      71507
                              GTTCCTATCCTTGTTG
                              ||||||||||||||||
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                                TAAGGGTGGGAACGGT

GAM378  LOC93259  5'  TGGTGGGGATGAAAGACAGGT  71828    C  G  CC     TG
                                ACC GT TT  TATCCT  TTG
                                ||| || ||  ||||||  |||
                                TGG CA AA  GTAGGG  GGT
                                  A  G  A_     GT
GAM378  LOC93589  3'  TGTGTTGGGGTGGGGGTTGGGT 72673      T TT      TGTTG
                                ACCCG G  CCTATCCT
                                ||||| |  ||||||||
                                TGGGT T  GGGTGGGG
                                   _ GG      TTGTGTC
GAM378  LOC93622  3'  CGGCGAGGCCGCGCGGGT    56931        TCCTAT
                                ACCCGTGT     CCTTGTTG
                                ||||||||     ||||||||
                                TGGGCGCG     GGAGCGGC
                                     CC_____
GAM379  ABCC3     3'  AGTCCTGTACTCTGGGGTG   13692     A   CAGC
                                CACC CAGA    TGCAGGACT
                                |||| ||||    |||||||||
                                GTGG GTCT    ATGTCCTGA
                                  G    C___
GAM379  ABCC3     3'  AGTCCTGTACTCTGGGGTG   39139     A   CAGC
                                CACC CAGA    TGCAGGACT
                                |||| ||||    |||||||||
                                GTGG GTCT    ATGTCCTGA
                                  G    C___
GAM379  ABCC3     3'  AGTCCTGTACTCTGGGGTG   39151     A   CAGC
                                CACC CAGA    TGCAGGACT
                                |||| ||||    |||||||||
                                GTGG GTCT    ATGTCCTGA
                                  G    C___
GAM379  ARVCF     3'  AGCCCTGCAGTCACGTGAGG   8026     A  GACA      A
                                CC CA    GCTGCAGG CT
                                || ||    |||||||| ||
                                GG GT    TGACGTCC GA
                                 A  GCAC       C
GAM379  CCS       3'  AGCTGCTGTGGTGTT       17609          A
                                AACACCACAG CAGCT
                                |||||||||| |||||
                                TTGTGGTGTC GTCGA
                                          _
GAM379  CELSR1    3'  TTTGTACTTCTGCGGTG     26492      A    C  C
                                CACC CAGA AG TGCAGG
                                |||| |||| || ||||||
                                GTGG GTCT TC ATGTTT
                                  C    _  _
GAM379  CELSR3    3'  GCAAAAGTTGTCTGTGGTG   7401             ___
                                CACCACAGACAGCT   GC
                                ||||||||||||||   ||
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                                GTGGTGTCTGTTGA  CG
                                       AAA
GAM379  COL19A1  3'  AGCCACCAAGCTGTCTTTGGT  8506      C      GCA_  A
                                ACCA AGACAGCT   GG CT
                                |||| ||||||||   || ||
                                TGGT TCTGTCGA   CC GA
                                  T       ACCA  _
GAM379  DDC      3'  CTCAGCTGTCTGTGG       5797            C
                                CCACAGACAGCTG AG
                                |||||||||||| ||
                                GGTGTCTGTCGAC TC
                                        _
GAM379  DLEC1    3'  AGTCCTGCACCCTGCGG     23685    A  ACAGC
                                CC CAG    TGCAGGACT
                                || |||    |||||||||
                                GG GTC    ACGTCCTGA
                                 C  CC___
GAM379  DLEC1    3'  AGTCCTGCACCCTGCGG     23696    A  ACAGC
                                CC CAG    TGCAGGACT
                                || |||    |||||||||
                                GG GTC    ACGTCCTGA
                                 C  CC___
GAM379  DUSP2    3'  GCCCTGTCTGTGGGTT      15347    A       CT
                                AAC CCACAGACAG  GC
                                ||| ||||||||||  ||
                                TTG GGTGTCTGTC  CG
                                  _       C_
GAM379  ERN2     5'  AGCCGTGCAGCTGCCCAGG   52701    ACAGA      _  A
                                CC    CAGCTGCA GG CT
                                ||    |||||||| || ||
                                GG    GTCGACGT CC GA
                                 ACCC_      G  _
GAM379  EZH1     3'  TCTGCTTTCCTGTCTGTAGTG  8830     C      CT__
                                CAC ACAGACAG   GCAGG
                                ||| ||||||||   |||||
                                GTG TGTCTGTC   CGTCT
                                  A       CTTT
GAM379  FUT4     3'  AGTCCTGCAGGAGTGCTG    8961     _  AG
                                CAG AC  CTGCAGGACT
                                ||| ||  ||||||||||
                                GTC TG  GACGTCCTGA
                                  G  AG
GAM379  GGA3     3'  AGCCCTGGGAATGTCTGTGG  56825        GCTG   A
                                CCACAGACA   CAGG CT
                                |||||||||   |||| ||
                                GGTGTCTGT   GTCC GA
                                      AAGG   C
GAM379  GGA3     3'  AGCCCTGGGAATGTCTGTGG  25741        GCTG   A
                                CCACAGACA   CAGG CT
                                |||||||||   |||| ||
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                                GGTGTCTGT   GTCC GA
                                     AAGG   C
GAM379  GPC1    3'  AGCCCCGCACGGGCTGTCTGGG 9098      A      ___  A  A
          TGT                    ACACC CAGACAGCT   GC GG CT
                                 ||||| |||||||||   || || ||
                                 TGTGG GTCTGTCGG   CG CC GA
                                   _       GCA  C  C
GAM379  HMGN3   3'  AGTCCTGTGCATACTGTGGTGT 14902         ACA  T
          T                     AACACCACAG   GC GCAGGACT
                                 ||||||||||   || ||||||||
                                 TTGTGGTGTC   CG TGTCCTGA
                                      ATA  _
GAM379  HPS1    3'  AGCCTCCTGTCTGCAGTG    3964     CA     CTGC   A
                                 CAC  CAGACAG    AGG CT
                                 |||  |||||||    ||| ||
                                 GTG  GTCTGTC    TCC GA
                                   AC      C___   _
GAM379  IGFBP1  3'  TCAAAGCTACCTGTGGTG    5180        AC    GCAG
                                 CACCACAG  AGCT    GA
                                 ||||||||  ||||    ||
                                 GTGGTGTC  TCGA    CT
                                      CA    AA__
GAM379  IGFBP3  3'  AGCTCACAGCCTTCTGTGGTGT 5185         CA    CA  A
                                 ACACCACAGA  GCTG  GG CT
                                 ||||||||||  ||||  || ||
                                 TGTGGTGTCT  CGAC  TC GA
                                      TC    AC  _
GAM379  IGFBP4  3'  AGTCCTGTCTCTGCCTGCGG   7758     A   A   CT
                                 CC CAG CAG  GCAGGACT
                                 || ||| |||  ||||||||
                                 GG GTC GTC  TGTCCTGA
                                  C   C   TC
GAM379  IL19    3'  GTCCATGTCTGTGATGT     25360     C       GCTGCA
                                 ACA CACAGACA     GGAC
                                 ||| ||||||||     ||||
                                 TGT GTGTCTGT     CCTG
                                   A       A_____
GAM379  INPP5B  5'  AGTCCCGTGCGCCCTGTGGTG  95521        ACA  T  A
                                 CACCACAG   GC GC GGACT
                                 ||||||||   || || |||||
                                 GTGGTGTC   CG TG CCTGA
                                      CCG  _  C
GAM379  ISLR    3'  CTCACTGTCTGCGGTG      18669      A      C  C
                                 CACC CAGACAG TG AG
                                 |||| ||||||| || ||
                                 GTGG GTCTGTC AC TC
                                   C       _ _
GAM379  KAI1    3'  AGCCCTGGCTGTTCTGTGGT   9495         _    TG    A
                                 ACCACAGA CAGC  CAGG CT
                                 |||||||| ||||  |||| ||
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                                TGGTGTCT GTCG  GTCC GA
                                     T   __   C
GAM379  KDR      3'  TGAAGCTGTGTGTGGTGT    9596         G     G
                                ACACCACA ACAGCT CA
                                |||||||| |||||| ||
                                TGTGGTGT TGTCGA GT
                                     G     A
GAM379  MLLT4    3'  AGTTATGGGCTCTCTGCAGTGT 72482      CA    C    G  G
              T                  AACAC  CAGA AGCT CA GACT
                                |||||  |||| |||| || ||||
                                TTGTG  GTCT TCGG GT TTGA
                                   AC    C    _  A
GAM379  MPO      3'  TCCTGGCTCTGTGG       4204         CA  TG
                                CCACAGA  GC  CAGGA
                                |||||||  ||  |||||
                                GGTGTCT  CG  GTCCT

                                   __  __
GAM379  PACSIN1  3'  AGTCCTGCAGCACCAGGTG   92253     ACAGACA
                                CACC       GCTGCAGGACT
                                ||||       ||||||||||||
                                GTGG       CGACGTCCTGA
                                  ACCA____
GAM379  PCLO     3'  CAGTGTCTGTGATGTT      94224      C       G
                                AACA CACAGACA CTG
                                |||| |||||||| |||
                                TTGT GTGTCTGT GAC
                                  A       _
GAM379  PLOD3    5'  TCCTCGCCTTGTCTGTGG    6558          CT  _
                                CCACAGACAG  GC AGGA
                                ||||||||||  || ||||
                                GGTGTCTGTT  CG TCCT
                                      C_  C
GAM379  PPP1R8   5'  AGCCCCGCATCCCTCTGTGGT  10722         CAGC   A  A
                                ACCACAGA    TGC GG CT
                                ||||||||    ||| || ||
                                TGGTGTCT    ACG CC GA
                                     CCCT   C  C
GAM379  PPP2R2B  3'  TGAGGTTGTCTGTAGT      15909    C        G
                                AC ACAGACAGCT CA
                                || ||||||||||  ||
                                TG TGTCTGTTGG GT
                                 A         A
GAM379  RAX      3'  AGCCCTGCAGCTGGAGGG    25536    ACAGA        A
                                CC     CAGCTGCAGG CT
                                ||     ||||||||||  ||
                                GG     GTCGACGTCC GA
                                 GAG__         C
GAM379  REGL     3'  AGTCCTGCAGCCAGGAGGGT   21485     ACAGACA
                                ACC       GCTGCAGGACT
                                |||       ||||||||||
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                                TGG      CGACGTCCTGA
                                  GAGGAC_
GAM379  RFC1     3'  GTCCTGTCCTGTGATGG     11302     CAG    CT
                                CCA   ACAG  GCAGGAC
                                |||   ||||  |||||||
                                GGT   TGTC  TGTCCTG
                                  AG_   C_
GAM379  RRM2     3'  AGTCCTGTCTGTTTATAGTG  6407      CAC     CT
                                CAC   AGACAG  GCAGGACT
                                |||   ||||||  ||||||||
                                GTG   TTTGTC  TGTCCTGA
                                  ATA     __
GAM379  RU2      5'  AGTCCTGCAAGCTCCTAGTG  33020     _ AC    _
                                CAC AG  AGCT GCAGGACT
                                ||| ||  |||| ||||||||
                                GTG TC  TCGA CGTCCTGA
                                  A  C_   A
GAM379  RXRA     3'  CCTGCAGCCATCTGTG      11407       CA
                                CACAGA  GCTGCAGG
                                ||||||  ||||||||
                                GTGTCT  CGACGTCC
                                   AC
GAM379  SH3BP2   3'  AGCCCTGCAGCTACAGCTG   11589     AC__       A
                                CAG    AGCTGCAGG CT
                                |||    |||||||||| ||
                                GTC    TCGACGTCC GA
                                  GACA        C
GAM379  SLC1A4   3'  TTGTATGTCTGTGGT       11721          GC
                                ACCACAGACA  TGCAG
                                ||||||||||  |||||
                                TGGTGTCTGT  ATGTT
                                      __
GAM379  TBXA2R   5'  AGCCTGCCCTGTCTG       6478        CT     A
                                CAGACAG  GCAGG CT
                                |||||||  ||||| ||
                                GTCTGTC  CGTCC GA
                                   C_    _
GAM379  TEM7     3'  AGCCCCAGCTTCTGT       39880       C     CA  A
                                ACAGA AGCTG  GG CT
                                ||||| |||||  || ||
                                TGTCT TCGAC  CC GA
                                  _    C_ _
GAM379  UNC13    3'  AGTCCTGCTCATCTGTGG    21055        CAGCT
                                CCACAGA    GCAGGACT
                                |||||||    ||||||||
                                GGTGTCT    CGTCCTGA
                                   ACT__
GAM379  WASF3    3'  AGCCCTGCAGCTGTAGTACAGT 21823     CACAG_         A
           G                     CAC     ACAGCTGCAGG CT
                                |||     |||||||||| ||
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                                GTG     TGTCGACGTCC GA
                                  ACATGA         C
GAM379  ZNF138   5' AGGCCCAGCCTCTGTGG     81184        CA    CA  A
                                CCACAGA  GCTG  GG CT
                                |||||||  ||||  || ||
                                GGTGTCT  CGAC  CC GA
                                    C_   __  G
GAM379  ABCA9    3' AGTCCATGTTTTGTCTGTTGTG 54409     C       CT  _
                                CAC ACAGACAG  GCA GGACT
                                ||| ||||||||  ||| |||||
                                GTG TGTCTGTT  TGT CCTGA
                                  T       T_  A
GAM379  APCL     5' GTTCAGCTGTCTGT       19684          CAG
                                ACAGACAGCTG   GAC
                                ||||||||||   |||
                                TGTCTGTCGAC   TTG
                                      ___
GAM379  BRD1     5' AGTCCTGCAACTGTGG      27413       ACAGC
                                CCACAG    TGCAGGACT
                                ||||||    |||||||||
                                GGTGTC    ACGTCCTGA
                                   A____
GAM379  C16orf5  3' AGTCCCCAGGCCTGTGG     25445       ACA   GCA
                                CCACAG   GCT   GGACT
                                ||||||   |||   |||||
                                GGTGTC   CGG   CCTGA
                                   ___   ACC
GAM379  C1orf24  3' AGTCTCTGCTTTCTGCAGTG   53707     CA    CAGCT   _
                                CAC  CAGA    GCAG GACT
                                |||  ||||    |||| ||||
                                GTG  GTCT    CGTC CTGA
                                  AC   TT___    T
GAM379  C1orf34  3' AGTCCCGGTCTGCTGTGGTGTT 60661          A  _  CA
                                AACACCACAG CAG CTG  GGACT
                                |||||||||| ||| |||  |||||
                                TTGTGGTGTC GTC GGC  CCTGA
                                      _   T   __
GAM379  C20orf82 5' AGTCTCTGGTCTGTCTG     84711        CTG  _
                                CAGACAG   CAG GACT
                                |||||||   ||| ||||
                                GTCTGTC   GTC CTGA
                                    TG_   T
GAM379  DKFZP434C171 3' AGTCCTGATAGTCTGTGG    31551         AGCTG
                                CCACAGAC    CAGGACT
                                ||||||||    |||||||
                                GGTGTCTG    GTCCTGA
                                    ATA__
GAM379  DKFZP434P211 3' AGTCCTGCGATGCTAAGTG   27260     CAC  A  GC
                                CAC   AG CA  TGCAGGACT
                                |||   || ||  |||||||||
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                                GTG   TC GT  GCGTCCTGA
                                  AA_  _  A_
GAM379  DMWD     3' AGCCCCAGGTCTGCAGTGT   60876     CA    AG   CA  A
                                ACAC  CAGAC  CTG  GG CT
                                ||||  |||||  |||  || ||
                                TGTG  GTCTG  GAC  CC GA
                                  AC     __   C_  _
GAM379  DOCK3    3' AGTCCTGCATGTTCAGG    66495    ACA   GC
                                CC   GACA  TGCAGGACT
                                ||   ||||  |||||||||
                                GG   TTGT  ACGTCCTGA
                                 AC_   __
GAM379  FLJ10094 3' AGTTATATCTGTGGCGTT    35807     A      C__
                                AAC CCACAGA   AGCT
                                ||| |||||||   ||||
                                TTG GGTGTCT   TTGA
                                  C      ATA
GAM379  FLJ10178 3' AGCCCTATAGTTCTGTG     35869       CA   C   A
                                CACAGA  GCTG AGG CT
                                ||||||  |||| ||| ||
                                GTGTCT  TGAT TCC GA
                                   __   A   C
GAM379  FLJ10637 5' AGTCCCCTGTCTGTGG      68586          CTGCA
                                CCACAGACAG    GGACT
                                ||||||||||    |||||
                                GGTGTCTGTC    CCTGA
                                      C____
GAM379  FLJ12891 5' AGTCCTGCAGCCTCGCTGG   46336    CA  CA
                                CCA  GA  GCTGCAGGACT
                                |||  ||  ||||||||||
                                GGT  CT  CGACGTCCTGA
                                  CG  C_
GAM379  FLJ12903 3' GTGCTATTGTGGTGT       42778         AC   T
                                ACACCACAG  AGC GC
                                |||||||||  ||| ||
                                TGTGGTGTT  TCG TG
                                     A_   _
GAM379  FLJ13902 3' AGCCCTGTAGCATCTGTG    45038       CA       A
                                CACAGA  GCTGCAGG CT
                                ||||||  |||||||| ||
                                GTGTCT  CGATGTCC GA
                                   A_       C
GAM379  FLJ20033 3' TTTTGCTAGCTGTGGTGTT   34351          ACAGCT
                                AACACCACAG     GCAGGA
                                ||||||||||     ||||||
                                TTGTGGTGTC     CGTTTT
                                      GAT___
GAM379  FLJ20315 3' CCAGCTGCTGCCTGTGGCGT  34933    A     A   T  A
                                AC CCACAG CAGC GC GG
                                || |||||| |||| || ||
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                                TG GGTGTC GTCG CG CC
                                 C     C    T  A
GAM379  FLJ20374  3'  AGCCCTGCAGCTGGCTGGAGT  35077    CA   A        A
                                AC  CAG CAGCTGCAGG CT
                                ||  ||| |||||||||| ||
                                TG  GTC GTCGACGTCC GA
                                 AG   G         C
GAM379  FLJ22127  3'  AGTCCTGTGGCTGGCCCGTGAT 42881    C   AGA_   TG
          G                      CA CAC    CAGC  CAGGACT
                                || |||    ||||  |||||||
                                GT GTG    GTCG  GTCCTGA
                                 A  CCCG    GT
GAM379  FLJ23185  5'  GTCCTGCAGTATGGCGT     46833    A   CAGACA
                                AC CCA     GCTGCAGGAC
                                || |||     ||||||||||
                                TG GGT     TGACGTCCTG
                                 C  A_____
GAM379  FLJ31762  5'  AGTCCTGCAGATGTGCGTG    58139    _    GACAG
                                CAC CACA    CTGCAGGACT
                                ||| ||||    ||||||||||
                                GTG GTGT    GACGTCCTGA
                                  C   A____
GAM379  GIOT-2    3'  CCTTCAGTTATCTGCAGT    32749    CA   C    C
                                AC  CAGA AGCTG AGG
                                ||  |||| ||||| |||
                                TG  GTCT TTGAC TCC
                                 AC    A    T
GAM379  HRH3      3'  AGCCCCGCCGTGTCTGTGG   23364        G T  A  A
                                CCACAGACA C GC GG CT
                                ||||||||| | || || ||
                                GGTGTCTGT G CG CC GA
                                      _ C  C  C
GAM379  HYA22     3'  TCCTACGTGTTGGTCTGTGGT  19429        _  _  C
                                ACCACAGAC AGC TG AGGA
                                ||||||||| ||| || ||||
                                TGGTGTCTG TTG GC TCCT
                                      G   T  A
GAM379  KCNB2     5'  TCCCACAGCCCTTTGTGGTG   96102        CA   CA
                                CACCACAGA  GCTG  GGA
                                |||||||||  ||||  |||
                                GTGGTGTTT  CGAC  CCT
                                     CC    AC
GAM379  KCNT1     3'  AGTCCTGCAGATCCCTCTGTGG 61826        CAG__
          T                     ACCACAGA    CTGCAGGACT
                                ||||||||    ||||||||||
                                TGGTGTCT    GACGTCCTGA
                                    CCCTA
GAM379  KIAA0218  3'  GTCCCTCGTCTGTGGT      28623         _  CTGCA
                                ACCACAGAC AG    GGAC
                                ||||||||| ||    ||||
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                                TGGTGTCTG TC    CCTG
                                    C _____
GAM379  KIAA0828 3' TCCTGTGCCTGTAGTGTT   81199     C   ACA  T
                                AACAC ACAG  GC GCAGGA
                                ||||| ||||  || ||||||
                                TTGTG TGTC  CG TGTCCT
                                  A  ___ _
GAM379  KIAA0953 3' AGTCCTGCATGTAGTTGGTG  66780     CAG  GC
                                CACCA  ACA  TGCAGGACT
                                |||||  |||  |||||||||
                                GTGGT  TGT  ACGTCCTGA
                                  TGA  __
GAM379  KIAA1157 3' AGTCCGTCCATGCTCTGTGG  72239      _ GCT  A
                                CCACAGA CA  GC GGACT
                                ||||||| ||  || |||||
                                GGTGTCT GT  TG CCTGA
                                    C  ACC  _
GAM379  KIAA1183 3' GCAGCCTGTGGTGTT      62535       ACA
                                AACACCACAG  GCTGC
                                ||||||||||  |||||
                                TTGTGGTGTC  CGACG
                                     ___
GAM379  KIAA1280 5' AGCCTGACTGTCCGTGGTG  69710     A   CTG   A
                                CACCAC GACAG  CAGG CT
                                |||||| |||||  |||| ||
                                GTGGTG CTGTC  GTCC GA
                                   C   A__  _
GAM379  KIAA1336 3' TCCTGGGTTTTGTAATGTT  72325    CC   CA  G
                                AACA  ACAGA  GCT CAGGA
                                ||||  |||||  ||| |||||
                                TTGT  TGTTT  TGG GTCCT
                                  AA   __  _
GAM379  KIAA1505 5' AGTCCCACCCATCTGTGGT  94185      CAGC  CA
                                ACCACAGA   TG  GGACT
                                ||||||||   ||  |||||
                                TGGTGTCT   AC  CCTGA
                                    ACCC  __
GAM379  KIAA1786 3' AGTCCTTCCTTATCTGTGGT  66022      CAGCTGC
                                ACCACAGA    AGGACT
                                ||||||||    ||||||
                                TGGTGTCT    TCCTGA
                                    ATTCCT_
GAM379  MAD4    3' CCTGTACCGGTCTGTGG    21271      AGC
                                CCACAGAC  TGCAGG
                                ||||||||  ||||||
                                GGTGTCTG  ATGTCC
                                    GCC
GAM379  MGC10940 3' AGCCCCCCAATCTGTGGT  50214      CAGC  CA  A
                                ACCACAGA   TG  GG CT
                                ||||||||   ||  || ||
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                                TGGTGTCT   AC  CC GA
                                    A___  CC  C
GAM379  MGC2654  5' AGCTTGGACCTGTCTGCAGT  44103   CA     CTG   A
                                AC  CAGACAG   CAGG CT
                                ||  |||||||   |||| ||
                                TG  GTCTGTC   GTTC GA
                                 AC      CAG   _
GAM379  MVD      3' AGTCCTGCGGCCGCCCAGGTGT 10138      ACAGACA
                                ACACC      GCTGCAGGACT
                                ||||||      ||||||||||||
                                TGTGG      CGGCGTCCTGA
                                   ACCCGC_
GAM379  NIN283   3' AGCCCTCTGCCGGCTGTGGTGT 50065        ACA  TGC   A
                                ACACCACAG   GC   AGG CT
                                |||||||||   ||   ||| ||
                                TGTGGTGTC   CG   TCC GA
                                     GGC  TC_   C
GAM379  NTT5     3' AGTCCTGCTACTTCTGGGGTG  25880     A   C  CT
                                CACC CAGA AG  GCAGGACT
                                |||| |||| ||  ||||||||
                                GTGG GTCT TC  CGTCCTGA
                                   G   _ AT
GAM379  P2RX1    3' TCCTGGGCTCCCTGCCTGTGG  67172      A  ____  G
                                CCACAG CA   GCT CAGGA
                                |||||| ||   ||| |||||
                                GGTGTC GT   CGG GTCCT
                                   C  CCCT  _
GAM379  PMAIP1   5' TGCAGCTGTCCGAGGTG    40892     ACA
                                CACC   GACAGCTGCA
                                ||||   ||||||||||
                                GTGG   CTGTCGACGT
                                   AGC
GAM379  PMVK     3' AGTCCCCTCAGCCTGTGGTG  94612       ACA   CA_
                                CACCACAG   GCTG   GGACT
                                ||||||||   ||||   |||||
                                GTGGTGTC   CGAC   CCTGA
                                     ___   TCC
GAM379  PMVK     3' AGTCCCCTCAGCCTGTGGTG  21610       ACA   CA_
                                CACCACAG   GCTG   GGACT
                                ||||||||   ||||   |||||
                                GTGGTGTC   CGAC   CCTGA
                                     ___   TCC
GAM379  POLD3    3' TCTGAGCTGTCTGCAAGG    91646    A__      G
                                CC   CAGACAGCT CAGG
                                ||   ||||||||| ||||
                                GG   GTCTGTCGA GTCT
                                 AAC       _
GAM379  PRO2958  3' AGTCCTAAACTGGCATCTGT  37651      CA   C___
                                ACAGA  GCTG   AGGACT
                                |||||  ||||   ||||||
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                                TGTCT  CGGT   TCCTGA
                                  A_   CAAA
GAM379  RAN     3'  GCAGCTGTCCTGTGATGT   20907    C   _
                                ACA CACAG ACAGCTGC
                                ||| ||||| ||||||||
                                TGT GTGTC TGTCGACG
                                  A    C
GAM379  RMP     3'  AGTTTTGTGCCAGCTGTG   13707     ACA  T
                                CACAG   GC GCAGGACT
                                |||||   || ||||||||
                                GTGTC   CG TGTTTTGA
                                  GAC  _
GAM379  RMP     3'  AGTTTTGTGCCAGCTGTG   56242     ACA  T
                                CACAG   GC GCAGGACT
                                |||||   || ||||||||
                                GTGTC   CG TGTTTTGA
                                  GAC  _
GAM379  SCYD1   3'  AGTCACCCCGGCCACCTGCGGT 90924     A  ACA   CAG_
          G                      CACC CAG   GCTG   GACT
                                |||| |||   ||||   ||||
                                GTGG GTC   CGGC   CTGA
                                  C   CAC   CCCA
GAM379  SHAPY   5'  AGTCCCGCCTGTCTGT     57108       CT  A
                                ACAGACAG  GC GGACT
                                ||||||||  || |||||
                                TGTCTGTC  CG CCTGA
                                    __  C
GAM379  SMOC1   3'  AGTCCTGCAATTGTACTGCGG  42147   A  _   C
                                CC CAG ACAG TGCAGGACT
                                || ||| |||| |||||||||
                                GG GTC TGTT ACGTCCTGA
                                 C  A   A
GAM379  SRPUL   3'  TCCTGCAGTGTTTCCAGG   27101   AC_   G
                                CC   AGACA CTGCAGGA
                                ||   ||||| ||||||||
                                GG   TTTGT GACGTCCT
                                 ACC    _
GAM379  SSH-3   3'  AGCCCTGCACACTCACCTGTGG 35339      AC_  C_    A
                                CCACAG   AG  TGCAGG CT
                                ||||||   ||  |||||| ||
                                GGTGTC   TC  ACGTCC GA
                                   CAC  AC     C
GAM379  TOSO    3'  CCCAGGCTCGGACTGTGGTG   18389       AC__   GCA
                                CACCACAG    AGCT   GG
                                ||||||||    ||||   ||
                                GTGGTGTC    TCGG   CC
                                    AGGC    AC_
GAM379  TPC2    3'  CCTGCAGCTTCCGTGGTG    57446      A  C
                                CACCAC GA AGCTGCAGG
                                |||||| || |||||||||
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                                GTGGTG CT TCGACGTCC
                                   C  _
GAM379  TRIM11    3'  CCATGCCTGTCTGTG       72831          CT  _
                                CACAGACAG  GCA GG
                                |||||||||  ||| ||
                                GTGTCTGTC  CGT CC
                                     __   A
GAM379  UGT2B10   3'  AGCCCCAGTAATGCTCTGTGG  6540          _ __   CA  A
                                CCACAGA CA  GCTG  GG CT
                                |||||||  ||  ||||  || ||
                                GGTGTCT GT  TGAC  CC GA
                                    C  AA   C_  _
GAM379  LOC113386 3'  AGTCCTGCATGTGTTGATG   57077    CA    GC
                                CA  GACA  TGCAGGACT
                                ||  ||||  |||||||||
                                GT  TTGT  ACGTCCTGA
                                  AG    GT
GAM379  LOC130814 3'  AGTGCTCAGACATCTGCAGTGT 74984      CA    CAG   C  G
           T                     AACAC  CAGA   CTG AG ACT
                                |||||  ||||   ||| || |||
                                TTGTG  GTCT   GAC TC TGA
                                   AC    ACA   _  G
GAM379  LOC131870 3'  AGTCCTGCAGCCTCATATGG   75013     CAGACA
                                CCA     GCTGCAGGACT
                                |||     ||||||||||
                                GGT     CGACGTCCTGA
                                  ATACTC
GAM379  LOC133491 5'  GTCTGGCGCCTGTGGCGT    75096    A     ACA  T  A
                                AC CCACAG   GC GC GGAC
                                || ||||||   || || ||||
                                TG GGTGTC   CG CG TCTG
                                 C     ___  _  G
GAM379  LOC139065 3'  TCCTTTTGATTTGTGG      75817        _  CTGC
                                CCACAGA CAG    AGGA
                                |||||||  |||    ||||
                                GGTGTTT GTT    TCCT
                                    A   T___
GAM379  LOC145622 5'  AGTCCTGCAAAGGTGATGGTGG 77291      AGA  G  __
           T                     ACCAC   CA CT  GCAGGACT
                                |||||   ||  ||  ||||||||
                                TGGTG   GT GA  CGTCCTGA
                                   GTA  G  AA
GAM379  LOC145676 5'  AGTCCTGTCCAGGGTCT     77333      AG  __
                                AGAC  CTG  CAGGACT
                                ||||  |||  |||||||
                                TCTG  GAC  GTCCTGA
                                  G_   CT
GAM379  LOC145955 5'  AGCCCTGAGATGTCCATGGT   83586     CA   G  G   A
                                ACCA  GACA CT CAGG CT
                                ||||  |||| || |||| ||
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                                TGGT  CTGT GA GTCC GA
                                  AC    A  _    C
GAM379   LOC145957 5'  CTGCTGTTGTCTGCGGT     56794     A       T
                                ACC CAGACAGC GCAG
                                ||| |||||||| ||||
                                TGG GTCTGTTG CGTC
                                  C       T
GAM379   LOC146287 5'  TTGCAGCTGCCTCGGT      83654     AC  A
                                ACC  AG CAGCTGCAG
                                |||  || |||||||||
                                TGG  TC GTCGACGTT
                                  C_  C
GAM379   LOC146669 3'  AGCCCTGCAGCCTGGG      78049     A   ACA       A
                                CC CAG   GCTGCAGG CT
                                || |||   |||||||| ||
                                GG GTC   CGACGTCC GA
                                 _  ___       C
GAM379   LOC147040 3'  CAGTGTCTGTGATGT       78230     C       G
                                ACA CACAGACA CTG
                                ||| |||||||| |||
                                TGT GTGTCTGT GAC
                                  A       _
GAM379   LOC147160 5'  AGCCCTGCAGTGCGTGTACAGG 83956     ACAG  ___       A
                                CC    ACA   GCTGCAGG CT
                                ||    |||   |||||||| ||
                                GG    TGT   TGACGTCC GA
                                 ACA_   GCG       C
GAM379   LOC149111 3'  CCTGCGTGTCTGTG        79181         GC
                                CACAGACA  TGCAGG
                                ||||||||  ||||||
                                GTGTCTGT  GCGTCC
                                      __
GAM379   LOC150174 3'  AGTCCTGCGATGCTAAGTG    79604     CAC  A  GC
                                CAC   AG CA  TGCAGGACT
                                |||   || ||  |||||||||
                                GTG   TC GT  GCGTCCTGA
                                  AA_  _  A_
GAM379   LOC150213 3'  AGTCCTGCGATGCTAAGTG    74851     CAC  A  GC
                                CAC   AG CA  TGCAGGACT
                                |||   || ||  |||||||||
                                GTG   TC GT  GCGTCCTGA
                                  AA_  _  A_
GAM379   LOC150236 3'  AGTCCTGCGATGCTAAGTG    79683     CAC  A  GC
                                CAC   AG CA  TGCAGGACT
                                |||   || ||  |||||||||
                                GTG   TC GT  GCGTCCTGA
                                  AA_  _  A_
GAM379   LOC154559 3'  GCAGCTGTCCTGTGATGT     81096     C    _
                                ACA CACAG ACAGCTGC
                                ||| ||||| ||||||||
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                                TGT GTGTC TGTCGACG
                                  A    C
GAM379  LOC158117 3'  CCTGGTCTGTTCTGTATTGTT  81703     CC    _  CTG
                                AACA  ACAGA CAG   CAGG
                                ||||  ||||| |||   ||||
                                TTGT  TGTCT GTC   GTCC
                                  TA    T   TG_
GAM379  LOC160897 3'  CCAGCTATTGTCTGTTGTGTT  82245      C      CT  A
                                AACAC ACAGACAG  GC GG
                                ||||| ||||||||  || ||
                                TTGTG TGTCTGTT  CG CC
                                   T       AT  A
GAM379  LOC161482 3'  GCACTTACCTGTGGTGTT    87089         AC_  C
                                AACACCACAG   AG TGC
                                ||||||||||   || |||
                                TTGTGGTGTC   TC ACG
                                      CAT  _
GAM379  LOC164382 3'  AGTCTCCCTGTCTGTGGT    87203         CTGCA
                                ACCACAGACAG    GGACT
                                ||||||||||    |||||
                                TGGTGTCTGTC    TCTGA
                                      CC___
GAM379  LOC200301 5'  AGCCTGTCTGTGTGTT      88736      C      _
                                AACAC ACAGACAG CT
                                ||||| |||||||| ||
                                TTGTG TGTCTGTC GA
                                   _       C
GAM379  LOC203275 3'  CCTGGTCTGTTCTGTATTGTT  89319     CC    _  CTG
                                AACA  ACAGA CAG   CAGG
                                ||||  ||||| |||   ||||
                                TTGT  TGTCT GTC   GTCC
                                  TA    T   TG_
GAM379  LOC219920 5'  TTGGGCACTGCCTGTGG     93323       A   C   AG
                                CCACAG CAG TGC  GA
                                |||||| ||| |||  ||
                                GGTGTC GTC ACG  TT
                                   C   _  GG
GAM379  LOC220932 3'  AGTCCTGTTCTCTGTTAATGT  93135     __    CT_
                                ACA  GACAG   GCAGGACT
                                |||  |||||   ||||||||
                                TGT  TTGTC   TGTCCTGA
                                  AA    TCT
GAM379  LOC221466 5'  GTCCTGTGTCCAGGGTG     93693     ACA   AGCT
                                CACC   GAC    GCAGGAC
                                ||||   |||    |||||||
                                GTGG   CTG    TGTCCTG
                                  GAC   _____
GAM379  LOC221547 3'  GCAGCTGTCCTGTGATGT    91007     C    _
                                ACA CACAG ACAGCTGC
                                ||| ||||| ||||||||
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                                TGT GTGTC TGTCGACG
                                  A     C
GAM379  LOC221935 3'  AGCCGTCACTGTCTGTG     92615          CT  A  A
                                CACAGACAG  GC GG CT
                                |||||||||  || || ||
                                GTGTCTGTC  TG CC GA
                                     AC  _  _
GAM379  LOC253681 3'  CAGTGTCTGTGATGT       95127     C       G
                                ACA CACAGACA CTG
                                ||| |||||||| |||
                                TGT GTGTCTGT GAC
                                  A       _
GAM379  LOC257115 3'  AGTCCTGCAAGGTGAAGGCGTT 96523     A  ACAGA  G  _
                                AAC CC     CA CT GCAGGACT
                                ||| ||     || || ||||||||
                                TTG GG     GT GA CGTCCTGA
                                  C  AA___  G  A
GAM379  LOC257577 3'  GCAGCTGTCCTGTGATGT     97838     C     _
                                ACA CACAG ACAGCTGC
                                ||| ||||| ||||||||
                                TGT GTGTC TGTCGACG
                                  A     C
GAM379  LOC51112  5'  AGTCCTGCGGGCCGTGG      32082      AGACAG
                                CCAC      CTGCAGGACT
                                ||||      ||||||||||
                                GGTG      GGCGTCCTGA
                                  CCG___
GAM379  LOC51236  3'  TCCTGCAGCTGTCTGCAGG    33205    A_
                                CC  CAGACAGCTGCAGGA
                                ||  ||||||||||||||
                                GG  GTCTGTCGACGTCCT
                                 AC
GAM379  LOC51713  3'  TTTGTACTGTCTGCGG      32762     A      C
                                CC CAGACAG TGCAGG
                                || ||||||| ||||||
                                GG GTCTGTC ATGTTT
                                 C      _
GAM379  LOC56920  3'  AGCCTTCCAGCCTGCGGTG    39379      A  ACA   C_  A
                                CACC CAG   GCTG  AGG CT
                                |||| |||   ||||  ||| ||
                                GTGG GTC   CGAC  TCC GA
                                  C  ___    CT  _
GAM379  LOC90408  3'  AGTCCTGTGGTCCTGTG     62655      ACA  TG
                                CACAG   GC  CAGGACT
                                |||||   ||  |||||||
                                GTGTC   TG  GTCCTGA
                                   C__  GT
GAM379  LOC91397  5'  GCAGTATCTGTGGTG       65910          CA
                                CACCACAGA  GCTGC
                                |||||||||  |||||
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                                GTGGTGTCT  TGACG
                                     A_
GAM380  A1BG     3'  TGTGGTCTTGTCCTCCC     55438        C   G
                                GGGAGGAC AGG CATG
                                |||||||| ||| ||||
                                CCCTCCTG TCT GTGT
                                     T   G
GAM380  ABCA1    5'  TTTGCTCCTTGTTTTTTCC   18554        C    CATGT
                                GGGAGGA CAGGG    GCAGG
                                ||||||| |||||    |||||
                                CCTTTTT GTTCC    CGTTT
                                    T    T____
GAM380  ABCD3    3'  CCTTGTGTGTGTCTTGG     11155         TG
                                CCAGGGCATG  CAGGG
                                ||||||||||  |||||
                                GGTTCTGTGT  GTTCC
                                      GT
GAM380  ABCD3    3'  TTTTGCATAACTGGTTTT    11156        GGCA
                                AGGACCAG   TGTGCAGGG
                                ||||||||   |||||||||
                                TTTTGGTC   ATACGTTTT
                                    A___
GAM380  ABL1     3'  GTTCTGTATATGATTCTCTGTG 23614     G _____
           GTTTTTTT               ACCA GG    CATGTGCAGGG   T
                                ||||  ||    ||||||||||   |
                                TGGT TC    GTATATGTCTT   G
                                  G  TCTTA
GAM380  ABL1     3'  GTTCTGTATATGATTCTCTGTG 17679     G _____
           GTTTTTTT               ACCA GG    CATGTGCAGGG   T
                                ||||  ||    ||||||||||   |
                                TGGT TC    GTATATGTCTT   G
                                  G  TCTTA
GAM380  ACADVL   3'  CCTTAAGGCCCTGGTTTGTCC  3414     AG       ATG  C
                                GGG  GACCAGGGC   TG AGG
                                |||  |||||||||   || |||
                                CCT  TTGGTCCCG   AT TCC
                                  GT       GA_  _
GAM380  ACCN1    3'  TCTTGTACATGACACTCCTCC  6586       CCAGGG
                                GGAGGA     CATGTGCAGGG
                                ||||||     ||||||||||
                                CCTCCT     GTACATGTTCT
                                   CACA__
GAM380  ACCN1    3'  TTCTGAGGTTTGCTTTGGTTTT 6588             TGTG_
           TCC                    GGGAGGACCAGGGCA    CAGGG
                                ||||||||||||||    |||||
                                CCTTTTTGGTTTCGT    GTCTT
                                        TTGGA
GAM380  ACTB     3'  TTTTGTTTTGTTTTGGTTTTTT 6590             TGT
           T                     GGGAGGACCAGGGCA   GCAGGG
                                ||||||||||||||   ||||||
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                                TTTTTTTGGTTTTGT  TGTTTT
                                       TT_
GAM380  ACYP1   5' CCTGTACGTGCTGTGTCC   6615     C G
                                GGAC A GGCATGTGCAGG
                                |||| | ||||||||||||
                                CCTG T TCGTGCATGTCC
                                  _ G
GAM380  ADAM17  3' TCTTGTGTGGTTTGGCCCTTCT 41558      A   G  GT
                                GGGAGG CCAGG CAT  GCAGGG
                                |||||| ||||| |||  ||||||
                                TCTTCC GGTTT GTG  TGTTCT
                                   C    G  __
GAM380  ADAM17  3' TCTTGTGTGGTTTGGCCCTTCT 12084      A   G  GT
                                GGGAGG CCAGG CAT  GCAGGG
                                |||||| ||||| |||  ||||||
                                TCTTCC GGTTT GTG  TGTTCT
                                   C    G  __
GAM380  ADAMTS13 3' TCCTGTGCATGGACTCTGCCC 57376    AGGAC   __   TG
                                GGG    CAGGG  CATG  CAGGG
                                |||    |||||  ||||  |||||
                                CCC    GTCTC  GTAC  GTCCT
                                  _____   AG   GT
GAM380  ADCY2   3' CTCTGTGTGTACCTGGTCCCTT 65017      _    GC  TG
          CT                    GGGAGG ACCAGG  ATG  CAGGG
                                |||||| ||||||  |||  |||||
                                TCTTCC TGGTCC  TGT  GTCTC
                                   C    A_  GT
GAM380  ADRBK2  3' CCCTGTGAAGTTTGTTTTCTC  17682       CA   ATG
                                GGGAGGAC  GGGC  TGCAGGG
                                ||||||||  ||||  |||||||
                                CTCTTTTG  TTTG  GTGTCCC
                                   __   AA_
GAM380  AGL     3' TATGCCTTGGTTTTTC     5352
                                GGAGGACCAGGGCATG
                                ||||||||||||||||
                                CTTTTTGGTTCCGTAT

GAM380  AGL     3' TATGCCTTGGTTTTTC     5359
                                GGAGGACCAGGGCATG
                                ||||||||||||||||
                                CTTTTTGGTTCCGTAT

GAM380  AGL     3' TATGCCTTGGTTTTTC     5365
                                GGAGGACCAGGGCATG
                                ||||||||||||||||
                                CTTTTTGGTTCCGTAT

GAM380  AGL     3' TATGCCTTGGTTTTTC     5371
                                GGAGGACCAGGGCATG
                                ||||||||||||||||
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                                CTTTTTGGTTCCGTAT

GAM380  AGL      3'  TATGCCTTGGTTTTTC      5380
                                GGAGGACCAGGGCATG
                                ||||||||||||||||
                                CTTTTTGGTTCCGTAT

GAM380  AGL      3'  TATGCCTTGGTTTTTC      3452
                                GGAGGACCAGGGCATG
                                ||||||||||||||||
                                CTTTTTGGTTCCGTAT

GAM380  AGR2     3'  TTTTGGGGGTGTTCTGTTTTCT 21145         C      GTG
              C                  GGGAGGAC AGGGCAT   CAGGG
                                ||||||||| |||||||   |||||
                                CTCTTTTG TCTTGTG   GTTTT
                                     _      GGG
GAM380  AGRN     3'  TCCTGTGTGTGCTCTGGGCCCT 78840    G   A_        TG
              GC                   G AGG  CCAGGGCATG  CAGGG
                                | |||  ||||||||||  |||||
                                C TCC  GGTCTCGTGT  GTCCT
                                 G   CG         GT
GAM380  AICDA    3'  TTTTGTATGTGTGTGATGCTTC 40332       C  GG__
              TCCC                  GGAGGA CA    GCATGTGCAGGG
                                |||||| ||    ||||||||||||
                                CCTCTT GT    TGTGTATGTTTT
                                   C  AGTG
GAM380  AKAP13   3'  TTTGCTTTTGCTTTTCCC    23250       ACCAG    TGT
                                GGGAGG    GGCA   GCAGG
                                ||||||    ||||   |||||
                                CCCTTT    TCGT   CGTTT
                                   ______   TTT
GAM380  AKAP13   3'  CATCTGCTTTGGTTGTTTT    89680      G         T
                                GGGA GACCAGGGCA GTG
                                |||| |||||||||| |||
                                TTTT TTGGTTTCGT TAC
                                  G        C
GAM380  AKAP13   3'  TCTGTAGCCAGGTCTTCCC    89689          AG   ATG
                                GGGAGGACC  GGC   TGCAGG
                                |||||||||  |||   ||||||
                                CCCTTCTGG  CCG   ATGTCT
                                     A_  ___
GAM380  AKAP13   5'  TTTGCTTTTGCTTTTCCC    89691       ACCAG    TGT
                                GGGAGG    GGCA   GCAGG
                                ||||||    ||||   |||||
                                CCCTTT    TCGT   CGTTT
                                   ______   TTT
GAM380  ALDH3B2  3'  CTCTGTGTATGCCTGGGATCCT 5504         _ A      TG
              TC                   GGAGGA CC GGGCATG  CAGGG
                                |||||| || |||||||  |||||
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                                CTTCCT GG TCCGTAT  GTCTC
                                   A  G      GT
GAM380  ALMS1    3'  TTTTGTATGTGTTTTTATACTT 30673       GACC
                TT                  GGGAG    AGGGCATGTGCAGGG
                                    |||||    ||||||||||||||||
                                    TTTTC    TTTTGTGTATGTTTT
                                      ATAT
GAM380  AMD1     3'  TTTTGTTTTGTTTTGGTTTTGT 7904     G          TGT
                T                    GG AGGACCAGGGCA   GCAGGG
                                    || ||||||||||||   ||||||
                                    TT TTTTGGTTTTGT   TGTTTT
                                     G          TT_
GAM380  AMPD3    3'  TCTGAGTCTTGGTTTCTTC    4902        _      ATGTG
                                    GGAGGA CCAGGGC     CAGG
                                    ||||||| |||||||     ||||
                                    CTTCTT GGTTCTG     GTCT
                                       T      A____
GAM380  ANKRA2   3'  TTTTGTTTACTTCTTGGTCCTT 43529           CA  T
                                    GAGGACCAGGG  TG GCAGGG
                                    ||||||||||  || ||||||
                                    TTCCTGGTTCT  AT TGTTTT
                                          TC  T
GAM380  AOAH     5'  TTTGTGTGTGGCTCTCTC    91119       GACCA  G    TG
                                    GGGAG    GG CATG  CAGG
                                    |||||    || ||||  ||||
                                    CTCTC    TC GTGT  GTTT
                                      _____  G    GT
GAM380  AP1B1    3'  CCCTGGCTCCTTGGTCTCTCC  6668       _       CAT  G
                                    GGAG GACCAGGG   GT CAGGG
                                    |||| ||||||||   || |||||
                                    CCTC CTGGTTCC   CG GTCCC
                                      T       T__  _
GAM380  AP1M1    3'  CCCTGTGTGTGTTTATGTC    50667      CA       TG
                                    GAC  GGGCATG  CAGGG
                                    |||  |||||||  |||||
                                    CTG  TTTGTGT  GTCCC
                                      TA      GT
GAM380  AQP1     3'  CTTTCCACTTGCCCTGTGTTCT 4606     GG    _      T   C
                TTC                   G  AGGAC CAGGGCA GTG AGGG
                                    |  ||||| ||||||| ||| ||||
                                    C  TCTTG GTCCCGT CAC TTTC
                                     TT    T      T   C
GAM380  ARF3     3'  TCTGCAGGTAGGTTTTTCT    8010          AGGGC  G
                                    GGGAGGACC     AT TGCAGG
                                    |||||||||     || ||||||
                                    TCTTTTTGG     TG ACGTCT
                                          A____  G
GAM380  ARHA     3'  TTTTGTATAATTGGATTTCCT  70700        A    GGCA
                                    GGGAGG CCAG    TGTGCAGGG
                                    |||||| ||||    |||||||||
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                                TCCTTT GGTT    ATATGTTTT
                                   A   A___
GAM380  ASIC4    3'  CTTTGCACAAAGGTCCTTCT   37920         AGGGCA
                                GGGAGGACC     TGTGCAGGG
                                |||||||||     |||||||||
                                TCTTCCTGG     ACACGTTTC
                                    AA____
GAM380  ASPH     3'  CCTGCTTCCCTGTTTTCTC    39395        C    CATGT
                                GGGAGGAC AGGG    GCAGG
                                |||||||| ||||    |||||
                                CTCTTTTG TCCC    CGTCC
                                    _   TT___
GAM380  ASPH     3'  CCTGCTTCCCTGTTTTCTC    50624        C    CATGT
                                GGGAGGAC AGGG    GCAGG
                                |||||||| ||||    |||||
                                CTCTTTTG TCCC    CGTCC
                                    _   TT___
GAM380  ASS      3'  TTTGTTCCCTGGTCCCCC    53948     A       CATGT
                                GGG GGACCAGGG    GCAGG
                                ||| |||||||||    |||||
                                CCC CCTGGTCCC    TGTTT
                                  _       T____
GAM380  ASS      3'  TTTGTTCCCTGGTCCCCC    3507      A       CATGT
                                GGG GGACCAGGG    GCAGG
                                ||| |||||||||    |||||
                                CCC CCTGGTCCC    TGTTT
                                  _       T____
GAM380  ASTN     3'  CCTTGTCTGTGTCTCCTGGTTT 69332          __    GT
            TCTT                  GGAGGACCAGG  GCAT  GCAGGG
                                ||||||||||  ||||  ||||||
                                TCTTTTGGTCC  TGTG  TGTTCC
                                     TC   TC
GAM380  ATF4     5'  CTCTGCGCGTGTGCGTTTTCCC 8037         CAGG
                                GGGAGGAC   GCATGTGCAGGG
                                ||||||||   ||||||||||||
                                CCCTTTTG   TGTGCGCGTCTC
                                    CG__
GAM380  ATF5     3'  TCTTGCGTATTTCTGGATCTCC 23808       A     C
            T                    GGGAGG CCAGGG ATGTGCAGGG
                                ||||||| |||||| ||||||||||
                                TCCTCT GGTCTT TATGCGTTCT
                                   A     _
GAM380  ATP6V0C  3'  TCTTGTACATGCGCAGTGTCCT 87316      CAGG_
                                AGGAC    GCATGTGCAGGG
                                |||||    ||||||||||||
                                TCCTG    CGTACATGTTCT
                                   TGACG
GAM380  ATP7B    3'  TCCTGCATAGTCTGTTCCTTTC 3543    GG   CCA   A
                                G  AGGA   GGGC TGTGCAGGG
                                |  ||||   |||| |||||||||
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                                C  TCCT   TCTG ATACGTCCT
                                 TT   TG_   _
GAM380  ATP8B2   3'  TATTTTTTGGTTCTCTC     65235           C
                                GGGAGGACCAGGG ATG
                                ||||||||||||| |||
                                CTCTCTTGGTTTT TAT
                                      T
GAM380  AVPR2    5'  TCTGTGCATCCGTCTGTCT   3546     GA   CAG  C   TG
                                GG  GGAC   GG ATG  CAGG
                                ||  ||||   || |||  ||||
                                TC  TCTG   CC TAC  GTCT
                                 TG   ___  _  GT
GAM380  B3GAT1   3'  CTCTGTGGCTCTCCTCTGGTTC 37830    A       CAT_ _
           ACCT                   GG GGACCAGGG    GT GCAGGG
                                || |||||||||    || ||||||
                                CC CTTGGTCTC    CG TGTCTC
                                 A        CTCT  G
GAM380  B3GAT1   5'  GCTGCTCTGTCCTCTC     53976        C     T
                                GGGAGGAC AGGGCA GT
                                |||||||| |||||| ||
                                CTCTCCTG TCTCGT CG
                                      _     _
GAM380  B4GALT5  3'  CGTGTTCTGTCTTTTC     16497   GG    C
                                G  AGGAC AGGGCATG
                                |  ||||| ||||||||
                                C  TTCTG TCTTGTGC
                                 TT   _
GAM380  B4GALT5  3'  CTTTGTCCCTGCCTTGGCTTTT 16502   GG   A      TGT
           C                    G  AGG CCAGGGCA   GCAGGG
                                |  ||| ||||||||   ||||||
                                C  TTC GGTTCCGT   TGTTTC
                                 TT   _       CCC
GAM380  B4GALT5  3'  TTTGTTTGTGTTTTTGTTCTTT 16518        C      T    G
           T                    GGGAGGAC AGGGCATG GCAGG
                                |||||||| |||||||| |||||
                                TTTTCTTG TTTTGTGT TGTTT
                                      T       T
GAM380  BACH2    3'  TTTTGTTTTTGTTTTTGTTTTC 41496        C     TGT
           CT                    GGGAGGAC AGGGCA   GCAGGG
                                ||||||| ||||||   ||||||
                                TCCTTTTG TTTTGT   TGTTTT
                                      T     TTT
GAM380  BCL6     5'  TGTCTTTTTCTGTCTTCTC   57224        C____
                                GGGAGGAC    AGGGCA
                                ||||||||    ||||||
                                CTCTTCTG    TTCTGT
                                      TCTTT
GAM380  BGN      3'  TCCAGACACACATGTTCTGTTC 8145       C        CAG__
           CTCCT                    GAGGA CAGGGCATGTG    GG
                                ||||| ||||||||||    ||
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                                CTCCT GTCTTGTACAC    CC
                                   T         ACAGA  T
GAM380  BIN3     3'  CCCTGTGCGGGAGAGCTGGTCC 37956         GGCA__  TG
              TCC                   GGAGGACCAG     TG  CAGGG
                                |||||||||     ||  |||||
                                CCTCCTGGTC     GC  GTCCC
                                     GAGAGG  GT
GAM380  BMPR2    5'  TCTGCAGCTAGGTCCTCTC   6836         AG   ATG
                                GGGAGGACC  GGC   TGCAGG
                                |||||||||  |||   ||||||
                                CTCTCCTGG  TCG   ACGTCT
                                     A_  ___
GAM380  BPAG1    3'  TTCTGTATATAGTGACCTTCT  8173        ACCAGG  _
                                GGGAGG     GC ATGTGCAGGG
                                ||||||     || ||||||||||
                                TCTTCC     TG TATATGTCTT
                                   AG____  A
GAM380  BRS3     5'  TCTGGATGTCTTGGATTTTCT  8179        _       GTG
                                GGAGGA CCAGGGCAT   CAGG
                                ||||||| |||||||||   ||||
                                TCTTTT GGTTCTGTA   GTCT
                                   A       G__
GAM380  BRS3     5'  TTCTGTTCTGTTCTGTTCTCCT 8180         C     TGT
                                GGGAGGAC AGGGCA   GCAGGG
                                |||||||| ||||||   ||||||
                                TCCTCTTG TCTTGT   TGTCTT
                                     _     CT_
GAM380  BSG      3'  TTCTGTTCCTTAGGTTTTTTT  67799         _   CATGT
                                GGGAGGACC AGGG    GCAGGG
                                ||||||||| ||||    ||||||
                                TTTTTTTGG TTCC    TGTCTT
                                     A   T____
GAM380  BTRC     3'  TCTGCACCTAGTTTTTTC    53311   GG    C   GCATG
                                G  AGGAC AGG    TGCAGG
                                |  ||||| |||    ||||||
                                C  TTTTG TCC    ACGTCT
                                 TT    A  _____
GAM380  BTRC     3'  TCTGCACCTAGTTTTTTC    14140   GG    C   GCATG
                                G  AGGAC AGG    TGCAGG
                                |  ||||| |||    ||||||
                                C  TTTTG TCC    ACGTCT
                                 TT    A  _____
GAM380  C21orf2  3'  TTTGCAGGCTGTCCTCCC    17019        CAG   ATG
                                GGGAGGAC   GGC   TGCAGG
                                ||||||||   |||   ||||||
                                CCCTCCTG   TCG   ACGTTT
                                     ___   G__
GAM380  C7       3'  CCGTCTGCCTTGGCCTCCC   5157         A      TGT  A
                                GGGAGG CCAGGGCA   GC GG
                                |||||| ||||||||   || ||
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                                CCCTCC GGTTCCGT   TG CC
                                  _       C__  _
GAM380  C7      3'  TCTGGGCCTTGGTTTTTT    5168            ATGTG
                                GGAGGACCAGGGC    CAGG
                                ||||||||||||    ||||
                                TTTTTTGGTTCCG    GTCT
                                   G____
GAM380  CACNB2   3'  TGCCCTTTTGTGTTTTTTT   5581         _ ___
                                GGGAGGAC CA   GGGCA
                                |||||||| ||   |||||
                                TTTTTTTG GT   CCCGT
                                    T  TTT
GAM380  CALM3    3'  CTTTGTAATGTGCTGGTTCTCT 17743          G   G
           T                     GGGAGGACCAG GCAT TGCAGGG
                                ||||||||||| |||| |||||||
                                TTCTCTTGGTC TGTA ATGTTTC
                                   G   _
GAM380  CAPZA1   3'  CCCTGCACATGAACATGTTTGC 72626     AG   CAGGG
           TT                    GGG  GAC    CATGTGCAGGG
                                |||  |||    ||||||||||
                                TTC  TTG    GTACACGTCCC
                                  GT   TACAA
GAM380  CARD10   3'  CTCACATGGGTGTCTGTGGTTC 27274       G _____    C  GG
           TCTC                   GGACCA GG    CATGTG AG
                                |||||| ||    |||||| ||
                                CTTGGT TC    GTACAC TC
                                   G  TGTGG    _
GAM380  CARD15   3'  CCTGCACACGCTCCTTCC    42212       CCAGG  A
                                GGGAGGA    GC TGTGCAGG
                                |||||||    || ||||||||
                                CCTTCCT    CG ACACGTCC
                                    _____  C
GAM380  CASP6    3'  CTCTGTATTGAAAATGGCTTTC 6909       A   GGG_  T
           T                     GGGAGG CCA    CA GTGCAGGG
                                |||||| |||    || ||||||||
                                TCTTTC GGT    GT TATGTCTC
                                   _   AAAA  _
GAM380  CASP6    3'  CTCTGTATTGAAAATGGCTTTC 52202       A   GGG_  T
           T                     GGGAGG CCA    CA GTGCAGGG
                                |||||| |||    || ||||||||
                                TCTTTC GGT    GT TATGTCTC
                                   _   AAAA  _
GAM380  CASQ1    3'  TCCTGCCTTCCCTTGTCCTTCC 6933         C    CATGT
                                GGGAGGAC AGGG    GCAGGG
                                |||||||| ||||    ||||||
                                CCTTCCTG TCCC    CGTCCT
                                    T   TTC__
GAM380  CBFA2T2  3'  TGTTCTGTGTCCTTTT     17480        _
                                GGGAGGAC CAGGGCA
                                |||||||| |||||||
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                                TTTTCCTG GTCTTGT
                                    T
GAM380  CCBL1    3'  TCTTGTGTTGCTTCTGGTCTCT 14484      _      _  T TG
                CC                   GGAG GACCAGG GCA G  CAGGG
                                |||| ||||||| ||| |  |||||
                                CCTC CTGGTCT CGT T  GTTCT
                                  T      T  _ GT
GAM380  CCNB1    5'  GTGTTCTGCTTCTCCC      49238        C
                                GGGAGGA CAGGGCAT
                                ||||||| ||||||||
                                CCCTCTT GTCTTGTG
                                    C
GAM380  CCND2    3'  TCCAAATTATCCTGGTCTTTTT 8298             CAT  GCA
                                GGGAGGACCAGGG  GT  GGG
                                |||||||||||||  ||  |||
                                TTTTTCTGGTCCT  TA  CCT
                                       AT_  AA_
GAM380  CCND2    3'  TTTTGTTCAGTTTGGTTTTTTT 8302            G A  T
                                GGGAGGACCAGG C TG GCAGGG
                                |||||||||||| | || ||||||
                                TTTTTTTGGTTT G AC TGTTTT
                                       _ _  T
GAM380  CCNF     3'  CCCATGTGTGTCCTGGTGTTCC 8316       G        GT  _
                C                    GGGAG ACCAGGGCAT  GCA GGG
                                ||||| ||||||||||  ||| |||
                                CCCTT TGGTCCTGTG  TGT CCC
                                  G         __  A
GAM380  CCR9     3'  CTTTGCATCTTTTGTGTCTTTC 48298         _    CAT
                T                    GGGAGGAC CAGGG  GTGCAGGG
                                |||||||| |||||  ||||||||
                                TCTTTCTG GTTTT  TACGTTTC
                                    T   C__
GAM380  CCR9     3'  CTTTGCATCTTTTGTGTCTTTC 21814         _    CAT
                T                    GGGAGGAC CAGGG  GTGCAGGG
                                |||||||| |||||  ||||||||
                                TCTTTCTG GTTTT  TACGTTTC
                                    T   C__
GAM380  CD34     3'  CCCTGGAGCAGACTCTGGTCTT 8343            CA  G_
                CTT                  GGGAGGACCAGGG  TGT  CAGGG
                                ||||||||||||  |||  |||||
                                TTCTTCTGGTCTC  ACG  GTCCC
                                       AG  AG
GAM380  CD3E     3'  CTTGCATGTAAGTTGTCCC   5591      G  CAGG  TG
                                GGGA GAC   GCA  TGCAGG
                                |||| |||   |||  ||||||
                                CCCT TTG   TGT  ACGTTC
                                  G  AA__  __
GAM380  CD3Z     3'  TCCTGGCGGTTCCTCGTTCTCC 5594         C   CA  G
                C                    GGGAGGAC AGGG  TGT CAGGG
                                ||||||| ||||  ||| |||||
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                                CCCTCTTG TCCT  GCG GTCCT
                                    C   TG  _
GAM380  CDC42   3'  CTTTGTATATGCATTCTTTTC  8371    GG   CCAGG
                                G  AGGA    GCATGTGCAGGG
                                |  ||||    ||||||||||||
                                C  TTCT    CGTATATGTTTC
                                 TT   TA___
GAM380  CDH17   3'  TCTGCCTGCCTTGGTCTCCC   14509      G       TGT
                                GGGAG ACCAGGGCA   GCAGG
                                ||||| |||||||||   |||||
                                CCCTC TGGTTCCGT   CGTCT
                                   _       C__
GAM380  CDH18   5'  TCCTAAAGATGCTCTGGCTTCT 17034       A       GTGC
            C                    GGGAGG CCAGGGCAT    AGGG
                                ||||||| |||||||||    ||||
                                CTCTTC GGTCTCGTA    TCCT
                                   _       GAAA
GAM380  CDKN2A  5'  CTCTGACCATTCTGTTCTCTC  54233        C   GC   TG
                                GGGAGGAC AGG  ATG  CAGGG
                                |||||||| |||  |||  |||||
                                CTCTCTTG TCT  TAC  GTCTC
                                    _  __   CA
GAM380  CEBPA   3'  TTTTGTTTTGTTTGGTTTTCTC 15165          G  TGT
                                GGGAGGACCAGG CA   GCAGGG
                                |||||||||||| ||   ||||||
                                CTCTTTTGGTTT GT   TGTTTT
                                      _  TT_
GAM380  CELSR1  3'  TTCTGCGGTGCTGGTTTTTCT  26489          G  ATG
                                GGGAGGACCAG GC   TGCAGGG
                                |||||||||||| ||   |||||||
                                TCTTTTTGGTC TG   GCGTCTT
                                      G  ___
GAM380  CELSR1  3'  TTGCACTGATCTTTCT     26491        C  GGGCAT
                                GGGAGGA CA     GTGCAG
                                ||||||| ||     ||||||
                                TCTTTCT GT     CACGTT
                                   A  _______
GAM380  CENTD1  5'  CTTGTGTGTGTGTCTCATC   30851    GA   CAGG    TG
                                GG  GGAC    GCATG  CAGG
                                ||  ||||    |||||  ||||
                                CT  TCTG    TGTGT  GTTC
                                 AC    _____     GT
GAM380  CH25H   3'  TTTTGTGTTCTTGGTATTCTT  14211       G      CAT TG
                                GGGAG ACCAGGG   G  CAGGG
                                ||||| |||||||   |  |||||
                                TTCTT TGGTTCT   T  GTTTT
                                   A       ___ GT
GAM380  CHD2    3'  CTCATAGCAGCTTTGGTTTTCC 7030             A   GCA
            C                    GGGAGGACCAGGGC TGT   GGG
                                |||||||||||||| |||   |||
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                                CCCTTTTGGTTTCG ACG   CTC
                                       _   ATA
GAM380  CHD2     3'  TGCCCTGCGTTCTTCT      7035          _
                                GGGAGGAC CAGGGCA
                                |||||||| |||||||
                                TCTTCTTG GTCCCGT
                                     C
GAM380  CHES1    3'  TCTTGTTTGGGGTTTGGTTTTC 17770           G ATGT_
             TT                   GGGAGGACCAGG C     GCAGGG
                                |||||||||||| |     ||||||
                                TTCTTTTGGTTT G     TGTTCT
                                       _ GGGTT
GAM380  CHST2    3'  CTTTGCCTTCTCTTGTCCTCTT 62694         C    CATGT
                                GGGAGGAC AGGG     GCAGGG
                                |||||||| ||||     ||||||
                                TTCTCCTG TCTC     CGTTTC
                                     T    TTC__
GAM380  CHST5    3'  CCTGATTCTCGGTTTTCCT    24023         A   CATGTG
                                GGGAGGACC GGG      CAGG
                                ||||||||| |||      ||||
                                TCCTTTTGG CTC      GTCC
                                     _   TTA___
GAM380  CHST6    3'  CTTGATTCTTGGTTTTCCT    41226            CATGTG
                                GGGAGGACCAGGG      CAGG
                                ||||||||||||      ||||
                                TCCTTTTGGTTCT      GTTC
                                       TA____
GAM380  CISH     3'  GCCCTGGCTTCTCTGGTTCTTC 59016            CAT  G
             C                   GGGAGGACCAGGG   GT CAGGG
                                ||||||||||||   || |||||
                                CCTTCTTGGTCTC   CG GTCCC
                                       TT_ _     GT
GAM380  CISH     3'  GCCCTGGCTTCTCTGGTTCTTC 25279            CAT  G
             C                   GGGAGGACCAGGG   GT CAGGG
                                ||||||||||||   || |||||
                                CCTTCTTGGTCTC   CG GTCCC
                                       TT_ _     GT
GAM380  CKAP1    5'  CTTCGCCGCCTGTTCTGGTCCT 73537    GG          T   _ AG
             TTC                   G  AGGACCAGGGCA GTG C  GG
                                |  |||||||||||| ||| |  ||
                                C  TCCTGGTCTTGT CGC G  TC
                                 TT          C   C CT  T
GAM380  CKAP1    3'  TCCTGTGTGTGCCCATGGCCCT 73540       A  _      TG
             TT                   GGAGG CCA GGGCATG  CAGGG
                                ||||| ||| |||||||  |||||
                                TTTCC GGT CCCGTGT  GTCCT
                                   C  A      GT
GAM380  CLN2     3'  CTCTGACTACTCTTGTCTTCCT 4613          C   CAT  G
                                GGGAGGAC AGGG   GT CAGGG
                                |||||||| ||||   || |||||
```

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                                TCCTTCTG TCTC   CA GTCTC
                                     T    AT_  _
GAM380  CLTC     3'  TCTTGTGTGTGTTTACTAACCC 16784     AGGACCA      TG
                                GGG      GGGCATG  CAGGG
                                |||      |||||||  |||||
                                CCC      TTTGTGT  GTTCT
                                  AATCA__      GT
GAM380  CNTNAP2  3'  TTTTGTGTGTGTTTAGAGGTGT 26235     G   A__      TG
           TC                     GAG ACC   GGGCATG  CAGGG
                                ||| |||   |||||||  |||||
                                CTT TGG   TTTGTGT  GTTTT
                                  G   AGA      GT
GAM380  COIL     3'  TTTTGTAGATCTTTGGTTTTTT 67853            C  G
           T                     GGGAGGACCAGGG AT TGCAGGG
                                |||||||||||| || |||||||
                                TTTTTTTGGTTTC TA ATGTTTT
                                       _  G
GAM380  COL4A6   5'  CCCTGGGCTGCTGGTCTTCTT  8471           GG   T  G
                                GGGAGGACCA  GCA GT CAGGG
                                ||||||||||  ||| || |||||
                                TTCTTCTGGT  CGT CG GTCCC
                                      __  _  G
GAM380  CPNE3    3'  TATGAGCATTCCTGGTTTTCTT 14033            C    G  GGG
                                GGGAGGACCAGGG ATGT CA
                                |||||||||||| |||| ||
                                TTCTTTTGGTCCT TACG GT
                                       _   A  ATT
GAM380  CPO      3'  CGTGCCTTAGTCTTCTC     3636          C
                                GGGAGGAC AGGGCATG
                                |||||||| ||||||||
                                CTCTTCTG TTCCGTGC
                                     A
GAM380  CPSF4    3'  TTCTGTGTGGCGGTGGTCATTC 21957       _    GG  A  TG
           CC                     GGGAG GACCA  GC TG  CAGGG
                                ||||| |||||  || ||  |||||
                                CCCTT CTGGT  CG GT  GTCTT
                                   A    GG  _  GT
GAM380  CREBL2   3'  TGCCATCTGGTCCACTC     7147      A      __
                                GGG GGACCAG  GGCA
                                ||| |||||||  ||||
                                CTC CCTGGTC  CCGT
                                  A      TA
GAM380  CRMP1    3'  TTTGTACAAAGTTTTCCT     7154          CAGGGCA
                                GGGAGGAC      TGTGCAGG
                                ||||||||      ||||||||
                                TCCTTTTG      ACATGTTT
                                     AA_____
GAM380  CRTAP    3'  CATCTGCCTTGGGCCTCCC    21032        A       T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
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                                CCCTCC GGTTCCGT TAC
                                   G      C
GAM380  CSNK1E   3'  TCCTGTGTAAATATTGGACTTT 95630       A   GGCA  TG
            TT                   GGGAGG CCAG   TG  CAGGG
                                ||||||| ||||   ||  |||||
                                TTTTTC GGTT   AT  GTCCT
                                   A   ATAA  GT
GAM380  CSNK1E   5'  TGCCCTTCGTTTTTCC     8553         C_
                                GGGAGGAC  AGGGCA
                                ||||||||  ||||||
                                CCTTTTTG  TCCCGT
                                     CT
GAM380  CSPG3    3'  TTCTGCATGTGTGATGAATCTC 15241       AC  GG
            TT                   GGGAGG  CA  GCATGTGCAGGG
                                ||||||  ||  ||||||||||||
                                TTCTCT  GT  TGTGTACGTCTT
                                   AA  AG
GAM380  CTSD     3'  TGTTCTGTGGTTTTCCC     8587          __
                                GGGAGGACCA  GGGCA
                                ||||||||||  |||||
                                CCCTTTTGGT  CTTGT
                                      GT
GAM380  CUL4B    3'  CCCTGTGTACGTGGTGGTTCT  13139       GG  A  TG
                                AGGACCA  GC TG  CAGGG
                                |||||||  || ||  |||||
                                TCTTGGT  TG AT  GTCCC
                                    GG  C  GT
GAM380  CUL4B    3'  TTCTGTGTCATGCTGGTTTTCC 13146         GG    _
            T                    GGGAGGACCA  GCATG TGCAGGG
                                ||||||||||  ||||| |||||||
                                TCCTTTTGGT  CGTAC GTGTCTT
                                      __    T
GAM380  CXCL16   3'  TTTTGTAATGATTGAGTCTTCT 41930        _  GG   G
            T                    GGGAGGAC CAG  CAT TGCAGGG
                                |||||||| |||  ||| |||||||
                                TTCTTCTG GTT  GTA ATGTTTT
                                    A  A_  _
GAM380  CYB561   3'  CCTTGCGGCTCAGCTCTGGTTT 8598     AG       AT_ _
            CCTC                    GG  GACCAGGGC   GT GCAGGG
                                ||  |||||||||   || ||||||
                                TC  TTGGTCTCG   CG CGTTCC
                                 CT       ACT  G
GAM380  CYLN2    3'  TCTTAGCGGCCCTGTCCTCTT  12638        C    A   GC
                                GGGAGGAC AGGGC TGT  AGGG
                                |||||||| ||||| |||  ||||
                                TTCTCCTG TCCCG GCG  TTCT
                                    _    _  A_
GAM380  CYP1A2   3'  CACCTGCCTTGGCTTCCC    5678        A       T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
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                                CCCTTC GGTTCCGT CAC
                                   _       C
GAM380  CYP1A2   3'  CACCTGCCTTGGCTTCCC    69097       A       T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTTC GGTTCCGT CAC
                                   _       C
GAM380  CYP2B6   3'  CCCTGTCAATCTGGTTTTT   5726          GCATGT
                                GAGGACCAGG     GCAGGG
                                ||||||||||     ||||||
                                TTTTTGGTCT     TGTCCC
                                     AAC___
GAM380  CYP2B6   3'  TGTGTCTGGTTGCTTTC     5745    GG _     G
                                G  AG GACCAGG CATG
                                |  || ||||||| ||||
                                C  TC TTGGTCT GTGT
                                 TT  G      _
GAM380  CYP4F3   3'  CCCTGTATTTATTTGTTTTCTT 6113         C   GCAT
                                GGGAGGAC AGG    GTGCAGGG
                                |||||||| |||    ||||||||
                                TTCTTTTG TTT    TATGTCCC
                                     _   ATT_
GAM380  CYP8B1   3'  CCCAGCTTGCTTTAGTTTTTTC 15261    GG    C     TGT  A
                                G  AGGAC AGGGCA   GC GGG
                                |  ||||| ||||||   || |||
                                C  TTTTG TTTCGT   CG CCC
                                 TT    A     T__  A
GAM380  DAZL     5'  CCTTGTCACCCGCTCTTGGTTT 68140          _ AT   _
           TCCT                   GGAGGACCAGG GC  GTG CAGGG
                                ||||||||||| ||  ||| |||||
                                CCTTTTGGTTC CG  CAC GTTCC
                                      T  CC   T
GAM380  DBT      3'  TTTGTGGTAATGCTTTGGTATT 8614    GG  G        GT__    G
           TTC                    AG ACCAGGGCAT    GCAGG
                                 || ||||||||||    |||||
                                 TT TGGTTTCGTA    TGTTT
                                TT  A         ATGG
GAM380  DEFA5    3'  CTCTGTGTACCTTGTGTCTTTC 40666        _    CA  TG
           T                     GGGAGGAC CAGGG  TG  CAGGG
                                ||||||| |||||  ||  |||||
                                TCTTTCTG GTTCC  AT  GTCTC
                                     T    __  GT
GAM380  DEK      3'  TTTTGTACATTTTGGATTTCTT 12959       A    GC
                                GGGAGG CCAGG  ATGTGCAGGG
                                |||||| |||||  ||||||||||
                                TTCTTT GGTTT  TACATGTTTT
                                   A    __
GAM380  DGAT2    5'  CTCTGTATTCACTGTTCCTCCC 50789        C   GGCAT
                                GGGAGGA CAG    GTGCAGGG
                                ||||||| |||    ||||||||
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                                CCCTCCT GTC    TATGTCTC
                                    T  ACT__
GAM380  DGAT2   3'  TTTTGTATATGCCTTG     50793
                                CAGGGCATGTGCAGGG
                                ||||||||||||||||
                                GTTCCGTATATGTTTT

GAM380  DNMT1   5'  CCTTGCGCATGCGTGTTCCC  7268       G  CAGG
                                GGGAG AC   GCATGTGCAGGG
                                ||||| ||   ||||||||||||
                                CCCTT TG   CGTACGCGTTCC
                                  G  ____
GAM380  DPH2L1  3'  CCTTGTGTGTGCCCTGGGCC  7277     A        TG
                                GG CCAGGGCATG  CAGGG
                                || ||||||||||  |||||
                                CC GGTCCCGTGT  GTTCC
                                 G         GT
GAM380  DRIL1   3'  TTTTGTCTGCTTTAGTTCTCTT 17833         C     TGT
                                GGGAGGAC AGGGCA   GCAGGG
                                |||||||| ||||||   ||||||
                                TTCTCTTG TTTCGT   TGTTTT
                                    A    C__
GAM380  DSCR3   3'  CCTCCTGTCTTGGCCTCCC   20177       A      TGTGC
                                GGGAGG CCAGGGCA    AGG
                                |||||| ||||||||    |||
                                CCCTCC GGTTCTGT    TCC
                                   _       CC___
GAM380  DSCR3   3'  TTCTGTAGTTTTTTGGTTTTGT 20199    G        C  G
          T                      GG AGGACCAGGG AT TGCAGGG
                                || ||||||||||  || |||||||
                                TT TTTTGGTTTT TG ATGTCTT
                                 G         T  _
GAM380  DUSP5   3'  TCTTGTGACAATTGTTTTCCT  15355         CAGGGCA  _
                                GGGAGGAC      TGT GCAGGG
                                ||||||||      ||| ||||||
                                TCCTTTTG      ACA TGTTCT
                                    TTA____   G
GAM380  DVL3    3'  CCTGCGTGCTGGTTCCTTC   15366       _   G  ATGT
                                GGAGGA CCAG GC    GCAGG
                                |||||| |||| ||    |||||
                                CTTCCT GGTC TG    CGTCC
                                   T   G  ____
GAM380  DVL3    3'  CTGCGCAGGACTTCCC      15367       A  AGGGCA
                                GGGAGG CC     TGTGCAG
                                |||||| ||     |||||||
                                CCCTTC GG     ACGCGTC
                                   A  _______
GAM380  DYT1    3'  CCTTGTGTGTGTGTTTTTTTTT 3671       CC  G    TG
                                GAGGA  AG GCATG  CAGGG
                                |||||  || |||||  |||||
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                                TTTTT  TT TGTGT  GTTCC
                                   TT  G    GT
GAM380  EBAF    3'  GTCCTGTGTGACCTTCGCCCTG 65425   _    AT_____ TG
            TGTCCTTCC                C CAGGGC      G  CAGGG   T
                                | ||||||      |  |||||  |
                                G GTCCCG      T  GTCCT   G
                                 T     CTTCCAG GT
GAM380  EBP     5'  CCGTCGCGCGCCTTGGTTTTTC 21666            A   CA  G
            T                    GGGAGGACCAGGGC TGTG  GG
                                ||||||||||||| ||||  ||
                                TCTTTTTGGTTCCG GCGC  CC
                                         C   TG
GAM380  ED1     3'  CCTTGTACAGTCTGCTCCTCTT 7366         CCA   A
                                GGGAGGA   GGGC TGTGCAGGG
                                |||||||   |||| |||||||||
                                TTCTCCT   TCTG ACATGTTCC
                                    CG_   _
GAM380  EDAR    3'  CTTGGGCCTTGTCTTTTC    42267   GG    C    ATGTG
                                G  AGGAC AGGGC    CAGG
                                |  ||||| |||||    ||||
                                C  TTCTG TTCCG    GTTC
                                 TT    _    G____
GAM380  EEF1A1  3'  TTGTGGACCACTTTGGTTTTCT 7389            CAT  G  GGG
            T                    GGGAGGACCAGGG   GT CA
                                ||||||||||||   || ||
                                TTCTTTTGGTTTC   CA GT
                                       AC_  G  GTTT
GAM380  EFNB2   3'  TCTGCGTTGGGTTTTCCC    14577         AG   ATGT
                                GGGAGGACC  GGC    GCAGG
                                |||||||||  |||   |||||
                                CCCTTTTGG  TTG    CGTCT
                                     G_  _____
GAM380  EGFL6   3'  CTTTGTATGTCAGTTCCCTGGT 31324         C____
            TTTTTT                GGACCAGGG    ATGTGCAGGG
                                |||||||||    ||||||||||
                                TTTGGTCCC    TGTATGTTTC
                                     TTGAC
GAM380  EGR1    3'  ATATGGTTTGGTTTTTCT    8739            G
                                GGGAGGACCAGG CATGT
                                |||||||||||| |||||
                                TCTTTTTGGTTT GTATA
                                       G
GAM380  EGR4    3'  TGCTTTGGGTTTTTTT      8746          _
                                GGGAGGACC AGGGCA
                                ||||||||| ||||||
                                TTTTTTTGG TTTCGT
                                     G
GAM380  EHD3    3'  CCCTATCTGCTTTGGCTTCCT  27477       A       T  GC
                                GGGAGG CCAGGGCA GT  AGGG
                                |||||| |||||||| ||  ||||
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                                TCCTTC GGTTTCGT TA  TCCC
                                   _       C  __
GAM380  EIF1A    3'  CTTTGTGTTTTTGGTTTACCC  88602     AG       CAT TG
                                GGG  GACCAGGG   G  CAGGG
                                |||  ||||||||   |  |||||
                                CCC  TTGGTTTT   T  GTTTC
                                  AT       ___ GT
GAM380  EIF1A    3'  TTCTGTACATAAAAGTGTTTTT 88608    G     CAGGGC
           GC                     G GAGGAC     ATGTGCAGGG
                                | ||||||     ||||||||||
                                C TTTTTG     TACATGTCTT
                                 G     TGAAAA
GAM380  EIF4G2   3'  TCTGCATAAGGTTTTTTT     7424          AGGGCA
                                GGGAGGACC     TGTGCAGG
                                |||||||||     ||||||||
                                TTTTTTTGG     ATACGTCT
                                     A_____
GAM380  ELAVL2   5'  CTTTGTTCCTTGGTTT      15413          CATGT
                                GGACCAGGG     GCAGGG
                                |||||||||     ||||||
                                TTTGGTTCC     TGTTTC
                                     T____
GAM380  ELMO1    3'  TTTTGCCTTGCTCTGTTCCTCT 55287        C      TGT
           T                     GGGAGGA CAGGGCA   GCAGGG
                                ||||||| |||||||   ||||||
                                TTCTCCT GTCTCGT   CGTTTT
                                     T      TC_
GAM380  EMS1     3'  TCTTGGGTGGTTTTGGGTTTTT 17855    GG     _     ATG G
           TC                     G  AGGACC AGGGC   T CAGGG
                                |  |||||| |||||   | |||||
                                C  TTTTGG TTTTG   G GTTCT
                                 TT     G     GT_ G
GAM380  EMS1     3'  TCTTGGGTGGTTTTGGGTTTTT 56755    GG     _     ATG G
           TC                     G  AGGACC AGGGC   T CAGGG
                                |  |||||| |||||   | |||||
                                C  TTTTGG TTTTG   G GTTCT
                                 TT     G     GT_ G
GAM380  EP300    5'  TCCTGAGGATTCTGGTTTTCCT 7477             CATGTG
                                GGGAGGACCAGGG     CAGGG
                                ||||||||||||     |||||
                                TCCTTTTGGTCTT     GTCCT
                                       AGGA__
GAM380  EPB72    3'  GTTCCTTGAGTTCTCCT     14608         _     C
                                GGGAGGAC CAGGG AT
                                |||||||| ||||| ||
                                TCCTCTTG GTTCC TG
                                     A     T
GAM380  EPHB4    3'  TCCAGAACAGTGCCTTGGTCAT 15463      G        _   GCA
           CCC                     GGGA GACCAGGGCA TGT   GGG
                                |||| |||||||||| |||   |||
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                                CCCT CTGGTTCCGT ACA   CCT
                                  A        G   AGA
GAM380  ESRRG    3'  TTTAAAAATGTTTTGTTTCTTC 66397        C       GTGCAGGG
            T                    GGGAGGA CAGGGCAT
                                |||||||  ||||||||
                                TCTTCTT GTTTTGTA
                                   T       AAAATTTT
GAM380  ETV5     3'  TTTTGTTTGTGTTTTTGGTTGT 15491      G       _    T
            TCC                    GGGA GACCAGGG CATG GCAGGG
                                |||| |||||||| |||| ||||||
                                CCTT TTGGTTTT GTGT TGTTTT
                                  G       T   T
GAM380  FACL5    3'  CCCAGTTTATGTTCTGTGTCCT 64187         _       T  A
            TCC                    GGGAGGAC CAGGGCATG GC GGG
                                |||||||| |||||||| || |||
                                CCTTCCTG GTCTTGTAT TG CCC
                                   T       T  A
GAM380  FANCC    3'  CTGTGTACAGGGTTGGCCTCTT 70522       A   GGCA     G
                                GGGAGG CCAG    TGTGCA GG
                                ||||||  ||||    ||||||  ||
                                TTCTCC GGTT    ACATGT TC
                                   _   GGG_     G
GAM380  FBLN5    3'  TATGTTCTGTCTTCCC      20918         C
                                GGGAGGAC AGGGCATG
                                |||||||| ||||||||
                                CCCTTCTG TCTTGTAT
                                   _
GAM380  FBXL7    3'  TCCTGTGCATACTGTCGTCTT  24555      G   CA  GC   TG
                                GGGA GAC  GG  ATG  CAGGG
                                ||||  |||  ||  |||  |||||
                                TTCT CTG  TC  TAC  GTCCT
                                  G   __  A_   GT
GAM380  FBXW7    3'  TCTGCTAGCCTGTTCTTTT    53305        CA    ATGT
                                GGGAGGAC  GGGC    GCAGG
                                ||||||||  ||||    |||||
                                TTTTCTTG  TCCG    CGTCT
                                   __    AT__
GAM380  FBXW7    3'  TCTGCTAGCCTGTTCTTTT    37027        CA    ATGT
                                GGGAGGAC  GGGC    GCAGG
                                ||||||||  ||||    |||||
                                TTTTCTTG  TCCG    CGTCT
                                   __    AT__
GAM380  FCAR     3'  TTCTGCACATAAGTTATGGTTT 8860          GG  __
            TCC                    GGAGGACCA  GC  ATGTGCAGGG
                                |||||||||  ||  ||||||||||
                                CCTTTTGGT  TG  TACACGTCTT
                                    AT  AA
GAM380  FCAR     3'  TTCTGCACATAAGTTATGGTTT 55755         GG  __
            TCC                    GGAGGACCA  GC  ATGTGCAGGG
                                |||||||||  ||  ||||||||||
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                                CCTTTTGGT  TG  TACACGTCTT
                                     AT  AA
GAM380  FCAR    3'  TTCTGCACATAAGTTATGGTTT 55766        GG  __
          TCC                  GGAGGACCA  GC  ATGTGCAGGG
                               |||||||||  ||  ||||||||||
                               CCTTTTGGT  TG  TACACGTCTT
                                     AT  AA
GAM380  FCAR    3'  TTCTGCACATAAGTTATGGTTT 55777        GG  __
          TCC                  GGAGGACCA  GC  ATGTGCAGGG
                               |||||||||  ||  ||||||||||
                               CCTTTTGGT  TG  TACACGTCTT
                                     AT  AA
GAM380  FCAR    3'  TTCTGCACATAAGTTATGGTTT 55788        GG  __
          TCC                  GGAGGACCA  GC  ATGTGCAGGG
                               |||||||||  ||  ||||||||||
                               CCTTTTGGT  TG  TACACGTCTT
                                     AT  AA
GAM380  FCMD    3'  TTCTGTACATGTACTGTTTTC  22099      C  GG
                               GAGGAC AG  CATGTGCAGGG
                               ||||||  ||  ||||||||||||
                               CTTTTG TC  GTACATGTCTT
                                  _  AT
GAM380  FCN2    3'  CCTGTCCCCTGGCTTCTC    31731      A    CATGT
                               GGGAGG CCAGGG    GCAGG
                               ||||||  ||||||    |||||
                               CTCTTC GGTCCC    TGTCC
                                  _     C____
GAM380  FCN2    3'  CCTGTCCCCTGGCTTCTC    31738      A    CATGT
                               GGGAGG CCAGGG    GCAGG
                               ||||||  ||||||    |||||
                               CTCTTC GGTCCC    TGTCC
                                  _     C____
GAM380  FGF2    3'  CCCTGGATATGCTCTTGTTTTT 8868    GG    C      G
          TC                   G  AGGAC AGGGCATGT CAGGG
                               |  |||||  |||||||||  |||||
                               C  TTTTG TCTCGTATA GTCCC
                                TT    T       G
GAM380  FGF23   3'  CTTTCAAGCCTTCGTTCTTCC  40193        C    A  TGC
                               GGGAGGAC AGGGC TG   AG
                               |||||||  |||||  ||   ||
                               CCTTCTTG TTCCG AC   TC
                                    C    A  TT_
GAM380  FGFR3   3'  TATTTGCTTTGTCCTTTT    3776         C     T
                               GGGAGGAC AGGGCA GTG
                               ||||||||  ||||||  |||
                               TTTTCCTG TTTCGT TAT
                                  _     T
GAM380  FHL2    3'  CTTGCCTTCTGGTTTCTTC   7563        _     CATGT
                               GGAGGA CCAGGG    GCAGG
                               ||||||  ||||||    |||||
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                                CTTCTT GGTCTT    CGTTC
                                   T     C____
GAM380  FKBP1B   3'  CTCTGTATGTGTTCGTCAGTGT 14648     G  CA__
            TC                   GAG AC    GGGCATGTGCAGGG
                                ||| ||    ||||||||||||||
                                CTT TG    CTTGTGTATGTCTC
                                  G  ACTG
GAM380  FKBP1B   3'  CTCTGTATGTGTTCGTCAGTGT 54008     G  CA__
            TC                   GAG AC    GGGCATGTGCAGGG
                                ||| ||    ||||||||||||||
                                CTT TG    CTTGTGTATGTCTC
                                  G  ACTG
GAM380  FLOT2    3'  CTCTGTGCATCTGTCCATCCT  15574      _    CAG  C   TG
                                GGGA GGAC   GG ATG  CAGGG
                                |||| ||||   || |||  |||||
                                TCCT CCTG   TC TAC  GTCTC
                                  A   ___  _   GT
GAM380  FLRT2    3'  TCTGTGTTTGGGCCTCTC    25067       A  AG   ATGT
                                GGGAGG CC  GGC    GCAGG
                                |||||| ||  |||    |||||
                                CTCTCC GG  TTG    TGTCT
                                   _  GT   ____
GAM380  FMR1     3'  GTCCTGTGTCAGTTTATGTTTT 8939          _______ TG
            GGTCCACTT               CCAGGGCAT     G  CAGGG   T
                                |||||||||     |  |||||  |
                                GGTTTTGTA     T  GTCCT   G
                                     TTTGAC GT
GAM380  FOSB     5'  CTTACTTTTTTTGGTCTTCTT  22104           CAT   C
                                GGGAGGACCAGGG   GTG AG
                                ||||||||||||   ||| ||
                                TTCTTCTGGTTTT   CAT TC
                                      TTT   _
GAM380  FOSB     5'  CTTGATTGTTGTGGTTCTTCT  22105          G    TGTG
                                GGGAGGACCA GGCA    CAGG
                                |||||||||| ||||    ||||
                                TCTTCTTGGT TTGT    GTTC
                                     G    TA__
GAM380  FOXO1A   3'  GTATTTGTGTGTTTTTGGTT 8905           _   TG    G
            TTTCT                GGAGGACCAGGG CATG  CAGG
                                |||||||||||| ||||  ||||
                                CTTTTTGGTTTT GTGT  GTTT
                                      T   GT    ATGT
GAM380  FPGS     3'  TTTTGGCTTTCCTGGTTCTGTC 17093    G        CAT  G
                                GG AGGACCAGGG   GT CAGGG
                                || ||||||||||   || |||||
                                CT TCTTGGTCCT   CG GTTTT
                                 G         TT_  _
GAM380  FUT1     3'  CACCTGTCTTGGCCTCCC    3785        A       T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
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                                CCCTCC GGTTCTGT CAC
                                   _       C
GAM380  FUT8     3'  TTTTGTTTTTGTTTTTGTTTTT 15592   GG    C     TGT
             TC                   G  AGGAC AGGGCA   GCAGGG
                                  |  ||||| ||||||   ||||||
                                  C  TTTTG TTTTGT   TGTTTT
                                   TT    T     TTT
GAM380  FXYD7    3'  TTAATAAATGTGCATTTGGTTT 41840   GG       _     GCAGGG
             TTTC                    AGGACCAGG GCATGT
                                   |||||||||| ||||||
                                   TTTTGGTTT CGTGTA
                                  TT        A     AATAATTC
GAM380  FY       5'  CCAGCTGCCCTGGCTTCCC    8969        A       TGT  A
                                  GGGAGG CCAGGGCA   GC GG
                                  |||||| ||||||||   || ||
                                  CCCTTC GGTCCCGT   CG CC
                                     _      ___  A
GAM380  FY       5'  TCCTGCAGAGACCTTGTTCTCC 8973          C   GCATG
             C                    GGGAGGAC AGG     TGCAGGG
                                  |||||||| |||     |||||||
                                  CCCTCTTG TCC     ACGTCCT
                                       T   AGAG_
GAM380  FZD10    3'  TTTTGTTTTGTTTTGGTTTTCC 23244             TGT
                                  GGAGGACCAGGGCA   GCAGGG
                                  ||||||||||||||   ||||||
                                  CCTTTTGGTTTTGT   TGTTTT
                                        TT_
GAM380  G6PC     3'  CACCTGCCTTGGCCTCCC     3821        A       T
                                  GGGAGG CCAGGGCA GTG
                                  |||||| |||||||| |||
                                  CCCTCC GGTTCCGT CAC
                                     _       C
GAM380  GABRE    5'  TCCGTCAACAGCCTTGGTCCTC 41777             A   GCA_
             TC                     GGGAGGACCAGGGC TGT    GGG
                                  |||||||||||||| |||    |||
                                  CTCTCCTGGTTCCG ACA    CCT
                                        _   ACTG
GAM380  GABRE    5'  TCCGTCAACAGCCTTGGTCCTC 41786             A   GCA_
             TC                     GGGAGGACCAGGGC TGT    GGG
                                  |||||||||||||| |||    |||
                                  CTCTCCTGGTTCCG ACA    CCT
                                        _   ACTG
GAM380  GABRE    5'  CCCACAATTTTCTGGTCCTCTC 41802           CA_   CA
                                  GGGAGGACCAGGG   TGTG  GG
                                  ||||||||||||   ||||  ||
                                  CTCTCCTGGTCTT   ACAC  CC
                                        TTA   __
GAM380  GABRE    5'  TCCGTCAACAGCCTTGGTCCTC 41809             A   GCA_
             TC                     GGGAGGACCAGGGC TGT    GGG
                                  |||||||||||||| |||    |||
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                                CTCTCCTGGTTCCG ACA   CCT
                                       _  ACTG
GAM380  GALNS   3'  TCTGGCCTCGGTCCTCCC   4967        AG  ATGTG
                                GGGAGGACC GGC    CAGG
                                ||||||||| |||    ||||
                                CCCTCCTGG CCG    GTCT
                                    CT  _____
GAM380  GATA6   3'  TTCTGATCAATTTTGGTTGTTC 17920     G      CA TG
          C                      GGGA GACCAGGG  TG  CAGGG
                                |||| ||||||||  ||  |||||
                                CCTT TTGGTTTT  AC  GTCTT
                                  G      A_  TA
GAM380  GDI1    3'  CCTTGTGTGTGTCTCTTCCCCC 59976    A  CCA     TG
                                GGG GGA   GGGCATG  CAGGG
                                ||| |||   |||||||  |||||
                                CCC CCT   TCTGTGT  GTTCC
                                  _  TC_     GT
GAM380  GHR     3'  CTTTGCTGCTATGGTTTTCTC  3882          G   TGT
                                GGGAGGACCA GGCA   GCAGGG
                                |||||||||| ||||   ||||||
                                CTCTTTTGGT TCGT   CGTTTC
                                    A   ___
GAM380  GJA1    3'  TCCTGAACATCTTAGGTCTTTT 3906    GG    AG  C   G
          C                      G  AGGACC  GG ATGT CAGGG
                                |  ||||||  || |||| |||||
                                C  TTCTGG  TC TACA GTCCT
                                 TT     AT  _   A
GAM380  GJA1    3'  TTTTGCAGTAACTGGTATTCTT 3910       G    GGCATG
                                GGGAG ACCAG     TGCAGGG
                                ||||| |||||     |||||||
                                TTCTT TGGTC     ACGTTTT
                                   A    AATG__
GAM380  GLI2    3'  CCAGCTGTCTTGTCTTTTT   47524        C    TGT  A
                                GGGAGGAC AGGGCA   GC GG
                                |||||||| ||||||   || ||
                                TTTTTCTG TTCTGT   CG CC
                                    _     ___  A
GAM380  GLRA2   5'  TCTGAGGCTTTGTCTTTCT   9033         C    ATGTG
                                GGGAGGAC AGGGC    CAGG
                                ||||||| |||||    ||||
                                TCTTTCTG TTTCG    GTCT
                                    _    GA___
GAM380  GLRA3   5'  TCTGTCTTTCTGGTTCCCC   60074    A       CATGT
                                GGG GGACCAGGG    GCAGG
                                ||| |||||||||    |||||
                                CCC CTTGGTCTT    TGTCT
                                  _       TC___
GAM380  GM2A    3'  GACCGTGCATGCCTTGTCCTCT 67776        C       TG A  G
          T                      GGGAGGAC AGGGCATG  C GG
                                |||||||| ||||||||  | ||
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                                TTCTCCTG TTCCGTAC  G CC
                                   _       GT _  AGA
GAM380  GNA11    5'  CTCTGTGCGTGGCCTTGTCC   76097      C   G    TG
                                GGAC AGG CATG  CAGGG
                                |||| ||| ||||  |||||
                                CCTG TCC GTGC  GTCTC
                                  T   G    GT
GAM380  GNAI3    3'  TTCTGCAATAAGATTCTAGTTC 21446        C    CATG__
           TCTC                   GGAGGAC AGGG     TGCAGGG
                                |||||||  ||||     |||||||
                                TCTCTTG TCTT     ACGTCTT
                                   A    AGAATA
GAM380  GNAZ     3'  TTTTGTTTTTTGTTTTTTGGTT 9067          __   TGT_
           TTTTT                  AGGACCAGG  GCA    GCAGGG
                                |||||||||  |||   ||||||
                                TTTTGGTTT  TGT    TGTTTT
                                     TT   TTTT
GAM380  GOCAP1   3'  TTTTGTACATATCTAACTCTGT 42706     C    C_____
           TCTCTT                  GAC AGGG     ATGTGCAGGG
                                |||  ||||     ||||||||||
                                TTG TCTC     TACATGTTTT
                                  _    AATCTA
GAM380  GOT1     3'  CCTAAGCTTTGGTTCTTT    9095            ATGTGC
                                GGAGGACCAGGGC     AGG
                                ||||||||||||      |||
                                TTTCTTGGTTTCG     TCC
                                      AA____
GAM380  GPR4     3'  CCTCCTGCCTTGGCCTCCC    59904       A       TGTGC
                                GGGAGG CCAGGGCA     AGG
                                ||||||  ||||||||     |||
                                CCCTCC GGTTCCGT     TCC
                                   _       CC___
GAM380  GPR75    5'  CTTATCTGTCTTGGGCCTCTT  22305       A       T   C
                                GGGAGG CCAGGGCA GTG AG
                                |||||| |||||||| ||| ||
                                TTCTCC GGTTCTGT TAT TC
                                   G       C   _
GAM380  GPR81    3'  CGCCTGCCTTGGCCTCCC     50755       A       T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTCC GGTTCCGT CGC
                                   _       C
GAM380  GPRK6    3'  TTTGCACAGTGATCTTCCC    9116        C AGG  A
                                GGGAGGA C   GC TGTGCAGG
                                |||||||  |   || ||||||||
                                CCCTTCT G   TG ACACGTTT
                                   A ___  _
GAM380  GRB10    3'  CCTAGATGTTTTGTCTTCTC   17976        C      G GC
                                GGGAGGAC AGGGCAT T  AGG
                                |||||||| |||||||  |  |||
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                                CTCTTCTG TTTTGTA A  TCC
                                    _      G __
GAM380  GRM4     3'  CCTGTCTTTCTGTTCTCTT   5921         C   CATGT
                                GGGAGGAC AGGG    GCAGG
                                |||||||| ||||    |||||
                                TTCTCTTG TCTT    TGTCC
                                    _   TC___
GAM380  GRM6     3'  TCCTGCATTTGCTGTTTTCTC  5940         CAG   T
                                GGGAGGAC   GGCA GTGCAGGG
                                ||||||||   |||| ||||||||
                                CTCTTTTG   TCGT TACGTCCT
                                    ___    T
GAM380  H1F0     3'  CCCTGTTGAAACTTAGGTTTTT 18015         AG  CATGT
              CC                   GGGAGGACC  GG    GCAGGG
                                |||||||||  ||    ||||||
                                CCTTTTTGG  TC    TGTCCC
                                     AT  AAAGT
GAM380  HDAC4    3'  TGTGGCTGGGTTTTCT     20123         A  G
                                GGAGGACC GG CATG
                                |||||||| || ||||
                                TCTTTTGG TC GTGT
                                    G  G
GAM380  HDAC5    3'  CCCTGTGGCTGGTCTGGTTCTC 57607          G  TG
                                GAGGACCAGG CA  TGCAGGG
                                |||||||||| ||  |||||||
                                CTCTTGGTCT GT  GTGTCCC
                                     G  CG
GAM380  HDAC5    3'  TCCTGCATTCTGTCTGTCCTTT 57615         CA    T_
              T                   GGGAGGAC  GGGCA  GTGCAGGG
                                ||||||||  |||||  ||||||||
                                TTTTCCTG  TCTGT  TACGTCCT
                                    __     CT
GAM380  HDAC7A   3'  CCCTGTGTATGTATGCATGTTT 33450       ___ GG    TG
              TT                   GAGGAC   CA  GCATG  CAGGG
                                ||||||   ||  |||||  |||||
                                TTTTTG   GT  TGTAT  GTCCC
                                   TAC  A_    GT
GAM380  HDAC7A   3'  CTTGGGACCTGGTTCTCTT   33451          GCATGTG
                                GGGAGGACCAGG      CAGG
                                ||||||||||||      ||||
                                TTCTCTTGGTCC      GTTC
                                     AGG____
GAM380  HDAC7A   3'  CCCTGTGTATGTATGCATGTTT 31209       ___ GG    TG
              TT                   GAGGAC   CA  GCATG  CAGGG
                                ||||||   ||  |||||  |||||
                                TTTTTG   GT  TGTAT  GTCCC
                                   TAC  A_    GT
GAM380  HDAC7A   3'  CTTGGGACCTGGTTCTCTT   31210          GCATGTG
                                GGGAGGACCAGG      CAGG
                                ||||||||||||      ||||
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                                TTCTCTTGGTCC      GTTC
                                      AGG____
GAM380  HDAC8    3'  TATATCTTTGGTTTTTTT    37492           C
                                GGGAGGACCAGGG ATGTG
                                ||||||||||||| |||||
                                TTTTTTTGGTTTC TATAT
                                      _
GAM380  HHLA1    5'  CTCTAATTAGATGTCCTAGGTC 19129       _     G  C__
              CTCCC                  AGGACC AGGGCAT TG   AGGG
                                ||||||| ||||||| ||   ||||
                                TCCTGG TCCTGTA AT   TCTC
                                   A      G  TAA
GAM380  HIS1     3'  CTTTCTAGTGCCTTGGTTTTCT 21315             GTGC   G
              T                  GGGAGGACCAGGGCAT    AGG
                                |||||||||||||||    |||
                                TTCTTTTGGTTCCGTG    TTC
                                      ATCT
GAM380  HMG20A   3'  TGTGTCCTGTCTTCCT      36544         C
                                GGGAGGAC AGGGCATG
                                |||||||| ||||||||
                                TCCTTCTG TCCTGTGT
                                      _
GAM380  HMGA2    3'  TTCTGTATTGCCATGGTCTTTC 13005          G    T
              C                  GGGAGGACCA GGCA GTGCAGGG
                                |||||||||| |||| ||||||||
                                CCTTTCTGGT CCGT TATGTCTT
                                      A   _
GAM380  HMGN3    3'  TCCTGTGCATACTGTGGTGTTT 14905       G    G  C   TG
              TT                  GGGAG ACCA GG ATG  CAGGG
                                ||||| |||| || |||  |||||
                                TTTTT TGGT TC TAC  GTCCT
                                   G    G  A   GT
GAM380  HNMT     5'  CCTTGCTTCCTGCTCTGTCTTT 22568         C      TGT_
              CT                  GGGAGGAC AGGGCA    GCAGGG
                                |||||||| ||||||    ||||||
                                TCTTTCTG TCTCGT    CGTTCC
                                      _     CCTT
GAM380  HOXC10   3'  TTGCATGTAGCTTCCT      61274      CCAG   _
                                AGGA    GGC ATGTGCAG
                                ||||    ||| |||||||||
                                TCCT    TCG TGTACGTT
                                   ____   A
GAM380  HOXD4    3'  CAAGCCTTGGTCTTTT      27521            A
                                GGAGGACCAGGGC TG
                                |||||||||||| ||
                                TTTTCTGGTTCCG AC
                                      A
GAM380  HPCA     3'  CTGTGTTTGGCCTCTC      9255         A    GGCAT TG
                                GGGAGG CCAG     G  CAG
                                |||||| ||||     |  |||
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                                CTCTCC GGTT    T  GTC
                                  _   _____ GT
GAM380  HS3ST3B1  3'  CCTTGTCTTGTCTTGGGTCTCC 20149      GA      TGT
              C                    GGGAG  CCAGGGCA   GCAGGG
                                   |||||  ||||||||   ||||||
                                   CCCTC  GGTTCTGT   TGTTCC
                                     TG       TC_
GAM380  HSPA1B   3'  TTCTGTACGAGTTTGTTTTTTT 18077        CA    A
                                   GGGAGGAC  GGGC TGTGCAGGG
                                   ||||||||  ||||  |||||||||
                                   TTTTTTTG  TTTG GCATGTCTT
                                       __    A
GAM380  HUNK     3'  CCCTGTGTGTGTTTTG      27446         TG
                                   CAGGGCATG  CAGGG
                                   |||||||||  |||||
                                   GTTTTGTGT  GTCCC
                                        GT
GAM380  HUNK     3'  CTTTGGGAACTCTGTCTTTCT  27451         C    CATGTG
                                   GGGAGGAC AGGG     CAGGG
                                   ||||||||| ||||     |||||
                                   TCTTTCTG TCTC     GTTTC
                                       _    AAGG__
GAM380  ICAM1    3'  CCCAAGCTATGCCTTGTCCTCT 71575         C       T  A_
              T                    GGGAGGAC AGGGCATG GC  GGG
                                   |||||||| |||||||| ||  |||
                                   TTCTCCTG TTCCGTAT CG  CCC
                                       _       _  AA
GAM380  IGF1R    3'  CCCTGTCCTTCCCTGTTCTCCC 6048          C    CATGT
                                   GGGAGGAC AGGG     GCAGGG
                                   |||||||| ||||     ||||||
                                   CCCTCTTG TCCC     TGTCCC
                                       _    TTCC_
GAM380  IKBKB    3'  CCTGCTCCCTGTCCTCTC     63205         C    CATGT
                                   GGGAGGAC AGGG     GCAGG
                                   |||||||| ||||     |||||
                                   CTCTCCTG TCCC     CGTCC
                                       _    T____
GAM380  IL1F5    3'  TTCTGTGTGTGTCCCCTCCC   24386        ACCA      TG
                                   GGGAGG    GGGCATG  CAGGG
                                   ||||||    |||||||  |||||
                                   CCCTCC    CCTGTGT  GTCTT
                                       ____       GT
GAM380  IL21R    3'  CCCTGTGCATGTCTGGACTC   41426     GA    G    TG
                                   GAG  CCAGG CATG  CAGGG
                                   |||  ||||| ||||  |||||
                                   CTC  GGTCT GTAC  GTCCC
                                     A_     _    GT
GAM380  IL22RA2  3'  TGCCTTTTGTCCTTTT      53695         C_
                                   GGGAGGAC  AGGGCA
                                   ||||||||  ||||||
```

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                                TTTTCCTG  TTCCGT
                                     TT
GAM380  IL8     3'  CCTTGTTCCACTGTGCCTTGGT 94479    _       _  ___
             TTCTCC                  GA CCAGGGCAT GTG   CAGGG
                                || |||||||| |||   |||||
                                TT GGTTCCGTG CAC   GTTCC
                                 T       T   CTT
GAM380  IMPDH1   3'  TCCTGGCCCTGCTCTGGCCCTT 6085        A      T_  G
             CC                    GGGAGG CCAGGGCA  GT CAGGG
                                |||||| ||||||||  || |||||
                                CCTTCC GGTCTCGT  CG GTCCT
                                   C       CC  _
GAM380  INPP5B   3'  CCCAGCTGTTTTGGGTCTCCC  95525      GA      TGT  A
                                GGGAG  CCAGGGCA   GC GGG
                                |||||  ||||||||   || |||
                                CCCTC  GGTTTTGT   CG CCC
                                   TG       ___  A
GAM380  IRF1     3'  GTGTCTGGGTTTTTCT      64347         A
                                GGGAGGACC GGGCAT
                                ||||||||| ||||||
                                TCTTTTTGG TCTGTG
                                     G
GAM380  ISL1     3'  AATTCTATGTGTTTTGTCTTTT 9360         C        CAGGG
             T                   GGGAGGAC AGGGCATGTG
                                |||||||| ||||||||||
                                TTTTTCTG TTTTGTGTAT
                                     _        CTTAAT
GAM380  ITGA1    3'  CTTTGTATGTGCTTCTTTGTTC 63530       C_  _
             TT                   GAGGAC  AGG GCATGTGCAGGG
                                ||||||  ||| ||||||||||||
                                TTCTTG  TCT CGTGTATGTTTC
                                   TT   T
GAM380  ITGA3    3'  TTTGTATATAGGCTTCTC    9380        A  AGGGC
                                GGGAGG CC    ATGTGCAGG
                                |||||| ||    |||||||||
                                CTCTTC GG    TATATGTTT
                                   _  A____
GAM380  ITGA3    3'  TTTGTATATAGGCTTCTC    18542       A  AGGGC
                                GGGAGG CC    ATGTGCAGG
                                |||||| ||    |||||||||
                                CTCTTC GG    TATATGTTT
                                   _  A____
GAM380  ITSN1    3'  TCCTGTACTAGATGGTGTTCTC 11620      G   GGGCAT
                                GGGAG ACCA     GTGCAGGG
                                ||||| ||||    ||||||||
                                CTCTT TGGT     CATGTCCT
                                   G   AGAT__
GAM380  IVD      3'  TCCTGCACCTAGTGGCCTTTC  9465    GG  A  G_  CAT
                                G  AGG CCA  GG   GTGCAGGG
                                |  ||| |||  ||   ||||||||
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                                C  TCC GGT  TC   CACGTCCT
                                 TT  _  GA  ___
GAM380  JAM3     3'  GTGTCTTGGGTTTTTT     51428        _
                                GGAGGACC AGGGCAT
                                |||||||| |||||||
                                TTTTTTGG TTCTGTG
                                    G
GAM380  JJAZ1    3'  TTTTGCTTGTTTTGTTTTTCT  31082       C      TGT
                                GGAGGA CAGGGCA   GCAGGG
                                |||||| |||||||   ||||||
                                TCTTTT GTTTTGT   CGTTTT
                                   T      T__
GAM380  KAL1     3'  TTTGTGTATGTCTGTC      4019      CA      TG
                                GAC  GGGCATG  CAGG
                                |||  |||||||  ||||
                                CTG  TCTGTAT  GTTT
                                  __      GT
GAM380  KCNA6    3'  CCCTGTAACAACCACTGGTCCT 9510           _  CATG
            CCT                   GGGAGGACCAG GG    TGCAGGG
                                |||||||||| ||    |||||||
                                TCCTCCTGGTC CC    ATGTCCC
                                      A  AACA
GAM380  KCNAB1   3'  ACATGTTTTGTTTTTTTT    60925        C
                                GGGAGGA CAGGGCATGT
                                ||||||| ||||||||||
                                TTTTTTT GTTTTGTACA
                                    T
GAM380  KCNH3    3'  CCCTGCATGTGCCCCTGCCTCT 64606       ACCA
                                GGAGG    GGGCATGTGCAGGG
                                |||||    ||||||||||||||
                                TCTCC    CCCGTGTACGTCCC
                                   GTC_
GAM380  KCNK10   5'  CTTTGCGCCACGATGTTTTGTT 40970      C      _____
            TTCCT                  GGAC AGGGCAT    GTGCAGGG
                                |||| |||||||    ||||||||
                                TTTG TTTTGTA    CGCGTTTC
                                  _      GCAC
GAM380  KCNK2    3'  TTTTGTGCCCAGACTGTTTTCC 26423        CA___      TGCAGGG
            T                   GGAGGAC     GGGCATG
                                |||||||     |||||||
                                CCTTTTG     CCCGTGT
                                    TCAGA      TTT   G
GAM380  KCNK6    3'  CTTGTTCTCTGTCCTTTC    16693    GG    C    CATGT
                                G  AGGAC AGGG     GCAGG
                                |  ||||| ||||     |||||
                                C  TCCTG TCTC     TGTTC
                                 TT     _    T_____
GAM380  KCNMB1   3'  TCTGTGCCTGAGTTCTCCC    14710        CA    ATGT
                                GGGAGGAC  GGGC    GCAGG
                                ||||||||  ||||    |||||
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                                CCCTCTTG  TCCG    TGTCT
                                    AG    ____
GAM380  KDR      3'  GGTTTTGCCCTTGTTCTGTCC  9594      _    C     TGTGCAGGG
                                GGG AGGAC AGGGCA
                                ||| ||||| ||||||
                                CCT TCTTG TCCCGT
                                  G    T     TTT   GGG
GAM380  KIAA0442 3'  TCCTGTATGTAATAAAGTCCTT 31475    GG    CAGGGC
             TC                   G  AGGAC     ATGTGCAGGG
                                |  |||||     ||||||||||
                                C  TCCTG     TGTATGTCCT
                                 TT    AAATAA
GAM380  KIAA0442 3'  TCTTGTGTGTGAGTGTGTTTTT 31476        _ GGG    TG
             T                    GGAGGAC CA   CATG  CAGGG
                                |||||||  ||   ||||  |||||
                                TTTTTTG GT   GTGT  GTTCT
                                     T  GA_    GT
GAM380  KIAA0857 3'  CTTTGGGAGCCCTGGGTCTTTC 66675          _    ATGTG
             C                    GGGAGGACC AGGGC     CAGGG
                                |||||||||  |||||     |||||
                                CCTTTCTGG TCCCG     GTTTC
                                     G    AGG__
GAM380  KLHL3    3'  ATGTCCTTGTCTTCTT      87454         C
                                GGGAGGAC AGGGCAT
                                ||||||||  |||||||
                                TTCTTCTG TCCTGTA
                                     T
GAM380  KLHL3    3'  CTTTGGGCTTTGTTTTGGTGTT 87456       G        T_  G
             TCT                    GGGAG ACCAGGGCA  GT CAGGG
                                |||||  |||||||||  ||  |||||
                                TCTTT TGGTTTTGT  CG GTTTC
                                   G        TT  G
GAM380  KPNA1    3'  TTTTGCTTCTCTTTGGTCTTTT 80323           CATGT
                                GGAGGACCAGGG    GCAGGG
                                ||||||||||||    ||||||
                                TTTTCTGGTTTC    CGTTTT
                                       TCTT_
GAM380  KRT2A    3'  CTGTGTATATAGCTCCTCTT   4709         CCAGG  _      G
                                GGGAGGA    GC ATGTGCA GG
                                |||||||    || ||||||| ||
                                TTCTCCT    CG TATATGT TC
                                     _____  A      G
GAM380  KRT5     5'  CCCACTAGTGCCTGGTTCTCTT 4710            G   GTGCA
                                GGGAGGACCAGG CAT    GGG
                                ||||||||||||| |||    |||
                                TTCTCTTGGTCC GTG    CCC
                                       _  ATCA_
GAM380  KRT5     5'  TCCTGCTGAGCTCTGTTCTCTC 4712          C    ATGT
                                GGGAGGAC AGGGC    GCAGGG
                                ||||||||  |||||   ||||||
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                                CTCTCTTG TCTCG   CGTCCT
                                   _    AGT_
GAM380  KRTHA8   3'  CCTTGTATCAAATCCTGAGTTT 22258       _    CA _
           TCTC                  GGAGGAC CAGGG  TG TGCAGGG
                                 ||||||| |||||  || |||||||
                                 TCTTTTG GTCCT  AC ATGTTCC
                                    A    AA  T
GAM380  LAMC2    3'  TTCTGTATTTCCTTGGATTTTC 18716       _    CAT
           CT                    GGGAGGA CCAGGG   GTGCAGGG
                                 ||||||| ||||||   ||||||||
                                 TCCTTTT GGTTCC   TATGTCTT
                                    A     TT_
GAM380  LAPTM5   3'  CCCTGTGTGTCGGGGTCCTCC 22202       AG    GT
                                 GGAGGACC  GGCAT  GCAGGG
                                 ||||||||  |||||  ||||||
                                 CCTCCTGG  CTGTG  TGTCCC
                                    GG    __
GAM380  LARGE    3'  TCCTGTTTTGTTTTGTTTTTCT 56111       C     TGT
                                 GGAGGA CAGGGCA   GCAGGG
                                 ||||||| |||||||   ||||||
                                 TCTTTT GTTTTGT   TGTCCT
                                    T      TT_
GAM380  LARGE    3'  TCCTGTTTTGTTTTGTTTTTCT 16437       C     TGT
                                 GGAGGA CAGGGCA   GCAGGG
                                 ||||||| |||||||   ||||||
                                 TCTTTT GTTTTGT   TGTCCT
                                    T      TT_
GAM380  LCN1     3'  CCCTGCGCCCCCTCTCCTGGTT 64229         CAT___
           CTCC                  AGGACCAGGG     GTGCAGGG
                                 ||||||||||     ||||||||
                                 TCTTGGTCCT     CGCGTCCC
                                    CTCCCC
GAM380  LCN1     3'  CCCTGCGCCCCCTCTCCTGGTT 9689          CAT___
           CTCC                  AGGACCAGGG     GTGCAGGG
                                 ||||||||||     ||||||||
                                 TCTTGGTCCT     CGCGTCCC
                                    CTCCCC
GAM380  LFG      3'  TCCTGCATCCAGTCTGTGTCCT 76727        _   GCAT
           CCT                   GGGAGGAC CAGG    GTGCAGGG
                                 ||||||| ||||    ||||||||
                                 TCCTCCTG GTCT    TACGTCCT
                                    T    GACC
GAM380  LIF      3'  AGAGCAGTGTTCTGGCTTCTT  9726       A       G   AGGG
                                 GGGAGG CCAGGGCAT TGC
                                 |||||| ||||||||| |||
                                 TTCTTC GGTCTTGTG ACG
                                    _       _  AGAC
GAM380  LIMD1    3'  TTTTGTGTGTGCGAGATCTCT  26469      ACCAGG    TG
                                 GGAGG     GCATG  CAGGG
                                 |||||     |||||  |||||
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                                TCTCT     CGTGT  GTTTT
                                   AGAG__     GT
GAM380  LIMK1    3'  CTCTGTCCTCTGCGTTTTTTC  9785    GG    _    CATGT
                                G  AGGAC CAGGG    GCAGGG
                                |  ||||| |||||    ||||||
                                C  TTTTG GTCTC    TGTCTC
                                 TT    C    C____
GAM380  LIMK1    3'  CTCTGTCCTCTGCGTTTTTTC  33645    GG    _    CATGT
                                G  AGGAC CAGGG    GCAGGG
                                |  ||||| |||||    ||||||
                                C  TTTTG GTCTC    TGTCTC
                                 TT    C    C____
GAM380  LIPA     3'  TTCTGTAAAACACTTGTTTTTC 4084         C    GCATG
              TT                   GGGAGGA CAGG    TGCAGGG
                                |||||||  ||||    |||||||
                                TTCTTTT GTTC    ATGTCTT
                                    T    ACAAA
GAM380  LMNB1    3'  TTTTGTATGTGTGTTTTTTCTT 18737         CC  G
              TT                   GGGAGGA  AG GCATGTGCAGGG
                                |||||||  ||  ||||||||||||
                                TTTTCTT  TT TGTGTATGTTTT
                                    TT  G
GAM380  LPL      3'  CTCTGCATGTGTGTTGTCCTTC 4087         C  G
                                GGAGGAC AG GCATGTGCAGGG
                                |||||||  ||  ||||||||||||
                                CTTCCTG TT TGTGTACGTCTC
                                    _  G
GAM380  LTA      5'  CCTGGGCCTGGGCCTTGGTTCT 5174              AT__  G    G
              CCC                   GGAGGACCAGGGC    GT CAGG
                                ||||||||||||||    ||  ||||
                                CCTCTTGGTTCCG    CG GTCC
                                       GGTC  G
GAM380  LZTFL1   3'  TTTGTATTGGCCTGGTTTTCTC 39761           G  T
                                GGGAGGACCAGG CA GTGCAGG
                                ||||||||||||  ||  |||||||
                                CTCTTTTGGTCC GT TATGTTT
                                       G  _
GAM380  LZTS1    3'  CACCTGCCTTGGCCTCCC    40681        A       T
                                GGGAGG CCAGGGCA GTG
                                ||||||  ||||||||  |||
                                CCCTCC GGTTCCGT CAC
                                    _       C
GAM380  LZTS1    3'  TCTTGTTTGGTTTGGTTTGCTT 40698     AG      G  TGT
                                GGG  GACCAGG CA   GCAGGG
                                |||  |||||||  ||   ||||||
                                TTC  TTGGTTT GT   TGTTCT
                                  GT      G  T__
GAM380  MADD     5'  TGTGTAGCATGCCTTGGTTTTT 55335              _    GGG
              CC                   GGGAGGACCAGGGCATG TGCA
                                ||||||||||||||||  ||||
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                                CCTTTTTGGTTCCGTAC ATGT
                                          G    GT
GAM380  MAFF     3'  CCTTCGTGGGCCCTGTCTTCCT 24647        C     ATG  C
                                GGGAGGAC AGGGC   TG AGG
                                |||||||| |||||   || |||
                                TCCTTCTG TCCCG   GC TCC
                                     _    GGT  T
GAM380  MAP3K14  5'  TCTGTGTTTGGTCTCTCTC    14209      _     GGCAT TG
                                GGGAG GACCAG    G  CAGG
                                ||||| ||||||    |  ||||
                                CTCTC CTGGTT    T  GTCT
                                   T     _____ GT
GAM380  MAP3K7IP2 3'  TCTTGGCCTTGTCTTTGTCTTC 30662        C     T_  G
             CC                   GGGAGGAC AGGGCA  GT CAGGG
                                |||||||| ||||||  || |||||
                                CCCTTCTG TTCTGT  CG GTTCT
                                     T     TC  _
GAM380  MAP3K9   3'  TTCTGTGATTGATTTTGGTCCT 60710           _  TG
             CCT                    GGGAGGACCAGGG CA  TGCAGGG
                                |||||||||||| ||  |||||||
                                TCCTCCTGGTTTT GT  GTGTCTT
                                       A  TA
GAM380  MAPRE3   3'  CCTTGCACTTTACCTGTTCTTT 24665   GG   C   GCAT
             TC                   G  AGGA CAGG   GTGCAGGG
                                |  |||| ||||   ||||||||
                                C  TTCT GTCC   CACGTTCC
                                 TT   T   ATTT
GAM380  MAZ      3'  CTCTGTAAGCCCATGCCCTGTC 73389      C      ____
             TTCCC                  GGAC AGGGCATG   TGCAGGG
                                |||| ||||||||   |||||||
                                TCTG TCCCGTAC   ATGTCTC
                                   _      CCGA
GAM380  MDFI     3'  CCTCTCCCTGGTCCTCTC    18770           CATGTGC
                                GGGAGGACCAGGG      AGG
                                ||||||||||||      |||
                                CTCTCCTGGTCCC      TCC
                                       TC_____
GAM380  MIF      5'  CTCTGCGCGGGTCTCCTGGTCC 10034          CA__
             TTCT                   GGAGGACCAGGG   TGTGCAGGG
                                ||||||||||||   |||||||||
                                CTTCCTGGTCCT   GCGCGTCTC
                                       CTGG
GAM380  MJD      3'  TCTGCTACCTGGTTTTC     17164          GCATGT
                                GAGGACCAGG     GCAGG
                                ||||||||||     |||||
                                CTTTTGGTCC     CGTCT
                                      AT_____
GAM380  MJD      3'  TCTGCTACCTGGTTTTC     47683          GCATGT
                                GAGGACCAGG     GCAGG
                                ||||||||||     |||||
```

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                                CTTTTGGTCC     CGTCT
                                      AT____
GAM380  MKI67   3' CTCTGCTCCCGCCTGTTTTCTT 10043        CA   ATGT
                                GGGAGGAC  GGGC   GCAGGG
                                ||||||||  ||||   ||||||
                                TTCTTTTG  TCCG   CGTCTC
                                    __   CCCT
GAM380  MKI67   3' TTTGCCCCCTGTCCTCTC    10052        C   CATGT
                                GGGAGGAC AGGG    GCAGG
                                |||||||| ||||    |||||
                                CTCTCCTG TCCC    CGTTT
                                    _   C____
GAM380  MLLT2   3' TTTTGTTTTGTTTTGTTTTCTT 19858        C    TGT
                                GGGAGGAC AGGGCA   GCAGGG
                                |||||||| ||||||   ||||||
                                TTCTTTTG TTTTGT   TGTTTT
                                    _    TT_
GAM380  MLPH    3' CTGCACTGTTTTCCC      44080        CAGGGCAT
                                GGGAGGAC      GTGCAG
                                ||||||||      ||||||
                                CCCTTTTG      CACGTC
                                     T_______
GAM380  MME     3' CTCTGCATCTCCTGTCTTTTC 23488   GG    C   CAT
                                G  AGGAC AGGG   GTGCAGGG
                                |  ||||| ||||   ||||||||
                                C  TTCTG TCCT   TACGTCTC
                                 TT    _   C__
GAM380  MME     3' TGTGCCTGGCTTCTT      23491       A    G
                                GGGAGG CCAGG CATG
                                |||||| ||||| ||||
                                TTCTTC GGTCC GTGT
                                   _    _
GAM380  MME     3' CTCTGCATCTCCTGTCTTTTC 23498   GG    C   CAT
                                G  AGGAC AGGG   GTGCAGGG
                                |  ||||| ||||   ||||||||
                                C  TTCTG TCCT   TACGTCTC
                                 TT    _   C__
GAM380  MME     3' TGTGCCTGGCTTCTT      23501       A    G
                                GGGAGG CCAGG CATG
                                |||||| ||||| ||||
                                TTCTTC GGTCC GTGT
                                   _    _
GAM380  MME     3' CTCTGCATCTCCTGTCTTTTC 23509   GG    C   CAT
                                G  AGGAC AGGG   GTGCAGGG
                                |  ||||| ||||   ||||||||
                                C  TTCTG TCCT   TACGTCTC
                                 TT    _   C__
GAM380  MME     3' TGTGCCTGGCTTCTT      23513       A    G
                                GGGAGG CCAGG CATG
                                |||||| ||||| ||||
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                                TTCTTC GGTCC GTGT
                                    _    _
GAM380  MME     3'  CTCTGCATCTCCTGTCTTTTC  6141    GG    C   CAT
                                G  AGGAC AGGG   GTGCAGGG
                                |  ||||| ||||   ||||||||
                                C  TTCTG TCCT   TACGTCTC
                                 TT    _   C__
GAM380  MME     3'  TGTGCCTGGCTTCTT      6144        A    G
                                GGGAGG CCAGG CATG
                                |||||| ||||| ||||
                                TTCTTC GGTCC GTGT
                                    _    _
GAM380  MMP2    3'  CTTTGTATGCACTTTGTTTTTT 15766   GG   C    CA
            TC                    G  AGGA CAGGG  TGTGCAGGG
                                |  |||| |||||  |||||||||
                                C  TTTT GTTTC  GTATGTTTC
                                 TT   T    AC
GAM380  MPP2    3'  CCTTGACCTTGGTCC       59820          _  TGTGC
                                GGACCAGGG CA    AGG
                                ||||||||| ||    |||
                                CCTGGTTCC GT    TCC
                                     A _____
GAM380  MPP2    3'  TCCTGTCTCTTCTCGGTCTTTC 59832          A   CATGT
            C                    GGGAGGACC GGG    GCAGGG
                                ||||||||| |||    ||||||
                                CCTTTCTGG CTC    TGTCCT
                                     _  TTCTC
GAM380  MRPL49  3'  CCTTGGCCTGTTTTGTTTTTCT 69568       C      T  G
                                GGAGGA CAGGGCA GT CAGGG
                                |||||| ||||||| || |||||
                                TCTTTT GTTTTGT CG GTTCC
                                   T     C  _
GAM380  MTA1L1  3'  TCTGTAATTGGTTCTT      16444         GGGCATG
                                GAGGACCA      TGCAGG
                                ||||||||      ||||||
                                TTCTTGGT      ATGTCT
                                     TA_____
GAM380  MTAP    5'  CTCTGTGGCTCGCTTGGTTCCC 10130     A       G AT  _
            T                    GGG GGACCAGG C  GT GCAGGG
                                ||| |||||||  |  || ||||||
                                TCC CTTGGTTC G  CG TGTCTC
                                  _       _ CT  G
GAM380  MTF1    3'  CCTTGCCTTCCTGGTTCTTTC  19883   GG        CATGT
                                G  AGGACCAGGG    GCAGGG
                                |  ||||||||||    ||||||
                                C  TCTTGGTCCT    CGTTCC
                                 TT        TC___
GAM380  MTMR1   3'  TTTGCTCCCTGGTCTTTTT   70161            CATGT
                                GGGAGGACCAGGG    GCAGG
                                ||||||||||||    |||||
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                                TTTTTCTGGTCCC    CGTTT
                                      T____
GAM380  MTMR2    3'  TCTTGTCCCCTTGGTCTTTT  32386          CATGT
                                GGAGGACCAGGG    GCAGGG
                                ||||||||||||    ||||||
                                TTTTCTGGTTCC    TGTTCT
                                      CC___
GAM380  MTNR1B   3'  CCTCCTGCCTTGGCCTCCT   19895      A      TGTGC
                                GGGAGG CCAGGGCA    AGG
                                |||||| ||||||||    |||
                                TCCTCC GGTTCCGT    TCC
                                   _      CC___
GAM380  MTR      3'  TCCTGTGGTTTCCCTGGTCCCT 4221     A      CATGT
              C                  GGG GGACCAGGG    GCAGGG
                                ||| |||||||||    ||||||
                                CTC CCTGGTCCC    TGTCCT
                                  _       TTTGG
GAM380  MTR      3'  TTCTGGGCATTTTCGTCCTCCC 4223        CA  C   G
                                GGGAGGAC  GGG ATGT CAGGG
                                ||||||||  ||| |||| |||||
                                CCCTCCTG  CTT TACG GTCTT
                                     __  T   G
GAM380  MTR      3'  TTTTGTTTTGTTTTGGTTTTTT 4224             TGT
              T                  GGGAGGACCAGGGCA  GCAGGG
                                ||||||||||||||  ||||||
                                TTTTTTTGGTTTTGT  TGTTTT
                                      TT_
GAM380  MYCN     3'  CTTTGCACATTTTGATTTTTTT 18192       C   GC
                                GGGAGGA CAGG  ATGTGCAGGG
                                |||||||  ||||  ||||||||||
                                TTTTTTT GTTT  TACACGTTTC
                                   A   __
GAM380  MYO1C    3'  CCAATGCTTTGCTTTTCTC   61203       C      GTGCA
                                GGGAGGA CAGGGCAT    GG
                                |||||||  ||||||||    ||
                                CTCTTTT GTTTCGTA    CC
                                   C      A____
GAM380  MYO1E    3'  TTAAAGATGTGCTCTGCTTTTT 17191   GG   C       GCAGGG
              TC                  G  AGGA CAGGGCATGT
                                |  |||| ||||||||||
                                C  TTTT GTCTCGTGTA
                                 TT   C        GAAATTC
GAM380  MYO1F    3'  CCTGGGCCCTGGTCTTCCT   82423           ATGTG
                                GGGAGGACCAGGGC    CAGG
                                ||||||||||||||    ||||
                                TCCTTCTGGTCCCG    GTCC
                                      G____
GAM380  NAPB     3'  CCTTGTGCATTTATTGTTTCTC 70180       C  GGC  TG
              CT                  GGGAGGA CAG   ATG  CAGGG
                                |||||||  |||   |||  |||||
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                                TCCTCTT GTT   TAC  GTTCC
                                    T  ATT  GT
GAM380  NAT2    3'  CTTGTGTATGTATCACCC   3401     AG  CCAGG    TG
                                GGG  GA    GCATG  CAGG
                                |||  ||    |||||  ||||
                                CCC  CT    TGTAT  GTTC
                                  A_  A____    GT
GAM380  NCAM2   3'  CCCTGCATGTGTATGAGTCCT  15800      _ GG
                                AGGAC CA  GCATGTGCAGGG
                                |||||  ||  ||||||||||||
                                TCCTG GT  TGTGTACGTCCC
                                   A  A_
GAM380  NDUFS6  3'  TTCTGTGCGAAGGGTATTCCT  15848      G   AGGGCA  TG
                                GGGAG ACC     TG  CAGGG
                                |||||  |||     ||  |||||
                                TCCTT TGG     GC  GTCTT
                                   A   GAA___  GT
GAM380  NEB     3'  CTCAAGCTGCCTATGGTTTTTC 15810          _    T  GCA
            T                    GGGAGGACCA GGGCA GT   GGG
                                ||||||||||  |||||  ||   |||
                                TCTTTTTGGT TCCGT CG   CTC
                                      A    _  AA_   T
GAM380  NESH    3'  CTGTGAGCTGTGTTCTGTCCTT 33146        C     _  __   GG
            CC                    GGAGGAC AGGGCAT GT  GCAG
                                |||||||  |||||||  ||  ||||
                                CTTCCTG TCTTGTG CG  TGTC
                                    _      T  AG
GAM380  NFIA    3'  TTTTGTTTTTCTAGTCCTTTC  70369   GG    C   CATGT
                                G  AGGAC AGGG    GCAGGG
                                |  |||||  ||||    ||||||
                                C  TCCTG TCTT    TGTTTT
                                 TT    A   TT___
GAM380  NLGN1   3'  TCTGTATTTTGTTCCTTTT   30025       C   GCAT
                                GGGAGGA CAGG   GTGCAGG
                                |||||||  ||||   |||||||
                                TTTTCCT GTTT   TATGTCT
                                    T   _____
GAM380  NLGN1   3'  TTGCTGTTTTGTCTTTCT    30029       C    TGT
                                GGGAGGAC AGGGCA   GCAG
                                |||||||  ||||||   ||||
                                TCTTTCTG TTTTGT   CGTT
                                      _     ___
GAM380  NLGN2   5'  TCTTGGGGTGCTCGGTTTTCTC 88158         A    GTG
                                GGGAGGACC GGGCAT   CAGGG
                                |||||||||  ||||||   |||||
                                CTCTTTTGG CTCGTG   GTTCT
                                      _     GG_
GAM380  NLGN3   3'  TTTTGTTGTTGTTGGTTTTTTT 38604         GG   TGT
                                GGGAGGACCA  GCA   GCAGGG
                                ||||||||||  |||   ||||||
```

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                                TTTTTTTGGT  TGT   TGTTTT
                                      __  TGT
GAM380  NONO     3'  TCTTGATCATTCCGGTTTTTTT 82025         A   C   TG
                                GGGAGGACC GGG ATG  CAGGG
                                ||||||||| ||| |||  |||||
                                TTTTTTTGG CCT TAC  GTTCT
                                      _  _  TA
GAM380  NOS1     3'  CCTTGTCGCTGTGCCCTGGTTT 5248       G        _  _
           CCC                    GGAG ACCAGGGCAT GTG CAGGG
                                |||| |||||||||| ||| |||||
                                CCTT TGGTCCCGTG CGC GTTCC
                                  _        T  T
GAM380  NPAT     3'  CTCTGATCACTCTGTTCTCTT  67235         C    CA  TG
                                GGGAGGAC AGGG  TG  CAGGG
                                |||||||| ||||  ||  |||||
                                TTCTCTTG TCTC  AC  GTCTC
                                      _   __  TA
GAM380  NR1I2    5'  TTGGCAATCCCAGGTTCTCTT  13976         A   CATG   AGGG
                                GGGAGGACC GGG   TGC
                                ||||||||| |||   |||
                                TTCTCTTGG CCC   ACG
                                      A   TA__   GTTT
GAM380  NR3C1    3'  TGAGGACATGTTTTTGTTTTCT 3926         C        GCAGGG
           T                     GGGAGGAC AGGGCATGT
                                |||||||| |||||||||
                                TTCTTTTG TTTTGTACA
                                      T        GGAGT
GAM380  NRAS     3'  GTTTTGTACATGTATGAAATTG 10276      GG_____
           GTTTTCC                  ACCA      GCATGTGCAGGG   T
                                ||||      ||||||||||||  |
                                TGGT      TGTACATGTTTT   G
                                  TAAAGTA
GAM380  NRAS     3'  TGCCCTGGGTTCTTCC      10278          _
                                GGGAGGACC AGGGCA
                                ||||||||| ||||||
                                CCTTCTTGG TCCCGT
                                      G
GAM380  NRG1     5'  TCCTGCATGACAGTTGTTTTCT 25650         CAGGGCAT
           T                     GGGAGGAC       GTGCAGGG
                                ||||||||       ||||||||
                                TTCTTTTG       TACGTCCT
                                      TTGACAG_
GAM380  NRG1     3'  CCTTGTGCTTTCCTTGTGGTTT 15689         __  CAT TG
           TCTT                     GGAGGACCA  GGG   G  CAGGG
                                |||||||||  |||  |  |||||
                                TCTTTTGGT  TCC   C  GTTCC
                                      GT   TTT GT
GAM380  NSF      3'  TGTTTTGGGTTTTCTT      63072          _
                                GGGAGGACC AGGGCA
                                ||||||||| ||||||
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                                TTCTTTTGG TTTTGT
                                     G
GAM380  NSMAF    3'  TTCTGAATCTGTTTTGTCTTCC 13121        C     T  G
             T                    GGGAGGAC AGGGCA GT CAGGG
                                  |||||||| |||||| || |||||
                                  TCCTTCTG TTTTGT TA GTCTT
                                       _     C  A
GAM380  NTRK2    3'  CTCTGTGCCATGGATGATTCTT 20523        C  GGG  _ TG
             TT                    GGGAGGA CA   CAT G  CAGGG
                                  ||||||| ||   ||| |  |||||
                                  TTTTCTT GT   GTA C  GTCTC
                                     A  AG_   C GT
GAM380  NUMB     3'  CTTTGTGTGTGTCCTCTTCCCC 13622     A   CC       TG
             C                    GGG GGA  AGGGCATG  CAGGG
                                  ||| |||  ||||||||  |||||
                                  CCC CCT  TCCTGTGT  GTTTC
                                   _  TC       GT
GAM380  NUP62    3'  GCTGTGTGCTTTGCGTTTTTCC 33329         _      GT   GG
                                  GGGAGGAC CAGGGCAT  GCAG
                                  |||||||| ||||||||  ||||
                                  CCTTTTTG GTTTCGTG  TGTC
                                       C       __   GC
GAM380  NXF5     3'  CTTTGATGTCATCTTTGTCTTC 51967        C   C  TG__
             CT                    GGGAGGAC AGGG ATG    CAGGG
                                  |||||||| |||| |||    |||||
                                  TCCTTCTG TTTC TAC    GTTTC
                                       _   _  TGTA
GAM380  NXF5     3'  CTTTGATGTCATCTTTGTCTTC 52510        C   C  TG__
             CT                    GGGAGGAC AGGG ATG    CAGGG
                                  |||||||| |||| |||    |||||
                                  TCCTTCTG TTTC TAC    GTTTC
                                       _   _  TGTA
GAM380  NXF5     3'  CTTTGATGTCATCTTTGTCTTC 52515        C   C  TG__
             CT                    GGGAGGAC AGGG ATG    CAGGG
                                  |||||||| |||| |||    |||||
                                  TCCTTCTG TTTC TAC    GTTTC
                                       _   _  TGTA
GAM380  NXF5     3'  CTTTGATGTCATCTTTGTCTTC 52519        C   C  TG__
             CT                    GGGAGGAC AGGG ATG    CAGGG
                                  |||||||| |||| |||    |||||
                                  TCCTTCTG TTTC TAC    GTTTC
                                       _   _  TGTA
GAM380  NXF5     3'  CTTTGATGTCATCTTTGTCTTC 52523        C   C  TG__
             CT                    GGGAGGAC AGGG ATG    CAGGG
                                  |||||||| |||| |||    |||||
                                  TCCTTCTG TTTC TAC    GTTTC
                                       _   _  TGTA
GAM380  OSM      3'  TCTGTGGACCTGTTTTCTC   40077        C  GCATGT
                                  GGGAGGAC AGG     GCAGG
                                  |||||||| |||     |||||
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                                CTCTTTTG TCC     TGTCT
                                    _  AGG___
GAM380  OSR1    3'  TTTGTGAAATGTTTGGTCTTTC 17572          G  GT_   G
          T                      GGGAGGACCAGG CAT  GCAGG
                                 |||||||||||| |||  |||||
                                 TCTTTCTGGTTT GTA  TGTTT
                                       _  AAG
GAM380  OTOR    3'  TCCTGCTGGCCTGGTCTGCCC  39347    A      G  TGT
                                 GGG GGACCAGG CA  GCAGGG
                                 ||| |||||||| ||  ||||||
                                 CCC TCTGGTCC GT  CGTCCT
                                   G      G ___
GAM380  OTP     3'  CTCTGTGCCCTTGGTTGTTTT  49497     G      CAT TG
                                 GGGA GACCAGGG  G  CAGGG
                                 |||| ||||||||  |  |||||
                                 TTTT TTGGTTCC  C  GTCTC
                                   G       ___ GT
GAM380  OVOL1   3'  TTCTGGAGGGCTCTGTCCTTCC 15861        C    ATGTG
                                 GGGAGGAC AGGGC    CAGGG
                                 |||||||| |||||    |||||
                                 CCTTCCTG TCTCG    GTCTT
                                     _    GGAG_
GAM380  PACE4   3'  TTCTGTGTGACCATGTTTTCCC 56352        CAG  _  GT
                                 GGGAGGAC  GG CAT  GCAGGG
                                 ||||||||  || |||  ||||||
                                 CCCTTTTG  CC GTG  TGTCTT
                                     TA_  A  __
GAM380  PAFAH1B2 3'  TCCTGTACATAGAAGGTTT   10406      AGGGC
                                 GGACC    ATGTGCAGGG
                                 |||||    ||||||||||
                                 TTTGG    TACATGTCCT
                                   AAGA_
GAM380  PAG     3'  TTTTGCAATCAGCCTGGTCTCT 37406     _     GCATG
          CC                     GGAG GACCAGG    TGCAGGG
                                 |||| |||||||    |||||||
                                 CCTC CTGGTCC    ACGTTTT
                                   T      GACTA
GAM380  PARK2   3'  CTCTGCATACCAGGGGTTCCCC 15863    A    AG_  CA
                                 GGG GGACC  GG  TGTGCAGGG
                                 ||| |||||  ||  |||||||||
                                 CCC CTTGG  CC  ATACGTCTC
                                   _    GGA  __
GAM380  PARK2   3'  CTCTGCATACCAGGGGTTCCCC 25669    A    AG_  CA
                                 GGG GGACC  GG  TGTGCAGGG
                                 ||| |||||  ||  |||||||||
                                 CCC CTTGG  CC  ATACGTCTC
                                   _    GGA  __
GAM380  PARK2   3'  CTCTGCATACCAGGGGTTCCCC 25672    A    AG_  CA
                                 GGG GGACC  GG  TGTGCAGGG
                                 ||| |||||  ||  |||||||||
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                                CCC CTTGG   CC  ATACGTCTC
                                  _    GGA  __
GAM380  PARN     3'  TTTTGTGGCTGTGGTTTTTTC  10427   GG      G   ATG
                                G  AGGACCA GGC   TGCAGGG
                                |  ||||||| |||   |||||||
                                C  TTTTGGT TCG   GTGTTTT
                                 TT      G  ___
GAM380  PAX5     3'  CTTTGGGGAGATGTCCTGGTTT 33635      G        GTG__
             CCT                   GGAG ACCAGGGCAT     CAGGG
                                |||| ||||||||||     |||||
                                CCTT TGGTCCTGTA     GTTTC
                                  _        GAGGG
GAM380  PCDH11X  3'  TTCTGTATTGCATGTTTTCTT  52032        CAGG   T
                                GGGAGGAC    GCA GTGCAGGG
                                ||||||||    ||| ||||||||
                                TTCTTTTG    CGT TATGTCTT
                                     TA__   _
GAM380  PCDH11X  3'  TTCTGTATTGCATGTTTTCTT  52054        CAGG   T
                                GGGAGGAC    GCA GTGCAGGG
                                ||||||||    ||| ||||||||
                                TTCTTTTG    CGT TATGTCTT
                                     TA__   _
GAM380  PCDH11Y  3'  TTCTGTATTGCATGTTTTCTT  52088        CAGG   T
                                GGGAGGAC    GCA GTGCAGGG
                                ||||||||    ||| ||||||||
                                TTCTTTTG    CGT TATGTCTT
                                     TA__   _
GAM380  PCDH7    3'  TTCTGTAAAGTTTTGTCTTCTC 50600         C     ATG
                                GGGAGGAC AGGGC   TGCAGGG
                                |||||||| |||||   |||||||
                                CTCTTCTG TTTTG   ATGTCTT
                                     _    AA_
GAM380  PCDHA2   3'  TTTTGTTGTTGTTTTGGTTTTT 48986             TGT
                                GAGGACCAGGGCA   GCAGGG
                                ||||||||||||   ||||||
                                TTTTTGGTTTTGT   TGTTTT
                                       TGT
GAM380  PCDHB4   3'  ATATGTGTATATTTTTTGGTTT 38435             C      GGG
             TCCT                   GGGAGGACCAGGG ATGTGCA
                                |||||||||||| |||||||
                                TCCTTTTGGTTTT TATATGT
                                       T      GTATAA
GAM380  PCSK1    3'  TCGTGCTGCATGCCTGGTCTTT 4775            G    _  G
             CC                    GGGAGGACCAGG CATGT GCA GG
                                |||||||||||| ||||| ||| ||
                                CCTTTCTGGTCC GTACG CGT CT
                                       _    T  G  C
GAM380  PCTK1    3'  CCTGCGTGTGGCCCTCCC    20577       ACCAG G  TG
                                GGGAGG    G CA  TGCAGG
                                ||||||    | ||  ||||||
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                                CCCTCC    C GT  GCGTCC
                                   _____ G  GT
GAM380  PCTK1    3'  CCTGCGTGTGGCCCTCCC    52261       ACCAG G  TG
                                GGGAGG    G CA  TGCAGG
                                ||||||    | ||  ||||||
                                CCCTCC    C GT  GCGTCC
                                   _____ G  GT
GAM380  PCTK1    3'  CCTGCGTGTGGCCCTCCC    52266       ACCAG G  TG
                                GGGAGG    G CA  TGCAGG
                                ||||||    | ||  ||||||
                                CCCTCC    C GT  GCGTCC
                                   _____ G  GT
GAM380  PDE4C    3'  TCTTACGATGCCCTGGTGTCTT 6237    GG  _       _  C   G
              TC                   G  AGG ACCAGGGCAT GTG AGG
                                |  ||| |||||||||| ||| |||
                                C  TCT TGGTCCCGTA CAT TCT
                                 TT   G        G  _
GAM380  PDGFB    5'  CCTGCGCCCAGGTCCTCCC    10497         A    ATGT
                                GGGAGGACC GGGC    GCAGG
                                ||||||||| ||||    |||||
                                CCCTCCTGG CCCG    CGTCC
                                     A   ____
GAM380  PDGFB    3'  CTCTGTGCACAGTGGCTTCTT  10498       A   GGGCA  TG
                                GGGAGG CCA    TG  CAGGG
                                |||||| |||    ||  |||||
                                TTCTTC GGT    AC  GTCTC
                                   _   GAC__  GT
GAM380  PDLIM1   3'  CTCTGCTTACTTTGGTTTTCCC 40634           CATGT
                                GGGAGGACCAGGG    GCAGGG
                                ||||||||||||    ||||||
                                CCCTTTTGGTTTC    CGTCTC
                                      ATT__
GAM380  PELO     5'  CTTTGGTTCCTTTGGTTCTGTC 31955    G        CATGTG
                                GG AGGACCAGGG     CAGGG
                                || ||||||||||     |||||
                                CT TCTTGGTTTC     GTTTC
                                 G        CTTG__
GAM380  PHLDA3   3'  TCCTGCTGCTTAGGTCCTTTT  24767         AG   TGT
                                GGGAGGACC  GGCA   GCAGGG
                                |||||||||  ||||   ||||||
                                TTTTCCTGG  TCGT   CGTCCT
                                     AT   ___
GAM380  PIGR     3'  CTCTAACACCTGCCTAGGTTTT 72600         A    T   C_
              TCC                   GGGAGGACC GGGCA GTG  AGGG
                                |||||||||  |||||  |||  ||||
                                CCTTTTTGG TCCGT CAC  TCTC
                                     A    C   AA
GAM380  PIK3C2B  3'  TCTGCCTGCCTTGGCCTCCC   10579       A       TGT
                                GGGAGG CCAGGGCA   GCAGG
                                ||||||  ||||||||   |||||
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                                CCCTCC GGTTCCGT   CGTCT
                                   _       C__
GAM380  PITPNB   3'  CCCTGCCTGCTCCTCGTTTTCC 24779        C   _   TGT
           C                     GGGAGGAC AGG GCA   GCAGGG
                                 |||||||| ||| |||   ||||||
                                 CCCTTTTG TCC CGT   CGTCCC
                                     C   T   C__
GAM380  PK428    5'  TGCAGCAACATTTTTGGTTTTC 13213           C   _  AGGG
           CC                      GGGAGGACCAGGG ATGT GC
                                 |||||||||||| |||| ||
                                 CCCTTTTGGTTTT TACA CG
                                        _   A  ACGTT
GAM380  PKIA     5'  TTCTGAGAAGCCCTGGTTTCCC 22388     AG       ATGTG
           C                     GGG  GACCAGGGC    CAGGG
                                 |||  |||||||||    |||||
                                 CCC  TTGGTCCCG    GTCTT
                                   CT       AAGA_
GAM380  PLA2G2D  3'  CTCTGTTTCCCCTGTTTTCCC  24793        C   CATGT
                                 GGGAGGAC AGGG    GCAGGG
                                 |||||||| ||||    ||||||
                                 CCCTTTTG TCCC    TGTCTC
                                     _   CTT__
GAM380  PLP2     3'  CCATATGTGTGTGCCTAGGTCC 10651        A     TG ___ G
           TCCT                    GAGGACC GGGCATG  CA   GG
                                 ||||||| |||||||  ||   ||
                                 CTCCTGG TCCGTGT  GT   CC
                                     A      GT  ATA
GAM380  PML      3'  CTCTAGGTGGCCCTGGTCTTGC 52656    G        ATGTGC
           C                     GG AGGACCAGGGC     AGGG
                                 || ||||||||||     ||||
                                 CC TTCTGGTCCCG     TCTC
                                  G         GTGGA_
GAM380  PMX1     3'  TTCTGTGTGTGTTTATTTTGTT 22599      CA___     TG
           TTTCT                   AGGAC    GGGCATG  CAGGG
                                 |||||    |||||||  |||||
                                 TTTTG    TTTGTGT  GTCTT
                                    TTTTA      GT
GAM380  PMX1     3'  TTCTGTGTGTGTTTATTTTGTT 42666      CA___     TG
           TTTCT                   AGGAC    GGGCATG  CAGGG
                                 |||||    |||||||  |||||
                                 TTTTG    TTTGTGT  GTCTT
                                    TTTTA      GT
GAM380  PNUTL2   5'  TTCTGTGTGTGAGGAACTTTGC 54423    __  GA  AGGG   TG
           C                     GG  GAG  CC   CATG  CAGGG
                                 ||  |||  ||   ||||  |||||
                                 CC  TTC  GG   GTGT  GTCTT
                                  GT   AA  A___    GT
GAM380  PNUTL2   5'  TTCTGTGTGTGAGGAACTTTGC 15898    __  GA  AGGG   TG
           C                     GG  GAG  CC   CATG  CAGGG
                                 ||  |||  ||   ||||  |||||
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                              CC  TTC  GG   GTGT  GTCTT
                               GT   AA  A___   GT
GAM380  POU2F2   3'  CTCTGGTCCCTGCCTTGGTCCC 10689     A        TGTG_
           TT                   GGG GGACCAGGGCA    CAGGG
                              ||| ||||||||||    |||||
                              TTC CCTGGTTCCGT    GTCTC
                               _         CCCTG
GAM380  PPIG     5'  CCTTGTTTTTTTTTGGTCTTTT 16576   GG       CATGT
           C                    G  AGGACCAGGG    GCAGGG
                              |  ||||||||||    ||||||
                              C  TTCTGGTTTT    TGTTCC
                               TT        TTTT_
GAM380  PPIL1    3'  CTTGTGCATGTCTGCTCT    32142     GACCA     TG
                              GGAG    GGGCATG  CAGG
                              ||||    |||||||  ||||
                              TCTC    TCTGTAC  GTTC
                                G____      GT
GAM380  PPP1CB   3'  CCTTCACCTGCATTGGTTTTCT 10712          G   T   C   G
           T                    GGGAGGACCAG GCA GTG AGG
                              |||||||||||| ||| ||| |||
                              TTCTTTTGGTT CGT CAC TCC
                                    A   C   T
GAM380  PPP1R12B 3'  CTCTGCACTTTCAATGCCCTGT 49468    C      _____
           TCTTCC                GA CAGGGCAT    GTGCAGGG
                              || ||||||||    ||||||||
                              CT GTCCCGTA    CACGTCTC
                               T       ACTTT
GAM380  PPP1R12B 3'  CTCTGCACTTTCAATGCCCTGT 49479    C      _____
           TCTTCC                GA CAGGGCAT    GTGCAGGG
                              || ||||||||    ||||||||
                              CT GTCCCGTA    CACGTCTC
                               T       ACTTT
GAM380  PPP1R2   3'  CCCTCTGATTTTGGTTTTCTT  20688          _ TGTGC
                              GGGAGGACCAGGG CA    AGGG
                              |||||||||||| ||    ||||
                              TTCTTTTGGTTTT GT    TCCC
                                    A  C____
GAM380  PPP1R3D  3'  GTTTTGCATGTGTCCTGAATGT 20705   _ ___
           GTCTCT                G AC   CAGGGCATGTGCAGGG   T
                              | ||   ||||||||||||||||  |
                              T TG   GTCCTGTGTACGTTTT   G
                               G  TAA
GAM380  PPP2R5C  3'  CCTTGTGCAGCTCTGGTACCTC 10757       _      A  TG
           CT                    GGGAGG ACCAGGGC TG  CAGGG
                              |||||| |||||||| ||  |||||
                              TCCTCC TGGTCTCG AC  GTTCC
                                 A       _  GT
GAM380  PPP3CB   3'  TTCTGTAACATAGTCTTGGTAT 40901      G      _   _
           TTTT                  GGAG ACCAGGGC ATGT GCAGGG
                              |||| |||||||| |||| ||||||
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                                TTTT TGGTTCTG TACA TGTCTT
                                  A       A   A
GAM380  PPP3CB   3'  TTTTGTGTATGCATGTTTTC  40903       CAGG    TG
                                GAGGAC   GCATG  CAGGG
                                ||||||   |||||  |||||
                                CTTTTG   CGTAT  GTTTT
                                   TA__    GT
GAM380  PRKAB1   3'  TTCATACCTGCCCTGGTCCTGC 20740    G         T  CAGGG
           T                     GG AGGACCAGGGCA GTG
                                 || ||||||||||| |||
                                 TC TCCTGGTCCCGT CAT
                                  G         C  ACTT
GAM380  PRKAR2B  3'  TTCTGTGATTTCAGGTTTTTTC 10806   GG    A  CATG
                                G  AGGACC GGG   TGCAGGG
                                |  |||||| |||   |||||||
                                C  TTTTGG CTT   GTGTCTT
                                 TT    A  TA__
GAM380  PRPF31   3'  TCTTCATCATGCCTTGTCTTTT 31572        C      _  C
           T                     GGGAGGAC AGGGCATG TG AGGG
                                 |||||||| |||||||| || ||||
                                 TTTTTCTG TTCCGTAC AC TTCT
                                      _       T  _
GAM380  PRSS16   3'  CCCTGTCACTATTTGTCTTTCT 19628        C  GCAT  _
                                GGGAGGAC AGG   GTG CAGGG
                                |||||||| |||   ||| |||||
                                TCTTTCTG TTT   CAC GTCCC
                                   _  AT__  T
GAM380  PSMD9    3'  CCTCCTGCCTTGGCCTCCT   10983      A      TGTGC
                                GGGAGG CCAGGGCA    AGG
                                ||||||| ||||||||    |||
                                TCCTCC GGTTCCGT    TCC
                                   _       CC___
GAM380  PTGES    3'  CCTGAGTCCTGGTTTCCT    16858      G      ATGTG
                                GGGAG ACCAGGGC    CAGG
                                ||||| ||||||||    ||||
                                TCCTT TGGTCCTG    GTCC
                                   _       A____
GAM380  PTGFRN   3'  CCCTGCACAGCACTGGCCTTTC 67187   GG  A   G  A
                                G  AGG CCAG GC TGTGCAGGG
                                |  ||| |||| || |||||||||
                                C  TCC GGTC CG ACACGTCCC
                                 TT  _   A  _
GAM380  PTGS1    3'  CCTCTGCTCTGTCCTCCC    54570       C    TGTGC
                                GGGAGGAC AGGGCA    AGG
                                |||||||| ||||||    |||
                                CCCTCCTG TCTCGT    TCC
                                   _     C____
GAM380  PTGS1    3'  CCTCTGCTCTGTCCTCCC    6351        C    TGTGC
                                GGGAGGAC AGGGCA    AGG
                                |||||||| ||||||    |||
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                                CCCTCCTG TCTCGT    TCC
                                   _    C____
GAM380  PTPN23   3'  TTTTGCCTACCTGGTCCTT   63730        GCATGT
                                GAGGACCAGG    GCAGGG
                                ||||||||||    ||||||
                                TTCCTGGTCC    CGTTTT
                                    ATC___
GAM380  PTPN7    3'  CCCAGGTGTCCTGGTGTTCTC  54547     G       G  CA
                                GGGAG ACCAGGGCAT TG  GG
                                ||||| |||||||||| ||  ||
                                CTCTT TGGTCCTGTG AC  CC
                                   G       G __
GAM380  PTPN7    3'  CCCAGGTGTCCTGGTGTTCTC  54558     G       G  CA
                                GGGAG ACCAGGGCAT TG  GG
                                ||||| |||||||||| ||  ||
                                CTCTT TGGTCCTGTG AC  CC
                                   G       G __
GAM380  PTPN7    3'  CCCAGGTGTCCTGGTGTTCTC  11065     G       G  CA
                                GGGAG ACCAGGGCAT TG  GG
                                ||||| |||||||||| ||  ||
                                CTCTT TGGTCCTGTG AC  CC
                                   G       G __
GAM380  PXN      3'  CTCTGACGTCTCTTTGGTCTTG 11160   G       C_   G
           TT                    GG AGGACCAGGG  ATGT CAGGG
                                || ||||||||||  ||||| |||||
                                TT TTCTGGTTTC  TGCA GTCTC
                                 G       TC   _
GAM380  RAB13    3'  TTCTGTCACTTGTCATGGTCTT 11204        G   T  _
           TCT                     GGGAGGACCA GGCA GTG CAGGG
                                |||||||||| ||||| ||| |||||
                                TCTTTCTGGT CTGT CAC GTCTT
                                     A   T   T
GAM380  RAB26    3'  CCTTGCACTCAACTTGGCCTTT 26823      A    GCAT
           T                     GGGAGG CCAGG    GTGCAGGG
                                ||||||| |||||    ||||||||
                                TTTTCC GGTTC    CACGTTCC
                                   _    AACT
GAM380  RAB30    3'  TCTGGGGGCCCTGGTTTTCTT  27168          ATGTG
                                GGGAGGACCAGGGC    CAGG
                                ||||||||||||||    ||||
                                TTCTTTTGGTCCCG    GTCT
                                      GGG__
GAM380  RAB38    3'  CTTTCACCTTGCCCTGGTGTCT 60288      _      T_  C  G
           TTT                     GGAGG ACCAGGGCA  GTG AGG
                                ||||| |||||||||  ||| |||
                                TTTCT TGGTCCCGT  CAC TTC
                                   G       TC  T
GAM380  RABL2A   3'  TTTTGTTTTTGTTTTTGTTTTC 25508       C     TGT
           TT                     GGGAGGAC AGGGCA   GCAGGG
                                |||||||| ||||||   ||||||
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                                TTCTTTTG TTTTGT   TGTTTT
                                    T     TTT
GAM380  RABL2B   3'  TTTTGTTTTTGTTTTTGTTTTC 23009        C     TGT
           TT                    GGGAGGAC AGGGCA   GCAGGG
                                 |||||||| ||||||   ||||||
                                 TTCTTTTG TTTTGT   TGTTTT
                                    T     TTT
GAM380  RAD21    3'  TTTTGTTAGTCTGGTTTTT   20764          G ATGT
                                 GAGGACCAGG C    GCAGGG
                                 |||||||||| |    ||||||
                                 TTTTTGGTCT G    TGTTTT
                                      _ AT__
GAM380  RDX      3'  CATGCTTGGTTTTCTT      11278           G
                                 GGGAGGACCAGG CATG
                                 |||||||||||| ||||
                                 TTCTTTTGGTTC GTAC
                                      _
GAM380  RDX      3'  TTTTGCATATATGTTCTTC    11282        CAGGGC
                                 GGAGGAC     ATGTGCAGGG
                                 |||||||     ||||||||||
                                 CTTCTTG     TATACGTTTT
                                    TA____
GAM380  RERE     3'  CTCTGTGTGTGTCCGTATCTTG 23965    G    CCA      TG
           TT                    GG AGGA   GGGCATG  CAGGG
                                 || ||||   |||||||  |||||
                                 TT TTCT   CCTGTGT  GTCTC
                                  G    ATG      GT
GAM380  RFC1     3'  CTCTGTGTGTGTTGACCACGTC 11301      CA ___    TG
           T                     GGAC  GG   GCATG  CAGGG
                                 ||||  ||   |||||  |||||
                                 TCTG  CC   TGTGT  GTCTC
                                   CA  AGT    GT
GAM380  RGL      3'  TCCAATTTCCTTTGGTCTTTCC 30738            CATGTGCA
                                 GGGAGGACCAGGG       GGG
                                 ||||||||||||        |||
                                 CCTTTCTGGTTTC       CCT
                                       CTTTAA__
GAM380  RNF26    3'  CCCTGTCTGCTTCTGGTTTTTC 49310           _   TGT
           T                     GGGAGGACCAGG GCA   GCAGGG
                                 |||||||||||| |||   ||||||
                                 TCTTTTTGGTCT CGT   TGTCCC
                                       T   C__
GAM380  RNF4     3'  CCCACCTGTCTTGGCTTTCT   11356       A       T   CA
                                 GGGAGG CCAGGGCA GTG  GG
                                 |||||| |||||||| |||  ||
                                 TCTTTC GGTTCTGT CAC  CC
                                    _       C   __
GAM380  RNMT     3'  CCTTGTGCATTTGGGTTATCTC 13718      G    AGGGC   TG
                                 GGGA GACC    ATG  CAGGG
                                 |||| ||||    |||  |||||
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                                CTCT TTGG    TAC  GTTCC
                                  A   GTT__   GT
GAM380  RP2     3'  CTCTGCATATGATATTCTT   22618      CCAGGG
                                GAGGA     CATGTGCAGGG
                                |||||     ||||||||||
                                TTCTT     GTATACGTCTC
                                  ATA___
GAM380  RP2     3'  TTTTGTGTATTAGCAATGGTTT 22623        GG __   TG
            TT                   GAGGACCA  GC  ATG  CAGGG
                                |||||||  ||  |||  |||||
                                TTTTTGGT  CG  TAT  GTTTT
                                    AA  AT   GT
GAM380  RPLP1   5'  GTGCTCGGTCCTTCC      6401          A
                                GGGAGGACC GGGCAT
                                |||||||| ||||||
                                CCTTCCTGG CTCGTG
                                    _
GAM380  RPS6KA1  3'  CCTGAGCCTTAGTTTTCCC   59316        C    ATGTG
                                GGGAGGAC AGGGC    CAGG
                                |||||||| |||||    ||||
                                CCCTTTTG TTCCG    GTCC
                                    A    A____
GAM380  SCML1   3'  TGATTCTGGTTCATCT     22168    _       _
                                GGA GGACCAGGG CA
                                ||| ||||||||| ||
                                TCT CTTGGTCTT GT
                                  A       A
GAM380  SCNN1A   3'  CTCTGAACACTCTGGTTTCCCC 6424     AG      CA   G
                                GGG  GACCAGGG  TGT CAGGG
                                |||  ||||||||  ||| |||||
                                CCC  TTGGTCTC  ACA GTCTC
                                  CT       __   A
GAM380  SCNN1A   3'  TCTTGTACATTTGTGTCTCCC  6426       AC   GGC
                                GGGAGG  CAG   ATGTGCAGGG
                                ||||||  |||   ||||||||||
                                CCCTCT  GTT   TACATGTTCT
                                   GT  ____
GAM380  SCNN1A   3'  TTCTGCCACATCTTGTCTTCCC 6428        C    CA  T
                                GGGAGGAC AGGG  TG GCAGGG
                                |||||||| ||||  || ||||||
                                CCCTTCTG TTCT  AC CGTCTT
                                    _   AC  _
GAM380  SERPINB13 3'  TACATTTTTCTGGTTTTTTT  24772          C_
                                GGGAGGACCAGGG  ATGTG
                                ||||||||||||  |||||
                                TTTTTTTGGTCTT  TACAT
                                       TT
GAM380  SERPINB9  3'  TGTGTCTGGCTTCTT      14771       A    G
                                GGGAGG CCAGG CATG
                                |||||| ||||| ||||
```

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                                TTCTTC GGTCT GTGT
                                    _   _
GAM380  SET7    3'  GTCTTGCAATAGAATGGCTTTG 47638        ATG_____
            GTTTTTTT                ACCAGGGC      TGCAGGG  T
                                |||||||       |||||||  |
                                TGGTTTCG      ACGTTCT  G
                                    GTAAGATA
GAM380  SH3GL3  3'  TCCTGATGACGTCTGGTCTTTT 11637   GG       G ATGTG
            C                    G  AGGACCAGG C    CAGGG
                                |  |||||||||  |    |||||
                                C  TTCTGGTCT G    GTCCT
                                 TT       _ CAGTA
GAM380  SH3GL3  3'  TTTTGTATGTGTGCTCTCTTT  11639      CC  G
                                GAGGA  AG GCATGTGCAGGG
                                |||||  ||  ||||||||||||
                                TTTCT  TC TGTGTATGTTTT
                                   C_  G
GAM380  SHANK2  3'  CCCTGGGACTCTGGTCTGCCC  55734    A       CATGTG
                                GGG GGACCAGGG     CAGGG
                                |||  |||||||||     |||||
                                CCC TCTGGTCTC     GTCCC
                                  G       AGG___
GAM380  SHANK2  3'  TCTGAGCCCTGGGCCTCTC   55738      A     ATGTG
                                GGGAGG CCAGGGC    CAGG
                                ||||||  |||||||    ||||
                                CTCTCC GGTCCCG    GTCT
                                   G      A_____
GAM380  SHMT2   3'  CTCTGTCATTCTGCTGGTTTTC 18265          _  C   T
            TC                    GGGAGGACCAG GG ATG GCAGGG
                                ||||||||||  ||  |||  ||||||
                                CTCTTTTGGTC TC TAC TGTCTC
                                      G  T   _
GAM380  SHMT2   3'  CTTTGCACAGAGGGGCCTCTC  18266       A  AGGGCA
                                GGGAGG CC     TGTGCAGGG
                                ||||||  ||    |||||||||
                                CTCTCC GG     ACACGTTTC
                                   _  GGAG__
GAM380  SIAH1   3'  TTCTGTAATTCAGGTTTTTCC  11660         AG  CATG
                                GGGAGGACC  GG    TGCAGGG
                                |||||||||  ||    |||||||
                                CCTTTTTGG  CT    ATGTCTT
                                     A_  TA__
GAM380  SIAT7D  3'  CCTTGTGCCAGTCCTGGTCCTC 26949            AT TG
            CC                    GGGAGGACCAGGGC  G  CAGGG
                                ||||||||||||||  |  |||||
                                CCCTCCTGGTCCTG  C  GTTCC
                                       AC GT
GAM380  SIGLEC6 3'  CCTTGTGTCTTCACATGGTCTT 59927          GGGCAT_ TG
            TCC                   GGGAGGACCA      G  CAGGG
                                ||||||||||      |  |||||
```

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                                CCTTTCTGGT      T  GTTCC
                                      ACACTTC GT
GAM380  SIP1     3'  TCTTGGTGCTGTTTTGTTCTTT 13234       C      T TG _
             T                    GGAGGA CAGGGCA G  C AGGG
                                  |||||| ||||||| |  | ||||
                                  TTTTCT GTTTTGT C  G TTCT
                                     T      _ GT G
GAM380  SIX2     3'  TCTGCTTTCTGTCTTTCT    33725        C    CATGT
                                  GGGAGGAC AGGG     GCAGG
                                  |||||||| ||||     |||||
                                  TCTTTCTG TCTT     CGTCT
                                       _    T_____
GAM380  SIX2     3'  TCTTGTACTCTGTGTCCTGGTC 33726   A         ___
             CCTCC                    GGACCAGGGCAT   GTGCAGGG
                                   ||||||||||||   ||||||||
                                   CCTGGTCCTGTG   CATGTTCT
                                  C          TCT
GAM380  SIX3     5'  TCTGTCTCGGGTTCTCTC     18279         A   CATGT
                                  GGGAGGACC GGG     GCAGG
                                  |||||||| |||     |||||
                                  CTCTCTTGG CTC     TGTCT
                                       G  ______
GAM380  SLC14A1  3'  CCTTGTGTGTGTGACATTCTCT 31838        CCAGG     TG
             C                    GGGAGGA     GCATG  CAGGG
                                  |||||||     |||||  |||||
                                  CTCTCTT     TGTGT  GTTCC
                                      ACAG_     GT
GAM380  SLC21A2  3'  CCCTGCAACTAACCCTGGTCTT 18856           CATG_
             TCC                    GGGAGGACCAGGG     TGCAGGG
                                  ||||||||||||||     |||||||
                                  CCTTTCTGGTCCC     ACGTCCC
                                         AATCA
GAM380  SLC25A15 3'  TGCTTTTTGTCTTCCC      26514         C_
                                  GGGAGGAC  AGGGCA
                                  ||||||||  ||||||
                                  CCCTTCTG  TTTCGT
                                       TT
GAM380  SLC29A1  3'  CCCTGCGCCTCCTCCTCTGTGT 17073      _     CAT___
             TTTTTC                  GGAC CAGGG      GTGCAGGG
                                  |||| |||||      ||||||||
                                  TTTG GTCTC      CGCGTCCC
                                    T    CTCCTC
GAM380  SLC2A4   5'  CCCTGCGCGTCCAGCTCTTCT  6441        CCAG  C
                                  GGAGGA    GG ATGTGCAGGG
                                  ||||||    || ||||||||||
                                  TCTTCT    CC TGCGCGTCCC
                                     CGA_  _
GAM380  SLC35A1  3'  TTCTGTACTAACTGTTCTCTT  21179         C  GGCAT
                                  GGGAGGAC AG     GTGCAGGG
                                  |||||||| ||     ||||||||
```

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                                TTCTCTTG TC    CATGTCTT
                                    _ AAT__
GAM380  SLC4A1AP  3'  TCTGTGTTCTTGGCTTCCT   36363      A    CAT TG
                                GGGAGG CCAGGG  G  CAGG
                                |||||| ||||||  |  ||||
                                TCCTTC GGTTCT  T  GTCT
                                   _    ___ GT
GAM380  SLC7A6   3'  CTTTGTGCATGCCTAGG    14306    A     TG
                                CC GGGCATG  CAGGG
                                || |||||||  |||||
                                GG TCCGTAC  GTTTC
                                 A      GT
GAM380  SLC8A2   3'  CTTGGACCCTGGTCTCCT    66331      G     CATG G
                                GGGAG ACCAGGG   T CAGG
                                ||||| |||||||   | ||||
                                TCCTC TGGTCCC   A GTTC
                                   _     _____ G
GAM380  SMARCC1  3'  GTGTGCCCTGGTCATCCT    11802     G       TG
                                GGGA GACCAGGGCA  T
                                |||| ||||||||||  |
                                TCCT CTGGTCCCGT  G
                                  A        GT
GAM380  SMCY     5'  CTGTGACTGTTTTCCT      16208        C  GG ATGT
                                GGGAGGAC AG  C   GCAG
                                |||||||| ||  |   ||||
                                TCCTTTTG TC  G   TGTC
                                    _  A_ _____
GAM380  SMP1     3'  CCCTGCATGGGTTTGTTTGTTT 26698       CA__   AT
            TTTT                  GGAGGAC   GGGC  GTGCAGGG
                                |||||||   ||||  ||||||||
                                TTTTTTG   TTTG  TACGTCCC
                                   TTTG   GG
GAM380  SNAP25   3'  TGTGTCTTTTGTTCTCTC    55528       C_
                                GGGAGGAC  AGGGCATG
                                ||||||||  ||||||||
                                CTCTCTTG  TTCTGTGT
                                     TT
GAM380  SNAP25   3'  TTTTGTTCTCTCTTGGTCTCTT 55529     _      CATGT
            T                   GGAG GACCAGGG    GCAGGG
                                |||| ||||||||    ||||||
                                TTTC CTGGTTCT    TGTTTT
                                  T      CTCT_
GAM380  SNAP25   3'  TGTGTCTTTTGTTCTCTC    11835       C_
                                GGGAGGAC  AGGGCATG
                                ||||||||  ||||||||
                                CTCTCTTG  TTCTGTGT
                                     TT
GAM380  SNAP25   3'  TTTTGTTCTCTCTTGGTCTCTT 11836     _      CATGT
            T                   GGAG GACCAGGG    GCAGGG
                                |||| ||||||||    ||||||
```

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                                TTTC CTGGTTCT    TGTTTT
                                  T      CTCT_
GAM380  SNL     3'  CTCTGGGTGTCTTGGTCTTTT  11852           GTG
                                GGAGGACCAGGGCAT   CAGGG
                                |||||||||||||||   |||||
                                TTTTCTGGTTCTGTG   GTCTC
                                        G__
GAM380  SNRPN   5'  TTTTGCATAAGAAAGGCTTTTC 42996   GG   A  AGGGCA
                                G  AGG CC     TGTGCAGGG
                                |  ||| ||     |||||||||
                                C  TTC GG     ATACGTTTT
                                 TT   _  AAAGA_
GAM380  SNRPN   5'  TTTTGCATAAGAAAGGCTTTTC 43003   GG   A  AGGGCA
                                G  AGG CC     TGTGCAGGG
                                |  ||| ||     |||||||||
                                C  TTC GG     ATACGTTTT
                                 TT   _  AAAGA_
GAM380  SNRPN   5'  TTTTGCATAAGAAAGGCTTTTC 43011   GG   A  AGGGCA
                                G  AGG CC     TGTGCAGGG
                                |  ||| ||     |||||||||
                                C  TTC GG     ATACGTTTT
                                 TT   _  AAAGA_
GAM380  SNRPN   5'  TTTTGCATAAGAAAGGCTTTTC 43018   GG   A  AGGGCA
                                G  AGG CC     TGTGCAGGG
                                |  ||| ||     |||||||||
                                C  TTC GG     ATACGTTTT
                                 TT   _  AAAGA_
GAM380  SORD    5'  CCCTGCGTGCGGCGCTTCTCCC 11870       ACC  G  ATG_
                                GGGAGG   AG GC    TGCAGGG
                                ||||||   || ||    |||||||
                                CCCTCT   TC CG    GCGTCCC
                                    ___  G  GCGT
GAM380  SOX12   3'  TTCTGCATGTCTGTGCTCTTCC 22703        C  G  C
          T                      GGGAGGA CA GG ATGTGCAGGG
                                |||||||  ||  ||  ||||||||||
                                TCCTTCT GT TC TGTACGTCTT
                                    C  G  _
GAM380  SOX4    3'  TCCTGCATCACCACCTTGGTTT 11878   G        CA_  _
            TGTT                  G AGGACCAGGG   TG TGCAGGG
                                | ||||||||||   ||  |||||||
                                T TTTTGGTTCC   AC ACGTCCT
                                 G         ACC  T
GAM380  SPG3A   3'  CTTTGTATATGTGAGTTTCACT 31915    GA    CAGG
                                GG  GGAC    GCATGTGCAGGG
                                ||  ||||    ||||||||||||
                                TC  TTTG    TGTATATGTTTC
                                 AC    AG__
GAM380  SPOCK   3'  TGGGTGGTTTTGGTCTTTTT   62822            ATG G
                                GGGAGGACCAGGGC   T CA
                                ||||||||||||||   | ||
```

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                                TTTTTCTGGTTTTG  G GT
                                      GT_ G
GAM380  SPOCK   3'  TTTGTATCTGTTTCTCCT   62823       C  GGCAT
                                GGGAGGA CAG    GTGCAGG
                                ||||||| |||    |||||||
                                TCCTCTT GTC    TATGTTT
                                   T  _____
GAM380  SPTBN2  3'  TCTGCCTTCTGGTTCCTC    22707      _    CATGT
                                GAGGA CCAGGG    GCAGG
                                ||||| ||||||    |||||
                                CTCCT GGTCTT    CGTCT
                                  T     C____
GAM380  SRC     3'  CTCTGCCTGCCTGCTGTTGGTC 18286        _   T __
            CTCTC                   AGGACCAG GGCA GT  GCAGGG
                                ||||||||| |||| ||  ||||||
                                TCCTGGTT TCGT CG  CGTCTC
                                     G   C  TC
GAM380  SRD5A1  3'  TTTTGTAGATTTTGAGTTTTCC 6462         _   GC  G
            C                    GGGAGGAC CAGG  AT TGCAGGG
                                ||||||||| ||||  || |||||||
                                CCCTTTTG GTTT  TA ATGTTTT
                                     A   __ G
GAM380  STAU    3'  CGTGTTTGGTCTTTTT     16001          G
                                GGGAGGACCAGG CATG
                                |||||||||||| ||||
                                TTTTTCTGGTTT GTGC
                                      _
GAM380  STAU    3'  CGTGTTTGGTCTTTTT     33894          G
                                GGGAGGACCAGG CATG
                                |||||||||||| ||||
                                TTTTTCTGGTTT GTGC
                                      _
GAM380  STAU    3'  CGTGTTTGGTCTTTTT     33900          G
                                GGGAGGACCAGG CATG
                                |||||||||||| ||||
                                TTTTTCTGGTTT GTGC
                                      _
GAM380  STAU    3'  CGTGTTTGGTCTTTTT     33907          G
                                GGGAGGACCAGG CATG
                                |||||||||||| ||||
                                TTTTTCTGGTTT GTGC
                                      _
GAM380  STAU2   3'  TGCATGTTCGGATTTTTTT   26909       _ A
                                GGGAGGA CC GGGCATGTG
                                ||||||| || |||||||||
                                TTTTTTT GG CTTGTACGT
                                   A  _
GAM380  STS     3'  CCCTGAGCATTCTTGGTTTTCC 4451          C   G
                                GGAGGACCAGGG ATGT CAGGG
                                |||||||||||| |||| |||||
```

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                                CCTTTTGGTTCT TACG GTCCC
                                       _   A
GAM380  SUDD    3'  TGTGTTGCGTCTTTCC     13820        _  G
                                GGGAGGAC CAG GCA
                                |||||||| ||| |||
                                CCTTTCTG GTT TGT
                                     C  G
GAM380  SUFU    3'  CTCTGATCATGTTTGGTTTTCT 32409          G   TG
          T                      GGGAGGACCAGG CATG  CAGGG
                                 |||||||||||| ||||  |||||
                                 TTCTTTTGGTTT GTAC  GTCTC
                                       _   TA
GAM380  SUFU    3'  TGTGTCTGGTCTTCCC     32414          G
                                GGGAGGACCAGG CATG
                                |||||||||||| ||||
                                CCCTTCTGGTCT GTGT
                                       _
GAM380  SUFU    3'  TGTGTCTGGTCTTCCC     32415          G
                                GGGAGGACCAGG CATG
                                |||||||||||| ||||
                                CCCTTCTGGTCT GTGT
                                       _
GAM380  SYNGR2  3'  CCTCTGCCCTGGACTTTCC   16306      A      TGTGC
                                GGGAGG CCAGGGCA    AGG
                                |||||| ||||||||    |||
                                CCTTTC GGTCCCGT    TCC
                                   A      C____
GAM380  TACC1   3'  TGCTGCTGTGTTTTGGTGTTTT 20802   GG  G       T   GG
          C                      G  AG ACCAGGGCATG GCAG
                                 |  || ||||||||||| ||||
                                 C  TT TGGTTTTGTGT CGTC
                                  TT  G        _   GTT
GAM380  TAF12   5'  CTTTAATTGGCCTTGGTCCTC  18918          ATGTGC  G
                                GAGGACCAGGGC     AGG
                                ||||||||||||    |||
                                CTCCTGGTTCCG     TTC
                                      GTTAAT
GAM380  TAF1A   3'  CTTTGTAACTATGTCTGTTTTC 19061        CA     __
          TT                     GGGAGGAC  GGGCATG  TGCAGGG
                                 |||||||  |||||||  |||||||
                                 TTCTTTTG  TCTGTAT  ATGTTTC
                                      __      CA
GAM380  TAF1A   3'  CTTTGTAACTATGTCTGTTTTC 57813        CA     __
          TT                     GGGAGGAC  GGGCATG  TGCAGGG
                                 |||||||  |||||||  |||||||
                                 TTCTTTTG  TCTGTAT  ATGTTTC
                                      __      CA
GAM380  TAF7    3'  CCTTGCTCTTCCTAGTCCTTTT 18907        C   CATGT
                                GGGAGGAC AGGG    GCAGGG
                                |||||||| ||||    ||||||
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                                TTTTCCTG TCCT    CGTTCC
                                    A   TCT__
GAM380  TAP2    3'  CTTTGCATATGGTGTTTTCTT  5028        CAGGG
                                GGGAGGAC    CATGTGCAGGG
                                ||||||||    ||||||||||
                                TTCTTTTG    GTATACGTTTC
                                    TG___
GAM380  TARDBP  3'  CACAGTGTTTGGTTCTTTT   23770          G _
                                GGGAGGACCAGG CA TGTG
                                |||||||||||| || ||||
                                TTTTCTTGGTTT GT ACAC
                                      _ G
GAM380  TBX3    3'  TGTGTTCTTGTTTTCCT    33358        C
                                GGGAGGAC AGGGCATG
                                |||||||| ||||||||
                                TCCTTTTG TCTTGTGT
                                    T
GAM380  TCF12   3'  TGTTCTCTAGGTTTTCCC   12180        ___
                                GGGAGGACC   AGGGCA
                                |||||||||   ||||||
                                CCCTTTTGG   TCTTGT
                                     ATC
GAM380  TCF3    3'  TTTTGCATATGTTTTG     70738
                                CAGGGCATGTGCAGGG
                                ||||||||||||||||
                                GTTTTGTATACGTTTT

GAM380  TCFL4   3'  CCTCTGTTTTGGTCTCTT   63462      G       TGTGC
                                GGGAG ACCAGGGCA    AGG
                                ||||| |||||||||    |||
                                TTCTC TGGTTTTGT    TCC
                                   _       C____
GAM380  TCFL4   3'  CTTGGTGTTTGGTTTTTCC  63464          G  GTG   G
                                GGGAGGACCAGG CAT   CAGG
                                |||||||||||| |||   ||||
                                CCTTTTTGGTTT GTG   GTTC
                                      _  ___   A
GAM380  TCTA    3'  TTCTGAATCTCTGGTTTTGCT  42243   G       CATGTG
                                GG AGGACCAGGG     CAGGG
                                || ||||||||||     |||||
                                TC TTTTGGTCTC     GTCTT
                                 G        TAA___
GAM380  TEM6    3'  ATGCCCTGGTTTTCCT      42741
                                GGGAGGACCAGGGCAT
                                ||||||||||||||||
                                TCCTTTTGGTCCCGTA

GAM380  TES     3'  CGCCTGCCTTGGCCTCCC    72003       A      T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
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                                CCCTCC GGTTCCGT CGC
                                   _       C
GAM380  TFAP4    3'  TTCTGTTTTTGTTTTGTTTTTC 12242       C      TGT
           T                    GGAGGA CAGGGCA   GCAGGG
                                |||||| |||||||   ||||||
                                TCTTTT GTTTTGT   TGTCTT
                                   T      TTT
GAM380  TGFB3    3'  CCCTGTGTTCATTTGGTGTTCC 12259       G     GCAT TG
           T                    GGGAG ACCAGG    G  CAGGG
                                ||||| ||||||    |  |||||
                                TCCTT TGGTTT    T  GTCCC
                                   G     ACT_ GT
GAM380  TIM3     3'  TTGAGCTTGGTGTTTTGTCTTT 51351         C      GT_  AGGG
           TT                    GGGAGGAC AGGGCAT   GC
                                |||||||| |||||||   ||
                                TTTTTCTG TTTTGTG   CG
                                   _      GTT  AGTTT
GAM380  TJP1     5'  TCTTGCTCTTCCAGGTCCTTCT 12300          A   CATGT
                                GGGAGGACC GGG    GCAGGG
                                ||||||||| |||    ||||||
                                TCTTCCTGG CCT    CGTTCT
                                     A   TCT__
GAM380  TLL2     3'  CCTTGTCCCTTTGGTTTCCCC  24962     AG       CATGT
                                GGG  GACCAGGG    GCAGGG
                                |||  ||||||||    ||||||
                                CCC  TTGGTTTC    TGTTCC
                                  CT       CC___
GAM380  TMEM2    3'  CTTGCACTTGGGTTTTTT    25419         AGGG  T
                                GGAGGACC    CA GTGCAGG
                                ||||||||    || |||||||
                                TTTTTTGG    GT CACGTTC
                                     _____  T
GAM380  TNFRSF10B 3'  TCCAGGAGTTTTTGGTCTTTTC 13880    GG        C  GTGCA
                                G  AGGACCAGGG AT     GGG
                                |  ||||||||| ||     |||
                                C  TTCTGGTTTT TG     CCT
                                 TT         _  AGGA_
GAM380  TNFRSF17  5'  TTCTGTAGCTCCCTTGTTTTCT 6821          C    CATG
           T                    GGGAGGAC AGGG    TGCAGGG
                                ||||||| ||||    |||||||
                                TTCTTTTG TCCC    ATGTCTT
                                     T    TCG_
GAM380  TNFRSF1B  3'  CCCTGCGAAGGGGCCCTGGTCC 6519             ATG__
           TTCC                    GGAGGACCAGGGC     TGCAGGG
                                ||||||||||||||     |||||||
                                CTTCCTGGTCCCG    GCGTCCC
                                      GGGAA
GAM380  TNFRSF1B  3'  CTCTGTGGGGCCTTGGTTCCCT 6520      A         ATG
                                GGG GGACCAGGGC   TGCAGGG
                                ||| ||||||||||   |||||||
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                                TCC CTTGGTTCCG   GTGTCTC
                                  _        GG_
GAM380  TNFRSF1B  3'  TTCTGGAGCCCTTGGGTTTTTT 6527          __     ATGTG
                                GGAGGACC  AGGGC    CAGGG
                                ||||||||  |||||    |||||
                                TTTTTTGG  TCCCG    GTCTT
                                    GT    AG___
GAM380  TNFSF5   3'  CTTTGCGTGCAGTGTCTTTCC  3572          CAGG   GT
                                GGGAGGAC    GCAT  GCAGGG
                                ||||||||    ||||  ||||||
                                CCTTTCTG    CGTG  CGTTTC
                                    TGA_    __
GAM380  TOP1MT   3'  TTTTGTATGTGTGTGTGTTTTT 53698          _  GG
            TT                    GGGAGGAC CA  GCATGTGCAGGG
                                ||||||||  ||  ||||||||||||
                                TTTTTTTG GT  TGTGTATGTTTT
                                    T  G_
GAM380  TOP2B    3'  TCTTGTGTTGTCCTTTTGTCTT 6534          C__      T TG
            CTC                     GGAGGAC   AGGGCA G  CAGGG
                                |||||||   ||||||  |  |||||
                                TCTTCTG   TCCTGT T  GTTCT
                                    TTT     _ GT
GAM380  TRAF5    5'  TCCTGCGCGTCCGCTCTTCCC  16089         CCA    AT
                                GGGAGGA   GGGC  GTGCAGGG
                                |||||||   ||||  ||||||||
                                CCCTTCT   CCTG  CGCGTCCT
                                    CG_   __
GAM380  TRIM14   3'  TTCTGCATATGCTGCTTTCTC  52636       CC  _
                                GAGGA  AG GGCATGTGCAGGG
                                |||||  ||  ||||||||||||
                                CTCTT  TC TCGTATACGTCTT
                                   __  G
GAM380  TRIM9    3'  TCCTGTTTATGTGTGTCTTGGT 30768           TG ____
            TTTTCT                  GGACCAGGGCA  T    GCAGGG
                                ||||||||||  |   ||||||
                                TTTGGTTCTGT  G    TGTCCT
                                      GT TATT
GAM380  TRPM6    3'  CACCTGCCTTGGCTTCCC    34533        A       T
                                GGGAGG CCAGGGCA GTG
                                ||||||  |||||||| |||
                                CCCTTC GGTTCCGT CAC
                                   _       C
GAM380  TRPV1    3'  CTCTGTGCCGTGCTTGCTCCTC 38078        CCA     _ TG
            TT                    GGGAGGA   GGGCAT G  CAGGG
                                |||||||   ||||||  |  |||||
                                TTCTCCT   TTCGTG C  GTCTC
                                    CG_     C GT
GAM380  TRPV1    3'  CTCTGTGCCGTGCTTGCTCCTC 54799        CCA     _ TG
            TT                    GGGAGGA   GGGCAT G  CAGGG
                                |||||||   ||||||  |  |||||
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                                TTCTCCT  TTCGTG C  GTCTC
                                   CG_    C GT
GAM380  TRPV1   3'  CTCTGTGCCGTGCTTGCTCCTC 54832       CCA    _ TG
          TT                    GGGAGGA  GGGCAT G  CAGGG
                                ||||||| ||||||  |  |||||
                                TTCTCCT  TTCGTG C  GTCTC
                                   CG_    C GT
GAM380  TRPV1   3'  CTCTGTGCCGTGCTTGCTCCTC 54864       CCA    _ TG
          TT                    GGGAGGA  GGGCAT G  CAGGG
                                ||||||| ||||||  |  |||||
                                TTCTCCT  TTCGTG C  GTCTC
                                   CG_    C GT
GAM380  TRRAP   3'  CCTTCGCTAGCTTTAGTCTTTC 13022       C    AT  C  G
          T                     GGGAGGAC AGGGC  GTG AGG
                                |||||||| |||||  ||| |||
                                TCTTTCTG TTTCG  CGC TCC
                                    A    AT  T
GAM380  TSNAX   5'  TCTGCAGGCTGTTTTCCC    20004       CAG  ATG
                                GGGAGGAC  GGC  TGCAGG
                                ||||||||  |||  ||||||
                                CCCTTTTG  TCG  ACGTCT
                                    ____  G__
GAM380  TUFT1   3'  CCCTGCAGGTCATCATGGTTTT 39258        _ GC  G
          CTT                     GGGAGGACCA GG  AT TGCAGGG
                                ||||||||||  ||  || |||||||
                                TTCTTTTGGT CT  TG ACGTCCC
                                    A  AC  G
GAM380  TUFT1   3'  CCTACGCTGCCCTGGCCTCCT  39259      A      T  C
                                GGGAGG CCAGGGCA GTG AGG
                                ||||||  |||||||| ||| |||
                                TCCTCC GGTCCCGT CGC TCC
                                   _      _  A
GAM380  TXNIP   3'  TCCTGTCAAATTTTTTGTTCTC 21352       C   C  G  _
          CC                    GGGAGGAC AGGG AT TG CAGGG
                                |||||||| |||| || || |||||
                                CCCTCTTG TTTT TA AC GTCCT
                                    _   T  A  T
GAM380  UBE2H   3'  TCTTGATTTCTTGGTCATTTC  12490   GG G      CATGTG
                                G  A GACCAGGG     CAGGG
                                |  | ||||||||     |||||
                                C  T CTGGTTCT     GTTCT
                                 TT A       TTA___
GAM380  USP5    3'  CCCTGTCTCTTCCTTGTCCTTC 12992       C   CATGT
          T                     GGGAGGAC AGGG    GCAGGG
                                |||||||| ||||    ||||||
                                TCTTCCTG TCCT    TGTCCC
                                    T   TCTC_
GAM380  VANGL2  3'  CTTTGTGCTCTCTTTGTTTTTT 71648       C    CAT TG
          CT                    GGGAGGA CAGGG  G  CAGGG
                                ||||||| |||||  |  |||||
```

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                                TCTTTTT GTTTC  C  GTTTC
                                    T    TCT GT
GAM380  VASP    3'  CCTTCAAAGTTTTGGTTTTTTT 12566           ATG  C
                                GGGAGGACCAGGGC  TG AGG
                                |||||||||||||  || |||
                                TTTTTTTGGTTTTG  AC TCC
                                      AA_  T
GAM380  VCAM1   3'  TTTTGTAAATGTTTAGGTTTTT 54772         AG    G
          TT                    GGGAGGACC  GGCAT TGCAGGG
                                |||||||||  ||||| |||||||
                                TTTTTTTGG  TTGTA ATGTTTT
                                     AT    A
GAM380  VCAM1   3'  TTTTGTAAATGTTTAGGTTTTT 6548          AG    G
          TT                    GGGAGGACC  GGCAT TGCAGGG
                                |||||||||  ||||| |||||||
                                TTTTTTTGG  TTGTA ATGTTTT
                                     AT    A
GAM380  VCL     3'  TGTGTCCTGGTGCTCTC    25740      G
                                GGGAG ACCAGGGCATG
                                ||||| ||||||||||
                                CTCTC TGGTCCTGTGT
                                   G
GAM380  VCL     3'  TGTGTCCTGGTGCTCTC    12581      G
                                GGGAG ACCAGGGCATG
                                ||||| ||||||||||
                                CTCTC TGGTCCTGTGT
                                   G
GAM380  VEGF    3'  TCCTCCATCCCCTGGTCCTTCC 12589           CAT   C
                                GGGAGGACCAGGG   GTG AGGG
                                |||||||||||||  ||| ||||
                                CCTTCCTGGTCCC   TAC TCCT
                                      C__   C
GAM380  VHL     3'  TCCTGATTGATTTGGGTTTTTT 5089          AGGG_  TGTG
          T                     GGGAGGACC    CA   CAGGG
                                |||||||||    ||   |||||
                                TTTTTTTGG    GT   GTCCT
                                     GTTTA  TA__
GAM380  VPS41   3'  TCCTGTACTAATGGTTTCTCTT 26927       _  GGGCAT
                                GGGAGGA CCA     GTGCAGGG
                                ||||||| |||     ||||||||
                                TTCTCTT GGT     CATGTCCT
                                   T   AAT___
GAM380  VPS41   3'  TCCTGTACTAATGGTTTCTCTT 54658       _  GGGCAT
                                GGGAGGA CCA     GTGCAGGG
                                ||||||| |||     ||||||||
                                TTCTCTT GGT     CATGTCCT
                                   T   AAT___
GAM380  WHSC1   3'  CTCGCCTGCCTTGGGCTTTCC  55828       A      T   C
                                GGGAGG CCAGGGCA GTG AG
                                |||||| |||||||| ||| ||
```

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                                CCTTTC GGTTCCGT CGC TC
                                   G      C  _
GAM380  WHSC1    3'  CTCGCCTGCCTTGGGCTTTCC  55845      A      T  C
                                GGGAGG CCAGGGCA GTG AG
                                |||||| |||||||| ||| ||
                                CCTTTC GGTTCCGT CGC TC
                                   G      C  _
GAM380  WHSC1    3'  TCTTGTTATTTGGTTCTCC   23672         GCATGT
                                GGAGGACCAGG    GCAGGG
                                ||||||||||     ||||||
                                CCTCTTGGTTT    TGTTCT
                                      AT____
GAM380  WHSC1    3'  CTTTGCATGTTTGTATTTCCT  23659      AC  GGC
                                GGGAGG  CAG  ATGTGCAGGG
                                ||||||  |||  ||||||||||
                                TCCTTT  GTT  TGTACGTTTC
                                   AT  ___
GAM380  WHSC1    5'  CTCGCCTGCCTTGGGCTTTCC  55858      A      T  C
                                GGGAGG CCAGGGCA GTG AG
                                |||||| |||||||| ||| ||
                                CCTTTC GGTTCCGT CGC TC
                                   G      C  _
GAM380  WIG1     3'  CCTGCTTTGTGGTCTTTTT   94465        AGG  TGT
                                GGGAGGACC  GCA  GCAGG
                                |||||||||  |||  |||||
                                TTTTTCTGG  TGT  CGTCC
                                     ___  TT_
GAM380  WNT1     3'  CCTTTGTCCTGCGTTTTCTC  18311        _     TGTGC
                                GGGAGGAC CAGGGCA    AGG
                                |||||||| |||||||    |||
                                CTCTTTTG GTCCTGT    TCC
                                     C     T____
GAM380  WNT1     3'  TCCTGCGTTTTCTCCGGGTCCT 18313        A  CATG_
            CCT                   GGGAGGACC GGG    TGCAGGG
                                |||||||||  |||    |||||||
                                TCCTCCTGG CCT    GCGTCCT
                                     G  CTTTT
GAM380  WNT3A    3'  TGCGTTGGCTTCTCCC     52438       _  G
                                GGGAGGA CCAG GCA
                                ||||||| |||| |||
                                CCCTCTT GGTT CGT
                                   C   G
GAM380  WT1      3'  TTTTGTGTATGTTTTTGACTCT 44368      GACC      TG
            T                    GGGAG   AGGGCATG  CAGGG
                                |||||   ||||||||  |||||
                                TTCTC   TTTTGTAT  GTTTT
                                  AGT_      GT
GAM380  WT1      3'  TTTTGTGTATGTTTTTGACTCT 44378      GACC      TG
            T                    GGGAG   AGGGCATG  CAGGG
                                |||||   ||||||||  |||||
```

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                              TTCTC   TTTTGTAT  GTTTT
                                AGT_     GT
GAM380  WT1     3'  TTTTGTGTATGTTTTTGACTCT 44358     GACC     TG
            T                  GGGAG   AGGGCATG  CAGGG
                               |||||   ||||||||  |||||
                              TTCTC   TTTTGTAT  GTTTT
                                AGT_     GT
GAM380  WT1     3'  TTTTGTGTATGTTTTTGACTCT 4593      GACC     TG
            T                  GGGAG   AGGGCATG  CAGGG
                               |||||   ||||||||  |||||
                              TTCTC   TTTTGTAT  GTTTT
                                AGT_     GT
GAM380  WTAP    3'  TGGGTGTACGTTTTGGTTTTTT 16929          AT   GGG
            T                  GGGAGGACCAGGGC  GTGCA
                               ||||||||||||||  |||||
                              TTTTTTTGGTTTTG  CATGT
                                      __    GGGTG
GAM380  WWOX    3'  CCTGTGTGTGTCCCCTC    33045    ACCA     TG
                              GAGG   GGGCATG  CAGG
                              ||||   |||||||  ||||
                              CTCC   CCTGTGT  GTCC
                                ____     GT
GAM380  XPR1    3'  CTTAACATCTTTGGTTTTCCT  16427          C   GC
                              GGGAGGACCAGGG ATGT  AGG
                              ||||||||||||| ||||  |||
                              TCCTTTTGGTTTC TACA  TTC
                                      _   A_
GAM380  XRCC3   5'  CATTGTTCTGTCTTTCC    18336       C    T
                              GGGAGGAC AGGGCA GTG
                              |||||||| |||||| |||
                              CCTTTCTG TCTTGT TAC

                                 _    _
GAM380  XRCC5   3'  CTCTGTATATAGGTGGTTTTCT 40932        GGGC
            T                  GGGAGGACCA   ATGTGCAGGG
                               ||||||||||   ||||||||||
                              TTCTTTTGGT   TATATGTCTC
                                   GGA_
GAM380  YWHAE   3'  TCCTGCCCTGTTGGTTTTTTT  22197        GG  TGT
                              GGGAGGACCA  GCA  GCAGGG
                              |||||||||  |||  ||||||
                              TTTTTTTGGT  TGT  CGTCCT
                                   __  CC_
GAM380  YWHAG   5'  TCTGTGGGTCGGTCCTCTC   25023       AG  ATGT
                              GGGAGGACC  GGC   GCAGG
                              |||||||||  |||   |||||
                              CTCTCCTGG  CTG   TGTCT
                                   __  GG__
GAM380  ZFP37   3'  CTCTGTATGTGTATGTATCTTT 12716     AC  GG
                              GGAGG  CA  GCATGTGCAGGG
                              |||||  ||  ||||||||||||
```

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                                TTTCT  GT  TGTGTATGTCTC
                                   AT  A_
GAM380  ZNF141   3'  TTTTGCACATGATATCCTTT   12874       CCAGGG
                                GGAGGA     CATGTGCAGGG
                                ||||||     ||||||||||
                                TTTCCT     GTACACGTTTT
                                   ATA___
GAM380  ZNF144   3'  TCCTGTGTGTGTGGCCTTT   23082      A  AGG    TG
                                GGAGG CC   GCATG  CAGGG
                                ||||| ||   |||||  |||||
                                TTTCC GG   TGTGT  GTCCT
                                   _ ___    GT
GAM380  ZNFN1A3  3'  TTTTGTGAAACCTTTGTTTTCC 60243        C    CATG
           C                     GGGAGGAC AGGG    TGCAGGG
                                ||||||||| ||||    |||||||
                                CCCTTTTG TTCC    GTGTTTT
                                     T    AAA_
GAM380  AAK1     3'  CGCCTGCCTTGGCCTCCC    29843       A       T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTCC GGTTCCGT CGC
                                   _       C
GAM380  ABCA5    5'  TTTTGCAGTACCTTTTTGGTCT 37919   GA     ___   C  G
           GTCT                    GGACCA   GGG AT TGCAGGG
                                  ||||||   ||| || |||||||
                                  TCTGGT   TCC TG ACGTTTT
                                TG     TTT   A  _
GAM380  ABCA5    3'  CTGTGGTTGTGTGTTTTGCTTT 37914      C      TG _____   GG
           TCTT                    AGGA CAGGGCA  T    GCAG
                                |||| |||||||  |    ||||
                                TTTT GTTTTGT  G    TGTC
                                  C      GT TTGG
GAM380  ABCA5    5'  TCTTGTGTGTGCCTTG      37917          TG
                                CAGGGCATG  CAGGG
                                |||||||||  |||||
                                GTTCCGTGT  GTTCT
                                     GT
GAM380  ABCA8    3'  TCCTGTTTAAACCCGTGGTTTT 23152          _  CATGT
           TTT                     GGGAGGACCA GGG     GCAGGG
                                |||||||||| |||     ||||||
                                TTTTTTTGGT CCC     TGTCCT
                                     G   AAATT
GAM380  ABHD2    3'  TTTTGTGCTTAGTTACTGGTTT 22811          _  AT_ TG
           TCTC                    GGAGGACCAG GGC   G  CAGGG
                                |||||||||| |||   |  |||||
                                TCTTTTGGTC TTG   C  GTTTT
                                     A   ATT GT
GAM380  AGPAT1   3'  TGCGTGGTTGGTTTTT      21153         G G
                                GAGGACCA G CATGTG
                                |||||||| | ||||||
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                                TTTTTGGT T GTGCGT
                                     _ G
GAM380  AGPAT1   3'  TGCGTGGTTGGTTTTT     51237        G G
                                GAGGACCA G CATGTG
                                |||||||| | ||||||
                                TTTTTGGT T GTGCGT
                                     _ G
GAM380  AIF1     3'  CCCTGTACTTACCTGTTTTCTC 16753        C   GCAT
                                GGGAGGAC AGG   GTGCAGGG
                                |||||||| |||   ||||||||
                                CTCTTTTG TCC   CATGTCCC
                                     _  ATT_
GAM380  AK5      3'  CCCTGATCATCTGGTTCTCCT  23910          GCATGTG
                                GGGAGGACCAGG      CAGGG
                                ||||||||||||      |||||
                                TCCTCTTGGTCT      GTCCC
                                      ACTA___
GAM380  AKAP11   3'  TTCTGTCCTTGGTTCTGTCCTC 57835        C    ATGT_
           CT                     GGGAGGAC AGGGC    GCAGGG
                                |||||||| |||||    ||||||
                                TCCTCCTG TCTTG    TGTCTT
                                     _    GTTCC
GAM380  AKAP5    5'  TCCTGCACTTCATTTTTGGTTC 16776          CAT__
           TT                     GAGGACCAGGG    GTGCAGGG
                                ||||||||||    ||||||||
                                TTCTTGGTTTT    CACGTCCT
                                      TACTT
GAM380  AKAP6    3'  TCTGAATGTGTGCGCTGGTTCT 14997         G   TG G__   G
           CTT                    GGAGGACCAG GCA  T   CAGG
                                |||||||||| |||  |   ||||
                                TCTCTTGGTC CGT  G   GTCT
                                     G   GT TAA
GAM380  AKR7A2   3'  TTCTGTCACCTCTTTTGTTCTC 13493        C    CAT  _
           TC                     GGGAGGAC AGGG   GTG CAGGG
                                |||||||| ||||   ||| |||||
                                CTCTCTTG TTTC   CAC GTCTT
                                     T    TC_   T
GAM380  APCL     5'  CTTTGCACGTCATCTGGTCCTT 19673          GC
           CC                     GGGAGGACCAGG  ATGTGCAGGG
                                ||||||||||||  ||||||||||
                                CCTTCCTGGTCT  TGCACGTTTC
                                      AC
GAM380  APOA5    3'  CCTGCATATCCAGCCTCCT   53728       ACCAG  C
                                GGGAGG    GG ATGTGCAGG
                                ||||||    || |||||||||
                                TCCTCC    CC TATACGTCC
                                   GA___  _
GAM380  ARFGAP1  3'  CTTTGGTTTTGCTCTAGTTCTT 36590   GG    C     TGTG
           TC                     G  AGGAC AGGGCA    CAGGG
                                |  ||||| ||||||    |||||
```

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                                C  TCTTG TCTCGT    GTTTC
                                 TT    A     TTTG
GAM380  ARHGAP5  3'  TTTGATTTGCTCTGTTTTTTC  77085   GG    C     TGTG
                                G  AGGAC AGGGCA    CAGG
                                |  ||||| ||||||    ||||
                                C  TTTTG TCTCGT    GTTT
                                 TT    _     TTA_
GAM380  ARHGEF9  3'  GTGTCCTGGTTGTCCC      30818      G
                                GGGA GACCAGGGCAT
                                |||| ||||||||||
                                CCCT TTGGTCCTGTG
                                  G
GAM380  ARHGEF9  3'  TTTTGCATTCAGGCTGTTTCTT 30828         C   GGCAT
             CT                   GGGAGGA CAG     GTGCAGGG
                                |||||||| |||     ||||||||
                                TCTTCTT GTC     TACGTTTT
                                    T   GGACT
GAM380  ARNTL2   3'  CCTTCAAAATGTTTTAGTTTTC 39460         C      G_  C   G
             TT                   GGGAGGAC AGGGCAT  TG AGG
                                |||||||| |||||||  || |||
                                TTCTTTTG TTTTGTA  AC TCC
                                    A      AA  T
GAM380  ARPP-19  3'  TTCTATATCTAGTCTTGGTTTT 21807             AT_   C
             TTT                   GGGAGGACCAGGGC   GTG AGGG
                                ||||||||||||||   ||| ||||
                                TTTTTTTGGTTCTG   TAT TCTT
                                       ATC   A
GAM380  ARPP-21  3'  TTTTGTTTGGTTTGGTTTTGCT 32830     G       G  TGT
                                GG AGGACCAGG CA   GCAGGG
                                || |||||||| ||   ||||||
                                TC TTTTGGTTT GT   TGTTTT
                                 G       G  T__
GAM380  ARSDR1   3'  TTCTGTATATGTTGGTAACTAC 32077     _  G_   GG
             CC                   GGG AG  ACCA  GCATGTGCAGGG
                                ||| ||  ||||  ||||||||||||
                                CCC TC  TGGT  TGTATATGTCTT
                                  A  AA   __
GAM380  ASB16    3'  CCACGTGCTGTCCTGGTCCACC 55105     A         T TG AG
             T                    GGG GGACCAGGGCA G  C  GG
                                ||| |||||||||| |  |  ||
                                TCC CCTGGTCCTGT C  G  CC
                                  A          _ GT CA
GAM380  ASB16    5'  TCTTGGACCCTCTGTCTTCCC  69948         C    CAT  G
                                GGGAGGAC AGGG   GT CAGGG
                                |||||||| ||||   || |||||
                                CCCTTCTG TCTC   CA GTTCT
                                     _    C__  G
GAM380  ATP1B4   3'  CCTGCAAACAGGTTTTTCT   23814          AGGGCATG
                                GGGAGGACC       TGCAGG
                                |||||||||       ||||||
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                                TCTTTTTGG       ACGTCC
                                     ACAA____
GAM380  ATP6M8-9  3'  TTTTGTGTGTGCCTGTGATGTT 19279      CA___      TG
            TTTCT                  AGGAC    GGGCATG  CAGGG
                                |||||    |||||||  |||||
                                TTTTG    TCCGTGT  GTTTT
                                   TAGTG      GT
GAM380  ATP6V1EL2 3'  CTCTGATACTGTTCTGTTTTTC 54685       C      T  _
            T                   GGAGGA CAGGGCA GTG CAGGG
                                |||||| ||||||| ||| |||||
                                TCTTTT GTCTTGT CAT GTCTC
                                   T      _  A
GAM380  AUTL1    3'  TTTTGCATATGTCTTG      51663
                                CAGGGCATGTGCAGGG
                                ||||||||||||||||
                                GTTCTGTATACGTTTT

GAM380  B3GNT6   3'  CCTAAAATTCCTGGTTCTCTC  22504           C  GTGC
                                GGGAGGACCAGGG AT    AGG
                                ||||||||||||| ||    |||
                                CTCTCTTGGTCCT TA    TCC
                                      _  AAA_
GAM380  BA108L7.2 3'  CACCTGCCTTGGCCTCCC    48257       A       T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTCC GGTTCCGT CAC
                                   _       C
GAM380  BCAS4    3'  CTTTGTGAGCTTTGTGGTCTTC 35256          __    ATG
            CC                    GGGAGGACCA  GGGC   TGCAGGG
                                ||||||||||  ||||   |||||||
                                CCCTTCTGGT  TTCG   GTGTTTC
                                      GT    A__
GAM380  BIA2     3'  TTCTGTTTCTCCTCGTTTTCCT 71285         C    CATGT
                                GGGAGGAC AGGG    GCAGGG
                                |||||||| ||||    ||||||
                                TCCTTTTG TCCT    TGTCTT
                                     C    CTT__
GAM380  BITE     3'  CCCTGCTCATCCTGTTCTTTT  60450         CA   C   T
                                GGGAGGAC  GGG ATG GCAGGG
                                ||||||||  ||| ||| ||||||
                                TTTTCTTG  TCC TAC CGTCCC
                                     __   _   T
GAM380  BM045    3'  CTCTGCATGGGTTGGATTTTCC 37459       _   GG  AT
                                GGAGGA CCA  GC  GTGCAGGG
                                ||||||| |||  ||  ||||||||
                                CCTTTT GGT  TG  TACGTCTC
                                   A   __ GG
GAM380  BOP      5'  TTCTGTGTCTGTGCTCCTCCT  85055         CCA G   T TG
                                GGGAGGA   G GCA G  CAGGG
                                |||||||   | ||| |  |||||
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                                TCCTCCT  C TGT T  GTCTT
                                   ___ G  C GT
GAM380  BRD1    5'  CCTGTATGTGGACTTCCT   27415     CC  GG
                                AGGA  AG  CATGTGCAGG
                                ||||  ||  ||||||||||
                                TCCT  TC  GTGTATGTCC
                                  __  AG
GAM380  BTN1A1  3'  CTCTGCGCCCTCCTGTTTCTCC 8193        C    CAT
          C                      GGGAGGA CAGGG  GTGCAGGG
                                |||||||  |||||  ||||||||
                                CCCTCTT GTCCT  CGCGTCTC
                                   T    CC_
GAM380  C14orf4 3'  TGTTGTTTTGTTTTGTTTTTCT 67342       C      TGT   GG
                                GGAGGA CAGGGCA  GCAG
                                ||||||  |||||||  ||||
                                TCTTTT GTTTTGT  TGTT
                                   T      TT_   GTT
GAM380  C1orf17 3'  ACATCCTCTGGTTTTTCT    68208           C
                                GGGAGGACCAGGG ATGT
                                ||||||||||||| ||||
                                TCTTTTTGGTCTC TACA
                                        C
GAM380  C1orf34 3'  CTCTGCATGGAGGTCTCTTCC  60669      _   AGGGCA
                                GGGAG GACC     TGTGCAGGG
                                |||||  ||||     |||||||||
                                CCTTC CTGG     GTACGTCTC
                                  T   AG____
GAM380  C1QR1   3'  TCTTCAAGTTGCTTTGTCTTTT 23846   GG    C     TG_  C
          C                      G  AGGAC AGGGCA  TG AGGG
                                |  |||||  ||||||  ||  ||||
                                C  TTCTG TTTCGT  AC TTCT
                                 TT    _     TGA  _
GAM380  C1QTNF3 3'  TTGTGTATGTTCCCCC     48201     A   CCAGG    TG
                                GGG GGA    GCATG  CAG
                                |||  |||    |||||  |||
                                CCC CCT    TGTAT  GTT
                                  _  _____    GT
GAM380  C20orf150 3'  TTCTGTGCAGACTGGTGCTTCC 65405      G    GGCA  TG
                                GGGAG ACCAG   TG  CAGGG
                                |||||  |||||   ||  |||||
                                CCTTC TGGTC   AC  GTCTT
                                  G    AG__  GT
GAM380  C20orf178 3'  CCTTGCTCCCCTGGTCTTCT   74792          CATGT
                                GGAGGACCAGGG    GCAGGG
                                ||||||||||||    ||||||
                                TCTTCTGGTCCC    CGTTCC
                                       CT___
GAM380  C20orf18  3'  CCAGTGCCTTTGTCCTTCC   48340        C      GTGCA
                                GGGAGGAC AGGGCAT    GG
                                ||||||||  |||||||    ||
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                                CCTTCCTG TTCCGTG    CC
                                     T      A____
GAM380  C20orf18  3'  CCAGTGCCTTTGTCCTTCC   48346        C      GTGCA
                                GGGAGGAC AGGGCAT    GG
                                |||||||| |||||||    ||
                                CCTTCCTG TTCCGTG    CC
                                     T      A____
GAM380  C20orf188 3'  TCCTGTAGCTCCTCTGGTTCTG 31581    G        CATG
           TT                    GG AGGACCAGGG   TGCAGGG
                                || ||||||||||   |||||||
                                TT TCTTGGTCTC   ATGTCCT
                                 G        CTCG
GAM380  C20orf27  3'  CCCTGCCCCTCCCTCGTCCTCC 35383        C   CATGT
           T                     GGGAGGAC AGGG    GCAGGG
                                |||||||| ||||    ||||||
                                TCCTCCTG TCCC    CGTCCC
                                     C   TCCC_
GAM380  C20orf36  3'  CCTTGTGTGTGGAGAGCTTTCT 36797       ACCAGGG   TG
                                GGGAGG      CATG  CAGGG
                                ||||||      ||||  |||||
                                TCTTTC      GTGT  GTTCC
                                   GAGAG__   GT
GAM380  C20orf43  3'  CCTGCAGGTGCATTTGGTCCTT 59936   GG       _   G    G
           TC                    G  AGGACCAGG GCAT TGCAGG
                                |  |||||||| |||| ||||||
                                C  TCCTGGTTT CGTG ACGTCC
                                 TT       A   G
GAM380  C21orf108 3'  CCCTGCACATGCCCTTTTGCCT 88717    AG  CC
                                GGG  GA  AGGGCATGTGCAGGG
                                |||  ||  ||||||||||||||
                                TCC  TT  TCCCGTACACGTCCC
                                  GT  __
GAM380  C21orf108 3'  CTGACAATGCCTTGGTTTTGTC 88721    G         GTG
                                GG AGGACCAGGGCAT   CAG
                                || ||||||||||||   |||
                                CT TTTTGGTTCCGTA   GTC
                                 G          ACA
GAM380  C21orf108 3'  TCTTGCTTTTCTTTGTTCTCCC 88727        C   CATGT
                                GGGAGGAC AGGG    GCAGGG
                                |||||||| ||||    ||||||
                                CCCTCTTG TTCT    CGTTCT
                                     T   TTT__
GAM380  C21orf108 3'  TTTTGTAAGGTTTTTGTGTTTT 88728       _    _ ATG
           CCT                    GGAGGAC CAGGG C   TGCAGGG
                                |||||||| ||||| |   |||||||
                                CCTTTTG GTTTT G   ATGTTTT
                                     T    T GA_
GAM380  C2F      3'  TCTTGCAAACCTGGTTGTTTT  20934      G      GCATG
                                GGGA GACCAGG    TGCAGGG
                                |||| |||||||    |||||||
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                                TTTT TTGGTCC     ACGTTCT
                                  G      AA___
GAM380  C5orf6   3'  TTCTGCCTCCATCCTGGTTTCC 33489     AG       CATGT
              CC                  GGG  GACCAGGG    GCAGGG
                                  |||  ||||||||    ||||||
                                  CCC  TTGGTCCT    CGTCTT
                                    CT       ACCTC
GAM380  C6orf5   3'  CACCTGCCTTGGCCTCCC    31340       A       T
                                  GGGAGG CCAGGGCA GTG
                                  ||||||| |||||||| |||
                                  CCCTCC GGTTCCGT CAC
                                     _       C
GAM380  C7orf13  5'  CCCTGCGTGGCCCGCTGGCCTT 50927       A  __   ATG
              TT                   GGGAGG CCA  GGGC   TGCAGGG
                                  |||||| |||  ||||   |||||||
                                  TTTTCC GGT  CCCG   GCGTCCC
                                     _  CG   GT_
GAM380  C7orf14  3'  CTTTGTATATGGACATCTTTTC 73853   GG   CCAGGG
                                  G  AGGA     CATGTGCAGGG
                                  |  ||||     ||||||||||
                                  C  TTCT     GTATATGTTTC
                                   TT   ACAG__
GAM380  C9orf7   3'  CTTTGCACGTGTCCCTACACCT 34172     ACC   _
                                  AGG   AGGG CATGTGCAGGG
                                  |||   |||| ||||||||||
                                  TCC   TCCC GTGCACGTTTC
                                    ACA   T
GAM380  CAPS2    3'  TTTTGTTTTGTTTTGTTTTCTC 70605        C     TGT
                                  GGGAGGAC AGGGCA   GCAGGG
                                  |||||||| ||||||   ||||||
                                  CTCTTTTG TTTTGT   TGTTTT
                                       _     TT_
GAM380  CAT56    3'  CTTGTGCATCTGTCCACCT   47514     A   CAG  C   TG
                                  GGG GGAC   GG ATG  CAGG
                                  ||| ||||   || |||  ||||
                                  TCC CCTG   TC TAC  GTTC
                                    A   ___ _  GT
GAM380  CBX6     3'  CTTGTACGTTTGTTCTG     26616        __
                                  CAGGGCA  TGTGCAGG
                                  |||||||  ||||||||
                                  GTCTTGT  GCATGTTC
                                      TT
GAM380  CCNA2    3'  TTTTGTATATGTATCTGTCTT  6947       C  _
                                  AGGAC AGG GCATGTGCAGGG
                                  ||||| ||| ||||||||||||
                                  TTCTG TCT TGTATATGTTTT
                                     _  A
GAM380  CCNB2    3'  TTTTGTACATAGTCCTCTGGTC 16289   A     _ _ _
              TATCT                   GGACCAG GG C ATGTGCAGGG
                                   ||||||| || | ||||||||||
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                                TCTGGTC CC G TACATGTTTT
                               A      T  T A
GAM380  CDC14B   3'  TCTGCCTGCCTTGGCCTCCC   52863       A       TGT
                               GGGAGG CCAGGGCA   GCAGG
                               ||||||| ||||||||   |||||
                               CCCTCC GGTTCCGT   CGTCT
                                  _       C__
GAM380  CDH24    3'  CCCTGTGACTGGCTTTTTGTTT 94930        C_    ATG_
           TTTT                   GGAGGAC  AGGGC    TGCAGGG
                               |||||||  |||||   |||||||
                               TTTTTTG  TTTCG    GTGTCCC
                                  TT    GTCA
GAM380  CDW92    3'  TTTGCTAAATGCCTTGGTTTCT 54507       _       GT_    G
           TT                    GGAGGA CCAGGGCAT   GCAGG
                               |||||| |||||||||   |||||
                               TTTCTT GGTTCCGTA   CGTTT
                                  T        AAT
GAM380  CECR1    3'  CTCTATACCGTGCCTGGGTCTT 33813    GG     A      _ C
           TTC                    G  AGGACC GGGCATG TG AGGG
                               |  |||||| ||||||| || ||||
                               C  TTCTGG TCCGTGC AT TCTC
                                TT     G      C  A
GAM380  CECR1    3'  TCCTGTGCTCGCCCTGTTTCTC 33820        C     AT TG
           TC                     GGGAGGA CAGGGC  G  CAGGG
                               ||||||| ||||||  |  |||||
                               CTCTCTT GTCCCG  C  GTCCT
                                  T     CT GT
GAM380  CECR6    3'  CTCTGTGTGTGTAGTGTTGTTT 49086        __ GG    TG
           TCTC                   GGAGGAC  CA  GCATG  CAGGG
                               |||||||  ||  |||||  |||||
                               TCTTTTG  GT  TGTGT  GTCTC
                                  TT  GA    GT
GAM380  CED-6    3'  CAACGATATGTTTGGTTTTCCT 32853           G    GCAGGG
                               GGGAGGACCAGG CATGT
                               |||||||||||| |||||
                               TCCTTTTGGTTT GTATA
                                     _    GCAACT
GAM380  CENPH    3'  TTGCATTTGTCTGTCC      43280      CA    T    G
                               GGAC  GGGCA GTGCA G
                               ||||  ||||| ||||| |
                               CCTG  TCTGT TACGT T
                                  __    T    G
GAM380  CEP3     3'  TGTGTTGGGTTTTCT       21252         AG
                               GGAGGACC  GGCATG
                               ||||||||  ||||||
                               TCTTTTGG  TTGTGT
                                  G_
GAM380  cerk     3'  ATATGCCCTGGCTCTTTC    42843    GG  GA
                               G  AG  CCAGGGCATGT
                               |  ||  ||||||||||
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                                C  TC  GGTCCCGTATA
                                 TT  TC
GAM380  CGI-57   3'  CCTCTCTTCTGGTTCTTCT   73878          CATGTGC
                                GGGAGGACCAGGG      AGG
                                ||||||||||||      |||
                                TCTTCTTGGTCTT      TCC
                                      CTC____
GAM380  CHIT1    3'  TCCTGCAGGCCTTTCTGTGGTC 12950      _____   ATG
           TTCCT                 GACCA    GGGC   TGCAGGG
                                |||||    ||||   |||||||
                                CTGGT    TCCG   ACGTCCT
                                   GTCTT    G__
GAM380  CHSY1    3'  GTTTGTTTTGTTTTGTTCTTTT 29903       C      TGT    G
                                GGAGGA CAGGGCA   GCAGG
                                |||||| |||||||   |||||
                                TTTTCT GTTTTGT   TGTTT
                                    T      TT_    GT
GAM380  CKAP2    3'  TATGCCCTTGTTTTTTC     36563   GG    C
                                G  AGGAC AGGGCATG
                                |  ||||| ||||||||
                                C  TTTTG TCCCGTAT
                                 TT    T
GAM380  CKAP4    3'  TTCTGCATTTGGTTGGTTTCCT 22392       G    G G  T
                                GGGAG ACCA G CA GTGCAGGG
                                ||||| |||| | || ||||||||
                                TCCTT TGGT T GT TACGTCTT
                                   _   _ G  T
GAM380  CLDN8    3'  AGAAAAATATGTCTTGGTTTTC 24034             GCAGGG
                                GAGGACCAGGGCATGT
                                ||||||||||||||||
                                CTTTTGGTTCTGTATA
                                        AAAAGAC
GAM380  CLECSF9  3'  TCTGTAGCAGGTCCTCTT    26841         AGG  ATG
                                GGGAGGACC   GC   TGCAGG
                                |||||||||   ||   ||||||
                                TTCTCCTGG   CG   ATGTCT
                                     A__  ____
GAM380  CLPX     3'  TCTTGTATATACAGCTTTTCCT 21856      CC    ___
                                AGGA  AGGGC   ATGTGCAGGG
                                ||||  |||||   ||||||||||
                                TCCT  TTTCG   TATATGTTCT
                                   __     ACA
GAM380  CNNM1    3'  ACTGGATCTCTGGTTTTTCT   39767           CAT  G   GG
                                GGGAGGACCAGGG   GT CAG
                                ||||||||||||   || |||
                                TCTTTTTGGTCTC   TA GTC
                                       ___  G   AT
GAM380  COQ7     3'  CTCTGCAGTGTTGATTTTTCT  32330        C   G  ATG
                                GGGAGGA CAG GC   TGCAGGG
                                |||||||  ||| ||   |||||||
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                                TCTTTTT GTT TG   ACGTCTC
                                    A  G ___
GAM380  CPLX1    3'  CCTGCGTGTGTTCTCTCC    21836     GACC     TG
                                GGAG   AGGGCA  TGCAGG
                                ||||   ||||||  ||||||
                                CCTC   TCTTGT  GCGTCC
                                  ____     GT
GAM380  CPSF2    3'  TCTGTATTTGCGTCTTTCT   61603        CAGG   T
                                GGGAGGAC   GCA GTGCAGG
                                ||||||||   ||| |||||||
                                TCTTTCTG   CGT TATGTCT
                                    ____  T
GAM380  CREG     3'  TTTTGTGTGTTCCTGGTATTCT 13899      G      C   TG
            T                    GGGAG ACCAGGG ATG  CAGGG
                                |||||  |||||||  |||  |||||
                                TTCTT TGGTCCT TGT  GTTTT
                                   A      _  GT
GAM380  CRK7     3'  TAGGTGTTTTGGGTTTTTTT   33255        _      G
                                GGGAGGACC AGGGCAT TG
                                |||||||||  |||||||  ||
                                TTTTTTTGG TTTTGTG AT
                                     G      G
GAM380  CSL4     3'  CCTCCTGCCTTGGCCTCCC   32109       A       TGTGC
                                GGGAGG CCAGGGCA    AGG
                                ||||||  ||||||||    |||
                                CCCTCC GGTTCCGT    TCC
                                   _       CC___
GAM380  CST9L    3'  TTTTGCATGTGTTTGAGATCTC 54621      ACCA
                                GAGG   GGGCATGTGCAGGG
                                ||||   ||||||||||||||
                                CTCT   TTTGTGTACGTTTT
                                  AGAG
GAM380  CTPS2    3'  TGTGTCTGGCTTCTTCT     39092       _    G
                                GGGAGGA CCAGG CATG
                                |||||||  |||||  ||||
                                TCTTCTT GGTCT GTGT
                                    C    _
GAM380  CUGBP2   3'  CCCAGCCTTTTTGGTTTTTTT  21628          CATGT  A
                                GGGAGGACCAGGG    GC GGG
                                ||||||||||||    || |||
                                TTTTTTTGGTTTT    CG CCC
                                        TC___  A
GAM380  CXorf15  3'  CACTGCCTTGTCCTTTC    37161   GG    C     T
                                G  AGGAC AGGGCA GTG
                                |  |||||  ||||||  |||
                                C  TCCTG TTCCGT CAC
                                 TT    _     _
GAM380  CYorf15B 3'  TGTACATGTTTCTCTT     50820       CCAGG
                                GGGAGGA    GCATGTGCA
                                |||||||    |||||||||
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                                TTCTCTT    TGTACATGT
                                   _____
GAM380  CYP3A7   3'  TTCTGTACGTGCATTGTGCTCT 5717       G  CAGG
            C                    GGGAG AC   GCATGTGCAGGG
                                 ||||| ||   ||||||||||||
                                 CTCTC TG   CGTGCATGTCTT
                                   G  TTA_
GAM380  D4ST-1   3'  CCTTGTAAGGGCTTTGTTTTCC 55323        C    ATG
            T                    GGGAGGAC AGGGC   TGCAGGG
                                 |||||||| |||||   |||||||
                                 TCCTTTTG TTTCG   ATGTTCC
                                      _    GGA
GAM380  DBR1     3'  CACCTGTCTTGGCCTTCT    32529       A      T
                                 GGGAGG CCAGGGCA GTG
                                 |||||| |||||||| |||
                                 TCTTCC GGTTCTGT CAC
                                    _       C
GAM380  DCOHM    3'  CCTCCTGCCTTGGCCTCTC   49595       A      TGTGC
                                 GGGAGG CCAGGGCA    AGG
                                 |||||| ||||||||    |||
                                 CTCTCC GGTTCCGT    TCC
                                    _       CC___
GAM380  DCOHM    3'  CCTGCCTGCCTTGGCCTCCC   49596       A      TGT
                                 GGGAGG CCAGGGCA   GCAGG
                                 |||||| ||||||||   |||||
                                 CCCTCC GGTTCCGT   CGTCC
                                    _       C__
GAM380  DCOHM    3'  CTTTGCTTCTCTTGTTTTCTT  49602        C   CATGT
                                 GGGAGGAC AGGG    GCAGGG
                                 |||||||| ||||    ||||||
                                 TTCTTTTG TCTC    CGTTTC
                                     T   TT___
GAM380  DCTN4    3'  TTTTGTTTACCTTGGTCTTGTT 67790    G       CATGT
                                 GG AGGACCAGGG    GCAGGG
                                 || ||||||||||    ||||||
                                 TT TTCTGGTTCC    TGTTTT
                                  G        ATT__
GAM380  DF       3'  TCCTGCATCTGGTTGGTCTTT  8632         G G  T
                                 GAGGACCA G CA GTGCAGGG
                                 |||||||| | || ||||||||
                                 TTTCTGGT T GT TACGTCCT
                                    _ G  C
GAM380  DF       3'  TCCTGCATCTGGTTGGTCTTT  76330        G G  T
                                 GAGGACCA G CA GTGCAGGG
                                 |||||||| | || ||||||||
                                 TTTCTGGT T GT TACGTCCT
                                    _ G  C
GAM380  DHRS2    5'  CTTTGTTCTTTTGGTCTTC   19381          CATGT
                                 GAGGACCAGGG    GCAGGG
                                 ||||||||||    ||||||
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                                CTTCTGGTTTT    TGTTTC
                                      CT___
GAM380  Di-Ras2   3'  CTCTCAATATGTCCTAGTTTTC 34187        C       GC
            TT                   GGGAGGAC AGGGCATGT  AGGG
                                ||||||||| |||||||||  ||||
                                TTCTTTTG TCCTGTATA  TCTC
                                    A        AC
GAM380  DICER1    3'  TCTTGCATAAAAAAGGGTTCTT 47609    G      AGGGCA
            GC                   G GAGGACC     TGTGCAGGG
                                | |||||||     |||||||||
                                C TTCTTGG     ATACGTTCT
                                 G      GAAAAA
GAM380  DJ37E16.5 3'  CCCTGTTGTGACCTGTCCTTCC 39730        C   G    T
                                GGGAGGAC AGG CATG GCAGGG
                                |||||||| ||| |||| ||||||
                                CCTTCCTG TCC GTGT TGTCCC
                                    _   A   _
GAM380  DKFZP434A043 3'  TCTTGTGTTTTGTTTTGGTTTT 31195            T_ TG
            TTT                  GGGAGGACCAGGGCA  G  CAGGG
                                |||||||||||||||  |  |||||
                                TTTTTTTGGTTTTGT  T  GTTCT
                                      TT GT
GAM380  DKFZp434C0328 5'  TCTGTTCCTTGGTTTTTTT    34137           CATGT
                                GGGAGGACCAGGG    GCAGG
                                ||||||||||||    |||||
                                TTTTTTTGGTTCC    TGTCT
                                      T_____
GAM380  DKFZP434C0826 5'  TGTCTCTTTGTTCTCTT     84038        C_  _
                                GGGAGGAC  AG GGCA
                                ||||||||  || ||||
                                TTCTCTTG  TC CTGT
                                    TT  T
GAM380  DKFZP434C0826 5'  CCTGTGCTCGGGTTCTCTT    84035         A    ATGT
                                GGGAGGACC GGGC    GCAGG
                                ||||||||| ||||    |||||
                                TTCTCTTGG CTCG    TGTCC
                                     G   _____
GAM380  DKFZP434C171 3'  CTTTGCTCTGTTTTTCT     31554       C      TGTGC
                                GGAGGA CAGGGCA     AG
                                ||||||| |||||||     ||
                                TCTTTT GTCTCGT     TC
                                   T      T_____
GAM380  DKFZP434D146 3'  TATATCCTGGTTTTCTC     31528           GC
                                GGGAGGACCAGG  ATG
                                ||||||||||||  |||
                                CTCTTTTGGTCC  TAT
                                      TA
GAM380  DKFZp434E0519 3'  CCCTAGATTAGTCTTTGGTTTT 49985           _   AT  GC
            CTT                  GGGAGGACCAG GGC  GT  AGGG
                                |||||||||| |||  ||  ||||
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                                TTCTTTTGGTT CTG  TA  TCCC
                                      T   AT  GA
GAM380  DKFZp434E2220 3'  TTTGTACATTGTTTTCCC    34306        CAGGGC
                                GGGAGGAC     ATGTGCAGG
                                ||||||||     |||||||||
                                CCCTTTTG     TACATGTTT
                                     T_____
GAM380  DKFZP434H0820 3'  CTTGCTCCCTGTTTTCTC    63850        C    CATGT
                                GGGAGGAC AGGG    GCAGG
                                |||||||| ||||    |||||
                                CTCTTTTG TCCC    CGTTC
                                     _   T____
GAM380  DKFZP434I1735 3'  TTTTGTTTTGTTTTGTTTTTCT 87802       C      TGT
                                GGAGGA CAGGGCA   GCAGGG
                                |||||| |||||||   ||||||
                                TCTTTT GTTTTGT   TGTTTT
                                    T      TT_
GAM380  DKFZp434I1930 3'  TTTGTACATGTCAACTC     50035     GACCAG
                                GAG     GGCATGTGCAGG
                                |||     ||||||||||||
                                CTC     CTGTACATGTTT
                                  AA____
GAM380  DKFZP434J037 3'  CTCTGTACACATGGTGCCTTCT 48212       _   GGGCA
                                GGGAGG ACCA    TGTGCAGGG
                                |||||| ||||    |||||||||
                                TCTTCC TGGT    ACATGTCTC
                                   G   AC___
GAM380  DKFZP434J1813 3'  CTTTCGTAGTTTTGGTTTTTC  61787           A   C
                                GGAGGACCAGGGC TGTG AGG
                                |||||||||||||| |||| |||
                                CTTTTTGGTTTTG ATGC TTC
                                      _   T
GAM380  DKFZp434K1210 3'  TCCTGTTACTTTCTGGTCATCC 34276     G      CATGT
          C                      GGGA GACCAGGG    GCAGGG
                                |||| ||||||||    ||||||
                                CCCT CTGGTCTT    TGTCCT
                                  A      TCAT_
GAM380  DKFZP434K2235 3'  TTTTGTGTAAAACTTGTCTTCC 83501       C  GCA  TG
          C                      GGGAGGAC AGG   TG  CAGGG
                                |||||||| |||   ||  |||||
                                CCCTTCTG TTC   AT  GTTTT
                                     _   AAA  GT
GAM380  DKFZP434L0117 3'  TCCTCAGGGCTCTTGTTCTCCC 42920       C    ATG  C
                                GGGAGGAC AGGGC   TG AGGG
                                |||||||| |||||   || ||||
                                CCCTCTTG TCTCG   AC TCCT
                                     T    GG_  _
GAM380  DKFZP434O125 3'  TGCTTTTTGTTTTCCC      64962        C_
                                GGGAGGAC  AGGGCA
                                ||||||||  ||||||
```

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                                CCCTTTTG  TTTCGT
                                    TT
GAM380  DKFZP434P1750 3'  CTTTGTCTTCTGTCCTTTGGTT 31375       __    TGT_
          CTCCT                   AGGACCA  GGGCA   GCAGGG
                                  |||||||  |||||   ||||||
                                  TCTTGGT  CCTGT   TGTTTC
                                     TT    CTTC
GAM380  DKFZp547M072 3'  CTCTGCGCCAGGTCGGTCCTCC 61080        AG  AT_
          C                    GGGAGGACC  GGC   GTGCAGGG
                               |||||||||  |||   ||||||||
                               CCCTCCTGG  CTG   CGCGTCTC
                                    __   GAC
GAM380  DKFZP564G202 3'  TCTTGTCACTCTTTTGGTTTTC 65291          CAT  _
          TT                    GGGAGGACCAGGG   GTG CAGGG
                                ||||||||||||   ||| |||||
                                TTCTTTTGGTTTT   CAC GTTCT
                                      CT_   T
GAM380  DKFZP564K0322 3'  TTTTGTTCATGCTTTGATTTTT 49366       C       T
          TT                    GGGAGGA CAGGGCATG GCAGGG
                                |||||||  |||||||| ||||||
                                TTTTTTT GTTTCGTAC TGTTTT
                                    A       T
GAM380  DKFZP564K2062 3'  TTTGAATCTTGGTTTTC     31241          CATGTG
                                GAGGACCAGGG     CAGG
                                ||||||||||     ||||
                                CTTTTGGTTCT     GTTT
                                     AA____
GAM380  DKFZp566H0824 5'  CTGTGGTGGTTTTTCT      34051          GGGCATGT
                                GGGAGGACCA      GCAG
                                ||||||||||      ||||
                                TCTTTTTGGT      TGTC
                                     GG_______
GAM380  DKFZp566H0824 5'  TTCTGAGTTTCTGGTCCTTTT  34061          CATGTG
                                GGGAGGACCAGGG     CAGGG
                                ||||||||||||     |||||
                                TTTTCCTGGTCTT     GTCTT
                                      TGA___
GAM380  DKFZP566K0524 3'  TTTTGCCATGCCTGAGTTCTTT 69354   GG    CA     T
          C                    G  AGGAC  GGGCATG GCAGGG
                               |  |||||  ||||||| ||||||
                               C  TCTTG  TCCGTAC CGTTTT
                                TT    AG     _
GAM380  DKFZP586J0619 3'  TCCTGCACGTGCTGGGCCTGCT 81393    G  A  AG
                                GG AGG CC  GGCATGTGCAGGG
                                || ||| ||  ||||||||||||
                                TC TCC GG  TCGTGCACGTCCT
                                 G  _  G_
GAM380  DKFZP727C091 3'  CATCTGCATTTGGTCTTCTC   66208          GGCAT     G
                                GGGAGGACCAG    GTGCAGG
                                ||||||||||    |||||||
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                                CTCTTCTGGTT    TACGTCT
                                      _____      ACT
GAM380  DKFZP727G051 3'  TCCTGTGTGTGCACAGCTGTCC 69480     _ ACCAGG    TG
           C                     GGGA GG     GCATG  CAGGG
                                 |||| ||     |||||  |||||
                                 CCCT TC     CGTGT  GTCCT
                                   G  GACA__     GT
GAM380  DKFZp761G2113 3'  TTTTGCATATGTAATCCATTCT 69913     _  CCAGG
                                 GGGA GGA    GCATGTGCAGGG
                                 |||| |||    ||||||||||||
                                 TCTT CCT    TGTATACGTTTT
                                   A  AA___
GAM380  DKFZP761I2123 3'  CCCTGCGCGCTCTGCTCCTTCC 48761       C     AT
                                 GGGAGGA CAGGGC  GTGCAGGG
                                 ||||||| ||||||  ||||||||
                                 CCTTCCT GTCTCG  CGCGTCCC
                                     C     __
GAM380  DKFZp762P2111 3'  CCTGTGGGTCTTTTGGTTTTTT 86355          C  G     G
           T                     GGGAGGACCAGGG AT TGCAGG
                                 |||||||||||||  || ||||||
                                 TTTTTTTGGTTTT TG GTGTCC
                                        C  G
GAM380  DKK2     5'  CCCTCCGGGCTTTGCGTCTTCC 27014        _     ATGT C
           T                     GGGAGGAC CAGGGC    G AGGG
                                 |||||||| ||||||    | ||||
                                 TCCTTCTG GTTTCG    C TCCC
                                     C     GG__ C
GAM380  DNAJB11   3'  TTTTGTGTGTGTTTTTGTTTTT 32839       C       TG
                                 GAGGAC AGGGCATG  CAGGG
                                 |||||| ||||||||  |||||
                                 TTTTTG TTTTGTGT  GTTTT
                                    T       GT
GAM380  DNAL4    3'  CCCTAGGCAGGTCCTGGTTTTT 19214           A   GC
           CC                     GGGAGGACCAGGGC TGT  AGGG
                                  |||||||||||||| |||  ||||
                                  CCTTTTTGGTCCTG ACG  TCCC
                                        G   GA
GAM380  DOK4     3'  TCTGCACAGGCTCCTTCC    36183        CCAGG  A
                                 GGGAGGA    GC TGTGCAGG
                                 |||||||    || ||||||||
                                 CCTTCCT    CG ACACGTCT
                                     _____  G
GAM380  DUSP10   3'  TTGTGTGTTTCATGCTCTGGAT 58564      _       T_  GGG
           TTTTT                   GAGGA CCAGGGCATG  GCA
                                   |||||| ||||||||||  |||
                                   TTTTT GGTCTCGTAC  TGT
                                     A         TT   GTGTTT
GAM380  DUSP10   3'  TTGTGTGTTTCATGCTCTGGAT 23284      _       T_  GGG
           TTTTT                   GAGGA CCAGGGCATG  GCA
                                   |||||| ||||||||||  |||
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                                TTTTT GGTCTCGTAC  TGT
                                   A        TT   GTGTTT
GAM380  DYRK4    3'  GCTTTGCTGAGGGTATGTCCTG 64227    C       T_____
             CTCCTTTC                 A CAGGGCATG     GCAGGG   C
                                | |||||||||     ||||||  |
                                T GTCCTGTAT     CGTTTC   G
                                 C        GGGAGT
GAM380  EFA6R    3'  CCTTCTCTTTTGGTTTTCTC   30983           CATGTGC
                                GGGAGGACCAGGG      AGG
                                ||||||||||||      |||
                                CTCTTTTGGTTTT      TCC
                                       CTCT___
GAM380  ENAH     3'  TCTGCGTGTGTGTGCTCTC   36619      G  CAGG   TG
                                GGGAG AC    GCA  TGCAGG
                                ||||| ||    |||  ||||||
                                CTCTC TG    TGT  GCGTCT
                                   G  _____   GT
GAM380  ENDOGLYX1 3'  CCTTGTGAAGATGCCTTGGTTC 45401       _       G__
             CTCT                    GAGGA CCAGGGCAT   TGCAGGG
                                ||||| |||||||||   |||||||
                                CTCCT GGTTCCGTA   GTGTTCC
                                   T        GAA
GAM380  EPB41L1   3'  CCCTCTGTGTCCTGGTCCTTCT 70588              TGC
                                GGGAGGACCAGGGCATG   AGGG
                                ||||||||||||||||   ||||
                                TCTTCCTGGTCCTGTGT   TCCC
                                       C__
GAM380  EPSIN    5'  CCTGCCTCCCTGTCTTCCC    25296         C    CATGT
                                GGGAGGAC AGGG     GCAGG
                                |||||||| ||||     |||||
                                CCCTTCTG TCCC     CGTCC
                                     _    TC___
GAM380  EPSIN    5'  TTCTGGCTTCCCCGGTTCTTCC 25300          A   CAT  G
                                GGGAGGACC GGG   GT CAGGG
                                ||||||||| |||   || |||||
                                CCTTCTTGG CCC   CG GTCTT
                                     C   TT_  _
GAM380  ESDN     3'  TTCTGCAGGCTTCCTGTCCTTT 55181         C    CATG
             T                    GGGAGGAC AGGG    TGCAGGG
                                |||||||| ||||    |||||||
                                TTTTCCTG TCCT    ACGTCTT
                                     _    TCGG
GAM380  EZF-2    3'  CTCTGTGTGAAGGGGCCTCTC  37100       A  AGGG   GT
                                GGGAGG CC    CAT  GCAGGG
                                ||||||  ||    |||  ||||||
                                CTCTCC GG    GTG  TGTCTC
                                   _ GGAA   ___
GAM380  FASTK    3'  CCTGCACTTTGTTTTTTCC    46988       CCAG    T_
                                GGAGGA    GGCA  GTGCAGG
                                ||||||    ||||  |||||||
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                                CCTTTT   TTGT  CACGTCC
                                   ____   TT
GAM380  FBXO27   3'  TTCTGCCCACTCTGGTTTCTCT 74516      _    CA  T
                                GGAGGA CCAGGG  TG GCAGGG
                                |||||| ||||||  || ||||||
                                TCTCTT GGTCTC  AC CGTCTT
                                   T    __ C
GAM380  FHX      3'  TCCTGTTTTTTCCTAGTTCTTT 37309        C   CATGT
           T                     GGGAGGAC AGGG    GCAGGG
                                |||||||| ||||    ||||||
                                TTTTCTTG TCCT    TGTCCT
                                    A   TTTT_
GAM380  FKBP4    3'  CCCTGTTCCCTGTTCTGGTATT 8899      G       TGT_
           TCC                    GGGAG ACCAGGGCA   GCAGGG
                                ||||| |||||||||   ||||||
                                CCTTT TGGTCTTGT   TGTCCC
                                   A       CCCT
GAM380  FKBP5    3'  TTCTCATTTATGCTTTTGTCTT 14654       C     __  C
           TTT                    GGAGGAC AGGGCAT  GTG AGGG
                                ||||||| |||||||  ||| ||||
                                TTTTCTG TTTCGTA  TAC TCTT
                                    T      TT  _
GAM380  FLB6421  3'  TTTTGGGTGTCTTTTGTTTTCC 39236       C_     GTGCAGGG
           T                     GGGAGGAC  AGGGCAT
                                ||||||||  |||||||
                                TCCTTTTG  TTCTGTG
                                     TT      GGTTTT
GAM380  FLJ00026 3'  TCCGATAATGCTTTGCTTTTTT 64996       C      GTGCA
           T                     GGGAGGA CAGGGCAT    GGG
                                ||||||| ||||||||    |||
                                TTTTTTT GTTTCGTA    CCT
                                    C       ATAG_  C
GAM380  FLJ10079 3'  CTTGTGTGTTGCTTTTCCC   60203       C   G  ATGT
                                GGGAGGA CAG GC   GCAGG
                                ||||||| ||| ||   |||||
                                CCCTTTT GTT TG   TGTTC
                                    C   G  ____
GAM380  FLJ10101 3'  CTGCAGCAGCCTTGGTCTTTCT 45265            A  _
                                GGGAGGACCAGGGC TG TGCAG
                                |||||||||||||| || |||||
                                TCTTTCTGGTTCCG AC ACGTC
                                        _ G
GAM380  FLJ10251 3'  TTTTGCCATACTTTTGTTCTTC 35945       C   C   T
           C                     GGGAGGAC AGGG ATG GCAGGG
                                |||||||| |||| ||| ||||||
                                CCTTCTTG TTTC TAC CGTTTT
                                     T   A  _
GAM380  FLJ10420 3'  CCCTGTCCCCATCTGTCCTCTT 36107       CA__   CATGT
                                GGGAGGAC   GGG    GCAGGG
                                ||||||||   |||    ||||||
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                              TTCTCCTG   CCC    TGTCCC
                                   TCTA  C____
GAM380  FLJ10420 3' TCCTGGCAGACTTGGGTTTTCT 36111        AG  CA   G
            C                   GGGAGGACC  GG  TGT CAGGG
                                |||||||||  ||  ||| |||||
                                CTCTTTTGG  TC  ACG GTCCT
                                     GT  AG  _
GAM380  FLJ10525 3' TTGTGTATGTGGCTAGTCTT  36227      CA  G      GGG
                                AGGAC  GG CATGTGCA
                                |||||  || ||||||||
                                TTCTG  TC GTGTATGT
                                   A_  G       GTTT
GAM380  FLJ10697 3' TTTGGTTTTGTTTTGTGTTTTC 36423        _      TGT  AGGG
            TT                   GGGAGGAC CAGGGCA   GC
                                |||||||| |||||||   ||
                                TTCTTTTG GTTTTGT   TG
                                     T      TT_  GTTTT
GAM380  FLJ10716 3' GTCGTTTTTGGTCTTCTT    36486          C   T
                                GGGAGGACCAGGG ATG GC
                                |||||||||||| ||| ||
                                TTCTTCTGGTTTT TGC TG
                                      _  _
GAM380  FLJ10751 3' CCCTGATGACCTGGTTCTTCT  36568          G   GTG
                                GGGAGGACCAGG CAT   CAGGG
                                |||||||||||| |||   |||||
                                TCTTCTTGGTCC GTA   GTCCC
                                      A  ___
GAM380  FLJ10751 3' CCCTGATGACCTGGTTCTTCT  36729          G   GTG
                                GGGAGGACCAGG CAT   CAGGG
                                |||||||||||| |||   |||||
                                TCTTCTTGGTCC GTA   GTCCC
                                      A  ___
GAM380  FLJ10769 3' TTTGTGGATGGTTTTCCT    36601          GGGCA G
                                GGGAGGACCA    T TGCAGG
                                ||||||||||    | ||||||
                                TCCTTTTGGT    A GTGTTT
                                     _____ G
GAM380  FLJ10826 3' GTGTTTCGGTTTTTTT     36704         AG
                                GGGAGGACC  GGCAT
                                |||||||||  |||||
                                TTTTTTTGG  TTGTG
                                     CT
GAM380  FLJ10858 3' TCTTGTGTGTGCCATCTTTCC  36778       CCAG     TG
                                GGGAGGA   GGCATG  CAGGG
                                |||||||   ||||||  |||||
                                CCTTTCT   CCGTGT  GTTCT
                                   A___     GT
GAM380  FLJ10884 5' CTCTGCGGAGTTCGTCTTCCC  38836       CA   ATG
                                GGGAGGAC  GGGC   TGCAGGG
                                ||||||||  ||||  |||||||
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                                CCCTTCTG  CTTG   GCGTCTC
                                    __    AG_
GAM380  FLJ10901  3' CACCTGCCTTGGCCTTTC    36817   GG   A      T
                                G  AGG CCAGGGCA GTG
                                |  ||| |||||||| |||
                                C  TCC GGTTCCGT CAC
                                 TT  _      C
GAM380  FLJ11210  3' CCCACTGGGCTCTGGTCCTTCC 59575            AT_   CA
                                GGGAGGACCAGGGC   GTG  GG
                                ||||||||||||||   |||  ||
                                CCTTCCTGGTCTCG   CAC  CC
                                         GGT   __
GAM380  FLJ11210  3' TTCTGTTTTGTTTTGTTTTTTT 59577        C     TGT
                                GGGAGGAC AGGGCA   GCAGGG
                                |||||||| ||||||   ||||||
                                TTTTTTTG TTTTGT   TGTCTT
                                    _     TT_
GAM380  FLJ11275  3' TCCTGCATATTCATTGTTTTTT 37206        CAG  C
           T                     GGGAGGAC   GG ATGTGCAGGG
                                |||||||||   || ||||||||||
                                TTTTTTTG   CT TATACGTCCT
                                     TTA  _
GAM380  FLJ11286  3' CCTGACCTTTGTTCTCTT    37218        C    CATGTG
                                GGGAGGAC AGGG     CAGG
                                |||||||| ||||     ||||
                                TTCTCTTG TTCC     GTCC
                                     T    A_____
GAM380  FLJ11320  3' TCTGAGTTTTTGTCCTTCC    37246        C    ATGTG
                                GGGAGGAC AGGGC    CAGG
                                |||||||| |||||    ||||
                                CCTTCCTG TTTTG    GTCT
                                     T    A____
GAM380  FLJ11362  3' TCCTGAGGCTTTGGTGCTCCC  41683      G      ATGTG
                                GGGAG ACCAGGGC    CAGGG
                                ||||| ||||||||    |||||
                                CCCTC TGGTTTCG    GTCCT
                                   G      GA___
GAM380  FLJ11506  3' TCCTGAGCACCTTGTTTTTCT  45113      C    CA   G
                                GGAGGA CAGGG  TGT CAGGG
                                |||||| |||||  ||| |||||
                                TCTTTT GTTCC  ACG GTCCT
                                   T    __   A
GAM380  FLJ11506  3' TCCTGGGTGATTTGGGTTTTCT 45114        AGGG_   GTG
           C                     GGGAGGACC    CAT   CAGGG
                                |||||||||    |||   |||||
                                CTCTTTTGG    GTG   GTCCT
                                     GTTTA   G__
GAM380  FLJ11850  3' TTTGCTTCCTGGTTTGCCT    42725     AG      CATGT
                                GGG  GACCAGGG    GCAGG
                                |||  ||||||||    |||||
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                                TCC  TTGGTCCT    CGTTT
                                  GT       T____
GAM380  FLJ11850  3'  CTTGTCTATGTGTTTTGTTTTT 42720       C        __    G
                TTT                GGAGGA CAGGGCATGT  GCAGG
                                   |||||| ||||||||||  |||||
                                   TTTTTT GTTTTGTGTA  TGTTC
                                      T        TC
GAM380  FLJ12076  3'  TTTTGTGACTGACTGGTGTCTT 47238       _    GG  T  _
                CC                 GGGAGG ACCAG  CA GT GCAGGG
                                   |||||| |||||  || || ||||||
                                   CCTTCT TGGTC  GT CA TGTTTT
                                      G    A_ _ G
GAM380  FLJ12132  3'  CTTTGCAAGAACCTGTTCTCTT 46469         C   GCATG
                                   GGGAGGAC AGG    TGCAGGG
                                   |||||||| |||    |||||||
                                   TTCTCTTG TCC    ACGTTTC
                                       _   AAGA_
GAM380  FLJ12363  3'  TCTGCCTGCCTTGGCCTCCC   49694       A       TGT
                                   GGGAGG CCAGGGCA   GCAGG
                                   |||||| ||||||||   |||||
                                   CCCTCC GGTTCCGT   CGTCT
                                      _       C__
GAM380  FLJ12409  3'  TTTGTGCGTTGCTTTTCC    47056     CC     _  TG
                                   GGA  AGGGCA TG  CAGG
                                   |||  |||||| ||  ||||
                                   CCT  TTTCGT GC  GTTT
                                     __      T  GT
GAM380  FLJ12598  3'  TTCTGTATGTGTCTGGTGTTTT 45398      G     G
                                   GGAG ACCAGG CATGTGCAGGG
                                   |||| |||||| ||||||||||
                                   TTTT TGGTCT GTGTATGTCTT
                                     G     _
GAM380  FLJ12704  3'  CCTGCCCATCTGTTCTCCC    46532         CAG  C   T
                                   GGGAGGAC   GG ATG GCAGG
                                   ||||||||   || ||| |||||
                                   CCCTCTTG   TC TAC CGTCC
                                       ___  _   C
GAM380  FLJ12707  3'  TTCTGTGACTGAACTGGGTTTT 41951         _  GG  T  _
                TCT                GGAGGACC AG  CA GT GCAGGG
                                   |||||||| ||  || || ||||||
                                   CTTTTTGG TC  GT CA TGTCTT
                                      G  AA  _  G
GAM380  FLJ12788  3'  CCCAGCTCGTGCCCTGTTTTTC 42541       C        T  A
                T                   GGAGGA CAGGGCATG GC GGG
                                    ||||||| |||||||| || |||
                                    TCTTTT GTCCCGTGC CG CCC
                                       T        T  A
GAM380  FLJ12876  3'  CCTTGTGTCTGTGTTTCTCTT  42784        C  G  CAT TG
                                   GGGAGGA CA GG   G  CAGGG
                                   ||||||| || ||   |  |||||
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                                TTCTCTT GT TC   T  GTTCC
                                    T  G  ___ GT
GAM380  FLJ12876  3'  TCCTGTTCAACCTGGGTTCTCC 42790         A   CA  T
              C                  GGGAGGACC GGG  TG GCAGGG
                                 ||||||||| |||  || ||||||
                                 CCCTCTTGG TCC  AC TGTCCT
                                     G   A_  T
GAM380  FLJ13057  3'  TCTTGTCTTACATGGTCTTTTC 42458   GG      GGGCATGT
                                 G  AGGACCA       GCAGGG
                                 |  |||||||       ||||||
                                 C  TTCTGGT       TGTTCT
                                  TT      ACATTC__
GAM380  FLJ13072  5'  TGTGCTTTGGGTTTCTT     89832       GA
                                 GGGAG  CCAGGGCATG
                                 |||||  ||||||||||
                                 TTCTT  GGTTTCGTGT
                                    TG
GAM380  FLJ13105  3'  CTTGCCTACCTGTCTTCCC    46545         C   GCATGT
                                 GGGAGGAC AGG     GCAGG
                                 |||||||| |||     |||||
                                 CCCTTCTG TCC     CGTTC
                                     _   ATC___
GAM380  FLJ13111  3'  CCTTTGCTCTGGGCTTCCT    46937       A       TGTGC
                                 GGGAGG CCAGGGCA     AGG
                                 |||||| ||||||||     |||
                                 TCCTTC GGTCTCGT     TCC
                                    G       T____
GAM380  FLJ13154  3'  CCTTCCACAGCCCGGGTTCTCC 44796         A   A   C
              T                   GGGAGGACC GGGC TGTG AGGG
                                  ||||||||| |||| |||| ||||
                                  TCCTCTTGG CCCG ACAC TTCC
                                      G   _   C
GAM380  FLJ13158  3'  CTCTGACTTCTCTGTTTTTCT  46111       C    CAT  G
                                 GGAGGA CAGGG   GT CAGGG
                                 |||||| |||||   || |||||
                                 TCTTTT GTCTC   CA GTCTC
                                    T    TT_ _
GAM380  FLJ13162  5'  CCTGTGTGTGCCAGGCCCT   46554     A  AG     TG
                                 AGG CC  GGCATG  CAGG
                                 ||| ||  ||||||  ||||
                                 TCC GG  CCGTGT  GTCC
                                   C  A_     GT
GAM380  FLJ13204  3'  TCTGTGATTGGTTTTTT     45419          GGCATGT
                                 GGAGGACCAG      GCAGG
                                 ||||||||||      |||||
                                 TTTTTTGGTT      TGTCT
                                      AG_____
GAM380  FLJ13441  3'  TTTTGCACGTGTAGAGTTTTT  43676       CAGG
                                 GAGGAC    GCATGTGCAGGG
                                 ||||||    ||||||||||||
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                                TTTTTG   TGTGCACGTTTT
                                   AGA_
GAM380  FLJ13456 3' TTTTGTGTTAATCTGTTTTCTC 65948       C  GCAT TG
                                GGGAGGAC AGG   G  CAGGG
                                |||||||| |||   |  |||||
                                CTCTTTTG TCT   T  GTTTT
                                     _  AAT_ GT
GAM380  FLJ13544 5' TCTGTTCCTTGGTCTTC    46579          CATGT
                                GAGGACCAGGG    GCAGG
                                ||||||||||    |||||
                                CTTCTGGTTCC    TGTCT
                                      T____
GAM380  FLJ13852 3' CCTGCATGAGGGTCTCCT    43576      G  AGGG  TG
                                GGGAG ACC    CA  TGCAGG
                                ||||| |||    ||  ||||||
                                TCCTC TGG    GT  ACGTCC
                                   _  GA__  __
GAM380  FLJ14146 3' CTTTGTAGCATCCTGTCTTCTT 45243       CA  C  _
                                GGGAGGAC  GGG ATG TGCAGGG
                                ||||||||  ||| ||| |||||||
                                TTCTTCTG  TCC TAC ATGTTTC
                                     __  _  G
GAM380  FLJ14154 3' CCCTGCGCATGCACCATCCCC  45813    A  CCA  _
                                GG GGA   GG GCATGTGCAGGG
                                || |||   || ||||||||||||
                                CC CCT   CC CGTACGCGTCCC
                                  _  A__  A
GAM380  FLJ14251 3' CACAGTGTTTTGGTTCCCT    45967     A        _
                                GGG GGACCAGGGCA TGTG
                                ||| ||||||||||| ||||
                                TCC CTTGGTTTTGT ACAC
                                  _        G
GAM380  FLJ14280 3' CCTGCACTTGTTTCTCTC    45998       CCAGG  T
                                GGGAGGA    GCA GTGCAGG
                                |||||||    ||| |||||||
                                CTCTCTT    TGT CACGTCC
                                     _____  T
GAM380  FLJ14327 3' TCCTGTTTGAACTTGGTTCTCT 46147          GCATGT
                                GGAGGACCAGG     GCAGGG
                                ||||||||||     ||||||
                                TCTCTTGGTTC     TGTCCT
                                      AAGTT_
GAM380  FLJ14327 3' TCTGAGACTCGGTTTTCTC    46150        A  CATGTG
                                GGGAGGACC GGG     CAGG
                                ||||||||| |||     ||||
                                CTCTTTTGG CTC     GTCT
                                     _  AGA___
GAM380  FLJ14427 3' CTCTGCGTGTGTTCCCATGTCC 51335     CA  __  TG
                                GGAC  GGG  CA  TGCAGGG
                                ||||  |||  ||  |||||||
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                              CCTG  CCC  GT  GCGTCTC
                                TA   TT  GT
GAM380  FLJ14442  3' CTTTGCCTGTCTTCTGTCTTCC 51367        C_     TGT
             T                  GGGAGGAC  AGGGCA   GCAGGG
                                ||||||||  ||||||   ||||||
                                TCCTTCTG  TTCTGT   CGTTTC
                                    TC     C__
GAM380  FLJ14442  3' TTCTGTCTTCCTTGTCTTTCC  51378        C    CATGT
                                GGGAGGAC AGGG    GCAGGG
                                |||||||| ||||    ||||||
                                CCTTTCTG TCCT    TGTCTT
                                    T   TC___
GAM380  FLJ14454  3' CTTACCTGTTGTGGTCTTTTT  51380         G   T   C
                                GGGAGGACCA GGCA GTG AG
                                |||||||||| |||| ||| ||
                                TTTTTCTGGT TTGT CAT TC
                                     G   C  _
GAM380  FLJ14564  3' CCTTGTGCTGCCCCTGTCTTTT 76501   GG    CA    T TG
             C                   G  AGGAC  GGGCA G  CAGGG
                                 |  |||||  |||||  |  |||||
                                 C  TTCTG  CCCGT C  GTTCC
                                 TT    TC    _ GT
GAM380  FLJ14621  3' TCCTGTGGTGATGGTTTTCCC  51477         GG  ATG
                                GGGAGGACCA  GC   TGCAGGG
                                ||||||||||  ||   |||||||
                                CCCTTTTGGT  TG   GTGTCCT
                                     AG  ___
GAM380  FLJ14668  3' TCTGGGTCTTTGTTTTCTT   51514        C    ATGTG
                                GGGAGGAC AGGGC    CAGG
                                |||||||| |||||    ||||
                                TTCTTTTG TTCTG    GTCT
                                    T    G____
GAM380  FLJ14675  3' CCCTGTTCACGTCTTGGTGCTT 51519      G      A  T
             CT                   GGGAG ACCAGGGC TG GCAGGG
                                  |||||  |||||||  ||  ||||||
                                  TCTTC TGGTTCTG AC TGTCCC
                                     G       C  T
GAM380  FLJ14675  3' CTCTGAGATTTTGAGTTCTTCT 51520        _    CATGTG
                                GGGAGGAC CAGGG     CAGGG
                                |||||||| |||||     |||||
                                TCTTCTTG GTTTT     GTCTC
                                    A     AGA___
GAM380  FLJ14681  5' CCTTGCACGTTCCGGCTCCTCC 51523       _ A   C
             T                   GGGAGGA CC GGG ATGTGCAGGG
                                 |||||||  ||  |||  ||||||||||
                                 TCCTCCT GG CCT TGCACGTTCC
                                     C  _   _
GAM380  FLJ14800  3' CTTTGGTCATCTCTGTCCTTTC 51613   GG    C   C   TG
                                G  AGGAC AGGG ATG  CAGGG
                                |  ||||| |||| |||  |||||
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                              C  TCCTG TCTC TAC  GTTTC
                               TT    _   _   TG
GAM380  FLJ14824  3' CTTTGCACATGCCCTACTCTCC 51644      ACC
                              GGAGG   AGGGCATGTGCAGGG
                              |||||   ||||||||||||||||
                              CCTCT   TCCCGTACACGTTTC
                                 CA_
GAM380  FLJ14824  3' TTTTGTGTGGAATCTTGTCTTT 51647        C   GCA  TG
           CC                   GGGAGGAC AGG   TG  CAGGG
                              |||||||| |||   ||  |||||
                              CCTTTCTG TCT   GT  GTTTT
                                   T   AAG  GT
GAM380  FLJ14957  3' TCCTGTATCTTTTATGGTTTTT 51763          GGGCAT
           CC                   GGGAGGACCA     GTGCAGGG
                              ||||||||||     ||||||||
                              CCTTTTTGGT     TATGTCCT
                                    ATTTTC
GAM380  FLJ20019  3' CCCTGCGTAGCAGGTCCCCT   34345     A    AGG  A
                              GGG GGACC   GC TGTGCAGGG
                              ||| |||||   || |||||||||
                              TCC CCTGG   CG ATGCGTCCC
                                _    A__  _
GAM380  FLJ20034  3' CCCTGCATAAAAGGTCTCTCTT 34366      _   AGGGCA
                              GGGAG GACC     TGTGCAGGG
                              ||||| ||||     |||||||||
                              TTCTC CTGG     ATACGTCCC
                                 T    AAA___
GAM380  FLJ20034  3' TTTTGTAAGAATTTTGTCTTTC 34393        C   GCATG
           T                   GGGAGGAC AGG     TGCAGGG
                              |||||||| |||     |||||||
                              TCTTTCTG TTT     ATGTTTT
                                   T   AAGA_
GAM380  FLJ20045  3' TTGCACTGTTCTCCT      34434         CAGGGCAT
                              GGGAGGAC      GTGCAG
                              ||||||||      ||||||
                              TCCTCTTG      CACGTT
                                   T_______
GAM380  FLJ20069  3' TCTTGTACAAGCTTGTTTTTTT 34469   GG   CCA   A
           C                    G  AGGA   GGGC TGTGCAGGG
                              |  ||||   |||| |||||||||
                              C  TTTT   TTCG ACATGTTCT
                               TT   TG_   A
GAM380  FLJ20079  3' CACCTGCCTTGGCCTCCC    34489       A      T
                              GGGAGG CCAGGGCA GTG
                              |||||| |||||||| |||
                              CCCTCC GGTTCCGT CAC
                                 _      C
GAM380  FLJ20154  3' CCCTGTGCATATGAAGTCTTTC 72925         CAGGGC   TG
           T                    GGGAGGAC     ATG  CAGGG
                              ||||||||     |||  |||||
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                                TCTTTCTG     TAC  GTCCC
                                    AAGTA_   GT
GAM380  FLJ20189  3'  TCCTGTGTGTGAGATGTATTCC 34701      GAC  GGG    TG
          C                  GGGAG   CA   CATG  CAGGG
                             |||||   ||   ||||  |||||
                             CCCTT   GT   GTGT  GTCCT
                               AT_  AGA    GT
GAM380  FLJ20211  5'  CTCTGCAGCACTCCGGGTTCTC 34750         AG  CA  _
          CT                  GGGAGGACC  GG  TG TGCAGGG
                              |||||||||  ||  || |||||||
                              TCCTCTTGG  CC  AC ACGTCTC
                                   G_  TC  G
GAM380  FLJ20225  3'  CTTATTCCAATGTTCTTGGTTT 38806           _  GTGCAGGG
          TTCT                   GGAGGACCAGGG CAT
                                 ||||||||||||| |||
                                 CTTTTTGGTTCT GTA
                                       T   ACCTTATTCT
GAM380  FLJ20274  3'  TCTTGTTTATGTCTGTTTTTTT 62646         CA      T
                             GGGAGGAC  GGGCATG GCAGGG
                             ||||||||  ||||||| ||||||
                             TTTTTTTG  TCTGTAT TGTTCT
                                  __      T
GAM380  FLJ20276  3'  CCCACATTTGCCCTTGGTCTTC 34829          _    T   CA
          TC                   GGGAGGACCA GGGCA GTG  GGG
                               |||||||||| ||||| |||  |||
                               CTCTTCTGGT CCCGT TAC  CCC
                                    T    T   A_
GAM380  FLJ20331  3'  TTTTGTAGAACTGGTTTTTTT  34955          GGCATG
                             GGGAGGACCAG     TGCAGGG
                             ||||||||||      |||||||
                             TTTTTTTGGTC     ATGTTTT
                                   AAG___
GAM380  FLJ20344  3'  TTTTGCACTGTCCTGCTCTTTC 35020        C      T
          C                   GGGAGGA CAGGGCA GTGCAGGG
                              ||||||| ||||||| ||||||||
                              CCTTTCT GTCCTGT CACGTTTT
                                  C      _
GAM380  FLJ20359  3'  CCCTCCCAGCCCTGGGTCCTCC 35039          _    A  TGC
          C                   GGGAGGACC AGGGC TG   AGGG
                              ||||||||| ||||| ||   ||||
                              CCCTCCTGG TCCCG AC   TCCC
                                   G    _  CC_
GAM380  FLJ20514  3'  TTTTGCATATACTATACTGGTT 35338         ___  C
          TTTT                   AGGACCAG   GG ATGTGCAGGG
                                 ||||||||   || ||||||||||
                                 TTTTGGTC   TC TATACGTTTT
                                      ATA  A
GAM380  FLJ20548  3'  AAGGGTGCAGCTCTGGTTCTTC 35373            A  TG AGGG
          C                   GGGAGGACCAGGGC TG  C
                              |||||||||||||| ||  |
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                                CCTTCTTGGTCTCG AC  G
                                      _  GT GGAAG
GAM380  FLJ20625  3'  GCCCTGGGTTTTTACATGTTTG 35469      G     _______
              GTCTTTTT                CCAGG CATGTG     CAGGG   C
                                |||||  ||||||     |||||   |
                                GGTTT GTACAT     GTCCC   G
                                   _     TTTTGG
GAM380  FLJ20793  3'  TTTTGTGTGTGTTTTGCTTT   91809      AC       TG
                                GAGG  CAGGGCATG  CAGGG
                                ||||  |||||||||  |||||
                                TTTC  GTTTTGTGT  GTTTT
                                   __       GT
GAM380  FLJ20958  3'  CCTCCCGCCTTGGTCTCCC    42056      G       ATGTGC
                                GGGAG ACCAGGGC     AGG
                                |||||  ||||||||     |||
                                CCCTC TGGTTCCG     TCC
                                   _       CCC___
GAM380  FLJ21032  3'  CTTTGCACGTGAGGTGGGTCTC 46088      GA   GGG
              CT                  GGGAG  CCA   CATGTGCAGGG
                                |||||  |||   ||||||||||
                                TCCTC  GGT   GTGCACGTTTC
                                   TG   GGA
GAM380  FLJ21103  3'  TTTTGTACTCTATACTTGGTTT 44649          GCAT__
              TTC                  GGAGGACCAGG     GTGCAGGG
                                ||||||||||     ||||||||
                                CTTTTTGGTTC     CATGTTTT
                                      ATATCT
GAM380  FLJ21140  3'  TCTTGCATGTGCAATTCTCT   45482       CCAGG
                                GGAGGA    GCATGTGCAGGG
                                ||||||    ||||||||||||
                                TCTCTT    CGTGTACGTTCT
                                   AA___
GAM380  FLJ21148  3'  TTTTGAACTGTTTTGTCCTCTC 45861        C     T  G
                                GGGAGGAC AGGGCA GT CAGGG
                                |||||||| |||||| || |||||
                                CTCTCCTG TTTTGT CA GTTTT
                                      _     _ A
GAM380  FLJ21324  5'  TTTGATTCTTGGTTCTTT    91215          CATGTG
                                GGAGGACCAGGG     CAGG
                                ||||||||||||     ||||
                                TTTCTTGGTTCT     GTTT
                                      TA____
GAM380  FLJ21415  3'  CTTTGTAATTTTTTTGGTTCAC 45354     A       CATG
              TT                  GGG GGACCAGGG    TGCAGGG
                                |||  |||||||||   |||||||
                                TTC CTTGGTTTT    ATGTTTC
                                  A       TTTA
GAM380  FLJ21596  5'  TTCTGTACATGATTTCCTT    45708      CCAGGG
                                GAGGA     CATGTGCAGGG
                                |||||     ||||||||||
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                                TTCCT     GTACATGTCTT
                                  TTA___
GAM380  FLJ21919  3'  CCTTCAGGTCTTGGTTTGTTC  43456     AG       A  TGC
                                GGG  GACCAGGGC TG   AGG
                                |||  |||||||| ||   |||
                                CTT  TTGGTTCTG AC   TCC
                                  GT       G  T__
GAM380  FLJ21952  3'  TTCTGCATATGCCTTTGAATTC 42557      GACC
              CT                  GGGAG    AGGGCATGTGCAGGG
                                |||||    ||||||||||||||||
                                TCCTT    TTCCGTATACGTCTT
                                  AAGT
GAM380  FLJ22029  3'  TTTTGTTTTGGTGTTTGGTTTT 46334          G   GT__
              TTT                 GGAGGACCAGG CAT    GCAGGG
                                |||||||||| |||    ||||||
                                TTTTTTGGTTT GTG    TGTTTT
                                      _   GTTT
GAM380  FLJ22059  5'  CCCTGTGCAGTCGTGTCTTCCC 42768        C G   A  TG
                                GGGAGGAC A GGC TG  CAGGG
                                |||||||| | ||| ||  |||||
                                CCCTTCTG T CTG AC  GTCCC
                                     _ G   _  GT
GAM380  FLJ22167  3'  CCTGATTCTCGGTTTTCCT    44569         A   CATGTG
                                GGGAGGACC GGG     CAGG
                                |||||||| |||     ||||
                                TCCTTTTGG CTC     GTCC
                                     _   TTA___
GAM380  FLJ22318  3'  CTCTGTGCTCCTGCTGTCTTTT 42831    GG    __    CAT TG
              C                   G  AGGAC  CAGGG   G  CAGGG
                                |  |||||  |||||   |  |||||
                                C  TTCTG  GTCCT   C  GTCTC
                                 TT    TC    ___ GT
GAM380  FLJ22378  3'  TCTTGTCAGCCTCTGGTTCTCC 46909          _   A  T
              T                   GGGAGGACCAG GGC TG GCAGGG
                                |||||||||| ||| || ||||||
                                TCCTCTTGGTC CCG AC TGTTCT
                                      T  _ _
GAM380  FLJ22476  3'  TTTTGTGCGTGCTTTCACTCT  46777     GACC       TG
                                GGAG    AGGGCATG  CAGGG
                                ||||    ||||||||  |||||
                                TCTC    TTTCGTGC  GTTTT
                                  AC__       GT
GAM380  FLJ22529  3'  TCTGCCTGCCTTGGTCTCCC   45579      G       TGT
                                GGGAG ACCAGGGCA   GCAGG
                                ||||| |||||||||   |||||
                                CCCTC TGGTTCCGT   CGTCT
                                  _       C__
GAM380  FLJ22596  5'  CGTTCTTGGTCTTCTT      46962           CATGT  A
                                GGGAGGACCAGGG    GC G
                                ||||||||||||     || |
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                                TTCTTCTGGTTCT    TG C
                                      _____ A
GAM380  FLJ22709  3' CCTTGCATTTCTTGGTATCTCT 44718      _     CAT
          C                    GGGAGG ACCAGGG  GTGCAGGG
                               |||||| |||||||  ||||||||
                               CTCTCT TGGTTCT  TACGTTCC
                                  A     T__
GAM380  FLJ22724  3' CCTTGTGTATTTGATAGTCTTT 44564   GG   CAGGGC  TG
          TC                   G  AGGAC    ATG  CAGGG
                               |  |||||    |||  |||||
                               C  TTCTG    TAT  GTTCC
                                TT    ATAGTT  GT
GAM380  FLJ22814  3' TCCTGCACGGGCTCTGTTCTTT 46179      C     A
          T                    GGAGGA CAGGGC TGTGCAGGG
                               |||||| |||||| |||||||||
                               TTTTCT GTCTCG GCACGTCCT
                                  T     G
GAM380  FLJ22833  3' CTCTGCATTTGTTGCTTTGTTT 43103      C     T___
          TTTT                   GAGGAC AGGGCA   GTGCAGGG
                               |||||| ||||||   ||||||||
                               TTTTTG TTTCGT   TACGTCTC
                                  _     TGTT
GAM380  FLJ23024  3' TTTGCCTGCCTTGGCCTCCC  46278      A      TGT
                               GGGAGG CCAGGGCA  GCAGG
                               |||||| ||||||||  |||||
                               CCCTCC GGTTCCGT  CGTTT
                                  _      C__
GAM380  FLJ23112  3' CTTTGTGCAGGGAGCTCCTCTC 46248       CCAGGGCA  TG
                               GGGAGGA       TG  CAGGG
                               |||||||       ||  |||||
                               CTCTCCT       AC  GTTTC
                                   CGAGGG__  GT
GAM380  FLJ23132  3' TTTTGCATATGGTCTCTTACCT 96138    _   CCA  G
                               GGG AGGA   GG CATGTGCAGGG
                               ||| ||||   || ||||||||||
                               TCC TTCT   CT GTATACGTTTT
                                 A   ___  G
GAM380  FLJ23185  5' TCCTGCAACACTGTGTTTTTCC 46835       _  GGCATG
                               GGGAGGAC CAG     TGCAGGG
                               |||||||| |||     |||||||
                               CCTTTTTG GTC     ACGTCCT
                                    T   ACA___
GAM380  FLJ23416  3' ATGCTCTGGGTTTTCTC     49946        _
                               GGGAGGACC AGGGCAT
                               ||||||||| |||||||
                               CTCTTTTGG TCTCGTA
                                     G
GAM380  FLJ23548  3' TCCTGTGAAAAGCTGTTTTTCT 44749       CAG   ATG_
                               GGGAGGAC   GGC    TGCAGGG
                               ||||||||   |||    |||||||
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                                TCTTTTTG  TCG   GTGTCCT
                                    ___  AAAA
GAM380  FLJ23604  3'  TTGTACATGTCACCTC     46862     ACCAG
                                GAGG   GGCATGTGCAG
                                ||||    ||||||||||
                                CTCC    CTGTACATGTT
                                  A____
GAM380  FLJ25416  5'  CCTGGGCCCGTTCCTGGTCTTC 58805          _ AT  G   G
          TC                     GGGAGGACCAGGG C  GT CAGG
                                ||||||||||||| |  || ||||
                                CTCTTCTGGTCCT G  CG GTCC
                                       T CC  G
GAM380  FLJ31547  3'  TTCTGTGATTTTGGTTTCCC  58834      G     GCATG
                                GGGAG ACCAGG    TGCAGGG
                                ||||| ||||||    |||||||
                                CCCTT TGGTTT    GTGTCTT
                                  _     TA___
GAM380  FLJ31564  5'  TTCTGTTCCGTTTTGTCCTTTT 58530        C    ATGT
                                GGGAGGAC AGGGC   GCAGGG
                                |||||||| |||||   ||||||
                                TTTTCCTG TTTTG   TGTCTT
                                    _    CCT_
GAM380  FLJ31762  3'  TCTTGCGTGTGAATCTCTTACC 58146    _   CCAGGG  TG
          C                     GGG AGGA     CA  TGCAGGG
                                ||| ||||     ||  |||||||
                                CCC TTCT     GT  GCGTTCT
                                  A   CTAA__  GT
GAM380  FLJ32332  3'  CCTTGTGCAGTGAGTTCTCCT  58303        CAGG  A  TG
                                GGGAGGAC   GC TG  CAGGG
                                ||||||||   || ||  |||||
                                TCCTCTTG   TG AC  GTTCC
                                    AG__  _  GT
GAM380  FLJ32865  3'  TCTGAGATCTTGGTCTCCT   58187      G     CATGTG
                                GGGAG ACCAGGG     CAGG
                                ||||| |||||||     ||||
                                TCCTC TGGTTCT     GTCT
                                  _      AGA___
GAM380  FLJ32894  3'  TCTTGCCAACTCTGGTTTCCTC 58343     AG      CA  T
                                GGG  GACCAGGG  TG GCAGGG
                                |||  ||||||||  || ||||||
                                CTC  TTGGTCTC  AC CGTTCT
                                  CT       A_  _
GAM380  FLJ32926  3'  CCTGTTCTCTGGGCTTCCT   58021       A     CATGT
                                GGGAGG CCAGGG    GCAGG
                                |||||| ||||||    |||||
                                TCCTTC GGTCTC    TGTCC
                                   G     T____
GAM380  FLJ32926  3'  CCTTGTGGGTCTCTGTCTTTTT 58023        C   C  G
                                GGGAGGAC AGGG AT TGCAGGG
                                |||||||| |||| || |||||||
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                                TTTTTCTG TCTC TG GTGTTCC
                                    _   _ G
GAM380  FRAG1   3'  CCCTGGTATCTCCTGTCTTCCC 27169        C   CAT   _
                                GGGAGGAC AGGG  GTGC AGGG
                                |||||||| ||||  |||| ||||
                                CCCTTCTG TCCT  TATG TCCC
                                    _   C__   G
GAM380  FREQ    3'  CCTGCCCTTTGGCCTTTT    26573       A     CATGT
                                GGGAGG CCAGGG    GCAGG
                                |||||| ||||||    |||||
                                TTTTCC GGTTTC    CGTCC
                                   _    C____
GAM380  FREQ    3'  TCTTGCGCGTGTGCTTTTGTTT 26589       C__  G
            TTT                   GGAGGAC   AG GCATGTGCAGGG
                                |||||||  || ||||||||||||
                                TTTTTTG  TC TGTGCGCGTTCT
                                    TTT  G
GAM380  FUBP3   3'  TACAGTTTCTGGTTTTTTC   63733   GG       CA
                                G  AGGACCAGGG  TGTG
                                |  ||||||||||  ||||
                                C  TTTTGGTCTT  ACAT
                                 TT        TG
GAM380  FYCO1   3'  CCCTGTTCTCTGTGGTCCTTTT 44491         G  CATGT
                                GGGAGGACCA GG    GCAGGG
                                |||||||||| ||    ||||||
                                TTTTCCTGGT TC    TGTCCC
                                      G  TCT__
GAM380  GBTS1   3'  TTCTGTACCATGTGGGTCTCTC 59065      GA  AGG   _
                                GGGAG  CC   GCATG TGCAGGG
                                |||||  ||   ||||| |||||||
                                CTCTC  GG   TGTAC ATGTCTT
                                   TG  ___    C
GAM380  GCHFR   3'  CCGGTGCCCTGGTGCTCCC   17922      G       GTGCA
                                GGGAG ACCAGGGCAT    GG
                                ||||| ||||||||||    ||
                                CCCTC TGGTCCCGTG    CC
                                   G        G____
GAM380  GGA2    3'  CGCCTGCCTTGGCCTCCC    30463       A      T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTCC GGTTCCGT CGC
                                   _       C
GAM380  GGA2    3'  TCTTGTGTGTGTTCTGGAAGAT 30478    GGA_       TG
            CT                    GGA   CCAGGGCATG  CAGGG
                                |||   ||||||||||  |||||
                                TCT   GGTCTTGTGT  GTTCT
                                  AGAA        GT
GAM380  GGA2    3'  CGCCTGCCTTGGCCTCCC    56877       A      T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
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                                CCCTCC GGTTCCGT CGC
                                   _      C
GAM380  GGA2    3'  TCTTGTGTGTGTTCTGGAAGAT 56892    GGA_       TG
            CT                   GGA   CCAGGGCATG  CAGGG
                                 |||   ||||||||||  |||||
                                 TCT   GGTCTTGTGT  GTTCT
                                   AGAA        GT
GAM380  GMEB1   5'  CTCTGCGCATGCTCCGTCGCCT 21668    AG   CA
                                 GGG  GAC  GGGCATGTGCAGGG
                                 |||  |||  ||||||||||||||
                                 TCC  CTG  CTCGTACGCGTCTC
                                   G_   C_
GAM380  GMEB1   5'  CTCTGCGCATGCTCCGTCGCCT 44402    AG   CA
                                 GGG  GAC  GGGCATGTGCAGGG
                                 |||  |||  ||||||||||||||
                                 TCC  CTG  CTCGTACGCGTCTC
                                   G_   C_
GAM380  GMFB    3'  TTCTGTATCTTCTTTGGTTTCC 14673      G      CAT
            T                    GGGAG ACCAGGG   GTGCAGGG
                                 |||||| |||||||   ||||||||
                                 TCCTT TGGTTTC   TATGTCTT
                                   _      TTC
GAM380  GMPPB   5'  CACCTGCCTTGGCTTCCC    95723       A      T
                                 GGGAGG CCAGGGCA GTG
                                 |||||| |||||||| |||
                                 CCCTTC GGTTCCGT CAC
                                   _      C
GAM380  GOLGA1  3'  CCTGTTCCTTTGTCTTCTC   9089        C   CATGT
                                 GGGAGGAC AGGG    GCAGG
                                 |||||||| ||||    |||||
                                 CTCTTCTG TTCC    TGTCC
                                     T   T____
GAM380  GOLPH3  3'  TTCTGTTGACTTCTGGTTTTCT 42117          CATGT
                                 GGAGGACCAGGG    GCAGGG
                                 ||||||||||||    ||||||
                                 TCTTTTGGTCTT    TGTCTT
                                       CAGT_
GAM380  GPR88   3'  TTTTGTGCATGCACCATTTCTC 41883       CCA _    TG
            TC                   GGGAGGA   GG GCATG  CAGGG
                                 |||||||   || |||||  |||||
                                 CTCTCTT   CC CGTAC  GTTTT
                                    TA_  A    GT
GAM380  GRIN3A  3'  TTTTGTATATCGGGTTTACCT  55976    AG   AGGGC
                                 GGG  GACC    ATGTGCAGGG
                                 |||  ||||    ||||||||||
                                 TCC  TTGG    TATATGTTTT
                                   AT   GC___
GAM380  GRP3    3'  TTTTGTTTTGTTTTGTTCTTCT 31125       C      TGT
                                 GGAGGA CAGGGCA   GCAGGG
                                 ||||||  |||||||  ||||||
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                                TCTTCT GTTTTGT   TGTTTT
                                   T      TT_
GAM380  H       3'  TTCTGTCTCCTTGGTCC     54578          CATGT
                                GGACCAGGG     GCAGGG
                                |||||||||     ||||||
                                CCTGGTTCC     TGTCTT
                                   TC___
GAM380  H-plk   5'  TTAATTAGGTTTTTGGTTTTCT 31815            C  G  CAGGG
          T                     GGGAGGACCAGGG AT TG
                                |||||||||||| || ||
                                TTCTTTTGGTTTT TG AT
                                      _  G  TAATTT
GAM380  H-plk   5'  TTTTGTAAGTTCTTGTTTTTCT 31816         C     ATG
                                GGGAGGAC AGGGC   TGCAGGG
                                |||||||| |||||   |||||||
                                TCTTTTTG TCTTG   ATGTTTT
                                     T    A__
GAM380  H326    5'  TCTTAGCGCTCAGGTCTTTTC  31710   GG     A   ATGT  _
                                G  AGGACC GGGC    GC AGGG
                                |  |||||| ||||    || ||||
                                C  TTCTGG CTCG    CG TTCT
                                 TT     A    _____ A
GAM380  H326    3'  TTCTGCCCTTCCTGGTTCCCT  31712     A       CATGT
                                GGG GGACCAGGG    GCAGGG
                                ||| |||||||||    ||||||
                                TCC CTTGGTCCT    CGTCTT
                                  _       TCC__
GAM380  HCA4    3'  CCTGCCTCCTGGTCCCCT    77583     A       CATGT
                                GGG GGACCAGGG    GCAGG
                                ||| |||||||||    |||||
                                TCC CCTGGTCCT    CGTCC
                                  _       C____
GAM380  HEAB    5'  TTCTGCACGGGAGGACCTTCT  22415       A  AGGGCA
                                GGGAGG CC     TGTGCAGGG
                                |||||| ||     |||||||||
                                TCTTCC GG     GCACGTCTT
                                   A  AGG___
GAM380  HERC3   3'  CCCTGTGTCCTCCCTGATTTTC 27512        C    CAT TG
          CT                     GGGAGGA CAGGG   G  CAGGG
                                |||||||| |||||   |  |||||
                                TCCTTTT GTCCC   T  GTCCC
                                    A    TCC GT
GAM380  HERC3   3'  CCTTGTATGGGAGGTGTTTTT  27513      G   AGGGCA
                                GGGAG ACC     TGTGCAGGG
                                ||||| |||     |||||||||
                                TTTTT TGG     GTATGTTCC
                                   G   AGG___
GAM380  HEY1    3'  CCTTGTATAGTTATGGTCT   91250       GG  A
                                GGACCA  GC TGTGCAGGG
                                ||||||  || |||||||||
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                                TCTGGT  TG ATATGTTCC
                                   AT  _
GAM380  HGC6.1.1  3'  TCCTGCGTGGAAAGTCCTCTT  26831        CAGGG   GT
                                GGGAGGAC    CAT  GCAGGG
                                ||||||||    |||  ||||||
                                TTCTCCTG    GTG  CGTCCT
                                    AAAG_  __
GAM380  HN1L     3'  TCCTGCGCATGCAAGCCCTGCT 58005    G   ACCAGG
                                GG AGG     GCATGTGCAGGG
                                || |||     ||||||||||||
                                TC TCC     CGTACGCGTCCT
                                 G  CGAA__
GAM380  HOOK3    3'  CTTTGTATGAAAATGTCCTCTT 50548        CAGGG   GT
                                GGGAGGAC    CAT  GCAGGG
                                ||||||||    |||  ||||||
                                TTCTCCTG    GTA  TGTTTC
                                    TAAAA  __
GAM380  HRH4     3'  TTTGGTTATGTTTTGTCCTTTT 41259        C       TG
                                GGGAGGAC AGGGCATG  CAGG
                                |||||||| ||||||||  ||||
                                TTTTCCTG TTTTGTAT  GTTT
                                   _       TG
GAM380  HRI      3'  CCTCTGTCTGGTCTTCCT    26981         G    TGTGC
                                GGGAGGACCA GGCA    AGG
                                |||||||||| ||||    |||
                                TCCTTCTGGT CTGT    TCC
                                    _   C____
GAM380  HRMT1L3  3'  CTCTGTACTAGTTCTGGTCTCC 39073      G       AT
           T                     GGGAG ACCAGGGC  GTGCAGGG
                                ||||| ||||||||  ||||||||
                                TCCTC TGGTCTTG  CATGTCTC
                                   _       AT
GAM380  HSPC047  3'  CTCTGTATGGCCTGGTGTTTCC 26258      G     G   GT
                                GGGAG ACCAGG CAT  GCAGGG
                                ||||| |||||| |||  ||||||
                                CCTTT TGGTCC GTA  TGTCTC
                                   G     G  __
GAM380  HSPC065  3'  CTGGCCGTGCTCTGGGTCTTCC 26299         _      T  A  G
           C                     GGGAGGACC AGGGCATG GC GG
                                |||||||| |||||||| || ||
                                CCCTTCTGG TCTCGTGC CG TC
                                    G       _ G
GAM380  HSPC129  3'  CAAGCCTTGGTTCTCT      33069            A
                                GGAGGACCAGGGC TG
                                |||||||||||| ||
                                TCTCTTGGTTCCG AC
                                       A
GAM380  HSPC156  5'  CTTTGTGTGTGGAGTTTTCC   26355        CAGGG   TG
                                GGAGGAC    CATG  CAGGG
                                |||||||    ||||  |||||
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                                CCTTTTG    GTGT  GTTTC
                                    AG___    GT
GAM380  HT002    3'  CTCTGTAGGACCTGGTCCTGCC 25939    G       GCATG
                                GG AGGACCAGG    TGCAGGG
                                || |||||||||    |||||||
                                CC TCCTGGTCC    ATGTCTC
                                 G       AGG__
GAM380  HTCD37   3'  TTCTGCATGTGTAGAGTCTCCC 67682       ACCAGG
                                GGGAGG    GCATGTGCAGGG
                                ||||||    ||||||||||||
                                CCCTCT    TGTGTACGTCTT
                                   GAGA__
GAM380  HTR3A    3'  CTGTACGAGGCTTCTC      6026        A  AGGGCA
                                GGGAGG CC     TGTGCAG
                                |||||| ||     |||||||
                                CTCTTC GG     GCATGTC
                                   _ A_____
GAM380  HYA22    3'  CATCTCTTGGTCTTCTC     19420            C
                                GGGAGGACCAGGG ATG
                                |||||||||||| |||
                                CTCTTCTGGTTCT TAC
                                       C
GAM380  IBTK     5'  CCTTTGTGTCCTGGCTTTTT  67486       A        TGC
                                GGGAGG CCAGGGCATG   AGG
                                |||||| ||||||||||   |||
                                TTTTTC GGTCCTGTGT   TCC
                                   _        T__
GAM380  ITGB8    3'  CTTTGCCTTTATGTTTTGTTTT 9407        C       T__
            CTT                   GGAGGAC AGGGCATG   GCAGGG
                                |||||||| ||||||||   ||||||
                                TCTTTTG TTTTGTAT   CGTTTC
                                   _       TTC
GAM380  JAM1     3'  CCTCTGCCCTGTCCTCCT    57919        C     TGTGC
                                GGGAGGAC AGGGCA     AGG
                                |||||||| ||||||     |||
                                TCCTCCTG TCCCGT     TCC
                                   _      C____
GAM380  JAM1     3'  CGCCTGCCTTGGCCTCCC    57920       A       T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTCC GGTTCCGT CGC
                                   _       C
GAM380  JAM1     3'  TCCTGCCCCTTCCTGGTTCTT  57935          CATGT
                                GAGGACCAGGG    GCAGGG
                                ||||||||||     ||||||
                                TTCTTGGTCCT    CGTCCT
                                      TCCC_
GAM380  JAM1     3'  CCTCTGCCCTGTCCTCCT    57946        C     TGTGC
                                GGGAGGAC AGGGCA     AGG
                                |||||||| ||||||     |||
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                                TCCTCCTG TCCCGT    TCC
                                   _     C____
GAM380  JAM1    3' CGCCTGCCTTGGCCTCCC   57947      A      T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTCC GGTTCCGT CGC
                                   _      C
GAM380  JAM1    3' TCCTGCCCCTTCCTGGTTCTT 57959          CATGT
                                GAGGACCAGGG    GCAGGG
                                ||||||||||    ||||||
                                TTCTTGGTCCT    CGTCCT
                                      TCCC_
GAM380  JAM1    3' CCTCTGCCCTGTCCTCCT   57880       C    TGTGC
                                GGGAGGAC AGGGCA    AGG
                                |||||||| ||||||    |||
                                TCCTCCTG TCCCGT    TCC
                                   _     C____
GAM380  JAM1    3' CCTCTGCCCTGTCCTCCT   57891       C    TGTGC
                                GGGAGGAC AGGGCA    AGG
                                |||||||| ||||||    |||
                                TCCTCCTG TCCCGT    TCC
                                   _     C____
GAM380  JAM1    3' CGCCTGCCTTGGCCTCCC   57892      A      T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTCC GGTTCCGT CGC
                                   _      C
GAM380  JAM1    3' TCCTGCCCCTTCCTGGTTCTT 57904          CATGT
                                GAGGACCAGGG    GCAGGG
                                ||||||||||    ||||||
                                TTCTTGGTCCT    CGTCCT
                                      TCCC_
GAM380  JAM1    3' CCTCTGCCCTGTCCTCCT   33753       C    TGTGC
                                GGGAGGAC AGGGCA    AGG
                                |||||||| ||||||    |||
                                TCCTCCTG TCCCGT    TCC
                                   _     C____
GAM380  JAM1    3' CGCCTGCCTTGGCCTCCC   33754      A      T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTCC GGTTCCGT CGC
                                   _      C
GAM380  JAM1    3' TCCTGCCCCTTCCTGGTTCTT 33766          CATGT
                                GAGGACCAGGG    GCAGGG
                                ||||||||||    ||||||
                                TTCTTGGTCCT    CGTCCT
                                      TCCC_
GAM380  JM11    3' CTCTGCCTCCTGGGTTCTCCT 53256        A  CATGT
                                GGGAGGACC GGG    GCAGGG
                                ||||||||| |||    ||||||
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                                TCCTCTTGG TCC    CGTCTC
                                     G  TC___
GAM380  JM11    3'  TTCTGTGTCTTGTCTGTCTTTT 53273   GG    CA    T_ TG
            C                    G  AGGAC  GGGCA  G  CAGGG
                                 |  |||||  |||||  |  |||||
                                 C  TTCTG  TCTGT  T  GTCTT
                                  TT    __    TC GT
GAM380  KCNE4   3'  TTTTGCCTAGAGCTTTGTCCTT 54756        C    A_  T
            CT                    GGGAGGAC AGGGC  TG GCAGGG
                                 ||||||||  |||||  ||  ||||||
                                 TCTTCCTG TTTCG  AT CGTTTT
                                     _    AG  C
GAM380  KIAA0014 3' CCTGTCTTCTGTTTTCCC    27841        C    CATGT
                                 GGGAGGAC AGGG    GCAGG
                                 ||||||||  ||||    |||||
                                 CCCTTTTG TCTT    TGTCC
                                     _    C____
GAM380  KIAA0014 3' CTCTGCACACATGATCTTCCT  27842        C  GGGCA
                                 GGGAGGA CA    TGTGCAGGG
                                 |||||||  ||    |||||||||
                                 TCCTTCT GT    ACACGTCTC
                                     A  AC___
GAM380  KIAA0020 3' CTCTGTATATGTGTTTCTTCTT 29651        CC  G
                                 GGGAGGA  AG GCATGTGCAGGG
                                 |||||||  ||  ||||||||||||
                                 TTCTTCT  TT TGTATATGTCTC
                                     __  G
GAM380  KIAA0057 3' TGTTTTTGGTTTCTCCC    24445        _    _
                                 GGGAGGA CCAGGG CA
                                 |||||||  ||||||  ||
                                 CCCTCTT GGTTTT GT
                                     T    T
GAM380  KIAA0063 3' TCTGCACATGTATCTTC    29646      CCAGG
                                 GAGGA    GCATGTGCAGG
                                 |||||    ||||||||||
                                 CTTCT    TGTACACGTCT
                                    A____
GAM380  KIAA0090 3' TCTTGTATACAGTGTTTTCTT  88450        CAGG  A_
                                 GGGAGGAC   GC  TGTGCAGGG
                                 ||||||||   ||  |||||||||
                                 TTCTTTTG   TG  ATATGTTCT
                                      _____  AC
GAM380  KIAA0102 3' TCTTGTGTATGACAGCTTTCC  28567      ACCAGGG   TG
                                 GGGAGG     CATG  CAGGG
                                 ||||||     ||||  |||||
                                 CCTTTC     GTAT  GTTCT
                                    GACA___    GT
GAM380  KIAA0121 3' TCTGTGGCCTGTTTTTCC    72662       C    G ATGT
                                 GGAGGA CAGG C    GCAGG
                                 ||||||  ||||  |    |||||
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                                CCTTTT GTCC G    TGTCT
                                   T    G ____
GAM380  KIAA0125 3' CCTGGGCCCTGGTCCTTC    60506           ATGTG
                                GGAGGACCAGGGC     CAGG
                                ||||||||||||     ||||
                                CTTCCTGGTCCCG     GTCC
                                     G____
GAM380  KIAA0133 3' TCTGTGTTTGGTTCTC      28770         GGCAT TG
                                GAGGACCAG     G  CAGG
                                |||||||||     |  ||||
                                CTCTTGGTT     T  GTCT
                                     _____ GT
GAM380  KIAA0141 3' TATGCCTGGGTTTTCTC     28734          A
                                GGGAGGACC GGGCATG
                                ||||||||| |||||||
                                CTCTTTTGG TCCGTAT
                                      G
GAM380  KIAA0152 3' TGGGTATGCTTTGGGCTTTCT  28305       A         G
                                GGGAGG CCAGGGCATGT CA
                                |||||| |||||||||| ||
                                TCTTTC GGTTTCGTATG GT
                                   G          G
GAM380  KIAA0161 3' CTTTGTGTGTGTTTGACTTCT  28506       ACCA      TG
                                GGAGG    GGGCATG  CAGGG
                                |||||    |||||||  |||||
                                TCTTC    TTTGTGT  GTTTC
                                   AG__      GT
GAM380  KIAA0161 3' TTTTGCATGTGTAAAGCTTC   28517      ACCAGG
                                GAGG     GCATGTGCAGGG
                                ||||     ||||||||||||
                                CTTC     TGTGTACGTTTT
                                  GAAA__
GAM380  KIAA0173 3' CCCTGCCAGCAGCCCTAGGTCT 27668        _     A   __
           TCCT                   GAGGACC AGGGC TGT  GCAGGG
                                |||||||  |||||  |||  ||||||
                                CTTCTGG TCCCG ACG  CGTCCC
                                    A    _   AC
GAM380  KIAA0182 3' TTTTGTTTGTTGTTTTGGTTTT 72039             TGT_
           TTT                   GGGAGGACCAGGGCA    GCAGGG
                                |||||||||||||||    ||||||
                                TTTTTTTGGTTTTGT    TGTTTT
                                      TGTT
GAM380  KIAA0212 3' ATGCCTTTGTTTTTTT      27931         C
                                GGGAGGAC AGGGCAT
                                |||||||| |||||||
                                TTTTTTTG TTCCGTA
                                     T
GAM380  KIAA0218 3' CTCCTGTGTCCTGTCTTTCT   28618         C     ATGT
                                GGGAGGAC AGGGC    GCAGGG
                                |||||||| |||||    ||||||
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                                TCTTTCTG TCCTG    TGTCCT
                                   _    ____     CT
GAM380  KIAA0222 3' TTCTGCATTTTCTGGCTTTTGT 27685     C    AT____
            TTTCTT                GGAC AGGGC     GTGCAGGG
                                |||| |||||     ||||||||
                                TTTG TTTCG     TACGTCTT
                                  T    GTCTTT
GAM380  KIAA0226 3' TCCTGCAGCAGAGCTGGGTCCT 63524        AG   A_ _
            TCC                   GGAGGACC  GGC  TG TGCAGGG
                                |||||||| |||  || |||||||
                                CTTCCTGG  TCG  AC ACGTCCT
                                    G_   AG  G
GAM380  KIAA0229 3' CTCTGCGTGTGCAGCTCTC   92426      GACCAGG   TG
                                GGGAG      GCA  TGCAGGG
                                |||||      |||  |||||||
                                CTCTC      CGT  GCGTCTC
                                   GA_____   GT
GAM380  KIAA0232 3' CCTGTGTGGTGGTTTTGCT   72746    G     GG  ATGT
                                GG AGGACCA  GC    GCAGG
                                || |||||||  ||    |||||
                                TC TTTTGGT  TG    TGTCC
                                 G      GG  ____
GAM380  KIAA0240 3' TTTTGTGTGTGTTTTGTTGTT  92445    G   C      TG
                                GA GAC AGGGCATG  CAGGG
                                || ||| ||||||||  |||||
                                TT TTG TTTTGTGT  GTTTT
                                 G   _       GT
GAM380  KIAA0247 3' CCCACAGCAGTGCCCTTGTCTT 28392        C      G   A__
            CCT                   GGAGGAC AGGGCAT TGC   GGG
                                ||||||| ||||||| |||   |||
                                CCTTCTG TCCCGTG ACG   CCC
                                    T      _   ACA
GAM380  KIAA0247 3' CCCTGTGCTGCATGTCTGCTCC 28395      C    ___   T TG
            TCCC                  GAGGA CAGG   GCA G  CAGGG
                                ||||| ||||   ||| |  |||||
                                CTCCT GTCT   CGT C  GTCCC
                                   C    GTA   _ GT
GAM380  KIAA0258 3' CTTTGGCATTTATTTGGTTTTT 28814          GC_    G
            CT                    GGGAGGACCAGG   ATGT CAGGG
                                ||||||||||||   |||| |||||
                                TCTTTTTGGTTT   TACG GTTTC
                                       ATT    _
GAM380  KIAA0265 3' TCCTGTAAGCACCTGTTTTTCC 69883       C    _ ATG
                                GGAGGA CAGG GC   TGCAGGG
                                ||||||| |||| ||   |||||||
                                CCTTTT GTCC CG   ATGTCCT
                                   T    A  A__
GAM380  KIAA0265 3' TCTGTAAATTGGTTTTTC    69886          GGCATG
                                GGAGGACCAG     TGCAGGG
                                ||||||||||     ||||||
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                                CTTTTTGGTT     ATGTCT
                                     AA____
GAM380  KIAA0284  3'  CCCTGTGCGTGTGCGTCTCTGC 63116    G  _  CAGG    TG
            C                    GG AG GAC    GCATG  CAGGG
                                 || || |||    |||||  |||||
                                 CC TC CTG    TGTGC  GTCCC
                                  G  T   CG__     GT
GAM380  KIAA0293  3'  TTCTGCACCCCCCTGCTCCTCT 60610        C     CAT
            T                    GGGAGGA CAGGG   GTGCAGGG
                                 |||||||| |||||   ||||||||
                                 TTCTCCT GTCCC   CACGTCTT
                                     C     CC_
GAM380  KIAA0295  3'  CTCTGTGCCCTGGCCTCCC    68103        A      ATGT
                                 GGGAGG CCAGGGC    GCAGGG
                                 |||||| |||||||    ||||||
                                 CCCTCC GGTCCCG    TGTCTC
                                    _      _____
GAM380  KIAA0317  3'  CTTTGGCAATGCCTTGGCCTCC 29083        A        G  _
            T                    GGGAGG CCAGGGCAT TGC AGGG
                                 |||||| ||||||||| ||| ||||
                                 TCCTCC GGTTCCGTA ACG TTTC
                                    _        _  G
GAM380  KIAA0318  3'  CTTTGTATGTGTCGTGCATTC  68955     GAC  G
                                 GAG   CA GGCATGTGCAGGG
                                 |||   || ||||||||||||||
                                 CTT   GT CTGTGTATGTTTC
                                   AC_  G
GAM380  KIAA0321  5'  CCTCTGCCTTGGCCTTTC     62393    GG   A       TGTGC
                                 G  AGG CCAGGGCA     AGG
                                 |  ||| ||||||||     |||
                                 C  TCC GGTTCCGT     TCC
                                  TT   _       C_____
GAM380  KIAA0323  3'  CCCTGGGTGTCCTTGGTCCTGC 63261    G         C TG G
            C                    GG AGGACCAGGG A  T CAGGG
                                 || |||||||||| |  | |||||
                                 CC TCCTGGTTCC T  G GTCCC
                                  G         _ GT G
GAM380  KIAA0337  3'  TTCTGTTTGGTTTTGGTTTTGT 28839    G         ATGT
            T                    GG AGGACCAGGGC    GCAGGG
                                 || ||||||||||    ||||||
                                 TT TTTTGGTTTTG    TGTCTT
                                  G         GTT_
GAM380  KIAA0342  3'  GCCCTGTACATCTAGTTTTCTT 70619      ___  ___
            GGTTCTCCC               CCAGG   GC   ATGTGCAGGG   C
                                 |||||   ||   ||||||||||   |
                                 GGTTC   TG   TACATGTCCC   G
                                    TTT  ATC
GAM380  KIAA0355  3'  TATGTTCTCGTTTTTCT     28032         C
                                 GGGAGGAC AGGGCATG
                                 |||||||| ||||||||
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                                TCTTTTTG TCTTGTAT
                                     C
GAM380  KIAA0375 3' CCCTGTGCATGCTGGTGGCCTC 71020     A  G_    TG
                                GAGG CCA  GGCATG  CAGGG
                                |||| |||  ||||||  |||||
                                CTCC GGT  TCGTAC  GTCCC
                                  _  GG     GT
GAM380  KIAA0408 3' ATGTTCTGTTTTCTC      28133        C
                                GGGAGGAC AGGGCAT
                                |||||||| |||||||
                                CTCTTTTG TCTTGTA
                                     _
GAM380  KIAA0416 3' ATGTCCTGTTCTTTTT      31464        C
                                GGGAGGA CAGGGCAT
                                ||||||| ||||||||
                                TTTTTCT GTCCTGTA
                                     T
GAM380  KIAA0417 3' CCTGTGTACTGTTTCTCTT    71243       C  GGCA  TG
                                GGGAGGA CAG   TG  CAGG
                                ||||||| |||   ||  ||||
                                TTCTCTT GTC   AT  GTCC
                                     T  ____  GT
GAM380  KIAA0429 5' CTCTGTGTGTGCCCTTCCCC  28555    A  CC      TG
                                GG GGA  AGGGCATG  CAGGG
                                || |||  ||||||||  |||||
                                CC CCT  TCCCGTGT  GTCTC
                                  _  __       GT
GAM380  KIAA0429 5' CTGTGTATATGTCTGTCT    28556     CA        G
                                GGAC  GGGCATGTGCA GG
                                ||||  |||||||||| ||
                                TCTG  TCTGTATATGT TC
                                   __         G
GAM380  KIAA0435 3' GTGTTCAGGTTTTCCT      28981         A
                                GGGAGGACC GGGCAT
                                ||||||||| ||||||
                                TCCTTTTGG CTTGTG
                                     A
GAM380  KIAA0436 3' TCCTAATGTGTTCTGGTCATCC 60058     G          GC
          C                      GGGA GACCAGGGCATGT  AGGG
                                |||| ||||||||||||  ||||
                                CCCT CTGGTCTTGTGTA  TCCT
                                  A          A_
GAM380  KIAA0444 3' CTGTGTGTATGTTTTGGTTTTC 62341             TG  G
          T                      GGAGGACCAGGGCATG  CA GG
                                |||||||||||||||  || ||
                                TCTTTTGGTTTTGTAT  GT TC
                                          GT  G  T
GAM380  KIAA0444 3' CTGTGTGTATGTTTTGGTTTTC 62342             TG  G
          T                      GGAGGACCAGGGCATG  CA GG
                                |||||||||||||||  || ||
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                                TCTTTTGGTTTTGTAT  GT TC
                                          GT  G  T
GAM380  KIAA0450 3' TTTGTGCGGCGCTCCTCCT   27659       CCA G  A  TG
                                GGGAGGA   G GC TG  CAGG
                                |||||||   | || ||  ||||
                                TCCTCCT   C CG GC  GTTT
                                   ___ G  _  GT
GAM380  KIAA0469 3' TCTGGGTTCCTGTTTTCTC   29358       C    CATG G
                                GGGAGGAC AGGG    T CAGG
                                |||||||| ||||    | ||||
                                CTCTTTTG TCCT    G GTCT
                                     _    T___ G
GAM380  KIAA0470 3' TCTTGGAATCCCTGTCTTCTT  29056       C    C  GTG
                                GGGAGGAC AGGG AT   CAGGG
                                |||||||| |||| ||   |||||
                                TTCTTCTG TCCC TA   GTTCT
                                     _    _ AG_
GAM380  KIAA0471 3' ATGCCTTGGTTTTGTT     29384    G
                                GG AGGACCAGGGCAT
                                || ||||||||||||
                                TT TTTTGGTTCCGTA
                                 G
GAM380  KIAA0472 3' TTCTGTGTGTGCCCCTCACCCC 71873     AG  CCA      TG
                                GGG  GA   GGGCATG  CAGGG
                                |||  ||   |||||||  |||||
                                CCC  CT   CCCGTGT  GTCTT
                                  CA  C__      GT
GAM380  KIAA0475 3' CTTTGCAATCTCTTTGTCTTTT 29491        C    CATG
           T                     GGGAGGAC AGGG    TGCAGGG
                                 |||||||| ||||    |||||||
                                 TTTTTCTG TTCT    ACGTTTC
                                      T   CTA_
GAM380  KIAA0515 3' TCCTGCCCTCACCTGGTCTTTT 63815    GG       GCATGT
           C                     G  AGGACCAGG     GCAGGG
                                 |  |||||||||     ||||||
                                 C  TTCTGGTCC     CGTCCT
                                 TT       ACTCC_
GAM380  KIAA0515 3' TTTTGTTTATGTTTTGGCCTTT 63820    GG   A        T
           C                     G  AGG CCAGGGCATG GCAGGG
                                 |  ||| |||||||||| ||||||
                                 C  TCC GGTTTTGTAT TGTTTT
                                 TT  _        T
GAM380  KIAA0522 3' CTTTGCTTCCTCGGTTTTTTC  71968    GG     AG  CATGT
                                 G  AGGACC  GG    GCAGGG
                                 |  ||||||  ||    ||||||
                                 C  TTTTGG  CC    CGTTTC
                                 TT     CT  TT___
GAM380  KIAA0534 3' CTTTGAATCTGTTGGTTTTTCC 71429         GG   T  G
                                 GGGAGGACCA  GCA GT CAGGG
                                 ||||||||||  ||| || |||||
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                                CCTTTTTGGT  TGT TA GTTTC
                                      __  C  A
GAM380  KIAA0546 3' TCTGCATGTGCCATATCC    71313     CCAG
                                GGA   GGCATGTGCAGG
                                |||   ||||||||||||
                                CCT   CCGTGTACGTCT
                                  ATA_
GAM380  KIAA0561 3' CTTGTGCAATGTTTTTTCC   65883       CCAG    _ TG
                                GGAGGA   GGCAT G  CAGG
                                ||||||   ||||| |  ||||
                                CCTTTT   TTGTA C  GTTC
                                    ____    A GT
GAM380  KIAA0633 3' CTTTGTATGATATCGTGGTCTT 94053          G GC  _
           CTC                    GGGAGGACCA G  AT GTGCAGGG
                                ||||||||||  |  || ||||||||
                                CTCTTCTGGT C  TA TATGTTTC
                                      G TA  G
GAM380  KIAA0644 3' TGTGCTCCTGGCTTTTTTC   29068   GG   _    _
                                G  AGGA CCAGG GCATG
                                |  |||| ||||| |||||
                                C  TTTT GGTCC CGTGT
                                 TT   C    T
GAM380  KIAA0669 3' CCTTGTGTGCCACTGGTGTTCT 28786      G    _    GT
           T                     GGGAG ACCAG GGCAT  GCAGGG
                                ||||| ||||| |||||  ||||||
                                TTCTT TGGTC CCGTG  TGTTCC
                                   G    A   __
GAM380  KIAA0673 3' CCTGCAGGCTGTCCTCCC    62269        CAG   ATG
                                GGGAGGAC   GGC   TGCAGG
                                ||||||||   |||   ||||||
                                CCCTCCTG   TCG   ACGTCC
                                    ___   G__
GAM380  KIAA0682 3' TCTGCCCGCTTGTTTTTCC   29374        C  _  CATGT
                                GGGAGGAC AG GG    GCAGG
                                |||||||| || ||    |||||
                                CCTTTTTG TC CC    CGTCT
                                     T  G  _____
GAM380  KIAA0700 3' CTTTGTACACATCCTGGTTTTC 72056           CA
           T                     GGAGGACCAGGG  TGTGCAGGG
                                ||||||||||||  |||||||||
                                TCTTTTGGTCCT  ACATGTTTC
                                      AC
GAM380  KIAA0757 3' CCCTGTTCAGTTGGTTCTTTT  20128          GG  A  T
                                GGGAGGACCA  GC TG GCAGGG
                                ||||||||||  || || ||||||
                                TTTTCTTGGT  TG AC TGTCCC
                                      __  _  T
GAM380  KIAA0775 3' CCCTGCAGGCCAGTCCTGTCCT 28278       C    A  ___
           CCT                    GAGGAC AGGGC TG   TGCAGGG
                                ||||||  |||||  ||   |||||||
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                                CTCCTG TCCTG AC   ACGTCCC
                                   _    _ CGG
GAM380  KIAA0794 3' TTTTCAGATGTCTTGGGCTTTT 80419       A       G  CAGGG
              T                  GGGAGG CCAGGGCAT TG
                                 |||||| ||||||||| ||
                                 TTTTTC GGTTCTGTA AC
                                    G        G  TTTT
GAM380  KIAA0828 3' TTTTGTATTAATTGGTTCCCT  81207     A      GGCAT
                                 GGG GGACCAG     GTGCAGGG
                                 ||| |||||||     ||||||||
                                 TCC CTTGGTT     TATGTTTT
                                   _      AAT__
GAM380  KIAA0831 3' CGCTTGCCTTGGCCTCCT     29970       A       T
                                 GGGAGG CCAGGGCA GTG
                                 |||||| |||||||| |||
                                 TCCTCC GGTTCCGT CGC
                                    _       T
GAM380  KIAA0841 3' CCTGGACCCTGTCCTTTC     71381    GG    C    CATG G
                                 G  AGGAC AGGG    T CAGG
                                 |  ||||| ||||    | ||||
                                 C  TCCTG TCCC    A GTCC
                                  TT    _   _____ G
GAM380  KIAA0876 3' CCAGTGCCCTGGTTTTTCC    64676              GTGCA
                                 GGGAGGACCAGGGCAT     GG
                                 ||||||||||||||||    ||
                                 CCTTTTTGGTCCCGTG     CC
                                             A_____
GAM380  KIAA0894 3' TCAAGCTGTGCTTTGTTTTCTT 29707         C       T  AGGG
                                 GGGAGGAC AGGGCATG GC
                                 |||||||| |||||||| ||
                                 TTCTTTTG TTTCGTGT CG
                                    _       _ AACTT
GAM380  KIAA0894 3' TCTGTGCATGGTGCTCTC     29708       G    GGGCA  TG
                                 GGGAG ACCA     TG  CAGG
                                 ||||| ||||     ||  ||||
                                 CTCTC TGGT     AC  GTCT
                                    G    ______  GT
GAM380  KIAA0939 3' TCCTGCGTGTGTATTTATTTTC 62020       CCAGG   TG
              T                  GGAGGA    GCA  TGCAGGG
                                 ||||||    |||  |||||||
                                 TCTTTT    TGT  GCGTCCT
                                    ATTTA   GT
GAM380  KIAA0945 3' TTTTGTGTGTTGATCCTGGTTT 30221      G      _ _  TG
              CCC                   GGAG ACCAGGG CA TG  CAGGG
                                 |||| ||||||| || ||  |||||
                                 CCTT TGGTCCT GT GT  GTTTT
                                    _      A  T  GT
GAM380  KIAA0978 3' CCCTGTGTGTGTTTTCCCTTGC 70479    _   ACC       TG
              C                  GG GAGG   AGGGCATG  CAGGG
                                 || ||||   ||||||||  |||||
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                              CC TTCC   TTTTGTGT  GTCCC
                               G   C__      GT
GAM380  KIAA0981 3' TCCTGTTGATTTTGTTTTCCT  61425        C   G  TGT
                              GGGAGGAC AGG CA   GCAGGG
                              |||||||| ||| ||   ||||||
                              TCCTTTTG TTT GT   TGTCCT
                                   T   A  ___
GAM380  KIAA0982 3' TCTTGTATATTCAGTCCTTTC  25850   GG    CAG  C
                              G  AGGAC   GG ATGTGCAGGG
                              |  |||||   || ||||||||||
                              C  TCCTG   CT TATATGTTCT
                               TT    A__ _
GAM380  KIAA0993 3' TGTGTTCTGTTTTCCT      64149        C
                              GGGAGGAC AGGGCATG
                              |||||||| ||||||||
                              TCCTTTTG TCTTGTGT

                                   _
GAM380  KIAA1028 3' CCCTGCACTGGTACTGGCTCTT 91935      GA    GG AT
           TT                  GGGAG  CCAG  C  GTGCAGGG
                              |||||  ||||  |  ||||||||
                              TTTTC  GGTC  G  CACGTCCC
                                 TC    AT GT
GAM380  KIAA1030 3' GCTTTGCATGTGTGCCCTCTTG 93336     ___     __
           GTCTTGCT              ACCA   GGGCAT  GTGCAGGG   C
                              ||||   ||||||  ||||||||  |
                              TGGT   CCCGTG  TACGTTTC   G
                                TCT     TG
GAM380  KIAA1034 3' TTTTATGTCTGTTTTGTTTTTC 62476       CA___      TGCAGGG
           T                   GGAGGAC    GGGCATG
                              |||||||    |||||||
                              CTTTTTG    TCTGTAT
                                  TTTTG      TTT   G
GAM380  KIAA1042 3' CCTTGTGTCCGCCCTGCTCTTT 30335       C     AT TG
           CT                    GGGAGGA CAGGGC  G  CAGGG
                              |||||||  ||||||  |  |||||
                              TCTTTCT GTCCCG  T  GTTCC
                                  C     CC GT
GAM380  KIAA1052 3' CTCTGCAGGCACTGTGTTTTCC 30249        _  G  ATG
           T                   GGGAGGAC CAG GC   TGCAGGG
                              |||||||| ||| ||   |||||||
                              TCCTTTTG GTC CG   ACGTCTC
                                   T   A  G__
GAM380  KIAA1102 3' TCCTGTTTATTGTTTTGGTTTT 69016            TGT_
           TTT                   GGGAGGACCAGGGCA    GCAGGG
                              ||||||||||||||||    ||||||
                              TTTTTTTGGTTTTGT    TGTCCT
                                        TATT
GAM380  KIAA1110 3' GTCCTTGCTGCCCTGGCCCTCC 61850       A       TGT
           T                   GGGAGG CCAGGGCA   GCAGGG
                              ||||||  ||||||||   ||||||
```

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                                TCCTCC GGTCCCGT   CGTTCC
                                   C       ___      TGT
GAM380  KIAA1117 3' CTCTGCGTTGTATAGTTTTTCC 61119        CAGG   TGT
                                GGGAGGAC   GCA   GCAGGG
                                ||||||||   |||   ||||||
                                CCTTTTTG   TGT   CGTCTC
                                    ATA_   TG_
GAM380  KIAA1157 3' CCCTGCATGACAGAGGGTCTTT 72240        AGGGCAT
                                GAGGACC      GTGCAGGG
                                |||||||      ||||||||
                                TTTCTGG      TACGTCCC
                                   GAGACAG
GAM380  KIAA1193 3' TGACCTTGTGTTCTCCC     67653         _    _
                                GGGAGGAC CAGGG CA
                                |||||||| ||||| ||
                                CCCTCTTG GTTCC GT
                                    T     A
GAM380  KIAA1196 3' TCCTGTGTGACCGTTGGCCCTC 61480       A   _ _   GT
           CT                    GGGAGG CCAG GG CAT  GCAGGG
                                ||||||| |||| || |||  ||||||
                                TCCTCC GGTT CC GTG  TGTCCT
                                   C   G  A   __
GAM380  KIAA1198 3' CACCTGCCTTGGCCTCCC    63292       A       T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTCC GGTTCCGT CAC
                                   _       C
GAM380  KIAA1209 3' CTTTGCACATGCACCCTCCT   60755       ACCAGG
                                GGGAGG     GCATGTGCAGGG
                                ||||||     ||||||||||||
                                TCCTCC     CGTACACGTTTC
                                   CA____
GAM380  KIAA1238 3' TTTGTTAGTGTTTTAGTCTTTT 71084        C      GT    G
           T                     GGGAGGAC AGGGCAT  GCAGG
                                |||||||| |||||||  |||||
                                TTTTTCTG TTTTGTG  TGTTT
                                    A      AT
GAM380  KIAA1257 3' GCAGAAGCGCGTGCGTTGGTCT 62742    GG       G       AGGG
           TTTC                    G  AGGACCAG GCATGTGC
                                |  |||||||| ||||||||
                                C  TTCTGGTT CGTGCGCG
                                 TT       G       AAGACGT
GAM380  KIAA1265 3' CCCTGCACGTAGGGGTCTTTT  70788        AGGGC
                                GGAGGACC    ATGTGCAGGG
                                ||||||||    ||||||||||
                                TTTTCTGG    TGCACGTCCC
                                    GGA__
GAM380  KIAA1265 3' TAGGTGCCCTGTTCTCCT    70793        C      G
                                GGGAGGAC AGGGCAT TG
                                |||||||| ||||||| ||
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                                TCCTCTTG TCCCGTG AT
                                   _     G
GAM380  KIAA1297 3' TCCTGTGTATGTGGTGACTTCC 72187     G_  AGG    TG
                                GGGAG  ACC   GCATG  CAGGG
                                |||||  |||   |||||  |||||
                                CCTTC  TGG   TGTAT  GTCCT
                                  AG   ___     GT
GAM380  KIAA1300 5' CTTTAGATGGCCCTGTCTTCTC 62863       C    _ G  C
                                GGGAGGAC AGGGC AT TG AG
                                |||||||| ||||| || || ||
                                CTCTTCTG TCCCG TA AT TC
                                   _    G  G  T
GAM380  KIAA1321 3' CCTTGATCTTTTTGGTTTTACT 62225    G       CATGTG
                                GG AGGACCAGGG     CAGGG
                                || ||||||||||     |||||
                                TC TTTTGGTTTT     GTTCC
                                 A        TCTA__
GAM380  KIAA1337 3' CCCTGTGGCCCTCCCTGGGCCT 72679      A     CAT _
           TTT                   GGGAGG CCAGGG   GT GCAGGG
                                |||||| ||||||   || ||||||
                                TTTTCC GGTCCC   CG TGTCCC
                                   G     TCC  G
GAM380  KIAA1354 3' TTTTGTGCAGAAAATTTAGGTT 60918      _  GCA__  TG
           CTTTT                  AGGACC AGG    TG  CAGGG
                                |||||| |||    ||  |||||
                                TCTTGG TTT    AC  GTTTT
                                   A   AAAAG  GT
GAM380  KIAA1364 3' CTCTGTGTGTCTCGGTTTCTTC 63592       _ AG    GT
           T                    GGGAGGA CC  GGCAT  GCAGGG
                                ||||||| ||  |||||  ||||||
                                TCTTCTT GG  CTGTG  TGTCTC
                                   T  CT    __
GAM380  KIAA1371 3' TTTAAGACAGTGTTTGGGTTCT 89050   GG    AG   _  GCAGGG
           TTC                    G  AGGACC  GGCA TGT
                                |  ||||||  |||| |||
                                C  TCTTGG  TTGT ACA
                                 TT     GT   G  GAATTTT
GAM380  KIAA1399 3' CTTTGTGCTCCCTGCTCCTTCC 70250       C    CAT TG
                                GGGAGGA CAGGG   G  CAGGG
                                |||||||  |||||   |  |||||
                                CCTTCCT GTCCC   C  GTTTC
                                   C    T__ GT
GAM380  KIAA1416 3' CTTACATAATGCTCTGCTTTTT 86459       C      _  C  G
           TT                     GGGAGGA CAGGGCAT GTG AGG
                                ||||||| |||||||| ||| |||
                                TTTTTTT GTCTCGTA TAC TTC
                                   C       A  A
GAM380  KIAA1434 3' TCCTGCTCCTTTGCTCCTCTC  69621       C    CATGT
                                GGGAGGA CAGGG    GCAGGG
                                ||||||| |||||    ||||||
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                              CTCTCCT GTTTC    CGTCCT
                                  C    CT___
GAM380  KIAA1437 3' CCCTGTCACCACCTGGTCCTTC 60583         GCAT  _
                              GGAGGACCAGG   GTG CAGGG
                              ||||||||||    ||| |||||
                              CTTCCTGGTCC   CAC GTCCC
                                   AC__  T
GAM380  KIAA1437 3' GTGTCTTGTTTTCTT      60591        C
                              GGGAGGAC AGGGCAT
                              |||||||| |||||||
                              TTCTTTTG TTCTGTG
                                  _
GAM380  KIAA1456 3' CTTTGTATGAAAGGGTTCTCT  66996       AGGG  GT
                              GGAGGACC   CAT  GCAGGG
                              ||||||||   |||  ||||||
                              TCTCTTGG   GTA  TGTTTC
                                   GAAA  __
GAM380  KIAA1456 3' TCTTGGAGTTTGGTTTGGTTCT 67007         G  TG G_
           CTT                  GGGAGGACCAGG CA  T  CAGGG
                              |||||||||||| ||  |  |||||
                              TTCTCTTGGTTT GT  G  GTTCT
                                    G  TT AG
GAM380  KIAA1462 3' TTTTGTATTTGTCTTTGTTCTT 91394       C     T
           CT                   GGGAGGAC AGGGCA GTGCAGGG
                              |||||||| |||||| ||||||||
                              TCTTCTTG TTCTGT TATGTTTT
                                   T     T
GAM380  KIAA1464 3' TTTGCATTGGGTTTTCCT    68280        AGGGCAT
                              GGGAGGACC      GTGCAGG
                              |||||||||      |||||||
                              TCCTTTTGG      TACGTTT
                                   GT_____
GAM380  KIAA1493 3' TTCTGTAATATTGAGTCTTTTT 64169       _  GGCATG
                              GGGAGGAC CAG     TGCAGGG
                              |||||||| |||     |||||||
                              TTTTTCTG GTT     ATGTCTT
                                   A   ATA___
GAM380  KIAA1500 3' CCTTGTGTGTGTTTTACTAACC 64118    GA  ACC      TG
                              GG  GG   AGGGCATG  CAGGG
                              ||  ||   ||||||||  |||||
                              CC  TC   TTTTGTGT  GTTCC
                                AA  A__       GT
GAM380  KIAA1538 3' CTTTGTGTGAGATGTAGTTTTC 71545       __ GGG  GT
           CC                   GGGAGGAC  CA   CAT  GCAGGG
                              ||||||||  ||   |||  ||||||
                              CCCTTTTG  GT   GTG  TGTTTC
                                   AT  AGA  __
GAM380  KIAA1546 3' CTTTGTAAGCTGGCTTTTGTCT 67906       C    ATG__
           TTTT                 GGAGGAC AGGGC    TGCAGGG
                              ||||||| |||||    |||||||
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                                TTTTCTG TTTCG    ATGTTTC
                                    T    GTCGA
GAM380  KIAA1554 3' CAGGGCCTTGGTTTTCTC    95147           A_
                                GGGAGGACCAGGGC  TG
                                |||||||||||||  ||
                                CTCTTTTGGTTCCG  AC
                                      GG
GAM380  KIAA1554 3' TTGTGCTGCTTTTCTC     95158      CCA    T TG
                                GAGGA   GGGCA G  CAG
                                |||||   ||||| |  |||
                                CTCTT   TTCGT C  GTT
                                   ____    _ GT
GAM380  KIAA1557 3' GAAGGTATTTTTTGGTTTTCCT 61135          CAT    AGGG
                                GGGAGGACCAGGG   GTGC
                                ||||||||||||   ||||
                                TCCTTTTGGTTTT   TATG
                                      T__   GAAGT
GAM380  KIAA1559 3' TTTTGTATGTGTTTGAAATTTC 73080     GACCA
                                GGAG    GGGCATGTGCAGGG
                                ||||    ||||||||||||||
                                CTTT    TTTGTGTATGTTTT
                                  AAAG_
GAM380  KIAA1598 3' TCCTAGTAGGTTTTGGTTTTTT 37080          ATG  _
                                GGAGGACCAGGGC   TGC AGGG
                                ||||||||||||   ||| ||||
                                TTTTTTGGTTTTG   ATG TCCT
                                      G__   A
GAM380  KIAA1615 3' CTTTGTGTGTGTTTTTTTCCTT 68711       CC      TG
           CC                  GGGAGGA  AGGGCATG  CAGGG
                                |||||||  ||||||||  |||||
                                CCTTCCT  TTTTGTGT  GTTTC
                                    TT      GT
GAM380  KIAA1635 3' ATTGCCAGTTTTGGTTCTCCT  67860          A  T   GG
                                GGGAGGACCAGGGC TG GCAG
                                |||||||||||||| || ||||
                                TCCTCTTGGTTTTG AC CGTT
                                      _ _   AT
GAM380  KIAA1641 5' CATGTTCTGATTCTTTC    80207   GG   C
                                G  AGGA CAGGGCATG
                                |  |||| |||||||||
                                C  TCTT GTCTTGTAC
                                 TT   A
GAM380  KIAA1656 3' CTCTGCCTGCCCTGTCCTTCC  65792       C     TGT
                                GGGAGGAC AGGGCA   GCAGGG
                                |||||||| ||||||   ||||||
                                CCTTCCTG TCCCGT   CGTCTC
                                    _     C__
GAM380  KIAA1656 3' CCTGTGGCTGGTTCCCT    65789    A     GGCATGT
                                GGG GGACCAG     GCAGG
                                ||| |||||||     |||||
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                                TCC CTTGGTC      TGTCC
                                  _      GG_____
GAM380  KIAA1668 3' TCTGAGTCTCTGTCTTCCT   66483        C   CATGTG
                                GGGAGGAC AGGG     CAGG
                                |||||||| ||||     ||||
                                TCCTTCTG TCTC     GTCT
                                    _   TGA___
GAM380  KIAA1671 3' TTTTGTTTTGTTTTGTTTTTCT 65702       C      TGT
                                GGAGGA CAGGGCA   GCAGGG
                                |||||| |||||||   ||||||
                                TCTTTT GTTTTGT   TGTTTT
                                   T      TT_
GAM380  KIAA1677 3' CCTTAAATTCTTTGGTTTTCTT 67065           C  GTGC
                                GGGAGGACCAGGG AT    AGG
                                |||||||||||| ||    |||
                                TTCTTTTGGTTTC TA    TCC
                                       T  AAT_
GAM380  KIAA1728 3' TTCTGTGTTATGGTTCTT    68420        GG  ATGT
                                GAGGACCA  GC    GCAGGG
                                ||||||||  ||    ||||||
                                TTCTTGGT  TG    TGTCTT
                                    AT  ____
GAM380  KIAA1808 3' CTTTGTGTGTGTCCCGATGTTC 85863      GACCA      TG
           CT                    GGGAG    GGGCATG  CAGGG
                                |||||    |||||||  |||||
                                TCCTT    CCTGTGT  GTTTC
                                   GTAGC      GT
GAM380  KIAA1811 3' CCCTCCTCCCCTGGTCCTCCC  64794           CATGTGC
                                GGGAGGACCAGGG      AGGG
                                ||||||||||||      ||||
                                CCCTCCTGGTCCC      TCCC
                                       CTCC___
GAM380  KIAA1819 5' TTTTGTTTTGTTTTGGTTTTTT 69682            TGT
                                GGAGGACCAGGGCA   GCAGGG
                                ||||||||||||||   ||||||
                                TTTTTTGGTTTTGT   TGTTTT
                                       TT_
GAM380  KIAA1831 3' TTCTGTGCTCCTTTGTTTTTTT 63787        C   CAT TG
                                GGGAGGAC AGGG   G  CAGGG
                                |||||||| ||||   |  |||||
                                TTTTTTTG TTCC   C  GTCTT
                                    T   T__ GT
GAM380  KIAA1878 3' TCCTGAACCGCTCTGGTCTGCT 91716     A        AT  G
           C                     GGG GGACCAGGGC  GT CAGGG
                                ||| ||||||||||  || |||||
                                CTC TCTGGTCTCG  CA GTCCT
                                  G        C_  A
GAM380  KIAA1881 3' CTTAGATGCCCTGGTTTGTCC  95340     AG         G  C
                                GGG  GACCAGGGCAT TG AG
                                |||  |||||||||| || ||
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                              CCT  TTGGTCCCGTA AT TC
                                GT         G  _
GAM380  KIAA1884  3'  CTCTGTATATGAGGCTTCCC   73336       A  AGGG
                              GGGAGG CC    CATGTGCAGGG
                              |||||| ||    ||||||||||
                              CCCTTC GG    GTATATGTCTC
                                 _  A___
GAM380  KIAA1884  3'  TCCTGCATTATGGTACTTTCC  73341       _   GGGCAT
                              GGGAGG ACCA     GTGCAGGG
                              |||||| ||||     ||||||||
                              CCTTTC TGGT     TACGTCCT
                                 A    AT____
GAM380  KIAA1894  3'  CCTTGCTTCAATATGGTTTTTT 73842    GG      GGGCATGT
              C                   G  AGGACCA       GCAGGG
                              |  |||||||       ||||||
                              C  TTTTGGT       CGTTCC
                               TT      ATAACTT_
GAM380  KIAA1922  5'  CGCCTGCCTTGGCCTCCC    73624       A       T
                              GGGAGG CCAGGGCA GTG
                              |||||| |||||||| |||
                              CCCTCC GGTTCCGT CGC
                                 _       C
GAM380  KIAA1925  5'  CTCTGTGCTCACTATTTCTGGT 92078         CAT____ TG
              CTTTTC                GGACCAGGG      G  CAGGG
                              |||||||||      |  |||||
                              TCTGGTCTT      C  GTCTC
                                    TATCACT GT
GAM380  KIAA1925  5'  TCCTGTGTTGAGTGTTTTCTT  92080        CAGGG  T TG
                              GGGAGGAC    CA G  CAGGG
                              ||||||||    || |  |||||
                              TTCTTTTG    GT T  GTCCT
                                   TGA__  _ GT
GAM380  KIAA1937  3'  CCCTCTGACCCTGGTTCTCCT  73698           _  TGTGC
                              GGGAGGACCAGGG CA    AGGG
                              |||||||||||| ||    ||||
                              TCCTCTTGGTCCC GT    TCCC
                                      A  C____
GAM380  KIAA1938  3'  TCTGTACATAGTTTTCT     92203        CAGGGC
                              GGAGGAC     ATGTGCAGG
                              |||||||     |||||||||
                              TCTTTTG     TACATGTCT
                                 A_____
GAM380  KIAA1938  3'  TGTTTTCTCGTTCTCCC     92204        C  __
                              GGGAGGAC AGG  GCA
                              |||||||| |||  |||
                              CCCTCTTG TCT  TGT
                                   C   TT
GAM380  KIAA1940  3'  CCTTGGATTTCTTGGTCCTGCC 79981    G        CAT  G
                              GG AGGACCAGGG   GT CAGGG
                              || ||||||||||   || |||||
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                                CC TCCTGGTTCT   TA GTTCC
                                 G        T__  G
GAM380  KIAA1962  3'  TGCCTTTTTTGGTTTTTT    81920         ____
                                GGAGGACCA    GGGCA
                                |||||||||    |||||
                                TTTTTTGGT    TCCGT
                                     TTTT
GAM380  KIAA1975  5'  TGTGCTGTGGTTTTCTC     73981          G
                                GGGAGGACCA GGCATG
                                |||||||||| ||||||
                                CTCTTTTGGT TCGTGT
                                     G
GAM380  KIAA1975  5'  TGTGCTGTGGTTTTCTC     73980          G
                                GGGAGGACCA GGCATG
                                |||||||||| ||||||
                                CTCTTTTGGT TCGTGT
                                     G
GAM380  KIAA1987  3'  TCCTGTATTGACTGTTTTCCT  88022         C  GG  T
                                GGGAGGAC AG  CA GTGCAGGG
                                |||||||| ||  || ||||||||
                                TCCTTTTG TC  GT TATGTCCT
                                     _ A_ _
GAM380  KIF13B    3'  TTTTGTACCATATGTGTCTTTC 82831         _ GGGCAT
          C                      GGGAGGAC CA     GTGCAGGG
                                |||||||| ||     ||||||||
                                CCTTTCTG GT     CATGTTTT
                                     T  ATAC__
GAM380  KIF13B    3'  CCTTGCACGTTGCAGCCTCTC  30906       ACCAGG  _
                                GGGAGG     GCA TGTGCAGGG
                                ||||||     ||| |||||||||
                                CTCTCC     CGT GCACGTTCC
                                   GA_____   T
GAM380  KIF13B    3'  TTTTGTACCATATGTGTCTTTC 30918         _ GGGCAT
          C                      GGGAGGAC CA     GTGCAGGG
                                |||||||| ||     ||||||||
                                CCTTTCTG GT     CATGTTTT
                                     T  ATAC__
GAM380  KLF5      3'  TTTTGTATTGTGGTCATTTCC  8188        _    G GCAT
                                GGGAG GACCA G    GTGCAGGG
                                ||||| ||||| |    ||||||||
                                CCTTT CTGGT T    TATGTTTT
                                   A    G _____
GAM380  KLHL8     3'  GATGTATTTCTGTCTTTCT    62856         C   CAT    GGG
                                GGGAGGAC AGGG   GTGCA
                                |||||||| ||||   |||||
                                TCTTTCTG TCTT   TATGT
                                     _   ____    AGT
GAM380  KLK6      3'  TCCTGATTCTCCCTGGTTTTAC 10922     G        CAT  G
          C                      GG AGGACCAGGG   GT CAGGG
                                || ||||||||||   || |||||
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                                CC TTTTGGTCCC   TA GTCCT
                                 A        TCT  _
GAM380  KOC1     5'  CTTGTGCTTGGTTCTTAC    91074   GG      GGCAT TG
                                G  AGGACCAG    G  CAGG
                                |  ||||||||    |  ||||
                                C  TCTTGGTT    C  GTTC
                                 AT       _____ GT
GAM380  KPNA6    3'  CCTTGTACCTGGTTTGGGTTTT 24604         AG   AT_
             CCC                   GGGAGGACC  GGC   GTGCAGGG
                                ||||||||||  |||   ||||||||
                                CCCTTTTGG  TTG   CATGTTCC
                                      GT   GTC
GAM380  KPNA6    3'  TCTTGTATTAAGATTGCTCTTC 24614        C   GGCAT
             CC                    GGGAGGA CAG    GTGCAGGG
                                |||||||  |||    ||||||||
                                CCCTTCT GTT    TATGTTCT
                                    C   AGAAT
GAM380  KRTAP17-1 3'  CCCAAGACAGTGTCTTGTCTTT 49235         C     _   GCA
             CT                    GGGAGGAC AGGGCA TGT   GGG
                                |||||||| ||||||  |||   |||
                                TCTTTCTG TTCTGT ACA   CCC
                                    _     G   GAA
GAM380  KRTAP4-14 3'  TCCTGCTTTCTCCCTGTTCTCT 52342         C    CATGT
             C                     GGGAGGAC AGGG    GCAGGG
                                |||||||| ||||    ||||||
                                CTCTCTTG TCCC    CGTCCT
                                    _   TCTTT
GAM380  KRTHB5   3'  CCCGTTCATGTTTTGCTTCTCT 9652         C        T  A
             C                     GGGAGGA CAGGGCATG GC GGG
                                |||||||  |||||||||  ||  |||
                                CTCTCTT GTTTTGTAC TG CCC
                                    C        T  _
GAM380  LAMP3    3'  CAAGGTCTTTGGTCTTCTC    59487           _  ATG
                                GGGAGGACCAG GGC   TG
                                ||||||||||  |||   ||
                                CTCTTCTGGTT CTG   AC
                                       T   GA_
GAM380  LAP1B    3'  TCTGTCAAATGCTATGGTTTTC 64589          G    G  _   G
             TT                    GGGAGGACCA GGCAT TG CAGG
                                |||||||||  |||||  ||  ||||
                                TTCTTTTGGT TCGTA AC GTCT
                                      A    A  T
GAM380  LASP1    3'  CTTGATTCATCTCTGGTTTTCT 20454           C   TG_   G
             T                     GGGAGGACCAGGG ATG   CAGG
                                ||||||||||||  |||   ||||
                                TTCTTTTGGTCTC TAC   GTTC
                                       _  TTA
GAM380  LEC3     3'  TTCTGCATGTGAAAAACGGTTT 30864         AGGG__
             TCC                   GGAGGACC     CATGTGCAGGG
                                ||||||||     ||||||||||
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                                CCTTTTGG     GTGTACGTCTT
                                     CAAAAA
GAM380  LEPROTL1  3'  GGAAGTGCATTCTCTGGTCCTT 31062           C   TG AGGG
              CC                   GGGAGGACCAGGG ATG  C
                                   ||||||||||||| |||  |
                                   CCTTCCTGGTCTC TAC  G
                                         T   GT AAGGA
GAM380  LGI3     3'  TTCTGCCCCTCTGGTCTTTCC  57750           CATGT
                                   GGGAGGACCAGGG    GCAGGG
                                   ||||||||||||     ||||||
                                   CCTTTCTGGTCTC    CGTCTT
                                         CC___
GAM380  LHFPL2   3'  TCTTGTTTTCCTCTGTTCTTTC 69954   GG    C   CATGT
                                   G  AGGAC AGGG    GCAGGG
                                   |  ||||| ||||    ||||||
                                   C  TCTTG TCTC    TGTTCT
                                    TT    _   CTTT_
GAM380  LPAAT-delta 3'  CTTTAGTGGGCTTTGGTTTTCT 39289           ATGTGC   G
              T                     GGGAGGACCAGGGC     AGG
                                   ||||||||||||||     |||
                                   TTCTTTTGGTTTCG     TTC
                                         GGTGAT
GAM380  LRG      3'  CTGACTCTGTCTTCCC      53748        C    CATGTG
                                   GGGAGGAC AGGG     CAG
                                   |||||||| ||||     |||
                                   CCCTTCTG TCTC     GTC
                                        _   A_____
GAM380  LRG      3'  TCTTGAACTCTGGGTTCTCCC  53753         _   CATGTG
                                   GGGAGGACC AGGG     CAGGG
                                   ||||||||| ||||     |||||
                                   CCCTCTTGG TCTC     GTTCT
                                        G   AA____
GAM380  LSFR2    3'  CTCTGAATATGTCCTTGTCCTT 60565        C       G
              CC                   GGGAGGAC AGGGCATGT CAGGG
                                   |||||||| ||||||||| |||||
                                   CCTTCCTG TCCTGTATA GTCTC
                                        T       A
GAM380  LSM6     3'  TTTTGTGATACAATTTGTCCTC 22999        C  GGCATG
              TT                    GGGAGGAC AG     TGCAGGG
                                   |||||||| ||     |||||||
                                   TTCTCCTG TT     GTGTTTT
                                        T  AACATA
GAM380  LYPLA3   3'  TTCTGTGCAGCTGGATTTTCTC 24636       _  GG  A  TG
                                   GGGAGGA CCA  GC TG  CAGGG
                                   ||||||| |||  || ||  |||||
                                   CTCTTTT GGT  CG AC  GTCTT
                                        A  __  _  GT
GAM380  MACF1    3'  TCCTGTTTGCTTTCGTCTTTTT 23894        C     TGT
                                   GGGAGGAC AGGGCA   GCAGGG
                                   |||||||| ||||||   ||||||
```

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                                TTTTTCTG TTTCGT   TGTCCT
                                    C     T__
GAM380  MACMARCKS 3'  GCCCTGCATAAGGCAGTTGTTG 43448      GG____  A_
          GTTTTCTT               ACCA     GC  TGTGCAGGG   C
                                ||||     ||  |||||||||  |
                                TGGT     CG  ATACGTCCC   G
                                  TGTTGA  GA
GAM380  MAD4     3'  CTCTGCGTGTGCCCTCCCAGCC 21274     A_  ACC     TG
          C                    GGG  GG   AGGGCA  TGCAGGG
                               |||  ||   ||||||  |||||||
                               CCC  CC   TCCCGT  GCGTCTC
                                 GA  C__     GT
GAM380  MAL2     3'  TCCTACTACTTTGGTTTTCCT  53556           CAT  GC
                               GGGAGGACCAGGG   GT  AGGG
                               ||||||||||||   ||  ||||
                               TCCTTTTGGTTTC   CA  TCCT
                                      AT_  __
GAM380  MAN1     3'  TCCTGTTTGGCTTTTTGTCTTC 26716         C_    ATGT
          CT                   GGGAGGAC  AGGGC    GCAGGG
                               ||||||||  |||||    ||||||
                               TCCTTCTG  TTTCG    TGTCCT
                                   TT    GTT_
GAM380  MAP2K5   3'  CCCTGCCCACTTCTGTTTTCCT 10864         C    CA  T
                               GGGAGGAC AGGG  TG GCAGGG
                               ||||||||  ||||  ||  ||||||
                               TCCTTTTG TCTT  AC CGTCCC
                                   _    C_  C
GAM380  MAPK11   3'  CCCTGGGCCTACCTTGGTCCTC 10845           CAT  G
          CT                   GGGAGGACCAGGG   GT CAGGG
                               ||||||||||||   ||  |||||
                               TCCTCCTGGTTCC   CG GTCCC
                                      ATC  G
GAM380  MAPK6    3'  TCATGAAATGTGTTTTGTCTTT 10837         C        GCAGGG
          TT                   GGGAGGAC AGGGCATGT
                               ||||||||  |||||||||
                               TTTTTCTG TTTTGTGTA
                                   _        AAGTACTT
GAM380  MCF2L    3'  TTTTGTATGTGTGCACCTCT   60847      ACCAGG
                               GGAGG     GCATGTGCAGGG
                               |||||     ||||||||||||
                               TCTCC     TGTGTATGTTTT
                                 ACG___
GAM380  MDS018   3'  CCTGCTTCTTGGTTTCCTC    41531     AG      CATGT    G
                               GGG  GACCAGGG    GCAGG
                               |||  ||||||||    |||||
                               CTC  TTGGTTCT    CGTCC
                                 CT       T_____    G
GAM380  MGC10561 3'  CTGATGATGTGCTTTGGCCTTC 50999        A         G__   GG
          T                    GGGAGG CCAGGGCATGT   CAG
                               ||||||  ||||||||||   |||
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                                TCTTCC GGTTTCGTGTA  GTC
                                  _        GTA
GAM380  MGC10870 3' CTTGGGCCCTGGTTTTGTT   50206   G       ATGTG
                                GG AGGACCAGGGC    CAGG
                                || ||||||||||    ||||
                                TT TTTTGGTCCCG    GTTC
                                 G        G____
GAM380  MGC10902 3' CTCTGCCTTTCTGGTTTCTCT 47547      _    CATGT
                                GGAGGA CCAGGG    GCAGGG
                                |||||| ||||||    ||||||
                                TCTCTT GGTCTT    CGTCTC
                                   T     TC___
GAM380  MGC11034 3' TCTTGCTGATCTAGTTCTTTC 48790   GG   C  GG  TGT
                                G  AGGAC AG  CA   GCAGGG
                                |  ||||| ||  ||   ||||||
                                C  TCTTG TC  GT   CGTTCT
                                 TT    A  TA  ___
GAM380  MGC12538 3' CATGTTCTGATTCTTTC    51243   GG   C
                                G  AGGA CAGGGCATG
                                |  |||| |||||||||
                                C  TCTT GTCTTGTAC
                                 TT   A
GAM380  MGC13007 3' CTTTGTATGGGGGATGGTCCTT 50304        GGGCA
           TT                    GGGAGGACCA    TGTGCAGGG
                                ||||||||||    |||||||||
                                TTTTCCTGGT    GTATGTTTC
                                      AGGGG
GAM380  MGC14376 3' CATCTTTGGTTTTTCT     51846          C
                                GGGAGGACCAGGG ATG
                                |||||||||||| |||
                                TCTTTTTGGTTTC TAC
                                      _
GAM380  MGC15429 3' TTTTGTGGTCTGTTTGTCTTTT 51252  GG   ___   G   TGCAGGG
           C                     AGGAC   CAGG CATG
                                 |||||   |||| ||||
                                 TTCTG   GTCT GTGT
                                TT    TTT   G   TTT  G
GAM380  MGC15730 3' CTTTCCATCTGTGTCTTGGCTT 51801      A      __  C
           CTT                    GGAGG CCAGGGCAT  GTG AGGG
                                |||||| |||||||||  ||| ||||
                                TCTTC GGTTCTGTG  TAC TTTC
                                  _       TC  C
GAM380  MGC16386 3' CTTGTCGTCCTGTCCTTCC   54733       C   ATGT
                                GGGAGGAC AGGGC   GCAGG
                                |||||||| |||||   |||||
                                CCTTCCTG TCCTG   TGTTC
                                    _   C___
GAM380  MGC20253 3' TCCTGCTACAATCCAGGTTCTC 58063        A  CA  _
           CT                    GGGAGGACC GGG  TGT GCAGGG
                                ||||||||| |||  ||| ||||||
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                                TCCTCTTGG CCT  ACA CGTCCT
                                     A  A_  T
GAM380  MGC20255  3'  TTCTGTCTCTTTCTGTCTTTCT 53449       C   CATGT
                                GGGAGGAC AGGG    GCAGGG
                                |||||||| ||||    ||||||
                                TCTTTCTG TCTT    TGTCTT
                                     _   TCTC_
GAM380  MGC22014  3'  TTCTGCTCTGTTTTGTTTTCCC 64501       C     TGT
                                GGGAGGAC AGGGCA  GCAGGG
                                |||||||| ||||||  ||||||
                                CCCTTTTG TTTTGT  CGTCTT
                                     _    CT_
GAM380  MGC22014  3'  CTTTGTTGGAGTGTTGGTTTTT 64494         G  ATGT
           CT                    GGGAGGACCAG GC   GCAGGG
                                ||||||||||| ||   ||||||
                                TCTTTTTGGTT TG   TGTTTC
                                      G  AGGT
GAM380  MGC23980  3'  CCTTGCTTGATTCTGGTTTCTT 58759      G     _  TGT
                                GGGAG ACCAGGG CA  GCAGGG
                                ||||| ||||||| ||  ||||||
                                TTCTT TGGTCTT GT  CGTTCC
                                   _     A  T__
GAM380  MGC2477   5'  CTTGGTATTGTTTGGGTTTTTT 44063        AG   T   _  G
           T                     GGGAGGACC  GGCA GTGC AGG
                                |||||||||  |||| |||| |||
                                TTTTTTTGG  TTGT TATG TTC
                                     GT   _   G
GAM380  MGC2477   5'  TTTTGTTTTGCTTCGTTTTCTT 44078       CA    TGT
                                GGGAGGAC  GGGCA  GCAGGG
                                ||||||||  |||||  ||||||
                                TTCTTTTG  TTCGT  TGTTTT
                                     C_    TT_
GAM380  MGC26954  3'  TGTGCCTGGCTTCTT      58840       A    G
                                GGGAGG CCAGG CATG
                                |||||| ||||| ||||
                                TTCTTC GGTCC GTGT
                                     _   _
GAM380  MGC29898  3'  TTTTGTGCTCAGATGATCCTTT 58932       C ___      TGCAGGG
           T                     GGAGGA CA  GGGCATG
                                |||||| ||  |||||||
                                TTTCCT GT  CTCGTGT
                                   A  AGA     TTT  G
GAM380  MGC3178   3'  TTTGTGTGTGTGTTTTCC    47993       CAGG    TG
                                GGAGGAC   GCATG  CAGG
                                |||||||   |||||  ||||
                                CCTTTTG   TGTGT  GTTT
                                     ____   GT
GAM380  MGC3222   3'  CTTGGGCTTTGGTTTTTTT   44296          ATGTG
                                GGGAGGACCAGGGC    CAGG
                                ||||||||||||||    ||||
```

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                                TTTTTTTGGTTTCG    GTTC
                                      G____
GAM380  MGC3413  3' TTTTGCACATGCCATGTTTTC 51051      CAG
                                GAGGAC  GGCATGTGCAGGG
                                ||||||  ||||||||||||||
                                CTTTTG  CCGTACACGTTTT
                                   TA_
GAM380  MGC39350 3' TGTTGTTTTGTCCTGGACTTTC 58656      A      TGT   GG
          C                     GGGAGG CCAGGGCA  GCAG
                                |||||| ||||||||  ||||
                                CCTTTC GGTCCTGT  TGTT
                                   A      TT_   GTT
GAM380  MGC4607  3' TTTGCACATGATGTTCCT    48742     C  GGG
                                AGGA CA  CATGTGCAGG
                                |||| ||  ||||||||||
                                TCCT GT  GTACACGTTT
                                  T  A__
GAM380  MGC4618  3' TCTTGCGTGGCCTGGTTTT   50318       G  GT
                                AGGACCAGG CAT  GCAGGG
                                ||||||||| |||  ||||||
                                TTTTGGTCC GTG  CGTTCT
                                     G  __
GAM380  MGC4638  3' CCTAAGAAGTTCCCTGGTTTTT 48941          C  GTGC_  G
          CC                  GGGAGGACCAGGG AT    AGG
                              ||||||||||||| ||    |||
                              CCTTTTTGGTCCC TG    TCC
                                    T  AAGAA
GAM380  MGC4643  3' TGGAGTGTGTTTTGGGTTTTTT 51158        _    TG G_  GGG
          T                   GGGAGGACC AGGGCA  T  CA
                              ||||||||| ||||||  |  ||
                              TTTTTTTGG TTTTGT  G  GT
                                    G     GT AG
GAM380  MGC4655  3' TGGATATGTCTGGTCCTCCT  52805          G    G
                              GGGAGGACCAGG CATGT CA
                              |||||||||||| ||||| ||
                              TCCTCCTGGTCT GTATA GT
                                    _    G
GAM380  MGC4766  5' CGCCTGCCTTGGCCTCCC    48776      A      T
                              GGGAGG CCAGGGCA GTG
                              |||||| |||||||| |||
                              CCCTCC GGTTCCGT CGC
                                 _      C
GAM380  MGC4796  3' CCCTGCGTATGTGGCTCCTCC  61483      _ AGG
                              GGAGGA CC   GCATGTGCAGGG
                              |||||| ||  ||||||||||||
                              CCTCCT GG   TGTATGCGTCCC
                                 C  ___
GAM380  MGC5469  3' CTCTGGACCTCCTGTCTTCTC  50394       C   CAT  G
                              GGGAGGAC AGGG   GT CAGGG
                              |||||||| ||||   || |||||
```

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                                CTCTTCTG TCCT   CA GTCTC
                                    _   C__  G
GAM380  MGC5469  3' CTTGTCCTCTGGACCTCCT   50395       A     CATGT
                                GGGAGG CCAGGG    GCAGG
                                |||||| ||||||    |||||
                                TCCTCC GGTCTC    TGTTC
                                   A     C____
GAM380  MGC5508  3' CTCTGCTGCTGCCTTGGCTTCC 44037       A       T _
           T                    GGGAGG CCAGGGCA GT GCAGGG
                                |||||| |||||||| || ||||||
                                TCCTTC GGTTCCGT CG CGTCTC
                                   _       _ T
GAM380  MMD     3' TTTTGTATATGTTTAGAACTCT 59812       GACCA
           C                    GGGAG    GGGCATGTGCAGGG
                                |||||    ||||||||||||||
                                CTCTC    TTTGTATATGTTTT
                                   AAGA_
GAM380  MMPL1   3' CTCTGTGTGTTCTCTGGATCTT 14718       _     C   TG
           TT                    GGAGGA CCAGGG ATG  CAGGG
                                |||||| |||||| |||  |||||
                                TTTTCT GGTCTC TGT  GTCTC
                                   A     T   GT
GAM380  MMRN    3' TCTGCTCTGTTTTGGTTTTTCT 23724             TGT
                                GGGAGGACCAGGGCA   GCAGG
                                ||||||||||||||   |||||
                                TCTTTTTGGTTTTGT   CGTCT
                                      CT_
GAM380  MO25    3' CTTTGTGTGTGTGGGAAATCTC 32808     GGA_  AGG    TG
                                GGGA   CC   GCATG  CAGGG
                                ||||   ||   |||||  |||||
                                CTCT   GG   TGTGT  GTTTC
                                  AAAG  ___    GT
GAM380  MRG15   3' TCCATTTGTGCTTTTGTTTTTT 22302        C       TGCA
           T                    GGGAGGAC AGGGCATG    GGG
                                |||||||| ||||||||   |||
                                TTTTTTTG TTTCGTGT    CCT
                                     T       TTA_
GAM380  MRPL10  3' TGTCCTTAGTTTTCCC     59155        C_
                                GGGAGGAC  AGGGCA
                                ||||||||  ||||||
                                CCCTTTTG  TCCTGT
                                     AT
GAM380  MRPL34  3' CCCTGCCCCATCCTGAGTTCTT 43741        _    CATGT
           TT                    GGGAGGAC CAGGG    GCAGGG
                                |||||||| |||||    ||||||
                                TTTTCTTG GTCCT    CGTCCC
                                     A    ACCC_
GAM380  MSTP032 3' TCTTGCAAGTTACTTGTTCTCT 47443        C   GCATG
           C                    GGGAGGAC AGG    TGCAGGG
                                |||||||| |||    |||||||
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                                CTCTCTTG TTC     ACGTTCT
                                     _  ATTGA
GAM380  MUC13    3'  ATGCCTTGTCCTCTT       52329         C
                                GGGAGGAC AGGGCAT
                                |||||||| |||||||
                                TTCTCCTG TTCCGTA
                                     _
GAM380  MYO18B   5'  TCCTGTGATCTGTGTCCTCTT  50889         _   GCATGT
                                GGGAGGAC CAGG     GCAGGG
                                |||||||| ||||     ||||||
                                TTCTCCTG GTCT     TGTCCT
                                     T   AG____
GAM380  N4BP3    3'  CCCTGGGCCTCTTGGTCCATCC 66259     _       CAT  G
                                GGA GGACCAGGG   GT CAGGG
                                ||| |||||||||   || |||||
                                CCT CCTGGTTCT   CG GTCCC
                                  A        C__  G
GAM380  NAALAD2  3'  TTGATTATAGGCTTTGGTCTTT 18441    GG         A    CAGGG
           TC                     G  AGGACCAGGGC TGTG
                                |  ||||||||||| ||||
                                C  TTCTGGTTTCG ATAT
                                 TT          G    TAGTTT
GAM380  NAG14    3'  CTCTGTTATTCTGGTCCATCT  42166     _       CATGT
                                GGA GGACCAGGG     GCAGGG
                                ||| |||||||||     ||||||
                                TCT CCTGGTCTT     TGTCTC
                                  A        AT___
GAM380  NAG73    3'  TGTGTCTTTGTTCTTCC     50808         C
                                GGGAGGAC AGGGCATG
                                |||||||| ||||||||
                                CCTTCTTG TTCTGTGT
                                     T
GAM380  NAP1L2   5'  TCCTGTGGAGGTTTGGTCTCCC 41736       G      G ATG
                                GGGAG ACCAGG C   TGCAGGG
                                ||||| |||||| |   |||||||
                                CCCTC TGGTTT G   GTGTCCT
                                   _     _ GAG
GAM380  NAPG     5'  TCTGCCTGCCTTGGCCTCCC   96733        A       TGT
                                GGGAGG CCAGGGCA   GCAGG
                                ||||||| ||||||||   |||||
                                CCCTCC GGTTCCGT   CGTCT
                                   _       C__
GAM380  NDP52    3'  CTCTGTGTTCCTACTGGGCTTT 19529        A    GGCAT TG
           CC                     GGGAGG CCAG     G  CAGGG
                                ||||||| ||||     |  |||||
                                CCTTTC GGTC     T  GTCTC
                                   G    ATCCT GT
GAM380  NDST3    5'  TCTTGCATGTGACACTCTTGCC 16551     _    CCAGGG
           C                      GGG AGGA     CATGTGCAGGG
                                ||| ||||     ||||||||||
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                                CCC TTCT     GTGTACGTTCT
                                  G   CACA__
GAM380  NDUFC2   3'  CACCTGCCTTGGCCTTCC    15826       A       T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCTTCC GGTTCCGT CAC
                                   _       C
GAM380  NEDD5    3'  TTCTGATCCCCTTTGGTTTTAC 15316    G        CATGTG
           T                     GG AGGACCAGGG     CAGGG
                                || ||||||||||      |||||
                                TC TTTTGGTTTC     GTCTT
                                 A         CCCTA_
GAM380  NESCA    3'  TCCTGCGTATGTGTCTCCTTCC 26746        CCAGG
                                GGGAGGA    GCATGTGCAGGG
                                |||||||    ||||||||||||
                                CCTTCCT    TGTATGCGTCCT
                                    CTG__
GAM380  NETO1    3'  CATTTTTTGGTCTTTCC     57252            C
                                GGGAGGACCAGGG ATG
                                |||||||||||| |||
                                CCTTTCTGGTTTT TAC
                                       T
GAM380  NEUGRIN  5'  TGCCATTGGTTCTCTT      33574           _
                                GGGAGGACCAG GGCA
                                |||||||||| ||||
                                TTCTCTTGGTT CCGT
                                      A
GAM380  NICN1    3'  TCTGCCTGCCTTGGCCTTCC   50295       A       TGT
                                GGGAGG CCAGGGCA   GCAGG
                                |||||| ||||||||   |||||
                                CCTTCC GGTTCCGT   CGTCT
                                   _       C__
GAM380  NIN283   3'  CTTTGGGTTTGTTTGGTTTTTT 50071    GG       G  TG G
           C                     G  AGGACCAGG CA  T CAGGG
                                |  ||||||||| ||  | |||||
                                C  TTTTGGTTT GT  G GTTTC
                                 TT        _  TT G
GAM380  NKX2B    3'  TTTGTTTTTGCGTTTTCCC    10238         CAGG   TGT
                                GGGAGGAC    GCA   GCAGG
                                ||||||||    |||   |||||
                                CCCTTTTG    CGT   TGTTT
                                     _____   TTT
GAM380  NKX2C    3'  CCCTGGCCGCGCTTGGTTCTTC 59218           _ AT  G
           C                      GGGAGGACCAGG GC  GT CAGGG
                                |||||||||||| ||  || |||||
                                CCTTCTTGGTTC CG  CG GTCCC
                                       G  C_  _
GAM380  NPD009   5'  CTTGTACTTGATCCTCCT    95048         C   GGCAT
                                GGGAGGA CAG     GTGCAGG
                                ||||||| |||     |||||||
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                                TCCTCCT GTT    CATGTTC
                                   A  _____
GAM380  NUDC     3'  CTTGGGACCTTGTCCTCCC   21714        C  GCATGTG
                                GGGAGGAC AGG     CAGG
                                |||||||| |||     ||||
                                CCCTCCTG TCC     GTTC
                                   T  AGG____
GAM380  NUDEL    3'  CTTTGGAGTGTTTTTGTTTTCT 47968        C     GTG
             C                   GGGAGGAC AGGGCAT  CAGGG
                                |||||||| |||||||  |||||
                                CTCTTTTG TTTTGTG  GTTTC
                                   T     AG_
GAM380  NUDT11   3'  TTTTGTATATGTTTGAAATTTT 59997       CCA_
             CC                   GGAGGA   GGGCATGTGCAGGG
                                ||||||   ||||||||||||||
                                CCTTTT   TTTGTATATGTTTT
                                   AAAG
GAM380  NUDT3    3'  TTTTGTGCATGATCTGTCCCTC 21990       AC  GG   TG
             CC                   GGGAGG  CAG  CATG  CAGGG
                                ||||||  |||  ||||  |||||
                                CCCTCC  GTC  GTAC  GTTTT
                                   CT  TA   GT
GAM380  NXP-2    3'  CTTTGTGCAATTTTTTCTGGTT 71107   A       CA___  TG
             CCCC                 G GGACCAGGG    TG  CAGGG
                                | |||||||||    ||  |||||
                                C CTTGGTCTT    AC  GTTTC
                                _       TTTTA  GT
GAM380  NXPH3    3'  TTCTGTGCCCGCTTGGTCCTC  65772         G AT TG
                                GAGGACCAGG C  G  CAGGG
                                |||||||||| |  |  |||||
                                CTCCTGGTTC G  C  GTCTT
                                      _ CC GT
GAM380  NY-REN-41 3'  CTTTGGCTTGTTTTGTTTTTCT 54688       C      T  G
                                GGAGGA CAGGGCA GT CAGGG
                                |||||| ||||||| || |||||
                                TCTTTT GTTTTGT CG GTTTC
                                   T      T  _
GAM380  OCIA     5'  CCCTGATCGCTTGGTTTTCCT  35209          G ATGTG
                                GGGAGGACCAGG C    CAGGG
                                |||||||||||| |    |||||
                                TCCTTTTGGTTC G    GTCCC
                                      _ CTA__
GAM380  OGFR     3'  CCCGTCGGCGTCTTGGTCCTCC 61335           A_  T  A
             T                   GGGAGGACCAGGGC  TG GC GGG
                                ||||||||||||||  || || |||
                                TCCTCCTGGTTCTG  GC TG CCC
                                      CG  _  _
GAM380  OSAP     3'  CATCTTTGGTTTTTTT      50924            C
                                GGGAGGACCAGGG ATG
                                |||||||||||| |||
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```
                                TTTTTTTGGTTTC TAC
                                          _
GAM380  OSBPL2   3'  TCTTGTGTTTCTGTTTTTCCC  29224        C     CAT TG
                                GGGAGGA CAGGG   G  CAGGG
                                ||||||| |||||   |  |||||
                                CCCTTTT GTCTT   T  GTTCT
                                    T    ___ GT
GAM380  OSBPL2   3'  TCTTGTGTTTCTGTTTTTCCC  57875        C     CAT TG
                                GGGAGGA CAGGG   G  CAGGG
                                ||||||| |||||   |  |||||
                                CCCTTTT GTCTT   T  GTTCT
                                    T    ___ GT
GAM380  OSBPL3   3'  CTTTGGTGTATGCTTTGTTCTT 31437        C        TG _
            TCC                    GGGAGGA CAGGGCATG  C AGGG
                                ||||||| |||||||||  | ||||
                                CCTTTCT GTTTCGTAT  G TTTC
                                    T        GT G
GAM380  P450RAI-2 3'  CCCTGTGTTGTAATTGGTCCCT 39100    GA      G_   T TG
            CC                     GG  GGACCAG  GCA G  CAGGG
                                ||  |||||||  ||| |  |||||
                                CC  CCTGGTT  TGT T  GTCCC
                                 TC      AA   _ GT
GAM380  PABPC5   5'  TTTTGCCTGCCTTGGCTTTTT  55075       A       TGT
                                GGGAGG CCAGGGCA   GCAGGG
                                |||||| ||||||||   ||||||
                                TTTTTC GGTTCCGT   CGTTTT
                                   _       C__
GAM380  PAGE-5   5'  TGTGTCTTCGTTCTTTC     55322    GG    C
                                G  AGGAC AGGGCATG
                                |  ||||| ||||||||
                                C  TCTTG TTCTGTGT
                                 TT    C
GAM380  PARVA    3'  TTTTGTCTCTTTTTTGGTCTCT 36657      _       CATGT
            TT                     GGAG GACCAGGG     GCAGGG
                                |||| ||||||||     ||||||
                                TTTC CTGGTTTT     TGTTTT
                                  T       TTCTC
GAM380  PASK     5'  CTTTGTTAGGCTGTTGGTTCTC 30716          _   ATGT
            CT                     GGGAGGACCAG GGC    GCAGGG
                                |||||||||||| |||    ||||||
                                TCCTCTTGGTT TCG    TGTTTC
                                      G   GAT_
GAM380  PCANAP7  5'  CCTTATCTTGTCCTGGTTTCCT 93364       G        T_   C   G
                                GGGAG ACCAGGGCA  GTG AGG
                                ||||| |||||||||  ||| |||
                                TCCTT TGGTCCTGT  TAT TCC
                                   _        TC   _
GAM380  PCSK7    3'  TCCTGCCACCACCCTGTCTTCC 16338         C    CA_  T
            T                      GGGAGGAC AGGG   TG GCAGGG
                                |||||||| ||||   || ||||||
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                                TCCTTCTG TCCC   AC CGTCCT
                                    _    ACC  _
GAM380  PEGASUS  3'  TTTGCTGTTTTTGTGGTTTGGT 42433          G   GT__    GG
          TTTTTT                  GAGGACCAGG CAT    GCAG
                                |||||||||| |||    ||||
                                TTTTTGGTTT GTG    TGTC
                                    G   TTTT    GTTTT
GAM380  PEGASUS  3'  TTTTGTTTTTTGTTTTGGTCAT 42435      G        TGT_
          CCC                   GGGA GACCAGGGCA    GCAGGG
                                |||| ||||||||||    ||||||
                                CCCT CTGGTTTTGT    TGTTTT
                                  A        TTTT
GAM380  PFDN1    3'  CTCTGCTAAGCCTGGTTTTCTT 10510           G A  T
                                GGGAGGACCAGG C TG GCAGGG
                                |||||||||||| | || ||||||
                                TTCTTTTGGTCC G AT CGTCTC
                                    _ A  _
GAM380  PFTK1    3'  TTTTGCAAATGTGGTTTTTTT  24763         AGG    G
                                GGGAGGACC   GCAT TGCAGGG
                                |||||||||   |||| |||||||
                                TTTTTTTGG   TGTA ACGTTTT
                                    ___    A
GAM380  phospho1  3'  GTATTTCCTGGTCCTCCC    82371            CAT
                                GGGAGGACCAGGG   GTGC
                                ||||||||||||   ||||
                                CCCTCCTGGTCCT   TATG
                                    T__
GAM380  PI15     3'  TTTTGTGCTAATCTTGTTTTCC 31894         C   GCAT TG
          T                     GGGAGGAC AGG    G  CAGGG
                                |||||||| |||    |  |||||
                                TCCTTTTG TCT    C  GTTTT
                                    T   AAT_ GT
GAM380  PIG7     3'  CCTTCTGCCTTGGCCTCCC    16793       A       TGTGC
                                GGGAGG CCAGGGCA     AGG
                                |||||| ||||||||     |||
                                CCCTCC GGTTCCGT     TCC
                                    _       CT___
GAM380  PILB     3'  TCCTGTGTGTTAGGCTGTTCTT 24236       CAG   ___   TG
                                GAGGAC   GGC   ATG  CAGGG
                                ||||||   |||   |||  |||||
                                TTCTTG   TCG   TGT  GTCCT
                                    ___   GAT   GT
GAM380  PLA2G3   3'  TTTGCGCAAAGGACCTCCC    31688       A  AGGGCA
                                GGGAGG CC      TGTGCAGG
                                |||||| ||      ||||||||
                                CCCTCC GG      ACGCGTTT
                                    A  AA____
GAM380  PLAGL2   3'  CTTTGTTGTATCTGGTTTTC   70448          _   TGT
                                GAGGACCAGG GCA   GCAGGG
                                |||||||||| |||   ||||||
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                                CTTTTGGTCT TGT   TGTTTC
                                     A  ___
GAM380  PLP1     3'  ATGTCTTTGGTCCTCTC     5005          _
                                GGGAGGACCAG GGCAT
                                |||||||||| |||||
                                CTCTCCTGGTT CTGTA
                                      T
GAM380  PLU-1    3'  TCTGCCTCCTGGTTTCCT    21758      G     CATGT
                                GGGAG ACCAGGG    GCAGG
                                ||||| |||||||    |||||
                                TCCTT TGGTCCT    CGTCT
                                   _     C____
GAM380  PLU-1    3'  TCTGCCTCCTGGTTTCCT    87417      G     CATGT
                                GGGAG ACCAGGG    GCAGG
                                ||||| |||||||    |||||
                                TCCTT TGGTCCT    CGTCT
                                   _     C____
GAM380  PLUNC    3'  CTCTGCTGAGCTGGGTCTTCCC 55641        AG   ATGT
                                GGGAGGACC  GGC   GCAGGG
                                |||||||||  |||   ||||||
                                CCCTTCTGG  TCG   CGTCTC
                                     G_   AGT_
GAM380  POMT1    3'  CATGCCTTTGTCTTTTT     23153        C
                                GGGAGGAC AGGGCATG
                                |||||||| ||||||||
                                TTTTTCTG TTCCGTAC
                                     T
GAM380  POU4F2   3'  TTCTGTATATGGCCTGGTTTCT 15901      G     G
           T                     GGGAG ACCAGG CATGTGCAGGG
                                |||||| |||||| ||||||||||
                                TTCTT TGGTCC GTATATGTCTT
                                   _     G
GAM380  PP1628   3'  CACAGCAACATGCCCTGGCCTT 47292   GG   A        _  AGGG
           TC                    G  AGG CCAGGGCATGT GC
                                |  ||| |||||||||| ||
                                C  TCC GGTCCCGTACA CG
                                TT  _         A  ACACT
GAM380  PPIL2    3'  AGCTGTATATGTCTGGTTTTCT 26763          G       GG
           T                     GGGAGGACCAGG CATGTGCAG
                                |||||||||||| |||||||||
                                TTCTTTTGGTCT GTATATGTC
                                        _       GAC
GAM380  PPP1R3B  3'  CTTGTGCTTGGATTTTCC    44817       _   GGCAT TG
                                GGAGGA CCAG    G  CAGG
                                |||||| ||||    |  ||||
                                CCTTTT GGTT    C  GTTC
                                   A   _____ GT
GAM380  PPP1R9A  3'  TGTGTTTTGCTCTTCTC    34464        C
                                GGGAGGA CAGGGCATG
                                ||||||| |||||||||
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                                CTCTTCT GTTTTGTGT
                                    C
GAM380  PRAX-1   3' CTGATCCTGTCTTCCC      16470        C   GCATGTG
                                GGGAGGAC AGG       CAG
                                |||||||| |||       |||
                                CCCTTCTG TCC       GTC
                                     _   TA_____
GAM380  PREI3    3' TTTTGTATGCTGGGTTTGCCT  66326     AG    AG    GT
                                GGG  GACC  GGCAT  GCAGGG
                                |||  ||||  |||||  ||||||
                                TCC  TTGG  TCGTA  TGTTTT
                                  GT   G_    __
GAM380  PRMT6    3' TTTTGTTTTGTTTTGTTTTTCT 36273       C      TGT
                                GGAGGA CAGGGCA   GCAGGG
                                ||||||| |||||||   ||||||
                                TCTTTT GTTTTGT   TGTTTT
                                    T      TT_
GAM380  PRO0233  3' TTTTGTGCTTTCTGGCCTTCT  26120       A     CAT TG
                                GGGAGG CCAGGG   G  CAGGG
                                |||||| ||||||   |  |||||
                                TCTTCC GGTCTT   C  GTTTT
                                    _     T__ GT
GAM380  PRO0767  5' TTTTGTAGGACCATCTTGGTTT 26026    G        CATG__
           TACC                  G AGGACCAGGG      TGCAGGG
                                | ||||||||||      |||||||
                                C TTTTGGTTCT      ATGTTTT
                                 A         ACCAGG
GAM380  PRO0971  3' CTGTTTTTTGGTTTTTCC    37703            CATGT
                                GGGAGGACCAGGG     GCAG
                                ||||||||||||     ||||
                                CCTTTTTGGTTTT     TGTC
                                        T_____
GAM380  PRO1048  3' TTCTGTAGGAGTCTTAGGTTTT 37527          _     ATG
           TTT                    GGGAGGACC AGGGC   TGCAGGG
                                |||||||| |||||   |||||||
                                TTTTTTTGG TTCTG   ATGTCTT
                                     A     AGG
GAM380  PRO1257  5' TCTTGCATATGTATAGTTC   37711      CAGG
                                GGAC    GCATGTGCAGGG
                                ||||    ||||||||||||
                                CTTG    TGTATACGTTCT
                                  ATA_
GAM380  PRO1580  5' CCAGGGAAGTGTGCCTTGTCTT 37531         C      TG GCAG__
           TCT                    GGAGGAC AGGGCA  T      GG
                                ||||||| ||||||  |     ||
                                CTTTCTG TTCCGT  G     CC
                                     _     GT AAGGGA
GAM380  PROL2    3' CTTTGTGTGTGACTGTTTCTC  22345       C   GG    TG
                                GAGGA CAG  CATG  CAGGG
                                ||||| |||  ||||  |||||
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                                CTCTT GTC  GTGT  GTTTC
                                   T  A_   GT
GAM380  PRRG1    3'  TATGCTTTTGTCTTTCT     6288         C
                                GGGAGGAC AGGGCATG
                                |||||||| ||||||||
                                TCTTTCTG TTTCGTAT
                                     T
GAM380  PRSS21   3'  CCAAGTCAGGCCCTGGTTCTCT 22306            A  T  AG
           T                     GGGAGGACCAGGGC TG GC  GG
                                |||||||||||||| || ||  ||
                                TTCTCTTGGTCCCG AC TG  CC
                                        G  _  AA
GAM380  PRSS21   3'  CCAAGTCAGGCCCTGGTTCTCT 58617            A  T  AG
           T                     GGGAGGACCAGGGC TG GC  GG
                                |||||||||||||| || ||  ||
                                TTCTCTTGGTCCCG AC TG  CC
                                        G  _  AA
GAM380  PSKH1    3'  CCTGCATGTGCCACCTCC     68238       ACCAG
                                GGAGG     GGCATGTGCAGG
                                |||||     ||||||||||||
                                CCTCC     CCGTGTACGTCC
                                   A____
GAM380  PTE1     5'  TTCTGTGTATGTCTCCGCGTCT 18443        CA__      TG
           TC                     GAGGAC    GGGCATG  CAGGG
                                |||||||   |||||||  |||||
                                CTTCTG    TCTGTAT  GTCTT
                                    CGCC      GT
GAM380  PTPN3    3'  CTCTCAGTGTGTTCTGGTCATC 11058      G          _  C
           TT                     GGGA GACCAGGGCATG TG AGGG
                                |||| |||||||||||| || ||||
                                TTCT CTGGTCTTGTGT AC TCTC
                                   A          G  _
GAM380  QKI      3'  GTGTCTTGTCTTTTT       65446         C
                                GGGAGGAC AGGGCAT
                                |||||||| |||||||
                                TTTTTCTG TTCTGTG
                                      _
GAM380  RAB10    3'  TTACTTCTATGTTCTGCTTTTC 85180         C        TGCAGGG
           CT                     GGGAGGA CAGGGCATG
                                |||||||| |||||||||
                                TCCTTTT GTCTTGTAT
                                    C        CTTCATTT
GAM380  RAB11B   3'  TCTTGTAGCCTTTGGTTTTT   73907          _  ATG
                                GAGGACCAG GGC   TGCAGGG
                                ||||||||| |||   |||||||
                                TTTTTGGTT CCG   ATGTTCT
                                      T  ____
GAM380  RAB20    3'  CTGTGAGTTGTCTTTGGTCCTC 35155          _   TG_    GG
           CC                     GGGAGGACCAG GGCA   TGCAG
                                |||||||||| ||||   |||||
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                                CCCTCCTGGTT CTGT   GTGTC
                                      T    TGA
GAM380  RAB32    3'  TCTTGTGTGTGCCTCAGCTCT  22417     GACCA      TG
                                GGAG    GGGCATG  CAGGG
                                ||||    |||||||  |||||
                                TCTC    TCCGTGT  GTTCT
                                  GAC__      GT
GAM380  RAB4B    5'  CCTGCACATGTACTCCC     32374      GACCAGG
                                GGGAG      GCATGTGCAGG
                                |||||      ||||||||||
                                CCCTC      TGTACACGTCC
                                  A_______
GAM380  RAI15    3'  ATGCTCTGGTATTCCT      66665       G
                                GGGAG ACCAGGGCAT
                                ||||| ||||||||||
                                TCCTT TGGTCTCGTA
                                  A
GAM380  RAI17    3'  CCTCTGTCCTAGTTCTCTT    91277         C     TGTGC
                                GGGAGGAC AGGGCA     AGG
                                |||||||| ||||||     |||
                                TTCTCTTG TCCTGT     TCC
                                    A     C_____
GAM380  RAI17    3'  CTCTCCGTCTGTTCTGTTTTTC 91280       C      TG  C
          T                      GGAGGA CAGGGCA  TG AGGG
                                ||||||| |||||||  || ||||
                                TCTTTT GTCTTGT  GC TCTC
                                   T      CT  C
GAM380  RALGPS1A 3'  CTCTGCAAACTGTCCTGGTTTT 27602             TG_
          TC                     GGAGGACCAGGGCA   TGCAGGG
                                ||||||||||||||   |||||||
                                CTTTTTGGTCCTGT   ACGTCTC
                                      CAA
GAM380  RAP140   5'  CTCTGCATTTGCTGTTCTCTC  30843         CAG    T
                                GGGAGGAC   GGCA GTGCAGGG
                                ||||||||   |||| ||||||||
                                CTCTCTTG   TCGT TACGTCTC
                                    ___    T
GAM380  RBT1     3'  TTCTGTGAAGGTGGGTCTTCCT 25356          AGG  ATG
                                GGGAGGACC   GC   TGCAGGG
                                |||||||||   ||   |||||||
                                TCCTTCTGG   TG   GTGTCTT
                                     G__  GAA
GAM380  RIL      3'  TCTGTTCCAGGTTTTTCT    13490          A   CATGT
                                GGGAGGACC GGG    GCAGG
                                ||||||||| |||    |||||
                                TCTTTTTGG CCT    TGTCT
                                     A  _____
GAM380  RIN      3'  CTCTGCATATCTGTACCTCTT  11343        AC   GGC
                                GGGAGG  CAG   ATGTGCAGGG
                                ||||||  |||   ||||||||||
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                                TTCTCC  GTC   TATACGTCTC
                                   AT  ___
GAM380  RNAC     3'  CTTGAGCCTTGGTTTTT     19311           ATGTG
                                GAGGACCAGGGC    CAGG
                                ||||||||||||    ||||
                                TTTTTGGTTCCG    GTTC
                                      A____
GAM380  RNF11    3'  TGCCTTAGGTCTTTTT      26875         _
                                GGGAGGACC AGGGCA
                                ||||||||| ||||||
                                TTTTTCTGG TTCCGT
                                     A
GAM380  RNF2     3'  TCTTGTATATTTATAGTTTTCC 23299         CAG  C
              T                  GGGAGGAC   GG ATGTGCAGGG
                                ||||||||   || ||||||||||
                                TCCTTTTG   TT TATATGTTCT
                                    ATA  _
GAM380  RNF38    3'  TTTTGTGTGTGCACTAACATTC 42942       GACC  G    TG
              CC                   GGGAG    AG GCATG  CAGGG
                                |||||    || |||||  |||||
                                CCCTT    TC CGTGT  GTTTT
                                   ACAA  A    GT
GAM380  RNF8     3'  CCTTGTGTCTTGGTTTTGGTTT 14222       _      AT__ TG
              CTTC                 GAGGA CCAGGGC    G  CAGGG
                                ||||| |||||||    |  |||||
                                TTCTT GGTTTTG    T  GTTCC
                                   T      GTTC GT
GAM380  RoXaN    3'  CCCTGCCTTTCTCTGTCTTTTC 46640    GG    C    CATGT
                                G  AGGAC AGGG    GCAGGG
                                |  ||||| ||||    ||||||
                                C  TTCTG TCTC    CGTCCC
                                 TT    _    TTTC_
GAM380  S164     3'  TCTGAATCCTTGGTTCTCTT   60783           CATGTG
                                GGGAGGACCAGGG     CAGG
                                ||||||||||||     ||||
                                TTCTCTTGGTTCC     GTCT
                                      TAA___
GAM380  SCGN     5'  CCCAAAGTTGTCTAGGTCCTTC 22786         A    TGTGCA
              C                  GGGAGGACC GGGCA     GGG
                                ||||||||| |||||     |||
                                CCTTCCTGG TCTGT     CCC
                                     A    TGAAA_
GAM380  SCYA22   3'  TACAAGTGTCTGGTCCTTTC   90953   GG       _  A
                                G  AGGACCAGG GC TGTG
                                |  ||||||||| || ||||
                                C  TCCTGGTCT TG ACAT
                                 TT       G  A
GAM380  SCYA25   3'  CCCTGCACCTGAGTTGGTCCTC 18838          GG  T
              CC                   GGGAGGACCAG  CA GTGCAGGG
                                ||||||||||  || ||||||||
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                                CCCTCCTGGTT  GT CACGTCCC
                                      GA  C
GAM380  SCYA28   3'  CATCTGCCTTGGCCTCCC    39057       A       T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTCC GGTTCCGT TAC
                                   _       C
GAM380  SDC3     3'  TCCTGTGTTCTCTGGATTTCTT 27765       A     CAT TG
                                GGGAGG CCAGGG   G  CAGGG
                                |||||| ||||||   |  |||||
                                TTCTTT GGTCTC   T  GTCCT
                                   A     T__ GT
GAM380  SDCCAG33 3'  TCTGGACCTTGGTTTTCTT    19366           CATG G
                                GGGAGGACCAGGG    T CAGG
                                |||||||||||||    | ||||
                                TTCTTTTGGTTCC    A GTCT
                                      _____ G
GAM380  SDS3     3'  AATGATCATGTGTTTTGTCCTC 69222         C        CAGGG
             CT                   GGGAGGAC AGGGCATGTG
                                |||||||| ||||||||||
                                TCCTCCTG TTTTGTGTAC
                                   _        TAGTAAC
GAM380  SEMA3E   3'  TCTATGCTGTTCTGTCCTTCT  24887        C     T  GC
                                GGGAGGAC AGGGCA GT  AGG
                                |||||||| |||||| ||  |||
                                TCTTCCTG TCTTGT CG  TCT
                                   _     _ TA
GAM380  SEMA3E   5'  TGCGTGTGCTCGGTTTTTTT   24888         A     TG
                                GGGAGGACC GGGCA  TGCA
                                ||||||||| |||||  ||||
                                TTTTTTTGG CTCGT  GCGT
                                   _    GT
GAM380  SEMA4G   5'  CCCGAGGTGCCCTGTTCTCTC  94676         C      GTGCA
                                GGGAGGAC AGGGCAT    GGG
                                |||||||| |||||||    |||
                                CTCTCTTG TCCCGTG    CCC
                                   _      GAG__
GAM380  SEMA5A   3'  CTTTCATGTTTTGGGCTTCTT  14255       A        TGC
                                GGGAGG CCAGGGCATG   AG
                                |||||| ||||||||||   ||
                                TTCTTC GGTTTTGTAC   TC
                                   G         TT_
GAM380  SEMA6B   3'  CCTTATGCGCGTAGGTTTTGGT 49490          __      __
             TTTTTT                GGACCAGGGC  ATGTGCA  GGG
                                ||||||||||  |||||||  |||
                                TTTGGTTTTG  TGCGCGT  TCC
                                      GA      AT
GAM380  SEPT3    3'  CCCAACCTATGCTCTCGGTCTT 38891         _       TGCA
             TCC                   GGGAGGACC AGGGCATG    GGG
                                |||||||| ||||||||    |||
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                                CCTTTCTGG TCTCGTAT    CCC
                                     C       CCAA
GAM380  SEPW1    3'  TCTTGTGGACACCTGGTCTTTC 11542           GCATGT
              C                   GGGAGGACCAGG     GCAGGG
                                  ||||||||||||     ||||||
                                  CCTTTCTGGTCC     TGTTCT
                                        ACAGG_
GAM380  SHAPY    3'  TTTTGTTTTGTTTTGTTCTTTT 57117       C      TGT
                                  GGAGGA CAGGGCA   GCAGGG
                                  ||||||| |||||||   ||||||
                                  TTTTCT GTTTTGT   TGTTTT
                                     T      TT_
GAM380  SIAT4A   3'  TTTTGCACGAAGCCTGGCCTCT 11678       A     GCA
              T                   GGGAGG CCAGG   TGTGCAGGG
                                  |||||| |||||   |||||||||
                                  TTCTCC GGTCC   GCACGTTTT
                                     _    GAA
GAM380  SIRPB1   3'  CACCTGTCTTGGCCTCCC    20242       A       T
                                  GGGAGG CCAGGGCA GTG
                                  |||||| |||||||| |||
                                  CCCTCC GGTTCTGT CAC
                                     _       C
GAM380  SLC12A8  5'  TTCTGTACATCGTCTTCGTCTT 44905         C    _
              CCT                   GGGAGGAC AGGGC ATGTGCAGGG
                                  |||||||| ||||| ||||||||||
                                  TCCTTCTG TTCTG TACATGTCTT
                                      C    C
GAM380  SLC21A6  3'  TTTTGAGGAGTTCCTGGTCCTT 21242   GG        C  GTG_
              TC                    G  AGGACCAGGG AT    CAGGG
                                  |  |||||||||| ||    |||||
                                  C  TCCTGGTCCT TG    GTTTT
                                   TT        _  AGGA
GAM380  SLC2A11  3'  TCCTGCCAGGGCCCTGGTCCTC 47967           A_  T
                                  GAGGACCAGGGC  TG GCAGGG
                                  ||||||||||||  || ||||||
                                  CTCCTGGTCCCG  AC CGTCCT
                                        GG  _
GAM380  SLC38A4  3'  TCTTGCACCAAAGTCTCTGGTC 35877        _  AT__
              T                   GGACCAG GGC    GTGCAGGG
                                  ||||||| |||    ||||||||
                                  TCTGGTC CTG    CACGTTCT
                                     T   AAAC
GAM380  SLC5A6   3'  GTGTCCCTGGTCCTCT      40833           _
                                  GGAGGACCAGGG CAT
                                  |||||||||||| |||
                                  TCTCCTGGTCCC GTG
                                        T
GAM380  SLC5A7   3'  ATGCTTTGTTTTCCC       41504         C
                                  GGGAGGAC AGGGCAT
                                  |||||||| |||||||
```

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                                CCCTTTTG TTTCGTA
                                     _
GAM380  SLPI    3'  CTCTGTGTGGTCCAGGTCCTTT 11772   GG    A   A  TG
            C                    G  AGGACC GGGC TG  CAGGG
                                 |  |||||| |||| ||  |||||
                                 C  TCCTGG CCTG GT  GTCTC
                                  TT     A   _  GT
GAM380  SMARCF1  3'  TTTTGTTTTGTTTTGTTTTCTT 20048       C     TGT
                                 GGGAGGAC AGGGCA   GCAGGG
                                 ||||||||| ||||||   ||||||
                                 TTCTTTTG TTTTGT   TGTTTT
                                      _     TT_
GAM380  SMARCF1  3'  TTTTGTTTTGTTTTGTTTTCTT 37449       C     TGT
                                 GGGAGGAC AGGGCA   GCAGGG
                                 ||||||||| ||||||   ||||||
                                 TTCTTTTG TTTTGT   TGTTTT
                                      _     TT_
GAM380  SMARCF1  3'  TTTTGTTTTGTTTTGTTTTCTT 57494       C     TGT
                                 GGGAGGAC AGGGCA   GCAGGG
                                 ||||||||| ||||||   ||||||
                                 TTCTTTTG TTTTGT   TGTTTT
                                      _     TT_
GAM380  SMCR5   5'  CCCACGCTGTCCTGGCCTCCC  58593      A      T   CA
                                 GGGAGG CCAGGGCA GTG  GGG
                                 ||||||  |||||||| |||  |||
                                 CCCTCC GGTCCTGT CGC  CCC
                                      _      _  A_
GAM380  SMCR7   3'  TTCTGTGCGTTTAGTTTTCTT  57509       CAGGGC   TG
                                 GGGAGGAC     ATG  CAGGG
                                 ||||||||     |||  |||||
                                 TTCTTTTG     TGC  GTCTT
                                      ATT___   GT
GAM380  SMOC2   3'  CTTGTCTGCCTGGTTTTCCT   72373          G  TGT
                                 GGGAGGACCAGG CA   GCAGG
                                 ||||||||||||  ||   |||||
                                 TCCTTTTGGTCC GT   TGTTC
                                        _  C__
GAM380  SNAP29   3'  CTGTAATTGTTTCTGGTTCTTT 16541    GG        _  TG    GG
            C                    G  AGGACCAGGG CA  TGCAG
                                 |  ||||||||||  ||  |||||
                                 C  TCTTGGTCTT GT  ATGTC
                                  TT         T  TA
GAM380  SNAPC2   3'  CCTGCTGCCAGGTCCTTCC    11846         AG    TGT
                                 GGGAGGACC  GGCA   GCAGG
                                 |||||||||  ||||   |||||
                                 CCTTCCTGG  CCGT   CGTCC
                                      A_   ____
GAM380  SNPH    3'  TCTTGCGTCTGTGGCCTTCC   28246       A   G  CATG
                                 GGGAGG CCA GG    TGCAGGG
                                 ||||||  ||| ||    |||||||
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                                CCTTCC GGT TC   GCGTTCT
                                   _  G  T___
GAM380  SNPH    3'  TCTTGTCTCCTTTGTCCTTTT  28247       C   CATGT
                                GGGAGGAC AGGG    GCAGGG
                                |||||||| ||||    ||||||
                                TTTTCCTG TTCC    TGTTCT
                                     T   TC___
GAM380  SP2     3'  CCTTGGCTCTGCCTTGGCCCTT 11886      A      T_  G
            CC                    GGGAGG CCAGGGCA  GT CAGGG
                                |||||| ||||||||  || |||||
                                CCTTCC GGTTCCGT  CG GTTCC
                                   C       CT  _
GAM380  SP2     3'  CTGTATTGTCCTCCT      11889        CAGGGCAT
                                GGGAGGAC      GTGCAG
                                ||||||||      ||||||
                                TCCTCCTG      TATGTC
                                     T________
GAM380  Spir-1  3'  CCTTCCGTGTCCTGGTTTCTT  64697      G        TGC
                                GGGAG ACCAGGGCATG   AGG
                                ||||| ||||||||||   |||
                                TTCTT TGGTCCTGTGC   TCC
                                   _         CT_
GAM380  Spir-1  3'  CTGCACTAGTTTTCCT     64698        CAGGGCAT
                                GGGAGGAC      GTGCAG
                                ||||||||      ||||||
                                TCCTTTTG      CACGTC
                                     AT_______
GAM380  SPRY1   5'  CCTGCGCTGGCTTCTTTC    65002       CCA  G  T
                                GGAGGA   GG CA GTGCAGG
                                ||||||   || || |||||||
                                CTTTCT   TC GT CGCGTCC
                                   ___  G  _
GAM380  SPRY1   3'  TTTTGTTTTTGTTTTTGTTTTC 65008        C     TGT
            TT                    GGGAGGAC AGGGCA   GCAGGG
                                |||||||| ||||||   ||||||
                                TTCTTTTG TTTTGT   TGTTTT
                                     T     TTT
GAM380  SQV7L   5'  CCTCCTGCCTTGGCCTCCC   70574       A      TGTGC
                                GGGAGG CCAGGGCA    AGG
                                |||||| ||||||||    |||
                                CCCTCC GGTTCCGT    TCC
                                   _       CC___
GAM380  SRPK2   3'  GTGTTTTGGTTTTTTT     11971
                                GGGAGGACCAGGGCAT
                                ||||||||||||||||
                                TTTTTTTGGTTTTGTG

GAM380  SS-56   3'  TTTTGCACATGGTGACTTTCC  59609       AC  GGG
                                GGGAGG  CA   CATGTGCAGGG
                                ||||||  ||   ||||||||||
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                                CCTTTC  GT   GTACACGTTTT
                                   A_  G__
GAM380  SS18L1   3'  TTGATGGTGCTTTGTTTTTTTC 65350   GG   C      GTG
                                G  AGGA CAGGGCAT   CAG
                                |  |||| ||||||||   |||
                                C  TTTT GTTTCGTG   GTT
                                 TT   T      GTA
GAM380  SSH-3    3'  CCCTGCACCTCCTGTCCTCTC  36889        C   CAT
                                GGGAGGAC AGGG   GTGCAGGG
                                |||||||| ||||   ||||||||
                                CTCTCCTG TCCT   CACGTCCC
                                     _   C__
GAM380  SSH-3    3'  CCCTGCACCTCCTGTCCTCTC  35341        C   CAT
                                GGGAGGAC AGGG   GTGCAGGG
                                |||||||| ||||   ||||||||
                                CTCTCCTG TCCT   CACGTCCC
                                     _   C__
GAM380  SSH2     3'  CTTGGACTTTGTTTTCCC    62205        CAGGGCAT  G
                                GGGAGGAC       GT CAGG
                                ||||||||       || ||||
                                CCCTTTTG       CA GTTC
                                     TTT_____  G
GAM380  SSH2     3'  TTCTGTTGGATTTTGGTTTGCT 62218     AG       CATGT
           T                     GGG  GACCAGGG    GCAGGG
                                |||  ||||||||    ||||||
                                TTC  TTGGTTTT    TGTCTT
                                  GT       AGGT_
GAM380  ST7L     3'  TTTTGCATATGAAAAAGCTTCT 34860       ACCAGGG
           T                     GGGAGG      CATGTGCAGGG
                                ||||||      ||||||||||
                                TTCTTC      GTATACGTTTT
                                   GAAAAA_
GAM380  ST7L     3'  TTTTGCATATGAAAAAGCTTCT 57581       ACCAGGG
           T                     GGGAGG      CATGTGCAGGG
                                ||||||      ||||||||||
                                TTCTTC      GTATACGTTTT
                                   GAAAAA_
GAM380  ST7L     3'  TTTTGCATATGAAAAAGCTTCT 57004       ACCAGGG
           T                     GGGAGG      CATGTGCAGGG
                                ||||||      ||||||||||
                                TTCTTC      GTATACGTTTT
                                   GAAAAA_
GAM380  STARD7   3'  TTTTGTTTTTGTTTTTGTTTTC 57700        C     TGT
           CT                      GGGAGGAC AGGGCA   GCAGGG
                                ||||||||| ||||||   ||||||
                                TCCTTTTG TTTTGT   TGTTTT
                                     T     TTT
GAM380  STARD7   3'  TTTTGTTTTTGTTTTTGTTTTC 39333        C     TGT
           CT                      GGGAGGAC AGGGCA   GCAGGG
                                ||||||||| ||||||   ||||||
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                                TCCTTTTG TTTTGT   TGTTTT
                                    T     TTT
GAM380  STATI2   3'  CCTTGCCTTCTTAGGTTCTTTT 94552        AG  CATGT
                                GGGAGGACC  GG    GCAGGG
                                |||||||||  ||    ||||||
                                TTTTCTTGG  TC    CGTTCC
                                    AT  TTC__
GAM380  STATI2   3'  CCTTGCCTTCTTAGGTTCTTTT 13922        AG  CATGT
                                GGGAGGACC  GG    GCAGGG
                                |||||||||  ||    ||||||
                                TTTTCTTGG  TC    CGTTCC
                                    AT  TTC__
GAM380  STK38L   3'  ACCGTGTGTTTTTGGTTTTTCT 69171          CAT TG  G
                                GGGAGGACCAGGG   G  CA GG
                                ||||||||||||   |  || ||
                                TCTTTTTGGTTTT   T  GT CC
                                    ___ GT  G  AA
GAM380  STOML2   3'  CCCTGCCAAGATTTTGGTTTTT 25556         CA_  T
                                GAGGACCAGGG   TG GCAGGG
                                ||||||||||   || ||||||
                                TTTTTGGTTTT   AC CGTCCC
                                    AGA  _
GAM380  STX5A    3'  CTCTGGCCACCCTGTCCTCCC  12043       C   CA  TG
                                GGGAGGAC AGGG  TG  CAGGG
                                |||||||| ||||  ||  |||||
                                CCCTCCTG TCCC  AC  GTCTC
                                    _   __ CG
GAM380  SUPT4H1  3'  CCCTGTAGGAGGTAGGTCCTTT 12060        AGG  ATG_
            T                    GGGAGGACC   GC    TGCAGGG
                                |||||||||   ||    |||||||
                                TTTTCCTGG   TG    ATGTCCC
                                    A__  GAGG
GAM380  SYNE-1   5'  TTCTGTACTCTAATGTTCTTTC 30969   GG    CAG  CAT
                                G  AGGAC   GG   GTGCAGGG
                                |  |||||   ||   ||||||||
                                C  TCTTG   TC   CATGTCTT
                                 TT    TAA  T__
GAM380  SYNE-2   3'  CTTTGTGAATTCTGGTTT    30798         CATG
                                GGACCAGGG    TGCAGGG
                                |||||||||    |||||||
                                TTTGGTCTT    GTGTTTC
                                    AA__
GAM380  SYNJ2    3'  CCTATTAAATGTTTTTGTCTTT 61765        C      GTGC_  G
            TT                    GGGAGGAC AGGGCAT     AGG
                                ||||||||| |||||||     |||
                                TTTTTCTG TTTTGTA     TCC
                                    T      AATTA
GAM380  SYT12    5'  CTTTGCCTAGGGCCTGGGTCTT 94730         A    A_  T
            CTT                    GGGAGGACC GGGC  TG GCAGGG
                                |||||||||  ||||  ||  ||||||
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                                TTCTTCTGG TCCG  AT CGTTTC
                                     G   GG  C
GAM380  SYT13    3' CCTTGCATATGTCTGTCC    93454     CA
                                GGAC  GGGCATGTGCAGGG
                                ||||  ||||||||||||||
                                CCTG  TCTGTATACGTTCC
                                  __
GAM380  SYTL2    3' CCCTGCATATATATGATTGTTT 51959       ___  GGGC
           TTCT                  GAGGAC   CA   ATGTGCAGGG
                                ||||||  ||   ||||||||||
                                TTTTTG  GT   TATACGTCCC
                                   TTA  ATA_
GAM380  SYTL2    3' CCCTGCATATATATGATTGTTT 50471       ___  GGGC
           TTCT                  GAGGAC   CA   ATGTGCAGGG
                                ||||||  ||   ||||||||||
                                TTTTTG  GT   TATACGTCCC
                                   TTA  ATA_
GAM380  SYTL2    5' TCCTGTGCATGTGGACTACTC  50473    A  A  AGG    TG
                                GGG GG CC   GCATG  CAGGG
                                ||| || ||   |||||  |||||
                                CTC TC GG   TGTAC  GTCCT
                                  A  A ___    GT
GAM380  T2BP     3' CCTGTGTCTGGTTTTCCT    69995          GGCAT TG
                                GGGAGGACCAG    G  CAGG
                                ||||||||||    |  ||||
                                TCCTTTTGGTC    T  GTCC
                                      _____ GT
GAM380  TA-NFKBH 3' CCCTGCACCCCTAGTCCTTTC  51171   GG    C    CAT
                                G  AGGAC AGGG   GTGCAGGG
                                |  ||||| ||||   ||||||||
                                C  TCCTG TCCC   CACGTCCC
                                 TT    A   ___
GAM380  TA-PP2C  3' CTCGTCAAGTTTCTGGTTTTTC 57758           _ A  T  AG G
           T                    GGGAGGACCAGGG C TG GC  G
                                |||||||||||||  | || ||  |
                                TCTTTTTGGTCTT G AC TG  C
                                       T A  _  CT
GAM380  TACTILE  5' TTTTGTGCGTCAAGTTGGCCTT 19476       A   GGC_   TG
           TT                    GGGAGG CCAG    ATG  CAGGG
                                ||||||  ||||    |||  |||||
                                TTTTCC GGTT    TGC  GTTTT
                                   _    GAAC   GT
GAM380  TBLR1    3' CTCTGTTGGTTTTGTTTTTTT  45100        C    ATGT
                                GGGAGGAC AGGGC    GCAGGG
                                ||||||||  |||||    ||||||
                                TTTTTTTG TTTTG    TGTCTC
                                   _    GT__
GAM380  TBX19    3' TTTGCACAGCGATCCTTCC    17654        CCAGG  A
                                GGGAGGA    GC TGTGCAGG
                                |||||||    || ||||||||
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                                CCTTCCT    CG ACACGTTT
                                   AG___ _
GAM380  TCL6    3'  CCTCCTGCCTTGGCCTCCC   40097      A      TGTGC
                                GGGAGG CCAGGGCA    AGG
                                |||||| ||||||||    |||
                                CCCTCC GGTTCCGT    TCC
                                   _      CC___
GAM380  TCL6    5'  CCCTGCCTCCACCTTGTTTTCT 40127       C   GCATGT
          T                      GGGAGGAC AGG     GCAGGG
                                |||||||| |||     ||||||
                                TTCTTTTG TCC     CGTCCC
                                   T   ACCTC_
GAM380  TCL6    3'  CCTCCTGCCTTGGCCTCCC   40128      A      TGTGC
                                GGGAGG CCAGGGCA    AGG
                                |||||| ||||||||    |||
                                CCCTCC GGTTCCGT    TCC
                                   _      CC___
GAM380  TCL6    5'  CCCTGCCTCCACCTTGTTTTCT 40155       C   GCATGT
          T                      GGGAGGAC AGG     GCAGGG
                                |||||||| |||     ||||||
                                TTCTTTTG TCC     CGTCCC
                                   T   ACCTC_
GAM380  TED     3'  CTCTGTATATGTACTGCTTTCT 31635      AC   GG
                                GGGAGG  CAG  CATGTGCAGGG
                                ||||||  |||  ||||||||||
                                TCTTTC  GTC  GTATATGTCTC
                                   __   AT
GAM380  TFIP11   3'  TCCTGATAATCTGGTTCTTCC  24057          GCATGTG
                                GGGAGGACCAGG      CAGGG
                                ||||||||||||      |||||
                                CCTTCTTGGTCT      GTCCT
                                      AATA___
GAM380  TGIF2    3'  CTTTGTTCCAGCCTGGTTTCCT 41451      G     G A  T_
                                GGGAG ACCAGG C TG  GCAGGG
                                ||||| |||||| | ||  ||||||
                                TCCTT TGGTCC G AC  TGTTTC
                                   _     _ _ CT
GAM380  TGIF2    3'  GTGTTTGGTTTTTCT       41458           G
                                GGGAGGACCAGG CAT
                                |||||||||||| |||
                                TCTTTTTGGTTT GTG
                                      _
GAM380  TGOLN2   3'  CCTTGAGAACCTTGTCCTCCC  64047        C   GCATGTG
                                GGGAGGAC AGG      CAGGG
                                |||||||| |||      |||||
                                CCCTCCTG TCC      GTTCC
                                   T   AAGA___
GAM380  THEA     3'  TCCTCCTGCCTTGGATCTCCC  66300       A      TGTGC
                                GGGAGG CCAGGGCA    AGGG
                                |||||| ||||||||    ||||
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                                CCCTCT GGTTCCGT    TCCT
                                   A      CC___
GAM380  THEA    3'  TTTGTGTGTGTGTCTTT    66304      CAGG    TG
                                GAGGAC   GCATG  CAGG
                                ||||||   |||||  ||||
                                TTTCTG   TGTGT  GTTT
                                   ____    GT
GAM380  TLN2    3'  CTTTGGCTTTTGTTGGTCCTTC 61687        GG   TGT  _
           T                     GGGAGGACCA  GCA   GC AGGG
                                ||||||||||  |||   || ||||
                                TCTTCCTGGT  TGT   CG TTTC
                                      __  TTT  G
GAM380  TMSNB   3'  CTTTGTGTATGTAGTTCTTGC  41811   G    CAGG    TG
                                G GAGGAC   GCATG  CAGGG
                                | ||||||   |||||  |||||
                                C TTCTTG   TGTAT  GTTTC
                                 G     A___    GT
GAM380  TNRC6   3'  CTCTGCACATTTTCCACTTTGT 70507     C_  _  C__
           TTTCCC                 GGAC  AG GG   ATGTGCAGGG
                                ||||  || ||   ||||||||||
                                TTTG  TC CC   TACACGTCTC
                                  TT  A  TTT
GAM380  TOPK    3'  TCTTGATCTCTTGGATCTCCT  37506      A    CATGTG
                                GGGAGG CCAGGG     CAGGG
                                |||||| ||||||     |||||
                                TCCTCT GGTTCT     GTTCT
                                   A     CTA___
GAM380  TP53INP1  3'  TTCTGTGTGTATGGTTTTTCC  52734        GG   GT
                                GGGAGGACCA  GCAT  GCAGGG
                                ||||||||||  ||||  ||||||
                                CCTTTTTGGT  TGTG  TGTCTT
                                      A_   __
GAM380  TP53INP1  3'  TTCTGTGTGTATGGTTTTTCC  72961        GG   GT
                                GGGAGGACCA  GCAT  GCAGGG
                                ||||||||||  ||||  ||||||
                                CCTTTTTGGT  TGTG  TGTCTT
                                      A_   __
GAM380  TPRA40   3'  CCCATGGTGCTTTGGCCTCCT  33039      A       GTG  _
                                GGGAGG CCAGGGCAT   CA GGG
                                |||||| |||||||||   || |||
                                TCCTCC GGTTTCGTG   GT CCC
                                   _       ___  A
GAM380  TRAF4   3'  TCTGGGCTTTGGTTATCCC   62630     G       ATGTG
                                GGGA GACCAGGGC    CAGG
                                |||| |||||||||    ||||
                                CCCT TTGGTTTCG    GTCT
                                  A       G____
GAM380  TREX1   5'  TCTGGCACCACTGCCCTGGTCC 33059           T__   A
           TTCC                   GGAGGACCAGGGCA   GTGC GGG
                                ||||||||||||||   |||| |||
```

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                                CTTCCTGGTCCCGT   CACG TCT
                                      CAC    G
GAM380  TREX1    5'  TCTGGCACCACTGCCCTGGTCC 53283           T__    A
           TTCC                  GGAGGACCAGGGCA   GTGC GGG
                                ||||||||||||||   |||| |||
                                CTTCCTGGTCCCGT   CACG TCT
                                      CAC    G
GAM380  TREX1    5'  TCTGGCACCACTGCCCTGGTCC 53293           T__    A
           TTCC                  GGAGGACCAGGGCA   GTGC GGG
                                ||||||||||||||   |||| |||
                                CTTCCTGGTCCCGT   CACG TCT
                                      CAC    G
GAM380  TRIM11   3'  TCTGGATCCTGGTCTTCCT   72835          GCAT  G
                                GGGAGGACCAGG    GT CAGG
                                ||||||||||||    || ||||
                                TCCTTCTGGTCC    TA GTCT
                                      _____  G
GAM380  TRIM22   3'  TTTTGTTTTTGTTCTGTTTTCT 20288        C     TGT
           T                    GGGAGGAC AGGGCA   GCAGGG
                                |||||||| ||||||   ||||||
                                TTCTTTTG TCTTGT   TGTTTT
                                     _     TTT
GAM380  TRIM26   3'  CTTTGTGTGTGTCACATGCTGC 12888     A  ACCAG     TG
           CT                     GGG GG    GGCATG  CAGGG
                                ||| ||    ||||||  |||||
                                TCC TC    CTGTGT  GTTTC
                                  G  GTACA     GT
GAM380  TTTY9    3'  GTGTACTGGTTTTTCC      49186          GG
                                GGGAGGACCAG  CAT
                                ||||||||||  |||
                                CCTTTTTGGTC  GTG
                                       AT
GAM380  TU12B1-TY 3'  CACCTGCCTTGGCCTCCC    33370       A       T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTCC GGTTCCGT CAC
                                     _       C
GAM380  TU12B1-TY 3'  TGTACCAGGTTTTTCT      33410          A  _
                                GGGAGGACC GG GCA
                                ||||||||| || |||
                                TCTTTTTGG CC TGT
                                      A  A
GAM380  TUB      3'  TCTGTATATAGGCCTTCC     12430       A  AGGGC
                                GGGAGG CC     ATGTGCAGG
                                |||||| ||     |||||||||
                                CCTTCC GG     TATATGTCT
                                     _  A_____
GAM380  TUSP     3'  TTTTGTTTTTGTTTTTGTTTTT 39647         C     TGT
           CT                     GGGAGGAC AGGGCA   GCAGGG
                                ||||||||| ||||||   ||||||
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                                TCTTTTTG TTTTGT   TGTTTT
                                    T     TTT
GAM380  UACA     3'  CTTTGTGCAACTCCATGGTCTT 72391          _  CA  TG
            TCT                   GGGAGGACCA GGG  TG  CAGGG
                                  |||||||||| |||  ||  |||||
                                  TCTTTCTGGT CCT  AC  GTTTC
                                      A   CA  GT
GAM380  UBCE7IP5 3'  TCCTGTGTGCCCCTGGCTTTCT 30162        A     _  GT
                                  GGGAGG CCAGGG CAT  GCAGGG
                                  |||||| |||||| |||  ||||||
                                  TCTTTC GGTCCC GTG  TGTCCT
                                     _     C  __
GAM380  UBE2G1   3'  TAGGTGCTTTGTCCTTTT    12485         C      G
                                  GGGAGGAC AGGGCAT TG
                                  |||||||| ||||||| ||
                                  TTTTCCTG TTTCGTG AT
                                     _      G
GAM380  UPB1     3'  CTTAACATGTCCAGGTTCTCCC 32887          A       GC
                                  GGGAGGACC GGGCATGT  AGG
                                  ||||||||| ||||||||  |||
                                  CCCTCTTGG CCTGTACA  TTC
                                      A       A_
GAM380  VEGFC    3'  TCTTGTAAAGACTGGTTTTCT  18309          GGCATG
                                  GGAGGACCAG     TGCAGGG
                                  ||||||||||     |||||||
                                  TCTTTTGGTC     ATGTTCT
                                      AGAA__
GAM380  VPS29    3'  TCTTGATGATTTTTGGTTTTTT 54115           CATGTG
            T                     GGGAGGACCAGGG     CAGGG
                                  ||||||||||||||     |||||
                                  TTTTTTTGGTTTT     GTTCT
                                        TAGTA_
GAM380  VPS29    3'  TCTTGATGATTTTTGGTTTTTT 32632           CATGTG
            T                     GGGAGGACCAGGG     CAGGG
                                  ||||||||||||||     |||||
                                  TTTTTTTGGTTTT     GTTCT
                                        TAGTA_
GAM380  VPS39    3'  CCTGCCTCCTGTCCTCCC    62844         C   CATGT
                                  GGGAGGAC AGGG     GCAGG
                                  |||||||| ||||     |||||
                                  CCCTCCTG TCCT     CGTCC
                                      _    C____
GAM380  WDR18    3'  TTCTGTGTCGTGTTCGGGTTTT 65552          A     _
            TCC                     GGGAGGACC GGGCATG TGCAGGG
                                  ||||||||| ||||||| |||||||
                                  CCTTTTTGG CTTGTGC GTGTCTT
                                      G      T
GAM380  WIRE     3'  CAGATGCTTTGGTTTTCT    78300             G
                                  GGAGGACCAGGGCAT TG
                                  |||||||||||||| ||
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                                TCTTTTGGTTTCGTA AC
                                       G
GAM380  WS-3     3'  TCCTATATCCTTGGTTCTTTT  21648           C    GC
                                GGGAGGACCAGGG ATGT  AGGG
                                |||||||||||| ||||  ||||
                                TTTTCTTGGTTCC TATA  TCCT
                                       _   __
GAM380  X123     5'  CTCTGTGGTTTGTGTCCTCTT  69923        _    G ATGT
                                GGGAGGAC CAGG C    GCAGGG
                                |||||||| |||| |    ||||||
                                TTCTCCTG GTTT G    TGTCTC
                                     T    G ____
GAM380  XYLT1    3'  CCTGCCCTTTGGTTC       77848          CATGT
                                GGACCAGGG    GCAGG
                                |||||||||    |||||
                                CTTGGTTTC    CGTCC
                                     C____
GAM380  YAP1     3'  CATTTCCTGGTTTTTTT     20348            C
                                GGGAGGACCAGGG ATG
                                |||||||||||| |||
                                TTTTTTTGGTCCT TAC
                                       T
GAM380  YWHAQ    3'  TTTGTGTTTGTCTTGGCCTTCC 22398       A       T TG    G
                                GGGAGG CCAGGGCA G  CAGG
                                |||||| |||||||| |  ||||
                                CCTTCC GGTTCTGT T  GTTT
                                   _       T GT
GAM380  ZAP3     5'  TCCTGTGTCTTTTGGTTCTGCC 77225     _        CAT TG
            C                    GGG AGGACCAGGG   G  CAGGG
                                ||| ||||||||||   |  |||||
                                CCC TCTTGGTTTT   T  GTCCT
                                  G        C__ GT
GAM380  ZDHHC5   5'  TTCTGTTTCCCTGGTTTTCTT  91565           CATGT
                                GGGAGGACCAGGG    GCAGGG
                                ||||||||||||    ||||||
                                TTCTTTTGGTCCC    TGTCTT
                                       TT___
GAM380  ZFD25    5'  CCTGTGTTTGCTCCTCCC    32579        CCAGG   T TG
                                GGGAGGA    GCA G  CAGG
                                |||||||    ||| |  ||||
                                CCCTCCT    CGT T  GTCC
                                   _____  T GT
GAM380  ZFP106   3'  CATATGCTCTGGTTTGCTC   42463     AG
                                GGG  GACCAGGGCATGTG
                                |||  ||||||||||||||
                                CTC  TTGGTCTCGTATAC
                                  GT
GAM380  ZIC4     3'  CCCTGTGTGTGCAAACATGTGC 49617      G  CAGG__    TG
            TCTC                   GGAG AC     GCATG  CAGGG
                                |||| ||     |||||  |||||
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                                TCTC TG     CGTGT  GTCCC
                                  G  TACAAA    GT
GAM380  ZID      3'  CTTTGAAGCTGTTCTAGTCCTC 21777        C     T  G_
              CT                   GGGAGGAC AGGGCA GT  CAGGG
                                |||||||| |||||| ||  |||||
                                TCCTCCTG TCTTGT CG  GTTTC
                                   A     _  AA
GAM380  ZIM2     3'  TGTGTTCTGGGTTTTTTT    31088         _
                                GGGAGGACC AGGGCATG
                                ||||||||| ||||||||
                                TTTTTTTGG TCTTGTGT
                                     G
GAM380  ZIN      3'  TCTTGTATGTGAAAACTTGTCT 25494      C  GG__
                                GGAC AG    CATGTGCAGGG
                                |||| ||    ||||||||||
                                TCTG TC    GTGTATGTTCT
                                  T  AAAA
GAM380  ZNF212   3'  CCTTCAGGTCTCTGGTTTTCTC 24304           C  G  C
                                GGGAGGACCAGGG AT TG AGG
                                |||||||||||| || || |||
                                CTCTTTTGGTCTC TG AC TCC
                                       _  G  T
GAM380  ZNF220   3'  TTTTGTTGTGGGTTTTGGTTTT 22229            ATGT_
              CTT                   GGGAGGACCAGGGC    GCAGGG
                                |||||||||||||    ||||||
                                TTCTTTTGGTTTTG    TGTTTT
                                      GGTGT
GAM380  ZNF230   5'  TTCTGCGTCTGGCGGGTCCTTC 20860         AGGG  TG
              T                   GGGAGGACC    CA  TGCAGGG
                                |||||||||    ||  |||||||
                                TCTTCCTGG    GT  GCGTCTT
                                     GCG_  CT
GAM380  ZNF238   3'  TTCTGTGGCAACTTCTGGTTTT 20972           CA  _
              CT                   GGAGGACCAGGG  TGT GCAGGG
                                |||||||||||  ||| ||||||
                                TCTTTTGGTCTT  ACG TGTCTT
                                      CA   G
GAM380  ZNF238   3'  TTTTGCACAGTGTTTGTTTTCC 20978         C  G  A
              T                   GGGAGGAC AG GC TGTGCAGGG
                                |||||||| || || |||||||||
                                TCCTTTTG TT TG ACACGTTTT
                                     T  G  _
GAM380  ZNF297B  3'  CTCTGTTGTCTGGTTTTAGTCT 25780        C    ATGT__
              TTCT                   GGAGGAC AGGGC     GCAGGG
                                |||||||| |||||     ||||||
                                CTTTCTG TTTTG     TGTCTC
                                   A    GTCTGT
GAM380  ZNF297B  3'  TTTTGTAAACTCTGGTTTTT   25792          CATG
                                GAGGACCAGGG    TGCAGGG
                                ||||||||||    |||||||
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                                TTTTTGGTCTC   ATGTTTT
                                      AA__
GAM380  ZNF297B  3'  CTCTGTTGTCTGGTTTTAGTCT 81808       C    ATGT__
          TTCT                  GGAGGAC AGGGC     GCAGGG
                                ||||||| |||||     ||||||
                                CTTTCTG TTTTG     TGTCTC
                                   A    GTCTGT
GAM380  LOC112476 3'  CCCTGCATCTCTCCTGGCCTCC 59111       A     CAT
          C                     GGGAGG CCAGGG   GTGCAGGG
                                |||||| ||||||   ||||||||
                                CCCTCC GGTCCT   TACGTCCC
                                   _     CTC
GAM380  LOC112724 3'  TCTGAGCCTTGGTTTCTTC   56504       _     ATGTG
                                GGAGGA CCAGGGC    CAGG
                                |||||| |||||||    ||||
                                CTTCTT GGTTCCG    GTCT
                                   T      A____
GAM380  LOC112724 3'  CCTTGTGCATGCATGGTCCTCT 56494         GG    TG
          C                     GGGAGGACCA  GCATG  CAGGG
                                ||||||||||  |||||  |||||
                                CTCTCCTGGT  CGTAC  GTTCC
                                      A_    GT
GAM380  LOC112885 3'  TTCTGTTGGTTTGGTTTTCTT  56533          G  TGT
                                GGGAGGACCAGG CA   GCAGGG
                                |||||||||||| ||   ||||||
                                TTCTTTTGGTTT GT   TGTCTT
                                      G  ___
GAM380  LOC113386 3'  TTGTGTCTGGCTTTTT     57082       A    GGCAT TG
                                GGGAGG CCAG    G  CAG
                                |||||| ||||    |  |||
                                TTTTTC GGTC    T  GTT
                                   _   _____ GT
GAM380  LOC113386 3'  TCCTGCATGTGTTGATGCCACC 57081     A  ACCAG
          T                     GGG GG    GGCATGTGCAGGG
                                ||| ||    ||||||||||||
                                TCC CC    TTGTGTACGTCCT
                                  A  GTAG_
GAM380  LOC114926 3'  TCTGTGCATTGTTTTGCCT   56589     AC     _  TG
                                AGG  CAGGGCA TG  CAGG
                                |||  ||||||| ||  ||||
                                TCC  GTTTTGT AC  GTCT
                                  __      T  GT
GAM380  LOC114971 3'  CTCTGACTTGTTTTGTTTTCTT 73147        C     T  G
                                GGGAGGAC AGGGCA GT CAGGG
                                |||||||| |||||| || |||||
                                TTCTTTTG TTTTGT CA GTCTC
                                   _     T  _
GAM380  LOC115129 5'  TTTTGATAGCCCCTGGTTTTGT 73245    G        CA   G
          T                     GG AGGACCAGGG  TGT CAGGG
                                || ||||||||||  ||| |||||
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                                TT TTTTGGTCCC  ATA GTTTT
                                 G         CG  _
GAM380  LOC115219 3'  CTTTGTCGTTTTGGTTTTGTC  73306    G         ATGT
                                GG AGGACCAGGGC    GCAGGG
                                || ||||||||||    ||||||
                                CT TTTTGGTTTTG    TGTTTC
                                 G         C___
GAM380  LOC115294 5'  CTCTGCGCATGCCCGGACCCC  73014    A  A  A
                                GG GG CC GGGCATGTGCAGGG
                                || || || ||||||||||||||
                                CC CC GG CCCGTACGCGTCTC
                                 _ A  _
GAM380  LOC115817 3'  CCTTGGTTTTCCTTGTCCTTCT 56616         C    CATGTG
                                GGGAGGAC AGGG     CAGGG
                                |||||||| ||||      |||||
                                TCTTCCTG TCCT     GTTCC
                                     T    TTTG__
GAM380  LOC115817 3'  TGTGCCTTGGTTTTCCT     56618
                                GGGAGGACCAGGGCATG
                                |||||||||||||||||
                                TCCTTTTGGTTCCGTGT

GAM380  LOC115817 3'  TGTGCCTTGGTTTTCCT     56619
                                GGGAGGACCAGGGCATG
                                |||||||||||||||||
                                TCCTTTTGGTTCCGTGT

GAM380  LOC116411 5'  GTGTTTTGGCCTCTC       73870       A
                                GGGAGG CCAGGGCAT
                                ||||||| |||||||||
                                CTCTCC GGTTTTGTG
                                   _
GAM380  LOC118668 5'  CCTTGGAGTGTTGGTTCTTCC  75481          GG    GTG
                                GGGAGGACCA  GCAT   CAGGG
                                ||||||||||  ||||   |||||
                                CCTTCTTGGT  TGTG   GTTCC
                                     __    AG_
GAM380  LOC118812 3'  CCTTGTATGTGCCCTGTCACCT 73930     AG   C
                                GGG  GAC AGGGCATGTGCAGGG
                                |||  ||| ||||||||||||||||
                                TCC  CTG TCCCGTGTATGTTCC
                                  A_  _
GAM380  LOC120425 3'  TCCTGTGTGTGTCCTGGGCCAC 74011     A  A        TG
           TC                    GGG GG CCAGGGCATG  CAGGG
                                ||| || ||||||||||  |||||
                                CTC CC GGTCCTGTGT  GTCCT
                                  A  G         GT
GAM380  LOC122700 3'  CTTTGAAAATGATGTTTTGTTC 74148      C       GTG___
           CTTTT                   AGGA CAGGGCAT      CAGGG
                                |||| ||||||||      |||||
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                                TCCT GTTTTGTA     GTTTC
                                  T       GTAAAA
GAM380  LOC124045 3'  CCTTGCCAGCGCTGTCCTGTCT 76034       C     _  __
                TTCT                  GAGGAC AGGGCA TGT  GCAGGG
                                |||||| |||||| |||  ||||||
                                TTTCTG TCCTGT GCG  CGTTCC
                                  _     C   AC
GAM380  LOC124446 5'  CTTTGCGTAAAAGCGGTGCTCT 74289      G   AGG  A__
                T                  GGGAG ACC   GC   TGTGCAGGG
                                ||||| |||   ||   |||||||||
                                TTCTC TGG   CG   ATGCGTTTC
                                  G   ___  AAA
GAM380  LOC124460 3'  TTTGCTCCCTGGTTTCCT    76049      G      CATGT
                                GGGAG ACCAGGG    GCAGG
                                ||||| |||||||    |||||
                                TCCTT TGGTCCC    CGTTT
                                  _      T_____
GAM380  LOC124512 5'  TTCTGCGCGTGTGAGTCTCTTT 74304    GG  _   CAGG
                C                  G  AG GAC    GCATGTGCAGGG
                                |  || |||    ||||||||||||
                                C  TC CTG    TGTGCGCGTCTT
                                 TT  T   AG__
GAM380  LOC124739 5'  TCCTGTGTGTGTCCCTACCTAT 74332     _  ACC    _   TG
                CC                   GGG AGG   AGGG CATG  CAGGG
                                ||| |||   |||| ||||  |||||
                                CCT TCC   TCCC GTGT  GTCCT
                                  A   A__    T    GT
GAM380  LOC126133 3'  CTTGCTCTCTGGTTTTCTC    74442           CATGT
                                GGGAGGACCAGGG    GCAGG
                                ||||||||||||    |||||
                                CTCTTTTGGTCTC    CGTTC
                                        T_____
GAM380  LOC126528 5'  CTCTGATCTCTGAGTCTTCTC  74528         _    CATGTG
                                GGGAGGAC CAGGG     CAGGG
                                |||||||| |||||     |||||
                                CTCTTCTG GTCTC     GTCTC
                                     A     TA_____
GAM380  LOC126669 3'  CTCTGAATGCTCTGGCTTTTT  75405       A       GTG
                                GGGAGG CCAGGGCAT   CAGGG
                                |||||| |||||||||   |||||
                                TTTTTC GGTCTCGTA   GTCTC
                                  _        A__
GAM380  LOC126964 3'  CAGGGTTCTTGTTTTTCC    74616        C    A_
                                GGGAGGAC AGGGC  TG
                                |||||||| |||||  ||
                                CCTTTTTG TCTTG  AC
                                     T    GG
GAM380  LOC127262 3'  CTCTGTAACTTCAGTTCTGGTG 76109    G       ATG___
                TTTTC                  AG ACCAGGGC     TGCAGGG
                                || ||||||||     |||||||
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                                TT TGGTCTTG     ATGTCTC
                                 G       ACTTCA
GAM380  LOC128272 3'  TCCTGCCTGACTCTTGGTCCTT 74730           CATGT
                CT                GGGAGGACCAGGG    GCAGGG
                                  ||||||||||||     ||||||
                                  TCTTCCTGGTTCT    CGTCCT
                                        CAGTC
GAM380  LOC130162 3'  TCCTGTGTGTTAGACTGTCTTC 74913       C  GGC_   TG
                CC                GGGAGGAC AG   ATG  CAGGG
                                  |||||||| ||   |||  |||||
                                  CCCTTCTG TC   TGT  GTCCT
                                      _ AGAT   GT
GAM380  LOC130355 5'  CCCTGTGTTACTTTGGTTCATC 74929     _       CAT TG
                TT                GGGA GGACCAGGG   G  CAGGG
                                  |||| |||||||||   |  |||||
                                  TTCT CTTGGTTTC   T  GTCCC
                                    A       AT_ GT
GAM380  LOC131000 5'  CTTTGGAAGCCTCGGTTTTTCC 75853        AG   ATGTG
                                  GGGAGGACC  GGC    CAGGG
                                  |||||||||  |||    |||||
                                  CCTTTTTGG  CCG    GTTTC
                                       CT   AAG__
GAM380  LOC131583 3'  TTCTGTACATAACTGTGTTCTC 75867       _   GGC
                                  GAGGAC CAG   ATGTGCAGGG
                                  ||||||  |||   ||||||||||
                                  CTCTTG GTC   TACATGTCTT
                                     T   AA_
GAM380  LOC131870 3'  CTCTGCACACACCTGTCTTCCC 75017       C   GCA
                                  GGGAGGAC AGG   TGTGCAGGG
                                  |||||||| |||   |||||||||
                                  CCCTTCTG TCC   ACACGTCTC
                                       _   AC_
GAM380  LOC132001 5'  CCTTGCGTGTGCTTGCAGTCC  57154     CA_    TG
                                  GGAC   GGGCA  TGCAGGG
                                  ||||   |||||  |||||||
                                  CCTG   TTCGT  GCGTTCC
                                    ACG    GT
GAM380  LOC132112 5'  TCCTGCTTCCTCCTGGTCTTGT 75036    G       CATGT
                C                  GG AGGACCAGGG    GCAGGG
                                   || ||||||||||    ||||||
                                   CT TTCTGGTCCT    CGTCCT
                                    G        CCTT_
GAM380  LOC132671 3'  TCTGAGCCTTGGTTTT      59171          ATGTG
                                  AGGACCAGGGC    CAGG
                                  ||||||||||     ||||
                                  TTTTGGTTCCG    GTCT
                                        A____
GAM380  LOC133418 3'  ATGCCTTGATTTTCCT      75089        C
                                  GGGAGGA CAGGGCAT
                                  ||||||| ||||||||
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                                TCCTTTT GTTCCGTA
                                    A
GAM380  LOC133634 3'  CTCTGTATATGCTTTTGACTTT 75103       ACC
                CC                  GGGAGG  AGGGCATGTGCAGGG
                                    ||||||  ||||||||||||||||
                                    CCTTTC  TTTCGTATATGTCTC
                                       AGT
GAM380  LOC134111 3'  CTCTGTATCTCTGTTTTTCTT  75136       C    CAT
                                    GGGAGGA CAGGG  GTGCAGGG
                                    ||||||| |||||  ||||||||
                                    TTCTTTT GTCTC  TATGTCTC
                                       T    ___
GAM380  LOC134111 3'  TTTGTGTTCCTGTCTTCTC   75140       C   CAT TG
                                    GGGAGGAC AGGG  G  CAGG
                                    |||||||| ||||  |  ||||
                                    CTCTTCTG TCCT  T  GTTT
                                       _   ___ GT
GAM380  LOC134145 3'  TCTGAGCCTTGGCTTTCT    75145       A     ATGTG
                                    GGGAGG CCAGGGC    CAGG
                                    |||||| |||||||    ||||
                                    TCTTTC GGTTCCG    GTCT
                                       _      A____
GAM380  LOC134187 3'  TTTTGTGTTTTCCCTTTGTTTT 75931        C_   CAT TG
                TCC                 GGGAGGAC  AGGG  G  CAGGG
                                    ||||||||  ||||  |  |||||
                                    CCTTTTTG  TCCC  T  GTTTT
                                       TT   TTT GT
GAM380  LOC134265 3'  TCTGATTCTTGTTTTCCT    75176       C   CATGTG
                                    GGGAGGAC AGGG     CAGG
                                    |||||||| ||||     ||||
                                    TCCTTTTG TTCT     GTCT
                                       _   TA____
GAM380  LOC135293 3'  CCTCCTGTCTTGGCCTCCC   76176       A      TGTGC
                                    GGGAGG CCAGGGCA    AGG
                                    |||||| ||||||||    |||
                                    CCCTCC GGTTCTGT    TCC
                                       _      CC___
GAM380  LOC136345 3'  CGTGCCCTGGCTTCTC      76206       A
                                    GGGAGG CCAGGGCATG
                                    |||||| ||||||||||
                                    CTCTTC GGTCCCGTGC
                                       _
GAM380  LOC138389 3'  TCGCGCTGTGGGTTCTGGTCTT 76235          AT___   AGGG
                CCT                 GAGGACCAGGGC    GTGC
                                    ||||||||||||    ||||
                                    CTTCTGGTCTTG    CGCG
                                          GGTGT   CT
GAM380  LOC142955 3'  TTCTGTGCTGCTGCTTCTCCT  76450       C  GG   T TG
                                    GGGAGGA CA  GCA G  CAGGG
                                    ||||||| ||  ||| |  |||||
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                                TCCTCTT GT  CGT C  GTCTT
                                    C __  _ GT
GAM380  LOC143287 3'  CCCTGACCCAGCCTGGTCCTTC 82929          G A  TG_
          C                      GGGAGGACCAGG C TG   CAGGG
                                 |||||||||||| | ||   |||||
                                 CCTTCCTGGTCC G AC   GTCCC
                                       _ _  CCA
GAM380  LOC143384 3'  TTTTGCACATGGGTCGGATTTT 76556       _ AGGG
          CCC                    GGGAGGA CC    CATGTGCAGGG
                                 |||||||  ||    ||||||||||
                                 CCCTTTT GG    GTACACGTTTT
                                    A  CTGG
GAM380  LOC143524 3'  CCCTGTGTATTATCCTTGTTTT 76594    GG    C    C_   TG
          TTC                    G  AGGAC AGGG  ATG  CAGGG
                                 |  ||||| ||||  |||  |||||
                                 C  TTTTG TCCT  TAT  GTCCC
                                  TT    T    AT   GT
GAM380  LOC143914 5'  CTCTGCCCACATTTTGGTCTGT 76611      _       CA  T
          TCT                    GGGA GGACCAGGG  TG GCAGGG
                                 |||| |||||||||  || ||||||
                                 TCTT TCTGGTTTT  AC CGTCTC
                                   G        AC  C
GAM380  LOC144182 3'  CCTGTATCGTGGACCTTTT    57495       A   G GCAT
                                 GGGAGG CCA G    GTGCAGG
                                 ||||||| ||| |   |||||||
                                 TTTTCC GGT C    TATGTCC
                                    A   G ____
GAM380  LOC144438 3'  TTCTGCCATTGCCTCTGTCTTC 76840        CA    _ T
          CT                     GGGAGGAC  GGGCA TG GCAGGG
                                 ||||||||  ||||| || ||||||
                                 TCCTTCTG  TCCGT AC CGTCTT
                                     TC    T _
GAM380  LOC144473 3'  CCTTGCGGTCACATTCTGGTTC 83070          CA __
          TCT                    GGAGGACCAGGG  TG  TGCAGGG
                                 ||||||||||||  ||  |||||||
                                 TCTCTTGGTCTT  AC  GCGTTCC
                                       AC  TG
GAM380  LOC144519 5'  CACCTGCCTTGGCTTCCC    76866       A       T
                                 GGGAGG CCAGGGCA GTG
                                 |||||| |||||||| |||
                                 CCCTTC GGTTCCGT CAC
                                    _       C
GAM380  LOC144695 5'  GTGCCTCTGGTTTTCTT     83181          _
                                 GGGAGGACCAG GGCAT
                                 |||||||||||| |||||
                                 TTCTTTTGGTC CCGTG
                                       T
GAM380  LOC144698 5'  TGTGTCTGTCTTCTC       76912         CA
                                 GGGAGGAC  GGGCATG
                                 ||||||||  |||||||
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                                CTCTTCTG  TCTGTGT
                                   __
GAM380  LOC144715 5'  TCCTGTTCTCTCCTGTGTTTTT 76932   GG    _    CATGT
              TC                  G  AGGAC CAGGG    GCAGGG
                                  |  ||||| |||||    ||||||
                                  C  TTTTG GTCCT    TGTCCT
                                   TT    T    CTCT_
GAM380  LOC144715 5'  TGGATGTGTCCTGTTCTCTC   76933        C       G
                                  GGGAGGAC AGGGCATGT CA
                                  |||||||| ||||||||| ||
                                  CTCTCTTG TCCTGTGTA GT
                                      _       G
GAM380  LOC144747 5'  TTCTGTGTGTGTTTTTTTAGTT 76954      C___       TG
              CTTTT                 AGGAC    AGGGCATG  CAGGG
                                  |||||    ||||||||  |||||
                                  TCTTG    TTTTGTGT  GTCTT
                                     ATTT       GT
GAM380  LOC144840 3'  CTCTGTGTAACAGATTCTCCT  76973        CCAGGGCA  TG
                                  GGGAGGA       TG  CAGGG
                                  |||||||       ||  |||||
                                  TCCTCTT       AT  GTCTC
                                      AGACA___  GT
GAM380  LOC145009 3'  TCTTGTAGTGTACTGTTTTTTT 60353        C  GG   G
                                  GGGAGGAC AG  CAT TGCAGGG
                                  |||||||| ||  ||| |||||||
                                  TTTTTTTG TC  GTG ATGTTCT
                                      _ AT  _
GAM380  LOC145225 3'  CTCTGTGTCTCCGTTGGTCCCT 83304     A      _  CAT TG
              C                    GGG GGACCAG GG   G  CAGGG
                                  ||| ||||||| ||   |  |||||
                                  CTC CCTGGTT CC   T  GTCTC
                                    _      G  TC_ GT
GAM380  LOC145268 5'  CTTGATTTTGGTCTTCT     77057          GCATGTG
                                  GGAGGACCAGG      CAGG
                                  ||||||||||       ||||
                                  TCTTCTGGTTT      GTTC
                                        TA_____
GAM380  LOC145355 5'  TCCTGCAGCTGGTTGAGTTCTT 77100   GG    CA  G  TG
              TC                   G  AGGAC  GG CA  TGCAGGG
                                  |  |||||  || ||  |||||||
                                  C  TCTTG  TT GT  ACGTCCT
                                   TT    AG  G  CG
GAM380  LOC145453 5'  TCTGTCTGCTTTGGTCTCCC   77148      G       TGT
                                  GGGAG ACCAGGGCA   GCAGG
                                  ||||| |||||||||   |||||
                                  CCCTC TGGTTTCGT   TGTCT
                                     _       C__
GAM380  LOC145508 3'  TCTTGTATAATTTGGTCCTATC 77261   GG       GCA
                                  G  AGGACCAGG   TGTGCAGGG
                                  |  |||||||||   |||||||||
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                                C  TCCTGGTTT   ATATGTTCT
                                 TA        A__
GAM380   LOC145601 3'  CAAAGGCCCTGGTCTTTCC    83362             ATG
                                GGGAGGACCAGGGC   TG
                                |||||||||||||   ||
                                CCTTTCTGGTCCCG   AC
                                      GAA
GAM380   LOC145608 3'  TTCTGGAATTGTCCTTGGTTTT 83389            _  TGTG
           TCC                    GGGAGGACCAGGG CA    CAGGG
                                |||||||||||| ||    |||||
                                CCTTTTTGGTTCC GT    GTCTT
                                      T  TAAG
GAM380   LOC145622 5'  CCTGGTTCCCTGGTCTCTT    77298       G      C  GTG
                                GGGAG ACCAGGG AT   CAGG
                                ||||| ||||||| ||   ||||
                                TTCTC TGGTCCC TG   GTCC
                                  _       T  ____
GAM380   LOC145623 5'  CTCTATTATATATTTTGGTTTT 83394            C     C_
           CTT                    GGGAGGACCAGGG ATGTG  AGGG
                                |||||||||||| |||||  ||||
                                TTCTTTTGGTTTT TATAT  TCTC
                                      A     TA
GAM380   LOC145652 3'  CCTTGCTTTGTTTTTGTTTTTT 83411         C      TGT
           T                     GGGAGGAC AGGGCA   GCAGGG
                                |||||||| ||||||   ||||||
                                TTTTTTTG TTTTGT   CGTTCC
                                    T      TT_
GAM380   LOC145757 5'  CTCTGTGCCTGTTCTGCTCCTC 77460         C       T TG
           TC                     GGGAGGA CAGGGCA G  CAGGG
                                ||||||| ||||||| |  |||||
                                CTCTCCT GTCTTGT C  GTCTC
                                   C      C GT
GAM380   LOC145813 5'  CCTCCTGCTTTGGCCTCCC    83504        A       TGTGC
                                GGGAGG CCAGGGCA     AGG
                                ||||||| ||||||||     |||
                                CCCTCC GGTTTCGT     TCC
                                  _       CC___
GAM380   LOC145813 5'  CCTGTCTCCTGTCTTCCT     83505         C    CATGT
                                GGGAGGAC AGGG     GCAGG
                                |||||||| ||||     |||||
                                TCCTTCTG TCCT     TGTCC
                                   _    C____
GAM380   LOC145815 5'  TCTGCCTCTTGATTTTTCT    83525         C     CATGT
                                GGGAGGA CAGGG     GCAGG
                                ||||||| |||||     |||||
                                TCTTTTT GTTCT     CGTCT
                                   A    C____
GAM380   LOC145826 5'  CCCTGTACCTATTTGTCTTTCC 83529         C   GCAT
                                GGGAGGAC AGG    GTGCAGGG
                                |||||||| |||    ||||||||
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                                CCTTTCTG TTT    CATGTCCC
                                     _  ATC_
GAM380  LOC145828 5'  TTCTGTTTCTTCTGTCTTCTT  83539        C    CATGT
                                GGGAGGAC AGGG    GCAGGG
                                |||||||| ||||    ||||||
                                TTCTTCTG TCTT    TGTCTT
                                     _   CTT__
GAM380  LOC145871 5'  TCTTGCATCCTGTGGTCTT   83564        G  CAT
                                AGGACCA GG   GTGCAGGG
                                ||||||| ||   ||||||||
                                TTCTGGT TC   TACGTTCT
                                   G  C__
GAM380  LOC145945 5'  CTCTGCATATAAAATGGTATTT 83574       G    GGGC
           CC                     GGGAG ACCA    ATGTGCAGGG
                                |||||| ||||    ||||||||||
                                CCTTT TGGT    TATACGTCTC
                                   A    AAAA
GAM380  LOC145980 3'  TTTGCATAAGTGGTTCCTT    83608       _ AGG  A
                                GAGGA CC   GC TGTGCAGG
                                |||||| ||   || ||||||||
                                TTCCT GG   TG ATACGTTT
                                   T  ___  A
GAM380  LOC145989 3'  CCTCCGCCCTGGTTCCCT     59544     A        ATGT C
                                GGG GGACCAGGGC    G AGG
                                ||| ||||||||||    | |||
                                TCC CTTGGTCCCG    C TCC
                                  _         _____ C
GAM380  LOC145989 3'  CTCTGGGTGTCCTGGTCTTTT  59545             GTG
                                GGAGGACCAGGGCAT   CAGGG
                                ||||||||||||||   |||||
                                TTTTCTGGTCCTGTG   GTCTC
                                         G__
GAM380  LOC146108 5'  TCTCATGTCTATGCCTTGGTCC 77670     A          T  _
           CTT                    GG GGACCAGGGCATG GCA GGG
                                || |||||||||||| ||| |||
                                TC CCTGGTTCCGTAT TGT CTC
                                 _           C   A   TC
GAM380  LOC146174 3'  TTTTGCAAAGACTTGGTCCTGC 77704    G       GCATG
           C                     GG AGGACCAGG     TGCAGGG
                                || |||||||||     |||||||
                                CC TCCTGGTTC     ACGTTTT
                                 G        AGAA_
GAM380  LOC146229 3'  TTTTGATTTGCCCTGTGTTCTC 77785         _      TGTG
           CT                     GGGAGGAC CAGGGCA    CAGGG
                                |||||||| |||||||    |||||
                                TCCTCTTG GTCCCGT    GTTTT
                                     T      TTA_
GAM380  LOC146332 3'  CTTTGCAACCAGCTGTCTTCTC 77825         CAG   ATG_
                                GGGAGGAC   GGC    TGCAGGG
                                ||||||||   |||    |||||||
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                                CTCTTCTG  TCG   ACGTTTC
                                    ___   ACCA
GAM380  LOC146346 5'  CCTGACCCGTGGTCCTCTC   77838         G  CAT  G
                                GGGAGGACCA GG  GT CAGG
                                |||||||||| ||  || ||||
                                CTCTCCTGGT CC  CA GTCC
                                    G  ___  _
GAM380  LOC146381 5'  CTTTGTCCCTCCCTGGTTCCTT 77867       _     CATGT
          C                      GGAGGA CCAGGG    GCAGGG
                                |||||| ||||||    ||||||
                                CTTCCT GGTCCC    TGTTTC
                                   T     TCCC_
GAM380  LOC146429 5'  CGCCTGCCTTGGCCTCCC    83671       A       T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTCC GGTTCCGT CGC
                                   _       C
GAM380  LOC146452 3'  CTCTGTTATGACTCTGTCTTCC 77915        C   _   T
          C                      GGGAGGAC AGGG CATG GCAGGG
                                |||||||| |||| |||| ||||||
                                CCCTTCTG TCTC GTAT TGTCTC
                                    _   A   _
GAM380  LOC146488 5'  CTCTGGGCTGCCCTGTTCTTCT 70810       C      T  G
                                GGAGGA CAGGGCA GT CAGGG
                                |||||| ||||||| || |||||
                                TCTTCT GTCCCGT CG GTCTC
                                   T      _ G
GAM380  LOC146488 5'  CTTTGCTGGCTTCGTGGTCTTC 70811         __   ATGT
          TC                     GGGAGGACCA  GGGC   GCAGGG
                                ||||||||||  ||||   ||||||
                                CTCTTCTGGT  TTCG   CGTTTC
                                    GC   GT__
GAM380  LOC146520 3'  TTTTGTATGTGTTTGTTTTTGT 77961     CA____
          CCTTTC                  GGAC     GGGCATGTGCAGGG
                                ||||     ||||||||||||||
                                CCTG     TTTGTGTATGTTTT
                                  TTTTTG
GAM380  LOC146542 3'  CATGCCCTGGGCTTTCC     59180       A
                                GGGAGG CCAGGGCATG
                                |||||| ||||||||||
                                CCTTTC GGTCCCGTAC
                                   G
GAM380  LOC146713 3'  TCTGTGTCGTGTTCTCTC    83735        C G   ATGT
                                GGGAGGAC A GGC   GCAGG
                                |||||||| | |||   |||||
                                CTCTCTTG T CTG   TGTCT
                                    _ G  ____
GAM380  LOC146733 5'  TCTTGATCTCTGCGTTTTTCT  83772        _    CATGTG
                                GGGAGGAC CAGGG     CAGGG
                                |||||||| |||||     |||||
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                                TCTTTTTG GTCTC     GTTCT
                                    C    TA____
GAM380  LOC146823 3'  CCTGACAGTCCCTTGGTTCTCT 83793          CA_  G   G
           T                     GGGAGGACCAGGG   TGT CAGG
                                 |||||||||||||   ||| ||||
                                 TTCTCTTGGTTCC   ACA GTCC
                                       CTG   _
GAM380  LOC146880 3'  TCTTGCACATAAGTTCTGTCT  78160     C    __
                                 GGAC AGGGC  ATGTGCAGGG
                                 |||| |||||  ||||||||||
                                 TCTG TCTTG  TACACGTTCT
                                   _    AA
GAM380  LOC147080 5'  CTTTGCGTTTGGTGTCCTCCC  83933       CAGGG  TG
                                 GGGAGGAC    CA  TGCAGGG
                                 ||||||||    ||  |||||||
                                 CCCTCCTG    GT  GCGTTTC
                                      TG___  TT
GAM380  LOC147622 5'  CTTTGCAAGTGTTAGTCCTTCC 84051       CAG    G
                                 GGGAGGAC   GGCAT TGCAGGG
                                 ||||||||   ||||| |||||||
                                 CCTTCCTG   TTGTG ACGTTTC
                                      A__    A
GAM380  LOC147694 3'  TCTGCCTGCCTTGGCCTCTC   78456       A       TGT
                                 GGGAGG CCAGGGCA   GCAGG
                                 |||||| ||||||||   |||||
                                 CTCTCC GGTTCCGT   CGTCT
                                    _       C__
GAM380  LOC147741 5'  TCCACCGTGTTCGGGTCTTTCT 78474         A      TGCA
                                 GGGAGGACC GGGCATG    GGG
                                 ||||||||| |||||||    |||
                                 TCTTTCTGG CTTGTGC    CCT
                                      G      CA__
GAM380  LOC147858 3'  CTCTGTACCTTTTCTGGCTTCC 78571       A     CAT
           C                      GGGAGG CCAGGG   GTGCAGGG
                                  ||||||  ||||||   ||||||||
                                  CCCTTC GGTCTT   CATGTCTC
                                     _     TTC
GAM380  LOC148056 3'  TCTTGCGCTCCTTGGCCTCCT  84110       A     CAT
                                  GGGAGG CCAGGG   GTGCAGGG
                                  ||||||  ||||||   ||||||||
                                  TCCTCC GGTTCC   CGCGTTCT
                                     _     T__
GAM380  LOC148195 5'  CCCTGTGCATTCTGGTGCTTTT 84125      G     GC   TG
                                  GGGAG ACCAGG  ATG  CAGGG
                                  |||||  ||||||  |||  |||||
                                  TTTTC TGGTCT  TAC  GTCCC
                                    G      __   GT
GAM380  LOC148293 3'  TTTTGCAAACCTGGTTCCCT   78788     A      GCATG
                                  GGG GGACCAGG     TGCAGGG
                                  ||| ||||||||     |||||||
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                                TCC CTTGGTCC    ACGTTTT
                                  _      AA___
GAM380  LOC148371 3'  TTGTGGACCACTTTGGTTTTCT 78810          CAT  G  GGG
          T                      GGGAGGACCAGGG   GT CA
                                 ||||||||||||   || ||
                                 TTCTTTTGGTTTC   CA GT
                                       AC_  G  GTTT
GAM380  LOC148397 3'  CCCTGCCTGCTCTGGTCCACCC 78814    A        TGT
                                 GGG GGACCAGGGCA   GCAGGG
                                 ||| ||||||||||   ||||||
                                 CCC CCTGGTCTCGT   CGTCCC
                                   A        C__
GAM380  LOC148413 3'  CTCTGCCACATCCCTGTCTTCC 78829       C   C    _
          T                      GGGAGGAC AGGG ATGTG CAGGG
                                 |||||||| |||| ||||| |||||
                                 TCCTTCTG TCCC TACAC GTCTC
                                     _   _    C
GAM380  LOC148490 3'  CTTGGGTCCCTGTCTTTCT   78885       C   CATG G
                                 GGGAGGAC AGGG   T CAGG
                                 |||||||| ||||   | ||||
                                 TCTTTCTG TCCC   G GTTC
                                     _   T___ G
GAM380  LOC148545 3'  TCCTGTATTCTAGTGATCTTCT 78899       C  G_  CAT
          T                      GGGAGGA CA  GG   GTGCAGGG
                                 ||||||| ||  ||   ||||||||
                                 TTCTTCT GT  TC   TATGTCCT
                                     A  GA  T__
GAM380  LOC148734 5'  TGTGCTCTGGTTTCTCCC    78958       _
                                 GGGAGGA CCAGGGCATG
                                 ||||||| ||||||||||
                                 CCCTCTT GGTCTCGTGT
                                     T
GAM380  LOC149182 5'  TCTGGGCTTGGTTTTCCC    84378          GGCAT  G
                                 GGGAGGACCAG    GT CAGG
                                 ||||||||||    || ||||
                                 CCCTTTTGGTT    CG GTCT
                                       _____  G
GAM380  LOC149302 5'  TCCAGTGGTGCTTGGTTCTCTC 79272          G   G   A
                                 GGGAGGACCAGG CAT TGC GGG
                                 |||||||||||| ||| ||| |||
                                 CTCTCTTGGTTC GTG GTG CCT
                                       _  _   A
GAM380  LOC149386 5'  TTTTGTGGTCACTGTTCTCTT  84411       C  _   ATG
                                 GGGAGGAC AG GGC   TGCAGGG
                                 |||||||| || |||   |||||||
                                 TTCTCTTG TC CTG   GTGTTTT
                                     _ A   ___
GAM380  LOC149420 3'  TCTGCTGGTCTGTTTTTTC   79371   GG    CA   ATGT
                                 G  AGGAC  GGGC    GCAGG
                                 |  |||||  ||||    |||||
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                                C  TTTTG  TCTG   CGTCT
                                 TT    __   GT__
GAM380  LOC149461 5'  TCCTGGGACCCTCGGTCCTCTC 79405        _   CATGTG
                                GGGAGGACC AGGG     CAGGG
                                ||||||||| ||||     |||||
                                CTCTCCTGG TCCC     GTCCT
                                     C   AGG___
GAM380  LOC149506 3'  TTCTGCGCCTCCCTTGGTCTTT 84485   G        CAT
          GC                     G GAGGACCAGGG   GTGCAGGG
                                | ||||||||||   ||||||||
                                C TTTCTGGTTCC   CGCGTCTT
                                 G         CTC
GAM380  LOC149684 5'  CTCTGTGCCTCGGGTCCTCCT  84613        A   CAT TG
                                GGGAGGACC GGG   G  CAGGG
                                ||||||||| |||   |  |||||
                                TCCTCCTGG CTC   C  GTCTC
                                     G   ___ GT
GAM380  LOC149685 5'  TCCTGGTTTTCTGGTTCTGCC  79482    G       C  GTG
                                GG AGGACCAGGG AT   CAGGG
                                || ||||||||| ||   |||||
                                CC TCTTGGTCTT TG   GTCCT
                                 G        T  ___
GAM380  LOC149692 3'  TCTGCCTGCCTTGGCCTCCC   84597       A       TGT
                                GGGAGG CCAGGGCA   GCAGG
                                |||||| ||||||||   |||||
                                CCCTCC GGTTCCGT   CGTCT
                                   _       C__
GAM380  LOC149706 5'  CTTGCCTGTTTGTTTTTCT    84641        CA    TGT
                                GGGAGGAC  GGGCA   GCAGG
                                ||||||||  |||||   |||||
                                TCTTTTTG  TTTGT   CGTTC
                                     __    C__
GAM380  LOC149711 3'  TTCTGCAAATTTTGGTCTTTT  84693          CATG
                                GGAGGACCAGGG    TGCAGGG
                                ||||||||||||    |||||||
                                TTTTCTGGTTTT    ACGTCTT
                                      AA__
GAM380  LOC149837 5'  CTCTGTGGCTACCCTGGTCTTG 84732    G        CAT  _
          CT                     GG AGGACCAGGG   GT GCAGGG
                                || ||||||||||   || ||||||
                                TC TTCTGGTCCC   CG TGTCTC
                                 G        AT_  G
GAM380  LOC149837 5'  TTCTGCTGTATTCCTGTCTTTC 84750        C   CATGT
          T                      GGGAGGAC AGGG    GCAGGG
                                |||||||| ||||    ||||||
                                TCTTTCTG TCCT    CGTCTT
                                     _   TATGT
GAM380  LOC149837 3'  TTCTGTGTGTGTTCACCTGCTC 84751    _  ACCA     TG
                                GGG AGG   GGGCATG  CAGGG
                                ||| |||   |||||||  |||||
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                                CTC TCC    CTTGTGT  GTCTT
                                  G  A___      GT
GAM380  LOC150054 5'  CCTCCTGCCTTGGCCTCCC   84828       A       TGTGC
                                GGGAGG CCAGGGCA     AGG
                                |||||| ||||||||     |||
                                CCCTCC GGTTCCGT     TCC
                                   _       CC___
GAM380  LOC150054 5'  CTCTGGGCTTTTGGTCCTCC   84830           CAT  G
                                GGAGGACCAGGG   GT CAGGG
                                ||||||||||||   || |||||
                                CCTCCTGGTTTT   CG GTCTC
                                       ___  G
GAM380  LOC150166 5'  GTCTTGCTTTTGTTGTGTTTTG 84888          GT_____
           GTTTTTT                  ACCAGGGCAT      GCAGGG   T
                                ||||||||||      ||||||  |
                                TGGTTTTGTG      CGTTCT   G
                                     TTGTTTT
GAM380  LOC150225 5'  CACATGCTTTGGGTCCTTCC   84983         _
                                GGGAGGACC AGGGCATGTG
                                ||||||||| ||||||||||
                                CCTTCCTGG TTTCGTACAC
                                     G
GAM380  LOC150244 3'  CCTGTGCCCGTGTCCTCCT    79734        CA    ATGT
                                GGGAGGAC  GGGC    GCAGG
                                |||||||  ||||   |||||
                                TCCTCCTG  CCCG    TGTCC
                                    TG   _____
GAM380  LOC150271 5'  TAGTGGTCATTCTCTGGTCTTC 84954           C   TG  GGG
           TC                     GGGAGGACCAGGG ATG  CA
                                |||||||||||| |||  ||
                                CTCTTCTGGTCTC TAC  GT
                                       T   TG  GATT
GAM380  LOC150282 5'  TTCTGTATATGCTTGTTCT    79733       CA
                                AGGAC  GGGCATGTGCAGGG
                                |||||  ||||||||||||||
                                TCTTG  TTCGTATATGTCTT
                                   __
GAM380  LOC150297 5'  CCTTGTGCCTCTTGGACTTTTT 79811        A     CAT TG
                                GGGAGG CCAGGG   G  CAGGG
                                |||||| ||||||   |  |||||
                                TTTTTC GGTTCT   C  GTTCC
                                   A     C__ GT
GAM380  LOC150311 5'  CCTGACTCTGGTTCTC      79752           CATGTG
                                GAGGACCAGGG     CAGG
                                ||||||||||      ||||
                                CTCTTGGTCTC     GTCC
                                      A_____
GAM380  LOC150372 3'  CCCTGCCCTCCTAGGTCTTCCC 79795          A   CATGT
                                GGGAGGACC GGG    GCAGGG
                                ||||||||| |||    ||||||
```

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                                CCCTTCTGG TCC    CGTCCC
                                     A  TCC__
GAM380  LOC150481 3'  CCTGTGGTTGGGCTTCCC   79883      A  AG  ATG
                                GGGAGG CC  GGC  TGCAGG
                                |||||| ||  |||  ||||||
                                CCCTTC GG  TTG  GTGTCC
                                   _ G_  ___
GAM380  LOC150481 3'  TCTGGGCCTTGGTCTTCTC   79898          ATGTG
                                GGGAGGACCAGGGC   CAGG
                                ||||||||||||||   ||||
                                CTCTTCTGGTTCCG   GTCT
                                       G____
GAM380  LOC150481 3'  TTCTGTATATGTTCTGTGCTTT 79900     AC
                                GAGG  CAGGGCATGTGCAGGG
                                ||||  ||||||||||||||||
                                TTTC  GTCTTGTATATGTCTT
                                  GT
GAM380  LOC150606 5'  TTCTGTATGTGTGTGTTTGTCC 85094    G  C  GG
                                GGA GA CA  GCATGTGCAGGG
                                ||| || ||  ||||||||||||
                                CCT TT GT  TGTGTATGTCTT
                                  G  T  G_
GAM380  LOC150630 3'  CTCTGAGCAGCTGTCCTAGTTC 85104       C    __  G
           TCTC                  GGAGGAC AGGGCA  TGT CAGGG
                                ||||||| ||||||  ||| |||||
                                TCTCTTG TCCTGT  ACG GTCTC
                                    A     CG   A
GAM380  LOC150819 5'  CTTTGTGCTGCTGGCTTTTC  85120   GG   A   GG   T TG
                                G  AGG CCA  GCA G  CAGGG
                                |  ||| |||  ||| |  |||||
                                C  TTC GGT  CGT C  GTTTC
                                 TT  _  __  _ GT
GAM380  LOC150960 3'  CCCAGCCCATGTGTCTTGGTCT 80055             CA__
           TTTT                  GGAGGACCAGGGCATGTG   GGG
                                ||||||||||||||||||   |||
                                TTTTCTGGTTCTGTGTAC   CCC
                                        CCGA
GAM380  LOC151005 3'  CTGTAACTGTCTTTCC     80098    CC    TG
                                GGA  AGGGCA  TGCAG
                                |||  ||||||  |||||
                                CCT  TTCTGT  ATGTC
                                  __     CA
GAM380  LOC151176 3'  TCTGGGCTCCTTGGTCTTCCC  85264          CAT  G
                                GGGAGGACCAGGG   GT CAGG
                                ||||||||||||   || ||||
                                CCCTTCTGGTTCC   CG GTCT
                                       T__  G
GAM380  LOC151188 3'  TTTTGTGTGTGTAGTTCTTTC  80163   GG    CAGG    TG
                                G  AGGAC   GCATG  CAGGG
                                |  |||||   |||||  |||||
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                                C  TCTTG   TGTGT  GTTTT
                                 TT    A___    GT
GAM380  LOC151278 3'  TCCTGTTCTTCTTCGTCTTCTT 80202       C   CATGT
                                GGGAGGAC AGGG    GCAGGG
                                |||||||| ||||    ||||||
                                TTCTTCTG TTCT    TGTCCT
                                    C   TCT__
GAM380  LOC151361 3'  TTCTGCATGCAGGAGTTTCTCC 85330      CCAGG_  TG
           T                     GGGAGGA    GCA  TGCAGGG
                                |||||||     |||  |||||||
                                TCCTCTT     CGT  ACGTCTT
                                   TGAGGA  __
GAM380  LOC151465 3'  TTTTGTATCAGCTGGACCTTCC 62782      A   GGCAT
                                GGGAGG CCAG    GTGCAGGG
                                |||||| ||||    ||||||||
                                CCTTCC GGTC    TATGTTTT
                                   A   GAC__
GAM380  LOC151525 5'  CCTGCAGGCTGTTTTTCT    80272       CAG  ATG
                                GGGAGGAC  GGC  TGCAGG
                                ||||||||  |||  ||||||
                                TCTTTTTG  TCG  ACGTCC
                                    ___  G__
GAM380  LOC151742 3'  CTCTGTATCCACCTGGTTTT  57667        GCAT
                                AGGACCAGG   GTGCAGGG
                                |||||||||   ||||||||
                                TTTTGGTCC   TATGTCTC
                                     ACC_
GAM380  LOC151742 3'  TCCTGAGAATGCTTTGTCCTTC 57671       C     GTG
           T                     GGGAGGAC AGGGCAT   CAGGG
                                |||||||| |||||||   |||||
                                TCTTCCTG TTTCGTA   GTCCT
                                    _      AGA
GAM380  LOC151963 3'  CTTTGCATTTGCTTAGTTCTCC 80401       CA    T
           T                     GGGAGGAC  GGGCA GTGCAGGG
                                ||||||||  ||||| ||||||||
                                TCCTCTTG  TTCGT TACGTTTC
                                    A_    T
GAM380  LOC152059 5'  CTCTGCTGGATCAGGTCCTCCT 80445        A  GCATGT
                                GGGAGGACC GG     GCAGGG
                                |||||||||  ||     ||||||
                                TCCTCCTGG CT     CGTCTC
                                     A  AGGT__
GAM380  LOC152141 3'  TTCTGTACATGACTTTACTCTT 85555      GACC   G
                                GGGAG    AGG CATGTGCAGGG
                                |||||    ||| ||||||||||||
                                TTCTC    TTC GTACATGTCTT
                                   AT__   A
GAM380  LOC152245 3'  TTTTGTGGGGGCCCTTGGTTCC 85606     A     _   ATG
           CC                    GGG GGACCA GGGC   TGCAGGG
                                ||| |||||| ||||   |||||||
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                                CCC CTTGGT CCCG   GTGTTTT
                                  _     T    GGG
GAM380  LOC152317 5'  TTTTGTTCTGGCCTGTGGTCCT 85655          _    ATGT
                TCT                   GGGAGGACCA GGGC    GCAGGG
                                |||||||||| ||||    ||||||
                                TCTTCCTGGT TCCG    TGTTTT
                                     G    GTCT
GAM380  LOC152765 5'  TCCTGTCTGTGCTCTGATTCTC 80663        C       GT
                CC                    GGGAGGA CAGGGCAT  GCAGGG
                                |||||||| ||||||||  ||||||
                                CCCTCTT GTCTCGTG  TGTCCT
                                   A       TC
GAM380  LOC152790 5'  CTCTGTGGACTCCTTAGTTCTT 85874         C    CATGT
                CC                    GGGAGGAC AGGG     GCAGGG
                                |||||||| ||||     ||||||
                                CCTTCTTG TTCC     TGTCTC
                                     A    TCAGG
GAM380  LOC152991 5'  TCTGTGTACGTGTGTGTGGTTT 85897          GG_       G
                TCCT                  GGAGGACCA   GCATGTGCA GG
                                |||||||||   |||||||||  ||
                                CCTTTTGGT   TGTGCATGT TC
                                     GTG       G  TC
GAM380  LOC152992 3'  TTGCACAGGCCCTTCC      80760     CC     A
                                GGA  AGGGC TGTGCAG
                                |||  ||||| |||||||
                                CCT  TCCCG ACACGTT
                                  __     G
GAM380  LOC153196 5'  CTCTGTGTATGTATATGTTTTC 85958         CAGG     TG
                TC                    GGGAGGAC    GCATG  CAGGG
                                |||||||||   |||||  |||||
                                CTCTTTTG    TGTAT  GTCTC
                                     TATA     GT
GAM380  LOC153277 3'  CCTTGCTAGCCTAGTCCTCTT  85989         CA    ATGT
                                GGGAGGAC  GGGC    GCAGGG
                                |||||||||  ||||    ||||||
                                TTCTCCTG  TCCG    CGTTCC
                                     A_    AT__
GAM380  LOC153525 5'  TTCTGCATGTTCTCATTTGTTC 86048         CA__   C
                TTTT                  GGAGGAC    GGG ATGTGCAGGG
                                |||||||    ||| ||||||||||
                                TTTCTTG    CTC TGTACGTCTT
                                     TTTA   T
GAM380  LOC153642 3'  TTTTGACTTTGTTCTGGTATTT 80914       G        T_  G
                TT                    GGGAG ACCAGGGCA  GT CAGGG
                                ||||| |||||||||  || |||||
                                TTTTT TGGTCTTGT  CA GTTTT
                                   A        TT  _
GAM380  LOC153688 5'  CATGCCTTGTTTTCTT      86098          C
                                GGGAGGAC AGGGCATG
                                |||||||| ||||||||
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                                TTCTTTTG TTCCGTAC
                                        _
GAM380  LOC153856 3'  TCTGTACATGTATCTG      80971      _
                                CAGG GCATGTGCAGG
                                |||| ||||||||||
                                GTCT TGTACATGTCT
                                  A
GAM380  LOC154452 3'  CCCTGCTACCTTCCTGGCCTCT 81097       A     CAT  _
          C                      GGGAGG CCAGGG  GT GCAGGG
                                |||||| ||||||  || ||||||
                                CTCTCC GGTCCT  CA CGTCCC
                                   _     TC_  T
GAM380  LOC154789 5'  TGTCCCAGGTTCTCTT      81145          A_
                                GGGAGGACC  GGGCA
                                |||||||||  |||||
                                TTCTCTTGG  CCTGT
                                     AC
GAM380  LOC154792 3'  TTTTGTATATGTTACGTGTTT  86251     G  CAG
                                GAG AC   GGCATGTGCAGGG
                                ||| ||   ||||||||||||
                                TTT TG   TTGTATATGTTTT
                                  G  CA_
GAM380  LOC154877 3'  CCTCCTGCCTTGGCCTCCC    86289       A       TGTGC
                                GGGAGG CCAGGGCA     AGG
                                |||||| ||||||||     |||
                                CCCTCC GGTTCCGT     TCC
                                   _       CC___
GAM380  LOC155032 5'  CGTGCCCTGGCTTCTC      86320       A
                                GGGAGG CCAGGGCATG
                                |||||| ||||||||||
                                CTCTTC GGTCCCGTGC
                                   _
GAM380  LOC155038 3'  CTTTGTACATGCTTTG      81257
                                CAGGGCATGTGCAGGG
                                ||||||||||||||||
                                GTTTCGTACATGTTTC

GAM380  LOC155061 3'  TCCTGTGTGTGCCCCTGCTCTG 81270    A  C    _   TG
          CC                      GG GGA CAGGG CATG  CAGGG
                                || ||| ||||| ||||  |||||
                                CC TCT GTCCC GTGT  GTCCT
                                 G  C    C   GT
GAM380  LOC155081 3'  CTCTGCATTTTATTGGTTT   81290        GGCAT
                                GGACCAG    GTGCAGGG
                                |||||||    ||||||||
                                TTTGGTT    TACGTCTC
                                    ATTT_
GAM380  LOC157254 3'  GTGTGTTCTGCTTTTCTT    81390        C       TG
                                GGGAGGA CAGGGCA  T
                                ||||||| |||||||  |
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                                TTCTTTT GTCTTGT  G
                                    C      GT
GAM380  LOC157355 3'  CTTGCATTCGTGGCCTCCT   81426       A   G  CAT
                                GGGAGG CCA GG   GTGCAGG
                                ||||||| ||| ||   |||||||
                                TCCTCC GGT CT   TACGTTC
                                   _   G  ___
GAM380  LOC157577 3'  TTTTGTACCATATGTGTCTTTC 81488        _  GGGCAT
          C                     GGGAGGAC CA     GTGCAGGG
                                |||||||| ||     ||||||||
                                CCTTTCTG GT     CATGTTTT
                                     T  ATAC__
GAM380  LOC157651 3'  CCTTGTGTGTGATCTTTTCTGT 81540     C___   _   TG
          CTTCCC                  GGAC   AGGG CATG  CAGGG
                                ||||   |||| ||||  |||||
                                TCTG   TTCT GTGT  GTTCC
                                  TCTT   A   GT
GAM380  LOC157653 5'  TCTTGCACATCGGTCCTCTT   81529         AGGGC
                                GGGAGGACC    ATGTGCAGGG
                                |||||||||    ||||||||||
                                TTCTCCTGG    TACACGTTCT
                                     C____
GAM380  LOC157858 5'  TGTTTTGTGTTCTCCC      86607        _
                                GGGAGGAC CAGGGCA
                                |||||||| |||||||
                                CCCTCTTG GTTTTGT
                                     T
GAM380  LOC157860 5'  CCTGGCCCCCTGTCCTTTT   86567        C   CAT  G
                                GGGAGGAC AGGG   GT CAGG
                                |||||||| ||||   || ||||
                                TTTTCCTG TCCC   CG GTCC
                                     _   C__  _
GAM380  LOC157919 3'  CTTTGTTTTGTTTTCCT     81633        C     TGTGC
                                GGGAGGAC AGGGCA    AG
                                |||||||| ||||||    ||
                                TCCTTTTG TTTTGT    TC
                                     _     T____
GAM380  LOC158117 3'  CTGCATGGGGCCTCTC      81704       A  AGGGCAT
                                GGGAGG CC      GTGCAG
                                |||||| ||      ||||||
                                CTCTCC GG      TACGTC
                                   _  GG_____
GAM380  LOC158117 3'  TCTTGTAGTCAACCCTGGTCT  81712         CATG_
                                GGACCAGGG    TGCAGGG
                                |||||||||    |||||||
                                TCTGGTCCC    ATGTTCT
                                     AACTG
GAM380  LOC158125 5'  TTTGCACGAGGTCCCCC     81720     A    AGGGCA
                                GGG GGACC     TGTGCAGG
                                ||| |||||     ||||||||
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                                CCC CCTGG     GCACGTTT
                                  _    A_____
GAM380  LOC158191 3'  TCTGGGCCTTGGTCTTCTT   81784           ATGTG
                                GGGAGGACCAGGGC    CAGG
                                ||||||||||||||    ||||
                                TTCTTCTGGTTCCG    GTCT
                                      G____
GAM380  LOC158191 3'  TTCTGTATATGTTCTGTGCTTT 81786     AC
                                GAGG  CAGGGCATGTGCAGGG
                                ||||  ||||||||||||||||
                                TTTC  GTCTTGTATATGTCTT
                                  GT
GAM380  LOC158237 5'  TCTTGCACATGCAAATCTTTGC 60455   G    CCAGG
                                G GAGGA    GCATGTGCAGGG
                                | |||||    ||||||||||||
                                C TTTCT    CGTACACGTTCT
                                 G    AAA__
GAM380  LOC158364 3'  CCTTTCATGTCCTGGTCTTTTT 81875             TGC
                                GGGAGGACCAGGGCATG   AGG
                                ||||||||||||||||   |||
                                TTTTTCTGGTCCTGTAC   TCC
                                      TT_
GAM380  LOC158364 5'  TTTTGCACAGCTGTGGTTCTGC 81878    G      G   A
          C                      GG AGGACCA GGC TGTGCAGGG
                                || ||||||| ||| |||||||||
                                CC TCTTGGT TCG ACACGTTTT
                                 G      G  _
GAM380  LOC158654 5'  CTTTGAGCAATCTAGGTTTTTT 81964         A   CA   G
          T                      GGGAGGACC GGG  TGT CAGGG
                                ||||||||| |||  ||| |||||
                                TTTTTTTGG TCT  ACG GTTTC
                                     A  A_  A
GAM380  LOC158709 3'  CTCTGTGTGTGTCTGTGTCCTC 81980       CA      TG
                                GAGGAC  GGGCATG  CAGGG
                                ||||||  |||||||  |||||
                                CTCCTG  TCTGTGT  GTCTC
                                   TG      GT
GAM380  LOC158714 5'  CTTGTGTGGGTGTTTTCC    81989        CAGG  AT TG
                                GGAGGAC    GC  G  CAGG
                                |||||||    ||  |  ||||
                                CCTTTTG    TG  T  GTTC
                                    ____  GG GT
GAM380  LOC158722 3'  CTCTGCTCTATTTGGTTTCTTT 81994       _    GCATGT
                                GGAGGA CCAGG     GCAGGG
                                |||||| |||||     ||||||
                                TTTCTT GGTTT     CGTCTC
                                   T    ATCT__
GAM380  LOC158819 3'  CTTGATCATGGTTCTCTT    86905          GGGCA  TG
                                GGGAGGACCA    TG  CAGG
                                ||||||||||    ||  ||||
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                                TTCTCTTGGT    AC  GTTC
                                      _____  TA
GAM380  LOC158819 3'  TCCTGTGTGATAGGTTTTTTT  86911        AGGG  GT
                                GGGAGGACC    CAT  GCAGGG
                                |||||||||    |||  ||||||
                                TTTTTTTGG    GTG  TGTCCT
                                     ATA_  __
GAM380  LOC158954 3'  TACTGCTCTGTTCTCCC     60436        C     T
                                GGGAGGAC AGGGCA GTG
                                |||||||| |||||| |||
                                CCCTCTTG TCTCGT CAT
                                     _     _
GAM380  LOC160717 5'  TTCTGTGAGGACCGGTTCTCCC 82238         A  GCATG
                                GGGAGGACC GG     TGCAGGG
                                ||||||||| ||     |||||||
                                CCCTCTTGG CC     GTGTCTT
                                     _  AGGA_
GAM380  LOC161489 5'  CCTTGCCTTCCAGGTCCTCTT  87092         A   CATGT
                                GGGAGGACC GGG    GCAGGG
                                ||||||||| |||    ||||||
                                TTCTCCTGG CCT    CGTTCC
                                     A   TC___
GAM380  LOC161527 5'  CTCTAGAGATGTTTTGTTCTTC 82276        C       GTGC
          CT                    GGGAGGA CAGGGCAT    AGGG
                                ||||||| ||||||||    ||||
                                TCCTTCT GTTTTGTA    TCTC
                                    T       GAGA
GAM380  LOC161734 3'  CCAAATGTTCTGTTTTCTT    87098        C      GTGCA
                                GGGAGGAC AGGGCAT     GG
                                |||||||| |||||||     ||
                                TTCTTTTG TCTTGTA     CC
                                     _      AA___
GAM380  LOC162333 5'  TGTCCCTGTGTCCTCTT     87144        _    _
                                GGGAGGAC CAGGG CA
                                |||||||| ||||| ||
                                TTCTCCTG GTCCC GT
                                     T    T
GAM380  LOC162417 5'  CCTTTGCCCTGGCCTTCT    82346       A      TGTGC
                                GGGAGG CCAGGGCA    AGG
                                |||||| ||||||||    |||
                                TCTTCC GGTCCCGT    TCC
                                    _       T_____
GAM380  LOC163782 5'  CTGTACATAGCTTCCT      82157      CCAG  _
                                AGGA   GGC ATGTGCAG
                                ||||   ||| |||||||||
                                TCCT   TCG TACATGTC
                                  _____  A
GAM380  LOC163833 5'  CTCTGTGTGGAGTGGCTTTCC  82160       A  GGGCA  TG
                                GGGAGG CCA    TG  CAGGG
                                |||||| |||    ||  |||||
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                                CCTTTC GGT    GT  GTCTC
                                   _  GAG__  GT
GAM380  LOC163911 5'  TTCTGCTCACCTTCGGGTCCTC 87046        __   CA  T
          CT                     GGGAGGACC  AGGG  TG GCAGGG
                                 |||||||||  ||||  || ||||||
                                 TCCTCCTGG  TTCC  AC CGTCTT
                                    GC   __  T
GAM380  LOC164582 5'  CCCTGTCCCAGGCTCTGGTTCC 82541     A       A  T_
          CC                     GGG GGACCAGGGC TG  GCAGGG
                                 ||| ||||||||||  ||  ||||||
                                 CCC CTTGGTCTCG AC  TGTCCC
                                   _       G  CC
GAM380  LOC167153 5'  TTGTGTTGCTCCTCCC      82676       CCAGG   T TG
                                 GGGAGGA    GCA G  CAG
                                 |||||||    ||| |  |||
                                 CCCTCCT    CGT T  GTT
                                    _____  _ GT
GAM380  LOC168537 5'  TCTTGTACGTGCCTAAGTTCT  82718      CA
                                 AGGAC  GGGCATGTGCAGGG
                                 |||||  ||||||||||||||
                                 TCTTG  TCCGTGCATGTTCT
                                   AA
GAM380  LOC170082 3'  TTTTGTTTTTGTTTTTGTTTTT 82570   GG    C     TGT
          TC                     G  AGGAC AGGGCA   GCAGGG
                                 |  ||||| ||||||   ||||||
                                 C  TTTTG TTTTGT   TGTTTT
                                  TT    T     TTT
GAM380  LOC170261 3'  TTCTGTGTGTGCCCATTTCCTT 82588      CCA      TG
                                 GAGGA   GGGCATG  CAGGG
                                 |||||   |||||||  |||||
                                 TTCCT   CCCGTGT  GTCTT
                                   TTA      GT
GAM380  LOC170372 3'  TTCTGCATGAAATGTGTTTTGT 76363     C      _____
          CTTTTT                   GAC AGGGCAT    GTGCAGGG
                                 ||| |||||||    ||||||||
                                 CTG TTTTGTG    TACGTCTT
                                   _      TAAAG
GAM380  LOC170409 3'  CCCTGCAGCCCCTGGTCTGCCC 82859     A       CATG
                                 GGG GGACCAGGG    TGCAGGG
                                 ||| |||||||||    |||||||
                                 CCC TCTGGTCCC    ACGTCCC
                                   G        CG__
GAM380  LOC196382 3'  TTTTGCAGTAAGCTAGTCTTCC 89626        CAG   A  _
          C                      GGGAGGAC   GGC TG TGCAGGG
                                 ||||||||   ||| || |||||||
                                 CCCTTCTG   TCG AT ACGTTTT
                                    A__   A  G
GAM380  LOC196411 3'  TTCTGTACAAGGCTGCTTGTTT 87691        C  _   A_
          TTTT                     GGAGGAC AG GGC  TGTGCAGGG
                                 |||||||  ||  |||  |||||||||
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                                TTTTTTG TC TCG  ACATGTCTT
                                    T  G   GA
GAM380  LOC196418 5'  CCCTGCCTCTGCCTGTTCTTCT 87695       CA    TGT
                                GGGAGGAC  GGGCA   GCAGGG
                                |||||||  |||||   ||||||
                                TCTTCTTG  TCCGT   CGTCCC
                                   __     CTC
GAM380  LOC196549 5'  GTGTCCTGGCCTCTT      59234       A
                                GGGAGG CCAGGGCAT
                                |||||| |||||||||
                                TTCTCC GGTCCTGTG
                                   _
GAM380  LOC196812 3'  TTCTGCACTTTGGTGGTTCTCC 89579         GGGCAT
          C                      GGGAGGACCA     GTGCAGGG
                                ||||||||||     ||||||||
                                CCCTCTTGGT     CACGTCTT
                                     GGTTT_
GAM380  LOC197131 3'  TTTTGTATTTGGTGTTTTCCC  87889        CAGG  AT_
                                GGGAGGAC   GC   GTGCAGGG
                                ||||||||   ||   ||||||||
                                CCCTTTTG   TG   TATGTTTT
                                     _____  GTT
GAM380  LOC197319 3'  TCTTGTTTTTTCCTGGTTT   87974         CATGT
                                GGACCAGGG    GCAGGG
                                |||||||||    ||||||
                                TTTGGTCCT    TGTTCT
                                     TTTT_
GAM380  LOC197342 5'  CCCACTGGGTGCCCTGGATCTC 87996       A       G  CA
          CC                     GGGAGG CCAGGGCAT TG  GGG
                                |||||| |||||||||  ||  |||
                                CCCTCT GGTCCCGTG GT  CCC
                                   A       G  CA
GAM380  LOC197439 5'  CTTTGTCCCTCCCTGGTTCCTT 88075       _     CATGT
          C                      GGAGGA CCAGGG    GCAGGG
                                ||||||  ||||||    ||||||
                                CTTCCT GGTCCC    TGTTTC
                                   T     TCCC_
GAM380  LOC199786 3'  CCTCCTGCCTTGGCCTCCC   88376       A       TGTGC
                                GGGAGG CCAGGGCA    AGG
                                |||||| ||||||||    |||
                                CCCTCC GGTTCCGT    TCC
                                   _       CC___
GAM380  LOC199786 3'  CTCTGTATGGCCTGGTTTTTCC 88379           G   GT
                                GGGAGGACCAGG CAT  GCAGGG
                                |||||||||||| |||  ||||||
                                CCTTTTTGGTCC GTA  TGTCTC
                                     G   __
GAM380  LOC200035 3'  CTTTGGAGTATTTTGGTTTTTC 73253           C  GTG
          T                      GGGAGGACCAGGG AT   CAGGG
                                |||||||||||| ||   |||||
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                                TCTTTTTGGTTTT TG   GTTTC
                                      A  AG_
GAM380   LOC200107 5'  CCTGCGTCTCCTGGTTTTCTC  88573           CATG
                                GGGAGGACCAGGG    TGCAGG
                                |||||||||||||    ||||||
                                CTCTTTTGGTCCT    GCGTCC
                                      CT__
GAM380   LOC200269 3'  TGTGTCCCTGGATCTTCC     88669       _     _
                                GGAGGA CCAGGG CATG
                                |||||| |||||| ||||
                                CCTTCT GGTCCC GTGT
                                   A     T
GAM380   LOC200301 3'  TGTGCTTTGGTTTTGCT     88756    G
                                GG AGGACCAGGGCATG
                                || ||||||||||||||
                                TC TTTTGGTTTCGTGT
                                 G
GAM380   LOC200314 5'  TATGTCCTGCTTTTCCC     90015        C
                                GGGAGGA CAGGGCATG
                                ||||||| |||||||||
                                CCCTTTT GTCCTGTAT
                                    C
GAM380   LOC200492 3'  TGCCTTCCTGTTCTTCT     90089        C__
                                GGGAGGAC   AGGGCA
                                ||||||||   ||||||
                                TCTTCTTG   TTCCGT
                                     TCC
GAM380   LOC200597 5'  CCTGCATATGGGACCTCTC    88839       A  AGGG
                                GGGAGG CC    CATGTGCAGG
                                |||||| ||    ||||||||||
                                CTCTCC GG    GTATACGTCC
                                   A  _____
GAM380   LOC200982 3'  TCTTACTTATCTCTGGTCTTTT 90227           CAT_  C   G
            T                    GGGAGGACCAGGG    GTG AGG
                                |||||||||||||    ||| |||
                                TTTTTCTGGTCTC    CAT TCT
                                       TATT  _
GAM380   LOC200985 3'  CTCTAAGCTGCCTGGGTCTTTT 88962         A    T  GC
            T                    GGGAGGACC GGGCA GT  AGGG
                                |||||||| ||||| ||  ||||
                                TTTTTCTGG TCCGT CG  TCTC
                                     G    _  AA
GAM380   LOC201115 5'  TTGCATGGGGCTTCCC      88108       A  AGGGCAT
                                GGGAGG CC      GTGCAG
                                |||||| ||      ||||||
                                CCCTTC GG      TACGTT
                                   _  GG_____
GAM380   LOC201294 3'  CTCTGAGTGCTTTGAGTTCTTC 88207         _       GTG
            C                    GGGAGGAC CAGGGCAT   CAGGG
                                |||||||| ||||||||   |||||
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                                CCTTCTTG GTTTCGTG   GTCTC
                                    A       A__
GAM380   LOC201304 3'  CCCACAGCTATGCTTTGGCCTC 88230       A        T  A__
             TC                   GGGAGG CCAGGGCATG GC   GGG
                                  |||||| |||||||||| ||   |||
                                  CTCTCC GGTTTCGTAT CG   CCC
                                    _        _ ACA
GAM380   LOC202047 3'  ACATTTTTGGTTTTTTT     90301            C
                                  GGGAGGACCAGGG ATGT
                                  |||||||||||| ||||
                                  TTTTTTTGGTTTT TACA
                                           _
GAM380   LOC202108 3'  TTGTGGACCACTTTGGTTTTCT 89156           CAT  G  GGG
             T                    GGGAGGACCAGGG   GT CA
                                  |||||||||||||   || ||
                                  TTCTTTTGGTTTC   CA GT
                                         AC_  G  GTTT
GAM380   LOC202152 3'  TCCTGATTTTTTAGTCCTGGTT 89158          ATGTG___
             CTTCT                   AGGACCAGGGC       CAGGG
                                  ||||||||||       |||||
                                  TCTTGGTCCTG       GTCCT
                                       ATTTTTTA
GAM380   LOC202347 5'  CTTTGTGGTTTTATTTTGGTTC 90345   GG        CATGT__
             TTTC                    AGGACCAGGG      GCAGGG
                                   |||||||||      ||||||
                                   TCTTGGTTTT      TGTTTC
                                  TT        ATTTTGG
GAM380   LOC202546 5'  CCTGCTCTCTGGTCTTTTC   90359   GG        CATGT
                                  G  AGGACCAGGG    GCAGG
                                  |  ||||||||||    |||||
                                  C  TTCTGGTCTC    CGTCC
                                   TT        T____
GAM380   LOC202802 3'  CTCTGCATTTTATTGGTTT   89204        GGCAT
                                  GGACCAG    GTGCAGGG
                                  |||||||    ||||||||
                                  TTTGGTT    TACGTCTC
                                       ATTT_
GAM380   LOC202934 5'  CTCTGTTGCATTTGGTTCTGCT 90410    G       _   TGT
                                  GG AGGACCAGG GCA   GCAGGG
                                  || |||||||| |||   ||||||
                                  TC TCTTGGTTT CGT   TGTCTC
                                   G        A  ___
GAM380   LOC203069 5'  CTTTGTATGTGCCCCGGGTGCT 89260    G   A_
                                  AG ACC  GGGCATGTGCAGGG
                                  || |||  ||||||||||||||
                                  TC TGG  CCCGTGTATGTTTC
                                   G   GC
GAM380   LOC203275 3'  CTGCATGGGGCCTCTC      89320        A  AGGGCAT
                                  GGGAGG CC      GTGCAG
                                  |||||| ||      ||||||
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                                CTCTCC GG      TACGTC
                                   _ GG_____
GAM380  LOC203275 3'  TCTTGTAGTCAACCCTGGTCT  89328         CATG_
                                GGACCAGGG    TGCAGGG
                                |||||||||    |||||||
                                TCTGGTCCC    ATGTTCT
                                     AACTG
GAM380  LOC203339 3'  CTCTGTGTGTGCCTCTGCGTTC 90544   A  _  _    TG
          CCT                    G GGAC CAG GGCATG  CAGGG
                                | |||| ||| ||||||  |||||
                                C CTTG GTC CCGTGT  GTCTC
                                 _   C  T     GT
GAM380  LOC203350 3'  CACCTGCCTTGGCCTCCC    90564       A      T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTCC GGTTCCGT CAC
                                   _       C
GAM380  LOC203378 5'  TTTTGCCAATTTCTGGTTTTTC 90623           CA  T
          T                     GGGAGGACCAGGG  TG GCAGGG
                                ||||||||||||  || ||||||
                                TCTTTTTGGTCTT  AC CGTTTT
                                      TA  _
GAM380  LOC203427 3'  CCTCCTGCCTTGGCCTCCC   89357       A      TGTGC
                                GGGAGG CCAGGGCA    AGG
                                |||||| ||||||||    |||
                                CCCTCC GGTTCCGT    TCC
                                   _       CC___
GAM380  LOC203523 3'  CTCTGTATGTAATGGTTTTTTT 89375         GG   GT
                                GGGAGGACCA  GCAT  GCAGGG
                                ||||||||||  ||||  ||||||
                                TTTTTTTGGT  TGTA  TGTCTC
                                      AA   __
GAM380  LOC203523 3'  CTCTGTCTCCTTGGTTTTGTT  89376   G       CATGT
                                GG AGGACCAGGG    GCAGGG
                                || ||||||||||    ||||||
                                TT TTTTGGTTCC    TGTCTC
                                 G        TC___
GAM380  LOC203636 3'  CTCTGCAGGCCCCATGGTCCTC 89424         __   ATG
          CC                     GGGAGGACCA  GGGC   TGCAGGG
                                ||||||||||  ||||   |||||||
                                CCCTCCTGGT  CCCG   ACGTCTC
                                      AC   G__
GAM380  LOC219404 3'  CTGCATTTGTTTTCCC      93494         CAGGGCAT
                                GGGAGGAC       GTGCAG
                                ||||||||       ||||||
                                CCCTTTTG       TACGTC
                                     TT_______
GAM380  LOC219540 5'  CTCTGTATTCCTTTTTGTCCTT 93597        C__   CAT
          CC                     GGGAGGAC   AGGG   GTGCAGGG
                                ||||||||   ||||   ||||||||
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                                CCTTCCTG  TTCC  TATGTCTC
                                    TTT   T__
GAM380  LOC219540 5'  CTTGCTCTTCTGTTCTTTT  93599      C    CATGT
                                GGAGGA CAGGG   GCAGG
                                |||||| |||||   |||||
                                TTTTCT GTCTT   CGTTC
                                   T   CT___
GAM380  LOC219540 5'  TTTTGTCCTTCCTGGTTCTTTT 93604          CATGT
                                GGGAGGACCAGGG   GCAGGG
                                ||||||||||||   ||||||
                                TTTTCTTGGTCCT   TGTTTT
                                       TCC__
GAM380  LOC219700 5'  CCCTGTTCTTTTCTGTCCTCCC 93061       C   CATGT
                                GGGAGGAC AGGG   GCAGGG
                                |||||||| ||||   ||||||
                                CCCTCCTG TCTT   TGTCCC
                                    _   TTCT_
GAM380  LOC219731 5'  CGCCTGCCTTGGCCTCCC   93094      A      T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTCC GGTTCCGT CGC
                                   _      C
GAM380  LOC219790 3'  TATGAATCTCTGGTTTTTCT  91359          ___
                                GGGAGGACCAGGG  CATG
                                ||||||||||||  ||||
                                TCTTTTTGGTCTC  GTAT
                                       TAA
GAM380  LOC219848 3'  TCTGAGCCTTGGTTTCCTC   91496    AG      ATGTG
                                GGG  GACCAGGGC   CAGG
                                |||  |||||||||   ||||
                                CTC  TTGGTTCCG   GTCT
                                  CT       A____
GAM380  LOC219894 3'  CTTGTATCATGTTTTCCT   93282     CCA     _
                                AGGA  GGGCATG TGCAGG
                                ||||  ||||||| ||||||
                                TCCT  TTTGTAC ATGTTC
                                  ___      T
GAM380  LOC219940 3'  TCTTGCTGTATTTTGTCTTCTT 93359       CAGG_  TGT
                                GGGAGGAC   GCA  GCAGGG
                                ||||||||   |||  ||||||
                                TTCTTCTG   TGT  CGTTCT
                                   TTTTA  ___
GAM380  LOC219988 3'  TTTTGCACACTTGCCCTGTCTT 91630       C    __
            CCT                 GGAGGAC AGGGCA  TGTGCAGGG
                                ||||||| ||||||  |||||||||
                                CCTTCTG TCCCGT  ACACGTTTT
                                   _    TC
GAM380  LOC220047 3'  CCCTGTGTATTAGTCTGTTCT  91642     CA   __  TG
                                AGGAC  GGGC  ATG  CAGGG
                                |||||  ||||  |||  |||||
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                                TCTTG  TCTG  TAT  GTCCC
                                  __   AT   GT
GAM380  LOC220064 3'  CTTTGTTTTTGTTTTGTTTTTT 93426   GG    C     TGT
            C                    G  AGGAC AGGGCA   GCAGGG
                                 |  ||||| ||||||   ||||||
                                 C  TTTTG TTTTGT   TGTTTC
                                  TT    _     TTT
GAM380  LOC220074 3'  CCGTCTGCTTTGGCCTCCC   59267       A      TGT  A
                                 GGGAGG CCAGGGCA   GC GG
                                 |||||| ||||||||   || ||
                                 CCCTCC GGTTTCGT   TG CC
                                    _       C__  _
GAM380  LOC220565 3'  TACCTGCTCTGTCCTCTT    90755        C     T
                                 GGGAGGAC AGGGCA GTG
                                 |||||||| |||||| |||
                                 TTCTCCTG TCTCGT CAT
                                     _     C
GAM380  LOC220739 3'  GTGCCCTGGGTTCTTCC     92937         _
                                 GGGAGGACC AGGGCAT
                                 ||||||||| |||||||
                                 CCTTCTTGG TCCCGTG
                                      G
GAM380  LOC220929 3'  TTTTGTACATGGTTTTATTTTC 91406      CC   G
                                 GAGGA  AGG CATGTGCAGGG
                                 |||||  ||| ||||||||||
                                 CTTTT  TTT GTACATGTTTT
                                    AT   G
GAM380  LOC220932 3'  TCCCGGCCGTGCTCTGCGTCCT 93137        _       T  A
            CCC                     GGAGGAC CAGGGCATG GC GGG
                                 ||||||| ||||||||| || |||
                                 CCTCCTG GTCTCGTGC CG CCC
                                     C        _ G   TC
GAM380  LOC220936 3'  CATGGCCTGGTTCTTCC     91409           G
                                 GGGAGGACCAGG CATG
                                 |||||||||||| ||||
                                 CCTTCTTGGTCC GTAC
                                       G
GAM380  LOC220936 3'  CCATAGTGTTCTGGCCCTTCT  91410       A       GTGCA
                                 GGGAGG CCAGGGCAT    GG
                                 |||||| |||||||||    ||
                                 TCTTCC GGTCTTGTG    CC
                                    C        ATA__
GAM380  LOC220980 5'  CCCTGTATGTGGTGCTGCCTTT 93151       AC   G  _
            T                    GGGAGG  CAG GC ATGTGCAGGG
                                 ||||||  ||| || ||||||||||
                                 TTTTCC  GTC TG TGTATGTCCC
                                    __   G  G
GAM380  LOC221061 3'  TTTTGTTGTTGTTGGTTTTCTT 93224          GG   TGT
                                 GGGAGGACCA  GCA   GCAGGG
                                 ||||||||||  |||   ||||||
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                                TTCTTTTGGT  TGT   TGTTTT
                                      __  TGT
GAM380  LOC221288 3'  TCTTGTGTGTGATTTTGTTCT  93618      C   G    TG
                                AGGAC AGG CATG  CAGGG
                                ||||| ||| ||||  |||||
                                TCTTG TTT GTGT  GTTCT
                                   T   A    GT
GAM380  LOC221288 5'  TTTTGTGTGTGTTTTAATTCTC 93624      CC       TG
                                GAGGA  AGGGCATG  CAGGG
                                |||||  ||||||||  |||||
                                CTCTT  TTTTGTGT  GTTTT
                                   AA       GT
GAM380  LOC221296 3'  CTGCACAAGGTCTCCT      91962      G   AGGGCA
                                GGGAG ACC     TGTGCAG
                                ||||| |||     |||||||
                                TCCTC TGG     ACACGTC
                                   _   A_____
GAM380  LOC221337 3'  GCTAGGCACATCCTTTGGTTTT 92111           C     AG
           CTC                    GGGAGGACCAGGG ATGTGC  GG
                                |||||||||||| ||||||  ||
                                CTCTTTTGGTTTC TACACG  TC
                                      C     GA  GT
GAM380  LOC221393 3'  CCCTGCAAGAGGCTGGCTTCTT 92295       A    GGCATG
                                GGGAGG CCAG     TGCAGGG
                                |||||| ||||     |||||||
                                TTCTTC GGTC     ACGTCCC
                                   _    GGAGA_
GAM380  LOC221477 3'  CCTTGCATGTGTTGGTATTCT  92151     G    GG
                                GGAG ACCA  GCATGTGCAGGG
                                |||| ||||  ||||||||||||
                                TCTT TGGT  TGTGTACGTTCC
                                  A   __
GAM380  LOC221486 3'  TCCTGGGTCCTGCCTGGTCCTC 91017           G  TG_ G
           CC                    GGGAGGACCAGG CA   T CAGGG
                                |||||||||||| ||   | |||||
                                CCCTCCTGGTCC GT   G GTCCT
                                      _  CCT G
GAM380  LOC221490 5'  CCCTGCATGGAGAGGGCTCTCT 93656      GA  AGGGCA
           C                     GGGAG  CC     TGTGCAGGG
                                |||||  ||     |||||||||
                                CTCTC  GG     GTACGTCCC
                                   TC  GAGAG_
GAM380  LOC221490 5'  TTCTGTGCAGATCTGTTCCTCC 93671       C    GCA  TG
           T                     GGGAGGA CAGG   TG  CAGGG
                                |||||||  ||||   ||  |||||
                                TCCTCCT GTCT   AC  GTCTT
                                   T    AG_  GT
GAM380  LOC221540 3'  CCTCCTGCCTTGGCCTCCC    93836       A       TGTGC
                                GGGAGG CCAGGGCA     AGG
                                ||||||  ||||||||     |||
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                                CCCTCC GGTTCCGT     TCC
                                   _       CC___
GAM380  LOC221552 3'  TTTTGGAATCTCTAGTTCTTCC 93806         C    C  GTG
                                GGGAGGAC AGGG AT   CAGGG
                                |||||||| |||| ||   |||||
                                CCTTCTTG TCTC TA   GTTTT
                                     A    _  AG_
GAM380  LOC221596 3'  TTAGTTACTGCTCTGGTCTT   91984           T   CAGGG
                                AGGACCAGGGCA GTG
                                |||||||||||| |||
                                TTCTGGTCTCGT CAT
                                       _  TGATTT
GAM380  LOC221755 3'  TTCTGTCCCTTCTTGGTCTCTT 92398      _       CATGT
           C                     GGAG GACCAGGG     GCAGGG
                                |||| ||||||||     ||||||
                                CTTC CTGGTTCT     TGTCTT
                                  T       TCCC_
GAM380  LOC221830 3'  TGTGTGTCCTTGTCTTCTT    92513         C      GT
                                GGGAGGAC AGGGCAT  GCA
                                |||||||| |||||||  |||
                                TTCTTCTG TCCTGTG  TGT
                                     T      __
GAM380  LOC221830 3'  TTTTGTGTGTGTTTAATAGGCT 92516      A  A___      TG
           TC                     GAGG CC    GGGCATG  CAGGG
                                |||| ||    |||||||  |||||
                                CTTC GG    TTTGTGT  GTTTT
                                  _ ATAA      GT
GAM380  LOC221838 3'  TTGTGGACCACTTTGGTTTTCT 92547           CAT  G  GGG
           T                     GGGAGGACCAGGG   GT CA
                                ||||||||||||   || ||
                                TTCTTTTGGTTTC   CA GT
                                       AC_  G  GTTT
GAM380  LOC222068 3'  TTCTGCATTCTGGGTTTTGTTT 92715      C     AT___
           TTCC                    GAGGA CAGGGC     GTGCAGGG
                                ||||| ||||||     ||||||||
                                CTTTT GTTTTG     TACGTCTT
                                  T     GGTCT
GAM380  LOC222228 3'  CTCTGCATTTTATTGGTTT    94295        GGCAT
                                GGACCAG     GTGCAGGG
                                |||||||     ||||||||
                                TTTGGTT     TACGTCTC
                                     ATTT_
GAM380  LOC222237 3'  CTCTGTGTGTGGTGGGCCCTTT 94289   GG   A_   GG    GT
           C                      G  AGG  CCA  GCAT  GCAGGG
                                |  |||  |||  ||||  ||||||
                                C  TCC  GGT  TGTG  TGTCTC
                                 TT   CG   GG   __
GAM380  LOC222237 3'  TTCTGCATCCCACTTGTTCCTC 94291        C    GCAT
           TT                     GGGAGGA CAGG    GTGCAGGG
                                |||||||  ||||    ||||||||
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                                TTCTCCT GTTC    TACGTCTT
                                    T    ACCC
GAM380   LOC222256 3'  TCCTGCATGTGAGATTCATCC  94262     G  CCAGGG
                                GGA GA      CATGTGCAGGG
                                ||| ||      ||||||||||
                                CCT CT      GTGTACGTCCT
                                  A  TAGA__
GAM380   LOC245771 5'  CACCTGCCTTGGCCTTTC    92882    GG   A       T
                                G  AGG CCAGGGCA GTG
                                |  ||| |||||||| |||
                                C  TCC GGTTCCGT CAC
                                 TT   _       C
GAM380   LOC245811 3'  TCTTGAGCTCTTTGGTCATCTT 93911      G       CAT  G
                                GGGA GACCAGGG   GT CAGGG
                                |||| ||||||||   || |||||
                                TTCT CTGGTTTC   CG GTTCT
                                  A       T__  A
GAM380   LOC253299 5'  CCTTGCATGTGGATTGGTTTTG 96453    G       GG
            CT                    GG AGGACCAG  CATGTGCAGGG
                                || ||||||||  ||||||||||
                                TC TTTTGGTT  GTGTACGTTCC
                                 G       AG
GAM380   LOC253348 5'  CTCTGAGGCCTCTGGTTTGTTC 96356     AG     _   ATGTG
                                GGG  GACCAG GGC     CAGGG
                                |||  |||||| |||     |||||
                                CTT  TTGGTC CCG     GTCTC
                                  GT     T   GA___
GAM380   LOC253499 3'  CTGTGTTTATGTGTTCTCCC   96531        CAGG    T   G
                                GGGAGGAC    GCATG GCA GG
                                ||||||||    ||||| ||| ||
                                CCCTCTTG    TGTAT TGT TC
                                     _____    T   G
GAM380   LOC253612 5'  TTCTGCCTTGCTTTGGTTTCTC 96758       _       TGT
            C                     GGAGGA CCAGGGCA   GCAGGG
                                |||||| ||||||||   ||||||
                                CCTCTT GGTTTCGT   CGTCTT
                                    T       TC_
GAM380   LOC253613 3'  CCTTTCATGTCCTGGTCTTTTT 96192              TGC
                                GGGAGGACCAGGGCATG   AGG
                                ||||||||||||||||   |||
                                TTTTTCTGGTCCTGTAC   TCC
                                          TT_
GAM380   LOC253664 3'  CTAGGCCGTGTCTTGTTCTTCC 94810        C       T  AG
            T                     GGGAGGA CAGGGCATG GC  GG
                                ||||||| |||||||| ||  ||
                                TCCTTCT GTTCTGTGC CG  TC
                                    T       _  GA
GAM380   LOC253769 5'  TTCTGCATGTGGATGTCTTTCT 97227        CAGGG
                                GGGAGGAC    CATGTGCAGGG
                                ||||||||    ||||||||||
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                                TCTTTCTG    GTGTACGTCTT
                                    TAG__
GAM380  LOC254057 3'  CCTGTGTGTGTGTTGTCT    96997     C  G    TG
                                GGAC AG GCATG  CAGG
                                |||| || |||||  ||||
                                TCTG TT TGTGT  GTCC
                                  _ G    GT
GAM380  LOC254228 3'  ATATGTATTTGGTCTTTCT    95951          _
                                GGGAGGACCAGG GCATGT
                                |||||||||||| ||||||
                                TCTTTCTGGTTT TGTATA
                                       A
GAM380  LOC254249 3'  TTCTGCATTCTTGCCTAGTTTT 95451       CA    T__
          CCT                    GGAGGAC  GGGCA   GTGCAGGG
                                |||||||  |||||   ||||||||
                                CCTTTTG  TCCGT   TACGTCTT
                                    A_    TCT
GAM380  LOC254428 3'  CCCTGTGATCCCAGTTCTGTTC 95456       C    ATG___
          TCTT                   GAGGAC AGGGC     TGCAGGG
                                |||||| |||||     |||||||
                                CTCTTG TCTTG     GTGTCCC
                                   _    ACCCTA
GAM380  LOC254428 3'  CTCTGGATTTTTGGTTTT    95458         CAT  G
                                AGGACCAGGG   GT CAGGG
                                ||||||||||   || |||||
                                TTTTGGTTTT   TA GTCTC
                                     ___  G
GAM380  LOC254610 5'  TCCTGCCTTCCTTTGGTTTTAC 96277    G        CATGT
          T                     GG AGGACCAGGG     GCAGGG
                                || ||||||||||     ||||||
                                TC TTTTGGTTTC     CGTCCT
                                 A        CTTC_
GAM380  LOC254655 3'  CACCTGCCTTGGCCTCTC    95468       A       T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CTCTCC GGTTCCGT CAC
                                   _       C
GAM380  LOC254672 3'  CACCTGCCTTGGCTTCCC    94641       A       T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTTC GGTTCCGT CAC
                                   _       C
GAM380  LOC254873 5'  CCCTGCGCGTCCAGCTCTTCT  94571       CCAG  C
                                GGAGGA    GG ATGTGCAGGG
                                ||||||    || ||||||||||
                                TCTTCT    CC TGCGCGTCCC
                                   CGA_  _
GAM380  LOC254986 5'  CTCTGCGCATGCCCGGACCCC  96084    A  A  A
                                GG GG CC GGGCATGTGCAGGG
                                || || || ||||||||||||||
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                                CC CC GG CCCGTACGCGTCTC
                                 _ A _
GAM380  LOC255042 5'  CTGATTCTGGTCCCCC     95314     A      GCATGTG
                                GGG GGACCAGG      CAG
                                ||| ||||||||      |||
                                CCC CCTGGTCT      GTC
                                  _       TA_____
GAM380  LOC255196 5'  CTCTGTACATGTTCTTCCTC  97168      CC
                                GAGGA  AGGGCATGTGCAGGG
                                |||||  |||||||||||||||
                                CTCCT  TCTTGTACATGTCTC
                                   __
GAM380  LOC255242 3'  CTCTGGACCTCCTGTCTTCTC  95926        C    CAT  G
                                GGGAGGAC AGGG   GT CAGGG
                                |||||||| ||||   || |||||
                                CTCTTCTG TCCT   CA GTCTC
                                     _   C__  G
GAM380  LOC255242 3'  CTTGTCCTCTGGACCTCCT    95927       A     CATGT
                                GGGAGG CCAGGG    GCAGG
                                |||||| ||||||    |||||
                                TCCTCC GGTCTC    TGTTC
                                   A     C____
GAM380  LOC255465 5'  CTCTGTTGCATTTGGTTCTGCT 97288    G       _   TGT
                                GG AGGACCAGG GCA   GCAGGG
                                || |||||||| |||   ||||||
                                TC TCTTGGTTT CGT   TGTCTC
                                 G       A  ___
GAM380  LOC255465 3'  TTTTGTATTCATTATCTGTGTT 97312      _   GCAT__
           CTCTT                  AGGAC CAGG     GTGCAGGG
                                |||||| ||||     ||||||||
                                TCTTG GTCT     TATGTTTT
                                   T    ATTACT
GAM380  LOC255520 5'  TCCTGCTCCCCCTAGTTCTTCC 95865        C    CATGT
                                GGGAGGAC AGGG    GCAGGG
                                |||||||| ||||    ||||||
                                CCTTCTTG TCCC    CGTCCT
                                     A    CCT__
GAM380  LOC255671 3'  TCCTAGGGTTCTCGTTCTCCC  97263        C    ATGTGC
                                GGGAGGAC AGGGC     AGGG
                                |||||||| |||||     ||||
                                CCCTCTTG TCTTG     TCCT
                                     C    GGA___
GAM380  LOC255671 3'  TCTTGGAATTTCTTGTTCTCTT 97265        C   C  GTG
                                GGGAGGAC AGGG AT   CAGGG
                                |||||||| |||| ||   |||||
                                TTCTCTTG TTCT TA   GTTCT
                                     _   T  AG_
GAM380  LOC255838 3'  TTTTGTGCATGGAGTGCTTTT  96005      G  CAGGG   TG
                                GGGAG AC    CATG  CAGGG
                                ||||| ||    ||||  |||||
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                                TTTTC TG    GTAC  GTTTT
                                   G  AG___   GT
GAM380  LOC255849 3'  TTTTGTGTGTGTCATGTCT   96445     CAG     TG
                                GGAC  GGCATG  CAGGG
                                ||||  ||||||  |||||
                                TCTG  CTGTGT  GTTTT
                                  TA_     GT
GAM380  LOC255919 3'  GTGCTTTGGTACTTTT      95039      G
                                GGGAG ACCAGGGCAT
                                ||||| ||||||||||
                                TTTTC TGGTTTCGTG
                                   A
GAM380  LOC256416 5'  TCCTGCGTCGTTCTGTCCTTCC 94409        C    ATG
                                GGGAGGAC AGGGC   TGCAGGG
                                |||||||| |||||   |||||||
                                CCTTCCTG TCTTG   GCGTCCT
                                     _    CT_
GAM380  LOC256476 3'  TTTTGTTGATGTTGGGTTCTTC 96823        AG    GT
           T                     GGGAGGACC  GGCAT  GCAGGG
                                |||||||||  |||||  ||||||
                                TCTTCTTGG  TTGTA  TGTTTT
                                     G_    GT
GAM380  LOC256537 5'  CTCTGCGTGAGGGTTCTTCT   95226        AGGG   GT
                                GGGAGGACC    CAT  GCAGGG
                                |||||||||    |||  ||||||
                                TCTTCTTGG    GTG  CGTCTC
                                     GA__   __
GAM380  LOC256815 3'  CTTGTGCAATGTTTCTCTC    94708       CCAGG   _ TG
                                GGGAGGA    GCAT G  CAGG
                                |||||||    |||| |  ||||
                                CTCTCTT    TGTA C  GTTC
                                     _____   A GT
GAM380  LOC256974 3'  CCCTGGGACCCCGGGTCCTTCC 97246         A   CATGTG
                                GGGAGGACC GGG     CAGGG
                                ||||||||| |||     |||||
                                CCTTCCTGG CCC     GTCCC
                                     G   CAGG__
GAM380  LOC256980 3'  CCTACTCCCTGGTTCTCTC    95217          CAT  GC
                                GGGAGGACCAGGG   GT  AGG
                                ||||||||||||   ||  |||
                                CTCTCTTGGTCCC   CA  TCC
                                       T__  __
GAM380  LOC257000 5'  TTCTGCAACCTGTGTCTTTCT  96784        _   GCATG
                                GGGAGGAC CAGG    TGCAGGG
                                |||||||| ||||    |||||||
                                TCTTTCTG GTCC    ACGTCTT
                                     T   A____
GAM380  LOC257051 3'  TTCTGTGTGTGCCCATTTCCTT 96322      CCA      TG
                                GAGGA   GGGCATG  CAGGG
                                |||||   |||||||  |||||
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                                TTCCT  CCCGTGT  GTCTT
                                  TTA     GT
GAM380  LOC257095 5'  CTCTGCGTGGTGTGGCTCCTCC 96938      _  GG  ATG
          T                     GGGAGGA CCA  GC   TGCAGGG
                                ||||||| |||  ||   |||||||
                                TCCTCCT GGT  TG   GCGTCTC
                                   C  G_  GT_
GAM380  LOC257282 5'  TTCTGCATCATTGGTTCTCCC  96402         GGCAT
                                GGGAGGACCAG    GTGCAGGG
                                ||||||||||    ||||||||
                                CCCTCTTGGTT    TACGTCTT
                                      AC___
GAM380  LOC257364 3'  TCTGTGGCACTGTCTTCCC   94968       C  G  ATG
                                GGGAGGAC AG GC   TGCAGG
                                |||||||| || ||   ||||||
                                CCCTTCTG TC CG   GTGTCT
                                    _  A  ___
GAM380  LOC257446 5'  CATGTTCTGATTCTTTC     79999    GG    C
                                G  AGGA CAGGGCATG
                                |  |||| |||||||||
                                C  TCTT GTCTTGTAC
                                 TT   A
GAM380  LOC257492 3'  CCCTGCTACCTTCCTGGCCTCT 97716       A     CAT  _
          C                     GGGAGG CCAGGG   GT GCAGGG
                                |||||| ||||||   || ||||||
                                CTCTCC GGTCCT   CA CGTCCC
                                   _     TC_  T
GAM380  LOC257493 3'  TTTTGGAATCTCTAGTTCTTCC 97801        C   C  GTG
                                GGGAGGAC AGGG AT   CAGGG
                                |||||||| |||| ||   |||||
                                CCTTCTTG TCTC TA   GTTTT
                                    A   _  AG_
GAM380  LOC257494 3'  CTTTGTGTGTGTCACATGCTGC 97792     A  ACCAG     TG
          CT                      GGG GG    GGCATG  CAGGG
                                ||| ||    ||||||  |||||
                                TCC TC    CTGTGT  GTTTC
                                  G  GTACA     GT
GAM380  LOC257545 3'  CCTCCTGCCTTGGCCTCCC   97804       A       TGTGC
                                GGGAGG CCAGGGCA    AGG
                                |||||| ||||||||    |||
                                CCCTCC GGTTCCGT    TCC
                                   _       CC___
GAM380  LOC257598 3'  CCTCCTGCCTTGGCCTCCC   97919       A       TGTGC
                                GGGAGG CCAGGGCA    AGG
                                |||||| ||||||||    |||
                                CCCTCC GGTTCCGT    TCC
                                   _       CC___
GAM380  LOC257606 3'  CCCTGCTACCTTCCTGGCCTCT 97892       A     CAT  _
          C                     GGGAGG CCAGGG   GT GCAGGG
                                |||||| ||||||   || ||||||
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                                CTCTCC GGTCCT   CA CGTCCC
                                   _     TC_  T
GAM380  LOC257609 3'  TTTTGGAATCTCTAGTTCTTCC 97941        C    C  GTG
                                GGGAGGAC AGGG AT   CAGGG
                                |||||||| |||| ||   |||||
                                CCTTCTTG TCTC TA   GTTTT
                                    A    _  AG_
GAM380  LOC51008  3'  CCCTTAGTGTGTTCTGGTTTTT 31960             TG GC
             TT                   GGGAGGACCAGGGCA  T  AGGG
                                |||||||||||||||  |  ||||
                                TTTTTTTGGTCTTGT  G  TCCC
                                       GT AT
GAM380  LOC51008  5'  CACCTGCCTTGGCCTCCC    31959       A       T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTCC GGTTCCGT CAC
                                   _       C
GAM380  LOC51028  3'  CATTTTTGGTTTTTCC      32180            C
                                GGGAGGACCAGGG ATG
                                |||||||||||| |||
                                CCTTTTTGGTTTT TAC
                                          _
GAM380  LOC51031  3'  TCTGTGCGAGCTTCTTTC    32199       CCAG   A  TG
                                GGAGGA    GGC TG  CAGG
                                ||||||    ||| ||  ||||
                                CTTTCT    TCG GC  GTCT
                                   _____   A  GT
GAM380  LOC51049  3'  CTTTGCATATGTACTTTTCTCT 31887        CC  GG
             T                   GGGAGGA  AG  CATGTGCAGGG
                                |||||||  ||  ||||||||||||
                                TTCTCTT  TC  GTATACGTTTC
                                    T_  AT
GAM380  LOC51159  5'  TCTGCCTGCCTTGGCCCTCCC  32502       A       TGT
                                GGGAGG CCAGGGCA   GCAGG
                                |||||| ||||||||   |||||
                                CCCTCC GGTTCCGT   CGTCT
                                   C       C__
GAM380  LOC51200  3'  CCCTGCAAGAACTGGTTCTGCC 32993    G       GGCATG
                                GG AGGACCAG     TGCAGGG
                                || ||||||||     |||||||
                                CC TCTTGGTC     ACGTCCC
                                 G       AAGA__
GAM380  LOC51285  3'  CCCTCCAGGCCTTGGTCTTC   33345           A  TGC
                                GAGGACCAGGGC TG   AGGG
                                ||||||||||| ||   ||||
                                CTTCTGGTTCCG AC   TCCC
                                       G  C__
GAM380  LOC51580  3'  CTTTGTTTGGTTCTTCT     31863          G   TGTGC
                                GGGAGGACCA GGCA     AG
                                |||||||||| ||||     ||
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                                TCTTCTTGGT TTGT    TC
                                      _   T____
GAM380  LOC51608 3' CCTTTGTTCTGGGTCCTTTC  63673   GG    _    TGTGC
                                G  AGGACC AGGGCA    AGG
                                |  |||||| ||||||    |||
                                C  TCCTGG TCTTGT    TCC
                                 TT    G    T____
GAM380  LOC51652 3' TTTGTGCAGGTTTTTCT    32197        AGGGCA  TG
                                GGGAGGACC    TG  CAGG
                                |||||||||    ||  ||||
                                TCTTTTTGG    AC  GTTT
                                      ______ GT
GAM380  LOC51673 5' TCCTGCGTCGTTCTGTCCTTCC 94568        C    ATG
                                GGGAGGAC AGGGC   TGCAGGG
                                |||||||| |||||   |||||||
                                CCTTCCTG TCTTG   GCGTCCT
                                     _    CT_
GAM380  LOC51701 3' TATGTTTTGTTTTTCTT    32653       C
                                GGGAGGA CAGGGCATG
                                ||||||| |||||||||
                                TTCTTTT GTTTTGTAT
                                    T
GAM380  LOC51706 3' TCTGTGTGTGTCTCTCTC    70318      GACCA     TG
                                GGGAG    GGGCATG  CAGG
                                |||||    |||||||  ||||
                                CTCTC    TCTGTGT  GTCT
                                   _____     GT
GAM380  LOC51713 3' TTTTGCTGGGTTGGTTTTTTT  32763         GG  TGT
                                GGGAGGACCAG  CA   GCAGGG
                                ||||||||||  ||   ||||||
                                TTTTTTTGGTT  GT   CGTTTT
                                      GG  ___
GAM380  LOC51754 5' CCTGTACAAGGTCTTT     71029       AGGGCA
                                GAGGACC     TGTGCAGG
                                |||||||     ||||||||
                                TTTCTGG     ACATGTCC
                                    A_____
GAM380  LOC54103 5' CCTGTGTTATGTTTTCTC    94211        CAG   ATGT
                                GGGAGGAC   GGC    GCAGG
                                ||||||||   |||    |||||
                                CTCTTTTG   TTG    TGTCC
                                    TA_  _____
GAM380  LOC54103 5' CCTTGCACGTGCTTTGCGTATA 94212    GAGG  _
           CT                    GG    AC CAGGGCATGTGCAGGG
                                ||    || ||||||||||||||||
                                TC    TG GTTTCGTGCACGTTCC
                                 ATA_  C
GAM380  LOC56181 5' CTCTGCAGGGCCTGGTTTTTT  95535          G ATG
                                GGAGGACCAGG C   TGCAGGG
                                |||||||||| |   |||||||
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                                TTTTTTGGTCC G   ACGTCTC
                                      _ GG_
GAM380  LOC56181  5' CTTTATCATGCTCTGCTCCTCT 95536       C       TGC   G
             T                   GGGAGGA CAGGGCATG   AGG
                                 ||||||| |||||||||   |||
                                 TTCTCCT GTCTCGTAC   TTC
                                     C        TAT
GAM380  LOC56181  3' TGTTTCTGGTTTTTCC      95545          _
                                 GGGAGGACCAGGG CA
                                 |||||||||||||| ||
                                 CCTTTTTGGTCTT GT
                                       T
GAM380  LOC57146  3' CACCTGCCTTGGCCTCCC    39915       A       T
                                 GGGAGG CCAGGGCA GTG
                                 |||||| |||||||| |||
                                 CCCTCC GGTTCCGT CAC
                                    _       C
GAM380  LOC57826  3' TTTGTGATGTGTTTTGTTTTTT 41021       C       _    G
             TT                   GGGAGGA CAGGGCATGT GCAGG
                                 ||||||| |||||||||| |||||
                                 TTTTTTT GTTTTGTGTA TGTTT
                                     T        G
GAM380  LOC63928  5' CCTGCACATTGTTTTCC     42033        CAGGGC
                                 GGAGGAC     ATGTGCAGG
                                 |||||||     |||||||||
                                 CCTTTTG     TACACGTCC
                                     T_____
GAM380  LOC64116  5' CTCTGTCCCCCTTTGTCCTCTT 42199        C_   CATGT
                                 GGGAGGAC  AGGG    GCAGGG
                                 |||||||| ||||    ||||||
                                 TTCTCCTG  TCCC    TGTCTC
                                      TT   CC___
GAM380  LOC64744  3' TCCTGTGTATGTGTAAATTCCT 61801      CCAGG_    TG
             T                   GAGGA     GCATG  CAGGG
                                 |||||     |||||  |||||
                                 TTCCT     TGTAT  GTCCT
                                    TAAATG    GT
GAM380  LOC81034  3' CGCCTGCCTTGGCCTCCC    47849       A       T
                                 GGGAGG CCAGGGCA GTG
                                 |||||| |||||||| |||
                                 CCCTCC GGTTCCGT CGC
                                    _       C
GAM380  LOC90110  5' CACCTGCCTTGGCCTCCC    61507       A       T
                                 GGGAGG CCAGGGCA GTG
                                 |||||| |||||||| |||
                                 CCCTCC GGTTCCGT CAC
                                    _       C
GAM380  LOC90288  3' TCCTGCATGTGTCACCACCC   62107     A  ACCAG
                                 GGG GG    GGCATGTGCAGGG
                                 ||| ||    ||||||||||||
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                                CCC CC    CTGTGTACGTCCT
                                  A  A____
GAM380  LOC90459  3' CTCTGTTGAGTCTCTGTCCTCC 62886        C    C  GT_
             C                   GGGAGGAC AGGG AT   GCAGGG
                                 |||||||| |||| ||   ||||||
                                 CCCTCCTG TCTC TG   TGTCTC
                                    _   _ AGT
GAM380  LOC90620  5' TCGTGTTGTGTGTTTTGGGTTT 63571        _     GT_  G
             TCTC                  GGAGGACC AGGGCAT   GCA GG
                                 |||||||| |||||||   ||| ||
                                 TCTTTTGG TTTTGTG   TGT CT
                                    G      TGT   G
GAM380  LOC90630  5' CCTGCCAACCTGTCTTCTC    63631        C   GCA  T
                                 GGGAGGAC AGG   TG GCAGG
                                 |||||||| |||   || |||||
                                 CTCTTCTG TCC   AC CGTCC
                                    _   A__  _
GAM380  LOC90639  5' TCTTGATTCTTTCTGGTTTTGC 63663    G        CAT  G
             C                   GG AGGACCAGGG   GT CAGGG
                                 || ||||||||||   || |||||
                                 CC TTTTGGTCTT   TA GTTCT
                                  G         TCT  _
GAM380  LOC90750  3' TTCTGGCACCTCTGGTTCTGCT 63929    G        CAT   _
                                 GG AGGACCAGGG   GTGC AGGG
                                 || ||||||||||   |||| ||||
                                 TC TCTTGGTCTC   CACG TCTT
                                  G         ___    G
GAM380  LOC90841  5' CCAGTGGGGCTCTGGTCTTTTC 64196    GG         ATG   A
                                 G  AGGACCAGGGC   TGC GG
                                 |  ||||||||||   ||| ||
                                 C  TTCTGGTCTCG   GTG CC
                                  TT         GG_   A
GAM380  LOC90906  5' TCCTGCTACATTTCTTGGTTCC 64314     A       C   _
             CT                    GGG GGACCAGGG ATGT GCAGGG
                                 ||| ||||||||| |||| ||||||
                                 TCC CTTGGTTCT TACA CGTCCT
                                   _        T   T
GAM380  LOC90982  5' TTTTGTGTGTGCCCTGCTCCC  64540      GAC        TG
                                 GGGAG   CAGGGCATG  CAGGG
                                 |||||   |||||||||  |||||
                                 CCCTC   GTCCCGTGT  GTTTT
                                    ___         GT
GAM380  LOC91010  3' TTTTGTACATGTACCACCTCCC 64620       ACCA  _
                                 GGGAGG    GG GCATGTGCAGGG
                                 ||||||    || ||||||||||||
                                 CCCTCC    CC TGTACATGTTTT
                                    A___  A
GAM380  LOC91012  5' TTTGCAGTTTGGGTTTTTT    64645         AG   ATG
                                 GGAGGACC  GGC   TGCAGG
                                 ||||||||  |||   ||||||
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                                TTTTTTGG  TTG   ACGTTT
                                    GT  ___
GAM380  LOC91050  3' CCCAGTGGTGGTCTGGTTTTTT 64743          G   G   A
           T                    GGGAGGACCAGG CAT TGC GGG
                                |||||||||||| ||| ||| |||
                                TTTTTTTGGTCT GTG GTG CCC
                                    G   _   A
GAM380  LOC91097  3' TTTGATTCTTGGTTCTTT    64842          CATGTG
                                GGAGGACCAGGG     CAGG
                                ||||||||||||     ||||
                                TTTCTTGGTTCT     GTTT
                                    TA____
GAM380  LOC91145  3' TTCTACATTATGCCCAGGTTCT 65059         A     _  C
           TCT                    GGGAGGACC GGGCATG TG AGGG
                                |||||||| ||||||| || ||||
                                TCTTCTTGG CCCGTAT AC TCTT
                                    A      T  A
GAM380  LOC91208  5' CCTGCCAACCTGTCTTCTC   65246        C   GCA  T
                                GGGAGGAC AGG   TG GCAGG
                                |||||||| |||   || |||||
                                CTCTTCTG TCC   AC CGTCC
                                    _   A__  _
GAM380  LOC91266  5' CTGATAGGGCCCTGGTCTTTCT 65414           A_   G
                                GGGAGGACCAGGGC  TGT CAG
                                |||||||||||||  ||| |||
                                TCTTTCTGGTCCCG  ATA GTC
                                    GG  _
GAM380  LOC91272  3' CTTGTACATGAATCTTCT    65429       CCAGGG
                                GGAGGA     CATGTGCAGG
                                ||||||     ||||||||||
                                TCTTCT     GTACATGTTC
                                   AA____
GAM380  LOC91300  3' TCCTGTGTCCCCATGCTGGTCC 57072        GG    ____
           TCCT                    AGGACCA  GCATG    TGCAGGG
                                |||||||  |||||   |||||||
                                TCCTGGT  CGTAC    GTGTCCT
                                    __     CCCT
GAM380  LOC91300  3' TCCTGTGTCCCCATGCTGGTCC 94599        GG    ____
           TCCT                    AGGACCA  GCATG    TGCAGGG
                                |||||||  |||||   |||||||
                                TCCTGGT  CGTAC    GTGTCCT
                                    __     CCCT
GAM380  LOC91397  3' TCTTGCCTGCTCTGGCCTCCT  65914       A       TGT
                                GGGAGG CCAGGGCA   GCAGGG
                                |||||| ||||||||   ||||||
                                TCCTCC GGTCTCGT   CGTTCT
                                    _       C__
GAM380  LOC91464  5' TCCTGTGCCTTATTGTTTCTCC 66145        C   GGCAT TG
           C                     GGGAGGA CAG    G  CAGGG
                                ||||||| |||    |  |||||
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                                CCCTCTT GTT    C  GTCCT
                                    T  ATTC_ GT
GAM380  LOC91547  3' CGCCTGCCTTGGCCTCCC    66402       A      T
                                GGGAGG CCAGGGCA GTG
                                ||||||| |||||||| |||
                                CCCTCC GGTTCCGT CGC
                                   _       C
GAM380  LOC91571  3' CTTTGCATGTGTAGTTACTTCT 66509       CCAGG_
           CC                    GGAGGA     GCATGTGCAGGG
                                ||||||     ||||||||||||
                                CCTCTT     TGTGTACGTTTC
                                   CATTGA
GAM380  LOC91628  3' TTTTGTATATGTATGCCATTTT 66765      CCA ___
           CTCC                    GAGGA   GG   GCATGTGCAGGG
                                |||||   ||   ||||||||||||
                                CTCTT   CC   TGTATATGTTTT
                                   TTA  GTA
GAM380  LOC91948  3' CTTTGCACATGCTATGTCTTTT 67618        CAG
                                GGAGGAC   GGCATGTGCAGGG
                                |||||||   ||||||||||||||
                                TTTTCTG   TCGTACACGTTTC
                                    TA_
GAM380  LOC92080  5' TCCGGGTTGTCCTGTTCTTTC  68060   GG    C     TGT  A_
                                G  AGGAC AGGGCA   GC  GGG
                                |  ||||| ||||||   ||  |||
                                C  TCTTG TCCTGT   TG  CCT
                                 TT    _     ___  GG
GAM380  LOC92148  5' CCTTGATCTATGTTCTGTTTTT 68332        C       TG_
           TTT                   GGGAGGA CAGGGCATG   CAGGG
                                ||||||| |||||||||   |||||
                                TTTTTTT GTCTTGTAT   GTTCC
                                    T       CTA
GAM380  LOC92170  3' CTCCGCATGCTTGGTTCTCCC  68368           G     C
                                GGGAGGACCAGG CATGTG AG
                                |||||||||||| |||||| ||
                                CCCTCTTGGTTC GTACGC TC
                                      _     C
GAM380  LOC92231  3' CCTGTATTTGCTTTTCCC    68551       ACCAG    T
                                GGGAGG    GGCA GTGCAGG
                                ||||||    |||| |||||||
                                CCCTTT    TCGT TATGTCC
                                   _____    T
GAM380  LOC92267  3' CGCCTGCCTTGGCCTCCC    68608       A      T
                                GGGAGG CCAGGGCA GTG
                                |||||| |||||||| |||
                                CCCTCC GGTTCCGT CGC
                                   _       C
GAM380  LOC92335  3' TCCTGCCAGCTGCCCTGGTGCT 68972   GG  G       __  T
           TTC                    AG ACCAGGGCA  TG GCAGGG
                                 || |||||||||  || ||||||
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                                TC TGGTCCCGT  AC CGTCCT
                               TT  G        CG  _
GAM380  LOC92597  3'  TTTTGCACAAGTTTTTGTTTTT 69974         C     A
                 CT                  GGGAGGAC AGGGC TGTGCAGGG
                                     |||||||| ||||| |||||||||
                                     TCTTTTTG TTTTG ACACGTTTT
                                          T     A
GAM380  LOC92719  3'  CCCAAAGTGCCTTGTTTTCTC  70381         C      GTGCA
                                     GGGAGGAC AGGGCAT     GGG
                                     |||||||| |||||||     |||
                                     CTCTTTTG TTCCGTG     CCC
                                          _      AAA__
GAM380  LOC93268  5'  ATGCCCTGGTTTTGCC      71876     G
                                     GG AGGACCAGGGCAT
                                     || ||||||||||||
                                     CC TTTTGGTCCCGTA
                                      G
GAM380  LOC93538  3'  TTATATCATAAGTTCTGGTCTT 72565              A    CAGGG
                 TCC                   GGGAGGACCAGGGC TGTG
                                     |||||||||||||| ||||
                                     CCTTTCTGGTCTTG ATAC
                                               A    TATATTT
GAM380  LOC93587  3'  TCTTAGCAGCTGTGGTTTTTTT 72649           G   A   GC
                                     GGGAGGACCA GGC TGT  AGGG
                                     |||||||||| ||| |||  ||||
                                     TTTTTTTGGT TCG ACG  TTCT
                                           G   _   A_
GAM380  LOC93622  3'  TTTTGTCTCCCCTGTTTTTCT  56934        C     CATGT
                                     GGAGGA CAGGG     GCAGGG
                                     |||||| |||||     ||||||
                                     TCTTTT GTCCC     TGTTTT
                                        T     CTC__
GAM380  LOC96597  5'  CTCTAGAGGTCTTGTCTTCCC  66912         C     ATGTGC
                                     GGGAGGAC AGGGC      AGGG
                                     |||||||| |||||      ||||
                                     CCCTTCTG TTCTG      TCTC
                                          _     GAGA__
GAM381  ARHGEF6   3'  CAAACTTGAAGCCAGGC     68197        ACCA
                                     GCCTGG    CAAGTTTG
                                     ||||||    ||||||||
                                     CGGACC    GTTCAAAC
                                        GAA_
GAM381  CNTN2     3'  GTCACAACCCAGGTGA      17411         ACCACAA   _
                                     TCGCCTGG      GTT TGAC
                                     ||||||||      ||| ||||
                                     AGTGGACC      CAA ACTG
                                          ________  C
GAM381  CORO2A    3'  AAACTGTGGTCCAGAGA     12642     GC         A
                                     TC  CTGGACCACA GTTT
                                     ||  |||||||||| ||||
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                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM381  CORO2A   3'  AAACTGTGGTCCAGAGA     53398    GC        A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM381  GRLF1    3'  AGGTCAGAAAGTGGCCCAGG   78551      A    AAG
                                CCTGG CCAC   TTTGACCT
                                ||||| ||||   ||||||||
                                GGACC GGTG   AGACTGGA
                                   C    AA_
GAM381  LAPTM5   3'  AGGCTTGTGGTCAAGC      22199    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCGGA
                                 AA_
GAM381  POU2AF1  3'  AGATTTACAGTCCAGGC     20647        CAC
                                GCCTGGAC   AAGTTT
                                ||||||||   ||||||
                                CGGACCTG   TTTAGA
                                     ACA
GAM381  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  6355         C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM381  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  54574        C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM381  TRIM34   5'  AGGTCAAGTTGAGCCCAG    55224     ACCA   G
                                CTGG    CAA TTTGACCT
                                ||||    ||| ||||||||
                                GACC    GTT GAACTGGA
                                  CGA_   _
GAM381  TRIM9    5'  AGGCCAGGCAAGTCCAGGC   30749        CACAA    A
                                GCCTGGAC    GTTTG CCT
                                ||||||||    ||||| |||
                                CGGACCTG    CGGAC GGA
                                     AA___    C
GAM381  ABLIM    5'  GATATGTAACCCAGGCGG    22030        ACC   A
                                TCGCCTGG   ACA GTT
                                ||||||||   ||| |||
                                GGCGGACC   TGT TAG
                                     CAA   A
GAM381  AMOT     3'  AGGCATCTTCATGGTCCAGGGA 55716    G       C_   TT  A
                                TC CCTGGACCA  AAG  TG CCT
                                || |||||||||  |||  || |||
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                                AG GGACCTGGT  TTC  AC GGA
                                 _       AC   T_ _
GAM381  DKFZp434D177 5'  TTAGACCCAGGCGA       79443        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                          _______
GAM381  DKFZp434D177 5'  TTAGACCCAGGCGA       50056        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                          _______
GAM381  FLJ23420  3'  CAAGTGGGTCCAGGC       46845         A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                          _ __
GAM381  HSA249128 5'  GGCGCGGTCCAGGCGG      34152          ACAA
                                TCGCCTGGACC    GTT
                                ||||||||||    |||
                                GGCGGACCTGG    CGG
                                       CG__
GAM381  MGC15668  5'  AGACCCGGTGGTCCAGACG   51277    C       AA_
                                CG CTGGACCAC   GTTT
                                || |||||||||   ||||
                                GC GACCTGGTG   CAGA
                                 A        GCC
GAM381  MGC22014  3'  AGGTCCCGAGTGTAACCCAGGT 64486        ACC   AGTTT
           GA                     TCGCCTGG   ACA    GACCT
                                ||||||||   |||    |||||
                                AGTGGACC   TGT    CTGGA
                                     CAA   GAGCC
GAM381  SDCCAG10  5'  AGAGTTGTGGTCCAAAGA    19641    GCC        G
                                TC   TGGACCACAA TTT
                                ||   |||||||||| |||
                                AG   ACCTGGTGTT AGA
                                 AA_         G
GAM381  LOC115442 3'  AGGTCAGGGATGGTCCAG    72676        CAAG
                                CTGGACCA    TTTGACCT
                                ||||||||    ||||||||
                                GACCTGGT    GGACTGGA
                                     AG__
GAM381  LOC129011 5'  AGACCTGCGGTCCAGGC     74862         A  A
                                GCCTGGACC CA GTTT
                                ||||||||| || ||||
                                CGGACCTGG GT CAGA
                                       C  C
GAM381  LOC130536 5'  GCAAAGTCCAGGCG        75746         CACAAG    A
                                CGCCTGGAC     TTTG C
                                |||||||||     |||| |
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                                GCGGACCTG     AAAC G
                                      _____   C
GAM381  LOC149108 3'  AGACTTCACTGTGGTCCA    84357        ____
                                TGGACCACA   AGTTT
                                |||||||||   |||||
                                ACCTGGTGT   TCAGA
                                     CACT
GAM381  LOC221688 5'  AGACTCGGGCCCAGACGA    93674    C   A  ACA
                                TCG CTGG CC   AGTTT
                                ||| |||| ||   |||||
                                AGC GACC GG   TCAGA
                                  A   C  GC_
GAM381  LOC256228 5'  AGACTTGTGGTCAAAGC     96233    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCAGA
                                 AAA
GAM381  LOC257441 5'  TTAGACCCAGGCGA        95566        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                      _______
GAM381  LOC91960  3'  AGGTGCCTCTCGTGGTCCAAGC 67657    C       A  TTTG
                                GC TGGACCAC AG    ACCT
                                || |||||||| ||    ||||
                                CG ACCTGGTG TC    TGGA
                                 A       C  TCCG
GAM381  LOC92840  3'  GTCCCTCGGGTCCAGGC     56435        ACA  TTT
                                GCCTGGACC   AG   GAC
                                |||||||||   ||   |||
                                CGGACCTGG   TC   CTG
                                     GC_  C__
GAM382  ABCB4     5'  GCTCCAGGTGGCAGGCA     4794       A       CT
                                TGCCTG CTACCTGG  GC
                                ||||||  ||||||||  ||
                                ACGGAC GGTGGACC  CG
                                   _       T_
GAM382  ABCB4     5'  GCTCCAGGTGGCAGGCA     38143      A       CT
                                TGCCTG CTACCTGG  GC
                                ||||||  ||||||||  ||
                                ACGGAC GGTGGACC  CG
                                   _       T_
GAM382  ABL1      3'  GCAGTCAGGGGTCAGGT     23613        A
                                GCCTGACT CCTGGCTGC
                                ||||||||  |||||||||
                                TGGACTGG GGACTGACG
                                          _
GAM382  ABL1      3'  GCAGTCAGGGGTCAGGT     17676        A
                                GCCTGACT CCTGGCTGC
                                ||||||||  |||||||||
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                                TGGACTGG GGACTGACG
                                       _
GAM382  ADRBK1   3'  CGGCCAGGTGGGCGGGCA    7868        A
                                TGCCTG CTACCTGGCTG
                                |||||| ||||||||||
                                ACGGGC GGTGGACCGGC
                                   G
GAM382  AES      3'  TTATGGTGGCCGCCGGCGGG   6678      A  ACC    TG
                                CCTG CT   TGGC  CCATAG
                                |||| ||   ||||  ||||||
                                GGGC GG   GCCG  GGTATT
                                  _ CC_   GT
GAM382  ALDH3B1  3'  CCAACAGCAGCCAGGTGGTCAA 91523    C            CATAG
           GC                     GC TGACTACCTGGCTGC
                                || ||||||||||||||
                                CG ACTGGTGGACCGACG
                                 A            ACAACCT
GAM382  AMFR     3'  TTGTGGTAGTCCTTTTGGG   6698     TG CTACCT
                                CC  A     GGCTGCCATAG
                                ||  |     ||||||||||
                                GG  T     CTGATGGTGTT
                                 GT TTC___
GAM382  AMFR     3'  TTGTGGTAGTCCTTTTGGG   57248    TG CTACCT
                                CC  A     GGCTGCCATAG
                                ||  |     ||||||||||
                                GG  T     CTGATGGTGTT
                                 GT TTC___
GAM382  CALU     3'  CTGTGGTGGGAAGAGTTAGG   6886        AC  GG TG
                                CCTGACT  CT  C  CCATAG
                                |||||||  ||  |  ||||||
                                GGATTGA  GA  G  GGTGTC
                                   __  AG GT
GAM382  CLDN14   5'  GTGGGCAGGTGGTCAGG     57841           G TG
                                CCTGACTACCTG C  C
                                ||||||||||| |  |
                                GGACTGGTGGAC G  G
                                       G GT
GAM382  CLN5     5'  TTGTGGTGGTCATCTCCGGC   21435     T  CTACC    TG
                                GCC GA    TGGC  CCATAG
                                ||| ||    ||||  ||||||
                                CGG CT    ACTG  GGTGTT
                                  C  CT___    GT
GAM382  COX7A2   5'  TTGTGGCGGTTGCTGGTCAG   8519        CCT
                                CTGACTA   GGCTGCCATAG
                                |||||||   ||||||||||
                                GACTGGT   TTGGCGGTGTT
                                    CG_
GAM382  DDEF2    5'  GCGGCTGGGTGGCGGGTA    13953       A     TG
                                TGCCTG CTACC  GCTGC
                                |||||| |||||  |||||
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                                ATGGGC GGTGG  CGGCG
                                   _    GT
GAM382  DLG4    3'  GGGGTCGGGGGTCGGGT    7255        A     G
                                GCCTGACT CCTGGCT CC
                                |||||||| ||||||| ||
                                TGGGCTGG GGGCTGG GG
                                   _      _
GAM382  DYRK1A  3'  TTGTGGTGAAGTTTGTCAGGCA 7359        TAC  GGCT
                                TGCCTGAC  CT   GCCATAG
                                ||||||||  ||   |||||||
                                ACGGACTG  GA   TGGTGTT
                                    TTT  AG__
GAM382  DYRK1A  3'  TTGTGGTGAAGTTTGTCAGGCA 55210       TAC  GGCT
                                TGCCTGAC  CT   GCCATAG
                                ||||||||  ||   |||||||
                                ACGGACTG  GA   TGGTGTT
                                    TTT  AG__
GAM382  DYRK1A  3'  TTGTGGTGAAGTTTGTCAGGCA 55256       TAC  GGCT
                                TGCCTGAC  CT   GCCATAG
                                ||||||||  ||   |||||||
                                ACGGACTG  GA   TGGTGTT
                                    TTT  AG__
GAM382  EPB41L2 3'  CTGTGGTGGTGTTCTGTTGGT  7482     T  TACCTG  TG
                                GCC GAC     GC  CCATAG
                                ||| |||     ||  ||||||
                                TGG TTG     TG  GGTGTC
                                  _  TCTTG_  GT
GAM382  FCMD    3'  GTTGGTAGTTAGGCA      22096          T
                                TGCCTGACTACC GGC
                                ||||||||||||  |||
                                ACGGATTGATGG TTG
                                      _
GAM382  FPGS    3'  CTGTGGCAGCTGCCCCTGGCA  17085     TGACTACCT
                                TGCC       GGCTGCCATAG
                                ||||       ||||||||||
                                ACGG       TCGACGGTGTC
                                  TCCCCG___
GAM382  GAB2    3'  TTATGGTGGCATGTGTTGTGTA 24506    C   T  CTG  TG
                                TGC TGAC AC   GC  CCATAG
                                ||| |||| ||   ||  ||||||
                                ATG GTTG TG   CG  GGTATT
                                  T   _  TA_  GT
GAM382  GAB2    3'  TTATGGTGGCATGTGTTGTGTA 54463    C   T  CTG  TG
                                TGC TGAC AC   GC  CCATAG
                                ||| |||| ||   ||  ||||||
                                ATG GTTG TG   CG  GGTATT
                                  T   _  TA_  GT
GAM382  HD      3'  TGTGGCAGTGGCCAGGCA    9195       A  ACCTG
                                TGCCTG CT    GCTGCCATA
                                |||||| ||    |||||||||
```

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                                ACGGAC GG    TGACGGTGT
                                   C _____
GAM382  HIP1    3'  TATGGTGGTTGGTTGGGT   18066    TG   CCTG  TG
                                GCC  ACTA   GC  CCATA
                                |||  ||||   ||  |||||
                                TGG  TGGT   TG  GGTAT
                                  GT   ____  GT
GAM382  IFNAR1  3'  TAGCCGGGTAGTAGGTA    5286       A
                                TGCCTG CTACCTGGCTG
                                |||||| ||||||||||
                                ATGGAT GATGGGCCGAT
                                   _
GAM382  JMJ     3'  TTGTGGCAGCTGAAGGCGG   17135   TA  __
                                C  CCT  GGCTGCCATAG
                                |  |||  ||||||||||
                                G  GGA  TCGACGGTGTT
                                 GC   AG
GAM382  LAPTM5  3'  TGTGGCAGCTGGGGAGGTT   22205     A_  TG
                                GACT  CC  GCTGCCATA
                                ||||  ||  |||||||||
                                TTGG  GG  CGACGGTGT
                                  AG  GT
GAM382  LENG4   5'  CTGTGGCGGGCCCCATTAGGTA 44165       CTACCT   _
                                TGCCTGA     GGCT GCCATAG
                                |||||||     |||| |||||||
                                ATGGATT     CCGG CGGTGTC
                                    ACC___   G
GAM382  MCM6    5'  TTGTGGCGGTCGAGCGTGGCGC 19791     CT A   _ _
          A                      TGC  G CTAC CT GGCTGCCATAG
                                |||  | |||| || ||||||||||
                                ACG  C GGTG GA CTGGCGGTGTT
                                  __ _   C  G
GAM382  NAPB    5'  CTGTGGCGGCCGCGGCGGGCG  70181       ACTA  _
                                TGCCTG   CC TGGCTGCCATAG
                                ||||||   || ||||||||||||
                                GCGGGC   GG GCCGGCGGTGTC
                                   ____  C
GAM382  NDUFA5  3'  TTATGGTAATATGGTCATGT   17196    C     CC  GC
                                GC TGACTA  TG  TGCCATAG
                                || ||||||  ||  ||||||||
                                TG ACTGGT  AT  ATGGTATT
                                 T     __  A_
GAM382  P3      3'  AGTTAGGTAGGTGGGC     39064     GA
                                GCCT  CTACCTGGCT
                                ||||  ||||||||||
                                CGGG  GATGGATTGA
                                  TG
GAM382  PCTP    3'  CTGTGGCAGCTAGCAAAAGCA  41097    CTGACTAC
                                TGC      CTGGCTGCCATAG
                                |||      ||||||||||||
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                              ACG      GATCGACGGTGTC
                                AAAAC___
GAM382  PPP1R12B 3' TGTGGTAGCCACTCCAGG   49475    ACTACC
                              CCTG     TGGCTGCCATA
                              ||||     ||||||||||
                              GGAC     ACCGATGGTGT
                                CTC___
GAM382  PPP1R12B 3' TGTGGTAGCCACTCCAGG   49486    ACTACC
                              CCTG     TGGCTGCCATA
                              ||||     ||||||||||
                              GGAC     ACCGATGGTGT
                                CTC___
GAM382  PTGFRN   3' TGTGGTGGGAAGACGGGCA  67195      A A  GGCT
                              TGCCTG CT CCT    GCCATA
                              |||||| || |||    ||||||
                              ACGGGC GA GGG    TGGTGT
                                 A A  _____
GAM382  PYGB     3' GTGGCTGTGGTTGGCA     11178     T    CT  TG
                              TGCC GACTAC  GGC  C
                              |||| ||||||  |||  |
                              ACGG TTGGTG  TCG  G
                                _     __  GT
GAM382  PYGO2    3' TATGGCAGTTTCTTGGT    63991     CCT
                              ACTA   GGCTGCCATA
                              ||||   ||||||||||
                              TGGT   TTGACGGTAT
                                TCT
GAM382  RAB27A   3' TTATGGTGGCAAATGTTTGGTA 15928     T  TACCTG  TG
                              TGCC GAC     GC  CCATAG
                              |||| |||     ||  ||||||
                              ATGG TTG     CG  GGTATT
                                T   TAAA__  GT
GAM382  RPL36AL  5' GCGAAGGGCCAGGTGTCGGGC  6398       T      GCCATAG
                              GCCTGAC ACCTGGCT
                              ||||||| ||||||||
                              CGGGCTG TGGACCGG
                                  _      GAAGCGT
GAM382  RPN1     3' CTGTGGCAGGCAGATTGGGT   11390    TG CTAC   G
                              GCC  A    CTG CTGCCATAG
                              |||  |    ||| |||||||||
                              TGG  T    GAC GACGGTGTC
                                GT A___   G
GAM382  SCN3A    3' TGTGGTGCATGTTTGGGCA   22633     TG CT  CTG  T
                              TGCC  A  AC   GC GCCATA
                              ||||  |  ||   || ||||||
                              ACGG  T  TG   CG TGGTGT
                                GT __  TA_  _
GAM382  SDC4     3' GATGTTGCTGGGTGGTTGAGT  11479    CT     TG  TGC   AG
                              GC  GACTACC  GC   CAT
                              ||  |||||||  ||   |||
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                                TG  TTGGTGG  CG   GTA
                                 AG      GT  TT_   GT
GAM382  SF3B3    3'  CTGTGGTGGGACTGGGTAGGGT 24857     TGA    TG __ TG
             A                    TGCC   CTACC  G  C  CCATAG
                                  ||||   |||||  |  |  ||||||
                                  ATGG   GATGG  C  G  GGTGTC
                                    ___     GT AG GT
GAM382  SFRP4    3'  CTGTACCATTAGGAGTTAGGTA 11577         A    C  CC
                                  TGCCTGACT CCTGG TG  ATAG
                                  |||||||||| ||||| ||  ||||
                                  ATGGATTGA GGATT AC  TGTC
                                        _    _ CA
GAM382  SFTPA2   3'  CTGTGGCAGGCCTGGTCAGGC  22647         CCT  _
                                  GCCTGACTA   GGC TGCCATAG
                                  |||||||||   ||| ||||||||
                                  CGGACTGGT   CCG ACGGTGTC
                                        ___  G
GAM382  SLA      3'  GTTAGGTGTCAGGCA       22172         T
                                  TGCCTGAC ACCTGGC
                                  |||||||| |||||||
                                  ACGGACTG TGGATTG

                                        _
GAM382  SLC12A2  5'  GCCGGGGGTCGGGCA       6453          A
                                  TGCCTGACT CCTGGC
                                  ||||||||| ||||||
                                  ACGGGCTGG GGGCCG

                                        _
GAM382  TAF4B    3'  CTGTGGTGACTTTGGTCGGC   87168     T    CCT  CT
                                  GCC GACTA   GG  GCCATAG
                                  ||| |||||   ||  |||||||
                                  CGG CTGGT   TC  TGGTGTC
                                    _    T__  AG
GAM382  TAGLN2   3'  CTGTGGCAGCTGCTGCCCCAGC 13096    C   ACTACCT
             CA                     TG CTG      GGCTGCCATAG
                                    || |||      ||||||||||
                                    AC GAC      TCGACGGTGTC
                                     C   CCCGTCG
GAM382  TSPY     5'  TGTGGCGTGGGTCGGGCA    82109         ACCTGGC
                                  TGCCTGACT      TGCCATA
                                  |||||||||      |||||||
                                  ACGGGCTGG      GCGGTGT
                                       GT_____
GAM382  UNC13    3'  GTGCCTGGCTGGCTGGGTAGTC 21059    C       TG  _   TAG
             AGC                      GC TGACTACC  GCT GCCA
                                      || ||||||||  ||| ||||
                                      CG ACTGATGG  CGG CGGT
                                       _      GT   T    CCGTGT
GAM382  VCP      3'  CTATCCAACCTGGGTAGGTGGG 75369      GA    TG CTGCC
             TA                       TGCCT  CTACC  G    ATAG
                                      |||||  |||||  |    ||||
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                                ATGGG  GATGG  C    TATC
                                  TG    GT CAACC
GAM382  VIPR2   3'  GTTGATGGTCGGTGGTTGGGT  12615    TG    T   GC  TAG
                                GCC  ACTACC GGCT  CA
                                |||  |||||| ||||  ||
                                TGG  TGGTGG CTGG  GT
                                  GT     _    TA  TGT
GAM382  WFS1    3'  CTGTCCAGCAGGTAGTGGGT   20009     G      G   CC
                                GCCT ACTACCTG CTG  ATAG
                                |||| |||||||| |||  ||||
                                TGGG TGATGGAC GAC  TGTC
                                  _       _  C_
GAM382  XKRY    3'  GCAACCAAGGTGGTCGGGCA   16257           _ C
                                TGCCTGACTACCT GG TGC
                                |||||||||||| || |||
                                ACGGGCTGGTGGA CC ACG
                                       A  A
GAM382  XKRY    3'  GCAACCAAGGTGGTCGGGCA   60019           _ C
                                TGCCTGACTACCT GG TGC
                                |||||||||||| || |||
                                ACGGGCTGGTGGA CC ACG
                                       A  A
GAM382  ZNF192   3'  CTGTGGTACAGATAGTTGGCA  20855     T    C   GC
                                TGCC GACTA CTG  TGCCATAG
                                |||| ||||| |||  ||||||||
                                ACGG TTGAT GAC  ATGGTGTC
                                  _    A  __
GAM382  ATP6V0A1  5'  TGTGGCGGTTGCTGTGGC    17733     TG  TACC
                                GCC  AC   TGGCTGCCATA
                                |||  ||   ||||||||||
                                CGG  TG   GTTGGCGGTGT
                                  __  TC__
GAM382  C1QTNF6  3'  CTGTGTTCTGGGTGTTCAGGT  49144       C   TG CTGC
                                GCCTGA TACC  G   CATAG
                                ||||||  ||||  |   |||||
                                TGGACT GTGG  C   GTGTC
                                   T   GT TT__
GAM382  CBX6    3'  GTATGCAGGTAGTCAGCCA   26623    C        G _
                                TG CTGACTACCTG C TGC
                                || ||||||||||| | |||
                                AC GACTGATGGAC G ATG
                                 C         _ T
GAM382  CBX6    3'  TGGGGCTGGGTAGTTGGG    26632    TG    TG  G
                                CC  ACTACC  GCT CCA
                                ||  ||||||  ||| |||
                                GG  TGATGG  CGG GGT
                                 GT     GT  _
GAM382  CCNI    5'  CTACAGCAAGCTGGGTAGCAGG 22419       A    TG  _ CA
            CA                    TGCCTG CTACC  GCT GC  TAG
                                |||||| |||||  ||| ||  |||
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                                ACGGAC GATGG  CGA CG  ATC
                                   _    GT   A  AC
GAM382  CDT1     3'  CTGTGGCAATATGGGGTTGGGT 77673     TG   A  TGGC
            A                    TGCC  ACT CC    TGCCATAG
                                 ||||  ||| ||   ||||||||
                                 ATGG  TGG GG    ACGGTGTC
                                   GT   _  TATA
GAM382  COE2     3'  TGTGCAGCTGGTTGGGCA    64257     TG   ACCT    _
                                 TGCC  ACT    GGCTGC CA
                                 ||||  |||    |||||| ||
                                 ACGG  TGG    TCGACG GT
                                   GT  _____     T
GAM382  CSEN     3'  GTGGCTGGGTGGTCAGCA    25534     C      TG  TG
                                 TGC TGACTACC  GC  C
                                 ||| ||||||||  ||  |
                                 ACG ACTGGTGG  CG  G
                                   _       GT  GT
GAM382  dJ309H15.1 3'  CTGTGGTAGTTAGCGGGCAGG  56796     A  AC
                                 CCTG CT  CTGGCTGCCATAG
                                 |||| ||  ||||||||||||||
                                 GGAC GG  GATTGATGGTGTC
                                   _  GC
GAM382  DKFZP434H204 5'  GCCCTGCCAGGTGGTGGGCA   66429      G        T__
                                 TGCCT ACTACCTGGC   GC
                                 ||||| ||||||||||   ||
                                 ACGGG TGGTGGACCG   CG
                                   _         TCC
GAM382  DKFZP564O0423 3'  TGTGGTGGCCATGTGGT     91705      C    TG
                                 ACTAC TGGC  CCATA
                                 ||||| ||||  |||||
                                 TGGTG ACCG  GGTGT
                                    T    GT
GAM382  DNAJC5   3'  TGGTTTCTTGGGAGTCGGGCA  61457         A  TG CT_
                                 TGCCTGACT CC  G   GCCA
                                 |||||||||  ||  |   ||||
                                 ACGGGCTGA GG  T   TGGT
                                       _  GT CTT
GAM382  DTX2     3'  TGGCTGGGTGGCCAGGCA    71955       A    TG
                                 TGCCTG CTACC  GCTG
                                 ||||||  |||||  ||||
                                 ACGGAC GGTGG  CGGT
                                    C     GT
GAM382  ERG-1    5'  TGTGGCGGTTACCTGG      41845     CC
                                 CTA  TGGCTGCCATA
                                 |||  ||||||||||
                                 GGT  ATTGGCGGTGT
                                   CC
GAM382  FEM-2    3'  GCACTGGGTGGCGGGCA     27582       A    TG C
                                 TGCCTG CTACC  G TGC
                                 ||||||  |||||  | |||
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                                ACGGGC GGTGG  C ACG
                                   _    GT _
GAM382  FLJ00001  3'  TGTGGTAGCTTTTAGGC     81823       CTACCT
                                GCCTGA     GGCTGCCATA
                                ||||||     ||||||||||
                                CGGATT     TCGATGGTGT
                                   T_____
GAM382  FLJ10468  3'  TGTGGGAGGTGGTCAG      36150         GGCTG
                                CTGACTACCT    CCATA
                                ||||||||||    |||||
                                GACTGGTGGA    GGTGT
                                     G____
GAM382  FLJ10853  3'  CTGTGGCAGTTGTTGCCTGAGC 36767     CTGACT_  CT
          A                      TGC      AC  GGCTGCCATAG
                                |||      ||  ||||||||||
                                ACG      TG  TTGACGGTGTC
                                  AGTCCGT  __
GAM382  FLJ10901  3'  TTGTGGCATGTTCTGGTTGGG  36835    TG    CCT   _
                                CC  ACTA   GGC TGCCATAG
                                ||  ||||   ||| ||||||||
                                GG  TGGT   TTG ACGGTGTT
                                 GT    C__   T
GAM382  FLJ10989  5'  TGTGGTGGCAGGCTGGGCA   36953       ACTA    G TG
                                TGCCTG    CCTG C  CCATA
                                ||||||    |||| |  |||||
                                ACGGGT    GGAC G  GGTGT
                                   C___    _ GT
GAM382  FLJ12428  3'  CTATGGTTGGGGGTAGTTAGG  42944          GGCT
                                CCTGACTACCT    GCCATAG
                                ||||||||||    |||||||
                                GGATTGATGGG    TGGTATC
                                     GGT_
GAM382  FLJ13193  3'  TTATGTTAAGGAAGTCAGGTA  49776         A   GGCTGC
                                TGCCTGACT CCT     CATAG
                                ||||||||| |||     |||||
                                ATGGACTGA GGA     GTATT
                                     A   ATT___
GAM382  FLJ14490  3'  TTGTGGCAGCTGGTGCCGGGT  51401      AC    T
                                GCCTG  TACC GGCTGCCATAG
                                |||||  |||| ||||||||||
                                TGGGC  GTGG TCGACGGTGTT
                                   C_   _
GAM382  FLJ20506  5'  TATGGCGGCTACCAG      35268     ACTACC
                                CTG     TGGCTGCCATA
                                |||     ||||||||||
                                GAC     ATCGGCGGTAT
                                  C_____
GAM382  FLJ20986  3'  TTATGGTGGGAGGTGGTTGGG  44548    TG      GG TG
                                CC  ACTACCT  C  CCATAG
                                ||  |||||||  |  ||||||
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                                GG  TGGTGGA  G  GGTATT
                                 GT      G_ GT
GAM382  FLJ22477  5'  TTGTGGCAGCCAGATATCGGGC 45348       C  C
                                GCCTGA TA CTGGCTGCCATAG
                                |||||| || ||||||||||||
                                CGGGCT AT GACCGACGGTGTT
                                   _  A
GAM382  FLJ22679  3'  TTGTGGCGGGTAGAGTCAG   34682       AC   G
                                CTGACT  CTG CTGCCATAG
                                ||||||  ||| |||||||||
                                GACTGA  GAT GGCGGTGTT
                                   __  G
GAM382  FLJ22679  3'  TTGTGGCGGGTAGAGTCAG   49926       AC   G
                                CTGACT  CTG CTGCCATAG
                                ||||||  ||| |||||||||
                                GACTGA  GAT GGCGGTGTT
                                   __  G
GAM382  FLJ23231  3'  TTGGCCTTGGCTGGCTAGTTGG 46916    TG   C TG  ___   TAG
          GCA                    CC  ACTA C  GCT   GCCA
                                ||  |||| |  |||   ||||
                                GG  TGAT G  CGG   CGGT
                                 GT   C GT   TTC   T
GAM382  GGA2     3'  GGCCTGGTAGTCAGGT      30474          T
                                GCCTGACTACC GGCT
                                |||||||||| ||||
                                TGGACTGATGG CCGG
                                      T
GAM382  GGA2     3'  GGCCTGGTAGTCAGGT      56888          T
                                GCCTGACTACC GGCT
                                |||||||||| ||||
                                TGGACTGATGG CCGG
                                      T
GAM382  GLP      3'  TATGGTAGTTCCCTTAGG    37848      CTACCT
                                CCTGA     GGCTGCCATA
                                |||||     ||||||||||
                                GGATT     TTGATGGTAT
                                   CCC___
GAM382  H2-ALPHA  5'  CTGTGGCAGCCGGTTGAGGT   73010     GACT   T
                                GCCT   ACC GGCTGCCATAG
                                ||||   ||| ||||||||||
                                TGGA   TGG CCGACGGTGTC
                                  GT__  _
GAM382  IL-17RE   3'  TGGCTCCAGGTGGTCAGGACA  58297    _         CT
                                TG CCTGACTACCTGG  GCCA
                                || ||||||||||||  ||||
                                AC GGACTGGTGGACC  CGGT
                                 A          T_
GAM382  KIAA0212  3'  CTGTGGCGGCAGTGGTGGGTA  27939      G    CTG
                                TGCCT ACTAC   GCTGCCATAG
                                ||||| |||||   ||||||||||
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                                ATGGG TGGTG   CGGCGGTGTC
                                  _    A__
GAM382  KIAA0237  3'  TTGTGGTTCCCGGGTGGCAGGT 28540      A      CT
                                GCCTG CTACCTGG  GCCATAG
                                ||||| ||||||||  |||||||
                                TGGAC GGTGGGCC  TGGTGTT
                                  _      CT
GAM382  KIAA0317  3'  TGTGGTGGTCCTTAGGCA    29091       CTACCT   TG
                                TGCCTGA     GGC  CCATA
                                |||||||     |||  |||||
                                ACGGATT     CTG  GGTGT
                                   C_____   GT
GAM382  KIAA0523  3'  CTATGGTGACTGGGTTAGGTA  67735      ACT   TG CT
                                TGCCTG   ACC  G  GCCATAG
                                ||||||   |||  |  |||||||
                                ATGGAT   TGG  C  TGGTATC
                                   ___   GT AG
GAM382  KIAA0544  3'  TGGTGGCTGGGTGTCAGGCA   70911       T   TG  TG
                                TGCCTGAC ACC  GC  CCA
                                |||||||| |||  ||  |||
                                ACGGACTG TGG  CG  GGT
                                   _  GT  GT
GAM382  KIAA0547  3'  GTTAGGAGTCAGGTA      28916        A
                                TGCCTGACT CCTGGC
                                |||||||||| ||||||
                                ATGGACTGA GGATTG
                                          _
GAM382  KIAA0721  3'  TTATGGTAAGCTATTTGGGTA  41351     TG CTACC    _
                                TGCC  A    TGGCT GCCATAG
                                ||||  |    ||||| |||||||
                                ATGG  T    ATCGA TGGTATT
                                  GT T____    A
GAM382  KIAA0721  3'  TTATGGTAAGCTATTTGGGTA  95979     TG CTACC    _
                                TGCC  A    TGGCT GCCATAG
                                ||||  |    ||||| |||||||
                                ATGG  T    ATCGA TGGTATT
                                  GT T____    A
GAM382  KIAA1023  3'  TGTGGCGGTCAGAAGGC    34272     GACTAC
                                GCCT     CTGGCTGCCATA
                                ||||     ||||||||||||
                                CGGA     GACTGGCGGTGT
                                  A_____
GAM382  KIAA1094  5'  TGTGGGGGGTGGCCGGGC    29807      A     GGCTG
                                GCCTG CTACCT    CCATA
                                ||||| ||||||    |||||
                                CGGGC GGTGGG    GGTGT
                                  C     G____
GAM382  KIAA1257  3'  CTGTGGTGGTTATCATAGTTA  62739       CC_   TG
                                TGACTA   TGGC  CCATAG
                                ||||||   ||||  ||||||
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                                ATTGAT   ATTG  GGTGTC
                                   ACT    GT
GAM382  KIAA1280 5' TTGTGGTGGCTGTCTGTGGGG 69735    G  TACCT   TG
                                CCT AC    GGC  CCATAG
                                ||| ||    |||  ||||||
                                GGG TG    TCG  GGTGTT
                                  G  TCTG_   GT
GAM382  KIAA1320 5' TTATGGCAGCTGGGTG     69314     TG
                                TACC  GCTGCCATAG
                                ||||  ||||||||||
                                GTGG  CGACGGTATT
                                  GT
GAM382  KIAA1414 3' GTATCATGTAGTCGGGCA    67991          C   C
                                TGCCTGACTAC TGG TGC
                                |||||||||||| ||| |||
                                ACGGGCTGATG ACT ATG
                                       T  _
GAM382  KIAA1553 5' CTGTGGCAGCACCGGGGCAGGC 91919       A  A  TG_
           A                     TGCCTG CT CC   GCTGCCATAG
                                ||||||| || ||   ||||||||||
                                ACGGAC GG GG   CGACGGTGTC
                                   _ _  CCA
GAM382  KIAA1644 3' GTCTAGGTAGGTAGGTA     85031       A      _
                                TGCCTG CTACCTGG C
                                |||||| |||||||| |
                                ATGGAT GATGGATC G
                                   G       T
GAM382  KIAA1751 3' GTGGTGGAAGTCAGG       71704       A  TGGCT
                                CCTGACT CC     GCCAT
                                ||||||| ||     |||||
                                GGACTGA GG     TGGTG
                                   A  _____
GAM382  KIAA1863 3' TGTGGCGATGGTGGGGT     64876     TGA    TGGC
                                GCC   CTACC    TGCCATA
                                |||   |||||    |||||||
                                TGG   GGTGG    GCGGTGT
                                  ___    TA__
GAM382  KIAA1951 3' CTGTGGTGGCCAGCTACTCAGG 73762      C  C    TG
                                CCTGA TA CTGGC  CCATAG
                                ||||| || |||||  ||||||
                                GGACT AT GACCG  GGTGTC
                                   C  C    GT
GAM382  MGC10701 3' CTGTGGTAAGGCTCTGTCGGGC 51027        TACCT   __
           A                     TGCCTGAC    GGCT  GCCATAG
                                ||||||||    ||||  |||||||
                                ACGGGCTG    TCGG  TGGTGTC
                                     TC___    AA
GAM382  MGC10814 5' TTGTGGCTGCAGGTGTTAGGT  51044       T    G T
                                GCCTGAC ACCTG C GCCATAG
                                ||||||| ||||| | |||||||
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                                TGGATTG TGGAC G CGGTGTT
                                   _    _ T
GAM382  MGC16733 3' TTGTGGTAGCTGTTACAAGTA 53212    C  ACT  CT
                                TGC TG   AC  GGCTGCCATAG
                                ||| ||   ||  ||||||||||||
                                ATG AC   TG  TCGATGGTGTT
                                  A  AT_  __
GAM382  MGC2452  5' CTGTGGCCTCTGTAGTTAGGGC 50982     _     CT  CT
           A                     TGCC TGACTAC  GG  GCCATAG
                                ||||  |||||||  ||  |||||||
                                ACGG ATTGATG  TC  CGGTGTC
                                  G      __  TC
GAM382  MGC2477  5' TTGTGGTGGAATCCAGTGAGGT 44077     G   ACCTGG TG
                                GCCT ACT     C  CCATAG
                                ||||  |||     |  ||||||
                                TGGA TGA     G  GGTGTT
                                  G   CCTAA_ GT
GAM382  MGC26655 5' CTGCGGAGTGTGGGTGGTTGGG 56290     TG      _   G  A
           C                     GCC  ACTACCTG GCT CC TAG
                                |||  |||||||| ||| || |||
                                CGG  TGGTGGGT TGA GG GTC
                                  GT       G   _  C
GAM382  MGC3195  5' CTGTGGCGGCTAGGCCCGCGTG 49123    C  ACTA
           C                     GC TG    CCTGGCTGCCATAG
                                || ||    ||||||||||||||
                                CG GC    GGATCGGCGGTGTC
                                 T  GCCC
GAM382  MGC4643  3' TTATGGTGATGTGTAGTCAGTG 51159     _      C  GC
           TA                     TGC CTGACTAC TG  TGCCATAG
                                ||| ||||||||  ||  ||||||||
                                ATG GACTGATG GT  GTGGTATT
                                  T       T  A_
GAM382  MIC2L1   3' CTGTGGTGGAGGGTGGTCAGTC 48823    C        GG TG
           G                     TG CTGACTACCT  C  CCATAG
                                || ||||||||||  |  ||||||
                                GC GACTGGTGGG  G  GGTGTC
                                 T         A_ GT
GAM382  MKNK1    3' TGTGGCGGCTGGGGCTGCA   13481     CTGACTA  TG
                                TGC      CC  GCTGCCATA
                                |||      ||  |||||||||
                                ACG      GG  CGGCGGTGT
                                  TCG____  GT
GAM382  NAP1L2   5' CTGTGGTAGCCACCTTAGGC   41735       CTACC
                                GCCTGA    TGGCTGCCATAG
                                ||||||    ||||||||||||
                                CGGATT    ACCGATGGTGTC
                                   CC___
GAM382  NIBAN    5' CTGTGGCAGCCCTTCTTCAGAC 42001    C   CTACCT
           A                     TG CTGA     GGCTGCCATAG
                                || ||||     ||||||||||
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                                AC GACT     CCGACGGTGTC
                                 A   TCTTC_
GAM382  PCF11    5'  CTGTGGCGGCTGGAAGTGG   31891      __ TG
                                CTAC  C  GCTGCCATAG
                                ||||  |  ||||||||||
                                GGTG  G  CGGCGGTGTC
                                  AA GT
GAM382  PRO0650  5'  TTATGCACCTACCAGGGGTCAG 26216        A    C___   C
           GCA                    CCTGACT CCTGG    TGC ATAG
                                ||||||| |||||    ||| ||||
                                GGACTGG GGACC    ACG TATT
                                    _    ATCC  _
GAM382  PRO2730  5'  TGAGGCTAGGTGGTTGGGCA  47420      TG         GC
                                TGCC  ACTACCTGGCT  CA
                                ||||  ||||||||||  ||
                                ACGG  TGGTGGATCGG  GT
                                  GT         A_
GAM382  RER1     3'  GCCAGGTGGGCAGGCA      22864       A
                                TGCCTG CTACCTGGC
                                |||||| |||||||||
                                ACGGAC GGTGGACCG
                                   G
GAM382  SLC39A3  3'  GTCCTCGGGCTGGTCAGGC   57978         _    CT
                                GCCTGACTA CCTGG  GC
                                ||||||||| |||||  ||
                                CGGACTGGT GGGCT  TG
                                     C    CC
GAM382  SPEC1    3'  TTATGGTAGTGGGGTCAGG   39614      CTA   G
                                CCTGA   CCT GCTGCCATAG
                                |||||   ||| ||||||||||
                                GGACT   GGG TGATGGTATT
                                  ___   G
GAM382  STI2     3'  TTGTGTAGCTTGGGAGTCAGGC 88969         A  T     _  TAG
           A                     TGCCTGACT CC GGCTGC CA
                                ||||||||| || |||||| ||
                                ACGGACTGA GG TCGATG GT
                                     G  T     T  T
GAM382  STK25    3'  TGTGGTGTTGGATCAGGTA   21053        CTAC TG  T
                                TGCCTGA   C  GC GCCATA
                                |||||||   |  || ||||||
                                ATGGACT   G  TG TGGTGT
                                   A___ GT  _
GAM382  SYNCOILIN 3'  CTGTGGTATAACTGTCAGGTA  47895        TACCTGGC
                                TGCCTGAC       TGCCATAG
                                ||||||||       ||||||||
                                ATGGACTG       ATGGTGTC
                                    TCAAT___
GAM382  TBX21    3'  TTGTGGTGGTTGTGTGTGGGT  25329     G  T  C   TG
                                GCCT AC AC TGGC  CCATAG
                                |||| || || ||||  ||||||
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                                TGGG TG TG GTTG  GGTGTT
                                  _ _ T   GT
GAM382  TRIP13   5' CTGTGGCGGCGACGCTGGGC  14895     GACTACCTG
                                GCCT       GCTGCCATAG
                                ||||       ||||||||||
                                CGGG       CGGCGGTGTC
                                  TCGCAG___
GAM382  VEZATIN  3' GTTAGGTGGTTGGCA      34227     T
                                TGCC GACTACCTGGC
                                |||| ||||||||||
                                ACGG TTGGTGGATTG
                                  _
GAM382  WFDC3    3' TGGATTGGGTAGTGGGT    96926     G     TG CTG
                                GCCT ACTACC  G   CCA
                                |||| ||||||  |   |||
                                TGGG TGATGG  T   GGT
                                  _     GT A__
GAM382  ZNF297   3' GGTCAGGGGTCAGGT      18392       A
                                GCCTGACT CCTGGCT
                                |||||||| |||||||
                                TGGACTGG GGACTGG
                                  _
GAM382  LOC112714 5' CTGTGGCAGCCGGTTGAGGT  72872     GACT   T
                                GCCT    ACC GGCTGCCATAG
                                ||||    ||| ||||||||||
                                TGGA    TGG CCGACGGTGTC
                                  GT__   _
GAM382  LOC113675 5' TGGTCTGGGATAGTTGGGCA  56574     TG   _  TG CT
                                TGCC  ACTA CC  G  GCCA
                                ||||  |||| ||  |  ||||
                                ACGG  TGAT GG  C  TGGT
                                  GT    A  GT __
GAM382  LOC121219 5' CTATGGTGGTTGGGCGGCTGGT 74044    _  GA TA  TG  TG
           GC                     GC CT  C  CC  GC  CCATAG
                                || ||  |  ||  ||  ||||||
                                CG GG  G  GG  TG  GGTATC
                                 T  TC GC  GT  GT
GAM382  LOC124460 3' CAGCCAGGTGGTCAGG      76041
                                CCTGACTACCTGGCTG
                                ||||||||||||||||
                                GGACTGGTGGACCGAC

GAM382  LOC124997 5' TGTGGCAGCAGCTGGGC     74389      GA  ACCTG
                                GCCT  CT    GCTGCCATA
                                ||||  ||    |||||||||
                                CGGG  GA    CGACGGTGT
                                  TC  _____
GAM382  LOC125929 3' TTGTGGTAGTGGTTGTAGTTAG 75675         CTG_
                                CTGACTAC    GCTGCCATAG
                                ||||||||    ||||||||||
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                                GATTGATG   TGATGGTGTT
                                    TTGG
GAM382  LOC132720 5'  CGGCCGGGGGTTGGGC     75064    TG  A
                                GCC  ACT CCTGGCTG
                                |||  ||| ||||||||
                                CGG  TGG GGGCCGGC
                                  GT  _
GAM382  LOC139231 3'  TATGGCGGTGAAGTGGGC    75378    G  ACCTG
                                GCCT ACT    GCTGCCATA
                                |||| |||    |||||||||
                                CGGG TGA    TGGCGGTAT
                                  _  AG___
GAM382  LOC144347 3'  AGCCAGGAGGTTGGGCA    76810    TG  A
                                TGCC  ACT CCTGGCT
                                ||||  ||| |||||||
                                ACGG  TGG GGACCGA
                                  GT  A
GAM382  LOC145497 3'  TGTGGCAGGGGCTGGGCA    77220      ACTA  GG
                                TGCCTG   CCT  CTGCCATA
                                ||||||   |||  ||||||||
                                ACGGGT   GGG  GACGGTGT
                                   C___  __
GAM382  LOC145761 5'  CTGCATTCCCAGGAGGTTAGGC 83475        A   C__  CATAG
          A                      TGCCTGACT CCTGG  TGC
                                |||||||| |||||  |||
                                ACGGATTGG GGACC  ACG
                                     A   CTT  TC
GAM382  LOC146599 5'  GCCCACCAGGGGTCAGGT    78025       A   CT_
                                GCCTGACT CCTGG  GC
                                |||||||| |||||  ||
                                TGGACTGG GGACC  CG
                                     _   ACC
GAM382  LOC147299 3'  CTGTGGCGTCCCTCGTCGGGTA 78346       TACCT  C
                                TGCCTGAC    GG TGCCATAG
                                ||||||||    || ||||||||
                                ATGGGCTG    CC GCGGTGTC
                                     CTC__  T
GAM382  LOC147622 5'  CTGTGGCGCACTTGGTTGGG  84050   TG   CCTG  T
                                CC  ACTA   GC GCCATAG
                                ||  ||||   || |||||||
                                GG  TGGT   CG CGGTGTC
                                 GT   TCA_  _
GAM382  LOC147976 5'  TGTGGCATTTGGTAGGCA    78590      ACTAC TG C
                                TGCCTG    C  G TGCCATA
                                ||||||    |  | |||||||
                                ACGGAT    G  T ACGGTGT
                                   _____ GT T
GAM382  LOC150005 5'  TGTGGTGGTGTCAGGT     84823       TACCTG  TG
                                GCCTGAC    GC  CCATA
                                |||||||    ||  |||||
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                                TGGACTG     TG  GGTGT
                                   _______ GT
GAM382  LOC151273 5'  CTGTGGCAGTTCAGTCAG    67016       ACCT
                                CTGACT    GGCTGCCATAG
                                ||||||    ||||||||||
                                GACTGA    TTGACGGTGTC
                                   C___
GAM382  LOC151429 5'  TGTGGTGACTGTTCAGGT    85362       CT  CT  CT
                                GCCTGA  AC  GG  GCCATA
                                ||||||  ||  ||  ||||||
                                TGGACT  TG  TC  TGGTGT
                                   __  __  AG
GAM382  LOC152805 5'  CTGTGGCGGGGCCAAGTGAGGC 80688      G   ACC    __
                                GCCT ACT   TGGCT  GCCATAG
                                |||| |||   |||||  |||||||
                                CGGA TGA   ACCGG  CGGTGTC
                                  G  ___     GG
GAM382  LOC152845 5'  GCCGGGTAGCAGGCA       60333       A
                                TGCCTG CTACCTGGC
                                |||||| |||||||||
                                ACGGAC GATGGGCCG
                                   _
GAM382  LOC153222 3'  CTATGGCAGTTTTGCAATCAGG 80784       CTACCT
          T                      GCCTGA     GGCTGCCATAG
                                ||||||     ||||||||||
                                TGGACT     TTGACGGTATC
                                   AACGTT
GAM382  LOC153339 5'  CTATGGCAGTTAAAAGTGGT   86006      C__
                                ACTAC   TGGCTGCCATAG
                                |||||   ||||||||||||
                                TGGTG   ATTGACGGTATC
                                   AAA
GAM382  LOC153454 3'  AGTTAGATGGTTAGGT      80830         C
                                GCCTGACTA CTGGCT
                                ||||||||| ||||||
                                TGGATTGGT GATTGA
                                     A
GAM382  LOC155060 3'  TTATGGTGGCCGGCCAGTTTGG 86334    T   AC    TG
                                CC GACT  CTGGC  CCATAG
                                || ||||  |||||  ||||||
                                GG TTGA  GGCCG  GGTATT
                                 T   CC    GT
GAM382  LOC155179 3'  TGTGGCGGTCAGAAGGC     81326      GACTAC
                                GCCT     CTGGCTGCCATA
                                ||||     ||||||||||||
                                CGGA     GACTGGCGGTGT
                                  A_____
GAM382  LOC168966 5'  TGTGGTGGTTGCTCAGACA   87278    C   CTACC   TG
                                TG CTGA    TGGC  CCATA
                                || ||||    ||||  |||||
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                                AC GACT    GTTG  GGTGT
                                 A   C____   GT
GAM382  LOC196812 3' CTGTGGCACCCTGTTTGGGT  89569    TG CT  CT  C
                                GCC  A  AC  GG TGCCATAG
                                |||  |  ||  || ||||||||
                                TGG  T  TG  CC ACGGTGTC
                                  GT __  T_  C
GAM382  LOC197342 3' CTGTGGTAGCTGGAAGTGGGGC 88000      G   A  T
          A                      TGCCT ACT CC GGCTGCCATAG
                                |||||| ||| || ||||||||||
                                ACGGG TGA GG TCGATGGTGTC
                                  G   A  _
GAM382  LOC199870 3' TTGTGGTGGTCACTGCTCAGTG 88433    _   CTACC   TG
          TA                     TGC CTGA    TGGC  CCATAG
                                ||| ||||    ||||  ||||||
                                ATG GACT    ACTG  GGTGTT
                                  T   CGTC_   GT
GAM382  LOC201736 5' TAGCTGGGCTGGTTGGGTA   89053     TG   _  TG
                                TGCC  ACTA CC  GCTG
                                ||||  |||| ||  ||||
                                ATGG  TGGT GG  CGAT
                                  GT   C  GT
GAM382  LOC202934 3' TGGGCCAGGTGGGCAGGT    90432      A       TG
                                GCCTG CTACCTGGC  CCA
                                ||||| |||||||||  |||
                                TGGAC GGTGGACCG  GGT
                                  G        __
GAM382  LOC203365 3' CTGTGGTAGTTTTTTTGAGCA  89348    CT  CTACCT
                                TGC  GA     GGCTGCCATAG
                                |||  ||     ||||||||||||
                                ACG  TT     TTGATGGTGTC
                                 AG  TTT___
GAM382  LOC205418 3' CTGTGGCGGCTCCCATTCAG   90684     CTACCT
                                CTGA     GGCTGCCATAG
                                ||||     ||||||||||||
                                GACT     TCGGCGGTGTC
                                  TACCC_
GAM382  LOC206480 5' CTGTGGCAGCCTCAGTTGGC   90718    T   ACCT
                                GCC GACT   GGCTGCCATAG
                                ||| ||||   ||||||||||||
                                CGG TTGA   CCGACGGTGTC
                                  _   CT__
GAM382  LOC220534 3' TATGGTAGTTCCCTTAGG    90722      CTACCT
                                CCTGA     GGCTGCCATA
                                |||||     ||||||||||
                                GGATT     TTGATGGTAT
                                  CCC___
GAM382  LOC220538 3' TATGGTAGTTCCCTTAGG    90734      CTACCT
                                CCTGA     GGCTGCCATA
                                |||||     ||||||||||
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                                GGATT     TTGATGGTAT
                                   CCC___
GAM382  LOC220662 3'  TCAGGTAGTTGAGGCA      91183       _
                                TGCCT GACTACCTGG
                                ||||| ||||||||||
                                ACGGA TTGATGGACT
                                   G
GAM382  LOC220827 3'  CTGCATTCCCAGGAGGTTAGGC 91242          A    C__   CATAG
          A                      TGCCTGACT CCTGG   TGC
                                ||||||||| |||||   |||
                                ACGGATTGG GGACC   ACG
                                      A    CTT   TC
GAM382  LOC221143 3'  CTGTGGTAGCTGAAATTTGGG  93567    TG CTACCT
                                CC  A     GGCTGCCATAG
                                ||  |     ||||||||||
                                GG  T     TCGATGGTGTC
                                 GT TAAAG_
GAM382  LOC253216 5'  GCCCTGCCAGGTGGTGGGCA   94960       G         T__
                                TGCCT ACTACCTGGC   GC
                                ||||| ||||||||||   ||
                                ACGGG TGGTGGACCG   CG
                                   _         TCC
GAM382  LOC254528 3'  TTATGGTGGAGGTGGTCTGGGT 95056      _       GG TG
                                GCCT GACTACCT  C  CCATAG
                                |||| ||||||||  |  ||||||
                                TGGG CTGGTGGA  G  GGTATT
                                  T       __ GT
GAM382  LOC255426 5'  TGGGAGCCGGGCGGTCGGGC   97161        TA      G
                                GCCTGAC  CCTGGCT CCA
                                |||||||  ||||||| |||
                                CGGGCTG  GGGCCGA GGT
                                    GC       G
GAM382  LOC256041 5'  GCTGTCGGGTATCAGGCA     97606        C       T
                                TGCCTGA TACCTGGC GC
                                ||||||| |||||||| ||
                                ACGGACT ATGGGCTG CG
                                   _       T
GAM382  LOC257054 5'  CTGTGTGCATGCAGCTGGTCGG 95660          C   G _   _
          GC                      GCCTGACTA CTG C TGC CATAG
                                ||||||||| ||| | ||| |||||
                                CGGGCTGGT GAC G ACG GTGTC
                                     C   _ T   T
GAM382  LOC257286 3'  TATGGTAGTTCCCTTAGG    94556       CTACCT
                                CCTGA     GGCTGCCATA
                                |||||     ||||||||||
                                GGATT     TTGATGGTAT
                                   CCC___
GAM382  LOC257451 3'  TATGGCAGTTTCTTGGT     95561       CCT
                                ACTA   GGCTGCCATA
                                ||||   ||||||||||
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                                TGGT  TTGACGGTAT
                                  TCT
GAM382  LOC63923  3'  GTGGCAGCTTGGGGC      67123     TGACTA  T
                                GCC     CC GGCTGCCAT
                                |||     || |||||||||
                                CGG     GG TCGACGGTG
                                 _______  T
GAM382  LOC91301  5'  TATGGTGGCCGGGGAGGC    65547     GACTA     TG
                                GCCT    CCTGGC  CCATA
                                ||||    ||||||  |||||
                                CGGA    GGGCCG  GGTAT
                                  G____     GT
GAM382  LOC91516  5'  TTGTGGTGGCCCTGCTCATGT  66306    C   C  CCT   TG
                                GC TGA TA   GGC  CCATAG
                                || ||| ||   |||  ||||||
                                TG ACT GT   CCG  GGTGTT
                                 T   C  C__   GT
GAM382  LOC91759  5'  TGGCACCTAGGAGTCAGGCA   67091         A    C
                                TGCCTGACT CCTGG TGCCA
                                ||||||||| ||||| |||||
                                ACGGACTGA GGATC ACGGT
                                      _    C
GAM382  LOC91963  5'  AGACTAGGCTAGTTGGGT    67688     TG   _    _
                                GCC  ACTA CCTGG CT
                                |||  |||| ||||| ||
                                TGG  TGAT GGATC GA
                                  GT   C    A
GAM382  LOC93622  3'  TGTGCACAGGTGGTTGGGT   56932     TG      GC  _
                                GCC  ACTACCTG  TGC CA
                                |||  ||||||||  ||| ||
                                TGG  TGGTGGAC  ACG GT
                                  GT      __   T
GAM383  GRIN2A    3'  TAATGGTTTCTCTAATACA   5898      GA__
                                TGTA   AGAAGCCATTA
                                ||||   ||||||||||
                                ACAT   TCTTTGGTAAT
                                  AATC
GAM383  SURF4     3'  AATGGCTTCAGGACATGGG   52537     TA   AGAA
                                CCCA  TGT   GAAGCCATT
                                ||||  |||   |||||||||
                                GGGT  ACA   CTTCGGTAA
                                  __  GGA_
GAM383  CECR1     3'  AATGGCCTCTGTATGG      33804       GTAGA   A
                                CCATAT    AGA GCCATT
                                ||||||    ||| ||||||
                                GGTATG    TCT CGGTAA
                                   _____  C
GAM383  FLJ22639  3'  GCTTCCTCTATTCCTTTATATG 45609       _______    A
                                CATAT     GTAGA GAAGC
                                |||||     ||||| |||||
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                                GTATA     TATCT CTTCG
                                   TTTCCT    C
GAM383  KIAA0040  3'  AATGGCTTCTTAAAGGA    27772    CATATGTAG
                                TCC       AAGAAGCCATT
                                |||       ||||||||||
                                AGG       TTCTTCGGTAA
                                  AAA_____
GAM383  KIAA0471  3'  TAATGGCTTCCATTTAATACAG 29399    CA   GTAGAA
           G                     CC  TAT     GAAGCCATTA
                                || |||     |||||||||
                                GG  ATA     CTTCGGTAAT
                                 AC   ATTTAC
GAM383  KIAA0748  5'  AATGGCTTCTGCAGCCATGGGA 28928       AT  AGA
                                TCCCAT  GT   AGAAGCCATT
                                ||||||  ||   ||||||||||
                                AGGGTA  CG   TCTTCGGTAA
                                   C_  ACG
GAM383  PRO2949   3'  TAATGATCACATTTTACATATG 37623    C         GAAGC_
           AGA                     TC CATATGTAGAA     CATTA
                                || ||||||||||     |||||
                                AG GTATACATTTT     GTAAT
                                 A          ACACTA
GAM383  RFX4      3'  TGGTTCTTCTACATACAAGG   50664    CA_         G
                                CC   TATGTAGAAGAA CCA
                                ||   ||||||||||| |||
                                GG   ATACATCTTCTT GGT
                                 AAC          _
GAM383  SBB103    3'  AATGGCTTCCTCTCA      19355    T   A
                                TG AGA GAAGCCATT
                                || ||| |||||||||
                                AC TCT CTTCGGTAA
                                 _   C
GAM383  VEST1     5'  AATGGACTACATATTGGA    53681     C       AAGAAG
                                TCC ATATGTAG     CCATT
                                ||| ||||||||     |||||
                                AGG TATACATC     GGTAA
                                  T       A_____
GAM383  LOC165476 5'  AATGGCTTCCCCGTGGG     87195       ATGTAGAA
                                CCCAT       GAAGCCATT
                                |||||       |||||||||
                                GGGTG       CTTCGGTAA
                                   CCC_____
GAM383  LOC201182 5'  AATGGCTTCTCCCTCTTTAAGG 89761     A  TGT  A_
                                CC TA   AG  AGAAGCCATT
                                || ||   ||  ||||||||||
                                GG AT   TC  TCTTCGGTAA
                                 A  TTC  CC
GAM383  LOC220824 3'  GCTTCCTCTATTCCTTTATATG 90806       _______    A
                                CATAT     GTAGA GAAGC
                                |||||     ||||| |||||
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                                GTATA     TATCT CTTCG
                                   TTTCCT    C
GAM383  LOC255520 3'  GCTCTACCTACATATG     95860        A_  A
                                CATATGTAG  AGA GC
                                |||||||||  ||| ||
                                GTATACATC  TCT CG
                                     CA  _
GAM383  LOC57105  5'  TAATGGCTATTCTACAT     39820        GA
                                ATGTAGAA  AGCCATTA
                                ||||||||  ||||||||
                                TACATCTT  TCGGTAAT
                                     A_
GAM383  LOC92597  3'  TAATAACTTTTTCTGCATAT   69972           CC
                                ATATGTAGAAGAAG  ATTA
                                ||||||||||||||  ||||
                                TATACGTCTTTTTC  TAAT
                                        AA
GAM384  ADAMTS13  3'  GGCGTGCATGTGTTGGTGCTGA 57375        TGTG  AT
                                TCAGCACCA   ACA  CATGCC
                                |||||||||   |||  ||||||
                                AGTCGTGGT   TGT  GTGCGG
                                     TG__   AC
GAM384  AMFR      3'  GGTATGATCTCTTCTGGTGTTG 57247        TGT  CA
           A                     TCAGCACCA   GA  ATCATGCC
                                |||||||||   ||  ||||||||
                                AGTTGTGGT   CT  TAGTATGG
                                     CTT  C_
GAM384  AMFR      3'  GGTATGATCTCTTCTGGTGTTG 6697         TGT  CA
           A                     TCAGCACCA   GA  ATCATGCC
                                |||||||||   ||  ||||||||
                                AGTTGTGGT   CT  TAGTATGG
                                     CTT  C_
GAM384  ASNS      5'  TGTCGCGTGGTCCTGA     55943      C
                                TCAG ACCATGTGACA
                                ||||  ||||||||||
                                AGTC TGGTGCGCTGT
                                  C
GAM384  BPGM      3'  GGAGTGTGTTATGGGTGCTGA  8176         A      AT   G
                                TCAGCACC TGTGACA  CAT CC
                                |||||||| |||||||  ||| ||
                                AGTCGTGG GTATTGT  GTG GG
                                     _      __   A
GAM384  CBFA2T3   3'  GGCATCTGTGTGCGTGGTGT   17758         G   ATC
                                GCACCATGT ACA   ATGCC
                                |||||||||  |||   |||||
                                TGTGGTGCG TGT   TACGG
                                     _  GTC
GAM384  COL4A3    3'  GTGGAGTTGGTGGTGCTGA   48559         GTGA   CA
                                TCAGCACCAT   CAAT  TGC
                                ||||||||||   ||||  |||
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                                AGTCGTGGTG   GTTG  GTG
                                      _____    AG
GAM384  COL4A3   3'  GTGGAGTTGGTGGTGCTGA   3624          GTGA   CA
                                TCAGCACCAT   CAAT  TGC
                                ||||||||||   ||||  |||
                                AGTCGTGGTG   GTTG  GTG
                                      _____    AG
GAM384  COL4A3   3'  GTGGAGTTGGTGGTGCTGA   48570         GTGA   CA
                                TCAGCACCAT   CAAT  TGC
                                ||||||||||   ||||  |||
                                AGTCGTGGTG   GTTG  GTG
                                      _____    AG
GAM384  FBN1     3'  GCTACCTTGTCATATGTGTTGA 64400        C       TCAT
                                TCAGCAC ATGTGACAA   GC
                                |||||||  |||||||||   ||
                                AGTTGTG TATACTGTT   CG
                                    _       CCAT
GAM384  GJA1     3'  GGTGTGGGCCAATATGGTGTT  3903          GACAA
                                AGCACCATGT    TCATGCC
                                ||||||||||    |||||||
                                TTGTGGTATA    GGTGTGG
                                      ACCG_
GAM384  GRHPR    3'  TTGTCACATTGGTGTTGG    24193         _
                                TCAGCACCA TGTGACAA
                                |||||||||  ||||||||
                                GGTTGTGGT ACACTGTT
                                      T
GAM384  GUCY1A3  5'  GGCGTGATCTCACCATGGTGCG 63491    A      _  CA
           GA                     TC GCACCATG TGA  ATCATGCC
                                ||  ||||||||  |||  ||||||||
                                AG CGTGGTAC ACT  TAGTGCGG
                                 G       C   C_
GAM384  KCNA7    3'  GGTCTTGGGTTGTGTGGTTTGG 49058     C     TG  AA   T_
                                TCAG ACCATG  AC  TCA  GCC
                                ||||  ||||||  ||  |||  |||
                                GGTT TGGTGT  TG  GGT  TGG
                                   _     GT  __   TC
GAM384  MAGEL2   3'  GTACATTTTTTATGTGGTGTTG 38819           C  TCA   C
           A                     TCAGCACCATGTGA AA   TGC
                                ||||||||||||||  ||   |||
                                AGTTGTGGTGTATT TT   ATG
                                      T  TAC
GAM384  MAML1    3'  GGCATCAGTACCTGGTGTTGG  28592         T   ACAATC
                                TCAGCACCA GTG     ATGCC
                                |||||||||  |||     |||||
                                GGTTGTGGT CAT     TACGG
                                      C   GAC___
GAM384  MC1R     3'  GTGATATTGTGTGGTCTGG   9956      C     TG CA
                                TCAG ACCATG  A  ATCAT
                                ||||  ||||||  |  |||||
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                                GGTC TGGTGT  T  TAGTG
                                  _     GT A_
GAM384  MYEOV    3'  GCATGAGCCAGGTGCTGG    57050        A  TGACAA
                                TCAGCACC TG     TCATGC
                                |||||||| ||     ||||||
                                GGTCGTGG AC     AGTACG
                                    _ CG____
GAM384  PFKFB4   3'  GGCATGGTCTCCGCATGGGCTG 15871      A      ACA
           A                     TCAGC CCATGTG   ATCATGCC
                                |||||| |||||||   ||||||||
                                AGTCG GGTACGC   TGGTACGG
                                  _      CTC
GAM384  SCAMP2   3'  GGTGCCTTATGTGGTGGTGG   19101     G        CA_
                                TCA CACCATGTGA   ATC
                                ||| ||||||||||   |||
                                GGT GTGGTGTATT   TGG
                                  G        CCG
GAM384  SLC12A7  3'  GGCACAGCGGCCACATGGTGCT 21703           ACAATCA
           GG                     TCAGCACCATGTG      TGCC
                                ||||||||||||       ||||
                                GGTCGTGGTACAC      ACGG
                                       CGGCGAC
GAM384  STK10    3'  GGTGTGGCACGTGCGGGGTGTT 19988        A   ACAA
           GG                     TCAGCACC TGTG    TCATGCC
                                |||||||| ||||    |||||||
                                GGTTGTGG GCGT    GGTGTGG
                                    G    GCAC
GAM384  TAL1     3'  CGTACGCTGGTGCTGA      12103         T   ACAATC
                                TCAGCACCA GTG     ATG
                                ||||||||| |||     |||
                                AGTCGTGGT CGC     TGC
                                    _  A_____
GAM384  TNFAIP1  3'  CACTGCATGGTGTTG       40916           ACAATCA
                                CAGCACCATGTG      TG
                                ||||||||||||      ||
                                GTTGTGGTACGT      AC
                                       C______
GAM384  VCX      5'  GGCGTGATTGTCTCGTCCTGG  69190      CACC   T
                                TCAG    ATG GACAATCATGCC
                                ||||    ||| ||||||||||||
                                GGTC    TGC CTGTTAGTGCGG
                                  C___   T
GAM384  C11orf25 5'  GGTGTTGATTTATGTGGTCTTG 48644      C        CA   _
           A                     TCAG ACCATGTGA  ATCA TGCC
                                |||| |||||||||  |||| ||||
                                AGTT TGGTGTATT  TAGT GTGG
                                  C        __    T
GAM384  CBCIP2   3'  GGTGGACTTCATGGGTGCTGA  51593        A    CAA  A
                                TCAGCACC TGTGA   TC TGCC
                                |||||||| |||||   || ||||
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                                AGTCGTGG GTACT   AG GTGG
                                     _    TC_  _
GAM384  DKFZP564I052 5'  GGCTGTCAATGGTGTTGA    66715          G    AT
                                TCAGCACCAT TGACA  C
                                |||||||||| |||||  |
                                AGTTGTGGTA ACTGT  G
                                     _    CG
GAM384  FLJ11850  3'  GATCCTGTTATGTGTGCTGA   42721        C       __
                                TCAGCAC ATGTGACA  ATC
                                ||||||| ||||||||  |||
                                AGTCGTG TGTATTGT  TAG
                                     _      CC
GAM384  FLJ12425  3'  TGTTATATGTGTTGA       85896        C
                                TCAGCAC ATGTGACA
                                ||||||| ||||||||
                                AGTTGTG TATATTGT
                                     _
GAM384  FLJ14753  3'  GGTGACTTCATGGTGCTGG    50777           TGACA
                                TCAGCACCATG     ATC
                                ||||||||||     |||
                                GGTCGTGGTAC     TGG
                                      TTCAG
GAM384  FLJ20281  3'  GTGACAGTCATATGGTTTTGA  90983      C         AA
                                TCAG ACCATGTGAC  TCAT
                                |||| ||||||||||  ||||
                                AGTT TGGTATACTG  AGTG
                                   T         AC
GAM384  FLJ20446  3'  GGTGCCTCGCTGGTGCTGG    35186          T    CA_
                                TCAGCACCA GTGA   ATC
                                ||||||||| ||||   |||
                                GGTCGTGGT CGCT   TGG
                                     _    CCG
GAM384  FLJ23790  5'  GCGTGGTGGGTGGTGC      58621         G GACA
                                GCACCAT T    ATCATGC
                                ||||||| |    |||||||
                                CGTGGTG G    TGGTGCG
                                     G _____
GAM384  HSA243396 5'  GGCGACTGTCCGTGGTGCTGA  37256           T    A  AT
                                TCAGCACCATG GACA TC  GCC
                                |||||||||| |||| ||  |||
                                AGTCGTGGTGC CTGT AG  CGG
                                      _    C  __
GAM384  IL18BP    5'  GTGTGATGGTGGGTGCTGG    19111         ATGTGACA
                                TCAGCACC        ATCATGC
                                ||||||||        |||||||
                                GGTCGTGG        TAGTGTG
                                     GTGG_____
GAM384  KIAA0186  3'  GCGTGAGCCTTGGTGCTGG    40754          TGTGACAA
                                TCAGCACCA       TCATGC
                                |||||||||       ||||||
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                                GGTCGTGGT       AGTGCG
                                     TCCG_____
GAM384  KIAA0222 3' TTGTTGTGTGTGTTGG     27686        C   TG
                                TCAGCAC ATG  ACAA
                                ||||||| |||  ||||
                                GGTTGTG TGT  TGTT
                                   _  GT
GAM384  KIAA0493 5' GCATGGTGGGTGGTGC      64277        G GACA
                                GCACCAT T    ATCATGC
                                ||||||| |    |||||||
                                CGTGGTG G    TGGTACG
                                   G _____
GAM384  KIAA0870 3' GTGTGGTTGTTGGAGCCGG   81471    A  A   TGTG
                                TC GC CCA    ACAATCATGC
                                || || |||    ||||||||||
                                GG CG GGT    TGTTGGTGTG
                                 C  A  _____
GAM384  KIAA1434 3' GGTATTTTTTACATGGGTTGA  69618      A       C  TC
                                TCAGC CCATGTGA AA  ATGCC
                                ||||| |||||||| ||  |||||
                                AGTTG GGTACATT TT  TATGG
                                   _       T  __
GAM384  KIAA1656 3' CGGCTTGATCTGATTGTATGCA 65790       _      T_____
           TGGTGTTGG                CATGTG ACAATCA     GCC   G
                                |||||| |||||||     |||   |
                                GTACGT TGTTAGT     CGG   C
                                   A      CTAGTT
GAM384  KIAA1719 5' GCGAGCGCGTGGTGCTGG    68165           ACAATCA
                                TCAGCACCATGTG      TGC
                                ||||||||||||||      |||
                                GGTCGTGGTGCGC      GCG
                                      GA_____
GAM384  LASP1    3' GACTGTCACACTGGTGCTGA   20455         _      A
                                TCAGCACCA TGTGACA TC
                                ||||||||| ||||||| ||
                                AGTCGTGGT ACACTGT AG
                                     C      C
GAM384  MGC12966 3' TGTCCTGCAGTGGTGTTGA    51128         _  __
                                TCAGCACCA TGT  GACA
                                ||||||||| |||  ||||
                                AGTTGTGGT ACG  CTGT
                                     G   TC
GAM384  MGC17998 3' GGTGTTCCCCTGCAGGTGCTGG 58744         A   GACAATC
                                TCAGCACC TGT      ATGCC
                                |||||||| |||      |||||
                                GGTCGTGG ACG      TGTGG
                                   _  TCCCCT_
GAM384  PSKH1    3' TGTCTGCATGGGTGTTGG    68245         _   _
                                TCAGCACC ATGT GACA
                                |||||||| |||| ||||
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                                GGTTGTGG TACG CTGT
                                     G   T
GAM384  TRIM7    3'  GGCTCGGTGTGTGTGGTGTTGG 52907        TG G   A  AT
                                TCAGCACCA  T ACA TC  GCC
                                |||||||||  | ||| ||  |||
                                GGTTGTGGT  G TGT GG  CGG
                                     GT _   _  CT
GAM384  Ubc6p    3'  CGTCCGCGGGTGCTGG     54150        A    ACAATC
                                TCAGCACC TGTG     ATG
                                |||||||| ||||     |||
                                GGTCGTGG GCGC     TGC
                                     _    C_____
GAM384  VPS39    3'  GGTGTGGTTGGAGAGTTGTGCT 62848       C  GTGA
           GG                     TCAGCAC AT    CAATCATGCC
                                |||||||  ||    ||||||||||
                                GGTCGTG TG    GTTGGTGTGG
                                     T  AGAG
GAM384  LOC113523 3'  TTATGATCATATGGTGTTGG   73052           CAA    CC
                                TCAGCACCATGTGA   TCATG
                                ||||||||||||||   |||||
                                GGTTGTGGTATACT   AGTAT
                                       ___     TA
GAM384  LOC128977 3'  GGTGGCCCTGTTGTGTGATGCT 74826       C    TG   ATCA
           GA                     TCAGCA CATG  ACA    TGCC
                                ||||||  ||||  |||    ||||
                                AGTCGT GTGT  TGT    GTGG
                                   A    GT   CCCG
GAM384  LOC138389 5'  CGCTCTATGGTGCTGG      76222          T  CAATCA
                                TCAGCACCATG GA     TG
                                ||||||||||| ||     ||
                                GGTCGTGGTAT CT     GC
                                      _ C_____
GAM384  LOC146901 3'  GGTTTTTGTTGTTGGTGTTGA  83846         T TG    TCAT
                                TCAGCACCA G  ACAA    GCC
                                |||||||| |  ||||    |||
                                AGTTGTGGT T  TGTT    TGG
                                     _ GT    TT__
GAM384  LOC147669 5'  GGTAGAGGTCATGGGTGCTGG  84065         A     AA  A
                                TCAGCACC TGTGAC  TC TGCC
                                |||||||| ||||||  || ||||
                                GGTCGTGG GTACTG  AG ATGG
                                     _     G_  _
GAM384  LOC148758 5'  TGTGGCAGGTGCTGG       78978         A   G
                                TCAGCACC TGT ACA
                                |||||||| ||| |||
                                GGTCGTGG ACG TGT
                                     _  G
GAM384  LOC154092 3'  GGTGTGGTCCTGCACGTGGGGT 86160      __     A  __
           GTTGG                     CACC  ATGTG CA  ATCATGCC
                                ||||  ||||| ||  ||||||||
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                                GTGG  TGCAC GT  TGGTGTGG
                                  GG    _  CC
GAM384  LOC158014 5'  GGTGTGTGTGTGTGTGGTGGTG 81656    G    TG G  AT
           G                     TCA CACCA  T ACA  CATGCC
                                 ||| |||||  | |||  ||||||
                                 GGT GTGGT  G TGT  GTGTGG
                                   G    GT _  GT
GAM384  LOC163412 5'  GGCGTGCGGCGCATGGTGGTGA 82136    G       ACAAT
                                 TCA CACCATGTG    CATGCC
                                 ||| |||||||||    ||||||
                                 AGT GTGGTACGC    GTGCGG
                                   G       GGC__
GAM384  LOC202559 5'  GGCGGGAGTCGCAGGTGCTGG  89197        A     AA  A
                                 TCAGCACC TGTGAC  TC TGCC
                                 |||||||| ||||||  || ||||
                                 GGTCGTGG ACGCTG  AG GCGG
                                     _     __ G
GAM384  LOC222060 5'  ATTGTCATATGCTGCTGG    94102       C
                                 TCAGCA CATGTGACAAT
                                 |||||| ||||||||||
                                 GGTCGT GTATACTGTTA
                                    C
GAM384  LOC255249 5'  GGCGTGATTGTCTCGTCCTGG  97434     CACC   T
                                 TCAG    ATG GACAATCATGCC
                                 ||||    ||| ||||||||||||
                                 GGTC    TGC CTGTTAGTGCGG
                                   C___   T
GAM384  LOC51195  3'  GTGGATGTTGTGTGTGCTGG   32948       C   TG   A
                                 TCAGCAC ATG  ACA TCAT
                                 ||||||| |||  ||| ||||
                                 GGTCGTG TGT  TGT GGTG
                                     _  GT   A
GAM384  LOC92078  3'  GCTCTGTCGTAGGTGCTGG    67983        A      ATCAT
                                 TCAGCACC TGTGACA     GC
                                 |||||||| |||||||    ||
                                 GGTCGTGG ATGCTGT     CG
                                     _      CT___
GAM384  LOC92080  3'  GGTGACCCTGGTCACTTGGTGC 68055        T    AA___    GCC
           TGG                     AGCACCA GTGAC     TCAT
                                 ||||||| |||||     ||||
                                 TCGTGGT CACTG     AGTG
                                    T    GTCCC    G
GAM384  LOC92340  3'  GCCTGTTGCATGGGCTGG    68993      A    TG   ATCAT
                                 TCAGC CCATG  ACA    GC
                                 ||||| |||||  |||    ||
                                 GGTCG GGTAC  TGT    CG
                                   _    GT   C____
GAM384  LOC95244  5'  GGCGTGATTGTCTCGTCCTGG  60441     CACC   T
                                 TCAG    ATG GACAATCATGCC
                                 ||||    ||| ||||||||||||
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                                GGTC    TGC CTGTTAGTGCGG
                                  C___   T
GAM385  CCND2    3'  GCTAGCACATACACC       8292          T  CAC
                                GGTGTATGT GC   AGT
                                ||||||||| ||   |||
                                CCACATACA CG   TCG
                                     _  A__
GAM385  CYLN2    3'  AACACCAACACACACACACCTC 12626         A   TGCCACA
           T                     AGAGGTGT TGT       GTGTT
                                |||||||| |||       |||||
                                TCTCCACA ACA       CACAA
                                     C   CACAAC_
GAM385  DNMT2    3'  ATTGTAGCAACATACACTCT   15330      G         C
                                AGAG TGTATGTTGC ACAGT
                                |||| |||||||||| |||||
                                TCTC ACATACAACG TGTTA
                                  _         A
GAM385  GLRA3    5'  AACACTGTGACTCTCCACTTCT 60073        TAT_  TGC
                                AGAGGTG    GT   CACAGTGTT
                                |||||||    ||   |||||||||
                                TCTTCAC    CA   GTGTCACAA
                                    CTCT  ____
GAM385  IFI16    3'  AACACTATACATACAC      71219         TGCCAC
                                GTGTATGT     AGTGTT
                                ||||||||     ||||||
                                CACATACA     TCACAA
                                     TA_____
GAM385  PDE6D    3'  TGACACATACACCCCT      10494    A       T C
                                AG GGTGTATGT G CA
                                || ||||||||| | ||
                                TC CCACATACA C GT
                                 C        _ A
GAM385  PMM2     3'  AACACTGAGCCATACACCCT   72088    A       TT  CA
                                AG GGTGTATG  GC  CAGTGTT
                                || ||||||||  ||  |||||||
                                TC CCACATAC  CG  GTCACAA
                                 _       ___  A_
GAM385  TNFRSF10B 3'  AACACTGTGGCAACAGGACCT  13864      GTA
                                AGGT   TGTTGCCACAGTGTT
                                ||||   ||||||||||||||||
                                TCCA   ACAACGGTGTCACAA
                                  GG_
GAM385  KIAA0089  3'  AACACTATGTCTGTACACCTCT 69959           TTGC  C
                                AGAGGTGTATG    CA AGTGTT
                                ||||||||||    || ||||||
                                TCTCCACATGT    GT TCACAA
                                       CT___  A
GAM385  TM9SF2   3'  AACACCGTAATTCTAAATAAAC 16626       G   GTTGCC__  A
           CTCT                    AGAGGT TAT       AC GTGTT
                                |||||| |||       || |||||
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                                TCTCCA ATA       TG CACAA
                                   A   AATCTTAA  C
GAM385  LOC115509 3'  CACAGTGCCACTACACCTT   73459        T  T  C  A
                                GAGGTGTA GT GC AC GTG
                                |||||||| || || || |||
                                TTCCACAT CA CG TG CAC
                                     _  C  _  A
GAM385  LOC148188 5'  GGCCAACACACACATCT     78726     G    A    _
                                AGA GTGT TGTTG CC
                                ||| |||| ||||| ||
                                TCT CACA ACAAC GG
                                  A   C    C
GAM385  LOC51301  5'  ACACTGTAGGGAACCTCT    33437       GTATGT G  _
                                AGAGGT     T CC ACAGTGT
                                ||||||     | || |||||||
                                TCTCCA     A GG TGTCACA
                                   _______ G  A
GAM385  LOC91012  3'  TGGCAACATACTCCTCT     64644       T
                                AGAGG GTATGTTGCCA
                                ||||| ||||||||||
                                TCTCC CATACAACGGT
                                   T
GAM386  ACP2     3'  AGAAAGTTCTAGACTG      7851       GC  TC
                                CAGT  CT  AGAACTTTCT
                                ||||  ||  ||||||||||
                                GTCA  GA  TCTTGAAAGA
                                   __  __
GAM386  APTX     5'  AAGAGAAAGAGATCAGGCA    34655       TCAGAA
                                TGCCT     CTTTCTCTT
                                |||||     |||||||||
                                ACGGA     GAAAGAGAA
                                   CTAGA_
GAM386  BCL7A    3'  AGGCTGTCTCCTTAAGGCACTG 40637         C  A__  TT
                                CAGTGCCTT AG   AC  TCT
                                ||||||||| ||   ||  |||
                                GTCACGGAA TC   TG  GGA
                                      T  CTC  TC
GAM386  CLC      3'  AAGAGAAAATACTGAAAGCACA 25105    A    C    AAC
           GG                     CC GTGC TTCAG   TTTCTCTT
                                || |||| |||||   ||||||||
                                GG CACG AAGTC   AAAGAGAA
                                 A    A     ATA
GAM386  CNK      3'  AAGCCCTGAAGGCCTG      14517     T       AA
                                CAG GCCTTCAG  CTT
                                ||| ||||||||  |||
                                GTC CGGAAGTC  GAA
                                  _       CC
GAM386  COL4A3   3'  AAGTGCAGGTTCTGAGGGCACC 48549    A            TCT
           GG                     CC GTGCCTTCAGAACTT   CTT
                                || ||||||||||||||   |||
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                                GG CACGGGAGTCTTGGA   GAA
                                 C            CGT
GAM386  CSPG4    3'  AAGAGAGACCTGGAGACAC    8570     C     AAC
                                GTG CTTCAG   TTTCTCTT
                                ||| ||||||   ||||||||
                                CAC GAGGTC   AGAGAGAA
                                  A     C__
GAM386  CYP1B1   3'  AAGAGAAAAGAGAGAAACACTG 3651       CC   AGAAC
                                CAGTG  TTC    TTTCTCTT
                                |||||  |||    ||||||||
                                GTCAC  AAG    AAAGAGAA
                                   A_   AGAGA
GAM386  DLG3     3'  AAGAGAAAAGAGGAGGACTG   40880     G    AGAAC
                                CAGT CCTTC    TTTCTCTT
                                |||| |||||    ||||||||
                                GTCA GGAGG    AAAGAGAA
                                  _    AGA__
GAM386  DLG5     5'  AGGCAGACTCTGAAGGC     82909         A_  T
                                GCCTTCAGA  CT TCT
                                |||||||||  || |||
                                CGGAAGTCT  GA GGA
                                     CA  C
GAM386  FLT1     3'  AAGAGAAACCGGGAGAAGGCAT 8910         AGAAC_
                                GTGCCTTC     TTTCTCTT
                                ||||||||     ||||||||
                                TACGGAAG     AAAGAGAA
                                    AGGGCC
GAM386  GRB10    3'  AGAGAAAATGGCACCTGG    17971     _   TTCAGAAC
                                CCAG TGCC       TTTCTCT
                                |||| ||||       |||||||
                                GGTC ACGG       AAAGAGA
                                  C   TA_______
GAM386  LFG      3'  AAGAGAAAAGGAGCCAAGAACT 76711      GC   CAGAA   _
           GG                   CCAGT  CTT    CTTT CTCTT
                                |||||  |||    |||| |||||
                                GGTCA  GAA    GAAA GAGAA
                                  A_   CCGAG   A
GAM386  MAN2A2   3'  AAGAGAAAGTTCATTCAC    20391     CCTTCA
                                GTG     GAACTTTCTCTT
                                |||     ||||||||||||
                                CAC     CTTGAAAGAGAA
                                  TTA___
GAM386  NLGN3    3'  AAGAAAAGTTCTTAAAACACT  38596     CC  C       C
                                AGTG  TT AGAACTTT TCTT
                                ||||  || |||||||| ||||
                                TCAC  AA TCTTGAAA AGAA
                                  AA  T       _
GAM386  NPAS1    5'  AAGGTCTCCCGAGGGCACT    59879         A_  _
                                AGTGCCTTC  GA ACTTT
                                |||||||||  || |||||
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                                TCACGGGAG  CT TGGAA
                                     CC  C
GAM386  PLAG1    3'  AGTGTGTTCCAAAGGCATT   10605        CA   TTT
                                AGTGCCTT  GAAC   CT
                                ||||||||  ||||   ||
                                TTACGGAA  CTTG   GA
                                    AC    TGT
GAM386  PLXNA1   3'  AGAAAATGAAGGCAGTGG    72309     G       GAAC
                                CCA TGCCTTCA    TTTCT
                                ||| ||||||||    |||||
                                GGT ACGGAAGT    AAAGA
                                  G       A___
GAM386  PPP4R1   3'  AAGAGAAAGTACAGTAAACACT 17620      CCTTCAGA
                                AGTG       ACTTTCTCTT
                                ||||       ||||||||||
                                TCAC       TGAAAGAGAA
                                  AAATGACA
GAM386  ACYP2    3'  AAGAGAAAAATTGTAACACACT 56612      CC  _   AAC
           G                     CAGTG  TT CAG   TTTCTCTT
                                ||||||  || |||   ||||||||
                                GTCAC  AA GTT   AAAGAGAA
                                  AC  T   AA_
GAM386  B3GNT6   3'  AGAAATCAGATGAAGGCAT    22503         GAAC_
                                GTGCCTTCA     TTTCT
                                |||||||||     |||||
                                TACGGAAGT     AAAGA
                                     AGACT
GAM386  BAG5     3'  AAGAGAAGGGATAAAGGAC    16835    G    CAGAA
                                GT CCTT     CTTTCTCTT
                                || ||||     |||||||||
                                CA GGAA     GGAAGAGAA
                                 _    ATAG_
GAM386  BIVM     3'  AAGAGAAAAGACTCAAGAAACT 34665      GC   C  AAC
           G                     CAGT  CTT AG   TTTCTCTT
                                ||||  ||| ||   ||||||||
                                GTCA  GAA TC   AAAGAGAA
                                  AA   C  AGA
GAM386  C15orf5  3'  AGAGAAAAGAAAGCAC      48195      C   AGAAC
                                GTGC TTC     TTTCTCT
                                |||| |||     |||||||
                                CACG AAG     AAAGAGA
                                  A   A____
GAM386  C20orf80 5'  AAGAGAAGAAGATGAAGAAAC  65282    GC    GAAC
                                GT  CTTCA    TTTCTCTT
                                ||  |||||    ||||||||
                                CA  GAAGT    GAAGAGAA
                                 AA     AGAA
GAM386  CLSTN1   3'  AGTTCTGAGGACACTGG     30103        C
                                CCAGTG CTTCAGAACT
                                |||||| ||||||||||
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                                GGTCAC GGAGTCTTGA
                                   A
GAM386  DKFZP434P0111 3'  AAGAGAAAGTTTCTGCAC    67368     CTTCA
                                GTGC    GAACTTTCTCTT
                                ||||    ||||||||||||
                                CACG    TTTGAAAGAGAA
                                  TC___
GAM386  DORFIN   5'  AGAATTCTCTGAAGGAAC    31257    G      ACT
                                GT CCTTCAGA   TTCT
                                || ||||||||   ||||
                                CA GGAAGTCT   AAGA
                                 A       CTT
GAM386  FLJ10300 5'  AAGAGAAAGATGAAGACTCTG  35997    TGC    GAA
                                CAG   CTTCA   CTTTCTCTT
                                |||   |||||   |||||||||
                                GTC   GAAGT   GAAAGAGAA
                                  TCA    A__
GAM386  FLJ20373  3'  AAGAGAAGAAGGAAAGGCACAG 35070    A     _ AGAAC
           G                     CC GTGCCTT C    TTTCTCTT
                                || |||||||  |    ||||||||
                                GG CACGGAA G    GAAGAGAA
                                 A      A GAA__
GAM386  FLJ23511  5'  AGAGAAAAACAAGGCAT    49956       CAGAAC
                                GTGCCTT     TTTCTCT
                                |||||||     |||||||
                                TACGGAA     AAAGAGA
                                    CAA___
GAM386  FLJ30681  3'  AGAGAAGAAAGACCACTGG   91782      CCT  AGAAC
                                CCAGTG   TC    TTTCTCT
                                ||||||   ||    |||||||
                                GGTCAC   AG    GAAGAGA
                                   C__   AAA__
GAM386  HDAC11    3'  GAGCTATAGGCACTGG     45717       TC  AACTTT
                                CCAGTGCCT  AG     CTC
                                |||||||||  ||     |||
                                GGTCACGGA  TC     GAG
                                     TA  _______
GAM386  IKKE     5'  AGTGAGCCCTGAAAGCTCTGG  25745     T  C    AA   T
                                CCAG GC TTCAG  CTT CT
                                |||| || |||||  ||| ||
                                GGTC CG AAGTC  GAG GA
                                  T  A    CC   T
GAM386  KIAA0680  3'  AGAGAAAATTGAAGCAT     28232     C    AAC
                                GTGC TTCAG   TTTCTCT
                                |||| |||||   |||||||
                                TACG AAGTT   AAAGAGA
                                  _    A__
GAM386  KIAA1228  3'  AGGGGGTGATTCTGAGGCACTG 65035       T   ___   TT
                                CAGTGCCT CAGA   ACT  CT
                                |||||||| ||||   |||  ||
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                                GTCACGGA GTCT   TGG  GA
                                     _   TAG   GG
GAM386  KIAA1300  5'  AGGAACCCTGAAGGCA     62860         AAC
                                TGCCTTCAG   TTTCT
                                |||||||||   |||||
                                ACGGAAGTC   AAGGA
                                     CC_
GAM386  KIAA1805  3'  AAGAGAAAGTAGAAGCAGCA   79966     __    AGA
                                TGC  CTTC   ACTTTCTCTT
                                |||  ||||   ||||||||||
                                ACG  GAAG   TGAAAGAGAA
                                  AC    A__
GAM386  LENG1     5'  AAGAGAAAGCTCTGGGCATCCT 84074     __    TT    A
            G                    CAG  TGCC  CAGA CTTTCTCTT
                                |||  ||||  |||| |||||||||
                                GTC  ACGG  GTCT GAAAGAGAA
                                  CT    __    C
GAM386  LHX6      3'  AAGAGAAAACTCTGGGGTCA   26854    C      AC
                                TG CTTCAGA  TTTCTCTT
                                || |||||||  ||||||||
                                AC GGGGTCT  AAAGAGAA
                                 T      CA
GAM386  N4BP3     3'  AGCTCCAGAAGGCACTGG     66250          A_  A
                                CCAGTGCCTTC  GA CT
                                ||||||||||  || ||
                                GGTCACGGAAG  CT GA
                                      AC  C
GAM386  NASP      3'  AGAGGGTGAAGAAACTG     67966      GC    AGA
                                CAGT  CTTC   ACTTTCT
                                ||||  ||||   |||||||
                                GTCA  GAAG   TGGGAGA
                                  AA    ___
GAM386  SMARCF1   3'  AAAATTCTGAAGGAC       57480    G       C
                                GT CCTTCAGAA TTT
                                || ||||||||| |||
                                CA GGAAGTCTT AAA
                                 _       A
GAM386  SMARCF1   3'  AAAATTCTGAAGGAC       20034    G       C
                                GT CCTTCAGAA TTT
                                || ||||||||| |||
                                CA GGAAGTCTT AAA
                                 _       A
GAM386  SMARCF1   3'  AAAATTCTGAAGGAC       37430    G       C
                                GT CCTTCAGAA TTT
                                || ||||||||| |||
                                CA GGAAGTCTT AAA
                                 _       A
GAM386  TED       3'  AAGAGAAAGTCCAGGGACTGG  31630      G   TCA  A
                                CCAGT CCT   GA CTTTCTCTT
                                ||||| |||   || |||||||||
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                                GGTCA GGA   CT GAAAGAGAA
                                   G   C__ _
GAM386  TGIF2     3'  AGAAGGGTGCTGAAGGC     41447         AA_
                                GCCTTCAG   CTTTCT
                                ||||||||   ||||||
                                CGGAAGTC   GGAAGA
                                    GTG
GAM386  WBSCR20A  3'  AAGAGAAAGAAGAGACAGCA   35958     CT  AGAA
                                TGC  TC    CTTTCTCTT
                                |||  ||    |||||||||
                                ACG  AG    GAAAGAGAA
                                  AC  AGAA
GAM386  LOC115273 3'  AGAAAGTTCTGATGGCCAGG   73356     AGT   T
                                CC   GCC TCAGAACTTTCT
                                ||   ||| ||||||||||||
                                GG   CGG AGTCTTGAAAGA
                                  AC_   T
GAM386  LOC145761 5'  AAGAGAAAGTGGAAGGCATGG  83472     G      AGA
                                CCA TGCCTTC   ACTTTCTCTT
                                ||| |||||||   ||||||||||
                                GGT ACGGAAG   TGAAAGAGAA
                                  _     G__
GAM386  LOC146179 5'  AGAAAGTTTTGGGCCT      77700     T   TT
                                AG GCC  CAGAACTTTCT
                                || |||  ||||||||||
                                TC CGG  GTTTTGAAAGA
                                  _  __
GAM386  LOC147072 3'  AAGAGAAAGTGAGAAGAAACTG 60407      GC    AGA
                                CAGT  CTTC   ACTTTCTCTT
                                ||||  ||||   ||||||||||
                                GTCA  GAAG   TGAAAGAGAA
                                  AA    AG_
GAM386  LOC148758 5'  AGAAAGTTCTGAGAAAC     78962     GCC
                                GT   TTCAGAACTTTCT
                                ||   ||||||||||||
                                CA   GAGTCTTGAAAGA
                                  AA_
GAM386  LOC148932 3'  AGGAATCTGAAGGCACTGG    79103             AC
                                CCAGTGCCTTCAGA  TTTCT
                                ||||||||||||||  |||||
                                GGTCACGGAAGTCT  AAGGA
                                                __
GAM386  LOC149386 5'  AAGTTTTGAAAGCACT      84400       C
                                AGTGC TTCAGAACTT
                                ||||| ||||||||||
                                TCACG AAGTTTTGAA
                                   A
GAM386  LOC150139 3'  AGAAAATAGAAAAAGGCGCTGG 79583           CAGAAC_
                                CCAGTGCCTT       TTTCT
                                ||||||||||       |||||
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                                GGTCGCGGAA      AAAGA
                                      AAAGATA
GAM386  LOC152756 3'  AAGATGCAGTTCTGAAAACCTG 85871     TGCC       TTC
                                CAG    TTCAGAACT   TCTT
                                |||    |||||||||   ||||
                                GTC    AAGTCTTGA   AGAA
                                  CAA_        CGT
GAM386  LOC162333 5'  AAGAGAAAGCGATGACACTG   87114      CCT   GAA
                                CAGTG   TCA   CTTTCTCTT
                                |||||   |||   |||||||||
                                GTCAC   AGT   GAAAGAGAA
                                   ___   AGC
GAM386  LOC199221 3'  AAGAGAAGCTCGAAAGCATGG  80347     G   C   A A   T
                                CCA TGC TTC GA CTT CTCTT
                                ||| ||| ||| || ||| |||||
                                GGT ACG AAG CT GAA GAGAA
                                  _   A   _ C   _
GAM386  LOC203339 3'  AGAGAAAATTGGGCCTG     90542     T   TCAGAAC
                                CAG GCCT      TTTCTCT
                                ||| ||||      |||||||
                                GTC CGGG      AAAGAGA
                                  _    TTA____
GAM386  LOC255017 3'  AGAAAGAGGAACTGG       94624       G   TCAGAA
                                CCAGT CCT     CTTTCT
                                ||||| |||     ||||||
                                GGTCA GGA     GAAAGA
                                   A  _______
GAM386  LOC256021 3'  AAGAGAAACAAAGACAACACTG 96512       CCT  AGAAC
            G                    CCAGTG   TC    TTTCTCTT
                                ||||||  ||    ||||||||
                                GGTCAC   AG    AAAGAGAA
                                   AAC  AAAC_
GAM386  LOC90139  3'  AGAATCCCGAAGGCAT      55396        A_  ACT
                                GTGCCTTC  GA   TTCT
                                ||||||||  ||   ||||
                                TACGGAAG  CT   AAGA
                                     CC  ___
GAM387  ALX4     3'  CCACGCCCATGTTTTCCA    41629    A      AGTTT   A
                                TG AAGACATG    GTG TGG
                                || ||||||||    ||| |||
                                AC TTTTGTAC    CGC ACC
                                 C       C_____  _
GAM387  BCLG     3'  CCATCTCTGGACTCACAGCTTC 56985    A   ACA      GT_
            CA                    TG AAG   TGAGTTT   GATGG
                                || |||   |||||||   |||||
                                AC TTC   ACTCAGG   CTACC
                                 C  GAC      TCT
GAM387  CHGB     3'  GCCATCACATGATCTGTTTTTC 8430          T  GTT
            A                     TGAAAGACA GA   TGTGATGGC
                                |||||||||  ||   |||||||||
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                                ACTTTTTGT CT   ACACTACCG
                                     _ AGT
GAM387  HUNK     3'  CAAACTCATGTTTTCA      27442      A
                                TGAA GACATGAGTTTG
                                |||| ||||||||||||
                                ACTT TTGTACTCAAAC
                                  _
GAM387  KIF3C    3'  CCAACATAGCTCATGCCCTTCA 9599       AGA       T   A
                                TGAA   CATGAGTT GTG TGG
                                ||||   |||||||| ||| |||
                                ACTT   GTACTCGA TAC ACC
                                  CCC       _  A
GAM387  PAG      3'  CCCAGAACTCATTCCTTCA   37402      A  C       GTGAT
                                TGAA GA ATGAGTTT    GG
                                |||| || ||||||||    ||
                                ACTT CT TACTCAAG    CC
                                  C  _       AC___
GAM387  RGL      3'  CCATCACACTCTTCCTTC    30731     A  CAT    TT
                                GAA GA   GAGT  GTGATGG
                                ||| ||   ||||  |||||||
                                CTT CT   CTCA  CACTACC
                                  C  T__   __
GAM387  SNX5     3'  GCCATCACCTGGCCCATGTC   27035       A   T_
                                GACATG GTT  GTGATGGC
                                |||||| |||  ||||||||
                                CTGTAC CGG  CACTACCG
                                    C   TC
GAM387  FLJ10738 3'  CACAAACTCCATCTCCCA    36528    AA   CAT
                                TG  AGA   GAGTTTGTG
                                ||  |||   |||||||||
                                AC  TCT   CTCAAACAC
                                 CC   AC_
GAM387  HABP2    3'  CCATCACATCTTTATTCCTCA  14695     AA  C    TT
                                TGA  GA ATGAG  TGTGATGG
                                |||  || |||||  ||||||||
                                ACT  CT TATTT  ACACTACC
                                  C_  _    CT
GAM387  HIF1AN   3'  GCCATCATTCACATCTATTCA  61975      _   CA   GTTT
                                TGAA AGA  TGA    GTGATGGC
                                |||| |||  |||    ||||||||
                                ACTT TCT  ACT    TACTACCG
                                  A   AC   _____
GAM387  KIAA1937 5'  CCATCACATATCCCCTTCCA   73696    A   ACAT  GTT
                                TG AAG    GA   TGTGATGG
                                || |||    ||   ||||||||
                                AC TTC    CT   ACACTACC
                                 C   CC__  AT_
GAM387  TRIM2    3'  GCCATCATATCATATCCTATCA 30942     AA_  C    GTT
                                TGA   GA ATGA   TGTGATGGC
                                |||   || ||||   |||||||||
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                                ACT   CT TACT   ATACTACCG
                                  ATC  A   ___
GAM387   LOC120973 5'  CATCACCAATCTTTCA      75553        CA  AGTTT
                                TGAAAGA  TG    GTGATG
                                |||||||  ||    ||||||
                                ACTTTCT  AC    CACTAC
                                   A_  _____
GAM387   LOC122830 3'  CCACACAGTACTCAGCCTTTCA 74164       ACA    _    A
                                TGAAAG   TGAGT TTGTG TGG
                                ||||||   ||||| ||||| |||
                                ACTTTC   ACTCA GACAC ACC
                                   CG_    T    _
GAM387   LOC146337 3'  GCCATCACCCCATGCCGTC    83661    AAGA    AGTTT
                                GA    CATG    GTGATGGC
                                ||    ||||    ||||||||
                                CT    GTAC    CACTACCG
                                 GCC_    CC___
GAM387   LOC149566 3'  CCATCACAACCCTCTTTCA    84487        CATGAGT
                                TGAAAGA      TTGTGATGG
                                |||||||      |||||||||
                                ACTTTCT      AACACTACC
                                   CCC____
GAM387   LOC151405 5'  CCATCACCAAACATCTTATC   85335    CAT  _    _
                                GA   GA GTTTG TGATGG
                                ||   || ||||| ||||||
                                CT   CT CAAAC ACTACC
                                 ATT  A    C
GAM387   LOC197335 5'  GCCACCTATGACCTCGTGTC   87976         T TG  A_
                                GACATGAG T  TG  TGGC
                                |||||||| |  ||  ||||
                                CTGTGCTC A  AT  ACCG
                                     C GT  CC
GAM387   LOC253272 5'  CCATCACAGAATATCTTT    95360       CATGAG
                                AAAGA     TTTGTGATGG
                                |||||     ||||||||||
                                TTTCT     AGACACTACC
                                   ATA___
GAM387   LOC254440 3'  GCCATCACAAATGGGTCCTTTC 97070        _  ATGA
            A                    TGAAAG AC    GTTTGTGATGGC
                                ||||||  ||    ||||||||||||
                                ACTTTC TG    TAAACACTACCG
                                   C  GG__
GAM387   LOC255736 5'  GCTGGTAAAATTCACGTCTTTC 95334         A      GTGA
            A                    TGAAAGAC TGAGTTT    TGGC
                                |||||||| |||||||    ||||
                                ACTTTCTG ACTTAAA    GTCG
                                     C      ATG_
GAM387   LOC57019  3'  CCACCCTCTTGTCTTTCA    39723         T   TTTGTGA
                                TGAAAGACA GAG      TGG
                                ||||||||| |||      |||
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                                ACTTTCTGT CTC      ACC
                                     T  CC_____
GAM388  FST      3'  CATAAAAATGCAACGCTGTAAT 20956        _ C   TCA
            A                    TATTACAG GT TGT   TTTTATG
                                 |||||||| || |||   |||||||
                                 ATAATGTC CA ACG   AAAATAC
                                     G  _   TA_
GAM388  FLJ11539 3'  TGAACAAAACTGTAATA     45381        GTC
                                 TATTACAG   TGTTCA
                                 ||||||||   ||||||
                                 ATAATGTC   ACAAGT
                                     AAA
GAM388  FLJ11753 3'  CATAAAATGAACACTGAC    45079     __
                                 GTC  TGTTCATTTTATG
                                 |||  |||||||||||||
                                 CAG  ACAAGTAAAATAC
                                   TC
GAM388  KIAA1573 3'  GATGAACAGACCTGCCATA    62687     TA
                                 TAT  CAGGTCTGTTCATT
                                 |||  ||||||||||||||
                                 ATA  GTCCAGACAAGTAG
                                   CC
GAM388  TLK2     3'  CATAAAGTGAAACCCGTA     78198     A   CTG
                                 TAC GGT   TTCATTTTATG
                                 ||| |||   ||||||||||
                                 ATG CCA   AAGTGAAATAC
                                   C  ___
GAM388  TLK2     3'  CATAAAGTGAAACCCGTA     22449     A   CTG
                                 TAC GGT   TTCATTTTATG
                                 ||| |||   ||||||||||
                                 ATG CCA   AAGTGAAATAC
                                   C  ___
GAM388  LOC150208 3'  CATAAAACTCTTTTGACCTGTA 84915          TGTTCA_
            A                    TTACAGGTC      TTTTATG
                                 |||||||||      |||||||
                                 AATGTCCAG      AAAATAC
                                      TTTTCTC
GAM389  ADRA1A   3'  GCACAAATCCAACATG      52784      AAGCC  A
                                 CATGT    TG ATTTGTGC
                                 |||||    || ||||||||
                                 GTACA    AC TAAACACG
                                    _____  C
GAM389  AEGL1    5'  GCACAAATACACTACAT      6679       AGCC  A
                                 ATGTA    TG ATTTGTGC
                                 |||||    || ||||||||
                                 TACAT    AC TAAACACG
                                    C___  A
GAM389  CDH2     3'  GCACAAATGTTTTACAT      8377        CCTGA
                                 ATGTAAG    ATTTGTGC
                                 |||||||    ||||||||
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                                TACATTT    TAAACACG
                                   TG___
GAM389  CHRNE   3'  GCCCTCAGGCCCACAGGT   3586     A  AA    ATTTGT
                                ACC TGT  GCCTGA    GC
                                ||| |||  ||||||     ||
                                TGG ACA  CGGACT    CG
                                  _  CC     CC____
GAM389  COL4A3  3'  GGCCATGGCTCACATGGT   3622       A   TGAATT  T
                                ACCATGT AGCC    TG GCC
                                ||||||| ||||     || |||
                                TGGTACA TCGG    AC CGG
                                   C   T_____ _
GAM389  COL4A3  3'  GGCCATGGCTCACATGGT   48557      A   TGAATT  T
                                ACCATGT AGCC    TG GCC
                                ||||||| ||||     || |||
                                TGGTACA TCGG    AC CGG
                                   C   T_____ _
GAM389  COL4A3  3'  GGCCATGGCTCACATGGT   48568      A   TGAATT  T
                                ACCATGT AGCC    TG GCC
                                ||||||| ||||     || |||
                                TGGTACA TCGG    AC CGG
                                   C   T_____ _
GAM389  CYP3A4  3'  ACAAGCCTGGCCTACATGGT  33923       A  TGAA
                                ACCATGTA GCC   TTTGT
                                |||||||| |||   |||||
                                TGGTACAT CGG   GAACA
                                    C  TCC_
GAM389  HIVEP3  5'  GGCACAAACCCAGCAGCCTCA  44439   TAA __  AA
                                TG  GC  CTG  TTTGTGCC
                                ||  ||  |||  ||||||||
                                AC  CG  GAC  AAACACGG
                                 TC_  AC  CC
GAM389  RECK    3'  GCAACAGGCTCACTGGT    40869     T  A    AAT
                                ACCA GT AGCCTG  TTGT
                                |||| || ||||||  ||||
                                TGGT CA TCGGAC  AACG
                                  _  C     ___
GAM389  TNFSF8  3'  GCACAAATTTAATACA     6966      AGCC
                                TGTA   TGAATTTGTGC
                                ||||   ||||||||||
                                ACAT   ATTTAAACACG
                                  A___
GAM389  ADAR3   3'  CACAAATTCAGAACGTG    38018      AAGC
                                CATGT   CTGAATTTGTG
                                |||||   ||||||||||
                                GTGCA   GACTTAAACAC
                                  A___
GAM389  BIVM    3'  CACAAATTCACTTA       34667     CC
                                TAAG  TGAATTTGTG
                                ||||  ||||||||||
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                                ATTC  ACTTAAACAC
                                  __
GAM389  C20orf160 3'  GCAGTTACAGGATTACATGGT  54648         G    AAT
                                ACCATGTAA CCTG   TTGT
                                ||||||||| ||||   ||||
                                TGGTACATT GGAC   GACG
                                     A    ATT
GAM389  EPHA7    3'  CACAAATTTGCTGCACA     15433     A_   CT
                                TGT  AGC  GAATTTGTG
                                |||  |||  |||||||||
                                ACA  TCG  TTTAAACAC
                                  CG  __
GAM389  FLJ12783  3'  AGTTCAGGCTCACTG       48675     T  A
                                CA GT AGCCTGAATT
                                || || ||||||||||
                                GT CA TCGGACTTGA
                                 _  C
GAM389  HSC3     3'  CACAGGTTCAGACTACA     59067      A C
                                TGTA G CTGAATTTGTG
                                |||| | ||||||||||||
                                ACAT C GACTTGGACAC
                                  _ A
GAM389  KIAA0316  3'  GCACAAATGCTCTTCACAGTGG 69674      _  _   CCTGA
           T                     ACCA TGT AAG     ATTTGTGC
                                |||| ||| |||     ||||||||
                                TGGT ACA TTC     TAAACACG
                                  G   C   TCG__
GAM389  KIAA0453  3'  GCACAAGTAGCTACATAGT    69047    C     A  CTGA
                                AC ATGTA GC    ATTTGTGC
                                || ||||| ||    ||||||||
                                TG TACAT CG    TGAACACG
                                 A     _  A___
GAM389  KIAA1423  3'  AATTCAAGTTTACATG       61719          C
                                CATGTAAGC TGAATT
                                ||||||||| ||||||
                                GTACATTTG ACTTAA
                                     A
GAM389  KIAA1691  3'  GCACAAATGCTGTCCATGG    92556       TA_   CTGA
                                CCATG   AGC    ATTTGTGC
                                |||||   |||    ||||||||
                                GGTAC   TCG    TAAACACG
                                   CTG   _____
GAM389  PPP1R3B   3'  GCCAGGTTCAGATTACA     44820       GC        T
                                TGTAA  CTGAATTTG GC
                                |||||  ||||||||| ||
                                ACATT  GACTTGGAC CG
                                  A_        _
GAM389  SFXN2     3'  GCAGCAGAGTTACATGGT     73946          GC   AATTTG
                                ACCATGTAA  CTG     TGC
                                |||||||||  |||     |||
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                                TGGTACATT  GAC     ACG
                                    GA   G_____
GAM389  TBC1D2   5'  TAAATTCAGACCTACTGGT   37321     T   AGC
                                ACCA GTA   CTGAATTTG
                                |||| |||   |||||||||
                                TGGT CAT   GACTTAAAT
                                  _   CCA
GAM389  ZNF347   3'  GGCTTTATTCAGGCCTCACA  50848     AA_      TTGT
                                TGT   GCCTGAAT   GCC
                                |||   ||||||||   |||
                                ACA   CGGACTTA   CGG
                                  CTC       TTT_
GAM389  LOC134147 3'  CACAAATTCAGTAGGACGT   57158     AAGC
                                ATGT    CTGAATTTGTG
                                ||||    ||||||||||
                                TGCA    GACTTAAACAC
                                  GGAT
GAM389  LOC151195 5'  GCACAAATTTATTTACA     80169       CC
                                TGTAAG  TGAATTTGTGC
                                ||||||  ||||||||||
                                ACATTT  ATTTAAACACG
                                  __
GAM389  LOC152860 3'  AATTCCAGCTTACATGG     80695         CT
                                CCATGTAAGC  GAATT
                                |||||||||  |||||
                                GGTACATTCG  CTTAA
                                    AC
GAM389  LOC200382 3'  ACAGGGGCCAGACTTACATG  88801        C   AA_
                                CATGTAAG CTG   TTTGT
                                |||||||| |||   |||||
                                GTACATTC GAC   GGACA
                                    A   CGG
GAM389  LOC93622  3'  ACAGTCATTCCAGGCTTAGATG 56929     G      _   __
                                CAT TAAGCCTG AAT  TTGT
                                ||| |||||||| |||  ||||
                                GTA ATTCGGAC TTA  GACA
                                  G       C   CT
GAM390  A1BG     3'  CACAGCAACCTCTACCTC    55411           A
                                GAGGTAGAGGTTGC GTG
                                |||||||||||||| |||
                                CTCCATCTCCAACG CAC
                                      A
GAM390  ACVR1    5'  CACTGCAGCCTCCACCTC    6604       A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTCCGACGTCAC
                                  C
GAM390  AHR      3'  TGGCTCACTGCAACCTCTACCT 7885
            C                    GAGGTAGAGGTTGCAGTGAGTCA
                                ||||||||||||||||||||||||
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                                CTCCATCTCCAACGTCACTCGGT

GAM390  AIM1     3'  CACTGCAGCCTCTACCTC    91818
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCATCTCCGACGTCAC

GAM390  ALDH1B1  3'  CACTGCAACCTCCGCCTC    5491      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  ALDH3B1  3'  GACTCACCCCCTGCC      91526      A  TTGCA
                                GGTAG GG    GTGAGTC
                                ||||| ||    |||||||
                                CCGTC CC    CACTCAG
                                  C  _____
GAM390  AP3B2    5'  CGCCGCAACCTCCTCCTC    16188     TA      A
                                GAGG  GAGGTTGC GTG
                                ||||  |||||||| |||
                                CTCC  CTCCAACG CGC
                                  TC       C
GAM390  APPBP2   3'  CACTGCAACCTCCGCCTC    21074     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  AQP6     3'  GGCTCACTGCAACCTCTACCTC 7958
                                GAGGTAGAGGTTGCAGTGAGTC
                                ||||||||||||||||||||||
                                CTCCATCTCCAACGTCACTCGG

GAM390  AQP6     3'  GGCTCACTGCAACCTCTACCTC 53938
                                GAGGTAGAGGTTGCAGTGAGTC
                                ||||||||||||||||||||||
                                CTCCATCTCCAACGTCACTCGG

GAM390  ARCN1    3'  CACTGCAACCTCCGCCTC    7972      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  ATP8B2   3'  GCTCACTGCAACCTCCACCTC  65227      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                  C
GAM390  BRIP1    3'  CACTGCAACCTTCACCTC    49397      AG
                                GAGGT  AGGTTGCAGTG
                                |||||  ||||||||||
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                                CTCCA  TCCAACGTCAC
                                   CT
GAM390  C7      3'  CTGCAACCTCCGCCTC     5162      TA
                                GAGG  GAGGTTGCAG
                                ||||  ||||||||||
                                CTCC  CTCCAACGTC
                                   GC
GAM390  CAMLG    3'  CACCGCAACCTCCACCTT    8233       A      A
                                GAGGT GAGGTTGC GTG
                                ||||| |||||||| |||
                                TTCCA CTCCAACG CAC
                                   C       C
GAM390  CCNF     3'  ACTCACTGTAACCTCCGCCTC  8312       TA
                                GAGG  GAGGTTGCAGTGAGT
                                ||||  ||||||||||||||
                                CTCC  CTCCAATGTCACTCA
                                   GC
GAM390  CDH17    3'  CACTGCAACCTCCGCCTC    14501     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  CIAS1    5'  CACTGCAGCCTCCACCTC    16899      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTCCGACGTCAC
                                   C
GAM390  CLECSF12 3'  GACTCACTGCAGCTATCTC   76690      AGA
                                GAGGT   GGTTGCAGTGAGTC
                                |||||   ||||||||||||||
                                CTCTA   TCGACGTCACTCAG
                                   ___
GAM390  COX15    3'  ACTCTGCAACCTCCACTTC   54308      A       GT
                                GAGGT GAGGTTGCA  GAGT
                                ||||| |||||||||  ||||
                                CTTCA CTCCAACGT  CTCA
                                   C       __
GAM390  CRHR1    3'  TGACTCACCACGATGACGCCTC 15215      AGAG    CA
                                GAGGT   GTTG  GTGAGTCA
                                |||||   ||||  ||||||||
                                CTCCG   TAGC  CACTCAGT
                                   CAG_   AC
GAM390  CRTAP    3'  CACTGCAACCTCCGCCTC    21030     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  CSNK2A2  5'  GCTCACTGCAACCTCCACCTC  8564       A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| |||||||||||||||
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                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390  CXCL16   3' GGCTCACTGCAACCCCCATCTC 41923      AGA
                                GAGGT  GGTTGCAGTGAGTC
                                |||||  ||||||||||||||
                                CTCTA  CCAACGTCACTCGG
                                   CCC
GAM390  CYLN2    3' CTGCAGCCTCCACCTC     12633      A
                                GAGGT GAGGTTGCAG
                                ||||| ||||||||||
                                CTCCA CTCCGACGTC
                                   C
GAM390  CYP1A2   3' GCTCACTGCAACCTCCACCTC  5693       A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| |||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390  CYP1A2   3' CACTGCAACCTCTGCCTC    5680
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  CYP1A2   3' CACTGCAACCTCTGCCTC    69099
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  CYP1A2   3' GCTCACTGCAACCTCCACCTC  69113      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| |||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390  CYP2B6   3' GGCTCACTGCAACCTCCACC   5738     A
                                GGT GAGGTTGCAGTGAGTC
                                ||| ||||||||||||||
                                CCA CTCCAACGTCACTCGG
                                  C
GAM390  CYP4F3   3' CATTGCAACCTCCGCCTC    6112      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTTAC
                                   GC
GAM390  CYP8B1   3' CACTACAACCTCTGCCTC    15258          C
                                GAGGTAGAGGTTG AGTG
                                |||||||||||| ||||
                                CTCCGTCTCCAAC TCAC
                                        A
GAM390  CYP8B1   3' CACTGCAACCTCTGCCTC    15260
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
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                                CTCCGTCTCCAACGTCAC

GAM390  DFFB    3'  CACTGCAACCTCCGCCTC    87378      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  DISC1   3'  GGCTCACTGCAACCTCTACCTC 37886
                                GAGGTAGAGGTTGCAGTGAGTC
                                ||||||||||||||||||||||
                                CTCCATCTCCAACGTCACTCGG

GAM390  DSCR3   3'  GCTCACTGCAACCTCCACCTC  20185       A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390  EHD2    3'  GCTCACTGCAACCTCCACCTC  27496       A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390  EPB72   3'  CACTGCAACCTCCGCCTC    14600      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  F2RL2   3'  CATTGCAACCTCTGCCTC    14620
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTTAC

GAM390  FANCF   3'  CAGTGCAACCTCTGCCTC    42671             G
                                GAGGTAGAGGTTGCA TG
                                |||||||||||||| ||
                                CTCCGTCTCCAACGT AC
                                         G
GAM390  FBXL11  3'  TGATAGCACAACCTCTTCC    24576    T      CA  GA
                                GG AGAGGTTG  GT  GTCA
                                || ||||||||  ||  ||||
                                CC TCTCCAAC  CG  TAGT
                                 T       A_  A_
GAM390  FCAR    3'  GACTCACTGCAACCTTCGCCTC 55797      TA
                                GAGG  GAGGTTGCAGTGAGTC
                                ||||  ||||||||||||||||
                                CTCC  TTCCAACGTCACTCAG
                                  GC
GAM390  FCAR    3'  GACTCACTGCAACCTTCGCCTC 55813      TA
                                GAGG  GAGGTTGCAGTGAGTC
                                ||||  ||||||||||||||||
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                                CTCC  TTCCAACGTCACTCAG
                                  GC
GAM390   FEZ1     3'  TGGCTCACTGCAACCTCCACCT 42582       A
                C                  GAGGT GAGGTTGCAGTGAGTCA
                                   ||||| ||||||||||||||||
                                   CTCCA CTCCAACGTCACTCGGT
                                     C
GAM390   FGF5     3'  GGCTCACTGCAACCTCCAACTC 52492     GTA
                                   GAG   GAGGTTGCAGTGAGTC
                                   |||   ||||||||||||||||
                                   CTC   CTCCAACGTCACTCGG
                                     AAC
GAM390   FGF5     3'  GGCTCACTGCAACCTCCAACTC 15546     GTA
                                   GAG   GAGGTTGCAGTGAGTC
                                   |||   ||||||||||||||||
                                   CTC   CTCCAACGTCACTCGG
                                     AAC
GAM390   FHL2     5'  GCTCACTGCAAGCTCTACCTC  7565          G
                                   GAGGTAGAG TTGCAGTGAGT
                                   ||||||||| ||||||||||
                                   CTCCATCTC AACGTCACTCG
                                        G
GAM390   FZD4     3'  CACTGCAACCTCTGCCTC    24129
                                   GAGGTAGAGGTTGCAGTG
                                   ||||||||||||||||||
                                   CTCCGTCTCCAACGTCAC

GAM390   G6PC     3'  CACTGCAACCTCTTCCTC    3822       T
                                   GAGG AGAGGTTGCAGTG
                                   |||| ||||||||||||
                                   CTCC TCTCCAACGTCAC
                                     T
GAM390   GHR      3'  TGACTCACTGCAATCTCCACCT 3891        A
                C                  GAGGT GAGGTTGCAGTGAGTCA
                                   ||||| ||||||||||||||||
                                   CTCCA CTCTAACGTCACTCAGT
                                     C
GAM390   GM2A     3'  CACTGCAACCTCCGCCTC    67774      TA
                                   GAGG  GAGGTTGCAGTG
                                   ||||  ||||||||||||
                                   CTCC  CTCCAACGTCAC
                                     GC
GAM390   GNE      3'  CAATGCAACCTCTGCC      18476           G
                                   GGTAGAGGTTGCA TG
                                   |||||||||||| ||
                                   CCGTCTCCAACGT AC
                                            A
GAM390   GPR4     3'  CACTGCAGCCTCCACCTC    59901       A
                                   GAGGT GAGGTTGCAGTG
                                   ||||| ||||||||||||
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                                CTCCA CTCCGACGTCAC
                                   C
GAM390  GPR56    5'  CATCGTAACCTCCACCTC    19066      A      A
                                GAGGT GAGGTTGC GTG
                                ||||| |||||||| |||
                                CTCCA CTCCAATG TAC
                                   C       C
GAM390  GPR81    3'  CACTGCAACCTCTGCCTC    50754
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  GRAF     3'  CACTGCAACCTCCGCCTC    30551      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  HTR1E    5'  CATTGCAACCTCCGCCTC    6012       TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTTAC
                                   GC
GAM390  IL11     3'  TCACTGCAAGCTCCACCTC    5334       A   G
                                GAGGT GAG TTGCAGTGA
                                ||||| ||| |||||||||
                                CTCCA CTC AACGTCACT
                                   C   G
GAM390  INHBB    5'  TGACCCGCGACCTCCGCC     9344     TA       AGT A
                                GG  GAGGTTGC   G GTCA
                                ||  ||||||||   | ||||
                                CC  CTCCAGCG   C CAGT
                                 GC       ___ C
GAM390  INMT     3'  GACTCACTGCAAGCTCCGCCTC 22271      TA   G
                                GAGG  GAG TTGCAGTGAGTC
                                ||||  ||| ||||||||||||
                                CTCC  CTC AACGTCACTCAG
                                   GC   G
GAM390  ITGAM    3'  CACTGCAACCTCCGCCTC    71836      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  KMO      3'  CACTGCAACCTCTGCCTC    13447
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  LANCL1   3'  ACTCACTGCATGACCCT     20206    A  __
                                AG GGT  TGCAGTGAGT
                                || |||  ||||||||||
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                                TC CCA  ACGTCACTCA
                                 _  GT
GAM390  LILRA3   3'  CACTGCAACCTCCGCCTC    95308      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  LNK      3'  CACTGCAACCTCCACCTT    18459      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TTCCA CTCCAACGTCAC
                                  C
GAM390  LSS      3'  CTCAACCTCTATCTC       9817       C
                                GAGGTAGAGGTTG AG
                                |||||||||||| ||
                                CTCTATCTCCAAC TC

                                                   _
GAM390  LYZ      3'  GGCTCACTGCAACCTCCACCTC 4106       A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                  C
GAM390  MAK      3'  TACTGCAACCTCCACCTC    19767      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTCCAACGTCAT
                                  C
GAM390  MEF2A    5'  CACTGCAACCTCCGCCTC    18781      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  MEFV     3'  CACTGCAACCTCCGCCTC    4128       TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  MEFV     3'  GCTCACTGCAACCTCCACCTC  4142       A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                  C
GAM390  MHC2TA   3'  CACTGCAACCTCCGCCTC    4166       TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  MICB     3'  CACTGCAACCTCTGCCTC    19822
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
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                                CTCCGTCTCCAACGTCAC

GAM390  MPL      3'  CACTGCAACCTCTGCCTC    18133
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  MPL      3'  GCTCACTGCAACCTCCACCTC  18145       A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390  MRPL49   3'  CACTGCAACTTCCACCTC    69567       A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTTCAACGTCAC
                                   C
GAM390  MYCL2    3'  CACTGCAACCTCTGCCTC    18177
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  NDRG3    3'  CACTGCAACCTCTGCC       49293
                                GGTAGAGGTTGCAGTG
                                ||||||||||||||||
                                CCGTCTCCAACGTCAC

GAM390  NQO1     3'  CACTGCAACCTCTGCCTC    6154
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  PCDHB11  3'  CACTGCAACCTCTGCCTC    38411
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  PCDHB16  3'  CACTGCAACCTCTGCCTC    40551
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  PCDHB9   3'  CACTGCAACCTCCGCCTC    38936       TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  PDCL     3'  GGCTCACTGCAACCTCCACCTC 18216       A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
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                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  PDE6B    3'  GCTCACTGCAACCTCCACCTC  4283       A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390  PER2     3'  CACTGCAACCTCTGCCTC    43029
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  PIGR     3'  CACTGCAACCTCCGCCTC    72592      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  PIK3C2B  3'  GACTCACTGCAAAATCTGCCTC 10567        GG
                                GAGGTAGA  TTGCAGTGAGTC
                                ||||||||  ||||||||||||
                                CTCCGTCT  AACGTCACTCAG
                                    AA
GAM390  PON1     3'  CACTGCAACTTCTACCTC    4802
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCATCTTCAACGTCAC

GAM390  PRKWNK3  3'  TGCTGCAACCTCCCCCTC    61559      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCGT
                                   CC
GAM390  PSMB2    3'  CACTGCAACCTCCGCCTC    10950      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  RAB36    3'  CAGTGCAACCTCTGCCTC    16951            G
                                GAGGTAGAGGTTGCA TG
                                ||||||||||||||| ||
                                CTCCGTCTCCAACGT AC
                                        G
GAM390  RHD      3'  TGGCTCACTGCAACCTCTACCT 32322
              C                  GAGGTAGAGGTTGCAGTGAGTCA
                                ||||||||||||||||||||||||
                                CTCCATCTCCAACGTCACTCGGT

GAM390  RHD      3'  CACTGCAACCTCCGCCTC    32607      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  RHD     3'  TGGCTCACTGCAACCTCTACCT 32631
              C                  GAGGTAGAGGTTGCAGTGAGTCA
                                 ||||||||||||||||||||||
                                 CTCCATCTCCAACGTCACTCGGT

GAM390  RHD     3'  CACTGCAACCTCCGCCTC    32298     TA
                                 GAGG  GAGGTTGCAGTG
                                 ||||  ||||||||||||
                                 CTCC  CTCCAACGTCAC
                                   GC
GAM390  RPH3AL  3'  GGCTCACTGCAACCTCCACCTC 22751      A
                                 GAGGT GAGGTTGCAGTGAGTC
                                 ||||| ||||||||||||||||
                                 CTCCA CTCCAACGTCACTCGG
                                    C
GAM390  SAS     3'  CACCGCAACCTCTGCCTC    19950          A
                                 GAGGTAGAGGTTGC GTG
                                 |||||||||||||| |||
                                 CTCCGTCTCCAACG CAC
                                         C
GAM390  SEDL    3'  CACTGCAACCTCCGCCTC    27328     TA
                                 GAGG  GAGGTTGCAGTG
                                 ||||  ||||||||||||
                                 CTCC  CTCCAACGTCAC
                                   GC
GAM390  SEDL    3'  TGGCTCACTGCAACCTCCACCT 27366      A
              C                  GAGGT GAGGTTGCAGTGAGTCA
                                 ||||| ||||||||||||||||
                                 CTCCA CTCCAACGTCACTCGGT
                                    C
GAM390  SEDL    3'  TGGCTCACTGCAACCTCCACCT 27367      A
              C                  GAGGT GAGGTTGCAGTGAGTCA
                                 ||||| ||||||||||||||||
                                 CTCCA CTCCAACGTCACTCGGT
                                    C
GAM390  SEPN1   3'  TGGCTCACTGCAACCTCCACCT 66383      A
              C                  GAGGT GAGGTTGCAGTGAGTCA
                                 ||||| ||||||||||||||||
                                 CTCCA CTCCAACGTCACTCGGT
                                    C
GAM390  SERPINB9 3' CACTGCAACCTCCTCCTC    14749     TA
                                 GAGG  GAGGTTGCAGTG
                                 ||||  ||||||||||||
                                 CTCC  CTCCAACGTCAC
                                   TC
GAM390  SHOX    3'  GACTCACTGCAACCTCCGCCTC 22538      TA
                                 GAGG  GAGGTTGCAGTGAGTC
                                 ||||  ||||||||||||||||
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                                CTCC  CTCCAACGTCACTCAG
                                  GC
GAM390  SIL     3'  CACTGCAACCTCTGCCTC    11686
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  SLA2    3'  GCTCACTGCAACCTCCATCTC  49899      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||
                                CTCTA CTCCAACGTCACTCG
                                  C
GAM390  SLC14A2  5'  TGGCTCACTGCAACCTCCACCT 23143      A
          C                      GAGGT GAGGTTGCAGTGAGTCA
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGGT
                                  C
GAM390  SLC15A1  3'  CACTGCAACCTCCGCCTC    17398     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  SMAC    5'  CACTGCAACCTCTGCCTC    57204
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  SNAP23  3'  CACTGCAACCTCCGCCTC    13806     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  SNAP23  3'  CACTGCAACCTCCGCCTC    55459     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  SNX15   3'  GGCTCACTGCAACCTCCACCTC 73747      A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                  C
GAM390  SPN     3'  CACTGCAACCTCTGCCTC    11917
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  SS18    3'  CACTGCAACCTCCGCCTC    18883     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  STAU     5'  ACTGCAACCTCCACCTC     15994       A
                                GAGGT GAGGTTGCAGT
                                ||||| ||||||||||
                                CTCCA CTCCAACGTCA
                                   C
GAM390  STAU     5'  GGCTCACTGCAACCTCCACCTC 16007       A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  SULT2B1  5'  CACTGCAACCTCCGCCTC    16023      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  TAF4     3'  CGTTGCACCCCCACCTC     12091       AGA  T
                                GAGGT   GG TGCAGTG
                                |||||   || |||||||
                                CTCCA   CC ACGTTGC
                                   CC_  C
GAM390  TAPBP    3'  TACTGCAACCTCCGCCTC    12134      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAT
                                  GC
GAM390  TAT      3'  GGCTCACTGCAACCTCCACCTC 4473       A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  TBXA2R   3'  GCTCACTGCAACCTCCACCTC  6496       A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| |||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390  TBXA2R   3'  CACTGCAACCTCCGCCTC    6483       TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  TMC1     5'  CTGCAACCTCCGCCTC      56903      TA
                                GAGG  GAGGTTGCAG
                                ||||  ||||||||||
                                CTCC  CTCCAACGTC
                                  GC
GAM390  TNFRSF10B 3'  CAGTGCAACCTCCGCCTC    13867      TA       G
                                GAGG  GAGGTTGCA TG
                                ||||  ||||||||| ||
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                                CTCC  CTCCAACGT AC
                                  GC        G
GAM390  TPMT    3' CACTGCAACCTCTGCCTC    4534
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  TRIM9   5' CACTGCAACCTCCGCCTC    30755     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  TRPM6   3' CACTGCAACCTCTGCCTC    34535
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  TRPV1   3' CACTGCAACCTCTGCCTC    38073
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  TRPV1   3' CTGCAACCTCCGCCTC      38081     TA
                                GAGG  GAGGTTGCAG
                                ||||  |||||||||
                                CTCC  CTCCAACGTC
                                  GC
GAM390  TRPV1   3' CTGCAACCTCCGCCTC      54835     TA
                                GAGG  GAGGTTGCAG
                                ||||  |||||||||
                                CTCC  CTCCAACGTC
                                  GC
GAM390  TRPV1   3' CTGCAACCTCCGCCTC      54867     TA
                                GAGG  GAGGTTGCAG
                                ||||  |||||||||
                                CTCC  CTCCAACGTC
                                  GC
GAM390  TRPV1   3' CACTGCAACCTCTGCCTC    54859
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  TRPV1   3' CACTGCAACCTCTGCCTC    54792
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  TRPV1   3' CTGCAACCTCCGCCTC      54802     TA
                                GAGG  GAGGTTGCAG
                                ||||  |||||||||
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                                CTCC  CTCCAACGTC
                                  GC
GAM390  TRPV1    3'  CACTGCAACCTCTGCCTC    54827
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  TUFT1    3'  CACTGCAACCTCTGCCTC    39252
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  VENTX2   3'  CACTGCAACCTCCGCCTC    27108     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  VHL      3'  CACTGCAACCTCTGCCTC    5064
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  ZNF133   5'  ACTCACTGCAACCTCCACC    12829     A
                                GGT GAGGTTGCAGTGAGT
                                ||| ||||||||||||||
                                CCA CTCCAACGTCACTCA
                                  C
GAM390  ZNF264   3'  CACTGCAACCTCCGCCTC    12746     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  ZNF264   3'  CTGCAACCTCTGCCTC      12754
                                GAGGTAGAGGTTGCAG
                                ||||||||||||||||
                                CTCCGTCTCCAACGTC

GAM390  20D7-FC4 5'  CACTGCAGCCTCCACCTC    60896      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTCCGACGTCAC
                                  C
GAM390  ARHF     3'  TGGCTCACTGCAAGCTCCACCT 38751      A   G
          C                      GAGGT GAG TTGCAGTGAGTCA
                                ||||| ||| ||||||||||||
                                CTCCA CTC AACGTCACTCGGT
                                  C   G
GAM390  ARPP-19  3'  CACTGCAACCTCTGCCTC    21791
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
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                                CTCCGTCTCCAACGTCAC

GAM390  ASB16    5'  CACTGCAACCTCCGCCTC    69932      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  ASE-1    3'  CACTGCAACCTCCGCCTC    23946      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  ATP1B4   3'  GGCTCACTGCAACCTCCACCTC 23825       A
                                GAGGT GAGGTTGCAGTGAGTC
                                |||||  ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  BA108L7.2 3'  CACTGCAACCTCTGCCTC    48259
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  BAG5     3'  GCTCACTGCAACCTCCACCTC  16845       A
                                GAGGT GAGGTTGCAGTGAGT
                                |||||  |||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390  BNIP-S   3'  CACTGCAACCTCCGCCTC    56257      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  BTN3A1   3'  CTGCAACCTCCACCTC      22919       A
                                GAGGT GAGGTTGCAG
                                |||||  |||||||||
                                CTCCA CTCCAACGTC
                                   C
GAM390  C1orf24  3'  CACTGCAACCTCCGCCTC    53710      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  C1QTNF6  3'  CACTGCAACCTCTGCCTC    49139
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  C20orf167 3'  TGACTCACTGCACAGCACC   53664     AGAG  T
                                GGT   GT GCAGTGAGTCA
                                |||   || ||||||||||
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                                CCA    CA CGTCACTCAGT
                                  CGA_ _
GAM390  C21orf25  3'  TACTGCAACCTCCACCTC    63556       A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTCCAACGTCAT
                                   C
GAM390  C21orf93  3'  TGACCCTCACCTCTCACCTC   59090       _     T C  TGA
                                GAGGT AGAGGT G AG   GTCA
                                ||||| |||||| | ||   ||||
                                CTCCA TCTCCA C TC   CAGT
                                   C      _ _  C__
GAM390  C3F       3'  GCTCACCGCAACCTCCACCTC  19293       A       A
                                GAGGT GAGGTTGC GTGAGT
                                ||||| |||||||| ||||||
                                CTCCA CTCCAACG CACTCG
                                   C       C
GAM390  C9orf9    3'  CACTGCAACCTCCGCCTC    38506      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  C9orf9    3'  TGGCTCACTGCAACCTCCACCT 38532       A
           C                     GAGGT GAGGTTGCAGTGAGTCA
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGGT
                                   C
GAM390  CEACAM8   3'  ACTCACTGCAAGCTCCGCCTC  8420       TA   G
                                GAGG  GAG TTGCAGTGAGT
                                ||||  ||| ||||||||||
                                CTCC  CTC AACGTCACTCA
                                  GC   G
GAM390  CENPH     3'  CACTGCAACCTCTGCCTC    43271
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  CHRAC1    3'  CACTGCAACCTCCGCCTC    33867      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  CLSTN2    3'  ACTCACTGTGCGTCTCCTC   42120      T   G  T
                                GAGG AGA GT GCAGTGAGT
                                |||| ||| || |||||||||
                                CTCC TCT CG TGTCACTCA
                                   _   G  _
GAM390  CPSF2     3'  CACCGCAACCTCTGCCTC    61574            A
                                GAGGTAGAGGTTGC GTG
                                |||||||||||||| |||
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                                  CTCCGTCTCCAACG CAC
                                            C
GAM390  CYP4F8   3'  GACCCACCCACCTACCTT   23410       A_  TTGCA  A
                                  GAGGTAG  GG    GTG GTC
                                  |||||||  ||    ||| |||
                                  TTCCATC  CC    CAC CAG
                                     CA  _____   C
GAM390  DBR1     3'  CACCGCAACCTCCGCCTC   32528     TA      A
                                  GAGG  GAGGTTGC GTG
                                  ||||  |||||||| |||
                                  CTCC  CTCCAACG CAC
                                    GC       C
GAM390  DKFZp434A2417 3'  CACTGCAACTTCCACCTC   66097      A
                                  GAGGT GAGGTTGCAGTG
                                  ||||| ||||||||||||
                                  CTCCA CTTCAACGTCAC
                                     C
GAM390  DKFZP434C212 3'  TGGCTCACTGCAACCTCCACCT 68921      A
          C                        GAGGT GAGGTTGCAGTGAGTCA
                                  ||||| ||||||||||||||||||
                                  CTCCA CTCCAACGTCACTCGGT
                                     C
GAM390  DKFZp434E2220 5'  CACTGCAACCTCCGCCTC   34294     TA
                                  GAGG  GAGGTTGCAGTG
                                  ||||  ||||||||||||
                                  CTCC  CTCCAACGTCAC
                                    GC
GAM390  DKFZp547H025 3'  GCTCACTGCAACCTCCACCTC  39359      A
                                  GAGGT GAGGTTGCAGTGAGT
                                  ||||| |||||||||||||||
                                  CTCCA CTCCAACGTCACTCG
                                     C
GAM390  DKFZP564O0523 3'  GGCTCACTGCAACCTCCACCTC 49518      A
                                  GAGGT GAGGTTGCAGTGAGTC
                                  ||||| ||||||||||||||||
                                  CTCCA CTCCAACGTCACTCGG
                                     C
GAM390  DKFZp761J139 5'  CACTGCAACGTCCACCTC   50104      A  G
                                  GAGGT GA GTTGCAGTG
                                  ||||| || |||||||||
                                  CTCCA CT CAACGTCAC
                                     C  G
GAM390  DKFZp761N1114 3'  CACTGCAACCTCCGCCTC   79015     TA
                                  GAGG  GAGGTTGCAGTG
                                  ||||  ||||||||||||
                                  CTCC  CTCCAACGTCAC
                                    GC
GAM390  DKFZp762P2111 3'  CACTGCAACCTCCGCCTC   86353     TA
                                  GAGG  GAGGTTGCAGTG
                                  ||||  ||||||||||||
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                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  DRIL2    3'  CAATAAACCTCTACCTC    21323          GCAG
                                GAGGTAGAGGTT   TG
                                ||||||||||||  ||
                                CTCCATCTCCAA   AC
                                      ATA_
GAM390  DSCR6    3'  CACTGCAACCTCCACTTC    38543      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTTCA CTCCAACGTCAC
                                  C
GAM390  EREG     3'  GGCTCACTGCAACCTCACCTC  7507       A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                  _
GAM390  FBP17    3'  GGCTCACTACAACCTCCACCTC 72801      A     C
                                GAGGT GAGGTTG AGTGAGTC
                                ||||| ||||||| ||||||||
                                CTCCA CTCCAAC TCACTCGG
                                  C     A
GAM390  FER1L4   3'  ACTGCAACCTCCACCTC     47325      A
                                GAGGT GAGGTTGCAGT
                                ||||| ||||||||||
                                CTCCA CTCCAACGTCA
                                  C
GAM390  FER1L4   3'  ACTGCAACCTCCACCTC     47327      A
                                GAGGT GAGGTTGCAGT
                                ||||| ||||||||||
                                CTCCA CTCCAACGTCA
                                  C
GAM390  FLJ00024 5'  CACTGCAACCTCTGCCTC    63753
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  FLJ10232 3'  CACTGCAACCTCCGCCTC    35922      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  FLJ10346 5'  GGCTCACTGCAAGCTCCACCTC 36047      A   G
                                GAGGT GAG TTGCAGTGAGTC
                                ||||| ||| ||||||||||||
                                CTCCA CTC AACGTCACTCGG
                                  C   G
GAM390  FLJ10535 3'  CACTGCAACCTCTGCCTC    36235
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
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                                CTCCGTCTCCAACGTCAC

GAM390  FLJ10922 3' CACTGCAACCTCCGCCTC    36871     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  FLJ11004 5' GGCTCACTGCAACCTCTACCTC 36971
                                GAGGTAGAGGTTGCAGTGAGTC
                                ||||||||||||||||||||||
                                CTCCATCTCCAACGTCACTCGG

GAM390  FLJ11106 5' TCTTGCAACCTCACCTC     37056      A        T
                                GAGGT GAGGTTGCAG GA
                                ||||| |||||||||| ||
                                CTCCA CTCCAACGTT CT
                                  _       _
GAM390  FLJ12287 3' TGACCCCTTCACCTCTCCC    42320    T     T C  TGA
                                GG AGAGGT G AG   GTCA
                                || |||||| | ||   ||||
                                CC TCTCCA C TC   CAGT
                                 C     _ T  CC_
GAM390  FLJ12363 3' GCTCACTGCAACCTCCACCTC  49684      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390  FLJ12409 3' TGACTCACTGCAACCTCCGCCT 47053     TA
           C                     GAGG  GAGGTTGCAGTGAGTCA
                                ||||  ||||||||||||||||
                                CTCC  CTCCAACGTCACTCAGT
                                  GC
GAM390  FLJ12572 5' CACTGCAACCTCTGCCTC    43247
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  FLJ12649 3' CACTGCAACCTCCGCCTC    44777     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  FLJ12668 3' TGGTCACTGCAACCTCCATCTC 46529      A          G
                                GAGGT GAGGTTGCAGTGA TCA
                                ||||| |||||||||||| |||
                                CTCTA CTCCAACGTCACT GGT
                                  C         _
GAM390  FLJ12687 3' CACTGCAACCTCCGCCTC    46188     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  FLJ12747  3'  CACTGCAACCTCTGCCTC    49712
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  FLJ12973  3'  CACCGCAACCTCCGCCTC    46103      TA       A
                                GAGG  GAGGTTGC GTG
                                ||||  |||||||| |||
                                CTCC  CTCCAACG CAC
                                  GC       C
GAM390  FLJ13072  5'  CACTGCAACCTCTGCCTC    89804
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  FLJ13197  3'  GGCTCACTGCAACCTCTACCTC 44861
                                GAGGTAGAGGTTGCAGTGAGTC
                                |||||||||||||||||||||||
                                CTCCATCTCCAACGTCACTCGG

GAM390  FLJ14950  3'  GGCTCACTGCAACCTCCACCTC 51726       A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  FLJ14957  3'  CACTGCAACCTCTGCCTC    51742
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  FLJ20004  3'  CATTGCAACCTCCGCCTC    95291      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTTAC
                                  GC
GAM390  FLJ20034  3'  CACTGCAACCTCTGCCTC    34359
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  FLJ20045  3'  CACTGCAACCTCTGCCTC    34416
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  FLJ20079  3'  TGGCTCACCGCAACCTCCACCT 34505       A       A
             C                   GAGGT GAGGTTGC GTGAGTCA
                                ||||| |||||||| ||||||||
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                                CTCCA CTCCAACG CACTCGGT
                                   C       C
GAM390  FLJ20342 3' CACTGCAACCTCTGCCTC    34987
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  FLJ20344 3' CACTGCAACCTCCGCCTC    35006     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  FLJ20507 3' CACTGCAACCTCTGCCTC    35275
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  FLJ20507 3' CACTGCAACCTCTGCCTC    60210
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  FLJ20511 3' GGCTCACTGCAAGCTCCACCTC 35329      A   G
                                GAGGT GAG TTGCAGTGAGTC
                                ||||| ||| ||||||||||||
                                CTCCA CTC AACGTCACTCGG
                                   C   G
GAM390  FLJ20542 3' ACTCACCCAGCCGCCACCTC  49780      AGA    CA
                                GAGGT   GGTTG  GTGAGT
                                |||||   |||||  ||||||
                                CTCCA   CCGAC  CACTCA
                                   CCG    C_
GAM390  FLJ20813 3' CACTGCAACTCCACCTC     35679      A   G
                                GAGGT GAG TTGCAGTG
                                ||||| ||| ||||||||
                                CTCCA CTC AACGTCAC
                                   C   _
GAM390  FLJ21302 3' CACTGCAACCTCCGCCTC    43212     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  FLJ22002 3' CACTGCAACCTCCGCCTC    45768     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  FLJ22531 5' GGCTCACTGCAACCTCCACCTC 45033      A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
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                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  FLJ22794  3'  CACTGCAACTTCCACCTC    91603      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTTCAACGTCAC
                                   C
GAM390  FLJ22965  3'  CACTGCAACCTCCGCCTC    42049      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  FLJ22969  3'  CACTGCAACCTCTGCCTC    68646
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  FLJ23024  3'  CACTGCAACCTCTGCCTC    46266
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  FLJ23392  3'  CACTGCAACCTCTGCCTC    45527
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  FLJ23563  3'  CACTGCAACCTCTGCCTC    67592
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  FLJ31101  3'  CACTGCAACCTCTGCCTC    35706
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  FLJ32865  3'  CACTGCAACCTCTGCCTC    58168
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  GAL3ST-4  3'  CACTGCAACCTCTGCCTC    44934
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  GMPPB     5'  GGCTCACTGCAACCTCCACCTC 95749      A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
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                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  GNG4    3'  GCTCACTGCGACCTCCACCTC  15618      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||||
                                CTCCA CTCCAGCGTCACTCG
                                   C
GAM390  GP5     3'  GGCCCGCAACCCCTCCTC    15655     T  A    AGT A
                                GAGG AG GGTTGC   G GTC
                                |||| || ||||||   | |||
                                CTCC TC CCAACG   C CGG
                                  _  C     ___ C
GAM390  GREB1   3'  CACTGCAACCTCTGCCTC    27865
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  GRWD    3'  CACTGCAACCTCCGCCTC    48963     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  GTF2E1  3'  CACTGCAACCTCTGCCTC    18611
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  GTPBG3  3'  TGGCTCACTGCAACCTCCATCT 50914      A
            C                    GAGGT GAGGTTGCAGTGAGTCA
                                ||||| ||||||||||||||||||
                                CTCTA CTCCAACGTCACTCGGT
                                   C
GAM390  GTPBG3  3'  TACTGCAACCTCCACCTC    50907      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTCCAACGTCAT
                                   C
GAM390  H-plk   5'  GACTCACTGCAACCTCCACCTC 31809      A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCAG
                                   C
GAM390  HRH4    3'  CACTGCAACCTCTGCCTC    41248
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  HSPC065 3'  CGCTGCAACCTCCTCCTC    26293     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                CTCC  CTCCAACGTCGC
                                  TC
GAM390  HSPC065  3'  TGGCTCACTGCAACCTCCACCT 26331      A
          C                      GAGGT GAGGTTGCAGTGAGTCA
                                 ||||| ||||||||||||||||
                                 CTCCA CTCCAACGTCACTCGGT
                                   C
GAM390  ICK      3'  CTGCAACCTCTGCCTC      29928
                                 GAGGTAGAGGTTGCAG
                                 ||||||||||||||||
                                 CTCCGTCTCCAACGTC

GAM390  JAM1     5'  CACTGCAACCTCCTCCTC    57916      TA
                                 GAGG  GAGGTTGCAGTG
                                 ||||  ||||||||||||
                                 CTCC  CTCCAACGTCAC
                                   TC
GAM390  JM11     3'  CACTGCAACCTCTGCCTC    53252
                                 GAGGTAGAGGTTGCAGTG
                                 ||||||||||||||||||
                                 CTCCGTCTCCAACGTCAC

GAM390  KCNMB3L  5'  ACCCACGGTGGCCTCTCCTC  26957      T     TG A   A
                                 GAGG AGAGGT  C GTG GT
                                 |||| ||||||  | ||| ||
                                 CTCC TCTCCG  G CAC CA
                                   _     GT G   C
GAM390  KIAA0063 3'  GGCTCACTGCAACCTCCACCTC 29636      A
                                 GAGGT GAGGTTGCAGTGAGTC
                                 ||||| ||||||||||||||||
                                 CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  KIAA0391 3'  CACTGCAACCTCTGCCTC    27909
                                 GAGGTAGAGGTTGCAGTG
                                 ||||||||||||||||||
                                 CTCCGTCTCCAACGTCAC

GAM390  KIAA0426 3'  CACTGCAACCTCCGCCTC    28255      TA
                                 GAGG  GAGGTTGCAGTG
                                 ||||  ||||||||||||
                                 CTCC  CTCCAACGTCAC
                                   GC
GAM390  KIAA0459 3'  GGCTCACTGCAACCTCCACCTC 61002      A
                                 GAGGT GAGGTTGCAGTGAGTC
                                 ||||| ||||||||||||||||
                                 CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  KIAA0469 3'  CACTGCAGCCTCCACCTC    29323      A
                                 GAGGT GAGGTTGCAGTG
                                 ||||| ||||||||||||
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                                CTCCA CTCCGACGTCAC
                                   C
GAM390  KIAA0513 3' ACTCACTGCAACCTCCACCTC 28327      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCA
                                   C
GAM390  KIAA0513 5' CACTGCAGCCTCCACCTC    28343      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTCCGACGTCAC
                                   C
GAM390  KIAA0527 3' CACTGCAACCTCTGCCTC    95795
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  KIAA0544 3' CACTGCAACCTCCGCCTC    70896      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  KIAA0544 3' CACGCACCTCTACC        70894         T  A
                                GGTAGAGGT GC GTG
                                ||||||||| || |||
                                CCATCTCCA CG CAC
                                      _  _
GAM390  KIAA0557 3' TGGCTCACCACAACCTCCACCT 78012       A      CA
           C                     GAGGT GAGGTTG  GTGAGTCA
                                ||||| |||||||  ||||||||
                                CTCCA CTCCAAC  CACTCGGT
                                   C      AC
GAM390  KIAA0561 3' CACTGCAACCTCCGCCTC    65875      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  KIAA0562 3' CTGCAACCTCCGCCTC      28153      TA
                                GAGG  GAGGTTGCAG
                                ||||  ||||||||||
                                CTCC  CTCCAACGTC
                                   GC
GAM390  KIAA0563 5' CACTGCAACCTCTGCCTC    29184
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  KIAA0594 3' TACTGCAACCTCCGCCTC    64901      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                CTCC  CTCCAACGTCAT
                                  GC
GAM390  KIAA0599 3' CACTGCAACCTCCGCCTC    77169     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  KIAA0599 3' TACTGCAACCTCCGCCTC    77189     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAT
                                  GC
GAM390  KIAA0630 3' ACCACCACCTCTACC       89386        TGCA   A
                                GGTAGAGGT    GTG GT
                                |||||||||    ||| ||
                                CCATCTCCA    CAC CA
                                     C___   _
GAM390  KIAA0720 3' CACTGCAACCTCTGCCTC    62318
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  KIAA0841 3' CACTGCAACCTCCGCCTC    71376     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  KIAA0841 3' CACTGCAACCTCTGCCTC    71377
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  KIAA1041 3' CACTGCAACCTCCGCCTC    30128     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  KIAA1054 3' CACTGCAACCTCCGCCTC    68429     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  KIAA1161 5' CACTGCAACCCCTCCTC     81736     T  A
                                GAGG AG GGTTGCAGTG
                                |||| || ||||||||||
                                CTCC TC CCAACGTCAC
                                  _  C
GAM390  KIAA1170 3' CACTGCAACCTCCGCCTC    69846     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  KIAA1193  3'  CACTGCAACCTCCGCCTC    67632     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  KIAA1198  3'  CACTGCAACCTCCACTTC    63293     A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTTCA CTCCAACGTCAC
                                   C
GAM390  KIAA1198  3'  CACCGCAACCTCCGCCTC    63291     TA      A
                                GAGG  GAGGTTGC GTG
                                ||||  |||||||| |||
                                CTCC  CTCCAACG CAC
                                  GC       C
GAM390  KIAA1209  3'  CACTGCAGCCTCCACCTC    60751     A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTCCGACGTCAC
                                   C
GAM390  KIAA1257  3'  CACCGCAACCTCCGCCTC    62730     TA      A
                                GAGG  GAGGTTGC GTG
                                ||||  |||||||| |||
                                CTCC  CTCCAACG CAC
                                  GC       C
GAM390  KIAA1320  5'  CACTGCAACCTCTGCCTC    69297
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  KIAA1373  3'  GCTCACTGCAACCTCCACCTC  70942     A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390  KIAA1497  5'  CACTGCAACCTCTGCCTC    67505
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  KIAA1508  3'  CACTGCAACCTCCGCCTC    61879     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  KIAA1571  3'  GCTCACCGCAACCTCCACCTC  60955     A       A
                                GAGGT GAGGTTGC GTGAGT
                                ||||| |||||||| ||||||
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                                CTCCA CTCCAACG CACTCG
                                  C       C
GAM390  KIAA1615 3' GATCACTGCAACCTCCACCTC 68713      A          G
                                GAGGT GAGGTTGCAGTGA TC
                                ||||| |||||||||||||| ||
                                CTCCA CTCCAACGTCACT AG
                                  C          _
GAM390  KIAA1655 3' CACTGTAACCTCCACCTC    66597      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTCCAATGTCAC
                                  C
GAM390  KIAA1655 3' CATTGCAACCTCCGCCTC    66601     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTTAC
                                  GC
GAM390  KIAA1737 3' CACTGCAACCTCCGCCTC    67351     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  KIAA1775 3' TGACTCACACACCTCTACTTC 52386          TGCA
                                GAGGTAGAGGT   GTGAGTCA
                                ||||||||||   ||||||||
                                CTTCATCTCCA   CACTCAGT
                                     CA__
GAM390  KIAA1784 3' CACTGCAACCTCCGCCTC    65145     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  KIAA1922 5' CACTGCAACCTCCGCCTC    73617     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  KIAA1956 3' CACTGCAGCCTCCACCTC    78431      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTCCGACGTCAC
                                  C
GAM390  KIAA1971 3' TACTGCAACCTCCACCTC    74227      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTCCAACGTCAT
                                  C
GAM390  KLK7     3' CACTGCAACCTCCGCCTC    57729     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  KLK7     3'  CACTGCAACCTCCGCCTC    17289      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  MCLC     3'  GGCTCACTGCAACCTCCACCTC 30691       A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  MEF-2    3'  CACTGCAACCTCCGCCTC    64379      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  MGC12518 3'  TACTGCAACCTCTGCC      64083
                                GGTAGAGGTTGCAGTG
                                ||||||||||||||||
                                CCGTCTCCAACGTCAT

GAM390  MGC13138 3'  CACTGCAACCTCTGCCTC    53014
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  MGC14836 3'  CACTGCAACCTCCGCCTC    53037      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  MGC1842  3'  TACTACAACCTCCGCCTC    65657      TA      C
                                GAGG  GAGGTTG AGTG
                                ||||  ||||||| ||||
                                CTCC  CTCCAAC TCAT
                                  GC      A
GAM390  MGC2474  3'  GACTCACTGCAACTTCCACCTC 43724       A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTTCAACGTCACTCAG
                                   C
GAM390  MGC29891 3'  CACTGCAACCTCCGCCTC    58202      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  MGC3113  3'  CACTGCAGCCTCCACCTC    43840       A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
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                                CTCCA CTCCGACGTCAC
                                   C
GAM390  MGC3329  3' CACTGCAACCCCCGCCTC    44015      AGA
                                GAGGT  GGTTGCAGTG
                                |||||  ||||||||||
                                CTCCG  CCAACGTCAC
                                   CCC
GAM390  MGC5149  3' CACTGCAACCTCTGCCTC    72286
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  MGC9912  3' GGCTCACTGCAACCTCCACCTC 54722       A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  MLZE     5' CACTGCAACCTCTGCCTC    48615
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  MMPL1    3' CACTGCAGCCTCCACCTC    14717      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTCCGACGTCAC
                                   C
GAM390  moblak   3' CACTGCATCCTCCACCTC    55488      A   T
                                GAGGT GAGG TGCAGTG
                                ||||| |||| |||||||
                                CTCCA CTCC ACGTCAC
                                   C   T
GAM390  MOCS3    3' CACTGCAACCTCCGCCTC    27149      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  MRPL44   3' GGCTCACTGCAACCTCCACCTC 43323       A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  MtFMT    3' CACTGCAACCTCCGCCTC    57649      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  NDP52    3' TGACTCACTACAGCCTCTGCCT 19535           C
             C                   GAGGTAGAGGTTG AGTGAGTCA
                                ||||||||||||| |||||||||
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                                CTCCGTCTCCGAC TCACTCAGT
                                      A
GAM390  NDUFB1   5'  CACTGCAACCTCTGCCTC    15815
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  NDUFC2   3'  GGCTCACTGCAACCTCCACCTC 15840      A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  Nup43    3'  GGCTCACTGCAACCTCCACCTC 45006      A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  OSBPL2   3'  CACCGCAACCTCCGCCTC    29205     TA      A
                                GAGG  GAGGTTGC GTG
                                ||||  |||||||| |||
                                CTCC  CTCCAACG CAC
                                   GC       C
GAM390  OSBPL2   3'  CACCGCAACCTCCGCCTC    57856     TA      A
                                GAGG  GAGGTTGC GTG
                                ||||  |||||||| |||
                                CTCC  CTCCAACG CAC
                                   GC       C
GAM390  PASK     5'  CACTGCAACCTCTGCCTC    30713
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  PELI1    5'  CACTGCAACCTCCTCCTC    40255     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   TC
GAM390  PELI1    5'  CACTGCAACCTCTGCCTC    40257
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  PIP3-E   3'  CACTGCAACCTCTGCCTC    66801
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  PRO0365  5'  GCTCACTGCAACCTCCACCTC  26162      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||
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                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390  PRO1992  5'  CACTGCAACCTCTGCCTC    26054
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  PRO2955  3'  CACTGCAACCTCTGCCTC    37632
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  PSTPIP2  3'  CACTGCAACCTCTGCCTC    44384
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  RAB21    3'  GGCTCACTGCAAGCTCCACCTC 30390      A   G
                                GAGGT GAG TTGCAGTGAGTC
                                ||||| ||| ||||||||||||
                                CTCCA CTC AACGTCACTCGG
                                   C   G
GAM390  RAB33B   3'  CACTGCAACCTCCGCCTC    48489     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  RAI      5'  CACTGCAACCTCCGCCTC    21874     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  RASAL2   3'  GACCCACTCTCCTATCTC    16723       AG TTGC    A
                                GAGGTAG  G    AGTG GTC
                                |||||||  |    |||| |||
                                CTCTATC  C    TCAC CAG
                                    CT _____    C
GAM390  RNF20    3'  ACCACCAAACCTCTACCTC    38963          GCA   A
                                GAGGTAGAGGTT   GTG GT
                                ||||||||||||   ||| ||
                                CTCCATCTCCAA   CAC CA
                                       AC_   _
GAM390  RNF8     3'  GCTCACTGCAACCTCCACCTC  14230      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390  RNO2     5'  CACTGCAACCTCCACCTT    52764      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
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                                TTCCA CTCCAACGTCAC
                                   C
GAM390  SC4MOL   3'  CACTGCAACCTCTGCCTC    22151
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  SCAMP-4  3'  CACTGCAACCTCTGCCTC    54391
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  SCAND2   3'  TGACTCACTGCAACATCTGCCT 41891        G
            C                    GAGGTAGA GTTGCAGTGAGTCA
                                ||||||||| ||||||||||||||
                                CTCCGTCT CAACGTCACTCAGT
                                     A
GAM390  SCYA16   3'  CACTGTAACCTCCACCTC    15956      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTCCAATGTCAC
                                   C
GAM390  SCYA22   3'  ACCCATCCTCTGCCTC      90935         T  CA
                                GAGGTAGAGG TG  GT
                                |||||||||| ||  ||
                                CTCCGTCTCC AC  CA
                                      T  C_
GAM390  SCYA22   3'  GGCTCACTACAACCTCGACCTC 90952      A     C
                                GAGGT GAGGTTG AGTGAGTC
                                ||||| ||||||| ||||||||
                                CTCCA CTCCAAC TCACTCGG
                                   G      A
GAM390  SERF1B   3'  CACTGCAACCTCCGCCTC    43410     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  SIRPB1   3'  CACTGCAACCCCCGCCTC    20244      AGA
                                GAGGT   GGTTGCAGTG
                                |||||   ||||||||||
                                CTCCG   CCAACGTCAC
                                   CCC
GAM390  SLC11A1  3'  ACTCATTGCAACCTCCACCTT  59450      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||
                                TTCCA CTCCAACGTTACTCA
                                   C
GAM390  SLC2A10  3'  CACTGCAACCTCCACTTC    47817      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
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                                CTTCA CTCCAACGTCAC
                                   C
GAM390  SP2      3'  CGCCACAACCTCTCCTC     11888      T       CA
                                GAGG AGAGGTTG  GTG
                                ||||| ||||||||  |||
                                CTCC TCTCCAAC  CGC
                                   _       AC
GAM390  STAF65(gamma) 3'  GACTCACTGCAACCTCTGCCTC 29436
                                GAGGTAGAGGTTGCAGTGAGTC
                                ||||||||||||||||||||||
                                CTCCGTCTCCAACGTCACTCAG

GAM390  SUN1     3'  CACTGCAGCCTCCACCTC    47155       A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTCCGACGTCAC
                                   C
GAM390  SYT13    3'  CACTGCAACCTCCGCCTC    93451      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  TOLLIP   3'  TGGTTCACAACCCCCACCCTC  38690      TAGA_   GCA   GT
                                GAGG    GGTT   GTGA  CA
                                ||||    ||||   ||||  ||
                                CTCC    CCAA   CACT  GT
                                   CACCC   ___    TG
GAM390  TOR1B    3'  ACTCACTGCAACCTCCGCT   27195    TA
                                GG  GAGGTTGCAGTGAGT
                                ||  ||||||||||||||
                                TC  CTCCAACGTCACTCA
                                  GC
GAM390  TRIM5    3'  GGTTCACTGCAACCTCCACCTC 52301       A          GT
                                GAGGT GAGGTTGCAGTGA  C
                                ||||| ||||||||||||  |
                                CTCCA CTCCAACGTCACT  G
                                   C          TG
GAM390  TRIM6    3'  CACTGCAACCTCTGCCTC    54135
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  TU12B1-TY 3'  CACTGCAACCTCTGCCTC    33371
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  TUCAN    3'  CACTGCAACCTCTGCCTC    30271
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
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                                CTCCGTCTCCAACGTCAC

GAM390  UBF-fl   3'  CACTGCAACCTCTGCCTC    51555
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  USP22    3'  GGCTCACTGCAACCTCCACCTC 68019      A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  VDU1     3'  CACTGCAGCCTCCACCTC    30414      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTCCGACGTCAC
                                   C
GAM390  VPS33A   3'  CTCACTGCAACCTCCACCTC   43338      A
                                GAGGT GAGGTTGCAGTGAG
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTC
                                   C
GAM390  WBSCR20A 5'  CACCGCAACCTCTGCCTC    49650           A
                                GAGGTAGAGGTTGC GTG
                                |||||||||||||| |||
                                CTCCGTCTCCAACG CAC
                                      C
GAM390  ZTL1     3'  CACTGCAACCTCTGCCTC    43911
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  LOC112724 5' GGCTCACTGCAACCTCCACCTC 56501      A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  LOC113675 5' CACTGCAACCTCCGCCTC    56570      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  LOC115219 5' CACTGCAACCTCCGCCTC    73298      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  LOC116411 5' CGCTACAACCTCCACCTC    73860      A      C
                                GAGGT GAGGTTG AGTG
                                ||||| ||||||| ||||
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                                CTCCA CTCCAAC TCGC
                                  C      A
GAM390  LOC119392 3'  TGACTCACTGCAACCTCTGCCT 59140
          C                    GAGGTAGAGGTTGCAGTGAGTCA
                               ||||||||||||||||||||||
                               CTCCGTCTCCAACGTCACTCAGT

GAM390  LOC120114 3'  GCTCACTGCAATCTCCACCTC  75531      A
                               GAGGT GAGGTTGCAGTGAGT
                               ||||| ||||||||||||||
                               CTCCA CTCTAACGTCACTCG
                                  C
GAM390  LOC120939 3'  CACTGTAACCTCCACCTC    76248      A
                               GAGGT GAGGTTGCAGTG
                               ||||| ||||||||||||
                               CTCCA CTCCAATGTCAC
                                  C
GAM390  LOC121219 5'  TGACTCAGGCCCTCAACCTC  74050      A   TT  AG
                               GAGGT GAGG  GC  TGAGTCA
                               ||||| ||||  ||  |||||||
                               CTCCA CTCC  CG  ACTCAGT
                                  A   __  G_
GAM390  LOC126364 3'  CACTGCAACCTCCGCCTC    75684      TA
                               GAGG  GAGGTTGCAGTG
                               ||||  ||||||||||||
                               CTCC  CTCCAACGTCAC
                                 GC
GAM390  LOC126661 3'  CACTGCAACCTCCGCCTC    74545      TA
                               GAGG  GAGGTTGCAGTG
                               ||||  ||||||||||||
                               CTCC  CTCCAACGTCAC
                                 GC
GAM390  LOC128077 3'  CACTGCAACCTCCGCCTC    74707      TA
                               GAGG  GAGGTTGCAGTG
                               ||||  ||||||||||||
                               CTCC  CTCCAACGTCAC
                                 GC
GAM390  LOC128077 3'  CACTGCAACCTCTGCCTC    74709
                               GAGGTAGAGGTTGCAGTG
                               ||||||||||||||||||
                               CTCCGTCTCCAACGTCAC

GAM390  LOC128387 3'  CACTGCAACCTCCACTTC    74747      A
                               GAGGT GAGGTTGCAGTG
                               ||||| ||||||||||||
                               CTTCA CTCCAACGTCAC
                                  C
GAM390  LOC128989 3'  CACTGCAACCTCCGCCTC    74806      TA
                               GAGG  GAGGTTGCAGTG
                               ||||  ||||||||||||
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                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  LOC130813 3'  CACCGCAACCTCCGCCTC    75764     TA      A
                                GAGG  GAGGTTGC GTG
                                ||||  |||||||| |||
                                CTCC  CTCCAACG CAC
                                  GC      C
GAM390  LOC132625 3'  TGGCTCACTGCAACCTCCACCT 75917      A
          C                      GAGGT GAGGTTGCAGTGAGTCA
                                 ||||| ||||||||||||||||||
                                 CTCCA CTCCAACGTCACTCGGT
                                   C
GAM390  LOC133686 3'  CTGCAACCTCCATCTC      75121      A
                                GAGGT GAGGTTGCAG
                                ||||| ||||||||||
                                CTCTA CTCCAACGTC
                                   C
GAM390  LOC135154 3'  ACTCACTGCAACTTCCGCC    75212    TA
                                GG  GAGGTTGCAGTGAGT
                                ||  ||||||||||||||
                                CC  CTTCAACGTCACTCA
                                 GC
GAM390  LOC135293 3'  CACTGCAACCTCTGCCTC    76175
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  LOC135763 3'  CACTGCAACCTCCGCCTC    56787      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  LOC142913 5'  TGACCACTGCAGCCTCCACCTC 76419       A          A
                                GAGGT GAGGTTGCAGTG GTCA
                                ||||| |||||||||||| ||||
                                CTCCA CTCCGACGTCAC CAGT
                                   C          _
GAM390  LOC143187 3'  TGGCTCACTGCAACCTCCACCT 59103       A
          C                      GAGGT GAGGTTGCAGTGAGTCA
                                 ||||| ||||||||||||||||||
                                 CTCCA CTCCAACGTCACTCGGT
                                   C
GAM390  LOC143241 5'  CACTGCAACCTCTGCCTC    57174
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  LOC144248 5'  GCTCACTGCAACCTCCACCTC  76738       A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||
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                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390   LOC144317 5'  ACTCACTGCAACCTCTTCCTC  76782      T
                                GAGG AGAGGTTGCAGTGAGT
                                |||| ||||||||||||||||
                                CTCC TCTCCAACGTCACTCA
                                  T
GAM390   LOC144524 5'  GCTCACTGCAACCTCCACCTC  83130       A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390   LOC145216 3'  ACCCACTGCTTTTCCCC     83260    TA    TT     A
                                GG  GAGG  GCAGTG GT
                                ||  ||||  |||||| ||
                                CC  CTTT  CGTCAC CA
                                 C_   T_     C
GAM390   LOC145268 5'  CACTGCAACCTCCACCC     77055    A   A
                                G GGT GAGGTTGCAGTG
                                | ||| ||||||||||||
                                C CCA CTCCAACGTCAC
                                 _   C
GAM390   LOC145725 3'  GCTCACTGCAGCCTCCACCTC  77409       A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM390   LOC145732 3'  GCTCACTGCAGCCTCCACCTC  77431       A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM390   LOC145757 5'  CACTACAACCTCTGCCTC     77457            C
                                GAGGTAGAGGTTG AGTG
                                |||||||||||| ||||
                                CTCCGTCTCCAAC TCAC
                                        A
GAM390   LOC146229 3'  CTGCAACCTCCACCTC       77750       A
                                GAGGT GAGGTTGCAG
                                ||||| |||||||||
                                CTCCA CTCCAACGTC
                                   C
GAM390   LOC146229 3'  GGCTCACTGCAACCTCCACCTC 77768       A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| |||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390   LOC146784 5'  GGCTCACTGCAACCTCCACCTC 78122       A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| |||||||||||||||
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                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  LOC146901 3'  CATTGCAACCTCCACCTT    83835      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TTCCA CTCCAACGTTAC
                                   C
GAM390  LOC146909 3'  CACTGCAACCTCCGCCTC    78168      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  LOC146952 5'  GCTCACTGCAACCTCCACCTC  83869      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390  LOC147071 5'  CACTGCAACCTCTGCCTC    72995
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  LOC147407 3'  CACTGCAACCTCCGCCTC    76324      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  LOC147660 3'  TGACTCACAGCAACCTCCGCCT 78398      TA       A
           C                     GAGG  GAGGTTGC GTGAGTCA
                                ||||  |||||||| ||||||||
                                CTCC  CTCCAACG CACTCAGT
                                  GC       A
GAM390  LOC147817 3'  TGGCTCACTGCAACCTCCACCT 78509      A
           C                     GAGGT GAGGTTGCAGTGAGTCA
                                ||||| ||||||||||||||||||
                                CTCCA CTCCAACGTCACTCGGT
                                   C
GAM390  LOC147990 3'  CACTACAACCTCTGCCTC    84090           C
                                GAGGTAGAGGTTG AGTG
                                |||||||||||| ||||
                                CTCCGTCTCCAAC TCAC
                                        A
GAM390  LOC148137 3'  CACGGCAACCTCCACCTC    58421      A      A
                                GAGGT GAGGTTGC GTG
                                ||||| |||||||| |||
                                CTCCA CTCCAACG CAC
                                   C       G
GAM390  LOC148189 5'  GGCTCACTGCAACCTCCACCTC 78717      A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
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                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  LOC148198 3'  GCTCACTGCAACCTCCATCTC  70683      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||||
                                CTCTA CTCCAACGTCACTCG
                                   C
GAM390  LOC148709 3'  CACTACAACCTCCGCCTC    78935     TA     C
                                GAGG  GAGGTTG AGTG
                                ||||  ||||||| ||||
                                CTCC  CTCCAAC TCAC
                                  GC      A
GAM390  LOC148918 5'  ACTCAGCTTCTTCTACCTC   79054         TT  AG
                                GAGGTAGAGG  GC  TGAGT
                                ||||||||||  ||  |||||
                                CTCCATCTTC  CG  ACTCA
                                      TT  __
GAM390  LOC148918 5'  CACTGCAGCCTCCACCTC    79064      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTCCGACGTCAC
                                   C
GAM390  LOC149506 3'  CACTGCAACCTCTGCCTC    84453
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  LOC149506 3'  CACTGCAACTTCCACCTC    84454      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTTCAACGTCAC
                                   C
GAM390  LOC150397 3'  CATTGCAACCTCCGCCTC    79843     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTTAC
                                  GC
GAM390  LOC150519 3'  CTGCAACCTGCCACCTC     79917      AG_
                                GAGGT   AGGTTGCAG
                                |||||   |||||||||
                                CTCCA   TCCAACGTC
                                   CCG
GAM390  LOC150696 3'  CACTGCAGCCTCCACCTC    58478      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTCCA CTCCGACGTCAC
                                   C
GAM390  LOC150960 3'  CGCTGCAACCTCCGCCTC    80058      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                CTCC  CTCCAACGTCGC
                                  GC
GAM390   LOC151057 3'  CACTGCAACCTCTGCCTC    85208
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390   LOC151201 3'  GCTCACTGCAACCTCCACCTC  85283       A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390   LOC151475 5'  CACTGCAACCTCTGCCTC    85394
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390   LOC151475 5'  TGGCTCACTGCAACCTCCACCT 85423       A
           C                     GAGGT GAGGTTGCAGTGAGTCA
                                ||||| ||||||||||||||||||
                                CTCCA CTCCAACGTCACTCGGT
                                   C
GAM390   LOC151826 3'  CACTGCAACCTCCGCCTC    80354      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390   LOC151877 3'  GGCTCACTACAACCACCACCTC 85508       AGA    C
                                GAGGT   GGTTG AGTGAGTC
                                |||||   ||||| ||||||||
                                CTCCA   CCAAC TCACTCGG
                                   CCA    A
GAM390   LOC152343 3'  GACTCAGTGCAACCTCCGCCTC 80565      TA       G
                                GAGG  GAGGTTGCA TGAGTC
                                ||||  ||||||||| ||||||
                                CTCC  CTCCAACGT ACTCAG
                                  GC        G
GAM390   LOC152445 3'  CACTGCAACCTCTGCCTC    85749
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390   LOC152582 5'  CACCGCAACCTCTGCCTC    85789            A
                                GAGGTAGAGGTTGC GTG
                                |||||||||||||| |||
                                CTCCGTCTCCAACG CAC
                                          C
GAM390   LOC152620 3'  CACTACAACCTCTGCCTC    60078            C
                                GAGGTAGAGGTTG AGTG
                                |||||||||||| ||||
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                                CTCCGTCTCCAAC TCAC
                                      A
GAM390   LOC152719 5'  CACTGCAACCTCTGCCTC    85848
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390   LOC152794 5'  CTCACTGCAACCTCTACCTC   80675
                                GAGGTAGAGGTTGCAGTGAG
                                ||||||||||||||||||||
                                CTCCATCTCCAACGTCACTC

GAM390   LOC152851 3'  CGCTGCAACCTCCACCC     80708   A   A
                                G GGT GAGGTTGCAGTG
                                | ||| ||||||||||||
                                C CCA CTCCAACGTCGC
                                 _  C
GAM390   LOC153077 3'  CACTGCAACCTCCGCCTC    85907     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390   LOC153688 3'  GGCTCACTGCAACCTCCACCTC 86117      A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390   LOC153883 5'  CACTGCAACCTCCACC      80979     A
                                GGT GAGGTTGCAGTG
                                ||| ||||||||||||
                                CCA CTCCAACGTCAC
                                  C
GAM390   LOC154075 3'  CACTGCAACCTCCGCCTC    81044     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390   LOC154282 5'  GGCTCACTGCAACCTCCACCTC 86207      A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390   LOC154877 3'  GCTCACTGCAACCTCTACCTC  86298
                                GAGGTAGAGGTTGCAGTGAGT
                                |||||||||||||||||||||
                                CTCCATCTCCAACGTCACTCG

GAM390   LOC155100 5'  ACCCACGGTGGCCTCTCCTC   73023     T     TG A   A
                                GAGG AGAGGT  C GTG GT
                                |||| ||||||  | ||| ||
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                                CTCC TCTCCG  G CAC CA
                                  _     GT G   C
GAM390   LOC157247 5'  GCTCACTGCAACCTCCACC   81368     A
                                GGT GAGGTTGCAGTGAGT
                                ||| ||||||||||||||
                                CCA CTCCAACGTCACTCG
                                  C
GAM390   LOC157798 5'  CACTGCAACCTCCGCCTC    86548     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390   LOC157858 5'  CACTGCAACCTCTGCCTC    86584
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390   LOC158476 3'  CACTGCAACCTCCGCC      86838    TA
                                GG  GAGGTTGCAGTG
                                ||  ||||||||||||
                                CC  CTCCAACGTCAC
                                 GC
GAM390   LOC158668 3'  CACTGCAACCTCTGCCTC    69365
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390   LOC158865 5'  CACTGCAACCTCTGCCTC    86933
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390   LOC161829 3'  CACTGCAACCTCCGCCTC    82312     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390   LOC196047 5'  CACTGCAACCTCCGCCTC    89594     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390   LOC196264 3'  CACTGCAACCTCTGCCTC    87603
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390   LOC196411 3'  CACTGCAACCTCCGCCTC    87668     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                CTCC  CTCCAACGTCAC
                                  GC
GAM390   LOC196529 3'  GCTCACTGCAACCTCCACCTC  87775      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390   LOC196761 3'  ACCCACAACACCTCTGCC    89550        T CA   A
                                GGTAGAGGT G  GTG GT
                                ||||||||| |  ||| ||
                                CCGTCTCCA C  CAC CA
                                     _ AA   C
GAM390   LOC196957 3'  GCTCACTGCAGCCTCCACCTC  87825      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM390   LOC196961 3'  GCTCACTGCAGCCTCCACCTC  87846      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM390   LOC197138 3'  GCTCACTGCAGCCTCCACCTC  87919      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||||
                                CTCCA CTCCGACGTCACTCG
                                   C
GAM390   LOC197358 3'  CTGCAACCTCCGCCTC      88033      TA
                                GAGG  GAGGTTGCAG
                                ||||  |||||||||
                                CTCC  CTCCAACGTC
                                  GC
GAM390   LOC199699 3'  GCTCACTGCAAGCTCCACCTC  88309      A   G
                                GAGGT GAG TTGCAGTGAGT
                                ||||| ||| ||||||||||
                                CTCCA CTC AACGTCACTCG
                                   C   G
GAM390   LOC199786 3'  CACTGCAACCTCCGCCTC    88370      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390   LOC200014 3'  CGCTGCAACCCCCACCTC    88523      AGA
                                GAGGT   GGTTGCAGTG
                                |||||   ||||||||||
                                CTCCA   CCAACGTCGC
                                   CCC
GAM390   LOC200169 5'  CACTGCAACCTCTGCCTC    89945
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
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                                CTCCGTCTCCAACGTCAC

GAM390  LOC200268 3'  CACTGCAACCTCTGCCTC    88678
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  LOC200310 3'  CACTACAACCTCTGCCTC    65729            C
                                GAGGTAGAGGTTG AGTG
                                |||||||||||| ||||
                                CTCCGTCTCCAAC TCAC
                                      A
GAM390  LOC200314 3'  TGGCTCACTGCAACCTCCACCT 90020      A
          C                    GAGGT GAGGTTGCAGTGAGTCA
                               ||||| ||||||||||||||||
                               CTCCA CTCCAACGTCACTCGGT
                                  C
GAM390  LOC200339 3'  CACTGCAACCTCTGCCTC    90033
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  LOC200845 5'  CACTGCAACCTCCGCCTC    88896     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  LOC200860 3'  TGGTTCACTGCAACCTCCACCT 90178      A          GT
          C                    GAGGT GAGGTTGCAGTGA  CA
                               ||||| ||||||||||||  ||
                               CTCCA CTCCAACGTCACT  GT
                                  C          TG
GAM390  LOC201173 5'  CACTGCAACCTCTGCCTC    87325
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  LOC201220 5'  CACTGCAACCTCTGCCTC    87345
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  LOC201294 3'  CACTGCAACCTCCGCCTC    88203     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  LOC201294 3'  CACTGCAACCTCCGCCTC    88204     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                CTCC  CTCCAACGTCAC
                                  GC
GAM390   LOC201411 3'  CACTGCAACCTCTGCCTC    62952
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390   LOC201626 3'  CACTGCAACCTCCGCC      88988    TA
                                GG  GAGGTTGCAGTG
                                ||  ||||||||||||
                                CC  CTCCAACGTCAC
                                 GC
GAM390   LOC201627 3'  ACTGCAACCTCCACCTC     89003      A
                                GAGGT GAGGTTGCAGT
                                ||||| ||||||||||
                                CTCCA CTCCAACGTCA
                                   C
GAM390   LOC201696 3'  TGACTCACTATCACTTTACCTC 63138         GTTGC
                                GAGGTAGAG    AGTGAGTCA
                                |||||||||    |||||||||
                                CTCCATTTC    TCACTCAGT
                                     ACTA_
GAM390   LOC202025 3'  CACTGCAACCTCCGCCTC    90284      TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390   LOC202934 3'  CACTACAACCTCTGCCTC    90404           C
                                GAGGTAGAGGTTG AGTG
                                |||||||||||| ||||
                                CTCCGTCTCCAAC TCAC
                                       A
GAM390   LOC203297 5'  CACTGCAACCTCTGCCTC    75349
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390   LOC203350 3'  ACTGCAACCTCCGCCTC     90557      TA
                                GAGG  GAGGTTGCAGT
                                ||||  ||||||||||
                                CTCC  CTCCAACGTCA
                                  GC
GAM390   LOC204804 3'  GCTCACTGCAACCTCGACCTC  89475       A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| |||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   G
GAM390   LOC204804 3'  GGCTCACTGCCACCTCCACCTC 89481       A    T
                                GAGGT GAGGT GCAGTGAGTC
                                ||||| ||||| ||||||||||
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                                CTCCA CTCCA CGTCACTCGG
                                  C     C
GAM390   LOC219735 3'  CACTGCAACCTCTGCCTC    93107
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390   LOC219894 3'  TGGTTCACTGCAAGCTCCACCT 93291      A   G       GT
           C                     GAGGT GAG TTGCAGTGA  CA
                                ||||| ||| |||||||||  ||
                                CTCCA CTC AACGTCACT  GT
                                  C   G       TG
GAM390   LOC220662 3'  TGGTTCACTGCAACCTCCACCT 91185      A          GT
           C                     GAGGT GAGGTTGCAGTGA  CA
                                ||||| ||||||||||||  ||
                                CTCCA CTCCAACGTCACT  GT
                                  C           TG
GAM390   LOC220662 3'  CACTGCAACCTCCACTTC    91167      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
                                CTTCA CTCCAACGTCAC
                                  C
GAM390   LOC221035 3'  CACTACAACCTCTGCCTC    93162           C
                                GAGGTAGAGGTTG AGTG
                                |||||||||||| ||||
                                CTCCGTCTCCAAC TCAC
                                       A
GAM390   LOC221174 5'  GCTCACTGCGACCTCCACCTC  93503      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||
                                CTCCA CTCCAGCGTCACTCG
                                  C
GAM390   LOC221271 3'  CACTGCAACCTCTGCCTC    91850
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390   LOC221296 3'  GGCTCACTGCAACCTCCACCTC 91968      A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                  C
GAM390   LOC221495 3'  TGACTCACCTTCTTCTGCC    93865       TTGCA
                                GGTAGAGG    GTGAGTCA
                                ||||||||    ||||||||
                                CCGTCTTC    CACTCAGT
                                     TTC__
GAM390   LOC221663 5'  TGGCTCACTGCAACCTCCACCT 93826      A
           C                     GAGGT GAGGTTGCAGTGAGTCA
                                ||||| ||||||||||||||||
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                                CTCCA CTCCAACGTCACTCGGT
                                   C
GAM390  LOC221715 5'  ACCCAAATGCCTCTACCTT   93748          TGCAG  A
                                GAGGTAGAGGT    TG GT
                                ||||||||||    || ||
                                TTCCATCTCCG    AC CA
                                      TAA__  C
GAM390  LOC222070 5'  CACTGCAACCTCTGCCTC    94152
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  LOC253612 5'  CACTGCAACCTCCGCCTC    96742     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  LOC253664 3'  CATTGCAACCTCTGCCTC    94809
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTTAC

GAM390  LOC253666 5'  CACTGCAACCTCCGCCTC    95060     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  LOC253779 3'  CACTGCAACCTCCGCCTC    97144     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  LOC255497 3'  CACTGCAACCTCCGCCTC    97188     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  LOC255919 3'  CTGCAACCTCTGCCTC      95032
                                GAGGTAGAGGTTGCAG
                                ||||||||||||||||
                                CTCCGTCTCCAACGTC

GAM390  LOC256267 3'  CACTGCAACCTCCGCCTC    96798     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  LOC256306 3'  GCTCACTGCAACCTCCACCTC 96692       A
                                GAGGT GAGGTTGCAGTGAGT
                                |||||  ||||||||||||||
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                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390  LOC51200  3' CACCACAACCTCTGCCTC    32991           CA
                                GAGGTAGAGGTTG GTG
                                |||||||||||||  |||
                                CTCCGTCTCCAAC  CAC
                                      AC
GAM390  LOC51219  5' CACCGCAACCTCCGCCTC    33112     TA      A
                                GAGG  GAGGTTGC GTG
                                ||||  |||||||| |||
                                CTCC  CTCCAACG CAC
                                   GC       C
GAM390  LOC51696  3' CACTGCAACCTCTGCCTC    32543
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  LOC57107  3' TGACTCACTGCAACCTCCGCCT 39846     TA
             C                   GAGG  GAGGTTGCAGTGAGTCA
                                ||||  ||||||||||||||||||
                                CTCC  CTCCAACGTCACTCAGT
                                   GC
GAM390  LOC57146  3' GGCTCACTGCAACCTCCAACTC 39926     GTA
                                GAG   GAGGTTGCAGTGAGTC
                                |||   ||||||||||||||||
                                CTC   CTCCAACGTCACTCGG
                                  AAC
GAM390  LOC64102  5' GACTCACTTGCAACTCCACCTC 42173      A  G   _
                                GAGGT GAG TTGCA GTGAGTC
                                ||||| ||| ||||| |||||||
                                CTCCA CTC AACGT CACTCAG
                                   C  _    T
GAM390  LOC81034  3' GCTCACTGCAACCTCCACCTC  47853      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390  LOC89932  3' TGGCTCACTGCAACCTCCACCT 60822      A
             C                   GAGGT GAGGTTGCAGTGAGTCA
                                ||||| ||||||||||||||||||
                                CTCCA CTCCAACGTCACTCGGT
                                   C
GAM390  LOC90288  3' CTCACTGCAACCTCCACCTC   62090      A
                                GAGGT GAGGTTGCAGTGAG
                                ||||| |||||||||||||
                                CTCCA CTCCAACGTCACTC
                                   C
GAM390  LOC90333  5' CACTGCAACCTCCACTTC    62283      A
                                GAGGT GAGGTTGCAGTG
                                ||||| ||||||||||||
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                                CTTCA CTCCAACGTCAC
                                   C
GAM390  LOC90333  3' CACTGCAACCTCCTCCTC    62284     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  TC
GAM390  LOC90371  5' TGGCTCACTGCAACCTCCACCT 62505      A
          C                      GAGGT GAGGTTGCAGTGAGTCA
                                |||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGGT
                                   C
GAM390  LOC90408  5' TGGCTCACTGCAACCTCTACCT 62671
          C                      GAGGTAGAGGTTGCAGTGAGTCA
                                ||||||||||||||||||||||
                                CTCCATCTCCAACGTCACTCGGT

GAM390  LOC90459  3' CACTGCAACCTCCGCCTC    62883     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  LOC90485  3' CACTGCAACCTCCGCCTC    63008     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  LOC90591  3' GCTCACTGCAAGCTCCACCTC  63433      A  G
                                GAGGT GAG TTGCAGTGAGT
                                ||||| ||| ||||||||||
                                CTCCA CTC AACGTCACTCG
                                   C  G
GAM390  LOC90591  3' TGTTCACTGCCACCTCCACCTC 63448      A    T      T
                                GAGGT GAGGT GCAGTGAG CA
                                ||||| ||||| |||||||| ||
                                CTCCA CTCCA CGTCACTT GT
                                   C    C      _
GAM390  LOC91115  3' CACTGCAACCTCCGCCTC    64927     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  LOC91115  3' GGCTCACTGCAACCTCCACCTC 64946      A
                                GAGGT GAGGTTGCAGTGAGTC
                                ||||| ||||||||||||||||
                                CTCCA CTCCAACGTCACTCGG
                                   C
GAM390  LOC91291  5' GCTCACTGCAACCTCGACCTC  65481      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| |||||||||||||||
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                                CTCCA CTCCAACGTCACTCG
                                   G
GAM390  LOC91373  3' ACTCATCCTCTGCC       65831        TTGCA
                                GGTAGAGG    GTGAGT
                                ||||||||    ||||||
                                CCGTCTCC    TACTCA
                                   _____
GAM390  LOC92267  3' GCTCACTGCAACCTCCACCTC  68617      A
                                GAGGT GAGGTTGCAGTGAGT
                                ||||| ||||||||||||||
                                CTCCA CTCCAACGTCACTCG
                                   C
GAM390  LOC92303  3' ACTCACTGCAACCTCTGCC   68819
                                GGTAGAGGTTGCAGTGAGT
                                ||||||||||||||||||
                                CCGTCTCCAACGTCACTCA

GAM390  LOC92466  3' CACTGCAACCTCCGCCTC    69423     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  LOC92661  5' TGGCTCACTGCAAGCTCCACCT 70090      A   G
          C                     GAGGT GAG TTGCAGTGAGTCA
                                ||||| ||| ||||||||||||
                                CTCCA CTC AACGTCACTCGGT
                                   C   G
GAM390  LOC92689  3' CACTGCAACCTCCGCCTC    70219     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CTCC  CTCCAACGTCAC
                                   GC
GAM390  LOC92697  5' CACCGCAACCTCCGCCTC    70262     TA       A
                                GAGG  GAGGTTGC GTG
                                ||||  |||||||| |||
                                CTCC  CTCCAACG CAC
                                   GC       C
GAM390  LOC92697  5' CGCTACAACCTCCACCTC    70264      A      C
                                GAGGT GAGGTTG AGTG
                                ||||| ||||||| ||||
                                CTCCA CTCCAAC TCGC
                                   C      A
GAM390  LOC92841  3' CACCGCAACCTCCTCCTC    70706     TA       A
                                GAGG  GAGGTTGC GTG
                                ||||  |||||||| |||
                                CTCC  CTCCAACG CAC
                                   TC       C
GAM390  LOC93132  5' CACTGCAACCTCCGCCTC    71485     TA
                                GAGG  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                CTCC  CTCCAACGTCAC
                                  GC
GAM390  LOC93349  3'  CACTGCAACCTCTGCCTC    56453
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM390  LOC93408  5'  CACTGCAACCTCTGCCTC    56475
                                GAGGTAGAGGTTGCAGTG
                                ||||||||||||||||||
                                CTCCGTCTCCAACGTCAC

GAM391  PCDHB7    5'  ACAGTGGTAATAGGAATTGGG  38441       G  AGG
                                CTCAAT CC   TATTACCACTGT
                                |||||| ||   ||||||||||||
                                GGGTTA GG   ATAATGGTGACA
                                   A  ___
GAM391  PTPN13    3'  GTAATATTGGCATAGA      20759    A     G
                                TC ATGCCAG TATTAC
                                || ||||||| ||||||
                                AG TACGGTT ATAATG
                                 A      _
GAM391  PTPN13    3'  GTAATATTGGCATAGA      54775    A     G
                                TC ATGCCAG TATTAC
                                || ||||||| ||||||
                                AG TACGGTT ATAATG
                                 A      _
GAM391  PTPN13    3'  GTAATATTGGCATAGA      54773    A     G
                                TC ATGCCAG TATTAC
                                || ||||||| ||||||
                                AG TACGGTT ATAATG
                                 A      _
GAM391  PYGB      3'  CAGCAGGCCTGGCACTGGG    11171      A       ATTACCA
                                CTCA TGCCAGGT      CTG
                                |||| ||||||||      |||
                                GGGT ACGGTCCG      GAC
                                  C       GAC____
GAM391  FLJ10482  3'  ACAGAATCCACACCTGCATTGA 36159        C    ATTACCA
                                TCAATGC AGGT      CTGT
                                ||||||| ||||      ||||
                                AGTTACG TCCA      GACA
                                   _    CACCTAA
GAM391  FLJ10781  3'  ACAGTAGTAATATTCTATCAT  36628     CC  _     C
                                ATG  AGG TATTAC ACTGT
                                |||  ||| |||||| |||||
                                TAC  TCT ATAATG TGACA
                                  TA  T     A
GAM391  FLJ23120  3'  ACAATGACATATTTGGCA    85141          TAC  C
                                TGCCAGGTAT   CA TGT
                                ||||||||||   || |||
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                                ACGGTTTATA   GT ACA
                                     CA_  A
GAM391  KIAA0316  3'  ACAGTGGTTCTAGCATT     69667       C   TATT
                                AATGC AGG    ACCACTGT
                                ||||| |||    ||||||||
                                TTACG TCT    TGGTGACA
                                  A  _____
GAM391  KIAA0970  3'  ACAGTGGCATTTAGCACTGGCA 29954           _  ATTA__
          TTGAG                    CTCAATGCCAG GT     CCACTGT
                                ||||||||||| ||     |||||||
                                GAGTTACGGTC CG     GGTGACA
                                      A  ATTTAC
GAM391  MDS031    3'  ACAGTGGTAATGAAACATT    37468      CCAGG
                                AATG    TATTACCACTGT
                                ||||    ||||||||||||
                                TTAC    GTAATGGTGACA
                                  AAA__
GAM391  SNRK      3'  ACAGTGAGTGTCTGCACTGAG  34763      A   C  GT   AC
                                CTCA TGC AG  ATT  CACTGT
                                |||| ||| ||  |||  ||||||
                                GAGT ACG TC  TGA  GTGACA
                                  C   _  TG   __
GAM391  LOC145225 3'  ACAGCAATAATACCTAGGGAG  83299     AATG  _      CCA
                                CTC    CC AGGTATTA   CTGT
                                |||    || ||||||||   ||||
                                GAG    GG TCCATAAT   GACA
                                  _____  A       AAC
GAM391  LOC145624 5'  AATACCTGGCATAGAG      83403     A
                                CTC ATGCCAGGTATT
                                ||| ||||||||||||
                                GAG TACGGTCCATAA
                                  A
GAM391  LOC150005 3'  ACAGTGGTGGTATCCACCACTG 84814      A  CCA
          AG                      CTCA TG   GGTATTACCACTGT
                                ||||| ||   ||||||||||||||
                                GAGT AC   CTATGGTGGTGACA
                                  C  CAC
GAM391  LOC158835 3'  ACAGCCCCATCTCCCGGCATTG 82006          A  TATTACCA
          AG                      CTCAATGCC GG       CTGT
                                |||||||||  ||       ||||
                                GAGTTACGG CC       GACA
                                     C  TCTACCCC
GAM391  LOC197201 3'  ACAGTACCTTACCTGGCTCTGA 87928      AT       TTACC
          G                       CTCA  GCCAGGTA     ACTGT
                                ||||  ||||||||     |||||
                                GAGT  CGGTCCAT     TGACA
                                  CT       TCCA_
GAM391  LOC200078 3'  ACAGTGGGGCATCCGGCACTGA 88569     A    A  TATTA
                                TCA TGCC GG     CCACTGT
                                ||| |||| ||     |||||||
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                                AGT ACGG CC    GGTGACA
                                  C   _ TACGG
GAM391  LOC220739 3'  AGTGCCTGGCACTGAG     92923     A
                                CTCA TGCCAGGTATT
                                |||| ||||||||||
                                GAGT ACGGTCCGTGA
                                  C
GAM391  LOC221322 5'  GCAGCAGGTGGCATTG     91930       AGGTATT  A_
                                CAATGCC     ACC  CTGT
                                |||||||     |||  ||||
                                GTTACGG     TGG  GACG
                                   ________  AC
GAM391  LOC91351  3'  ACAATGTAGTCCTGGCATT   65703        T    CAC
                                AATGCCAGG ATTAC   TGT
                                ||||||||| |||||   |||
                                TTACGGTCC TGATG   ACA
                                     _    TA_
GAM392  BCLG    3'  CCATCTCTGGACTCACAGCTTC 56984    A   ACA    GT__
          CA                    TG AAG   TGAGTT    GATGG
                                || |||   ||||||    |||||
                                AC TTC   ACTCAG    CTACC
                                 C   GAC     GTCT
GAM392  DLD     3'  CGTCAACTCATATTTTCA    3662       AC     TG
                                TGAAAG  ATGAGT  TGATG
                                ||||||  ||||||  |||||
                                ACTTTT  TACTCA  ACTGC
                                   A_     __
GAM392  HUNK    3'  CACCAAACTCATGTTTTCA    27445     A       __
                                TGAA GACATGAGTT  GTG
                                |||| ||||||||||  |||
                                ACTT TTGTACTCAA  CAC
                                  _        AC
GAM392  KIF3C   3'  CCAACATAGCTCATGCCCTTCA 9598      AGA        A
                                TGAA   CATGAGTTGTG TGG
                                ||||   |||||||||||| |||
                                ACTT   GTACTCGATAC ACC
                                  CCC         A
GAM392  PKDREJ  3'  TGCTTTCTACTCATGTCCTTCA 20280     A       TGT  T
                                TGAA GACATGAGT   GA GGCA
                                |||| |||||||||   || ||||
                                ACTT CTGTACTCA   CT TCGT
                                  C        T__  T
GAM392  PPP1R3C  3'  CACAACTCACATCCTTCA    18249     A  CA
                                TGAA GA  TGAGTTGTG
                                |||| ||  |||||||||
                                ACTT CT  ACTCAACAC
                                  C  AC
GAM392  PRG2    5'  GCCACACTCATCATAGCCTTCA 10782     AGAC   GTT   A
                                TGAA    ATGA   GTG TGGC
                                ||||    ||||   ||| ||||
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                                ACTT   TACT  CAC ACCG
                                  CCGA   ACT  _
GAM392  RGL      3'  CCATCACACTCTTCCTTC   30730    A  CAT   T
                                GAA GA   GAGT GTGATGG
                                ||| ||   |||| |||||||
                                CTT CT   CTCA CACTACC
                                  C  T__   _
GAM392  DKFZp434E0519 3'  CTGTATCTCATGTCTTTCA   49988          TTGTG
                                TGAAAGACATGAG    ATGG
                                ||||||||||||    ||||
                                ACTTTCTGTACTC    TGTC
                                        TA___
GAM392  DKFZp434J0226 3'  CATCCACTCATGTC       72331        T T
                                GACATGAGT G GATG
                                ||||||||| | ||||
                                CTGTACTCA C CTAC

                                     _ _
GAM392  DKFZP761I2123 5'  GCAACCATGTCTTCCA     48763    A      A
                                TG AAGACATG GTTGT
                                || |||||||| |||||
                                AC TTCTGTAC CAACG
                                 C      _
GAM392  FADS2    3'  TGCCATTGGTCCACCCTTTCA  14958      ACA  AG  GT
                                TGAAAG   TG  TT  GATGGCA
                                ||||||   ||  ||  |||||||
                                ACTTTC   AC  GG  TTACCGT
                                   CC_  CT  __
GAM392  FLJ22944  3'  CCAATTTCTCATGTCTCTC   47122    A       TT  GA
                                GA AGACATGAG  GT  TGG
                                || |||||||||  ||  |||
                                CT TCTGTACTC  TA  ACC
                                 C       TT  __
GAM392  HABP2    3'  CCATCACATCTTTATTCCTCA  14694     AA  CAT   T
                                TGA  GA   GAG TGTGATGG
                                |||  ||   ||| ||||||||
                                ACT  CT   TTC ACACTACC
                                  C_  TAT   T
GAM392  KIAA0435  3'  CATGGCTCATGCTTTC      28970      A     TG
                                GAAAG CATGAGT  TG
                                ||||| |||||||  ||
                                CTTTC GTACTCG  AC
                                   _      GT
GAM392  KIAA0987  3'  ACAATTCATGCCTTTCA     24558       A
                                TGAAAG CATGAGTTGT
                                |||||| ||||||||||
                                ACTTTC GTACTTAACA
                                   C
GAM392  KIAA1219  3'  CAACTCATGTTCTTCA      61365      AG
                                TGAA  ACATGAGTTG
                                ||||  ||||||||||
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                                ACTT  TGTACTCAAC
                                  CT
GAM392  KIAA1937  5'  CCATCACATATCCCCTTCCA  73695    A   ACAT  GT
                                TG AAG    GA  TGTGATGG
                                || |||    ||  ||||||||
                                AC TTC    CT  ACACTACC
                                 C   CC__  AT
GAM392  MGC27044  3'  CAGTCAACTCATATCTT     58669     C      TGA
                                AAGA ATGAGTTG   TG
                                |||| ||||||||   ||
                                TTCT TACTCAAC   AC
                                  A       TG_
GAM392  MGC3222   3'  CACCAGCTCATGTCTT      44292           _
                                AAGACATGAGTTG TG
                                |||||||||||| ||
                                TTCTGTACTCGAC AC
                                        C
GAM392  MGC5466   5'  GCAACTCATTCCTTTCA     73055       AC
                                TGAAAG  ATGAGTTGT
                                ||||||  |||||||||
                                ACTTTC  TACTCAACG
                                   CT
GAM392  SKD3      3'  GCCAGACTTTCTCATGTT    47995        TT_  GA
                                GACATGAG   GT  TGGC
                                ||||||||   ||  ||||
                                TTGTACTC   CA  ACCG
                                     TTT  G_
GAM392  LOC144997 3'  CAATTCATATCTTTCA      83210        C
                                TGAAAGA ATGAGTTG
                                ||||||| ||||||||
                                ACTTTCT TACTTAAC
                                   A
GAM392  LOC149566 3'  TGCCATCACAACCCTCTTTCA  84496        CATGA
                                TGAAAGA    GTTGTGATGGCA
                                |||||||    ||||||||||||
                                ACTTTCT    CAACACTACCGT
                                   CC___
GAM392  LOC199766 5'  CACCATTATGTCCTTCA     89494     A      GTT
                                TGAA GACATGA   GTG
                                |||| |||||||   |||
                                ACTT CTGTATT   CAC
                                  C      AC_
GAM392  LOC253272 5'  CCATCACAGAATATCTTT    95359       CATGAG
                                AAAGA     TTGTGATGG
                                |||||     |||||||||
                                TTTCT     GACACTACC
                                  ATAA__
GAM392  LOC253776 3'  TGCCATCTGAGCACACCTGTC  97432      __  A   GT
                                GACA  TG GTT  GATGGCA
                                ||||  || |||  |||||||
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                                CTGT  AC CGA  CTACCGT
                                  CC  A   GT
GAM392  LOC254440 3'  TGCCATCACAAATGGGTCCTTT 97072       _  ATGAG
            CA                    TGAAAG AC    TTGTGATGGCA
                                  |||||| ||    ||||||||||
                                  ACTTTC TG    AACACTACCGT
                                     C  GGTA_
GAM392  LOC255328 3'  TGCCATCAAATACATGTTT   96566       A   G
                                  AGACATG GTT TGATGGCA
                                  ||||||| ||| ||||||||
                                  TTTGTAC TAA ACTACCGT
                                     A  _
GAM392  LOC57019  3'  GCCACCCTCTTGTCTTTCA   39725        T   TTGTGA
                                  TGAAAGACA GAG     TGGC
                                  ||||||||| |||     ||||
                                  ACTTTCTGT CTC     ACCG
                                        T   CC____
GAM393  AASS    3'  GTTTGCTAATGTGCTGTTTTA  19268         ATTGT   TG
                                  TGAGGCAGTG    TTAG  AAT
                                  |||||||||     ||||  |||
                                  ATTTTGTCGT    AATC  TTG
                                        GT___   GT
GAM393  ABCB11   3'  AATAATTCTGCTTTA      13615        T
                                  TGAGGCAG GATTGTT
                                  |||||||| |||||||
                                  ATTTCGTC TTAATAA
                                           _
GAM393  ACADSB   3'  TTAAACGGTTGTGTCTT     7850        G
                                  GAGGCA TGATTGTTTAG
                                  |||||| ||||||||||
                                  TTCTGT GTTGGCAAATT
                                           _
GAM393  ACADVL   3'  GAGCACTTACTGCCTC      3415          T
                                  GAGGCAGTGA TGTTT
                                  |||||||||| |||||
                                  CTCCGTCATT ACGAG
                                        C
GAM393  ACLY    3'  TTCATTGGACACTATCTT    65063     GC   GATT
                                  GAG  AGT   GTTTAGTGAA
                                  |||  |||   ||||||||||
                                  TTC  TCA   CAGGTTACTT
                                    TA  ____
GAM393  ACTC    3'  TTTGTGCTTCTAATATTTATTG 60188         T   T__   AAT
            CTTTA                   AGGCAGTGA TGTT   AGTG
                                  |||||||| ||||   ||||
                                  TTCGTTATT ATAA   TCGT
                                        T   TCT    GTTTG
GAM393  ACVR1B   3'  TAAACAAACAAACATTGTTTTA 39741          A     A  GAAT
                                  TGAGGCAGTG TTGTTT GT
                                  |||||||||| |||||| ||
```

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                                ATTTTGTTAC AACAAA CA
                                     A     _ AATA
GAM393  ADAM17   3'  ATTTGCTGGGCAGTTTTTCTGT 41554     T__       TG
                                GCAG   GATTGTTTAG  AAT
                                ||||   ||||||||||  |||
                                TGTC   TTGACGGGTC  TTA
                                  TTT        GT
GAM393  ADAM17   3'  ATTTGCTGGGCAGTTTTTCTGT 12082     T__       TG
                                GCAG   GATTGTTTAG  AAT
                                ||||   ||||||||||  |||
                                TGTC   TTGACGGGTC  TTA
                                  TTT        GT
GAM393  ADCY7    3'  ATTTGTTTCAAAATGCTGTTTC 6637        G  GTTT  TG
            A                    TGAGGCAGT ATT    AG  AAT
                                |||||||||  |||    ||  |||
                                ACTTTGTCG TAA    TT  TTA
                                     _  AACT  GT
GAM393  ADSS     3'  ATTAGGCATAACATTGTTTT   71756       AT_
                                GAGGCAGTG   TGTTTAGT
                                |||||||||   ||||||||
                                TTTTGTTAC   ACGGATTA
                                     AAT
GAM393  ADSS     3'  ATTTGTTGCTCCTGCTGCTCTC 71757     _     ATT  TT  TG
            A                    TGAG GCAGTG   GT  AG  AAT
                                ||||  ||||||   ||  ||  |||
                                ACTC CGTCGT   CG  TT  TTA
                                  T     CCT  __  GT
GAM393  AEGL1    3'  TCCTGAAGTAACACTGTTTTA  6680        A  _    T
                                TGAGGCAGTG TTG TTTAG GA
                                |||||||||| ||| ||||| ||
                                ATTTTGTCAC AAT AAGTC CT
                                     _  G    _
GAM393  AGL      5'  ATTCATTCTCTTTCATTGCTCT 3448     _     TTGTTT
                                AG GCAGTGA     AGTGAAT
                                || |||||||     |||||||
                                TC CGTTACT     TTACTTA
                                 T      TTCTC_
GAM393  ALDOB    5'  ATTTGGCAGCTGCTGCCTCA   68085       GA   TT
                                TGAGGCAGT  TTGT  AGT
                                |||||||||  ||||  |||
                                ACTCCGTCG  GACG  TTA
                                     TC    GT
GAM393  ALOX12   3'  CGCATAGTCACTGTCTCA    5516           TTA
                                TGAGGCAGTGATTGT   GTG
                                ||||||||||||||||  |||
                                ACTCTGTCACTGATA   CGC
                                                ___
GAM393  ALS2     3'  GTTTATTAAAATACTGTTTT   40507       ATTG
                                GAGGCAGTG   TTTAGTGAAT
                                |||||||||   ||||||||||
```

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                                TTTTGTCAT   AAATTATTTG
                                    A___
GAM393  AMT     3'  TCAGGAATGATTGCTGACTCA  4906      G   TG  TG   AG
                                TGAG CAG  AT  TTT  TGA
                                |||| |||  ||  |||  |||
                                ACTC GTC  TA  AAG  ACT
                                  A   GT  GT   G_
GAM393  ANGPT1  3'  ATTTACTGTTTTGTTGTCT   6701       TG TTGTT
                                AGGCAG  A    TAGTGAAT
                                ||||||  |    ||||||||
                                TCTGTT  T    GTCATTTA
                                   GT TT___
GAM393  ANGPT2  5'  GTTTGCTAAGCTGCTGGTTTA  6706      G    ATT     TG
                                TGAG CAGTG   GTTTAG  AAT
                                |||| |||||   ||||||  |||
                                ATTT GTCGT   CGAATC  TTG
                                  G    ___     GT
GAM393  ANXA7   3'  GTTTGCACATGTTGTTATTGCC 6720           TGTTTA_ TG
            TTA                   TGAGGCAGTGAT      G  AAT
                                ||||||||||||      | |||
                                ATTCCGTTATTG      C  TTG
                                      TTGTACA GT
GAM393  ANXA7   3'  GTTTGCACATGTTGTTATTGCC 14452          TGTTTA_ TG
            TTA                   TGAGGCAGTGAT      G  AAT
                                ||||||||||||      | |||
                                ATTCCGTTATTG      C  TTG
                                      TTGTACA GT
GAM393  ANXA9   3'  TTTCTTTGATAGTTTCTGCCTC 13106        T      TAGT   T
            A                    TGAGGCAG GATTGTT    GAA
                                |||||||| |||||||    |||
                                ACTCCGTC TTGATAG    CTT
                                     T      TTT_   TT
GAM393  APC     3'  TTGAAGGGTCTTGTTTCA    3482         T    G
                                TGAGGCAG GATT TTTAG
                                |||||||| |||| |||||
                                ACTTTGTT CTGG AAGTT
                                     _   G
GAM393  APPL    3'  GTTCTATAACAATTATGTTTCA 23929        G       TAGT
                                TGAGGCA TGATTGTT    GAAT
                                ||||||| ||||||||    ||||
                                ACTTTGT ATTAACAA    CTTG
                                     _       TAT_
GAM393  ARHGEF7  3'  GTTTATTGGAGTTTGCTGTT   14012      TG TTG
                                GGCAG  A   TTTAGTGAAT
                                |||||  |   ||||||||||
                                TTGTC  T   AGGTTATTTG
                                   GT TG_
GAM393  ASTN    3'  ATTTATTGAGTGCTTGCTGT   69329      TG T GT
                                GCAG  A T  TTAGTGAAT
                                ||||  | |  |||||||||
```

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                                TGTC  T G  AGTTATTTA
                                  GT C TG
GAM393  ASTN    3'  CACCATGGTCACTGCCCA   69330   A      TG TTA
                                TG GGCAGTGAT  T   GTG
                                || |||||||||  |   |||
                                AC CCGTCACTG  A   CAC
                                 _       GT C__
GAM393  ATM     5'  GTTTATTGTCACCCTGCTGCCC 3514    A    GATTGTT
          A                      TG GGCAGT      TAGTGAAT
                                 || ||||||      ||||||||
                                 AC CCGTCG      GTTATTTG
                                  _     TCCCACT
GAM393  ATP1A2  3'  AGGGAGTCATTGCCTT     5519          G
                                GAGGCAGTGATT TTT
                                |||||||||||| |||
                                TTCCGTTACTGA GGA
                                       G
GAM393  ATP6V1A1  3'  GAGCAACATTGTCTTA     8077          A
                                TGAGGCAGTG TTGTTT
                                |||||||||| ||||||
                                ATTCTGTTAC AACGAG
                                          _
GAM393  ATP7A   3'  TATTCACTAAATTTGTTTGTTG 3529       TG TT__
          TT                     GGCAG  A   GTTTAGTGAAT  A
                                 |||||  |   ||||||||||  |
                                 TTGTT  T   TAAATCACTTA  T
                                    GT TGTT
GAM393  ATP8A2  3'  AGGCAGTTAACTGTCTCA   93507        _
                                TGAGGCAGT GATTGTTT
                                ||||||||| ||||||||
                                ACTCTGTCA TTGACGGA
                                      A
GAM393  B29     3'  TTAAACAGTCATTGCTTT   49198
                                GAGGCAGTGATTGTTTAG
                                ||||||||||||||||||
                                TTTCGTTACTGACAAATT

GAM393  B4GALT6  3'  AATAGCATTGTCTTA      59861          A
                                TGAGGCAGTG TTGTT
                                |||||||||| |||||
                                ATTCTGTTAC GATAA
                                          _
GAM393  BACH1   3'  GTTTGCTATAGCTTACTGCTT  6801         TT  _  TG
                                AGGCAGTGA  GTT TAG  AAT
                                |||||||||  ||| |||  |||
                                TTCGTCATT  CGA ATC  TTG
                                      __  T  GT
GAM393  BACH1   3'  TTCACATGATCATTGCTCA   6804      G      TG TTA
                                TGAG CAGTGAT  T   GTGAA
                                |||| |||||||  |   |||||
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                                ACTC GTTACTA  A   CACTT
                                  _      GT ___
GAM393  BAI3     3'  GTTTGTTGAGCTACATTCTTCA 8124       C    ATT     TG
                                TGAGG AGTG   GTTTAG  AAT
                                ||||| ||||   ||||||  |||
                                ACTTC TTAC   CGAGTT  TTG
                                  _   AT_     GT
GAM393  BCL11B   3'  ATTCTGTGGCAATTATTGTTCT 56799    AG         TAGT
            A                    TG  GCAGTGATTGTT    GAAT
                                ||  ||||||||||||    ||||
                                AT  TGTTATTAACGG    CTTA
                                 CT          TGT_
GAM393  BCS1L    5'  ATTTGCTAAACAGGTAGTGTT  15076     G  A      TG
                                GGCA TG TTGTTTAG  AAT
                                ||||  ||  ||||||||  |||
                                TTGT AT GACAAATC  TTA
                                  G  G       GT
GAM393  BDKRB2   3'  TTGAGGGACAGTTGCTTTTCA  5265      C  TG     AG
                                TGAGG AG  ATTGTTT  TGA
                                ||||| ||  |||||||  |||
                                ACTTT TC  TGACAGG  GTT
                                  _ GT      GA
GAM393  BPAG1    3'  ATTTATTAAATGATAAATTGC  8171      G_  TG
                                GCAGT  AT  TTTAGTGAAT
                                |||||  ||  ||||||||||
                                CGTTA  TA  AAATTATTTA
                                   AA  GT
GAM393  C4BPA    3'  ATTTGCTAAAGTTTAGTGCTTT 5549       G   TTG    TG
                                GAGGCA TGA   TTTAG  AAT
                                ||||||  |||   |||||  |||
                                TTTCGT ATT   AAATC  TTA
                                   G   TG_    GT
GAM393  CA12     3'  GAGCAGTTATGTTTTA      6879        G
                                TGAGGCA TGATTGTTT
                                |||||||  |||||||||
                                ATTTTGT ATTGACGAG
                                  _
GAM393  CALB1    3'  CTAGTCAACTGCTGTTTTA   17024        GA   T
                                TGAGGCAGT  TTG TTAG
                                |||||||||  |||  ||||
                                ATTTTGTCG  AAC GATC
                                     TC   T
GAM393  CARP     3'  GTTTATTTATTTACTGCC    26899        TTGTTT
                                GGCAGTGA     AGTGAAT
                                ||||||||     |||||||
                                CCGTCATT     TTATTTG
                                     TAT___
GAM393  CARPX    3'  ATTTGCTAAGCAAGTATGACTT 39416      CA   A      TG
            TA                    TGAGG  GTG TTGTTTAG  AAT
                                |||||  |||  ||||||||  |||
```

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                                ATTTC  TAT AACGAATC  TTA
                                  AG   G       GT
GAM393  CAV2     3'  AAAGGCAGACAGTTTTGCTTTA 6940         T       A  GAAT
                                TGAGGCAG GATTGTTT GT
                                |||||||| |||||||| ||
                                ATTTCGTT TTGACAGA CG
                                    _       _ GAAAT
GAM393  CCND1    3'  ATTCCAAAAAGGTTGCTGTTTC 53884        TG  TG   AGT
            A                    TGAGGCAG  AT  TTT   GAAT
                                |||||||| ||  |||  ||||
                                ACTTTGTC  TG  AAA   CTTA
                                    GT  GA   AC_
GAM393  CCND2    3'  ATTTGTTAAAATATTTGCCTT  8288        TGATTG    TG
                                GAGGCAG     TTTAG  AAT
                                |||||||     |||||  |||
                                TTCCGTT     AAATT  TTA
                                    TATA__    GT
GAM393  CCR2     3'  GTTTGTTGAACAATAGAAACCT 5389      CAGTG       TG
                                AGG    ATTGTTTAG  AAT
                                |||    |||||||||  |||
                                TCC    TAACAAGTT  TTG
                                  AAAGA       GT
GAM393  CD44     3'  TTGTAAAAACAGCATTGCTTT  5210         A     AGTGAAT
                                GAGGCAGTG TTGTTT
                                ||||||||| ||||||
                                TTTCGTTAC GACAAA
                                    _     AATGTTT
GAM393  CDK2AP1  3'  TTCAAAATGGTTACAGTTTC   16173      A    TG   AG   T
                                GAGGC GTGAT  TTT  TGAA
                                ||||| |||||  |||  ||||
                                CTTTG CATTG  AAA  ACTT
                                   A    GT   __    T
GAM393  CDO1     3'  GTTCGCTGTATGTTTGCCTT   8400        TGATTGTT
                                GAGGCAG       TAGTGAAT
                                |||||||       ||||||||
                                TTCCGTT       GTCGCTTG
                                    TGTAT___
GAM393  CGA      3'  TTTACCAAGTGCTGTCTT    5598         GA   TTTA
                                GAGGCAGT  TTG    GTGAA
                                ||||||||  |||    |||||
                                TTCTGTCG  AAC    CATTT
                                    TG  _____
GAM393  CHD2     5'  TTTAGTATTAATTATTGCTTTA 7038             TT  G    T
                                TGAGGCAGTGATTG  TA TGAA
                                ||||||||||||||  || ||||
                                ATTTCGTTATTAAT  AT ATTT
                                        T_  G    T
GAM393  CHRNA3   3'  ATTCATTGTTAATATAACTGTC 5606         GAT    __
            TTA                    GAGGCAGT   TGTT  TAGTGAAT
                                ||||||||   ||||  ||||||||
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                                TTCTGTCA  ATAA  GTTACTTA
                                   AT_   TT
GAM393  CIS4    3'  TTAGAAATTGTTGCCTT    14881       TG  G
                                GAGGCAG  ATT TTTAG
                                |||||||  ||| |||||
                                TTCCGTT  TAA AGATT
                                   GT  _
GAM393  CIT     3'  GTTTACTGTTTTCATTGCCTT  69748         TTGTT
                                GAGGCAGTGA    TAGTGAAT
                                ||||||||||    ||||||||
                                TTCCGTTACT    GTCATTTG
                                     TTT__
GAM393  CIT     3'  GTTTGCTGAAGTTTTGTCTC   69749       T  TG    TG
                                GAGGCAG GAT  TTTAG  AAT
                                ||||||| |||  |||||  |||
                                CTCTGTT TTG  AAGTC  TTG
                                   _  __    GT
GAM393  CLASP1  3'  GTTGATGAAATAGTCACTGTTT 65309            A  G
                                AGGCAGTGATTGTTT GT AAT
                                |||||||||||||| || |||
                                TTTGTCACTGATAAA TA TTG
                                      G  G
GAM393  CLCA3   3'  ATTTACTATACTTATTGTCT   16993         TT  T
                                AGGCAGTGA  GT TAGTGAAT
                                |||||||||  || ||||||||
                                TCTGTTATT  CA ATCATTTA
                                   __ T
GAM393  CLCN3   3'  ATTTGTTGAATAGCACAACTC  8437     GCA  A      TG
                                GAG   GTG TTGTTTAG  AAT
                                |||   ||| ||||||||  |||
                                CTC   CAC GATAAGTT  TTA
                                  AA_  _       GT
GAM393  CLCN5   3'  TTATAAGACAATGCTGCTTT   3597         G      A
                                GAGGCAGT ATTGTTT GTGA
                                |||||||| ||||||| ||||
                                TTTCGTCG TAACAGA TATT
                                   _      A
GAM393  CNR1    3'  AACAATTAATTGTCTT      32211         _
                                GAGGCAGT GATTGTT
                                |||||||| |||||||
                                TTCTGTTA TTAACAA
                                   A
GAM393  COG3    3'  GTTTGCTAAATGATTATTTGTT 48700       _   TG    TG
           T                     AGGCAG TGAT  TTTAG  AAT
                                 ||||||  ||||  |||||  |||
                                 TTTGTT ATTA  AAATC  TTG
                                    T   GT    GT
GAM393  COL19A1  3'  ATTCATTCCATATGTTTTGCTT 8507         TGAT   TT
           TA                     TGAGGCAG    TGT  AGTGAAT
                                  ||||||||    |||  |||||||
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                                ATTTCGTT   ATA  TTACTTA
                                    TTGT   CC
GAM393  COL4A1   3'  GTTTGTTTATATCACTGTCT  8463         TGTTT  TG
                                AGGCAGTGAT    AG  AAT
                                ||||||||||    ||  |||
                                TCTGTCACTA    TT  TTG
                                    TAT__  GT
GAM393  CPNE3    3'  GTTCATTATAGTGGTGCCTTA  14032       G G    TT
                                TGAGGCA T ATTGT  AGTGAAT
                                ||||||| | |||||  |||||||
                                ATTCCGT G TGATA  TTACTTG
                                    _ G    __
GAM393  CREB1    3'  ATTTACTGTTGCCCATTGCACT 15201     _     ATT  T_
           TA                     TGAG GCAGTG   GT  TAGTGAAT
                                ||||  ||||||   ||  ||||||||
                                ATTC CGTTAC   CG  GTCATTTA
                                  A     C__  TT
GAM393  CREB1    3'  GGGCAGTTGTTGCTTC      15202        TG
                                GAGGCAG  ATTGTTT
                                |||||||  |||||||
                                CTTCGTT  TGACGGG
                                    GT
GAM393  CREBL2   3'  TTTACTACCTACTGCTCA    7150      G    ATTGTT
                                TGAG CAGTG     TAGTGAA
                                |||| |||||     |||||||
                                ACTC GTCAT     ATCATTT
                                  _    CC____
GAM393  CSRP1    3'  AGGTAGGCACTGCCTCA     14525         A   TT
                                TGAGGCAGTG TTG  T
                                |||||||||| |||  |
                                ACTCCGTCAC GAT  A
                                    G   GG
GAM393  CTNND2   3'  CTAAATATTGCTTCA      7184         GATT
                                TGAGGCAGT   GTTTAG
                                |||||||||   ||||||
                                ACTTCGTTA   TAAATC

                                    ____
GAM393  CUL3     3'  GTTTAAGTTTACGTCATTGTCT 13165          T  TTAG_
           CA                     TGAGGCAGTGAT GT    TGAAT
                                ||||||||||| ||    |||||
                                ACTCTGTTACTG CA    ATTTG
                                    _ TTTGA
GAM393  CUL3     3'  ATTTATTAGAATGTATGTCTCA 13162       GTGATTG
                                TGAGGCA     TTTAGTGAAT
                                |||||||     ||||||||||
                                ACTCTGT     AGATTATTTA
                                    ATGTA__
GAM393  CXorf6   3'  GTTCACTAAAAATCCTATTGCC 18518       __   G
           TT                     GAGGCAGT  GATT TTTAGTGAAT
                                |||||||  |||| ||||||||||
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                                TTCCGTTA  CTAA AAATCACTTG
                                    TC   _
GAM393  CXorf6   3' GTTTACTATGCATTGTTTT   18519        ATTGTT
                                GAGGCAGTG    TAGTGAAT
                                |||||||||    ||||||||
                                TTTTGTTAC    ATCATTTG
                                    GT____
GAM393  CYP3A43  3' ATTCATTGAGCTCTCATTGTCT 54046        TT
                                AGGCAGTGA  GTTTAGTGAAT
                                |||||||||  ||||||||||
                                TCTGTTACT  CGAGTTACTTA
                                    CT
GAM393  CYP3A43  3' ATTCATTGAGCTCTCATTGTCT 54047        TT
                                AGGCAGTGA  GTTTAGTGAAT
                                |||||||||  ||||||||||
                                TCTGTTACT  CGAGTTACTTA
                                    CT
GAM393  CYP3A43  3' ATTCATTGAGCTCTCATTGTCT 43056        TT
                                AGGCAGTGA  GTTTAGTGAAT
                                |||||||||  ||||||||||
                                TCTGTTACT  CGAGTTACTTA
                                    CT
GAM393  D10S170  3' TTCAGCAGTTGCTGTTTT   18368      TG   TTAG   T
                                GAGGCAG  ATTGT   TGAA
                                |||||||  |||||   ||||
                                TTTTGTC  TGACG   ACTT
                                    GT    _____   T
GAM393  DDEF1    3' TTAAGCAATTGCTTCCTCA   59565     C  TG
                                TGAGG AG  ATTGTTTAG
                                ||||| ||  |||||||||
                                ACTCC TC  TAACGAATT
                                   T  GT
GAM393  DDX1     3' TTTACTGAATAAGATTTG    17051     TGA
                                CAG   TTGTTTAGTGAA
                                |||   ||||||||||||
                                GTT   AATAAGTCATTT
                                  TAG
GAM393  DDX6     3' GTTTGCTGCCACACTGTCTCA  15289        AT  TT   TG
                                TGAGGCAGTG  TG  TAG  AAT
                                ||||||||||  ||  |||  |||
                                ACTCTGTCAC  AC  GTC  TTG
                                     __  C_   GT
GAM393  DGCR2    3' TGCTGAGGCAGTGCTGTCTC   17634       G   _
                                GAGGCAGT ATTGT TTAGTG
                                |||||||| ||||| ||||||
                                CTCTGTCG TGACG AGTCGT
                                    _    G
GAM393  DMD      5' GTTTGTTGGTTTCTCATTGTTT 14361        TTGT   TG
           T                    GAGGCAGTGA   TTAG  AAT
                                ||||||||||   ||||  |||
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                                TTTTGTTACT   GGTT  TTG
                                     CTTT   GT
GAM393  DMRT2    3'  TTCCCTGGTGCTGCCTCA   21617         ATTGT   T
                                TGAGGCAGTG    TTAG GAA
                                ||||||||||    |||| |||
                                ACTCCGTCGT    GGTC CTT
                                     _____   C
GAM393  DPYS     3'  AAGCAATTGCTGTCTT     7283        TG
                                GAGGCAG  ATTGTTT
                                |||||||  |||||||
                                TTCTGTC  TAACGAA
                                    GT
GAM393  DPYSL2   3'  AAACAATTTTTGTTTCA    7288         T
                                TGAGGCAG GATTGTTT
                                |||||||| ||||||||
                                ACTTTGTT TTAACAAA
                                     T
GAM393  DVL1     3'  ATTTATTTATTTATTGCCT   59333         TTGTTT
                                AGGCAGTGA     AGTGAAT
                                |||||||||     |||||||
                                TCCGTTATT     TTATTTA
                                     TAT___
GAM393  EFG2     3'  TATTTATTGGACGAATAAAGTA 50478      A_____
           CTGTTTCA               AGTG     TTGTTTAGTGAAT   A
                                ||||     ||||||||||||   |
                                TCAT     AGCAGGTTATTTA   T
                                  GAAATA
GAM393  EGLN1    5'  TTGGGAGGGACATTCATTGCCT 41899          T    AGTGAAT
           CA                    TGAGGCAGTGA TGTTT
                                ||||||||||| |||||
                                ACTCCGTTACT ACAGG
                                     T    GAGGGTTA
GAM393  EIF1AY   3'  ATTCATTGTAATCCACTGTTTT 16260         _   TT
                                GAGGCAGTG ATTG  TAGTGAAT
                                ||||||||| ||||  ||||||||
                                TTTTGTCAC TAAT  GTTACTTA
                                     C   __
GAM393  EIF4EBP2 3'  TTACCCTGTGACACTGTTTT   14592         A TG TTA
                                GAGGCAGTG T  T   GTGA
                                ||||||||| |  |   ||||
                                TTTTGTCAC A  G   CATT
                                     _ GT TCC
GAM393  EMP1     3'  ATTCCTGGTTAAGCAGGCATTG 7443        A       T___
           CTTT                  GGCAGTG TTGTTTAG    GAAT
                                |||||||| ||||||||    ||||
                                TCGTTAC GACGAATT    CTTA
                                    G       GGTC
GAM393  EN2      3'  TAAATAATCATTTCTTA     7469       C
                                TGAGG AGTGATTGTTTA
                                ||||| ||||||||||||
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                                ATTCT TTACTAATAAAT
                                    _
GAM393  ENC1    3'  GTTTACTAAGCATGTGCCGTC  13283    _   GTGAT
                                GA GGCA    TGTTTAGTGAAT
                                || ||||    ||||||||||||
                                CT CCGT    ACGAATCATTTG
                                 G   GT___
GAM393  EPHA3   3'  AAACAATTACTGGCTCA     17862     G
                                TGAG CAGTGATTGTTT
                                |||| ||||||||||||
                                ACTC GTCATTAACAAA
                                  G
GAM393  EPHA3   3'  ATTTACTACCTTATCACTGC   17865       TGTT
                                GCAGTGAT   TAGTGAAT
                                ||||||||   ||||||||
                                CGTCACTA   ATCATTTA
                                     TTCC
GAM393  EPHA3   3'  ATTTACTGGACATAACATTTTC 17866      CA  GAT
            A                    TGAGG  GT   TGTTTAGTGAAT
                                ||||||  ||   ||||||||||||
                                ACTTT  CA   ACAGGTCATTTA
                                   TA  AT_
GAM393  EPS15   3'  GTTTAACACGGTTACTGACTTA 8794      G       TTAG
                                TGAG CAGTGATTGT   TGAAT
                                |||| ||||||||||   |||||
                                ATTC GTCATTGGCA   ATTTG
                                  A        CA__
GAM393  ESR1    3'  GTTTTCTAAGTAATTGCTGCCT 3706       TG       T
            C                    GAGGCAG  ATTGTTTAG GAAT
                                |||||||  ||||||||| ||||
                                CTCCGTC  TAATGAATC TTTG
                                    GT       T
GAM393  ETF1    3'  TTCCAATAATCCTGTTTCA   16401       T     TAGT
                                TGAGGCAG GATTGTT   GAA
                                |||||||| |||||||   |||
                                ACTTTGTC CTAATAA   CTT
                                    _      C___
GAM393  ETFA    3'  TGGTTCCAAACAATTATTGTTT 3713            AGT
                                AGGCAGTGATTGTTT   GAAT
                                ||||||||||||||   ||||
                                TTTGTTATTAACAAA   CTTG
                                         C__   GTG
GAM393  EVA1    3'  ATTCATTACATATCTGTCTCA  19393       TGAT   TT
                                TGAGGCAG   TGT  AGTGAAT
                                ||||||||   |||  |||||||
                                ACTCTGTC   ACA  TTACTTA
                                     TAT_  __
GAM393  EYA2    3'  GGACAATCATTCTTT      17885     C
                                GAGG AGTGATTGTTT
                                |||| ||||||||||
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                                TTTC TTACTAACAGG
                                  _
GAM393  EYA3    5'  ATTCTCTCAGTTCCTGTTTC  8809       TG   TTT  T
                                GAGGCAG  ATTG   AG GAAT
                                |||||||  ||||   || ||||
                                CTTTGTC  TGAC   TC CTTA
                                    CT   ___  T
GAM393  EYA4    5'  AAGTTGTCGCTGCCTTA    14614          TG
                                TGAGGCAGTGAT  TTT
                                ||||||||||||  |||
                                ATTCCGTCGCTG  GAA
                                      TT
GAM393  EZH1    3'  ATTCTCCTCCAGTCCTGTCTCA 8813        T    TTTAGT
                                TGAGGCAG GATTG     GAAT
                                |||||||| |||||     ||||
                                ACTCTGTC CTGAC     CTTA
                                    _    CTCCT_
GAM393  F8      3'  TCCTAGCAGACACTGCCTT   3734         A    T  T
                                GAGGCAGTG TTGTT AG GA
                                ||||||||| ||||| || ||
                                TTCCGTCAC GACGA TC CT
                                    A    _ _
GAM393  F9      3'  ATTCTATGATCATTGCTTT   3737          TG TT
                                GAGGCAGTGAT  T  AGT
                                ||||||||||  |  |||
                                TTTCGTTACTA  A  TTA
                                      GT TC
GAM393  FACL3   3'  CTAGATAATCATTATTTCA   15498      C
                                TGAGG AGTGATTGTTTAG
                                ||||| ||||||||||||
                                ACTTT TTACTAATAGATC
                                   A
GAM393  FACL3   3'  TTGTTGCTGTGTAATTATTGTC 15502          TT   TG AT
          TT                     GAGGCAGTGATTG  TAG  A
                                ||||||||||||  |||  |
                                TTCTGTTATTAAT  GTC  T
                                      GT   GT GTTT
GAM393  FANCF   3'  GTTTATTAAACAGTTAT    42678
                                GTGATTGTTTAGTGAAT
                                ||||||||||||||||
                                TATTGACAAATTATTTG

GAM393  FCN2    3'  GTCAAACCTGAATGGTCGCTAC 31734    C     TG    ___  AT
          CTCA                   AGG AGTGAT  TTTAG   TGA
                                ||| ||||||  |||||   |||
                                TCC TCGCTG  AAGTC   ACT
                                  A     GT    CAA   G
GAM393  FGF2    3'  GAAGAATTATATAATCACTGCT 8872           T   GAAT
          TTA                    TGAGGCAGTGATTGT TAGT
                                ||||||||||||||| ||||
```

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                                ATTTCGTCACTAATA ATTA
                                      T   AGAAGT
GAM393  FGF5    3'  ATTTATTGAGATCTAAGTCTGT 52478       TGATTG__
          CTT                  GAGGCAG      TTTAGTGAAT
                               |||||||      ||||||||||
                               TTCTGTC      GAGTTATTTA
                                  TGAATCTA
GAM393  FGF5    3'  ATTTATTGAGATCTAAGTCTGT 15532       TGATTG__
          CTT                  GAGGCAG      TTTAGTGAAT
                               |||||||      ||||||||||
                               TTCTGTC      GAGTTATTTA
                                  TGAATCTA
GAM393  FGFR2   3'  ATTTGCTAAATGCTGTTCTTA  3759      _   GATT    TG
                               TGAGG CAGT   GTTTAG  AAT
                               ||||| ||||   ||||||  |||
                               ATTCT GTCG   TAAATC  TTA
                                  T  _____     GT
GAM393  FGFR2   3'  ATTTGCTAAATGCTGTTCTTA  43487     _   GATT    TG
                               TGAGG CAGT   GTTTAG  AAT
                               ||||| ||||   ||||||  |||
                               ATTCT GTCG   TAAATC  TTA
                                  T  _____     GT
GAM393  FGFR2   3'  ATTTGCTAAATGCTGTTCTTA  43497     _   GATT    TG
                               TGAGG CAGT   GTTTAG  AAT
                               ||||| ||||   ||||||  |||
                               ATTCT GTCG   TAAATC  TTA
                                  T  _____     GT
GAM393  FGFR2   3'  ATTTGCTAAATGCTGTTCTTA  43355     _   GATT    TG
                               TGAGG CAGT   GTTTAG  AAT
                               ||||| ||||   ||||||  |||
                               ATTCT GTCG   TAAATC  TTA
                                  T  _____     GT
GAM393  FGFR2   3'  ATTTGCTAAATGCTGTTCTTA  43367     _   GATT    TG
                               TGAGG CAGT   GTTTAG  AAT
                               ||||| ||||   ||||||  |||
                               ATTCT GTCG   TAAATC  TTA
                                  T  _____     GT
GAM393  FGFR2   3'  ATTTGCTAAATGCTGTTCTTA  43478     _   GATT    TG
                               TGAGG CAGT   GTTTAG  AAT
                               ||||| ||||   ||||||  |||
                               ATTCT GTCG   TAAATC  TTA
                                  T  _____     GT
GAM393  FGFRL1  3'  AGATAATGCTGCCTCA     41616        G
                               TGAGGCAGT ATTGTTT
                               ||||||||| |||||||
                               ACTCCGTCG TAATAGA
                                     _
GAM393  FGFRL1  3'  AGATAATGCTGCCTT      41617        G
                               GAGGCAGT ATTGTTT
                               |||||||| |||||||
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                                TTCCGTCG TAATAGA
                                      _
GAM393  FOXG1B   5'  ATTCCTGAGGGGTGGTTGCTGC 17899      TG  TG ___   T
            TTT                   AGGCAG  AT  T   TTAG GAAT
                                  ||||||  ||  |   |||| ||||
                                  TTCGTC  TG  G   AGTC CTTA
                                     GT  GT GGG   _
GAM393  FOXG1B   3'  CTAAATAGTGACTGCTTT    17901        G
                                  GAGGCAGT ATTGTTTAG
                                  |||||||| |||||||||
                                  TTTCGTCA TGATAAATC
                                       G
GAM393  FUT1     3'  TTCATGCCATTCTGCCTCA    3799         T   T  TTA
                                  TGAGGCAG GAT GT   GTGAA
                                  |||||||| ||| ||   |||||
                                  ACTCCGTC TTA CG   TACTT
                                       _   C  ___
GAM393  FZD4     3'  TTTATTAATTCATGCCTTA    24159        G   TTGT
                                  TGAGGCA TGA    TTAGTGAA
                                  |||||||| |||    ||||||||
                                  ATTCCGT ACT    AATTATTT
                                       _   T___
GAM393  GAB2     3'  ATTTATTAATGGCTGCTGTCTC 24487         GA TG  T
                                  GAGGCAGT  T  TT AGTGAAT
                                  |||||||  |  || |||||||
                                  CTCTGTCG  G  AA TTATTTA
                                       TC GT  _
GAM393  GAB2     3'  ATTTATTAATGGCTGCTGTCTC 54444         GA TG  T
                                  GAGGCAGT  T  TT AGTGAAT
                                  |||||||  |  || |||||||
                                  CTCTGTCG  G  AA TTATTTA
                                       TC GT  _
GAM393  GABRA5   3'  TACAAATAATATTGCCTT    60192         A     A
                                  GAGGCAGTG TTGTTT GTG
                                  ||||||||| |||||| |||
                                  TTCCGTTAT AATAAA CAT
                                       _     _
GAM393  GABRB1   5'  ATTCGGGAATTACTGCCCA    5870     A        G TT
                                  TG GGCAGTGATT T  AGT
                                  || |||||||||| |  |||
                                  AC CCGTCATTAA G  TTA
                                   _         G GC
GAM393  GALC     3'  GTTCAGAGCCAATTCTTGTTTC 3848         T    T  AG
              A                    TGAGGCAG GATTG TT  TGAAT
                                  |||||||| ||||| ||  |||||
                                  ACTTTGTT TTAAC GA  ACTTG
                                       C    C  G_
GAM393  GAS1     3'  TTCATTCTTTCACTGTTT    8995          TTGTTT
                                  AGGCAGTGA     AGTGAA
                                  |||||||||     ||||||
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                                TTTGTCACT     TTACTT
                                     TTC___
GAM393  GATM    3'  TCATTCTCCTGCTTTA     7629         T  TTGTTT
                                TGAGGCAG GA     AGTGA
                                |||||||| ||     |||||
                                ATTTCGTC CT     TTACT
                                     _  C_____
GAM393  GEMIN5  3'  GAATAAATTACTGTTTCA    89164          _
                                TGAGGCAGTGATT GTTT
                                |||||||||||| ||||
                                ACTTTGTCATTAA TAAG
                                       A
GAM393  GHR     3'  GTTTAGTAGCAGTGATTGTCTT 3885         G     T G
           A                     TGAGGCAGT ATTGTT A TGAAT
                                 ||||||||| |||||| | |||||
                                 ATTCTGTTA TGACGA T ATTTG
                                      G     _ G
GAM393  GOLGA4  5'  ATTAAGAAGCAGTTGTTATCTC 60069     GC  TG     AG   AT
           A                     TGAG  AG  ATTGTTT  TGA
                                 ||||  ||  |||||||  |||
                                 ACTC  TT  TGACGAA  ATT
                                   TA  GT      GA   A
GAM393  GRAF    3'  GGCAGCGTTGCTTCA      30571          A
                                TGAGGCAGTG TTGTT
                                |||||||||| |||||
                                ACTTCGTTGC GACGG
                                      _
GAM393  GRB10   3'  GTTCTAGAACGATCACTGCCTT 17985              AGT
           A                     TGAGGCAGTGATTGTTT   GAAT
                                 ||||||||||||||||   ||||
                                 ATTCCGTCACTAGCAAG   CTTG
                                        AT_
GAM393  GRM6    3'  ATTTATTACATTCATTGCTT   5926         T   TT
                                AGGCAGTGA TGT  AGTGAAT
                                ||||||||| |||  |||||||
                                TTCGTTACT ACA  TTATTTA
                                     T  __
GAM393  GRM6    3'  ATTTGTTAAATTGACCACTGTT 5927         ATT_     TG
           T                     AGGCAGTG   GTTTAG  AAT
                                 ||||||||   ||||||  |||
                                 TTTGTCAC   TAAATT  TTA
                                     CAGT     GT
GAM393  GRPR    3'  GGACGGTTTTGCTTTA      18001         T
                                TGAGGCAG GATTGTTT
                                |||||||| ||||||||
                                ATTTCGTT TTGGCAGG
                                      _
GAM393  H3F3B   5'  GTTCGTTGGGCGGTGCTGGTTT 18023     G   G
                                GAG CAGT ATTGTTTAGTGAAT
                                ||| |||| ||||||||||||||
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                                TTT GTCG TGGCGGGTTGCTTG
                                  G   _
GAM393  HADHSC   3' CTGAATGATTACTGTCT     18031          TG
                                AGGCAGTGAT  TTTAG
                                ||||||||||  |||||
                                TCTGTCATTA  AAGTC
                                      GT
GAM393  HDAC4    3' ACTGACAGTCACGTTTTA    20104       A       T
                                TGAGGC GTGATTGTT AGT
                                |||||| ||||||||| |||
                                ATTTTG CACTGACAG TCA
                                   _       _
GAM393  HDAC4    3' TCCTGAATAAGCATTGTTTTA 20116          A      T
                                TGAGGCAGTG TTGTTTAG GA
                                |||||||||| |||||||| ||
                                ATTTTGTTAC AATAAGTC CT
                                      G       _
GAM393  HGF      3' ATTTGCTGGATGATAAAGATTT 94232      CAGTG  TG    TG
              CA                  TGAGG    AT  TTTAG  AAT
                                |||||    ||  |||||  |||
                                ACTTT    TA  AGGTC  TTA
                                   AGAAA  GT    GT
GAM393  HLA-DOB  3' ATGCTCAGGTAGTCACTGTTTC 9210            TT _   AAT
                                GAGGCAGTGATTG  T AGTG
                                ||||||||||||  | ||||
                                CTTTGTCACTGAT  A TCGT
                                       GG C    A
GAM393  HLF      3' ATTTATTGGATGATACAGTGTT 9218       G  _  TG
              TT                   GAGGCA TG AT  TTTAGTGAAT
                                |||||| || ||  ||||||||||
                                TTTTGT AC TA  AGGTTATTTA
                                   G  A  GT
GAM393  HNRPA1   3' TGAACTGATAGTTACTGTT   48296          T   GAAT
                                GGCAGTGATTGTT AGT
                                |||||||||||| |||
                                TTGTCATTGATAG TCA
                                       _  AGTT
GAM393  HOXD9    3' ATTTGTTGTTGTTGCTGTTTC 26404       TG  TGTT   TG
                                GAGGCAG  AT    TAG  AAT
                                |||||||  ||    |||  |||
                                CTTTGTC  TG    GTT  TTA
                                    GT  TT__   GT
GAM393  HRMT1L1  3' GACAGTTGATGCTTTA     65201       GT
                                TGAGGCA  GATTGTT
                                |||||||  |||||||
                                ATTTCGT  TTGACAG
                                    AG
GAM393  HS3ST3B1 3' TTCTCCAGTTGCTGCCTC    20151       TG   TTTAGT
                                GAGGCAG  ATTG     GAA
                                |||||||  ||||     |||
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                                CTCCGTC  TGAC     CTT
                                    GT    CT____
GAM393  HSPA1B   3'  GTTCATTAGAATTCTTTGC   18076     T  TTG
                                GCAG GA   TTTAGTGAAT
                                |||| ||   ||||||||||
                                CGTT CT   AGATTACTTG
                                  T  TA_
GAM393  HSPD1    3'  GTTTACTGCTGTCATTGTCCA  60173    A       T  TT
                                TG GGCAGTGAT GT  AGTGAAT
                                || |||||||| ||  |||||||
                                AC CTGTTACTG CG  TCATTTG
                                 _       T  __
GAM393  HTR1D    3'  TTCAAGAGATTCTGCCTCA   6005         T   GTTTAG
                                TGAGGCAG GATT     TGAA
                                |||||||| ||||     ||||
                                ACTCCGTC TTAG     ACTT
                                    _   AGA___
GAM393  ID4      3'  GTTTACGAAATCTGCTGTTTTA 7756          _   GTTTA
                                TGAGGCAGT GATT    GTGAAT
                                ||||||||| ||||    ||||||
                                ATTTTGTCG CTAA    CATTTG
                                     T   AG___
GAM393  IFNA2    3'  GTTCATTGAACTTTTGCT    5207     TG TT
                                AG  A  GTTTAGTGAAT
                                ||  |  ||||||||||
                                TC  T  CAAGTTACTTG
                                 GT TT
GAM393  IGJ      3'  CTTTATTAGGTAATCACTTCTT 58314      C      TT     T
            A                    TGAGG AGTGATTG  TAGTGAA
                                ||||| ||||||||  |||||||
                                ATTCT TCACTAAT  ATTATTT
                                  _      GG      CT
GAM393  IL11     3'  ATTTATTTAAGCAATTACTTTT 5323       C          _
            CA                     TGAGG AGTGATTGTTTAG TGAAT
                                ||||| |||||||||||| |||||
                                ACTTT TCATTAACGAATT ATTTA
                                  _          T
GAM393  IL11RA   3'  TCCACCTATAATTCTGTCTT   15713       T    TTA   AAT
                                GAGGCAG GATTGT   GTG
                                ||||||| ||||||   |||
                                TTCTGTC TTAATA   CAC
                                    _    TC_   CTT
GAM393  IL22RA2  3'  GTTTAGTTTTTAATCCTGTCTT 53694        T    TTTAG
            A                    TGAGGCAG GATTG    TGAAT
                                ||||||||| |||||    |||||
                                ATTCTGTC CTAAT    ATTTG
                                    _    TTTTG
GAM393  IL7      3'  ATTCAAAATTGACATTGCTTTA 6079          ATT   AG
                                TGAGGCAGTG   GTTT  TGAAT
                                ||||||||||   ||||  |||||
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                                ATTTCGTTAC  TAAA  ACTTA
                                     AGT   __
GAM393  IMPA1    3'  TTCTTAGTGGTCATTGCTCT  18650   _     TG  TAGT  T
                                AG GCAGTGAT  TT   GAA
                                || ||||||||  ||   |||
                                TC CGTTACTG  GA   CTT
                                 T      GT  TT__  T
GAM393  ING1     3'  ATTTATTACATTGCTGCCTT  18652      TG  T  TT
                                GAGGCAG  AT GT  AGTGAAT
                                |||||||  || ||  |||||||
                                TTCCGTC  TA CA  TTATTTA
                                    GT  _ __
GAM393  INPP5B   3'  ATTTGGCAGCTTATTGCTTC  95522        _   TT
                                GAGGCAGTGA TTGT  AGT
                                |||||||||| ||||  |||
                                CTTCGTTATT GACG  TTA
                                      C   GT
GAM393  INSL4    3'  GCCCAATTAAATGATTGCTGTT 9348      TG  TG    GAAT
             T                   AGGCAG  AT  TTTAGT
                                 ||||||  ||  ||||||
                                 TTTGTC  TA  AAATTA
                                    GT  GT    ACCCGT
GAM393  IRTA1    5'  TAGGCAAGTGCTGCTTT    48421       GA
                                GAGGCAGT  TTGTTTA
                                ||||||||  |||||||
                                TTTCGTCG  AACGGAT
                                     TG
GAM393  ISL1     3'  GTTTCTATATTGGTCATTGCCT 9368          TT_  T
             T                   GAGGCAGTGATTG   TAG GAAT
                                 ||||||||||||||  ||| ||||
                                 TTCCGTTACTGGT   ATC TTTG
                                       TAT  _
GAM393  ITGA6    3'  TAAAAGTGTTCATTGTTTC   3987         TTG__
                                GAGGCAGTGA    TTTA
                                ||||||||||    ||||
                                CTTTGTTACT    AAAT
                                      TGTGA
GAM393  KCNJ15   3'  ATTCATTGATCTCACTGCTTTA 9542          TTGT
                                TGAGGCAGTGA   TTAGTGAAT
                                ||||||||||   |||||||||
                                ATTTCGTCACT   AGTTACTTA
                                      CT__
GAM393  KIF3B    3'  TTTACTAAGAATTTGCCT    16616      TGATTG
                                AGGCAG     TTTAGTGAA
                                ||||||     |||||||||
                                TCCGTT     GAATCATTT
                                   TAA___
GAM393  KIN      5'  TCCAGAAAGTGATCGCTGCC  24595       TG  AG  AAT
                                GGCAGTGAT  TTT  TG
                                |||||||||  |||  ||
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                                CCGTCGCTA  GAA  AC
                                     GT   AG  CTG
GAM393  KLHL3    3'  TAGTGGATAATTACAGCCTCA  87463       A         G
                                TGAGGC GTGATTGTTTA TG
                                |||||| |||||||||||  ||
                                ACTCCG CATTAATAGGT AT
                                   A         G
GAM393  KRTHA8   3'  ATTTGCTAAGTATGATGTGCTT 22257       GTGAT      TG
           C                     GAGGCA    TGTTTAG  AAT
                                |||||||   |||||||  |||
                                CTTCGT    ATGAATC  TTA
                                   GTAGT      GT
GAM393  LAMC2    3'  ATTTACTGGACCCTGTTTTA   38146        TGATT
                                TGAGGCAG    GTTTAGTGAAT
                                ||||||||    ||||||||||
                                ATTTTGTC    CAGGTCATTTA
                                     C____
GAM393  LANCL1   3'  GGCATCATTGTTTCA       20214           T
                                TGAGGCAGTGAT GTT
                                |||||||||||| |||
                                ACTTTGTTACTA CGG
                                                _
GAM393  LBR      3'  AAATTGTCATTGTTTTA     59350           T
                                TGAGGCAGTGAT GTTT
                                |||||||||||| ||||
                                ATTTTGTTACTG TAAA
                                      T
GAM393  LBR      3'  ATTCACTAAACTTTTGTGTTCA 59351      G  G   TT
                                TGAG CA TGA  GTTTAGTGAAT
                                |||| || |||  ||||||||||
                                ACTT GT GTT  CAAATCACTTA
                                  _ _   TT
GAM393  LCP1     3'  ATTTACTGGACAAAGAATTCC  9693     C   GA_
                                GG AGT   TTGTTTAGTGAAT
                                || |||   ||||||||||||
                                CC TTA   AACAGGTCATTTA
                                 _   AGA
GAM393  LNK      3'  GTTCTACCTGGCTACTGCTTCA 18469         ATT   TA  _
                                TGAGGCAGTG   GTT  GT GAAT
                                ||||||||||   |||  || ||||
                                ACTTCGTCAT   CGG  CA CTTG
                                      ____   TC  T
GAM393  LPL      3'  ATTCAATATCTGACAGTTACTC 4086      C        TAG___
           TTCA                    AGG AGTGATTGTT     TGAAT
                                |||  ||||||||||     |||||
                                TTC TCATTGACAG     ACTTA
                                  _        TCTATA
GAM393  LPXN     3'  ATTTGCCCTGTGGCTCACTGTC 16676          _ TG TTA TG
           TTA                     TGAGGCAGTGA T  T   G  AAT
                                |||||||||||  |  |   |  |||
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                                ATTCTGTCACT G  G   C  TTA
                                      C GT TCC GT
GAM393  LYZ     3'  GTTCACTAATGTGGTTATT   4107       TG _
                                AGTGAT  T TTAGTGAAT
                                ||||||  | |||||||||
                                TTATTG  G AATCACTTG
                                   GT T
GAM393  MAGEB3   3'  TTAAAGAGGGCAGTCACTGTTC 9888     AG          AGTGAAT
           CA                    TG  GCAGTGATTGTTT
                                ||  ||||||||||||
                                AC  TGTCACTGACGGG
                                 CT          AGAAATTG
GAM393  MAK     3'  GTTCATTGGACTTTTCAAATTG 19766      __   TT_
           TTTT                    GGCAG  TGA   GTTTAGTGAAT
                                |||||  |||   ||||||||||
                                TTGTT  ACT   CAGGTTACTTG
                                   AA   TTT
GAM393  MAN1A1   3'  AGACAATTATTTTCTTA     91900      C
                                TGAGG AGTGATTGTTT
                                |||||| ||||||||||
                                ATTCT TTATTAACAGA
                                   T
GAM393  MATN3    3'  ATTCACTTTATTATTTTGCTTC 9935         T   T  TT
           A                     TGAGGCAG GAT GT  AGTGAAT
                                |||||||| ||| ||  |||||||
                                ACTTCGTT TTA TA  TCACTTA
                                     _  T  TT
GAM393  MCL1     3'  AAAGCAAATACTTACTGTTTT  41710          T    A  GAAT
                                GAGGCAGTGA TGTTT GT
                                |||||||||| ||||| ||
                                TTTTGTCATT ATAAA CG
                                      C    _  AAAT
GAM393  MDH2     3'  ATTTGCTTTGGTGATGATTACT 19794         TG  T____  TG
           GT                     GCAGTGAT  TT    AG  AAT
                                ||||||||  ||    ||  |||
                                TGTCATTA  AG    TC  TTA
                                     GT  TGGTT  GT
GAM393  MDM1     3'  GTTTATTGGATGGACCTCCTGC 39275      T  ___ TG
                                GCAG GA   T  TTTAGTGAAT
                                ||||  ||   |  ||||||||||
                                CGTC CT   G  AGGTTATTTG
                                   _  CCA GT
GAM393  ME1      3'  AGACAATTTTGCTTCA      9984          T
                                TGAGGCAG GATTGTTT
                                ||||||||  ||||||||
                                ACTTCGTT TTAACAGA
                                     _
GAM393  MEN1     5'  TTAAACAATCTTGTTTCA     93386         T
                                TGAGGCAG GATTGTTTAG
                                ||||||||  |||||||||
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                                ACTTTGTT CTAACAAATT
                                    _
GAM393  MEOX2   3' GACAGACATTGTCTTA     19804         A
                                TGAGGCAGTG TTGTT
                                |||||||||| |||||
                                ATTCTGTTAC GACAG
                                     A
GAM393  MGEA5   3' GTTTATTGAGTGAAATGCCTC 24217      GTGA TG
                                GAGGCA   T TTTAGTGAAT
                                ||||||   | ||||||||||
                                CTCCGT   A GAGTTATTTG
                                   AA__ GT
GAM393  MID1    3' ATTTGCTAGATTCATGCCTCA 4600       G  TT    TG
                                TGAGGCA TGA GTTTAG AAT
                                ||||||| ||| |||||| |||
                                ACTCCGT ACT TAGATC TTA
                                   _ __    GT
GAM393  MLC1    3' AGGCGGTCACTGCCCA     30775    A
                                TG GGCAGTGATTGTTT
                                || ||||||||||||||
                                AC CCGTCACTGGCGGA
                                 _
GAM393  MLC1    5' GTTTGCTGAGCTTTTGTTTCA 30784       TGATT    TG
                                TGAGGCAG   GTTTAG AAT
                                ||||||||   |||||| |||
                                ACTTTGTT   CGAGTC TTG
                                     TT___    GT
GAM393  MLC1    3' AGGCGGTCACTGCCCA     57586    A
                                TG GGCAGTGATTGTTT
                                || ||||||||||||||
                                AC CCGTCACTGGCGGA
                                 _
GAM393  MLH3    5' TTTGTTAAGCGGGACTCC    26886    C  GA      TG
                                GG AGT  TTGTTTAG  AA
                                || |||  ||||||||  ||
                                CC TCA  GGCGAATT  TT
                                 _  G_      GT
GAM393  MMP14   3' GTTCGGCTAGATTTCTGTCTT 17174       TGATT     _
                                GAGGCAG    GTTTAGT GAAT
                                |||||||    ||||||| ||||
                                TTCTGTC    TAGATCG CTTG
                                   TT___     G
GAM393  MMP7    3' ATTCATTGGATTGTATATCATT 60439       T____
          GTTGCA                 GCAGTGAT    GTTTAGTGAAT
                                ||||||||   ||||||||||
                                TGTTACTA    TAGGTTACTTA
                                     TATGT
GAM393  MOX2    3' TTCCTGCTTACTGCTTT    66931         TTGTT  T
                                GAGGCAGTGA    TAG GAA
                                |||||||||    ||| |||
```

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                                TTTCGTCATT     GTC CTT
                                      C____  _
GAM393  MTF1     3'  GAACATCGCTGTTTT       19884          T
                                GAGGCAGTGAT GTTT
                                |||||||||| ||||
                                TTTTGTCGCTA CAAG
                                      _
GAM393  MTMR1    3'  TTTGTTATCTAAGCAATTTTTG 70162        T       _  AT
           TTTTA                  GAGGCAG GATTGTTTAG TGA
                                ||||||| |||||||||| |||
                                TTTTGTT TTAACGAATC ATT
                                    T        T  GTTTT
GAM393  MTMR2    3'  ATTTACCTTGATCACTTTTCA  32381      C      TTTA
                                TGAGG AGTGATTG   GTGAAT
                                ||||| ||||||||   ||||||
                                ACTTT TCACTAGT   CATTTA
                                   _      TC__
GAM393  MTMR8    3'  ATTCACTAGGTGATAATTTCC  31289    C  G  TG
                                GG AGT AT  TTTAGTGAAT
                                || ||| ||  ||||||||||
                                CC TTA TA  GGATCACTTA
                                 T  A  GT
GAM393  MYB      3'  GTTGATAGCCAGTCACTGCCTT 59541            T  GTGAAT
           A                    TGAGGCAGTGATTG TTA
                                |||||||||||||| |||
                                ATTCCGTCACTGAC GAT
                                      C  AGTTG
GAM393  MYH4     5'  ATTCTTGAAGTAGTTGTCTGCT 34039       _    _   T
           TT                    GAGGCAG TGATTG TTTAG GAAT
                                ||||||| |||||| ||||| ||||
                                TTTCGTC GTTGAT AAGTT CTTA
                                    T    G   _
GAM393  MYLK     3'  GTTTGCTGAAAAGTTAGTCTTA 97021       AG   G    TG
                                TGAGGC  TGATT TTTAG  AAT
                                ||||||  ||||| |||||  |||
                                ATTCTG  ATTGA AAGTC  TTG
                                   __    A    GT
GAM393  NBS1     3'  GTTTATTAAATAGTTAATATAG 69500     AG___
           TC                    GGC    TGATTGTTTAGTGAAT
                                |||    ||||||||||||||||
                                CTG    ATTGATAAATTATTTG
                                  ATATA
GAM393  NCOA6    5'  ATTTATTGAATGGGGCTTGCTT 25956       _ GA TG
           T                     GAGGCA GT  T  TTTAGTGAAT
                                |||||| ||  |  ||||||||||
                                TTTCGT CG  G  AAGTTATTTA
                                   T  G_ GT
GAM393  NEDD4    3'  GTTTATTGAATGCTGCGTGCCT 70012       _  ATT
                                AGGCA GTG   GTTTAGTGAAT
                                ||||| |||   ||||||||||
```

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                                TCCGT CGT   TAAGTTATTTG
                                   G   CG_
GAM393  NEUROD1  3'  ATTTATTGTCATTACTGCCTT  10209          T TT
                                GAGGCAGTGAT G  TAGTGAAT
                                |||||||||| |  ||||||||
                                TTCCGTCATTA C  GTTATTTA
                                      _ T_
GAM393  NFRKB    5'  TACCGGCAGTTATGCTTCA   20498       G       TA
                                TGAGGCA TGATTGTT  GTG
                                ||||||| ||||||||  |||
                                ACTTCGT ATTGACGG  CAT
                                    _       C_
GAM393  NFRKB    5'  TTCGCTAGGCTGGTCTCA    20499       AGTGATT
                                TGAGGC      GTTTAGTGAA
                                ||||||      ||||||||||
                                ACTCTG      CGGATCGCTT
                                   GT_____
GAM393  NOTCH2   3'  TTGTTCATTCTCTGCTTTA   44317        T  T  TT
                                TGAGGCAG GA TG  TAG
                                |||||||| || ||  |||
                                ATTTCGTC CT AC  GTT
                                     T  T  TT
GAM393  NOTCH2   3'  TAAGATGGATAATCACTTTCTC 44314      C          GTGAAT
           A                     TGAGG AGTGATTGTTTA
                                 ||||| ||||||||||||
                                 ACTCT TCACTAATAGGT
                                    T          AGAATG
GAM393  NOV      3'  GTTTACTAAGTGGACTGGTGTC 10242     G  _   GA TG
           A                     TGA GC AGT  T  TTTAGTGAAT
                                 ||| || |||  |  ||||||||||
                                 ACT TG TCA  G  GAATCATTTG
                                   G  G   __ GT
GAM393  NR1D1    3'  ATTTGTTCTGTTCCTGTCTCA  41362        TG  TGTTT  TG
                                 TGAGGCAG  AT    AG  AAT
                                 |||||||  ||    ||  |||
                                 ACTCTGTC  TG    TT  TTA
                                      CT  TC___  GT
GAM393  NRBP     3'  ATTCGCCTCAGTTGCTGCT   25430      TG   TTTA
                                 GGCAG  ATTG   GTGAAT
                                 |||||  ||||   ||||||
                                 TCGTC  TGAC   CGCTTA
                                    GT   TC__
GAM393  NRG1     3'  TGCATCATGTTGAATAATGCTG 15691        G      __   AT
           TTTTA                   AGGCAGT ATTGTTTA  GTGA
                                   ||||||| ||||||||  ||||
                                   TTTGTCG TAATAAGT  TACT
                                      _       TG   ACGTT
GAM393  NTRK2    3'  ATTTATTATTATTACTGTTCTT 20521      _      TGTT
           A                     TGAGG CAGTGAT   TAGTGAAT
                                 ||||| |||||||   ||||||||
```

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                                ATTCT GTCATTA   ATTATTTA
                                  T     TT__
GAM393  NUP153   3' TTGTTTAGTCTTGTCTCA   17608       T   TT
                                TGAGGCAG GATTG  TAG
                                |||||||| |||||  |||
                                ACTCTGTT CTGAT  GTT
                                   _    TT
GAM393  OLR1     5' GTTTGTTGAAGTTCGTGACTGC 10339       G  TG__    TG
           TTCA                  GAGGCAGT AT   TTTAG  AAT
                                |||||||| ||   |||||  |||
                                CTTCGTCA TG   AAGTT  TTG
                                    G  CTTG    GT
GAM393  OPA1     3' TTGATTCAGTTGCTGTTTT   55536      TG   T_
                                GAGGCAG  ATTG  TTAG
                                |||||||  ||||  ||||
                                TTTTGTC  TGAC  AGTT
                                    GT    TT
GAM393  OPA1     3' TTGATTCAGTTGCTGTTTT   55545      TG   T_
                                GAGGCAG  ATTG  TTAG
                                |||||||  ||||  ||||
                                TTTTGTC  TGAC  AGTT
                                    GT    TT
GAM393  OPA1     3' TTGATTCAGTTGCTGTTTT   55554      TG   T_
                                GAGGCAG  ATTG  TTAG
                                |||||||  ||||  ||||
                                TTTTGTC  TGAC  AGTT
                                    GT    TT
GAM393  OPA1     3' TTGATTCAGTTGCTGTTTT   55563      TG   T_
                                GAGGCAG  ATTG  TTAG
                                |||||||  ||||  ||||
                                TTTTGTC  TGAC  AGTT
                                    GT    TT
GAM393  OPA1     3' TTGATTCAGTTGCTGTTTT   55572      TG   T_
                                GAGGCAG  ATTG  TTAG
                                |||||||  ||||  ||||
                                TTTTGTC  TGAC  AGTT
                                    GT    TT
GAM393  OPHN1    3' ATTTATTAACTGCTCAGTGTTT 10354       G   T GT
             CA                   TGAGGCA TGA T  TTAGTGAAT
                                |||||||  ||| |  |||||||||
                                ACTTTGT ACT G  AATTATTTA
                                    G   C TC
GAM393  OSCAR    5' TTTTCTGATGTTGCCTCA    55667       GT ATTGT    T
                                TGAGGCA  G     TTAG GAA
                                |||||||  |    |||| |||
                                ACTCCGT  T    AGTC TTT
                                    TG _____    T
GAM393  OSCAR    5' TTTTCTGATGTTGCCTCA    55671       GT ATTGT    T
                                TGAGGCA  G     TTAG GAA
                                |||||||  |    |||| |||
```

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                                ACTCCGT  T    AGTC TTT
                                   TG _____   T
GAM393  OSCAR    5'  TTTTCTGATGTTGCCTCA    55374       GT ATTGT   T
                                TGAGGCA  G    TTAG GAA
                                |||||||  |    |||| |||
                                ACTCCGT  T    AGTC TTT
                                   TG _____   T
GAM393  PAFAH1B1 3'  TTCAGGACAATATTGCCTCA  4735         A    AG   T
                                TGAGGCAGTG TTGTTT  TGAA
                                |||||||||| ||||||  ||||
                                ACTCCGTTAT AACAGG  ACTT
                                      _    __   T
GAM393  PAFAH1B2 3'  ATTCATTGAATTATTATCACTG 10405        T___
           TTTT                  GGCAGTGAT   GTTTAGTGAAT
                                |||||||||   ||||||||||
                                TTGTCACTA   TAAGTTACTTA
                                     TTAT
GAM393  PATE     3'  TTTCTGGGTGAGGTTGTTGCCT 56316       TG  GTTTAGT  T
           CA                    TGAGGCAG  ATT     GAA
                                |||||||  |||     |||
                                ACTCCGTT  TGG     CTT
                                   GT   AGTGGGT   TA
GAM393  PCDH11X  3'  TCAAAAAATGGTTCTGTTTTA  52029       T  TG  AG
                                TGAGGCAG GAT  TTT  TGA
                                |||||||| |||  |||  |||
                                ATTTTGTC TTG  AAA  ACT
                                   _  GT   AA
GAM393  PCDH11X  3'  TCAAAAAATGGTTCTGTTTTA  52051       T  TG  AG
                                TGAGGCAG GAT  TTT  TGA
                                |||||||| |||  |||  |||
                                ATTTTGTC TTG  AAA  ACT
                                   _  GT   AA
GAM393  PCDH11Y  5'  GAGCGGTTTTGCCTCA     52061       T
                                TGAGGCAG GATTGTTT
                                |||||||| ||||||||
                                ACTCCGTT TTGGCGAG
                                   _
GAM393  PCDH11Y  3'  TCGAAAAATGGTTCTGTTTTA  52085       T  TG  AG
                                TGAGGCAG GAT  TTT  TGA
                                |||||||| |||  |||  |||
                                ATTTTGTC TTG  AAA  GCT
                                   _  GT   AA
GAM393  PCDHA12  5'  TTTACTAAATATGTACTTA   49036   C   AT
                                G AGTG  TGTTTAGTGAA
                                | ||||  ||||||||||
                                A TCAT  ATAAATCATTT
                                 T   GT
GAM393  PCDHA12  5'  TTTACTAAATATGTACTTA   38214   C   AT
                                G AGTG  TGTTTAGTGAA
                                | ||||  ||||||||||
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                                A TCAT  ATAAATCATTT
                                 T   GT
GAM393  PDE1A   3'  ATTTACTTCCTTGCACTGTCTT 17215          ATTGTTT
              A                  TGAGGCAGTG      AGTGAAT
                                 ||||||||||      |||||||
                                 ATTCTGTCAC      TCATTTA
                                       GTTCCT_
GAM393  PDE4D   3'  ATTTACTTTGCATTTTGTTTCA 73580        TGAT   TT
                                 TGAGGCAG   TGT  AGTGAAT
                                 ||||||||   |||  |||||||
                                 ACTTTGTT   ACG  TCATTTA
                                      TT__   TT
GAM393  PDE4D   3'  GTTTGCTAGATGAGGTCTTGTC 73583      T   __     TG
                                 GGCAG GATT  GTTTAG  AAT
                                 ||||| ||||  ||||||  |||
                                 CTGTT CTGG  TAGATC  TTG
                                    _   AG     GT
GAM393  PDE4D   3'  GTTTGTTGAACAAAACTGACCT 73584      _   GA       TG
              T                  GAGG CAGT  TTGTTTAG  AAT
                                 |||| ||||  ||||||||  |||
                                 TTCC GTCA  AACAAGTT  TTG
                                   A   A_       GT
GAM393  PDE6B   3'  AGGTGATCACCGCCTCA     4272        A    TG
                                 TGAGGC GTGAT  TTT
                                 ||||||| |||||  |||
                                 ACTCCG CACTA  GGA
                                     C     GT
GAM393  PDGFRB  3'  GGACAGTTATGTCTT       65977       G
                                 GAGGCA TGATTGTTT
                                 |||||| |||||||||
                                 TTCTGT ATTGACAGG

                                    _
GAM393  PDGFRB  3'  TTGAGCAGTGTTGCCTCA    65982         G
                                 TGAGGCAGT ATTGTTTAG
                                 ||||||||| |||||||||
                                 ACTCCGTTG TGACGAGTT

                                     _
GAM393  PGF     3'  ATTTATTAGCCAACTGTTTC   10532         GAT  T
                                 GAGGCAGT   TG TTAGTGAAT
                                 ||||||||   || |||||||||
                                 CTTTGTCA   AC GATTATTTA
                                      ___  C
GAM393  PHTF1   3'  GTTTACTGGACATAGTCTT   21731       AGTGAT
                                 GAGGC     TGTTTAGTGAAT
                                 |||||     ||||||||||||
                                 TTCTG     ACAGGTCATTTG
                                   AT____
GAM393  PHYH    3'  AAATATTACTGTTTTA      20607           T
                                 TGAGGCAGTGAT GTTT
                                 |||||||||||| ||||
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                                ATTTTGTCATTA TAAA
                                           _
GAM393  PIK3CG   3'  AAATAATTACTTCTCA      10585      C
                                TGAGG AGTGATTGTTT
                                ||||| ||||||||||
                                ACTCT TCATTAATAAA
                                  _
GAM393  PITPNB   3'  TTATTTCTGGATGGTCATTATC 24782     GC     TG    T  AT
           TT                    GAG  AGTGAT  TTTAG GA
                                |||  ||||||  ||||| ||
                                TTC  TTACTG  AGGTC TT
                                  TA     GT    T  ATTT
GAM393  PLAG1    3'  ATTCACTGAATAATTATAGGCT 10606      A_
           TT                    GAGGC  GTGATTGTTTAGTGAAT
                                |||||  ||||||||||||||||
                                TTTCG  TATTAATAAGTCACTTA
                                   GA
GAM393  PLIN     3'  ATTTGCATCATTACTGCCTT   10639          T TTTA TG
                                GAGGCAGTGAT G    G  AAT
                                |||||||||| |    |  |||
                                TTCCGTCATTA C    C  TTA
                                      _ TA__ GT
GAM393  PLOD     3'  TTCACTTTTACTGCTTT     4322          TTGTTT
                                GAGGCAGTGA     AGTGAA
                                |||||||||      ||||||
                                TTTCGTCATT     TCACTT
                                     T_____
GAM393  PODXL    3'  TTCAGAGGTTACTGCTTTA    18244           GTTTAG
                                TGAGGCAGTGATT     TGAA
                                ||||||||||||      ||||
                                ATTTCGTCATTGG     ACTT
                                      AG____
GAM393  POLS     3'  ATAAGCTTGGGAGGTCATTGTT 22789           GTTT_   GAAT
           TTA                   TGAGGCAGTGATT     AGT
                                ||||||||||||     |||
                                ATTTTGTTACTGG     TCG
                                      AGGGT   AATA
GAM393  POU2F2   3'  ATTCCTCTGGTCCCTGCCTT   10688       T    TTT  T
                                GAGGCAG GATTG   AG GAAT
                                ||||||| |||||   || ||||
                                TTCCGTC CTGGT   TC CTTA
                                   C    C__  _
GAM393  PPP1R2   3'  ATTGTTAAATAGTCCCTGCTTT 20685        T        TG AT
           A                     TGAGGCAG GATTGTTTAG  A
                                ||||||||| ||||||||||  |
                                ATTTCGTC CTGATAAATT  T
                                     C         GT A
GAM393  PPP1R3A  3'  ATTTATTAAGCAGGTCTATCTT 10717     GC  TGA
                                GAG  AG   TTGTTTAGTGAAT
                                |||  ||   ||||||||||||
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                                TTC  TC   GACGAATTATTTA
                                  TA  TG_
GAM393  PPP1R3A  3'  TTGAATGATCATGTTTTA    10719       G    TG
                                TGAGGCA TGAT  TTTAG
                                ||||||| ||||  |||||
                                ATTTTGT ACTA  AAGTT
                                    _   GT
GAM393  PPP2CB   3'  ATTTAAACTAAATTACTGTTTT 14773           __     TGAAT
          A                      TGAGGCAGTGATT  GTTTAG
                                ||||||||||||  ||||||
                                ATTTTGTCATTAA  CAAATT
                                      AT     TA
GAM393  PRDM2    3'  ATTTGTTGTGCTATTGCTGC   31846     TG  T  T   TG
                                GCAG  AT GT TAG  AAT
                                ||||  || || |||  |||
                                CGTC  TA CG GTT  TTA
                                  GT  T  T   GT
GAM393  PROC     3'  ATTTACTGAGCACCTGTT    4342       TGAT
                                GGCAG    TGTTTAGTGAAT
                                |||||    ||||||||||||
                                TTGTC    ACGAGTCATTTA
                                  C___
GAM393  PTGFR    3'  TAGGGAAGGTAGTCCTGCTTTA 6318         T     TT AGTGAAT
                                TGAGGCAG GATTG  T
                                |||||||| |||||  |
                                ATTTCGTC CTGAT  A
                                    _    GG AGGGATT
GAM393  PTPN7    3'  GCTAAGCAGTCTCTGTTTT    11070       T
                                GAGGCAG GATTGTTTAGT
                                ||||||| ||||||||||
                                TTTTGTC CTGACGAATCG
                                    T
GAM393  PTPN7    3'  GCTAAGCAGTCTCTGTTTT    54552       T
                                GAGGCAG GATTGTTTAGT
                                ||||||| ||||||||||
                                TTTTGTC CTGACGAATCG
                                    T
GAM393  PTPN7    3'  GCTAAGCAGTCTCTGTTTT    54563       T
                                GAGGCAG GATTGTTTAGT
                                ||||||| ||||||||||
                                TTTTGTC CTGACGAATCG
                                    T
GAM393  PUM2     3'  TTTAATACAATTACTGCC     31017          TTAG   T
                                GGCAGTGATTGT   TGAA
                                ||||||||||||   ||||
                                CCGTCATTAACA   ATTT
                                      TA__   T
GAM393  PXF      3'  TCTTTGAGTAGCACTGTTTT   11153        A      T
                                GAGGCAGTG TTGTTTAG GA
                                ||||||||| |||||||| ||
```

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                                TTTTGTCAC GATGAGTT CT
                                      _       T
GAM393  RAB30    3'  AACAATCATTGTTTTA      27167
                                TGAGGCAGTGATTGTT
                                ||||||||||||||||
                                ATTTTGTTACTAACAA

GAM393  RAB36    3'  GTTTGCTGGGCATAAGCTTCA  16971       AGTGAT      TG
                                TGAGGC     TGTTTAG  AAT
                                ||||||     |||||||  |||
                                ACTTCG     ACGGGTC  TTG
                                   AAT___      GT
GAM393  RAD18    3'  GTTTGTTAGACCTGTGTC    39397    G   TGATT     TG
                                GA GCAG    GTTTAG  AAT
                                || ||||    ||||||  |||
                                CT TGTC    CAGATT  TTG
                                 G  _____     GT
GAM393  RAD21    3'  TGTGAACTCGTAATTACTGTTT 20761           TTT   GAAT
             TA                   TGAGGCAGTGATTG   AGT
                                ||||||||||||||   |||
                                ATTTTGTCATTAAT   TCA
                                       GC_   AGTGTT
GAM393  RAD50    3'  AGATAATTACTGCCTT      56005
                                GAGGCAGTGATTGTTT
                                ||||||||||||||||
                                TTCCGTCATTAATAGA

GAM393  RAD50    3'  AGATAATTACTGCCTT      19191
                                GAGGCAGTGATTGTTT
                                ||||||||||||||||
                                TTCCGTCATTAATAGA

GAM393  RAD51C   3'  ATTTATTATTTTCGCTGTC    54254        TTGTT
                                GGCAGTGA    TAGTGAAT
                                ||||||||    ||||||||
                                CTGTCGCT    ATTATTTA
                                     TTT__
GAM393  RAD54B   3'  ATTCGTTGGAAAAATTCATTGT 56234         TTG__
             CTC                   AGGCAGTGA    TTTAGTGAAT
                                |||||||||    ||||||||||
                                TCTGTTACT    AGGTTGCTTA
                                     TAAAA
GAM393  RAP1B    3'  ATTTGCAGTAACTATTGCTGTT 31597        TG  T   TA_ TG
             TTA                   TGAGGCAG  AT GTT   G  AAT
                                ||||||||  || |||   |  |||
                                ATTTTGTC  TA CAA   C  TTA
                                     GT  T   TGA GT
GAM393  RELN     3'  ATTTGTAAAACAGTGGTTGTTT 94303        TG      A TG
             T                    GAGGCAG  ATTGTTT G  AAT
                                |||||||  |||||||  |  |||
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                                TTTTGTT  TGACAAA T  TTA
                                    GG      A GT
GAM393  RGL      3'  TCTTGGAATGTCACTGCTTCA  30739          TG    T
                                TGAGGCAGTGAT  TTTAG GA
                                |||||||||||  ||||| ||
                                ACTTCGTCACTG  AGGTT CT
                                      TA    _
GAM393  RGS9     5'  AAACAGTCGTTGCTGTCA    13830    _
                                TGA GGCAGTGATTGTTT
                                ||| ||||||||||||||
                                ACT TCGTTGCTGACAAA
                                  G
GAM393  SACM1L   3'  ATTGATCTGATGTTACTGCCTT 25819          TGT   _ G
                                GAGGCAGTGAT   TTAG T AAT
                                ||||||||||   |||| | |||
                                TTCCGTCATTG   AGTC A TTA
                                      T__    T G
GAM393  SCG2     3'  ATTTATTGAATTATTTTGTTAC 12953       T_____
            TGTCT                   CAGTGAT     GTTTAGTGAAT
                                |||||||     ||||||||||
                                GTCATTG     TAAGTTATTTA
                                    TTTTAT
GAM393  SCML2    3'  TTTCTCTTAGCAGTTTTTGTTT 20327       T     T  T   T
            T                    GAGGCAG GATTGTT AG GAA
                                ||||||| ||||||| || |||
                                TTTTGTT TTGACGA TC CTT
                                    T      T  T   TA
GAM393  SEL1L    3'  GTTTGTTTATGCATTGCCTT   17363        ATTGTTT  TG
                                GAGGCAGTG      AG  AAT
                                |||||||||      ||  |||
                                TTCCGTTAC      TT  TTG
                                     GTAT___  GT
GAM393  SELE     3'  ATTACACAGTTGCTGTC     4827       TG    T
                                GGCAG  ATTGT TAGT
                                |||||  ||||| ||||
                                CTGTC  TGACA ATTA
                                   GT    C
GAM393  SELENBP1 3'  ATTTACTGACCACTGTT     14152       ATTGT
                                GGCAGTG    TTAGTGAAT
                                |||||||    |||||||||
                                TTGTCAC    AGTCATTTA
                                    C_____
GAM393  SHANK2   3'  GTTTATTTTTACACTGTCTTA  24589         ATTGTTT
                                TGAGGCAGTG      AGTGAAT
                                ||||||||||      |||||||
                                ATTCTGTCAC      TTATTTG
                                      ATTT___
GAM393  SIM2     3'  ATTCACTAGGCTCGTGTTTGCT 17383    A    TGATT_
            ACA                   TG GGCAG     GTTTAGTGAAT
                                || |||||     ||||||||||
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                                AC TCGTT     CGGATCACTTA
                                 A    TGTGCT
GAM393  SLC12A4  3'  ATTTATTGCATATTTATTGTTT 17389        T  T
                                AGGCAGTGA TGT TAGTGAAT
                                ||||||||| ||| ||||||||
                                TTTGTTATT ATA GTTATTTA
                                     T  C
GAM393  SLC16A1  3'  ATTTAAAATTAATCTTGCTTCA 11740       T    TTTAG
                                TGAGGCAG GATTG    TGAAT
                                |||||||| |||||    ||||||
                                ACTTCGTT CTAAT    ATTTA
                                     _    TAAA_
GAM393  SLC1A3   5'  ATTCACCTCGTTACTGCTT   14797         TGTTTA
                                AGGCAGTGAT    GTGAAT
                                ||||||||||    ||||||
                                TTCGTCATTG    CACTTA
                                      CTC___
GAM393  SLC25A15 3'  AGGTGATCATTTCTCA     26509      C     TG
                                TGAGG AGTGAT  TTT
                                ||||| ||||||  |||
                                ACTCT TTACTA  GGA
                                   _     GT
GAM393  SLC2A3   3'  ATTATCTAAAGTGTGTTGTTGC 22658       TG  TG__    _  AT
           TTTA                    AGGCAG  AT    TTTAG TGA
                                ||||||  ||    ||||| |||
                                TTCGTT  TG    AAATC ATT
                                   GT  TGTG    T  A
GAM393  SLC2A8   3'  GTTTATTCCCATCACTGCCCA  27423    A       T TTT
                                TG GGCAGTGAT G   AGTGAAT
                                || |||||||| |   |||||||
                                AC CCGTCACTA C   TTATTTG
                                 _       _ CC_
GAM393  SLC6A6   3'  AGGCAGTCACTGCTC       11727     G
                                GAG CAGTGATTGTTT
                                ||| ||||||||||||
                                CTC GTCACTGACGGA
                                  _
GAM393  SLC7A2   5'  GTTTATTGGAACACCTGCCCCA 11738    A    TGAT    _
                                TG GGCAG    TGTTT AGTGAAT
                                || |||||    ||||| |||||||
                                AC CCGTC    ACAAG TTATTTG
                                 C    C___     G
GAM393  SLC9A6   3'  CTGAGTAGCATTGCCTTA    21002          A
                                TGAGGCAGTG TTGTTTAG
                                |||||||||| ||||||||
                                ATTCCGTTAC GATGAGTC
                                          _
GAM393  SMP1     3'  ATTTGCTGGGTGATTTAAATGT 26696     GT__  TG    TG
                                GCA    GAT  TTTAG  AAT
                                |||    |||  |||||  |||
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                                TGT   TTA  GGGTC  TTA
                                  AAAT   GT    GT
GAM393  SNAI2    3'  GAACAGTATTGCTTT      11776        G
                                GAGGCAGT ATTGTTT
                                |||||||| |||||||
                                TTTCGTTA TGACAAG
                                        _
GAM393  SOD3     5'  ATTTACTGACGTTGTTGTCTC  11859       TG  T   T
                                GAGGCAG  AT GTT AGTGAAT
                                |||||||  || ||| |||||||
                                CTCTGTT  TG CAG TCATTTA
                                    GT  _   _
GAM393  SORCS1   3'  ATTTATTAAACAGATAATGTCT 53581       G  A
          C                      GAGGCA TG TTGTTTAGTGAAT
                                |||||| || ||||||||||||||
                                CTCTGT AT GACAAATTATTTA
                                   A  A
GAM393  SOS2     3'  TCAGTAGCATTGCCTT      68538         ATTGT   G
                                GAGGCAGTG    TTA TGA
                                |||||||||    ||| |||
                                TTCCGTTAC    GAT ACT
                                      _____  G
GAM393  SOX12    3'  AATAATAGCTGCTTCA      22692         G
                                TGAGGCAGT ATTGTT
                                ||||||||| ||||||
                                ACTTCGTCG TAATAA
                                     A
GAM393  SOX12    3'  GGGCGTCGCTGCCTTA      22699          T
                                TGAGGCAGTGAT GTTT
                                |||||||||||| ||||
                                ATTCCGTCGCTG CGGG
                                       _
GAM393  SPON1    3'  TATTGTTGAAAACTATTGTTTC 62457         ATTG    TG AT
          A                      TGAGGCAGTG   TTTAG  A
                                |||||||||   |||||  |
                                ACTTTGTTAT   AAGTT  T
                                     CAA_    GT ATT
GAM393  SPR      3'  GGGCAGTCCTGCCTTA      11933        T
                                TGAGGCAG GATTGTTT
                                |||||||| ||||||||
                                ATTCCGTC CTGACGGG
                                       _
GAM393  SRD5A1   3'  TTCATCTGGCATTGCTTT    6460         ATTGT   _
                                GAGGCAGTG    TTAG TGAA
                                |||||||||    |||| ||||
                                TTTCGTTAC    GGTC ACTT
                                      _____   T
GAM393  SRP46    3'  TTCTATAGTGATGACTGTTTT  49466        G  TG  TAGT   T
                                GAGGCAGT AT  TT   GAA
                                |||||||| ||  ||   |||
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                                TTTTGTCA TA  GA    CTT
                                     G  GT  TAT_   T
GAM393  ST5     3'  GAGCAGATGCTGTCTT      18291          A
                                GAGGCAGTG TTGTTT
                                ||||||||| ||||||
                                TTCTGTCGT GACGAG
                                     A
GAM393  ST5     3'  GAGCAGATGCTGTCTT      57497          A
                                GAGGCAGTG TTGTTT
                                ||||||||| ||||||
                                TTCTGTCGT GACGAG
                                     A
GAM393  STATH   3'  ATTTACTGTATACTCTTTGTTT 12027         T  T   T
            CA                    TGAGGCAG GA TGT TAGTGAAT
                                ||||||||| || ||| ||||||||
                                ACTTTGTT CT ATA GTCATTTA
                                     T  C   T
GAM393  STAU2   3'  TACCAACAATTCTGTTTCA   26908         T      TA
                                TGAGGCAG GATTGTT  GTG
                                ||||||||| |||||||  |||
                                ACTTTGTC TTAACAA  CAT
                                     _      C_
GAM393  SULT1A3 5'  TGAGAAGTCACTGCTTT     12055           G
                                GAGGCAGTGATT TTTA
                                |||||||||||| ||||
                                TTTCGTCACTGA GAGT
                                      A
GAM393  SURF4   3'  TTTTCTAACACTGCCTTA    52549          ATTGT    T
                                TGAGGCAGTG    TTAG GAA
                                ||||||||||    |||| |||
                                ATTCCGTCAC    AATC TTT
                                     _____    T
GAM393  SURF6   3'  GGGGGTGGGCAGTCACTGCCT  22190              GTGAAT
                                AGGCAGTGATTGTTTA
                                ||||||||||||||||
                                TCCGTCACTGACGGGT
                                          GGGGGT
GAM393  SYNGR1  3'  TGGGTGGTCCCTGCTTC     16325        T   TG
                                GAGGCAG GAT  TTTA
                                ||||||| |||  ||||
                                CTTCGTC CTG  GGGT
                                     C   GT
GAM393  SYNGR3  3'  TCCCTGTGGGTAGTGACTGTCT 14856         G    TT  GTGAAT
            C                    GAGGCAGT ATTG  TA
                                ||||||||| ||||  ||
                                CTCTGTCA TGAT  GT
                                     G    GG  GTCCCTG
GAM393  TAC1    3'  AGAAATAAGTGGTTATTTCTCA 25725       C      TG    GTGAAT
                                TGAGG AGTGAT  TTTA
                                ||||| ||||||  ||||
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                                ACTCT TTATTG  GAAT
                                  _     GT    AAAGAT
GAM393  TAC1    3'  AGAAATAAGTGGTTATTTCTCA 25726      C     TG    GTGAAT
                                TGAGG AGTGAT  TTTA
                                ||||| ||||||  ||||
                                ACTCT TTATTG  GAAT
                                  _     GT    AAAGAT
GAM393  TAC1    3'  AGAAATAAGTGGTTATTTCTCA 12078      C     TG    GTGAAT
                                TGAGG AGTGAT  TTTA
                                ||||| ||||||  ||||
                                ACTCT TTATTG  GAAT
                                  _     GT    AAAGAT
GAM393  TAC1    3'  AGAAATAAGTGGTTATTTCTCA 25724      C     TG    GTGAAT
                                TGAGG AGTGAT  TTTA
                                ||||| ||||||  ||||
                                ACTCT TTATTG  GAAT
                                  _     GT    AAAGAT
GAM393  TAF1    5'  GTCACTTCTGGGCGACTGTTGT 57189      GT A    ___    AT
          TTTA                    AGGCA  G TTGTTT   AGTGA
                                ||||| | ||||||   |||||
                                TTTGT  T AGCGGG   TCACT
                                  TG C     TCT    G
GAM393  TAF1    5'  GTCACTTCTGGGCGACTGTTGT 16035      GT A    ___    AT
          TTTA                    AGGCA  G TTGTTT   AGTGA
                                ||||| | ||||||   |||||
                                TTTGT  T AGCGGG   TCACT
                                  TG C     TCT    G
GAM393  TAF4B   3'  TTACTACCTGCCTCA      87170        TGATTGTT
                                TGAGGCAG      TAGTGA
                                ||||||||      ||||||
                                ACTCCGTC      ATCATT
                                    C_______
GAM393  TAGLN   3'  AAGCATCACTGCCTT      59631          T
                                GAGGCAGTGAT GTTT
                                |||||||||| ||||
                                TTCCGTCACTA CGAA
                                          _
GAM393  TBL1X   3'  GTTCATTGGGTGGTTTTTCA  18936      CAGT  TG
                                TGAGG   GAT  TTTAGTGAAT
                                |||||   |||  ||||||||||
                                ACTTT   TTG  GGGTTACTTG
                                  _____  GT
GAM393  TCF1    3'  TAGGAGGGACTGTCGCTGCTTC 5036          T   AGTGAAT
                                GAGGCAGTGAT GTTT
                                |||||||||| ||||
                                CTTCGTCGCTG CAGG
                                      T   GAGGATG
GAM393  TEM5    3'  TTGGAGAAGCAGTTACTTTTCA 51320      C        AGTGAAT
                                TGAGG AGTGATTGTTT
                                ||||| ||||||||||
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                                ACTTT TCATTGACGAA
                                  _         GAGGTTT
GAM393  TIF1    3'  GTTTACTAGACTTTGATTTCCT 60380      C   GATT
           TA                    TGAGG AGT    GTTTAGTGAAT
                                 ||||| |||    ||||||||||
                                 ATTCC TTA    CAGATCATTTG
                                    T   GTTT
GAM393  TIMP3   3'  GAATAGTTTTTGCTTT      4509         T
                                 GAGGCAG GATTGTTT
                                 ||||||| ||||||||
                                 TTTCGTT TTGATAAG
                                     T
GAM393  TMC1    5'  AGGAATCATTGCCCCA      56897    A        G
                                 TG GGCAGTGATT TT
                                 || |||||||||| ||
                                 AC CCGTTACTAA GA
                                  C         G
GAM393  TMC1    5'  TGAAAGATCACTGTTTTA    56909            G
                                 TGAGGCAGTGATT TTTA
                                 |||||||||||||| ||||
                                 ATTTTGTCACTAG AAGT
                                         A
GAM393  TMEM1   3'  ATTTACTGGGCAAATGTGCTT  12334      GTGA
                                 AGGCA    TTGTTTAGTGAAT
                                 |||||    ||||||||||||||
                                 TTCGT    AACGGGTCATTTA
                                    GTA_
GAM393  TMOD2   3'  TTTAGAAGCATTTATTGCTTT  27256          T    AG    T
                                 GAGGCAGTGA TGTTT  TGAA
                                 |||||||||| |||||  ||||
                                 TTTCGTTATT ACGAA  ATTT
                                       T    G_   T
GAM393  TMOD3   3'  TCAGAATTGTTATTGCTTCA   27246           T   AG
                                 TGAGGCAGTGAT GTTT  TGA
                                 |||||||||||| ||||  |||
                                 ACTTCGTTATTG TAAG  ACT
                                         T   __
GAM393  TOP1    3'  AAGCAGTCGTGGCTTT      12357       AG
                                 GAGGC  TGATTGTTT
                                 |||||  |||||||||
                                 TTTCG  GCTGACGAA
                                    GT
GAM393  TP53    3'  GCTCGAGCAGTCCTGCCTCA   5041         T       _
                                 TGAGGCAG GATTGTTT AGT
                                 |||||||| |||||||| |||
                                 ACTCCGTC CTGACGAG TCG
                                      _       C
GAM393  TP53BP2 3'  ATTTATTGGGCAGTTGGGAAAT 18299     GGCAGT
           CA                    TGA     GATTGTTTAGTGAAT
                                 |||     ||||||||||||||||
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                                ACT     TTGACGGGTTATTTA
                                  AAAGGG
GAM393  TRHDE    3'  GTCTGGCAATGATTACTGTGTT 25387    G      TG  TAGT  AT
                                GA GCAGTGAT  TT    GA
                                || ||||||||  ||    ||
                                TT TGTCATTA  AA    CT
                                 G       GT  CGGT  G
GAM393  TRIM14   3'  ATAATGCACTGTTTTA      28850          _
                                TGAGGCAGTG ATTGT
                                |||||||||| |||||
                                ATTTTGTCAC TAATA
                                      G
GAM393  TRO      3'  TTTGCTGTTCCTGCTTTA    32389        T  TTGTT   TG
                                TGAGGCAG GA     TAG  AA
                                |||||||| ||     |||  ||
                                ATTTCGTC CT     GTC  TT
                                     _  T____   GT
GAM393  TRPS1    3'  TAAACAATCACTTTTTA     26077      C
                                TGAGG AGTGATTGTTTA
                                ||||| ||||||||||||
                                ATTTT TCACTAACAAAT
                                  _
GAM393  TSGA10   5'  GTTCCTGACATAATCATTGTTC 47500      G        _    T
          A                      TGAG CAGTGATTGT TTAG GAAT
                                |||| |||||||||| |||| ||||
                                ACTT GTTACTAATA AGTC CTTG
                                  _         C    _
GAM393  TSN      3'  AACAGTCATGTTTTA       16098        G
                                TGAGGCA TGATTGTT
                                ||||||| ||||||||
                                ATTTTGT ACTGACAA
                                  _
GAM393  UBE2L3   3'  TTAAAAATCACTGCTTCA    12509             G
                                TGAGGCAGTGATT TTTAG
                                |||||||||||| |||||
                                ACTTCGTCACTAA AAATT
                                        _
GAM393  UBE4A    3'  GTTTACTAACATACTCATTCTT 16565       C     T   _
          CA                     TGAGG AGTGA TGT TTAGTGAAT
                                ||||| ||||| ||| |||||||||
                                ACTTC TTACT ATA AATCATTTG
                                  _    C   C
GAM393  UMPS     3'  GTTTGTTAGACAGCCACAGTCC 4556     _ A   AT      TG
          T                      AGG C GTG  TGTTTAG  AAT
                                ||| | |||  |||||||  |||
                                TCC G CAC  ACAGATT  TTG
                                 T A  CG      GT
GAM393  UNRIP    3'  GTTCATTGTACACTGCCTC    23203          ATTGTT
                                GAGGCAGTG     TAGTGAAT
                                |||||||||     ||||||||
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                                CTCCGTCAC     GTTACTTG
                                     AT____
GAM393  WEE1    3'  TAGCATTAAACAATCATTGTT  12654              AAT
                                GGCAGTGATTGTTTAGTG
                                ||||||||||||||||||
                                TTGTTACTAACAAATTAC
                                          GATG
GAM393  WFS1    3'  TTGTTTGGTCACTGCTACA   20013    A        TT
                                TG GGCAGTGATTG  TAG
                                || ||||||||||  |||
                                AC TCGTCACTGGT  GTT
                                 A         TT
GAM393  WHSC1   3'  ATTCACTTGAGTTGTTGCTT  23654      TG   GTTT
                                AGGCAG  ATT   AGTGAAT
                                ||||||  |||   |||||||
                                TTCGTT  TGA   TCACTTA
                                   GT   GT__
GAM393  WRB     3'  ATTTGTTGAGCAAGAGTTGT   16125     GA      TG
                                GCAGT  TTGTTTAG  AAT
                                |||||  ||||||||  |||
                                TGTTG  AACGAGTT  TTA
                                  AG       GT
GAM393  XRCC2   3'  TTCGTTGCAGCACTGCCCA   18333    A     A   TTAG
                                TG GGCAGTG TTGT   TGAA
                                || ||||||| ||||   ||||
                                AC CCGTCAC GACG   GCTT
                                 _      _   TT__
GAM393  XRCC4   3'  TTCACTAGACTATGTTTT    42587      GTGATT
                                GAGGCA    GTTTAGTGAA
                                ||||||    ||||||||||
                                TTTTGT    CAGATCACTT
                                   AT____
GAM393  XRCC4   3'  TTCACTAGACTATGTTTT    42357      GTGATT
                                GAGGCA    GTTTAGTGAA
                                ||||||    ||||||||||
                                TTTTGT    CAGATCACTT
                                   AT____
GAM393  XRCC4   3'  TTCACTAGACTATGTTTT    12687      GTGATT
                                GAGGCA    GTTTAGTGAA
                                ||||||    ||||||||||
                                TTTTGT    CAGATCACTT
                                   AT____
GAM393  YWHAH   3'  ATTCAATGGGTAAATAAATGCT 12693      A     G____
            GCTTT                GCAGTG TTGTTTA    TGAAT
                                ||||||| |||||||    |||||
                                CGTCGT AATAAAT    ACTTA
                                   A      GGGTA
GAM393  ZFP37   3'  ATTTGCATATCTGTTTATTGCC 12713          TTGTT _ TG
            TTA                  TGAGGCAGTGA    TA G  AAT
                                ||||||||||    || |  |||
```

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                                ATTCCGTTATT    AT C  TTA
                                     TGTCT  A GT
GAM393  ZNF10    3'  ATTTACTGAGTTCTCACTTCCC 31176      C_    TT
          TTA                  TGAGG  AGTGA  GTTTAGTGAAT
                               |||||  |||||  ||||||||||
                               ATTCC  TCACT  TGAGTCATTTA
                                  CT    CT
GAM393  ZNF18    3'  GCTGTAGTCACTGCTT     78141          TT
                               AGGCAGTGATTG  TAGT
                               ||||||||||||  ||||
                               TTCGTCACTGAT  GTCG
                                          __
GAM393  ZNF6     5'  TAAAGGAAGCAGTCATGTTTCA 41819       G       AGTGAAT
                               TGAGGCA TGATTGTTT
                               |||||||  |||||||||
                               ACTTTGT ACTGACGAA
                                  _       GGAAATA
GAM393  3-PAP    5'  TCGCGGCGGTCGCGGCCTT   38805      A       TA
                               GAGGC GTGATTGTT  GTGA
                               |||||  |||||||||  ||||
                               TTCCG CGCTGGCGG  CGCT
                                  G       __
GAM393  AAK1     3'  GTTTGCTGAGCGGCTTATGTTC 29854     CA   _      TG
          T                    AGG  GTGA TTGTTTAG  AAT
                               |||  ||||  ||||||||  |||
                               TCT  TATT GGCGAGTC  TTG
                                 TG   C       GT
GAM393  ABHD2    5'  TTTGCAAGCCACTGCTTTA   22810         ATT    A TG
                               TGAGGCAGTG   GTTT G  AA
                               ||||||||||   |||| |  ||
                               ATTTCGTCAC   CGAA C  TT
                                     ____   _ GT
GAM393  ABLIM    3'  TGGAATGAACAGTCACTGTTCT 22040    AG          GTGAAT
          A                     TG  GCAGTGATTGTTTA
                                ||  ||||||||||||||
                                AT  TGTCACTGACAAGT
                                 CT           AAGGTG
GAM393  ABLIM    3'  TGGAATGAACAGTCACTGTTCT 9778     AG          GTGAAT
          A                     TG  GCAGTGATTGTTTA
                                ||  ||||||||||||||
                                AT  TGTCACTGACAAGT
                                 CT           AAGGTG
GAM393  ACAA2    3'  AAATAAATGTTGCCTTA     91764       GT A
                               TGAGGCA  G TTGTTT
                               |||||||  | ||||||
                               ATTCCGT  T AATAAA
                                   TG A
GAM393  AD-020   3'  AGCAGTATTGCCTCA       39307         G
                               TGAGGCAGT ATTGTT
                               |||||||| ||||||
```

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                                ACTCCGTTA TGACGA
                                        _
GAM393  AD-020   3' AGCAGTATTGCCTCA      59383        G
                                TGAGGCAGT ATTGTT
                                ||||||||| ||||||
                                ACTCCGTTA TGACGA
                                        _
GAM393  AKAP6    3' ATTTATTAAAAAGCTGCTTT  14988        GATTG
                                GAGGCAGT    TTTAGTGAAT
                                ||||||||    ||||||||||
                                TTTCGTCG    AAATTATTTA
                                     AA___
GAM393  AKAP6    3' GTTTGTTGAACAATGCCTT   14995      GTGA      TG
                                GAGGCA   TTGTTTAG  AAT
                                ||||||   ||||||||  |||
                                TTCCGT   AACAAGTT  TTG
                                   ____      GT
GAM393  AKAP7    3' GTTTATTGAACAATAGTACTT 16726    GCAGTG
                                GAG     ATTGTTTAGTGAAT
                                |||     ||||||||||||||
                                TTC     TAACAAGTTATTTG
                                  ATGA__
GAM393  AKAP7    3' GTTTATTGAACAATAGTACTT 33051    GCAGTG
                                GAG     ATTGTTTAGTGAAT
                                |||     ||||||||||||||
                                TTC     TAACAAGTTATTTG
                                  ATGA__
GAM393  AKAP7    3' GTTTATTGAACAATAGTACTT 56839    GCAGTG
                                GAG     ATTGTTTAGTGAAT
                                |||     ||||||||||||||
                                TTC     TAACAAGTTATTTG
                                  ATGA__
GAM393  AKR1D1   3' ATTCACATTAGGTCACTGTC  19973        GTTTA
                                GGCAGTGATT    GTGAAT
                                ||||||||||    ||||||
                                CTGTCACTGG    CACTTA
                                     ATTA_
GAM393  ALS2CR3  3' AAGTAATTACTGTTTC     30482
                                GAGGCAGTGATTGTTT
                                ||||||||||||||||
                                CTTTGTCATTAATGAA

GAM393  ALY      3' TTTACTGGTTGCTGTT     19353      TG  TGTT
                                GGCAG  AT   TAGTGAA
                                |||||  ||   |||||||
                                TTGTC  TG   GTCATTT
                                   GT  _____
GAM393  AMOTL1   3' GTTCATCTCTGTCTCTGCTTTA 73655        T   TGTTTA
                                TGAGGCAG GAT     GTGAAT
                                |||||||| |||     ||||||
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                                ATTTCGTC CTG     TACTTG
                                     T  TCTC__
GAM393  ANKRD6   3'  TTTATTGAGAACTGCCT    30094       GATTGT
                                AGGCAGT     TTAGTGAA
                                |||||||     ||||||||
                                TCCGTCA     AGTTATTT
                                    AG____
GAM393  ANP32B   3'  TAAACAGTTACTCTTT     21133     C
                                GAGG AGTGATTGTTTA
                                |||| ||||||||||||
                                TTTC TCATTGACAAAT

                                  _
GAM393  AP1S2    3'  ATTCAGGCCACGTGAGCACTGT 14039        AT__  TTAG
           CTTA                   GAGGCAGTG   TGT   TGAAT
                                |||||||||   |||   |||||
                                TTCTGTCAC   GCA   ACTTA
                                     GAGT   CCGG
GAM393  APG-1    3'  GTTCATTTCCATTGCTGCTT  26552      TG  T TTT
                                AGGCAG  AT G   AGTGAAT
                                ||||||  || |   |||||||
                                TTCGTC  TA C   TTACTTG
                                   GT  _ CT_
GAM393  ARF4     3'  GTTTATTGGGCAGACATATCTT 82815      CA   A
           CA                    TGAGG  GTG TTGTTTAGTGAAT
                                |||||  ||| ||||||||||||
                                ACTTC  TAC GACGGGTTATTTG
                                   TA   A
GAM393  ARHE     3'  AGGTAGTTACTGTTTT     17711           TT
                                GAGGCAGTGATTG  T
                                ||||||||||||  |
                                TTTTGTCATTGAT  A
                                       GG
GAM393  ARHGEF10 3'  AACAGTTAATGTTTCA     60418       G
                                TGAGGCA TGATTGTT
                                ||||||| ||||||||
                                ACTTTGT ATTGACAA
                                    A
GAM393  ARHGEF9  3'  TGAGTGATTCACTGCCTT   30823         _ TG
                                GAGGCAGTGA T  TTTA
                                |||||||||| |  ||||
                                TTCCGTCACT A  GAGT
                                     T GT
GAM393  ASAH     3'  ATTCACTGAGTTTTGTTTCA  15047       TGATTG
                                TGAGGCAG    TTTAGTGAAT
                                ||||||||    ||||||||||
                                ACTTTGTT    GAGTCACTTA
                                    TT_____
GAM393  ATP6M8-9 3'  TTTATTAGACAAACTTAC    19277     __
                                GTGA  TTGTTTAGTGAA
                                ||||  ||||||||||||
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```
                                CATT  AACAGATTATTT
                                  CA
GAM393  ATP6V0A2  3'  ATTCCATCTTCATTACTGCCTT 24945           T TTTAGT
            A                    TGAGGCAGTGAT G     GAAT
                                 |||||||||||| |     ||||
                                 ATTCCGTCATTA C     CTTA
                                       _ TTCTAC
GAM393  ATP9A    3'  TTCACTGGACGGTCCCTG    62054     T
                                 CAG GATTGTTTAGTGAA
                                 ||| ||||||||||||||
                                 GTC CTGGCAGGTCACTT
                                   C
GAM393  ATP9A    3'  ATTCATTGAGTGAGTTTCTGT  62037      TGA_ TG
                                 GCAG   T  TTTAGTGAAT
                                 ||||   |  ||||||||||
                                 TGTC   A  GAGTTACTTA
                                   TTTG GT
GAM393  B3GALT1   5'  ATTTATTAGTAATATGCTGCCT 40612         GATTGT
            T                    GAGGCAGT     TTAGTGAAT
                                 ||||||||     |||||||||
                                 TTCCGTCG     GATTATTTA
                                      TATAAT
GAM393  BANP     5'  GTTTATTGAGCACCTGCC    66218       TGAT
                                 GGCAG   TGTTTAGTGAAT
                                 |||||   ||||||||||||
                                 CCGTC   ACGAGTTATTTG
                                   C___
GAM393  BFAR     3'  ATTCAATCAACAATTCTGTCTT 60769         T      TAG
            A                    TGAGGCAG GATTGTT   TGAAT
                                 |||||||| |||||||   |||||
                                 ATTCTGTC TTAACAA   ACTTA
                                      _      CTA
GAM393  BLP1     3'  GTTTACTAAAAAGAGCTGCCAT 49200     _     GATTG
            CA                     TGA GGCAGT     TTTAGTGAAT
                                 ||| ||||||    ||||||||||
                                 ACT CCGTCG     AAATCATTTG
                                   A     AGAA_
GAM393  BNIP2    3'  GTTCACTGCTGTACTGGTTT   66768     G    ATT  TT
                                 GAG CAGTG   GT  AGTGAAT
                                 ||| |||||   ||  |||||||
                                 TTT GTCAT   CG  TCACTTG
                                   G    GT_ __
GAM393  BNIP2    3'  GTTTATTGAATGATGCATCTTC 66769      CA  _  TG
                                 GAGG  GTG AT  TTTAGTGAAT
                                 ||||  ||| ||  ||||||||||
                                 CTTC  TAC TA  AAGTTATTTG
                                   __  G  GT
GAM393  BTN2A2   3'  AAACGATTAATGTTTCA     22774        G
                                 TGAGGCA TGATTGTTT
                                 ||||||| |||||||||
```

```
                                ACTTTGT ATTAGCAAA
                                    A
GAM393  C11orf25  3'  ATGGATAGATGATAGCTGTTTC 48637        G  TG   GTGAAT
           A                     TGAGGCAGT AT  TTTA
                                 ||||||||| ||  ||||
                                 ACTTTGTCG TA  AGAT
                                     A  GT   AGGTA
GAM393  C1orf9   3'  GTTTGTTTAAGTTGCTGCTTTA 32638       TG  GTTT  TG
                                 TGAGGCAG  ATT   AG  AAT
                                 ||||||||  |||   ||  |||
                                 ATTTCGTC  TGA   TT  TTG
                                     GT   AT__  GT
GAM393  C1QTNF6  3'  ATTCATTAAACACTGAGCACTC 49136     _  AGTGAT
           A                     TGAG GC     TGTTTAGTGAAT
                                 |||| ||     ||||||||||||
                                 ACTC CG     ACAAATTACTTA
                                   A  AGTC__
GAM393  C1QTNF7  3'  GTTGGCGATAATATTGCCTTA  49161         A    TA  G
                                 TGAGGCAGTG TTGTT  GT AAT
                                 |||||||||| |||||  || |||
                                 ATTCCGTTAT AATAG  CG TTG
                                     _    __ G
GAM393  C20orf177 3'  ATTTATTAGTAATTCTACTTGC 62144       _ _  TTGT
           CTT                     GAGGCA GT GA    TTAGTGAAT
                                 ||||||| || ||   |||||||||
                                 TTCCGT CA CT    GATTATTTA
                                    T  T  TAAT
GAM393  C20orf177 3'  GTTTATGCTGAGTTGCTGCCTT 62153       TG   GTTTA
                                 GAGGCAG  ATT    GTGAAT
                                 |||||||  |||    ||||||
                                 TTCCGTC  TGA    TATTTG
                                    GT   GTCG_
GAM393  C20orf177 3'  TGTATTTTGAGTAGTCATTTCT 62155      C          TGAAT
           CA                      TGAGG AGTGATTGTTTAG
                                 ||||| ||||||||||||
                                 ACTCT TTACTGATGAGTT
                                   _          TTATGTT
GAM393  C20orf36  3'  TTCATAGTTGTTGCCTT     36802        TG   GTTTA
                                 GAGGCAG  ATT    GTGAA
                                 |||||||  |||    |||||
                                 TTCCGTT  TGA    TACTT
                                    GT  _____
GAM393  C20orf48  3'  ATTTGCTGTATATAAGTTGCCT 46366     _ TG   GTT___   TG
           GCTTT                   GCA G  ATT     TAG  AAT
                                 ||| |  |||     |||  |||
                                 CGT C  TGA     GTC  TTA
                                   C GT   ATATAT   GT
GAM393  C20orf72  3'  ATTTAAGTTATACAGTTGCTGC 53495        TG    TTAG__
           CTTA                    GAGGCAG  ATTGT     TGAAT
                                 |||||||  |||||     |||||
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                                TTCCGTC  TGACA     ATTTA
                                   GT    TATTGA
GAM393  C21orf109 3'  AGATAATTCCTGTTTTA     57265        TG
                                TGAGGCAG  ATTGTTT
                                ||||||||  |||||||
                                ATTTTGTC  TAATAGA
                                   CT
GAM393  C21orf25  3'  ATTCGAAACACAATACACTGCC 63542         _    TTAG
           TC                    GAGGCAGTG ATTGT    TGAAT
                                ||||||||| |||||    |||||
                                CTCCGTCAC TAACA    GCTTA
                                   A    CAAA
GAM393  C21orf41  3'  TAAATGATTGTTGTTTTA    56358        TG  TG
                                TGAGGCAG  AT  TTTA
                                ||||||||  ||  ||||
                                ATTTTGTT  TA  AAAT
                                   GT  GT
GAM393  C21orf51  3'  ATTGGCTTGTGGTCATTTTCTC 54198      C     TG TT   G
           A                     TGAGG AGTGAT  T  AGT AAT
                                ||||| ||||||  |  ||| |||
                                ACTCT TTACTG  G  TCG TTA
                                   T     GT T_   G
GAM393  C21orf59  3'  GCGGATAACACTGCTTT     35238         A     A
                                GAGGCAGTG TTGTTT GT
                                ||||||||| |||||| ||
                                TTTCGTCAC AATAGG CG
                                      _     _
GAM393  C3IP1     3'  GTTCAGCTACCTGATTACTGCC 41284    A         TT   _
           CCA                     TG GGCAGTGATTG  TAG TGAAT
                                || ||||||||||  ||| |||||
                                AC CCGTCATTAGT  ATC ACTTG
                                 C         CC   G
GAM393  C5orf5    3'  ATTCTGCTAATCATTGTTACA  33464    AG       TGTT   _
                                TG  GCAGTGAT    TAGT GAAT
                                ||  ||||||||    |||| ||||
                                AC  TGTTACTA    ATCG CTTA
                                 AT       ____    T
GAM393  C5orf6    3'  AGGCAATTGCTCCTTA      33477       C  TG
                                TGAGG AG  ATTGTTT
                                ||||| ||  |||||||
                                ATTCC TC  TAACGGA
                                   _ GT
GAM393  C5orf7    3'  TTGTAGTGAAATAGTTACTATT 63873       C         AGTGAAT
           TCA                     TGAGG AGTGATTGTTT
                                ||||| ||||||||||
                                ACTTT TCATTGATAAA
                                   A          GTGATGTTT
GAM393  C6orf33   3'  TCTCAGGCAGGCAGTTCTGCTT 55889         T       AG_   AT
           CA                      TGAGGCAG GATTGTTT   TGA
                                |||||||| ||||||||   |||
```

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                                ACTTCGTC TTGACGGA   ACT
                                    _       CGG   CTT
GAM393  C8orf2   3'  ATTCACTAAGTAGCCTGTGTT  23158    G    TGA
                                GA GCAG   TTGTTTAGTGAAT
                                || ||||   ||||||||||||
                                TT TGTC   GATGAATCACTTA
                                 G   C__
GAM393  C9orf12  3'  TTACATGGTCACTTTTTCA   42796      C     TG TTA
                                TGAGG AGTGAT  T   GTGA
                                ||||| ||||||  |   ||||
                                ACTTT TCACTG  A   CATT
                                   T     GT ___
GAM393  C9orf5   3'  AGACAGTCACTTTTCA     49272      C
                                TGAGG AGTGATTGTTT
                                ||||| ||||||||||
                                ACTTT TCACTGACAGA
                                  _
GAM393  CAPS2    3'  TTCAGTAATTATTGCCT     70604          TGTT  G
                                AGGCAGTGAT    TA TGAA
                                ||||||||||    || ||||
                                TCCGTTATTA    AT ACTT
                                      _____ G
GAM393  CARD14   5'  TTCACCTGGTGCTGCTTT    44109         ATTGTTTA
                                GAGGCAGTG       GTGAA
                                |||||||||       |||||
                                TTTCGTCGT       CACTT
                                     GGTC_____
GAM393  CARD9    3'  TTTGTTAAGCGGCACTCA    53379   C   A      TG
                                G AGTG TTGTTTAG  AA
                                | |||| ||||||||  ||
                                A TCAC GGCGAATT  TT
                                 C   _       GT
GAM393  CARD9    3'  TTTGTTAAGCGGCACTCA    42293   C   A      TG
                                G AGTG TTGTTTAG  AA
                                | |||| ||||||||  ||
                                A TCAC GGCGAATT  TT
                                 C   _       GT
GAM393  CCRK     3'  ATGGCTAAGGTGGCATTGTCTC 24012          ATTG     GAAT
           A                     TGAGGCAGTG    TTTAGT
                                ||||||||||    ||||||
                                ACTCTGTTAC    GAATCG
                                      GGTG     GTA
GAM393  CCRL2    3'  ATTTGCTAAGCACTGAATTTGT 14248       TGAT__     TG
           CTCA                    AGGCAG     TGTTTAG  AAT
                                ||||||     |||||||  |||
                                TCTGTT     ACGAATC  TTA
                                   TAAGTC      GT
GAM393  CDH26    3'  TTAACGTAATCATTGGCTCA  41467      G       TTTAG
                                TGAG CAGTGATTG    TGA
                                |||| |||||||||     |||
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                                ACTC GTTACTAAT    ATT
                                  G       GCA__
GAM393  CDK5RAP3 5' ATTCACTACTTTCACTGCCT  47280        TT  TT
                                AGGCAGTGA  GT  AGTGAAT
                                |||||||||  ||  |||||||
                                TCCGTCACT  CA  TCACTTA
                                     TT  __
GAM393  CDKL2    5' GTTTGCTAGGCAGCATCTTT  14162     CA   A      TG
                                GAGG  GTG TTGTTTAG  AAT
                                ||||  ||| ||||||||  |||
                                TTTC  TAC GACGGATC  TTG
                                  __  _      GT
GAM393  CEZANNE  3' GGCGATTCTGTCTTA      39513        T
                                TGAGGCAG GATTGTT
                                |||||||| |||||||
                                ATTCTGTC TTAGCGG

                                     _
GAM393  CG012    3' TTCAGGCAGTTATATGCCTCA  83230       _       TAG    T
                                TGAGGCA GTGATTGTT   TGAA
                                ||||||| |||||||||   ||||
                                ACTCCGT TATTGACGG   ACTT
                                    A       ___    T
GAM393  CG018    3' ATTACAAAATGAGCAGTTGATG 53391     GT       ____    AT
           TTTTA                 GCA  GATTGTTTA    GTGA
                                |||  |||||||||   ||||
                                TGT  TTGACGAGT    CATT
                                  AG       AAAA    A
GAM393  CHFR     3' GTTTATCAAAAACATTGTTTCA 36658         ATTG   A
                                TGAGGCAGTG    TTT GTGAAT
                                ||||||||||    ||| ||||||
                                ACTTTGTTAC    AAA TATTTG
                                     AA__   C
GAM393  CHL1     3' ATTTGTTGAGCTCCTATTTGCC 21744    A    TGATT_     TG
           CA                    TG GGCAG     GTTTAG  AAT
                                || |||||     ||||||  |||
                                AC CCGTT     CGAGTT  TTA
                                 _    TATCCT     GT
GAM393  CHRAC1   3' TTGCGGTGGCGCTGTCTCA   33881         A TG  TA TG
                                TGAGGCAGTG T  TT  G  A
                                |||||||||| |  ||  |  |
                                ACTCTGTCGC G  GG  C  T
                                     _ GT  __ GT
GAM393  CHSY1    3' GATAATAGCTGTTTCA      29900         G
                                TGAGGCAGT ATTGTT
                                ||||||||| ||||||
                                ACTTTGTCG TAATAG
                                     A
GAM393  CKAP4    3' TTCTTTAATGGCTGTCTT    22393         G    TTTAGT
                                GAGGCAGT ATTG     GAA
                                |||||||| ||||     |||
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                                TTCTGTCG TAAT      CTT
                                    G    TT____
GAM393  CLDN1     3'  ATTTACTCTTCTTCATTAGCTT 40847       _     TTGTTT
              T                  GAGGC AGTGA      AGTGAAT
                                 ||||| |||||      |||||||
                                 TTTCG TTACT      TCATTTA
                                   A     TCTTC_
GAM393  COL21A1   3'  TTACTACAGTGTCTCA      48023        G  ATTGTT
                                 TGAGGCA TG     TAGTGA
                                 ||||||| ||     ||||||
                                 ACTCTGT AC     ATCATT
                                    G  _______
GAM393  CXYorf1   3'  GTTTGTTAAGTGGTCAGAAATT 82051     GCAG    TG    TG
              C                  GAG    TGAT  TTTAG  AAT
                                 |||    ||||  |||||  |||
                                 CTT    ACTG  GAATT  TTG
                                   AAAG    GT    GT
GAM393  CYP-M     3'  ATTCATTGGACACATTTGACTT 40338      G   TGAT
              A                  TGAG CAG    TGTTTAGTGAAT
                                 |||| |||    ||||||||||||
                                 ATTC GTT    ACAGGTTACTTA
                                   A   TAC_
GAM393  DCTN4     3'  GACAGGTTACTGTTTT      67787          _
                                 GAGGCAGTGAT TGTT
                                 |||||||||||| ||||
                                 TTTTGTCATTG ACAG
                                       G
GAM393  DDX35     3'  GTTTGCTGGGCTGGCTTTGCTT 41641        TGATT     TG
              T                  GAGGCAG     GTTTAG  AAT
                                 |||||||     ||||||  |||
                                 TTTCGTT     CGGGTC  TTG
                                    TCGGT     GT
GAM393  DEPP      3'  ATTTGTTAAATGTTTTCTGTCT 22819        T  TT     TG
              T                  GAGGCAG GA  GTTTAG  AAT
                                 ||||||| ||  ||||||  |||
                                 TTCTGTC TT  TAAATT  TTA
                                    T  TG     GT
GAM393  DKFZP434A0225 3'  ATTTGCTGTGTGATTACTGTTT 93907          TG T   TG
                                 AGGCAGTGAT  T TAG  AAT
                                 |||||||||  | |||  |||
                                 TTTGTCATTA  G GTC  TTA
                                      GT T   GT
GAM393  DKFZP434A043 3'  ATTTATTGAAACAAAGCTGTTT 31185        GA    _
                                 AGGCAGT  TTGTT TAGTGAAT
                                 |||||||  ||||| ||||||||
                                 TTTGTCG  AACAA GTTATTTA
                                    A_     A
GAM393  DKFZP434B205 3'  AGCAGTTACGCCTTA       75316        A
                                 TGAGGC GTGATTGTT
                                 ||||||| |||||||||
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                                ATTCCG CATTGACGA
                                     _
GAM393  DKFZp434C0328 5'  ATTCATTGGGCATTTGTTAGCT 34131      _  TG T
          TT                  GAGGC AG  A TGTTTAGTGAAT
                              |||||  ||  | ||||||||||||
                              TTTCG TT  T ACGGGTTACTTA
                                 A  GT T
GAM393  DKFZp434E169 3'  GAGTAATTACTGTTTTA     50060
                              TGAGGCAGTGATTGTTT
                              |||||||||||||||||
                              ATTTTGTCATTAATGAG

GAM393  DKFZP434E2135 3'  GACAGCACTGTTTCA       47955          A
                              TGAGGCAGTG TTGTT
                              ||||||||||  |||||
                              ACTTTGTCAC GACAG
                                     _
GAM393  DKFZP434E2135 3'  ATTCATTAGGCTGTTGCCTC   47951        TGATT
                              GAGGCAG    GTTTAGTGAAT
                              |||||||    ||||||||||||
                              CTCCGTT    CGGATTACTTA
                                   GT___
GAM393  DKFZp434E2220 5'  TTTACTAATTTTTGCCTT    34305        TGATTGT
                              GAGGCAG      TTAGTGAA
                              |||||||      ||||||||
                              TTCCGTT      AATCATTT
                                   TTT_____
GAM393  DKFZP434I1735 3'  AAACTTACTAAACAATCCACTG 87799          _          AT
          CTTTA                   GAGGCAGTG ATTGTTTAGTGA
                              |||||||||  ||||||||||||
                              TTTCGTCAC TAACAAATCATT
                                   C          CAAAT
GAM393  DKFZP434J193 3'  GTTTACTGCCTCCACTGCCTC  71006          ATTGTT
                              GAGGCAGTG     TAGTGAAT
                              |||||||||     ||||||||
                              CTCCGTCAC     GTCATTTG
                                   CTCC__
GAM393  DKFZP434J214 3'  AAGCATCACTGCTTT       60929          T
                              GAGGCAGTGAT GTTT
                              ||||||||||| ||||
                              TTTCGTCACTA CGAA
                                     _
GAM393  DKFZp547E052 5'  TTCGTGTAATTATTGCCCA    50102     A         TTTAG
                              TG GGCAGTGATTG     TGAA
                              || ||||||||||     ||||
                              AC CCGTTATTAAT     GCTT
                                _         GT___
GAM393  DKFZp547G183 3'  AGGTGATCACTGGCTCA      38024      G      TG
                              TGAG CAGTGAT  TTT
                              |||| |||||||  |||
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                                ACTC GTCACTA  GGA
                                  G      GT
GAM393   DKFZp547M236 3'  GTTCACTAGGGGTTGGCTGTTT 38039        GATTG
                                AGGCAGT     TTTAGTGAAT
                                |||||||     ||||||||||
                                TTTGTCG     GGATCACTTG
                                    GTTGG
GAM393   DKFZp564B0769 3'  TAAATAATCATAGTCTTA     51772        A
                                TGAGGC GTGATTGTTTA
                                |||||| ||||||||||
                                ATTCTG TACTAATAAAT
                                   A
GAM393   DKFZP564O092 3'  ATTCATTAATTGTTTGCTTT   63795       GT   TGT
                                GAGGCA  GAT   TTAGTGAAT
                                ||||||  |||   |||||||||
                                TTTCGT  TTG   AATTACTTA
                                   __   TT_
GAM393   DKFZP566G1424 3'  GTTCATTTTCAAAATGCTGCTT 84788        GA_   TTT
            T                   GAGGCAGT   TTG   AGTGAAT
                                ||||||||   |||   |||||||
                                TTTCGTCG   AAC   TTACTTG
                                     TAA   TT_
GAM393   DKFZP586B2420 3'  ATGACTCAAGTGATACTGTTTT 74994          A TG   _   GAAT
            A                   TGAGGCAGTG T  TTT AGT
                                |||||||||| |  ||| |||
                                ATTTTGTCAT A  GAA TCA
                                      _ GT   C   GTA
GAM393   DKFZP586M0622 5'  TAAACAATTATGCTTT      31485        G
                                GAGGCA TGATTGTTTA
                                |||||| ||||||||||
                                TTTCGT ATTAACAAAT
                                   _
GAM393   DKFZP727G051 3'  ATTCATGGTTTTTAATTGCTGC 69471        TG    TTTA__
            TTT                   GAGGCAG  ATTG     GTGAAT
                                |||||||  ||||     ||||||
                                TTTCGTC  TAAT     TACTTA
                                    GT    TTTTGG
GAM393   DKFZP727G051 3'  TGGACAATCACTTTTT      69482      C
                                GAGG AGTGATTGTTTA
                                |||| ||||||||||||
                                TTTT TCACTAACAGGT
                                   _
GAM393   DKFZP761E1824 3'  GTCTGTTAGGCAGCATTGCTTT 66441          A      GT AAT
                                GAGGCAGTG TTGTTTA  G
                                ||||||||| |||||||  |
                                TTTCGTTAC GACGGAT  T
                                      _      TG CTGT
GAM393   DKFZP761F241 3'  GTTTGCTGAGTAATTGTTTC   48799        GATTG    TG
                                GAGGCAGT    TTTAG  AAT
                                ||||||||    |||||  |||
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                                CTTTGTTA    GAGTC  TTG
                                    AT___    GT
GAM393  DKFZp761G0313 3'  ATTTGCCCCTATCAGTTGCTCC 65814     C  TG   TTTA__ TG
          TCA                   GAGG AG  ATTG     G  AAT
                                |||| ||  ||||     |  |||
                                CTCC TC  TGAC     C  TTA
                                  _  GT    TATCCC GT
GAM393  DKFZp761G2113 3'  GAACGGTGCTGCTTTA     69903         G
                                TGAGGCAGT ATTGTTT
                                ||||||||| |||||||
                                ATTTCGTCG TGGCAAG
                                          _
GAM393  DKFZp761P1010 3'  ATTTATTAAATGGAAATATGCT 37337       GTGA_ TG
          TT                    GAGGCA    T  TTTAGTGAAT
                                ||||||    |  ||||||||||
                                TTTCGT    G  AAATTATTTA
                                   ATAAA GT
GAM393  DNAJA3    3'  ATTCAGTGCTAATCATTGTTTT 60485           TT  G
                                GAGGCAGTGATTG  TA TGAAT
                                ||||||||||||  ||  |||||
                                TTTTGTTACTAAT  GT ACTTA
                                       C_  G
GAM393  DNAJA4    5'  GTTCACCCCTGGCACTGTCTCA 37756         ATTGTTTA
                                TGAGGCAGTG       GTGAAT
                                ||||||||||       ||||||
                                ACTCTGTCAC       CACTTG
                                     GGTCCC__
GAM393  DNCLI1    3'  ATACACTAGTCATTGTCTCA   59504          TGTT    AAT
                                TGAGGCAGTGAT    TAGTG
                                ||||||||||||    |||||
                                ACTCTGTTACTG    ATCAC
                                      _____     ATAG
GAM393  DSCR1L1   3'  GACAATTAGCTGCTTCA     19497         _
                                TGAGGCAG TGATTGTT
                                |||||||| ||||||||
                                ACTTCGTC ATTAACAG
                                     G
GAM393  EDG1      3'  TTCATTAGATAGTAATTG    59332      G
                                CAGT ATTGTTTAGTGAA
                                |||| ||||||||||||
                                GTTA TGATAGATTACTT
                                  A
GAM393  EDG7      3'  AGGTGATGACTGTCTTA     24060         G  TG
                                TGAGGCAGT AT  TTT
                                ||||||||| ||  |||
                                ATTCTGTCA TA  GGA
                                     G  GT
GAM393  EEA1      3'  ATTCAAAAATGGTTTTTGTTTT 13097         T   TG   AG
          A                     TGAGGCAG GAT  TTT  TGAAT
                                |||||||| |||  |||  |||||
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                                ATTTTGTT TTG  AAA  ACTTA
                                     T  GT   A_
GAM393  EFS2    3'  ATTCACTGGACAAGTTCTCTG  19619     T __
                                CAG GA  TTGTTTAGTGAAT
                                ||| ||  ||||||||||||||
                                GTC CT  AACAGGTCACTTA
                                  T  TG
GAM393  ELF4    3'  ATTCATTGAGTATTTGTGCCT  7429       G   T
                                AGGCA TGA TGTTTAGTGAAT
                                ||||| ||| ||||||||||||
                                TCCGT GTT ATGAGTTACTTA
                                   _  T
GAM393  ELL2    3'  TTAAAAAAATAAACATTGTCTT 23875         A     AGTGAAT
                                GAGGCAGTG TTGTTT
                                ||||||||| ||||||
                                TTCTGTTAC AATAAA
                                     A     AAAATTA
GAM393  EMR3    3'  ATTCATTAAACATATCATCCTT 50810      CA    _
                                GAGG  GTGAT TGTTTAGTGAAT
                                ||||  ||||| ||||||||||||
                                TTCC  TACTA ACAAATTACTTA
                                   __    T
GAM393  EREG    3'  ATTTATGTGAGGTAATTATTGC 7492      G       TT A__
           TCA                    GAG CAGTGATTG  T   GTGAAT
                                ||| |||||||||  |   ||||||
                                CTC GTTATTAAT  A   TATTTA
                                  _       GG GTG
GAM393  EZFIT   3'  AACAGTAACTACTGCTTT    41104         ___
                                GAGGCAGTG   ATTGTT
                                |||||||||   ||||||
                                TTTCGTCAT   TGACAA
                                     CAA
GAM393  FADS2   3'  TGGACGGCGCTGCCTCA     14959         A
                                TGAGGCAGTG TTGTTTA
                                |||||||||| |||||||
                                ACTCCGTCGC GGCAGGT
                                          _
GAM393  FAM3C   3'  GTTCACTAAATAACTCAGTTTT 29686      AG  _
                                GAGGC  TGA TTGTTTAGTGAAT
                                |||||  ||| ||||||||||||
                                TTTTG  ACT AATAAATCACTTG
                                   __  C
GAM393  FBXO30  3'  ATTTGCTAGTTATCTAATGTTT 49574       GT_  TGT   TG
           TA                    TGAGGCA   GAT   TTAG  AAT
                                |||||||   |||   ||||  |||
                                ATTTTGT   CTA   GATC  TTA
                                    AAT   TT_   GT
GAM393  FBXO30  3'  TTTGTTAAGCACTGCC     49582       GATT     TG
                                GGCAGT    GTTTAG  AA
                                ||||||    ||||||  ||
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                                CCGTCA   CGAATT  TT
                                  ____     GT
GAM393  FENS-1   3'  TAGGCTGATGGTTATTGCCTTA 40443          TG  T   GAAT
                                TGAGGCAGTGAT  TT AGT
                                ||||||||||||  || |||
                                ATTCCGTTATTG  AG TCG
                                      GT  _  GATA
GAM393  FKSG14   3'  ATTCATTTTTAAATGGTCATTT 67805     C     TG   ___
          CTTA                    AGG AGTGAT  TTTA   GTGAAT
                                ||| ||||||  ||||   ||||||
                                TCT TTACTG  AAAT   TACTTA
                                  _     GT    TTT
GAM393  FKSG14   3'  ATTTGTTTCATATATACTGTCT 67806          AT   TT  TG
          TA                     TGAGGCAGTG  TGT  AG  AAT
                                ||||||||||  |||  ||  |||
                                ATTCTGTCAT  ATA  TT  TTA
                                      AT   CT  GT
GAM393  FKSG32   3'  ATTAAGGAAGTTATTGCTTTA  48545          G_
                                TGAGGCAGTGATT  TTTAGT
                                ||||||||||||||  ||||||
                                ATTTCGTTATTGA  GAATTA
                                      AG
GAM393  FLJ10036 3'  GATAATCCTGTCTCA       94949         T
                                TGAGGCAG GATTGTT
                                ||||||||  |||||||
                                ACTCTGTC CTAATAG
                                        _
GAM393  FLJ10081 3'  ATTCATGACTTAAGTTGTTGGC 35799      G   TG   GTTTA_
          TCA                     TGAG CAG  ATT     GTGAAT
                                ||||  |||  |||     ||||||
                                ACTC GTT  TGA     TACTTA
                                  G   GT   ATTCAG
GAM393  FLJ10116 3'  ATTTAGTGCTTAATCTTTGCCT 35828         T    TT  G
          CA                      TGAGGCAG GATTG  TA TGAAT
                                ||||||||  |||||  || |||||
                                ACTCCGTT CTAAT  GT ATTTA
                                      T    TC  G
GAM393  FLJ10193 3'  ATTCACTGGACGAATTAAGCCT 35881      AG    _
                                AGGC  TGATT GTTTAGTGAAT
                                ||||  ||||| ||||||||||
                                TCCG  ATTAA CAGGTCACTTA
                                  A_    G
GAM393  FLJ10199 5'  GTTTTTGTTGTGACTGCTGCCT 71236         GA TG TTAGT
          T                      GAGGCAGT  T  T    GAAT
                                ||||||||  |  |    ||||
                                TTCCGTCG  A  G    TTTG
                                     TC GT TTGTT
GAM393  FLJ10252 3'  ATTCACTATGTCCCATTGTTCT 35948    AG     ATTGTT
          A                      TG  GCAGTG     TAGTGAAT
                                ||  ||||||     ||||||||
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                                AT  TGTTAC     ATCACTTA
                                 CT     CCTGT_
GAM393  FLJ10408  3'  CAGTGATTCGTTGCCTCA    36091          TTGT   G
                                TGAGGCAGTGA    TTA TG
                                ||||||||||    ||| ||
                                ACTCCGTTGCT    AGT AC
                                      T___   G
GAM393  FLJ10525  3'  GTGGAAAAATAATCATTTTCTT 36226      C         AGTGAAT
                                GAGG AGTGATTGTTT
                                |||| ||||||||||
                                TTCT TTACTAATAAA
                                  T         AAGGTG
GAM393  FLJ10546  5'  TGATGGATCATTGTTTT     59480           GT
                                GAGGCAGTGATT  TTA
                                ||||||||||||  |||
                                TTTTGTTACTAG  AGT
                                       GT
GAM393  FLJ10618  3'  TTGGCAGTAGTCACTGTTTT   36347           TTTA  G  T
                                GAGGCAGTGATTG    GT AA
                                ||||||||||||    || ||
                                TTTTGTCACTGAT    CG TT
                                       GA__  G  T
GAM393  FLJ10656  3'  ATTTATTTTCATTCATTGCTTT 36385          T  TTT
          A                     TGAGGCAGTGA TG   AGTGAAT
                                ||||||||||| ||   |||||||
                                ATTTCGTTACT AC   TTATTTA
                                      T  TT_
GAM393  FLJ10701  3'  GTTTATACCTGGGTATTGCTTC 36432          ATTGTTTA
          A                     TGAGGCAGTG       GTGAAT
                                ||||||||||       ||||||
                                ACTTCGTTAT       TATTTG
                                     GGGTCCA_
GAM393  FLJ10716  3'  GTTTGTAACAATCACTGTTCTA 36487    AG          TA TG
                                TG  GCAGTGATTGTT  G  AAT
                                ||  ||||||||||||  |  |||
                                AT  TGTCACTAACAA  T  TTG
                                 CT          __ GT
GAM393  FLJ10830  3'  GGATGATTTTGTCTCA      36722         T   TG
                                TGAGGCAG GAT  TTT
                                |||||||| |||  |||
                                ACTCTGTT TTA  AGG
                                     _   GT
GAM393  FLJ10876  3'  GTTCACTAGACTAAAATGTTTT 36793        GTGATT
          A                     TGAGGCA     GTTTAGTGAAT
                                |||||||     ||||||||||||
                                ATTTTGT     CAGATCACTTG
                                    AAAAT_
GAM393  FLJ10876  3'  TTAAAGGTCATTGACTCA    36794      G       G
                                TGAG CAGTGATT TTTAG
                                |||| |||||||| |||||
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```
                                ACTC GTTACTGG AAATT
                                  A      _
GAM393  FLJ10921  3' ATTCCTTTCATTATTGCTTT  36860          T TTT  T
                                GAGGCAGTGAT G   AG GAAT
                                |||||||||||  |   || ||||
                                TTTCGTTATTA C   TC CTTA
                                      _ TT_  _
GAM393  FLJ10997  3' TTCTGATGACACTGTTTCA   36958          A TG  TAGT
                                TGAGGCAGTG T  TT    GAA
                                ||||||||||  |  ||    |||
                                ACTTTGTCAC A  AG    CTT
                                      _ GT  T___
GAM393  FLJ11036  3' TGGATGGTCCACTGCTTT    37000         _  TG
                                GAGGCAGTG AT  TTTA
                                |||||||||  ||  ||||
                                TTTCGTCAC TG  AGGT
                                     C  GT
GAM393  FLJ11053  3' TTTGCTAGACTGTCTCA     88733         GATTGT    TG
                                TGAGGCAGT     TTAG  AA
                                |||||||||     ||||  ||
                                ACTCTGTCA     GATC  TT
                                      _______   GT
GAM393  FLJ11078  3' AGACGATTGATGTCTT      37028       GT
                                GAGGCA  GATTGTTT
                                ||||||  ||||||||
                                TTCTGT  TTAGCAGA
                                   AG
GAM393  FLJ11088  3' GTAGTAAATATATTATTGTTTC 37042           _     G  AAT
          A                      TGAGGCAGTGAT TGTTTA TG
                                ||||||||||||  ||||||  ||
                                ACTTTGTTATTA ATAAAT AT
                                       T     G  G
GAM393  FLJ11149  3' TTATTCATTCACTGTTTT    37115          T  TT
                                GAGGCAGTGA TG  TAG
                                ||||||||||  ||  |||
                                TTTTGTCACT AC  ATT
                                      T  TT
GAM393  FLJ11252  3' GTTTATTAAATAATTGTGT    67609     G
                                GCA TGATTGTTTAGTGAAT
                                |||  ||||||||||||||||
                                TGT GTTAATAAATTATTTG
                                  _
GAM393  FLJ11275  3' GATAACTCATTGCTTTA      37205          _
                                TGAGGCAGTGA TTGTT
                                ||||||||||  |||||
                                ATTTCGTTACT AATAG
                                       C
GAM393  FLJ11370  3' TTTGCTAGACCCTTTCTCA    46374       C  TGATT     TG
                                TGAGG AG    GTTTAG  AA
                                |||||  ||    ||||||  ||
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                                ACTCT TC    CAGATC  TT
                                  T  C____    GT
GAM393  FLJ11383  5'  AGATAGTTCTGTCTT      46281       T
                                GAGGCAG GATTGTTT
                                ||||||| ||||||||
                                TTCTGTC TTGATAGA
                                  _
GAM393  FLJ11710  3'  TTCATTAAACAACTTATTG   45835       _
                                CAGTGA TTGTTTAGTGAA
                                |||||| ||||||||||||
                                GTTATT AACAAATTACTT
                                   C
GAM393  FLJ11838  3'  TGAATGGTCATGCTTT     45095       G   TG
                                GAGGCA TGAT  TTTA
                                |||||| ||||  ||||
                                TTTCGT ACTG  AAGT
                                   _   GT
GAM393  FLJ12363  3'  ATTCATTCTTCAGTTGTTGATT 49671     G   TG   TTT
          TA                      TGAG CAG  ATTG   AGTGAAT
                                |||| |||  ||||   |||||||
                                ATTT GTT  TGAC   TTACTTA
                                  A   GT   TTC
GAM393  FLJ12476  3'  AAACCATTATTGTTTTA     42945          T
                                TGAGGCAGTGAT GTTT
                                |||||||||||| ||||
                                ATTTTGTTATTA CAAA
                                      C
GAM393  FLJ12505  3'  TTTTTTTAAGCAGTTATTACCT 45391      C         T   T
          CA                      TGAGG AGTGATTGTTTAG GAA
                                ||||| |||||||||||||| |||
                                ACTCC TTATTGACGAATT TTT
                                   A          T   TT
GAM393  FLJ12568  3'  TTAGATGATCACTCTTTCA   46502      C     TG
                                TGAGG AGTGAT  TTTAG
                                ||||| ||||||  |||||
                                ACTTT TCACTA  AGATT
                                   C     GT
GAM393  FLJ12643  3'  GAATAGTGACTGTTTCA     82785         G
                                TGAGGCAGT ATTGTTT
                                ||||||||| |||||||
                                ACTTTGTCA TGATAAG
                                     G
GAM393  FLJ12770  3'  ATGAAGAGGCAGTTATTGCTTT 49736             AGTGAAT
          A                       TGAGGCAGTGATTGTTT
                                |||||||||||||||||
                                ATTTCGTTATTGACGGA
                                          GAAGTA
GAM393  FLJ12783  3'  ATTTATTAAGCACTTGCTGT   48676      TG T
                                GCAG  A TGTTTAGTGAAT
                                ||||  | ||||||||||||
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                                TGTC  T ACGAATTATTTA
                                  GT C
GAM393  FLJ12806  3'  TTTACTAGACGGATGTT     43090      GTGAT
                                GGCA     TGTTTAGTGAA
                                ||||     ||||||||||
                                TTGT     GCAGATCATTT
                                  AG___
GAM393  FLJ12895  3'  AGGCAAATACTGTTTT      43680         A
                                GAGGCAGTG TTGTTT
                                ||||||||| ||||||
                                TTTTGTCAT AACGGA
                                     A
GAM393  FLJ12910  3'  TTTATTGGTCATTGTC      44706         TGTT
                                GGCAGTGAT    TAGTGAA
                                |||||||||    |||||||
                                CTGTTACTG    GTTATTT
                                             ____
GAM393  FLJ13114  3'  AAATAGCTGCTGCTTC      44591         GA
                                GAGGCAGT  TTGTTT
                                ||||||||  ||||||
                                CTTCGTCG  GATAAA
                                     TC
GAM393  FLJ13188  3'  GTTATAAAAGTAGTTACTGTTT 41940           _  A    AT
        T                     GAGGCAGTGATTG TTT GTGA
                              ||||||||||||| ||| ||||
                              TTTTGTCATTGAT AAA TATT
                                    G   A   G
GAM393  FLJ13197  3'  ACCTCAAGTGATCCACTGCCTC 44844          _  TG   AGTGAAT
        A                     TGAGGCAGTG AT  TTT
                              |||||||||| ||  |||
                              ACTCCGTCAC TA  GAA
                                    C  GT   CTCCA
GAM393  FLJ13490  3'  GTCCTTTGAGGGATCATTGTCT 46303           G     T_  AT
        TA                    TGAGGCAGTGATT TTTAG  GA
                              |||||||||||| |||||  ||
                              ATTCTGTTACTAG GAGTT  CT
                                    G    TC  G
GAM393  FLJ13848  3'  GATGCTAAATATTTATTGTCTT 45466          T        AAT
        A                     TGAGGCAGTGA TGTTTAGTG
                              |||||||||| |||||||||
                              ATTCTGTTATT ATAAATCGT
                                    T        AG
GAM393  FLJ13855  3'  GTTTGTTCCCGCAATCACTGAT 43590     G        TT_  TG
        TT                    GAG CAGTGATTGT   AG  AAT
                              ||| ||||||||||   ||  |||
                              TTT GTCACTAACG   TT  TTG
                                A         CCC  GT
GAM393  FLJ14007  3'  ATTGGCTGTGACACTGCTTT   45209         A TG TT   G
                              GAGGCAGTG T  T  AGT AAT
                              ||||||||| |  |  ||| |||
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                                TTTCGTCAC A  G  TCG TTA
                                     _ GT __   G
GAM393  FLJ14327  5' GTTTATTCTGTTCACTGCT   46145       TTGTTT
                                GGCAGTGA     AGTGAAT
                                ||||||||     |||||||
                                TCGTCACT     TTATTTG
                                    TGTC__
GAM393  FLJ14442  3' GTTTGTTGTTTTTTGCTGTCCA 51372    A    TG TTGTT   TG
                                TG GGCAG  A     TAG  AAT
                                || |||||  |    |||  |||
                                AC CTGTC  T    GTT  TTG
                                 _    GT TTTT_   GT
GAM393  FLJ14547  3' TTGCTGGCAGTGTTGTCTCA   51440        G     T  TG
                                TGAGGCAGT ATTGTT AG  A
                                ||||||||| |||||| ||  |
                                ACTCTGTTG TGACGG TC  T
                                     _     _  GT
GAM393  FLJ14566  3' ATTTATTGAGCAGGCCTGTGCC 51444       GTGA_
           TC                    GAGGCA    TTGTTTAGTGAAT
                                 ||||||    ||||||||||||
                                 CTCCGT    GACGAGTTATTTA
                                    GTCCG
GAM393  FLJ14751  3' GTTTATTAAAACTGGGTATGCT 51597       GTGATTG_
           TCA                   TGAGGCA       TTTAGTGAAT
                                 |||||||       ||||||||||
                                 ACTTCGT       AAATTATTTG
                                     ATGGGTCA
GAM393  FLJ14827  3' ATTTGTGAGTGAACACTGTTTC 51649         A TG    GTGAAT
           A                     TGAGGCAGTG T  TTTA
                                 ||||||||||  |  ||||
                                 ACTTTGTCAC A  GAGT
                                       A GT    GTTTA
GAM393  FLJ20033  5' TTGGGCAGTTGCTTGTTTT   34350       _ TG
                                GAGGCA G  ATTGTTTAG
                                ||||||  |  |||||||||
                                TTTTGT C  TGACGGGTT
                                    T GT
GAM393  FLJ20039  3' ATTCCAGTCAATTATTCCTCA  34404      C       TTTAGT
                                TGAGG AGTGATTG     GAAT
                                ||||| ||||||||     ||||
                                ACTCC TTATTAAC     CTTA
                                   _       TGAC__
GAM393  FLJ20060  3' GTTCACTAAGTGGTTA     34451      TG
                                TGAT  TTTAGTGAAT
                                ||||  ||||||||||
                                ATTG  GAATCACTTG
                                  GT
GAM393  FLJ20093  3' TGAAGATCACTGCCTT      34555           G
                                GAGGCAGTGATT TTTA
                                ||||||||||| ||||
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                                TTCCGTCACTAG AAGT
                                           _
GAM393  FLJ20097  3'  TTAAGTAGTTACTGTCCT    34566     _
                                AGG CAGTGATTGTTTAG
                                ||| |||||||||||||
                                TCC GTCATTGATGAATT
                                  T
GAM393  FLJ20128  3'  TGGACAGTCACAGCCTCA    34600       A
                                TGAGGC GTGATTGTTTA
                                ||||||| ||||||||||
                                ACTCCG CACTGACAGGT
                                   A
GAM393  FLJ20147  3'  GTTTGCTGTGTGATTGCAGTTT 34641       A TG  TG T   TG
          TA                     TGAGGC G  AT  T TAG  AAT
                                |||||| |  ||  | |||  |||
                                ATTTTG C  TA  G GTC  TTG
                                   A GT  GT T   GT
GAM393  FLJ20150  3'  ATTCAAAGGGTTGGAGATTGCT 34645     TG   GTTTAG____
            GCTTT                  GCAG  ATT        TGAAT
                                |||| |||        |||||
                                CGTC  TAG        ACTTA
                                  GT   AGGTTGGGAA
GAM393  FLJ20209  3'  TTTGCTGGTCACTGTTT     85520         TGTT   TG
                                AGGCAGTGAT    TAG  AA
                                ||||||||||    |||  ||
                                TTTGTCACTG    GTC  TT
                                     _____   GT
GAM393  FLJ20273  3'  GTTTATTAAATGGGCCTC    38730      AGTGA TG
                                GAGGC    T  TTTAGTGAAT
                                |||||    |  ||||||||||
                                CTCCG    G  AAATTATTTG
                                   ______ GT
GAM393  FLJ20275  3'  ATTTATTTTATTGCTGTCT    34818       TG  TGTTT
                                AGGCAG  AT    AGTGAAT
                                ||||||  ||    |||||||
                                TCTGTC  TA    TTATTTA
                                   GT  TT___
GAM393  FLJ20276  3'  GAATGGTTTTTGCCTTA     34830        T   TG
                                TGAGGCAG GAT  TTT
                                |||||||| |||  |||
                                ATTCCGTT TTG  AAG
                                     T   GT
GAM393  FLJ20296  3'  ATTTATTGATTCCATTGCTTTA 34887          ATTGT
                                TGAGGCAGTG    TTAGTGAAT
                                ||||||||||    |||||||||
                                ATTTCGTTAC    AGTTATTTA
                                      CTT__
GAM393  FLJ20300  3'  TTACCACAGTTGCTGCCTC    34909       TG    TTA
                                GAGGCAG  ATTGT   GTGA
                                |||||||  |||||   ||||
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                                CTCCGTC  TGACA   CATT
                                   GT    C__
GAM393  FLJ20340 3' TTTGCTGAAACTGCTTC     34982        GATTG    TG
                                GAGGCAGT    TTTAG  AA
                                ||||||||    |||||  ||
                                CTTCGTCA    AAGTC  TT
                                   _____    GT
GAM393  FLJ20445 3' GTGACTTAATTAGTCACTGCCT 35179          TTT_  GAAT
           T                     GAGGCAGTGATTG   AGT
                                ||||||||||||||   |||
                                TTCCGTCACTGAT   TCA
                                      TAAT  GTG
GAM393  FLJ20552 3' TTAAATTATTACTGCTTT    35392         T
                                GAGGCAGTGAT GTTTAG
                                |||||||||| ||||||
                                TTTCGTCATTA TAAATT
                                      T
GAM393  FLJ20559 3' GACAGCCATTGTTTCA      35398         AT
                                TGAGGCAGTG  TGTT
                                |||||||||  ||||
                                ACTTTGTTAC  ACAG
                                     CG
GAM393  FLJ20689 3' TTGTTACCTTGTTATTGCTGTC 35540        TG  TGTTTA   AT
           TCA                    TGAGGCAG  AT     GTGA
                                |||||||  ||     ||||
                                ACTCTGTC  TA     CATT
                                   GT  TTGTTC   GTTT
GAM393  FLJ20689 3' TTGTTACCTTGTTATTGCTGTC 35744        TG  TGTTTA   AT
           TCA                    TGAGGCAG  AT     GTGA
                                |||||||  ||     ||||
                                ACTCTGTC  TA     CATT
                                   GT  TTGTTC   GTTT
GAM393  FLJ20694 3' TTAAAAATACTGTCTCA     35551         ATTG
                                TGAGGCAGTG   TTTAG
                                |||||||||    |||||
                                ACTCTGTCAT   AAATT
                                     AA__
GAM393  FLJ20716 3' ATTAGTATTTGCTGCTTTA   35599        TG TTGT
                                TGAGGCAG  A   TTAGT
                                |||||||  |   |||||
                                ATTTCGTC  T   GATTA
                                   GT TAT_
GAM393  FLJ20716 3' ATTTTGTAATATTTACTGCTTT 35601          T   TAGT
           A                     TGAGGCAGTGA TGTT   GAAT
                                ||||||||||| ||||   ||||
                                ATTTCGTCATT ATAA   TTTA
                                      T   TGT_
GAM393  FLJ20730 5' GCTAGACAGTTACTGTCTCA  35619
                                TGAGGCAGTGATTGTTTAGT
                                ||||||||||||||||||||
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                                ACTCTGTCATTGACAGATCG

GAM393  FLJ20753  3'  TAGATAATCTTGTTTTA     35633        T
                                TGAGGCAG GATTGTTTA
                                |||||||| |||||||||
                                ATTTTGTT CTAATAGAT
                                        _
GAM393  FLJ20783  3'  TTGAACAATCATGCTTCA    35666        G
                                TGAGGCA TGATTGTTTAG
                                ||||||| ||||||||||
                                ACTTCGT ACTAACAAGTT
                                       _
GAM393  FLJ20967  5'  GTTTGCTGAATTATTGTCCCA  41965    A       TGT    TG
                                TG GGCAGTGAT   TTAG  AAT
                                || |||||||||   ||||  |||
                                AC CTGTTATTA   AGTC  TTG
                                 C        ___    GT
GAM393  FLJ21172  3'  ATTTGCTACACAAGTCACTGTT 45644          _  T   TG
           TT                    GAGGCAGTGATT GT TAG  AAT
                                ||||||||||||| || |||  |||
                                TTTTGTCACTGA CA ATC  TTA
                                       A  C   GT
GAM393  FLJ21240  5'  ATTTGTTAAGCACAATCGCCTC 45838      A  GAT      TG
                                GAGGC GT   TGTTTAG  AAT
                                ||||| ||   |||||||  |||
                                CTCCG TA   ACGAATT  TTA
                                   C  AC_      GT
GAM393  FLJ21369  3'  ATTCGCTAGATATAGAGACTC  45634     GCAGTGAT
                                GAG       TGTTTAGTGAAT
                                |||       ||||||||||||
                                CTC       ATAGATCGCTTA
                                  AGAGAT__
GAM393  FLJ21432  3'  TTTTACCTCTGGTACACTGTCT 44640         ATTGTTTA    T
           T                     GAGGCAGTG       GTGAA
                                |||||||||       |||||
                                TTCTGTCAC       CATTT
                                      ATGGTCTC     TG
GAM393  FLJ21562  3'  TTGAATAGTTATGTTTCA    47078        G
                                TGAGGCA TGATTGTTTAG
                                ||||||| ||||||||||
                                ACTTTGT ATTGATAAGTT
                                       _
GAM393  FLJ21617  3'  ATTTTATAATTACTGTTT    48074            TT
                                AGGCAGTGATTGT  AGT
                                ||||||||||||  |||
                                TTTGTCATTAATA  TTA
                                        TT
GAM393  FLJ21657  3'  ATTTATAATGTTAGTGATTGGT 42508     G   TG  TA____
           GCCTTA                  GCA TGAT  TT     GTGAAT
                                ||| ||||  ||     ||||||
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                                CGT GTTA  GA     TATTTA
                                  G    GT  TTGTAA
GAM393  FLJ21802  3'  ATTTACCTTTATCACTGCTTCA 44979           TGTTTA
                                TGAGGCAGTGAT     GTGAAT
                                ||||||||||||     ||||||
                                ACTTCGTCACTA     CATTTA
                                      TTTC__
GAM393  FLJ21865  3'  ATTTATAGTGGCAATTATTTTC 42803       C        TA_
          TCA                     TGAGG AGTGATTGTT   GTGAAT
                                ||||| ||||||||||   ||||||
                                ACTCT TTATTAACGG   TATTTA
                                   T         TGA
GAM393  FLJ21919  3'  AGATAATCGTGTCTTA      43455        G
                                TGAGGCA TGATTGTTT
                                ||||||| |||||||||
                                ATTCTGT GCTAATAGA
                                   _
GAM393  FLJ22035  3'  ATTTATTTCTTCACTGTGTT   44535    G      TTGTTT
                                GA GCAGTGA     AGTGAAT
                                || |||||||     |||||||
                                TT TGTCACT     TTATTTA
                                 G      TCT___
GAM393  FLJ22282  3'  TTTACTAGATAACCCATTG    45595       A_
                                CAGTG  TTGTTTAGTGAA
                                |||||  ||||||||||||
                                GTTAC  AATAGATCATTT
                                   CC
GAM393  FLJ22329  3'  ATTTATTAAGCACCTGCTGT   45062       AT
                                GCAGTG  TGTTTAGTGAAT
                                ||||||  ||||||||||||
                                TGTCGT  ACGAATTATTTA
                                    CC
GAM393  FLJ22378  3'  GTTTGTAGCGGTAATTGCCTCA 46906         G     TA TG
                                TGAGGCAGT ATTGTT  G  AAT
                                ||||||||| ||||||  |  |||
                                ACTCCGTTA TGGCGA  T  TTG
                                      A     __ GT
GAM393  FLJ22684  3'  GTTCAAAACCCAGTAGTCATTG 46798           TTTAG___
          TTT                     AGGCAGTGATTG       TGAAT
                                ||||||||||||       |||||
                                TTTGTTACTGAT       ACTTG
                                      GACCCAAA
GAM393  FLJ22833  3'  ATCAAAGAAGCAATTGCAGCTT 43101       A TG      AG_   AT
          TA                      TGAGGC G  ATTGTTT   TGA
                                ||||||  |  |||||||   |||
                                ATTTCG C  TAACGAA   ACT
                                   A GT      GAA   A
GAM393  FLJ23049  3'  TTGTTCATTACTGTTTC     45196           T TT
                                GAGGCAGTGAT G  TAG
                                ||||||||||| |  |||
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                                CTTTGTCATTA C  GTT
                                      _ TT
GAM393  FLJ23132  3'  ATTTATTAGACAGTGGAATGC  96134    GTG_
                                GCA   ATTGTTTAGTGAAT
                                |||   ||||||||||||||
                                CGT   TGACAGATTATTTA
                                  AAGG
GAM393  FLJ23323  5'  ATTTGTTAAATAGTCTTCCCTG 45050     T___       TG
          C                      GCAG   GATTGTTTAG  AAT
                                ||||   ||||||||||  |||
                                CGTC   CTGATAAATT  TTA
                                  CCTT       GT
GAM393  FLJ23550  5'  TCACTACTTTGTCTCA     46856       TGATTGTT
                                TGAGGCAG      TAGTGA
                                ||||||||      ||||||
                                ACTCTGTT      ATCACT
                                     TC_______
GAM393  FLJ23556  3'  TTAATAAATTACTGTTTTA   45962          GT
                                TGAGGCAGTGATT  TTAG
                                ||||||||||||  ||||
                                ATTTTGTCATTAA  AATT
                                       AT
GAM393  FLJ23594  3'  ATAGTTTATTGCTTCA     45506          _
                                TGAGGCAGTGA TTGT
                                ||||||||||| ||||
                                ACTTCGTTATT GATA
                                       T
GAM393  FLJ32122  3'  ATTTGCTTAATTATTGCTT   58328          TTT  TG
                                AGGCAGTGATTG   AG  AAT
                                ||||||||||||   ||  |||
                                TTCGTTATTAAT   TC  TTA
                                      ___  GT
GAM393  FNBP3     3'  TTAAATATATTGCCTTA     80153         AT
                                TGAGGCAGTG  TGTTTAG
                                ||||||||||  |||||||
                                ATTCCGTTAT  ATAAATT
                                      __
GAM393  FRAT1     3'  TTCAAGGTCACTGTTTC     18497          TGTTTAG
                                GAGGCAGTGAT      TGAA
                                ||||||||||       ||||
                                CTTTGTCACTG      ACTT
                                      GA_____
GAM393  GAB3      3'  ATTCATTTTGTTTTTGCTGTTT 54625        TG TTGTTT
          CA                     TGAGGCAG  A     AGTGAAT
                                ||||||||  |     |||||||
                                ACTTTGTC  T     TTACTTA
                                     GT TTTGTT
GAM393  GABPB2    3'  TATTACTGACAGTATTGTTTT  8980         G     T    AT
                                GAGGCAGT ATTGTT AGTGA
                                |||||||| |||||| |||||
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                                TTTTGTTA TGACAG TCATT
                                   _     _    ATT
GAM393  gm117   3'  TGAACTAATAAGTATTGCCTCA 78846          A    T  GAAT
                                TGAGGCAGTG TTGTT AGT
                                |||||||||| ||||| |||
                                ACTCCGTTAT AATAA TCA
                                      G    _  AGTA
GAM393  GMEB1   3'  GTTTATTTTTATCATTGTCCCA 21670    A       TGTTT
                                TG GGCAGTGAT    AGTGAAT
                                || |||||||||    |||||||
                                AC CTGTTACTA    TTATTTG
                                 C       TTT__
GAM393  GMEB1   3'  GTTTATTTTTATCATTGTCCCA 44404    A       TGTTT
                                TG GGCAGTGAT    AGTGAAT
                                || |||||||||    |||||||
                                AC CTGTTACTA    TTATTTG
                                 C       TTT__
GAM393  GNB4    3'  GTTTCTAAGTGGTTTTGCTTCA 41271        T  TG   T
                                TGAGGCAG GAT  TTTAG GAAT
                                |||||||| |||  ||||| ||||
                                ACTTCGTT TTG  GAATC TTTG
                                     _  GT   _
GAM393  GPR72   3'  GGGCAGCTGCTGCCTTA    69761         GA
                                TGAGGCAGT  TTGTTT
                                |||||||||  ||||||
                                ATTCCGTCG  GACGGG
                                     TC
GAM393  GRP3    3'  ATACCTGGATGTTTACTGCCTT 31116         TT    TGAAT
                                GAGGCAGTGA  GTTTAG
                                ||||||||||  ||||||
                                TTCCGTCATT  TAGGTC
                                      TG    CATA
GAM393  H2AV    3'  GTTCATTTTTCGGGTTTTGTTT 56856        TGA  TTT
           CA                     TGAGGCAG   TTG   AGTGAAT
                                |||||||   |||   |||||||
                                ACTTTGTT   GGC   TTACTTG
                                     TTG   TTT
GAM393  H2BFB   3'  TTTGCTGCACACTGGTTCA   56971     G    AT   TT  TG
                                TGAG CAGTG  TGT  AG  AA
                                |||| |||||  |||  ||  ||
                                ACTT GTCAC  ACG  TC  TT
                                  G    __   __  GT
GAM393  HBXAP   5'  ATTTACTGAATATAGCTTT   33419      AGTGAT
                                GAGGC     TGTTTAGTGAAT
                                |||||     ||||||||||||
                                TTTCG     ATAAGTCATTTA
                                  AT____
GAM393  HCA4    3'  ATTTACCATCGATAATCTTGTT 77581        T      TA__
           TCA                    GAGGCAG GATTGTT    GTGAAT
                                ||||||| |||||||    ||||||
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                                CTTTGTT CTAATAG    CATTTA
                                   _      CTAC
GAM393  HCC-4    3'  GAATATTACTGCTTT       56819          T
                                GAGGCAGTGAT GTTT
                                |||||||||| ||||
                                TTTCGTCATTA TAAG
                                   _
GAM393  HGC6.1.1 3'  CTAGCCGGTCATTTTCTTA    26828       C       T
                                TGAGG AGTGATTG TTAG
                                ||||| |||||||| ||||
                                ATTCT TTACTGGC GATC
                                   T       C
GAM393  HIRIP5   5'  GAGCGGTCGCCGCCTT      31654       A
                                GAGGC GTGATTGTTT
                                ||||| ||||||||||
                                TTCCG CGCTGGCGAG
                                   C
GAM393  HM74     5'  ATTCACTAGGCGAGGCGCTCC  20056    C    A_
                                GG AGTG  TTGTTTAGTGAAT
                                || ||||  ||||||||||||
                                CC TCGC  AGCGGATCACTTA
                                 _   GG
GAM393  HNRPC    3'  GTTCATTAATTCATATTGCCCC 48548    A      ATTGT
          G                      TG GGCAGTG    TTAGTGAAT
                                || |||||||    |||||||||
                                GC CCGTTAT    AATTACTTG
                                 C      ACTT_
GAM393  HRASLS2  3'  GTTTACTGATTTTACTGTTTT  35395          TTGT
                                GAGGCAGTGA   TTAGTGAAT
                                ||||||||||   |||||||||
                                TTTTGTCATT   AGTCATTTG
                                      TT__
GAM393  HS6ST    3'  ATTTGCTAGCAGGCTGCCCCA  62024    A     GA    T  TG
                                TG GGCAGT  TTGTT AG  AAT
                                || ||||||  ||||| ||  |||
                                AC CCGTCG  GACGA TC  TTA
                                 C     __    _ GT
GAM393  HSH2     3'  TTCATTATTTTACGCCTCA    51678       A   TTGTT
                                TGAGGC GTGA    TAGTGAA
                                |||||| ||||    |||||||
                                ACTCCG CATT    ATTACTT
                                   _   TT___
GAM393  HSJ1     3'  ATTTATTGGATGGGGAGCTCC  22125    C   GA_ TG
                                GG AGT   T  TTTAGTGAAT
                                || |||   |  ||||||||||
                                CC TCG   G  AGGTTATTTA
                                 _  AGG GT
GAM393  HSNOV1   3'  AGGCAGTTATTGTCCA     34004    A
                                TG GGCAGTGATTGTTT
                                || ||||||||||||||
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                                AC CTGTTATTGACGGA
                                  _
GAM393  HSPC019  3' ATGCAAGAACAATCATTATTTT 25855      C         AGTGAAT
             A                    TGAGG AGTGATTGTTT
                                  ||||| ||||||||||
                                  ATTTT TTACTAACAAG
                                     A          AACGTA
GAM393  HSPC019  3' GTTTGTTCTGCTGTCACTGTTT 25860          T  TT  TG
                                  AGGCAGTGAT GT  AG  AAT
                                  |||||||||| ||  ||  |||
                                  TTTGTCACTG CG  TT  TTG
                                        T  TC  GT
GAM393  HSPC063  3' GTTCGCTGAGTGATCAGC    26272    AG    TG
                                  GC  TGAT  TTTAGTGAAT
                                  ||  ||||  ||||||||||
                                  CG  ACTA  GAGTCGCTTG
                                   __    GT
GAM393  HSPC156  5' ATTCACTGCGTGCTGTCCTCA  26353      _    ATTGTT
                                  TGAGG CAGTG     TAGTGAAT
                                  ||||| |||||     ||||||||
                                  ACTCC GTCGT     GTCACTTA
                                     T     GC_____
GAM393  HSPC228  3' ATTTACTGAATGGCTACT    33226      A TG
                                  AGTG T  TTTAGTGAAT
                                  |||| |  ||||||||||
                                  TCAT G  AAGTCATTTA
                                    C GT
GAM393  HTCD37   3' ATTTATTGAATACCTGCCTCA  67671         TGAT
                                  TGAGGCAG    TGTTTAGTGAAT
                                  ||||||||    ||||||||||||
                                  ACTCCGTC    ATAAGTTATTTA
                                       C___
GAM393  ICK      3' ATTTGTTGGGCAGAGGCTGTTC 29924    AG    GA       TG
             CA                     TG  GCAGT  TTGTTTAG  AAT
                                  ||  |||||  ||||||||  |||
                                  AC  TGTCG  GACGGGTT  TTA
                                   CT     GA       GT
GAM393  IL10RB   3' GAACTCACTGCCTTA       5276           TT
                                  TGAGGCAGTGA  GTTT
                                  ||||||||||  ||||
                                  ATTCCGTCACT  CAAG
                                              __
GAM393  IRS4     3' TGAATGGTCATTGTCT      13196          TG
                                  AGGCAGTGAT  TTTA
                                  ||||||||||  ||||
                                  TCTGTTACTG  AAGT
                                        GT
GAM393  IRX4     3' GTTCACACCAATAATTGCCTGC 33023       _ TG     TA_
             TTCA                    GAGGCA G  ATTGTT   GTGAAT
                                  ||||||  |  ||||||   ||||||
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                                CTTCGT C  TAATAA   CACTTG
                                   C GT     CCA
GAM393  KCNS1    3' ATTTGCTAAGCAATAATCTTCC 9572     C  TG_       TG
                                GG AG   ATTGTTTAG  AAT
                                || ||   |||||||||  |||
                                CC TC   TAACGAATC  TTA
                                 T  TAA        GT
GAM393  KDELR3   3' ATTTGCACAATCACTGTTTTA  22456            TTA TG
                                TGAGGCAGTGATTGT   G  AAT
                                ||||||||||||||   |  |||
                                ATTTTGTCACTAACA   C  TTA
                                         ___ GT
GAM393  KIAA0009 3' TAAGGAAGTTACTGTTTTA    27613           G_
                                TGAGGCAGTGATT  TTTA
                                ||||||||||||  ||||
                                ATTTTGTCATTGA  GAAT
                                       AG
GAM393  KIAA0016 3' ATTCTCCGTAGTCACAGTTTCA 28644       A      TTTAGT
                                TGAGGC GTGATTG     GAAT
                                |||||| |||||||     ||||
                                ACTTTG CACTGAT     CTTA
                                   A      GCCT__
GAM393  KIAA0040 3' AGATGGTTACTCTCTTA     27774      C     TG
                                TGAGG AGTGAT  TTT
                                ||||| ||||||  |||
                                ATTCT TCATTG  AGA
                                   C     GT
GAM393  KIAA0062 3' GTTCACTAGGTGAATTGATTTA 70243     G    GA TG
                                TGAG CAGT  T  TTTAGTGAAT
                                |||| ||||  |  ||||||||||
                                ATTT GTTA  A  GGATCACTTG
                                  A    __ GT
GAM393  KIAA0087 3' ATTTATTAGGTGATCTGC    28695     GT   TG
                                GCA  GAT  TTTAGTGAAT
                                |||  |||  ||||||||||
                                CGT  CTA  GGATTATTTA
                                  __   GT
GAM393  KIAA0087 3' TTTGCTCTCTTACTGCTCA    28708     G     TTGTTT  TG
                                TGAG CAGTGA     AG  AA
                                |||| ||||||     ||  ||
                                ACTC GTCATT     TC  TT
                                  _     CTC___  GT
GAM393  KIAA0121 3' GTTTGTTGTTGTTACTGTTTT  72660          TGTT   TG
                                GAGGCAGTGAT    TAG  AAT
                                ||||||||||    |||  |||
                                TTTTGTCATTG    GTT  TTG
                                       TT__   GT
GAM393  KIAA0144 3' TGCACTGAAGTCTTGTTTCA   29287        T   TG      AAT
                                TGAGGCAG GAT  TTTAGTG
                                |||||||| |||  |||||||
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                                ACTTTGTT CTG  AAGTCAC
                                   _  __      GTT
GAM393  KIAA0164  3'  TTCAAATGCATTGCTTTA    28453          ATTGTTTAG
                                TGAGGCAGTG       TGAA
                                ||||||||||       ||||
                                ATTTCGTTAC       ACTT
                                     GTAA_____
GAM393  KIAA0202  3'  ATTGCATAATTTTGCCTTA    64367        T     T
                                TGAGGCAG GATTGT TAGT
                                |||||||| |||||| ||||
                                ATTCCGTT TTAATA GTTA
                                   _     C
GAM393  KIAA0205  3'  GTTTTTTGACAATCACTTCCTT 29590       C         TAGT
          A                      TGAGG AGTGATTGTT    GAAT
                                |||||| ||||||||||    ||||
                                ATTCC TCACTAACAG    TTTG
                                   T         TTT_
GAM393  KIAA0212  3'  GTTTACTGAATGATTACCACCT 27943     CA     TG
                                AGG  GTGAT  TTTAGTGAAT
                                |||  |||||  ||||||||||
                                TCC  CATTA  AAGTCATTTG
                                  AC     GT
GAM393  KIAA0255  3'  ATTTCTCAATCTTGCCTCA    28464         T     TTT
                                TGAGGCAG GATTG   AGT
                                |||||||| |||||   |||
                                ACTCCGTT CTAAC   TTA
                                   _     TCT
GAM393  KIAA0256  3'  GTTTGCTGTGAAGATTACTTCT 64423       C      GTT_   TG
          CA                     TGAGG AGTGATT    TAG  AAT
                                |||||| |||||||    |||  |||
                                ACTCT TCATTAG    GTC  TTG
                                   _      AAGT   GT
GAM393  KIAA0284  3'  AAGTGGTCACGCTTCA      63113        A     TG
                                TGAGGC GTGAT  TTT
                                |||||| |||||  |||
                                ACTTCG CACTG  GAA
                                   _     GT
GAM393  KIAA0286  3'  TGATTCTAGATGGTTACTACCT 68330      C     TG     TGAAT
          T                      GAGG AGTGAT  TTTAG
                                |||| ||||||  |||||
                                TTCC TCATTG  AGATC
                                  A     GT     TTAGTT
GAM393  KIAA0296  3'  TCACAGATAATTGTTTCCTT   28117      C  TG      A
                                GAGG AG  ATTGTTT GTGA
                                |||| ||  ||||||| ||||
                                TTCC TT  TAATAGA CACT
                                  T  GT      _
GAM393  KIAA0310  3'  ATTCATTGAAGCCGGAGCTGTC 81675         GATTG_
          TC                     GAGGCAGT     TTTAGTGAAT
                                ||||||||     ||||||||||
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                                CTCTGTCG     AAGTTACTTA
                                     AGGCCG
GAM393  KIAA0319 3' GGATGATTTCTGTCTTA     29037        T   TG
                                TGAGGCAG GAT  TTT
                                |||||||| |||  |||
                                ATTCTGTC TTA  AGG
                                     T   GT
GAM393  KIAA0332 3' TGAGCCAATCACTGTTTTA   62705           _
                                TGAGGCAGTGATTG TTTA
                                |||||||||||||| ||||
                                ATTTTGTCACTAAC GAGT
                                       C
GAM393  KIAA0332 3' TTCCTTATTCACTGTTTT    62707         TTGTTT  T
                                GAGGCAGTGA     AG GAA
                                ||||||||||     || |||
                                TTTTGTCACT     TC CTT
                                     TAT___  _
GAM393  KIAA0367 3' ATTCATTGGGGAGAGCTGTCCA 67293    A     GA  G
                                TG GGCAGT  TT TTTAGTGAAT
                                || ||||||  || ||||||||||
                                AC CTGTCG  GA GGGTTACTTA
                                 _     A_  G
GAM393  KIAA0372 3' AAACCATTATTGCCTT      27660          T
                                GAGGCAGTGAT GTTT
                                |||||||||| ||||
                                TTCCGTTATTA CAAA
                                       C
GAM393  KIAA0420 3' ATGGCTGAAGGTGGGTGCTGCT 63353        GA TG __     GAAT
           TCA                    GAGGCAGT  T  T  TTAGT
                                ||||||||  |  |  |||||
                                CTTCGTCG  G  G  AGTCG
                                     TG GT GA     GTA
GAM393  KIAA0430 3' ATTCACTGGAGTTGCTGCTT   38838       TG  TG
                                AGGCAG  AT  TTTAGTGAAT
                                ||||||  ||  ||||||||||
                                TTCGTC  TG  AGGTCACTTA
                                   GT  __
GAM393  KIAA0431 3' GTTTTAGAATCATCACTGCCTT 30897           T    AGTGAAT
           A                     TGAGGCAGTGAT GTTT
                                ||||||||||| ||||
                                ATTCCGTCACTA TAAG
                                       C    ATTTTG
GAM393  KIAA0435 3' GTTTGCTGAGCTGTTCACTGTT 28983         TT_     TG
           TC                     GAGGCAGTGA   GTTTAG  AAT
                                ||||||||||   ||||||  |||
                                CTTTGTCACT   CGAGTC  TTG
                                     TGT     GT
GAM393  KIAA0451 5' ATTTATGCCGATTACTGTTCA  29102      G       TTTA
                                TGAG CAGTGATTG    GTGAAT
                                |||| |||||||||    ||||||
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                                ACTT GTCATTAGC    TATTTA
                                  _       CG__
GAM393  KIAA0461  3'  GGGCAGTCCCTGCTTTA     70838         T
                                TGAGGCAG GATTGTTT
                                |||||||| ||||||||
                                ATTTCGTC CTGACGGG
                                     C
GAM393  KIAA0469  3'  GTTTATTGAGTATCTGCTGT   29345       AT
                                GCAGTG  TGTTTAGTGAAT
                                ||||||  ||||||||||||
                                TGTCGT  ATGAGTTATTTG
                                   CT
GAM393  KIAA0471  3'  AGCGATCATTGGTTTA      29382      G
                                TGAG CAGTGATTGTT
                                |||| ||||||||||
                                ATTT GTTACTAGCGA
                                  G
GAM393  KIAA0471  3'  ATTTGTTGATATTAATCATTGG 29387     _      T__    TG
           CCTCA                  GGC AGTGATTG   TTAG  AAT
                                ||| ||||||||   ||||  |||
                                CCG TTACTAAT   AGTT  TTA
                                  G       TAT    GT
GAM393  KIAA0475  3'  CATTGGGTAGTATTGTTTT    29487        G    TT
                                GAGGCAGT ATTG  TAGTG
                                |||||||| ||||  |||||
                                TTTTGTTA TGAT  GTTAC
                                     _   GG
GAM393  KIAA0481  3'  ATTCGTGTGGAGGAGGTTGTTG 71844      TG   G_   AG__
           CTTTA                  GGCAG  ATT  TTT    TGAAT
                                |||||  |||  |||   |||||
                                TCGTT  TGG  GAG    GCTTA
                                  GT   AG   GTGT
GAM393  KIAA0483  3'  TTCAATTATCACTGTCTTA    30794          TGTTTAG
                                TGAGGCAGTGAT      TGAA
                                ||||||||||||      ||||
                                ATTCTGTCACTA      ACTT
                                      TTA____
GAM393  KIAA0493  3'  GAGCAATTCTTGCTTTA     64276         T
                                TGAGGCAG GATTGTTT
                                |||||||| ||||||||
                                ATTTCGTT TTAACGAG
                                     C
GAM393  KIAA0534  3'  ATTGTACAGTTTTTGCCTCA   71428         T     T
                                TGAGGCAG GATTGT TAGT
                                |||||||| |||||| ||||
                                ACTCCGTT TTGACA GTTA
                                     T     T
GAM393  KIAA0546  3'  ATTTGCTGGGTAGTCTTG    71307     T    TT   TG
                                CAG GATTG  TAG  AAT
                                ||| |||||  |||  |||
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                                GTT CTGAT  GTC  TTA
                                  _    GG   GT
GAM393  KIAA0596 3' TTTCCCTGACTGTTGCCTCA  62840       TGATT   T  T   T
                                TGAGGCAG    GTT AG GAA
                                ||||||||    ||| || |||
                                ACTCCGTT    CAG TC CTT
                                    GT___   _ C   TA
GAM393  KIAA0638 3' TTACCATAGTGACTGCTTCA  72401        G    TTA
                                TGAGGCAGT ATTGT   GTGA
                                ||||||||| |||||   ||||
                                ACTTCGTCA TGATA   CATT
                                     G    C__
GAM393  KIAA0649 5' TTTGCAGACGTTGTCTCA    29053       TGAT    A TG
                                TGAGGCAG   TGTTT G  AA
                                ||||||||   ||||| |  ||
                                ACTCTGTT   GCAGA C  TT
                                    _____    _ GT
GAM393  KIAA0663 3' ATTTACCTGAGATGATCATTTC 29125     C     TG   A__
           TTTA                  GAGG AGTGAT  TTT   GTGAAT
                                ||||| ||||||  |||   ||||||
                                TTTC TTACTA  AGA   CATTTA
                                  T     GT   GTC
GAM393  KIAA0708 3' GTTTGCTGAATAAAGGTCTC  92205      AGTGA      TG
                                GAGGC    TTGTTTAG  AAT
                                |||||    ||||||||  |||
                                CTCTG    AATAAGTC  TTG
                                  GA___       GT
GAM393  KIAA0766 3' ATCTGCGTGGGTATTGCTGCTT 29003        TG  TGTTTA  _  AT
           TA                   TGAGGCAG  AT     GT GA
                                ||||||||  ||     || ||
                                ATTTCGTC  TA     CG CT
                                    GT  TGGGTG  T  A
GAM393  KIAA0794 3' AAATAGTCATTCCTT      80405     C
                                GAGG AGTGATTGTTT
                                |||| ||||||||||
                                TTCC TTACTGATAAA
                                  _
GAM393  KIAA0820 3' ATTCACTGAGTAGGGGTGTCCC 69020    A   GTGA
           A                    TG GGCA   TTGTTTAGTGAAT
                                || ||||   ||||||||||||
                                AC CTGT   GATGAGTCACTTA
                                 C   GGG_
GAM393  KIAA0884 3' ATTCGTTAACTTGCAATTGCCT 70200        GATTGT
           T                    GAGGCAGT     TTAGTGAAT
                                ||||||||     |||||||||
                                TTCCGTTA     AATTGCTTA
                                    ACGTTC
GAM393  KIAA0895 3' AACATTATTGTTTCA      92721           T
                                TGAGGCAGTGAT GTT
                                |||||||||||| |||
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```
                                ACTTTGTTATTA CAA

                                          _
GAM393  KIAA0903 3' CTGGATAATTATTTCTTA    71407      C
                                TGAGG AGTGATTGTTTAG
                                ||||| ||||||||||||
                                ATTCT TTATTAATAGGTC

                                  _
GAM393  KIAA0907 3' ATTTGCTGATGCTGGTGCTGTT 30171         ATT _   TG
           TT                    GAGGCAGTG   GT TTAG  AAT
                                ||||||||||   || ||||  |||
                                TTTTGTCGT   CG AGTC  TTA
                                     GGT  T    GT
GAM393  KIAA0916 3' TTTATTGTATACTGCCTT    30495         ATTGTT
                                GAGGCAGTG     TAGTGAA
                                |||||||||     |||||||
                                TTCCGTCAT     GTTATTT
                                     AT_____
GAM393  KIAA0931 3' TTGTGCAATCATTGTC      67428           T
                                GGCAGTGATTGT TAG
                                |||||||||||| |||
                                CTGTTACTAACG GTT
                                       T
GAM393  KIAA0939 3' TTGAGCCATTGCCTT       62021         ATT
                                GAGGCAGTG   GTTTAG
                                |||||||||   ||||||
                                TTCCGTTAC   CGAGTT

                                          ___
GAM393  KIAA0981 3' ATTCTGAAACAATAGTTGCTGC 61419       TG ___    AGT
           CTT                   AGGCAG  AT   TGTTT   GAAT
                                ||||||  ||   |||||   ||||
                                TCCGTC  TG   ACAAA   CTTA
                                   GT  ATA    GT_
GAM393  KIAA0981 3' ATTTGCTAGCTTAATTGTTTTA 61420         GATT   T  TG
                                TGAGGCAGT    GTT AG  AAT
                                |||||||||    ||| ||  |||
                                ATTTTGTTA    CGA TC  TTA
                                     ATT_  _  GT
GAM393  KIAA0981 3' TGGGCATTTATTGTTTTA    61428           T
                                TGAGGCAGTGA TGTTTA
                                |||||||||||| ||||||
                                ATTTTGTTATT ACGGGT
                                       T
GAM393  KIAA0981 3' TTAAAAGATAACTGCCTT    61429         G   G
                                GAGGCAGT ATT TTTAG
                                |||||||| ||| |||||
                                TTCCGTCA TAG AAATT
                                     A   A
GAM393  KIAA0992 3' AAACAGCCATTGCCTT      32202         AT
                                GAGGCAGTG  TGTTT
                                |||||||||  |||||
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                                TTCCGTTAC  ACAAA
                                     CG
GAM393  KIAA0997 3' ATTTACTAAATAAAAATGGCTT 30187     G  GTGA
            A                    TGAG CA    TTGTTTAGTGAAT
                                 |||| ||    ||||||||||||
                                 ATTC GT    AATAAATCATTTA
                                   G  AAA_
GAM393  KIAA1028 3' ATTTACCTATGTGTGCTGCCTC 91933         ATTGTTTA
            A                    TGAGGCAGTG       GTGAAT
                                 ||||||||||       ||||||
                                 ACTCCGTCGT       CATTTA
                                      GTGTATC_
GAM393  KIAA1041 3' GTTTGCTTAAGTCACTGTTTT  30137          GTTT  TG
                                 GAGGCAGTGATT    AG  AAT
                                 ||||||||||||    ||  |||
                                 TTTTGTCACTGA    TC  TTG
                                       AT__  GT
GAM393  KIAA1041 3' CTGCTGTTGGACAGTCAGTGTT 30132        G        GT AAT
            TTA                    TGAGGCA TGATTGTTTA  G
                                 |||||||  ||||||||||  |
                                 ATTTTGT ACTGACAGGT  T
                                     G         TG CGTCA
GAM393  KIAA1055 3' TAGGCCAGAGGGTTGCTGCCTC 66067        TG   G   A  GAAT
            A                    TGAGGCAG  ATT TTT GT
                                 ||||||||  ||| ||| ||
                                 ACTCCGTC  TGG AGA CG
                                      GT   G   C  GATG
GAM393  KIAA1068 3' GTTCTCCAGGGACTGGTCACTG 31038          _   AGT__
            CCTCA                    GGCAGTGATT GTTT    GAAT
                                 ||||||||||  ||||    ||||
                                 CCGTCACTGG CAGG    CTTG
                                       T   GACCT
GAM393  KIAA1084 3' GTTTACTAGATTTTATGTTGC  29840     __   TT
                                 GCA  GTGA  GTTTAGTGAAT
                                 |||  ||||  ||||||||||||
                                 CGT  TATT  TAGATCATTTG
                                   TG   T_
GAM393  KIAA1136 3' ATTTGCTAGGTTGTCCTTCTCA 91316      C  T   TG    TG
                                 TGAGG AG GAT  TTTAG  AAT
                                 |||||  || |||  |||||  |||
                                 ACTCT TC CTG  GGATC  TTA
                                   _  _   TT    GT
GAM393  KIAA1136 3' TTTGTTATACTGTCTTA     91324          ATTGTT   TG
                                 TGAGGCAGTG     TAG  AA
                                 ||||||||||     |||  ||
                                 ATTCTGTCAT     ATT  TT
                                       _______  GT
GAM393  KIAA1161 3' GTTCATTAAACCTCTTTTTCTT 81758      CAGT_  TT
            CA                     TGAGG    GA  GTTTAGTGAAT
                                 |||||    ||  ||||||||||
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                                ACTTC    CT  CAAATTACTTG
                                   TTTTT  C_
GAM393  KIAA1171  3'  GTTCATTAAACATGGTCTT   87985      AGTGAT
                                GAGGC     TGTTTAGTGAAT
                                |||||     ||||||||||||
                                TTCTG     ACAAATTACTTG
                                   GT____
GAM393  KIAA1189  3'  GTTTGCTAAATGTTGCCTT   72046       TGAT     TG
                                GAGGCAG   TGTTTAG  AAT
                                |||||||   |||||||  |||
                                TTCCGTT   GTAAATC  TTG
                                    ____     GT
GAM393  KIAA1189  3'  TTCACTGAATCTTCTCTCA   72049      CAGT  TT
                                TGAGG   GA  GTTTAGTGAA
                                |||||   ||  ||||||||||
                                ACTCT   CT  TAAGTCACTT
                                   _____ TC
GAM393  KIAA1198  3'  TCAAAGCAATCCTGCCTCA   63331        T      AG
                                TGAGGCAG GATTGTTT  TGA
                                |||||||| ||||||||  |||
                                ACTCCGTC CTAACGAA  ACT
                                    _      __
GAM393  KIAA1210  3'  ATTTATTAAGCAAAATAGCCTT 96325       A  GA
          A                      TGAGGC GT  TTGTTTAGTGAAT
                                 ||||||  ||  ||||||||||||
                                 ATTCCG TA  AACGAATTATTTA
                                    A  A_
GAM393  KIAA1211  3'  TTCACTTTTATTGCC      68897        TTGTTT
                                GGCAGTGA     AGTGAA
                                ||||||||     ||||||
                                CCGTTATT     TCACTT
                                    T_____
GAM393  KIAA1257  3'  GTTTGTTAAGAAGATGCTGCTT 62756        GATTG    TG
          T                      GAGGCAGT    TTTAG  AAT
                                 ||||||||    |||||  |||
                                 TTTCGTCG    GAATT  TTG
                                     TAGAA    GT
GAM393  KIAA1340  3'  ATTCATTGGGTCTATTTGCCT  69180      TGATT TT
                                AGGCAG    G  TAGTGAAT
                                ||||||    |  ||||||||
                                TCCGTT    T  GTTACTTA
                                   TATC_ GG
GAM393  KIAA1344  3'  GTTTGTAGCAGTTGTTTGTCTC 72450       _ TG     TA TG
          A                      TGAGGCA G  ATTGTT  G  AAT
                                 |||||||  |  ||||||  |  |||
                                 ACTCTGT T  TGACGA  T  TTG
                                     T GT     __ GT
GAM393  KIAA1364  3'  GTTTGCTGGGCCGAGCTGCTTT 63597        GATT     TG
                                GAGGCAGT   GTTTAG  AAT
                                ||||||||   ||||||  |||
```

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                                TTTCGTCG   CGGGTC  TTG
                                    AGC_     GT
GAM393  KIAA1430  3'  ATTTGTTGAGGCTGCTGCTTTA 80766         ATTG    TG
                                TGAGGCAGTG   TTTAG  AAT
                                ||||||||||   |||||  |||
                                ATTTCGTCGT   GAGTT  TTA
                                     CG__     GT
GAM393  KIAA1432  5'  TAACCAAGAGCAGGTGTTGCTT 66749       GT A     AGTGAAT
          CA                    TGAGGCA  G TTGTTT
                                |||||||  | ||||||
                                ACTTCGT  T GACGAG
                                   TG G     AACCAATG
GAM393  KIAA1453  3'  CTCGACGGCGCTGCCTCA    46973         A    T
                                TGAGGCAGTG TTGTT AG
                                |||||||||| ||||| ||
                                ACTCCGTCGC GGCAG TC
                                      _    C
GAM393  KIAA1462  3'  AAATAATTGCTGGTTTA     91380     G   TG
                                TGAG CAG  ATTGTTT
                                |||| |||  |||||||
                                ATTT GTC  TAATAAA
                                  G   GT
GAM393  KIAA1492  3'  TTCATCTGTTACTGTTT     64511         TGTTTA
                                AGGCAGTGAT     GTGAA
                                ||||||||||     |||||
                                TTTGTCATTG     TACTT
                                     TC____
GAM393  KIAA1511  3'  TGGGCAGTCCTGTCTTA     70172        T
                                TGAGGCAG GATTGTTTA
                                |||||||| |||||||||
                                ATTCTGTC CTGACGGGT
                                      _
GAM393  KIAA1511  3'  TTTACTGTTTCATGTCTTA    70173       G   TTGTT
                                TGAGGCA TGA    TAGTGAA
                                ||||||| |||    |||||||
                                ATTCTGT ACT    GTCATTT
                                   _  TT___
GAM393  KIAA1511  3'  TCTTGGTGTTTACTGTTTCA   70171          TTGT   T
                                TGAGGCAGTGA    TTAG GA
                                ||||||||||    |||| ||
                                ACTTTGTCATT    GGTT CT
                                     TGT_   _
GAM393  KIAA1522  3'  GTTCACCTCTGGCAGTTGCCGC 64977      A TG     TA__
          TTCA                  GAGGC G  ATTGTT    GTGAAT
                                |||||  |  ||||||    ||||||
                                CTTCG C  TGACGG    CACTTG
                                  C GT     TCTC
GAM393  KIAA1524  3'  ATTTAACACAATAGCTGTCTCA 73454         G    TTAG
                                TGAGGCAGT ATTGT    TGAAT
                                |||||||| |||||    |||||
```

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                                ACTCTGTCG TAACA    ATTTA
                                     A    CA__
GAM393  KIAA1550 3' ATTTGCTGGATGGAAGCTGC  66547      GA TG    TG
                                GCAGT  T  TTTAG  AAT
                                |||||  |  |||||  |||
                                CGTCG  G  AGGTC  TTA
                                   AA GT    GT
GAM393  KIAA1553 3' ATTTTTATACAAACACTGTTTT 91914         A   T   TGAAT
           A                    TGAGGCAGTG TTGT TAG
                                |||||||||| |||| |||
                                ATTTTGTCAC AACA ATT
                                     A   T   TTTA
GAM393  KIAA1571 3' TGTTTACTAAGTTCTTGTAATC 60965       _______
           ATTATTTTA               GTGATTG     TTTAGTGAAT   G
                                |||||||     ||||||||||  |
                                TACTAAT     GAATCATTTG   T
                                    GTTCTT
GAM393  KIAA1577 3' ATTTATGTAACTAAATCACTGT 64474          __   TA
           TTTA                   GAGGCAGTGATT  GTT  GTGAAT
                                ||||||||||||  |||  ||||||
                                TTTTGTCACTAA  CAA  TATTTA
                                      AT   TG
GAM393  KIAA1610 3' CACAATAATCATTGCTCT    67157    _        TA
                                AG GCAGTGATTGTT  GTG
                                || ||||||||||||  |||
                                TC CGTTACTAATAA  CAC
                                 T         __
GAM393  KIAA1613 3' ATTTGCTACTTTTGCTCTTCA  64815      C  TG TT  TT  TG
                                TGAGG AG  A  GT  AG  AAT
                                |||||  ||  |  ||  ||  |||
                                ACTTC TC  T  CA  TC  TTA
                                   _  GT TT  __  GT
GAM393  KIAA1613 3' ATTCTTCTGTAGTCATTGTTT  64814          TT   T_
                                AGGCAGTGATTG  TAG  GAAT
                                ||||||||||||  |||  ||||
                                TTTGTTACTGAT  GTC  CTTA
                                      __   TT
GAM393  KIAA1635 3' GTGCTGAAACAGATTGTTGCTT 67862       TG  _   _    AAT
           C                    GAGGCAG  AT TGTT TAGTG
                                |||||||  ||  |||| |||||
                                CTTCGTT  TA ACAA GTCGT
                                    GT  G    A    G
GAM393  KIAA1643 3' ATTGCAATGACGATTGCAGTTT 64546       A TG     TA_ TG AT
           TA                    TGAGGC G  ATTGTT   G  A
                                ||||||  |  ||||||   |  |
                                ATTTTG C  TAGCAG   C  T
                                   A GT     TAA GT A
GAM393  KIAA1644 3' ATAACCAAGTGGTCAGTGTCTC 85023       G    TG   A  GAAT
                                GAGGCA TGAT  TTT GT
                                ||||||  ||||  |||  ||
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                                CTCTGT ACTG  GAA CA
                                   G   GT   C  ATA
GAM393  KIAA1644 5' TCACGGTACTTGCTGTCTCA  85032       TG TT  TTA
                                TGAGGCAG  A  GT   GTGA
                                |||||||| | ||  ||||
                                ACTCTGTC  T  CA   CACT
                                     GT __  TGG
GAM393  KIAA1671 3' AGGCAGTTGCTGTTCA     65666     G   TG
                                TGAG CAG  ATTGTTT
                                |||| |||  |||||||
                                ACTT GTC  TGACGGA
                                  _  GT
GAM393  KIAA1671 3' GTTCATTTGTCTCTCTGTCTCA 65687       T  TTGTTT
                                TGAGGCAG GA     AGTGAAT
                                |||||||| ||     |||||||
                                ACTCTGTC CT     TTACTTG
                                     T  CTGT__
GAM393  KIAA1674 3' ATTTGCTGTTTGTCTTCTGTCT 68774       T_  TGTT  TG
           CA                  TGAGGCAG  GAT   TAG  AAT
                               |||||||| |||   |||  |||
                               ACTCTGTC  CTG   GTC  TTA
                                    TT  TTT_  GT
GAM393  KIAA1674 3' GTTCATTGTTATTTGTTGCTCC 68792     C  TG  TGTT__
           TT                   GAGG AG  AT     TAGTGAAT
                                |||| ||  ||     ||||||||
                                TTCC TC  TG     GTTACTTG
                                  _ GT  TTTATT
GAM393  KIAA1676 3' GTTTATTGCTTCAGCTGCTTCA 93124       GATT  TT
                                TGAGGCAGT   GT  AGTGAAT
                                |||||||||   ||  |||||||
                                ACTTCGTCG   CG  TTATTTG
                                     ACTT  __
GAM393  KIAA1678 3' ATTATAAAGAGATTATTGTCTT 72304         G   A   AT
           A                    TGAGGCAGTGATT TTT GTGA
                                |||||||||||||| ||| ||||
                                ATTCTGTTATTAG GAA TATT
                                       A   A   A
GAM393  KIAA1679 3' ATTGCAAAAGTAATATTGCCTC 70147        A  _  A TG AT
           A                    TGAGGCAGTG TTG TTT G  A
                                |||||||||| ||| ||| |  |
                                ACTCCGTTAT AAT AAA C  T
                                     _  G   A GT A
GAM393  KIAA1705 3' AGACATTACTGTTTTA     72422          T
                                TGAGGCAGTGAT GTTT
                                |||||||||||| ||||
                                ATTTTGTCATTA CAGA
                                          _
GAM393  KIAA1715 3' GTTTGCTAGTTTACTGTCTT  68126        TTGT   TG
                                GAGGCAGTGA   TTAG  AAT
                                |||||||||   ||||  |||
```

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                                TTCTGTCATT   GATC  TTG
                                     T___    GT
GAM393  KIAA1727 3' GTGAGCAGATGATCATTGT   64060       TG   A  GA
                                GCAGTGAT  TTT GT  AT
                                ||||||||  ||| ||  ||
                                TGTTACTA  AGA CG  TG
                                    GT   _  AG
GAM393  KIAA1729 3' GTTTATTGGGTAGTCGATTG  89131     _    TT
                                CAGT GATTG  TAGTGAAT
                                |||| |||||  ||||||||
                                GTTA CTGAT  GTTATTTG
                                  G    GG
GAM393  KIAA1729 3' TAAACAGTTACTCTTTA     89132      C
                                TGAGG AGTGATTGTTTA
                                ||||| ||||||||||||
                                ATTTC TCATTGACAAAT
                                  _
GAM393  KIAA1819 5' AAACAGCACTGTTTT       69678        A
                                GAGGCAGTG TTGTTT
                                ||||||||| ||||||
                                TTTTGTCAC GACAAA
                                   _
GAM393  KIAA1843 3' ATTCATTAGGTGATCTCAGTTC 62189     G AGT   TG
          A                  TGAG C   GAT  TTTAGTGAAT
                             |||| |   |||  ||||||||||
                             ACTT G   CTA  GGATTACTTA
                               _ ACT   GT
GAM393  KIAA1877 3' ATTGAGTATGTATTACTGCTTT 66164         TG___    GAAT
                                GAGGCAGTGAT    TTTAGT
                                ||||||||||     ||||||
                                TTTCGTCATTA    GAGTTA
                                     TGTAT       T
GAM393  KIAA1877 3' ATTTATAACAAATCCTGTTTTA 66165       T   _   TA
                                TGAGGCAG GATT GTT  GTGAAT
                                |||||||| |||| |||  ||||||
                                ATTTTGTC CTAA CAA  TATTTA
                                    _   A  __
GAM393  KIAA1899 5' ATTCGTTAGACGCGCGCTGC   73211       AT
                                GCAGTG  TGTTTAGTGAAT
                                ||||||  ||||||||||||
                                CGTCGC  GCAGATTGCTTA
                                   GC
GAM393  KIAA1900 3' ATTTATTGGACACAATGGCATC 73247    G  AG_  AT
                                GA GC   TG  TGTTTAGTGAAT
                                || ||   ||  ||||||||||||
                                CT CG   AC  ACAGGTTATTTA
                                 A  GTA  __
GAM393  KIAA1912 3' ATTCTCTGTTGTTGTTGTTTTA 73364        TG  TGTT   T
                                TGAGGCAG  AT    TAG GAAT
                                ||||||||  ||    ||| ||||
```

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                                ATTTTGTT  TG   GTC CTTA
                                    GT  TT__   T
GAM393  KIAA1913  3'  ATTTTCTGAATAATTGTTCTTT 73884     C  TG       T
                                GAGG AG  ATTGTTTAG GAAT
                                |||| ||  |||||||||| ||||
                                TTTC TT  TAATAAGTC TTTA
                                  _ GT       T
GAM393  KIAA1915  3'  ATAATCATCTGCTTCA     73276       _
                                TGAGGCAG TGATTGT
                                |||||||| |||||||
                                ACTTCGTC ACTAATA
                                    T
GAM393  KIAA1918  3'  ATTCATTAAACTTTTGTTGT  73159     TG TT
                                GCAG  A  GTTTAGTGAAT
                                ||||  |  ||||||||||
                                TGTT  T  CAAATTACTTA
                                  GT TT
GAM393  KIAA1932  3'  GTTCACTAGACATTGCGCCT  73446     A TG  T
                                AGGC G  AT GTTTAGTGAAT
                                |||| |  || ||||||||||
                                TCCG C  TA CAGATCACTTG
                                  _ GT  _
GAM393  KIAA1939  3'  ATTCACTGAATGGATCCTCA  45762      CAGTGA TG
                                TGAGG     T  TTTAGTGAAT
                                |||||     |  ||||||||||
                                ACTCC     G  AAGTCACTTA
                                   TA____ GT
GAM393  KIAA1940  5'  TTCATTGAGGAGCTCCTT    79995     C   GAT G
                                GAGG AGT   T TTTAGTGAA
                                |||| |||   | |||||||||
                                TTCC TCG   A GAGTTACTT
                                  _  ___ G
GAM393  KLF12     3'  GTTTATTGAAAATAGCTGCTTT 32805       GATTG
                                GAGGCAGT    TTTAGTGAAT
                                ||||||||    ||||||||||
                                TTTCGTCG    AAGTTATTTG
                                    ATAA_
GAM393  KLF5      3'  AAATCGGTTGCTGTTTT     8184        TG   _
                                GAGGCAG  ATTG TTT
                                |||||||  |||| |||
                                TTTTGTC  TGGC AAA
                                    GT   T
GAM393  KPNA6     3'  GAATTACGGTAGTGCATTGCCT 24607        _   TTTA   AT
          TA                  GAGGCAGTG ATTG   GTGA
                              |||||||||| ||||   ||||
                              TTCCGTTAC TGAT   CATT
                                   G   GG__   AAGT
GAM393  KRTHB2    3'  GTTTACTGGACAGTTGGAAAAC 52288    CAGT__
          C                   GG     GATTGTTTAGTGAAT
                              ||     ||||||||||||||
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                                CC     TTGACAGGTCATTTG
                                 AAAAGG
GAM393  LC27     3'  ATTGTGTAATCATTGTTCTA  60125    AG       TT
                                TG  GCAGTGATTG  TAGT
                                ||  ||||||||||  ||||
                                AT  TGTTACTAAT  GTTA
                                 CT        GT
GAM393  LIM      3'  TTCATTGTGTATGCTTCA    21308       GTGATTGTT
                                TGAGGCA       TAGTGAA
                                |||||||       |||||||
                                ACTTCGT       GTTACTT
                                    ATGT_____
GAM393  LY75     3'  ATTTGTTAGACTAGTTCTCTTG 9834      _ T  TT__     TG
              TCTT                  GGCA G GA    GTTTAG  AAT
                                |||| | ||    ||||||  |||
                                CTGT C CT    CAGATT  TTA
                                  T T  TGAT     GT
GAM393  MAGEH1   3'  ATTTGTGATCAGTGATCATTGT 25923     G      TG  TA__ TG
              TCA                   GAG CAGTGAT  TT    G  AAT
                                ||| |||||||  ||    |  |||
                                CTT GTTACTA  GA    T  TTA
                                  _      GT  CTAG GT
GAM393  MAPK8IP3 3'  TTGGAGGTCACTGCTACA    52999    A        G
                                TG GGCAGTGATT TTTAG
                                || ||||||||||  |||||
                                AC TCGTCACTGG AGGTT
                                 A        _
GAM393  MARCKS   3'  AAACGATCATAGTCTTA     9865        A
                                TGAGGC GTGATTGTTT
                                ||||||  ||||||||||
                                ATTCTG TACTAGCAAA
                                    A
GAM393  MATR3    3'  GTTAATGAATAGTTTTTGTTTT 38116         T       G   AT
              A                   TGAGGCAG GATTGTTTA TGA
                                ||||||||  |||||||||  |||
                                ATTTTGTT TTGATAAGT ATT
                                     T       A   G
GAM393  MBLL39   3'  ATTCTAGCTCTAATTACTGTC  58605          TTTAGT
                                GGCAGTGATTG     GAAT
                                ||||||||||      ||||
                                CTGTCATTAAT     CTTA
                                      CTCGAT
GAM393  MBLL39   3'  ATTCTAGCTCTAATTACTGTC  19247          TTTAGT
                                GGCAGTGATTG     GAAT
                                ||||||||||      ||||
                                CTGTCATTAAT     CTTA
                                      CTCGAT
GAM393  MCM10    3'  ATTCACTGAAGTTTTTGCCCA  37570    A    T   TG
                                TG GGCAG GAT  TTTAGTGAAT
                                || ||||| |||  ||||||||||
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                                AC CCGTT TTG  AAGTCACTTA
                                 _    T  __
GAM393  MEGF10   3' TTGACATTAATTGCTGTCCT  50589    _  TG   TTTA  G  T
                                AGG CAG  ATTG   GT AA
                                ||| |||  ||||   || ||
                                TCC GTC  TAAT   CA TT
                                  T  GT   TA__  G  T
GAM393  MESDC2   3' TTGAACCACTGTTTCA     72506        ATT
                                TGAGGCAGTG   GTTTAG
                                ||||||||||   ||||||
                                ACTTTGTCAC   CAAGTT
                                      ____
GAM393  METL     3' AACAATTATGCTTCA      37251       G
                                TGAGGCA TGATTGTT
                                ||||||| ||||||||
                                ACTTCGT ATTAACAA
                                     _
GAM393  MFN1     3' GAATAGTCACTTTTTTA    53203      C
                                TGAGG AGTGATTGTTT
                                ||||| ||||||||||
                                ATTTT TCACTGATAAG
                                   T
GAM393  MFN1     3' GAATAGTCACTTTTTTA    35544      C
                                TGAGG AGTGATTGTTT
                                ||||| ||||||||||
                                ATTTT TCACTGATAAG
                                   T
GAM393  MGC10067 3' TTTTGTGTTGACAATATTGCTT 58943         A    TA_ TG  T
           TA                    TGAGGCAGTG TTGTT   G  AA
                                ||||||||| |||||   |  ||
                                ATTTCGTTAT AACAG   T  TT
                                      _    TTG GT  TG
GAM393  MGC10924 3' GAATAATCACCTGCTTTA   47552        _
                                TGAGGCAG TGATTGTTT
                                |||||||| |||||||||
                                ATTTCGTC ACTAATAAG
                                     C
GAM393  MGC10924 3' GGGCAGTCTTGCTTTA     47553        T
                                TGAGGCAG GATTGTTT
                                |||||||| ||||||||
                                ATTTCGTT CTGACGGG
                                     _
GAM393  MGC11242 3' ATTTATTGAGATGACTGTTTC 44237        G   GT
                                GAGGCAGT ATT  TTAGTGAAT
                                |||||||| |||  |||||||||
                                CTTTGTCA TAG  AGTTATTTA
                                     G  __
GAM393  MGC11287 3' TTTACCATGTCACTGCCT   48835         TGTTTA
                                AGGCAGTGAT     GTGAA
                                ||||||||||     |||||
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```
                                TCCGTCACTG     CATTT
                                     TAC___
GAM393  MGC11316 3' TTTGTTAGATGGCCTC     51944      AGTGAT     TG
                                GAGGC     TGTTTAG  AA
                                |||||     |||||||  ||
                                CTCCG     GTAGATT  TT
                                  _____      GT
GAM393  MGC12945 5' GTTTGCTAAGTGGTCGGTTCCT 50298     CAG    TG    TG
                                AGG   TGAT  TTTAG  AAT
                                |||   ||||  |||||  |||
                                TCC   GCTG  GAATC  TTG
                                  TTG    GT    GT
GAM393  MGC13007 3' ATTTACTAAATGATTGTAAACT 50303     GCA TG  TG
           T                     GAG   G  AT  TTTAGTGAAT
                                |||   |  ||  ||||||||||
                                TTC   T  TA  AAATCATTTA
                                  AAA GT  GT
GAM393  MGC13090 3' ATTTATTGCTAAATTATTGTCC 51137    A        GTT
           A                     TG GGCAGTGATT   TAGTGAAT
                                ||  ||||||||||   ||||||||
                                AC CTGTTATTAA   GTTATTTA
                                  _        ATC
GAM393  MGC14353 3' TTTTAGGATGGCAATCATGTCT 51196       G       TAG_   T
           T                     GAGGCA TGATTGTT    TGAA
                                ||||||  ||||||||    ||||
                                TTCTGT ACTAACGG    ATTT
                                   _       TAGG    TA
GAM393  MGC14433 3' GTTTATTATACATTTAGTGTTT 51868       G   T   T
           CA                      TGAGGCA TGA TGT TAGTGAAT
                                |||||||  |||  |||  ||||||||
                                ACTTTGT ATT ACA ATTATTTG
                                    G   T   T
GAM393  MGC15873 3' ATTCATTGAAACCGCTATTGCT 51900     TG  TG____
           GT                      GCAG  AT     TTTAGTGAAT
                                ||||  ||     ||||||||||
                                TGTC  TA     AAGTTACTTA
                                  GT  TCGCCA
GAM393  MGC16386 3' GGGCAATTCTGTCTT       54735        T
                                GAGGCAG GATTGTTT
                                |||||||  ||||||||
                                TTCTGTC TTAACGGG
                                      _
GAM393  MGC19556 3' ATTCATTATTCTAGTCCTGCTT 53226         T    TT_
           TA                      TGAGGCAG GATTG   TAGTGAAT
                                ||||||||  |||||   ||||||||
                                ATTTCGTC CTGAT   ATTACTTA
                                   _    CTT
GAM393  MGC20460 5' CTGGACGATTACGTTTCA    53847       A
                                TGAGGC GTGATTGTTTAG
                                ||||||  ||||||||||||
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                                ACTTTG CATTAGCAGGTC
                                      _
GAM393  MGC20481  5' GTTTACTGGGCAGCTGTTACG  62714    AG    GAT
                                TG  GCAGT   TGTTTAGTGAAT
                                ||  |||||   ||||||||||||
                                GC  TGTCG   ACGGGTCATTTG
                                 AT    ____
GAM393  MGC21675  3' GTTTTGGATGGACGAATGCTGC 53487         A      GT__
           TTCA                    GAGGCAGTG TTGTTTA    GAAT
                                |||||||||  |||||||    ||||
                                CTTCGTCGT AGCAGGT    TTTG
                                      A      AGGT
GAM393  MGC22014  3' ATTTACTGAGCAGTTGTATTCA 64489      GCA TG
                                TGAG   G  ATTGTTTAGTGAAT
                                ||||   |  ||||||||||||||
                                ACTT   T  TGACGAGTCATTTA
                                  A__ GT
GAM393  MGC2488   3' TGATGTTAAGCAATTGACTGTC 43878         _       GT AAT
           TTA                     TGAGGCAGT GATTGTTTA  G
                                |||||||||  |||||||||  |
                                ATTCTGTCA TTAACGAAT  T
                                      G        TG AGTG
GAM393  MGC2647   3' GAGCAGTTACTCTTCA      73703       C
                                TGAGG AGTGATTGTTT
                                |||||  ||||||||||
                                ACTTC TCATTGACGAG
                                      _
GAM393  MGC2663   5' AAATAATTGCTGCCTT      44092        TG
                                GAGGCAG  ATTGTTT
                                |||||||  |||||||
                                TTCCGTC  TAATAAA
                                    GT
GAM393  MGC27277  3' TTGGGTTATTACTGCTTCA   58707           TG
                                TGAGGCAGTGAT  TTTAG
                                ||||||||||||  |||||
                                ACTTCGTCATTA  GGGTT
                                       TT
GAM393  MGC27434  3' ATTTGTTAAATTCACTTGTCT  58946      _   TT     TG
                                AGGCA GTGA  GTTTAG  AAT
                                |||||  ||||  ||||||  |||
                                TCTGT CACT  TAAATT  TTA
                                   T   __      GT
GAM393  MGC29898  3' AAGCGGTCTTGCTTT       58925        T
                                GAGGCAG GATTGTTT
                                |||||||  ||||||||
                                TTTCGTT CTGGCGAA
                                      _
GAM393  MGC3040   3' AGATGATTACTGCTTT      66841           TG
                                GAGGCAGTGAT  TTT
                                ||||||||||  |||
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```
                                TTTCGTCATTA  AGA
                                      GT
GAM393  MGC3040   3'  ATTTTCTAGCGTGTTGTTGTCT 66844        TG  TGT    T
           TA                    TGAGGCAG  AT   TTAG GAAT
                                 ||||||||  ||   |||| |||||
                                 ATTCTGTT  TG   GATC TTTA
                                     GT  TGC    T
GAM393  MGC3295   3'  TACCTGATTATTATTGTCTCA  47503          T   TA
                                 TGAGGCAGTGAT GTT  GTG
                                 ||||||||||||| |||  |||
                                 ACTCTGTTATTA TAG  CAT
                                       T   TC
GAM393  MGC35570  3'  TGAGAGATTGTTGTCTT     58117        TG   G
                                 GAGGCAG  ATT TTTA
                                 |||||||  ||| ||||
                                 TTCTGTT  TAG GAGT
                                     GT   A
GAM393  MGC5338   3'  ATTCAGAAATTACTGTTTC    43936          GTTTAG
                                 GAGGCAGTGATT     TGAAT
                                 ||||||||||||     |||||
                                 CTTTGTCATTAA     ACTTA
                                       AG____
GAM393  MIG2      3'  ATTCACCAGCATAATCACTGTC 72423           _  A
           T                      AGGCAGTGATTGT TT GTGAAT
                                  |||||||||||||| || ||||||
                                  TCTGTCACTAATA GA CACTTA
                                        C  C
GAM393  MKNK1     3'  AAGCAATCACTTCTCA      13476      C
                                 TGAGG AGTGATTGTTT
                                 ||||| ||||||||||
                                 ACTCT TCACTAACGAA
                                   _
GAM393  MKP-7     3'  TCGCTAGTTGCTGCCTC     66422        TG  TGTT
                                 GAGGCAG  AT   TAGTGA
                                 |||||||  ||   ||||||
                                 CTCCGTC  TG   ATCGCT
                                     GT  ____
GAM393  MKRN1     3'  TTGTCCATCTACTGCTTT    25578         AT  TT
                                 GAGGCAGTG  TG  TAG
                                 |||||||||  ||  |||
                                 TTTCGTCAT  AC  GTT
                                      CT  CT
GAM393  MRPL10    3'  TTGGGAGCACTGCTTTA     59156         ATTG
                                 TGAGGCAGTG   TTTAG
                                 ||||||||||   |||||
                                 ATTTCGTCAC   GGGTT
                                       GA__
GAM393  MRPL19    3'  AAGTGAACTAAGCATTCATTGT 28637          T      GAAT
           TTTA                    TGAGGCAGTGA TGTTTAGT
                                   |||||||||| ||||||||
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```
                                ATTTTGTTACT ACGAATCA
                                      T       AGTGAAT
GAM393  MRPL35   3'  ATTATGCATGAATTACTGTTTC 33540          GTTTA   AT
            A                    TGAGGCAGTGATT    GTGA
                                 ||||||||||||    ||||
                                 ACTTTGTCATTAA    TATT
                                       GTACG   A
GAM393  MRPS10   3'  ATTCTTTTTATTCATTGTTTCA 36291          T  TTTAGT
                                 TGAGGCAGTGA TG     GAAT
                                 |||||||||| ||     ||||
                                 ACTTTGTTACT AT     CTTA
                                       T  TTTT__
GAM393  MTCH1    3'  TTTGCTGAGTCTGTCTT     26783       TGATTG    TG
                                 GAGGCAG     TTTAG  AA
                                 |||||||     |||||  ||
                                 TTCTGTC     GAGTC  TT
                                     T_____     GT
GAM393  MTHFS    3'  GCCAAATAATCAGTGTTTTA   21237       G       A
                                 TGAGGCA TGATTGTTT GT
                                 ||||||| ||||||||| ||
                                 ATTTTGT ACTAATAAA CG
                                     G        C
GAM393  NAV3     3'  TTCCTATGGTGCTGTCTCA    29777         ATTGTT   T
                                 TGAGGCAGTG     TAG GAA
                                 ||||||||||     ||| |||
                                 ACTCTGTCGT     ATC CTT
                                       GGT___   _
GAM393  NDUFA4   3'  TTCACTATAACGCTGCTTTA   10192         A    TT
                                 TGAGGCAGTG TTGT  AGTGAA
                                 |||||||||| ||||  ||||||
                                 ATTTCGTCGC AATA  TCACTT
                                           _   __
GAM393  NEIL2    3'  ATTTGTTGAACAATTCAGGAAT 58906     GGCAGT        TG
            CA                     TGA     GATTGTTTAG  AAT
                                 |||     ||||||||||  |||
                                 ACT     TTAACAAGTT  TTA
                                   AAGGAC         GT
GAM393  NET-6    3'  ATTCTAGAAATAGTTATGTCTT 26937       G       AGT
            A                    TGAGGCA TGATTGTTT   GAAT
                                 ||||||| |||||||||   ||||
                                 ATTCTGT ATTGATAAA   CTTA
                                     _       GAT
GAM393  NEUGRIN  5'  AGGCAGTTATTGTTCTA     33572    AG
                                 TG  GCAGTGATTGTTT
                                 ||  ||||||||||||
                                 AT  TGTTATTGACGGA
                                   CT
GAM393  NIT1     3'  TTATATAGTCATTGTTT     18809           T
                                 AGGCAGTGATTGT TAG
                                 |||||||||||| |||
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                                TTTGTTACTGATA ATT
                                       T
GAM393  NOLC1   3'  ATTCATTTTCATTGTTGTCTC  16445       TG  T TTT
                                GAGGCAG  AT G   AGTGAAT
                                |||||||  || |   |||||||
                                CTCTGTT  TA C   TTACTTA
                                   GT  _ TT_
GAM393  NP220   3'  ATTCACTAGAAATTTGTTT   27171       TGATTG
                                AGGCAG     TTTAGTGAAT
                                ||||||     ||||||||||
                                TTTGTT     AGATCACTTA
                                   TAA___
GAM393  NRF     3'  ATTGTGCAGTTACTGTTT    34081           T
                                AGGCAGTGATTGT TAGT
                                |||||||||||| ||||
                                TTTGTCATTGACG GTTA
                                       T
GAM393  Nup43   5'  GAATTGTCGCTGCTTCA     45001           T
                                TGAGGCAGTGAT GTTT
                                |||||||||||| ||||
                                ACTTCGTCGCTG TAAG
                                       T
GAM393  NUP54   3'  GTTTACTGACAAATTACTGTTC 60101      G       GT
          A                     TGAG CAGTGATT  TTAGTGAAT
                                |||| ||||||||  |||||||||
                                ACTT GTCATTAA  AGTCATTTG
                                  _       AC
GAM393  NXPH2   5'  GTTTGTTAAACAGTCTCCGGT  72720    AGT_        TG
                                GC   GATTGTTTAG  AAT
                                ||   ||||||||||  |||
                                TG   CTGACAAATT  TTG
                                 GCCT        GT
GAM393  NXPH3   3'  ATTTATTAGACGTGTGGCTTT  65749       AGTGAT
                                GAGGC     TGTTTAGTGAAT
                                |||||     ||||||||||||
                                TTTCG     GCAGATTATTTA
                                   GTGT__
GAM393  OBTP    3'  AACAGTGCTGTTTTA       34239          G
                                TGAGGCAGT ATTGTT
                                ||||||||| ||||||
                                ATTTTGTCG TGACAA
                                          _
GAM393  OR2C3   3'  ATTTGCTAATTATCATAGTTTT 75445       A    TGT   TG
                                GAGGC GTGAT   TTAG  AAT
                                ||||| |||||   ||||  |||
                                TTTTG TACTA   AATC  TTA
                                   A    TT_   GT
GAM393  OR51E2  3'  TGCAGAATAATCCTGTTTTA  47801         T       A
                                TGAGGCAG GATTGTTT GTG
                                |||||||| |||||||| |||
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                                ATTTTGTC CTAATAAG CGT
                                   _       A
GAM393  OSBPL8   3'  ATTTACTTTTTGTTACTCTTTA 40455       C     TGTTT
                                TGAGG AGTGAT     AGTGAAT
                                ||||| ||||||     |||||||
                                ATTTC TCATTG     TCATTTA
                                   _     TTTT_
GAM393  OSRF     3'  ATTTGCTGTCTTTTTCTTGCTT 59523         T  TTGTT_   TG
          CA                      TGAGGCAG GA     TAG  AAT
                                |||||||| ||      |||  |||
                                ACTTCGTT CT     GTC  TTA
                                   _ TTTTCT   GT
GAM393  PABPC5   3'  TTAAATAATTACTTTTTTA   55074       C
                                TGAGG AGTGATTGTTTAG
                                ||||| ||||||||||||||
                                ATTTT TCATTAATAAATT
                                   T
GAM393  PARVA    3'  ATACAAAGGCAATGTACTGTTT 36652          _      AGTGAAT
          T                       GAGGCAGTG ATTGTTT
                                |||||||||  |||||||
                                TTTTGTCAT TAACGGA
                                     G      AACATA
GAM393  PC4      3'  CTGTGTAGTTATTGCTT     22013            TT
                                AGGCAGTGATTG  TAG
                                ||||||||||||  |||
                                TTCGTTATTGAT  GTC
                                      GT
GAM393  PCDH10   3'  GCAATATCACTGTTTTA     51991            __
                                TGAGGCAGTGAT  TGT
                                ||||||||||||  |||
                                ATTTTGTCACTA  ACG
                                      TA
GAM393  PDCD10   5'  AGATAATTTTGCCTTA      23307         T
                                TGAGGCAG GATTGTTT
                                ||||||||  ||||||||
                                ATTCCGTT TTAATAGA
                                   _
GAM393  PDCD5    3'  ATTTACTTTGTTTATTGTCT   16300          TTGTTT
                                AGGCAGTGA     AGTGAAT
                                |||||||||     |||||||
                                TCTGTTATT     TCATTTA
                                     TGTT__
GAM393  PDCD7    3'  ATTCATTAATAAATGCTGTT   72135        A    T
                                GGCAGTG TTGTT AGTGAAT
                                ||||||| ||||| |||||||
                                TTGTCGT AATAA TTACTTA
                                   A    _
GAM393  PEG10    3'  ATTTGCTAATATTGCATTGCT  30520        ATTGT    TG
                                GGCAGTG    TTAG  AAT
                                |||||||    ||||  |||
```

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                                TCGTTAC    AATC  TTA
                                   GTTAT   GT
GAM393  PEPP3    3'  ATGGCTGGGACAGTTACTGGTT 30036     G         _  GAAT
           CA                    TGAG CAGTGATTGTTT AGT
                                ||||| |||||||||||| |||
                                ACTT GTCATTGACAGG TCG
                                  G          G  GTA
GAM393  PIP3-E   3'  TTAGAAATCATTGTGTTA    66818    G       G
                                TGA GCAGTGATT TTTAG
                                ||| ||||||||| |||||
                                ATT TGTTACTAA AGATT
                                  G       _
GAM393  PLCL1    3'  ATTTACTAAACATATGATTTCA 20633      _ GTGAT
                                TGAGG CA    TGTTTAGTGAAT
                                ||||| ||    ||||||||||||
                                ACTTT GT    ACAAATCATTTA
                                   A  AT___
GAM393  PLEKHA3  3'  ATTTATTTTCTTGTTGCCTCA  38859        TG TTGTTT
                                TGAGGCAG  A     AGTGAAT
                                ||||||||  |     |||||||
                                ACTCCGTT  T     TTATTTA
                                     GT CTT___
GAM393  PM5      3'  GGACAGTTGCAGTCTCA     26597       A TG
                                TGAGGC G  ATTGTTT
                                |||||| |  |||||||
                                ACTCTG C  TGACAGG
                                   A GT
GAM393  POLYDOM  3'  GTTTGCTAGCATTGTTGTTCTT 44428     _  TG  T   T  TG
                                GAGG CAG  AT GTT AG  AAT
                                |||| |||  || ||| ||  |||
                                TTCT GTT  TA CGA TC  TTG
                                  T  GT  _  _ GT
GAM393  PPAP2C   3'  AGATAGTTGCTGTTTT      13543        TG
                                GAGGCAG  ATTGTTT
                                |||||||  |||||||
                                TTTTGTC  TGATAGA
                                   GT
GAM393  PPP2R2A  3'  GTTGGCTGTAATCACTCCTC   10747     C      TT   G
                                GAGG AGTGATTG  TAGT AAT
                                |||| ||||||||  |||| |||
                                CTCC TCACTAAT  GTCG TTG
                                  _       __   G
GAM393  PRO0233  3'  ATTCGTTGAATTGGCTGTTTTA 26115         GATT
                                TGAGGCAGT   GTTTAGTGAAT
                                |||||||||   ||||||||||||
                                ATTTTGTCG   TAAGTTGCTTA
                                     GT__
GAM393  PRO0246  5'  ATTTACTGAAGGAATTGCCTGC 26137    _     GA  G
           A                     TG AGGCAGT  TT TTTAGTGAAT
                                || |||||||  || ||||||||||
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                                AC TCCGTTA  AG AAGTCATTTA
                                 G      __ G
GAM393  PRO0611  3' ATAATTAAGTAATTCCTGCTTT 26006        TG        GAAT
                A                 TGAGGCAG  ATTGTTTAGT
                                  |||||||| ||||||||||
                                  ATTTCGTC  TAATGAATTA
                                      CT        ATA
GAM393  PRO0641  3' TTTGCTAAACATTGTTCA    26213     G  TGAT     TG
                                  TGAG CAG   TGTTTAG  AA
                                  |||| |||   ||||||| ||
                                  ACTT GTT   ACAAATC  TT
                                    _  ____     GT
GAM393  PRO0800  3' TTTCCCAGAGACAAACATTGCT 37745         A    AGT_  T
                TT                  GAGGCAGTG TTGTTT   GAA
                                  ||||||||| ||||||   |||
                                  TTTCGTTAC AACAGA   CTT
                                       A    GACC  TG
GAM393  PRO1048  3' AAACAAGGTTGTTGCTTT    37508       TG __
                                  GAGGCAG  AT  TGTTT
                                  ||||||| ||  |||||
                                  TTTCGTT  TG  ACAAA
                                      GT  GA
GAM393  PRO1596  3' ATTTGTTATCAACATTTCCTCA 48383      C   A  TT  TG
                                  TGAGG AGTG TTG  TAG  AAT
                                  ||||| |||| |||  |||  |||
                                  ACTCC TTAC AAC  ATT  TTA
                                     T   _  T_  GT
GAM393  PRO1843  5' ATTCATTATGCCCACTGCTGCA 37541    A     ATT  T
                                  TG GGCAGTG   GT TAGTGAAT
                                  || |||||||   || ||||||||
                                  AC TCGTCAC   CG ATTACTTA
                                   G      C__  T
GAM393  PRO1866  3' GTTTAACATGGTTACTGACTTA 37552      G      TG TTAG
                                  TGAG CAGTGAT  T   TGAAT
                                  |||| |||||||  |   |||||
                                  ATTC GTCATTG  A   ATTTG
                                     A      GT CA__
GAM393  PRO1992  5' ATTTATTTTCACGAATCAGTTG 26052      _   _ TT_
                CTTT                  GGCAG TGATT GT   AGTGAAT
                                  ||||| ||||| ||   |||||||
                                  TCGTT ACTAA CA   TTATTTA
                                     G    G  CTT
GAM393  PRO2133  3' GAGCGATCCTGTTTCA      37788        T
                                  TGAGGCAG GATTGTTT
                                  |||||||| ||||||||
                                  ACTTTGTC CTAGCGAG
                                          _
GAM393  PRO2730  3' TTAAGCAATTACTTTTT     47421      C
                                  GAGG AGTGATTGTTTAG
                                  |||| ||||||||||||
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                                TTTT TCATTAACGAATT
                                  _
GAM393  PROL2   3' AACAGACGCTGTCTCA     22344          A
                                TGAGGCAGTG TTGTT
                                |||||||||| |||||
                                ACTCTGTCGC GACAA
                                      A
GAM393  PTD004  3' GTTCACTAAATGTGAACAGCTT 25317      A  GAT
          T                     GAGGC GT   TGTTTAGTGAAT
                                ||||| ||   ||||||||||||
                                TTTCG CA   GTAAATCACTTG
                                   A  AGT
GAM393  PTPRR   5' GGCAGTCTGTTGTCTTA    55616       GT_
                                TGAGGCA   GATTGTT
                                |||||||   |||||||
                                ATTCTGT   CTGACGG
                                     TGT
GAM393  PYPAF4  5' ATTTATTGTTCCTGGTCACTGT 78578           TT__
          CTC                     GAGGCAGTGATTG    TAGTGAAT
                                ||||||||||||||    ||||||||
                                CTCTGTCACTGGT    GTTATTTA
                                       CCTT
GAM393  QKI     3' TGCAATAGACATTCATTGTTTT 65448          T     G  AAT
                                GAGGCAGTGA TGTTTA TG
                                |||||||||| |||||| ||
                                TTTTGTTACT ACAGAT AC
                                      T     A  GTA
GAM393  RAB10   3' GTTTGCTGAGTCTTGTTTTA  85178        T   TGT   TG
                                TGAGGCAG GAT   TTAG  AAT
                                |||||||| |||   ||||  |||
                                ATTTTGTT CTG   AGTC  TTG
                                     _  ___    GT
GAM393  RAB9A   3' TAAACTAATGTTGCTGCTTCA 14913        TG  TGT    GAAT
                                TGAGGCAG  AT   TTAGT
                                ||||||||  ||   |||||
                                ACTTCGTC  TG   AATCA
                                     GT  T__     AATT
GAM393  RBBP1   3' ACCCAGCTGAATAGTTACTGCT 11256    A            GAAT
          GCA                     TG GGCAGTGATTGTTTAGT
                                || ||||||||||||||||
                                AC TCGTCATTGATAAGTCG
                                 G              ACCCAT
GAM393  RBBP1   3' ACCCAGCTGAATAGTTACTGCT 43427    A            GAAT
          GCA                     TG GGCAGTGATTGTTTAGT
                                || ||||||||||||||||
                                AC TCGTCATTGATAAGTCG
                                 G              ACCCAT
GAM393  RBM11   3' GTTTGCTGTTCAATTTTTGCCT 58583        T    TT   TG
          T                     GAGGCAG GATTG  TAG  AAT
                                |||||||  |||||  |||  |||
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                                TTCCGTT TTAAC  GTC  TTG
                                   T    TT   GT
GAM393  RBM12    3'  TAGACAGTCCTGCTTCA     20160        T
                                TGAGGCAG GATTGTTTA
                                |||||||| |||||||||
                                ACTTCGTC CTGACAGAT
                                   _
GAM393  RDH-E2   3'  TCAAAGAGTGGTTGCTTCTTA  57273      C  TG  TG   AG
                                TGAGG AG  AT  TTT  TGA
                                ||||| ||  ||  |||  |||
                                ATTCT TC  TG  GAG  ACT
                                   _ GT  GT   AA
GAM393  RFX3     5'  TTATAGCAACCGTTGCCTT   56226        A    TA
                                GAGGCAGTG TTGTT  GTGA
                                ||||||||| |||||  ||||
                                TTCCGTTGC AACGA  TATT
                                    C    __
GAM393  RFX3     5'  TTATAGCAACCGTTGCCTT   11316        A    TA
                                GAGGCAGTG TTGTT  GTGA
                                ||||||||| |||||  ||||
                                TTCCGTTGC AACGA  TATT
                                    C    __
GAM393  RGS7     3'  ATTTATTAAACAATAAATTCCG 11328    A  CAGTG
           CA                     TG GG    ATTGTTTAGTGAAT
                                || ||    ||||||||||||||
                                AC CC    TAACAAATTATTTA
                                 G  TTAAA
GAM393  RI58     3'  ATTTATTGAATAGTTATTGT   24846
                                GCAGTGATTGTTTAGTGAAT
                                ||||||||||||||||||||
                                TGTTATTGATAAGTTATTTA

GAM393  RNF38    3'  ATTTGCTGAGTCATTTTCTCA  42934      C     TGT   TG
                                TGAGG AGTGAT   TTAG  AAT
                                ||||| ||||||   ||||  |||
                                ACTCT TTACTG   AGTC  TTA
                                   T     ___   GT
GAM393  RNF8     3'  ATTTGTTGTTGTTGTTACTGTT 14216         TGTT_  TG
           TT                     GAGGCAGTGAT    TAG  AAT
                                ||||||||||    |||  |||
                                TTTTGTCATTG    GTT  TTA
                                     TTGTT   GT
GAM393  RoXaN    3'  ATTTGTTGAATGATTGAATGAC 46635      _____  TG    TG
           TGC                    GCAGT    GAT  TTTAG  AAT
                                |||||    |||  |||||  |||
                                CGTCA    TTA  AAGTT  TTA
                                   GTAAG   GT    GT
GAM393  RRN3     3'  TTTACGGGTTGCTGTTTTA   37360        TG  TGTTTA
                                TGAGGCAG  AT     GTGAA
                                ||||||||  ||     |||||
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                                ATTTTGTC  TG     CATTT
                                    GT  GG____
GAM393  SARCOSIN 3' ATTCAAGAAGTTATTGTCT   20231          GTTTAG
                                AGGCAGTGATT     TGAAT
                                ||||||||||      |||||
                                TCTGTTATTGA     ACTTA
                                    AGA___
GAM393  SDCBP    3' TTCAAAATAGTTGTAGCCTTA  18843       A TG      AG    T
                                TGAGGC G  ATTGTTT  TGAA
                                ||||||  |  |||||||  ||||
                                ATTCCG T  TGATAAA  ACTT
                                   A GT       __    T
GAM393  SDR1     3' GTTTATTGTCAATTGCTTCTCA 16463      C  TG    TT
                                TGAGG AG  ATTG  TAGTGAAT
                                |||||  ||  ||||  ||||||||
                                ACTCT TC  TAAC  GTTATTTG
                                   _  GT    T_
GAM393  SE57-1   3' ATTTATTGGATAAGAAGGTCT  47396      AGTGA
                                AGGC    TTGTTTAGTGAAT
                                ||||    ||||||||||||
                                TCTG    AATAGGTTATTTA
                                  GAAG_
GAM393  SEC24A   3' TCAAAATAATCATGTTTTA   82684        G        AG
                                TGAGGCA TGATTGTTT  TGA
                                |||||||  |||||||||  |||
                                ATTTTGT ACTAATAAA  ACT
                                    _       __
GAM393  SEC24B   3' AACGATGATGCTGTTTCA    20896          __
                                TGAGGCAGTG  ATTGTT
                                ||||||||||  ||||||
                                ACTTTGTCGT  TAGCAA
                                      AG
GAM393  SEMA3E   3' ATTCACACTATTTTTGCTTTA  24878         T   T  TTA
                                TGAGGCAG GAT GT   GTGAAT
                                ||||||||  |||  ||   ||||||
                                ATTTCGTT TTA CA   CACTTA
                                     T   T  ____
GAM393  SERP1    3' GTTTGCTTTGTTAATTGCCTCA 27064         GATTGTTT  TG
                                TGAGGCAGT       AG  AAT
                                |||||||||       ||  |||
                                ACTCCGTTA       TC  TTG
                                     ATTGTT__  GT
GAM393  SGT1     3' ATTTATTAGACCTGGCAGCTTT 21991       A  GATT
                                GAGGC GT    GTTTAGTGAAT
                                |||||  ||    ||||||||||||
                                TTTCG CG    CAGATTATTTA
                                  A  GTC_
GAM393  SH3BGRL2 3' GATAATCACAGTCTTA      48887        A
                                TGAGGC GTGATTGTT
                                ||||||  |||||||||
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                                ATTCTG CACTAATAG
                                   A
GAM393  SLC12A5  3'  ATTTATTACTATTACTGCT   40378        TGTT
                                GGCAGTGAT   TAGTGAAT
                                |||||||||   ||||||||
                                TCGTCATTA   ATTATTTA
                                    TC__
GAM393  SLC31A2  3'  TTTATTACTTACTGCTT    60131        TTGTT
                                AGGCAGTGA    TAGTGAA
                                |||||||||    |||||||
                                TTCGTCATT    ATTATTT
                                    C____
GAM393  SLK      3'  AGACAATCACCTGCCTCA    28223        _
                                TGAGGCAG TGATTGTTT
                                |||||||| |||||||||
                                ACTCCGTC ACTAACAGA
                                    C
GAM393  SLU7     3'  GTTTATTCTTCTTGCTGCCT  21213       TG TTGTTT
                                AGGCAG  A     AGTGAAT
                                ||||||  |     |||||||
                                TCCGTC  T     TTATTTG
                                   GT CTTC__
GAM393  SMBP     3'  AAGCATTATTGCTTTA      72157          T
                                TGAGGCAGTGAT GTTT
                                |||||||||||| ||||
                                ATTTCGTTATTA CGAA
                                          _
GAM393  SNRK     3'  TTGCTGTGGTCACTGTTTC   34775          TG TT  TG
                                GAGGCAGTGAT  T  AG  A
                                ||||||||||  |  ||  |
                                CTTTGTCACTG  G  TC  T
                                      GT __  GT
GAM393  SNRPD1   3'  ATTAAGGGTCATTGCTTT    22677          G
                                GAGGCAGTGATT TTTAGT
                                |||||||||||| ||||||
                                TTTCGTTACTGG GAATTA
                                          _
GAM393  SNX10    3'  ATAACTAGGATAACTTGTTGCT 25263        TG _    _   GAAT
           TT                    GAGGCAG  A TTGTT TAGT
                                |||||||  | ||||| ||||
                                TTTCGTT  T AATAG ATCA
                                   GT C    G    ATA
GAM393  SNX10    3'  GTTCACACTATTTCTGTTTTA  25266        T   T  TTA
                                TGAGGCAG GAT GT   GTGAAT
                                |||||||| ||| ||   ||||||
                                ATTTTGTC TTA CA   CACTTG
                                     T   T ____
GAM393  SPTLC2   3'  TGGGCAGTTGTTGTTT     16813        TG
                                AGGCAG  ATTGTTTA
                                ||||||  ||||||||
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                                TTTGTT  TGACGGGT
                                   GT
GAM393  SRPK2    3'  TCATTAAGGTGCCTC       11972       GTGATTG
                                GAGGCA      TTTAGTGA
                                ||||||      ||||||||
                                CTCCGT      GAATTACT
                                   G_______
GAM393  SS18L1   3'  ATTTATTGAACAGGTCAAATTT 65343      ___   _
            GTCTT                GCAG   TGAT TGTTTAGTGAAT
                                ||||   |||| ||||||||||||
                                TGTT   ACTG ACAAGTTATTTA
                                  TAA    G
GAM393  ST7L     3'  ATTTGTATATAGTTGCTGCC   57006      TG    TTA TG
                                GGCAG  ATTGT   G  AAT
                                |||||  |||||   |  |||
                                CCGTC  TGATA   T  TTA
                                   GT    TA_ GT
GAM393  ST7L     3'  ATTTGTATATAGTTGCTGCC   57569      TG    TTA TG
                                GGCAG  ATTGT   G  AAT
                                |||||  |||||   |  |||
                                CCGTC  TGATA   T  TTA
                                   GT    TA_ GT
GAM393  STC2     3'  GTTTATATTTTAACCACTGCTT 13551          A   TTTA
            CA                    TGAGGCAGTG TTG    GTGAAT
                                ||||||||||| |||    ||||||
                                ACTTCGTCAC AAT    TATTTG
                                      C   TTTA
GAM393  STIM2    3'  CAACCAAGGGATATTTACTGCT 40472          T    AG  AAT
            TTA                   TGAGGCAGTGA TGTTT  TG
                                ||||||||||| |||||  ||
                                ATTTCGTCATT ATAGG  AC
                                      T    GA  CAACT
GAM393  STIP-1   3'  ATTTACTAAGTGCACTCTTTCA 69662      C    ATTG
                                TGAGG AGTG    TTTAGTGAAT
                                ||||| ||||    ||||||||||
                                ACTTT TCAC    GAATCATTTA
                                   C    GT__
GAM393  STK38L   3'  GGATATTGCTGCTTTA      69174        TG  T
                                TGAGGCAG  AT GTTT
                                ||||||||  || ||||
                                ATTTCGTC  TA TAGG
                                     GT  _
GAM393  STRIN    3'  ATTCTACCAACCACTGTTTCA  32766          A   TTTA  _
                                TGAGGCAGTG TTG    GT GAAT
                                |||||||||| |||    || ||||
                                ACTTTGTCAC AAC    CA CTTA
                                      C   _____  T
GAM393  STX12    3'  TTCAATAAAATTACTGTCTT   66356          GTTTAG    T
                                GAGGCAGTGATT     TGAA
                                ||||||||||||     ||||
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                                TTCTGTCATTAA     ACTT
                                      AATA__    T
GAM393  SV2B    3'  ATTCATTGAGCAGCTACCACTT 29294     GCA   A
            A                    TGAG   GTG TTGTTTAGTGAAT
                                 ||||   ||| ||||||||||||
                                 ATTC   CAT GACGAGTTACTTA
                                   AC_   C
GAM393  TA-LRRP  5'  AGCAGTCAATGCCTTA     31067       G
                                 TGAGGCA TGATTGTT
                                 ||||||| ||||||||
                                 ATTCCGT ACTGACGA
                                     A
GAM393  TACTILE  3'  ATTAATATAGTCGCTCTTCA  19467     C       _
                                 TGAGG AGTGATTGT TTAGT
                                 ||||| ||||||||| |||||
                                 ACTTC TCGCTGATA AATTA
                                   _       T
GAM393  TBLR1    3'  TTCAGCATTCGTTGCTTT    45107         T   TTAG
                                 GAGGCAGTGA TGT    TGAA
                                 |||||||||| |||    ||||
                                 TTTCGTTGCT ACG    ACTT
                                       T  _____
GAM393  TESK2    3'  TTGAGTAATTGCTGTTT     63185       TG
                                 AGGCAG  ATTGTTTAG
                                 ||||||  |||||||||
                                 TTTGTC  TAATGAGTT
                                    GT
GAM393  TEX27    3'  TTCACTAATGTTAGCCTTA   41668      AG    TGT
                                 TGAGGC  TGAT   TTAGTGAA
                                 ||||||  ||||   ||||||||
                                 ATTCCG  ATTG   AATCACTT
                                    __    T__
GAM393  TFEC     3'  AGGTGGTCATTGCCTT      24291          TG
                                 GAGGCAGTGAT  TTT
                                 ||||||||||  |||
                                 TTCCGTTACTG  GGA
                                       GT
GAM393  TIGD1    5'  TTGCTATTGTCATTGTTTT   88871          TGTT   TG
                                 GAGGCAGTGAT    TAG  A
                                 ||||||||||    |||  |
                                 TTTTGTTACTG    ATC  T
                                       TT__   GT
GAM393  TNRC4     3'  GTTCTGGGGCAAACGCTGCTTC 23224         A     AGT
                                 GAGGCAGTG TTGTTT   GAAT
                                 |||||||| ||||||   ||||
                                 CTTCGTCGC AACGGG   CTTG
                                       A     GT_
GAM393  TPD52    3'  ATTTTGGAATAAGCATTGTTTT 17424         A     AGT
                                 GAGGCAGTG TTGTTT   GAAT
                                 |||||||| ||||||   ||||
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                                TTTTGTTAC AATAAG   TTTA
                                     G     GT_
GAM393   TPD52    3'  ATTTATTAAATTGTGATTGTTT 17423         G  T
            TA                    TGAGGCAGT AT GTTTAGTGAAT
                                  ||||||||| || ||||||||||
                                  ATTTTGTTA TG TAAATTATTTA
                                     G  T
GAM393   TRAF3    3'  ATTCAAGAGTGCAATTTTGTTT 12383        T     TTAG_
            CA                    TGAGGCAG GATTGT    TGAAT
                                  |||||||| ||||||    |||||
                                  ACTTTGTT TTAACG    ACTTA
                                     _     TGAGA
GAM393   TRAF3    5'  ATTCAAGAGTGCAATTTTGTTT 59735        T     TTAG_
            CA                    TGAGGCAG GATTGT    TGAAT
                                  |||||||| ||||||    |||||
                                  ACTTTGTT TTAACG    ACTTA
                                     _     TGAGA
GAM393   TREX1    5'  TCCTGAGTCATTGCTTT     33058          TGT   T
                                  GAGGCAGTGAT   TTAG GA
                                  |||||||||||   |||| ||
                                  TTTCGTTACTG   AGTC CT
                                        ___   _
GAM393   TREX1    5'  TCCTGAGTCATTGCTTT     53281          TGT   T
                                  GAGGCAGTGAT   TTAG GA
                                  |||||||||||   |||| ||
                                  TTTCGTTACTG   AGTC CT
                                        ___   _
GAM393   TREX1    5'  TCCTGAGTCATTGCTTT     53291          TGT   T
                                  GAGGCAGTGAT   TTAG GA
                                  |||||||||||   |||| ||
                                  TTTCGTTACTG   AGTC CT
                                        ___   _
GAM393   TRIM22   3'  AGGCAGGCATTGTCTCA     20285          A
                                  TGAGGCAGTG TTGTTT
                                  |||||||||| ||||||
                                  ACTCTGTTAC GACGGA
                                        G
GAM393   TRIM4    3'  ATTTATTGGATGTTGATCTTTG 52251       T   ___
            TTTCA                   GGCAG GATT   GTTTAGTGAAT
                                  ||||| ||||   ||||||||||
                                  TTGTT CTAG   TAGGTTATTTA
                                     T   TTG
GAM393   UNC5D    3'  ATTTAAGTCCAATAGTCATGCT 55134       G      TAG__
            TTA                   GAGGCA TGATTGTT    TGAAT
                                  |||||| ||||||||    |||||
                                  TTTCGT ACTGATAA    ATTTA
                                     _       CCTGA
GAM393   UQCR     3'  TTCATCCGTTGCTGCCTTA   22411         TG  TGTTTA
                                  TGAGGCAG  AT     GTGAA
                                  ||||||||  ||     |||||
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                                ATTCCGTC  TG     TACTT
                                    GT  CC____
GAM393  USP20    3'  GTCAGGGAGTAGCTGCTGCTTC 21927         GA     AG   AT
            A                    TGAGGCAGT  TTGTTT  TGA
                                 |||||||||  ||||||  |||
                                 ACTTCGTCG  GATGAG  ACT
                                     TC     GG   G
GAM393  VEST1    5'  ATTTACTTCTCTGTTATTGTTT 53684           TGTTT
            C                    GAGGCAGTGAT    AGTGAAT
                                 ||||||||||     |||||||
                                 CTTTGTTATTG    TCATTTA
                                       TCTCT
GAM393  WDF2     3'  ATTTACTAAAGAAACGGTTGTT 53661         TGA_  G
            TTA                    TGAGGCAG    TT TTTAGTGAAT
                                 ||||||||    || ||||||||||
                                 ATTTTGTT    AA AAATCATTTA
                                     GGCA  G
GAM393  XLKD1    3'  ATTTGCTGAATAGCTACT    21948      A       TG
                                 AGTG TTGTTTAG  AAT
                                 ||||| ||||||||  |||
                                 TCAT GATAAGTC  TTA
                                   C       GT
GAM393  YAP1     3'  GTTTGTTCAACAGTTGTTTCTT 20357       C  TG     T  TG
            CA                     TGAGG AG  ATTGTT AG  AAT
                                 |||||  ||  ||||||  ||  |||
                                 ACTTC TT  TGACAA TT  TTG
                                    T  GT     C  GT
GAM393  ZDHHC3   3'  AAGCAATTGCCTGCCTT     33455       _ TG
                                 GAGGCA G  ATTGTTT
                                 ||||||  |  |||||||
                                 TTCCGT C  TAACGAA
                                    C GT
GAM393  ZFP91    3'  ATTACAGATAGATGATTGTTTC 53818         G  _    A    AT
                                 GAGGCAGT AT TGTTT GTGA
                                 ||||||||  ||  |||||  ||||
                                 CTTTGTTA TA ATAGA CATT
                                     G  G    _    A
GAM393  ZIC4     5'  GTTCACTGCTGGCGCTGTCT   49623         ATT  TT
                                 AGGCAGTG   GT  AGTGAAT
                                 ||||||||   ||  |||||||
                                 TCTGTCGC   CG  TCACTTG
                                     GGT  __
GAM393  ZNF177   3'  GAACTAGTTGCTGTCTCA    12900         TG  _
                                 TGAGGCAG  ATT GTTT
                                 ||||||||  |||  ||||
                                 ACTCTGTC  TGA CAAG
                                     GT   T
GAM393  ZNF31    3'  GTTTATTGAGCTGTTGCTCTTT 64989      C  TG  T
                                 GAGG AG  AT GTTTAGTGAAT
                                 ||||  ||  ||  ||||||||||
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                                TTTC TC  TG CGAGTTATTTG
                                  _ GT  T
GAM393  ZNF345   3'  TTTATTATATTTTGCCTCA   12775        TGATTGTT
                                TGAGGCAG       TAGTGAA
                                ||||||||       |||||||
                                ACTCCGTT       ATTATTT
                                    TTAT____
GAM393  LOC115051 3'  ATTTGCTAGCAGGCTGCCCCA  60035    A     GA    T  TG
                                TG GGCAGT  TTGTT AG  AAT
                                || ||||||  ||||| ||  |||
                                AC CCGTCG  GACGA TC  TTA
                                 C     __    _ GT
GAM393  LOC115123 3'  AAGCAAATGCTGTTTTA     73219          A
                                TGAGGCAGTG TTGTTT
                                |||||||||| ||||||
                                ATTTTGTCGT AACGAA
                                      A
GAM393  LOC115123 5'  TTAGCAGAGTAATTGCTGTCT  73224       TG      A  GAAT
                                AGGCAG  ATTGTTT GT
                                ||||||  ||||||| ||
                                TCTGTC  TAATGAG CG
                                   GT      A  ATTA
GAM393  LOC115207 3'  GTTTACTTAACTTACTGTTTT  56604          TT   T
                                GAGGCAGTGA  GTT AGTGAAT
                                ||||||||||  ||| |||||||
                                TTTTGTCATT  CAA TCATTTG
                                     __  T
GAM393  LOC116028 3'  ATTTAAGTACGGTCGTTGCCCA 73716    A          TTAG
                                TG GGCAGTGATTGT    TGAAT
                                || ||||||||||||    |||||
                                AC CCGTTGCTGGCA    ATTTA
                                 _          TGA_
GAM393  LOC116068 3'  TGTTGATTAAAAATCATTTGTC 73728        _    G     G
           TT                    GAGGCAG TGATT TTTAGT AAT
                                |||||||  ||||| |||||| |||
                                TTCTGTT ACTAA AAATTA TTG
                                    T    _     G   TT
GAM393  LOC116143 3'  GTTTGCTGACTTGCTGCTGCA  73773    A    TG TTGT    TG
                                TG GGCAG  A    TTAG  AAT
                                || |||||  |    ||||  |||
                                AC TCGTC  T    AGTC  TTG
                                 G    GT C___    GT
GAM393  LOC118851 5'  AGACAGTGCTGCCTTA      75499          G
                                TGAGGCAGT ATTGTTT
                                |||||||||  |||||||
                                ATTCCGTCG TGACAGA
                                          _
GAM393  LOC119548 3'  AATAATCATTGTTCTA      73995    AG
                                TG  GCAGTGATTGTT
                                ||  ||||||||||||
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                                AT  TGTTACTAATAA
                                 CT
GAM393   LOC121219 5'  AGACGATCTTGCTTTA      74039         T
                                TGAGGCAG GATTGTTT
                                |||||||| ||||||||
                                ATTTCGTT CTAGCAGA

                                   _
GAM393   LOC121642 5'  TAGAACTTGAGCAATTTCTGTC 74101        T       _ GAAT
           TT                    GAGGCAG GATTGTTTA GT
                                |||||||| ||||||||| ||
                                TTCTGTC TTAACGAGT CA
                                    T        T  AGATA
GAM393   LOC122553 3'  GTTTGTTAGACATTCATATGCC 74134       _   T      TG
           T                     AGGCA GTGA TGTTTAG  AAT
                                ||||| |||| |||||||  |||
                                TCCGT TACT ACAGATT  TTG
                                   A    T      GT
GAM393   LOC122704 3'  GTTCAGCTAAGTCTTGCTTTA  74143         T   TGT   _
                                TGAGGCAG GAT   TTAG TGAAT
                                |||||||| |||   |||| |||||
                                ATTTCGTT CTG   AATC ACTTG
                                   _  ___   G
GAM393   LOC122786 3'  ATTACTGTAAACAGGTACTGCT 74156         A    __     AT
           TTA                    GAGGCAGTG TTGTT  TAGTGA
                                |||||||| |||||  ||||||
                                TTTCGTCAT GACAA  GTCATT
                                     G    AT     A
GAM393   LOC122786 3'  TAGGCAACATTGCCTTA     74160          A
                                TGAGGCAGTG TTGTTTA
                                |||||||||| |||||||
                                ATTCCGTTAC AACGGAT

                                   _
GAM393   LOC123876 3'  ATTTATTAAGCATTTGCC     74243       TGAT
                                GGCAG    TGTTTAGTGAAT
                                |||||    ||||||||||||
                                CCGTT    ACGAATTATTTA
                                   T___
GAM393   LOC124987 5'  AGACAGTTACGCTTC       75662       A
                                GAGGC GTGATTGTTT
                                ||||| ||||||||||
                                CTTCG CATTGACAGA

                                   _
GAM393   LOC125228 3'  ATTAAGCAGTGGTTAATGTCTT 74401       G   ___       GAAT
           A                     GAGGCA TGAT   TGTTTAGT
                                |||||| ||||   ||||||||
                                TTCTGT ATTG   ACGAATTA
                                   A   GTG         T
GAM393   LOC126231 3'  ATTCAATGTCAGTCCTGTTTTA 74466         T    TTTAG
                                TGAGGCAG GATTG     TGAAT
                                |||||||| |||||     |||||
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                                ATTTTGTC CTGAC     ACTTA
                                    _     TGTA_
GAM393   LOC126526 3'  AGACAGCTGCTGTTTTA     74531          GA
                                TGAGGCAGT  TTGTTT
                                |||||||||  ||||||
                                ATTTTGTCG  GACAGA
                                     TC
GAM393   LOC126669 3'  ATTTATTGAGCTTCTGTC     75397       TGATT
                                GGCAG     GTTTAGTGAAT
                                |||||     ||||||||||||
                                CTGTC     CGAGTTATTTA
                                   TT___
GAM393   LOC130535 5'  AGACATCATTGTTTT       76146           T
                                GAGGCAGTGAT GTTT
                                |||||||||||| ||||
                                TTTTGTTACTA CAGA
                                          _
GAM393   LOC130574 3'  GAATAAATGTTGCTTCA      74956         GT A
                                TGAGGCA  G TTGTTT
                                |||||||  | ||||||
                                ACTTCGT  T AATAAG
                                     TG A
GAM393   LOC131368 3'  GAACGGCTGCTGTTTCA      75860          GA
                                TGAGGCAGT  TTGTTT
                                |||||||||  ||||||
                                ACTTTGTCG  GGCAAG
                                     TC
GAM393   LOC131873 3'  AGAAAATCATTGTTTTA      75875            G
                                TGAGGCAGTGATT TTT
                                |||||||||||||| |||
                                ATTTTGTTACTAA AGA
                                       A
GAM393   LOC133688 3'  GGTCACAGATGATACTGCTTTA 75115          A TG   A    AT
                                TGAGGCAGTG T  TTT GTGA
                                |||||||||| |  ||| ||||
                                ATTTCGTCAT A  AGA CACT
                                     _ GT   _    GGT
GAM393   LOC134265 3'  ATTCTACAGTCATTCCTCA    75171       C        TT
                                TGAGG AGTGATTGT  AGT
                                ||||| |||||||||  |||
                                ACTCC TTACTGACA  TTA
                                   _        TC
GAM393   LOC134266 3'  AAGCAATCCTGCCTCA       75160         T
                                TGAGGCAG GATTGTTT
                                |||||||| ||||||||
                                ACTCCGTC CTAACGAA
                                          _
GAM393   LOC136288 3'  TTATAACATTTGCTGTTTTA   75256          TG T    TA
                                TGAGGCAG  A TGTT  GTGA
                                |||||||  | ||||  ||||
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                                ATTTTGTC  T ACAA  TATT
                                    GT T   __
GAM393   LOC137781 5'  GTTCAAAAGCATTGCTGTTTCA 75271        TG  T   AG
                                TGAGGCAG  AT GTTT  TGAAT
                                |||||||  || ||||  |||||
                                ACTTTGTC  TA CGAA  ACTTG
                                    GT  _   A_
GAM393   LOC139422 3'  TTAAGAGTAAGCGATTTATTGC 75848         _     GTGAAT
           TTTA                   GAGGCAGTGA TTGTTTA
                                |||||||||| |||||||
                                TTTCGTTATT AGCGAAT
                                      T      GAGAATTA
GAM393   LOC142955 5'  ATTTACTGAGCAGCTGCTGT   76442      GA
                                GCAGT  TTGTTTAGTGAAT
                                |||||  ||||||||||||
                                TGTCG  GACGAGTCATTTA
                                   TC
GAM393   LOC142973 3'  TGAACTGATAGTTACTGTT    60281           T   GAAT
                                GGCAGTGATTGTT AGT
                                |||||||||||| |||
                                TTGTCATTGATAG TCA
                                      _  AGTT
GAM393   LOC143196 3'  GTTTGTTAGATTTATTATTACT 82907        T____     TG
           GTC                    GCAGTGAT    GTTTAG  AAT
                                |||||||    ||||||  |||
                                TGTCATTA    TAGATT  TTG
                                    TTATT     GT
GAM393   LOC143308 5'  TCTCAATGAATGGTCATTGATT 82940     G      TG    G   AT
           TA                     TGAG CAGTGAT  TTTA TGA
                                |||| |||||||  |||| |||
                                ATTT GTTACTG  AAGT ACT
                                  A      GT    A   CTT
GAM393   LOC143381 3'  GTTTACTGAGTGAGTACTCT   76550    C    A TG
                                GG AGTG T  TTTAGTGAAT
                                || |||| |  ||||||||||
                                TC TCAT A  GAGTCATTTG
                                 _   G GT
GAM393   LOC143465 5'  GTCCTTTAGATAGGTACTGTTT 82968         A       T_  AT
           CA                     TGAGGCAGTG TTGTTTAG  GA
                                |||||||||| ||||||||  ||
                                ACTTTGTCAT GATAGATT  CT
                                      G       TC  G
GAM393   LOC143785 5'  AGGCGGACGCTGTCTCA     76606          A
                                TGAGGCAGTG TTGTTT
                                |||||||||| ||||||
                                ACTCTGTCGC GGCGGA
                                      A
GAM393   LOC144245 3'  GTTTATTAAAACTGGGTATGCT 70817        GTGATTG_
           TCA                    TGAGGCA       TTTAGTGAAT
                                |||||||       ||||||||||
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                                ACTTCGT       AAATTATTTG
                                    ATGGGTCA
GAM393  LOC144248 3'  TAAAATAGATAATTATGTTTCA 76744        G         GTGAAT
                                TGAGGCA TGATTGTTTA
                                ||||||| ||||||||||
                                ACTTTGT ATTAATAGAT
                                    _         AAAATT
GAM393  LOC144266 5'  TTTGCTGTCCTCTGCTTT    76766        T_   TGTTT  TG
                                GAGGCAG  GAT    AG  AA
                                |||||||  |||    ||  ||
                                TTTCGTC  CTG    TC  TT
                                    TC  _____  GT
GAM393  LOC144742 5'  AGATAATAGCTGTTTTA     76940         G
                                TGAGGCAGT ATTGTTT
                                ||||||||| |||||||
                                ATTTTGTCG TAATAGA
                                     A
GAM393  LOC144871 3'  ATTCTCTGCAATCTGTTGTTTC 83196       GT_     TT  T
                                GAGGCA   GATTGT  AG GAAT
                                ||||||   ||||||  || ||||
                                CTTTGT   CTAACG  TC CTTA
                                    TGT      __  T
GAM393  LOC144997 3'  ATTTACTAGTGTTAGCTGTTT  83209        GATTGT
                                AGGCAGT     TTAGTGAAT
                                |||||||     |||||||||
                                TTTGTCG     GATCATTTA
                                    ATTGT_
GAM393  LOC145225 3'  TCTCTCTGGGCAATTGTTTCCT 83309      C  TG       T  AT
          T                      GAGG AG  ATTGTTTAG GA
                                |||| ||  |||||||||| ||
                                TTCC TT  TAACGGGTC CT
                                  T  GT       T  CTT
GAM393  LOC145608 5'  TTTATGTTGTTACTGCTCA    83390      G      TGTTTA
                                TGAG CAGTGAT     GTGAA
                                |||| |||||||     |||||
                                ACTC GTCATTG     TATTT
                                  _      TTG___
GAM393  LOC145623 3'  ATTTTTATATGATCATTGTGTC 83393     G       TG T   TGAAT
          A                      TGA GCAGTGAT  T TAG
                                ||| ||||||||  | |||
                                ACT TGTTACTA  A ATT
                                  G       GT T   TTTA
GAM393  LOC145676 5'  TTTCAGTGTGACTGTTGTTGCT 77344        TG  T  _ G   T
          TTA                    TGAGGCAG  AT GTT TA TGAA
                                ||||||||  || ||| || ||||
                                ATTTCGTT  TG CAG GT ACTT
                                     GT  T   T  G   TA
GAM393  LOC145773 3'  AGGCGAATGCTGTTTT      77495         A
                                GAGGCAGTG TTGTTT
                                ||||||||| ||||||
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                                TTTTGTCGT AGCGGA
                                     A
GAM393  LOC145788 5'  ATTCATCTTCTGTTTGCTGCTT 77494        TG TTGTTTA
                TA                  TGAGGCAG  A      GTGAAT
                                    |||||||| |      ||||||
                                    ATTTCGTC  T      TACTTA
                                        GT TGTCTTC
GAM393  LOC145815 3'  TCATGACTGATTACTGCTTT   83524          _  TA
                                    GAGGCAGTGATT GTT  GTGA
                                    |||||||||||| |||  ||||
                                    TTTCGTCATTAG CAG  TACT
                                          T  __
GAM393  LOC145820 3'  ATCCTTAAGCAATCACTGATTT 77510     G          T  AT
                                    GAG CAGTGATTGTTTAG GA
                                    ||| |||||||||||||| ||
                                    TTT GTCACTAACGAATT CT
                                      A           C  A
GAM393  LOC145845 3'  ATTTATTAAAAGTTCAAGTTGC 83551       __  TTG
                TTT                 GAGGCAG  TGA   TTTAGTGAAT
                                    |||||||  |||  ||||||||||
                                    TTTCGTT  ACT   AAATTATTTA
                                        GA   TGA
GAM393  LOC146229 3'  ATTTGCTGATCTACCAGCTGTT 77729        GATTGT_   TG
                TTA                 TGAGGCAGT      TTAG  AAT
                                    |||||||||      ||||  |||
                                    ATTTTGTCG      AGTC  TTA
                                         ACCATCT    GT
GAM393  LOC146268 3'  TTCTGACTTACTGCTTCA    77815          TT   TAGT
                                    TGAGGCAGTGA  GTT    GAA
                                    ||||||||||  |||    |||
                                    ACTTCGTCATT  CAG    CTT
                                          __   T___
GAM393  LOC146337 3'  GTGAGGAGGCAGTGCACTGTTT 83663         _      AGTGAAT
                T                    GAGGCAGTG ATTGTTT
                                    |||||||| |||||||
                                    TTTTGTCAC TGACGGA
                                         G      GGAGTG
GAM393  LOC146714 5'  ATTCATTGAGCACCTGCTGCCT 83739        AT
                                    AGGCAGTG  TGTTTAGTGAAT
                                    |||||||  ||||||||||||
                                    TCCGTCGT  ACGAGTTACTTA
                                         CC
GAM393  LOC146784 5'  GACAGTCATTTTCTCA      78114       C
                                    TGAGG AGTGATTGTT
                                    ||||| ||||||||||
                                    ACTCT TTACTGACAG
                                       T
GAM393  LOC146818 5'  TTGAGAGGTTGCTGCTTCA    78145        TG  TG
                                    TGAGGCAG  AT  TTTAG
                                    ||||||||  ||  |||||
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                                ACTTCGTC  TG  GAGTT
                                    GT  GA
GAM393   LOC146952 5'  ATTCTTTCAGTTACTGT     83859          TTTAGT
                                GCAGTGATTG     GAAT
                                ||||||||||     ||||
                                TGTCATTGAC     CTTA
                                    TTT___
GAM393   LOC147172 3'  GTTCACTGAACAGCTATTTTC  78297    C    A
                                GG AGTG TTGTTTAGTGAAT
                                || |||| ||||||||||||
                                CT TTAT GACAAGTCACTTG
                                 T   C
GAM393   LOC147429 3'  ATTTTAATCAATCCACTGCTTT 78354          _   T    TGAAT
           A                     TGAGGCAGTG ATTG TTAG
                                ||||||||||| |||| ||||
                                ATTTCGTCAC TAAC AATT
                                    C   T   TTA
GAM393   LOC147429 3'  TTTCACTGATGGTTGGCTGTTT 78368         _  TG  T     T
           CA                    TGAGGCAGT GAT  TT AGTGAA
                                ||||||||| |||  || ||||||
                                ACTTTGTCG TTG  AG TCACTT
                                    G   GT  _     TT
GAM393   LOC148293 3'  AAATAGTTGCTGTTCA      78776      G   TG
                                TGAG CAG  ATTGTTT
                                |||| |||  |||||||
                                ACTT GTC  TGATAAA
                                  _  GT
GAM393   LOC148753 3'  AACGGCACTGCTTCA       84208          A
                                TGAGGCAGTG TTGTT
                                |||||||||| |||||
                                ACTTCGTCAC GGCAA
                                    _
GAM393   LOC149301 3'  TTTCCCGGGGCAAGCATTGTTT 79254          A     AGT   T
           CA                    TGAGGCAGTG TTGTTT   GAA
                                |||||||||| ||||||   |||
                                ACTTTGTTAC AACGGG   CTT
                                    G     GCC   TA
GAM393   LOC149420 3'  TAAGCAATTGTTCCTCA     79369      C  TG
                                TGAGG AG  ATTGTTTA
                                ||||| ||  ||||||||
                                ACTCC TT  TAACGAAT
                                  _  GT
GAM393   LOC149506 3'  GCAGTGGCGCTGTCTC      84465         __
                                GAGGCAGTG  ATTGT
                                |||||||||  |||||
                                CTCTGTCGC  TGACG
                                    GG
GAM393   LOC149506 3'  GGCCATCACTGTCTCA      84474           T
                                TGAGGCAGTGAT GTT
                                ||||||||||| |||
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                                ACTCTGTCACTA CGG
                                       C
GAM393  LOC149684 5'  GTTTATTGAGCACCTGCTCT  84617   _   TGAT
                                AG GCAG   TGTTTAGTGAAT
                                || ||||   ||||||||||||
                                TC CGTC   ACGAGTTATTTG
                                 T   C___
GAM393  LOC149821 3'  TTTGCTAATCACTCCTCA    84769     C    TGTT  TG
                                TGAGG AGTGAT   TAG  AA
                                ||||| ||||||   |||  ||
                                ACTCC TCACTA   ATC  TT
                                   _    ____  GT
GAM393  LOC149837 3'  GGACAGTTGCTGTTTT     84743       TG
                                GAGGCAG  ATTGTTT
                                |||||||  |||||||
                                TTTTGTC  TGACAGG
                                     GT
GAM393  LOC149935 5'  ATTCACTACTTTCACTGCCT  60295       TT  TT
                                AGGCAGTGA  GT  AGTGAAT
                                |||||||||  ||  |||||||
                                TCCGTCACT  CA  TCACTTA
                                      TT  __
GAM393  LOC149995 3'  GGCAGCATTGTTTCA      84846         A
                                TGAGGCAGTG TTGTT
                                |||||||||| |||||
                                ACTTTGTTAC GACGG
                                          _
GAM393  LOC150005 5'  GAATGGTTCTGCCTTA     84820       T  TG
                                TGAGGCAG GAT  TTT
                                |||||||| |||  |||
                                ATTCCGTC TTG  AAG
                                      _  GT
GAM393  LOC150159 3'  AAATATTTATTGCTTTA    57536         T
                                TGAGGCAGTGA TGTTT
                                |||||||||| |||||
                                ATTTCGTTATT ATAAA
                                       T
GAM393  LOC150225 3'  AAGCAGTTCTGCCTCA     84975       T
                                TGAGGCAG GATTGTTT
                                |||||||| ||||||||
                                ACTCCGTC TTGACGAA
                                          _
GAM393  LOC150319 5'  AGACGATTGCTCCTCA     79645      C  TG
                                TGAGG AG  ATTGTTT
                                ||||| ||  |||||||
                                ACTCC TC  TAGCAGA
                                   _  GT
GAM393  LOC150333 5'  TTCTCTAGCTATTGCCTTA  85019         ATT  T  T
                                TGAGGCAGTG   GTT AG GAA
                                ||||||||||   ||| || |||
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                                ATTCCGTTAT   CGA TC CTT
                                     ___   _ T
GAM393   LOC150397 3'  TGGTAGGGAGTCACTGTTTTA  79854           G    G
                                TGAGGCAGTGATT TTTA TG
                                |||||||||||| |||| ||
                                ATTTTGTCACTGA GGAT GT
                                      G    G
GAM393   LOC150759 3'  ATTTATTGAATATACTTTTTCA 80003      C    AT
                                TGAGG AGTG  TGTTTAGTGAAT
                                ||||| ||||  ||||||||||||
                                ACTTT TCAT  ATAAGTTATTTA
                                   T   __
GAM393   LOC150848 5'  ATTCACTAAATGGGCTCCTGCC 85128    A    T __ TG
            CA                    TG GGCAG GA  T  TTTAGTGAAT
                                || ||||| ||  |  ||||||||||
                                AC CCGTC CT  G  AAATCACTTA
                                 _    _ CG GT
GAM393   LOC150848 3'  TTGCTAGTGATTATTGCTT    85140         TG  T  TG
                                AGGCAGTGAT  TT AG  A
                                ||||||||||  || ||  |
                                TTCGTTATTA  GA TC  T
                                      GT  _  GT
GAM393   LOC151098 5'  ATTTATAAAAAGCGCTGTTTT  80114         ATTG   A
                                GAGGCAGTG    TTT GTGAAT
                                |||||||||    ||| ||||||
                                TTTTGTCGC    AAA TATTTA
                                      GA__   A
GAM393   LOC151176 3'  ATTTATTAAAGTATTTATTGTC 85258         T  _
            T                    AGGCAGTGA TG TTTAGTGAAT
                                |||||||||| || ||||||||||
                                TCTGTTATT AT AAATTATTTA
                                      T  G
GAM393   LOC151249 3'  TGAACTGATAGTTACTGTT    60063           T   GAAT
                                GGCAGTGATTGTT AGT
                                |||||||||||| |||
                                TTGTCATTGATAG TCA
                                       _   AGTT
GAM393   LOC151318 3'  GTTTTTGAAAGAGGTTGCTGCT 80228        TG   G_   AGT
            TT                    GAGGCAG  ATT  TTT   GAAT
                                |||||||  |||  |||   ||||
                                TTTCGTC  TGG  AAA   TTTG
                                    GT   AG   GTT
GAM393   LOC151323 3'  ATTTATTGAATATACTTTTTCA 80216      C    AT
                                TGAGG AGTG  TGTTTAGTGAAT
                                ||||| ||||  ||||||||||||
                                ACTTT TCAT  ATAAGTTATTTA
                                   T   __
GAM393   LOC151475 5'  ATTGCTCAGTGATAACTGTTTC 85391         G  TG  T  TG AT
            A                     TGAGGCAGT AT  TT AG  A
                                |||||||||  ||  ||  ||  |
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                                ACTTTGTCA TA  GA TC  T
                                     A  GT  C  GT A
GAM393   LOC151827 5'  TAGGCGGTCACTGCCTTA    80371
                                TGAGGCAGTGATTGTTTA
                                ||||||||||||||||||
                                ATTCCGTCACTGGCGGAT

GAM393   LOC151959 3'  ATTTTTCAGTAGTTGCCTTA   85521        TG    TTT
                                TGAGGCAG  ATTG   AGT
                                ||||||||  ||||   |||
                                ATTCCGTT  TGAC   TTA
                                     GA    TTT
GAM393   LOC151959 3'  GTTTACTGGGCGGTTTCC    85525    CAGT
                                GG    GATTGTTTAGTGAAT
                                ||    ||||||||||||||
                                CC    TTGGCGGGTCATTTG
                                 T___
GAM393   LOC151963 3'  GTTTACTTTTTGTAGTTATTGT 80404          TTT__
           C                     GGCAGTGATTG    AGTGAAT
                                ||||||||||     |||||||
                                CTGTTATTGAT    TCATTTG
                                      GTTTT
GAM393   LOC152059 3'  TCCTGGTTCTGCCTCA      80450        TGATTGT   T
                                TGAGGCAG      TTAG GA
                                ||||||||      |||| ||
                                ACTCCGTC      GGTC CT
                                     TT_____   _
GAM393   LOC152330 5'  TCAGGATAATCGCCGCTTT   80540      A        AG
                                GAGGC GTGATTGTTT  TGA
                                ||||| ||||||||||  |||
                                TTTCG CGCTAATAGG  ACT
                                   C        __
GAM393   LOC152518 3'  GTTCATTGGGCTTCCTTGTACT 80613     _   T  TT
           TA                    TGAG GCAG GA  GTTTAGTGAAT
                                ||||  |||| ||  ||||||||||
                                ATTC TGTT CT  CGGGTTACTTG
                                  A   C  T_
GAM393   LOC152790 5'  TGATGTGTTACTGCTTT     85876          TGT
                                GAGGCAGTGAT   TTA
                                ||||||||||   |||
                                TTTCGTCATTG   AGT
                                      TGT
GAM393   LOC152804 3'  TTGGATGTTCATTGTCTT    85891          TT
                                GAGGCAGTGA  GTTTAG
                                ||||||||||  ||||||
                                TTCTGTTACT  TAGGTT
                                      TG
GAM393   LOC153163 3'  TTTGCTGGACAAATTCC     80773    C   GA      TG
                                GG AGT  TTGTTTAG  AA
                                || |||  ||||||||  ||
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                                CC TTA  AACAGGTC  TT
                                 _  __      GT
GAM393  LOC153416 3'  ATTTGCAGTAACTATTGCTGTT 60538       TG  T   TA_ TG
            TTA                   TGAGGCAG  AT GTT   G  AAT
                                  ||||||||  || |||   |  |||
                                  ATTTTGTC  TA CAA   C  TTA
                                       GT  T   TGA GT
GAM393  LOC153514 3'  GTTTATTCTAACTTAATTCTGC 80853       TGATT_  T_
            CTTA                    GAGGCAG     GTT  AGTGAAT
                                  |||||||     |||  |||||||
                                  TTCCGTC     CAA  TTATTTG
                                       TTAATT   TC
GAM393  LOC153651 3'  TTTAGATGGTGATTGTTGTCT  80917      TG  TG  TAG   T
                                  AGGCAG  AT  TT   TGAA
                                  ||||||  ||  ||   ||||
                                  TCTGTT  TA  GG   ATTT
                                      GT  GT  TAG   T
GAM393  LOC153688 5'  AGACAATGCTGTCTTA      86093        G
                                  TGAGGCAGT ATTGTTT
                                  |||||||||  |||||||
                                  ATTCTGTCG TAACAGA
                                            _
GAM393  LOC153733 5'  GAGTGATGGCTGTTTTA     80921        G  TG
                                  TGAGGCAGT AT  TTT
                                  |||||||||  ||  |||
                                  ATTTTGTCG TA  GAG
                                       G  GT
GAM393  LOC153937 5'  TTTACCTAGTACTGCCTT    81007        ATTGTTTA
                                  GAGGCAGTG       GTGAA
                                  |||||||||       |||||
                                  TTCCGTCAT       CATTT
                                       GATC____
GAM393  LOC154007 3'  TTTATTCTTCATTGCCT     81027        TTGTTT
                                  AGGCAGTGA     AGTGAA
                                  |||||||||     ||||||
                                  TCCGTTACT     TTATTT
                                       TC____
GAM393  LOC154386 3'  GTTTACTGGGTACAGAGTTTCA 81083       AG  AT  TT
                                  TGAGGC  TG  TG  TAGTGAAT
                                  ||||||  ||  ||  ||||||||
                                  ACTTTG  AC  AT  GTCATTTG
                                      AG  __  GG
GAM393  LOC154442 3'  TATTTACTGAGCAGATAGTTTT 86220      _______
            ATTGTCCA                GTGA     TTGTTTAGTGAAT   A
                                  ||||     ||||||||||||||  |
                                  TATT     GACGAGTCATTTA   T
                                    TTGATA
GAM393  LOC154877 3'  TTGAAAACCGCTGCCTCA    86318         ATTG
                                  TGAGGCAGTG    TTTAG
                                  ||||||||||    |||||
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                                ACTCCGTCGC    AAGTT
                                      CAA_
GAM393   LOC154881 3'  GTTCATTAAGCCCATTGCTTT  81172          ATT
                                GAGGCAGTG   GTTTAGTGAAT
                                |||||||||   ||||||||||
                                TTTCGTTAC   CGAATTACTTG
                                     C__
GAM393   LOC155435 3'  ATTCTGCTTCTTGTCACTGTTT 81346           TGTTT  _
           CA                     TGAGGCAGTGAT     AGT GAAT
                                |||||||||||     ||| ||||
                                ACTTTGTCACTG     TCG CTTA
                                      TTCT_   T
GAM393   LOC155435 3'  ATTTGGTGGCCACTGCTTCA   81347          A TG TT
                                TGAGGCAGTG T  T  AGT
                                |||||||||| |  |  |||
                                ACTTCGTCAC G  G  TTA
                                      C GT GT
GAM393   LOC155438 3'  GGACAGTGACTGCCTC      86394         G
                                GAGGCAGT ATTGTTT
                                |||||||| |||||||
                                CTCCGTCA TGACAGG
                                     G
GAM393   LOC157349 5'  GTTCATTAGGTGGCCTAGTGCC 81422       G  A_ TG
           T                     AGGCA TG  T  TTTAGTGAAT
                                ||||| ||  |  ||||||||||
                                TCCGT AT  G  GGATTACTTG
                                   G  CC GT
GAM393   LOC157562 5'  ATTTATTGGGAACCAATCATTG 86476   A         ___
           TCCA                    GGCAGTGATTG   TTTAGTGAAT
                                 ||||||||||   ||||||||||
                                 CTGTTACTAAC   GGGTTATTTA
                                _         CAA
GAM393   LOC157653 3'  ATTTATTGGGTGATGTCTGTC  81522       TG  TG
                                GGCAG  AT  TTTAGTGAAT
                                |||||  ||  ||||||||||
                                CTGTC  TA  GGGTTATTTA
                                   TG  GT
GAM393   LOC157740 3'  ATTTATTCAAATAATTACTCCT 81561       C         _
           T                     GAGG AGTGATTGTTT AGTGAAT
                                |||| ||||||||||| |||||||
                                TTCC TCATTAATAAA TTATTTA
                                  _         C
GAM393   LOC157931 3'  ATTAACGTGGTCACTTTCTCA  86656       C      TG _
                                TGAGG AGTGAT  T TTAGT
                                ||||| ||||||  | |||||
                                ACTCT TCACTG  G AATTA
                                   T     GT C
GAM393   LOC158014 5'  ATTCTCCATGTTATTGTCTCA  81644           TGTTTAGT
                                TGAGGCAGTGAT       GAAT
                                ||||||||||||       ||||
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                                ACTCTGTTATTG       CTTA
                                      TACCT___
GAM393  LOC158156 3'  ATTTATTTTTTTCACTTGCTGC 81724        TG T  TTT__
          TTTA                   GAGGCAG  A TG     AGTGAAT
                                 |||||||  | ||    |||||||
                                 TTTCGTC  T AC     TTATTTA
                                    GT C  TTTTT
GAM393  LOC158187 3'  ATTCACTGTGCTTTTACAGCTT 86688        A    TT  T
          CA                     TGAGGC GTGA  GT TAGTGAAT
                                 |||||| ||||  || ||||||||
                                 ACTTCG CATT  CG GTCACTTA
                                    A    TT  T
GAM393  LOC158219 3'  ATTTGTTGGGTAGTTAAACTTC 81789      CAG     TT   TG
          A                      TGAGG   TGATTG  TAG  AAT
                                 |||||   ||||||  |||  |||
                                 ACTTC   ATTGAT  GTT  TTA
                                    AA_     GG   GT
GAM393  LOC158427 3'  GTTTATTGAACAGCCACACCC  57680    CA   AT
                                 GG  GTG  TGTTTAGTGAAT
                                 ||  |||  ||||||||||||
                                 CC  CAC  ACAAGTTATTTG
                                  CA   CG
GAM393  LOC158581 5'  GTTCACTGGTTGGCTGCTGC   86871      GA  GT
                                 GCAGT  TT  TTAGTGAAT
                                 |||||  ||  |||||||||
                                 CGTCG  GG  GGTCACTTG
                                    TC  TT
GAM393  LOC158777 3'  ATTTCCAAATAGTTGTAGCCTT 82000       A TG      AGTGAAT
          A                      TGAGGC G  ATTGTTT
                                 ||||||| |  |||||||
                                 ATTCCG T  TGATAAA
                                    A GT      CCTTTA
GAM393  LOC158865 5'  ATTGGCTGTAAGTGTTGCCTCA 86931        GT ATTGTT    G
                                 TGAGGCA  G     TAGT AAT
                                 |||||||  |     |||| |||
                                 ACTCCGT  T     GTCG TTA
                                      TG GAAT__    G
GAM393  LOC159089 3'  ATTGACTTATATAATCACTGTT 86985              TT_   G
          TCA                      TGAGGCAGTGATTGT   AGT AAT
                                 ||||||||||||||||   ||| |||
                                 ACTTTGTCACTAATA   TCA TTA
                                         TAT   G
GAM393  LOC160711 5'  GGCAGTTCTTGCTTTA      87071         T
                                 TGAGGCAG GATTGTT
                                 |||||||| |||||||
                                 ATTTCGTT TTGACGG
                                      C
GAM393  LOC161482 3'  TTAAGAAAGCAGTTGCTGTTCA 87091      G   TG      AGTGAAT
                                 TGAG CAG  ATTGTTT
                                 |||| |||  |||||||
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                                ACTT GTC  TGACGAA
                                  _  GT      AGAATTA
GAM393  LOC161734 3'  TTTACTAGGCATGTATT     87105      AT
                                AGTG  TGTTTAGTGAA
                                ||||  ||||||||||
                                TTAT  ACGGATCATTT
                                  GT
GAM393  LOC163231 5'  GTTCACTATCACCCACTCTTTC 82441       C    AT  TT
          A                      TGAGG AGTG  TG  TAGTGAAT
                                ||||| ||||  ||  ||||||||
                                ACTTT TCAC  AC  ATCACTTG
                                  C    CC  T_
GAM393  LOC163231 5'  GTTCACTGTCACCCACTGTCTC 82442          AT  TT
          A                      TGAGGCAGTG  TG  TAGTGAAT
                                ||||||||||  ||  ||||||||
                                ACTCTGTCAC  AC  GTCACTTG
                                      CC  T_
GAM393  LOC164312 5'  GTTCATAGCTGAGTTGCTGTCC 82506    A    TG   GTTTA
          A                      TG GGCAG  ATT     GTGAAT
                                || |||||  |||    ||||||
                                AC CTGTC  TGA     TACTTG
                                 _    GT   GTCGA
GAM393  LOC168667 3'  GAGCAGTCCTGTTTCA      92757         T
                                TGAGGCAG GATTGTTT
                                |||||||| ||||||||
                                ACTTTGTC CTGACGAG
                                        _
GAM393  LOC169611 3'  ATTCACTAGGCCTCTTCTGTTT 82756        T_  TT
          T                      GAGGCAG  GA  GTTTAGTGAAT
                                |||||||  ||  ||||||||||
                                TTTTGTC  CT  CGGATCACTTA
                                    TT  C_
GAM393  LOC170261 5'  GAACGGCGCTGCCTC       82583         A
                                GAGGCAGTG TTGTTT
                                ||||||||| ||||||
                                CTCCGTCGC GGCAAG
                                        _
GAM393  LOC196485 3'  GGCAGTAGTGCTGCCTT     87733          __
                                GAGGCAGTG  ATTGTT
                                |||||||||  ||||||
                                TTCCGTCGT  TGACGG
                                     GA
GAM393  LOC196812 3'  ATTCATTAGATGACTACAGCCT 89564      A   A TG
                                AGGC GTG T  TTTAGTGAAT
                                |||| ||| |  ||||||||||
                                TCCG CAT A  AGATTACTTA
                                  A   C GT
GAM393  LOC196812 3'  TTCATTTATGACTGCTTT    89578         G  TGTTT
                                GAGGCAGT AT     AGTGAA
                                |||||||| ||     ||||||
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                                TTTCGTCA TA    TTACTT
                                    G  T____
GAM393  LOC197003 3'  ATTTGCTGCCTATCACTGTC  87869        TGTT  TG
                                GGCAGTGAT   TAG  AAT
                                |||||||||   |||  |||
                                CTGTCACTA   GTC  TTA
                                    TCC_  GT
GAM393  LOC197131 3'  ATTTGCTAAGTGATTAGTGATG 87886   AGG  G   TG    TG
          CA                     TG  CA TGAT  TTTAG  AAT
                                ||  || ||||  |||||  |||
                                AC  GT ATTA  GAATC  TTA
                                 GTA  G   GT    GT
GAM393  LOC197423 5'  GTTCAGCATGGCAGTTGTGCTT 77862       G      TAG_
          TA                     TGAGGCA TGATTGTT   TGAAT
                                |||||||  ||||||||   |||||
                                ATTTCGT GTTGACGG   ACTTG
                                   _      TACG
GAM393  LOC199907 3'  TTTACCAGTCATTGTT     88472          TTTA
                                GGCAGTGATTG   GTGAA
                                ||||||||||   |||||
                                TTGTTACTGAC   CATTT
                                      ____
GAM393  LOC199923 3'  GCAGATAATGACTGCTTT    88499        G     A
                                GAGGCAGT ATTGTTT GT
                                |||||||| ||||||| ||
                                TTTCGTCA TAATAGA CG
                                    G    _
GAM393  LOC199923 3'  TTGAAAGTCACTGCTTTA    88501          G
                                TGAGGCAGTGATT TTTAG
                                |||||||||||| |||||
                                ATTTCGTCACTGA AAGTT
                                      _
GAM393  LOC200014 3'  ATTCAATTTCAGTCTGCTGCTT 88518       _    TTTAG
          T                     GAGGCAGT GATTG    TGAAT
                                |||||||| |||||    |||||
                                TTTCGTCG CTGAC    ACTTA
                                    T    TTTA_
GAM393  LOC200093 3'  GTTTGTTAAGTGGTCAGAAATT 63099    GCAG   TG    TG
          C                     GAG   TGAT  TTTAG  AAT
                                |||   ||||  |||||  |||
                                CTT   ACTG  GAATT  TTG
                                  AAAG   GT    GT
GAM393  LOC200107 3'  TTAATGAATTATTGCTTT    88578          GT
                                GAGGCAGTGATT  TTAG
                                ||||||||||||  ||||
                                TTTCGTTATTAA  AATT
                                      GT
GAM393  LOC200132 3'  ATTCATTAAGTGCAATTATTGT 88581   AG       __
          TACA                    G  GCAGTGATTGT  TTAGTGAAT
                                |  ||||||||||  |||||||||
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                                C  TGTTATTAACG  AATTACTTA
                                 AT         TG
GAM393   LOC200268 3'  ATTCTTGGAAATATATCATTGT 88676          _    AGT_
              TTT                  GAGGCAGTGAT TGTTT    GAAT
                                |||||||||| |||||    ||||
                                TTTTGTTACTA ATAAA    CTTA
                                      T    GGTT
GAM393   LOC200269 3'  TTCAATTAAATTATTGCTTTA  88670          GTTTAG    T
                                TGAGGCAGTGATT     TGAA
                                ||||||||||||     ||||
                                ATTTCGTTATTAA     ACTT
                                       ATTA__    T
GAM393   LOC200282 3'  ATTTATTTTGTTTGCTGTCT   88705       TG TTGTTT
                                AGGCAG  A     AGTGAAT
                                ||||||  |     |||||||
                                TCTGTC  T     TTATTTA
                                   GT TGTT__
GAM393   LOC200314 5'  TTGTGTATGTGTAATCATTGTT 90021            TT  GTGAAT
              TTA                  TGAGGCAGTGATTG  TA
                                |||||||||||||  ||
                                ATTTTGTTACTAAT  GT
                                       GT  ATGTGTTT
GAM393   LOC200314 3'  AAGCAAGTCGCTGCCTT     89999          _
                                GAGGCAGTGATT GTTT
                                |||||||||||| ||||
                                TTCCGTCGCTGA CGAA
                                       A
GAM393   LOC200399 3'  ATTTATTGAATATACTTTTTCA 88807      C    AT
                                TGAGG AGTG  TGTTTAGTGAAT
                                ||||| ||||  ||||||||||||
                                ACTTT TCAT  ATAAGTTATTTA
                                   T   __
GAM393   LOC200531 5'  AAACAATCATTCCTTA      88819      C
                                TGAGG AGTGATTGTTT
                                ||||| ||||||||||
                                ATTCC TTACTAACAAA
                                   _
GAM393   LOC200609 5'  ATTCTGTCAGTTTTTGCTTCA  90095        T    TTTAGT
                                TGAGGCAG GATTG     GAAT
                                |||||||| |||||     ||||
                                ACTTCGTT TTGAC     CTTA
                                      T    TGT___
GAM393   LOC200734 3'  ATTCATTGGAGTAACTGGTTTA 88859      G    GATTG
                                TGAG CAGT    TTTAGTGAAT
                                |||| ||||    ||||||||||
                                ATTT GTCA    AGGTTACTTA
                                  G   ATG__
GAM393   LOC200760 3'  ATTCACTGGGCATCTGCTGC   90134       AT
                                GCAGTG  TGTTTAGTGAAT
                                ||||||  ||||||||||||
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                                CGTCGT  ACGGGTCACTTA
                                   CT
GAM393   LOC200830 3'  ATCTCTGGGTAGTCACTGCCTC 90147          TT   T  AT
                                GAGGCAGTGATTG  TAG GA
                                |||||||||||||  ||| ||
                                CTCCGTCACTGAT  GTC CT
                                     GG   T  A
GAM393   LOC201564 3'  TTGACTAAATCATTGTTTCA   80440          GTT    G
                                TGAGGCAGTGATT   TAGT AA
                                |||||||||||||   |||| ||
                                ACTTTGTTACTAA   ATCA TT
                                     ____   G
GAM393   LOC201627 3'  ATTCTGTTGAGTGATCATTGTT 89005         TG    GT_
           T                     AGGCAGTGAT  TTTA   GAAT
                                ||||||||||  ||||   ||||
                                TTTGTTACTA  GAGT   CTTA
                                     GT    TGT
GAM393   LOC201627 3'  TCAGGAGGAATCACTGCTTTA  89024          G   AG
                                TGAGGCAGTGATT TTT  TGA
                                |||||||||||||  |||  |||
                                ATTTCGTCACTAA GAG  ACT
                                     G   G_
GAM393   LOC201725 3'  ATTTATTTCTGTGGTTACTGCT 89037         TG TT_
           TT                    GAGGCAGTGAT  T   AGTGAAT
                                ||||||||||  |  |||||||
                                TTTCGTCATTG  G   TTATTTA
                                     GT TCT
GAM393   LOC201931 3'  GTTTGCTGTTAGCACTGTT   89114       A   TT   TG
                                GGCAGTG TTG  TAG  AAT
                                |||||||  |||  |||  |||
                                TTGTCAC GAT  GTC  TTG
                                   _  T_   GT
GAM393   LOC202025 5'  ATTTACAGCTGATCACTGC   90280         _   TA
                                GCAGTGATT GTT  GTGAAT
                                |||||||||  |||  ||||||
                                CGTCACTAG CGA  CATTTA
                                     T  __
GAM393   LOC202025 3'  GAATTATCATTGTTTTA     90289          T
                                TGAGGCAGTGAT GTTT
                                ||||||||||| ||||
                                ATTTTGTTACTA TAAG
                                     T
GAM393   LOC202347 3'  GAATAGATCATTGTTTT     90346          _
                                GAGGCAGTGAT TGTTT
                                |||||||||| |||||
                                TTTTGTTACTA ATAAG
                                     G
GAM393   LOC202460 5'  GTTCACCAAATCACTGCCTCA  89187          GTTTA
                                TGAGGCAGTGATT    GTGAAT
                                ||||||||||||    ||||||
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                                ACTCCGTCACTAA    CACTTG
                                      AC___
GAM393  LOC202986 3' GGCAGTAATGCTGCCTT    90444        __
                                GAGGCAGTG  ATTGTT
                                |||||||||  ||||||
                                TTCCGTCGT  TGACGG
                                     AA
GAM393  LOC203276 3' ATTTATTGATGCCAGCTGCTCC 90473    AG    GATTGT
           A                     TG  GCAGT     TTAGTGAAT
                                ||  |||||     |||||||||
                                AC  CGTCG     AGTTATTTA
                                 CT    ACCGT_
GAM393  LOC203305 3' ATTTATTGATGCCAGCTGCTCC 90517    AG    GATTGT
           A                     TG  GCAGT     TTAGTGAAT
                                ||  |||||     |||||||||
                                AC  CGTCG     AGTTATTTA
                                 CT    ACCGT_
GAM393  LOC203369 3' TTCAAGAACTGCTGCCTTA    89346         ATT    AG
                                TGAGGCAGTG   GTTT  TGAA
                                ||||||||||   ||||  ||||
                                ATTCCGTCGT   CAAG  ACTT
                                      ___    A_
GAM393  LOC203378 5' ATTTGTTGAACAGAGATGCCCT 90594      TGA____       TG
           GTCTCA                  GCAG      TTGTTTAG  AAT
                                ||||      ||||||||  |||
                                TGTC      GACAAGTT  TTA
                                  CCGTAGA       GT
GAM393  LOC203427 5' GAACAGTAACTGTTTC      89358         G
                                GAGGCAGT ATTGTTT
                                |||||||| |||||||
                                CTTTGTCA TGACAAG
                                     A
GAM393  LOC203504 3' GCTGGACAGTGGCTGCCTC    90638         G
                                GAGGCAGT ATTGTTTAGT
                                |||||||| ||||||||||
                                CTCCGTCG TGACAGGTCG
                                     G
GAM393  LOC204804 3' TTACATAGTTGCTCCTTA     89490      C  TG    TTA
                                TGAGG AG  ATTGT   GTGA
                                ||||| ||  |||||   ||||
                                ATTCC TC  TGATA   CATT
                                   _  GT    ___
GAM393  LOC206338 5' TTTATGTTATGGCATTGCCTT  89528         A TG TTA    T
                                GAGGCAGTG T  T   GTGAA
                                |||||||||  |  |   |||||
                                TTCCGTTAC G  A   TATTT
                                      _ GT TTG    T
GAM393  LOC219404 3' GAGGAATTATTGCTTCA     93495           G
                                TGAGGCAGTGATT TTT
                                |||||||||||| |||
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                                ACTTCGTTATTAA GAG
                                      G
GAM393  LOC219540 5'  TGACTTTAGGTAATTATTGCTT 93603          TT   TGAAT
          T                    GAGGCAGTGATTG  TAG
                               ||||||||||||  |||
                               TTTCGTTATTAAT  ATT
                                     GG   TCAGTG
GAM393  LOC219621 3'  ATTTGTTAAACAATAGCAATTC 91458     GCA  G       TG
          A                    TGAG   GT ATTGTTTAG  AAT
                               ||||   || |||||||||  |||
                               ACTT   CG TAACAAATT  TTA
                                 AA_  A       GT
GAM393  LOC219686 3'  GTTTATTCTATATGAATATTGT 90843         A TG T   __
          TTCA                   GAGGCAGTG T  T TAG  TGAAT
                               |||||||||  |  | |||  |||||
                               CTTTGTTAT A  A ATC  ATTTG
                                    A GT T   TT
GAM393  LOC219899 3'  TTCACTGGGATTTGCCT     91506       TGATTG
                               AGGCAG     TTTAGTGAA
                               ||||||     |||||||||
                               TCCGTT     GGGTCACTT
                                  TA____
GAM393  LOC220038 5'  ATTCACTAAATAAACATTGT   91720       A
                               GCAGTG TTGTTTAGTGAAT
                               |||||| ||||||||||||
                               TGTTAC AATAAATCACTTA
                                  A
GAM393  LOC220058 3'  GAGTGACACTGCTTTA      91726          A TG
                               TGAGGCAGTG T  TTT
                               ||||||||||  |  |||
                               ATTTCGTCAC A  GAG
                                     _ GT
GAM393  LOC220565 5'  GTTCAGCATGGCAGTCGTGCTT 90754        G       TAG_
          TA                     TGAGGCA TGATTGTT    TGAAT
                               |||||||  ||||||||    |||||
                               ATTTCGT GCTGACGG    ACTTG
                                  _       TACG
GAM393  LOC220672 3'  ATTTACTAGAATTTTGTGTCA  60424     G    TGATTG
                               TGA GCAG     TTTAGTGAAT
                               ||| ||||     ||||||||||
                               ACT TGTT     AGATCATTTA
                                 G    TTA___
GAM393  LOC220840 3'  TGAACTGATAGTTACTGTT    90810           T   GAAT
                               GGCAGTGATTGTT AGT
                               |||||||||||| |||
                               TTGTCATTGATAG TCA
                                     _  AGTT
GAM393  LOC220930 3'  CTCAGAATAAATTACTGCTTTA 93131            _   AG   AT
                               TGAGGCAGTGATT GTTT  TGA
                               |||||||||||| ||||  |||
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                                ATTTCGTCATTAA TAAG  ACT
                                      A   __  CT
GAM393  LOC221181 3'  ATTCAGTGTAGCAATTACTGTC 92901           _ G
          TT                   GAGGCAGTGATTGTT TA TGAAT
                               ||||||||||||||| || |||||
                               TTCTGTCATTAACGA GT ACTTA
                                      T  G
GAM393  LOC221272 3'  TGTTCACGGTGAAAAACAGTAA 93610    G     A_____
          CTGCCTCA               AGT ATTGTTT    GTGAAT  G
                               ||| |||||||     ||||||  |
                               TCA TGACAAA     CACTTG  T
                                 A      AAGTGG
GAM393  LOC221337 3'  ATTTGCTAGGCACATCCTT   92106     CA  AT     TG
                               GAGG  GTG  TGTTTAG  AAT
                               ||||  |||  |||||||  |||
                               TTCC  TAC  ACGGATC  TTA
                                 __  __     GT
GAM393  LOC221354 3'  GCAGTAATGCTGCTTT     92413        __
                               GAGGCAGTG  ATTGT
                               |||||||||  |||||
                               TTTCGTCGT  TGACG
                                    AA
GAM393  LOC221437 5'  ATTTAAATTGTGAACATTGCCT 92839        A TG TTAG
          T                    GAGGCAGTG T  T   TGAAT
                               |||||||||  |  |   |||||
                               TTCCGTTAC A  G   ATTTA
                                    A GT TTAA
GAM393  LOC221477 3'  ATTCACTATGTGCATTGTTTT  92148        ATTGTT
                               GAGGCAGTG     TAGTGAAT
                               |||||||||     ||||||||
                               TTTTGTTAC     ATCACTTA
                                    GTGT__
GAM393  LOC221490 5'  GAACAGTTAGTGTTTT     93659       G
                               GAGGCA TGATTGTTT
                               ||||||  |||||||||
                               TTTTGT ATTGACAAG
                                  G
GAM393  LOC221511 3'  AAGCAGTCATTCCTTA     90989       C
                               TGAGG AGTGATTGTTT
                               |||||  ||||||||||
                               ATTCC TTACTGACGAA
                                  _
GAM393  LOC221687 5'  TTTGCTAGAGCTGGCCTT    92250      _  GATTG    TG
                               GAGGC AGT    TTTAG  AA
                               |||||  |||    |||||  ||
                               TTCCG TCG    AGATC  TT
                                  G  _____    GT
GAM393  LOC221710 3'  TTAACTCAAAGCGCTGTTTCA  92416        ATTG  T   GAAT
                               TGAGGCAGTG    TT AGT
                               ||||||||||    || |||
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                                ACTTTGTCGC    AA TCA
                                      GA__  C   ATTT
GAM393   LOC221755 3'  ATTTATTTTGCAGTCATTCTTT 92392      C        TT
                                GAGG AGTGATTGT  AGTGAAT
                                |||| |||||||||  |||||||
                                TTTC TTACTGACG  TTATTTA
                                  _        TT
GAM393   LOC221773 3'  ATTTACTGAAATGCGCTCTTTA 91037      C    ATTG
                                TGAGG AGTG    TTTAGTGAAT
                                ||||| ||||    ||||||||||
                                ATTTC TCGC    AAGTCATTTA
                                  _    GTA_
GAM393   LOC221814 5'  ATTTACTAAAGGAATAATGTTT 93942        G  A  G
            TA                    TGAGGCA TG TT TTTAGTGAAT
                                ||||||| || || ||||||||||
                                ATTTTGT AT AG AAATCATTTA
                                     A  A  G
GAM393   LOC221895 3'  GTTTGTTAGATGAGTAAACCTC 92527      CAG  A TG     TG
                                GAGG   TG T  TTTAG  AAT
                                ||||   || |  |||||  |||
                                CTCC   AT A  AGATT  TTG
                                  AA_  G GT     GT
GAM393   LOC221929 3'  AGGTAGTTGTGCCTCA      92672        G      TT
                                TGAGGCA TGATTG  T
                                ||||||| ||||||  |
                                ACTCCGT GTTGAT  A
                                     _     GG
GAM393   LOC222001 3'  GTTCACTAAGTGGTTA      92906      TG
                                TGAT  TTTAGTGAAT
                                ||||  ||||||||||
                                ATTG  GAATCACTTG
                                  GT
GAM393   LOC222008 3'  GTTCACTAAACATATCTGCTT  94013        TGAT
                                AGGCAG    TGTTTAGTGAAT
                                ||||||    ||||||||||||
                                TTCGTC    ACAAATCACTTG
                                   TAT_
GAM393   LOC222159 5'  GTTCACCATAGAAAACAATTTT 94080      T       A_____
            GTCTT                   CAG GATTGTTT      GTGAAT
                                ||| ||||||||      ||||||
                                GTT TTAACAAA      CACTTG
                                  _       AGATAC
GAM393   LOC253019 3'  ATTTACCTGAGATGATCATTTC 95365      C      TG   A__
            TTTA                    GAGG AGTGAT  TTT   GTGAAT
                                |||| ||||||  |||   ||||||
                                TTTC TTACTA  AGA   CATTTA
                                  T     GT   GTC
GAM393   LOC253443 5'  ATTTATTAGACATCTGTTT    95869        TGAT
                                AGGCAG    TGTTTAGTGAAT
                                ||||||    ||||||||||||
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                                TTTGTC    ACAGATTATTTA
                                   T___
GAM393   LOC253549 3'  GCAGGTGATGCATTGCTTC    96777         _  TG   A
                                GAGGCAGTG AT  TTT GT
                                ||||||||| ||  ||| ||
                                CTTCGTTAC TA  GGA CG
                                     G  GT   _
GAM393   LOC253639 3'  ATTTATTCTCATTGCTGTTTCA 95819         TG  T TTT
                                TGAGGCAG  AT G   AGTGAAT
                                ||||||||  || |   |||||||
                                ACTTTGTC  TA C   TTATTTA
                                     GT  _ TC_
GAM393   LOC253975 3'  ATTTACCTGAGATGATCATTTC 95994      C      TG   A__
            TTTA                   GAGG AGTGAT  TTT   GTGAAT
                                |||| ||||||  |||   ||||||
                                TTTC TTACTA  AGA   CATTTA
                                  T     GT   GTC
GAM393   LOC253982 3'  AATAAATACTGCTTTA      95077          A
                                TGAGGCAGTG TTGTT
                                |||||||||| |||||
                                ATTTCGTCAT AATAA
                                      A
GAM393   LOC254028 3'  GACATCACTGCTTCA       96540           T
                                TGAGGCAGTGAT GTT
                                |||||||||||| |||
                                ACTTCGTCACTA CAG
                                           _
GAM393   LOC254243 3'  ATTTATTGATGCCAGCTGCTCC 97402    AG     GATTGT
            A                   TG  GCAGT     TTAGTGAAT
                                ||  |||||     |||||||||
                                AC  CGTCG     AGTTATTTA
                                 CT     ACCGT_
GAM393   LOC254250 3'  GTTTACTAACACCGGGCTGTCT 97016         GAT_    T
            C                   GAGGCAGT    TGTT AGTGAAT
                                ||||||||    |||| |||||||
                                CTCTGTCG    ACAA TCATTTG
                                     GGCC    _
GAM393   LOC254848 3'  ATCCCAAGACAGATGCTGCCTT 97089          A      AGTGAAT
                                GAGGCAGTG TTGTTT
                                ||||||||| ||||||
                                TTCCGTCGT GACAGA
                                      A      ACCCTA
GAM393   LOC255652 3'  ATTTATTGGAGCCGCTGTCT   96719         ATTG
                                AGGCAGTG    TTTAGTGAAT
                                ||||||||    ||||||||||
                                TCTGTCGC    AGGTTATTTA
                                     CG__
GAM393   LOC255779 3'  GTTTGCTGGATGGGATTGGCTC 96016     G    GA TG     TG
                                GAG CAGT  T  TTTAG  AAT
                                ||| ||||  |  |||||  |||
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                                CTC GTTA  G  AGGTC  TTG
                                  G    G_ GT    GT
GAM393   LOC255862 3'  AAGCAATGTTGCCTTA      94483        GT A
                                TGAGGCA  G TTGTTT
                                |||||||  | ||||||
                                ATTCCGT  T AACGAA
                                    TG _
GAM393   LOC255870 3'  AAATAAATGTTGCCTTA     94655        GT A
                                TGAGGCA  G TTGTTT
                                |||||||  | ||||||
                                ATTCCGT  T AATAAA
                                    TG A
GAM393   LOC256096 5'  ATTAATAAATGATTGTTGCCT  97198        TG  TG    G   AT
                                AGGCAG  AT  TTTA TGA
                                ||||||  ||  |||| |||
                                TCCGTT  TA  AAAT ATT
                                   GT  GT    A   A
GAM393   LOC256236 3'  GTTTGCTAAGCAGTTGGGGGCT 95268      AG_         TG
           T                     AGGC   TGATTGTTTAG  AAT
                                ||||   ||||||||||  |||
                                TTCG   GTTGACGAATC  TTG
                                  GGG         GT
GAM393   LOC256454 3'  ATTTGCTAAATATTTTGTCTT  96529        TGAT      TG
                                GAGGCAG    TGTTTAG  AAT
                                |||||||    |||||||  |||
                                TTCTGTT    ATAAATC  TTA
                                    TT__      GT
GAM393   LOC256536 3'  GTTCTCAGAGGATTACTGTTTC 94712            G   AGT
           A                     TGAGGCAGTGATT TTT   GAAT
                                ||||||||||||| |||   ||||
                                ACTTTGTCATTAG AGA   CTTG
                                       G   CT_
GAM393   LOC256691 3'  ATTTACTAGACGAAAAC     96196    GA
                                GT  TTGTTTAGTGAAT
                                ||  ||||||||||||
                                CA  AGCAGATCATTTA
                                 AA
GAM393   LOC256905 3'  ATTCATTAGATATTTGTCCT   96865     CA TG T
                                AGG  G  A TGTTTAGTGAAT
                                |||  |  | ||||||||||||
                                TCC  T  T ATAGATTACTTA
                                  __ GT T
GAM393   LOC256995 5'  GTTTATTAAGTGCACTTTCTTC 97591       C_   ATTG
           A                     TGAGG  AGTG    TTTAGTGAAT
                                |||||  ||||    ||||||||||
                                ACTTC  TCAC    GAATTATTTG
                                   TT    GT__
GAM393   LOC257051 5'  GAACGGCGCTGCCTC       96317          A
                                GAGGCAGTG TTGTTT
                                ||||||||| ||||||
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                                CTCCGTCGC GGCAAG
                                          _
GAM393  LOC257054 5'  TTGGCCCGGTTCTGCTTCA   95671        T    TTTA  G
                                TGAGGCAG GATTG    GT AA
                                |||||||| |||||    || ||
                                ACTTCGTC TTGGC    CG TT
                                      _    C___  G
GAM393  LOC257319 3'  GTTTATGATGGCATAACCATTG 95776       AT__   TA_
          CTTTA                    GGCAGTG    TGTT   GTGAAT
                                |||||||    ||||   ||||||
                                TCGTTAC    ACGG   TATTTG
                                    CAAT    TAG
GAM393  LOC257354 3'  ATGGCTGAAGGTGGGTGCTGCT 95086        GA TG __    GAAT
          TCA                     GAGGCAGT  T  T  TTAGT
                                |||||||| |  |  |||||
                                CTTCGTCG  G  G  AGTCG
                                     TG GT GA    GTA
GAM393  LOC257407 3'  ATTCACTGATTTTATTGATTTT 96985     _     TTGT
                                GAGG CAGTGA    TTAGTGAAT
                                |||| ||||||    |||||||||
                                TTTT GTTATT    AGTCACTTA
                                  A     TT__
GAM393  LOC257486 3'  ATTTATTAAGCAAAATAGCCTT 69242       A  GA
          A                      TGAGGC GT  TTGTTTAGTGAAT
                                |||||| ||  ||||||||||||||
                                ATTCCG TA  AACGAATTATTTA
                                   A  A_
GAM393  LOC257569 3'  AAGCAGTCATTCCTTA      97830      C
                                TGAGG AGTGATTGTTT
                                ||||| ||||||||||
                                ATTCC TTACTGACGAA
                                  _
GAM393  LOC50999  3'  AAACGATAATTGCTTTA     32098         G
                                TGAGGCAGT ATTGTTT
                                ||||||||| |||||||
                                ATTTCGTTA TAGCAAA
                                     A
GAM393  LOC51015  3'  ATTTTGTGGTCATTGTTTC    32118          TG TT
                                GAGGCAGTGAT  T  AGT
                                |||||||||||  |  |||
                                CTTTGTTACTG  G  TTA
                                      GT TT
GAM393  LOC51055  3'  TTAAATGGTTACTGTTT     31910          TG
                                AGGCAGTGAT  TTTAG
                                ||||||||||  |||||
                                TTTGTCATTG  AAATT
                                      GT
GAM393  LOC51074  3'  ATTCATTAGAAAATTTCCTCA  31983       C   GATTG
                                TGAGG AGT    TTTAGTGAAT
                                ||||| |||    ||||||||||
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                                ACTCC TTA    AGATTACTTA
                                   T  AA___
GAM393  LOC51122  3' AGCAATTACTTTTCA      65588      C
                                TGAGG AGTGATTGTT
                                ||||| ||||||||||
                                ACTTT TCATTAACGA
                                   _
GAM393  LOC51152  3' TTTACCAGGTTGCTGCTCA   32457     G  TG  GTTTA
                                TGAG CAG  ATT    GTGAA
                                |||| |||  |||    |||||
                                ACTC GTC  TGG    CATTT
                                   _  GT  AC___
GAM393  LOC51175  3' CTTTTTAAATAATTGCTTTCTT 32746      C  TG       TGAAT
          A                     TGAGG AG  ATTGTTTAG
                                ||||| ||  |||||||||
                                ATTCT TC  TAATAAATT
                                   T  GT       TTTCA
GAM393  LOC51194  3' ATTCATTAAATTTGGCTGCCTT 32933         GATT
          A                     TGAGGCAGT   GTTTAGTGAAT
                                |||||||||   ||||||||||
                                ATTCCGTCG   TAAATTACTTA
                                     GTT_
GAM393  LOC51313  3' TTGATTTAATGGTTACTGCCCA 33512   A       TG  T  G  T
                                TG GGCAGTGAT  TT AGT AA
                                || |||||||||  || ||| ||
                                AC CCGTCATTG  AA TTA TT
                                 _       GT  T  G  T
GAM393  LOC51316  5' GTTTACTAATTTCCACTGCTTT 59513         ATTGT
                                GAGGCAGTG    TTAGTGAAT
                                |||||||||    |||||||||
                                TTTCGTCAC    AATCATTTG
                                     CTTT_
GAM393  LOC51619  3' TTCAGCAATTACGGCTTT    32019      A      TTAG
                                GAGGC GTGATTGT   TGAA
                                ||||| ||||||||   ||||
                                TTTCG CATTAACG   ACTT
                                   G      _____
GAM393  LOC51754  5' TTTGCTGGACGTCGCTGT    71032        T    TG
                                GCAGTGAT GTTTAG  AA
                                ||||||| ||||||  ||
                                TGTCGCTG CAGGTC  TT
                                     _     GT
GAM393  LOC51762  3' GTTCATATGGTCAAATATTACT 33269        ___  T  _
          GCCTT                   GCAGTGAT   TG TTA GTGAAT
                                ||||||||   || ||| ||||||
                                CGTCATTA   AC GGT TACTTG
                                     TAA  T   A
GAM393  LOC57107  5' GTTCGTTTCTGGTCACTGCTCC 39840    AG       TTT
          A                     TG  GCAGTGATTG   AGTGAAT
                                ||  ||||||||||   |||||||
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                                AC  CGTCACTGGT   TTGCTTG
                                 CT        CT_
GAM393  LOC57147  5' GGCAGTACTGCCTCA      39932         G
                                TGAGGCAGT ATTGTT
                                ||||||||| ||||||
                                ACTCCGTCA TGACGG
                                          _
GAM393  LOC57406  3' ATTCGCTGAACCCTGTT     40344       TGATT
                                GGCAG    GTTTAGTGAAT
                                |||||    ||||||||||
                                TTGTC    CAAGTCGCTTA
                                   C____
GAM393  LOC57826  3' ATTTGCACAGATGCTGCTTT   41016         A    TTA TG
                                GAGGCAGTG TTGT   G  AAT
                                ||||||||| ||||  |  |||
                                TTTCGTCGT GACA   C  TTA
                                      A   ___ GT
GAM393  LOC81034  3' TTTACTGAATAAGGTGTT    47860     GTGA
                                GGCA   TTGTTTAGTGAA
                                ||||   ||||||||||||
                                TTGT   AATAAGTCATTT
                                  GG__
GAM393  LOC88584  3' ATTTGTTAAACAATATGCT   60489     GTG       TG
                                GGCA   ATTGTTTAG  AAT
                                ||||   |||||||||  |||
                                TCGT   TAACAAATT  TTA
                                  A__       GT
GAM393  LOC90038  3' ATTTATTGATGCCAGCTGCTCC 61146    AG    GATTGT
           A                     TG  GCAGT     TTAGTGAAT
                                ||  |||||     |||||||||
                                AC  CGTCG     AGTTATTTA
                                 CT    ACCGT_
GAM393  LOC90155  3' GTTCATTGTCACACTGCT    61697       AT  TT
                                GGCAGTG  TG  TAGTGAAT
                                |||||||  ||  ||||||||
                                TCGTCAC  AC  GTTACTTG
                                    __  T_
GAM393  LOC90190  3' ATTTATACCTCATCACTGTTTC 61774          T TTTA
                                GAGGCAGTGAT G    GTGAAT
                                ||||||||||| |    ||||||
                                CTTTGTCACTA C    TATTTA
                                      _ TCCA
GAM393  LOC90288  3' AAGCAATTCTGCCTCA      62072         T
                                TGAGGCAG GATTGTTT
                                |||||||| ||||||||
                                ACTCCGTC TTAACGAA
                                          _
GAM393  LOC90538  3' TGAATGGTTCTGTCTC      63197        T   TG
                                GAGGCAG GAT  TTTA
                                ||||||| |||  ||||
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                                CTCTGTC TTG  AAGT
                                    _  GT
GAM393  LOC90624  3' ATTCACTGATAAATTCTCTCA  63602      C   GATTGT
                                TGAGG AGT     TTAGTGAAT
                                ||||| |||     |||||||||
                                ACTCT TTA     AGTCACTTA
                                   C  AAT___
GAM393  LOC90625  3' GTTTAACATCTCCAATTGCTGT 63613       TG   TTTAG__
           CTTA                    GAGGCAG  ATTG      TGAAT
                                ||||||| ||||      |||||
                                TTCTGTC  TAAC      ATTTG
                                    GT   CTCTACA
GAM393  LOC90750  3' AGGCAGTCTTGTTTTA      63913        T
                                TGAGGCAG GATTGTTT
                                |||||||| ||||||||
                                ATTTTGTT CTGACGGA
                                    _
GAM393  LOC90750  5' ATTTGCTCATTTAGTCATTGTT 63916          TTT_  TG
           T                     AGGCAGTGATTG   AG  AAT
                                ||||||||||||   ||  |||
                                TTTGTTACTGAT   TC  TTA
                                      TTAC  GT
GAM393  LOC90777  3' ATTTATTAAATGTAATTGCTTT 63965        GAT
           A                     TGAGGCAGT   TGTTTAGTGAAT
                                |||||||||   ||||||||||||
                                ATTTCGTTA   GTAAATTATTTA
                                     AT_
GAM393  LOC90841  3' GTTCTGTAAAAAGTAATACTGC 64201        __  G   GT
           TTTA                    GAGGCAGTG  ATT TTTA  GAAT
                                |||||||||  ||| ||||  ||||
                                TTTCGTCAT  TGA AAAT  CTTG
                                     AA  A   GT
GAM393  LOC90850  3' GTTGTGTAAACAGTTGGCTGTT 64215        _       GTGAAT
           TCA                     TGAGGCAGT GATTGTTTA
                                |||||||||  |||||||||
                                ACTTTGTCG TTGACAAAT
                                     G       GTGTTG
GAM393  LOC91040  3' GTTTGTTAAGTGGTCAGAAATT 64723    GCAG   TG    TG
           C                      GAG   TGAT  TTTAG  AAT
                                |||   ||||  |||||  |||
                                CTT   ACTG  GAATT  TTG
                                  AAAG   GT    GT
GAM393  LOC91050  3' ATTTATTAAATGTAGGTCCTCA 64742      _ AGTGAT
                                TGAGG C     TGTTTAGTGAAT
                                ||||| |     ||||||||||||
                                ACTCC G     GTAAATTATTTA
                                   T GAT___
GAM393  LOC91308  3' TTCAAGGGATTCTGCCTCA   65569        T   G  TAG
                                TGAGGCAG GATT TT   TGAA
                                |||||||| |||| ||   ||||
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                                ACTCCGTC TTAG GA   ACTT
                                    _    G ____
GAM393  LOC91380  3' ATTTTATAGTTACTTCCTTA   65858       C        TT
                                TGAGG AGTGATTGT  AGT
                                ||||| |||||||||  |||
                                ATTCC TCATTGATA  TTA
                                   T        TT
GAM393  LOC91585  3' GAACTGTTACTGCCTT      66576           T
                                GAGGCAGTGAT GTTT
                                |||||||||||| ||||
                                TTCCGTCATTG CAAG
                                       T
GAM393  LOC91585  5' GTGAGCGGGAACGGTGCTGCTT 66581          G      A_  GA
           TA                    TGAGGCAGT ATTGTTT  GT  AT
                                ||||||||| |||||||  ||  ||
                                ATTTCGTCG TGGCAAG  CG  TG
                                    _      GG  AG
GAM393  LOC92154  3' ATTTAAATATAGTCACTGCTAC 68355    A          TTAG
           A                     TG GGCAGTGATTGT    TGAAT
                                || ||||||||||||    |||||
                                AC TCGTCACTGATA    ATTTA
                                 A          TAA_
GAM393  LOC92170  3' AAATGGATGCTGTCTCA     68366          A TG
                                TGAGGCAGTG T  TTT
                                |||||||||| |  |||
                                ACTCTGTCGT G  AAA
                                      A GT
GAM393  LOC92230  5' TTGAGATGTGCTGCCTTA    68549          ATTG
                                TGAGGCAGTG    TTTAG
                                ||||||||||    |||||
                                ATTCCGTCGT    GAGTT
                                      GTA_
GAM393  LOC92293  3' ATTCATTAGATAGGTTCCT    68760     CAGTGA
                                AGG     TTGTTTAGTGAAT
                                |||     ||||||||||||||
                                TCC     GATAGATTACTTA
                                  TTG___
GAM393  LOC93132  5' ATTCAAGTGGTTATTGTGTTA  71482     G       TG  TAG
                                TGA GCAGTGAT  TT   TGAAT
                                ||| ||||||||  ||   |||||
                                ATT TGTTATTG  GA   ACTTA
                                  G       GT  ___
GAM393  LOC93134  3' GAACAGTTTTGCCTTA      71519         T
                                TGAGGCAG GATTGTTT
                                |||||||| ||||||||
                                ATTCCGTT TTGACAAG
                                       _
GAM393  LOC93206  5' TTCATTTCACTGTT        71727         TTGTTT     T
                                GGCAGTGA     AGTGAA
                                ||||||||     ||||||
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                                TTGTCACT     TTACTT
                                   _______     T
GAM393  LOC93356  5'  TAAACAGTAATTACTGTTT   72079          ___
                                AGGCAGTGAT   TGTTTA
                                ||||||||||   ||||||
                                TTTGTCATTA   ACAAAT
                                     ATG
GAM393  LOC96652  3'  TTCGCTTTTGCTGCTGCA    65474    A    TG TTGTTT
                                TG GGCAG  A     AGTGAA
                                || |||||  |     ||||||
                                AC TCGTC  T     TCGCTT
                                 G    GT T_____
GAM394  A1BG      3'  GGGCCAGGCTGGTCTCCA    55425     A     GATTTT  TG
                                TGGA GACTAGT     GT  T
                                |||| |||||||     ||  |
                                ACCT CTGGTCG     CG  G
                                  _      GAC___  GT
GAM394  ACADL     3'  CAAAATTCTAGTTTTCCA    7840           T
                                TGGAAGACTAG GATTTTG
                                |||||||||||  |||||||
                                ACCTTTTGATC TTAAAAC
                                           _
GAM394  ACPT      3'  AGCAAGCCCACGGTCTTCCA  54978         A   AT
                                TGGAAGACT GTG  TTTGTT
                                |||||||||  |||  ||||||
                                ACCTTCTGG CAC  GAACGA
                                     _  CC
GAM394  ADORA2B   5'  GGCAATTTGTTAGTTATCC   5436     A     TG TT
                                GGA GACTAG  A  TTGTT
                                |||  ||||||  |  |||||
                                CCT TTGATT  T  AACGG
                                  A     GT T_
GAM394  AGL       3'  AACAATGGACTATGCCTTGGTT 5373        __  AT_  TG
           TTTCA                   AAGACTA  GTG   TT  TTGTT
                                |||||||  |||   ||  |||||
                                TTTTGGT  CGT   AG  AACAA
                                    TC   ATC  GT
GAM394  AGL       3'  AACAATGGACTATGCCTTGGTT 5341        __  AT_  TG
           TTTCA                   AAGACTA  GTG   TT  TTGTT
                                |||||||  |||   ||  |||||
                                TTTTGGT  CGT   AG  AACAA
                                    TC   ATC  GT
GAM394  AGL       3'  AACAATGGACTATGCCTTGGTT 5353        __  AT_  TG
           TTTCA                   AAGACTA  GTG   TT  TTGTT
                                |||||||  |||   ||  |||||
                                TTTTGGT  CGT   AG  AACAA
                                    TC   ATC  GT
GAM394  AGL       3'  AACAATGGACTATGCCTTGGTT 5360        __  AT_  TG
           TTTCA                   AAGACTA  GTG   TT  TTGTT
                                |||||||  |||   ||  |||||
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                              TTTTGGT  CGT   AG  AACAA
                                  TC   ATC  GT
GAM394  AGL     3'  AACAATGGACTATGCCTTGGTT 5366        __   AT_  TG
           TTTCA                  AAGACTA  GTG   TT  TTGTT
                              |||||||  |||   ||  |||||
                              TTTTGGT  CGT   AG  AACAA
                                  TC   ATC  GT
GAM394  AGL     3'  AACAATGGACTATGCCTTGGTT 3445        __   AT_  TG
           TTTCA                  AAGACTA  GTG   TT  TTGTT
                              |||||||  |||   ||  |||||
                              TTTTGGT  CGT   AG  AACAA
                                  TC   ATC  GT
GAM394  ALDH2   3'  GACAACAATACTGCTAGCTTTC 59712       A     ATT
           A                    TGGAAG CTAGTG   TTGTTGTT
                              ||||||  ||||||   ||||||||
                              ACTTTC GATCGT   AACAACAG
                                 _     CAT
GAM394  ALEX2   3'  AATTGAAAGTTACTGCTTTTCC 28791        C        GTTGTT
           A                    TGGAAGA TAGTGATTTT
                              |||||||  ||||||||||
                              ACCTTTT GTCATTGAAA
                                  C        GTTAA
GAM394  AMD1    3'  AGCAGCCCTTTCCACTAGTTTC 7899      A       ATTTT_
           CCA                    TGG AGACTAGTG     GTTGTT
                              |||  |||||||||      ||||||
                              ACC TTTGATCAC     CGACGA
                                C        CTTTCC
GAM394  ANGPT1   5'  AACAAATGGCTAGTTTTCTA   6700          G   T
                              TGGAAGACTAGT ATTT GTT
                              ||||||||||||  ||||  |||
                              ATCTTTTGATCG TAAA CAA
                                     G   _
GAM394  ANGPT1   5'  AACAAATGGCTAGTTTTCTA   57770         G   T
                              TGGAAGACTAGT ATTT GTT
                              ||||||||||||  ||||  |||
                              ATCTTTTGATCG TAAA CAA
                                     G   _
GAM394  APOBEC1  3'  GATGGCAAAATCATCTTACA   19701   G   CTAG      TG
                              TG AAGA   TGATTTTGT  TT
                              ||  ||||   |||||||||  ||
                              AC TTCT   ACTAAAACG  AG
                               A   _____       GT
GAM394  ARHGEF7  3'  AACAACAAAATACACTGTTTT  13999     T   _
                              AAGAC AGTG ATTTTGTTGTT
                              |||||  ||||  ||||||||||
                              TTTTG TCAC TAAAACAACAA
                                 _   A
GAM394  ARHI    5'  GCAGCGCATTTGTCTTCTA   16248       T   ATTT
                              TGGAAGAC AGTG   TGTTGT
                              |||||||  ||||   ||||||
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                                ATCTTCTG TTAC    GCGACG
                                     T   _____
GAM394  ARSF     5'  ACAACAAGAAGGTATTCCA   64596       G   AGTGA
                                TGGAA ACT     TTTTGTTGT
                                ||||| |||     |||||||||
                                ACCTT TGG     AGAACAACA
                                   A   A_____
GAM394  ASS      3'  GACAATTAAAAGAGACACTAGT 3506           A    _____
             CTTTTA                 AGACTAGTG TTTT    GTTGTT
                                ||||||||| ||||    ||||||
                                TCTGATCAC GAGA    TAACAG
                                     A    AAAT
GAM394  ASS      3'  GACAATTAAAAGAGACACTAGT 53947          A    _____
             CTTTTA                 AGACTAGTG TTTT    GTTGTT
                                ||||||||| ||||    ||||||
                                TCTGATCAC GAGA    TAACAG
                                     A    AAAT
GAM394  ATP1A2   3'  AATAATAAAGTGGCATTTCTTT 5518       CTA  G
                                GAAGA   GT ATTTTGTTGTT
                                |||||   || ||||||||||
                                TTTCT   CG TGAAATAATAA
                                   TTA  G
GAM394  ATP1B1   3'  AGCAACAAAATATTTATTCTA  8038       GACT    A
                                TGGAA    AGTG TTTTGTTGTT
                                |||||    |||| ||||||||||
                                ATCTT    TTAT AAAACAACGA
                                   AT__   _
GAM394  ATP2A2   3'  CCAATGGGGTTGTTAGCTTTTA 8062       A    TG    TG   TT
                                TGGAAG CTAG  ATTT  TTG
                                |||||| ||||  ||||  |||
                                ATTTTC GATT  TGGG  AAC
                                   _   GT    GT   CA
GAM394  ATRX     3'  AGAATCACTGGCTTCTA     4915        A
                                TGGAAG CTAGTGATTTT
                                |||||| ||||||||||
                                ATCTTC GGTCACTAAGA
                                   _
GAM394  ATRX     3'  AGAATCACTGGCTTCTA     56245       A
                                TGGAAG CTAGTGATTTT
                                |||||| ||||||||||
                                ATCTTC GGTCACTAAGA
                                   _
GAM394  AVPR1A   5'  GCAACCAGCAGTCTTCC     5538         A  GATTTT
                                GGAAGACT GT     GTTGT
                                |||||||| ||     |||||
                                CCTTCTGA CG     CAACG
                                     _ AC_____
GAM394  B3GAT1   3'  ACCACTGTTTTCCA       53967         T    ATTTT
                                TGGAAGAC AGTG    GT
                                |||||||| ||||    ||
```

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                                ACCTTTTG TCAC    CA
                                   _   _____
GAM394  B3GAT1   3'  ACCACTGTTTTCCA       37823        T   ATTTT
                                TGGAAGAC AGTG    GT
                                |||||||| ||||    ||
                                ACCTTTTG TCAC    CA
                                   _   _____
GAM394  B4GALT1  3'  GGTGATAGAATTGCTAAATTGT 7674     ____  TG     TG
            C                    GAC   TAG  ATTTTGT  TT
                                |||   |||  |||||||  ||
                                CTG   ATC  TAAGATA  GG
                                  TTAA  GT     GT
GAM394  BACH1    3'  AATGACAGGATTATGAGT    6795     A       TG
                                ACT GTGATTTTGT  TT
                                ||| ||||||||||  ||
                                TGA TATTAGGACA  AA
                                  G        GT
GAM394  BAIAP3   3'  GGCGGTGGGCAGCTGGTCTCCA 14126     A     GAT  TG
                                TGGA GACTAGT   TT  TTGTT
                                |||| |||||||   ||  |||||
                                ACCT CTGGTCG   GG  GGCGG
                                  _      AC_  GT
GAM394  BAZ2B    3'  TTTAACAGGGTGTAGGGGATAT 25625     ________      GTT
           TAGTTTTCCA               AGTG       ATTTTGTT     A
                                ||||       ||||||||     |
                                TTAT       TGGGACAA     T
                                  AGGGGATG         TTG
GAM394  BCL7A    3'  GGCGGCAGGATTAGCTGGTGCT 40642    _    _
                                AG ACTAG TGATTTTGTTGTT
                                || ||||| ||||||||||||
                                TC TGGTC ATTAGGACGGCGG
                                 G    G
GAM394  BVES     5'  ATCATCTGGTTTTTCA      69315          _
                                TGGAAGACTAG TGAT
                                |||||||||| ||||
                                ACTTTTTGGTC ACTA
                                       T
GAM394  CACNA1C  5'  AATGACAGAGTCTTTCTCTTC  5556       CT  T      TG
                                GAAGA  AG GATTTTGT  TT
                                |||||  || ||||||||  ||
                                CTTCT  TT CTGAGACA  AA
                                   CT  _       GT
GAM394  CALCB    3'  AGCAAACTGGTTCTTTC     87569       _    GATT
                                GGAAGA CTAGT    TTGTT
                                |||||| |||||    |||||
                                CTTTCT GGTCA    AACGA
                                   T    ____
GAM394  CALCR    3'  AACAATGAAATTGACCTAGTT  8215        T__    TG
                                GACTAG   GATTT  TTGTT
                                ||||||   |||||  |||||
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                                TTGATC   TTAAA  AACAA
                                   CAG    GT
GAM394  CAPN7    3'  AAGTTACTGGCTTTTA     26660       A
                                TGGAAG CTAGTGATTT
                                |||||| ||||||||||
                                ATTTTC GGTCATTGAA
                                   _
GAM394  CASP10   3'  GACAGTGAGGTCACAGTC    52102      A      TG
                                GACT GTGATTT  TTGTT
                                |||| |||||||  |||||
                                CTGA CACTGGA  GACAG
                                  _      GT
GAM394  CASP10   3'  GACAGTGAGGTCACAGTC    52119      A      TG
                                GACT GTGATTT  TTGTT
                                |||| |||||||  |||||
                                CTGA CACTGGA  GACAG
                                  _      GT
GAM394  CASP7    5'  AGCAGTGGGATTTGTGCTTCT  52898      ACTAGT    TG
                                GGAAG     GATTT  TTGTT
                                |||||     |||||  |||||
                                TCTTC     TTAGG  GACGA
                                   GTGT__    GT
GAM394  CASQ2    3'  GTAACAAAATTGACAGCTTTC  6938       A  AG        GTT
                                GGAAG CT  TGATTTTGTT
                                ||||| ||  ||||||||||
                                CTTTC GA  GTTAAAACAA
                                  _ CA        TGA
GAM394  CCND1    3'  TGTTTATGAGATGCTGGTTTTC 53895          G    TG TGTT
          TA                    TGGAAGACTAGT ATTT  T
                                |||||||||||| ||||  |
                                ATCTTTTGGTCG TAGA  A
                                      _   GT TTTGTC
GAM394  CD28     3'  AGTGATAAAATTACTAAACTAC 20435    A  AC         TG
          T                     GG AG  TAGTGATTTTGT  TT
                                || ||  ||||||||||||  ||
                                TC TC  ATCATTAAAATA  GA
                                 A  AA          GT
GAM394  CD3Z     3'  AATGACAAAATCATCTTT    5592       CTAG       TG
                                GAAGA   TGATTTTGT  TT
                                |||||   |||||||||  ||
                                TTTCT   ACTAAAACA  AA
                                   _____        GT
GAM394  CD53     3'  GCAGCAAGACAATCTTTCA   5110        CTAG  A
                                TGGAAGA   TG TTTTGTTGT
                                |||||||   || |||||||||
                                ACTTTCT   AC AGAACGACG
                                    A___  _
GAM394  CD80     5'  AAATTGTTGGCTTTCA     17764       A    TG
                                TGGAAG CTAG  ATTT
                                |||||| ||||  ||||
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                                ACTTTC GGTT  TAAA
                                   _   GT
GAM394  CDC5L    5'  GATGGTTTTGTGTTAGTCTTCC 6981          __ TG TT TG  GTT
                                GGAAGACTA  G  A  T  TT
                                |||||||||  |  |  |  ||
                                CCTTCTGAT  T  T  G  AG
                                     TG GT TT GT
GAM394  CEACAM6  3'  AATAATAGAATTGCTCCCTACC 10183     A  ACT  TG
           A                     TGG AG   AG  ATTTTGTTGTT
                                |||  ||   ||  ||||||||||||
                                ACC TC   TC  TAAGATAATAA
                                  A  CC_  GT
GAM394  CEACAM6  3'  GATGATGCTGTCATTAGTATTT 10186      G       TT   TG
           CA                     TGGAA ACTAGTGAT  TGT  TT
                                |||||  |||||||||  |||  ||
                                ACTTT TGATTACTG  GTA  AG
                                   A       TC   GT
GAM394  CELL     3'  GCTGCAGTCATTAGTTTCTA   8411      A       TT   T  T
                                TGGA GACTAGTGAT  TGT GT
                                ||||  ||||||||||  |||  ||
                                ATCT TTGATTACTG  ACG CG
                                  _        __   T  T
GAM394  CEP2     3'  GGCGGCGGAGTCAGGGTCCCA  22283     AA    AG
                                TGG  GACT  TGATTTTGTTGTT
                                |||  ||||  ||||||||||||||
                                ACC  CTGG  ACTGAGGCGGCGG
                                  __   G_
GAM394  CHST6    3'  AGCGATGCTGGTGGTCACTAGC 41221    A       TT____
           TTCT                    AG CTAGTGATT     GTTGTT
                                || |||||||||     ||||||
                                TC GATCACTGG     TAGCGA
                                 _       TGGTCG
GAM394  CHST6    3'  GACAACAGTTTTAGGCTTCCA  41227       A    TGATT
                                TGGAAG CTAG    TTGTTGTT
                                ||||||  ||||    ||||||||
                                ACCTTC GATT    GACAACAG
                                   G    TT___
GAM394  CLCA3    3'  AGCAGCAGAATTGTACTTGATT 16991     GACT   __
           C                     GAA    AGT  GATTTTGTTGTT
                                |||    |||  ||||||||||||
                                CTT    TCA  TTAAGACGACGA
                                  AGT_   TG
GAM394  CLCN5    3'  GATGGTGAAGTCACATTAGT   3593       __      TG TG
                                ACTA  GTGATTT  T  TT
                                ||||  |||||||  |  ||
                                TGAT  CACTGAA  G  AG
                                  TA      GT GT
GAM394  CLCN7    3'  CGGAGTCACTGGTTTCTC    7088    GA
                                G  AGACTAGTGATTTTG
                                |  |||||||||||||||
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                                C  TTTGGTCACTGAGGC
                                 TC
GAM394  CLN5    3'  AATGAAGTCAGGTCTT     21422       AG     TG
                                AAGACT  TGATTT  TT
                                ||||||  ||||||  ||
                                TTCTGG  ACTGAA  AA
                                   __     GT
GAM394  CNP     3'  GGCAGTGGGGCTGGGGGTAGTT 52445       GTGA___   TG
          TTCCA                   AAGACTA     TTT  TTGTT
                                |||||||     |||  |||||
                                TTTTGAT     GGG  GACGG
                                   GGGGGTC   GT
GAM394  CNTN3   3'  GATGGCAGAGATGGTTTTTTA  66695        GTGAT    TG
                                TGGAAGACTA    TTTGT  TT
                                ||||||||||    |||||  ||
                                ATTTTTTGGT    AGACG  AG
                                     AG___    GT
GAM394  COL13A1  5'  AGCAGCGGAAAGGGACGTTTTC 55011       TAGTGA
          CA                    TGGAAGAC    TTTTGTTGTT
                                ||||||||    ||||||||||
                                ACCTTTTG    AAGGCGACGA
                                   CAGGGA
GAM394  COL13A1  5'  AGCAGCGGAAAGGGACGTTTTC 55014       TAGTGA
          CA                    TGGAAGAC    TTTTGTTGTT
                                ||||||||    ||||||||||
                                ACCTTTTG    AAGGCGACGA
                                   CAGGGA
GAM394  COL13A1  5'  AGCAGCGGAAAGGGACGTTTTC 55017       TAGTGA
          CA                    TGGAAGAC    TTTTGTTGTT
                                ||||||||    ||||||||||
                                ACCTTTTG    AAGGCGACGA
                                   CAGGGA
GAM394  COL13A1  5'  AGCAGCGGAAAGGGACGTTTTC 55020       TAGTGA
          CA                    TGGAAGAC    TTTTGTTGTT
                                ||||||||    ||||||||||
                                ACCTTTTG    AAGGCGACGA
                                   CAGGGA
GAM394  COL13A1  5'  AGCAGCGGAAAGGGACGTTTTC 55023       TAGTGA
          CA                    TGGAAGAC    TTTTGTTGTT
                                ||||||||    ||||||||||
                                ACCTTTTG    AAGGCGACGA
                                   CAGGGA
GAM394  COL13A1  5'  AGCAGCGGAAAGGGACGTTTTC 55026       TAGTGA
          CA                    TGGAAGAC    TTTTGTTGTT
                                ||||||||    ||||||||||
                                ACCTTTTG    AAGGCGACGA
                                   CAGGGA
GAM394  COL13A1  5'  AGCAGCGGAAAGGGACGTTTTC 17785       TAGTGA
          CA                    TGGAAGAC    TTTTGTTGTT
                                ||||||||    ||||||||||
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                                ACCTTTTG     AAGGCGACGA
                                     CAGGGA
GAM394  COL9A1   3'  GACAGCAGAGTCATCAGTT   8484      A
                                GACT GTGATTTTGTTGTT
                                |||| ||||||||||||||
                                TTGA TACTGAGACGACAG
                                  C
GAM394  COL9A1   3'  GACAGCAGAGTCATCAGTT   54351     A
                                GACT GTGATTTTGTTGTT
                                |||| ||||||||||||||
                                TTGA TACTGAGACGACAG
                                  C
GAM394  COPA     3'  ATTTGAAGAAGTTATTTGGTTT 15186         _     GTTGTT
            TCCA                    GGAAGACTAG TGATTTT
                                |||||||||| |||||||
                                CCTTTTGGTT ATTGAAG
                                       T      AAGTTTAA
GAM394  COX6A1   3'  TGATGACTGGTATACTGGTCTC 15190    A       ATTTT  TG
            CCA                     TGG AGACTAGTG    GT  TT
                                ||| |||||||||    ||  ||
                                ACC TCTGGTCAT    CA  AG
                                  C       ATGGT  GT  TA
GAM394  CR1      3'  AGCAGAACCCTAGTCTTTTA  5131          TGA
                                TGGAAGACTAG   TTTTGTT
                                ||||||||||   |||||||
                                ATTTTCTGATC   AAGACGA
                                       CC_
GAM394  CR2      3'  AATAATGTGTACATTAGTCATT 8532      A      ATTT
            CA                      TGGA GACTAGTG    TGTTGTT
                                |||| ||||||||   |||||||
                                ACTT CTGATTAC    GTAATAA
                                  A       ATGT
GAM394  CRYZ     3'  GACAATTTATTAGTTTTCT   8545           TT
                                GGAAGACTAGTGA  TTGTT
                                ||||||||||||  |||||
                                TCTTTTGATTATT  AACAG
                                       T_
GAM394  CTSB     3'  TAACAGCGGGAGACCTGTGCTA 64730       GA_____
            GTTTT                   ACTAGT      TTTTGTTGTT   A
                                ||||||      ||||||||||  |
                                TGATCG      AGGGCGACAA   T
                                   TGTCCAG
GAM394  CTSZ     3'  AACGATGGGACCTCAGTCTTCT 62114        _ TGA   TG
                                GGAAGACT AG   TTT  TTGTT
                                |||||||| ||   |||  |||||
                                TCTTCTGA TC   AGG  AGCAA
                                     C  C__   GT
GAM394  CUL4B    3'  AATGGCAAAAGTACTGTTTTTC 13137        T   A     TG
            G                     TGGAAGAC AGTG TTTTGT  TT
                                |||||||| |||| ||||||  ||
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                                  GCTTTTTG TCAT AAAACG  AA
                                     _   G     GT
GAM394  CXCL6    3'  ATCACTGGTTATTAGTCTTTCA 11464            TT  TGTT
                                  TGGAAGACTAGTGATT  GT
                                  ||||||||||||||||  ||
                                  ACTTTCTGATTATTGG  CA
                                        T_  CTAA
GAM394  CXCR4    3'  TGGTATAGAAATGCTGGTTTTT 12952          A     TGTT
          CA                        TGGAAGACTAGTG TTTTGT
                                  ||||||||||||| ||||||
                                  ACTTTTTGGTCGT AAGATA
                                        A     TGGTG
GAM394  CYP39A1  3'  GTAATAAAATGGTAGTTTTCT  33447        G G       GTT
                                  GGAAGACTA T ATTTTGTT
                                  ||||||||| | ||||||||
                                  TCTTTTGAT G TAAAATAA
                                     _ G       TGA
GAM394  DAZL     3'  AGCCTTTGTCACTAGTCTTT   68139          TTT_
                                  GAAGACTAGTGAT   GTT
                                  ||||||||||||    |||
                                  TTTCTGATCACTG   CGA
                                        TTTC
GAM394  DIO1     3'  AATAACAGAATTATTA      5819
                                  TAGTGATTTTGTTGTT
                                  ||||||||||||||||
                                  ATTATTAAGACAATAA

GAM394  DKC1     3'  GATGGGCCTGGTAGTTTTCCA  7247          G  AT  TG
                                  TGGAAGACTA TG  TT  TT
                                  |||||||||| ||  ||  ||
                                  ACCTTTTGAT GT  GG  AG
                                        G  CC  GT
GAM394  DR1      3'  TGGACTTGTCATTGGTATTCTA 59372       G        TTT   GTT
                                  TGGAA ACTAGTGAT   GTT
                                  ||||| |||||||||   |||
                                  ATCTT TGGTTACTG   CAG
                                     A        TT_   GTG
GAM394  DSG1     3'  GGCAATAGGATGAGGTTTCTTC 8685       CTAGTG
                                  GAAGA     ATTTTGTTGTT
                                  |||||     ||||||||||||
                                  CTTCT     TAGGATAACGG
                                     TTGGAG
GAM394  DVL3     3'  AACATAATGAGTCACTAGGCTT 15363       A         TGT_
          CT                        GGAAG CTAGTGATTT    TGTT
                                  ||||| ||||||||||    ||||
                                  TCTTC GATCACTGAG    ACAA
                                     G         TAAT
GAM394  EBF      3'  ATTCTGCAATCATTTGTCTTTT 66047         T      TTGTTGTT
          A                         TGGAAGAC AGTGATT
                                  |||||||| |||||||
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                                ATTTTCTG TTACTAA
                                    T      CGTCTTAA
GAM394  EDAR     3'  AACAATGAGATCATAATAATTC 42262      GACTA      TG
                T                    GGAA    GTGATTT  TTGTT
                                     ||||    |||||||  |||||
                                     TCTT    TACTAGA  AACAA
                                       AATAA      GT
GAM394  EEF1A1   3'  GGCAGTTTTAAGTTATTAGTTT 7388             TG__
                TT                    GAAGACTAGTGATTT    TTGTT
                                      ||||||||||||||||   |||||
                                      TTTTTGATTATTGAA    GACGG
                                              TTTT
GAM394  EGFL6    3'  AGTGGCTTAGCTGGGTCTTTCA 31323         _  GATTTT  TG
                                      TGGAAGACT AGT     GT  TT
                                      |||||||||  |||     ||  ||
                                      ACTTTCTGG TCG     CG  GA
                                            G   ATT___  GT
GAM394  EHD3     3'  AGTGCATTTGTCATTAGTCTTC 27475           TT_  TGTT
                                      GAAGACTAGTGAT   TGT
                                      ||||||||||||   |||
                                      CTTCTGATTACTG   ACG
                                              TTT   TGA
GAM394  EHHADH   3'  AATGGAGTATAAGTTTTCC    8748         A  G    TG
                                      GGAAGACT GT ATTT  TT
                                      ||||||||  ||  ||||  ||
                                      CCTTTTGA TA TGAG  AA
                                            A  _    GT
GAM394  EIF3S10  3'  ATAGCAAACTGCTTTTCCA    71707        C    GATT
                                      TGGAAGA TAGT    TTGTTGT
                                      |||||||  ||||    |||||||
                                      ACCTTTT GTCA    AACGATA
                                         C    _____
GAM394  ELAVL2   5'  GGCAATAGGAGGGTAGTCTCTC 15415     _     GTGA
                C                     GGA AGACTA    TTTTGTTGTT
                                      |||  ||||||    ||||||||||
                                      CCT TCTGAT    AGGATAACGG
                                        C     GGG_
GAM394  ELMO1    3'  AATGGTGAAATCAGTAGTCTC  55279    A    G     TG TG
                                      GA GACTA TGATTT  T  TT
                                      ||  |||||  ||||||  |  ||
                                      CT CTGAT ACTAAA  G  AA
                                        _    G     GT GT
GAM394  EMS1     3'  AGCAATGAGGTCGGGTTTT    17849       AG     TG
                                      AAGACT  TGATTT  TTGTT
                                      ||||||  ||||||  |||||
                                      TTTTGG  GCTGGA  AACGA
                                         __     GT
GAM394  EMS1     3'  AGCAATGAGGTCGGGTTTT    56749       AG     TG
                                      AAGACT  TGATTT  TTGTT
                                      ||||||  ||||||  |||||
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                                TTTTGG  GCTGGA  AACGA
                                   __     GT
GAM394  EN1     5'  GACAGCGAGATCTATCTGCTA  7451     A   CTAGT
                                TGG AGA    GATTTTGTTGTT
                                ||| |||    ||||||||||||
                                ATC TCT    CTAGAGCGACAG
                                  G  AT___
GAM394  EPHB4    3'  AGTGACAAAATCATTGGGGTTT 15461     GA          TG
                                GAA  CTAGTGATTTTGT  TT
                                |||  ||||||||||||  ||
                                TTT  GGTTACTAAAACA  GA
                                  GG          GT
GAM394  EVA1    3'  AACAATGTGGGTCTTTCA    19391         AGTGATT
                                TGGAAGACT     TTGTT
                                |||||||||     |||||
                                ACTTTCTGG     AACAA
                                      GTGT___
GAM394  F2R     3'  GACGGCAAGGTTTAAGTT    8838      AGT
                                GACT   GATTTTGTTGTT
                                ||||   ||||||||||||
                                TTGA   TTGGAACGGCAG
                                  AT_
GAM394  F8      3'  GATGATGACATTAGGCTTCTA  3729        A     ATT TG TG
                                TGGAAG CTAGTG   T  T  TT
                                |||||| ||||||   |  |  ||
                                ATCTTC GATTAC   A  A  AG
                                   G     ___ GT GT
GAM394  FACL4    3'  GGTGATAAAATCATAAGTATTT 43401     G   A        TG
                                GAA ACT GTGATTTTGT  TT
                                ||| ||| ||||||||||  ||
                                TTT TGA TACTAAAATA  GG
                                  A   A         GT
GAM394  FACL4    3'  GGTGATAAAATCATAAGTATTT 15511     G   A        TG
                                GAA ACT GTGATTTTGT  TT
                                ||| ||| ||||||||||  ||
                                TTT TGA TACTAAAATA  GG
                                  A   A         GT
GAM394  FADD     3'  GGCAGCGGGATCTCGTATCTTT 13796      CTAGT
                                GAAGA    GATTTTGTTGTT
                                |||||    ||||||||||||
                                TTTCT    CTAGGGCGACGG
                                   ATGCT
GAM394  FAP     3'  AATAATAAAGTCAGAAGTT    15514     AG
                                GACT  TGATTTTGTTGTT
                                ||||  ||||||||||||
                                TTGA  ACTGAAATAATAA
                                  AG
GAM394  FCAR     3'  AAGTTATGGTTTTCCA      8850          G
                                TGGAAGACTA TGATTT
                                |||||||||| ||||||
```

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                                ACCTTTTGGT ATTGAA
                                           _
GAM394  FCAR    3' AAGTTATGGTTTTCCA    55745        G
                                TGGAAGACTA TGATTT
                                |||||||||| ||||||
                                ACCTTTTGGT ATTGAA
                                           _
GAM394  FCAR    3' AAGTTATGGTTTTCCA    55756        G
                                TGGAAGACTA TGATTT
                                |||||||||| ||||||
                                ACCTTTTGGT ATTGAA
                                           _
GAM394  FCAR    3' AAGTTATGGTTTTCCA    55767        G
                                TGGAAGACTA TGATTT
                                |||||||||| ||||||
                                ACCTTTTGGT ATTGAA
                                           _
GAM394  FCAR    3' AAGTTATGGTTTTCCA    55778        G
                                TGGAAGACTA TGATTT
                                |||||||||| ||||||
                                ACCTTTTGGT ATTGAA
                                           _
GAM394  FGD1    3' GACAATGGATACTCAGTTTTTT 15524       _   AT  TG
                                GGAAGACT AGTG  TT  TTGTT
                                |||||||| ||||  ||  |||||
                                TTTTTTGA TCAT  AG  AACAG
                                     C   __  GT
GAM394  FGF7    3' GATAACAGGATTATTA    8884
                                TAGTGATTTTGTTGTT
                                ||||||||||||||||
                                ATTATTAGGACAATAG

GAM394  FGFR2   3' GATAGCAGAATGTGCTTCTCTC 43479    A  CT   _
          T                      GGA GA  AGTG ATTTTGTTGTT
                                 ||| ||  |||| ||||||||||||
                                 TCT CT  TCGT TAAGACGATAG
                                   _  CT    G
GAM394  FGFR2   3' GATAGCAGAATGTGCTTCTCTC 43356    A  CT   _
          T                      GGA GA  AGTG ATTTTGTTGTT
                                 ||| ||  |||| ||||||||||||
                                 TCT CT  TCGT TAAGACGATAG
                                   _  CT    G
GAM394  FGFR2   3' GATAGCAGAATGTGCTTCTCTC 43489    A  CT   _
          T                      GGA GA  AGTG ATTTTGTTGTT
                                 ||| ||  |||| ||||||||||||
                                 TCT CT  TCGT TAAGACGATAG
                                   _  CT    G
GAM394  FGFR2   3' GATAGCAGAATGTGCTTCTCTC 43499    A  CT   _
          T                      GGA GA  AGTG ATTTTGTTGTT
                                 ||| ||  |||| ||||||||||||
```

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                                TCT CT  TCGT TAAGACGATAG
                                  _ CT    G
GAM394  FGFR2    3'  GATAGCAGAATGTGCTTCTCTC 43368     A  CT   _
            T                    GGA GA  AGTG ATTTTGTTGTT
                                 ||| ||  |||| ||||||||||
                                TCT CT  TCGT TAAGACGATAG
                                  _ CT    G
GAM394  FGFR2    3'  GATAGCAGAATGTGCTTCTCTC 3760      A  CT   _
            T                    GGA GA  AGTG ATTTTGTTGTT
                                 ||| ||  |||| ||||||||||
                                TCT CT  TCGT TAAGACGATAG
                                  _ CT    G
GAM394  FIGF     5'  AACTGATTATTTGGTTTTCT   15554          _    TT
                                GGAAGACTAG TGATT  GTT
                                |||||||||| |||||  |||
                                TCTTTTGGTT ATTAG  CAA
                                      T    T_
GAM394  FUT8     5'  ACAACAGAAGTCTATTC     15589    C   TGA
                                GA TAG   TTTTGTTGT
                                || |||   |||||||||
                                CT ATC   AAGACAACA
                                 T  TG_
GAM394  FZD6     3'  GACAAAATGTTAGTCTTTT    13042          GT A
                                GGAAGACTA  G TTTTGTT
                                |||||||||  | |||||||
                                TTTTCTGAT  T AAAACAG
                                      TG _
GAM394  FZD6     3'  TAGACAAAATGTTAGTCTTTT  13043         GT A      GTT
                                GGAAGACTA  G TTTTGTT
                                |||||||||  | |||||||
                                TTTTCTGAT  T AAAACAG
                                      TG _      ATG
GAM394  G22P1    5'  GGCAGCAGGATTTACCGTCCA  7602       AGACTAGT
                                TGGA       GATTTTGTTGTT
                                ||||       ||||||||||||
                                ACCT       TTAGGACGACGG
                                  GCCAT___
GAM394  GAD1     3'  AGCAGAGTCATTGTT       5872      T
                                GAC AGTGATTTTGTT
                                ||| ||||||||||||
                                TTG TTACTGAGACGA
                                  _
GAM394  GAGED2   3'  AACAACGCAAGCTGGTTTT   55926         GATTT
                                AAGACTAGT    TGTTGTT
                                |||||||||    |||||||
                                TTTTGGTCG    GCAACAA
                                      AAC__
GAM394  GAGED2   3'  AACAACGCAAGCTGGTTTT   55930         GATTT
                                AAGACTAGT    TGTTGTT
                                |||||||||    |||||||
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                                TTTTGGTCG    GCAACAA
                                     AAC__
GAM394  GAGED2   3' AACAACGCAAGCTGGTTTT   39905        GATTT
                                AAGACTAGT    TGTTGTT
                                |||||||||    |||||||
                                TTTTGGTCG    GCAACAA
                                     AAC__
GAM394  GALNT3   3' AATAGCAAAATTCCTGTGTTC  15603     G  T  TG
                                GAA AC AG  ATTTTGTTGTT
                                ||| || ||  ||||||||||
                                CTT TG TC  TAAAACGATAA
                                  G  _  CT
GAM394  GCLC     3' AATGATAGAACTGTACTGTTTT 7676        T   A__     TG
           CT                     GGAAGAC AGTG   TTTTGT  TT
                                |||||||| ||||   ||||||  ||
                                TCTTTTG TCAT   AAGATA  AA
                                   _   GTC     GT
GAM394  GLI2     3' ACAATGAAAAAAGTCTCCA   47523     A   AGTGA   TG
                                TGGA GACT    TTT  TTGT
                                |||| ||||    |||  ||||
                                ACCT CTGA    AAA  AACA
                                  _   AA___   GT
GAM394  GLI2     3' GGCATCCTCTCTGGTCTTTT   47525         T  TTT
                                GGAAGACTAG GA   TGTT
                                |||||||||| ||   ||||
                                TTTTCTGGTC CT   ACGG
                                     T  CCT
GAM394  GOCAP1   3' GTAGCAAAATACAGGTTTTTT  42702        A  A     GTT
                                GGAAGACT GTG TTTTGTT
                                |||||||| ||| |||||||
                                TTTTTTGG CAT AAAACGA
                                    A  _      TGA
GAM394  GP1BA    3' AGCATTTTCTAGTTTTCCA   3915          TGATTT
                                TGGAAGACTAG     TGTT
                                ||||||||||     ||||
                                ACCTTTTGATC     ACGA
                                     TTTT__
GAM394  GPR65    5' GATAATGAACACATGGACTTCT 59748      A  _  AT  TG
                                GGAAG CTA GTG  TT  TTGTT
                                ||||| ||| |||  ||  |||||
                                TCTTC GGT CAC  AA  AATAG
                                  A  A  __  GT
GAM394  GRIN2C   3' AGTGACAGATGATGTCTTCCA  5910        TAGTGAT    TG
                                TGGAAGAC      TTTGT  TT
                                ||||||||      |||||  ||
                                ACCTTCTG      AGACA  GA
                                    TAGT___     GT
GAM394  HCRT     3' GGCAATAAAGACGAGTCTCCA  7727      A   A  GA
                                TGGA GACT GT  TTTTGTTGTT
                                |||| |||| ||  ||||||||||
```

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                                ACCT CTGA CA  GAAATAACGG
                                  _   G  __
GAM394  HGD     3'  AATAAACTTGCTGGTGTTCT  3947      G    TG T
                                GGAA ACTAG  A TTTGTT
                                |||| |||||  | ||||||
                                TCTT TGGTC  T AAATAA
                                  G    GT C
GAM394  HGF     3'  AACTAGTTGCTGGTCTCTA   94230     A    TG   TT
                                TGGA GACTAG  ATT  GTT
                                |||| ||||||  |||  |||
                                ATCT CTGGTC  TGA  CAA
                                  _    GT   T_
GAM394  HIP2    3'  GTTTGAAAATTATTAGTTTTGC 18068    G          GTTGTT
            A                    TG AAGACTAGTGATTTT
                                || ||||||||||||||
                                AC TTTTGATTATTAAAA
                                 G           GTTTGA
GAM394  HLCS    3'  AGCAGATGCTGCGTTTTCCA  4658        _    AT
                                TGGAAGAC TAGTG  TTTGTT
                                |||||||| |||||  ||||||
                                ACCTTTTG GTCGT  AGACGA
                                    C    __
GAM394  HLF     3'  AATAATAAAATCAAAAACTTTT 9212       ACTAG
                                GGAAG    TGATTTTGTTGTT
                                |||||    ||||||||||||
                                TTTTC    ACTAAAATAATAA
                                  AAAA_
GAM394  HMG20A  3'  AGCAACAAAATCTGTTTTT   36531      TAGT
                                GAAGAC   GATTTTGTTGTT
                                ||||||   ||||||||||||
                                TTTTTG   CTAAAACAACGA
                                   T___
GAM394  HMGN3   3'  AGCAATAATCAGTGGTGCTTTT 14901     _   G   TT
                                GGAAG ACTA TGAT  TGTTGTT
                                ||||| |||| ||||  |||||||
                                TTTTC TGGT ACTA  ATAACGA
                                  G   G   __
GAM394  HNRPD   3'  GGTGGTGAAGCAGTATTTTCCA 9245       C  G  A   TG TG
                                TGGAAGA TA TG TTT  T  TT
                                ||||||| || || |||  |  ||
                                ACCTTTT AT AC GAA  G  GG
                                   _ G  _   GT GT
GAM394  HNRPD   3'  GGTGGTGAAGCAGTATTTTCCA 48576      C  G  A   TG TG
                                TGGAAGA TA TG TTT  T  TT
                                ||||||| || || |||  |  ||
                                ACCTTTT AT AC GAA  G  GG
                                   _ G  _   GT GT
GAM394  HNRPDL  3'  GACGACATTGAAGATTGGTCTT 18426         GA  T_
            CT                   GGAAGACTAGT  TT  TGTTGTT
                                ||||||||||  ||  |||||||
```

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                                TCTTCTGGTTA  AG  ACAGCAG
                                      GA  TT
GAM394  HNRPH3   3'  GACAACAGCATCTGGTCTACTA 24200     A     _ ATT
                                TGG AGACTAG TG   TTGTTGTT
                                ||| ||||||| ||   ||||||||
                                ATC TCTGGTC AC   GACAACAG
                                  A      T ___
GAM394  HOXA3    3'  GATAACGCAGGGCGGTCTTCT  47688        A  GA  T
                                GGAAGACT GT  TT TGTTGTT
                                |||||||| ||  || |||||||
                                TCTTCTGG CG  GA GCAATAG
                                     _ G_  C
GAM394  HPGD     3'  AACAGTGAAAGCACAAGATTTC 5975       A  A   A   TG
           CA                     TGGAAG CT GTG TTT  TTGTT
                                |||||| || ||| |||  |||||
                                ACCTTT GA CAC AAA  GACAA
                                   A  A   G   GT
GAM394  HPGD     3'  ATCTCCATAAATTACTTAGTCT 5978          _      TGTTGTT
           TCTA                    GGAAGACTA GTGATTT
                                |||||||||  |||||||
                                TCTTCTGAT CATTAAA
                                     T      TACCTCTAG
GAM394  HPRT1    3'  TAAAGAGAAGATATATTAGTTT 3963           _    G  GTT
           TTTA                    GGAAGACTAGTG ATTTT TT
                                ||||||||||||  ||||| ||
                                TTTTTTGATTAT TAGAA AG
                                       A    G  AAATA
GAM394  HRY      5'  AACAGCGGAATCCCCCGTCT   18636      TAGT
                                AGAC    GATTTTGTTGTT
                                ||||    ||||||||||||
                                TCTG    CTAAGGCGACAA
                                  CCCC
GAM394  HSPA9B   3'  AGCAATGAAGGTAGTCATCCA  14703      A    GTGA   TG
                                TGGA GACTA    TTT  TTGTT
                                |||| |||||    |||  |||||
                                ACCT CTGAT    GAA  AACGA
                                  A    G___   GT
GAM394  HYAL4    5'  AGCAGCAAACAAAACGTTTGGT 24371       ___  GAT_
           CTTCTA                   AGACTA   GT    TTTGTTGTT
                                ||||||   ||    |||||||||
                                TCTGGT   CA    AAACGACGA
                                   TTG  AAAC
GAM394  IAPP     3'  AGACAGAATGCTGTTTT     4692        T   G      TG
                                AAGAC AGT ATTTTGT  T
                                ||||| ||| |||||||  |
                                TTTTG TCG TAAGACA  A
                                  _  _       GT
GAM394  ID3      3'  AATGGCAGAGTCAGTTTCCA   79045      A    AGT       TG
                                TGGA GACT   GATTTTGT  TT
                                |||| ||||   ||||||||  ||
```

```
                                ACCT TTGA   CTGAGACG  AA
                                  _   ___       GT
GAM394  IFNAR1   3'  AACACGTTATCACTTGGTTTTC 5279          _    TT   T
             T                   GGAAGACTA GTGAT  TGT GTT
                                 ||||||||| |||||  ||| |||
                                 TCTTTTGGT CACTA  GCA CAA
                                     T    TT  _
GAM394  IL1A     3'  AATAGCAGACAGTGTTTTCT   62462        T G  AT
                                 GGAAGAC A TG  TTTGTTGTT
                                 ||||||| | ||  |||||||||
                                 TCTTTTG T AC  AGACGATAA
                                    _ G  __
GAM394  IL1RAPL2 5'  GGCGACAGGGCAGCTGGTGTTT 33794      G     GA
             C                   GGAA ACTAGT  TTTTGTTGTT
                                 |||| ||||||  ||||||||||
                                 CTTT TGGTCG  GGGACAGCGG
                                   G     AC
GAM394  IL27     3'  AGCACATCACTGGTTTTCTA   64692            TT
                                 TGGAAGACTAGTGAT  TGTT
                                 ||||||||||||||  ||||
                                 ATCTTTTGGTCACTA  ACGA
                                          C_
GAM394  IL6R     3'  GCAGCAGGGAGGGCTTCT    5122       A  AGTGA
                                 GGAAG CT    TTTTGTTGT
                                 ||||| ||    |||||||||
                                 TCTTC GG    GGGACGACG
                                   _  GA___
GAM394  IL8      3'  ACAATGAATAGTTTTTCA    94477          GTGAT  TG
                                 TGGAAGACTA    TT  TTGT
                                 ||||||||||    ||  ||||
                                 ACTTTTTGAT    AA  AACA
                                       _____  GT
GAM394  ITPR1    3'  AACAATAGAGTTTATTTTTTCT 9440        CTAGT
                                 GGAAGA    GATTTTGTTGTT
                                 ||||||    ||||||||||||
                                 TCTTTT    TTGAGATAACAA
                                    TTAT_
GAM394  ITSN1    3'  GACAACAAAGTTTACATTTCA  11619       GACTAGT
                                 TGGAA      GATTTTGTTGTT
                                 |||||      ||||||||||||
                                 ACTTT      TTGAAACAACAG
                                   ACAT___
GAM394  JPH2     3'  AGCGGACCGTATTAGTCTTTC  94444           AT_
                                 GGAAGACTAGTG   TTTGTT
                                 ||||||||||||   ||||||
                                 CTTTCTGATTAT   AGGCGA
                                        GCC
GAM394  JRK      3'  AGCAGCAAAGTTCTGTTGTTTC 86520       _  T  T
             A                   TGGAA GAC AG GATTTTGTTGTT
                                 ||||| ||| || ||||||||||||
```

```
                                ACTTT TTG TC TTGAAACGACGA
                                  G  _ _
GAM394  KCND2   3' AAAGTTACTAATTTTCCA    24389       C
                                TGGAAGA TAGTGATTTT
                                ||||||| ||||||||||
                                ACCTTTT ATCATTGAAA
                                    A
GAM394  KCND2   3' AATCAGAATTACTATGTCTTTT 24390       _       TTGTT
                                GGAAGAC TAGTGATTTTG
                                ||||||| ||||||||||
                                TTTTCTG ATCATTAAGAC
                                    T         TAA
GAM394  KCND2   3' GTAGTGAAACACAAAGCTTCCA 24400      ACTA  A  TG  GTT
                                TGGAAG   GTG TTT  TT
                                ||||||   ||| |||  ||
                                ACCTTC   CAC AAA  GA
                                   GAAA  _  GT  TGG
GAM394  KCNK5   3' AGTGGCAGACGCAAGGCTTTC  13609     A  A  AT   TG
                                GGAAG CT GTG  TTTGT  TT
                                ||||| || |||  |||||  ||
                                CTTTC GA CGC  AGACG  GA
                                  G  A  __    GT
GAM394  KCNS2   3' AATCTGATGGTTTTCCA    68298        GT_
                                TGGAAGACTA   GATT
                                ||||||||||   ||||
                                ACCTTTTGGT   CTAA
                                     AGT
GAM394  KCNS2   3' AATGACACTCACTGGTCTTT  68299         TTT  TG
                                GAAGACTAGTGA   TGT  TT
                                ||||||||||||   |||  ||
                                TTTCTGGTCACT   ACA  AA
                                     C__   GT
GAM394  KIAA0442 3' GATGGCAGAAAAAAAAGTCTT 31469      AGTGA    TG
                                AAGACT    TTTTGT  TT
                                ||||||    ||||||  ||
                                TTCTGA    AAGACG  AG
                                   AAAAA     GT
GAM394  KIR2DL1  3' AATAACTTCAATGTAGTTTTCC 26424       G__  TT   GTT
          A                      TGGAAGACTA   TGA  TTGTT
                                ||||||||||   |||  |||||
                                ACCTTTTGAT   ACT  AATAA
                                     GTA   TC
GAM394  KIR2DL2  3' AATAACTTCAATGTAGTTTTCC 26426       G__  TT   GTT
          A                      TGGAAGACTA   TGA  TTGTT
                                ||||||||||   |||  |||||
                                ACCTTTTGAT   ACT  AATAA
                                     GTA   TC
GAM394  KLRD1   3' GGGCAAGATCATAGCTC    23680   _  G      TG
                                GA CTA TGATTTTGT  T
                                || ||| |||||||||  |
```

```
                                CT GAT ACTAGAACG  G
                                 C  _       GT
GAM394  KLRD1   3'  GGGCAAGATCATAGCTC    9621    _  G       TG
                                GA CTA TGATTTTGT  T
                                || ||| |||||||||  |
                                CT GAT ACTAGAACG  G
                                 C  _       GT
GAM394  KPNB1   3'  AACAATGGAGTTACTTATTT  9625    CT      TG
                                AGA  AGTGATTT  TTGTT
                                |||  ||||||||  |||||
                                TTT  TCATTGAG  AACAA
                                  AT       GT
GAM394  KRT12   3'  GACAACTGGAGTAGTCTTTTA 4041         GTGA  TT
                                TGGAAGACTA   TT  GTTGTT
                                ||||||||||   ||  ||||||
                                ATTTTCTGAT   AG  CAACAG
                                      G___  GT
GAM394  LANCL1  3'  AATAACAGGGTCTAAGTATTTT 20204      G   AGT
            A                    TGGAA ACT   GATTTTGTTGTT
                                |||||  |||  ||||||||||||
                                ATTTT TGA   CTGGGACAATAA
                                   A  AT_
GAM394  LGS     3'  AATAACAAGATTACGAATGCTT 33359      ACTA_
            TT                   GGAAG    GTGATTTTGTTGTT
                                |||||    ||||||||||||||
                                TTTTC    CATTAGAACAATAA
                                   GTAAG
GAM394  LNK     3'  GACAGTGGAGTCAGCTGCTCTT 18463     C  _    TG
                                AAGA TAG TGATTT  TTGTT
                                ||||  ||| ||||||  |||||
                                TTCT GTC ACTGAG  GACAG
                                  C  G     GT
GAM394  LPP     5'  GACAGAACCTGGTCTTCT    18747         TGA
                                GGAAGACTAG   TTTTGTT
                                ||||||||||   |||||||
                                TCTTCTGGTC   AAGACAG
                                      C__
GAM394  LZTS1   3'  AACGACAGAGGAGCTTTTCT   40674    CT   GA
                                AGA  AGT  TTTTGTTGTT
                                |||  |||  ||||||||||
                                TCT  TCG  GAGACAGCAA
                                  TT   AG
GAM394  M6PR    3'  GGTGGTGGGATCCTGATGTCTT 9863        __  T    TG TG
            TCA                   GGAAGAC  TAG GATTT  T  TT
                                |||||||  ||| |||||  |  ||
                                CTTTCTG  GTC CTAGG  G  GG
                                    TA  _    GT GT
GAM394  MAML1   3'  GATAGCAGAATTATTTGCAATT 28589     GACT_
            T                    GAA    AGTGATTTTGTTGTT
                                |||    ||||||||||||||
```

```
                                TTT    TTATTAAGACGATAG
                                  AACGT
GAM394  MAN2A1   3'  AGAATCATTGGCTTTTA    9893       A
                                TGGAAG CTAGTGATTTT
                                |||||| ||||||||||
                                ATTTTC GGTTACTAAGA
                                   _
GAM394  MAN2A2   3'  GGTGGCAGGGGTGTGGGGTCCT 20400     A   AGTGA_    TG
           TCA                    TGGA GACT     TTTTGT  TT
                                |||| ||||     ||||||  ||
                                ACTT CTGG     GGGACG  GG
                                  C   GGTGTG     GT
GAM394  MBL2     3'  AATATTTTGCTAGTTTTT    4112          TG TTT
                                GAAGACTAG  A   TGTT
                                |||||||||  |   ||||
                                TTTTTGATC  T   ATAA
                                     GT TT_
GAM394  MDM4     3'  GGCGACAGGGTCTGTCTT    9979       TAGT
                                AAGAC    GATTTTGTTGTT
                                |||||    ||||||||||||
                                TTCTG    CTGGGACAGCGG
                                   T___
GAM394  MEN1     5'  GACACAGAGTCACCAGTTTTCC 93371        A        T
                                GGAAGACT GTGATTTTGT GTT
                                |||||||| |||||||||| |||
                                CCTTTTGA CACTGAGACA CAG
                                     C         _   T
GAM394  MGAT5    5'  AGCAGTGAGGTGTACCTTTTCC 10020       CTA   _    TG
                                GGAAGA   GTG ATTT  TTGTT
                                ||||||   ||| ||||  |||||
                                CCTTTT   CAT TGGA  GACGA
                                   C__   G    GT
GAM394  MGAT5    5'  GATAGCAACTTTTTAGCTTCT  10023      A    T  TT
                                GGAAG CTAG GA  TTGTTGTT
                                ||||| |||| ||  ||||||||
                                TCTTC GATT TT  AACGATAG
                                   _    _ TC
GAM394  MKKS     5'  GGTGGCAGTGACTAGTTTTTC  38139          G  TT   TG
                                GGAAGACTAGT AT  TGT  TT
                                |||||||||| ||  |||  ||
                                CTTTTTGATCA TG  ACG  GG
                                      G  __   GT
GAM394  MYBL1    3'  AATAGCAGAATCGGCTTGCTGC 64071     A  ACT   _
           TA                     TGG AG   AGT GATTTTGTTGTT
                                ||| ||   ||| ||||||||||||
                                ATC TC   TCG CTAAGACGATAA
                                  G  GT_   G
GAM394  MYBL2    3'  AACAACAAAGTTCCACTTCCA  10153       ACTAGT
                                TGGAAG     GATTTTGTTGTT
                                ||||||     ||||||||||||
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```
                                ACCTTC     TTGAAACAACAA
                                   ACC___
GAM394  MYEOV    3'  GGCTCCAGGGTCCCTGGTTTTC 57051         T      TT
             T                   GGAAGACTAG GATTTTG  GTT
                                 |||||||||| |||||||  |||
                                 TCTTTTGGTC CTGGGAC  CGG
                                      C      CT
GAM394  MYO1F    3'  AACAGCAGAATCTACCTCCCA  82421     A  ACTA  _
                                 TGG AG    GT GATTTTGTTGTT
                                 ||| ||    || ||||||||||||
                                 ACC TC    CA CTAAGACGACAA
                                   C  ____  T
GAM394  MYO1F    5'  GCAGCAAGGAGCGCTTCCA    82426       ACTA  GA
                                 TGGAAG    GT  TTTTGTTGT
                                 ||||||    ||  |||||||||
                                 ACCTTC    CG  GGAACGACG
                                    G___   A_
GAM394  NAT1     5'  GCAGCAATCTGTCTTCT      5406         T  TGATT
                                 GGAAGAC AG     TTGTTGT
                                 ||||||| ||     |||||||
                                 TCTTCTG TC     AACGACG
                                    _  T_____
GAM394  NCOA6    5'  GATGGCAAGGTCTATTGTTCT  25965     C   _       TG
                                 AGA TAGT GATTTTGT  TT
                                 ||| |||| ||||||||  ||
                                 TCT GTTA CTGGAACG  AG
                                   T   T       GT
GAM394  NDP      3'  AATGGTGGCCTGGCTTGTCTTC 4242         T   GATT TG TG
             T                   GGAAGAC AGT    T  T  TT
                                 ||||||| |||    |  |  ||
                                 TCTTCTG TCG    G  G  AA
                                     T   GTCC GT GT
GAM394  NKTR     3'  GGCAGTGTATTAGTTTTCTA   18202            ATT
                                 TGGAAGACTAGTG   TTGTT
                                 ||||||||||||   |||||
                                 ATCTTTTGATTAT   GACGG
                                         GT_
GAM394  NME2     3'  GGCAACAGGATTGATCATTCTT 10240       CTAG_
             TT                   GGAAGA     TGATTTTGTTGTT
                                  ||||||     ||||||||||||
                                  TTTTCT     GTTAGGACAACGG
                                     TACTA
GAM394  NOS1     3'  TAACAATATGATTATTATTTTT 5253         C       T
             TTA                    TGGAAGA TAGTGATT TGTTGTT
                                    ||||||| |||||||| |||||||
                                    ATTTTTT ATTATTAG ATAACAA
                                       T       T      TG
GAM394  NR3C2    3'  GGCAACATTACCTTGTCTTTCA 6132          TA_    TTT
                                 TGGAAGAC   GTGA   TGTTGTT
                                 ||||||||   ||||   |||||||
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                                ACTTTCTG  CATT  ACAACGG
                                    TTC   ___
GAM394  NRXN3   5' AGTGATGAAATCACCCTCTCC 16580    A CTA     TG TG
                                GGA GA  GTGATTT  T  TT
                                ||| ||  |||||||  |  ||
                                CCT CT  CACTAA  A  GA
                                  _ CC_     GT GT
GAM394  NTSR1   5' GACGGCGCGCCCGCTGGTCTTC 10294         ATTT
                                GAAGACTAGTG   TGTTGTT
                                ||||||||||   |||||||
                                CTTCTGGTCGC   GCGGCAG
                                      CCGC
GAM394  NTSR1   3' GGCGATGGTGCCTGGTCTCT  10297    A    TGATT TG
                                GGA GACTAG    T  TTGTT
                                ||| ||||||    |  |||||
                                TCT CTGGTC    G  AGCGG
                                  _     CGT__ GT
GAM394  NUP62   3' ACAGCAGCCTAGTTTTC    33326        TGATT
                                GAAGACTAG    TTGTTGT
                                |||||||||    |||||||
                                CTTTTGATC    GACGACA
                                    C____
GAM394  OCLN    3' AATAATAAATTCCCTGGCCTTT 10312      A   T  T
          CA                    TGGAAG CTAG GA TTTGTTGTT
                                |||||| |||| || |||||||||
                                ACTTTC GGTC CT AAATAATAA
                                   C   C  T
GAM394  OGN     5' AGCAGGCCACTAGTTT     25919        AT
                                AGACTAGTG  TTTGTT
                                |||||||||  ||||||
                                TTTGATCAC  GGACGA
                                    C_
GAM394  OGN     5' AGCAGGCCACTAGTTT     44324        AT
                                AGACTAGTG  TTTGTT
                                |||||||||  ||||||
                                TTTGATCAC  GGACGA
                                    C_
GAM394  OGN     5' AGCAGGCCACTAGTTT     52242        AT
                                AGACTAGTG  TTTGTT
                                |||||||||  ||||||
                                TTTGATCAC  GGACGA
                                    C_
GAM394  PAX4    5' GGCAGCAAGGATGCAGTCTCCC 20556    A   A  A
          A                     TGG AGACT GTG TTTTGTTGTT
                                ||| ||||| ||| ||||||||||
                                ACC TCTGA CGT GGAACGACGG
                                  C    _  A
GAM394  PAX9    5' GACAGCGGAAGGAGTTTCC   20560    A   AGTGA
                                GGA GACT    TTTTGTTGTT
                                ||| ||||    ||||||||||
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                                CCT TTGA    AAGGCGACAG
                                  _   GG___
GAM394  PCDH9   5' AATGGCAAAGTGATCTGTTTT 82789     TA G     TG
                                AAGAC  GT ATTTTGT  TT
                                |||||  || |||||||  ||
                                TTTTG  TA TGAAACG  AA
                                   TC  G      GT
GAM394  PCDHA9  3' AATTTAGTTGTTAGTCATTCA 25752     A    TG   TT
                                TGGA GACTAG  ATT  GTT
                                |||| ||||||  |||  |||
                                ACTT CTGATT  TGA  TAA
                                  A     GT   TT
GAM394  PCK1    3' AGACCTACTAGTTTTCC    59943         ATTTT  TG
                                GGAAGACTAGTG    GT  T
                                ||||||||||||    ||  |
                                CCTTTTGATCAT    CA  A
                                       C_____  GT
GAM394  PCLO    3' AAAATTGTAGTCTTCT     94219        G
                                GGAAGACTA TGATTTT
                                ||||||||| |||||||
                                TCTTCTGAT GTTAAAA
                                          _
GAM394  PCLO    3' AGTGGCTGCCAGTTTTCCA   94222        ___  G
                                TGGAAGACT   AGT ATT
                                |||||||||   ||| |||
                                ACCTTTTGA   TCG TGA
                                      CCG   G
GAM394  PDE4B   3' GGCAATGGGATGTAGTTTTT  10483       GTG   TG
                                GAAGACTA   ATTT  TTGTT
                                ||||||||   ||||  |||||
                                TTTTTGAT   TAGG  AACGG
                                     G__    GT
GAM394  PIP5K1A 3' AGAGTTGTGGTTTTCCA    13053        G
                                TGGAAGACTA TGATTTT
                                |||||||||| |||||||
                                ACCTTTTGGT GTTGAGA
                                          _
GAM394  PK428   5' AGCAACATTTTTGGTTTTCC  13207        TGATTT
                                GGAAGACTAG     TGTTGTT
                                ||||||||||     |||||||
                                CCTTTTGGTT     ACAACGA
                                      TTT___
GAM394  PKD2    3' GACCGATTGCTAATCTTCT   60093      C   TG   TT
                                GGAAGA TAG  ATT  GTT
                                |||||| |||  |||  |||
                                TCTTCT ATC  TAG  CAG
                                   A   GT   C_
GAM394  PKDREJ  3' ACAGCAGGATCACAGT     20275     A
                                ACT GTGATTTTGTTGT
                                ||| ||||||||||||
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                                TGA CACTAGGACGACA
                                  _
GAM394  PKP2     3'  AATGGCAAAATTATTGGTTTCT 15886     A           TG
                                GGA GACTAGTGATTTTGT  TT
                                ||| ||||||||||||||  ||
                                TCT TTGGTTATTAAAACG  AA
                                  _          GT
GAM394  PLA2R1   5'  GGGCGGAGTGGGTCTCCA    23753     A   AGTG     TG
                                TGGA GACT    ATTTTGT  T
                                |||| ||||   |||||||  |
                                ACCT CTGG    TGAGGCG  G
                                  _   G___     GT
GAM394  PLN      3'  AACAACAGAATCTAATCTTC   10646      CTAGT
                                GAAGA    GATTTTGTTGTT
                                |||||    ||||||||||||
                                CTTCT    CTAAGACAACAA
                                   AAT__
GAM394  PLN      3'  GACAGTGAGATTAGTC      10647      GTG   TG
                                GACTA   ATTT  TTGTT
                                |||||   ||||  |||||
                                CTGAT   TAGA  GACAG
                                   ___   GT
GAM394  POLI     3'  AATAACGGAGTAAACTGTTCCA 23237      GAC   G_
                                TGGAA   TAGT  ATTTTGTTGTT
                                |||||   ||||  ||||||||||
                                ACCTT   GTCA  TGAGGCAATAA
                                   ___   AA
GAM394  POU3F2   3'  GGCAATGGAGTGGAGTGTCTCC 18814    A   TAGTG   TG
                                GGA GAC    ATTT  TTGTT
                                ||| |||    ||||  |||||
                                CCT CTG    TGAG  AACGG
                                  _  TGAGG   GT
GAM394  PPAT     3'  GACAACTCATGATTGTTAGCTT 10698      A   TG   TT__
           TCA                   GGAAG CTAG  ATT    GTTGTT
                                |||||  ||||  |||    ||||||
                                CTTTC GATT  TAG    CAACAG
                                  _   GT   TACT
GAM394  PPP1R12B 5'  GCAATAGAGTTCCTTGCCA   49471    AAGACT  TG
                                TGG     AG  ATTTTGTTGT
                                |||     ||  ||||||||||
                                ACC     TC  TGAGATAACG
                                  GT____  CT
GAM394  PPP1R12B 5'  GCAATAGAGTTCCTTGCCA   49482    AAGACT  TG
                                TGG     AG  ATTTTGTTGT
                                |||     ||  ||||||||||
                                ACC     TC  TGAGATAACG
                                  GT____  CT
GAM394  PPP1R3A  3'  AATGGCAGAGGACTTTTTTGGT 10716       TGA____     TG
           CTTTTA                  AGACTAG     TTTTGT  TT
                                |||||||      ||||||  ||
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                                TCTGGTT      GAGACG  AA
                                    TTTTCAG     GT
GAM394  PPP1R3D  3'  GGCAGTGGCCCATCCTGTCTTC 20704        T  T   T__ TG
            TA                    TGGAAGAC AG GAT   T  TTGTT
                                  |||||||| || |||   |  |||||
                                  ATCTTCTG TC CTA   G  GACGG
                                      _ _   CCC GT
GAM394  PPP6C    3'  AGCAGCAAAGTTGTTATTC    10767    C   TG
                                  GA TAG  ATTTTGTTGTT
                                  || |||  ||||||||||
                                  CT ATT  TGAAACGACGA
                                   T   GT
GAM394  PRKCN    3'  AGCAATAACTGGTTTTGTA    19444    G       GATT
                                  TG AAGACTAGT    TTGTT
                                  || |||||||||    |||||
                                  AT TTTTGGTCA    AACGA
                                   G        AT__
GAM394  PRLR     3'  GATGACAAAAGAAAATTTTCCA 6279         CTAGTGA     TG
                                  TGGAAGA      TTTTGT  TT
                                  |||||||      ||||||  ||
                                  ACCTTTT      AAAACA  AG
                                      AAAAG__     GT
GAM394  PROML1   3'  GGCAACGGCACCATTGGTCTCT 20055     A       ATT
                                  GGA GACTAGTG   TTGTTGTT
                                  ||| ||||||||   ||||||||
                                  TCT CTGGTTAC   GGCAACGG
                                    _       CAC
GAM394  PTGER2   3'  AATGACAAAGTATGTGGTTTTG 6303     G      GTG      TG
            TA                    TG AAGACTA   ATTTTGT  TT
                                  || |||||||   |||||||  ||
                                  AT TTTTGGT   TGAAACA  AA
                                   G      GTA      GT
GAM394  PTPRO    3'  GGCAACAAACAGGAGCTTCT   47716      A  AG  AT
                                  GGAAG CT  TG  TTTGTTGTT
                                  ||||| ||  ||  |||||||||
                                  TCTTC GA  AC  AAACAACGG
                                    _ GG  __
GAM394  PVR      3'  AGTGGTGAGATCACAGTT    21471      A      TG TG
                                  GACT GTGATTT  T  TT
                                  |||| |||||||  |  ||
                                  TTGA CACTAGA  G  GA
                                    _      GT GT
GAM394  PVR      3'  GACAGCAGAATTCCTCTT    21477      CTA TG
                                  AAGA   G  ATTTTGTTGTT
                                  ||||   |  ||||||||||
                                  TTCT   C  TAAGACGACAG
                                    ___ CT
GAM394  QPCT     3'  AATGGCAAAATAAATATCTTTC 24836       AC  GTG      TG
            CA                    TGGAAG  TA   ATTTTGT  TT
                                  ||||||  ||   |||||||  ||
```

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                                ACCTTT  AT   TAAAACG  AA
                                   CT  AAA      GT
GAM394  RAB2L    3'  GGCAGTGAAGTGCCACTGGTTT 16479    A       __    TG
            ACCA                    GG AGACTAGTG  ATTT  TTGTT
                                || |||||||||  ||||  |||||
                                CC TTTGGTCAC  TGAA  GACGG
                                 A        CG    GT
GAM394  RAB36    3'  GGCGGCGGGATGGAGTCTCT   16969     A    AGTG
                                GGA GACT    ATTTTGTTGTT
                                ||| ||||    ||||||||||
                                TCT CTGA    TAGGGCGGCGG
                                  _   GG__
GAM394  RAD21    3'  TTTTAGAAAGGTCATTAGTTTC 20763     A          GTTGTT
            T                    GGA GACTAGTGATTTT
                                ||| ||||||||||||
                                TCT TTGATTACTGGAA
                                  _          AGATTTTA
GAM394  RAD54B   3'  AGCAATGGAAACATTTTTCT   56232     CT    A   TG
                                AGA  AGTG TTT  TTGTT
                                |||  |||| |||  |||||
                                TCT  TTAC AAG  AACGA
                                  TT    A   GT
GAM394  RAD9     3'  AGTGGCAGAACTGGGTCTCTCA 15932    GA    _  GAT    TG
                                TG  AGACT AGT   TTTGT  TT
                                ||  ||||| |||   |||||  ||
                                AC  TCTGG TCA   AGACG  GA
                                 TC    G  ___     GT
GAM394  RASGRP1  3'  AACAGCAGGGTCACTTCTC    19200    CT
                                GA  AGTGATTTTGTTGTT
                                ||  ||||||||||||||
                                CT  TCACTGGGACGACAA
                                 CT
GAM394  RBM8A    3'  AATAATAAAATTTAACATTTTC 17542        CTAGT
            CA                    TGGAAGA    GATTTTGTTGTT
                                |||||||    ||||||||||||
                                ACCTTTT    TTAAAATAATAA
                                    ACAAT
GAM394  RBMX     3'  GCAATGAAGTTATCTCCA    68220      A  CTAG     TG
                                TGGA GA    TGATTT  TTGT
                                |||| ||    ||||||  ||||
                                ACCT CT    ATTGAA  AACG
                                  _ _____     GT
GAM394  RCN1     3'  AAAATGGACATCACTAGTCTTT 59627             _  TG  GTT
            CA                    TGGAAGACTAGTGAT TT  TT
                                ||||||||||||||| ||  ||
                                ACTTTCTGATCACTA AG  AA
                                          C  GT  AA
GAM394  RCN1     3'  AAAATGGACATCACTAGTCTTT 11267             _  TG  GTT
            CA                    TGGAAGACTAGTGAT TT  TT
                                ||||||||||||||| ||  ||
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                                ACTTTCTGATCACTA AG  AA
                                        C  GT  AA
GAM394  REGL    3'  AGTAGTGGGTCCCTGGTCTCC  21484     A     T    TGTTGTT
                                GGA GACTAG GATTT
                                ||| |||||| |||||
                                CCT CTGGTC CTGGG
                                  _     C    TGATGA
GAM394  RET     3'  AACAGCAAAATTGTGGCATTTT 4368       GA   G
                                GGAA  CTA TGATTTTGTTGTT
                                ||||  ||| ||||||||||||
                                TTTT  GGT GTTAAAACGACAA
                                  AC  _
GAM394  RET     3'  AACAGCAAAATTGTGGCATTTT 40590      GA   G
                                GGAA  CTA TGATTTTGTTGTT
                                ||||  ||| ||||||||||||
                                TTTT  GGT GTTAAAACGACAA
                                  AC  _
GAM394  RET     3'  AACAGCAAAATTGTGGCATTTT 40166      GA   G
                                GGAA  CTA TGATTTTGTTGTT
                                ||||  ||| ||||||||||||
                                TTTT  GGT GTTAAAACGACAA
                                  AC  _
GAM394  RET     3'  AACAGCAAAATTGTGGCATTTT 40172      GA   G
                                GGAA  CTA TGATTTTGTTGTT
                                ||||  ||| ||||||||||||
                                TTTT  GGT GTTAAAACGACAA
                                  AC  _
GAM394  RGR     3'  AGTGGTGAAGTCTGGGCTTTTA 11322        A  AGT    TG TG
                                TGGAAG CT   GATTT  T  TT
                                |||||| ||   |||||  |  ||
                                ATTTTC GG   CTGAA  G  GA
                                  _ GT_    GT GT
GAM394  RGS3    3'  GGTGGCAGGCAGCTGGCCTTCT 35057       A    GAT    TG
                                GGAAG CTAGT   TTTGT  TT
                                ||||| |||||   |||||  ||
                                TCTTC GGTCG   GGACG  GG
                                  C    AC_    GT
GAM394  RGS3    3'  GGTGGCAGGCAGCTGGCCTTCT 56223       A    GAT    TG
                                GGAAG CTAGT   TTTGT  TT
                                ||||| |||||   |||||  ||
                                TCTTC GGTCG   GGACG  GG
                                  C    AC_    GT
GAM394  RGS3    3'  GGTGGCAGGCAGCTGGCCTTCT 57826       A    GAT    TG
                                GGAAG CTAGT   TTTGT  TT
                                ||||| |||||   |||||  ||
                                TCTTC GGTCG   GGACG  GG
                                  C    AC_    GT
GAM394  RGS3    3'  GGTGGCAGGCAGCTGGCCTTCT 57823       A    GAT    TG
                                GGAAG CTAGT   TTTGT  TT
                                ||||| |||||   |||||  ||
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                                TCTTC GGTCG   GGACG  GG
                                  C    AC_    GT
GAM394  RGS3    3'  GGTGGCAGGCAGCTGGCCTTCT 40862      A    GAT    TG
                                GGAAG CTAGT   TTTGT  TT
                                ||||| |||||   |||||  ||
                                TCTTC GGTCG   GGACG  GG
                                  C    AC_    GT
GAM394  RGS3    3'  GGTGGCAGGCAGCTGGCCTTCT 55445      A    GAT    TG
                                GGAAG CTAGT   TTTGT  TT
                                ||||| |||||   |||||  ||
                                TCTTC GGTCG   GGACG  GG
                                  C    AC_    GT
GAM394  RNF3    5'  AGCAGTGGGATTGCTGGATCTT 20885     _   TG   TG
                                AAGA CTAG  ATTT  TTGTT
                                |||| ||||  ||||  |||||
                                TTCT GGTC  TAGG  GACGA
                                  A   GT   GT
GAM394  RNTRE   3'  GATCCTAGTTTTTCA      28036          T
                                TGGAAGACTAG GATT
                                |||||||||||| ||||
                                ACTTTTTGATC CTAG
                                          _
GAM394  RP42    3'  AATGGTGGTTTGGGCTTGTCTT 40201        T   GATT_ TG TG
          CTA                     TGGAAGAC AGT    T  T  TT
                                ||||||||| |||    |  |  ||
                                ATCTTCTG TCG    G  G  AA
                                     T   GGTTT GT GT
GAM394  RPL28   3'  AGCAATAAAGTCAGCTGGCTTT 6391       A   _
          C                      GGAAG CTAG TGATTTTGTTGTT
                                ||||| |||| ||||||||||||
                                CTTTC GGTC ACTGAAATAACGA
                                  _   G
GAM394  RPL5    5'  AGCAGCGGACGCCGGTCTCT   6386     A   TA   AT
                                GGA GAC  GTG  TTTGTTGTT
                                ||| |||  |||  |||||||||
                                TCT CTG  CGC  AGGCGACGA
                                  _  GC  __
GAM394  RPS13   3'  GCAATAAAATGATTGTTT    6405      T   G
                                AGAC AGT ATTTTGTTGT
                                |||| ||| ||||||||||
                                TTTG TTA TAAAATAACG
                                  _  G
GAM394  RPS6KA5 3'  AAGTCACAGGTTTTCCA     16465         A
                                TGGAAGACT GTGATTT
                                ||||||||| |||||||
                                ACCTTTTGG CACTGAA
                                     A
GAM394  SCA7    3'  AGCAACGGAATTCGAGCTCC   4402      A A  AGT
                                GGA G CT   GATTTTGTTGTT
                                ||| | ||   ||||||||||||
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                                CCT C GA   TTAAGGCAACGA
                                  _ _  GC_
GAM394  SCP2     3'  AACAATAAAGTTTGCTTTCA   11441       ACTAGT
                                TGGAAG     GATTTTGTTGTT
                                ||||||     ||||||||||||
                                ACTTTC     TTGAAATAACAA
                                   GT____
GAM394  SDHA     3'  GATGACAGAATCAGCTTTT    73835       A  AGT       TG
                                GGAAG CT   GATTTTGT  TT
                                ||||| ||   ||||||||  ||
                                TTTTC GA   CTAAGACA  AG
                                  _ ___       GT
GAM394  SDHB     3'  AAGATCTTGGTTTTCCA     60509           T
                                TGGAAGACTAG GATTTT
                                |||||||||||| ||||||
                                ACCTTTTGGTT CTAGAA
                                          _
GAM394  SDHC     3'  AATAGTGGAAAAGGGTCTAGTT 69383         TGA___   TG
             TTCC                   AAGACTAG     TTT  TTGTT
                                ||||||||     |||  |||||
                                TTTTGATC     AAG  GATAA
                                   TGGGAA   GT
GAM394  SEPP1    3'  AACAACAAAGACATGCTTTCCA 60108        ACTA   A
                                TGGAAG    GTG TTTTGTTGTT
                                ||||||    ||| ||||||||||
                                ACCTTT    TAC GAAACAACAA
                                   CG__   A
GAM394  SEPP1    3'  AACAACAAAGACATGCTTTCCA 18259        ACTA   A
                                TGGAAG    GTG TTTTGTTGTT
                                ||||||    ||| ||||||||||
                                ACCTTT    TAC GAAACAACAA
                                   CG__   A
GAM394  SERPINB2 3'  TGACAACCCTATTAATCATTTG 10408       _    TT____
             GTCTTCTA                ACTAG TGATT     GTTGTT   G
                                ||||| |||||     ||||||   |
                                TGGTT ACTAA     CAACAG   T
                                   T     TTATCC
GAM394  SFRP1    3'  GGCCTGGTCATTGGTCTCC    11572     A         TT
                                GGA GACTAGTGATT  GTT
                                ||| ||||||||||  |||
                                CCT CTGGTTACTGG  CGG
                                  _          TC
GAM394  SGCB     3'  AACAATGGTTCCTTAGTTTTGC 4065     G       T  TT TG
             A                   TG AAGACTAG GA  T  TTGTT
                                || ||||||| ||  |  |||||
                                AC TTTTGATT CT  G  AACAA
                                 G       C  T_ GT
GAM394  SGT      3'  AGCAGCAGGGTTGTCAGTC    11587      A TG
                                GACT G  ATTTTGTTGTT
                                |||| |  ||||||||||
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```
                                CTGA T  TGGGACGACGA
                                  C GT
GAM394  SHANK2   3'  GACAGCAGAATCTTTCTATCA  55737     A   CTAGT
                                TGG AGA    GATTTTGTTGTT
                                ||| |||    ||||||||||||
                                ACT TCT    CTAAGACGACAG
                                  A  TT___
GAM394  SHOC2    5'  GATGGCGGAGTCGGGGCTCC   23765     A A  AG       TG
                                GGA G CT  TGATTTTGT  TT
                                ||| | ||  |||||||||  ||
                                CCT C GG  GCTGAGGCG  AG
                                  _ _ G_       GT
GAM394  SHOX     3'  AGCAATAAGGAAATAGTTCTCT 4830      AG    GTGA
                                GGA  ACTA   TTTTGTTGTT
                                |||  ||||   ||||||||||
                                TCT  TGAT   GGAATAACGA
                                  CT   AAA_
GAM394  SIM1     3'  AACAACAAACTTGGTCTTACA  17375    G      TGAT
                                TG AAGACTAG   TTTGTTGTT
                                || ||||||||   |||||||||
                                AC TTCTGGTT   AAACAACAA
                                 A      C___
GAM394  SKI      3'  GCGGCCTGCTGGTCCTCT    11704     A      ATTTT
                                GGA GACTAGTG    GTTGT
                                ||| ||||||||    |||||
                                TCT CTGGTCGT    CGGCG
                                  C      C____
GAM394  SLC12A6  3'  AACAATGCTCAAGTCTTTCA   17623        AG   TT_
                                TGGAAGACT  TGA   TTGTT
                                |||||||||  |||   |||||
                                ACTTTCTGA  ACT   AACAA
                                     __   CGT
GAM394  SLC16A7  3'  AATGGCAAATTTTAAATTAGTT 16402        GAT___    TG
           TTT                    AAGACTAGT     TTTGT  TT
                                |||||||||     |||||  ||
                                TTTTGATTA     AAACG  AA
                                     AATTTT    GT
GAM394  SLC17A4  3'  AACAACAGAAAGCATAGTGTTT 18523       TA_   A_
           TCCA                   GGAAGAC   GTG  TTTTGTTGTT
                                |||||||   |||  ||||||||||
                                CCTTTTG   TAC  AAGACAACAA
                                    TGA   GA
GAM394  SLC1A5   3'  GCAATAAAATTGAGTGTC    18846     TAG
                                GAC   TGATTTTGTTGT
                                |||   ||||||||||||
                                CTG   GTTAAAATAACG
                                  TGA
GAM394  SLC1A5   3'  GCAATAAAATTGAGTGTC    78537     TAG
                                GAC   TGATTTTGTTGT
                                |||   ||||||||||||
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```
                                CTG  GTTAAAATAACG
                                  TGA
GAM394  SLC22A12  3'  AGCAGTAGAGTCTCAGCTCCA  58066     A A  AGT
                                TGGA G CT  GATTTTGTTGTT
                                |||| | ||  ||||||||||||
                                ACCT C GA  CTGAGATGACGA
                                  _ _ CT_
GAM394  SLC22A2  3'  GACATTGGACATTGGTTTTCT  59531          A  TGT
                                GGAAGACTAGTG TTT  TGTT
                                |||||||||||| |||  ||||
                                TCTTTTGGTTAC AGG  ACAG
                                       _  TT_
GAM394  SLC25A15  3'  AGCTATTATGGCTGGTCTTCCA 26508          G  TTT_
                                TGGAAGACTAGT AT   GTT
                                |||||||||||| ||   |||
                                ACCTTCTGGTCG TA   CGA
                                       G  TTAT
GAM394  SLC3A2   5'  AGCGGTGAGATCACTGCCTCAC 9982    GA  AC      TG
          G                     TG  AG  TAGTGATTT  TTGTT
                                ||  ||  |||||||||  |||||
                                GC  TC  GTCACTAGA  GGCGA
                                 AC  C_      GT
GAM394  SMARCD1  3'  GATAACAGAATCCAATTTCC  11817     ACTAGT
                                GGAAG     GATTTTGTTGTT
                                |||||     ||||||||||||
                                CCTTT     CTAAGACAATAG
                                   AAC___
GAM394  SMARCD1  3'  GATAACAGAATCCAATTTCC  57435     ACTAGT
                                GGAAG     GATTTTGTTGTT
                                |||||     ||||||||||||
                                CCTTT     CTAAGACAATAG
                                   AAC___
GAM394  SMOH    3'  GACTGTGTCATTAGTCCTTT  18865    A       TTT
                                GGA GACTAGTGAT  GTT
                                ||| ||||||||||  |||
                                TTT CTGATTACTG  CAG
                                  C       TGT
GAM394  SP3     3'  AATAAAGTTACATTGCTGGTCT 82491        _____       GTT
          TGTA                    AGACTAGT    GATTTTGTT
                                |||||||    |||||||||
                                TCTGGTCG    TTGAAATAA
                                     TTACA          T
GAM394  SP3     5'  AGCGACAGGTGATTTGGCTTCT 82494      A   TGAT
                                GGAAG CTAG    TTTGTTGTT
                                ||||| ||||   |||||||||
                                TCTTC GGTT    GGACAGCGA
                                   _   TAGT
GAM394  SPK     5'  GTGGCATCACAGTTTTTCA   16685        A   TTT  TG
                                TGGAAGACT GTGA  TGT  T
                                ||||||||| ||||  |||  |
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                                ACTTTTTGA CACT   ACG  G
                                      _   ___   GT
GAM394  SREBF2   5'  ACGGCAGGGGGGGCTTCT    15988      A  AGTGA
                                GGAAG CT    TTTTGTTGT
                                ||||| ||    |||||||||
                                TCTTC GG    GGGACGGCA
                                  _ GG___
GAM394  SSPN     3'  GACAATAAAAGTCACTCTTCTA 17442       CTA      _
                                TGGAAGA   GTGATTTT GTTGTT
                                |||||||   |||||||| ||||||
                                ATCTTCT   CACTGAAA TAACAG
                                   ___       A
GAM394  STAC     3'  AGCAATAAAATCATTAG     11986
                                CTAGTGATTTTGTTGTT
                                ||||||||||||||||
                                GATTACTAAAATAACGA

GAM394  STC1     3'  GTTCTCACATGTTGCTAGTTTT 12032         TG  TT   TGTT
           TT                    GGAAGACTAG  AT  TGT
                                ||||||||||  ||  |||
                                TTTTTTGATC  TG  ACA
                                     GT  T_  CTCTTGA
GAM394  STK10    3'  GGCTGGAATTCTTGGTTTTTCA 19987          T     _
                                TGGAAGACTAG GATTTT GTT
                                |||||||||| |||||| |||
                                ACTTTTTGGTT TTAAGG CGG
                                      C     T
GAM394  TAL1     3'  GATGGTGGGATGTGGTTTTCT  12104         GTG    TG TG
                                GGAAGACTA   ATTT  T  TT
                                |||||||||   ||||  |  ||
                                TCTTTTGGT   TAGG  G  AG
                                     G__    GT GT
GAM394  TBXAS1   5'  GGCGGCGAGATCAGCCTCC    6509      A A  AGT
                                GGA G CT   GATTTTGTTGTT
                                ||| | ||   ||||||||||||
                                CCT C GA   CTAGAGCGGCGG
                                  _ C  ___
GAM394  TBXAS1   5'  GGCGGCGAGATCAGCCTCC    48293     A A  AGT
                                GGA G CT   GATTTTGTTGTT
                                ||| | ||   ||||||||||||
                                CCT C GA   CTAGAGCGGCGG
                                  _ C  ___
GAM394  TCF2     3'  AACAACAAGGACCCTGTTTTCC 4855         T  TGA
           A                     TGGAAGAC AG   TTTTGTTGTT
                                ||||||||  ||   ||||||||||
                                ACCTTTTG TC   GGAACAACAA
                                     _  CCA
GAM394  TCTE1L   3'  GATAATAAAATTCTCTTTCA   70973        CTAGT
                                TGGAAGA    GATTTTGTTGTT
                                |||||||    ||||||||||||
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                                ACTTTCT    TTAAAATAATAG
                                   C____
GAM394  TDO2    3'  AATAATAAAGTATTAATCTTTC 18944       C   G
           A                    TGGAAGA TAGT ATTTTGTTGTT
                                ||||||| |||| ||||||||||
                                ACTTTCT ATTA TGAAATAATAA
                                   A   _
GAM394  TFDP1   3'  AACAGCAGAATGCAACTTTC  23047      ACTA  G
                                GGAAG   GT ATTTTGTTGTT
                                |||||   || ||||||||||
                                CTTTC   CG TAAGACGACAA
                                  AA__  _
GAM394  TFRC    3'  AACAGCAGGGTAGTCTGGTTTC 12246     A     TG_
           TA                    TGGA GACTAG   ATTTTGTTGTT
                                |||| ||||||   ||||||||||
                                ATCT TTGGTC   TGGGACGACAA
                                  _     TGA
GAM394  TGFA    3'  AATGGACACTGGTTTTT     12248          AT  TG
                                GAAGACTAGTG  TT  TT
                                |||||||||||  ||  ||
                                TTTTTGGTCAC  AG  AA
                                      __ GT
GAM394  THBS1   3'  ATTGAAGAATTGTTGGTTTTTT 12282          TG    GTTGTT
                                GGAAGACTAG  ATTTT
                                ||||||||||  |||||
                                TTTTTTGGTT  TAAGA
                                      GT    AGTTAA
GAM394  TIAL1   3'  ATAACAGAGTCCTATTC    42259    C   T
                                GA TAG GATTTTGTTGT
                                || ||| ||||||||||
                                CT ATC CTGAGACAATA
                                 T  _
GAM394  TIRAP   3'  AGCAACAAGAATCCAGTCCTTC 53565     A   AGT     _
           A                    TGGA GACT   GATTTT GTTGTT
                                |||| ||||   |||||| ||||||
                                ACTT CTGA   CTAAGA CAACGA
                                  C   C__     A
GAM394  TLR4    5'  AGCAACAAGATTCAAAGTATTT 56735     G   AGT
                                GAA ACT   GATTTTGTTGTT
                                ||| |||   ||||||||||||
                                TTT TGA   TTAGAACAACGA
                                  A   AAC
GAM394  TMOD3   3'  GATAATAAATATGATAGATTTC 27244       A   GTGAT
           CA                   TGGAAG CTA    TTTGTTGTT
                                |||||| |||    |||||||||
                                ACCTTT GAT    AAATAATAG
                                   A   AGTAT
GAM394  TMPRSS2 3'  AGGTGAAAACGTCTTCC     18964       TA  GA   TG TG
                                GGAAGAC  GT  TTT  T  T
                                |||||||  ||  |||  |  |
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                                CCTTCTG  CA  AAA  G  A
                                   __ __   GT GT
GAM394  TNC     3'  AGTGACAACATCGCAATAGTTT 9287          __    T   TG
             TTTA                   GGAAGACTA  GTGAT TTGT  TT
                                |||||||||  ||||| ||||  ||
                                TTTTTTTGAT  CGCTA AACA  GA
                                     AA    C    GT
GAM394  TOB1    3'  AGTGGGTTTATTGGTCTTTT   19236           T  TG
                                GGAAGACTAGTGA TT  TT
                                |||||||||||||| ||  ||
                                TTTTCTGGTTATT GG  GA
                                       T  GT
GAM394  TP63    3'  AACAGTGAAGTTTTACTGTCT  13563     T   __    TG
                                AGAC AGT  GATTT  TTGTT
                                |||| |||  |||||  |||||
                                TCTG TCA  TTGAA  GACAA
                                  _  TT    GT
GAM394  TP63    3'  AGCTTCAGTTGCTTGTCTTCT  13566       T  TG   TT_
                                GGAAGAC AG  ATT   GTT
                                |||||||  ||  |||   |||
                                TCTTCTG TC  TGA   CGA
                                    T  GT   CTT
GAM394  TRAM    3'  AATAGCAGAGTGGCCTGTTCTA 26656      AG  TA  G
                                TGGA  AC  GT ATTTTGTTGTT
                                ||||  ||  || ||||||||||
                                ATCT  TG  CG TGAGACGATAA
                                  __  TC  G
GAM394  TRIM    3'  GATAACAAGATTACAAATTC   33065     GACTA
                                GAA    GTGATTTTGTTGTT
                                |||    ||||||||||||||
                                CTT    CATTAGAACAATAG
                                 AAA__
GAM394  TRPC1   3'  GATGAAAAGCATTGGTTTTTTA 12388           A_   TG
                                TGGAAGACTAGTG  TTT  TT
                                ||||||||||||  |||  ||
                                ATTTTTTGGTTAC  AAA  AG
                                       GA   GT
GAM394  TRPM8   3'  AACAATTTCTGGATGGTTTTTC 43980         GT__  TT    GTT
             A                   TGGAAGACTA    GA  TTGTT
                                ||||||||||    ||  |||||
                                ACTTTTTGGT    CT  AACAA
                                     AGGT  TT
GAM394  TSN     3'  AGCAATAAAATTTTTTTGGTCT 16102          T__
             TTT                  GGAAGACTAG   GATTTTGTTGTT
                                ||||||||||   ||||||||||||
                                TTTTCTGGTT   TTAAAATAACGA
                                     TTT
GAM394  TSN     3'  ATCATTTTGTTTTCCA      16104         T_
                                TGGAAGAC  AGTGAT
                                ||||||||  ||||||
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                                ACCTTTTG  TTACTA
                                     TT
GAM394  TTC3     5'  AGCAACAGGAAGATGTCTTTT  12414       TAGTGA
                                GGAAGAC     TTTTGTTGTT
                                |||||||     ||||||||||
                                TTTTCTG     AGGACAACGA
                                    TAGA__
GAM394  TUFT1    3'  AGCAACAAACTGTTTGTTTTTC 39249       TAGTGAT
                                GGAAGAC      TTTGTTGTT
                                |||||||      |||||||||
                                CTTTTTG      AAACAACGA
                                    TTTGTC_
GAM394  UBE2A    3'  GTTTCAGAATTATTGGTCTTCT 12468             TTGTT
                                GGAAGACTAGTGATTTTG
                                |||||||||||||||||
                                TCTTCTGGTTATTAAGAC
                                          TTTGA
GAM394  UBE2G2   3'  AACAGTGAAACCCTGTCTCCA  64849     A  T  TGA  TG
                                TGGA GAC AG   TTT  TTGTT
                                |||| ||| ||   |||  |||||
                                ACCT CTG TC   AAA  GACAA
                                  _  _ CC_   GT
GAM394  UBL3     3'  AATAATTCTCTATTGGTTTTTC 23028           ATTTT
           A                     TGGAAGACTAGTG    GTTGTT
                                 ||||||||||||     ||||||
                                 ACTTTTTGGTTAT    TAATAA
                                       CTCT_
GAM394  VENTX2   3'  GATAAAAGGATCATTTGTTTTT 27112        T       G
           TA                    TGGAAGAC AGTGATTTT TTGTT
                                 |||||||| ||||||||| |||||
                                 ATTTTTTG TTACTAGGA AATAG
                                      T       A
GAM394  VIL2     3'  AACAGGATTATTATTAGTGTTT 12596     G   ___        GTT
           TA                    GGAA ACTA   GTGATTTTGTT
                                 |||| ||||   ||||||||||
                                 TTTT TGAT   TATTAGGACAA
                                   G   TAT
GAM394  WEE1     3'  ATAATAATTACTGGTTTTGTA  12649    G         TT     T
                                 TG AAGACTAGTGAT  TGTTGT
                                 || ||||||||||||  ||||||
                                 AT TTTTGGTCATTA  ATAATA
                                  G          __     T
GAM394  WNT5A    3'  AACAGTGAAATCCACCTTCC   12659      ACTA  _   TG
                                 GGAAG   GTG ATTT  TTGTT
                                 |||||   ||| ||||  |||||
                                 CCTTC   CAC TAAA  GACAA
                                    _____  C   GT
GAM394  YES1     3'  AGTGACAGAATGGCTTTGCT   18349    ACT   G     TG
                                 AG   AGT ATTTTGT  TT
                                 ||   ||| |||||||  ||
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                                TC   TCG TAAGACA  GA
                                 GTT   G      GT
GAM394  YES1     3'  AATAATGAAGTTATGGCTTC   18344      A   G     TG
                                GAAG CTA TGATTT  TTGTT
                                |||| ||| ||||||  |||||
                                CTTC GGT ATTGAA  AATAA
                                  _  _     GT
GAM394  ZNF20    3'  AGCAACGGGAGAAGCTTTCT   63400     CT   GA_
                                AGA  AGT   TTTTGTTGTT
                                |||  |||   ||||||||||
                                TCT  TCG   AGGGCAACGA
                                  T_   AAG
GAM394  ZNF22    3'  TAACTGCTGTGTCGTTTGTTTT 91465        T     TTT  T
             CCA                    TGGAAGAC AGTGAT   GT GTT
                                |||||||| ||||||   || |||
                                ACCTTTTG TTGCTG   CG CAA
                                     T     TGT  T   TG
GAM394  ZNF236   3'  AGAATCATTGTCTTTCA     23711         T
                                TGGAAGAC AGTGATTTT
                                |||||||| |||||||||
                                ACTTTCTG TTACTAAGA
                                       _
GAM394  ZNF80    3'  AGCATGTCACTAGTTTTCTA   23073             TT
                                TGGAAGACTAGTGAT  TGTT
                                ||||||||||||||  ||||
                                ATCTTTTGATCACTG  ACGA
                                        T_
GAM394  ZNFN1A3  3'  ATTTGGTCATTATCTTCTA   60241        C       TT
                                TGGAAGA TAGTGATT  GT
                                ||||||| ||||||||  ||
                                ATCTTCT ATTACTGG  TA
                                     _       TT
GAM394  7h3      3'  GATAACAGAGTCTGGCCTTTCC 52272       A_   GT
             A                   TGGAAG  CTA  GATTTTGTTGTT
                                ||||||  |||  ||||||||||||
                                ACCTTT  GGT  CTGAGACAATAG
                                   CC  __
GAM394  AASDHPPT 5'  AGCGGCGAGGTCCGCTTTCA  31242       ACTAGT
                                TGGAAG     GATTTTGTTGTT
                                ||||||     ||||||||||||
                                ACTTTC     CTGGAGCGGCGA
                                   GC____
GAM394  ACTR2    3'  ACAATGGGTGGTCTTCT     19148         GTGAT  TG
                                GGAAGACTA    TT  TTGT
                                |||||||||    ||  ||||
                                TCTTCTGGT    GG  AACA
                                      _____  GT
GAM394  AD-020   3'  ACAACAAACTTATTTTCT    59382       CT   GATT
                                GGAAGA  AGT    TTGTTGT
                                ||||||  |||   |||||||
```

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                                TCTTTT  TCA    AACAACA
                                   AT  ____
GAM394  AD-020    3'  ACAACAAACTTATTTTCT    39306       CT   GATT
                                GGAAGA  AGT    TTGTTGT
                                ||||||  |||    |||||||
                                TCTTTT  TCA    AACAACA
                                   AT  ____
GAM394  AKAP10    3'  ACTAGAAAATTATTAGTTTTCC 23251              GTTGTT
           A                     TGGAAGACTAGTGATTTT
                                 ||||||||||||||||||
                                 ACCTTTTGATTATTAAAA
                                          GATCA
GAM394  AKAP10    3'  GATGGCAGTATATAGTTTTC   23253        GTGATT    TG
                                GAAGACTA     TTGT  TT
                                ||||||||     ||||  ||
                                CTTTTGAT     GACG  AG
                                   ATAT__    GT
GAM394  AKAP8     3'  GATGATGGATGCGTTGGTCTTT 19603           AT  TG TG
           C                     GGAAGACTAGTG  TT  T  TT
                                 ||||||||||||  ||  |  ||
                                 CTTTCTGGTTGC  AG  A  AG
                                       GT  GT GT
GAM394  AMOTL1    3'  AGCAATGAAATTCCTTTCTT   73646      CT  TG    TG
                                AAGA  AG  ATTT  TTGTT
                                ||||  ||  ||||  |||||
                                TTCT  TC  TAAA  AACGA
                                  T_  CT    GT
GAM394  AP3M2     3'  GATGGTATCGGACTAGTTTTC  22314          __   T TG  GTT
                                GAAGACTAGT  GAT T  TT
                                ||||||||||  ||| |  ||
                                CTTTTGATCA  CTA G  AG
                                      GG   T GT
GAM394  APG3      5'  GCAGCGAGGACATTTTCT    42531     CT    A
                                AGA  AGTG TTTTGTTGT
                                |||  |||| |||||||||
                                TCT  TTAC GGAGCGACG
                                  T_    A
GAM394  ARFD1     3'  GATAATAGGATTACTTTATGTT 7992       AGACT
           TA                    TGGA     AGTGATTTTGTTGTT
                                 ||||     |||||||||||||||
                                 ATTT     TCATTAGGATAATAG
                                   GTATT
GAM394  ARFGAP1   3'  GACAGTGGGATGTGGTGTTCCA 36591       G    GTG    TG
                                TGGAA ACTA   ATTT  TTGTT
                                ||||| ||||   ||||  |||||
                                ACCTT TGGT   TAGG  GACAG
                                   G    G__    GT
GAM394  ARHGAP9   3'  GGTGGTGAGAGGCTGGTGTTCT 50681      G     GA   TG TG
                                GGAA ACTAGT  TTT  T  TT
                                |||| ||||||  |||  |  ||
```

```
                                TCTT TGGTCG  AGA  G  GG
                                  G     G_   GT GT
GAM394  ARHGEF15 3'  AGCAATGACTGGTCCTGTCTTT 30255       T  T   __ TG
           T                     GGAAGAC AG GATT  T  TTGTT
                                 ||||||| || ||||  |  |||||
                                 TTTTCTG TC CTGG  A  AACGA
                                    _ _    TC GT
GAM394  ASB16    3'  GACAACAGAATTGGAAGGTC   69936     AG_
                                 GACT   TGATTTTGTTGTT
                                 ||||   ||||||||||||||
                                 CTGG   GTTAAGACAACAG
                                   AAG
GAM394  ASPN     5'  GACAGTCCTAGACTGGTCTTCT 34601          GATT__    GTT
           A                     TGGAAGACTAGT     TTGTT
                                 ||||||||||||     |||||
                                 ATCTTCTGGTCA     GACAG
                                       GATCCT
GAM394  ATPW     5'  ACAGCCCGCAGTCTTCT     31627        A   ATTTT
                                 GGAAGACT GTG     GTTGT
                                 |||||||| |||     |||||
                                 TCTTCTGA CGC     CGACA
                                    _   C_____
GAM394  B3GNT5   3'  AATGACGTTTTCAACTGGTTTT 49421         _  TTT   TG
           T                     GAAGACTAGT GA   TGT  TT
                                 |||||||||| ||   |||  ||
                                 TTTTTGGTCA CT   GCA  AA
                                      A  TTT   GT
GAM394  BAIAP1   3'  GCAGCAGGAAAGTCTTTT    16450        AGTGA
                                 GGAAGACT    TTTTGTTGT
                                 ||||||||    |||||||||
                                 TTTTCTGA    AGGACGACG
                                    A_____
GAM394  BANK     3'  GATGACAAGTTCCGTGGTCTTC 35595        GT  T    TG
           C                     GGAAGACTA  GA TTTGT  TT
                                 |||||||||  || |||||  ||
                                 CCTTCTGGT  CT GAACA  AG
                                      GC  T    GT
GAM394  BFAR     3'  GACTTGTAGTCACTGGGCTTTT 60772      A       TT__   GTT
                                 GGAAG CTAGTGATT    GTT
                                 ||||| |||||||||    |||
                                 TTTTC GGTCACTGA    CAG
                                    G        TGTT
GAM394  BIRC2    3'  TAAAAAGGGAATTATGAGTTTT 67202         A      G  GTT
           TCA                     TGGAAGACT GTGATTTT TT
                                 |||||||||  |||||||| ||
                                 ACTTTTTGA TATTAAGG AA
                                      G       G  AAATG
GAM394  BM-002   3'  AACAGCAGGATTATGAATTATC 33521    A  CTA
                                 GA GA   GTGATTTTGTTGTT
                                 || ||   ||||||||||||||
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                                CT TT   TATTAGGACGACAA
                                 A  AAG
GAM394  BRAL1    5'  GACAATGGGAAATTGTGCTTCC 41518      AC    GA   TG
                                GGAAG  TAGT  TTT  TTGTT
                                |||||  ||||  |||  |||||
                                CCTTC  GTTA  AGG  AACAG
                                   GT    A_   GT
GAM394  C15orf15  5'  GGTGACGGGGTTGCATCACTTC 32832      ACTA TG      TG
           C                     GGAAG    G  ATTTTGT  TT
                                |||||    |  |||||||  ||
                                CCTTC    C  TGGGGCA  GG
                                   ACTA GT      GT
GAM394  C16orf44  3'  AGCAGCAACTTCTTAGTATTCC 45314     G     T  TT
                                GGAA ACTAG GA  TTGTTGTT
                                ||||  |||||  ||  ||||||||
                                CCTT TGATT CT  AACGACGA
                                   A    _  TC
GAM394  C17orf26  3'  AACAGCAGTGGTTGGCTTCTA  57541       A    TG  TT
                                TGGAAG CTAG  AT  TGTTGTT
                                |||||| ||||  ||  |||||||
                                ATCTTC GGTT  TG  ACGACAA
                                   _   GG  __
GAM394  C1orf25   5'  CAGGATTTGGTCACTGGTTCTT 72534       _        TT   GTT
           C                     GAAGA CTAGTGATT  GTT
                                |||||  |||||||||  |||
                                CTTCT GGTCACTGG  TAG
                                   T        TT   GACA
GAM394  C20orf103 3'  AACAACAAAAGCACTTTTCCA  24325       ACT    A
                                TGGAAG   AGTG TTTTGTTGTT
                                ||||||   ||||  ||||||||||
                                ACCTTT   TCAC AAAACAACAA
                                   ___    G
GAM394  C20orf142 3'  AGCAATAAGATTACTTTTTTTC 74766       CT
           T                     GGAAGA  AGTGATTTTGTTGTT
                                ||||||  ||||||||||||||
                                TCTTTT  TCATTAGAATAACGA
                                   TT
GAM394  C20orf177 3'  GACAGTGGAATCTAGTACTTT  62148      _   GT    TG
                                GAAG ACTA  GATTT  TTGTT
                                ||||  ||||  |||||  |||||
                                TTTC TGAT  CTAAG  GACAG
                                   A   __     GT
GAM394  C21orf18  3'  GATGGCAGGTCTAATGCTCTTC 33845       C  GT_    T  TG
           C                     GGAAGA TA   GATTT GT  TT
                                ||||||  ||   |||||  ||  ||
                                CCTTCT GT   CTGGA CG  AG
                                   C  AAT    _  GT
GAM394  C22orf2   3'  AGCAGCAAGCACCAGCCTTCCA 94452       A  A   AT
                                TGGAAG CT GTG  TTTGTTGTT
                                ||||||  ||  |||  |||||||||
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                                ACCTTC GA CAC  GAACGACGA
                                   C  C  __
GAM394  C5orf6   3'  AATAGTTTGCTTGTCTTCCA  33475        T  TG TT
                                TGGAAGAC AG  A  TTGTT
                                |||||||| ||  |  |||||
                                ACCTTCTG TC  T  GATAA
                                     T  GT T_
GAM394  C7orf13  3'  GATGGGGTCTGGTTTTCT    50931        GT    TG
                                GGAAGACTA  GATTT  TT
                                |||||||||  |||||  ||
                                TCTTTTGGT  CTGGG  AG
                                     __    GT
GAM394  C9orf9   3'  GGCGATGACCTGGTTTTC    38521        TGATT TG
                                GAAGACTAG    T  TTGTT
                                |||||||||    |  |||||
                                CTTTTGGTC    A  AGCGG
                                     C____ GT
GAM394  CACNG4   3'  GGCAACAGGAGCCTGGACTTCT 26954      A    TGA
                                GGAAG CTAG   TTTTGTTGTT
                                ||||| ||||  ||||||||||
                                TCTTC GGTC   AGGACAACGG
                                   A   CG_
GAM394  CAP      3'  GATAGCAGGTCAGTTGATCTTC 21022      C  _     T
           T                     GGAAGA TAG TGATTT GTTGTT
                                ||||||| ||| |||||| ||||||
                                TCTTCT GTT ACTGGA CGATAG
                                   A  G    _
GAM394  CASPR3   3'  GACAATAGACACAGGTTTTC   45935       A  AT
                                GAAGACT GTG  TTTGTTGTT
                                ||||||| |||  |||||||||
                                CTTTTGG CAC  AGATAACAG
                                     A  __
GAM394  CDC37    3'  CAGCAATGATCTTCCA     22956        C  GTGATT
                                TGGAAGA TA     TTGTTG
                                ||||||| ||     ||||||
                                ACCTTCT GT     AACGAC
                                     A  _______
GAM394  CDKL2    5'  AACAGCGCTGGAATTGCTAGTT 14161  A     TG   ___
           TGCTA                    AGACTAG  ATTT   TGTTGTT
                                |||||||  ||||  |||||||
                                TTTGATC  TAAG   GCGACAA
                                G      GT    GTC
GAM394  CEACAM7  3'  GATAACAGAATTGCTG     22560     TG
                                TAG  ATTTTGTTGTT
                                |||  ||||||||||
                                GTC  TAAGACAATAG
                                  GT
GAM394  CED-6    3'  AACGATATGTTTGGTTTTCC  32851         TGATTT
                                GGAAGACTAG     TGTTGTT
                                ||||||||||     |||||||
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                                CCTTTTGGTT     ATAGCAA
                                      TGT___
GAM394  cerk     3'  AACAACAAAAAAAGTTTCCCA  42840     A    AGTGA
                                TGG AGACT    TTTTGTTGTT
                                ||| |||||    ||||||||||
                                ACC TTTGA    AAAACAACAA
                                  C    AA___
GAM394  CGGBP1   3'  AGTGATAGGATTTTAGTCTCT  13358     A     T      TG
                                GGA GACTAG GATTTTGT  TT
                                ||| |||||| ||||||||  ||
                                TCT CTGATT TTAGGATA  GA
                                  _     _      GT
GAM394  CGI-127  3'  CAGCAGAGTCTGTCT      32154      TAGT
                                AGAC    GATTTTGTTG
                                ||||    ||||||||||
                                TCTG    CTGAGACGAC
                                  T___
GAM394  CGI-94   3'  AATGGCATGGTTTTCC      32095          _  G
                                GGAAGACTA GT ATT
                                ||||||||| || |||
                                CCTTTTGGT CG TAA
                                     A  G
GAM394  CHRFAM7A 3'  GGCGACAAAGCAAGACTTTGTT 95021       T_   GA__
           TTTTA                 AAGAC  AGT    TTTTGTTGTT
                                |||||  |||    ||||||||||
                                TTTTG  TCA    GAAACAGCGG
                                   TT   GAAC
GAM394  CHRNA9   3'  GATAACAAAATACACTTTACT  34142    ACT    _
                                AG   AGTG ATTTTGTTGTT
                                ||   |||| ||||||||||
                                TC   TCAC TAAAACAATAG
                                 ATT    A
GAM394  CL24751  3'  GACAGTGGAAGATGAGGTCATC 64687     A    AGTGA   TG
           T                     GGA GACT    TTT  TTGTT
                                ||| ||||    |||  |||||
                                TCT CTGG    AAG  GACAG
                                  A    AGTAG   GT
GAM394  CLIC4    3'  AGCAGTGAGGTTTGTTCTTTCC 25629       ACTAGT    TG
           A                     TGGAAG     GATTT  TTGTT
                                ||||||     |||||  |||||
                                ACCTTT     TTGGA  GACGA
                                   CTTGT_    GT
GAM394  CLTH     3'  AGCAGCAAAATCCTTACTTCCA 23144       ACT  T
                                TGGAAG   AG GATTTTGTTGTT
                                ||||||   || ||||||||||||
                                ACCTTC   TC CTAAAACGACGA
                                   AT_  _
GAM394  COTL1    3'  AGCGACAAGATCGTTAG     87952
                                CTAGTGATTTTGTTGTT
                                ||||||||||||||||
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                                GATTGCTAGAACAGCGA

GAM394  CRIPT    3'  CAGCAACAGTGTAACTAGTCTT 73805          GATT
             TT                  GGAAGACTAGT   TTGTTGTT
                                 ||||||||||    ||||||||
                                 TTTTCTGATCA   GACAACGA
                                       ATGT      CA
GAM394  CRNKL1   3'  ACAATGGAGTCATTTCT    33598    CT      TG
                                 AGA  AGTGATTT  TTGT
                                 |||  ||||||||  ||||
                                 TCT  TTACTGAG  AACA
                                   __      GT
GAM394  CROC4    5'  AGCAGCCTCATTTGTTTTCT  21019       T    TTTT
                                 GGAAGAC AGTGA   GTTGTT
                                 |||||||  |||||   ||||||
                                 TCTTTTG TTACT   CGACGA
                                     T    C___
GAM394  CRSP3    3'  AATGACATATTTAGTCTTC   60633        TGATTT  TG
                                 GAAGACTAG     TGT  TT
                                 |||||||||     |||  ||
                                 CTTCTGATT     ACA  AA
                                       TAT___   GT
GAM394  CUL4A    3'  AATAATAAAGTTTGGTTTGGTT 13148        T___
             TTT                   GAAGACTAG   GATTTTGTTGTT
                                   |||||||||   ||||||||||||
                                   TTTTTGGTT   TTGAAATAATAA
                                       TGGT
GAM394  CYB5-M   3'  ACAACAGACCGTTTTCCA    47565        TAGTGAT
                                 TGGAAGAC      TTTGTTGT
                                 ||||||||      ||||||||
                                 ACCTTTTG      AGACAACA
                                     CC_____
GAM394  CYB5-M   3'  ACAACAGACCGTTTTCCA    94561        TAGTGAT
                                 TGGAAGAC      TTTGTTGT
                                 ||||||||      ||||||||
                                 ACCTTTTG      AGACAACA
                                     CC_____
GAM394  CYorf14  3'  ACAGCAAGATCTTGTCT     37605      TAGT
                                 AGAC    GATTTTGTTGT
                                 ||||    ||||||||||||
                                 TCTG    CTAGAACGACA
                                   TT__
GAM394  DATF1    3'  GACTTCCTGTCACTGTTTTCCA 55005        T     TTT__
                                 TGGAAGAC AGTGAT    GTT
                                 |||||||| ||||||    |||
                                 ACCTTTTG TCACTG    CAG
                                     _     TCCTT
GAM394  DATF1    3'  GACTTCCTGTCACTGTTTTCCA 42069        T     TTT__
                                 TGGAAGAC AGTGAT    GTT
                                 |||||||| ||||||    |||
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                                ACCTTTTG TCACTG    CAG
                                   _     TCCTT
GAM394  DC11     3'  TCCAACAAGGTTATTATTTTTT 39489      C          TT
                                GAAGA TAGTGATTTTGTTG
                                ||||| ||||||||||||||
                                TTTTT ATTATTGGAACAAC
                                   T          CTT
GAM394  DC2      3'  AGTGGCATTTTCTTTTTAGTTT 64262         T__  TTT   TG
           TTCA                   GGAAGACTAG   GA   TGT  TT
                                ||||||||||   ||   |||  ||
                                CTTTTTGATT   CT   ACG  GA
                                      TTT  TTT   GT
GAM394  DC8      3'  AGCAGCAGATGCAGGGTTTTTT 31304        AG  AT
                                GGAAGACT  TG  TTTGTTGTT
                                ||||||||  ||  |||||||||
                                TTTTTTGG  AC  AGACGACGA
                                     G_  GT
GAM394  DCLRE1A  5'  GGCAGTGACTTCGCAGTTTTTT 69165        A    TT TG
                                GGAAGACT GTGA  T  TTGTT
                                ||||||||  ||||  |  |||||
                                TTTTTTGA CGCT  A  GACGG
                                   _    TC GT
GAM394  DDA3     3'  GGCAGCAGGCACCTGGTCTTC  50955         _  AT
                                GAAGACTAG TG  TTTGTTGTT
                                |||||||||  ||  |||||||||
                                CTTCTGGTC AC  GGACGACGG
                                     C  __
GAM394  DDM36    3'  AACAATGTCATTTATTTGGTTT 40567       _____    T    GTT
           TTCA                   AGACTA     GTGAT TTGTT
                                ||||||     ||||| |||||
                                TTTGGT     TACTG AACAA
                                   TTATT     T       T
GAM394  DDR1     3'  AATAATAAAGGTTGAGTTTTCC 8719          AGTGA
           A                     TGGAAGACT     TTTTGTTGTT
                                |||||||||     ||||||||||
                                ACCTTTTGA     GAAATAATAA
                                     GTTG_
GAM394  DDR1     3'  AATAATAAAGGTTGAGTTTTCC 25692         AGTGA
           A                     TGGAAGACT     TTTTGTTGTT
                                |||||||||     ||||||||||
                                ACCTTTTGA     GAAATAATAA
                                     GTTG_
GAM394  DDR1     3'  AATAATAAAGGTTGAGTTTTCC 25701         AGTGA
           A                     TGGAAGACT     TTTTGTTGTT
                                |||||||||     ||||||||||
                                ACCTTTTGA     GAAATAATAA
                                     GTTG_
GAM394  DF       3'  AGCAATGAAGTCATCCACTCC  8630      AGACTA      TG
                                GGA     GTGATTT  TTGTT
                                |||     |||||||  |||||
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                                CCT     TACTGAA  AACGA
                                  CACC__      GT
GAM394  DF      3'  AGCAATGAAGTCATCCACTCC  76328     AGACTA      TG
                                GGA     GTGATTT  TTGTT
                                |||     |||||||  |||||
                                CCT     TACTGAA  AACGA
                                  CACC__      GT
GAM394  DICER1   3'  GGTGAATCACATTTTAGTTTTC 47608        ____      TGTTGTT
           T                     GAAGACTA    GTGATTT
                                |||||||||    |||||||
                                CTTTTGAT    CACTAAG
                                     TTTA      TGG   T
GAM394  DJ1042K10.2 5'  GATAGCAGGATAGGAGACTTCT 31666       A  AGTG
           A                     TGGAAG CT    ATTTTGTTGTT
                                ||||||| ||    ||||||||||
                                ATCTTC GA    TAGGACGATAG
                                   A  GGA_
GAM394  DJ122O8.2 3'  GGTGACAGAGTGAGACAGTCTC 39993      A    A  G__      TG
           CA                     TGGA GACT GT   ATTTTGT  TT
                                |||| |||| ||   |||||||  ||
                                ACCT CTGA CA   TGAGACA  GG
                                  _   _  GAG      GT
GAM394  DJ37E16.5 3'  GATAGTGACCCAGTGGTCTTTT 39731          G  ATT TG
           A                     TGGAAGACTA TG   T  TTGTT
                                |||||||||| ||   |  |||||
                                ATTTTCTGGT AC   A  GATAG
                                     G  CC_ GT
GAM394  DKFZP434A043 3'  GACTTCCAAGTTACTATTTTTT 31192        C        TGTT
           CA                     TGGAAGA TAGTGATTT    GTT
                                |||||||| |||||||||    |||
                                ACTTTTT ATCATTGAA    CAG
                                    T        CCTT
GAM394  DKFZp434C0923 3'  GGCCTCAGGGTCATGAGTTTTC 34216         A        TT
           T                     GGAAGACT GTGATTTTG  GTT
                                |||||||| |||||||||  |||
                                TCTTTTGA TACTGGGAC  CGG
                                    G        TC
GAM394  DKFZP434C1715 3'  AACAGTGCCAAATTGGTTTTTC 86142           GATT__    GTT
           A                     TGGAAGACTAGT     TTGTT
                                ||||||||||||     |||||
                                ACTTTTTGGTTA     GACAA
                                      AACCGT
GAM394  DKFZP434D0127 3'  GACAATGGGGTTTTCTTCC    49586       CTAGT    TG
                                GGAAGA    GATTT  TTGTT
                                ||||||    |||||  |||||
                                CCTTCT    TTGGG  AACAG
                                   T_____    GT
GAM394  DKFZP434D193 3'  AACAGATGAGTCTTTCA     88874         AGTGAT
                                TGGAAGACT     TTTGTT
                                |||||||||     ||||||
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                                ACTTTCTGA     AGACAA
                                     GT____
GAM394  DKFZP434K1772 3'  GGCACCTTCACGGTTTTCT   67715        A   TTT
                                GGAAGACT GTGA   TGTT
                                |||||||| ||||   ||||
                                TCTTTTGG CACT   ACGG
                                     _   TCC
GAM394  DKFZp434K2435 3'  AGCAGCAGAGTTGGTGACTTT  50036     AC  G
                                GAAG  TA TGATTTTGTTGTT
                                ||||  || ||||||||||||||
                                TTTC  GT GTTGAGACGACGA
                                  A_  G
GAM394  DKFZp547I224 3'  AATGACAGGATCAAATTC    39550     GACTAG       TG
                                GAA     TGATTTTGT  TT
                                |||     |||||||||  ||
                                CTT     ACTAGGACA  AA
                                  AA____       GT
GAM394  DKFZp547M236 3'  GATAATGATTTACTTATTTTTC 38035       CT_    TT TG
           CA                     TGGAAGA   AGTGA  T  TTGTT
                                |||||||   |||||  |  |||||
                                ACCTTTT   TCATT  A  AATAG
                                    TAT    T_ GT
GAM394  DKFZP564D0462 3'  GATAATGAGGTAGTGGGTTTTT 70498         AGTG   TG
           TA                     TGGAAGACT    ATTT  TTGTT
                                |||||||||   ||||  |||||
                                ATTTTTTGG    TGGA  AATAG
                                     GTGA    GT
GAM394  DKFZP564D1378 3'  AGCAACAAAGTGAATTGTTCTT 49527      C    G_
           T                     GAAGA TAGT  ATTTTGTTGTT
                                |||||  ||||  ||||||||||
                                TTTCT GTTA  TGAAACAACGA
                                   T    AG
GAM394  DKFZP564I1171 5'  AGTGGCAGGAACGTCTTCC    71583       TA  GA     TG
                                GGAAGAC  GT  TTTTGT  TT
                                |||||||  ||  ||||||  ||
                                CCTTCTG  CA  AGGACG  GA
                                    __  __     GT
GAM394  DKFZP564I122 3'  GGCAGTAGAATCATTTGAACCA 63175     AAGACT
                                TGG     AGTGATTTTGTTGTT
                                |||     ||||||||||||||||
                                ACC     TTACTAAGATGACGG
                                  AAGT__
GAM394  DKFZP564O0463 3'  GATGGCAGAGTTAAGTAATTGC 26278     AAG__   AG       TG
           CA                     TGG    ACT  TGATTTTGT  TT
                                |||    |||  |||||||||  ||
                                ACC    TGA  ATTGAGACG  AG
                                  GTTAA   __       GT
GAM394  DKFZp566H0824 5'  AGCAGATTGTTGTTTTTCCA   34043       C   TG    T
                                TGGAAGA TAG  ATTT GTT
                                ||||||| |||  |||| |||
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                                ACCTTTT GTT  TAGA CGA
                                    T  GT   _
GAM394  DKFZP566J2046 3'  GATTTTGAAATTACTGTTTTCC 48307        T        TT
          A                      TGGAAGAC AGTGATTTTG  GTT
                                 |||||||| ||||||||||  |||
                                 ACCTTTTG TCATTAAAGT  TAG
                                     _        TT   T
GAM394  DKFZP586B2420 5'  AACAACGGGATCATCTCCTTCC 74993      ACTA
                                 GGAAG   GTGATTTTGTTGTT
                                 |||||   ||||||||||||||
                                 CCTTC   TACTAGGGCAACAA
                                   CTC_
GAM394  DKFZP586D0623 3'  AGCAGAATCATCTTCCA     71973        CTAG
                                 TGGAAGA   TGATTTTGTT
                                 |||||||   ||||||||||
                                 ACCTTCT   ACTAAGACGA
                                    _____
GAM394  DKFZP586D0623 3'  AGCAGCAGTCTTTACTTTTCCA 71974       ACT    TT_
                                 TGGAAG  AGTGA  TTGTTGTT
                                 ||||||  |||||  ||||||||
                                 ACCTTT  TCATT  GACGACGA
                                     ___    TCT
GAM394  DKFZP586L151 5'  AGCAGCAAGATGAGTTTTTCA  63960         AGTG
                                 TGGAAGACT   ATTTTGTTGTT
                                 |||||||||   ||||||||||
                                 ACTTTTTGA   TAGAACGACGA
                                      G___
GAM394  DKFZp761D112 3'  ATAATATGTAGTCTTCT     50187         GTGATTT
                                 GGAAGACTA      TGTTGT
                                 |||||||||      ||||||
                                 TCTTCTGAT      ATAATA
                                      GT_____
GAM394  DKFZp761F2014 3'  GGATGCTGGTCTTTT       39540          G
                                 GGAAGACTAGT ATTT
                                 |||||||||| ||||
                                 TTTTCTGGTCG TAGG
                                      _
GAM394  DKFZp761G2113 3'  GGCAGCAGGAGCTGTCCTTTT  69906       AC   GA
                                 GGAAG  TAGT  TTTTGTTGTT
                                 |||||  ||||  ||||||||||
                                 TTTTC  GTCG  AGGACGACGG
                                   CT   __
GAM394  DKFZp761H079 3'  ACCCCTAAAGTCACTAGACTTC 58728       A         TTGTT
          CA                     TGGAAG CTAGTGATTTTG
                                 ||||||| ||||||||||||
                                 ACCTTC GATCACTGAAAT
                                    A          CCCCAA
GAM394  DKFZp761N0624 3'  AGCAGTGAAGGCTGCACTAGTT 50178          AT___  TG
          TTCTA                   AAGACTAGTG    TT  TTGTT
                                 ||||||||||    ||  |||||
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                                TTTTGATCAC    AA  GACGA
                                      GTCGG  GT
GAM394  DKFZp761O0113 5'  AGTGGTTAATCATTAGTCCTTT 37275      _       TTGTTGTT
          T                    GGAAG ACTAGTGATT
                               ||||| ||||||||||
                               TTTTC TGATTACTAA
                                  C        TTGGTGA
GAM394  DSCR1L1  3'  GAGGTTTTTGGTTTTTCA    19498          T
                               TGGAAGACTAG GATTTT
                               |||||||||||| ||||||
                               ACTTTTTGGTT TTGGAG
                                      T
GAM394  DUSP12   3'  GGCAGATTGTTAGTGCTTTCA  23379      _    TG   T
                               TGGAAG ACTAG  ATTT GTT
                               |||||| |||||  |||| |||
                               ACTTTC TGATT  TAGA CGG
                                  G    GT   _
GAM394  EHM2     3'  AATAATTCTTTATTGCTGGTTT 38909         TG  TTT__
          TTCA                   GGAAGACTAG  AT    GTTGTT
                               ||||||||||  ||    ||||||
                               CTTTTTGGTC  TA    TAATAA
                                     GT  TTTCT
GAM394  ELF2     3'  GAGGTTATATAGTTTTTCA   22498          _
                               TGGAAGACTA GTGATTTT
                               |||||||||| ||||||||
                               ACTTTTTGAT TATTGGAG
                                     A
GAM394  ENPP4    3'  ATCTTTTGGTCTTTCA      30047          T_
                               TGGAAGACTAG  GAT
                               ||||||||||  |||
                               ACTTTCTGGTT  CTA
                                      TT
GAM394  EPS8R1   3'  AATAGCGGAAGTCGATCTTCT  34801       CTAG      _
                               GGAAGA   TGATTTT GTTGTT
                               ||||||   ||||||| ||||||
                               TCTTCT   GCTGAAG CGATAA
                                  A___      G
GAM394  EPS8R1   3'  AATAGCGGAAGTCGATCTTCT  55699       CTAG      _
                               GGAAGA   TGATTTT GTTGTT
                               ||||||   ||||||| ||||||
                               TCTTCT   GCTGAAG CGATAA
                                  A___      G
GAM394  EPS8R1   3'  AATAGCGGAAGTCGATCTTCT  57600       CTAG      _
                               GGAAGA   TGATTTT GTTGTT
                               ||||||   ||||||| ||||||
                               TCTTCT   GCTGAAG CGATAA
                                  A___      G
GAM394  EZF-2    3'  GTAATAAAGTCACTGTGT    37104    _         GTT
                               AC TAGTGATTTTGTT
                               || ||||||||||||
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                                TG GTCACTGAAATAA
                                 T          TGA
GAM394  F23149_1  3'  GCAGCAAAGCACTTTTCT   69983    CT   A
                                AGA  AGTG TTTTGTTGT
                                |||  |||| |||||||||
                                TCT  TCAC GAAACGACG
                                  TT   _
GAM394  FABP7     5'  AAATCACTGGATTTTT     7541      _
                                GAAGA CTAGTGATTT
                                ||||| ||||||||||
                                TTTTT GGTCACTAAA
                                   A
GAM394  FADS1     3'  GGTGGCAGGATTACTACTTT  25483    AC        TG
                                GAAG  TAGTGATTTTGT  TT
                                ||||  ||||||||||||  ||
                                TTTC  ATCATTAGGACG  GG
                                  __         GT
GAM394  FBXL9     5'  GATGGCGGAGTCGCTGCCCC  24083   AAGAC       TG
                                GG    TAGTGATTTTGT  TT
                                ||    ||||||||||||  ||
                                CC    GTCGCTGAGGCG  AG
                                 CC___         GT
GAM394  FBXO21    3'  TCTCTATAAATCATTAGTTTTC 53241            TGTTGTT
                  TA                TGGAAGACTAGTGATTT
                                    ||||||||||||||||
                                    ATCTTTTGATTACTAAA
                                              TATCTCTA
GAM394  FENS-1    3'  GTAACAGTTTACTGGTTGTTCC 40441     _      TT    GTT
                  A                 TGGAA GACTAGTGA  TTGTT
                                    ||||| |||||||||  |||||
                                    ACCTT TTGGTCATT  GACAA
                                      G       T_    TGA
GAM394  FER1L4    3'  GTAATAAGATCAGTATCTTCT  47360      C  G       GTT
                                GGAAGA TA TGATTTTGTT
                                |||||| || ||||||||||
                                TCTTCT AT ACTAGAATAA
                                   _ G        TGG
GAM394  FJX1      3'  GATGGTGAGATCACTGTTCCA  26787     GAC       TG TG
                                TGGAA   TAGTGATTT  T  TT
                                |||||   |||||||||  |  ||
                                ACCTT   GTCACTAGA  G  AG
                                   ____       GT GT
GAM394  FKBP14    3'  GGCGGCAGAATCACTTGAACCC 35626    AAGACT
                  G                 TGG     AGTGATTTTGTTGTT
                                    |||     ||||||||||||||
                                    GCC     TCACTAAGACGGCGG
                                      CAAGT_
GAM394  FLJ10103  3'  AGCCAGATTATCTGGTCTTCCA 35816          _     T
                                TGGAAGACTAG TGATTT GTT
                                |||||||||| |||||| |||
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                                ACCTTCTGGTC ATTAGA CGA
                                      T     C
GAM394  FLJ10244 3' GACACATCGTTGTTTGTTTTTC 35941       T  TG  TT   T
            A                    TGGAAGAC AG  AT  TGT GTT
                                 |||||||| ||  ||  ||| |||
                                 ACTTTTTG TT  TG  ACA CAG
                                      T  GT  CT  _
GAM394  FLJ10292 3' AAATCTTGGTTTTTCA     35974          T
                                 TGGAAGACTAG GATTT
                                 |||||||||||| |||||
                                 ACTTTTTGGTT CTAAA
                                                _
GAM394  FLJ10314 3' GACTCCGAATTACTGTTCTTCC 36012       C       T TT
            A                    TGGAAGA TAGTGATTT G  GTT
                                 ||||||| ||||||||| |  |||
                                 ACCTTCT GTCATTAAG C  CAG
                                      T       _ CT
GAM394  FLJ10352 3' AGACAAAACCGCCTTCCA    49556      ACTA  A    TG
                                 TGGAAG   GTG TTTTGT  T
                                 ||||||   ||| ||||||  |
                                 ACCTTC   CGC AAAACA  A
                                     ____  C     GT
GAM394  FLJ10468 3' AGCAGTGAGGTCCTCATTCTCC 36142     AG CT  T    TG
            A                    TGGA  A  AG GATTT  TTGTT
                                 ||||  |  || |||||  |||||
                                 ACCT  T  TC CTGGA  GACGA
                                   CT AC  _    GT
GAM394  FLJ10493 3' AGTGGCTACTGTTTTAGTTTTC 36186         TGATTTT  TG
            TA                    TGGAAGACTAG      GT  TT
                                  ||||||||||      ||  ||
                                  ATCTTTTGATT      CG  GA
                                        TTGTCAT  GT
GAM394  FLJ10618 3' GACAATGAGATCGTCAGT    36345    AG     TG
                                 ACT  TGATTT  TTGTT
                                 |||  ||||||  |||||
                                 TGA  GCTAGA  AACAG
                                   CT     GT
GAM394  FLJ10619 3' TCTGCAAAACATTGGTTTTCTA 36353          A     TGTT
                                 TGGAAGACTAGTG TTTTGT
                                 |||||||||||| ||||||
                                 ATCTTTTGGTTAC AAAACG
                                        _     TCTC
GAM394  FLJ10716 3' GGCAGTGAAGAGAACAGGTCTT 36485        A  GA_   TG
            TCA                   TGGAAGACT GT   TTT  TTGTT
                                  ||||||||| ||   |||  |||||
                                  ACTTTCTGG CA   GAA  GACGG
                                       A  AGA   GT
GAM394  FLJ10829 3' AACAGTGGGGAGCAACTTTTCC 36706       CTA  GA   TG
            A                    TGGAAGA   GT  TTT  TTGTT
                                 |||||||   ||  |||  |||||
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                                ACCTTTT  CG  GGG  GACAA
                                    CAA  A_  GT
GAM394  FLJ10961  3'  AGCAATAAAATAATTGTCTTGC 63484    _   T  G
          CA                  TGG AAGAC AGT ATTTTGTTGTT
                              ||| ||||| ||| ||||||||||
                              ACC TTCTG TTA TAAAATAACGA
                                G   _  A
GAM394  FLJ10989  3'  TAAGGCTTCATCACTGGATTTC 36952     A     TTT  GTT
          T                   GGAAG CTAGTGAT  GTT
                              ||||| ||||||||  |||
                              TCTTT GGTCACTA  CGG
                                A      CTT  AATA
GAM394  FLJ10996  5'  GCGGCAGAGGGAGTTTCC   38776    A   AGTGA
                              GGA GACT    TTTTGTTGT
                              ||| ||||    |||||||||
                              CCT TTGA    GAGACGGCG
                                _   GG___
GAM394  FLJ10997  3'  AACAAACTATTAGTCTGCCA  36956    A      AT
                              TGG AGACTAGTG  TTTGTT
                              ||| |||||||||  ||||||
                              ACC TCTGATTAT  AAACAA
                                G       C_
GAM394  FLJ11021  3'  GATAATAAAAATGGTTTTCT  66442       GTGA
                              GGAAGACTA   TTTTGTTGTT
                              |||||||||   ||||||||||
                              TCTTTTGGT   AAAATAATAG
                                   A___
GAM394  FLJ11082  3'  GGCAACACATCTAGTTTTTCA  37035        _ ATTT
                              TGGAAGACTAG TG   TGTTGTT
                              |||||||||||| ||   |||||||
                              ACTTTTTGATC AC   ACAACGG
                                     T ____
GAM394  FLJ11132  3'  GACGCTCATGAGTTTTTCA   37092       A   TTT
                              TGGAAGACT GTGA  TGTT
                              ||||||||| ||||  ||||
                              ACTTTTTGA TACT  GCAG
                                   G  C__
GAM394  FLJ11155  3'  AATGACAGGCATGCTAGTTTTT 37117         AT   TG
          T                   GGAAGACTAGTG  TTTGT  TT
                              |||||||||||  |||||  ||
                              TTTTTTGATCGT  GGACA  AA
                                     AC    GT
GAM394  FLJ11722  5'  GATGGCAGATGTGGTTCTCCA  46392    AG   GTGAT   TG
                              TGGA  ACTA    TTTGT  TT
                              ||||  ||||    |||||  ||
                              ACCT  TGGT    AGACG  AG
                                CT   GT___    GT
GAM394  FLJ11783  3'  AGTGGCGTTGCGCATTTGTTTT 46029       T   ATTT_  TG
          CCA                 TGGAAGAC AGTG    TGT  TT
                              ||||||| ||||    |||  ||
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                                ACCTTTTG TTAC    GCG  GA
                                    T   GCGTT   GT
GAM394  FLJ11996  3' GGTGACAGAGCAAGAGTCTGTC 46442   GA    AG  A    TG
           A                 TG  AGACT  TG TTTTGT  TT
                             ||  |||||  || ||||||  ||
                             AC  TCTGA  AC GAGACA  GG
                              TG    GA  _    GT
GAM394  FLJ12076  3' GATGACAATTTTGTGAGTTTTT 47235        A TG TT   TG
           CA                 TGGAAGACT G  A  TTGT  TT
                             |||||||||  |  |  ||||  ||
                             ACTTTTTGA T  T  AACA  AG
                                 G GT TT   GT
GAM394  FLJ12294  3' AATAATGTCAGTGCTGTTTTCC 47004       __  G   T   GTT
           A                 TGGAAGAC  TA TGAT TTGTT
                             ||||||||  || |||| |||||
                             ACCTTTTG  GT ACTG AATAA
                                 TC  G   T
GAM394  FLJ12572  5' AACGATGGAGTCTCGCTCTGTC 43240    T_  __   TG
                             GAC  AGT  GATTT  TTGTT
                             |||  |||  |||||  |||||
                             CTG  TCG  CTGAG  AGCAA
                               TC   CT    GT
GAM394  FLJ12587  5' GCGGCGGGGATCGTCTCC    42497    A   TAGT    _
                             GGA GAC    GATTTT GTTGT
                             ||| |||    |||||| |||||
                             CCT CTG    CTAGGG CGGCG
                              _  _____     G
GAM394  FLJ12604  3' AGTGATGGGATCATCTCTCCCA 64437    A   CTA     TG TG
                             TGG AGA   GTGATTT  T  TT
                             ||| |||   |||||||  |  ||
                             ACC TCT   TACTAGG  A  GA
                               C   C__      GT GT
GAM394  FLJ12666  3' GGCAGTAGAATCACTTGAACCC 44769    AAGACT
                             GG     AGTGATTTTGTTGTT
                             ||     ||||||||||||||
                             CC     TCACTAAGATGACGG
                              CAAGT_
GAM394  FLJ12688  3' AACAACAGGATATTTCTCTCT  73177    A  CT   A
                             GGA GA  AGTG TTTTGTTGTT
                             ||| ||  |||| ||||||||||
                             TCT CT  TTAT AGGACAACAA
                               _ CT   _
GAM394  FLJ12747  3' AGCAATACCAACCATTGTCTTT 49709       T   ATTT_
           TA                  TGGAAGAC AGTG    TGTTGTT
                             ||||||||  ||||    |||||||
                             ATTTTCTG TTAC    ATAACGA
                                 _   CAACC
GAM394  FLJ12770  3' GGCAGTTATTGCTTTAGTCTTT 49741       __  TG  T_   GTT
           CA                  GGAAGACT  AG  AT  TTGTT
                             ||||||||  ||  ||  |||||
```

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                                CTTTCTGA  TC  TA  GACGG
                                    TT  GT  TT
GAM394  FLJ12783  3'  AATGGCAGAAGAGAGGGTTTTC 48672       AGTGA    TG
          T                  GGAAGACT    TTTTGT  TT
                             ||||||||    ||||||  ||
                             TCTTTTGG    AAGACG  AA
                                 GAGAG     GT
GAM394  FLJ12785  3'  GGCAGCAAAATGGATTTCTCC  45854    A  CTAGTG
                             GGA GA     ATTTTGTTGTT
                             ||| ||     ||||||||||
                             CCT CT     TAAAACGACGG
                               _  TTAGG_
GAM394  FLJ12838  3'  AATAACAAAATCACTGTACCTT 44966      AC_
          CC                   GGAAG   TAGTGATTTTGTTGTT
                             |||||   ||||||||||||||||
                             CCTTC   GTCACTAAAACAATAA
                                CAT
GAM394  FLJ13072  3'  AACAATTAGTCATTGGTTTTCT 89796           TT
                             GGAAGACTAGTGATT  GTTGTT
                             ||||||||||||||  ||||||
                             TCTTTTGGTTACTGA  TAACAA
                                      T_
GAM394  FLJ13162  3'  ACGATGGGGTCGGGGTC    46549     AG    TG
                             GACT  TGATTT  TTGT
                             ||||  ||||||  ||||
                             CTGG  GCTGGG  AGCA
                               G_     GT
GAM394  FLJ13220  3'  ATAACCTACTAGTCTTTC    41632          ATTTT
                             GGAAGACTAGTG    GTTGT
                             ||||||||||||    |||||
                             CTTTCTGATCAT    CAATA
                                    C____
GAM394  FLJ13315  3'  GGCGGCAGGATCACTTGAACCA 46571    AAGACT
                             TGG     AGTGATTTTGTTGTT
                             |||     ||||||||||||||||
                             ACC     TCACTAGGACGGCGG
                               AAGT__
GAM394  FLJ13612  3'  AGTGACAGATCCAGGGCCTTTC 47311      A  AG  AT    TG
          A                   TGGAAG CT  TG  TTTGT  TT
                             ||||||  ||  ||  |||||  ||
                             ACTTTC GG  AC  AGACA  GA
                                C  G_  CT    GT
GAM394  FLJ14001  3'  AACAATTGTAATAGTTTTTCA  45166        G  ATT
                             TGGAAGACTA TG   TTGTT
                             ||||||||||  ||   |||||
                             ACTTTTTGAT AT   AACAA
                                    A  GTT
GAM394  FLJ14007  3'  AAATTATGAGTTTTCTA     45207         A
                             TGGAAGACT GTGATTT
                             |||||||||  |||||||
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                                ATCTTTTGA TATTAAA
                                     G
GAM394  FLJ14281  3'  AACTATTTGATTTCTAGTCTTC 46211          T   TT  T
              T                   GGAAGACTAG GATT  GT GTT
                                  |||||||||| ||||  || |||
                                  TCTTCTGATC TTAG  TA CAA
                                       T   TT  T
GAM394  FLJ14356  5'  GGCAGTGGGGCTCAGGTTTCCA 48034      A   AG  _  TG
                                  TGGA GACT  TGA TTT  TTGTT
                                  |||| ||||  ||| |||  |||||
                                  ACCT TTGG  ACT GGG  GACGG
                                    _   __  C  GT
GAM394  FLJ14511  3'  CGGGATTATTGCTCTTCT    52362        C
                                  GGAAGA TAGTGATTTTG
                                  |||||| ||||||||||
                                  TCTTCT GTTATTAGGGC
                                     C
GAM394  FLJ14642  3'  GCAACAAGGTTCTGCTCCA   51502      AGAC  T
                                  TGGA   TAG GATTTTGTTGT
                                  ||||   ||| ||||||||||
                                  ACCT   GTC TTGGAACAACG
                                    C___  _
GAM394  FLJ14743  3'  GGCAGCACAGCCCCACTGTGTC 68065       _    ATTT__
              TTCC                 AAGAC TAGTG     TGTTGTT
                                   ||||| |||||     |||||||
                                   TTCTG GTCAC     ACGACGG
                                     T    CCCGAC
GAM394  FLJ20004  3'  GAATCACATGGTCTTCC     95293         _
                                  GGAAGACTA GTGATTT
                                  ||||||||| |||||||
                                  CCTTCTGGT CACTAAG
                                       A
GAM394  FLJ20054  3'  AAGTTATTAGTGTTCT      38780      G
                                  GGAA ACTAGTGATTT
                                  |||| ||||||||||
                                  TCTT TGATTATTGAA
                                    G
GAM394  FLJ20136  3'  AATAGCTAGTATTGGGTTTTCT 34608         AGTG  TT
              A                    TGGAAGACT   ATT  GTTGTT
                                   |||||||||   |||  ||||||
                                   ATCTTTTGG   TGA  CGATAA
                                       GTTA  T_
GAM394  FLJ20171  3'  AATAATAAAATCACAATCTT   34674      CTA
                                  AAGA   GTGATTTTGTTGTT
                                  ||||   ||||||||||||||
                                  TTCT   CACTAAAATAATAA
                                    AA_
GAM394  FLJ20190  5'  GATGATAAAGTCTTTGCTTC   34703      ACTAGT       TG
                                  GAAG     GATTTTGT  TT
                                  ||||     ||||||||  ||
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                                CTTC     CTGAAATA  AG
                                  GTTT__       GT
GAM394  FLJ20208  3' ACAACAAAAGTGTTTTCC    34739       TAGTGA
                                GGAAGAC     TTTTGTTGT
                                |||||||     |||||||||
                                CCTTTTG     AAAACAACA
                                   TG____
GAM394  FLJ20274  3' GGTGATGAAGAACTTCAGTCTT 62645        __  GA   TG TG
          CT                     GGAAGACT  AGT  TTT  T  TT
                                |||||||| |||  |||  |  ||
                                TCTTCTGA  TCA  GAA  A  GG
                                    CT   A_   GT GT
GAM394  FLJ20296  3' GGCAATGGAATCACTGCTTCCA 34891       AC       TG
                                TGGAAG  TAGTGATTT  TTGTT
                                ||||||  |||||||||  |||||
                                ACCTTC  GTCACTAAG  AACGG
                                   __       GT
GAM394  FLJ20298  3' GTAACAGAATTGCTGACATCT  34903    C__  TG      GTT
                                AGA   TAG  ATTTTGTT
                                |||   |||  ||||||||
                                TCT   GTC  TAAGACAA
                                  ACA   GT       TGG
GAM394  FLJ20312  3' CCTTATAGATTGTTGGCTTTCA 34926      A   TG   TGTTGTT
                                TGGAAG CTAG  ATTT
                                |||||| ||||  ||||
                                ACTTTC GGTT  TAGA
                                   _   GT    TATTCCA
GAM394  FLJ20313  5' ACGATAAGATCAATTC     34930    CTAG
                                GA   TGATTTTGTTGT
                                ||   ||||||||||||
                                CT   ACTAGAATAGCA
                                 TA__
GAM394  FLJ20399  3' AGTGACAGGGTCAAGTTCTCT  35124    AG   AG       TG
                                GGA  ACT  TGATTTTGT  TT
                                |||  |||  |||||||||  ||
                                TCT  TGA  ACTGGGACA  GA
                                  CT   __       GT
GAM394  FLJ20425  5' GGCAATGTTTGCTGTCTTCCA  35151       T  TG TT_
                                TGGAAGAC AG  A   TTGTT
                                |||||||| ||  |  |||||
                                ACCTTCTG TC  T   AACGG
                                    _  GT TGT
GAM394  FLJ20432  3' GATAATAAAAAGAGTTGTCCA  35161     A   AGTGA
                                TGGA GACT    TTTTGTTGTT
                                |||| ||||    ||||||||||
                                ACCT TTGA    AAAATAATAG
                                  G   GA___
GAM394  FLJ20456  5' GCGGCGGAGGTGGCTTCT    35213      A  GTGA
                                GGAAG CTA    TTTTGTTGT
                                ||||| |||   |||||||||
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                                TCTTC GGT    GAGGCGGCG
                                  _  G___
GAM394  FLJ20507  3'  AACCGGAGGTCCACTGGTTTTC 35269          _    GTTGTT
            TA                   TGGAAGACTAGTG ATTTT
                                 |||||||||||| |||||
                                 ATCTTTTGGTCAC TGGAG
                                       C    GCCAA
GAM394  FLJ20507  3'  AACCGGAGGTCCACTGGTTTTC 60204          _    GTTGTT
            TA                   TGGAAGACTAGTG ATTTT
                                 |||||||||||| |||||
                                 ATCTTTTGGTCAC TGGAG
                                       C    GCCAA
GAM394  FLJ20519  3'  AGCAGCCTCTGGCTTGTTTTCT 35343       T  GATTTT
            A                    TGGAAGAC AGT    GTTGTT
                                 |||||||| |||    ||||||
                                 ATCTTTTG TCG    CGACGA
                                      T  GTCTC_
GAM394  FLJ20527  3'  AGGCAGGATGTCTTTTA    35351       TAGTG    TG
                                 TGGAAGAC    ATTTTGT  T
                                 ||||||||    |||||||  |
                                 ATTTTCTG    TAGGACG  A
                                      _____     GT
GAM394  FLJ20558  3'  AGCAGTGTCACTAGTTTTTC  35396          T
                                 GGAAGACTAGTGAT TTGTT
                                 |||||||||||||| |||||
                                 CTTTTTGATCACTG GACGA
                                       T
GAM394  FLJ20618  3'  TTATTCTTAGATCATTGGTTTT 35460           TGTTGTT
            CCA                   TGGAAGACTAGTGATTT
                                  ||||||||||||||||
                                  ACCTTTTGGTTACTAGA
                                        TTCTTATTC
GAM394  FLJ20640  5'  AGCGACGAGGAGACGGTCTTT  35487       A  GA
                                 GAAGACT GT  TTTTGTTGTT
                                 |||||||  ||  ||||||||||
                                 TTTCTGG CA  GGAGCAGCGA
                                    _  GA
GAM394  FLJ20725  3'  GGCAACAAAAGGACCGGTTTCT 35611     A  TA  GA
            A                     TGGA GAC  GT  TTTTGTTGTT
                                  |||| |||  ||  ||||||||||
                                  ATCT TTG  CA  AAAACAACGG
                                    _  GC  GG
GAM394  FLJ20793  3'  GATAATGGGGAAAAAAAGTCTT 91806       AGTGA_  TG
            CT                    GGAAGACT     TTT  TTGTT
                                  ||||||||     |||  |||||
                                  TCTTCTGA     GGG  AATAG
                                       AAAAAA   GT
GAM394  FLJ21302  3'  GACAACAAAACCCATTCTTTCA 43214       CTA  A_
                                 TGGAAGA  GTG  TTTTGTTGTT
                                 |||||||  |||  ||||||||||
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                                ACTTTCT  TAC  AAAACAACAG
                                   ___  CC
GAM394  FLJ22054  3' GTAATGGAATCACTCATGTTCA 94401     AGACT      TG  GTT
                                TGGA    AGTGATTT  TT
                                ||||    ||||||||  ||
                                ACTT    TCACTAAG  AA
                                  GTAC_      GT  TGA
GAM394  FLJ22169  5' GATGGTGAACCACAGTCTTC  44003       A  AT  TG TG
                                GAAGACT GTG  TT  T  TT
                                ||||||| |||  ||  |  ||
                                CTTCTGA CAC  AA  G  AG
                                   _  C_  GT GT
GAM394  FLJ22215  3' AGCGACAAGGTTGTGATCCA  96832     AGACTA TG
                                TGGA     G  ATTTTGTTGTT
                                ||||     |  ||||||||||
                                ACCT     T  TGGAACAGCGA
                                  AG____ GT
GAM394  FLJ22313  3' GTAACAATATTGGTCTTCCA  42343          ATT    GTT
                                TGGAAGACTAGTG  TTGTT
                                ||||||||||||  |||||
                                ACCTTCTGGTTAT  AACAA
                                       ___   TGC
GAM394  FLJ22318  3' AGTGGCAAGGGATTTGGTCTTC 42830        TGA    TG
                                GAAGACTAG  TTTTGT  TT
                                |||||||||  ||||||  ||
                                CTTCTGGTT  GGAACG  GA
                                     TAG    GT
GAM394  FLJ22347  3' GGCAATAAAGCTGCTAGTTT  43083        GA
                                AGACTAGT  TTTTGTTGTT
                                ||||||||  ||||||||||
                                TTTGATCG  GAAATAACGG
                                    TC
GAM394  FLJ22389  5' GGCAGTGGGAACTTCAGCTGGT 46236       _  ___  TG
           CTTC                   AGACTAG TGA  TTT  TTGTT
                                ||||||| |||  |||  |||||
                                TCTGGTC ACT  AGG  GACGG
                                   G  TCA  GT
GAM394  FLJ22415  3' AACTTATTGGATTATTAGTTAT 91489     A        TT  T_
           TCA                    TGGA GACTAGTGATT  GT  GTT
                                |||| ||||||||||  ||  |||
                                ACTT TTGATTATTAG  TA  CAA
                                  A        GT  TT
GAM394  FLJ22569  3' GACAATAAAAGGATGGTGTTCT 43678      G   GTGA
           A                     TGGAA ACTA   TTTTGTTGTT
                                ||||| ||||   ||||||||||
                                ATCTT TGGT   AAAATAACAG
                                  G   AGG_
GAM394  FLJ22969  3' AACAGTGGCCCCCTGCATTAGT 68639        ATT____ TG
           TTTCT                  AGACTAGTG     T  TTGTT
                                |||||||||     |  |||||
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                                TTTGATTAC      G  GACAA
                                     GTCCCCC GT
GAM394  FLJ23040  3' AGTGGTGAAATTACAGCTCACA 47196    GA  A  A      TG TG
                                TG  AG CT GTGATTT  T  TT
                                ||  || || |||||||  |  ||
                                AC  TC GA CATTAAA  G  GA
                                 AC  _  _      GT GT
GAM394  FLJ23053  5' ACGGCGAAATTGGTGTTT    43260     G   AGT
                                GAA ACT   GATTTTGTTGT
                                |||  |||   ||||||||||
                                TTT TGG   TTAAAGCGGCA
                                  G  ___
GAM394  FLJ23056  3' GGCAGCAAGCAGGGACTTTCA  44723       A  AG  AT
                                TGGAAG CT  TG  TTTGTTGTT
                                ||||||  ||  ||  |||||||||
                                ACTTTC GG  AC  GAACGACGG
                                    A  G_  __
GAM394  FLJ23129  3' GATGGCAAAAGAGAAATACTAG 45429        A_____     TG
           TTTCTA                GACTAGTG     TTTTGT  TT
                                |||||||||     ||||||  ||
                                TTGATCAT     AAAACG  AG
                                     AAAGAG     GT
GAM394  FLJ23151  3' ACAGTGAAGTCTCCTTCC    45477      ACTAGT    TG
                                GGAAG     GATTT  TTGT
                                |||||     |||||  ||||
                                CCTTC     CTGAA  GACA
                                   CT_____     GT
GAM394  FLJ23186  3' AGCAACTGTATTGGTTGTCTA  60401      A       ATTTT
                                TGGA GACTAGTG     GTTGTT
                                ||||  |||||||||     ||||||
                                ATCT TTGGTTAT     CAACGA
                                  G       GT___
GAM394  FLJ23186  3' AGTGATGGAGGCTGGTCTCT   60402     A      GA   TG TG
                                GGA GACTAGT  TTT  T  TT
                                |||  |||||||  |||  |  ||
                                TCT CTGGTCG  GAG  A  GA
                                  _      __   GT GT
GAM394  FLJ23186  3' GAGGTCACTGGTATTCT     60403      G
                                GGAA ACTAGTGATTTT
                                ||||  ||||||||||||
                                TCTT TGGTCACTGGAG
                                  A
GAM394  FLJ23209  3' AGCAGCAAGATCACTTGAGCCC 46052     AAGACT
             A                   TGG     AGTGATTTTGTTGTT
                                |||     ||||||||||||||||
                                ACC     TCACTAGAACGACGA
                                  CGAGT_
GAM394  FLJ23259  5' AGCAACAGGAAGATGTCTT    45308       TAGTGA
                                AAGAC     TTTTGTTGTT
                                |||||     ||||||||||
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                                TTCTG     AGGACAACGA
                                   TAGA__
GAM394  FLJ23306  5'  GCAGCAGGTGGCTCTTCT    44559       CTA  G    T
                                GGAAGA   GT ATTT GTTGT
                                ||||||   || |||| |||||
                                TCTTCT   CG TGGA CGACG
                                   ___  G   _
GAM394  FLJ23510  5'  AATCACAGTCTTCTA       45278          A
                                TGGAAGACT GTGATT
                                ||||||||| ||||||
                                ATCTTCTGA CACTAA
                                      _
GAM394  FLJ30046  3'  GACAGCAGAATTAAATGGTC   58101      G_
                                GACTA  TGATTTTGTTGTT
                                |||||  ||||||||||||
                                CTGGT  ATTAAGACGACAG
                                   AA
GAM394  FLJ31737  3'  GAGATAAAATTGCTTGTCTTTC 58695        T  TG      GTT
          A                      TGGAAGAC AG  ATTTTGTT
                                |||||||| ||  ||||||||
                                ACTTTCTG TC  TAAAATAG
                                     T  GT       AG
GAM394  FLJ31762  3'  GGTGGCGGGGGGTCGGGGGTCTT 58144         AG     _  TG
          CT                     GGAAGACT  TGATTTT GT  TT
                                |||||||  ||||||| ||  ||
                                TCTTCTGG  GCTGGGG CG  GG
                                     GG      G  GT
GAM394  FLJ32421  5'  GGCGCCGTCCTGGTTTTCC    58449         T   TT
                                GGAAGACTAG GAT  TGTT
                                |||||||||| |||  ||||
                                CCTTTTGGTC CTG  GCGG
                                      _  CC
GAM394  FLJ32915  3'  AACAACAGACCTGGTCTTTC   58789         TGAT
                                GGAAGACTAG    TTTGTTGTT
                                ||||||||||    |||||||||
                                CTTTCTGGTC    AGACAACAA
                                     C___
GAM394  FOXD4     5'  GACGGTAAAATCGATGTC    82749     TAG      TT
                                GAC   TGATTTTG  GTT
                                |||   ||||||||  |||
                                CTG   GCTAAAAT  CAG
                                  TA_      GG
GAM394  FOXP1     3'  AGCAGTGAAATTGTTCTCCA  51062     AG  TAGT    TG
                                TGGA  AC    GATTT  TTGTT
                                ||||  ||    |||||  |||||
                                ACCT  TG    TTAAA  GACGA
                                  CT  ____     GT
GAM394  FUK       5'  GACAGTGTCCAGGTCTTTCA   58975         AGT   T
                                TGGAAGACT   GAT TTGTT
                                |||||||||   ||| |||||
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                                ACTTTCTGG  CTG GACAG
                                     AC_  T
GAM394  FUSIP1   3'  AACACTTGTTAGTTTTCC    53954         TG TTT
                                GGAAGACTAG  A  TGTT
                                ||||||||||  |  ||||
                                CCTTTTGATT  T  ACAA
                                      GT C__
GAM394  G2       3'  AGTGGTAGAACCACAGTCTTCC 66657        A  A    TG
                                GGAAGACT GTG TTTTGT  TT
                                |||||||| ||| ||||||  ||
                                CCTTCTGA CAC AAGATG  GA
                                     _  C     GT
GAM394  G2       3'  GCAATGGGTGAGTCTTTC    66660        AGTGAT  TG
                                GGAAGACT     TT  TTGT
                                ||||||||     ||  ||||
                                CTTTCTGA     GG  AACG
                                     GT____  GT
GAM394  GAB3     3'  GGGCAGAATCTTACTCCA    54632     AGAC  T      TG
                                TGGA   TAG GATTTTGT  T
                                ||||   ||| ||||||||  |
                                ACCT   ATT CTAAGACG  G
                                  C___  _      GT
GAM394  GOLGA3   3'  AACAACGTAACTTGGTTTTC  19712        _ GATTT
                                GAAGACTA GT    TGTTGTT
                                |||||||| ||    |||||||
                                CTTTTGGT CA    GCAACAA
                                     T  AT___
GAM394  GOLPH3   3'  GATGGCAAAATCGACCTCTTGT 42113     T ____       TG
            C                    GAC AG   TGATTTTGT  TT
                                ||| ||   |||||||||  ||
                                CTG TC   GCTAAAACG  AG
                                  T  TCCA       GT
GAM394  GPNMB    3'  AAGATGAGGTCCCTGGTTTTTC 10239          T    TG  GTT
            A                    TGGAAGACTAG GATTT  TT
                                ||||||||||| |||||  ||
                                ACTTTTTGGTC CTGGA  AG
                                      C    GT  AA
GAM394  GREAT    3'  GGATCACTGGACTTTCA     55483       A
                                TGGAAG CTAGTGATTT
                                ||||||  ||||||||||
                                ACTTTC GGTCACTAGG
                                   A
GAM394  GREB1    3'  ACAGCGGCGAGTTTTCT     27858        A  GATTT
                                GGAAGACT GT    TGTTGT
                                |||||||| ||    ||||||
                                TCTTTTGA CG    GCGACA
                                     G  _____
GAM394  GREB1    3'  AGATAGGGTCATGGTT      72404       G       TG
                                GACTA TGATTTTGT  T
                                |||||  |||||||||  |
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                                TTGGT ACTGGGATA  A
                                  _       GT
GAM394  GS3955   3'  GGCAGCGGAAAGGAGTTCTTCC 41318       _  AGTGA
                                GGAAGA CT    TTTTGTTGTT
                                |||||| ||    ||||||||||
                                CCTTCT GA    AAGGCGACGG
                                   T  GGA__
GAM394  GW112    3'  AAAATTAATAGTTTTCTA    21181          G
                                TGGAAGACTA TGATTTT
                                |||||||||| |||||||
                                ATCTTTTGAT ATTAAAA
                                      A
GAM394  H2AFJ    3'  AATGATGGAATTACTTCTCCCA 36837    A   CT       TG TG
                                TGG AGA  AGTGATTT  T  TT
                                ||| |||  ||||||||  |  ||
                                ACC TCT  TCATTAAG  A  AA
                                  C  __       GT GT
GAM394  HBXAP    5'  AACAAATATAGTCTTCT     33415         GTGAT
                                GGAAGACTA    TTTGTT
                                |||||||||    ||||||
                                TCTTCTGAT    AAACAA
                                     AT___
GAM394  HCC-4    3'  AATGGTAAATTAAGTTGTCTTC 56816         TAG_     T TT
           CA                     TGGAAGAC    TGATTT G  GTT
                                  ||||||||    |||||| |  |||
                                  ACCTTCTG    ATTAAA T  TAA
                                       TTGA     _ GG
GAM394  HERC3    3'  AATTGCTAAATTGGTAGTTTTT 27511          G     T  T
           CA                     TGGAAGACTA TGATTT GT GTT
                                  |||||||||| |||||| || |||
                                  ACTTTTTGAT GTTAAA CG TAA
                                        G     T  T
GAM394  HES2     3'  AATAACAAGATAAATGCCTTCC 38852        ACTAGTG
           A                       TGGAAG      ATTTTGTTGTT
                                   ||||||      ||||||||||
                                   ACCTTC      TAGAACAATAA
                                      CGTAAA_
GAM394  HIC      5'  AGCAACAGAGGGAGAAGTGTTT 67445       G   AGTGA
           CA                     TGGAA ACT    TTTTGTTGTT
                                  ||||| |||    ||||||||||
                                  ACTTT TGA    GAGACAACGA
                                     G   AGAGG
GAM394  HN1L     3'  GATGGCAAAGGTGGTGGTGCTT 57997       _   G GA     TG
           TCA                      TGGAAG ACTA T  TTTTGT  TT
                                    |||||| |||| |  ||||||  ||
                                    ACTTTC TGGT G  GAAACG  AG
                                       G   G TG     GT
GAM394  HN1L     3'  GTAGCAAAGTCACACCTGTCCA 58000      AGACTA         GTT
                                TGGA     GTGATTTTGTT
                                ||||     ||||||||||
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                                ACCT     CACTGAAACGA
                                  GTCCA_         TGA
GAM394  HNRPA0   5'  AGCGGTGGCCTTGGTTGTCTTC 22319        TAGTGATT TG
           CA                    TGGAAGAC       T  TTGTT
                                 ||||||||       |  |||||
                                 ACCTTCTG       G  GGCGA
                                     TTGGTTCC GT
GAM394  HPCAL4   3'  CTTCTGAGATTGTGGTCTTCCA 32735          G       TTGTT
                                 TGGAAGACTA TGATTTTG
                                 |||||||||| ||||||||
                                 ACCTTCTGGT GTTAGAGT
                                       _      CTTCG
GAM394  HRIHFB2436 3'  GAATCATTGGCTTCTA      26792        A
                                 TGGAAG CTAGTGATTT
                                 |||||| ||||||||||
                                 ATCTTC GGTTACTAAG

                                   _
GAM394  HSA404617 3'  AGCAGCAGGGGCTGGGGTCTTC 72707         AGTGA
           T                      GGAAGACT    TTTTGTTGTT
                                  ||||||||    ||||||||||
                                  TCTTCTGG    GGGACGACGA
                                      GGTCG
GAM394  HSFY     3'  AACAATAAAATTGCATGTTT   68638      TA TG
                                 AGAC  G  ATTTTGTTGTT
                                 ||||  |  ||||||||||
                                 TTTG  C  TAAAATAACAA
                                   TA GT
GAM394  ITGA10   3'  AGTTATTGGTCTCCA       59374      A
                                 TGGA GACTAGTGATT
                                 |||| ||||||||||
                                 ACCT CTGGTTATTGA

                                   _
GAM394  JWA      3'  GACAATAATAGCTGATCTTTT  21141        C    GATT
                                 GGAAGA TAGT    TTGTTGTT
                                 |||||| ||||    ||||||||
                                 TTTTCT GTCG    AATAACAG
                                     A    AT__
GAM394  KCNJ2    5'  AGCAACAGGACATGTTCTCT   6098      AG  TA   A
                                 GGA  AC  GTG TTTTGTTGTT
                                 |||  ||  ||| ||||||||||
                                 TCT  TG  TAC AGGACAACGA
                                   CT  __   _
GAM394  KCNS1    3'  GGGCAGAGTCAGGTTT      9578        AG        TG
                                 AGACT  TGATTTTGT  T
                                 |||||  |||||||||  |
                                 TTTGG  ACTGAGACG  G
                                     __        GT
GAM394  KHDRBS1  3'  AACAACAAAATTAGGCTTGTA  21622    G   A  AG
                                 TG AAG CT  TGATTTTGTTGTT
                                 || ||| ||  ||||||||||||
```

```
                                AT TTC GG  ATTAAAACAACAA
                                 G  _ __
GAM394  KHSRP    3' GATAGCGAGATCTAAATCTCT  13484     A  CTAGT
                                GGA GA    GATTTTGTTGTT
                                ||| ||    ||||||||||||
                                TCT CT    CTAGAGCGATAG
                                  _ AAAT_
GAM394  KIAA0014 3' AGCACTGGTTACTGGTTTCC   27837     A        T_
                                GGA GACTAGTGATT  TGTT
                                ||| ||||||||||  ||||
                                CCT TTGGTCATTGG  ACGA
                                  _        TC
GAM394  KIAA0022 3' GGCAACAAAGTTCCAGCTTGT  29669    T  ___
                                AC AGT   GATTTTGTTGTT
                                || |||   ||||||||||||
                                TG TCG   TTGAAACAACGG
                                 T   ACC
GAM394  KIAA0040 3' AGTGGCAAAATTGCTATCT    27776     C   TG     TG
                                AGA TAG  ATTTTGT  TT
                                ||| |||  |||||||  ||
                                TCT ATC  TAAAACG  GA
                                  _  GT      GT
GAM394  KIAA0052 3' TGATAGTGATTCCCAGTTGTTG 67835      TG  _____ TG
           GTGTTTCA               ACTAG  ATT    T  TTGTT   G
                                |||||  |||    |  |||||  |
                                TGGTT  TGA    A  GATAG   T
                                   GT   CCCTT GT
GAM394  KIAA0087 3' AACAGCAAGGTCTAGACATTTC 28690      GA_   GT
           A                    TGGAA   CTA  GATTTTGTTGTT
                                |||||   |||  ||||||||||||
                                ACTTT   GAT  CTGGAACGACAA
                                   ACA   __
GAM394  KIAA0092 3' AACAGATTACCAGTTTTTTA   27965        A      T
                                TGGAAGACT GTGATTT GTT
                                ||||||||| ||||||| |||
                                ATTTTTTGA CATTAGA CAA
                                      C      _
GAM394  KIAA0125 5' GGTGACAGAGTTGCTTCT    28902     CT  TG     TG
                                AGA  AG  ATTTTGT  TT
                                |||  ||  |||||||  ||
                                TCT  TC  TGAGACA  GG
                                  __ GT      GT
GAM394  KIAA0125 3' AGTGGCAGGATCCTCTCCTTT  60503     ACT  T      TG
                                GAAG   AG GATTTTGT  TT
                                ||||   || ||||||||  ||
                                TTTC   TC CTAGGACG  GA
                                  CTC  _       GT
GAM394  KIAA0179 3' GTGTTTAGAATACTGGTTTTCT 64830           A    TTGTT
           A                    TGGAAGACTAGTG TTTTG
                                |||||||||||| |||||
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                                ATCTTTTGGTCAT AAGAT
                                      _    TTGTGT
GAM394  KIAA0179 3' GCAGCAGAGTCCCTTGT    64827    T  T
                                AC AG GATTTTGTTGT
                                || || ||||||||||
                                TG TC CTGAGACGACG
                                 T  C
GAM394  KIAA0182 3' GCAACGGGCGAGTCTTCC    72029        A  GATT
                                GGAAGACT GT    TTGTTGT
                                |||||||| ||    |||||||
                                CCTTCTGA CG    GGCAACG
                                     G  ____
GAM394  KIAA0193 3' GGCAATGGACACATTAGCCTTT 28657       A     AT  TG
           TA                     TGGAAG CTAGTG  TT  TTGTT
                                |||||| ||||||  ||  |||||
                                ATTTTC GATTAC  AG  AACGG
                                   C     AC  GT
GAM394  KIAA0210 3' AATAATAACTCTGGTTTTGCCA 28468    _       TGATT
                                TGG AAGACTAG    TTGTTGTT
                                ||| ||||||||    ||||||||
                                ACC TTTTGGTC    AATAATAA
                                  G       TC___
GAM394  KIAA0226 3' GACAGCAAGACCAAGTTCTTCC 63516       CTAG  A
           A                    TGGAAGA    TG TTTTGTTGTT
                                |||||||    || ||||||||||
                                ACCTTCT    AC AGAACGACAG
                                    TGA_  C
GAM394  KIAA0226 3' GGCGGTAAGAAGGAGTCTCCCA 63520    A    AGTGA    TT
                                TGG AGACT    TTTTG  GTT
                                ||| |||||    |||||  |||
                                ACC TCTGA    AGAAT  CGG
                                  C    GGA__    GG
GAM394  KIAA0232 3' GCGGGTAGAGTCATGAGTTTTC 72749        A         GTT
           CA                     TGGAAGACT GTGATTTTGTT
                                ||||||||| ||||||||||
                                ACCTTTTGA TACTGAGATGG
                                     G         GCGG
GAM394  KIAA0335 3' GACAACAGAATCATAG      28991     G
                                CTA TGATTTTGTTGTT
                                ||| ||||||||||||
                                GAT ACTAAGACAACAG
                                  _
GAM394  KIAA0339 3' GACAACAAGATCCCGTGTCT   71474      TAGT
                                AGAC    GATTTTGTTGTT
                                ||||    ||||||||||||
                                TCTG    CTAGAACAACAG
                                  TGCC
GAM394  KIAA0372 3' AGCAATGAATCAAGACTTCTA  27661       A  AG    T TG
                                TGGAAG CT  TGAT T  TTGTT
                                |||||| ||  |||| |  |||||
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                                ATCTTC GA  ACTA A  AACGA
                                   A  __   _ GT
GAM394  KIAA0391  3'  AATAGCAGAATCAATCCATCT  27899    CTAG_
                                AGA    TGATTTTGTTGTT
                                |||    ||||||||||||
                                TCT    ACTAAGACGATAA
                                  ACCTA
GAM394  KIAA0416  3'  GACAGCAGAGGAGTATTTTCCA 31465       CTAGTGA
                                TGGAAGA      TTTTGTTGTT
                                |||||||      ||||||||||
                                ACCTTTT      GAGACGACAG
                                   ATGAG__
GAM394  KIAA0438  3'  AATGGAATGCAAGTTTTTCA   29069        A  G   TG
                                TGGAAGACT GT ATTT  TT
                                ||||||||| || ||||  ||
                                ACTTTTTGA CG TAAG  AA
                                     A  _   GT
GAM394  KIAA0450  3'  GGTGGCAGGGGGCCCTGGTTTT 27646       TGA_    TG
                                AAGACTAG   TTTTGT  TT
                                ||||||||   ||||||  ||
                                TTTTGGTC   GGGACG  GG
                                     CCGG    GT
GAM394  KIAA0494  5'  GACAGCGGGGCGGGGGTCTATC 28742    A    AG  A
          A                      TGG AGACT  TG TTTTGTTGTT
                                ||| |||||  || ||||||||||
                                ACT TCTGG  GC GGGGCGACAG
                                  A    GG  _
GAM394  KIAA0495  3'  AACAGTGGCTGTTTTCCA    62571       T   G  TT
                                TGGAAGAC AGT AT  TGTT
                                |||||||| ||| ||  ||||
                                ACCTTTTG TCG TG  ACAA
                                     _  G  __
GAM394  KIAA0528  3'  GACAATGGAGAAAAGTTTTC   72381       AGTGA   TG
                                GAAGACT    TTT  TTGTT
                                |||||||    |||  |||||
                                CTTTTGA    GAG  AACAG
                                     AAA__   GT
GAM394  KIAA0543  3'  GATGGTGGAGCTGGGCTCTTCT 68935       __    GAT  TG TG
                                GGAAGA  CTAGT   TT  T  TT
                                ||||||  |||||   ||  |  ||
                                TCTTCT  GGTCG   AG  G  AG
                                   CG    ____  GT GT
GAM394  KIAA0546  3'  AGCAGTAAGCTTGTTTTCCA   71304       T   GATT
                                TGGAAGAC AGT    TTGTT
                                |||||||| |||    |||||
                                ACCTTTTG TCG    GACGA
                                     T  AAT_
GAM394  KIAA0555  3'  GATGGCAAAATTGTTTACACCA 28884    AAGACT  TG     TG
                                TGG     AG  ATTTTGT  TT
                                |||     ||  |||||||  ||
```

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                                ACC     TT  TAAAACG  AG
                                  ACAT__  GT      GT
GAM394  KIAA0555  3'  GCAATGGAACTAGTTTCT    28885     A      GAT  TG
                                GGA GACTAGT   TT  TTGT
                                ||| |||||||   ||  ||||
                                TCT TTGATCA   AG  AACG
                                  _     ____  GT
GAM394  KIAA0565  3'  AACAATAGATAAATAGTTTTCT 66882         GTGAT
                                GGAAGACTA    TTTGTTGTT
                                |||||||||    |||||||||
                                TCTTTTGAT    AGATAACAA
                                     AAAT_
GAM394  KIAA0594  3'  TAGTAAAAGTTAAGTCTTCT   64902        AG      GTTGTT
                                GGAAGACT  TGATTTT
                                ||||||||  |||||||
                                TCTTCTGA  ATTGAAA
                                    __      ATGATG
GAM394  KIAA0644  3'  GACAGTGGAATCTTCTGTTT   29061      T  T_    TG
                                AGAC AG  GATTT  TTGTT
                                ||||  ||  |||||  |||||
                                TTTG TC  CTAAG  GACAG
                                  _ TT    GT
GAM394  KIAA0731  5'  GGCAGCAAGGTTGGTGACTTT  66932      AC  G
                                GAAG  TA TGATTTTGTTGTT
                                ||||  || ||||||||||||||
                                TTTC  GT GTTGGAACGACGG
                                  A_  G
GAM394  KIAA0766  3'  AGTGACAAAGTCATTGTCTTTT 29002         T         TG
          A                      TGGAAGAC AGTGATTTTGT  TT
                                 ||||||||| ||||||||||  ||
                                 ATTTTCTG TTACTGAAACA  GA
                                     _         GT
GAM394  KIAA0783  3'  GACAATGCATTCCATTAGTCTG 27800     A       ATTTT_
          CTA                      TGG AGACTAGTG     GTTGTT
                                 ||| |||||||||     ||||||
                                 ATC TCTGATTAC     TAACAG
                                   G       CTTACG
GAM394  KIAA0798  3'  AGCAGCCTGTTGCTAGATTTTC 27716      _   TG  TTT
                                 GAAGA CTAG  AT   GTTGTT
                                 ||||| ||||  ||   ||||||
                                 CTTTT GATC  TG   CGACGA
                                    A    GT  TC_
GAM394  KIAA0853  3'  GGCAGCAGGATTGCTGGAGCCC 30541    AAGA    TG
          A                       TGG    CTAG  ATTTTGTTGTT
                                  |||    ||||  ||||||||||
                                  ACC    GGTC  TAGGACGACGG
                                    CGA_    GT
GAM394  KIAA0854  3'  GGTGACAGACGGCAGATCTTCC 30100       _ A  GAT    TG
          A                       TGGAAGA CT GT   TTTGT  TT
                                  ||||||| || ||   |||||  ||
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                                ACCTTCT GA CG   AGACA  GG
                                    A  _  GC_     GT
GAM394  KIAA0865 3' AACAACAGAAGGCTGCCTTCT  61246      AC    GA
                                GGAAG  TAGT  TTTTGTTGTT
                                |||||  ||||  ||||||||||
                                TCTTC  GTCG  AAGACAACAA
                                  C_    G_
GAM394  KIAA0869 3' AATAATAAGATTGTATAGTTT  70854       _ TG
                                AGACTA G  ATTTTGTTGTT
                                |||||| |  ||||||||||
                                TTTGAT T  TAGAATAATAA
                                   A GT
GAM394  KIAA0895 3' AGCAGTAAGGTCAGTTTTTTTC 92722       CTAG
            C                    GGAAGA    TGATTTTGTTGTT
                                ||||||    ||||||||||||
                                CCTTTT    ACTGGAATGACGA
                                   TTTG
GAM394  KIAA0930 3' GGACACCTAGTTTTCC      70545          TGATTT   TG
                                GGAAGACTAG     TGT  T
                                ||||||||||     |||  |
                                CCTTTTGATC     ACA  G
                                     C_____   GT
GAM394  KIAA0940 3' AATAGATTTAAGTCGCTGTGTT 29861       _        TG__
            TTCT                   AAGAC TAGTGATTT    TTGTT
                                ||||| |||||||||    |||||
                                TTTTG GTCGCTGAA    GATAA
                                   T        TTTA
GAM394  KIAA0970 3' AACAGTGATTGCGATTGTTTTC 29953        TAG  ATT TG
            TA                    TGGAAGAC   TG   T  TTGTT
                                ||||||||   ||   |  |||||
                                ATCTTTTG   GC   A  GACAA
                                     TTA  GTT GT
GAM394  KIAA0976 5' CAAAGTCACTGATCTTTT    29887       C
                                GGAAGA TAGTGATTTTG
                                |||||| ||||||||||
                                TTTTCT GTCACTGAAAC
                                   A
GAM394  KIAA0993 3' GACAGCGGCTTTGGCTTTTCCA 64140        _   TGATT
                                TGGAAGA CTAG    TTGTTGTT
                                ||||||| ||||    ||||||||
                                ACCTTTT GGTT    GGCGACAG
                                    C   TC___
GAM394  KIAA1016 3' AACAATGGAACGGATCACTGCT 91729     C       ____ TG
            TTTTT                  AGA TAGTGATT    T  TTGTT
                                ||| ||||||||   |  |||||
                                TTT GTCACTAG    G  AACAA
                                  C       GCAA GT
GAM394  KIAA1025 3' GGCAGCAAAGGGTAGTTTTC   63977        GTGA
                                GAAGACTA    TTTTGTTGTT
                                ||||||||    ||||||||||
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                                CTTTTGAT   GAAACGACGG
                                    GG__
GAM394  KIAA1041 3' AACAGCAGGGCAGGGTTTCTA 30119     A   AG  A
                                TGGA GACT  TG TTTTGTTGTT
                                |||| ||||  || ||||||||||
                                ATCT TTGG  AC GGGACGACAA
                                  _   G_  _
GAM394  KIAA1041 3' GGTTTGCTTAAGTCACTGTTTT 30136       T      T_  TGTT
          CTA                     GGAAGAC AGTGATTT  GT
                                |||||||  ||||||||  ||
                                TCTTTTG TCACTGAA  CG
                                   _      TT  TTTGGT
GAM394  KIAA1042 3' GGCAGCAGAAGATGTGTCCTTC 30343       _  TAGTGA
          CA                      TGGAAG AC     TTTTGTTGTT
                                ||||||  ||     ||||||||||
                                ACCTTC TG     AAGACGACGG
                                   C  TGTAG_
GAM394  KIAA1061 3' AGTGACAGAGTCAACTTCT   71174      ACTAG       TG
                                GGAAG    TGATTTTGT  TT
                                |||||    |||||||||  ||
                                TCTTC    ACTGAGACA  GA
                                   A____       GT
GAM394  KIAA1191 5' GGCAGCAGGATCACAG     39958    A
                                CT GTGATTTTGTTGTT
                                || ||||||||||||||
                                GA CACTAGGACGACGG
                                 _
GAM394  KIAA1204 5' AGCGACAGGATGCTTGTTTTTC 69215       T   G
                                GGAAGAC AGT ATTTTGTTGTT
                                ||||||| ||| ||||||||||
                                CTTTTTG TCG TAGGACAGCGA
                                    T  _
GAM394  KIAA1209 3' GGCAGCAAGGAGACTTTTTC   60760      CT   GA
                                GAAGA  AGT  TTTTGTTGTT
                                |||||  |||  ||||||||||
                                CTTTT  TCA  GGAACGACGG
                                   __  GA
GAM394  KIAA1211 3' GATGGCAAAGTTATTTACCA   68893     AAGACT        TG
                                TGG     AGTGATTTTGT  TT
                                |||     ||||||||||  ||
                                ACC     TTATTGAAACG  AG
                                  AT____         GT
GAM394  KIAA1229 3' AGCTCATCACTGGTCATTCA   62061      A        TTT
                                TGGA GACTAGTGAT   GTT
                                |||| ||||||||||   |||
                                ACTT CTGGTCACTA   CGA
                                  A        CT_
GAM394  KIAA1233 3' AAAGTTACTATTTTTC      63077       C
                                GAAGA TAGTGATTTT
                                ||||| ||||||||||
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                                CTTTT ATCATTGAAA
                                   T
GAM394  KIAA1233  3'  GCAACAAAGTTACCTGCCA   63081     A  ACTA
                                TGG AG   GTGATTTTGTTGT
                                ||| ||   ||||||||||||
                                ACC TC   CATTGAAACAACG
                                  G  ____
GAM394  KIAA1240  3'  AATTATGGGTTACTAGTTTTAC 66727    G          TGTTGTT
          A                      TG AAGACTAGTGATTT
                                || ||||||||||||||
                                AC TTTTGATCATTGGG
                                 A           TATTAA
GAM394  KIAA1271  3'  GCGACAGAGTGGTATTCT    69548     G   AGTG
                                GGAA ACT    ATTTTGTTGT
                                |||| |||    ||||||||||
                                TCTT TGG    TGAGACAGCG
                                  A  _____
GAM394  KIAA1280  5'  GGCAACAGGGCTTGGTTTTTC  69725         TGA
                                GGAAGACTAG   TTTTGTTGTT
                                ||||||||||   ||||||||||
                                CTTTTTGGTT   GGGACAACGG
                                     C__
GAM394  KIAA1317  3'  AATAATGAAATGAAGTGGCTTC 86027       A   GTG_   TG
          CA                     TGGAAG CTA    ATTT  TTGTT
                                |||||| |||    ||||  |||||
                                ACCTTC GGT    TAAA  AATAA
                                   _  GAAG    GT
GAM394  KIAA1318  3'  GGTGGTGGGGTTATGGGTAGTT 67308        ___      TG TG
          TTT                    AAGACTA   GTGATTT  T  TT
                                |||||||   |||||||  |  ||
                                TTTTGAT   TATTGGG  G  GG
                                    GGG      GT GT
GAM394  KIAA1321  3'  AGAGTTGTAGTCTTCT      62221         G
                                GGAAGACTA TGATTTT
                                ||||||||| |||||||
                                TCTTCTGAT GTTGAGA
                                          _
GAM394  KIAA1336  3'  AGCAATAGCTTGCCTATTAGTC 72322   A       ATT___
          TGCT                     AGACTAGTG     TTGTTGTT
                                  |||||||||     ||||||||
                                  TCTGATTAT     GATAACGA
                                 G        CCGTTC
GAM394  KIAA1357  3'  GGCAGTAGAGTTGCTGGTTCTT 71980     _   TG
                                AAGA CTAG  ATTTTGTTGTT
                                |||| ||||  ||||||||||
                                TTCT GGTC  TGAGATGACGG
                                  T   GT
GAM394  KIAA1371  3'  AATAGTCATTGCTCACTGGTCT 89039   G        TTT_ _
          TGTA                    G AAGACTAGTGA    TG TTGTT
                                | ||||||||||    || |||||
```

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                                T TTCTGGTCACT    AC GATAA
                                 G         CGTT  T
GAM394  KIAA1371  3'  GACAGACATTTGTTTTTCA   89043        T    AT
                                TGGAAGAC AGTG  TTTGTT
                                |||||||| ||||  ||||||
                                ACTTTTTG TTAC  AGACAG
                                     T   __
GAM394  KIAA1391  3'  GACAACGAAATAATTCTCTTT  67262      CT   G
                                GAAGA  AGT ATTTTGTTGTT
                                |||||  ||| ||||||||||
                                TTTCT  TTA TAAAGCAACAG
                                   C_   A
GAM394  KIAA1393  3'  AATAGCAGAGTTGAGTGGTT   72093      G_
                                GACTA  TGATTTTGTTGTT
                                |||||  ||||||||||||
                                TTGGT  GTTGAGACGATAA
                                   GA
GAM394  KIAA1431  3'  AGCAGCAGAGTTGAGCAGTT   62997      AG_
                                GACT   TGATTTTGTTGTT
                                ||||   ||||||||||||
                                TTGA   GTTGAGACGACGA
                                  CGA
GAM394  KIAA1492  3'  GGTTAATAGTTTTCCA      64507          G
                                TGGAAGACTA TGATT
                                |||||||||| |||||
                                ACCTTTTGAT ATTGG
                                      A
GAM394  KIAA1494  5'  GGCAGCAGAGAGGAGTCTCCC  68461    A    AGTGA
                                GG AGACT    TTTTGTTGTT
                                || |||||    ||||||||||
                                CC TCTGA    GAGACGACGG
                                 C    GGA__
GAM394  KIAA1495  3'  GGTCTTAGTTTTCTA       73187          T
                                TGGAAGACTAG GATT
                                |||||||||| ||||
                                ATCTTTTGATT CTGG
                                          _
GAM394  KIAA1505  3'  AGCAACAGAGTACAACAGGGTT 94184      A_  AG  _
           TCTA                   GGAAG  CT  TG ATTTTGTTGTT
                                |||||  ||  || ||||||||||
                                TCTTT  GA  AC TGAGACAACGA
                                   GG  CA  A
GAM394  KIAA1530  3'  AGTGGCAGAATCATAGCTC   67944    _  G       TG
                                GA CTA TGATTTTGT  TT
                                || ||| |||||||||  ||
                                CT GAT ACTAAGACG  GA
                                 C  _        GT
GAM394  KIAA1560  3'  ACATTCTCATTGTTTTCCA   64170        T    TTT
                                TGGAAGAC AGTGA   TGT
                                |||||||| |||||   |||
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                                ACCTTTTG TTACT   ACA
                                     _    CTT
GAM394  KIAA1560 3' AGCATAATTATTGGTTT     64172           T
                                AGACTAGTGATT TGTT
                                |||||||||||| ||||
                                TTTGGTTATTAA ACGA
                                      T
GAM394  KIAA1582 3' AACGGTTGTTATTATTAGCTTC 65363       A       TTT_ TT
           TA                    TGGAAG CTAGTGAT    G  GTT
                                |||||| ||||||||    |  |||
                                ATCTTC GATTATTA    T  CAA
                                   _       TTGT GG
GAM394  KIAA1596 5' GACGATGTGAGTCTTTCA    70915         AGTGATT
                                TGGAAGACT      TTGTT
                                |||||||||      |||||
                                ACTTTCTGA      AGCAG
                                     GTGT___
GAM394  KIAA1634 3' TAAAGTCATTAGTCTTT     63393
                                GAAGACTAGTGATTTTG
                                |||||||||||||||||
                                TTTCTGATTACTGAAAT

GAM394  KIAA1644 5' CATAGCTAGAGTTACTGTTTTT 85026         T       _    T
           TA                    TGGAAGAC AGTGATTTT GTTGT
                                |||||||| ||||||||| |||||
                                ATTTTTTG TCATTGAGA CGATA
                                   _        T    CG
GAM394  KIAA1649 3' GGCAGTAGGACCTGGTTTTTCA 66979           TGA
                                TGGAAGACTAG   TTTTGTTGTT
                                ||||||||||   ||||||||||
                                ACTTTTTGGTC   AGGATGACGG
                                      C__
GAM394  KIAA1649 3' GGCAGTAGGACCTGGTTTTTCA 50274           TGA
                                TGGAAGACTAG   TTTTGTTGTT
                                ||||||||||   ||||||||||
                                ACTTTTTGGTC   AGGATGACGG
                                      C__
GAM394  KIAA1679 3' GATAATGAAATCAAATGGTTTC 70151     A    G_     TG
           C                     GGA GACTA  TGATTT  TTGTT
                                ||| |||||  ||||||  |||||
                                CCT TTGGT  ACTAAA  AATAG
                                  _    AA     GT
GAM394  KIAA1691 3' GGCGGTGAGGCCAGGGCTTCCA 92560       A  AG  AT  TG
                                TGGAAG CT  TG  TT  TTGTT
                                |||||| ||  ||  ||  |||||
                                ACCTTC GG  AC  GA  GGCGG
                                   _ G_  CG  GT
GAM394  KIAA1754 3' AGCAGTGGGGCTCTTGGTGTTT 63233      G    T  _   TG
           CA                    TGGAA ACTAG GA TTT  TTGTT
                                ||||| ||||| || |||  |||||
```

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                                ACTTT TGGTT CT GGG  GACGA
                                  G    _ C   GT
GAM394  KIAA1762 3' AACGGCAAATCCAAAGTTCTTT 63788       _ AG  AT
            CA                    TGGAAGA CT  TG  TTTGTTGTT
                                ||||||| ||  ||  |||||||||
                                ACTTTCT GA  AC  AAACGGCAA
                                   T  A_  CT
GAM394  KIAA1853 3' GATAACGGGGTCAGGCCTTT   69393     A  AG
                                GAAG CT  TGATTTTGTTGTT
                                |||| ||  ||||||||||||
                                TTTC GG  ACTGGGGCAATAG
                                  C  __
GAM394  KIAA1856 3' GGAATTATTGGTTTTTT     92664
                                GGAAGACTAGTGATTTT
                                |||||||||||||||||
                                TTTTTTGGTTATTAAGG

GAM394  KIAA1870 3' GGCGGCAGGATCACTAG     51832
                                CTAGTGATTTTGTTGTT
                                |||||||||||||||||
                                GATCACTAGGACGGCGG

GAM394  KIAA1872 3' AACGATGAGTTTTGCGGTTTTT 62919         A TG T_  TG
            CA                    TGGAAGACT G  A  TT  TTGTT
                                |||||||||  |  |  ||  |||||
                                ACTTTTTGG C  T  GA  AGCAA
                                     _ GT TT  GT
GAM394  KIAA1878 3' GGCAGCAAAGTCTCTGCTTACA 91714    G   AC   T
                                TG AAG  TAG GATTTTGTTGTT
                                || |||  ||| ||||||||||||
                                AC TTC  GTC CTGAAACGACGG
                                 A   __   T
GAM394  KIAA1879 3' GCAGCAGGGATGTCTACCA    73569     A    TAGTGA
                                TGG AGAC     TTTTGTTGT
                                ||| ||||     |||||||||
                                ACC TCTG     GGGACGACG
                                  A   TA____
GAM394  KIAA1884 3' ACAGCAAGGTCAATGCCA     73333     AAGACTAG
                                TGG       TGATTTTGTTGT
                                |||       ||||||||||||
                                ACC       ACTGGAACGACA
                                  GTA_____
GAM394  KIAA1911 3' GGCAACAACCATATGGTTGTTC 73508      _    _  ATT
            CA                    TGGAA GACTA GTG   TTGTTGTT
                                ||||| ||||| |||   ||||||||
                                ACCTT TTGGT TAC   AACAACGG
                                  G    A  C__
GAM394  KIAA1912 3' AATACAAGGGACACTGGTCTTT 73362          A_     TGTT
            T                     GGAAGACTAGTG  TTTTGT
                                ||||||||||||  ||||||
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                                TTTTCTGGTCAC  GGAACA
                                      AG     TAA
GAM394  KIAA1912  3'  AACAACAAACATAATTTTTCTA 73361        CTA   AT
                                TGGAAGA   GTG  TTTGTTGTT
                                |||||||   |||  |||||||||
                                ATCTTTT   TAC  AAACAACAA
                                    TAA   __
GAM394  KIAA1913  5'  GGTGGCAGGACTGGGGTTTCC  73887      A_    GAT    TG
                                GGAAG  CTAGT   TTTGT  TT
                                |||||  |||||   |||||  ||
                                CCTTT  GGTCA   GGACG  GG
                                   GG    ___    GT
GAM394  KIAA1924  3'  GACAGCTGGAAGGGTCTTGGTT 73672        T    _____
            TTCT                    AGACTAG GATTTT    GTTGTT
                                |||||||  ||||||   ||||||
                                TTTGGTT CTGGGA    CGACAG
                                    _     AGGT
GAM394  KIAA1938  3'  ACAGCGGGATTGCCTCC     92191     A ACTA TG
                                GGA G    G  ATTTTGTTGT
                                |||  |    |  ||||||||||
                                CCT C    C  TAGGGCGACA
                                  _ _____ GT
GAM394  KIAA1950  3'  ACAGCGGAATCCCTTC      92586      ACTAGT
                                GAAG     GATTTTGTTGT
                                ||||     ||||||||||
                                CTTC     CTAAGGCGACA
                                  C_____
GAM394  LALP1     3'  GGCAATAAAATCAAAGTTTTT  39785        AG
                                GAAGACT  TGATTTTGTTGTT
                                |||||||  ||||||||||||
                                TTTTTGA  ACTAAAATAACGG
                                    A_
GAM394  LIM       3'  AATAACAGAATTATTGTATTT  21299     G  T
                                GAA AC AGTGATTTTGTTGTT
                                |||  ||  ||||||||||||||
                                TTT TG TTATTAAGACAATAA
                                  A  _
GAM394  LIPI      3'  AACAATGCAATCAGTCTTTTA  79563         AGT    T
                                TGGAAGACT   GATT TGTTGTT
                                |||||||||   ||||  |||||||
                                ATTTTCTGA   CTAA GTAACAA
                                      ___    C
GAM394  LNX       3'  AATAACAAGATTTATAGTATCT 50917      AG    GT
              A                   TGGA  ACTA  GATTTTGTTGTT
                                ||||  ||||  ||||||||||||
                                ATCT  TGAT  TTAGAACAATAA
                                  A_    AT
GAM394  LOXL4     3'  GATGGCAAGATCACCAATCCA  49868      AGACTA         TG
                                TGGA     GTGATTTTGT  TT
                                ||||     ||||||||||  ||
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                                ACCT     CACTAGAACG  AG
                                  AAC___         GT
GAM394  LSM1     3'  AATAACAAAATCACTGTTT   27092      T
                                AGAC AGTGATTTTGTTGTT
                                |||| ||||||||||||||
                                TTTG TCACTAAAACAATAA
                                  _
GAM394  LSR7     5'  AGCGATGAAGACAGTAGTTCTT 37676       _  G  A   TG
           T                     GAAGA CTA TG TTT  TTGTT
                                ||||| ||| || |||  |||||
                                TTTCT GAT AC GAA  AGCGA
                                   T   G  A   GT
GAM394  MACMARCKS 3'  GGCAGTTGTTGGTTTTCT    43449          TG  TT
                                GGAAGACTAG  AT  TGTT
                                ||||||||||  ||  ||||
                                TCTTTTGGTT  TG  ACGG
                                      GT  __
GAM394  MEF-2    3'  GACAGCAAGTCTGGTCATTCA  64384      A     TGAT
                                TGGA GACTAG    TTTGTTGTT
                                |||| ||||||    |||||||||
                                ACTT CTGGTC    GAACGACAG
                                  A     T___
GAM394  MESDC2   3'  AGCAGTAGAATTATTAG     72489
                                CTAGTGATTTTGTTGTT
                                ||||||||||||||||
                                GATTATTAAGATGACGA

GAM394  METL     5'  AGCGATCCGGCGCGGGTCTTCC 37252         A   ATTTT
           A                     TGGAAGACT GTG     GTTGTT
                                ||||||||| |||     ||||||
                                ACCTTCTGG CGC     TAGCGA
                                      G   GGCC_
GAM394  MGC10940 3'  AGCAGTAAAATTAGCTCTTTCA 50213        _    GATT    GTT
                                TGGAAGA CTAGT    TTGTT
                                ||||||| |||||    |||||
                                ACTTTCT GATTA    GACGA
                                    C     AAAT
GAM394  MGC11324 3'  GTAACAAAGAGCTTAGTTTTCC 51169         _ GA      GTT
                                GGAAGACTA GT  TTTTGTT
                                ||||||||| ||  |||||||
                                CCTTTTGAT CG  GAAACAA
                                      T  A_      TGG
GAM394  MGC13008 5'  GGTGGTGAGGTCACTGTCCA   51081      AGAC        TG TG
                                TGGA    TAGTGATTT  T  TT
                                ||||    |||||||||  |  ||
                                ACCT    GTCACTGGA  G  GG
                                  _____         GT GT
GAM394  MGC13010 5'  GGCTCCAGGTCGCTGGCTTCT  51083       A         T TT
                                GGAAG CTAGTGATTT G  GTT
                                ||||| ||||||||||  |  |||
```

```
                                TCTTC GGTCGCTGGA C  CGG
                                  _       _ CT
GAM394  MGC13057 5' GACAAATTTCATTGTTTTCTA 50307       T    T_
                                TGGAAGAC AGTGA  TTTGTT
                                |||||||| |||||  ||||||
                                ATCTTTTG TTACT  AAACAG
                                   _    TT
GAM394  MGC13114 3' AACAACAAATGCCTGATCTTCC 50412      C   TGAT
                                GGAAGA TAG    TTTGTTGTT
                                |||||| |||   |||||||||
                                CCTTCT GTC    AAACAACAA
                                   A  CGT_
GAM394  MGC13125 3' GACAGCACCGGCTGTTGCTGGC 51178    A   TG  TT____
           TTTCA                 AG CTAG  AT     TGTTGTT
                                || ||||  ||     |||||||
                                TC GGTC  TG     ACGACAG
                                 _   GT  TCGGCC
GAM394  MGC14161 3' GACAATGGGGACTGTTTAGTTT 51844        TGA__  TG
           TTT                   GGAAGACTAG    TTT  TTGTT
                                ||||||||||    |||  |||||
                                TTTTTTGATT    GGG  AACAG
                                     TGTCA   GT
GAM394  MGC14386 3' AACAATGAAACCAGAGCTTCTA 53205      A  AG  A   TG
                                TGGAAG CT  TG TTT  TTGTT
                                |||||| ||  || |||  |||||
                                ATCTTC GA  AC AAA  AACAA
                                   _ G_  C   GT
GAM394  MGC15397 3' GATGGTGAAATCCTGTCTCTA  54680     A   T  T    TG TG
                                TGGA GAC AG GATTT  T  TT
                                |||| ||| || |||||  |  ||
                                ATCT CTG TC CTAAA  G  AG
                                  _  _ _    GT GT
GAM394  MGC15548 5' GCAACACCATTGTTTTTCA   51254       T   ATTT
                                TGGAAGAC AGTG   TGTTGT
                                |||||||| ||||   ||||||
                                ACTTTTTG TTAC   ACAACG
                                   _   C___
GAM394  MGC15737 5' GCAGCGAGCGGGCTTCC     51929      A  A  GATT
                                GGAAG CT GT   TTGTTGT
                                ||||| || ||   |||||||
                                CCTTC GG CG   AGCGACG
                                   _ G  _____
GAM394  MGC15937 5' GATAATAGAGTTTCTTCTTC   54708      CT  T
                                GAAGA  AG GATTTTGTTGTT
                                |||||  || ||||||||||||
                                CTTCT  TC TTGAGATAATAG
                                   __  T
GAM394  MGC16025 3' AGGCAGGCTGGTCTCT      51913     A     GATT   TG
                                GGA GACTAGT   TTGT  T
                                ||| |||||||   ||||  |
```

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                                TCT CTGGTCG   GACG  A
                                  _     ____   GT
GAM394  MGC17337  3'  TAGTGGCAAAGAAGCTGTTATA 54691    _____  GA    TG
              GTCTTCT                ACT    AGT  TTTTGT  TT   A
                                |||    |||  ||||||  ||  |
                                TGA    TCG  GAAACG  GA   T
                                  TATTG   AA     GT
GAM394  MGC1842   3'  GACAGCAGGGTCTGCCCTCTT  65649     CTAGT
                                AAGA    GATTTTGTTGTT
                                ||||    ||||||||||||
                                TTCT    CTGGGACGACAG
                                  CCCGT
GAM394  MGC20235  3'  GGCAGCAGAATCACTTGAAACC 58899     AAGACT
              G                  TGG     AGTGATTTTGTTGTT
                                |||     ||||||||||||||
                                GCC     TCACTAAGACGACGG
                                  AAAGT_
GAM394  MGC20460  5'  ACAGCGAAGTCCCCCTCCA   53843     AGACTAGT
                                TGGA      GATTTTGTTGT
                                ||||      ||||||||||
                                ACCT      CTGAAGCGACA
                                  CCCC____
GAM394  MGC22679  5'  GACGGCGGGACTGGGTTTTCTA 58498         AGTGA
                                TGGAAGACT    TTTTGTTGTT
                                |||||||||    ||||||||||
                                ATCTTTTGG    AGGGCGGCAG
                                     GTC__
GAM394  MGC2488   5'  CTGTGCCAAAGTCACAGGTTTT 43869         A       TTGTT
              TCA                  TGGAAGACT GTGATTTTG
                                |||||||||  |||||||||
                                ACTTTTTGG  CACTGAAAC
                                     A       CGTGTCT
GAM394  MGC2541   3'  AGCAATAAGATCTTAATAAAGT 54744      AGT____
              CTTCTA                 AGACT     GATTTTGTTGTT
                                |||||     ||||||||||||
                                TCTGA     CTAGAATAACGA
                                  AATAATT
GAM394  MGC2628   3'  AGCGGTGGGATCTCTGCTGCCA 43967    A  AC   T    TG
                                TGG AG  TAG GATTT  TTGTT
                                ||| ||  ||| |||||  |||||
                                ACC TC  GTC CTAGG  GGCGA
                                  G __   T    GT
GAM394  MGC27016  3'  AATAACAAGTGTTATGGGTTTT 58677       A    _
              T                   GAAGACT GTGAT TTTGTTGTT
                                |||||||  |||||  |||||||||
                                TTTTTGG  TATTG  GAACAATAA
                                     G    T
GAM394  MGC27016  3'  GGCAATAGAACCTAGTC     58679       TGA
                                GACTAG   TTTTGTTGTT
                                ||||||   ||||||||||
```

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                                CTGATC   AAGATAACGG
                                   C__
GAM394  MGC2734  3' AGCAGCAAAAGCAAATTGGTCT 52413     A      GA__
            CCA                   GGA GACTAGT    TTTTGTTGTT
                                  ||| |||||||    ||||||||||
                                  CCT CTGGTTA    AAAACGACGA
                                    _      AACG
GAM394  MGC29654 3' GACAGTGAGGCAAGTCTTC   66638       AG  A   TG
                                  GAAGACT  TG TTT  TTGTT
                                  |||||||  || |||  |||||
                                  CTTCTGA  AC GGA  GACAG
                                      __ _  GT
GAM394  MGC3020  5' GGTGGCAGGATGGGTCTTCCA  43896        AGTG     TG
                                  TGGAAGACT    ATTTTGT  TT
                                  |||||||||    |||||||  ||
                                  ACCTTCTGG    TAGGACG  GG
                                       G___      GT
GAM394  MGC3048  3' GGGCAGTTTGGTCTTC      43900        TGATT    TG
                                  GAAGACTAG    TTGT  T
                                  |||||||||    ||||  |
                                  CTTCTGGTT    GACG  G
                                       T_____   GT
GAM394  MGC33182 3' AGTGAAACGTGGTGTCTGGTTT 75576          TG  TT   GTT
            TCTA                    TGGAAGACTAG  AT  TGTT
                                    ||||||||||  ||  ||||
                                    ATCTTTTGGTC  TG  GCAA
                                         TG  GT   AGTGAT
GAM394  MGC3731  3' AGTGACAAGGTCATTTACAACT 44228     ACT__        TG
            T                    AAG    AGTGATTTTGT  TT
                                 |||    ||||||||||  ||
                                 TTC    TTACTGGAACA  GA
                                   AACAT         GT
GAM394  MGC4161  3' AACGATCATCTTATTAGTTTTC 44190           TTTT
                                 GAAGACTAGTGA   GTTGTT
                                 ||||||||||||   ||||||
                                 CTTTTGATTATT    TAGCAA
                                        CTAC
GAM394  MGC4189  3' GACATCTGTTCTTGGTCTTTT  50231         T   TT_
                                 GGAAGACTAG GAT   TGTT
                                 |||||||||| |||   ||||
                                 TTTTCTGGTT TTG   ACAG
                                       C   TCT
GAM394  MGC4677  5' AGCGGCAGGGCCAGTGGGTTTT 53506        _ G  AT
            C                    GAAGACT A TG  TTTGTTGTT
                                 ||||||| | ||  |||||||||
                                 CTTTTGG T AC  GGACGGCGA
                                     G G  CG
GAM394  MGC4832  3' AGGATTATTAGTGTTTCA    58998       G
                                 TGGAA ACTAGTGATTTT
                                 ||||| ||||||||||||
```

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                                ACTTT TGATTATTAGGA
                                   G
GAM394  MGC4840  3'  AACGGCGAAACTCTGTCTCTA  71564     A   T  TGA
                                TGGA GAC AG   TTTTGTTGTT
                                |||| ||| ||   ||||||||||
                                ATCT CTG TC   AAAGCGGCAA
                                  _  _  TC_
GAM394  MGC955   3'  ATTGAGACAGAGTCACTGTCTT 44049       T         GTT
           TC                     GGAAGAC AGTGATTTTGTT
                                  ||||||| ||||||||||||
                                  CTTTCTG TCACTGAGACAG
                                     _          AGTTAC
GAM394  MGEA6    3'  AATAATAAAATCAGTAGTTTTT 19815        G
           C                      GGAAGACTA TGATTTTGTTGTT
                                  |||||||||  ||||||||||||
                                  CTTTTTGAT ACTAAAATAATAA
                                       G
GAM394  MKRN1    3'  AGTGATAAGTCATACTTTTCCA 25572       CTA     T  TG
                                  TGGAAGA   GTGATTT GT  TT
                                  |||||||   |||||||  ||  ||
                                  ACCTTTT   TACTGAA TA  GA
                                     CA_      _  GT
GAM394  MO25     3'  GGCAGTGAGGTCGTAGCCTTTT 32812       A   G     TG
           A                      TGGAAG CTA TGATTT  TTGTT
                                  ||||||  ||| ||||||  |||||
                                  ATTTTC GAT GCTGGA  GACGG
                                     C   _     GT
GAM394  MRG15    3'  TGCATTGTGTAGCTAGTTTTCT 22303          GATTTTGT   T
                                  GGAAGACTAGT       TGT
                                  ||||||||||        |||
                                  TCTTTTGATCG       ACG
                                        ATGTGTT_   TA
GAM394  MRPL13   3'  AATAATAAAATCACTTACTT   26016     ACT
                                  AAG   AGTGATTTTGTTGTT
                                  |||   ||||||||||||||
                                  TTC   TCACTAAAATAATAA
                                    AT_
GAM394  MRPL35   3'  CAATAAATGTCTTTCA      33541         TAGTGAT
                                  TGGAAGAC      TTTGTTG
                                  ||||||||      |||||||
                                  ACTTTCTG      AAATAAC
                                       T_______
GAM394  MST4     3'  AACTTATTATTGGCTTCT    33298       A       TTT
                                  GGAAG CTAGTGAT   GTT
                                  |||||  ||||||||   |||
                                  TCTTC GGTTATTA   CAA
                                     _       TT_
GAM394  MYOM1    3'  AATAATGTCAGGTCTTTCA   13735         AG   T
                                  TGGAAGACT  TGAT TTGTT
                                  |||||||||  ||||  |||||
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                                ACTTTCTGG  ACTG AATAA
                                     __    T
GAM394  NAP1L1   3'  GTAGCAAAATCATCTTTTTCA  57621        CTA         GTT
                                TGGAAGA   GTGATTTTGTT
                                |||||||   ||||||||||
                                ACTTTTT   TACTAAAACGA
                                   C__          TGA
GAM394  NDP52    3'  GATACTAAGTGATTAGTTTTCC 19530           G    T  TGTT
           A                     TGGAAGACTAGT ATTT GT
                                ||||||||||| |||| ||
                                ACCTTTTGATTA TGAA CA
                                      G    T  TAG
GAM394  NEDD5    3'  GATAATAGATAACTGCTCTTTT 15313        C    GAT
           A                     TGGAAGA TAGT   TTTGTTGTT
                                ||||||| ||||   |||||||||
                                ATTTTCT GTCA   AGATAATAG
                                   C    AT_
GAM394  NEK1     3'  AATAGCAAAATTATATTTCTT  95874      CTA
                                AAGA   GTGATTTTGTTGTT
                                ||||   ||||||||||||||
                                TTCT   TATTAAAACGATAA
                                  TTA
GAM394  NET-6    3'  AATGATAATTTACTTGTAGTCT 26936        ___     TT    TG
           TTTA                   GAAGACT   AGTGA  TTGT  TT
                                |||||||   |||||  ||||  ||
                                TTTCTGA   TCATT  AATA  AA
                                   TGT    T_    GT
GAM394  NIFU     3'  GATAATGAAGTTGCAAGTTTT  67314       A TG    TG
                                AAGACT G  ATTT  TTGTT
                                ||||||  |  ||||  |||||
                                TTTTGA C  TGAA  AATAG
                                   A GT    GT
GAM394  NLI-IF   3'  GGCAGCAGGAGTCTGTCCTTCA 41050      A   T  TGA
                                TGGA GAC AG   TTTTGTTGTT
                                |||| ||| ||   ||||||||||
                                ACTT CTG TC   AGGACGACGG
                                  C   _  TG_
GAM394  NMNAT    5'  TGACAACAAGGGAGGTGTCACA 42962    A    _______
           GTTTTCCA                CT GTGAT     TTTGTTGTT   G
                                ||  |||||     |||||||||   |
                                GA CACTG     GAACAACAG   T
                                 _     TGGAGG
GAM394  NMT1     3'  GGCAACAGAAGTGGTTTCCCA  40786     A     GTGA
                                TGG AGACTA    TTTTGTTGTT
                                |||  ||||||    ||||||||||
                                ACC TTTGGT    AAGACAACGG
                                  C     G___
GAM394  NS1-BP   5'  GGCGGCGGAGGCAGTGTCTCCC 72546    A    T G  A
                                GG AGAC A TG TTTTGTTGTT
                                ||  ||||  |  ||  ||||||||||
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                                CC TCTG T AC GAGGCGGCGG
                                 C   _ G  G
GAM394  NTN4     3'  AGTCAAAAAATCACAGTTTTTC 62912          A       GTTGTT
              A                   TGGAAGACT GTGATTTT
                                  ||||||||| ||||||||
                                  ACTTTTTGA CACTAAAA
                                        _       AACTGAT
GAM394  NUP160   3'  AATAATAAAATCATCTTGGATT 87593      A   __
              TT                   GAAG CTA  GTGATTTTGTTGTT
                                  |||| |||  ||||||||||||||
                                  TTTT GGT  TACTAAAATAATAA
                                    A  TC
GAM394  NXN      3'  AGCGGCAGAGTCCACCGTGTTT 42416      TA_  _
                                  AGAC   GTG ATTTTGTTGTT
                                  ||||   ||| ||||||||||
                                  TTTG   CAC TGAGACGGCGA
                                    TGC   C
GAM394  NXN      3'  TTTCGCAAAGTCACTAGCTTTT 42429       A          TGTT
                                  GGAAG CTAGTGATTTTGT
                                  ||||| ||||||||||||
                                  TTTTC GATCACTGAAACG
                                     _          CTTTC
GAM394  OLIG1    3'  GACGGCGGGAAGGCGCTTTCC  95590       ACTA  GA
                                  GGAAG   GT  TTTTGTTGTT
                                  |||||   ||  ||||||||||
                                  CCTTT   CG  AGGGCGGCAG
                                     CG__  GA
GAM394  OMD      3'  AACAACAAAATTATAAAGCT   17211    ACTA
                                  AG   GTGATTTTGTTGTT
                                  ||   ||||||||||||||
                                  TC   TATTAAAACAACAA
                                   GAAA
GAM394  ORCTL4   5'  GGTGGCTCCATGCTGGTCTCT  16651     A      GATTTT  TG
                                  GGA GACTAGT     GT  TT
                                  ||| |||||||     ||  ||
                                  TCT CTGGTCG     CG  GG
                                    _      TACCT_  GT
GAM394  OSBPL11  3'  AACAGCAAAACAATAATTTTTT 42890        CTAG_  A
              CA                   TGGAAGA    TG TTTTGTTGTT
                                  |||||||    || ||||||||||
                                  ACTTTTT    AC AAAACGACAA
                                      TAATA  _
GAM394  OSGEP    3'  AGCAATAAAATATTTTTGGTTT 35128         TG__
              TTT                   GAAGACTAG   ATTTTGTTGTT
                                  |||||||||   ||||||||||
                                  TTTTTGGTT   TAAAATAACGA
                                       TTTA
GAM394  P37NB    3'  AATGATGGCATTAGACTTTCA  19503       A     ATT TG
                                  TGGAAG CTAGTG   T  TT
                                  |||||| ||||||  |  ||
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                                ACTTTC GATTAC   A  AA
                                   A     GGT GT
GAM394  PAK6    3'  GGCAGACTGCTGGTCTCCA   39410      A      GAT
                                TGGA GACTAGT   TTTGTT
                                |||| |||||||   ||||||
                                ACCT CTGGTCG   AGACGG
                                  _      TC_
GAM394  PB1     3'  GCAACAGAGTGAGTCTCT    37022     A    AGTG
                                GGA GACT    ATTTTGTTGT
                                ||| ||||    ||||||||||
                                TCT CTGA    TGAGACAACG
                                  _   G___
GAM394  PDZD2   5'  AGTGACTGTCGCTGGCTTTCA  80860       A       TTT  TG
                                TGGAAG CTAGTGAT   GT  TT
                                |||||| ||||||||   ||  ||
                                ACTTTC GGTCGCTG   CA  GA
                                   _       T__  GT
GAM394  PDZD2   3'  AGTCACTGGGTTTCCA      80859       A
                                TGGAAG CTAGTGATT
                                |||||| |||||||||
                                ACCTTT GGTCACTGA
                                   G
GAM394  PECI    5'  AGGTCACTAGTTTCCC      20382     A
                                GG AGACTAGTGATTT
                                || ||||||||||||
                                CC TTTGATCACTGGA
                                 C
GAM394  PELI1   5'  AATAGCAATATATTGGTTTCT  40243     A       ATT
                                GGA GACTAGTG   TTGTTGTT
                                ||| ||||||||   ||||||||
                                TCT TTGGTTAT   AACGATAA
                                  _       AT_
GAM394  PHF5A   3'  ATAATATTTTAGTCTTCT    51284          TGATTT
                                GGAAGACTAG     TGTTGT
                                ||||||||||     ||||||
                                TCTTCTGATT     ATAATA
                                      TT_____
GAM394  PIG11   3'  CAACAGGTGTCTTCC       61611        TAGTGAT
                                GGAAGAC      TTTGTTG
                                |||||||      |||||||
                                CCTTCTG      GGACAAC
                                   T_______
GAM394  PKNOX2  3'  AACAACAGGACAATGGTTTTTT 90873          G  A
          A                      TGGAAGACTA TG TTTTGTTGTT
                                ||||||||||  || ||||||||||
                                ATTTTTTGGT AC AGGACAACAA
                                      A  _
GAM394  PNMA5   5'  GCAGTGAGGCTGTCTCC     73597     A   T   GAT  TG
                                GGA GAC AGT   TT  TTGT
                                ||| ||| |||   ||  ||||
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                                CCT CTG TCG   GA  GACG
                                  _  _  ___  GT
GAM394  POF1B    3'  AACAGGTGTGAGTTTTCCA   46217        AGTGAT
                                TGGAAGACT     TTTGTT
                                |||||||||     ||||||
                                ACCTTTTGA     GGACAA
                                     GTGT__
GAM394  POLE3    3'  AGCAGAATCCTGTTTT     33854      T  T
                                AAGAC AG GATTTTGTT
                                ||||| || |||||||||
                                TTTTG TC CTAAGACGA
                                  _ _
GAM394  POP5     3'  AACAGCATCTTCCACAGTTTTC 31922        A  ATTT_
           CA                     TGGAAGACT GTG    TGTTGTT
                                |||||||||| |||    |||||||
                                ACCTTTTGA CAC    ACGACAA
                                     _  CTTCT
GAM394  POT1     3'  AATGGCAAAGTTGCTTTGTT  31278    T_ TG     TG
                                GAC  AG  ATTTTGT  TT
                                |||  ||  |||||||  ||
                                TTG  TC  TGAAACG  AA
                                  TT  GT     GT
GAM394  PP1628   3'  GGTGGCATTCTGTGTCTTCT  47306       _  TGATTT  TG
                                GGAAGAC TAG     TGT  TT
                                ||||||| |||     |||  ||
                                TCTTCTG GTC     ACG  GG
                                    T  TT____  GT
GAM394  PPP2R3A  5'  GGCAACGAGGTTTCTCTGTC  10750    T_ T
                                GAC  AG GATTTTGTTGTT
                                |||  || ||||||||||||
                                CTG  TC TTGGAGCAACGG
                                  TC  T
GAM394  PRO0159  5'  GATAATGAGGTAGTGATACTGT 26112    T  _____  TG
           CTTCTA                  GAC AGTG    ATTT  TTGTT
                                |||| ||||    ||||  |||||
                                CTG TCAT    TGGA  AATAG
                                  _   AGTGA   GT
GAM394  PRO0478  3'  AGTGGTGAGATCATAGCTCACA 26182    GA  A  G    TG TG
                                TG  AG CTA TGATTT  T  TT
                                ||  || ||| ||||||  |  ||
                                AC  TC GAT ACTAGA  G  GA
                                 AC  _  _     GT GT
GAM394  PRO1257  3'  AATGGTTTGTTACTAGTCT   37706         TTT TT
                                AGACTAGTGAT   G  GTT
                                ||||||||||   |  |||
                                TCTGATCATTG   T  TAA
                                      TT_ GG
GAM394  PRO1483  3'  ATAAACAGATTCGGTTTTCTA  37717        AGT  T    GTT
                                TGGAAGACT   GA TTTGTT
                                |||||||||   || ||||||
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                                ATCTTTTGG  CT AGACAA
                                    ___ T    ATAG
GAM394  PROZ    3'  AGCAGCAGAGCCGCCGTTTGCT 13978   A   TA  AT
                                GG AGAC  GTG  TTTGTTGTT
                                || ||||  |||  |||||||||
                                TC TTTG  CGC  AGACGACGA
                                 G   C_  CG
GAM394  PRRG2   3'  AATGGTGGGAGTAGGGGTCATC 6290    A   AG  A   TG TG
          C                      GGA GACT  TG TTT  T  TT
                                ||| ||||  || |||  |  ||
                                CCT CTGG  AT AGG  G  AA
                                  A   GG  G   GT GT
GAM394  PRSS12  3'  AATGGCAAGATCTGTTTTT   13246      TAGT      TG
                                GAAGAC   GATTTTGT  TT
                                ||||||   ||||||||  ||
                                TTTTTG   CTAGAACG  AA
                                   T___      GT
GAM394  PRTD-NY3 3'  AGCAATAAAATCACTGTATATC 48147    AG_  T
          T                     GGA   AC AGTGATTTTGTTGTT
                                |||   || ||||||||||||||
                                TCT   TG TCACTAAAATAACGA
                                  ATA  _
GAM394  PTBP2   3'  GCAGCATTTTTAGTTTTT    41037        TGATTT
                                GAAGACTAG     TGTTGT
                                |||||||||     ||||||
                                TTTTTGATT     ACGACG
                                     TTT___
GAM394  PTBP2   3'  ACAACAAAGTGATTTCT    41029    CT   G
                                AGA  AGT ATTTTGTTGT
                                |||  ||| ||||||||||
                                TCT  TTA TGAAACAACA
                                  __   G
GAM394  PTK6    3'  AATAGTAAGTCACACTAAGTCT 19932       _   AT_
          TCT                     GGAAGACT AGTG   TTTGTTGTT
                                |||||||| ||||   |||||||||
                                TCTTCTGA TCAC   GAATGATAA
                                    A   ACT
GAM394  PTK9    3'  AACATTGTAATACTAGTTTTTT 11022          __ TT   GTT
          A                      TGGAAGACTAGTG  AT  TGTT
                                ||||||||||||  ||  ||||
                                ATTTTTTGATCAT  TG  ACAA
                                       AA  TT
GAM394  PTRF    3'  GCAGCAGGACCATTTTTC    63501    CT   A
                                GA  AGTG TTTTGTTGT
                                ||  |||| |||||||||
                                CT  TTAC AGGACGACG
                                 TT   C
GAM394  RAB10   3'  ACAACGAAAGGCTTTTC    85172    CT   GA
                                GA  AGT  TTTTGTTGT
                                ||  |||  |||||||||
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                                CT  TCG  AAAGCAACA
                                 TT   G_
GAM394  RAB10    3'  ACAGTGGAATTTTCTGTC    85173     T  T_    TG
                                GAC AG  GATTT  TTGT
                                ||| ||  |||||  ||||
                                CTG TC  TTAAG  GACA
                                  _ TT    GT
GAM394  RAB20    3'  AACAGCAAGGAATTATTTTCCA 35152        C    GA
                                TGGAAGA TAGT  TTTTGTTGTT
                                |||||||  ||||  ||||||||||
                                ACCTTTT ATTA  GGAACGACAA
                                    _   A_
GAM394  RAB40B   3'  GATAAAGTTTTTGCTAGTTATT 22375     A      ___       GTT
              TA                  GGA GACTAGT   GATTTTGTT
                                ||| |||||||   |||||||||
                                TTT TTGATCG   TTGAAATAG
                                  A      TTT
GAM394  RAN      3'  GATGACAGGTCAGCAGTATTCT 20906      G   AG     T  TG
              A                   TGGAA ACT  TGATTT GT  TT
                                ||||| |||  ||||||  ||  ||
                                ATCTT TGA  ACTGGA CA  AG
                                   A  CG     _ GT
GAM394  RBAK     3'  AATGGTAAAATACCTAGTTTTC 40974          TG     TT
              TA                  TGGAAGACTAG  ATTTTG  GTT
                                ||||||||||  ||||||  |||
                                ATCTTTTGATC  TAAAAT  TAA
                                      CA     GG
GAM394  RBBP1    3'  TAACAATGAAGTTATTTAACAA 43430   A  _____      TG
              GATTTCTA               CT    AGTGATTT  TTGTT   A
                                ||    ||||||||  |||||  |
                                GA    TTATTGAA  AACAA   T
                                A  ACAAT      GT
GAM394  RBBP1    3'  TAACAATGAAGTTATTTAACAA 11259   A  _____      TG
              GATTTCTA               CT    AGTGATTT  TTGTT   A
                                ||    ||||||||  |||||  |
                                GA    TTATTGAA  AACAA   T
                                A  ACAAT      GT
GAM394  RGS13    3'  AGCAATGGAATCTAGAATTCT  11338     GA   GT    TG
                                GGAA  CTA  GATTT  TTGTT
                                ||||  |||  |||||  |||||
                                TCTT  GAT  CTAAG  AACGA
                                  AA   __    GT
GAM394  RGS13    3'  AGCAATGGAATCTAGAATTCT  58575     GA   GT    TG
                                GGAA  CTA  GATTT  TTGTT
                                ||||  |||  |||||  |||||
                                TCTT  GAT  CTAAG  AACGA
                                  AA   __    GT
GAM394  RHOBTB1  3'  ACAGCAGGGGAGCTTTC    91437    CT   GA
                                GA  AGT  TTTTGTTGT
                                ||  |||  |||||||||
```

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                                CT  TCG  GGGACGACA
                                 T_  AG
GAM394  RIP5    3'  AATGGCATTTCAAGTCTTCT  38122       AG  TTT  TG
                                GGAAGACT  TGA  TGT  TT
                                ||||||||  |||  |||  ||
                                TCTTCTGA  ACT  ACG  AA
                                    __  TT_  GT
GAM394  S164    3'  AATTAGGTTATTAGTTTCCCA  60775    A        T
                                TGG AGACTAGTGATTT GTT
                                ||| ||||||||||||| |||
                                ACC TTTGATTATTGGA TAA
                                  C          T
GAM394  SAE1    3'  GATAATAAAGTTACTTGCTTT  18532    ACT
                                GAAG  AGTGATTTTGTTGTT
                                ||||  ||||||||||||||
                                TTTC  TCATTGAAATAATAG
                                  GT_
GAM394  SCDGF-B  3'  AATTAAATCATTGTGTTTTTTA 47374       _      T
                                TGGAAGAC TAGTGATTT GTT
                                |||||||| ||||||||| |||
                                ATTTTTTG GTTACTAAA TAA
                                     T       T
GAM394  SCDGF-B  3'  AATTAAATCATTGTGTTTTTTA 52446       _      T
                                TGGAAGAC TAGTGATTT GTT
                                |||||||| ||||||||| |||
                                ATTTTTTG GTTACTAAA TAA
                                     T       T
GAM394  SEC61A1  3'  AGTGACAAATAAAGCCAGTTTT 25306       A  GAT_   TG
           TTA                  TGGAAGACT GT   TTTGT  TT
                                |||||||||  ||   |||||  ||
                                ATTTTTTGA CG   AAACA  GA
                                     C  AAAT    GT
GAM394  SEMA5B   3'  GACAGTGGAGCCAGTTTGGTTT 63125        __  AT  TG
           TCT                  GGAAGACTAG  TG  TT  TTGTT
                                ||||||||||  ||  ||  |||||
                                TCTTTTGGTT  AC  AG  GACAG
                                     TG  CG  GT
GAM394  SEMA5B   3'  GATGGCAAGAGGGCAGGCTTTT 63126      A  A  GA    TG
           A                    TGGAAG CT GT  TTTTGT  TT
                                ||||||  ||  ||  ||||||  ||
                                ATTTTC GG CG  AGAACG  AG
                                   _  A  GG     GT
GAM394  SENP3    3'  GACAATAGGATCACTGCCTGCC 31614    A  AC
           A                    TGG AG  TAGTGATTTTGTTGTT
                                |||  ||  |||||||||||||||
                                ACC TC  GTCACTAGGATAACAG
                                  G  C_
GAM394  SEPT1    3'  ACCGCATCACTGTCTTCC    53422       T    TTT   T
                                GGAAGAC AGTGA   TGT GT
                                |||||||  |||||   |||  ||
```

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                                CCTTCTG TCACT   ACG CA
                                  _   ___  C
GAM394  SFXN2    3'  GTAGCAAAGGCCAATGTCTTCT 73952       TAG  A_     GTT
            A                    TGGAAGAC   TG  TTTTGTT
                                 ||||||||   ||  |||||||
                                 ATCTTCTG   AC  GAAACGA
                                     TA_  CG      TGG
GAM394  SFXN2    3'  GGCAGCAGAGTTACATGGTTCT 73951     _  _
            T                    AAGA CTA GTGATTTTGTTGTT
                                 |||| ||| ||||||||||||||
                                 TTCT GGT CATTGAGACGACGG
                                   T   A
GAM394  SH3BGRL  3'  AATAGCAGAATTAGCTTTGCTT 61939     ACT  _
            C                    GAAG   AG TGATTTTGTTGTT
                                 ||||   || ||||||||||||
                                 CTTC   TC ATTAAGACGATAA
                                   GTT  G
GAM394  SHARP    3'  AACATTTCATTGGTTTTTT   30394          TTT
                                 GGAAGACTAGTGA   TGTT
                                 ||||||||||||   ||||
                                 TTTTTTGGTTACT   ACAA
                                        TT_
GAM394  SIMRP7   5'  AATAGCGCCGGCTAGGTCTTCC 92357        _   GATTT
            A                    TGGAAGAC TAGT    TGTTGTT
                                 |||||||| ||||    |||||||
                                 ACCTTCTG ATCG    GCGATAA
                                     G   GCC__
GAM394  SKRP1    3'  GACAATGGACAACTGTAGTTTT 55146       __  GAT  TG
            T                    GAAGACT  AGT   TT  TTGTT
                                 |||||||  |||   ||  |||||
                                 TTTTTGA  TCA   AG  AACAG
                                    TG   AC_  GT
GAM394  SLC15A2  3'  AATAACAAAGAAATGGTATTTC 40794     G   GTGA
            A                    TGGAA ACTA    TTTTGTTGTT
                                 |||||  ||||   ||||||||||
                                 ACTTT TGGT    GAAACAATAA
                                   A   AAA_
GAM394  SLC1A7   3'  GGCGGCAGGCAGGGGTTATCC  21909    A   AG  AT
                                 GGA GACT  TG  TTTGTTGTT
                                 |||  ||||  ||  |||||||||
                                 CCT TTGG  AC  GGACGGCGG
                                   A   GG  __
GAM394  SLC2A10  3'  AATGACATCATGTTAGTCTTT  47811       __   TTT   TG
                                 GAAGACTA  GTGA   TGT  TT
                                 ||||||||  ||||   |||  ||
                                 TTTCTGAT  TACT   ACA  AA
                                     TG    ___   GT
GAM394  SLC31A2  3'  GGTGGCAGGGTTACTGAGCCCA 60129     AAGAC         TG
                                 TGG    TAGTGATTTTGT  TT
                                 |||    ||||||||||||  ||
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                                ACC    GTCATTGGGACG  GG
                                  CGA__         GT
GAM394  SLC7A11  3'  GGACAAAGTCAGACTCCA    26754     AGACTAG       TG
                                TGGA      TGATTTTGT  T
                                ||||      |||||||||  |
                                ACCT      ACTGAAACA  G
                                  CAG____       GT
GAM394  SMARCF1  3'  AGCAGCAAGCTGTAGTTTTT   57481       GTGAT
                                GAAGACTA    TTTGTTGTT
                                ||||||||    |||||||||
                                TTTTTGAT    GAACGACGA
                                    GTC__
GAM394  SMARCF1  3'  AGCAGCAAGCTGTAGTTTTT   37431       GTGAT
                                GAAGACTA    TTTGTTGTT
                                ||||||||    |||||||||
                                TTTTTGAT    GAACGACGA
                                    GTC__
GAM394  SMARCF1  3'  AGCAGCAAGCTGTAGTTTTT   20035       GTGAT
                                GAAGACTA    TTTGTTGTT
                                ||||||||    |||||||||
                                TTTTTGAT    GAACGACGA
                                    GTC__
GAM394  SMCR7    3'  GATGGCATTTTCCTGCTGTCTT 57508       T  __  TTT  TG
           CT                    GGAAGAC AGT  GA   TGT  TT
                                |||||||  |||  ||   |||  ||
                                TCTTCTG TCG  CT   ACG  AG
                                   _  TC  TTT   GT
GAM394  SNAP29   3'  AACAGTGCATTAGTTTTT    16535         ATT
                                GAAGACTAGTG   TTGTT
                                ||||||||||   |||||
                                TTTTTGATTAC   GACAA
                                     GT_
GAM394  SNRPF    3'  GACAATAAAGATTTGTTTGTTT 60170       T  TG __
           TTCA                   GGAAGAC AG  A  TTTTGTTGTT
                                |||||||  ||  |  ||||||||||
                                CTTTTTG TT  T  GAAATAACAG
                                    T  GT TA
GAM394  SS18L2   3'  AGCAATAGAATAATCTTCCA   32838       CTAGTG
                                TGGAAGA     ATTTTGTTGTT
                                |||||||     ||||||||||||
                                ACCTTCT     TAAGATAACGA
                                    AA_____
GAM394  ST7L     3'  AACAATGAATATAAGCCTTCCA 57572       A  A   AT  TG
                                TGGAAG CT GTG  TT  TTGTT
                                ||||||  ||  |||  ||  |||||
                                ACCTTC GA TAT  AA  AACAA
                                   C  A   __  GT
GAM394  STAM2    3'  AACAATGGACATTAGTTTTT   19559         AT  TG
                                GAAGACTAGTG  TT  TTGTT
                                ||||||||||  ||  |||||
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                                TTTTTGATTAC  AG  AACAA
                                     __ GT
GAM394  STK17A   3' GTCTACTAAAATTGCTACTTTT 16476       C  TG    TTGTT
           TCA                   TGGAAGA TAG  ATTTTG
                                 ||||||| |||  ||||||
                                 ACTTTTT ATC  TAAAAT
                                    C  GT    CATCTGT
GAM394  STK33    5' AACTTTTAGGATTAGCTAGTTT 62896         _      TT_
           TCTA                   GGAAGACTAG TGATTTTG  GTT
                                 |||||||||| ||||||||  |||
                                 TCTTTTGATC ATTAGGAT  CAA
                                      G      TTT
GAM394  STK38L   3' AGCAGCAGCTATCTGTCTTTT 69172       TA  ATT
                                 GGAAGAC  GTG  TTGTTGTT
                                 |||||||  |||  ||||||||
                                 TTTTCTG  TAT  GACGACGA
                                    TC  C__
GAM394  STRN3    3' AACAGTGGGGTTTAGTACTCCA 27404     AG   GT   TG
                                 TGGA  ACTA  GATTT  TTGTT
                                 ||||  ||||  |||||  |||||
                                 ACCT  TGAT  TTGGG  GACAA
                                   CA   __    GT
GAM394  STRN3    3' TGACAATAAAGTATTTTTTCTA 27409      TG_____
           GTCTTCC                ACTAG     ATTTTGTTGTT  G
                                 |||||     ||||||||||  |
                                 TGATC     TGAAATAACAG  T
                                   TTTTTTA
GAM394  TCL6     3' GGCAGCAAGAATTTGGCTCTTC 40109      _   TGA
           T                     GGAAGA CTAG  TTTTGTTGTT
                                 ||||||| ||||  ||||||||||
                                 TCTTCT GGTT  AGAACGACGG
                                    C   TA_
GAM394  TCL6     3' GGCAGCAAGAATTTGGCTCTTC 40142      _   TGA
           T                     GGAAGA CTAG  TTTTGTTGTT
                                 ||||||| ||||  ||||||||||
                                 TCTTCT GGTT  AGAACGACGG
                                    C   TA_
GAM394  TGIF2    3' GACGACAGCCTTTAGTTTTCC  41452        TGATT
                                 GGAAGACTAG    TTGTTGTT
                                 ||||||||||    ||||||||
                                 CCTTTTGATT    GACAGCAG
                                      TCC__
GAM394  TINAG    3' GACAGTGGAATCTTTGTCTCTT 27097     _   TAGT   TG
           CA                    TGGA AGAC   GATTT  TTGTT
                                 |||| ||||   |||||  |||||
                                 ACTT TCTG   CTAAG  GACAG
                                   C   TTT_    GT
GAM394  TLR8     3' AATGACATTTCTGTATTAGTTA 56862     A      ATTT__  TG
           TCTA                   GGA GACTAGTG     TGT  TT
                                 ||| ||||||||     |||  ||
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                                TCT TTGATTAT     ACA  AA
                                  A       GTCTTT   GT
GAM394  TLR8     3'  AATGACATTTCTGTATTAGTTA 33502     A      ATTT__   TG
             TCTA                   GGA GACTAGTG     TGT  TT
                                ||| ||||||||     |||  ||
                                TCT TTGATTAT     ACA  AA
                                  A       GTCTTT   GT
GAM394  TPARL    3'  AACAGTAGTTTAATCATTGGTC 37476           ___
             TTTT                   AAGACTAGTGATT   TTGTTGTT
                                ||||||||||||   ||||||||
                                TTCTGGTTACTAA   GATGACAA
                                       TTT
GAM394  TPD52    3'  AATAATGGAGAATCACTTTTCT 17418     CT       __
                                AGA  AGTGATTTT  GTTGTT
                                |||  |||||||||  ||||||
                                TCT  TCACTAAGA  TAATAA
                                  TT       GG
GAM394  TRIM6    3'  AACAATAAAAAAAAATACGTCT 54126        _ GTGA_
             TTCA                   GGAAGAC TA    TTTTGTTGTT
                                ||||||| ||    ||||||||||
                                CTTTCTG AT    AAAATAACAA
                                    C  AAAAA
GAM394  TSPEAR   3'  GGACGGTCTGGTCTTGCA    58722    G      TGATT   TG
                                TG AAGACTAG    TTGT  T
                                || ||||||||    ||||  |
                                AC TTCTGGTC    GGCA  G
                                 G       T____    GT
GAM394  TTTY8    3'  AGCAATAAGGTGGGTCTTCC   50849        AGTG
                                GGAAGACT    ATTTTGTTGTT
                                ||||||||    ||||||||||
                                CCTTCTGG    TGGAATAACGA
                                     G___
GAM394  U5-100K  3'  GACAGTGGAATCTTACTGTC   59679     T  __    TG
                                GAC AGT  GATTT  TTGTT
                                ||| |||  |||||  |||||
                                CTG TCA  CTAAG  GACAG
                                  _  TT    GT
GAM394  UBN1     3'  GGCAGTGGGGTTATGTGTC    33731     TA      TG
                                GAC  GTGATTT  TTGTT
                                |||  |||||||  |||||
                                CTG  TATTGGG  GACGG
                                  TG      GT
GAM394  UCH37    3'  ACAACTGTTAGTTTTCT     32021          TGATTTT
                                GGAAGACTAG      GTTGT
                                ||||||||||      |||||
                                TCTTTTGATT      CAACA
                                      GT_____
GAM394  USP22    3'  AAAATTGCTGTTCTTTT     67994       C   TG
                                GGAAGA TAG  ATTTT
                                |||||| |||  |||||
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                                TTTTCT GTC  TAAAA
                                   T   GT
GAM394  USP22    3'  AGCATCTCGCGGTTTTCTA    68000         A    TTT
                                TGGAAGACT GTGA   TGTT
                                ||||||||| ||||   ||||
                                ATCTTTTGG CGCT   ACGA
                                      _   CT_
GAM394  USP25    3'  AGCAGATTTCTGCATTGGTTTT 25439          AT____     GTT
           CCA                    AAGACTAGTG     TTTGTT
                                ||||||||||     ||||||
                                TTTTGGTTAC     AGACGA
                                      GTCTTT       T
GAM394  XRN2     3'  TGGAATAGGAGTACTGGTTTTT 24302           A      GTT
           CA                     TGGAAGACTAGTG TTTTGTT
                                |||||||||||| |||||||
                                ACTTTTTGGTCAT AGGATAA
                                      G      GGTA
GAM394  YKT6     3'  AGCAGCAGGTGCTGTGGTCTCT 21596    GA     GTGAT
           CA                     TG  AGACTA    TTTGTTGTT
                                ||  ||||||    |||||||||
                                AC  TCTGGT    GGACGACGA
                                 TC     GTCGT
GAM394  ZDHHC2   3'  AACAATAGAAATATCTGCAGTC 33006       A  _  ___
           TTTCA                    AGACT GT GAT   TTTGTTGTT
                                ||||| || |||   ||||||||
                                TCTGA CG CTA   AGATAACAA
                                   _ T   TAA
GAM394  ZDHHC7   3'  ACAGTGAAGGTGGCTTCC    34837      A   GTGA   TG
                                GGAAG CTA    TTT  TTGT
                                ||||| |||    |||  ||||
                                CCTTC GGT    GAA  GACA
                                   _  G___   GT
GAM394  ZNF185   3'  AGCAGTTTTTCATTTGGTCTTC 23106          _   TT__    GTT
           CA                     GGAAGACTAG TGA    TTGTT
                                |||||||||| |||    |||||
                                CCTTCTGGTT ACT    GACGA
                                      T   TTTT
GAM394  ZNF220   5'  AACAACAGGTTGTTTTGGTTTC 22223     A     TGAT_
           TA                     TGGA GACTAG     TTTGTTGTT
                                ||||| ||||||     |||||||||
                                ATCT TTGGTT     GGACAACAA
                                   _     TTGTT
GAM394  ZNF238   3'  GCAACTTCTGGTTTTCT     20962          TGATTTT
                                GGAAGACTAG      GTTGT
                                ||||||||||      |||||
                                TCTTTTGGTC      CAACG
                                      TT_____
GAM394  ZNF287   5'  AGCGACAGGGTCTCTTATCCA  40296     AGACT  T
                                TGGA    AG GATTTTGTTGTT
                                ||||    || ||||||||||||
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                                ACCT    TC CTGGGACAGCGA
                                  AT___ T
GAM394  ZNF294   3' AATAATGGAGCATTGTTTTTCC 70824       C    A  TG
           A                     TGGAAGA TAGTG TTT  TTGTT
                                 ||||||| ||||| |||  |||||
                                 ACCTTTT GTTAC GAG  AATAA
                                    T   _  GT
GAM394  ZNF294   3' AATAATTTTATTGCAGTCTTCC 70825        A TG  TTT
           A                     TGGAAGACT G  AT   GTTGTT
                                 ||||||||| |  ||   ||||||
                                 ACCTTCTGA C  TA   TAATAA
                                      _ GT  TTT
GAM394  ZNF300   3' AGTGGCTCATTTTACTGTCTTC 53473       T    TTTT_ TG
           T                     GGAAGAC AGTGA    GT  TT
                                 ||||||| |||||    ||  ||
                                 TCTTCTG TCATT    CG  GA
                                    _    TTACT  GT
GAM394  ZNF304   3' GGGATTGCTGTCTTCT     40317       T  TG
                                 GGAAGAC AG  ATTTT
                                 ||||||| ||  |||||
                                 TCTTCTG TC  TAGGG
                                    _ GT
GAM394  ZNF333   3' AGACAGAATTTCCTTCC     50568      ACTAGT      TG
                                 GGAAG     GATTTTGT  T
                                 |||||     ||||||||  |
                                 CCTTC     TTAAGACA  A
                                   CT____       GT
GAM394  ZNF387   3' GCAACAAAATTGTGTTC     27995     G  TAGT
                                 GAA AC    GATTTTGTTGT
                                 ||| ||    ||||||||||
                                 CTT TG    TTAAAACAACG
                                   G  ____
GAM394  ZNF396   3' AACAACAAAATTATCTATTTTC 75666        C  _
           CA                      TGGAAGA TAG TGATTTTGTTGTT
                                 ||||||| ||| ||||||||||||
                                 ACCTTTT ATC ATTAAAACAACAA
                                    _  T
GAM394  ZNF396   3' AATAATACATGTATTGTGTTTT 75667         _    ATTT
           CCA                     TGGAAGAC TAGTG    TGTTGTT
                                 ||||||| |||||    |||||||
                                 ACCTTTTG GTTAT    ATAATAA
                                     T    GTAC
GAM394  LOC114971 3' AGTGGCAGGGTCAAGCTTGTA  73146    G   A  AG       TG
                                 TG AAG CT  TGATTTTGT  TT
                                 || ||| ||  |||||||||  ||
                                 AT TTC GA  ACTGGGACG  GA
                                  G  _ __        GT
GAM394  LOC114987 3' GACAATGAGATTAAGCTTC    59123      A  AG     TG
                                 GAAG CT  TGATTT  TTGTT
                                 |||| ||  ||||||  |||||
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                                CTTC GA  ATTAGA  AACAG
                                  _ __     GT
GAM394   LOC115708 3'  AGCGGCAGAGTGGGTTGTCTGC 73545    A    TAGTG
             C                    GG AGAC     ATTTTGTTGTT
                                  || ||||     ||||||||||
                                  CC TCTG     TGAGACGGCGA
                                   G    TTGGG
GAM394   LOC116068 3'  AACAGCAGAATCATTGCATTT  73722     GAC
                                  GAA   TAGTGATTTTGTTGTT
                                  |||   ||||||||||||||||
                                  TTT   GTTACTAAGACGACAA
                                    AC_
GAM394   LOC116236 3'  GGCAACAGGACATATGTTTCCA 73816       ACTA   A
                                  TGGAAG    GTG TTTTGTTGTT
                                  ||||||    ||| ||||||||||
                                  ACCTTT    TAC AGGACAACGG
                                     GTA_   _
GAM394   LOC118611 5'  GACGACAAAGAGACCAGTTTTT 75474        A  GA
             C                    GGAAGACT GT  TTTTGTTGTT
                                  |||||||| ||  ||||||||||
                                  CTTTTTGA CA  GAAACAGCAG
                                       C  GA
GAM394   LOC118851 3'  GAAATCACTGATTTTTT     75501        C
                                  GGAAGA TAGTGATTTT
                                  |||||| ||||||||||
                                  TTTTTT GTCACTAAAG
                                     A
GAM394   LOC118851 3'  GCAGCAGAATTCCTGCCA    75502     AAGAC   TG
                                  TGG     TAG  ATTTTGTTGT
                                  |||     |||  ||||||||||
                                  ACC     GTC  TAAGACGACG
                                    ______   CT
GAM394   LOC120103 3'  AAAGCAGAATCATGAGTCTTCT 74001          A         GTT
             A                     TGGAAGACT GTGATTTTGTT
                                   |||||||||  ||||||||||
                                   ATCTTCTGA TACTAAGACGA
                                         G          AA
GAM394   LOC120196 3'  ACTAAATTATTAGTTTTGTA   75545    G           T
                                  TG AAGACTAGTGATTT GT
                                  || |||||||||||||| ||
                                  AT TTTTGATTATTAAA CA
                                   G            T
GAM394   LOC120939 3'  AGTGACACACGCTAGTCTCTA  76246      A      ATTT   TG
                                  TGGA GACTAGTG    TGT  TT
                                  |||| ||||||||    |||  ||
                                  ATCT CTGATCGC    ACA  GA
                                    _       AC__   GT
GAM394   LOC121504 3'  GGCAGTAGGATTGCTGGAGGCC 74099     AAGA    TG
             A                     TGG    CTAG  ATTTTGTTGTT
                                   |||    ||||  ||||||||||
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                                ACC   GGTC  TAGGATGACGG
                                  GGA_   GT
GAM394   LOC121504 3'  GACAGTAATCATATCTTCCA  74097       CTA    _
                                TGGAAGA  GTGATT TTGTT
                                |||||||  |||||| |||||
                                ACCTTCT  TACTAA GACAG
                                   A__     T
GAM394   LOC121506 3'  AACAACAGGATCACTAGGCCTG 74092    A  A_
           CC                     GG AG  CTAGTGATTTTGTTGTT
                                || ||  ||||||||||||||||
                                CC TC  GATCACTAGGACAACAA
                                 G  CG
GAM394   LOC122330 5'  AATGACCATTATCAGTTTTCCA 76264        A    TTT  TG
                                TGGAAGACT GTGAT   GT  TT
                                |||||||| |||||   ||  ||
                                ACCTTTTGA TATTA   CA  AA
                                     C    C__  GT
GAM394   LOC124739 5'  AGCGGCGAAACCCAGGTCTGTC 74326   GA    AG  A_
                                G  AGACT  TG  TTTTGTTGTT
                                |  |||||  ||  ||||||||||
                                C  TCTGG  AC  AAAGCGGCGA
                                 TG    __  CC
GAM394   LOC125058 3'  AGACAAAATTAGAGTCT     59855      AG       TG
                                AGACT  TGATTTTGT  T
                                |||||  |||||||||  |
                                TCTGA  ATTAAAACA  A
                                   G_       GT
GAM394   LOC126231 3'  AATGATGGAATGTTAGTCTT   74465       GT A   TG TG
                                AAGACTA  G TTT  T  TT
                                |||||||  | |||  |  ||
                                TTCTGAT  T AAG  A  AA
                                    TG _   GT GT
GAM394   LOC127841 5'  AGTGGCAGAATTATTTATGATT 74693     GACT_        TG
           CT                     GGAA    AGTGATTTTGT  TT
                                ||||    ||||||||||  ||
                                TCTT    TTATTAAGACG  GA
                                  AGTAT         GT
GAM394   LOC129607 3'  AGCAGCAGACAAGATCTTCCA  74884       CTAG  AT
                                TGGAAGA   TG  TTTGTTGTT
                                |||||||   ||  |||||||||
                                ACCTTCT   AC  AGACGACGA
                                    AGA_  __
GAM394   LOC130355 5'  GATGGTGGAAAGCTGGACTGGT 74930        GA____   TG TG
           CTCCC                  AGACTAGT     TTT  T  TT
                                ||||||||     |||  |  ||
                                TCTGGTCA     AAG  G  AG
                                     GGTCGA   GT GT
GAM394   LOC130436 3'  CAGCAAGATCCTTTGG      74934      T_
                                CTAG  GATTTTGTTG
                                ||||  ||||||||||
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                                GGTT  CTAGAACGAC
                                  TC
GAM394   LOC131368 3'  GATAGTGAAAATAGTTGTTAGC 75861    A   TG ____  TG
           TTCCA                  AG CTAG  AT   TT  TTGTT
                                || ||||  ||   ||  |||||
                                TC GATT  TG   AA  GATAG
                                 _   GT  ATAA  GT
GAM394   LOC132112 3'  TTTGGGCAAGATCATTGGTTTA 75037    A            GTT
           TCA                    TGG AGACTAGTGATTTTGTT
                                ||| ||||||||||||||||
                                ACT TTTGGTTACTAGAACGG
                                  A             GTTTG
GAM394   LOC132625 3'  AACAGCAAGAGCCCATCTTTTA 75893       CTA  GA
                                TGGAAGA   GT  TTTTGTTGTT
                                |||||||   ||  ||||||||||
                                ATTTTCT   CG  AGAACGACAA
                                    ACC  __
GAM394   LOC133383 3'  AATCAGAAATTATTAGGTTTTC 75087        _       GTTGTT
           TA                     TGGAAGAC TAGTGATTTT
                                |||||||| ||||||||||
                                ATCTTTTG ATTATTAAAG
                                    G         ACTAA
GAM394   LOC135932 3'  GGTGGCATAATTTGAGTCTTCT 76199        AGT   T   TG
                                GGAAGACT   GATT TGT  TT
                                ||||||||   |||| |||  ||
                                TCTTCTGA   TTAA ACG  GG
                                    GT_   T   GT
GAM394   LOC138389 5'  GACACGATGCTGGTCTTCCA   76225          G   T
                                TGGAAGACTAGT ATT TGTT
                                |||||||||||| ||| ||||
                                ACCTTCTGGTCG TAG ACAG
                                       _  C
GAM394   LOC138693 5'  GATGATGAAATCAGAGCTCTCA 75951    GA  A  AG     TG TG
                                TG  AG CT  TGATTT  T  TT
                                ||  || ||  ||||||  |  ||
                                AC  TC GA  ACTAAA  A  AG
                                 TC  _  G_     GT GT
GAM394   LOC139231 3'  GGCGGTGAAGTGGGCGTCTTC  75376       TAGTG   TG
                                GAAGAC    ATTT  TTGTT
                                ||||||    ||||  |||||
                                CTTCTG    TGAA  GGCGG
                                   CGGG_   GT
GAM394   LOC143098 5'  AACAGTGAGATCAGAGAGCT   76453    A  AG_     TG
                                AG CT   TGATTT  TTGTT
                                || ||   ||||||  |||||
                                TC GA   ACTAGA  GACAA
                                 _ GAG     GT
GAM394   LOC143286 3'  AATGGTGGCTTTATGTTTTCCA 82942        TA    TT TG TG
                                TGGAAGAC  GTGA  T  T  TT
                                ||||||||  ||||  |  |  ||
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                                ACCTTTTG  TATT  G  G  AA
                                    __    TC GT GT
GAM394   LOC143381 3'  AATGGCAAATCCAGCTCTTCCA 76542       CTAG  AT    TG
                                TGGAAGA   TG  TTTGT  TT
                                |||||||   ||  |||||  ||
                                ACCTTCT   AC  AAACG  AA
                                   CG__  CT    GT
GAM394   LOC143677 3'  GGCAGCCCTGGGCAGTCTTCT  82978        A  GATTTT
                                GGAAGACT GT     GTTGTT
                                ||||||||  ||    ||||||
                                TCTTCTGA CG     CGACGG
                                   _ GGTCC_
GAM394   LOC143914 5'  AGCAGTGAGGGGCAGGCTCTTC 76610       _  A  GA   TG
           T                     GGAAGA CT GT  TTT  TTGTT
                                ||||||  ||  ||  |||  |||||
                                TCTTCT GG CG  GGA  GACGA
                                   C  A  G_   GT
GAM394   LOC144245 5'  AACAGCGACCCGCTGTTTTCC  70816        T    ATT
                                GGAAGAC AGTG   TTGTTGTT
                                |||||||  ||||   ||||||||
                                CCTTTTG TCGC   AGCGACAA
                                   _   CC_
GAM394   LOC144305 3'  AACAATAACATCTCTAGATTTC 83030       A    T   T
           CA                     TGGAAG CTAG GAT TTGTTGTT
                                ||||||  ||||  |||  ||||||||
                                ACCTTT GATC CTA AATAACAA
                                   A   T   C
GAM394   LOC144747 3'  CCTTCCCGGGGTTTCTGGTTTT 76952          T      TTGTT
           TCA                     TGGAAGACTAG GATTTTG
                                ||||||||||  |||||||
                                ACTTTTTGGTC TTGGGGC
                                      T      CCTTCCA
GAM394   LOC144817 5'  GCAGCAGACAGGGTCTCCA   76969      A   AG  AT
                                TGGA GACT  TG  TTTGTTGT
                                ||||  ||||  ||  ||||||||
                                ACCT CTGG  AC  AGACGACG
                                   _   G_  __
GAM394   LOC144817 3'  GGCAATGAAAACAGAAGTTTTT 76970        AG  A   TG
                                GAAGACT  TG TTT  TTGTT
                                |||||||  || |||  |||||
                                TTTTTGA  AC AAA  AACGG
                                    AG  A   GT
GAM394   LOC145082 5'  GGGCAAAATCGTGGCTC     83244    _  G       TG
                                GA CTA TGATTTTGT  T
                                || ||| |||||||||  |
                                CT GGT GCTAAAACG  G
                                 C  _        GT
GAM394   LOC145453 3'  AACAATAAAACGTAGGGGTTTC 77132      GA  AG  A
                                GGAA  CT  TG TTTTGTTGTT
                                ||||  ||  || ||||||||||
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                                CTTT  GG  GC AAAATAACAA
                                  GG  AT  _
GAM394   LOC145553 5'  GGCAGCAAGATCACACACTTT  56667      ACTA
                                GAAG    GTGATTTTGTTGTT
                                ||||    ||||||||||||||
                                TTTC    CACTAGAACGACGG
                                  ACA_
GAM394   LOC145566 5'  GATGATGGGATCAGTGTGTTTT 77274       _  G      TG TG
                                AAGAC TA TGATTT  T  TT
                                ||||| || ||||||  |  ||
                                TTTTG GT ACTAGG  A  AG
                                  T  G     GT GT
GAM394   LOC145623 5'  TAAAGTAACTGGTTTTCCA    83400            G
                                TGGAAGACTAGT ATTTTG
                                |||||||||||| ||||||
                                ACCTTTTGGTCA TGAAAT
                                       A
GAM394   LOC145644 3'  GACTGCATCGATCGCTGGTTAT 64661     A         T_   T
           CT                     GGA GACTAGTGATT  TGT GTT
                                ||| ||||||||||  ||| |||
                                TCT TTGGTCGCTAG  ACG CAG
                                  A          CT   T
GAM394   LOC145748 3'  GGCAACAAAGTCCAGCTTGT   83468    T   __
                                AC AGT  GATTTTGTTGTT
                                || |||  ||||||||||||
                                TG TCG  CTGAAACAACGG
                                 T   AC
GAM394   LOC145919 3'  GACAACGAGGATGAAGACTTCT 77570       A  AGTGA
           A                     TGGAAG CT     TTTTGTTGTT
                                ||||||| ||     ||||||||||
                                ATCTTC GA     GGAGCAACAG
                                   A  AGTA_
GAM394   LOC145945 5'  GGCAACAGGGCACGTGTTTTT  83577       TA   A
                                GAAGAC  GTG TTTTGTTGTT
                                ||||||  ||| ||||||||||
                                TTTTTG  CAC GGGACAACGG
                                   TG  _
GAM394   LOC145955 5'  GCAGCAAGAGCGTCTCC     83592     A   TAGTGA
                                GGA GAC      TTTTGTTGT
                                ||| |||      |||||||||
                                CCT CTG      AGAACGACG
                                  _   CG____
GAM394   LOC146489 3'  AGCAGTGGTTCCTGTGTTTTTC 70800        _   T  TT TG
           A                     TGGAAGAC TAG GA  T  TTGTT
                                |||||||| ||| ||  |  |||||
                                ACTTTTTG GTC CT  G  GACGA
                                     T   _  T_ GT
GAM394   LOC146503 3'  AGCAGTGGTTCCTGTGTTTTTC 77929        _   T  TT TG
           A                     TGGAAGAC TAG GA  T  TTGTT
                                |||||||| ||| ||  |  |||||
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                                ACTTTTTG GTC CT  G  GACGA
                                     T   _  T_ GT
GAM394   LOC146565 5'  AACAATGGGAACCAGTCTTTCA 60500         A  GA   TG
                                TGGAAGACT GT  TTT  TTGTT
                                ||||||||| ||  |||  |||||
                                ACTTTCTGA CA  AGG  AACAA
                                     C  __  GT
GAM394   LOC146782 5'  ATAACAAAATCGCCTTT     76290      ACTA
                                GAAG   GTGATTTTGTTGT
                                ||||   |||||||||||||
                                TTTC   CGCTAAAACAATA
                                  ____
GAM394   LOC146783 3'  AGCAATAAAAAGCAAGTTTTC  83787        A  GA
                                GAAGACT GT  TTTTGTTGTT
                                ||||||| ||  ||||||||||
                                CTTTTGA CG  AAAATAACGA
                                    A  A_
GAM394   LOC146795 3'  AGCAACGGGATTGCTTC     78130    CT  TG
                                GA  AG  ATTTTGTTGTT
                                ||  ||  ||||||||||||
                                CT  TC  TAGGGCAACGA
                                 __ GT
GAM394   LOC146839 3'  GAAATTGCTGGTTTCC      83811     A     TG
                                GGA GACTAG  ATTTT
                                ||| ||||||  |||||
                                CCT TTGGTC  TAAAG
                                  _     GT
GAM394   LOC146845 3'  GATAACTCCAACACTAGTCTTC 58966          ATTTT
                                GAAGACTAGTG    GTTGTT
                                ||||||||||     ||||||
                                CTTCTGATCAC    CAATAG
                                       AACCT
GAM394   LOC146894 3'  AGCGGTGGCCTTGCTCTTCC   59183       CTA TG TT TG
                                GGAAGA   G  A  T  TTGTT
                                ||||||   |  |  |  |||||
                                CCTTCT   C  T  G  GGCGA
                                   ___ GT CC GT
GAM394   LOC146923 3'  TAGGGATAGATGTGCTAGTCTT 78195           AT     GTT
            CTA                   TGGAAGACTAGTG  TTTGTT
                                ||||||||||||  ||||||
                                ATCTTCTGATCGT  AGATAG
                                       GT     GGATG
GAM394   LOC147599 3'  GGCAACAGAGAGACTGTCTCCA 84041      A   T   GA
                                TGGA GAC AGT  TTTTGTTGTT
                                |||| ||| |||  ||||||||||
                                ACCT CTG TCA  GAGACAACGG
                                  _  _  GA
GAM394   LOC147791 5'  GGTGGCGGGGGAAGCGTCTCCA 84073      A   TA  GA_     TG
                                TGGA GAC  GT   TTTTGT  TT
                                |||| |||  ||   ||||||  ||
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                                ACCT CTG  CG   GGGGCG  GG
                                  _  __ AAG     GT
GAM394   LOC148021 3'  GACAGTGGAAGATGAGGTCATC 78615     A    AGTGA   TG
                T                  GGA GACT     TTT  TTGTT
                                   ||| ||||     |||  |||||
                                   TCT CTGG     AAG  GACAG
                                     A    AGTAG   GT
GAM394   LOC148195 3'  AACAACCCGAACAGGTTTTCT  84122        A  GATTTT
                                   GGAAGACT GT     GTTGTT
                                   |||||||| ||     ||||||
                                   TCTTTTGG CA     CAACAA
                                        A  AGCC__
GAM394   LOC148371 3'  AGCAGTTTTAAGTTATTAGTTT 78805             TG__
                TT                   GAAGACTAGTGATTT    TTGTT
                                   ||||||||||||||    |||||
                                   TTTTTGATTATTGAA    GACGA
                                            TTTT
GAM394   LOC148438 3'  AACAGCAGAATCATTTTTCTTC 84154       CT
                C                   GGAAGA  AGTGATTTTGTTGTT
                                   ||||||  ||||||||||||||
                                   CCTTCT  TTACTAAGACGACAA
                                      TT
GAM394   LOC148645 5'  GGGCGAGATCATAGCTC     84183    _  G        TG
                                   GA CTA TGATTTTGT  T
                                   || ||| |||||||||  |
                                   CT GAT ACTAGAGCG  G
                                    C  _        GT
GAM394   LOC148709 3'  GACCACAAATTTTGGTTTTCCA 78943           TGAT    T
                                   TGGAAGACTAG    TTTGT GTT
                                   ||||||||||    ||||| |||
                                   ACCTTTTGGTT    AAACA CAG
                                         TT__     C   T
GAM394   LOC148789 3'  AGCAGTAGACTGTATGGTCTTT 78991          GTGAT
                CA                   TGGAAGACTA     TTTGTTGTT
                                   ||||||||||     |||||||||
                                   ACTTTCTGGT     AGATGACGA
                                         ATGTC
GAM394   LOC148898 3'  AGCAGCACAATTGTCATAGTTT 84251         __ TG   T
                TTT                  GGAAGACTA  G  ATT TGTTGTT
                                   |||||||||  |  ||| |||||||
                                   TTTTTTGAT  T  TAA ACGACGA
                                        AC GT   C
GAM394   LOC148936 5'  GACAATGGGGAAAATGTCTCCA 84292     A   TAGTGA   TG
                                   TGGA GAC      TTT  TTGTT
                                   |||| |||     |||  |||||
                                   ACCT CTG     GGG  AACAG
                                     _   TAAAA_   GT
GAM394   LOC148938 5'  GACAATGGGGAAAATGTCTCCA 84272     A   TAGTGA   TG
                                   TGGA GAC      TTT  TTGTT
                                   |||| |||     |||  |||||
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                                ACCT CTG     GGG  AACAG
                                  _  TAAAA_  GT
GAM394  LOC149013 3'  TGACGGTGAGAAGTCTCCACCT 79132     _ A_____  TG
            GGTCTTCCA               CTAG TG     TTT  TTGTT   G
                                |||| ||     |||  |||||  |
                                GGTC AC     AGA  GGCAG   T
                                  C  CTCTGA   GT
GAM394  LOC149127 3'  GGCAGCTCCTGCTGTCTTCCA  84348        T   GATTTT
                                TGGAAGAC AGT     GTTGTT
                                |||||||| |||     ||||||
                                ACCTTCTG TCG     CGACGG
                                    _  TCCT__
GAM394  LOC149146 5'  AACGACAAAAGCCGGTTTCTCA 79198    GA    TA  GA
                                TG  AGAC  GT  TTTTGTTGTT
                                ||  ||||  ||  ||||||||||
                                AC  TTTG  CG  AAAACAGCAA
                                 TC    GC  __
GAM394  LOC149271 3'  GGTGGCAAAATCACAGGTT   79246     A        TG
                                GACT GTGATTTTGT  TT
                                |||| ||||||||||  ||
                                TTGG CACTAAAACG  GG
                                  A        GT
GAM394  LOC149506 3'  GCAGCGAGATCCCCTTC     84464      ACTAGT
                                GAAG     GATTTTGTTGT
                                ||||     ||||||||||
                                CTTC     CTAGAGCGACG
                                  CC____
GAM394  LOC149672 5'  ATGAACACCAGATTATTATCTT 79510       C        __   GTT
            CT                    GGAAGA TAGTGATTT  TGTT
                                ||||||  |||||||||  ||||
                                TCTTCT ATTATTAGA  ACAA
                                  _       CC    GTAA
GAM394  LOC149707 5'  GGCAGTTGTTAGTCTTC     79486         TG  TT
                                GAAGACTAG  AT  TGTT
                                |||||||||  ||  ||||
                                CTTCTGATT  TG  ACGG
                                     GT  __
GAM394  LOC149837 3'  GACAGTTGCTGTTTTCT     84735       T  TG  TT
                                GGAAGAC AG  AT  TGTT
                                |||||||  ||  ||  ||||
                                TCTTTTG TC  TG  ACAG
                                   _  GT  __
GAM394  LOC149844 3'  GGGTAAAGTCAAGGTCT     79518      AG       TG
                                AGACT  TGATTTTGT  T
                                |||||  |||||||||  |
                                TCTGG  ACTGAAATG  G
                                  A_       GT
GAM394  LOC149992 5'  GGTGGCAAAATTGCTGTC    79558     T  TG      TG
                                GAC AG  ATTTTGT  TT
                                |||  ||  |||||||  ||
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                                CTG TC  TAAAACG  GG
                                  _ GT      GT
GAM394  LOC150082 5'  AACAGCGCGGAGCAGGTTTTTT 79567         A  GA TT
          A                      TGGAAGACT GT  T  TGTTGTT
                                 ||||||||| ||  |  |||||||
                                 ATTTTTTGG CG  G  GCGACAA
                                      A  A_ GC
GAM394  LOC150290 3'  AGTGGCCCAGTTCTGGTTTTCT 79768          T    TT  TG
          A                      TGGAAGACTAG GATT  GT  TT
                                 |||||||||||| ||||  ||  ||
                                 ATCTTTTGGTC TTGA  CG  GA
                                       _   CC  GT
GAM394  LOC150397 3'  AGCGATGGAGACGGTCTTT   79836       A  GA   TG
                                 GAAGACT GT  TTT  TTGTT
                                 |||||||  ||  |||  |||||
                                 TTTCTGG CA  GAG  AGCGA
                                     _ __  GT
GAM394  LOC150426 3'  GGTGGCAAAATTGCTGTC    79869     T  TG      TG
                                 GAC AG  ATTTTGT  TT
                                 ||| ||  |||||||  ||
                                 CTG TC  TAAAACG  GG
                                   _ GT      GT
GAM394  LOC150587 3'  AATAACATTTTTCACAGTTTTC 85056          A    TTT_
          CA                     TGGAAGACT GTGA    TGTTGTT
                                 |||||||||  ||||    |||||||
                                 ACCTTTTGA CACT    ACAATAA
                                      _   TTTT
GAM394  LOC150622 3'  GGCAACAAGAGCAAAACTCTTT 79962        CTAG  A
          CA                     TGGAAGA    TG TTTTGTTGTT
                                 |||||||    || ||||||||||
                                 ACTTTCT    AC AGAACAACGG
                                     CAAA  G
GAM394  LOC151098 5'  AACAACAGAATGTACATTTTTC 80113        CTA   _
          T                      GGAAGA   GTG ATTTTGTTGTT
                                 ||||||   ||| ||||||||||||
                                 TCTTTT   CAT TAAGACAACAA
                                    TA_   G
GAM394  LOC151126 5'  GATGATGGAATTATTTACTTTT 80126        ACT       TG TG
          A                      TGGAAG   AGTGATTT  T  TT
                                 ||||||   ||||||||  |  ||
                                 ATTTTC   TTATTAAG  A  AG
                                    AT_       GT GT
GAM394  LOC151162 5'  AATATTGTTATTAGTGTTTC   85237      G       TT
                                 GGAA ACTAGTGAT  TGTT
                                 |||| |||||||||  ||||
                                 CTTT TGATTATTG  ATAA
                                   G        TT
GAM394  LOC151248 5'  AGCAATAGAATTACTGGCTT   80183     A
                                 AAG CTAGTGATTTTGTTGTT
                                 ||| ||||||||||||||||
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                                TTC GGTCATTAAGATAACGA
                                  _
GAM394  LOC151457 5'  TGGATTTGTTGGTTTTCCA   80245          TG T TT
                                TGGAAGACTAG  A T  G
                                ||||||||||  | |  |
                                ACCTTTTGGTT  T A  T
                                      GT T GG
GAM394  LOC151808 5'  AATGGCAGAAGGTCACTTTTCC 85497       ACT    __    TG
          A                      TGGAAG   AGTGAT  TTTGT  TT
                                ||||||   ||||||  |||||  ||
                                ACCTTT   TCACTG  AGACG  AA
                                   ___     GA    GT
GAM394  LOC151959 3'  TAAGCTTTCTGCTGGTCTCTA  85527      A     _  TTTT   GTT
                                TGGA GACTAGT GA    GTT
                                |||| |||||||  ||    |||
                                ATCT CTGGTCG CT    CGA
                                  _      T  TT__   ATA
GAM394  LOC152018 3'  GATGACTGGTGCTTTCA     85545        _     G
                                TGGAAG ACTAGT ATT
                                |||||| |||||| |||
                                ACTTTC TGGTCA TAG
                                   G     G
GAM394  LOC152059 3'  GATAGCAGGTCAGTTGATCTTC 80446       C  _     T
          T                      GGAAGA TAG TGATTT GTTGTT
                                |||||| ||| |||||| ||||||
                                TCTTCT GTT ACTGGA CGATAG
                                   A  G    _
GAM394  LOC152195 3'  AATGACAGAATTTTCTTCTA   85561        CTAGT       TG
                                TGGAAGA    GATTTTGT  TT
                                |||||||    ||||||||  ||
                                ATCTTCT    TTAAGACA  AA
                                    T____       GT
GAM394  LOC152559 3'  AACAGTAAAATTACTGAATATC 80615    AGAC
                                GA   TAGTGATTTTGTTGTT
                                ||   ||||||||||||||||
                                CT   GTCATTAAAATGACAA
                                 ATAA
GAM394  LOC152627 3'  GGCAATAGAATTGCTTGAACC  80630    AAGACT  TG
                                GG     AG  ATTTTGTTGTT
                                ||     ||  ||||||||||
                                CC     TC  TAAGATAACGG
                                 AAGT__  GT
GAM394  LOC152674 3'  AGAGTTGTGGTTTTCTA     85831          G
                                TGGAAGACTA TGATTTT
                                |||||||||| |||||||
                                ATCTTTTGGT GTTGAGA
                                          _
GAM394  LOC152762 3'  GGCAGCAGGCAGCGTCTGTTTT 80654        TA__  GAT
          CT                     GGAAGAC   GT   TTTGTTGTT
                                |||||||   ||  |||||||||
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                                TCTTTTG   CG  GGACGACGG
                                    TCTG  AC_
GAM394  LOC152920 5'  AATAGCAAAGTCACAGTTATTC 80739     _   A
          C                      GGAA GACT GTGATTTTGTTGTT
                                 |||| |||| ||||||||||||||
                                 CCTT TTGA CACTGAAACGATAA
                                   A   _
GAM394  LOC153205 3'  AACAATAAAGTTATTG      85940
                                 TAGTGATTTTGTTGTT
                                 ||||||||||||||||
                                 GTTATTGAAATAACAA

GAM394  LOC153222 3'  GACAACAAAATAGATTATTTTT 80787      C   G_
                                 GAAGA TAGT  ATTTTGTTGTT
                                 ||||| ||||  ||||||||||
                                 TTTTT ATTA  TAAAACAACAG
                                   _   GA
GAM394  LOC153232 5'  AACATTATTAATCATTAGCTTT 85984      A       TTGT_
          TA                     TGGAAG CTAGTGATT    TGTT
                                 |||||| |||||||||    ||||
                                 ATTTTC GATTACTAA    ACAA
                                   _       TTATT
GAM394  LOC153338 3'  AGCAGTAGAATCGCTTAAACCC 85993    AAGACT
          A                      TGG     AGTGATTTTGTTGTT
                                 |||     ||||||||||||||
                                 ACC     TCGCTAAGATGACGA
                                   CAAAT_
GAM394  LOC153628 3'  GATGACAGAATCAGCTTTT   75156      A  AGT      TG
                                 GGAAG CT   GATTTTGT  TT
                                 ||||| ||   ||||||||  ||
                                 TTTTC GA   CTAAGACA  AG
                                   _ ___       GT
GAM394  LOC153711 3'  AACAGTAGCTTCAGCGGTTTTT 86130        AG   TT
          CA                     TGGAAGACT  TGA  TTGTTGTT
                                 |||||||||  |||  ||||||||
                                 ACTTTTTGG  ACT  GATGACAA
                                      CG   TC
GAM394  LOC153937 5'  AATGGTGAAAATGCAGTTTTTC 81004       A   A   TG TG
                                 GGAAGACT GTG TTT  T  TT
                                 ||||||| ||| |||  |  ||
                                 CTTTTTGA CGT AAA  G  AA
                                      _  A   GT GT
GAM394  LOC154092 3'  AACATAACTCATTTTGGTCTTT 86157        __   _ T   GTT
          CA                     GGAAGACTA  GTGA TT TGTT
                                 |||||||||  |||| || ||||
                                 CTTTCTGGT  TACT AA ACAA
                                      TT   C  T
GAM394  LOC154141 5'  AGTGGCAGAGTTGAGTAGTT   86167      G_       TG
                                 GACTA  TGATTTTGT  TT
                                 |||||  |||||||||  ||
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                                TTGAT  GTTGAGACG  GA
                                  GA       GT
GAM394   LOC154336 3'  AATGGCAAAATTAGTCGCC   59392    AA     GAT    TG
                                GG  GACTAGT   TTTGT  TT
                                ||  |||||||   |||||  ||
                                CC  CTGATTA   AAACG  AA
                                 G_      ___     GT
GAM394   LOC154386 5'  AGCAGGTATTGGTCTTTC    81079          AT
                                GGAAGACTAGTG  TTTGTT
                                ||||||||||||  ||||||
                                CTTTCTGGTTAT  GGACGA
                                              __
GAM394   LOC155038 3'  AGTGGGACATAGTCTTCCA    81255         G  A   TG
                                TGGAAGACTA TG TTT  TT
                                ||||||||||  ||  |||  ||
                                ACCTTCTGAT AC AGG  GA
                                      _ _  GT
GAM394   LOC155038 3'  GGTGACAAAATTACCTGT    81261    TA       TG
                                AC  GTGATTTTGT  TT
                                ||  ||||||||||  ||
                                TG  CATTAAAACA  GG
                                 TC        GT
GAM394   LOC155066 3'  GGCATGGAATTGTTAATTTTCT 81282       C   TG    TG T
                                GGAAGA TAG  ATTT  T GTT
                                ||||||  |||  ||||  |  |||
                                TCTTTT ATT  TAAG  A CGG
                                   A   GT    GT _
GAM394   LOC155179 3'  AGTGGACCCGCTGGTCTTT    81311          AT  TG
                                GAAGACTAGTG  TT  TT
                                ||||||||||  ||  ||
                                TTTCTGGTCGC  AG  GA
                                      CC  GT
GAM394   LOC157503 5'  AATGACAGAGTCTAGATTCTTC 86466       CTAGT       TG
                                GAAGA    GATTTTGT  TT
                                |||||    ||||||||  ||
                                CTTCT    CTGAGACA  AA
                                   TAGAT       GT
GAM394   LOC157695 3'  AATGGTGAAGTTGTGGAGGTTT 86515        A__ TG    TG TG
           TCT                   GGAAGACT   G  ATTT  T  TT
                                ||||||||  |  ||||  |  ||
                                TCTTTTGG   T  TGAA  G  AA
                                    AGG GT    GT GT
GAM394   LOC157739 3'  GGCTACCGGTGGTTATTAGTTT 81583            TT__  T
           TCT                   GGAAGACTAGTGATT    GT GTT
                                ||||||||||||||||    || |||
                                TCTTTTGATTATTGG    CA CGG
                                        TGGC  T
GAM394   LOC157858 5'  AACGGTGGAATAAAATATCTTC 86575       CTAGTG    TG
           CA                    TGGAAGA     ATTT  TTGTT
                                |||||||     ||||  |||||
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                                ACCTTCT     TAAG  GGCAA
                                    ATAAAA    GT
GAM394   LOC158038 5'  GACGGCAAGGGTTGGATTTTTC 81663       _  GTGA
           A                     TGGAAGA CTA    TTTTGTTGTT
                                 ||||||| |||    ||||||||||
                                 ACTTTTT GGT    GGAACGGCAG
                                    A  TG__
GAM394   LOC158056 5'  GCACAGGCTGGTCTTCTA    81686          GATT    T  T
                                 TGGAAGACTAGT    TTGT GT
                                 ||||||||||||    |||| ||
                                 ATCTTCTGGTCG    GACA CG
                                       _____   _ T
GAM394   LOC158116 3'  GATAACAGGATTATTA      60321
                                 TAGTGATTTTGTTGTT
                                 ||||||||||||||||
                                 ATTATTAGGACAATAG

GAM394   LOC158191 3'  AACGACAGAATGAGGGATTTTC 81767      _  AGTG
                                 GAAGA CT    ATTTTGTTGTT
                                 ||||| ||    ||||||||||
                                 CTTTT GG    TAAGACAGCAA
                                    A  GAG_
GAM394   LOC158236 5'  AACAACAAGTTCCTGGTCTTC  86704         T  T
                                 GAAGACTAG GA TTTGTTGTT
                                 ||||||||| || |||||||||
                                 CTTCTGGTC CT GAACAACAA
                                       _ T
GAM394   LOC158363 3'  AGCTCAAGTTGCTGGTTTTTT  86776         TG    T_
                                 GGAAGACTAG  ATTT  GTT
                                 ||||||||||  ||||  |||
                                 TTTTTTGGTC  TGAA  CGA
                                       GT    CT
GAM394   LOC158654 3'  AATTATTGGTCTCTTCA     81961      _
                                 TGGA AGACTAGTGATT
                                 |||| ||||||||||||
                                 ACTT TCTGGTTATTAA
                                    C
GAM394   LOC158654 3'  GGCATCTGACTGGTCTTCCA   81966          GATTT
                                 TGGAAGACTAGT    TGTT
                                 ||||||||||||    ||||
                                 ACCTTCTGGTCA    ACGG
                                       GTCT_
GAM394   LOC158709 5'  AGATTGCTGTTTTTCCA     81977        C   TG
                                 TGGAAGA TAG  ATTT
                                 ||||||| |||  ||||
                                 ACCTTTT GTC  TAGA
                                    T   GT
GAM394   LOC158747 3'  ACAGCTTATAAGTCTTTTA    81999         A    TTTT
                                 TGGAAGACT GTGA    GTTGT
                                 ||||||||| ||||    |||||
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                                ATTTTCTGA TATT    CGACA
                                     A    ____
GAM394   LOC158848 3'  GATCAGATTGCTGTTTTCTA   82031        T  TG    T
                                TGGAAGAC AG  ATTT GTT
                                |||||||| ||  |||| |||
                                ATCTTTTG TC  TAGA TAG
                                     _ GT    C
GAM394   LOC158852 3'  GATCAGATTGCTGTTTTCTA   82033        T  TG    T
                                TGGAAGAC AG  ATTT GTT
                                |||||||| ||  |||| |||
                                ATCTTTTG TC  TAGA TAG
                                     _ GT    C
GAM394   LOC158972 3'  GGCAACAAGGTTCCCATCTTC  86954       CTAGT
                                GAAGA    GATTTTGTTGTT
                                |||||    ||||||||||||
                                CTTCT    TTGGAACAACGG
                                   ACCC_
GAM394   LOC158978 3'  AACAATAAAAAAGAGTTTTC   82075        AGTGA
                                GAAGACT    TTTTGTTGTT
                                |||||||    ||||||||||
                                CTTTTGA    AAAATAACAA
                                    GAA__
GAM394   LOC159089 3'  GATAATAGATGGTTTTGTCTTT 86987         TAGTGAT
           CA                     TGGAAGAC      TTTGTTGTT
                                |||||||      |||||||||
                                ACTTTCTG      AGATAATAG
                                     TTTTGGT
GAM394   LOC159091 5'  GGCGGCAGATTGTAGTTTTT   57187        GTGAT
                                GAAGACTA    TTTGTTGTT
                                ||||||||    |||||||||
                                TTTTTGAT    AGACGGCGG
                                    GTT__
GAM394   LOC159119 3'  AACAATAAAATTGCATGTTT   76359      TA TG
                                AGAC  G  ATTTTGTTGTT
                                ||||  |  ||||||||||||
                                TTTG  C  TAAAATAACAA
                                  TA GT
GAM394   LOC159989 5'  AGCGGTGAAATCCAGCTCCTCC 82202     A  _  AGT    TG
                                GGA GA CT   GATTT  TTGTT
                                ||| || ||   |||||  |||||
                                CCT CT GA   CTAAA  GGCGA
                                  C  C  C__     GT
GAM394   LOC160897 3'  AATGACAAAGTTACCAAGTT   82243      A_        TG
                                GACT  GTGATTTTGT  TT
                                ||||  ||||||||||  ||
                                TTGA  CATTGAAACA  AA
                                  AC         GT
GAM394   LOC161054 5'  GGCTTTCGCAGTTTTTC     87078        A    TTTT
                                GGAAGACT GTGA    GTT
                                |||||||| ||||    |||
```

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                                CTTTTTGA CGCT    CGG
                                     _    TT__
GAM394   LOC161589 3'  TAGTGACAGTTTTTAAGTTATT 82282          _______  TG
                AGTTTTT                  CTAGTGATTT     TGT  TT   A
                                |||||||||     |||  ||  |
                                GATTATTGAA     ACA  GA   T
                                      TTTTTG   GT
GAM394   LOC161635 5'  GCAGCAGAATTCATTGTC    96572     T    _
                                GAC AGTGA TTTTGTTGT
                                ||| ||||| |||||||||
                                CTG TTACT AAGACGACG
                                  _    T
GAM394   LOC161725 3'  GGCGGCGAGGTTCTACCTTC   55655      AC   T
                                GAAG  TAG GATTTTGTTGTT
                                ||||  ||| ||||||||||||
                                CTTC  ATC TTGGAGCGGCGG
                                  C_  _
GAM394   LOC162333 5'  GCAACAGAGCGGCCTTCT    87133      A  A  GAT
                                GGAAG CT GT   TTTGTTGT
                                ||||| || ||   ||||||||
                                TCTTC GG CG   AGACAACG
                                   C  _  ___
GAM394   LOC162461 3'  GGTGATGGGGTCGCTGCGCC   82363    AAGAC       TG TG
                                GG    TAGTGATTT  T  TT
                                ||    |||||||||  |  ||
                                CC    GTCGCTGGG  A  GG
                                 GC___        GT GT
GAM394   LOC162962 3'  GACAGCGAGACCCTGTCTCCA  82376     A   T  TGA
                                TGGA GAC AG   TTTTGTTGTT
                                |||| ||| ||   ||||||||||
                                ACCT CTG TC   AGAGCGACAG
                                  _   _  CC_
GAM394   LOC164390 5'  AACAGCAAGGAGCCATTCTTCT 82513       CTA  GA
                A                    TGGAAGA   GT  TTTTGTTGTT
                                |||||||   ||  ||||||||||
                                ATCTTCT   CG  GGAACGACAA
                                     TAC  A_
GAM394   LOC164397 5'  GACGATGGAGTTTGCTGTGTCT 82525     _   TG _   TG
                                AGAC TAG  A TTT  TTGTT
                                |||| |||  | |||  |||||
                                TCTG GTC  T GAG  AGCAG
                                  T   GT T   GT
GAM394   LOC166316 5'  AGCGGCATCACTTGTTTTTCA  87259        T    TTT
                                TGGAAGAC AGTGA   TGTTGTT
                                |||||||| |||||   |||||||
                                ACTTTTTG TCACT   ACGGCGA
                                     T    ___
GAM394   LOC169693 5'  AGCAGCAGGGTCAGGGTGCT   87289    _   AG
                                AG ACT  TGATTTTGTTGTT
                                || |||  ||||||||||||
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                                TC TGG  ACTGGGACGACGA
                                 G  G_
GAM394  LOC170063 3'  GGCAGCAGGGCTTCAGTTCTCC 87246     AG  __  GAT
                A                TGGA  ACT  AGT  TTTGTTGTT
                                 ||||  |||  |||  |||||||||
                                 ACCT  TGA  TCG  GGACGACGG
                                   CT  CT  ___
GAM394  LOC170082 3'  GACATTAATGGTCATTAGTCTG 82560   GA        TTGT_
                TCA                TG  AGACTAGTGATT   TGTT
                                 ||  ||||||||||||   ||||
                                 AC  TCTGATTACTGG   ACAG
                                  TG         TAATT
GAM394  LOC196424 3'  GGCAATGAGATAGTTTTCT   87702       GTGA  TG
                                 GGAAGACTA   TTT  TTGTT
                                 |||||||||   |||  |||||
                                 TCTTTTGAT   AGA  AACGG
                                       ____  GT
GAM394  LOC196446 5'  AACAACAAGGTTTATTTTTCA  87705      CTAGT
                                 TGGAAGA   GATTTTGTTGTT
                                 |||||||   ||||||||||||
                                 ACTTTTT   TTGGAACAACAA
                                    AT___
GAM394  LOC196446 3'  AACAGAGCCATTGATAGTCTTC 87706       ___  AT    GTT
                CA                 GGAAGACTA  GTG  TTTGTT
                                 |||||||||  |||  ||||||
                                 CCTTCTGAT  TAC  AGACAA
                                      AGT  CG
GAM394  LOC196472 5'  AGCAGTGGGATTGCCAGTT   87717     A TG   TG
                                 GACT G  ATTT  TTGTT
                                 |||| |  ||||  |||||
                                 TTGA C  TAGG  GACGA
                                   C GT   GT
GAM394  LOC196540 5'  AGCAAATGATGGTCTTCTA   89633       GTGAT
                                 TGGAAGACTA    TTTGTT
                                 ||||||||||    ||||||
                                 ATCTTCTGGT    AAACGA
                                       AGT__
GAM394  LOC196955 5'  GATGACAGGGAATGTGTCTTCT 77379      TA  GA    TG
                                 GGAAGAC  GT  TTTTGT  TT
                                 |||||||  ||  ||||||  ||
                                 TCTTCTG  TA  GGGACA  AG
                                    TG  A_     GT
GAM394  LOC199725 5'  AATAGTGAGACACCGTCTTT   89834      TA   A   TG
                                 GAAGAC  GTG TTT  TTGTT
                                 ||||||  ||| |||  |||||
                                 TTTCTG  CAC AGA  GATAA
                                    C_  _  GT
GAM394  LOC199870 3'  AACAGCAAATGGAGTTGTCCA  88428     A   AGTGAT
                                 TGGA GACT     TTTGTTGTT
                                 |||| ||||     |||||||||
```

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                                ACCT TTGA     AAACGACAA
                                  G   GGT___
GAM394  LOC199907 3'  AACAGATGTACTGTCTTTCA  88456       T   AT
                                TGGAAGAC AGTG  TTTGTT
                                |||||||| ||||  ||||||
                                ACTTTCTG TCAT  AGACAA
                                    _   GT
GAM394  LOC199907 3'  ATTTTCAGGATTGTGTGGTCTT 88463       _ TG     TTGTT
          TT                     GGAAGACTA G  ATTTTG
                                |||||||||  |  ||||||
                                TTTTCTGGT T  TAGGAC
                                     G GT     TTTTAA
GAM394  LOC199923 3'  AGTGGCAAGTCATAGTTTTT  88495       G     T  TG
                                GAAGACTA TGATTT GT  TT
                                |||||||| ||||||  ||  ||
                                TTTTTGAT ACTGAA CG  GA
                                    _     _  GT
GAM394  LOC200227 5'  GGCAGTTGTTAGTCTTC     88644        TG  TT
                                GAAGACTAG  AT  TGTT
                                |||||||||  ||  ||||
                                CTTCTGATT  TG  ACGG
                                     GT  __
GAM394  LOC201626 3'  AATTTCAAAATTGTTGGTTTTT 88983        TG     TT
                                GAAGACTAG  ATTTTG  GTT
                                |||||||||  ||||||  |||
                                TTTTTGGTT  TAAAAC  TAA
                                     GT     TT   T
GAM394  LOC201685 5'  GGCAGCAGGGTCAATTTGCT   90246    ACTAG
                                AG     TGATTTTGTTGTT
                                ||    ||||||||||||
                                TC    ACTGGGACGACGG
                                 GTTTA
GAM394  LOC201915 3'  GTAGTGGAGTTACTGAGTAATC 89104     AG  _      TG  GTT
          C                      GGA  ACT AGTGATTT  TT
                                |||  ||| ||||||||  ||
                                CCT  TGA TCATTGAG  GA
                                  AA   G       GT  TGG
GAM394  LOC201931 3'  AACAATGAGACACTGTCTCTCA 89106    GA   T   A   TG
                                TG  AGAC AGTG TTT  TTGTT
                                ||  |||| |||| |||  |||||
                                AC  TCTG TCAC AGA  AACAA
                                 TC   _   _  GT
GAM394  LOC201952 3'  AGCAATGAAATCACCTTTC   90267      ACTA      TG
                                GGAAG    GTGATTT  TTGTT
                                |||||    |||||||  |||||
                                CTTTC    CACTAAA  AACGA
                                   _____      GT
GAM394  LOC202459 3'  AGTGGCATTTTCTTCTTAGTTT 59252         T__  TTT   TG
          TTCA                    GGAAGACTAG   GA   TGT  TT
                                ||||||||||   ||   |||  ||
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                                CTTTTTGATT  CT   ACG  GA
                                      CTT  TTT   GT
GAM394   LOC203274 3'  GACACGATGCTGGTCTTCCA  90468          G   T
                                TGGAAGACTAGT ATT TGTT
                                |||||||||||| ||| ||||
                                ACCTTCTGGTCG TAG ACAG
                                       _  C
GAM394   LOC203297 5'  GGCAACAGGGTCTGGCTCTGTC 75352     T_  __
                                GAC  AGT  GATTTTGTTGTT
                                |||  |||  ||||||||||||
                                CTG  TCG  CTGGGACAACGG
                                  TC   GT
GAM394   LOC203377 5'  AATATTGTTATTAGTGTTTC  90575      G       TT
                                GGAA ACTAGTGAT  TGTT
                                |||| |||||||||  ||||
                                CTTT TGATTATTG  ATAA
                                   G        TT
GAM394   LOC203522 3'  GGCAGTGAAAGCTGGGCTTTT  89371      A    GA   TG
                                GGAAG CTAGT  TTT  TTGTT
                                ||||| |||||  |||  |||||
                                TTTTC GGTCG  AAA  GACGG
                                   G    __  GT
GAM394   LOC203523 3'  AACAATAAGCAGTGTAGTCTTT 89373        GTGAT
                                GAAGACTA    TTTGTTGTT
                                ||||||||    |||||||||
                                TTTCTGAT    GAATAACAA
                                     GTGAC
GAM394   LOC204804 3'  AGTGGCGGGATTACTGCTC   89469   C         TG
                                GA TAGTGATTTTGT  TT
                                || ||||||||||||  ||
                                CT GTCATTAGGGCG  GA
                                 C          GT
GAM394   LOC204931 5'  AGCAATAAAATTGATTTCTTT  90646      CTAG
                                GAAGA   TGATTTTGTTGTT
                                |||||   ||||||||||||||
                                TTTCT   GTTAAAATAACGA
                                   TTA_
GAM394   LOC206426 3'  AGAGTTGTGGTTTTCCA     89532          G
                                TGGAAGACTA TGATTTT
                                |||||||||| |||||||
                                ACCTTTTGGT GTTGAGA
                                          _
GAM394   LOC219300 5'  GATGGAGTTTGTGGTCTTCT   94313        GT    TG
                                GGAAGACTA  GATTT  TT
                                |||||||||  |||||  ||
                                TCTTCTGGT  TTGAG  AG
                                      GT    GT
GAM394   LOC219347 3'  GACGGTGAAACACTGTCTCTA  92982     A  T   A  TG
                                TGGA GAC AGTG TTT  TTGTT
                                |||| ||| |||| |||  |||||
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                                ATCT CTG TCAC AAA  GGCAG
                                  _  _   _  GT
GAM394  LOC219445 3'  GCAATAAACCTGTTTTCCA   91574        T  TGAT
                                TGGAAGAC AG   TTTGTTGT
                                |||||||| ||   ||||||||
                                ACCTTTTG TC   AAATAACG
                                     _  C___
GAM394  LOC219513 5'  GGCAGCGGGGCGAGGGGCTTCT 94333      A  AG  A
                                GGAAG CT  TG TTTTGTTGTT
                                ||||| ||  || ||||||||||
                                TCTTC GG  GC GGGGCGACGG
                                   G  GA  _
GAM394  LOC219894 3'  AAATTCTGGTCTTTTA      93273          T
                                TGGAAGACTAG GATTT
                                |||||||||||| |||||
                                ATTTTCTGGTC TTAAA
                                          _
GAM394  LOC219938 3'  AGCAACAGGTGGAAGTCCTTCA 91551     A    AGTGAT
                                TGGA GACT     TTTGTTGTT
                                |||| ||||     |||||||||
                                ACTT CTGA     GGACAACGA
                                  C    AGGT__
GAM394  LOC220038 5'  GGCAACAGAGCAGGCTTTTCA  91721      GA  AG  A
                                TGGAA  CT  TG TTTTGTTGTT
                                |||||  ||  || ||||||||||
                                ACTTT  GG  AC GAGACAACGG
                                   TC  __  _
GAM394  LOC220115 5'  GATAGCAAAGTTTATATTCC   91744     GACTAGT
                                GGAA      GATTTTGTTGTT
                                ||||      ||||||||||||
                                CCTT      TTGAAACGATAG
                                  ATAT___
GAM394  LOC220370 3'  GGCAGTAGAATCGCTTGAACCC 92830     AAGACT
           A                     TGG     AGTGATTTTGTTGTT
                                |||     ||||||||||||||||
                                ACC     TCGCTAAGATGACGG
                                  CAAGT_
GAM394  LOC220729 3'  GATGACAGAATCAGCTTTT    71599      A  AGT       TG
                                GGAAG CT   GATTTTGT  TT
                                ||||| ||   ||||||||  ||
                                TTTTC GA   CTAAGACA  AG
                                  _  ___       GT
GAM394  LOC220936 3'  GACAATGAGGGTCTGGTTTTTT 91411          TGA   TG
           A                     TGGAAGACTAG   TTT  TTGTT
                                ||||||||||||   |||  |||||
                                ATTTTTTGGTC   GGA  AACAG
                                       TG_   GT
GAM394  LOC221002 3'  AGCATGGAGTTGTCAGTTTTCT 91474        A TG    TG T
                                GGAAGACT G  ATTT  T GTT
                                |||||||| |  ||||  | |||
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                                TCTTTTGA T  TGAG  A CGA
                                    C GT    GT _
GAM394   LOC221336 3'  AGCAATAAAATTACAGGATTAT 92269      GA__  A
                TCT                   GGAA    CT GTGATTTTGTTGTT
                                |||||    || ||||||||||||||
                                TCTT    GG CATTAAAATAACGA
                                  ATTA  A
GAM394   LOC221495 3'  AACAGTGGGATTAGGGCTCCA  93853      A A  AG     TG
                                TGGA G CT  TGATTT  TTGTT
                                ||||| | ||  ||||||  |||||
                                ACCT C GG  ATTAGG  GACAA
                                  _ _  G_     GT
GAM394   LOC221662 3'  GACAACAAGGTTACTG      92404
                                TAGTGATTTTGTTGTT
                                ||||||||||||||||
                                GTCATTGGAACAACAG

GAM394   LOC221683 5'  AATAACATTAGCCTGTCTTTCA 93708         TA  GATTT
                                TGGAAGAC  GT    TGTTGTT
                                ||||||||  ||    |||||||
                                ACTTTCTG  CG    ACAATAA
                                    TC  ATT__
GAM394   LOC221749 5'  GGCGACGAAGAGGAGTTCTTC  92007       _  AGTGA
                                GAAGA CT    TTTTGTTGTT
                                |||||  ||    ||||||||||
                                CTTCT GA    GAAGCAGCGG
                                   T  GGA__
GAM394   LOC221751 5'  ACAATGAAGTGACTTCCA    92043     AGACT   G    TG
                                TGGA    AGT ATTT  TTGT
                                ||||    ||| ||||  ||||
                                ACCT    TCA TGAA  AACA
                                  _____  G   GT
GAM394   LOC221763 5'  GACAGCAAAATCTTGGTTT   93797        T
                                AGACTAG GATTTTGTTGTT
                                ||||||| ||||||||||||
                                TTTGGTT CTAAAACGACAG
                                  _
GAM394   LOC221773 3'  GCAATGGGGTCCACTTCC    91045      ACTAGT    TG
                                GGAAG     GATTT  TTGT
                                |||||     |||||  ||||
                                CCTTC     CTGGG  AACG
                                  AC____     GT
GAM394   LOC221838 3'  GGCAGTTTTAAGTTATTAGTTT 92544             TG__
                TT                  GAAGACTAGTGATTT    TTGTT
                                ||||||||||||||||   |||||
                                TTTTTGATTATTGAA    GACGG
                                        TTTT
GAM394   LOC221933 3'  AGCAATAAAATCTTGCTTT   92585      ACTAGT
                                GAAG     GATTTTGTTGTT
                                ||||     ||||||||||||
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                                TTTC     CTAAAATAACGA
                                  GTT___
GAM394   LOC222066 3'  AGCAGCAGAACACACGTTTCTA 92739       ACTA   A
                                TGGAAG   GTG TTTTGTTGTT
                                ||||||   ||| ||||||||||
                                ATCTTT   CAC AAGACGACGA
                                   GCA_  _
GAM394   LOC222070 5'  AATAACCATACTCTGGTCTTTC 94144          TGATTTT
           A                     TGGAAGACTAG      GTTGTT
                                ||||||||||      ||||||
                                ACTTTCTGGTC      CAATAA
                                      TCATAC_
GAM394   LOC222160 3'  GGCAGCAGAATCGCTTGAACC  94130    AAGACT
                                GG     AGTGATTTTGTTGTT
                                ||     ||||||||||||||
                                CC     TCGCTAAGACGACGG
                                 AAGT__
GAM394   LOC222161 5'  AGTGATAAAATTGTGTTTTCTA 92794        TA TG      TG
                                TGGAAGAC  G  ATTTTGT  TT
                                ||||||||  |  |||||||  ||
                                ATCTTTTG  T  TAAAATA  GA
                                     __ GT      GT
GAM394   LOC222484 5'  GATGACCTAGTCTGCCA     94341     A      _ G
                                TGG AGACTAG T ATT
                                ||| ||||||| | |||
                                ACC TCTGATC A TAG
                                  G      C G
GAM394   LOC222681 3'  AATGACAAGATCACCTCATCT  92849     A  CTA        TG
                                GGA GA   GTGATTTTGT  TT
                                ||| ||   ||||||||||  ||
                                TCT CT   CACTAGAACA  AA
                                  A  C__         GT
GAM394   LOC253003 3'  AATAGGCCACTTGTTTTCTA   96891         T    AT
                                TGGAAGAC AGTG  TTTGTT
                                |||||||| ||||  ||||||
                                ATCTTTTG TCAC  GGATAA
                                     T    C_
GAM394   LOC253143 3'  AGCAGAATCAGCTGTC      96955     T  _
                                GAC AG TGATTTTGTT
                                ||| || ||||||||||
                                CTG TC ACTAAGACGA
                                  _  G
GAM394   LOC253502 3'  GGACAAGAGGTTTTCC      94581         AGTGA     TG
                                GGAAGACT     TTTTGT  T
                                ||||||||     ||||||  |
                                CCTTTTGG     AGAACA  G
                                     _____      GT
GAM394   LOC253783 5'  AGTGGTGAGATCACAGTT    95266      A      TG TG
                                GACT GTGATTT  T  TT
                                |||| |||||||  |  ||
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                                TTGA CACTAGA  G  GA
                                  _      GT GT
GAM394   LOC253890 5'  AGCAGTGGAGTCATTCAG    95675    _      TG
                                CT AGTGATTT  TTGTT
                                || ||||||||  |||||
                                GA TTACTGAG  GACGA
                                 C       GT
GAM394   LOC253890 3'  GACGACACCTCTGGTTTTTCA  95678          TGATTT
                                TGGAAGACTAG     TGTTGTT
                                ||||||||||     |||||||
                                ACTTTTTGGTC     ACAGCAG
                                       TCC___
GAM394   LOC253926 5'  AGCAGTGGAATTGCTGGATC   94922    _   TG   TG
                                GA CTAG  ATTT  TTGTT
                                || ||||  ||||  |||||
                                CT GGTC  TAAG  GACGA
                                 A   GT   GT
GAM394   LOC254065 5'  GACAACAAGATTCATCTCTTTC 97427       CTA   _
                                GGAAGA   GTGA TTTTGTTGTT
                                ||||||   |||| ||||||||||
                                CTTTCT   TACT AGAACAACAG
                                   C__    T
GAM394   LOC254122 3'  AAGTCACTAGTTTTCC      94750
                                GGAAGACTAGTGATTT
                                ||||||||||||||||
                                CCTTTTGATCACTGAA

GAM394   LOC254249 3'  AATAATAAAACTTCAGTCTTTC 95443        AGTGA
                                GGAAGACT    TTTTGTTGTT
                                ||||||||    ||||||||||
                                CTTTCTGA    AAAATAATAA
                                     CTTC_
GAM394   LOC254479 5'  AGCAGCAGAGTCAGCCTTCTA  97083       A  AGT
                                TGGAAG CT   GATTTTGTTGTT
                                |||||| ||   ||||||||||||
                                ATCTTC GA   CTGAGACGACGA
                                   C  ___
GAM394   LOC255231 3'  GATAATAAAATTCTCTATTAGT 95374        ____
           CT                     AGACTAGT    GATTTTGTTGTT
                                ||||||||    ||||||||||||
                                TCTGATTA    TTAAAATAATAG
                                     TCTC
GAM394   LOC255766 3'  AATGACAAAATATTGTTATCCA 96299      A  T   A     TG
                                TGGA GAC AGTG TTTTGT  TT
                                |||| ||| |||| ||||||  ||
                                ACCT TTG TTAT AAAACA  AA
                                  A  _   _     GT
GAM394   LOC255812 3'  GATGACAGAATCAGCTTTT   95705      A  AGT      TG
                                GGAAG CT   GATTTTGT  TT
                                ||||| ||   ||||||||  ||
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                                TTTTC GA   CTAAGACA  AG
                                  _ ___       GT
GAM394   LOC255849 5'  GATGACAGACTAGCTTTTCT   96443       _    GATT    TG
                                GGAAGA CTAGT    TTGT  TT
                                |||||| |||||    ||||  ||
                                TCTTTT GATCA    GACA  AG
                                   C     ____    GT
GAM394   LOC255861 3'  GCAGCAGGAGGCTTTCT     94633     CT   GA
                                AGA  AGT  TTTTGTTGT
                                |||  |||  |||||||||
                                TCT  TCG  AGGACGACG
                                  T_   G_
GAM394   LOC256021 3'  AACAATAGGACAGCTGCTCTTC 96511        C    GA
            CA                    TGGAAGA TAGT  TTTTGTTGTT
                                |||||||| ||||  ||||||||||
                                ACCTTCT GTCG  AGGATAACAA
                                    C    AC
GAM394   LOC256207 3'  AACAATAGATAAATAGTTTTCT 95162         GTGAT
                                GGAAGACTA     TTTGTTGTT
                                |||||||||     |||||||||
                                TCTTTTGAT     AGATAACAA
                                     AAAT_
GAM394   LOC256239 5'  GAGCATGGGATTCTTAGTTTTT 94488          T     TG T
            CA                    TGGAAGACTAG GATTT  T GTT
                                ||||||||||| |||||  | |||
                                ACTTTTTGATT TTAGG  A CGA
                                      C     GT _   GC
GAM394   LOC257060 3'  GCGATGGAGCAGTCTCC     94462     A    A  GAT  TG
                                GGA GACT GT   TT  TTGT
                                ||| |||| ||   ||  ||||
                                CCT CTGA CG   AG  AGCG
                                  _    _ ___  GT
GAM394   LOC257122 3'  GATCAGATTGCTGTTTTCTA   96213        T  TG    T
                                TGGAAGAC AG  ATTT GTT
                                |||||||| ||  |||| |||
                                ATCTTTTG TC  TAGA TAG
                                     _ GT    C
GAM394   LOC257418 5'  ACAGTGAAATCATCGTT     97564     TA      TG
                                GAC  GTGATTT  TTGT
                                |||  |||||||  ||||
                                TTG  TACTAAA  GACA
                                  C_      GT
GAM394   LOC257471 5'  AGCGACAGGTGATTTGGCTTCT 95685       A    TGAT
                                GGAAG CTAG    TTTGTTGTT
                                ||||| ||||    |||||||||
                                TCTTC GGTT    GGACAGCGA
                                   _    TAGT
GAM394   LOC257471 3'  AATAAAGTTACATTGCTGGTCT 95682          _____        GTT
            TGTA                   AGACTAGT    GATTTTGTT
                                ||||||||    |||||||||
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                                TCTGGTCG    TTGAAATAA
                                    TTACA         T
GAM394  LOC257507 3'  AATGACAAGATCACCTCATCT  97771    A  CTA       TG
                                GGA GA   GTGATTTTGT  TT
                                ||| ||   ||||||||||  ||
                                TCT CT   CACTAGAACA  AA
                                  A  C__        GT
GAM394  LOC257625 3'  AATGACAAGATCACCTCATCT  97902    A  CTA       TG
                                GGA GA   GTGATTTTGT  TT
                                ||| ||   ||||||||||  ||
                                TCT CT   CACTAGAACA  AA
                                  A  C__        GT
GAM394  LOC51003  3'  GTAGCGGAGTCACTGACCTCTT 32150      C__         GTT
          T                    GAAGA   TAGTGATTTTGTT
                               |||||   ||||||||||||
                               TTTCT   GTCACTGAGGCGA
                                  CCA          TGA
GAM394  LOC51008  3'  GGTGACAGGATTTCCTTCC    31968      ACTAGT      TG
                                GGAAG     GATTTTGT  TT
                                |||||     ||||||||  ||
                                CCTTC     TTAGGACA  GG
                                  CT____       GT
GAM394  LOC51018  3'  AAAATTTAAAATTATAGTTTTT 32123        G       TTGTT
          CA                     TGGAAGACTA TGATTTTG
                                 ||||||||||  ||||||||
                                 ACTTTTTGAT ATTAAAAT
                                       _       TTAAAAT
GAM394  LOC51020  3'  AACAAACATTATTTTTCCA    32159       C     AT
                                TGGAAGA TAGTG  TTTGTT
                                |||||||  |||||  ||||||
                                ACCTTTT ATTAC  AAACAA
                                    T    __
GAM394  LOC51026  3'  AGCAGTGAAAACAGGCTTCTA  32166       A  A  GA   TG
                                TGGAAG CT GT  TTT  TTGTT
                                ||||||  ||  ||  |||  |||||
                                ATCTTC GG CA  AAA  GACGA
                                   _  A  __   GT
GAM394  LOC51026  3'  AGCAGTGGCTTATTATTTGTTT 32167       T     T__ TG
          TTCA                    GGAAGAC AGTGAT   T  TTGTT
                                  |||||||  ||||||   |  |||||
                                  CTTTTTG TTATTA   G  GACGA
                                    T     TTC GT
GAM394  LOC51093  3'  AGTGGCAGAGTACATCTCATCC 32042      A  CTA  _      TG
          A                     TGGA GA   GTG ATTTTGT  TT
                                ||||  ||   |||  |||||||  ||
                                ACCT CT   TAC TGAGACG  GA
                                  A  C__   A      GT
GAM394  LOC51112  5'  GATGGTGAAGTCGCCCAGCTTC 32089      A  A_      TG TG
                                GAAG CT  GTGATTT  T  TT
                                ||||  ||  |||||||  |  ||
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                                CTTC GA  CGCTGAA  G  AG
                                  _ CC      GT GT
GAM394  LOC51652  3' ACAATGGGGTCCTTCCA     32189       ACTAGT    TG
                                TGGAAG     GATTT  TTGT
                                ||||||     |||||  ||||
                                ACCTTC     CTGGG  AACA
                                   _______    GT
GAM394  LOC54543  3' AGGATTATTTGGTCTTCT    38801         _
                                GGAAGACTAG TGATTTT
                                |||||||||| |||||||
                                TCTTCTGGTT ATTAGGA
                                      T
GAM394  LOC56961  5' GGCGGCGGGGAAAGTCTCTCC  62909     _    AGTGA
                                GGA AGACT    TTTTGTTGTT
                                ||| |||||    ||||||||||
                                CCT TCTGA    GGGGCGGCGG
                                  C    AA___
GAM394  LOC81034  3' AATGATTAATCTTCATTGGTTT 47839   GA       TTTT__  TG
          CTCA                    G  AGACTAGTGA     GT  TT
                                |  ||||||||||     ||  ||
                                C  TTTGGTTACT     TA  AA
                                 TC        TCTAAT  GT
GAM394  LOC85414  3' GGTGACAAAATTAAAGGCTTTC 52400      A  AG       TG
                                GGAAG CT  TGATTTTGT  TT
                                ||||| ||  |||||||||  ||
                                CTTTC GG  ATTAAAACA  GG
                                   _ AA       GT
GAM394  LOC90321  3' AACAATAAAGTTGAAATTTTCC 62259       CTAG
          A                      TGGAAGA   TGATTTTGTTGTT
                                |||||||   ||||||||||||
                                ACCTTTT   GTTGAAATAACAA
                                    AAA_
GAM394  LOC90632  3' GACAATGGAATCCACACTCT   63646    CTA  _   TG
                                AGA   GTG ATTT  TTGTT
                                |||   ||| ||||  |||||
                                TCT   CAC TAAG  AACAG
                                  CA_   C   GT
GAM394  LOC91351  3' AGCATTCATTGCTGTCTTTTA  65705       T  TG  TT_
                                TGGAAGAC AG  AT   TGTT
                                |||||||| ||  ||   ||||
                                ATTTTCTG TC  TA   ACGA
                                     _ GT  CTT
GAM394  LOC91523  5' AGCTTCGGTCATTAGTCTTCC  56392            TT_
                                GGAAGACTAGTGATT   GTT
                                ||||||||||||||   |||
                                CCTTCTGATTACTGG   CGA
                                          CTT
GAM394  LOC91549  3' AGCCAGATTGCTTAGTTTTTC  66426         _ TG   T
                                GGAAGACTA G  ATTT GTT
                                |||||||| |  |||| |||
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                                CTTTTTGAT C  TAGA CGA
                                     T GT    C
GAM394  LOC91585  3' AATAGCAGAATTCCTATTTTTC 66571       C   TG
             C                    GGAAGA TAG  ATTTTGTTGTT
                                  ||||||| |||  ||||||||||
                                  CCTTTT ATC  TAAGACGATAA
                                     T   CT
GAM394  LOC91748  5' GCAACAAAGTTAGAGTCT    67056      AG
                                  AGACT  TGATTTTGTTGT
                                  |||||  ||||||||||||
                                  TCTGA  ATTGAAACAACG
                                    G_
GAM394  LOC91974  5' AGCAACGGAGCAAAGGCTTTC  67748      A  AG  A
                                  GGAAG CT  TG TTTTGTTGTT
                                  ||||| ||  || ||||||||||
                                  CTTTC GG  AC GAGGCAACGA
                                     _  AA  _
GAM394  LOC91974  3' AGTGGCAGGACTTGAGGTTGGC 67751    A   ___  _     TG
             TTCCA                  AG CTAG   TGA TTTTGT  TT
                                  || ||||   ||| ||||||  ||
                                  TC GGTT   GTT AGGACG  GA
                                   _   GGA   C     GT
GAM394  LOC91974  5' GTAGCAGAGGCCCTGTCTTCT  67757       T  TGA     GTT
                                  GGAAGAC AG   TTTTGTT
                                  ||||||| ||   |||||||
                                  TCTTCTG TC   GAGACGA
                                      _ CCG      TGA
GAM394  LOC92095  3' GGCGGCAAGGTCCTTGCTCCCA 68094     A  ACT  T
                                  TGG AG   AG GATTTTGTTGTT
                                  ||| ||   || ||||||||||||
                                  ACC TC   TC CTGGAACGGCGG
                                    C  GT_  _
GAM394  LOC92231  3' CTCCAGCAGTCACAGTTTTTCA 68553         A    TT    TT
                                  TGGAAGACT GTGAT  TGTTG
                                  ||||||||| |||||  |||||
                                  ACTTTTTGA CACTG  ACGAC
                                        _    __     CTCG
GAM394  LOC92283  3' AACAGTGGGATTAAAGAGTATC 68742     AG   AG_     TG
             T                    GGA  ACT   TGATTT  TTGTT
                                  |||  |||   ||||||  |||||
                                  TCT  TGA   ATTAGG  GACAA
                                    A_   GAA     GT
GAM394  LOC92340  3' GATGATGAGGTCTCCTTCCA   68992       ACTAGT    TG TG
                                  TGGAAG     GATTT  T  TT
                                  ||||||     |||||  |  ||
                                  ACCTTC     CTGGA  A  AG
                                     CT_____     GT GT
GAM394  LOC92346  3' TAAGATTGCTGGTATTCTA    57640       G     TG
                                  TGGAA ACTAG  ATTTTG
                                  ||||| |||||  ||||||
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                                ATCTT TGGTC  TAGAAT
                                   A    GT
GAM394  LOC92597  3'  GATAGTAAAATCACTGGCTTTT 69971      A
                                GGAAG CTAGTGATTTTGTTGTT
                                ||||| ||||||||||||||||
                                TTTTC GGTCACTAAAATGATAG
                                  _
GAM394  LOC92606  3'  AACAACAGTGTATTTGTTTTTC 69984       _ T   ATT
          CA                     TGGAAGA C AGTG   TTGTTGTT
                                ||||||| | ||||  ||||||||
                                ACCTTTT G TTAT   GACAACAA
                                   T T   GT_
GAM394  LOC92606  3'  GTGAACAGAATACTGTTTTCT  69987       T   A     GTT
                                GGAAGAC AGTG TTTTGTT
                                ||||||| |||| |||||||
                                TCTTTTG TCAT AAGACAA
                                   _   _     GTGA
GAM394  LOC93097  5'  GATAATGAAACAGGTTGTCCA  71362     A   AG  A   TG
                                TGGA GACT  TG TTT  TTGTT
                                |||| ||||  || |||  |||||
                                ACCT TTGG  AC AAA  AATAG
                                  G   __ _  GT
GAM394  LOC93624  5'  GGTGACAGGAGCAGTGTTTTCC 72728       T G  A    TG
                                GGAAGAC A TG TTTTGT  TT
                                ||||||| | || ||||||  ||
                                CCTTTTG T AC AGGACA  GG
                                   _ G  G     GT
GAM394  LOC95915  3'  GCAGCAGGAGGCTTTCT    59469    CT   GA
                                AGA  AGT  TTTTGTTGT
                                |||  |||  |||||||||
                                TCT  TCG  AGGACGACG
                                  T_   G_
GAM395  BACH2    3'  AGACCTGTTTGGCAGCCAT   41482       T   TTGA  A
                                ATGGCTGC CAG    AG TCT
                                |||||||| |||    || |||
                                TACCGACG GTT    TC AGA
                                   _   TG__  C
GAM395  EVPL     3'  AGACCAGGACAGCAGCCA    8801        CA   GAAGA
                                TGGCTGCT  GTT    TCT
                                ||||||||  |||    |||
                                ACCGACGA  CAG    AGA
                                   __   GACC_
GAM395  MYLK2    3'  AGATCCCCAGGGCAGCC     52416       AGT  AA
                                GGCTGCTC   TG  GATCT
                                ||||||||   ||  |||||
                                CCGACGGG   AC  CTAGA
                                   ___  CC
GAM395  NPC1     3'  TAGATCTGGAGGCAACCA    4252     C   CAGTTGA
                                TGG TGCT      AGATCTA
                                ||| ||||      |||||||
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                                ACC ACGG      TCTAGAT
                                  A   AGG____
GAM395  PLA2G2D  3' CTACAACCGCAGCAGCCA    24792        CA_   A
                                TGGCTGCT   GTTG AG
                                ||||||||   |||| ||
                                ACCGACGA   CAAC TC
                                     CGC    A
GAM395  DKFZP586B2420 3' ATGTTACAACCAAAGCAGCCA  74995        CA_   _ G
                                TGGCTGCT   GTTG AA AT
                                ||||||||   |||| || ||
                                ACCGACGA   CAAC TT TA
                                     AAC    A  G
GAM395  KIAA0237  3' AGGGGCAACTGAGCATCCA   28520     C        AAGA
                                TGG TGCTCAGTTG    TCT
                                ||| ||||||||||    |||
                                ACC ACGAGTCAAC    GGA
                                  T         GG__
GAM395  KIF13B   3' AGACCCTCACAGCAGCCA    30902        CAGT   AGA
                                TGGCTGCT    TGA   TCT
                                ||||||||    |||   |||
                                ACCGACGA    ACT   AGA
                                     C___   CCC
GAM395  KIF13B   3' AGACCCTCACAGCAGCCA    82818        CAGT   AGA
                                TGGCTGCT    TGA   TCT
                                ||||||||    |||   |||
                                ACCGACGA    ACT   AGA
                                     C___   CCC
GAM395  ZFP106   3' TAGACCGATGGCAGCCAT    42478         CA    AAGA
                                ATGGCTGCT  GTTG    TCTA
                                |||||||||  ||||    ||||
                                TACCGACGG  TAGC    AGAT
                                      __    C___
GAM395  LOC145678 3' AGATGGCTGAGAAGCCA     83417      G      GAAG
                                TGGCT CTCAGTT    ATCT
                                |||||  |||||||    ||||
                                ACCGA GAGTCGG    TAGA
                                   A      _____
GAM395  LOC150370 3' TGGGTCCAACTGAGCAGCCAT  84943             AA
                                ATGGCTGCTCAGTTG  GATCTA
                                ||||||||||||||  ||||||
                                TACCGACGAGTCAAC  CTGGGT
                                                 __
GAM396  CASP2    3' GCTCTTTGACAACGCCAACCGC 52172    AA   A       T  C
                                GC  TTG TGTTGTCA AG AGC
                                ||  ||| ||||||||  || |||
                                CG  AAC GCAACAGT TC TCG
                                 CC   C       T  _
GAM396  CASP2    3' GCTCTTTGACAACGCCAACCGC 52157    AA   A       T  C
                                GC  TTG TGTTGTCA AG AGC
                                ||  ||| ||||||||  || |||
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                                CG  AAC GCAACAGT TC TCG
                                 CC   C       T  _
GAM396  CLCN3    3'  CTACTATGATATACAAGTGCT  8438      A  A  T     C
                                AGCA TTG TGT GTCATAG AG
                                |||| ||| ||| ||||||| ||
                                TCGT AAC ATA TAGTATC TC
                                  G   _   _     A
GAM396  EGFL5    5'  GCTACCATGACAGCATT     86622          ___
                                GATGTTGTCA   TAGC
                                ||||||||||   ||||
                                TTACGACAGT   ATCG
                                      ACC
GAM396  ESRRBL1  3'  GCTGCTGTCACAACATGAACTG 35849     A  G     C
             CT                   AGCA TT ATGTTGT ATAGCAGC
                                |||| || ||||||| ||||||||
                                TCGT AA TACAACA TGTCGTCG
                                  C  G      C
GAM396  TLR4     5'  CTGCTTTGAATACACCAATTGC 56728        A   TG   T
             T                   AGCAATTG TGT  TCA AGCAG
                                |||||||| |||  ||| |||||
                                TCGTTAAC ACA  AGT TCGTC
                                     C   TA   T
GAM396  TLR4     5'  CTGCTTTGAATACACCAATTGC 56733        A   TG   T
             T                   AGCAATTG TGT  TCA AGCAG
                                |||||||| |||  ||| |||||
                                TCGTTAAC ACA  AGT TCGTC
                                     C   TA   T
GAM396  TLR4     5'  CTGCTTTGAATACACCAATTGC 12318        A   TG   T
             T                   AGCAATTG TGT  TCA AGCAG
                                |||||||| |||  ||| |||||
                                TCGTTAAC ACA  AGT TCGTC
                                     C   TA   T
GAM396  TLR4     5'  CTGCTTTGAATACACCAATTGC 56737        A   TG   T
             T                   AGCAATTG TGT  TCA AGCAG
                                |||||||| |||  ||| |||||
                                TCGTTAAC ACA  AGT TCGTC
                                     C   TA   T
GAM396  API5     3'  GCTATTCAAATCAACTGC    21690     A    G   TC
                                GCA TTGAT TTG  ATAGC
                                ||| ||||| |||  |||||
                                CGT AACTA AAC  TATCG
                                  C     _   T_
GAM396  C2orf9   5'  GCCGCCATGACAACCGAT    50234      AT      A  A
                                ATTG  GTTGTCAT GC GC
                                ||||  |||||||| || ||
                                TAGC  CAACAGTA CG CG
                                  __       C  C
GAM396  FLJ14950 3'  CTGCTATGTGGCTTCAACCAGC 51720    AA_   T   T
                                GC   TTGA GTTG CATAGCAG
                                ||   |||| |||| ||||||||
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                                CG   AACT CGGT GTATCGTC
                                 ACC    T   _
GAM396  NYD-SP11  5'  GCCGCTTCAACATCAGCTGC   49212     A       TCAT   A
                                GCA TTGATGTTG    AGC GC
                                ||| |||||||||    ||| ||
                                CGT GACTACAAC    TCG CG
                                  C        T___   C
GAM396  VRP       5'  GCTGTACCTCAGCATCAA    22947         TCATA
                                TTGATGTTG    GCAGC
                                |||||||||    |||||
                                AACTACGAC    TGTCG
                                     TCCA_
GAM396  LOC143437 3'  CTACAATAACAACAATTGCT   82953         A     CA
                                AGCAATTG TGTTGT  TAG
                                |||||||| ||||||  |||
                                TCGTTAAC ACAATA  ATC
                                     A     AC
GAM396  LOC146782 5'  GCTACAACAACAACATCGATCA 76293    CA         CA___
          CT                      AG  ATTGATGTTGT     TAGC
                                ||  ||||||||||     ||||
                                TC  TAGCTACAACA     ATCG
                                 AC          ACAAC
GAM396  LOC149086 3'  GCCGCTGTCAACATCATTGC   84339      T      TC     A
                                GCAAT GATGTTG  ATAGC GC
                                ||||| |||||||  ||||| ||
                                CGTTA CTACAAC  TGTCG CG
                                  _      __     C
GAM396  LOC158709 3'  GCTGCTATAACAGAACACCA   81982    A   __   C
                                TG TGT  TGT ATAGCAGC
                                || |||  ||| ||||||||
                                AC ACA  ACA TATCGTCG
                                 C  AG   A
GAM396  LOC253531 3'  CTACAATAACAACAATTGCT   96468         A     CA
                                AGCAATTG TGTTGT  TAG
                                |||||||| ||||||  |||
                                TCGTTAAC ACAATA  ATC
                                     A     AC
GAM396  LOC253971 3'  GACAACATCATCTGCT      96140      AT
                                AGCA  TGATGTTGTC
                                ||||  ||||||||||
                                TCGT  ACTACAACAG
                                  CT
GAM396  LOC256158 5'  GCTGACCAACATCACTGCT    97673      AT       TCA
                                AGCA  TGATGTTG   TAGC
                                ||||  ||||||||  ||||
                                TCGT  ACTACAAC   GTCG
                                  C_       CA_
GAM396  LOC90190  3'  CTGTTCCAACACCACCTGCT   61777      AT  A    TC
                                AGCA  TG TGTTG  ATAG
                                ||||  ||  |||||  ||||
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                                TCGT  AC ACAAC  TGTC
                                  CC  C    CT
GAM397  ADAMTS13 3'  TCTGCAGGGGAGAAGGCTCC  57378      TC  AG
                                GGAGC  TC  CTTTGCAGA
                                |||||  ||  |||||||||
                                CCTCG  AG  GGGACGTCT
                                   GA  AG
GAM397  ADRA2A   3'  CTACAAGGGAAGCTTCTT    5451        C  AG    C
                                AAGGAGCT TC  CTTTG AG
                                ||||||||  ||  ||||| ||
                                TTCTTCGA AG  GGAAC TC
                                     _  __    A
GAM397  AP2M1    3'  CTCACCTCAGAGCTCC      14515        C  CTT  C
                                GGAGCTCT AG   TG AG
                                ||||||||  ||   || ||
                                CCTCGAGA TC   AC TC
                                     C  C__  _
GAM397  ATP2A3   3'  CTTCCACAAAGTCGGCTCC   17724       CTCA     CA
                                GGAGCT   GCTTTG  GAAG
                                ||||||   ||||||  ||||
                                CCTCGG   TGAAAC  CTTC
                                   C___     AC
GAM397  BCL7A    3'  TCTGCAAAGTGCCCT      40644     A  TCTCA
                                AGG GC    GCTTTGCAGA
                                |||  ||    ||||||||||
                                TCC CG    TGAAACGTCT
                                  _  _____
GAM397  CACNA1C  3'  TCTGCGGGAGAGCACC     5564     A     AGCT
                                GG GCTCTC    TTGCAGA
                                || ||||||    |||||||
                                CC CGAGAG    GGCGTCT
                                 A     _____
GAM397  CHGA     3'  CTTTTGGTGAAAGCTGAGAACT 7043       C        G__
           CCT                    AGGAG TCTCAGCTTT   CAGAAG
                                |||||  ||||||||||   ||||||
                                TCCTC AGAGTCGAAA   GTTTTC
                                   A         GTG
GAM397  CHI3L1   3'  CTGCAAAGCCAGCTT      7046       CTCA
                                GAGCT    GCTTTGCAG
                                |||||    |||||||||
                                TTCGA    CGAAACGTC
                                   C___
GAM397  CLN6     3'  GCAAAAGCCAGAGCTCCT    35406        CA    _
                                AGGAGCTCT  GCTTT GC
                                |||||||||  |||||  ||
                                TCCTCGAGA  CGAAA CG
                                     C_     A
GAM397  DEDD     3'  CTTCTGGCTTTATGAGAGCTCT 52224          GCTTT  _
           T                     AGGAGCTCTCA    GC AGAAG
                                ||||||||||     || |||||
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                                TTCTCGAGAGT    CG TCTTC
                                      ATTT_ G
GAM397  DXYS155E  3'  CTGCAAAGCCAAGACCCTTCT  17452      C_  CA
                                AGGAG  TCT  GCTTTGCAG
                                |||||  |||  |||||||||
                                TCTTC  AGA  CGAAACGTC
                                   CC   AC
GAM397  GNRHR    5'  CTTCTGTGGTAACAAGCTCCTT 4641        CTCA  TT
                                AAGGAGCT   GCT  GCAGAAG
                                ||||||||   |||  |||||||
                                TTCCTCGA   TGG  TGTCTTC
                                     ACAA  __
GAM397  HS3ST2   3'  CAAAGCTGAAAGCACCT    20154    A  C
                                AGG GCT TCAGCTTTG
                                ||| ||| |||||||||
                                TCC CGA AGTCGAAAC
                                  A  A
GAM397  ITK      3'  CTGTGTTTGTAGAGAACTCC  18682     C   A  TT_
                                GGAG TCTC GC   TGCAG
                                |||| |||| ||   |||||
                                CCTC AGAG TG   GTGTC
                                   A   A  TTT
GAM397  KCNC3    3'  CTGGAAAAGCCACAGAGCTCC  17138       CA_   G_
                                GGAGCTCT   GCTTT  CAG
                                ||||||||   |||||  |||
                                CCTCGAGA   CGAAA  GTC
                                     CAC    AG
GAM397  KIF3C    3'  CTTCTGACTTGAGAGCTCC   9602          CTTTG
                                GGAGCTCTCAG    CAGAAG
                                ||||||||||     ||||||
                                CCTCGAGAGTT    GTCTTC
                                      CA___
GAM397  LAIR1    3'  CTTCTACAATCGAGCAGCTCCT 9661        _  AGCT  C
           T                     AAGGAGCT CTC    TTG AGAAG
                                |||||||| |||    ||| |||||
                                TTCCTCGA GAG    AAC TCTTC
                                     C   CT__   A
GAM397  LAIR1    3'  CTTCTACAATCGAGCAGCTCCT 41356       _  AGCT  C
           T                     AAGGAGCT CTC    TTG AGAAG
                                |||||||| |||    ||| |||||
                                TTCCTCGA GAG    AAC TCTTC
                                     C   CT__   A
GAM397  LAMB3    3'  TTGAAACTAAGAGCTCT     4043         C  C   G
                                GGAGCTCT AG TTT CAG
                                |||||||| || ||| |||
                                TCTCGAGA TC AAA GTT
                                     A  _   _
GAM397  LZTR1    5'  CTCCAGGACCGAGAGCTC    22236        AGC   C
                                GAGCTCTC   TTTG AG
                                ||||||||   |||| ||
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                                CTCGAGAG   GGAC TC
                                     CCA    C
GAM397  MYOZ1    3'  TCACCAACTCAGAGCTCC    41152        C  CT   CA
                                GGAGCTCT AG  TTG  GA
                                |||||||| ||  |||  ||
                                CCTCGAGA TC  AAC  CT
                                     C  __   CA
GAM397  NEDD4L   3'  TCTGCAGGCAAAGCCCTT    30953     A   CTCA    T
                                AAGG GCT    GCTT GCAGA
                                |||| |||    |||| |||||
                                TTCC CGA    CGGA CGTCT
                                  _   AA__    _
GAM397  PCDH1    3'  TCTGCAATGACTGGGCTCCTT  50565         TCAGCT
                                AAGGAGCTC     TTGCAGA
                                |||||||||     |||||||
                                TTCCTCGGG     AACGTCT
                                     TCAGT_
GAM397  PLA2G5   3'  TCTGGTGCCAAGAGCTCTCC   6250    A      CA  TTTG
                                A GGAGCTCT  GC    CAGA
                                | ||||||||  ||    ||||
                                C TCTCGAGA  CG    GTCT
                                 C       AC  TG__
GAM397  PLXNB2   3'  CTGAGGTACCTGAGAGCCCCT  24803     A       CT_ TG
                                AGG GCTCTCAG   T  CAG
                                ||| ||||||||   |  |||
                                TCC CGAGAGTC   G  GTC
                                  C       CAT GA
GAM397  PRKCL1   3'  CTGCCCGAGAGCTCTT      62515          AGCTTT
                                AGGAGCTCTC     GCAG
                                ||||||||||     ||||
                                TTCTCGAGAG     CGTC
                                     CC_____
GAM397  RABIF    3'  CAAACTTTCTAAGGGCTCC    11206        C  C___
                                GGAGCTCT AG    TTTG
                                |||||||| ||    ||||
                                CCTCGGGA TC    AAAC
                                     A  TTTC
GAM397  RCE1     3'  TCTGCCTCTGAAAAGCTGCT   17619    G   C_   CTTT
                                AG AGCT  TCAG    GCAGA
                                || ||||  ||||    |||||
                                TC TCGA  AGTC    CGTCT
                                 G   AA    TC__
GAM397  SFRP5    3'  CAAGGCCCAGAGCTCC      11580        CA
                                GGAGCTCT  GCTTTG
                                ||||||||  ||||||
                                CCTCGAGA  CGGAAC
                                     CC
GAM397  SH3BP5   3'  TTCTGGGTAAGAGCTCTT    16746        CA   TTG
                                AGGAGCTCT  GCT   CAGAA
                                |||||||||  |||   |||||
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                                TTCTCGAGA  TGG   GTCTT
                                     A_  ___
GAM397  SREBF2   3' CTGGGCAGAGCCCCTT     15989     A    CA   TTG
                                AAGG GCTCT  GCT   CAG
                                |||| |||||  |||   |||
                                TTCC CGAGA  CGG   GTC
                                  C    __  ___
GAM397  TEX15    3' CTTCTGCAAAAGTAAAAACTCT 48388     CTCTCA   _
                                GGAG     GCTTT GCAGAAG
                                ||||     ||||| |||||||
                                TCTC     TGAAA CGTCTTC
                                  AAAAA_    A
GAM397  TNFAIP2  3' CTGGGCCTGAAAGTTCCTT   20830       C   _ TTG
                                AAGGAGCT TCAG CT   CAG
                                |||||||| |||| ||   |||
                                TTCCTTGA AGTC GG   GTC
                                     A   C ___
GAM397  TRPS1    5' TCCGCGAAGGCTCCTT     26080       TCTCAG    A
                                AAGGAGC     CTTTGC GA
                                |||||||     |||||| ||
                                TTCCTCG     GAAGCG CT
                                   _______     C
GAM397  WEE1     5' CTGCTTGGGAGAGCTCTT    12651         AG  TT
                                AGGAGCTCTC  CT  GCAG
                                ||||||||||  ||  ||||
                                TTCTCGAGAG  GG  CGTC
                                     __  TT
GAM397  WNT3A    3' CTGCGGGGGCGAGGCCCCT   52430    A  T   AG
                                AGG GC CTC  CTTTGCAG
                                ||| || |||  ||||||||
                                TCC CG GAG  GGGGCGTC
                                  C _   CG
GAM397  ARTN     3' CTCAAAGCTGAGAGGCCCCT  14276    A _        C
                                AGG GC TCTCAGCTTTG AG
                                ||| || ||||||||||| ||
                                TCC CG AGAGTCGAAAC TC
                                  C  G         _
GAM397  ARTN     3' CTCAAAGCTGAGAGGCCCCT  54036    A _        C
                                AGG GC TCTCAGCTTTG AG
                                ||| || ||||||||||| ||
                                TCC CG AGAGTCGAAAC TC
                                  C  G         _
GAM397  ARTN     3' CTCAAAGCTGAGAGGCCCCT  54039    A _        C
                                AGG GC TCTCAGCTTTG AG
                                ||| || ||||||||||| ||
                                TCC CG AGAGTCGAAAC TC
                                  C  G         _
GAM397  ARTN     3' CTCAAAGCTGAGAGGCCCCT  54068    A _        C
                                AGG GC TCTCAGCTTTG AG
                                ||| || ||||||||||| ||
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                                TCC CG AGAGTCGAAAC TC
                                  C  G         _
GAM397  C11orf24  5'  CTGCAAAGCCAGACTTC     42273      C   CA
                                GGAG TCT  GCTTTGCAG
                                |||| |||  |||||||||
                                CTTC AGA  CGAAACGTC
                                  _   C_
GAM397  C1orf35   3'  CTGCCTCGGAAGCTCCTT    44233         CT _  CTTT
                                AAGGAGCT  C AG    GCAG
                                ||||||||  | ||    ||||
                                TTCCTCGA  G TC    CGTC
                                     AG C  ____
GAM397  C7orf13   3'  CTTCCTAAACCATGAGCTCCTT 50930          TCAGC    CA
                                AAGGAGCTC    TTTG  GAAG
                                |||||||||    ||||  ||||
                                TTCCTCGAG    AAAT  CTTC
                                     TACC_   C_
GAM397  CALN1     3'  TCTGCAAAACTTCCT      48878      GCTCTC  C
                                AGGA     AG TTTGCAGA
                                ||||     || ||||||||
                                TCCT     TC AAACGTCT
                                  _______  A
GAM397  CGI-96    3'  CTTCCACAAACTGGAACTGCTC 31662      TC__    C    CA
                                GAGC    TCAG TTTG  GAAG
                                ||||    |||| ||||  ||||
                                CTCG    GGTC AAAC  CTTC
                                  TCAA    _    AC
GAM397  CNOT3     5'  CTTCCCTTGGACTAAAGCTCCT 27220         CTC  _  TTGCA
            T                    AAGGAGCT   AG CT    GAAG
                                ||||||||   || ||    ||||
                                TTCCTCGA   TC GG    CTTC
                                     AA_  A  TTCC_
GAM397  DKFZp434J1015 3'  CTCCACCTGAAAAGCTCCTT   92635         C_    CTT  C
                                AAGGAGCT  TCAG   TG AG
                                ||||||||  ||||   || ||
                                TTCCTCGA  AGTC   AC TC
                                     AA    C__  C
GAM397  DKFZP761F241 3'  CTTCTGCAAAGACACCTCCTT  48794       CTCTCAG
                                AAGGAG      CTTTGCAGAAG
                                ||||||      ||||||||||||
                                TTCCTC      GAAACGTCTTC
                                   CACA___
GAM397  DOK4      3'  TCTGCACAGGCTCCTT      36182        TCTCAG  T
                                AAGGAGC     CT TGCAGA
                                |||||||     || ||||||
                                TTCCTCG     GA ACGTCT
                                   _______  C
GAM397  FLJ10315  3'  TTCAGCCAAGGGCTCC      36023        CA   TTGCA
                                GGAGCTCT  GCT    GAA
                                ||||||||  |||    |||
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                                CCTCGGGA CGA    CTT
                                    AC  _____
GAM397  FLJ14525  3'  TCTGTTTCATCTGGGAGCCCCT 51418    A      CTTT_
                                AGG GCTCTCAG    GCAGA
                                ||| ||||||||    |||||
                                TCC CGAGGGTC    TGTCT
                                  C       TACTT
GAM397  FLJ20079  3'  TCTAGTGAGAGCTCT      34503         G  TTGC
                                GGAGCTCTCA CT   AGA
                                |||||||||| ||   |||
                                TCTCGAGAGT GA   TCT
                                     _ _____
GAM397  FLJ20113  3'  AGGCTGTGAGCTCCTT     34572         T
                                AAGGAGCTC CAGCTT
                                ||||||||| ||||||
                                TTCCTCGAG GTCGGA
                                     T
GAM397  FLJ23403  3'  CTTCTGCAGTAAAAGCTACCT  41954    _   CTCAGCT
                                AGG AGCT      TTGCAGAAG
                                ||| ||||      |||||||||
                                TCC TCGA      GACGTCTTC
                                  A   AAAT___
GAM397  FLJ32771  5'  TCTGCAGAGGAAAGGCCCC   58801    A  T  CAG
                                GG GC CT   CTTTGCAGA
                                || || ||   |||||||||
                                CC CG GA   GAGACGTCT
                                 C  _  AAG
GAM397  GAS2L1    3'  CTTCTGCATCAGGGAGCCCC   21362    A     AGCTT
                                GG GCTCTC    TGCAGAAG
                                || ||||||    ||||||||
                                CC CGAGGG    ACGTCTTC
                                 C     ACT__
GAM397  GBA2      5'  CTGAAGCAAGAGCTCC      71024        CA    TG
                                GGAGCTCT  GCTT  CAG
                                ||||||||  ||||  |||
                                CCTCGAGA  CGAA  GTC
                                    A_   __
GAM397  HRI       3'  CTTCCTGCCCCACAAGCTCCTT 26985        CTCAGCTTT   _
                                AAGGAGCT       GCAG AAG
                                ||||||||       |||| |||
                                TTCCTCGA       CGTC TTC
                                    ACACCC___    C
GAM397  IGF2AS    3'  CTGCCTAGAGCTCC       33097        C  CTTT
                                GGAGCTCT AG    GCAG
                                |||||||| ||    ||||
                                CCTCGAGA TC    CGTC
                                     _ _____
GAM397  IMP13     5'  GCCTGAGAGCTCCT       27734          CTTT
                                AGGAGCTCTCAG    GC
                                ||||||||||||    ||
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                                TCCTCGAGAGTC   CG
                                      ____
GAM397  KIAA0472 3' TCTGCAAAGAGTAGCTC    71872      _  AGC
                                GAGCT CTC   TTTGCAGA
                                ||||| |||   ||||||||
                                CTCGA GAG   AAACGTCT
                                   T  ___
GAM397  KIAA0700 3' TCCCTGGGGCTGAGATCTCC  72057     C      TT CA
                                GGAG TCTCAGCT  G  GA
                                |||| ||||||||  |  ||
                                CCTC AGAGTCGG  T  CT
                                  T       GG CC
GAM397  KIAA0852 5' TAATGCTAAAAGCTCCTT    30082       CTC   T
                                AAGGAGCT   AGC TTG
                                ||||||||   ||| |||
                                TTCCTCGA   TCG AAT
                                     AAA   T
GAM397  KIAA1126 3' CTGCTTCCGAGAGCTCCT    71927        AGCTTT
                                AGGAGCTCTC     GCAG
                                ||||||||||     ||||
                                TCCTCGAGAG     CGTC
                                     CCTT__
GAM397  KIAA1719 3' TGAAAGCCAAGAGCCCT     68173     A    CA    G
                                AGG GCTCT  GCTTT CA
                                ||| |||||  ||||| ||
                                TCC CGAGA  CGAAA GT
                                  _    AC    _
GAM397  KIAA1918 3' TCTGCCCCAGAGAGCTCC    73166        AGCTTT
                                GGAGCTCTC     GCAGA
                                |||||||||     |||||
                                CCTCGAGAG     CGTCT
                                     ACCC__
GAM397  MGC13114 3' CTGCCCTGCTGAGAGTCCT   50414     G      TTT
                                AGGA CTCTCAGC   GCAG
                                |||| ||||||||   ||||
                                TCCT GAGAGTCG   CGTC
                                  _       TCC
GAM397  MGC14258 3' TCCGCAAAGGAAAGCTCTTT  51861       C  AG    A
                                AAGGAGCT TC  CTTTGC GA
                                |||||||| ||  |||||| ||
                                TTTCTCGA AG  GAAACG CT
                                     A __     C
GAM397  MGC15606 5' TCTGCATAAGAGCTCTT     58880        CAGCTT
                                AGGAGCTCT     TGCAGA
                                |||||||||     ||||||
                                TTCTCGAGA     ACGTCT
                                     AT____
GAM397  MGC1842  3' CAGGGCTGAGGACCCCT     65646     AGC
                                AGG   TCTCAGCTTTG
                                |||   ||||||||||
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                                TCC   GGAGTCGGGAC
                                  CCA
GAM397  MGC32043  3'  GTAGACTGTAAGCTCCTT    58055        CT   C
                                AAGGAGCT  CAG TTTGC
                                ||||||||  ||| |||||
                                TTCCTCGA  GTC AGATG
                                    AT   _
GAM397  MGC5442   3'  CTCCAATCCCTGACAGCTCCTT 48709        C    CT_   C
                                AAGGAGCT TCAG   TTG AG
                                |||||||| ||||   ||| ||
                                TTCCTCGA AGTC   AAC TC
                                    C    CCT   C
GAM397  MPN       3'  CGGGGCCAGGAGCCCCTT    49208      A     CA
                                AAGG GCTCT  GCTTTG
                                |||| |||||  ||||||
                                TTCC CGAGG  CGGGGC
                                  C     AC
GAM397  PRO0132   5'  CTCCAACAGTAACAAGAGCTCC 26104        CA__   _   C
                                GGAGCTCT    GCT TTG AG
                                ||||||||    ||| ||| ||
                                CCTCGAGA    TGA AAC TC
                                    ACAA   C   C
GAM397  RIP60     3'  TCCCAGCGCTGAGAGCCTCC   25460      _       T   CA
                                GGAG CTCTCAGC TTG  GA
                                |||| ||||||| |||  ||
                                CCTC GAGAGTCG GAC  CT
                                  C       C   C_
GAM397  SMARCF1   3'  TCCCAGGGTTGCTAGAGCTCCT 37445          __       CA
          T                      AAGGAGCTCT  CAGCTTTG  GA
                                 ||||||||||  ||||||||  ||
                                 TTCCTCGAGA  GTTGGGAC  CT
                                     TC       C_
GAM397  SPIB      3'  CTTCCAGAGTCCCAAGAGCTTC 11908         CA__     CA
          T                      AGGAGCTCT    GCTTTG  GAAG
                                 |||||||||    ||||||  ||||
                                 TCTTCGAGA    TGAGAC  CTTC
                                     ACCC     __
GAM397  SSR3      3'  CTTCTGCAATTCTGAGAACTCT 23038    A   C     CT
          CC                      A GGAG TCTCAG  TTGCAGAAG
                                  | |||| ||||||  |||||||||
                                  C TCTC AGAGTC  AACGTCTTC
                                   C   A     TT
GAM397  STK36     3'  TTCCTTTCTGGAGCTCCTT    72107         T   CTTTGCA
                                AAGGAGCTC CAG       GAA
                                |||||||||  |||      |||
                                TTCCTCGAG GTC       CTT
                                    _   TTTC___
GAM397  TOB2      3'  CTGCCTGGTTGAGAGCTTCTT  95624             TT
                                AAGGAGCTCTCAGCT  GCAG
                                ||||||||||||||  ||||
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                                TTCTTCGAGAGTTGG  CGTC
                                         TC
GAM397  URG4     3'  CAGACTGTGAGCTCCTT     35503         T   C
                                AAGGAGCTC CAG TTTG
                                ||||||||| ||| ||||
                                TTCCTCGAG GTC AGAC
                                     T  _
GAM397  LOC115219 5'  TTCTGTCCAGGAGCTCCTT   73324          CAGCTTT
                                AAGGAGCTCT      GCAGAA
                                ||||||||||      ||||||
                                TTCCTCGAGG      TGTCTT
                                     ACC____
GAM397  LOC123242 5'  TCTGTAGTCCTGGGAGCCCC   75602    A       CT
                                GG GCTCTCAG  TTGCAGA
                                || ||||||||  |||||||
                                CC CGAGGGTC  GATGTCT
                                 C       CT
GAM397  LOC124302 3'  TTCTGCAAGAAAGCCTCTT   74276    GA   C  AGCT
                                AAG  GCT TC    TTGCAGAA
                                |||  ||| ||    ||||||||
                                TTC  CGA AG    AACGTCTT
                                  TC   A  ____
GAM397  LOC124801 3'  TCTGCAGGAAGAACTCTCTT   74340     _  C   CAGC
                                AAG GAG TCT    TTTGCAGA
                                ||| ||| |||    ||||||||
                                TTC CTC AGA    GGACGTCT
                                  T   A   A___
GAM397  LOC126767 5'  CTGTGAAACTGAGAGTCCT   75432      G      C  TG
                                AGGA CTCTCAG TT  CAG
                                |||| ||||||| ||  |||
                                TCCT GAGAGTC AA  GTC
                                  _      A  GT
GAM397  LOC129011 3'  CTTCTGCAAAATACAAGCTC   74867       CTCAGC
                                GAGCT     TTTGCAGAAG
                                |||||     ||||||||||
                                CTCGA     AAACGTCTTC
                                   ACATA_
GAM397  LOC132241 5'  TAGAGCTAAGAGCTCTCC    75054    A       C
                                A GGAGCTCT AGCTTTG
                                | ||||||| |||||||
                                C TCTCGAGA TCGAGAT
                                 C       A
GAM397  LOC146310 5'  CTTCTGCAAAAAGTGCATCCT  77818      _  T  CAGC
                                AGGA GC CT    TTTGCAGAAG
                                |||| || ||    ||||||||||
                                TCCT CG GA    AAACGTCTTC
                                  A  T  A___
GAM397  LOC146445 3'  TCCACAAAGCTGCGGCCCC    83684    A  T T       CA
                                GG GC C CAGCTTTG  GA
                                || || | ||||||||  ||
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                                CC CG G GTCGAAAC  CT
                                 C  _ C       AC
GAM397   LOC147639 3'  CTGAAACCGGAAGCTCCTT   78380        CT AGC   G
                                AAGGAGCT  C   TTT CAG
                                ||||||||  |   ||| |||
                                TTCCTCGA  G   AAA GTC
                                    AG CC_  _
GAM397   LOC148697 3'  CTTCTGCATTTCAAAGTCCT   78924     G  CTCAGCTT
                                AGGA CT       TGCAGAAG
                                ||||  ||       ||||||||
                                TCCT GA       ACGTCTTC
                                  _  AACTTT__
GAM397   LOC148697 3'  GCGATGAGAGCTGCT       78927    G       GCT
                                AG AGCTCTCA   TTGC
                                ||  ||||||||   ||||
                                TC TCGAGAGT   AGCG
                                 G       ___
GAM397   LOC149670 3'  CTTCTGTCTTCAAAAGGCTCCT 79489        T  CAGCTTT
            T                    AAGGAGC CT      GCAGAAG
                                |||||||  ||      |||||||
                                TTCCTCG GA      TGTCTTC
                                    _  AAACTTC
GAM397   LOC149912 5'  TCTGGAGCTGAGAATCCT    84720      GC        TG
                                AGGA  TCTCAGCTT  CAGA
                                ||||  |||||||||  ||||
                                TCCT  AGAGTCGAG  GTCT
                                  A_        __
GAM397   LOC152849 3'  CTTCTGGCCCAAGAGCTCC    80694        CA_  TTTG
                                GGAGCTCT   GC    CAGAAG
                                ||||||||   ||    ||||||
                                CCTCGAGA   CG    GTCTTC
                                    ACC  _____
GAM397   LOC152920 5'  CTGAGCTTGAGAGCCCT     80740     A      _   TTG
                                AGG GCTCTCA GCT   CAG
                                ||| ||||||| |||   |||
                                TCC CGAGAGT CGA   GTC
                                  _      T  ___
GAM397   LOC196955 5'  TCTGTAGTCCTGGGAGCCCC   77392    A       CT
                                GG GCTCTCAG  TTGCAGA
                                ||  ||||||||  |||||||
                                CC CGAGGGTC  GATGTCT
                                 C       CT
GAM397   LOC199986 3'  TCTGCAGAGAGATCC       89911     G     AGCTT
                                GGA CTCTC     TGCAGA
                                ||| |||||     ||||||
                                CCT GAGAG     ACGTCT
                                  A    ______
GAM397   LOC202546 3'  TCCCGCAACTTGCGGAGCTCCT 90360          _   CT    A_
                                AGGAGCTCT CAG  TTGC  GA
                                |||||||||  |||  ||||  ||
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                                TCCTCGAGG GTT  AACG  CT
                                     C   C_   CC
GAM397   LOC219653 3'  CTGCCCACATGAGAGCTTC   91293         GCTTT
                                GGAGCTCTCA    GCAG
                                ||||||||||    ||||
                                CTTCGAGAGT    CGTC
                                     ACACC
GAM397   LOC221416 3'  CTCAGACTGGAGCTCC     93764       T   C   C
                                GGAGCTC CAG TTTG AG
                                ||||||| ||| |||| ||
                                CCTCGAG GTC AGAC TC
                                   _  _   _
GAM397   LOC221416 3'  CTCAGACTGGAGCTCC     93765       T   C   C
                                GGAGCTC CAG TTTG AG
                                ||||||| ||| |||| ||
                                CCTCGAG GTC AGAC TC
                                   _  _   _
GAM397   LOC221416 3'  CTCCATCTGGAGCTCC     93766       T   CTT  C
                                GGAGCTC CAG   TG AG
                                ||||||| |||   || ||
                                CCTCGAG GTC   AC TC
                                   _  T__  C
GAM397   LOC253181 5'  CTGGGCTGAGAACCCCT    97557     AGC      TTG
                                AGG   TCTCAGCT   CAG
                                |||   ||||||||   |||
                                TCC   AGAGTCGG   GTC
                                  CCA       ___
GAM397   LOC255271 3'  CTTCTCACCTGCTGAGAGGTCC 95500      G      TT_  C
            TT                    AAGGA CTCTCAGC   TG AGAAG
                                |||||  ||||||||   ||  |||||
                                TTCCT GAGAGTCG   AC TCTTC
                                   G       TCC  _
GAM397   LOC255506 5'  CTTCTACCAGAAGAGGCTCCTT 97040       T   AG  TTGC
                                AAGGAGC CTC  CT    AGAAG
                                ||||||| |||  ||    |||||
                                TTCCTCG GAG  GA    TCTTC
                                   _   AA  CCA_
GAM397   LOC257460 5'  TCCCGCAACTTGCGGAGCTCCT 81061         _   CT    A_
                                AGGAGCTCT CAG  TTGC  GA
                                |||||||||  |||  ||||  ||
                                TCCTCGAGG GTT  AACG  CT
                                     C   C_   CC
GAM397   LOC257484 5'  GCCCCTGAGAGCCCCTT    88816     A      CTTT
                                AAGG GCTCTCAG    GC
                                ||||  ||||||||    ||
                                TTCC CGAGAGTC    CG
                                  C       CC__
GAM397   LOC56963  3'  CTGCAGATGCAAGAGCTCCT  71453         CA  _
                                AGGAGCTCT  GC TTTGCAG
                                |||||||||  ||  |||||||
```

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                                TCCTCGAGA  CG AGACGTC
                                     A_  T
GAM397  LOC91056  3'  TCCCAAGGTTTGCAAGCTCC  94764      CT  _   CA
                                GGAGCT  CAG CTTTG  GA
                                ||||||  ||| |||||  ||
                                CCTCGA  GTT GGAAC  CT
                                   AC   T    C_
GAM397  LOC92095  3'  CTGCAAAGGCTCCT      68093      TCTCAG
                                AGGAGC     CTTTGCAG
                                ||||||     ||||||||
                                TCCTCG     GAAACGTC

                                _______
GAM397  LOC92096  3'  CTGCAAAGGCTCCT      68099      TCTCAG
                                AGGAGC     CTTTGCAG
                                ||||||     ||||||||
                                TCCTCG     GAAACGTC

                                _______
GAM397  LOC92716  3'  CTGCAGCCCTGTGAGGCCCC  70379   A _ T  CT
                                GG GC TC CAG  TTGCAG
                                || || || |||  ||||||
                                CC CG AG GTC  GACGTC
                                 C  G  T   CC
GAM398  ABCB4     5'  GCTCCAGGTGGCAGGCA     38143      A      CT
                                TGCCTG CTACCTGG  GC
                                |||||| ||||||||  ||
                                ACGGAC GGTGGACC  CG
                                   _       T_
GAM398  ABCB4     5'  GCTCCAGGTGGCAGGCA     4794       A      CT
                                TGCCTG CTACCTGG  GC
                                |||||| ||||||||  ||
                                ACGGAC GGTGGACC  CG
                                   _       T_
GAM398  ABL1      3'  GCAGTCAGGGGTCAGGT     17676      A
                                GCCTGACT CCTGGCTGC
                                |||||||| |||||||||
                                TGGACTGG GGACTGACG

                                   _
GAM398  ABL1      3'  GCAGTCAGGGGTCAGGT     23613      A
                                GCCTGACT CCTGGCTGC
                                |||||||| |||||||||
                                TGGACTGG GGACTGACG

                                   _
GAM398  ADRBK1    3'  CGGCCAGGTGGGCGGGCA    7868       A
                                TGCCTG CTACCTGGCTG
                                |||||| ||||||||||
                                ACGGGC GGTGGACCGGC
                                   G
GAM398  AES       3'  TTATGGTGGCCGCCGGCGGG  6678      A ACC   TG
                                CCTG CT   TGGC  CCATAG
                                |||| ||   ||||  ||||||
```

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                                GGGC GG   GCCG  GGTATT
                                  _ CC_   GT
GAM398  ALDH3B1  3'  CCAACAGCAGCCAGGTGGTCAA 91523    C          CATAG
              GC                  GC TGACTACCTGGCTGC
                                  || ||||||||||||||
                                  CG ACTGGTGGACCGACG
                                   A           ACAACCT
GAM398  AMFR     3'  TTGTGGTAGTCCTTTTGGG   57248    TG CTACCT
                                  CC  A     GGCTGCCATAG
                                  ||  |     ||||||||||
                                  GG  T     CTGATGGTGTT
                                   GT TTC___
GAM398  AMFR     3'  TTGTGGTAGTCCTTTTGGG   6698     TG CTACCT
                                  CC  A     GGCTGCCATAG
                                  ||  |     ||||||||||
                                  GG  T     CTGATGGTGTT
                                   GT TTC___
GAM398  CALU     3'  CTGTGGTGGGAAGAGTTAGG  6886        AC  GG TG
                                  CCTGACT  CT  C  CCATAG
                                  |||||||  ||  |  ||||||
                                  GGATTGA  GA  G  GGTGTC
                                     __  AG GT
GAM398  CLDN14   5'  GTGGGCAGGTGGTCAGG     57841           G TG
                                  CCTGACTACCTG C  C
                                  ||||||||||||  |  |
                                  GGACTGGTGGAC G  G
                                        G GT
GAM398  CLN5     5'  TTGTGGTGGTCATCTCCGGC  21435     T  CTACC   TG
                                  GCC GA    TGGC  CCATAG
                                  ||| ||    ||||  ||||||
                                  CGG CT    ACTG  GGTGTT
                                    C  CT___    GT
GAM398  COX7A2   5'  TTGTGGCGGTTGCTGGTCAG  8519        CCT
                                  CTGACTA   GGCTGCCATAG
                                  |||||||   ||||||||||
                                  GACTGGT   TTGGCGGTGTT
                                     CG_
GAM398  DDEF2    5'  GCGGCTGGGTGGCGGGTA    13953       A    TG
                                  TGCCTG CTACC  GCTGC
                                  |||||| |||||  |||||
                                  ATGGGC GGTGG  CGGCG
                                     _    GT
GAM398  DLG4     3'  GGGGTCGGGGGTCGGGT     7255         A      G
                                  GCCTGACT CCTGGCT CC
                                  |||||||| ||||||| ||
                                  TGGGCTGG GGGCTGG GG
                                        _     _
GAM398  DYRK1A   3'  TTGTGGTGAAGTTTGTCAGGCA 7359         TAC  GGCT
                                  TGCCTGAC   CT   GCCATAG
                                  ||||||||   ||   |||||||
```

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                              ACGGACTG  GA   TGGTGTT
                                  TTT  AG__
GAM398  DYRK1A   3'  TTGTGGTGAAGTTTGTCAGGCA 55256       TAC  GGCT
                              TGCCTGAC  CT   GCCATAG
                              ||||||||  ||   |||||||
                              ACGGACTG  GA   TGGTGTT
                                  TTT  AG__
GAM398  DYRK1A   3'  TTGTGGTGAAGTTTGTCAGGCA 55210       TAC  GGCT
                              TGCCTGAC  CT   GCCATAG
                              ||||||||  ||   |||||||
                              ACGGACTG  GA   TGGTGTT
                                  TTT  AG__
GAM398  EPB41L2  3'  CTGTGGTGGTGTTCTGTTGGT  7482     T  TACCTG  TG
                              GCC GAC     GC  CCATAG
                              ||| |||     ||  ||||||
                              TGG TTG     TG  GGTGTC
                                _  TCTTG_  GT
GAM398  FCMD     3'  GTTGGTAGTTAGGCA      22096          T
                              TGCCTGACTACC GGC
                              |||||||||||| |||
                              ACGGATTGATGG TTG
                                        _
GAM398  FPGS     3'  CTGTGGCAGCTGCCCCTGGCA  17085     TGACTACCT
                              TGCC       GGCTGCCATAG
                              ||||       ||||||||||
                              ACGG       TCGACGGTGTC
                                TCCCCG___
GAM398  GAB2     3'  TTATGGTGGCATGTGTTGTGTA 24506     C   T  CTG  TG
                              TGC TGAC AC   GC  CCATAG
                              ||| |||| ||   ||  ||||||
                              ATG GTTG TG   CG  GGTATT
                                T   _  TA_  GT
GAM398  GAB2     3'  TTATGGTGGCATGTGTTGTGTA 54463     C   T  CTG  TG
                              TGC TGAC AC   GC  CCATAG
                              ||| |||| ||   ||  ||||||
                              ATG GTTG TG   CG  GGTATT
                                T   _  TA_  GT
GAM398  HD       3'  TGTGGCAGTGGCCAGGCA    9195        A  ACCTG
                              TGCCTG CT    GCTGCCATA
                              |||||| ||    |||||||||
                              ACGGAC GG    TGACGGTGT
                                 C  _____
GAM398  HIP1     3'  TATGGTGGTTGGTTGGGT    18066     TG   CCTG  TG
                              GCC  ACTA   GC  CCATA
                              |||  ||||   ||  |||||
                              TGG  TGGT   TG  GGTAT
                                GT   ____  GT
GAM398  IFNAR1   3'  TAGCCGGGTAGTAGGTA     5286        A
                              TGCCTG CTACCTGGCTG
                              |||||| ||||||||||
```

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                                ATGGAT GATGGGCCGAT
                                      _
GAM398  JMJ     3'  TTGTGGCAGCTGAAGGCGG   17135   TA  __
                                C  CCT  GGCTGCCATAG
                                |  |||  ||||||||||
                                G  GGA  TCGACGGTGTT
                                 GC   AG
GAM398  LAPTM5   3'  TGTGGCAGCTGGGGAGGTT   22205     A_  TG
                                GACT  CC  GCTGCCATA
                                ||||  ||  |||||||||
                                TTGG  GG  CGACGGTGT
                                  AG  GT
GAM398  LENG4    5'  CTGTGGCGGGCCCCATTAGGTA 44165        CTACCT   _
                                TGCCTGA     GGCT GCCATAG
                                |||||||     |||| |||||||
                                ATGGATT     CCGG CGGTGTC
                                     ACC___    G
GAM398  MCM6     5'  TTGTGGCGGTCGAGCGTGGCGC 19791     CT A   _ _
            A                    TGC  G CTAC CT GGCTGCCATAG
                                |||  | |||| || ||||||||||
                                ACG  C GGTG GA CTGGCGGTGTT
                                  __ _   C  G
GAM398  NAPB     5'  CTGTGGCGGCCGCGGCGGGCG  70181       ACTA  _
                                TGCCTG   CC TGGCTGCCATAG
                                ||||||   || ||||||||||||
                                GCGGGC   GG GCCGGCGGTGTC
                                    _____  C
GAM398  NDUFA5   3'  TTATGGTAATATGGTCATGT   17196    C     CC  GC
                                GC TGACTA  TG  TGCCATAG
                                || ||||||  ||  ||||||||
                                TG ACTGGT  AT  ATGGTATT
                                 T     __  A_
GAM398  P3       3'  AGTTAGGTAGGTGGGC      39064      GA
                                GCCT  CTACCTGGCT
                                ||||  ||||||||||
                                CGGG  GATGGATTGA
                                  TG
GAM398  PCTP     3'  CTGTGGCAGCTAGCAAAAGCA  41097     CTGACTAC
                                TGC       CTGGCTGCCATAG
                                |||       ||||||||||||
                                ACG       GATCGACGGTGTC
                                  AAAAC____
GAM398  PPP1R12B 3'  TGTGGTAGCCACTCCAGG    49475     ACTACC
                                CCTG     TGGCTGCCATA
                                ||||     ||||||||||
                                GGAC     ACCGATGGTGT
                                  CTC___
GAM398  PPP1R12B 3'  TGTGGTAGCCACTCCAGG    49486     ACTACC
                                CCTG     TGGCTGCCATA
                                ||||     ||||||||||
```

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                                GGAC     ACCGATGGTGT
                                  CTC___
GAM398  PTGFRN   3'  TGTGGTGGGAAGACGGGCA   67195       A  A   GGCT
                                TGCCTG CT CCT    GCCATA
                                |||||| || |||    ||||||
                                ACGGGC GA GGG    TGGTGT
                                   A  A  _____
GAM398  PYGB     3'  GTGGCTGTGGTTGGCA     11178      T     CT   TG
                                TGCC GACTAC  GGC  C
                                |||| ||||||  |||  |
                                ACGG TTGGTG  TCG  G
                                  _     __  GT
GAM398  PYGO2    3'  TATGGCAGTTTCTTGGT     63991      CCT
                                ACTA   GGCTGCCATA
                                ||||   ||||||||||
                                TGGT   TTGACGGTAT
                                  TCT
GAM398  RAB27A   3'  TTATGGTGGCAAATGTTTGGTA 15928      T   TACCTG  TG
                                TGCC GAC     GC  CCATAG
                                |||| |||     ||  ||||||
                                ATGG TTG     CG  GGTATT
                                  T   TAAA__  GT
GAM398  RPL36AL  5'  GCGAAGGGCCAGGTGTCGGGC  6398        T       GCCATAG
                                GCCTGAC ACCTGGCT
                                ||||||| ||||||||
                                CGGGCTG TGGACCGG
                                    _       GAAGCGT
GAM398  RPN1     3'  CTGTGGCAGGCAGATTGGGT   11390     TG CTAC   G
                                GCC  A    CTG CTGCCATAG
                                |||  |    ||| ||||||||||
                                TGG  T    GAC GACGGTGTC
                                  GT A___   G
GAM398  SCN3A    3'  TGTGGTGCATGTTTGGGCA   22633      TG CT  CTG  T
                                TGCC  A  AC   GC GCCATA
                                ||||  |  ||   || ||||||
                                ACGG  T  TG   CG TGGTGT
                                  GT __  TA_  _
GAM398  SDC4     3'  GATGTTGCTGGGTGGTTGAGT  11479    CT      TG  TGC   AG
                                GC  GACTACC  GC   CAT
                                ||  |||||||  ||   |||
                                TG  TTGGTGG  CG   GTA
                                  AG      GT  TT_   GT
GAM398  SF3B3    3'  CTGTGGTGGGACTGGGTAGGGT 24857      TGA     TG __ TG
           A                     TGCC   CTACC  G  C  CCATAG
                                ||||   |||||  |  |  ||||||
                                ATGG   GATGG  C  G  GGTGTC
                                  ___     GT AG GT
GAM398  SFRP4    3'  CTGTACCATTAGGAGTTAGGTA 11577         A    C  CC
                                TGCCTGACT CCTGG TG  ATAG
                                |||||||| ||||| ||  ||||
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                                ATGGATTGA GGATT AC  TGTC
                                      _    _ CA
GAM398  SFTPA2   3'  CTGTGGCAGGCCTGGTCAGGC  22647        CCT  _
                                GCCTGACTA   GGC TGCCATAG
                                |||||||||   ||| ||||||||
                                CGGACTGGT   CCG ACGGTGTC
                                     ___  G
GAM398  SLA      3'  GTTAGGTGTCAGGCA      22172        T
                                TGCCTGAC ACCTGGC
                                |||||||| |||||||
                                ACGGACTG TGGATTG

                                      _
GAM398  SLC12A2  5'  GCCGGGGGTCGGGCA      6453         A
                                TGCCTGACT CCTGGC
                                ||||||||| ||||||
                                ACGGGCTGG GGGCCG

                                      _
GAM398  TAF4B    3'  CTGTGGTGACTTTGGTCGGC  87168    T    CCT  CT
                                GCC GACTA   GG  GCCATAG
                                ||| |||||   ||  |||||||
                                CGG CTGGT   TC  TGGTGTC
                                  _    T__  AG
GAM398  TAGLN2   3'  CTGTGGCAGCTGCTGCCCCAGC 13096    C   ACTACCT
           CA                     TG CTG      GGCTGCCATAG
                                || |||      ||||||||||
                                AC GAC      TCGACGGTGTC
                                 C   CCCGTCG
GAM398  TSPY     5'  TGTGGCGTGGGTCGGGCA    82109        ACCTGGC
                                TGCCTGACT      TGCCATA
                                |||||||||      |||||||
                                ACGGGCTGG      GCGGTGT
                                     GT_____
GAM398  UNC13    3'  GTGCCTGGCTGGCTGGGTAGTC 21059    C       TG  _   TAG
           AGC                      GC TGACTACC  GCT GCCA
                                || ||||||||  ||| ||||
                                CG ACTGATGG  CGG CGGT
                                 _       GT   T    CCGTGT
GAM398  VCP      3'  CTATCCAACCTGGGTAGGTGGG 75369      GA    TG CTGCC
           TA                     TGCCT  CTACC  G    ATAG
                                |||||  |||||  |    ||||
                                ATGGG  GATGG  C    TATC
                                   TG    GT CAACC
GAM398  VIPR2    3'  GTTGATGGTCGGTGGTTGGGT  12615     TG     T   GC  TAG
                                GCC  ACTACC GGCT  CA
                                |||  |||||| ||||  ||
                                TGG  TGGTGG CTGG  GT
                                  GT     _    TA  TGT
GAM398  WFS1     3'  CTGTCCAGCAGGTAGTGGGT   20009     G      G   CC
                                GCCT ACTACCTG CTG  ATAG
                                |||| |||||||| |||  ||||
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                                TGGG TGATGGAC GAC  TGTC
                                  _      _  C_
GAM398  XKRY     3'  GCAACCAAGGTGGTCGGGCA  16257          _ C
                                TGCCTGACTACCT GG TGC
                                |||||||||||| || |||
                                ACGGGCTGGTGGA CC ACG
                                       A  A
GAM398  XKRY     3'  GCAACCAAGGTGGTCGGGCA  60019          _ C
                                TGCCTGACTACCT GG TGC
                                |||||||||||| || |||
                                ACGGGCTGGTGGA CC ACG
                                       A  A
GAM398  ZNF192   3'  CTGTGGTACAGATAGTTGGCA  20855     T    C  GC
                                TGCC GACTA CTG  TGCCATAG
                                |||| ||||| |||  ||||||||
                                ACGG TTGAT GAC  ATGGTGTC
                                  _    A  __
GAM398  ATP6V0A1 5'  TGTGGCGGTTGCTGTGGC   17733    TG  TACC
                                GCC  AC   TGGCTGCCATA
                                |||  ||   ||||||||||
                                CGG  TG   GTTGGCGGTGT
                                  __  TC__
GAM398  C1QTNF6  3'  CTGTGTTCTGGGTGTTCAGGT  49144      C   TG CTGC
                                GCCTGA TACC  G   CATAG
                                |||||| ||||  |   |||||
                                TGGACT GTGG  C   GTGTC
                                   T   GT TT__
GAM398  CBX6     3'  GTATGCAGGTAGTCAGCCA   26623    C       G _
                                TG CTGACTACCTG C TGC
                                || ||||||||||| | |||
                                AC GACTGATGGAC G ATG
                                 C         _ T
GAM398  CBX6     3'  TGGGGCTGGGTAGTTGGG    26632    TG    TG  G
                                CC  ACTACC  GCT CCA
                                ||  ||||||  ||| |||
                                GG  TGATGG  CGG GGT
                                 GT     GT  _
GAM398  CCNI     5'  CTACAGCAAGCTGGGTAGCAGG 22419      A    TG  _ CA
           CA                    TGCCTG CTACC  GCT GC  TAG
                                ||||||| |||||  ||| ||  |||
                                ACGGAC GATGG  CGA CG  ATC
                                   _    GT   A  AC
GAM398  CDT1     3'  CTGTGGCAATATGGGGTTGGGT 77673     TG   A  TGGC
           A                     TGCC  ACT CC   TGCCATAG
                                ||||  ||| ||   ||||||||
                                ATGG  TGG GG   ACGGTGTC
                                  GT   _  TATA
GAM398  COE2     3'  TGTGCAGCTGGTTGGGCA    64257     TG   ACCT    _
                                TGCC  ACT   GGCTGC CA
                                ||||  |||   |||||| ||
```

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                                ACGG  TGG    TCGACG GT
                                  GT  _____     T
GAM398  CSEN     3'  GTGGCTGGGTGGTCAGCA    25534     C       TG  TG
                                TGC TGACTACC  GC  C
                                ||| ||||||||  ||  |
                                ACG ACTGGTGG  CG  G
                                  _       GT  GT
GAM398  dJ309H15.1 3'  CTGTGGTAGTTAGCGGGCAGG  56796      A  AC
                                CCTG CT  CTGGCTGCCATAG
                                |||| ||  ||||||||||||||
                                GGAC GG  GATTGATGGTGTC
                                  _ GC
GAM398  DKFZP434H204 5'  GCCCTGCCAGGTGGTGGGCA   66429       G        T__
                                TGCCT ACTACCTGGC   GC
                                ||||| ||||||||||   ||
                                ACGGG TGGTGGACCG   CG
                                  _        TCC
GAM398  DKFZP564O0423 3'  TGTGGTGGCCATGTGGT     91705      C    TG
                                ACTAC TGGC  CCATA
                                ||||| ||||  |||||
                                TGGTG ACCG  GGTGT
                                   T    GT
GAM398  DNAJC5    3'  TGGTTTCTTGGGAGTCGGGCA  61457          A  TG CT_
                                TGCCTGACT CC  G   GCCA
                                |||||||| ||  |   ||||
                                ACGGGCTGA GG  T   TGGT
                                     _ GT CTT
GAM398  DTX2      3'  TGGCTGGGTGGCCAGGCA    71955       A     TG
                                TGCCTG CTACC  GCTG
                                |||||| |||||  ||||
                                ACGGAC GGTGG  CGGT
                                   C     GT
GAM398  ERG-1     5'  TGTGGCGGTTACCTGG      41845     CC
                                CTA  TGGCTGCCATA
                                |||  ||||||||||
                                GGT  ATTGGCGGTGT
                                  CC
GAM398  FEM-2     3'  GCACTGGGTGGCGGGCA     27582       A     TG C
                                TGCCTG CTACC  G TGC
                                |||||| |||||  | |||
                                ACGGGC GGTGG  C ACG
                                   _    GT _
GAM398  FLJ00001  3'  TGTGGTAGCTTTTAGGC     81823       CTACCT
                                GCCTGA     GGCTGCCATA
                                ||||||     ||||||||||
                                CGGATT     TCGATGGTGT
                                   T_____
GAM398  FLJ10468  3'  TGTGGGAGGTGGTCAG      36150          GGCTG
                                CTGACTACCT    CCATA
                                ||||||||||    |||||
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                                GACTGGTGGA    GGTGT
                                      G____
GAM398  FLJ10853  3' CTGTGGCAGTTGTTGCCTGAGC 36767    CTGACT_ CT
             A                   TGC      AC  GGCTGCCATAG
                                 |||      ||  ||||||||||
                                 ACG      TG  TTGACGGTGTC
                                   AGTCCGT  __
GAM398  FLJ10901  3' TTGTGGCATGTTCTGGTTGGG  36835    TG   CCT  _
                                 CC  ACTA   GGC TGCCATAG
                                 ||  ||||   ||| ||||||||
                                 GG  TGGT   TTG ACGGTGTT
                                  GT   C__   T
GAM398  FLJ10989  5' TGTGGTGGCAGGCTGGGCA   36953      ACTA   G TG
                                 TGCCTG   CCTG C  CCATA
                                 ||||||   |||| |  |||||
                                 ACGGGT   GGAC G  GGTGT
                                    C___   _ GT
GAM398  FLJ12428  3' CTATGGTTGGGGGGTAGTTAGG  42944         GGCT
                                 CCTGACTACCT   GCCATAG
                                 ||||||||||   |||||||
                                 GGATTGATGGG   TGGTATC
                                       GGT_
GAM398  FLJ13193  3' TTATGTTAAGGAAGTCAGGTA  49776        A   GGCTGC
                                 TGCCTGACT CCT     CATAG
                                 |||||||| |||     |||||
                                 ATGGACTGA GGA     GTATT
                                      A   ATT___
GAM398  FLJ14490  3' TTGTGGCAGCTGGTGCCGGGT  51401      AC   T
                                 GCCTG  TACC GGCTGCCATAG
                                 |||||  |||| ||||||||||
                                 TGGGC  GTGG TCGACGGTGTT
                                    C_   _
GAM398  FLJ20506  5' TATGGCGGCTACCAG      35268     ACTACC
                                 CTG     TGGCTGCCATA
                                 |||     ||||||||||
                                 GAC     ATCGGCGGTAT
                                   C_____
GAM398  FLJ20986  3' TTATGGTGGGAGGTGGTTGGG  44548    TG      GG TG
                                 CC  ACTACCT  C  CCATAG
                                 ||  |||||||  |  ||||||
                                 GG  TGGTGGA  G  GGTATT
                                  GT      G_ GT
GAM398  FLJ22477  5' TTGTGGCAGCCAGATATCGGGC 45348       C  C
                                 GCCTGA TA CTGGCTGCCATAG
                                 |||||| || ||||||||||||
                                 CGGGCT AT GACCGACGGTGTT
                                    _ A
GAM398  FLJ22679  3' TTGTGGCGGGTAGAGTCAG   49926       AC   G
                                 CTGACT  CTG CTGCCATAG
                                 ||||||  ||| |||||||||
```

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                                GACTGA  GAT GGCGGTGTT
                                   __   G
GAM398  FLJ22679  3'  TTGTGGCGGGTAGAGTCAG   34682       AC   G
                                CTGACT  CTG CTGCCATAG
                                ||||||  ||| |||||||||
                                GACTGA  GAT GGCGGTGTT
                                   __   G
GAM398  FLJ23231  3'  TTGGCCTTGGCTGGCTAGTTGG 46916    TG    C TG  ___    TAG
           GCA                    CC  ACTA C  GCT   GCCA
                                ||  |||| |  |||   ||||
                                GG  TGAT G  CGG   CGGT
                                 GT    C GT   TTC    T
GAM398  GGA2     3'  GGCCTGGTAGTCAGGT      56888          T
                                GCCTGACTACC GGCT
                                |||||||||| ||||
                                TGGACTGATGG CCGG
                                       T
GAM398  GGA2     3'  GGCCTGGTAGTCAGGT      30474          T
                                GCCTGACTACC GGCT
                                |||||||||| ||||
                                TGGACTGATGG CCGG
                                       T
GAM398  GLP      3'  TATGGTAGTTCCCTTAGG    37848       CTACCT
                                CCTGA     GGCTGCCATA
                                |||||     |||||||||
                                GGATT     TTGATGGTAT
                                   CCC___
GAM398  H2-ALPHA  5'  CTGTGGCAGCCGGTTGAGGT   73010      GACT   T
                                GCCT    ACC GGCTGCCATAG
                                ||||    ||| ||||||||||
                                TGGA    TGG CCGACGGTGTC
                                  GT__   _
GAM398  IL-17RE   3'  TGGCTCCAGGTGGTCAGGACA  58297    _          CT
                                TG CCTGACTACCTGG  GCCA
                                || ||||||||||||  ||||
                                AC GGACTGGTGGACC  CGGT
                                 A           T_
GAM398  KIAA0212  3'  CTGTGGCGGCAGTGGTGGGTA  27939      G    CTG
                                TGCCT ACTAC   GCTGCCATAG
                                ||||| |||||   ||||||||||
                                ATGGG TGGTG   CGGCGGTGTC
                                   _    A__
GAM398  KIAA0237  3'  TTGTGGTTCCCGGGTGGCAGGT 28540       A       CT
                                GCCTG CTACCTGG  GCCATAG
                                ||||| ||||||||  |||||||
                                TGGAC GGTGGGCC  TGGTGTT
                                   _       CT
GAM398  KIAA0317  3'  TGTGGTGGTCCTTAGGCA    29091        CTACCT   TG
                                TGCCTGA     GGC  CCATA
                                |||||||     |||  |||||
```

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                                ACGGATT     CTG  GGTGT
                                   C_____   GT
GAM398  KIAA0523 3' CTATGGTGACTGGGTTAGGTA 67735       ACT   TG CT
                                TGCCTG   ACC  G  GCCATAG
                                ||||||   |||  |  |||||||
                                ATGGAT   TGG  C  TGGTATC
                                   ___   GT AG
GAM398  KIAA0544 3' TGGTGGCTGGGTGTCAGGCA  70911        T   TG  TG
                                TGCCTGAC ACC  GC  CCA
                                |||||||| |||  ||  |||
                                ACGGACTG TGG  CG  GGT
                                    _  GT  GT
GAM398  KIAA0547 3' GTTAGGAGTCAGGTA       28916         A
                                TGCCTGACT CCTGGC
                                ||||||||| ||||||
                                ATGGACTGA GGATTG
                                          _
GAM398  KIAA0721 3' TTATGGTAAGCTATTTGGGTA 41351      TG CTACC    _
                                TGCC  A    TGGCT GCCATAG
                                ||||  |    ||||| |||||||
                                ATGG  T    ATCGA TGGTATT
                                  GT T____    A
GAM398  KIAA0721 3' TTATGGTAAGCTATTTGGGTA 95979      TG CTACC    _
                                TGCC  A    TGGCT GCCATAG
                                ||||  |    ||||| |||||||
                                ATGG  T    ATCGA TGGTATT
                                  GT T____    A
GAM398  KIAA1023 3' TGTGGCGGTCAGAAGGC     34272      GACTAC
                                GCCT     CTGGCTGCCATA
                                ||||     ||||||||||||
                                CGGA     GACTGGCGGTGT
                                  A_____
GAM398  KIAA1094 5' TGTGGGGGGTGGCCGGGC    29807      A     GGCTG
                                GCCTG CTACCT     CCATA
                                ||||| ||||||    |||||
                                CGGGC GGTGGG     GGTGT
                                   C     G____
GAM398  KIAA1257 3' CTGTGGTGGTTATCATAGTTA 62739       CC_   TG
                                TGACTA   TGGC  CCATAG
                                ||||||   ||||  ||||||
                                ATTGAT   ATTG  GGTGTC
                                   ACT    GT
GAM398  KIAA1280 5' TTGTGGTGGCTGTCTGTGGGG 69735     G  TACCT   TG
                                CCT AC     GGC  CCATAG
                                ||| ||     |||  ||||||
                                GGG TG     TCG  GGTGTT
                                  G  TCTG_   GT
GAM398  KIAA1320 5' TTATGGCAGCTGGGTG      69314      TG
                                TACC  GCTGCCATAG
                                ||||  ||||||||||
```

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                                GTGG  CGACGGTATT
                                  GT
GAM398  KIAA1414  3'  GTATCATGTAGTCGGGCA    67991          C   C
                                TGCCTGACTAC TGG TGC
                                |||||||||||  ||| |||
                                ACGGGCTGATG ACT ATG
                                      T  _
GAM398  KIAA1553  5'  CTGTGGCAGCACCGGGGCAGGC 91919       A  A  TG_
          A                      TGCCTG CT CC   GCTGCCATAG
                                 ||||||  || ||   ||||||||||
                                 ACGGAC GG GG   CGACGGTGTC
                                    _ _  CCA
GAM398  KIAA1644  3'  GTCTAGGTAGGTAGGTA     85031       A      _
                                 TGCCTG CTACCTGG C
                                 ||||||  ||||||||  |
                                 ATGGAT GATGGATC G
                                    G       T
GAM398  KIAA1751  3'  GTGGTGGAAGTCAGG       71704        A  TGGCT
                                 CCTGACT CC     GCCAT
                                 |||||||  ||     |||||
                                 GGACTGA GG     TGGTG
                                     A  _____
GAM398  KIAA1863  3'  TGTGGCGATGGTGGGGT     64876     TGA    TGGC
                                 GCC   CTACC    TGCCATA
                                 |||   |||||    |||||||
                                 TGG   GGTGG    GCGGTGT
                                   ____    TA__
GAM398  KIAA1951  3'  CTGTGGTGGCCAGCTACTCAGG 73762       C  C    TG
                                 CCTGA TA CTGGC  CCATAG
                                 |||||  ||  |||||  ||||||
                                 GGACT AT GACCG  GGTGTC
                                    C  C    GT
GAM398  MGC10701  3'  CTGTGGTAAGGCTCTGTCGGGC 51027         TACCT   __
          A                      TGCCTGAC    GGCT  GCCATAG
                                 ||||||||    ||||  |||||||
                                 ACGGGCTG    TCGG  TGGTGTC
                                      TC___    AA
GAM398  MGC10814  5'  TTGTGGCTGCAGGTGTTAGGT  51044        T    G T
                                 GCCTGAC ACCTG C GCCATAG
                                 |||||||  |||||  |  |||||||
                                 TGGATTG TGGAC G CGGTGTT
                                    _    _ T
GAM398  MGC16733  3'  TTGTGGTAGCTGTTACAAGTA  53212     C  ACT  CT
                                 TGC TG   AC  GGCTGCCATAG
                                 |||  ||   ||  ||||||||||
                                 ATG AC   TG  TCGATGGTGTT
                                   A  AT_  __
GAM398  MGC2452   5'  CTGTGGCCTCTGTAGTTAGGGC 50982      _      CT  CT
          A                      TGCC TGACTAC  GG  GCCATAG
                                 ||||  |||||||  ||  |||||||
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                                ACGG ATTGATG  TC  CGGTGTC
                                  G      __  TC
GAM398  MGC2477  5'  TTGTGGTGGAATCCAGTGAGGT 44077     G   ACCTGG TG
                                GCCT ACT     C  CCATAG
                                |||| |||     |  ||||||
                                TGGA TGA     G  GGTGTT
                                  G   CCTAA_ GT
GAM398  MGC26655 5'  CTGCGGAGTGTGGGTGGTTGGG 56290     TG      _   G  A
          C                      GCC  ACTACCTG GCT CC TAG
                                 |||  |||||||| ||| || |||
                                 CGG  TGGTGGGT TGA GG GTC
                                   GT       G   _  C
GAM398  MGC3195  5'  CTGTGGCGGCTAGGCCCGCGTG 49123    C  ACTA
          C                      GC TG    CCTGGCTGCCATAG
                                 || ||    ||||||||||||||
                                 CG GC    GGATCGGCGGTGTC
                                  T  GCCC
GAM398  MGC4643  3'  TTATGGTGATGTGTAGTCAGTG 51159     _       C  GC
          TA                      TGC CTGACTAC TG  TGCCATAG
                                 ||| |||||||| ||  ||||||||
                                 ATG GACTGATG GT  GTGGTATT
                                   T       T  A_
GAM398  MIC2L1   3'  CTGTGGTGGAGGGTGGTCAGTC 48823    C        GG TG
          G                      TG CTGACTACCT  C  CCATAG
                                 || ||||||||||  |  ||||||
                                 GC GACTGGTGGG  G  GGTGTC
                                  T         A_ GT
GAM398  MKNK1    3'  TGTGGCGGCTGGGGCTGCA   13481     CTGACTA  TG
                                TGC      CC  GCTGCCATA
                                |||      ||  |||||||||
                                ACG      GG  CGGCGGTGT
                                  TCG_____  GT
GAM398  NAP1L2   5'  CTGTGGTAGCCACCTTAGGC   41735       CTACC
                                GCCTGA    TGGCTGCCATAG
                                ||||||    ||||||||||||
                                CGGATT    ACCGATGGTGTC
                                    CC___
GAM398  NIBAN    5'  CTGTGGCAGCCCTTCTTCAGAC 42001    C    CTACCT
          A                      TG CTGA     GGCTGCCATAG
                                 || ||||     ||||||||||||
                                 AC GACT     CCGACGGTGTC
                                  A   TCTTC_
GAM398  PCF11    5'  CTGTGGCGGCTGGAAGTGG    31891     __ TG
                                CTAC  C  GCTGCCATAG
                                ||||  |  ||||||||||
                                GGTG  G  CGGCGGTGTC
                                  AA GT
GAM398  PRO0650  5'  TTATGCACCTACCAGGGGTCAG 26216        A    C___   C
          GCA                     CCTGACT CCTGG    TGC ATAG
                                 ||||||| |||||    ||| ||||
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                                GGACTGG GGACC   ACG TATT
                                   _    ATCC  _
GAM398  PRO2730  5'  TGAGGCTAGGTGGTTGGGCA  47420     TG        GC
                                TGCC  ACTACCTGGCT  CA
                                ||||  ||||||||||  ||
                                ACGG  TGGTGGATCGG  GT
                                  GT         A_
GAM398  RER1     3'  GCCAGGTGGGCAGGCA     22864       A
                                TGCCTG CTACCTGGC
                                |||||| |||||||||
                                ACGGAC GGTGGACCG
                                   G
GAM398  SLC39A3  3'  GTCCTCGGGCTGGTCAGGC   57978         _    CT
                                GCCTGACTA CCTGG  GC
                                ||||||||| |||||  ||
                                CGGACTGGT GGGCT  TG
                                     C    CC
GAM398  SPEC1    3'  TTATGGTAGTGGGGTCAGG   39614      CTA   G
                                CCTGA   CCT GCTGCCATAG
                                |||||   ||| ||||||||||
                                GGACT   GGG TGATGGTATT
                                   ___  G
GAM398  STI2     3'  TTGTGTAGCTTGGGAGTCAGGC 88969         A  T     _  TAG
           A                     TGCCTGACT CC GGCTGC CA
                                |||||||| || |||||| ||
                                ACGGACTGA GG TCGATG GT
                                     G  T     T  T
GAM398  STK25    3'  TGTGGTGTTGGATCAGGTA   21053        CTAC TG  T
                                TGCCTGA    C  GC GCCATA
                                |||||||    |  || ||||||
                                ATGGACT    G  TG TGGTGT
                                   A___ GT  _
GAM398  SYNCOILIN 3'  CTGTGGTATAACTGTCAGGTA  47895         TACCTGGC
                                TGCCTGAC       TGCCATAG
                                ||||||||       ||||||||
                                ATGGACTG       ATGGTGTC
                                     TCAAT___
GAM398  TBX21    3'  TTGTGGTGGTTGTGTGTGGGT  25329     G  T  C    TG
                                GCCT AC AC TGGC  CCATAG
                                |||| || || ||||  ||||||
                                TGGG TG TG GTTG  GGTGTT
                                  _ _  T   GT
GAM398  TRIP13   5'  CTGTGGCGGCGACGCTGGGC   14895     GACTACCTG
                                GCCT       GCTGCCATAG
                                ||||       ||||||||||
                                CGGG       CGGCGGTGTC
                                  TCGCAG___
GAM398  VEZATIN  3'  GTTAGGTGGTTGGCA      34227      T
                                TGCC GACTACCTGGC
                                |||| ||||||||||
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                                ACGG TTGGTGGATTG
                                   _
GAM398  WFDC3     3'  TGGATTGGGTAGTGGGT     96926      G     TG CTG
                                GCCT ACTACC  G   CCA
                                |||| ||||||  |   |||
                                TGGG TGATGG  T   GGT
                                  _     GT A__
GAM398  ZNF297    3'  GGTCAGGGGTCAGGT       18392        A
                                GCCTGACT CCTGGCT
                                |||||||| |||||||
                                TGGACTGG GGACTGG
                                   _
GAM398  LOC112714 5'  CTGTGGCAGCCGGTTGAGGT   72872      GACT   T
                                GCCT    ACC GGCTGCCATAG
                                ||||    ||| ||||||||||
                                TGGA    TGG CCGACGGTGTC
                                  GT__   _
GAM398  LOC113675 5'  TGGTCTGGGATAGTTGGGCA   56574      TG   _  TG CT
                                TGCC  ACTA CC  G  GCCA
                                ||||  |||| ||  |  ||||
                                ACGG  TGAT GG  C  TGGT
                                  GT    A  GT __
GAM398  LOC121219 5'  CTATGGTGGTTGGGCGGCTGGT 74044    _  GA TA  TG  TG
          GC                      GC CT  C  CC  GC  CCATAG
                                || ||  |  ||  ||  ||||||
                                CG GG  G  GG  TG  GGTATC
                                 T  TC GC  GT  GT
GAM398  LOC124460 3'  CAGCCAGGTGGTCAGG      76041
                                CCTGACTACCTGGCTG
                                ||||||||||||||||
                                GGACTGGTGGACCGAC

GAM398  LOC124997 5'  TGTGGCAGCAGCTGGGC     74389      GA  ACCTG
                                GCCT  CT    GCTGCCATA
                                ||||  ||    |||||||||
                                CGGG  GA    CGACGGTGT
                                  TC  _____
GAM398  LOC125929 3'  TTGTGGTAGTGGTTGTAGTTAG 75675         CTG_
                                CTGACTAC    GCTGCCATAG
                                ||||||||    ||||||||||
                                GATTGATG    TGATGGTGTT
                                    TTGG
GAM398  LOC132720 5'  CGGCCGGGGGTTGGGC      75064     TG   A
                                GCC  ACT CCTGGCTG
                                |||  ||| ||||||||
                                CGG  TGG GGGCCGGC
                                  GT  _
GAM398  LOC139231 3'  TATGGCGGTGAAGTGGGC    75378      G   ACCTG
                                GCCT ACT    GCTGCCATA
                                |||| |||    |||||||||
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                                CGGG TGA    TGGCGGTAT
                                  _  AG___
GAM398  LOC144347 3'  AGCCAGGAGGTTGGGCA    76810     TG  A
                                TGCC  ACT CCTGGCT
                                |||| ||| |||||||
                                ACGG  TGG GGACCGA
                                  GT  A
GAM398  LOC145497 3'  TGTGGCAGGGGCTGGGCA    77220      ACTA  GG
                                TGCCTG   CCT  CTGCCATA
                                ||||||   |||  ||||||||
                                ACGGGT   GGG  GACGGTGT
                                   C___  __
GAM398  LOC145761 5'  CTGCATTCCCAGGAGGTTAGGC 83475        A   C__  CATAG
          A                     TGCCTGACT CCTGG  TGC
                                ||||||||| |||||  |||
                                ACGGATTGG GGACC  ACG
                                     A   CTT  TC
GAM398  LOC146599 5'  GCCCACCAGGGGTCAGGT    78025       A   CT_
                                GCCTGACT CCTGG  GC
                                |||||||| |||||  ||
                                TGGACTGG GGACC  CG
                                   _    ACC
GAM398  LOC147299 3'  CTGTGGCGTCCCTCGTCGGGTA 78346       TACCT  C
                                TGCCTGAC    GG TGCCATAG
                                ||||||||    || ||||||||
                                ATGGGCTG    CC GCGGTGTC
                                     CTC__  T
GAM398  LOC147622 5'  CTGTGGCGCACTTGGTTGGG  84050   TG   CCTG  T
                                CC  ACTA   GC GCCATAG
                                ||  ||||   || |||||||
                                GG  TGGT   CG CGGTGTC
                                 GT   TCA_  _
GAM398  LOC147976 5'  TGTGGCATTTGGTAGGCA    78590      ACTAC TG C
                                TGCCTG    C  G TGCCATA
                                ||||||    |  | |||||||
                                ACGGAT    G  T ACGGTGT
                                   _____ GT T
GAM398  LOC150005 5'  TGTGGTGGTGTCAGGT     84823      TACCTG  TG
                                GCCTGAC    GC  CCATA
                                |||||||    ||  |||||
                                TGGACTG    TG  GGTGT
                                   ______  GT
GAM398  LOC151273 5'  CTGTGGCAGTTCAGTCAG    67016      ACCT
                                CTGACT   GGCTGCCATAG
                                ||||||   ||||||||||||
                                GACTGA   TTGACGGTGTC
                                   C___
GAM398  LOC151429 5'  TGTGGTGACTGTTCAGGT    85362      CT  CT  CT
                                GCCTGA  AC  GG  GCCATA
                                ||||||  ||  ||  ||||||
```

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                                TGGACT  TG  TC  TGGTGT
                                   __  __  AG
GAM398  LOC152805 5'  CTGTGGCGGGGCCAAGTGAGGC 80688     G   ACC    __
                                GCCT ACT   TGGCT  GCCATAG
                                |||| |||   |||||  |||||||
                                CGGA TGA   ACCGG  CGGTGTC
                                  G  ___     GG
GAM398  LOC152845 5'  GCCGGGTAGCAGGCA       60333       A
                                TGCCTG CTACCTGGC
                                |||||| |||||||||
                                ACGGAC GATGGGCCG
                                   _
GAM398  LOC153222 3'  CTATGGCAGTTTTGCAATCAGG 80784       CTACCT
              T                  GCCTGA     GGCTGCCATAG
                                |||||||     ||||||||||
                                TGGACT     TTGACGGTATC
                                   AACGTT
GAM398  LOC153339 5'  CTATGGCAGTTAAAAGTGGT   86006      C__
                                ACTAC   TGGCTGCCATAG
                                |||||   ||||||||||||
                                TGGTG   ATTGACGGTATC
                                  AAA
GAM398  LOC153454 3'  AGTTAGATGGTTAGGT      80830         C
                                GCCTGACTA CTGGCT
                                ||||||||| ||||||
                                TGGATTGGT GATTGA
                                     A
GAM398  LOC155060 3'  TTATGGTGGCCGGCCAGTTTGG 86334    T   AC    TG
                                CC GACT  CTGGC  CCATAG
                                || ||||  |||||  ||||||
                                GG TTGA  GGCCG  GGTATT
                                 T   CC    GT
GAM398  LOC155179 3'  TGTGGCGGTCAGAAGGC     81326      GACTAC
                                GCCT     CTGGCTGCCATA
                                ||||     ||||||||||||
                                CGGA     GACTGGCGGTGT
                                  A_____
GAM398  LOC168966 5'  TGTGGTGGTTGCTCAGACA   87278    C   CTACC   TG
                                TG CTGA    TGGC  CCATA
                                || ||||    ||||  |||||
                                AC GACT    GTTG  GGTGT
                                 A   C____    GT
GAM398  LOC196812 3'  CTGTGGCACCCTGTTTGGGT   89569     TG CT  CT  C
                                GCC  A  AC  GG TGCCATAG
                                |||  |  ||  || ||||||||
                                TGG  T  TG  CC ACGGTGTC
                                  GT __  T_  C
GAM398  LOC197342 3'  CTGTGGTAGCTGGAAGTGGGGC 88000      G   A  T
              A                  TGCCT ACT CC GGCTGCCATAG
                                ||||| ||| || ||||||||||
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                                ACGGG TGA GG TCGATGGTGTC
                                  G   A _
GAM398  LOC199870 3'  TTGTGGTGGTCACTGCTCAGTG 88433    _   CTACC   TG
          TA                     TGC CTGA    TGGC  CCATAG
                                ||| ||||    ||||  ||||||
                                ATG GACT    ACTG  GGTGTT
                                  T   CGTC_   GT
GAM398  LOC201736 5'  TAGCTGGGCTGGTTGGGTA   89053     TG   _  TG
                                TGCC  ACTA CC  GCTG
                                ||||  |||| ||  ||||
                                ATGG  TGGT GG  CGAT
                                  GT    C  GT
GAM398  LOC202934 3'  TGGGCCAGGTGGGCAGGT    90432      A       TG
                                GCCTG CTACCTGGC  CCA
                                ||||| |||||||||  |||
                                TGGAC GGTGGACCG  GGT
                                  G       __
GAM398  LOC203365 3'  CTGTGGTAGTTTTTTTGAGCA  89348    CT  CTACCT
                                TGC  GA     GGCTGCCATAG
                                |||  ||     ||||||||||||
                                ACG  TT     TTGATGGTGTC
                                 AG  TTT___
GAM398  LOC205418 3'  CTGTGGCGGCTCCCATTCAG   90684     CTACCT
                                CTGA     GGCTGCCATAG
                                ||||     ||||||||||||
                                GACT     TCGGCGGTGTC
                                  TACCC_
GAM398  LOC206480 5'  CTGTGGCAGCCTCAGTTGGC   90718    T    ACCT
                                GCC GACT    GGCTGCCATAG
                                ||| ||||    ||||||||||||
                                CGG TTGA    CCGACGGTGTC
                                 _    CT__
GAM398  LOC220534 3'  TATGGTAGTTCCCTTAGG    90722      CTACCT
                                CCTGA     GGCTGCCATA
                                |||||     ||||||||||
                                GGATT     TTGATGGTAT
                                  CCC___
GAM398  LOC220538 3'  TATGGTAGTTCCCTTAGG    90734      CTACCT
                                CCTGA     GGCTGCCATA
                                |||||     ||||||||||
                                GGATT     TTGATGGTAT
                                  CCC___
GAM398  LOC220662 3'  TCAGGTAGTTGAGGCA      91183      _
                                TGCCT GACTACCTGG
                                ||||| ||||||||||
                                ACGGA TTGATGGACT
                                  G
GAM398  LOC220827 3'  CTGCATTCCCAGGAGGTTAGGC 91242         A    C__   CATAG
          A                      TGCCTGACT CCTGG   TGC
                                |||||||| |||||   |||
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                                ACGGATTGG GGACC   ACG
                                     A    CTT   TC
GAM398  LOC221143 3'  CTGTGGTAGCTGAAATTTGGG  93567    TG CTACCT
                                CC  A     GGCTGCCATAG
                                ||  |     ||||||||||
                                GG  T     TCGATGGTGTC
                                 GT TAAAG_
GAM398  LOC253216 5'  GCCCTGCCAGGTGGTGGGCA   94960      G        T__
                                TGCCT ACTACCTGGC   GC
                                ||||| ||||||||||   ||
                                ACGGG TGGTGGACCG   CG
                                   _         TCC
GAM398  LOC254528 3'  TTATGGTGGAGGTGGTCTGGGT 95056      _       GG TG
                                GCCT GACTACCT  C  CCATAG
                                |||| ||||||||  |  ||||||
                                TGGG CTGGTGGA  G  GGTATT
                                  T       __ GT
GAM398  LOC255426 5'  TGGGAGCCGGGCGGTCGGGC   97161        TA      G
                                GCCTGAC  CCTGGCT CCA
                                |||||||  ||||||| |||
                                CGGGCTG  GGGCCGA GGT
                                    GC      G
GAM398  LOC256041 5'  GCTGTCGGGTATCAGGCA    97606        C       T
                                TGCCTGA TACCTGGC GC
                                ||||||| |||||||| ||
                                ACGGACT ATGGGCTG CG
                                   _       T
GAM398  LOC257054 5'  CTGTGTGCATGCAGCTGGTCGG 95660          C   G _   _
          GC                      GCCTGACTA CTG C TGC CATAG
                                |||||||||| ||| | ||| |||||
                                CGGGCTGGT GAC G ACG GTGTC
                                     C   _ T   T
GAM398  LOC257286 3'  TATGGTAGTTCCCTTAGG    94556       CTACCT
                                CCTGA     GGCTGCCATA
                                |||||     ||||||||||
                                GGATT     TTGATGGTAT
                                   CCC___
GAM398  LOC257451 3'  TATGGCAGTTTCTTGGT     95561      CCT
                                ACTA   GGCTGCCATA
                                ||||   ||||||||||
                                TGGT   TTGACGGTAT
                                  TCT
GAM398  LOC63923  3'  GTGGCAGCTTGGGGC       67123     TGACTA  T
                                GCC     CC GGCTGCCAT
                                |||     || |||||||||
                                CGG     GG TCGACGGTG
                                  _______ T
GAM398  LOC91301  5'  TATGGTGGCCGGGGAGGC    65547      GACTA     TG
                                GCCT    CCTGGC  CCATA
                                ||||    ||||||  |||||
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                                CGGA    GGGCCG  GGTAT
                                  G____     GT
GAM398  LOC91516  5'  TTGTGGTGGCCCTGCTCATGT  66306    C   C  CCT   TG
                                GC TGA TA   GGC  CCATAG
                                || ||| ||   |||  ||||||
                                TG ACT GT   CCG  GGTGTT
                                 T  C  C__   GT
GAM398  LOC91759  5'  TGGCACCTAGGAGTCAGGCA  67091         A    C
                                TGCCTGACT CCTGG TGCCA
                                ||||||||| ||||| |||||
                                ACGGACTGA GGATC ACGGT
                                      _    C
GAM398  LOC91963  5'  AGACTAGGCTAGTTGGGT    67688     TG   _    _
                                GCC  ACTA CCTGG CT
                                |||  |||| ||||| ||
                                TGG  TGAT GGATC GA
                                  GT   C    A
GAM398  LOC93622  3'  TGTGCACAGGTGGTTGGGT   56932     TG      GC  _
                                GCC  ACTACCTG  TGC CA
                                |||  ||||||||  ||| ||
                                TGG  TGGTGGAC  ACG GT
                                  GT       __   T
GAM399  ADH4      3'  TAAAAAGATTTTTACTGGA   5408         CGT
                                TCCAGTGG   TCTTTTTA
                                ||||||||   ||||||||
                                AGGTCATT   AGAAAAAT
                                     TTT
GAM399  B4GALT2   3'  AGTAAAAAACGTGAATGGA   47580     GTG    CT
                                TCCA   GCGTT  TTTTACT
                                ||||   |||||  |||||||
                                AGGT   TGCAA  AAAATGA
                                  AAG    __
GAM399  CTBP1     3'  AAAAAGAAAACCTGAAGGAG   67941     AGT_  CG
                                CTCC    GG  TTCTTTTT
                                ||||    ||  ||||||||
                                GAGG    CC  AAGAAAAA
                                  AAGT  AA
GAM399  ENPP3     3'  TAAAAAGAACAGCAGAGAG    17226     CAGTG  _
                                CTC     GC GTTCTTTTTA
                                |||     || ||||||||||
                                GAG     CG CAAGAAAAAT
                                  AGA__  A
GAM399  F8        3'  TAAAAAAATAAGTCAGGAGGA  3732        AG    GTTC_
                                TCCTCC  TGGC    TTTTTA
                                ||||||  ||||    ||||||
                                AGGAGG  ACTG    AAAAAT
                                    __    AATAA
GAM399  GK        3'  AGCAAAAAGAATGCTAT     3911             A
                                GTGGCGTTCTTTTT CT
                                |||||||||||||| ||
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                                TATCGTAAGAAAAA GA
                                        C
GAM399  ID4      3'  GAAAAAAAGCCACCGGAGGA  7755        A     GTTC
                                TCCTCC GTGGC    TTTTT
                                ||||||| |||||    |||||
                                AGGAGG CACCG    AAAAG
                                   C     AAA_
GAM399  PITX1    3'  GAAAAAGACGTCGGAG      10599      AGT    T     A
                                CTCC   GGCGT CTTTTT C
                                ||||   ||||| |||||| |
                                GAGG   CTGCA GAAAAA G
                                  ____    _     C
GAM399  TDG      3'  GAAAAAGATGCTGGAG      12191         GCGT      A
                                CTCCAGTG    TCTTTTT C
                                ||||||||    ||||||| |
                                GAGGTCGT    AGAAAAA G
                                    _____       C
GAM399  XRCC2    3'  AGCAAAAAGAACAAAGCTGGAG 18318         GGC        A
              G                  CCTCCAGT   GTTCTTTTT CT
                                ||||||||   ||||||||| ||
                                GGAGGTCG   CAAGAAAAA GA
                                     AAA        C
GAM399  DKFZP727M111 5'  AAAAGGAAAAGCCCTGAAG    31401    C   T   G_
                                CT CAG GGC  TTCTTTTT
                                || ||| |||  ||||||||
                                GA GTC CCG  AAGGAAAA
                                 A   _   AA
GAM399  ELKS     3'  AGTGGTCAACGCCCTGGAAGA  30501    C     T     CTTT
                                TC TCCAG GGCGTT    TTACT
                                || ||||| ||||||    |||||
                                AG AGGTC CCGCAA    GGTGA
                                 A     _      CT__
GAM399  FLJ10648 3'  AGCAAAAAGAACAAAGTCCTGG 36378          T   ___        A
              AGGA                    TCCTCCAG GGC   GTTCTTTTT CT
                                ||||||||| |||   ||||||||| ||
                                AGGAGGTC CTG   CAAGAAAAA GA
                                     _   AAA        C
GAM399  FLJ20151 3'  AAAGACCCTGGAGGA       34648         T  CGT
                                TCCTCCAG GG   TCTTT
                                |||||||| ||   |||||
                                AGGAGGTC CC   AGAAA
                                     _ ____
GAM399  FLJ20435 3'  TAAAAAGAGCCATCTGGAGGA  35162         _    GT
                                TCCTCCAG TGGC  TCTTTTTA
                                |||||||| ||||  ||||||||
                                AGGAGGTC ACCG  AGAAAAAT
                                     T   __
GAM399  MDS024   3'  AAAAAGAATTGCCAAGGA    41522     AG    _
                                TCC  TGGCG TTCTTTTT
                                |||  ||||| ||||||||
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                                AGG  ACCGT AAGAAAAA
                                  A_    T
GAM399  ShrmL    5'  AGAGCGCCACTGAAGGA     40463      C
                                TCCT CAGTGGCGTTCT
                                |||| ||||||||||||
                                AGGA GTCACCGCGAGA
                                  A
GAM399  SIAT8C   5'  TAAAAAAGCCCCACAGAGGA   31883      CA   C  C
                                TCCTC  GTGG GTT TTTTTA
                                |||||  |||| ||| ||||||
                                AGGAG  CACC CGA AAAAAT
                                  A_   C  _
GAM399  VEST1    5'  AAAAAGATGCACTGGGGA    53678     T    G  T
                                TCC CCAGTG CGT CTTTTT
                                ||| |||||| ||| ||||||
                                AGG GGTCAC GTA GAAAAA
                                  _    _  _
GAM399  ZFD25    5'  AAAAAGAGCCCTGGA       32573      T  GT
                                TCCAG GGC  TCTTTTT
                                ||||| |||  |||||||
                                AGGTC CCG  AGAAAAA
                                  _  __
GAM399  LOC124626 3'  AGTAAGACCAAACCACTGGA  74313        CGTTCT
                                TCCAGTGG     TTTTACT
                                ||||||||     |||||||
                                AGGTCACC     AGAATGA
                                     AAACC_
GAM399  LOC144577 3'  TAAAAAGAAGCCACAAAGAG  76902     CA_    G
                                CTC   GTGGC TTCTTTTTA
                                |||   ||||| |||||||||
                                GAG   CACCG AAGAAAAAT
                                  AAA    _
GAM399  LOC145837 5'  AGCAAAAAGAACCAAAGAGGA 83542      CAG  CG      A
                                TCCTC   TGG  TTCTTTTT CT
                                |||||   |||  |||||||| ||
                                AGGAG   ACC  AAGAAAAA GA
                                  AA_  __       C
GAM399  LOC151194 3'  TAAAAAAACTGGGGA      59215     T    GGCGTTC
                                TCC CCAGT      TTTTTA
                                ||| |||||      ||||||
                                AGG GGTCA      AAAAAT
                                  _    A_____
GAM399  LOC154789 5'  AGTAAAATCTCAGGCCACTAGA 81131     C     GTTCT_
          G                      CTC AGTGGC     TTTTACT
                                ||| ||||||     |||||||
                                GAG TCACCG     AAAATGA
                                  A     GACTCT
GAM399  LOC197322 3'  AAAGACTCCACTGGAGGA    89736          C  T
                                TCCTCCAGTGG GT CTTT
                                |||||||||| || ||||
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                                AGGAGGTCACC CA GAAA
                                      T  _
GAM399  LOC221596 3'  TAAAAACCTCACACTGGAGAGA 91980    _       GCGTTC
                                TC CTCCAGTG     TTTTTA
                                || ||||||||     ||||||
                                AG GAGGTCAC     AAAAAT
                                 A       ACTCC_
GAM399  LOC91796  3'  AGCAAAAAGAACAAGGCTGGA  67208       GGC       A
                                TCCAGT   GTTCTTTTT CT
                                ||||||   ||||||||| ||
                                AGGTCG   CAAGAAAAA GA
                                   GAA       C
GAM399  LOC92539  5'  TAAAAAGTGTCACTG       69638        TT
                                CAGTGGCG  CTTTTTA
                                ||||||||  |||||||
                                GTCACTGT  GAAAAAT

                                  __
GAM400  ARHGEF6   3'  CAAACTTGAAGCCAGGC     68197       ACCA
                                GCCTGG   CAAGTTTG
                                ||||||   ||||||||
                                CGGACC   GTTCAAAC
                                   GAA_
GAM400  CNTN2     3'  GTCACAACCCAGGTGA      17411        ACCACAA  _
                                TCGCCTGG      GTT TGAC
                                ||||||||      ||| ||||
                                AGTGGACC      CAA ACTG
                                     _______  C
GAM400  CORO2A    3'  AAACTGTGGTCCAGAGA     12642    GC       A
                                TC  CTGGACCACA GTTT
                                ||  ||||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_       _
GAM400  CORO2A    3'  AAACTGTGGTCCAGAGA     53398    GC       A
                                TC  CTGGACCACA GTTT
                                ||  ||||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_       _
GAM400  GRLF1     3'  AGGTCAGAAAGTGGCCCAGG   78551      A   AAG
                                CCTGG CCAC   TTTGACCT
                                ||||| ||||   ||||||||
                                GGACC GGTG   AGACTGGA
                                   C    AA_
GAM400  LAPTM5    3'  AGGCTTGTGGTCAAGC      22199    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCGGA
                                 AA_
GAM400  POU2AF1   3'  AGATTTACAGTCCAGGC     20647        CAC
                                GCCTGGAC   AAGTTT
                                ||||||||   ||||||
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                                CGGACCTG   TTTAGA
                                     ACA
GAM400  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  54574        C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM400  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  6355         C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM400  TRIM34   5'  AGGTCAAGTTGAGCCCAG    55224      ACCA   G
                                CTGG    CAA TTTGACCT
                                ||||    ||| ||||||||
                                GACC    GTT GAACTGGA
                                  CGA_   _
GAM400  TRIM9    5'  AGGCCAGGCAAGTCCAGGC   30749        CACAA    A
                                GCCTGGAC    GTTTG CCT
                                ||||||||    ||||| |||
                                CGGACCTG    CGGAC GGA
                                     AA___    C
GAM400  ABLIM    5'  GATATGTAACCCAGGCGG    22030        ACC   A
                                TCGCCTGG   ACA GTT
                                ||||||||   ||| |||
                                GGCGGACC   TGT TAG
                                     CAA   A
GAM400  AMOT     3'  AGGCATCTTCATGGTCCAGGGA 55716    G       C_   TT  A
                                TC CCTGGACCA  AAG  TG CCT
                                || |||||||||  |||  || |||
                                AG GGACCTGGT  TTC  AC GGA
                                  _       AC   T_ _
GAM400  DKFZp434D177 5'  TTAGACCCAGGCGA       50056        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                              _______
GAM400  DKFZp434D177 5'  TTAGACCCAGGCGA       79443        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                              _______
GAM400  FLJ23420  3'  CAAGTGGGTCCAGGC       46845         A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                           _ __
GAM400  HSA249128 5'  GGCGCGGTCCAGGCGG      34152          ACAA
                                TCGCCTGGACC    GTT
                                ||||||||||    |||
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                                GGCGGACCTGG   CGG
                                      CG__
GAM400  MGC15668  5'  AGACCCGGTGGTCCAGACG   51277    C       AA_
                                CG CTGGACCAC   GTTT
                                || |||||||||  ||||
                                GC GACCTGGTG   CAGA
                                 A       GCC
GAM400  MGC22014  3'  AGGTCCCGAGTGTAACCCAGGT 64486        ACC   AGTTT
           GA                    TCGCCTGG   ACA    GACCT
                                |||||||||  |||    |||||
                                AGTGGACC   TGT    CTGGA
                                     CAA   GAGCC
GAM400  SDCCAG10  5'  AGAGTTGTGGTCCAAAGA    19641    GCC        G
                                TC   TGGACCACAA TTT
                                ||   |||||||||| |||
                                AG   ACCTGGTGTT AGA
                                 AA_        G
GAM400  LOC115442 3'  AGGTCAGGGATGGTCCAG    72676        CAAG
                                CTGGACCA    TTTGACCT
                                ||||||||    ||||||||
                                GACCTGGT    GGACTGGA
                                     AG__
GAM400  LOC129011 5'  AGACCTGCGGTCCAGGC     74862         A  A
                                GCCTGGACC CA GTTT
                                ||||||||| || ||||
                                CGGACCTGG GT CAGA
                                      C  C
GAM400  LOC130536 5'  GCAAAGTCCAGGCG        75746         CACAAG    A
                                CGCCTGGAC     TTTG C
                                |||||||||     |||| |
                                GCGGACCTG     AAAC G
                                      _______   C
GAM400  LOC149108 3'  AGACTTCACTGTGGTCCA    84357         _____
                                TGGACCACA    AGTTT
                                |||||||||    |||||
                                ACCTGGTGT    TCAGA
                                      CACT
GAM400  LOC221688 5'  AGACTCGGGCCCAGACGA    93674     C    A  ACA
                                TCG CTGG CC   AGTTT
                                ||| |||| ||   |||||
                                AGC GACC GG   TCAGA
                                  A   C  GC_
GAM400  LOC256228 5'  AGACTTGTGGTCAAAGC     96233     CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCAGA
                                 AAA
GAM400  LOC257441 5'  TTAGACCCAGGCGA        95566         ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
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                                AGCGGACC      CAGATT
                                        _______
GAM400  LOC91960  3'  AGGTGCCTCTCGTGGTCCAAGC 67657    C      A  TTTG
                                GC TGGACCAC AG    ACCT
                                || |||||||| ||    ||||
                                CG ACCTGGTG TC    TGGA
                                 A       C  TCCG
GAM400  LOC92840  3'  GTCCCTCGGGTCCAGGC     56435         ACA  TTT
                                GCCTGGACC   AG   GAC
                                |||||||||   ||   |||
                                CGGACCTGG   TC   CTG
                                      GC_  C__
GAM401  ADH1B     3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM401  AHR       3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM401  FDFT1     3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM401  JTB       3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM401  KLF4      3'  TCCCAGACAGTGGATATG     14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM401  PHYH      3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM401  PKD2      3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                       T__    _
GAM401  WRN       3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
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                                AAAGT AAAGTGACGGG
                                   A
GAM401  ZNF216   3' ATCTGCACAGCAAAGTGAAA  20017        CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM401  CG012    5' CTCACTCTGAAAGTGAA    83218        CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM401  EIF2C2   3' ATCTTCTGAGAGTGAAAG   71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM401  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||         |||||||||
                                GTAAAG         CAGACTCTA
                                   AAACATTT_
GAM401  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM401  KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM401  KLHL6    3' ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM401  NIR3     3' GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM401  PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM401  PP35     3' ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
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                                AAAGT  CAGACTCTA
                                  __
GAM401  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148          TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM401  SEP15     3'  TCCTACAGTAAGAGTGAAA   14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM401  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM401  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM401  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM401  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226     A      GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _      ATTT
GAM401  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM402  ALK       3'  CAATGGCTCCTTCAC       73381        ACTC
                                GTGAAGGA   CTGTTG
                                ||||||||   ||||||
                                CACTTCCT   GGTAAC
                                     C___
GAM402  ARAF1     5'  CAACAGGAGGGCCTGAGC    63936    GA   AA
                                GT  AGG  CTCCTGTTG
                                ||  |||  |||||||||
                                CG  TCC  GAGGACAAC
                                 AG   GG
GAM402  KIF3C     3'  ACGGAAGTCCCTCCACTGG   9597       A   A   C
                                TCAGTG AGG ACT CTGT
                                |||||| ||| ||| ||||
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                                GGTCAC TCC TGA GGCA
                                   C   C   A
GAM402  MAP2     3'  CAACAGGAAGACACTGG     48995       AAGGAAC
                                TCAGTG      TCCTGTTG
                                ||||||      ||||||||
                                GGTCAC      AGGACAAC
                                   AGA____
GAM402  PPP2R5A  3'  CAACCTGTCCTTCACCTAGT   20706     CA       ACTCCT
                                ACT  GTGAAGGA     GTTG
                                |||  ||||||||     ||||
                                TGA  CACTTCCT     CAAC
                                  TC       GTC___
GAM402  SHANK2   3'  ACAGGCTCCTGTCACTGAG    24582         _    ACT
                                CTCAGTGA AGGA   CCTGT
                                |||||||| ||||   |||||
                                GAGTCACT TCCT   GGACA
                                     G   C__
GAM402  SYNGR1   3'  AGGTGGGCTCTTCACTGAG    16309          AA  _
                                CTCAGTGAAGG  CT CCT
                                ||||||||||  || |||
                                GAGTCACTTCT  GG GGA
                                      CG  T
GAM402  TDE1     3'  CAAAGGTCTCCTTCACCGA    22341    A       ACT   G
                                TC GTGAAGGA   CCT TTG
                                || ||||||||   ||| |||
                                AG CACTTCCT   GGA AAC
                                 C       CT_  _
GAM402  TGFB3    3'  CAACAAACCTCACTGAG      12258         A  AACTCC
                                CTCAGTGA GG     TGTTG
                                |||||||| ||     |||||
                                GAGTCACT CC     ACAAC
                                    _  AA____
GAM402  TRAF5    3'  CAACAGGAATATACTGA      16074        AAGGAAC
                                TCAGTG      TCCTGTTG
                                ||||||      ||||||||
                                AGTCAT      AGGACAAC
                                   ATA____
GAM402  ZNF24    3'  CAACAGGAATTACAAAGT     22726     CA   AGGAAC
                                ACT  GTGA     TCCTGTTG
                                |||  ||||     ||||||||
                                TGA  CATT     AGGACAAC
                                  AA   A_____
GAM402  ADAMTSL1 3'  ACAAAAGACTCTTCACTGAG   57685          AA  CC
                                CTCAGTGAAGG  CT  TGT
                                ||||||||||  ||  |||
                                GAGTCACTTCT  GA  ACA
                                      CA  AA
GAM402  C1QTNF7  3'  GCACCTTGTTCTTCACTGA    49160          ACTCC
                                TCAGTGAAGGA    TGT
                                ||||||||||     |||
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                                AGTCACTTCTT    ACG
                                      GTTCC
GAM402  DGS-A    3'  GCAACAGGGAGATTCC     84899     _   _
                                GGAA CTCC TGTTGC
                                |||| |||| ||||||
                                CCTT GAGG ACAACG
                                  A   G
GAM402  FLJ10607 3'  CAACAGAAATCCTTCAC    77106        ACTC
                                GTGAAGGA   CTGTTG
                                ||||||||   ||||||
                                CACTTCCT   GACAAC
                                     AAA_
GAM402  FLJ13340 3'  GCACTGGATTCTTTCACTGAG  54104          C   T  T
                                CTCAGTGAAGGAA TCC GT GC
                                |||||||||||| ||| || ||
                                GAGTCACTTTCTT AGG CA CG
                                       _   T  _
GAM402  FLJ14721 3'  GCAGGAGTCCCCTCACGAAGT  51583    CA   A  A
                                ACT  GTGA GG ACTCCTGT
                                |||  |||| || ||||||||
                                TGA  CACT CC TGAGGACG
                                  AG   C  C
GAM402  FLJ25359 5'  GGAGTTCCTCCACTCAG    58075    C   A
                                CT AGTG AGGAACTCC
                                || |||| |||||||||
                                GA TCAC TCCTTGAGG
                                 C   C
GAM402  FLJ31547 3'  GCAACAAGATTTCTTCA    58831        C  C
                                TGAAGGAA TC TGTTGC
                                |||||||| || ||||||
                                ACTTCTTT AG ACAACG
                                     _ A
GAM402  FYCO1    3'  GCAACAAGAACCACCATTCACT 44495         _ AAC_  C
           GAGT                    ACTCAGTGAA GG   TC TGTTGC
                                |||||||||| ||   || ||||||
                                TGAGTCACTT CC   AG ACAACG
                                      A  ACCA  A
GAM402  KIAA1323 5'  GCAACAGGAATCCTGGTGGA  63043   AGTGA   AC
                                TC    AGGA  TCCTGTTGC
                                ||    ||||  |||||||||
                                AG    TCCT  AGGACAACG
                                 GTGG_   A_
GAM402  MGC12538 3'  CAACAAAAGCTTTGCTGG   51242    TG   GAA  CC
                                TCAG  AAG   CT  TGTTG
                                ||||  |||   ||  |||||
                                GGTC  TTC   GA  ACAAC
                                  GT   ___  AA
GAM402  MGC29761 5'  CAACAGGACGCCGCCGAGT   58326     A  GAA  AAC
                                ACTC GT   GG   TCCTGTTG
                                |||| ||   ||   ||||||||
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                                TGAG CG   CC   AGGACAAC
                                  C ___  GC_
GAM402  SCOP     3'  CAACTCACCCTCACTTCACTGA 91778         _  ACTCCT
                                TCAGTGAAG GA      GTTG
                                |||||||||  ||     ||||
                                AGTCACTTC CT      CAAC
                                     A  CCCACT
GAM402  SNAP29   3'  CAACAGGTCTTCCACTGG    16538       A    ACT
                                TCAGTG AGGA   CCTGTTG
                                ||||||  ||||   |||||||
                                GGTCAC TTCT   GGACAAC
                                   C   ___
GAM402  TBDN100  3'  GCACTGGATTCTTTCACTGAG  46953           C   T  T
                                CTCAGTGAAGGAA TCC GT GC
                                ||||||||||||| ||| || ||
                                GAGTCACTTTCTT AGG CA CG
                                       _   T  _
GAM402  UBE4B    3'  CAGCATCCCTTCATGA      20163     G     AACTCC
                                TCA TGAAGG     TGTTG
                                |||  ||||||     |||||
                                AGT ACTTCC     ACGAC
                                  _     CT_____
GAM402  LOC145438 3'  GCAAAAACGCCCTCACTGAG   83338        A  AACTCCTG
                                CTCAGTGA GG       TTGC
                                ||||||||  ||       ||||
                                GAGTCACT CC       AACG
                                     C  GCAAA___
GAM402  LOC148764 5'  CAACAACCTGTCACTGAGT    78982         _  AACTCC
                                ACTCAGTGA AGG     TGTTG
                                |||||||||  |||     |||||
                                TGAGTCACT TCC     ACAAC
                                     G   A_____
GAM402  LOC151623 5'  ACATGGACCCCCTCACTGG    85454        A  AAC  _
                                TCAGTGA GG   TCC TGT
                                |||||||  ||   ||| |||
                                GGTCACT CC   AGG ACA
                                     C  CC_   T
GAM402  LOC158696 3'  GGAGCTCCCCCACAGAGT    81973      A   AA   A
                                ACTC GTG  GGA CTCC
                                ||||  |||  |||  ||||
                                TGAG CAC  CCT GAGG
                                  A   CC   C
GAM402  LOC199837 5'  CAACAAGAAAATTGACTTCACT 88406           GAAC___  C
           GAGT                    ACTCAGTGAAG       TC TGTTG
                                |||||||||||       || |||||
                                TGAGTCACTTC       AG ACAAC
                                      AGTTAAA  A
GAM402  LOC200261 3'  AGTTGCTCCACTGAGT      88652         A  G
                                ACTCAGTG AG AACT
                                ||||||||  || ||||
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                                TGAGTCAC TC TTGA
                                     C  G
GAM402  LOC219735 3'  GCAACAAGAATTCCTTTA    93109        C  C
                                TGAAGGAA TC TGTTGC
                                |||||||| || ||||||
                                ATTTCCTT AG ACAACG
                                     A  A
GAM402  LOC220370 3'  GCAAGTCACTCACCTCACTGAG 92827        A  AACTCCTG
                                CTCAGTGA GG       TTGC
                                |||||||| ||       ||||
                                GAGTCACT CC       AACG
                                     _ ACTCACTG
GAM402  LOC220686 3'  GCAACAGGAGCCGGACCTACA  92921    A   AA___
                                TG AGG    CTCCTGTTGC
                                || |||    ||||||||||
                                AC TCC    GAGGACAACG
                                 A  AGGCC
GAM402  LOC245757 3'  CAACAAGGGAGCTCACTGAGT  90775        AGGAA    __
                                ACTCAGTGA    CTCCT  GTTG
                                |||||||||    |||||  ||||
                                TGAGTCACT    GAGGG  CAAC
                                     C____    AA
GAM402  LOC51651  3'  CAACAAAAGCTGAATTTCTTCA 32182        _____  CC
          C                      GTGAAGGAA    CT  TGTTG
                                |||||||||    ||  |||||
                                CACTTCTTT    GA  ACAAC
                                     AAGTC  AA
GAM402  LOC91137  3'  GGTTCCTTCACTGAGT     57066
                                ACTCAGTGAAGGAACT
                                ||||||||||||||||
                                TGAGTCACTTCCTTGG

GAM403  ARCN1    3'  AGACTGCACTCTCTGTCA    7970         CA_
                                TGACAGAGA   CAGTTT
                                |||||||||   ||||||
                                ACTGTCTCT   GTCAGA
                                     CAC
GAM403  CBFA2T2  3'  GAGCAAAACTCTGTCT     17466      C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                   C
GAM403  CTLA4    3'  CAGAGCTGGGATGTTTCTGTCA 17807         CAGTTTT
                                TGACAGAGACA      GCTCTG
                                ||||||||||||     ||||||
                                ACTGTCTTTGT      CGAGAC
                                      AGGGT__
GAM403  ITK      3'  CAGAACAGGAGTGATGTCTCTG 18674        _  G    C
                                CAGAGACA CA TTTTG TCTG
                                |||||||| || ||||| ||||
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                                GTCTCTGT GT AGGAC AGAC
                                     A G    A
GAM403  LAMP2    3' GGTGAAACCCCATCTCTATCA 25716    C    CACA   TG
                                TGA AGAGA   GTTT  CT
                                ||| |||||   ||||  ||
                                ACT TCTCT   CAAA  GG
                                  A    ACCC   GT
GAM403  MRPS12   3' CAAAGGGTGCCCCTCTGTCA  40865       A__  AG
                                TGACAGAG  CAC  TTTTG
                                ||||||||  |||  |||||
                                ACTGTCTC  GTG  GAAAC
                                     CCC  G_
GAM403  MRPS12   3' CAAAGGGTGCCCCTCTGTCA  52960       A__  AG
                                TGACAGAG  CAC  TTTTG
                                ||||||||  |||  |||||
                                ACTGTCTC  GTG  GAAAC
                                     CCC  G_
GAM403  MRPS12   3' CAAAGGGTGCCCCTCTGTCA  52963       A__  AG
                                TGACAGAG  CAC  TTTTG
                                ||||||||  |||  |||||
                                ACTGTCTC  GTG  GAAAC
                                     CCC  G_
GAM403  PDGFRB   5' CAGAGCCTGGAACTGTG    65969        __
                                CACAGTTTT  GCTCTG
                                |||||||||  ||||||
                                GTGTCAAGG  CGAGAC
                                     TC
GAM403  PTPRA    3' AGAGCGGTATCTCTG      55087      C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM403  PTPRA    3' AGAGCGGTATCTCTG      55079      C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM403  PTPRA    3' AGAGCGGTATCTCTG      11088      C  AGTTT
                                CAGAGA AC    TGCTCT
                                |||||| ||    ||||||
                                GTCTCT TG    GCGAGA
                                   A _____
GAM403  RAD51L3  3' CAAAACTCAGGTATGTCTCTGT 56065       C_____
                                ACAGAGACA     AGTTTTG
                                |||||||||     |||||||
                                TGTCTCTGT     TCAAAAC
                                     ATGGAC
GAM403  TBL2     3' CAGAACTGTGTTCCATCA    24924    CA  A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
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                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM403  TBL2     3'  CAGAACTGTGTTCCATCA    52178     CA   A
                                TGA  GAG CACAGTTTTG
                                |||  ||| ||||||||||
                                ACT  CTT GTGTCAAGAC
                                  AC  _
GAM403  AGTRL2   5'  CAGAGCAAGAACTGTTC     17691    C      _
                                GA ACAGTTTT GCTCTG
                                || |||||||| ||||||
                                CT TGTCAAGA CGAGAC
                                 _       A
GAM403  CABP5    3'  AGAGCGGTATCTTTGCCA    39079    A     C  AGTTT
                                TG CAGAGA AC     TGCTCT
                                || |||||| ||     ||||||
                                AC GTTTCT TG     GCGAGA
                                 C     A  _____
GAM403  CUL4A    5'  AGAGCAGCACCTCCATCA    13149     CA   ACACA  T
                                TGA  GAG    GT TTGCTCT
                                |||  |||    || |||||||
                                ACT  CTC    CA GACGAGA
                                  AC  _____  C
GAM403  DKFZp761O17121 3'  CAGACAGCCCCTGTGTCTCTGT 50136            TT_  C
           C                     GACAGAGACACAG   TTG TCTG
                                ||||||||||||   ||| ||||
                                CTGTCTCTGTGTC   GAC AGAC
                                       CCC  _
GAM403  FLJ10375 3'  CAGAGGCCTGTGTCTGTGCCA  36073    A  G      TTTTG
                                TG CA AGACACAG    CTCTG
                                || || ||||||||    |||||
                                AC GT TCTGTGTC    GAGAC
                                 C  G      CG___
GAM403  FLJ10738 5'  CAAAGCCAGCCCTCTGTCA   36527        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
                                ACTGTCTC    CGAAAC
                                     CCGAC
GAM403  FLJ10803 3'  CAAAACAAAACTCTGTCA    36660        ACACA
                                TGACAGAG    GTTTTG
                                ||||||||    ||||||
                                ACTGTCTC    CAAAAC
                                     AAAA_
GAM403  FLJ10842 3'  AAAGTGTGCTCTGTCA      36723        A   G
                                TGACAGAG CACA TTT
                                |||||||| |||| |||
                                ACTGTCTC GTGT AAA
                                     _   G
GAM403  FLJ13153 3'  CAGAGCCCAGCATCCATCTCTG 45555         CACA_  TT
           TCA                    TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
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                                ACTGTCTCT    CGA  CGAGAC
                                     ACCTA   CC
GAM403  FLJ20035  3'  CAAACCTGCCATGTTCTGTCA  34395        A ___   T
                                TGACAGAG CA   CAG TTTG
                                |||||||| ||   ||| ||||
                                ACTGTCTT GT   GTC AAAC
                                     _ ACC   C
GAM403  FLJ22195  5'  CAGAGCAGAGGGAAGTCTCTGC 42800    A      ACAG
          CA                     TG CAGAGAC    TTTTGCTCTG
                                || |||||||    ||||||||||
                                AC GTCTCTG    GAGACGAGAC
                                 C      AAGG
GAM403  FLJ32191  5'  GAACTGCACCTCTGTCA     58411         ACA
                                TGACAGAG   CAGTTT
                                ||||||||   ||||||
                                ACTGTCTC   GTCAAG
                                     CAC
GAM403  KIAA1023  3'  CAAAGCTGTATCTGCTATCA   34255     C _   C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G   A
GAM403  KIAA1586  5'  AGTGTGATGTGTCTCTG     92326          GTT TG T
                                CAGAGACACA   T  C CT
                                ||||||||||   |  | ||
                                GTCTCTGTGT   A  G GA
                                     ___ GT T
GAM403  KIAA1754  3'  GACTAACGTCTCTGTCA     63236          AC_
                                TGACAGAGAC   AGTT
                                ||||||||||   ||||
                                ACTGTCTCTG   TCAG
                                     CAA
GAM403  LANCL2    3'  CAGAGTGCACTGCAGCTCTGTC 37995        ACA    TTT
          A                      TGACAGAG   CAGT   GCTCTG
                                ||||||||   ||||   ||||||
                                ACTGTCTC   GTCA   TGAGAC
                                     GAC    CG_
GAM403  LIG-1     3'  CAGAGCAGGCCTGTCCATGCCA 63893    A  GAGAC    TT
                                TG CA    ACAG  TTGCTCTG
                                || ||    ||||  ||||||||
                                AC GT    TGTC  GACGAGAC
                                 C  ACC__    CG
GAM403  MGC5242   3'  AGAGTACATGTCTCTG      43823         CAGTTT
                                CAGAGACA     TGCTCT
                                ||||||||     ||||||
                                GTCTCTGT     ATGAGA
                                     AC____
GAM403  OSMR      3'  CAGAGCTGGCACCCTGTCA    14345       AGACA
                                TGACAG    CAGTTTTG
                                ||||||    ||||||||
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                                ACTGTC    GTCGAGAC
                                   CCACG
GAM403  RAB21    3'  CAGAACAAAACTGTGGATC   30383    GA       C
                                GA  CACAGTTTTG TCTG
                                ||  |||||||||| ||||
                                CT  GTGTCAAAAC AGAC
                                 AG        A
GAM403  SPTLC2   3'  CAGAGCAAAACTGTGTCTC   16799
                                GAGACACAGTTTTGCTCTG
                                |||||||||||||||||||
                                CTCTGTGTCAAAACGAGAC

GAM403  TGIF2    3'  GAGTCATGCTCTGTCA     41454        A  CAGTTT  _
                                TGACAGAG CA     TG CTC
                                |||||||| ||     || |||
                                ACTGTCTC GT     AC GAG
                                    _ _______  T
GAM403  WBSCR23  5'  GCTGACTGTGTCTCCATCA   46765    CA       TT
                                TGA  GAGACACAGTT  GC
                                |||  ||||||||||  ||
                                ACT  CTCTGTGTCAG  CG
                                  AC         T_
GAM403  LOC115129 3' GGCAAAACCCCGTCTCT     73235       ACA
                                AGAGAC   GTTTTGCT
                                ||||||   ||||||||
                                TCTCTG   CAAAACGG
                                   CCC
GAM403  LOC129198 3' AGCAAGCTGTGCCTC       76117     A       T
                                GAG CACAGTTT GCT
                                ||| |||||||| |||
                                CTC GTGTCGAA CGA
                                  C       _
GAM403  LOC145231 3' GGTGAAACTATGTCTCT     83293       C     TG
                                AGAGACA AGTTT  CT
                                ||||||| |||||  ||
                                TCTCTGT TCAAA  GG
                                    A     GT
GAM403  LOC145483 3' GAGCAAAACTCTGTCT      77243      C
                                AGACA AGTTTTGCTC
                                ||||| ||||||||||
                                TCTGT TCAAAACGAG
                                   C
GAM403  LOC146713 3' GAGCAAAACTCCGTCT      83726      AC
                                AGAC  AGTTTTGCTC
                                ||||  ||||||||||
                                TCTG  TCAAAACGAG
                                  CC
GAM403  LOC149175 3' CAGGGTGAAACCACGTCTCT  79208       ACA    TG
                                AGAGAC   GTTT  CTCTG
                                ||||||   ||||  |||||
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                                TCTCTG  CAAA  GGGAC
                                   CAC   GT
GAM403  LOC150299 3'  CAGAACCTGCATCTTTGTCA  84968        CA  _
                                TGACAGAGA  CAG TTTTG
                                |||||||||  ||| |||||
                                ACTGTTTCT  GTC AAGAC
                                     AC   C
GAM403  LOC153277 3'  TAAAACTGTGCCTGTGCCA   85990    A  G  A
                                TG CA AG CACAGTTTTG
                                || || || ||||||||||
                                AC GT TC GTGTCAAAAT
                                 C  G  C
GAM403  LOC155179 3'  CAAAGCTGTATCTGCTATCA  81312     C  _  C
                                TGA AG AGA ACAGTTTTG
                                ||| || ||| |||||||||
                                ACT TC TCT TGTCGAAAC
                                  A  G  A
GAM403  LOC221074 3'  AAAGTGTGTCTCTTTCA     93177     C        G
                                TGA AGAGACACA TTT
                                ||| ||||||||| |||
                                ACT TCTCTGTGT AAA
                                  T        G
GAM403  LOC221103 5'  AGTTTATGTGTGCTCTGTCA  93244         _    GTTTT
                                TGACAGAG ACACA    GCT
                                |||||||| |||||    |||
                                ACTGTCTC TGTGT    TGA
                                     G    ATT__
GAM403  LOC255988 5'  CAGAGCCCAGCATCCATCTCTG 97608         CACA_  TT
           TCA                    TGACAGAGA    GTT  GCTCTG
                                |||||||||    |||  ||||||
                                ACTGTCTCT    CGA  CGAGAC
                                     ACCTA   CC
GAM404  ACO1     3'  TTGGTCGTGCGCCCAGGGA   9353         AAA   TC
                                TCCCTGGGC   GTAT  CCAA
                                |||||||||   ||||  ||||
                                AGGGACCCG   CGTG  GGTT
                                     ___    CT
GAM404  CD8A     3'  TGGGATACTGTGCCCAG     8336         A    T
                                CTGGGCA AGTAT CCCA
                                ||||||| ||||| ||||
                                GACCCGT TCATA GGGT
                                     G    _
GAM404  COG2     3'  ATTTGGGTCTTCTTTGCCCA  23736         TATT
                                TGGGCAAAG   CCCAAAT
                                |||||||||   |||||||
                                ACCCGTTTC   GGGTTTA
                                     TTCT
GAM404  EPB41L2  3'  TTTGAGAATTTCACAGGGA   7484        GGCAAAGT   C
                                TCCCTG       ATTC CAAA
                                ||||||       |||| ||||
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                                AGGGAC       TAAG GTTT
                                   ACTT____    A
GAM404  GAC1     3'  ATTTGGGAGAGGGATGCCCAGG 20941        AAGTA
                                CCTGGGCA    TTCCCAAAT
                                ||||||||    |||||||||
                                GGACCCGT    GAGGGTTTA
                                   AGGGA
GAM404  HSD17B1  5'  GGGAATCTGCCCAGGGG     4688          AA T
                                TCCCTGGGCA  G ATTCCC
                                ||||||||||  | ||||||
                                GGGGACCCGT  C TAAGGG
                                     __ _
GAM404  HSPA5    3'  AATACTGCCCAAGGA       18078     C     AA
                                TCC TGGGCA  GTATT
                                ||| ||||||  |||||
                                AGG ACCCGT  CATAA
                                  A     __
GAM404  ID3      5'  TGGGGTGCTGCCAGG       79050      G  AA    T
                                CCTGG CA  GTAT CCCA
                                ||||| ||  |||| ||||
                                GGACC GT  CGTG GGGT
                                   _ __   _
GAM404  PCOLN3   3'  TTGGGAGCCCCCAGGGA     10915        CAAA  AT
                                TCCCTGGG   GT  TCCCAA
                                ||||||||   ||  ||||||
                                AGGGACCC   CG  AGGGTT
                                   C___  __
GAM404  PON1     3'  AGTACTCACCCAGGGA      4800         CAA
                                TCCCTGGG   AGTATT
                                ||||||||   ||||||
                                AGGGACCC   TCATGA
                                   AC_
GAM404  PRKCABP  3'  TGGGCTCCTGCCCAGG      24832        A_  TATT
                                CCTGGGCA  AG    CCCA
                                ||||||||  ||    ||||
                                GGACCCGT  TC    GGGT
                                   CC  _____
GAM404  RASA1    5'  ATTTGGGAAGCTGGCTCCAG   42633      _  AA   A
                                CTGG GC  AGT TTCCCAAAT
                                |||| ||  ||| |||||||||
                                GACC CG  TCG AAGGGTTTA
                                  T  G_  _
GAM404  SERPINB13 3'  ATTTGGGAATACAGTAGC    24770    AAA_
                                GC    GTATTCCCAAAT
                                ||    ||||||||||||
                                CG    CATAAGGGTTTA
                                 ATGA
GAM404  SLC25A13  3'  ATTTGGCCCTCTGCCCAG    26502        A  TATTC
                                CTGGGCA AG    CCAAAT
                                ||||||| ||    ||||||
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                                GACCCGT TC    GGTTTA
                                   C  CC___
GAM404  SMP1     3'  GAATATGCTCAGGGA      26700         AAG
                                TCCCTGGGCA   TATTC
                                ||||||||||   |||||
                                AGGGACTCGT   ATAAG
                                      ___
GAM404  ZFP93    5'  TGAGATATCTCCCAGGGA    14889        CAA  TAT  C
                                TCCCTGGG   AG   TC CA
                                ||||||||   ||   || ||
                                AGGGACCC   TC   AG GT
                                   ___  TAT  A
GAM404  ARHGAP8  3'  GAGTCAGCGTTTACCCAGGGG  34697        C  _  __
                                TCCCTGGG AAA GT  ATTC
                                |||||||| ||| ||  ||||
                                GGGGACCC TTT CG  TGAG
                                   A   G  AC
GAM404  C20orf112 3'  GGAGCGCACTGCCCTAGGGA   54644      _    AA TA
                                TCCCT GGGCA  G  TTCC
                                ||||| |||||  |  ||||
                                AGGGA CCCGT  C  GAGG
                                  T    CA GC
GAM404  C20orf36  3'  TTGGGAAAATCCAGGGA     36803        CAAAGTA
                                TCCCTGGG      TTCCCAA
                                ||||||||      |||||||
                                AGGGACCT      AAGGGTT
                                   AA_____
GAM404  C20orf85  3'  GGAGTTCTGCCCAGGGG     74757         AAGT
                                TCCCTGGGCA    ATTCC
                                ||||||||||    |||||
                                GGGGACCCGT    TGAGG
                                   CT__
GAM404  DKFZP564D116 3'  TGGGCACACCCTTTGCCCAG   72214         TATT__
                                CTGGGCAAAG     CCCA
                                ||||||||||     ||||
                                GACCCGTTTC     GGGT
                                   CCACAC
GAM404  DKFZp761J139 5'  TTGGGGGGTTGCCAGGGA    50121       G   AGTAT
                                TCCCTGG CAA    TCCCAA
                                ||||||| |||    ||||||
                                AGGGACC GTT    GGGGTT
                                   _  GG___
GAM404  EPN2     3'  TGCTTTTACCCAGGGA     30331        C_
                                TCCCTGGG  AAAGTA
                                ||||||||  ||||||
                                AGGGACCC  TTTCGT
                                   AT
GAM404  FLJ10898 3'  ATTTAGGAATACTCCTA     59422      CAA       C
                                TGGG   AGTATTCC AAAT
                                ||||   |||||||| ||||
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                                ATCC   TCATAAGG TTTA
                                  ___       A
GAM404  FLJ11608  3'  TGAGAATGAGCCCAGAGG    44652    _     AAAG    C
                                CC CTGGGC    TATTC CA
                                || ||||||    ||||| ||
                                GG GACCCG    GTAAG GT
                                 A     A___     A
GAM404  FLJ12190  3'  TTGGAGCTGCCTAGGGA     46876          AA  ATTC
                                TCCCTGGGCA  GT    CCAA
                                ||||||||||  ||    ||||
                                AGGGATCCGT  CG    GGTT
                                      __  A___
GAM404  FLJ12242  3'  GGAACTGCCCGGGGA       45180          AAGTA
                                TCCCTGGGCA     TTCC
                                ||||||||||     ||||
                                AGGGGCCCGT     AAGG
                                      C____
GAM404  FLJ13187  3'  TTGGAAATACTTTGGC      44843    G       C
                                G CAAAGTATT CCAA
                                | |||||||||| ||||
                                C GTTTCATAA GGTT
                                 G        A
GAM404  FLJ13263  3'  ATTTGGGGTACCCTCACCCCA  47089      CAAA__    T
                                TGGG      GTAT CCCAAAT
                                ||||      |||| |||||||
                                ACCC      CATG GGGTTTA
                                  CACTCC    _
GAM404  FLJ14346  5'  GGGAAGTGCCCAGGGA      46718          AAGTA
                                TCCCTGGGCA     TTCCC
                                ||||||||||     |||||
                                AGGGACCCGT     AAGGG
                                      G____
GAM404  FLJ14642  3'  GGATACCTCAGGGA        51503          CAAA
                                TCCCTGGG    GTATTC
                                ||||||||    ||||||
                                AGGGACTC    CATAGG
                                      ____
GAM404  FLJ22729  5'  ATACTTTGTCCAAAGA      45187    CC
                                TC  TGGGCAAAGTAT
                                ||  ||||||||||||
                                AG  ACCTGTTTCATA
                                 AA
GAM404  FLJ30058  3'  ATTTGTGGTAAACACCTTTCCC 58637        C    TATT___  _
           AGGGA                    CCCTGGG AAAG       CC CAAAT
                                ||||||| ||||      || |||||
                                GGGACCC TTTC      GG GTTTA
                                    _   CACAAAT  T
GAM404  FSBP     3'  TTTGGGAATATCCT       21591      CAAA
                                GGG    GTATTCCCAAA
                                |||    ||||||||||
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                                TCC   TATAAGGGTTT
                                      ____
GAM404  GAB3     3'  GGGAACACTTTGCCCA      54631          A
                                TGGGCAAAGT TTCCC
                                |||||||||| |||||
                                ACCCGTTTCA AAGGG
                                      C
GAM404  HZFW1    3'  TGGGAATACTTCAG       47464     GCAA
                                CTGG   AGTATTCCCA
                                ||||   ||||||||||
                                GACT   TCATAAGGGT
                                      ____
GAM404  KIAA0141 3'  ATTTGGGAAACATGTGCCAG   28729     G  AA_  A
                                CTGG CA   GT TTCCCAAAT
                                |||| ||   || |||||||||
                                GACC GT   CA AAGGGTTTA
                                  _  GTA  _
GAM404  KIAA0296 5'  ATTTGGGAAGCTTGTGCACAGG 28108       G  _   A
           GA                     TCCCTG GCA AAGT TTCCCAAAT
                                |||||| ||| |||| |||||||||
                                AGGGAC CGT TTCG AAGGGTTTA
                                   A  G   _
GAM404  KIAA0792 3'  TGGGCCTTCTCACTCAGGGA   28106        CAA  TATT
                                TCCCTGGG   AG    CCCA
                                ||||||||   ||    ||||
                                AGGGACTC   TC    GGGT
                                     AC_  TTCC
GAM404  KIAA0931 3'  GAGTACTTTACCCAGAGG    67421    _    C
                                CC CTGGG AAAGTATTC
                                || ||||| |||||||||
                                GG GACCC TTTCATGAG
                                 A    A
GAM404  KIAA1199 3'  TTTGCTCTTCATCCAGGGA    72523        CA   TATTCC
                                TCCCTGGG  AAG     CAAA
                                ||||||||  |||     ||||
                                AGGGACCT  TTC     GTTT
                                     AC   TC____
GAM404  KIAA1503 5'  GGAACACTTTGCCCAGG     68350           A
                                CCTGGGCAAAGT TTCC
                                |||||||||||| ||||
                                GGACCCGTTTCA AAGG
                                      C
GAM404  KIAA1536 3'  TGGCTCTTTTGTCCCAGGGA   40492        _    TATTC
                                TCCCTGGG CAAAG    CCA
                                |||||||| |||||    |||
                                AGGGACCC GTTTT    GGT
                                     T    CTC__
GAM404  KIAA1560 3'  TTTGGAGGATACCCAGGGA    64182        CAAAG    _
                                TCCCTGGG    TATTC CCAAA
                                ||||||||    ||||| |||||
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                                AGGGACCC    ATAGG GGTTT
                                      _____    A
GAM404  KIAA1755 3'  GAATACTTGGGCGGGA     61345     TGG  A_
                                TCCC   GC  AAGTATTC
                                ||||   ||  ||||||||
                                AGGG   CG  TTCATAAG
                                  ___  GG
GAM404  KIAA1900 3'  TTTGTAATACTTTGCCCA    73251           CC
                                TGGGCAAAGTATT  CAAA
                                ||||||||||||  ||||
                                ACCCGTTTCATAA  GTTT
                                       T_
GAM404  KIAA1940 3'  AGTCCTTCCCAGGGA       79975        CA   T
                                TCCCTGGG  AAG ATT
                                ||||||||  ||| |||
                                AGGGACCC  TTC TGA
                                     __  C
GAM404  MRPS7    3'  TTGGGAATTTCCTCCAGG    31998       CAAAGT
                                CCTGGG     ATTCCCAA
                                ||||||     ||||||||
                                GGACCT     TAAGGGTT
                                   CCTT__
GAM404  PALM     3'  TTGGTCCCTGCCCTAGGGA   10418      _    AAGTATTC
                                TCCCT GGGCA       CCAA
                                ||||| |||||       ||||
                                AGGGA CCCGT       GGTT
                                   T    CCCT____
GAM404  PRO1331  5'  GATATTTCTCCAGCCCAGGGA  47835         A____
                                TCCCTGGGC    AAGTATT
                                |||||||||    |||||||
                                AGGGACCCG    TTTATAG
                                     ACCTC
GAM404  PTP4A1   3'  ATTTGAGAATACTTTAAAGGGA 12936      GGGC       C
                                TCCCT    AAAGTATTC CAAAT
                                |||||    ||||||||| |||||
                                AGGGA    TTTCATAAG GTTTA
                                   AA__        A
GAM404  SHARP    3'  TTGGACTTTTGCCCAGTGA   30399    C       _  ATTC
                                TC CTGGGCAAA GT    CCAA
                                || |||||||| ||    ||||
                                AG GACCCGTTT CA    GGTT
                                 T        T  ____
GAM404  TACTILE  3'  GAATACTTTGCACAGG      19470      G
                                CCTG GCAAAGTATTC
                                |||| ||||||||||
                                GGAC CGTTTCATAAG
                                  A
GAM404  USP3     5'  TGAAAATACTTTGTACAG    89679     GG       CC
                                CTG  CAAAGTATT  CA
                                |||  |||||||||  ||
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                                GAC  GTTTCATAA  GT
                                  AT        AA
GAM404  VIT1     5'  AATATTAATACCCAGGGA    37967        CAA_
                                TCCCTGGG    AGTATT
                                ||||||||    ||||||
                                AGGGACCC    TTATAA
                                    ATAA
GAM404  LOC116437 3'  GAGACCTTTGTCCAAAGA    73891    CC       TA
                                TC  TGGGCAAAG  TTC
                                ||  |||||||||  |||
                                AG  ACCTGTTTC  GAG
                                 AA        CA
GAM404  LOC122970 5'  GGACCCTTCCCAGGGA      74181        CA   TAT
                                TCCCTGGG  AAG   TCC
                                ||||||||  |||   |||
                                AGGGACCC  TTC   AGG
                                    __   CC_
GAM404  LOC123242 3'  TGGTGAACTTCACTCAGGGA   75604        CA    AT  _
                                TCCCTGGG  AAGT  TC CCA
                                ||||||||  ||||  || |||
                                AGGGACTC  TTCA  AG GGT
                                    AC    __  T
GAM404  LOC143677 3'  ATTTAGGAGACTTTTTACCCAG 82975        C__     A    C
          GGG                     TCCCTGGG   AAAGT TTCC AAAT
                                ||||||||   ||||| |||| ||||
                                GGGGACCC   TTTCA GAGG TTTA
                                    ATT    _    A
GAM404  LOC146520 5'  GGAAAACCTCAGGGA       77955        CAAA  A
                                TCCCTGGG    GT TTCC
                                ||||||||    || ||||
                                AGGGACTC    CA AAGG
                                    _____  A
GAM404  LOC148824 3'  GAAACTAACCCAGGGA      84226        CAA   A
                                TCCCTGGG   AGT TTC
                                ||||||||   ||| |||
                                AGGGACCC   TCA AAG
                                    AA_   _
GAM404  LOC158428 3'  AATTCTTTGCCCAGAGA     70556    C        T
                                TC CTGGGCAAAG ATT
                                || ||||||||||  |||
                                AG GACCCGTTTC TAA
                                 A         T
GAM404  LOC159110 3'  GAATACTTCTCAGG        82098       CA
                                CCTGGG  AAGTATTC
                                ||||||  ||||||||
                                GGACTC  TTCATAAG
                                    __
GAM404  LOC159116 3'  GAATACTTCTCAGG        82093       CA
                                CCTGGG  AAGTATTC
                                ||||||  ||||||||
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                                GGACTC  TTCATAAG
                                  __
GAM404  LOC203080 5'  GACTCTTTACCCAGGGA     89266        C    TA
                                TCCCTGGG AAAG  TT
                                |||||||| ||||  ||
                                AGGGACCC TTTC  AG
                                    A    TC
GAM404  LOC203378 5'  TGGCGCTTCTCCCAGGGA    90619        CA    ATTC
                                TCCCTGGG  AAGT    CCA
                                |||||||| ||||    |||
                                AGGGACCC  TTCG    GGT
                                    TC    C___
GAM404  LOC219654 3'  ATTTGGGGAGTTTCACCCAG   91299      CAAAGTA
                                CTGGG      TTCCCAAAT
                                |||||      |||||||||
                                GACCC      AGGGGTTTA
                                   ACTTTG_
GAM404  LOC222161 3'  GGCACTGCTTTGCCCAGGG    92798           TTC
                                CCCTGGGCAAAGTA   CC
                                ||||||||||||||   ||
                                GGGACCCGTTTCGT   GG
                                       CAC
GAM404  LOC254226 5'  GAGTCTTTCTCCGGCCCAGGGA 96242         _____   T
                                TCCCTGGGC     AAAG ATTC
                                |||||||||     |||| ||||
                                AGGGACCCG     TTTC TGAG
                                    GCCTC   _
GAM404  LOC54466  3'  ATTTGGAAAGTACTTTATCCAG 38651      GC       C_
                                CTGG  AAAGTATT  CCAAAT
                                ||||  ||||||||  ||||||
                                GACC  TTTCATGA  GGTTTA
                                  TA       AA
GAM404  LOC89958  3'  GGAGCCCGCCCTAGGGA     60922       _    AAA  AT
                                TCCCT GGGC   GT  TCC
                                ||||| ||||   ||  |||
                                AGGGA CCCG   CG  AGG
                                   T    CC_  __
GAM404  LOC93129  3'  ATTTGGGTGTTTCTACCCAAGG 71461    C    CAA  TATT_
                                CC TGGG   AG     CCCAAAT
                                || ||||   ||     |||||||
                                GG ACCC   TC     GGGTTTA
                                 A    A__  TTTGT
GAM404  LOC93538  5'  TGAGAATACTTTTAAAGG    72563     GGGC       C
                                CCT    AAAGTATTC CA
                                |||    ||||||||| ||
                                GGA    TTTCATAAG GT
                                  AAT_       A
GAM405  ADCY6     3'  CCTCCTCATGCCCCTTCTGA   30926     _  ACA  TC
                                TCA AAG   GC  TGAGGAGG
                                ||| |||   ||  ||||||||
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                                AGT TTC  CG  ACTCCTCC
                                  C  CC_  T_
GAM405  ADCY6   3'  CCTCCTCATGCCCCTTCTGA  40616    _  ACA  TC
                                TCA AAG  GC  TGAGGAGG
                                ||| |||  ||  ||||||||
                                AGT TTC  CG  ACTCCTCC
                                  C  CC_  T_
GAM405  AK1     3'  CCTCCTCAGCCTCCCTTTG   4883      AC  CT
                                CAAAG  AG  CTGAGGAGG
                                |||||  ||  |||||||||
                                GTTTC  TC  GACTCCTCC
                                   CC  C_
GAM405  ATM     5'  CCTTTTGAGCTGTCTTGA   56300     A      T_
                                TCAA GACAGCTC  GAGG
                                ||||  ||||||||  ||||
                                AGTT CTGTCGAG  TTCC
                                  _      TT
GAM405  ATM     5'  CCTTTTGAGCTGTCTTGA   56294     A      T_
                                TCAA GACAGCTC  GAGG
                                ||||  ||||||||  ||||
                                AGTT CTGTCGAG  TTCC
                                  _      TT
GAM405  B3GAT1  3'  CTCCTCAGACCCTGTT     53974      C_
                                GACAG  TCTGAGGAG
                                |||||  |||||||||
                                TTGTC  AGACTCCTC
                                   CC
GAM405  B3GAT1  3'  CTCCTCAGACCCTGTT     37829      C_
                                GACAG  TCTGAGGAG
                                |||||  |||||||||
                                TTGTC  AGACTCCTC
                                   CC
GAM405  BRF1    3'  CCTCCCCAGGCCTCTT     7711      CA  T   A
                                AAGA  GC CTG GGAGG
                                ||||  || ||| |||||
                                TTCT  CG GAC CCTCC
                                  C_  _   C
GAM405  CARD10  3'  CCCCCAAGGCTGTCTCTGG   27273     A      TC  A  A
                                TCA AGACAGC  TG GG GG
                                |||  |||||||  || || ||
                                GGT TCTGTCG  AC CC CC
                                  C      GA  _  _
GAM405  CD28    3'  CCCAAGTCTGTCTTTGA     20438          _  C  A
                                TCAAAGACAG CT TG GG
                                ||||||||||  || || ||
                                AGTTTCTGTC GA AC CC
                                       T  _  _
GAM405  CDK5R2  3'  CCTCCTTTTTGTGTCTT     14133       G TCT
                                AAGACA C   GAGGAGG
                                ||||||  |   |||||||
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                                TTCTGT G   TTCCTCC
                                   _ TTT
GAM405  CPNE3    3'  CCTGGAAAGCTGTCTT      14026         __   G
                                AAGACAGC  TCT AGG
                                ||||||||  ||| |||
                                TTCTGTCG  AGG TCC
                                    AA  _
GAM405  DLEU2    5'  CCTCACTTCTTTGAT       20060        C  CTC
                                ATCAAAGA AG   TGAGG
                                |||||||| ||   |||||
                                TAGTTTCT TC   ACTCC
                                   _ ____
GAM405  DNAJB9   3'  CCTCATTATCTTTGAT      24679        C  CTC
                                ATCAAAGA AG   TGAGG
                                |||||||| ||   |||||
                                TAGTTTCT TT   ACTCC
                                    A ____
GAM405  DPP6     3'  CCTCCTCAAGGTTGTCTT    55447        TC
                                AAGACAGC  TGAGGAGG
                                ||||||||  ||||||||
                                TTCTGTTG  ACTCCTCC
                                    GA
GAM405  DPYSL3   3'  CCTCCTCATATTGCCTCTGA  7314     A  A   CTC
                                TCA AG CAG   TGAGGAGG
                                ||| || |||   ||||||||
                                AGT TC GTT   ACTCCTCC
                                  C  C   AT_
GAM405  EDAR     3'  CCTCCTCAGAATGTTTT     42266       GC
                                AAGACA  TCTGAGGAGG
                                ||||||  ||||||||||
                                TTTTGT  AGACTCCTCC
                                   A_
GAM405  EPHB4    3'  CCCCCAGCTGCTGCCTT     15462     A    T_   A  A
                                AAG CAGC  CTG GG GG
                                ||| ||||  ||| || ||
                                TTC GTCG  GAC CC CC
                                  C    TC   _ _
GAM405  EVA1     3'  CCTCCTCGGTGTTTCTGAT   19395     A    GCT
                                ATCA AGACA   CTGAGGAGG
                                |||| |||||   |||||||||
                                TAGT TTTGT   GGCTCCTCC
                                  C    ____
GAM405  FBLN5    5'  CCTCCTCGCGCGTCTTGGA   20914    A    A  TC
                                TC AAGAC GC  TGAGGAGG
                                || ||||| ||  ||||||||
                                AG TTCTG CG  GCTCCTCC
                                 G    _ C_
GAM405  FGD1     3'  CCTCCTCAGCCAGGTCTT    15522       AGCT
                                AAGAC    CTGAGGAGG
                                |||||    |||||||||
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                                TTCTG   GACTCCTCC
                                  GACC
GAM405  FNTB    3'  CCTCCTCACCAGCTCTC    8951    C   C_
                                GA AGCT  TGAGGAGG
                                || ||||  ||||||||
                                CT TCGA  ACTCCTCC
                                 C   CC
GAM405  FUT3    5'  CCTCCTGGTGAGCTGTC    3801        TG_
                                GACAGCTC  AGGAGG
                                ||||||||  ||||||
                                CTGTCGAG  TCCTCC
                                    TGG
GAM405  G2A     5'  CTCCTCATGTTCTTGA     25320     AG  GCTC
                                TCAA  ACA   TGAGGAG
                                ||||  |||   |||||||
                                AGTT  TGT   ACTCCTC
                                  CT  _____
GAM405  GRIK3   3'  CTCCTCAGATCTTCT      5887     C  C
                                AGA AG TCTGAGGAG
                                ||| || |||||||||
                                TCT TC AGACTCCTC
                                  _  T
GAM405  HLF     3'  CCTCCTCAGCTTTGCTT    9219     A  CT
                                AAG CAG  CTGAGGAGG
                                ||| |||  |||||||||
                                TTC GTT  GACTCCTCC
                                  _  TC
GAM405  HMGA1   3'  CCCCCAGCCAAACTGTCTTTG  76935        CT___  A  A
                                CAAAGACAG    CTG GG GG
                                |||||||||    ||| || ||
                                GTTTCTGTC    GAC CC CC
                                    AAACC  _ _
GAM405  HOXC13  3'  CCTCCTCAAAGGCCACCTTGGT 59682      AGACA  C_
                                ATCAA    GCT  TGAGGAGG
                                |||||    |||  ||||||||
                                TGGTT    CGG  ACTCCTCC
                                  CCAC_  AA
GAM405  HPS1    3'  CCTCTTCCAGAGCTGCCTCTG  3965    A  A     _
                                CA AG CAGCTCTG AGGAGG
                                || || |||||||| ||||||
                                GT TC GTCGAGAC TTCTCC
                                 C  C       C
GAM405  HS3ST2  3'  CCTCCTCAGACCTTATC    20156    C_  C
                                GA  AG TCTGAGGAGG
                                ||  || ||||||||||
                                CT  TC AGACTCCTCC
                                 AT  C
GAM405  LAG3    5'  CCTCCTCAGGCTGCCT     9659     A   T
                                AG CAGC CTGAGGAGG
                                || |||| |||||||||
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                                TC GTCG GACTCCTCC
                                 C   _
GAM405  LSP1     3'  CCTCGCCTCTTTGAT      9808         CA  TCT
                                ATCAAAGA  GC   GAGG
                                ||||||||  ||   ||||
                                TAGTTTCT  CG   CTCC
                                    C_  ___
GAM405  MOCS2    3'  CCTCCTCAGTGACTTT     15769      A  GCT
                                AAAG CA   CTGAGGAGG
                                |||| ||   |||||||||
                                TTTC GT   GACTCCTCC
                                  A  ___
GAM405  MYLK2    3'  CCTCCCCAGCTCCTCGTCTTTG 52418         _ CT_   A
            A                    TCAAAGAC AG   CTG GGAGG
                                ||||||||  ||   |||  |||||
                                AGTTTCTG TC   GAC CCTCC
                                     C  CTC   C
GAM405  NHLH1    3'  CCTTGAGCTGCCTTTGG     18798       A     T
                                TCAAAG CAGCTC GAGG
                                ||||||  ||||||  ||||
                                GGTTTC GTCGAG TTCC
                                   C     _
GAM405  NPEPPS   5'  CCTCCTCCTTCTCGTCTT    20874       _ CTCT
                                AAGAC AG    GAGGAGG
                                |||||  ||    |||||||
                                TTCTG TC    CTCCTCC
                                  C  TTC_
GAM405  NPR2L    5'  CCTCGAGGCTGTCTCTGA    21559     A      TC
                                TCA AGACAGC  TGAGG
                                |||  |||||||  |||||
                                AGT TCTGTCG  GCTCC
                                  C      GA
GAM405  NRAS     3'  CCTCCTCACTTGGCTGTCT    10270        C__
                                AGACAGCT   TGAGGAGG
                                ||||||||   ||||||||
                                TCTGTCGG   ACTCCTCC
                                     TTC
GAM405  P29      3'  CCTCCTCATGGCGGCCTGTGA  31311     A  ACA   C
                                TCA AG   GCT TGAGGAGG
                                |||  ||   |||  ||||||||
                                AGT TC   CGG ACTCCTCC
                                  G  CGG   T
GAM405  PEX6     3'  CCTCCTCAGGCTGCT       4300     A    T
                                AG CAGC CTGAGGAGG
                                ||  ||||  |||||||||
                                TC GTCG GACTCCTCC
                                  _   _
GAM405  PPP1R3D  3'  CCTCCTCAGGAATATTCTCGAT 20702     AA   CAGC_
                                ATC  AGA    TCTGAGGAGG
                                |||  |||    ||||||||||
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                                TAG  TCT    GGACTCCTCC
                                  C_   TATAA
GAM405  PTGS2    3'  CCAAAAAGAAGCTGTCTTGGAT 6360      A       _  GA__
                                ATC AAGACAGCT CT    GG
                                ||| ||||||||| ||    ||
                                TAG TTCTGTCGA GA    CC
                                  G        A  AAAA
GAM405  RARA     3'  CCTCCTCAGTTTTCTCTTT   6366       C  CT
                                AAAGA AG  CTGAGGAGG
                                ||||| ||  |||||||||
                                TTTCT TT  GACTCCTCC
                                   C  TT
GAM405  SCGB2A1  5'  CCTCCACAGCAACTTCCTTGAT 10013      A  C  CT_  A
                                ATCAA GA AG   CTG GGAGG
                                ||||| || ||   ||| |||||
                                TAGTT CT TC   GAC CCTCC
                                   C  _  AAC   A
GAM405  SP100    3'  CCTTCAGTTGTCTCTGAT    11894      A      CT
                                ATCA AGACAGCT  GAGG
                                |||| ||||||||  ||||
                                TAGT TCTGTTGA  TTCC
                                  C       C_
GAM405  SRD5A1   3'  CTTTACAACTGTCTTTGAT   6456           CTC
                                ATCAAAGACAG   TGAGG
                                ||||||||||   |||||
                                TAGTTTCTGTC   ATTTC
                                      AAC
GAM405  UGT1A1   3'  CCCCTCCGGTGTCTTTGAT   4874          G  CT   A
                                ATCAAAGACA CT  GAGG GG
                                |||||||||| ||  |||| ||
                                TAGTTTCTGT GG  CTCC CC
                                      _  C_   _
GAM405  UGT1A4   3'  CCCCTCCGGTGTCTTTGAT   23059         G  CT   A
                                ATCAAAGACA CT  GAGG GG
                                |||||||||| ||  |||| ||
                                TAGTTTCTGT GG  CTCC CC
                                      _  C_   _
GAM405  UGT1A9   3'  CCCCTCCGGTGTCTTTGAT   40710         G  CT   A
                                ATCAAAGACA CT  GAGG GG
                                |||||||||| ||  |||| ||
                                TAGTTTCTGT GG  CTCC CC
                                      _  C_   _
GAM405  ACTR1A   3'  CCTCCTCAGGTGGCCTCTGG  62966    A  ACA  T
                                TCA AG   GC CTGAGGAGG
                                ||| ||   || |||||||||
                                GGT TC   TG GACTCCTCC
                                  C  CGG  _
GAM405  ATP10D   5'  CCTATCAGGAAGCTGTCTCTGA 73143    A      __    GG
                                TCA AGACAGCT  CTGA  AGG
                                ||| ||||||||  ||||  |||
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                                AGT TCTGTCGA  GACT  TCC
                                  C       AG    A_
GAM405  ATP6V1EL2 3'  CCTCCTCTTTGATGCTCTGAT  54684      A  A  GCTCT
                                ATCA AG CA     GAGGAGG
                                |||| || ||     |||||||
                                TAGT TC GT     CTCCTCC
                                  C  _  AGTTT
GAM405  BHMT     3'  CCTCGATAGAAGCTATTTTTGA 8153         C    _   AG
          T                      ATCAAAGA AGCT CTG  GAGG
                                |||||||| |||| |||  ||||
                                TAGTTTTT TCGA GAT  CTCC
                                     A    A   AG
GAM405  BRD4     3'  CCTCTAGAGCTGTCCTAGAT   26666     AAA        _
                                ATC   GACAGCTCT GAGG
                                |||   ||||||||| ||||
                                TAG   CTGTCGAGA CTCC
                                  ATC        T
GAM405  C20orf162 5'  TCTGAGGAGGCAAAGTGTCTTT 54604          G_________   TGAG
            GA                    TCAAAGACA        CTC    GA
                                |||||||||        |||    ||
                                AGTTTCTGT        GAG    CT
                                     GAAACIIIG   GAGT
GAM405  C2orf6   3'  CCTCCTCGATGGCTTTGAT    36644        A  GC  T
                                ATCAAAG CA  TC GAGGAGG
                                ||||||| ||  || |||||||
                                TAGTTTC GT  AG CTCCTCC
                                     G  __  _
GAM405  C5orf6   3'  CCTCCACTTTAGCTGTTTTGA  33479      A      CTGA_
                                TCAA GACAGCT     GGAGG
                                |||| |||||||     |||||
                                AGTT TTGTCGA     CCTCC
                                  _      TTTCA
GAM405  C9orf7   3'  CCTCCCCACACAGAGCTGTC   34167          A____
                                GACAGCTCTG     GGAGG
                                ||||||||||     |||||
                                CTGTCGAGAC     CCTCC
                                     ACACC
GAM405  CAPN6    3'  CCTACAGATGTCTTTGAT    26604          GC   _
                                ATCAAAGACA  TCTG AGG
                                |||||||||  |||| |||
                                TAGTTTCTGT  AGAC TCC
                                     __    A
GAM405  CHRNA6   3'  CCTCCTCAGCATTATTTGAT   14838       GACAGCT
                                ATCAAA      CTGAGGAGG
                                ||||||      |||||||||
                                TAGTTT      GACTCCTCC
                                   ATTAC__
GAM405  CTCF     5'  CCTCCTCAAACTGACTTTG    21634       A   CTC
                                CAAAG CAG   TGAGGAGG
                                ||||| |||   ||||||||
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                                GTTTC GTC   ACTCCTCC
                                   A   AA_
GAM405  DGS-A    3'  CCTCACTCACTGTCTTTGA   84897          CTC   _
                                TCAAAGACAG   TGAG GAGG
                                ||||||||||   |||| ||||
                                AGTTTCTGTC   ACTC CTCC
                                     ____   A
GAM405  DKFZp434E1822 3'  CCTCACAGCTGTCTTTGG    68503           C
                                TCAAAGACAGCT TGAGG
                                |||||||||||| |||||
                                GGTTTCTGTCGA ACTCC
                                      C
GAM405  DKFZp547I094 5'  CCTCCTCTCTGAAGCTGTCTCT 49636     A       CT___
           GA                     TCA AGACAGCT     GAGGAGG
                                ||| ||||||||     |||||||
                                AGT TCTGTCGA     CTCCTCC
                                  C       AGTCT
GAM405  DKFZp547I224 5'  CCTCCTCAAGTGGGTCCCTGA  39556     AA   A_   C
                                TCA  GAC  GCT TGAGGAGG
                                |||  |||  ||| ||||||||
                                AGT  CTG  TGA ACTCCTCC
                                  CC   GG   _
GAM405  DKFZP566G1424 3'  CCTCCTCAATGCTCTCT     84784     C   TC
                                AGA AGC  TGAGGAGG
                                ||| |||  ||||||||
                                TCT TCG  ACTCCTCC
                                  C   TA
GAM405  DKFZP727C091 3'  CCTCCTCATGCCCCTTGGT    66209      A ACA  TC
                                ATCAA G   GC  TGAGGAGG
                                ||||| |   ||  ||||||||
                                TGGTT C   CG  ACTCCTCC
                                   _ CC_  T_
GAM405  DRIL2    3'  CCTCCCCAGCCTTCTT      21325      C  CT   A
                                AAGA AG  CTG GGAGG
                                |||| ||  ||| |||||
                                TTCT TC  GAC CCTCC
                                   _  C_   C
GAM405  E2F6     3'  CCTCCTCAAGTAGCTTC     8713     C    _ _
                                GA AGCT CT GAGGAGG
                                || |||| || |||||||
                                CT TCGA GA CTCCTCC
                                 _    T  A
GAM405  EDG1     3'  CCTCCTCAACGTTCTTT     59327      CA  TC
                                AAAGA  GC  TGAGGAGG
                                |||||  ||  ||||||||
                                TTTCT  TG  ACTCCTCC
                                   __  CA
GAM405  ENPP4    3'  TCTGAGGAGGCAAAGTGTCTTT 30050         G_________   TGAG
           GAT                    TCAAAGACA       CTC    GA
                                |||||||||       |||   ||
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                                AGTTTCTGT       GAG   CT
                                    GAAACIIIG   GAGT
GAM405  EPI64    3' CCTCCGTTCTGCCTCTGGT   95632     A  A  CTCTGA
                                ATCA AG CAG     GGAGG
                                |||| || |||     |||||
                                TGGT TC GTC     CCTCC
                                  C  C   TTG___
GAM405  FHOD2    5' CCGGGAGCTGTTCTGAT     73824     AA       GA
                                ATCA  GACAGCTCT  GG
                                ||||  |||||||||  ||
                                TAGT  TTGTCGAGG  CC
                                  C_       G_
GAM405  FKBP5    3' CCTCCTCAGCCAGCCTCCTTG 14652     A  CA   __
                                CAA GA  GCT  CTGAGGAGG
                                ||| ||  |||  |||||||||
                                GTT CT  CGA  GACTCCTCC
                                  C  C_  CC
GAM405  FLJ10482 3' CCTCCTTGTGCCTCTGGAT   36160     AA   CA  TCT
                                ATC  AGA  GC   GAGGAGG
                                |||  |||  ||   |||||||
                                TAG  TCT  CG   TTCCTCC
                                  G_   C_  TG_
GAM405  FLJ10989 3' CCTCTTGACTGTCTTT      36947       C  T_
                                AAAGACAG TC  GAGG
                                |||||||| ||  ||||
                                TTTCTGTC AG  CTCC
                                     _  TT
GAM405  FLJ12505 3' CCTCTGGCTTTCTTTGA     45386       C    CT
                                TCAAAGA AGCT  GAGG
                                ||||||| ||||  ||||
                                AGTTTCT TCGG  CTCC
                                    T   T_
GAM405  FLJ12587 3' CCTCCTCAGAGCCCACCCTGA 42496     AAGACA
                                TCA     GCTCTGAGGAGG
                                |||     ||||||||||||
                                AGT     CGAGACTCCTCC
                                  CCCACC
GAM405  FLJ13265 3' CCTGGAGCTGTCTTTG      45923          G
                                CAAAGACAGCTCT AGG
                                |||||||||||| |||
                                GTTTCTGTCGAGG TCC
                                          _
GAM405  FLJ20034 3' CCCCTGCAGCCTCTTTGAT   34365       CA  CTG  A
                                ATCAAAGA  GCT   AGG GG
                                ||||||||  |||   ||| ||
                                TAGTTTCT  CGA   TCC CC
                                    C_   CG_  _
GAM405  FLJ21140 3' CCTCCTCAGAATGTT       45480     GC
                                GACA  TCTGAGGAGG
                                ||||  ||||||||||
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                                TTGT  AGACTCCTCC
                                  A_
GAM405  FLJ22969  3'  CCTCCCACTTCCCTCTTTGA  68649       CAGCTC  A
                                TCAAAGA     TG GGAGG
                                |||||||     || |||||
                                AGTTTCT     AC CCTCC
                                    CCCTTC  _
GAM405  FLJ23042  3'  CCTTTCAGATGAGCTGTCCTTG 47171      A      ___   G
          A                      TCAA GACAGCTC   TGAG AGG
                                |||| ||||||||   |||| |||
                                AGTT CTGTCGAG   ACTT TCC
                                  C       TAG   _
GAM405  FLJ32389  3'  CCTCCTCAGGCTCCCTCT    58191     C__   T
                                AGA   AGC CTGAGGAGG
                                |||   ||| |||||||||
                                TCT   TCG GACTCCTCC
                                  CCC   _
GAM405  GABBR1    3'  CCTCCTCAGCAGCCTC      7607     CA   _
                                GA  GCT CTGAGGAGG
                                ||  ||| |||||||||
                                CT  CGA GACTCCTCC
                                 C_   C
GAM405  GABBR1    3'  CCTCCTCAGCAGCCTC      41572    CA   _
                                GA  GCT CTGAGGAGG
                                ||  ||| |||||||||
                                CT  CGA GACTCCTCC
                                 C_   C
GAM405  GTF3C2    3'  CCTCCCCAGGACTCCTTAGAT  7722     A   AC  CT   A
                                ATC AAG  AG  CTG GGAGG
                                ||| |||  ||  ||| |||||
                                TAG TTC  TC  GAC CCTCC
                                  A   C_  AG   C
GAM405  HCA4      3'  CCTCCTCATGCCCTCTGAT   77582     A  ACA  TC
                                ATCA AG   GC  TGAGGAGG
                                |||| ||   ||  ||||||||
                                TAGT TC   CG  ACTCCTCC
                                  C  C__  T_
GAM405  HTEX4     5'  CCTCCTCAGTTTTCTGTTTTT  97721       CT__
                                AAAGACAG    CTGAGGAGG
                                ||||||||    |||||||||
                                TTTTTGTC    GACTCCTCC
                                    TTTT
GAM405  HTEX4     5'  CCTCCTCAGTTTTCTGTTTTT  97896       CT__
                                AAAGACAG    CTGAGGAGG
                                ||||||||    |||||||||
                                TTTTTGTC    GACTCCTCC
                                    TTTT
GAM405  HTEX4     5'  CCTCCTCAGTTTTCTGTTTTT  92095       CT__
                                AAAGACAG    CTGAGGAGG
                                ||||||||    |||||||||
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                                TTTTTGTC   GACTCCTCC
                                    TTTT
GAM405  IL-17RE  3' CCTCCTCATACTTTCCCTTGA 58293     A_ C CTC
                                TCAA GA AG  TGAGGAGG
                                |||| || ||  ||||||||
                                AGTT CT TC  ACTCCTCC
                                  CC T AT_
GAM405  KIAA0152 3' CCTCAGATCGCCTCTGA    28297    A ACA __
                                TCA AG  GC TCTGAGG
                                ||| ||  || |||||||
                                AGT TC  CG AGACTCC
                                  C ___ CT
GAM405  KIAA0173 3' CCTCCTCAGAGTATTTTTTGA 27669       CA
                                TCAAAGA GCTCTGAGGAGG
                                ||||||| ||||||||||||
                                AGTTTTT TGAGACTCCTCC
                                    TA
GAM405  KIAA0318 3' CCTTTAAGCTTTCTTTGAT   68951       C   CT
                                ATCAAAGA AGCT GAGG
                                |||||||| |||| ||||
                                TAGTTTCT TCGA TTCC
                                     T   AT
GAM405  KIAA0450 5' CCTCCTCAGAGTTCTC     27632    C
                                GA AGCTCTGAGGAGG
                                || ||||||||||||
                                CT TTGAGACTCCTCC
                                 C
GAM405  KIAA0620 3' CCTCCTTGAACTGACCTTTGAT 62121       A_  C T
                                ATCAAAG CAG TC GAGGAGG
                                ||||||| ||| || |||||||
                                TAGTTTC GTC AG TTCCTCC
                                    CA  A _
GAM405  KIAA0970 3' CCTCCTCATTTGTCTT     29957       CTC
                                AAGACAG  TGAGGAGG
                                |||||||  ||||||||
                                TTCTGTT  ACTCCTCC
                                    T__
GAM405  KIAA1076 3' CCTCCAAAGGGCTGTCT    65513        GA
                                AGACAGCTCT GGAGG
                                |||||||||| |||||
                                TCTGTCGGGA CCTCC
                                     AA
GAM405  KIAA1077 3' CCTCCTCTTCACTCTCCTCTGA 72905     AA_ C CTCT
           T                     ATCA  GA AG   GAGGAGG
                                ||||  || ||   |||||||
                                TAGT  CT TC   CTCCTCC
                                  CTC C ACTT
GAM405  KIAA1130 3' CCTCCTCAGAAGCCCTCCCTG 62416   AA CA  _
                                CA GA GCT CTGAGGAGG
                                ||  ||  ||| |||||||||
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                              GT  CT  CGA GACTCCTCC
                               CC  CC   A
GAM405  KIAA1210 3' CCTCAGCTGTCTTTG      96327          CT
                              CAAAGACAGCT  GAGG
                              ||||||||||  ||||
                              GTTTCTGTCGA  CTCC
                                        __
GAM405  KIAA1240 3' CTTTAGAACTGCCTTT      66731      A   C
                              AAAG CAG TCTGAGG
                              |||| ||| |||||||
                              TTTC GTC AGATTTC
                                C   A
GAM405  KIAA1396 3' CCTCCTCAAGTGGGTCCCTGA  62987     AA  A_  C
                              TCA  GAC  GCT TGAGGAGG
                              |||  |||  ||| ||||||||
                              AGT  CTG  TGA ACTCCTCC
                                CC   GG  _
GAM405  KIAA1409 3' CCCCTGTTGCTATTTTTGAT   61215        C   TCTG   A
                              ATCAAAGA AGC    AGG GG
                              |||||||| |||    ||| ||
                              TAGTTTTT TCG    TCC CC
                                   A   TTG_  _
GAM405  KIAA1554 3' CCTCAGCTATCTTTGG      95149        C    CT
                              TCAAAGA AGCT  GAGG
                              |||||||| ||||  ||||
                              GGTTTCT TCGA  CTCC
                                   A   __
GAM405  KIAA1604 5' CCAGTTTGAAGCATCTTTGAT  64235         CA   CT   GA
                              ATCAAAGA  GCT  GAG  GG
                              ||||||||  |||  |||  ||
                              TAGTTTCT  CGA  TTT  CC
                                   A_   AG   GA
GAM405  KIAA1668 3' CCTCCTCAGGGACCTCTGA   66471     A  ACAG
                              TCA AG    CTCTGAGGAGG
                              ||| ||    ||||||||||
                              AGT TC    GGGACTCCTCC
                                C  CA__
GAM405  KIAA1676 5' CCTGCAGCTGTCTTGAT     93123      A      CTG
                              ATCAA GACAGCT   AGG
                              ||||| |||||||   |||
                              TAGTT CTGTCGA   TCC
                                 _      CG_
GAM405  KIAA1944 3' CAGAGCTGTCTCAGAT      75557     AA
                              ATC  AGACAGCTCTG
                              |||  ||||||||||
                              TAG  TCTGTCGAGAC
                                AC
GAM405  MGC11034 5' CCTCCTCAGGGGCTGTCTCTG  48788    A       _
                              CA AGACAGCTC TGAGGAGG
                              || |||||||| ||||||||
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                                GT TCTGTCGGG ACTCCTCC
                                 C        G
GAM405  MGC22014  3'  CCCGAGCTGTCTCTG      64493    A       T A
                                CA AGACAGCTC G GG
                                || |||||||||| | ||
                                GT TCTGTCGAG C CC
                                 C        _ _
GAM405  MGC35558  3'  CCTGGGGAGCTGTCACTGA   58781     AA      _ G
                                TCA  GACAGCTC T AGG
                                |||  |||||||| | |||
                                AGT  CTGTCGAG G TCC
                                  CA       G G
GAM405  MMP28     3'  CTCCCCAGGCCTTTG      51968      ACA  T   A
                                CAAAG   GC CTG GGAG
                                |||||   || ||| ||||
                                GTTTC   CG GAC CCTC
                                   ____ _   C
GAM405  MMP28     3'  CTCCCCAGGCCTTTG      44189      ACA  T   A
                                CAAAG   GC CTG GGAG
                                |||||   || ||| ||||
                                GTTTC   CG GAC CCTC
                                   ____ _   C
GAM405  MOST2     5'  CCTTCTCAGCCTTCTTTGA   39680       C  CT
                                TCAAAGA AG  CTGAGGAGG
                                |||||||  ||  |||||||||
                                AGTTTCT TC  GACTCTTCC
                                    _  C_
GAM405  MYO18B    3'  CCTCCTTGAAGCTGCCCTTGA 50887     AGA    CT
                                TCAA   CAGCT  GAGGAGG
                                ||||   |||||  |||||||
                                AGTT   GTCGA  TTCCTCC
                                  CCC    AG
GAM405  NAG14     3'  CCGAGAGCTGTCTTTG      42164          GA
                                CAAAGACAGCTCT  GG
                                ||||||||||||||  ||
                                GTTTCTGTCGAGA  CC
                                       G_
GAM405  P5-1      3'  CTGTAGAGATGTCTTTGAT   21917         G    A
                                ATCAAAGACA CTCTG GG
                                |||||||||| ||||| ||
                                TAGTTTCTGT GAGAT TC
                                     A    G
GAM405  P5326     3'  CTTCCTTGGCTACTTTGA    48772       AC   CT
                                TCAAAG  AGCT  GAGGAGG
                                ||||||  ||||  |||||||
                                AGTTTC  TCGG  TTCCTTC
                                   A_   __
GAM405  PDE10A    3'  CCTCATCTTGCTTCTTTGA   21862       C   TCT  G
                                TCAAAGA AGC   GA GAGG
                                |||||||  |||   || ||||
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                                AGTTTCT TCG   CT CTCC
                                    _  TT_  A
GAM405  PORIMIN  3'  CTGTAGAGCTGCTTT      53604      A       A
                                AAAG CAGCTCTG GG
                                |||| |||||||| ||
                                TTTC GTCGAGAT TC
                                  _       G
GAM405  RNB6     5'  CCTCCTCAGGGTTCCCT     32928     AC
                                AG  AGCTCTGAGGAGG
                                ||  ||||||||||||
                                TC  TTGGGACTCCTCC
                                 CC
GAM405  RNO2     5'  CCTGATAGAGCTGTCTCTG    52768     A         __
                                CA AGACAGCTCTG  AGG
                                || ||||||||||  |||
                                GT TCTGTCGAGAT  TCC
                                 C          AG
GAM405  S164     3'  CCTGGAGAGCTGTATTT     60777     G       G_
                                AAA ACAGCTCT  AGG
                                ||| ||||||||  |||
                                TTT TGTCGAGA  TCC
                                  A       GG
GAM405  SE57-1   3'  CCTCCCGAGTAGCTGTCTTT   47397          _  GA
                                AAAGACAGCT CT  GGAGG
                                |||||||||| ||  |||||
                                TTTCTGTCGA GA  CCTCC
                                      T  GC
GAM405  SEMA4G   3'  CCTCCCTTGCTGTCTTGGA   35434     A       TCTGA
                                TC AAGACAGC    GGAGG
                                || ||||||||    |||||
                                AG TTCTGTCG    CCTCC
                                 G       TTC__
GAM405  SEMA4G   3'  CCTCCCTTGCTGTCTTGGA   94677     A       TCTGA
                                TC AAGACAGC    GGAGG
                                || ||||||||    |||||
                                AG TTCTGTCG    CCTCC
                                 G       TTC__
GAM405  SIAT9    3'  CTGAGAGCTGTTTTTGA     13989             G
                                TCAAAGACAGCTCT AG
                                |||||||||||||| ||
                                AGTTTTTGTCGAGA TC
                                         G
GAM405  SUI1     3'  CCTCCTCAGCTCTCCCTCTG   19403     A  AC  CT
                                CA AG  AG  CTGAGGAGG
                                || ||  ||  |||||||||
                                GT TC  TC  GACTCCTCC
                                 C  CC  TC
GAM405  TM4-B    3'  CCTGAGAGGAGCTGTCCCTGA  24969     AA        GAGG
                                TCA  GACAGCTCT    AGG
                                |||  |||||||||    |||
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                                AGT  CTGTCGAGG   TCC
                                  CC       AGAG
GAM405  TNFRSF19L 3'  CCTCCCCCAGCTGTTTTT   51775         CTGA
                                AAAGACAGCT   GGAGG
                                ||||||||||   |||||
                                TTTTTGTCGA   CCTCC
                                     CCC_
GAM405  TOMM34   3'  CCTCCTCAATCCCTTGAT   22335      A_ CAGCTC
                                ATCAA  GA     TGAGGAGG
                                |||||  ||     ||||||||
                                TAGTT  CT     ACTCCTCC
                                   CC  A_____
GAM405  LOC123775 3'  CCTCCCCGTCAGTCTGTCTTT  75623        CT   ___
                                AAAGACAG  CTGA   GGAGG
                                ||||||||  ||||   |||||
                                TTTCTGTC  GACT   CCTCC
                                     T_   GCC
GAM405  LOC131377 3'  CCCCCTAGGTTGTCTTGAT   76269      A     T   A  A
                                ATCAA GACAGC CTG GG GG
                                ||||| |||||| ||| || ||
                                TAGTT CTGTTG GAT CC CC
                                   _     _  C  _
GAM405  LOC145135 5'  CCTCGGCTGCCCTTGGA    83251    A   A_    CT
                                TC AAG  CAGCT  GAGG
                                || |||  |||||  ||||
                                AG TTC  GTCGG  CTCC
                                 G   CC    __
GAM405  LOC145693 5'  CCTGGAGAGCCTCCTTGAT   77350      A  CA    G_
                                ATCAA GA  GCTCT  AGG
                                |||||  ||  |||||  |||
                                TAGTT CT  CGAGA  TCC
                                   C  C_    GG
GAM405  LOC146332 3'  CCTCCTCAGGTTCCTT      77822     AC   T
                                AAG  AGC CTGAGGAGG
                                |||  ||| |||||||||
                                TTC  TTG GACTCCTCC
                                  C_  _
GAM405  LOC146909 3'  CCTGCAGAGCTGCCCTTGA   78170      AGA      _
                                TCAA   CAGCTCTG AGG
                                ||||   |||||||| |||
                                AGTT   GTCGAGAC TCC
                                   CCC       G
GAM405  LOC148137 3'  CCTTAGAGCTGTCTTTGA    58423
                                TCAAAGACAGCTCTGAGG
                                ||||||||||||||||||
                                AGTTTCTGTCGAGATTCC

GAM405  LOC148183 5'  CCTCCTCACTCTCTCCCTGG  84116     AA  C  CTC
                                TCA  GA AG   TGAGGAGG
                                |||  || ||   ||||||||
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                                GGT  CT TC   ACTCCTCC
                                  CC  C  TC_
GAM405   LOC148809 5'  CCTCCATCCCTTCTTTGAT   79002        C  CTCT  _
                                ATCAAAGA AG    GA GGAGG
                                |||||||| ||    || |||||
                                TAGTTTCT TC    CT CCTCC
                                     _  C___  A
GAM405   LOC149711 5'  CCTCCTCAAAGATCACTTGA   84678      AGACAG  C
                                TCAA     CT TGAGGAGG
                                ||||     || ||||||||
                                AGTT     GA ACTCCTCC
                                  CACTA_  A
GAM405   LOC150287 3'  CCTCCTCTTTGATCTCTGA    79782     A  _  CTCT
                                TCA AGA CAG    GAGGAGG
                                ||| ||| |||    |||||||
                                AGT TCT GTT    CTCCTCC
                                  C   A   T___
GAM405   LOC150423 5'  CCTGGAGCTGCCTTTGA     79864       A      G
                                TCAAAG CAGCTCT AGG
                                |||||| ||||||| |||
                                AGTTTC GTCGAGG TCC
                                   C      _
GAM405   LOC152018 5'  CTTAAGACTGTCTTTGAT    85544          C   G
                                ATCAAAGACAG TCT AGG
                                |||||||||||| ||| |||
                                TAGTTTCTGTC AGA TTC
                                     _   A
GAM405   LOC152897 5'  CCTCCTTCTTGTCTGTGA    80725     A     CTCT
                                TCA AGACAG    GAGGAGG
                                ||| ||||||    |||||||
                                AGT TCTGTT    TTCCTCC
                                  G     C___
GAM405   LOC153565 5'  CCTCCTCACCGCGCCCTCGGA  80891    AA  ACA  TC
                                TC  AG   GC  TGAGGAGG
                                ||  ||   ||  ||||||||
                                AG  TC   CG  ACTCCTCC
                                 GC  CCG  CC
GAM405   LOC155032 3'  CTTTGTTAGTATCTTTGAT    86321        CAGCT   G
                                ATCAAAGA     CTGA GAGG
                                ||||||||     |||| ||||
                                TAGTTTCT     GATT TTTC
                                     AT___    G
GAM405   LOC157349 5'  CCTCACGGCTGTCTCCGG    81413    AA       C
                                TC  AGACAGCT TGAGG
                                ||  |||||||| |||||
                                GG  TCTGTCGG ACTCC
                                 CC       C
GAM405   LOC157355 3'  CCTCCTCAGAGAAGCCTCT    81425     CAG__
                                AGA    CTCTGAGGAGG
                                |||    ||||||||||
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                                TCT    GAGACTCCTCC
                                  CCGAA
GAM405  LOC158158 3'  CCTCCTCAAGTGGGTCCCTGA  81722    AA  A_  C
                                TCA  GAC  GCT TGAGGAGG
                                |||  |||  ||| ||||||||
                                AGT  CTG  TGA ACTCCTCC
                                  CC   GG  _
GAM405  LOC158438 5'  CCTCCTTTGCTTCCTTGA    86832     A  C   TCT
                                TCAA GA AGC   GAGGAGG
                                |||| || |||   |||||||
                                AGTT CT TCG   TTCCTCC
                                  C  _   T__
GAM405  LOC158856 5'  CCTCCCCAGTCTTCTT     86914     C  CT   A
                                AAGA AG  CTG GGAGG
                                |||| ||  ||| |||||
                                TTCT TC  GAC CCTCC
                                  _  T_   C
GAM405  LOC164582 5'  CCTCCTCAAAGCCTGT     82542     _  C
                                ACAG CT TGAGGAGG
                                |||| || ||||||||
                                TGTC GA ACTCCTCC
                                  C  A
GAM405  LOC199906 3'  CTCCCCTCGTTTTTGA     88482       _  CTCTGA
                                TCAAAGAC AG     GGAG
                                |||||||| ||     ||||
                                AGTTTTTG TC     CCTC
                                     C  C_____
GAM405  LOC200470 5'  CTCCCAGCGTCTTTGA     90060       AGCT   A
                                TCAAAGAC    CTG GGAG
                                ||||||||    ||| ||||
                                AGTTTCTG    GAC CCTC
                                     C___   _
GAM405  LOC200918 3'  CCTCCTCATGCTCATCTT    88940     C_   TC
                                AAGA  AGC  TGAGGAGG
                                ||||  |||  ||||||||
                                TTCT  TCG  ACTCCTCC
                                  AC   T_
GAM405  LOC203871 3'  CAGAGCTGTCTCCGGT     89441     AA
                                ATC  AGACAGCTCTG
                                |||  ||||||||||
                                TGG  TCTGTCGAGAC
                                  CC
GAM405  LOC219988 5'  CCTCCTGTTAGAGCTGTC    91620         __
                                GACAGCTCTG  AGGAGG
                                ||||||||||  ||||||
                                CTGTCGAGAT  TCCTCC
                                      TG
GAM405  LOC221143 3'  CCCCCAAACTGGAGCTGTCCCT 93566     AA        A___  A
          GG                    TCA  GACAGCTCTG    GG GG
                                |||  ||||||||||    || ||
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                                GGT  CTGTCGAGGT    CC CC
                                  CC         CAAA  C
GAM405   LOC221218 3'  CCTAGCAGCTGTCCTTG     91759     A      _  G
                                CAA GACAGCT CT AGG
                                ||| ||||||| || |||
                                GTT CTGTCGA GA TCC
                                  C      C  _
GAM405   LOC253219 3'  CCTCCTCTTTAGTCTTTG     97484        AGCTCT
                                CAAAGAC     GAGGAGG
                                |||||||     |||||||
                                GTTTCTG     CTCCTCC
                                    ATTT__
GAM405   LOC253868 3'  CCTCCTCACCTCTCTTCGG    95580     A    C  CTC
                                TC AAGA AG   TGAGGAGG
                                || |||| ||   ||||||||
                                GG TTCT TC   ACTCCTCC
                                 C    C  C__
GAM405   LOC254528 3'  CTCCTACTGTCTTTG       95053         CTCTG
                                CAAAGACAG    AGGAG
                                |||||||||    |||||
                                GTTTCTGTC    TCCTC
                                     A____
GAM405   LOC255515 3'  CCTCAAGCTTCCTTGAT     96094       A  C    C
                                ATCAA GA AGCT TGAGG
                                ||||| || |||| |||||
                                TAGTT CT TCGA ACTCC
                                  C  _   _
GAM405   LOC255645 3'  CCTCCTCACTGTCT        96650        CTC
                                AGACAG   TGAGGAGG
                                ||||||   ||||||||
                                TCTGTC   ACTCCTCC
                                   ___
GAM405   LOC256158 5'  CCTACAGAGCTGTCGCTGA   97658     AA        _
                                TCA  GACAGCTCTG AGG
                                |||  |||||||||| |||
                                AGT  CTGTCGAGAC TCC
                                  CG         A
GAM405   LOC256337 3'  CCTCCCACTGGCCTCTTTGAT  94694         CA   C_  A
                                ATCAAAGA  GCT  TG GGAGG
                                ||||||||  |||  || |||||
                                TAGTTTCT  CGG  AC CCTCC
                                    C_   TC  _
GAM405   LOC257106 3'  CCTCCAGCTTCTCTCTTTGA   95386        C___    CTGA
                                TCAAAGA    AGCT    GGAGG
                                |||||||    ||||    |||||
                                AGTTTCT    TCGA    CCTCC
                                    CTCT    ____
GAM405   LOC257484 3'  CCCGAGCTGTCTCTG       88815     A       T A
                                CA AGACAGCTC G GG
                                || |||||||| | ||
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                                GT TCTGTCGAG C CC
                                 C       _ _
GAM405  LOC257486 3'  CCTCAGCTGTCTTTG       69244          CT
                                CAAAGACAGCT  GAGG
                                ||||||||||  ||||
                                GTTTCTGTCGA  CTCC
                                          __
GAM405  LOC51112  5'  CCTCGGACTTCTTCGA      32086    A   C  C
                                TC AAGA AG TCTGAGG
                                || |||| || |||||||
                                AG TTCT TC AGGCTCC
                                 C   _ _
GAM405  LOC51312  3'  CCTCCTCCCTGGATCCTTAGAT 33507     A  A___   CTCT
                                ATC AAG    CAG    GAGGAGG
                                ||| |||    |||    |||||||
                                TAG TTC    GTC    CTCCTCC
                                  A   CTAG   C___
GAM405  LOC51644  3'  CCTCTAGGCTGTCTCTG     32137    A      CT
                                CA AGACAGCT  GAGG
                                || ||||||||  ||||
                                GT TCTGTCGG  CTCC
                                 C       AT
GAM405  LOC90593  3'  CCTCCTCAAGTGGGTCCCTGAT 63453     AA   A_   C
                                ATCA  GAC  GCT TGAGGAGG
                                ||||  |||  ||| ||||||||
                                TAGT  CTG  TGA ACTCCTCC
                                  CC   GG   _
GAM405  LOC90786  5'  CCTCTTAGAGAGGCTGTCTTTG 64031          _   G_
            A                    TCAAAGACAGC TCT  AGGAGG
                                ||||||||||| |||  ||||||
                                AGTTTCTGTCG AGA  TTCTCC
                                       G   GA
GAM405  LOC92095  3'  CCTCCTCATTGTCCTTG     68092     A    CTC
                                CAA GACAG   TGAGGAGG
                                ||| |||||   ||||||||
                                GTT CTGTT   ACTCCTCC
                                  C    ___
GAM405  LOC92096  3'  CCTCCTCATTGTCCTTG     68098     A    CTC
                                CAA GACAG   TGAGGAGG
                                ||| |||||   ||||||||
                                GTT CTGTT   ACTCCTCC
                                  C    ___
GAM405  LOC92539  3'  CCTCCTCAAATGGGTCCCTGA  69633     AA   AGCTC
                                TCA  GAC    TGAGGAGG
                                |||  |||    ||||||||
                                AGT  CTG    ACTCCTCC
                                  CC   GGTAA
GAM405  LOC92539  5'  CCTGGAGCTTTCTTTGAT    69634        C     G
                                ATCAAAGA AGCTCT AGG
                                |||||||| |||||| |||
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                                TAGTTTCT TCGAGG TCC
                                    T    _
GAM405  LOC96597  3'  CCTCCTGCCACCCTCTCTTTGA 66910       C  CTCTG_
                                TCAAAGA AG     AGGAGG
                                ||||||| ||     ||||||
                                AGTTTCT TC     TCCTCC
                                    C  CCACCG
GAM406  TNFAIP1   3'  CATCAGCTGAGGACAGCAAACT 40917     AG     G
              CC                  GGA  TTGCTG CTTCAGCTGATG
                                  |||  |||||| ||||||||||||
                                  CCT  AACGAC GGAGTCGACTAC
                                    CA     A
GAM406  C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 21681     AA       _ ___
              CCC                   GG  GTTGCTGG CT   TCAGCTG
                                  ||  |||||||| ||   |||||||
                                  CC  CGACGACC GG   GGTCGAC
                                   CC       A  GTT
GAM406  C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 94622     AA       _ ___
              CCC                   GG  GTTGCTGG CT   TCAGCTG
                                  ||  |||||||| ||   |||||||
                                  CC  CGACGACC GG   GGTCGAC
                                   CC       A  GTT
GAM406  C20orf59  3'  CATCCCTAGCCAGCAGCTCC   41992     A        TC  CT
                                GGA GTTGCTGGCT  AG  GATG
                                ||| ||||||||||  ||  ||||
                                CCT CGACGACCGA  TC  CTAC
                                  _        __  C_
GAM406  FLJ20079  3'  CATTCTGGTAAACCAGCAGCCT 34490     A       CT__    CT
              CC                  GGA GTTGCTGG    TCAG  GATG
                                  ||| ||||||||    ||||  ||||
                                  CCT CGACGACC    GGTC  TTAC
                                    C       AAAT   __
GAM406  SSAT2     3'  CATCAGCTGAAGCACTCTTC   56041      TTGCTG
                                GAAG     GCTTCAGCTGATG
                                ||||     ||||||||||||||
                                CTTC     CGAAGTCGACTAC
                                   TCA___
GAM406  SYNJ2     3'  ATCAGCTTAAGCAATTCC     61763      GTTGCTG    C
                                GGAA      GCTT AGCTGAT
                                ||||      |||| |||||||
                                CCTT      CGAA TCGACTA
                                  AA_____    T
GAM406  LOC162333 5'  CTGAAGCCAGCAATTCC     87131      G
                                GGAA TTGCTGGCTTCAG
                                |||| ||||||||||||
                                CCTT AACGACCGAAGTC
                                  _
GAM406  LOC222060 5'  CACCTCCCACCAGCAACCCCC  94104     AA       CTTC  C
                                GG  GTTGCTGG    AG TG
                                ||  ||||||||    || ||
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                                CC  CAACGACC    TC AC
                                 CC       ACCC  C
GAM406  LOC255650 3'  CATCAGCCCCAGGCAACTTCC  96711         _   CTTCA
                                GGAAGTTGC TGG    GCTGATG
                                ||||||||| |||    |||||||
                                CCTTCAACG ACC    CGACTAC
                                     G   C____
GAM407  ANXA5     3'  CTGTAAAATTATGATG      6716          __
                                CATCATGAT  TACAG
                                |||||||||  |||||
                                GTAGTATTA  ATGTC
                                     AA
GAM407  APBA1     3'  ATCTGTGGGAATGTGGTAGTA  69915     C      CATGA
                                TAC ACCACAT    TTACAGAT
                                ||| |||||||    ||||||||
                                ATG TGGTGTA    GGTGTCTA
                                  A      AG___
GAM407  CENTD1    3'  GTACAGTGATGTGGTGGTA   30853           GAT
                                TACCACCACATCAT   TAC
                                ||||||||||||||   |||
                                ATGGTGGTGTAGTG   ATG
                                       AC_
GAM407  CENTD1    3'  GTACAGTGATGTGGTGGTA   57563           GAT
                                TACCACCACATCAT   TAC
                                ||||||||||||||   |||
                                ATGGTGGTGTAGTG   ATG
                                       AC_
GAM407  HNRPD     3'  GTGTCATGATGTAGTAGTG   48577     C  C       T
                                TAC AC ACATCATGAT AC
                                ||| || |||||||||| ||
                                GTG TG TGTAGTACTG TG
                                  A  A       _
GAM407  HNRPD     3'  GTGTCATGATGTAGTAGTG   9246      C  C       T
                                TAC AC ACATCATGAT AC
                                ||| || |||||||||| ||
                                GTG TG TGTAGTACTG TG
                                  A  A       _
GAM407  PTGS2     3'  ATCTGTAACCAAGATG      6359      A  A
                                CATC TG TTACAGAT
                                |||| || ||||||||
                                GTAG AC AATGTCTA
                                   A  C
GAM407  SGCB      3'  TTGTTCACAATGTGGTGG    4068          CA   TT
                                CCACCACAT  TGA  ACAG
                                |||||||||  |||  ||||
                                GGTGGTGTA  ACT  TGTT
                                     AC   __
GAM407  FLJ12949  3'  ATCTCTACAAAATGTGGTG   43441         CA  AT  C
                                CACCACAT  TG  TA AGAT
                                ||||||||  ||  || ||||
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                                GTGGTGTA  AC  AT TCTA
                                    AA  __  C
GAM407  FLJ21369  3'  TAGCCAGATGTGGTGG     45637         A  AT
                                CCACCACATC TG  TA
                                |||||||||| ||  ||
                                GGTGGTGTAG AC  AT
                                     _  CG
GAM407  FLJ23514  3'  ATCTGTAATGAATAGTGG    41542     CACA   GAT
                                CCAC   TCAT   TACAGAT
                                ||||   ||||  |||||||
                                GGTG   AGTA   ATGTCTA
                                  ATA_   ___
GAM407  FLJ23556  3'  ATCATGATTGTGATGG      45942     C   _
                                CCA CACA TCATGAT
                                ||| |||| |||||||
                                GGT GTGT AGTACTA
                                  A   T
GAM407  FPGT      3'  ATCTGTGGGGGAAGTGGTAGTA 13845     C    A  ATGA
                                TAC ACCAC TC    TTACAGAT
                                ||| |||||| ||   ||||||||
                                ATG TGGTG AG    GGTGTCTA
                                  A    A  GG__
GAM407  HSPC043   3'  TAGCCATGTGTGGTGG      67722        T   AT
                                CCACCACA CATG  TA
                                |||||||| ||||  ||
                                GGTGGTGT GTAC  AT
                                     _   CG
GAM407  KIAA0721  3'  TGATCATGTGTGGTG       95975        T
                                CACCACA CATGATTA
                                ||||||| ||||||||
                                GTGGTGT GTACTAGT
                                     _
GAM407  KIAA0721  3'  TGATCATGTGTGGTG       41347        T
                                CACCACA CATGATTA
                                ||||||| ||||||||
                                GTGGTGT GTACTAGT
                                     _
GAM407  LAT1-3TM  3'  ATCTGTAATGCAGCTTGTAATG 48312    CC   TCA  _
                                CA  ACA   TG ATTACAGAT
                                ||  |||   || |||||||||
                                GT  TGT   AC TAATGTCTA
                                  AA   TCG  G
GAM407  LAT1-3TM  5'  ATCTGTAATGCAGCTTGTAATG 68598    CC   TCA  _
                                CA  ACA   TG ATTACAGAT
                                ||  |||   || |||||||||
                                GT  TGT   AC TAATGTCTA
                                  AA   TCG  G
GAM407  MGC4268   3'  ATCTGTTTTCCATGATGTGTTG 48743    C       _ TT
                                CA CACATCATG A  ACAGAT
                                || |||||||| |  ||||||
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                                GT GTGTAGTAC T  TGTCTA
                                 T       C TT
GAM407  PCANAP7   5' ATCTGTAAAATGATG      93363       GA
                                CATCAT  TTACAGAT
                                ||||||  ||||||||
                                GTAGTA  AATGTCTA
                                   A_
GAM407  PRIC285   3' CTGTAATCACTCTGGATGGTG  61435      _  CATCA
                                TACCA CCA    TGATTACAG
                                ||||| |||    |||||||||
                                GTGGT GGT    ACTAATGTC
                                   A  CTC__
GAM407  UBPH      3' ATCTGAGGTGATGTGGTG    38917         GATTA
                                CACCACATCAT    CAGAT
                                ||||||||||    |||||
                                GTGGTGTAGTG    GTCTA
                                      GA___
GAM407  LOC146957 3' TGATCTAATATGGTGGTG    78208        C  CAT
                                TACCACCA AT   GATTA
                                |||||||| ||   |||||
                                GTGGTGGT TA   CTAGT
                                     A  AT_
GAM407  LOC197003 5' ATCCATAAGCATGACTGGTGGT 87868        CA    A  CA
          A                      TACCACCA  TCATG TTA  GAT
                                ||||||||  ||||| |||  |||
                                ATGGTGGT  AGTAC AAT  CTA
                                     C_    G   AC
GAM407  LOC197423 5' ATCTGTAATGCAGCTTGTAATG 77856    CC   TCA  _
                                CA  ACA   TG ATTACAGAT
                                ||  |||   || |||||||||
                                GT  TGT   AC TAATGTCTA
                                 AA   TCG  G
GAM407  LOC200310 3' CTGGCCTGATGTGGAGTA    65735     CA       TGATTA
                                TAC  CCACATCA     CAG
                                |||  ||||||||     |||
                                ATG  GGTGTAGT     GTC
                                  A_       CCG___
GAM407  LOC220565 5' ATCTGTAATGCAGCTTGTAATG 90743    CC   TCA  _
                                CA  ACA   TG ATTACAGAT
                                ||  |||   || |||||||||
                                GT  TGT   AC TAATGTCTA
                                 AA   TCG  G
GAM407  LOC255328 3' TGTAGTCATAATATATGGTA   96568      CCAC  C
                                TACCA    AT ATGATTACA
                                |||||    || |||||||||
                                ATGGT    TA TACTGATGT
                                   ATA_  A
GAM407  LOC256273 3' ATCTATAAAGTTGTGGTGG    96403        TCATGA   C
                                CCACCACA     TTA AGAT
                                ||||||||     ||| ||||
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                                GGTGGTGT     AAT TCTA
                                     TGA___   A
GAM407  LOC51026  3'  ATCTGTGAAAATGGGATG    32168    CA    GA
                                CA  TCAT  TTACAGAT
                                ||  ||||  ||||||||
                                GT  GGTA  AGTGTCTA
                                 AG    AA
GAM407  LOC54516  3'  ATCTGTAATCATGATGTGGTGG 38760
           TA                    TACCACCACATCATGATTACAGAT
                                ||||||||||||||||||||||||
                                ATGGTGGTGTAGTACTAATGTCTA

GAM407  LOC91408  3'  TCTGTAGACATGAAGG      65928    ACA    A
                                CC   TCATG TTACAGA
                                ||   ||||| |||||||
                                GG   AGTAC GATGTCT
                                 A__     A
GAM408  AK1       3'  CAGCGGAGTAGCAGAAGAC    4881      CC      AAG  T
                                GTC  CTGCTAC   TG CTG
                                |||  |||||||   || |||
                                CAG  GACGATG   GC GAC
                                  AA      AG_  _
GAM408  ARHGDIA   3'  CAGGAACAAACAAGGGACCAA  15042         C  CTACAA  GT
                                TTGGTCCC TG     GT  CTG
                                |||||||| ||     ||  |||
                                AACCAGGG AC     CA  GAC
                                     A  AAA___  AG
GAM408  DBP       5'  AGACACTCGTCCAAACCA    7214       CCCC  CT  A
                                TGGT    TG  AC AGTGTCT
                                ||||    ||  || |||||||
                                ACCA    AC  TG TCACAGA
                                  A___  C_  C
GAM408  ED1       3'  CAGTTGTAGCAGAAACCAA    7363        CCC        G
                                TTGGT   CTGCTACAA TG
                                |||||   ||||||||| ||
                                AACCA   GACGATGTT AC
                                   AA_        G
GAM408  ELF3      3'  CAGACACTTGGACTGAGCCAA  15420       CCCCTGCTA
                                TTGGT        CAAGTGTCTG
                                |||||        ||||||||||
                                AACCG        GTTCACAGAC
                                   AGTCAG___
GAM408  KLK3      3'  CAGACACTCACAGCAAGGATGG 7919     G    CC    ACA
           A                     TT GTCC  TGCT   AGTGTCTG
                                || ||||  ||||   ||||||||
                                AG TAGG  ACGA   TCACAGAC
                                 G   A_    CAC
GAM408  MMP14     3'  GGGGGCAGGAGGGGACCAA    17172          G  ACAA  G
                                TTGGTCCCCT CT    GT TCT
                                |||||||||| ||    || |||
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                                AACCAGGGGA GA    CG GGG
                                      G _____ G
GAM408  PRKCQ    3'  TATCTGTAGCAGAAACCAA   20744      CCC       AG
                                TTGGT   CTGCTACA  TG
                                |||||   ||||||||  ||
                                AACCA   GACGATGT  AT
                                   AA_      CT
GAM408  TCF7     3'  AGACACTTCATGGACCAA    12155       CC  CTAC
                                TTGGTCC  TG    AAGTGTCT
                                |||||||  ||    ||||||||
                                AACCAGG  AC    TTCACAGA
                                   T_ _____
GAM408  APOL6    5'  CAGACACTCACAGCCCCCTGCC 47618      CCCCT   ACA
           AG                     TTGGT    GCT   AGTGTCTG
                                |||||    |||   ||||||||
                                GACCG    CGA   TCACAGAC
                                   TCCCC   CAC
GAM408  FLJ22529  3'  CAGGAGGATAGAAGAGGACCAA 45565       C  G   CAAGTG
                                TTGGTCC CT CTA     TCTG
                                ||||||| || |||     ||||
                                AACCAGG GA GAT     GGAC
                                   A  A   AGGA__
GAM408  MGC13168  3'  CAGACACGTGCAGGGAACCAA  51209      C     TACAA
                                TTGGT CCCTGC    GTGTCTG
                                ||||| ||||||    |||||||
                                AACCA GGGACG    CACAGAC
                                   A     TG___
GAM408  RP4-622L5 3'  ACAACAGCAGGGACCAA     38926        C    ACAAG
                                TTGGTCCC TGCT    TGT
                                |||||||| ||||    |||
                                AACCAGGG ACGA    ACA
                                   _   CA___
GAM408  SEC3     3'  CAGACACTATACCAAAATACCA 36811      CCCC  C  CA
           A                     TTGGT   TG TA  AGTGTCTG
                                |||||   || ||  ||||||||
                                AACCA   AC AT  TCACAGAC
                                   TAAA  C  A_
GAM408  LOC127428 3'  CAGACACTCCAGCTAGGAACTC 74663     _  C  CT   ACA
           AA                     TTG GT CC  GCT   AGTGTCTG
                                ||| || ||  |||   ||||||||
                                AAC CA GG  CGA   TCACAGAC
                                  T  A  AT   CC_
GAM408  LOC146784 5'  CAGACACTGAGCCAGGGGCCCA 78105      T     _  A  A
           A                     TTGG CCCCTG CT CA GTGTCTG
                                |||| |||||| || || |||||||
                                AACC GGGGAC GA GT CACAGAC
                                  C     C  _  _
GAM408  LOC90092  5'  CAGACACTCACAGCCCCACC   61402     CCCCT   ACA
                                GGT    GCT   AGTGTCTG
                                |||    |||   ||||||||
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                                CCA    CGA   TCACAGAC
                                  CCC__   CAC
GAM409  A1BG     3'  GGGGTCTCTGGGGGGCTGG   55426      G      ACTT
                                CCAGT CCTTCAGA   TCTC
                                ||||| ||||||||   ||||
                                GGTCG GGGGGTCT   GGGG
                                   _      CT__
GAM409  ABCB9    3'  GGGGGAGTGAGGGGCTGG   39036      G   CAGA   TT
                                CCAGT CCTT   ACT  CTC
                                ||||| ||||   |||  |||
                                GGTCG GGAG   TGA  GGG
                                   G   ____  GG
GAM409  ABCC3    3'  GGAGAAAGCAGCCATTGG   39158      C  TCAGAA
                                CCAGTG CT    CTTTCTCT
                                |||||| ||    ||||||||
                                GGTTAC GA    GAAAGAGG
                                   C  C_____
GAM409  ABL1     5'  AGGAGGGGGTTAAGGCGCAGG  17673    A     CAG   TT
                                CC GTGCCTT   AACT  CTCTT
                                || |||||||  ||||  |||||
                                GG CGCGGAA   TTGG  GAGGA
                                 A      ___   GG
GAM409  ACVRL1   5'  AGGAGGGAGTGGTGGAGCTGG  3417      TGC    GA   TT
                                CCAG   CTTCA  ACT  CTCTT
                                ||||   |||||  |||  |||||
                                GGTC   GAGGT  TGA  GAGGA
                                   ___    GG   GG
GAM409  ACVRL1   3'  GGGGGGGGTGGGGGGCAGTGG   3420     G     AGA   TT
                                CCA TGCCTTC   ACT  CTC
                                ||| |||||||   |||  |||
                                GGT ACGGGGG   TGG  GGG
                                  G      G__   GG
GAM409  ADAM15   3'  GGGAGGGGCTGGGGGGTTGG   13772     GT      AA
                                CCA  GCCTTCAG  CTTTCT
                                |||  ||||||||  ||||||
                                GGT  TGGGGGTC  GGAGGG
                                   __       GG
GAM409  ADAMTS4  3'  GGGGGAAGGCAGGGAGGGCCTG 17516      T     AGAA
           G                     CCAG GCCTTC    CTTTCTCTT
                                ||||  ||||||    |||||||||
                                GGTC CGGGAG    GGAAGGGGG
                                   _     GGAC
GAM409  ADAMTS8  3'  AGGGGGAAGAGGAGAGGGTATG 22882     G     AGAA
           G                     CCA TGCCTTC    CTTTCTCTT
                                |||  |||||||    |||||||||
                                GGT ATGGGAG    GAAGGGGGA
                                   _     AGGA
GAM409  ADCY9    3'  GGGAGTGGAGGCGTTGG     6658          AGA   TT
                                CCAGTGCCTTC   ACT  C
                                ||||||||||   |||  |
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                                GGTTGCGGAGG  TGA  G
                                     ___  GG
GAM409  ADH5    3'  AAGGGAAAGGAAGCAGGGCAGT 5413     G     CAGAA
          GG                    CCA TGCCTT    CTTTCTCTT
                                ||| ||||||    |||||||||
                                GGT ACGGGA    GAAAGGGAA
                                  G     CGAAG
GAM409  ADORA1  3'  AGGAGAGAGGTTGAGGATGCAC 5422        __     AA
          TGG                   CAGTGC  CTTCAG  CTTTCTCTT
                                ||||||  ||||||  |||||||||
                                GTCACG  GGAGTT  GAGAGAGGA
                                   TA     G_
GAM409  ADORA2A 3'  GGGGAGAGGTTGGGGCTGG   5435       G  TTCAGAA
                                CCAGT CC      CTTTCTCT
                                ||||| ||      ||||||||
                                GGTCG GG      GAGAGGGG
                                   G  TTG____
GAM409  ADRA2B  3'  GGGAGGTCTTGGAGGCCTGG  5464      T     GA
                                CCAG GCCTTCA  ACTTTCT
                                |||| |||||||  |||||||
                                GGTC CGGAGGT  TGGAGGG
                                  _      TC
GAM409  AES     3'  GGGGAGACAGAGGCACGG    6677     A     CAGAAC
                                CC GTGCCTT     TTTCTCT
                                || |||||||     |||||||
                                GG CACGGAG     AGAGGGG
                                  _      AC____
GAM409  AGPAT2  3'  GGGAGAGGAGGGGCCTGG    65824     T    CAGAA
                                CCAG GCCTT     CTTTCTC
                                |||| |||||     |||||||
                                GGTC CGGGG     GAGAGGG
                                  _     AG___
GAM409  AICDA   3'  GAGAGAGGGCCGGGCGTGG   40327     G    TCAGAA
                                CCA TGCCT      CTTTCTC
                                ||| |||||      |||||||
                                GGT GCGGG      GAGAGAG
                                  _     CCGG__
GAM409  AMN     3'  GGGGAGGGTGAGGAGCTGG    48192      G   CAGA
                                CCAGT CCTT    ACTTTCTCT
                                ||||| ||||    |||||||||
                                GGTCG GGAG    TGGGAGGGG
                                   A   ____
GAM409  ANK1    3'  AGAGAGAGACAGGGCTGG     40023      G   TCAGAA
                                CCAGT CCT     CTTTCTCT
                                ||||| |||     ||||||||
                                GGTCG GGA     GAGAGAGA
                                  _  CA____
GAM409  ANK1    3'  AGAGAGAGACAGGGCTGG     3469       G   TCAGAA
                                CCAGT CCT     CTTTCTCT
                                ||||| |||     ||||||||
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                                GGTCG GGA     GAGAGAGA
                                  _  CA____
GAM409  ANK1    3' AGAGAGAGACAGGGCTGG    60384      G  TCAGAA
                                CCAGT CCT     CTTTCTCT
                                ||||| |||     ||||||||
                                GGTCG GGA     GAGAGAGA
                                  _  CA____
GAM409  AP1S1   3' GGGAAGGAAGGGTTGG     54034     GT    CAGAA
                                CCA  GCCTT    CTTTCTC
                                |||  |||||    |||||||
                                GGT  TGGGA    GGAAGGG
                                  __    A____
GAM409  APBA1   5' GGGAGAAGATGGTGGCGCTGG  69920        T  GAACT
                                CCAGTGCC TCA     TTCTCTT
                                |||||||| |||    |||||||
                                GGTCGCGG GGT    AAGAGGG
                                     T  AG___
GAM409  APC4    5' GAGGGAGGGGAGAGGCCACTGG 95903      _   CAGAA
                                CCAGTG CCTT    CTTTCTCTT
                                |||||| ||||    |||||||||
                                GGTCAC GGAG    GGGAGGGAG
                                   C   AG___
GAM409  ARHGAP6 5' AGGGGGAGTGGCGCTGG     20403       TTCAGA  TT
                                CCAGTGCC     ACT  CTCT
                                ||||||||     |||  ||||
                                GGTCGCGG     TGA  GGGA
                                     _____  GG
GAM409  ARHGAP6 5' GGGAGGAAGTTCTCGCGGCGCC 20410    A    TTC
           GG                    CC GTGCC   AGAACTTTCTCTT
                                || |||||  ||||||||||||||
                                GG CGCGG   TCTTGAAGGAGGG
                                 C    CGC
GAM409  ARHGAP6 5' AGGGGGAGTGGCGCTGG     6758        TTCAGA  TT
                                CCAGTGCC     ACT  CTCT
                                ||||||||     |||  ||||
                                GGTCGCGG     TGA  GGGA
                                     _____  GG
GAM409  ARHGAP6 3' GGGAAAGTTCTCCTGG      6767      TGCCTTC
                                CCAG      AGAACTTTCTC
                                ||||      ||||||||||
                                GGTC      TCTTGAAAGGG
                                  C_____
GAM409  ARHGAP6 5' GGGAGGAAGTTCTCGCGGCGCC 6768    A    TTC
           GG                    CC GTGCC   AGAACTTTCTCTT
                                || |||||  ||||||||||||||
                                GG CGCGG   TCTTGAAGGAGGG
                                 C    CGC
GAM409  ARNT2   3' GAGGGGGAGAAGCCCAGGACTG 29460      G  TCAGAA  TT
           G                     CCAGT CCT     CT  CTCTT
                                ||||| |||     ||  |||||
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                                GGTCA GGA     GA  GGGAG
                                  _  CCCGAA  GG
GAM409  ATP1A2   3'  GGGAGCTCTGGAGGTGTTG   5528      TG       A  TT
                                CAG  CCTTCAGA CT  C
                                |||  |||||||| ||  |
                                GTT  GGAGGTCT GA  G
                                  GT       C  GG
GAM409  ATP5B    5'  GGGCTTTTTGGTGGTGCTGG   59663     TG  T     CTTT
                                CCAG  CC TCAGAA   CTC
                                ||||  || ||||||   |||
                                GGTC  GG GGTTTT   GGG
                                  GT  T     TC__
GAM409  AXL      5'  GAGGGAAGGAGGCAGGGGTGCT 8099      TG   CAGAA
           G                     CAG  CCTT    CTTTCTCTT
                                |||  ||||    |||||||||
                                GTC  GGGG    GGAAGGGAG
                                  GT    ACGGA
GAM409  AXL      5'  GAGGGAAGGAGGCAGGGGTGCT 41596     TG   CAGAA
           G                     CAG  CCTT    CTTTCTCTT
                                |||  ||||    |||||||||
                                GTC  GGGG    GGAAGGGAG
                                  GT    ACGGA
GAM409  B3GAT1   3'  AAGAGGGGGCAGGGGCTGCTGG 37822      _    CAGAA  TT
                                CCAGT GCCTT    CT  CTCTT
                                |||||  |||||    ||  |||||
                                GGTCG CGGGG    GG  GAGAA
                                  T    AC___  GG
GAM409  B3GAT1   3'  AAGAGGGGGCAGGGGCTGCTGG 53966      _    CAGAA  TT
                                CCAGT GCCTT    CT  CTCTT
                                |||||  |||||    ||  |||||
                                GGTCG CGGGG    GG  GAGAA
                                  T    AC___  GG
GAM409  BAX      3'  GGGAGGGGTGGGGATTGG    57038      G   TCAGAA
                                CCAGT CCT     CTTTCTC
                                |||||  |||     |||||||
                                GGTTA GGG     GGGAGGG
                                  G   TG____
GAM409  BAX      3'  GGGAGGGGTGGGGATTGG    57040      G   TCAGAA
                                CCAGT CCT     CTTTCTC
                                |||||  |||     |||||||
                                GGTTA GGG     GGGAGGG
                                  G   TG____
GAM409  BAX      3'  GGGAGGGGTGGGGATTGG    57042      G   TCAGAA
                                CCAGT CCT     CTTTCTC
                                |||||  |||     |||||||
                                GGTTA GGG     GGGAGGG
                                  G   TG____
GAM409  BAX      3'  GGGAGGGGTGGGGATTGG    57044      G   TCAGAA
                                CCAGT CCT     CTTTCTC
                                |||||  |||     |||||||
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                                GGTTA GGG     GGGAGGG
                                  G   TG____
GAM409  BAZ2A    3'  GAGGGGGAGACGGCGTTGG   25602        T  AGAA  TT
                                CCAGTGCC TC    CT  CTC
                                |||||||| ||    ||  |||
                                GGTTGCGG AG    GG  GAG
                                    C  A___  GG
GAM409  BCL2     3'  AGGGAGGGTTCCTGTGGG    5297      T  _
                                CCT CAG AACTTTCTCT
                                ||| ||| ||||||||||
                                GGG GTC TTGGGAGGGA
                                  T  C
GAM409  BCL2     3'  GAGGGAAGGAACAGAGGCCCTG 5302      T    CAGAA
              G                  CCAG GCCTT    CTTTCTCTT
                                |||| |||||    |||||||||
                                GGTC CGGAG    GGAAGGGAG
                                  C    ACAA_
GAM409  BCL2L11  3'  AGGAGGAGGTGAGAGAGGCACA 56833    A      CAGA
              GG                  CC GTGCCTT    ACTTTCTCTT
                                || |||||||    ||||||||||
                                GG CACGGAG    TGGAGGAGGA
                                 A      AGAG
GAM409  BCL2L11  3'  AGGAGGAGGTGAGAGAGGCACA 56832    A      CAGA
              GG                  CC GTGCCTT    ACTTTCTCTT
                                || |||||||    ||||||||||
                                GG CACGGAG    TGGAGGAGGA
                                 A      AGAG
GAM409  BCL6     3'  GGGGGTTGGGGGTGGTGG    57223     G      GA   TT
                                CCA TGCCTTCA  ACT  C
                                ||| ||||||||  |||  |
                                GGT GTGGGGGT  TGG  G
                                  G       __   GG
GAM409  BCL6     3'  GGGGGTTGGGGGTGGTGG    8126      G      GA   TT
                                CCA TGCCTTCA  ACT  C
                                ||| ||||||||  |||  |
                                GGT GTGGGGGT  TGG  G
                                  G       __   GG
GAM409  BCRP2    3'  GGAGTCAGAAGGTGTTGG    62404     TG    A  A
                                CCAG  CCTTC GA CTTT
                                ||||  ||||| || ||||
                                GGTT  GGAAG CT GAGG
                                  GT    A  _
GAM409  BSN      3'  GAGGGCTGGGGGCCCTGG    12923     T      AA
                                CCAG GCCTTCAG  CTT
                                |||| ||||||||  |||
                                GGTC CGGGGGTC  GAG
                                  C       GG
GAM409  BTG2     3'  GGGGGGGAGGAGGGAACTGG  22217      G    AGAA  TT
                                CCAGT CCTTC    CT  CTC
                                ||||| |||||    ||  |||
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                                GGTCA GGGAG   GG  GGG
                                  A    GA__  GG
GAM409  BTG2    3'  GGGAGGAGGGAACTGGAGGTTA 22215      _      AA_
          TTGG                   CAGTG CCTTCAG   CTTTCTCTT
                                |||||| |||||||   |||||||||
                                GTTAT GGAGGTC   GGAGGAGGG
                                  T      AAG
GAM409  C21orf2  3'  GGGAGAGAGTTTTGTTTTCTTG 17015      TGCCTT
          G                     CCAG     CAGAACTTTCTCTT
                                ||||     ||||||||||||||
                                GGTT     GTTTTGAGAGAGGG
                                  CTTTT_
GAM409  CA11    5'  GAGAGGGGGGCAGGGCGTTGG  6873          CAGAA  TT
                                CCAGTGCCTT    CT  CTCTT
                                ||||||||||    ||  |||||
                                GGTTGCGGGA    GG  GAGAG
                                     CG___  GG
GAM409  CARPX   3'  AGGATCCTTTGAGGGTGCTGG  39414      TG       ACT
                                CCAG  CCTTCAGA   TTCT
                                ||||  ||||||||   ||||
                                GGTC  GGGAGTTT   AGGA
                                  GT       CCT
GAM409  CASP6   5'  AAGAGGAGGGCAAGGTGTCTGG 52199      _     CAGAA
                                CCAG TGCCTT    CTTTCTCTT
                                |||| ||||||    |||||||||
                                GGTC GTGGAA    GGAGGAGAA
                                  T     CG___
GAM409  CASP6   5'  AAGAGGAGGGCAAGGTGTCTGG 6906       _     CAGAA
                                CCAG TGCCTT    CTTTCTCTT
                                |||| ||||||    |||||||||
                                GGTC GTGGAA    GGAGGAGAA
                                  T     CG___
GAM409  CBLB    5'  GGGAGAGCGGGTGTGG      15122     G    TCAGAA
                                CCA TGCCT     CTTTCTC
                                ||| |||||     |||||||
                                GGT GTGGG     GAGAGGG
                                  _     C_____
GAM409  CD34    3'  GGGGAAAGCCAAGGTCTGG   8346       T    CAGAA
                                CCAG GCCTT    CTTTCTCT
                                |||| |||||    ||||||||
                                GGTC TGGAA    GAAAGGGG
                                  _     CC___
GAM409  CDC2    5'  GGGGGGGGGGGGGCACTTGG   8361      _      AGAA  TT
                                CCA GTGCCTTC   CT  CTC
                                ||| ||||||||   ||  |||
                                GGT CACGGGGG   GG  GGG
                                  T       ____  GG
GAM409  CDC27   5'  GGGGGGGCCTGAGGCACTG   6988         T   AA  TT
                                CAGTGCCT CAG  CT  CT
                                |||||||| |||  ||  ||
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                                GTCACGGA GTC  GG  GG
                                    _  CG  GG
GAM409  CDK10    3'  AGAGGGACAAGGTATGG     53765     G     CAGAAC TT
                                CCA TGCCTT     T  CTCT
                                ||| ||||||     |  ||||
                                GGT ATGGAA     A  GAGA
                                  _     C_____ GG
GAM409  CDK10    3'  AGAGGGACAAGGTATGG     53773     G     CAGAAC TT
                                CCA TGCCTT     T  CTCT
                                ||| ||||||     |  ||||
                                GGT ATGGAA     A  GAGA
                                  _     C_____ GG
GAM409  CDK10    3'  AGAGGGACAAGGTATGG     13398     G     CAGAAC TT
                                CCA TGCCTT     T  CTCT
                                ||| ||||||     |  ||||
                                GGT ATGGAA     A  GAGA
                                  _     C_____ GG
GAM409  CDKN1A   3'  GGGGAAGGTGGGGTCCTGG    54301      TG    CAGA
                                CCAG  CCTT    ACTTTCTCT
                                ||||  ||||    |||||||||
                                GGTC  GGGG    TGGAAGGGG
                                  CT    ____
GAM409  CEP2     5'  AAGAGGAGGTTGAAGTGGCATG 23225     G    TTCAG
          G                      CCA TGCC     AACTTTCTCTT
                                ||| ||||     ||||||||||
                                GGT ACGG     TTGGAGGAGAA
                                  _    TGAAG
GAM409  CHD4     3'  GGGAGGGAGTGAGGGGCAGTGG 7041      G     CAGA   TT
                                CCA TGCCTT    ACT  CTCTT
                                ||| ||||||    |||  |||||
                                GGT ACGGGG    TGA  GAGGG
                                  G     AG__   GG
GAM409  CHRM1    3'  GAGGGAAACCCGGGGAACTGG  94791      G    CAGAAC
                                CCAGT CCTT     TTTCTCTT
                                ||||| ||||     ||||||||
                                GGTCA GGGG     AAAGGGAG
                                   A    CCC___
GAM409  CHRNB2   3'  GAGGGGAAGAGAGAGGCCTGG  5626      T    CAGAA
                                CCAG GCCTT     CTTTCTCTT
                                |||| |||||    |||||||||
                                GGTC CGGAG     GAAGGGGAG
                                  _     AGA__
GAM409  CHRNB2   3'  GGAGAAGAGGGGTATAGG    5627     A     CAGAAC
                                CC GTGCCTT     TTTCTCT
                                || |||||||     |||||||
                                GG TATGGGG     GAAGAGG
                                 A      A_____
GAM409  CHST5    3'  GAGAGGGAGCTGGGGCGCATGG 24026     _     T   AA
                                CCA GTGCCT CAG  CTTTCTC
                                ||| |||||| |||  |||||||
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                                GGT CGCGGG GTC  GGGAGAG
                                  A     _  GA
GAM409  CHST6    3'  GAGAGAAGGCTGGGGAGGGCTG 41228      G    AGAA
                G                  CCAGT CCTTC   CTTTCTCTT
                                   ||||| |||||   |||||||||
                                   GGTCG GGAGG   GGAAGAGAG
                                     _    GGTC
GAM409  CLCN4    3'  GAGGGGAAGTTTGCTGTATTGG 8445       CTTCA
                                   CCAGTGC    GAACTTTCTCTT
                                   |||||||    ||||||||||||
                                   GGTTATG    TTTGAAGGGGAG
                                      TCG__
GAM409  COL4A3   3'  AAGTGCAGGTTCTGAGGGCACC 48549    A          TCT
                GG                   CC GTGCCTTCAGAACTT  CTT
                                   || ||||||||||||||  |||
                                   GG CACGGGAGTCTTGGA  GAA
                                    C           CGT
GAM409  COL5A1   5'  AGGAGGAGGCGAGAAGGAGTTG 3632     TG    AGAA
                G                  CCAG  CCTTC   CTTTCTCTT
                                   ||||  |||||   |||||||||
                                   GGTT  GGAAG   GGAGGAGGA
                                     GA    AGC_
GAM409  CPSF4    3'  GGGAGGGAGGCAGCTGCTGG  21954     _____    AGAA  TT
                                   CCAGT   GCCTTC   CT  C
                                   |||||   ||||||   ||  |
                                   GGTCG   CGGAGG   GA  G
                                     TCGA    _____  GG
GAM409  CRY2     3'  AGGGGAGCAGGGCACAGG   72204    A     CAGAAC
                                   CC GTGCCTT     TTTCTCT
                                   || |||||||     |||||||
                                   GG CACGGGA     GAGGGGA
                                    A      C_____
GAM409  CSNK1G2  3'  GGAGGGGGACAGGCATTG    7169        TCAGAA  TT
                                   CAGTGCCT     CT  CTCT
                                   ||||||||     ||  ||||
                                   GTTACGGA     GG  GAGG
                                      CA____  GG
GAM409  CSRP1    3'  GGGAGGAAGGGGAAAGGGCTGG 14536     G   _ AGAA
                                   CCAGT CCTT C   CTTTCTCTT
                                   ||||| |||| |   |||||||||
                                   GGTCG GGAA G   GAAGGAGGG
                                     _   A GG__
GAM409  CTNND2   3'  GGAGAGACGAGGCATTCGG   7185    _     CAGAAC
                                   CC AGTGCCTT     TTTCTCT
                                   || ||||||||     |||||||
                                   GG TTACGGAG     AGAGAGG
                                    C       C_____
GAM409  CTSZ     3'  GGGAGGGAGGGAGGGAGTTGG  62116     TG    AGAA  TT
                                   CCAG  CCTTC   CT  CTCTT
                                   ||||  |||||   ||  |||||
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                                GGTT  GGGAG   GA  GAGGG
                                  GA    G___  GG
GAM409  CYP4A11  3'  GGGAGAAAAGCTGAGTGTTGG  5757      TG CT   AAC
                                CCAG  C  TCAG   TTTCTCTT
                                ||||  |  ||||   ||||||||
                                GGTT  G  AGTC   AAAGAGGG
                                  GT __    GA_
GAM409  CYP4F3   5'  GAGGAGGTTGTGTGGG      6116      T  G
                                CCT CA AACTTTCTC
                                ||| || |||||||||
                                GGG GT TTGGAGGAG
                                  T  G
GAM409  D1S155E  5'  GAGAGGGGGCGCTGAGCTGTTG 23124     GT_  CT    AA  TT
           G                     CCA   GC  TCAG  CT  CTCTT
                                |||   ||  ||||  ||  |||||
                                GGT   CG  AGTC  GG  GAGAG
                                  TGT  __    GC  GG
GAM409  DAG1     3'  GGGGGAGAGTTCTCTGTCCTAC 15281      CCTTC_
           TG                    CAGTG     AGAACTTTCTCTT
                                |||||     ||||||||||||
                                GTCAT     TCTTGAGAGGGGG
                                   CCTGTC
GAM409  DCTN1    5'  GGGAGGGGGCTAGGGTACTTGG 14554     _      C  AA
                                CCA GTGCCTT AG  CTTTCTC
                                ||| ||||||| ||  |||||||
                                GGT CATGGGA TC  GGGAGGG
                                  T     _ GG
GAM409  DES      3'  AAGAGGGAATCCCCGAAGGTGC 72121      TG    AGAAC_ TT
           TGG                   CCAG  CCTTC     T  CTCTT
                                ||||  |||||     |  |||||
                                GGTC  GGAAG     A  GAGAA
                                  GT    CCCCTA GG
GAM409  DES      3'  GAGAGAAAGTGGGTGAGATGCT 72127      GC   CAGA
           GG                    CCAGT  CTT    ACTTTCTCTT
                                |||||  |||   ||||||||||
                                GGTCG  GAG    TGAAAGAGAG
                                   TA   TGGG
GAM409  DES      3'  GAGGGAATCCCCGAAGGTGCTG 72128      TG    AGAACT
           G                     CCAG  CCTTC     TTCTCTT
                                ||||  |||||     |||||||
                                GGTC  GGAAG     AAGGGAG
                                  GT    CCCCT_
GAM409  DIO3     5'  AGATTTCTAGGGCATTGG     7241          C   CTT
                                CCAGTGCCTT AGAA   TCT
                                |||||||||| ||||   |||
                                GGTTACGGGA TCTT   AGA
                                      _    T__
GAM409  DLG4     5'  AAGAGGGGGCCAGGGTGTGTGG 7248      _ TG   CAGAA  TT
                                CCA G  CCTT    CT  CTCTT
                                ||| |  ||||    ||  |||||
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                                GGT T  GGGA    GG  GAGAA
                                  G GT   CC___  GG
GAM409  DMD    3' AAGAGGAAAAGCTAAGGACTGG 3663      G   C  AAC
                                CCAGT CCTT AG   TTTCTCTT
                                ||||| |||| ||   ||||||||
                                GGTCA GGAA TC   AAGGAGAA
                                  _   _ GAA
GAM409  DMD    3' AAGAGGAAAAGCTAAGGACTGG 14415     G   C  AAC
                                CCAGT CCTT AG   TTTCTCTT
                                ||||| |||| ||   ||||||||
                                GGTCA GGAA TC   AAGGAGAA
                                  _   _ GAA
GAM409  DMD    3' AAGAGGAAAAGCTAAGGACTGG 14422     G   C  AAC
                                CCAGT CCTT AG   TTTCTCTT
                                ||||| |||| ||   ||||||||
                                GGTCA GGAA TC   AAGGAGAA
                                  _   _ GAA
GAM409  DMD    3' AAGAGGAAAAGCTAAGGACTGG 14400     G   C  AAC
                                CCAGT CCTT AG   TTTCTCTT
                                ||||| |||| ||   ||||||||
                                GGTCA GGAA TC   AAGGAGAA
                                  _   _ GAA
GAM409  DMD    3' AAGAGGAAAAGCTAAGGACTGG 14405     G   C  AAC
                                CCAGT CCTT AG   TTTCTCTT
                                ||||| |||| ||   ||||||||
                                GGTCA GGAA TC   AAGGAGAA
                                  _   _ GAA
GAM409  DMD    3' AAGAGGAAAAGCTAAGGACTGG 14410     G   C  AAC
                                CCAGT CCTT AG   TTTCTCTT
                                ||||| |||| ||   ||||||||
                                GGTCA GGAA TC   AAGGAGAA
                                  _   _ GAA
GAM409  DMD    3' AAGAGGAAAAGCTAAGGACTGG 14356     G   C  AAC
                                CCAGT CCTT AG   TTTCTCTT
                                ||||| |||| ||   ||||||||
                                GGTCA GGAA TC   AAGGAGAA
                                  _   _ GAA
GAM409  DMD    3' AAGAGGAAAAGCTAAGGACTGG 14362     G   C  AAC
                                CCAGT CCTT AG   TTTCTCTT
                                ||||| |||| ||   ||||||||
                                GGTCA GGAA TC   AAGGAGAA
                                  _   _ GAA
GAM409  DMD    3' AAGAGGAAAAGCTAAGGACTGG 14367     G   C  AAC
                                CCAGT CCTT AG   TTTCTCTT
                                ||||| |||| ||   ||||||||
                                GGTCA GGAA TC   AAGGAGAA
                                  _   _ GAA
GAM409  DMD    3' AAGAGGAAAAGCTAAGGACTGG 14374     G   C  AAC
                                CCAGT CCTT AG   TTTCTCTT
                                ||||| |||| ||   ||||||||
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                                GGTCA GGAA TC   AAGGAGAA
                                  _   _ GAA
GAM409  DMD     3' AAGAGGAAAAGCTAAGGACTGG 14382      G   C  AAC
                                CCAGT CCTT AG   TTTCTCTT
                                ||||| |||| ||   ||||||||
                                GGTCA GGAA TC   AAGGAGAA
                                  _   _ GAA
GAM409  DMD     3' AAGAGGAAAAGCTAAGGACTGG 14387      G   C  AAC
                                CCAGT CCTT AG   TTTCTCTT
                                ||||| |||| ||   ||||||||
                                GGTCA GGAA TC   AAGGAGAA
                                  _   _ GAA
GAM409  DMD     3' AAGAGGAAAAGCTAAGGACTGG 14392      G   C  AAC
                                CCAGT CCTT AG   TTTCTCTT
                                ||||| |||| ||   ||||||||
                                GGTCA GGAA TC   AAGGAGAA
                                  _   _ GAA
GAM409  DMPK    5' AGGAGGGAGCTTGGGGGGCTGG 15322      G     AA  TT
                                CCAGT CCTTCAG  CT  CTCTT
                                ||||| |||||||  ||  |||||
                                GGTCG GGGGGTT  GA  GAGGA
                                  _     C_  GG
GAM409  DNAJB1  3' GGGAGGGAAGGGGAGTTGG   20447     TG   CAGAA
                                CCAG  CCTT    CTTTCTC
                                ||||  ||||    |||||||
                                GGTT  GGGG    GGGAGGG
                                  GA   AA___
GAM409  DRD5    3' GAGAGAAGAGAGTATGGTGCTG 5847      TG  TTCAGAAC
          G                      CCAG  CC      TTTCTCTT
                                ||||  ||      ||||||||
                                GGTC  GG      GAAGAGAG
                                  GT  TATGAGA_
GAM409  DSCR3   5' AGGAGGAAGGCGTGGGGCATT  20172       T  GAA
                                AGTGCCT CA   CTTTCTCTT
                                ||||||| ||   |||||||||
                                TTACGGG GT   GAAGGAGGA
                                   _ GCG
GAM409  DUSP5   3' GGAGGAGAAGGGTACT      15353        CAGAAC
                                AGTGCCTT     TTTCTCT
                                ||||||||     |||||||
                                TCATGGGA     GAGGAGG
                                   A_____
GAM409  DXYS155E 3' AGGAGAAGGAGCGCGCGCTGG  17449       CTTCAGAA
                                CCAGTGC      CTTTCTCTT
                                |||||||      |||||||||
                                GGTCGCG      GGAAGAGGA
                                   CGCGA___
GAM409  DYRK1A  5' GGAATTGGAGGCATTGG     55246          AACT
                                CCAGTGCCTTCAG   TTCT
                                ||||||||||||   ||||
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                              GGTTACGGAGGTT  AAGG
                                      ____
GAM409  E2F1    3' AGGGGAGGAGGGGTGTGGG  84793    G    CAGAA
                              CCA TGCCTT   CTTTCTCT
                              ||| ||||||   ||||||||
                              GGT GTGGGG   GGAGGGGA
                                _    A____
GAM409  EFNA3   3' GAGAGATGGGGCGGGGCTTGG 17067    T   CAGAA T
                              CCAG GCCTT   CT TCTCTT
                              |||| |||||   || ||||||
                              GGTT CGGGG   GG AGAGAG
                                _   CGG__ T
GAM409  EGFL4   3' GGGGGTGCTGGGGGCAGTGG  61818    G      A  TT
                              CCA TGCCTTCAG ACT  C
                              ||| ||||||||| |||  |
                              GGT ACGGGGGTC TGG  G
                                G       G  GG
GAM409  EGFL4   3' GGGGGTGGTGGGGGTGCTGG  61819    TG    GA  TT
                              CCAG  CCTTCA  ACT  C
                              ||||  ||||||  |||  |
                              GGTC  GGGGGT  TGG  G
                                GT    GG  GG
GAM409  EGFL5   5' GGAGGAAGGCAGCATTGG   86623      CTTCAGAA
                              CCAGTGC      CTTTCTCT
                              |||||||      ||||||||
                              GGTTACG      GAAGGAGG
                                  ACG_____
GAM409  EGLN3   3' GGGGAGGTGGAGTTGG    41972    TG TTCAGA
                              CCAG  CC    ACTTTCTC
                              ||||  ||    ||||||||
                              GGTT  GG    TGGAGGGG
                                GA  _______
GAM409  EGR3    3' GAGAGAAGGAACAAAGGTCTGG 59554    T   CAGAA
                              CCAG GCCTT   CTTTCTCTT
                              |||| |||||   |||||||||
                              GGTC TGGAA   GGAAGAGAG
                                _   ACAA_
GAM409  EIF4G1  5' GAGGGAGGGAGGGGCATTG  17070       CAGAA  TT
                              CAGTGCCTT   CT  CTC
                              |||||||||   ||  |||
                              GTTACGGGG   GA  GAG
                                   AGG__  GG
GAM409  EIF5A   3' GGGAGAAGGGGGGTGGGTGCTG 8768    TG  TCAGAA
                              CAG  CCT    CTTTCTCTT
                              |||  |||    |||||||||
                              GTC  GGG    GGAAGAGGG
                                GT  TGGG__
GAM409  EMP3    5' GAGAGAGAAAGGGTTCTGG  7448     T   CAGAA
                              CCAG GCCTT   CTTTCTC
                              |||| |||||   |||||||
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                                GGTC TGGGA    GAGAGAG
                                  T    AA___
GAM409  EMP3    5'  GGAGAAGGGCGGGGCACGG   7449    A     CAGAA
                                CC GTGCCTT    CTTTCTCT
                                || |||||||    ||||||||
                                GG CACGGGG    GGAAGAGG
                                 _     CG___
GAM409  EN1     5'  GGGGGAGGGACGCGGGTGCGG  7452    A TG   TCAGAA
                                CC G  CCT     CTTTCTCT
                                || |  |||     ||||||||
                                GG C  GGG     GGAGGGGG
                                 _ GT   CGCAG_
GAM409  ENPP3   3'  AGGGAAGGCAGGTGGTGG    17223    G    TCAGAA
                                CCA TGCCT     CTTTCTCT
                                ||| |||||     ||||||||
                                GGT GTGGA     GGAAGGGA
                                  G    C_____
GAM409  ENTPD1  5'  AGGGGAAGTTTTCCTTGG    8347    TTC_
                                CC    AGAACTTTCTCT
                                ||    ||||||||||||
                                GG    TTTTGAAGGGGA
                                 TTCC
GAM409  EPB49   3'  GAGAGGAATGAGGGGCATTGG  8787         _  GAA
                                CCAGTGCCT TCA   CTTTC
                                ||||||||| |||   |||||
                                GGTTACGGG AGT   GAGAG
                                      G   AAG
GAM409  ESRRG   3'  AGAGAAAATGGGTGTTGG    66386    TG   TCAGAAC
                                CCAG  CCT     TTTCTCT
                                ||||  |||     |||||||
                                GGTT  GGG     AAAGAGA
                                  GT   TA_____
GAM409  FABP2   3'  AGAGTTGGAGGGTTGG     3741     GT    AG
                                CCA  GCCTTC  AACTTT
                                |||  ||||||  ||||||
                                GGT  TGGGAG  TTGAGA
                                  __     G_
GAM409  FANCC   3'  GAGGGGGCCTTGACGGCGTTGG 70523        T   AA  TT
                                CCAGTGCC TCAG  CT  CTC
                                |||||||| ||||  ||  |||
                                GGTTGCGG AGTT  GG  GAG
                                     C    CC  GG
GAM409  FANCG   5'  AGGAGGACCTGGGGGTGTGG   16140    G       AA
                                CCA TGCCTTCAG  CTTTCT
                                ||| |||||||||  ||||||
                                GGT GTGGGGGTC  GGAGGA
                                  _       CA
GAM409  FGF2    5'  AGGAGGGAGGAGAACTGGGGGC 8866         AA___  TT
            GCGG                  GTGCCTTCAG    CT  CTCTT
                                ||||||||||    ||  |||||
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                                CGCGGGGGTC    GA  GAGGA
                                     AAGAG  GG
GAM409  FGFR1   5' AGGAGGGGGGCACAAGGTCTGG 5200      T    CAGAA  TT
                                CCAG GCCTT    CT  CTCTT
                                |||| |||||    ||  |||||
                                GGTC TGGAA    GG  GAGGA
                                  _    CACG_  GG
GAM409  FGFR1   5' AGGAGGGGGGCACAAGGTCTGG 43612     T    CAGAA  TT
                                CCAG GCCTT    CT  CTCTT
                                |||| |||||    ||  |||||
                                GGTC TGGAA    GG  GAGGA
                                  _    CACG_  GG
GAM409  FGFR1   5' AGGAGGGGGGCACAAGGTCTGG 43619     T    CAGAA  TT
                                CCAG GCCTT    CT  CTCTT
                                |||| |||||    ||  |||||
                                GGTC TGGAA    GG  GAGGA
                                  _    CACG_  GG
GAM409  FGFR1   5' AGGAGGGGGGCACAAGGTCTGG 43626     T    CAGAA  TT
                                CCAG GCCTT    CT  CTCTT
                                |||| |||||    ||  |||||
                                GGTC TGGAA    GG  GAGGA
                                  _    CACG_  GG
GAM409  FGFR1   5' AGGAGGGGGGCACAAGGTCTGG 43635     T    CAGAA  TT
                                CCAG GCCTT    CT  CTCTT
                                |||| |||||    ||  |||||
                                GGTC TGGAA    GG  GAGGA
                                  _    CACG_  GG
GAM409  FGFR1   5' AGGAGGGGGGCACAAGGTCTGG 31793     T    CAGAA  TT
                                CCAG GCCTT    CT  CTCTT
                                |||| |||||    ||  |||||
                                GGTC TGGAA    GG  GAGGA
                                  _    CACG_  GG
GAM409  FGFR4   5' AGGAGGAGCCAGGAAGGCAGTT 8891      _     AGAAC
          GG                      CCAG TGCCTTC    TTTCTCTT
                                |||| |||||||    ||||||||
                                GGTT ACGGAAG    GAGGAGGA
                                  G     GACC_
GAM409  FGFR4   5' AGGAGGAGCCAGGAAGGCAGTT 43351     _     AGAAC
          GG                      CCAG TGCCTTC    TTTCTCTT
                                |||| |||||||    ||||||||
                                GGTT ACGGAAG    GAGGAGGA
                                  G     GACC_
GAM409  FKRP    3' AGAGAAGGCTGGCATTGG    44182        TTCAGAA
                                CCAGTGCC      CTTTCTCT
                                ||||||||      ||||||||
                                GGTTACGG      GGAAGAGA
                                    TC_____
GAM409  FLNB    3' AGGAGAGGGGCGATTATGTGCT 62171     TG CTTCAGAA
          GG                      CCAG  C       CTTTCTCTT
                                ||||  |       |||||||||
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                                GGTC  G       GGGAGAGGA
                                  GT TATTAGCG
GAM409  FOLR1    5'  AGGAGAAGGTGGAGTGAGGGCT 33612     GT      GA__
              GG                  CCA  GCCTTCA    ACTTTCTCTT
                                  |||  |||||||   ||||||||||
                                  GGT  CGGGAGT    TGGAAGAGGA
                                    __      GAGG
GAM409  FPGS     3'  AAGAGAAGGTGGACCTGGCAGT 17079     G    TTCAGA
              GG                  CCA TGCC     ACTTTCTCTT
                                  ||| ||||     ||||||||||
                                  GGT ACGG     TGGAAGAGAA
                                    G   TCCAGG
GAM409  FXR2     5'  GGGGGAGTCGGAGGCGGTGG   16788     G      A  A  TT
                                  CCA TGCCTTC GA CT  CTC
                                  ||| ||||||| || ||  |||
                                  GGT GCGGAGG CT GA  GGG
                                    G      _ _  GG
GAM409  GAB2     3'  GGAGGAGGGCAGGGCTTGG   54455     T    CAGAA
                                  CCAG GCCTT    CTTTCTCT
                                  |||| |||||    ||||||||
                                  GGTT CGGGA    GGAGGAGG
                                    _    CG___
GAM409  GAB2     3'  GGAGGGAGTGTGGTGTGG    54456     G   TTCAGA   TT
                                  CCA TGCC     ACT  CTCT
                                  |||  ||||     |||  ||||
                                  GGT GTGG     TGA  GAGG
                                    _   TG____   GG
GAM409  GAB2     3'  GGAGGAGGGCAGGGCTTGG   24498     T    CAGAA
                                  CCAG GCCTT    CTTTCTCT
                                  |||| |||||    ||||||||
                                  GGTT CGGGA    GGAGGAGG
                                    _    CG___
GAM409  GAB2     3'  GGAGGGAGTGTGGTGTGG    24499     G   TTCAGA   TT
                                  CCA TGCC     ACT  CTCT
                                  |||  ||||     |||  ||||
                                  GGT GTGG     TGA  GAGG
                                    _   TG____   GG
GAM409  GATA4    3'  GGGGAAGCGGGTGTTGG     9007      TG   TCAGAA
                                  CCAG  CCT     CTTTCTC
                                  ||||  |||     |||||||
                                  GGTT  GGG     GAAGGGG
                                    GT   C_____
GAM409  GCN5L2   3'  AGAGCTTTGGAGGCTTGG    59838      T       A
                                  CCAG GCCTTCAGA CTTT
                                  |||| ||||||||| ||||
                                  GGTT CGGAGGTTT GAGA
                                    _       C
GAM409  GCNT1    3'  AGAGGGGACCAGGGTGGCTGG  7652       _    CAGAA
                                  CCAGT GCCTT    CTTTCT
                                  ||||| |||||    ||||||
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                                GGTCG TGGGA    GGGAGA
                                  G    CCAG_
GAM409  GDF5    3'  GAGAGAAGAGGAGAGGGCTTGG 5105      T    AGAA   _
                                CCAG GCCTTC   CTTT CTCTT
                                |||| ||||||   |||| |||||
                                GGTT CGGGAG   GAGA GAGAG
                                  _    AG__   A
GAM409  GDI1    5'  AGGAGGAGGAGCCGAGCGGGCG 59975        __ AGAA
          CTGG                    CAGTGCCT  TC   CTTTCTCTT
                                |||||||| ||   |||||||||
                                GTCGCGGG  AG   GGAGGAGGA
                                    CG  CCGA
GAM409  GDI1    3'  GGGAGATGGGGGGTTGG    59978    GT    AGAAC
                                CCA  GCCTTC    TTTCTC
                                |||  ||||||    ||||||
                                GGT  TGGGGG    AGAGGG
                                  __     GT___
GAM409  GDI1    3'  GGGGGAGTGGGGAAGGCTTGG  59979     T    AGA   TT
                                CCAG GCCTTC   ACT  CTC
                                |||| ||||||   |||  |||
                                GGTT CGGAAG   TGA  GGG
                                  _     GGG   GG
GAM409  GFAP    3'  GAGAGGGATGAGGTGCTGG   9014      TG   T  GAA
                                CCAG  CCT CA   CTTTCTC
                                ||||  ||| ||   |||||||
                                GGTC  GGA GT   GGGAGAG
                                  GT   _  A__
GAM409  GJB3    5'  AGGGAAGAGGAGGTGGTGG   43762    G     AGAAC
                                CCA TGCCTTC    TTTCTCT
                                ||| |||||||    |||||||
                                GGT GTGGAGG    GAAGGGA
                                  G      A____
GAM409  GLUL    3'  AGAGAAGGTAGGGGTTGG    9038      G   TCAGA
                                CCAGT CCT    ACTTTCTCT
                                ||||| |||    |||||||||
                                GGTTG GGA    TGGAAGAGA
                                  G  _____
GAM409  GOLGA4  5'  AAGAGGAGGAGTTAAAGGCATT 60068         C  AA
          GG                    CCAGTGCCTT AG  CTTTCTCTT
                                |||||||||| ||  |||||||||
                                GGTTACGGAA TT  GGAGGAGAA
                                    A  GA
GAM409  GPC1    3'  GGGAGGAGGACTTGGAGGGTCT 9104      TG     AA
          GG                    CCAG  CCTTCAG  CTTTCTCTT
                                ||||  |||||||  |||||||||
                                GGTC  GGAGGTT  GGAGGAGGG
                                  TG      CA
GAM409  GPC1    3'  GGGAGGGGTGGTGTGGTGTTGG 9105      TG  TT  GA   T
                                CCAG  CC  CA  ACTT CTCTT
                                ||||  ||  ||  |||| |||||
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                                GGTT  GG  GT  TGGG GAGGG
                                  GT  T_  GG   _
GAM409  GPR61    3'  AGGGGAGGGAACCTGGGTATGG 78908     G    TCAGAA
                                CCA TGCCT     CTTTCTCT
                                ||| |||||     ||||||||
                                GGT ATGGG     GGAGGGGA
                                  _    TCCAAG
GAM409  GPX4     5'  GAGGGGAGGAGCCGCTGG    9129        C    AGAA
                                CCAGTG CTTC    CTTTC
                                |||||| ||||    |||||
                                GGTCGC GAGG    GGGAG
                                   C   AG__
GAM409  GRLF1    3'  GGTACCTGCTGAGGGCGCTGG  78562            AACTTT
                                CCAGTGCCTTCAG     CT
                                ||||||||||||      ||
                                GGTCGCGGGAGTC     GG
                                       GTCCAT
GAM409  GRM6     3'  AAGGGAAAGTTTTCCTGCATT  5924       CTTC
                                AGTGC    AGAACTTTCTCTT
                                |||||    ||||||||||||
                                TTACG    TTTTGAAAGGGAA
                                   TCC_
GAM409  H1F0     3'  GAGGGGGAGTGGGCGGGCAGTG 18017     G    TCAGA   TT
           G                     CCA TGCCT    ACT  CTCTT
                                ||| |||||    |||  |||||
                                GGT ACGGG    TGA  GGGAG
                                  G    CGGG_   GG
GAM409  HCFC1    3'  AGGGAGGCTAGGGCAATGG    70988     G     C  AA  TT
                                CCA TGCCTT AG  CT  CT
                                ||| |||||| ||  ||  ||
                                GGT ACGGGA TC  GA  GA
                                  A     _  G_  GG
GAM409  HD       3'  AGGAGCTGGCTGGCAGGTGTTG 9180      TG  _    AA  TT
           G                     CCAG  CCT TCAG  CT  CTCTT
                                ||||  ||| ||||  ||  |||||
                                GGTT  GGA GGTC  GG  GAGGA
                                  GT   C    __  TC
GAM409  HDAC4    3'  AAGGCCTTGGGGGCACTGG   20102           AA
                                CCAGTGCCTTCAG  CTTT
                                ||||||||||||  ||||
                                GGTCACGGGGGTT  GGAA
                                       CC
GAM409  HDAC5    3'  GGAGGGGGCTGGGCGCTG    57610       TT   AA
                                CAGTGCC  CAG  CTTTCT
                                |||||||  |||  ||||||
                                GTCGCGG  GTC  GGGAGG
                                    __   GG
GAM409  HEXA     3'  GAGAGAAAGGGGCCGGTGCTGG 4975      TG  TTCAGAA
                                CCAG  CC      CTTTCTCTT
                                ||||  ||      |||||||||
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                                GGTC  GG      GAAAGAGAG
                                  GT  CCGGG__
GAM409  HIRA     3'  GGGGGAGGAGACACTGG     12439       C   CAGAA  TT
                                CCAGTG CTT     CT  CTC
                                |||||| |||     ||  |||
                                GGTCAC GAG     GA  GGG
                                   A  _____  GG
GAM409  HOXB3    5'  AAGGGCTGGAGGTGGTGG    9258      G        AA
                                CCA TGCCTTCAG  CTT
                                ||| |||||||||  |||
                                GGT GTGGAGGTC  GAA
                                  G        GG
GAM409  HOXD4    5'  GAGGGGAATGGGGTGCTGG   27524     TG   T  GAA
                                CCAG  CCT CA   CTTTC
                                ||||  ||| ||   |||||
                                GGTC  GGG GT   GGGAG
                                  GT   _  AAG
GAM409  HSF4     5'  GGGAGAGGGAGGGCACGG    59776    A       AGAA
                                CC GTGCCTTC    CTTTCTC
                                || ||||||||    |||||||
                                GG CACGGGAG    GAGAGGG
                                 _       G___
GAM409  HSPB2    3'  GGGGGAAGGGAAAGGTGCATGG 7743      _ TG    CAGAA
                                CCA G  CCTT     CTTTCTCTT
                                ||| |  ||||     |||||||||
                                GGT C  GGAA     GGAAGGGGG
                                  A GT    AG___
GAM409  HUNK     3'  GGGAGAAAGCTGAGGAGGCTTT 27459      T      AGAA
            GG                    CCAG GCCTTC    CTTTCTCTT
                                ||||| ||||||    |||||||||
                                GGTT CGGAGG    GAAAGAGGG
                                  T     AGTC
GAM409  HYAL1    5'  GGGGGCTGAGGGCCTGG     23608      T       AA
                                CCAG GCCTTCAG  CTT
                                |||| ||||||||  |||
                                GGTC CGGGAGTC  GGG
                                  _       GG
GAM409  HYOU1    3'  GGAGGAGGGTCAGGGCTGG   59652       G   TCA  A
                                CCAGT CCT   GA CTTTCTCT
                                ||||| |||   || ||||||||
                                GGTCG GGA   CT GGAGGAGG
                                  _  ____  G
GAM409  IGFBP5   5'  GGAGAAAAGAGGTGTTAGG   5192     _ TG    CAGAAC
                                CC AG  CCTT     TTTCTCT
                                || ||  ||||     |||||||
                                GG TT  GGAG     AAAGAGG
                                 A  GT    A_____
GAM409  IL22RA2  3'  GGAGAAGGACCGGTGTTGG   53693      TG  TTCAGAA
                                CCAG  CC      CTTTCTCT
                                ||||  ||      ||||||||
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                                GGTT  GG      GGAAGAGG
                                  GT  CCA____
GAM409  IL4R     3'  GAGAGTAGAGGGCACTGG    4701           AGA
                                CCAGTGCCTTC   ACTTTC
                                ||||||||||   ||||||
                                GGTCACGGGAG   TGAGAG
                                      A__
GAM409  IL6R     3'  AGAGGAGAGGGGCACAGG    5117     A     CAGAAC
                                CC GTGCCTT     TTTCTCT
                                || |||||||     |||||||
                                GG CACGGGG     GAGGAGA
                                 A      A_____
GAM409  INHA     5'  AGGGGAGAGTGGAAAGGCCCTG 9335      T    CAGA
             G                   CCAG GCCTT    ACTTTCTCTT
                                |||| |||||   ||||||||||
                                GGTC CGGAA    TGAGAGGGGA
                                  C     AGG_
GAM409  IRS2     3'  GGGAGGGAAGGGCTTTGG    59721      T    CAGAA
                                CCAG GCCTT    CTTTCTC
                                |||| |||||    |||||||
                                GGTT CGGGA    GGGAGGG
                                  T     A____
GAM409  ITPR2    5'  AGGAGGAGGAGCAAAGGTGTTG 9446       TG   CAGAA
             G                   CCAG  CCTT    CTTTCTCTT
                                ||||  ||||    |||||||||
                                GGTT  GGAA    GGAGGAGGA
                                  GT    ACGA_
GAM409  ITPR2    5'  GAGAGAGGGCGGCGAGGGCGCA 9449     A       AGAA
             GG                    CC GTGCCTTC    CTTTCTCTT
                                || ||||||||    |||||||||
                                GG CGCGGGAG    GGGAGAGAG
                                 A       CGGC
GAM409  JAM2     5'  AGGGGAAGAAAGGAGTTGG   41115      TG   CAGAA
                                CCAG  CCTT    CTTTCTCT
                                ||||  ||||    ||||||||
                                GGTT  GGAA    GAAGGGGA
                                  GA    A____
GAM409  KAI1     3'  GGAGGGGGCCGGGCGCGG    9501     A     TCAGAA  TT
                                CC GTGCCT     CT  CTCT
                                || ||||||     ||  ||||
                                GG CGCGGG     GG  GAGG
                                 _      CC_____  GG
GAM409  KCNAB2   3'  GGGAGAGGGAAAGGGTCTGG   13308      T    CAGAA
                                CCAG GCCTT    CTTTCTC
                                |||| |||||    |||||||
                                GGTC TGGGA    GAGAGGG
                                  _     AAGG_
GAM409  KCNN3    3'  GAGGGAGGGTTGTGTCAGGCTT 9559       T   T_  G
             GG                    CCAG GCCT  CA AACTTTCTCTT
                                |||| ||||  || ||||||||||
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                                GGTT CGGA  GT TTGGGAGGGAG
                                  _   CT  G
GAM409  KIT     3'  AGAGAGGGAGGTATGG     4039     G     AGAA
                                CCA TGCCTTC   CTTTCT
                                ||| |||||||   ||||||
                                GGT ATGGAGG   GAGAGA
                                  _     _____
GAM409  KPNB2   3'  GGGAGGGGCGGGAGGGAGGTGT 9631    TG    AGAA___     TT
          TG                     AG  CCTTC     CTTTCTC
                                || |||||     |||||||
                                TT  GGAGG     GGGAGGG
                                 GT    GAGGGCG
GAM409  KRT13   3'  AGGAGAGAGGAGGGGCTGCTGG 9640      _    CAGAA
                                CCAGT GCCTT    CTTTCTCTT
                                ||||| |||||    |||||||||
                                GGTCG CGGGG    GAGAGAGGA
                                   T    AG___
GAM409  LAMA4   5'  GAGAGGAGGTGGCCTAGCGCTG 9668       CTTCAGA
          G                     CCAGTGC      ACTTTCTCTT
                                |||||||      ||||||||||
                                GGTCGCG      TGGAGGAGAG
                                   ATCCGG_
GAM409  LAMB2   5'  AGGGAAGGGGTAGGGTTGG   9671     GT    CAGAA
                                CCA  GCCTT    CTTTCTCT
                                |||  |||||    ||||||||
                                GGT  TGGGA    GGAAGGGA
                                  __    TGG__
GAM409  LAMC3   5'  AGGGGAAGGCGGGTCCTGG   20225     TG   TCAGAA
                                CCAG  CCT     CTTTCTCT
                                ||||  |||     ||||||||
                                GGTC  GGG     GAAGGGGA
                                  CT   CG____
GAM409  LAMP1   3'  GAGGGGGTGGGGGTGCTG    18702     TG    AGA   TT
                                CAG  CCTTC   ACT  CTC
                                |||  |||||   |||  |||
                                GTC  GGGGG   TGG  GAG
                                  GT    ___   GG
GAM409  LASS2   5'  AAGAGGGAGGAGAGGCGCGG   67683    A      CAGAA  TT
                                CC GTGCCTT    CT  CTCTT
                                || |||||||    ||  |||||
                                GG CGCGGAG    GA  GAGAA
                                  _      AG___  GG
GAM409  LIF     3'  GGAGGAGGAGAGGCCTGG    9738      T    CAGAA
                                CCAG GCCTT    CTTTCTCT
                                |||| |||||    ||||||||
                                GGTC CGGAG    GGAGGAGG
                                  _    A____
GAM409  LMO4    3'  GGGAGGGGGAGGGAGCTGG   22254      G    AGAA
                                CCAGT CCTTC   CTTTCTC
                                ||||| |||||   |||||||
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                                GGTCG GGGAG    GGGAGGG
                                  A    G___
GAM409  LRP1     3'  AGGGAGAGTTCTTTGCTG    9796       CCTTC
                                CAGTG    AGAACTTTCTCT
                                |||||    ||||||||||||
                                GTCGT    TCTTGAGAGGGA
                                  T____
GAM409  LRP4     3'  AGGAGAGAACAACAGGGGCTGG 64441      G   TCAGAAC
                                CCAGT CCT      TTTCTCTT
                                ||||| |||      ||||||||
                                GGTCG GGA      AGAGAGGA
                                  G   CAACA__
GAM409  LTB4R    5'  AAGGGGAGGAAAGGGGGTGCTG 5639      TG    AGAA
              G                  CCAG  CCTTC   CTTTCTCTT
                                ||||  |||||   |||||||||
                                GGTC  GGGGG   GGAGGGGAA
                                  GT    AAA_
GAM409  LTB4R    3'  GGAGGAGCAGGGGCGTGG    5650     G    CAGAAC
                                CCA TGCCTT     TTTCTCT
                                ||| |||||||    |||||||
                                GGT GCGGGG     GAGGAGG
                                  _     AC_____
GAM409  LY64     3'  GGGAGGAAGCAGAGGGAGGGAC 18757      G    AGAA_
              TGG                  CCAGT CCTTC    CTTTCTCTT
                                ||||| |||||    |||||||||
                                GGTCA GGAGG    GAAGGAGGG
                                  G    GAGAC
GAM409  LZTR1    3'  AGAGAGAGCAGGAGCTGG    22230      G   TCAGAA
                                CCAGT CCT     CTTTCTCT
                                ||||| |||     ||||||||
                                GGTCG GGA     GAGAGAGA
                                  A   C_____
GAM409  MADH3    3'  GGGGAGGGCAGGCTTGG     19739      T   TCAGAA
                                CCAG GCCT     CTTTCTC
                                |||| ||||     |||||||
                                GGTT CGGA     GGAGGGG
                                  _   CG____
GAM409  MAGEA8   5'  AGAGAAGCGAGGGCCTGG    18105     T    AGAAC
                                CCAG GCCTTC    TTTCTCT
                                |||| ||||||    |||||||
                                GGTC CGGGAG    GAAGAGA
                                  _     C____
GAM409  MAML1    3'  AGGGGAGAAGGAGGCCACTGG  28587      _    AGAAC
                                CCAGTG CCTTC    TTTCTCTT
                                |||||| |||||    ||||||||
                                GGTCAC GGAGG    AGAGGGGA
                                  C    A____
GAM409  MAP2     5'  AGGAGAAATAACAAGGCATTG  48993        CAGAAC
                                CAGTGCCTT     TTTCTCTT
                                |||||||||     ||||||||
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                                GTTACGGAA     AAAGAGGA
                                     CAAT__
GAM409  MAP2K1   5' GGGAGGAAGCGAGAGGTGCTG 10858    TG   CAGAA
                                CAG  CCTT    CTTTCTCTT
                                |||  ||||    |||||||||
                                GTC  GGAG    GAAGGAGGG
                                  GT   AGC__
GAM409  MAP3K5   3' AAGGGAGAGGAGAAAGGCGCTG 19802        CAGAA
                                CAGTGCCTT    CTTTCTCTT
                                |||||||||    |||||||||
                                GTCGCGGAA    GAGAGGGAA
                                     AGAG_
GAM409  MAP3K7IP1 3' GGGAGAGGTGAGGACTGG    20380      G   CAGAA
                                CCAGT CCTT    CTTTCTC
                                ||||| ||||    |||||||
                                GGTCA GGAG    GAGAGGG
                                   _   TG___
GAM409  MAP4K5   5' GGGAGGAGGACGCGGGTGCGG 21655    A TG   TCAGAA
                                CC G  CCT     CTTTCTCTT
                                || |  |||     |||||||||
                                GG C  GGG     GGAGGAGGG
                                 _ GT   CGCA__
GAM409  MAPK14   5' GGGAGAGGGTGCGGGTGCAGG  57339    A TG   TCAGA
                                CC G  CCT     ACTTTCTCTT
                                || |  |||     ||||||||||
                                GG C  GGG     TGGGAGAGGG
                                 A GT   CG___
GAM409  MAPK14   5' GGGAGAGGGTGCGGGTGCAGG  57345    A TG   TCAGA
                                CC G  CCT     ACTTTCTCTT
                                || |  |||     ||||||||||
                                GG C  GGG     TGGGAGAGGG
                                 A GT   CG___
GAM409  MAPK14   5' GGGAGAGGGTGCGGGTGCAGG  57334    A TG   TCAGA
                                CC G  CCT     ACTTTCTCTT
                                || |  |||     ||||||||||
                                GG C  GGG     TGGGAGAGGG
                                 A GT   CG___
GAM409  MAPK14   5' GGGAGAGGGTGCGGGTGCAGG  7160     A TG   TCAGA
                                CC G  CCT     ACTTTCTCTT
                                || |  |||     ||||||||||
                                GG C  GGG     TGGGAGAGGG
                                 A GT   CG___
GAM409  MAPK8IP1 3' GGGAGGGACAGGGCTTGG     18406      T     CAGAA
                                CCAG GCCTT    CTTTCTC
                                |||| |||||    |||||||
                                GGTT CGGGA    GGGAGGG
                                   _    CA___
GAM409  MAPRE3   3' GAGGGGGGCTTGGGGGCATGG  24666     G        AA  TT
                                CCA TGCCTTCAG  CT  CTC
                                ||| |||||||||  ||  |||
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                                GGT ACGGGGGTT  GG  GAG
                                  _       CG  GG
GAM409  MB      3'  AGGAGGAGCTGAGGGGCTGG   18114      G      AA
                                CCAGT CCTTCAG  CTTTCT
                                ||||| |||||||  ||||||
                                GGTCG GGGAGTC  GGAGGA
                                  _      GA
GAM409  MET     5'  GAGAGGAGGCGGGGAGGCGCGG 71269    A       AGAA
                                CC GTGCCTTC    CTTTCTCTT
                                || ||||||||    |||||||||
                                GG CGCGGAGG    GGAGGAGAG
                                  _      GGC_
GAM409  MGA     3'  GGGAGAAAGGGGGTAGGGTGCT 62809     TG    CAGAA
            G                    CAG  CCTT    CTTTCTCTT
                                |||  ||||    |||||||||
                                GTC  GGGA    GAAAGAGGG
                                  GT    TGGGG
GAM409  MGEA5   3'  GAGAGAAGGTTTTTAGGT    24211      TC
                                GCCT  AGAACTTTCTCTT
                                ||||  ||||||||||||
                                TGGA  TTTTGGAAGAGAG
                                  T_
GAM409  MGEA5   5'  GAGGGAGAGCTCGGGGCTTGG  24212      T    TC  AA  TT
                                CCAG GCCT  AG  CT  CTC
                                |||| ||||  ||  ||  |||
                                GGTT CGGG  TC  GA  GAG
                                  _   GC  GA  GG
GAM409  MLLT7   3'  GGGAGAGGGTTTTTCTCACTG  19864      CCTTC
                                CAGTG    AGAACTTTCTCTT
                                |||||    ||||||||||||
                                GTCAC    TTTTGGGAGAGGG
                                   TCT__
GAM409  MLLT7   3'  GGGAGAGTACATTGAAGGCCTG 19865      T      A__      TT
            G                    CCAG GCCTTCAG   ACTTTCTC
                                |||| ||||||||   ||||||||
                                GGTC CGGAAGTT   TGAGAGGG
                                  _       ACA
GAM409  MLLT7   3'  GGGAGCTTGGCTGAGGGTCTGG 19866      T      AACT_
                                CCAG GCCTTCAG    TTCTC
                                |||| ||||||||    |||||
                                GGTC TGGGAGTC    GAGGG
                                  _       GGTTC
GAM409  MMP14   3'  AGGGGAAATGGGGTGAACGGTG 17167     TG  _   GAAC_
            CTGG                   CAG  CC TTCA    TTTCTCTT
                                |||  || ||||    ||||||||
                                GTC  GG AAGT    AAAGGGGA
                                  GT  C    GGGGT
GAM409  MRPL49  3'  AGGAGGAGGGAGGTGGGTGTTG 69565      TG   TCAGAA
            G                    CCAG  CCT     CTTTCTCTT
                                ||||  |||     |||||||||
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                                GGTT GGG    GGAGGAGGA
                                  GT  TGGAG_
GAM409  MRPL49   3' AGGAGGGAGGTGGGTGTTGG 69566    TG  TCAGAA TT
                                CCAG CCT    CT CTCTT
                                |||| |||    || |||||
                                GGTT GGG    GA GAGGA
                                  GT  TG____ GG
GAM409  MTR      5' GAGAGAGGCCCTAGGGCGCTG 4211       C AA_    TT
                                CAGTGCCTT AG  CTTTCTC
                                ||||||||| ||  |||||||
                                GTCGCGGGA TC  GAGAGAG
                                     _ CCG
GAM409  MUC4     3' GAGGGGCTCCTGGGGGTCTGG 56327    T      AAC TT
                                CCAG GCCTTCAG  T CTC
                                |||| ||||||||  |  |||
                                GGTC TGGGGGTC  G GAG
                                  _      CTC GG
GAM409  MYCBP    3' AGGGGAAGAGGGGTGCTG   24693    TG   CAGAA
                                CAG CCTT   CTTTCTCT
                                |||  ||||   ||||||||
                                GTC GGGG   GAAGGGGA
                                 GT   A____
GAM409  MYO15A   3' GGAGGAGGCAGGAGTTGG   32672    TG  TCAGAA
                                CCAG CCT    CTTTCTCT
                                |||| |||    ||||||||
                                GGTT GGA    GGAGGAGG
                                  GA  C_____
GAM409  MYO1D    3' AGGAGGAGGGCCTGGGTTTGG 71764    T  TT  AA
                                CCAG GCC CAG CTTTCTCTT
                                |||| |||  |||  |||||||||
                                GGTT TGG GTC GGAGGAGGA
                                  _  __  CG
GAM409  NEUD4    3' AGGGGGAAGCCGAGAGGGGGCT 16194     G   AGAA
          GG                    CCAGT CCTTC   CTTTCTCTT
                                ||||| |||||   |||||||||
                                GGTCG GGGAG   GAAGGGGGA
                                  G    AGCC
GAM409  NEURL    3' GGAGGGAGCGGGGGGCTGG   14860    G  TCAGAA TT
                                CCAGT CCT    CT CTCT
                                ||||| |||    || ||||
                                GGTCG GGG    GA GAGG
                                  G  C_____ GG
GAM409  NLGN3    3' AGGAGAAAGGGGCTAGCACTGG 38597      CTTC AA_
                                CCAGTGC   AG  CTTTCTCTT
                                |||||||   ||  |||||||||
                                GGTCACG   TC  GAAAGAGGA
                                   A___ GGG
GAM409  NPDC1    3' GGGAGGGGCAGGGCCTGG   31173    T   CAGAA
                                CCAG GCCTT    CTTTCTC
                                |||| |||||    |||||||
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                                GGTC CGGGA    GGGAGGG
                                  _    CG___
GAM409  NRXN1   5'  GAGAGAGGGCGGGGTTATTGG  16631      _   CAGAA
                                CCAGTG CCTT    CTTTCTC
                                |||||| ||||    |||||||
                                GGTTAT GGGG    GAGAGAG
                                   T   CGG__
GAM409  NRXN2   3'  AGAGGGAGCAAGGCATTG    57007       CAGAA  TT
                                CAGTGCCTT    CT  CTCT
                                |||||||||    ||  ||||
                                GTTACGGAA    GA  GAGA
                                     C____  GG
GAM409  NRXN2   3'  AGAGGGAGCAAGGCATTG    57018       CAGAA  TT
                                CAGTGCCTT    CT  CTCT
                                |||||||||    ||  ||||
                                GTTACGGAA    GA  GAGA
                                     C____  GG
GAM409  NRXN2   3'  AGAGGGAGCAAGGCATTG    30621       CAGAA  TT
                                CAGTGCCTT    CT  CTCT
                                |||||||||    ||  ||||
                                GTTACGGAA    GA  GAGA
                                     C____  GG
GAM409  NYX     3'  GGGGGAAAGTTTGCTTAACTGG 42603     GCCTTCA
                                CCAGT      GAACTTTCTCTT
                                |||||      ||||||||||||
                                GGTCA      TTTGAAAGGGGG
                                   ATTCG__
GAM409  OGDH    3'  GAGGGAGAGGAGGGGCTGG   91108     G    AGAA  TT
                                CCAGT CCTTC    CT  CTC
                                ||||| |||||    ||  |||
                                GGTCG GGAGG    GA  GAG
                                   G    A___  GG
GAM409  PACSIN1 3'  GAGAGGGTGCGGGGGCTTGG  92260     T     AGA
                                CCAG GCCTTC   ACTTTCTC
                                |||| ||||||   ||||||||
                                GGTT CGGGGG   TGGGAGAG
                                  _     CG_
GAM409  PAK4    5'  GAGGGAGGCGCGAGGGCGCGG  19687    A      AGAA  TT
                                CC GTGCCTTC    CT  CTC
                                || ||||||||    ||  |||
                                GG CGCGGGAG    GA  GAG
                                  _      CGCG  GG
GAM409  PBX2    3'  GGGGGGGTGGGAGGCATGG   10446     G     AGA   TT
                                CCA TGCCTTC   ACT  CTC
                                ||| |||||||   |||  |||
                                GGT ACGGAGG   TGG  GGG
                                  _     G__  GG
GAM409  PCDHGA1 3'  GAGGGGCCTCTGTGGGTGCTGG 38284     TG   T    AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
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                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGA10  3'  GAGGGGCCTCTGTGGGTGCTGG 38291     TG   T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGA11  3'  GAGGGGCCTCTGTGGGTGCTGG 38298     TG   T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGA11  3'  GAGGGGCCTCTGTGGGTGCTGG 49462     TG   T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGA12  3'  GAGGGGCCTCTGTGGGTGCTGG 13594     TG   T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGA2   5'  AGGGGGTGGAGGTTTGG    49266     T    AGA   TT
                                CCAG GCCTTC   ACT  CT
                                |||| ||||||   |||  ||
                                GGTT TGGAGG   TGG  GA
                                  _    ___   GG
GAM409  PCDHGA2   5'  AGGGGGTGGAGGTTTGG    38302     T    AGA   TT
                                CCAG GCCTTC   ACT  CT
                                |||| ||||||   |||  ||
                                GGTT TGGAGG   TGG  GA
                                  _    ___   GG
GAM409  PCDHGA2   3'  GAGGGGCCTCTGTGGGTGCTGG 38308     TG   T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGA3   3'  GAGGGGCCTCTGTGGGTGCTGG 38315     TG   T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGA4   3'  GAGGGGCCTCTGTGGGTGCTGG 38322     TG   T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGA5   3'  GAGGGGCCTCTGTGGGTGCTGG 38329     TG   T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
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                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGA6  3'  GAGGGGCCTCTGTGGGTGCTGG 38336    TG  T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGA7  3'  GAGGGGCCTCTGTGGGTGCTGG 38343    TG  T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGA8  3'  GAGGGGCCTCTGTGGGTGCTGG 49454    TG  T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGA9  3'  GAGGGGCCTCTGTGGGTGCTGG 38350    TG  T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGB1  3'  GAGGGGCCTCTGTGGGTGCTGG 38357    TG  T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGB2  3'  GAGGGGCCTCTGTGGGTGCTGG 38364    TG  T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGB3  3'  GAGGGGCCTCTGTGGGTGCTGG 38371    TG  T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGB4  3'  GAGGGGCCTCTGTGGGTGCTGG 13601    TG  T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGB5  3'  GAGGGGCCTCTGTGGGTGCTGG 38378    TG  T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T   CC GG
GAM409  PCDHGB6  3'  GAGGGGCCTCTGTGGGTGCTGG 38385    TG  T   AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
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                                GGTC  GGG GTCT  G  GAG
                                  GT   T    CC GG
GAM409  PCDHGB7  3'  GAGGGGCCTCTGTGGGTGCTGG 38392     TG   T    AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T    CC GG
GAM409  PCDHGC3  3'  GAGGGGCCTCTGTGGGTGCTGG 50518     TG   T    AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T    CC GG
GAM409  PCDHGC3  3'  GAGGGGCCTCTGTGGGTGCTGG 10455     TG   T    AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T    CC GG
GAM409  PCDHGC4  3'  GAGGGGCCTCTGTGGGTGCTGG 38399     TG   T    AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T    CC GG
GAM409  PCDHGC5  3'  GAGGGGCCTCTGTGGGTGCTGG 38406     TG   T    AC TT
                                CCAG  CCT CAGA  T  CTC
                                ||||  ||| ||||  |  |||
                                GGTC  GGG GTCT  G  GAG
                                  GT   T    CC GG
GAM409  PEA15    3'  GGGGAGGGCTGGCTGCTGG   13653      _  TTC  AA  TT
                                CCAGT GCC   AG  CT  CT
                                ||||| |||   ||  ||  ||
                                GGTCG CGG   TC  GA  GG
                                  T   ___  GG  GG
GAM409  PFKFB4   3'  GAGGGGAGTTAGGAGTTGCTGG 15868      GC    AG    TT T
                                CCAGT  CTTC  AACT  C CTT
                                |||||  ||||  ||||  | |||
                                GGTCG  GAGG  TTGA  G GAG
                                  TT    A_    GG _
GAM409  PIK3CG   5'  GGGAGGAAAAGGGAGGGCACGG 10587    A       AGAAC
                                CC GTGCCTTC     TTTCTCTT
                                || ||||||||     ||||||||
                                GG CACGGGAG     AAGGAGGG
                                 _       GGAA_
GAM409  PIK3R3   5'  AAGATTTGGAGGCGGTGG    61045     G        A
                                CCA TGCCTTCAGA CTT
                                ||| |||||||||| |||
                                GGT GCGGAGGTTT GAA
                                  G         A
GAM409  PIK4CB   3'  GTACTGAGGGTACTGG      10594             A
                                CCAGTGCCTTCAG AC
                                |||||||||||| ||
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                                GGTCATGGGAGTC TG
                                       A
GAM409  PIP5K1A  3'  AGGGGAAGAAGGGGGCCTGG  13055     T     AGAA
                                CCAG GCCTTC   CTTTCTCT
                                |||| ||||||   ||||||||
                                GGTC CGGGGG   GAAGGGGA
                                  _     AA__
GAM409  PK428    5'  GAGGGAAGGCGGGGGAGGGCTG 13209      G    AGAA
           G                     CCAGT CCTTC   CTTTCTCTT
                                |||||| |||||   |||||||||
                                GGTCG GGAGG   GGAAGGGAG
                                  _    GGGC
GAM409  PKDREJ   3'  GAGAAACAAGGGCTGG      20277      G   CAGAAC
                                CCAGT CCTT     TTTCTC
                                ||||| ||||     ||||||
                                GGTCG GGAA     AAAGAG
                                  _   C_____
GAM409  PKM2     3'  AGGGGCCTTAGGGCACTGG   10601         C  AA
                                CCAGTGCCTT AG  CTTT
                                |||||||||| ||  ||||
                                GGTCACGGGA TC  GGGA
                                      T  CG
GAM409  PLAB     5'  GGAGAGCCAGGAGGAGCTGG  65855      G    AGAA
                                CCAGT CCTTC   CTTTCT
                                ||||| |||||   ||||||
                                GGTCG GGAGG   GAGAGG
                                   A    ACC_
GAM409  PNUTL2   3'  AAGGGAGAGAAGATTGGCGCTG 54419        T_  AGAA
           G                     CCAGTGCC  TC   CTTTCTCTT
                                ||||||||  ||   |||||||||
                                GGTCGCGG  AG   GAGAGGGAA
                                     TT  AA__
GAM409  PPARBP   3'  GGGAGGGGGGTGGGAGGGGTGT 16490    A TG  _  AGAA  TT
           AGG                     CC G  CCT TC   CT  CTCTT
                                || |  ||| ||   ||  |||||
                                GG T  GGG AG   GG  GAGGG
                                 A GT   G  GGTG  GG
GAM409  PPP1CC   5'  GGGGAAAGCAGTCATTGG    73588       C  TCAGAA
                                CCAGTG CT     CTTTCTCT
                                |||||| ||     ||||||||
                                GGTTAC GA     GAAAGGGG
                                   T  C_____
GAM409  PPP2R5B  3'  GGGGGAGACGAGGAGAGGCAAT 20710     G    _  AGAA_  TT   TT
           GG                     CCA TGCCT TC     CT  CTC
                                ||| ||||| ||     ||  |||
                                GGT ACGGA AG     GA  GGG
                                  A    G  GAGCA  GG
GAM409  PPP2R5B  3'  GGGGGAGGGGGAGGGCACAGG  20711    A       AGAA
                                CC GTGCCTTC   CTTTCTCT
                                || ||||||||   ||||||||
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                                GG CACGGGAG   GGAGGGGG
                                 A      GG__
GAM409  PPP2R5E  5' AGGAGAGAGAAAGGGGCATTG 20721        CAGAA
                                CAGTGCCTT    CTTTCTCTT
                                |||||||||    |||||||||
                                GTTACGGGG    GAGAGAGGA
                                     AAA__
GAM409  PREB     3' AGAGCCTGGAGGCACTG     25409          AACTTT
                                CAGTGCCTTCAG     CTCT
                                ||||||||||||     ||||
                                GTCACGGAGGTC     GAGA
                                      C_____
GAM409  PRKACA   3' GGGGGGGTGGGAGGGTTGG   10792    GT     AGA   TT
                                CCA  GCCTTC   ACT  CTC
                                |||  ||||||   |||  |||
                                GGT  TGGGAG   TGG  GGG
                                  __     GG_   GG
GAM409  PRKRA    5' AGGAGGTGGCGGCGCTGG    13494        T  AGA
                                CCAGTGCC TC   ACTTTCT
                                |||||||| ||   |||||||
                                GGTCGCGG GG   TGGAGGA
                                     C  ___
GAM409  PRV1     3' GGGAGGTAGGCTGGGGGCCTGG 73533      T       AA  T
                                CCAG GCCTTCAG  CT TCTCTT
                                |||| ||||||||  || ||||||
                                GGTC CGGGGGTC  GA GGAGGG
                                  _       G_  T
GAM409  PRX      3' AGGAGGAGGAAGAGGGCAGTGG 40516     G      AGAA
                                CCA TGCCTTC    CTTTCTCTT
                                ||| |||||||    |||||||||
                                GGT ACGGGAG    GGAGGAGGA
                                  G      AA__
GAM409  PSA      3' AAGAGAAAGTTGATTGGTTGG  40954     GT   T_   GA
                                CCA  GCC  TCA  ACTTTCTCTT
                                |||  |||  |||  ||||||||||
                                GGT  TGG  AGT  TGAAAGAGAA
                                  __   TT   __
GAM409  PSA      3' AAGAGAAAGTTGATTGGTTGG  54192     GT   T_   GA
                                CCA  GCC  TCA  ACTTTCTCTT
                                |||  |||  |||  ||||||||||
                                GGT  TGG  AGT  TGAAAGAGAA
                                  __   TT   __
GAM409  PSCD4    3' AAGGGAGAGTTTCGTGCACTG  25398       CTTCA
                                CAGTGC    GAACTTTCTCTT
                                ||||||    ||||||||||||
                                GTCACG    TTTGAGAGGGAA
                                   TGC__
GAM409  PSCD4    3' AGGAGGGCCGCCTGGAGGCAGT 25400     G        AACT
             GG                   CCA TGCCTTCAG    TTCTCTT
                                ||| |||||||||    |||||||
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                                GGT ACGGAGGTC    GGGAGGA
                                  G        CGCC
GAM409   PSMD9    3'  TTCTGGCAGGTACTGG      10992          _
                                CCAGTGCCT TCAGAA
                                ||||||||| ||||||
                                GGTCATGGA GGTCTT
                                     C
GAM409   PTBP1    3'  GAGAGAGGCAGGGGGCCTGG   11006      T     AGAA
                                CCAG GCCTTC    CTTTCTC
                                |||| ||||||    |||||||
                                GGTC CGGGGG    GAGAGAG
                                  _     ACG_
GAM409   PTBP1    3'  GAGAGAGGCAGGGGGCCTGG   49251      T     AGAA
                                CCAG GCCTTC    CTTTCTC
                                |||| ||||||    |||||||
                                GGTC CGGGGG    GAGAGAG
                                  _     ACG_
GAM409   PTPN6    3'  AAGAGGAAGTGAGCGGTGCTG  54510     TG _   AGA
                                CAG  CC TTC   ACTTTCTCTT
                                |||  || |||   ||||||||||
                                GTC  GG GAG   TGAAGGAGAA
                                  GT  C  ___
GAM409   RAB26    3'  GAGGGAGGGCTGGGGCTGG    26824     GT    T   AA  TT
                                CCA  GCCT CAG  CT  CTC
                                |||  |||| |||  ||  |||
                                GGT  CGGG GTC  GA  GAG
                                  __   _  GG  GG
GAM409   RANBP3   3'  AGGAGGAGGTCCCCTGGGCACA 13256    A     TCAGA
           GG                     CC GTGCCT     ACTTTCTCTT
                                || ||||||     ||||||||||
                                GG CACGGG     TGGAGGAGGA
                                 A     TCCCC
GAM409   REG1A    5'  AAGAGAAACATTTGAAGGTGTG 88848      G         AC
           G                      CCA TGCCTTCAGA  TTTCTCTT
                                ||| ||||||||||  ||||||||
                                GGT GTGGAAGTTT  AAAGAGAA
                                  _         AC
GAM409   RENBP    5'  GGGGGAGGGTGAGCCGGGCGCG 11285    A     TCAGA
           G                      CC GTGCCT     ACTTTCTCTT
                                || ||||||     ||||||||||
                                GG CGCGGG     TGGGAGGGGG
                                  _     CCGAG
GAM409   RENT1    5'  GAGGGGAGCTGAGGCGCGG    11288    A     T   AAC TT
                                CC GTGCCT CAG   T  CTC
                                || |||||| |||   |  |||
                                GG CGCGGA GTC   G  GAG
                                  _     _  GA_ GG
GAM409   RGS3     3'  AGAGAGGCCCAGGCTACTGG   35055       _    TCAGAA
                                CCAGT GCCT      CTTTCT
                                ||||| ||||     ||||||
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                                GGTCA CGGA     GAGAGA
                                   T    CCCG__
GAM409   RGS3     3'  AGAGAGGCCCAGGCTACTGG   40859      _    TCAGAA
                                CCAGT GCCT     CTTTCT
                                ||||| ||||     ||||||
                                GGTCA CGGA     GAGAGA
                                   T    CCCG__
GAM409   RGS3     3'  AGAGAGGCCCAGGCTACTGG   55443      _    TCAGAA
                                CCAGT GCCT     CTTTCT
                                ||||| ||||     ||||||
                                GGTCA CGGA     GAGAGA
                                   T    CCCG__
GAM409   RGS3     3'  AGAGAGGCCCAGGCTACTGG   56220      _    TCAGAA
                                CCAGT GCCT     CTTTCT
                                ||||| ||||     ||||||
                                GGTCA CGGA     GAGAGA
                                   T    CCCG__
GAM409   RGS3     3'  AGAGAGGCCCAGGCTACTGG   57821      _    TCAGAA
                                CCAGT GCCT     CTTTCT
                                ||||| ||||     ||||||
                                GGTCA CGGA     GAGAGA
                                   T    CCCG__
GAM409   RGS3     3'  AGAGAGGCCCAGGCTACTGG   57824      _    TCAGAA
                                CCAGT GCCT     CTTTCT
                                ||||| ||||     ||||||
                                GGTCA CGGA     GAGAGA
                                   T    CCCG__
GAM409   ROM1     5'  GGGAGGATGCTCAGGGTATTGG 4384          C  AACT
                                CCAGTGCCTT AG    TTCTCTT
                                |||||||||| ||    |||||||
                                GGTTATGGGA TC    AGGAGGG
                                      C  GT__
GAM409   RP42     5'  GGGGGGGAGAGGCCTGG     40203      T    CAGAA  TT
                                CCAG GCCTT     CT  CTC
                                |||| |||||    ||  |||
                                GGTC CGGAG     GG  GGG
                                  _    A____  GG
GAM409   RXRA     3'  GAGAGAGGGGCTCAGGAACTGG 11411       G   TCA  A_
                                CCAGT CCT   GA  CTTTCTCTT
                                ||||| |||   ||  |||||||||
                                GGTCA GGA   CT  GGGAGAGAG
                                   A  ___  CG
GAM409   RYR3     5'  GGGGGAAGCAGAGGCGCCGG   6416     A      CAGAA
                                CC GTGCCTT     CTTTCTCT
                                || |||||||    ||||||||
                                GG CGCGGAG     GAAGGGGG
                                 C      AC___
GAM409   S100A10  5'  AGGGGGAGGAGACAGGGCTGG  59321       G  _  AGAA  TT
                                CCAGT CCT TC    CT  CTCT
                                ||||| ||| ||    ||  ||||
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                                GGTCG GGA AG    GA  GGGA
                                  _  C  AG__  GG
GAM409  SACM1L   3'  AGAGGAGGATGAGGTCTGG   25818     T   T  GAA
                                CCAG GCCT CA   CTTTCTCT
                                |||| |||| ||   ||||||||
                                GGTC TGGA GT   GGAGGAGA
                                  _   _  A__
GAM409  SCN1B    3'  GGGAGGGGGCAGGGGGCTTGG  6418      T     AGAA  TT
                                CCAG GCCTTC    CT  CTCTT
                                |||| ||||||    ||  |||||
                                GGTT CGGGGG    GG  GAGGG
                                  _     AC__  GG
GAM409  SEPN1    3'  AGGAGAAAGGAGGGGCAGTGG  66359     G     CAGAA
                                CCA TGCCTT     CTTTCTCTT
                                ||| ||||||     |||||||||
                                GGT ACGGGG     GAAAGAGGA
                                  G     AG___
GAM409  SEPX1    5'  GAGGGGAGGTGGACGCGGGTAC 32915    A     TCAGA_
            CGG                   CC GTGCCT     ACTTTCTCTT
                                || ||||||     ||||||||||
                                GG CATGGG     TGGAGGGGAG
                                 C     CGCAGG
GAM409  SERPINF2 3'  GGAGGAGGGCAGGCATCGG   6257     A     TCAGAA
                                CC GTGCCT     CTTTCTCT
                                || ||||||     ||||||||
                                GG TACGGA     GGAGGAGG
                                 C     CG____
GAM409  SHANK2   3'  GGGAGGGAGTTTTTCTAACATG 24588     _ GCCTTC     TT
            G                    CCA GT     AGAACT  CTCTT
                                ||| ||     ||||||  |||||
                                GGT CA     TTTTGA  GAGGG
                                  A  ATCT__     GG
GAM409  SHB      3'  GGGGGCTGGAGGCCTGG     11643      T       AA
                                CCAG GCCTTCAG  CTT
                                |||| ||||||||  |||
                                GGTC CGGAGGTC  GGG
                                  _       GG
GAM409  SHOX     3'  AAGGGGATAAAAGAGGGCACGG 4829     A       AGAACT
                                CC GTGCCTTC     TTCTCTT
                                || ||||||||     |||||||
                                GG CACGGGAG     AGGGGAA
                                  _       AAAAT_
GAM409  SIAT4C   3'  AGGAGGGCAGGGGCATTGG   20784          CAGAA
                                CCAGTGCCTT    CTTTCT
                                ||||||||||    ||||||
                                GGTTACGGGG    GGAGGA
                                      ACG__
GAM409  SIAT4C   3'  GGGAGGGAGTTCTGGGCCTGG  20787     T  TT      TT
                                CCAG GCC  CAGAACT  CTCTT
                                |||| |||  |||||||  |||||
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                                GGTC CGG  GTCTTGA  GAGGG
                                  _  __      GG
GAM409  SLC16A2  5'  AAGGGAGCTGGGGGAGGCAGTG 21497     G      AGAACT
           G                     CCA TGCCTTC     TTCTCTT
                                 ||| |||||||     |||||||
                                 GGT ACGGAGG     GAGGGAA
                                   G      GGGTC_
GAM409  SLC16A2  5'  GGGAGGAAGAGGTGGGGGGTGT 21503     G      AGAA_
           GG                    CCA TGCCTTC     CTTTCTCTT
                                 ||| |||||||     |||||||||
                                 GGT GTGGGGG     GAAGGAGGG
                                   _      GTGGA
GAM409  SLN      5'  GGGAGGGAGAAGGAGTTGG    11771      TG     AGAA
                                 CCAG  CCTTC    CTTTCTC
                                 ||||  |||||    |||||||
                                 GGTT  GGAAG    GGGAGGG
                                   GA     A___
GAM409  SOST     3'  AGGAGAGGGTCCGAGGGTGGTG 47467     G      A  A
           G                     CCA TGCCTTC GA CTTTCTCTT
                                 ||| ||||||| || |||||||||
                                 GGT GTGGGAG CT GGGAGAGGA
                                   G      C  _
GAM409  SOX10    3'  GAGGGGAAGCACCAGGGTTGG  22686     GT     CAGAA
                                 CCA  GCCTT    CTTTCTCTT
                                 |||  |||||    |||||||||
                                 GGT  TGGGA    GAAGGGGAG
                                   __     CCAC_
GAM409  SPAG8    3'  GAGAGGAGGAAAGCAGGCATT  24902        TCAGAA
                                 AGTGCCT     CTTTCTCTT
                                 |||||||     |||||||||
                                 TTACGGA     GGAGGAGAG
                                     CGAAA_
GAM409  SPR      3'  AGGAGAGAGGTTATGGGTATTG 11931          TCAGAA
           G                     CCAGTGCCT     CTTTCTCTT
                                 |||||||||     |||||||||
                                 GGTTATGGG     GAGAGAGGA
                                     TATTG_
GAM409  SRC      3'  AAGAGGAACCAGGAGAAGGGCT 18282       G     AGAAC_
           GG                    CCAGT CCTTC     TTTCTCTT
                                 |||||  |||||     ||||||||
                                 GGTCG GGAAG     AAGGAGAA
                                   _     AGGACC
GAM409  SURF6    3'  GAGGGAGACTGGGGCCTGG    22189      T    T   AA  TT
                                 CCAG GCCT CAG  CT  CTC
                                 ||||  |||| |||  ||  |||
                                 GGTC CGGG GTC  GA  GAG
                                   _    _   A_  GG
GAM409  TACSTD2  5'  GAGAGAAATCAAGGGAGGGCTG 9858        G     AGAAC
           G                     CCAGT CCTTC     TTTCTCTT
                                 |||||  |||||     ||||||||
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                                GGTCG GGAGG    AAAGAGAG
                                  _    GAACT
GAM409  TACSTD2  5' AGGGAGGGCTGGGGCTGG   9853     GT   T  AA  TT
                                CCA  GCCT CAG  CT  CT
                                |||  |||| |||  ||  ||
                                GGT  CGGG GTC  GA  GA
                                 __   _  GG  GG
GAM409  TARBP2   5' GGGAGAGAGGGGGGCGCGG   56160    A      AGAA
                                CC GTGCCTTC   CTTTCTC
                                || ||||||||   |||||||
                                GG CGCGGGGGG   GAGAGGG
                                 _      A___
GAM409  TARBP2   5' GGGAGAGAGGGGGGCGCGG   56168    A      AGAA
                                CC GTGCCTTC   CTTTCTC
                                || ||||||||   |||||||
                                GG CGCGGGGGG   GAGAGGG
                                 _      A___
GAM409  TBXA2R   3' AGGGGCTGGGGGGTGCTGG   6481      TG     AA
                                CCAG  CCTTCAG  CTT
                                ||||  |||||||  |||
                                GGTC  GGGGGTC  GGA
                                  GT      GG
GAM409  TCAP     3' AGGAGAAGGGACAAAAGGTACT 13397         CAGAA
           GG                    CCAGTGCCTT    CTTTCTCTT
                                ||||||||||    |||||||||
                                GGTCATGGAA    GGAAGAGGA
                                     AACAG
GAM409  TGM2     3' GAGAGGGGACTGGGGGACTGG  16053      G      AA
                                CCAGT CCTTCAG  CTTTCTC
                                |||||  |||||||  |||||||
                                GGTCA GGGGGTC  GGGAGAG
                                  _      AG
GAM409  TGT      3' AGGGAGGGAGGGGCTGG    48310      G    AGAA  TT
                                CCAGT CCTTC   CT  CT
                                |||||  |||||   ||  ||
                                GGTCG GGAGG   GA  GA
                                  G    ____  GG
GAM409  TIMM17A  3' GGTTTTGAGGATATTGG    20936       C
                                CCAGTG CTTCAGAACT
                                ||||||  ||||||||||
                                GGTTAT GGAGTTTTGG
                                   A
GAM409  TIMP3    3' GGGGGAGAATGGGAGGCTTGG  4512      T     AGAA  TT
                                CCAG GCCTTC   CT  CTC
                                ||||  ||||||   ||  |||
                                GGTT CGGAGG   GA  GGG
                                  _     GTAA  GG
GAM409  TK1      3' AGGAGGAAGTCGGGAGGCGTGG 12303     G      A  A
                                CCA TGCCTTC GA CTTTCTCTT
                                ||| ||||||| || |||||||||
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                                GGT GCGGAGG CT GAAGGAGGA
                                  _     G  _
GAM409  TNFRSF10C 3'  GAGGGCGGGGGGCGCTGG    13862          AGAA
                                CCAGTGCCTTC   CTTTC
                                ||||||||||   |||||
                                GGTCGCGGGGG   GGGAG
                                      GC__
GAM409  TNXB    5'  GGGAGGGAAAGGCCCTGG    50640     T    CAGAA
                                CCAG GCCTT    CTTTCTC
                                |||| |||||    |||||||
                                GGTC CGGAA    GGGAGGG
                                  C    A____
GAM409  TRIM9   5'  AGAGAGAGGCTGGGCGCGG   30747    A    TT   AA
                                CC GTGCC  CAG  CTTTCTCT
                                || |||||  |||  ||||||||
                                GG CGCGG  GTC  GAGAGAGA
                                 _    __   G_
GAM409  TRPC5   5'  AGAGTTTCAGGGCACTGG    24996         CA
                                CCAGTGCCTT  GAACTTT
                                ||||||||||  |||||||
                                GGTCACGGGA  TTTGAGA
                                      C_
GAM409  TRPC5   3'  AGGAGGAGGTTTTGAAG     24997
                                CTTCAGAACTTTCTCTT
                                |||||||||||||||||
                                GAAGTTTTGGAGGAGGA

GAM409  TRPV1   3'  GGGTGGTTTGGGGGTGTTGG  38094     TG      A  TT
                                CCAG  CCTTCAGA CT  CTC
                                ||||  |||||||| ||  |||
                                GGTT  GGGGGTTT GG  GGG
                                  GT       _  T_
GAM409  TRPV1   3'  GGGTGGTTTGGGGGTGTTGG  54877     TG      A  TT
                                CCAG  CCTTCAGA CT  CTC
                                ||||  |||||||| ||  |||
                                GGTT  GGGGGTTT GG  GGG
                                  GT       _  T_
GAM409  TRPV1   3'  GGGTGGTTTGGGGGTGTTGG  54811     TG      A  TT
                                CCAG  CCTTCAGA CT  CTC
                                ||||  |||||||| ||  |||
                                GGTT  GGGGGTTT GG  GGG
                                  GT       _  T_
GAM409  TRPV1   3'  GGGTGGTTTGGGGGTGTTGG  54844     TG      A  TT
                                CCAG  CCTTCAGA CT  CTC
                                ||||  |||||||| ||  |||
                                GGTT  GGGGGTTT GG  GGG
                                  GT       _  T_
GAM409  TTN     3'  GGAGAAAGTTTCTTATGG    55921    TTC   _
                                CC   AGAA CTTTCTCT
                                ||   |||| ||||||||
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                              GG   TCTT GAAAGAGG
                               TAT    T
GAM409  TTN     3'  GGAGAAAGTTTCTTATGG    55939    TTC   _
                              CC   AGAA CTTTCTCT
                              ||   |||| ||||||||
                              GG   TCTT GAAAGAGG
                               TAT    T
GAM409  TTN     3'  GGAGAAAGTTTCTTATGG    55951    TTC   _
                              CC   AGAA CTTTCTCT
                              ||   |||| ||||||||
                              GG   TCTT GAAAGAGG
                               TAT    T
GAM409  TULP1   3'  GGAGGGGGTAGGTGATGG    12432    GT   TCAGA   TT
                              CCA  GCCT    ACT  CTCT
                              |||  ||||    |||  ||||
                              GGT  TGGA    TGG  GAGG
                                AG   _____  GG
GAM409  UMPK    3'  GGAGGGGTCAGGAGGCACTG   25011         A  A
                              CAGTGCCTTC GA CTTTCT
                              |||||||||| || ||||||
                              GTCACGGAGG CT GGGAGG
                                    A  G
GAM409  VANGL2  3'  GAGGGGGTGGGAGGGGGCTTGG 71649     _ G    AGA   TT
                              CCA GT CCTTC   ACT  CTC
                              ||| || |||||   |||  |||
                              GGT CG GGGAG   TGG  GAG
                                T  G    GG_  GG
GAM409  VIL2    3'  AGGGAAAGTTTTGTTCTG    12597    TGCCTT
                              CAG     CAGAACTTTCTCT
                              |||     ||||||||||||
                              GTC     GTTTTGAAAGGGA
                                TT____
GAM409  WBSCR1  3'  GGGAGGGAATGGGGCGTGG   49261    G    T  GAA
                              CCA TGCCT CA   CTTTCTC
                              ||| ||||| ||   |||||||
                              GGT GCGGG GT   GGGAGGG
                                _    _  AA_
GAM409  WBSCR1  3'  GGGAGGGAATGGGGCGTGG   42229    G    T  GAA
                              CCA TGCCT CA   CTTTCTC
                              ||| ||||| ||   |||||||
                              GGT GCGGG GT   GGGAGGG
                                _    _  AA_
GAM409  WHSC1L1 5'  AAGGGAAAGTTAAGGATGCTGG 43517       _   CAG
                              CCAGTG CCTT   AACTTTCTCTT
                              |||||| ||||  ||||||||||
                              GGTCGT GGAA   TTGAAAGGGAA
                                 A   ___
GAM409  WHSC1L1 5'  AAGGGAAAGTTAAGGATGCTGG 35026       _   CAG
                              CCAGTG CCTT   AACTTTCTCTT
                              |||||| ||||  ||||||||||
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                                GGTCGT GGAA   TTGAAAGGGAA
                                   A   ___
GAM409  WNT5A    5'  GAGAGGGGTCAGGGGGTGCGG  12666    A TG    A  A
                                CC G  CCTTC GA CTTTCTC
                                || |  ||||| || |||||||
                                GG C  GGGGG CT GGGAGAG
                                 _ GT    A  G
GAM409  WNT7A    5'  AGGGAGGGGCGGGGGCTGG   16118      G   TCAGAA
                                CCAGT CCT     CTTTCTCT
                                ||||| |||     ||||||||
                                GGTCG GGG     GGGAGGGA
                                   G   CG____
GAM409  ZNF179   3'  GGGAGGCAGCATCTGGGGGCAG 23104     G        A_  T
           TGG                     CCA TGCCTTCAGA  CT TCTCTT
                                ||| ||||||||||  || ||||||
                                GGT ACGGGGGTCT  GA GGAGGG
                                  G         AC  C
GAM409  ZNF198   5'  GAGGGGAGGTTCGTTCCGCG   12906     CTTCA
                                TGC     GAACTTTCTCTT
                                |||     ||||||||||||
                                GCG     CTTGGAGGGGAG
                                  CCTTG
GAM409  ZNF217   3'  GGGGAAAAAAGGTCTTGG     21518      T    CAGAAC
                                CCAG GCCTT     TTTCTCT
                                |||| |||||     |||||||
                                GGTT TGGAA     AAAGGGG
                                  C     A_____
GAM409  A4GALT   3'  GAGAGGAGAGGAGGCTGTTGG  33837     GT_     AGAAC
                                CCA   GCCTTC    TTTCTCTT
                                |||   ||||||    ||||||||
                                GGT   CGGAGG    GAGGAGAG
                                  TGT     A____
GAM409  AAMP     3'  AAGAGGAGGGTGGGGCCCTGG  6559       T    CAGAA
                                CCAG GCCTT    CTTTCTCTT
                                |||| |||||    |||||||||
                                GGTC CGGGG    GGAGGAGAA
                                  C     TG___
GAM409  ABCA8    3'  AGGAGGAGGTTCGGGTGCTGG  23148      TG   TCA
                                CCAG  CCT   GAACTTTCTCTT
                                ||||  |||  ||||||||||||
                                GGTC  GGG   CTTGGAGGAGGA
                                  GT   ___
GAM409  ADIR     3'  GAGGTGTTTGAGGGTGTGG    42331     G        ACTT
                                CCA TGCCTTCAGA    TCTC
                                ||| ||||||||||    ||||
                                GGT GTGGGAGTTT    GGAG
                                  _         GT__
GAM409  AF053356_CDS3 5'  AAGAGGAAAGGTCTTGGGGGCC 43750     T      GA   __
           CTGG                    CAG GCCTTCA  ACT  TTCTCTT
                                ||| |||||||  |||  |||||||
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                                GTC CGGGGGT  TGG  AGGAGAA
                                  C      TC   AA
GAM409  AGPAT1   5'  GGGAGGGAGGGAGGGTGCTGG  21151     TG    AGAA  TT
                                CCAG  CCTTC    CT  CTCTT
                                ||||  |||||    ||  |||||
                                GGTC  GGGAG    GA  GAGGG
                                  GT    G___  GG
GAM409  ALS2CR3  3'  GTTCTGAGGGGTTGG      30484      G
                                CCAGT CCTTCAGAAC
                                ||||| ||||||||||
                                GGTTG GGGAGTCTTG
                                   _
GAM409  AMOT     3'  GAGGGAAGTGGGGGGTGTTAGG 55720    _  TG    AGAAC
                                CC AG  CCTTC    TTTCTCTT
                                || ||  |||||    ||||||||
                                GG TT  GGGGG    GAAGGGAG
                                 A  GT    GT___
GAM409  AMOTL2   3'  GGGAGGGAGTGGCTGTGTTGG  32484     TG CTTC  A_   TT
                                CCAG  C    AG  ACT  CTCTT
                                ||||  |    ||  |||  |||||
                                GGTT  G    TC  TGA  GAGGG
                                  GT _____  GG   GG
GAM409  APCL     5'  AGGGGAGGGGATGAGGGGGCAC 19662     _      AGAA_
           CTGG                   CAG TGCCTTC    CTTTCTCTT
                                ||| |||||||    |||||||||
                                GTC ACGGGGG    GGGAGGGGA
                                  C      AGTAG
GAM409  APELIN   3'  GGAGGGGAGGGTGCTGG     33785      TG    AGAA
                                CCAG  CCTTC    CTTTCT
                                ||||  |||||    ||||||
                                GGTC  GGGAG    GGGAGG
                                  GT    _____
GAM409  APOL3    3'  AGGGAGGAGAGGGGACTGG    26811      G    AGAA  TT
                                CCAGT CCTTC    CT  CT
                                ||||| |||||    ||  ||
                                GGTCA GGGAG    GA  GA
                                   G     AG__  GG
GAM409  APOL4    3'  AGGGAGGAGAGGGGACTGG    47622      G    AGAA  TT
                                CCAGT CCTTC    CT  CT
                                ||||| |||||    ||  ||
                                GGTCA GGGAG    GA  GA
                                   G     AG__  GG
GAM409  ARHGAP9  5'  AGGAGGTGGTGGTATTGG     50676        TTCAGA
                                CCAGTGCC      ACTTTCT
                                ||||||||      |||||||
                                GGTTATGG      TGGAGGA
                                    TGG___
GAM409  ARHGDIG  3'  GGAGGGGCCTGGGGGTCTGG   6780       T       AA
                                CCAG GCCTTCAG  CTTTCT
                                |||| ||||||||  ||||||
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                                GGTC TGGGGGTC  GGGAGG
                                  _      CG
GAM409  ARTN     5'  GGGGAGAGCCCAGCACTGG   54041       CTTCAGAA
                                CCAGTGC      CTTTCTCT
                                |||||||      ||||||||
                                GGTCACG      GAGAGGGG
                                   ACCC____
GAM409  BET3     3'  GAGGGAGGAAGGGCTGG    26963      G    AGAA  TT
                                CCAGT CCTTC   CT  CTC
                                ||||| |||||   ||  |||
                                GGTCG GGAAG   GA  GAG
                                  _   _____ GG
GAM409  BRD2     5'  AAGGGGAGGCGGGGAGAGAGTG 17533    TG ___    AGAA
           CTGG                   AG  C   CTTC   CTTTCTCTT
                                || |   ||||   |||||||||
                                TC  G   GAGG   GGAGGGGAA
                                 GT AGA   GGC_
GAM409  BRD2     5'  GGGAGAGAGTGCTGGAGGCTCT 17537     T      A
           GG                     CCAG GCCTTCAG ACTTTCTCTT
                                |||| |||||||| ||||||||||
                                GGTC CGGAGGTC TGAGAGAGGG
                                  T       G
GAM409  BRUNOL6  3'  AGGGGAACCAGCAGAGGGCGTT 53428          AGAACT
           GG                     CCAGTGCCTTC     TTCTCTT
                                ||||||||||     |||||||
                                GGTTGCGGGAG     AAGGGGA
                                      ACGACC
GAM409  C1orf17  3'  GGGAGGTGGCTGGGGTGCTGG  68216     TG  T  A_
                                CCAG  CCT CAG  ACTTTCT
                                ||||  ||| |||  |||||||
                                GGTC  GGG GTC  TGGAGGG
                                  GT   _  GG
GAM409  C1orf2   5'  AGGAGAAAGGACGGGGCCTTGG 21680     T    CAGAA
                                CCAG GCCTT    CTTTCTCTT
                                |||| |||||    |||||||||
                                GGTT CGGGG    GAAAGAGGA
                                  C    CAG__
GAM409  C1orf2   5'  AGGAGAAAGGACGGGGCCTTGG 94621     T    CAGAA
                                CCAG GCCTT    CTTTCTCTT
                                |||| |||||    |||||||||
                                GGTT CGGGG    GAAAGAGGA
                                  C    CAG__
GAM409  C1orf34  5'  GGGGGAAAGGGGCCAGAGTGTT 60679     TG _  TCAGAA
           GG                     CCAG  C CT     CTTTCTCTT
                                ||||  | ||     |||||||||
                                GGTT  G GA     GAAAGGGGG
                                  GT A  CCGGG_
GAM409  C20orf161 3'  GGGAGGCTGCAGAGGGTGCTGG 53071     TG    AGAAC
                                CCAG  CCTTC    TTTCTC
                                ||||  |||||    ||||||
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                                GGTC  GGGAG    GGAGGG
                                  GT    ACGTC
GAM409  C20orf162 5'  AGGAGGACACTGAAGGCCTGG  54597     T      AACT
                                CCAG GCCTTCAG    TTCTCTT
                                |||| ||||||||    |||||||
                                GGTC CGGAAGTC    AGGAGGA
                                  _       AC__
GAM409  C20orf27  3'  AGGGAGAGGGAGGGCCTGG    35382     T     AGAA
                                CCAG GCCTTC    CTTTCTCT
                                |||| ||||||    ||||||||
                                GGTC CGGGAG    GAGAGGGA
                                  _     G___
GAM409  C20orf28  3'  GAGAGGAAGGGGTGAGGCGTGG 31223     G    T  GAA
                                CCA TGCCT CA   CTTTCTCTT
                                ||| ||||| ||   |||||||||
                                GGT GCGGA GT   GAAGGAGAG
                                  _    _ GGG
GAM409  C20orf45  3'  AGGATTTGGGGGCGGTGG    32106     G        A
                                CCA TGCCTTCAGA CTT
                                ||| |||||||||| |||
                                GGT GCGGGGGTTT GGA
                                  G        A
GAM409  C20orf67  3'  AGGAGGAGCCCCAGGGGTGCT  42067    TG    CAGAAC
                                AG  CCTT     TTTCTCTT
                                ||  ||||     ||||||||
                                TC  GGGG     GAGGAGGA
                                 GT    ACCCC_
GAM409  C20orf72  3'  GGGGGGGGGGGGGCGTGG     53497     G      AGAA  TT
                                CCA TGCCTTC    CT  CTC
                                ||| |||||||    ||  |||
                                GGT GCGGGGG    GG  GGG
                                  _      _____ GG
GAM409  C22orf2   5'  GAGAAGGGAGCACTGG      94455        CTTCAGAA
                                CCAGTGC       CTTTCTC
                                |||||||       |||||||
                                GGTCACG       GGAAGAG
                                    AG_______
GAM409  CACNA1H   5'  GGGGGCGGAGGCGCTGG     40844          AGAA  TT
                                CCAGTGCCTTC    CT  C
                                ||||||||||    ||  |
                                GGTCGCGGAGG    GG  G
                                       C___  GG
GAM409  CACNA1H   5'  GGGGGCGGAGGCGCTGG     40845          AGAA  TT
                                CCAGTGCCTTC    CT  C
                                ||||||||||    ||  |
                                GGTCGCGGAGG    GG  G
                                       C___  GG
GAM409  CALN1     3'  AGGGGGGAGGGGACTGG     48855       G    AGAA  TT
                                CCAGT CCTTC    CT  CT
                                ||||| |||||    ||  ||
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                                GGTCA GGGAG   GG  GA
                                  G    ____  GG
GAM409  CALN1    3'  GGGGGAGGGGACTGGGACTGG  48874      G  TT   AA
                                CCAGT CC  CAG  CTTTCTCTT
                                ||||| ||  |||  |||||||||
                                GGTCA GG  GTC  GGGAGGGGG
                                  _ __   AG
GAM409  CARHSP1  3'  GGGAGGAGGCAGCAGACACTGG 26707       C  TCAGAA
                                CCAGTG CT     CTTTCTCTT
                                |||||| ||     |||||||||
                                GGTCAC GA     GGAGGAGGG
                                   A  CGAC__
GAM409  CAT56    3'  GAGGGAGGGGTGAGAGCTGTTG 47515     GT_  C   GAA  TT   TT
          G                      CCA   GC TTCA   CT  CTC
                                |||   || ||||   ||  |||
                                GGT   CG GAGT   GA  GAG
                                  TGT  A    GGG  GG
GAM409  CBX6     3'  GGGGCATTGAAGGCCTGG    26621      T       AA
                                CCAG GCCTTCAG  CTTT
                                |||| ||||||||  ||||
                                GGTC CGGAAGTT  GGGG
                                  _       AC
GAM409  CDH24    3'  GGGGGGGGGCAGCGGGCACAGG 94932    A     TCAGAA  TT
                                CC GTGCCT     CT  CTCT
                                || ||||||     ||  ||||
                                GG CACGGG     GG  GGGG
                                 A     CGACG_  GG
GAM409  CECR6    3'  GAGGGAGGGCTTGGGTGCCTGG 49088      T  _  TC  AA  TT
                                CCAG GC CT  AG  CT  CTC
                                |||| || ||  ||  ||  |||
                                GGTC CG GG  TC  GA  GAG
                                  _ T  GT  GG  GG
GAM409  CECR6    3'  GGAGGAGAGGGGTGCTGG    49091      TG    CAGAAC
                                CCAG  CCTT     TTTCTCT
                                ||||  ||||     |||||||
                                GGTC  GGGG     GAGGAGG
                                  GT    A_____
GAM409  CECR6    3'  GTTTTGGGGGCTTGG       49092      T
                                CCAG GCCTTCAGAAC
                                |||| ||||||||||
                                GGTT CGGGGGTTTTG
                                  _
GAM409  CENTG1   3'  GAGGGAGGGTTTAGTACATGG  28709     _    CTTCA
                                CCA GTGC     GAACTTTCTCTT
                                ||| ||||     ||||||||||||
                                GGT CATG     TTTGGGAGGGAG
                                  A   A____
GAM409  CEZANNE  3'  AGGGGAAGGTTTGGTGTGTGG  39512     _ TG  TTCA
                                CCA G  CC    GAACTTTCTCTT
                                ||| |  ||    ||||||||||||
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                                GGT T  GG    TTTGGAAGGGGA
                                  G GT  ____
GAM409  CG018    3'  GAGAGAAGTGGTGGGGGGGCAT 53392          AGA  __
             TG                   CAGTGCCTTC   ACT  TTCTCTT
                                  ||||||||||   |||  |||||||
                                  GTTACGGGGG   TGG  AAGAGAG
                                       GG_   TG
GAM409  CKLF1    5'  GAGGGAAAGTGCTGCTGCTGG  33771       CCTT   A
                                  CCAGTG    CAG ACTTTCTCTT
                                  ||||||    ||| ||||||||||
                                  GGTCGT    GTC TGAAAGGGAG
                                     C___   G
GAM409  CKLF1    5'  GAGGGAAAGTGCTGCTGCTGG  32885       CCTT   A
                                  CCAGTG    CAG ACTTTCTCTT
                                  ||||||    ||| ||||||||||
                                  GGTCGT    GTC TGAAAGGGAG
                                     C___   G
GAM409  CLDN4    3'  AGGGGAGGGGCGAAGGTGCTG  7134      TG    AGAA
                                  CAG  CCTTC    CTTTCTCTT
                                  |||  |||||    |||||||||
                                  GTC  GGAAG    GGGAGGGGA
                                    GT    CG__
GAM409  CLSTN1   3'  ACTGCTAGTTCTGAGGACACTG 30102       C         TTCTCTT
             G                    CCAGTG CTTCAGAACT
                                  |||||| ||||||||||
                                  GGTCAC GGAGTCTTGA
                                     A         TCGTCAG
GAM409  CNR2     3'  AGAGAGAGAGGGGTCTTGG   8453       T    CAGAA
                                  CCAG GCCTT     CTTTCTCT
                                  |||| |||||     ||||||||
                                  GGTT TGGGG     GAGAGAGA
                                    C    A____
GAM409  COLEC12  3'  GAGAGAGAGCCACTGG      47867       C  TCAGAA
                                  CCAGTG CT     CTTTCTC
                                  |||||| ||     |||||||
                                  GGTCAC GA     GAGAGAG
                                     C _______
GAM409  COVA1    3'  GAGAGGATGGAGGTTTGG    73260      T     GAA
                                  CCAG GCCTTCA   CTTTC
                                  |||| |||||||   |||||
                                  GGTT TGGAGGT   GAGAG
                                    _      AG_
GAM409  CRF      3'  GGGGGAGGGGGGGAGTTGG    21936     TG    AGAA  TT
                                  CCAG  CCTTC    CT  CTC
                                  ||||  |||||    ||  |||
                                  GGTT  GGGGG    GA  GGG
                                    GA     _____  GG
GAM409  CRF      3'  GGGGGGAGTTGGGGGCTGG   21937      G   TCAG    TT
                                  CCAGT CCT    AACT  CTCT
                                  ||||| |||    ||||  ||||
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                                GGTCG GGG   TTGA  GGGG
                                  G  ____   GG
GAM409  CSEN     3'  AGGGGGGAGAGGGGGTAATGG  25528    G     AGAA  TT
                                CCA TGCCTTC   CT  CTCTT
                                ||| |||||||   ||  |||||
                                GGT ATGGGGG   GA  GGGGA
                                  A     A___  GG
GAM409  CSPG5    3'  AGAGGAAGCGGGGGTAGTGG   21654    G    CAGAA
                                CCA TGCCTT    CTTTCTCT
                                ||| ||||||    ||||||||
                                GGT ATGGGG    GAAGGAGA
                                  G    C____
GAM409  CTNNBIP1 3'  AGGGGCCTGGAGGTCTGG    39660     T      AA
                                CCAG GCCTTCAG  CTTT
                                |||| ||||||||  ||||
                                GGTC TGGAGGTC  GGGA
                                  _      CG
GAM409  CTRP5    5'  GAGAGGGAGCGAACCAGGACTG 31595      G   TCAGAA  TT
           G                     CCAGT CCT     CT  CTCTT
                                |||||| |||     ||  |||||
                                GGTCA GGA     GA  GAGAG
                                  _  CCAAGC  GG
GAM409  CTRP5    5'  GGAGAAGCGCGGGGGCTGG   31596      G   TCAGAAC
                                CCAGT CCT      TTTCTCT
                                ||||| |||      |||||||
                                GGTCG GGG      GAAGAGG
                                  G  CGC____
GAM409  CX46.6   3'  AGGGGGAGTGGGGCATTG    39941        CAGA   TT
                                CAGTGCCTT   ACT  CTCT
                                |||||||||   |||  ||||
                                GTTACGGGG   TGA  GGGA
                                     ____   GG
GAM409  D21S2056E 3'  GGGAGGGAAGGGCGGCACTGG  13474        T  AGAA
                                CCAGTGCC TC   CTTTCTC
                                |||||||| ||   |||||||
                                GGTCACGG GG   GGGAGGG
                                    C  GAA_
GAM409  DKFZP434A1319 5'  GGAGGGGGCCCGGGGTTGG   49551    GT    CAGAA  TT
                                CCA  GCCTT    CT  CTCT
                                |||  |||||    ||  ||||
                                GGT  TGGGG    GG  GAGG
                                  __    CCC__  GG
GAM409  DKFZp434K1210 5'  AGGAGGAAGACGTGGGTTTGG  34273     T   TCAGAA
                                CCAG GCCT     CTTTCTCTT
                                |||| ||||     |||||||||
                                GGTT TGGG     GAAGGAGGA
                                  _   TGCA__
GAM409  DKFZp434O0320 3'  GGGAGAGGGGCTGGGCATGG  83695    G   TT  AA_
                                CCA TGCC  CAG   CTTTCTC
                                ||| ||||  |||   |||||||
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                                GGT ACGG  GTC   GAGAGGG
                                  _   __   GGG
GAM409  DKFZP434P0111 3'  GGGGGGGAGGGGGTGTGG    67372     G      AGAA  TT
                                CCA TGCCTTC    CT  CTC
                                ||| |||||||    ||  |||
                                GGT GTGGGGG    GG  GGG
                                  _      A___  GG
GAM409  DKFZp547D155 3'  GGGAGAAAACGGGAGGTGCT   70436    TG    AGAAC
                                AG  CCTTC     TTTCTCTT
                                ||  |||||     ||||||||
                                TC  GGAGG     AAAGAGGG
                                 GT    GCA__
GAM409  DKFZP564D166 3'  GAGAGGAGATCAGAGAGAGTGC 47677     TG _  _  A  A   T
           TGG                    CAG  C CT TC GA CTT CTCTT
                                ||| | || || || ||| |||||
                                GTC  G GA AG CT GAG GAGAG
                                  GT A  G  A  A  _
GAM409  DKFZP564K2062 3'  AAGAGAAAGGCAAAGAGGTGTG 31235     G     CAGAA
           G                     CCA TGCCTT     CTTTCTCTT
                                ||| ||||||     |||||||||
                                GGT GTGGAG     GAAAGAGAA
                                  _      AAACG
GAM409  DKFZP586C1619 5'  AGGAGGAGTACAACGAGGAGCT 61932       G    CAGAAC
           GG                     CCAGT CCTT      TTTCTCTT
                                ||||| ||||     ||||||||
                                GGTCG GGAG     GAGGAGGA
                                   A    CAACAT
GAM409  DKFZp586H0623 3'  AAGAGGAACAGAGGTGCTG    34063     TG    CAGAAC
                                CAG  CCTT     TTTCTCTT
                                |||  ||||     ||||||||
                                GTC  GGAG     AAGGAGAA
                                  GT    AC____
GAM409  DKFZp761O17121 3'  GGGAGAAGGTTGGGGTGTAGG  50141    A TG    CAG
                                CC G  CCTT   AACTTTCTCTT
                                || |  ||||   ||||||||||
                                GG T  GGGG   TTGGAAGAGGG
                                 A GT   ___
GAM409  DKFZp762P2111 3'  AGGGCTGCTTCTGGGGGTCTTG 86351      T        CTTT    T
           G                     CCAG GCCTTCAGAA    CTCT
                                |||| ||||||||||    ||||
                                GGTT TGGGGGTCTT    GGGA
                                   C         CGTC
GAM409  DNPEP    3'  GAGGGGAAGTTCTCAGCTG    23956      GCCTTC
                                CAGT     AGAACTTTCTCTT
                                ||||     ||||||||||||
                                GTCG     TCTTGAAGGGGAG
                                  AC____
GAM409  DTX2     3'  GGGAGGTTTGTTGAGGGTGTGG 71953     G       __        CTT
                                CCA TGCCTTCA  GAACTTTCT
                                ||| ||||||||  |||||||||
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                                GGT GTGGGAGT  TTTGGAGGG
                                  _       TG
GAM409  E2-EPF    3'  GGGAGGGTACAGGGGGCACTGG 27173          AGA
                                CCAGTGCCTTC   ACTTTCTC
                                ||||||||||   ||||||||
                                GGTCACGGGGG   TGGGAGGG
                                      ACA
GAM409  ECE2      3'  AGAGGGTGGGAGGGTGTGG   28065     G      AGA
                                CCA TGCCTTC   ACTTTCT
                                ||| |||||||   |||||||
                                GGT GTGGGAG   TGGGAGA
                                  _      GG_
GAM409  ENDO180   3'  GGGAGGAGCTGGGGAGCTGG   20147      GC     AA
                                CCAGT  CTTCAG  CTTTCT
                                |||||  ||||||  ||||||
                                GGTCG  GGGGTC  GGAGGG
                                   A_     GA
GAM409  ENDOGLYX1 3'  GAGAGATCAGGTGGAGGTAATT 45403      _      GAACTT
           GG                     CCAGT GCCTTCA      TCTCTT
                                |||||| |||||||      ||||||
                                GGTTA TGGAGGT      AGAGAG
                                   A      GGACT_
GAM409  ERF       3'  GGGGGGAGTAGAGGGGCCGCTG 21438       __     AGA   TT    T
           G                     CCAGTG  CCTTC   ACT  CTCT
                                ||||||  |||||   |||  ||||
                                GGTCGC  GGGAG   TGA  GGGG
                                   CG    A__   GG
GAM409  ESAM      3'  AAGAGGAAGTGGATCTGGAATT 57251      GCC     ___
           GG                     CAGT   TTCAGA   ACTTTCTCTT
                                ||||   ||||||   ||||||||||
                                GTTA   AGGTCT   TGAAGGAGAA
                                  ___      AGG
GAM409  FADS2     3'  AGGAGGAGGCTGCCCTGAGGGG 14948     G      AA___
           CTGG                    AGT CCTTCAG     CTTTCTCTT
                                ||| |||||||     |||||||||
                                TCG GGGAGTC     GGAGGAGGA
                                  _      CCGTC
GAM409  FADS2     3'  AGGAGGAGGTGGGGGCTGGAGG 14949   TG      A____
           TGCTGG                    CCTTCAG     ACTTTCTCTT
                                 |||||||     ||||||||||
                                 GGAGGTC     TGGAGGAGGA
                                GT      GGGGG
GAM409  FADS2     3'  AGGAGGGGGCGGCAGGGCTGG  14950      G   TCAGAA  TT
                                CCAGT CCT      CT  CTCTT
                                ||||| |||      ||  |||||
                                GGTCG GGA      GG  GAGGA
                                   _  CGGC__  GG
GAM409  FAM3D     3'  AGGAGGAGGAGCAGGGGGTGCT 57150     TG     AGAA
           G                      CAG  CCTTC    CTTTCTCTT
                                |||  |||||    |||||||||
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                                GTC  GGGGG   GGAGGAGGA
                                  GT    ACGA
GAM409  FAP48   5'  GGGAGAGGCGAGGGTTCTGG  53901     T    AGAA
                                CCAG GCCTTC   CTTTCTC
                                |||| ||||||   |||||||
                                GGTC TGGGAG   GAGAGGG
                                  T    CG__
GAM409  FAP48   5'  GGGAGAGGCGAGGGTTCTGG  22981     T    AGAA
                                CCAG GCCTTC   CTTTCTC
                                |||| ||||||   |||||||
                                GGTC TGGGAG   GAGAGGG
                                  T    CG__
GAM409  FBXO21  3'  AGGGGAAAGTTTGATAATACGG 53236    A  CCT   A
                                CC GTG   TCAGA CTTTCTCTT
                                || |||   ||||| |||||||||
                                GG CAT   AGTTT GAAAGGGGA
                                 _   AAT    _
GAM409  FGF19   5'  GGGAGGGGGCTGGGGCTGG   17589    GT   T  AA
                                CCA  GCCT CAG  CTTTCTC
                                |||  |||| |||  |||||||
                                GGT  CGGG GTC  GGGAGGG
                                  __   _  GG
GAM409  FKBP4   3'  AGGGGAAGGGGGAAAGGTGTAG 8898    A TG   _ AGAA
          G                      CC G  CCTT C   CTTTCTCTT
                                || |  |||| |   |||||||||
                                GG T  GGAA G   GGAAGGGGA
                                 A GT   A GG__
GAM409  FKSG43  3'  AGGAGGAGGGCAACTGGGGGCC 49337    T     AA__
          CTGG                    CAG GCCTTCAG   CTTTCTCTT
                                ||| ||||||||   |||||||||
                                GTC CGGGGGTC   GGAGGAGGA
                                  C      AACG
GAM409  FKSG44  3'  AGGAGGAGGGCGACTGGGGGCC 49121    T     AA__
          CTGG                    CAG GCCTTCAG   CTTTCTCTT
                                ||| ||||||||   |||||||||
                                GTC CGGGGGTC   GGAGGAGGA
                                  C      AGCG
GAM409  FLJ10206 5' AGGAGAAAGAGGAAAGGCGTTT 35897    GT_   _ AGAA
          GG                    CCA   GCCTT C   CTTTCTCTT
                                |||   ||||| |   |||||||||
                                GGT   CGGAA G   GAAAGAGGA
                                  TTG    A GA__
GAM409  FLJ10535 3' AGAGAGGGTGTGGGATTGG   36233     G  TTCAGA
                                CCAGT CC     ACTTTCTCT
                                ||||| ||     |||||||||
                                GGTTA GG     TGGGAGAGA
                                  G  TG____
GAM409  FLJ10607 5' GAGGAGGTGGGGCTGG     77115     G  TTCAGA
                                CCAGT CC     ACTTTCTC
                                ||||| ||     ||||||||
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                                GGTCG GG     TGGAGGAG
                                  G _______
GAM409  FLJ10648 5' GGGAGGAGGATGGCCGGGGGTG 36379     TG    AGAA__
           CTGG                  CAG  CCTTC     CTTTCTCTT
                                |||  |||||     |||||||||
                                GTC  GGGGG     GGAGGAGGG
                                  GT    CCGGTA
GAM409  FLJ10697 3' GAGGGAAAGTAACGAAAGGGCT 36419      G   _ AGA
           GG                    CCAGT CCTT C   ACTTTCTCTT
                                ||||| |||| |   ||||||||||
                                GGTCG GGAA G   TGAAAGGGAG
                                  _    A CAA
GAM409  FLJ10737 3' ACACCCCAGCTTTTGAGGGTGC 36517     TG       _ TTCTCTT
           TGG                   CCAG  CCTTCAGAA CT
                                ||||  ||||||||| ||
                                GGTC  GGGAGTTTT GA
                                  GT       C  CCCCACAG
GAM409  FLJ10743 3' GGGAGAAGGAAGAGGGGGAGCT 36551      G    AGAA
           GG                    CCAGT CCTTC    CTTTCTCTT
                                ||||| |||||    |||||||||
                                GGTCG GGGGG    GGAAGAGGG
                                  A     AGAA
GAM409  FLJ10748 5' GAGGGAGAGGCGCGGAGACACT 36557      C    AGAA
           GG                    CCAGTG CTTC    CTTTCTCTT
                                ||||||| ||||    |||||||||
                                GGTCAC GAGG    GAGAGGGAG
                                   A    CGCG
GAM409  FLJ10761 3' GAGAGGGAGTGGTGAGGCCCTG 36581     T   T  GA   TT
           G                     CCAG GCCT CA  ACT  CTCTT
                                |||| |||| ||  |||  |||||
                                GGTC CGGA GT  TGA  GAGAG
                                  C   _  GG   GG
GAM409  FLJ10761 5' GAGGGGGTGGGGCTGCTGG   36582      _    CAGA   TT
                                CCAGT GCCTT    ACT  CTC
                                |||||  |||||    |||  |||
                                GGTCG CGGGG    TGG  GAG
                                  T    _____   GG
GAM409  FLJ10811 3' GAGATCTTGAGGCACTGG    36682         C   ACTT
                                CCAGTGCCTT AGA    TCTC
                                ||||||||||  |||    ||||
                                GGTCACGGAG TCT    AGAG
                                     T  _____
GAM409  FLJ11160 3' AGAGAGTGCAGGAGGGCTGG   37121      G    AGA
                                CCAGT CCTTC   ACTTTCT
                                |||||  |||||   |||||||
                                GGTCG GGAGG   TGAGAGA
                                  _     ACG
GAM409  FLJ11160 3' AAGGGAGGACACAAGGACATTG 37120       _   CAGAA  TT  CTT
           G                     CCAGTG CCTT     CT  CT
                                ||||||  ||||     ||  ||
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                                GGTTAC GGAA    GA  GA
                                   A   CACAG  GG  A
GAM409  FLJ11218  3'  AGAGGAGAAGGGCATT     37167        CAGAAC
                                AGTGCCTT     TTTCTCT
                                ||||||||     |||||||
                                TTACGGGA     GAGGAGA
                                   A_____
GAM409  FLJ11726  3'  GGAGGGGAGAGGCACGG     46415    A      CAGAA
                                CC GTGCCTT     CTTTCT
                                || |||||||     ||||||
                                GG CACGGAG     GGGAGG
                                 _      AG___
GAM409  FLJ11743  3'  GGGGGGGGGGATGGGGGGGCTGG 44551       G     GAA  TT
                                CCAGT CCTTCA   CT  CTCT
                                ||||| ||||||   ||  ||||
                                GGTCG GGGGGT   GG  GGGG
                                   G     AG_  GG
GAM409  FLJ12168  5'  GGAGGAGGCGGGGCAGTGG    45185     G     CAGAA
                                CCA TGCCTT     CTTTCTCT
                                ||| ||||||     ||||||||
                                GGT ACGGGG     GGAGGAGG
                                  G     C____
GAM409  FLJ12171  3'  GGAGAAACCAAGCTGCTGG    44872       GC   CAGAAC
                                CCAGT  CTT     TTTCTCT
                                |||||  |||     |||||||
                                GGTCG  GAA     AAAGAGG
                                   TC   CC____
GAM409  FLJ12221  5'  AGGAGGGCAGGGGGCGCGG    62548    A       AGAA
                                CC GTGCCTTC    CTTTCT
                                || ||||||||    ||||||
                                GG CGCGGGGG    GGAGGA
                                 _       ACG_
GAM409  FLJ12242  3'  GGGAGAGGCAGCAGAAGGGGCT 45181       G     AGAA__      TT
          GG                    CCAGT CCTTC     CTTTCTC
                                |||||  |||||     |||||||
                                GGTCG GGAAG     GAGAGGG
                                   G    ACGACG
GAM409  FLJ12484  3'  AAGTGACAGTTTTGAAGTATTG 42855        C        T  T
          G                     CCAGTGC TTCAGAACT TC CTT
                                ||||||| ||||||||| || |||
                                GGTTATG AAGTTTTGA AG GAA
                                   _       C  T
GAM409  FLJ12484  3'  AAGTGACAGTTTTGAAGTATTG 69652        C        T  T
          G                     CCAGTGC TTCAGAACT TC CTT
                                ||||||| ||||||||| || |||
                                GGTTATG AAGTTTTGA AG GAA
                                   _       C  T
GAM409  FLJ12650  3'  GGAGACATGGAGGAACTGG    44528       G     GAACTT
                                CCAGT CCTTCA     TCTCT
                                ||||| ||||||     |||||
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                                GGTCA GGAGGT     AGAGG
                                  A     AC____
GAM409  FLJ12671  3'  GGAGAAACAGGGCAGTGG    48278     G     CAGAAC
                                CCA TGCCTT     TTTCTCT
                                ||| ||||||     |||||||
                                GGT ACGGGA     AAAGAGG
                                  G     C_____
GAM409  FLJ12687  5'  GAGAGGAGTCGAGGTGCCGG   46194    A TG    CA  AC
                                CC G  CCTT  GA  TTTCTC
                                || |  ||||  ||  ||||||
                                GG C  GGAG  CT  GGAGAG
                                 C GT    __  GA
GAM409  FLJ12700  3'  AGGGGGGTGGGAGGCACATGG  46114     _       AGAA  TT
                                CCA GTGCCTTC    CT  CT
                                ||| ||||||||    ||  ||
                                GGT CACGGAGG    GG  GA
                                  A       GTG_  GG
GAM409  FLJ12770  3'  AGGGAAATAAGGCAGTTGG    49735     _     CAGAAC
                                CCAG TGCCTT     TTTCTCT
                                |||| ||||||     |||||||
                                GGTT ACGGAA     AAAGGGA
                                  G     T_____
GAM409  FLJ12783  3'  AAGAGAGGGTTTTCTCATTG   48671      CCTTC
                                CAGTG    AGAACTTTCTCTT
                                |||||    |||||||||||||
                                GTTAC    TTTTGGGAGAGAA
                                   TC___
GAM409  FLJ12800  3'  GAGAGGGGGCTGGGCCCTGG   43233     T   TT   AA
                                CCAG GCC  CAG  CTTTCTC
                                |||| |||  |||  |||||||
                                GGTC CGG  GTC  GGGAGAG
                                  C   __   GG
GAM409  FLJ13456  5'  GAGGGAAAGAGGCCGAGGCCTG 65941      T    CAGAA
          G                      CCAG GCCTT     CTTTCTCTT
                                |||| |||||     |||||||||
                                GGTC CGGAG     GAAAGGGAG
                                  _     CCGGA
GAM409  FLJ13769  3'  AGGGGAGGGAAGAGAGAGGTGT 46597     G     CAGAA_
          GG                     CCA TGCCTT     CTTTCTCTT
                                ||| ||||||     |||||||||
                                GGT GTGGAG     GGGAGGGGA
                                  _     AGAGAA
GAM409  FLJ13842  3'  GAGGAAAGGGGGTTGG      44984     GT     AGAAC
                                CCA  GCCTTC    TTTCTC
                                |||  ||||||    ||||||
                                GGT  TGGGGG    AAGGAG
                                  __     A____
GAM409  FLJ14129  3'  GAGAGGGAGTTGGAGAGCTGG  48065      GC    GA   TT
                                CCAGT  CTTCA  ACT  CTCTT
                                |||||  |||||  |||  |||||
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                                GGTCG  GAGGT  TGA  GAGAG
                                  A_    __  GG
GAM409  FLJ14129  5' GGGAGGGCTGAGGGCGCGG   48068   A       AA  TT
                                CC GTGCCTTCAG  CT  C
                                || ||||||||||  ||  |
                                GG CGCGGGAGTC  GA  G
                                 _       GG  GG
GAM409  FLJ14351  3' GGAGAGGGCAGGTTTTGG    45328    T   TCAGAA
                                CCAG GCCT     CTTTCTCT
                                |||| ||||     ||||||||
                                GGTT TGGA     GGGAGAGG
                                  T   C_____
GAM409  FLJ14427  3' AGGGGAGGGGAGCTCAAGGTTT 51334     T    C  AA_
           GG                     CCAG GCCTT AG   CTTTCTCTT
                                |||| ||||| ||   |||||||||
                                GGTT TGGAA TC   GGGAGGGGA
                                  _    C  GAG
GAM409  FLJ14442  3' AGGGGGGAGTACAGAAGGTATG 51359    G     AGA   TT
           G                     CCA TGCCTTC   ACT  CTCTT
                                ||| |||||||   |||  |||||
                                GGT ATGGAAG   TGA  GGGGA
                                  _      ACA   GG
GAM409  FLJ14708  3' GAGAGGGAGGCTGGGGTGCCTG 51543     T  _     AA  TT
           G                     CCAG GC CTTCAG  CT  CTCTT
                                |||| || ||||||  ||  |||||
                                GGTC CG GGGGTC  GA  GAGAG
                                  _ T     G_  GG
GAM409  FLJ14728  5' AAGGGGAGCGTGGGGCCGCTGG 51586       _   CAGA  _
                                CCAGTG CCTT    AC TTTCTCTT
                                |||||| ||||    || ||||||||
                                GGTCGC GGGG    TG GAGGGGAA
                                   C    _____  C
GAM409  FLJ14957  3' GGGGGAATAAGAGGGTATGG   51755    G     AGAACT
                                CCA TGCCTTC     TTCTCTT
                                ||| |||||||     |||||||
                                GGT ATGGGAG     AAGGGGG
                                  _      AAT___
GAM409  FLJ14966  5' GGGGGAAGGACAGGAGCTGG   51771      G   TCAGAA
                                CCAGT CCT     CTTTCTCT
                                ||||| |||     ||||||||
                                GGTCG GGA     GAAGGGGG
                                   A   CAG___
GAM409  FLJ20040  3' GGAGGAAGGCGGCCGCTGG    38633       _ TTCAGAA
                                CCAGTG CC      CTTTCTCT
                                |||||| ||      ||||||||
                                GGTCGC GG      GAAGGAGG
                                   C  CG_____
GAM409  FLJ20209  3' AGTCCCTGTTCTGGGAGGTGCT 85517     TG    _    TTTCTCTT
           GG                     CCAG  CCTTC AGAAC
                                ||||  ||||| |||||
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                                GGTC  GGAGG TCTTG
                                  GT    G    TCCCTGA
GAM409  FLJ20274  3'  GAGGGGAGGATAGGAGGGGGAT 62644  GT ___    AGAA
          GTTGG                    G   CCTTC    CTTTCTCTT
                                   |  |||||   |||||||||
                                   T  GGGAG   GGAGGGGAG
                                  TG AGG    GATA
GAM409  FLJ20281  5'  AAGAGAAAGTTTTGAAAGT   90975    C
                                  GC TTCAGAACTTTCTCTT
                                  || ||||||||||||||||
                                  TG AAGTTTTGAAAGAGAA
                                   A
GAM409  FLJ20306  3'  AGAGAAGGCCGGGTGCGG    34913    A TG   TCAGAA
                                  CC G  CCT     CTTTCTCT
                                  || |  |||     ||||||||
                                  GG C  GGG     GGAAGAGA
                                   _ GT   CC____
GAM409  FLJ20373  3'  AAGAGAAGAAGGAAAGGCACAG 35070    A      _ AGAAC
          G                        CC GTGCCTT C     TTTCTCTT
                                  || ||||||| |     ||||||||
                                  GG CACGGAA G     GAAGAGAA
                                   A      A GAA__
GAM409  FLJ20378  3'  GAGAGGTGGGGTGGGGGGCTGG 35092      G     GAA  T
                                  CCAGT CCTTCA   CT TCTCTT
                                  ||||| ||||||   || ||||||
                                  GGTCG GGGGGT   GG GGAGAG
                                     _     GG_  T
GAM409  FLJ20457  5'  GGGGGGGGCGGGGGGGGTGGTG 35222     G      AGAA  TT    T
          G                        CCA TGCCTTC    CT  CTCT
                                  ||| |||||||    ||  ||||
                                  GGT GTGGGGG    GG  GGGG
                                    G      GGGC  GG
GAM409  FLJ20464  3'  AAGAGAAAGGGGCCGGGCGCGG 35224    A     TCAGAA
                                  CC GTGCCT     CTTTCTCTT
                                  || ||||||     |||||||||
                                  GG CGCGGG     GAAAGAGAA
                                   _     CCGGG_
GAM409  FLJ20548  3'  GAGGAACAGGGCTTGG      35378      T    CAGAAC
                                  CCAG GCCTT     TTTCTC
                                  |||| |||||     ||||||
                                  GGTT CGGGA     AAGGAG
                                     _    C_____
GAM409  FLJ20584  5'  AAGAGAAACCCGGAGGGCGCCG 35426    A       AGAAC
          G                        CC GTGCCTTC    TTTCTCTT
                                  || ||||||||    ||||||||
                                  GG CGCGGGAG    AAAGAGAA
                                   C       GCCC_
GAM409  FLJ20627  5'  GAGAGGCTGGGGGTGCGG    35473    A TG      AA
                                  CC G  CCTTCAG  CTTTC
                                  || |  |||||||  |||||
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                                GG C  GGGGGTC  GAGAG
                                 _ GT      G_
GAM409  FLJ20986  5' GGGAGAGGGAGGGTGTT     44546    TG    AGAA
                                AG  CCTTC    CTTTCTC
                                ||  |||||    |||||||
                                TT  GGGAG    GAGAGGG
                                 GT    G___
GAM409  FLJ21126  3' GAGGGAGAGCAAATCAGATGCT 90327      GC  TCAGAA
           GG                     CCAGT  CT     CTTTCTCTT
                                |||||  ||     |||||||||
                                GGTCG  GA     GAGAGGGAG
                                   TA  CTAAAC
GAM409  FLJ22167  3' GAGAGGGAGCTGGGGCGCATGG 44573     _     T   AA
                                CCA GTGCCT CAG  CTTTCTC
                                |||  |||||| |||  |||||||
                                GGT CGCGGG GTC  GGGAGAG
                                  A     _   GA
GAM409  FLJ22349  3' GGGAGGAAGAAGAGGTGGAGGT 45693    G      GAA___
           GTGG                    A TGCCTTCA     CTTTCTCTT
                                | ||||||||     |||||||||
                                T GTGGAGGT     GAAGGAGGG
                                 _       GGAGAA
GAM409  FLJ22494  5' AGGGGAGACCATCGTGGAGGCG 45673          _  AC_
           CTG                     CAGTGCCTTCA GA   TTTCTCTT
                                ||||||||||| ||   |||||||
                                GTCGCGGAGGT CT   AGAGGGGA
                                      G  ACC
GAM409  FLJ22494  5' GAGGGCCTGGCGGGGGCGCTGG 45677          AGAACT
                                CCAGTGCCTTC     TTCTC
                                ||||||||||     |||||
                                GGTCGCGGGGG     GGGAG
                                      CGGTCC
GAM409  FLJ22692  3' AAGAGGGAGTTTTGGGGGCTGG 46801     GT         TT
                                CCA  GCCTTCAGAACT  CTCTT
                                |||  ||||||||||||  |||||
                                GGT  CGGGGGTTTTGA  GAGAA
                                  __          GG
GAM409  FLJ22795  3' AGGGGAAGGCGTAGGTGTGG   46941     G    TCAGAA
                                CCA TGCCT     CTTTCTCT
                                ||| |||||     ||||||||
                                GGT GTGGA     GAAGGGGA
                                  _    TGCG__
GAM409  FLJ23185  5' GGGGTCCCTGGAGGTTTGG    46831      T      A_
                                CCAG GCCTTCAG  ACTTT
                                ||||  ||||||||  |||||
                                GGTT TGGAGGTC  TGGGG
                                   _       CC
GAM409  FLJ23375  5' GAGAGGGGCAGGTGCTGG    46356      TG   TCAGAA
                                CCAG  CCT     CTTTCTC
                                ||||  |||     |||||||
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                                GGTC  GGA     GGGAGAG
                                  GT   CG____
GAM409  FLJ23416  3'  AGAGGAGGCCGAGGGCTGG   49944     GT     AGAA
                                CCA  GCCTTC    CTTTCTCT
                                |||  ||||||    ||||||||
                                GGT  CGGGAG    GGAGGAGA
                                  __     CC__
GAM409  FLJ23436  3'  GAGAGAGGTCAGCGGAGGGCTG 45142       G    A__  A      TT
            G                    CCAGT CCTTC   GA CTTTCTC
                                |||||  |||||   ||  |||||||
                                GGTCG GGAGG   CT GAGAGAG
                                  _    CGA  G
GAM409  FLJ23550  3'  GAGGGAGAAAGGAACTGG    46853       G    CAGAA  TT
                                CCAGT CCTT     CT  CTC
                                |||||  ||||     ||  |||
                                GGTCA GGAA     GA  GAG
                                  A    A_____  GG
GAM409  FLJ30294  5'  AAGGGTTCTTCTGGAGGTGTTG 58248      TG        CTTT
            G                    CCAG  CCTTCAGAA    CTCTT
                                ||||  |||||||||    |||||
                                GGTT  GGAGGTCTT    GGGAA
                                  GT        CTT_
GAM409  FLJ31762  5'  AGAGAGAGAGATGTGTTGG    58138      TG CT  AGAA
                                CCAG  C  TC    CTTTCTCT
                                ||||  |  ||    ||||||||
                                GGTT  G  AG    GAGAGAGA
                                  GT T_  A___
GAM409  GBTS1     3'  GAGGGAAGGTGAGATGGAGGTT 59056     T      GA__
            TTGG                   CAG GCCTTCA    ACTTTCTCTT
                                |||  |||||||    ||||||||||
                                GTT TGGAGGT    TGGAAGGGAG
                                  T      AGAG
GAM409  GBTS1     3'  GCTTCTGGGTTCTGAAGGTGCC 59057     A TG          TCTCTT
            GG                     CC G  CCTTCAGAACTT
                                ||  |  ||||||||||||
                                GG C  GGAAGTCTTGGG
                                 C GT          TCTTCGA
GAM409  GENX-3414 3'  AAGGGAAAGTGAGTGGGGTTGG 14144     GT     CAGA
                                CCA  GCCTT    ACTTTCTCTT
                                |||  |||||    ||||||||||
                                GGT  TGGGG    TGAAAGGGAA
                                  __     TGAG
GAM409  GP3ST     3'  AGGGCTTCTGGGGCGTTGG    42142         T     CTTT
                                CCAGTGCCT CAGAA    CTCT
                                |||||||||  |||||    ||||
                                GGTTGCGGG GTCTT    GGGA
                                      _    C___
GAM409  GPA33     5'  GGGAGAAGGCAGGGGAGGTGGC 19456       _      AGAA
            TGG                    CCAGT GCCTTC    CTTTCTCTT
                                |||||  ||||||    |||||||||
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                                GGTCG TGGAGG   GGAAGAGGG
                                   G    GGAC
GAM409  GPR     5'  GGAGGGAGTGGGCATGG    23335    G   TCAGA  TT
                                CCA TGCCT    ACT  CTCT
                                ||| |||||    |||  ||||
                                GGT ACGGG    TGA  GAGG
                                  _    _____  GG
GAM409  GSK3A   3'  AAGAGAAGGACAGGGTGTTGG  95272     TG   CAGAA
                                CCAG  CCTT    CTTTCTCTT
                                ||||  ||||    |||||||||
                                GGTT  GGGA    GGAAGAGAA
                                  GT    CA___
GAM409  GTF3C4  3'  GAGAAGGATGCACTGG     24194       CTTCAGAA
                                CCAGTGC      CTTTCTC
                                |||||||      |||||||
                                GGTCACG      GGAAGAG
                                   TA_______
GAM409  H2AFY2  3'  AGGAGAGAGGAGGGGTGATGG  37840    GT    CAGAA
                                CCA  GCCTT    CTTTCTCTT
                                |||  |||||    |||||||||
                                GGT  TGGGG    GAGAGAGGA
                                  AG    AG___
GAM409  H2BFB   3'  AGGGGAAGGAACTAAAGGTGTT 56969    TG   C  AA
                                AG  CCTT AG  CTTTCTCTT
                                ||  |||| ||  |||||||||
                                TT  GGAA TC  GGAAGGGGA
                                 GT    A  AA
GAM409  HBP1    5'  GAGAGGGGGTACGAGAGCTGCT 24312      _ C   AGA   TT
           GG                     CCAGT GC TTC   ACT  CTCTT
                                |||||| || |||   |||  |||||
                                GGTCG CG GAG   TGG  GAGAG
                                   T  A   CA_   GG
GAM409  HMP19   3'  GAGGGAGGGAAGGAAGGTGCGG 87472    A TG    AGAA
                                CC G  CCTTC    CTTTCTCTT
                                || |  |||||    |||||||||
                                GG C  GGAAG    GGGAGGGAG
                                 _ GT    GAA_
GAM409  HPCAL4  3'  GGAGTTGGGGGCCTGG     32740     T     GA
                                CCAG GCCTTCA  ACTTT
                                |||| |||||||  |||||
                                GGTC CGGGGGT  TGAGG
                                   _      __
GAM409  HSPC155 3'  AAGGGAAAGACTGGGCTTTGG  33086     T   TT   AA
                                CCAG GCC  CAG  CTTTCTCTT
                                |||| |||  |||  |||||||||
                                GGTT CGG  GTC  GAAAGGGAA
                                  T   __   A_
GAM409  HSPC195 5'  GGGAGGAGGGGCAGGTGCTG   80967    TG   TCAGAA
                                CAG  CCT     CTTTCTCTT
                                |||  |||     |||||||||
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                                GTC  GGA     GGAGGAGGG
                                  GT   CGG___
GAM409  HSU79266 3'  AGGAGGAAGATGAGGGCACGG  25248    A       GAA
                                CC GTGCCTTCA   CTTTCTCTT
                                || |||||||||   |||||||||
                                GG CACGGGAGT   GAAGGAGGA
                                  _       A__
GAM409  HTMP10   5'  GAGGGATGGACTGAGGGCTTGG 52611      T       AA  T
                                CCAG GCCTTCAG  CT TCTCTT
                                |||| ||||||||  || ||||||
                                GGTT CGGGAGTC  GG AGGGAG
                                  _       A_  T
GAM409  IGF2AS   3'  AGTTCTGGGAGCGCTGG     33094        CT
                                CCAGTGC  TCAGAACT
                                |||||||  ||||||||
                                GGTCGCG  GGTCTTGA
                                    AG
GAM409  IRX1     3'  GGGGGAGGGGGGAGGAGTTGG  85938      TG    AGAA
                                CCAG  CCTTC    CTTTCTCT
                                ||||  |||||    ||||||||
                                GGTT  GGAGG    GGAGGGGG
                                  GA    GG__
GAM409  ITPK1    3'  AGGAGGGAGGCACAGGGCTTGG 26406      T    CAGAA  TT
                                CCAG GCCTT     CT  CTCTT
                                |||| |||||    ||  |||||
                                GGTT CGGGA     GA  GAGGA
                                  _    CACG_  GG
GAM409  KCNH4    5'  GGGAGGAGGCAGGAGGGCGCAT 24407     _       AGAA
           GG                     CCA GTGCCTTC    CTTTCTCTT
                                ||| ||||||||    |||||||||
                                GGT CGCGGGAG    GGAGGAGGG
                                  A       GAC_
GAM409  KCNJ9    3'  AGAGAGAGAGAGGTTCTGG    17151      T    CAGAA
                                CCAG GCCTT     CTTTCTCT
                                |||| |||||    ||||||||
                                GGTC TGGAG     GAGAGAGA
                                  T    A____
GAM409  KIAA0057 3'  GAGAGGGAGGTGGCGCTGG    24427        TTCAGAA  TT
                                CCAGTGCC       CT  CTCTT
                                ||||||||       ||  |||||
                                GGTCGCGG       GA  GAGAG
                                    TG_____  GG
GAM409  KIAA0087 3'  AGAGGAAGAGGAGGCCTGG    28694      T     AGAA
                                CCAG GCCTTC    CTTTCTCT
                                |||| ||||||    ||||||||
                                GGTC CGGAGG    GAAGGAGA
                                  _     A___
GAM409  KIAA0121 3'  GGGAGGGGTCGGCGGTGCTGG  72659      TG  T  A  A
                                CCAG  CC TC GA CTTTCTC
                                ||||  || || || |||||||
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                                GGTC  GG GG CT GGGAGGG
                                  GT  C  _  G
GAM409  KIAA0161  3'  AGGGGAGGCAGGTGTGG     28497     G     TCAGAA
                                CCA TGCCT     CTTTCTCT
                                ||| |||||     ||||||||
                                GGT GTGGA     GGAGGGGA
                                  _     C_____
GAM409  KIAA0211  3'  GAGGGAAATGAGGGGTGCTG   27548     TG  _  GAAC
                                CAG  CCT TCA    TTTCTCTT
                                |||  ||| |||    ||||||||
                                GTC  GGG AGT    AAAGGGAG
                                  GT   G  ____
GAM409  KIAA0237  3'  GGAGGGGTCTGATGTGCTGG   28529      TG CT     A
                                CCAG  C  TCAGA CTTTCT
                                ||||  |  ||||| ||||||
                                GGTC  G  AGTCT GGGAGG
                                  GT T_    G
GAM409  KIAA0321  3'  AGGGGAGGCGGTGGGGGGTGGT 62387     G      AGAA_       T
          GG                    CCA TGCCTTC     CTTTCTCT
                                ||| |||||||     ||||||||
                                GGT GTGGGGG     GGAGGGGA
                                  G      GTGGC
GAM409  KIAA0365  3'  AGGGGAAGGGTTGGGTGCTG   78663     TG  TT   AA
                                CAG  CC  CAG  CTTTCTCT
                                |||  ||  |||  ||||||||
                                GTC  GG  GTT  GAAGGGGA
                                  GT  __   GG
GAM409  KIAA0391  3'  GGGAGGAGTCAGGGCATGG    27919     G     CA  AC
                                CCA TGCCTT  GA  TTTCTC
                                ||| ||||||  ||  ||||||
                                GGT ACGGGA  CT  GGAGGG
                                  _     __  GA
GAM409  KIAA0418  3'  AGGGGTTGTTTGGGGGCCTGG  27551      T        A TT
                                CCAG GCCTTCAGA C  TCTCT
                                |||| |||||||| |  |||||
                                GGTC CGGGGGTTT G  GGGGA
                                  _       _ TT
GAM409  KIAA0429  5'  AAGGGAGAGGAAGGGGTATGG  28547     G     CAGAA
                                CCA TGCCTT     CTTTCTCTT
                                ||| ||||||     |||||||||
                                GGT ATGGGG     GAGAGGGAA
                                  _      AAG__
GAM409  KIAA0447  3'  AAGGGAGGGGACAGAGGGCCCT 71662      T     AGAA
          GG                    CCAG GCCTTC    CTTTCTCTT
                                |||| ||||||    |||||||||
                                GGTC CGGGAG    GGGAGGGAA
                                  C     ACAG
GAM409  KIAA0450  5'  GGGAGAGGGCAGGACAGGGGCT 27644       G  _  AGAA
          GG                    CCAGT CCT TC    CTTTCTCTT
                                ||||| ||| ||    |||||||||
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                                GGTCG GGA AG    GGGAGAGGG
                                   G   C  GAC_
GAM409  KIAA0455  5'  GGGAGAAGGCGGGGGCGCTG   72470          AGAA
                                CAGTGCCTTC    CTTTCTCTT
                                ||||||||||    |||||||||
                                GTCGCGGGGG    GGAAGAGGG
                                     C____
GAM409  KIAA0476  3'  GGGGGAGATCTGGGGGGAGTTG 29378      G_      A  TT   TT
          G                      CCAGT  CCTTCAGA CT  CTC
                                |||||  |||||||| ||  |||
                                GGTTG  GGGGGTCT GA  GGG
                                   AG       A  GG
GAM409  KIAA0493  5'  AGGAGGAAATACAGGAAGTATT 64269        C   AGAAC_
          GG                     CCAGTGC TTC     TTTCTCTT
                                |||||||  |||     ||||||||
                                GGTTATG AAG     AAGGAGGA
                                    _  GACATA
GAM409  KIAA0514  5'  AGGAGGAAGTAGCCCAGTATTG 28074        CTTCAGA
          G                      CCAGTGC      ACTTTCTCTT
                                |||||||      ||||||||||
                                GGTTATG      TGAAGGAGGA
                                    ACCCGA_
GAM409  KIAA0537  5'  GGGAGGGGTTGGGGGGCGCGG  29252    A       AGAA
                                CC GTGCCTTC    CTTTCTC
                                || ||||||||    |||||||
                                GG CGCGGGGG    GGGAGGG
                                 _       GTTG
GAM409  KIAA0537  3'  GGGGGGGGGGTGGGGGTGTGG   29254    G       GAA  TT
                                CCA TGCCTTCA   CT  CTC
                                ||| ||||||||   ||  |||
                                GGT GTGGGGGT   GG  GGG
                                  _      GG_  GG
GAM409  KIAA0544  3'  AGGGGAGAGGCCTGGGCCTGG  70886     T   TT   AA
                                CCAG GCC  CAG  CTTTCTCTT
                                |||| |||  |||  |||||||||
                                GGTC CGG  GTC  GAGAGGGGA
                                  _  __  CG
GAM409  KIAA0552  3'  AGGGGAGGACTGGGGCTGG   28307      G  TTCAGAA
                                CCAGT CC      CTTTCTCT
                                |||||  ||      ||||||||
                                GGTCG GG      GGAGGGGA
                                   G  TCA____
GAM409  KIAA0552  3'  GGAGAAGAGAAGGCATT     28317          AGAAC
                                AGTGCCTTC     TTTCTCT
                                |||||||||     |||||||
                                TTACGGAAG     GAAGAGG
                                     A____
GAM409  KIAA0557  3'  GGGAGAGGGCCTGGGGGCTGG  78004     GT       AA
                                CCA  GCCTTCAG  CTTTCTCTT
                                |||  ||||||||  |||||||||
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                                GGT  CGGGGGTC  GGGAGAGGG
                                  __       C_
GAM409  KIAA0594  3'  GGGAAAAAAGCACTGG      64900        C  CAGAAC
                                CCAGTGC TT     TTTCTC
                                ||||||| ||     ||||||
                                GGTCACG AA     AAAGGG
                                   A _______
GAM409  KIAA0620  3'  AGGGGAGGGATGGGGGGCACAG 62119    A       AGAA       T
          G                      CC GTGCCTTC    CTTTCTCT
                                || ||||||||    ||||||||
                                GG CACGGGGGG    GGAGGGGA
                                 A       GTAG
GAM409  KIAA0668  3'  AGCCCCGTTCTGTGGGGCACTG 66522          _     TTTCTCTT
          G                      CCAGTGCCTT CAGAAC
                                |||||||||| ||||||
                                GGTCACGGGG GTCTTG
                                      T     CCCCGA
GAM409  KIAA0668  3'  GAGAGGGGCCTGGGGCACTGG  66524         T   AA
                                CCAGTGCCT CAG  CTTTCTC
                                ||||||||| |||  |||||||
                                GGTCACGGG GTC  GGGAGAG
                                     _  CG
GAM409  KIAA0682  3'  GAGGGGAGGAACAGGCACAGG  29365    A     TCAGAA
                                CC GTGCCT     CTTTCTCTT
                                || ||||||     |||||||||
                                GG CACGGA     GGAGGGGAG
                                 A     CAA___
GAM409  KIAA0694  3'  AGGGAGAGTCCAGGCCTGG    72578      T    TCA  A
                                CCAG GCCT   GA CTTTCTCT
                                |||| ||||   || ||||||||
                                GGTC CGGA   CT GAGAGGGA
                                  _    C__  _
GAM409  KIAA0773  3'  AAGAGGGAGACTGAGGAGCTGG 28044       GC     AA  TT
                                CCAGT  CTTCAG  CT  CTCTT
                                |||||  ||||||  ||  |||||
                                GGTCG  GGAGTC  GA  GAGAA
                                   A_     A_  GG
GAM409  KIAA0775  3'  GAGAGGGAGGATCCTGGAGGAC 28280      G      AA__  TT
          TGG                    CAGT CCTTCAG    CT  CTCTT
                                |||| |||||||    ||  |||||
                                GTCA GGAGGTC    GA  GAGAG
                                  _      CTAG  GG
GAM409  KIAA0779  3'  AAGACTTAAGTTTTGTGGGCAC 85721          T       TC_
          TGG                    CCAGTGCCT CAGAACTT   TCTT
                                |||||||||| ||||||||   ||||
                                GGTCACGGG GTTTTGAA   AGAA
                                     T       TTC
GAM409  KIAA0819  3'  GGAGACATGGAGGTGCGG    63579    A TG     GAACTT
                                CC G  CCTTCA     TCTCT
                                || |  ||||||     |||||
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                              GG C  GGAGGT     AGAGG
                               _ GT     AC____
GAM409  KIAA0821  3'  GAGAGGGAGACAGATGGAGGCA 29945    G      GAA__  TT
            GTGG                  CA TGCCTTCA    CT  CTCTT
                              || ||||||||    ||  |||||
                              GT ACGGAGGT    GA  GAGAG
                               G       AGACA  GG
GAM409  KIAA0870  3'  GAGGGTCTCTGGGGGTGTT   81468    TG      _
                              AG  CCTTCAGA ACTTTC
                              ||  |||||||| ||||||
                              TT  GGGGGTCT TGGGAG
                               GT       C
GAM409  KIAA0876  3'  AGGGGAAGCCCGGGGGTCTGG  64675     T     AGAA
                              CCAG GCCTTC    CTTTCTCT
                              |||| ||||||    ||||||||
                              GGTC TGGGGG    GAAGGGGA
                                _     CCC_
GAM409  KIAA0931  3'  GAGAGAGAACTGGGTGTTGG   67419     TG  TT   AA
                              CCAG  CC  CAG  CTTTCTC
                              ||||  ||  |||  |||||||
                              GGTT  GG  GTC  GAGAGAG
                                GT  __  AA
GAM409  KIAA0934  5'  AAGAGGAGGCCGTGCGGGGCGC 64216    A      _  GAA
            GG                  CC GTGCCTT CA   CTTTCTCTT
                              || ||||||| ||   |||||||||
                              GG CGCGGGG GT   GGAGGAGAA
                               _      C  GCC
GAM409  KIAA0939  3'  GAGGGCGGGGCGAGGTACTGG  62015          CAGAA  TT
                              CCAGTGCCTT    CT  CTCTT
                              ||||||||||    ||  |||||
                              GGTCATGGAG    GG  GGGAG
                                    CG___  GC
GAM409  KIAA0940  3'  GAGGGAAAAGAGAGGGCACTG  29869          AGAAC
                              CAGTGCCTTC    TTTCTCTT
                              ||||||||||    ||||||||
                              GTCACGGGAG    AAAGGGAG
                                    AGA__
GAM409  KIAA0945  3'  GGGAGGGAAGATGGGTGCTGG  30213     TG   TCAGAA
                              CCAG  CCT     CTTTCTC
                              ||||  |||     |||||||
                              GGTC  GGG     GGGAGGG
                                GT   TAGAA_
GAM409  KIAA0979  5'  GGGGGGGGGGAGAAGGCGATTGG 30444      _     AGAA  TT
                              CCAGT GCCTTC    CT  CTCT
                              ||||| ||||||    ||  ||||
                              GGTTA CGGAAG    GG  GGGG
                                 G     AG__  GG
GAM409  KIAA0995  5'  AGGAGGAGCTGGAGGGGGCGCG 72875    A      AGAAC
            G                   CC GTGCCTTC    TTTCTCTT
                              || ||||||||    ||||||||
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                                GG CGCGGGGG    GAGGAGGA
                                 _      AGGTC
GAM409  KIAA1016 3' AAGGGAGCCGCGAAGGGCGCTG 91730       _  AGAA  TT  CTT
            G                    CCAGTGCC TTC    CT  CT
                                 |||||||| |||    ||  ||
                                 GGTCGCGG AAG    GA  GA
                                     G   CGCC  GG  A
GAM409  KIAA1023 3' GAGAGAGTGCAGGGAGGGGCTG 34260      G    AGA_      TT
            G                    CCAGT CCTTC    ACTTTCTC
                                 ||||| |||||    ||||||||
                                 GGTCG GGAGG    TGAGAGAG
                                    G    GACG
GAM409  KIAA1032 3' GGGGAAAGTTCAGCGTGG    66159    G   CTTCA
                                 CCA TGC    GAACTTTCTCT
                                 ||| |||    ||||||||||
                                 GGT GCG    CTTGAAAGGGG
                                  _  A____
GAM409  KIAA1042 3' GGGGAAACAAGGCTTTGG    30344     T    CAGAAC
                                 CCAG GCCTT     TTTCTCT
                                 |||| |||||     |||||||
                                 GGTT CGGAA     AAAGGGG
                                   T    C_____
GAM409  KIAA1054 3' GGGGGAAGACTGGTGTTGG    68445     TG  TTCAGAA
                                 CCAG  CC      CTTTCTCT
                                 ||||  ||      ||||||||
                                 GGTT  GG      GAAGGGGG
                                   GT  TCA____
GAM409  KIAA1094 5' GAGGGAGAAGGTTGCTGG    29805       _    AGAAC TT
                                 CCAGTG CCTTC    T  CTC
                                 |||||| |||||    |  |||
                                 GGTCGT GGAAG    A  GAG
                                    T    _____ GG
GAM409  KIAA1110 3' GAGGGGAGGAGGGTTGG     61844     GT     AGAA
                                 CCA  GCCTTC    CTTTC
                                 |||  ||||||    |||||
                                 GGT  TGGGAG    GGGAG
                                   __     GAG_
GAM409  KIAA1190 3' GGGGGATTGGGGGGACTGG    71102      G      AAC TT
                                 CCAGT CCTTCAG   T  CTC
                                 ||||| |||||||   |  |||
                                 GGTCA GGGGGTT   A  GGG
                                    G      ___ GG
GAM409  KIAA1196 3' AGGGGAGGGGAGCAGGCACTGG 61458         TCAGAA
                                 CCAGTGCCT     CTTTCTCTT
                                 |||||||||     |||||||||
                                 GGTCACGGA     GGGAGGGGA
                                       CGAG__
GAM409  KIAA1196 3' GGGAGAAGAGAAGAGGGTCTGG 61475     T     AGAAC
                                 CCAG GCCTTC    TTTCTCTT
                                 |||| ||||||    ||||||||
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                                GGTC TGGGAG    GAAGAGGG
                                  _     AAGA_
GAM409  KIAA1199  3'  AGGAGGTAGTCTGGAGGGCTGG 72508      G       A  T
                                CCAGT CCTTCAGA CT TCTCTT
                                ||||| |||||||| || ||||||
                                GGTCG GGAGGTCT GA GGAGGA
                                  _       _  T
GAM409  KIAA1202  3'  GGAGGGGGTTCTTATTG    72020      CCTTC     TT
                                CAGTG    AGAACT  CTCT
                                |||||    ||||||  ||||
                                GTTAT    TCTTGG  GAGG
                                  ______     GG
GAM409  KIAA1357  3'  GAGAGAGGGGAAGGGTTGG   71979      G    AGAA
                                CCAGT CCTTC    CTTTCTC
                                ||||| |||||    |||||||
                                GGTTG GGAAG    GAGAGAG
                                  _    GG__
GAM409  KIAA1373  5'  AGGAGAAGGGGGAGGAGGCACG 70928    A       AGAA
            G                    CC GTGCCTTC    CTTTCTCTT
                                || ||||||||    |||||||||
                                GG CACGGAGG    GGAAGAGGA
                                 _       AGGG
GAM409  KIAA1441  3'  GGGGGGGTGGGGGGGTTGG    88413     GT     AGA   TT
                                CCA  GCCTTC   ACT  CTC
                                |||  ||||||   |||  |||
                                GGT  TGGGGG   TGG  GGG
                                  __     G__   GG
GAM409  KIAA1465  3'  GAGGGAAGGGGAGGGGCGCGG  60830    A      CAGAA
                                CC GTGCCTT     CTTTCTCTT
                                || |||||||     |||||||||
                                GG CGCGGGG    GGAAGGGAG
                                 _      AGG__
GAM409  KIAA1492  3'  GAGAGAGGTCAAAGGGTTGG   64505     GT    CA  A
                                CCA  GCCTT  GA CTTTCTC
                                |||  |||||  || |||||||
                                GGT  TGGGA  CT GAGAGAG
                                  __     AA  G
GAM409  KIAA1503  5'  GAGGGAAGGAGGGAAGGAGTGC 68347      G__    AGAA
            TGG                   CAGT   CCTTC    CTTTCTCTT
                                ||||   |||||   |||||||||
                                GTCG   GGAAG   GGAAGGGAG
                                  TGA    GGA_
GAM409  KIAA1511  3'  GGAGAAGATGAAGGTCTGG    70168      T      GAACT
                                CCAG GCCTTCA     TTCTCT
                                |||| |||||||     ||||||
                                GGTC TGGAAGT     AAGAGG
                                  _      AG___
GAM409  KIAA1538  3'  AAGAGAGACTGAGGAAGGCCTG 71525      T     AGAAC
            G                    CCAG GCCTTC     TTTCTCTT
                                |||| ||||||     ||||||||
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                                GGTC CGGAAG    AGAGAGAA
                                  _    GAGTC
GAM409  KIAA1538 3' AGGGGAGGTTTTAGACAGG   71528    _ _
                                CCT TC AGAACTTTCTCT
                                ||| || ||||||||||||
                                GGA AG TTTTGGAGGGGA
                                  C  A
GAM409  KIAA1538 5' GGGAGCTGGGGGGCGCTGG    71548          AA  TT
                                CCAGTGCCTTCAG  CT  C
                                ||||||||||||  ||  |
                                GGTCGCGGGGGTC  GA  G
                                       __  GG
GAM409  KIAA1571 3' AGATATTTGTGGGTATTGG   60948        T   ACTT
                                CCAGTGCCT CAGA   TCT
                                ||||||||| ||||   |||
                                GGTTATGGG GTTT   AGA
                                     T   AT__
GAM409  KIAA1580 5' AGGAGAAGGGGACCCGGGGGCT 69441     G  TCAGAA
           GG                    CCAGT CCT     CTTTCTCTT
                                ||||| |||     |||||||||
                                GGTCG GGG     GGAAGAGGA
                                   G   CCCAGG
GAM409  KIAA1580 5' GGGAGAGGGGAAGGTGGCTGG  69447     _    AGAA
                                CCAGT GCCTTC    CTTTCTC
                                ||||| ||||||    |||||||
                                GGTCG TGGAAG    GAGAGGG
                                   G     GG__
GAM409  KIAA1607 3' AAGAGAGAGGCAGCAGAGGCTC 63796     T    CAGAA_
           TGG                   CCAG GCCTT     CTTTCTCTT
                                |||| |||||     |||||||||
                                GGTC CGGAG     GAGAGAGAA
                                  T    ACGACG
GAM409  KIAA1609 5' GAGAGGAGCCCGTGGGCTGCTG 74235     _   TCAGAAC
           G                     CCAGT GCCT      TTTCTCTT
                                ||||| ||||      ||||||||
                                GGTCG CGGG      GAGGAGAG
                                   T   TGCCC__
GAM409  KIAA1614 5' GGGAGGGAGAAGGGGCTGG   70121     G    AGAA
                                CCAGT CCTTC    CTTTCTC
                                ||||| |||||    |||||||
                                GGTCG GGAAG    GGGAGGG
                                   G    A___
GAM409  KIAA1656 3' GGGAGAGAGTAGAGAGGGAGGT 65803   _    AGA___
           GACTGG                  T GCCTTC     ACTTTCTCTT
                                | ||||||     ||||||||||
                                A TGGAGG     TGAGAGAGGG
                                 G     GAGAGA
GAM409  KIAA1719 3' GAGGAGAGAGGCCTGG      68162     T    CAGAAC
                                CCAG GCCTT     TTTCTC
                                |||| |||||     ||||||
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                                GGTC CGGAG     GAGGAG
                                  _    A_____
GAM409  KIAA1753 3' AGAGGGCTGAGAGGGTCTGG  64877     T   __   AA
                                CCAG GCCT  TCAG  CTTT
                                |||| ||||  ||||  ||||
                                GGTC TGGG  AGTC  GAGA
                                  _   AG   GG
GAM409  KIAA1755 3' GGAGAGAGGCAGGCCTGG    61350     T   TCAGAA
                                CCAG GCCT     CTTTCTCT
                                |||| ||||     ||||||||
                                GGTC CGGA     GAGAGAGG
                                  _   CG____
GAM409  KIAA1795 3' AGGGGGAGGGAGAGGTGTTGG 72147     TG   CAGAA
                                CCAG  CCTT    CTTTCTCTT
                                ||||  ||||    |||||||||
                                GGTT  GGAG    GGAGGGGGA
                                  GT   AG___
GAM409  KIAA1795 3' GGGGGAGGGAGAGGTGTTGG  72153     TG   CAGAA
                                CCAG  CCTT    CTTTCTCT
                                ||||  ||||    ||||||||
                                GGTT  GGAG    GGAGGGGG
                                  GT   AG___
GAM409  KIAA1811 3' GGGGGAGGGACGGGAGCTGG  64797     G  TCAGAA
                                CCAGT CCT     CTTTCTCT
                                ||||| |||     ||||||||
                                GGTCG GGG     GGAGGGGG
                                   A  CAG___
GAM409  KIAA1813 5' GAGGGAGGCAGGGCACTG    70299       CAGAA  TT
                                CAGTGCCTT    CT  CTC
                                |||||||||    ||  |||
                                GTCACGGGA    GA  GAG
                                     CG___  GG
GAM409  KIAA1821 3' AGGGGCAGAGGGTACTGG    71776        AGAACTT
                                CCAGTGCCTTC      TCTCT
                                ||||||||||      |||||
                                GGTCATGGGAG      GGGGA
                                      AC_____
GAM409  KIAA1855 3' GGAGGGAGGGAGGGCTGG    92345     G    AGAA  TT
                                CCAGT CCTTC   CT  CTCT
                                ||||| |||||   ||  ||||
                                GGTCG GGAGG   GA  GAGG
                                  _    ____ GG
GAM409  KIAA1863 3' AGGGGGAGCGGGCATTG     64867       TCAGAA  TT
                                CAGTGCCT     CT  CTCT
                                ||||||||     ||  ||||
                                GTTACGGG     GA  GGGA
                                     C_____  GG
GAM409  KIAA1872 3' AAGAGGAAGATACAGGGTATCG 62920    A     CAGAA
            G                    CC GTGCCTT    CTTTCTCTT
                                || |||||||    |||||||||
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                                GG TATGGGA    GAAGGAGAA
                                 C      CATA_
GAM409  KIAA1904  3'  AAGAGAGGGTGTGGGGTCTGG  73475     T   T  GA
                                CCAG GCCT CA  ACTTTCTCTT
                                |||| |||| ||  ||||||||||
                                GGTC TGGG GT  TGGGAGAGAA
                                  _   _ G_
GAM409  KIAA1952  5'  GAGGGAGGCAGGGGGCCTGG   73171     T    AGAA  TT
                                CCAG GCCTTC   CT  CTC
                                |||| ||||||   ||  |||
                                GGTC CGGGGG   GA  GAG
                                  _    ACG_  GG
GAM409  KIAA1981  3'  GGGAGAGTGAGGTTGCTGG   88345      GC   AGA
                                CCAGT  CTTC   ACTTTCTC
                                |||||  ||||   ||||||||
                                GGTCG  GGAG   TGAGAGGG
                                   TT   ___
GAM409  KOC1      3'  AAGGGAAGTGCTGAATGGTGTT 91068     TG _    A     CTT
           GG                     CCAG  CC TTCAG ACTTTCT
                                |||||  || ||||| |||||||
                                GGTT  GG AAGTC TGAAGGG
                                  GT  T    G      AA
GAM409  KR18      3'  AGAGAGAGGCCAGGCGCGG   52737    A    TCAGAA
                                CC GTGCCT     CTTTCTCT
                                || ||||||     ||||||||
                                GG CGCGGA     GAGAGAGA
                                 _     CCG___
GAM409  LASP1     3'  GAGGGGCAGGACCTGAAGGTAT 20456          AA_  T
           TGG                    CCAGTGCCTTCAG   CT TCTCTT
                                ||||||||||||||  || ||||||
                                GGTTATGGAAGTC   GA GGGGAG
                                       CAG  C
GAM409  LASP1     3'  GGGAGTCTTGGGTGGCGCTGG  20460       _   GA   TT
                                CCAGTGCC TTCA  ACT  C
                                |||||||| ||||  |||  |
                                GGTCGCGG GGGT  TGA  G
                                     T   TC   GG
GAM409  LIP8      5'  AAGGGAAAGTACAAGGGAGCTG 88148      G   CAGA
           G                     CCAGT CCTT    ACTTTCTCTT
                                |||||| ||||   ||||||||||
                                GGTCG GGGA    TGAAAGGGAA
                                  A    ACA_
GAM409  LPAAT-delta 3'  GGGGAGGGCAGGGCTGG     39291      G   TCAGAA
                                CCAGT CCT     CTTTCTC
                                ||||| |||     |||||||
                                GGTCG GGA     GGAGGGG
                                  _  CG_____
GAM409  LSM1      5'  GAGGGAAGAGGTTTTGGACGCG 27094       C       __
           CTGG                    CAGTGC TTCAGAACT  TTCTCTT
                                |||||| |||||||||  |||||||
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                                GTCGCG AGGTTTTGG  AAGGGAG
                                   C        AG
GAM409  LSM1     5'  GGAGGGAAGAGGTTTTGG    27095      T    CAGAAC TT
                                CCAG GCCTT     T  CTCT
                                |||| |||||     |  ||||
                                GGTT TGGAG     A  GAGG
                                  T    A_____ GG
GAM409  LSR68    5'  GAGGGGGGCTGCTGAAGGCATG 37935     G       AA__  TT   TT
              G                  CCA TGCCTTCAG    CT  CTC
                                ||| |||||||||    ||  |||
                                GGT ACGGAAGTC    GG  GAG
                                  _       GTCG  GG
GAM409  MANBAL   3'  AAGAGGAGGCCTGAGGAGCTGG 41976      GC     AA
                                CCAGT  CTTCAG  CTTTCTCTT
                                |||||  ||||||  |||||||||
                                GGTCG  GGAGTC  GGAGGAGAA
                                   A_     C_
GAM409  MAP4K3   5'  GGGAGGGAGGCGGGGGGCACCT 13242      _      AGAA  TT
              GG                   CCAG TGCCTTC    CT  CTCTT
                                |||| |||||||    ||  |||||
                                GGTC ACGGGGG    GA  GAGGG
                                  C      GCG_  GG
GAM409  MAPKAPK2 5'  GGGAGGGAGGGAGGGCGCCGG  16473    A      AGAA  TT
                                CC GTGCCTTC    CT  CTCTT
                                || ||||||||    ||  |||||
                                GG CGCGGGAG    GA  GAGGG
                                 C       G___  GG
GAM409  MAPKAPK2 5'  GGGAGGGAGGGAGGGCGCCGG  51984    A      AGAA  TT
                                CC GTGCCTTC    CT  CTCTT
                                || ||||||||    ||  |||||
                                GG CGCGGGAG    GA  GAGGG
                                 C       G___  GG
GAM409  MCC2     5'  AGGAGAAGCATTCAGAGGGCAC 72062          A   C_
              TGG                    CCAGTGCCTTC GAA  TTTCTCTT
                                |||||||||| |||  ||||||||
                                GGTCACGGGAG CTT  GAAGAGGA
                                      A   AC
GAM409  MDS025   3'  GGATTTTGTGGGTATTGG    41540          T    CTT
                                CCAGTGCCT CAGAA   TCT
                                ||||||||| |||||   |||
                                GGTTATGGG GTTTT   AGG
                                     T    ___
GAM409  MGC10200 3'  GAGAGGGGAGAGGGGCTGG    58987      G    CAGAA
                                CCAGT CCTT     CTTTCTC
                                ||||| ||||     |||||||
                                GGTCG GGAG     GGGAGAG
                                   G    AG___
GAM409  MGC10561 3'  GGGGGAGGAGGGCCTGG     51001      T     AGAA  TT
                                CCAG GCCTTC    CT  CTC
                                |||| ||||||    ||  |||
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                                GGTC CGGGAG   GA  GGG
                                  _    _____ GG
GAM409  MGC10992  5' GGGAAGCGGGGCACGG     52626    A     CAGAAC
                                CC GTGCCTT     TTTCTC
                                || |||||||     ||||||
                                GG CACGGGG     GAAGGG
                                  _     C_____
GAM409  MGC11266  5' GGAGAAGCAAGGACATTGG   44241      _   CAGAAC
                                CCAGTG CCTT     TTTCTCT
                                |||||| ||||     |||||||
                                GGTTAC GGAA     GAAGAGG
                                   A   C_____
GAM409  MGC1203   3' GGGGGAGGGGGGGCGTTG    44154        AGAA  TT
                                CAGTGCCTTC   CT  CTC
                                ||||||||||   ||  |||
                                GTTGCGGGGG   GA  GGG
                                      _____ GG
GAM409  MGC13057  5' GAGAGGGAAAGCACTGG     50308       C   AGAAC
                                CCAGTGC TTC    TTTCTC
                                ||||||| |||    ||||||
                                GGTCACG AAG    GGAGAG
                                   A  _____
GAM409  MGC14386  5' GAGAGGGTAGAGGGCATAGG   53208    A      AGA
                                CC GTGCCTTC   ACTTTCTC
                                || ||||||||   ||||||||
                                GG TACGGGAG   TGGGAGAG
                                 A      A__
GAM409  MGC14425  5' AGGGGAAAAGGGGGGCGCTGG  51864          AGAAC
                                CCAGTGCCTTC    TTTCTCTT
                                ||||||||||    ||||||||
                                GGTCGCGGGGG    AAAGGGGA
                                      GA___
GAM409  MGC14839  3' GGGGGAAGGGGGCTGAGGCGTG 54697    G    T   AA_
           G                     CCA TGCCT CAG   CTTTCTCTT
                                ||| ||||| |||   |||||||||
                                GGT GCGGA GTC   GGAAGGGGG
                                  _    _  GGG
GAM409  MGC15631  3' AGGAGGGGGCCCTGAGGCATGG 51258    G    T   AA  TT
                                CCA TGCCT CAG  CT  CTCTT
                                ||| ||||| |||  ||  |||||
                                GGT ACGGA GTC  GG  GAGGA
                                  _    _  CC  GG
GAM409  MGC15677  5' GGGAGAAAGTTACAGAACTGG  51799      GC  TCAG
                                CCAGT  CT   AACTTTCTCTT
                                |||||  ||   ||||||||||
                                GGTCA  GA   TTGAAAGAGGG
                                   A_  CA__
GAM409  MGC16063  5' GGAGAGAGTTACAGGTTGG   53860    GT   TCAG
                                CCA  GCCT   AACTTTCTCT
                                |||  ||||   |||||||||
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                                GGT  TGGA   TTGAGAGAGG
                                  __   CA__
GAM409  MGC21688 3' AGAGGAGGCAGGGGCTGG   58264     G  TCAGAA
                                CCAGT CCT     CTTTCTCT
                                ||||| |||     ||||||||
                                GGTCG GGA     GGAGGAGA
                                  G  C_____
GAM409  MGC23401 5' GAGAGAGAGCTGGGGTGCTGG 58684     TG  T  AA
                                CCAG  CCT CAG  CTTTCTC
                                ||||  ||| |||  |||||||
                                GGTC  GGG GTC  GAGAGAG
                                  GT  _  GA
GAM409  MGC2705  3' GGGGGAAGGTTGGGGGGTGTCT 51115     _     AG
           GG                     CCAG TGCCTTC  AACTTTCTCTT
                                ||||  |||||||  ||||||||||
                                GGTC GTGGGGG  TTGGAAGGGGG
                                  T     G_
GAM409  MGC2705  3' AAGGGGTATGTTGGGGGCTTGG 51110     T      AACTT
                                CCAG GCCTTCAG    TCTCTT
                                |||| ||||||||    ||||||
                                GGTT CGGGGGTT    GGGGAA
                                  _      GTAT_
GAM409  MGC2865  3' GGAGAGAGTGAGGGGTTGG   50452     G   CAGA
                                CCAGT CCTT   ACTTTCTCT
                                ||||| ||||   |||||||||
                                GGTTG GGAG   TGAGAGAGG
                                  G   _____
GAM409  MGC35558 5' GAGAGAAGGGGAGGAGGTCTGG 58782     T    AGAA
                                CCAG GCCTTC   CTTTCTCTT
                                |||| ||||||   |||||||||
                                GGTC TGGAGG   GGAAGAGAG
                                  _    AGG_
GAM409  MGC4604  5' GAGAGAGAGAGAGGGCATTG  48978         AGAA
                                CAGTGCCTTC   CTTTCTCTT
                                ||||||||||   |||||||||
                                GTTACGGGAG   GAGAGAGAG
                                     A___
GAM409  MGC4638  3' AAGAGGGAGATGGGCAAGGCGC 48937        CAGAA_  TT
           TG                    CAGTGCCTT     CT  CTCTT
                                |||||||||     ||  |||||
                                GTCGCGGAA     GA  GAGAA
                                     CGGGTA  GG
GAM409  MGC5469  3' GAGGGGAATGGAAGGGCATGG  50396    G   _  AGAAC
                                CCA TGCC TTC    TTTCTCTT
                                ||| |||| |||    ||||||||
                                GGT ACGG AAG    AAGGGGAG
                                  _   G  GT___
GAM409  MGC9564  3' GGGAGGGAGGTAAGAGGGGCTT 54742    _ G   CAGAA  TT
           GG                    CCA GT CCTT    CT  CTCTT
                                ||| || ||||    ||  |||||
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                                GGT CG GGAG    GA  GAGGG
                                  T  G   AATG_  GG
GAM409  MIDORI   5'  AGTTACTGGGGGTGTTGG   73783     TG     _
                                CCAG  CCTTCAG AACT
                                ||||  ||||||| ||||
                                GGTT  GGGGGTC TTGA
                                  GT      A
GAM409  MLLT10   5'  AGGAGGAGGCGGAGGAGGCGGT 16165    G     AGAA
          GG                    CCA TGCCTTC   CTTTCTCTT
                                ||| |||||||   |||||||||
                                GGT GCGGAGG   GGAGGAGGA
                                  G      AGGC
GAM409  MY014    5'  GGGAGGCCTTGGAGGCGTAGG  48141    AG       AA
                                CC  TGCCTTCAG  CTTTCT
                                ||  |||||||||  ||||||
                                GG  GCGGAGGTT  GGAGGG
                                 AT        CC
GAM409  NAG14    3'  AAGAGAAAGGGTGGGCGTGG   42159    G    TCAGAA
                                CCA TGCCT     CTTTCTCTT
                                ||| |||||     |||||||||
                                GGT GCGGG     GAAAGAGAA
                                  _    TGG___
GAM409  NAG14    3'  AAGGGAGAGACGAAAAGGGTAC 42160    A     CAGAA_
          AGG                     CC GTGCCTT     CTTTCTCTT
                                || |||||||     |||||||||
                                GG CATGGGA     GAGAGGGAA
                                 A      AAAGCA
GAM409  NAV1     5'  AGGAGAAGGACACTGAGCTGCT 39949      _ CT    AA_
          GG                    CCAGT GC  TCAG   CTTTCTCTT
                                ||||| ||  ||||   |||||||||
                                GGTCG CG  AGTC   GGAAGAGGA
                                  T  __    ACA
GAM409  NCOR1    3'  AGGGGAACAGGGTGCAGG    20877    A TG   CAGAAC
                                CC G  CCTT     TTTCTCT
                                || |  ||||     |||||||
                                GG C  GGGA     AAGGGGA
                                 A GT   C_____
GAM409  NDRG4    3'  GGGGGCTGAAGGTTCTGG    39987     T      AA
                                CCAG GCCTTCAG  CTT
                                |||| ||||||||  |||
                                GGTC TGGAAGTC  GGG
                                  T       GG
GAM409  NDRG4    3'  GGGGGCTGAAGGTTCTGG    43290     T      AA
                                CCAG GCCTTCAG  CTT
                                |||| ||||||||  |||
                                GGTC TGGAAGTC  GGG
                                  T       GG
GAM409  NET-7    3'  GGAGGGAAGGGCATCTGG    24710     _     CAGAAC TT
                                CCAG TGCCTT     T  CTCT
                                |||| ||||||     |  ||||
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                                GGTC ACGGGA     A  GAGG
                                  T     _______ GG
GAM409  NGEF     3'  GGGGGGGGGGGGGGCTCTGG   69163      T     AGAA  TT
                                CCAG GCCTTC    CT  CTCT
                                |||| ||||||    ||  ||||
                                GGTC CGGGGG    GG  GGGG
                                  T     _____  GG
GAM409  NPEPL1   3'  GGGAGGGGACCGGGAAGCGCTG 45091        C   AGAA_      TT
          G                      CCAGTGC TTC     CTTTCTC
                                |||||||  |||     |||||||
                                GGTCGCG AGG     GGGAGGG
                                    A   GCCAG
GAM409  NUDC     3'  AGGAGAAAGGCTGGGTCTTGG  21713      T   TT   AA
                                CCAG GCC  CAG  CTTTCTCTT
                                |||| |||  |||  |||||||||
                                GGTT TGG  GTC  GAAAGAGGA
                                  C   __   G_
GAM409  NXPH3    3'  GGGAGGGGTGACCAGGTGCTGG 65767      TG   TCAGAA
                                CCAG  CCT     CTTTCTC
                                ||||  |||     |||||||
                                GGTC  GGA     GGGAGGG
                                  GT   CCAGTG
GAM409  ODZ2     3'  AAGAGGAGGAGTGAGCACTGG  70858        CT   GAA
                                CCAGTGC  TCA   CTTTCTCTT
                                |||||||  |||   |||||||||
                                GGTCACG  AGT   GGAGGAGAA
                                    __   GA_
GAM409  PADI3    3'  GAGAGGGGGCTAAGGGGCTGG  32659       G    C  AA
                                CCAGT CCTT AG  CTTTCTC
                                ||||| |||| ||  |||||||
                                GGTCG GGAA TC  GGGAGAG
                                  G    _  GG
GAM409  PASK     5'  GAGAGAGAGTGGCCAGTGCTGG 30717      TG CTTCAGA
                                CCAG  C       ACTTTCTCTT
                                ||||  |       ||||||||||
                                GGTC  G       TGAGAGAGAG
                                  GT ACCGG__
GAM409  PCAF     5'  AGGGGGCGGGAGGGCGTGG    13945     G      AGAA  TT
                                CCA TGCCTTC    CT  CT
                                |||  |||||||    ||  ||
                                GGT GCGGGAG    GG  GA
                                  _      GGC_  GG
GAM409  pcnp     3'  AGAGGGAGTATTGTATTGG    39788        CTTC  A   TT
                                CCAGTGC    AG ACT  CTCT
                                |||||||    || |||  ||||
                                GGTTATG    TT TGA  GAGA
                                    _____  A   GG
GAM409  PEX11B   3'  AGGGGAGGTATAAGGTTTGG   13888      T    CAGA
                                CCAG GCCTT    ACTTTCTCT
                                |||| |||||    |||||||||
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                                GGTT TGGAA   TGGAGGGGA
                                  _    TA__
GAM409  PHYHIP   3' GGAGGCCTGGAGGCTTGG   28612     T      AA
                                CCAG GCCTTCAG  CTTT
                                |||| ||||||||  ||||
                                GGTT CGGAGGTC  GAGG
                                  _       CG
GAM409  PIP5K2B  5' GGGGGAGGCCTGAGGCCGCTGG 13078       C     AA  TT
                                CCAGTG CTTCAG  CT  CTC
                                |||||| ||||||  ||  |||
                                GGTCGC GGAGTC  GA  GGG
                                   C     CG  GG
GAM409  PIP5K2B  5' GGGGGAGGCCTGAGGCCGCTGG 56895       C     AA  TT
                                CCAGTG CTTCAG  CT  CTC
                                |||||| ||||||  ||  |||
                                GGTCGC GGAGTC  GA  GGG
                                   C     CG  GG
GAM409  PITPNM   3' GGAGGGAGGAGGGCGTGG    16934     G      AGAA  TT
                                CCA TGCCTTC    CT  CTCT
                                ||| |||||||    ||  ||||
                                GGT GCGGGAG    GA  GAGG
                                  _     _____ GG
GAM409  PITPNM   3' GGGAGGAGGGCGTGGGCATGG  16935     G    TCAGAA
                                CCA TGCCT     CTTTCTCTT
                                ||| |||||     |||||||||
                                GGT ACGGG     GGAGGAGGG
                                  _    TGCG__
GAM409  PLP1     3' AGAGAAACAGGGTGTTG     5004      TG    CAGAAC
                                CAG  CCTT     TTTCTCT
                                |||  ||||     |||||||
                                GTT  GGGA     AAAGAGA
                                  GT   C_____
GAM409  PMVK     3' TAGGGGGGGTCTAGATTCTGAG 21611        _______  TT   T
           GGGGTTGG                CTTCAGA     ACT  CTCT   A
                                |||||||     |||  ||||   |
                                GGAGTCT     TGG  GGGA   T
                                   TAGATC   GG      T
GAM409  PMVK     3' TAGGGGGGGTCTAGATTCTGAG 94613        _______  TT   T
           GGGGTTGG                CTTCAGA     ACT  CTCT   A
                                |||||||     |||  ||||   |
                                GGAGTCT     TGG  GGGA   T
                                   TAGATC   GG      T
GAM409  PNMA5    3' AAGAGAAGAGAGGATGTGTTGG 73589      TG CT  AGAAC
                                CCAG  C  TC    TTTCTCTT
                                ||||  |  ||    ||||||||
                                GGTT  G  AG    GAAGAGAA
                                  GT T_  GAGA_
GAM409  POLM     3' GAGAGGGAGAGGGCCTGG    91089      T     AGAA
                                CCAG GCCTTC    CTTTCTC
                                |||| ||||||    |||||||
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                                GGTC CGGGAG    GGGAGAG
                                  _     A___
GAM409   PP1628    5'  GGGAGAAGCGGAAGGAGCTGG  47303      G    AGAAC
                                CCAGT CCTTC    TTTCTCTT
                                ||||| |||||    ||||||||
                                GGTCG GGAAG    GAAGAGGG
                                   A    GC___
GAM409   PP3501    3'  GGAGGGAGGGAGGGGCTGG   41372      G    AGAA  TT
                                CCAGT CCTTC    CT  CTCT
                                ||||| |||||    ||  ||||
                                GGTCG GGAGG    GA  GAGG
                                   G    ____ GG
GAM409   PQBP1     5'  AGAGGAACAGGGCCCTGG    19125      T    CAGAAC
                                CCAG GCCTT     TTTCTCT
                                |||| |||||     |||||||
                                GGTC CGGGA     AAGGAGA
                                  C    C_____
GAM409   PRPF8     3'  AGGGGGAGGTTTACTCTGCG   61182     CTTCA
                                TGC    GAACTTTCTCTT
                                |||    ||||||||||||
                                GCG    TTTGGAGGGGGA
                                 TCTCA
GAM409   PSK      5'  AGGAGAGGCAGAGAGGGCGCGG 32359    A      AGAA_     CTT
                                CC GTGCCTTC    CTTTCT
                                || ||||||||    ||||||
                                GG CGCGGGAG    GAGAGG
                                 _      AGACG     A
GAM409   PSMD3     3'  AGGGGGTGGGGGTGCTGG    10970     TG    AGA   TT
                                CCAG  CCTTC   ACT  CT
                                ||||  |||||   |||  ||
                                GGTC  GGGGG   TGG  GA
                                  GT    ___   GG
GAM409   PTRF      3'  AGGGAGAGCAGGGTGCCGG   63495    A TG   CAGAA
                                CC G  CCTT    CTTTCTCT
                                || |  ||||    ||||||||
                                GG C  GGGA    GAGAGGGA
                                 C GT   C____
GAM409   RAB17     3'  AAGGGCAGCTGGGGGCAGTGG  42388     G       AACTTT
                                CCA TGCCTTCAG     CTCTT
                                ||| |||||||||     |||||
                                GGT ACGGGGGTC     GGGAA
                                  G       GAC___
GAM409   RAB20     5'  GGGAGAGGGCGCGGGGGCGCTG 35156          AGAA
           G                     CCAGTGCCTTC   CTTTCTCTT
                                ||||||||||    |||||||||
                                GGTCGCGGGGG   GGGAGAGGG
                                      CGC_
GAM409   RAB3IL1   5'  GGGAGGACGCGGCGGCGCTGG  25465       T  AGAACT
                                CCAGTGCC TC     TTCTCTT
                                |||||||| ||     |||||||
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                                GGTCGCGG GG     AGGAGGG
                                    C  CGC___
GAM409  RBT1     3'  GAGGGGGTGGGAGGGGCTGG  25352      G    AGA   TT
                                CCAGT CCTTC   ACT  CTC
                                ||||| |||||   |||  |||
                                GGTCG GGAGG   TGG  GAG
                                   G    G__   GG
GAM409  RERG     3'  AGGAGAAGAAGCTGAGCTATTG 51894      _ CT    AAC
           G                     CCAGT GC  TCAG   TTTCTCTT
                                ||||| ||  ||||   ||||||||
                                GGTTA CG  AGTC   GAAGAGGA
                                   T __    GAA
GAM409  RHOBTB2  3'  GGAGGAGGGCGGGGCTGG    60944      G  TTCAGAA
                                CCAGT CC      CTTTCTCT
                                ||||| ||      ||||||||
                                GGTCG GG      GGAGGAGG
                                   G  CG_____
GAM409  RIP60    5'  GGGAGAGGGCAGCATAAGGCAC 25457         CAGAA_
           TG                    CAGTGCCTT     CTTTCTCTT
                                |||||||||     |||||||||
                                GTCACGGAA     GGGAGAGGG
                                    TACGAC
GAM409  RNF20    3'  AGAGAAGAAGAGGAGCTGG   38964      G    CAGAAC
                                CCAGT CCTT     TTTCTCT
                                ||||| ||||     |||||||
                                GGTCG GGAG     GAAGAGA
                                   A    AA____
GAM409  RoXaN    3'  AGGAGGTGCAGGGTGTTGG   46628      TG    CAGA
                                CCAG  CCTT    ACTTTCT
                                ||||  ||||    |||||||
                                GGTT  GGGA    TGGAGGA
                                  GT    CG__
GAM409  RoXaN    3'  AGGGGGGGTGAGGCAGGGCCTG 46629      T    CAGA_   TT    T
           G                     CCAG GCCTT     ACT  CTCT
                                |||| |||||    |||  ||||
                                GGTC CGGGA    TGG  GGGA
                                  _    CGGAG   GG
GAM409  RP4-622L5 3'  GGGGAGGCAGCACTGG      38931        CTTCAGAA
                                CCAGTGC       CTTTCTC
                                |||||||       |||||||
                                GGTCACG       GGAGGGG
                                    AC_______
GAM409  RPIA     5'  GGGAGGGCCGGGGGGCGCGG   57967    A       AGAA
                                CC GTGCCTTC    CTTTCTC
                                || ||||||||    |||||||
                                GG CGCGGGGG    GGGAGGG
                                  _       CC__
GAM409  SARM     3'  GAGGGAAGGGAAGTCAGGCTTG 30608      T    TCAGAA
           G                     CCAG GCCT     CTTTCTCTT
                                |||| ||||     |||||||||
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                                GGTT CGGA     GGAAGGGAG
                                  _   CTGAAG
GAM409  SARM    3'  AGGGAAATAGGGGAACTGG   30595      G   CAGAAC
                                CCAGT CCTT     TTTCTCT
                                |||||| ||||     |||||||
                                GGTCA GGGG     AAAGGGA
                                   A   AT____
GAM409  SARM    3'  AGTTCTGGAGACACTGG     30596      C
                                CCAGTG CTTCAGAACT
                                |||||| ||||||||||
                                GGTCAC GAGGTCTTGA
                                   A
GAM409  SCAND2  3'  AAGAGGAATCCTGGAGGCTTGG 53312     T      AAC
                                CCAG GCCTTCAG   TTTCTCTT
                                |||| ||||||||   ||||||||
                                GGTT CGGAGGTC   AAGGAGAA
                                  _       CT_
GAM409  SCYD1   3'  AGGGGAGATAAGGGTATCTGG  90923     _     CAGAAC
                                CCAG TGCCTT     TTTCTCTT
                                |||| ||||||     ||||||||
                                GGTC ATGGGA     AGAGGGGA
                                  T     AT____
GAM409  SEC24C  3'  GGGAGAGAGGCAGAGGCAGCTG 16999     _     CAGAA
           G                     CCAG TGCCTT     CTTTCTCTT
                                |||| ||||||     |||||||||
                                GGTC ACGGAG     GAGAGAGGG
                                  G     ACG__
GAM409  SEF     3'  GGGAGAGAATGGAGGACTGG   69466      G     GAA
                                CCAGT CCTTCA   CTTTCTC
                                ||||| ||||||   |||||||
                                GGTCA GGAGGT   GAGAGGG
                                  _     AA_
GAM409  SELB    3'  GAGGGGGATGGGTTGCTGG   61915      _  TCAGAA  TT
                                CCAGTG CCT     CT  CTC
                                |||||| |||     ||  |||
                                GGTCGT GGG     GG  GAG
                                   T   TA____  GG
GAM409  SEMA4F  3'  AGAGCCCTGGAGGTGGTTGG   14938     GT_      AA
                                CCA   GCCTTCAG  CTTT
                                |||   ||||||||  ||||
                                GGT   TGGAGGTC  GAGA
                                  TGG       CC
GAM409  SEMA4G  5'  GAGGGGGCTGGGGGCCTGG   94680     T      AA
                                CCAG GCCTTCAG  CTTTC
                                |||| ||||||||  |||||
                                GGTC CGGGGGTC  GGGAG
                                  _       GG
GAM409  SEMA6B  3'  AAGGGCTTGGGGGCCTGG    39615     T      AA
                                CCAG GCCTTCAG  CTTT
                                |||| ||||||||  ||||
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                                GGTC CGGGGGTT  GGAA
                                  _      CG
GAM409  SEMA6B   3' AAGGGCTTGGGGGCCTGG   49488     T      AA
                                CCAG GCCTTCAG  CTTT
                                |||| ||||||||  ||||
                                GGTC CGGGGGTT  GGAA
                                  _      CG
GAM409  SEMA6B   3' AAGGGCTTGGGGGCCTGG   55822     T      AA
                                CCAG GCCTTCAG  CTTT
                                |||| ||||||||  ||||
                                GGTC CGGGGGTT  GGAA
                                  _      CG
GAM409  SERPING1 3' AGGGCTCCTGAGGGTCTGG   3555      T      AACTTT
                                CCAG GCCTTCAG     CTCT
                                |||| ||||||||     ||||
                                GGTC TGGGAGTC     GGGA
                                  _      CTC___
GAM409  SHANK3   3' GGGGGAGGGGGGGAGACATTGG 65502       C    AGAA
                                CCAGTG CTTC    CTTTCTCT
                                |||||| ||||    ||||||||
                                GGTTAC GAGG    GGAGGGGG
                                   A   GG__
GAM409  SIAT8D   5' AAGAGAAGGTGCGGGAGCTGG  19028      G   TCAGA
                                CCAGT CCT    ACTTTCTCTT
                                ||||| |||    ||||||||||
                                GGTCG GGG    TGGAAGAGAA
                                   A   CG___
GAM409  SLC26A9  3' AAGAGGGGGATGGGTAGCTGG  53613     _    TCAGAA  TT
                                CCAG TGCCT     CT  CTCTT
                                |||| |||||     ||  |||||
                                GGTC ATGGG     GG  GAGAA
                                  G    TA____  GG
GAM409  SLC26A9  3' AAGAGGGGGATGGGTAGCTGG  56174     _    TCAGAA  TT
                                CCAG TGCCT     CT  CTCTT
                                |||| |||||     ||  |||||
                                GGTC ATGGG     GG  GAGAA
                                  G    TA____  GG
GAM409  SLC37A1  5' GGGGGAGGTGGGGGCTGG    38566      G   TCAGA
                                CCAGT CCT    ACTTTCTCT
                                ||||| |||    |||||||||
                                GGTCG GGG    TGGAGGGGG
                                   G  _____
GAM409  SLC38A5  3' GGAGGAGGCCAGGTCCTGG   53192     TG   TCAGAA
                                CCAG  CCT     CTTTCTCT
                                ||||  |||     ||||||||
                                GGTC  GGA     GGAGGAGG
                                  CT   CC____
GAM409  SLC39A3  3' GAGGGGGTGGGCCTGG      57974     T   TCAGA   TT
                                CCAG GCCT    ACT  CTC
                                |||| ||||    |||  |||
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                                GGTC CGGG    TGG  GAG
                                  _   _____  GG
GAM409  SLC4A11  3'  GAGGGGAGGTGTAGGTGTGTGG 49340    _ TG   TCAGA
                                CCA G  CCT    ACTTTCTCTT
                                ||| |  |||    ||||||||||
                                GGT T  GGA    TGGAGGGGAG
                                  G GT   TG___
GAM409  SMOC1    3'  GGGGGGGTGGGGGAGGGTGTTG 42153    TG    AGA_  TT   TT
                                CAG  CCTTC    ACT  CTC
                                |||  |||||    |||  |||
                                GTT  GGGAG    TGG  GGG
                                  GT    GGGG   GG
GAM409  SPEC1    3'  GGAGGAAGAGGGGTCTGG    39611      T    CAGAA
                                CCAG GCCTT    CTTTCTCT
                                |||| |||||    ||||||||
                                GGTC TGGGG    GAAGGAGG
                                  _    A____
GAM409  SS18L2   3'  AAGAGGAAACTCAGTAGGTGTT 32837     TG   TCA  AC
            GG                    CCAG  CCT   GA  TTTCTCTT
                                ||||  |||   ||  ||||||||
                                GGTT  GGA   CT  AAGGAGAA
                                  GT   TGA  CA
GAM409  SSH-3    3'  AGGAGAAGGTTGTAGGCATGG  36887    G    T  GA
                                CCA TGCCT CA  ACTTTCTCTT
                                ||| ||||| ||  ||||||||||
                                GGT ACGGA GT  TGGAAGAGGA
                                  _    T  __
GAM409  ST7L     3'  AGGAGAGATACCAATGTACTGG 57568       CTTCAGAAC
                                CCAGTGC       TTTCTCTT
                                |||||||       ||||||||
                                GGTCATG       AGAGAGGA
                                    TAACCAT__
GAM409  STAF42   3'  AGGATTTGAGGGTGTGG    53874    G       A
                                CCA TGCCTTCAGA CTT
                                ||| |||||||||| |||
                                GGT GTGGGAGTTT GGA
                                  _       A
GAM409  STAG3    3'  AGGGGAAAGAGTTGGGCATTG  24911       TT   AA
                                CAGTGCC  CAG  CTTTCTCTT
                                |||||||  |||  |||||||||
                                GTTACGG  GTT  GAAAGGGGA
                                    __   GA
GAM409  STAT5A   5'  GGGAGGGAGCAAGCGGGGCTGG 12014      G  TTCAGAA  TT
                                CCAGT CC      CT  CTCTT
                                ||||| ||      ||  |||||
                                GGTCG GG      GA  GAGGG
                                   G  CGAAC__  GG
GAM409  STK29    3'  GGGAGGAAAGGAAAGGGGCGTT 87578         CAGAA    _
            GG                    CCAGTGCCTT    CTTTC TCTT
                                ||||||||||    ||||| ||||
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                                GGTTGCGGGG    GAAAG AGGG
                                      AAAG_    G
GAM409  STK36   3'  GGTGTTGGAGGTGCTGG    72105     TG     A
                                CCAG  CCTTCAG ACT
                                ||||  ||||||| |||
                                GGTC  GGAGGTT TGG
                                  GT      G
GAM409  STMN3   3'  GGGGGAGGGGGGGTGATGG   31901    GT    AGAA  TT
                                CCA  GCCTTC   CT  CTC
                                |||  ||||||   ||  |||
                                GGT  TGGGGG   GA  GGG
                                 AG     _____  GG
GAM409  STX6    5'  GAGGGAGACCGGGAGGCACGG  19489    A      AGAA  TT
                                CC GTGCCTTC   CT  CTC
                                || ||||||||   ||  |||
                                GG CACGGAGG   GA  GAG
                                 _      GCCA  GG
GAM409  SV2     3'  GAGGGAAAGAAACCAGGCATCT 29308     _    TCAGAA
            GG                   CCAG TGCCT     CTTTCTCTT
                                ||||  |||||     |||||||||
                                GGTC ACGGA     GAAAGGGAG
                                  T    CCAAA_
GAM409  SYTL3   5'  GGAGGGAAGAGGCGTTG     81002         CAGAAC TT
                                CAGTGCCTT     T  CTCT
                                |||||||||     |  ||||
                                GTTGCGGAG     A  GAGG
                                     A_____ GG
GAM409  SZF1    3'  AGGGGAAGGGCTAGGGGTACCT 32231     _    TC  AA      T
            GG                   CCAG TGCCT  AG  CTTTCTCT
                                ||||  |||||  ||  ||||||||
                                GGTC ATGGG  TC  GAAGGGGA
                                  C    GA  GG
GAM409  TBC1D1  3'  GAGAGGGACAGAAGACGCTGG  64663       C    AGAA
                                CCAGTG CTTC    CTTTCTC
                                ||||||  ||||    |||||||
                                GGTCGC GAAG    GGGAGAG
                                   A    ACA_
GAM409  TBLR1   5'  GGGAGGGGGGAGCGGCGTTGG  45103        _  AGAA
                                CCAGTGCC TTC    CTTTCTC
                                ||||||||  |||    |||||||
                                GGTTGCGG GAG    GGGAGGG
                                     C   GG__
GAM409  TBLR1   5'  GGGGGTGGTTGGAGGCGGTGG  45104     G       A_   TT
                                CCA TGCCTTCAG  ACT  C
                                |||  |||||||||  |||  |
                                GGT GCGGAGGTT  TGG  G
                                  G       GG   GG
GAM409  TED     3'  AAGAGAAAGTCCAGGGACTGG  31630      G   TCA  A
                                CCAGT CCT   GA CTTTCTCTT
                                |||||  |||   ||  |||||||||
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                                GGTCA GGA   CT GAAAGAGAA
                                  G   C__  _
GAM409  TED      3'  GGAGGAAGTGGGGGCTGG    31641       G   TCAGA
                                CCAGT CCT    ACTTTCTCT
                                ||||| |||    |||||||||
                                GGTCG GGG    TGAAGGAGG
                                  G  _____
GAM409  TEKT2    3'  GGAGGAGGGCAGGGTTGG    27099     GT    CAGAA
                                CCA  GCCTT    CTTTCTCT
                                |||  |||||    ||||||||
                                GGT  TGGGA    GGAGGAGG
                                  __    CG___
GAM409  TIX1     3'  GAGAGAGGGCAAGGGCTTTGG  61744      T    CAGAA
                                CCAG GCCTT    CTTTCTC
                                |||| |||||    |||||||
                                GGTT CGGGA    GAGAGAG
                                  T    ACGG_
GAM409  TMPRSS5  3'  GGAGAGAGGTAGGAGCTGG   47786      G   TCAGAA
                                CCAGT CCT     CTTTCTCT
                                ||||| |||     ||||||||
                                GGTCG GGA     GAGAGAGG
                                  A   TG____
GAM409  TRIM22   3'  AAGATAATATTTGGAGGTATTG 20284            ACT  C
           G                     CCAGTGCCTTCAGA   TT TCTT
                                ||||||||||||||   || ||||
                                GGTTATGGAGGTTT   AA AGAA
                                        AT_  T
GAM409  TSPAN-5  5'  GAGGGGCTGGAGGTGCGG    19158    A TG      AAC TT
                                CC G  CCTTCAG   T  CTC
                                || |  |||||||   |  |||
                                GG C  GGAGGTC   G  GAG
                                 _ GT      ___ GG
GAM409  TU12B1-TY 3'  GAGAAAGTTCTGTAGG      33382     T
                                CCT CAGAACTTTCTC
                                ||| ||||||||||||
                                GGA GTCTTGAAAGAG
                                  T
GAM409  TUB      3'  GAGAGAAGTTGGGAGGGTGGTG 12426     G      AG    T
           G                     CCA TGCCTTC  AACTT CTCTT
                                ||| |||||||  ||||| |||||
                                GGT GTGGGAG  TTGAA GAGAG
                                  G      GG   _
GAM409  TUBB5    3'  GAGAAACAAGGCCTGG      20302      T    CAGAAC
                                CCAG GCCTT     TTTCTC
                                |||| |||||     ||||||
                                GGTC CGGAA     AAAGAG
                                  _    C_____
GAM409  U2AF65   3'  GGGGGTTGGGGGGGTTGG     23461     GT     AG    TT
                                CCA  GCCTTC  AACT  C
                                |||  ||||||  ||||  |
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                                GGT  TGGGGG  TTGG  G
                                  __     G_   GG
GAM409  UBE3B    5'  GGGACTTTGAGGGAGTTGG   76923     TG      ACTT
                                CCAG  CCTTCAGA   TCTC
                                ||||  ||||||||   ||||
                                GGTT  GGGAGTTT   AGGG
                                  GA       C___
GAM409  UBN1     3'  AGGATTTGAGGGCACT     33729          A
                                AGTGCCTTCAGA CTT
                                |||||||||||| |||
                                TCACGGGAGTTT GGA
                                       A
GAM409  UNC5D    3'  GGGGGAGGTGGGGAGTTGG   55141     TG   CAGA
                                CCAG  CCTT   ACTTTCTCT
                                ||||  ||||   |||||||||
                                GGTT  GGGG   TGGAGGGGG
                                  GA   _____
GAM409  UREB1    5'  AGGAGAAGAAGGGCAGGATGCT 48579       _  _  AGAAC
          GG                      CCAGTG CCT TC    TTTCTCTT
                                ||||||| ||| ||    ||||||||
                                GGTCGT GGA GG    GAAGAGGA
                                   A  C  GAA__
GAM409  VEGFC    5'  AGGAGGGGGACGAGGGCTCTGG 18307     T     AGAA  TT
                                CCAG GCCTTC   CT  CTCTT
                                |||| ||||||   ||  |||||
                                GGTC CGGGAG   GG  GAGGA
                                  T     CA__  GG
GAM409  WBSCR17  3'  GGGAGGGAGCTGGGGCACTGG  81302         T   AA
                                CCAGTGCCT CAG  CTTTCTC
                                |||||||||| |||  |||||||
                                GGTCACGGG GTC  GGGAGGG
                                      _  GA
GAM409  WFDC2    3'  AGAGAAAGTTTCTGCCTGG   20345     T  CTTCA
                                CCAG GC    GAACTTTCTCT
                                |||| ||    ||||||||||
                                GGTC CG    TTTGAAAGAGA
                                  _ TC___
GAM409  WFDC2    3'  AGAGAAAGTTTCTGCCTGG   54935     T  CTTCA
                                CCAG GC    GAACTTTCTCT
                                |||| ||    ||||||||||
                                GGTC CG    TTTGAAAGAGA
                                  _ TC___
GAM409  WFDC2    3'  AGAGAAAGTTTCTGCCTGG   54936     T  CTTCA
                                CCAG GC    GAACTTTCTCT
                                |||| ||    ||||||||||
                                GGTC CG    TTTGAAAGAGA
                                  _ TC___
GAM409  WFDC2    3'  AGAGAAAGTTTCTGCCTGG   54934     T  CTTCA
                                CCAG GC    GAACTTTCTCT
                                |||| ||    ||||||||||
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                                GGTC CG    TTTGAAAGAGA
                                  _ TC___
GAM409  YAP     5'  AAGAGGAGGTGGAGAAGGCTTG 36783     T     AGA
              G                   CCAG GCCTTC   ACTTTCTCTT
                                  |||| ||||||   ||||||||||
                                  GGTT CGGAAG   TGGAGGAGAA
                                    _     AGG
GAM409  YAP     5'  AAGAGGAGGTGGAGAAGGCTTG 57458     T     AGA
              G                   CCAG GCCTTC   ACTTTCTCTT
                                  |||| ||||||   ||||||||||
                                  GGTT CGGAAG   TGGAGGAGAA
                                    _     AGG
GAM409  YAP     5'  AAGAGGAGGTGGAGAAGGCTTG 57460     T     AGA
              G                   CCAG GCCTTC   ACTTTCTCTT
                                  |||| ||||||   ||||||||||
                                  GGTT CGGAAG   TGGAGGAGAA
                                    _     AGG
GAM409  YKT6    3'  GGGGGGAGGCCAAGGGTTTGG  21606     T    CAGAA  TT
                                  CCAG GCCTT    CT  CTCT
                                  |||| |||||    ||  ||||
                                  GGTT TGGGA    GA  GGGG
                                    _    ACCG_  GG
GAM409  ZDHHC4  3'  GAGAGAGGGGAAAATGGGTGTT 36157     TG   TCAGAA
              G                   CAG  CCT     CTTTCTCTT
                                  |||  |||     |||||||||
                                  GTT  GGG     GGGAGAGAG
                                    GT   TAAAAG
GAM409  ZER6    3'  GGGAAAATTTAGGGGTGCTGG  63380     TG   TC   AC
                                  CCAG  CCT  AGA  TTTCTC
                                  ||||  |||  |||  ||||||
                                  GGTC  GGG  TTT  AAAGGG
                                    GT   GA   A_
GAM409  ZFPL1   3'  GGAGAGGCGGGGTAATGG    59656     G     CAGAA
                                  CCA TGCCTT    CTTTCT
                                  ||| ||||||    ||||||
                                  GGT ATGGGG    GAGAGG
                                    A     CG___
GAM409  ZNF282  5'  GAGAGGGGGAAGGCGCCTGG   89213     _     AGAA
                                  CCAG TGCCTTC    CTTTCTC
                                  |||| |||||||    |||||||
                                  GGTC GCGGAAG    GGGAGAG
                                    C      G___
GAM409  ZWINT   3'  GGGAGGGGGTACTGGCCTTGG  22936     T   TTC  A   TT
                                  CCAG GCC   AG ACT  CTCTT
                                  |||| |||   || |||  |||||
                                  GGTT CGG   TC TGG  GAGGG
                                    C  ___ A   GG
GAM409  ZWINT   3'  GGGAGGGGGTACTGGCCTTGG  52222     T   TTC  A   TT
                                  CCAG GCC   AG ACT  CTCTT
                                  |||| |||   || |||  |||||
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                                GGTT CGG   TC TGG  GAGGG
                                  C  ___  A   GG
GAM409   LOC112885 3'  GGGAGGAAAGAAAGGGCGGTGG 56528     G     CAGAAC
                                CCA TGCCTT     TTTCTCTT
                                ||| ||||||     ||||||||
                                GGT GCGGGA     AAGGAGGG
                                  G     AAGA__
GAM409   LOC115110 5'  AAGGGAGAGGACTTGGGGGTTG 71709     GT      _ AA
           G                     CCA  GCCTTCA G  CTTTCTCTT
                                ||| |||||||  |  |||||||||
                                GGT  TGGGGGT C  GAGAGGGAA
                                  __      T AG
GAM409   LOC115110 5'  GGGAGGGATCTGGGGCAGCTGG 71720      _    T    A
                                CCAG TGCCT CAGA CTTTCTC
                                |||| ||||| |||| |||||||
                                GGTC ACGGG GTCT GGGAGGG
                                  G    _    A
GAM409   LOC115708 3'  GGAGGGAGGGGGGGCATTG    73554          AGAA  TT
                                CAGTGCCTTC    CT  CTCT
                                ||||||||||    ||  ||||
                                GTTACGGGGG    GA  GAGG
                                      _____  GG
GAM409   LOC116412 5'  AGGGGAAGTCCAGCATTGG    73877        CTTCA  A
                                CCAGTGC     GA CTTTCTCT
                                |||||||     || ||||||||
                                GGTTACG     CT GAAGGGGA
                                    AC___  _
GAM409   LOC121274 3'  AGAGGAGAGTGGTACTGG     74058        TTCAGA     _
                                CCAGTGCC      ACTTTC TCT
                                ||||||||      |||||| |||
                                GGTCATGG      TGAGAG AGA
                                    _______      G
GAM409   LOC121457 5'  GAGGGAAGGGGCTGGGCTCTGG 74070      T   TT   AA
                                CCAG GCC  CAG  CTTTCTCTT
                                |||| |||  |||  |||||||||
                                GGTC CGG  GTC  GGAAGGGAG
                                  T   __   GG
GAM409   LOC121457 5'  GGGAGAGGGAAGGGGCTGG    74074      G    AGAA
                                CCAGT CCTTC    CTTTCTC
                                ||||| |||||    |||||||
                                GGTCG GGAAG    GAGAGGG
                                  G    G___
GAM409   LOC123628 5'  AGGAGGAAGTGAGATAAGGCAC 75618         CAGA_
           TG                    CAGTGCCTT     ACTTTCTCTT
                                |||||||||     ||||||||||
                                GTCACGGAA     TGAAGGAGGA
                                    TAGAG
GAM409   LOC124446 5'  GGGAGGGGACGAGGGCGTTG   74291          AGAA
                                CAGTGCCTTC    CTTTCTC
                                ||||||||||    |||||||
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                                GTTGCGGGAG   GGGAGGG
                                     CAG_
GAM409  LOC124930 5'  GGGAGGGGGTTTTGGAGGAGAG 74360   G___       TT
          GCTG                  GT   CCTTCAGAACT  CTCTT
                                ||   ||||||||||  |||||
                                CG   GGAGGTTTTGG  GAGGG
                                 GAGA         GG
GAM409  LOC124944 3'  GAGAGAGGGCTGAAAGGCTGCT 74373     _   _  AA     TT
          GG                    CCAGT GCCTT CAG  CTTTCTC
                                ||||| ||||| |||  |||||||
                                GGTCG CGGAA GTC  GAGAGAG
                                   T    A  GG
GAM409  LOC125875 5'  GGAGCCCTAGGGCACTGG    74417         C  AA
                                CCAGTGCCTT AG  CTTT
                                |||||||||| ||  ||||
                                GGTCACGGGA TC  GAGG
                                      _ CC
GAM409  LOC125875 5'  GGGGAACGAGGTCTGG     74419     T    CAGAAC
                                CCAG GCCTT     TTTCTC
                                |||| |||||     ||||||
                                GGTC TGGAG     AAGGGG
                                  _    C_____
GAM409  LOC126917 3'  GAGAGAAGCAGGGTGGGCTGCT 74583     _   TCAGAAC
          GG                    CCAGT GCCT      TTTCTCTT
                                ||||| ||||      ||||||||
                                GGTCG CGGG      GAAGAGAG
                                   T   TGGGAC_
GAM409  LOC126917 3'  GGGGGAGGGATCAGGGTGCTGG 74591     TG   CA  A
                                CCAG  CCTT  GA CTTTCTCTT
                                ||||  ||||  || |||||||||
                                GGTC  GGGA  CT GGGAGGGGG
                                  GT   __  A
GAM409  LOC126961 3'  GGAGAGACGGGGCGTCGG   74630   AG    CAGAAC
                                CC  TGCCTT     TTTCTCT
                                ||  ||||||     |||||||
                                GG  GCGGGG     AGAGAGG
                                 CT     C_____
GAM409  LOC127281 3'  AAGAACTGTTCCGGAGGCGCTG 74641         A   T_   CTT
          G                     CCAGTGCCTTC GAAC  TTCT
                                ||||||||||| ||||  ||||
                                GGTCGCGGAGG CTTG  AAGA
                                      C   TC   A
GAM409  LOC129563 3'  GAGAGGGTGGGGCTGG     74879      G  TTCAGA
                                CCAGT CC     ACTTTCTC
                                ||||| ||     ||||||||
                                GGTCG GG     TGGGAGAG
                                  G  _______
GAM409  LOC130074 3'  GGGAGGGAGTTGCGAGGTTTGG 76135     T    CAG   TT
                                CCAG GCCTT   AACT  CTCTT
                                |||| |||||   ||||  |||||
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                                GGTT TGGAG   TTGA  GAGGG
                                  _    CG_    GG
GAM409   LOC130327 3'  AGGAGGCAGTAAAGGTACTGG  74915         CAGA   T
                                CCAGTGCCTT    ACT TCTCTT
                                ||||||||||    ||| ||||||
                                GGTCATGGAA    TGA GGAGGA
                                     A___   C
GAM409   LOC130470 5'  GAGGGGGGTCCAAGGCTTGG   74944     T    CA  A  TT
                                CCAG GCCTT  GA CT  CTC
                                |||| |||||  || ||  |||
                                GGTT CGGAA  CT GG  GAG
                                  _    C_  G  GG
GAM409   LOC131873 5'  AGGAGAAAAAGGAGGTGTGG   75876     G      AGAAC
                                CCA TGCCTTC     TTTCTCTT
                                |||  |||||||    ||||||||
                                GGT GTGGAGG     AAAGAGGA
                                  _      AA___
GAM409   LOC133482 5'  GGGGAGTAGAGCCGCTGG    75095       C   CAGA   TT
                                CCAGTG CTT    ACT  CT
                                ||||||  |||    |||  ||
                                GGTCGC GAG    TGA  GG
                                   C   A___   GG
GAM409   LOC133993 5'  TGAGGGGTCCGCGGGCTCTGGA 75930         A  _____
           GGTGCTGG                CCTTCAGA CTT     TCTCTT   G
                                ||||||||  |||    ||||||   |
                                GGAGGTCT GGG    GGGGAG   T
                                     C   CGCCT
GAM409   LOC137990 5'  AGAGAAAGCCCAGGATTGG    75941       G   TCAGAA
                                CCAGT CCT     CTTTCTCT
                                |||||  |||     ||||||||
                                GGTTA GGA     GAAAGAGA
                                  _   CCC___
GAM409   LOC138429 3'  GGAGAAGCAGGGGTCCTGG    75342      TG    CAGAAC
                                CCAG  CCTT     TTTCTCT
                                ||||  ||||     |||||||
                                GGTC  GGGG     GAAGAGG
                                  CT    AC____
GAM409   LOC143243 3'  GGGAGAAGGGGGTGGGTGCTG  60307     TG   TCAGAA
                                CAG  CCT     CTTTCTCTT
                                |||  |||     |||||||||
                                GTC  GGG     GGAAGAGGG
                                  GT   TGGG__
GAM409   LOC143286 5'  GGGAGAGGGAAGGTAGCTGG   82948      _      AGAA
                                CCAG TGCCTTC    CTTTCTC
                                |||| |||||||    |||||||
                                GGTC ATGGAAG    GAGAGGG
                                  G      G___
GAM409   LOC143287 3'  GGGAGAGGGAAGGTAGCTGG   82931      _      AGAA
                                CCAG TGCCTTC    CTTTCTC
                                |||| |||||||    |||||||
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                                GGTC ATGGAAG   GAGAGGG
                                  G     G___
GAM409  LOC143310 3'  GGGAGTCTGCTGGAGGCCTGG  76538     T      AACT
                                CCAG GCCTTCAG   TTCTC
                                |||| ||||||||   |||||
                                GGTC CGGAGGTC   GAGGG
                                  _      GTCT
GAM409  LOC143437 5'  GGAGGAAGAGCAGGTCTGG   82956     T   TCAGAA
                                CCAG GCCT     CTTTCTCT
                                |||| ||||     ||||||||
                                GGTC TGGA     GAAGGAGG
                                  _   CGA___
GAM409  LOC143465 5'  GGGGGGCGGGGGGTATTGG   82966          AGAA  TT
                                CCAGTGCCTTC   CT  C
                                ||||||||||   ||  |
                                GGTTATGGGGG   GG  G
                                      GCG_  GG
GAM409  LOC143903 5'  GAGGGGGACAGGGAGCTGG   76620      G   CAGAA  TT
                                CCAGT CCTT    CT  CTC
                                ||||| ||||    ||  |||
                                GGTCG GGGA    GG  GAG
                                  A   CA___  GG
GAM409  LOC143915 3'  AGGAGGGAGCCTTAGGGTGCTG 82992     TG   C  AA  TT
          G                    CCAG  CCTT AG  CT  CTCTT
                               |||| |||| ||  ||  |||||
                               GGTC  GGGA TC  GA  GAGGA
                                 GT   T  C_  GG
GAM409  LOC144262 5'  GGGAGGGGCTGTGAGGGGCTGG 76753      G   _   AA
                               CCAGT CCTT CAG  CTTTCT
                               ||||| |||| |||  ||||||
                               GGTCG GGAG GTC  GGAGGG
                                  G   T  GG
GAM409  LOC144347 3'  GGGAAGGTTCCCTGG      76815      TGCCTTCA
                               CCAG       GAACTTTCTC
                               ||||       ||||||||||
                               GGTC       CTTGGAAGGG
                                 C________
GAM409  LOC144519 3'  AGGAGGAGGGTGGGGAGCTGG  76865      G   CAGAA
                               CCAGT CCTT    CTTTCTCTT
                               ||||| ||||    |||||||||
                               GGTCG GGGG    GGAGGAGGA
                                  A   TG___
GAM409  LOC144811 3'  GAGAGAGAAGGGTGTGG     83184     G     CAGAA
                               CCA TGCCTT    CTTTCTC
                               ||| ||||||    |||||||
                               GGT GTGGGA    GAGAGAG
                                 _     A____
GAM409  LOC145622 3'  GAGAGGGGGTTTCACCACGTTG 77300       CCTTCA    TT
          G                    CCAGTG     GAACT  CTCTT
                               ||||||     |||||  |||||
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                                GGTTGC     TTTGG  GAGAG
                                   ACCAC_    GG
GAM409   LOC145717 3'  AGGGGAAGGCGTAGGTGTGG   66827     G    TCAGAA
                                CCA TGCCT     CTTTCTCT
                                ||| |||||     ||||||||
                                GGT GTGGA     GAAGGGGA
                                  _    TGCG__
GAM409   LOC145719 5'  GAGGGAAGCCCGAGGGAGCTGG 83451      G    AGAAC
                                CCAGT CCTTC     TTTCTCTT
                                ||||| |||||     ||||||||
                                GGTCG GGGAG     GAAGGGAG
                                   A     CCC__
GAM409   LOC145720 5'  GAGGGAAGCCCGAGGGAGCTGG 83433      G    AGAAC
                                CCAGT CCTTC     TTTCTCTT
                                ||||| |||||     ||||||||
                                GGTCG GGGAG     GAAGGGAG
                                   A     CCC__
GAM409   LOC145748 3'  AGGGGGAGGCCAGTGGGGGCGT 83462          GAA_
            TGG                   CCAGTGCCTTCA    CTTTCTCTT
                                ||||||||||||    |||||||||
                                GGTTGCGGGGGT    GGAGGGGGA
                                      GACC
GAM409   LOC145758 5'  AGGAGGAGGCAGAGGGGTGCCT 83482      T  _   AGAA
            GG                    CCAG GC CTTC    CTTTCTCTT
                                |||| || ||||    |||||||||
                                GGTC CG GGGG    GGAGGAGGA
                                  _ T    AGAC
GAM409   LOC145761 5'  AAGAGAAAGTGGAAGGCATGG  83472     G      AGA
                                CCA TGCCTTC   ACTTTCTCTT
                                ||| |||||||   ||||||||||
                                GGT ACGGAAG   TGAAAGAGAA
                                  _      G__
GAM409   LOC145783 5'  GGGAGGGGCATGAGGCGCT    77481        T  GAA
                                AGTGCCT CA   CTTTCTC
                                ||||||| ||   |||||||
                                TCGCGGA GT   GGGAGGG
                                    _ ACG
GAM409   LOC145980 5'  GGAGAAGGCGGGTACCTGG    83607      _    TCAGAA
                                CCAG TGCCT     CTTTCTCT
                                |||| |||||     ||||||||
                                GGTC ATGGG     GGAAGAGG
                                   C     C_____
GAM409   LOC146057 5'  AGGAGGGGGAGCAGGTGCTGG  77656      TG   TCAGAA  TT
                                CCAG  CCT     CT  CTCTT
                                ||||  |||     ||  |||||
                                GGTC  GGA     GG  GAGGA
                                   GT   CGA___  GG
GAM409   LOC146272 5'  GGGAGGGGCACAGGGAGGTGGT 77793     G      AGAA__      TT
            GG                    CCA TGCCTTC     CTTTCTC
                                ||| |||||||     |||||||
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                                GGT GTGGAGG     GGGAGGG
                                  G      GACACG
GAM409   LOC146488 5'  GAGGCTGTCTGGGGGACTGG   70813      G       A TT
                                CCAGT CCTTCAGA C  TCTC
                                ||||| |||||||| |  ||||
                                GGTCA GGGGGTCT G  GGAG
                                  _       _ TC
GAM409   LOC146712 5'  AGGAACTTGTTCAGGAGGTGCT 83714     TG    A    TTTC
           GG                     CCAG  CCTTC GAAC    TCTT
                                |||| ||||| ||||    ||||
                                GGTC  GGAGG CTTG    AGGA
                                  GT     A    TTCA
GAM409   LOC146714 5'  GGGGGAGAACAGAGAAGGTGTG 83740     G      AGAAC
           G                      CCA TGCCTTC     TTTCTCTT
                                ||| |||||||     ||||||||
                                GGT GTGGAAG     AGAGGGGG
                                  _      AGACA
GAM409   LOC146795 5'  GAGAGGAGGGGTGAGAGGGCAC 78132    A       AGAA_
           GG                     CC GTGCCTTC     CTTTCTCTT
                                || ||||||||     |||||||||
                                GG CACGGGAG     GGAGGAGAG
                                  _       AGTGG
GAM409   LOC146880 5'  GGAGGAAGTTCTGCCGG     78158    TT
                                CC  CAGAACTTTCTCT
                                ||  |||||||||||||
                                GG  GTCTTGAAGGAGG
                                  CC
GAM409   LOC147040 3'  AGGAGAGAGAATGGGGTACT   78227       T  GAA
                                AGTGCCT CA   CTTTCTCTT
                                |||||||  ||   |||||||||
                                TCATGGG GT   GAGAGAGGA
                                    _  AA_
GAM409   LOC147515 3'  AAGGGGGAGTAGGAGGGCTTTG 84017     T     AGA   TT
           G                      CCAG GCCTTC   ACT  CTCTT
                                |||| ||||||   |||  |||||
                                GGTT CGGGAG   TGA  GGGAA
                                  T     GA_   GG
GAM409   LOC147645 5'  GGGGGAGGCAGAGGTGGCACTG 78424       T  AGAA_  TT   TT
           G                      CCAGTGCC TC     CT  CTC
                                |||||||| ||     ||  |||
                                GGTCACGG GG     GA  GGG
                                    T  AGACG  GG
GAM409   LOC147658 3'  AAGGGGATCAGGAGGTTTTGG  78412     T     A  ACT
                                CCAG GCCTTC GA   TTCTCTT
                                |||| |||||| ||   |||||||
                                GGTT TGGAGG CT   AGGGGAA
                                  T     A  ___
GAM409   LOC147669 5'  AAGAGGAACCCTGAGGTGGCTG 84057      GC     AAC
           G                      CCAGT  CTTCAG   TTTCTCTT
                                |||||  ||||||   ||||||||
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                                GGTCG  GGAGTC   AAGGAGAA
                                  GT     CC_
GAM409  LOC147685 3'  AGGAGAAACTATGGGGGTGCTG 78443     TG     GAAC
          G                     CCAG  CCTTCA    TTTCTCTT
                                ||||  ||||||    ||||||||
                                GGTC  GGGGGT    AAAGAGGA
                                  GT     ATC_
GAM409  LOC148046 3'  GGGGGGGAGTTGGAGGGGGTGC 84106    _ TG    AG_   TT
          CTGG                    CA G  CCTTC   AACT  CTCTT
                                || |  |||||   ||||  |||||
                                GT C  GGGGG   TTGA  GGGGG
                                 C GT    AGG    GG
GAM409  LOC148114 5'  AGGGGAAGGGATGGGGCTTGG  78659     T    T  GAA
                                CCAG GCCT CA   CTTTCTCTT
                                |||| |||| ||   |||||||||
                                GGTT CGGG GT   GGAAGGGGA
                                  _    _ AG_
GAM409  LOC148166 5'  AGGAGAAAGTTCTGGAGAGGAT 78689     GTGC
          GG                    CCA    CTTCAGAACTTTCTCTT
                                |||    ||||||||||||||||
                                GGT    GAGGTCTTGAAAGAGGA
                                 AGGA
GAM409  LOC148394 3'  AGGGGAAACAAGAGGGCACTG  84143          AGAAC
                                CAGTGCCTTC     TTTCTCTT
                                ||||||||||     ||||||||
                                GTCACGGGAG     AAAGGGGA
                                     AAC__
GAM409  LOC148430 5'  GGGGGGGGGCCCGGAGGCCCTG 67924      T     AGAA  TT    T
          G                     CCAG GCCTTC    CT  CTCT
                                ||||  ||||||    ||  ||||
                                GGTC CGGAGG    GG  GGGG
                                  C     CCCG  GG
GAM409  LOC148490 5'  GGGCTTCTGAGGGACTGG     78888       G        CTTT
                                CCAGT CCTTCAGAA    CTC
                                |||||  |||||||||    |||
                                GGTCA GGGAGTCTT    GGG
                                  _        C___
GAM409  LOC148534 3'  AGAGAAGGCCGGGCACGG     78893     A     TCAGAA
                                CC GTGCCT      CTTTCTCT
                                || ||||||      ||||||||
                                GG CACGGG      GGAAGAGA
                                 _      CC_____
GAM409  LOC148887 5'  GGGGGCTTCAGAAGGCACTGG  84246          A  _  TT
                                CCAGTGCCTTC GAA CT  C
                                |||||||||||  ||| ||  |
                                GGTCACGGAAG CTT GG  G
                                       A   C  GG
GAM409  LOC148932 3'  GGAATCTGAAGGCACTGG     79110            ACT
                                CCAGTGCCTTCAGA   TTCT
                                ||||||||||||||   ||||
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                                GGTCACGGAAGTCT  AAGG
                                      ___
GAM409  LOC148960 5' GGGGGGGGGCCCGGAGGCCCTG 79124     T    AGAA  TT   T
            G                  CCAG GCCTTC   CT  CTCT
                               |||| ||||||   ||  ||||
                               GGTC CGGAGG   GG  GGGG
                                 C    CCCG  GG
GAM409  LOC149076 3' GAGGGAGTGGGCCTGG     79152     T   TCAGA   TT
                               CCAG GCCT    ACT  CTC
                               |||| ||||    |||  |||
                               GGTC CGGG    TGA  GAG
                                 _   _____  GG
GAM409  LOC149086 3' GAGAGGAAGGGCAGAGGGTTGG 84338    GT    AGAA
                               CCA  GCCTTC   CTTTCTCTT
                               |||  ||||||   |||||||||
                               GGT  TGGGAG   GAAGGAGAG
                                 __    ACGG
GAM409  LOC149111 3' GGGAGGGGCTGGAGGGTGTGTG 79185    _ TG    AGAA     TT
            G                  CCA G  CCTTC   CTTTCTC
                               ||| |  |||||   |||||||
                               GGT T  GGGAG   GGGAGGG
                                 G GT    GTCG
GAM409  LOC149300 5' AGGGAAGGCAGGGTTTGG    79285     T    CAGAA
                               CCAG GCCTT    CTTTCTCT
                               |||| |||||    ||||||||
                               GGTT TGGGA    GGAAGGGA
                                 _    C____
GAM409  LOC149706 5' AGGGGGAGCAGGGGCTTGG   84637     T    CAGAA  TT
                               CCAG GCCTT    CT  CTCT
                               |||| |||||    ||  ||||
                               GGTT CGGGG    GA  GGGA
                                 _    AC___  GG
GAM409  LOC149837 3' GAGAGGGAGATAGCACTGG   84736       CT  AGAA
                               CCAGTGC  TC   CTTTCTC
                               |||||||  ||   |||||||
                               GGTCACG  AG   GGGAGAG
                                    AT  A___
GAM409  LOC149844 5' GGGGGAGAAGGAGGAGCTGG  79517      G    AGAA  TT
                               CCAGT CCTTC   CT  CTC
                               ||||| |||||   ||  |||
                               GGTCG GGAGG   GA  GGG
                                  A    AA__  GG
GAM409  LOC149995 3' AAGGGGGAGTAGGAGGGCTTTG 84839     T    AGA   TT
            G                  CCAG GCCTTC   ACT  CTCTT
                               |||| ||||||   |||  |||||
                               GGTT CGGGAG   TGA  GGGAA
                                 T    GA_   GG
GAM409  LOC150135 3' GGGAGGTGGGGTGCTG     79572     TG   CAGA
                               CAG  CCTT    ACTTTCT
                               |||  ||||    |||||||
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                                GTC  GGGG    TGGAGGG
                                  GT   _____
GAM409   LOC150225 3'  AGGAGGAGCTGCAGGGGGGCTT 84981      T     AGAAC_
                GG                  CCAG GCCTTC      TTTCTCTT
                                    |||| ||||||      ||||||||
                                    GGTT CGGGGG      GAGGAGGA
                                      _     GACGTC
GAM409   LOC150225 3'  GAGGGGATGGTGGCATTGG    84996        T   GAA
                                    CCAGTGCC TCA   CTTTC
                                    |||||||| |||   |||||
                                    GGTTACGG GGT   GGGAG
                                        T   AG_
GAM409   LOC150225 3'  GGGGAGGGGCAGGCAATGG    85007     G    TCAGAA
                                    CCA TGCCT      CTTTCTCT
                                    ||| |||||      ||||||||
                                    GGT ACGGA      GGGAGGGG
                                      A     CG_____
GAM409   LOC150271 3'  GGGAGGAGGAGCAGAGAGGTAT 84952      G     CAGAA_
                GG                  CCA TGCCTT      CTTTCTCTT
                                    ||| ||||||      |||||||||
                                    GGT ATGGAG      GGAGGAGGG
                                      _     AGACGA
GAM409   LOC150279 3'  AGGAGAATGAACAGAAGGTGCT 79663      TG    AGAACT
                GG                  CCAG  CCTTC      TTCTCTT
                                    ||||  |||||      |||||||
                                    GGTC  GGAAG      AAGAGGA
                                      GT     ACAAGT
GAM409   LOC150279 3'  GAGGGCTGATTTGAAGGTGCTG 79668     TG       ACT_    TT
                                    CAG  CCTTCAGA    TTCTC
                                    |||  ||||||||    |||||
                                    GTC  GGAAGTTT    GGGAG
                                      GT       AGTC
GAM409   LOC150290 5'  GGAGAGAGTTTTCCATGG     79775     TTC_
                                    CC    AGAACTTTCTCT
                                    ||    ||||||||||||
                                    GG    TTTTGAGAGAGG
                                     TACC
GAM409   LOC150378 5'  AAGAGGCCAAATTTGAAGGCCT 79736      T       ACTT_
                TGG                   CCAG GCCTTCAGA     TCTCTT
                                    |||| |||||||||     ||||||
                                    GGTT CGGAAGTTT     GGAGAA
                                      C        AAACC
GAM409   LOC150384 5'  GGAGAGAGCCAGGGGCTGG    85036      G   TCAGAA
                                    CCAGT CCT      CTTTCTCT
                                    ||||| |||      ||||||||
                                    GGTCG GGA      GAGAGAGG
                                      G   CC_____
GAM409   LOC150481 3'  GGAGGGTCGGGGGGCACGG     79892     A       A  A
                                    CC GTGCCTTC GA CTTTCT
                                    || |||||||| || ||||||
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                                GG CACGGGGG CT GGGAGG
                                 _      _ _
GAM409  LOC150481 3'  GGGAGGCTTGGAGGCAGTGG  79894     G       AA  TT
                                CCA TGCCTTCAG  CT  C
                                ||| |||||||||  ||  |
                                GGT ACGGAGGTT  GA  G
                                  G        CG  GG
GAM409  LOC150577 3'  AAGAGGAGGCTCAGGTGCTG  85069     TG   TCA  A
                                CAG  CCT   GA CTTTCTCTT
                                |||  |||   || |||||||||
                                GTC  GGA   CT GGAGGAGAA
                                  GT   ___  C
GAM409  LOC150630 5'  AGAGGGGGTTTCACCGTGG   85098     __   CCTTCA    TT
                                CCA  GTG     GAACT  CTCT
                                |||  |||     |||||  ||||
                                GGT  CAC     TTTGG  GAGA
                                  GC  _______     GG
GAM409  LOC151174 5'  GGAGTTGGGGGGCGTTG      85251          GA
                                CAGTGCCTTCA  ACTTT
                                ||||||||||  |||||
                                GTTGCGGGGGT  TGAGG
                                            __
GAM409  LOC151742 5'  AGAGGGTAGGAGGGATGCTGG  57665       _    AGA
                                CCAGTG CCTTC   ACTTTCT
                                |||||| |||||   |||||||
                                GGTCGT GGGAG   TGGGAGA
                                   A    GA_
GAM409  LOC151987 5'  GAGGGAGGGGGAGGGCGTCGG  67466    AG     AGAA  TT
                                CC  TGCCTTC    CT  CTC
                                ||  |||||||    ||  |||
                                GG  GCGGGAG    GA  GAG
                                 CT      GGG_  GG
GAM409  LOC152200 3'  AGGAGAAGAAGAGGGCAGTGG  85573     G      AGAAC
                                CCA TGCCTTC     TTTCTCTT
                                ||| |||||||     ||||||||
                                GGT ACGGGAG     GAAGAGGA
                                  G      AA___
GAM409  LOC152275 3'  GGGAGAGAAAGGCACTG     85619         CAGAA
                                CAGTGCCTT     CTTTCTC
                                |||||||||     |||||||
                                GTCACGGAA     GAGAGGG
                                     A____
GAM409  LOC152283 5'  AGGAGGGAGGCGAGGCATGTGG 85679     _      CAGAA  TT
                                CCA GTGCCTT     CT  CTCTT
                                ||| |||||||     ||  |||||
                                GGT TACGGAG     GA  GAGGA
                                  G      CG___  GG
GAM409  LOC152317 5'  GAGAGGCTGAAGGTGCTG    85641     TG      AA
                                CAG  CCTTCAG  CTTTC
                                |||  |||||||  |||||
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                                GTC  GGAAGTC  GAGAG
                                  GT      G_
GAM409   LOC152453 5'  GGAGGGGGAAGGGCCCTGG   80601     T    CAGAA  TT
                                CCAG GCCTT    CT  CTCT
                                |||| |||||    ||  ||||
                                GGTC CGGGA    GG  GAGG
                                  C    A____  GG
GAM409   LOC152580 5'  GAGGAAAATGTACTGG      85778       C  CAGAAC
                                CCAGTGC TT     TTTCTC
                                ||||||| ||     ||||||
                                GGTCATG AA     AAGGAG
                                   T _______
GAM409   LOC152633 5'  GGAGGGGGCCAAGGGCTGG   85814      G   CAGAA  TT
                                CCAGT CCTT    CT  CTCT
                                ||||| ||||    ||  ||||
                                GGTCG GGAA    GG  GAGG
                                  _   CC___  GG
GAM409   LOC153196 3'  AGGAGAGGGTTTTCTATGACTG 85954     GCCTTC
                                CAGT     AGAACTTTCTCTT
                                ||||     |||||||||||||
                                GTCA     TTTTGGGAGAGGA
                                  GTATC_
GAM409   LOC153688 3'  GAGAGGGAAAGGGCTTGG    86107     T    CAGAA
                                CCAG GCCTT    CTTTCTC
                                |||| |||||    |||||||
                                GGTT CGGGA    GGGAGAG
                                  _    AA___
GAM409   LOC153711 3'  AAGGGAAAGTGGTAAGGGAGAG 86131   TG _   AGA___
           TGCTGG                   C CTTC     ACTTTCTCTT
                                | ||||     ||||||||||
                                G GAGG     TGAAAGGGAA
                                GT A   GAATGG
GAM409   LOC153811 3'  AGGAGCTACTGAAGGCAATGG  80940     G       AACTTT
                                CCA TGCCTTCAG     CTCTT
                                ||| |||||||||     |||||
                                GGT ACGGAAGTC     GAGGA
                                  A       ATC___
GAM409   LOC155038 3'  GGGGAGGGGCGGGGCATGG    81260     G     CAGAA
                                CCA TGCCTT    CTTTCTCT
                                ||| ||||||    ||||||||
                                GGT ACGGGG    GGGAGGGG
                                  _     CG___
GAM409   LOC155060 3'  AGGGGAAGGCCTGGGCTTGG   86327     T   TT   AA
                                CCAG GCC  CAG  CTTTCTCT
                                |||| |||  |||  ||||||||
                                GGTT CGG  GTC  GAAGGGGA
                                  _  __   CG
GAM409   LOC155179 3'  GAGAGAGTGCAGGGAGGGGCTG 81314      G    AGA_      TT
             G                   CCAGT CCTTC    ACTTTCTC
                                ||||| |||||    ||||||||
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                                GGTCG GGAGG    TGAGAGAG
                                  G    GACG
GAM409  LOC157254 5'  AGGAGGTCTTTTGGGGGCCTGG 81381     T       CTT
                                CCAG GCCTTCAGAA   TCTCTT
                                |||| ||||||||||   ||||||
                                GGTC CGGGGGTTTT   GGAGGA
                                  _       CT_
GAM409  LOC157280 3'  GGGAGGTGAGCTGGGGGCCCTG 73912     T      AACTT
          G                      CCAG GCCTTCAG    TCTCTT
                                |||| ||||||||    ||||||
                                GGTC CGGGGGTC    GGAGGG
                                  C       GAGT_
GAM409  LOC157280 5'  AGGAGAAAACACATGAGGGTGT 73911     G       GAAC_
          GG                     CCA TGCCTTCA    TTTCTCTT
                                ||| ||||||||    ||||||||
                                GGT GTGGGAGT    AAAGAGGA
                                  _       ACACA
GAM409  LOC157349 5'  GGAGGAAGATGGGCCCTGG    81419     T    TCAGAA
                                CCAG GCCT     CTTTCTCT
                                |||| ||||     ||||||||
                                GGTC CGGG     GAAGGAGG
                                  C    TA____
GAM409  LOC157507 5'  AAGAGGGAGCTTGAGAGTGCTG 81449     TG C    AA  TT
          G                      CCAG  C TTCAG  CT  CTCTT
                                ||||  | |||||  ||  |||||
                                GGTC  G GAGTT  GA  GAGAA
                                  GT A    C_  GG
GAM409  LOC157848 3'  GGAGGAAAGGAAGGGCTGG    81619     G    AGAAC
                                CCAGT CCTTC    TTTCTCT
                                ||||| |||||    |||||||
                                GGTCG GGAAG    AAGGAGG
                                  _    GA___
GAM409  LOC157848 3'  GGGGGAGGCGGGTGAGGGCTGG 81621     GT      GAA__  TT
                                CCA  GCCTTCA    CT  CTC
                                |||  |||||||    ||  |||
                                GGT  CGGGAGT    GA  GGG
                                  __      GGGCG  GG
GAM409  LOC158056 5'  AGGGGAGGGCGGGTGGGCAGCT 81681     _    TCAGAA      T
          GG                     CCAG TGCCT     CTTTCTCT
                                |||| |||||     ||||||||
                                GGTC ACGGG     GGAGGGGA
                                  G    TGGGCG
GAM409  LOC158117 3'  AAGAGGTTAGATTGGGGGCTCT 81701     T       AACTT
          GG                     CCAG GCCTTCAG    TCTCTT
                                |||| ||||||||    ||||||
                                GGTC CGGGGGTT    GGAGAA
                                  T       AGATT
GAM409  LOC158117 3'  GGGAGGAGGTGGGGTCAGGGCT 81710      G  __  AGA
          GG                     CCAGT CCT  TC   ACTTTCTCTT
                                ||||| |||  ||   ||||||||||
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                                GGTCG GGA  GG   TGGAGGAGGG
                                  _  CT  GG_
GAM409   LOC158191 3'  GGAGGGTTGGGGGCATGG    81779     G      GA
                                CCA TGCCTTCA  ACTTTCT
                                ||| ||||||||  |||||||
                                GGT ACGGGGGT  TGGGAGG
                                  _       __
GAM409   LOC158263 5'  GAGGGCAGGGGGCGCTGG    81847          AGAA
                                CCAGTGCCTTC    CTTTC
                                ||||||||||    |||||
                                GGTCGCGGGGG    GGGAG
                                       AC__
GAM409   LOC158267 3'  GGAGAAGCAGAGGCATGG    81834     G     CAGAAC
                                CCA TGCCTT     TTTCTCT
                                ||| ||||||     |||||||
                                GGT ACGGAG     GAAGAGG
                                  _     AC____
GAM409   LOC158629 5'  GGGAAGTTAAGGTACATGG    86879     _      CAG
                                CCA GTGCCTT   AACTTTCT
                                ||| |||||||   ||||||||
                                GGT CATGGAA   TTGAAGGG
                                  A      ___
GAM409   LOC158987 5'  GAGAGGAGGAGGAGGTATGG   86963     G      AGAA
                                CCA TGCCTTC    CTTTCTCTT
                                ||| |||||||    |||||||||
                                GGT ATGGAGG    GGAGGAGAG
                                  _      A___
GAM409   LOC159199 5'  GGGAGGGCGGCCTCAAGGTGCT 82184      TG    C  AA__      TT
           GG                     CCAG  CCTT AG    CTTTCTC
                                ||||  |||| ||    |||||||
                                GGTC  GGAA TC    GGGAGGG
                                  GT    C  CGGC
GAM409   LOC160717 5'  AGGAGGAGGAGGAGGTGTTTGG 82235     _ TG     AGAA
                                CCA G  CCTTC    CTTTCTCTT
                                ||| |  |||||    |||||||||
                                GGT T  GGAGG    GGAGGAGGA
                                  T GT     A___
GAM409   LOC163682 5'  AGGAGAAGGTGCCAGGAACTGG 87023       G   TCAGA
                                CCAGT CCT     ACTTTCTCTT
                                ||||| |||     ||||||||||
                                GGTCA GGA     TGGAAGAGGA
                                   A   CCG__
GAM409   LOC168574 5'  AGGGGAGGGTTTTGTCCCCGTG 82720     G  CCTT
           G                     CCA TG    CAGAACTTTCTCTT
                                ||| ||    ||||||||||||||
                                GGT GC    GTTTTGGGAGGGGA
                                  _  CCCT
GAM409   LOC169026 5'  GAGAGAGACCAGAGGAGCTGG  82725       G    CAGAA
                                CCAGT CCTT     CTTTCTC
                                ||||| ||||     |||||||
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                                GGTCG GGAG    GAGAGAG
                                  A   ACCA_
GAM409  LOC170370 3'  GGGGGAAGGAAAGGCATGG   82841    G    CAGAA
                                CCA TGCCTT    CTTTCTCT
                                ||| ||||||    ||||||||
                                GGT ACGGAA    GAAGGGGG
                                  _     AG___
GAM409  LOC196205 3'  AGGAGGAGGTGATAGGAATTGG 87588      G   TCAGA
                                CCAGT CCT    ACTTTCTCTT
                                ||||| |||    ||||||||||
                                GGTTA GGA    TGGAGGAGGA
                                  A   TAG__
GAM409  LOC196337 5'  GGAGAAGACAGAGGGCTGG   87649    GT    AGAAC
                                CCA  GCCTTC    TTTCTCT
                                |||  ||||||    |||||||
                                GGT  CGGGAG    GAAGAGG
                                  __     ACA__
GAM409  LOC196394 5'  GGCTGGGTTCTGGAGGCCCTGG 87655     T          TC
                                CCAG GCCTTCAGAACTT  TC
                                |||| ||||||||||||  ||
                                GGTC CGGAGGTCTTGGG  GG
                                  C          TC
GAM409  LOC196446 3'  AGGGGAACCAAAGGGCTGG   87707      G   CAGAAC
                                CCAGT CCTT     TTTCTCT
                                ||||| ||||     |||||||
                                GGTCG GGAA     AAGGGGA
                                  _   ACC___
GAM409  LOC196510 3'  GAGGGAGAGACGGGGACGTTGG 87749       _   CAGAA
                                CCAGTG CCTT    CTTTCTCTT
                                |||||| ||||    |||||||||
                                GGTTGC GGGG    GAGAGGGAG
                                   A   CA___
GAM409  LOC196955 5'  AGGAGGAGACCTGAGTTGCTGG 77362      GC  T   AAC
                                CCAGT  CT CAG   TTTCTCTT
                                |||||  || |||   ||||||||
                                GGTCG  GA GTC   GAGGAGGA
                                   TT  _   CA_
GAM409  LOC196989 3'  GGGAGGGGGCCGGGGGCGGTGG 89667    G     AGAA  TT
                                CCA TGCCTTC    CT  CTCTT
                                ||| |||||||    ||  |||||
                                GGT GCGGGGG    GG  GAGGG
                                  G      CC__  GG
GAM409  LOC196993 3'  GAGAAGGCGGGGCTGG      89668      G  TTCAGAA
                                CCAGT CC       CTTTCTC
                                ||||| ||       |||||||
                                GGTCG GG       GGAAGAG
                                   G  C_______
GAM409  LOC197085 5'  AGAGGGAGAGGCTGCTGG    87878      _   TCAGAA  TT
                                CCAGT GCCT     CT  CTCT
                                ||||| ||||     ||  ||||
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                                GGTCG CGGA     GA  GAGA
                                  T   _______  GG
GAM409   LOC197085 5'  AGGAGGAGCAGGAGAGGCTGCT 87879      _    CAGAAC
           GG                     CCAGT GCCTT     TTTCTCTT
                                  ||||| |||||     ||||||||
                                  GGTCG CGGAG     GAGGAGGA
                                    T     AGGAC_
GAM409   LOC197115 5'  AGAGGGAGAGGCTGCTGG    87883      _   TCAGAA  TT
                                  CCAGT GCCT     CT  CTCT
                                  ||||| ||||     ||  ||||
                                  GGTCG CGGA     GA  GAGA
                                    T   _______  GG
GAM409   LOC197115 5'  AGGAGGAGCAGGAGAGGCTGCT 87884      _    CAGAAC
           GG                     CCAGT GCCTT     TTTCTCTT
                                  ||||| |||||     ||||||||
                                  GGTCG CGGAG     GAGGAGGA
                                    T     AGGAC_
GAM409   LOC197201 3'  AGGAGGGGGTTCCTCCCGCTGG 87931       CCTTCA    TT
                                  CCAGTG     GAACT  CTCTT
                                  ||||||     |||||  |||||
                                  GGTCGC     CTTGG  GAGGA
                                     CCTC__     GG
GAM409   LOC197358 3'  GGGAGGAAGGAGAGGTGCTG   88045     TG    CAGAA
                                  CAG  CCTT    CTTTCTCTT
                                  |||  ||||    |||||||||
                                  GTC  GGAG    GAAGGAGGG
                                    GT    AG___
GAM409   LOC199863 3'  GGAGGAAGTCCGTGCTGG    89866     TG CTTCA  A
                                  CCAG  C    GA CTTTCTCT
                                  ||||  |    || ||||||||
                                  GGTC  G    CT GAAGGAGG
                                    GT C_____  _
GAM409   LOC199882 3'  GGGAACTTGGAGGCATTGG    88453           AACT
                                  CCAGTGCCTTCAG    TTCTC
                                  ||||||||||||||   |||||
                                  GGTTACGGAGGTT    AAGGG
                                           C___
GAM409   LOC200019 3'  GGGAACTTGGAGGCATTGG    88548           AACT
                                  CCAGTGCCTTCAG    TTCTC
                                  ||||||||||||||   |||||
                                  GGTTACGGAGGTT    AAGGG
                                           C___
GAM409   LOC200205 3'  GAGGGGTCTGGGGCATTGG    88625         T    A
                                  CCAGTGCCT CAGA CTTTC
                                  ||||||||| |||| |||||
                                  GGTTACGGG GTCT GGGAG
                                        _   G
GAM409   LOC200220 3'  GAGGGAGAGACGGGGACGTTGG 88638        _    CAGAA
                                  CCAGTG CCTT    CTTTCTCTT
                                  |||||| ||||    |||||||||
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                                GGTTGC GGGG    GAGAGGGAG
                                   A   CA___
GAM409  LOC200471 5'  AAGATTTGGGGGTTTGG    90048     T       A
                                CCAG GCCTTCAGA CTT
                                |||| ||||||||| |||
                                GGTT TGGGGGTTT GAA
                                  _       A
GAM409  LOC200781 3'  GGGGAAAGACAGGAGCTGG   90140     G   TCAGAA
                                CCAGT CCT     CTTTCTCT
                                ||||| |||     ||||||||
                                GGTCG GGA     GAAAGGGG
                                   A   CA____
GAM409  LOC200860 3'  GAGGGGGTGGGGGAGGGCACTG 90164          AGA_   TT   TT
           G                     CCAGTGCCTTC    ACT  CTC
                                ||||||||||    |||  |||
                                GGTCACGGGAG    TGG  GAG
                                      GGGG   GG
GAM409  LOC200933 3'  AGTTTTGAAGGTGCTG     90193     TG
                                CAG  CCTTCAGAACT
                                |||  ||||||||||
                                GTC  GGAAGTTTTGA
                                  GT
GAM409  LOC201175 5'  GGAGGAAGTTCTGCCCGG    88136    TT_
                                CC   CAGAACTTTCTCT
                                ||   |||||||||||||
                                GG   GTCTTGAAGGAGG
                                 CCC
GAM409  LOC201194 3'  GGGGGAGTCTGAGGGCGCGG   89778    A        A  TT
                                CC GTGCCTTCAGA CT  CTC
                                || |||||||||| ||  |||
                                GG CGCGGGAGTCT GA  GGG
                                 _         _  GG
GAM409  LOC202754 3'  GAGAGAGCTGGAAGGCATGG   82706     G      AGAA
                                CCA TGCCTTC    CTTTCTC
                                ||| |||||||    |||||||
                                GGT ACGGAAG    GAGAGAG
                                  _      GTC_
GAM409  LOC202781 3'  AAGAGAAGGGGCCGGGCGCGG  90362    A     TCAGAA
                                CC GTGCCT     CTTTCTCTT
                                || ||||||     |||||||||
                                GG CGCGGG     GGAAGAGAA
                                  _     CCGG__
GAM409  LOC202915 3'  GAGGGAGGGGCGCCGGGGCGCT 90392          CAGAA
           GG                    CCAGTGCCTT    CTTTCTCTT
                                ||||||||||    |||||||||
                                GGTCGCGGGGG    GGGAGGGAG
                                      CCGCG
GAM409  LOC203245 5'  AAGAGAAGGGGAATTGGGGCGC 89298         CAGAA_
           T                     AGTGCCTT     CTTTCTCTT
                                ||||||||     |||||||||
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                                TCGCGGGG     GGAAGAGAA
                                    TTAAGG
GAM409  LOC203275 3'  AAGAGGTTAGATTGGGGGCTCT 89317      T       AACTT
          GG                      CCAG GCCTTCAG     TCTCTT
                                  |||| ||||||||     ||||||
                                  GGTC CGGGGGTT     GGAGAA
                                    T       AGATT
GAM409  LOC203275 3'  GGGAGGAGGTGGGGTCAGGGCT 89326       G  __  AGA
          GG                      CCAGT CCT  TC   ACTTTCTCTT
                                  ||||| |||  ||   ||||||||||
                                  GGTCG GGA  GG   TGGAGGAGGG
                                    _  CT  GG_
GAM409  LOC204823 5'  AGGAGGAGCTGGGGCTGCTGG  89493       _   T   AA
                                  CCAGT GCCT CAG  CTTTCT
                                  ||||| |||| |||  ||||||
                                  GGTCG CGGG GTC  GGAGGA
                                    T   _   GA
GAM409  LOC206426 3'  GGAGAAGAAGGGGGCCTGG    89535      T     AGAAC
                                  CCAG GCCTTC     TTTCTCT
                                  |||| ||||||     |||||||
                                  GGTC CGGGGG     GAAGAGG
                                    _      AA___
GAM409  LOC219686 5'  AGGAGGAGGCCGAGGCGCCGG  90838     A      CAGAA
                                  CC GTGCCTT     CTTTCTCTT
                                  || |||||||     |||||||||
                                  GG CGCGGAG     GGAGGAGGA
                                   C       CC___
GAM409  LOC219690 5'  GGAGGGGAAGGCACTGG     93075           AGAA
                                  CCAGTGCCTTC    CTTTCT
                                  ||||||||||    ||||||
                                  GGTCACGGAAG    GGGAGG
                                                 ____
GAM409  LOC219700 3'  AGGGGTTCTCCTGAGGGTGCAG 93059     A TG       AACTT     T
          G                       CC G  CCTTCAG     TCTCT
                                  || |  |||||||     |||||
                                  GG C  GGGAGTC     GGGGA
                                   A GT       CTCTT
GAM409  LOC219854 5'  GGGGGAGAGTGGATCCAGGACT 91488       G   TCAGA_
          GG                      CCAGT CCT      ACTTTCTCTT
                                  ||||| |||      ||||||||||
                                  GGTCA GGA      TGAGAGGGGG
                                    _   CCTAGG
GAM409  LOC219855 3'  GGGAGAGTAGAAAGAGGGGTTG 91514       G    CAGA_       TT
          G                       CCAGT CCTT     ACTTTCTC
                                  ||||| ||||     ||||||||
                                  GGTTG GGAG     TGAGAGGG
                                    G    AAAGA
GAM409  LOC219920 3'  AGGAGGAGGAGTGGGGCAGTGG 93300     G     T  GAA
                                  CCA TGCCT CA   CTTTCTCTT
                                  ||| ||||| ||   |||||||||
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                                GGT ACGGG GT   GGAGGAGGA
                                  G    _ GA_
GAM409   LOC219942 5'  AAGAGAAAACGTGGGGTGTGG  93341    G    T  GAAC
                                CCA TGCCT CA    TTTCTCTT
                                ||| ||||| ||    ||||||||
                                GGT GTGGG GT    AAAGAGAA
                                  _    _ GCA_
GAM409   LOC220045 5'  GGGAGGGAGGCTGAGGGGGCAC 93411        __   AA  TT
           TG                     CAGTGCCT  TCAG  CT  CTCTT
                                ||||||||  ||||  ||  |||||
                                GTCACGGG  AGTC  GA  GAGGG
                                    GG   G_  GG
GAM409   LOC220107 5'  AGGAGGAGGTAGTGCGAGGCGC 93467        _  GA
           TG                     CAGTGCCTT CA  ACTTTCTCTT
                                |||||||||  ||  ||||||||||
                                GTCGCGGAG GT  TGGAGGAGGA
                                     C  GA
GAM409   LOC220537 3'  AGGGGAAGGCGTAGGTGTGG   90727    G    TCAGAA
                                CCA TGCCT     CTTTCTCT
                                ||| |||||     ||||||||
                                GGT GTGGA     GAAGGGGA
                                  _    TGCG__
GAM409   LOC220776 3'  GAGGGGGGTGAGGGGGCATT   68392        AGAA  TT
                                AGTGCCTTC    CT  CTC
                                |||||||||    ||  |||
                                TTACGGGGG    GG  GAG
                                     AGTG  GG
GAM409   LOC220930 5'  GGGGAAGGGCAGGTTTGG    93132     T   TCAGAA
                                CCAG GCCT     CTTTCTCT
                                |||| ||||     ||||||||
                                GGTT TGGA     GGAAGGGG
                                  _    CG____
GAM409   LOC220936 3'  GGGGGGTTGAGGGTATTG    91413         GA   TT
                                CAGTGCCTTCA  ACT  CT
                                ||||||||||  |||  ||
                                GTTATGGGAGT  TGG  GG
                                      __  GG
GAM409   LOC221002 3'  GGGAGGGGCAGGGGGCACCTGG 91478     _     AGAA
                                CCAG TGCCTTC    CTTTCTC
                                |||| |||||||    |||||||
                                GGTC ACGGGGG    GGGAGGG
                                  C      ACG_
GAM409   LOC221178 5'  AGAGGAGATGGGGCTCTGG    93524     T   T  GAACT
                                CCAG GCCT CA     TTCTCT
                                |||| |||| ||     ||||||
                                GGTC CGGG GT     AGGAGA
                                  T    _ AG___
GAM409   LOC221336 5'  GGGGGAAAACCGAGAGGCGCTG 92273        CAGAAC
                                CAGTGCCTT     TTTCTCTT
                                |||||||||     ||||||||
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                                GTCGCGGAG     AAAGGGGG
                                     AGCCA_
GAM409  LOC221418 5'  AGGGAAGGTGACGGCCTGG   93634      T   T  AGA
                                CCAG GCC TC   ACTTTCTCT
                                |||| ||| ||   |||||||||
                                GGTC CGG AG   TGGAAGGGA
                                  _   C  ___
GAM409  LOC221463 3'  GGAGGGTGAGGGCGTGG     92073     G      AGA
                                CCA TGCCTTC   ACTTTCT
                                ||| |||||||   |||||||
                                GGT GCGGGAG   TGGGAGG
                                  _     ____
GAM409  LOC221495 3'  GGAGAAGGTTCTAGTAGG    93860     TC_
                                CCT   AGAACTTTCTCT
                                |||   ||||||||||||
                                GGA   TCTTGGAAGAGG
                                  TGA
GAM409  LOC221501 3'  GAGGGGGGGCGGGGTGTGG   93794     G     CAGAA  TT
                                CCA TGCCTT    CT  CTC
                                ||| ||||||    ||  |||
                                GGT GTGGGG    GG  GAG
                                  _     CGG__  GG
GAM409  LOC221543 5'  AGAGAAAAGGGGCAGCTGG   93733      _     CAGAAC
                                CCAG TGCCTT     TTTCTCT
                                |||| ||||||     |||||||
                                GGTC ACGGGG     AAAGAGA
                                  G     A_____
GAM409  LOC221833 3'  GAGGGAGAGGCTGGAGGCCTGG 92540      T       AA
                                CCAG GCCTTCAG  CTTTCTCTT
                                |||| ||||||||  |||||||||
                                GGTC CGGAGGTC  GAGAGGGAG
                                  _       G_
GAM409  LOC221876 5'  AGGGGGAAGAGCGCAGAGGGCT 93918       G    CAGAA_
           GG                     CCAGT CCTT     CTTTCTCTT
                                ||||| ||||     |||||||||
                                GGTCG GGAG     GAAGGGGGA
                                  _    ACGCGA
GAM409  LOC221914 3'  GGGAGGGGTGGGGGCATCTGG  93951      _      GAA
                                CCAG TGCCTTCA   CTTTCTC
                                |||| |||||||   |||||||
                                GGTC ACGGGGGT   GGGAGGG
                                  T       G__
GAM409  LOC221922 5'  GAGGGAGGGCCATTGGGCGTGG 92694     G    TCAGAA
                                CCA TGCCT     CTTTCTCTT
                                ||| |||||     |||||||||
                                GGT GCGGG     GGGAGGGAG
                                  _    TTACC_
GAM409  LOC221922 5'  GAGGGGGAGCAGGAGGGCAGGC 92695  ____      AGAA  TT
           GTTGG                     TGCCTTC    CT  CTCTT
                                  |||||||    ||  |||||
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                                  ACGGGAG   GA  GGGAG
                                GCGG      GAC_  GG
GAM409   LOC222183 3'  GGGAGGAAAGAGACTGAGGGCC 94166     T       AA_    _
           CTGG                   CAG GCCTTCAG   CTTTC TCTT
                                ||| ||||||||   ||||| ||||
                                GTC CGGGAGTC   GAAAG AGGG
                                  C       AGA     G
GAM409   LOC222183 3'  GGGGGAGGGGTCTGGGGTCTGG 94167      T    T    A
                                CCAG GCCT CAGA CTTTCTCTT
                                |||| |||| |||| |||||||||
                                GGTC TGGG GTCT GGGAGGGGG
                                  _   _   G
GAM409   LOC222936 5'  AAGGGAAGGTGAGTGGGGCAGT 94362     G     CAGA
           GG                     CCA TGCCTT    ACTTTCTCTT
                                ||| ||||||    ||||||||||
                                GGT ACGGGG    TGGAAGGGAA
                                  G     TGAG
GAM409   LOC245727 3'  AGGAGGAAGCCCAGGAGCTGG  91122      G   TCAGAA
                                CCAGT CCT     CTTTCTCTT
                                ||||| |||     |||||||||
                                GGTCG GGA     GAAGGAGGA
                                   A   CCC___
GAM409   LOC253070 3'  GGGAGGGCTCGGAAGGCGCT   97012         A  A
                                AGTGCCTTC GA CTTTCTC
                                ||||||||| || |||||||
                                TCGCGGAAG CT GGGAGGG
                                     G  C
GAM409   LOC253115 3'  GAGGGAAAGAAATGGGGGGCCT 94495     T     AGAA_
           GG                     CCAG GCCTTC     CTTTCTCTT
                                |||| ||||||     |||||||||
                                GGTC CGGGGG     GAAAGGGAG
                                  _     GTAAA
GAM409   LOC253531 5'  GGAGGAAGAGCAGGTCTGG    96471      T    TCAGAA
                                CCAG GCCT     CTTTCTCT
                                |||| ||||     ||||||||
                                GGTC TGGA     GAAGGAGG
                                  _    CGA___
GAM409   LOC253681 3'  AGGAGAGAGAATGGGGTACT   95124        T  GAA
                                AGTGCCT CA   CTTTCTCTT
                                ||||||| ||   |||||||||
                                TCATGGG GT   GAGAGAGGA
                                   _  AA_
GAM409   LOC253767 3'  GGGAGAGGGAGGGCACGG    94402    A       AGAA
                                CC GTGCCTTC    CTTTCTC
                                || ||||||||    |||||||
                                GG CACGGGAG    GAGAGGG
                                  _       G___
GAM409   LOC253866 5'  GGGGGAAGGGCAGGGGTGTGG  95589     G     CAGAA
                                CCA TGCCTT     CTTTCTCTT
                                ||| ||||||     |||||||||
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                                GGT GTGGGG    GGAAGGGGG
                                  _     ACG__
GAM409   LOC253869 3'  AGGAGGGCAGGAGGCATTGG  94904         AGAA
                                CCAGTGCCTTC   CTTTCT
                                ||||||||||   ||||||
                                GGTTACGGAGG   GGAGGA
                                      ACG_
GAM409   LOC253893 3'  GGAGGAAAGGAAGGGCTGG   96113     G   AGAAC
                                CCAGT CCTTC    TTTCTCT
                                ||||| |||||    |||||||
                                GGTCG GGAAG    AAGGAGG
                                  _    GA___
GAM409   LOC253893 3'  GGGGGAGGCGGGTGAGGGCTGG 96115    GT     GAA__ TT
                                CCA  GCCTTCA    CT  CTC
                                |||  |||||||    ||  |||
                                GGT  CGGGAGT    GA  GGG
                                  __     GGGCG  GG
GAM409   LOC253992 3'  AGAGGGGAGGGGGACACTGG  96622      _   AGAA
                                CCAGTG CCTTC   CTTTCT
                                ||||||| |||||   ||||||
                                GGTCAC GGGGG   GGGAGA
                                   A    AG__
GAM409   LOC254020 5'  GGGAGGGAAGGGCACTGG    96143        CAGAA
                                CCAGTGCCTT    CTTTCTC
                                ||||||||||    |||||||
                                GGTCACGGGA    GGGAGGG
                                      A____
GAM409   LOC254196 3'  AGGGGAAACAAGAGGGCACTG  97346        AGAAC
                                CAGTGCCTTC    TTTCTCTT
                                ||||||||||    ||||||||
                                GTCACGGGAG    AAAGGGGA
                                      AAC__
GAM409   LOC254263 3'  GGGAGGGAGGGGGCACTGG   94719         AGAA
                                CCAGTGCCTTC   CTTTCTC
                                ||||||||||   |||||||
                                GGTCACGGGGG   GGGAGGG
                                      A___
GAM409   LOC254517 5'  AGAGGGAGAGGCTGCTGG    94963      _  TCAGAA  TT
                                CCAGT GCCT     CT  CTCT
                                ||||| ||||     ||  ||||
                                GGTCG CGGA     GA  GAGA
                                  T   _______  GG
GAM409   LOC254517 5'  AGGAGGAGCAGGAGAGGCTGCT 94964      _   CAGAAC
           GG                    CCAGT GCCTT     TTTCTCTT
                                ||||| |||||     ||||||||
                                GGTCG CGGAG     GAGGAGGA
                                  T    AGGAC_
GAM409   LOC254532 5'  GGGAGGGAGGAAAGGGGCCTGG 96642     T   CAGAA  TT
                                CCAG GCCTT    CT  CTCTT
                                |||| |||||    ||  |||||
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                                GGTC CGGGG    GA  GAGGG
                                  _    AAAG_  GG
GAM409  LOC254617 5'  GAGAGGAGCTGCAGGAGGGCTG 97422       G    AGAAC
                 G                 CCAGT CCTTC    TTTCTCTT
                                   ||||| |||||    ||||||||
                                   GGTCG GGAGG    GAGGAGAG
                                     _    ACGTC
GAM409  LOC254643 3'  GGGAGAGGGAGGGCAATGG   95569     G      AGAA
                                   CCA TGCCTTC    CTTTCTC
                                   ||| |||||||    |||||||
                                   GGT ACGGGAG    GAGAGGG
                                     A      G___
GAM409  LOC254826 5'  GGGAGGAAGAGAAGGGAGGTAG 97243     _      AGAA_
                 CTGG                  CAG TGCCTTC    CTTTCTCTT
                                   ||| |||||||    |||||||||
                                   GTC ATGGAGG    GAAGGAGGG
                                     G      GAAGA
GAM409  LOC254876 5'  AAGATCTGAGGGTGTCGG    96050    A TG       A
                                   CC G  CCTTCAGA CTT
                                   || |  |||||||| |||
                                   GG T  GGGAGTCT GAA
                                    C GT       A
GAM409  LOC254910 5'  GGGAAGGTTCTTCTGG      96790      TGCCTTC
                                   CCAG      AGAACTTTCTC
                                   ||||      ||||||||||
                                   GGTC      TCTTGGAAGGG
                                     T_______
GAM409  LOC254964 5'  AGAGGGAGAGGCTGCTGG    94999       _   TCAGAA  TT
                                   CCAGT GCCT     CT  CTCT
                                   ||||| ||||     ||  ||||
                                   GGTCG CGGA     GA  GAGA
                                      T   _______  GG
GAM409  LOC254964 5'  AGGAGGAGCAGGAGAGGCTGCT 95000       _    CAGAAC
                 GG                  CCAGT GCCTT     TTTCTCTT
                                   ||||| |||||     ||||||||
                                   GGTCG CGGAG     GAGGAGGA
                                      T     AGGAC_
GAM409  LOC255031 3'  GGGGGGGGGGTGCGGGGCACGG  97238    A      CAGA   TT
                                   CC GTGCCTT    ACT  CTCTT
                                   || |||||||    |||  |||||
                                   GG CACGGGG    TGG  GGGGG
                                     _      CG__   GG
GAM409  LOC255104 5'  GGAGAAGCCAAGCATTGG    95397        CTTCAGAAC
                                   CCAGTGC        TTTCTCT
                                   |||||||        |||||||
                                   GGTTACG        GAAGAGG
                                       AACC_____
GAM409  LOC255104 3'  GGAGCTCTGGAGGTACAGG   95398    A          A
                                   CC GTGCCTTCAGA CTTT
                                   || ||||||||||| ||||
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                                GG CATGGAGGTCT GAGG
                                 A          C
GAM409   LOC255189 5'  AGGGGCTGAGGGCACTG     96587            AA
                                CAGTGCCTTCAG  CTT
                                ||||||||||||  |||
                                GTCACGGGAGTC  GGA
                                      GG
GAM409   LOC255242 3'  GAGGGGAATGGAAGGGCATGG  95928     G   _  AGAAC
                                CCA TGCC TTC     TTTCTCTT
                                ||| |||| |||     ||||||||
                                GGT ACGG AAG     AAGGGGAG
                                  _   G  GT___
GAM409   LOC255276 3'  GGGAGGGGGGCCCGGGGCCTGG 96354      T    CAGAA  TT
                                CCAG GCCTT     CT  CTCTT
                                |||| |||||     ||  |||||
                                GGTC CGGGG     GG  GAGGG
                                  _     CCCG_  GG
GAM409   LOC255448 5'  AGGAGAAAACACATGAGGGTGT 94649     G       GAAC_
            GG                    CCA TGCCTTCA     TTTCTCTT
                                ||| ||||||||     ||||||||
                                GGT GTGGGAGT     AAAGAGGA
                                  _       ACACA
GAM409   LOC255448 3'  GGGAGGTGAGCTGGGGGCCCTG 94650      T       AACTT
            G                     CCAG GCCTTCAG     TCTCTT
                                |||| ||||||||     ||||||
                                GGTC CGGGGGTC     GGAGGG
                                  C       GAGT_
GAM409   LOC255452 3'  AGGGGCCTGGGGGTGCCGG    97524    A TG      AA
                                CC G  CCTTCAG  CTTT
                                || |  |||||||  ||||
                                GG C  GGGGGTC  GGGA
                                 C GT      CG
GAM409   LOC255480 3'  AAGGGAGGTAGGTGGGGGTGTG 96518     G       GA_      CTT
            G                     CCA TGCCTTCA   ACTTTCT
                                ||| ||||||||   |||||||
                                GGT GTGGGGGT   TGGAGGG
                                  _       GGA      AA
GAM409   LOC255520 3'  GAGAGGAATGATGACTGGAGGT 95856    TG      AAC___
            GTT                     G  CCTTCAG      TTTCTCTT
                                |  |||||||      ||||||||
                                T  GGAGGTC      AAGGAGAG
                                 GT       AGTAGT
GAM409   LOC255645 3'  GGGAGAGTATGGGGGGCTGG   96653       G     GA
                                CCAGT CCTTCA  ACTTTCTC
                                ||||| ||||||  ||||||||
                                GGTCG GGGGGT  TGAGAGGG
                                  _     A_
GAM409   LOC255809 3'  GGGAGAGGGGACACAGGCATGG 96780     G     TCAGAA
                                CCA TGCCT      CTTTCTCTT
                                ||| |||||      |||||||||
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                                GGT ACGGA     GGGAGAGGG
                                  _     CACAG_
GAM409   LOC255849 3'  GAGGGTTTTCTGGGGTTGCTGG 96442       GC       CT
                                CCAGT  CTTCAGAA  TTCTC
                                |||||  ||||||||  |||||
                                GGTCG  GGGGTCTT  GGGAG
                                   TT       TT
GAM409   LOC255971 3'  GGGAGGGGCGGGGGGCTGG    96536      G    CAGAA
                                CCAGT CCTT     CTTTCTC
                                ||||| ||||     |||||||
                                GGTCG GGGG     GGGAGGG
                                   G    CG___
GAM409   LOC256021 3'  AAGAGAGGGTTCTGACTCTG   96513     TGCCT
                                CAG     TCAGAACTTTCTCTT
                                |||     ||||||||||||||
                                GTC     AGTCTTGGGAGAGAA
                                  TC___
GAM409   LOC256158 5'  GAGGGGAGCCCCAGGGGAGCTG 97666       G    CAGAAC
            G                    CCAGT CCTT      TTTCTCTT
                                ||||| ||||      ||||||||
                                GGTCG GGGG      GAGGGGAG
                                   A    ACCCC_
GAM409   LOC256905 5'  GGAGGGGTAGGGGGCGGTGG   96869     G      AGAA
                                CCA TGCCTTC    CTTTCT
                                ||| |||||||    ||||||
                                GGT GCGGGGG    GGGAGG
                                  G      ATG_
GAM409   LOC257395 3'  GGAGAGACGGGGCGTCGG     95422     AG     CAGAAC
                                CC  TGCCTT     TTTCTCT
                                ||  ||||||     |||||||
                                GG  GCGGGG     AGAGAGG
                                 CT     C_____
GAM409   LOC257447 5'  AGGAGGAACAGGAGAGGCTGCT 83441       _    CAGAAC
            GG                    CCAGT GCCTT      TTTCTCTT
                                ||||| |||||      ||||||||
                                GGTCG CGGAG      AAGGAGGA
                                   T     AGGAC_
GAM409   LOC257457 3'  GAGGGAAAGACCCAGGGTCTGG 62628      T    CAGAA
                                CCAG GCCTT     CTTTCTCTT
                                |||| |||||     |||||||||
                                GGTC TGGGA     GAAAGGGAG
                                  _     CCCA_
GAM409   LOC257556 3'  GAGGGAAAGAAATGGGGGGCCT 97708      T     AGAA_
            GG                    CCAG GCCTTC     CTTTCTCTT
                                |||| ||||||     |||||||||
                                GGTC CGGGGG     GAAAGGGAG
                                  _     GTAAA
GAM409   LOC257596 5'  AGAGAAAAGGGGCAGCTGG    97926      _     CAGAAC
                                CCAG TGCCTT      TTTCTCT
                                |||| ||||||      |||||||
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                                GGTC ACGGGG     AAAGAGA
                                  G     A_____
GAM409  LOC257617 3'  GAGGGAAAGAAATGGGGGGCCT 97814     T     AGAA_
            GG                    CCAG GCCTTC     CTTTCTCTT
                                  |||| ||||||     |||||||||
                                  GGTC CGGGGG     GAAAGGGAG
                                    _     GTAAA
GAM409  LOC51000  3'  AGGATCTGGAGGCATTG     31974           A
                                  CAGTGCCTTCAGA CTT
                                  |||||||||||| |||
                                  GTTACGGAGGTCT GGA
                                         A
GAM409  LOC51030  3'  AGGAGAAAGTTTTGCTTCTATG 32184     GTGCCTT
            G                     CCA      CAGAACTTTCTCTT
                                  |||      ||||||||||||||
                                  GGT      GTTTTGAAAGAGGA
                                    ATCTTC_
GAM409  LOC51087  5'  GGGGGAGGGGCCGGGGCGGTGG 32013     G     CAGAA
                                  CCA TGCCTT     CTTTCTCTT
                                  ||| ||||||     |||||||||
                                  GGT GCGGGG     GGGAGGGGG
                                    G     CCG__
GAM409  LOC51102  3'  GAGGGGAGGCGGATCTGAGGGG 63878     G      A___
            CTGG                    AGT CCTTCAGA    CTTTCTCTT
                                  ||| ||||||||    |||||||||
                                  TCG GGGAGTCT    GGAGGGGAG
                                    _       AGGC
GAM409  LOC51281  5'  GAGGGCCCGCTGAGGGCGCAGG 33324     A        AACT
                                  CC GTGCCTTCAG    TTCTC
                                  || ||||||||||    |||||
                                  GG CGCGGGAGTC    GGGAG
                                   A         GCCC
GAM409  LOC51725  3'  AAGGGAACAAAGCTGGAGGCTC 69863      T      AACT_
            TGG                     CCAG GCCTTCAG     TTCTCTT
                                  |||| ||||||||     |||||||
                                  GGTC CGGAGGTC     AAGGGAA
                                    T       GAAAC
GAM409  LOC54466  5'  GGAGGGTAGTGGGTGCTGG    38655      TG   TCAGA
                                  CCAG  CCT     ACTTTCT
                                  ||||  |||     |||||||
                                  GGTC  GGG     TGGGAGG
                                    GT   TGA__
GAM409  LOC56920  3'  GGGAGGGAACACAGAGGTGTTG 39389      TG    CAGAA_     TT
            G                     CCAG  CCTT     CTTTCTC
                                  ||||  ||||     |||||||
                                  GGTT  GGAG     GGGAGGG
                                    GT    ACACAA
GAM409  LOC56930  5'  AGAGGGCTGAGGGCCTGG     62059      T       AA
                                  CCAG GCCTTCAG  CTTT
                                  |||| ||||||||  ||||
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                                GGTC CGGGAGTC  GAGA
                                  _      GG
GAM409  LOC57105  3'  AGGAGGAGGATCTGGGGCATTG 39815        T   A
                                CAGTGCCT CAGA CTTTCTCTT
                                |||||||| |||| |||||||||
                                GTTACGGG GTCT GGAGGAGGA
                                   _   A
GAM409  LOC57105  3'  GGGGGAGAAGGATTGG      39819      G    AGAAC TT
                                CCAGT CCTTC    T  CTC
                                ||||| |||||    |  |||
                                GGTTA GGAAG    A  GGG
                                  _    _____ GG
GAM409  LOC63928  5'  AGGAGAGGCACGCCGGGGTTCT 42029     T    CAGAAC
          GG                      CCAG GCCTT     TTTCTCTT
                                |||| |||||     ||||||||
                                GGTC TGGGG     GGAGAGGA
                                  T    CCGCAC
GAM409  LOC80298  5'  AGGGAAGGACGGGGCCTGG   47288     T    CAGAA
                                CCAG GCCTT    CTTTCTCT
                                |||| |||||    ||||||||
                                GGTC CGGGG    GGAAGGGA
                                  _    CA___
GAM409  LOC87769  5'  AGGGGAAACACCAGAAGGTGTG 71320     G      AGAAC
          G                      CCA TGCCTTC    TTTCTCTT
                                ||| |||||||    ||||||||
                                GGT GTGGAAG    AAAGGGGA
                                  _      ACCAC
GAM409  LOC90019  3'  GTTCTGGAGCACTGG       56771        C
                                CCAGTGC TTCAGAAC
                                ||||||| ||||||||
                                GGTCACG AGGTCTTG
                                   _
GAM409  LOC90092  5'  AGGGGAAGAGACACGGGCGCTG 61399         TCAGAA       T
          G                      CCAGTGCCT     CTTTCTCT
                                |||||||||     ||||||||
                                GGTCGCGGG     GAAGGGGA
                                     CACAGA
GAM409  LOC90170  5'  AAGAGGAGCCCAAGGCTCTGG  61705     T    CAGAAC
                                CCAG GCCTT     TTTCTCTT
                                |||| |||||     ||||||||
                                GGTC CGGAA     GAGGAGAA
                                  T    CCC___
GAM409  LOC90342  5'  AAGAGGATGGCCATTGAGGTGC 62351     TG   T   AA_ _
          TGG                     CAG  CCT CAG   CT TTCTCTT
                                |||  ||| |||   || |||||||
                                GTC  GGA GTT   GG AGGAGAA
                                  GT   _   ACC  T
GAM409  LOC90342  5'  GAGAGAAACGAAGAGGTTCTGG 62357     T    CAGAAC
                                CCAG GCCTT     TTTCTCTT
                                |||| |||||     ||||||||
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                                GGTC TGGAG     AAAGAGAG
                                  T    AAGC__
GAM409  LOC90342  5'  GGGAGAAACTGCTGAGGGAGCT 62361      G      AAC
              GG                   CCAGT CCTTCAG   TTTCTCTT
                                |||||| |||||||   ||||||||
                                GGTCG GGGAGTC   AAAGAGGG
                                  A      GTC
GAM409  LOC90495  3'  GGGAGAAGAAAAGGAGGTTTGG 63060     T     AGAAC
                                CCAG GCCTTC     TTTCTCTT
                                |||| ||||||     ||||||||
                                GGTT TGGAGG     GAAGAGGG
                                  _     AAAA_
GAM409  LOC90550  3'  AAGAGAAAACAATGCTGGGGGT 73089    TG      AAC___
              GTT                   G  CCTTCAG     TTTCTCTT
                                |  |||||||     ||||||||
                                T  GGGGGTC     AAAGAGAA
                                 GT      GTAACA
GAM409  LOC90736  3'  AGAGGAGGTTCCAGCTGG     63901      GCCTTCA
                                CCAGT      GAACTTTCTCT
                                ||||||      ||||||||||
                                GGTCG      CTTGGAGGAGA
                                  AC_____
GAM409  LOC90850  3'  GAGGGAAGGGCTGGGATGCTGG 64213      GC  T   AA
                                CCAGT  CT CAG  CTTTCTCTT
                                |||||  || |||  ||||||||
                                GGTCG  GG GTC  GGAAGGGAG
                                  TA  _   G_
GAM409  LOC90906  5'  AAGGGAAAAGGGGGGCCCTGG  64291     T     AGAAC
                                CCAG GCCTTC     TTTCTCTT
                                |||| ||||||     ||||||||
                                GGTC CGGGGG     AAAGGGAA
                                  C     GA___
GAM409  LOC90918  5'  GGGGGAGGGATAGCATTGG    64360       CT  AGAA
                                CCAGTGC  TC    CTTTCTCT
                                |||||||  ||    ||||||||
                                GGTTACG  AG    GGAGGGGG
                                    AT  _____
GAM409  LOC91064  5'  GGGGAGAGACGGGTCCTGG    64765     TG   TCAGAA
                                CCAG  CCT     CTTTCTCT
                                ||||  |||     ||||||||
                                GGTC  GGG     GAGAGGGG
                                  CT   CA_____
GAM409  LOC91149  5'  AGGGGAGGGCGAGGAAGGCTTG 65067     T     AGAA
              G                   CCAG GCCTTC    CTTTCTCTT
                                |||| ||||||    |||||||||
                                GGTT CGGAAG    GGGAGGGGA
                                  _     GAGC
GAM409  LOC91156  5'  GGGAGAGAACTGGGGGTGCCTG 65112     _ TG      AA      TT
              G                   CCA G  CCTTCAG  CTTTCTC
                                ||| |  |||||||  |||||||
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                                GGT C  GGGGGTC  GAGAGGG
                                  C GT      AA
GAM409  LOC91266  5' GAGGGGAAGCTGATAGGGCCCT 65416     T   __   AA
             GG                    CCAG GCCT  TCAG  CTTTCTCTT
                                |||| ||||  ||||  |||||||||
                                GGTC CGGG  AGTC  GAAGGGGAG
                                  C   AT   __
GAM409  LOC91286  3' GGGAGGGAAGGAGGCACT    65453         AGAA
                                AGTGCCTTC   CTTTCTC
                                |||||||||   |||||||
                                TCACGGAGG   GGGAGGG
                                     AA__
GAM409  LOC91363  5' AAGAGGAAGTTTGTCACTG   65773      CCTTCA
                                CAGTG     GAACTTTCTCTT
                                |||||     ||||||||||||
                                GTCAC     TTTGAAGGAGAA
                                   TG____
GAM409  LOC91813  5' GGGGTTTCTGGGGGTGTTG   67257     TG       C TT
                                CAG  CCTTCAGAA T  C
                                |||  |||||||||  |  |
                                GTT  GGGGGTCTT G  G
                                  GT        T GG
GAM409  LOC91875  3' AGAGGAGACAAGGCTCTGG   67436      T    CAGAAC
                                CCAG GCCTT     TTTCTCT
                                |||| |||||     |||||||
                                GGTC CGGAA     GAGGAGA
                                  T    CA____
GAM409  LOC91947  3' AAGAGAAAGTTTAATTATTTGG 67610      TGCCTTCA
                                CCAG       GAACTTTCTCTT
                                ||||       ||||||||||||
                                GGTT       TTTGAAAGAGAA
                                  TATTAA__
GAM409  LOC91974  3' AGGGGAAAAGGAAGGGGTGTGG 67749     GTG_    AGAAC
                                CCA   CCTTC    TTTCTCTT
                                |||   |||||    ||||||||
                                GGT   GGAAG    AAAGGGGA
                                  GTGG    GA___
GAM409  LOC92080  3' GAGAGGGGCTGGGGGCGTGG   68050     G       AA
                                CCA TGCCTTCAG  CTTTCTC
                                ||| |||||||||  |||||||
                                GGT GCGGGGGTC  GGGAGAG
                                  _       G_
GAM409  LOC92140  5' GAGGGAGGACAGCGGGGCCTGG 68283      T    CAGAA_  TT
                                CCAG GCCTT     CT  CTC
                                |||| |||||     ||  |||
                                GGTC CGGGG     GA  GAG
                                  _    CGACAG  GG
GAM409  LOC92170  3' GGGAGGGCCGGAGGCATGTGG  68370     _      AGAA
                                CCA GTGCCTTC    CTTTCTC
                                ||| ||||||||    |||||||
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                                GGT TACGGAGG   GGGAGGG
                                  G      CC__
GAM409  LOC92568  3' GGGGGAGGGATAGCATTGG   69775      CT  AGAA
                                CCAGTGC  TC   CTTTCTCT
                                |||||||  ||   ||||||||
                                GGTTACG  AG   GGAGGGGG
                                   AT  _____
GAM409  LOC92710  3' AAGAGGAGACCAAGGCCCTGG  70351     T    CAGAAC
                                CCAG GCCTT     TTTCTCTT
                                |||| |||||     ||||||||
                                GGTC CGGAA     GAGGAGAA
                                  C    CCA___
GAM409  LOC92822  3' GGGAGGGTCGGAGGGTGCTG   70649    TG    A  A
                                CAG  CCTTC GA CTTTCTC
                                |||  ||||| || |||||||
                                GTC  GGGAG CT GGGAGGG
                                  GT    G  _
GAM409  LOC93082  3' GAGAGGAAGGCAGGGAGGTGCT 56444     TG    AGAA
           G                     CAG  CCTTC   CTTTCTCTT
                                |||  |||||   |||||||||
                                GTC  GGAGG   GAAGGAGAG
                                  GT    GACG
GAM409  LOC93097  5' AGGAGAGGGTGAGTGGGGTATA 71358    A      CAGA
           GG                     CC GTGCCTT    ACTTTCTCTT
                                || |||||||   ||||||||||
                                GG TATGGGG    TGGGAGAGGA
                                 A      TGAG
GAM409  LOC93259  5' GAGAGAGAGAAAGAGGGTACTG 71821          AGAA
           G                     CCAGTGCCTTC   CTTTCTCTT
                                ||||||||||   |||||||||
                                GGTCATGGGAG   GAGAGAGAG
                                      AAA_
GAM409  LOC93268  5' GAGGAGCAGGGTCTGG      71879      T    CAGAAC
                                CCAG GCCTT     TTTCTC
                                |||| |||||     ||||||
                                GGTC TGGGA     GAGGAG
                                  _    C_____
GAM409  LOC93268  5' GGGAGCTGCTGGTGGCACTGG  71884        T   AA_  TT
                                CCAGTGCC TCAG   CT  C
                                |||||||| ||||   ||  |
                                GGTCACGG GGTC   GA  G
                                     T   GTC  GG
GAM409  LOC93624  5' AGGAGAAGGAAAAGGCGCTG   72725        CAGAA
                                CAGTGCCTT    CTTTCTCTT
                                |||||||||    |||||||||
                                GTCGCGGAA    GGAAGAGGA
                                      AA___
GAM410  ADH1B    3' CTTAGACATAAAGTAAAAT   72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
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                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM410  AHR     3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM410  FDFT1   3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                      _
GAM410  JTB     3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM410  KLF4    3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM410  PHYH    3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM410  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                       T__    _
GAM410  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM410  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_    CG_
GAM410  CG012   5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM410  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
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                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM410  FLJ23462  3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
            G                     CATTTC        GTCTGAGAT
                                  ||||||        |||||||||
                                  GTAAAG        CAGACTCTA
                                     AAACATTT_
GAM410  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                  CATTTCA   TCACTGTCTGAGAT
                                  |||||||   ||||||||||||||
                                  GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM410  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                  TTCA TTTCACTG  TGAG
                                  |||| ||||||||  ||||
                                  AAGT AAAGTGAC  GTTT
                                    A       CT
GAM410  KLHL6     3'  ATCTCAGAGCAGGAAA      55299     A  _
                                  TTTC CTG TCTGAGAT
                                  |||| ||| ||||||||
                                  AAAG GAC AGACTCTA
                                    _  G
GAM410  NIR3      3'  GCAGTGAAAGTGCAAT      66242     T
                                  ATT CACTTTCACTGT
                                  ||| ||||||||||||
                                  TAA GTGAAAGTGACG
                                   C
GAM410  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                  TTCACTTT  CT TCTGAGAT
                                  ||||||||  || ||||||||
                                  AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM410  PP35      3'  ATCTCAGACTGAAA       22814       CT
                                  TTTCA  GTCTGAGAT
                                  |||||  |||||||||
                                  AAAGT  CAGACTCTA
                                     __
GAM410  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148         TCAC   C_
                                  CATTTCACTT    TGT  TGAG
                                  ||||||||||    |||  ||||
                                  GTAAAGTGAA    ACG  ACTC
                                       TA__   TT
GAM410  SEP15     3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                  TTTCACTTT ACTGT  GA
                                  ||||||||| |||||  ||
                                  AAAGTGAGA TGACA  CT
                                       A    TC
GAM410  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                  TTTCACTTT    TCTGAG
                                  |||||||||    ||||||
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                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM410  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM410  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM410  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226     A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM410  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM411  DUSP4    5'  ACCGCCCTAGAGCGGCAGCTC  54052       AC   GGA  AA
                                GAGCTGCC  CTT   AG  CGGT
                                ||||||||  |||   ||  ||||
                                CTCGACGG  GAG   TC  GCCA
                                    C_   A__  CC
GAM411  IL13RA1   3'  ACCATTTAAAAACAGGCAGCTC 7773        ACCTTGGAA   C
                                GAGCTGCC        GAA GGT
                                ||||||||        ||| |||
                                CTCGACGG        TTT CCA
                                    ACAAAAA__   A
GAM411  PAPPA    5'  CTCCCAAAGCTGGCAGCTC    10422        C   _  A
                                GAGCTGCCA CTT GG AG
                                ||||||||| ||| || ||
                                CTCGACGGT GAA CC TC
                                     C   A  C
GAM411  WNT5A    3'  CGTTTCCAAACGGCAGCTC    12664        ACC     GA
                                GAGCTGCC   TTGGAA  ACG
                                ||||||||   ||||||  |||
                                CTCGACGG   AACCTT  TGC
                                    CA_     __
GAM411  FLJ23392  3'  TCCTTAGATGGCAGCTC     45549        C  T_
                                GAGCTGCCA CT  GGA
                                ||||||||| ||  |||
                                CTCGACGGT GA  CCT
                                     A  TT
GAM411  KIAA0453  3'  CTGCACAAGATGGCAGCTC    69046        C    GAAGAA
                                GAGCTGCCA CTTG     CGG
                                ||||||||| ||||     |||
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                                CTCGACGGT GAAC     GTC
                                     A    AC____
GAM411  KIAA1940  3'  ACCACCCTTCCAAGGTGGGGG  79973    G          AAC
                                CT CCACCTTGGAAG   GGT
                                || ||||||||||||   |||
                                GG GGTGGAACCTTC   CCA
                                 G          CCA
GAM411  PRO1617   5'  ACCATTCTTCCACATCACAACT 37728     C  CCACCT       C
          T                      GAG TG     TGGAAGAA GGT
                                ||| ||     |||||||| |||
                                TTC AC     ACCTTCTT CCA
                                  A  ACTAC_       A
GAM411  TOR1B    3'  CCACCCTTTGTGGCAGC     27197        CTTG    AAC
                                GCTGCCAC    GAAG   GG
                                ||||||||    ||||   ||
                                CGACGGTG    TTTC   CC
                                     ____    CCA
GAM411  TRF4-2   3'  CTTCCAAGGTACAACTC     42386     C  CC
                                GAG TG  ACCTTGGAAG
                                ||| ||  ||||||||||
                                CTC AC  TGGAACCTTC
                                  A  A_
GAM411  LOC123095 3'  ACCGTAGGTAAAAATGGCAGCT 76010          CC  GGAAGA
          C                      GAGCTGCCA  TT     ACGGT
                                |||||||||  ||     |||||
                                CTCGACGGT  AA     TGCCA
                                     AA  ATGGA_
GAM411  LOC147343 5'  CTCCCAAGTGGCAGCTC     83999          C    A
                                GAGCTGCCAC TTGG AG
                                |||||||||| |||| ||
                                CTCGACGGTG AACC TC
                                     _    C
GAM411  LOC148696 5'  TCCAAAATGGCAGCTC      84189          CC
                                GAGCTGCCA  TTGGA
                                |||||||||  |||||
                                CTCGACGGT  AACCT
                                     AA
GAM411  LOC196860 3'  ACCGTAGGTAAAAATGGCAGCT 89641          CC  GGAAGA
          C                      GAGCTGCCA  TT     ACGGT
                                |||||||||  ||     |||||
                                CTCGACGGT  AA     TGCCA
                                     AA  ATGGA_
GAM411  LOC200862 5'  CCAGGCAAAATGGCAGTTC    90180         C____
                                GAGCTGCCA    CTTGG
                                |||||||||    |||||
                                CTTGACGGT    GGACC
                                     AAAAC
GAM411  LOC255193 5'  CGTTCTGGGCAGCTC       95354          ACCTTGGA
                                GAGCTGCC       AGAACG
                                ||||||||       ||||||
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                                CTCGACGG      TCTTGC
                                   G_______
GAM412  ADAR    3'  GTGGCTACTGTGCATTCCTTG  6626        TTT___
                                TAAGGAATGC    GCCAT
                                ||||||||||    |||||
                                GTTCCTTACG    CGGTG
                                   TGTCAT
GAM412  ADAR    3'  GTGGCTACTGTGCATTCCTTG  31751       TTT___
                                TAAGGAATGC    GCCAT
                                ||||||||||    |||||
                                GTTCCTTACG    CGGTG
                                   TGTCAT
GAM412  ADAR    3'  GTGGCTACTGTGCATTCCTTG  31761       TTT___
                                TAAGGAATGC    GCCAT
                                ||||||||||    |||||
                                GTTCCTTACG    CGGTG
                                   TGTCAT
GAM412  ALOX15  3'  GTGGTTATAGCCCTGCCCTCC  6686    AT  TTT  C
                                GGA  GC   GC ATAACCAC
                                |||  ||   || ||||||||
                                CCT  CG   CG TATTGGTG
                                  CC  TCC  A
GAM412  BCL11A  3'  GCAATGCTCTATTCCTTA    56723       ___  T
                                TAAGGAAT   GC TTGC
                                ||||||||   || ||||
                                ATTCCTTA   CG AACG
                                     TCT  T
GAM412  BCL11A  3'  GCAATGCTCTATTCCTTA    35866       ___  T
                                TAAGGAAT   GC TTGC
                                ||||||||   || ||||
                                ATTCCTTA   CG AACG
                                     TCT  T
GAM412  CHST6   3'  GTGGTTATAACAAAATACCTTA 41234     A  GC   CC
                                TAAGG AT  TTTG  ATAACCAC
                                ||||| ||  ||||  ||||||||
                                ATTCC TA  AAAC  TATTGGTG
                                   A  __   AA
GAM412  CLN5    5'  GTGACTATGGCAAGGCCCT   21432    AAT       AC
                                AGG  GCTTTGCCATA  CAC
                                |||  ||||||||||| |||
                                TCC  CGGAACGGTAT  GTG
                                  ___        CA
GAM412  LPIN1   3'  GTGAAAAGCATTCCT      67394         GC
                                AGGAATGCTTT  CAT
                                |||||||||||  |||
                                TCCTTACGAAA  GTG
                                      A_
GAM412  MASP2   3'  GTGGCTCGAGAAGCATTC    21739       ____
                                GAATGCTTT   GCCAT
                                |||||||||   |||||
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                                CTTACGAAG   CGGTG
                                     AGCT
GAM412  RET     3'  GTGGTTAAGCATTCCTT    40181          T
                                AAGGAATGCTT GCCAT
                                |||||||||| |||||
                                TTCCTTACGAA TGGTG
                                      T
GAM412  RET     3'  GTGGTTAAGCATTCCTT    40597          T
                                AAGGAATGCTT GCCAT
                                |||||||||| |||||
                                TTCCTTACGAA TGGTG
                                      T
GAM412  CSEN    3'  GCACAAGCATTCCTTA     25531          _
                                TAAGGAATGCTT TGC
                                |||||||||||| |||
                                ATTCCTTACGAA ACG
                                       C
GAM412  DKFZP564G0222 3'  TGGTCAGGTACATTCCTTA   25899        CTT   ATA
                                TAAGGAATG   TGCC   ACCA
                                |||||||||   ||||   ||||
                                ATTCCTTAC   ATGG   TGGT
                                     ___    AC_
GAM412  DKFZp761B0514 3'  GGTTATGGAAGCCCTTA    50158      AAT   TG
                                TAAGG   GCTT  CCATAACC
                                |||||   ||||  ||||||||
                                ATTCC   CGAA  GGTATTGG
                                   ___   __
GAM412  FLJ12770  3'  ATGGTATAAAGCATCCCCTT   49737     A_    __
                                AAGG  ATGCTT  TGCCAT
                                ||||  ||||||  ||||||
                                TTCC  TACGAA  ATGGTA
                                  CC     AT
GAM412  FLJ20707  3'  GTAGTGAAAGCATTTCT     35597          GC   A
                                AGGAATGCTTT  CAT AC
                                ||||||||||  ||| ||
                                TCTTTACGAAA  GTG TG
                                      __  A
GAM412  FLJ21162  3'  TGGTTAATTGGAAGCTATTCCT 45897        _   TG  __
           TA                    TAAGGAAT GCTT  CCA  TAACCA
                                |||||||| ||||  |||  ||||||
                                ATTCCTTA CGAA  GGT  ATTGGT
                                     T   __   TA
GAM412  FLJ23441  3'  GTTAAGGAAAAGCACCCC    45170    AA    G  A
                                GG  TGCTTT CC TAAC
                                ||  |||||| || ||||
                                CC  ACGAAA GG ATTG
                                 CC     A  A
GAM412  KEAP1    5'  GGCCATGGCGGGGTCCCT    24452    AAT       AA
                                AGG   GCTTTGCCAT  CC
                                |||   ||||||||||  ||
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                                TCC  TGGGGCGGTA GG
                                  C__        CC
GAM412  KIAA0329  3'  GGATGGCAAAGCTCTCCT   29277     AT       AA
                                AGGA GCTTTGCCAT CC
                                |||| |||||||||| ||
                                TCCT CGAAACGGTA GG
                                  CT        __
GAM412  KIAA1643  3'  GGCGTGCAAAGCACCCTT   64553     AA      CATAA
                                AAGG TGCTTTGC   CC
                                |||| ||||||||   ||
                                TTCC ACGAAACG   GG
                                  C_      TGC__
GAM412  KIAA1877  3'  TTATGTGAAAGCATTGCTTA  66188     G       GC
                                TAAG AATGCTTT CATAA
                                |||| |||||||| |||||
                                ATTC TTACGAAA GTATT
                                  G       GT
GAM412  MGC9564   3'  GCAGTCATCAGCCATTCCTTA 54740         _ _____
                                TAAGGAATG CT    TTGC
                                ||||||||| ||    ||||
                                ATTCCTTAC GA    GACG
                                     C CTACT
GAM412  MYT1      3'  GCAACCACAGTATTCCTT    15774         ____
                                AAGGAATGCT   TTGC
                                ||||||||||   ||||
                                TTCCTTATGA   AACG
                                     CACC
GAM412  PARVA     3'  ATGTCCAAAACATTCCTT    36653        C   C_
                                AAGGAATG TTTG CAT
                                |||||||| |||| |||
                                TTCCTTAC AAAC GTA
                                     A   CT
GAM412  SCYB11    3'  TGTCGTAAAACATTCCT     87446        C   C
                                AGGAATG TTTGC ATA
                                ||||||| ||||| |||
                                TCCTTAC AAATG TGT
                                    A    C
GAM412  LOC121274 3'  ATGGCCAGAGCATTTCT     74060          _
                                AGGAATGCTTTG CCAT
                                |||||||||||| ||||
                                TCTTTACGAGAC GGTA
                                       C
GAM412  LOC146378 3'  GGTCTGTAAAGCACCTCC    77854     A_      CATA
                                GGA TGCTTTGC   ACC
                                |||  ||||||||   |||
                                CCT ACGAAATG   TGG
                                  CC       TC__
GAM412  LOC150157 3'  GTTGGAAGTAAAGCACTCCT  84880      A       CA_
                                AGGA TGCTTTGC   TAAC
                                |||| ||||||||  ||||
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                                TCCT ACGAAATG   GTTG
                                  C       AAG
GAM412  LOC152702 5'  TGACAAAGCATTCACT      80646    _        C
                                AG GAATGCTTTG CA
                                || |||||||||| ||
                                TC CTTACGAAAC GT
                                 A         A
GAM412  LOC196890 3'  GTTGGAAGTAAAGCACTCCT   89650      A       CA_
                                AGGA TGCTTTGC   TAAC
                                |||| ||||||||   ||||
                                TCCT ACGAAATG   GTTG
                                  C       AAG
GAM413  CAPON    3'  GGACATTGAATGTTGCTACA   63963    _  C    C
                                TG AGC GCGT CAATGTCC
                                || ||| |||| ||||||||
                                AC TCG TGTA GTTACAGG
                                 A  T   A
GAM413  KIF5C    3'  TGAACAACTAAGCTCATGA    15742        CGC  CCAA   C
                                TCATGAGC   GT    TGT CA
                                ||||||||   ||    ||| ||
                                AGTACTCG   CA    ACA GT
                                     AAT  ____   A
GAM413  OPHN1    3'  CTGAACATTGGAGAATCTCA   10357      CCGCG       C
                                TGAG    TCCAATGT CAG
                                ||||    |||||||| |||
                                ACTC    AGGTTACA GTC
                                  TAAG_       A
GAM413  FLJ10619  3'  CTGGACTTCACATAGCTCATGA 36350        CGC  CCAAT
                                TCATGAGC   GT    GTCCAG
                                ||||||||   ||    ||||||
                                AGTACTCG   CA    CAGGTC
                                     ATA  CTT__
GAM413  KIAA1981  3'  GGGCAGGACGCGGCTCA     88346           AA
                                TGAGCCGCGTCC  TGTCC
                                ||||||||||||  |||||
                                ACTCGGCGCAGG  ACGGG
                                              __
GAM413  SIMRP7    3'  CTGGACATTCGGCTACAGCTCA 92364        CGC_   C
           TGG                    TCATGAGC    GTC AATGTCCAG
                                ||||||||    ||| |||||||||
                                GGTACTCG    CGG TTACAGGTC
                                     ACAT   C
GAM413  TEKT2    5'  ACACTGGAGCTCAGA      27098    A    CGCG    A
                                TC TGAGC    TCCA TGT
                                || |||||    |||| |||
                                AG ACTCG    AGGT ACA
                                 _    ____    C
GAM413  LOC152580 5'  CTGGACATACTTTCCAAGCCAT 85777       A  CGCGTCCA_
           GA                     TCATG GC       ATGTCCAG
                                |||||  ||       ||||||||
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                                AGTAC CG        TACAGGTC
                                  _ AACCTTTCA
GAM413  LOC220827 3'  TGGACATTGGAGACTATGA   91246      G  CCGCG
                                TCAT AG     TCCAATGTCCA
                                |||| ||     ||||||||||
                                AGTA TC     AGGTTACAGGT
                                  _ AG___
GAM413  LOC255598 5'  CAGTGCGAAACACAGCTCATGA 97481         CGCG__ _ A
                                TCATGAGC     TC CA TG
                                ||||||||     || || ||
                                AGTACTCG     AG GT AC
                                     ACACAA  C  G
GAM413  LOC51112  5'  GGCAGGACGCGGCCCGCGA   32090    A  A       AA
                                TC TG GCCGCGTCC  TGTC
                                || || |||||||||  ||||
                                AG GC CGGCGCAGG  ACGG
                                 C  C       __
GAM414  CD8A     3'  CACACAGCCCTGGCCTCTGCTC 8332       A  TTT  A__
                                GAGCA AG   GC   GGCTGTGTG
                                ||||| ||   ||   |||||||||
                                CTCGT TC   CG   CCGACACAC
                                   C ___ GTC
GAM414  CLC      3'  CCTTCAAACCCTGCTCC     25108       AA    C
                                GGAGCA  GTTTG AGG
                                ||||||  ||||| |||
                                CCTCGT  CAAAC TCC
                                    CC    T
GAM414  DNASE1    5'  CACACAGCCTATTGTCTACCTC 17822     CAA  TTTGC
                                GAG   AG    AGGCTGTGTG
                                |||   ||    ||||||||||
                                CTC   TC    TCCGACACAC
                                  CA_  TGTTA
GAM414  DNM2     3'  CACACAGCCTGAGCCTGGCCC  17054    A  AAA   TG
                                GG GC   GTT  CAGGCTGTGTG
                                || ||   |||  ||||||||||
                                CC CG   CGA  GTCCGACACAC
                                 _ GTC   __
GAM414  KRT15    3'  CACATGCAAACTCCAGTCC    9642      GCAA      GGC
                                GGA    AGTTTGCA   TGTG
                                |||    ||||||||   ||||
                                CCT    TCAAACGT   ACAC
                                  GACC       ___
GAM414  LENG4     3'  ACACAGCCTCCTGACTCC    44160      CAA  TTTGC
                                GGAG   AG    AGGCTGTGT
                                ||||   ||    |||||||||
                                CCTC   TC    TCCGACACA
                                  AG_  C____
GAM414  MOCS1     3'  CACACAGCCCACACCTGGCCC  92030    A  AAA  T  CA
                                GG GC   GT TG  GGCTGTGTG
                                || ||   || ||  |||||||||
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                                CC CG   CA AC  CCGACACAC
                                 _ GTC  C  __
GAM414  NPTX1    3' ACACAGCCTGGTTTTGTCC   10254     G    TTTG
                                GGA CAAAG   CAGGCTGTGT
                                ||| |||||   ||||||||||
                                CCT GTTTT   GTCCGACACA
                                  _    G___
GAM414  NTSR1    3' CACTTCCTGCCAAACTTTGCCC 10287    A       _   CT
                                GG GCAAAGTTTG CAGG  GTG
                                || |||||||||| ||||  |||
                                CC CGTTTCAAAC GTCC  CAC
                                 _       C   TT
GAM414  SLC7A8   3' CACACAGCCAGCACCACCGCCC 24276    A  AAAGTT   A
                                GG GC     TGC GGCTGTGTG
                                || ||     ||| |||||||||
                                CC CG     ACG CCGACACAC
                                 _ CCACC_   A
GAM414  FLJ20507 3' CACACAGCCTACACCCAGCCC  35274    A  AAAGTT  C
                                GG GC     TG AGGCTGTGTG
                                || ||     || ||||||||||
                                CC CG     AC TCCGACACAC
                                 _ ACCC__  A
GAM414  FLJ20507 3' CACACAGCCTACACCCAGCCC  60209    A  AAAGTT  C
                                GG GC     TG AGGCTGTGTG
                                || ||     || ||||||||||
                                CC CG     AC TCCGACACAC
                                 _ ACCC__  A
GAM414  FLJ21324 5' CTGCAAACTCCGCTTC      91201       AA
                                GGAGC  AGTTTGCAG
                                |||||  |||||||||
                                CTTCG  TCAAACGTC
                                   CC
GAM414  FLJ23462 3' CACACAGCACTTACTATGCTCC 45804       A   TTGCAG
                                GGAGCA AGT     GCTGTGTG
                                |||||| |||     ||||||||
                                CCTCGT TCA     CGACACAC
                                   A   TTCA__
GAM414  FLJ32499 5' CGTGCAGTCCAAACCCCGCCC  58157    A  AAA    CA    TG
                                GG GC   GTTTG  GGCTG  TG
                                || ||   |||||  |||||  ||
                                CC CG   CAAAC  CTGAC  GC
                                 _ CCC     __     GT
GAM414  KCNK16   3' CACACAGCCTAGACGCTTCCTC 49505     CA    TTGC
           C                     GGAG  AAGT    AGGCTGTGTG
                                ||||  ||||    ||||||||||
                                CCTC  TTCG    TCCGACACAC
                                  C_    CAGA
GAM414  KIAA0544 3' CACAGCCACCTGCTCC      70889       AA  TTGCA
                                GGAGCA  GT    GGCTGTG
                                ||||||  ||    |||||||
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                              CCTCGT  CA    CCGACAC
                                 C_ _____
GAM414  MAPK8IP2  3'  GCCTGCAAACCTTATCC    57467    GC  A
                              GGA  AA GTTTGCAGGC
                              |||  || ||||||||||
                              CCT  TT CAAACGTCCG
                                A_  C
GAM414  MAPK8IP2  3'  GCCTGCAAACCTTATCC    24658    GC  A
                              GGA  AA GTTTGCAGGC
                              |||  || ||||||||||
                              CCT  TT CAAACGTCCG
                                A_  C
GAM414  MAPK8IP2  3'  GCCTGCAAACCTTATCC    33157    GC  A
                              GGA  AA GTTTGCAGGC
                              |||  || ||||||||||
                              CCT  TT CAAACGTCCG
                                A_  C
GAM414  MGC20255  3'  CACACAGCCTGCCCCAGCGTCC 53439    _  AAAGTTT
                              GGA GC      GCAGGCTGTGTG
                              ||| ||      ||||||||||||
                              CCT CG      CGTCCGACACAC
                                G  ACCC___
GAM414  N-PAC     3'  CACACAGCAGCACCCTTCC   70879    GCAA  TT   AG
                              GGA   AG  TGC  GCTGTGTG
                              |||   ||  |||  ||||||||
                              CCT   TC  ACG  CGACACAC
                                _____  CC   A_
GAM414  PLP1      3'  ACACAGCCTACAATGCTGC   5002    G   AAGT   C
                              G AGCA   TTG AGGCTGTGT
                              | ||||   ||| |||||||||
                              C TCGT   AAC TCCGACACA
                               G   _____  A
GAM414  LOC128061 3'  CCAGCAAACTTCACTCC    74697     CA      A
                              GGAG  AAGTTTGC GG
                              ||||  |||||||| ||
                              CCTC  TTCAAACG CC
                                AC       A
GAM414  LOC131870 3'  CACACAGCCTGACACCTTCC  75016     CAAA  TTG
                              GGAG   GT   CAGGCTGTGTG
                              ||||   ||   ||||||||||||
                              CCTT   CA   GTCCGACACAC
                                C___  CA_
GAM414  LOC145719 5'  CACACAGCCCCCTTCCCTCC  83449     CA  TTTGCA
                              GGAG  AAG     GGCTGTGTG
                              ||||  |||     |||||||||
                              CCTC  TTC     CCGACACAC
                                CC   CC_____
GAM414  LOC145720 5'  CACACAGCCCCCTTCCCTCC  83431     CA  TTTGCA
                              GGAG  AAG     GGCTGTGTG
                              ||||  |||     |||||||||
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                                CCTC  TTC     CCGACACAC
                                  CC   CC____
GAM414   LOC146853 3'  CACACAGCCTCACCTTCACCTC 59182     CA_   TT  C
                                GAG   AAG  TG AGGCTGTGTG
                                |||   |||  || ||||||||||
                                CTC   TTC  AC TCCGACACAC
                                  CAC   C_  _
GAM414   LOC146894 3'  CACGATCTGCAAACTCCGCCTC 59186   GA  AA       GC
                                G  GC  AGTTTGCAG  TGTG
                                |  ||  |||||||||  ||||
                                C  CG  TCAAACGTC  GCAC
                                 TC  CC        TA
GAM414   LOC151040 5'  AGTCTCCGCAAACTTGCTCC   80101        A     __
                                GGAGCAA GTTTGC  AGGCT
                                |||||||  ||||||  |||||
                                CCTCGTT CAAACG  TCTGA
                                    _     CC
GAM414   LOC157247 5'  CACACAGCCAGTTCTCTGCTTC 81358       A  TTT  A
                                GGAGCA AG   GC GGCTGTGTG
                                ||||||  ||   ||  |||||||||
                                CTTCGT TC   TG CCGACACAC
                                   C  T__  A
GAM414   LOC197114 5'  CACACAGCCCCCTTCCCTCC   89701     CA   TTTGCA
                                GGAG  AAG     GGCTGTGTG
                                ||||  |||     |||||||||
                                CCTC  TTC     CCGACACAC
                                  CC   CC____
GAM414   LOC197117 5'  CACACAGCCCCCTTCCCTCC   89716     CA   TTTGCA
                                GGAG  AAG     GGCTGTGTG
                                ||||  |||     |||||||||
                                CCTC  TTC     CCGACACAC
                                  CC   CC____
GAM414   LOC203197 3'  ACACAGCCAACCCTGCTGC    89282    G    AA   TGCA
                                G AGCA  GTT    GGCTGTGT
                                |  ||||  |||   ||||||||
                                C TCGT  CAA    CCGACACA
                                 G    CC  ____
GAM414   LOC257065 5'  CAGGACCCTGCAGACCTTGCCC 97636    A    A       ___
                                GG GCAA GTTTGCAGG   CTG
                                || |||| |||||||||   |||
                                CC CGTT CAGACGTCC   GAC
                                  _   C        CAG
GAM414   LOC51157  3'  ACACAGCGTCACTCACTCC    32486     CAA   TT  AG
                                GGAG   AGT  GC  GCTGTGT
                                ||||   |||  ||  |||||||
                                CCTC   TCA  TG  CGACACA
                                  AC_   C_  __
GAM414   LOC51246  3'  ACACAGCCTAGCTGCCCC    33213    A   AAGTTT  _
                                GG GCA     GC AGGCTGTGT
                                || |||     || |||||||||
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                                CC CGT     CG TCCGACACA
                                 C  _______  A
GAM414  LOC92360  5'  CACACAGCCTGAGGGCCCTCC  69070     CAAA   TG
                                GGAG   GTT  CAGGCTGTGTG
                                ||||   |||  ||||||||||||
                                CCTC   CGG  GTCCGACACAC
                                  C___   GA
GAM414  LOC92973  5'  CACAGCCCACTGGCCC     71036    A  AA   TTGCA
                                GG GC  AGT    GGCTGTG
                                || ||  |||    |||||||
                                CC CG  TCA    CCGACAC
                                 _ G_  C____
GAM415  BIN3      3'  CACCCTCCAGCAGGCAGCCCAG 37955         C    AT  CA
            CA                    TGCTGGGCT CCTGC  GA  GTG
                                |||||||||  |||||  ||  |||
                                ACGACCCGA GGACG  CT  CAC
                                      C    AC  CC
GAM415  CRSP8     3'  CACGCAGGAAGCCCACA     80963    C     C    A
                                TG TGGGCT CCTGC TG
                                || ||||||  ||||| ||
                                AC ACCCGA GGACG AC
                                 _     A    C
GAM415  ENG       5'  CACTGCCATCCATTGGAGCCCA 3687           C_  C   A
            GCA                     TGCTGGGCTCC  TG ATG CAGTG
                                ||||||||||  ||  ||| |||||
                                ACGACCCGAGG  AC TAC GTCAC
                                       TT  C   C
GAM415  HD        3'  CACTGTTAGTGACAGAGCCCAG 9181           CC  _  _
            CA                    TGCTGGGCTC  TG CA TGACAGTG
                                ||||||||||  ||  ||  ||||||||
                                ACGACCCGAG  AC GT ATTGTCAC
                                      __  A  G
GAM415  IGLL1     5'  CACTCTCTAGGGAGCCCACA  39174    C        CAT  C
                                TG TGGGCTCCCTG   GA AGTG
                                ||  ||||||||||   ||  ||||
                                AC ACCCGAGGGAT   CT TCAC
                                 _         ___  C
GAM415  THBD      3'  CACTGCCACACAGGGTCTGCA  4494     T   CT    CA  A
                                TGC GGG  CCCTG  TG CAGTG
                                ||| |||  |||||  ||  |||||
                                ACG TCT  GGGAC  AC GTCAC
                                  _  __     AC  C
GAM415  ARHGEF16  3'  CACCGTGTCCCAGGGAGCCCAG 27069           CAT   __
            C                     GCTGGGCTCCCTG   GACA  GTG
                                ||||||||||||   ||||  |||
                                CGACCCGAGGGAC   CTGT  CAC
                                       C__    GC
GAM415  CABIN1    3'  ACCACATGGGAGCCCAG     24479          TGC   ACA
                                CTGGGCTCCC   ATG   GT
                                |||||||||   |||   ||
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                                GACCCGAGGG  TAC  CA
                                     ___  AC_
GAM415  FLJ10232  3'  ACTGTCAGGAACCCAG     35920     C  CTGCA
                                CTGGG TCC    TGACAGT
                                ||||| |||    |||||||
                                GACCC AGG    ACTGTCA
                                  A  _____
GAM415  FLJ20154  5'  GCCTTCAGGCCCAGCA     72927       CCCTGCA  CA
                                TGCTGGGCT     TGA  GT
                                |||||||||     |||  ||
                                ACGACCCGG     ACT  CG
                                     ________  TC
GAM415  FLJ21865  3'  CACCGCCATGCAGGGCTCGC  42805   T   TC      ACA
                                GC GGGC  CCTGCATG   GTG
                                || ||||  ||||||||   |||
                                CG CTCG  GGACGTAC   CAC
                                 _   __      CGC
GAM415  IRF7      3'  CACCGCGGTGCAAGAGCCCAGC 14443       CC    GACA
                                GCTGGGCTC  TGCAT   GTG
                                |||||||||  |||||   |||
                                CGACCCGAG  ACGTG   CAC
                                     A_    GCGC
GAM415  KIAA0864  3'  CACTGTCAGTATTAAGGCCCAG 63247       CCC_  A
          CA                   TGCTGGGCT   TGC TGACAGTG
                               |||||||||   ||| ||||||||
                               ACGACCCGG   ATG ACTGTCAC
                                    AATT  _
GAM415  MFN2      3'  ACAAGGCAGGGGCCCAGCA   29595       T     ATGACA
                                TGCTGGGC CCCTGC     GT
                                |||||||| ||||||     ||
                                ACGACCCG GGGACG     CA
                                     _     GAA___
GAM415  MGC3101   3'  GTCACACAGAGCCCAGCA    43883        CC  CA
                                TGCTGGGCTC  TG  TGAC
                                ||||||||||  ||  ||||
                                ACGACCCGAG  AC  ACTG
                                     __  AC
GAM415  SCYB11    3'  CACTGCCCAAAGGAGTCCAACA 87442    C      CTGCATGA
                                TG TGGGCTCC       CAGTG
                                || ||||||||       |||||
                                AC ACCTGAGG       GTCAC
                                 A       AAACCC__
GAM415  TIX1      3'  CATGTAAGGAGCCCAGCA    61739          C
                                TGCTGGGCTCC TGCATG
                                |||||||||||| ||||||
                                ACGACCCGAGG ATGTAC
                                       A
GAM415  UBP1      3'  CTGCCATAGCCAAGCA      27224      G   CCCTGC   A
                                TGCT GGCT     ATG CAG
                                |||| ||||     ||| |||
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                                ACGA CCGA     TAC GTC
                                  A   _______  C
GAM415  LOC123242 3'  ACCATTAAGCAGCCCAGCA   75589        CCCT  A   CA
                                TGCTGGGCT   GC TGA  GT
                                |||||||||   || |||  ||
                                ACGACCCGA   CG ATT  CA
                                     ____  A   AC
GAM415  LOC144058 5'  CTGGATGCAGGGCACCCAACA  76666    C   CT      GA
                                TG TGGG  CCCTGCAT  CAG
                                || ||||  ||||||||  |||
                                AC ACCC  GGGACGTA  GTC
                                 A   AC       G_
GAM415  LOC147160 5'  CACAGGGGAGCCCAGCA     83958          GCA
                                TGCTGGGCTCCCT   TG
                                ||||||||||||   ||
                                ACGACCCGAGGGG   AC
                                       AC_
GAM415  LOC148870 5'  CACTGCTCCCAGGAGCCCACA  79041    C      C  CAT  _
                                TG TGGGCTCC TG   GA CAGTG
                                || ||||||||  ||   || |||||
                                AC ACCCGAGG AC   CT GTCAC
                                 _       _  C__  C
GAM415  LOC149421 5'  CACTGCCAACGTAGAGGGCCCA 79355         C   A_  A
          GCA                    TGCTGGGCTC CTGC  TG CAGTG
                                |||||||||| ||||  || |||||
                                ACGACCCGGG GATG  AC GTCAC
                                      A   CA  C
GAM415  LOC151360 3'  CACTGTCACACCGTAGCCCACA 85311    C     CCCTGCA
                                TG TGGGCT      TGACAGTG
                                || ||||||      ||||||||
                                AC ACCCGA      ACTGTCAC
                                 _     TGCCAC_
GAM415  LOC151361 3'  CACTGTCACACCGTAGCCCACA 85320    C     CCCTGCA
                                TG TGGGCT      TGACAGTG
                                || ||||||      ||||||||
                                AC ACCCGA      ACTGTCAC
                                 _     TGCCAC_
GAM415  LOC152286 3'  CACTAGACAGCCAGGAGCCCAG 85626         CT  A  AC_
          CA                     TGCTGGGCTCC  GC TG   AGTG
                                ||||||||||  || ||   ||||
                                ACGACCCGAGG  CG AC   TCAC
                                      AC  _  AGA
GAM415  LOC152674 3'  CACTGTCACCTGGAAGCCCAG  85834       C  TGCA
                                CTGGGCT CC    TGACAGTG
                                ||||||| ||    ||||||||
                                GACCCGA GG    ACTGTCAC
                                    A  TCC_
GAM415  LOC253001 3'  ACCATTAAGCAGCCCAGCA   96249        CCCT  A   CA
                                TGCTGGGCT   GC TGA  GT
                                |||||||||   || |||  ||
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                                ACGACCCGA   CG ATT  CA
                                     _____  A   AC
GAM415  LOC255030 3'  ACTGAGAAGAAGCCCAGC    97267        CC  GCATGA
                                GCTGGGCT  CT     CAGT
                                ||||||||  ||     ||||
                                CGACCCGA  GA     GTCA
                                    A_  AGA___
GAM415  LOC51131  3'  ACTGTCACACTCCCAGCA    32277        CTCCC  CA
                                TGCTGGG    TG  TGACAGT
                                |||||||    ||  |||||||
                                ACGACCC    AC  ACTGTCA
                                   TC___  __
GAM416  BPAG1     3'  GCCCTTCCTTGAGCATTTA    31430        T   ACTCCTGA
                                TAAATGCTC AAG       GC
                                ||||||||| |||       ||
                                ATTTACGAG TTC       CG
                                    _  CTTCC___
GAM416  CDKN2D    3'  AGGGCAGAGCATTTA       8395          AAGAC
                                TAAATGCTCT    TCCT
                                ||||||||||    ||||
                                ATTTACGAGA    GGGA
                                     C_____
GAM416  CDKN2D    3'  AGGGCAGAGCATTTA       54379         AAGAC
                                TAAATGCTCT    TCCT
                                ||||||||||    ||||
                                ATTTACGAGA    GGGA
                                     C_____
GAM416  COL17A1   3'  GGCTCAGGAGTCTTAGAGCTTT 4935       T
          A                      TAAA GCTCTAAGACTCCTGAGCC
                                 |||| ||||||||||||||||||
                                 ATTT CGAGATTCTGAGGACTCGG
                                   _
GAM416  FBXL3A    3'  GCTCAGGAAAGTGAGCATTT   24067        TAAGAC
                                AAATGCTC     TCCTGAGC
                                ||||||||     ||||||||
                                TTTACGAG     AGGACTCG
                                    TGAA__
GAM416  FDFT1     3'  GCTCATGGCAGAGCATT     15517        AAGACT  _
                                AATGCTCT     CC TGAGC
                                ||||||||     || |||||
                                TTACGAGA     GG ACTCG
                                    C_____  T
GAM416  HMGA2     3'  TCAGCCTCAGAGCATTTA    13003         A  ACTC
                                TAAATGCTCT AG    CTGA
                                |||||||||| ||    ||||
                                ATTTACGAGA TC    GACT
                                     C  C___
GAM416  KLK4      3'  GGCCCAGGAGTCCAGGC     62870    T  AA       A
                                GC CT  GACTCCTG GCC
                                || ||  |||||||| |||
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                                CG GA  CTGAGGAC CGG
                                 _ C_       C
GAM416  MAT1A    3'  CTCAGGAGCCTGTGACAT    90831     C  TA  A
                                ATG TC  AG CTCCTGAG
                                ||| ||  || ||||||||
                                TAC AG  TC GAGGACTC
                                  _  TG  C
GAM416  RAI14    3'  GCTCAGGAAATCCAAACATTTG 31479       CTCTAAGAC
                                TAAATG        TCCTGAGC
                                ||||||        ||||||||
                                GTTTAC        AGGACTCG
                                   AAACCTAA_
GAM416  RBBP9    3'  GCCCAGGAGTTTGAGC      70134      TA        A
                                GCTC  AGACTCCTG GC
                                ||||  ||||||||| ||
                                CGAG  TTTGAGGAC CG
                                  __        C
GAM416  RPA3     5'  GGCCCAGGAATCTGGAGCAT   11380         A  C    A
                                ATGCTCTA GA TCCTG GCC
                                |||||||| || ||||| |||
                                TACGAGGT CT AGGAC CGG
                                     _ A    C
GAM416  ZNF74    3'  GCCCAGGAGTCTAGGACCA    12797    C   A        A
                                TG TCT AGACTCCTG GC
                                || ||| ||||||||| ||
                                AC AGG TCTGAGGAC CG
                                 C   A        C
GAM416  A4GALT   3'  GCTCAGGAGAAGCATTT     33838        CTAAGA
                                AAATGCT     CTCCTGAGC
                                |||||||     |||||||||
                                TTTACGA     GAGGACTCG
                                   A_____
GAM416  AAK1     3'  GCTCAGGAGCAAGACA      29849    C   AAGA
                                TG TCT    CTCCTGAGC
                                || |||    |||||||||
                                AC AGA    GAGGACTCG
                                 _   AC__
GAM416  ATPAF1   3'  CTCAAGAGCTCAGCATTTA    60773        CTA  A   C
                                TAAATGCT   AG CTC TGAG
                                ||||||||   || ||| ||||
                                ATTTACGA   TC GAG ACTC
                                     C__  _   A
GAM416  DKFZp761F2014 3'  GCTCAGACCTTGAGCATTTA   39539         T   ACTC
                                TAAATGCTC AAG    CTGAGC
                                ||||||||| |||    ||||||
                                ATTTACGAG TTC    GACTCG
                                      _   CA__
GAM416  FLJ11506 3'  GCTCAGTGACTGGAGCATT    45110         AGAC  _
                                AATGCTCTA    TC CTGAGC
                                |||||||||    || ||||||
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                                TTACGAGGT   AG GACTCG
                                    C___  T
GAM416  FLJ14327  3'  GGCCAGTGTTCTTGGAGCA   46144        CTC  A
                                TGCTCTAAGA  CTG GCC
                                ||||||||||  ||| |||
                                ACGAGGTTCT  GAC CGG
                                    TGT  _
GAM416  FLJ21945  3'  AGCTGTCTTAGGAGCACTTA  47314    A   _    TC
                                TAA TGCTC TAAGAC  CT
                                ||| ||||| ||||||  ||
                                ATT ACGAG ATTCTG  GA
                                  C   G     TC
GAM416  FLJ25415  3'  GCTGGTATCCCAGAAGCATTTA 58494       _ AA  CT  TG
                                TAAATGCT CT  GA  CC  AGC
                                |||||||| ||  ||  ||  |||
                                ATTTACGA GA  CT  GG  TCG
                                    A  CC  AT  __
GAM416  FLJ30213  3'  GGCTCAGGAGTGGGCA     58768      TAAG
                                TGCTC   ACTCCTGAGCC
                                |||||   ||||||||||
                                ACGGG   TGAGGACTCGG
                                  _____
GAM416  GLP       3'  CTTTTCTAGCTTAGAGCATTTA 37847          ACTCCT
                                TAAATGCTCTAAG     GAG
                                ||||||||||||      |||
                                ATTTACGAGATTC     TTC
                                      GATCTT
GAM416  GPT2      3'  GCTCAGGAGCCTGGGA     55958     A  A
                                TCT AG CTCCTGAGC
                                ||| || |||||||||
                                AGG TC GAGGACTCG
                                  G  C
GAM416  HEI10     3'  GCCCAGGAGTCTGAGGCTTTA  40998     T  T  A       A
                                TAAA GC CT AGACTCCTG GC
                                |||| || || ||||||||| ||
                                ATTT CG GA TCTGAGGAC CG
                                  _ _  G        C
GAM416  KIAA0326  3'  GGCCCAGGGGTCAAAGCATTTG 64329        CTAA      A
                                TAAATGCT   GACTCCTG GCC
                                ||||||||   |||||||| |||
                                GTTTACGA   CTGGGGAC CGG
                                    AA__       C
GAM416  KIAA0494  5'  GCTCAGGAGTCGGGGC     28744      AA
                                GCTCT  GACTCCTGAGC
                                |||||  ||||||||||
                                CGGGG  CTGAGGACTCG
                                  __
GAM416  KIAA0720  5'  GGCCCGAGCCTTAGAGC     62325        A  CTGA
                                GCTCTAAG CTC   GCC
                                |||||||| |||   |||
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                                CGAGATTC GAG   CGG
                                    C  CC__
GAM416  KIAA1598  3'  CTCAGGAGCTGGCAT      37077      CTA  A
                                ATGCT  AG CTCCTGAG
                                ||||||  || ||||||||
                                TACGG  TC GAGGACTC
                                  ____ _
GAM416  KIAA1713  3'  GCCCAGAGGATTTTAGAGC   72349        CT _  A
                                GCTCTAAGA  C CTG GC
                                |||||||||  | ||| ||
                                CGAGATTTT  G GAC CG
                                     AG A  C
GAM416  KIAA1753  3'  GGCCCAGGAGTTCCAGC    64885    CTAA      A
                                GCT   GACTCCTG GCC
                                |||   |||||||| |||
                                CGA   TTGAGGAC CGG
                                  CC__      C
GAM416  KIAA1755  3'  GGCATCCAGAGCATTTA    61351         AA  CT
                                TAAATGCTCT  GA  CC
                                ||||||||||  ||  ||
                                ATTTACGAGA  CT  GG
                                     C_  AC
GAM416  KIAA1821  3'  GCTCAGGAGTCCTAAACCAGC  71788    C___  A
                                GCT   TA GACTCCTGAGC
                                |||   || ||||||||||
                                CGA   AT CTGAGGACTCG
                                  CCAA  C
GAM416  LCE       3'  GCTCCATCCCAGAGCATTT   44028        AA  CTCCT
                                AAATGCTCT  GA   GAGC
                                |||||||||  ||   ||||
                                TTTACGAGA  CT   CTCG
                                     CC  AC___
GAM416  MGC22805  3'  CTCAGGAGTTTGAGAGCA   58082      A
                                TGCTCT AGACTCCTGAG
                                ||||||  ||||||||||
                                ACGAGA TTTGAGGACTC
                                   G
GAM416  PPFIBP2   3'  CTCAGGAGGAAAGACACTTA  76600    A  C  AAGA
                                TAA TG TCT   CTCCTGAG
                                ||| || |||   ||||||||
                                ATT AC AGA   GAGGACTC
                                  C  _  AAG_
GAM416  PRO0365   3'  GCTCAAGCAGAGTATTTA    26160        AAGA  CC
                                TAAATGCTCT   CT  TGAGC
                                ||||||||||   ||  |||||
                                ATTTATGAGA   GA  ACTCG
                                     C____  __
GAM416  PSK       3'  GCCCAAATCTAGAGCATT    32361        A  CTCC  A
                                AATGCTCTA GA   TG GC
                                |||||||| ||   || ||
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                                TTACGAGAT CT    AC CG
                                    _  AA__  C
GAM416  RAD51    3'  GAGTCTTAAAGCATTT      11222        C
                                AAATGCT TAAGACTC
                                ||||||| ||||||||
                                TTTACGA ATTCTGAG
                                    A
GAM416  RAD51    3'  GAGTCTTAAAGCATTT      56016        C
                                AAATGCT TAAGACTC
                                ||||||| ||||||||
                                TTTACGA ATTCTGAG
                                    A
GAM416  UPLC1    3'  CTCAGGAGCCTTTTAGT     34723     CT   A
                                GCT  AAG CTCCTGAG
                                |||  ||| ||||||||
                                TGA  TTC GAGGACTC
                                  TT   C
GAM416  ZNF262   3'  CAGGTCTTAGAGCATT      17485          CT
                                AATGCTCTAAGA  CCTG
                                ||||||||||||  ||||
                                TTACGAGATTCT  GGAC
                                          __
GAM416  ZNF313   3'  GCTCAAGAACCTTGGAGT    37941        AC  C
                                GCTCTAAG  TC TGAGC
                                ||||||||  || |||||
                                TGAGGTTC  AG ACTCG
                                    CA  A
GAM416  LOC115219 3'  GGCTGTCGTCTTGGAGCA    73314          TCCTG
                                TGCTCTAAGAC     AGCC
                                ||||||||||     ||||
                                ACGAGGTTCTG     TCGG
                                      CTG__
GAM416  LOC125268 3'  GGCTCAGGACAGAGCATT    76077        AAGAC
                                AATGCTCT    TCCTGAGCC
                                ||||||||    |||||||||
                                TTACGAGA    AGGACTCGG
                                    C____
GAM416  LOC128346 3'  GCTCAGTGCACAGAGTATT   74740        AAGACTC
                                AATGCTCT      CTGAGC
                                ||||||||      ||||||
                                TTATGAGA      GACTCG
                                    CACGT__
GAM416  LOC143188 5'  AGTCTCAGAGCATTTG      82896          A
                                TAAATGCTCT AGACT
                                |||||||||| |||||
                                GTTTACGAGA TCTGA
                                      C
GAM416  LOC143384 3'  CTCTCCTAGAGCATTT      76553          A  CTCCT
                                AAATGCTCTA GA     GAG
                                |||||||||| ||     |||
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                                TTTACGAGAT CT    CTC
                                      C _____
GAM416  LOC144519 3'  CTCAGGGGGAAAGAGCA    76868       AAGA
                                TGCTCT   CTCCTGAG
                                ||||||   ||||||||
                                ACGAGA   GGGGACTC
                                   AAG_
GAM416  LOC146728 3'  GCCCAGGAGTCTTGAG     83749    T       A
                                CTC AAGACTCCTG GC
                                ||| |||||||||| ||
                                GAG TTCTGAGGAC CG
                                  _       C
GAM416  LOC151904 5'  CAGGAGTCAGGGCA       80386       AA
                                TGCTCT  GACTCCTG
                                ||||||  ||||||||
                                ACGGGA  CTGAGGAC
                                  __
GAM416  LOC152359 3'  GCTCAAGGAAGAGCATTTG   85704         AAGAC   _
                                TAAATGCTCT    TCCT GAGC
                                ||||||||||    |||| ||||
                                GTTTACGAGA    AGGA CTCG
                                      _____   A
GAM416  LOC200138 5'  GGCCACCTCCTTGGAGCACTTA 89935    A       ACTCC  A
                                TAA TGCTCTAAG    TG GCC
                                ||| |||||||||    || |||
                                ATT ACGAGGTTC    AC CGG
                                  C       CTCC_ _
GAM416  LOC200213 5'  GCTCAGGAGCCTCAGACGC   88634    _  A  A
                                GC TCT AG CTCCTGAGC
                                || ||| || |||||||||
                                CG AGA TC GAGGACTCG
                                 C  C  C
GAM416  LOC220538 3'  CTTTTCTAGCTTAGAGCATTTA 90733           ACTCCT
                                TAAATGCTCTAAG     GAG
                                ||||||||||||     |||
                                ATTTACGAGATTC     TTC
                                       GATCTT
GAM416  LOC222236 3'  CAGGAGTTTGACAT       94307    C  TA
                                ATG TC  AGACTCCTG
                                ||| ||  |||||||||
                                TAC AG  TTTGAGGAC
                                  _ __
GAM416  LOC253666 3'  GCTCAGGAAGGAAGGAGCA   95065       AAGAC
                                TGCTCT    TCCTGAGC
                                ||||||    ||||||||
                                ACGAGG    AGGACTCG
                                   AAGGA
GAM416  LOC256158 5'  GCTCAGGAAGGAACAT     97672    C   AAGAC
                                ATG TCT    TCCTGAGC
                                ||| |||    ||||||||
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                                TAC AGG     AGGACTCG
                                  A   A____
GAM416  LOC257286 3'  CTTTTCTAGCTTAGAGCATTTA 94555            ACTCCT
                                TAAATGCTCTAAG      GAG
                                ||||||||||||      |||
                                ATTTACGAGATTC      TTC
                                      GATCTT
GAM416  LOC51049  5'  CTCAAAGCAAAATAGAGCATTT 31886          AGACTCC_
                                AAATGCTCTA       TGAG
                                ||||||||||       ||||
                                TTTACGAGAT       ACTC
                                     AAAACGAA
GAM416  LOC93132  3'  GGAGTCTTAAAGAATTTA     71493       G  C
                                TAAAT CT TAAGACTCC
                                ||||| || |||||||||
                                ATTTA GA ATTCTGAGG
                                   A  A
GAM417  ACTN2     3'  TTTAGCTAGTGTGCGG      6597
                                TTGCACATTAGCTAGA
                                ||||||||||||||||
                                GGCGTGTGATCGATTT

GAM417  AQP2      3'  TTTACTAGTGTGCAAG      4911             C
                                TTTGCACATTAG TAGA
                                |||||||||||| ||||
                                GAACGTGTGATC ATTT
                                             _
GAM417  ARHGEF6   3'  TCTGCCTAGTGTGTAAG     68206            C
                                TTTGCACATTAG TAGA
                                |||||||||||| ||||
                                GAATGTGTGATC GTCT
                                      C
GAM417  BAZ2A     3'  TCTAGTGAATGTGTGAA     25612     TG     A
                                TT  CACATT GCTAGA
                                ||  |||||| ||||||
                                AA  GTGTAA TGATCT
                                  GT     G
GAM417  C21orf2   3'  TCAGCCTTCCAGCTGGTGTGTA 17017            A  TT  CAT
              G                  TTGCACATTAGCT GA  GC
                                ||||||||||||| ||  ||
                                GATGTGTGGTCGA CT  CG
                                      C  TC  ACTG
GAM417  CAPS      3'  TGGGAGGCTGTGTGTGGA     14482     TG     T    AGAT G
                                TT  CACAT AGCT    T CCA
                                ||  ||||| ||||    | |||
                                AG  GTGTG TCGG    A GGT
                                  GT     _    ____ G
GAM417  CARD4     3'  TGGAAAGTTAATGTCAAG     20333      C        AGATTG
                                TTTG ACATTAGCT      CCA
                                ||||| |||||||||      |||
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                                GAAC TGTAATTGA     GGT
                                  _       AA____
GAM417  CLASP1   3'  ATGGCGAAACCCTGTGTGTGG  65297   TG    T  CTAGA
                                T  CACAT AG    TTGCCAT
                                |  ||||| ||    |||||||
                                G  GTGTG TC    AGCGGTA
                                 GT    _  CCAA_
GAM417  CNTNAP2  3'  TGGCACCTGGTGTGTAA     26234          CTAGAT
                                TTGCACATTAG     TGCCA
                                ||||||||||     |||||
                                AATGTGTGGTC     ACGGT
                                      C_____
GAM417  COL13A1  3'  GTGCTGGCTAGCTCATGTGTGA 55013    TG    T    ATT  CAT
           A                     TT  CACAT AGCTAG   GC
                                ||  ||||| ||||||   ||
                                AA  GTGTA TCGATC   CG
                                 GT    C     GGT  TG
GAM417  COL13A1  3'  GTGCTGGCTAGCTCATGTGTGA 55016    TG    T    ATT  CAT
           A                     TT  CACAT AGCTAG   GC
                                ||  ||||| ||||||   ||
                                AA  GTGTA TCGATC   CG
                                 GT    C     GGT  TG
GAM417  COL13A1  3'  GTGCTGGCTAGCTCATGTGTGA 55019    TG    T    ATT  CAT
           A                     TT  CACAT AGCTAG   GC
                                ||  ||||| ||||||   ||
                                AA  GTGTA TCGATC   CG
                                 GT    C     GGT  TG
GAM417  COL13A1  3'  GTGCTGGCTAGCTCATGTGTGA 55022    TG    T    ATT  CAT
           A                     TT  CACAT AGCTAG   GC
                                ||  ||||| ||||||   ||
                                AA  GTGTA TCGATC   CG
                                 GT    C     GGT  TG
GAM417  COL13A1  3'  GTGCTGGCTAGCTCATGTGTGA 55025    TG    T    ATT  CAT
           A                     TT  CACAT AGCTAG   GC
                                ||  ||||| ||||||   ||
                                AA  GTGTA TCGATC   CG
                                 GT    C     GGT  TG
GAM417  COL13A1  3'  GTGCTGGCTAGCTCATGTGTGA 55028    TG    T    ATT  CAT
           A                     TT  CACAT AGCTAG   GC
                                ||  ||||| ||||||   ||
                                AA  GTGTA TCGATC   CG
                                 GT    C     GGT  TG
GAM417  COL13A1  3'  GTGCTGGCTAGCTCATGTGTGA 17787    TG    T    ATT  CAT
           A                     TT  CACAT AGCTAG   GC
                                ||  ||||| ||||||   ||
                                AA  GTGTA TCGATC   CG
                                 GT    C     GGT  TG
GAM417  COX17    3'  ATGGTGGTCTGCTGTGTG    19100      T  T   TG
                                CACAT AGC AGAT  CCAT
                                ||||| ||| ||||  ||||
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                                GTGTG TCG TCTG  GGTA
                                  _  _   GT
GAM417  CPSF6    3'  TAGCAATCTAGTCAATGTGTAA 22802         AG       CAT
                G                  TTTGCACATT  CTAGATTGC
                                   ||||||||||  |||||||||
                                   GAATGTGTAA  GATCTAACG
                                        CT        ATA
GAM417  CRYZL1   5'  GTGGCGGTGGTGAAGGTGCAG  17581       ATTA   AG
                                   TTGCAC    GCT  ATTGCCAT
                                   ||||||    |||  ||||||||
                                   GACGTG    TGG  TGGCGGTG
                                      GAAG   __
GAM417  CUL4B    3'  ATGTTATTTAGTATGATGTGCA 13138          _      T  CAT
                GA                   TTTGCACATTA GCTAGAT GC
                                     ||||||||||| ||||||| ||
                                     AGACGTGTAGT TGATTTA TG
                                           A      T  TA
GAM417  CYP17    3'  GTGGCAATGCCAGTGATGTGCA 3646         G  AG_
                                     TGCACATTA CT   ATTGCCAT
                                     |||||||| ||   ||||||||
                                     ACGTGTAGT GA   TAACGGTG
                                          _ CCG
GAM417  DHCR24   3'  GTGGCAGTGTATGGTGTGTGA  28633    TG      GC  G
                                     T  CACATTA  TA ATTGCCAT
                                     |  |||||||  || ||||||||
                                     A  GTGTGGT  AT TGACGGTG
                                      GT      __  G
GAM417  E2F3     3'  GTGGCAATTGTCAGGGTGTGGG 8701      G     AGCTA
                AA                     TTT CACATT    GATTGCCAT
                                       ||| ||||||    |||||||||
                                       AAG GTGTGG    TTAACGGTG
                                         G     GACTG
GAM417  EGR2     5'  GTGGTGGTTGTTTTTAAGTGTG 4631     TG   A   CTA_  TG
                GA                     TT  CAC TTAG    GAT  CCAT
                                       ||  ||| ||||    |||  ||||
                                       AG  GTG AATT    TTG  GGTG
                                        GT  _    TTTG   GT
GAM417  EPHA3    3'  GTGCAGTTTTGGTGTGTAA   17871          CTA     CAT
                                     TTGCACATTAG   GATTGC
                                     ||||||||||   ||||||
                                     AATGTGTGGTT   TTGACG
                                           ___      TGG
GAM417  EPS8     5'  GCTCTTTAGCTGGGTGCAGA   15470        A       TT
                                     TTTGCAC TTAGCTAGA  GC
                                     |||||||  |||||||||  ||
                                     AGACGTG GGTCGATTT  CG
                                        _       CT
GAM417  ESRRG    3'  ATGGCAGTCTTATGTGCAAA   66387         TAGCT
                                     TTTGCACAT    AGATTGCCAT
                                     |||||||||    ||||||||||
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                                AAACGTGTA    TCTGACGGTA
                                     T____
GAM417  FACL4   3'  ATGGTGATTTTAAATGTGTGAG 15506    TG    AGCT   TG
                                TT  CACATT   AGAT  CCAT
                                ||  ||||||   ||||  ||||
                                GA  GTGTAA   TTTA  GGTA
                                  GT    AT__   GT
GAM417  FACL4   3'  ATGGTGATTTTAAATGTGTGAG 43396    TG    AGCT   TG
                                TT  CACATT   AGAT  CCAT
                                ||  ||||||   ||||  ||||
                                GA  GTGTAA   TTTA  GGTA
                                  GT    AT__   GT
GAM417  FGB     3'  TCTAGTTGATTGCGAG     17638       C
                                TTTGCA ATTAGCTAGA
                                ||||||  ||||||||||
                                GAGCGT TAGTTGATCT

                                  _
GAM417  FUS1    3'  GTGGTGAAGGCTAATGGCAGA  23451      A      AGA TG
                                TTTGC CATTAGCT   T  CCAT
                                |||||  ||||||||   |  ||||
                                AGACG GTAATCGG   A  GGTG
                                   _      A__ GT
GAM417  GARP    3'  GGCTCAGTAATGTGCGAG    18597         G  A  TT
                                TTTGCACATTA CT GA  GCC
                                ||||||||||  ||  ||  |||
                                GAGCGTGTAAT GA CT  CGG

                                      _  _  __
GAM417  GPR17   3'  CTTGCTAGTGTGCAGA      17954          T
                                TTTGCACATTAGC AG
                                ||||||||||||  ||
                                AGACGTGTGATCG TC
                                        T
GAM417  GUCY1B3  3'  ATGGTGATCTGCAAGTAGTAG  5964      _  A  A  T   TG
                                TTGC AC TT GC AGAT  CCAT
                                ||||  ||  ||  ||  ||||  ||||
                                GATG TG AA CG TCTA  GGTA
                                  A  _  _  _   GT
GAM417  HIVEP2  3'  ATGGCTTTTGGTTAGTGT    22118          TT
                                ACATTAGCTAGA  GCCAT
                                ||||||||||||  |||||
                                TGTGATTGGTTT  CGGTA
                                       T_
GAM417  HSPA6   5'  GTGGCCTATGGGGCTGCTGTGC 76334       T    AG  T_
          AG                    TTGCACA TAGCT  AT  GCCAT
                                |||||||  |||||  ||  |||||
                                GACGTGT GTCGG  TA  CGGTG
                                   C    GG  TC
GAM417  ITGA1   3'  ATGTATAGTAGCTGCATGTGTG 63528    TG    _     GAT   CAT
          AA                    TT  CACAT TAGCTA   TGC
                                ||  |||||  ||||||   |||
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                                AA  GTGTA GTCGAT   ATG
                                 GT    C     GAT   TA
GAM417  KCNK2    3'  TCTAGCTAATGTGTGG      26422    TG
                                T  CACATTAGCTAGA
                                |  ||||||||||||
                                G  GTGTAATCGATCT
                                 GT
GAM417  KIAA0857 3'  TGGTGGATGATGTGT       66681         G  AGATT
                                GCACATTA CT    GCCA
                                |||||||| ||    ||||
                                TGTGTAGT GG    TGGT
                                    A  _____
GAM417  LENG4    3'  GTGGCGGGTGCGCTGCTGTGCG 44170         T    TAGA
              G                  TTGCACA TAGC    TTGCCAT
                                |||||||| ||||    |||||||
                                GGCGTGT GTCG    GGCGGTG
                                    C    CGTG
GAM417  LFG      3'  TGGAAAGTTACTGTGTGGA    76729    TG    T    AGATTG
                                TT  CACA TAGCT     CCA
                                ||  |||| |||||      |||
                                AG  GTGT ATTGA     GGT
                                 GT    C     AA____
GAM417  LIF      3'  ATGGCGCGTGGGCAGTGTGCAG 9727           A   AGAT
                                TTGCACATT GCT    TGCCAT
                                |||||||||| |||    ||||||
                                GACGTGTGA CGG    GCGGTA
                                     _   GTGC
GAM417  LPHH1    5'  GCCTCTGGCTCGGTGTGTGGA  24538    TG     _      TT
                                TT  CACATT AGCTAGA  GC
                                ||  |||||| |||||||  ||
                                AG  GTGTGG TCGGTCT  CG
                                 GT     C      C_
GAM417  MAP3K7IP2 3'  ATGGTGTTCTGCTAATGTTAAA 30660      C       T   TT
                                TTTG ACATTAGC AGA  GCCAT
                                |||| |||||||| |||  |||||
                                AAAT TGTAATCG TCT  TGGTA
                                  _       _   TG
GAM417  MLANA    3'  ATGGCAATTTAGCTCTCTTGGG 18581    A  TT__
              T                  GC CA    AGCTAGATTGCCAT
                                || ||    ||||||||||||||
                                TG GT    TCGATTTAACGGTA
                                 G  TCTC
GAM417  MMP14    3'  GTGGCAGCAGGTGGTGGTGG   17173    TG A    G  AGA
                                T  C CATTA CT   TTGCCAT
                                |  | ||||| ||   |||||||
                                G  G GTGGT GA   GACGGTG
                                 GT _     G  C__
GAM417  MYOM2    3'  TGGCGGTCTCTGTGTGAA    14270    TG    TTAGCT
                                TT  CACA     AGATTGCCA
                                ||  ||||     |||||||||
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                                AA  GTGT     TCTGGCGGT
                                 GT    C_____
GAM417  NEDD4L   3'  CAACTGGTTGATGTGTA     30947            A
                                TGCACATTAGCTAG TTG
                                |||||||||||||| |||
                                ATGTGTAGTTGGTC AAC
                                          _
GAM417  NUP98    3'  ATGGCATGAGATAGCTGGTGT  32860          GAT__
                                ACATTAGCTA     TGCCAT
                                ||||||||||     ||||||
                                TGTGGTCGAT     ACGGTA
                                      AGAGT
GAM417  OGT      3'  ATGGGATGGTTAGTGTGGAG   13199    G        GATTG
                                TT CACATTAGCTA     CCAT
                                || ||||||||||     ||||
                                GA GTGTGATTGGT     GGTA
                                 G         AG___
GAM417  PAX4     5'  GTGGGAGAGGTGGTGTGTGGA  20557    TG      G  AGA  G
                                TT  CACATTA CT   TT CCAT
                                ||  ||||||| ||   || ||||
                                AG  GTGTGGT GA   GA GGTG
                                 GT      G ___  G
GAM417  PDE4D    3'  CAACTAGTTAATTGCAAG    73581       C        A
                                TTTGCA ATTAGCTAG TTG
                                |||||| |||||||| |||
                                GAACGT TAATTGATC AAC
                                          _       _
GAM417  PDGFRA   3'  ATGGTGTGGTGAATGTGTGAG  20591    TG     A    GAT
                                TT  CACATT GCTA   TGCCAT
                                ||  |||||| ||||   ||||||
                                GA  GTGTAA TGGT   GTGGTA
                                 GT     G   ___
GAM417  PER2     3'  GTGGTTTGTTTGTGTGCAAA   43040         T   T    TG
                                TTTGCACAT AGC AGAT  C
                                ||||||||| ||| ||||  |
                                AAACGTGTG TTG TTTG  G
                                      T   _    GT
GAM417  PGM1     3'  GTGGCAATGAAATGATGGTGCA 10539         _   GCTAG
             AG                   TTTGCAC ATTA     ATTGCCAT
                                ||||||| ||||     ||||||||
                                GAACGTG TAGT     TAACGGTG
                                    G    AAAG_
GAM417  PROS1    3'  TGGCACAGCTGTGTGCAAG    87426         T    AGAT
                                TTTGCACAT AGCT    TGCCA
                                ||||||||| ||||    |||||
                                GAACGTGTG TCGA    ACGGT
                                      _   C___
GAM417  RLN2     3'  TTTATTTGATGTGTAAG     56241           C
                                TTTGCACATTAG TAGA
                                |||||||||||| ||||
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                                GAATGTGTAGTT ATTT
                                       T
GAM417  RLN2     3'  TTTATTTGATGTGTAAG     17342           C
                                TTTGCACATTAG TAGA
                                |||||||||||| ||||
                                GAATGTGTAGTT ATTT
                                       T
GAM417  RNASE1   5'  GTGTCCACTGGTTAGTGTGTGA 11348    TG         ATTGCCAT
           G                     TT  CACATTAGCTAG
                                ||  ||||||||||||
                                GA  GTGTGATTGGTC
                                 GT          ACCTGTG
GAM417  SDC2     3'  ATGGTAATTTAGTGTATATGTG 67131      TA__
                                CACAT    GCTAGATTGCCAT
                                |||||    ||||||||||||
                                GTGTA    TGATTTAATGGTA
                                   TATG
GAM417  SLC25A17 3'  GTGGCAGTTGGACTAATGTG   20999        _  G
                                CACATTAG CTA ATTGCCAT
                                |||||||| ||| ||||||||
                                GTGTAATC GGT TGACGGTG
                                     A  _
GAM417  SLC26A4  3'  TTTAGCAGTGTGTAAA      4791          A
                                TTTGCACATT GCTAGA
                                |||||||||| ||||||
                                AAATGTGTGA CGATTT
                                                _
GAM417  SMCX     3'  ATGGATGGGCTGGTGGGCAG   14822      A      AGATTG
                                TTGC CATTAGCT      CCAT
                                |||| ||||||||      ||||
                                GACG GTGGTCGG      GGTA
                                  G       GTA___
GAM417  SP3      3'  TTTATTGATGTGCAAA      82499           C
                                TTTGCACATTAG TAGA
                                |||||||||||| ||||
                                AAACGTGTAGTT ATTT
                                                _
GAM417  TACSTD2  3'  ATGGCACAGCGTTATGTGTAAA 9854          TA_   AGAT
                                TTTGCACAT   GCT    TGCCAT
                                |||||||||   |||    ||||||
                                AAATGTGTA   CGA    ACGGTA
                                      TTG   C___
GAM417  TEM8     3'  ATGTTGCTATGTTGATGTGTAA 49850           _   ATT  CAT
           G                     TTTGCACATTAGC TAG   GC
                                ||||||||||||| |||   ||
                                GAATGTGTAGTTG ATC   TG
                                       T   GT_  TA
GAM417  TGFBR3   5'  GTGGCAGTTTGAAAATTGCAAG 12276       C   AGC
                                TTTGCA ATT   TAGATTGCCAT
                                |||||| |||   ||||||||||
```

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                                GAACGT TAA   GTTTGACGGTG
                                   _   AA_
GAM417  TP63     3'  GTGGCTCTAAAAGGTAATGTGT 13570   TG      G ___   TT
             GGA                    CACATTA CT   AGA  GCCAT
                                    ||||||| ||   |||  |||||
                                    GTGTAAT GA   TCT  CGGTG
                                   GT      G  AAA  __
GAM417  TRPC1    3'  GTCCCTCTTGTTTGGTGTGTAG 12392          _ T   TTGCCAT
             A                      TTTGCACATTAG C AGA
                                   |||||||||||| | |||
                                   AGATGTGTGGTT G TCT
                                          T T   CCCTG
GAM417  USP9X    3'  ATGGCCTGATGCTAATGTGTAA 16206           TAGATT
             A                      TTTGCACATTAGC     GCCAT
                                   ||||||||||||      |||||
                                   AAATGTGTAATCG     CGGTA
                                          TAGTC_
GAM417  ZHX1     3'  ATGGTAATTTGGATAGGGTG  23330     A   G
                                   CAC TTA CTAGATTGCCAT
                                   ||| ||| ||||||||||||
                                   GTG GAT GGTTTAATGGTA
                                     G   A
GAM417  ZNF76    5'  TGGCGGTCTGTCGGCGGA    12814      ACATTA  T
                                   TTTGC     GC AGATTGCCA
                                   |||||     || |||||||||
                                   AGGCG     TG TCTGGCGGT
                                      GC____  _
GAM417  ACAS2L   3'  GTGGCAGTGCCAGTGTTCGG  68076     C    A  TAG
                                   TTG ACATT GC   ATTGCCAT
                                   ||| ||||| ||   ||||||||
                                   GGC TGTGA CG   TGACGGTG
                                     T    C  ___
GAM417  AP1GBP1  3'  AAATTGGCTGATGTGGGAG   23386     G         A
                                   TTT CACATTAGCTAG TT
                                   ||| |||||||||||| ||
                                   GAG GTGTAGTCGGTT AA
                                     G          A
GAM417  AP1GBP1  3'  AAATTGGCTGATGTGGGAG   54512     G         A
                                   TTT CACATTAGCTAG TT
                                   ||| |||||||||||| ||
                                   GAG GTGTAGTCGGTT AA
                                     G          A
GAM417  AP1GBP1  3'  AAATTGGCTGATGTGGGAG   54526     G         A
                                   TTT CACATTAGCTAG TT
                                   ||| |||||||||||| ||
                                   GAG GTGTAGTCGGTT AA
                                     G          A
GAM417  APMCF1   3'  GTGGTAGTCTGGAGTTGATG  41068         __
                                   CATTAGCT  AGATTGCCAT
                                   ||||||||  ||||||||||
```

```
                                GTAGTTGA  TCTGATGGTG
                                    GG
GAM417  APOL3    3'  GTGGTGGTTGTAGTGTGATG  26815      _   _  TG
                                CATTA GCTA GAT  CCAT
                                ||||| |||| |||  ||||
                                GTAGT TGAT TTG  GGTG
                                   G   G  GT
GAM417  APOL4    3'  GTGGTGGTTGTAGTGTGACAG  47630    _     GCTA  TG
                                TTG CACATTA   GAT  CCAT
                                ||| |||||||   |||  ||||
                                GAC GTGTGAT   TTG  GGTG
                                  A     G___  GT
GAM417  ARFD1    3'  TGGTAATTTAGGATGCA    7994      CATTAG
                                TGCA    CTAGATTGCCA
                                ||||    ||||||||||
                                ACGT    GATTTAATGGT
                                  AG____
GAM417  ARHF     3'  TGGTGATGTGGGTGCAG    38752      ATTAG  G  TG
                                TTGCAC    CTA AT  CCA
                                ||||||    ||| ||  |||
                                GACGTG    GGT TA  GGT
                                   _____  G  GT
GAM417  ASAHL    3'  ATGGCAGTCTAGCCTGGGCAA  63562     A  TTA
                                TTGC CA   GCTAGATTGCCAT
                                |||| ||   ||||||||||||
                                AACG GT   CGATCTGACGGTA
                                  G  C__
GAM417  AWP1     3'  TTTAGTTGAGTGCAGA     38664       A
                                TTTGCAC TTAGCTAGA
                                ||||||| |||||||||
                                AGACGTG AGTTGATTT
                                   _
GAM417  BART1    3'  CTGCTGGTGTGTAAG      23983          T
                                TTTGCACATTAGC AG
                                |||||||||||| ||
                                GAATGTGTGGTCG TC
                                    _
GAM417  BPESC1   3'  TGAGGATTGATTGGGCTGATGT 41477          A   G__  AT
          GTAGA                   TGCACATTAGCT GATT   CC
                                ||||||||||| ||||   ||
                                ATGTGTAGTCGG TTAG   GG
                                      G    TTA  AGTA
GAM417  C11orf9  3'  GTCTTGGCTGGTGGGCAGA   25212      A      _
                                TTTGC CATTAGCTA GAT
                                ||||| ||||||||| |||
                                AGACG GTGGTCGGT CTG
                                   G        T
GAM417  C1QR1    3'  TCTAGGTGATGTGTGAA     23845    TG     G
                                TT  CACATTA CTAGA
                                ||  ||||||| |||||
```

```
                                AA  GTGTAGT GATCT
                                 GT      G
GAM417  C20orf111 3'  AAAGAGATTTAGTTAATGGCAG 33208       A          GCCAT
            A                    TTTGC CATTAGCTAGATT
                                 |||||| |||||||||||||
                                 AGACG GTAATTGATTTAG
                                   _           AGAAAC
GAM417  C20orf21  3'  ATGGTGTTGGGGCATGATGTGT 35110    TG     _  AGAT
            GGA                    TT  CACATTA GCT   TGCCAT
                                 ||  ||||||| |||   ||||||
                                 AG  GTGTAGT CGG   GTGGTA
                                  GT      A   GGTT
GAM417  C22orf20  3'  GTGGCGATGAGAGAGTGTAGA  47435        ATTAG  AG
                                 TTTGCAC    CT  ATTGCCAT
                                 |||||||    ||  ||||||||
                                 AGATGTG    GA  TAGCGGTG
                                     AGA__  G_
GAM417  C2orf7    3'  GTGGTTTAAAGAGCTGGTGTTT 50302    TT C       AGATT_
            GGG                    T  G ACATTAGCT     GCCAT
                                 |  | |||||||||     |||||
                                 G  T TGTGGTCGA     TGGTG
                                  GG T        GAAATT
GAM417  CNNM3     3'  GGCCGTGATGTGCAGA      34341          AGCTAG  T
                                 TTTGCACATT     AT GCC
                                 ||||||||||     || |||
                                 AGACGTGTAG     TG CGG
                                       _______  C
GAM417  COASTER   3'  TTTGTGCTAATGTGCAAA    31451           _
                                 TTTGCACATTAGC TAGA
                                 |||||||||||| ||||
                                 AAACGTGTAATCG GTTT
                                        T
GAM417  DIS3      3'  GTGTTCATGGTTAGTGTGT   30235          _  TT
                                 GCACATTAGCTA GA  GC
                                 |||||||||||| ||  ||
                                 TGTGTGATTGGT CT  TG
                                       A  TG
GAM417  DKFZP434D1335 3'  TGGCAATACATGTGTAGA    65116         TAGCTAG
                                 TTTGCACAT      ATTGCCA
                                 |||||||||      |||||||
                                 AGATGTGTA      TAACGGT
                                     CA_____
GAM417  DKFZP434J037 3'  GTGGCACCCCTAATGTGCA   48218         CTAGAT
                                 TGCACATTAG     TGCCAT
                                 ||||||||||     ||||||
                                 ACGTGTAATC     ACGGTG
                                      CCC___
GAM417  DKFZP564F013 3'  GTGGCAGATGTTGTGTGTGAA  94208    TG    T   TAGA
                                 TT  CACAT AGC    TTGCCAT
                                 ||  ||||| |||    |||||||
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                                AA  GTGTG TTG    GACGGTG
                                 GT     _   TA__
GAM417  DKFZP564I052 3'  GTGGTGATCTTAAATGGGTGAG 66717    TG A    AGCT    TG
                                TT  C CATT    AGAT  CCAT
                                ||  | ||||    ||||  ||||
                                GA  G GTAA    TCTA  GGTG
                                 GT G    AT__    GT
GAM417  DKFZP564I052 3'  TGGTAGTAACTGTGTAAA    66722        TTAGCTAG
                                TTTGCACA       ATTGCCA
                                ||||||||       |||||||
                                AAATGTGT       TGATGGT
                                     CAA_____
GAM417  DKFZp586I021 3'  GTGGCCTTGAGGTTGGTGTGCA 50091           AGATT
                                TGCACATTAGCT    GCCAT
                                ||||||||||||    |||||
                                ACGTGTGGTTGG    CGGTG
                                       AGTTC
GAM417  DNCI2    5'  GTGGTGGCTACAGTTGGTGTTG 60967    _      __  A TG
                                CA CATTAGCT  AG T  CCAT
                                || ||||||||  || |  ||||
                                GT GTGGTTGA  TC G  GGTG
                                 T       CA  _ GT
GAM417  DRG1     5'  GTGGCAGTTTGCCGCGGGTGTG 14733    TG    TA  __
           TGAA                   T  CACAT  GC  TAGATTGCCAT
                                |  |||||  ||  ||||||||||
                                A  GTGTG  CG  GTTTGACGGTG
                                 GT    GG  CC
GAM417  EVI5     3'  GTATATGGTTAATGTGTAAA   19006            GAT
                                TTTGCACATTAGCTA   TGC
                                ||||||||||||||   |||
                                AAATGTGTAATTGGT   ATG
                                       AT_
GAM417  FIGN     3'  ATGGTGGTGGTAGTTTGCAAG  95639       C   G  AG  TG
                                TTTGCA ATTA CT  AT  CCAT
                                ||||||  |||| ||  ||  ||||
                                GAACGT TGAT GG  TG  GGTA
                                    T   _  __  GT
GAM417  FLJ10242  3'  TGGTGGCTGGTGTCAAA     35936      C       AGATT
                                TTTG ACATTAGCT    GCCA
                                ||||  |||||||||    ||||
                                AAAC TGTGGTCGG    TGGT
                                   _       ______
GAM417  FLJ10813  3'  GGGTTGTAGATAATGTGCAAG  36685          G   GATT   AT
                                TTTGCACATTA CTA    GCC
                                ||||||||||| |||    |||
                                GAACGTGTAAT GAT    TGG
                                       A  GT__   GT
GAM417  FLJ10829  3'  TGGTATAACTGTGTGCAAA   36716         T  CTAGAT
                                TTTGCACAT AG     TGCCA
                                |||||||| ||     |||||
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                              AAACGTGTG TC     ATGGT
                                    _ AAT___
GAM417  FLJ11342  3' GTTTAGTTGGTATGTAAA    37250       C
                              TTTGCA ATTAGCTAGAT
                              ||||||| ||||||||||
                              AAATGT TGGTTGATTTG
                                 A
GAM417  FLJ11710  3' GGGCTGGGGTGTAATGTGCAGA 45830          _  AGATT  AT
                              TTTGCACATTA GCT    GCC
                              |||||||||||| |||    |||
                              AGACGTGTAAT TGG    CGG
                                     G  GGT__  GT
GAM417  FLJ11807  3' GTGTGGCTGGTGGGTGAG    46353    TG A       G
                              TT  C CATTAGCTA AT
                              ||  | |||||||| ||
                              GA  G GTGGTCGGT TG
                               GT G        G
GAM417  FLJ11939  3' ATGGTGGTTTGTCCCGTGTAAG 45173       ATTA  T   TG
                              TTTGCAC    GC AGAT  CCAT
                              |||||||    || ||||  ||||
                              GAATGTG    TG TTTG  GGTA
                                  CCC_ _    GT
GAM417  FLJ12270  5' GGCGGCGATGTGCGGA     47574         A  AGATT
                              TTTGCACATT GCT    GCC
                              |||||||||| |||    |||
                              AGGCGTGTAG CGG    CGG
                                     _  _____
GAM417  FLJ13456  3' GTGGTAGTTTGGAAATTGC   65945     CATTAG
                              GCA     CTAGATTGCCAT
                              |||     ||||||||||||
                              CGT     GGTTTGATGGTG
                                TAAA__
GAM417  FLJ13614  3' ATTTGGCTGATGGGTAAA    57448      A
                              TTTGC CATTAGCTAGAT
                              ||||| ||||||||||||
                              AAATG GTAGTCGGTTTA
                                 G
GAM417  FLJ14494  3' CTGGCTGGGTGTAAG       90870       A
                              TTTGCAC TTAGCTAG
                              ||||||| ||||||||
                              GAATGTG GGTCGGTC
                                    _
GAM417  FLJ14708  3' CTGGCTGAGTGCAAG       51542       A
                              TTTGCAC TTAGCTAG
                              ||||||| ||||||||
                              GAACGTG AGTCGGTC
                                    _
GAM417  FLJ20758  3' ATGGCAGTTTAGGCTGCA    35641     CATTA _
                              TGCA    GC TAGATTGCCAT
                              ||||    || ||||||||||||
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                                ACGT    CG ATTTGACGGTA
                                  _____ G
GAM417  FLJ22794  5'  TTGGTCAATGTGTAAG     91616         AG
                                TTTGCACATT  CTAG
                                ||||||||||  ||||
                                GAATGTGTAA  GGTT
                                      CT
GAM417  FLJ23511  3'  ATGGTAGTTTCAGTTTTTGTG  49958     TT   _
                                CACA  AGCT AGATTGCCAT
                                ||||  |||| ||||||||||
                                GTGT  TTGA TTTGATGGTA
                                  TT    C
GAM417  FLJ23556  3'  ATGGCAGGGCGAGTTGTGTGTG 45943    TG    T    AGA_
           AG                     TT  CACAT AGCT    TTGCCAT
                                ||  ||||| ||||    |||||||
                                GA  GTGTG TTGA    GACGGTA
                                 GT    _    GCGG
GAM417  FREQ     3'  TGGCTGCTGGTGTGTGG     26591    TG       TAGATT
                                T  CACATTAGC     GCCA
                                |  |||||||||     ||||
                                G  GTGTGGTCG     CGGT
                                 GT        T_____
GAM417  GAJ      3'  ATGGTGGTGAAGGATGTACAAG 49508      C    AG  AG  TG
                                TTTG ACATT  CT  AT  CCAT
                                |||| |||||  ||  ||  ||||
                                GAAC TGTAG  GA  TG  GGTA
                                  A    __  AG  GT
GAM417  GEMIN4   3'  TGGCAATAATGGTGTAAA    31700        ATTAGCTAG
                                TTTGCAC        ATTGCCA
                                |||||||        |||||||
                                AAATGTG        TAACGGT
                                    GTAA_____
GAM417  GMPPB    5'  GTGGTGGTCGAAGATGGTGTGT 95751         G  A_   TG
                                GCACATTA CT  GAT  CCAT
                                |||||||| ||  |||  ||||
                                TGTGTGGT GA  CTG  GGTG
                                     A  AG   GT
GAM417  HIP-55   3'  ATGGTGGTTTGGCAGCAGG    25926       ACATTA      TG
                                TTTGC     GCTAGAT  CCAT
                                |||||     |||||||  ||||
                                GGACG     CGGTTTG  GGTA
                                  A_____       GT
GAM417  HNRPA3   3'  ATGGCGCATGCTAGTGTTTGAA 19254      C       TAGAT
                                TTTG ACATTAGC     TGCCAT
                                |||| ||||||||     ||||||
                                AAGT TGTGATCG     GCGGTA
                                  T       TAC__
GAM417  HNRPA3   3'  GTGGTGGTTATGGATCTGGTGG 19257   TG A     __   _   TG
           TGGA                    C CATTAG  CTA GAT  CCAT
                                | ||||||  ||| |||  ||||
```

```
                                 G GTGGTC  GGT TTG  GGTG
                               GT _     TA   A   GT
GAM417  HSPC189   3'  GTGGGGAGTGTGGTGTGTAAA  95278          G TAGA  G
                               TTTGCACATTA C    TT CCAT
                               |||||||||||  |    || ||||
                               AAATGTGTGGT G    AG GGTG
                                      _ TG__  G
GAM417  HUMAGCGB  5'  ATGGCTACCCAGCTGTGTGTGA 25228    TG    T    AGATT
          G                     TT  CACAT AGCT    GCCAT
                               ||  ||||| ||||    |||||
                               GA  GTGTG TCGA    CGGTA
                                GT    _   CCCAT
GAM417  IMAGE:4907098 3'  TGGAGGCAGGTGTGTAGA    91667         TA   AGATTG
                               TTTGCACAT  GCT     CCA
                               |||||||||  |||     |||
                               AGATGTGTG  CGG     GGT
                                     GA   A_____
GAM417  IRF5     3'  GTGGCGGTGCGGACTGATGTGG 50975     G       _  AG
          AGA                    TTT CACATTAG CT  ATTGCCAT
                               |||  ||||||||  ||  ||||||||
                               AGA GTGTAGTC GG  TGGCGGTG
                                 G       A  CG
GAM417  KCNK13    3'  ATGGTGGTGTAGGGGTGTGGGA 41906    G     AG   G  TG
                               TT CACATT  CTA AT  CCAT
                               || ||||||  ||| ||  ||||
                               AG GTGTGG  GAT TG  GGTA
                                G     G_  G  GT
GAM417  KCNMB2    3'  TGGCAAATTAATGTGT      19541          CTAGA
                               GCACATTAG     TTGCCA
                               |||||||||     ||||||
                               TGTGTAATT     AACGGT
                                     A____
GAM417  KCNS1     3'  GCCTCTTTAGCTGGTATGCAAG 9577        C         TT_
                               TTTGCA ATTAGCTAGA   GC
                               |||||| ||||||||||   ||
                               GAACGT TGGTCGATTT   CG
                                   A         CTC
GAM417  KIAA0205  3'  GTGGTAGTTTACTGTGATGTG  29589        GC_
                               CACATTA   TAGATTGCCAT
                               |||||||   ||||||||||
                               GTGTAGT   ATTTGATGGTG
                                    GTC
GAM417  KIAA0265  3'  TTTAGCTTATGTGTGGA     69889    TG    T
                               TT  CACAT AGCTAGA
                               ||  ||||| |||||||
                               AG  GTGTA TCGATTT
                                GT    T
GAM417  KIAA0417  3'  TTTAGCTGGTGGTAGA      71247       A
                               TTTGC CATTAGCTAGA
                               ||||| ||||||||||
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                              AGATG GTGGTCGATTT
                                _
GAM417  KIAA0630 3' GTGGTGGTTTTATTATATGCAA 89395      CAT  CT   TG
            A                  TTTGCA  TAG  AGAT  CCAT
                               ||||||  |||  ||||  ||||
                               AAACGT  ATT  TTTG  GGTG
                                  AT_  AT   GT
GAM417  KIAA0672 3' GTGGTGATGCTGGTGGTGCAG  29416      _    TAG  TG
                               TTGCAC ATTAGC  AT  CCAT
                               |||||| ||||||  ||  ||||
                               GACGTG TGGTCG  TA  GGTG
                                  G    ___  GT
GAM417  KIAA0753 3' GTGGCAGTTTGTACTGTGC   29000      TTA  T
                               GCACA  GC AGATTGCCAT
                               |||||  || ||||||||||
                               CGTGT  TG TTTGACGGTG
                                  CA_  _
GAM417  KIAA0774 3' ATGGTAAAGTCTGATGTGCAAA 91749          _  AGA
                               TTTGCACATTAG CT  TTGCCAT
                               |||||||||||| ||  |||||||
                               AAACGTGTAGTC GA  AATGGTA
                                     T  ___
GAM417  KIAA0978 3' GTGGTGATTTAGAATGCAG   70482      CATTAG    TG
                               TTGCA    CTAGAT  CCAT
                               |||||    ||||||  ||||
                               GACGT    GATTTA  GGTG
                                  AA____     GT
GAM417  KIAA1075 3' ATGGCAGAGATGGGTGTGTGAG 61715   TG    AG_  AGA
                               TT  CACATT  CT  TTGCCAT
                               ||  ||||||  ||  |||||||
                               GA  GTGTGG  GA  GACGGTA
                                GT    GTA  ___
GAM417  KIAA1117 3' TTGGTGAATGTGTAAA     61122         A
                               TTTGCACATT GCTAG
                               |||||||||| |||||
                               AAATGTGTAA TGGTT
                                     G
GAM417  KIAA1126 3' GTGGCACCCTTGGGGTGTG   71937      AGCT  AT
                               CACATT   AG  TGCCAT
                               ||||||   ||  ||||||
                               GTGTGG   TC  ACGGTG
                                  GGT_  CC
GAM417  KIAA1163 3' TGGCAATTTGGAGTGCAG    78906      ATTAG
                               TTGCAC    CTAGATTGCCA
                               ||||||    ||||||||||
                               GACGTG    GGTTTAACGGT
                                  A____
GAM417  KIAA1431 3' TTCTTTAAATTGGTTAATGTGT 62999    TG        A  CCAT
            GAG                   TT  CACATTAGCTAG TTG
                               ||  |||||||||||| |||
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                                GA  GTGTAATTGGTT AAT
                                 GT         A   TTCTTT
GAM417  KIAA1437  3'  GTGGCAGTTTCCCTTGAGCAAA 60590      A  TT  CT
                                TTTGC CA  AG  AGATTGCCAT
                                ||||| ||  ||  ||||||||||
                                AAACG GT  TC  TTTGACGGTG
                                   A  __  CC
GAM417  KIAA1493  3'  ATGGTGATTTGGAGGGCTGATG 64154         ____   TG
           TG                    CACATTAGCT    AGAT  CCAT
                                ||||||||||    ||||  ||||
                                GTGTAGTCGG    TTTA  GGTA
                                      GAGG    GT
GAM417  KIAA1546  3'  ATGGCAGTCTGCCTTTGTGT   67902      TTA  T
                                GCACA   GC AGATTGCCAT
                                |||||   || ||||||||||
                                TGTGT   CG TCTGACGGTA
                                   TTC  _
GAM417  KIAA1550  3'  TGGAAGCTGCGTGTGTGAA    66570    TG    TA  T  ATTG
                                TT  CACAT  GC AG    CCA
                                ||  |||||  || ||    |||
                                AA  GTGTG  CG TC    GGT
                                 GT    __  _  GAA_
GAM417  KIAA1655  3'  ATGGTACAAGTTGGTGTGTA   66591          AGAT
                                TGCACATTAGCT    TGCCAT
                                ||||||||||||    ||||||
                                ATGTGTGGTTGA    ATGGTA
                                      AC__
GAM417  KIAA1677  3'  TGGCTGCTGATGTATAAA    67072      C       TAGATT
                                TTTG ACATTAGC     GCCA
                                ||||| ||||||||     ||||
                                AAAT TGTAGTCG     CGGT
                                  A       T_____
GAM417  KIAA1863  3'  GTGGCGATGGTGGGGTGTGGGG 64874     G     A_   AG
           A                     TTT CACATT  GCT  ATTGCCAT
                                ||| ||||||  |||  ||||||||
                                AGG GTGTGG  TGG  TAGCGGTG
                                  G     GG   __
GAM417  KIAA1924  3'  GTGGGACGTGGGTAGTGTGTGA 73686    TG      G   GA  G
           A                     TT  CACATTA CTA  TT CCAT
                                ||  ||||||| |||  || ||||
                                AA  GTGTGAT GGT  AG GGTG
                                 GT      G   GC  _
GAM417  KIAA1940  3'  TCTGGCTGTGTGTGAA      79993    TG    T
                                TT  CACAT AGCTAGA
                                ||  ||||| |||||||
                                AA  GTGTG TCGGTCT
                                 GT    _
GAM417  MACF1     5'  GTGGCTCAGTGCAAATGTGCAA 52269          A  TAGATT
           A                     TTTGCACATT GC     GCCAT
                                |||||||||| ||     |||||
```

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                                AAACGTGTAA CG     CGGTG
                                      A  TGACT_
GAM417  MANBAL   5'  ATGGTAGACAGAGCTGATGTG  41978         AGA_
                                CACATTAGCT    TTGCCAT
                                ||||||||||    |||||||
                                GTGTAGTCGA    GATGGTA
                                      GACA
GAM417  MEGF10   3'  ATGGTGGTTTGGTCAGATG    50582      A_     TG
                                CATT  GCTAGAT  CCAT
                                ||||  |||||||  ||||
                                GTAG  TGGTTTG  GGTA
                                  AC      GT
GAM417  MGC20255 5'  GGGCCGGAGGTTAGTGTGCGG  53444           AGATT   AT
                                TTGCACATTAGCT    GCC
                                ||||||||||||     |||
                                GGCGTGTGATTGG    CGG
                                        AGGC_   GT
GAM417  MGC4309  3'  TGGTCTGTGAGTGTGTGAG    44136    TG     A  T  ATT
                                TT  CACATT GC AG   GCCA
                                ||  ||||||  || ||   ||||
                                GA  GTGTGA TG TC   TGGT
                                 GT     G  _  ___
GAM417  MGC9753  5'  GTGGTGGTCTTGCTGCTGCAG  53058      CAT    T    TG
                                TTGCA   TAGC AGAT  CCAT
                                |||||   |||| ||||  ||||
                                GACGT   GTCG TCTG  GGTG
                                   C__    T    GT
GAM417  MKRN2    3'  GTCGTCTGGTTGGTGTTG    72414    _         T
                                CA CATTAGCTAGAT GC
                                ||  ||||||||||||  ||
                                GT GTGGTTGGTCTG TG
                                 T          C
GAM417  MR       5'  TGGCAGGTGATGTGC       48326         G  AGATT
                                GCACATTA CT    GCCA
                                ||||||||  ||    ||||
                                CGTGTAGT GA    CGGT
                                     G  _____
GAM417  MRPL19   3'  AATTTGGTTAGTTGCAGA    28638       C
                                TTTGCA ATTAGCTAGATT
                                ||||||  ||||||||||||
                                AGACGT TGATTGGTTTAA
                                     _
GAM417  NEIL2    3'  GTAACTTTGGTTGATGTTAAG  58910      C         _
                                TTTG ACATTAGCTAGA TTGC
                                ||||  ||||||||||||  ||||
                                GAAT TGTAGTTGGTTT AATG
                                   _          C
GAM417  NMT2     3'  GTGGTGGTTGTTTAAGTGCAGA 16669        A   CTA   TG
                                TTTGCAC TTAG   GAT  CCAT
                                |||||||  ||||   |||  ||||
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                                AGACGTG AATT   TTG  GGTG
                                    _   TG_   GT
GAM417  NS1-BP   3'  GTGGCAGTCTTCAGTTTGCAGA 72547       CATT   __
                                TTTGCA   AGCT  AGATTGCCAT
                                |||||||   ||||  ||||||||||
                                AGACGT   TTGA  TCTGACGGTG
                                    ____   CT
GAM417  NUP107   5'  TTTGGTTGTGTGTGGA     39874    TG    T
                                TT  CACAT AGCTAGA
                                ||  ||||| |||||||
                                AG  GTGTG TTGGTTT
                                 GT    _
GAM417  Nup43    3'  ATGGCAGGGTTTTAGTGTGTGA 44994    TG      CTAGA
           G                     TT  CACATTAG    TTGCCAT
                                ||  ||||||||    |||||||
                                GA  GTGTGATT    GACGGTA
                                 GT      TTGG_
GAM417  OSBPL2   3'  ATGGCCACCACTTAATGTGTGG 29201    TG      CTAGATT
           A                     TT  CACATTAG     GCCAT
                                ||  ||||||||     |||||
                                AG  GTGTAATT     CGGTA
                                 GT      CACCAC_
GAM417  OSBPL2   3'  ATGGCCACCACTTAATGTGTGG 57852    TG      CTAGATT
           A                     TT  CACATTAG     GCCAT
                                ||  ||||||||     |||||
                                AG  GTGTAATT     CGGTA
                                 GT      CACCAC_
GAM417  PLK      3'  TGGGGGTTGCTGTGTAAG    17269       TTA  TA   G
                                TTTGCACA   GC  GATT CCA
                                ||||||||   ||  |||| |||
                                GAATGTGT   CG  TTGG GGT
                                    ___  __    G
GAM417  POF1B    3'  TGGTAGTAGTAGGTGTAAG   46222       ATTA   AG
                                TTTGCAC    GCT  ATTGCCA
                                |||||||    |||  |||||||
                                GAATGTG    TGA  TGATGGT
                                    GA__   __
GAM417  PP1665   3'  GTGGCAATGGAGTGTGTGGA   47920    TG     AGCTAG
                                TT  CACATT     ATTGCCAT
                                ||  ||||||     ||||||||
                                AG  GTGTGA     TAACGGTG
                                 GT     GG____
GAM417  PRDM10   3'  TTTATTGATGTGTAGA      39580           C
                                TTTGCACATTAG TAGA
                                |||||||||||| ||||
                                AGATGTGTAGTT ATTT
                                                _
GAM417  PRO0943  5'  ATGGCTAAATGGCTAATTTGCA 37700       C       GATT
           AA                     TTTGCA ATTAGCTA    GCCAT
                                ||||||  ||||||||    |||||
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                                AAACGT TAATCGGT    CGGTA
                                   T       AAAT
GAM417  PTD012   3'  AATGGCAATCTAGCTAATGTGC 25887
              AAA                  TTTGCACATTAGCTAGATTGCCAT
                                   ||||||||||||||||||||||
                                   AAACGTGTAATCGATCTAACGGTA
                                                 AT
GAM417  RAB14    3'  AGGCTTTGGTTAATTTGTGGA  32867    TG  C        TT   AT
                                   TT  CA ATTAGCTAGA  GCC
                                   ||  || ||||||||||  |||
                                   AG  GT TAATTGGTTT  CGG
                                    GT  T         __   AT
GAM417  RANBP6   3'  GTGGTAAAAGTTATTAAGTGTG 61638        ____     AGA
              CAAA                   GCACAT    TAGCT   TTGCCAT
                                   ||||||    |||||   |||||||
                                   CGTGTG    ATTGA   AATGGTG
                                      AATT    A__
GAM417  RBM14    3'  TCTAGCTGATGGTGAG      20912    TG A
                                   TT  C CATTAGCTAGA
                                   ||  | ||||||||||
                                   GA  G GTAGTCGATCT
                                    GT _
GAM417  RDH-E2   3'  TGGCAGTCTGGCTAAAGGC   57275    ACA
                                   GC   TTAGCTAGATTGCCA
                                   ||   ||||||||||||||
                                   CG   AATCGGTCTGACGGT
                                    GA_
GAM417  RODH-4   5'  GGCAGCTGTGTGTAAG      13537         T    AGATT
                                   TTTGCACAT AGCT    GCC
                                   |||||||| ||||    |||
                                   GAATGTGTG TCGA    CGG
                                             _   _____
GAM417  SEMA4F   3'  GCTTTCTCTGGCTGGAGTGTAG 14942        A       TT__  CAT
                                   TTGCAC TTAGCTAGA    GC
                                   |||||| |||||||||    ||
                                   GATGTG GGTCGGTCT    CG
                                      A        CTTT
GAM417  SFXN5    3'  TGGCAGTGAGATGTCAGA    58041      C    TAG  AG
                                   TTTG ACAT   CT  ATTGCCA
                                   |||| ||||   ||  |||||||
                                   AGAC TGTA   GA  TGACGGT
                                     _   ____ G_
GAM417  ShrmL    5'  ATGGCAGTGCTTACTGTGCAGA 40466         TT_   TAG
                                   TTTGCACA   AGC   ATTGCCAT
                                   ||||||||   |||   ||||||||
                                   AGACGTGT   TCG   TGACGGTA
                                        CAT   ___
GAM417  SLC34A1  3'  TGGGAGGCTGTGTGCAG     11749         T    AGAT G
                                   TTGCACAT AGCT    T CCA
                                   |||||||| ||||    | |||
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                                GACGTGTG TCGG   A GGT
                                   _   ____ G
GAM417  SLK     3'  TGGTTGCTGGTGTGTGTAA   28229       TA    ATT
                                TTGCACAT  GCTAG   GCCA
                                ||||||||  |||||   ||||
                                AATGTGTG  TGGTC   TGGT
                                   __    GT_
GAM417  ST13    3'  GTGTTCTTTTGTTAATGTGTAG 14117          T   TT  CAT
          A                      TTTGCACATTAGC AGA  GC
                                 |||||||||||||| |||  ||
                                 AGATGTGTAATTG TTT  TG
                                       T   CT  TG
GAM417  SYT6    3'  GTGAGCCTTCAGCTGATGTGCA 78773          A  TT  _
          G                      TTGCACATTAGCT GA  GC CAT
                                 |||||||||||||| ||  || |||
                                 GACGTGTAGTCGA CT  CG GTG
                                       _  TC  A
GAM417  TA-KRP  3'  TGGGGGCAAATGTGTAGA    50696        A   AGATTG
                                TTTGCACATT GCT     CCA
                                |||||||||| |||     |||
                                AGATGTGTAA CGG     GGT
                                     A   G_____
GAM417  TIX1    3'  GTGGCAGTGGGGGATGTGGGA  61748    G     AG  AG
                                TT CACATT  CT  ATTGCCAT
                                || ||||||  ||  ||||||||
                                AG GTGTAG  GG  TGACGGTG
                                 G     G_  G_
GAM417  TTY7    5'  ATGTGGTTAGTGTGAGGA    49178    TG        G
                                TT  CACATTAGCTA AT
                                ||  ||||||||||| ||
                                AG  GTGTGATTGGT TA
                                 GA         G
GAM417  UBF-fl  3'  ATGGTAATATGGTGGTGTGCAG 51550          G   G
                                TTGCACATTA CTA ATTGCCAT
                                |||||||||| ||| ||||||||
                                GACGTGTGGT GGT TAATGGTA
                                      _   A
GAM417  VILL    5'  TGGACAGCTGTGTGCAG     68416        T    AGATTG
                                TTGCACAT AGCT     CCA
                                |||||||| ||||     |||
                                GACGTGTG TCGA     GGT
                                      _    CA____
GAM417  ZAK     3'  ATGGCAATTATCAGTGTTG    56120    TTA   A__
                                CA   GCT   GATTGCCAT
                                ||   |||   |||||||||
                                GT   TGA   TTAACGGTA
                                 TG_   CTA
GAM417  LOC115110 3'  GTGGAGGGTGGCTGGTGTGGAA 71722    G         GA  G
                                TT CACATTAGCTA  TT CCAT
                                || ||||||||||  || ||||
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                                AA GTGTGGTCGGT  GA GGTG
                                 G          GG  _
GAM417  LOC118668 5'  TGGTGGCTGATGTGGAG     75484    G        AGATT
                                TT CACATTAGCT     GCCA
                                || ||||||||||     ||||
                                GA GTGTAGTCGG     TGGT
                                 G          _____
GAM417  LOC123628 5'  GGCCACAGCTAATGGTGAA    75619    TG A       AGATT
                                TT  C CATTAGCT     GCC
                                ||  | ||||||||     |||
                                AA  G GTAATCGA     CGG
                                 GT _       CAC__
GAM417  LOC124976 3'  GTGGCTTCAGTGGTGTGTAAG  74383           G  A  TT
                                TTTGCACATTA CT GA  GCCAT
                                |||||||||||| || ||  |||||
                                GAATGTGTGGT GA CT  CGGTG
                                       _ _  T_
GAM417  LOC126917 3'  TGGCAGTCTGGCTGTG      74595     T
                                CAT AGCTAGATTGCCA
                                ||| ||||||||||||
                                GTG TCGGTCTGACGGT
                                 _
GAM417  LOC127703 3'  TTTGGCAGTGTGTGGA      74686     TG     A
                                TT  CACATT GCTAGA
                                ||  |||||| ||||||
                                AG  GTGTGA CGGTTT
                                 GT     _
GAM417  LOC130074 3'  GTGGTGGTTTGAGTGCTGTG   76139      TTA  _   TG
                                CACA   GCT AGAT  CCAT
                                ||||   ||| ||||  ||||
                                GTGT   TGA TTTG  GGTG
                                  CG_   G    GT
GAM417  LOC144266 5'  ATGGTAATTTTGACAGATTGTA 76760       CATTAGCT
              GA                  TTTGCA       AGATTGCCAT
                                ||||||       ||||||||||
                                AGATGT       TTTAATGGTA
                                   TAGACAGT
GAM417  LOC144308 3'  ATGGCGGTTTTTTCTGGTGTG  83042        CT_
                                CACATTAG   AGATTGCCAT
                                ||||||||   ||||||||||
                                GTGTGGTC   TTTGGCGGTA
                                     TTT
GAM417  LOC144776 3'  TGGAGGCTGGTGTGTAAG    76962           AGATTG
                                TTTGCACATTAGCT     CCA
                                ||||||||||||||     |||
                                GAATGTGTGGTCGG     GGT
                                       A_____
GAM417  LOC146520 3'  GTGGTGGTTAGGGAATATGTG  77958      TAG  A_   TG
                                CACAT   CT  GAT  CCAT
                                |||||   ||  |||  ||||
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                                GTGTA  GG  TTG  GGTG
                                   TAA  GA   GT
GAM417  LOC146956 5'  GTGGCAGTTGAAAGAGTGGCGG 78211      A    AGCTA
                                TTGC CATT     GATTGCCAT
                                |||| ||||     |||||||||
                                GGCG GTGA     TTGACGGTG
                                  _    GAAAG
GAM417  LOC147353 3'  ATGGTTATTGTGGTGTAGTGTG 84006          _    _  T
          CAAA                    TTGCACATTA GCTA GAT GCCAT
                                |||||||||| |||| ||| |||||
                                AACGTGTGAT TGGT TTA TGGTA
                                     G   G   T
GAM417  LOC147649 3'  TGGTAAATAGTGTGCA      78418          GCTAGA
                                TGCACATTA     TTGCCA
                                |||||||||     ||||||
                                ACGTGTGAT     AATGGT
                                     A_____
GAM417  LOC148479 3'  GTGCCCTCTTAGTTGGTGTGTG 78878    TG         _ TT  CAT
          AG                      TT  CACATTAGCTA GA  GC
                                ||  ||||||||||| ||  ||
                                GA  GTGTGGTTGAT CT  CG
                                 GT         T  CC  TG
GAM417  LOC148918 5'  ATGGTGGTGACCAGGTGGGCAG 79060      A    AGCTAG  TG
                                TTGC CATT     AT  CCAT
                                |||| ||||     ||  ||||
                                GACG GTGG     TG  GGTA
                                  G   ACCAG_  GT
GAM417  LOC148930 3'  CTGGCTAGGTGTAGA       79095        A
                                TTTGCAC TTAGCTAG
                                ||||||| ||||||||
                                AGATGTG GATCGGTC
                                    _
GAM417  LOC148981 3'  ATGGTGGTTATGGATCTGGTGG 84313   TG A    __  _  TG
          TGG                     C CATTAG  CTA GAT  CCAT
                                 | ||||||  ||| |||  ||||
                                 G GTGGTC  GGT TTG  GGTA
                                GT _     TA   A   GT
GAM417  LOC149711 5'  GTGGTGGTCCCGTGGTGTG    84687        G TA   TG
                                CACATTA C  GAT  CCAT
                                ||||||| |  |||  ||||
                                GTGTGGT G  CTG  GGTG
                                   _ CC   GT
GAM417  LOC149844 5'  TGGTGGGGGTGGTGGTAG     79522      A    G  AGA TG
                                TTGC CATTA CT   T  CCA
                                |||| ||||| ||   |  |||
                                GATG GTGGT GG   G  GGT
                                  _    G  ___ GT
GAM417  LOC150139 5'  GTGGTGGTCTGTCACGTGGTGG 79586   TG A   TAGC    TG
                                T  C CAT    TAGAT  CCAT
                                |  | |||    |||||  ||||
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                                G  G GTG   GTCTG  GGTG
                                 GT _   CACT    GT
GAM417   LOC151126 3'  TTTAGTTGCTGTGTAAA     80134        T
                                TTTGCACA TAGCTAGA
                                |||||||| ||||||||
                                AAATGTGT GTTGATTT
                                     C
GAM417   LOC151457 5'  TGGTGGTGGAGGTGCAGA    80246       ATTAG  AG  TG
                                TTTGCAC    CT  AT  CCA
                                |||||||    ||  ||  |||
                                AGACGTG    GA  TG  GGT
                                     _____  GG  GT
GAM417   LOC151568 5'  TGGAGGGCTGGTGTGGAG    56705    G       AGATTG
                                TT CACATTAGCT     CCA
                                || ||||||||||     |||
                                GA GTGTGGTCGG     GGT
                                  G        GA____
GAM417   LOC151610 3'  TGGTAGTTAAGAGTGCAGA   80291       ATTAG  A
                                TTTGCAC    CT GATTGCCA
                                |||||||    || ||||||||
                                AGACGTG    GA TTGATGGT
                                     A____  A
GAM417   LOC151979 3'  ATGGTGGTGATGTGTGTGTGAG 80421    TG    TA  TAG  TG
                                TT  CACAT  GC   AT  CCAT
                                ||  |||||  ||   ||  ||||
                                GA  GTGTG  TG   TG  GGTA
                                  GT    __  TAG  GT
GAM417   LOC152098 3'  ATGGTATTTAAGTTAGTGTTAA 80460     C       A  T
            A                    TTTG ACATTAGCT GA TGCCAT
                                |||| ||||||||| || ||||||
                                AAAT TGTGATTGA TT ATGGTA
                                  _       A  T
GAM417   LOC152273 3'  TGGCTTGCTGGTGTGCAAG   80539           TAGATT
                                TTTGCACATTAGC     GCCA
                                ||||||||||||      ||||
                                GAACGTGTGGTCG     CGGT
                                        TT____
GAM417   LOC152445 5'  ATGGGGAGCTTGATGTGTGAG  85747    TG     _   AGAT G
                                TT  CACATTA GCT    T CCAT
                                ||  ||||||| |||    | ||||
                                GA  GTGTAGT CGA    G GGTA
                                  GT      T   ____ G
GAM417   LOC152674 5'  ATGGCAATCAAGGTGTGTCAA  85832    _    TAG  A
                                TTG CACAT   CT GATTGCCAT
                                ||| |||||   || |||||||||
                                AAC GTGTG   GA CTAACGGTA
                                  T    ___  A
GAM417   LOC153243 3'  TGGGAAGCTGGTGTCCGAG   80800     C       AGAT G
                                TTTG ACATTAGCT    T CCA
                                |||| |||||||||    | |||
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                                GAGC TGTGGTCGA    A GGT
                                  C        ____ G
GAM417   LOC153577 5' ATGGTGCAGGCTGGTGTGGGG  86052    G        AGAT
                                TT CACATTAGCT    TGCCAT
                                || ||||||||||    ||||||
                                GG GTGTGGTCGG    GTGGTA
                                 G         AC__
GAM417   LOC154141 5' GTGGTGTGGCGATGTGTAGA   86173          A    G  TG
                                TTTGCACATT GCTA AT  C
                                |||||||||| |||| ||  |
                                AGATGTGTAG CGGT TG  G
                                      _    G  GT
GAM417   LOC155061 3' GTGGTGTCCCCTAGTGTGTGA  81268   TG      CTA   T
                                T  CACATTAG   GAT GCCAT
                                |  ||||||||   ||| |||||
                                A  GTGTGATC   CTG TGGTG
                                 GT       CC_  _
GAM417   LOC158381 3' TTTAGTTGAGTGCAGA      71018        A
                                TTTGCAC TTAGCTAGA
                                ||||||| |||||||||
                                AGACGTG AGTTGATTT
                                   _
GAM417   LOC158714 5' GTGGCATTTTTGATGTGTCAA  81990     _      CTA  T
                                TTG CACATTAG   GA TGCCAT
                                ||| ||||||||   || ||||||
                                AAC GTGTAGTT   TT ACGGTG
                                  T       ___  T
GAM417   LOC159176 3' TCACTGTCTAGTTAATTGTAGA 82118       C         TGCCAT
                                TTTGCA ATTAGCTAGAT
                                |||||| ||||||||||
                                AGATGT TAATTGATCTG
                                   _          TCACTA
GAM417   LOC168283 5' GTGAGCTGGCTGATCTGCAAG  82690       C        A TG
                                TTTGCA ATTAGCTAG T  C
                                |||||| |||||||| |  |
                                GAACGT TAGTCGGTC A  G
                                    C        G GT
GAM417   LOC169966 3' TAAAACATTTAGTTAATTTGTG 82556    TG  C         TGCCAT
            GA                    TT  CA ATTAGCTAGAT
                                ||  || ||||||||||
                                AG  GT TAATTGATTTA
                                 GT  T         CAAAATA
GAM417   LOC199870 3' ATGGTGGTCTAGCTAGTTCTTG 88430      C__         TG
            TA                    TGCA   ATTAGCTAGAT  CCAT
                                ||||   |||||||||||  ||||
                                ATGT   TGATCGATCTG  GGTA
                                  TCT         GT
GAM417   LOC200597 3' GTGGCAGCCGCCTGCTGTGCGA 88843         T   CTAGA
            G                     TTTGCACA TAG     TTGCCAT
                                ||||||| |||     |||||||
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                                GAGCGTGT GTC    GACGGTG
                                    C  CGCC_
GAM417  LOC202018 3'  TGGCTGTTGGTGTGGGGA   89144    G       TAGATT
                                TTT CACATTAGC     GCCA
                                ||| |||||||||     ||||
                                AGG GTGTGGTTG     CGGT
                                  G       T_____
GAM417  LOC202934 3'  GTGGTGGTAGACCTGGTGTGTC 90425    _      CTAG  TG
          AA                      TTG CACATTAG    AT  CCAT
                                ||| ||||||||   ||  ||||
                                AAC GTGTGGTC    TG  GGTG
                                  T       CAGA  GT
GAM417  LOC205313 5'  ATGTGGATGGTGTGCGG    90675         G  G
                                TTGCACATTA CTA AT
                                |||||||||| ||| ||
                                GGCGTGTGGT GGT TA
                                      A  G
GAM417  LOC219649 3'  ATGGCGCATGTGCAGTGTGCAG 92951         A  TAGAT
                                TTGCACATT GC    TGCCAT
                                ||||||||| ||    ||||||
                                GACGTGTGA CG    GCGGTA
                                     _ TGTAC
GAM417  LOC219688 5'  GTGGTGGTGGTGGTGGTGCGGA 93054       ATTA  AG  TG
                                TTTGCAC   GCT  AT  CCAT
                                |||||||   |||  ||  ||||
                                AGGCGTG   TGG  TG  GGTG
                                    GTGG  __  GT
GAM417  LOC219754 3'  TGTTTCTTTAGCTAGTGAGTAA 91355      A        TTGCCAT
          A                      TTTGC CATTAGCTAGA
                                ||||| ||||||||||
                                AAATG GTGATCGATTT
                                   A         CTTTGTG
GAM417  LOC220018 5'  GCATTAGCTGGTGTTG      93402    _       AT
                                CA CATTAGCTAG  TGC
                                || ||||||||||  |||
                                GT GTGGTCGATT  ACG
                                 T        __
GAM417  LOC220662 3'  TGGTAGTTTTGTGTGTGT    91184       TA  T
                                GCACAT  GC AGATTGCCA
                                ||||||  || |||||||||
                                TGTGTG  TG TTTGATGGT
                                   __  T
GAM417  LOC220936 3'  ATGCAAGCTGGCTGGAGTGCAG 91408       A      A   CAT
          A                      TTTGCAC TTAGCTAG TTGC
                                ||||||| |||||||| ||||
                                AGACGTG GGTCGGTC AACG
                                    A       G   TA
GAM417  LOC221271 3'  ATGGCGGTGGAGAAGTTAATGG 91847     A      AG___
          TAAA                    TGC CATTAGCT    ATTGCCAT
                                ||| ||||||||    ||||||||
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                                ATG GTAATTGA    TGGCGGTA
                                  _      AGAGG
GAM417  LOC221271 5'  TGGTGGTCTCCTGGCAGA    91882      ACAT  CT   TG
                                TTTGC   TAG  AGAT  CCA
                                |||||   |||  ||||  |||
                                AGACG   GTC  TCTG  GGT
                                   _____  C_   GT
GAM417  LOC221656 3'  TAGCTGGTTGTGTAAA      92232       _
                                TTTGCACA TTAGCTA
                                |||||||| |||||||
                                AAATGTGT GGTCGAT
                                     T
GAM417  LOC221687 3'  ATGGTTTAGGTTTATGTGCAAG 92247        T   AGATT
                                TTTGCACAT AGCT    GCCAT
                                ||||||||| ||||    |||||
                                GAACGTGTA TTGG    TGGTA
                                     T   ATT__
GAM417  LOC221876 5'  GTGGACAAATGGCTGATGGTGG 93923    TG A       GA  _
          A                      TT  C CATTAGCTA  TTG CCAT
                                ||  | |||||||||  ||| ||||
                                AG  G GTAGTCGGT  AAC GGTG
                                 GT _       A_  A
GAM417  LOC253869 3'  ATGGCAAAGGATGAGTGTGTAA 94905         AG_  AGA
          A                      TTTGCACATT   CT   TTGCCAT
                                ||||||||||   ||   |||||||
                                AAATGTGTGA   GG   AACGGTA
                                     GTA  A__
GAM417  LOC254018 3'  ATTTGGTTATTGTGCAAA    96965        T
                                TTTGCACA TAGCTAGAT
                                |||||||| |||||||||
                                AAACGTGT ATTGGTTTA
                                     T
GAM417  LOC254057 3'  TGGCAATGTGATGGCAGA    97003      A   AGCT G
                                TTTGC CATT    A ATTGCCA
                                ||||| ||||    | |||||||
                                AGACG GTAG    T TAACGGT
                                  _   ____ G
GAM417  LOC254302 5'  GTGGCAGTGCTTGGGTGT    96185     ATT   TAG
                                GCAC   AGC   ATTGCCAT
                                ||||   |||   ||||||||
                                TGTG   TCG   TGACGGTG
                                  GGT   ___
GAM417  LOC254387 3'  ATGGTACAGAACTAAATGTGTG 94907    TG    _ CTAGAT
          AA                     TT  CACATT AG     TGCCAT
                                ||  |||||| ||     ||||||
                                AA  GTGTAA TC     ATGGTA
                                 GT     A  AAGAC_
GAM417  LOC254874 5'  GTGGCAGTGCTTGGGTGT    96182     ATT   TAG
                                GCAC   AGC   ATTGCCAT
                                ||||   |||   ||||||||
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                                TGTG   TCG   TGACGGTG
                                  GGT   ___
GAM417   LOC255037 3'  ATGGTGGGAAGTGGTGTGCAGA 96627          G  AGA TG
                                TTTGCACATTA CT   T  CCAT
                                |||||||||| ||   |  ||||
                                AGACGTGTGGT GA   G  GGTA
                                      _  AG_ GT
GAM417   LOC255520 3'  GTGGCAATTTAGCTTTTCAGTA 95864     ACATT
                                TGC    AGCTAGATTGCCAT
                                |||    ||||||||||||||
                                ATG    TCGATTTAACGGTG
                                  ACTTT
GAM417   LOC256158 5'  GTGGACAGAGCCGATGTGTGG  97679   TG    TA   AGA   _
                                T  CACAT  GCT   TTG CCAT
                                |  |||||  |||   ||| ||||
                                G  GTGTA  CGA   GAC GGTG
                                 GT    GC   ___   A
GAM417   LOC256414 3'  ATGGTAGTTTGAAGATGTG    96827       AGC
                                CACATT   TAGATTGCCAT
                                ||||||   ||||||||||
                                GTGTAG   GTTTGATGGTA
                                   AA_
GAM417   LOC257436 3'  ATGTCAATGTTGATGTGTAAA  95680           TAG    C
                                TTTGCACATTAGC   ATTG CAT
                                ||||||||||||   |||| |||
                                AAATGTGTAGTTG   TAAC GTA
                                      ___    T
GAM417   LOC257471 3'  TTTATTGATGTGCAAA      95690           C
                                TTTGCACATTAG TAGA
                                |||||||||||| ||||
                                AAACGTGTAGTT ATTT
                                      _
GAM417   LOC51204  5'  ATGGCGATCCCGGAATGTGCAG 33027         AGCTA
                                TTGCACATT    GATTGCCAT
                                |||||||||    |||||||||
                                GACGTGTAA    CTAGCGGTA
                                     GGCC_
GAM417   LOC51312  5'  CTGGCTGGTTTGCAGA      37714        C
                                TTTGCA ATTAGCTAG
                                |||||| |||||||||
                                AGACGT TGGTCGGTC
                                   T
GAM417   LOC51336  5'  GTGGTGATAAGTAGTGGGTGGA 33581    TG A    G  AG  TG
                                TT  C CATTA CT  AT  CCAT
                                ||  | ||||| ||  ||  ||||
                                AG  G GTGAT GA  TA  GGTG
                                 GT G    _  A_  GT
GAM417   LOC51337  3'  GTGCCCCATCTAGCTGGGTGCA 33590       A        T__  CAT
            G                    TTGCAC TTAGCTAGAT   GC
                                |||||| ||||||||||   ||
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                                GACGTG GGTCGATCTA   CG
                                   _        CCC  TG
GAM417  LOC51611  5' GTGGTAGTTAAGAATTTGTAAA 31986       C   AG  A
                                TTTGCA ATT  CT GATTGCCAT
                                ||||||| |||  || |||||||||
                                AAATGT TAA  GA TTGATGGTG
                                   T   __  A
GAM417  LOC51706  3' GTGGCAGGAACCCCTGGCTGTG 70317      TTA     A_____
           CAAA                    CACA   GCTAG     TTGCCAT
                                ||||   |||||     |||||||
                                GTGT   CGGTC     GACGGTG
                                  ___    CCCAAG
GAM417  LOC57107  3' CTGGTTGGATGTGCAG      39835         _
                                TTGCACATT AGCTAG
                                ||||||||| ||||||
                                GACGTGTAG TTGGTC
                                     G
GAM417  LOC84524  3' ATGGCAGAGGTGATGGCTGGTG 50669    A       GA____
           GGTAAA                   C CATTAGCTA     TTGCCAT
                                | |||||||||      |||||||
                                G GTGGTCGGT     GACGGTA
                                 G        AGTGGA
GAM417  LOC90133  3' TGGGAAGCTGGTGTCTGAG    61609      C        AGAT G
                                TTTG ACATTAGCT    T CCA
                                |||| |||||||||    | |||
                                GAGT TGTGGTCGA    A GGT
                                  C        _____ G
GAM417  LOC90750  3' ATGGTAACTTTTTAATGTG    63914         CT  A
                                CACATTAG  AG TTGCCAT
                                ||||||||  || |||||||
                                GTGTAATT  TC AATGGTA
                                     TT  _
GAM417  LOC90826  5' ATGGCAGTAGAATGTGCAGA   64087          AGCTAG
                                TTTGCACATT     ATTGCCAT
                                ||||||||||     ||||||||
                                AGACGTGTAA     TGACGGTA
                                     GA____
GAM417  LOC90841  5' ATGGCAGTCTGTGGTTTGTAGA 64193       C    GC
                                TTTGCA ATTA  TAGATTGCCAT
                                |||||| ||||  ||||||||||
                                AGATGT TGGT  GTCTGACGGTA
                                   T   __
GAM417  LOC91050  3' GTGGTGGTCTGGTTTTTTTTGT 64749     TT___       TG
           G                     CACA    AGCTAGAT  CCAT
                                ||||    ||||||||  ||||
                                GTGT    TTGGTCTG  GGTG
                                  TTTTT       GT
GAM417  LOC91149  3' GTGGCAGTATGCTTGGTGTGT  65083        _  TAG
                                GCACATTA GC   ATTGCCAT
                                |||||||| ||   ||||||||
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                                TGTGTGGT CG   TGACGGTG
                                     T  TA_
GAM417  LOC91250  5'  TTTAGCTAATGGGTGAA     65331     TG A
                                TT  C CATTAGCTAGA
                                ||  | ||||||||||
                                AA  G GTAATCGATTT
                                 GT G
GAM417  LOC91355  5'  GTGGTTGGGGCTGGTGTGTGG  65720    TG        AGATT
                                T  CACATTAGCT    GCCAT
                                |  ||||||||||    |||||
                                G  GTGTGGTCGG    TGGTG
                                 GT        GGT__
GAM417  LOC92249  5'  GTGGTGGGGGGCCTGGTGTGC  68567          _  AGA TG
                                GCACATTAG CT   T  CCAT
                                ||||||||| ||   |  ||||
                                CGTGTGGTC GG   G  GGTG
                                      C  GG_ GT
GAM417  LOC92876  5'  ATGGTAGTTTCTTTTGCTGTGC 70803         T   CT_
            AGA                    TTTGCACA TAG   AGATTGCCAT
                                ||||||||| |||   ||||||||||
                                AGACGTGT GTT   TTTGATGGTA
                                     C   TTC
GAM418  ENG      5'  CAGCAACTCCAGCCCAGC    3688      AT   TAA
                                GCT  GTT   AGTTGCTG
                                |||  |||   ||||||||
                                CGA  CGA   TCAACGAC
                                  CC   CC_
GAM418  ESR1     3'  CAGTAGACAAAATAGCACT   3701         GTTTAAAG
                                AGTGCTAT      TTGCTG
                                ||||||||      ||||||
                                TCACGATA      GATGAC
                                     AAACA___
GAM418  GABRA3   3'  AGCAACCAGAGCACTG      5867         A  TTTAAA
                                CAGTGCT TG     GTTGCT
                                ||||||| ||     ||||||
                                GTCACGA AC     CAACGA
                                     G _______
GAM418  GPR44    3'  CAGCAACTCTAAGACTACAGCA 16523      AT_    AA_
                                TGCT   GTTT   AGTTGCTG
                                ||||   ||||   ||||||||
                                ACGA   CAGA   TCAACGAC
                                   CAT    ATC
GAM418  HOXD4    3'  GCTCCTTCTCAAACATAGC   27525         A__   TT
                                GCTATGTTT   AAG  GC
                                |||||||||   |||  ||
                                CGATACAAA   TTC  CG
                                      CTC   CT
GAM418  MAT1A    3'  GCAGCAACTTGTCCTAGCAC  90834       TGTTTA
                                GTGCTA     AAGTTGCTGC
                                ||||||     ||||||||||
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                                CACGAT     TTCAACGACG
                                   CCTG__
GAM418  MEIS1     3'  GCAGCTCTAAAACATAGACTG  9995       G       AA_
                                CAGT CTATGTTT   AGTTGC
                                |||| ||||||||   ||||||
                                GTCA GATACAAA   TCGACG
                                  _       ATC
GAM418  SEC22L1   3'  GCATTTTAAAAACAGCACTG   16888        ATG      T
                                CAGTGCT   TTTAAAGT GC
                                |||||||   |||||||| ||
                                GTCACGA   AAATTTTA CG
                                    CAA       _
GAM418  SORCS1    3'  CAGCAACTTTGAGAGCAGTG   53583    G   ATG
                                CA TGCT   TTTAAAGTTGCTG
                                || ||||   ||||||||||||
                                GT ACGA   GAGTTTCAACGAC
                                 G   ____
GAM418  TBX3      5'  CAACAAAACACAGCAGCTG    19994     _   A    AAA
                                CAG TGCT TGTTT   GTTG
                                ||| |||| |||||   ||||
                                GTC ACGA ACAAA   CAAC
                                  G   C    A__
GAM418  TBX3      5'  CAACAAAACACAGCAGCTG    33351     _   A    AAA
                                CAG TGCT TGTTT   GTTG
                                ||| |||| |||||   ||||
                                GTC ACGA ACAAA   CAAC
                                  G   C    A__
GAM418  ARHGEF15  3'  CAGCAACTTGCCCAGGACTG   30257     G  AT  TTA
                                CAGT CT  GT   AAGTTGCTG
                                |||| ||  ||   |||||||||
                                GTCA GA  CG   TTCAACGAC
                                  G  CC  ____
GAM418  BIKE      3'  CAGCAACTCCATTTACAGCAT  34183      A  TTTAA
                                GTGCT TG    AGTTGCTG
                                ||||| ||    ||||||||
                                TACGA AT    TCAACGAC
                                   C  TTACC
GAM418  DKFZP586M1120 3'  GCTTCTTCAAAACATAGCAC   48463          A_   TT
                                GTGCTATGTTT  AAG  GC
                                ||||||||||  |||  ||
                                CACGATACAAA  TTC  CG
                                      AC   TT
GAM418  DKFZp761O132 5'  GCAGCAACCAGCACAGCAC    50198      A   TAAA
                                GTGCT TGTT    GTTGCTGC
                                ||||| ||||    ||||||||
                                CACGA ACGA    CAACGACG
                                   C    C____
GAM418  KIAA0542  3'  AGCAACTACTGCACT      66078      TAT  TTAA
                                AGTGC   GT    AGTTGCT
                                |||||   ||    |||||||
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                                TCACG  CA   TCAACGA
                                  T__ ____
GAM418  KIAA0644  3'  GCTTTTTTCAATCATAGCACT  29062        _ T   TT
                                AGTGCTATG TT AAAG  GC
                                ||||||||| || ||||  ||
                                TCACGATAC AA TTTT  CG
                                     T  C    TT
GAM418  MGC32104  3'  CAGCAACTAAAACAGCAT    58403      AT   AA
                                GTGCT  GTTT  AGTTGCTG
                                |||||  ||||  ||||||||
                                TACGA  CAAA  TCAACGAC
                                  __   A_
GAM418  PDE8A     3'  CAACAACTTTAAATACTG    62633      GCTAT        C
                                CAGT    GTTTAAAGTTG TG
                                ||||    |||||||||||| ||
                                GTCA    TAAATTTCAAC AC
                                  _____         A
GAM418  PRO0478   3'  CAGCAACTTCAAACTCCTGAGC 26186     AT___   A
          A                      TGCT    GTTT AAGTTGCTG
                                ||||    |||| |||||||||
                                ACGA    CAAA TTCAACGAC
                                  GTCCT   C
GAM418  UTS2      5'  GCAGCCCTAAACACAGCAT   41815      A     AA
                                GTGCT TGTTTA  GTTGC
                                ||||| ||||||  |||||
                                TACGA ACAAAT  CGACG
                                  C     CC
GAM418  LOC152282 3'  GCAGCAACTCCAGTAGCA    80553      GTTTAA
                                TGCTAT     AGTTGCTGC
                                ||||||     |||||||||
                                ACGATG     TCAACGACG
                                   ACC___
GAM418  LOC222029 5'  GCAGCAACTCCTGAGACACT   94038     _ ATGTTTAA
                                AGTG CT       AGTTGCTGC
                                |||| ||       |||||||||
                                TCAC GA       TCAACGACG
                                  A  GTCC____
GAM418  LOC222112 3'  GCAGTATTCTAAAATAGCACTG 92805        G   AAGT
                                CAGTGCTAT TTTA    TGCTGC
                                ||||||||| ||||    ||||||
                                GTCACGATA AAAT    ATGACG
                                     _   CTT_
GAM419  BCL11A    3'  TCAAGTGGACAATCAAATG    43168       A_
                                CATTTGAT  TCTACTTGA
                                ||||||||  |||||||||
                                GTAAACTA  AGGTGAACT
                                   AC
GAM419  NCALD     3'  ATATCAATGGTGATG       49369         T
                                TATCACCATT GATAT
                                |||||||||| |||||
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                                GTAGTGGTAA CTATA
                                      _
GAM419  SP3      5'  AGATTCATCAAATGGT      82493          __
                                ACCATTTGAT  ATCT
                                ||||||||||  ||||
                                TGGTAAACTA  TAGA
                                     CT
GAM419  KIAA0460 3'  TCAAGCATGTTAAGTGGTAATA 78891     C          CTA
                                TAT ACCATTTGATAT   CTTGA
                                ||| ||||||||||||   ||||||
                                ATA TGGTGAATTGTA   GAACT
                                  A          C__
GAM419  KIAA1829 3'  AGAGATATCAAACAAAGATA   61944      ACCA        A
                                TATC    TTTGATATCT CT
                                ||||    |||||||||| ||
                                ATAG    AAACTATAGA GA
                                  AAAC         _
GAM419  KIAA1946 3'  TCAAGCAGAGTAAATGGT    82473        ATA   A
                                ACCATTTG   TCT CTTGA
                                ||||||||   ||| |||||
                                TGGTAAAT   AGA GAACT
                                    G__   C
GAM419  SMARCA4   3'  TCACTGGATGTCAAACAGTAAT 11796     C  CA         CT
          A                      TAT AC  TTTGATATCTA  TGA
                                ||| ||  ||||||||||  |||
                                ATA TG  AAACTGTAGGT  ACT
                                  A  AC         C_
GAM419  LOC155411 3'  CAAGTAGATCACATG      86391     T   TA
                                CAT TGA  TCTACTTG
                                ||| |||  ||||||||
                                GTA ACT  AGATGAAC
                                  C  __
GAM419  LOC219731 5'  GGTACACATCAAATGGCGAT   93097     A        ATC
                                ATC CCATTTGAT   TACT
                                ||| |||||||||   ||||
                                TAG GGTAAACTA   ATGG
                                  C        CAC
GAM419  LOC257471 5'  AGATTCATCAAATGGT      95684          __
                                ACCATTTGAT  ATCT
                                ||||||||||  ||||
                                TGGTAAACTA  TAGA
                                     CT
GAM420  ABCB1    5'  CCAGAACATTCCTCCTGGAA  6247      CTGT  CT
                                TTCC    GG  ATGTTCTGG
                                ||||    ||  |||||||||
                                AAGG    CC  TACAAGACC
                                  TCCT  T_
GAM420  AGT      3'  CCAGAACACAGTGCCTGGCA  3454      __   TA__
                                TGT  GGC    TGTTCTGG
                                |||  |||    ||||||||
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                                ACG  CCG    ACAAGACC
                                  GT   TGAC
GAM420  ALDOB    3'  CCAGAATACCCACCCAAGAA  68087     CCT_   CTA
                                TTC   GTGG   TGTTCTGG
                                |||   ||||   ||||||||
                                AAG   CACC   ATAAGACC
                                  AACC   C__
GAM420  ARL4     3'  CCAGAACACAGTTGTGGGAA  19198      T TG   A
                                TTCCC G  GCT TGTTCTGG
                                ||||| |  ||| ||||||||
                                AAGGG T  TGA ACAAGACC
                                   _ GT   C
GAM420  B3GAT1   3'  CCAGAACAAAGGACAGAGAA  53972     C    GG  A
                                TTC CTGT  CT TGTTCTGG
                                ||| ||||  || ||||||||
                                AAG GACA  GA ACAAGACC
                                  A   G_  A
GAM420  B3GAT1   3'  CCAGAACAAAGGACAGAGAA  37827     C    GG  A
                                TTC CTGT  CT TGTTCTGG
                                ||| ||||  || ||||||||
                                AAG GACA  GA ACAAGACC
                                  A   G_  A
GAM420  CD79B    3'  CCAGAAGAGCCACAGG      41207         ATG
                                CCTGTGGCT   TTCTGG
                                |||||||||   ||||||
                                GGACACCGA   AAGACC
                                     G__
GAM420  CD79B    3'  CCAGAAGAGCCACAGG      5271          ATG
                                CCTGTGGCT   TTCTGG
                                |||||||||   ||||||
                                GGACACCGA   AAGACC
                                     G__
GAM420  CDH3     3'  CCAAACGTCAGGCCACAG    8380          __     C
                                CTGTGGCT  ATGTT TGG
                                ||||||||  ||||| |||
                                GACACCGG  TGCAA ACC
                                     AC    _
GAM420  COL5A1   5'  GCCAGAACAGCCGCCGCCACAA 3634    CC     TA____       III
          AGAA                    C  TGTGGC     TGTTCTGG   C
                                |  ||||||     ||||||||  |
                                G  ACACCG     ACAAGACC   G
                                 AA     CCGCCG       III
GAM420  CRIM1    3'  CCAGAACAAAGGCAG       33173      GG  A
                                CTGT  CT TGTTCTGG
                                ||||  || ||||||||
                                GACG  GA ACAAGACC
                                   __ A
GAM420  DIAPH2   3'  CCAAAACAAGTCTAGCAGGGAA 22063         __    A    C
                                TTCCCTGT  GGCT TGTT TGG
                                ||||||||  |||| |||| |||
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                                AAGGGACG  CTGA ACAA ACC
                                    AT   _   A
GAM420  DMD     3'  AGAAAATATAGTCACAGG    14414          __
                                CCTGTGGCTATGT  TCT
                                ||||||||||||  |||
                                GGACACTGATATA  AGA
                                     AA
GAM420  ED1     3'  TTGGAACAATCACAGGGAA   7376         CTA    TG
                                TTCCCTGTGG   TGTTC  G
                                ||||||||||   |||||  |
                                AAGGGACACT   ACAAG  T
                                     A__    GT
GAM420  EXTL3   3'  CCAAAACATGCCGCAGGGAG  7528          T    C
                                TTCCCTGTGGC ATGTT TGG
                                |||||||||||  ||||| |||
                                GAGGGACGCCG TACAA ACC
                                     _    A
GAM420  FCRH3   3'  CCAGAGTGGCCCACAGG     53630       _   GT
                                CCTGTGG CTAT  TCTGG
                                |||||||  ||||  |||||
                                GGACACC GGTG  AGACC
                                    C   __
GAM420  FECH    3'  CGTGGTGCCACAGGGAA     3753          __
                                TTCCCTGTGGC  TATG
                                ||||||||||  ||||
                                AAGGGACACCG  GTGC
                                     TG
GAM420  FGFRL1  3'  CCAGAACATACAAGGA     41619    C   GGCT
                                TCC TGT   ATGTTCTGG
                                ||| |||   |||||||||
                                AGG ACA   TACAAGACC
                                  A  _____
GAM420  GATA4   3'  CCAGAACAACAACTGGGAA   9004       T  GGCTA
                                TTCCC GT    TGTTCTGG
                                ||||| ||    ||||||||
                                AAGGG CA    ACAAGACC
                                   T  ACA__
GAM420  GNRH1   5'  CCATCACCAGCCACAGAGA   5883    C      AT  TC
                                TC CTGTGGCT  GT  TGG
                                || ||||||||  ||  |||
                                AG GACACCGA  CA  ACC
                                  A       C_  CT
GAM420  HAMP    3'  CCAGAACATAGGTCTTGGAA  40991     CTGT  _
                                TTCC   GGC TATGTTCTGG
                                ||||   ||| ||||||||||
                                AAGG   CTG ATACAAGACC
                                   TT__   G
GAM420  IPP     3'  TAGTTTGAGCCACAGAGAA   19729    C      ATGTT
                                TTC CTGTGGCT    CTG
                                ||| ||||||||    |||
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                                AAG GACACCGA    GAT
                                  A       GTTT_
GAM420  ITGB1    3'  CCAGTGTGGCCCAGGGAA    53369       T     GTT
                                TTCCCTG GGCTAT   CTGG
                                ||||||| ||||||   ||||
                                AAGGGAC CCGGTG   GACC
                                    _     T__
GAM420  KCNQ1    3'  CCAGCTGCTGAGCCGCAGAGAA 4021      C       AT  T_
                                TTC CTGTGGCT  GT  CTGG
                                ||| ||||||||  ||  ||||
                                AAG GACGCCGA  CG  GACC
                                  A       GT  TC
GAM420  KDR      3'  CAGAATACCACAAAGAA     9591      CC    CTA
                                TTC  TGTGG   TGTTCTG
                                |||  |||||   |||||||
                                AAG  ACACC   ATAAGAC
                                  AA    ___
GAM420  LEP      3'  CCAGGGGCCCACAGGGAA    4047          _  ATGT
                                TTCCCTGTGG CT    TCTGG
                                |||||||||| ||    |||||
                                AAGGGACACC GG    GGACC
                                      C  _____
GAM420  MKI67    3'  CCAGTGACCAGCCACAGGAGA  10041    _       AT   _
                                TC CCTGTGGCT  GTT CTGG
                                || |||||||||  ||| ||||
                                AG GGACACCGA  CAG GACC
                                 A        C_   T
GAM420  NEFH     3'  CCGGAACAGCCAAAG      40780    G    AT
                                CT TGGCT  GTTCTGG
                                || |||||  |||||||
                                GA ACCGA  CAAGGCC
                                 A    __
GAM420  NXF2     5'  CCAGAACATCACCAAG      35136    G   CT
                                CT TGG  ATGTTCTGG
                                || |||  |||||||||
                                GA ACC  TACAAGACC
                                 _   AC
GAM420  PDE6D    3'  CCAGCATACACACAGGGAA    10489        GC    TT
                                TTCCCTGTG  TATG  CTGG
                                |||||||||  ||||  ||||
                                AAGGGACAC  ATAC  GACC
                                      AC   __
GAM420  PHEMX    5'  CCAGCTGGAAACCACAGGGAG  57359         CTATGTT
                                TTCCCTGTGG      CTGG
                                ||||||||||      ||||
                                GAGGGACACC      GACC
                                      AAAGGTC
GAM420  PHEMX    5'  CCAGCTGGAAACCACAGGGAG  57364         CTATGTT
                                TTCCCTGTGG      CTGG
                                ||||||||||      ||||
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                                GAGGGACACC     GACC
                                     AAAGGTC
GAM420  PODXL    3'  CCAGAATGACACAAAGGA    18230    C_   GCTAT
                                TCC  TGTG    GTTCTGG
                                |||  ||||    |||||||
                                AGG  ACAC    TAAGACC
                                  AA   AG___
GAM420  PRODH    3'  CTGGGACAGCCACTGGAA    32925     CT    AT   TG
                                TTCC  GTGGCT  GTTC  G
                                ||||  ||||||  ||||  |
                                AAGG  CACCGA  CAGG  C
                                  T_     __   GT
GAM420  RANBP2L1 3'  CCAGAATAAAACCACCAGGAA 17313     CT   CTA
                                TTCC  GTGG   TGTTCTGG
                                ||||  ||||   ||||||||
                                AAGG  CACC   ATAAGACC
                                  AC   AAA
GAM420  REGL     3'  CCAGAACATGAATTCAGG    21486     TGGC
                                CCTG   TATGTTCTGG
                                ||||   ||||||||||
                                GGAC   GTACAAGACC
                                  TTAA
GAM420  SLC19A1  5'  CCAGAATGCATCCAGAGGGAA 11755      G  CTA
                                TTCCCT TGG   TGTTCTGG
                                |||||| |||   ||||||||
                                AAGGGA ACC   GTAAGACC
                                   G   TAC
GAM420  ST14     3'  CCAGAACATACACTGTGAA   41765    CCT   GC
                                TTC   GTG  TATGTTCTGG
                                |||   |||  ||||||||||
                                AAG   CAC  ATACAAGACC
                                  TGT   __
GAM420  TBL2     3'  CCAGAACAACCTAGAGAA    24926    C   T  CTA
                                TTC CTG GG   TGTTCTGG
                                ||| ||| ||   ||||||||
                                AAG GAT CC   ACAAGACC
                                  A   _  A__
GAM420  TBL2     3'  CCAGAACAACCTAGAGAA    52182    C   T  CTA
                                TTC CTG GG   TGTTCTGG
                                ||| ||| ||   ||||||||
                                AAG GAT CC   ACAAGACC
                                  A   _  A__
GAM420  TCFL4    3'  CCAGGATAAGACCACAGGGAA 63461         _  A
                                TTCCCTGTGG CT TGTTCTGG
                                |||||||||| || ||||||||
                                AAGGGACACC GA ATAGGACC
                                     A  _
GAM420  TFAP4    3'  CCGGGGCAGCCACAGGGAG   12237          AT
                                TTCCCTGTGGCT  GTTCTGG
                                ||||||||||||  |||||||
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                                GAGGGACACCGA  CGGGGCC
                                          __
GAM420  UBE2L6   3'  CCAGGGGGAGCCACGG     14873        ATG
                                CTGTGGCT   TTCTGG
                                ||||||||   ||||||
                                GGCACCGA   GGGACC
                                    GG_
GAM420  UBQLN3   3'  CAAAACATAGTGGAG      33926     CTGTG      C
                                TTCC    GCTATGTT TG
                                ||||    |||||||| ||
                                GAGG    TGATACAA AC
                                  _____       A
GAM420  UMOD     3'  CCAGTGCTCCAGCCACAG    12548        AT_  T
                                CTGTGGCT   GT CTGG
                                ||||||||   || ||||
                                GACACCGA   CG GACC
                                    CCT  T
GAM420  WBSCR5   3'  CCAGAACAGGGCAGAG     41856    G  G  A
                                CT TG CT TGTTCTGG
                                || || || ||||||||
                                GA AC GG ACAAGACC
                                 G  G  _
GAM420  WBSCR5   3'  CCAGAACAGGGCAGAG     26256    G  G  A
                                CT TG CT TGTTCTGG
                                || || || ||||||||
                                GA AC GG ACAAGACC
                                 G  G  _
GAM420  WBSCR5   3'  CCAGAACAGGGCAGAG     50610    G  G  A
                                CT TG CT TGTTCTGG
                                || || || ||||||||
                                GA AC GG ACAAGACC
                                 G  G  _
GAM420  ZNF134   3'  CAGTTTAAGCCACAGGGAA   12846          A  TT
                                TTCCCTGTGGCT TG  CTG
                                |||||||||||| ||  |||
                                AAGGGACACCGA AT  GAC
                                       _  TT
GAM420  ZNF36    3'  CCTTCGTAGCCACAAGG     93960    C       TTCT
                                CC TGTGGCTATG    GG
                                || ||||||||||    ||
                                GG ACACCGATGC    CC
                                 A        TT__
GAM420  ABCA9    5'  CAGAACATGCAGAGA       54410    C    GGCT
                                TC CTGT    ATGTTCTG
                                || ||||    ||||||||
                                AG GACG    TACAAGAC
                                 A   _____
GAM420  ADAMTSL1 3'  CCTCAAATAGCACAGGGAA   57686        G   GTTCT
                                TTCCCTGTG CTAT     GG
                                ||||||||| ||||     ||
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                                AAGGGACAC GATA    CC
                                    _   AACT_
GAM420  BAIAP1   3'  CCAGAACGGCAGCAGG     16449     G  AT
                                CCTGT GCT  GTTCTGG
                                ||||| |||  |||||||
                                GGACG CGG  CAAGACC
                                  A  __
GAM420  BCKDK    3'  CCAGAACTTGGAGCAGGGAA  59793       GG  T
                                TTCCCTGT  CTA GTTCTGG
                                ||||||||  ||| |||||||
                                AAGGGACG  GGT CAAGACC
                                    A_  T
GAM420  C11orf25 3'  CCAAATTAGGGCCACAG    48639       AT_  C
                                CTGTGGCT   GTT TGG
                                ||||||||   ||| |||
                                GACACCGG   TAA ACC
                                    GAT  _
GAM420  C20orf112 3'  CCAGTGCTGCCACAGGGA   54640        TAT  T
                                TCCCTGTGGC   GT CTGG
                                ||||||||||   || ||||
                                AGGGACACCG   CG GACC
                                     T__  T
GAM420  C6orf26  3'  CCAAAACACAGAGCAGG    47509     GG  A   C
                                CCTGT  CT TGTT TGG
                                |||||  || |||| |||
                                GGACG  GA ACAA ACC
                                  A_  C   A
GAM420  CGGBP1   5'  CTGGCACCACAGGGAA     13362        CTA   CT
                                TTCCCTGTGG   TGTT  G
                                ||||||||||   ||||  |
                                AAGGGACACC   ACGG  C
                                     ____   T_
GAM420  DKFZP566G1424 5'  CCAGTGCTGCCACAGGGA   84779        TAT  T
                                TCCCTGTGGC   GT CTGG
                                ||||||||||   || ||||
                                AGGGACACCG   CG GACC
                                     T__  T
GAM420  DKFZp586I021 5'  CCAGACGTCACCACAGGGA   50088       CT   T
                                TCCCTGTGG  ATGT CTGG
                                |||||||||  |||| ||||
                                AGGGACACC  TGCA GACC
                                    AC   _
GAM420  DKFZP727M111 5'  CCAATCTGGTCACAGGGAA   31407          T  TC
                                TTCCCTGTGGCTA GT  TGG
                                |||||||||||||| ||  |||
                                AAGGGACACTGGT TA  ACC
                                     C  __
GAM420  ELF4     3'  CCGTGGATCAGCCACAGGGA  7431          AT   _
                                TCCCTGTGGCT  GTTC TGG
                                ||||||||||  |||| |||
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                                AGGGACACCGA  TAGG GCC
                                      C_   T
GAM420  ERG-1    3' CCAGGATGCCAAAGG      41842    G   TAT
                                CCT TGGC   GTTCTGG
                                ||| ||||   |||||||
                                GGA ACCG   TAGGACC
                                  A   ___
GAM420  FLJ00058 5' CCAGAAATGCCAGCAGGGAA  78765       _   TATG
                                TTCCCTG TGGC    TTCTGG
                                ||||||| ||||    ||||||
                                AAGGGAC ACCG    AAGACC
                                    G   TA__
GAM420  FLJ12816 3' CCAGAACAGGACGACAGTGAA 41932    C   GGCTA
                                TTC CTGT    TGTTCTGG
                                ||| ||||    ||||||||
                                AAG GACA    ACAAGACC
                                  T   GCAGG
GAM420  FLJ13315 3' CCAGAACATAATACA      46568     GC
                                TGTG  TATGTTCTGG
                                ||||  ||||||||||
                                ACAT  ATACAAGACC
                                  A_
GAM420  FLJ20010 3' CCAGAACGATTGGAACAGG   38716      GG  __
                                CCTGT  CTA  TGTTCTGG
                                |||||  |||  ||||||||
                                GGACA  GGT  GCAAGACC
                                   A_   TA
GAM420  FLJ22369 5' ATGGCGCGACAGGGAA     49918       _ _
                                TTCCCTGT G GCTAT
                                |||||||| | |||||
                                AAGGGACA C CGGTA
                                     G G
GAM420  FLJ23563 3' CCAGAATGCTACAAAAGAA  67593    CC_    TAT
                                TTC   TGTGGC   GTTCTGG
                                |||   ||||||   |||||||
                                AAG   ACATCG   TAAGACC
                                  AAA    ___
GAM420  FLJ32332 3' CACAGCACACAGGGAA     58299        _  A
                                TTCCCTGTG GCT TG
                                ||||||||| ||| ||
                                AAGGGACAC CGA AC
                                     A  C
GAM420  GRIN3A   3' CCAAGTGAAGCAGCCACAGGGA 55968         ATG  ___
                                TCCCTGTGGCT   TTC   TGG
                                ||||||||||   |||   |||
                                AGGGACACCGA   AAG   ACC
                                      CG_   TGA
GAM420  HSPC166  3' CCAGAACACATGGAGGGAA   26366      G  GCTA
                                TTCCCT TG    TGTTCTGG
                                |||||| ||    ||||||||
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                                AAGGGA GT    ACAAGACC
                                   G  AC__
GAM420  HSPC251  3' CCAGGCTAGAGCCACAGAGA  33249    C       A  TT
                                TC CTGTGGCT TG  CTGG
                                || |||||||| ||  ||||
                                AG GACACCGA AT  GACC
                                 A       G  CG
GAM420  IGF2AS   3' CCAGGGTGCAACAGAGAA    33095     C    G  TAT TT
                                TTC CTGT GC   G  CTGG
                                ||| |||| ||   |  ||||
                                AAG GACA CG   T  GACC
                                  A   A  ___ GG
GAM420  ILF3     3' CCAAAACACGCTGGGAA     15722      T   GCTA   C
                                TTCCC GTG    TGTT TGG
                                ||||| |||    |||| |||
                                AAGGG CGC    ACAA ACC
                                   T  ____   A
GAM420  KIAA0040 3' CCAAAGTTTCCAGCAGGGAA  27780       _  CT  GTTC
                                TTCCCTG TGG  AT    TGG
                                ||||||| |||  ||    |||
                                AAGGGAC ACC  TG    ACC
                                    G   TT  AA__
GAM420  KIAA0254 3' CAGACAGTCACAGGGAA     28596          ATGT
                                TTCCCTGTGGCT    TCTG
                                ||||||||||||    ||||
                                AAGGGACACTGA    AGAC
                                      C___
GAM420  KIAA0336 3' CCAGAATAAAACCACCAGGAA 27589     CT   CTA
                                TTCC  GTGG   TGTTCTGG
                                ||||  ||||   ||||||||
                                AAGG  CACC   ATAAGACC
                                  AC    AAA
GAM420  KIAA0494 3' CCAGAACACATTTGGG      28740     T_  GCTA
                                CCC  GTG    TGTTCTGG
                                |||  |||    ||||||||
                                GGG  TAC    ACAAGACC
                                  TT  _____
GAM420  KIAA0537 3' CCAGAACAGCCTACAGGGGA  29244        _   AT
                                TTCCCTGT GGCT  GTTCTGG
                                ||||||| ||||  |||||||
                                AGGGGACA CCGA  CAAGACC
                                     T   __
GAM420  KIAA0774 5' CGGGATGCCACAAGGAA     91752     C     TAT   TG
                                TTCC TGTGGC   GTTC  G
                                |||| ||||||   ||||  |
                                AAGG ACACCG   TAGG  C
                                  A     ____   GT
GAM420  KIAA0828 3' CCATGAAAGCCACAGAGGA   81194     _      ATG  _
                                TCC CTGTGGCT   TTC TGG
                                ||| ||||||||   ||| |||
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                                AGG GACACCGA   AAG ACC
                                  A       ___   T
GAM420  KIAA1118  3'  CCAGAGGCCCACAGGGA     69606         _  ATGT
                                TCCCTGTGG CT    TCTGG
                                ||||||||| ||    |||||
                                AGGGACACC GG    AGACC
                                    C  ____
GAM420  KIAA1742  3'  CAGATCCACAGGGAG       77657          CTATGT
                                TTCCCTGTGG     TCTG
                                ||||||||||     ||||
                                GAGGGACACC     AGAC
                                     T_____
GAM420  KIAA1944  5'  CCAACCTAGCCACAGGGA    75558           T  TC
                                TCCCTGTGGCTA GT  TGG
                                |||||||||||| ||  |||
                                AGGGACACCGAT CA  ACC
                                      C  __
GAM420  KIAA1981  3'  CGGAACAGCACAAGGAA     88342     C    G  AT    TG
                                TTCC TGTG CT  GTTC  G
                                |||| |||| ||  ||||  |
                                AAGG ACAC GA  CAAG  C
                                  A   _ __    GT
GAM420  NXPH3     3'  ACGGAGCCACAGAGAG      65747     C       A
                                TTC CTGTGGCT TGT
                                ||| |||||||| |||
                                GAG GACACCGA GCA
                                  A       G
GAM420  PP5395    3'  TCAGGATAGCACAGGGAA    72110         G  AT
                                TTCCCTGTG CT  GTTCTGG
                                ||||||||| ||  |||||||
                                AAGGGACAC GA  TAGGACT
                                     _  __
GAM420  PRDM7     3'  CCAGAAGGGCCACAGAGAA   53788     C       ATG
                                TTC CTGTGGCT   TTCTGG
                                ||| ||||||||   ||||||
                                AAG GACACCGG   AAGACC
                                  A       G__
GAM420  PRDM9     3'  CCAGAAGGGCCACAGAGAA   39575     C       ATG
                                TTC CTGTGGCT   TTCTGG
                                ||| ||||||||   ||||||
                                AAG GACACCGG   AAGACC
                                  A       G__
GAM420  PXR2b     3'  ATATAGCCCAAGGAA       33337     C  T
                                TTCC TG GGCTATGT
                                |||| || ||||||||
                                AAGG AC CCGATATA
                                  A  _
GAM420  RAB33B    3'  CCAGCTTAGCCACAAAGAA   48490     CC       TGTT
                                TTC  TGTGGCTA    CTGG
                                |||  ||||||||    ||||
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                                AAG  ACACCGAT   GACC
                                  AA       TC__
GAM420  SH120    3'  CCAGAACATGAGAGGGAG    32920      GTGGC
                                TTCCCT    TATGTTCTGG
                                ||||||    ||||||||||
                                GAGGGA    GTACAAGACC
                                   GA___
GAM420  SH120    3'  CCAGAACATGAGAGGGAG    94606      GTGGC
                                TTCCCT    TATGTTCTGG
                                ||||||    ||||||||||
                                GAGGGA    GTACAAGACC
                                   GA___
GAM420  SLC2A12  3'  CCAGAACACACAGTGTGGA   59078    ___    GCTA
                                TCC   CTGTG   TGTTCTGG
                                |||   |||||   ||||||||
                                AGG   GACAC   ACAAGACC
                                  TGT    _____
GAM420  SP329    3'  CCAGAGTGCTCCACAGGGA   47924       CTA GT
                                TCCCTGTGG   T  TCTGG
                                |||||||||   |  |||||
                                AGGGACACC   G  AGACC
                                     TC_ TG
GAM420  SSH2     3'  TCAGTAAGCCCACAGGGAA   62213        _  ATGTT
                                TTCCCTGTGG CT    CTGG
                                |||||||||| ||    ||||
                                AAGGGACACC GA    GACT
                                     C  AT___
GAM420  SYTL4    5'  CCAGTCAGCCACAGGGAA    54939         ATGTT
                                TTCCCTGTGGCT    CTGG
                                ||||||||||||    ||||
                                AAGGGACACCGA    GACC
                                      CT___
GAM420  TNRC4     3'  CCAGTCAGCCACAGAGA     23221    C      ATGTT
                                TC CTGTGGCT    CTGG
                                || ||||||||    ||||
                                AG GACACCGA    GACC
                                 A       CT___
GAM420  UBE3B    3'  CCAGACTGTCAGCACAGGGAA  76919        G  _  GT
                                TTCCCTGTG CT AT  TCTGG
                                ||||||||| || ||  |||||
                                AAGGGACAC GA TG  AGACC
                                     _  C  TC
GAM420  VPS4A    3'  CCTTGCAGCCACAGAGA     25102    C      AT  TCT
                                TC CTGTGGCT  GT   GG
                                || ||||||||  ||   ||
                                AG GACACCGA  CG   CC
                                 A       __  TT_
GAM420  XYLT1    5'  CCAACAGCAGCCACGGGAA   77847      T     A_   TC
                                TTCCC GTGGCT  TGT  TGG
                                ||||| ||||||  |||  |||
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                                AAGGG CACCGA  ACA  ACC
                                  _     CG  __
GAM420  ZFP100    3'  CCAGAAAGCCAAAAAGAA    70050     CCTG    ATG
                                TTC    TGGCT   TTCTGG
                                |||    |||||  ||||||
                                AAG    ACCGA   AAGACC
                                  AAAA    ____
GAM420  ZNF213    5'  CAGCTACCACAGGGGA      65091          C  TGTT
                                TTCCCTGTGG TA    CTG
                                |||||||||| ||    |||
                                AGGGGACACC AT    GAC
                                      _  C___
GAM420  LOC112609 3'  CCAGTGTGGCACAGGGAA    72837         G    GTT
                                TTCCCTGTG CTAT   CTGG
                                ||||||||| ||||   ||||
                                AAGGGACAC GGTG   GACC
                                     _   T__
GAM420  LOC115073 5'  CCAGGCGTCAAACCACAGGGA  73204         CT__    T
                                TCCCTGTGG    ATGT CTGG
                                |||||||||    |||| ||||
                                AGGGACACC    TGCG GACC
                                     AAAC   _
GAM420  LOC122962 5'  CCAGACAGTGGCCACTGAGAA  75587     CCT      GT
                                TTC   GTGGCTAT  TCTGG
                                |||   ||||||||  |||||
                                AAG   CACCGGTG  AGACC
                                  AGT       AC
GAM420  LOC124044 3'  CCAGAACACTCAGAGGGA    76025      G   CTA
                                TCCCT TGG   TGTTCTGG
                                ||||| |||   ||||||||
                                AGGGA ACT   ACAAGACC
                                   G   C__
GAM420  LOC143308 5'  CCAAATTTGGCCACAG      82936         T   C
                                CTGTGGCTA GTT TGG
                                ||||||||| ||| |||
                                GACACCGGT TAA ACC
                                     T   _
GAM420  LOC145314 3'  CCAGAACACATCACCTGAG   77086     CCT    CTA
                                TTC   GTGG   TGTTCTGG
                                |||   ||||   ||||||||
                                GAG   CACT   ACAAGACC
                                  TC_    AC_
GAM420  LOC146420 3'  CCAGAACCAGTTACAG      83667         AT
                                CTGTGGCT  GTTCTGG
                                ||||||||  |||||||
                                GACATTGA  CAAGACC
                                     C_
GAM420  LOC146445 3'  CCAGAGCCACCACAGGGA    83678         CTAT
                                TCCCTGTGG    GTTCTGG
                                |||||||||    |||||||
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                                AGGGACACC    CGAGACC
                                     AC__
GAM420   LOC147178 3'  CCAGCCAGCCACGGAGAA    61323     C       ATGTT
                                TTC CTGTGGCT     CTGG
                                ||| ||||||||     ||||
                                AAG GGCACCGA     GACC
                                  A       CC___
GAM420   LOC148529 5'  CACAGCCACAGGAGAA      84166     _       A
                                TTC CCTGTGGCT TG
                                ||| ||||||||| ||
                                AAG GGACACCGA AC
                                  A       C
GAM420   LOC148930 5'  CCAGGGGCAGACCACGGGGAA  79093          CTA    _
                                TTCCCTGTGG   TGTTC TGG
                                ||||||||||   ||||| |||
                                AAGGGGCACC   ACGGG ACC
                                     AG_    G
GAM420   LOC149950 5'  CCAGAACATGATCTCAGG     79551      T GC
                                CCTG G  TATGTTCTGG
                                |||| |  ||||||||||
                                GGAC C  GTACAAGACC
                                  T TA
GAM420   LOC150378 5'  CCAGAAACAAGCCACGGGAA   79742       T     ATG
                                TTCCC GTGGCT   TTCTGG
                                ||||| ||||||   ||||||
                                AAGGG CACCGA   AAGACC
                                   _     ACA
GAM420   LOC150951 5'  CCAGGGCCACACAGGGAA    85167         GCTAT
                                TTCCCTGTG    GTTCTGG
                                |||||||||    |||||||
                                AAGGGACAC    CGGGACC
                                     AC___
GAM420   LOC151429 3'  CCAGGAGACCACAGGGA     85347         _ ATGT
                                TCCCTGTGG CT    TCTGG
                                ||||||||| ||    |||||
                                AGGGACACC GA    GGACC
                                     A _____
GAM420   LOC158434 3'  CCAGAATAAACCACTGGGAA   86819       T   CTA
                                TTCCC GTGG   TGTTCTGG
                                ||||| ||||   ||||||||
                                AAGGG CACC   ATAAGACC
                                   T    AA_
GAM420   LOC170106 5'  CCAAGGCAGTCAGCCACAGG   82571         A__   TC
                                CCTGTGGCT   TGT  TGG
                                |||||||||   |||  |||
                                GGACACCGA   ACG  ACC
                                     CTG   GA
GAM420   LOC196446 3'  CGGAAAGCCACAGAGAA     87708     C       ATG   TG
                                TTC CTGTGGCT   TTC  G
                                ||| ||||||||   |||  |
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                                AAG GACACCGA   AAG  C
                                  A       ___   GT
GAM420   LOC197136 3'  CCAGAACACTCAGAGGGA    89728      G   CTA
                                TCCCT TGG   TGTTCTGG
                                ||||| |||   ||||||||
                                AGGGA ACT   ACAAGACC
                                   G   C__
GAM420   LOC197342 3'  CCAGGAGAAGCCACAGGGGA   87993          ATG
                                TTCCCTGTGGCT   TTCTGG
                                ||||||||||||   ||||||
                                AGGGGACACCGA   AGGACC
                                       AG_
GAM420   LOC200734 3'  CCATCCGCAGCCACAGGGGA   88860          A  TTC
                                TTCCCTGTGGCT TG   TGG
                                |||||||||||| ||   |||
                                AGGGGACACCGA GC   ACC
                                       C  CT_
GAM420   LOC201102 3'  CCTGACCAGCCACAGGAGA    88090    _       AT   CT
                                TC CCTGTGGCT  GTT  GG
                                || |||||||||  |||  ||
                                AG GGACACCGA  CAG  CC
                                 A        C_   T_
GAM420   LOC201283 3'  CCAGAACACAGTCGTGAGGA   60413     CT     A
                                TCC  GTGGCT TGTTCTGG
                                |||  |||||| ||||||||
                                AGG  TGCTGA ACAAGACC
                                  AG     C
GAM420   LOC202915 3'  CCACACGCCAGCCACAGGGGA  90388          A_   TC
                                TTCCCTGTGGCT  TGT  TGG
                                ||||||||||||  |||  |||
                                AGGGGACACCGA  GCA  ACC
                                       CC   C_
GAM420   LOC204965 5'  CAGAGTGCACAGAGAA      90647     C     G TATG
                                TTC CTGTG C    TTCTG
                                ||| ||||| |    |||||
                                AAG GACAC G    GAGAC
                                  A    _ T____
GAM420   LOC205418 3'  CACAGCCAGCAGGGAA      90681        _    A
                                TTCCCTG TGGCT TG
                                ||||||| ||||| ||
                                AAGGGAC ACCGA AC
                                    G    C
GAM420   LOC220692 3'  CCAGAATAAAACCACCAGGAA  91220      CT    CTA
                                TTCC  GTGG   TGTTCTGG
                                ||||  ||||   ||||||||
                                AAGG  CACC   ATAAGACC
                                  AC    AAA
GAM420   LOC222631 5'  CCAGAACACAGCTGGAA     92838      CTGT    A
                                TTCC    GGCT TGTTCTGG
                                ||||    |||| ||||||||
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                                AAGG   TCGA ACAAGACC
                                  ____   C
GAM420  LOC253039 3'  CCAAATACATCTACAGGGAA  96153        CT   TC_
                                TTCCCTGTGG  ATGT   TGG
                                ||||||||||  ||||   |||
                                AAGGGACATC  TACA   ACC
                                     __    TAA
GAM420  LOC253841 5'  CCAGAATGTAGCCACAG    96342
                                CTGTGGCTATGTTCTGG
                                |||||||||||||||||
                                GACACCGATGTAAGACC

GAM420  LOC254028 3'  CCAGAACAGAAGCACCAAGAA 96539    CC  TG   A_
                                TTC  TG  GCT  TGTTCTGG
                                |||  ||  |||  ||||||||
                                AAG  AC  CGA  ACAAGACC
                                  A_  CA   AG
GAM420  LOC257449 3'  CAGATCCACAGGGAG      62718        CTATGT
                                TTCCCTGTGG     TCTG
                                ||||||||||     ||||
                                GAGGGACACC     AGAC
                                     T_____
GAM420  LOC89231  3'  GGACAGCACAGGGAA      92733        G  AT
                                TTCCCTGTG CT  GTTC
                                |||||||| ||  ||||
                                AAGGGACAC GA  CAGG
                                      _  __
GAM420  LOC90550  3'  CCAGAACACAAATCAGAGGGA  73090      G   CTA_
                                TCCCT TGG    TGTTCTGG
                                ||||| |||    ||||||||
                                AGGGA ACT    ACAAGACC
                                   G   AAAC
GAM420  LOC91373  3'  CCAGCAAGGCCACAG      65834        A  TT
                                CTGTGGCT TG  CTGG
                                |||||||| ||  ||||
                                GACACCGG AC  GACC
                                     A  __
GAM420  LOC91445  3'  CCAGAACCTGCCACAGG     60547        TAT
                                CCTGTGGC   GTTCTGG
                                ||||||||   |||||||
                                GGACACCG   CAAGACC
                                     TC_
GAM421  SLC17A4   3'  CAACAGTTCTTCATGTAGC   18525      CAGT
                                GCTGC   TGAAGAACTGTTG
                                |||||   |||||||||||||
                                CGATG   ACTTCTTGACAAC
                                   T____
GAM421  CITED1    5'  CAACAGCTCCAGCTGGCAGC  14729         AA  A
                                GCTGCCAGTTG  GA CTGTTG
                                ||||||||||  || ||||||
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                                CGACGGTCGAC  CT GACAAC
                                      __ C
GAM421  FLJ10900  5'  CAACAGTTCTTGCTGAAGCAGT 65590       __   TG
           T                   AGCTGC  CAGT  AAGAACTGTTG
                               ||||||  ||||  ||||||||||
                               TTGACG  GTCG  TTCTTGACAAC
                                  AA   __
GAM421  HS6ST    3'  CAACAGTTCCTTTGCCAGCAGC 62025      CA  T  A
                               GCTGC  GT GA GAACTGTTG
                               |||||  || || |||||||||
                               CGACG  CG TT CTTGACAAC
                                  AC  T  C
GAM421  MGC4638  3'  CAACAGTTCTTCAAGTG    48939    G
                               CA TTGAAGAACTGTTG
                               || ||||||||||||||
                               GT AACTTCTTGACAAC
                                G
GAM421  ZNF262   3'  TTCCCCAATGGCAGCTT    17492        G   AA
                               AAGCTGCCA TTG  GAA
                               ||||||||| |||  |||
                               TTCGACGGT AAC  CTT
                                     _  CC
GAM421  LOC115051 3'  CAACAGTTCCTTTGCCAGCAGC 60036      CA  T  A
                               GCTGC  GT GA GAACTGTTG
                               |||||  || || |||||||||
                               CGACG  CG TT CTTGACAAC
                                  AC  T  C
GAM421  LOC143153 3'  CAGCCTCAAGCTGGCAGC    76463        GA  AA
                               GCTGCCAGTT  AG  CTG
                               ||||||||||  ||  |||
                               CGACGGTCGA  TC  GAC
                                     AC  C_
GAM421  LOC168512 5'  CAACAGCCTCTCTGGCAGCTT  82714         TTGA  A_
                               AAGCTGCCAG   AGA  CTGTTG
                               ||||||||||   |||  ||||||
                               TTCGACGGTC   TCT  GACAAC
                                     ____  CC
GAM421  LOC199923 3'  AACAGTTCCAGACCAGC    88494     CCA  GAA
                               GCTG  GTT  GAACTGTT
                               ||||  |||  ||||||||
                               CGAC  CAG  CTTGACAA
                                  ___  AC_
GAM421  LOC199926 3'  TAGTCCTTCAACTCACAGCTT  89880      CC      A
                               AAGCTG  AGTTGAAG ACTG
                               ||||||  |||||||| ||||
                               TTCGAC  TCAACTTC TGAT
                                  AC      C
GAM421  LOC202316 3'  TAGTCCTTCAACTCACAGCTT  90340      CC      A
                               AAGCTG  AGTTGAAG ACTG
                               ||||||  |||||||| ||||
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                                TTCGAC  TCAACTTC TGAT
                                   AC       C
GAM421  LOC221479 3'  CAACAACTACAGCAGCAGC   92222      CA   A  AAC
                                GCTGC  GTTG AG   TGTTG
                                |||||  |||| ||   |||||
                                CGACG  CGAC TC   ACAAC
                                  A_    A  A__
GAM422  DDEF1    3'  GAGCTTTAGCAGCCTC      59564    A   AGATAC      A
                                GA GCT     CTAAAGCT C
                                || |||     |||||||| |
                                CT CGA     GATTTCGA G
                                 C   C_____       C
GAM422  DDX3     3'  GAGCCTTAGGTATTTG      43759          A   A
                                TAGATACCTAA GCT C
                                |||||||||| ||| |
                                GTTTATGGATT CGA G
                                      C   C
GAM422  GRAF     3'  GGTAACTCCCTCCCTAGCTTC  30573        ATACCTAA  C
                                GAAGCTAG       AG TACC
                                ||||||||       || ||||
                                CTTCGATC       TC ATGG
                                     CCTCCC__  A
GAM422  MAT1A    3'  AGCTTTAGAATCCCAGC     90825     A_   AC
                                GCT  GAT  CTAAAGCT
                                |||  |||  ||||||||
                                CGA  CTA  GATTTCGA
                                  CC   A_
GAM422  MYLK     3'  AGCTTCAGACATTTGGTT    97018        AC  A
                                AGCTAGAT  CT AAGCT
                                ||||||||  || |||||
                                TTGGTTTA  GA TTCGA
                                     CA  C
GAM422  RGL      3'  GTAGCTAAAACTTAGCTTCA   30736         ATACCTAA
                                TGAAGCTAG       AGCTAC
                                |||||||||       ||||||
                                ACTTCGATT       TCGATG
                                     CAAAA___
GAM422  ZFP93    3'  GTAGCCTTAATAACGTTAGTTT 14887         ATACC_   A
             CA                   TGAAGCTAG     TAA GCTAC
                                |||||||||     ||| |||||
                                ACTTTGATT     ATT CGATG
                                     GCAATA   C
GAM422  C3orf4   3'  AGCATTGACACATAGCTTCA   39118        GATACC   A
                                TGAAGCTA     TAA GCT
                                ||||||||     ||| |||
                                ACTTCGAT     GTT CGA
                                     ACACA_   A
GAM422  D2S448   3'  GGCAGGAGTCCTAGCTTCA    73527         _  A   AAA
                                TGAAGCTAG AT CCT   GCT
                                ||||||||| || |||   |||
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                                ACTTCGATC TG GGA   CGG
                                     C  A  ___
GAM422  FLJ12604  3'  AGCTTTAGTATTGACTTCA   64436      CTA    C
                                TGAAG   GATAC TAAAGCT
                                |||||   ||||| |||||||
                                ACTTC   TTATG ATTTCGA
                                   AG_    _
GAM422  FLJ14280  5'  GGTAGCTCCTGGCCAGCTCA   45999     A   AGATA  TAA
                                TGA GCT    CC   AGCTACC
                                ||| |||    ||   |||||||
                                ACT CGA    GG   TCGATGG
                                  _  CC___  TCC
GAM422  H2AFJ    3'  GTTGTCAAGTTTCTAGCTTCA  36842         T  CTAA_
                                TGAAGCTAGA AC     AGC
                                |||||||||| ||     |||
                                ACTTCGATCT TG     TTG
                                      T  AACTG
GAM422  KIAA0441  3'  TAGCTTTGTTAATCTAGCCTC  28960    A      ACC
                                GA GCTAGAT   TAAAGCTA
                                || |||||||   ||||||||
                                CT CGATCTA   GTTTCGAT
                                 C      ATT
GAM422  KIAA1128  3'  TAGCTTTATGTGCAGCTTGCA  68483    _    AGA   C
                                TG AAGCT   TAC TAAAGCTA
                                || |||||   ||| ||||||||
                                AC TTCGA   GTG ATTTCGAT
                                 G    C__   T
GAM422  KIAA1750  3'  TAGCCCCAGGAGTGGGCTTTA  68254       AG  A   AAA
                                TGAAGCT  AT CCT   GCTA
                                |||||||  || |||   ||||
                                ATTTCGG  TG GGA   CGAT
                                    G_  A   CCC
GAM422  KPNA5    3'  GGTAGCTTCAGGTAACT     9629     A    A
                                AG TACCT AAGCTACC
                                || ||||| ||||||||
                                TC ATGGA TTCGATGG
                                 A    C
GAM422  MAGEH1    5'  GGTAGCTTCAGCGGCAGCAGCT 25924       AGATAC_  A
           TC                    GAAGCT      CT AAGCTACC
                                ||||||      || ||||||||
                                CTTCGA      GA TTCGATGG
                                   CGACGGC  C
GAM422  MGC12921  3'  AGCCCTATTTAGCTTC      63774          CCTAAA
                                GAAGCTAGATA     GCT
                                ||||||||||     |||
                                CTTCGATTTAT     CGA
                                      CC_____
GAM422  MGC30052  3'  AGCTTTAGAATAGCTTC     58532        GATAC
                                GAAGCTA    CTAAAGCT
                                |||||||    ||||||||
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                                CTTCGAT    GATTTCGA
                                   AA___
GAM422  RNF34    3'  AGCAAGGGCTGCATCTAGCTTC 47094         A___  AAA
                                GAAGCTAGAT   CCT  GCT
                                ||||||||||   |||  |||
                                CTTCGATCTA   GGG  CGA
                                     CGTC  AA_
GAM422  TNFRSF19L 3'  GTAGCTTTTATCCCAGC    51779    A_   CCT
                                GCT  GATA  AAAGCTAC
                                |||  ||||  ||||||||
                                CGA  CTAT  TTTCGATG
                                  CC   ___
GAM422  LOC121536 3'  AGCAAATCACATTTAGCTTCA  74082          ACCTAAA
                                TGAAGCTAGAT     GCT
                                ||||||||||      |||
                                ACTTCGATTTA     CGA
                                      CACTAAA
GAM422  LOC255452 3'  TAGGTACCTACCTTCA     97544      C  A
                                TGAAG TAG TACCTA
                                ||||| ||| ||||||
                                ACTTC ATC ATGGAT
                                   C  C
GAM422  LOC257396 3'  GGCAGCTTTAGGCTTAACTT  97139    C  ATA      A
                                AAG TAG  CCTAAAGCT CC
                                ||| |||  ||||||||| ||
                                TTC ATT  GGATTTCGA GG
                                  A  C__       C
GAM422  LOC92710  3'  GTACAAGGCATCTAGCTT    70359        A  AAAGC
                                AAGCTAGAT CCT    TAC
                                ||||||||| |||    |||
                                TTCGATCTA GGA    ATG
                                     C  AC___
GAM423  ADAR     3'  TTCAGGCATACTTTTCCA    6629        C  GGA
                                TGGAGAAG ATG  CCTGAA
                                |||||||| |||  ||||||
                                ACCTTTTC TAC  GGACTT
                                     A  ___
GAM423  ADAR     3'  TTCAGGCATACTTTTCCA    31754       C  GGA
                                TGGAGAAG ATG  CCTGAA
                                |||||||| |||  ||||||
                                ACCTTTTC TAC  GGACTT
                                     A  ___
GAM423  ADAR     3'  TTCAGGCATACTTTTCCA    31764       C  GGA
                                TGGAGAAG ATG  CCTGAA
                                |||||||| |||  ||||||
                                ACCTTTTC TAC  GGACTT
                                     A  ___
GAM423  ARL2     3'  AGTCCAGGTCCCTCAACCTTC  8022      CAT__      A
                                GAAG    GGGACCTG ACT
                                ||||    |||||||| |||
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                                CTTC    CCCTGGAC TGA
                                  CAACT       C
GAM423  ATSV    3'  GGGCCCCAGGCTTCTCCA   15058        A   A
                                TGGAGAAGC TGGG CCT
                                ||||||||| |||| |||
                                ACCTCTTCG ACCC GGG
                                     G   C
GAM423  BCL10   5'  TTCATCCACACTTCTC     14065       CA   ACC
                                GAGAAG  TGGG  TGAA
                                ||||||  ||||  ||||
                                CTCTTC  ACCT  ACTT
                                   AC   ___
GAM423  CELL    3'  GTTCCATGCCCTCCA      8414       AA
                                TGGAG  GCATGGGAC
                                |||||  |||||||||
                                ACCTC  CGTACCTTG
                                   C_
GAM423  CELSR1  3'  GTCCGTGTCCCATGCTCCCTC  26486    A_       C  A
                                GAG  AGCATGGGAC TG AC
                                |||  |||||||||| || ||
                                CTC  TCGTACCCTG GC TG
                                  CC        T  C
GAM423  CHD2    5'  CAGGTCGTTGTTTTTTCCA   7029         _  TGG
                                TGGAGAAG CA   GACCTG
                                |||||||| ||   ||||||
                                ACCTTTTT GT   CTGGAC
                                     T  TG_
GAM423  FN1     3'  TCAACTCACAGCTTCTCCA   8948         A  G  CC
                                TGGAGAAGC TG GA  TGA
                                ||||||||| || ||  |||
                                ACCTCTTCG AC CT  ACT
                                     _  A  CA
GAM423  FUT1    3'  AGTTCAGGTTGCCTCTC    3784      A   TGGG
                                GAGA GCA    ACCTGAACT
                                |||| |||    |||||||||
                                CTCT CGT    TGGACTTGA
                                  C   ____
GAM423  GNAI2   3'  GGGCCCCTGCTTCTCCA    67548         T   A
                                TGGAGAAGCA GGG CCT
                                |||||||||| ||| |||
                                ACCTCTTCGT CCC GGG
                                     C   _
GAM423  HSD3B1  3'  TCAGGTCCTGCTGCCTCC   5990      A_   TG
                                GGAG  AGCA  GGACCTGA
                                ||||  ||||  ||||||||
                                CCTC  TCGT  CCTGGACT
                                  CG    __
GAM423  ITK     3'  AGTTCAGGTCCCATGCTT    18672
                                AAGCATGGGACCTGAACT
                                ||||||||||||||||||
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                                TTCGTACCCTGGACTTGA

GAM423  MEF2D   3'  TCAAGTCCCTCTTCCTCC   96917     _  CAT   C
                                GGAG AAG  GGGAC TGA
                                |||| |||  ||||| |||
                                CCTC TTC  CCCTG ACT
                                  C  T__   A
GAM423  PCDH9   5'  CCCAGTTGTCATTTCTCCA  82795      ___  __
                                TGGAGAA  GCA  TGGG
                                |||||||  |||  ||||
                                ACCTCTT  TGT  ACCC
                                    TAC  TG
GAM423  PLS1    3'  CAGAAATCTACTTTCTCCA   10658      CA   AC_
                                TGGAGAAG  TGGG  CTG
                                ||||||||  ||||  |||
                                ACCTCTTT  ATCT  GAC
                                    C_   AAA
GAM423  POLA    3'  TCCAAATGCTTCTCCA     33739        G_
                                TGGAGAAGCAT  GGA
                                ||||||||||  |||
                                ACCTCTTCGTA  CCT
                                      AA
GAM423  SMARCC1  3'  CGTGTCCCGTGCCTCCCCA   11797    A  A      C
                                TGG GA GCATGGGAC TG
                                ||| || |||||||| ||
                                ACC CT CGTGCCCTG GC
                                  C  C       T
GAM423  TRIM9   3'  AGTTCACACACATACTTTCTCC 53755      _ C  GGACC
          A                      TGGAGAA G ATG    TGAACT
                                |||||||  | |||    ||||||
                                ACCTCTT C TAC    ACTTGA
                                    T A  ACAC_
GAM423  TRPM7   3'  CAGAACTTACAAACTTCTCCA  62127      CA__   AC
                                TGGAGAAG   TGGG  CTG
                                ||||||||   ||||  |||
                                ACCTCTTC   ATTC  GAC
                                    AAAC   AA
GAM423  TYRO3   3'  AGTTCAGGAACCCTTCTCCA  20842      CAT  GA
                                TGGAGAAG  GG  CCTGAACT
                                ||||||||  ||  ||||||||
                                ACCTCTTC  CC  GGACTTGA
                                    ___  AA
GAM423  ZNF36   3'  GTTTTTTCCCACGCTTTTCCA  93967      A   CCT
                                TGGAGAAGC TGGGA  GAAC
                                ||||||||| |||||  ||||
                                ACCTTTTCG ACCCT  TTTG
                                    C    TT_
GAM423  C17     3'  TTAGCAACCATGCTTCTC   37858        GAC
                                GAGAAGCATGG  CTGA
                                ||||||||||  ||||
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                                CTCTTCGTACC   GATT
                                      AAC
GAM423  DKFZP586B1621 3'  TGGGTCCCCATGCCTCTCC   31386      A     _
                                GGAGA GCATGGG ACCTG
                                ||||| ||||||| |||||
                                CCTCT CGTACCC TGGGT
                                   C      C
GAM423  EDR1     3'  CAGGTCTTAATTCTCCA     15380       GCA
                                TGGAGAA   TGGGACCTG
                                |||||||   |||||||||
                                ACCTCTT   ATTCTGGAC
                                    A__
GAM423  FLJ00001  3'  GGAGCCATCTTCTCCA      81817       C   GA
                                TGGAGAAG ATGG  CC
                                |||||||| ||||  ||
                                ACCTCTTC TACC  GG
                                    _   GA
GAM423  FLJ10193  3'  CAGGCCCCATACTCCCTCCA   56552      A_  C    A
                                TGGAG  AG ATGGG CCTG
                                |||||  || ||||| ||||
                                ACCTC  TC TACCC GGAC
                                   CC  A    C
GAM423  FLJ10815  3'  AGTTCTCAACTTCTCCA     36693       CA    C
                                TGGAGAAG  TGGGA CT
                                ||||||||  ||||| ||
                                ACCTCTTC  ACTCT GA
                                    A_    T
GAM423  FLJ11342  3'  AGTTCAGGGGGCTTCCACCA   37247    A_    ATGGGA
                                TGG  GAAGC     CCTGAACT
                                |||  |||||     ||||||||
                                ACC  CTTCG     GGACTTGA
                                  AC    GG____
GAM423  FLJ12960  3'  TTCACTTAACTTCTCCA     44956       CA   ACC
                                TGGAGAAG  TGGG   TGAA
                                ||||||||  ||||   ||||
                                ACCTCTTC  ATTC   ACTT
                                    A_   ___
GAM423  FLJ20371  5'  GTCCTCACCACTTCTCCA    35066       CA_ _
                                TGGAGAAG   TG GGAC
                                ||||||||   || ||||
                                ACCTCTTC   AC CCTG
                                    ACC  T
GAM423  FLJ21276  3'  AGTCCAGAGTTTTTATGCCTCT 44914      A      _ _  A
          CC                      GGAGA GCATGGGA C CTG ACT
                                |||||  |||||||| | ||| |||
                                CCTCT CGTATTTT G GAC TGA
                                   C       T A   C
GAM423  GOLGA1   3'  TCAGGCTCTCTGCCTTCCA   9092       AA   T   _
                                TGGAG  GCA GGGA CCTGA
                                |||||  ||| |||| |||||
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                                ACCTT  CGT CTCT GGACT
                                  C_  _   C
GAM423  GREB1    3'  AGTCCAGGTCTCCCTTCTCC  27863       CAT      A
                                GGAGAAG  GGGACCTG ACT
                                |||||||  |||||||| |||
                                CCTCTTC  CTCTGGAC TGA
                                   C__      C
GAM423  HBP1     3'  GTTCATCACACTTCTTCA    24314       CA  GACC
                                TGGAGAAG  TGG   TGAAC
                                ||||||||  |||   |||||
                                ACTTCTTC  ACT   ACTTG
                                    AC  ____
GAM423  HSPC065  3'  GTTCAGGACTCCTCTC     26319     AGCAT  A
                                GAGA    GGG CCTGAAC
                                ||||    ||| |||||||
                                CTCT    CTC GGACTTG
                                  C____  A
GAM423  KIAA0193 3'  AGTTCAGGCCCCACCATTCC  28650     AAGCA  A
                                GGAG    TGGG CCTGAACT
                                ||||    |||| ||||||||
                                CCTT    ACCC GGACTTGA
                                  ACC__  C
GAM423  KIAA0607 3'  TCCGCATGTTTCCCCA     72571     A      _
                                TGG GAAGCATG GGA
                                ||| |||||||| |||
                                ACC CTTTGTAC CCT
                                  C       G
GAM423  KIAA0750 5'  CAGTGTGACGTTTCTCCA    27567       AT GG  _
                                TGGAGAAGC  G  AC CTG
                                |||||||||  |  || |||
                                ACCTCTTTG  C  TG GAC
                                     __ AG  T
GAM423  KIAA0828 3'  TTCAGCAAGCTGCTTCTCCA  81202         TGGGAC
                                TGGAGAAGCA     CTGAA
                                ||||||||||     |||||
                                ACCTCTTCGT     GACTT
                                     CGAAC_
GAM423  KIAA1033 3'  TCAGGTTTCTTCTACA     64519    G    CATG
                                TG AGAAG    GGACCTGA
                                || |||||    ||||||||
                                AC TCTTC    TTTGGACT
                                 A    ____
GAM423  KIAA1209 3'  CAAGTTTCTTGCTTCTCCA   60750         T GG  C
                                TGGAGAAGCA G  AC TG
                                |||||||||| |  || ||
                                ACCTCTTCGT C  TG AC
                                     T TT  A
GAM423  KIAA1751 3'  TTCAGGTCCTCCTCCA      71706       AAGCAT
                                TGGAG     GGGACCTGAA
                                |||||     ||||||||||
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                                ACCTC     TCCTGGACTT
                                  C_____
GAM423  KIAA1813  5'  AGGCCTCCCATGCCTCTC    70289      A      __
                                GAGA GCATGGGA  CCT
                                |||| ||||||||  |||
                                CTCT CGTACCCT  GGA
                                  C       CC
GAM423  KIAA1819  5'  TCTGTCCAACTTCTCCA     69680        CATG    CT
                                TGGAGAAG    GGAC  GA
                                ||||||||    ||||  ||
                                ACCTCTTC    CCTG  CT
                                    AA__    T_
GAM423  KLHL4     3'  TTCAGATCCTTTCTCCA     38925        GCAT    C
                                TGGAGAA    GGGA CTGAA
                                |||||||    |||| |||||
                                ACCTCTT    TCCT GACTT
                                   ____    A
GAM423  LASP1     5'  TCAGGCGTCCCCGCCCCA    20462     AGAA  AT   __
                                TGG    GC  GGGA  CCTGA
                                |||    ||  ||||  |||||
                                ACC    CG  CCCT  GGACT
                                  C___  C_    GC
GAM423  MGC10986  5'  CGGGTGCCGCTTCTCCA     47562         AT  G
                                TGGAGAAGC  GG ACCTG
                                |||||||||  || |||||
                                ACCTCTTCG  CC TGGGC
                                    __  G
GAM423  MGC20255  3'  CAGGCGTCCCGCCTTCCCA   53440     A   CA    __
                                TGG GAAG  TGGGA  CCTG
                                ||| ||||  |||||  ||||
                                ACC CTTC  GCCCT  GGAC
                                  _   C_    GC
GAM423  MGC4415   3'  TCAGGTCCATCCTTCTC     48954       CATG
                                GAGAAG    GGACCTGA
                                ||||||    ||||||||
                                CTCTTC    CCTGGACT
                                   CTA_
GAM423  MGC8407   3'  AGGTCCCACACTCTCC      43887      A CA
                                GGAGA G  TGGGACCT
                                ||||| |  ||||||||
                                CCTCT C  ACCCTGGA
                                  _ AC
GAM423  MSP       3'  CATGGTCCCATGCCTTCCA   49413      AA       _
                                TGGAG  GCATGGGACC TG
                                |||||  |||||||||| ||
                                ACCTT  CGTACCCTGG AC
                                  C_        T
GAM423  MST4      5'  CAGGTCCCAGTCATCACCA   33300     A  AGCA
                                TGG GA    TGGGACCTG
                                ||| ||    |||||||||
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                                ACC CT    ACCCTGGAC
                                  A  ACTG
GAM423  OATPRP4  3'  TTCAAAGCTCATGCTCCCC   48233    A  A      ACC
                                GG GA GCATGGG   TGAA
                                || || |||||||   ||||
                                CC CT CGTACTC   ACTT
                                 C  _      GAA
GAM423  PRDM8    5'  TCTGTCACAGCTTCTCCA    39571         A  G   CT
                                TGGAGAAGC TG GAC  GA
                                ||||||||| || |||  ||
                                ACCTCTTCG AC CTG  CT
                                      _ A   T_
GAM423  PSK      5'  TCAGGCCCCTGGGTCCCA    32363     A  AG  T   A
                                TGG GA  CA GGG CCTGA
                                ||| ||  || ||| |||||
                                ACC CT  GT CCC GGACT
                                  _  GG  C   _
GAM423  RBT1     5'  CAGGTCTCTGTGCTCCA     25351      AA   T
                                TGGAG  GCA GGGACCTG
                                |||||  ||| ||||||||
                                ACCTC  TGT CTCTGGAC
                                   G_   _
GAM423  RERG     3'  GTTCAAGCATCTTCTC      51898       C   GGACC
                                GAGAAG ATG    TGAAC
                                |||||| |||    |||||
                                CTCTTC TAC    ACTTG
                                    _   GA___
GAM423  TOM1     3'  CAGGTCCCCACTGCTCTC    18506     A   T__
                                GAGA GCA   GGGACCTG
                                |||| |||   ||||||||
                                CTCT CGT   CCCTGGAC
                                   _   CAC
GAM423  TRIM38   3'  AGTTCAAACTATTGCCCATGTT 20984    A   G     ACC_____
            CCCCA                    GG GAA CATGGG       TGAACT
                                || ||| ||||||       ||||||
                                CC CTT GTACCC       ACTTGA
                                 C   _     GTTATCAA
GAM423  WDR18    3'  CAGGCCTGGACTCTCC      65550      A CA    A
                                GGAGA G  TGGG CCTG
                                ||||| |  |||| ||||
                                CCTCT C  GTCC GGAC
                                   _ AG    _
GAM423  WIRE     3'  AGCTCCTAACATGTTTCTCCA  78298           ___   C
                                TGGAGAAGCATG   GGA CT
                                ||||||||||||   ||| ||
                                ACCTCTTTGTAC   CCT GA
                                       AAT   C
GAM423  XLKD1    3'  TCAGACCCTTTCTTCA      21950        CAT   AC
                                TGGAGAAG   GGG  CTGA
                                ||||||||   |||  ||||
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                                ACTTCTTT  CCC  GACT
                                    ___   A_
GAM423  LOC113386 3'  TCAGGTCCCTGTTCCC     57080    A  G  T
                                GG GAA CA GGGACCTGA
                                || ||| || |||||||||
                                CC CTT GT CCCTGGACT
                                 _  _ _
GAM423  LOC124801 3'  TTCAAGCCCTGCCTTCA     74341      AA  T  ACC
                                TGGAG  GCA GGG  TGAA
                                |||||  ||| |||  ||||
                                ACTTC  CGT CCC  ACTT
                                   __  _  GA_
GAM423  LOC144110 3'  TCAGGTCCCATACGCTACC   76676    AGA  __
                                GG  AGC  ATGGGACCTGA
                                ||  |||  ||||||||||
                                CC  TCG  TACCCTGGACT
                                 A__  CA
GAM423  LOC146159 5'  GGGCTCTCCCATCTTCTCCA  77684       C    ___
                                TGGAGAAG ATGGGA  CCT
                                |||||||| ||||||  |||
                                ACCTCTTC TACCCT  GGG
                                    _    CTC
GAM423  LOC146823 3'  GTCCCATGCTCCTCTA     83801      A
                                TGGAG AGCATGGGAC
                                ||||| ||||||||||
                                ATCTC TCGTACCCTG
                                   C
GAM423  LOC149464 5'  AGTTCAGGCCTGTTCTGCCCCA 84426    AGA  C    A
                                TGG  AG ATGGG CCTGAACT
                                |||  || ||||| ||||||||
                                ACC  TC TGTCC GGACTTGA
                                  CCG  T   _
GAM423  LOC152274 3'  CAGGTCCCTGCCTCC      80502     AA  T
                                GGAG  GCA GGGACCTG
                                ||||  ||| ||||||||
                                CCTC  CGT CCCTGGAC
                                   __  _
GAM423  LOC153516 3'  CAGATCTGATTTTCTCCA    56706       C  G  C
                                TGGAGAAG AT GGA CTG
                                |||||||| || ||| |||
                                ACCTCTTT TA TCT GAC
                                    _ G  A
GAM423  LOC197387 5'  AGTTCTCAGGCTTCTCCA    89746       A   C
                                TGGAGAAGC TGGGA CT
                                ||||||||| ||||| ||
                                ACCTCTTCG ACTCT GA
                                     G   T
GAM423  LOC204820 3'  AGTTCAGGCAAACTGCCCGTCC 90663     GAA  TGGGA
           A                     TGGA  GCA   CCTGAACT
                                ||||  |||   ||||||||
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                                ACCT   CGT    GGACTTGA
                                  GCC   CAAAC
GAM423  LOC220573 3'  TTCAATTGTGCTTGTCCA    69605     G    TG GACC
                                TGGA AAGCA  G    TGAA
                                |||| |||||  |    ||||
                                ACCT TTCGT  T    ACTT
                                  G    GT A___
GAM423  LOC221632 3'  TCAGGTCCTCTCTCCA      93803       A CAT
                                TGGAGA G   GGGACCTGA
                                |||||| |   |||||||||
                                ACCTCT C   TCCTGGACT
                                  _ ___
GAM423  LOC255231 3'  AGTTCAGGCATCCTTATCCA  95369     G   C   GGA
                                TGGA AAG ATG   CCTGAACT
                                |||| ||| |||   ||||||||
                                ACCT TTC TAC   GGACTTGA
                                  A   C   ___
GAM423  LOC255252 3'  TCAGCATGCTTCCCCA      95010     A      GGAC
                                TGG GAAGCATG    CTGA
                                ||| ||||||||    ||||
                                ACC CTTCGTAC    GACT
                                  C       _____
GAM423  LOC55885  3'  GTTCCATGTTCCCCA       37818     A   G
                                TGG GAA CATGGGAC
                                ||| ||| ||||||||
                                ACC CTT GTACCTTG
                                  C   _
GAM423  LOC89932  5'  TCACCCAACTTCTCCA      60814        CA    ACC
                                TGGAGAAG  TGGG   TGA
                                ||||||||  ||||   |||
                                ACCTCTTC  ACCC   ACT
                                    A_    ___
GAM423  LOC90342  5'  CAGGCACTTCCTGCTTCTTCA  62355          T    ___
                                TGGAGAAGCA GGGA   CCTG
                                |||||||||| ||||   ||||
                                ACTTCTTCGT CCTT   GGAC
                                      _    CAC
GAM423  LOC91628  3'  AGTTCTTCTCCATGTTTCTCCA 66757             ACCT
                                TGGAGAAGCATGGG    GAACT
                                ||||||||||||||    |||||
                                ACCTCTTTGTACCT    CTTGA
                                      CTT_
GAM424  CLCN5     5'  TGAAATACCTAAGCTGCTCCAA 3595          ________
                                TTGGAGCAG      GTTTCA
                                |||||||||      ||||||
                                AACCTCGTC      TAAAGT
                                    GAATCCA
GAM424  CLCN5     5'  TGAAATACCTAAGCTGCTCCAA 3595          ________
                                TTGGAGCAG      GTTTCA
                                |||||||||      ||||||
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                                AACCTCGTC     TAAAGT
                                     GAATCCA
GAM424  FLRT2   5' ATTGAAAAATGAGGTCTGC  25056    GT    CTC
                                GCAG TTCATT  CAAT
                                |||| ||||||  ||||
                                CGTC GAGTAA  GTTA
                                  TG    AAA
GAM424  FLRT2   5' ATTGAAAAATGAGGTCTGC  25056    GT    CTC
                                GCAG TTCATT  CAAT
                                |||| ||||||  ||||
                                CGTC GAGTAA  GTTA
                                  TG    AAA
GAM424  IL17    3' TGGGGAAAATGAAACCCTCC  9333     CA     __
                                GGAG GGTTTCAT TCTCCA
                                |||| |||||||| ||||||
                                CCTC CCAAAGTA AGGGGT
                                  __     AA
GAM424  IL17    3' TGGGGAAAATGAAACCCTCC  9333     CA     __
                                GGAG GGTTTCAT TCTCCA
                                |||| |||||||| ||||||
                                CCTC CCAAAGTA AGGGGT
                                  __     AA
GAM424  NLGN1   5' TGAAGATGCTGCTCCAA   30026       G__
                                TTGGAGCAG  TTTCA
                                |||||||||  |||||
                                AACCTCGTC  GAAGT
                                     GTA
GAM424  NLGN1   5' TGAAGATGCTGCTCCAA   30026       G__
                                TTGGAGCAG  TTTCA
                                |||||||||  |||||
                                AACCTCGTC  GAAGT
                                     GTA
GAM424  POLG    3' GTGATAAACCTGCTCCAA   10682        __
                                TTGGAGCAGGTT TCAT
                                |||||||||||  ||||
                                AACCTCGTCCAA AGTG
                                       AT
GAM424  POLG    3' GTGATAAACCTGCTCCAA   10682        __
                                TTGGAGCAGGTT TCAT
                                |||||||||||  ||||
                                AACCTCGTCCAA AGTG
                                       AT
GAM424  TPK1    3' GGAGAACCTGTCCAA     42384     G   TTCAT
                                TTGGA CAGGT   TCTCC
                                ||||| |||||   |||||
                                AACCT GTCCA   AGAGG
                                  _   _____
GAM424  TPK1    3' GGAGAACCTGTCCAA     42384     G   TTCAT
                                TTGGA CAGGT   TCTCC
                                ||||| |||||   |||||
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                                AACCT GTCCA    AGAGG
                                  _   _____
GAM424  C1orf8   5' GAGAATGAAACCCTC      16832    CA
                                GAG  GGTTTCATTCTC
                                |||  ||||||||||||
                                CTC  CCAAAGTAAGAG
                                  __
GAM424  C1orf8   5' GAGAATGAAACCCTC      16832    CA
                                GAG  GGTTTCATTCTC
                                |||  ||||||||||||
                                CTC  CCAAAGTAAGAG
                                  __
GAM424  CLIC6    3' TGGAGAACATGTTCCAA     82536       G  TTCAT
                                TTGGAGCA GT    TCTCCA
                                |||||||| ||    ||||||
                                AACCTTGT CA    AGAGGT
                                    A _____
GAM424  CLIC6    3' TGGAGAACATGTTCCAA     82536       G  TTCAT
                                TTGGAGCA GT    TCTCCA
                                |||||||| ||    ||||||
                                AACCTTGT CA    AGAGGT
                                    A _____
GAM424  CLIPR-59 3' TGGAGAATTTCAATGCCCCGA 31374     A  GGTTTC
                                TTGG GCA     ATTCTCCA
                                |||| |||     ||||||||
                                AGCC CGT     TAAGAGGT
                                  C  AACTT_
GAM424  CLIPR-59 3' TGGAGAATTTCAATGCCCCGA 31374     A  GGTTTC
                                TTGG GCA     ATTCTCCA
                                |||| |||     ||||||||
                                AGCC CGT     TAAGAGGT
                                  C  AACTT_
GAM424  DKFZP547L112 3' TGGAGAACTCTTGCTCCA   66532       TTTCA
                                TGGAGCAGG    TTCTCCA
                                |||||||||    |||||||
                                ACCTCGTTC    AAGAGGT
                                     TC___
GAM424  DKFZP547L112 3' TGGAGAACTCTTGCTCCA   66532       TTTCA
                                TGGAGCAGG    TTCTCCA
                                |||||||||    |||||||
                                ACCTCGTTC    AAGAGGT
                                     TC___
GAM424  EPS8R3   5' GGACCACCTGCTCCAA     55701         TTCATTC
                                TTGGAGCAGGT      TCC
                                ||||||||||       |||
                                AACCTCGTCCA      AGG
                                    CC_____
GAM424  EPS8R3   5' GGACCACCTGCTCCAA     57404         TTCATTC
                                TTGGAGCAGGT      TCC
                                ||||||||||       |||
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                                AACCTCGTCCA      AGG
                                      CC_____
GAM424  EPS8R3   5' GGACCACCTGCTCCAA     57404          TTCATTC
                                TTGGAGCAGGT      TCC
                                ||||||||||       |||
                                AACCTCGTCCA      AGG
                                      CC_____
GAM424  EPS8R3   5' GGACCACCTGCTCCAA     55701          TTCATTC
                                TTGGAGCAGGT      TCC
                                ||||||||||       |||
                                AACCTCGTCCA      AGG
                                      CC_____
GAM424  FLJ20552 3' AGAACAAAACTGCTCCAA    35389          G   CA
                                TTGGAGCAG TTT  TTCT
                                ||||||||| |||  ||||
                                AACCTCGTC AAA  AAGA
                                     _  AC
GAM424  FLJ20552 3' AGAACAAAACTGCTCCAA    35389          G   CA
                                TTGGAGCAG TTT  TTCT
                                ||||||||| |||  ||||
                                AACCTCGTC AAA  AAGA
                                     _  AC
GAM424  FLJ22865 5' TGGAGAAAACTGCTCTAA    47071          GTTTCA
                                TTGGAGCAG     TTCTCCA
                                |||||||||     |||||||
                                AATCTCGTC     AAGAGGT
                                      AA_____
GAM424  FLJ22865 5' TGGAGAAAACTGCTCTAA    47071          GTTTCA
                                TTGGAGCAG     TTCTCCA
                                |||||||||     |||||||
                                AATCTCGTC     AAGAGGT
                                      AA_____
GAM424  KIAA0372 5' ATTGAAATTTGTTACCTACTCC 27663       C    TT  TTCTC
          AA                      TTGGAG AGGT  CA    CAAT
                                |||||| ||||  ||    ||||
                                AACCTC TCCA  GT    GTTA
                                   A   TT  TTAAA
GAM424  KIAA0372 5' ATTGAAATTTGTTACCTACTCC 27663       C    TT  TTCTC
          AA                      TTGGAG AGGT  CA    CAAT
                                |||||| ||||  ||    ||||
                                AACCTC TCCA  GT    GTTA
                                   A   TT  TTAAA
GAM424  PRO0132  5' ATGAAACCACTCCAA      26101       CA
                                TTGGAG  GGTTTCAT
                                ||||||  ||||||||
                                AACCTC  CCAAAGTA
                                   A_
GAM424  PRO0132  5' ATGAAACCACTCCAA      26101       CA
                                TTGGAG  GGTTTCAT
                                ||||||  ||||||||
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                                AACCTC  CCAAAGTA
                                   A_
GAM424  TEX27    3'  AGAGTGGAACCCGCTGCAA   41658     G   A
                                TTG AGC GGTTTCATTCT
                                ||| ||| ||||||||||
                                AAC TCG CCAAGGTGAGA
                                  G   C
GAM424  TEX27    3'  AGAGTGGAACCCGCTGCAA   41658     G   A
                                TTG AGC GGTTTCATTCT
                                ||| ||| ||||||||||
                                AAC TCG CCAAGGTGAGA
                                  G   C
GAM424  LOC149373 3'  ATTGGGGTGATGATACCCACCC 79312      AGCA   T    _
           CAA                    TTGG    GGT TCATT CTCCAAT
                                ||||    ||| ||||| |||||||
                                AACC    CCA AGTAG GGGGTTA
                                  CCAC   T    T
GAM424  LOC149373 3'  ATTGGGGTGATGATACCCACCC 79312      AGCA   T    _
           CAA                    TTGG    GGT TCATT CTCCAAT
                                ||||    ||| ||||| |||||||
                                AACC    CCA AGTAG GGGGTTA
                                  CCAC   T    T
GAM424  LOC152687 3'  TTGGAGAATATTGCTCC     80643        GTTTC
                                GGAGCAG     ATTCTCCAA
                                |||||||     |||||||||
                                CCTCGTT     TAAGAGGTT
                                   A_____
GAM424  LOC152687 3'  TTGGAGAATATTGCTCC     80643        GTTTC
                                GGAGCAG     ATTCTCCAA
                                |||||||     |||||||||
                                CCTCGTT     TAAGAGGTT
                                   A_____
GAM424  LOC51202  3'  ATTGGAGAATGAAACCTGCTCC 33017
           AA                     TTGGAGCAGGTTTCATTCTCCAAT
                                ||||||||||||||||||||||||
                                AACCTCGTCCAAAGTAAGAGGTTA

GAM424  LOC51202  3'  ATTGGAGAATGAAACCTGCTCC 33017
           AA                     TTGGAGCAGGTTTCATTCTCCAAT
                                ||||||||||||||||||||||||
                                AACCTCGTCCAAAGTAAGAGGTTA

GAM425  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM425  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875        CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
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                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM425  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM425  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                  CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM425  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||  ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM425  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM425  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM425  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM425  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_    CG_
GAM425  CG012    5'  CTCACTCTGAAAGTGAA     83218          CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM425  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM425  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
              G                   CATTTC        GTCTGAGAT
                                ||||||        |||||||||
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                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM425  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA  TCACTGTCTGAGAT
                                |||||||  ||||||||||||||
                                GTAAAGT  AGTGACAGACTCTA
                                   C__
GAM425  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM425  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM425  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                 C
GAM425  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM425  PP35      3'  ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM425  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148        TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM425  SEP15     3'  TCCTACAGTAAGAGTGAAA   14934       C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM425  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA  73941       CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM425  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
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                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM425  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM425  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM425  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA

                                          _
GAM426  A1BG    3'  CAGGGTCTCACTGTGTTGC    55413        TAT_
                                GCAACACA    GGCTTTG
                                ||||||||    |||||||
                                CGTTGTGT    CTGGGAC
                                     CACT
GAM426  ACPT    3'  CACCCCGCCATATGCTGC     54986     ACA       TTT
                                GCA   CATATGGC   GTG
                                |||   ||||||||   |||
                                CGT   GTATACCG   CAC
                                  C__       CCC
GAM426  ACPT    3'  CACCCCGCCATATGCTGC     54980     ACA       TTT
                                GCA   CATATGGC   GTG
                                |||   ||||||||   |||
                                CGT   GTATACCG   CAC
                                  C__       CCC
GAM426  AHCY    3'  CACAAAGCCCATGTGTTTTGC  5473       C       _
                                GCAA ACATATGG CTTTGTG
                                |||| |||||||| |||||||
                                CGTT TGTGTACC GAAACAC
                                  T       C
GAM426  BCL7A   3'  CAGGATTCCATTTGTGTTGCT  40638          T    CT  G
                                AGCAACACA ATGG  TT TG
                                ||||||||| ||||  || ||
                                TCGTTGTGT TACC  AG AC
                                     T    TT  G
GAM426  CDK5R2  3'  CACAAAGCCACCGCCGCTGTT  14132      ACACATA
                                AGCA      TGGCTTTGTG
                                ||||      ||||||||||
                                TTGT      ACCGAAACAC
                                  CGCCGCC
GAM426  CHC1    3'  CACAAAGCATACTCTTGC     7019       CACA    G
                                GCAA    TATG CTTTGTG
                                ||||    |||| |||||||
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                                CGTT   ATAC GAAACAC
                                  CTC_   _
GAM426  CIT     3'  CACAAGGCATCTGTTGCT    69741       CATATG
                                AGCAACA     GCTTTGTG
                                |||||||     ||||||||
                                TCGTTGT     CGGAACAC
                                   CTA___
GAM426  COL6A2  5'  CAGGGCCACAGGTGCTGC    54168     A  ATA
                                GCA CAC   TGGCTTTG
                                ||| |||   ||||||||
                                CGT GTG   ACCGGGAC
                                  C   GAC
GAM426  COL6A2  5'  CAGGGCCACAGGTGCTGC    8480      A  ATA
                                GCA CAC   TGGCTTTG
                                ||| |||   ||||||||
                                CGT GTG   ACCGGGAC
                                  C   GAC
GAM426  EYA1    3'  CACAGCGTTATGTGTCTGC    4952      AC       T
                                GCA  ACATATGGC TTGTG
                                |||  ||||||||| |||||
                                CGT  TGTGTATTG GACAC
                                  C_       C
GAM426  FBN2    3'  CAAGGAACCATATGTG      8844          __
                                CACATATGG  CTTTG
                                |||||||||  |||||
                                GTGTATACC  GGAAC
                                     AA
GAM426  FMO1    3'  CACAAATGATTGTGTTGT    8924        TATGGC
                                GCAACACA     TTTGTG
                                ||||||||     ||||||
                                TGTTGTGT     AAACAC
                                   TAGT__
GAM426  GALNT2  3'  CACAAAGCCGAGTCGTGT    15593      _  A
                                ACAC AT TGGCTTTGTG
                                |||| || ||||||||||
                                TGTG TG GCCGAAACAC
                                  C  A
GAM426  GALNT2  3'  CACAAAGCCGTTCGCAGCT   15594     AACACAT
                                AGC      ATGGCTTTGTG
                                |||      ||||||||||
                                TCG      TGCCGAAACAC
                                  ACGCT__
GAM426  GPR4    3'  CAGGGTCTCACTGTGTTGC    59902        TAT_
                                GCAACACA    GGCTTTG
                                ||||||||    |||||||
                                CGTTGTGT    CTGGGAC
                                     CACT
GAM426  HNMT    3'  CACAAAGCCTGTGTTACT    22567    C     TAT
                                AG AACACA   GGCTTTGTG
                                || ||||||   |||||||||
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                                TC TTGTGT   CCGAAACAC
                                 A     ___
GAM426  IL1RN    3' CACAAAGCCCTTCCATGTCGC 5141     A   CATAT_
                                GC ACA     GGCTTTGTG
                                || |||     |||||||||
                                CG TGT     CCGAAACAC
                                 C   ACCTTC
GAM426  IL2RB    3' CACAAAGTGGATGCCTGCT   6069      ACA   ATG
                                AGCA  CAT   GCTTTGTG
                                ||||  |||   ||||||||
                                TCGT  GTA   TGAAACAC
                                  CC_  GG_
GAM426  ITSN2    3' CACAAAGCCATGCACGCT    38971     AACACA
                                AGC     TATGGCTTTGTG
                                |||     ||||||||||||
                                TCG     GTACCGAAACAC
                                  CAC___
GAM426  JRK      3' CAGGGTCTCACTGTGTTGC   86524       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                     CACT
GAM426  LANCL1   3' CACAATTTTATATGTATGCT  20210     AC      CT
                                AGCA  ACATATGG  TTGTG
                                ||||  ||||||||  |||||
                                TCGT  TGTATATT  AACAC
                                  A_      TT
GAM426  LGR6     5' GGCCATCGTGTTGCT      84200       AT
                                AGCAACAC  ATGGCT
                                ||||||||  ||||||
                                TCGTTGTG  TACCGG
                                     C_
GAM426  LRRC2    3' CAAGGCACCATGTGTTACT   44465    C      ATG
                                AG AACACAT   GCTTTG
                                || |||||||   ||||||
                                TC TTGTGTA   CGGAAC
                                 A      CCA
GAM426  MYBL2    3' CAGGGCCATGTGCTGC      10154     ACA
                                GCA   CATATGGCTTTG
                                |||   ||||||||||||
                                CGT   GTGTACCGGGAC
                                  C__
GAM426  OCLN     3' CACAAAGTTTTGGTTGCT    10314       A  TAT
                                AGCAAC CA   GGCTTTGTG
                                ||||||  ||   |||||||||
                                TCGTTG GT   TTGAAACAC
                                    _ T__
GAM426  OSR1     3' CACAAAGTAATATGTG      17566       G
                                CACATAT GCTTTGTG
                                |||||||  ||||||||
```

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                                GTGTATA TGAAACAC
                                    A
GAM426  PCDH9    5'  CACAAAGTGACAGTGCTGGCT  82794     AA_  ATATG
                                AGC  CAC    GCTTTGTG
                                |||  |||    ||||||||
                                TCG  GTG    TGAAACAC
                                  GTC  ACAG_
GAM426  PRDM2    5'  CACAAAGCCACATCCTGC    24246     ACAC  A
                                GCA   AT TGGCTTTGTG
                                |||   || ||||||||||
                                CGT   TA ACCGAAACAC
                                  CC__  C
GAM426  PRDM2    5'  CACAAAGCCACATCCTGC    31847     ACAC  A
                                GCA   AT TGGCTTTGTG
                                |||   || ||||||||||
                                CGT   TA ACCGAAACAC
                                  CC__  C
GAM426  PRG4     3'  CACAAAGCTTTATCGTGTTGT  19415       _  T
                                GCAACAC ATA GGCTTTGTG
                                ||||||| ||| |||||||||
                                TGTTGTG TAT TCGAAACAC
                                    C  T
GAM426  RXRB     3'  CACAAAGCACTGGCCTTGC    41757     CA_  TATG
                                GCAA  CA   GCTTTGTG
                                ||||  ||   ||||||||
                                CGTT  GT   CGAAACAC
                                  CCG  CA__
GAM426  SMARCD1  3'  CACAAAGTTCCCATGTG     57429       ___
                                CATATGG  CTTTGTG
                                |||||||  |||||||
                                GTGTACC  GAAACAC
                                    CTT
GAM426  SMARCD1  3'  CACAAAGTTCCCATGTG     11811       ___
                                CATATGG  CTTTGTG
                                |||||||  |||||||
                                GTGTACC  GAAACAC
                                    CTT
GAM426  SMURF1   3'  CACGTGTGATCTGTGTTGC   92448       T  G  TT
                                GCAACACA AT GC  TGTG
                                |||||||| || ||  ||||
                                CGTTGTGT TA TG  GCAC
                                    C  G  T_
GAM426  STX7     3'  CACCAAGATGTGTGTTACT   13108    C      GG  T
                                AG AACACATAT  CTT GTG
                                || |||||||||  ||| |||
                                TC TTGTGTGTA  GAA CAC
                                 A       __  C
GAM426  TAF4B    3'  CACAAAGCATTGTTGC      87167      CATATG
                                GCAACA     GCTTTGTG
                                ||||||     ||||||||
```

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                              CGTTGT     CGAAACAC
                                 TA____
GAM426  TF      3'  CACAGCTCTGTGTTGC      6512         TAT   T
                              GCAACACA   GGCT TG
                              ||||||||   |||| ||
                              CGTTGTGT   TCGA AC
                                   C__    C
GAM426  TLR4    5'  CACAGGGCCACTGCTGCT    12317      A  CATA
                              AGCA CA    TGGCTTTGTG
                              |||| ||    ||||||||||
                              TCGT GT    ACCGGGACAC
                                C  C___
GAM426  TLR4    5'  CACAGGGCCACTGCTGCT    56732      A  CATA
                              AGCA CA    TGGCTTTGTG
                              |||| ||    ||||||||||
                              TCGT GT    ACCGGGACAC
                                C  C___
GAM426  TLR4    5'  CACAGGGCCACTGCTGCT    56727      A  CATA
                              AGCA CA    TGGCTTTGTG
                              |||| ||    ||||||||||
                              TCGT GT    ACCGGGACAC
                                C  C___
GAM426  TLR4    5'  CACAGGGCCACTGCTGCT    56736      A  CATA
                              AGCA CA    TGGCTTTGTG
                              |||| ||    ||||||||||
                              TCGT GT    ACCGGGACAC
                                C  C___
GAM426  VIPR2   3'  CACAGTCTCCATGTGTGTGC  12605     A       CT_
                              GCA CACATATGG   TTGTG
                              ||| |||||||||   |||||
                              CGT GTGTGTACC   GACAC
                                _       TCT
GAM426  ANKT    3'  CAGGGTCTCACTGTGTTGC   33024        TAT_
                              GCAACACA    GGCTTTG
                              ||||||||    |||||||
                              CGTTGTGT    CTGGGAC
                                   CACT
GAM426  ATP9A   3'  CACAAAGCCAGTGGCTGTT   62039      A_  ATA
                              AGCA  CAC   TGGCTTTGTG
                              ||||  |||   ||||||||||
                              TTGT  GTG   ACCGAAACAC
                                CG  ___
GAM426  CETN2   3'  CACATGTTACACCTGTGTTGC 15093        TA GCTT_
                              GCAACACA  TG    TGTG
                              ||||||||  ||    ||||
                              CGTTGTGT  AC    ACAC
                                   CC  ATTGT
GAM426  CYLD    3'  CACAAGGTTTTATACTGCT   30883     ACAC  TG
                              AGCA   ATA  GCTTTGTG
                              ||||   |||  ||||||||
```

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                                TCGT   TAT  TGGAACAC
                                  CA__   TT
GAM426  DKFZP586A0522 3'  CAGGGTCTCACTGTGTTGC   25871       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM426  DKFZp762K222 3'  ACAGATGCGTGTTGCT     71116       ATATG _
                                AGCAACAC    GC TTTGT
                                ||||||||    || |||||
                                TCGTTGTG    CG AGACA
                                    _____ T
GAM426  FLJ10297  3'  CAGGGCTTCACTGTGTTGC   35979       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   TCGGGAC
                                    CACT
GAM426  FLJ10511  3'  CACATGTGTATGTGCAGCT   36204    AA      G TT
                                AGC  CACATATG C  TGTG
                                |||  |||||||| |  ||||
                                TCG  GTGTATGT G  ACAC
                                  AC       _ T_
GAM426  FLJ11029  5'  CACTAGCACCTGTGTTGCT   60973       TATG   TT
                                AGCAACACA   GCT  GTG
                                |||||||||   |||  |||
                                TCGTTGTGT   CGA  CAC
                                    CCA_   T_
GAM426  FLJ11117  3'  CACAAAGCTTGTATGTG    37073       _
                                CACATATG GCTTTGTG
                                |||||||| ||||||||
                                GTGTATGT CGAAACAC
                                    T
GAM426  FLJ11715  3'  CAGGGTCTCCATATGTTGC   44668      C  AT_
                                GCAACA AT   GGCTTTG
                                |||||| ||   |||||||
                                CGTTGT TA   CTGGGAC
                                   A  CCT
GAM426  FLJ20275  3'  CACAAAGGGCTTTATGTGTCAG 34819    A_     T   __
          CT                      AGC  ACACATA GGCT  TTGTG
                                |||  ||||||| ||||  |||||
                                TCG  TGTGTAT TCGG  AACAC
                                  AC      T   GA
GAM426  FLJ20413  3'  CAGAGCCGCATGCACTGCT   35131     ACA  A
                                AGCA   CAT TGGCTTTG
                                ||||   ||| ||||||||
                                TCGT   GTA GCCGAGAC
                                  CAC   C
GAM426  FLJ20450  3'  CACCTGGGACCTGTGTTGCT   35192       TAT  _   T_
                                AGCAACACA   GG CTT  GTG
                                |||||||||   || |||  |||
```

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                                TCGTTGTGT  CC GGG  CAC
                                     ___  A  TC
GAM426  FLJ20671  3'  CAATTCAAATGTGTTGC    35516        A  CT
                                GCAACACAT TGG  TTG
                                ||||||||| |||  |||
                                CGTTGTGTA ACT  AAC
                                      A  T_
GAM426  FLJ23598  3'  CACAAAGAGAGGCTGTGCTGC  45521    A   TATGG_
                                GCA CACA     CTTTGTG
                                ||| ||||     |||||||
                                CGT GTGT     GAAACAC
                                  C   CGGAGA
GAM426  FRSB    3'  CATAGGCCATACATGTTACT  19090   C   CA      T
                                AG AACA  TATGGCTT GTG
                                || ||||  |||||||| |||
                                TC TTGT  ATACCGGA TAC
                                 A   AC      _
GAM426  H2AV    3'  CACAGCCATATGTATTGTT   56845     C       T
                                AGCAA ACATATGGCT TG
                                ||||| |||||||||| ||
                                TTGTT TGTATACCGA AC
                                   A        C
GAM426  HIC2    3'  CACAAAGTCTGTACCGC    65256   AAC  TAT
                                GC  ACA  GGCTTTGTG
                                ||  |||  |||||||||
                                CG  TGT  CTGAAACAC
                                 CCA  ___
GAM426  KIAA0140  3'  CACATGGCCATGTCTTGC   27806    CAC      T
                                GCAA  ATATGGCT TGTG
                                ||||  |||||||| ||||
                                CGTT  TGTACCGG ACAC
                                  C__      T
GAM426  KIAA0215  3'  CAAATTCCATATGTAATGC   28416    AC      C_
                                GCA  ACATATGG  TTTG
                                |||  ||||||||  ||||
                                CGT  TGTATACC  AAAC
                                  AA       TT
GAM426  KIAA0254  3'  AGCCACCTGTGTTGCT     28595        TA
                                AGCAACACA  TGGCT
                                |||||||||  |||||
                                TCGTTGTGT  ACCGA
                                     CC
GAM426  KIAA0618  3'  CACAAAAACATGTGTTGT   29162       TA  GC
                                GCAACACA  TG  TTTGTG
                                ||||||||  ||  ||||||
                                TGTTGTGT  AC  AAACAC
                                     __  AA
GAM426  KIAA0953  3'  AGCTTTCATAGTGTTGCT   66778       A   ___
                                AGCAACAC TATG   GCT
                                |||||||| ||||   |||
```

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                                TCGTTGTG ATAC   CGA
                                     _   TTT
GAM426  KIAA1193  3'  CACAGAGCCATATACCTCGCT  67630     AACAC
                                AGC    ATATGGCTTTGTG
                                |||    |||||||||||||
                                TCG    TATACCGAGACAC
                                  CTCCA
GAM426  KIAA1281  3'  CACAGAGTAACAAATGTTGCT  89151       CATATG
                                AGCAACA     GCTTTGTG
                                |||||||     ||||||||
                                TCGTTGT     TGAGACAC
                                   AAACAA
GAM426  KIAA1466  5'  AGCCATATGTGCGCT      71913     AA
                                AGC  CACATATGGCT
                                |||  ||||||||||
                                TCG  GTGTATACCGA
                                  C_
GAM426  KIAA1821  3'  CAGGGTCTCACTGTGTTGC   71780       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                     CACT
GAM426  KIF13B    3'  CACAAAGTCCGTGGTGC     82820     A   ATAT
                                GCA CAC    GGCTTTGTG
                                ||| |||    |||||||||
                                CGT GTG    CTGAAACAC
                                  G   C___
GAM426  KIF13B    3'  CACAAAGTCCGTGGTGC     30904     A   ATAT
                                GCA CAC    GGCTTTGTG
                                ||| |||    |||||||||
                                CGT GTG    CTGAAACAC
                                  G   C___
GAM426  MGC12921  3'  CACAAAGGCCGTTATTGC    63775     CACAT    _
                                GCAA    ATGGC TTTGTG
                                ||||    ||||| ||||||
                                CGTT    TGCCG AAACAC
                                  AT___    G
GAM426  MGC14836  5'  CACAAAGCTATCATCCTGC   53035     ACACAT
                                GCA     ATGGCTTTGTG
                                |||     ||||||||||
                                CGT     TATCGAAACAC
                                  CCTAC_
GAM426  MGC15429  3'  CACATTGTCATGTGCAGCT   51249     AACA      TT
                                AGC    CATATGGC  TGTG
                                |||    ||||||||  ||||
                                TCG    GTGTACTG  ACAC
                                  AC__       TT
GAM426  MGC15875  3'  CGAGGCCATAATGCT       51908     ACACA
                                AGCA    TATGGCTTTG
                                ||||    ||||||||||
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                                TCGT    ATACCGGAGC
                                  A____
GAM426  MGC16279 5' GAAGCCATCGTGTCGCT    51888    A   AT
                                AGC ACAC  ATGGCTTT
                                ||| ||||  ||||||||
                                TCG TGTG  TACCGAAG
                                  C   C_
GAM426  MGC27434 3' CACAATAAGTATGTGTT    58947       GGCT
                                AACACATAT   TTGTG
                                |||||||||   |||||
                                TTGTGTATG   AACAC
                                     AAT_
GAM426  MGC3048  3' CACAAAGCATGAATGTT    43899    CA   G
                                AACA  TATG CTTTGTG
                                ||||  |||| |||||||
                                TTGT  GTAC GAAACAC
                                  AA   _
GAM426  MIG-6    3' CACAAGCTGGCCTTGTGTTGCT 38486       TAT   ___
                                AGCAACACA   GGCT   TTGTG
                                |||||||||   ||||   |||||
                                TCGTTGTGT   CCGG   AACAC
                                     T__    TCG
GAM426  MUC17    3' CACTGCCCCATATGTGTCCCT  94271    CA       CTTT
                                AG  ACACATATGG    GTG
                                ||  ||||||||||    |||
                                TC  TGTGTATACC    CAC
                                 CC        CCGT
GAM426  MYO3B    3' CACTCTCCCACATGTGTTGT   57301       A   CTTT
                                GCAACACAT TGG    GTG
                                ||||||||| |||    |||
                                TGTTGTGTA ACC    CAC
                                     C   CTCT
GAM426  NS1-BP   3' CACAAAGCTTTTGCATATTGC  72542     CA__  TAT
                                GCAA    CA   GGCTTTGTG
                                ||||    ||   |||||||||
                                CGTT    GT   TCGAAACAC
                                  ATAC  TT_
GAM426  OR51E2   3' CACAGGTTTTATGTGTTCT    47791    C      TG   T
                                AG AACACATA  GCTT GTG
                                || ||||||||  |||| |||
                                TC TTGTGTAT  TGGA CAC
                                 _       TT   _
GAM426  PRDM11   3' CAGGTGCTCCATGTGTTGC    39581       AT  _
                                GCAACACAT  GGC TTTG
                                |||||||||  ||| ||||
                                CGTTGTGTA  TCG GGAC
                                     CC   T
GAM426  PRO0943  5' CACAAAAGTGTTATATGTG   37701        ___
                                CACATATGGC   TTTGTG
                                ||||||||||   ||||||
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                                GTGTATATTG   AAACAC
                                     TGA
GAM426  SULT1C2   5'  CACAACGCAGCCATATGCTG  21674    _      ___
                                CA CATATGGCT   TTGTG
                                || |||||||||  |||||
                                GT GTATACCGA   AACAC
                                 C        CGC
GAM426  VEST1     3'  CACCTGCCATACATGTTGT   53685      CA     TTT
                                GCAACA  TATGGC   GTG
                                ||||||  ||||||   |||
                                TGTTGT  ATACCG   CAC
                                   AC     TC_
GAM426  ZFP100    3'  AGTCACCTGTGTTGCT     70049        TA
                                AGCAACACA  TGGCT
                                |||||||||  |||||
                                TCGTTGTGT  ACTGA
                                     CC
GAM426  ZNF363    5'  AGCCATATTGTCGCT      73452     A   C
                                AGC ACA ATATGGCT
                                ||| ||| ||||||||
                                TCG TGT TATACCGA
                                 C  _
GAM426  LOC118611 5'  CACAGAGCATTTGCGTTACT  75469    C   A  TATG
                                AG AAC CA    GCTTTGTG
                                || ||| ||    ||||||||
                                TC TTG GT    CGAGACAC
                                 A   C  TTA_
GAM426  LOC120526 3'  CAGGGCCATTGCACTGCT    74015     ACA  T
                                AGCA   CA ATGGCTTTG
                                ||||   || |||||||||
                                TCGT   GT TACCGGGAC
                                  CAC  _
GAM426  LOC126669 3'  CACAAAGTTCCATATGT     75399        __
                                ACATATGG  CTTTGTG
                                ||||||||  |||||||
                                TGTATACC  GAAACAC
                                     TT
GAM426  LOC139840 5'  CACAAGAGCCATGGGT      76266    A       _
                                AC TATGGCTTT GTG
                                || |||||||| |||
                                TG GTACCGAGA CAC
                                 G        A
GAM426  LOC143465 5'  CACATGCACATATGTG      82962        _  TT
                                CACATATG GC  TGTG
                                |||||||| ||  ||||
                                GTGTATAC CG  ACAC
                                     A  T_
GAM426  LOC146774 3'  CACTGACATGTGTGTGC     78094     A      GCTTT
                                GCA CACATATG    GTG
                                ||| ||||||||    |||
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```
                                CGT GTGTGTAC    CAC
                                  _      AGT__
GAM426  LOC147407 5'  CACAAAGCTATCATCCTGC   76322    ACACAT
                                GCA     ATGGCTTTGTG
                                |||     ||||||||||
                                CGT     TATCGAAACAC
                                  CCTAC_
GAM426  LOC151057 3'  ACAGAGCACATACTGT     85199    _  _
                                ACA TATG GCTTTGT
                                ||| |||| |||||||
                                TGT ATAC CGAGACA
                                  C   A
GAM426  LOC151473 3'  CACAACAACCTATGTGTT   80254       T  CT_
                                AACACATA GG   TTGTG
                                |||||||| ||   |||||
                                TTGTGTAT CC   AACAC
                                     _ AAC
GAM426  LOC154739 5'  CACAAAGTTCAAATGTATGC  86227    AC   A  _
                                GCA  ACAT TGG CTTTGTG
                                |||  |||| ||| |||||||
                                CGT  TGTA ACT GAAACAC
                                  A_   A  T
GAM426  LOC157507 5'  CACAGCTGTGTATGTGTGCT  81454     A     __   T
                                AGCA CACATAT  GGCT TG
                                |||| |||||||  |||| ||
                                TCGT GTGTATG  TCGA AC
                                  _     TG   C
GAM426  LOC161734 3'  CACAAACATTTAGTGTTGCT  87097       AT_  GC
                                AGCAACAC   ATG  TTTGTG
                                ||||||||   |||  ||||||
                                TCGTTGTG   TAC  AAACAC
                                     ATT  __
GAM426  LOC196410 3'  CACAAAAGTCATGGTG     87657    A       _
                                CAC TATGGCTTT GTG
                                ||| |||||||| |||
                                GTG GTACTGAAA CAC
                                  _       A
GAM426  LOC196485 3'  CACAAAAACCTGTGTTGT   87730       TAT  C_
                                GCAACACA   GG  TTTGTG
                                ||||||||   ||  ||||||
                                TGTTGTGT   CC  AAACAC
                                     ___  AA
GAM426  LOC196529 3'  CAGGGTCTCACTGTGTTGC   87771       TAT_
                                GCAACACA    GGCTTTG
                                ||||||||    |||||||
                                CGTTGTGT    CTGGGAC
                                     CACT
GAM426  LOC197003 5'  CACAAAGCTCCATGCTGT    87870    _  AT
                                ACA CAT  GGCTTTGTG
                                ||| |||  |||||||||
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```
                                TGT GTA  TCGAAACAC
                                  C   CC
GAM426   LOC202025 5'  CACAGTTGTATGGTTGCT    90281      A   TG   T
                                AGCAAC CATA  GCT TG
                                |||||| ||||  ||| ||
                                TCGTTG GTAT  TGA AC
                                   _   GT   C
GAM426   LOC203276 3'  CACAAAGTTCAAGTGTATGC   90475    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM426   LOC203292 3'  CAGGGTTTCATATGTGTT    90509        __
                                AACACATATG  GCTTTG
                                ||||||||||  ||||||
                                TTGTGTATAC  TGGGAC
                                      TT
GAM426   LOC203305 3'  CACAAAGTTCAAGTGTATGC   90519    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM426   LOC221354 3'  CACAAAAACATGTGTTGT    92409       TA  GC
                                GCAACACA  TG  TTTGTG
                                ||||||||  ||  ||||||
                                TGTTGTGT  AC  AAACAC
                                   __  AA
GAM426   LOC254243 3'  CACAAAGTTCAAGTGTATGC   97404    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM426   LOC255870 3'  CACAACTGGCCATGTCCTGC   94657    ACAC      __
                                GCA   ATATGGCT  TTGTG
                                |||   ||||||||  |||||
                                CGT   TGTACCGG  AACAC
                                  CC__       TC
GAM426   LOC90038  3'  CACAAAGTTCAAGTGTATGC   61148    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM426   LOC90321  3'  CACAAATGGATTGTGTGTGC   62262    A    TGGC_
                                GCA CACATA    TTTGTG
                                ||| ||||||    ||||||
                                CGT GTGTGT    AAACAC
                                  _     TAGGT
GAM426   LOC90750  3'  CACAAAGTTAAGATTGCT    63917      CACATA
                                AGCAA     TGGCTTTGTG
                                |||||     ||||||||||
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                                TCGTT     ATTGAAACAC
                                  AGA___
GAM426  LOC91069  3'  GAAGCCATCGTGTCACT     64778    CA    AT
                                AG  ACAC  ATGGCTTT
                                ||  ||||  ||||||||
                                TC  TGTG  TACCGAAG
                                 AC    C_
GAM426  LOC92539  3'  CACAAAGCCACTGTAGC     69630    A   CATA
                                GC ACA    TGGCTTTGTG
                                || |||    ||||||||||
                                CG TGT    ACCGAAACAC
                                 A   C___
GAM427  ABCG1     3'  CCTAGAACCGCGTTGGGTT   16982       TAGATCA
                                AACCCG      GTTCTAGG
                                ||||||      ||||||||
                                TTGGGT      CAAGATCC
                                   TGCGC__
GAM427  ADORA2A   3'  CCTAGACTCTCCTAGGGTT   5433       G   ATC   T
                                AACCC TAG   AGT CTAGG
                                ||||| |||   ||| |||||
                                TTGGG ATC   TCA GATCC
                                  _  CTC  _
GAM427  AIM1      3'  CCCAGGCTGATCTCG       91819    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTAGTCG GA CC
                                 _      _ C
GAM427  B4GALT5   3'  CCCAGGCTGGTCTCG       16495    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM427  CBFA2T2   3'  CCCAGAGGCTGATCTGC     17460         _  A
                                GTAGATCAGT TCT GG
                                |||||||||| ||| ||
                                CGTCTAGTCG AGA CC
                                      G   C
GAM427  CBFB      3'  CCCAGGCTGGTCTCG       43141    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM427  CBFB      3'  CCCAGGCTGGTCTCG       8274     T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM427  CIT       3'  CCTAGGGCTAGACCTA      69745    A  _
                                TAG TC AGTTCTAGG
                                ||| || |||||||||
```

```
                                ATC AG TCGGGATCC
                                  C  A
GAM427  CRLF1    3'  CCTAGAACCCCTGCCAGGG   16452     __   ATCA
                                CCC  GTAG   GTTCTAGG
                                |||  ||||   ||||||||
                                GGG  CGTC   CAAGATCC
                                  AC   CC__
GAM427  DMPK     3'  CCTAGAACTGTCTTCG      15323    T   T
                                CG AGA CAGTTCTAGG
                                || ||| ||||||||||
                                GC TCT GTCAAGATCC
                                 T   _
GAM427  EDAR     5'  CCCAGAACTGGATGG       42265      AGA       A
                                CCGT   TCAGTTCT GG
                                ||||   |||||||| ||
                                GGTA   GGTCAAGA CC
                                  ___       C
GAM427  EPHB3    5'  CCTAGAGCTGCCACGG      15455      AGAT
                                CCGT   CAGTTCTAGG
                                ||||   ||||||||||
                                GGCA   GTCGAGATCC
                                  CC__
GAM427  GAB2     3'  CCCAGAACTCTGGAGCTACAGG 24492    C    A ___     A
                                CC GTAG TC   AGTTCT GG
                                || |||| ||   |||||| ||
                                GG CATC AG   TCAAGA CC
                                 A   G  GTC     C
GAM427  GAB2     3'  CCCAGAACTCTGGAGCTACAGG 54449    C    A ___     A
                                CC GTAG TC   AGTTCT GG
                                || |||| ||   |||||| ||
                                GG CATC AG   TCAAGA CC
                                 A   G  GTC     C
GAM427  GRM6     3'  CCCAGGCTGGTCTCG       5929     T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _  C
GAM427  ITGAL    3'  CCCAGAACTGGACTCAGG     9389     GT  A       A
                                CC  AG TCAGTTCT GG
                                ||  || |||||||| ||
                                GG  TC GGTCAAGA CC
                                 AC  A       C
GAM427  MIPOL1   5'  CCCAGACTGGTCTCG       77066    T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCA GA CC
                                 _       _  C
GAM427  MTR      3'  CCTAAAATTGATCTATGG     4208             C
                                CCGTAGATCAGTT TAGG
                                |||||||||||| ||||
```

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                                GGTATCTAGTTAA ATCC
                                      A
GAM427  NGFR    3'  CCTAGAATCAGCCTAGGGGT  10224     G  ATCA
                                ACCC TAG   GTTCTAGG
                                |||| |||   ||||||||
                                TGGG ATC   TAAGATCC
                                  G  CGAC
GAM427  RFXANK  3'  CCCAGAACTGACTTCAAAGG  13561    GT___ A      A
                                CC    AG TCAGTTCT GG
                                ||    || |||||||| ||
                                GG    TC AGTCAAGA CC
                                 AAACT _       C
GAM427  RFXANK  3'  CCCAGAACTGACTTCAAAGG  56239    GT___ A      A
                                CC    AG TCAGTTCT GG
                                ||    || |||||||| ||
                                GG    TC AGTCAAGA CC
                                 AAACT _       C
GAM427  SLC3A2  5'  CCCAGACTGGTCTCG      9983     T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCA GA CC
                                 _       _ C
GAM427  TEM5    3'  CCAAGGTCTGACCTAGGGTT  51318      G   A   TT  A
                                AACCC TAG TCAG  CT GG
                                ||||| ||| ||||  || ||
                                TTGGG ATC AGTC  GA CC
                                  _  C    TG  A
GAM427  WHSC1   5'  CCCAGGCTGGTCTCG      29907    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM427  WHSC1   5'  CCCAGGCTGGTCTCG      55825    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM427  WHSC1   5'  CCCAGGCTGGTCTCG      55842    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM427  WHSC1   5'  CCCAGGCTGGTCTCG      23656    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM427  ZFX     5'  CCCAGGCTGGTCTCG      12717    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
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                                GC TCTGGTCG GA CC
                                 _      _ C
GAM427  ALDH9    5' CCTAGAACCGATCCCGTGG   5512    _ TA   A
                                CC CG  GATC GTTCTAGG
                                || ||  |||| ||||||||
                                GG GC  CTAG CAAGATCC
                                 T  C_   C
GAM427  C22orf19 3' CCCAGGCTGGTCTCG      13418    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM427  CBX6     3' CTAGAAACTAGGGTT      26612      G   ATCAG
                                AACCC TAG    TTCTAG
                                ||||| |||    ||||||
                                TTGGG ATC    AAGATC
                                   _  A____
GAM427  CHL1     3' CCTAGAGAACTGTCCAAGGGTT 21745      GTA  T   __
                                AACCC   GA CAGT  TCTAGG
                                |||||   || ||||  ||||||
                                TTGGG   CT GTCA  AGATCC
                                   AAC  _    AG
GAM427  CIP29    3' CCCAGGCTGGTCTCG      50402    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM427  FLJ10483 3' CCTAGAACCTCTACAGGT    36168    C    TCA
                                ACC GTAGA   GTTCTAGG
                                ||| |||||   ||||||||
                                TGG CATCT   CAAGATCC
                                  A    C__
GAM427  FLJ10815 3' CTGGAATCCACGGGT      36694       A   CAGT
                                ACCCGT GAT    TCTAG
                                |||||| |||    |||||
                                TGGGCA CTA    AGGTC
                                   C  _____
GAM427  FLJ10898 5' CCCAGAGGTAGATCGACAGGTT 59427     C  A   AG_   A
                                AACC GT GATC   TTCT GG
                                |||| || ||||   |||| ||
                                TTGG CA CTAG   GAGA CC
                                  A  G    ATG    C
GAM427  FLJ11715 3' CCCAGGCTGGTCTCG      44669    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM427  FLJ12448 3' CCTAGAACTGTCTGAGG     43176    G   T
                                CC TAGA CAGTTCTAGG
                                || |||| ||||||||||
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                                GG GTCT GTCAAGATCC
                                 A   _
GAM427  FLJ20147  3' CCCAGACTGGTCTCG      34637    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCA GA CC
                                 _      _  C
GAM427  FLJ30532  3' CCTCAGATGATCTAC      58543        GT  _
                                GTAGATCA  TCT AGG
                                ||||||||  ||| |||
                                CATCTAGT  AGA TCC
                                     __   C
GAM427  FLJ32334  3' CCCAGGCTGGTCTCG      57981    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _  C
GAM427  KIAA0205  3' CCTGAATAATCTATGGGTT   29579          CA   T
                                AACCCGTAGAT  GTTC AGG
                                ||||||||||  |||| |||
                                TTGGGTATCTA  TAAG TCC
                                      A_   _
GAM427  KIAA0268  3' CCCAGAACTGAAGATGG     70001      AGA      A
                                CCGT   TCAGTTCT GG
                                ||||   |||||||| ||
                                GGTA   AGTCAAGA CC
                                  GA_      C
GAM427  KIAA0318  3' CCTACGTCATCTATGGGTT   68950          CAGTTC
                                AACCCGTAGAT     TAGG
                                ||||||||||     ||||
                                TTGGGTATCTA     ATCC
                                      CTGC__
GAM427  KIAA0552  3' CCTAGAACCTGGGCCTAGG   28311    G   A_   _
                                CC TAG  TCAG TTCTAGG
                                || |||  |||| |||||||
                                GG ATC  GGTC AAGATCC
                                 _  CG   C
GAM427  KIAA0710  3' CCCAGAACTGGGAGATGG    29566     AGA      A
                                CCGT   TCAGTTCT GG
                                ||||   |||||||| ||
                                GGTA   GGTCAAGA CC
                                  GAG      C
GAM427  KIAA0907  3' CCCAGAACTGGTTGC       30172     G       A
                                GTA ATCAGTTCT GG
                                ||| ||||||||| ||
                                CGT TGGTCAAGA CC
                                  _       C
GAM427  KIAA1157  3' AGCTTATCTACGGGTT      72237          C
                                AACCCGTAGAT AGTT
                                |||||||||| ||||
```

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                                TTGGGCATCTA TCGA
                                       T
GAM427  KIAA1671  3'  CCCAGGCTGGTCTCG      65669    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM427  KIAA1715  3'  CCTGAGCATGATCTAC      68118        _   T
                                GTAGATCA GTTC AGG
                                |||||||| |||| |||
                                CATCTAGT CGAG TCC
                                     A   _
GAM427  KIAA1814  3'  CCTAGAGCAGTCTCCAGGG   70360    GT_   CA
                                CCC   AGAT  GTTCTAGG
                                |||   ||||  ||||||||
                                GGG   TCTG  CGAGATCC
                                  ACC    A_
GAM427  LIECG3    3'  CCCAGGCTGGTCTCG      87409    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM427  MGC10812  3'  CCTAGAACTTTTGCCAGT    48666    CC    TC
                                AC  GTAGA  AGTTCTAGG
                                ||  |||||  |||||||||
                                TG  CGTTT  TCAAGATCC
                                 AC    __
GAM427  PELI1     5'  CCCAGGCTGGTCTCG      40258    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM427  PGGT1B    5'  AGTGCTGATCTAGGG       17230    G       T
                                CCC TAGATCAGT CT
                                ||| ||||||||| ||
                                GGG ATCTAGTCG GA
                                  _       T
GAM427  PIP3-E    3'  CCTAGAACTGGGAGATG     66803    AGA
                                CGT   TCAGTTCTAGG
                                |||   ||||||||||
                                GTA   GGTCAAGATCC
                                  GAG
GAM427  PIP5K2B   3'  CCTCAGAACTGAGCCACAGG   13070    C  AGA      _
                                CC GT   TCAGTTCT AGG
                                || ||   |||||||| |||
                                GG CA   AGTCAAGA TCC
                                 A  CCG       C
GAM427  PTDSS1    3'  CCTAGAACTGAGAGGG      28571    GTAGA
                                CCC    TCAGTTCTAGG
                                |||    ||||||||||
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                                GGG    AGTCAAGATCC
                                  AG___
GAM427  PYPAF3   3'  CCTGGGATCGCTCTACG    57539      TCA
                                CGTAGA  GTTCTAGG
                                ||||||  ||||||||
                                GCATCT  TAGGGTCC
                                   CGC
GAM427  SDS3     3'  CCCAGAGGCTGATCTGC    69226        _  A
                                GTAGATCAGT TCT GG
                                |||||||||| ||| ||
                                CGTCTAGTCG AGA CC
                                      G  C
GAM427  SRF      3'  CCCAGAACTGGCTGGG     11943    GT  A     A
                                CCC  AG TCAGTTCT GG
                                |||  || |||||||| ||
                                GGG  TC GGTCAAGA CC
                                  __ _      C
GAM427  TRIM2    5'  CCCAGTTGTCTGCGGG     30941       T  TT  A
                                CCCGTAGA CAG  CT GG
                                |||||||| |||  || ||
                                GGGCGTCT GTT  GA CC
                                    _  __ C
GAM427  TSPEAR   3'  CCTAGGGCATCCCGGG     58719     TA  CA
                                CCCG  GAT  GTTCTAGG
                                ||||  |||  ||||||||
                                GGGC  CTA  CGGGATCC
                                  C_  __
GAM427  LOC113026 3'  CCCAGGCTGGTCTCG      55899    T     T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM427  LOC125144 3'  CCCAGGCTGGTCTCAGG    74393    GT      T  A
                                CC  AGATCAGT CT GG
                                ||  |||||||| || ||
                                GG  TCTGGTCG GA CC
                                 AC       _ C
GAM427  LOC126549 5'  CCTAGAACTGGCTGC      75708     A
                                GTAG TCAGTTCTAGG
                                |||| ||||||||||
                                CGTC GGTCAAGATCC
                                  _
GAM427  LOC126661 3'  CCCAGGCTGGTCTCG      74547    T     T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM427  LOC127702 3'  CCTGGGACACCTACAGG    75458    C   ATCA
                                CC GTAG   GTTCTAGG
                                || ||||   ||||||||
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                                GG CATC    CAGGGTCC
                                 A    CA__
GAM427   LOC143920 3'  CCCAGAGTCCTATCTAGGGT   76624      G     C __    A
                                ACCC TAGAT AG  TTCT GG
                                |||| ||||| ||  |||| ||
                                TGGG ATCTA TC  GAGA CC
                                  _    _ CT    C
GAM427   LOC145725 3'  CCCAGGCTGGTCTCG       77403     T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM427   LOC145732 3'  CCCAGGCTGGTCTCG       77425     T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM427   LOC146733 3'  CCTGGCTTGATCTACAGGT    83759     C        TT
                                ACC GTAGATCAG  CTAGG
                                ||| |||||||||  |||||
                                TGG CATCTAGTT  GGTCC
                                  A        C_
GAM427   LOC154877 3'  CCCAGGCTGGTCTCG       86286     T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM427   LOC154881 3'  CCCAGAACAGAAGAAGGGTT   81170       GTAGA  A     A
                                AACCC     TC GTTCT GG
                                |||||     || ||||| ||
                                TTGGG     AG CAAGA CC
                                   AAGA_  A     C
GAM427   LOC163998 5'  CCCAGAACTGGATGG       87053      AGA       A
                                CCGT   TCAGTTCT GG
                                ||||   |||||||| ||
                                GGTA   GGTCAAGA CC
                                  ___        C
GAM427   LOC170261 3'  CTGCAGCCTACGGGT       82582         ATCA   C
                                ACCCGTAG    GTT TAG
                                ||||||||    ||| |||
                                TGGGCATC    CGA GTC
                                    _____   C
GAM427   LOC196463 3'  CCTAGAGTGGGTCACG      87710     A    AG
                                CGT GATC  TTCTAGG
                                ||| ||||  |||||||
                                GCA CTGG  GAGATCC
                                  _    GT
GAM427   LOC196957 3'  CCCAGGCTGGTCTCG       87820     T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
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                                GC TCTGGTCG GA CC
                                 _      _ C
GAM427  LOC196961 3'  CCCAGGCTGGTCTCG      87841   T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM427  LOC197138 3'  CCCAGGCTGGTCTCG      87914   T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM427  LOC197423 5'  CCCAGAACTGATAGTGC     77857    G_       A
                                GTA  ATCAGTTCT GG
                                |||  ||||||||| ||
                                CGT  TAGTCAAGA CC
                                  GA       C
GAM427  LOC200268 3'  CCCAGGCTGGTCTCG      88681   T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM427  LOC200339 3'  AACTGATCTACAGGTT      90022     C
                                AACC GTAGATCAGTT
                                |||| ||||||||||
                                TTGG CATCTAGTCAA
                                  A
GAM427  LOC219653 3'  CCCAGAACTGAACACTAGGT  91292    CG   A__      A
                                ACC  TAG   TCAGTTCT GG
                                |||  |||   |||||||| ||
                                TGG  ATC   AGTCAAGA CC
                                  __   ACA       C
GAM427  LOC220565 5'  CCCAGAACTGATAGTGC     90748    G_       A
                                GTA  ATCAGTTCT GG
                                |||  ||||||||| ||
                                CGT  TAGTCAAGA CC
                                  GA       C
GAM427  LOC221895 3'  CCTATTGATATCTGCGG     92524        __    TCT
                                CCGTAGA  TCAGT   AGG
                                |||||||  |||||   |||
                                GGCGTCT  AGTTA   TCC
                                    AT    ___
GAM427  LOC221960 3'  CCCAGGCTGGTCTCG      91081   T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM427  LOC253228 3'  CTAGTGCTGACCTACGGG    95940        A    T
                                CCCGTAG TCAGT CTAG
                                ||||||| ||||| ||||
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                                GGGCATC AGTCG GATC
                                    C    T
GAM427  LOC254181 5'  CCCAGAACTGGCTCAGG     97583    GT  A      A
                                CC  AG TCAGTTCT GG
                                ||  || |||||||| ||
                                GG  TC GGTCAAGA CC
                                 AC  _       C
GAM427  LOC257051 3'  CTGCAGCCTACGGGT       96316        ATCA   C
                                ACCCGTAG    GTT TAG
                                ||||||||    ||| |||
                                TGGGCATC    CGA GTC
                                     _____  C
GAM427  LOC51226  3'  CCCAGAACTGACTCCTAAGG   33150    G   A__      A
                                CC TAG   TCAGTTCT GG
                                || |||   |||||||| ||
                                GG ATC   AGTCAAGA CC
                                 A  CTC       C
GAM427  LOC51622  3'  CCCAGGCTGGTCTCG       31566    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _  C
GAM427  LOC90139  3'  CCCAGAACTGAGGCTTGG     55402     T  A_      A
                                CCG AG  TCAGTTCT GG
                                ||| ||  |||||||| ||
                                GGT TC  AGTCAAGA CC
                                  _ GG       C
GAM427  LOC90979  3'  CCTGCAGGCTGATCCAGGG    64525     GTA      C_
                                CCC   GATCAGTT  TAGG
                                |||   ||||||||  ||||
                                GGG   CTAGTCGG  GTCC
                                  AC_       AC
GAM427  LOC91012  5'  CCCAGGCTGGTCTCGG      64639     T      T  A
                                CCG AGATCAGT CT GG
                                ||| |||||||| || ||
                                GGC TCTGGTCG GA CC
                                  _       _  C
GAM427  LOC92568  5'  CTGGAGATTCTACGGG      69772        TCAG
                                CCCGTAGA    TTCTAG
                                ||||||||    ||||||
                                GGGCATCT    GAGGTC
                                     TA__
GAM427  LOC93550  5'  CCTAGAACTGGAATAC      72584     GA
                                GTA  TCAGTTCTAGG
                                |||  ||||||||||
                                CAT  GGTCAAGATCC
                                  AA
GAM427  LOC93550  5'  GGTGCTGATCTCCGAGT     72586    C  T      T
                                AC CG AGATCAGT CT
                                || || |||||||| ||
```

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                                TG GC TCTAGTCG GG
                                 A  C       T
GAM428  ARF3    3'  CACTGCCCACTGGAGCCT    7998        CGA_   C
                                AGGCTCCA    GCAG TG
                                ||||||||    |||| ||
                                TCCGAGGT    CGTC AC
                                    CACC    _
GAM428  ARF3    3'  CACTGCCCACTGGAGCCT    7998        CGA_   C
                                AGGCTCCA    GCAG TG
                                ||||||||    |||| ||
                                TCCGAGGT    CGTC AC
                                    CACC    _
GAM428  ARVCF   3'  CTGCCGCATCTGCCTGGAGCCT 8027        CGA   C   AA
                                AGGCTCCA   GCAG TGC  CAG
                                ||||||||   |||| |||  |||
                                TCCGAGGT   CGTC ACG  GTC
                                    C__    T   CC
GAM428  ARVCF   3'  CTGCCGCATCTGCCTGGAGCCT 8027        CGA   C   AA
                                AGGCTCCA   GCAG TGC  CAG
                                ||||||||   |||| |||  |||
                                TCCGAGGT   CGTC ACG  GTC
                                    C__    T   CC
GAM428  B4GALT5 3'  CTGCCGTGGTCCTGCCGTGGAG 16498         A   __ TG AA
          CCT                   AGGCTCCACG GCAG  C  C  CAG
                                |||||||||| ||||  |  |  |||
                                TCCGAGGTGC CGTC  G  G  GTC
                                    _   CT GT CC
GAM428  B4GALT5 3'  CTGCCGTGGTCCTGCCGTGGAG 16498         A   __ TG AA
          CCT                   AGGCTCCACG GCAG  C  C  CAG
                                |||||||||| ||||  |  |  |||
                                TCCGAGGTGC CGTC  G  G  GTC
                                    _   CT GT CC
GAM428  CALM3   5'  CTGCTGCAGCTGCTGCCGCC  17742    TCCACG       A
                                GGC     AGCAGCTGCA CAG
                                |||     |||||||||| |||
                                CCG     TCGTCGACGT GTC
                                  CCG___        C
GAM428  CALM3   5'  CTGCTGCAGCTGCTGCCGCC  17742    TCCACG       A
                                GGC     AGCAGCTGCA CAG
                                |||     |||||||||| |||
                                CCG     TCGTCGACGT GTC
                                  CCG___        C
GAM428  CYP1A1  3'  TAGATGCTGATGGAGCCT    4947        CG   G
                                AGGCTCCA  AGCA CTG
                                ||||||||  |||| |||
                                TCCGAGGT  TCGT GAT
                                    AG    A
GAM428  CYP1A1  3'  TAGATGCTGATGGAGCCT    4947        CG   G
                                AGGCTCCA  AGCA CTG
                                ||||||||  |||| |||
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                              TCCGAGGT  TCGT GAT
                                  AG    A
GAM428  GFPT2    3'  CTGTTCTCTGACATCCGTGGAG 17576        AG___  CTGC
          CC                  GGCTCCACG    CAG   AACAG
                              |||||||||    |||   |||||
                              CCGAGGTGC    GTC   TTGTC
                                  CTACA  TC__
GAM428  GFPT2    3'  CTGTTCTCTGACATCCGTGGAG 17576        AG___  CTGC
          CC                  GGCTCCACG    CAG   AACAG
                              |||||||||    |||   |||||
                              CCGAGGTGC    GTC   TTGTC
                                  CTACA  TC__
GAM428  GJA4     3'  TTGCTGGCCATGGAGCCT   59370       CGA  AGCT
                              AGGCTCCA  GC   GCAA
                              ||||||||  ||   ||||
                              TCCGAGGT  CG   CGTT
                                  AC_  GT__
GAM428  GJA4     3'  TTGCTGGCCATGGAGCCT   59370       CGA  AGCT
                              AGGCTCCA  GC   GCAA
                              ||||||||  ||   ||||
                              TCCGAGGT  CG   CGTT
                                  AC_  GT__
GAM428  GLI2     5'  GTAGCTGCCCAAGGAGCC   47528      ACGA
                              GGCTCC   GCAGCTGC
                              ||||||   ||||||||
                              CCGAGG   CGTCGATG
                                 AACC
GAM428  GLI2     5'  GTAGCTGCCCAAGGAGCC   47528      ACGA
                              GGCTCC   GCAGCTGC
                              ||||||   ||||||||
                              CCGAGG   CGTCGATG
                                 AACC
GAM428  HDAC7A   3'  TGCCCACTCGGGGAGCCT   31213       A   CAGCT
                              AGGCTCC CGAG   GCA
                              ||||||| ||||   |||
                              TCCGAGG GCTC   CGT
                                  G   ACC__
GAM428  HDAC7A   3'  TGCCCACTCGGGGAGCCT   33454       A   CAGCT
                              AGGCTCC CGAG   GCA
                              ||||||| ||||   |||
                              TCCGAGG GCTC   CGT
                                  G   ACC__
GAM428  HDAC7A   3'  TGCCCACTCGGGGAGCCT   33454       A   CAGCT
                              AGGCTCC CGAG   GCA
                              ||||||| ||||   |||
                              TCCGAGG GCTC   CGT
                                  G   ACC__
GAM428  HDAC7A   3'  TGCCCACTCGGGGAGCCT   31213       A   CAGCT
                              AGGCTCC CGAG   GCA
                              ||||||| ||||   |||
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                                TCCGAGG GCTC    CGT
                                   G   ACC__
GAM428  HSD17B1  5' CACCTGCTTGTAAAGCCT   4682      CC      C
                                AGGCT  ACGAGCAG TG
                                |||||  |||||||| ||
                                TCCGA  TGTTCGTC AC
                                   AA      C
GAM428  HSD17B1  5' CACCTGCTTGTAAAGCCT   4682      CC      C
                                AGGCT  ACGAGCAG TG
                                |||||  |||||||| ||
                                TCCGA  TGTTCGTC AC
                                   AA      C
GAM428  LGALS3BP 5' GTTGCAGCTACCGCAGCC   69319     CCA  AGC
                                GGCT   CG   AGCTGCAAC
                                ||||   ||   |||||||||
                                CCGA   GC   TCGACGTTG
                                  C__  CA_
GAM428  LGALS3BP 5' GTTGCAGCTACCGCAGCC   69319     CCA  AGC
                                GGCT   CG   AGCTGCAAC
                                ||||   ||   |||||||||
                                CCGA   GC   TCGACGTTG
                                  C__  CA_
GAM428  NRL      5' GCCCTGCTCCATGGAGCCT   20515       C_    CT
                                AGGCTCCA  GAGCAG  GC
                                ||||||||  ||||||  ||
                                TCCGAGGT  CTCGTC  CG
                                    AC     C_
GAM428  NRL      5' GCCCTGCTCCATGGAGCCT   20515       C_    CT
                                AGGCTCCA  GAGCAG  GC
                                ||||||||  ||||||  ||
                                TCCGAGGT  CTCGTC  CG
                                    AC     C_
GAM428  SLC2A3   3' CTGTTCCCTCTGCTCCTGGAGC 22661       C     CTGC
           CT                    AGGCTCCA GAGCAG    AACAG
                                 ||||||||  ||||||   |||||
                                 TCCGAGGT CTCGTC    TTGTC
                                    C     TCCC
GAM428  SLC2A3   3' CTGTTCCCTCTGCTCCTGGAGC 22661       C     CTGC
           CT                    AGGCTCCA GAGCAG    AACAG
                                 ||||||||  ||||||   |||||
                                 TCCGAGGT CTCGTC    TTGTC
                                    C     TCCC
GAM428  SLC9A1   3' TGCCTGCTGTGGAGCC     70415       G    CT
                                GGCTCCAC AGCAG  GCA
                                ||||||||  |||||  |||
                                CCGAGGTG TCGTC  CGT
                                   _    __
GAM428  SLC9A1   3' TGCCTGCTGTGGAGCC     70415       G    CT
                                GGCTCCAC AGCAG  GCA
                                ||||||||  |||||  |||
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                                CCGAGGTG TCGTC  CGT
                                   _   __
GAM428  SRRM1    3' CTGCTGCAGCTGCTGTGACCC  19553    CTC  G       A
                                GG  CAC AGCAGCTGCA CAG
                                ||  ||| |||||||||| |||
                                CC  GTG TCGTCGACGT GTC
                                 CA_  _       C
GAM428  SRRM1    3' CTGCTGCAGCTGCTGTGACCC  19553    CTC  G       A
                                GG  CAC AGCAGCTGCA CAG
                                ||  ||| |||||||||| |||
                                CC  GTG TCGTCGACGT GTC
                                 CA_  _       C
GAM428  USP14    5' GCAGCTGCTCCTGGTCCC    17659    CT  C
                                GG  CCA GAGCAGCTGC
                                ||  ||| ||||||||||
                                CC  GGT CTCGTCGACG
                                 CT  C
GAM428  USP14    5' GCAGCTGCTCCTGGTCCC    17659    CT  C
                                GG  CCA GAGCAGCTGC
                                ||  ||| ||||||||||
                                CC  GGT CTCGTCGACG
                                 CT  C
GAM428  VWF      3' CTGCTGCAGCTGCATGGGTGCC 5093      T  A  A       A
           T                     AGGC CC CG GCAGCTGCA CAG
                                ||||  ||  ||  ||||||||| |||
                                TCCG GG GT CGTCGACGT GTC
                                  T  _  A       C
GAM428  VWF      3' CTGCTGCAGCTGCATGGGTGCC 5093      T  A  A       A
           T                     AGGC CC CG GCAGCTGCA CAG
                                ||||  ||  ||  ||||||||| |||
                                TCCG GG GT CGTCGACGT GTC
                                  T  _  A       C
GAM428  XPNPEP2  3' CTGCTACAGCTGCTCCCCTCCC 12682    CTCCAC       CAA
                                GG     GAGCAGCTG   CAG
                                ||     |||||||||   |||
                                CC     CTCGTCGAC   GTC
                                 CTCCC_       ATC
GAM428  XPNPEP2  3' CTGCTACAGCTGCTCCCCTCCC 12682    CTCCAC       CAA
                                GG     GAGCAGCTG   CAG
                                ||     |||||||||   |||
                                CC     CTCGTCGAC   GTC
                                 CTCCC_       ATC
GAM428  ZNFN2A1  3' GCTGCTCTTGGAGCCT      60739        C
                                AGGCTCCA GAGCAGC
                                |||||||| |||||||
                                TCCGAGGT CTCGTCG
                                     T
GAM428  ZNFN2A1  3' GCTGCTCTTGGAGCCT      60739        C
                                AGGCTCCA GAGCAGC
                                |||||||| |||||||
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                                TCCGAGGT CTCGTCG
                                     T
GAM428  AIP     3'  TGCTGCAGCTGCCAGCC     14280      CCACGA       A
                                GGCT     GCAGCTGCA CA
                                ||||     ||||||||| ||
                                CCGA     CGTCGACGT GT
                                  C_____       C
GAM428  AIP     3'  TGCTGCAGCTGCCAGCC     14280      CCACGA       A
                                GGCT     GCAGCTGCA CA
                                ||||     ||||||||| ||
                                CCGA     CGTCGACGT GT
                                  C_____       C
GAM428  ARHGEF3  5'  GCCGCCCGGCATCGTGGAGCT  38955          _ A__  T
                                GGCTCCACGA GC   GC GC
                                |||||||||| ||   || ||
                                TCGAGGTGCT CG   CG CG
                                      A  GCC  C
GAM428  ARHGEF3  5'  GCCGCCCGGCATCGTGGAGCT  38955          _ A__  T
                                GGCTCCACGA GC   GC GC
                                |||||||||| ||   || ||
                                TCGAGGTGCT CG   CG CG
                                      A  GCC  C
GAM428  C14orf4  5'  GCTGCCCGGGCGGTGGAGCC   67339         _____ A
                                GGCTCCAC    G GCAGC
                                ||||||||    | |||||
                                CCGAGGTG    C CGTCG
                                     GCGGG C
GAM428  C14orf4  5'  GCTGCCCGGGCGGTGGAGCC   67339         _____ A
                                GGCTCCAC    G GCAGC
                                ||||||||    | |||||
                                CCGAGGTG    C CGTCG
                                     GCGGG C
GAM428  C8orf2   3'  CTGCTGCAGCTGCCCCACCCC  23160    CTCCACGA       A
                                GG       GCAGCTGCA CAG
                                ||       ||||||||| |||
                                CC       CGTCGACGT GTC
                                 CCACCC__       C
GAM428  C8orf2   3'  CTGCTGCAGCTGCCCCACCCC  23160    CTCCACGA       A
                                GG       GCAGCTGCA CAG
                                ||       ||||||||| |||
                                CC       CGTCGACGT GTC
                                 CCACCC__       C
GAM428  Dlc2     5'  CTGCTGCAGCTGCAGGAGGAGC 54759       ACGA       A
          C                      GGCTCC    GCAGCTGCA CAG
                                 ||||||    ||||||||| |||
                                 CCGAGG    CGTCGACGT GTC
                                    AGGA       C
GAM428  Dlc2     5'  CTGCTGCAGCTGCAGGAGGAGC 54759       ACGA       A
          C                      GGCTCC    GCAGCTGCA CAG
                                 ||||||    ||||||||| |||
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                                CCGAGG   CGTCGACGT GTC
                                   AGGA       C
GAM428  FBXO27   3' TGCAGCTGCTGCTT      74515     TCCACG
                                AGGC     AGCAGCTGCA
                                ||||     ||||||||||
                                TTCG     TCGTCGACGT
                                  _______
GAM428  FBXO27   3' TGCAGCTGCTGCTT      74515     TCCACG
                                AGGC     AGCAGCTGCA
                                ||||     ||||||||||
                                TTCG     TCGTCGACGT
                                  _______
GAM428  FLJ10898 5' GCAGCTGCTGCAGCC      59435     C  CGA
                                GGCT CA   GCAGCTGC
                                |||| ||   ||||||||
                                CCGA GT   CGTCGACG
                                  C  ___
GAM428  FLJ10898 5' GCAGCTGCTGCAGCC      59435     C  CGA
                                GGCT CA   GCAGCTGC
                                |||| ||   ||||||||
                                CCGA GT   CGTCGACG
                                  C  ___
GAM428  FLJ11710 3' TGCAGACGTGGAGCT      45834        AGCAG
                                GGCTCCACG    CTGCA
                                |||||||||    |||||
                                TCGAGGTGC    GACGT
                                     A____
GAM428  FLJ11710 3' TGCAGACGTGGAGCT      45834        AGCAG
                                GGCTCCACG    CTGCA
                                |||||||||    |||||
                                TCGAGGTGC    GACGT
                                     A____
GAM428  FLJ13456 5' GCCGCTCGCCGGAGCCT    65942       A_    A
                                AGGCTCC  CGAGC GC
                                |||||||  ||||| ||
                                TCCGAGG  GCTCG CG
                                   CC    C
GAM428  FLJ13456 5' GCCGCTCGCCGGAGCCT    65942       A_    A
                                AGGCTCC  CGAGC GC
                                |||||||  ||||| ||
                                TCCGAGG  GCTCG CG
                                   CC    C
GAM428  FLJ20034 3' AGCTGCTCGTGCAGCC     34357     C
                                GGCT CACGAGCAGCT
                                |||| ||||||||||
                                CCGA GTGCTCGTCGA
                                  C
GAM428  FLJ20034 3' AGCTGCTCGTGCAGCC     34357     C
                                GGCT CACGAGCAGCT
                                |||| ||||||||||
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                                CCGA GTGCTCGTCGA
                                  C
GAM428  FLJ20275 3' TGCAGCTGCCGATGTAGCCT  34827     C _ A
                                AGGCT CA CG GCAGCTGCA
                                ||||| || || |||||||||
                                TCCGA GT GC CGTCGACGT
                                   T A _
GAM428  FLJ20275 3' TGCAGCTGCCGATGTAGCCT  34827     C _ A
                                AGGCT CA CG GCAGCTGCA
                                ||||| || || |||||||||
                                TCCGA GT GC CGTCGACGT
                                   T A _
GAM428  FLJ20507 3' CTGGGGCCTTCTCGTGGAACC 35284   C      C CT AA
                                GG TCCACGAG AG  GC  CAG
                                || ||||||| ||  ||  |||
                                CC AGGTGCTC TC  CG  GTC
                                 A       T __ GG
GAM428  FLJ20507 3' CTGGGGCCTTCTCGTGGAACC 35284   C      C CT AA
                                GG TCCACGAG AG  GC  CAG
                                || ||||||| ||  ||  |||
                                CC AGGTGCTC TC  CG  GTC
                                 A       T __ GG
GAM428  FLJ20507 3' CTGGGGCCTTCTCGTGGAACC 60219   C      C CT AA
                                GG TCCACGAG AG  GC  CAG
                                || ||||||| ||  ||  |||
                                CC AGGTGCTC TC  CG  GTC
                                 A       T __ GG
GAM428  FLJ20507 3' CTGGGGCCTTCTCGTGGAACC 60219   C      C CT AA
                                GG TCCACGAG AG  GC  CAG
                                || ||||||| ||  ||  |||
                                CC AGGTGCTC TC  CG  GTC
                                 A       T __ GG
GAM428  FLJ21865 3' TGCAGCTGCACAGCCT     42812      CCACGA
                                AGGCT     GCAGCTGCA
                                |||||     |||||||||
                                TCCGA     CGTCGACGT
                                   CA____
GAM428  FLJ21865 3' TGCAGCTGCACAGCCT     42812      CCACGA
                                AGGCT     GCAGCTGCA
                                |||||     |||||||||
                                TCCGA     CGTCGACGT
                                   CA____
GAM428  HEMK    3' TGCTGCAGCTGGGAGAGCT   32444      CACGAG      A
                                GGCTC     CAGCTGCA CA
                                |||||     |||||||| ||
                                TCGAG     GTCGACGT GT
                                   AGG___       C
GAM428  HEMK    3' TGCTGCAGCTGGGAGAGCT   32444      CACGAG      A
                                GGCTC     CAGCTGCA CA
                                |||||     |||||||| ||
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                                TCGAG     GTCGACGT GT
                                  AGG___      C
GAM428  JAM1     3' CAGCTGCTCAGGAGCCT    33750       AC
                                AGGCTCC  GAGCAGCTG
                                |||||||  |||||||||
                                TCCGAGG  CTCGTCGAC
                                   A_
GAM428  JAM1     3' CAGCTGCTCAGGAGCCT    33750       AC
                                AGGCTCC  GAGCAGCTG
                                |||||||  |||||||||
                                TCCGAGG  CTCGTCGAC
                                   A_
GAM428  JAM1     3' CAGCTGCTCAGGAGCCT    57888       AC
                                AGGCTCC  GAGCAGCTG
                                |||||||  |||||||||
                                TCCGAGG  CTCGTCGAC
                                   A_
GAM428  JAM1     3' CAGCTGCTCAGGAGCCT    57943       AC
                                AGGCTCC  GAGCAGCTG
                                |||||||  |||||||||
                                TCCGAGG  CTCGTCGAC
                                   A_
GAM428  JAM1     3' CAGCTGCTCAGGAGCCT    57943       AC
                                AGGCTCC  GAGCAGCTG
                                |||||||  |||||||||
                                TCCGAGG  CTCGTCGAC
                                   A_
GAM428  JAM1     3' CAGCTGCTCAGGAGCCT    57888       AC
                                AGGCTCC  GAGCAGCTG
                                |||||||  |||||||||
                                TCCGAGG  CTCGTCGAC
                                   A_
GAM428  JAM1     3' CAGCTGCTCAGGAGCCT    57917       AC
                                AGGCTCC  GAGCAGCTG
                                |||||||  |||||||||
                                TCCGAGG  CTCGTCGAC
                                   A_
GAM428  JAM1     3' CAGCTGCTCAGGAGCCT    57917       AC
                                AGGCTCC  GAGCAGCTG
                                |||||||  |||||||||
                                TCCGAGG  CTCGTCGAC
                                   A_
GAM428  KIAA0062 3' TAGCCACTGTGGAGCC     70244        G  CA
                                GGCTCCAC AG  GCTG
                                |||||||| ||  ||||
                                CCGAGGTG TC  CGAT
                                    _ AC
GAM428  KIAA0062 3' TAGCCACTGTGGAGCC     70244        G  CA
                                GGCTCCAC AG  GCTG
                                |||||||| ||  ||||
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                                CCGAGGTG TC  CGAT
                                    _ AC
GAM428  KIAA0140 3' TGCCGTCCACCCGTGGGGCC  27817       AGCA_ T
                                GGCTCCACG    GC GCA
                                |||||||||    || |||
                                CCGGGGTGC    TG CGT
                                     CCACC  C
GAM428  KIAA0140 3' TGCCGTCCACCCGTGGGGCC  27817       AGCA_ T
                                GGCTCCACG    GC GCA
                                |||||||||    || |||
                                CCGGGGTGC    TG CGT
                                     CCACC  C
GAM428  KIAA0828 3' TGCTGTTTCTCAGCAAAGCCT 81201     CCAC_  C  T
                                AGGCT    GAG AGC GCA
                                |||||    ||| ||| |||
                                TCCGA    CTC TTG CGT
                                   AACGA  T  T
GAM428  KIAA0828 3' TGCTGTTTCTCAGCAAAGCCT 81201     CCAC_  C  T
                                AGGCT    GAG AGC GCA
                                |||||    ||| ||| |||
                                TCCGA    CTC TTG CGT
                                   AACGA  T  T
GAM428  KIAA0982 3' CTGCCACAGCTGCTCACCTTGT 25848    TCCAC      CAA
          CT                  AGGC    GAGCAGCTG  CAG
                              ||||    |||||||||  |||
                              TCTG    CTCGTCGAC  GTC
                                TTCCA       ACC
GAM428  KIAA0982 3' CTGCCACAGCTGCTCACCTTGT 25848    TCCAC      CAA
          CT                  AGGC    GAGCAGCTG  CAG
                              ||||    |||||||||  |||
                              TCTG    CTCGTCGAC  GTC
                                TTCCA       ACC
GAM428  KIAA1068 5' CTGCTGCAGCTGAGAAGGAGCC 31031     ACGAG      A
                                GGCTCC    CAGCTGCA CAG
                                ||||||    |||||||| |||
                                CCGAGG    GTCGACGT GTC
                                   AAGA_      C
GAM428  KIAA1068 5' CTGCTGCAGCTGAGAAGGAGCC 31031     ACGAG      A
                                GGCTCC    CAGCTGCA CAG
                                ||||||    |||||||| |||
                                CCGAGG    GTCGACGT GTC
                                   AAGA_      C
GAM428  KIAA1157 5' TGCTGCAGCTGCAGCC     72252     CCACGA      A
                                GGCT     GCAGCTGCA CA
                                ||||     ||||||||| ||
                                CCGA     CGTCGACGT GT
                                  _______        C
GAM428  KIAA1157 5' TGCTGCAGCTGCAGCC     72252     CCACGA      A
                                GGCT     GCAGCTGCA CA
                                ||||     ||||||||| ||
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                                CCGA     CGTCGACGT GT
                                  _______        C
GAM428  KIAA1838  3'  CTGTTGCAGCTGCAAGGAGACC 64731    _    ACGA
                                GG CTCC    GCAGCTGCAACAG
                                || ||||    ||||||||||||||
                                CC GAGG    CGTCGACGTTGTC
                                 A    AA__
GAM428  KIAA1838  3'  CTGTTGCAGCTGCAAGGAGACC 64731    _    ACGA
                                GG CTCC    GCAGCTGCAACAG
                                || ||||    ||||||||||||||
                                CC GAGG    CGTCGACGTTGTC
                                 A    AA__
GAM428  KIAA1922  5'  CTGCTGCAGCTGGGAGGGGAGC 73627       ACGAG       A
          T                      GGCTCC     CAGCTGCA CAG
                                ||||||     |||||||| |||
                                TCGAGG     GTCGACGT GTC
                                   GGAGG       C
GAM428  KIAA1922  5'  CTGCTGCAGCTGGGAGGGGAGC 73627       ACGAG       A
          T                      GGCTCC     CAGCTGCA CAG
                                ||||||     |||||||| |||
                                TCGAGG     GTCGACGT GTC
                                   GGAGG       C
GAM428  MEF-2    3'  TTGCAGCTTGAGGGACCT    64399     CT  A  AGC
                                AGG  CC CG   AGCTGCAA
                                |||  || ||   ||||||||
                                TCC  GG GT   TCGACGTT
                                  AG  A  ___
GAM428  MEF-2    3'  TTGCAGCTTGAGGGACCT    64399     CT  A  AGC
                                AGG  CC CG   AGCTGCAA
                                |||  || ||   ||||||||
                                TCC  GG GT   TCGACGTT
                                  AG  A  ___
GAM428  MGC4415  3'  TGGCCGCCATGGAGCCT     48955        CGA  A
                                AGGCTCCA   GC GCTG
                                ||||||||   || ||||
                                TCCGAGGT   CG CGGT
                                     AC_  C
GAM428  MGC4415  3'  TGGCCGCCATGGAGCCT     48955        CGA  A
                                AGGCTCCA   GC GCTG
                                ||||||||   || ||||
                                TCCGAGGT   CG CGGT
                                     AC_  C
GAM428  SAE1     3'  GTTGCTCGGGAGCCT       18533        A
                                AGGCTCC CGAGCAGC
                                ||||||| ||||||||
                                TCCGAGG GCTCGTTG
                                        _
GAM428  SAE1     3'  GTTGCTCGGGAGCCT       18533        A
                                AGGCTCC CGAGCAGC
                                ||||||| ||||||||
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                                TCCGAGG GCTCGTTG
                                   _
GAM428  SHANK3   3' TGCAGCTGCCCAGTCT     65505      CCACGA
                                AGGCT     GCAGCTGCA
                                |||||     |||||||||
                                TCTGA     CGTCGACGT
                                  CC_____
GAM428  SHANK3   3' TGCAGCTGCCCAGTCT     65505      CCACGA
                                AGGCT     GCAGCTGCA
                                |||||     |||||||||
                                TCTGA     CGTCGACGT
                                  CC_____
GAM428  TP53TG3  3' CTGGGAGCTGCTGTGGAGCCT  31104        G     GCAA
                                AGGCTCCAC AGCAGCT   CAG
                                ||||||||| |||||||   |||
                                TCCGAGGTG TCGTCGA   GTC
                                    _     GG__
GAM428  TP53TG3  3' CTGGGAGCTGCTGTGGAGCCT  31104        G     GCAA
                                AGGCTCCAC AGCAGCT   CAG
                                ||||||||| |||||||   |||
                                TCCGAGGTG TCGTCGA   GTC
                                    _     GG__
GAM428  VAV3     3' TGTTGCATTTCATGGGCCT   20367     T  C  CAGC
                                AGGC CCA GAG   TGCAACA
                                |||| ||| |||   |||||||
                                TCCG GGT CTT   ACGTTGT
                                  _  A  T___
GAM428  VAV3     3' TGTTGCATTTCATGGGCCT   20367     T  C  CAGC
                                AGGC CCA GAG   TGCAACA
                                |||| ||| |||   |||||||
                                TCCG GGT CTT   ACGTTGT
                                  _  A  T___
GAM428  ZDHHC5   3' TGGCCCCTTGGAGCCT     91563       CG  CA
                                AGGCTCCA  AG  GCTG
                                ||||||||  ||  ||||
                                TCCGAGGT  TC  CGGT
                                    __  CC
GAM428  ZDHHC5   3' TGGCCCCTTGGAGCCT     91563       CG  CA
                                AGGCTCCA  AG  GCTG
                                ||||||||  ||  ||||
                                TCCGAGGT  TC  CGGT
                                    __  CC
GAM428  ZIN      3' TGTTTGCCATGGAGCCT    25495       CGA   CT
                                AGGCTCCA   GCAG  GCA
                                ||||||||   ||||  |||
                                TCCGAGGT   CGTT  TGT
                                   AC_   __
GAM428  ZIN      3' TGTTTGCCATGGAGCCT    25495       CGA   CT
                                AGGCTCCA   GCAG  GCA
                                ||||||||   ||||  |||
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                                TCCGAGGT  CGTT  TGT
                                   AC_   __
GAM428  ZNF304   5' GCGGCTCTCGTGGAACCT   40315    C      C
                                AGG TCCACGAG AGCTGC
                                ||| |||||||| ||||||
                                TCC AGGTGCTC TCGGCG
                                  A      _
GAM428  ZNF304   5' GCGGCTCTCGTGGAACCT   40315    C      C
                                AGG TCCACGAG AGCTGC
                                ||| |||||||| ||||||
                                TCC AGGTGCTC TCGGCG
                                  A      _
GAM428  LOC125268 3' TGCCCCTGCCCAGTGGAGCCT 76081        GA_   CT
                                AGGCTCCAC  GCAG  GCA
                                |||||||||  ||||  |||
                                TCCGAGGTG  CGTC  CGT
                                     ACC   CC
GAM428  LOC125268 3' TGCCCCTGCCCAGTGGAGCCT 76081        GA_   CT
                                AGGCTCCAC  GCAG  GCA
                                |||||||||  ||||  |||
                                TCCGAGGTG  CGTC  CGT
                                     ACC   CC
GAM428  LOC148443 3' CTGTTGCAACTCAAAGAGC   78856     CAC   CAGC
                                GCTC  GAG   TGCAACAG
                                ||||  |||   ||||||||
                                CGAG  CTC   ACGTTGTC
                                  AAA  A___
GAM428  LOC148443 3' CTGTTGCAACTCAAAGAGC   78856     CAC   CAGC
                                GCTC  GAG   TGCAACAG
                                ||||  |||   ||||||||
                                CGAG  CTC   ACGTTGTC
                                  AAA  A___
GAM428  LOC150157 5' CTGCACAGCTGCTCCCAGAGCC 84877       CAC       CAA
           T                     AGGCTC  GAGCAGCTG  CAG
                                ||||||  |||||||||  |||
                                TCCGAG  CTCGTCGAC  GTC
                                   ACC       AC_
GAM428  LOC150157 5' CTGCACAGCTGCTCCCAGAGCC 84877       CAC       CAA
           T                     AGGCTC  GAGCAGCTG  CAG
                                ||||||  |||||||||  |||
                                TCCGAG  CTCGTCGAC  GTC
                                   ACC       AC_
GAM428  LOC150984 5' TGCTGCAGCTGCAGCC     60371     CCACGA       A
                                GGCT     GCAGCTGCA CA
                                ||||     ||||||||| ||
                                CCGA     CGTCGACGT GT
                                  _______        C
GAM428  LOC150984 5' TGCTGCAGCTGCAGCC     60371     CCACGA       A
                                GGCT     GCAGCTGCA CA
                                ||||     ||||||||| ||
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                                CCGA     CGTCGACGT GT
                                  _______        C
GAM428  LOC161247 5'  GCAGCTGCCTGGCAGCC     82267      _  CGA
                                GGCT CCA   GCAGCTGC
                                |||| |||   ||||||||
                                CCGA GGT   CGTCGACG
                                  C  C__
GAM428  LOC161247 5'  GCAGCTGCCTGGCAGCC     82267      _  CGA
                                GGCT CCA   GCAGCTGC
                                |||| |||   ||||||||
                                CCGA GGT   CGTCGACG
                                  C  C__
GAM428  LOC166034 5'  TTGCAGCTGAAGAGCCT     87258       CACGAG
                                AGGCTC     CAGCTGCAA
                                ||||||     |||||||||
                                TCCGAG     GTCGACGTT
                                   AA____
GAM428  LOC166034 5'  TTGCAGCTGAAGAGCCT     87258       CACGAG
                                AGGCTC     CAGCTGCAA
                                ||||||     |||||||||
                                TCCGAG     GTCGACGTT
                                   AA____
GAM428  LOC166842 5'  TGCTGCAGCTGAGGGAGCT    82666       ACGAG       A
                                GGCTCC     CAGCTGCA CA
                                ||||||     |||||||| ||
                                TCGAGG     GTCGACGT GT
                                   GA___       C
GAM428  LOC166842 5'  TGCTGCAGCTGAGGGAGCT    82666       ACGAG       A
                                GGCTCC     CAGCTGCA CA
                                ||||||     |||||||| ||
                                TCGAGG     GTCGACGT GT
                                   GA___       C
GAM428  LOC196890 5'  CTGCACAGCTGCTCCCAGAGCC 89647       CAC       CAA
          T                     AGGCTC   GAGCAGCTG   CAG
                                ||||||   |||||||||   |||
                                TCCGAG   CTCGTCGAC   GTC
                                   ACC        AC_
GAM428  LOC196890 5'  CTGCACAGCTGCTCCCAGAGCC 89647       CAC       CAA
          T                     AGGCTC   GAGCAGCTG   CAG
                                ||||||   |||||||||   |||
                                TCCGAG   CTCGTCGAC   GTC
                                   ACC        AC_
GAM428  LOC200471 5'  GCAGCTGTGGAACCT      90054     C   ACGA
                                AGG TCC    GCAGCTGC
                                ||| |||    ||||||||
                                TCC AGG    TGTCGACG
                                  A  _____
GAM428  LOC200471 5'  GCAGCTGTGGAACCT      90054     C   ACGA
                                AGG TCC    GCAGCTGC
                                ||| |||    ||||||||
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                                TCC AGG    TGTCGACG
                                  A  _____
GAM428  LOC201115 5'  GCTGCTCGTGGGCCT       88106      T
                                AGGC CCACGAGCAGC
                                |||| ||||||||||
                                TCCG GGTGCTCGTCG
                                  _
GAM428  LOC201115 5'  GCTGCTCGTGGGCCT       88106      T
                                AGGC CCACGAGCAGC
                                |||| ||||||||||
                                TCCG GGTGCTCGTCG
                                  _
GAM428  LOC204970 3'  GTGCAGCTGCAGGCT       89415      CCACGA       A
                                GGCT     GCAGCTGCA C
                                ||||     ||||||||| |
                                TCGG     CGTCGACGT G
                                  A_____        C
GAM428  LOC204970 3'  GTGCAGCTGCAGGCT       89415      CCACGA       A
                                GGCT     GCAGCTGCA C
                                ||||     ||||||||| |
                                TCGG     CGTCGACGT G
                                  A_____        C
GAM428  LOC219513 3'  TGCGGCTGCTCACAGAGC    94335      CAC
                                GCTC   GAGCAGCTGCA
                                ||||   ||||||||||
                                CGAG   CTCGTCGGCGT
                                  ACA
GAM428  LOC219513 3'  TGCGGCTGCTCACAGAGC    94335      CAC
                                GCTC   GAGCAGCTGCA
                                ||||   ||||||||||
                                CGAG   CTCGTCGGCGT
                                  ACA
GAM428  LOC256848 5'  TGCTGCGGCTGCGGAACC    97515    C   ACGA       A
                                GG TCC    GCAGCTGCA CA
                                || |||    ||||||||| ||
                                CC AGG    CGTCGGCGT GT
                                 A  _____        C
GAM428  LOC256848 5'  TGCTGCGGCTGCGGAACC    97515    C   ACGA       A
                                GG TCC    GCAGCTGCA CA
                                || |||    ||||||||| ||
                                CC AGG    CGTCGGCGT GT
                                 A  _____        C
GAM428  LOC51083  5'  CTGTTGGAGCCCAGTGGAGCCT 31999          GAGCA   G
                                AGGCTCCAC     GCT CAACAG
                                |||||||||     ||| ||||||
                                TCCGAGGTG     CGA GTTGTC
                                     ACC__   G
GAM428  LOC51083  5'  CTGTTGGAGCCCAGTGGAGCCT 31999          GAGCA   G
                                AGGCTCCAC     GCT CAACAG
                                |||||||||     ||| ||||||
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                                TCCGAGGTG    CGA GTTGTC
                                     ACC__   G
GAM428  LOC51246  3' TTGCTCCCTGGAGCCT     33219       C_
                                AGGCTCCA  GAGCAG
                                ||||||||  ||||||
                                TCCGAGGT  CTCGTT
                                     CC
GAM428  LOC51246  3' TTGCTCCCTGGAGCCT     33219       C_
                                AGGCTCCA  GAGCAG
                                ||||||||  ||||||
                                TCCGAGGT  CTCGTT
                                     CC
GAM428  LOC91097  5' GCTGCGTGTGGAGCCT     64838        A
                                AGGCTCCACG GCAGC
                                |||||||||| |||||
                                TCCGAGGTGT CGTCG
                                      G
GAM428  LOC91097  5' GCTGCGTGTGGAGCCT     64838        A
                                AGGCTCCACG GCAGC
                                |||||||||| |||||
                                TCCGAGGTGT CGTCG
                                      G
GAM428  LOC93082  3' CTGTTGTGACTGGTGAAGCC  56443    C  GAG  CT
                                GGCT CAC   CAG  GCAACAG
                                |||| |||   |||  |||||||
                                CCGA GTG   GTC  TGTTGTC
                                  A  ___   AG
GAM428  LOC93082  3' CTGTTGTGACTGGTGAAGCC  56443    C  GAG  CT
                                GGCT CAC   CAG  GCAACAG
                                |||| |||   |||  |||||||
                                CCGA GTG   GTC  TGTTGTC
                                  A  ___   AG
GAM428  LOC93538  5' TGTTGCAGGTGATGGAACT   72564   C   CGAG  G
                                GG TCCA    CA CTGCAACA
                                || ||||    || ||||||||
                                TC AGGT    GT GACGTTGT
                                 A   A___  G
GAM428  LOC93538  5' TGTTGCAGGTGATGGAACT   72564   C   CGAG  G
                                GG TCCA    CA CTGCAACA
                                || ||||    || ||||||||
                                TC AGGT    GT GACGTTGT
                                 A   A___  G
GAM429  ADAR    3' CCCCTCTTTCCCTTCTGAGATT 31747     ACT  CT
                                AATC   GG  GGGAAAGAGGGG
                                ||||   ||  ||||||||||||
                                TTAG   TC  CCCTTTCTCCCC
                                  AG_  TT
GAM429  ADAR    3' CCCCTCTTTCCCTTCTGAGATT 6622      ACT  CT
                                AATC   GG  GGGAAAGAGGGG
                                ||||   ||  ||||||||||||
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                              TTAG  TC CCCTTTCTCCCC
                                AG_ TT
GAM429  ADAR    3' CCCCTCTTTCCCTTCTGAGATT 6622     ACT CT
                              AATC  GG GGGAAAGAGGGG
                              ||||  || ||||||||||||
                              TTAG  TC CCCTTTCTCCCC
                                AG_ TT
GAM429  ADAR    3' CCCCTCTTTCCCTTCTGAGATT 31757    ACT CT
                              AATC  GG GGGAAAGAGGGG
                              ||||  || ||||||||||||
                              TTAG  TC CCCTTTCTCCCC
                                AG_ TT
GAM429  ADAR    3' CCCCTCTTTCCCTTCTGAGATT 31757    ACT CT
                              AATC  GG GGGAAAGAGGGG
                              ||||  || ||||||||||||
                              TTAG  TC CCCTTTCTCCCC
                                AG_ TT
GAM429  ADAR    3' CCCCTCTTTCCCTTCTGAGATT 31747    ACT CT
                              AATC  GG GGGAAAGAGGGG
                              ||||  || ||||||||||||
                              TTAG  TC CCCTTTCTCCCC
                                AG_ TT
GAM429  BAT3    3' CCCCTCTTCCTTCACAGT   54779    GCT  A
                              ACTG  GGGAA GAGGGG
                              ||||  ||||| ||||||
                              TGAC  TCCTT CTCCCC
                                ACT   _
GAM429  BAT3    3' CCCCTCTTCCTTCACAGT   54779    GCT  A
                              ACTG  GGGAA GAGGGG
                              ||||  ||||| ||||||
                              TGAC  TCCTT CTCCCC
                                ACT   _
GAM429  BAT3    3' CCCCTCTTCCTTCACAGT   16159    GCT  A
                              ACTG  GGGAA GAGGGG
                              ||||  ||||| ||||||
                              TGAC  TCCTT CTCCCC
                                ACT   _
GAM429  BAT3    3' CCCCTCTTCCTTCACAGT   54782    GCT  A
                              ACTG  GGGAA GAGGGG
                              ||||  ||||| ||||||
                              TGAC  TCCTT CTCCCC
                                ACT   _
GAM429  BAT3    3' CCCCTCTTCCTTCACAGT   54782    GCT  A
                              ACTG  GGGAA GAGGGG
                              ||||  ||||| ||||||
                              TGAC  TCCTT CTCCCC
                                ACT   _
GAM429  BAT3    3' CCCCTCTTCCTTCACAGT   16159    GCT  A
                              ACTG  GGGAA GAGGGG
                              ||||  ||||| ||||||
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                                TGAC   TCCTT CTCCCC
                                  ACT    _
GAM429  CAPN1    3'  CCCCTCTCCTCCCAGCCA    17749        A_
                                TGGCTGGGA  AGAGGGG
                                |||||||||  |||||||
                                ACCGACCCT  TCTCCCC
                                     CC
GAM429  CAPN1    3'  CCCCTCTCCTCCCAGCCA    17749        A_
                                TGGCTGGGA  AGAGGGG
                                |||||||||  |||||||
                                ACCGACCCT  TCTCCCC
                                     CC
GAM429  CASQ1    5'  CCCCTCCCTACCCCAGCTA   6929         AAA__
                                TGGCTGGG    GAGGGG
                                ||||||||    ||||||
                                ATCGACCC    CTCCCC
                                     CATCC
GAM429  CASQ1    5'  CCCCTCCCTACCCCAGCTA   6929         AAA__
                                TGGCTGGG    GAGGGG
                                ||||||||    ||||||
                                ATCGACCC    CTCCCC
                                     CATCC
GAM429  CLTC     3'  CCCCTCTTTCTTTAAAG     16779    GGCT
                                CT   GGGAAAGAGGGG
                                ||   ||||||||||||
                                GA   TTCTTTCTCCCC
                                 AAT_
GAM429  CLTC     3'  CCCCTCTTTCTTTAAAG     16779    GGCT
                                CT   GGGAAAGAGGGG
                                ||   ||||||||||||
                                GA   TTCTTTCTCCCC
                                 AAT_
GAM429  CORO2B   3'  CCCCTCTTCCCTCAGC      64569     _ A
                                GCTG GG AAGAGGGG
                                |||| || ||||||||
                                CGAC CC TTCTCCCC
                                  T  C
GAM429  CORO2B   3'  CCCCTCTTCCCTCAGC      64569     _ A
                                GCTG GG AAGAGGGG
                                |||| || ||||||||
                                CGAC CC TTCTCCCC
                                  T  C
GAM429  DLX4     3'  CCCACCCACCCAGCGATT    8653      A   C   AAAGA
                                AATC CTGG TGGG    GGG
                                |||| |||| ||||    |||
                                TTAG GACC ACCC    CCC
                                  C   C   A____
GAM429  DLX4     3'  CCCACCCACCCAGCGATT    56276     A   C   AAAGA
                                AATC CTGG TGGG    GGG
                                |||| |||| ||||    |||
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                                TTAG GACC ACCC    CCC
                                  C   C   A____
GAM429  DLX4    3'  CCCACCCACCCAGCGATT   56276     A   C   AAAGA
                                AATC CTGG TGGG    GGG
                                |||| |||| ||||    |||
                                TTAG GACC ACCC    CCC
                                  C   C   A____
GAM429  DLX4    3'  CCCACCCACCCAGCGATT   8653      A   C   AAAGA
                                AATC CTGG TGGG    GGG
                                |||| |||| ||||    |||
                                TTAG GACC ACCC    CCC
                                  C   C   A____
GAM429  EGR3    3'  CCCCTCTTCCCCAGCT     59553       A
                                GGCTGGG AAGAGGGG
                                ||||||| ||||||||
                                TCGACCC TTCTCCCC
                                    C
GAM429  EGR3    3'  CCCCTCTTCCCCAGCT     59553       A
                                GGCTGGG AAGAGGGG
                                ||||||| ||||||||
                                TCGACCC TTCTCCCC
                                    C
GAM429  GA      5'  CCCCTCCTTCCCAGCCA    25173         A
                                TGGCTGGGAA GAGGGG
                                |||||||||| ||||||
                                ACCGACCCTT CTCCCC
                                     C
GAM429  GA      5'  CCCCTCCTTCCCAGCCA    25173         A
                                TGGCTGGGAA GAGGGG
                                |||||||||| ||||||
                                ACCGACCCTT CTCCCC
                                     C
GAM429  GALGT   3'  CCCCTCCTTTTTCCAGT    7615          __
                                GCTGGGAAA  GAGGGG
                                |||||||||  ||||||
                                TGACCTTTT  CTCCCC
                                     TC
GAM429  GALGT   3'  CCCCTCCTTTTTCCAGT    7615          __
                                GCTGGGAAA  GAGGGG
                                |||||||||  ||||||
                                TGACCTTTT  CTCCCC
                                     TC
GAM429  HD      3'  CCTCCCCCAGCCAGGA     9182    A       AAA
                                TC CTGGCTGGG   GAGG
                                || |||||||||   ||||
                                AG GACCGACCC   CTCC
                                 _       C__
GAM429  HD      3'  CCTCCCCCAGCCAGGA     9182    A       AAA
                                TC CTGGCTGGG   GAGG
                                || |||||||||   ||||
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                                AG GACCGACCC   CTCC
                                 _       C__
GAM429  HIP1    3'  CCCTCTTTGGGCAGTG      18058      G  GGG
                                CACTG CT   AAAGAGGG
                                ||||| ||   ||||||||
                                GTGAC GG   TTTCTCCC
                                  G  ___
GAM429  HIP1    3'  CCCTCTTTGGGCAGTG      18058      G  GGG
                                CACTG CT   AAAGAGGG
                                ||||| ||   ||||||||
                                GTGAC GG   TTTCTCCC
                                  G  ___
GAM429  ITGAL   3'  CCCCTCCTTCCTTGACCAGCAG 9390      A_   CT_    A
            AT                    ATC  CTGG   GGGAA GAGGGG
                                ||| ||||   ||||| ||||||
                                TAG  GACC   TCCTT CTCCCC
                                  AC    AGT    C
GAM429  ITGAL   3'  CCCCTCCTTCCTTGACCAGCAG 9390      A_   CT_    A
            AT                    ATC  CTGG   GGGAA GAGGGG
                                ||| ||||   ||||| ||||||
                                TAG  GACC   TCCTT CTCCCC
                                  AC    AGT    C
GAM429  LDB1    3'  CCCCTCCTCCCTGCTGCCA   13983      T___   AA
                                TGGC   GGGA  GAGGGG
                                ||||   ||||  ||||||
                                ACCG   CCCT  CTCCCC
                                  TCGT   C_
GAM429  LDB1    3'  CCCCTCCTCCCTGCTGCCA   13983      T___   AA
                                TGGC   GGGA  GAGGGG
                                ||||   ||||  ||||||
                                ACCG   CCCT  CTCCCC
                                  TCGT   C_
GAM429  MAG     3'  CCCCTCCTTCCCAGCT      54592        A
                                GGCTGGGAA GAGGGG
                                ||||||||| ||||||
                                TCGACCCTT CTCCCC
                                      C
GAM429  MAG     3'  CCCCTCCTTCCCAGCT      9880         A
                                GGCTGGGAA GAGGGG
                                ||||||||| ||||||
                                TCGACCCTT CTCCCC
                                      C
GAM429  MAG     3'  CCCCTCCTTCCCAGCT      9880         A
                                GGCTGGGAA GAGGGG
                                ||||||||| ||||||
                                TCGACCCTT CTCCCC
                                      C
GAM429  MAG     3'  CCCCTCCTTCCCAGCT      54592        A
                                GGCTGGGAA GAGGGG
                                ||||||||| ||||||
```

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                                TCGACCCTT CTCCCC
                                     C
GAM429  MAT1A    3'  CCCCCTTTCACAGGCAGCCAGT 90829        G____    A
                G                CACTGGCTG    GAAAG GGGG
                                 |||||||||    ||||| ||||
                                 GTGACCGAC    CTTTC CCCC
                                      GGACA   _
GAM429  MAT1A    3'  CCCCCTTTCACAGGCAGCCAGT 90829        G____    A
                G                CACTGGCTG    GAAAG GGGG
                                 |||||||||    ||||| ||||
                                 GTGACCGAC    CTTTC CCCC
                                      GGACA   _
GAM429  MAZ      3'  CCCCTCTTTTCCCACCA    73388    C    _
                                 TGG TGGGAAA GAGGGG
                                 ||| ||||||| ||||||
                                 ACC ACCCTTT CTCCCC
                                   _     T
GAM429  MAZ      3'  CCCCTCTTTTCCCACCA    73388    C    _
                                 TGG TGGGAAA GAGGGG
                                 ||| ||||||| ||||||
                                 ACC ACCCTTT CTCCCC
                                   _     T
GAM429  MFGE8    3'  TCCCTCTTTCCCACC      19813    C
                                 GG TGGGAAAGAGGGG
                                 || ||||||||||||
                                 CC ACCCTTTCTCCCT
                                  _
GAM429  MFGE8    3'  TCCCTCTTTCCCACC      19813    C
                                 GG TGGGAAAGAGGGG
                                 || ||||||||||||
                                 CC ACCCTTTCTCCCT
                                  _
GAM429  MYCL1    3'  CCCCTCTTCCCCAATGCT   18162    __   A
                                 GGC  TGGG AAGAGGGG
                                 |||  |||| ||||||||
                                 TCG  ACCC TTCTCCCC
                                   TA   C
GAM429  MYCL1    3'  CCCCTCTTCCCCAATGCT   18162    __   A
                                 GGC  TGGG AAGAGGGG
                                 |||  |||| ||||||||
                                 TCG  ACCC TTCTCCCC
                                   TA   C
GAM429  OTOF     3'  CCCTCTGCCCCAGCCAG    16640        AA
                                 CTGGCTGGG  AGAGGG
                                 |||||||||  ||||||
                                 GACCGACCC  TCTCCC
                                      CG
GAM429  OTOF     3'  CCCTCTGCCCCAGCCAG    16640        AA
                                 CTGGCTGGG  AGAGGG
                                 |||||||||  ||||||
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                                GACCGACCC  TCTCCC
                                     CG
GAM429  P23     3'  CCCCTCCTTCCCAGTCCCATGA 21716      CT _      A
             T                   ATCA  GG CTGGGAA GAGGGG
                                 ||||  || ||||||| ||||||
                                 TAGT  CC GACCCTT CTCCCC
                                   AC  T      C
GAM429  P23     3'  CCCCTCCTTCCCAGTCCCATGA 21716      CT _      A
             T                   ATCA  GG CTGGGAA GAGGGG
                                 ||||  || ||||||| ||||||
                                 TAGT  CC GACCCTT CTCCCC
                                   AC  T      C
GAM429  PACSIN1  3'  CCCCTCTCTGTGCCAGCGG   92256    A    TG   AA
                                 TC CTGGC  GGA  GAGGGG
                                 || |||||  |||  ||||||
                                 GG GACCG  TCT  CTCCCC
                                  C    TG  __
GAM429  PACSIN1  3'  CCCCTCTCTGTGCCAGCGG   92256    A    TG   AA
                                 TC CTGGC  GGA  GAGGGG
                                 || |||||  |||  ||||||
                                 GG GACCG  TCT  CTCCCC
                                  C    TG  __
GAM429  PCDH1    3'  CCCCTCCCCCAGCGCCGGCCAG 50562        GAAA____
                                 CTGGCTGG       GAGGGG
                                 ||||||||       ||||||
                                 GACCGGCC       CTCCCC
                                      GCGACCCC
GAM429  PCDH1    3'  CCCCTCCCCCAGCGCCGGCCAG 50562        GAAA____
                                 CTGGCTGG       GAGGGG
                                 ||||||||       ||||||
                                 GACCGGCC       CTCCCC
                                      GCGACCCC
GAM429  PLAC1    5'  CCCCTCTTCAGTTCCGGTGA   41420        __   GAA
                                 TCACTGG  CTGG   AGAGGGG
                                 |||||||  ||||   |||||||
                                 AGTGGCC  GACT   TCTCCCC
                                      TT   ___
GAM429  PLAC1    5'  CCCCTCTTCAGTTCCGGTGA   41420        __   GAA
                                 TCACTGG  CTGG   AGAGGGG
                                 |||||||  ||||   |||||||
                                 AGTGGCC  GACT   TCTCCCC
                                      TT   ___
GAM429  PXN      3'  CCCCCTTCCCCAGCCAG     11158         A  A
                                 CTGGCTGGG AAG GGGG
                                 |||||||||  ||| ||||
                                 GACCGACCC TTC CCCC
                                      C  _
GAM429  PXN      3'  CCCCCTTCCCCAGCCAG     11158         A  A
                                 CTGGCTGGG AAG GGGG
                                 |||||||||  ||| ||||
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                                GACCGACCC TTC CCCC
                                     C  _
GAM429  RAD50   5' CCCCTCTCTCCCGCTGTTGG  19193   CT  T   A
                                TCA  GGC GGGA AGAGGGG
                                |||  ||| |||| |||||||
                                GGT  TCG CCCT TCTCCCC
                                  TG  _   C
GAM429  RAD50   5' CCCCTCTCTCCCGCTGTTGG  19193   CT  T   A
                                TCA  GGC GGGA AGAGGGG
                                |||  ||| |||| |||||||
                                GGT  TCG CCCT TCTCCCC
                                  TG  _   C
GAM429  RAD50   5' CCCCTCTCTCCCGCTGTTGG  56007   CT  T   A
                                TCA  GGC GGGA AGAGGGG
                                |||  ||| |||| |||||||
                                GGT  TCG CCCT TCTCCCC
                                  TG  _   C
GAM429  RAD50   5' CCCCTCTCTCCCGCTGTTGG  56007   CT  T   A
                                TCA  GGC GGGA AGAGGGG
                                |||  ||| |||| |||||||
                                GGT  TCG CCCT TCTCCCC
                                  TG  _   C
GAM429  RAX     3' CCCCTCTTTCCCTGTC     25537    T
                                GGC GGGAAAGAGGGG
                                ||| ||||||||||||
                                CTG CCCTTTCTCCCC
                                  T
GAM429  RAX     3' CCCCTCTTTCCCTGTC     25537    T
                                GGC GGGAAAGAGGGG
                                ||| ||||||||||||
                                CTG CCCTTTCTCCCC
                                  T
GAM429  RFNG    3' CCCCTCTCCCAGCCCCTGGT  88173    CT     AA
                                ATCA  GGCTGGGA  GAGGGG
                                ||||  ||||||||  ||||||
                                TGGT  CCGACCCT  CTCCCC
                                  CC       __
GAM429  RFNG    3' CCCCTCTCCCAGCCCCTGGT  88173    CT     AA
                                ATCA  GGCTGGGA  GAGGGG
                                ||||  ||||||||  ||||||
                                TGGT  CCGACCCT  CTCCCC
                                  CC       __
GAM429  SHC1    3' CCCCTCCCTTGCTCAGTG    11646     _ T  AAA
                                CACTG GC GGG   GAGGGG
                                ||||| || |||   ||||||
                                GTGAC CG TCC   CTCCCC
                                  T T  ____
GAM429  SHC1    3' CCCCTCCCTTGCTCAGTG    11646     _ T  AAA
                                CACTG GC GGG   GAGGGG
                                ||||| || |||   ||||||
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                                GTGAC CG TCC   CTCCCC
                                  T  T  ____
GAM429  SIRT2    3'  CCCTCTTAACCAGCAGT     24261      G    GA
                                ACTG CTGG  AAGAGGG
                                |||| ||||  |||||||
                                TGAC GACC  TTCTCCC
                                  _    AA
GAM429  SIRT2    3'  CCCTCTTAACCAGCAGT     47591      G    GA
                                ACTG CTGG  AAGAGGG
                                |||| ||||  |||||||
                                TGAC GACC  TTCTCCC
                                  _    AA
GAM429  SIRT2    3'  CCCTCTTAACCAGCAGT     24261      G    GA
                                ACTG CTGG  AAGAGGG
                                |||| ||||  |||||||
                                TGAC GACC  TTCTCCC
                                  _    AA
GAM429  SIRT2    3'  CCCTCTTAACCAGCAGT     47591      G    GA
                                ACTG CTGG  AAGAGGG
                                |||| ||||  |||||||
                                TGAC GACC  TTCTCCC
                                  _    AA
GAM429  SOX10    5'  CCCCTCCCTCCCAGCC      22685        AA
                                GGCTGGGA  GAGGGG
                                ||||||||  ||||||
                                CCGACCCT  CTCCCC
                                     CC
GAM429  SOX10    5'  CCCCTCCCTCCCAGCC      22685        AA
                                GGCTGGGA  GAGGGG
                                ||||||||  ||||||
                                CCGACCCT  CTCCCC
                                     CC
GAM429  SPTBN2   3'  CCCCTCAGACCAGCCAGGA   22705    A      GAAA
                                TC CTGGCTGG   GAGGGG
                                || ||||||||   ||||||
                                AG GACCGACC   CTCCCC
                                  _      AGA_
GAM429  SPTBN2   3'  CCCCTCAGACCAGCCAGGA   22705    A      GAAA
                                TC CTGGCTGG   GAGGGG
                                || ||||||||   ||||||
                                AG GACCGACC   CTCCCC
                                  _      AGA_
GAM429  ST7      3'  CCCTCTTCCCCCACCA      41582    C    A_
                                TGG TGGG  AAGAGGG
                                ||| ||||  |||||||
                                ACC ACCC  TTCTCCC
                                  _    CC
GAM429  ST7      3'  CCCTCTTCCCCCACCA      41582    C    A_
                                TGG TGGG  AAGAGGG
                                ||| ||||  |||||||
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                                ACC ACCC  TTCTCCC
                                  _   CC
GAM429  TAGLN    3'  CCCCTCCCTCCCGGCT     59635        AA
                                GGCTGGGA  GAGGGG
                                ||||||||  ||||||
                                TCGGCCCT  CTCCCC
                                    CC
GAM429  TAGLN    3'  CCCCTCCCTCCCGGCT     59635        AA
                                GGCTGGGA  GAGGGG
                                ||||||||  ||||||
                                TCGGCCCT  CTCCCC
                                    CC
GAM429  TBXA2R   5'  CTGTTCCCAGCCAGT      6489          AG
                                ACTGGCTGGGAA  AG
                                ||||||||||||  ||
                                TGACCGACCCTT  TC
                                      G_
GAM429  TBXA2R   5'  CTGTTCCCAGCCAGT      6489          AG
                                ACTGGCTGGGAA  AG
                                ||||||||||||  ||
                                TGACCGACCCTT  TC
                                      G_
GAM429  TRH      3'  CCCCTCCCTCCCAGCC      23053        AA
                                GGCTGGGA  GAGGGG
                                ||||||||  ||||||
                                CCGACCCT  CTCCCC
                                    CC
GAM429  TRH      3'  CCCCTCCCTCCCAGCC      23053        AA
                                GGCTGGGA  GAGGGG
                                ||||||||  ||||||
                                CCGACCCT  CTCCCC
                                    CC
GAM429  TTYH1    3'  CCCCTCCTCCCGGCTGG     40321   TG     AA
                                C  GCTGGGA  GAGGGG
                                |  |||||||  ||||||
                                G  CGGCCCT  CTCCCC
                                 GT      C_
GAM429  TTYH1    3'  CCCCTCCTCCCGGCTGG     40321   TG     AA
                                C  GCTGGGA  GAGGGG
                                |  |||||||  ||||||
                                G  CGGCCCT  CTCCCC
                                 GT      C_
GAM429  TULP1    3'  CCCCTCCTCCCCGCGCCCCAGT 12431    __  _   AAA
                                ACT  GGC TGGG   GAGGGG
                                |||  ||| ||||   ||||||
                                TGA  CCG GCCC   CTCCCC
                                  CC   C    CTC
GAM429  TULP1    3'  CCCCTCCTCCCCGCGCCCCAGT 12431    __  _   AAA
                                ACT  GGC TGGG   GAGGGG
                                |||  ||| ||||   ||||||
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                                TGA  CCG GCCC   CTCCCC
                                  CC   C    CTC
GAM429  APPD     3'  CCCCGAAGCCCAGCCAGAGA  44215    A       AAAGA
                                TC CTGGCTGGG    GGGG
                                || |||||||||    ||||
                                AG GACCGACCC    CCCC
                                 A        GAAG_
GAM429  APPD     3'  CCCCGAAGCCCAGCCAGAGA  44215    A       AAAGA
                                TC CTGGCTGGG    GGGG
                                || |||||||||    ||||
                                AG GACCGACCC    CCCC
                                 A        GAAG_
GAM429  ARHGEF11 3'  CCCCTCTTTCTCCATAAG   28804    GGC  _
                                CT   TGG GAAAGAGGGG
                                ||   ||| ||||||||||
                                GA   ACC CTTTCTCCCC
                                 AT_   T
GAM429  ARHGEF11 3'  CCCCTCTTTCTCCATAAG   28804    GGC  _
                                CT   TGG GAAAGAGGGG
                                ||   ||| ||||||||||
                                GA   ACC CTTTCTCCCC
                                 AT_   T
GAM429  BRPF3    3'  CCCTCTCCCCAGGTAGT    92314     G    AA
                                ACTG CTGGG  AGAGGG
                                |||| |||||  ||||||
                                TGAT GACCC  TCTCCC
                                  G    C_
GAM429  BRPF3    3'  CCCTCTCCCCAGGTAGT    92314     G    AA
                                ACTG CTGGG  AGAGGG
                                |||| |||||  ||||||
                                TGAT GACCC  TCTCCC
                                  G    C_
GAM429  CECR7    5'  CCCCATCCAGCCAAAGA    79617    AC      AAAGA
                                TC  TGGCTGGG    GGGG
                                ||  ||||||||    ||||
                                AG  ACCGACCT    CCCC
                                 AA       A____
GAM429  CECR7    5'  CCCCATCCAGCCAAAGA    79617    AC      AAAGA
                                TC  TGGCTGGG    GGGG
                                ||  ||||||||    ||||
                                AG  ACCGACCT    CCCC
                                 AA       A____
GAM429  CNNM1    3'  CCCCTCTTCCCCAACA     39771    GC   A
                                TG  TGGG AAGAGGGG
                                ||  |||| ||||||||
                                AC  ACCC TTCTCCCC
                                 A_    C
GAM429  CNNM1    3'  CCCCTCTTCCCCAACA     39771    GC   A
                                TG  TGGG AAGAGGGG
                                ||  |||| ||||||||
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                                AC  ACCC TTCTCCCC
                                 A_   C
GAM429  CYP2S1   3'  CTCTCCCAGCCTGTGA     47615     T      AA
                                TCAC GGCTGGGA  GAG
                                |||| ||||||||  |||
                                AGTG CCGACCCT  CTC
                                  T      __
GAM429  CYP2S1   3'  CTCTCCCAGCCTGTGA     47615     T      AA
                                TCAC GGCTGGGA  GAG
                                |||| ||||||||  |||
                                AGTG CCGACCCT  CTC
                                  T      __
GAM429  DDR1     3'  CCCCTCCCTCAGGGAGCGAT  8723     A  GG    AAA
                                ATC CT  CTGGG   GAGGGG
                                |||  ||  |||||   ||||||
                                TAG GA  GACTC   CTCCCC
                                  C  GG    C__
GAM429  DDR1     3'  CCCCTCCCTCAGGGAGCGAT  25705    A  GG    AAA
                                ATC CT  CTGGG   GAGGGG
                                |||  ||  |||||   ||||||
                                TAG GA  GACTC   CTCCCC
                                  C  GG    C__
GAM429  DDR1     3'  CCCCTCCCTCAGGGAGCGAT  25696    A  GG    AAA
                                ATC CT  CTGGG   GAGGGG
                                |||  ||  |||||   ||||||
                                TAG GA  GACTC   CTCCCC
                                  C  GG    C__
GAM429  DDR1     3'  CCCCTCCCTCAGGGAGCGAT  25705    A  GG    AAA
                                ATC CT  CTGGG   GAGGGG
                                |||  ||  |||||   ||||||
                                TAG GA  GACTC   CTCCCC
                                  C  GG    C__
GAM429  DDR1     3'  CCCCTCCCTCAGGGAGCGAT  25696    A  GG    AAA
                                ATC CT  CTGGG   GAGGGG
                                |||  ||  |||||   ||||||
                                TAG GA  GACTC   CTCCCC
                                  C  GG    C__
GAM429  DDR1     3'  CCCCTCCCTCAGGGAGCGAT  8723     A  GG    AAA
                                ATC CT  CTGGG   GAGGGG
                                |||  ||  |||||   ||||||
                                TAG GA  GACTC   CTCCCC
                                  C  GG    C__
GAM429  DKFZp434J1015 3'  CCCCTCTCCCCCCAGCT    92633       AA_
                                GGCTGGG   AGAGGGG
                                |||||||   |||||||
                                TCGACCC   TCTCCCC
                                    CCC
GAM429  DKFZp434J1015 3'  CCCCTCTCCCCCCAGCT    92633       AA_
                                GGCTGGG   AGAGGGG
                                |||||||   |||||||
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                                TCGACCC  TCTCCCC
                                   CCC
GAM429  DKFZP564I1171 3'  CCCTGCCCAGTCAGTGA    71585          AAAG
                                TCACTGGCTGGG  AGGG
                                ||||||||||||  ||||
                                AGTGACTGACCC  TCCC
                                      G___
GAM429  DKFZP564I1171 3'  CCCTGCCCAGTCAGTGA    71585          AAAG
                                TCACTGGCTGGG  AGGG
                                ||||||||||||  ||||
                                AGTGACTGACCC  TCCC
                                      G___
GAM429  DKFZP564O1664 5'  CCCCTCTTTCCAAGAGAG   47936   GG  G
                                CT  CT GGAAAGAGGGG
                                ||  || ||||||||||
                                GA  GA CCTTTCTCCCC
                                 GA  A
GAM429  DKFZP564O1664 5'  CCCCTCTTTCCAAGAGAG   47936   GG  G
                                CT  CT GGAAAGAGGGG
                                ||  || ||||||||||
                                GA  GA CCTTTCTCCCC
                                 GA  A
GAM429  DMRTA2   3'  CCCCTCTTCGCCCAGC    60659      A_
                                GCTGGG  AAGAGGGG
                                ||||||  ||||||||
                                CGACCC  TTCTCCCC
                                   GC
GAM429  DMRTA2   3'  CCCCTCTTCGCCCAGC    60659      A_
                                GCTGGG  AAGAGGGG
                                ||||||  ||||||||
                                CGACCC  TTCTCCCC
                                   GC
GAM429  FLJ00024  3'  CCCCTCTCTTCCCAGC    63755       _
                                GCTGGGAA AGAGGGG
                                ||||||||| |||||||
                                CGACCCTT TCTCCCC
                                     C
GAM429  FLJ00024  3'  CCCCTCTCTTCCCAGC    63755       _
                                GCTGGGAA AGAGGGG
                                ||||||||| |||||||
                                CGACCCTT TCTCCCC
                                     C
GAM429  FLJ14800  3'  CCCCTCCCCGTAACAGTGA   51610      GC_   AAA
                                TCACTG  TGGG  GAGGGG
                                ||||||  ||||  ||||||
                                AGTGAC  GCCC  CTCCCC
                                   AAT  ____
GAM429  FLJ14800  3'  CCCCTCCCCGTAACAGTGA   51610      GC_   AAA
                                TCACTG  TGGG  GAGGGG
                                ||||||  ||||  ||||||
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                                AGTGAC  GCCC  CTCCCC
                                  AAT   ___
GAM429  FLJ14950  3'  CCCACCCAGCCAGTGGT    51716          AAAGA
                                ATCACTGGCTGGG   GGG
                                |||||||||||||   |||
                                TGGTGACCGACCC   CCC
                                      A____
GAM429  FLJ14950  3'  CCCACCCAGCCAGTGGT    51716          AAAGA
                                ATCACTGGCTGGG   GGG
                                |||||||||||||   |||
                                TGGTGACCGACCC   CCC
                                      A____
GAM429  FLJ21019  3'  CCTCCCCTCCCAGCCAG    46244         AA_
                                CTGGCTGGGA  GAGG
                                |||||||||   ||||
                                GACCGACCCT  CTCC
                                     CCC
GAM429  FLJ21019  3'  CCTCCCCTCCCAGCCAG    46244         AA_
                                CTGGCTGGGA  GAGG
                                |||||||||   ||||
                                GACCGACCCT  CTCC
                                     CCC
GAM429  FLJ23416  3'  CCCCTCTTTCCCATCGAGT   49947    _ C
                                ACT GG TGGGAAAGAGGGG
                                |||  ||  |||||||||||||
                                TGA CT ACCCTTTCTCCCC
                                  G  _
GAM429  FLJ23416  3'  CCCCTCTTTCCCATCGAGT   49947    _ C
                                ACT GG TGGGAAAGAGGGG
                                |||  ||  |||||||||||||
                                TGA CT ACCCTTTCTCCCC
                                  G  _
GAM429  GPS2      3'  CCCCTCTTCATGCACTGATT  50573     CTG  TGG   A
                                AATCA   GC   GAA GAGGGG
                                |||||   ||   |||  ||||||
                                TTAGT   CG   CTT CTCCCC
                                   CA_  TA_  _
GAM429  GPS2      3'  CCCCTCTTCATGCACTGATT  87154     CTG  TGG   A
                                AATCA   GC   GAA GAGGGG
                                |||||   ||   |||  ||||||
                                TTAGT   CG   CTT CTCCCC
                                   CA_  TA_  _
GAM429  GPS2      3'  CCCCTCTTCATGCACTGATT  50573     CTG  TGG   A
                                AATCA   GC   GAA GAGGGG
                                |||||   ||   |||  ||||||
                                TTAGT   CG   CTT CTCCCC
                                   CA_  TA_  _
GAM429  GPS2      3'  CCCCTCTTCATGCACTGATT  87154     CTG  TGG   A
                                AATCA   GC   GAA GAGGGG
                                |||||   ||   |||  ||||||
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                                TTAGT  CG  CTT CTCCCC
                                  CA_  TA_  _
GAM429  GTF3C1   3'  CCCCTCCCTCCCAGCCA    7717        AA
                                TGGCTGGGA  GAGGGG
                                |||||||||  ||||||
                                ACCGACCCT  CTCCCC
                                     CC
GAM429  GTF3C1   3'  CCCCTCCCTCCCAGCCA    7717        AA
                                TGGCTGGGA  GAGGGG
                                |||||||||  ||||||
                                ACCGACCCT  CTCCCC
                                     CC
GAM429  HSPC195  3'  CCCCCACCCCAACAGTGATT  80965       GC   AAAGA
                                AATCACTG  TGGG   GGGG
                                ||||||||  ||||   ||||
                                TTAGTGAC  ACCC   CCCC
                                    A_   CAC__
GAM429  HSPC195  3'  CCCCCACCCCAACAGTGATT  80965       GC   AAAGA
                                AATCACTG  TGGG   GGGG
                                |||||||  ||||   ||||
                                TTAGTGAC  ACCC   CCCC
                                    A_   CAC__
GAM429  KIAA0057 3'  CTCTCCCAGCCAGTGGT    24423          AA
                                ATCACTGGCTGGGA  GAG
                                |||||||||||||  |||
                                TGGTGACCGACCCT  CTC
                                          __
GAM429  KIAA0057 3'  CTCTCCCAGCCAGTGGT    24423          AA
                                ATCACTGGCTGGGA  GAG
                                |||||||||||||  |||
                                TGGTGACCGACCCT  CTC
                                          __
GAM429  KIAA0284 3'  CCCCTCGTCAGCTCCCAGCCAG 63115        AA____
                                CTGGCTGGGA    GAGGGG
                                ||||||||||    ||||||
                                GACCGACCCT    CTCCCC
                                      CGACTG
GAM429  KIAA0284 3'  CCCCTCGTCAGCTCCCAGCCAG 63115        AA____
                                CTGGCTGGGA    GAGGGG
                                ||||||||||    ||||||
                                GACCGACCCT    CTCCCC
                                      CGACTG
GAM429  KIAA0326 3'  CCCCTCTCCTCCTTAGCCAG  64322      _  A_
                                CTGGCTG GGA  AGAGGGG
                                |||||||  |||  |||||||
                                GACCGAT CCT  TCTCCCC
                                    T   CC
GAM429  KIAA0326 3'  CCCTGCCCAGCCAGGGA    64323    A      AAAG
                                TC CTGGCTGGG   AGGG
                                ||  |||||||||   ||||
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                                AG GACCGACCC   TCCC
                                 G       G___
GAM429  KIAA0326 3' CCCCTCTCCTCCTTAGCCAG  64322       _  A_
                                CTGGCTG GGA  AGAGGGG
                                ||||||| |||  |||||||
                                GACCGAT CCT  TCTCCCC
                                    T  CC
GAM429  KIAA0326 3' CCCTGCCCAGCCAGGGA    64323   A      AAAG
                                TC CTGGCTGGG   AGGG
                                || |||||||||   ||||
                                AG GACCGACCC   TCCC
                                 G       G___
GAM429  MGC10818 3' CCCCTGACCAACCATGAT   47537    C  C  GAA  A
                                ATCA TGG TGG   AG GGG
                                |||| ||| |||   || |||
                                TAGT ACC ACC   TC CCC
                                  _  A  AG_  _
GAM429  MGC10818 3' CCCCTGACCAACCATGAT   47537    C  C  GAA  A
                                ATCA TGG TGG   AG GGG
                                |||| ||| |||   || |||
                                TAGT ACC ACC   TC CCC
                                  _  A  AG_  _
GAM429  MGC11303 3' CCCCCAGGCCCAGCCAGGA   50704   A      AAAGA
                                TC CTGGCTGGG    GGGG
                                || |||||||||    ||||
                                AG GACCGACCC    CCCC
                                 _       GGAC_
GAM429  MGC11303 3' CCCCCAGGCCCAGCCAGGA   50704   A      AAAGA
                                TC CTGGCTGGG    GGGG
                                || |||||||||    ||||
                                AG GACCGACCC    CCCC
                                 _       GGAC_
GAM429  MGC13064 3' CCCCTCCCATTCCCAGT    50351       A__
                                GCTGGGAA  GAGGGG
                                ||||||||  ||||||
                                TGACCCTT  CTCCCC
                                    ACC
GAM429  MGC13064 3' CCCCTCCCATTCCCAGT    50351       A__
                                GCTGGGAA  GAGGGG
                                ||||||||  ||||||
                                TGACCCTT  CTCCCC
                                    ACC
GAM429  NLI-IF   5' CCCCTCCCCCCCGCGCCCCGAT 41046    ACT  _  AAA
          T                  AATC  GGC TGGG  GAGGGG
                             ||||  ||| ||||  ||||||
                             TTAG  CCG GCCC  CTCCCC
                               CC_  C   CCC
GAM429  NLI-IF   5' CCCCTCCCCCCCGCGCCCCGAT 41046    ACT  _  AAA
          T                  AATC  GGC TGGG  GAGGGG
                             ||||  ||| ||||  ||||||
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                                TTAG   CCG GCCC   CTCCCC
                                  CC_   C    CCC
GAM429  NLI-IF   3'  CCCCTCTTCCCCGCCCAG    41047     C    A
                                CTGG TGGG AAGAGGGG
                                |||| |||| ||||||||
                                GACC GCCC TTCTCCCC
                                  C    C
GAM429  NLI-IF   3'  CCCCTCTTCCCCGCCCAG    41047     C    A
                                CTGG TGGG AAGAGGGG
                                |||| |||| ||||||||
                                GACC GCCC TTCTCCCC
                                  C    C
GAM429  PAK6     3'  CCCCTCTCTCCCACTAAGT    39406     _ C    A
                                ACT GG TGGGA AGAGGGG
                                ||| || ||||| |||||||
                                TGA TC ACCCT TCTCCCC
                                  A _    C
GAM429  PAK6     3'  CCCCTCTCTCCCACTAAGT    39406     _ C    A
                                ACT GG TGGGA AGAGGGG
                                ||| || ||||| |||||||
                                TGA TC ACCCT TCTCCCC
                                  A _    C
GAM429  PSMD3    3'  CCTCCCCAGCCGGTGA      10971           AAA
                                TCACTGGCTGGG   GAGG
                                ||||||||||||   ||||
                                AGTGGCCGACCC   CTCC
                                               ____
GAM429  PSMD3    3'  CCTCCCCAGCCGGTGA      10971           AAA
                                TCACTGGCTGGG   GAGG
                                ||||||||||||   ||||
                                AGTGGCCGACCC   CTCC
                                               ____
GAM429  RALY     3'  CCCCAACGCATCCCAGCCAGTG 33617           AAGA__
                                CACTGGCTGGGA     GGGG
                                ||||||||||||     ||||
                                GTGACCGACCCT     CCCC
                                       ACGCAA
GAM429  RALY     3'  CCCCAACGCATCCCAGCCAGTG 33617           AAGA__
                                CACTGGCTGGGA     GGGG
                                ||||||||||||     ||||
                                GTGACCGACCCT     CCCC
                                       ACGCAA
GAM429  RLUCL    3'  CCCCTCCCTCCTCCTGGA    54216    ACT  CT   AA
                                TC   GG  GGGA  GAGGGG
                                ||   ||  ||||  ||||||
                                AG   CC  TCCT  CTCCCC
                                 GT_  __    CC
GAM429  RLUCL    3'  CCCCTCCCTCCTCCTGGA    54216    ACT  CT   AA
                                TC   GG  GGGA  GAGGGG
                                ||   ||  ||||  ||||||
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```
                                AG  CC  TCCT  CTCCCC
                                 GT_ __   CC
GAM429  SCRG1   5' CCCCTCCTCCCCACAGT    23462     GCT   AA
                                ACTG  GGGA  GAGGGG
                                ||||  ||||  ||||||
                                TGAC  CCCT  CTCCCC
                                  AC_   C_
GAM429  SCRG1   5' CCCCTCCTCCCCACAGT    23462     GCT   AA
                                ACTG  GGGA  GAGGGG
                                ||||  ||||  ||||||
                                TGAC  CCCT  CTCCCC
                                  AC_   C_
GAM429  SEMA4F  3' CCCCTCAAGCTCCAGTCAATGA 14940     C     _ AAA
           T                     ATCA TGGCTGG G   GAGGGG
                                ||||| ||||||| |   ||||||
                                TAGT ACTGACC C   CTCCCC
                                  A      T GAA
GAM429  SEMA4F  3' CCCCTCAAGCTCCAGTCAATGA 14940     C     _ AAA
           T                     ATCA TGGCTGG G   GAGGGG
                                ||||| ||||||| |   ||||||
                                TAGT ACTGACC C   CTCCCC
                                  A      T GAA
GAM429  SEMA6B  3' CCCCTCTGACCTCCAGCTGA  49489   _   CT   AA
                                TCA CTGG  GGG  AGAGGGG
                                ||| ||||  |||  |||||||
                                AGT GACC  TCC  TCTCCCC
                                  C   __   AG
GAM429  SEMA6B  3' CCCCTCTGACCTCCAGCTGA  39616   _   CT   AA
                                TCA CTGG  GGG  AGAGGGG
                                ||| ||||  |||  |||||||
                                AGT GACC  TCC  TCTCCCC
                                  C   __   AG
GAM429  SEMA6B  3' CCCCTCTGACCTCCAGCTGA  49489   _   CT   AA
                                TCA CTGG  GGG  AGAGGGG
                                ||| ||||  |||  |||||||
                                AGT GACC  TCC  TCTCCCC
                                  C   __   AG
GAM429  SEMA6B  3' CCCCTCTGACCTCCAGCTGA  55823   _   CT   AA
                                TCA CTGG  GGG  AGAGGGG
                                ||| ||||  |||  |||||||
                                AGT GACC  TCC  TCTCCCC
                                  C   __   AG
GAM429  SEMA6B  3' CCCCTCTGACCTCCAGCTGA  39616   _   CT   AA
                                TCA CTGG  GGG  AGAGGGG
                                ||| ||||  |||  |||||||
                                AGT GACC  TCC  TCTCCCC
                                  C   __   AG
GAM429  SEMA6B  3' CCCCTCTGACCTCCAGCTGA  55823   _   CT   AA
                                TCA CTGG  GGG  AGAGGGG
                                ||| ||||  |||  |||||||
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                                AGT GACC  TCC  TCTCCCC
                                  C   __  AG
GAM429  SIRPB1   3'  CCCCTCCCTGTCCCAGCCAG  20246        AA__
                                CTGGCTGGGA   GAGGGG
                                ||||||||||   ||||||
                                GACCGACCCT   CTCCCC
                                     GTCC
GAM429  SIRPB1   3'  CCCCTCCCTGTCCCAGCCAG  20246        AA__
                                CTGGCTGGGA   GAGGGG
                                ||||||||||   ||||||
                                GACCGACCCT   CTCCCC
                                     GTCC
GAM429  SLC26A10 5'  CCCCTCCTCCCCAACCTGGCTG 56027    _ _ C   AAA
          A                      TCA CT GG TGGG   GAGGGG
                                 ||| || || ||||   ||||||
                                 AGT GG CC ACCC   CTCCCC
                                   C  T  A   CTC
GAM429  SLC26A10 5'  CCCCTCCTCCCCAACCTGGCTG 56027    _ _ C   AAA
          A                      TCA CT GG TGGG   GAGGGG
                                 ||| || || ||||   ||||||
                                 AGT GG CC ACCC   CTCCCC
                                   C  T  A   CTC
GAM429  STRIN    3'  CCCCTCTTTTTGTCAGTGCATT 32768    _     TG
                                 AAT CACTGGC  GGAAAGAGGGG
                                 ||| |||||||  ||||||||||
                                 TTA GTGACTG  TTTTTCTCCCC
                                   C     __
GAM429  STRIN    3'  CCCCTCTTTTTGTCAGTGCATT 32768    _     TG
                                 AAT CACTGGC  GGAAAGAGGGG
                                 ||| |||||||  ||||||||||
                                 TTA GTGACTG  TTTTTCTCCCC
                                   C     __
GAM429  TM9SF2   5'  CCCCTCCTTCCCTCTTGA   16627    CT  CT   A
                                 TCA  GG  GGGAA GAGGGG
                                 |||  ||  ||||| ||||||
                                 AGT  TC  CCCTT CTCCCC
                                   __  T_   C
GAM429  TM9SF2   5'  CCCCTCCTTCCCTCTTGA   16627    CT  CT   A
                                 TCA  GG  GGGAA GAGGGG
                                 |||  ||  ||||| ||||||
                                 AGT  TC  CCCTT CTCCCC
                                   __  T_   C
GAM429  LOC121219 3' CCCCTCTCATGGCCCAGCCA  74043        AA___
                                 TGGCTGGG    AGAGGGG
                                 ||||||||    |||||||
                                 ACCGACCC    TCTCCCC
                                      GGTAC
GAM429  LOC121219 3' CCCCTCTCATGGCCCAGCCA  74043        AA___
                                 TGGCTGGG    AGAGGGG
                                 ||||||||    |||||||
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                                ACCGACCC    TCTCCCC
                                    GGTAC
GAM429  LOC143903 3'  CCTTTATCCCAGCCAGT    76617         A
                                ACTGGCTGGGA AGAGG
                                |||||||||| |||||
                                TGACCGACCCT TTTCC
                                      A
GAM429  LOC143903 3'  CCTTTATCCCAGCCAGT    76617         A
                                ACTGGCTGGGA AGAGG
                                |||||||||| |||||
                                TGACCGACCCT TTTCC
                                      A
GAM429  LOC143958 5'  CCCTCCTCTCAGCCA      76636        AA
                                TGGCTGGGA  GAGGG
                                |||||||||  |||||
                                ACCGACTCT  CTCCC
                                     C_
GAM429  LOC143958 5'  CCCTCCTCTCAGCCA      76636        AA
                                TGGCTGGGA  GAGGG
                                |||||||||  |||||
                                ACCGACTCT  CTCCC
                                     C_
GAM429  LOC145225 3'  CCCCTCTTCAATGCCAGTGA  83301       TGG  A
                                TCACTGGC   GAA GAGGGG
                                ||||||||   ||| ||||||
                                AGTGACCG   CTT CTCCCC
                                     TAA  _
GAM429  LOC145225 3'  CCCCTCTTCAATGCCAGTGA  83301       TGG  A
                                TCACTGGC   GAA GAGGGG
                                ||||||||   ||| ||||||
                                AGTGACCG   CTT CTCCCC
                                     TAA  _
GAM429  LOC145483 3'  CCCCTCTCCCCAGCTGTGA   77241     T     AA
                                TCAC GGCTGGG  AGAGGGG
                                |||| |||||||  |||||||
                                AGTG TCGACCC  TCTCCCC
                                  _     C_
GAM429  LOC145483 3'  CCCCTCTCCCCAGCTGTGA   77241     T     AA
                                TCAC GGCTGGG  AGAGGGG
                                |||| |||||||  |||||||
                                AGTG TCGACCC  TCTCCCC
                                  _     C_
GAM429  LOC145725 3'  CCCCCCCCCCCCGGCAGCCAGTG 77404        __ AAAGA
                                CACTGGCTG  GG    GGGG
                                |||||||||  ||    ||||
                                GTGACCGAC  CC    CCCC
                                     GG  CCCCC
GAM429  LOC145725 3'  CCCCCCCCCCCCGGCAGCCAGTG 77404        __ AAAGA
                                CACTGGCTG  GG    GGGG
                                |||||||||  ||    ||||
```

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                                GTGACCGAC  CC    CCCC
                                     GG  CCCCC
GAM429   LOC145732 3'  CCCCCCCCCCCCGGCAGCCAGTG 77426        __  AAAGA
                                CACTGGCTG  GG    GGGG
                                |||||||||  ||    ||||
                                GTGACCGAC  CC    CCCC
                                     GG  CCCCC
GAM429   LOC145732 3'  CCCCCCCCCCCCGGCAGCCAGTG 77426        __  AAAGA
                                CACTGGCTG  GG    GGGG
                                |||||||||  ||    ||||
                                GTGACCGAC  CC    CCCC
                                     GG  CCCCC
GAM429   LOC145919 3'  CCCTCCTCCTCAGCCA     77569       _  AA
                                TGGCTG GGA  GAGGG
                                ||||||  |||  |||||
                                ACCGAC CCT  CTCCC
                                    T   C_
GAM429   LOC145919 3'  CCCTCCTCCTCAGCCA     77569       _  AA
                                TGGCTG GGA  GAGGG
                                ||||||  |||  |||||
                                ACCGAC CCT  CTCCC
                                    T   C_
GAM429   LOC146957 3'  CCCCTCTTGTTACCAAAGATT  78203     AC   C   GA
                                AATC  TGG TGG  AAGAGGGG
                                ||||  |||  |||  ||||||||
                                TTAG  ACC ATT  TTCTCCCC
                                  AA   _   G_
GAM429   LOC146957 3'  CCCCTCTTGTTACCAAAGATT  78203     AC   C   GA
                                AATC  TGG TGG  AAGAGGGG
                                ||||  |||  |||  ||||||||
                                TTAG  ACC ATT  TTCTCCCC
                                  AA   _   G_
GAM429   LOC147669 5'  CCCCTCTCCCATCCAGAGA   84059    A    C    AA
                                TC CTGG TGGGA  GAGGGG
                                ||  ||||  |||||  ||||||
                                AG GACC ACCCT  CTCCCC
                                 A    T    __
GAM429   LOC147669 5'  CCCCTCTCCCATCCAGAGA   84059    A    C    AA
                                TC CTGG TGGGA  GAGGGG
                                ||  ||||  |||||  ||||||
                                AG GACC ACCCT  CTCCCC
                                 A    T    __
GAM429   LOC149506 3'  CCTCTCTTGTCTCCAGC     84459      _  _
                                GCTGG GA AAGAGGGG
                                |||||  ||  ||||||||
                                CGACC CT TTCTCTCC
                                   T  G
GAM429   LOC149506 5'  CCCCTCCTTCCCAGCTCAG   84458     _      A
                                CTG GCTGGGAA GAGGGG
                                |||  ||||||||  ||||||
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                                GAC CGACCCTT CTCCCC
                                  T       C
GAM429   LOC149506 5'  CCCCTCCTTCCCAGCTCAG   84458    _      A
                                CTG GCTGGGAA GAGGGG
                                ||| |||||||| ||||||
                                GAC CGACCCTT CTCCCC
                                  T       C
GAM429   LOC149506 3'  CCTCTCTTGTCTCCAGC     84459     _ _
                                GCTGG GA AAGAGGGG
                                ||||| || ||||||||
                                CGACC CT TTCTCTCC
                                   T  G
GAM429   LOC149668 5'  CCTGGCGCCAGCCAGTGA    84538         GAAAGA
                                TCACTGGCTGG     GGG
                                ||||||||||      |||
                                AGTGACCGACC     TCC
                                      GCGG__
GAM429   LOC149668 5'  CCTGGCGCCAGCCAGTGA    84538         GAAAGA
                                TCACTGGCTGG     GGG
                                ||||||||||      |||
                                AGTGACCGACC     TCC
                                      GCGG__
GAM429   LOC149910 3'  CCCCTCTTCCCTGTCAGTG   79531       T    A
                                CACTGGC GGGAA GAGGGG
                                ||||||| ||||| ||||||
                                GTGACTG CCCTT CTCCCC
                                    T    _
GAM429   LOC149910 3'  CCCCTCTTCCCTGTCAGTG   79531       T    A
                                CACTGGC GGGAA GAGGGG
                                ||||||| ||||| ||||||
                                GTGACTG CCCTT CTCCCC
                                    T    _
GAM429   LOC150605 5'  CCCCTCTTTCCCTTTCCCCA  85083    CT___
                                TGG    GGGAAAGAGGGG
                                |||    ||||||||||||
                                ACC    CCCTTTCTCCCC
                                  CCTTT
GAM429   LOC150605 5'  CCCCTCTTTCCCTTTCCCCA  85083    CT___
                                TGG    GGGAAAGAGGGG
                                |||    ||||||||||||
                                ACC    CCCTTTCTCCCC
                                  CCTTT
GAM429   LOC153474 3'  CCCTGCCCAGTCAGTGA     80844         AAAG
                                TCACTGGCTGGG   AGGG
                                ||||||||||||   ||||
                                AGTGACTGACCC   TCCC
                                      G___
GAM429   LOC153474 3'  CCCTGCCCAGTCAGTGA     80844         AAAG
                                TCACTGGCTGGG   AGGG
                                ||||||||||||   ||||
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                                AGTGACTGACCC  TCCC
                                      G___
GAM429  LOC155036 5' CCCCTCCCTCCCCCTGGCCA  86340     ___  AA
                                TGGCT  GGGA  GAGGGG
                                |||||  ||||  ||||||
                                ACCGG  CCCT  CTCCCC
                                   TCC  CC
GAM429  LOC155036 5' CCCCTCCCTCCCCCTGGCCA  86340     ___  AA
                                TGGCT  GGGA  GAGGGG
                                |||||  ||||  ||||||
                                ACCGG  CCCT  CTCCCC
                                   TCC  CC
GAM429  LOC161823 3' CCCATTCCACCAGTGATT   82302       C   AAGA
                                AATCACTGG TGGGA   GGG
                                ||||||||| |||||   |||
                                TTAGTGACC ACCTT   CCC
                                      _   A___
GAM429  LOC161823 3' CCCATTCCACCAGTGATT   82302       C   AAGA
                                AATCACTGG TGGGA   GGG
                                ||||||||| |||||   |||
                                TTAGTGACC ACCTT   CCC
                                      _   A___
GAM429  LOC165480 5' CCCCTCCAGCACAGCCAGTG  82483       GGAAA
                                CACTGGCTG   GAGGGG
                                |||||||||   ||||||
                                GTGACCGAC   CTCCCC
                                     ACGAC
GAM429  LOC165480 5' CCCCTCCAGCACAGCCAGTG  82483       GGAAA
                                CACTGGCTG   GAGGGG
                                |||||||||   ||||||
                                GTGACCGAC   CTCCCC
                                     ACGAC
GAM429  LOC196957 3' CCCCCCTGCAGCCAGTG    87821       GGAA  A
                                CACTGGCTG  AG GGGG
                                |||||||||  || ||||
                                GTGACCGAC  TC CCCC
                                     G___  C
GAM429  LOC196957 3' CCCCCCTGCAGCCAGTG    87821       GGAA  A
                                CACTGGCTG  AG GGGG
                                |||||||||  || ||||
                                GTGACCGAC  TC CCCC
                                     G___  C
GAM429  LOC196961 3' CCCCCCTGCAGCCAGTG    87842       GGAA  A
                                CACTGGCTG  AG GGGG
                                |||||||||  || ||||
                                GTGACCGAC  TC CCCC
                                     G___  C
GAM429  LOC196961 3' CCCCCCTGCAGCCAGTG    87842       GGAA  A
                                CACTGGCTG  AG GGGG
                                |||||||||  || ||||
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                                GTGACCGAC    TC CCCC
                                     G___  C
GAM429  LOC197138 3'  CCCCCTGCAGCCAGTG      87915         GGAA  A
                                CACTGGCTG    AG GGGG
                                |||||||||    || ||||
                                GTGACCGAC    TC CCCC
                                     G___  _
GAM429  LOC197138 3'  CCCCCTGCAGCCAGTG      87915         GGAA  A
                                CACTGGCTG    AG GGGG
                                |||||||||    || ||||
                                GTGACCGAC    TC CCCC
                                     G___  _
GAM429  LOC200014 3'  CCCCTCCTTTTACTCAACTA   88521     C   _  __
                                TGG TGGG AAA  GAGGGG
                                ||| |||| |||  ||||||
                                ATC ACTC TTT  CTCCCC
                                  A   A   TC
GAM429  LOC200014 3'  CCCCTCCTTTTACTCAACTA   88521     C   _  __
                                TGG TGGG AAA  GAGGGG
                                ||| |||| |||  ||||||
                                ATC ACTC TTT  CTCCCC
                                  A   A   TC
GAM429  LOC202050 5'  CCCCTCTTCTCCTCAGGA     89149    A   CT  GA
                                TC CTGG  GG  AAGAGGGG
                                || ||||  ||  ||||||||
                                AG GACT  CC  TTCTCCCC
                                 _   __  TC
GAM429  LOC202050 5'  CCCCTCTTCTCCTCAGGA     89149    A   CT  GA
                                TC CTGG  GG  AAGAGGGG
                                || ||||  ||  ||||||||
                                AG GACT  CC  TTCTCCCC
                                 _   __  TC
GAM429  LOC203292 3'  CCCCTCCTTCCCAGTCCCATGA 90510      CT  _      A
          T                      ATCA  GG CTGGGAA GAGGGG
                                ||||  || ||||||| ||||||
                                TAGT  CC GACCCTT CTCCCC
                                  AC  T      C
GAM429  LOC203292 3'  CCCCTCCTTCCCAGTCCCATGA 90510      CT  _      A
          T                      ATCA  GG CTGGGAA GAGGGG
                                ||||  || ||||||| ||||||
                                TAGT  CC GACCCTT CTCCCC
                                  AC  T      C
GAM429  LOC221914 3'  CCCCTCCTCCCCCCTCAG     93950     CT_   AA
                                CTGG   GGGA  GAGGGG
                                ||||   ||||  ||||||
                                GACT   CCCT  CTCCCC
                                  CCC    C_
GAM429  LOC221914 3'  CCCCTCCTCCCCCCTCAG     93950     CT_   AA
                                CTGG   GGGA  GAGGGG
                                ||||   ||||  ||||||
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                                GACT   CCCT  CTCCCC
                                  CCC    C_
GAM429   LOC245727 3'  CCCCCCTGCAGCCAGTG     91124        GGAA  A
                                CACTGGCTG    AG GGGG
                                |||||||||    || ||||
                                GTGACCGAC    TC CCCC
                                     G___  C
GAM429   LOC245727 3'  CCCCCCTGCAGCCAGTG     91124        GGAA  A
                                CACTGGCTG    AG GGGG
                                |||||||||    || ||||
                                GTGACCGAC    TC CCCC
                                     G___  C
GAM429   LOC253263 3'  CCATCCCCCAAACAGTGA    97028       GC    AAA  G
                                TCACTG  TGGG   GA GG
                                ||||||  ||||   || ||
                                AGTGAC  ACCC   CT CC
                                   AA    C__  A
GAM429   LOC253263 3'  CCATCCCCCAAACAGTGA    97028       GC    AAA  G
                                TCACTG  TGGG   GA GG
                                ||||||  ||||   || ||
                                AGTGAC  ACCC   CT CC
                                   AA    C__  A
GAM429   LOC257458 5'  CCCCTCTTCCCTTGGAGGA    67791    A  GGCT    A
                                TC CT    GGGAA GAGGGG
                                || ||    ||||| ||||||
                                AG GA    CCCTT CTCCCC
                                 _  GGTT     _
GAM429   LOC257458 5'  CCCCTCTTCCCTTGGAGGA    67791    A  GGCT    A
                                TC CT    GGGAA GAGGGG
                                || ||    ||||| ||||||
                                AG GA    CCCTT CTCCCC
                                 _  GGTT     _
GAM429   LOC84548  3'  CCCCTCTTCCCCGTCAG      71252      T     A
                                CTGGC GGGAA GAGGGG
                                ||||| ||||| ||||||
                                GACTG CCCTT CTCCCC
                                   C    _
GAM429   LOC84548  3'  CCCCTCTTCCCCGTCAG      71252      T     A
                                CTGGC GGGAA GAGGGG
                                ||||| ||||| ||||||
                                GACTG CCCTT CTCCCC
                                   C    _
GAM429   LOC90381  3'  CCCCTCTTCATCCAGCTA     62545        A_
                                TGGCTGGG  AAGAGGGG
                                ||||||||  ||||||||
                                ATCGACCT  TTCTCCCC
                                     AC
GAM429   LOC90381  3'  CCCCTCTTCATCCAGCTA     62545        A_
                                TGGCTGGG  AAGAGGGG
                                ||||||||  ||||||||
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                                ATCGACCT  TTCTCCCC
                                    AC
GAM429  LOC90499  3'  CCCCTCCTTCCCAGTCCCATGA 63063     CT  _      A
          T                  ATCA  GG CTGGGAA GAGGGG
                             ||||  || ||||||| ||||||
                             TAGT  CC GACCCTT CTCCCC
                               AC  T      C
GAM429  LOC90499  3'  CCCCTCCTTCCCAGTCCCATGA 63063     CT  _      A
          T                  ATCA  GG CTGGGAA GAGGGG
                             ||||  || ||||||| ||||||
                             TAGT  CC GACCCTT CTCCCC
                               AC  T      C
GAM429  LOC91263  5'  CCCCTCTTTGGGTTCAGTTA  65378        ___
                             TGGCTGGG  AAAGAGGGG
                             ||||||||  |||||||||
                             ATTGACTT  TTTCTCCCC
                                  GGG
GAM429  LOC91263  5'  CCCCTCTTTGGGTTCAGTTA  65378        ___
                             TGGCTGGG  AAAGAGGGG
                             ||||||||  |||||||||
                             ATTGACTT  TTTCTCCCC
                                  GGG
GAM429  LOC92736  5'  CCAAGCCCAGCCAGTGAT   70426          AAAGAG
                             ATCACTGGCTGGG    GG
                             ||||||||||||     ||
                             TAGTGACCGACCC    CC
                                   GAA___
GAM429  LOC92736  5'  CCAAGCCCAGCCAGTGAT   70426          AAAGAG
                             ATCACTGGCTGGG    GG
                             ||||||||||||     ||
                             TAGTGACCGACCC    CC
                                   GAA___
GAM430  ACTR1B   3'  GAGCGCCATGTCAGGCTGTTG  70820          CTACA
                             CAACGGCTTGACAT    TGTTC
                             ||||||||||||||    |||||
                             GTTGTCGGACTGTA    GCGAG
                                   CC___
GAM430  ADORA1   3'  GAGCATGTGGGGGAAGGCC   5425       GACA
                             GGCTT   TCTACATGTTC
                             |||||   ||||||||||
                             CCGGA   GGGTGTACGAG
                               AGG_
GAM430  BAI2     5'  GGCATGGCTCAGGTTGT    8120         CATCTA
                             ACGGCTTGA    CATGTT
                             |||||||||    ||||||
                             TGTTGGACT    GTACGG
                                  CG____
GAM430  CARD4    3'  GAATGTGTCTTGCGAGCTGTTG 20331         A  TCT
                             CAACGGCTTG CA   ACATGTTC
                             ||||||||| ||   ||||||||
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                                GTTGTCGAGC GT   TGTGTAAG
                                      _ TC_
GAM430  CD5L    3'  GCCTGTAGATGTGAGCTGTTG  19710         G       T
                                CAACGGCTT ACATCTACA GT
                                ||||||||| ||||||||| ||
                                GTTGTCGAG TGTAGATGT CG
                                      _       C
GAM430  CPSF4   3'  GGGCATGTGGGCCTGGCTGT   21955       TGACA
                                ACGGCT    TCTACATGTTC
                                ||||||    ||||||||||
                                TGTCGG    GGGTGTACGGG
                                   TCC__
GAM430  CRYZL1  5'  AGGTGCAGGCCGTTG       17579         A
                                CAACGGCTTG CATCT
                                |||||||||| |||||
                                GTTGCCGGAC GTGGA

                                      _
GAM430  ELMO2   3'  GGACAGGTGTGTTGGGCGTGTT 55675      _  TG   CT  A
           G                     CAACG GCT  ACAT  AC TGTTC
                                ||||| |||  ||||  || |||||
                                GTTGT CGG  TGTG  TG ACAGG
                                   G   GT   __ G
GAM430  FAT     3'  GAACATGTCTTACATGGGTTGC 17891     TTGA  CT___
           TG                    CGGC   CAT    ACATGTTC
                                ||||   |||    ||||||||
                                GTCG   GTA    TGTACAAG
                                  TTGG   CATTC
GAM430  IL1A    3'  AGCATGTACTGAGCC      62464       ACATC
                                GGCTTG    TACATGTT
                                ||||||    ||||||||
                                CCGAGT    ATGTACGA
                                   C____
GAM430  IRS2    3'  AGATGTAAGTTGTTG      59714         A
                                CAACGGCTTG CATCT
                                |||||||||| |||||
                                GTTGTTGAAT GTAGA

                                      _
GAM430  IRTA1   3'  AATGTGTGGGTCTTGTTTG   48414   C   TT   AT
                                A GGC  GAC  CTACATGTT
                                | |||  |||  |||||||||
                                G TTG  CTG  GGTGTGTAA
                                 T   TT   __
GAM430  MLC1    5'  ATGTTGTCAGGTGTTG     57587      G      TCT
                                CAACG CTTGACA   ACAT
                                ||||| |||||||   ||||
                                GTTGT GGACTGT   TGTA
                                   _     ____
GAM430  OLFM1   3'  GAGTGTGTAGAGTGAAGTTGCT 26555    A     G  A     TG
           G                     CA CGGCTT AC TCTACA  TTC
                                || |||||| || ||||||  |||
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                                GT GTTGAA TG AGATGT  GAG
                                 C     G _     GT
GAM430  OSM      3'  AGAGTCAGGCTGTTG       40073           A
                                CAACGGCTTGAC TCT
                                |||||||||||| |||
                                GTTGTCGGACTG AGA
                                          _
GAM430  PDHB     3'  GGACTTGAATATCAAGTCGTTG 87420          C  CTA  T
                                CAACGGCTTGA AT   CA GTTC
                                |||||||||||  ||   || ||||
                                GTTGCTGAACT TA   GT CAGG
                                       A  A__  T
GAM430  PIK3C2B  3'  GAGTGTGTGGGGTGGGCTGT   10569       G  A     TG
                                ACGGCTT AC TCTACA  TTC
                                |||||||  ||  ||||||  |||
                                TGTCGGG TG GGGTGT  GAG
                                   _ _     GT
GAM430  PXR1     3'  GGATGTGTTAGGAGTTGGCCTG 4352        C TG  AT  _
            TTG                    CAACGG T  AC  CTA CATGTTC
                                |||||||  |  ||  ||| |||||||
                                GTTGTC G  TG  GAT GTGTAGG
                                   C GT  AG   T
GAM430  RDS      3'  GGGTTGAGGAAGTCAGGCTGTT 4361           A   A  TGTTC
            G                   CAACGGCTTGAC TCT CA
                                |||||||||||| ||| ||
                                GTTGTCGGACTG AGG GT
                                       A   A  TGGG
GAM430  SCN4A    3'  AGTGTGTGGATGCGTGT     4408     T  A      TG
                                GC TG CATCTACA  TT
                                || || ||||||||  ||
                                TG GC GTAGGTGT  GA
                                 T  _       GT
GAM430  SHANK2   3'  GGATACTCGAATGTCAGGTTTT 24587     CG        CTACA
            TG                    CAA  GCTTGACAT     TGTTC
                                |||  |||||||||    |||||
                                GTT  TGGACTGTA     ATAGG
                                  TT        AGCTC
GAM430  SLC1A4   3'  GAGCGTGCTGTTTGTGGCTGTT 11716        TG   TC  _
            G                   CAACGGCT  ACA  TA CATGTTC
                                |||||||  |||  || |||||||
                                GTTGTCGG  TGT  GT GTGCGAG
                                     __  TT  C
GAM430  TFE3     3'  AGATGTCAGGATGTTG      21509       G
                                CAACG CTTGACATCT
                                ||||| ||||||||||
                                GTTGT GGACTGTAGA
                                   A
GAM430  TIA1     3'  GTGTAGTAAAGCCGTTG     41851          GACAT
                                CAACGGCTT    CTACAT
                                |||||||||    ||||||
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                                GTTGCCGAA    GATGTG
                                     AT___
GAM430  TIA1     3'  GTGTAGTAAAGCCGTTG     42248         GACAT
                                CAACGGCTT    CTACAT
                                |||||||||    ||||||
                                GTTGCCGAA    GATGTG
                                     AT___
GAM430  TSN      3'  GAGTAAGAAATTTCAGGTTGTT 16107         CA__  _ ATGTTC
              G                   AACGGCTTGA   TCT AC
                                |||||||||||   ||| ||
                                TTGTTGGACT   AGA TG
                                     TTAA  A  AG  C
GAM430  UBE2E3   3'  GAGTATGTGGTTCATGCTGTTG 20995       T  CAT
                                CAACGGC TGA  CTACATGTTC
                                ||||||| |||  ||||||||||
                                GTTGTCG ACT  GGTGTATGAG
                                     T  T__
GAM430  WBSCR14  3'  GGATGTGTGTGTGTGGGTT   51976      G   C
                                GGCTT ACAT TACATGTTC
                                ||||| |||| |||||||||
                                TTGGG TGTG GTGTGTAGG
                                   _   T
GAM430  WBSCR14  3'  GGATGTGTGTGTGTGGGTT   51971      G   C
                                GGCTT ACAT TACATGTTC
                                ||||| |||| |||||||||
                                TTGGG TGTG GTGTGTAGG
                                   _   T
GAM430  ADMP     3'  GAACATGTATTTGTTGAGTT   58867     TG  TC
                                GGCT  ACA  TACATGTTC
                                ||||  |||  |||||||||
                                TTGA  TGT  ATGTACAAG
                                  GT   TT
GAM430  BHLHB2   3'  GTAAATGTTAAGTAGTTG    13380      G       C
                                CAAC GCTTGACAT TAC
                                |||| ||||||||| |||
                                GTTG TGAATTGTA ATG
                                  A       A
GAM430  C20orf126 3'  GGGTGTGTGGGGCAGTGGCTGT 47999       TGACA       TT
                                ACGGCT    TCTACATG  C
                                ||||||    ||||||||  |
                                TGTCGG    GGGTGTGT  G
                                   TGACG       GG
GAM430  C20orf139 3'  AGGTGACAGGCTGTTG      84753          A
                                CAACGGCTTG CATCT
                                |||||||||| |||||
                                GTTGTCGGAC GTGGA
                                     A
GAM430  C22orf2  3'  GAATAGCTCTGTTGGGTTGT   94454       TG  TCTACA
                                ACGGCT  ACA     TGTTC
                                ||||||  |||     |||||
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                                TGTTGG  TGT     ATAAG
                                   GT   CTCG__
GAM430  C8orf14   5'  GGATGTGTGGAGGAGGTT    54002      GACA
                                GGCTT    TCTACATGTTC
                                |||||    ||||||||||
                                TTGGA    AGGTGTGTAGG
                                  GG__
GAM430  CAP350    3'  GGGCTTGTGATGTTGAGCTGT  29045       TG    T   T
                                ACGGCT  ACATC ACA GTTC
                                ||||||  ||||| ||| ||||
                                TGTCGA  TGTAG TGT CGGG
                                   GT    _   T
GAM430  DKFZP434G156 3'  AACATGTTTGGGTTGT      69778       TG CATCT
                                ACGGCT  A     ACATGTT
                                ||||||  |     |||||||
                                TGTTGG  T     TGTACAA
                                   GT _____
GAM430  ESM1      3'  GAATGTGTGTGGAAGGCCTTTG 22880     C     GA   CT
                                CAA GGCTT  CAT  ACATGTTC
                                ||| |||||  |||  ||||||||
                                GTT CCGGA  GTG  TGTGTAAG
                                  T    AG   __
GAM430  FBP17     3'  GGCATGTGGAATTCGTTG    72800       CTTGACA
                                CAACGG      TCTACATGTT
                                ||||||      ||||||||||
                                GTTGCT      AGGTGTACGG
                                   TA_____
GAM430  FLJ12221  3'  GTGTGTGCTTGGGCTGCTG   62554    A    TG _   C
                                CA CGGCT  A CAT TAC
                                || |||||  | ||| |||
                                GT GTCGG  T GTG GTG
                                 C    GT C   T
GAM430  FLJ13902  3'  GGTGTGTGGAAAGCGCTGT   45044      TTGACA      TT
                                ACGGC     TCTACATG  C
                                |||||     ||||||||  |
                                TGTCG     AGGTGTGT  G
                                   CGAA__       GG
GAM430  FLJ13962  3'  GGATATGTAGATGAGTTTTTG  45870    CG   TGA
                                CAA  GCT   CATCTACATGTTC
                                |||  |||   ||||||||||||
                                GTT  TGA   GTAGATGTATAGG
                                  TT   ___
GAM430  FLJ14007  3'  GGATGTCAGCTGTTG       45211        T
                                CAACGGCT GACATCT
                                |||||||| |||||||
                                GTTGTCGA CTGTAGG
                                          _
GAM430  FLJ14075  3'  GTGTACTTGCAAGTCGTTG   46049          A  TC
                                CAACGGCTTG CA  TACAT
                                |||||||||| ||  |||||
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                                GTTGCTGAAC GT  ATGTG
                                      _ TC
GAM430  FLJ20257  5'  AGCGTGGTCCGGGTCGTTG   38992         _ ATCTA
                                CAACGGCTTG AC    CATGTT
                                |||||||||| ||    ||||||
                                GTTGCTGGGC TG    GTGCGA
                                      C _____
GAM430  FLJ20294  3'  GGACATGTGGAAGAGCTGCTG  34878   A    GACA
                                CA CGGCTT   TCTACATGTTC
                                || ||||||   ||||||||||
                                GT GTCGAG   AGGTGTACAGG
                                 C    A___
GAM430  FLJ20986  5'  GAATATTATAGATAAGCTGTTG 44545       GAC   C_
                                CAACGGCTT  ATCTA  ATGTTC
                                |||||||||  |||||  ||||||
                                GTTGTCGAA  TAGAT  TATAAG
                                     ___   AT
GAM430  FLJ21736  3'  GGCATCCGTCGGGCTATTG   46231    CG     ATCTAC
                                CAA  GCTTGAC     ATGTT
                                |||  |||||||     |||||
                                GTT  CGGGCTG     TACGG
                                  AT      CC____
GAM430  HSJ1      3'  GGACATGTAGTAGCCCAGGTC  22133      ACAT_
                                GGCTTG    CTACATGTTC
                                ||||||    ||||||||||
                                CTGGAC    GATGTACAGG
                                   CCGAT
GAM430  KIAA0237  3'  GAGCAGTCACTGTCAGGGTGTT 28524     G     TCT  A
          G                     CAACG CTTGACA  AC TGTTC
                                ||||| |||||||  || |||||
                                GTTGT GGACTGT  TG ACGAG
                                   G     CAC  _
GAM430  KIAA0418  3'  GGGCTTATATGTCAGGCCTTTG 27561    C       CTACAT
                                CAA GGCTTGACAT     GTTC
                                ||| ||||||||||     ||||
                                GTT CCGGACTGTA     CGGG
                                  T        TATT__
GAM430  KIAA0672  3'  GGACGGCTCATGTCAGGTC   29413        CTACA
                                GGCTTGACAT    TGTTC
                                ||||||||||    |||||
                                CTGGACTGTA    GCAGG
                                      CTCG_
GAM430  KIAA0795  3'  GGACATGTGGAAGTTGTGTTG  46592     T   A
                                CGGC TGAC TCTACATGTTC
                                |||| |||| ||||||||||
                                GTTG GTTG AGGTGTACAGG
                                  T   A
GAM430  KIAA1068  3'  GGATGTGGAGTTGTTG     31034        G
                                CAACGGCTT ACATCT
                                ||||||||| ||||||
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                                GTTGTTGAG TGTAGG
                                     G
GAM430  KIAA1126 3' GGGTGTGTCGGTTGGTCGAGTC 71933        AT_ _    TT
                                GGCTTGAC  CT ACATG  C
                                ||||||||  || |||||  |
                                CTGAGCTG  GG TGTGT  G
                                    GTT  C    GG
GAM430  KIAA1130 3' GGTGTGTAGGTATCTCC    62425    CTT  C       TT
                                GG  GA ATCTACATG  C
                                ||  || |||||||||  |
                                CC  CT TGGATGTGT  G
                                 T__  A       GG
GAM430  KIAA1322 3' GAACGTGTGCTTCATGACCCGT 72736      CT__  CATC
           TG                    CAACGG   TGA   TACATGTTC
                                ||||||   |||   |||||||||
                                GTTGCC   ACT   GTGTGCAAG
                                   CAGT  TC__
GAM430  KIAA1674 3' ATGTATTTTGAGTTGTTG    68773        TG CATC
                                CAACGGCT  A   TACAT
                                ||||||||  |   |||||
                                GTTGTTGA  T   ATGTA
                                    GT TT__
GAM430  KIAA1958 3' GTTCGGGTGTCCTTCAGGTGAG 81911    _________     ACATGTTC
           CTGTTG                CTT      GACATCT
                                |||       |||||||
                                GAG       CTGTGGG
                                  TGGACTTC        CTTGT
GAM430  MGC2628  3' GGATGTGTGCTGCAGGGCTGCT 43976    A     GA  TC
           G                    CA CGGCTT  CA  TACATGTTC
                                || ||||||  ||  |||||||||
                                GT GTCGGG  GT  GTGTGTAGG
                                 C     AC  C_
GAM430  MGC2840  5' ATGTGGATCAAGTTG      43979        CA
                                CGGCTTGA  TCTACAT
                                ||||||||  |||||||
                                GTTGAACT  AGGTGTA
                                     __
GAM430  MGC4607  5' AGCATGTAGCGGCTGCTG    48740    A    TGACAT
                                CA CGGCT     CTACATGTT
                                || |||||     |||||||||
                                GT GTCGG     GATGTACGA
                                 C    C_____
GAM430  MGC4771  3' TGGATTCAGGCTGTTG      51033          C
                                CAACGGCTTGA ATCTA
                                |||||||||||| |||||
                                GTTGTCGGACT TAGGT
                                     _
GAM430  NPTXR    3' GAGTGAGCATGTCAAGTTGT   54179          _  A   GTTC
                                ACGGCTTGACAT CT CAT
                                |||||||||||| || |||
```

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                                TGTTGAACTGTA GA GTG
                                      C  _  AG
GAM430  NPTXR    3'  GAGTGAGCATGTCAAGTTGT  26643          _ A  GTTC
                                ACGGCTTGACAT CT CAT
                                |||||||||||| || |||
                                TGTTGAACTGTA GA GTG
                                      C  _  AG
GAM430  PP1201   3'  GATGTGTGGGTACTTGGT   42191    TGAC
                                GCT   ATCTACATGTT
                                |||   ||||||||||
                                TGG   TGGGTGTGTAG
                                  TTCA
GAM430  PP1665   3'  GAGTGTGTGGATGCTCACCTGT 47912     CT  _      TG
                                ACGG  TGA CATCTACA  TTC
                                ||||  ||| ||||||||  |||
                                TGTC  ACT GTAGGTGT  GAG
                                  C_  C       GT
GAM430  PPAP2B   5'  TGTGTGGCTGCTGTTG     13548       TTGACAT
                                CAACGGC      CTACATG
                                |||||||      |||||||
                                GTTGTCG      GGTGTGT
                                    TC_____
GAM430  PPFIBP1  5'  GAACGTGTGGATCACTTTGCTG 13252     TTGAC_
                                CGGC     ATCTACATGTTC
                                ||||     ||||||||||||
                                GTCG     TAGGTGTGCAAG
                                  TTTCAC
GAM430  PRO0902  5'  GTGGGGTGTTGGGCTGTT   53898       TG    A
                                AACGGCT  ACATCT CAT
                                |||||||  |||||| |||
                                TTGTCGG  TGTGGG GTG
                                    GT    _
GAM430  PTBP2    3'  GGGTGTGTAAAAAGGTTAAGTT 41038   CG     ATC__    TT
           TTTG                   AA  GCTTGAC    TACATG  C
                                ||  |||||||    ||||||  |
                                TT  TGAATTG    ATGTGT  G
                                 TT      GAAAA     GG
GAM430  SEMA5A   3'  GGATGTGTTCTGCAGGTTGCTG 14258   A     A  TCT
                                CA CGGCTTG CA   ACATGTTC
                                || ||||||| ||   ||||||||
                                GT GTTGGAC GT   TGTGTAGG
                                 C      _  CT_
GAM430  SLC11A2  5'  GGGCGGCGTGTCAGGTGGTTG  5237      G       CTACA
                                CAAC GCTTGACAT    TGTTC
                                |||| |||||||||    |||||
                                GTTG TGGACTGTG    GCGGG
                                  G       CG___
GAM430  TOB2     5'  GCGCGGGAAGGTGCGGGTTGTT 95625         A    ACA   TC
           G                     CAACGGCTTG CATCT   TGT
                                |||||||||| |||||   |||
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                                GTTGTTGGGC GTGGA   GCG
                                      _    AGG   CGG
GAM430  UBXD2    3'  AGCATCTGTTAAGTGTTG    68341      G      TCTAC
                                CAACG CTTGACA     ATGTT
                                ||||| |||||||     |||||
                                GTTGT GAATTGT     TACGA
                                  _      C____
GAM430  WBSCR20A  5'  GGGTGCTAGTGTATGAGTTGTT 49655          _  T  _  GTTC
          G                      CAACGGCTTG ACA CTA CAT
                                ||||||||||| ||| ||| |||
                                GTTGTTGAGT TGT GAT GTG
                                      A  _  C  GG
GAM430  ZFP106   3'  GTAGGTGAGGTGTTGGGCAGTT 42477      G  TG     A  GTTC
          G                      CAAC GCT  ACATCT CAT
                                |||| |||  |||||| |||
                                GTTG CGG  TGTGGA GTG
                                  A  GT     _  GATGG
GAM430  ZNF17    3'  ATACTGTAGGCTGTTG      82385        TTGACAT    _
                                CAACGGC      CTACA TGT
                                |||||||      ||||| |||
                                GTTGTCG      GATGT ATA
                                   ________    C
GAM430  ZW10     3'  GAATATGTGGATTCTTCCCTTG 16367     C  CTT  C
                                CAA GG   GA ATCTACATGTTC
                                ||| ||   || ||||||||||||
                                GTT CC   CT TAGGTGTATAAG
                                  C  TT_  _
GAM430  LOC118704 5'  GAGTGTGTGGCCAAAGCTGT   73923       GACAT    TG
                                ACGGCTT    CTACA  TTC
                                |||||||    |||||  |||
                                TGTCGAA    GGTGT  GAG
                                    ACC__    GT
GAM430  LOC123792 3'  GGCGTGTACCAGGCTGT     74232        ACATC
                                ACGGCTTG     TACATGTT
                                ||||||||     ||||||||
                                TGTCGGAC     ATGTGCGG
                                     C____
GAM430  LOC126961 3'  GGACATGTGGGCAGACGCTG   74629      _ GACA
                                CGGC TT    TCTACATGTTC
                                |||| ||    ||||||||||
                                GTCG AG    GGGTGTACAGG
                                  C  AC__
GAM430  LOC144305 3'  GAGCCACCGTGTTGGGCCTTTG 83033     C    TG    CTACAT
                                CAA GGCT  ACAT     GTTC
                                ||| ||||  ||||     ||||
                                GTT CCGG  TGTG     CGAG
                                  T   GT    CCAC__
GAM430  LOC144317 5'  GAACGTGTGGACGTGGGCT    76791      G  A
                                GGCTT AC TCTACATGTTC
                                ||||| || ||||||||||
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                                TCGGG TG AGGTGTGCAAG
                                  _ C
GAM430  LOC145757 3'  GAGTATATGTGTCGGGTACGTT 77461     _      C__  ATGTTC
            G                   AACG GCTTGACAT   TAC
                                |||| |||||||||  |||
                                TTGC TGGGCTGTG   ATG
                                  A       TAT   AG   C
GAM430  LOC147180 5'  CGGGTGGTCTCATGTTGAGGCT 83985     _   ____   ATGTTC
            GTTG                  GGCTT GACAT    CTAC
                                |||||| |||||    ||||
                                TCGGA TTGTA    GGTG
                                  G    CTCT    GG   CT
GAM430  LOC148734 5'  GGATGTCAGGTTTTTG      78956     CG
                                CAA  GCTTGACATCT
                                |||  ||||||||||
                                GTT  TGGACTGTAGG
                                  TT
GAM430  LOC149684 5'  GGGCATGTGGGTGTCACAGGAT 84615     _ __
            CG                    CGG CT  TGACATCTACATGTTC
                                ||| ||  ||||||||||||||||
                                GCT GG  ACTGTGGGTGTACGGG
                                  A  AC
GAM430  LOC151475 3'  AATGTGTGGGTGTGTGT     85382     TTG
                                GC   ACATCTACATGTT
                                ||   ||||||||||||
                                TG   TGTGGGTGTGTAA
                                 TG_
GAM430  LOC152190 5'  GAGTATGTAGAGAAGCC     69657      GACA
                                GGCTT    TCTACATGTTC
                                |||||    ||||||||||
                                CCGAA    AGATGTATGAG
                                   G___
GAM430  LOC164397 5'  AGTGTGTGGGAGGTCGT     82517       GACA     TG
                                ACGGCTT    TCTACA  TT
                                |||||||    ||||||  ||
                                TGCTGGA    GGGTGT  GA
                                    ____     GT
GAM430  LOC201848 3'  AACATGTTATAGGCTGT     89071        ACATCT
                                ACGGCTTG     ACATGTT
                                ||||||||     |||||||
                                TGTCGGAT     TGTACAA
                                   AT____
GAM430  LOC221354 3'  GAACGTGTGCTTAAGGTGGTTG 92412      G    GACATC
                                CAAC GCTT     TACATGTTC
                                |||| ||||     |||||||||
                                GTTG TGGA     GTGTGCAAG
                                  G    ATTC__
GAM430  LOC253974 3'  GAACATGTAGACCATGTAGTTG 97424      G  T  ACA
                                CAAC GC TG   TCTACATGTTC
                                |||| || ||   ||||||||||
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                                GTTG TG AC   AGATGTACAAG
                                  A  T  C__
GAM430  LOC254827 3'  GAATATGTAAAGCAAGTTATTG 96994     CG    ACATC
                                CAA  GCTTG    TACATGTTC
                                |||  |||||    |||||||||
                                GTT  TGAAC    ATGTATAAG
                                  AT    GAA__
GAM430  LOC256995 5'  ATGTTGATCGCAAGCTGTTG   97589         AC   T
                                CAACGGCTTG  ATC ACAT
                                ||||||||||  ||| ||||
                                GTTGTCGAAC  TAG TGTA
                                      GC   T
GAM430  LOC257395 3'  GGACATGTGGGCAGACGCTG   95421     _ GACA
                                CGGC TT    TCTACATGTTC
                                ||||  ||    ||||||||||||
                                GTCG AG    GGGTGTACAGG
                                  C  AC__
GAM430  LOC90346  3'  GTATGGTGCTGGGCTGTTG    56390        GA   _
                                CAACGGCTT  CATC TAC
                                |||||||||  ||||  |||
                                GTTGTCGGG  GTGG ATG
                                     TC    T
GAM430  LOC90631  3'  GGATGTGTGAAGTCAGGCT    63637        A  T
                                GGCTTGAC TC ACATGTTC
                                |||||||| ||  ||||||||
                                TCGGACTG AG TGTGTAGG
                                     A  _
GAM430  LOC91097  5'  GGATTTCAGATCTTAGGCTGTT 64839          C    ACATGTTC
          G                      CAACGGCTTGA ATCT
                                ||||||||||| ||||
                                GTTGTCGGATT TAGA
                                      C    CTTTAGG
GAM430  LOC91768  3'  GGGCGTGTGGGTGTGTGAATGT 67117     GCTTG
                                ACG    ACATCTACATGTTC
                                |||    ||||||||||||||
                                TGT    TGTGGGTGTGCGGG
                                  AAGTG
GAM430  LOC96652  3'  GAATGTGTACTGAGGAGCCGT  65468       GA  TC
                                ACGGCTT  CA  TACATGTTC
                                |||||||  ||  |||||||||
                                TGCCGAG  GT  ATGTGTAAG
                                    GA  C_
GAM431  HPN       5'  CCAGGGTCCCACCCTGG     9274         AA  AGCA
                                CCAGGGTG  ACT   TTGG
                                ||||||||  |||   ||||
                                GGTCCCAC  TGG   GACC
                                     CC  _____
GAM431  ITGA5     3'  CCCAACCCTTCCCTCACCTTGG 61280         AACT  CA
                                CCAGGGTGA   AG  TTGGG
                                |||||||||   ||  |||||
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                                GGTTCCACT   TC  AACCC
                                     CCCT  CC
GAM431  RXRA     3'  CCAACGCCAACACCTGGTG   11404       _ GAAACTA  A
                                TACCAGG GT      GC TTGG
                                ||||||| ||      || ||||
                                GTGGTCC CA      CG AACC
                                   A  AC_____  C
GAM431  C11orf21  5'  CCACCACCTCACCCTGGTG   26239         AACTAGCAT
                                TACCAGGGTGA       TGG
                                ||||||||||        |||
                                GTGGTCCCACT       ACC
                                     CCACC____
GAM431  CAPN6    3'  CCCAGCAGCATTTCACCC    26603        CTA  A_
                                GGGTGAAA   GC  TTGGG
                                ||||||||   ||  |||||
                                CCCACTTT   CG  GACCC
                                   A__  AC
GAM431  FLJ23392  5'  GCTAGTTCCCACCCTGGTA   45537         A_
                                TACCAGGGTG  AACTAGC
                                ||||||||||  |||||||
                                ATGGTCCCAC  TTGATCG
                                     CC
GAM431  KIAA1550  3'  CCCAAGCAGGCCCCACCCTGG  66555        AAA  A  A
                                CCAGGGTG   CT GC TTGGG
                                ||||||||   || || |||||
                                GGTCCCAC   GG CG AACCC
                                   CCC  A  _
GAM431  SPINT1    3'  CCCTTGATCAGCCCCACCCTGG 62649        AAA  AG_  TT
                                CCAGGGTG   CT   CA  GGG
                                ||||||||   ||   ||  |||
                                GGTCCCAC   GA   GT  CCC
                                   CCC  CTA  T_
GAM431  TU12B1-TY 3'  CCAGTGCCTCTCCCTG      33373       T  AACTA
                                CAGGG GA    GCATTGG
                                ||||| ||    |||||||
                                GTCCC CT    CGTGACC
                                   T  C_____
GAM431  LOC255147 5'  CCACAGTCCCATCCTGG     95701        AA   AGCAT
                                CCAGGGTG  ACT    TGG
                                ||||||||  |||    |||
                                GGTCCTAC  TGA    ACC
                                   CC   C_____
GAM431  LOC90092  3'  CCCAATGCCAGTCATGCTG   61403     G    AA  A
                                CAG GTGA  CT GCATTGGG
                                ||| ||||  || ||||||||
                                GTC TACT  GA CGTAACCC
                                  G    __  C
GAM431  LOC91759  5'  CCCAATGCTAATGAACAGCTC  67086      GAAAC__
                                GGGT      TAGCATTGGG
                                ||||      ||||||||||
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                                CTCG      ATCGTAACCC
                                  ACAAGTA
GAM432  ATP11B   3'  AGAGGCAAATCAACCCTAGG   80313    A  T    CACA   A
                                CC AG GTTGA    GCC TCT
                                || || |||||    ||| |||
                                GG TC CAACT    CGG AGA
                                 A  C    AAA_  _
GAM432  ATRN     3'  ATGGCTGTGCGGTGCGGGA    57795     AA TG   A
                                TCCC  G  TTG CACAGCCAT
                                ||||  |  ||| |||||||||
                                AGGG  C  GGC GTGTCGGTA
                                  __ GT   _
GAM432  FLG      3'  AGATGGCTCCAGACACCCCGGA 70876     CAA    GACAC
                                TCC   GTGTT    AGCCATCT
                                |||   |||||    ||||||||
                                AGG   CACAG    TCGGTAGA
                                  CCC    ACC__
GAM432  GYG      3'  AGATGGCTGTATCAGTTCTT   14688     TG    C
                                AAG  TTGA ACAGCCATCT
                                |||  |||| ||||||||||
                                TTC  GACT TGTCGGTAGA
                                  TT    A
GAM432  H4F2     3'  GTGGCTGCAAACACTTGAGA   59357    C       GACA
                                TC CAAGTGTT    CAGCCAT
                                || ||||||||    |||||||
                                AG GTTCACAA    GTCGGTG
                                 A       AC__
GAM432  HNRPH1   3'  AGACGCAATACCAATACTTAGG 18628     C       ACACA  CA
            A                    TCC AAGTGTTG     GC  TCT
                                ||| ||||||||     ||  |||
                                AGG TTCATAAC     CG  AGA
                                  A       CATAA  C_
GAM432  IPP      3'  GATGGCTTGAACTCGGGA    19726      A   GTTGACAC
                                TCCC AGT       AGCCATC
                                |||| |||       |||||||
                                AGGG TCA       TCGGTAG
                                  C   AGT_____
GAM432  JTB      5'  AGATGGCTGCGTCGGGGGCGGG 21958      AAGTG    A
            A                    TCCC     TTGAC CAGCCATCT
                                ||||     ||||| |||||||||
                                AGGG     GGCTG GTCGGTAGA
                                  CGGG_    C
GAM432  LZTR1    3'  GGATATGTCAGCACCTGG    22242     A       CAG
                                CCA GTGTTGACA   CC
                                ||| |||||||||   ||
                                GGT CACGACTGT   GG
                                  C        ATA
GAM432  MUCDHL   3'  AGATGGCTACGTCTGCATT    48362      T   AC
                                AGTGT GAC  AGCCATCT
                                ||||| |||  ||||||||
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                                TTACG CTG  TCGGTAGA
                                   T   CA
GAM432  MUCDHL   3'  AGATGGCTACGTCTGCATT   87297      T   AC
                                AGTGT GAC  AGCCATCT
                                ||||| |||  ||||||||
                                TTACG CTG  TCGGTAGA
                                   T   CA
GAM432  NFE2L1   3'  CTGTGTGAACACTTGGGA    12172          G
                                TCCCAAGTGTT ACACAG
                                |||||||||| ||||||
                                AGGGTTCACAA TGTGTC
                                       G
GAM432  PFKL     5'  GATGGCTGTGACCCTGGG    10518      A T  TGA
                                CCCA G GT   CACAGCCATC
                                |||| | ||   ||||||||||
                                GGGT C CA   GTGTCGGTAG
                                  _ C  ___
GAM432  PKIA     3'  ATGGCTGTGCTGCATTGCAGGA 22380     CA_    TGA
                                TCC   AGTGT   CACAGCCAT
                                |||   |||||   |||||||||
                                AGG   TTACG   GTGTCGGTA
                                  ACG    TC_
GAM432  PLGL     3'  ATGACTATGTTTGGGA      10635      AGTGTT   C  C
                                TCCCA     GACA AG CAT
                                |||||     |||| || |||
                                AGGGT     TTGT TC GTA
                                  _______   A  A
GAM432  SCNN1G   3'  CTGTGTCACTTTGCTTGGGG   6431          T__
                                TCCCAAGTG   TGACACAG
                                |||||||||   ||||||||
                                GGGGTTCGT   ACTGTGTC
                                      TTC
GAM432  TEM1     3'  ATGGGGTGTCAACCTT      39877     T      AG
                                AAG GTTGACAC  CCAT
                                ||| ||||||||  ||||
                                TTC CAACTGTG  GGTA
                                  _       G_
GAM432  APOL4    3'  GGCCAACACTTAGGG       47627     _      ACACA
                                CCC AAGTGTTG    GCC
                                ||| ||||||||    |||
                                GGG TTCACAAC    CGG
                                  A       _____
GAM432  C5orf5   3'  GCCATGTCAGTATGTAGGA   33467     CAA       CA
                                TCC   GTGTTGACA  GC
                                |||   |||||||||  ||
                                AGG   TATGACTGT  CG
                                  ATG       AC
GAM432  CCR8     3'  GTTGTTGCCAACACTT      17783         A  _
                                AAGTGTTG CA CAGC
                                |||||||| || ||||
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                                TTCACAAC GT GTTG
                                    C  T
GAM432  EVI5     3' AGATGAGTATCAACACTT    18988         C  AGC
                                AAGTGTTGA AC   CATCT
                                ||||||||| ||   |||||
                                TTCACAACT TG   GTAGA
                                    A  A__
GAM432  FLJ10704 3' ATGGCTGTTGCGTATTGG    36450      GTGT  AC
                                CCAA    TG  ACAGCCAT
                                ||||    ||  ||||||||
                                GGTT    GC  TGTCGGTA
                                  AT__  GT
GAM432  FLJ12783 3' AGACAGCCTCCAAGGTCAACAC 48674           ACA____  CA
           TTGG                   CCAAGTGTTGAC      GC  TCT
                                ||||||||||||      ||  |||
                                GGTTCACAACTG      CG  AGA
                                      GAACCTC  AC
GAM432  FLJ13055 3' AGATGGCTAGAAGGACATTTAG 42708     C      GACAC
           GA                   TCC AAGTGTT    AGCCATCT
                                ||| |||||||    ||||||||
                                AGG TTTACAG    TCGGTAGA
                                  A      GAAGA
GAM432  FLJ14547 3' GGCACCAAAACTTGGGA     51435        G   ACACA
                                TCCCAAGT TTG    GCC
                                |||||||| |||    |||
                                AGGGTTCA AAC    CGG
                                    A   CA___
GAM432  FLJ20004 3' AGATGACATTTGAGTCAACACC 95284     A      A   C___
           TGG                    CCA GTGTTGAC CAG    CATCT
                                ||| |||||||| |||    |||||
                                GGT CACAACTG GTT    GTAGA
                                  C       A   TACA
GAM432  FLJ20651 5' GACAGCTGTTACCAGGGA    35496     AA   TTGAC    CA
                                TCCC  GTG    ACAGC  TC
                                ||||  |||    |||||  ||
                                AGGG  CAT    TGTCG  AG
                                  AC  ______    AC
GAM432  FLJ22833 3' AGATAGGAGCAACACTT     43097        ACACAG  _
                                AAGTGTTG     CC ATCT
                                ||||||||     || ||||
                                TTCACAAC     GG TAGA
                                    GA____  A
GAM432  FLJ23309 3' AGATGGCTATGTAGCTTG    46060      GTTG   C
                                CAAGT    ACA AGCCATCT
                                |||||    ||| ||||||||
                                GTTCG    TGT TCGGTAGA
                                  A___   A
GAM432  FLJ23548 5' AGATGGCTATGATATCTGGGA  44746      AG   TGA  C
                                TCCCA  TGT   CA AGCCATCT
                                |||||  |||   || ||||||||
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                                AGGGT  ATA   GT TCGGTAGA
                                  CT   ___  A
GAM432  GT650    3'  AGATGGCTACATCCCTACT   53450     TT  CAC
                                AGTG  GA   AGCCATCT
                                ||||  ||   ||||||||
                                TCAT  CT   TCGGTAGA
                                  CC  ACA
GAM432  KIAA0140 5'  AGATGGCTGATACCCACCCTGG 27803      A_   TTGACA
            GA                    TCCCA  GTG     CAGCCATCT
                                |||||  |||     |||||||||
                                AGGGT  CAC     GTCGGTAGA
                                  CC   CCATA_
GAM432  KIAA0894 3'  AGATGGCCTGGACAC      29701       GACA   _
                                GTGTT    CAG CCATCT
                                |||||    ||| ||||||
                                CACAG    GTC GGTAGA
                                  _____  C
GAM432  KIAA0998 3'  TGTTCTGTGTCAGCACCCAGGA 30587     CAA          C_
                                TCC   GTGTTGACACAG  CA
                                |||   ||||||||||||  ||
                                AGG   CACGACTGTGTC  GT
                                  ACC          TT
GAM432  KIAA1165 3'  AGATGAAAACAACACTTGTGA  67403    C        ACACAGC
                                TC CAAGTGTTG      CATCT
                                || |||||||||      |||||
                                AG GTTCACAAC      GTAGA
                                  T       AAAA___
GAM432  KIAA1958 3'  GGATGGCACCAATACTTGGGA  81907           ACACA
                                TCCCAAGTGTTG    GCCATCT
                                ||||||||||||    |||||||
                                AGGGTTCATAAC    CGGTAGG
                                      CA___
GAM432  SEC15B   3'  AGATGCTTCTCACCAACACTTT 66683    CC       ACAC__   C
            AGA                   TC  AAGTGTTG     AGC ATCT
                                ||  ||||||||     ||| ||||
                                AG  TTCACAAC     TCG TAGA
                                  AT       CACTCT   _
GAM432  STHM     3'  AGATGACTCTCAGAACACTGGG 21296      A    GACAC  C
            A                    TCCCA GTGTT     AG CATCT
                                |||||  |||||     ||  |||||
                                AGGGT  CACAA     TC GTAGA
                                  _     GACTC  A
GAM432  USP24    3'  AGATGGAAGGGCCAGCACTT   91151         ACACAG
                                AAGTGTTG     CCATCT
                                ||||||||     ||||||
                                TTCACGAC     GGTAGA
                                     CGGGAA
GAM432  ZIM2     3'  CTGCGCCAACACTTTGGA    31085     C       ACA
                                TCC AAGTGTTG   CAG
                                ||| ||||||||   |||
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                                AGG TTCACAAC   GTC
                                  T       CGC
GAM432  LOC129563 3'  GCCGATGTCAACACCTGG    74880     A       CA_
                                CCA GTGTTGACA   GC
                                ||| |||||||||   ||
                                GGT CACAACTGT   CG
                                  C        AGC
GAM432  LOC132338 5'  AGATGGCTACTTTCACCAGGA  75886     CAA   TTGACAC
                                TCC   GTG      AGCCATCT
                                |||   |||      ||||||||
                                AGG   CAC      TCGGTAGA
                                  AC_   TTTCA__
GAM432  LOC145988 5'  ATGGCCTGCTGTCAACACCCAG 77606     CAA       _  _
           GA                     TCC   GTGTTGACA CAG CCAT
                                |||   ||||||||| ||| ||||
                                AGG   CACAACTGT GTC GGTA
                                  ACC        C   C
GAM432  LOC220883 3'  AGACGGCTGTGAATCCTGTGG  91258     _ TG  GA      A
                                CCA AG  TT  CACAGCC TCT
                                ||| ||  ||  ||||||| |||
                                GGT TC  AA  GTGTCGG AGA
                                  G  CT  __      C
GAM432  LOC256997 5'  GTGGCTGCCTACACTTGG    95336        TGACA
                                CCAAGTGT    CAGCCAT
                                ||||||||    |||||||
                                GGTTCACA    GTCGGTG
                                     TCC__
GAM432  LOC257358 3'  AGATGGCTATGGCTCTTGTGA  97097    C    T  TGA  C
                                TC CAAG GT   CA AGCCATCT
                                || |||| ||   || ||||||||
                                AG GTTC CG   GT TCGGTAGA
                                 T    T  ___  A
GAM432  LOC90917  3'  AGAGGGTATCAACATTT     64333         CACA   A
                                AAGTGTTGA    GCC TCT
                                |||||||||    ||| |||
                                TTTACAACT    TGG AGA
                                     A___   G
GAM433  CDR2      3'  AACATCCTCTCACTTGCATT   76020         TTC
                                GATGCAAGT   AGGATGTT
                                |||||||||   ||||||||
                                TTACGTTCA   TCCTACAA
                                     CTC
GAM433  FLT1      3'  AACATCCTGTGGCACTC     8908      A   AAGTTT
                                GAG TGC     CAGGATGTT
                                ||| |||     |||||||||
                                CTC ACG     GTCCTACAA
                                  _   GT____
GAM433  KAL1      3'  ATTCTGAAGCTTACATCTC    4011        C
                                GAGATG AAGTTTCAGGAT
                                |||||| ||||||||||||
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                                CTCTAC TTCGAAGTCTTA
                                   A
GAM433  PEX10    3'  AACAGAAATCTGCATCTC    10508        AG   AGGA
                                GAGATGCA  TTTC   TGTT
                                ||||||||  ||||   ||||
                                CTCTACGT  AAAG   ACAA
                                    CT   ____
GAM433  PRKR     5'  AACATCCTAAACAATCTT    10875      GCAA   C
                                GAGAT   GTTT AGGATGTT
                                |||||   |||| ||||||||
                                TTCTA   CAAA TCCTACAA
                                  A___   _
GAM433  SIM2     3'  GAACACCCCAGCTGCATTTC  23784        A  TCA  A
                                GAGATGCA GTT   GG TGTTC
                                |||||||| |||   || |||||
                                CTTTACGT CGA   CC ACAAG
                                     _  C__  C
GAM433  AKAP3    5'  GAACATCCCAGCATCTT     21211        AAGTTTCA
                                GAGATGC       GGATGTTC
                                |||||||       ||||||||
                                TTCTACG       CCTACAAG
                                    AC_______
GAM433  AP1GBP1  3'  GAACATCCTAAAAAAGCATT  23394       AAG  C
                                GATGC   TTT AGGATGTTC
                                |||||   ||| |||||||||
                                TTACG   AAA TCCTACAAG
                                  AA_   A
GAM433  FBXL9    3'  GGAACATCCTGCCACACCGC  24084    AA_  TT
                                GC   GT  CAGGATGTTCC
                                ||   ||  ||||||||||
                                CG   CA  GTCCTACAAGG
                                 CCA  CC
GAM433  FLJ11101 3'  CCGGATGAAACTTCCACCTC  37050     A  C      A_______
                                GAG TG AAGTTTC      GG
                                ||| || |||||||      ||
                                CTC AC TTCAAAG      CC
                                  C  C      TAGGIII
GAM433  FLJ11259 3'  CTGAAGCTCACATCTC      37187       CA
                                GAGATG  AGTTTCAG
                                ||||||  ||||||||
                                CTCTAC  TCGAAGTC
                                   AC
GAM433  FLJ23467 3'  GTGTTCCGAAGTGAAACTTGGA 44711    G       A________  ATGTT
           TCTC                    AT CAAGTTTC       GG    C
                                || ||||||||       ||    |
                                TA GTTCAAAG       CC    G
                                 G       TGAAGIII  TTGTA
GAM433  KIAA0090 3'  CCTGAAACCCCATCTC      88441       CAA
                                GAGATG   GTTTCAGG
                                ||||||   ||||||||
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                                CTCTAC   CAAAGTCC
                                   CC_
GAM433  KIAA0365  3'  GTCCCAAACACCTGCATCTC   78665        A  _  CA
                                GAGATGCA GT TT  GGAT
                                |||||||| || ||  ||||
                                CTCTACGT CA AA  CCTG
                                     C  C  AC
GAM433  KIAA0438  3'  GAACATAACACTTGCATT    29070         TTCAGG
                                GATGCAAGT     ATGTTC
                                |||||||||     ||||||
                                TTACGTTCA     TACAAG
                                      CAA___
GAM433  KIAA0595  3'  AACAAGTTAACTTGCATT    30496          TCAGGA
                                GATGCAAGTT     TGTT
                                ||||||||||     ||||
                                TTACGTTCAA     ACAA
                                      TTGA__
GAM433  KIAA1181  3'  GGAACATCCCAGAATGCATATC 68374    G    AGT   A_
                                GA ATGCA   TTC  GGATGTTCC
                                || |||||   |||  |||||||||
                                CT TACGT   AAG  CCTACAAGG
                                 A    ___   AC
GAM433  MGC16037  3'  CCTGAAACCCCATCTC      51820       CAA
                                GAGATG   GTTTCAGG
                                ||||||   ||||||||
                                CTCTAC   CAAAGTCC
                                   CC_
GAM433  TADA3L    3'  CCAGAGTGAAACTGCATCTC   55989        A    A_______
                                GAGATGCA GTTTC       GG
                                |||||||| |||||       ||
                                CTCTACGT CAAAG       CC
                                     _    TGAGAIII
GAM433  TADA3L    3'  CCAGAGTGAAACTGCATCTC   56001        A    A_______
                                GAGATGCA GTTTC       GG
                                |||||||| |||||       ||
                                CTCTACGT CAAAG       CC
                                     _    TGAGAIII
GAM433  LOC149373 3'  GAACTGAACAAGCTTGCATC   79314          CAGGAT
                                GATGCAAGTTT     GTTC
                                ||||||||||     ||||
                                CTACGTTCGAA     CAAG
                                      CAAGT_
GAM433  LOC158292 5'  AACATGCTGAAACTCCATCTC  86725       CA       G
                                GAGATG  AGTTTCAG ATGTT
                                ||||||  |||||||| |||||
                                CTCTAC  TCAAAGTC TACAA
                                   C_       G
GAM433  LOC200261 3'  AACACCTTTTCCCTGCGTCTC  88650        AGTTTC   A
                                GAGATGCA     AGG TGTT
                                ||||||||     ||| ||||
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                                CTCTGCGT     TCC ACAA
                                    CCCTTT  _
GAM433  LOC221585 3'  CTGAAACTTCATCTC      93630       C
                                GAGATG AAGTTTCAG
                                |||||| |||||||||
                                CTCTAC TTCAAAGTC
                                   _
GAM433  LOC222899 5'  AACATCCTGCTTCTCCATCTC  94363       CA  TTT
                                GAGATG  AG   CAGGATGTT
                                ||||||  ||   |||||||||
                                CTCTAC  TC   GTCCTACAA
                                   C_  TTC
GAM433  LOC254431 5'  AACAGAAATCTGCATCTC    96847        AG    AGGA
                                GAGATGCA  TTTC    TGTT
                                ||||||||  ||||    ||||
                                CTCTACGT  AAAG    ACAA
                                    CT   _____
GAM433  LOC254826 3'  CTGAAACTTGCATCTC      97241
                                GAGATGCAAGTTTCAG
                                ||||||||||||||||
                                CTCTACGTTCAAAGTC

GAM434  L1CAM    3'  TTTATTGCCAAAACCCAGCTGC 4718      _   A     CAA TG
          AC                      GTG AGCT GGTTT   G  ATGAG
                                ||| |||| |||||   |  |||||
                                CAC TCGA CCAAA   C  TATTT
                                  G   C     AC_ GT
GAM434  L1CAM    3'  TTTATTGCCAAAACCCAGCTGC 43756     _   A     CAA TG
          AC                      GTG AGCT GGTTT   G  ATGAG
                                ||| |||| |||||   |  |||||
                                CAC TCGA CCAAA   C  TATTT
                                  G   C     AC_ GT
GAM434  MYO15A   3'  CATCACTTGATGGGCCAC    32669     A   AGGTT
                                GTG GCT     TCAAGTGATG
                                ||| |||     ||||||||||
                                CAC CGG     AGTTCACTAC
                                  _  GT___
GAM434  PCDH15   3'  TCATCACTACTAACTCAC    52338       C   GTTTCA
                                GTGAG TAG      AGTGATGA
                                ||||| |||      ||||||||
                                CACTC ATC      TCACTACT
                                   A  A_____
GAM434  DKFZp727G131 5'  TCATAAAACCTAGGTCAC    59034      G       CAA
                                GTGA CTAGGTTT   GTGA
                                |||| ||||||||   ||||
                                CACT GATCCAAA   TACT
                                  G       A__
GAM434  FLJ10199  5'  GCTGAAACCAGCCCAC      71234     A   A      A
                                GTG GCT GGTTTCA GT
                                ||| ||| ||||||| ||
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                                CAC CGA CCAAAGT CG
                                  C  _     _
GAM434  FLJ20297  5'  TCATCACTCAGAAGCC      35639       A_
                                GGTTTC  AGTGATGA
                                ||||||  ||||||||
                                CCGAAG  TCACTACT
                                   AC
GAM434  FLJ21870  3'  TCATCACCTACAAACTCTC   43464    CTA    CAA_
                                GAG   GGTTT   GTGATGA
                                |||   |||||   |||||||
                                CTC   TCAAA   CACTACT
                                  ___    CATC
GAM434  KIAA0321  5'  TCATCACTCCCAGCCCTC    62397    CTA   TCA
                                GAG   GGTT   AGTGATGA
                                |||   ||||   ||||||||
                                CTC   CCGA   TCACTACT
                                  ___   CCC
GAM434  KIAA0323  3'  CATCACTTCCCCAGCCCA    63259    A  A  TTTC
                                TG GCT GG    AAGTGATG
                                || ||| ||    ||||||||
                                AC CGA CC    TTCACTAC
                                 C   C  C___
GAM434  KIAA1579  3'  CATAGAACAAATCTAGCCCAC  36606     A       CAAGTG
                                GTG GCTAGGTTT     ATG
                                ||| |||||||||     |||
                                CAC CGATCTAAA     TAC
                                  C       CAAGA_
GAM434  PRO1048   3'  CACCACTTTAGCTCA       37511       GGTTTC    A
                                TGAGCTA     AAGTG TG
                                |||||||     ||||| ||
                                ACTCGAT     TTCAC AC
                                    _______    C
GAM434  RP4-622L5 3'  CACCACCATGCCCCATGCTCAC 38928       TA__   TTCAA   A
                                GTGAGC    GGT    GTG TG
                                ||||||    |||    ||| ||
                                CACTCG    CCG    CAC AC
                                   TACC   TAC__   C
GAM434  SLC26A10  5'  CATCACTTGCCTTGGTAGTCAC 56025     __     TTT
                                GTGA  GCTAGG   CAAGTGATG
                                ||||  ||||||   |||||||||
                                CACT  TGGTTC   GTTCACTAC
                                  GA     C__
GAM434  LOC150776 5'  TCATCACTCAGAAGCC      63227       A_
                                GGTTTC  AGTGATGA
                                ||||||  ||||||||
                                CCGAAG  TCACTACT
                                   AC
GAM435  ADH1B     3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                ||||  |||||   ||||||||
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                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM435  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM435  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                        _
GAM435  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                  CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM435  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM435  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM435  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                       T__    _
GAM435  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM435  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_    CG_
GAM435  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM435  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
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                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM435  FLJ23462  3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
            G                    CATTTC        GTCTGAGAT
                                 ||||||        |||||||||
                                 GTAAAG        CAGACTCTA
                                    AAACATTT_
GAM435  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                 CATTTCA   TCACTGTCTGAGAT
                                 |||||||   |||||||||||||
                                 GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM435  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                 TTCA TTTCACTG  TGAG
                                 |||| ||||||||  ||||
                                 AAGT AAAGTGAC  GTTT
                                   A       CT
GAM435  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                 TTTC CTG TCTGAGAT
                                 |||| ||| ||||||||
                                 AAAG GAC AGACTCTA
                                   _  G
GAM435  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                 ATT CACTTTCACTGT
                                 ||| ||||||||||||
                                 TAA GTGAAAGTGACG
                                   C
GAM435  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                 TTCACTTT  CT TCTGAGAT
                                 ||||||||  || ||||||||
                                 AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM435  PP35      3'  ATCTCAGACTGAAA       22814      CT
                                 TTTCA  GTCTGAGAT
                                 |||||  |||||||||
                                 AAAGT  CAGACTCTA
                                    __
GAM435  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148         TCAC  C_
                                 CATTTCACTT   TGT  TGAG
                                 ||||||||||   |||  ||||
                                 GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM435  SEP15     3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                 TTTCACTTT ACTGT  GA
                                 ||||||||| |||||  ||
                                 AAAGTGAGA TGACA  CT
                                      A    TC
GAM435  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                 TTTCACTTT    TCTGAG
                                 |||||||||    ||||||
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                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM435  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM435  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM435  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226     A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM435  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM436  BRCA1    3'  CCACAGGTACAAGCCACAGGA  23558    A      CA  TCA
                                TC CTGTGGCT  GT   TGTGG
                                || ||||||||  ||   |||||
                                AG GACACCGA  CA   ACACC
                                 _       A_  TGG
GAM436  MXI1     3'  CCAAGGTCTGAGCCACAG     55259          TTCATG
                                CTGTGGCTCAG     TGG
                                ||||||||||      |||
                                GACACCGAGTC     ACC
                                      TGGA__
GAM436  MXI1     3'  CCAAGGTCTGAGCCACAG     19898          TTCATG
                                CTGTGGCTCAG     TGG
                                ||||||||||      |||
                                GACACCGAGTC     ACC
                                      TGGA__
GAM436  MYO1C    3'  CAGGCCGGGCCACAG       61202          A   CATG
                                CTGTGGCTC GTT    TG
                                ||||||||| |||    ||
                                GACACCGGG CGG    AC
                                     C  _____
GAM436  RBBP2    3'  ACTGAGCCACAGTGAT      17318
                                ATCACTGTGGCTCAGT
                                ||||||||||||||||
                                TAGTGACACCGAGTCA

GAM436  TCF3     3'  CCACACGAACTAGGGCAGTGGT 70731         GG TC     A
                                ATCACTGT  C  AGTTC TGTGG
                                ||||||||  |  ||||| |||||
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                                TGGTGACG  G  TCAAG ACACC
                                   __ GA    C
GAM436  C20orf20  3'  CCACCCCCCAGGCCACAGTGAT 36852          CAGTTCAT
                                ATCACTGTGGCT      GTGG
                                ||||||||||||      ||||
                                TAGTGACACCGG      CACC
                                     ACCCCC__
GAM436  FLJ12132  3'  CACCCCAAGCCACAGTGA    46466         CAGTTCAT
                                TCACTGTGGCT      GTG
                                ||||||||||||      |||
                                AGTGACACCGA      CAC
                                     ACCC____
GAM436  MGC2408   3'  CACATGAACCAATACAG     50324      GCTCA
                                CTGTG    GTTCATGTG
                                |||||    |||||||||
                                GACAT    CAAGTACAC
                                   AAC__
GAM436  LOC163231 5'  CACACATTCACCACAGTG    82436       CTC   TCA
                                CACTGTGG   AGT   TGTG
                                ||||||||   |||   ||||
                                GTGACACC   TTA   ACAC
                                     AC_   C__
GAM436  LOC201229 3'  CCACATGAACCAAGGAGAGAC  88142    GG   A___
                                GT  CTC    GTTCATGTGG
                                ||  |||    ||||||||||
                                CA  GAG    CAAGTACACC
                                 GA   GAAC
GAM437  CSNK1G2   3'  GGCCCAGCCCTGCAGGT     7170        AAC   ACTT
                                ACCTGTAG   CTG    GGCC
                                ||||||||   |||    ||||
                                TGGACGTC   GAC    CCGG
                                     CC_   ____
GAM437  PCDH11X   3'  CAATCATATTCTACAG      27238        CC   C
                                CTGTAGAA  TGA TTG
                                ||||||||  ||| |||
                                GACATCTT  ACT AAC
                                     AT   _
GAM437  SFTPA2    3'  GGTCAGGCTCTCCAGGTG    22650       T   A
                                CACCTG AGA CCTGACT
                                |||||| ||| |||||||
                                GTGGAC TCT GGACTGG
                                   C   C
GAM437  TBX5      5'  CCAAGTCCTATAGGTG      54888         AACCT
                                CACCTGTAG    GACTTGG
                                |||||||||    |||||||
                                GTGGATATC    CTGAACC
                                     _____
GAM437  TBX5      5'  CCAAGTCCTATAGGTG      3956          AACCT
                                CACCTGTAG    GACTTGG
                                |||||||||    |||||||
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                              GTGGATATC    CTGAACC
                                    _____
GAM437  ZNF132   3' GCCAAGTCAAACTTCATGCAG 12826     _  CC_
                              CTGTA GAA   TGACTTGGC
                              ||||| |||   |||||||||
                              GACGT CTT   ACTGAACCG
                                 A   CAA
GAM437  C9orf14  5' GCCAAGTCCATCTAAAGTG   86676    CTG   ACCT
                              CAC   TAGA   GACTTGGC
                              |||   ||||   |||||||||
                              GTG   ATCT   CTGAACCG
                                AA_   AC__
GAM437  DKFZP434J037 3' GCCCGGTCAGGCTCTCAG    48213    T  A     T
                              CTG AGA CCTGACT GGC
                              ||| ||| ||||||| |||
                              GAC TCT GGACTGG CCG
                                _  C      C
GAM437  ELOVL2   3' GCCTAGGTTATACAG      34959      G     ACTT
                              CTGTA AACCTG    GGC
                              ||||| ||||||    |||
                              GACAT TTGGAT    CCG
                                 A     ____
GAM437  FLJ11996 3' TTAGGTGCCTACAGGT     46447        A_
                              ACCTGTAG  ACCTGA
                              ||||||||  ||||||
                              TGGACATC  TGGATT
                                   CG
GAM437  FLJ13265 3' GCCAGAACTTTACAGGTG    45926         ACCTGAC
                              CACCTGTAGA      TTGGC
                              ||||||||||      |||||
                              GTGGACATTT      GACCG
                                    CAA____
GAM437  FLJ20038 5' CCAAGTCAGAACTGCG      34402      AAC
                              TGTAG   CTGACTTGG
                              |||||   |||||||||
                              GCGTC   GACTGAACC
                                 AA_
GAM437  FLJ20972 3' GCCAAGTCAGTTCCTGGTG   46725     TGTA   C
                              CACC    GAAC TGACTTGGC
                              ||||    |||| |||||||||
                              GTGG    CTTG ACTGAACCG
                                TC__    _
GAM437  KIAA0061 3' GCCAAGTTCTACATGTG     68292     C     ACCTG
                              CAC TGTAGA    ACTTGGC
                              ||| ||||||    |||||||
                              GTG ACATCT    TGAACCG
                                T     _____
GAM437  KIAA0141 3' CGGGAGTTCAGGTTCCCAAG  28732    GTA      _  GG
                              CT   GAACCTGA CTT  CCG
                              ||   |||||||| |||  |||
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                                GA  CTTGGACT GAG  GGC
                                 ACC      T  __
GAM437  KIAA1260  3'  GTCAGGTTGCACAGGTG    60029       AG
                                CACCTGT  AACCTGAC
                                |||||||  ||||||||
                                GTGGACA  TTGGACTG
                                    CG
GAM437  KIAA1301  3'  GCCTATGGGTTTACAGG    66342       A   ACTT
                                CCTGTAGA CCTG   GGC
                                |||||||| ||||   |||
                                GGACATTT GGGT   CCG
                                    _   AT__
GAM437  KIAA1485  3'  GGCTGCCAGGCTCTGCAGG   89262       A   ACT
                                CCTGTAGA CCTG   TGGCC
                                |||||||| ||||  |||||
                                GGACGTCT GGAC   GTCGG
                                    C   C__
GAM437  KIAA1546  3'  CAGGCAAACACCTACAGGT   67904       AACC_  A
                                ACCTGTAG    TG CTTG
                                ||||||||    || ||||
                                TGGACATC    AC GGAC
                                    CACAA  _
GAM437  KIAA1643  3'  CACCTCAGGTTCCCAGGTG   64548      TA      CT
                                CACCTG  GAACCTGA  TG
                                ||||||  ||||||||  ||
                                GTGGAC  CTTGGACT  AC
                                   C_      CC
GAM437  MGC10981  3'  CTGAGTCGATCCCACAGGTG   51017      A_  ACC    TG
                                CACCTGT  GA   TGACT  G
                                |||||||  ||   |||||  |
                                GTGGACA  CT   GCTGA  C
                                    CC  A__    GT
GAM437  MGC11324  3'  AGGCAGAACCTACAGGTG    51164       AAC   A
                                CACCTGTAG   CTG CTT
                                |||||||||   ||| |||
                                GTGGACATC   GAC GGA
                                     CAA  _
GAM437  MOST2     5'  CGGCCAAGCCTGTGCCTACGGT 39682     T   A_  CTGA
          G                      CACC GTAG  AC    CTTGGCCG
                                ||||  ||||  ||    ||||||||
                                GTGG CATC  TG    GAACCGGC
                                  _    CG  TCC_
GAM437  PADI3     3'  CGGCCAAGCTCCTGC      32657     AACCT  _
                                GTAG    GA CTTGGCCG
                                ||||    || ||||||||
                                CGTC    CT GAACCGGC
                                  _____  C
GAM437  phospho1  5'  CAGAGTCCCTACAGGTG     82367       A_  _
                                CACCTGTAG  AC CTG
                                |||||||||  || |||
```

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                                GTGGACATC  TG GAC
                                     CC  A
GAM437  RAB3D    3'  TGGCTGCCAGGTTCCTCAGG  15010     TA     ACT
                                CCTG  GAACCTG  TGGCCG
                                ||||  |||||||  ||||||
                                GGAC  CTTGGAC  GTCGGT
                                  TC      C__
GAM437  LOC122955 5'  GCTGTCAGTTCTACAG     75585        C    TT
                                CTGTAGAAC TGAC  GGC
                                ||||||||| ||||  |||
                                GACATCTTG ACTG  TCG
                                      _   __
GAM437  LOC149386 5'  CAAGTCAGGTCCACA      84404     A  A
                                TGT GA CCTGACTTG
                                ||| || |||||||||
                                ACA CT GGACTGAAC
                                  C  _
GAM437  LOC150197 5'  GCCAGGTCCTACGG       79598       AACCT
                                CTGTAG    GACTTGGC
                                ||||||    ||||||||
                                GGCATC    CTGGACCG
                                     _____
GAM437  LOC151878 5'  CTAGTTCAGACTCTAAGG    80374     G    AC    C
                                CCT TAGA  CTGA TTGG
                                ||| ||||  |||| ||||
                                GGA ATCT  GACT GATC
                                  _    CA    T
GAM437  LOC153146 5'  GCCAGAGCCTACAGGT     85929        AAC  GAC
                                ACCTGTAG   CT   TTGGC
                                ||||||||   ||   |||||
                                TGGACATC   GA   GACCG
                                     C__  ___
GAM437  LOC221931 3'  AAGTTGCAGGTTCTTCAG    93992     T      __
                                CTG AGAACCTG  ACTT
                                ||| ||||||||  ||||
                                GAC TCTTGGAC  TGAA
                                  T       GT
GAM437  LOC254848 5'  CGGCAGGCACAGGTTCTCCA  97090    T      A_    G
                                TG AGAACCTG  CTTG CCG
                                || ||||||||  |||| |||
                                AC TCTTGGAC  GGAC GGC
                                 C       AC    _
GAM438  ARNT2    3'  AAACAACCCGTGCATCCCTGC  29450     A    TTTTA
                                GTA GGAT     GGGTTGTTT
                                ||| ||||     |||||||||
                                CGT CCTA     CCCAACAAA
                                  C    CGTG_
GAM438  LCT      3'  AACCGTAAAAATCCTT      9697           G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
```

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                                TTCCTAAAAAT CCAA
                                      G
GAM438  RPL15    3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM438  FBXO30   3'  AACTAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                  G        AA
GAM438  KIAA0494 3'  AACAACCCTTACTTAC      28736      GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM438  PRO0641  5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                   ___    C
GAM438  SMT3H2   3'  AACAACATAAAAATCCTTGC   22670           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM438  LOC120103 3' AACCTATGAAAAATCCTTGC   74002           A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
                                CGTTCCTAAAAA   TCCAA
                                      GTA
GAM438  LOC129831 3' AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM438  LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                      GTA GGATTTTT     TTGTTT
                                ||| ||||||||     ||||||
                                CGT CCTAAAAA     AACAAA
                                  C       GATAA
GAM438  LOC148089 3' GGCCCTAAAAATTCCTAC    78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM438  LOC154547 3' AACAACATAAAAATCCTTGC   76050           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
```

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                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM438  LOC158104 3'  ACAGCCAAAAATCCTTA     60313          AG
                                TAAGGATTTTT  GGTTGT
                                |||||||||||  ||||||
                                ATTCCTAAAAA  CCGACA
                                      __
GAM438  LOC205880 5'  AAACAACCATCATCCTGAC   90709    A    TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM438  LOC221561 3'  AACAACATAAAAATCCTTGC  92130          GG
                                GTAAGGATTTTTA  GTTGTT
                                |||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM438  LOC257591 3'  AACAACATAAAAATCCTTGC  97840          GG
                                GTAAGGATTTTTA  GTTGTT
                                |||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM438  LOC51145  3'  AGCTAAAATCCTTAC       32393          TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
                                CATTCCTAAAA   TCGA
                                      ___
GAM439  ADCY7     3'  AGGCATGCAGATGGCTGTG   6636        AC     GC
                                CACAGCCA  TTTGTG  GCCT
                                ||||||||  ||||||  ||||
                                GTGTCGGT  AGACGT  CGGA
                                    __     A_
GAM439  APXL      3'  GGTGAAGCTGGCTGTG      7930         ACTTT  GG
                                CACAGCCA    GT  CGCC
                                ||||||||    ||  ||||
                                GTGTCGGT    CG  GTGG
                                    _____  AA
GAM439  INPPL1    3'  GGCACCACGAAGCTGTG     7803        CAAC      C
                                CACAGC    TTTGTGG GCC
                                ||||||    ||||||| |||
                                GTGTCG    AAGCACC CGG
                                    ____       A
GAM439  LGR6      5'  AGGCGCCAACACCTTGACTG  84199     C   CTTTG
                                CAG CAA     TGGCGCCT
                                ||| |||     ||||||||
                                GTC GTT     ACCGCGGA
                                  A   CCACA
GAM439  SH3GL3    5'  GTTCCACAAAGCCAGCCAGTA  11636     ACA  CAA       C
                                TAC   GC   CTTTGTGG GC
                                |||   ||   |||||||| ||
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                                ATG  CG  GAAACACC TG
                                  AC_ ACC      T
GAM439  SIAT8E   5' AGGCGCCAAGTCGGC     59857    A  TTG
                                GCC ACT  TGGCGCCT
                                ||| |||  ||||||||
                                CGG TGA  ACCGCGGA
                                  C  ___
GAM439  SRM      3' GCCTATACCAGCTGTGTA    11956       CAACTT   C
                                TACACAGC    TGTGG GC
                                ||||||||    ||||| ||
                                ATGTGTCG    ATATC CG
                                    ACC___   _
GAM439  WISP2    5' AGGCTCAAAGCTGGCTCTG   13932   C   A   TGGC
                                CA AGCCA CTTTG   GCCT
                                || ||||| |||||   ||||
                                GT TCGGT GAAAC   CGGA
                                 C   C   T___
GAM439  ACAS2    3' CAGGGAGGCAGCTGTGTA    37932       CAA   G
                                TACACAGC  CTTT TG
                                ||||||||  |||| ||
                                ATGTGTCG  GAGG AC
                                    ACG   G
GAM439  ACAS2    3' CAGGGAGGCAGCTGTGTA    57702       CAA   G
                                TACACAGC  CTTT TG
                                ||||||||  |||| ||
                                ATGTGTCG  GAGG AC
                                    ACG   G
GAM439  BRD1     3' ATAAAGTTATGCTGTGTA    27414       C_
                                TACACAGC  AACTTTGT
                                ||||||||  ||||||||
                                ATGTGTCG  TTGAAATA
                                    TA
GAM439  CARD9    3' AGGCGCAGCTACTGGCCGTG  42283    A   ACTTT  G
                                CAC GCCA    GT GCGCCT
                                ||| ||||    || ||||||
                                GTG CGGT    CG CGCGGA
                                  C   CAT__  A
GAM439  CASKIN1  3' AGGCGCTGCCGTCGGCTGTCA 40397   C    A  TTT TG
                                A ACAGCC AC  G  GCGCCT
                                | |||||| ||  |  ||||||
                                A TGTCGG TG  C  CGCGGA
                                 C    C  C__ GT
GAM439  CNOT7    3' CAGGAAAATTGGTTGTG     53983       C_  G
                                CACAGCCAA  TTT TG
                                |||||||||  ||| ||
                                GTGTTGGTT  AAG AC
                                     AA  G
GAM439  EHM2     3' ACAAGTTGGCTGTTA       38910   C       T
                                A ACAGCCAACTT GT
                                | ||||||||||| ||
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                                A TGTCGGTTGAA CA
                                 T        _
GAM439  FLJ10508  3'  ACTGAGAAATGGCTGTGTA   36198          A__   T
                                TACACAGCCA   CTT GT
                                ||||||||||   ||| ||
                                ATGTGTCGGT   GAG CA
                                      AAA   T
GAM439  FLJ14721  3'  GGCACCACAGGGGCT      51585      AAC      C
                                AGCC   TTTGTGG GCC
                                ||||   ||||||| |||
                                TCGG   GGACACC CGG
                                  ___      A
GAM439  FLJ22004  3'  TGCTATGTAGCTGTGTA     47214         CA  TTT
                                TACACAGC  AC   GTGGCG
                                ||||||||  ||   ||||||
                                ATGTGTCG  TG   TATCGT
                                    A_  ___
GAM439  HCBP6     3'  GTTGGAAAGTTGGCTG      80902          G
                                CAGCCAACTTT TGGC
                                |||||||||||| ||||
                                GTCGGTTGAAA GTTG
                                      G
GAM439  KIAA0527  3'  ACAAAGTTAGCTTTGTA     95787      C   C
                                TACA AGC AACTTTGT
                                |||| ||| ||||||||
                                ATGT TCG TTGAAACA
                                  T   A
GAM439  KIAA0648  3'  TCAAGAGTTGGCTGTGTA    82657            G
                                TACACAGCCAACTTT TGG
                                |||||||||||||| |||
                                ATGTGTCGGTTGAGA ACT
                                          _
GAM439  KIAA1157  3'  AGGCTTTGTGAAGTCAGCTGTG 72238       CA     TG C
                                CACAGC  ACTTTG  G GCCT
                                ||||||  ||||||  | ||||
                                GTGTCG  TGAAGT  T CGGA
                                    AC     GT T
GAM439  KIAA1979  3'  CGCATTGGTTGGCTGTGT    88276           T_
                                ACACAGCCAACT  TGTG
                                ||||||||||||  ||||
                                TGTGTCGGTTGG  ACGC
                                      TT
GAM439  KIAA1987  3'  GGAGCCAGGCTGTGTA      88019         AACTTTG   G
                                TACACAGCC      TGGC CC
                                |||||||||      |||| ||
                                ATGTGTCGG      ACCG GG
                                     _______   A
GAM439  MAPK8IP3  3'  GCCAGTATAAGTCAGCTGTG  52985       CA   TG__
                                CACAGC  ACTT    TGGC
                                ||||||  ||||    ||||
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                                GTGTCG  TGAA   ACCG
                                   AC   TATG
GAM439  MCM10    3'  GCAAAGGATTGGCTGTGTA   37573          __
                                TACACAGCCAA  CTTTGT
                                ||||||||||  ||||||
                                ATGTGTCGGTT  GAAACG
                                      AG
GAM439  PSR      3'  CCACAGAGCCAGCTGTGTA   65179        CAA
                                TACACAGC   CTTTGTGG
                                ||||||||   ||||||||
                                ATGTGTCG   GAGACACC
                                     ACC
GAM439  TRIM28   5'  GGCAGCAGTTGGCCGTG     19267     A      TTGTG  _
                                CAC GCCAACT    GC GCC
                                ||| |||||||    || |||
                                GTG CGGTTGA    CG CGG
                                  C      _____  A
GAM439  ZNF263   5'  AGGCGCCGGAGCCGGC      19222     AA   TG
                                GCC  CTT  TGGCGCCT
                                |||  |||  ||||||||
                                CGG  GAG  GCCGCGGA
                                  CC   __
GAM439  LOC118672 5'  AGGCGCCAATCCTACTGGCTG  73922       ACTTTG_
                                CAGCCA      TGGCGCCT
                                ||||||      ||||||||
                                GTCGGT      ACCGCGGA
                                   CATCCTA
GAM439  LOC149997 5'  GCCATAAAACTGGCTG      76341       AC
                                CAGCCA  TTTGTGGC
                                ||||||  ||||||||
                                GTCGGT  AAATACCG
                                   CA
GAM439  LOC151126 3'  CATTTTTAGTTGCTGTGTA   80125        C    TT__
                                TACACAGC AACT    GTG
                                |||||||| ||||    |||
                                ATGTGTCG TTGA    TAC
                                     _   TTTT
GAM439  LOC158852 5'  AGGCGCCACAACTTCACTG    82032     CCAACT
                                CAG     TTGTGGCGCCT
                                |||     ||||||||||
                                GTC     AACACCGCGGA
                                  ACTTC_
GAM439  LOC170221 3'  AGGCGCCGCTCCCTGGCT     82576      ACTTT
                                AGCCA    GTGGCGCCT
                                |||||    |||||||||
                                TCGGT    CGCCGCGGA
                                   CCCT_
GAM439  LOC201292 5'  GCAGTTGCTAAGCCGGCTGTGT 88188         AA   T TG  _
           G                     TACACAGCC  CTT G  GC GC
                                |||||||||  ||| |  || ||
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                                GTGTGTCGG  GAA C  TG CG
                                     CC   T GT  A
GAM439  LOC221154 5'  GCGCCGCCTAGCTGCGCT    93546    _  A  TT
                                AGC CA CT  GTGGCGC
                                ||| || ||  |||||||
                                TCG GT GA  CGCCGCG
                                  C  C  TC
GAM439  LOC221296 3'  AGGCAAAGAAGTTGGCCTGT   91955     _      GTGGC
                                ACAG CCAACTTT    GCCT
                                |||| ||||||||    ||||
                                TGTC GGTTGAAG    CGGA
                                  C       AAA__
GAM439  LOC221576 3'  GGGCATGCAAAGCCGGCTGTGT 93705         AA      GC
          G                      TACACAGCC  CTTTGTG  GCCT
                                |||||||||  |||||||  ||||
                                GTGTGTCGG  GAAACGT  CGGG
                                     CC      A_
GAM439  LOC257122 5'  AGGCGCCACAACTTCACTG   96212    CCAACT
                                CAG     TTGTGGCGCCT
                                |||     ||||||||||
                                GTC     AACACCGCGGA
                                  ACTTC_
GAM439  LOC257515 3'  GGGCATGCAAAGCCGGCTGTGT 97785         AA      GC
          G                      TACACAGCC  CTTTGTG  GCCT
                                |||||||||  |||||||  ||||
                                GTGTGTCGG  GAAACGT  CGGG
                                     CC      A_
GAM439  LOC257572 3'  GGGCATGCAAAGCCGGCTGTGT 97914         AA      GC
          G                      TACACAGCC  CTTTGTG  GCCT
                                |||||||||  |||||||  ||||
                                GTGTGTCGG  GAAACGT  CGGG
                                     CC      A_
GAM440  APG5L    3'  ATCCAGAGGTTACTGG     16758     AT
                                CCA  TAACCTCTGGAT
                                |||  ||||||||||||
                                GGT  ATTGGAGACCTA
                                  C_
GAM440  HELZ     3'  AGCCAAGAGGTTAATTG     29648           GGATCCA
                                CAATTAACCTCT      GCT
                                ||||||||||||      |||
                                GTTAATTGGAGA      CGA
                                       AC_____
GAM440  SEC22L1   5'  CAGCTGGATCTCCGGT     16887     TCT
                                ACC   GGATCCAGCTG
                                |||   ||||||||||
                                TGG   TCTAGGTCGAC
                                  CC_
GAM440  ZNF274    5'  AGCTGGACCCTAAATTGG    32881       AACCTCT  A
                                CCAATT      GG TCCAGCT
                                ||||||      || |||||||
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                                GGTTAA      CC AGGTCGA
                                   AT_____  C
GAM440  D2S448   3'  CAGCTGTGAGGAAGGTCATTGG 73518      TA   _  GGA  _
                                CCAAT  ACCT CT   TC CAGCTG
                                |||||  |||| ||   || ||||||
                                GGTTA  TGGA GG   AG GTCGAC
                                   C_    A  ___  T
GAM440  FUK      5'  CAGCCGAAGGGAGTTGATTGG  58972         _   GGA  CA
                                CCAATTAAC CTCT   TC  GCTG
                                |||||||||| ||||   ||  ||||
                                GGTTAGTTG GGGA   AG  CGAC
                                      A    ___  C_
GAM440  GFR      3'  CAGCCAGTGCAGGGAGGTTAAG 24468    A       __ G  CCA
           TG                     CA TTAACCTCT  G AT   GCTG
                                || |||||||||  | ||   ||||
                                GT AATTGGAGG  C TG   CGAC
                                 G        GA G  AC_
GAM440  HGC6.2   5'  CAGCTGGAGATGTGGTCAACGG 26834    AA  A   TCTGGA
           G                     CC  TT ACC     TCCAGCTG
                                ||  || |||     ||||||||
                                GG  AA TGG     AGGTCGAC
                                 GC  C   TGTAG_
GAM440  KIAA0551  3'  AGCTAAGAGGTCACTTGG    66837     TTA     GGATCC
                                CCAA   ACCTCT     AGCT
                                ||||   ||||||     ||||
                                GGTT   TGGAGA     TCGA
                                  CAC     A_____
GAM440  KIAA1908  5'  GCTGAAGGTTAATTCA     73399    C       CTGGATC
                                C AATTAACCT      CAGC
                                | |||||||||      ||||
                                A TTAATTGGA      GTCG
                                 C        A_______
GAM440  LOC121838 5'  CAGCTGGAAGGAGTCATATTGG 75997      TAAC    GGA
                                CCAAT    CTCT   TCCAGCTG
                                |||||    ||||   ||||||||
                                GGTTA    GAGG   AGGTCGAC
                                   TACT    A__
GAM440  LOC149414 3'  AGCTGGAACAGACTATTG    84412     TAACC    GA
                                CAAT     TCTG  TCCAGCT
                                ||||     ||||  |||||||
                                GTTA     AGAC  AGGTCGA
                                  TC___    A_
GAM440  LOC205272 5'  CAGCTGGATCAAGGGATTCACT 89496     ATTAAC    G
           GG                     CCA      CTCT GATCCAGCTG
                                |||      |||| ||||||||||
                                GGT      GGGA CTAGGTCGAC
                                  CACTTA    A
GAM440  LOC63928  3'  CAGCTGGATCCAAGGG      42031     TC
                                CC  TGGATCCAGCTG
                                ||  ||||||||||||
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                                GG  ACCTAGGTCGAC
                                 GA
GAM441  CABC1    5'  GCACAAACAGACGCTC      39654      CTGGC
                                GAGC    TCTGTTTGTGC
                                ||||    ||||||||||
                                CTCG    AGACAAACACG
                                  C____
GAM441  CEACAM5  3'  AACAGAGCAAGACTCCA     15153      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM441  F2R      3'  AACAGAGCAAGACTCCA     8831       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM441  FGFR2    3'  GACAGAGCGAGACTCCA     43377      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM441  FGFR2    3'  GACAGAGCGAGACTCCA     43383      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM441  FUT6     3'  GACAGAGCAAGACTCCA     3812       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441  GCLM     5'  GGCGCAGACCAGGCTCCA    9026          C    TTGT  _
                                TGGAGCCTGG TCTGT    GC C
                                |||||||||| |||||    || |
                                ACCTCGGACC AGACG    CG G
                                      _    _____  A
GAM441  GPC1     3'  GGCTGCAGAGCCCGGCCCCA  9103       A  T      TTGT
                                TGG GCC GGCTCTGT    GCC
                                ||| ||| ||||||||    |||
                                ACC CGG CCGAGACG    CGG
                                  C  C       T___
GAM441  HPSE     3'  CAAACAGGCCAGGCTCCA    21890          T
                                TGGAGCCTGGC CTGTTTG
                                |||||||||| |||||||
                                ACCTCGGACCG GACAAAC
                                          _
GAM441  IFIT4    3'  AACAGAGCAAGACTCCA     70918      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  A
GAM441  KCNJ5   3' GACAGAGCGAGACTCCA    6091      C  G
                                TGGAG CT GCTCTGTT
                                |||||  ||  ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM441  LY94    3' GACAGAGCGAGACTCCA    16705     C  G
                                TGGAG CT GCTCTGTT
                                |||||  ||  ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM441  LZTS1   3' ACAGAGCCTGGCCCCA    40676     A  T
                                TGG GCC GGCTCTGT
                                |||  |||  ||||||||
                                ACC CGG CCGAGACA
                                  C  T
GAM441  MSH3    3' AACAGAGCAAGACTCCA    10116     C  G
                                TGGAG CT GCTCTGTT
                                |||||  ||  ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM441  POLH    3' AACAGAGCGAGACTCCA    21461     C  G
                                TGGAG CT GCTCTGTT
                                |||||  ||  ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM441  PRKAB1  3' GCACACCACCAGGCTCCA   20736       CTC  TT
                                TGGAGCCTGG  TG TGTGC
                                ||||||||||  ||  |||||
                                ACCTCGGACC  AC ACACG
                                      ___ C_
GAM441  SIGLEC6 3' AACAGAGCGAGACTCCA    59925     C  G
                                TGGAG CT GCTCTGTT
                                |||||  ||  ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM441  SLC10A2 5' AGCAGAGCCAGGGCCCA    4840      AG
                                TGG  CCTGGCTCTGTT
                                |||  ||||||||||||
                                ACC  GGACCGAGACGA
                                  CG
GAM441  SNRPN   5' CAAGCAAAAACCAGGCTCCA  42991       CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM441  SNRPN   5' CAAGCAAAAACCAGGCTCCA  42998       CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
```

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                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM441  SNRPN    5'  CAAGCAAAAACCAGGCTCCA  43005        CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM441  SNRPN    5'  CAAGCAAAAACCAGGCTCCA  43013        CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM441  TNFSF11  5'  CAGGAGCCAAAGCCGGGCTCCA 13512          CT_   G
                                TGGAGCCTGGCT  GTTT TG
                                ||||||||||||  |||| ||
                                ACCTCGGGCCGA  CGAG AC
                                      AAC   G
GAM441  TSNAX    3'  GGTAACAGAGCAAGACTCCA  20002     C  G     TTG
                                TGGAG CT GCTCTGT  TGCC
                                ||||| || |||||||  ||||
                                ACCTC GA CGAGACA  ATGG
                                   A  A     ___
GAM441  UBE2L3   3'  GCCTTTGCAGAGTCAAGCTCCA 12503      C       TTGT
                                TGGAGC TGGCTCTGT   GC
                                ||||||  |||||||||  ||
                                ACCTCG ACTGAGACG   CG
                                    A       TTTC
GAM441  ZNF264   3'  AACAGAGCGAGACTCCA    12738     C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM441  ARNTL2   3'  GACAGAGCGAGACTCCA    39466     C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM441  C22orf5  3'  GGATCAGAGCCAGACACCA   24344    AGC      TTTGTG
                                TGG  CTGGCTCTG    CC
                                |||  |||||||||    ||
                                ACC  GACCGAGAC    GG
                                  ACA       TA____
GAM441  DKFZp547C176 3'  GACAGAGCAAGACTCCA    67223     C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441  DKFZp564K142 3'  AACAGAGCGAGACTCCA    49522     C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  G
GAM441  FADS1     3'  GACAGAGCAAGACTCCA     25477      C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441  FLJ12298  3'  AACAGAGCGAGACTCCA     49664      C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM441  FLJ14117  3'  AACAGAGCAAGACTCCA     42896      C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM441  FLJ14251  3'  GGTAACAGAGCGAGACTCCA   45977      C  G     TTG
                                TGGAG CT GCTCTGT   TGCC
                                |||||| || |||||||   ||||
                                ACCTC GA CGAGACA   ATGG
                                   A  G     ___
GAM441  FLJ14327  3'  AACAGAGCTAGACTCCA     46127      C
                                TGGAG CTGGCTCTGTT
                                ||||| ||||||||||
                                ACCTC GATCGAGACAA
                                   A
GAM441  FLJ14566  5'  GGCCACAGAGCCAGCCCCA   51446     A  C       TT T
                                TGG GC TGGCTCTGT  G GCC
                                ||| || |||||||||  | |||
                                ACC CG ACCGAGACA  C CGG
                                  C  _       __ _
GAM441  FLJ20084  3'  AACAGAGCGAGACTCCA     34511      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM441  FLJ20306  3'  GACAGAGCAAGACTCCA     34917      C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441  FLJ20456  3'  GGTAACAGAGCTAGACTCCA   35215      C       TTG
                                TGGAG CTGGCTCTGT   TGCC
                                ||||| ||||||||||   ||||
                                ACCTC GATCGAGACA   ATGG
                                   A        ___
GAM441  FLJ22054  3'  AACAGAGCAAGACTCCA     94391      C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  A
GAM441  FLJ22393  5'  AGCAGGAACCAGGCTCCA    47058          C_
                                TGGAGCCTGG  TCTGTT
                                ||||||||||  ||||||
                                ACCTCGGACC  GGACGA
                                      AA
GAM441  FLJ23598  3'  GCCAAGAGCCAGCTCCA     45522       C      GTT  T
                                TGGAGC TGGCTCT   TG GC
                                |||||| |||||||   || ||
                                ACCTCG ACCGAGA   AC CG
                                   _      ___  _
GAM441  FLJ31168  3'  GACAGAGCGAGACTCCA     58502       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM441  GP5       3'  GACAGAGCGAGACTCCA     15646       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM441  GTPBP5    3'  GACAGAGCAAGACTCCA     65357       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441  HIC       3'  AACAGAGCGAGACTCCA     67444       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM441  ING1-like 3'  GACAGAGCGAGACTCCA     54156       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM441  KBRAS2    3'  AACAGAGCAAGACTCCA     34191       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM441  KIAA0189  3'  CAGGAGCAGAGCCAGGCCCA  28273      A           G
                                TGG GCCTGGCTCTGTTT TG
                                ||| |||||||||||||| ||
                                ACC CGGACCGAGACGAG AC
                                  _            G
GAM441  KIAA0472  3'  AGCAGAGCAAGACTCCA     71853       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACGA
                                   A  A
GAM441  KIAA0563  3'  GACAGAGCAAGACTCCA     29188      C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441  KIAA0565  3'  GACAGAGCAAGACTCCA     66890      C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441  KIAA0648  3'  CAAACAGAAGCAGGCTCCA   82651         GC
                                TGGAGCCTG  TCTGTTTG
                                |||||||||  ||||||||
                                ACCTCGGAC  AGACAAAC
                                      GA
GAM441  KIAA0924  3'  AACAGAGCGAGACTCCA     29712      C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM441  KIAA1028  3'  CAGAGCACAGGCTCCA      91934         _
                                TGGAGCCTG GCTCTG
                                |||||||||| ||||||
                                ACCTCGGAC CGAGAC
                                      A
GAM441  KIAA1719  3'  GGCCAGGGCCAGGCCCCA    68169     A         TTTGT
                                TGG GCCTGGCTCTG    GCC
                                ||| ||||||||||     |||
                                ACC CGGACCGGGAC    CGG
                                  C         _____
GAM441  KIAA1940  3'  GGTCTCAGAACCAAGGCTCCA  79988         _  C    TTTGT
                                TGGAGCCT GG TCTG    GCC
                                |||||||| || ||||    |||
                                ACCTCGGA CC AGAC    TGG
                                     A  A   TC___
GAM441  LGI2      3'  CAAATCAAAGCCAGGCTC     36397          C  _
                                GAGCCTGGCT TG TTTG
                                |||||||||| || ||||
                                CTCGGACCGA AC AAAC
                                      A  T
GAM441  MGC10200  3'  AACAGAGCGAGACTCCA     58980      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM441  MGC2705   5'  GCACCAAGCCAGGCTCC     51113          C  TTT
                                GGAGCCTGGCT TG   GTGC
                                |||||||||| ||   ||||
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                                CCTCGGACCGA AC   CACG
                                          _  ___
GAM441  MGC4562  3'  AACAGAGCGAGACTCCA     55908      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM441  MGC4663  3'  AACAGAGCCAGACTCC      44501      C
                                GGAG CTGGCTCTGTT
                                |||| ||||||||||
                                CCTC GACCGAGACAA
                                  A
GAM441  NPTXR    3'  AACAGAGCAAGACTCCA     54171      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM441  NPTXR    3'  AACAGAGCAAGACTCCA     26635      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM441  OR7C1    5'  AACAGAGCCAAGTCCA      82428      G C
                                TGGA C TGGCTCTGTT
                                |||| | ||||||||||
                                ACCT G ACCGAGACAA
                                  _ A
GAM441  POFUT1   3'  AACAGAGCGAGACTCCA     70462      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM441  PTK6     3'  GACAGAGCGAGACTCCA     19936      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM441  RASGRF2  3'  GCACGAAGCCAGGCTCC     61042          CTGT
                                GGAGCCTGGCT   TTGTGC
                                ||||||||||    ||||||
                                CCTCGGACCGA   AGCACG
                                          ____
GAM441  SC65     3'  GACAGAGCGAGACTCCA     21289      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM441  SNURF    3'  CAAGCAAAAACCAGGCTCCA  19052          CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
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                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM441  TMG4     3' GACAGAGCAAGACTCCA    43989      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441  WBSCR23  3' GACAGAGCAAGACTCCA    46762      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441  WIRE     3' GACAGAGCCAGACTCC     78305     C
                                GGAG CTGGCTCTGTT
                                |||| ||||||||||
                                CCTC GACCGAGACAG
                                   A
GAM441  WSB1     3' AACAGAGCGAGACTCCA    56138      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM441  WSB1     3' AACAGAGCGAGACTCCA    56144      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM441  LOC115704 3' CAGCCAGAGCCAGGCCCC  73541    A        T
                                GG GCCTGGCTCTG TTG
                                || |||||||||| |||
                                CC CGGACCGAGAC GAC
                                 C         C
GAM441  LOC124220 5' GGCACAACCAGACGCC    59146    _   T
                                GGC TCTG TTGTGCC
                                ||| |||| |||||||
                                CCG AGAC AACACGG
                                  C   C
GAM441  LOC127262 3' GACAGAGCGAGACTCCA    76110      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM441  LOC129563 3' AGCAGAGCAGGCCCCA     74878    A    G
                                TGG GCCTG CTCTGTT
                                ||| ||||| |||||||
                                ACC CGGAC GAGACGA
                                  C    _
GAM441  LOC129880 3' AACAGAGCAAGACTCCA    74900      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  A
GAM441   LOC143196 3'  AACAGAGCGAGACTCCA     82903      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM441   LOC144319 3'  GGCACAAACAGGCGCCCC     83057    A  CTG  T
                                GG GC   GC CTGTTTGTGCC
                                || ||   || ||||||||||
                                CC CG   CG GACAAACACGG
                                 C  ___  _
GAM441   LOC145216 3'  GACAGAGCAAGACTCCA     83267      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441   LOC145820 3'  GACAGAGCAAGACTCCA     77514      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441   LOC146227 3'  GGTCAGAGCCAGACCCC     77711    AGC       TTTGT
                                GG   CTGGCTCTG    GCC
                                ||   |||||||||    |||
                                CC   GACCGAGAC    TGG
                                 CCA       _____
GAM441   LOC146713 3'  AACAGAGCAAGACTCCA     83720      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM441   LOC147071 3'  GACAGAGCAAGACTCCA     72999      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441   LOC147649 3'  GACAGAGCGAGACTCCA     78414      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM441   LOC148936 3'  AACAGAGCAAGACTCCA     84286      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM441   LOC149803 5'  CAGGCAGAGCAAGCTCCA     79538       CTG
                                TGGAGC   GCTCTGTTTG
                                ||||||   ||||||||||
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                                ACCTCG   CGAGACGGAC
                                   AA_
GAM441   LOC150299 3'  GACAGAGCAAGACTCCA     84970      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441   LOC151429 3'  GACAGAGCAAGACTCCA     85353      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441   LOC151904 3'  AACAGAGCGAGACTCCA     80382      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM441   LOC158292 5'  GACAGAGCGAGACTCCA     86730      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM441   LOC162137 5'  CAAGCAGGCCAAGCCCCA    87111     A  C   T
                                TGG GC TGGC CTGTTTG
                                ||| || |||| |||||||
                                ACC CG ACCG GACGAAC
                                  C  A   _
GAM441   LOC163033 5'  CGACCAGGACCAAGCCCCA   82396     A  C   CT   T
                                TGG GC TGG  CTG TTG
                                ||| || |||  ||| |||
                                ACC CG ACC  GAC AGC
                                  C  A   AG   C
GAM441   LOC163682 3'  ACACTCAAAGCCGGGCTCCA  87020           C  TT
                                TGGAGCCTGGCT TG  TGT
                                |||||||||||| ||  |||
                                ACCTCGGGCCGA AC  ACA
                                       A  TC
GAM441   LOC200261 3'  GCACAAACCTCTGGAGGCCCA 88655     A   GGCTCT
                                TGG GCCT     GTTTGTGC
                                ||| ||||     ||||||||
                                ACC CGGA     CAAACACG
                                  _   GGTCTC
GAM441   LOC201173 3'  GACAGAGCAAGACTCCA     87329      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441   LOC201182 5'  AACAGAGCAAGACTCCA     89760      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  A
GAM441   LOC219627 3'  GACAGAGCGAGACTCCA     92178      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM441   LOC221543 5'  GACAGAGCAAGACTCCA     93742      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441   LOC221943 5'  GACAGAGCAAGACTCCA     93989      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441   LOC222160 5'  GACAGAGCAAGACTCCA     94127      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441   LOC253039 5'  GGCTCCAAAACCAGGCTCTA   96159          CTCTG   T_
                                TGGAGCCTGG    TTTG  GCC
                                ||||||||||    ||||  |||
                                ATCTCGGACC    AAAC  CGG
                                      A____    CT
GAM441   LOC254659 3'  AAACAGAGCAAGACTCCA     95109      C  G
                                TGGAG CT GCTCTGTTT
                                ||||| || |||||||||
                                ACCTC GA CGAGACAAA
                                   A  A
GAM441   LOC256158 5'  AACATCGAGCCAGGCCCA     97639      A       __
                                TGG GCCTGGCTC  TGTT
                                ||| |||||||||  ||||
                                ACC CGGACCGAG  ACAA
                                  _       CT
GAM441   LOC256207 3'  GACAGAGCAAGACTCCA     95169      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441   LOC257596 5'  GACAGAGCAAGACTCCA     97935      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM441   LOC56963  3'  GCACAAAGCCAGGCTTCA    71455          CTGT
                                TGGAGCCTGGCT   TTGTGC
                                ||||||||||||   ||||||
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                                ACTTCGGACCGA   AACACG
                                      _____
GAM441  LOC91149  3'  GCTGAACCAGAGCCAGACTCCA 65079      C       _   T
                                TGGAG CTGGCTCTG TTTG GC
                                ||||| ||||||||| |||| ||
                                ACCTC GACCGAGAC AAGT CG
                                   A       C   _
GAM441  LOC91409  3'  AGGCAAGGCCAGGCCCCA   65951    A      TC
                                TGG GCCTGGC  TGTTT
                                ||| |||||||  |||||
                                ACC CGGACCG  ACGGA
                                  C      GA
GAM441  LOC91862  3'  GGTGACAGAGCGAGACTCCA  53470      C  G      TGT
                                TGGAG CT GCTCTGTT   GCC
                                ||||| || ||||||||   |||
                                ACCTC GA CGAGACAG   TGG
                                   A  G      ___
GAM441  LOC92482  3'  AACAGAGCAAGACTCCA    69485      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM442  RAB36    3'  ATGTTCAGCTCAGCGATTGCCA 16947    A      A   TCC
          A                      TTG CAGTCGCT AGTT   ACAT
                                ||| |||||||| ||||   ||||
                                AAC GTTAGCGA TCGA   TGTA
                                  C       C   CT_
GAM442  TGFBI    3'  ATGCAGAAACTTGGATGTCA  4489       GTCG       CA
                                TGACA   CTAAGTTTC  CAT
                                |||||   |||||||||  |||
                                ACTGT   GGTTCAAAG  GTA
                                   A___       AC
GAM442  TRPV1    3'  AGACAGCACTGTCAA      38071        C   AA
                                TTGACAGT GCT  GTTT
                                |||||||| |||  ||||
                                AACTGTCA CGA  CAGA
                                      _  __
GAM442  TRPV1    3'  AGACAGCACTGTCAA      54790        C   AA
                                TTGACAGT GCT  GTTT
                                |||||||| |||  ||||
                                AACTGTCA CGA  CAGA
                                      _  __
GAM442  TRPV1    3'  AGACAGCACTGTCAA      54825        C   AA
                                TTGACAGT GCT  GTTT
                                |||||||| |||  ||||
                                AACTGTCA CGA  CAGA
                                      _  __
GAM442  TRPV1    3'  AGACAGCACTGTCAA      54857        C   AA
                                TTGACAGT GCT  GTTT
                                |||||||| |||  ||||
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                                AACTGTCA CGA  CAGA
                                     _  __
GAM442  DIS3    3'  AAACTTAGCTGGGTGT     30223     G  _
                                ACA TC GCTAAGTTT
                                ||| || |||||||||
                                TGT GG CGATTCAAA
                                  G  T
GAM442  FBXO24  5'  AGGCGAGTGACTGTCAA     24091          AA
                                TTGACAGTCGCT  GTTT
                                ||||||||||||  ||||
                                AACTGTCAGTGA  CGGA
                                      G_
GAM442  FBXO24  5'  AGGCGAGTGACTGTCAA     53168          AA
                                TTGACAGTCGCT  GTTT
                                ||||||||||||  ||||
                                AACTGTCAGTGA  CGGA
                                      G_
GAM442  FLJ21941  5'  ATGTGGAAAAGGCTTCACTGTC 46746        C__  AAG
          AA                    TTGACAGT   GCT   TTTCCACAT
                                ||||||||   |||   |||||||||
                                AACTGTCA   CGG   AAAGGTGTA
                                    CTT   A__
GAM442  KIAA1577  3'  ATGTGGAAACTTAGCGACTGTC 64473
          AA                    TTGACAGTCGCTAAGTTTCCACAT
                                ||||||||||||||||||||||||
                                AACTGTCAGCGATTCAAAGGTGTA

GAM442  MGC14433  3'  ATGTGGAAAGGTTTGCAATTGT 51867        C  TAAG_
          CAA                     TTGACAGT GC    TTTCCACAT
                                ||||||||| ||    |||||||||
                                AACTGTTA CG    AAAGGTGTA
                                    A  TTTGG
GAM442  PRPF8   3'  AGACTCGCACTGTCAA     61181        C  TA
                                TTGACAGT GC  AGTTT
                                |||||||| ||  |||||
                                AACTGTCA CG  TCAGA
                                    _ C_
GAM442  LOC90906  3'  TGGAAACTGCATGCTG     64315     C_  TA
                                CAGT  GC  AGTTTCCA
                                ||||  ||  ||||||||
                                GTCG  CG  TCAAAGGT
                                  TA  __
GAM443  ASPH    5'  TGGATTGAAGAAATCAA     39396     GC      _
                                TTG  TTCTTCAA CCA
                                |||  |||||||| |||
                                AAC  AAGAAGTT GGT
                                  TA       A
GAM443  ASPH    5'  TGGATTGAAGAAATCAA     50626     GC      _
                                TTG  TTCTTCAA CCA
                                |||  |||||||| |||
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                                AAC  AAGAAGTT GGT
                                  TA       A
GAM443  ASPH    5'  TGGATTGAAGAAATCAA     50634     GC      _
                                TTG  TTCTTCAA CCA
                                |||  |||||||| |||
                                AAC  AAGAAGTT GGT
                                  TA       A
GAM443  FOS     5'  GCGAGCAACTGAGAAGCCAA   17906         T  ACCA  A_
                                TTGGCTTCT CA    GC  GT
                                ||||||||| ||    ||  ||
                                AACCGAAGA GT    CG  CG
                                     _  CAA_  AG
GAM443  FSTL1   3'  ATACTGCTAGTTAACCCAG    23010     C  CTTC   C
                                TTGG TT    AAC AGCAGTAT
                                ||||  ||    ||| ||||||||
                                GACC AA    TTG TCGTCATA
                                  C  ____   A
GAM443  NR4A2   3'  TGAGTTGAAGAAGGCAA     20535     G       _
                                TTG CTTCTTCAAC CA
                                |||  |||||||||| ||
                                AAC GAAGAAGTTG GT
                                  G        A
GAM443  NXF5    3'  CTGGCTGACCAAGAAGCCAA   51966         ___   A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
                                AACCGAAGA   AGT GGTC
                                     ACC   C
GAM443  NXF5    3'  CTGGCTGACCAAGAAGCCAA   52508         ___   A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
                                AACCGAAGA   AGT GGTC
                                     ACC   C
GAM443  NXF5    3'  CTGGCTGACCAAGAAGCCAA   52513         ___   A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
                                AACCGAAGA   AGT GGTC
                                     ACC   C
GAM443  NXF5    3'  CTGGCTGACCAAGAAGCCAA   52517         ___   A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
                                AACCGAAGA   AGT GGTC
                                     ACC   C
GAM443  NXF5    3'  CTGGCTGACCAAGAAGCCAA   52521         ___   A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
                                AACCGAAGA   AGT GGTC
                                     ACC   C
GAM443  POLG    5'  GCCAGTAAAAGAAGCCAA     10680         CA  CA
                                TTGGCTTCTT  AC  GC
                                ||||||||||  ||  ||
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                                AACCGAAGAA  TG  CG
                                      AA  AC
GAM443  FLJ12377  3'  TGTTGGATAAAGAAGCCAA   46487         CAA
                                TTGGCTTCTT   CCAGCA
                                ||||||||||   ||||||
                                AACCGAAGAA   GGTTGT
                                      ATA
GAM443  FLJ13102  3'  ACGGCGATTGAGAAGCCAA   46002        T   CCA  A
                                TTGGCTTCT CAA   GC GT
                                ||||||||| |||   || ||
                                AACCGAAGA GTT   CG CA
                                      _  AG_  G
GAM443  FLJ23120  3'  CATACTAAATGAAAGAAGCCAG 85145         CAAC  GC_
                                TTGGCTTCTT   CA   AGTATG
                                ||||||||||   ||   ||||||
                                GACCGAAGAA   GT   TCATAC
                                      A___  AAA
GAM443  FREQ     3'  GCGGCCAAGAAGCCAA     26582         CAA  A
                                TTGGCTTCTT   CC GC
                                ||||||||||   || ||
                                AACCGAAGAA   GG CG
                                      CC_  _
GAM443  KIAA0232  3'  TTGCTAACTGAAGAAGCCAA   72764          ACC
                                TTGGCTTCTTCA   AGCAG
                                ||||||||||||   |||||
                                AACCGAAGAAGT   TCGTT
                                       CAA
GAM443  KIAA0987  3'  GCAATTAAAGAGGCCAA     24563         C  CCA
                                TTGGCTTCTT AA   GC
                                |||||||||| ||   ||
                                AACCGGAGAA TT   CG
                                      A  AA_
GAM443  PPFIA2   5'  ATTGATCAATTGAAGAAGC    13261         CCAG_
                                GCTTCTTCAA    CAGT
                                ||||||||||    ||||
                                CGAAGAAGTT    GTTA
                                      AACTA
GAM443  SNPH     3'  ACAGCTTACTGAAAAAGCCAG  28236       C   ACC   A
                                TTGGCTT TTCA   AGC GT
                                ||||||| ||||   ||| ||
                                GACCGAA AAGT   TCG CA
                                    A   CAT   A
GAM443  LOC134957 3'  ACGTGACAGATGAAGAAACCAA 57661     C      ACCAG  _
                                TTGG TTCTTCA    CA GT
                                |||| |||||||    || ||
                                AACC AAGAAGT    GT CA
                                  A      AGACA  G
GAM443  LOC136895 5'  CTGCCAAAGAAGCCAA      57168         CAACCA
                                TTGGCTTCTT     GCAG
                                ||||||||||     ||||
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                                AACCGAAGAA     CGTC
                                      AC____
GAM443  LOC162333 5'  ACTAAGCTGAAGAGGCCAA   87115          ACCA __
                                TTGGCTTCTTCA   GC  AGT
                                ||||||||||||   ||  |||
                                AACCGGAGAAGT   CG  TCA
                                      ____  AA
GAM443  LOC253227 5'  ACTACTGGTAAGAAGCCA    97506        CA    C
                                TGGCTTCTT  ACCAG AGT
                                |||||||||  ||||| |||
                                ACCGAAGAA  TGGTC TCA
                                      __    A
GAM443  LOC255452 3'  GCAGCCGAAGAAGCCA      97538         AACCA  A
                                TGGCTTCTTC    GC GT
                                ||||||||||    || ||
                                ACCGAAGAAG    CG CG
                                      C____  A
GAM444  AGRN     3'  TGCAACGTCCCGTCCC      78841      AA
                                GGGAC  GATGTTGCG
                                |||||  |||||||||
                                CCCTG  CTGCAACGT
                                   CC
GAM444  CERD4    3'  TGCAACATTTTATCCC      23855      C
                                GGGA AAGATGTTGCG
                                ||||  ||||||||||
                                CCCT TTTTACAACGT
                                  A
GAM444  MNT      3'  CGCACACATCTTACCT      39711     AC      _
                                GGG  AAGATGT TGCG
                                |||  |||||||  ||||
                                TCC  TTCTACA ACGC
                                  A_      C
GAM444  APCL     3'  ATGCATGTCACCCTGCACCC   19663     ACA  ATGT  C
                                GGG   AG    TG GCATGCAT
                                |||   ||    || ||||||||
                                CCC   TC    AC TGTACGTA
                                  ACG  CC__  _
GAM444  CST7     3'  TGCATGCTCCTTGTCCC      13329         ATGTTGC
                                GGGACAAG      GCATGCA
                                ||||||||      |||||||
                                CCCTGTTC      CGTACGT
                                    CT_____
GAM444  DKFZP564D166 3'  CAGAAGCAACATCCCATCTC   47672      CAA       GCA
                                GGGA   GATGTTGC   TG
                                ||||   ||||||||   ||
                                CTCT   CTACAACG   AC
                                  ACC       AAG
GAM444  FLJ13057  5'  GCATGCGCCCTCCGTCCC    95648       AA  TGTT
                                GGGAC  GA    GCGCATGC
                                |||||  ||    ||||||||
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                                CCCTG  CT    CGCGTACG
                                  C_  CC__
GAM444  FLJ23071  3'  TGGAACATCCTGTCCC      47266       A     G
                                GGGACA GATGTT CG
                                |||||| |||||| ||
                                CCCTGT CTACAA GT
                                   C     G
GAM444  FREQ      3'  ATGTGGCACACCTTGTCCC    26570        A   T  _
                                GGGACAAG TGT GC GCAT
                                |||||||| ||| || ||||
                                CCCTGTTC ACA CG TGTA
                                     C   _  G
GAM444  KIAA0738  3'  ATGGCAACATCCCGTCTC     28215       AA       G
                                GGGAC  GATGTTGC CAT
                                |||||  |||||||| |||
                                CTCTG  CTACAACG GTA
                                   CC       _
GAM444  KIAA1530  3'  CATGTGTCCTCTTGTCCC     67947         TGTT
                                GGGACAAGA   GCGCATG
                                |||||||||   |||||||
                                CCCTGTTCT   TGTGTAC
                                     CC__
GAM444  PRO2435   5'  ATGCATGCTATTTCCTACCC   37590     ACAA  TGT  C
                                GGG   GA   TG GCATGCAT
                                |||   ||   || ||||||||
                                CCC   CT   AT CGTACGTA
                                  ATC_  TT_  _
GAM444  SIRPB1    3'  GCTTCCAACATCTTATCCC    20260      C        CGCAT
                                GGGA AAGATGTTG    GC
                                |||| |||||||||    ||
                                CCCT TTCTACAAC    CG
                                  A       CTT__
GAM444  SLC17A6   3'  GCACAACATCTCATCCT     39745      CA       C
                                GGGA  AGATGTTG GC
                                ||||  |||||||| ||
                                TCCT  TCTACAAC CG
                                  AC       A
GAM444  LOC91948  3'  ATGCATGCCTGGTTCCTTCCC  67615      CA  AT TT C
                                GGGA  AG  G  G GCATGCAT
                                ||||  ||  |  | ||||||||
                                CCCT  TC  T  T CGTACGTA
                                  __  CT GG C
GAM445  AKAP4     5'  AGTTCCATCTAAAGGGGCA    57769        C   CC_
                                TGCCCCTT AGA   AGCT
                                |||||||| |||   ||||
                                ACGGGGAA TCT   TTGA
                                     A   ACC
GAM445  CBR1      3'  AGTTGGTCCAAAGGGCAT     8282        C  CA
                                ATGCCC TT  GACCAGCT
                                |||||| ||  ||||||||
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                                TACGGG AA  CTGGTTGA
                                   _ AC
GAM445  DNAJB1   3'  GGAACAGCAGGAAAAGGCAT  20446      CC  AGACCA
                                ATGCC  TTC     GCTGTTCC
                                |||||  |||     ||||||||
                                TACGG  AAG     CGACAAGG
                                   AA   GA____
GAM445  FLI1     5'  GGCTAATCCGAAGGGGC     76609        A  CC
                                GCCCCTTC GA  AGCT
                                |||||||| ||  ||||
                                CGGGGAAG CT  TCGG
                                     C  AA
GAM445  GFAP     3'  GGCAGTCTGGAGGGGCAT    9018            CA
                                ATGCCCCTTCAGAC  GCT
                                ||||||||||||||  |||
                                TACGGGGAGGTCTG  CGG
                                        A_
GAM445  IL18R1   3'  AGTGTCTGAAGAGGCAT     13905      C      CA
                                ATGCC CTTCAGAC  GCT
                                |||||  ||||||||  |||
                                TACGG GAAGTCTG  TGA
                                   A       __
GAM445  MMP14    3'  GAACAGCCAGAGGGGGCA    17171         AGACCA
                                TGCCCCTTC     GCTGTTC
                                |||||||||     |||||||
                                ACGGGGGAG     CGACAAG
                                     AC____
GAM445  NDRG2    3'  GGTGCTGAAGGGGCAT      32718           _
                                ATGCCCCTTCAG ACC
                                |||||||||||| |||
                                TACGGGGAAGTC TGG
                                       G
GAM445  PTPRN    3'  AAAGCCAGAAGGGGCA      11127         AGACCA  G
                                TGCCCCTTC     GCT TT
                                |||||||||     ||| ||
                                ACGGGGAAG     CGA AA
                                     AC____  _
GAM445  RANBP3   5'  TAGCCTGCAAGGGGCAT     23634         _  ACCA
                                ATGCCCCTT CAG   GCTG
                                |||||||| |||   ||||
                                TACGGGGAA GTC   CGAT
                                     C  ____
GAM445  RS1      3'  GAACAGCTGGCCCAGGAGC   4393     C  TCAGA
                                GC CCT    CCAGCTGTTC
                                || |||    ||||||||||
                                CG GGA    GGTCGACAAG
                                 A  CCC__
GAM445  SMARCA3  3'  GAACACGTCTTCTAAAAGGGGC 11789         C_  CCA  _
           AT                    ATGCCCCTT  AGA  GC TGTTC
                                |||||||||  |||  || |||||
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                                TACGGGGAA  TCT   TG ACAAG
                                     AA   TC_  C
GAM445  ZNFN2A1   3'  AACAGCCTGAAGGG       60734        ACCA
                                CCCTTCAG    GCTGTT
                                ||||||||    ||||||
                                GGGAAGTC    CGACAA
                                    _____
GAM445  BRP44I    3'  GAACAAGGTCTTGAAGGGACA  32244    C     _   AGC
                                TG CCCTTCA GACC   TGTTC
                                || ||||||| ||||   |||||
                                AC GGGAAGT CTGG   ACAAG
                                 A      T   A__
GAM445  C1QR1     3'  GAACTCCCCATTCCAAAGGGGC 23840        CA  CCAGCT_
           A                     TGCCCCTT  GA      GTTC
                                ||||||||  ||      ||||
                                ACGGGGAA  CT      CAAG
                                     AC  TACCCCT
GAM445  DKFZP434I0714 3'  AACAGCTGGAACTGGAG     85796       A_
                                CTTCAG  CCAGCTGTT
                                ||||||  |||||||||
                                GAGGTC  GGTCGACAA
                                   AA
GAM445  DNAJC8    3'  GACAAGCCTGGAAGGGGCA    26559         AGACCA  _
                                TGCCCCTTC     GCT GTT
                                |||||||||     ||| |||
                                ACGGGGAAG     CGA CAG
                                      GTC___   A
GAM445  DNPEP     5'  GGCGCGGCCTGAAGGGGCA    23958          A  A_
                                TGCCCCTTCAG CC  GCT
                                |||||||||||  ||  |||
                                ACGGGGAAGTC GG  CGG
                                       C  CG
GAM445  FLJ10074  5'  AACAGCCAGGAGGCGT      35794       _   TCAGACCA
                                ATGCC CCT       GCTGTT
                                ||||| |||       ||||||
                                TGCGG GGA       CGACAA
                                   A   C________
GAM445  FLJ10504  3'  AACAGCTGGATGCAGGAGC    36197    C   T  GA
                                GC CCT CA  CCAGCTGTT
                                || ||| ||  |||||||||
                                CG GGA GT  GGTCGACAA
                                 A   C  A_
GAM445  FLJ12409  3'  TGATCTGAAGGGACAT      47054     C        C
                                ATG CCCTTCAGA CA
                                ||| |||||||| ||
                                TAC GGGAAGTCT GT
                                  A        A
GAM445  FLJ14082  5'  GGAACAGCCAGTGTCAGGCA   46673      CCTTCA   CA__
                                TGCC     GAC    GCTGTTCC
                                ||||     |||    ||||||||
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                                ACGG     CTG    CGACAAGG
                                  A_____   TGAC
GAM445  FLJ22686  3'  AACAGCTGCTGAGG       46361       AC
                                CTTCAG  CAGCTGTT
                                ||||||  ||||||||
                                GGAGTC  GTCGACAA
                                  __
GAM445  FLJ31762  5'  GGAACAGCCAACAAAGAGGC   58141     C   CAGACCA
                                GCC CTT      GCTGTTCC
                                ||| |||      ||||||||
                                CGG GAA      CGACAAGG
                                  A   ACAAC__
GAM445  HPCAL4    3'  CTGGCCAGAAGGGGCAT     32734          AGA
                                ATGCCCCTTC   CCAG
                                ||||||||||   ||||
                                TACGGGGAAG   GGTC
                                     ACC
GAM445  IDI2      3'  AACAGGGCAAAAGGGGCA    52692        CAGA  AG
                                TGCCCCTT    CC  CTGTT
                                ||||||||    ||  |||||
                                ACGGGGAA    GG  GACAA
                                    AAC_ __
GAM445  ING4      3'  GGCCCTAGTTGAAGGGGCA   59704          ACCA_
                                TGCCCCTTCAG    GCT
                                ||||||||||     |||
                                ACGGGGAAGTT    CGG
                                     GATCC
GAM445  KIAA0133  3'  GGCTGCATGGTCTGAAAGAGC  28768    CCC       _  T
                                GC   TTCAGACCA GC GTT
                                ||   |||||||| || |||
                                CG   AAGTCTGGT CG CGG
                                  AGA        A  T
GAM445  KIAA0172  3'  GGAATTCTGATCTGAAGGGGCA 64970           C   CT
                                TGCCCCTTCAGA CAG  GTTCC
                                |||||||||||| |||  |||||
                                ACGGGGAAGTCT GTC  TAAGG
                                     A   T_
GAM445  KIAA0215  3'  GGAACAGCTGGGCCCAGGGTAT 28419       CTTCAGA
                                ATGCCC      CCAGCTGTTCC
                                ||||||      ||||||||||
                                TATGGG      GGTCGACAAGG
                                   ACCCG__
GAM445  KIAA1941  3'  AACAAGTGAGGGGCA       74833        CAGACCA  _
                                TGCCCCTT      GCT GTT
                                ||||||||      ||| |||
                                ACGGGGAG      TGA CAA
                                    ________  A
GAM445  LUC7A     5'  GGAACAGCCGCCCGAAGGAAGC 33137     C_    AGACCA
              A                  TGC  CCTTC     GCTGTTCC
                                 |||  |||||     ||||||||
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                                ACG  GGAAG     CGACAAGG
                                  AA    CCCGC_
GAM445  MGC12760  3'  GGAACAGCTGAGTGAGGAG   51176     AG  _
                                CTTC  AC CAGCTGTTCC
                                ||||  || ||||||||||
                                GAGG  TG GTCGACAAGG
                                  AG  A
GAM445  MGC20235  3'  GGTCAGTCTGAAGGGGGCAT   58903       _     CA
                                ATGCCCC TTCAGAC  GCT
                                ||||||| |||||||  |||
                                TACGGGG AAGTCTG  TGG
                                    G      AC
GAM445  PDE11A    3'  ACAGCCTGAAGGGCCAT     33773     C      ACCA
                                ATG CCCTTCAG    GCTGT
                                ||| ||||||||    |||||
                                TAC GGGAAGTC    CGACA
                                  C       _____
GAM445  PDE1C     3'  AACAAAACATGAAGGGGCAT   17217          GACCAGC
                                ATGCCCCTTCA      TGTT
                                ||||||||||       ||||
                                TACGGGGAAGT      ACAA
                                      ACAAA__
GAM445  PPP1R16B  3'  GAAACTTGCCCTGAGGGGCA   61385       T   AC   CTG
                                TGCCCCT CAG  CAG   TTC
                                ||||||| |||  |||   |||
                                ACGGGGA GTC  GTT   AAG
                                    _  CC   CA_
GAM445  PRO0038   3'  AACAGCTGGGTGTGGTGGCA   26089     _ TT  GA
                                TGCC CC  CA  CCAGCTGTT
                                |||| ||  ||  |||||||||
                                ACGG GG  GT  GGTCGACAA
                                  T  T_  G_
GAM445  RALY      5'  AACAGCTGGCTAAG        33616     C  A
                                CTT AG CCAGCTGTT
                                ||| || |||||||||
                                GAA TC GGTCGACAA
                                  _  _
GAM445  SCOP      3'  GAACAGCTGATTGAG       91779       AC
                                TTCAG  CAGCTGTTC
                                |||||  |||||||||
                                GAGTT  GTCGACAAG
                                  A_
GAM445  SCYA13    5'  GAACAGCCAGAGGAGCA     18257     C   CAGACCA
                                TGC CCTT      GCTGTTC
                                ||| ||||      |||||||
                                ACG GGAG      CGACAAG
                                  A   AC_____
GAM445  SERF2     5'  GGATGGCTGACACGAAGGGGCA 19308         AGAC
                                TGCCCCTTC    CAGCTGTTC
                                |||||||||    |||||||||
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                                ACGGGGAAG   GTCGGTAGG
                                     CACA
GAM445  LOC124470 3'  GAACAGTGAGTTCTGCAAGGGG 75637        _   _ CA
           CAT                    ATGCCCCTT CAGA C  GCTGTTC
                                  ||||||||| |||| |  |||||||
                                  TACGGGGAA GTCT G  TGACAAG
                                       C    T AG
GAM445  LOC129676 5'  AACAGCTGAGTCAGGAGC    75730    C   TCA  _
                                  GC CCT   GAC CAGCTGTT
                                  || |||   ||| ||||||||
                                  CG GGA   CTG GTCGACAA
                                   A  ___   A
GAM445  LOC143381 3'  GAAAGGGTCTGAAAAAGCAT   76548     CCC      AGCTG
                                  ATGC   TTCAGACC    TTC
                                  ||||   ||||||||    |||
                                  TACG   AAGTCTGG    AAG
                                    AAA      GA___
GAM445  LOC148066 3'  GGAATGTTTCTGGTCTGAA   78624         C__
                                  TTCAGACCAG   TGTTCC
                                  ||||||||||   ||||||
                                  AAGTCTGGTC   GTAAGG
                                       TTT
GAM445  LOC149319 3'  GGAACAGCTGGGCTAAGG    79297     C  A
                                  CCTT AG CCAGCTGTTCC
                                  |||| || ||||||||||
                                  GGAA TC GGTCGACAAGG
                                    _ G
GAM445  LOC149579 3'  GGAACAGCTGAGTGAGGAG   71135     AG  _
                                  CTTC  AC CAGCTGTTCC
                                  ||||  || ||||||||||
                                  GAGG  TG GTCGACAAGG
                                    AG  A
GAM445  LOC151234 3'  GAAAGGTTGGGTCTGAA     80175        _   G
                                  TTCAGACC AGCT TTC
                                  |||||||| |||| |||
                                  AAGTCTGG TTGG AAG
                                       G    A
GAM445  LOC151568 5'  GAACAGCTTCTTGCAGAAGCA  56692    CC  T   ACC
                                  TGC  CT CAG   AGCTGTTC
                                  |||  || |||   ||||||||
                                  ACG  GA GTT   TCGACAAG
                                    AA  C   CT_
GAM445  LOC152286 3'  GACGGGACCTGAAGGGGC    85630         ACCAG
                                  GCCCCTTCAG    CTGTT
                                  ||||||||||    |||||
                                  CGGGGAAGTC    GGCAG
                                       CAG__
GAM445  LOC152579 3'  AACATTTCTGAAAAGGCA    80621     CC     CCAGC
                                  TGCC  TTCAGA    TGTT
                                  ||||  ||||||    ||||
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                                ACGG  AAGTCT    ACAA
                                  AA     TT___
GAM445  LOC153571 3'  GGAACAGCCGGCCCCGGAGGC  86049    _  TTCAGA  A
                                GCC CC     CC GCTGTTCC
                                ||| ||     || ||||||||
                                CGG GG     GG CGACAAGG
                                  A  CCCC__  C
GAM445  LOC157349 5'  GGAACAGCTGAGGTCCAGGG  81417     TCA   __
                                CCCT   GACC  AGCTGTTCC
                                ||||   ||||  |||||||||
                                GGGA   CTGG  TCGACAAGG
                                  C__    AG
GAM445  LOC157567 3'  AACAGCTGGCTTTGGA     81476       _
                                TTCAGA CCAGCTGTT
                                |||||| |||||||||
                                AGGTTT GGTCGACAA
                                   C
GAM445  LOC166793 5'  AGTAATTTGAAGGAGCA    59224    C      CCA
                                TGC CCTTCAGA   GCT
                                ||| ||||||||   |||
                                ACG GGAAGTTT   TGA
                                  A       AA_
GAM445  LOC196955 5'  AGTGTGACCTGAGGGGCA   77366       T   AC  _
                                TGCCCCT CAG  CA GCT
                                ||||||| |||  || |||
                                ACGGGGA GTC  GT TGA
                                    _  CA  G
GAM445  LOC200197 3'  GGCGGTCTGAAGGGCA     88620      C      A
                                TGCCC TTCAGACC GCT
                                ||||| |||||||| |||
                                ACGGG AAGTCTGG CGG
                                  _      _
GAM445  LOC219855 3'  GGTACATAATTTGAAGGGGCA  91515          CCAGC   T
                                TGCCCCTTCAGA    TGT CC
                                ||||||||||||    ||| ||
                                ACGGGGAAGTTT    ACA GG
                                       AAT__   T
GAM445  LOC220776 3'  AACTGAGGTCTGGAGAGGCAT  68379      C       AGCT
                                ATGCC CTTCAGACC   GTT
                                ||||| |||||||||   |||
                                TACGG GAGGTCTGG   CAA
                                   A       AGT_
GAM445  LOC257458 5'  GGAACAGCTGCGTCAGGAGC   67793    C   TCA  _
                                GC CCT   GAC CAGCTGTTCC
                                || |||   ||| ||||||||||
                                CG GGA   CTG GTCGACAAGG
                                 A  ____  C
GAM445  LOC57151  5'  AACAGCCAGGTTGGAGCA    39937     C  TTCA   A_
                                TGC CC    GACC  GCTGTT
                                ||| ||    ||||  ||||||
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                                ACG GG   TTGG  CGACAA
                                  A _____   AC
GAM445  LOC91548  5' GAACAGCTGGTTACTGAG    66413      __
                                TTCAG  ACCAGCTGTTC
                                |||||  ||||||||||
                                GAGTC  TGGTCGACAAG
                                   AT
GAM445  LOC92231  3' GAATGGCCCAGAAGGGGCA   68554        AGACCA
                                TGCCCCTTC     GCTGTTC
                                |||||||||     |||||||
                                ACGGGGAAG     CGGTAAG
                                     ACC___
GAM445  LOC92391  3' GGAACAGCTCTGTGG      69157    TT   CCA
                                CC  CAGA   GCTGTTCC
                                ||  ||||   ||||||||
                                GG  GTCT   CGACAAGG
                                 T_   ____
GAM446  CNGA1     3' CAACTGATAATGTGCAAA    59507         GC   A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                     A_  _
GAM446  ESRRG     3' TGGCAGTCTTATGTGCAAA   66396        TAGCT
                                TTTGCACAT    AGATTGCCA
                                |||||||||    |||||||||
                                AAACGTGTA    TCTGACGGT
                                     T_____
GAM446  KCNJ3     3' GCAATAATGTGCAAA       9525          GCTAGA
                                TTTGCACATTA     TTGC
                                ||||||||||     ||||
                                AAACGTGTAAT     AACG
                                      _______
GAM446  SDC2      3' GCAAATTAATGTGTAAA     67132          CTAGA
                                TTTGCACATTAG    TTGC
                                ||||||||||||    ||||
                                AAATGTGTAATT    AACG
                                      A_____
GAM446  USP9X     3' ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
                  A                TTTGCACATTAGC     GCCAT
                                   ||||||||||||      |||||
                                   AAATGTGTAATCG     CGGTA
                                         TAGTC_
GAM446  AMOTL1    3' GGCAAGTAATGTGCAAA     73650         G  AGAT
                                TTTGCACATTA CT    TGCC
                                |||||||||| ||    ||||
                                AAACGTGTAAT GA    ACGG
                                      _ _____
GAM446  BCAR3     3' AGTAATAATGTGCAAA      13098          __
                                TTTGCACATTA  GCT
                                ||||||||||  |||
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                                AAACGTGTAAT  TGA
                                      AA
GAM446  DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930          AGCTA    C
                                TTTGCACATT    GATTG CA
                                ||||||||||    ||||| ||
                                AGACGTGTAA    TTAAC GT
                                      A____    A
GAM446  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235           CT   T  C
                                TTTGCACATTAG  AGA TG CAT
                                ||||||||||||  ||| || |||
                                AGACGTGTAATC  TTT AC GTA
                                       __  T  A
GAM446  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
           AA                    TTTGCACATTAGCTAGATTGCCAT
                                ||||||||||||||||||||||||||
                                AAACGTGTAATCGATCTAACGGTA

GAM447  ARHGEF6  3'  CAAACTTGAAGCCAGGC    68198       ACCA
                                GCCTGG   CAAGTTTG
                                ||||||   ||||||||
                                CGGACC   GTTCAAAC
                                   GAA_
GAM447  BIG1     3'  TCAAACTTGCAACACTCCAG   21205      CCA___
                                CTGGA    CAAGTTTGA
                                |||||    |||||||||
                                GACCT    GTTCAAACT
                                   CACAAC
GAM447  CABC1    5'  TCAAGCTGACCCAGGCGG    39658        ACCACA
                                TCGCCTGG    AGTTTGA
                                ||||||||    |||||||
                                GGCGGACC    TCGAACT
                                     CAG___
GAM447  CORO2A   3'  TCAAACTGTGGTCCAGAGA   53403    GC        A
                                TC  CTGGACCACA GTTTGA
                                ||  |||||||||| ||||||
                                AG  GACCTGGTGT CAAACT
                                 A_        _
GAM447  CORO2A   3'  TCAAACTGTGGTCCAGAGA   12647    GC        A
                                TC  CTGGACCACA GTTTGA
                                ||  |||||||||| ||||||
                                AG  GACCTGGTGT CAAACT
                                 A_        _
GAM447  DISC1    3'  TCAAACTCCTGACCTCAGGCGA 37892        _ AC  CA
                                TCGCCTG G  CA  AGTTTGA
                                ||||||| |  ||  |||||||
                                AGCGGAC C  GT  TCAAACT
                                    T CA  CC
GAM447  EN2      5'  CGGGCGGCCCAGGCGG      7459          A  ACAA
                                TCGCCTGG CC    GTTTG
                                ||||||| ||    |||||
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                                GGCGGACC GG    CGGGC
                                    C _____
GAM447  FOXD2   5' CAGAGGGGGCCCAGGCGA   15562        A  ACAAG
                                TCGCCTGG CC    TTTG
                                |||||||| ||    ||||
                                AGCGGACC GG    AGAC
                                    C  GGG__
GAM447  GPX3    5' TCAGGCAGCGGCTCAGGCGA  9125        GA  ACAA
                                TCGCCTG  CC    GTTTGA
                                |||||||  ||    ||||||
                                AGCGGAC  GG    CGGACT
                                    TC  CGA_
GAM447  HNF3G   3' AACTCTGGTCCAGGAGA    72339    G       CA
                                TC CCTGGACCA  AGTT
                                || |||||||||  ||||
                                AG GGACCTGGT  TCAA
                                 A        C_
GAM447  IL13RA1 3' TCAAACTTGAGTCACAAAGA  7778     GCC  _   CA
                                TC   TG GAC  CAAGTTTGA
                                ||   || |||  |||||||||
                                AG   AC CTG  GTTCAAACT
                                 AA_  A  A_
GAM447  KCNS2   3' CAAACTTGTATTGAAGGGA   68300    G   GGACC
                                TC CCT     ACAAGTTTG
                                || |||     |||||||||
                                AG GGA     TGTTCAAAC
                                 _  AGTTA
GAM447  LMO4    5' CAAACTTGCAGCAGCGA     22251      __   GACCA
                                TCGC  CTG     CAAGTTTG
                                ||||  |||     ||||||||
                                AGCG  GAC     GTTCAAAC
                                  AC  _____
GAM447  LZTS1   3' TCAAACTTGTGGCCTCAAGC  40695    CT__  A
                                GC    GG CCACAAGTTTGA
                                ||    || ||||||||||||
                                CG    CC GGTGTTCAAACT
                                 AACT  _
GAM447  MATK    3' CAAGGAGGGTCCAGGCGG    57819          ACAAG
                                TCGCCTGGACC    TTTG
                                ||||||||||     ||||
                                GGCGGACCTGG    GAAC
                                     GAG__
GAM447  MATK    3' CAAGGAGGGTCCAGGCGG    57816          ACAAG
                                TCGCCTGGACC    TTTG
                                ||||||||||     ||||
                                GGCGGACCTGG    GAAC
                                     GAG__
GAM447  MATK    3' CAAGGAGGGTCCAGGCGG    9915           ACAAG
                                TCGCCTGGACC    TTTG
                                ||||||||||     ||||
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                                GGCGGACCTGG    GAAC
                                     GAG__
GAM447  MIR16    3'  TCAAACTTGTGGCCA      33565     A
                                TGG CCACAAGTTTGA
                                ||| ||||||||||||
                                ACC GGTGTTCAAACT
                                 _
GAM447  PIK3C2B  3'  AGCTCGGTCCAGGTGA      10559          ACA
                                TCGCCTGGACC   AGTT
                                ||||||||||   ||||
                                AGTGGACCTGG   TCGA
                                     C__
GAM447  PLCG2    5'  CAAACCCGGGGCAGGCGG    72463       GA  ACAA
                                TCGCCTG  CC    GTTTG
                                |||||||  ||    |||||
                                GGCGGAC  GG    CAAAC
                                    GG  CC__
GAM447  PLIN     3'  CAAACTTGTGGCCAAAAGA   10640    GCC   A
                                TC   TGG CCACAAGTTTG
                                ||   ||| ||||||||||||
                                AG   ACC GGTGTTCAAAC
                                 AAA  _
GAM447  POU2AF1  3'  CAGATTTACAGTCCAGGC    20648        CAC
                                GCCTGGAC   AAGTTTG
                                ||||||||   |||||||
                                CGGACCTG   TTTAGAC
                                    ACA
GAM447  SLC6A12  3'  CGAATGTGCTCCAGGCGA    11734         C    AG
                                TCGCCTGGA CACA  TTTG
                                ||||||||| ||||  ||||
                                AGCGGACCT GTGT  AAGC
                                     C   __
GAM447  STARD4   3'  TCAAACTTGTAGTACTACAGA  57516    GCC  _  C
                                TC   TGG AC ACAAGTTTGA
                                ||   ||| || ||||||||||
                                AG   ATC TG TGTTCAAACT
                                 AC_   A  A
GAM447  TP53     3'  TCAAACTCCTGGGCTCAGGCGA 5043         A_   CA
                                TCGCCTGG  CCA  AGTTTGA
                                ||||||||  |||  |||||||
                                AGCGGACT  GGT  TCAAACT
                                    CG   CC
GAM447  TR2      5'  CAAACTTTCCAGGC       72314        CCAC
                                GCCTGGA    AAGTTTG
                                |||||||    |||||||
                                CGGACCT    TTCAAAC
                                    ____
GAM447  C21orf42 5'  TCAAACTTGTAGCTGTATGA   54207     CC   ACC
                                TCG  TGG   ACAAGTTTGA
                                |||  |||   ||||||||||
```

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                                AGT  GTC   TGTTCAAACT
                                  AT   GA_
GAM447  DAZAP1   3'  CAAACTTGTGAACTCGTGA   38536     CT  AC
                                TCGC  GG  CACAAGTTTG
                                ||||  ||  ||||||||||
                                AGTG  TC  GTGTTCAAAC
                                  C_  AA
GAM447  DBR1     3'  AACTCCTGACCTCAGGCGA   32523       _ AC  CA
                                TCGCCTG G  CA  AGTT
                                |||||||  |  ||  ||||
                                AGCGGAC C  GT  TCAA
                                    T CA  CC
GAM447  DC-TM4F2 3'  CAAACTTGTGACTGC      48171    CT  AC
                                GC  GG  CACAAGTTTG
                                ||  ||  ||||||||||
                                CG  TC  GTGTTCAAAC
                                 __  A_
GAM447  DKFZp434N2030 5'  TCAAACTTGTCCTCGC     65525    CT   CAC
                                GC  GGAC   AAGTTTGA
                                ||  ||||   ||||||||
                                CG  CCTG   TTCAAACT
                                 CT   ___
GAM447  DKFZP564I1171 3'  TCAGAAGCTGAGTCCAGGC   71592        _  CAAG
                                GCCTGGAC CA    TTTGA
                                |||||||| ||    |||||
                                CGGACCTG GT    AGACT
                                     A  CGA_
GAM447  DKFZP564O0423 3'  TCAAACTCCTGGCCTCAGGCGA 91699        _ A   CA
                                TCGCCTG G CCA  AGTTTGA
                                |||||||  | |||  |||||||
                                AGCGGAC C GGT  TCAAACT
                                    T C   CC
GAM447  EPN2     5'  CAAACTTGTGGACAGG     30321     GA
                                CCTG  CCACAAGTTTG
                                ||||  ||||||||||
                                GGAC  GGTGTTCAAAC
                                  A_
GAM447  EREG     3'  TCAAACTTATGGGCAGGGA   7510     G   GA  C
                                TC CCTG  CCA AAGTTTGA
                                || ||||  ||| ||||||||
                                AG GGAC  GGT TTCAAACT
                                 _   G_  A
GAM447  FLJ10718 3'  TCAAACTCTTAGGCTCAGGCGA 36496       GA  ACA_
                                TCGCCTG  CC   AGTTTGA
                                |||||||  ||   |||||||
                                AGCGGAC  GG   TCAAACT
                                    TC  ATTC
GAM447  FLJ10803 3'  TCAAACTTGTATGGATGA    36671    _  TGGACC
                                TCG CC     ACAAGTTTGA
                                ||| ||     ||||||||||
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                                AGT GG     TGTTCAAACT
                                  A  TA____
GAM447  FLJ20312  5'  TCAAACTTGTGTGCTGAGG   34928    _  AC
                                CCT GG  CACAAGTTTGA
                                ||| ||  ||||||||||
                                GGA TC  GTGTTCAAACT
                                  G  GT
GAM447  FLJ23420  3'  CAAGTGGGTCCAGGC       46846        A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                     _  __
GAM447  FREQ    3'  TCAGCTGCTGGCCCGGGCGA  26585       A   CA   T
                                TCGCCTGG CCA  AGTT GA
                                |||||||| |||  |||| ||
                                AGCGGGCC GGT  TCGA CT
                                    C   CG   _
GAM447  H2AV    3'  TCAAACTCCTGACCTCAGGCGA 56858       _ AC  CA
                                TCGCCTG G  CA  AGTTTGA
                                ||||||| |  ||  |||||||
                                AGCGGAC C  GT  TCAAACT
                                   T CA  CC
GAM447  HSA249128 5'  GGCGCGGTCCAGGCGG     34153         ACAA
                                TCGCCTGGACC   GTT
                                ||||||||||   |||
                                GGCGGACCTGG   CGG
                                     CG__
GAM447  KIAA0089  5'  AAGCACGGTCCAGGCGG    69960         ACAA
                                TCGCCTGGACC   GTTT
                                ||||||||||   ||||
                                GGCGGACCTGG   CGAA
                                     CA__
GAM447  KIAA0256  3'  CAAACTTGTCCTGAGTGC    64417   _ __   CAC
                                GC CT  GGAC   AAGTTTG
                                || ||  ||||   |||||||
                                CG GA  CCTG   TTCAAAC
                                 T  GT   ___
GAM447  KIAA1026  3'  TCAACTCCTGACCTCAGGCGA  71207       _ AC  CA   T
                                TCGCCTG G  CA  AGTT GA
                                ||||||| |  ||  |||| ||
                                AGCGGAC C  GT  TCAA CT
                                   T CA  CC   _
GAM447  KIAA1981  3'  CAGAGGATGATTCAGGCGA   88341        C  CAAG
                                TCGCCTGGA CA   TTTG
                                ||||||||| ||   ||||
                                AGCGGACTT GT   AGAC
                                     A  AGG_
GAM447  MGC13090  5'  TCAAACTTGTCCGCCAAGT   51141    C   ACC
                                GC TGG   ACAAGTTTGA
                                || |||   ||||||||||
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                                TG ACC   TGTTCAAACT
                                 A   GCC
GAM447  MGC2452   5' TCAAGGAGATGTGGTCCAGG  50990          AG__
                                CCTGGACCACA    TTTGA
                                ||||||||||    |||||
                                GGACCTGGTGT    GAACT
                                      AGAG
GAM447  MYT1L     5' TCAAACTTGTGGTGG      66825    TGG
                                CC   ACCACAAGTTTGA
                                ||   ||||||||||||
                                GG   TGGTGTTCAAACT
                                 ___
GAM447  NUDT13    3' TCAGTTTGTGACCCAGGGA   63215    G    AC    AGT
                                TC CCTGG  CACA   TTGA
                                || |||||  ||||   ||||
                                AG GGACC  GTGT   GACT
                                 _    CA    TT_
GAM447  PCDH17    3' CAAACTTGTATTAGG      27087      ACC
                                CCTGG   ACAAGTTTG
                                |||||   |||||||||
                                GGATT   TGTTCAAAC
                                   A__
GAM447  PGRMC1    3' TCAAACTTGTAATTGTGGT   21895     TG  CC
                                GCC  GA  ACAAGTTTGA
                                |||  ||  ||||||||||
                                TGG  TT  TGTTCAAACT
                                  TG  AA
GAM447  PTDSS2    3' CATGGTGTGGTCCAGGC     47884           AGTT
                                GCCTGGACCACA    TG
                                ||||||||||||    ||
                                CGGACCTGGTGT    AC
                                      GGT_
GAM447  RPS6KB1   3' TCAAACTTTTCCCAGGC     12038       ACCAC
                                GCCTGG    AAGTTTGA
                                ||||||    ||||||||
                                CGGACC    TTCAAACT
                                   CTT__
GAM447  USP22     3' TCAAACTCCTGACCTCAGGCGA 68023        _ AC  CA
                                TCGCCTG G  CA  AGTTTGA
                                ||||||| |  ||  |||||||
                                AGCGGAC C  GT  TCAAACT
                                    T CA  CC
GAM447  LOC129011 5' CAGACCTGCGGTCCAGGC    74865         A  A
                                GCCTGGACC CA GTTTG
                                ||||||||| || |||||
                                CGGACCTGG GT CAGAC
                                      C  C
GAM447  LOC130595 5' CAGGCTCAGTCCAGGC      75748         CACA
                                GCCTGGAC    AGTTTG
                                ||||||||    ||||||
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                                CGGACCTG    TCGGAC
                                     AC__
GAM447   LOC131873 5'  CTGGTGGTCCAGGAGA      75879    G        A
                                TC CCTGGACCAC AG
                                || |||||||||| ||
                                AG GGACCTGGTG TC
                                 A         G
GAM447   LOC145978 3'  TCAAACTTTAACAGGTGA    77600        GACCAC
                                TCGCCTG     AAGTTTGA
                                |||||||     ||||||||
                                AGTGGAC     TTCAAACT
                                    AAT___
GAM447   LOC146890 5'  TCAGAAGTAGTCAGGCGA    83854        G  C  AAG
                                TCGCCTG AC AC   TTTGA
                                ||||||| || ||   |||||
                                AGCGGAC TG TG   AGACT
                                    _  A  A__
GAM447   LOC150622 5'  CTGGTGGTCCAGGGA       79957    G        A
                                TC CCTGGACCAC AG
                                || |||||||||| ||
                                AG GGACCTGGTG TC
                                 _         G
GAM447   LOC152002 3'  CAAACCAGCTCCAGGTGA    80431         CCACAA
                                TCGCCTGGA     GTTTG
                                |||||||||     |||||
                                AGTGGACCT     CAAAC
                                      CGAC__
GAM447   LOC153474 3'  TCAGAAGCTGAGTCCAGGC   80847         _ CAAG
                                GCCTGGAC CA    TTTGA
                                |||||||| ||    |||||
                                CGGACCTG GT    AGACT
                                     A  CGA_
GAM447   LOC154007 3'  TCAAACTCCTAGGCTCAGGCGA 81021        GA  ACA_
                                TCGCCTG  CC    AGTTTGA
                                |||||||  ||    |||||||
                                AGCGGAC  GG    TCAAACT
                                    TC  ATCC
GAM447   LOC154789 5'  TCAAACTTGAGCAGGC      81141       GACCA
                                GCCTG     CAAGTTTGA
                                |||||     |||||||||
                                CGGAC     GTTCAAACT
                                   GA____
GAM447   LOC158301 3'  CAAACCTGTGGTTCCA      81869      _    A
                                TGGA CCACA GTTTG
                                |||| ||||| |||||
                                ACCT GGTGT CAAAC
                                  T    C
GAM447   LOC199906 3'  TCAAACTCCTGACCTCAGGCGA 88487        _ AC  CA
                                TCGCCTG G  CA  AGTTTGA
                                ||||||| |  ||  |||||||
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                                AGCGGAC C  GT  TCAAACT
                                    T CA  CC
GAM447  LOC199991 5'  TCAGAGCGTTCCAGGCGA    89916        CC  AAG
                                TCGCCTGGA  AC   TTTGA
                                |||||||||  ||   |||||
                                AGCGGACCT  TG   AGACT
                                     __  CG_
GAM447  LOC219529 5'  TCAAACTCCTGAGCCCAGGTGA 92974        AC_  CA
                                TCGCCTGG   CA  AGTTTGA
                                ||||||||   ||  |||||||
                                AGTGGACC   GT  TCAAACT
                                    CGA  CC
GAM447  LOC220753 3'  CAAACTTGTAGAGGTGGGC   92941     GG  ___
                                GCCT  ACC   ACAAGTTTG
                                ||||  |||   |||||||||
                                CGGG  TGG   TGTTCAAAC
                                  __  AGA
GAM447  LOC221718 3'  TCAAACTTATTGGTGAAG    93632    GG   C_
                                CT  ACCA  AAGTTTGA
                                ||  ||||  ||||||||
                                GA  TGGT  TTCAAACT
                                 AG   TA
GAM447  LOC253927 3'  TCAAACTTAGACTTCAGGC    95025       CCAC
                                GCCTGGA    AAGTTTGA
                                |||||||    ||||||||
                                CGGACTT    TTCAAACT
                                    CAGA
GAM447  LOC51028  3'  CAAATATGGTCCAGG       32179        CAA
                                CCTGGACCA   GTTTG
                                |||||||||   |||||
                                GGACCTGGT   TAAAC
                                     A__
GAM448  ADAM19    3'  CAGGAAGAAGACTGGCCATTAT 52703      C   CTGAG
          G                      CATGA GGCT    TTCTTCCTG
                                 |||||  ||||    |||||||||
                                 GTATT CCGG    AAGAAGGAC
                                   A   TCAG_
GAM448  FACL5     5'  CAGGAAGAACTCAGAGCCG   64186
                                CGGCTCTGAGTTCTTCCTG
                                |||||||||||||||||||
                                GCCGAGACTCAAGAAGGAC

GAM448  GNAL      5'  CAGGAAAGAGAGGAGCCGTCG  9058         GAG TC
                                TGACGGCTCT   T  TTCCTG
                                ||||||||||   |  ||||||
                                GCTGCCGAGG   A  AAGGAC
                                     AG_ GA
GAM448  KAL1      3'  CAGGAAGAACTTCTGTCA    4013       CTCT
                                TGACGG   GAGTTCTTCCTG
                                ||||||   ||||||||||||
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                                ACTGTC   TTCAAGAAGGAC
                                      ____
GAM448  MYO1E    3' CAGGAGGACAAAACCACCATG 17187     AC  CTC  AGT
                                CATG  GG   TG   TCTTCCTG
                                ||||  ||   ||   ||||||||
                                GTAC  CC   AC   AGGAGGAC
                                  CA  AAA  ___
GAM448  PRKAR2B  3' CAGAAAGAACTCAGATGT    10804    _        C
                                GC TCTGAGTTCTT CTG
                                || ||||||||||| |||
                                TG AGACTCAAGAA GAC
                                 T         A
GAM448  PUM2     3' AGGATCAAAGCTGTCATG    31014         C   GTTCT
                                CATGACGGCT TGA    TCCT
                                |||||||||| |||    ||||
                                GTACTGTCGA ACT    AGGA
                                      A  _____
GAM448  SKI      3' CAGGAAGTGCAGAGCCGCA   11701    A      AGTT
                                TG CGGCTCTG   CTTCCTG
                                || ||||||||   |||||||
                                AC GCCGAGAC   GAAGGAC
                                 _      GT__
GAM448  TEM8     3' AGGAAGATGCAACCCCATG   36326     AC  CTC  AGT
                                CATG  GG   TG   TCTTCCT
                                ||||  ||   ||   |||||||
                                GTAC  CC   AC   AGAAGGA
                                  C_  A__  GT_
GAM448  ARHGEF4  5' AGAAAAAACTCAGGGC      52207         C  C
                                GCTCTGAGTT TT CT
                                |||||||||| || ||
                                CGGGACTCAA AA GA
                                      A  A
GAM448  FLJ31978 3' CAGGAAGGAACAAGCGCC    58348     T  GAG
                                GGC CT   TTCTTCCTG
                                ||| ||   |||||||||
                                CCG GA   AGGAAGGAC
                                  C  ACA
GAM448  HSU24186 5' AGAACTCAAAGCCGTC      25324        C
                                GACGGCT TGAGTTCT
                                ||||||| ||||||||
                                CTGCCGA ACTCAAGA
                                    A
GAM448  KCNT1    3' AGCTCCCAGGGCCGCCA     61825    A     __
                                TG CGGCTCT  GAGTT
                                || |||||||  |||||
                                AC GCCGGGA  CTCGA
                                 C      CC
GAM448  KIAA1867 3' CAGGAAGAACCCAAGAGCTCAT 94822      CG    GA_
                                ATGA  GCTCT   GTTCTTCCTG
                                ||||  |||||   ||||||||||
```

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                                TACT  CGAGA   CAAGAAGGAC
                                  __    ACC
GAM448  KIAA1878  3'  AATTCAGAGAATCGTCATG   91707        __
                                CATGACGG  CTCTGAGTT
                                ||||||||  |||||||||
                                GTACTGCT  GAGACTTAA
                                     AA
GAM448  MFN1      3'  CAGGAAGAACTCATGA      35541    _
                                TC TGAGTTCTTCCTG
                                || ||||||||||||
                                AG ACTCAAGAAGGAC
                                 T
GAM448  MIDORI    3'  CAGGGCCCTTCCAGAGCCTGTC 73784       _      AGTTCT
            ATG                    CATGAC GGCTCTG     TCCTG
                                |||||| |||||||     |||||
                                GTACTG CCGAGAC     GGGAC
                                    T      CTTCCC
GAM448  MYH7B     3'  CAGGAAGAACCTGGCTCGCATG 70530     A  _   CTGA
                                CATG CG GCT    GTTCTTCCTG
                                |||| || |||    ||||||||||
                                GTAC GC CGG    CAAGAAGGAC
                                  _ T   TC__
GAM448  RNAHP     3'  AGAAAGCAGCAGCCGTCAT    23761         _  AG
                                ATGACGGCT CTG  TTCT
                                |||||||| |||  ||||
                                TACTGCCGA GAC  AAGA
                                     C   GA
GAM448  SLC37A1   3'  AGACGGAGCTCAGACCC     38561    C        TC
                                GG TCTGAGTTCT  CT
                                || ||||||||||  ||
                                CC AGACTCGAGG  GA
                                 C         CA
GAM448  LOC116236 3'  CAGGAAAAGCACAAACCTCAT  73809     C  CTC  A   C
                                ATGA GG   TG GTT TTCCTG
                                |||| ||   || ||| ||||||
                                TACT CC   AC CGA AAGGAC
                                  _ AA_  A   A
GAM448  LOC124801 3'  CAGGAAGAACTCTCTTGCATG  74336     A   CTCT
                                CATG CGG    GAGTTCTTCCTG
                                |||| |||    ||||||||||||
                                GTAC GTT    CTCAAGAAGGAC
                                  _   CT__
GAM448  LOC222160 5'  AGGAAGAACTCACCCC      94117    CTC
                                GG   TGAGTTCTTCCT
                                ||   ||||||||||||
                                CC   ACTCAAGAAGGA
                                 CC_
GAM448  LOC51094  3'  CAGGAAGAATAAAGCC      32045      CTGA
                                GGCT    GTTCTTCCTG
                                ||||    ||||||||||
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                                CCGA   TAAGAAGGAC
                                  AA__
GAM448  LOC92078 3' CAGGAAGAAGAATCGACCGTC 67977      C  T  G__
                                GACGG TC GA   TTCTTCCTG
                                ||||| || ||   |||||||||
                                CTGCC AG CT   AAGAAGGAC
                                  _ _  AAG
GAM449  DDEF1    3' GAGCTTTAGCAGCCTC     59564    A   AGATAC      A
                                GA GCT     CTAAAGCT C
                                || |||     |||||||| |
                                CT CGA     GATTTCGA G
                                 C  C_____       C
GAM449  DDX3     3' GAGCCTTAGGTATTTG     43759          A   A
                                TAGATACCTAA GCT C
                                |||||||||| ||| |
                                GTTTATGGATT CGA G
                                      C   C
GAM449  GRAF     3' GGTAACTCCCTCCCTAGCTTC 30573        ATACCTAA  C
                                GAAGCTAG       AG TACC
                                ||||||||       || ||||
                                CTTCGATC       TC ATGG
                                    CCTCCC__  A
GAM449  MAT1A    3' AGCTTTAGAATCCCAGC     90825     A_   AC
                                GCT  GAT  CTAAAGCT
                                |||  |||  ||||||||
                                CGA  CTA  GATTTCGA
                                  CC   A_
GAM449  MYLK     3' AGCTTCAGACATTTGGTT    97018        AC  A
                                AGCTAGAT  CT AAGCT
                                ||||||||  || |||||
                                TTGGTTTA  GA TTCGA
                                    CA  C
GAM449  RGL      3' GTAGCTAAAACTTAGCTTCA  30736         ATACCTAA
                                TGAAGCTAG       AGCTAC
                                |||||||||       ||||||
                                ACTTCGATT       TCGATG
                                    CAAAA___
GAM449  ZFP93    3' GTAGCCTTAATAACGTTAGTTT 14887         ATACC_   A
            CA                    TGAAGCTAG     TAA GCTAC
                                |||||||||     ||| |||||
                                ACTTTGATT     ATT CGATG
                                    GCAATA   C
GAM449  C3orf4   3' AGCATTGACACATAGCTTCA  39118        GATACC   A
                                TGAAGCTA     TAA GCT
                                ||||||||     ||| |||
                                ACTTCGAT     GTT CGA
                                    ACACA_   A
GAM449  D2S448   3' GGCAGGAGTCCTAGCTTCA   73527         _  A   AAA
                                TGAAGCTAG AT CCT   GCT
                                ||||||||| || |||   |||
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                                ACTTCGATC TG GGA   CGG
                                     C  A  ___
GAM449  FLJ12604  3'  AGCTTTAGTATTGACTTCA   64436      CTA    C
                                TGAAG   GATAC TAAAGCT
                                |||||   ||||| |||||||
                                ACTTC   TTATG ATTTCGA
                                  AG_    _
GAM449  FLJ14280  5'  GGTAGCTCCTGGCCAGCTCA   45999     A   AGATA  TAA
                                TGA GCT    CC   AGCTACC
                                ||| |||    ||   |||||||
                                ACT CGA    GG   TCGATGG
                                  _  CC___  TCC
GAM449  H2AFJ    3'  GTTGTCAAGTTTCTAGCTTCA  36842         T  CTAA_
                                TGAAGCTAGA AC     AGC
                                |||||||||| ||     |||
                                ACTTCGATCT TG     TTG
                                      T  AACTG
GAM449  KIAA0441  3'  TAGCTTTGTTAATCTAGCCTC  28960    A      ACC
                                GA GCTAGAT   TAAAGCTA
                                || |||||||   ||||||||
                                CT CGATCTA   GTTTCGAT
                                 C      ATT
GAM449  KIAA1128  3'  TAGCTTTATGTGCAGCTTGCA  68483    _    AGA   C
                                TG AAGCT   TAC TAAAGCTA
                                || |||||   ||| ||||||||
                                AC TTCGA   GTG ATTTCGAT
                                 G    C__   T
GAM449  KIAA1750  3'  TAGCCCCAGGAGTGGGCTTTA  68254       AG  A   AAA
                                TGAAGCT  AT CCT   GCTA
                                |||||||  || |||   ||||
                                ATTTCGG  TG GGA   CGAT
                                    G_  A   CCC
GAM449  KPNA5    3'  GGTAGCTTCAGGTAACT     9629     A    A
                                AG TACCT AAGCTACC
                                || ||||| ||||||||
                                TC ATGGA TTCGATGG
                                 A    C
GAM449  MAGEH1    5'  GGTAGCTTCAGCGGCAGCAGCT 25924       AGATAC_  A
           TC                    GAAGCT      CT AAGCTACC
                                ||||||      || ||||||||
                                CTTCGA      GA TTCGATGG
                                   CGACGGC  C
GAM449  MGC12921  3'  AGCCCTATTTAGCTTC      63774          CCTAAA
                                GAAGCTAGATA     GCT
                                ||||||||||     |||
                                CTTCGATTTAT     CGA
                                      CC_____
GAM449  MGC30052  3'  AGCTTTAGAATAGCTTC     58532        GATAC
                                GAAGCTA    CTAAAGCT
                                |||||||    ||||||||
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                                CTTCGAT    GATTTCGA
                                   AA___
GAM449  RNF34    3'  AGCAAGGGCTGCATCTAGCTTC 47094         A___  AAA
                                GAAGCTAGAT   CCT  GCT
                                ||||||||||   |||  |||
                                CTTCGATCTA   GGG  CGA
                                     CGTC  AA_
GAM449  TNFRSF19L 3'  GTAGCTTTTATCCCAGC    51779    A_   CCT
                                GCT  GATA  AAAGCTAC
                                |||  ||||  ||||||||
                                CGA  CTAT  TTTCGATG
                                  CC   ___
GAM449  LOC121536 3'  AGCAAATCACATTTAGCTTCA  74082          ACCTAAA
                                TGAAGCTAGAT     GCT
                                ||||||||||      |||
                                ACTTCGATTTA     CGA
                                      CACTAAA
GAM449  LOC255452 3'  TAGGTACCTACCTTCA     97544      C  A
                                TGAAG TAG TACCTA
                                ||||| ||| ||||||
                                ACTTC ATC ATGGAT
                                   C  C
GAM449  LOC257396 3'  GGCAGCTTTAGGCTTAACTT  97139    C  ATA      A
                                AAG TAG  CCTAAAGCT CC
                                ||| |||  ||||||||| ||
                                TTC ATT  GGATTTCGA GG
                                  A  C__       C
GAM449  LOC92710  3'  GTACAAGGCATCTAGCTT    70359        A  AAAGC
                                AAGCTAGAT CCT    TAC
                                ||||||||| |||    |||
                                TTCGATCTA GGA    ATG
                                     C  AC___
GAM450  ADAT1    3'  ACCTGTAATCCTAGCTA    23896      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAT CT  TGTCCA
                                   C  AA
GAM450  ADCY2    3'  GCCTGTAGTCCCAGCTA    65019      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  AICDA    3'  ACCTGTAATCCCAGCTA    40322      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  AIRE     3'  GCCTGTAATCCCAGCTA    4601       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  AK1      3'  GCCTGTATTCCCAGCTA     4885        A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  TA
GAM450  ALDH3B1  3'  GCCTGTAATCCCAGCTA     91528       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  ALPP     3'  GCCTGTAGTCCCAGCTA     68835       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  ANKH     3'  ACCTGTAATCCCAGCTA     53986       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  ANKH     3'  ATCTGTAGTCCCAGCTA     39061       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCTA
                                   C   A
GAM450  APAF1    3'  GCCTGTAGTCCCAGCT      25039       A   C
                                AGCTG GAC ACAGGT
                                ||||| ||| ||||||
                                TCGAC CTG TGTCCG
                                  C   A
GAM450  APAF1    3'  GCCTGTAGTCCCAGCT      6730        A   C
                                AGCTG GAC ACAGGT
                                ||||| ||| ||||||
                                TCGAC CTG TGTCCG
                                  C   A
GAM450  APOC4    3'  GCCTGTAGTCCCAGCTA     7915        A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  APOL1    3'  GCCTGTAGTTCCAGCTA     13346       AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
                                ATCGAC  TG TGTCCG
                                   CT  A
GAM450  ARHGEF6  3'  CACACCTGTGGTCCCAGCTA  68199       A
                                TAGCTG GACCACAGGTGTG
                                |||||| |||||||||||||
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                                ATCGAC CTGGTGTCCACAC
                                   C
GAM450  ARSD    3'  TGCACCTGTGGTCCCAGCTA  23797      A
                                TAGCTG GACCACAGGTGTG
                                |||||| ||||||||||||
                                ATCGAC CTGGTGTCCACGT
                                   C
GAM450  ATM     3'  ACCTGTAATCCCAGCTA    56292      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  ATM     3'  ACCTGTAGTCTCACCTA    56298    C    C
                                TAG TGAGAC ACAGGT
                                ||| |||||| ||||||
                                ATC ACTCTG TGTCCA
                                  C     A
GAM450  ATM     3'  ACCTGTAGTCCCAGCTA    3508       A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  ATP1A2  3'  GCCTGTAATCTCAGCTA    5525        CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                     AA
GAM450  BCAS1   3'  CACACCTGTAGTCCCAGCTA  13338      A  C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACAC
                                   C   A
GAM450  BCL2    3'  GCCCTGAGTCTCAGCTA    5303        CA   T
                                TAGCTGAGAC  CAGG GT
                                ||||||||||  |||| ||
                                ATCGACTCTG  GTCC CG
                                     A_   _
GAM450  BHMT2   3'  GCCTGTAATCCCAGCTA    34310      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  BRCA1   3'  ACACCTGTAATCCCAGCTA  23549      A  CC
                                TAGCTG GA  ACAGGTGT
                                |||||| ||  ||||||||
                                ATCGAC CT  TGTCCACA
                                   C  AA
GAM450  BRCA1   3'  ACACCTGTAATCCCAGCTA  23557      A  CC
                                TAGCTG GA  ACAGGTGT
                                |||||| ||  ||||||||
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                                ATCGAC CT  TGTCCACA
                                   C  AA
GAM450  BRCA1   3' ACACCTGTAATCCCAGCTA   23565      A  CC
                                TAGCTG GA  ACAGGTGT
                                |||||| ||  ||||||||
                                ATCGAC CT  TGTCCACA
                                   C  AA
GAM450  BRCA1   3' ACACCTGTAATCCCAGCTA   23574      A  CC
                                TAGCTG GA  ACAGGTGT
                                |||||| ||  ||||||||
                                ATCGAC CT  TGTCCACA
                                   C  AA
GAM450  BRCA1   3' ACACCTGTAATCCCAGCTA   23582      A  CC
                                TAGCTG GA  ACAGGTGT
                                |||||| ||  ||||||||
                                ATCGAC CT  TGTCCACA
                                   C  AA
GAM450  BRCA1   3' ACACCTGTAATCCCAGCTA   23590      A  CC
                                TAGCTG GA  ACAGGTGT
                                |||||| ||  ||||||||
                                ATCGAC CT  TGTCCACA
                                   C  AA
GAM450  BRCA1   3' ACACCTGTAATCCCAGCTA   23516      A  CC
                                TAGCTG GA  ACAGGTGT
                                |||||| ||  ||||||||
                                ATCGAC CT  TGTCCACA
                                   C  AA
GAM450  BRCA1   3' ACACCTGTAATCCCAGCTA   23524      A  CC
                                TAGCTG GA  ACAGGTGT
                                |||||| ||  ||||||||
                                ATCGAC CT  TGTCCACA
                                   C  AA
GAM450  BRCA1   3' ACACCTGTAATCCCAGCTA   23534      A  CC
                                TAGCTG GA  ACAGGTGT
                                |||||| ||  ||||||||
                                ATCGAC CT  TGTCCACA
                                   C  AA
GAM450  BRCA1   3' ACACCTGTAATCCCAGCTA   23541      A  CC
                                TAGCTG GA  ACAGGTGT
                                |||||| ||  ||||||||
                                ATCGAC CT  TGTCCACA
                                   C  AA
GAM450  C1orf1  3' GCTTGTAGTCCCAGCTA    6863       A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTTCG
                                   C   A
GAM450  C21orf5 3' GCCTGTAATCCCAGCTA    17611      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  C5R1    3'  GCCTGTAATCCCAGCTA    8206       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  CAMLG   3'  ATAAATGTGGTCTCAGC    8231           GG
                                GCTGAGACCACA  TGT
                                ||||||||||||  |||
                                CGACTCTGGTGT  ATA
                                      AA
GAM450  CANX    3'  GTCACAGTGACCTTAGCTA   87483        AC  AGG
                                TAGCTGAG  CAC   TGTGAC
                                ||||||||  |||   ||||||
                                ATCGATTC  GTG   ACACTG
                                    CA  ___
GAM450  CARKL   3'  GCCTGTAATCCCAGCTA    25189      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  CASP10  3'  ACCTGTAATCCCAGCTA    52094      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  CASP10  3'  ACCTGTAATCCCAGCTA    52113      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  CD28    3'  ACCTGTAATCCCAGCTG    20434      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                GTCGAC CT  TGTCCA
                                   C  AA
GAM450  CEACAM5 3'  CGCACCTGTAGTCCCAGTTA  15158      A  C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATTGAC CTG TGTCCACGC
                                   C  A
GAM450  CLASP1  3'  ACATGGTCTCAGTTA      65295          CAGG
                                TAGCTGAGACCA   TGT
                                ||||||||||||   |||
                                ATTGACTCTGGT   ACA
                                              ____
GAM450  COL16A1 3'  ACCTGTAATCCTAGCTA    8497       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAT CT  TGTCCA
                                   C  AA
GAM450  CRACC   3'  TGCACCTGTAATCCCAGCTA  41011      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACGT
                                   C  AA
GAM450  CROT    3'  GCCTGTAGTCCAAGCTA    40950      GA  C
                                TAGCT  GAC ACAGGT
                                |||||  ||| ||||||
                                ATCGA  CTG TGTCCG
                                  AC   A
GAM450  CTMP    3'  GCCTGTAGTCCCAGCTA    53878      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  CTSS    3'  GCCTGTAATCCCAGCTA    14543      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  CYB561  3'  GCCTGTAGTCCCAGCTA    8601       A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  CYP19   3'  GTCGATTTATGCCTCAGC   48337      AC  C   G
                                GCTGAG  CA AGGT TGAC
                                ||||||  || |||| ||||
                                CGACTC  GT TTTA GCTG
                                   C_  A   _
GAM450  CYP19   3'  GTCGATTTATGCCTCAGC   3648       AC  C   G
                                GCTGAG  CA AGGT TGAC
                                ||||||  || |||| ||||
                                CGACTC  GT TTTA GCTG
                                   C_  A   _
GAM450  CYP4F3  3'  GCCTGTGGTCCCAGCTG    6117       A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                GTCGAC CTGGTGTCCG
                                   C
GAM450  CYP7A1  3'  ACCTGTAGTCTTAGCTA    5760         C
                                TAGCTGAGAC ACAGGT
                                |||||||||| ||||||
                                ATCGATTCTG TGTCCA
                                     A
GAM450  DAPP1   3'  GCCTGTAATCCCAGCTA    26918      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  DCLRE1C  3'  GCCTGTAATCCCAGCTA    42527      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  DDOST    3'  ACCTGTAGTCCCAGCTA    17814      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C  A
GAM450  DFFA     3'  GCCTGTAATCCCAGCTA    15303      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  DGAT2    3'  ATCTGGGTGGCTCAGCTA   50787      A  __
                                TAGCTGAG CCAC  AGGT
                                |||||||| ||||  ||||
                                ATCGACTC GGTG  TCTA
                                   _   GG
GAM450  DGKI     5'  ACCTGTTGTCCCAGCTA    16341      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C  T
GAM450  DGKI     5'  CACACCTGTAGTCCCAGCTA  16343      A  C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACAC
                                   C  A
GAM450  DHFR     3'  GCCTGTAGTCCCAGCTA    5805       A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  DMC1     3'  GCTTGTAATCCCAGCTA    22975      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTTCG
                                   C  AA
GAM450  DMPK     5'  TCACACCTGTGGCTTCCTCTG 15326     CT GA
                                TAG  GA  CCACAGGTGTGA
                                |||  ||  ||||||||||||
                                GTC  CT  GGTGTCCACACT
                                  TC  TC
GAM450  DVL3     3'  GCCTGTAATCTCAGCTA    15369      CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
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                                ATCGACTCT  TGTCCG
                                     AA
GAM450  EBI3    3'  TCGCACCTGTAATCCCAGT   19245     A  CC
                                GCTG GA  ACAGGTGTGA
                                |||| ||  ||||||||||
                                TGAC CT  TGTCCACGCT
                                  C  AA
GAM450  EGFL4   3'  ACTTGTAGTCCGAGCTA    61806     GA   C
                                TAGCT  GAC ACAGGT
                                |||||  ||| ||||||
                                ATCGA  CTG TGTTCA
                                   GC   A
GAM450  EGFL5   3'  GCCTGTAGTCTCAGCTA    86621         C
                                TAGCTGAGAC ACAGGT
                                |||||||||| ||||||
                                ATCGACTCTG TGTCCG
                                     A
GAM450  ENDOGL1 3'  CATCACCCTCAGCTA      17552        ACCACA   _
                                TAGCTGAG     GGTG TG
                                ||||||||     |||| ||
                                ATCGACTC     CCAC AC
                                     _______   T
GAM450  F2R     3'  ACCTGTAGTCCCAGCTA    8834       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  F2RL3   3'  GCCTGTAATCCCAGCTA    14186      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FANCC   3'  ATCTGTAATCCCAGCTA    70518      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCTA
                                   C  AA
GAM450  FANCD2  3'  GCCTGTTATCTCAGCTA    52356        CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                     AT
GAM450  FCN2    3'  CACCTGTGATCTCTGC     31730    T   C
                                GC GAGA CACAGGTG
                                || |||| ||||||||
                                CG CTCT GTGTCCAC
                                 T   A
GAM450  FCN2    3'  CACCTGTGATCTCTGC     31736    T   C
                                GC GAGA CACAGGTG
                                || |||| ||||||||
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                                CG CTCT GTGTCCAC
                                 T   A
GAM450  FGFR1   3' ACCTGTAGTCCCAGCTA    43610      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  FGFR1   3' ACCTGTAGTCCCAGCTA    43617      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  FGFR2   3' GCCTGTAATCCCAGCTA    43379      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FGFR2   3' GCCTGTAATCCCAGCTA    43385      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  GAB2    3' TCACAGCCCTCAGCTA     24504       ACCACA _
                                TAGCTGAG    GG TGTGA
                                ||||||||    || |||||
                                ATCGACTC    CC ACACT
                                     _____ G
GAM450  GAB2    3' TCACAGCCCTCAGCTA     54461       ACCACA _
                                TAGCTGAG    GG TGTGA
                                ||||||||    || |||||
                                ATCGACTC    CC ACACT
                                     _____ G
GAM450  GALNT3  3' ATCTGTAGTTCCAGCTA    15604      AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
                                ATCGAC  TG TGTCTA
                                   CT  A
GAM450  GALNT7  3' ACCTGTAATCCCAGCTA    54016      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  GP2     3' GCCTGTAATCCCAGCTA    7681       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  GPRK6   3' GTCACACCTGAGCCTTCAGC  9115       ACCA
                                GCTGAG   CAGGTGTGAC
                                ||||||   ||||||||||
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                                CGACTT   GTCCACACTG
                                   CCGA
GAM450  GRAF    3' GCCTGTAGTCCCAGCTA    30562      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  GRM6    3' GCCTGTAATCCCAGTTA    5936       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATTGAC CT  TGTCCG
                                   C  AA
GAM450  GSTM1   3' GCCCTTTGAAGCCTCAGCTA  59381       AC__  C   T
                                TAGCTGAG   CA AGG GT
                                ||||||||   || ||| ||
                                ATCGACTC   GT TCC CG
                                     CGAA  T   _
GAM450  GSTM2   3' GCCCTTTGAAGCCTCAGCTA  5950        AC__  C   T
                                TAGCTGAG   CA AGG GT
                                ||||||||   || ||| ||
                                ATCGACTC   GT TCC CG
                                     CGAA  T   _
GAM450  GSTM4   3' GCCCTTTGAAGCCTCAGCTA  5953        AC__  C   T
                                TAGCTGAG   CA AGG GT
                                ||||||||   || ||| ||
                                ATCGACTC   GT TCC CG
                                     CGAA  T   _
GAM450  HCS     3' ACCTGTAGTCTCAGCTA    38454        C
                                TAGCTGAGAC ACAGGT
                                |||||||||| ||||||
                                ATCGACTCTG TGTCCA
                                      A
GAM450  HIP1    3' GCCTGTAGTCTCAGCTA    18061        C
                                TAGCTGAGAC ACAGGT
                                |||||||||| ||||||
                                ATCGACTCTG TGTCCG
                                      A
GAM450  HS3ST2  3' GCCTATGGTCTCAACTG    20157    C      C
                                TAG TGAGACCA AGGT
                                ||| |||||||| ||||
                                GTC ACTCTGGT TCCG
                                  A       A
GAM450  HUNK    3' GCCTGTAGTCCCAGCTA    27454      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  IAPP    3' GCCTGTAATCCCAGCTA    4694       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  IFIT4    3'  ACCTGTAGTCCCAGCTA     70919       A   C
                                TAGCTG GAC ACAGGT
                                ||||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  IFNAR1   3'  CACACCTGTCTGTTCGC     5283     T   ACC
                                GC GAG   ACAGGTGTG
                                || |||   |||||||||
                                CG CTT   TGTCCACAC
                                 _  GTC
GAM450  IL10     3'  CGCACCTGTAATCCCAGCTA  5126       A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACGC
                                   C  AA
GAM450  IL12B    3'  GCTTGTGGTCCCAGCTG     9325       A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                GTCGAC CTGGTGTTCG
                                   C
GAM450  IL13RA1  3'  GCCTGTAATCCCAGCTA     7774       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  IL17R    3'  GCCTGTAGTCCTAGCTA     26778      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAT CTG TGTCCG
                                   C   A
GAM450  IL1R1    3'  GCCTGTAATCCCAGCTA     6061       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  IL5RA    3'  GCCAATTGTAGCACTCAGCTA 5115         ACC_  ___
                                TAGCTGAG   ACA  GGT
                                ||||||||   |||  |||
                                ATCGACTC   TGT  CCG
                                     ACGA  TAA
GAM450  IRAK1    3'  GCCTGTGGTCCCAGCTG     7809       A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                GTCGAC CTGGTGTCCG
                                   C
GAM450  IRAK4    3'  ACACCTGTAGTCCCAGCTA   61198      A   C
                                TAGCTG GAC ACAGGTGT
                                |||||| ||| ||||||||
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                                ATCGAC CTG TGTCCACA
                                   C   A
GAM450  ITGAL   3' CACACCTGTAGTCCCAGCTA  9386       A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACAC
                                   C   A
GAM450  KAI1    3' ACCTGTAGTCCCAGCTA    9494       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  KCNA5   3' GTCACACTGTAACCTCAGTCTA 59708    _    ACC    G
                                TAG CTGAG   ACAG TGTGAC
                                ||| |||||   |||| ||||||
                                ATC GACTC   TGTC ACACTG
                                  T    CAA   _
GAM450  KCNA7   3' ACCTGTAGTCCCAGCTA    49046      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  KCNA7   3' GCCTGTGATCCCAGCTA    49054      A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
                                ATCGAC CT GTGTCCG
                                   C  A
GAM450  KCNJ5   3' GCCTGTAGTCCCAGCTA    6093       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  KLRG1   3' ACCTGTAGTCCTAGCTA    19435      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAT CTG TGTCCA
                                   C   A
GAM450  LAMP2   3' GCCTGTAATCCCAGTTA    25713      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATTGAC CT  TGTCCG
                                   C  AA
GAM450  LDLR    3' ACCTGTAGTCCCAGCTA    4981       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  LDLR    3' GCCTGTGATCCCAGCTA    4990       A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
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                                ATCGAC CT GTGTCCG
                                   C  A
GAM450  LILRB1   3'  GCCTGTAATCCCAGCTA     21903       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LRRC2    3'  GCCTGTGGTCCCAGCTA     44472       A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAC CTGGTGTCCG
                                   C
GAM450  LUZP1    3'  GCCTGTAATCGCAGCTA     53300       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   G  AA
GAM450  LZTFL1   5'  TCTGTGGTCCAACTA      39757     C  A
                                TAG TG GACCACAGG
                                ||| || |||||||||
                                ATC AC CTGGTGTCT
                                  A  _
GAM450  LZTS1    3'  ACTTGTGGCCTCAAGC      40678     _  A
                                GCT GAG CCACAGGT
                                ||| ||| ||||||||
                                CGA CTC GGTGTTCA
                                  A  C
GAM450  MAFF     3'  GCCTGTAGTCCCAGCTA     24649       A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  MAPRE2   3'  TCATTGACCTTAGCTA      26543        AC  CAGGT
                                TAGCTGAG  CA    GTGA
                                ||||||||  ||    ||||
                                ATCGATTC  GT    TACT
                                     CA  _____
GAM450  MCM4     3'  GCCTGTAATCCCAGCTA     61904       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  MEN1     5'  GCCTGTGATCACAGCTA     55474       A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
                                ATCGAC CT GTGTCCG
                                   A  A
GAM450  MEN1     5'  GCCTGTGATCACAGCTA     55477       A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
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                                ATCGAC CT GTGTCCG
                                   A  A
GAM450  MIR16   3' GCCTGTATTCCCAGCTA    33564      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  TA
GAM450  MSH3    3' CACACCTGTAGTCCCAGCTA  10119      A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACAC
                                   C   A
GAM450  MTMR8   3' GCCTGTAGTCCCAGCTA    31293      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  MTNR1A  3' GCCTGTAATCCCAGCTA    19890      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  MYH11   3' CACACCTGTGGTCCCAGCTA  43134      A
                                TAGCTG GACCACAGGTGTG
                                |||||| |||||||||||||
                                ATCGAC CTGGTGTCCACAC
                                   C
GAM450  MYH11   3' CACACCTGTGGTCCCAGCTA  10173      A
                                TAGCTG GACCACAGGTGTG
                                |||||| |||||||||||||
                                ATCGAC CTGGTGTCCACAC
                                   C
GAM450  NPHP1   3' GCCTGTAATCCCAGCTA    62480      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  NPHS1   3' GCCTGTAGTCCCAGCTA    16192      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  NR4A2   3' GCCGTGTGAGCAGTCTCAGCT 20531        ____   _
                                AGCTGAGAC   CACA GGT
                                |||||||||   |||| |||
                                TCGACTCTG   GTGT CCG
                                     ACGA   G
GAM450  NT5M    3' GCCCCTCTTGGTCTCAGC    39511        C_  T
                                GCTGAGACCA  AGG GT
                                ||||||||||  ||| ||
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                                CGACTCTGGT  TCC CG
                                      TC   C
GAM450  OPA3     3'  GCCTGTAATCCTAGCTA     47110       A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAT CT  TGTCCG
                                   C  AA
GAM450  OPA3     3'  GCTTGTAATCCCAGCTA     47111       A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC CT  TGTTCG
                                   C  AA
GAM450  OPTN     3'  GCCTGTAGTCGCAGCTA     41768       A   C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   G   A
GAM450  P2RX7    3'  TGCACCTGCAATCCCAGCTA   10375       A  CCA
                                TAGCTG GA   CAGGTGTG
                                ||||||  ||   ||||||||
                                ATCGAC CT   GTCCACGT
                                   C  AAC
GAM450  P53AIP1  3'  GTCAGCATTTGAGCTCAGCTA  42083        ACCA     _
                                TAGCTGAG    CAGGTG TGAC
                                ||||||||    ||||||  ||||
                                ATCGACTC    GTTTAC ACTG
                                     GA__     G
GAM450  PAICS    3'  ACCTGTAATCCCAGCTA     21253       A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  PCDH11X  3'  GCCTGTAGTCCCAGCTA     52009       A   C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  PCDH11Y  3'  GCCTGTAGTCCCAGCTA     52062       A   C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  PCDH11Y  3'  GCCTGTAGTCCCAGCTA     52068       A   C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  PCDHB9   3'  GCTTGTAATCCCAGCTA     38943       A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
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                                ATCGAC CT  TGTTCG
                                   C  AA
GAM450  PDE4C    3'  GCCTGTAATCCCAGCTA     6234        A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  PDE6B    3'  GCCGTGGCACGATCTCAGCT   4281          _____   A
                                AGCTGAGA    CCAC GGT
                                ||||||||    |||| |||
                                TCGACTCT    GGTG CCG
                                    AGCAC   _
GAM450  PEX14    3'  GCCGTGTAATGGTTCAGCTA   63642         A ___  _
                                TAGCTGAG CC   ACA GGT
                                |||||||| ||   ||| |||
                                ATCGACTT GG   TGT CCG
                                    _ TAA   G
GAM450  PIK3CG   3'  GCCTGTAGTCCCAGGTA     10586    G  A  C
                                TA CTG GAC ACAGGT
                                || ||| ||| ||||||
                                AT GAC CTG TGTCCG
                                 G   C   A
GAM450  PLA2G2D  3'  GCCTGTAATCCCAGCTA     24795       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  POLH     3'  ACCTGTGATCCCAGCTA     21462       A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
                                ATCGAC CT GTGTCCA
                                   C  A
GAM450  POLH     3'  GCCTGTGATCCCAGCTA     21464       A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
                                ATCGAC CT GTGTCCG
                                   C  A
GAM450  POLK     3'  GCCTGTAATCCCAGCTA     32567       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  POLR2E   3'  CACCTGTGGTCCCAGC      59913      A
                                GCTG GACCACAGGTG
                                |||| ||||||||||
                                CGAC CTGGTGTCCAC
                                  C
GAM450  PSD      5'  GCCTGTAGTCCCAGCTA     10929       A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
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                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  PSMB9   3' ACCCCTGTAATCTCAGCTA  10955       CC    T
                                TAGCTGAGA  ACAGG GT
                                |||||||||  ||||| ||
                                ATCGACTCT  TGTCC CA
                                     AA    C
GAM450  PSMB9   3' ACCTGTAGTGCCAGCTA    10956      AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
                                ATCGAC  TG TGTCCA
                                   CG  A
GAM450  PSMD5   3' CACACCTATAATCTCAGCTA  17302       CCAC
                                TAGCTGAGA   AGGTGTG
                                |||||||||   |||||||
                                ATCGACTCT   TCCACAC
                                     AATA
GAM450  PTAFR   3' GCCTGTAGTCCCAGCTA    6296       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  PTGIS   3' GCCTGTAATCCCAGCTA    6334       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  RAB7L1  3' ACCTGTAATCCCAGCTA    14101      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  RBBP5   3' GCCTGTAATCCCAGCTA    17337      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  RFC2    3' ACCTGTAATCCCAGCTA    11303      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  RNMT    3' CACACCTGCAGGCGCTG    13710     TGAGA A_
                                TAGC   CC  CAGGTGTG
                                ||||   ||  ||||||||
                                GTCG   GG  GTCCACAC
                                  C____  AC
GAM450  RPN1    5' GCCTGTAATCCCAGCTA    11392      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  RPP30    3' ACATGGTCTCACTA       21159     C      CAGG
                                TAG TGAGACCA   TGT
                                ||| ||||||||   |||
                                ATC ACTCTGGT   ACA
                                  _      ____
GAM450  SCN2B    3' GCCTGTAATCCCAGCTA     15940       A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  SCN4A    3' GTCACACCCATGGCCTCAGC  4416        A   CA
                                GCTGAG CCA  GGTGTGAC
                                ||||||  |||  ||||||||
                                CGACTC GGT  CCACACTG
                                   C   AC
GAM450  SFRS2IP  5' GCCTGTAGTCCCAGCTA     16355       A   C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  SIM2     3' ACCTGTAATCCCAGCTA     23779       A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  SLC14A1  3' GCCTGTAGTTCCAGCTA     31840       AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC  TG TGTCCG
                                   CT  A
GAM450  SLC14A2  3' ACCTGTATTCCCAGCTA     23126       A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  TA
GAM450  SLC25A15 3' GCCTGTAGTCCCAGCTA     26510       A   C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  SLC26A4  3' GCCTGTAGTCCCAGCTA     4785        A   C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  SLC2A3   3' GCCTGTAATCCCAGCTA     22663       A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  SLC31A1  3'  GCCTGTAATCCCAGCTA     8513       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  SMG1     3'  GCCTGTAGTCCCAGCTA     30652      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  SRGAP1   3'  ACCTGTACTCCCAGCTA     72256      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  CA
GAM450  SRGAP1   5'  GCCTGTAGTCTCAGCTA     72263        C
                                TAGCTGAGAC ACAGGT
                                |||||||||| ||||||
                                ATCGACTCTG TGTCCG
                                     A
GAM450  SRGAP2   3'  ACACTGGTCTCAGC        74602        CAG
                                GCTGAGACCA  GTGT
                                ||||||||||  ||||
                                CGACTCTGGT  CACA
                                    ___
GAM450  STAT3    3'  GCCTGTAGTCCCAGCTA     57714      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  STAT3    3'  GCCTGTAGTCCCAGCTA     11999      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  SUV39H2  3'  GCCTGTAGTCCCAGCTA     45137      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  SWAP70   3'  GCCTGTAATCCCAGCTA     71350      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  TACC1    3'  GCCTGTGGTCCCAGCTA     20799      A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
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                                ATCGAC CTGGTGTCCG
                                   C
GAM450  TEM7    3' GCCTGTAGTCCCAGGTA    39886   G  A  C
                                TA CTG GAC ACAGGT
                                || ||| ||| ||||||
                                AT GAC CTG TGTCCG
                                 G  C  A
GAM450  TEM7    3' TGCACCTGTAGTCCCAGCTA  39897     A  C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                   C  A
GAM450  TERF1   3' TCACACAGTATACTCAGCTA  33978      ACC  AG
                                TAGCTGAG  AC  GTGTGA
                                ||||||||  ||  ||||||
                                ATCGACTC  TG  CACACT
                                     ATA  A_
GAM450  TGFB1   3' TACACCTGTGGTCCCAGCTA  5403      A
                                TAGCTG GACCACAGGTGTG
                                |||||| ||||||||||||
                                ATCGAC CTGGTGTCCACAT
                                   C
GAM450  TM7SF3  3' TCACACCTGTAATCCCA    59670   A  CC
                                TG GA  ACAGGTGTGA
                                || ||  ||||||||||
                                AC CT  TGTCCACACT
                                 C  AA
GAM450  TNFSF10 3' GCCTGTAGTCCCAGCTA    13749     A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  TPMT    3' GCCTGTGGTCCCAGCTG    4539      A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                GTCGAC CTGGTGTCCG
                                   C
GAM450  TRIM14  3' GCCTGTAATCCCAGCTA    28857     A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  TRIM9   5' GCCTGTAATCCCAGCTA    30761     A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  TRPM8   3' ACACCTGTAGTCCCAGCT   43981     A  C
                                AGCTG GAC ACAGGTGT
                                ||||| ||| ||||||||
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                                TCGAC CTG TGTCCACA
                                   C   A
GAM450  TSNAX    3'  GCCTGTAATCCCAGCTA     20000       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  TTF2     3'  ACCTGTAGTCCTAGCTA     13173       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAT CTG TGTCCA
                                   C   A
GAM450  UBE2B    3'  GCCTGTAGTCTCAGCTA     12474           C
                                TAGCTGAGAC ACAGGT
                                |||||||||| ||||||
                                ATCGACTCTG TGTCCG
                                      A
GAM450  UBE2G2   3'  GCCTGTAGTCCCAGCTA     64859       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  UBE2G2   3'  GCCTGTAGTCTCAGCTA     64860           C
                                TAGCTGAGAC ACAGGT
                                |||||||||| ||||||
                                ATCGACTCTG TGTCCG
                                      A
GAM450  UC28     3'  GCCTGTAATCCCAGCTA     41291       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  UPK1B    3'  GCCCTGAATGGTCTCAGCT   22718           __   T
                                AGCTGAGACCA  CAGG GT
                                ||||||||||  |||| ||
                                TCGACTCTGGT  GTCC CG
                                      AA   _
GAM450  UPK1B    3'  GCCTGTAATCCTAGCTA     22719       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAT CT  TGTCCG
                                   C  AA
GAM450  UQCRC1   5'  ACTTGTGGTCCCAGGTA     12551    G   A
                                TA CTG GACCACAGGT
                                || ||| ||||||||||
                                AT GAC CTGGTGTTCA
                                 G   C
GAM450  USP14    3'  CACACCTGTGATCCCAGCTA  17656       A  C
                                TAGCTG GA CACAGGTGTG
                                |||||| || ||||||||||
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                                ATCGAC CT GTGTCCACAC
                                   C  A
GAM450  VHL     3'  ATCTGTAATCCTAGCTA     5057        A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAT CT  TGTCTA
                                   C  AA
GAM450  VHL     3'  GCCTGTAATCCTAGCTA     5070        A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAT CT  TGTCCG
                                   C  AA
GAM450  VHL     3'  GCCTGTAGTCCCAGCTA     5071        A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  VPS41   3'  GCCTGTAATCCCAGCTA     26925       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  WIG1    3'  GCCTGTAGTCCCAGCTA     94467       A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  XRCC2   3'  GCCTGTAGTGCCAGCTA     18323       AG C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
                                ATCGAC  TG TGTCCG
                                   CG  A
GAM450  ZNF137  3'  CACACCTGTGGTCCCAGCTG  12860       A
                                TAGCTG GACCACAGGTGTG
                                |||||| |||||||||||||
                                GTCGAC CTGGTGTCCACAC
                                   C
GAM450  ZNF264  3'  GCCTGTGGTCCCAGCTG     12756       A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                GTCGAC CTGGTGTCCG
                                   C
GAM450  ZNF36   3'  ACCTGTAATCCCAGCTA     93957       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  ZNF91   3'  GCCTGTAGTCCCAGCTA     12820       A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
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                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  ABLIM    3'  CACCTGGGTCCCAGC      9759      A   A
                                GCTG GACC CAGGTG
                                |||| |||| ||||||
                                CGAC CTGG GTCCAC
                                  C   _
GAM450  ABLIM    3'  CACCTGGGTCCCAGC      22020     A   A
                                GCTG GACC CAGGTG
                                |||| |||| ||||||
                                CGAC CTGG GTCCAC
                                  C   _
GAM450  AF020591 3'  ACCTGTAGTCCCAGCTA    27134      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  AFAP     3'  GCCCAGAGTGGCCTCAGCTG  41306       A   A__  T
                                TAGCTGAG CCAC   GG GT
                                |||||||| ||||   || ||
                                GTCGACTC GGTG   CC CG
                                    C    AGA  _
GAM450  AKAP11   3'  ACCTGTAATCCCAGCTA    57827      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  AKR1B10  5'  GCCTGTAATCCCAGCTA    39696      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  AP1GBP1  3'  TGCACCTGTAGTCCCAGCTA  54536      A  C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                   C   A
GAM450  APOF     3'  GCTTGTAGTCCCAACTA     7911     C  A  C
                                TAG TG GAC ACAGGT
                                ||| || ||| ||||||
                                ATC AC CTG TGTTCG
                                  A  C   A
GAM450  ARNTL2   3'  CACACCTGTAATCCCAACTG  39455    C  A  CC
                                TAG TG GA  ACAGGTGTG
                                ||| || ||  |||||||||
                                GTC AC CT  TGTCCACAC
                                  A  C  AA
GAM450  ARNTL2   3'  GCCTGTGGTCCCAGCTG    39467      A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
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                                GTCGAC CTGGTGTCCG
                                   C
GAM450  BFAR    3' ACCTGTAATCCCAGCTA    60767      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  BIVM    3' ACCTGTAGTCCTAGCTA    34666      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAT CTG TGTCCA
                                   C  A
GAM450  BLOV1   3' CACACCTGTAATCCCAGCTA 76278      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AA
GAM450  BLOV1   3' GCCTGTAATCCCAGCTA    76282      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  BTN3A2  3' ACCTGTAGTCCCAGCTA    22909      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C  A
GAM450  C12orf2 3' GCCTGTAATCCCAGCTA    82787      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  C1orf24 3' GCCTGCAGTCCTAGCTA    53720      A  CA
                                TAGCTG GAC  CAGGT
                                |||||| |||  |||||
                                ATCGAT CTG  GTCCG
                                   C  AC
GAM450  C1orf33 3' GCCTGTAGTCCCAGCTA    32459      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  C1orf34 3' GCCTGCAGTCCCAGCTA    60674      A  CA
                                TAGCTG GAC  CAGGT
                                |||||| |||  |||||
                                ATCGAC CTG  GTCCG
                                   C  AC
GAM450  C1QTNF2 3' GCCTGTAATCCCAGCTA    49129      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  C20orf106 3'  GCCTGTAATCCCAGCTA     55057       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  C20orf108 3'  GCCTGTAGTCCCAGCTA     55047       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  C20orf12  3'  GCCTGTAATCCCAGTTA     36324       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATTGAC CT  TGTCCG
                                   C  AA
GAM450  C20orf142 3'  GCCTGTAATCCCAGCTA     74777       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  C20orf175 3'  GCCTGTAATCTCAGCTA     55065         CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                     AA
GAM450  C20orf177 3'  GCCTGTAATCCCAGCTA     62150       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  C21orf93  3'  CACACCTTTCGCTCTCAGCTA 59083         CCAC_
                                TAGCTGAGA    AGGTGTG
                                |||||||||    |||||||
                                ATCGACTCT    TCCACAC
                                     CGCTT
GAM450  C22orf20  3'  GCCTGTAATCCCAGCTA     47433       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  C3IP1     3'  GCCTAGTAGTTCAGCTA     41282       A C  _
                                TAGCTGAG C AC AGGT
                                |||||||| | || ||||
                                ATCGACTT G TG TCCG
                                     _ A  A
GAM450  C6orf29   3'  TGCACCTGTCATCCCAGCTA  51402       A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
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                                ATCGAC CT  TGTCCACGT
                                   C  AC
GAM450  C6orf5   3'  TGCACCTGTAATCCCAGCTA  31366      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACGT
                                   C  AA
GAM450  C6orf5   3'  GCCTGTAGTCCCAGCTA    31349      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  C6orf5   3'  TACACAGTCTCAGCT      31361      CACAG   G
                                AGCTGAGAC    GTGT A
                                |||||||||    |||| |
                                TCGACTCTG    CACA T
                                     A____   G
GAM450  C8orf17  3'  GCCTGTAGTCCCAGCTA    39600      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  C8orf2   3'  GTCAGGCACCTGTAATCCCAGC 23169      A  CC      __
           TA                    TAGCTG GA  ACAGGTGT  GAC
                                |||||| ||  ||||||||  |||
                                ATCGAC CT  TGTCCACG  CTG
                                   C  AA      GA
GAM450  CAMKK2   5'  GCCTGTAATCCCAGCTA    21583      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  CCR6     3'  GCCTGTAATCCCAGCTA    15169      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  CCR6     3'  GCCTGTAATCCCAGCTA    48585      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  CD109    3'  GCCCAGTGGTCTCAGT     56048        A  T
                                GCTGAGACCAC GG GT
                                |||||||||||| || ||
                                TGACTCTGGTG CC CG
                                      A  _
GAM450  CDT1     3'  ACCTGTCGTCCCAGCTA    77672      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
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                                ATCGAC CTG TGTCCA
                                   C   C
GAM450  CENTA2   3' GCCTGTAGTCCCAGCTA    37266      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  cerk     3' GCCTGTAATCTCAGCTA    42850       CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                     AA
GAM450  CES2     3' ACTTGTAATCCCAGCTA    13916      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTTCA
                                   C  AA
GAM450  CG012    3' GCCTGTAGTCCCAGCTA    83224      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  CG012    5' ACCTGTAATCCCAGCTA    83212      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  CG012    5' CACACCTGTAATCCCAGCTA 83217      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AA
GAM450  CG012    3' GCACCTGTAATCCCAGCTA  83220      A  CC
                                TAGCTG GA  ACAGGTGT
                                |||||| ||  ||||||||
                                ATCGAC CT  TGTCCACG
                                   C  AA
GAM450  CGI-203  3' GCCTGTAATCCCAGCTA    39903      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  CHRFAM7A 3' GCTTGTAATCCCAGCTA    95020      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTTCG
                                   C  AA
GAM450  CIP29    3' CACACCTGGCCCAGCTA    50400      AGACCA
                                TAGCTG    CAGGTGTG
                                ||||||    ||||||||
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                                ATCGAC     GTCCACAC
                                   CCG___
GAM450  CLONE24922 3'  ACTTGTAATCCCAGCTA     31622       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTTCA
                                   C  AA
GAM450  COE2     3'  GCCTGTAATCCCAGCTA     64254       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  COTL1    3'  CGCCGGCCTCAGCTA       87953        A  ACA
                                TAGCTGAG CC   GGTG
                                |||||||| ||   ||||
                                ATCGACTC GG   CCGC
                                    C  ___
GAM450  CPR2     3'  ACCTGTAATCCCAGCTA     48086       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  CRTAM    3'  CGCACCTGTAGTCTCAG     38979        C
                                CTGAGAC ACAGGTGTG
                                ||||||| |||||||||
                                GACTCTG TGTCCACGC
                                    A
GAM450  D21S2056E 3'  GCCTGTAATCCCAGCTA     13471       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  DCOHM    3'  TGCACCTGTTGTCCCAGCTA  49614       A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                   C   T
GAM450  DDX34    3'  GCCTGTAGTCCCAGCTA     27983       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  DEGS     3'  GCCTGTAATCCCAGCTA     13412       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  DEGS     3'  GCCTGTAATCCCAGCTA     58614       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  DF      3'  GCTTGTAGTTCCAGCTA     8631        AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
                                ATCGAC  TG TGTTCG
                                   CT  A
GAM450  DF      3'  GCTTGTAGTTCCAGCTA     76329       AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
                                ATCGAC  TG TGTTCG
                                   CT  A
GAM450  DIS3    3'  GCCTGTAATCCCAGCTA     30231       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  DKFZP434A0131 3'  GCCTGTGGTCCCAGCTA     38628       A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAC CTGGTGTCCG
                                   C
GAM450  DKFZP434B168 3'  GCCTGTAGTCCCAGCTA     31254       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  DKFZP434C1715 3'  CACACCTGTAGTCCCAGCTA   86145       A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACAC
                                   C   A
GAM450  DKFZp434E169 3'  GCCTGTAGTCCCAGCTA     50062       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  DKFZp434E2220 5'  GCTTGTAATCCCAGCTA     34298       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTTCG
                                   C  AA
GAM450  DKFZP434F1735 3'  CACACCTGTAGTCCCAGCTA   31496       A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACAC
                                   C   A
GAM450  DKFZp434G171 3'  GCCTGTAATCCCAGCTA     79433       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  DKFZp434G171 3'  GCCTGTAATCCCAGCTA    79434       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  DKFZP434I1735 3'  CACACCTGTAATCCCAGCTA  87800       A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AA
GAM450  DKFZP434K1421 3'  GCCTGTAGTCCCAGCTG    49552       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                GTCGAC CTG TGTCCG
                                   C   A
GAM450  DKFZP434L187 5'  GCCTGTAATCCCAGCTA    68805       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  DKFZP434N1511 3'  GCCTGTAGTCCCAGCTA    91417       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  DKFZp547C176 3'  GCCTGTAATCCCAGCTA    67227       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  DKFZp547H025 3'  GCAGCGTGATCTCAGCT    39357        C   AGG
                                AGCTGAGA CAC   TGT
                                |||||||| |||   |||
                                TCGACTCT GTG   ACG
                                    A   CG_
GAM450  DKFZp547I094 3'  CACACCTGTAGTCACAGCTA  49633       A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACAC
                                   A   A
GAM450  DKFZP564A022 3'  GCCTGTAGTCCCAGCTA    48227       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  DKFZP564B1023 3'  GCCTGTAATCCCAGCTA    48539       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  DKFZP564B1023 3'  TGCACCTGTAGTCCCAGCTA   48543       A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                   C   A
GAM450  DKFZP564I0422 3'  GCCTGTGTTCCCAGCTA     48714       A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
                                ATCGAC CT GTGTCCG
                                   C  T
GAM450  DKFZP564M182 3'  ACACCTGTAATCCCAGCTA    78031       A  CC
                                TAGCTG GA  ACAGGTGT
                                |||||| ||  ||||||||
                                ATCGAC CT  TGTCCACA
                                   C  AA
GAM450  DKFZP564M182 3'  ACCTGTAATCCCAGCTA     78032       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  DKFZP564M182 3'  GCCTGTGGTCCCAGCT      78037       A
                                AGCTG GACCACAGGT
                                ||||| ||||||||||
                                TCGAC CTGGTGTCCG
                                  C
GAM450  DKFZP566J2046 3'  GCCTGTAGTCCCAGCTA     48308       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  DKFZP586A011 3'  TCACACCTGTAAGGTACT    31220    _   __
                                AG ACC  ACAGGTGTGA
                                || |||  ||||||||||
                                TC TGG  TGTCCACACT
                                 A   AA
GAM450  DKFZP586C1324 3'  GCCTGTAATCCCAGCTA     69798       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  DKFZP586D2223 3'  ACCTGTGATCCTAGCTA     37678       A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
                                ATCGAT CT GTGTCCA
                                   C  A
GAM450  DKFZp727G131 3'  GCCTGCAGTCCCAGTTA     59031       A   CA
                                TAGCTG GAC  CAGGT
                                |||||| |||  |||||
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                                ATTGAC CTG  GTCCG
                                   C   AC
GAM450  DKFZP761G1913 3'  ACACCTGTAATCCCAGCTA   48908       A  CC
                                TAGCTG GA  ACAGGTGT
                                |||||| ||  ||||||||
                                ATCGAC CT  TGTCCACA
                                   C  AA
GAM450  DKFZp761J139 5'  GCCTGTAATCCCAGCTA    50109       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  DRF1    3'  CGCACCTGTAGTCCCCGCTA  47028     TGA   C
                                TAGC   GAC ACAGGTGTG
                                ||||   ||| |||||||||
                                ATCG   CTG TGTCCACGC
                                  CCC   A
GAM450  DRF1    3'  GCCTGTAATCCCAGCTA    47033       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  DSCR6   3'  GCCTGTGATCCCAGCTA    38547       A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
                                ATCGAC CT GTGTCCG
                                   C  A
GAM450  FADS1   3'  GCCTGTAATCCCAGCTA    25480       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FBXO27   3'  ACCTGTAGTCCAAGCTA    74503      GA   C
                                TAGCT  GAC ACAGGT
                                |||||  ||| ||||||
                                ATCGA  CTG TGTCCA
                                   AC   A
GAM450  FBXO6   3'  GCCTGTAGTCCCAGCTA    37384       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  FBXO9   3'  TGCACCTGTAGTCCCAGCTA  53106       A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                   C   A
GAM450  FKBP14   3'  GCCTGTAATCCCAGCTA    35625       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FKBP14   3' CACACCTGTAGTCCCAGCTA  35624      A  C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACAC
                                   C  A
GAM450  FKSG17   3' CACACCTGTAATCCCAGTTA  49328      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATTGAC CT  TGTCCACAC
                                   C  AA
GAM450  FLJ10008 3' GCCTGTAGTCCCAGCTA     35726      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  FLJ10043 3' GCCTGTAATCCCAGCTA     35761      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ10244 3' GCCTGTAATCCCAGCTG     35942      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                GTCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ10349 5' ACACGGTCTCAGCTG       36052        ACAG
                                TAGCTGAGACC   GTGT
                                ||||||||||    ||||
                                GTCGACTCTGG   CACA
                                      ____
GAM450  FLJ10460 3' GCCTGTAATCCCAGCTA     36130      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ10460 3' GCCTGTAGTCCCAGCTA     36131      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  FLJ10486 3' CACACCTGTAGTCCCAGCTG  36178      A  C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                GTCGAC CTG TGTCCACAC
                                   C  A
GAM450  FLJ10520 3' GCCTGTAGTCCCAGCTA     36211      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
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                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  FLJ10607  3' GCCTGTAATCCCAGCTA    77117      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ10613  3' GTGGCACCTGTAATCCCAGCTA 38826      A  CC      G
                                TAGCTG GA  ACAGGTGT AC
                                |||||| ||  |||||||| ||
                                ATCGAC CT  TGTCCACG TG
                                   C  AA      G
GAM450  FLJ10704  3' GCCTGTAATCCCAGCTA    36456      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ10781  3' GCCTGTAATCCCAGCTA    36634      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ10803  3' GCCTGTAATCTCAGCTA    36666        CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                     AA
GAM450  FLJ10826  3' GCCTGTAATCCCAGCTA    36702      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ10830  3' GCCTGTAGTTCCAGCTA    36721      AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
                                ATCGAC  TG TGTCCG
                                   CT  A
GAM450  FLJ10932  3' ACCTGTAGTCTTAGCTA    36891        C
                                TAGCTGAGAC ACAGGT
                                |||||||||| ||||||
                                ATCGATTCTG TGTCCA
                                     A
GAM450  FLJ10989  3' ATCTGTAGTCCCAGCTA    36944      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCTA
                                   C  A
GAM450  FLJ11036  3' ACCTGCGGTTCCAGCTA    36995      AG  A
                                TAGCTG  ACC CAGGT
                                ||||||  ||| |||||
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                                ATCGAC  TGG GTCCA
                                   CT   C
GAM450  FLJ11106 3' ACCTGTAGTCCCAGCTA    37052      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  FLJ11126 3' GCCTGTAGTCCCAGCTA    37084      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  FLJ11151 3' CACACCTGTAATCCCAGCTA  67871      A CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AA
GAM450  FLJ11301 3' CGCACCTGTAATCCCAGCTA  37227      A CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACGC
                                   C  AA
GAM450  FLJ11370 3' GCCTGTAATCCCAGCTA     46371      A CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ11577 3' ACCTGTAATCCCAGCTA     47177      A CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  FLJ11700 3' ACCTGTAATCCCAGCTA     46034      A CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  FLJ11710 5' GCCTGTAGTCCCAGCTA     45828      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  FLJ11715 3' GCCTGTGGTCCCAGCTA     44674      A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAC CTGGTGTCCG
                                   C
GAM450  FLJ11722 3' GCCTGTAATCCCAGCTA     46394      A CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ11722 3' GCCTGTAATCCCAGCTA    46395      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ11726 3' GCCTGTAATCCCAGCTA    46414      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ11800 3' ATCTGTGGTCCCAGCTG    46422      A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                GTCGAC CTGGTGTCTA
                                   C
GAM450  FLJ11996 3' GCCTGTAATCCCAGCTA    46436      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ12056 3' GCCTGTAATCCCAGCTA    46255      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ12132 3' GCCTGTAGTTCCAGCTA    46470      AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
                                ATCGAC  TG TGTCCG
                                   CT  A
GAM450  FLJ12190 3' GCTTGTAATCCCAGCTA    46875      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTTCG
                                   C  AA
GAM450  FLJ12363 3' GCCGTGGCGTGATCTCAGCT  49682        _____   A
                                AGCTGAGA    CCAC GGT
                                ||||||||    |||| |||
                                TCGACTCT    GGTG CCG
                                    AGTGC   _
GAM450  FLJ12409 3' ACACCTGTAGTCCCAGCTA   47039      A  C
                                TAGCTG GAC ACAGGTGT
                                |||||| ||| ||||||||
                                ATCGAC CTG TGTCCACA
                                   C  A
GAM450  FLJ12586 3' GCCTGTAATCCCAGCTA    44878      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ12592 3' GCTTGTAGTCCTAGCTA    49697      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAT CTG TGTTCG
                                   C   A
GAM450  FLJ12606 3' GCCTGTGGTCCCAGTTA    45641      A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATTGAC CTGGTGTCCG
                                   C
GAM450  FLJ12618 3' GCCTGTAATCTCAGCTA    45996       CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                     AA
GAM450  FLJ12660 3' GCCTGTAATCCCAGCTA    47144      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ12687 3' ACCTGTAATCCCAGCTG    46180      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                GTCGAC CT  TGTCCA
                                   C  AA
GAM450  FLJ12783 3' CACACCTGTGCAGGCAGCTG  48677       AGAC
                                TAGCTG   CACAGGTGTG
                                ||||||   ||||||||||
                                GTCGAC   GTGTCCACAC
                                   GGAC
GAM450  FLJ12921 3' GCCTGTAGTCCCAGCTA    45912      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  FLJ12949 3' GCCTGTAGTCCCAGCTA    43446      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  FLJ13117 3' GCCTGTAATCTCAGCTA    43544       CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                     AA
GAM450  FLJ13162 3' GCCTGTAATCCCAGCTA    46557      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ13193  3' GCCTGTAGTCCCAACTA    49769    C  A   C
                                TAG TG GAC ACAGGT
                                ||| || ||| ||||||
                                ATC AC CTG TGTCCG
                                  A C   A
GAM450  FLJ13273  3' TTATACAGTTCAGCTA     45393       ACCACAG
                                TAGCTGAG     GTGTGA
                                ||||||||     ||||||
                                ATCGACTT     CATATT
                                    GA_____
GAM450  FLJ13330  3' TCACACCTGTAATCTCAGC   46979       CC
                                GCTGAGA  ACAGGTGTGA
                                |||||||  ||||||||||
                                CGACTCT  TGTCCACACT
                                    AA
GAM450  FLJ13390  3' GCCTGTAATCCCAGCTA     42538      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ13448  3' CACACCTGTAATCCCAGTTA  47134      A  CC
                                TAGCTG GA  ACAGGTGTG
                                ||||||| ||  |||||||||
                                ATTGAC CT  TGTCCACAC
                                   C  AA
GAM450  FLJ13456  3' ACCTGTAATCCCAGCTA     65931      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  FLJ13621  3' GCCTGTAGTCCCAGCTA     46581      A   C
                                TAGCTG GAC ACAGGT
                                ||||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  FLJ13659  3' GCCTGTAATCCCAGCTA     47247      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ13769  3' GCCTGTAATCCCAGCTA     46616      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ13984  3' CACACCTGTGGTCCCAGCTA  45445       A
                                TAGCTG GACCACAGGTGTG
                                ||||||| |||||||||||||
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                                ATCGAC CTGGTGTCCACAC
                                   C
GAM450  FLJ14011 3' CGCACCTGTAATCTCAGCTA  42064        CC
                                TAGCTGAGA  ACAGGTGTG
                                |||||||||  |||||||||
                                ATCGACTCT  TGTCCACGC
                                   AA
GAM450  FLJ14100 3' GCCTGTAGTCCCAGCTA    46683      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  FLJ14117 3' GCCTGTAATCCCAGCTA    42909      A CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ14117 3' GCCTGTAGTCCCAGCTA    42910      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  FLJ14129 3' GCCTGTAATCTCAGCTA    48066       CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                   AA
GAM450  FLJ14251 3' GCCTGTAGTCCCAGCT     45973     A  C
                                AGCTG GAC ACAGGT
                                ||||| ||| ||||||
                                TCGAC CTG TGTCCG
                                  C  A
GAM450  FLJ14345 3' GCCTGTAATCCCAGCTA    45337      A CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ14346 3' GCCTGTAGTCCCAGCTA    46712      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  FLJ14397 3' GCCTGTAGTCCCAGCTA    51326      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  FLJ14399 3' ATCTGTAGTCCCAGCTA    51331      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
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                                ATCGAC CTG TGTCTA
                                   C   A
GAM450  FLJ14437  3' CTTGCAGTCTCAGCTG      50826         CA
                                TAGCTGAGAC  CAGG
                                ||||||||||  ||||
                                GTCGACTCTG  GTTC
                                     AC
GAM450  FLJ14457  3' GCCTGTAGTCCCAGCTA     51383       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  FLJ14466  3' ACCTGTGGTCTCAGCTA     51391
                                TAGCTGAGACCACAGGT
                                |||||||||||||||||
                                ATCGACTCTGGTGTCCA

GAM450  FLJ14466  3' GCTTGTAATCCCAGCTA     51393       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTTCG
                                   C  AA
GAM450  FLJ14490  3' GCCTGTAGTCCCAGCTA     51399       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  FLJ14549  3' GCTTTCTGGCCTCAGCTA    51443        A   C_
                                TAGCTGAG CCA  AGGT
                                |||||||| |||  ||||
                                ATCGACTC GGT  TTCG
                                     C   CT
GAM450  FLJ14621  3' GCCTGTAGTCCCAGCTA     51474       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  FLJ14641  3' GCCTGTAGTTCCAGCTA     51486       AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
                                ATCGAC  TG TGTCCG
                                   CT  A
GAM450  FLJ14840  5' GCCGGCGTGATCTCAGCT    51658        C   A__
                                AGCTGAGA CAC   GGT
                                |||||||| |||   |||
                                TCGACTCT GTG   CCG
                                     A   CGG
GAM450  FLJ20004  3' GCCTGTAAACCTCAGCTA    34313        ACC_
                                TAGCTGAG    ACAGGT
                                ||||||||    ||||||
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                                ATCGACTC   TGTCCG
                                    CAAA
GAM450  FLJ20006 3' GCCTGTAATCCCAGCTA    34322      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ20013 3' CACACCTGTAGTCCCAGCTA  34330      A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACAC
                                   C   A
GAM450  FLJ20019 3' ACCTGTAGTCTCAGCTA     34343        C
                                TAGCTGAGAC ACAGGT
                                |||||||||| ||||||
                                ATCGACTCTG TGTCCA
                                     A
GAM450  FLJ20045 3' GCTTGTAATCCCAGCTA     34425      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTTCG
                                   C  AA
GAM450  FLJ20055 3' GCCTGAAGTCCCAGCTA     34442      A   CA
                                TAGCTG GAC  CAGGT
                                |||||| |||  |||||
                                ATCGAC CTG  GTCCG
                                   C   AA
GAM450  FLJ20139 3' ACTTGTAGTTCAGCTA      34620       A C
                                TAGCTGAG C ACAGGT
                                |||||||| | ||||||
                                ATCGACTT G TGTTCA
                                     _ A
GAM450  FLJ20139 3' TGCACCTGTAGTCCCAGCTA  34631      A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                   C   A
GAM450  FLJ20241 3' GCCTGTAGTCCCAGCTA     34778      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  FLJ20306 3' CGCACCTGTAATCCCAGCTA  34915      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACGC
                                   C  AA
GAM450  FLJ20306 3' GCCTGTAGTACCAGCTA     34918      AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
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                                ATCGAC  TG TGTCCG
                                   CA  A
GAM450  FLJ20464  3' GCCTGTAATCTCAGCTA     35234         CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                     AA
GAM450  FLJ20546  3' GCCTGTGATTCCAGCTA     35367       AG C
                                TAGCTG  A CACAGGT
                                ||||||  | |||||||
                                ATCGAC  T GTGTCCG
                                   CT A
GAM450  FLJ20627  3' GCCCGTCATCTCAGCTA     35474         CC  A
                                TAGCTGAGA  AC GGT
                                |||||||||  || |||
                                ATCGACTCT  TG CCG
                                     AC  C
GAM450  FLJ20671  3' TGCACCTGTAGTCCCAGCTA   35532       A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                   C   A
GAM450  FLJ20700  3' GTGGCACCTGTAGTCCCAGCTA 35584       A   C       G
                                TAGCTG GAC ACAGGTGT AC
                                |||||| ||| |||||||| ||
                                ATCGAC CTG TGTCCACG TG
                                   C   A       G
GAM450  FLJ20729  3' ATTTGTGGCCTCAAGC      35646     _  A
                                GCT GAG CCACAGGT
                                ||| ||| ||||||||
                                CGA CTC GGTGTTTA
                                  A   C
GAM450  FLJ20783  3' GCCTGTGGTCCCAGCTA     35663       A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAC CTGGTGTCCG
                                   C
GAM450  FLJ20802  3' CGCACCTGTAGTCCCAGCTA   35668       A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGC
                                   C   A
GAM450  FLJ20825  3' GCCTGTAATCCCAGCTA     35697       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ20825  3' GCTTGTAGTCCCAGCTA     35699       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
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                                ATCGAC CTG TGTTCG
                                   C   A
GAM450  FLJ21144  3' GCCTGTAGTCCCAGCTA    42878      A  C
                                TAGCTG GAC ACAGGT
                                ||||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  FLJ21551  3' GCCTGTAATCCCAGCTA    45630      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ21657  3' ACCTGTAGTTTCAGCTA    42507         C
                                TAGCTGAGAC ACAGGT
                                |||||||||| ||||||
                                ATCGACTTTG TGTCCA
                                     A
GAM450  FLJ21687  3' GCCTGTAATCACAGCTA    45858      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   A  AA
GAM450  FLJ21870  3' GCCTGTAGTCCCAGCTA    43460      A  C
                                TAGCTG GAC ACAGGT
                                ||||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  FLJ21977  3' CACACCCCTTGCTGTCTCAGC 49881        CA ___
                                GCTGAGAC  CA   GGTGTG
                                |||||||| ||   ||||||
                                CGACTCTG  GT   CCACAC
                                     TC  TCC
GAM450  FLJ22313  3' GCCTGTAATCCCAGCTA    42341      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ22671  3' CACCTGGTCTCAGC       45863         CA
                                GCTGAGACCA  GGTG
                                ||||||||||  ||||
                                CGACTCTGGT  CCAC
                                           __
GAM450  FLJ22692  3' GCCTGTAGTCCCAGCTA    46804      A  C
                                TAGCTG GAC ACAGGT
                                ||||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  FLJ22692  3' GCCTGTAGTCCCAGCTA    46805      A  C
                                TAGCTG GAC ACAGGT
                                ||||||| ||| ||||||
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                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  FLJ22757 3' GTCACTTCCATCTCAGCTA   46069        CCACA  T_
                                TAGCTGAGA    GG  GTGAC
                                |||||||||    ||  |||||
                                ATCGACTCT    CC  CACTG
                                   A____  TT
GAM450  FLJ22814 3' ACCTGTAATCCCAGCTA     46173      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  FLJ22814 3' GCCTGTAGTCCCAGCTA     46175      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  FLJ23022 3' ACCTGTAATCCCAGCTA     46809      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  FLJ23042 3' GCCTGTAATCCCAGCTA     47173      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ23120 3' ACCTGTAATCCCAGCTA     85144      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  FLJ23235 3' GCCTGTAGTCCCAGCT      46306      A   C
                                AGCTG GAC ACAGGT
                                ||||| ||| ||||||
                                TCGAC CTG TGTCCG
                                   C   A
GAM450  FLJ23360 3' ACCTGTAGTCCCAGCTA     43566      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  FLJ23447 3' GCCTGTAGTCCCAGCTA     45713      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  FLJ23499 3' GCCTGTAATCCCAGCTA     42822      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ23499  3'  GCCTGTAATCCCAGCTA    42823      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  FLJ30092  3'  ATCTGTAGTCCCAGCTA    58685      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCTA
                                   C  A
GAM450  FLJ30681  3'  CACACCTGTAATCCCAGCTA  91784      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AA
GAM450  FLJ31455  3'  ACCTGTAGTCCCAGCTA    58622      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C  A
GAM450  FLJ31455  3'  GCCTGTAGTCTCAGCTA    58624         C
                                TAGCTGAGAC ACAGGT
                                |||||||||| ||||||
                                ATCGACTCTG TGTCCG
                                     A
GAM450  FLJ31737  3'  TGCACCTGTAATCCCAGCTA  58698      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACGT
                                   C  AA
GAM450  FLJ31952  3'  GCCTGTATCCCAGCTA     58384      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  A_
GAM450  FLJ31952  3'  TCACACCTGTAATCCCAGCTG 58388      A  CC
                                TAGCTG GA  ACAGGTGTGA
                                |||||| ||  ||||||||||
                                GTCGAC CT  TGTCCACACT
                                   C  AA
GAM450  FUSIP1    3'  GCCTGTAATCTCAGCTA    53959        CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                     AA
GAM450  GALNT6    3'  CGCACCTGCAGTCCCAGCTA  23291      A  CA
                                TAGCTG GAC  CAGGTGTG
                                |||||| |||  ||||||||
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                                ATCGAC CTG  GTCCACGC
                                   C   AC
GAM450  GALNT6   3'  GCCTGTAGTCGCAGCTA    23292       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   G   A
GAM450  GCN2     3'  GCCTGTAGTCCCAGCTA    62772       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  GLTP     3'  GCCTGTAGTTCCAGCTA    33161       AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
                                ATCGAC  TG TGTCCG
                                   CT  A
GAM450  GP5      3'  GCCTGTAGTCCCAGCTA    15648       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  GSG2     3'  GCCTGTAGTCCCAGCTA    49236       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  GTSE1    3'  GCCTGTAGTCCCAGCTA    33139       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  HEI10    3'  CGCACCTGTGATCCCAGCTA  40997       A  C
                                TAGCTG GA CACAGGTGTG
                                |||||| ||  ||||||||||
                                ATCGAC CT GTGTCCACGC
                                   C  A
GAM450  HES2     3'  ACCTGTGGTCCCAGCTA    38853       A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAC CTGGTGTCCA
                                   C
GAM450  HIC      3'  GCCTGTAGTCCCAGCTA    67450       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  HRH4     3'  GCCTGTAGTCCCAGCTA    41251       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
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                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  HRIHFB2072 3'  ATACTGTCTCAGCTA      50724         CACA
                                TAGCTGAGAC   GGTGT
                                ||||||||||   |||||
                                ATCGACTCTG   TCATA
                                             ____
GAM450  HSA250303 3'  CACACCTGTAGTCCCAGGTA  37410   G   A   C
                                TA CTG GAC ACAGGTGTG
                                || ||| ||| |||||||||
                                AT GAC CTG TGTCCACAC
                                 G   C   A
GAM450  HSC3    3'  TGCACCTGTAGTCCCAGCTA  59071      A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                   C   A
GAM450  HSH2    3'  GCCTGTAATCCCAGCTA    51675      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  HSPC043  3'  GCCTGTAATCCCAGCTA    67721      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  ICAM4   3'  CGCACCTGTGGTCCCAGCTA  42352      A
                                TAGCTG GACCACAGGTGTG
                                |||||| ||||||||||||
                                ATCGAC CTGGTGTCCACGC
                                   C
GAM450  ICAM4   3'  CGCACCTGTGGTCCCAGCTA  7748       A
                                TAGCTG GACCACAGGTGTG
                                |||||| ||||||||||||
                                ATCGAC CTGGTGTCCACGC
                                   C
GAM450  IL-23R  3'  GCTTGTAATCCCAGCTA    58454      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTTCG
                                   C  AA
GAM450  IMAGE:4907098 3'  GCCTGTAATCTCAGCTA    91660        CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                     AA
GAM450  INE1    3'  CACACCTGTGGTCCCAGCTA  13372      A
                                TAGCTG GACCACAGGTGTG
                                |||||| ||||||||||||
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                                ATCGAC CTGGTGTCCACAC
                                   C
GAM450  ING1-like 3'  GCCTGTAGTCCCAGCTA    54157      A  C
                                TAGCTG GAC ACAGGT
                                ||||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  IRF7    5'  CACACCTGCAGTCACACCTG   14440    C  A  CA
                                TAG TG GAC  CAGGTGTG
                                ||| || |||  ||||||||
                                GTC AC CTG  GTCCACAC
                                  C  A  AC
GAM450  IRF7    5'  CACACCTGCAGTCACACCTG   14442    C  A  CA
                                TAG TG GAC  CAGGTGTG
                                ||| || |||  ||||||||
                                GTC AC CTG  GTCCACAC
                                  C  A  AC
GAM450  IRF7    5'  CACACCTGCAGTCACACCTG   14446    C  A  CA
                                TAG TG GAC  CAGGTGTG
                                ||| || |||  ||||||||
                                GTC AC CTG  GTCCACAC
                                  C  A  AC
GAM450  IRF7    5'  CACACCTGCAGTCACACCTG   7815     C  A  CA
                                TAG TG GAC  CAGGTGTG
                                ||| || |||  ||||||||
                                GTC AC CTG  GTCCACAC
                                  C  A  AC
GAM450  JAM1     3'  GCCTGTAATCCCAGCTG     57899      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                GTCGAC CT  TGTCCG
                                   C  AA
GAM450  JAM1     3'  GCCTGTAATCCCAGCTG     57927      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                GTCGAC CT  TGTCCG
                                   C  AA
GAM450  JAM1     3'  GCCTGTAATCCCAGCTG     57954      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                GTCGAC CT  TGTCCG
                                   C  AA
GAM450  JAM1     3'  GCCTGTAATCCCAGCTG     33761      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                GTCGAC CT  TGTCCG
                                   C  AA
GAM450  JDD1     3'  GCTTGTAGTCCCAGCTA     63218      A  C
                                TAGCTG GAC ACAGGT
                                ||||||  ||| ||||||
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                                ATCGAC CTG TGTTCG
                                   C   A
GAM450  KALI     3'  TCACACCTGTAATCCCAGT   53595     A  CC
                                GCTG GA  ACAGGTGTGA
                                |||| ||  ||||||||||
                                TGAC CT  TGTCCACACT
                                  C  AA
GAM450  KATII    3'  GTCACACCTATAATCCCAGC  32648     A  CCAC
                                GCTG GA   AGGTGTGAC
                                |||| ||   |||||||||
                                CGAC CT   TCCACACTG
                                  C  AATA
GAM450  KBRAS2   3'  GCCTGTAATCCCAGCTA    34196      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KCNH6    3'  GCCTGTAATCCCAGCTA    47836      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA0042 3'  GCCTGTAATCCCAGCTA    29612      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA0057 3'  ACCTGTAATCCCAGCTA    24414      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  KIAA0159 3'  GCCTGTAATCCCAGCTA    29508      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA0184 3'  GCCTGTAGTCCCAGCTA    65196      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  KIAA0226 3'  GCCTGTAATCCCAGCTA    63517      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA0252 3'  GCCTGTAATCCCAGCTA    62794      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA0266 3' ACCTGTAATCCCAGCTA    41324      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  KIAA0323 3' GCTTCTGGTCTCAGCTA    63266         C
                                TAGCTGAGACCA AGGT
                                |||||||||||| ||||
                                ATCGACTCTGGT TTCG
                                      C
GAM450  KIAA0355 3' GCCTGTAGTCCCAGCTA    28029      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  KIAA0391 3' GCCTGTGGTCCCAGCTA    27915      A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAC CTGGTGTCCG
                                   C
GAM450  KIAA0419 3' GCCTGTAGTTCCAGCTA    28191      AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
                                ATCGAC  TG TGTCCG
                                   CT  A
GAM450  KIAA0420 3' GCCTATAGTCTCAGCTG    63358        CAC
                                TAGCTGAGAC   AGGT
                                ||||||||||   ||||
                                GTCGACTCTG   TCCG
                                     ATA
GAM450  KIAA0431 3' GCCTGTGATCCCAGCTA    30892      A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
                                ATCGAC CT GTGTCCG
                                   C  A
GAM450  KIAA0445 5' ACCTGTAATCCCAGCTA    27948      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  KIAA0446 5' GCCTGTAGTCCCAGCTA    68870      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  KIAA0471 3' GCCTGTAATCCCAGCTA    29395      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA0475 3' GCCTGTAGTCCCAGCTA    29493      A  C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  KIAA0514 3' ATCTGTAGCCTCAGCTA    28076       ACC
                                TAGCTGAG   ACAGGT
                                ||||||||   ||||||
                                ATCGACTC   TGTCTA
                                    CGA
GAM450  KIAA0544 3' GCCTGTGGTCCCAGCTA    70903      A
                                TAGCTG GACCACAGGT
                                ||||||  ||||||||||
                                ATCGAC CTGGTGTCCG
                                   C
GAM450  KIAA0547 3' GCTTGTAATCCCAGCTA    28912      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC CT  TGTTCG
                                   C  AA
GAM450  KIAA0557 3' GCCTGTAGTCCCAGCTA    77996      A  C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  KIAA0557 3' GCCTGTAGTCCCAGCTA    77997      A  C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  KIAA0565 3' CACACCTGTAGTCCCAGCTG  66887      A  C
                                TAGCTG GAC ACAGGTGTG
                                ||||||  |||  |||||||||
                                GTCGAC CTG TGTCCACAC
                                   C   A
GAM450  KIAA0565 3' GCCTGCAGTCCCAGTTA    66891      A  CA
                                TAGCTG GAC  CAGGT
                                ||||||  |||  |||||
                                ATTGAC CTG  GTCCG
                                   C   AC
GAM450  KIAA0570 3' CACACCTGTAGTCTCAGCTA  28179        C
                                TAGCTGAGAC ACAGGTGTG
                                ||||||||||  |||||||||
                                ATCGACTCTG TGTCCACAC
                                      A
GAM450  KIAA0596 3' GCCTGTAATCCCAGCTA    62831      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA0643 3' GCCTGTGGTCTCAGCTA    45601
                                TAGCTGAGACCACAGGT
                                ||||||||||||||||
                                ATCGACTCTGGTGTCCG

GAM450  KIAA0652 3' ATCTGTGAAGAGTCTCAGC   28456       ____
                                GCTGAGAC   CACAGGT
                                ||||||||   |||||||
                                CGACTCTG   GTGTCTA
                                    AGAA
GAM450  KIAA0694 3' ACCTGTAGTCCTAGCTA    72577      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAT CTG TGTCCA
                                   C  A
GAM450  KIAA0711 5' CACAGCCGGTCTCAGCT    29514        ACA _
                                AGCTGAGACC  GG TGTG
                                ||||||||||  || ||||
                                TCGACTCTGG  CC ACAC
                                    ___ G
GAM450  KIAA0738 3' GCCTGTGGTCCTAGCTA    28219      A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAT CTGGTGTCCG
                                   C
GAM450  KIAA0752 3' GTCACATGCCTGCAATCCCAGC 67051      A  CCA   __
          TA                    TAGCTG GA  CAGGT  GTGAC
                                |||||| ||  |||||  |||||
                                ATCGAC CT  GTCCG  CACTG
                                   C  AAC   TA
GAM450  KIAA0794 3' TGCACCTGTAATCCCAGCTA  80416      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACGT
                                   C  AA
GAM450  KIAA0795 3' GCCTGTTATCCCAGCTA    46591      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AT
GAM450  KIAA0798 3' GCTTGTAATCCCAGCTA    27725      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTTCG
                                   C  AA
GAM450  KIAA0831 3' GCCTGTAATCCCAGCTA    29977      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA0872 3' GCCTGTAGTCCCAGCTA     30065       A   C
                                TAGCTG GAC ACAGGT
                                ||||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  KIAA0876 3' CGCACCTGTGGTCCCAGCTA  64677       A
                                TAGCTG GACCACAGGTGTG
                                ||||||| ||||||||||||
                                ATCGAC CTGGTGTCCACGC
                                   C
GAM450  KIAA0884 3' GCCTGTCATCCCAGCTA     70205       A  CC
                                TAGCTG GA  ACAGGT
                                ||||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AC
GAM450  KIAA0892 3' GCCTGTAGTCCCAGCTA     71013       A   C
                                TAGCTG GAC ACAGGT
                                ||||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  KIAA0930 3' ACCTGTAATCCCAGCTA     70535       A  CC
                                TAGCTG GA  ACAGGT
                                ||||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  KIAA0953 3' TGCACCTGTGGTCCCAGGTA  66791    G   A
                                TA CTG GACCACAGGTGTG
                                || ||| ||||||||||||
                                AT GAC CTGGTGTCCACGT
                                 G   C
GAM450  KIAA0961 3' CAGGCTGGTCTCAACT      29729    C      CAG  G
                                AG TGAGACCA   GT TG
                                || ||||||||   || ||
                                TC ACTCTGGT   CG AC
                                 A       ___  G
GAM450  KIAA0961 3' GCCTGTAATCCCAGCTA     29733       A  CC
                                TAGCTG GA  ACAGGT
                                ||||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA1026 3' TACGCAGTCTCAGCT       71205        CACAG    G
                                AGCTGAGAC     GTGT A
                                |||||||||     |||| |
                                TCGACTCTG     CGCA T
                                     A____    G
GAM450  KIAA1032 3' GCCTGTAGTCCCAGCTA     66156       A   C
                                TAGCTG GAC ACAGGT
                                ||||||| ||| ||||||
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                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  KIAA1040 3' ATCATGATGGTCTCAGT    72220        _ _
                                GCTGAGACCA CA GGT
                                |||||||||| || |||
                                TGACTCTGGT GT CTA
                                   A  A
GAM450  KIAA1056 3' GCCTGTAATCCCAGCTG    29697      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                GTCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA1086 3' TGCACCTGTAGTCCCAGCTA  70754      A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                   C   A
GAM450  KIAA1143 3' CACACCTGTAGTCCCAGCTG  68672      A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                GTCGAC CTG TGTCCACAC
                                   C   A
GAM450  KIAA1160 3' TGCACCTGTAGTCCCAGCTG  40376      A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                GTCGAC CTG TGTCCACGT
                                   C   A
GAM450  KIAA1164 3' ACCTGTCATCCCAGCTA     69502      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AC
GAM450  KIAA1164 3' GCCTGTAGTCCCAGCTA     69505      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  KIAA1164 3' TCATGCCTGTAATCCCAGT   69510      A  CC
                                GCTG GA  ACAGGTGTGA
                                |||| ||  ||||||||||
                                TGAC CT  TGTCCGTACT
                                  C  AA
GAM450  KIAA1191 3' GCCTGTAGTCCCAGCTA     39956      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  KIAA1228 3' GCCTGTAGTCCCAGCTA     65042      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
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                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  KIAA1244 3' TGCACCTGTAATCCCAGCTA  71995      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACGT
                                   C  AA
GAM450  KIAA1253 3' GCCTGTGGTCCCAGCTA    91897      A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAC CTGGTGTCCG
                                   C
GAM450  KIAA1257 3' ACCTGTAGTCCCAGCTA    62723      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  KIAA1276 3' GCCTGTGGTCCCAGGTA    66432    G  A
                                TA CTG GACCACAGGT
                                || ||| ||||||||||
                                AT GAC CTGGTGTCCG
                                 G   C
GAM450  KIAA1328 3' CGCACCTGTAGTCCCGGCTA  61644      A  C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGGC CTG TGTCCACGC
                                   C   A
GAM450  KIAA1348 3' GCCTGTAATCCCAGCTA    68577      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA1364 3' CACACCTGTAATCCCAGCTA  63587      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AA
GAM450  KIAA1373 3' TGCACAGTCTCAGCT      70957        CACAG   G
                                AGCTGAGAC    GTGT A
                                |||||||||    |||| |
                                TCGACTCTG    CACG T
                                     A____   G
GAM450  KIAA1377 3' TGCACCTGTAGTCCCAGCTA  67179      A  C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                   C   A
GAM450  KIAA1404 3' GCCTGTAATCCCAGCTA    61990      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA1473 3' GCCTGTAATCCCAGCTA    70668      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA1486 3' GCCTGTAGTCCCAGCTA    67380      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  KIAA1503 3' GCCATAATGGCTCAGCTA    68349       A  CA__
                                TAGCTGAG CCA   GGT
                                |||||||| |||   |||
                                ATCGACTC GGT   CCG
                                    _  AATA
GAM450  KIAA1554 3' CACACCTGTAATCCCAGCTA  95145      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AA
GAM450  KIAA1559 3' GCCTGTAATCCCAGCTA    73066      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA1559 3' GTCACACCTGTAATCCCAGC  73073     A  CC
                                GCTG GA  ACAGGTGTGAC
                                |||| ||  ||||||||||
                                CGAC CT  TGTCCACACTG
                                  C  AA
GAM450  KIAA1586 5' GCCTGTAATTTCAGCTA    92332       CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTTT  TGTCCG
                                     AA
GAM450  KIAA1630 3' ACCTGTGATCCCAGCT     38029      A  C
                                AGCTG GA CACAGGT
                                ||||| || |||||||
                                TCGAC CT GTGTCCA
                                   C  A
GAM450  KIAA1641 3' GCCTGTAGTCTCAGCTA    80209       C
                                TAGCTGAGAC ACAGGT
                                |||||||||| ||||||
                                ATCGACTCTG TGTCCG
                                     A
GAM450  KIAA1649 3' GCTTGTAATCCCAGCTA    50273      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
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                                ATCGAC CT  TGTTCG
                                   C  AA
GAM450  KIAA1715 3' GCCTGTAATCCTAGCTA    68122      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAT CT  TGTCCG
                                   C  AA
GAM450  KIAA1735 3' CACACCTGTAGTCCCAGCTA  87625       A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACAC
                                   C   A
GAM450  KIAA1751 3' GCCTGTAATCCCAGCTA    71695      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA1771 3' GCCTGTGGTCCCAGCTA    79137      A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAC CTGGTGTCCG
                                   C
GAM450  KIAA1829 3' GCTTGTAATCCCAGCTA    61953      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTTCG
                                   C  AA
GAM450  KIAA1841 3' TACACCTGTAGTCCCAGCTA  80051      A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACAT
                                   C   A
GAM450  KIAA1855 3' GTCACACCACCTCCCTCAGC  92346      ACCACA
                                GCTGAG     GGTGTGAC
                                ||||||     ||||||||
                                CGACTC     CCACACTG
                                   CCTCCA
GAM450  KIAA1870 3' ATCTGTAATCCCAGCTA    51825      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCTA
                                   C  AA
GAM450  KIAA1871 3' GCCTGTAGTCCCAGGTA    61234    G  A  C
                                TA CTG GAC ACAGGT
                                || ||| ||| ||||||
                                AT GAC CTG TGTCCG
                                 G   C   A
GAM450  KIAA1872 3' GCCTGTAATCCCAGCTA    62935      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA1872 3' GCCTGTAATCCCAGCTA    62936      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA1872 3' CGCACCTGTAGTCCCAGCTA  62928      A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGC
                                   C   A
GAM450  KIAA1884 3' TCACACCTCTCCAGCT      73340      A  CCAC
                                AGCTG GA    AGGTGTGA
                                ||||| ||    ||||||||
                                TCGAC CT    TCCACACT
                                  _ C___
GAM450  KIAA1908 3' GTCACACCCTGGGTCAGT    73402      GA   CA
                                GCTGA  CCA  GGTGTGAC
                                |||||  |||  ||||||||
                                TGACT  GGT  CCACACTG
                                  G_   C_
GAM450  KIAA1941 3' GCCTGTAATCCCAGCTA     74840      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA1948 3' GCCTGTAGTCCCAGCTA     82403      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  KIAA1948 3' GCCTGTAGTCCTAGCTA     82404      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAT CTG TGTCCG
                                   C   A
GAM450  KIAA1950 3' GCCTGTGTTCCCAGCTA     92593      A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
                                ATCGAC CT GTGTCCG
                                   C  T
GAM450  KIAA1958 3' GCCTGTAATCCCAGCTA     81904      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KIAA1979 3' GCCTGTAATCCCAGCTA     88283      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KR18    3'  GCCTGTGGTCTCAGCTA    52748
                                TAGCTGAGACCACAGGT
                                |||||||||||||||||
                                ATCGACTCTGGTGTCCG

GAM450  KR18    3'  TCACACCTGTAATCCCAGT   52753     A  CC
                                GCTG GA  ACAGGTGTGA
                                ||||  ||  ||||||||||
                                TGAC CT  TGTCCACACT
                                  C  AA
GAM450  KR18    3'  GCCTGTAATCCCAGCTA    52747      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  KREMEN  3'  CACACCTGTAATCCCAGCTA  49405      A  CC
                                TAGCTG GA  ACAGGTGTG
                                ||||||  ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AA
GAM450  LANO    3'  GCCTGTAGTCCCAGCTA    47189      A   C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LIAS    3'  GCCTGTAATCCCAGCTA    70636      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LIM     3'  GCCTGTAATCCCAGCTA    21305      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LY117   3'  GTCCCCCTGTGGTCCAGC   92353     A      TGT
                                GCTG GACCACAGG   GAC
                                ||||  |||||||||   |||
                                CGAC CTGGTGTCC   CTG
                                  _       CC_
GAM450  LY117   3'  GTCCCCCTGTGGTCCAGC   97747     A      TGT
                                GCTG GACCACAGG   GAC
                                ||||  |||||||||   |||
                                CGAC CTGGTGTCC   CTG
                                  _       CC_
GAM450  LY117   3'  GTCCCCCTGTGGTCCAGC   97848     A      TGT
                                GCTG GACCACAGG   GAC
                                ||||  |||||||||   |||
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                                CGAC CTGGTGTCC   CTG
                                  _       CC_
GAM450  MACF1    3'  GCCTGTAGTCCCAGCTA     52317       A   C
                                TAGCTG GAC ACAGGT
                                ||||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  MDS006   3'  GTCACACCCATGATGGTGGCTA 39585       GAG   _ __
                                TAGCT   ACCA CA  GGTGTGAC
                                |||||   |||| ||  ||||||||
                                ATCGG   TGGT GT  CCACACTG
                                   ____   A  AC
GAM450  MGC10814 5'  GCCTGTAGTCCAAGCTA     51039       GA   C
                                TAGCT  GAC ACAGGT
                                |||||  ||| ||||||
                                ATCGA  CTG TGTCCG
                                   AC   A
GAM450  MGC10999 3'  GCCTGTAATCCCAGTTA     50227       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATTGAC CT  TGTCCG
                                   C  AA
GAM450  MGC11352 3'  GCCTGTAGTCCCAGCTA     64802       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  MGC11386 3'  GCCTGTAGTCCCAGCTA     51954       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  MGC13017 3'  ATCTGTAATCCCAGCTA     54692       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCTA
                                   C  AA
GAM450  MGC14126 3'  GCCTGTAATCCCGGCTA     51855       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGGC CT  TGTCCG
                                   C  AA
GAM450  MGC14407 3'  TGCACCTGTAGTCACAGCTA  51882       A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                   A   A
GAM450  MGC14799 3'  TGCACCTGTAATCCCGGCTA  50334       A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
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                                ATCGGC CT  TGTCCACGT
                                   C  AA
GAM450  MGC15397 3' ACCTGTAATCCCAGCTA    54677      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  MGC15631 3' CACACCTGTCATCCCAGCTA  51261      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AC
GAM450  MGC16332 3' GCCTGTAGTCCCAGCTA     56776      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  MGC16703 3' ACACCTGTGGTCCCAGCTA   73097      A
                                TAGCTG GACCACAGGTGT
                                |||||| ||||||||||||
                                ATCGAC CTGGTGTCCACA
                                   C
GAM450  MGC20235 3' GCCTGTAATCCCGGCTA     58897      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGGC CT  TGTCCG
                                   C  AA
GAM450  MGC20235 3' TTACACCTGTAATCCCAGT   58904     A  CC
                                GCTG GA  ACAGGTGTGA
                                |||| ||  ||||||||||
                                TGAC CT  TGTCCACATT
                                  C  AA
GAM450  MGC20235 3' ACCTGTAGTCCCAGCTA     58891      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  MGC22805 3' GCCTGTAATCCCAGCTA     58083      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  MGC2396  3' GCCTGTAATCCCAGCTA     53461      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  MGC2562  3' CGCACCTGTAATCCCAGCTG  50436      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
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                                GTCGAC CT  TGTCCACGC
                                   C  AA
GAM450  MGC2562  3' GCCTGTAGTCCCAGCTA    50443      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  MGC2663  3' ACCTGTAATCCCAGCTA    44093      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  MGC26641 3' TGCACCTGTAATCCCAACTA  58659    C  A  CC
                                TAG TG GA  ACAGGTGTG
                                ||| || ||  |||||||||
                                ATC AC CT  TGTCCACGT
                                  A  C  AA
GAM450  MGC2721  3' GTCTGCAGTGGTCTCAGC    51221         AG   T
                                GCTGAGACCAC  GTG GAC
                                ||||||||||  ||| |||
                                CGACTCTGGTG  CGT CTG
                                     A_  _
GAM450  MGC2731  3' GCCTGTAATCCCAGCTA    43951      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  MGC29762 3' ACCTGTGATCCCAGCTA    58466      A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
                                ATCGAC CT GTGTCCA
                                   C  A
GAM450  MGC29891 3' GCCTGTAGTCCCAGTTA    58206      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATTGAC CTG TGTCCG
                                   C   A
GAM450  MGC29937 3' GCCTGTAATCCCAGTTA    58113      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATTGAC CT  TGTCCG
                                   C  AA
GAM450  MGC4248  3' ACCTGTAGTCCCAGCTA    50325      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  MGC4562  3' GCCTGTAGTCCCAGCTA    55909      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
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                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  MGC4663  3' ACCTGTAGTCCCAGCTA    44502      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  MGC4771  3' GCCTGTAATCCCAGCTA    51031      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  MGC5384  3' GCCTGTAGTCCCAGCTA    48270      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  MGC9753  5' CACACCTGTGTGGC       53045     AGAC
                                GCTG   CACAGGTGTG
                                ||||   ||||||||||
                                CGGT   GTGTCCACAC
                                    ____
GAM450  MKRN4    3' GCCTGTAGTCCCAGCTA    47747      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  MLZE     5' GCGCATGGTCTCAGCT     48620       CAG
                                AGCTGAGACCA  GTGT
                                ||||||||||   ||||
                                TCGACTCTGGT  CGCG
                                      A__
GAM450  MOST2    5' GCCTGTAGTCCCAGCTA    39686      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  MRPL48   5' ACCTGTAATCCCAGCTA    32131      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  MRPS10   3' GCCTGTAATCCCAGCTA    36296      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  MRPS18B  3' CACACCTGTAGTCTCAACTA  25906    C    C
                                TAG TGAGAC ACAGGTGTG
                                ||| |||||| |||||||||
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                                ATC ACTCTG TGTCCACAC
                                  A     A
GAM450  MRPS27   3'  GTCAGGCTGGTCTCA      30642       CAG  G
                                TGAGACCA   GT TGAC
                                ||||||||   || ||||
                                ACTCTGGT   CG ACTG
                                     ___  G
GAM450  MT-ACT48 3'  TGCACCTGTAGTCCCAGTTA  24692      A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATTGAC CTG TGTCCACGT
                                   C   A
GAM450  N4BP2    3'  GCCTGTAATCCCAGCTA    36405      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  NMNAT    3'  GCCTGTAGTCCCAGCTA    42957      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  NMT2     3'  GCCTGTAGTCCCAGCTG    16665      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                GTCGAC CTG TGTCCG
                                   C   A
GAM450  NPTXR    3'  GCCTGTAGTCCCAGCTA    26646      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  NPTXR    3'  GCCTGTAGTCCCAGCTA    54182      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  OSBPL2   3'  TCACACCTGTGACGGAAGC   57869    GAGAC
                                GCT    CACAGGTGTGA
                                |||    ||||||||||
                                CGA    GTGTCCACACT
                                  AGGCA
GAM450  OSBPL2   3'  TCACACCTGTGACGGAAGC   29218    GAGAC
                                GCT    CACAGGTGTGA
                                |||    ||||||||||
                                CGA    GTGTCCACACT
                                  AGGCA
GAM450  PDCD7    3'  CACACCTGTAGTCCCAGCTA  72136      A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
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                                ATCGAC CTG TGTCCACAC
                                   C   A
GAM450  PDE8A    3'  TCGACATGGTCTTAGC      62638          CAGG  _
                                GCTGAGACCA   TGT GA
                                ||||||||||   ||| ||
                                CGATTCTGGT   ACA CT
                                     ____   G
GAM450  PDEF     5'  GCCAGTGGCCTCAGCTG     24748        A   A
                                TAGCTGAG CCAC GGT
                                |||||||| |||| |||
                                GTCGACTC GGTG CCG
                                   C   A
GAM450  phorbolin-1 3'  GCCTGTAGTCCCAGCTA     88779       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  PILR(ALPHA) 3'  CACACCTGTAATCCCAGCTA   25545       A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AA
GAM450  PIWIL2   3'  GCCTGTAGTCCCAGCTA     36059       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  PNPASE   3'  GCCTGTAATCCTAGCTA     70871       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAT CT  TGTCCG
                                   C  AA
GAM450  PP591    5'  GCCTGTAGTCCCAGCTA     47369       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  PPP1R3B  3'  GCCTGTAATCCAGCTA      44821       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   _  AA
GAM450  PPP1R3B  3'  GCCTGTAGTCCCAGCTA     44822       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  PRIC285  3'  GCCTGTAATCCCAGCTA     61437       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  PRO0365  5' CACCTAGGCACGATCTCAGCT 26151        _____ AC
                                AGCTGAGA    CC  AGGTG
                                ||||||||    ||  |||||
                                TCGACTCT    GG  TCCAC
                                    AGCAC  A_
GAM450  PRO0456  3' GCCTGTAGTCCCATCTA    26176    C  A  C
                                TAG TG GAC ACAGGT
                                ||| || ||| ||||||
                                ATC AC CTG TGTCCG
                                  T  C  A
GAM450  PRO0478  5' CACACCTGTAATCCCAGGTA  26185   G  A  CC
                                TA CTG GA  ACAGGTGTG
                                || ||| ||  |||||||||
                                AT GAC CT  TGTCCACAC
                                 G  C  AA
GAM450  PRO0478  3' GCCTGTAATCCCAGCTA    26190      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  PRO0478  3' TCACACCTGTAATCCCAGC   26197     A  CC
                                GCTG GA  ACAGGTGTGA
                                |||| ||  ||||||||||
                                CGAC CT  TGTCCACACT
                                  C  AA
GAM450  PRO0618  3' GCCTGTAGTCCCAGCTA    26201      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  PRO1048  5' GCCTGTAGTCCCAGCTA    37517      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  PRO1257  3' TCACACAGACTCAGCTA    37710       ACCACAG
                                TAGCTGAG     GTGTGA
                                ||||||||     ||||||
                                ATCGACTC     CACACT
                                    AGA____
GAM450  PRO1496  3' GCCTGTAGTCCCAGCTA    37759      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  PRO2015  3' ACCTGTAGTTCCAGCTA    37555      AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
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                                ATCGAC  TG TGTCCA
                                   CT  A
GAM450  PRO2032  5' TCACAGCTGGTCTCAGGTA   37782    G       CA G
                                TA CTGAGACCA  G TGTGA
                                || |||||||||  | |||||
                                AT GACTCTGGT  C ACACT
                                 G       __ G
GAM450  PRO2133  3' GCCTGTGATCTCAGCTA     37789         C
                                TAGCTGAGA CACAGGT
                                ||||||||| |||||||
                                ATCGACTCT GTGTCCG
                                      A
GAM450  PRO2198  5' GCCTGTAATCCCAGTTA     37792       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATTGAC CT  TGTCCG
                                   C  AA
GAM450  PRO2859  3' ACTTGTAGTCCCAGCTA     37613       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTTCA
                                   C   A
GAM450  PRO2964  3' ACCTGTAGTCCCAGCTA     37654       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  PSR      3' GCCTGTAGTCCCAGCTA     65184       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  PTK6     3' GCCTGTGATCCCAGCTA     19937       A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
                                ATCGAC CT GTGTCCG
                                   C  A
GAM450  PTRF     3' GCCTGTAATCCCAGCTA     63502       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  PTRF     3' GCCTGTGGTCTCAGCTA     63503
                                TAGCTGAGACCACAGGT
                                |||||||||||||||||
                                ATCGACTCTGGTGTCCG

GAM450  RAB4B    5' GCCTGTAATCCCAGCTA     32376       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  RAD51    3'  GCCTGTAGTCCCAGCTA     11224       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  RAD51    3'  GCCTGTAGTCCCAGCTA     56018       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  RES4-25  3'  CGCACCTGTAGTCCCAACTA  64650     C A   C
                                TAG TG GAC ACAGGTGTG
                                ||| || ||| |||||||||
                                ATC AC CTG TGTCCACGC
                                  A C   A
GAM450  RFX4     3'  TCACACCTGTAGTCCCAGCTA  11319       A   C
                                TAGCTG GAC ACAGGTGTGA
                                |||||| ||| ||||||||||
                                ATCGAC CTG TGTCCACACT
                                   C   A
GAM450  RHOBTB3  3'  CACACCTGTAATCCCAGCTA   29742       A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AA
GAM450  RNO2     5'  GCCTGTAGTCCCAGCTA     52770       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  RNO2     5'  CACACCTGTGGCCCCAGCT   52763       AGA
                                AGCTG   CCACAGGTGTG
                                |||||   ||||||||||
                                TCGAC   GGTGTCCACAC
                                   CCC
GAM450  RoXaN    3'  GCCTGTAGTTCCAGCTA     46647       AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
                                ATCGAC  TG TGTCCG
                                   CT  A
GAM450  RoXaN    3'  GCCTGTAGTCCCAGCTA     46646       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  Rpo1-2   3'  GCCTGTAGTTCCAGCTA     38701       AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
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                                ATCGAC  TG TGTCCG
                                    CT  A
GAM450  RRP4     3'  TGCACCTGTAGTCCCAGCTA  26566       A  C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                    C   A
GAM450  SAMHD1   3'  GCTTGTAATCCCAGCTA    61314       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTTCG
                                    C  AA
GAM450  SAMHD1   3'  GCCTGTAGTCCCAGCTA    61313       A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                    C   A
GAM450  SC4MOL   3'  TGCACAGTCTCAGCT      22166        CACAG    G
                                AGCTGAGAC    GTGT A
                                |||||||||    |||| |
                                TCGACTCTG    CACG T
                                     A____   G
GAM450  SCN12A   3'  GCCTGTAGTCCCAGCTA    26223       A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                    C   A
GAM450  SCYA5    3'  GCCTGTAATCCCAGCTA    11451       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                    C  AA
GAM450  SCYA5    3'  GCCTGTAGTCCCAGCTA    11452       A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                    C   A
GAM450  SEMA3E   3'  GCCTGTAGTCCCAGCTA    24882       A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                    C   A
GAM450  SLC19A3  3'  GCCTGTAGTCTCAGCTA    47490         C
                                TAGCTGAGAC ACAGGT
                                |||||||||| ||||||
                                ATCGACTCTG TGTCCG
                                     A
GAM450  SLC7A11  3'  GCTGGTAATCTCAGCTA    26753         CC  A
                                TAGCTGAGA  AC GGT
                                |||||||||  || |||
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                                ATCGACTCT  TG TCG
                                     AA  G
GAM450  SMA3     3'  GCCTGTAGTCCCAGCTA     22288       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  SMAP-5   3'  GCCTGTAGTCCCAGCTA     47932       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  SNAPC1   3'  GCCTGTAATCCCAGCTA     11842       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  Spir-1   3'  CTGGCTGGTCTCAGCTA     64699          __
                                TAGCTGAGACCA  CAG
                                ||||||||||||  |||
                                ATCGACTCTGGT  GTC
                                      CG
GAM450  SPTLC2   3'  GCCTGTAATCCCAGCTA     16803       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  SS18L1   3'  ACCTGTAATCCCAGCTA     65342       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  SSR3     3'  GCCTGTAATCTCAGCTA     23040         CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                     AA
GAM450  STRBP    5'  CACTGTGCCTGGCCTCAACTG  37229     C   ACCA   ___
                                TAG TGAG   CAGGT  GTG
                                |||  ||||   |||||  |||
                                GTC ACTC   GTCCG  CAC
                                  A   CG__    TGT
GAM450  TA-LRRP  3'  GCCTGTAATCCCAGCTA     31070       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  TACTILE  3'  ACCTGTAGTCCCAGCTA     19465       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
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                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  TFEC    5'  TCTGCAAGGCCTCAGCTA    24293        A  A__
                                TAGCTGAG CC   CAGG
                                |||||||| ||   ||||
                                ATCGACTC GG   GTCT
                                     C  AAC
GAM450  TMG4    3'  GCCTGTAGTCCCACCTA     43990     C  A   C
                                TAG TG GAC ACAGGT
                                ||| || ||| ||||||
                                ATC AC CTG TGTCCG
                                  C  C   A
GAM450  TTYH2   3'  TAGGCATGGTCTCAGGTA    50997    G       CAG  G
                                TA CTGAGACCA   GT TG
                                || |||||||||   || ||
                                AT GACTCTGGT   CG AT
                                 G       A__  G
GAM450  VIT1    5'  GCTTGTAATCCCAGCTG     37976      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                GTCGAC CT  TGTTCG
                                   C  AA
GAM450  WBSCR21  3'  CACACCTGTAATCCCAGCTA  48474      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AA
GAM450  WBSCR23  5'  ACCTGTAGTCCTAGCTA     46752      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAT CTG TGTCCA
                                   C   A
GAM450  WBSCR23  3'  GCCTGTAATCCCAGCTA     46763      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  WSB1    3'  ACCTGTAGTCCTAGCTA     56145      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAT CTG TGTCCA
                                   C   A
GAM450  WSB1    3'  ACCTGTAGTCCTAGCTA     56139      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAT CTG TGTCCA
                                   C   A
GAM450  YEA     3'  TCACACCTGTAATCCCAGC   51535     A  CC
                                GCTG GA  ACAGGTGTGA
                                |||| ||  ||||||||||
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                                CGAC CT  TGTCCACACT
                                  C  AA
GAM450  YEA     3'  GCCTGTAATCCCAGCTA     51531       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  ZAK     3'  CACACCTGTAGTCCCAG     56122     A   C
                                CTG GAC ACAGGTGTG
                                ||| ||| |||||||||
                                GAC CTG TGTCCACAC
                                  C   A
GAM450  ZFP106  3'  TCACACCTGTAATCCCAGCT  42479       A  CC
                                AGCTG GA  ACAGGTGTGA
                                ||||| ||  ||||||||||
                                TCGAC CT  TGTCCACACT
                                   C  AA
GAM450  ZFP106  3'  GCCTGTAATCCCAGCTG     42471       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                GTCGAC CT  TGTCCG
                                   C  AA
GAM450  ZFP106  3'  GCCTGTAGTCTCAGCTA     42472          C
                                TAGCTGAGAC ACAGGT
                                |||||||||| ||||||
                                ATCGACTCTG TGTCCG
                                      A
GAM450  ZIM3    3'  ACCTGTAATCCCAGCTA     53535       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  ZIN     3'  TCACTGTGTGATGGTCTCAGT  25493          _  GGT_
                                GCTGAGACCA CA    GTGA
                                |||||||||| ||    ||||
                                TGACTCTGGT GT    CACT
                                      A  GTGT
GAM450  ZNF271  3'  GCCTGTAGTCCCAGCTA     95253       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  ZNF297B 3'  CACACCTGTAATCCCAGCTA  25777       A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AA
GAM450  ZNF333  3'  TGCACCTGTAATCCCAGCTA  50572       A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
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                                ATCGAC CT  TGTCCACGT
                                   C  AA
GAM450  ZNF339   3' ACCTGTAGTCCCAGCTA    41117      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  ZNF347   3' GCCTGTAATCCCAGCTA    50846      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC115129 3' TCACACCTATAATCCCAGC   73242     A  CCAC
                                GCTG GA   AGGTGTGA
                                |||| ||   ||||||||
                                CGAC CT   TCCACACT
                                  C  AATA
GAM450  LOC115129 5' TTACACCTGTAATCCCAGCTA 73244      A  CC
                                TAGCTG GA  ACAGGTGTGA
                                |||||| ||  ||||||||||
                                ATCGAC CT  TGTCCACATT
                                   C  AA
GAM450  LOC115196 3' GCCTGTAGTCCCAACTA    73265    C  A  C
                                TAG TG GAC ACAGGT
                                ||| || ||| ||||||
                                ATC AC CTG TGTCCG
                                  A  C   A
GAM450  LOC115273 3' GCCTGTAATCCCAGTTA    73359      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATTGAC CT  TGTCCG
                                   C  AA
GAM450  LOC115399 5' GCCTGTAGTCCCAGCTA    73434      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC115757 3' ACCTGTAGTCCCAGCTA    73573      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  LOC115761 3' GCCTGTAGTCCCAGCTA    91738      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC116143 3' ATCTGTAGTCCTAGCTA    73770      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
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                                ATCGAT CTG TGTCTA
                                   C   A
GAM450  LOC116143 3' GCCTGTAATCACAGCTA     73772       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   A  AA
GAM450  LOC116228 3' GCCTGTAGTCCCAGGTA     73801    G  A  C
                                TA CTG GAC ACAGGT
                                || ||| ||| ||||||
                                AT GAC CTG TGTCCG
                                 G   C   A
GAM450  LOC116236 3' GCCTGTAATCCCAGTTA     73811       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATTGAC CT  TGTCCG
                                   C  AA
GAM450  LOC116236 3' GCTCTGCAAGTCTCAGCTA   73812         CA_   T
                                TAGCTGAGAC   CAGG GT
                                ||||||||||   |||| ||
                                ATCGACTCTG   GTCT CG
                                      AAC   _
GAM450  LOC119504 5' GCCTGTAATCCCAGCTA     73991       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC120939 3' GCATGGTCTCAGCT        76255          CAGG
                                AGCTGAGACCA    TGT
                                ||||||||||    |||
                                TCGACTCTGGT    ACG
                                     ____
GAM450  LOC122704 3' GCTTGTAATCCCAGCTA     74140       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTTCG
                                   C  AA
GAM450  LOC122970 3' CACACCTGTAGTCCCAGCTA  74177       A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACAC
                                   C   A
GAM450  LOC122970 3' TCACACCTGTAATCCCAGT   74188     A  CC
                                GCTG GA  ACAGGTGTGA
                                ||||  ||  ||||||||||
                                TGAC CT  TGTCCACACT
                                  C  AA
GAM450  LOC123283 3' GTCCACTCATGGCCTCAGCTG 76012         A   CA   T
                                TAGCTGAG CCA  GGTG GAC
                                |||||||| |||  |||| |||
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                                GTCGACTC GGT  TCAC CTG
                                    C  AC   _
GAM450  LOC126282 3'  GCCTGTAGTCCCAGCTA     74475       A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  LOC126282 3'  GCCTGTAGTCCCAGCTA     74476       A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  LOC126297 5'  GCCTGTGATCGCAGCTA     74482       A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
                                ATCGAC CT GTGTCCG
                                   G  A
GAM450  LOC126669 3'  GCCTGTGGTTCCAGCTA     75408       AG
                                TAGCTG  ACCACAGGT
                                ||||||  |||||||||
                                ATCGAC  TGGTGTCCG
                                   CT
GAM450  LOC127262 3'  ATCTGTGGTCCCAGCTA     76106       A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAC CTGGTGTCTA
                                   C
GAM450  LOC127294 3'  GCCTGTAATCCCGGCTA     74655       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGGC CT  TGTCCG
                                   C  AA
GAM450  LOC127428 3'  GCCTGTAATCCCAGCTA     74670       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC128954 5'  CACACCTGCATGGTGC      75791     TGAG   __
                                GC   ACCA  CAGGTGTG
                                ||   ||||  ||||||||
                                CG   TGGT  GTCCACAC
                                 ____   AC
GAM450  LOC130026 3'  GCCTGTAGTCCCAGCTA     56647       A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  LOC130535 3'  GCCTGTAGTCCCAGCTA     76153       A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
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                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC130535 3' GCCTGTGATCCCAGCTA     76154       A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
                                ATCGAC CT GTGTCCG
                                   C  A
GAM450  LOC131965 3' GCCTGTAATCCCAGCTA     75031       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC132625 3' GCCTGTGTTCCCAGCTA     75907       A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
                                ATCGAC CT GTGTCCG
                                   C  T
GAM450  LOC133926 3' GCCTGTAGTCCCAGCTA     75133       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC134147 3' GCCTGTAATCCCAGCTA     57162       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC134147 3' GCCTGTAGTCCCAGCTA     57163       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC135154 3' TGCACCTGTAATCCCAACTA  75225     C  A  CC
                                TAG TG GA  ACAGGTGTG
                                ||| || ||  |||||||||
                                ATC AC CT  TGTCCACGT
                                  A  C  AA
GAM450  LOC138389 3' ACCTGTAATTTCAGCTA     76214         CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTTT  TGTCCA
                                     AA
GAM450  LOC142779 3' ACCTGTAATCTCAGCTA     76389         CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCA
                                     AA
GAM450  LOC142937 3' ACCTGTGGTTCCAGCTA     56653       AG
                                TAGCTG  ACCACAGGT
                                ||||||  |||||||||
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                                ATCGAC  TGGTGTCCA
                                   CT
GAM450  LOC142948 3' GCCTGTAGTCCCAGCTA    82889      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  LOC143196 3' GCCTGTAATCCCAGCTA    82905      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC143465 3' GCCTGTAATCACAGCTA    82963      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   A  AA
GAM450  LOC143943 3' GCTTGTACTCCCAGCTA    82995      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTTCG
                                   C  CA
GAM450  LOC144289 3' GCCTGTAATCCCAGCTA    83026      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC144308 5' GCCTGTGGTCCCAGCTA    83049      A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAC CTGGTGTCCG
                                   C
GAM450  LOC144465 3' GCCTGTAATCCCAGCTA    76854      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC144465 3' GCCTGTAATCCCAGCTA    76855      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC144481 3' GCCTGTAATCCCAGCTA    83098      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC144524 3' GCCTGTAGTCCCAGCTA    83128      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
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                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC144558 3'  GCCTGTGGTCTCAGCTA     83147
                                TAGCTGAGACCACAGGT
                                |||||||||||||||||
                                ATCGACTCTGGTGTCCG

GAM450  LOC144817 3'  CACACCTGTAATCTCAGCTA  76964        CC
                                TAGCTGAGA  ACAGGTGTG
                                |||||||||  |||||||||
                                ATCGACTCT  TGTCCACAC
                                      AA
GAM450  LOC144845 3'  GCCTGTAATCTCAGCTA     56660        CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                      AA
GAM450  LOC145082 5'  ACCTGTAGTACCAGCTA     83233       AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
                                ATCGAC  TG TGTCCA
                                   CA  A
GAM450  LOC145216 3'  ACCTGTAATCCCAGCTA     83261       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC145231 3'  GCCTGTAATCCCAGCTA     83289       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC145231 3'  GCCTGTAATCTCAGCTA     83290        CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                      AA
GAM450  LOC145299 3'  GCCTGTAGTCCCAGCTA     83315       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC145333 3'  GCCTGTAGTCCCAGCTA     83327       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC145387 3'  GCCTGTGGTCTCAGCTA     83357
                                TAGCTGAGACCACAGGT
                                |||||||||||||||||
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                                ATCGACTCTGGTGTCCG

GAM450  LOC145438 3'  GCCTGTAGTCCCAGCTA     83340       A   C
                      TAGCTG GAC ACAGGT
                      ||||||  |||  ||||||
                      ATCGAC CTG TGTCCG
                          C   A
GAM450  LOC145482 3'  GCCTGTAATCCCAGCTA     77230       A  CC
                      TAGCTG GA  ACAGGT
                      ||||||  ||  ||||||
                      ATCGAC CT  TGTCCG
                          C  AA
GAM450  LOC145483 3'  GCCTGTAATCCTAGCTA     77245       A  CC
                      TAGCTG GA  ACAGGT
                      ||||||  ||  ||||||
                      ATCGAT CT  TGTCCG
                          C  AA
GAM450  LOC145662 3'  GCCTGTAGTTCCAGCTA     77320       AG  C
                      TAGCTG  AC ACAGGT
                      ||||||   ||  ||||||
                      ATCGAC  TG TGTCCG
                          CT  A
GAM450  LOC145663 3'  GCCTGTAGTCTCAGCTA     83414         C
                      TAGCTGAGAC ACAGGT
                      ||||||||||  ||||||
                      ATCGACTCTG TGTCCG
                            A
GAM450  LOC145820 3'  GCCTGTAGTCCCAGCTA     77515       A   C
                      TAGCTG GAC ACAGGT
                      ||||||  |||  ||||||
                      ATCGAC CTG TGTCCG
                          C   A
GAM450  LOC145955 3'  ACCTGTAGTCCTAGCTA     83584       A   C
                      TAGCTG GAC ACAGGT
                      ||||||  |||  ||||||
                      ATCGAT CTG TGTCCA
                          C   A
GAM450  LOC146059 3'  GCCTGTAATCCCAGCTA     77620       A  CC
                      TAGCTG GA  ACAGGT
                      ||||||  ||  ||||||
                      ATCGAC CT  TGTCCG
                          C  AA
GAM450  LOC146316 5'  CACACTTCTCAGCTA       60868         CCACA
                      TAGCTGAGA    GGTGTG
                      |||||||||    ||||||
                      ATCGACTCT    TCACAC
                                   _____
GAM450  LOC146540 3'  GCCTGTAGTCCCAGCTA     77975       A   C
                      TAGCTG GAC ACAGGT
                      ||||||  |||  ||||||
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                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC146713 3'  GCCTGTAGTCCCAGCTA    83728      A   C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC146723 3'  GCCTGTAATCCCAGCTA    78085      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC146728 3'  GCCTGTGGTCCCAGCTA    83750      A
                                TAGCTG GACCACAGGT
                                ||||||  ||||||||||
                                ATCGAC CTGGTGTCCG
                                   C
GAM450  LOC146756 3'  GCCTGTAGTCCCAGCTA    83780      A   C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC146895 3'  GCCTGTAATCCCAGCTA    83824      A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC146923 3'  ACCTGTAGTCCCAGCTA    78189      A   C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  LOC147057 3'  GCCTGTAGTCCCAGCTA    83910      A   C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC147080 3'  ACCTGTGATCCCAGCTA    83930      A  C
                                TAGCTG GA CACAGGT
                                ||||||  ||  |||||||
                                ATCGAC CT GTGTCCA
                                   C  A
GAM450  LOC147180 5'  GCCTGTAGTCCCAGCTA    83987      A   C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC147649 3'  GCCTGTAGTCCCAGCTA    78415      A   C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
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                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC147660 3'  ACCTGTAGTCTCAGCTA     78390          C
                                TAGCTGAGAC ACAGGT
                                |||||||||| ||||||
                                ATCGACTCTG TGTCCA
                                     A
GAM450  LOC147664 3'  GCCTGTAATCCCAGCTA     78409       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC147669 3'  GCCTGTGGTCCCAGCTA     84063       A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAC CTGGTGTCCG
                                   C
GAM450  LOC147700 3'  GCCTGTAATCCCAGCTA     59198       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC147727 5'  GCCTGTAATCCCAGCTA     78469       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC147727 5'  GCCTGTAGTCCCACCTA     78470     C  A  C
                                TAG TG GAC ACAGGT
                                ||| || ||| ||||||
                                ATC AC CTG TGTCCG
                                  C  C   A
GAM450  LOC147837 3'  GCCTGTAATCCCAGCTA     78516       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC147990 3'  CACACCTGTAATCTCAGCTA  84088         CC
                                TAGCTGAGA  ACAGGTGTG
                                |||||||||  |||||||||
                                ATCGACTCT  TGTCCACAC
                                     AA
GAM450  LOC148147 3'  GCCTGTAGTCCCAGCTA     78681       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC148198 3'  GCCTGTAATCCCAGCTA     70682       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC148293 3'  TGCACCTGTAGTCCCAGCTA  78785      A  C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                   C   A
GAM450  LOC148397 3'  GCCTGTAATCCTAGCTA    78819      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAT CT  TGTCCG
                                   C  AA
GAM450  LOC148534 3'  GCCTGTAATCCCAGCTA    78895      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC148734 3'  GCCTGTAATCCCAGCTA    78955      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC148809 5'  ACCTGTAATCCCAGCTA    78996      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC148823 3'  CACACCTGTAGTCCCAGGTA  59207    G  A  C
                                TA CTG GAC ACAGGTGTG
                                || ||| ||| |||||||||
                                AT GAC CTG TGTCCACAC
                                 G  C  A
GAM450  LOC148887 5'  CACAGGGCGTGCTCAGCTA   84229       AC  AGG_
                                TAGCTGAG  CAC   TGTG
                                ||||||||  |||   ||||
                                ATCGACTC  GTG   ACAC
                                    __  CGGG
GAM450  LOC148918 5'  GCCTGTAGTGCCAGCTA    79073      AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
                                ATCGAC  TG TGTCCG
                                   CG  A
GAM450  LOC148936 3'  GCCTGTGATCCCAGCTA    84293      A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
                                ATCGAC CT GTGTCCG
                                   C  A
GAM450  LOC148938 3'  GCCTGTGATCCCAGCTA    84274      A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
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                                ATCGAC CT GTGTCCG
                                   C  A
GAM450  LOC149073 3' GCCTGTAATCCCAGCTA    84325      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC149113 3' GCCTGTAATCCCAGCTA    79167      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC149175 3' GCCTGTAGTCCCAGCTA    79210      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  LOC149194 5' ACCTGTAATCCCAGCTA    79220      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC149319 3' GCCTGTAATCCCAGCTA    79296      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC149448 3' GTCACATGCCTGTAAACCCAGC 84423      AGACC    __
           TA                    TAGCTG    ACAGGT  GTGAC
                                ||||||    ||||||  |||||
                                ATCGAC    TGTCCG  CACTG
                                   CCAAA     TA
GAM450  LOC149460 3' ACCTGTAATCCCAGCTA    84438      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC149464 5' GCTTGTAGTCCCAGCTA    84431      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTTCG
                                   C  A
GAM450  LOC149577 3' CGCGCCTGGCCTCAGC     84507      ACCA
                                GCTGAG   CAGGTGTG
                                ||||||   ||||||||
                                CGACTC   GTCCGCGC
                                   CG__
GAM450  LOC149579 5' ACCTGTAATCCCAGCTA    71128      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC149705 3'  GCCTGTAATCCCAGCTA     84624       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC150095 3'  GCCTGTGGTCCTAGCTA     84858       A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAT CTGGTGTCCG
                                   C
GAM450  LOC150139 3'  GCCTGTAATCCCAGCTG     79585       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                GTCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC150225 3'  GCCTGTAGTCCCAGCTA     84997       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC150225 3'  GCCTGTGGTCTCAACTA     84999     C
                                TAG TGAGACCACAGGT
                                ||| ||||||||||||
                                ATC ACTCTGGTGTCCG
                                  A
GAM450  LOC150299 3'  ACCTGTAGTCCCAGCTA     84965       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  LOC150319 3'  GCCTGTAATCCCAGTTA     79656       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATTGAC CT  TGTCCG
                                   C  AA
GAM450  LOC150356 3'  GCCCTGCCCAGTCTCAGC    79780         CA__    T
                                GCTGAGAC    CAGG GT
                                ||||||||    |||| ||
                                CGACTCTG    GTCC CG
                                     ACCC    _
GAM450  LOC150358 3'  ACACCTGTAATCCCAGGTA    84918    G   A  CC
                                TA CTG GA  ACAGGTGT
                                || ||| ||  ||||||||
                                AT GAC CT  TGTCCACA
                                 G   C  AA
GAM450  LOC150358 3'  ACCTGTAGTCCCAGCTA     84919       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
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                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  LOC150372 3'  CGCACCTGTAGTCCCAGCTA  79797      A  C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGC
                                   C   A
GAM450  LOC150577 3'  GCCTGGAGTCCCAGCTA    85077      A  CA
                                TAGCTG GAC  CAGGT
                                |||||| |||  |||||
                                ATCGAC CTG  GTCCG
                                   C   AG
GAM450  LOC150622 3'  ACTTGTAATCTCAGCTA    79953        CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTTCA
                                     AA
GAM450  LOC150889 3'  ACTTGTAATCCCAGCTA    80023      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTTCA
                                   C  AA
GAM450  LOC150960 3'  TGCACCTGTAGTCCCAGCTA  80076      A  C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                   C   A
GAM450  LOC150998 3'  GCCTGTGGTCCCAGCTA    85184      A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAC CTGGTGTCCG
                                   C
GAM450  LOC151195 3'  CATCCTCTAGCCTCAGCTA  80167        ACCAC  T
                                TAGCTGAG    AGG GTG
                                ||||||||    ||| |||
                                ATCGACTC    TCC TAC
                                     CGATC  _
GAM450  LOC151248 5'  GCCTGTAATCCCAGCTA    80188      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC151248 3'  GCCTGTAGTCCCAGCTA    80189      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC151429 3'  ACATGTAGTCTCAGCTA    85343        C  G
                                TAGCTGAGAC ACA GT
                                |||||||||| ||| ||
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                                ATCGACTCTG TGT CA
                                     A   A
GAM450   LOC151429 3'  GCCTGTAGTCCCAGCTA     85355       A   C
                                TAGCTG GAC ACAGGT
                                ||||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450   LOC151446 3'  GCCTGTAATCCCAGCTA     85376       A  CC
                                TAGCTG GA  ACAGGT
                                ||||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450   LOC151556 3'  GCCTGTAATCCCAGCTA     80275       A  CC
                                TAGCTG GA  ACAGGT
                                ||||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450   LOC151602 3'  GCCTGTAATCCCAGCTA     80296       A  CC
                                TAGCTG GA  ACAGGT
                                ||||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450   LOC151623 3'  GCCTGTGGTCTCAGCTA     85458
                                TAGCTGAGACCACAGGT
                                |||||||||||||||||
                                ATCGACTCTGGTGTCCG

GAM450   LOC151720 3'  TGCACCTGTAGTCCCAGCTA   80341       A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                   C   A
GAM450   LOC151979 5'  ACCTAGGGTGGTCTCGGCTA   80420           ___
                                TAGCTGAGACCAC   AGGT
                                ||||||||||||   ||||
                                ATCGGCTCTGGTG   TCCA
                                      GGA
GAM450   LOC152106 5'  GCCATGGCCGGCCTCAGCTA   70060        A  A__  _
                                TAGCTGAG CC   CA GGT
                                |||||||| ||   || |||
                                ATCGACTC GG   GT CCG
                                     C  CCG  A
GAM450   LOC152220 3'  TACATGATCTCAGCT       85588        C  CAGG   G
                                AGCTGAGA CA    TGT A
                                |||||||| ||    ||| |
                                TCGACTCT GT    ACA T
                                     A _____   G
GAM450   LOC152271 3'  ACCTGTAATCCCAGCTA     80513       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC152283 3'  TGCACCTGTAATCCCAGCTA  85689      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACGT
                                   C  AA
GAM450  LOC152313 3'  GCCTGTAGTCCCAGCTA    85665      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  LOC152316 3'  GCCTGTAGTCCCAGTTA    85613      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATTGAC CTG TGTCCG
                                   C  A
GAM450  LOC152426 3'  GCCTGTAGTCCCAGCTA    85715      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  LOC152453 3'  ACCTGTAATCCCAGTTA    80591      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATTGAC CT  TGTCCA
                                   C  AA
GAM450  LOC152453 3'  GCCTGTAATCCCAGCTA    80600      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC152804 3'  ACCTGTAATCCCAGCTA    85877      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC152804 3'  GCCTGTAATCCCAGCTA    85884      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC152845 5'  GCAGCGGTGACCTCAGCTG  60332       AC  AGG
                                TAGCTGAG  CAC  TGT
                                ||||||||  |||  |||
                                GTCGACTC  GTG  ACG
                                    CA  GCG
GAM450  LOC152897 3'  GCTTGTAGTCCCAGCTA    80728      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
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                                ATCGAC CTG TGTTCG
                                   C   A
GAM450  LOC153260 3'  GCCTGTAGTCTCAGCTA     80805          C
                                TAGCTGAGAC ACAGGT
                                |||||||||| ||||||
                                ATCGACTCTG TGTCCG
                                     A
GAM450  LOC153579 3'  GCCTGTAGTCCCAGCTA     80896       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC153579 3'  TCACACCTGTAATCCCAGT    80899      A  CC
                                GCTG GA  ACAGGTGTGA
                                |||| ||  ||||||||||
                                TGAC CT  TGTCCACACT
                                  C  AA
GAM450  LOC153642 3'  CACACCTATAGTCTCAGCTA   80903          CAC
                                TAGCTGAGAC   AGGTGTG
                                ||||||||||   |||||||
                                ATCGACTCTG   TCCACAC
                                     ATA
GAM450  LOC153682 3'  GCCTGTAGTCCCAGCTA     86085       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC153688 3'  GCCTGTAGTCCCAGCTA     86109       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC153727 3'  GCCTGTAATCTCAGCTA     86153         CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                     AA
GAM450  LOC154403 3'  GCCTGTAATCCCAGCTA     81073       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC154739 5'  TGCACCTGTAATCCCAGCTA   86242       A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACGT
                                   C  AA
GAM450  LOC154791 3'  GCCTGTAATCCCAGCTA     81157       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC154877 3'  GCCGTGGCGCAATCTCAGCT  86295        _____   A
                                AGCTGAGA    CCAC GGT
                                ||||||||    |||| |||
                                TCGACTCT    GGTG CCG
                                    AACGC   _
GAM450  LOC154881 3'  ACCTGTAGTACCAGCTA    81167       AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
                                ATCGAC  TG TGTCCA
                                   CA  A
GAM450  LOC154992 3'  ACCTGTAATCCCAGCTA    81209       A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC155006 3'  CACACCTGTAATCCCAGCTA  81231       A  CC
                                TAGCTG GA  ACAGGTGTG
                                ||||||  ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AA
GAM450  LOC155054 3'  GCTTGTGGTCCCAGCTA    81275       A
                                TAGCTG GACCACAGGT
                                ||||||  ||||||||||
                                ATCGAC CTGGTGTTCG
                                   C
GAM450  LOC155072 3'  GCCTGTAGTCCCAGCTA    86378       A   C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC155072 3'  GCCTGTAGTCCCAGCTA    86379       A   C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC155376 3'  ACCTGTAATCCCAGCTA    81332       A  CC
                                TAGCTG GA  ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC155438 3'  TCACACCTGTAATCCCAGT   86398      A  CC
                                GCTG GA  ACAGGTGTGA
                                ||||  ||  ||||||||||
                                TGAC CT  TGTCCACACT
                                  C  AA
GAM450  LOC157278 3'  GCCTGTGGTCTCAGCTA    86424
                                TAGCTGAGACCACAGGT
                                |||||||||||||||||
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                                ATCGACTCTGGTGTCCG

GAM450  LOC157292 5'  CACACCTGTAATCTCAGTTA  86411        CC
                                TAGCTGAGA  ACAGGTGTG
                                |||||||||  |||||||||
                                ATTGACTCT  TGTCCACAC
                                     AA
GAM450  LOC157660 3'  CGCACCTGTAATCCCAGCTG  86506      A  CC
                                TAGCTG GA  ACAGGTGTG
                                ||||||| ||  |||||||||
                                GTCGAC CT  TGTCCACGC
                                   C  AA
GAM450  LOC158088 3'  ACCTGTAGTCCCAGCTA    86681      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  LOC158187 3'  GCCTGTAGTCCCAGCTA    86692      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC158191 3'  CACACCTGTAGTCCCAGCTA  81772      A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACAC
                                   C   A
GAM450  LOC158337 3'  GCCTGTAGTCCCAGCTG    86774      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                GTCGAC CTG TGTCCG
                                   C   A
GAM450  LOC158382 5'  GCCTGTAGTCTCAGCTA    86786        C
                                TAGCTGAGAC ACAGGT
                                |||||||||| ||||||
                                ATCGACTCTG TGTCCG
                                     A
GAM450  LOC158382 5'  GCCTGTAGTTCAGCTA     86787       A C
                                TAGCTGAG C ACAGGT
                                |||||||| | ||||||
                                ATCGACTT G TGTCCG
                                     _ A
GAM450  LOC158434 5'  TCATTCCAGTCTCAGT     86826       CACA  T
                                GCTGAGAC    GG GTGA
                                ||||||||    || ||||
                                TGACTCTG    CC TACT
                                     A___   T
GAM450  LOC158677 5'  ACCTGTAATCCCAGCTA    86888      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC158819 3'  GCCTGTAATCCCAGCTA    86908      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC159036 3'  GCCTGTAATCCCAGCTA    86972      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC159053 3'  GCCTGTAGTCCCAGCTA    86979      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  LOC159110 3'  ACCTGTAATCCTAGCTA    82097      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAT CT  TGTCCA
                                   C  AA
GAM450  LOC159116 3'  ACCTGTAATCCTAGCTA    82092      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAT CT  TGTCCA
                                   C  AA
GAM450  LOC161190 5'  ACCATGTGGCCTCAGCTG   82262       A  _
                                TAGCTGAG CCACA GGT
                                |||||||| ||||| |||
                                GTCGACTC GGTGT CCA
                                    C    A
GAM450  LOC161823 3'  CACACCTGTAGTCCCAGC   82301     A  C
                                GCTG GAC ACAGGTGTG
                                |||| ||| |||||||||
                                CGAC CTG TGTCCACAC
                                  C  A
GAM450  LOC162545 3'  ACCTGGTGGCCTCAGC     87148      A  _
                                GCTGAG CCAC AGGT
                                |||||| |||| ||||
                                CGACTC GGTG TCCA
                                   C  G
GAM450  LOC170395 3'  GCCTGCAGTCCCAGCTA    76372      A  CA
                                TAGCTG GAC  CAGGT
                                |||||| |||  |||||
                                ATCGAC CTG  GTCCG
                                   C  AC
GAM450  LOC170395 3'  GCCTGTAACTCCAGCTA    76373      A  CC_
                                TAGCTG GA   ACAGGT
                                |||||| ||   ||||||
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                                ATCGAC CT   TGTCCG
                                   _ CAA
GAM450  LOC196047 5'  TGCACCTGTAGTCCCAGTTA  89614       A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATTGAC CTG TGTCCACGT
                                   C   A
GAM450  LOC196761 3'  GCCTGTAATCTAAGCTA     89554      G   CC
                                TAGCT AGA  ACAGGT
                                ||||| |||  ||||||
                                ATCGA TCT  TGTCCG
                                  A   AA
GAM450  LOC196872 3'  CATGCCTGTGGCCTCAGC    87795       A
                                GCTGAG CCACAGGTGTG
                                |||||| ||||||||||
                                CGACTC GGTGTCCGTAC
                                   C
GAM450  LOC197196 3'  GCCTGTAATCCCAGCTA     89734       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC197201 3'  GCCTGTAATCTCAGCTA     87937         CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                     AA
GAM450  LOC197201 3'  GCCTGTGGTCCTAGCTA     87938       A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAT CTGGTGTCCG
                                   C
GAM450  LOC199676 3'  GCCTGTAATCCCAGCTA     89789       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC199733 3'  CGCACCTGTAGTCCCTGCTA  89847     TGA   C
                                TAGC   GAC ACAGGTGTG
                                ||||   ||| |||||||||
                                ATCG   CTG TGTCCACGC
                                  TCC   A
GAM450  LOC199958 3'  GCCTGTAGTTCCAGCTA     89887       AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
                                ATCGAC  TG TGTCCG
                                   CT  A
GAM450  LOC200014 3'  GCCTGTAATCCCAGCTA     88530       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC200251 5'  ACCTGTAATCCCAGCTA    88661      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC200251 3'  GCCTGTAATCTCCGCTA    88666     T   CC
                                TAGC GAGA  ACAGGT
                                |||| ||||  ||||||
                                ATCG CTCT  TGTCCG
                                  C    AA
GAM450  LOC200317 3'  GCCTGTAATCCCAGCTA    88796      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC200728 3'  ACCTGTAGTCCCAGCTA    90114      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  LOC200803 3'  GCCTGTAATCCTAGCTA    88880      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAT CT  TGTCCG
                                   C  AA
GAM450  LOC200904 3'  ACCTGTAATCCCAGCTA    90184      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC200940 3'  GCCTGTAATCCCAGCTA    88955      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC201182 5'  GCCTGTAATCCCAGCTA    89765      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC201283 3'  TGCAGGTCTCAGCTA      60417         ACAGG  TG
                                TAGCTGAGACC    TG  A
                                ||||||||||    ||  |
                                ATCGACTCTGG    AC  T
                                      _____  GT
GAM450  LOC201564 3'  GCCTGTAATCCCAGCTA    80437      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC201627 3'  GCCTGTAATCCCAGCTA    89015      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC201685 3'  GCCTGTAATCCCAGCTA    90244      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC201689 3'  CACACCTGTAGTCCCAGCTA  67143       A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACAC
                                   C   A
GAM450  LOC201868 3'  GCCTGTAATCCCAGCTA    89079      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC201895 3'  GCCTGTAATCCCAGCTA    89089      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC202020 3'  GCCTGTATTCCCAGCTA    89136      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  TA
GAM450  LOC202052 3'  GCCTGTAGTCCCAGCTA    90309      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC202781 3'  ACCTGTAGTGCCAGCTA    90363      AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  || ||||||
                                ATCGAC  TG TGTCCA
                                   CG  A
GAM450  LOC202781 3'  GCCTGTAGTCCCAGCTA    90365      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC202868 3'  GCCTGTAGTCCCAGCTA    90376      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
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                                ATCGAC CTG TGTCCG
                                   C   A
GAM450   LOC202868 3'  GCCTGTAGTCCCAGCTA     90377       A   C
                                TAGCTG GAC ACAGGT
                                ||||||| ||| |||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450   LOC203246 3'  GCCTGTAGTCCCAGCTA     89305       A   C
                                TAGCTG GAC ACAGGT
                                ||||||| ||| |||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450   LOC203276 3'  TGCACCTGTAATCCCAGCTA   90490       A  CC
                                TAGCTG GA  ACAGGTGTG
                                ||||||| ||  |||||||||
                                ATCGAC CT  TGTCCACGT
                                   C  AA
GAM450   LOC203305 3'  TGCACCTGTAATCCCAGCTA   90534       A  CC
                                TAGCTG GA  ACAGGTGTG
                                ||||||| ||  |||||||||
                                ATCGAC CT  TGTCCACGT
                                   C  AA
GAM450   LOC203378 3'  ACCTGTAGTTCCAGCTA     90589       AG  C
                                TAGCTG  AC ACAGGT
                                |||||||  || ||||||
                                ATCGAC  TG TGTCCA
                                   CT  A
GAM450   LOC219347 3'  ACCTGTAGTCTCAACTA     92978     C     C
                                TAG TGAGAC ACAGGT
                                ||| ||||||| ||||||
                                ATC ACTCTG TGTCCA
                                  A     A
GAM450   LOC219406 3'  CACACCTGCAATCCCAGCTA   93557       A  CCA
                                TAGCTG GA   CAGGTGTG
                                ||||||| ||   ||||||||
                                ATCGAC CT   GTCCACAC
                                   C  AAC
GAM450   LOC219540 3'  CACACCTGTAATCCCAGCTA   93596       A  CC
                                TAGCTG GA  ACAGGTGTG
                                ||||||| ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AA
GAM450   LOC219627 3'  GCCTGTAATCCCAGCTA     92179       A  CC
                                TAGCTG GA  ACAGGT
                                ||||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450   LOC219627 3'  GCCTGTAGTCCCAGCTA     92180       A   C
                                TAGCTG GAC ACAGGT
                                ||||||| ||| |||||||
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                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC219649 3'  CACACCTGTAATCCCAGCTA  92952      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AA
GAM450  LOC219649 3'  GCCTGTAGTCCCAGCTA    92957      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC219672 5'  ACCTGTAATCCCAGCTA    91325      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC219672 3'  TCACACCTGTAGTCCCAGTTA 91334      A   C
                                TAGCTG GAC ACAGGTGTGA
                                |||||| ||| ||||||||||
                                ATTGAC CTG TGTCCACACT
                                   C   A
GAM450  LOC220070 3'  CACACCTGTAGTCCCAGCTA  59259      A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACAC
                                   C   A
GAM450  LOC220506 3'  GCCTGTAGTCCCAGCTA    74078      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC220575 3'  ATCTGTGGTCCCAGCTA    76306      A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAC CTGGTGTCTA
                                   C
GAM450  LOC220662 3'  GCCTGTAATCCCAGCTA    91173      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC220662 3'  CACACCTGTCATCCCAGCTA  91164      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AC
GAM450  LOC220906 3'  GCCTGTGATCCCAGCTG    91398      A  C
                                TAGCTG GA CACAGGT
                                |||||| || |||||||
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                                GTCGAC CT GTGTCCG
                                   C  A
GAM450  LOC220906 3'  GCCTGTGGTCCCAGCTA     91399       A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAC CTGGTGTCCG
                                   C
GAM450  LOC220980 5'  ATCTGTGGCCCCAGTTA     93145       AGA
                                TAGCTG   CCACAGGT
                                ||||||   ||||||||
                                ATTGAC   GGTGTCTA
                                   CCC
GAM450  LOC220992 3'  GCCTGTAGTCCCAGTTA     91470       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATTGAC CTG TGTCCG
                                   C   A
GAM450  LOC221042 3'  GCCTGTAATCCCAGCTA     93188       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC221069 3'  GCCTGTAGTCCCAGCTG     93201       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                GTCGAC CTG TGTCCG
                                   C   A
GAM450  LOC221178 3'  GCCTGTAATCCCAGCTA     93534       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC221271 3'  ACCTGTAGTCCCAGCTA     91840       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  LOC221271 3'  GCCTGTAGTCCCAGCTA     91862       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC221271 3'  TCACACCTGTAATCCCAGCTA 91873         A  CC
                                TAGCTG GA  ACAGGTGTGA
                                |||||| ||  ||||||||||
                                ATCGAC CT  TGTCCACACT
                                   C  AA
GAM450  LOC221288 3'  GCCTGTAGTCCCAGCTA     93615       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
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                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC221410 3' GCCTGTAGTCCCAGCTA    92060      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC221474 3' GCCTGTAATCCCAGCTA    92382      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC221477 3' GCCTGTAATCCCAGCTA    92155      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC221550 3' GCCTGTAATCCCAGCTA    92119      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC221641 5' ACCTGTAATCTCAGCTG    93723       CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                GTCGACTCT  TGTCCA
                                     AA
GAM450  LOC221641 3' GCTTGTAGTCCCAGCTA    93728      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTTCG
                                   C   A
GAM450  LOC221787 3' TCACACCTCCAGTCCCAGCTA 92471      A   CAC
                                TAGCTG GAC   AGGTGTGA
                                |||||| |||   ||||||||
                                ATCGAC CTG   TCCACACT
                                   C   ACC
GAM450  LOC221795 3' ACCTGTAATCCCAGCTA    92474      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC221813 5' CATCTTCATCTCAGCTA    93936       CCAC
                                TAGCTGAGA   AGGTG
                                |||||||||   |||||
                                ATCGACTCT   TCTAC
                                     ACT_
GAM450  LOC221954 5' ACCTGTAATCCCAGCTA    93997      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450   LOC221962 3'  GCCTGTGGTCTCAGCTA     92682
                                TAGCTGAGACCACAGGT
                                |||||||||||||||||
                                ATCGACTCTGGTGTCCG

GAM450   LOC221962 3'  TCACACCTGTAATCCCAGC    92685     A  CC
                                GCTG GA  ACAGGTGTGA
                                ||||  ||  ||||||||||
                                CGAC CT  TGTCCACACT
                                  C  AA
GAM450   LOC222066 3'  TCACACCTGTAATCCCAGCTA  92748      A  CC
                                TAGCTG GA  ACAGGTGTGA
                                ||||||  ||  ||||||||||
                                ATCGAC CT  TGTCCACACT
                                   C  AA
GAM450   LOC222070 5'  GTCACACTGCATCTACAGC    94159     _  CCACA
                                GCTG AGA    GGTGTGAC
                                ||||  |||    ||||||||
                                CGAC TCT    TCACACTG
                                  A  ACG__
GAM450   LOC222160 3'  CACACCTGTAATCCCAGCTA   94120      A  CC
                                TAGCTG GA  ACAGGTGTG
                                ||||||  ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AA
GAM450   LOC222160 3'  GCCTGTAGTCCCAGCTA     94128      A  C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450   LOC222160 5'  GCCTGTAGTTCCAGCTA     94129      AG  C
                                TAGCTG  AC ACAGGT
                                ||||||  ||  ||||||
                                ATCGAC  TG TGTCCG
                                   CT  A
GAM450   LOC222865 3'  GCCTGTAGTCCCAGCTA     92863      A  C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450   LOC253003 3'  GCCTGTAGTCCCAGCTA     96892      A  C
                                TAGCTG GAC ACAGGT
                                ||||||  |||  ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450   LOC253039 3'  CGCACCTGTAGTCCCAGCTA   96154      A  C
                                TAGCTG GAC ACAGGTGTG
                                ||||||  |||  |||||||||
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                                ATCGAC CTG TGTCCACGC
                                   C   A
GAM450  LOC253532 3'  ACCTGTAATCCCAGCTA    96024      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC253612 3'  GCCTGTAATCCCAGCTA    96750      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC253612 5'  GCCTGTAATCCTAGCTA    96751      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAT CT  TGTCCG
                                   C  AA
GAM450  LOC253639 3'  GCCTGTAATCCCAGCTA    95820      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC253786 3'  GCCTGTAATCCCAGCTA    97042      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC254041 5'  TGCACCTGTAATCCCAGCTA  94889      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACGT
                                   C  AA
GAM450  LOC254045 3'  GCCTGTAATCCCAGCTA    96507      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC254243 3'  TGCACCTGTAATCCCAGCTA  97421      A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACGT
                                   C  AA
GAM450  LOC254266 3'  GCCTGTAGTCCCAGCTA    97352      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC254531 5'  GCCTGTAATCCCAGCTA    94986      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC254808 3'  GCCTGTAGTCCCAGCTA    97023      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC254875 3'  ACCTGTAATCCCAGCTA    96054      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC255042 3'  GCCTGTAATCCTAGCTA    95319      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAT CT  TGTCCG
                                   C  AA
GAM450  LOC255231 3'  ATCTGTAGTCCCAGCTA    95371      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCTA
                                   C   A
GAM450  LOC255326 3'  GCCTGTAGTCCCAGCTA    96377      A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC255328 3'  ACCTGTAATCCCAGCTA    96555      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC255461 3'  GCCTGTGGTCTCAGCTA    97320
                                TAGCTGAGACCACAGGT
                                |||||||||||||||||
                                ATCGACTCTGGTGTCCG

GAM450  LOC255516 3'  GCCTGTGGTCTCAGCTA    97333
                                TAGCTGAGACCACAGGT
                                |||||||||||||||||
                                ATCGACTCTGGTGTCCG

GAM450  LOC255523 3'  GCCTGTGGTCCCAGCTA    95027      A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAC CTGGTGTCCG
                                   C
GAM450  LOC255671 3'  GCCTGTAATCCCAGCTG    97258      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                GTCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC255937 3'  GCCTGTAATCCCAGCTA     95990       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC255937 3'  TCACACCTGTAATCCCAGCT   95992       A  CC
                                AGCTG GA  ACAGGTGTGA
                                ||||| ||  ||||||||||
                                TCGAC CT  TGTCCACACT
                                  C  AA
GAM450  LOC256096 5'  TCAATGCTGATCTCAGCT    97199        CCA  GTG
                                AGCTGAGA  CAG  TGA
                                ||||||||  |||  |||
                                TCGACTCT  GTC  ACT
                                    A__  GTA
GAM450  LOC256174 5'  CTTGTAATCTCAGCTG      97613        CC
                                TAGCTGAGA  ACAGG
                                |||||||||  |||||
                                GTCGACTCT  TGTTC
                                    AA
GAM450  LOC256207 3'  CACACCTGTAGTCCCAGCTG   95166       A  C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                GTCGAC CTG TGTCCACAC
                                   C  A
GAM450  LOC256207 3'  GCCTGCAGTCCCAGTTA     95170       A  CA
                                TAGCTG GAC  CAGGT
                                |||||| |||  |||||
                                ATTGAC CTG  GTCCG
                                   C  AC
GAM450  LOC256267 3'  ACCAAGCTGGACGATCTCAGCT 96792        ____  CA__
                                AGCTGAGA  CCA  GGT
                                ||||||||  |||  |||
                                TCGACTCT  GGT  CCA
                                    AGCA  CGAA
GAM450  LOC256267 3'  GCCTGTAATCTCAGCTA     96803        CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                    AA
GAM450  LOC256306 3'  GCAGAGGTGCGATCTCAGCT  96689       C__  AGG
                                AGCTGAGA  CAC  TGT
                                ||||||||  |||  |||
                                TCGACTCT  GTG  ACG
                                    AGC  GAG
GAM450  LOC256594 3'  ACCTGTAATCCCAGCTA     97075       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC256980 3'  GCCTGTAATCCCAGCTA    95220      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC257017 5'  GCCTGTAGTCCCAGCTA    97374      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  LOC257115 3'  TGCACCTGTAGTCCCAGCTA  96527      A  C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                   C  A
GAM450  LOC257354 3'  GCCTATAGTCTCAGCTG    95091        CAC
                                TAGCTGAGAC  AGGT
                                ||||||||||  ||||
                                GTCGACTCTG  TCCG
                                     ATA
GAM450  LOC257495 3'  GCCTGTAATCCCAGCTA    97725      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC257576 3'  GCCTGTAATCCCAGCTA    97882      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC51024  3'  TCTGTGGCCTTCAGCTA    32163       A_
                                TAGCTGAG  CCACAGG
                                ||||||||  |||||||
                                ATCGACTT  GGTGTCT
                                     CC
GAM450  LOC51145  3'  GCCTGTAATCCCAGCTA    32395      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC51279  3'  GCCTGTAGTCCCAGCTA    33314      A  C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C  A
GAM450  LOC51333  3'  GCCTGTAATCCCAGCTA    33569      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC51759  3' GCCTGTAATCCCAGCTG     72814       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                GTCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC55954  5' TGCGCAATCTCAGCTG      38878        CCACAG   G
                                TAGCTGAGA     GTGT A
                                |||||||||     |||| |
                                GTCGACTCT     CGCG T
                                     AA____   G
GAM450  LOC64167  3' GCCTGTAGTCCCAGCTA     42280       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC89890  3' GCCTGTAATCCCAGCTA     60579       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC90038  3' TGCACCTGTAATCCCAGCTA   61163       A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACGT
                                   C  AA
GAM450  LOC90072  5' CACACCTGTAGTCCCAGCTA   61292       A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACAC
                                   C   A
GAM450  LOC90072  3' GCTTGTAATCTTAGCTA     61300        CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGATTCT  TGTTCG
                                     AA
GAM450  LOC90092  3' GCCTGTAATCCCAGCTA     61408       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC90141  3' ACCTGTAGTCCCAGCTA     61621       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  LOC90155  5' GCCTGTAATCCCAGCTA     61696       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC90393  5' ACCTGTAGTCCCAGCTA    62618       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCA
                                   C   A
GAM450  LOC90591  3' GCCTGTAATCCCAGCTA    63428       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC90591  3' GCCTGTAGTCCCAGCTA    63429       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC90591  3' GCCTGTAGTCCCAGCTA    63430       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC90624  3' GCCTGTAGTCCCAGCTA    63604       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC90750  3' GCATGGCCTCAGCTG      63922       A   CAGG
                                TAGCTGAG CCA   TGT
                                |||||||| |||   |||
                                GTCGACTC GGT   ACG
                                    C  ____
GAM450  LOC90784  5' GCCTGTGGTCCCAGCTA    64001       A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAC CTGGTGTCCG
                                   C
GAM450  LOC90918  5' GCCTGTAATCCCAGCTA    64358       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC90979  3' GCCTGTAGTCCCAGCTA    64527       A   C
                                TAGCTG GAC ACAGGT
                                |||||| ||| ||||||
                                ATCGAC CTG TGTCCG
                                   C   A
GAM450  LOC90979  5' TCACACCTTATTCAGC      64531       ACCAC
                                GCTGAG    AGGTGTGA
                                ||||||    ||||||||
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                                CGACTT    TCCACACT
                                   AT___
GAM450  LOC91035 3' GCCTGTAATCCCAGCTA    64671      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC91056 3' GCCTGTAATCCCAGCTA    94757      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC91064 3' TGCACCTGTAGTCCCAGCTA  64768      A   C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                   C   A
GAM450  LOC91151 5' CACATTGCATCTCTGCTA    52617     T   CCACA
                                TAGC GAGA    GGTGTG
                                |||| ||||    ||||||
                                ATCG CTCT    TTACAC
                                  T   ACG__
GAM450  LOC91250 5' GCCTGTAATCCCAGTTA     65324      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATTGAC CT  TGTCCG
                                   C  AA
GAM450  LOC91442 3' GCCTGTAATCCCAGCTA     66051      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC91547 3' GCCTGTGGTCCCAGCTG     66404      A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                GTCGAC CTGGTGTCCG
                                   C
GAM450  LOC91812 3' GCCTGTAATCCCAGCTA     67240      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC91813 3' GCCTGTAATCCCAGCTA     67254      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC91862 3' GCCTGTAATCCCAGCTA     53468      A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC91963  5' GCCTGTAATCCCAGCTA     67696       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC91963  3' GCCTGTGATCTTAGCTA     67697         C
                                TAGCTGAGA CACAGGT
                                ||||||||| |||||||
                                ATCGATTCT GTGTCCG
                                     A
GAM450  LOC92267  3' GCCGTGGCGTGATCTCAGCT  68615         _____   A
                                AGCTGAGA    CCAC GGT
                                ||||||||    |||| |||
                                TCGACTCT    GGTG CCG
                                     AGTGC   _
GAM450  LOC92270  5' GCCTGTAATCCCAGCTA     68631       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC92299  3' GCTTGTAGTCTGAGCTA     68813       G   C
                                TAGCT AGAC ACAGGT
                                ||||| |||| ||||||
                                ATCGA TCTG TGTTCG
                                   G   A
GAM450  LOC92421  3' ACCTGTAATCCCAGCTA     69211       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCA
                                   C  AA
GAM450  LOC92466  3' ACCAAGCTGGACGATCTCAGCT 69417         ____  CA__
                                AGCTGAGA   CCA   GGT
                                ||||||||   |||   |||
                                TCGACTCT   GGT   CCA
                                     AGCA  CGAA
GAM450  LOC92466  3' GCCTGTAATCTCAGCTA     69428         CC
                                TAGCTGAGA  ACAGGT
                                |||||||||  ||||||
                                ATCGACTCT  TGTCCG
                                     AA
GAM450  LOC92482  3' GCCTGTAATCCCAGCTA     69489       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC92499  5' TGCACCTGTAATCCCAGCTA  69534       A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
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                                ATCGAC CT  TGTCCACGT
                                   C  AA
GAM450  LOC92573 3' GCCTGTAATCTCACCTA     69807     C    CC
                                TAG TGAGA  ACAGGT
                                ||| |||||  ||||||
                                ATC ACTCT  TGTCCG
                                  C    AA
GAM450  LOC92659 3' CACACCTGTTGTCCCAGCTA  70070       A  C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACAC
                                   C   T
GAM450  LOC92736 3' GCCTGTAATCCCAGCTA     70428       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC92771 3' GCCTGTAATCCCAGCTA     53075       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
                                ATCGAC CT  TGTCCG
                                   C  AA
GAM450  LOC92973 5' ACCTGTGGTCACAGCTA     71033       A
                                TAGCTG GACCACAGGT
                                |||||| ||||||||||
                                ATCGAC CTGGTGTCCA
                                   A
GAM450  LOC93097 3' CACACAATCTCAGCTG      71359        CCACAG
                                TAGCTGAGA     GTGTG
                                |||||||||     |||||
                                GTCGACTCT     CACAC
                                     AA_____
GAM450  LOC93132 5' TGCACCTGTAATCCCAGCTA  71505       A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACGT
                                   C  AA
GAM450  LOC93132 5' TGCACCTGTAGTCCCAGCTA  71506       A  C
                                TAGCTG GAC ACAGGTGTG
                                |||||| ||| |||||||||
                                ATCGAC CTG TGTCCACGT
                                   C   A
GAM450  LOC93613 3' CACACCTGTAATCCCAGCTA  72695       A  CC
                                TAGCTG GA  ACAGGTGTG
                                |||||| ||  |||||||||
                                ATCGAC CT  TGTCCACAC
                                   C  AA
GAM450  LOC96597 5' ACCTGTAATCCCAGCTA     66904       A  CC
                                TAGCTG GA  ACAGGT
                                |||||| ||  ||||||
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                                ATCGAC CT  TGTCCA
                                   C  AA
GAM451  ARHGEF6  3'  CAAACTTGAAGCCAGGC     68197       ACCA
                                GCCTGG    CAAGTTTG
                                ||||||    ||||||||
                                CGGACC    GTTCAAAC
                                   GAA_
GAM451  CNTN2    3'  GTCACAACCCAGGTGA      17411        ACCACAA  _
                                TCGCCTGG      GTT TGAC
                                ||||||||      ||| ||||
                                AGTGGACC      CAA ACTG
                                    ________  C
GAM451  CORO2A   3'  AAACTGTGGTCCAGAGA     12642    GC        A
                                TC  CTGGACCACA GTTT
                                ||  ||||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM451  CORO2A   3'  AAACTGTGGTCCAGAGA     53398    GC        A
                                TC  CTGGACCACA GTTT
                                ||  ||||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM451  GRLF1    3'  AGGTCAGAAAGTGGCCCAGG   78551      A    AAG
                                CCTGG CCAC   TTTGACCT
                                ||||| ||||   ||||||||
                                GGACC GGTG   AGACTGGA
                                   C    AA_
GAM451  LAPTM5   3'  AGGCTTGTGGTCAAGC      22199    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCGGA
                                 AA_
GAM451  POU2AF1  3'  AGATTTACAGTCCAGGC     20647        CAC
                                GCCTGGAC   AAGTTT
                                ||||||||   ||||||
                                CGGACCTG   TTTAGA
                                     ACA
GAM451  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  6355         C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM451  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  54574        C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM451  TRIM34   5'  AGGTCAAGTTGAGCCCAG    55224     ACCA   G
                                CTGG    CAA TTTGACCT
                                ||||    ||| ||||||||
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                                GACC    GTT GAACTGGA
                                  CGA_  _
GAM451  TRIM9     5'  AGGCCAGGCAAGTCCAGGC    30749        CACAA     A
                                GCCTGGAC    GTTTG CCT
                                ||||||||    ||||| |||
                                CGGACCTG    CGGAC GGA
                                    AA___    C
GAM451  ABLIM     5'  GATATGTAACCCAGGCGG    22030        ACC   A
                                TCGCCTGG   ACA GTT
                                ||||||||   ||| |||
                                GGCGGACC   TGT TAG
                                    CAA   A
GAM451  AMOT      3'  AGGCATCTTCATGGTCCAGGGA 55716    G       C_   TT  A
                                TC CCTGGACCA  AAG  TG CCT
                                || |||||||||  |||  || |||
                                AG GGACCTGGT  TTC  AC GGA
                                 _       AC   T_ _
GAM451  DKFZp434D177 5'  TTAGACCCAGGCGA       79443        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                              _______
GAM451  DKFZp434D177 5'  TTAGACCCAGGCGA       50056        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                              _______
GAM451  FLJ23420  3'  CAAGTGGGTCCAGGC       46845         A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                              _ __
GAM451  HSA249128 5'  GGCGCGGTCCAGGCGG      34152          ACAA
                                TCGCCTGGACC    GTT
                                ||||||||||    |||
                                GGCGGACCTGG    CGG
                                      CG__
GAM451  MGC15668  5'  AGACCCGGTGGTCCAGACG    51277    C       AA_
                                CG CTGGACCAC   GTTT
                                || |||||||||   ||||
                                GC GACCTGGTG   CAGA
                                 A        GCC
GAM451  MGC22014  3'  AGGTCCCGAGTGTAACCCAGGT 64486        ACC   AGTTT
           GA                    TCGCCTGG   ACA    GACCT
                                ||||||||   |||    |||||
                                AGTGGACC   TGT    CTGGA
                                    CAA   GAGCC
GAM451  SDCCAG10  5'  AGAGTTGTGGTCCAAAGA    19641    GCC        G
                                TC   TGGACCACAA TTT
                                ||   |||||||||| |||
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                                AG   ACCTGGTGTT AGA
                                 AA_         G
GAM451   LOC115442 3'  AGGTCAGGGATGGTCCAG    72676         CAAG
                                CTGGACCA    TTTGACCT
                                ||||||||    ||||||||
                                GACCTGGT    GGACTGGA
                                     AG__
GAM451   LOC129011 5'  AGACCTGCGGTCCAGGC     74862          A  A
                                GCCTGGACC CA GTTT
                                ||||||||| || ||||
                                CGGACCTGG GT CAGA
                                      C  C
GAM451   LOC130536 5'  GCAAAGTCCAGGCG        75746          CACAAG    A
                                CGCCTGGAC     TTTG C
                                |||||||||     |||| |
                                GCGGACCTG     AAAC G
                                     _______   C
GAM451   LOC149108 3'  AGACTTCACTGTGGTCCA     84357          _____
                                TGGACCACA    AGTTT
                                |||||||||    |||||
                                ACCTGGTGT    TCAGA
                                      CACT
GAM451   LOC221688 5'  AGACTCGGGCCCAGACGA     93674     C    A  ACA
                                TCG CTGG CC   AGTTT
                                ||| |||| ||   |||||
                                AGC GACC GG   TCAGA
                                  A   C  GC_
GAM451   LOC256228 5'  AGACTTGTGGTCAAAGC      96233     CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCAGA
                                 AAA
GAM451   LOC257441 5'  TTAGACCCAGGCGA         95566          ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                     _______
GAM451   LOC91960  3'  AGGTGCCTCTCGTGGTCCAAGC 67657     C       A  TTTG
                                GC TGGACCAC AG    ACCT
                                || |||||||| ||    ||||
                                CG ACCTGGTG TC    TGGA
                                 A       C  TCCG
GAM451   LOC92840  3'  GTCCCTCGGGTCCAGGC      56435          ACA  TTT
                                GCCTGGACC   AG   GAC
                                |||||||||   ||   |||
                                CGGACCTGG   TC   CTG
                                      GC_  C__
GAM452   ADH1B     3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                ||||  |||||   ||||||||
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                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM452  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM452  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                        _
GAM452  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
             TG                   CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM452  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM452  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM452  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                       T__    _
GAM452  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM452  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_    CG_
GAM452  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM452  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
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                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM452  FLJ23462  3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
            G                    CATTTC        GTCTGAGAT
                                 ||||||        |||||||||
                                 GTAAAG        CAGACTCTA
                                    AAACATTT_
GAM452  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                 CATTTCA   TCACTGTCTGAGAT
                                 |||||||   |||||||||||||
                                 GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM452  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                 TTCA TTTCACTG  TGAG
                                 |||| ||||||||  ||||
                                 AAGT AAAGTGAC  GTTT
                                   A       CT
GAM452  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                 TTTC CTG TCTGAGAT
                                 |||| ||| ||||||||
                                 AAAG GAC AGACTCTA
                                   _  G
GAM452  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                 ATT CACTTTCACTGT
                                 ||| ||||||||||||
                                 TAA GTGAAAGTGACG
                                   C
GAM452  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                 TTCACTTT  CT TCTGAGAT
                                 ||||||||  || ||||||||
                                 AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM452  PP35      3'  ATCTCAGACTGAAA       22814      CT
                                 TTTCA  GTCTGAGAT
                                 |||||  |||||||||
                                 AAAGT  CAGACTCTA
                                    __
GAM452  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148         TCAC  C_
                                 CATTTCACTT    TGT  TGAG
                                 ||||||||||    |||  ||||
                                 GTAAAGTGAA    ACG  ACTC
                                       TA__   TT
GAM452  SEP15     3'  TCCTACAGTAAGAGTGAAA    14934        C    CT
                                 TTTCACTTT ACTGT  GA
                                 ||||||||| |||||  ||
                                 AAAGTGAGA TGACA  CT
                                       A    TC
GAM452  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                 TTTCACTTT    TCTGAG
                                 |||||||||    ||||||
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                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM452  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM452  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM452  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226     A      GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM452  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM453  AVPR1A   5'  CACAGCAGATAACTGCAGA   5535        GCACCG   CA
                                TCTGCAGT     TGT  TGTG
                                ||||||||     |||  ||||
                                AGACGTCA     ACG  ACAC
                                     ATAG__  __
GAM453  GLP1R    3'  CACACAGCAGCACTGCAGA   9028         ACCG   CA
                                TCTGCAGTGC    TGT  TGTG
                                ||||||||||    |||  ||||
                                AGACGTCACG    ACG  ACAC
                                      _____  AC
GAM453  IARS     3'  CACATGAACACACTGAAGA   9291      G   GCACC   _
                                TCT CAGT     GTGT CATGTG
                                ||| ||||     |||| ||||||
                                AGA GTCA     CACA GTACAC
                                  A  ______  A
GAM453  IARS     3'  CACATGAACACACTGAAGA   25511     G   GCACC   _
                                TCT CAGT     GTGT CATGTG
                                ||| ||||     |||| ||||||
                                AGA GTCA     CACA GTACAC
                                  A  ______  A
GAM453  LY9      3'  ACACATGACACAAGATGTAC  71682      CC__
                                GTGCA    GTGTCATGTGT
                                |||||    ||||||||||
                                CATGT    CACAGTACACA
                                   AGAA
GAM453  MLLT7    3'  ACATGATACAAACACTACAGA  19859     C    CACC
                                TCTG AGTG    GTGTCATGT
                                |||| ||||    |||||||||
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                                AGAC TCAC    CATAGTACA
                                  A   AAA_
GAM453  MYD88    3'  CACAACAATGAACTGCAGA   10164       GCACCG   CA
                                TCTGCAGT     TGT  TGTG
                                ||||||||     |||  ||||
                                AGACGTCA     ACA  ACAC
                                    AGTA__   __
GAM453  XT3      3'  GACACAATGCACAGCAGA    39524      A    CC
                                TCTGC GTGCA  GTGTC
                                ||||| |||||  |||||
                                AGACG CACGT  CACAG
                                  A    AA
GAM453  C5orf4   5'  GCTTGGACACAGCCCACTGCAG 50497        CACC    AT_
          A                      TCTGCAGTG   GTGTC   GT
                                |||||||||   |||||   ||
                                AGACGTCAC   CACAG   CG
                                    CCGA    GTT
GAM453  FLJ13490 3'  ACATAAACAGTGTACTGCAGA  46298          C  GTC
                                TCTGCAGTGCAC GT   ATGT
                                ||||||||||||| ||   ||||
                                AGACGTCATGTG CA   TACA
                                    A  AA_
GAM453  HSZFP36  3'  ACACATGATAAGGCACACTGGA 63474    G    CA  G
          GA                    TCT CAGTG  CC TGTCATGTGT
                                ||| |||||  || ||||||||||
                                AGA GTCAC  GG ATAGTACACA
                                  G    AC  A
GAM453  LOC51161 3'  ACCCATCACGGTGCCTACAGA  32505     C  T      TC   T
                                TCTG AG GCACCGTG  ATG GT
                                |||| || ||||||||  ||| ||
                                AGAC TC CGTGGCAC  TAC CA
                                  A  _       __   C
GAM453  LOC93132 5'  CACATGAAGGCACCACAG    71484     CA   ACCGTG
                                CTG  GTGC    TCATGTG
                                |||  ||||    |||||||
                                GAC  CACG    AGTACAC
                                  AC   GA____
GAM454  HTR2C    3'  GATTTCCAAAAGTACTA     6021           _
                                TAGTACTTTTG AAATC
                                |||||||||| |||||
                                ATCATGAAAAC TTTAG
                                    C
GAM454  PPP2R5C  3'  CAAACTGATTTCAAAAGTACTA 10754
                                TAGTACTTTTGAAATCAGTTTG
                                |||||||||||||||||||||
                                ATCATGAAAACTTTAGTCAAAC

GAM454  TAF4     3'  CAAACTGATTTTTTAGACTA   12090      A  TTT
                                TAGT CT   GAAATCAGTTTG
                                |||| ||   ||||||||||||
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                                ATCA GA   TTTTAGTCAAAC
                                  _ TT_
GAM454  ASAH     3'  CAAACTGCTTATGAAAAGTACT 15048          GAAAT_
              A                   TAGTACTTTT     CAGTTTG
                                  ||||||||||     |||||||
                                  ATCATGAAAA     GTCAAAC
                                       GTATTC
GAM454  ATP6V1B2 3'  AACTCCCTCAAGAGTAC     8084          AATC
                                  GTACTTTTGA    AGTT
                                  ||||||||||    ||||
                                  CATGAGAACT    TCAA
                                       CCC_
GAM454  C6orf5   3'  CAAACTGATTCATGTAC     31338     TTT    A
                                  GTAC   TGAA TCAGTTTG
                                  ||||   |||| ||||||||
                                  CATG   ACTT AGTCAAAC
                                    T__    _
GAM454  FLJ20203 3'  CAAACTGATAAGGAAGT     34733       GAA
                                  ACTTTT   ATCAGTTTG
                                  ||||||   |||||||||
                                  TGAAGG   TAGTCAAAC
                                     AA_
GAM454  KIAA0205 3'  ACTGAGAATTCCAAAAGTAT   29575         AAA___
                                  GTACTTTTG     TCAGT
                                  |||||||||     |||||
                                  TATGAAAAC     AGTCA
                                       CTTAAG
GAM454  KIAA0430 3'  CAAAAGTGGGTTTCAAAAATAC 38839     C        AG__
                                  GTA TTTTGAAATC    TTTG
                                  ||| ||||||||||    ||||
                                  CAT AAAACTTTGG    AAAC
                                    A         GTGA
GAM454  KLK7     3'  CAAACATGTTCCAAAAGTAC   17287         A   CA
                                  GTACTTTTG AAT  GTTTG
                                  ||||||||| |||  |||||
                                  CATGAAAAC TTG  CAAAC
                                       C   TA
GAM454  KLK7     3'  CAAACATGTTCCAAAAGTAC   57727         A   CA
                                  GTACTTTTG AAT  GTTTG
                                  ||||||||| |||  |||||
                                  CATGAAAAC TTG  CAAAC
                                       C   TA
GAM454  LATS1    3'  CAAACTGATTTCATGATAC    60273     C  T
                                  GTA TT TGAAATCAGTTTG
                                  ||| || ||||||||||||
                                  CAT AG ACTTTAGTCAAAC
                                    _  T
GAM454  LOC126302 3'  CAAACTGAGAGGCAAAAGCACT 74490     A     AAA_
                                  AGT CTTTTG    TCAGTTTG
                                  ||| ||||||    ||||||||
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                                TCA GAAAAC    AGTCAAAC
                                  C      GGAG
GAM454   LOC136288 3'  CAAACTGATATTCAAAATATTA 75251       C      _
                                TAGTA TTTTGAA ATCAGTTTG
                                ||||| ||||||| |||||||||
                                ATTAT AAAACTT TAGTCAAAC
                                   _      A
GAM454   LOC145268 3'  CAAACTGATTCCAATGAC    77052    ACTT   A
                                GT    TTG AATCAGTTTG
                                ||    ||| ||||||||||
                                CA    AAC TTAGTCAAAC
                                 GT__   C
GAM454   LOC149465 3'  CAAACTGATTTCTGGTGGCAC  79391    A  TTT_
                                GT CT    GAAATCAGTTTG
                                || ||    ||||||||||||
                                CA GG    CTTTAGTCAAAC
                                 C  TGGT
GAM454   LOC151429 3'  CAAACTGACCTCAGTGTTCTG  85345     T  TT    AA
                                TAG AC  TTGA  TCAGTTTG
                                ||| ||  ||||  ||||||||
                                GTC TG  GACT  AGTCAAAC
                                  T  T_   CC
GAM455   NRAS     3'  CACACCTCTGCCACCCCA    10267    A   _   AATT
                                TG GGTG CAGA    TGTG
                                || |||| ||||    ||||
                                AC CCAC GTCT    ACAC
                                 C    C    CC__
GAM455   PTPRO    3'  ACAGGAGCTTCTGCACATCA   47712     G       ATTT  G_
                                TGA GTGCAGAA    GT  CTGT
                                ||| ||||||||    ||  ||||
                                ACT CACGTCTT    CG  GACA
                                  A       _____  AG
GAM455   GALNT6   3'  ACAGCACCATTGCACCCCA   23287    A      AAATTT
                                TG GGTGCAG     GTGCTGT
                                || |||||||     |||||||
                                AC CCACGTT     CACGACA
                                 C      AC_____
GAM455   KIAA0420  3'  ACAACACCTCTGCACC      63350         AATTT   C
                                GGTGCAGA    GTG TGT
                                ||||||||    ||| |||
                                CCACGTCT    CAC ACA
                                     C_____   A
GAM455   KIAA0876  3'  GACAAAGCACCCCTGCACCTC  64679          AAATTT    __
                                GAGGTGCAG     GTGCT  GTC
                                |||||||||     |||||  |||
                                CTCCACGTC     CACGA  CAG
                                      CC_____    AA
GAM455   PRO1257   5'  ACAAATTTCCCACCCTCA    37707       _  CA
                                TGAGG TG  GAAATTTGT
                                ||||| ||  |||||||||
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                                ACTCC AC  CTTTAAACA
                                  C  C_
GAM455  ROBO2    3'  AGCACAAATCTCTACTCCTCA  62485      TGC   A
                                TGAGG   AGA ATTTGTGCT
                                |||||   ||| |||||||||
                                ACTCC   TCT TAAACACGA
                                   TCA   C
GAM455  SFRS12   3'  GACAAGTGTACCTCTGCACTCA 57527     G     AATT  TG  _
                                TGAG TGCAGA    TG  CT GTC
                                |||| ||||||    ||  || |||
                                ACTC ACGTCT    AT  GA CAG
                                  _     CC__  GT  A
GAM455  TP53TG3  3'  ACAAATCCTCTGCACCCCA   31100    A      A_
                                TG GGTGCAGA  ATTTGT
                                || ||||||||  ||||||
                                AC CCACGTCT  TAAACA
                                 C       CC
GAM455  LOC152897 5'  CAGAGATTTCTAGACCCCA   80723    A   GC      G
                                TG GGT  AGAAATTT TG
                                || |||  |||||||| ||
                                AC CCA  TCTTTAGA AC
                                 C   GA       G
GAM455  LOC199675 3'  CATTTATCTCTGCACTCA    88262      G     A  TT
                                TGAG TGCAGA AT  GTG
                                |||| |||||| ||  |||
                                ACTC ACGTCT TA  TAC
                                  _     C  TT
GAM455  LOC222066 3'  ACAGCACCACTGCACTCCA   92738    AG     AAATTT
                                TG  GTGCAG     GTGCTGT
                                ||  ||||||     |||||||
                                AC  CACGTC     CACGACA
                                 CT     AC_____
GAM455  LOC222776 5'  ACAGATCTTCCGCACTTCA   94355        A  _
                                TGAGGTGC GAA ATTTGT
                                |||||||| ||| ||||||
                                ACTTCACG CTT TAGACA
                                     C   C
GAM455  LOC256306 5'  GACAGCACAAAGAGTCCCCCA  96688    A  TG AGAAA
                                TG GG  C    TTTGTGCTGTC
                                || ||  |    ||||||||||
                                AC CC  G    AAACACGACAG
                                 C  CT AG___
GAM455  LOC257181 3'  ACAGCAGTGTGCTCCCACCTCA 94589       CA  A_  TTG
                                TGAGGTG  GA  AT   TGCTGT
                                |||||||  ||  ||   ||||||
                                ACTCCAC  CT  TG   ACGACA
                                   C_  CG  TG_
GAM455  LOC257354 3'  ACAACACCTCTGCACC      95083        AATTT   C
                                GGTGCAGA    GTG TGT
                                ||||||||    ||| |||
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                                CCACGTCT    CAC ACA
                                    C____   A
GAM456  ABCC12   5'  AAGAGGAATTAAATGGTCCTA  52644    C       AG
                                TAG ACCATTTGA  TTCTCTT
                                ||| |||||||||  |||||||
                                ATC TGGTAAATT  AGGAGAA
                                  C        A_
GAM456  ARCN1    3'  AGAAGCACCTTTCAAATGG   7969         TTCT
                                CCATTTGAAG   CTTCT
                                ||||||||||   |||||
                                GGTAAACTTT   GAAGA
                                     CCAC
GAM456  B4GALT4  3'  GACTTCAAATAGTAGC     13672    _ C
                                GC AC ATTTGAAGTT
                                || || ||||||||||
                                CG TG TAAACTTCAG
                                 A  A
GAM456  CCND2    3'  AGAAAAAAACTAATTTTTGGTG 8285       TTTGA_   CTC
           CTG                   TAGCACCA     AGTT   TTCT
                                ||||||||     ||||   ||||
                                GTCGTGGT     TCAA   AAGA
                                    TTTTAA    AAA
GAM456  CEACAM6  3'  AGCCCCAAATGGTGGTA     10185    G       AA
                                TA CACCATTTG  GTT
                                || |||||||||  |||
                                AT GTGGTAAAC  CGA
                                 G        CC
GAM456  COL11A2  3'  AGAAGAGAAAGGACATGGCGT  54764    A   TTGAAG
                                GC CCAT     TTCTCTTCT
                                || ||||     |||||||||
                                TG GGTA     AAGAGAAGA
                                 C   CAGGA_
GAM456  COL11A2  3'  AGAAGAGAAAGGACATGGCGT  54766    A   TTGAAG
                                GC CCAT     TTCTCTTCT
                                || ||||     |||||||||
                                TG GGTA     AAGAGAAGA
                                 C   CAGGA_
GAM456  IL1RAP   3'  AGAAATCTCCTAATGGTGCTA  9308         T_  AG_
                                TAGCACCATT  GA   TTCT
                                ||||||||||  ||   ||||
                                ATCGTGGTAA  CT   AAGA
                                     TC  CTA
GAM456  ITGA5    3'  AGAACTCAAATGGGGC     61276    A      A
                                GC CCATTTGA GTTCT
                                || |||||||| |||||
                                CG GGTAAACT CAAGA
                                 G       _
GAM456  LILRA3   3'  AGAAGAGAGAACAATGC     95306     CCAT   AAG
                                GCA    TTG   TTCTCTTCT
                                |||    |||   |||||||||
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                                CGT    AAC   GAGAGAAGA
                                  _____   AA_
GAM456  RPS3A    3'  GACTTCAAATAGTGGC      6403     _  C
                                GC AC ATTTGAAGTT
                                || || ||||||||||
                                CG TG TAAACTTCAG
                                 G  A
GAM456  SORL1    3'  AGAAACCAAATGGTGT      11874          AAG
                                GCACCATTTG   TTCT
                                ||||||||||   ||||
                                TGTGGTAAAC   AAGA
                                      CA_
GAM456  ACAA2    5'  AGAAGAAAACCCAGGAGGACGC 91766    A_  A    AA   C
                                GC  CC TTTG  GTT TCTTCT
                                ||  || ||||  ||| ||||||
                                CG  GG GGAC  CAA AGAAGA
                                 CA  A    C_   A
GAM456  BMF      3'  AGAAAAGACAACATTGGTGCTA 53151         TT  AA  T  C
                                TAGCACCA  TG  GT CT TTCT
                                ||||||||  ||  || || ||||
                                ATCGTGGT  AC  CA GA AAGA
                                     T_  AA  _  A
GAM456  CHUK     3'  AGAAGAAAACCTCAAGT     7053         A   C
                                ATTTGA GTT TCTTCT
                                |||||| ||| ||||||
                                TGAACT CAA AGAAGA
                                   C   A
GAM456  FADS1    3'  AGAAGAGAACCTCAAACTAGG  25470    A__     A
                                CC   TTTGA GTTCTCTTCT
                                ||   ||||| ||||||||||
                                GG   AAACT CAAGAGAAGA
                                 ATC    C
GAM456  FLJ14442 3'  AGAAGAGGAAACAAACTGC    51357     CCA    AAG
                                GCA   TTTG   TTCTCTTCT
                                |||   ||||   |||||||||
                                CGT   AAAC   AGGAGAAGA
                                  C__    AA_
GAM456  ING3     3'  AGAAGAGAAAGAAGAAACAATG 38831     CCA_   GAAG
           C                     GCA    TTT    TTCTCTTCT
                                 |||    |||    |||||||||
                                 CGT    AAG    AAGAGAAGA
                                   AACA   AAGA
GAM456  KIAA0884 5'  AGAAGAGGAAAATGG       70197       GAAG
                                CCATTT    TTCTCTTCT
                                ||||||    |||||||||
                                GGTAAA    AGGAGAAGA
                                          ____
GAM456  MGC2603  3'  AGAAGAGAGGTAGAATGGTGCT 43856           GAAG
           A                     TAGCACCATTT    TTCTCTTCT
                                 ||||||||||    |||||||||
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                                ATCGTGGTAAG   GAGAGAAGA
                                      ATG_
GAM456  MGC32104  3'  AAGAAAACTTCAGGCTGGTACT 58401    C   _       C
                                AG ACCA TTTGAAGTT TCTT
                                || |||| ||||||||| ||||
                                TC TGGT GGACTTCAA AGAA
                                 A   C       A
GAM456  NYD-SP25  3'  AGAGGGGAAAATAGTGGT    53184       TGAAG
                                ACCATT    TTCTCTTCT
                                ||||||    |||||||||
                                TGGTGA    AAGGGGAGA
                                   TAA__
GAM456  PPFIA4    3'  GAAGAGAACTCTGTGC      70323      CATTT  A
                                GCAC    GA GTTCTCTTC
                                ||||    || |||||||||
                                CGTG    CT CAAGAGAAG
                                  T____  _
GAM456  PRKRIR    3'  AGAAGAGAACGTTGAAAGTGC  16296      CA  TG A
                                GCAC  TT  A GTTCTCTTCT
                                ||||  ||  | ||||||||||
                                CGTG  AA  T CAAGAGAAGA
                                  A_  GT G
GAM456  PRO1768   5'  AGAATGGGCCCTCAAATGGTGC 26039           A TT  _
           T                     AGCACCATTTGA G  CTC TTCT
                                ||||||||||| |  ||| ||||
                                TCGTGGTAAACT C  GGG AAGA
                                      _ CC   T
GAM456  SURB7     3'  AGAAAAGAACTGTTTGAGTGC  14946      _  TTTGA     C
                                GCAC CA     AGTTCT TTCT
                                |||| ||     |||||| ||||
                                CGTG GT     TCAAGA AAGA
                                  A  TTG__      A
GAM456  TRIAD3    5'  AGAAGAGAAAACAAATG     94498       AAG
                                CATTTG   TTCTCTTCT
                                ||||||   |||||||||
                                GTAAAC   AAGAGAAGA
                                   AA_
GAM456  ZNF302    3'  AGAAATAAAATGGTGTTA    37416          GAAG
                                TAGCACCATTT    TTCT
                                ||||||||||    ||||
                                ATTGTGGTAAA    AAGA
                                      ATA_
GAM456  ZNF302    3'  AGAAATAAAATGGTGTTA    37925          GAAG
                                TAGCACCATTT    TTCT
                                ||||||||||    ||||
                                ATTGTGGTAAA    AAGA
                                      ATA_
GAM456  LOC133744 3'  GACTTCAAATAGTGGC      75130    _  C
                                GC AC ATTTGAAGTT
                                || || ||||||||||
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                                CG TG TAAACTTCAG
                                 G  A
GAM456  LOC145767 3'  GACTTCAAATAGTGGC      66766    _  C
                                GC AC ATTTGAAGTT
                                || || ||||||||||
                                CG TG TAAACTTCAG
                                 G  A
GAM456  LOC146053 3'  GACTTCAAATAGTGGC      60381    _  C
                                GC AC ATTTGAAGTT
                                || || ||||||||||
                                CG TG TAAACTTCAG
                                 G  A
GAM456  LOC146381 5'  AGAAGAGAACCTCACCAGC   77865    ACCATT   A
                                GC     TGA GTTCTCTTCT
                                ||     ||| ||||||||||
                                CG     ACT CAAGAGAAGA
                                 ACC___   C
GAM456  LOC147358 3'  GACTTCAAATAGTGGC      60072    _  C
                                GC AC ATTTGAAGTT
                                || || ||||||||||
                                CG TG TAAACTTCAG
                                 G  A
GAM456  LOC153792 3'  GACTTCAAATAGTGGC      60372    _  C
                                GC AC ATTTGAAGTT
                                || || ||||||||||
                                CG TG TAAACTTCAG
                                 G  A
GAM456  LOC162333 5'  AGAAGAGAAAGCGATGACACTG 87116    CAC    T AAG
                                TAG   CATT G   TTCTCTTCT
                                |||   |||| |   |||||||||
                                GTC   GTAG C   AAGAGAAGA
                                 ACA    _ GA_
GAM456  LOC165693 5'  AGAAAGGAAAATGGTGCTG   82592          GAAG
                                TAGCACCATTT    TTCT
                                ||||||||||    ||||
                                GTCGTGGTAAA    AAGA
                                       AGGA
GAM456  LOC197439 5'  AGAAGAGAACCTCACCAGC   88073    ACCATT   A
                                GC     TGA GTTCTCTTCT
                                ||     ||| ||||||||||
                                CG     ACT CAAGAGAAGA
                                 ACC___   C
GAM456  LOC200734 3'  AAGAGAACCTCATCCATGC   88855    CCATT   A
                                GCA    TGA GTTCTCTT
                                |||    ||| ||||||||
                                CGT    ACT CAAGAGAA
                                 ACCT_   C
GAM456  LOC222166 3'  AGATGCTTCAAACAGTGT    94089      CA       _
                                GCAC  TTTGAAGT TCT
                                ||||  |||||||| |||
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                                TGTG  AAACTTCG AGA
                                  AC       T
GAM457  CALM3    3'  TGAGGGCCCGTCCTAG      17748        A   _
                                TTAGGAC GGCT TCA
                                ||||||| |||| |||
                                GATCCTG CCGG AGT
                                    C   G
GAM457  OCM      3'  CCCTGGGAATGGGGAACCCC  20547    ACAGG         A
                                GG    CTTCATTCCCA GG
                                ||    |||||||||||| ||
                                CC    GGGGTAAGGGT CC
                                 CCAA_         C
GAM457  PTGER2   3'  AATGAAGCTGCCCTAA     6302       ACA
                                TTAGG   GGCTTCATT
                                |||||   |||||||||
                                AATCC   TCGAAGTAA
                                   CG_
GAM457  RXRB     3'  CCTGAAATGGCCTGTCC     41759         TCA   CCA
                                GGACAGGCT   TTC   AGG
                                |||||||||   |||   |||
                                CCTGTCCGG   AAG   TCC
                                     TA_  ___
GAM457  SPAG8    3'  CCTTGGGATTGCCCCTATCC   24900     C   CTT  T
                                GGA AGG   CA TCCCAAGG
                                ||| |||   || ||||||||
                                CCT TCC   GT AGGGTTCC
                                  A   CC_  T
GAM457  SRGAP2   3'  CCTTGAGAATGAAGCCCTTGG  74606      ACA        C
                                TTAGG   GGCTTCATTC CAAGG
                                |||||   |||||||||| |||||
                                GGTTC   CCGAAGTAAG GTTCC
                                   ___         A
GAM457  ADG-90   5'  CCTTAGGGATGCAGCCTGTCT  52351         T     C
                                GGACAGGCT CATTCC AAGG
                                ||||||||| |||||| ||||
                                TCTGTCCGA GTAGGG TTCC
                                     C     A
GAM457  CAPN6    3'  ATGAAGCCTTCCCTAA      26601       AC
                                TTAGG  AGGCTTCAT
                                |||||  |||||||||
                                AATCC  TCCGAAGTA
                                   CT
GAM457  CLIPR-59 3'  CCTTGTATGAAGCCCACCCC   31371    ACA_      TCC
                                GG   GGCTTCAT   CAAGG
                                ||   ||||||||   |||||
                                CC   CCGAAGTA   GTTCC
                                 CCAC       T__
GAM457  FLJ10193 3'  CCTTAAGAATGAAGCCAGCTTA 56554       ACA        CC
           G                     TTAGG   GGCTTCATTC  AAGG
                                |||||   ||||||||||  ||||
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                                GATTC  CCGAAGTAAG  TTCC
                                  GA_       AA
GAM457  HYA22    3'  CCTCAGGGGACCTGCCTGTCCT 19423        TTCA    A_
                                AGGACAGGC   TTCCC  AGG
                                |||||||||   |||||  |||
                                TCCTGTCCG   AGGGG  TCC
                                    TCC_    AC
GAM457  KIAA1856 3'  CCTTAGCATGGAGCCCACCCC  92662    ACA_     TCCC
                                GG   GGCTTCAT   AAGG
                                ||   ||||||||   ||||
                                CC   CCGAGGTA   TTCC
                                 CCAC      CGA_
GAM457  KIAA1870 3'  CCTTGGGAACAATGGATCC   49660    C    ___
                                GG TTCAT   TCCCAAGG
                                || |||||   ||||||||
                                CC AGGTA   AGGGTTCC
                                 T    ACA
GAM457  MGC2628  3'  CTCAGGAATGGGCCCC     43972    ACA   T     CA
                                GG   GGCT CATTCC  AG
                                ||   |||| ||||||  ||
                                CC   CCGG GTAAGG  TC
                                 ___   _     AC
GAM457  PCSK7    3'  CCTGGACATGCCTGTCCTGA   16335         TTCAT   CA
                                TTAGGACAGGC    TCC  AGG
                                ||||||||||    |||  |||
                                AGTCCTGTCCG    AGG  TCC
                                      TAC__   __
GAM457  SR-A1    3'  CCTTGCCCCCAAGCCTGTCC   70046         CATTCC
                                GGACAGGCTT     CAAGG
                                ||||||||||     |||||
                                CCTGTCCGAA     GTTCC
                                     CCCCC_
GAM457  VI       3'  CCCAGGAATGGACCCCCC    25558    ACA  C      CAA
                                GG   GG TTCATTCC   GG
                                ||   || ||||||||   ||
                                CC   CC AGGTAAGG   CC
                                 C__  C       AC_
GAM457  ZNF282   3'  CCTCGGCCCCAGCCTGTCC   89212         TCATTC  A
                                GGACAGGCT     CC AGG
                                |||||||||     || |||
                                CCTGTCCGA     GG TCC
                                     CCCC__   C
GAM457  LOC112616 3'  CCTTAAGAAACAAAGCCCTGTC 56486          _   CA_   CC
           CTAA                    TTAGGACAGG CTT   TTC  AAGG
                                ||||||||||| |||   |||  ||||
                                AATCCTGTCC GAA   AAG  TTCC
                                     C   ACA   AA
GAM457  LOC149461 3'  CCGGGAATGGGCCCC      79400    ACA   T     AA
                                GG   GGCT CATTCCC  G
                                ||   |||| |||||||  |
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                                CC   CCGG GTAAGGG  C
                                 ___   _      CC
GAM457   LOC221830 3'  CCCTGGAAATGTAGCTTGTCC  92506        T    C   A
                                GGACAGGCT CATT CCA GG
                                ||||||||| |||| ||| ||
                                CCTGTTCGA GTAA GGT CC
                                     T    A   C
GAM457   LOC255104 3'  CCTTGGGAAGCTGCCTGTCC   95395        TTCA
                                GGACAGGC    TTCCCAAGG
                                ||||||||    |||||||||
                                CCTGTCCG    AAGGGTTCC
                                    TCG_
GAM457   LOC256849 5'  CCCTGAGAATGAAGCC      96948          C  A
                                GGCTTCATTC CA GG
                                |||||||||| || ||
                                CCGAAGTAAG GT CC
                                     A  C
GAM457   LOC90785  3'  CCTCAAGAATGAAGCCGTGGAC 64015    GA  _       CCA
                                G  CA GGCTTCATTC   AGG
                                |  || ||||||||||   |||
                                C  GT CCGAAGTAAG   TCC
                                 AG  G        AAC
GAM457   LOC91133  3'  CCTCAGGGGACCCTGTCCTAA  65010         CTTCA    A_
                                TTAGGACAGG    TTCCC  AGG
                                |||||||||     |||||  |||
                                AATCCTGTCC    AGGGG  TCC
                                     C_____    AC
GAM458   GRAF      3'  ACAAAACTGGATAAACTTC   30545          _  GA_
                                GAAGTTTATC AG   TGT
                                |||||||||| ||   |||
                                CTTCAAATAG TC   ACA
                                     G  AAA
GAM458   KRTHA4    3'  ACTTCCCAATAAACTTC     40668         CA   T
                                GAAGTTTAT  GGA GT
                                |||||||||  ||| ||
                                CTTCAAATA  CCT CA
                                     AC   T
GAM458   PSG2      3'  AGCTCCTGATAACTTC      48355       T      T
                                GAAGTT ATCAGGA GTT
                                |||||| ||||||| |||
                                CTTCAA TAGTCCT CGA
                                   _     _
GAM458   TTN       3'  TGTGGATCTAATAAACTTC   55925         C  GAT
                                GAAGTTTAT AG   GTTCACA
                                |||||||||  ||   |||||||
                                CTTCAAATA TC   TAGGTGT
                                     A  ___
GAM458   DATF1     3'  TGAACACATTCGAACTTCGA   55007         ATC  GA
                                TCGAAGTTT   AG  TGTTCA
                                |||||||||   ||  ||||||
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                                AGCTTCAAG  TT ACAAGT
                                    C__ AC
GAM458  DATF1    3' TGAACACATTCGAACTTCGA 55010       ATC GA
                                TCGAAGTTT  AG TGTTCA
                                |||||||||  || ||||||
                                AGCTTCAAG  TT ACAAGT
                                    C__ AC
GAM458  DATF1    3' TGAACACATTCGAACTTCGA 42072       ATC GA
                                TCGAAGTTT  AG TGTTCA
                                |||||||||  || ||||||
                                AGCTTCAAG  TT ACAAGT
                                    C__ AC
GAM458  HTEX4    5' ATATCTGTAAACTTC     92094       CA
                                GAAGTTTAT GGATGT
                                |||||||||  ||||||
                                CTTCAAATG TCTATA
                                    __
GAM458  HTEX4    5' ATATCTGTAAACTTC     97720       CA
                                GAAGTTTAT GGATGT
                                |||||||||  ||||||
                                CTTCAAATG TCTATA
                                    __
GAM458  HTEX4    5' ATATCTGTAAACTTC     97895       CA
                                GAAGTTTAT GGATGT
                                |||||||||  ||||||
                                CTTCAAATG TCTATA
                                    __
GAM458  KIAA0970 3' GCACCAGTAAACTTC     29961       CA A
                                GAAGTTTAT GG TGT
                                |||||||||  || |||
                                CTTCAAATG CC ACG
                                    A_ _
GAM458  KIAA1579 3' CATCCCTAATAAACTTAGA 36607   G     CA_
                                TC AAGTTTAT  GGATG
                                || ||||||||  |||||
                                AG TTCAAATA  CCTAC
                                 A      ATC
GAM458  SYNE-2   3' TGAATAATGTAAACTTCGA 30803       T GGA
                                TCGAAGTTTA CA  TGTTCA
                                |||||||||| ||  ||||||
                                AGCTTCAAAT GT  ATAAGT
                                    _ A__
GAM458  ZNF212   3' TGAACATCCCCTTGGA    24309   G  TTTATCA
                                TC AAG     GGATGTTCA
                                || |||     |||||||||
                                AG TTC     CCTACAAGT
                                 G  C_____
GAM458  LOC146443 3' TGAACAAAGTAAACTTC  77887       CAGGA
                                GAAGTTTAT   TGTTCA
                                |||||||||   ||||||
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                                CTTCAAATG    ACAAGT
                                     AA___
GAM458  LOC146556 3'  TGTGAACGGATGAATAAAGTTC 77984    G    _ GGA
                                GAA TTTAT CA   TGTTCACA
                                ||| |||||| ||  ||||||||
                                CTT AAATA GT   GCAAGTGT
                                  G    A  AG_
GAM458  LOC149117 3'  TGTGGTAAACTGATGAACCCCG 84354    AA       GATGT
            A                    TCG  GTTTATCAG    TCACA
                                ||| |||||||||    |||||
                                AGC  CAAGTAGTC    GGTGT
                                  CC        AAAT_
GAM458  LOC149117 3'  TGTGGTAAACTGATGAACCCCG 84355    AA       GATGT
            A                    TCG  GTTTATCAG    TCACA
                                ||| |||||||||    |||||
                                AGC  CAAGTAGTC    GGTGT
                                  CC        AAAT_
GAM458  LOC149117 3'  TGTGGTAAACTGATGAACCCCG 84356    AA       GATGT
            A                    TCG  GTTTATCAG    TCACA
                                ||| |||||||||    |||||
                                AGC  CAAGTAGTC    GGTGT
                                  CC        AAAT_
GAM458  LOC149992 3'  TGTAAACATCCTTTAAAATTC  79560    G   TC       C
                                GAA TTTA  AGGATGTT ACA
                                ||| ||||  |||||||| |||
                                CTT AAAT  TCCTACAA TGT
                                  A   T_       A
GAM458  LOC151005 3'  TGTAAACATCCTTTAAAATTC  80100    G   TC       C
                                GAA TTTA  AGGATGTT ACA
                                ||| ||||  |||||||| |||
                                CTT AAAT  TCCTACAA TGT
                                  A   T_       A
GAM458  LOC64102  3'  ATGTTCTAATAAACTTC     42168         C
                                GAAGTTTAT AGGATGT
                                ||||||||| |||||||
                                CTTCAAATA TCTTGTA
                                     A
GAM459  CD7      3'  CTCACCCTGCTGTCCTCCCACG 20428        CCTC__   A
            G                    CCGTGGGA     CAG GTGAG
                                ||||||||     ||| |||||
                                GGCACCCT     GTC CACTC
                                    CCTGTC   C
GAM459  EGLN3    3'  TTCTTGCTTGAAAATCCCATG  41973       CCTCCA   TG
                                CGTGGGA     GAG  AGAA
                                |||||||     |||  ||||
                                GTACCCT     TTC  TCTT
                                   AAAAG_   GT
GAM459  EZH1     3'  TCCACTTGTTGTCCCATG    8828         CTCCA    A
                                CGTGGGAC    GAGTG GA
                                ||||||||    ||||| ||
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                                GTACCCTG    TTCAC CT
                                    TTG__   _
GAM459  FGR     3'  TTCTCACTCCATCCCCAC    17898      ACCTCCA
                                GTGGG      GAGTGAGAA
                                |||||      |||||||||
                                CACCC      CTCACTCTT
                                   CTAC___
GAM459  FUT3    3'  CTCACTCTAGAGGGGTTGG   3802      TGGGA   C
                                CCG    CCTC AGAGTGAG
                                |||    |||| ||||||||
                                GGT    GGAG TCTCACTC
                                  TGG__   A
GAM459  GPR56   3'  TCTCACTCAGCTCCCACGGG  19076        C  CCA
                                TCCGTGGGA CT   GAGTGAGA
                                ||||||||| ||   ||||||||
                                GGGCACCCT GA   CTCACTCT
                                     C  ___
GAM459  HDGF    3'  TTCCCACTCCAAGCCCAGCCCA 15686        ACCTCCA__    A
            TGGA                   TCCGTGGG        GAGTG GAA
                                |||||||||       ||||| |||
                                AGGTACCC        CTCAC CTT
                                     GACCCGAAC    C
GAM459  MSF     3'  CTCACCCTCTGTCCCCACG   88083      ACCTC   __
                                CGTGGG    CAGA  GTGAG
                                ||||||    ||||  |||||
                                GCACCC    GTCT  CACTC
                                   CT___   CC
GAM459  PRX     5'  CTCAGGCAGCAAGAACCCCACG 40530        AC_____ _  A
            GA                    TCCGTGGG      CT CC GAG
                                |||||||||      || || |||
                                AGGCACCC      GA GG CTC
                                     CAAGAAC  C  A
GAM459  PSME3   3'  CTCACCCTATCACCCATGGA  19371        ACCTCC  A
                                TCCGTGGG     AG GTGAG
                                |||||||||     || |||||
                                AGGTACCC     TC CACTC
                                     ACTA__  C
GAM459  SMTN    3'  CTGCTCGGGGCCCCACGGA   56154        A  T  A   G
                                TCCGTGGG CC CC GAGT AG
                                |||||||| || || |||| ||
                                AGGCACCC GG GG CTCG TC
                                     C  _  _   _
GAM459  SURF4   3'  CTCCCAGCACTGGAGACCCACG 52543        AC     A  ___
            GA                    TCCGTGGG  CTCCAG GT   GAG
                                |||||||||  |||||| ||   |||
                                AGGCACCC  GAGGTC CG   CTC
                                     A_     A  ACC
GAM459  VENTX2  3'  TCTCACCCTGACCCAC      27122       ACCTC   A
                                GTGGG    CAG GTGAGA
                                |||||    ||| ||||||
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                                CACCC    GTC CACTCT
                                  A____  C
GAM459  WNT3A    3'  CTCGCGAAGGTCCCAC     52428        CCAGA
                                GTGGGACCT    GTGAG
                                |||||||||    |||||
                                CACCCTGGA    CGCTC
                                     AG___
GAM459  ZNF200   5'  CTCTGGAGGCCCCGCG     12908      A
                                CGTGGG CCTCCAGAG
                                |||||| |||||||||
                                GCGCCC GGAGGTCTC
                                   C
GAM459  ACAS2L   3'  TCCCATCCATTGGAGGTCCCAG 68077    G        A__  A
           GA                     TCC TGGGACCTCCAG  GTG GA
                                ||| ||||||||||||  ||| ||
                                AGG ACCCTGGAGGTT  TAC CT
                                 _         ACC  C
GAM459  AHCYL1   3'  CTCACTCTAGTCACTA     21764    _  CTCC
                                TGG GAC   AGAGTGAG
                                ||| |||   ||||||||
                                ATC CTG   TCTCACTC
                                  A  A___
GAM459  CARD9    3'  CTCACTCCCCCAGGA      42285    G   ACCTCCA
                                TCC TGGG     GAGTGAG
                                ||| ||||     |||||||
                                AGG ACCC     CTCACTC
                                  _   C_______
GAM459  COLEC12  3'  CTCACTCTGGAGATAGATGGG  47865     GGGAC
                                TCCGT    CTCCAGAGTGAG
                                |||||    ||||||||||||
                                GGGTA    GAGGTCTCACTC
                                   GATA_
GAM459  FLJ13855 3'  CTCACTTCAACCCCAGGGA   43586    G   ACCTCCA
                                TCC TGGG     GAGTGAG
                                ||| ||||     |||||||
                                AGG ACCC     TTCACTC
                                  G   CAAC___
GAM459  FLJ14107 5'  TCCCACTCCCCAGGTCCCAT  46699        CCA    A
                                GTGGGACCT  GAGTG GA
                                |||||||||  ||||| ||
                                TACCCTGGA  CTCAC CT
                                     CCC    C
GAM459  FLJ20640 5'  CACTGAGGACCCCACGGA    35488       A_   CAG
                                TCCGTGGG  CCTC  AGTG
                                ||||||||  ||||  ||||
                                AGGCACCC  GGAG  TCAC
                                     CA   ___
GAM459  FLJ22477 3'  CTCCAGCCTGGAGACCCCATGG 45341       AC     A __
           A                     TCCGTGGG  CTCCAG GT  GAG
                                ||||||||  ||||||  ||  |||
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                                AGGTACCC  GAGGTC CG  CTC
                                    CA     _ AC
GAM459  KIAA1128  3'  TTCCAGGGGATCCCACGGA   68489        _   CA
                                TCCGTGGGA CCTC  GAG
                                ||||||||| ||||  |||
                                AGGCACCCT GGGG  CTT
                                    A    AC
GAM459  LYPLA3    3'  CTGTACCCAGAGGTCCCAGGGA 24629    G       CAGA  _
                                TCC TGGGACCTC    GTG AG
                                ||| |||||||||    ||| ||
                                AGG ACCCTGGAG    CAT TC
                                  G       ACC_   G
GAM459  PAPSS2    3'  TTCTCACTCTAAAAGAGGT   59597      C___
                                ACCTC    AGAGTGAGAA
                                |||||    ||||||||||
                                TGGAG    TCTCACTCTT
                                   AAAA
GAM459  TRAF3     3'  CACCTGAGGGTCCCAC      59736        TC   A
                                GTGGGACC  CAG GTG
                                ||||||||  ||| |||
                                CACCCTGG  GTC CAC
                                    GA  _
GAM459  LOC128439 3'  CTGACTTTGGAAGCCCCCA   57353     AC  _     G
                                TGGG  CT CCAGAGT AG
                                ||||  || ||||||| ||
                                ACCC  GA GGTTTCA TC
                                  CC  A      G
GAM459  LOC148394 5'  TTCTCACTCTAAAGCTCAC   84146      AC  CC
                                GTGGG  CT  AGAGTGAGAA
                                |||||  ||  ||||||||||
                                CACTC  GA  TCTCACTCTT
                                   __  AA
GAM459  LOC149911 3'  TCCACATGGAGGTCCCAGGA   84710     G        GA   A
                                TCC TGGGACCTCCA  GTG GA
                                ||| ||||||||||  ||| ||
                                AGG ACCCTGGAGGT  CAC CT
                                  _        A_  _
GAM459  LOC152402 3'  TCATCTGGAGACCCCATGGA   85707        AC      G
                                TCCGTGGG  CTCCAGA TGA
                                ||||||||  ||||||| |||
                                AGGTACCC  GAGGTCT ACT
                                    CA     _
GAM459  LOC154789 5'  TCTCACTTCTCATCTCCAC   81142     _  CCTCCA
                                GTGG GA     GAGTGAGA
                                |||| ||     ||||||||
                                CACC CT     TTCACTCT
                                  T  ACTC__
GAM459  LOC197419 5'  TTCCGGAAGTCCCACGG     89757         C   A
                                CCGTGGGAC TCC GAG
                                ||||||||| ||| |||
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                                GGCACCCTG AGG CTT
                                     A   C
GAM459  LOC200728 3'  TCTCACTCTGAAATTCCA    90119      CCTC
                                TGGGA   CAGAGTGAGA
                                |||||   ||||||||||
                                ACCTT   GTCTCACTCT
                                  AAA_
GAM459  LOC221178 3'  TCCCACCTACCTCCACGGA   93539       ACCTCC  A   A
                                TCCGTGGG    AG GTG GA
                                ||||||||    || ||| ||
                                AGGCACCT    TC CAC CT
                                    CCA___ _   C
GAM459  LOC51066  5'  TTCCCACCTTTGGAGGCCCCAG 31938    G   A      _  A
           GGA                    TCC TGGG CCTCCAGAG TG GAA
                                ||| |||| ||||||||| || |||
                                AGG ACCC GGAGGTTTC AC CTT
                                  G   C       C  C
GAM459  LOC90917  5'  CCACTCCTCCCAGGA     64337    G   CCTCCA    A
                                TCC TGGGA    GAGTG G
                                ||| |||||    ||||| |
                                AGG ACCCT    CTCAC C
                                  _    C_____    C
GAM459  LOC92017  5'  TTCTCACTCTAAAAATGCTGGT 67895    TG  ACCTCC_
           GG                    CCG  GG     AGAGTGAGAA
                                |||  ||     ||||||||||
                                GGT  TC     TCTCACTCTT
                                  GG  GTAAAAA
GAM460  ATRN    3'  CAACACTAACCCCACTCC    57796     AGATT
                                GGAGT    GTTAGTGTTG
                                |||||    ||||||||||
                                CCTCA    CAATCACAAC
                                  CCC__
GAM460  ATRN    3'  CAACACTAACCCCACTCC    57796     AGATT
                                GGAGT    GTTAGTGTTG
                                |||||    ||||||||||
                                CCTCA    CAATCACAAC
                                  CCC__
GAM460  CSAGE   3'  CAACACTATCCAGCCACTCTGA 86860    G   AGA   T_
                                TCAG AGT   TTG  TAGTGTTG
                                ||||  |||   |||  ||||||||
                                AGTC TCA   GAC  ATCACAAC
                                  _   CC_   CT
GAM460  CSAGE   3'  CAACACTATCCAGCCACTCTGA 86860    G   AGA   T_
                                TCAG AGT   TTG  TAGTGTTG
                                ||||  |||   |||  ||||||||
                                AGTC TCA   GAC  ATCACAAC
                                  _   CC_   CT
GAM460  DPP8    3'  CATGTAACATCTACTCCTGA  55233         T   _
                                TCAGGAGTAGAT GTTA GTG
                                |||||||||||| |||| |||
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                                AGTCCTCATCTA CAAT TAC
                                      _   G
GAM460  DPP8     3'  CATGTAACATCTACTCCTGA  55233          T   _
                                TCAGGAGTAGAT GTTA GTG
                                |||||||||||| |||| |||
                                AGTCCTCATCTA CAAT TAC
                                      _   G
GAM460  FLJ13197 5'  CAACACCAGCGCTGCACC    44847    A   AT   A
                                GG GTAG  TGTT GTGTTG
                                || ||||  |||| ||||||
                                CC CGTC  GCGA CACAAC
                                 A   __   C
GAM460  FLJ13197 5'  CAACACCAGCGCTGCACC    44847    A   AT   A
                                GG GTAG  TGTT GTGTTG
                                || ||||  |||| ||||||
                                CC CGTC  GCGA CACAAC
                                 A   __   C
GAM460  TRAG3    3'  CAACACTATCCAGCCACTCTGA 16932     G   AGA   T_
                                TCAG AGT   TTG  TAGTGTTG
                                |||| |||   |||  ||||||||
                                AGTC TCA   GAC  ATCACAAC
                                  _  CC_   CT
GAM460  TRAG3    3'  CAACACTATCCAGCCACTCTGA 67525     G   AGA   T_
                                TCAG AGT   TTG  TAGTGTTG
                                |||| |||   |||  ||||||||
                                AGTC TCA   GAC  ATCACAAC
                                  _  CC_   CT
GAM460  TRAG3    3'  CAACACTATCCAGCCACTCTGA 16932     G   AGA   T_
                                TCAG AGT   TTG  TAGTGTTG
                                |||| |||   |||  ||||||||
                                AGTC TCA   GAC  ATCACAAC
                                  _  CC_   CT
GAM460  TRAG3    3'  CAACACTATCCAGCCACTCTGA 67525     G   AGA   T_
                                TCAG AGT   TTG  TAGTGTTG
                                |||| |||   |||  ||||||||
                                AGTC TCA   GAC  ATCACAAC
                                  _  CC_   CT
GAM460  LOC196890 3'  AACAACCTGCTCCTGA     89642          A
                                TCAGGAGTAG TTGTT
                                |||||||||| |||||
                                AGTCCTCGTC AACAA
                                      C
GAM460  LOC196890 3'  AACAACCTGCTCCTGA     89642          A
                                TCAGGAGTAG TTGTT
                                |||||||||| |||||
                                AGTCCTCGTC AACAA
                                      C
GAM460  LOC92017  5'  AACCATCCACTCCTGA     67883         A   T
                                TCAGGAGT GAT GTT
                                |||||||| ||| |||
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                                AGTCCTCA CTA CAA
                                     C   C
GAM460  LOC92017  5'  AACCATCCACTCCTGA      67883         A   T
                                TCAGGAGT GAT GTT
                                |||||||| ||| |||
                                AGTCCTCA CTA CAA
                                     C   C
GAM461  CD5L      3'  AGGTGACCACAATAGCAAC    19709           AA TG
                                GTTGCTATTGT  T  CTT
                                ||||||||||  |  |||
                                CAACGATAACA  A  GGA
                                       CC GT
GAM461  EVA1      3'  CCAAGATTTACAATAGCA     19394           TTG   T
                                TGCTATTGTAA   CTT GG
                                ||||||||||   ||| ||
                                ACGATAACATT   GAA CC
                                       TA_  _
GAM461  TNC       3'  CAAAGCATCAATACAAC      9288       C    TAAT
                                GTTG TATTG    TGCTTTG
                                |||| |||||    |||||||
                                CAAC ATAAC    ACGAAAC
                                  _     T___
GAM461  TNFAIP6   3'  CCAAAGCAAGTCATAAAAAC   59465     GCTAT  TAA
                                GTT    TG   TTGCTTTGG
                                |||    ||   |||||||||
                                CAA    AC   AACGAAACC
                                  AAAT_  TG_
GAM461  CLIPR-59  3'  CCAAAGCAAAAGAGTAAC     31369       ATTGTAA
                                GTTGCT      TTGCTTTGG
                                ||||||      |||||||||
                                CAATGA      AACGAAACC
                                   GAA____
GAM461  EREG      3'  CCAAAGCAACCACAAATGCA   7494      TA   AA
                                TGC  TTGT  TTGCTTTGG
                                |||  ||||  |||||||||
                                ACG  AACA  AACGAAACC
                                  TA   CC
GAM461  KIAA0240  3'  CCAGTCTTCATAATAGCAAC   92434           AATTGCT
                                GTTGCTATTGT      TTGG
                                ||||||||||      ||||
                                CAACGATAATA      GACC
                                       CTTCT__
GAM461  MBLL39    3'  CAAAGCAATGAAGCGAC      19248       ATTGTA
                                GTTGCT     ATTGCTTTG
                                ||||||     |||||||||
                                CAGCGA     TAACGAAAC
                                   AG____
GAM461  MGC32104  3'  CCAAAGCAATTGCAACAAAAAC 58404      GCTA
                                GTT    TTGTAATTGCTTTGG
                                |||    ||||||||||||||
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                                CAA    AACGTTAACGAAACC
                                  AAAC
GAM461   ZFD25     3'  CCAAAGCAACAAGAGCAA     32578       A    AAT
                                TTGCT TTGT   TGCTTTGG
                                ||||| ||||   ||||||||
                                AACGA AACA   ACGAAACC
                                   G   ___
GAM461   LOC145622 3'  CAATATACAATAGTAAC      77294           _
                                GTTGCTATTGTA ATTG
                                |||||||||||| ||||
                                CAATGATAACAT TAAC
                                       A
GAM461   LOC151178 3'  CCAAAGCAATCTGGTCAC     80148     T    TTGTA
                                GT GCTA     ATTGCTTTGG
                                || ||||     ||||||||||
                                CA TGGT     TAACGAAACC
                                 C   C____
GAM461   LOC197196 3'  CCAAAGCAACTGTGGGCA     89732     TA TG  A
                                TGC  T  TA TTGCTTTGG
                                |||  |  || |||||||||
                                ACG  G  GT AACGAAACC
                                  __ GT  C
GAM461   LOC221760 3'  CCAAAGAGAGCAATGCAAC    93783       T     AATTG
                                GTTGC ATTGT     CTTTGG
                                ||||| |||||     ||||||
                                CAACG TAACG     GAAACC
                                   _     AGA__
GAM461   LOC51000  3'  CCAAAGCAATCAAGAGAGCCAC 31975     T   A  GTA
                                GT GCT TT   ATTGCTTTGG
                                || ||| ||   ||||||||||
                                CA CGA AG   TAACGAAACC
                                 C   G  AAC
GAM461   LOC85479  5'  CCAAAGCAATCAATGCCAA    52403     C     TA
                                TTG TATTG  ATTGCTTTGG
                                ||| |||||  ||||||||||
                                AAC GTAAC  TAACGAAACC
                                  C    __
GAM461   LOC91796  3'  CCAAAGCAACCCTGAGCAA    67211       ATTGTAA
                                TTGCT      TTGCTTTGG
                                |||||      |||||||||
                                AACGA      AACGAAACC
                                   GTCCC__
GAM462   CHAT      5'  TCCACACCTCTGCATCCCTGCA 40624       AAGTTTTT_
            C                    GTGCA        AGGTGTGGA
                                |||||        |||||||||
                                CACGT        TCCACACCT
                                   CCCTACGTC
GAM462   CHAT      5'  TCCACACCTCTGCATCCCTGCA 40625       AAGTTTTT_
            C                    GTGCA        AGGTGTGGA
                                |||||        |||||||||
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                                CACGT       TCCACACCT
                                   CCCTACGTC
GAM462  KIF5A    3'  CCACACCCACGGCTGCATAC  17157       AA  TTTA
                                GTGTGCA  GTT   GGTGTGG
                                |||||||  |||   |||||||
                                CATACGT  CGG   CCACACC
                                   __  CAC_
GAM462  SLC26A2  3'  TCCACAGTGGGAAATTTTGCAC 3670            AGG
           AC                    GTGTGCAAAGTTTTT  TGTGGA
                                |||||||||||||||  ||||||
                                CACACGTTTTAAAGG  ACACCT
                                       GTG
GAM462  TERT     3'  CCACACCCAGGCCCGCAC    12226     AAA   TTA
                                GTGC  GTTT  GGTGTGG
                                ||||  ||||  |||||||
                                CACG  CGGA  CCACACC
                                  CC_   C__
GAM462  TNNT2    3'  CCACACCCACTCCACAC     4523       CAA  TTTTA
                                GTGTG  AGT    GGTGTGG
                                |||||  |||    |||||||
                                CACAC  TCA    CCACACC
                                   C__   C____
GAM462  DKFZP434J037 3'  CCACACTCCACTCCACAC    48208      CAA  TTTTA
                                GTGTG  AGT    GGTGTGG
                                |||||  |||    |||||||
                                CACAC  TCA    TCACACC
                                   C__   CC___
GAM462  DKFZp761O132 5'  TCCACACCTGCCCACCCTGCAC 50199       AA  TTT
                                GTGCA  GT   TAGGTGTGGA
                                |||||  ||   ||||||||||
                                CACGT  CA   GTCCACACCT
                                   CC  CCC
GAM462  LIN-28   3'  CCCAAAAGAAAACTTACACAC  45147      CA      AGG  T
                                GTGTG  AAGTTTTT   TG GG
                                |||||  ||||||||   || ||
                                CACAC  TTCAAAAG   AC CC
                                   A_       AAA  _
GAM462  MGC15429  3'  TCCACACAAGCACTTGCACAC  51251        A  TTTTAG
                                GTGTGCAA GT     GTGTGGA
                                |||||||| ||     |||||||
                                CACACGTT CA     CACACCT
                                    _ CGAA__
GAM462  MGC2594   3'  TCCACACCCTGCGTCCACAC   43898      CAAA  TTTTA
                                GTGTG   GT    GGTGTGGA
                                |||||   ||    ||||||||
                                CACAC   CG    CCACACCT
                                   CTG_  TC___
GAM462  PRO2325   5'  CCAAAAAACTTTTCACAC    37587      C       A
                                GTGTG AAAGTTTTT GG
                                ||||| |||||||| ||
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                                CACAC TTTCAAAAA CC
                                  T       A
GAM462  SIRPB1   3'  TCCACACCTCTCACCTCCACC  20265   T  CAA  TTTTT
                                G GTG  AG    AGGTGTGGA
                                | |||  ||    |||||||||
                                C CAC  TC    TCCACACCT
                                _  C__  CACTC
GAM462  SQV7L    3'  CCTAATAAAAACTCTGAACAC  70572     G  A      GGTGT
                                GTGT CA AGTTTTTA    GG
                                |||| || ||||||||    ||
                                CACA GT TCAAAAAT    CC
                                  A  C       AAT__
GAM462  STAM2    3'  CCTAAAAATTTGCACAC     19561         G
                                GTGTGCAAA TTTTTAGG
                                ||||||||| ||||||||
                                CACACGTTT AAAAATCC

                                   _
GAM462  LOC139046 5'  TCCACACCGCCCCCCGCACAT  75814       AAAGTTTTTA
                                GTGTGC        GGTGTGGA
                                ||||||        ||||||||
                                TACACG        CCACACCT
                                   CCCCCCG___
GAM462  LOC146823 3'  TCCACCACCAAACCTCCACAC  83802      CAAA   TTA   _
                                GTGTG   GTTT  GGTG TGGA
                                |||||   ||||  |||| ||||
                                CACAC   CAAA  CCAC ACCT
                                   CTC_   ___   C
GAM462  LOC151438 5'  CCACACCACTCTTCGCCAC   85363    T  A   TTTTTA
                                GTG GC AAG     GGTGTGG
                                ||| || |||     |||||||
                                CAC CG TTC     CCACACC
                                  _ C   TCA___
GAM462  LOC152915 5'  CCACACAACCCGGCACAC    67023      AAA   TTTAG
                                GTGTGC  GTT    GTGTGG
                                ||||||  |||    ||||||
                                CACACG  CAA    CACACC
                                   GCC  _____
GAM462  LOC161247 5'  CCACACCTTCCTGCTCAC    82266    T  AAGTTTTT
                                GTG GCA       AGGTGTGG
                                ||| |||       ||||||||
                                CAC CGT       TCCACACC
                                  T  CCT_____
GAM462  LOC255218 3'  CCACACCTCCACGCACAC    95769      AAA  TTTT
                                GTGTGC  GT    AGGTGTGG
                                ||||||  ||    ||||||||
                                CACACG  CA    TCCACACC
                                   ___  CC__
GAM462  LOC90246  3'  CCAGAAAAATTTGCACAC    61906        G    A
                                GTGTGCAAA TTTTT GG
                                ||||||||| ||||| ||
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                                CACACGTTT AAAAG CC
                                     A    A
GAM462  LOC90785 3' CCACACCTTTCCCTCCACAC  64013      CAA  TTTTT
                                GTGTG  AG    AGGTGTGG
                                |||||  ||    ||||||||
                                CACAC  TC    TCCACACC
                                   C__  CCTT_
GAM463  ADH1B    3' CTTAGACATAAAGTAAAAT   72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM463  AHR      3' ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM463  FDFT1    3' TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                        _
GAM463  JTB      3' ATCTCAGACAGTGAAAGTGAAA 21959
           TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM463  KLF4     3' TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM463  PHYH     3' ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM463  PKD2     3' TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM463  WRN      3' GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM463  ZNF216   3' ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
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                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM463  CG012    5' CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                     CT  __
GAM463  EIF2C2   3' ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM463  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM463  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM463  KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM463  KLHL6    3' ATCTCAGAGCAGGAAA      55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM463  NIR3     3' GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM463  PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM463  PP35     3' ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM463  PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148         TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
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                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM463  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM463  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941        CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM463  LOC149703 3' ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM463  LOC154007 3' ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM463  LOC155004 3' TCATTTAAGTGAAAGGAAA    81226     A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM463  LOC222134 5' ACAGTGAAGTGAAATG       94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM464  ACADS    3'  ACATGGGAATGAGGCCCTCCGA 3405    A  AGA_   AAAG
                                TC GA    CTCA    TTCCATGT
                                || ||    ||||    ||||||||
                                AG CT    GAGT    AGGGTACA
                                 C  CCCG    A___
GAM464  DDB2     3'  ACATGGGATCAAGTCCTG     3659      AA    CAAAA
                                CAG  GACT    GTTCCATGT
                                |||  ||||    |||||||||
                                GTC  CTGA    TAGGGTACA
                                  __    AC___
GAM464  FBXW7    5'  AACCTTTGCATCTTCTGA     53303        CT    A
                                TCAGAAGA  CAAA GTT
                                ||||||||  |||| |||
                                AGTCTTCT  GTTT CAA
                                     AC    C
GAM464  RBM3     5'  GGACCTCGTGAGTCTTCTGA   70488          AA  T
                                TCAGAAGACTCA  AG TCC
                                ||||||||||||  || |||
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                                AGTCTTCTGAGT  TC AGG
                                      GC  C
GAM464  SEPP1    3'  CATGGAGAAATCTACTGA    60109     A   CTCAAAAG
                                TCAG AGA       TTCCATG
                                |||| |||       |||||||
                                AGTC TCT       GAGGTAC
                                  A   AAA_____
GAM464  SEPP1    3'  CATGGAGAAATCTACTGA    18260     A   CTCAAAAG
                                TCAG AGA       TTCCATG
                                |||| |||       |||||||
                                AGTC TCT       GAGGTAC
                                  A   AAA_____
GAM464  SLC16A2  3'  ACATGGGACATTTAAATCCTC  21498    A  CTC   A
                                GA GA   AAA GTTCCATGT
                                || ||   ||| |||||||||
                                CT CT   TTT CAGGGTACA
                                 C  AAA   A
GAM464  XPNPEP2  3'  ACATGGAACCCATGATTC    12680    C   AAA
                                GA TCA   GTTCCATGT
                                || |||   |||||||||
                                CT AGT   CAAGGTACA
                                 T   ACC
GAM464  ARHGAP9  5'  GCTCCTGAATCTTCTGA     50680        C   AA
                                TCAGAAGA TCA  AGT
                                |||||||| |||  |||
                                AGTCTTCT AGT  TCG
                                     A   CC
GAM464  C20orf177 3'  ACTTTTGAGTTCTCCGA     62141    A  AG
                                TC GA  ACTCAAAAGT
                                || ||  ||||||||||
                                AG CT  TGAGTTTTCA
                                 C  CT
GAM464  FLJ10751  3'  ACATGGAACTTTCAATGCT   36726    ACTCA
                                AG    AAAGTTCCATGT
                                ||    ||||||||||||
                                TC    TTTCAAGGTACA
                                 GTAAC
GAM464  FLJ10751  3'  ACATGGAACTTTCAATGCT   36565    ACTCA
                                AG    AAAGTTCCATGT
                                ||    ||||||||||||
                                TC    TTTCAAGGTACA
                                 GTAAC
GAM464  FLJ13110  3'  CTTTAAGTCTTCTGA      43301         CA
                                TCAGAAGACT  AAAG
                                ||||||||||  ||||
                                AGTCTTCTGA  TTTC
                                      A_
GAM464  FLJ14721  5'  CATGGAGGGAGCTCCCTGA   51578     A_  A   AAAAGT
                                TCAG  AG CTC     TCCATG
                                ||||  || |||     ||||||
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                                AGTC  TC GAG     AGGTAC
                                  CC  _   GG____
GAM464  FLJ20374  3'  ACACGGAACTTCACCTTTTCTG 35076        CTCAA      A
            G                    TCAGAAGA    AAGTTCC TGT
                                 ||||||||    ||||||| |||
                                 GGTCTTTT    TTCAAGG ACA
                                     CCAC_      C
GAM464  KIAA0565  3'  CTTTTGAGTTTCTGA      66889      A
                                 TCAGA GACTCAAAAG
                                 ||||| ||||||||||
                                 AGTCT TTGAGTTTTC
                                   _
GAM464  KIAA0677  3'  ACATGGAACGCTGAAGTCTCTG 27823      A   _  AAA
            A                    TCAGA GACT CA   GTTCCATGT
                                 ||||| |||| ||   |||||||||
                                 AGTCT CTGA GT   CAAGGTACA
                                   _   A  CG_
GAM464  KIAA0977  3'  ACATGGAACTCTTGTTTTTTT  29747      CT   A
                                 GAAGA  CAA AGTTCCATGT
                                 |||||  ||| ||||||||||
                                 TTTTT  GTT TCAAGGTACA
                                    TT   C
GAM464  KIAA1958  5'  ACATGGTTTGTGAGTCTTCTG  81898          AAAGTT
                                 CAGAAGACTCA     CCATGT
                                 ||||||||||      ||||||
                                 GTCTTCTGAGT     GGTACA
                                       GTTT__
GAM464  LBP-9     3'  GACCTTTAGTCTTCTGA     27277          C   A
                                 TCAGAAGACT AAA GTT
                                 |||||||||| ||| |||
                                 AGTCTTCTGA TTT CAG
                                       _   C
GAM464  PDE10A    5'  ACATGGAAGATGGACCTTCT   21857      AC   AAAG
                                 AGAAG  TCA    TTCCATGT
                                 |||||  |||    ||||||||
                                 TCTTC  GGT    AAGGTACA
                                    CA   AG__
GAM464  RIP5      3'  ATGGCATTTCAAGTCTTCTGA  38123         CAA    T
                                 TCAGAAGACT   AAGT CCAT
                                 ||||||||||   |||| ||||
                                 AGTCTTCTGA   TTTA GGTA
                                       AC_    C
GAM464  SLC7A11   3'  AATTCTTGAGTCTCTGA     26752      A      A
                                 TCAGA GACTCAA AGTT
                                 ||||| ||||||| ||||
                                 AGTCT CTGAGTT TTAA
                                    _      C
GAM464  LOC116064 3'  ACATGGGACAAACCTTTCTGA  73720        ACTCAAAA
                                 TCAGAAG       GTTCCATGT
                                 |||||||       |||||||||
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                                AGTCTTT       CAGGGTACA
                                    CCAAA___
GAM464   LOC121536 3'  ACATGAAAATGAGTCTT     74081        AAAG   C
                                AAGACTCA    TTC ATGT
                                ||||||||    ||| ||||
                                TTCTGAGT    AAG TACA
                                    AA__   _
GAM464   LOC129011 3'  CATGGAAGAAACTTCT      74866      AC  AAAAG
                                AGAAG  TC    TTCCATG
                                |||||  ||    |||||||
                                TCTTC  AG    AAGGTAC
                                  AA  _____
GAM464   LOC152245 3'  CATGTAACTGAGTCTTT     85598        AAA   C
                                GAAGACTCA   GTT CATG
                                |||||||||   ||| ||||
                                TTTCTGAGT   CAA GTAC
                                    ___   T
GAM464   LOC220739 3'  GGACCTCTGAGTTTTCTGA    92934          AA  T
                                TCAGAAGACTCA  AG TCC
                                ||||||||||||  || |||
                                AGTCTTTTGAGT  TC AGG
                                      C_  C
GAM464   LOC220963 3'  ACATAGAACTTTTAATTCTG   91445      GACTC       C
                                CAGAA     AAAAGTTC ATGT
                                |||||     |||||||| ||||
                                GTCTT     TTTTCAAG TACA
                                  AA___       A
GAM464   LOC253890 3'  CATGGAACTTTTCTGT      95676    TC
                                AC  AAAAGTTCCATG
                                ||  ||||||||||||
                                TG  TTTTCAAGGTAC
                                 TC
GAM464   LOC256207 3'  CTTTTGAGTTTCTGA       95168       A
                                TCAGA GACTCAAAAG
                                ||||| ||||||||||
                                AGTCT TTGAGTTTTC
                                   _
GAM465   JJAZ1    3'  AGTGCTTTTCTATATGTACCC  31077         A    TAT
                                GGGTACATA AGAAG   GTACT
                                ||||||||| |||||   |||||
                                CCCATGTAT TCTTT   CGTGA
                                    A    T__
GAM465   LECT2    3'  ACATATACACCTATGTACCC   9719         AAGAA
                                GGGTACATA     GTATGT
                                |||||||||     ||||||
                                CCCATGTAT     TATACA
                                    CCACA
GAM465   MAP3K1   3'  AGTTGATACTTCTTTATGACCC 67814      A          GT
                                GGGT CATAAAGAAGTAT  ACT
                                |||| ||||||||||||  |||
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                                CCCA GTATTTCTTCATA  TGA
                                  _          GT
GAM465  PPP2R5C  3'  TACATACTTCCTGTGCC     10761       TAAA
                                GGTACA   GAAGTATGTA
                                ||||||   ||||||||||
                                CCGTGT   CTTCATACAT
                                   C___
GAM465  PTPRN    3'  GCATCTCTGTGTACCC      11132        A  A
                                GGGTACATA AGA GT
                                ||||||||| ||| ||
                                CCCATGTGT TCT CG
                                     C  A
GAM465  SRD5A2   5'  AGTACATGTGGCTTCATACCC  59414      CATA  AA
                                GGGTA   AAG  GTATGTACT
                                |||||   |||  |||||||||
                                CCCAT   TTC  TGTACATGA
                                  AC__  GG
GAM465  ERO1L    3'  AGCACATACTTGGTATCC    27428       ATAAAG       A
                                GGGTAC     AAGTATGT CT
                                ||||||     |||||||| ||
                                CCTATG     TTCATACA GA
                                   G_____       C
GAM465  KIAA1695 3'  TACATACATGTACACC      47105   _    AAAGAA
                                GG GTACAT     GTATGTA
                                || ||||||     |||||||
                                CC CATGTA     CATACAT
                                 A    _______
GAM465  KIF13B   3'  GCTTTGTTTCTTCTGTACCC  30912       TA       T_
                                GGGTACA  AAGAAGTA  GT
                                |||||||  ||||||||  ||
                                CCCATGT  TTCTTTGT  CG
                                   C_       TT
GAM465  LY6G6C   3'  CAGGCTCCCATATGTACCC   47512        AAGA  A
                                GGGTACATA   AGT TG
                                |||||||||   ||| ||
                                CCCATGTAT   TCG AC
                                     ACCC  G
GAM465  MRPL19   3'  ATAAACATTCATGTACCC    28640        AAA  _  A
                                GGGTACAT   GAA GT TGT
                                ||||||||   ||| || |||
                                CCCATGTA   CTT CA ATA
                                    ___   A  A
GAM465  SCYB11   3'  TACACACTTCTTTCCCC     87444     TACAT       A
                                GGG    AAAGAAGT TGTA
                                |||    |||||||| ||||
                                CCC    TTTCTTCA ACAT
                                 C____       C
GAM465  ZNF220   3'  GAGCCTTACTTTCTTTACATAC 22226     CA      _   TGTA
            C                    GGTA  TAAAGAA GTA   CTC
                                ||||  ||||||| |||   |||
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                                CCAT  ATTTCTT CAT    GAG
                                  AC      T   TCC_
GAM465   LOC120939 3'  ACATACTTTTCTAACCC     76242      ACA  A
                                GGGT   TA AGAAGTATGT
                                ||||   || ||||||||||
                                CCCA   AT TTTTCATACA
                                  ___  C
GAM465   LOC126267 5'  TGTGTCTTCTTTACCCACCC   75678      ACA       T TG
                                GGGT   TAAAGAAG A  TA
                                ||||   |||||||| |  ||
                                CCCA   ATTTCTTC T  GT
                                  CCC       _ GT
GAM465   LOC196812 3'  AGTACATGCCATGTACTC    89561         AAAGAA
                                GGGTACAT     GTATGTACT
                                ||||||||     |||||||||
                                CTCATGTA     CGTACATGA
                                     C_____
GAM465   LOC200339 3'  AGTAACTCCTTATGTATCC    90030          A  A  ATG
                                GGGTACATAA GA GT   TACT
                                |||||||||| || ||   ||||
                                CCTATGTATT CT CA   ATGA
                                     C  _  ___
GAM465   LOC200488 5'  ATTTCTTTATATACCT      90082       C
                                GGGTA ATAAAGAAGT
                                ||||| ||||||||||
                                TCCAT TATTTCTTTA
                                   A
GAM465   LOC200982 3'  GTATTTCTCCATGTCCC     90225     T    AA
                                GGG ACAT  AGAAGTAT
                                ||| ||||  ||||||||
                                CCC TGTA  TCTTTATG
                                  _    CC
GAM465   LOC257463 3'  AGTACAGAGAGTTCCTATGTAC 71066          AA  AGTA_
            CC                    GGGTACATA  GA    TGTACT
                                |||||||||  ||    ||||||
                                CCCATGTAT  TT    ACATGA
                                     CC  GAGAG
GAM465   LOC51605  3'  ACATGTCTATGTACCC      31949         AA   AG
                                GGGTACAT  AGA  TATGT
                                ||||||||  |||  |||||
                                CCCATGTA  TCT  GTACA
                                     __   __
GAM465   LOC92336  3'  ATCTTCCTCATGTACCT     68974         AAA    T
                                GGGTACAT   GAAG AT
                                ||||||||   |||| ||
                                TCCATGTA   CTTC TA
                                     CTC    _
GAM466   ROBO1     3'  AAGCCCCTTATTTTTAGC    11372       TG   G
                                GCTAA  GTG AGGGGCTT
                                |||||  ||| ||||||||
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                                CGATT  TAT TCCCCGAA
                                   TT  _
GAM466  ROBO1    3'  AAGCCCCTTATTTTTAGC    56085      TG  G
                                GCTAA  GTG AGGGGCTT
                                |||||  ||| ||||||||
                                CGATT  TAT TCCCCGAA
                                   TT  _
GAM466  CHIT1    3'  AAGCCCCTCCAGTCCAGCTTTG 12948        AAT  __
           A                     TTAAAGCT   GG  TGGAGGGGCTT
                                ||||||||   ||  ||||||||||
                                AGTTTCGA   CC  ACCTCCCCGAA
                                     ___  TG
GAM466  HSPC166  3'  TTTCCAACATTAGCTCTAA   26369     A      G
                                TTA AGCTAATG TGGAGG
                                ||| |||||||| ||||||
                                AAT TCGATTAC ACCTTT
                                  C       A
GAM466  MGC10940 3'  GCCCCTCTGCTTTAA      50216       TAATGGT     _
                                TTAAAGC      GGAGGGG C
                                |||||||      ||||||| |
                                AATTTCG      TCTCCCC G
                                     ________     C
GAM466  UBF-fl   3'  CCCCATAGCTTTAA       51559         A  T
                                TTAAAGCTA TGG GG
                                ||||||||| ||| ||
                                AATTTCGAT ACC CC
                                     _  _
GAM466  LOC169026 3'  TTTTCCACAATTAGCTCTAA  82733     A      G
                                TTA AGCTAAT GTGGAGGG
                                ||| ||||||| ||||||||
                                AAT TCGATTA CACCTTTT
                                  C      A
GAM467  DDEF1    3'  GAGCTTTAGCAGCCTC      59564    A  AGATAC      A
                                GA GCT     CTAAAGCT C
                                || |||     |||||||| |
                                CT CGA     GATTTCGA G
                                 C  C_____       C
GAM467  DDX3     3'  GAGCCTTAGGTATTTG      43759          A  A
                                TAGATACCTAA GCT C
                                |||||||||| ||| |
                                GTTTATGGATT CGA G
                                      C  C
GAM467  GRAF     3'  GGTAACTCCCTCCCTAGCTTC  30573        ATACCTAA  C
                                GAAGCTAG       AG TACC
                                ||||||||       || ||||
                                CTTCGATC       TC ATGG
                                     CCTCCC__  A
GAM467  MAT1A    3'  AGCTTTAGAATCCCAGC     90825     A_  AC
                                GCT  GAT  CTAAAGCT
                                |||  |||  ||||||||
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                                CGA  CTA  GATTTCGA
                                  CC   A_
GAM467  MYLK     3'  AGCTTCAGACATTTGGTT    97018        AC  A
                                AGCTAGAT  CT AAGCT
                                ||||||||  || |||||
                                TTGGTTTA  GA TTCGA
                                    CA  C
GAM467  RGL      3'  GTAGCTAAAACTTAGCTTCA  30736         ATACCTAA
                                TGAAGCTAG       AGCTAC
                                |||||||||       ||||||
                                ACTTCGATT       TCGATG
                                    CAAAA___
GAM467  ZFP93    3'  GTAGCCTTAATAACGTTAGTTT 14887         ATACC_  A
             CA                   TGAAGCTAG     TAA GCTAC
                                |||||||||     ||| |||||
                                ACTTTGATT     ATT CGATG
                                    GCAATA   C
GAM467  C3orf4   3'  AGCATTGACACATAGCTTCA  39118        GATACC   A
                                TGAAGCTA     TAA GCT
                                ||||||||     ||| |||
                                ACTTCGAT     GTT CGA
                                    ACACA_   A
GAM467  D2S448   3'  GGCAGGAGTCCTAGCTTCA   73527         _  A   AAA
                                TGAAGCTAG AT CCT   GCT
                                |||||||| || |||   |||
                                ACTTCGATC TG GGA   CGG
                                    C  A   ___
GAM467  FLJ12604 3'  AGCTTTAGTATTGACTTCA   64436      CTA    C
                                TGAAG   GATAC TAAAGCT
                                |||||   ||||| |||||||
                                ACTTC   TTATG ATTTCGA
                                  AG_    _
GAM467  FLJ14280 5'  GGTAGCTCCTGGCCAGCTCA  45999     A   AGATA  TAA
                                TGA GCT    CC   AGCTACC
                                ||| |||    ||   |||||||
                                ACT CGA    GG   TCGATGG
                                  _  CC___  TCC
GAM467  H2AFJ    3'  GTTGTCAAGTTTCTAGCTTCA 36842         T  CTAA_
                                TGAAGCTAGA AC    AGC
                                |||||||||| ||    |||
                                ACTTCGATCT TG    TTG
                                    T  AACTG
GAM467  KIAA0441 3'  TAGCTTTGTTAATCTAGCCTC  28960    A      ACC
                                GA GCTAGAT   TAAAGCTA
                                || |||||||   ||||||||
                                CT CGATCTA   GTTTCGAT
                                 C      ATT
GAM467  KIAA1128 3'  TAGCTTTATGTGCAGCTTGCA  68483    _    AGA   C
                                TG AAGCT   TAC TAAAGCTA
                                || |||||   ||| ||||||||
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                                AC TTCGA   GTG ATTTCGAT
                                 G    C__   T
GAM467  KIAA1750  3'  TAGCCCCAGGAGTGGGCTTTA  68254       AG  A   AAA
                                TGAAGCT  AT CCT   GCTA
                                |||||||  || |||   ||||
                                ATTTCGG  TG GGA   CGAT
                                    G_  A   CCC
GAM467  KPNA5     3'  GGTAGCTTCAGGTAACT     9629     A    A
                                AG TACCT AAGCTACC
                                || ||||| ||||||||
                                TC ATGGA TTCGATGG
                                 A    C
GAM467  MAGEH1    5'  GGTAGCTTCAGCGGCAGCAGCT 25924       AGATAC_  A
              TC                   GAAGCT      CT AAGCTACC
                                |||||||      || ||||||||
                                CTTCGA      GA TTCGATGG
                                   CGACGGC  C
GAM467  MGC12921  3'  AGCCCTATTTAGCTTC      63774          CCTAAA
                                GAAGCTAGATA     GCT
                                ||||||||||      |||
                                CTTCGATTTAT     CGA
                                      CC____
GAM467  MGC30052  3'  AGCTTTAGAATAGCTTC     58532        GATAC
                                GAAGCTA    CTAAAGCT
                                |||||||    ||||||||
                                CTTCGAT    GATTTCGA
                                    AA___
GAM467  RNF34     3'  AGCAAGGGCTGCATCTAGCTTC 47094         A___   AAA
                                GAAGCTAGAT    CCT   GCT
                                ||||||||||    |||   |||
                                CTTCGATCTA    GGG   CGA
                                      CGTC   AA_
GAM467  TNFRSF19L 3'  GTAGCTTTTATCCCAGC     51779     A_   CCT
                                GCT  GATA   AAAGCTAC
                                |||  ||||   ||||||||
                                CGA  CTAT   TTTCGATG
                                  CC    ___
GAM467  LOC121536 3'  AGCAAATCACATTTAGCTTCA  74082          ACCTAAA
                                TGAAGCTAGAT      GCT
                                ||||||||||      |||
                                ACTTCGATTTA      CGA
                                      CACTAAA
GAM467  LOC255452 3'  TAGGTACCTACCTTCA      97544       C   A
                                TGAAG TAG TACCTA
                                ||||| ||| ||||||
                                ACTTC ATC ATGGAT
                                   C   C
GAM467  LOC257396 3'  GGCAGCTTTAGGCTTAACTT   97139     C   ATA       A
                                AAG TAG   CCTAAAGCT CC
                                ||| |||   ||||||||| ||
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                                TTC ATT   GGATTTCGA GG
                                  A  C__       C
GAM467  LOC92710  3'  GTACAAGGCATCTAGCTT    70359         A   AAAGC
                                AAGCTAGAT CCT     TAC
                                ||||||||| |||     |||
                                TTCGATCTA GGA     ATG
                                     C   AC___
GAM468  KCNJ6     5'  GTTGTGCTGGATATTGC     9532       C       A
                                GCAA ATCCAGCA AAC
                                |||| |||||||| |||
                                CGTT TAGGTCGT TTG
                                  A       G
GAM468  MBP       3'  TTTTGCTGGTCACTGCCA    9953        ACAT
                                TGGCA   CCAGCAAAA
                                |||||   |||||||||
                                ACCGT   GGTCGTTTT
                                   CACT
GAM468  ESPL1     5'  TTTTGCTGGAGCCGCCA     24464      AACA
                                TGGC   TCCAGCAAAA
                                ||||   ||||||||||
                                ACCG   AGGTCGTTTT
                                  CCG_
GAM468  HEY1      3'  CAGCTGGGCTGGACTGTTGCCA 91249         _     AAAA  _
                                TGGCAACA TCCAGC   CTA CTG
                                |||||||| ||||||   ||| |||
                                ACCGTTGT AGGTCG   GGT GAC
                                     C      _____  C
GAM468  HEYL      3'  AGTGGGACCAGTGTTGCCA   27390         CCAGCAAAA
                                TGGCAACAT       CTACT
                                |||||||||       |||||
                                ACCGTTGTG       GGTGA
                                     ACCAG_____
GAM468  IDI1      3'  AGTTATGCCGGATGTTGCCA  67043          A   A
                                TGGCAACATCC GCA AACT
                                |||||||||||| ||| ||||
                                ACCGTTGTAGG CGT TTGA
                                      C   A
GAM468  KIAA1189  3'  TTTGCTAAATGTTGCC     72050         CC
                                GGCAACAT  AGCAAA
                                ||||||||  ||||||
                                CCGTTGTA  TCGTTT
                                   AA
GAM468  KIAA1233  3'  CAGTAGTTGTTAAGATGTTGGC 63080    G      C_   AA
           A                     TG CAACATC  AGCA  ACTACTG
                                 || |||||||  ||||  |||||||
                                 AC GTTGTAG  TTGT  TGATGAC
                                  G      AA   __
GAM468  KIAA1389  3'  CAGTAGTTTTATTTCCACAGCC 69766      AACATCCAGC
           A                     TGGC        AAAACTACTG
                                 ||||        ||||||||||
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                                ACCG        TTTTGATGAC
                                  ACACCTTTA_
GAM468  KIAA1615  3'  TTTGTTAGATGTTGCCA     68741          C
                                TGGCAACATC AGCAAA
                                |||||||||| ||||||
                                ACCGTTGTAG TTGTTT
                                      A
GAM468  Rpo1-2    3'  TTTTGCTGGAGTTACCA     38712     C   A
                                TGG AAC TCCAGCAAAA
                                ||| ||| ||||||||||
                                ACC TTG AGGTCGTTTT
                                  A  _
GAM468  LOC133686 3'  AGTAGTTTTGGAATTGCC    75118      CA    GCA
                                GGCAA  TCCA   AAACTACT
                                |||||  ||||   ||||||||
                                CCGTT  AGGT   TTTGATGA
                                   A_   ___
GAM468  LOC150203 3'  GTCTTGCTGGAGCCA       60519      AACA       A
                                TGGC    TCCAGCAA AC
                                ||||    |||||||| ||
                                ACCG    AGGTCGTT TG
                                   ____       C
GAM468  LOC253150 3'  GTTCCCTGGATGTTGCCA    95519           CAA
                                TGGCAACATCCAG   AAC
                                ||||||||||||   |||
                                ACCGTTGTAGGTC   TTG
                                      CC_
GAM468  LOC254822 5'  AGTAGTTCTGCTTTTGCC    97211      CATCC    A
                                GGCAA     AGCA AACTACT
                                |||||     |||| |||||||
                                CCGTT     TCGT TTGATGA
                                   T____    C
GAM468  LOC254822 5'  AGTAGTTCTGCTTTTGCC    97212      CATCC    A
                                GGCAA     AGCA AACTACT
                                |||||     |||| |||||||
                                CCGTT     TCGT TTGATGA
                                   T____    C
GAM469  ACADVL    3'  CCAGTTATGTGCCTTCCCTCAA 3413     G   A      ____
          G                      CT GAG GAAGGCAC    TTGG
                                || ||| ||||||||    ||||
                                GA CTC CTTCCGTG    GACC
                                 A   C       TATT
GAM469  ALDH3B1   3'  TCCCTCTTCTCTCCAG      91533          CACTT
                                CTGGAGAGAAGG     GGA
                                ||||||||||||     |||
                                GACCTCTCTTCT     CCT
                                      C____
GAM469  ALPPL2    3'  CCCTGCTCCCCACCTCCAGTC  68840        AGAA__    CTT
                                GACTGGAG     GGCA   GG
                                ||||||||     ||||   ||
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                                CTGACCTC     TCGT   CC
                                     CACCCC    C__
GAM469  APOD     5'  TCCAGGTCCCTTCTCCAG    7918        GA   C
                                CTGGAGA  AGG ACTTGGA
                                |||||||  ||| |||||||
                                GACCTCT  TCC TGGACCT
                                     __   C
GAM469  APXL     3'  TTCCTCCTCCTCTCCAG     7933         A   CACTT
                                CTGGAGAG AGG    GGAA
                                |||||||| |||    ||||
                                GACCTCTC TCC    CCTT
                                     C   T____
GAM469  AR       5'  TTCCCCCCCTCCCCCGTC    3497      T  A   AA  CACTT
                                GAC GG GAG  GG    GGAA
                                ||| || |||  ||    ||||
                                CTG CC CTC  CC    CCTT
                                  C  C   CC  _____
GAM469  ARHGEF1  3'  CCAAGTGCCTTCGCTC      16299     A
                                GAG GAAGGCACTTGG
                                ||| ||||||||||||
                                CTC CTTCCGTGAACC
                                  G
GAM469  ASIC4    3'  TTCCTGCCCCTCTCCAG     37923        AA    CTT
                                CTGGAGAG  GGCA   GGAA
                                ||||||||  ||||   ||||
                                GACCTCTC  CCGT   CCTT
                                     C_    ___
GAM469  BCL6     5'  CCACTTCCTTCCCTCCAGTC   57221        A    CACT
                                GACTGGAG GAAGG    TGG
                                |||||||| |||||    |||
                                CTGACCTC CTTCC    ACC
                                     C    TTC_
GAM469  CABC1    5'  TCCACAGACTTCTCTTCAG    39659          GCACT
                                CTGGAGAGAAG    TGGA
                                ||||||||||     ||||
                                GACTTCTCTTC    ACCT
                                       AGAC_
GAM469  CACNA2D2 3'  TCCAAGTGCCCCCTCACCTCTC 20088    CT  A   AA
                                GA  GG GAG  GGCACTTGGA
                                ||  || |||  ||||||||||
                                CT  CC CTC  CCGTGAACCT
                                 CT  A   CC
GAM469  CALCR    3'  TCCAAATCTCCAGTC       8222          GAAGGCAC
                                GACTGGAGA       TTGGA
                                |||||||||       |||||
                                CTGACCTCT       AACCT
                                     A_______
GAM469  CD3E     3'  CCCAGGTCTCCTCTCCAGTC   5589          A   A  T
                                GACTGGAGAG AGGC CT GG
                                |||||||||| |||| || ||
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                                CTGACCTCTC TCTG GA CC
                                     C   _ C
GAM469  CDH5     3'  CCAACCCCTCTCCAG      8385         AA  CAC
                                CTGGAGAG  GG   TTGG
                                ||||||||  ||   ||||
                                GACCTCTC  CC   AACC
                                     C_  ___
GAM469  CENTD2   3'  TTCAGCCTTCCTTCCAGTC   30878        A     ACT
                                GACTGGAG GAAGGC   TGGA
                                |||||||| ||||||   ||||
                                CTGACCTT CTTCCG   ACTT
                                     C     ___
GAM469  CENTD2   3'  TTCAGCCTTCCTTCCAGTC   57559        A     ACT
                                GACTGGAG GAAGGC   TGGA
                                |||||||| ||||||   ||||
                                CTGACCTT CTTCCG   ACTT
                                     C     ___
GAM469  CGTHBA   3'  CCTACGCTTCCCTCCAGTC   23861        A   G ACTT
                                GACTGGAG GAAG C    GG
                                |||||||| |||| |    ||
                                CTGACCTC CTTC G    CC
                                     C    _ CAT_
GAM469  CLCN4    5'  CTTCCAGGGTCTTCCCCCCA  8444      AGA     A
                                TGG   GAAGGC CTTGGAAG
                                |||   |||||| ||||||||
                                ACC   CTTCTG GGACCTTC
                                  CCC     _
GAM469  COL1A1   3'  TTCCACCCTCTCTCCA      3610         A  CACT
                                TGGAGAGA GG    TGGAA
                                |||||||| ||    |||||
                                ACCTCTCT CC    ACCTT
                                     C  _____
GAM469  DIRC1    3'  CCTCTTGCACTTTCTCTCCAGT 53666          _ _   CTT
              C                  GACTGGAGAGAA G GCA   GG
                                ||||||||||||| | |||   ||
                                CTGACCTCTCTT C CGT   CC
                                       T A   TCT
GAM469  EGFL3    3'  CCGTGGAGCCCGCCTCTCCAGT 62614          AA_   A  _
              C                  GACTGGAGAG   GGC CT TGG
                                ||||||||||   ||| || |||
                                CTGACCTCTC   CCG GG GCC
                                     CGC   A  T
GAM469  EPB49    3'  CTTCCAAGCCTTTTGCTCCAG  8786        _      AC
                                CTGGAG AGAAGGC  TTGGAAG
                                ||||||  |||||||  |||||||
                                GACCTC TTTTCCG  AACCTTC
                                   G     ___
GAM469  EPHA2    3'  CCAAGCCGACCTTCCCTCC    15402      A    CA__
                                GGAG GAAGG    CTTGG
                                ||||  |||||    |||||
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                                CCTC CTTCC   GAACC
                                  C    AGCC
GAM469  FGR     3'  TCCCTCACTTCTCTCCTATC  17897   CT      GCACTT
                                GA  GGAGAGAAG    GGA
                                ||  |||||||||    |||
                                CT  CCTCTCTTC    CCT
                                 AT       ACTC__
GAM469  GPR86   3'  TCCAAACACCTTCTCACATTC  43652   C  GA     CAC
                                GA TG  GAGAAGG   TTGGA
                                || ||  |||||||   |||||
                                CT AC  CTCTTCC   AACCT
                                 T  A_     ACA
GAM469  GRAF    3'  CTTTCAGGTACCCCCTCCCCAG 30559     A   AA  C
                                CTGG GAG  GG ACTTGGAAG
                                |||| |||  || |||||||||
                                GACC CTC  CC TGGACTTTC
                                  C   CC  A
GAM469  GSTT2   3'  CCCAGTCCCTTCTCTCCAG   5959          C   T
                                CTGGAGAGAAGG ACT GG
                                |||||||||||| ||| ||
                                GACCTCTCTTCC TGA CC
                                       C   C
GAM469  KRT5    3'  CTTCCAAGTGCAGCAACCCAG  4711      AGAGAAG
                                CTGG      GCACTTGGAAG
                                ||||      ||||||||||
                                GACC      CGTGAACCTTC
                                  CAACGA_
GAM469  LOXL2   3'  CTTCCAATGAAACCCTCCAGTC 9795        AGAAGG  C
                                GACTGGAG     CA TTGGAAG
                                ||||||||     || |||||||
                                CTGACCTC     GT AACCTTC
                                    CCAAA_  _
GAM469  LY95    5'  CCAATTCCCTCTCCCCAGTC   16703       A   A  CAC
                                GACTGG GAGA GG   TTGG
                                |||||| |||| ||   ||||
                                CTGACC CTCT CC   AACC
                                   C   C  TT_
GAM469  MAF     5'  CCCCTCCCTCTCCTCCAGTC   18098        _  A  CACTT
                                GACTGGAG AGA GG    GG
                                |||||||| ||| ||    ||
                                CTGACCTC TCT CC    CC
                                    C   C  TCC__
GAM469  MGAT1   3'  TCCTGCCCTTCTCTCCTGTC   10012    T       _ CTT
                                GAC GGAGAGAAGG CA   GGA
                                ||| ||||||||| ||   |||
                                CTG CCTCTCTTCC GT   CCT
                                  T        C ___
GAM469  MPP1    5'  TCCCGCCTTCTCCGCAG     10112     GA      ACTT
                                CTG  GAGAAGGC    GGA
                                |||  ||||||||    |||
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                                GAC  CTCTTCCG   CCT
                                  GC       C___
GAM469  NOS1    3'  CCAAAGGCTTTCTTTCCAATC  5246     C          AC
                                GA TGGAGAGAAGGC  TTGG
                                || ||||||||||||  ||||
                                CT ACCTTTCTTTCG  AACC
                                 A          GA
GAM469  NPM1    5'  TCCGTCCGCCTTCTCTCC    10252          ACT
                                GGAGAGAAGGC   TGGA
                                ||||||||||   ||||
                                CCTCTCTTCCG   GCCT
                                       CCT
GAM469  NRXN3   5'  TCCTCTTTCCCTCCAGTC    57281        A    CACTT
                                GACTGGAG GAAGG    GGA
                                |||||||| |||||    |||
                                CTGACCTC CTTTC    CCT
                                     C    T____
GAM469  OTP     3'  CCGCCGCCTCCCCTCCGGTC  49495        AGA   ACT
                                GACTGGAG   AGGC   TGG
                                ||||||||   ||||   |||
                                CTGGCCTC   TCCG   GCC
                                     CCC    CC_
GAM469  PES1    3'  TCCTCCTTTCTCCAG       26672         A  CACTT
                                CTGGAGAGA GG    GGA
                                |||||||| ||    |||
                                GACCTCTTT CC    CCT
                                      _ T____
GAM469  PGM1    3'  AGTGCCTTCTGTCCAATC    10537    C   G
                                GA TGGA AGAAGGCACT
                                || |||| ||||||||||
                                CT ACCT TCTTCCGTGA
                                 A   G
GAM469  PKIG    3'  CCAACACCTCCTCTCCAG    22959        A  CAC
                                CTGGAGAG AGG   TTGG
                                |||||||| |||   ||||
                                GACCTCTC TCC   AACC
                                     C   AC_
GAM469  PKLR    3'  CCATCCCTTCCTCCCCAGTC  4315       A  _   CACT
                                GACTGG GAG AAGG   TGG
                                |||||| ||| ||||   |||
                                CTGACC CTC TTCC   ACC
                                   C   C   CT__
GAM469  PRDM1   5'  CCAAGTGTAACTCCAGC     6826    A     AGAAG
                                G CTGGAG    GCACTTGG
                                | ||||||    ||||||||
                                C GACCTC    TGTGAACC
                                 _     AA___
GAM469  RARA    3'  CCCAGTTCTCCTCCTCAG    6365     GA  A  C  T
                                CTG  GAG AGG ACT GG
                                |||  ||| ||| ||| ||
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                                GAC  CTC TCT TGA CC
                                  TC   C  _  C
GAM469  RFX1    3'  CCCAGCGTCTTCTCCCCAG   11309     A      A  T
                                CTGG GAGAAGGC CT GG
                                |||| |||||||| || ||
                                GACC CTCTTCTG GA CC
                                  C       C  C
GAM469  RORB    5'  TTCCTCCTCCTCCTCAGTC   22612     GA   A   CACTT
                                GACTG  GAG AGG    GGAA
                                |||||  ||| |||    ||||
                                CTGAC  CTC TCC    CCTT
                                   TC   C   T____
GAM469  SAC     5'  CCGGCCTCCTCTCCTGTC    37313    T    A    ACT
                                GAC GGAGAG AGGC   TGG
                                ||| |||||| ||||   |||
                                CTG CCTCTC TCCG   GCC
                                  T     C   ___
GAM469  SEPN1   3'  CAGGCTGCCCCCTCCCCAG   66364     A   AA   _
                                CTGG GAG  GGCA CTTG
                                |||| |||  |||| ||||
                                GACC CTC  CCGT GGAC
                                  C   CC    C
GAM469  SNAI2   3'  CTTCCAAGTGCCTTTTT     11775
                                GAGAAGGCACTTGGAAG
                                |||||||||||||||||
                                TTTTTCCGTGAACCTTC

GAM469  SNRP70  5'  CCACCCCCTGCTCCAGTC    78547        _  AA  CACT
                                GACTGGAG AG  GG   TGG
                                |||||||| ||  ||   |||
                                CTGACCTC TC  CC   ACC
                                     G  CC  ____
GAM469  SOX13   3'  CCCCGTCTTCTCTCCATC    19082    C         ACTT
                                GA TGGAGAGAAGGC   GG
                                || ||||||||||||   ||
                                CT ACCTCTCTTCTG   CC
                                 _          CC__
GAM469  SOX13   3'  CCACTTCTCTCCAG        19081          GCACT
                                CTGGAGAGAAG    TGG
                                ||||||||||     |||
                                GACCTCTCTTC    ACC
                                          _____
GAM469  TBL3    3'  TCCGGCCTCTCTCCAGTC    21267          A   ACT
                                GACTGGAGAGA GGC   TGGA
                                |||||||||| |||   ||||
                                CTGACCTCTCT CCG   GCCT
                                          _  ___
GAM469  TNFAIP1 5'  CTTCCAAGCCTACCTCC     40920     AGA   AC
                                GGAG   AGGC  TTGGAAG
                                ||||   ||||  |||||||
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                                CCTC  TCCG  AACCTTC
                                  CA_   __
GAM469  UBE2L3   3' CCACACCCCTCCTCCAGTC   12499       A  A  CACT
                                GACTGGAG GA GG   TGG
                                |||||||| || ||   |||
                                CTGACCTC CT CC   ACC
                                     _ C  CAC_
GAM469  UBE4A    3' CCATGCTGCCTCCAGTC    16562       AGAA   CT
                                GACTGGAG   GGCA  TGG
                                ||||||||   ||||  |||
                                CTGACCTC   TCGT  ACC
                                     CG__   __
GAM469  ALOXE3   3' CTTCCAAGCCTAGAGCCACCAG 41264     AGAGA__   AC
                                CTGG      AGGC  TTGGAAG
                                ||||      ||||  |||||||
                                GACC      TCCG  AACCTTC
                                  ACCGAGA   __
GAM469  AMOT     3' TTCCAAGTGCCATCCA     55730     GAGAA
                                TGGA    GGCACTTGGAA
                                ||||    ||||||||||
                                ACCT    CCGTGAACCTT
                                  A____
GAM469  ARHGAP4  3' CCCCTTGCTTCTCTCCAG    8019          G  CTT
                                CTGGAGAGAAG CA   GG
                                |||||||||| ||   ||
                                GACCTCTCTTC GT   CC
                                      _ TCC
GAM469  ART5     3' CCTAGCAGCCTTCTCCCCA   53814     A      A_  T
                                TGG GAGAAGGC  CT GG
                                ||| ||||||||  || ||
                                ACC CTCTTCCG  GA CC
                                  C       AC  T
GAM469  ASB16    3' TTCAGACCCTCTCTCCAGC   55111   A       A  CAC
                                G CTGGAGAGA GG   TTGGA
                                | |||||||||| ||   |||||
                                C GACCTCTCT CC   GACTT
                                 _       C  A__
GAM469  C20orf142 3' TTGATGCCCCTCTCTCCAATC  74790    C       A_   C TG
                                GA TGGAGAGA  GGCA T  G
                                || ||||||||  |||| |  |
                                CT ACCTCTCT  CCGT A  T
                                 A       CC    _ GT
GAM469  DKFZP434H132 5' TCCCAGCACCCTCTCCAG    73609        AA  CA  T
                                CTGGAGAG  GG  CT GGA
                                ||||||||  ||  || |||
                                GACCTCTC  CC  GA CCT
                                     __  AC  C
GAM469  DKFZP566H073 3' CCGTCGTCTTCCCTCCAGTC  31381         A     ACT
                                GACTGGAG GAAGGC   TGG
                                |||||||| ||||||   |||
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                                CTGACCTC CTTCTG   GCC
                                    C     CT_
GAM469  E1B-AP5  3'  TCCCACTGCCTCCTCTCCAGT  58570        A    CTT
                                ACTGGAGAG AGGCA   GGA
                                ||||||||| |||||   |||
                                TGACCTCTC TCCGT   CCT
                                    C     CAC
GAM469  E1B-AP5  3'  TCCCACTGCCTCCTCTCCAGT  22904        A    CTT
                                ACTGGAGAG AGGCA   GGA
                                ||||||||| |||||   |||
                                TGACCTCTC TCCGT   CCT
                                    C     CAC
GAM469  E2IG4    3'  CCAAGTGCCTTCCCTC      90909     A
                                GAG GAAGGCACTTGG
                                ||| ||||||||||||
                                CTC CTTCCGTGAACC
                                  C
GAM469  EPN2     3'  CTGAGGCCGCCCTCTCCAGTC  30323        AA_   A  TG
                                GACTGGAGAG   GGC CT  G
                                ||||||||||   ||| ||  |
                                CTGACCTCTC   CCG GA  C
                                     CCG   _  GT
GAM469  EPN2     3'  CTTCCAAGGCAGGCCCCTC   30325     AA   A___
                                GAG  GGC    CTTGGAAG
                                |||  |||    ||||||||
                                CTC  CCG    GAACCTTC
                                  C_   GACG
GAM469  FLJ10700 3'  CCTCTCGTCCTCCCCTCCAGC  36427   A     A_  A   ACTT
                                G CTGGAG  GA GGC    GG
                                | ||||||  || |||    ||
                                C GACCTC  CT CTG    CC
                                _     CC  C   CTCT
GAM469  FLJ11320 3'  CCCCTCCCTCTCCAGTC     37244         A_   CACTT
                                GACTGGAGAG  AGG    GG
                                ||||||||||  |||    ||
                                CTGACCTCTC  TCC    CC
                                     CC   _____
GAM469  FLJ12595 3'  TCCCACTGTTCTCTCCACTC   46507    C      AG   CTT
                                GA TGGAGAGA  GCA   GGA
                                || ||||||||  |||   |||
                                CT ACCTCTCT  TGT   CCT
                                 C       __   CAC
GAM469  FLJ12650 3'  TTCCTCTCTTCTCCAG      44531       GA   CACTT
                                CTGGAGA  AGG    GGAA
                                |||||||  |||    ||||
                                GACCTCT  TCT    CCTT
                                    TC   _____
GAM469  FLJ14100 5'  CCTCGCCCTCTCCAGTC     46677         AA   ACTT
                                GACTGGAGAG  GGC    GG
                                ||||||||||  |||    ||
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                                CTGACCTCTC  CCG   CC
                                     __  CT__
GAM469  FLJ14827  3'  CTAAGATGCCTCTCTCCAG   51652        A   _
                                CTGGAGAGA GGCA CTTGG
                                ||||||||| |||| |||||
                                GACCTCTCT CCGT GAATC
                                     _   A
GAM469  FLJ21034  3'  CCATGCCACCTCCCTTCCAGTC 46293       ___  AA   CT
                                GACTGGA  GAG  GGCA  TGG
                                |||||||  |||  ||||  |||
                                CTGACCT  CTC  CCGT  ACC
                                   TCC  CA  __
GAM469  FLJ22596  5'  CCACCTTCTCTCCA       46960          CACT
                                TGGAGAGAAGG   TGG
                                ||||||||||   |||
                                ACCTCTCTTCC   ACC

                                     ____
GAM469  GEMIN7   3'  TCCTCTCTTCTCTCCAG    45236          CACTT
                                CTGGAGAGAAGG    GGA
                                ||||||||||||    |||
                                GACCTCTCTTCT    CCT
                                      CT___
GAM469  ITGB8    5'  CTTGCAGAGCCCTCTCTCCAGT 9406          A  A  T G
          C                      GACTGGAGAGA GGC CT G AAG
                                ||||||||||| ||| || | |||
                                CTGACCTCTCT CCG GA C TTC
                                      C  A  _ G
GAM469  KIAA0321  3'  TCCTGCTTCCCTTCAGTC    62398       A   G  CTT
                                GACTGGAG GAAG CA   GGA
                                |||||||| |||| ||   |||
                                CTGACTTC CTTC GT   CCT
                                   C   _ ___
GAM469  KIAA0436  3'  TCCAGGCCTCCCTTCCAGTC   60057       AGA   A  T
                                GACTGGAG   AGGC CT GGA
                                ||||||||   |||| || |||
                                CTGACCTT   TCCG GA CCT
                                   CCC   _ _
GAM469  KIAA0574  3'  CCCAGAGCCTTCCTCCAGTC   69280       A    A  T
                                GACTGGAG GAAGGC CT GG
                                |||||||| |||||| || ||
                                CTGACCTC CTTCCG GA CC
                                   _    A  C
GAM469  KIAA1049  5'  CTTCCTTCTCCCTCTCTCCAG  30365       A  CACTT
                                CTGGAGAGA GG    GGAAG
                                ||||||||| ||    |||||
                                GACCTCTCT CC    CCTTC
                                   C  TCTT_
GAM469  KIAA1128  3'  TCCCCCATCTCCAGTC     68484        GAA  CACTT
                                GACTGGAGA   GG    GGA
                                |||||||||   ||    |||
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                                CTGACCTCT  CC    CCT
                                     AC_ _____
GAM469  KIAA1183 3' CTGGGTGCCCCCTCTCCAGT  62533       AA    TG
                                ACTGGAGAG  GGCACT  G
                                |||||||||  ||||||  |
                                TGACCTCTC  CCGTGG  C
                                     CC    GT
GAM469  KIAA1190 3' CCAAGTGCCCCCCCTTTCT   71099     AA__
                                GGAGAG   GGCACTTGG
                                ||||||   |||||||||
                                TCTTTC   CCGTGAACC
                                   CCCC
GAM469  KIAA1271 3' CCTGTGGAGCTCCTCTCCAG  69541      A  G__  TT
                                CTGGAGAG AG  CAC  GG
                                |||||||| ||  |||  ||
                                GACCTCTC TC  GTG  CC
                                     C  GAG  T_
GAM469  KIAA1538 3' TTCCATCCCTTCTCCAG    71562      GA  CACT
                                CTGGAGA  AGG   TGGAA
                                |||||||  |||   |||||
                                GACCTCT  TCC   ACCTT
                                   __  CT__
GAM469  KIAA1656 3' CCACTTCCTTCCAGTC     65787      A   GCACT
                                GACTGGAG GAAG    TGG
                                |||||||| ||||    |||
                                CTGACCTT CTTC    ACC
                                     C  _____
GAM469  KIAA1762 5' CCAACCCCCTTCTCCAG    63789      GA  CAC
                                CTGGAGA  AGG  TTGG
                                |||||||  |||  ||||
                                GACCTCT  TCC  AACC
                                   __  CCC
GAM469  KIAA1762 5' TCCAGCCCCATCTCCAGTC  63791       GAA  ACT
                                GACTGGAGA  GGC  TGGA
                                |||||||||  |||  ||||
                                CTGACCTCT  CCG  ACCT
                                     ACC  ___
GAM469  KIAA1817 5' CCAACCCATCTCTCCA     68224      A  CAC
                                TGGAGAGA GG  TTGG
                                |||||||| ||  ||||
                                ACCTCTCT CC  AACC
                                     A  C__
GAM469  KIAA1855 3' TCCGACCCCTTTCCAG     92347      AA  CAC
                                CTGGAGAG  GG  TTGGA
                                ||||||||  ||  |||||
                                GACCTTTC  CC  AGCCT
                                     C_  ___
GAM469  KIAA1881 3' CTTCCCAAGCCTTCTCCTCAG 95341    GA     ACTT
                                CTG  GAGAAGGC   GGAAG
                                |||  ||||||||   |||||
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                                GAC  CTCTTCCG   CCTTC
                                  TC       AAC_
GAM469  KIAA1887  5'  CCAAGGGGCAATGCCCCCTCTC 76772        AA   _______
              CAG                   CTGGAGAG  GGCA     CTTGG
                                |||||||| ||||     |||||
                                GACCTCTC  CCGT     GAACC
                                    CC    AACGGG
GAM469  KLHL6    3'  CCTCTCACCCTCCTCCAGTC   55301        A  A  CACTT
                                GACTGGAG GA GG     GG
                                |||||||| || ||     ||
                                CTGACCTC CT CC     CC
                                    _ C  ACTCT
GAM469  LIP8     5'  CCTCCCTTCTCCCAAGTC    88149      _ A      CACTT
                                GACT GG GAGAAGG     GG
                                |||| || |||||||     ||
                                CTGA CC CTCTTCC     CC
                                  A _      CT___
GAM469  MAPK8IP2  3'  CTTCCAAGTGATGCCCTCC   57466     AGAAGG
                                GGAG     CACTTGGAAG
                                ||||     ||||||||||
                                CCTC     GTGAACCTTC
                                  CCGTA_
GAM469  MAPK8IP2  3'  CTTCCAAGTGATGCCCTCC   33156     AGAAGG
                                GGAG     CACTTGGAAG
                                ||||     ||||||||||
                                CCTC     GTGAACCTTC
                                  CCGTA_
GAM469  MAPK8IP2  3'  CTTCCAAGTGATGCCCTCC   24657     AGAAGG
                                GGAG     CACTTGGAAG
                                ||||     ||||||||||
                                CCTC     GTGAACCTTC
                                  CCGTA_
GAM469  MGC4707  3'  CCAGCCTCCTCTCCAGC     44117   A      A    ACT
                                G CTGGAGAG AGGC   TGG
                                | |||||||| ||||   |||
                                C GACCTCTC TCCG   ACC
                                _       C    ____
GAM469  MGC5457  5'  TCCTTGCTCCTTTCCAGTC   50948         AA   CTT
                                GACTGGAGAG  GGCA   GGA
                                ||||||||||  ||||   |||
                                CTGACCTTTC  TCGT   CCT
                                    C_    T__
GAM469  MGC5590  3'  TCCCATCTCTCTCCCAGTC   43928       A    AG CACTT
                                GACTGG GAGA  G     GGA
                                |||||| ||||  |     |||
                                CTGACC CTCT  C     CCT
                                   _    CT TAC__
GAM469  MUC16    3'  CCTGGGGTGCCTTTCCCCCAG  60528      AGA        __
                                CTGG   GAAGGCACTT  GG
                                ||||   ||||||||||  ||
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                                GACC   TTTCCGTGGG  CC
                                  CCC         GT
GAM469  PP1201   3'  TTGAGGCCCATCTCTCCAG   42195         A_   A  TG
                                CTGGAGAGA  GGC CT  G
                                |||||||||  ||| ||  |
                                GACCTCTCT  CCG GA  T
                                     AC   _  GT
GAM469  RGS11    3'  CCAAGTGCCTCACCAGTC    13824       A  GAA
                                GACTGG GA   GGCACTTGG
                                ||||||  ||   |||||||||
                                CTGACC CT   CCGTGAACC
                                   A  ___
GAM469  RIP5     3'  CCAAGTGCTCCCTATCCAGTC  38124       G  AA
                                GACTGGA AG  GGCACTTGG
                                |||||||  ||  |||||||||
                                CTGACCT TC  TCGTGAACC
                                     A  CC
GAM469  SAE1     3'  TTCCAAGCACCCCTCTGCC    18536    _   AA  CA
                                GG AGAG  GG  CTTGGAA
                                ||  ||||  ||  |||||||
                                CC TCTC  CC  GAACCTT
                                 G   C_  AC
GAM469  SCYD1    3'  CTGAGGCCCTTCTCTCCAG    90930          CA  TG
                                CTGGAGAGAAGG  CT  G
                                ||||||||||||  ||  |
                                GACCTCTCTTCC  GA  C
                                      CG  GT
GAM469  SEC24B   5'  CTTCCTCTCTCCTCTCCGG    20898        A   CACTT
                                CTGGAGAG AGG    GGAAG
                                ||||||||  |||    |||||
                                GGCCTCTC TCT    CCTTC
                                     C   CT___
GAM469  SLC12A5  3'  CTTCCCACCCTCCTCTCCAGTC 40380          A   CACTT
                                GACTGGAGAG AGG    GGAAG
                                ||||||||||  |||    |||||
                                CTGACCTCTC TCC    CCTTC
                                      C   CAC__
GAM469  SNTA1    3'  CTTCCTGCTGCCCCCCTCCA   11858      AGAA   CTT
                                TGGAG   GGCA   GGAAG
                                |||||   ||||   |||||
                                ACCTC   CCGT   CCTTC
                                   CCC_    CGT
GAM469  TESK2    3'  CCAGACCCTCTCCAGT      63180         AA  CAC
                                ACTGGAGAG  GG   TTGG
                                |||||||||  ||   ||||
                                TGACCTCTC  CC   GACC
                                     __  A__
GAM469  TRIM5    3'  TCCCAGTTTTCTCTCAAGTC   52363      G        ACTT
                                GACT GAGAGAAGGC    GGA
                                ||||  ||||||||||    |||
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                                CTGA CTCTCTTTTG   CCT
                                  A       AC__
GAM469  WBSCR23  3'  CCGTGCACCTCCACCTCCAG  46755      A__  AG_   TT
                                CTGGAG  GA  GCAC  GG
                                ||||||  ||  ||||  ||
                                GACCTC  CT  CGTG  CC
                                   CAC  CCA   __
GAM469  ZDHHC7   5'  TCGCACCGCCCCGCTCTCCAG  34846       AA_  ACT  _
                                CTGGAGAG  GGC  TG GA
                                ||||||||  |||  || ||
                                GACCTCTC  CCG  AC CT
                                    GCC  CC_  G
GAM469  LOC112476 3'  TCCCTGCACTTCTTCCAG   59116      G   _  CTT
                                CTGGA AGAAG GCA  GGA
                                ||||| ||||| |||  |||
                                GACCT TCTTC CGT  CCT
                                  _   A  C__
GAM469  LOC120425 5'  TCCCCGCTCCACTCCAGTC   74010       AGAA  ACTT
                                GACTGGAG   GGC   GGA
                                ||||||||   |||   |||
                                CTGACCTC   TCG   CCT
                                    ACC_  CC__
GAM469  LOC126123 5'  TCCGCCCTCATCCCCAGTC   74437      A _ A  ACTT
                                GACTGG GA GA GGC   GGA
                                |||||| || || |||   |||
                                CTGACC CT CT CCG   CCT
                                   C  A  C  _____
GAM469  LOC144147 3'  CTTCTCACCTCCTCTCTAG   71730       A  CACTT
                                CTGGAGAG AGG    GGAAG
                                |||||||| |||    |||||
                                GATCTCTC TCC    TCTTC
                                    C  AC___
GAM469  LOC145725 5'  CCACAGCCCCACTCTCCAG   77401       AA_  ACT
                                CTGGAGAG  GGC  TGG
                                ||||||||  |||  |||
                                GACCTCTC  CCG  ACC
                                    ACC  AC_
GAM469  LOC145732 5'  CCACAGCCCCACTCTCCAG   77423       AA_  ACT
                                CTGGAGAG  GGC  TGG
                                ||||||||  |||  |||
                                GACCTCTC  CCG  ACC
                                    ACC  AC_
GAM469  LOC145813 5'  TCCAACATTCTCCCAATC   83513   C  A   GGCAC
                                GA TGG GAGAA    TTGGA
                                || ||| |||||    |||||
                                CT ACC CTCTT    AACCT
                                 A  _    AC___
GAM469  LOC146733 5'  CTTCCAAGATTCTTCCCTCCAT 83763   C    A    CA
          TC                    GA TGGAG GAAGG  CTTGGAAG
                                || ||||| |||||  ||||||||
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                                CT ACCTC CTTCT  GAACCTTC
                                 T    C    TA
GAM469  LOC149132 5'  TCCCAGCCTTCTCTCCAG    79179          ACTT
                                CTGGAGAGAAGGC   GGA
                                ||||||||||||   |||
                                GACCTCTCTTCCG   CCT
                                      AC__
GAM469  LOC149606 3'  CTTCCATTCCTCTCTCTA    79451       A  CACT
                                TGGAGAGA GG   TGGAAG
                                |||||||| ||   ||||||
                                ATCTCTCT CC   ACCTTC
                                    _ TT__
GAM469  LOC150793 3'  TCCCTTTCCCCCTCTCTCCAG 80014       A  CACTT_
                                CTGGAGAGA GG     GGA
                                ||||||||| ||     |||
                                GACCTCTCT CC     CCT
                                     C  CCTTTC
GAM469  LOC151996 5'  GAGCACCTTCCTCTCCAG    85533       _   CA
                                CTGGAGAG AAGG  CTT
                                |||||||| ||||  |||
                                GACCTCTC TTCC  GAG
                                    C    AC
GAM469  LOC158364 5'  CTTCCCTACACTTCTCTCCA  81876        GCACTT
                                TGGAGAGAAG     GGAAG
                                ||||||||||     |||||
                                ACCTCTCTTC     CCTTC
                                      ACATC_
GAM469  LOC158856 5'  CCACACCCCTCCCCAGTC    86913      A   AA  CACT
                                GACTGG GAG  GG    TGG
                                |||||| |||  ||    |||
                                CTGACC CTC  CC    ACC
                                   C   C_  AC__
GAM469  LOC162427 3'  CCAAGGGAGGCTTCTCTCCA  82349        GCA__
                                TGGAGAGAAG    CTTGG
                                ||||||||||    |||||
                                ACCTCTCTTC    GAACC
                                      GGAGG
GAM469  LOC196478 5'  CCACGGGCCCTCCCCCA     87725     A_  AA  A  _
                                TGG  GAG  GGC CT TGG
                                |||  |||  ||| || |||
                                ACC  CTC  CCG GG ACC
                                  CC   __   _  C
GAM469  LOC196957 5'  CCACAGCCCCACTCTCCAG   87818       AA_  ACT
                                CTGGAGAG   GGC   TGG
                                ||||||||   |||   |||
                                GACCTCTC   CCG   ACC
                                     ACC   AC_
GAM469  LOC196961 5'  CCACAGCCCCACTCTCCAG   87839       AA_  ACT
                                CTGGAGAG   GGC   TGG
                                ||||||||   |||   |||
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                                GACCTCTC  CCG  ACC
                                    ACC  AC_
GAM469  LOC197138 5'  CCACAGCCCCACTCTCCAG   87912       AA_  ACT
                                CTGGAGAG  GGC  TGG
                                ||||||||  |||  |||
                                GACCTCTC  CCG  ACC
                                    ACC  AC_
GAM469  LOC200312 3'  TTTGGGACCTTCTCTGCAATC  89998   C  G     CA  TG
                                GA TG AGAGAAGG  CT  GA
                                || || ||||||||  ||  ||
                                CT AC TCTCTTCC  GG  TT
                                 A  G      A_  GT
GAM469  LOC203504 5'  TCCCACACCCCTCCCCAGTC  90643      A  AA  CACTT
                                GACTGG GAG  GG    GGA
                                ||||||| |||  ||    |||
                                CTGACC CTC  CC    CCT
                                   C  C_  ACAC_
GAM469  LOC220739 3'  AGTGCCTTCCTCCAG      92924      A
                                CTGGAG GAAGGCACT
                                ||||||| |||||||||
                                GACCTC CTTCCGTGA
                                  _
GAM469  LOC220954 5'  CCAGCCACCTTGTCTCCAGTC  93140       G   CAC
                                GACTGGAGA AAGG  TTGG
                                ||||||||| ||||  ||||
                                CTGACCTCT TTCC  GACC
                                     G   ACC
GAM469  LOC221922 5'  CCATGCCTCTCCAG      92689      GAA  CT
                                CTGGAGA  GGCA  TGG
                                |||||||  ||||  |||
                                GACCTCT  CCGT  ACC
                                   ___  __
GAM469  LOC254263 3'  CCCAGGCTCTTTCTCCAG   94716       AG  A  T
                                CTGGAGAGA  GC CT GG
                                |||||||||  || || ||
                                GACCTCTTT  CG GA CC
                                     CT  _  C
GAM469  LOC255975 5'  TCCCAGCCTTCTCTCCAG   95899         ACTT
                                CTGGAGAGAAGGC   GGA
                                ||||||||||||   |||
                                GACCTCTCTTCCG   CCT
                                       AC__
GAM469  LOC51762  5'  TCCCCGCCTCTCTCCA     33270       A  ACTT
                                TGGAGAGA GGC   GGA
                                |||||||| |||   |||
                                ACCTCTCT CCG   CCT
                                     _  CC__
GAM469  LOC58486  5'  TCCCCTCCCCCTCCAGTC   41083       AGA_  CACTT
                                GACTGGAG   AGG   GGA
                                ||||||||   |||   |||
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                                CTGACCTC   TCC    CCT
                                    CCCC  _____
GAM469  LOC90591  3'  CCGGCCTTCTCCCCATTC   63419   C  A      ACT
                                GA TGG GAGAAGGC  TGG
                                || ||| ||||||||  |||
                                CT ACC CTCTTCCG  GCC
                                 T  C      ___
GAM469  LOC91373  3'  TCCTGCCTTCTCCCCA     65845    A       CTT
                                TGG GAGAAGGCA  GGA
                                ||| |||||||||  |||
                                ACC CTCTTCCGT  CCT
                                  C       ___
GAM470  ADD2      3'  GTGCTCCTTCTACTACA     33935         A  A
                                TGTAGTGGAA GA GCAT
                                |||||||||| || ||||
                                ACATCATCTT CT CGTG
                                      C  _
GAM470  ADD2      3'  GTGCTCCTTCTACTACA     33952         A  A
                                TGTAGTGGAA GA GCAT
                                |||||||||| || ||||
                                ACATCATCTT CT CGTG
                                      C  _
GAM470  ADD2      3'  GTGCTCCTTCTACTACA     33963         A  A
                                TGTAGTGGAA GA GCAT
                                |||||||||| || ||||
                                ACATCATCTT CT CGTG
                                      C  _
GAM470  ADD2      3'  GTGCTCCTTCTACTACA     33946         A  A
                                TGTAGTGGAA GA GCAT
                                |||||||||| || ||||
                                ACATCATCTT CT CGTG
                                      C  _
GAM470  ARHG      5'  ACTGCCTCCACTACA       76590         AAGAA   T
                                TGTAGTGGA    GCA GT
                                |||||||||    ||| ||
                                ACATCACCT    CGT CA
                                     C____  _
GAM470  AS3       3'  ACATGCTTTAGCCATACA    31933      G   AAA
                                TGTA TGG   GAAGCATGT
                                |||| |||   |||||||||
                                ACAT ACC   TTTCGTACA
                                  _  GA_
GAM470  ATF5      5'  ACAGTCTCTTCTCACTACA   23804        GA   AG A
                                TGTAGTG  AAGA  C TGT
                                |||||||  ||||  | |||
                                ACATCAC  TTCT  G ACA
                                    TC   CT _
GAM470  CD48      3'  ACATGCTTTTTTCCCAC     8351       _
                                GTGG AAAGAAGCATGT
                                |||| ||||||||||||
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                                CACC TTTTTTCGTACA
                                  C
GAM470  DIRC1    5'  ACATCTTTCTCCTCACTACA  53665       AA    C
                                TGTAGTGG  AGAAG ATGT
                                ||||||||  ||||| ||||
                                ACATCACT  TCTTT TACA
                                     CC    C
GAM470  FLRT2    3'  ACATGCTTGTACACACACA   25053    A  GAAAG
                                TGT GTG    AAGCATGT
                                ||| |||    ||||||||
                                ACA CAC    TTCGTACA
                                  _  ACATG
GAM470  FXYD6    3'  ACTTGCCTCCCCACTGCA    41835       AAA  A   T
                                TGTAGTGG   GA GCA GT
                                ||||||||   || ||| ||
                                ACGTCACC   CT CGT CA
                                     C__  C   T
GAM470  GPR17    3'  GCCTCCTTCCCGCTACA     17956       _  A  A
                                TGTAGTGG AA GA GC
                                |||||||| || || ||
                                ACATCGCC TT CT CG
                                     C  C  C
GAM470  MHC2TA   3'  CACCCTCCTTTCCACCACA   4164     A      A  CA
                                TGT GTGGAAAG AG  TG
                                ||| |||||||| ||  ||
                                ACA CACCTTTC TC  AC
                                  C       C  CC
GAM470  NR1I2    5'  ACATCCTGGTATCCACCACA  13960    A    AAGA  C
                                TGT GTGGA    AG ATGT
                                ||| |||||    || ||||
                                ACA CACCT    TC TACA
                                  C    ATGG  C
GAM470  PIK3R3   3'  ACATGTGCTTCCATACA     61047     G    AGAA
                                TGTA TGGAA    GCATGT
                                |||| |||||    ||||||
                                ACAT ACCTT    TGTACA
                                  _    CG__
GAM470  RAB11A   3'  GTTTTCTTCCACTACA      16233         AG
                                TGTAGTGGAA  AAGC
                                ||||||||||  ||||
                                ACATCACCTT  TTTG
                                      CT
GAM470  RNASE1   3'  ACATGCTTCCCTTTCC      63874      __
                                GGAAA  GAAGCATGT
                                |||||  |||||||||
                                CCTTT  CTTCGTACA
                                   CC
GAM470  RNASE1   3'  ACATGCTTCCCTTTCC      11346      __
                                GGAAA  GAAGCATGT
                                |||||  |||||||||
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                                CCTTT  CTTCGTACA
                                   CC
GAM470  RNPEP    3'  ACAGCTCTCCCCGCTACA    65109        AA   A  A
                                TGTAGTGG  AGA GC TGT
                                ||||||||  ||| || |||
                                ACATCGCC  TCT CG ACA
                                     CC  _ _
GAM470  SFRP4    3'  ATCCTACTCTCCACTACA    11575        A  A  C
                                TGTAGTGGA AG AG AT
                                ||||||||| || || ||
                                ACATCACCT TC TC TA
                                     C  A  C
GAM470  TNFAIP1  3'  ACATGCTTGGCCACACA     40913     A    AAAG
                                TGT GTGG    AAGCATGT
                                ||| ||||    ||||||||
                                ACA CACC    TTCGTACA
                                  _    GG__
GAM470  TRIM9    5'  ACCTGCTTTCACTACA      30742         AAGA    T
                                TGTAGTGGA    AGCA GT
                                |||||||||    |||| ||
                                ACATCACTT    TCGT CA
                                     ____    C
GAM470  USF2     3'  ACATGCCCCTCCCCCAGCTGC  12557       __  AA  AA
                                GTAGT  GG  AG  GCATGT
                                |||||  ||  ||  ||||||
                                CGTCG  CC  TC  CGTACA
                                   AC  CC  CC
GAM470  VDR      3'  TGTCCTTTTCACTACA      4575           AA
                                TGTAGTGGAAAG  GCA
                                ||||||||||||  |||
                                ACATCACTTTTC  TGT
                                      C_
GAM470  ZK1      3'  GTTTCTTTCCAGTACA      19464      G
                                TGTA TGGAAAGAAGC
                                |||| ||||||||||
                                ACAT ACCTTTCTTTG
                                   G
GAM470  ARNTL2   3'  CACTCTTCCCACTCCACTACA  39457         AA__    CA
                                TGTAGTGGA    GAAG  TG
                                |||||||||    ||||  ||
                                ACATCACCT    CTTC  AC
                                     CACC    TC
GAM470  B3GNT5   3'  TACACACTACCTCCCTTCACTA 49428         AA  ___  CA
           CA                    TGTAGTGGA  GA   AG  TGTA
                                 |||||||||  ||   ||  ||||
                                 ACATCACTT  CT   TC  ACAT
                                      CC  CCA  AC
GAM470  CALN1    3'  TACATGCTTCCCCCCTTCCA   48875      A____
                                TGGAA    GAAGCATGTA
                                |||||    ||||||||||
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                                ACCTT    CTTCGTACAT
                                   CCCCC
GAM470  ChGn     3'  TACATGTTATCCACCCCA    37196    TA    AAGA
                                TG  GTGGA    AGCATGTA
                                ||  |||||    ||||||||
                                AC  CACCT    TTGTACAT
                                 CC     A___
GAM470  CLECSF9  3'  ACAGGCCTCCACTGCA      26835         AAGAA  A
                                TGTAGTGGA     GC TGT
                                |||||||||     || |||
                                ACGTCACCT     CG ACA
                                      C____  G
GAM470  DKFZP434B205 3'  TACATCTGGGACCGCCACTACA 75323         AAAGA__  C
                                TGTAGTGG      AG ATGTA
                                ||||||||      || |||||
                                ACATCACC      TC TACAT
                                      GCCAGGG  _
GAM470  DKFZP564G202 3'  TTTCTTTCCTACTACA      65292         _
                                TGTAGT GGAAAGAAG
                                |||||| |||||||||
                                ACATCA CCTTTCTTT
                                    T
GAM470  DKK3     3'  GTGCTCTCTCCACTAC      25133         A   A
                                GTAGTGGA AGA GCAT
                                |||||||| ||| ||||
                                CATCACCT TCT CGTG
                                      C   _
GAM470  ENAH     3'  GCCTTTACCACTACA       36615         _   AA
                                TGTAGTGG AAAG  GC
                                |||||||| ||||  ||
                                ACATCACC TTTC  CG
                                      A    __
GAM470  FAM8A1   3'  TACATACTTCTTTGCA      32724    G      C
                                TG AAAGAAG ATGTA
                                || ||||||| |||||
                                AC TTTCTTC TACAT
                                 G      A
GAM470  FLJ10040 3'  TGCTCCATCCACTACA      35754         AA  A
                                TGTAGTGGA  GA GCA
                                |||||||||  || |||
                                ACATCACCT  CT CGT
                                      AC  _
GAM470  FLJ11110 3'  ACACACTTCTGCCCCCACTGCA 37058         AA__    CA
                                TGTAGTGG    AGAAG  TGT
                                ||||||||    |||||  |||
                                ACGTCACC    TCTTC  ACA
                                      CCCG    AC
GAM470  FLJ21272 3'  ACAATAGACTTTCCATTACA   46731           AAGCA
                                TGTAGTGGAAAG    TGT
                                ||||||||||||    |||
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                                ACATTACCTTTC    ACA
                                      AGATA
GAM470  FLJ22318  3'  ACCTCTTCCTCCCACTACA   42829       AAA   CAT
                                TGTAGTGG  GAAG  GT
                                ||||||||  ||||  ||
                                ACATCACC  CTTC  CA
                                    CTC   TC_
GAM470  FLJ23309  3'  ACATGTGGGTACTGCCACTACA 46058       AAAGAA__
                                TGTAGTGG      GCATGT
                                ||||||||      ||||||
                                ACATCACC      TGTACA
                                    GTCATGGG
GAM470  GABBR1    3'  GTGCTCTTTCCACCCCA    41576   TA      A
                                TG  GTGGAAAGA GCAT
                                ||  |||||||||| ||||
                                AC  CACCTTTCT CGTG
                                 CC       _
GAM470  GABBR1    3'  GTGCTCTTTCCACCCCA    7611    TA      A
                                TG  GTGGAAAGA GCAT
                                ||  |||||||||| ||||
                                AC  CACCTTTCT CGTG
                                 CC       _
GAM470  GRP3      3'  TACATCCTTCCCACTACA    31123       AAA   C
                                TGTAGTGG  GAAG ATGTA
                                ||||||||  |||| |||||
                                ACATCACC  CTTC TACAT
                                    ___   C
GAM470  GS3955    5'  ATACACGCCCCCCACCCTTTCC 41315       AA_______ A   III
           AC                     GTGGAAAG      GC TGTA  T
                                ||||||||      || ||||  |
                                CACCTTTC      CG ACAT  A
                                    CCACCCCC  C   III
GAM470  HCA127    3'  ACAGCTTTCCTTTCCAC    37947       __   A
                                GTGGAAAG  AAGC TGT
                                ||||||||  |||| |||
                                CACCTTTC  TTCG ACA
                                    CT    _
GAM470  HCGIX     3'  TATGATCTCACCACTACA    19573       AA  AG
                                TGTAGTGG  AGA  CATG
                                ||||||||  |||  ||||
                                ACATCACC  TCT  GTAT
                                    AC    A_
GAM470  HE3-ALPHA 5'  ACATGCTGATCCCCACTACA  60184       AAAGA
                                TGTAGTGG    AGCATGT
                                ||||||||    |||||||
                                ACATCACC    TCGTACA
                                    CCTAG
GAM470  KIAA0295  3'  TGCCCTTTCCACTCA      68111   T      AA
                                TG AGTGGAAAG  GCA
                                || |||||||||  |||
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                              AC TCACCTTTC  CGT
                               _       C_
GAM470  KIAA0574  3' ACATGCTTCTCCCCAC     69278     AA
                              GTGG  AGAAGCATGT
                              ||||  ||||||||||
                              CACC  TCTTCGTACA
                                CC
GAM470  KIAA0795  3' ACATGCACTTCCACTAC     46585        AGAA
                              GTAGTGGAA   GCATGT
                              |||||||||   ||||||
                              CATCACCTT   CGTACA
                                   CA__
GAM470  KIAA0960  3' ACACACTTCCTCATCACTGCA 92653       AAA_   CA
                              TGTAGTGG   GAAG  TGT
                              ||||||||   ||||  |||
                              ACGTCACT   CTTC  ACA
                                   ACTC   AC
GAM470  KIAA0979  3' ACATGCTTTAGCCATACA    30440     G   AAA
                              TGTA TGG   GAAGCATGT
                              |||| |||   |||||||||
                              ACAT ACC   TTTCGTACA
                                _  GA_
GAM470  KIAA1068  3' ACATGCTTTTGTCTCCAC    31026      A__
                              GTGGA   AGAAGCATGT
                              |||||   ||||||||||
                              CACCT   TTTTCGTACA
                                 CTG
GAM470  KIAA1613  3' ACATGCTTCTTTTTATTCA   64811    T
                              TG AGTGGAAAGAAGCATGT
                              || ||||||||||||||||
                              AC TTATTTTTCTTCGTACA
                               _
GAM470  KIAA1753  3' TGCCCTTCCCACTGCA      64888        A   AA
                              TGTAGTGG AAG  GCA
                              |||||||| |||  |||
                              ACGTCACC TTC  CGT
                                   C   C_
GAM470  KIAA1853  3' ACATGCTTCCACTCCAC     69387      AA_
                              GTGGA   GAAGCATGT
                              |||||   |||||||||
                              CACCT   CTTCGTACA
                                 CAC
GAM470  KIAA1871  3' ACATCTTATTGCACTACA    61229       G  AG   C
                              TGTAGTG AA  AAG ATGT
                              ||||||| ||  ||| ||||
                              ACATCAC TT  TTC TACA
                                  G  A_  _
GAM470  MGC1136   3' ACAGACTTTCCACTCCA     43802    T       AAGCA
                              TG AGTGGAAAG    TGT
                              || |||||||||    |||
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                                AC TCACCTTTC    ACA
                                 C       AG___
GAM470  PIG7    3'  GTGCCCCTTTCCATACA    16795     G     AA
                                TGTA TGGAAAG  GCAT
                                |||| |||||||  ||||
                                ACAT ACCTTTC  CGTG
                                  _     CC
GAM470  PP1057  3'  ACTTTCCTCCTCCCCACTGCA  48431       AA  A  CAT_
                                TGTAGTGG  AG AG   GT
                                ||||||||  || ||   ||
                                ACGTCACC  TC TC   CA
                                     CC  C  CTTT
GAM470  SEPT3   3'  TACTGCTGCTCTCCACTCA   38895   T    A  A   T
                                TG AGTGGA AG AGCA GTA
                                || |||||| || |||| |||
                                AC TCACCT TC TCGT CAT
                                 _     C  G   _
GAM470  SKIP    3'  TGCTCTCTCCACTAC      55370       A   A
                                GTAGTGGA AGA GCA
                                |||||||| ||| |||
                                CATCACCT TCT CGT
                                     C   _
GAM470  SKIP    3'  TGCTCTCTCCACTAC      33277       A   A
                                GTAGTGGA AGA GCA
                                |||||||| ||| |||
                                CATCACCT TCT CGT
                                     C   _
GAM470  SLAC2-B 3'  GCCTGCCTTTCCACCAC    30513   A     AA   T
                                GT GTGGAAAG  GCA GT
                                || ||||||||  ||| ||
                                CA CACCTTTC  CGT CG
                                 C       __   C
GAM470  SLC6A14 3'  TACATGCATTCTACCACTACA  23358       AA   _
                                TGTAGTGG  AGAA GCATGTA
                                ||||||||  |||| |||||||
                                ACATCACC  TCTT CGTACAT
                                     A_   A
GAM470  TERA    3'  TACATGCTACAAGCCACCATA  41136    A   AAAGA
                                TGT GTGG    AGCATGTA
                                ||| ||||    ||||||||
                                ATA CACC    TCGTACAT
                                  C   GAACA
GAM470  THTPA   3'  TACACACTTTCCACTTCA    44262    T      AAGCA
                                TG AGTGGAAAG    TGTA
                                || |||||||||    ||||
                                AC TCACCTTTC    ACAT
                                 T       AC___
GAM470  TRIM2   3'  ACTTGCTTCCACTAC      30939       AAGA   T
                                GTAGTGGA   AGCA GT
                                ||||||||   |||| ||
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                                CATCACCT   TCGT CA
                                    ____   T
GAM470  ZNF313   3'  TACAGAGCTTCCATTACA   37942       AAGA  A_
                                TGTAGTGGA   AGC  TGTA
                                |||||||||   |||  ||||
                                ACATTACCT   TCG  ACAT
                                    ____   AG
GAM470  LOC116236 3'  TACATGCTCCCTCTGGCAC   73817    GAA  ___
                                GTG   AGA   AGCATGTA
                                |||   |||   ||||||||
                                CAC   TCT   TCGTACAT
                                  GG_   CCC
GAM470  LOC130951 3'  TGCCCTTCCCACTACA     57148       A   AA
                                TGTAGTGG AAG  GCA
                                |||||||| |||  |||
                                ACATCACC TTC  CGT
                                     C   C_
GAM470  LOC133418 3'  TACATGCTTAAATAACTCCA   75091    T   GGAAAG
                                TG AGT     AAGCATGTA
                                || |||     |||||||||
                                AC TCA     TTCGTACAT
                                 C   ATAAA_
GAM470  LOC144363 3'  ACATACTCAAGGTTCACTACA  76822       AAGA_  C
                                TGTAGTGGA    AG ATGT
                                |||||||||    || ||||
                                ACATCACTT    TC TACA
                                     GGAAC  A
GAM470  LOC144571 3'  TACTTTCTTCTTTCCCCACA   83157    AGT      CAT
                                TGT   GGAAAGAAG   GTA
                                |||   |||||||||   |||
                                ACA   CCTTTCTTC   CAT
                                  CC_       TTT
GAM470  LOC144596 3'  ACATGCCCCTCCCCCAGCTGC  76906     __  AA  AA
                                GTAGT  GG  AG  GCATGT
                                |||||  ||  ||  ||||||
                                CGTCG  CC  TC  CGTACA
                                   AC  CC  CC
GAM470  LOC145945 5'  TACATGCTTAAACCACACA   83579    A   AAAG
                                TGT GTGG    AAGCATGTA
                                ||| ||||    |||||||||
                                ACA CACC    TTCGTACAT
                                  _    AAA_
GAM470  LOC151361 3'  ACTGTTCTTTCCAC       85315        G  T
                                GTGGAAAGAA CA GT
                                |||||||||| || ||
                                CACCTTTCTT GT CA
                                     _  _
GAM470  LOC165693 5'  CATCTGTCTCTCCACTAC    82595       A  _  C
                                GTAGTGGA AGA AG ATG
                                |||||||| ||| || |||
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                                CATCACCT TCT TC TAC
                                     C   G  _
GAM470   LOC196485 3'  TGCTCTCCTACTACA       87734         AA   A
                                TGTAGTGG  AGA GCA
                                ||||||||  ||| |||
                                ACATCATC  TCT CGT
                                     C_   _
GAM470   LOC196860 3'  ACATGCTTCTCTCCACT     89639        A
                                AGTGGA AGAAGCATGT
                                |||||| ||||||||||
                                TCACCT TCTTCGTACA
                                   C
GAM470   LOC197358 3'  TACTGCCCCTTTCCACTCA    88047    T        AA   T
                                TG AGTGGAAAG  GCA GTA
                                || |||||||||  ||| |||
                                AC TCACCTTTC  CGT CAT
                                 _        CC   _
GAM470   LOC199796 5'  GCAGCTTCCCATCTACA     74454       _  AAA    A
                                TGTAG TGG   GAAGC TGT
                                ||||| |||   ||||| |||
                                ACATC ACC   CTTCG ACG
                                   T  ___    _
GAM470   LOC200492 3'  TGTTCTTTCCACCGCA      90090    TA        G
                                TG  GTGGAAAGAA CA
                                ||  |||||||||| ||
                                AC  CACCTTTCTT GT
                                 GC         _
GAM470   LOC202181 3'  TACATGCTTCTCAT        89160     GAA
                                GTG   AGAAGCATGTA
                                |||   ||||||||||||
                                TAC   TCTTCGTACAT
                                  ___
GAM470   LOC203276 3'  TACATGCTTCTGGAACACT    90489      GAA_
                                AGTG    AGAAGCATGTA
                                ||||    ||||||||||||
                                TCAC    TCTTCGTACAT
                                  AAGG
GAM470   LOC203305 3'  TACATGCTTCTGGAACACT    90533      GAA_
                                AGTG    AGAAGCATGTA
                                ||||    ||||||||||||
                                TCAC    TCTTCGTACAT
                                  AAGG
GAM470   LOC203411 3'  TACATGCTTCTCTTGTATAC   90629     GTG  A
                                GTA   GA AGAAGCATGTA
                                |||   || ||||||||||||
                                CAT   TT TCTTCGTACAT
                                 ATG  C
GAM470   LOC203504 3'  ACCTCTTCTCTCCCCTACA    90637      T   A    CAT
                                TGTAG GGA AGAAG   GT
                                ||||| ||| |||||   ||
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                                ACATC CCT TCTTC   CA
                                   C   C     TC_
GAM470  LOC219376 3'  CATTCTGTCCTTCCACTATA  93897         A  _  C
                                TGTAGTGGAA GA AG ATG
                                |||||||||| || || |||
                                ATATCACCTT CT TC TAC
                                     C  G  T
GAM470  LOC219988 3'  TACTGACCATTTCCACTACA  91627          GAAG  T
                                TGTAGTGGAAA    CA GTA
                                ||||||||||    || |||
                                ACATCACCTTT    GT CAT
                                      ACCA  _
GAM470  LOC221463 3'  ACATGCTTCTTTTTAAACA   92062     AG
                                TGT  TGGAAAGAAGCATGT
                                |||  ||||||||||||||
                                ACA  ATTTTTCTTCGTACA
                                  A_
GAM470  LOC254243 3'  TACATGCTTCTGGAACACT   97419     GAA_
                                AGTG   AGAAGCATGTA
                                ||||   ||||||||||
                                TCAC   TCTTCGTACAT
                                  AAGG
GAM470  LOC51161  3'  ACGGTTCCTCTCTCCACTGCA  32506         A  __  A
                                TGTAGTGGA AGA  AGC TGT
                                |||||||| |||  ||| |||
                                ACGTCACCT TCT  TTG GCA
                                     C   CC  _
GAM470  LOC51285  3'  ACATGCTTGCAGTCCTACA   33343      T  AAAG
                                TGTAG GG   AAGCATGT
                                ||||| ||   ||||||||
                                ACATC CT   TTCGTACA
                                   _ GACG
GAM470  LOC90038  3'  TACATGCTTCTGGAACACT   61161     GAA_
                                AGTG   AGAAGCATGTA
                                ||||   ||||||||||
                                TCAC   TCTTCGTACAT
                                  AAGG
GAM470  LOC90494  5'  CAGGCTCCTCCCCACTGCA   63053        AA  A   A
                                TGTAGTGG  AG AGC TG
                                ||||||||  || ||| ||
                                ACGTCACC  TC TCG AC
                                     CC  C   G
GAM470  LOC90573  3'  GTGCCCCTCCCACTACA     63275        AA  AA
                                TGTAGTGG  AG  GCAT
                                ||||||||  ||  ||||
                                ACATCACC  TC  CGTG
                                     C_  CC
GAM470  LOC90576  3'  GTTTCTTTCCAGTACA      63345      G
                                TGTA TGGAAAGAAGC
                                |||| ||||||||||
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                                ACAT ACCTTTCTTTG
                                  G
GAM470  LOC92078 3'  ACATCTGGGCTCACTACA    67973        AAAGA  C
                                TGTAGTGG    AG ATGT
                                ||||||||    || ||||
                                ACATCACT    TC TACA
                                    CGGG_  _
GAM471  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM471  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM471  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM471  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
           TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM471  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM471  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM471  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM471  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM471  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
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                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM471  CG012    5' CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                     CT  __
GAM471  EIF2C2   3' ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM471  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC       GTCTGAGAT
                                ||||||       |||||||||
                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM471  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM471  KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM471  KLHL6    3' ATCTCAGAGCAGGAAA      55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM471  NIR3     3' GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM471  PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM471  PP35     3' ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM471  PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148         TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
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                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM471  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM471  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941        CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM471  LOC149703 3' ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM471  LOC154007 3' ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM471  LOC155004 3' TCATTTAAGTGAAAGGAAA    81226     A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM471  LOC222134 5' ACAGTGAAGTGAAATG       94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM472  CCND2    3'  CAGCAAGCAGCGTTTA       8289          C
                                TAAATGCTGC TGCTG
                                |||||||||| |||||
                                ATTTGCGACG ACGAC
                                     A
GAM472  COL4A2   3'  GGACAGACGAGACAACAGCA   8470       CC  _  GA   A
                                TGCTG  TG CT  TCT TCC
                                |||||  || ||  ||| |||
                                ACGAC  AC GA  AGA AGG
                                   A_  A  GC   C
GAM472  ELAVL3   3'  AGACAGCACAGGCAGC       7425         __    A
                                GCTGCCT  GCTG TCT
                                |||||||  |||| |||
                                CGACGGA  CGAC AGA
                                    CA   _
GAM472  FOXE3    3'  AGATTTCAGACAGGCAGCA    24102          _   __
                                TGCTGCCTG CTGA  TCT
                                ||||||||| ||||  |||
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                                ACGACGGAC GACT  AGA
                                     A    TT
GAM472  HMGN3    5'  GGCAGAGGCAGCAT       14903        G   A
                                ATGCTGCCT CTG TC
                                ||||||||| ||| ||
                                TACGACGGA GAC GG
                                      _   _
GAM472  IL1RAPL2 5'  AGACAGAGGCAGCAT      33790        G   A
                                ATGCTGCCT CTG TCT
                                ||||||||| ||| |||
                                TACGACGGA GAC AGA
                                      _   _
GAM472  MYO5A    3'  TCAGCTGGCAGCATTTA     59766          T
                                TAAATGCTGCC GCTGA
                                |||||||||| |||||
                                ATTTACGACGG CGACT
                                       T
GAM472  PRKCM    3'  ATCAACAGAAGCATTTG     10811        GC   C
                                TAAATGCT  CTG TGAT
                                ||||||||  ||| ||||
                                GTTTACGA  GAC ACTA
                                     A_   A
GAM472  PTGIS    3'  TCTGCAGGCAGATTTA      6347       G      T
                                TAAAT CTGCCTGC GA
                                ||||| |||||||| ||
                                ATTTA GACGGACG CT
                                   _       T
GAM472  TXNRD1   3'  ATAGAAGGCAGGCAGCATCA  12456   A         GA
                                A ATGCTGCCTGCT  TCTAT
                                | ||||||||||||  |||||
                                A TACGACGGACGG  AGATA
                                 C          A_
GAM472  AASDHPPT 3'  AGGTCAAGTAGCATTTA     31243         CTGC
                                TAAATGCTGC    TGATCT
                                ||||||||||    ||||||
                                ATTTACGATG    ACTGGA
                                     A___
GAM472  C1orf16  3'  CAGAAGGACAGCATTT      29227         _  G
                                AAATGCTG CCT CTG
                                |||||||| ||| |||
                                TTTACGAC GGA GAC
                                     A   A
GAM472  CCR5     3'  CACAGGCAGCATTTA       5148           C
                                TAAATGCTGCCTG TG
                                |||||||||||||| ||
                                ATTTACGACGGAC AC
                                       _
GAM472  CGI-01   3'  GACAGATTTGAGAGAGCATTTA 31942        GC  GCT    A
                                TAAATGCT  CT   GATCT TC
                                ||||||||  ||   ||||| ||
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                                ATTTACGA  GA   TTAGA AG
                                     GA  GT_    C
GAM472  FLJ10508  3'  GTCAGCAGAGAACATTTA    36200       CTGC
                                TAAATG    CTGCTGAT
                                ||||||    ||||||||
                                ATTTAC    GACGACTG
                                   AAGA
GAM472  FLJ12671  3'  GGAGGCAGAGGCAGCA      48279        G   A_
                                TGCTGCCT CTG  TCT
                                |||||||| |||  |||
                                ACGACGGA GAC  AGG
                                     _  GG
GAM472  FLJ14327  3'  GGACAGATCAGCAAAAGC    46143     GCC        A
                                GCT   TGCTGATCT TCC
                                |||   ||||||||| |||
                                CGA   ACGACTAGA AGG
                                  AA_       C
GAM472  FLJ20445  3'  GAACAGTTTTTAGGCAGCCTTT 35178      T      _____    A
          A                      TAAA GCTGCCT    GCTG TC
                                |||| |||||||    |||| ||
                                ATTT CGACGGA    TGAC AG
                                  C      TTTT    A
GAM472  GAB3      3'  GGATAGATCAAATTGGCAGTCA 54630    T     TGC_
                                A GCTGCC    TGATCTATCC
                                | ||||||    ||||||||||
                                A TGACGG    ACTAGATAGG
                                 C     TTAA
GAM472  KCNK13    3'  ATCACAAAAGCAGCATT     41905        C__  C
                                AATGCTGC   TG TGAT
                                ||||||||   || ||||
                                TTACGACG   AC ACTA
                                     AAA  _
GAM472  KIAA1328  5'  GAACAGAAGCAGCATTTG    61649         CTG   A
                                TAAATGCTGC   CTG TC
                                ||||||||||   ||| ||
                                GTTTACGACG   GAC AG
                                      AA_   A
GAM472  MGC2668   3'  GGACGGGGCAGGCAGCA     60576          GAT TA
                                TGCTGCCTGCT   C  TCC
                                ||||||||||   |  |||
                                ACGACGGACGG   G  AGG
                                       ___ GC
GAM472  NOPAR     5'  GGCAGCGGCAGCAT       53808        T   A
                                ATGCTGCC GCTG TC
                                |||||||| |||| ||
                                TACGACGG CGAC GG
                                     _   _
GAM472  p25       3'  GGACCTGGCAGGCAGC      22853          A_
                                GCTGCCTGCTG  TCT
                                ||||||||||  |||
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                                CGACGGACGGT  AGG
                                      CC
GAM472  ST7L     3'  GAACAGAGAGCAGCATTT    57570         _ G   A
                                AAATGCTGC CT CTG TC
                                |||||||||  || ||| ||
                                TTTACGACG GA GAC AG
                                     A  _   A
GAM472  ST7L     3'  GAACAGAGAGCAGCATTT    57575         _ G   A
                                AAATGCTGC CT CTG TC
                                |||||||||  || ||| ||
                                TTTACGACG GA GAC AG
                                     A  _   A
GAM472  LOC124783 5'  GGAGGCGGAGAGGCAGCAT   74335         G_   A_
                                ATGCTGCCT  CTG  TCT
                                |||||||||  |||  |||
                                TACGACGGA  GGC  AGG
                                     GA   GG
GAM472  LOC127841 5'  GACAGAGGGGAACAAGTAGCAT 74695         C  __  GA   A
          TTA                     TAAATGCTGC TG  CT  TCT TC
                                |||||||||| ||  ||  ||| ||
                                ATTTACGATG AC  GG  AGA AG
                                     A  AA  GG   C
GAM472  LOC157623 5'  GATGGGAGCAGAGCAGCATTTA 81498          _    GA
                                TAAATGCTGC CTGCT  TCTATC
                                |||||||||| |||||  ||||||
                                ATTTACGACG GACGA  GGGTAG
                                     A    __
GAM472  LOC202025 5'  GAATGCAGGCAGCATTT     90287           TGA
                                AAATGCTGCCTGC   TC
                                ||||||||||||   ||
                                TTTACGACGGACG   AG
                                       TA_
GAM472  LOC206280 5'  GGACAAAAAGTTCGGCAGCAT  90713         T_   GATCTA
                                ATGCTGCC  GCT     TCC
                                ||||||||  |||     |||
                                TACGACGG  TGA     AGG
                                     CT   AAAAC_
GAM472  LOC220020 5'  GGATTGAGAGCAGCAGCATT   93420         C    GA  T
                                AATGCTGC TGCT  TC ATCC
                                |||||||| ||||  || ||||
                                TTACGACG ACGA  AG TAGG
                                     _    G_  T
GAM472  LOC254842 5'  AGAGAGCAGGCAGCA       97595          GA
                                TGCTGCCTGCT  TCT
                                ||||||||||  |||
                                ACGACGGACGA  AGA
                                       G_
GAM472  LOC91250  5'  AGATTGTACAAGCAGCATTT   65319         C  CT_
                                AAATGCTGC TG   GATCT
                                |||||||| ||   |||||
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                                TTTACGACG AC   TTAGA
                                     A  ATG
GAM473  IL1R1    3'  ACAGGAGGGAGAGAACTT    6054       G   AG
                                AAGTT CTC  TCTCCTGT
                                ||||| |||  ||||||||
                                TTCAA GAG  GGAGGACA
                                  _  AG
GAM473  MAP3K8   3'  TGGGTGACTAGAACAACTTGA  17793        C  _   T
                                TCAAGTTG TC AGTC CCTG
                                |||||||| || |||| ||||
                                AGTTCAAC AG TCAG GGGT
                                     A A   T
GAM473  NAGA     3'  ACAGACGTTGCTGAGCAACT   4231          CTC__
                                AGTTGCTCAGT    CTGT
                                ||||||||||     ||||
                                TCAACGAGTCG    GACA
                                      TTGCA
GAM473  TCEB3    3'  TACAGGAGACTGGAGTCTTG   12148     TT   _
                                CAAG  GCTC AGTCTCCTGTA
                                ||||  |||| ||||||||||
                                GTTC  TGAG TCAGAGGACAT
                                  __   G
GAM473  ACF      5'  TACAAAAATTATTGAGCAAC   27411         CTCC__
                                GTTGCTCAGT     TGTA
                                |||||||||      ||||
                                CAACGAGTTA     ACAT
                                      TTAAAA
GAM473  ACF      5'  TACAAAAATTATTGAGCAAC   57226         CTCC__
                                GTTGCTCAGT     TGTA
                                |||||||||      ||||
                                CAACGAGTTA     ACAT
                                      TTAAAA
GAM473  C12orf22 3'  ACAGGAAAAGCTGGGTAACT   47974          C__
                                AGTTGCTCAGT   TCCTGT
                                ||||||||||   ||||||
                                TCAATGGGTCG   AGGACA
                                      AAA
GAM473  DEGS     3'  ACAGGAAACTTGTGACTTG    13407      TG TC   C
                                CAAGT  C  AGT TCCTGT
                                |||||  |  ||| ||||||
                                GTTCA  G  TCA AGGACA
                                   GT T_   A
GAM473  DKFZP564O0423 5'  ACAGGAGACTACCTGTAC    91674    T  TC__
                                GT GC    AGTCTCCTGT
                                || ||    ||||||||||
                                CA TG    TCAGAGGACA
                                  _ TCCA
GAM473  DKFZP727M111 5'  TACAGGAGCTGTTCCACCTGA  31414     A  TGCT   T
                                TCA GT    CAG CTCCTGTA
                                ||| ||    ||| ||||||||
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                                AGT CA    GTC GAGGACAT
                                  C  CCTT  _
GAM473  FLJ10607  3'  TTACCACTGAACAATTTGA   77131        C    CTCCT
                                TCAAGTTG TCAGT    GTAA
                                |||||||| |||||    ||||
                                AGTTTAAC AGTCA    CATT
                                    A    C____
GAM473  FLJ10898  5'  ACAGGAGACTAATATGA    59417    A   GCTC
                                TCA GTT   AGTCTCCTGT
                                ||| |||   ||||||||||
                                AGT TAA   TCAGAGGACA
                                  A  _____
GAM473  GALNAC4ST-2 3'  TACAGGAGATGTAAACAACTTG 48657        CTCA_
           A                     TCAAGTTG    GTCTCCTGTA
                                |||||||    ||||||||||
                                AGTTCAAC    TAGAGGACAT
                                    AAATG
GAM473  HN1      3'  GAGAACTGCACAACTTGA    32461        CT   _
                                TCAAGTTG  CAGT CTC
                                ||||||||  |||| |||
                                AGTTCAAC  GTCA GAG
                                    AC   A
GAM473  KIAA1550  3'  GGAAAAGACATGAGCAAC    66557        _  ___
                                GTTGCTCA GTC   TCC
                                |||||||| |||   |||
                                CAACGAGT CAG   AGG
                                    A   AAA
GAM473  LOXL4    3'  TTACAGGACTGACA       49873    C    TC
                                TG TCAG  TCCTGTAA
                                || ||||  ||||||||
                                AC AGTC  AGGACATT
                                  _   __
GAM473  LY75     3'  CAAGAACTAAGCCAACTTGA   9835         _ C   C  C
                                TCAAGTTG CT AGT TC TG
                                |||||||| || ||| || ||
                                AGTTCAAC GA TCA AG AC
                                    C  A   _  A
GAM473  LOC150225 3'  AGACTGAGCAATTGA       84980      G
                                TCAA TTGCTCAGTCT
                                |||| ||||||||||
                                AGTT AACGAGTCAGA
                                  _
GAM473  LOC151808 5'  TTACAGGAGAGGAAGC      85498     _ AG
                                GCT C  TCTCCTGTAA
                                ||| |  ||||||||||
                                CGA G  AGAGGACATT
                                  A G_
GAM473  LOC153688 3'  ACAGGGAGCAACTGA       86090     A      AGTCT
                                TCA GTTGCTC    CCTGT
                                ||| |||||||    |||||
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                                AGT CAACGAG    GGACA
                                  _    _____
GAM473  LOC157349 5'  ACAGGAGACTGACAC      81402    T C
                                GT G TCAGTCTCCTGT
                                || | ||||||||||||
                                CA C AGTCAGAGGACA
                                  _ _
GAM473  LOC157681 3'  TTACAAAAGAGGCAACT    81547      CAG   CC
                                AGTTGCT   TCT  TGTAA
                                |||||||   |||  |||||
                                TCAACGG   AGA  ACATT
                                    ___   AA
GAM473  LOC92697  5'  TTACAATGGAAAAACCAACTTG 70285       CTCAG   CC
            A                    TCAAGTTG    TCT  TGTAA
                                ||||||||    |||  |||||
                                AGTTCAAC    AGG  ACATT
                                     CAAAA   TA
GAM474  CAV3    3'  GCCCCACCATGATGCC     52892    AG      AA
                                GG  ATCATGGTG  GGC
                                ||  |||||||||  |||
                                CC  TAGTACCAC  CCG
                                 G_       C_
GAM474  CDKN1A   3'  CTCATGGCCCCTCTGACCTGC  54299   G  A   T_  TGAA
                                G AG TCA  GG   GGCCATGAG
                                | || |||  ||   |||||||||
                                C TC AGT  CC   CCGGTACTC
                                 G  C   CT  _____
GAM474  HLA-A   3'  CATGTCCACCATGACCCTC   9203     A_     AA   C
                                GAG  TCATGGTG  GGC ATG
                                |||  ||||||||  ||| |||
                                CTC  AGTACCAC  CTG TAC
                                  CC       __   _
GAM474  HLA-E   3'  CTCTGTGTCTACCATGACCCC  91023    AGA     GA   _  T
                                GG   TCATGGT  AGGC CA GAG
                                ||   |||||||  |||| || |||
                                CC   AGTACCA  TCTG GT CTC
                                 CC_      __    T  _
GAM474  HLA-G   3'  TGTGCCCACCATGACCCTC   9227     A_      AA   _
                                GAG  TCATGGTG  GGC CA
                                |||  ||||||||  ||| ||
                                CTC  AGTACCAC  CCG GT
                                  CC       __   T
GAM474  C5orf4   5'  CTCATCATCACCACCATCTCC  32981       CA     A GCC
                                GGAGAT  TGGTGA G   ATGAG
                                ||||||  |||||| |   |||||
                                CCTCTA  ACCACT C   TACTC
                                   CC     A ___
GAM474  C5orf4   3'  CTCATCATCACCACCATCTCC  50492       CA     A GCC
                                GGAGAT  TGGTGA G   ATGAG
                                ||||||  |||||| |   |||||
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                                CCTCTA  ACCACT C   TACTC
                                   CC     A ___
GAM474  DKFZp434F142 3'  CTCTTGCCTCACCATGGCCTCC 50023      AT       A   CAT
                                GGAG  CATGGTGA GGC   GAG
                                |||| |||||||| |||   |||
                                CCTC  GTACCACT CCG   CTC
                                  CG       _  TT_
GAM474  KIAA0545  3'  CCCTCACCATGCTCC       63147      AT       A
                                GGAG  CATGGTGA GG
                                |||| |||||||| ||
                                CCTC  GTACCACT CC
                                  __       C
GAM474  PRKWNK2   3'  CACAGCCCGTGGTCCC      90537    A       TGAAG  CA
                                GG GATCATGG     GC  TG
                                || ||||||||     ||  ||
                                CC CTGGTGCC     CG  AC
                                 _      _____  AC
GAM474  PSKH1     3'  CATGGCCTCAGAATTTCC     68235       CA  GTGA
                                GGAGAT  TG    AGGCCATG
                                ||||||  ||    ||||||||
                                CCTTTA  AC    TCCGGTAC
                                   AG  ____
GAM474  SDC3      5'  CACAGCCCTCGCCTCTGGTCTC 27740         T_    A   CA
           C                     GGAGATCA  GGTGA GGC  TG
                                |||||||| |||||| |||  ||
                                CCTCTGGT  CCGCT CCG  AC
                                     CT     C   AC
GAM474  SEC8      3'  TGGACCTCACCATGTCCCC    41443    A  T       A  _
                                GG GA CATGGTGA GG CCA
                                || || |||||||| || |||
                                CC CT GTACCACT CC GGT
                                 C  _       _  A
GAM474  ZSIG11    3'  CATGGCCTGCACCCTCC      31930      ATCAT    A
                                GGAG     GGTG AGGCCATG
                                ||||     |||| ||||||||
                                CCTC     CCAC TCCGGTAC
                                  _____    G
GAM474  LOC129138 3'  CATGGCCTTCATGGCGCGCTCC 57119      ATCATG
                                GGAG      GTGAAGGCCATG
                                ||||      ||||||||||||
                                CCTC      TACTTCCGGTAC
                                  GCGCGG
GAM474  LOC144742 5'  CTCATGGCCTCAAATGATCCAC 76942    GA     GG   A
                                G  GATCAT  TGA GGCCATGAG
                                |  ||||||  ||| |||||||||
                                C  CTAGTA  ACT CCGGTACTC
                                 AC     A_  _
GAM474  LOC157638 5'  CACGGCCTTCACCTCTCC    81510       TCAT         A
                                GGAGA    GGTGAAGGCC TG
                                |||||    |||||||||| ||
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                                CCTCT    CCACTTCCGG AC
                                   _____         C
GAM474   LOC197003 3'  CTCACTCTCCACCGTGACCTCC 87874      A       A   CCA
                                GGAG TCATGGTG AGG   TGAG
                                |||| |||||||| |||   ||||
                                CCTC AGTGCCAC TCT   ACTC
                                  C       C   C__
GAM474   LOC200597 3'  CCTTCACCAAGATCTCC     88840        A
                                GGAGATC TGGTGAAGG
                                ||||||| |||||||||
                                CCTCTAG ACCACTTCC
                                    A
GAM474   LOC201799 3'  CTCACACTTGTTTCACCATACC 89059      ATC       GCCA__
            TCC                   GGAG   ATGGTGAAG     TGAG
                                ||||   |||||||||     ||||
                                CCTC   TACCACTTT     ACTC
                                  CA_       GTTCAC
GAM474   LOC255426 3'  CATGGCCATCATCTCC      97158       TCATGG   A
                                GGAGA     TGA GGCCATG
                                |||||     ||| |||||||
                                CCTCT     ACT CCGGTAC
                                   _______  A
GAM474   LOC255925 3'  CCTCCACCATGGTCCC      96477    A        A
                                GG GATCATGGTG AGG
                                || ||||||||| |||
                                CC CTGGTACCAC TCC
                                 _        C
GAM474   LOC257490 3'  CATGTCCACCATGACCCTC    97713     A_       AA   C
                                GAG  TCATGGTG  GGC ATG
                                |||  ||||||||  ||| |||
                                CTC  AGTACCAC  CTG TAC
                                  CC       __  _
GAM474   LOC257539 3'  CTCTGTGTCTACCATGACCCC  97701    AGA      GA   _  T
                                GG   TCATGGT  AGGC CA GAG
                                ||   |||||||  |||| || |||
                                CC   AGTACCA  TCTG GT CTC
                                 CC_      __    T  _
GAM474   LOC257578 3'  CTCTGTGTCTACCATGACCCC  97821    AGA      GA   _  T
                                GG   TCATGGT  AGGC CA GAG
                                ||   |||||||  |||| || |||
                                CC   AGTACCA  TCTG GT CTC
                                 CC_      __    T  _
GAM474   LOC90786  5'  CATGGCCTCCAGGCCTCT    64029      AT A   TGA
                                GGAG  C TGG   AGGCCATG
                                ||||  | |||   ||||||||
                                TCTC  G ACC   TCCGGTAC
                                  CG _  ___
GAM475   ATP11A    3'  CCAGGGCTGCTGTGATA     77021          CA   AG
                                TATCACAGC  TCT  TGG
                                |||||||||  |||  |||
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                                ATAGTGTCG  GGG  ACC
                                     TC  __
GAM475  CABC1    5'  CAGCCCTGAAGGATGGCTGCCA 39652     CA       AGT_  A
            TA                    TAT  CAGCCATCT    GG GCTG
                                  |||  |||||||||    || ||||
                                  ATA  GTCGGTAGG    CC CGAC
                                    CC        AAGT  _
GAM475  FBXL7    3'  CAGCTCTGTCAATGACTATGA  24544     C  C   CTA TG
                                  TCA AG CAT   G  GAGCTG
                                  ||| || |||   |  ||||||
                                  AGT TC GTA   T  CTCGAC
                                    A  A   AC_ GT
GAM475  GBE1     3'  CAGCTCCACCAGATGC      3851     C    A
                                  GC ATCT GTGGAGCTG
                                  || |||| |||||||||
                                  CG TAGA CACCTCGAC
                                   _   C
GAM475  GPR30    5'  CAGCTCCACGCGGGACTGTG   7690       _  ATCTA
                                  CACAG CC    GTGGAGCTG
                                  |||||| ||    |||||||||
                                  GTGTC GG    CACCTCGAC
                                     A  GCG__
GAM475  NPC1     3'  CACTAGATGGCTGTGA      4251
                                  TCACAGCCATCTAGTG
                                  ||||||||||||||||
                                  AGTGTCGGTAGATCAC

GAM475  SLC15A1  3'  CAGGTTTAAAATGGCTGTGATA 17400           CTAG    G
                                  TATCACAGCCAT    TGGA CTG
                                  ||||||||||||    |||| |||
                                  ATAGTGTCGGTA    ATTT GAC
                                         AA__    G
GAM475  STAT6    3'  GGTCCAAGTGGCTGTGA     12025          CTAG    G
                                  TCACAGCCAT    TGGA C
                                  ||||||||||    |||| |
                                  AGTGTCGGTG    ACCT G
                                        A___    G
GAM475  TCF19    3'  CAGTGTGATGGCTGTGA     97734          _  G
                                  TCACAGCCATC TA TG
                                  |||||||||| || ||
                                  AGTGTCGGTAG GT AC
                                         T  G
GAM475  TCF19    3'  CAGTGTGATGGCTGTGA     97864          _  G
                                  TCACAGCCATC TA TG
                                  |||||||||| || ||
                                  AGTGTCGGTAG GT AC
                                         T  G
GAM475  CLECSF9  3'  CAGCTCCAAACAGGCTGT    26838       ATCTAG
                                  ACAGCC     TGGAGCTG
                                  ||||||     ||||||||
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                                TGTCGG     ACCTCGAC
                                   ACAA__
GAM475  DKFZP434C0826 5'  CAGCTCCACCTTTCTGTGAT   84034        CCATCTA
                                ATCACAG      GTGGAGCTG
                                |||||||      |||||||||
                                TAGTGTC      CACCTCGAC
                                   TTTC___
GAM475  DKFZP566H073 5'  CAGCTCCACTAAACGGGTTGGA 31380      A    ATC_
          TA                     TATC CAGCC    TAGTGGAGCTG
                                |||| |||||    ||||||||||
                                ATAG GTTGG    ATCACCTCGAC
                                  _    GCAA
GAM475  FBP17    3'  CAGCCTCCCAAATAGCTGTGAT 72783         CATCTAGT   _
                                ATCACAGC       GGAG CTG
                                ||||||||       |||| |||
                                TAGTGTCG       CCTC GAC
                                     ATAAAC__    C
GAM475  FLJ13993  3'  GCCCCACACTGTGATG      60461         CCATCTA    A
                                TATCACAG      GTGG GC
                                ||||||||      |||| ||
                                GTAGTGTC      CACC CG
                                     A_______    C
GAM475  FLJ14007  3'  CAGCTGTTGATTGGCTGTGA   45210         TC   TGG
                                TCACAGCCA  TAG   AGCTG
                                |||||||||  |||   |||||
                                AGTGTCGGT  GTT   TCGAC
                                      TA   G__
GAM475  FLJ20371  3'  CAGCCTGTGCTGGCTGCAATA  35058     CA     TCTA TG A
                                TAT  CAGCCA    G  G GCTG
                                |||  ||||||    |  | ||||
                                ATA  GTCGGT    T  C CGAC
                                  AC     CG__ GT _
GAM475  FLJ23548  5'  ACTAGATGGCTATGATA     44745       C
                                TATCA AGCCATCTAGT
                                |||||  ||||||||||
                                ATAGT TCGGTAGATCA
                                   A
GAM475  GMFB     3'  AGCAAAGAGCTGTGATA     14662         CA   AGTGGA
                                TATCACAGC  TCT     GCT
                                |||||||||  |||     |||
                                ATAGTGTCG  AGA     CGA
                                     __   AA____
GAM475  KIAA0212  3'  CAGAATGTTAACAGCTGTGATA 27933         CATC  GT GAG
                                TATCACAGC    TA  G   CTG
                                |||||||||    ||  |   |||
                                ATAGTGTCG    AT  T   GAC
                                     ACA_  TG AA_
GAM475  KIAA0252  3'  CAGCTTTGTGGTAGCTGTGA   62788        C   TA TG
                                TCACAGC ATC  G  GAGCTG
                                |||||||  |||  |  ||||||
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                                AGTGTCG TGG  T  TTCGAC
                                    A  __ GT
GAM475  KIAA0590  3'  CAGCTCCACTAGATTTTTGGAT 28196    A  CC
                                ATC CAG  ATCTAGTGGAGCTG
                                ||| |||  ||||||||||||||
                                TAG GTT  TAGATCACCTCGAC
                                  _  TT
GAM475  KIAA1257  3'  CAGCCTGTGCAGATGGCTGTG  62731          A_ TG A
                                CACAGCCATCT  G  G GCTG
                                ||||||||||  |  | ||||
                                GTGTCGGTAGA  T  C CGAC
                                      CG GT _
GAM475  MGC2474   3'  CAGCCTCTCAGATGGCTGTGA  43716          AGT GA
                                TCACAGCCATCT   G  GCTG
                                ||||||||||||   |  ||||
                                AGTGTCGGTAGA   C  CGAC
                                       CT_ TC
GAM475  LOC120227 5'  GTTCTAAATGGCTATGATG   74007      C     CTAG
                                TATCA AGCCAT    TGGAGC
                                ||||| ||||||    ||||||
                                GTAGT TCGGTA    ATCTTG
                                   A     A___
GAM475  LOC158333 3'  CAGCAGGCCTTAGATGGGTGCA 86780     CA  G       T  A__
           ATA                    TAT  CA CCATCTAG GG   GCTG
                                ||| || |||||||| ||   ||||
                                ATA  GT GGTAGATT CC   CGAC
                                  AC  G       _  GGA
GAM475  LOC163682 3'  GGTTGTAAACGGCTGTGA    87038        ATCTAG  G
                                TCACAGCC     TG AGCT
                                ||||||||     || ||||
                                AGTGTCGG     AT TTGG
                                     CAA___  G
GAM475  LOC222128 5'  CAGCTCCACTAGGGATTATGA  92716     CAG_  AT
                                TCA    CC  CTAGTGGAGCTG
                                |||    ||  ||||||||||||
                                AGT    GG  GATCACCTCGAC
                                  ATTA  __
GAM475  LOC90784  5'  CAGCTCCACCTGGGGCT     63999      A  TA
                                AGCC TC  GTGGAGCTG
                                |||| ||  |||||||||
                                TCGG GG  CACCTCGAC
                                  _  TC
GAM476  ABCD1     5'  ACAATCCTTCCAGCCA      3459     A    TT
                                TG CTGG  AGGATTGT
                                || ||||  ||||||||
                                AC GACC  TCCTAACA
                                 C    T_
GAM476  CXCL16    3'  ATAGGACTAACCAGCCACTG   41916    C  A       GA
                                CA TG CTGGTTAG  TTGT
                                || || ||||||||  ||||
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                                GT AC GACCAATC  GATA
                                 C  C       AG
GAM476  DDEF2    3'  AACAATCCTCCTGCATCTGT   13948     C_  ACT  TT
                                ACA  TG   GG  AGGATTGTT
                                |||  ||   ||  |||||||||
                                TGT  AC   CC  TCCTAACAA
                                  CT  GT_  __
GAM476  GDF8     3'  ACAATCCATGCCAACGGT    17925      AC    TA
                                ACTG  TGGT  GGATTGT
                                ||||  ||||  |||||||
                                TGGC  ACCG  CCTAACA
                                  A_    TA
GAM476  GRB10    3'  AACATGTTTTTAACCATCAGTG 17968        C        T__
                                CACTGA TGGTTAGGA   TGTT
                                ||||||  |||||||||   ||||
                                GTGACT ACCAATTTT   ACAA
                                   _        TGT
GAM476  ITK      3'  CCAACCAGTCATGTT       18676      C        A
                                AACA TGACTGGTT GG
                                |||| |||||||||  ||
                                TTGT ACTGACCAA CC
                                   _       _
GAM476  LANCL1   3'  ACAATAACAGTCTGTGTT    20205       T    GTTAGG
                                AACAC GACTG     ATTGT
                                |||||  |||||     |||||
                                TTGTG CTGAC     TAACA
                                   T    AA____
GAM476  MAPK7    3'  AACAATCCTTTTCAGT      10839      TT
                                ACTGG  AGGATTGTT
                                |||||  |||||||||
                                TGACT  TCCTAACAA
                                   TT
GAM476  MAPK7    3'  AACAATCCTTTTCAGT      57379      TT
                                ACTGG  AGGATTGTT
                                |||||  |||||||||
                                TGACT  TCCTAACAA
                                   TT
GAM476  MAPK7    3'  AACAATCCTTTTCAGT      57382      TT
                                ACTGG  AGGATTGTT
                                |||||  |||||||||
                                TGACT  TCCTAACAA
                                   TT
GAM476  MAPK7    3'  AACAATCCTTTTCAGT      57385      TT
                                ACTGG  AGGATTGTT
                                |||||  |||||||||
                                TGACT  TCCTAACAA
                                   TT
GAM476  MEF2C    3'  AACAATCCCGGTGTGTCAG   9986       TGG TA
                                CTGAC   T  GGATTGTT
                                |||||   |  ||||||||
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                                GACTG  G  CCTAACAA
                                   TGT GC
GAM476  RPL15    3' AACAATTTAGGACAGTCATGT  11383    C    GTTA
                                ACA TGACTG   GGATTGTT
                                ||| ||||||   ||||||||
                                TGT ACTGAC   TTTAACAA
                                  _    AGGA
GAM476  STAC     3' CCAATCAGTCAGTGT      11991          A
                                ACACTGACTGGTT GG
                                |||||||||||| ||
                                TGTGACTGACTAA CC
                                       _
GAM476  ARPP-19  3' AACAATATCCTAATCA     21782         __
                                TGGTTAGGAT  TGTT
                                ||||||||||  ||||
                                ACTAATCCTA  ACAA
                                      TA
GAM476  FLJ12700 3' TCCAACAGTCAGTGTT     46122         GTTA
                                AACACTGACTG   GGA
                                ||||||||||   |||
                                TTGTGACTGAC   CCT
                                      AA__
GAM476  FLJ20038 3' AATTATCAATCAGTCAG    34399         AG_
                                CTGACTGGTT  GATT
                                ||||||||||  ||||
                                GACTGACTAA  TTAA
                                      CTA
GAM476  FLJ20073 3' AACAGAGGACCAACCAGTC  34481        A  A___
                                GACTGGTT GG   TTGTT
                                |||||||| ||   |||||
                                CTGACCAA CC   GACAA
                                    _ AGGA
GAM476  FLJ23311 3' ACAATCCTCAATCAAGTC   45177     _   _
                                GACT GGTT AGGATTGT
                                |||| |||| ||||||||
                                CTGA CTAA TCCTAACA
                                  A   C
GAM476  FLJ23598 5' ACAACCCTATCCAGTC     45519       T   A
                                GACTGG TAGG TTGT
                                |||||| |||| ||||
                                CTGACC ATCC AACA
                                   T   C
GAM476  KIAA1364 3' AACATGAAATCAGTCAG    63585         AGGAT
                                CTGACTGGTT   TGTT
                                ||||||||||   ||||
                                GACTGACTAA   ACAA
                                      AGT__
GAM476  KIAA1399 3' TCCAATCAGTCAATG      70253    C       A
                                CA TGACTGGTT GGA
                                || ||||||||| |||
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                                GT ACTGACTAA CCT
                                 A       _
GAM476  RAB40A   5'  AACAATCGCTGAATCAGTTTC  82066   T     _  _
                                C GACTGGT TAG GATTGTT
                                | ||||||| ||| |||||||
                                C TTGACTA GTC CTAACAA
                                 T      A  G
GAM476  TTTY2    5'  CTACCAGTCATGTT       87002     C      T
                                AACA TGACTGGT AG
                                |||| |||||||| ||
                                TTGT ACTGACCA TC

                                  _      _
GAM476  YAP1     3'  AATTCATACCAATCAGTGTT  20346        C   TA
                                AACACTGA TGGT  GGATT
                                |||||||| ||||  |||||
                                TTGTGACT ACCA  CTTAA
                                     A   TA
GAM476  LOC132793 5'  AACAATCCTGTGCCCAATC   75918    C  T__
                                GA TGG   TAGGATTGTT
                                || |||   ||||||||||
                                CT ACC   GTCCTAACAA
                                 A  CGT
GAM476  LOC145858 3'  AACCATTTTAACCAGGCA    77541    A        T
                                TG CTGGTTAGGAT GTT
                                || ||||||||||| |||
                                AC GACCAATTTTA CAA
                                 G         C
GAM476  LOC148764 5'  AACAATCCTGCAGACAAGCGTT 78979     A  GA_   GT
                                AAC CT   CTG  TAGGATTGTT
                                ||| ||   |||  ||||||||||
                                TTG GA   GAC  GTCCTAACAA
                                  C  ACA  __
GAM476  LOC159148 5'  CTACCAGTCATGTT       87011     C      T
                                AACA TGACTGGT AG
                                |||| |||||||| ||
                                TTGT ACTGACCA TC

                                  _      _
GAM476  LOC169611 3'  AATCTTGTAACCAGTCATGTT  82752     C       __
                                AACA TGACTGGTTA  GGATT
                                |||| ||||||||||  |||||
                                TTGT ACTGACCAAT  TCTAA
                                  _        GT
GAM476  LOC200488 5'  AACAAGGAAGACCAGTCA    90076        AGGA
                                TGACTGGTT    TTGTT
                                |||||||||    |||||
                                ACTGACCAG    AACAA
                                     AAGG
GAM476  LOC253747 5'  CCTAATCAGCCAATGT      97474     C  A
                                ACA TG CTGGTTAGG
                                ||| || |||||||||
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                                TGT AC GACTAATCC
                                  A  C
GAM476  LOC254866 3'  AACAATCCTGCTAAATCACTG  96765    C  C_   T
                                CA TGA  TGGT AGGATTGTT
                                || |||  |||| |||||||||
                                GT ACT  ATCG TCCTAACAA
                                 C  AA   _
GAM476  LOC257436 3'  AACAATAGAATCAGTCA     95679         AGG
                                TGACTGGTT   ATTGTT
                                |||||||||   ||||||
                                ACTGACTAA   TAACAA
                                     GA_
GAM477  CABC1    5'  GCACAAACAGACGCTC      39654      CTGGC
                                GAGC    TCTGTTTGTGC
                                ||||    ||||||||||
                                CTCG    AGACAAACACG
                                  C____
GAM477  CEACAM5  3'  AACAGAGCAAGACTCCA     15153      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM477  F2R      3'  AACAGAGCAAGACTCCA     8831       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM477  FGFR2    3'  GACAGAGCGAGACTCCA     43377      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM477  FGFR2    3'  GACAGAGCGAGACTCCA     43383      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM477  FUT6     3'  GACAGAGCAAGACTCCA     3812       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM477  GCLM     5'  GGCGCAGACCAGGCTCCA    9026          C    TTGT _
                                TGGAGCCTGG TCTGT    GC C
                                |||||||||| |||||    || |
                                ACCTCGGACC AGACG    CG G
                                      _    ____  A
GAM477  GPC1     3'  GGCTGCAGAGCCCGGCCCCA  9103      A  T      TTGT
                                TGG GCC GGCTCTGT    GCC
                                ||| ||| ||||||||    |||
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                                ACC CGG CCGAGACG    CGG
                                  C   C       T___
GAM477  HPSE     3'  CAAACAGGCCAGGCTCCA    21890          T
                                TGGAGCCTGGC CTGTTTG
                                |||||||||| |||||||
                                ACCTCGGACCG GACAAAC
                                                _
GAM477  IFIT4    3'  AACAGAGCAAGACTCCA     70918      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM477  KCNJ5    3'  GACAGAGCGAGACTCCA     6091       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM477  LY94     3'  GACAGAGCGAGACTCCA     16705      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM477  LZTS1    3'  ACAGAGCCTGGCCCCA      40676     A   T
                                TGG GCC GGCTCTGT
                                ||| ||| ||||||||
                                ACC CGG CCGAGACA
                                  C   T
GAM477  MSH3     3'  AACAGAGCAAGACTCCA     10116      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM477  POLH     3'  AACAGAGCGAGACTCCA     21461      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM477  PRKAB1   3'  GCACACCACCAGGCTCCA    20736          CTC  TT
                                TGGAGCCTGG   TG  TGTGC
                                ||||||||||   ||  |||||
                                ACCTCGGACC   AC  ACACG
                                      ___  C_
GAM477  SIGLEC6  3'  AACAGAGCGAGACTCCA     59925      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM477  SLC10A2  5'  AGCAGAGCCAGGGCCCA     4840      AG
                                TGG  CCTGGCTCTGTT
                                |||  ||||||||||||
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                                ACC  GGACCGAGACGA
                                  CG
GAM477  SNRPN    5'  CAAGCAAAAACCAGGCTCCA  43013        CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM477  SNRPN    5'  CAAGCAAAAACCAGGCTCCA  42991        CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM477  SNRPN    5'  CAAGCAAAAACCAGGCTCCA  42998        CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM477  SNRPN    5'  CAAGCAAAAACCAGGCTCCA  43005        CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM477  TNFSF11  5'  CAGGAGCCAAAGCCGGGCTCCA 13512          CT_   G
                                TGGAGCCTGGCT  GTTT TG
                                ||||||||||||  |||| ||
                                ACCTCGGGCCGA  CGAG AC
                                      AAC   G
GAM477  TSNAX    3'  GGTAACAGAGCAAGACTCCA  20002     C  G     TTG
                                TGGAG CT GCTCTGT  TGCC
                                ||||| || |||||||  ||||
                                ACCTC GA CGAGACA  ATGG
                                   A  A     ____
GAM477  UBE2L3   3'  GCCTTTGCAGAGTCAAGCTCCA 12503       C       TTGT
                                TGGAGC TGGCTCTGT   GC
                                ||||||| |||||||||  ||
                                ACCTCG ACTGAGACG   CG
                                    A       TTTC
GAM477  ZNF264   3'  AACAGAGCGAGACTCCA     12738      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM477  ARNTL2   3'  GACAGAGCGAGACTCCA     39466      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM477  C22orf5  3'  GGATCAGAGCCAGACACCA   24344     AGC       TTTGTG
                                TGG  CTGGCTCTG     CC
                                |||  |||||||||     ||
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                                ACC   GACCGAGAC     GG
                                  ACA        TA____
GAM477  DKFZp547C176 3'  GACAGAGCAAGACTCCA     67223       C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM477  DKFZp564K142 3'  AACAGAGCGAGACTCCA     49522       C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM477  FADS1    3'  GACAGAGCAAGACTCCA     25477       C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM477  FLJ12298  3'  AACAGAGCGAGACTCCA     49664       C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM477  FLJ14117  3'  AACAGAGCAAGACTCCA     42896       C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM477  FLJ14251  3'  GGTAACAGAGCGAGACTCCA   45977       C  G      TTG
                                TGGAG CT GCTCTGT   TGCC
                                |||||| || |||||||   ||||
                                ACCTC GA CGAGACA   ATGG
                                   A  G      ____
GAM477  FLJ14327  3'  AACAGAGCTAGACTCCA     46127       C
                                TGGAG CTGGCTCTGTT
                                |||||| ||||||||||
                                ACCTC GATCGAGACAA
                                   A
GAM477  FLJ14566  5'  GGCCACAGAGCCAGCCCCA    51446     A  C       TT T
                                TGG GC TGGCTCTGT  G GCC
                                ||| || |||||||||  | |||
                                ACC CG ACCGAGACA  C CGG
                                  C  _        __ _
GAM477  FLJ20084  3'  AACAGAGCGAGACTCCA     34511       C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM477  FLJ20306  3'  GACAGAGCAAGACTCCA     34917       C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
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                                ACCTC GA CGAGACAG
                                   A  A
GAM477  FLJ20456  3'  GGTAACAGAGCTAGACTCCA  35215      C       TTG
                                TGGAG CTGGCTCTGT  TGCC
                                ||||| ||||||||||  ||||
                                ACCTC GATCGAGACA  ATGG
                                   A       ___
GAM477  FLJ22054  3'  AACAGAGCAAGACTCCA    94391      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM477  FLJ22393  5'  AGCAGGAACCAGGCTCCA   47058         C_
                                TGGAGCCTGG  TCTGTT
                                ||||||||||  ||||||
                                ACCTCGGACC  GGACGA
                                      AA
GAM477  FLJ23598  3'  GCCAAGAGCCAGCTCCA    45522       C     GTT  T
                                TGGAGC TGGCTCT  TG GC
                                |||||| |||||||  || ||
                                ACCTCG ACCGAGA  AC CG
                                   _     ___ _
GAM477  FLJ31168  3'  GACAGAGCGAGACTCCA    58502      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM477  GP5       3'  GACAGAGCGAGACTCCA    15646      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM477  GTPBP5    3'  GACAGAGCAAGACTCCA    65357      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM477  HIC       3'  AACAGAGCGAGACTCCA    67444      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM477  ING1-like 3'  GACAGAGCGAGACTCCA    54156      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM477  KBRAS2    3'  AACAGAGCAAGACTCCA    34191      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  A
GAM477  KIAA0189 3' CAGGAGCAGAGCCAGGCCCA  28273     A          G
                                TGG GCCTGGCTCTGTTT TG
                                ||| |||||||||||||| ||
                                ACC CGGACCGAGACGAG AC
                                  _          G
GAM477  KIAA0472 3' AGCAGAGCAAGACTCCA     71853      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACGA
                                   A  A
GAM477  KIAA0563 3' GACAGAGCAAGACTCCA     29188      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM477  KIAA0565 3' GACAGAGCAAGACTCCA     66890      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM477  KIAA0648 3' CAAACAGAAGCAGGCTCCA   82651         GC
                                TGGAGCCTG  TCTGTTTG
                                |||||||||  ||||||||
                                ACCTCGGAC  AGACAAAC
                                      GA
GAM477  KIAA0924 3' AACAGAGCGAGACTCCA     29712      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM477  KIAA1028 3' CAGAGCACAGGCTCCA      91934         _
                                TGGAGCCTG GCTCTG
                                ||||||||| ||||||
                                ACCTCGGAC CGAGAC
                                      A
GAM477  KIAA1719 3' GGCCAGGGCCAGGCCCCA    68169     A        TTTGT
                                TGG GCCTGGCTCTG    GCC
                                ||| ||||||||||     |||
                                ACC CGGACCGGGAC    CGG
                                  C          _____
GAM477  KIAA1940 3' GGTCTCAGAACCAAGGCTCCA 79988        _ C    TTTGT
                                TGGAGCCT GG TCTG    GCC
                                |||||||| || ||||    |||
                                ACCTCGGA CC AGAC    TGG
                                     A  A   TC___
GAM477  LGI2     3' CAAATCAAAGCCAGGCTC     36397          C  _
                                GAGCCTGGCT TG TTTG
                                |||||||||| || ||||
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                                CTCGGACCGA AC AAAC
                                     A  T
GAM477  MGC10200  3'  AACAGAGCGAGACTCCA     58980      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM477  MGC2705   5'  GCACCAAGCCAGGCTCC      51113          C  TTT
                                GGAGCCTGGCT TG   GTGC
                                |||||||||||  ||   ||||
                                CCTCGGACCGA AC   CACG
                                      _  ___
GAM477  MGC4562   3'  AACAGAGCGAGACTCCA      55908      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM477  MGC4663   3'  AACAGAGCCAGACTCC       44501      C
                                GGAG CTGGCTCTGTT
                                |||| ||||||||||
                                CCTC GACCGAGACAA
                                  A
GAM477  NPTXR     3'  AACAGAGCAAGACTCCA      54171      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM477  NPTXR     3'  AACAGAGCAAGACTCCA      26635      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM477  OR7C1     5'  AACAGAGCCAAGTCCA       82428      G C
                                TGGA C TGGCTCTGTT
                                |||| | ||||||||||
                                ACCT G ACCGAGACAA
                                  _ A
GAM477  POFUT1    3'  AACAGAGCGAGACTCCA      70462      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM477  PTK6      3'  GACAGAGCGAGACTCCA      19936      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM477  RASGRF2   3'  GCACGAAGCCAGGCTCC      61042          CTGT
                                GGAGCCTGGCT    TTGTGC
                                ||||||||||     ||||||
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                                CCTCGGACCGA  AGCACG
                                      ____
GAM477  SC65     3'  GACAGAGCGAGACTCCA    21289      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM477  SNURF    3'  CAAGCAAAAACCAGGCTCCA  19052          CTC_
                                TGGAGCCTGG  TGTTTG
                                ||||||||||  ||||||
                                ACCTCGGACC  ACGAAC
                                      AAAA
GAM477  TMG4     3'  GACAGAGCAAGACTCCA    43989      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM477  WBSCR23  3'  GACAGAGCAAGACTCCA    46762      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM477  WIRE     3'  GACAGAGCCAGACTCC     78305      C
                                GGAG CTGGCTCTGTT
                                |||| ||||||||||
                                CCTC GACCGAGACAG
                                  A
GAM477  WSB1     3'  AACAGAGCGAGACTCCA    56138      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM477  WSB1     3'  AACAGAGCGAGACTCCA    56144      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM477  LOC115704 3'  CAGCCAGAGCCAGGCCCC  73541    A        T
                                GG GCCTGGCTCTG TTG
                                || |||||||||| |||
                                CC CGGACCGAGAC GAC
                                 C         C
GAM477  LOC124220 5'  GGCACAACCAGACGCC     59146    _   T
                                GGC TCTG TTGTGCC
                                ||| |||| |||||||
                                CCG AGAC AACACGG
                                  C   C
GAM477  LOC127262 3'  GACAGAGCGAGACTCCA    76110      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAG
                                   A  G
GAM477   LOC129563 3'  AGCAGAGCAGGCCCCA      74878     A    G
                                TGG GCCTG CTCTGTT
                                ||| ||||| |||||||
                                ACC CGGAC GAGACGA
                                  C    _
GAM477   LOC129880 3'  AACAGAGCAAGACTCCA      74900      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM477   LOC143196 3'  AACAGAGCGAGACTCCA      82903      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM477   LOC144319 3'  GGCACAAACAGGCGCCCC     83057    A  CTG  T
                                GG GC   GC CTGTTTGTGCC
                                || ||   || ||||||||||
                                CC CG   CG GACAAACACGG
                                 C ___  _
GAM477   LOC145216 3'  GACAGAGCAAGACTCCA      83267      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM477   LOC145820 3'  GACAGAGCAAGACTCCA      77514      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM477   LOC146227 3'  GGTCAGAGCCAGACCCC      77711    AGC       TTTGT
                                GG   CTGGCTCTG    GCC
                                ||   |||||||||    |||
                                CC   GACCGAGAC    TGG
                                 CCA       _____
GAM477   LOC146713 3'  AACAGAGCAAGACTCCA      83720      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM477   LOC147071 3'  GACAGAGCAAGACTCCA      72999      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM477   LOC147649 3'  GACAGAGCGAGACTCCA      78414      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAG
                                   A  G
GAM477  LOC148936 3'  AACAGAGCAAGACTCCA     84286      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM477  LOC149803 5'  CAGGCAGAGCAAGCTCCA    79538       CTG
                                TGGAGC   GCTCTGTTTG
                                ||||||   ||||||||||
                                ACCTCG   CGAGACGGAC
                                   AA_
GAM477  LOC150299 3'  GACAGAGCAAGACTCCA     84970      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM477  LOC151429 3'  GACAGAGCAAGACTCCA     85353      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM477  LOC151904 3'  AACAGAGCGAGACTCCA     80382      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM477  LOC158292 5'  GACAGAGCGAGACTCCA     86730      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM477  LOC162137 5'  CAAGCAGGCCAAGCCCCA    87111     A  C   T
                                TGG GC TGGC CTGTTTG
                                ||| || |||| |||||||
                                ACC CG ACCG GACGAAC
                                  C  A   _
GAM477  LOC163033 5'  CGACCAGGACCAAGCCCCA   82396     A  C   CT   T
                                TGG GC TGG  CTG TTG
                                ||| || |||  ||| |||
                                ACC CG ACC  GAC AGC
                                  C  A   AG   C
GAM477  LOC163682 3'  ACACTCAAAGCCGGGCTCCA  87020           C  TT
                                TGGAGCCTGGCT TG  TGT
                                ||||||||||||| ||  |||
                                ACCTCGGGCCGA AC  ACA
                                       A  TC
GAM477  LOC200261 3'  GCACAAACCTCTGGAGGCCCA 88655     A   GGCTCT
                                TGG GCCT     GTTTGTGC
                                ||| ||||     ||||||||
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                                ACC CGGA     CAAACACG
                                  _   GGTCTC
GAM477  LOC201173 3'  GACAGAGCAAGACTCCA     87329      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM477  LOC201182 5'  AACAGAGCAAGACTCCA     89760      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM477  LOC219627 3'  GACAGAGCGAGACTCCA     92178      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM477  LOC221543 5'  GACAGAGCAAGACTCCA     93742      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM477  LOC221943 5'  GACAGAGCAAGACTCCA     93989      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM477  LOC222160 5'  GACAGAGCAAGACTCCA     94127      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM477  LOC253039 5'  GGCTCCAAAACCAGGCTCTA  96159          CTCTG   T_
                                TGGAGCCTGG    TTTG  GCC
                                ||||||||||    ||||  |||
                                ATCTCGGACC    AAAC  CGG
                                      A____    CT
GAM477  LOC254659 3'  AAACAGAGCAAGACTCCA     95109      C  G
                                TGGAG CT GCTCTGTTT
                                ||||| || |||||||||
                                ACCTC GA CGAGACAAA
                                   A  A
GAM477  LOC256158 5'  AACATCGAGCCAGGCCCA     97639      A       __
                                TGG GCCTGGCTC  TGTT
                                ||| |||||||||  ||||
                                ACC CGGACCGAG  ACAA
                                  _        CT
GAM477  LOC256207 3'  GACAGAGCAAGACTCCA     95169      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAG
                                  A  A
GAM477  LOC257596 5'  GACAGAGCAAGACTCCA     97935       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                  A  A
GAM477  LOC56963  3'  GCACAAAGCCAGGCTTCA    71455           CTGT
                                TGGAGCCTGGCT   TTGTGC
                                ||||||||||||   ||||||
                                ACTTCGGACCGA   AACACG
                                      _____
GAM477  LOC91149  3'  GCTGAACCAGAGCCAGACTCCA 65079       C       _   T
                                TGGAG CTGGCTCTG TTTG GC
                                ||||| ||||||||| |||| ||
                                ACCTC GACCGAGAC AAGT CG
                                  A       C   _
GAM477  LOC91409  3'  AGGCAAGGCCAGGCCCCA    65951     A      TC
                                TGG GCCTGGC  TGTTT
                                ||| |||||||  |||||
                                ACC CGGACCG  ACGGA
                                  C      GA
GAM477  LOC91862  3'  GGTGACAGAGCGAGACTCCA   53470       C  G       TGT
                                TGGAG CT GCTCTGTT   GCC
                                ||||| || ||||||||   |||
                                ACCTC GA CGAGACAG   TGG
                                  A  G      ___
GAM477  LOC92482  3'  AACAGAGCAAGACTCCA     69485       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                  A  A
GAM478  ADRB1     5'  CCAGCCCTGCCACACCCCCCGC 5468        AGAT       AA
          CC                      GGGCG   GTGTGGCA  GCTGG
                                |||||   ||||||||  |||||
                                CCCGC   CACACCGT  CGACC
                                  CCCC       CC
GAM478  CD7       3'  TGCCACACCCCTCACCC     20430     C   AT
                                GGG GAG  GTGTGGCA
                                ||| |||  ||||||||
                                CCC CTC  CACACCGT
                                  A  CC
GAM478  ESRRG     3'  CCAGCTTTACCACTTTTCAGCC 66390     GA  TGT   C
                                GGC  GA   GTGG AAAGCTGG
                                |||  ||   |||| ||||||||
                                CCG  CT   CACC TTTCGACC
                                  A_ TTT    A
GAM478  FOXE3     3'  CCAGCTTTGCGGCGCCCCCC   24103     CGAGAT   G
                                GGG     GTGT GCAAAGCTGG
                                |||     |||| ||||||||||
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                                CCC     CGCG CGTTTCGACC
                                  CC____    G
GAM478  GNAI2    3'  CCAGCTTTGCCCAACACCAGCC 67546      GAGAT   __
                C                  GGGC    GTGT  GGCAAAGCTGG
                                   ||||    ||||  ||||||||||
                                   CCCG    CACA  CCGTTTCGACC
                                     AC___    AC
GAM478  MYO15A   3'  CAACTCCACACCCTAGCCC   32668     G  AT     CAA  C
                                   GGGC AG  GTGTGG   AG TG
                                   |||| ||  ||||||   || ||
                                   CCCG TC  CACACC   TC AC
                                     A  C_     ___  A
GAM478  PCSK2    3'  CCAGCTCCGCCTCTGTCCTCGC 10464        ATGTGT   AA
                TC                   GGGCGAG     GGC  AGCTGG
                                   |||||||     |||  ||||||
                                   CTCGCTC     CCG  TCGACC
                                       CTGTCT   CC
GAM478  S100A7   5'  CCAAACACACACATCTCACTC  11428     C        GCAAAGC
                                   GGG GAGATGTGTG      TGG
                                   ||| ||||||||||      |||
                                   CTC CTCTACACAC      ACC
                                     A         ACAA___
GAM478  SIX2     5'  CCAGCCCCGCCCGCGTCTCGGC 33721    G        T   AAA
                C                   GG CGAGATGTG GGC   GCTGG
                                   || |||||||| |||   |||||
                                   CC GCTCTGCGC CCG   CGACC
                                    G        _   CCC
GAM478  TLX1     3'  CCAGGCCCCCACCACACATCCC 18631     GA_       CAAA_ _
                   AGCC                   GGC   GATGTGTGG    GC TGG
                                   |||   |||||||||     || |||
                                   CCG   CTACACACC     CG ACC
                                     ACC        ACCCC  G
GAM478  TRH      3'  GCCAGCCCCATATTCACACACA 23055         GCAAA_____     III
                   TCCCAGCC                 GATGTGTG        GCTGG   C
                                   ||||||||         |||||   |
                                   CTACACAC         CGACC   G
                                       ACTTATACCC     III
GAM478  TRPM2    5'  CCAGCCAAGGGACACATCTC   12397         GGCAAA
                                   GAGATGTGT      GCTGG
                                   |||||||||      |||||
                                   CTCTACACA      CGACC
                                        GGGAAC
GAM478  DKFZP434O125 3'  CCAGCCCTACCTGTCTTCCC   64958     C     T    CAAA
                                   GGG GAGATG GTGG    GCTGG
                                   ||| |||||| ||||    |||||
                                   CCC TTCTGT CATC    CGACC
                                     _     C    C___
GAM478  DKFZP566G1424 5'  CCAGCCATCCACACATCTGGCC 84778      G         CAAA
                C                   GGGC AGATGTGTGG    GCTGG
                                   |||| ||||||||||    |||||
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                                CCCG TCTACACACC    CGACC
                                  G        TAC_
GAM478  DKFZP761I2123 3'  GCCAGCCTTGTCCACACACACA 48766        _____   A    III
            TCTC                  GATGTGTG    GCAA GCTGG   C
                                |||||||||    |||| |||||  |
                                CTACACAC    TGTT CGACC   G
                                    ACACC    C    III
GAM478  DMTF1    5'  CCAGCTGCAGCCACTCTCGCCC 40937        TGT    AA_
                                GGGCGAGA   GTGGC   AGCTGG
                                |||||||||  |||||  ||||||
                                CCCGCTCT   CACCG   TCGACC
                                    ___     ACG
GAM478  HSPC195   5'  CCAGCCCTGCCCAGCCCGCGCC 80964      AGATG  T    AA
            C                    GGGCG    TG GGCA  GCTGG
                                |||||    || ||||  |||||
                                CCCGC    AC CCGT  CGACC
                                   GCCCG  _   CC
GAM478  IAN4L1   3'  CAGCCCTGCAGCCTGCCC    37223     G  ATGT  G   AA
                                GGGC AG    GT GCA  GCTG
                                |||| ||    || |||  ||||
                                CCCG TC    CG CGT  CGAC
                                  _ _____  A   CC
GAM478  KIAA0329  3'  CCGCCCTGCCACACATCCCGCC 29273       A         AA  T
            C                    GGGCG GATGTGTGGCA  GC GG
                                |||||| ||||||||||  || ||
                                CCCGC CTACACACCGT  CG CC
                                   C          CC  _
GAM478  KIAA0469  3'  CCAGCTCTGCCACTGTCAGCC  29324     GA    T     A
                                GGC  GATG GTGGCA AGCTGG
                                |||  |||| |||||| ||||||
                                CCG  CTGT CACCGT TCGACC
                                  A_   _     C
GAM478  LOC112476 3'  CAACTCTGCGCTCTCAGCC    59110     _    T   TG CAA  C
                                GGC GAGA GTG  G   AG TG
                                ||| |||| |||  |   || ||
                                CCG CTCT CGC  C   TC AC
                                  A    _   GT ___  A
GAM478  LOC145231 3'  CCAGCTTTGGGTGCACACCTCC 83282     C   A    GG_
            CC                    GGG GAG TGTGT   CAAAGCTGG
                                ||| ||| |||||   |||||||||
                                CCC CTC ACACG   GTTTCGACC
                                  _   C     TGG
GAM478  LOC148394 5'  CCAGCCTTGCCTGGCTCTCGCC 84144         T  GT    A
            T                    GGGCGAGA GT  GGCAA GCTGG
                                ||||||||| ||  ||||| |||||
                                TCCGCTCT CG  CCGTT CGACC
                                    _ GT    C
GAM478  LOC148870 3'  CCAGCTCCAGAACCACCCGCCC 79043      AGAT  G_   CAA
                                GGGCG    GT  TGG   AGCTGG
                                |||||    ||  |||   ||||||
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                                CCCGC   CA  ACC   TCGACC
                                  CCAC  AG  ___
GAM478  LOC149017 5'  CCAAACACACACATCTCACTC  70912     C        GCAAAGC
                                GGG GAGATGTGTG      TGG
                                ||| ||||||||||      |||
                                CTC CTCTACACAC      ACC
                                  A         ACAA___
GAM478  LOC254196 5'  CCAGCCTTGCCTGGTTCTCGCC 97347         TGTGT    A
           T                     GGGCGAGA    GGCAA GCTGG
                                ||||||||    ||||| |||||
                                TCCGCTCT    CCGTT CGACC
                                    TGGT_    C
GAM478  LOC93589  3'  CCAGCGCACACACATCTCCCC  72668     C        _  AAA
                                GGG GAGATGTGTG GC   GCTGG
                                ||| ||||||||| ||   |||||
                                CCC CTCTACACAC CG   CGACC
                                  _        A  ___
GAM479  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM479  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875        CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM479  FDFT1    3'  TAGGAAAGTGAAATG       15518            A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                        _
GAM479  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
           TG                     CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM479  KLF4     3'  TCCCAGACAGTGGATATG     14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM479  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM479  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
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                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM479  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM479  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM479  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM479  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM479  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||         |||||||||
                                GTAAAG         CAGACTCTA
                                   AAACATTT_
GAM479  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM479  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM479  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM479  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM479  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598         CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
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                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM479  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM479  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                     TA__    TT
GAM479  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A     TC
GAM479  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                     AAAGG
GAM479  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647       ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM479  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM479  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM479  LOC222134 5'  ACAGTGAAGTGAAATG       94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                      _
GAM480  A1BG     3'  CAGGGTCTCACTGTGTTGC    55413        TAT_
                                GCAACACA    GGCTTTG
                                ||||||||    |||||||
                                CGTTGTGT    CTGGGAC
                                     CACT
GAM480  ACPT     3'  CACCCCGCCATATGCTGC     54980     ACA       TTT
                                GCA   CATATGGC   GTG
                                |||   ||||||||   |||
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                                CGT   GTATACCG   CAC
                                  C__       CCC
GAM480  ACPT     3'  CACCCCGCCATATGCTGC    54986     ACA       TTT
                                GCA   CATATGGC   GTG
                                |||   ||||||||   |||
                                CGT   GTATACCG   CAC
                                  C__       CCC
GAM480  AHCY     3'  CACAAAGCCCATGTGTTTTGC  5473       C       _
                                GCAA ACATATGG CTTTGTG
                                |||| |||||||| |||||||
                                CGTT TGTGTACC GAAACAC
                                  T       C
GAM480  BCL7A    3'  CAGGATTCCATTTGTGTTGCT  40638          T    CT  G
                                AGCAACACA ATGG  TT TG
                                ||||||||| ||||  || ||
                                TCGTTGTGT TACC  AG AC
                                      T    TT  G
GAM480  CDK5R2   3'  CACAAAGCCACCGCCGCTGTT  14132      ACACATA
                                AGCA      TGGCTTTGTG
                                ||||      ||||||||||
                                TTGT      ACCGAAACAC
                                  CGCCGCC
GAM480  CHC1     3'  CACAAAGCATACTCTTGC    7019       CACA    G
                                GCAA    TATG CTTTGTG
                                ||||    |||| |||||||
                                CGTT    ATAC GAAACAC
                                  CTC_   _
GAM480  CIT      3'  CACAAGGCATCTGTTGCT    69741        CATATG
                                AGCAACA     GCTTTGTG
                                |||||||     ||||||||
                                TCGTTGT     CGGAACAC
                                    CTA___
GAM480  COL6A2   5'  CAGGGCCACAGGTGCTGC    8480      A   ATA
                                GCA CAC   TGGCTTTG
                                ||| |||   ||||||||
                                CGT GTG   ACCGGGAC
                                  C   GAC
GAM480  COL6A2   5'  CAGGGCCACAGGTGCTGC    54168     A   ATA
                                GCA CAC   TGGCTTTG
                                ||| |||   ||||||||
                                CGT GTG   ACCGGGAC
                                  C   GAC
GAM480  EYA1     3'  CACAGCGTTATGTGTCTGC   4952      AC       T
                                GCA  ACATATGGC TTGTG
                                |||  ||||||||| |||||
                                CGT  TGTGTATTG GACAC
                                  C_        C
GAM480  FBN2     3'  CAAGGAACCATATGTG      8844           __
                                CACATATGG  CTTTG
                                |||||||||  |||||
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                                GTGTATACC  GGAAC
                                     AA
GAM480  FMO1    3'  CACAAATGATTGTGTTGT    8924        TATGGC
                                GCAACACA    TTTGTG
                                ||||||||    ||||||
                                TGTTGTGT    AAACAC
                                     TAGT__
GAM480  GALNT2  3'  CACAAAGCCGAGTCGTGT    15593     _ A
                                ACAC AT TGGCTTTGTG
                                |||| || ||||||||||
                                TGTG TG GCCGAAACAC
                                  C  A
GAM480  GALNT2  3'  CACAAAGCCGTTCGCAGCT   15594    AACACAT
                                AGC     ATGGCTTTGTG
                                |||     ||||||||||
                                TCG     TGCCGAAACAC
                                  ACGCT__
GAM480  GPR4    3'  CAGGGTCTCACTGTGTTGC   59902       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                     CACT
GAM480  HNMT    3'  CACAAAGCCTGTGTTACT    22567    C    TAT
                                AG AACACA  GGCTTTGTG
                                || ||||||  |||||||||
                                TC TTGTGT  CCGAAACAC
                                 A    ____
GAM480  IL1RN   3'  CACAAAGCCCTTCCATGTCGC 5141    A  CATAT_
                                GC ACA     GGCTTTGTG
                                || |||     |||||||||
                                CG TGT     CCGAAACAC
                                 C  ACCTTC
GAM480  IL2RB   3'  CACAAAGTGGATGCCTGCT   6069     ACA  ATG
                                AGCA  CAT  GCTTTGTG
                                ||||  |||  ||||||||
                                TCGT  GTA  TGAAACAC
                                  CC_  GG_
GAM480  ITSN2   3'  CACAAAGCCATGCACGCT    38971    AACACA
                                AGC     TATGGCTTTGTG
                                |||     ||||||||||||
                                TCG     GTACCGAAACAC
                                  CAC____
GAM480  JRK     3'  CAGGGTCTCACTGTGTTGC   86524       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                     CACT
GAM480  LANCL1  3'  CACAATTTTATATGTATGCT  20210     AC     CT
                                AGCA  ACATATGG  TTGTG
                                ||||  ||||||||  |||||
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                                TCGT  TGTATATT  AACAC
                                  A_       TT
GAM480  LGR6    5'  GGCCATCGTGTTGCT      84200        AT
                                AGCAACAC  ATGGCT
                                ||||||||  ||||||
                                TCGTTGTG  TACCGG
                                    C_
GAM480  LRRC2    3'  CAAGGCACCATGTGTTACT   44465    C      ATG
                                AG AACACAT   GCTTTG
                                || |||||||   ||||||
                                TC TTGTGTA   CGGAAC
                                 A      CCA
GAM480  MYBL2    3'  CAGGGCCATGTGCTGC      10154     ACA
                                GCA   CATATGGCTTTG
                                |||   ||||||||||||
                                CGT   GTGTACCGGGAC
                                  C__
GAM480  OCLN     3'  CACAAAGTTTTGGTTGCT    10314       A  TAT
                                AGCAAC CA   GGCTTTGTG
                                |||||| ||   |||||||||
                                TCGTTG GT   TTGAAACAC
                                   _  T__
GAM480  OSR1     3'  CACAAAGTAATATGTG      17566        G
                                CACATAT GCTTTGTG
                                ||||||| ||||||||
                                GTGTATA TGAAACAC
                                    A
GAM480  PCDH9    5'  CACAAAGTGACAGTGCTGGCT  82794     AA_   ATATG
                                AGC   CAC    GCTTTGTG
                                |||   |||    ||||||||
                                TCG   GTG    TGAAACAC
                                  GTC   ACAG_
GAM480  PRDM2    5'  CACAAAGCCACATCCTGC    24246     ACAC  A
                                GCA    AT TGGCTTTGTG
                                |||    || ||||||||||
                                CGT    TA ACCGAAACAC
                                  CC__  C
GAM480  PRDM2    5'  CACAAAGCCACATCCTGC    31847     ACAC  A
                                GCA    AT TGGCTTTGTG
                                |||    || ||||||||||
                                CGT    TA ACCGAAACAC
                                  CC__  C
GAM480  PRG4     3'  CACAAAGCTTTATCGTGTTGT  19415        _   T
                                GCAACAC ATA GGCTTTGTG
                                ||||||| ||| |||||||||
                                TGTTGTG TAT TCGAAACAC
                                    C   T
GAM480  RXRB     3'  CACAAAGCACTGGCCTTGC    41757      CA_  TATG
                                GCAA   CA    GCTTTGTG
                                ||||   ||    ||||||||
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                                CGTT  GT   CGAAACAC
                                  CCG CA__
GAM480  SMARCD1  3' CACAAAGTTCCCATGTG    57429       ___
                                CATATGG  CTTTGTG
                                |||||||  |||||||
                                GTGTACC  GAAACAC
                                   CTT
GAM480  SMARCD1  3' CACAAAGTTCCCATGTG    11811       ___
                                CATATGG  CTTTGTG
                                |||||||  |||||||
                                GTGTACC  GAAACAC
                                   CTT
GAM480  SMURF1   3' CACGTGTGATCTGTGTTGC   92448       T  G  TT
                                GCAACACA AT GC  TGTG
                                |||||||| || ||  ||||
                                CGTTGTGT TA TG  GCAC
                                     C  G  T_
GAM480  STX7     3' CACCAAGATGTGTGTTACT   13108    C      GG   T
                                AG AACACATAT  CTT GTG
                                || |||||||||  ||| |||
                                TC TTGTGTGTA  GAA CAC
                                 A       __  C
GAM480  TAF4B    3' CACAAAGCATTGTTGC     87167      CATATG
                                GCAACA     GCTTTGTG
                                ||||||     ||||||||
                                CGTTGT     CGAAACAC
                                   TA____
GAM480  TF       3' CACAGCTCTGTGTTGC     6512        TAT   T
                                GCAACACA   GGCT TG
                                ||||||||   |||| ||
                                CGTTGTGT   TCGA AC
                                     C__   C
GAM480  TLR4     5' CACAGGGCCACTGCTGCT    12317     A  CATA
                                AGCA CA    TGGCTTTGTG
                                |||| ||    ||||||||||
                                TCGT GT    ACCGGGACAC
                                  C  C___
GAM480  TLR4     5' CACAGGGCCACTGCTGCT    56736     A  CATA
                                AGCA CA    TGGCTTTGTG
                                |||| ||    ||||||||||
                                TCGT GT    ACCGGGACAC
                                  C  C___
GAM480  TLR4     5' CACAGGGCCACTGCTGCT    56727     A  CATA
                                AGCA CA    TGGCTTTGTG
                                |||| ||    ||||||||||
                                TCGT GT    ACCGGGACAC
                                  C  C___
GAM480  TLR4     5' CACAGGGCCACTGCTGCT    56732     A  CATA
                                AGCA CA    TGGCTTTGTG
                                |||| ||    ||||||||||
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                                TCGT GT   ACCGGGACAC
                                  C  C___
GAM480  VIPR2    3' CACAGTCTCCATGTGTGTGC  12605    A      CT_
                                GCA CACATATGG  TTGTG
                                ||| |||||||||  |||||
                                CGT GTGTGTACC  GACAC
                                  _      TCT
GAM480  ANKT     3' CAGGGTCTCACTGTGTTGC   33024      TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM480  ATP9A    3' CACAAAGCCAGTGGCTGTT   62039    A_  ATA
                                AGCA  CAC  TGGCTTTGTG
                                ||||  |||  ||||||||||
                                TTGT  GTG  ACCGAAACAC
                                  CG  ___
GAM480  CETN2    3' CACATGTTACACCTGTGTTGC 15093      TA GCTT_
                                GCAACACA TG   TGTG
                                |||||||| ||   ||||
                                CGTTGTGT AC   ACAC
                                    CC ATTGT
GAM480  CYLD     3' CACAAGGTTTTATACTGCT   30883    ACAC  TG
                                AGCA   ATA GCTTTGTG
                                ||||   ||| ||||||||
                                TCGT   TAT TGGAACAC
                                  CA__  TT
GAM480  DKFZP586A0522 3' CAGGGTCTCACTGTGTTGC  25871      TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM480  DKFZp762K222 3' ACAGATGCGTGTTGCT     71116      ATATG _
                                AGCAACAC    GC TTTGT
                                ||||||||    || |||||
                                TCGTTGTG    CG AGACA
                                    _____ T
GAM480  FLJ10297  3' CAGGGCTTCACTGTGTTGC   35979      TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   TCGGGAC
                                    CACT
GAM480  FLJ10511  3' CACATGTGTATGTGCAGCT   36204    AA     G TT
                                AGC  CACATATG C  TGTG
                                |||  |||||||| |  ||||
                                TCG  GTGTATGT G  ACAC
                                  AC      _ T_
GAM480  FLJ11029  5' CACTAGCACCTGTGTTGCT   60973      TATG  TT
                                AGCAACACA   GCT  GTG
                                |||||||||   |||  |||
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                                TCGTTGTGT   CGA  CAC
                                     CCA_   T_
GAM480  FLJ11117  3'  CACAAAGCTTGTATGTG     37073        _
                                CACATATG GCTTTGTG
                                |||||||| ||||||||
                                GTGTATGT CGAAACAC
                                     T
GAM480  FLJ11715  3'  CAGGGTCTCCATATGTTGC   44668      C  AT_
                                GCAACA AT   GGCTTTG
                                |||||| ||   |||||||
                                CGTTGT TA   CTGGGAC
                                   A  CCT
GAM480  FLJ20275  3'  CACAAAGGGCTTTATGTGTCAG 34819    A_     T   __
           CT                     AGC  ACACATA GGCT  TTGTG
                                |||  ||||||| ||||  |||||
                                TCG  TGTGTAT TCGG  AACAC
                                  AC      T   GA
GAM480  FLJ20413  3'  CAGAGCCGCATGCACTGCT   35131     ACA   A
                                AGCA   CAT TGGCTTTG
                                ||||   ||| ||||||||
                                TCGT   GTA GCCGAGAC
                                  CAC   C
GAM480  FLJ20450  3'  CACCTGGGACCTGTGTTGCT   35192        TAT  _   T_
                                AGCAACACA   GG CTT  GTG
                                |||||||||   || |||  |||
                                TCGTTGTGT   CC GGG  CAC
                                     ___  A   TC
GAM480  FLJ20671  3'  CAATTCAAATGTGTTGC     35516        A   CT
                                GCAACACAT TGG  TTG
                                ||||||||| |||  |||
                                CGTTGTGTA ACT  AAC
                                     A   T_
GAM480  FLJ23598  3'  CACAAAGAGAGGCTGTGCTGC  45521     A    TATGG_
                                GCA CACA     CTTTGTG
                                ||| ||||     |||||||
                                CGT GTGT     GAAACAC
                                  C    CGGAGA
GAM480  FRSB      3'  CATAGGCCATACATGTTACT   19090    C    CA      T
                                AG AACA  TATGGCTT GTG
                                || ||||  |||||||| |||
                                TC TTGT  ATACCGGA TAC
                                 A    AC      _
GAM480  H2AV      3'  CACAGCCATATGTATTGTT    56845      C        T
                                AGCAA ACATATGGCT TG
                                ||||| |||||||||| ||
                                TTGTT TGTATACCGA AC
                                   A        C
GAM480  HIC2      3'  CACAAAGTCTGTACCGC     65256    AAC   TAT
                                GC   ACA   GGCTTTGTG
                                ||   |||   |||||||||
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                              CG  TGT  CTGAAACAC
                               CCA  ___
GAM480  KIAA0140 3' CACATGGCCATGTCTTGC   27806    CAC      T
                              GCAA  ATATGGCT TGTG
                              ||||  |||||||| ||||
                              CGTT  TGTACCGG ACAC
                                C__      T
GAM480  KIAA0215 3' CAAATTCCATATGTAATGC  28416    AC      C_
                              GCA  ACATATGG  TTTG
                              |||  ||||||||  ||||
                              CGT  TGTATACC  AAAC
                                AA      TT
GAM480  KIAA0254 3' AGCCACCTGTGTTGCT     28595        TA
                              AGCAACACA  TGGCT
                              |||||||||  |||||
                              TCGTTGTGT  ACCGA
                                   CC
GAM480  KIAA0618 3' CACAAAAACATGTGTTGT   29162       TA  GC
                              GCAACACA  TG  TTTGTG
                              ||||||||  ||  ||||||
                              TGTTGTGT  AC  AAACAC
                                   __  AA
GAM480  KIAA0953 3' AGCTTTCATAGTGTTGCT   66778       A   ___
                              AGCAACAC TATG  GCT
                              |||||||| ||||  |||
                              TCGTTGTG ATAC  CGA
                                   _  TTT
GAM480  KIAA1193 3' CACAGAGCCATATACCTCGCT 67630    AACAC
                              AGC    ATATGGCTTTGTG
                              |||    |||||||||||||
                              TCG    TATACCGAGACAC
                                CTCCA
GAM480  KIAA1281 3' CACAGAGTAACAAATGTTGCT 89151       CATATG
                              AGCAACA     GCTTTGTG
                              |||||||     ||||||||
                              TCGTTGT     TGAGACAC
                                  AAACAA
GAM480  KIAA1466 5' AGCCATATGTGCGCT      71913    AA
                              AGC  CACATATGGCT
                              |||  ||||||||||
                              TCG  GTGTATACCGA
                                C_
GAM480  KIAA1821 3' CAGGGTCTCACTGTGTTGC  71780       TAT_
                              GCAACACA   GGCTTTG
                              ||||||||   |||||||
                              CGTTGTGT   CTGGGAC
                                   CACT
GAM480  KIF13B   3' CACAAAGTCCGTGGTGC    82820    A  ATAT
                              GCA CAC   GGCTTTGTG
                              ||| |||   |||||||||
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                              CGT GTG   CTGAAACAC
                                G  C___
GAM480  KIF13B   3' CACAAAGTCCGTGGTGC    30904    A  ATAT
                              GCA CAC   GGCTTTGTG
                              ||| |||   |||||||||
                              CGT GTG   CTGAAACAC
                                G  C___
GAM480  MGC12921 3' CACAAAGGCCGTTATTGC   63775    CACAT   _
                              GCAA   ATGGC TTTGTG
                              ||||   ||||| ||||||
                              CGTT   TGCCG AAACAC
                                AT___   G
GAM480  MGC14836 5' CACAAAGCTATCATCCTGC  53035    ACACAT
                              GCA    ATGGCTTTGTG
                              |||    ||||||||||
                              CGT    TATCGAAACAC
                                CCTAC_
GAM480  MGC15429 3' CACATTGTCATGTGCAGCT  51249    AACA     TT
                              AGC   CATATGGC  TGTG
                              |||   ||||||||  ||||
                              TCG   GTGTACTG  ACAC
                                AC__      TT
GAM480  MGC15875 3' CGAGGCCATAATGCT     51908    ACACA
                              AGCA   TATGGCTTTG
                              ||||   |||||||||
                              TCGT   ATACCGGAGC
                                A____
GAM480  MGC16279 5' GAAGCCATCGTGTCGCT    51888    A   AT
                              AGC ACAC  ATGGCTTT
                              ||| ||||  ||||||||
                              TCG TGTG  TACCGAAG
                                C   C_
GAM480  MGC27434 3' CACAATAAGTATGTGTT    58947       GGCT
                              AACACATAT   TTGTG
                              |||||||||   |||||
                              TTGTGTATG   AACAC
                                   AAT_
GAM480  MGC3048  3' CACAAAGCATGAATGTT    43899    CA   G
                              AACA  TATG CTTTGTG
                              ||||  |||| |||||||
                              TTGT  GTAC GAAACAC
                                AA   _
GAM480  MIG-6    3' CACAAGCTGGCCTTGTGTTGCT 38486       TAT   ___
                              AGCAACACA  GGCT  TTGTG
                              |||||||||  ||||  |||||
                              TCGTTGTGT  CCGG  AACAC
                                   T__   TCG
GAM480  MUC17    3' CACTGCCCCATATGTGTCCCT  94271   CA      CTTT
                              AG  ACACATATGG   GTG
                              ||  ||||||||||   |||
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                                TC  TGTGTATACC   CAC
                                 CC        CCGT
GAM480  MYO3B    3'  CACTCTCCCACATGTGTTGT  57301        A   CTTT
                                GCAACACAT TGG   GTG
                                ||||||||| |||   |||
                                TGTTGTGTA ACC   CAC
                                     C   CTCT
GAM480  NS1-BP   3'  CACAAAGCTTTTGCATATTGC  72542     CA__  TAT
                                GCAA   CA   GGCTTTGTG
                                ||||   ||   |||||||||
                                CGTT   GT   TCGAAACAC
                                  ATAC  TT_
GAM480  OR51E2   3'  CACAGGTTTTATGTGTTCT   47791    C      TG   T
                                AG AACACATA  GCTT GTG
                                || ||||||||  |||| |||
                                TC TTGTGTAT  TGGA CAC
                                 _       TT   _
GAM480  PRDM11   3'  CAGGTGCTCCATGTGTTGC   39581        AT  _
                                GCAACACAT  GGC TTTG
                                |||||||||  ||| ||||
                                CGTTGTGTA  TCG GGAC
                                     CC   T
GAM480  PRO0943  5'  CACAAAAGTGTTATATGTG   37701         ___
                                CACATATGGC   TTTGTG
                                ||||||||||   ||||||
                                GTGTATATTG   AAACAC
                                      TGA
GAM480  SULT1C2  5'  CACAACGCAGCCATATGCTG  21674    _      ___
                                CA CATATGGCT   TTGTG
                                || |||||||||   |||||
                                GT GTATACCGA   AACAC
                                 C        CGC
GAM480  VEST1    3'  CACCTGCCATACATGTTGT   53685      CA     TTT
                                GCAACA  TATGGC   GTG
                                ||||||  ||||||   |||
                                TGTTGT  ATACCG   CAC
                                   AC     TC_
GAM480  ZFP100   3'  AGTCACCTGTGTTGCT     70049        TA
                                AGCAACACA  TGGCT
                                |||||||||  |||||
                                TCGTTGTGT  ACTGA
                                     CC
GAM480  ZNF363   5'  AGCCATATTGTCGCT      73452     A  C
                                AGC ACA ATATGGCT
                                ||| ||| ||||||||
                                TCG TGT TATACCGA
                                  C  _
GAM480  LOC118611 5'  CACAGAGCATTTGCGTTACT   75469    C   A  TATG
                                AG AAC CA    GCTTTGTG
                                || ||| ||    ||||||||
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                                TC TTG GT    CGAGACAC
                                 A   C  TTA_
GAM480   LOC120526 3'  CAGGGCCATTGCACTGCT    74015      ACA  T
                                AGCA   CA ATGGCTTTG
                                ||||   || |||||||||
                                TCGT   GT TACCGGGAC
                                  CAC  _
GAM480   LOC126669 3'  CACAAAGTTCCATATGT     75399         __
                                ACATATGG  CTTTGTG
                                ||||||||  |||||||
                                TGTATACC  GAAACAC
                                     TT
GAM480   LOC139840 5'  CACAAGAGCCATGGGT      76266    A        _
                                AC TATGGCTTT GTG
                                || |||||||| |||
                                TG GTACCGAGA CAC
                                 G        A
GAM480   LOC143465 5'  CACATGCACATATGTG      82962         _  TT
                                CACATATG GC  TGTG
                                |||||||| ||  ||||
                                GTGTATAC CG  ACAC
                                     A  T_
GAM480   LOC146774 3'  CACTGACATGTGTGTGC     78094     A       GCTTT
                                GCA CACATATG    GTG
                                ||| ||||||||    |||
                                CGT GTGTGTAC    CAC
                                  _       AGT__
GAM480   LOC147407 5'  CACAAAGCTATCATCCTGC    76322     ACACAT
                                GCA     ATGGCTTTGTG
                                |||     ||||||||||
                                CGT     TATCGAAACAC
                                  CCTAC_
GAM480   LOC151057 3'  ACAGAGCACATACTGT      85199     _   _
                                ACA TATG GCTTTGT
                                ||| |||| |||||||
                                TGT ATAC CGAGACA
                                  C    A
GAM480   LOC151473 3'  CACAACAACCTATGTGTT     80254         T  CT_
                                AACACATA GG   TTGTG
                                |||||||| ||   |||||
                                TTGTGTAT CC   AACAC
                                     _ AAC
GAM480   LOC154739 5'  CACAAAGTTCAAATGTATGC   86227     AC    A  _
                                GCA  ACAT TGG CTTTGTG
                                |||  |||| ||| |||||||
                                CGT  TGTA ACT GAAACAC
                                  A_   A  T
GAM480   LOC157507 5'  CACAGCTGTGTATGTGTGCT   81454      A      __    T
                                AGCA CACATAT  GGCT TG
                                |||| |||||||  |||| ||
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                                TCGT GTGTATG  TCGA AC
                                  _     TG   C
GAM480  LOC161734 3'  CACAAACATTTAGTGTTGCT   87097       AT_  GC
                                AGCAACAC   ATG  TTTGTG
                                ||||||||   |||  ||||||
                                TCGTTGTG   TAC  AAACAC
                                    ATT  __
GAM480  LOC196410 3'  CACAAAAGTCATGGTG     87657     A      _
                                CAC TATGGCTTT GTG
                                ||| ||||||||| |||
                                GTG GTACTGAAA CAC
                                  _       A
GAM480  LOC196485 3'  CACAAAAACCTGTGTTGT    87730       TAT  C_
                                GCAACACA   GG  TTTGTG
                                ||||||||   ||  ||||||
                                TGTTGTGT   CC  AAACAC
                                    ___  AA
GAM480  LOC196529 3'  CAGGGTCTCACTGTGTTGC   87771       TAT_
                                GCAACACA    GGCTTTG
                                ||||||||    |||||||
                                CGTTGTGT    CTGGGAC
                                    CACT
GAM480  LOC197003 5'  CACAAAGCTCCATGCTGT    87870    _  AT
                                ACA CAT  GGCTTTGTG
                                ||| |||  |||||||||
                                TGT GTA  TCGAAACAC
                                  C   CC
GAM480  LOC202025 5'  CACAGTTGTATGGTTGCT    90281      A   TG   T
                                AGCAAC CATA  GCT TG
                                |||||| ||||  ||| ||
                                TCGTTG GTAT  TGA AC
                                   _   GT   C
GAM480  LOC203276 3'  CACAAAGTTCAAGTGTATGC  90475    _   ATAT
                                GCA ACAC    GGCTTTGTG
                                ||| ||||    |||||||||
                                CGT TGTG    TTGAAACAC
                                  A   AAC_
GAM480  LOC203292 3'  CAGGGTTTCATATGTGTT    90509        __
                                AACACATATG  GCTTTG
                                ||||||||||  ||||||
                                TTGTGTATAC  TGGGAC
                                     TT
GAM480  LOC203305 3'  CACAAAGTTCAAGTGTATGC  90519    _   ATAT
                                GCA ACAC    GGCTTTGTG
                                ||| ||||    |||||||||
                                CGT TGTG    TTGAAACAC
                                  A   AAC_
GAM480  LOC221354 3'  CACAAAAACATGTGTTGT    92409       TA  GC
                                GCAACACA  TG  TTTGTG
                                ||||||||  ||  ||||||
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                                TGTTGTGT  AC  AAACAC
                                    __  AA
GAM480  LOC254243 3'  CACAAAGTTCAAGTGTATGC  97404    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM480  LOC255870 3'  CACAACTGGCCATGTCCTGC  94657    ACAC     __
                                GCA   ATATGGCT  TTGTG
                                |||   ||||||||  |||||
                                CGT   TGTACCGG  AACAC
                                  CC__      TC
GAM480  LOC90038  3'  CACAAAGTTCAAGTGTATGC  61148    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM480  LOC90321  3'  CACAAATGGATTGTGTGTGC  62262    A    TGGC_
                                GCA CACATA    TTTGTG
                                ||| ||||||    ||||||
                                CGT GTGTGT    AAACAC
                                  _    TAGGT
GAM480  LOC90750  3'  CACAAAGTTAAGATTGCT   63917     CACATA
                                AGCAA    TGGCTTTGTG
                                |||||    ||||||||||
                                TCGTT    ATTGAAACAC
                                   AGA___
GAM480  LOC91069  3'  GAAGCCATCGTGTCACT    64778   CA   AT
                                AG  ACAC  ATGGCTTT
                                ||  ||||  ||||||||
                                TC  TGTG  TACCGAAG
                                 AC   C_
GAM480  LOC92539  3'  CACAAAGCCACTGTAGC    69630   A  CATA
                                GC ACA   TGGCTTTGTG
                                || |||   ||||||||||
                                CG TGT   ACCGAAACAC
                                 A  C___
GAM481  CNGA1    3'  CAACTGATAATGTGCAAA   59507        GC  A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                      A_  _
GAM481  ESRRG    3'  TGGCAGTCTTATGTGCAAA  66396       TAGCT
                                TTTGCACAT   AGATTGCCA
                                |||||||||   |||||||||
                                AAACGTGTA   TCTGACGGT
                                     T____
GAM481  KCNJ3    3'  GCAATAATGTGCAAA     9525         GCTAGA
                                TTTGCACATTA    TTGC
                                ||||||||||    ||||
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                                AAACGTGTAAT     AACG
                                        _______
GAM481  SDC2     3'  GCAAATTAATGTGTAAA     67132          CTAGA
                                TTTGCACATTAG     TTGC
                                ||||||||||||    ||||
                                AAATGTGTAATT    AACG
                                      A_____
GAM481  USP9X    3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
          A                      TTTGCACATTAGC     GCCAT
                                ||||||||||||||     |||||
                                AAATGTGTAATCG     CGGTA
                                       TAGTC_
GAM481  AMOTL1   3'  GGCAAGTAATGTGCAAA     73650          G  AGAT
                                TTTGCACATTA CT    TGCC
                                |||||||||||| ||    ||||
                                AAACGTGTAAT GA    ACGG
                                        _ _____
GAM481  BCAR3    3'  AGTAATAATGTGCAAA      13098          __
                                TTTGCACATTA  GCT
                                ||||||||||  |||
                                AAACGTGTAAT  TGA
                                      AA
GAM481  DKFZP434B044 3'  TGACAATTAAATGTGCAGA    48930          AGCTA    C
                                TTTGCACATT     GATTG CA
                                |||||||||     ||||| ||
                                AGACGTGTAA     TTAAC GT
                                      A_____     A
GAM481  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                TTTGCACATTAG  AGA TG CAT
                                ||||||||||||  ||| || |||
                                AGACGTGTAATC  TTT AC GTA
                                       __  T  A
GAM481  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
          AA                     TTTGCACATTAGCTAGATTGCCAT
                                ||||||||||||||||||||||||||
                                AAACGTGTAATCGATCTAACGGTA

GAM482  ADRA1A   3'  GCACAAATCCAACATG      52784       AAGCC  A
                                CATGT     TG ATTTGTGC
                                |||||     || ||||||||
                                GTACA     AC TAAACACG
                                   ______  C
GAM482  AEGL1    5'  GCACAAATACACTACAT     6679        AGCC  A
                                ATGTA    TG ATTTGTGC
                                |||||    || ||||||||
                                TACAT    AC TAAACACG
                                   C___  A
GAM482  CDH2     3'  GCACAAATGTTTTACAT     8377         CCTGA
                                ATGTAAG     ATTTGTGC
                                |||||||     ||||||||
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                                TACATTT    TAAACACG
                                   TG___
GAM482  CHRNE   3'  GCCCTCAGGCCCACAGGT   3586     A  AA    ATTTGT
                                ACC TGT  GCCTGA    GC
                                ||| |||  ||||||     ||
                                TGG ACA  CGGACT    CG
                                  _  CC    CC____
GAM482  COL4A3  3'  GGCCATGGCTCACATGGT   3622       A   TGAATT  T
                                ACCATGT AGCC    TG GCC
                                ||||||| ||||    || |||
                                TGGTACA TCGG    AC CGG
                                   C   T_____ _
GAM482  COL4A3  3'  GGCCATGGCTCACATGGT   48557      A   TGAATT  T
                                ACCATGT AGCC    TG GCC
                                ||||||| ||||    || |||
                                TGGTACA TCGG    AC CGG
                                   C   T_____ _
GAM482  COL4A3  3'  GGCCATGGCTCACATGGT   48568      A   TGAATT  T
                                ACCATGT AGCC    TG GCC
                                ||||||| ||||    || |||
                                TGGTACA TCGG    AC CGG
                                   C   T_____ _
GAM482  CYP3A4  3'  ACAAGCCTGGCCTACATGGT  33923      A  TGAA
                                ACCATGTA GCC   TTTGT
                                |||||||| |||   |||||
                                TGGTACAT CGG   GAACA
                                    C  TCC_
GAM482  HIVEP3  5'  GGCACAAACCCAGCAGCCTCA  44439   TAA __  AA
                                TG  GC  CTG  TTTGTGCC
                                ||  ||  |||  ||||||||
                                AC  CG  GAC  AAACACGG
                                 TC_  AC  CC
GAM482  RECK    3'  GCAACAGGCTCACTGGT    40869    T  A    AAT
                                ACCA GT AGCCTG  TTGT
                                |||| || ||||||  ||||
                                TGGT CA TCGGAC  AACG
                                  _  C    ___
GAM482  TNFSF8  3'  GCACAAATTTAATACA     6966     AGCC
                                TGTA   TGAATTTGTGC
                                ||||   ||||||||||
                                ACAT   ATTTAAACACG
                                  A___
GAM482  ADAR3   3'  CACAAATTCAGAACGTG    38018     AAGC
                                CATGT   CTGAATTTGTG
                                |||||   ||||||||||
                                GTGCA   GACTTAAACAC
                                  A___
GAM482  BIVM    3'  CACAAATTCACTTA       34667     CC
                                TAAG  TGAATTTGTG
                                ||||  ||||||||||
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                                ATTC  ACTTAAACAC
                                  __
GAM482  C20orf160 3'  GCAGTTACAGGATTACATGGT  54648         G    AAT
                                ACCATGTAA CCTG   TTGT
                                ||||||||| ||||   ||||
                                TGGTACATT GGAC   GACG
                                     A    ATT
GAM482  EPHA7    3'  CACAAATTTGCTGCACA     15433     A_   CT
                                TGT  AGC  GAATTTGTG
                                |||  |||  |||||||||
                                ACA  TCG  TTTAAACAC
                                  CG  __
GAM482  FLJ12783  3'  AGTTCAGGCTCACTG       48675     T  A
                                CA GT AGCCTGAATT
                                || || ||||||||||
                                GT CA TCGGACTTGA
                                 _  C
GAM482  HSC3     3'  CACAGGTTCAGACTACA     59067      A C
                                TGTA G CTGAATTTGTG
                                |||| | ||||||||||||
                                ACAT C GACTTGGACAC
                                  _ A
GAM482  KIAA0316  3'  GCACAAATGCTCTTCACAGTGG 69674      _  _   CCTGA
           T                     ACCA TGT AAG     ATTTGTGC
                                |||| ||| |||     ||||||||
                                TGGT ACA TTC     TAAACACG
                                  G   C   TCG__
GAM482  KIAA0453  3'  GCACAAGTAGCTACATAGT    69047    C     A  CTGA
                                AC ATGTA GC    ATTTGTGC
                                || ||||| ||    ||||||||
                                TG TACAT CG    TGAACACG
                                 A     _  A___
GAM482  KIAA1423  3'  AATTCAAGTTTACATG       61719          C
                                CATGTAAGC TGAATT
                                ||||||||| ||||||
                                GTACATTTG ACTTAA
                                     A
GAM482  KIAA1691  3'  GCACAAATGCTGTCCATGG    92556       TA_   CTGA
                                CCATG   AGC    ATTTGTGC
                                |||||   |||    ||||||||
                                GGTAC   TCG    TAAACACG
                                  CTG   _____
GAM482  PPP1R3B   3'  GCCAGGTTCAGATTACA     44820       GC        T
                                TGTAA  CTGAATTTG GC
                                |||||  ||||||||| ||
                                ACATT  GACTTGGAC CG
                                  A_        _
GAM482  SFXN2    3'  GCAGCAGAGTTACATGGT     73946          GC   AATTTG
                                ACCATGTAA  CTG     TGC
                                |||||||||  |||     |||
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                                TGGTACATT  GAC     ACG
                                    GA   G_____
GAM482  TBC1D2   5'  TAAATTCAGACCTACTGGT   37321     T   AGC
                                ACCA GTA   CTGAATTTG
                                |||| |||   |||||||||
                                TGGT CAT   GACTTAAAT
                                  _   CCA
GAM482  ZNF347   3'  GGCTTTATTCAGGCCTCACA  50848     AA_      TTGT
                                TGT   GCCTGAAT   GCC
                                |||   ||||||||   |||
                                ACA   CGGACTTA   CGG
                                  CTC       TTT_
GAM482  LOC134147 3'  CACAAATTCAGTAGGACGT   57158     AAGC
                                ATGT    CTGAATTTGTG
                                ||||    ||||||||||
                                TGCA    GACTTAAACAC
                                  GGAT
GAM482  LOC151195 5'  GCACAAATTTATTTACA     80169       CC
                                TGTAAG  TGAATTTGTGC
                                ||||||  ||||||||||
                                ACATTT  ATTTAAACACG
                                   __
GAM482  LOC152860 3'  AATTCCAGCTTACATGG     80695         CT
                                CCATGTAAGC  GAATT
                                ||||||||||  |||||
                                GGTACATTCG  CTTAA
                                      AC
GAM482  LOC200382 3'  ACAGGGGCCAGACTTACATG   88801         C   AA_
                                CATGTAAG CTG   TTTGT
                                |||||||| |||   |||||
                                GTACATTC GAC   GGACA
                                    A   CGG
GAM482  LOC93622  3'  ACAGTCATTCCAGGCTTAGATG 56929     G       _   __
                                CAT TAAGCCTG AAT  TTGT
                                ||| |||||||| |||  ||||
                                GTA ATTCGGAC TTA  GACA
                                  G       C   CT
GAM483  FLT4     3'  TTGACCAAAGAGCCCTC     8923      ACTT   G    C
                                GAG    GGTT TTTGG CAA
                                |||    |||| ||||| |||
                                CTC    CCGA AAACC GTT
                                  ____   G    A
GAM483  FRAT2    5'  CGGGCAACCAAGCCCCCA    23880     AGA
                                TGG   CTTGGTTGTTTG
                                |||   ||||||||||||
                                ACC   GAACCAACGGGC
                                  CCC
GAM483  ITGA5    3'  TCATCAACCAAGGCCCCA    61282     AGA       TT
                                TGG   CTTGGTTG  TGG
                                |||   ||||||||  |||
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                                ACC   GAACCAAC  ACT
                                  CCG       T_
GAM483  KCNS2    3'  CTTGACCAATGCAAGTCTCTA  68305          GTTGT    C
                                TGGAGACTTG    TTGG CAAG
                                ||||||||||    |||| ||||
                                ATCTCTGAAC    AACC GTTC
                                     GT___    A
GAM483  PPP1R12B 5'  GCCAGACAAACCCACCA    49472    AGACT   __
                                TGG    TGG  TTGTTTGGC
                                |||    |||  |||||||||
                                ACC    ACC  AACAGACCG
                                  _____  CA
GAM483  PPP1R12B 5'  GCCAGACAAACCCACCA    49483    AGACT   __
                                TGG    TGG  TTGTTTGGC
                                |||    |||  |||||||||
                                ACC    ACC  AACAGACCG
                                  _____  CA
GAM483  TMOD     3'  TGGCCAAACCACCCCA     12342    AGACTT   T
                                TGG     GGT GTTTGGCCA
                                |||     ||| |||||||||
                                ACC     CCA CAAACCGGT
                                  _______  C
GAM483  VEGFB    3'  TGGTAAAAAACAGCCAAGCCCC 12591    AGA        G__
          CA                      TGG   CTTGGTTGTTT   GCCA
                                |||   ||||||||||   ||||
                                ACC   GAACCGACAAA   TGGT
                                  CCC         AAA
GAM483  DCNP1    3'  GCCCACCAAGTCTCCA     55622          TGTTT
                                TGGAGACTTGGT    GGC
                                ||||||||||||    |||
                                ACCTCTGAACCA    CCG
                                      C____
GAM483  FLJ20045 3'  TGGCCAAATGGTGAAACCCCA  34432    AGAC  G TT
                                TGG    TT G  GTTTGGCCA
                                |||    || |  |||||||||
                                ACC    AA T  TAAACCGGT
                                  CCA_  G GG
GAM483  FLJ32389 3'  TTGACCCCCAAGTCTTCA    58192         TTGTTT  C
                                TGGAGACTTGG     GG CAA
                                ||||||||||      || |||
                                ACTTCTGAACC     CC GTT
                                      C_____  A
GAM483  GPS2     5'  GCCACCATGACCAACCTCCA  87160      AC    TG T_
                                TGGAG  TTGGT  T  TGGC
                                |||||  |||||  |  ||||
                                ACCTC  AACCA  A  ACCG
                                   C_    GT CC
GAM483  HSA404617 5'  GGCCGGTGGCCAAGGCCCCA  72711    AGA    TG  T
                                TGG   CTTGGT  TT GGCC
                                |||   ||||||  || ||||
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                                ACC   GAACCG  GG CCGG
                                  CCG     GT _
GAM483  KIAA1940  3'  TCAGAACCAAGGCTCCA     79991       A     TG
                                TGGAG CTTGGT  TTTGG
                                ||||| ||||||  |||||
                                ACCTC GAACCA  AGACT
                                  G     __
GAM483  MYH10     3'  GCCACATCAAGTCTCC      69140           TGTT
                                GGAGACTTGGT    TGGC
                                ||||||||||    ||||
                                CCTCTGAACTA    ACCG
                                       C___
GAM483  PHCA      3'  CTTAGTTTTTAACCAAGTATCC 37176      G        TTT   C
              A                  TGGA ACTTGGTTG   GGC AAG
                                ||||| |||||||||   ||| |||
                                ACCT TGAACCAAT   TTG TTC
                                  A        TT_   A
GAM483  PRO0255   3'  TGGCCAAGGCGGCAAAACCCCA 26142     AGACTTG    _
                                TGG       GTTGT TTGGCCA
                                |||       ||||| |||||||
                                ACC       CGGCG AACCGGT
                                  CCAAAA_     G
GAM483  TREX2     5'  CCTACAGCCAAATCCCCA     23276     A  C       TT
                                TGG GA TTGGTTGT  GG
                                ||| || ||||||||  ||
                                ACC CT AACCGACA  CC
                                  C  A       T_
GAM483  VPS33B    3'  GCTGCTATAACCAAGTGTCCA  37903      G        TT_
                                TGGA ACTTGGTTGT   GGC
                                ||||| ||||||||||   |||
                                ACCT TGAACCAATA   TCG
                                  G         TCG
GAM483  ZDHHC7    3'  GCCAAGCGAGCAAACCTGCA   34841    G  AC   G
                                TG AG  TTG TTGTTTGGC
                                || ||  ||| |||||||||
                                AC TC  AAC AGCGAACCG
                                 G  CA   G
GAM483  LOC115704 3'  GCCAGAGCCAGGCCCCCA    73544     AGA     TG
                                TGG   CTTGGT  TTTGGC
                                |||   ||||||  ||||||
                                ACC   GGACCG  AGACCG
                                  CCC     __
GAM483  LOC138389 3'  TGGCCAAAATGATGAAACCCCA 76236     AGAC  G  TG  _
                                TGG    TT GT  TTT GGCCA
                                |||    || ||  ||| |||||
                                ACC    AA TA  AAA CCGGT
                                  CCA_  G  GT   A
GAM483  LOC147664 5'  CTCAGCGCACCAAGTCCCC    78407     A       _    T
                                GG GACTTGGT TGTT GG
                                || |||||||| |||| ||
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                                CC CTGAACCA GCGA TC
                                 C       C   C
GAM483  LOC150271 3'  TGGCCTGGGCCAAGTCCCCA  84958    A       GTTT
                                TGG GACTTGGTT   GGCCA
                                ||| |||||||||   |||||
                                ACC CTGAACCGG   CCGGT
                                  C       GT__
GAM483  LOC151057 3'  TGACCAAACAGAATATCTC   85217     CTTGG      C
                                GAGA    TTGTTTGG CA
                                ||||    |||||||| ||
                                CTCT    GACAAACC GT
                                  ATAA_      A
GAM483  LOC151632 5'  CCCAGCCCAAGTCTCCA     85468          TT   T
                                TGGAGACTTGG  GTT GG
                                ||||||||||  ||| ||
                                ACCTCTGAACC  CGA CC
                                       __  C
GAM483  LOC158490 3'  CTTGGCCTCCGGCCAAGTCCCA 81935     A       TTT
                                TGG GACTTGGTTG  GGCCAAG
                                ||| ||||||||||  |||||||
                                ACC CTGAACCGGC  CCGGTTC
                                  _       CT_
GAM483  LOC159184 3'  GCCAGACAAACCCACCA     60049     AGACT  __
                                TGG    TGG  TTGTTTGGC
                                |||    |||  |||||||||
                                ACC    ACC  AACAGACCG
                                  _____  CA
GAM483  LOC200311 3'  TGGCCTGGGCCAAGTCCCCA  89984     A       GTTT
                                TGG GACTTGGTT   GGCCA
                                ||| |||||||||   |||||
                                ACC CTGAACCGG   CCGGT
                                  C       GT__
GAM483  LOC221312 3'  CTTGTGATGCAACCAAGTCTC  91907          TTGGC
                                GAGACTTGGTTGT    CAAG
                                ||||||||||||    ||||
                                CTCTGAACCAACG    GTTC
                                        TAGT_
GAM483  LOC254219 3'  CCCAGCCCCCAAGGCTCCA   96548     A    TT   T
                                TGGAG CTTGG  GTT GG
                                ||||| |||||  ||| ||
                                ACCTC GAACC  CGA CC
                                   G    CC   C
GAM484  AKAP2    3'  CACACAAGCTTGTTAACCCCA  23258    AT  GA__
                                TG  GT   GAGCTTGTGTG
                                ||  ||   ||||||||||
                                AC  CA   TTCGAACACAC
                                 CC  ATTG
GAM484  HSF4     5'  CAAGTCTCCCACTCATCTCA   59774        T   A   _
                                TGAGATGA GTG GAG CTTG
                                |||||||| ||| ||| ||||
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                                ACTCTACT CAC CTC GAAC
                                     _  C   T
GAM484  PPEF1    5'  CACACAAGCCCTCTGCATTTC  20682       ATGT   A
                                GAGATG   GAG GCTTGTGTG
                                ||||||   ||| |||||||||
                                CTTTAC   CTC CGAACACAC
                                   GT__  C
GAM484  FLJ14827 3'  CACCTCCCACATCATCCA   51650   A       A   CTT
                                TG GATGATGTG GAG  GTG
                                || |||||||| |||  |||
                                AC CTACTACAC CTC  CAC
                                 _       C  ___
GAM484  LOC51015 3'  CACACAAGCTCTTCTTATCTC  32119       TGT
                                GAGATGA  GAGAGCTTGTGTG
                                |||||||  |||||||||||||
                                CTCTATT  TTCTCGAACACAC
                                    C__
GAM485  ALK      3'  CAATGGCTCCTTCAC      73381        ACTC
                                GTGAAGGA   CTGTTG
                                ||||||||   ||||||
                                CACTTCCT   GGTAAC
                                     C___
GAM485  ARAF1    5'  CAACAGGAGGGCCTGAGC   63936   GA   AA
                                GT  AGG  CTCCTGTTG
                                ||  |||  |||||||||
                                CG  TCC  GAGGACAAC
                                 AG   GG
GAM485  KIF3C    3'  ACGGAAGTCCCTCCACTGG   9597       A   A   C
                                TCAGTG AGG ACT CTGT
                                |||||| ||| ||| ||||
                                GGTCAC TCC TGA GGCA
                                   C   C   A
GAM485  MAP2     3'  CAACAGGAAGACACTGG    48995       AAGGAAC
                                TCAGTG     TCCTGTTG
                                ||||||     ||||||||
                                GGTCAC     AGGACAAC
                                   AGA_____
GAM485  PPP2R5A  3'  CAACCTGTCCTTCACCTAGT  20706    CA      ACTCCT
                                ACT  GTGAAGGA     GTTG
                                |||  ||||||||     ||||
                                TGA  CACTTCCT     CAAC
                                  TC       GTC___
GAM485  SHANK2   3'  ACAGGCTCCTGTCACTGAG   24582        _   ACT
                                CTCAGTGA AGGA   CCTGT
                                |||||||| ||||   |||||
                                GAGTCACT TCCT   GGACA
                                     G   C__
GAM485  SYNGR1   3'  AGGTGGGCTCTTCACTGAG   16309         AA  _
                                CTCAGTGAAGG  CT CCT
                                ||||||||||  || |||
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                                GAGTCACTTCT  GG GGA
                                      CG  T
GAM485  TDE1     3'  CAAAGGTCTCCTTCACCGA   22341    A      ACT   G
                                TC GTGAAGGA   CCT TTG
                                || ||||||||   ||| |||
                                AG CACTTCCT   GGA AAC
                                 C       CT_  _
GAM485  TGFB3    3'  CAACAAACCTCACTGAG     12258        A  AACTCC
                                CTCAGTGA GG     TGTTG
                                |||||||| ||     |||||
                                GAGTCACT CC     ACAAC
                                    _ AA____
GAM485  TRAF5    3'  CAACAGGAATATACTGA     16074       AAGGAAC
                                TCAGTG      TCCTGTTG
                                ||||||      ||||||||
                                AGTCAT      AGGACAAC
                                   ATA____
GAM485  ZNF24    3'  CAACAGGAATTACAAAGT    22726     CA   AGGAAC
                                ACT  GTGA     TCCTGTTG
                                |||  ||||     ||||||||
                                TGA  CATT     AGGACAAC
                                 AA   A_____
GAM485  ADAMTSL1 3'  ACAAAAGACTCTTCACTGAG  57685          AA  CC
                                CTCAGTGAAGG  CT  TGT
                                ||||||||||  ||  |||
                                GAGTCACTTCT  GA  ACA
                                      CA  AA
GAM485  C1QTNF7  3'  GCACCTTGTTCTTCACTGA   49160          ACTCC
                                TCAGTGAAGGA    TGT
                                ||||||||||     |||
                                AGTCACTTCTT    ACG
                                      GTTCC
GAM485  DGS-A    3'  GCAACAGGGAGATTCC      84899      _   _
                                GGAA CTCC TGTTGC
                                |||| |||| ||||||
                                CCTT GAGG ACAACG
                                  A   G
GAM485  FLJ10607 3'  CAACAGAAATCCTTCAC     77106        ACTC
                                GTGAAGGA   CTGTTG
                                ||||||||   ||||||
                                CACTTCCT   GACAAC
                                    AAA_
GAM485  FLJ13340 3'  GCACTGGATTCTTTCACTGAG  54104           C   T  T
                                CTCAGTGAAGGAA TCC GT GC
                                |||||||||||| ||| || ||
                                GAGTCACTTTCTT AGG CA CG
                                      _  T  _
GAM485  FLJ14721 3'  GCAGGAGTCCCCTCACGAAGT  51583     CA   A  A
                                ACT  GTGA GG ACTCCTGT
                                |||  |||| || ||||||||
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                                TGA  CACT CC TGAGGACG
                                  AG    C  C
GAM485  FLJ25359  5'  GGAGTTCCTCCACTCAG     58075    C    A
                                CT AGTG AGGAACTCC
                                || |||| |||||||||
                                GA TCAC TCCTTGAGG
                                 C    C
GAM485  FLJ31547  3'  GCAACAAGATTTCTTCA     58831         C  C
                                TGAAGGAA TC TGTTGC
                                |||||||| || ||||||
                                ACTTCTTT AG ACAACG
                                     _  A
GAM485  FYCO1     3'  GCAACAAGAACCACCATTCACT 44495          _  AAC_  C
           GAGT                    ACTCAGTGAA GG    TC TGTTGC
                                |||||||||| ||    || ||||||
                                TGAGTCACTT CC    AG ACAACG
                                      A  ACCA  A
GAM485  KIAA1323  5'  GCAACAGGAATCCTGGTGGA   63043    AGTGA    AC
                                TC    AGGA  TCCTGTTGC
                                ||    ||||  |||||||||
                                AG    TCCT  AGGACAACG
                                 GTGG_   A_
GAM485  MGC12538  3'  CAACAAAAGCTTTGCTGG    51242     TG   GAA  CC
                                TCAG  AAG   CT  TGTTG
                                ||||  |||   ||  |||||
                                GGTC  TTC   GA  ACAAC
                                  GT   ___  AA
GAM485  MGC29761  5'  CAACAGGACGCCGCCGAGT   58326     A  GAA  AAC
                                ACTC GT   GG   TCCTGTTG
                                |||| ||   ||   ||||||||
                                TGAG CG   CC   AGGACAAC
                                  C  ___  GC_
GAM485  SCOP      3'  CAACTCACCCTCACTTCACTGA 91778         _  ACTCCT
                                TCAGTGAAG GA     GTTG
                                ||||||||| ||     ||||
                                AGTCACTTC CT     CAAC
                                      A  CCCACT
GAM485  SNAP29    3'  CAACAGGTCTTCCACTGG    16538       A    ACT
                                TCAGTG AGGA   CCTGTTG
                                |||||| ||||   |||||||
                                GGTCAC TTCT   GGACAAC
                                   C   ___
GAM485  TBDN100   3'  GCACTGGATTCTTTCACTGAG  46953           C   T  T
                                CTCAGTGAAGGAA TCC GT GC
                                |||||||||||| ||| || ||
                                GAGTCACTTTCTT AGG CA CG
                                        _  T  _
GAM485  UBE4B     3'  CAGCATCCCTTCATGA     20163     G     AACTCC
                                TCA TGAAGG     TGTTG
                                ||| ||||||     |||||
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                                AGT ACTTCC     ACGAC
                                  _     CT_____
GAM485  LOC145438 3'  GCAAAAACGCCCTCACTGAG  83338        A  AACTCCTG
                                CTCAGTGA GG       TTGC
                                |||||||| ||       ||||
                                GAGTCACT CC       AACG
                                     C  GCAAA___
GAM485  LOC148764 5'  CAACAACCTGTCACTGAGT   78982         _  AACTCC
                                ACTCAGTGA AGG     TGTTG
                                ||||||||| |||     |||||
                                TGAGTCACT TCC     ACAAC
                                     G   A_____
GAM485  LOC151623 5'  ACATGGACCCCCTCACTGG   85454        A  AAC  _
                                TCAGTGA GG   TCC TGT
                                ||||||| ||   ||| |||
                                GGTCACT CC   AGG ACA
                                     C  CC_   T
GAM485  LOC158696 3'  GGAGCTCCCCCACAGAGT    81973     A   AA   A
                                ACTC GTG  GGA CTCC
                                |||| |||  ||| ||||
                                TGAG CAC  CCT GAGG
                                  A   CC   C
GAM485  LOC199837 5'  CAACAAGAAAATTGACTTCACT 88406          GAAC___  C
          GAGT                    ACTCAGTGAAG      TC TGTTG
                                ||||||||||       || |||||
                                TGAGTCACTTC       AG ACAAC
                                     AGTTAAA  A
GAM485  LOC200261 3'  AGTTGCTCCACTGAGT      88652         A  G
                                ACTCAGTG AG AACT
                                |||||||| || ||||
                                TGAGTCAC TC TTGA
                                     C  G
GAM485  LOC219735 3'  GCAACAAGAATTCCTTTA    93109         C  C
                                TGAAGGAA TC TGTTGC
                                |||||||| || ||||||
                                ATTTCCTT AG ACAACG
                                     A  A
GAM485  LOC220370 3'  GCAAGTCACTCACCTCACTGAG 92827         A  AACTCCTG
                                CTCAGTGA GG       TTGC
                                |||||||| ||       ||||
                                GAGTCACT CC       AACG
                                     _  ACTCACTG
GAM485  LOC220686 3'  GCAACAGGAGCCGGACCTACA  92921    A   AA___
                                TG AGG    CTCCTGTTGC
                                || |||    ||||||||||
                                AC TCC    GAGGACAACG
                                 A   AGGCC
GAM485  LOC245757 3'  CAACAAGGGAGCTCACTGAGT  90775         AGGAA    __
                                ACTCAGTGA    CTCCT  GTTG
                                |||||||||    |||||  ||||
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                                TGAGTCACT    GAGGG  CAAC
                                     C____    AA
GAM485  LOC51651  3'  CAACAAAAGCTGAATTTCTTCA 32182        _____  CC
            C                    GTGAAGGAA    CT  TGTTG
                                 |||||||||    ||  |||||
                                 CACTTCTTT    GA  ACAAC
                                      AAGTC  AA
GAM485  LOC91137  3'  GGTTCCTTCACTGAGT     57066
                                 ACTCAGTGAAGGAACT
                                 ||||||||||||||||
                                 TGAGTCACTTCCTTGG

GAM486  AP1B1    3'  CTCCACTGCCACCTCTC     6669      T       A
                                 GAGA GGTGGCAGTG AG
                                 |||| |||||||||| ||
                                 CTCT CCACCGTCAC TC
                                   _       C
GAM486  APLP2    3'  CCCTCACCTCCACCCCCTC   90894    AT    CA    A
                                 GAG  GGTGG  GTGA GG
                                 |||  |||||  |||| ||
                                 CTC  CCACC  CACT CC
                                   CC    TC   C
GAM486  ATP6IP1  3'  CTGCCCCCATCTCTCCCA    6789     AA      T
                                 TG  AGAGATGG GGCAG
                                 ||  |||||||| |||||
                                 AC  TCTCTACC CCGTC
                                  CC       C
GAM486  C5R1     3'  CCCCCACACACCATCTTT    8203          GCA   AA
                                 AGAGATGGTG   GTG  GG
                                 ||||||||||   |||  ||
                                 TTTCTACCAC   CAC  CC
                                      A__   CC
GAM486  CALR     3'  CCTCCACTCTCCCCCACCCCCT 62975    AT    C____    A
            C                    GAG  GGTGG    AGTG AGG
                                 |||  |||||    |||| |||
                                 CTC  CCACC    TCAC TCC
                                   CC    CCCTC   C
GAM486  CHRNB1   3'  CTCACTGTTCTTCTC      60534     T  T      A
                                 GAGA GG GGCAGTGA G
                                 |||| || |||||||| |
                                 CTCT TC TTGTCACT C
                                   _ _       C
GAM486  ECM2     3'  CTTCACTATTCCTCACTC    7330     A   T  C__
                                 GAG TGG GG   AGTGAAG
                                 ||| ||| ||   |||||||
                                 CTC ACT CC   TCACTTC
                                   _  _ TTA
GAM486  FKBP1A   3'  CCTTCACTGCCTTTGCTC    53953    ATGGT
                                 GAG    GGCAGTGAAGG
                                 |||    ||||||||||
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                                CTC    CCGTCACTTCC
                                  GTTT_
GAM486  GIP     3'  CCTTCACTTAGCACCTGCCTC  14661    AT_   GC_
                                GAG   GGTG   AGTGAAGG
                                |||   ||||   ||||||||
                                CTC   CCAC   TCACTTCC
                                  CGT    GAT
GAM486  HAP1    3'  CCTTCACTGGCCCATCCCTC   14167    AT    __
                                GAG  GGTGG  CAGTGAAGG
                                |||  |||||  |||||||||
                                CTC  CTACC  GTCACTTCC
                                  C_    CG
GAM486  HMGCS1  5'  CTTCACACAGCTCTTTCA    9231        ATG  GGCA
                                TGAAAGAG   GT    GTGAAG
                                ||||||||   ||    ||||||
                                ACTTTCTC   CA    CACTTC
                                     GA_  ____
GAM486  HOXC6   3'  CCCTCACCGCACAACTCTCTTT 15700        TGG  _  A    A
              C                  GAAAGAGA   TG GC GTGA GG
                                 ||||||||   || || |||| ||
                                 CTTTCTCT   AC CG CACT CC
                                     CA_  A  C    C
GAM486  IHPK3   5'  CCCCCACCACCACCATCT    54024        CA   AA
                                AGATGGTGG  GTG  GG
                                |||||||||  |||  ||
                                TCTACCACC  CAC  CC
                                     AC   CC
GAM486  JPH2    5'  CTCCACCCCACCCTTTC     94445     T    CA   A
                                GAGA GGTGG  GTG AG
                                ||||  |||||  |||  ||
                                CTTT  CCACC  CAC TC
                                  C    C_   C
GAM486  KIAA0857 3'  CAAAGCCCCATCCCCTTCA   66673     AGA    T   AG
                                TGAA   GATGG GGC  TG
                                ||||   |||||  |||  ||
                                ACTT   CTACC CCG  AC
                                  CCC    _   AA
GAM486  LDHB    5'  CCCCCATACACCATCTATTC   9709     AG      GCA   AA
                                GAA  AGATGGTG   GTG  GG
                                |||  ||||||||   |||  ||
                                CTT  TCTACCAC   TAC  CC
                                  A_      A__   CC
GAM486  LY9     3'  CTTTACACCACCTTCTC     71683     T    CA
                                GAGA GGTGG  GTGAAG
                                ||||  |||||  ||||||
                                CTCT  CCACC  CATTTC
                                  T    A_
GAM486  MS4A12  3'  CTTCACTGTCTCTTCCT     34759    AT  T
                                AG  GG GGCAGTGAAG
                                ||  ||  ||||||||||
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                                TC  TC CTGTCACTTC
                                 CT  T
GAM486  MYL1    5'  CCACCATCCTCTTCCA      54377    A    _
                                TG AAGAG ATGGTGG
                                || ||||| |||||||
                                AC TTCTC TACCACC
                                 C    C
GAM486  MYOZ1   5'  CCCCCACTGCCAGTGCT     41151    A  G       AA
                                AG TG TGGCAGTG  GG
                                || || ||||||||  ||
                                TC GT ACCGTCAC  CC
                                 _  G       CC
GAM486  NAP1L3  5'  CCTCCACTGCCGCTGCCACCTC 15795     A   ___      A
                                GAG TGGT   GGCAGTG AGG
                                ||| ||||   ||||||| |||
                                CTC ACCG   CCGTCAC TCC
                                  C    TCG      C
GAM486  OGDH    3'  CCTCGCTGTGCCACCACCCCTC 91107     A__      __   A
                                GAG   TGGTGGCA  GTGA GG
                                |||   ||||||||  |||| ||
                                CTC   ACCACCGT  CGCT CC
                                  CCC       GT   _
GAM486  PCDH9   5'  CCCCCATGTTTCCATCTCCTGT 82796     AA_      TG   G  AA
          CA                      TGA   GAGATGG  GCA TG  GG
                                |||   |||||||  ||| ||  ||
                                ACT   CTCTACC  TGT AC  CC
                                  GTC      TT  _  CC
GAM486  PRX     3'  CCCTCACTGCCCACTCT     40527     A   TG      A
                                AGAG TGG  GCAGTGA GG
                                |||| |||  ||||||| ||
                                TCTC ACC  CGTCACT CC
                                   _  __      C
GAM486  PTGIS   3'  CCCCCACTGCCGCCTCCTT    6329      A  T        AA
                                AAG GA GGTGGCAGTG  GG
                                ||| || ||||||||||  ||
                                TTC CT CCGCCGTCAC  CC
                                  _  _         CC
GAM486  PTPN1   3'  CCTCCACTCCACCTC       11048    T    C    A
                                GA GGTGG AGTG AGG
                                || ||||| |||| |||
                                CT CCACC TCAC TCC
                                  _    _   C
GAM486  SCN4A   3'  CCTCCACTCCTTCCATCTCTT  4411          T_  C    A
                                AAGAGATGG  GG AGTG AGG
                                |||||||||  || |||| |||
                                TTCTCTACC  CC TCAC TCC
                                      TT  _    C
GAM486  SCNN1G  3'  CCTCCACCACCAAAGGCCTGTC 6430    A       _____   CA   A
          TCTCA                    A AGAGATGG    TGG  GTG AGG
                                | ||||||||    |||  ||| |||
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                                A TCTCTGTC    ACC  CAC TCC
                                 C       CGGAA   AC   C
GAM486  TCF7     3'  CCCCCACTGCCACACCCTC   12159     ATG       AA
                                GAG   GTGGCAGTG  GG
                                |||   |||||||||  ||
                                CTC   CACCGTCAC  CC
                                  CCA       CC
GAM486  TRIM8    3'  CCTTCTCCTCACCATCTT    48115          CAGT
                                GAGATGGTGG   GAAGG
                                ||||||||||   |||||
                                TTCTACCACT   CTTCC
                                      CCT_
GAM486  XPC      3'  CTCACTGCCTCTTT       16132       TGGT      A
                                AGAGA   GGCAGTGA G
                                |||||   |||||||| |
                                TTTCT   CCGTCACT C
                                  ____       C
GAM486  YWHAH    3'  CCTTCACCCACCACCCCCATCA 12696     AAGAGA     CA
                                TGA     TGGTGG  GTGAAGG
                                |||     ||||||  |||||||
                                ACT     ACCACC  CACTTCC
                                  ACCCCC     __
GAM486  AKAP11   3'  CCCCCACCCCCCCACTCTCTCTC 32704     A    _   T  CA   AA
          A                      TGA AGAGA TGG GG  GTG  GG
                                ||| ||||| ||| ||  |||  ||
                                ACT TCTCT ACC CC  CAC  CC
                                  C    C   _ C_   CC
GAM486  ARF6     3'  CCACCATCACCTCTTTCA    8012         ___
                                TGAAAGA   GATGGTGG
                                |||||||   ||||||||
                                ACTTTCT   CTACCACC
                                    CCA
GAM486  C1QTNF6  3'  CTGCCATCATCCCTCCCA    49143    AA  A
                                TG  AG GATGGTGGCAG
                                ||  || ||||||||||
                                AC  TC CTACTACCGTC
                                 CC  C
GAM486  C5orf4   3'  CCTCATCATCACCACCATCTC  50491          CA   __
                                GAGATGGTGG  GTGA  AGG
                                ||||||||||  ||||  |||
                                CTCTACCACC  TACT  TCC
                                      AC    AC
GAM486  C5orf4   5'  CCTCATCATCACCACCATCTC  32980          CA   __
                                GAGATGGTGG  GTGA  AGG
                                ||||||||||  ||||  |||
                                CTCTACCACC  TACT  TCC
                                      AC    AC
GAM486  CALN1    3'  CCTCCACTCCCCATTCTTTCA  48863        A  T  C   A
                                TGAAAGAG TGG GG AGTG AGG
                                |||||||| ||| || |||| |||
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                                ACTTTCTT ACC CC TCAC TCC
                                   _  _ _   C
GAM486  COL12A1  3' CCCTCACCTCCTCATCTTT  54663       T  CA   A
                                AGAGATGG GG  GTGA GG
                                |||||||| ||  |||| ||
                                TTTCTACT CC  CACT CC
                                   _ TC   C
GAM486  COL12A1  3' CCCTCACCTCCTCATCTTT  15181       T  CA   A
                                AGAGATGG GG  GTGA GG
                                |||||||| ||  |||| ||
                                TTTCTACT CC  CACT CC
                                   _ TC   C
GAM486  DKFZp761O132 5' CCTTCACTGCCCTTCTCCATCT 50197        T____
          CTT                    AAGAGATGG    GGCAGTGAAGG
                                |||||||||    ||||||||||
                                TTCTCTACC    CCGTCACTTCC
                                     TCTTC
GAM486  FLJ11280  5' CCTTCATTGCACCTATCTC  37209       TG
                                GAGATGG  GCAGTGAAGG
                                |||||||  ||||||||||
                                CTCTATC  CGTTACTTCC
                                   CA
GAM486  FLJ13114  3' CCTCCACGTGTTCCACCCCCTT 44594     AT   __ _  A
                                GAG  GGTGG  CA GTG AGG
                                |||  |||||  || ||| |||
                                TTC  CCACC  GT CAC TCC
                                  CC    TT  G   C
GAM486  FLJ14800  3' CCTTCACTCCTTTCTC     51611     TGGT  C
                                GAGA   GG AGTGAAGG
                                ||||   || ||||||||
                                CTCT   CC TCACTTCC
                                  TT__  _
GAM486  FLJ30092  3' CCTTCAGACCACACCACCTCT  58688     A    GCAG_
                                AGAG TGGTG    TGAAGG
                                |||| |||||    ||||||
                                TCTC ACCAC    ACTTCC
                                  C    ACCAG
GAM486  KIAA0210  5' TCACTGCCACCTCTCCCTCA  28485     AA   T
                                TGA  GAGA GGTGGCAGTGA
                                |||  |||| ||||||||||
                                ACT  CTCT CCACCGTCACT
                                  CC   _
GAM486  KIAA0255  3' CCCTCACTGCCCCACATTCTC  28466     ___  T      A
                                GAGA   TGG GGCAGTGA GG
                                ||||   ||| |||||||| ||
                                CTCT   ACC CCGTCACT CC
                                  TAC  _       C
GAM486  KIAA0258  3' TTTCCCACCTCTTTCA     28826       GAT    CAGT
                                TGAAAGA   GGTGG   GAA
                                |||||||   |||||   |||
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                                ACTTTCT  CCACC   TTT
                                   ___   C___
GAM486  KIAA0446 3' CCTTCACCACCACCACT    68862   A    CA
                                AG TGGTGG  GTGAAGG
                                || ||||||  |||||||
                                TC ACCACC  CACTTCC
                                 _    AC
GAM486  KIAA0446 3' CTCACCCCATCTCTTT     68864        T  CAG  A
                                AAAGAGATGG GG   TGA G
                                |||||||||| ||   ||| |
                                TTTCTCTACC CC   ACT C
                                      _ ___  C
GAM486  KIAA0537 5' CCTTTAGAGCCCCATCTCTTCC 29247   A      T  AG
           A                     TG AAGAGATGG GGC  TGAAGG
                                || |||||||| |||  ||||||
                                AC TTCTCTACC CCG  ATTTCC
                                 C       _  AG
GAM486  KIAA1042 3' CTTCACTGCTCTGCCTC    30339    AT  T
                                GAG  GG GGCAGTGAAG
                                |||  || ||||||||||
                                CTC  TC TCGTCACTTC
                                  CG  _
GAM486  KIAA1643 3' CCCTCACCCCTCACCCCTC   64550    AT   CA_   A
                                GAG  GGTGG   GTGA GG
                                |||  |||||   |||| ||
                                CTC  CCACT   CACT CC
                                  C_    CCC   C
GAM486  KIAA1887 5' CCTCTCCAGCCCCACCTC    76774    A  T  AGT  _
                                GAG TGG GGC   GA AGG
                                ||| ||| |||   || |||
                                CTC ACC CCG   CT TCC
                                  C  _  AC_  C
GAM486  KIAA1944 3' CCTCCACTGCATTGCCATCCTC 75559    _   G__    A
                                GAG ATGGT   GCAGTG AGG
                                ||| |||||   |||||| |||
                                CTC TACCG   CGTCAC TCC
                                  C    TTA    C
GAM486  KRT6    3' CCTTCACTACCAAGGGACTCTC 82220     TGG___  C
           T                     AGAGA     TGG AGTGAAGG
                                |||||     ||| ||||||||
                                TCTCT     ACC TCACTTCC
                                   CAGGGA   A
GAM486  N4BP3   3' CCTTCACTCAGTGTCATCCCTT 66260    AT     ____
           C                     GAG  GGTGGCA   GTGAAGG
                                |||  |||||||   |||||||
                                CTT  CTACTGT   CACTTCC
                                  CC      GACT
GAM486  PDE1C   3' CTCACACCATCTCCTTC    17218    A      GGCA   A
                                GAA GAGATGGT   GTGA G
                                ||| ||||||||   |||| |
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                                CTT CTCTACCA   CACT C
                                  C      ____   C
GAM486  RAB3IL1  3'  TTGTCACCTTCCCTCCCA   25467   AA  A  T
                                TG  AG GA GGTGGCAG
                                ||  || || ||||||||
                                AC  TC CT CCACTGTT
                                 CC  C  T
GAM486  RAI      3'  CTGACACCATCTCTCCCA   21880   AA       G
                                TG  AGAGATGGTG CAG
                                ||  |||||||||| |||
                                AC  TCTCTACCAC GTC
                                 CC        A
GAM486  RFX3     5'  CACCACCACCATCTCCATCA  11313    AA       CA
                                TGA  GAGATGGTGG  GTG
                                |||  ||||||||||  |||
                                ACT  CTCTACCACC  CAC
                                  AC        AC
GAM486  RFX3     5'  CACCACCACCATCTCCATCA  56224    AA       CA
                                TGA  GAGATGGTGG  GTG
                                |||  ||||||||||  |||
                                ACT  CTCTACCACC  CAC
                                  AC        AC
GAM486  RNF9     3'  CCTTCACTGACAGTCTC    53411     GGTGG
                                GAGAT    CAGTGAAGG
                                |||||    |||||||||
                                CTCTG    GTCACTTCC
                                   ACA__
GAM486  SEMA3B   5'  CCCTCACTGCTGACTCCTCTTC 16154   A    AT  _      A
           CA                     TG AAGAG  GGT GGCAGTGA GG
                                || |||||  ||| |||||||| ||
                                AC TTCTC  TCA TCGTCACT CC
                                 C    C_  G       C
GAM486  SLC34A1  3'  CCTCCAAGATACCATCTCCTCA 11747    AA       GCAG  A
                                TGA  GAGATGGTG    TG AGG
                                |||  |||||||||    || |||
                                ACT  CTCTACCAT    AC TCC
                                  C_        AGA_  C
GAM486  TSC22    3'  CCTCCACAGTCACCCATTTC  20064       _   A  A
                                GAGATGG TGGC GTG AGG
                                ||||||| |||| ||| |||
                                CTTTACC ACTG CAC TCC
                                    C    A  C
GAM486  TU3A     3'  CCTTCATTATCCACCCCATC  23186   GAT    C_
                                GA   GGTGG  AGTGAAGG
                                ||   |||||  ||||||||
                                CT   CCACC  TTACTTCC
                                 ACC    TA
GAM486  WNT10A   3'  CTCCACCATTCCCTTCA    47403     AGA      C
                                TGAA   GATGGTGG AG
                                ||||   |||||||| ||
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                                ACTT   TTACCACC TC
                                  CCC      _
GAM486  LOC126528 3'  CCTGCCAACCACCATCCCTGCC 74527    AA  A      CAG  A_
          A                     TG  AG GATGGTGG   TG  AGG
                                || || ||||||||   ||  |||
                                AC  TC CTACCACC   AC  TCC
                                 CG  C       A__  CG
GAM486  LOC137964 3'  CCCCCACTGCTGTGTCCTTTC  75280      A   G TG     AA
                                GAAAG GAT G  GCAGTG  GG
                                ||||| ||| |  ||||||  ||
                                CTTTC CTG T  CGTCAC  CC
                                  _  _ GT     CC
GAM486  LOC143381 5'  CCTCCACCACCTTGTTCTTT   76545       AT_    CAG  A
                                AAAGAG   GGTGG   TG AGG
                                ||||||   |||||   || |||
                                TTTCTT   CCACC   AC TCC
                                   GTT    ___  C
GAM486  LOC145601 3'  CCGCTTTGCCACCATCTC    83365           TGAA
                                GAGATGGTGGCAG    GG
                                ||||||||||||    ||
                                CTCTACCACCGTT    CC
                                       TCG_
GAM486  LOC149401 5'  CCTTGAACACCATCTCTT    79333          GCAGTG
                                AAGAGATGGTG     AAGG
                                ||||||||||     ||||
                                TTCTCTACCAC     TTCC
                                      AAG___
GAM486  LOC157931 3'  CCCCCACTTGCCACCATC    86659          _   AA
                                GATGGTGGCA GTG  GG
                                |||||||||| |||  ||
                                CTACCACCGT CAC  CC
                                      T   CC
GAM486  LOC201456 3'  CCTTCACCACCATCACTCTC   88246      _     CA
                                GAGA TGGTGG  GTGAAGG
                                |||| ||||||  |||||||
                                CTCT ACTACC  CACTTCC
                                  C     AC
GAM486  LOC201952 5'  CCCCCACTGCCATAATATTCTC 90271      TG___       AA
                                GAGA    GTGGCAGTG  GG
                                ||||    |||||||||  ||
                                CTCT    TACCGTCAC  CC
                                  TATAA        CC
GAM486  LOC202860 3'  CCCTCACTGCCACTCCCTC    89221     AT         A
                                GAG  GGTGGCAGTGA GG
                                |||  |||||||||| ||
                                CTC  TCACCGTCACT CC
                                  CC          C
GAM486  LOC222193 5'  CCCACCGCCACCGTCTC     94180           A   AA
                                GAGATGGTGGC GTG  G
                                |||||||||| |||  |
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                                CTCTGCCACCG CAC  C
                                      C   CC
GAM486  LOC253897 3'  CCCCCACTGCTGTGTCCTTTC  96105      A   G TG     AA
                                GAAAG GAT G  GCAGTG  GG
                                ||||| ||| |  ||||||  ||
                                CTTTC CTG T  CGTCAC  CC
                                  _  _ GT     CC
GAM486  LOC90550  3'  CTGCCAACACCCCTTTCA    73091       AGA  G
                                TGAAAG   TG TGGCAG
                                ||||||   || ||||||
                                ACTTTC   AC ACCGTC
                                   CCC  A
GAM486  LOC92080  5'  CCTCCACTGCTGAAGTTCCT   68045    AG  GG       A
                                AG  AT  TGGCAGTG AGG
                                ||  ||  |||||||| |||
                                TC  TG  GTCGTCAC TCC
                                 CT  AA       C
GAM486  LOC95633  3'  CCTTGGCCCCCACCCCCTC    59871     AT     CA  G
                                GAG  GGTGG  GT AAGG
                                |||  |||||  || ||||
                                CTC  CCACC  CG TTCC
                                  CC    CC  G
GAM487  A1BG      3'  ACTCACCTCTACCTC       55410           T C
                                GAGGTAGAGGT G AGT
                                |||||||||||| | |||
                                CTCCATCTCCA C TCA
                                          _ _
GAM487  ACVR1     5'  ACTGCAGCCTCCACCTCC     6600        A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487  AHR       3'  GCTCACTGCAACCTCTACCTCC 7880                  _
                                GGAGGTAGAGGTTGCAGT AGC
                                |||||||||||||||||| |||
                                CCTCCATCTCCAACGTCA TCG
                                          C
GAM487  AIM1      3'  ACTGCAGCCTCTACCTCC    91814
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCATCTCCGACGTCA

GAM487  ALDH1B1   3'  ACTGCAACCTCCGCCTCC    5487        TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  APBA2     3'  GCCGTCACCCCTGCCTCC    18560         A   T  A
                                GGAGGTAG GGT GC GT
                                |||||||| ||| || ||
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                                CCTCCGTC CCA TG CG
                                     C   C  C
GAM487  APPBP2   3'  ACTGCAACCTCCGCCTCC    21070      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  AQP6     3'  GCTCACTGCAACCTCTACCTCC 7955                _
                                GGAGGTAGAGGTTGCAGT AGC
                                |||||||||||||||||| |||
                                CCTCCATCTCCAACGTCA TCG
                                           C
GAM487  AQP6     3'  GCTCACTGCAACCTCTACCTCC 53931               _
                                GGAGGTAGAGGTTGCAGT AGC
                                |||||||||||||||||| |||
                                CCTCCATCTCCAACGTCA TCG
                                           C
GAM487  ARCN1    3'  ACTGCAACCTCCGCCTCC    7968       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  ATBF1    5'  GCCACCATGAGCTCCCCTCC   22550      TA   G   CA  A
                                GGAGG  GAG TTG  GT GC
                                |||||  ||| |||  || ||
                                CCTCC  CTC AGT  CA CG
                                   C_   G   AC  C
GAM487  ATP8B2   3'  GCTCACTGCAACCTCCACCTCC 65229       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                ||||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                    C          C
GAM487  BRIP1    3'  ACTGCAACCTTCACCTCC    49395       AG
                                GGAGGT  AGGTTGCAGT
                                ||||||  ||||||||||
                                CCTCCA  TCCAACGTCA
                                    CT
GAM487  CAMLG    3'  ACCGCAACCTCCACCTTC    8230        A      A
                                GGAGGT GAGGTTGC GT
                                ||||||| |||||||| ||
                                CTTCCA CTCCAACG CA
                                    C       C
GAM487  CBFA2T2  3'  ACGGTAACCTCTGCCTCC    17456             A
                                GGAGGTAGAGGTTGC GT
                                |||||||||||||| ||
                                CCTCCGTCTCCAATG CA
                                          G
GAM487  CCND3    3'  GCCACCCACCTCCCTGCCTCC  8307         __    TGCA  A
                                GGAGGTA  GAGGT    GT GC
                                |||||||  |||||    || ||
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                                CCTCCGT  CTCCA    CA CG
                                   CC    CC__  C
GAM487  CCNF     3'  ACTGTAACCTCCGCCTCC    8313       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAATGTCA
                                   GC
GAM487  CDH17    3'  ACTGCAACCTCCGCCTCC    14499      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  CHAT     5'  GCTGCAGCCCCCACCCC     40623    A   AGA
                                GG GGT   GGTTGCAGT
                                || |||   |||||||||
                                CC CCA   CCGACGTCG
                                 _   CCC
GAM487  CIAS1    5'  ACTGCAGCCTCCACCTCC    16897       A
                                GGAGGT GAGGTTGCAGT
                                ||||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487  CLECSF12 3'  ACCGCAACCTCCGCCCC     76681    A  TA      A
                                GG GG  GAGGTTGC GT
                                || ||  |||||||| ||
                                CC CC  CTCCAACG CA
                                 _ GC       C
GAM487  COL9A2   3'  CTACTTCCTTCCCTGCCTCC   8487         A  TTGC_
                                GGAGGTAG GG     AGTAG
                                |||||||| ||     |||||
                                CCTCCGTC CC     TCATC
                                    _  TTCCT
GAM487  COX15    3'  CTCTGCAACCTCCACTTCC    54310       A        T
                                GGAGGT GAGGTTGCAG AG
                                |||||| |||||||||| ||
                                CCTTCA CTCCAACGTC TC
                                   C         _
GAM487  CRAT     5'  GCCACTGCCACCTGCCTCC    14354       AG   T    A
                                GGAGGT  AGGT GCAGT GC
                                ||||||  |||| ||||| ||
                                CCTCCG  TCCA CGTCA CG
                                   __    C    C
GAM487  CSNK2A2  5'  GCTCACTGCAACCTCCACCTCC 8566        A         _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  CXCL16   3'  GCTCACTGCAACCCCCATCTCC 41921       AGA       _
                                GGAGGT   GGTTGCAGT AGC
                                ||||||   ||||||||| |||
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                                CCTCTA   CCAACGTCA TCG
                                   CCC        C
GAM487  CYP1A2   3'  ACTGCAACCTCTGCCTCC    69092
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  CYP1A2   3'  GCTCACTGCAACCTCCACCTC  69114       A         _
                                GAGGT GAGGTTGCAGT AGC
                                ||||| |||||||||||| |||
                                CTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  CYP1A2   3'  GCTCACTGCAACCTCCACCTC  5694        A         _
                                GAGGT GAGGTTGCAGT AGC
                                ||||| |||||||||||| |||
                                CTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  CYP1A2   3'  ACTGCAACCTCTGCCTCC    5673
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  CYP2B6   3'  ACTGCAACCTCCACATCC    5720      G  A
                                GGA GT GAGGTTGCAGT
                                ||| || ||||||||||
                                CCT CA CTCCAACGTCA
                                  A  C
GAM487  CYP2B6   3'  GCTCACTGCAACCTCCACCCC  5734     A   A         _
                                GG GGT GAGGTTGCAGT AGC
                                || ||| |||||||||| |||
                                CC CCA CTCCAACGTCA TCG
                                  _  C          C
GAM487  CYP8B1   3'  GCTCACTACAACCTCTGCCTCC 15266             C   _
                                GGAGGTAGAGGTTG AGT AGC
                                |||||||||||||| ||| |||
                                CCTCCGTCTCCAAC TCA TCG
                                         A   C
GAM487  CYP8B1   3'  ACTGCAACCTCTGCCTCC    15254
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  DDX26    5'  GCCACCGGCGCCTCCACCTCT  24052       A    T  A_  A
                                GGAGGT GAGGT GC  GT GC
                                |||||| ||||| ||  || ||
                                TCTCCA CTCCG CG  CA CG
                                   C     _ GC  C
GAM487  DISC1    3'  GCTCACTGCAACCTCTACCTCC 37882                 _
                                GGAGGTAGAGGTTGCAGT AGC
                                |||||||||||||||||| |||
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                                CCTCCATCTCCAACGTCA TCG
                                          C
GAM487  DMD     5'  CTATGACTCTACCTCC     14368         GTTGCA
                                GGAGGTAGAG    GTAG
                                ||||||||||    ||||
                                CCTCCATCTC    TATC
                                   AG____
GAM487  DMD     5'  CTATGACTCTACCTCC     14376         GTTGCA
                                GGAGGTAGAG    GTAG
                                ||||||||||    ||||
                                CCTCCATCTC    TATC
                                   AG____
GAM487  DSCR3   3'  GCTCACTGCAACCTCCACCTCC 20187       A       _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C        C
GAM487  EFNB1   3'  CTCACACCATCCACCTCC    15397       A _  _ C
                                GGAGGT GA GGT TG AG
                                |||||| || ||| || ||
                                CCTCCA CT CCA AC TC
                                   C A  C _
GAM487  EHD2    3'  GCTCACTGCAACCTCCACCTCC 27498       A       _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C        C
GAM487  EPB72   3'  ACTGCAACCTCCGCCTCC    14597       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                  GC
GAM487  F8      3'  GCCACTGCAGCACCTGCC    3730        AG      A
                                GGTAG  GTTGCAGT GC
                                |||||  |||||||| ||
                                CCGTC  CGACGTCA CG
                                  CA       C
GAM487  FANCE   3'  ACTGTAACCTCTGCCTCC    41611
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAATGTCA

GAM487  FEZ1    3'  GCTCACTGCAACCTCCACCTCC 42574       A       _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C        C
GAM487  FGF5    3'  GCTCACTGCAACCTCCAACTCC 52489      GTA       _
                                GGAG   GAGGTTGCAGT AGC
                                ||||   |||||||||| |||
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                                CCTC   CTCCAACGTCA TCG
                                  AAC          C
GAM487   FGF5     3'  GCTCACTGCAACCTCCAACTCC 15543      GTA          _
                                GGAG   GAGGTTGCAGT AGC
                                ||||   |||||||||||| |||
                                CCTC   CTCCAACGTCA TCG
                                  AAC          C
GAM487   FZD4     3'  ACTGCAACCTCTGCCTCC    24122
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487   G6PC     3'  ACTGCAACCTCTTCCTCC    3818        T
                                GGAGG AGAGGTTGCAGT
                                ||||| ||||||||||||
                                CCTCC TCTCCAACGTCA
                                   T
GAM487   G6PC     3'  GCCACCGCACCGGGCCCTCC   3826       TAGA   T  A  A
                                GGAGG    GGT GC GT GC
                                |||||    ||| || || ||
                                CCTCC    CCA CG CA CG
                                   CGGG   _  C  C
GAM487   GAB2     3'  ACTGTCCTCTGCCCC       54440    A       TT
                                GG GGTAGAGG  GCAGT
                                || ||||||||  |||||
                                CC CCGTCTCC  TGTCA
                                _      __
GAM487   GAB2     3'  CTCCACCCACTACCTCC     54451         A  T  C
                                GGAGGTAG GG TG AG
                                |||||||| || || ||
                                CCTCCATC CC AC TC
                                     A  C  C
GAM487   GAB2     3'  ACTGTCCTCTGCCCC       24483    A       TT
                                GG GGTAGAGG  GCAGT
                                || ||||||||  |||||
                                CC CCGTCTCC  TGTCA
                                _      __
GAM487   GAB2     3'  CTCCACCCACTACCTCC     24494         A  T  C
                                GGAGGTAG GG TG AG
                                |||||||| || || ||
                                CCTCCATC CC AC TC
                                     A  C  C
GAM487   GHR      3'  ACTGCAATCTCCACCTCC    3876         A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCTAACGTCA
                                   C
GAM487   GM2A     3'  ACTGCAACCTCCGCCTCC    67768        TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
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                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  GPR4     3'  ACTGCAGCCTCCACCTCC    59899       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487  GPR62    3'  GCTACTGAAACTCCTCCACCTG 89520   G   A   TTG__
              C                  G AGGT GAGG    CAGTAGC
                                | |||| ||||    |||||||
                                C TCCA CTCC    GTCATCG
                                 G   C   TCAAA
GAM487  GPR81    3'  ACTGCAACCTCTGCCTCC    50751
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  GRAF     3'  ACTGCAACCTCCGCCTCC    30549      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  HAT1     3'  CTACTGCAATTGCTTCC     13317       GAG
                                GGAGGTA   GTTGCAGTAG
                                |||||||   ||||||||||
                                CCTTCGT   TAACGTCATC
                                      ___
GAM487  HOXC13   3'  GCTGTCGACCTCTACTCC    59686     G       _
                                GGAG TAGAGGTTG CAGT
                                |||| ||||||||| ||||
                                CCTC ATCTCCAGC GTCG
                                   _       T
GAM487  HPN      5'  GCCACCGCCTCTGCCTCC    9276           T___
                                GGAGGTAGAGGT   GC
                                ||||||||||||   ||
                                CCTCCGTCTCCG   CG
                                       CCAC
GAM487  IRS2     3'  GCTGTCGACCTCTCCTCC    59718      T      _
                                GGAGG AGAGGTTG CAGT
                                ||||| |||||||| ||||
                                CCTCC TCTCCAGC GTCG
                                   _       T
GAM487  ITGAM    3'  ACTGCAACCTCCGCCTCC    71834      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  KCNC4    5'  GCCACCGCCTCCTGCCTCC   17139        _   T___
                                GGAGGTAG AGGT   GC
                                |||||||| ||||   ||
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                                CCTCCGTC TCCG    CG
                                     C    CCAC
GAM487  KCND2    5'  ACTGCACATCACCTCC      24391       A  GGT
                                GGAGGT GA   TGCAGT
                                |||||| ||   ||||||
                                CCTCCA CT   ACGTCA
                                   _  AC_
GAM487  KIF5B    3'  ACTATAACCTCTACTCCC     15729     AG        C
                                GG  GTAGAGGTTG AGT
                                ||  |||||||||| |||
                                CC  CATCTCCAAT TCA
                                 CT         A
GAM487  KMO      3'  ACTGCAACCTCTGCCTCC     13441
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  LNK      3'  ACTGCAACCTCCACCTTC     18455       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CTTCCA CTCCAACGTCA
                                    C
GAM487  LYZ      3'  GCTCACTGCAACCTCCACCTCC 4104        A         _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                    C          C
GAM487  MAK      3'  GCTTACTGCAACCTCCACCTCC 19765       A         _
                                GGAGGT GAGGTTGCAGTA GC
                                |||||| |||||||||||| ||
                                CCTCCA CTCCAACGTCAT CG
                                    C          T
GAM487  MAPT     3'  GCCACTGCAGTCACCCC      19778     A   AGA GT     A
                                GG GGT   G  TGCAGT GC
                                || |||   |  |||||| ||
                                CC CCA   C  ACGTCA CG
                                 _  ___ TG     C
GAM487  MAPT     3'  GCCACTGCAGTCACCCC      33689     A   AGA GT     A
                                GG GGT   G  TGCAGT GC
                                || |||   |  |||||| ||
                                CC CCA   C  ACGTCA CG
                                 _  ___ TG     C
GAM487  MAPT     3'  GCCACTGCAGTCACCCC      33698     A   AGA GT     A
                                GG GGT   G  TGCAGT GC
                                || |||   |  |||||| ||
                                CC CCA   C  ACGTCA CG
                                 _  ___ TG     C
GAM487  MAPT     3'  GCCACTGCAGTCACCCC      33708     A   AGA GT     A
                                GG GGT   G  TGCAGT GC
                                || |||   |  |||||| ||
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                                CC CCA   C  ACGTCA CG
                                 _  ___ TG     C
GAM487  MCM5    3'  GCTGGGACCTCTGCCTCC    59965          G
                                GGAGGTAGAGGTT CAGT
                                |||||||||||| ||||
                                CCTCCGTCTCCAG GTCG
                                      G
GAM487  MEF2A   5'  ACTGCAACCTCCGCCTCC    18778      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  MEFV    3'  ACTGCAACCTCCGCCTCC    4123       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  MEFV    3'  GCTCACTGCAACCTCCACCTCC 4144        A       _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                    C         C
GAM487  MHC2TA  3'  GCTACTGTCCTACCCACC    4176    A  TAG   TT
                                GG GG   AGG  GCAGTAGC
                                || ||   |||  ||||||||
                                CC CC   TCC  TGTCATCG
                                 A  CA_  __
GAM487  MICB    3'  ACTGCAACCTCTGCCTCC    19818
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  MPL     3'  GCTCACTGCAACCTCCACCTCC 18147       A       _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                    C         C
GAM487  MPL     3'  ACTGCAACCTCTGCCTCC    18129
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  MTCP1   5'  CTACTGCAGTGCACCC     26430    AG   GAGG
                                GG  GTA   TTGCAGTAG
                                ||  |||   |||||||||
                                CC  CGT   GACGTCATC
                                 CA  _____
GAM487  MYCL2   3'  ACTGCAACCTCTGCCTCC    18172
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
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                                CCTCCGTCTCCAACGTCA

GAM487  NDRG3    3'  ACTGCAACCTCTGCCCC     49288    A
                                GG GGTAGAGGTTGCAGT
                                || ||||||||||||||
                                CC CCGTCTCCAACGTCA
                                 _
GAM487  NEDD4L   3'  CTCTGACACCTCCACCCTC   30948   GA  A    TG  T
                                G  GGT GAGGT  CAG AG
                                |  ||| |||||  ||| ||
                                C  CCA CTCCA  GTC TC
                                 TC  C    CA  _
GAM487  NLGN2    3'  ACGCGCCTGCCTCC       88154       AG   T  A
                                GGAGGT  AGGT GC GT
                                ||||||  |||| || ||
                                CCTCCG  TCCG CG CA
                                   __   _ _
GAM487  NQO1     3'  ACTGCAACCTCTGCCTCC    6150
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  NR2E3    3'  CTACTGCCACCTTCC       32971    TA    T
                                GG  GAGGT GCAGTAG
                                ||  ||||| |||||||
                                CC  TTCCA CGTCATC
                                 __    C
GAM487  PCDHB11  3'  ACTGCAACCTCTGCCTCC    38409
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  PCDHB16  3'  ACTGCAACCTCTGCCTCC    40547
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  PCDHB9   3'  ACTGCAACCTCCGCCTCC    38934      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  PDCL     3'  GCTCACTGCAACCTCCACCTCC 18215       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  PDE6B    3'  GCTCACTGCAACCTCCACCTCC 4285        A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
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                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  PER2     3'  ACTGCAACCTCTGCCTCC    43026
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  PIGR     3'  ACTGCAACCTCCGCCTCC    72590       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  PIK3CD   3'  ACTGTAACCTCCGCCTCC    17239       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAATGTCA
                                   GC
GAM487  PKM2     3'  CTACTGCAGCACCTCC      10602       AGAG
                                GGAGGT   GTTGCAGTAG
                                ||||||   ||||||||||
                                CCTCCA   CGACGTCATC
                                   ____
GAM487  PMCHL1   3'  ACTGAAACCTCTGCCTCC    49068           G
                                GGAGGTAGAGGTT CAGT
                                |||||||||||| ||||
                                CCTCCGTCTCCAA GTCA
                                      A
GAM487  PON1     3'  ACTGCAACTTCTACCTCC    4799
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCATCTTCAACGTCA

GAM487  PPP1R8   5'  GCCCCAACCCTACCTCC     10725        A    CA
                                GGAGGTAG GGTTG  GT
                                |||||||| |||||  ||
                                CCTCCATC CCAAC  CG
                                   _    CC
GAM487  PRDM2    5'  GCCACTATGTTTTCTACCTCC  31849          T GC   A
                                GGAGGTAGAGG T  AGT GC
                                |||||||||| |  ||| ||
                                CCTCCATCTTT G  TCA CG
                                      T TA   C
GAM487  PRDM2    5'  GCCACTATGTTTTCTACCTCC  24248          T GC   A
                                GGAGGTAGAGG T  AGT GC
                                |||||||||| |  ||| ||
                                CCTCCATCTTT G  TCA CG
                                      T TA   C
GAM487  PRKWNK3  3'  GCTGCAACCTCCCCCTCC    61554       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
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                                CCTCC  CTCCAACGTCG
                                   CC
GAM487  PSMB2    3'  ACTGCAACCTCCGCCTCC    10946      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  PSMB9    3'  GCCACCTGACCTTACCTCC   10962        ____   T
                                GGAGGTAG   AGGT GC
                                ||||||||   |||| ||
                                CCTCCATT   TCCA CG
                                     CCAG   C
GAM487  PTPRO    3'  ACTGCACCTCTACATCC     47713     G      T
                                GGA GTAGAGGT GCAGT
                                ||| |||||||| |||||
                                CCT CATCTCCA CGTCA
                                  A      _
GAM487  RAD9     3'  CTACTGACGTTCCTACCTCT   15934        A GT  _
                                GGAGGTAG G  TG CAGTAG
                                |||||||| |  || ||||||
                                TCTCCATC C  GC GTCATC
                                     _ TT  A
GAM487  RAMP3    3'  GCTACTGTGGCCACACCCC   19592    A   AGA   TG
                                GG GGT   GGT  CAGTAGC
                                || |||   |||  |||||||
                                CC CCA   CCG  GTCATCG
                                 _   CA_   GT
GAM487  RHD      3'  ACTGCAACCTCCGCCTCC    32292      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  RHD      3'  GCTCACTGCAACCTCTACCTCC 32309              _
                                GGAGGTAGAGGTTGCAGT AGC
                                |||||||||||||||| |||
                                CCTCCATCTCCAACGTCA TCG
                                           C
GAM487  RHD      3'  ACTGCAACCTCCGCCTCC    32601      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  RHD      3'  GCTCACTGCAACCTCTACCTCC 32618              _
                                GGAGGTAGAGGTTGCAGT AGC
                                |||||||||||||||| |||
                                CCTCCATCTCCAACGTCA TCG
                                           C
GAM487  RPH3AL   3'  GCTCACTGCAACCTCCACCTCC 22749       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
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                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  SAS      3'  ACCGCAACCTCTGCCTCC    19948             A
                                GGAGGTAGAGGTTGC GT
                                |||||||||||||| ||
                                CCTCCGTCTCCAACG CA
                                      C
GAM487  SDPR     5'  ACCGCAACTTCTCACC      16222     _       A
                                GGT AGAGGTTGC GT
                                ||| ||||||||| ||
                                CCA TCTTCAACG CA
                                  C        C
GAM487  SEDL     3'  GCTCACTGCAACCTCCACCTCC 27344       A       _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  SEDL     3'  GCTCACTGCAACCTCCACCTCC 27345       A       _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  SEDL     3'  ACCGTAACCTCTGCCTCC    27313             A
                                GGAGGTAGAGGTTGC GT
                                |||||||||||||| ||
                                CCTCCGTCTCCAATG CA
                                      C
GAM487  SEDL     3'  ACTGCAACCTCCGCCTCC    27321      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  SEPN1    3'  GCTCACTGCAACCTCCACCTCC 66372       A       _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  SERPINB9 3'  ACTGCAACCTCCTCCTCC    14746      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   TC
GAM487  SHOX     3'  ACTGCAACCTCCGCCTCC    22528      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  SIL      3'  ACTGCAACCTCTGCCTCC    11680
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
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                                CCTCCGTCTCCAACGTCA

GAM487  SLA2     3'  GCTCACTGCAACCTCCATCTCC 49901       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCTA CTCCAACGTCA TCG
                                   C         C
GAM487  SLC14A2  5'  GCTCACTGCAACCTCCACCTCC 23135       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  SLC15A1  3'  ACTGCAACCTCCGCCTCC    17395      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  SLC15A1  3'  GCCCTGACCTCTGCCCC     17403    A        ___
                                GG GGTAGAGGTT   GC
                                || ||||||||||   ||
                                CC CCGTCTCCAG   CG
                                 _        TCC
GAM487  SLC7A6   3'  CTACTGCAGGAGCCCC      14302    A   AGAGG
                                GG GGT    TTGCAGTAG
                                || |||    |||||||||
                                CC CCG    GACGTCATC
                                 _  AG___
GAM487  SLC7A8   3'  GCTACTCTCTCCTTCCTCC   24281      TA   TTGC
                                GGAGG  GAGG   AGTAGC
                                |||||  ||||   ||||||
                                CCTCC  TTCC   TCATCG
                                   __   TCTC
GAM487  SMAC     5'  ACTGCAACCTCTGCCTCC    57202
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  SNAP23   3'  ACTGCAACCTCCGCCTCC    13803      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  SNAP23   3'  ACTGCAACCTCCGCCTCC    55456      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  SNX15    3'  GCTCACTGCAACCTCCACCTCC 73743       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
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                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  SPN      3'  ACTGCAACCTCTGCCTCC    11913
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  SREBF2   3'  GCCAAGCCCCTGCCTCC     15990        A   __
                                GGAGGTAG GGTT  GC
                                |||||||| ||||  ||
                                CCTCCGTC CCGA  CG
                                     C    AC
GAM487  SS18     3'  ACTGCAACCTCCGCCTCC    18880       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  SSR2     3'  CTATCCCCTGCCTCC       11983        A  TTGCA
                                GGAGGTAG GG    GTAG
                                |||||||| ||    ||||
                                CCTCCGTC CC    TATC
                                     C  _____
GAM487  STAU     5'  GCTCACTGCAACCTCCACCTCC 16006       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  SULT2B1  5'  ACTGCAACCTCCGCCTCC    16019       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  TAPBP    3'  ACTGCAACCTCCGCCTCC    12118       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  TAT      3'  GCTCACTGCAACCTCCACCTCC 4471        A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  TBX6     3'  CTGCTGGGCCCCTCTGCCTCC  16037          TTG_
                                GGAGGTAGAGG   CAGTAG
                                ||||||||||   ||||||
                                CCTCCGTCTCC   GTCGTC
                                      CCGG
GAM487  TBXA2R   3'  ACTGCAACCTCCGCCTCC    6476        TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
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                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  TBXA2R   3'  GCTCACTGCAACCTCCACCTCC 6498        A         _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                    C          C
GAM487  TERF1    3'  ACTGAACCTCTGCCTCC     33968            G
                                GGAGGTAGAGGTT CAGT
                                |||||||||||| ||||
                                CCTCCGTCTCCAA GTCA
                                                _
GAM487  TFAP4    3'  GCCCCCACCTCTGCCTCC    12238           T___
                                GGAGGTAGAGGT   GC
                                ||||||||||||   ||
                                CCTCCGTCTCCA   CG
                                      CCCC
GAM487  TFEB     3'  GCCACCTGCCCTGCCTCC    92126         ___   T
                                GGAGGTAG  AGGT GC
                                ||||||||  |||| ||
                                CCTCCGTC  TCCA CG
                                     CCG   C
GAM487  TPMT     3'  ACTGCAACCTCTGCCTCC    4532
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  TRIM9    5'  ACTGCAACCTCCGCCTCC    30746       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  TRPM6    3'  ACTGCAACCTCTGCCTCC    34529
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  TRPV1    3'  ACTGCAACCTCTGCCTCC    54789
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  TRPV1    3'  ACTGCAACCTCTGCCTCC    38070
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  TRPV1    3'  ACTGCAACCTCTGCCTCC    54856
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
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                                CCTCCGTCTCCAACGTCA

GAM487  TRPV1    3'  ACTGCAACCTCTGCCTCC    54824
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  TTC3     5'  ACTCTAGCCCTACTCC      12413     G   A    C
                                GGAG TAG GGTTG AGT
                                |||| ||| ||||| |||
                                CCTC ATC CCGAT TCA
                                  _  _    C
GAM487  TUFT1    3'  ACTGCAACCTCTGCCTCC    39248
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  VENTX2   3'  ACTGCAACCTCCGCCTCC    27105      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  VHL      3'  ACTACAAGCTCTGCCTCC    5051         G   C
                                GGAGGTAGAG TTG AGT
                                |||||||||| ||| |||
                                CCTCCGTCTC AAC TCA
                                      G   A
GAM487  VHL      3'  ACTGCAACCTCTGCCTCC    5054
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  VIPR1    3'  GCCACTCAGCTTCCTACC    16113      _     C   A
                                GGTAG AGGTTG AGT GC
                                ||||| |||||| ||| ||
                                CCATC TTCGAC TCA CG
                                   C     _  C
GAM487  ZNF10    3'  CTACTAGTATCTACCTC     31177        GGT   _
                                GAGGTAGA   TGC AGTAG
                                ||||||||   ||| |||||
                                CTCCATCT   ATG TCATC
                                     ___   A
GAM487  ZNF133   5'  ACTGCAACCTCCACCCC     12830    A   A
                                GG GGT GAGGTTGCAGT
                                || ||| ||||||||||
                                CC CCA CTCCAACGTCA
                                 _  C
GAM487  ZNF264   3'  ACTGCAACCTCCGCCTCC    12743      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
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                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  20D7-FC4  5'  ACTGCAGCCTCCACCTCC    60893       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487  20D7-FC4  3'  GCTACTGCCATCAACCCC    60901    A  A  GGTT
                                GG GGT GA    GCAGTAGC
                                || ||| ||    ||||||||
                                CC CCA CT    CGTCATCG
                                 _  A  AC__
GAM487  AMOT      5'  GCTACAATCTCCACCATCC    55721    _  A      C
                                GGA GGT GAGGTTG AGT
                                ||| ||| ||||||| |||
                                CCT CCA CTCTAAC TCG
                                  A  C      A
GAM487  ANKT      5'  GCTACTGCAAAAGTTCCTTC   33025      T  AGG
                                GGAGG AG   TTGCAGTAGC
                                ||||| ||   ||||||||||
                                CTTCC TT   AACGTCATCG
                                   _  GAA
GAM487  ARGBP2    5'  GCCACTGACTCCTACTTCC    40774        AG  TG   A
                                GGAGGTAG  GT  CAGT GC
                                ||||||||  ||  |||| ||
                                CCTTCATC  CA  GTCA CG
                                     CT  __   C
GAM487  ARGBP2    5'  GCCACTGACTCCTACTTCC    13195        AG  TG   A
                                GGAGGTAG  GT  CAGT GC
                                ||||||||  ||  |||| ||
                                CCTTCATC  CA  GTCA CG
                                     CT  __   C
GAM487  ARPP-19   3'  ACTGCAACCTCTGCCTCC    21785
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  ASB16     5'  ACTGCAACCTCCGCCTCC    69930      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  ASE-1     3'  ACTGCAACCTCCGCCTCC    23942      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  ATIP1     3'  GCAAACCTTCTACCTCC     40392         _   _
                                GGAGGTAGA GGTT GC
                                ||||||||| |||| ||
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                                CCTCCATCT CCAA CG
                                     T   A
GAM487  ATP1B4   3'  GCTCACTGCAACCTCCACCTCC 23822       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  BA108L7.2 3'  ACTGCAACCTCTGCCTCC    48251
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  BAG5     3'  CTACTGCAGGTCCAACTCC    16842     GTA  GG
                                GGAG   GA  TTGCAGTAG
                                ||||   ||  |||||||||
                                CCTC   CT  GACGTCATC
                                  AAC  G_
GAM487  BAG5     3'  GCTCACTGCAACCTCCACCTCC 16847       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  BCL2L12   5'  TGTAAGCCTCTACCTCC     56865          _
                                GGAGGTAGAGGTT GCA
                                |||||||||||| |||
                                CCTCCATCTCCGA TGT
                                      A
GAM487  BNIP-S   3'  ACTGCAACCTCCGCCTCC    56255      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                  GC
GAM487  BTN3A1   3'  GCTCCCTGCAACCTCCACCTCC 22922       A        T_
                                GGAGGT GAGGTTGCAG  AGC
                                |||||| ||||||||||  |||
                                CCTCCA CTCCAACGTC  TCG
                                   C         CC
GAM487  C11orf14  3'  CGTAGCACCTGACCTTTACCTC 40227          T________  AGTA
          C                      GGAGGTAGAGGT       GC   G
                                ||||||||||||       ||   |
                                CCTCCATTTCCA       CG   C
                                      GTCCAIII  ATGA
GAM487  C11orf25  5'  GCTACTGTTCCTCCGCCTCC  48643      TA   TT
                                GGAGG  GAGG  GCAGTAGC
                                |||||  ||||  ||||||||
                                CCTCC  CTCC  TGTCATCG
                                  GC   T_
GAM487  C14orf4   3'  CTGGGCAGCCACCTCC      67336       AGA     AG
                                GGAGGT   GGTTGC  TAG
                                ||||||   ||||||  |||
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                                CCTCCA  CCGACG  GTC
                                   ___     G_
GAM487  C1orf24  3'  ACTGCAACCTCCGCCTCC    53704      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                  GC
GAM487  C1QTNF6  3'  ACTGCAACCTCTGCCTCC    49135
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  C21orf25  3'  GCTTACTGCAACCTCCACCTCC 63554       A          _
                                GGAGGT GAGGTTGCAGTA GC
                                |||||| |||||||||||| ||
                                CCTCCA CTCCAACGTCAT CG
                                   C          T
GAM487  C3F      3'  GCTCACCGCAACCTCCACCTCC 19295       A      A _
                                GGAGGT GAGGTTGC GT AGC
                                |||||| |||||||| || |||
                                CCTCCA CTCCAACG CA TCG
                                   C       C  C
GAM487  C9orf7   3'  CTACCCAGCCCTACTCC     34169      G   A    CA
                                GGAG TAG GGTTG  GTAG
                                |||| ||| |||||  ||||
                                CCTC ATC CCGAC  CATC
                                  _  _    C_
GAM487  C9orf9   3'  ACTGCAACCTCCGCCTCC    38502      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                  GC
GAM487  C9orf9   3'  GCTCACTGCAACCTCCACCTCC 38517       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  CABIN1   3'  GCCACTGCAGCCCCACCGCC   24480    A   AGA       A
                                GG GGT   GGTTGCAGT GC
                                || |||   ||||||||| ||
                                CC CCA   CCGACGTCA CG
                                 G   CC_       C
GAM487  CENPH    3'  ACTGCAACCTCTGCCTCC    43269
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  CHPT1    5'  GCCAGCCTCTCCCTCC      39621       T      _
                                GGAGG AGAGGTTG C
                                ||||| |||||||| |
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                                CCTCC TCTCCGAC G
                                   C       C
GAM487  CHRAC1   3'  ACTGCAACCTCCGCCTCC    33863      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  CNTNAP1  3'  GCCAGCCCTCTACTCC      13277      G    _  _
                                GGAG TAGAGG TTG C
                                |||| |||||| ||| |
                                CCTC ATCTCC GAC G
                                   _     C  C
GAM487  COLEC12  3'  ACTGCAACCCCCCACATCC    47861     G  AGA
                                GGA GT   GGTTGCAGT
                                ||| ||   |||||||||
                                CCT CA   CCAACGTCA
                                  A  CCC
GAM487  CPSF2    3'  ACCGCAACCTCTGCCTCC    61568            A
                                GGAGGTAGAGGTTGC GT
                                |||||||||||||| ||
                                CCTCCGTCTCCAACG CA
                                          C
GAM487  CPSF2    3'  ACTATAACCTCTTCCTCC    61570      T      C
                                GGAGG AGAGGTTG AGT
                                ||||| |||||||| |||
                                CCTCC TCTCCAAT TCA
                                   T       A
GAM487  CSAD     5'  GCTACCTGTGCACCCTGCCTCC 32031        A  _    _
                                GGAGGTAG GGT TGCAG TAGC
                                |||||||| ||| ||||| ||||
                                CCTCCGTC CCA GTGTC ATCG
                                     _  C    C
GAM487  DBR1     3'  ACCGCAACCTCCGCCTCC    32526      TA      A
                                GGAGG  GAGGTTGC GT
                                |||||  |||||||| ||
                                CCTCC  CTCCAACG CA
                                   GC       C
GAM487  DCOHM    3'  GCCACTATCCCTACCTC     49604       A  TTGC   A
                                GAGGTAG GG    AGT GC
                                |||||||  ||    ||| ||
                                CTCCATC CC    TCA CG
                                   _  TA__   C
GAM487  DIRC2    5'  ACAGCAGCCTCCGCCTCC    51609      TA      A
                                GGAGG  GAGGTTGC GT
                                |||||  |||||||| ||
                                CCTCC  CTCCGACG CA
                                   GC       A
GAM487  DKFZp434A2417 3'  ACTGCAACTTCCACCTCC    66093       A
                                GGAGGT GAGGTTGCAGT
                                ||||||  ||||||||||
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                                CCTCCA CTTCAACGTCA
                                   C
GAM487  DKFZP434C212 3'  GCTCACTGCAACCTCCACCTCC 68914       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  DKFZp434E2220 5'  ACTGCAACCTCCGCCTCC    34292      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                  GC
GAM487  DKFZP434F1735 5'  ACTGTACCCTACCTCC      31494        A  T
                                GGAGGTAG GGT GCAGT
                                |||||||| ||| |||||
                                CCTCCATC CCA TGTCA
                                    _  _
GAM487  DKFZp547H025 3'  GCTCACTGCAACCTCCACCTCC 39361       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  DKFZP564J157 3'  GCTCCCCACCCCCTACCTCC   37455        A  T  CAGT
                                GGAGGTAG GG TG    AGC
                                |||||||| || ||    |||
                                CCTCCATC CC AC    TCG
                                     C  C  CCC_
GAM487  DKFZP564O0523 3'  GCTCACTGCAACCTCCACCTCC 49517       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  DKFZP564O123 5'  GCCTGGCGACCCCGACCTCC   59468       AGA     AGTA
                                GGAGGT   GGTTGC    GC
                                ||||||   ||||||    ||
                                CCTCCA   CCAGCG    CG
                                   GCC     GTC_
GAM487  DKFZP566G1424 5'  CACTGCAGCCCTCC       84774       TAGAG       A
                                GGAGG    GTTGCAGT G
                                |||||    |||||||| |
                                CCTCC    CGACGTCA C
                                  _____       C
GAM487  DKFZp761N1114 3'  ACTGCAACCTCCGCCTCC    79012       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                  GC
GAM487  DPP8     5'  GCCACTGCAACCAGGACC    55234     AGA       A
                                GGT   GGTTGCAGT GC
                                |||   |||||||| ||
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                                CCA   CCAACGTCA CG
                                  GGA        C
GAM487  EREG     3'  GCTCACTGCAACCTCACCTCC  7504        A         _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   _          C
GAM487  ETL      5'  ACTGCGGCCACCGCC       42205    A   AGA
                                GG GGT   GGTTGCAGT
                                || |||   |||||||||
                                CC CCA   CCGGCGTCA
                                 G  ___
GAM487  FBXL9    5'  CGTAGCACCAGGCCTTACCTCC 24080       A    T_______  AGTA
                                GGAGGT GAGGT       GC    G
                                |||||| |||||       ||    |
                                CCTCCA TTCCG       CG    C
                                   _    GACCAIII  ATGA
GAM487  FER1L4   3'  GCTGACTGCAACCTCCACCTCC 47352       A         _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          G
GAM487  FER1L4   3'  GCTGACTGCAACCTCCACCTCC 47353       A         _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          G
GAM487  FLJ00024 5'  ACTGCAACCTCTGCCTCC    63746
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  FLJ10232 3'  ACTGCAACCTCCGCCTCC    35919       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  FLJ10535 3'  ACTGCAACCTCTGCCTCC    36232
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  FLJ10922 3'  ACTGCAACCTCCGCCTCC    36866       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  FLJ11004 5'  GCTCACTGCAACCTCTACCTCC 36970                 _
                                GGAGGTAGAGGTTGCAGT AGC
                                |||||||||||||||||| |||
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                                CCTCCATCTCCAACGTCA TCG
                                          C
GAM487  FLJ12363  3'  GCTCACTGCAACCTCCACCTCC 49686       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  FLJ12572  5'  ACTGCAACCTCTGCCTCC    43244
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  FLJ12649  3'  ACTGCAACCTCCGCCTCC    44773      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  FLJ12668  3'  GTCACTGCAACCTCCATCTCC  46522       A        AG
                                GGAGGT GAGGTTGCAGT  C
                                |||||| ||||||||||  |
                                CCTCTA CTCCAACGTCA  G
                                   C         CT
GAM487  FLJ12687  3'  ACTGCAACCTCCGCCTCC    46184      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  FLJ12747  3'  ACTGCAACCTCTGCCTCC    49708
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  FLJ12876  3'  ACTGCAACATGCCTTC      42782       GAG
                                GGAGGTA   GTTGCAGT
                                |||||||   ||||||||
                                CTTCCGT   CAACGTCA
                                    A__
GAM487  FLJ12973  3'  ACCGCAACCTCCGCCTCC    46100      TA      A
                                GGAGG  GAGGTTGC GT
                                |||||  |||||||| ||
                                CCTCC  CTCCAACG CA
                                   GC       C
GAM487  FLJ13193  3'  GCCCACCTCTGCCTCC      49768          T_
                                GGAGGTAGAGGT  GC
                                ||||||||||||  ||
                                CCTCCGTCTCCA  CG
                                      CC
GAM487  FLJ13197  3'  GCTCACTGCAACCTCTACCTCC 44857              _
                                GGAGGTAGAGGTTGCAGT AGC
                                |||||||||||||||||| |||
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                                CCTCCATCTCCAACGTCA TCG
                                           C
GAM487  FLJ13409  3'  CTACTGCTGTACTTCC      44868        G GGTT
                                GGAGGTA A    GCAGTAG
                                ||||||| |    |||||||
                                CCTTCAT T    CGTCATC
                                   G ____
GAM487  FLJ13848  3'  GCCTCTCACCTCTACCCC    45468    A       T C  TA
                                GG GGTAGAGGT G AG  GC
                                || |||||||| | ||  ||
                                CC CCATCTCCA C TC  CG
                                 _       _ _  TC
GAM487  FLJ14950  3'  GCTCACTGCAACCTCCACCTCC 51722       A         _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  FLJ14957  3'  ACTGCAACCTCTGCCTCC    51736
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  FLJ20034  3'  ACTGCAACCTCTGCCTCC    34354
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  FLJ20045  3'  ACTGCAACCTCTGCCTCC    34411
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  FLJ20079  3'  GCTCACCGCAACCTCCACCTCC 34497       A       A  _
                                GGAGGT GAGGTTGC GT AGC
                                |||||| |||||||| || |||
                                CCTCCA CTCCAACG CA TCG
                                   C       C  C
GAM487  FLJ20342  3'  ACTGCAACCTCTGCCTCC    34984
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  FLJ20507  3'  ACTGCAACCTCTGCCTCC    35271
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  FLJ20507  3'  ACTGCAACCTCTGCCTCC    60207
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
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                                CCTCCGTCTCCAACGTCA

GAM487  FLJ20813  3' ACTGCAACTCCACCTCC    35678      A  G
                                GGAGGT GAG TTGCAGT
                                ||||||| ||| |||||||
                                CCTCCA CTC AACGTCA
                                   C  _
GAM487  FLJ21302  3' ACTGCAACCTCCGCCTCC    43209      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  FLJ22002  3' ACTGCAACCTCCGCCTCC    45766      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  FLJ22169  5' GCTACTGGGAGATCCACTCC   44004     GTA  GG  G
                                GGAG   GA  TT CAGTAGC
                                ||||   ||  || |||||||
                                CCTC   CT  AG GTCATCG
                                  AC_  AG  G
GAM487  FLJ22531  5' GCTCACTGCAACCTCCACCTCC 45032       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  FLJ22794  3' ACTGCAACTTCCACCTCC    91600      A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTTCAACGTCA
                                   C
GAM487  FLJ22814  3' GCTGTCACCTCGACCTCC    46177      A    T
                                GGAGGT GAGGT GCAGT
                                |||||| ||||| |||||
                                CCTCCA CTCCA TGTCG
                                   G    C
GAM487  FLJ22965  3' ACTGCAACCTCCGCCTCC    42047      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  FLJ22969  3' ACTGCAACCTCTGCCTCC    68643
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  FLJ22969  3' GCCACTGCAACCTATTACT   68652      _        A
                                GGTAG AGGTTGCAGT GC
                                ||||| |||||||||| ||
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                                TCATT TCCAACGTCA CG
                                   A         C
GAM487   FLJ23024  3'  ACTGCAACCTCTGCCTCC    46264
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487   FLJ23047  3'  GCTAAAATCCTCTCCCTCC   44623      T    TTGCAG
                                GGAGG AGAGG     TAGC
                                ||||| |||||     ||||
                                CCTCC TCTCC     ATCG
                                   C    TAAA__
GAM487   FLJ23392  3'  ACTGCAACCTCTGCCTCC    45525
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487   FLJ23519  3'  CACTGCCTTTCCTCC       49963      T   GTT    A
                                GGAGG AGAG   GCAGT G
                                ||||| ||||   ||||| |
                                CCTCC TTTC   CGTCA C
                                   _   ___    C
GAM487   FLJ23556  3'  ACTGCACCTCTGCCTCC     45940          T
                                GGAGGTAGAGGT GCAGT
                                |||||||||||| |||||
                                CCTCCGTCTCCA CGTCA
                                          _
GAM487   FLJ23563  3'  ACTGCAACCTCTGCCTCC    67584
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487   FLJ31101  3'  ACTGCAACCTCTGCCTCC    35704
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487   FLJ32865  3'  ACTGCAACCTCTGCCTCC    58164
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487   GAL3ST-4  3'  ACTGCAACCTCTGCCTCC    44931
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487   GMPPB     5'  GCTCACTGCAACCTCCACCTCC 95744       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
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                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  GNG4     3'  ACTGCGACCTCCACCTCC    15606       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCAGCGTCA
                                   C
GAM487  GR6      5'  ACTGAAACCTCTGCCTCC    23726            G
                                GGAGGTAGAGGTT CAGT
                                |||||||||||| ||||
                                CCTCCGTCTCCAA GTCA
                                      A
GAM487  GREB1    5'  GCTACACGGCCCTTCCTCC   72406      T  A    CA
                                GGAGG AG GGTTG  GTAGC
                                ||||| || |||||  |||||
                                CCTCC TC CCGGC  CATCG
                                   T  _    A_
GAM487  GREB1    3'  ACTGCAACCTCTGCCTCC    27861
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  GRWD     3'  ACTGCAACCTCCGCCTCC    48960       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  GTF2E1   3'  ACTGCAACCTCTGCCTCC    18608
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  GTPBG3   3'  GCTCACTGCAACCTCCATCTCC 50902       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCTA CTCCAACGTCA TCG
                                   C          C
GAM487  GTPBG3   3'  GCTTACTGCAACCTCCACCTCC 50906       A        _
                                GGAGGT GAGGTTGCAGTA GC
                                |||||| |||||||||||| ||
                                CCTCCA CTCCAACGTCAT CG
                                   C          T
GAM487  H-plk    5'  ACTGCAACCTCCACCTCC    31803       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCAACGTCA
                                   C
GAM487  HIF1AN   3'  CTACCTGTGATCCACCTC    61972      AGA  TG  _
                                GAGGT   GGT  CAG TAG
                                |||||   |||  ||| |||
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                                CTCCA  CTA  GTC ATC
                                  C__  GT   C
GAM487  HOMER-2B 3'  GCTACTGCCCCCTGCCCC   16721   A    A  TT
                                GG GGTAG GG  GCAGTAGC
                                || ||||| ||  ||||||||
                                CC CCGTC CC  CGTCATCG
                                 _    _ C_
GAM487  HRH4     3'  ACTGCAACCTCTGCCTCC    41245
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  HSNOV1   3'  ACTGTAACCTCTGCCTCC    34003
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAATGTCA

GAM487  HSPC023  3'  ATCCCACCCCCTACCTCC    25908       A  T  CA
                                GGAGGTAG GG TG  GT
                                |||||||| || ||  ||
                                CCTCCATC CC AC  TA
                                     C  C  CC
GAM487  HSPC063  3'  CTACTGCAATAACCTTC     26271       AGAG
                                GGAGGT   GTTGCAGTAG
                                ||||||   ||||||||||
                                CTTCCA   TAACGTCATC
                                   A___
GAM487  HSPC065  3'  GCTCACTGCAACCTCCACCTCT 26308       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                TCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  HSPC065  3'  GCTGCAACCTCCTCCTCC    26312      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCG
                                  TC
GAM487  HU-K4    3'  GCTCTCCCACCTCTACCTCC  24369          TGC  T
                                GGAGGTAGAGGT   AG AGC
                                ||||||||||||  || |||
                                CCTCCATCTCCA   TC TCG
                                      CCC  _
GAM487  HZFW1    3'  CTACTACAGTACTTCC      47460       GAGG   C
                                GGAGGTA    TTG AGTAG
                                |||||||    ||| |||||
                                CCTTTCAT    GAC TCATC
                                    ____  A
GAM487  HZFW1    3'  GCTAGTTCCCCAACCTCC    47462       AGA  TT  AG
                                GGAGGT   GG  GC  TAGC
                                ||||||   ||  ||  ||||
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                                CCTCCA  CC  TG ATCG
                                   AC_  CT  __
GAM487  JAM1     3' ACTGTAACCTCCGCCTCC   57886     TA
                                GGAGG GAGGTTGCAGT
                                ||||| ||||||||||
                                CCTCC CTCCAATGTCA
                                   GC
GAM487  JAM1     3' ACTGTAACCTCCGCCTCC   33748     TA
                                GGAGG GAGGTTGCAGT
                                ||||| ||||||||||
                                CCTCC CTCCAATGTCA
                                   GC
GAM487  JAM1     5' ACTGCAACCTCCTCCTCC   57911     TA
                                GGAGG GAGGTTGCAGT
                                ||||| ||||||||||
                                CCTCC CTCCAACGTCA
                                   TC
GAM487  JAM1     3' ACTGTAACCTCCGCCTCC   57913     TA
                                GGAGG GAGGTTGCAGT
                                ||||| ||||||||||
                                CCTCC CTCCAATGTCA
                                   GC
GAM487  JAM1     3' ACTGTAACCTCCGCCTCC   57940     TA
                                GGAGG GAGGTTGCAGT
                                ||||| ||||||||||
                                CCTCC CTCCAATGTCA
                                   GC
GAM487  JM11     3' ACTGCAACCTCTGCCTCC   53250
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  K6HF     3' GCCAGCCTCTCCCTCC     16272     T     _
                                GGAGG AGAGGTTG C
                                ||||| |||||||| |
                                CCTCC TCTCCGAC G
                                   C      C
GAM487  KCNT1    3' GCCCGGCGACCTCCACCCTC  61834   GA  A     AGTA
                                G  GGT GAGGTTGC   GC
                                |  ||| ||||||||   ||
                                C  CCA CTCCAGCG   CG
                                 TC  C      GCC_
GAM487  KIAA0063 3' GCTCACTGCAACCTCCACCTCC 29632       A       _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C        C
GAM487  KIAA0182 3' GCTACTGCTTACCTCCTCC   72034     TAG   T_
                                GGAGG  AGGT  GCAGTAGC
                                |||||  ||||  ||||||||
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                                CCTCC   TCCA  CGTCATCG
                                   ___    TT
GAM487  KIAA0295  3'  CTACCTGACCCTACCTCT    68102        A    GCA
                                GGAGGTAG GGTT   GTAG
                                |||||||| ||||   ||||
                                TCTCCATC CCAG   CATC
                                   _    TC_
GAM487  KIAA0391  3'  ACTGCAACCTCTGCCTCC    27901
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  KIAA0397  3'  GCCACCAACCGACCCCACCTCT 61675       AGA    CA__  A
                                GGAGGT   GGTTG    GT GC
                                ||||||   |||||    || ||
                                TCTCCA   CCAGC    CA CG
                                   CC_    CAAC  C
GAM487  KIAA0426  3'  ACTGCAACCTCCGCCTCC    28253       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||||
                                CCTCC  CTCCAACGTCA
                                  GC
GAM487  KIAA0459  3'  GCTCACTGCAACCTCCACCTCC 61000        A         _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  KIAA0469  3'  ACTGCAGCCTCCACCTCC    29319       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487  KIAA0513  5'  ACTGCAGCCTCCACCTCC    28335       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487  KIAA0513  3'  ACTGCAACCTCCACCTCC    28331       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCAACGTCA
                                   C
GAM487  KIAA0514  3'  GCCACTCTGTGCTACCTCC    28085        ___  _  T
                                GGAGGTAG   AG GT GC
                                ||||||||   || || ||
                                CCTCCATC   TC CA CG
                                     GTG  T  C
GAM487  KIAA0527  3'  ACTGCAACCTCTGCCTCC    95790
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
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                                CCTCCGTCTCCAACGTCA

GAM487  KIAA0534  3'  GCCACTGGTTGTTTCTACTTCC 71430        GG TG_   A
                                GGAGGTAGA  T   CAGT GC
                                |||||||||  |   |||| ||
                                CCTTCATCT  G   GTCA CG
                                     TT TTG    C
GAM487  KIAA0544  3'  ACTGCAACCTCCGCCTCC    70885      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  KIAA0561  3'  ACTGCAACCTCCGCCTCC    65871      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  KIAA0563  5'  ACTGCAACCTCTGCCTCC    29181
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  KIAA0594  3'  ACTGCAACCTCCGCCTCC    64892      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  KIAA0599  3'  ACTGCAACCTCCGCCTCC    77165      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  KIAA0599  3'  ACTGCAACCTCCGCCTCC    77164      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  KIAA0720  3'  ACTGCAACCTCTGCCTCC    62316
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  KIAA0737  3'  ACTGAAACCTCTGCCTCC    29131          G
                                GGAGGTAGAGGTT CAGT
                                |||||||||||| ||||
                                CCTCCGTCTCCAA GTCA
                                      A
GAM487  KIAA0757  3'  CTATCTATACACCTACCTCC  20130        AG  TGCA
                                GGAGGTAG  GT    GTAG
                                ||||||||  ||    ||||
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                                CCTCCATC CA   TATC
                                    CA  TATC
GAM487  KIAA0841 3' ACTGCAACCTCCGCCTCC   71368     TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  KIAA0841 3' ACTGCAACCTCTGCCTCC   71369
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  KIAA0876 3' GCTACTGCAATGCCCTAC   64680     A  __
                                GTAG GGT  TGCAGTAGC
                                |||| |||  |||||||||
                                CATC CCG  ACGTCATCG
                                  _  TA
GAM487  KIAA0889 3' ACTGTAACCTCCGCCTCC   31127     TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAATGTCA
                                   GC
GAM487  KIAA0924 3' ACTGCAACCCCCGCCCC    29713    A   AGA
                                GG GGT   GGTTGCAGT
                                || |||   |||||||||
                                CC CCG   CCAACGTCA
                                 _  CCC
GAM487  KIAA1041 3' ACTGCAACCTCCGCCTCC   30123     TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  KIAA1054 3' ACTGCAACCTCCGCCTCC   68426     TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  KIAA1130 3' GCCACAGCCTCTCCCTCC   62423     T      CA
                                GGAGG AGAGGTTG  GT
                                ||||| |||||||  ||
                                CCTCC TCTCCGAC  CG
                                   C       AC
GAM487  KIAA1161 5' ACTGCAACCCCTCCTCC    81730     T  A
                                GGAGG AG GGTTGCAGT
                                ||||| || |||||||||
                                CCTCC TC CCAACGTCA
                                   _  C
GAM487  KIAA1170 3' ACTGCAACCTCCGCCTCC   69842     TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
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                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  KIAA1193  3'  ACTGCAACCTCCGCCTCC    67626      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  KIAA1198  3'  ACCGCAACCTCCGCCTCC    63282      TA       A
                                GGAGG  GAGGTTGC GT
                                |||||  ||||||| ||
                                CCTCC  CTCCAACG CA
                                   GC       C
GAM487  KIAA1209  3'  ACTGCAGCCTCCACCTCC    60747       A
                                GGAGGT GAGGTTGCAGT
                                ||||||  ||||||||||
                                CCTCCA CTCCGACGTCA
                                    C
GAM487  KIAA1223  3'  ACTGACCTCTTCCTCC      71141      T     TG
                                GGAGG AGAGGT  CAGT
                                |||||  ||||||  ||||
                                CCTCC TCTCCA  GTCA
                                   T     __
GAM487  KIAA1257  3'  ACCGCAACCTCCGCCTCC    62722      TA       A
                                GGAGG  GAGGTTGC GT
                                |||||  ||||||| ||
                                CCTCC  CTCCAACG CA
                                   GC       C
GAM487  KIAA1257  3'  ACTACAGCCTCTGCCCC     62724    A         C
                                GG GGTAGAGGTTG AGT
                                ||  ||||||||||  |||
                                CC CCGTCTCCGAC TCA
                                  _         A
GAM487  KIAA1320  5'  ACTGCAACCTCTGCCTCC    69293
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  KIAA1373  3'  GCTCACTGCAACCTCCACCTCC 70944        A         _
                                GGAGGT GAGGTTGCAGT AGC
                                ||||||  ||||||||||  |||
                                CCTCCA CTCCAACGTCA TCG
                                    C          C
GAM487  KIAA1497  5'  ACTGCAACCTCTGCCTCC    67502
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  KIAA1500  3'  ACGGGAGCCTCTGCCTCC    64114            GCA
                                GGAGGTAGAGGTT   GT
                                ||||||||||||   ||
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                                CCTCCGTCTCCGA  CA
                                      GGG
GAM487  KIAA1508 3' ACTGCAACCTCCGCCTCC   61873     TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                  GC
GAM487  KIAA1514 3' ACTGACCCCTGCCTCC     38816       A  TG
                                GGAGGTAG GGT  CAGT
                                ||||||||  |||  ||||
                                CCTCCGTC CCA  GTCA
                                   C  __
GAM487  KIAA1571 3' GCTCACCGCAACCTCCACCTCC 60957      A      A _
                                GGAGGT GAGGTTGC GT AGC
                                ||||||  |||||||  ||  |||
                                CCTCCA CTCCAACG CA TCG
                                  C      C  C
GAM487  KIAA1615 3' CTCAACCTCTGCCTCC     68707          C
                                GGAGGTAGAGGTTG AG
                                ||||||||||||||  ||
                                CCTCCGTCTCCAAC TC
                                                _
GAM487  KIAA1615 3' ACTGCAACCTCCACCTCC   68696      A
                                GGAGGT GAGGTTGCAGT
                                ||||||  ||||||||||
                                CCTCCA CTCCAACGTCA
                                  C
GAM487  KIAA1655 3' ACTGTAACCTCCACCTCC   66586      A
                                GGAGGT GAGGTTGCAGT
                                ||||||  ||||||||||
                                CCTCCA CTCCAATGTCA
                                  C
GAM487  KIAA1737 3' ACTGCAACCTCCGCCTCC   67347      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                  GC
GAM487  KIAA1755 5' GCCAGGGTGACTTCTACCTCC  61349          TG AGTA
                                GGAGGTAGAGGT  C   GC
                                ||||||||||||  |   ||
                                CCTCCATCTTCA  G   CG
                                      GT GGAC
GAM487  KIAA1784 3' ACTGCAACCTCCGCCTCC   65142      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                  GC
GAM487  KIAA1798 5' GCCCCGACCTCTCCCC     60620    A  T      CA
                                GG GG AGAGGTTG  GT
                                ||  ||  ||||||||  ||
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                                CC CC TCTCCAGC  CG
                                 _ _      CC
GAM487  KIAA1922 5' ACTGCAACCTCCGCCTCC    73613      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  KIAA1956 3' ACTGCAGCCTCCACCTCC    78427       A
                                GGAGGT GAGGTTGCAGT
                                ||||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487  KIAA1971 3' GCTTACTGCAACCTCCACCTCC 74224       A         _
                                GGAGGT GAGGTTGCAGTA GC
                                ||||||| |||||||||||| ||
                                CCTCCA CTCCAACGTCAT CG
                                   C         T
GAM487  KLK7     3' ACTGCAACCTCCGCCTCC    57723      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  KLK7     3' ACTGCAACCTCCGCCTCC    17283      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  KRT6     3' GCTACAAGCCCCTCTGCCCC  82221    A      TT  A_
                                GG GGTAGAGG  GC  GTAGC
                                || ||||||||  ||  |||||
                                CC CCGTCTCC  CG  CATCG
                                 _      C_  AA
GAM487  LBP-9    3' GCTGGTACCTTTACCTCC    27279          TG
                                GGAGGTAGAGGT  CAGT
                                ||||||||||||  ||||
                                CCTCCATTTCCA  GTCG
                                      TG
GAM487  LIMK2    3' GCCATCTGACTTCTACCTCC   18726          TG   TA_
                                GGAGGTAGAGGT  CAG   GC
                                ||||||||||||  |||   ||
                                CCTCCATCTTCA  GTC   CG
                                      __   TAC
GAM487  LIMK2    3' GCCATCTGACTTCTACCTCC   33624          TG   TA_
                                GGAGGTAGAGGT  CAG   GC
                                ||||||||||||  |||   ||
                                CCTCCATCTTCA  GTC   CG
                                      __   TAC
GAM487  LNIR     3' GCTTGACCTTTACCTCC     48133          C
                                GGAGGTAGAGGTTG AGT
                                |||||||||||||| |||
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                                CCTCCATTTCCAGT TCG
                                          _
GAM487  LYPLA3   3'  ACTCCACTCCTACCTCC     24628        AG  T C
                                GGAGGTAG  GT G AGT
                                ||||||||  || | |||
                                CCTCCATC  CA C TCA
                                     CT  _ C
GAM487  MAPK8IP3 3'  GCCACCTGGGCCCACCTCC   52984       AGA   G   TA_
                                GGAGGT   GGTT CAG   GC
                                ||||||   |||| |||   ||
                                CCTCCA   CCGG GTC   CG
                                   C__    _   CAC
GAM487  MCLC     3'  GCTCACTGCAACCTCCACCTCC 30687       A         _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  MEF-2    3'  ACTGCAACCTCCGCCTCC    64376      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                  GC
GAM487  MEIS3    3'  GCTCAACGCCTACCTCC     78282        AG   C
                                GGAGGTAG  GTTG AGT
                                ||||||||  |||| |||
                                CCTCCATC  CAAC TCG
                                     CG   _
GAM487  MGC13138 3'  ACTGCAACCTCTGCCTCC    53013
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  MGC13138 3'  CTACAGGCACCCACCACCTCC  53017       AGA  T   A_
                                GGAGGT   GG TGC  GTAG
                                ||||||   || |||  ||||
                                CCTCCA   CC ACG  CATC
                                   CCA  C   GA
GAM487  MGC14836 3'  ACTGCAACCTCCGCCTCC    53034      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                  GC
GAM487  MGC15437 3'  GCTACAGCCCTATCCCC     51782    A    A    C
                                GG GGTAG GGTTG AGT
                                || ||||| ||||| |||
                                CC CTATC CCGAC TCG
                                 C    _    A
GAM487  MGC2474  3'  ACTGCAACTTCCACCTCC    43710       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
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                                CCTCCA CTTCAACGTCA
                                   C
GAM487  MGC26877 5' GCCACTGCAACCCAGCCT    58242     AGA       A
                                AGGT   GGTTGCAGT GC
                                ||||   ||||||||| ||
                                TCCG   CCAACGTCA CG
                                  AC_       C
GAM487  MGC29891 3' ACTGCAACCTCCGCCTCC    58196     TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  MGC3113  3' ACTGCAGCCTCCACCTCC    43838      A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487  MGC3329  3' ACTGCAACCCCCGCCTCC    44011      AGA
                                GGAGGT   GGTTGCAGT
                                ||||||   |||||||||
                                CCTCCG   CCAACGTCA
                                   CCC
GAM487  MGC5149  3' ACTGCAACCTCTGCCTCC    72283
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  MGC9912  3' GCTCACTGCAACCTCCACCTCC 54720       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  MLZE     5' ACTGCAACCTCTGCCTCC    48613
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  MMPL1    3' ACTGCAGCCTCCACCTCC     14715       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487  MOCS3    3' ACTGCAACCTCCGCCTCC     27147      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  MRPL10   3' GCTATTGTCCCCTGCCTCC    59153        A  TT
                                GGAGGTAG GG  GCAGTAGC
                                |||||||| ||  ||||||||
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                                CCTCCGTC CC  TGTTATCG
                                     _ C_
GAM487  MRPL44   3'  GCTCACTGCAACCTCCACCTC  43321      A        _
                                GAGGT GAGGTTGCAGT AGC
                                ||||| |||||||||||| |||
                                CTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  MtFMT    3'  ACTGCAACCTCCGCCTCC    57647      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  MUC16    5'  GCCACCACATTCCTGCCTCC   60529        A GT  CA  A
                                GGAGGTAG G  TG  GT GC
                                |||||||| |  ||  || ||
                                CCTCCGTC C  AC  CA CG
                                     _ TT  AC  C
GAM487  NDP52    3'  ACTACAGCCTCTGCCTCC    19525           C
                                GGAGGTAGAGGTTG AGT
                                |||||||||||||| |||
                                CCTCCGTCTCCGAC TCA
                                        A
GAM487  NDUFB1   5'  ACTGCAACCTCTGCCTCC    15813
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  NDUFC2   3'  GCTCACTGCAACCTCCACCTCC 15837       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  Nup43    3'  GCTCACTGCAACCTCCACCTC 45004       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  OR51E2   3'  ACTGCAACCTCCACATCC    47788     G  A
                                GGA GT GAGGTTGCAGT
                                ||| || ||||||||||
                                CCT CA CTCCAACGTCA
                                  A  C
GAM487  OSBPL2   3'  ACCGCAACCTCCGCCTCC    57848      TA      A
                                GGAGG  GAGGTTGC GT
                                |||||  |||||||| ||
                                CCTCC  CTCCAACG CA
                                   GC       C
GAM487  OSBPL2   3'  ACCGCAACCTCCGCCTCC    29197      TA      A
                                GGAGG  GAGGTTGC GT
                                |||||  |||||||| ||
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                                CCTCC  CTCCAACG CA
                                   GC       C
GAM487  PASK     5'  ACTGCAACCTCTGCCTCC    30709
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  PELI1    5'  ACTGCAACCTCCTCCTCC    40247      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   TC
GAM487  PELI1    5'  ACTGCAACCTCTGCCTCC    40250
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  PIP3-E   3'  ACTGCAACCTCTGCCTCC    66795
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  PITPNM   5'  GCTAGGCTCGCCTCTGCCTCC  16933          T_  AG
                                GGAGGTAGAGGT  GC  TAGC
                                ||||||||||||  ||  ||||
                                CCTCCGTCTCCG  CG  ATCG
                                      CT  G_
GAM487  PNAS-131 5'  GCCAAGCCCGCTACCTCC    48749        A_   __
                                GGAGGTAG  GGTT  GC
                                ||||||||  ||||  ||
                                CCTCCATC  CCGA  CG
                                     GC    AC
GAM487  PRO0365  5'  GCTCACTGCAACCTCCACCTCC 26164       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                ||||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  PRO1992  5'  ACTGCAACCTCTGCCTCC    26050
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  PRO2955  3'  ACTGCAACCTCTGCCTCC    37629
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  PSTPIP2  3'  ACTGCAACCTCTGCCTCC    44380
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
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                                CCTCCGTCTCCAACGTCA

GAM487  RAB33B   3'  ACTGCAACCTCCGCCTCC    48485      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  RAB40C   3'  GCTCACCTCTACCTCC      40981          T_
                                GGAGGTAGAGGT  GC
                                ||||||||||  ||
                                CCTCCATCTCCA  CG
                                      CT
GAM487  RAI      5'  ACTGCAACCTCCGCCTCC    21870      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  RASGRP4  3'  GCTGAACAACCTCTACCTGC  53657   G        CAG
                                G AGGTAGAGGTTG   TAGC
                                | ||||||||||   ||||
                                C TCCATCTCCAAC   GTCG
                                 G          AA_
GAM487  RNF8     3'  GCTCACTGCAACCTCCACCTCC 14232       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                    C          C
GAM487  SC4MOL   3'  ACTGCAACCTCTGCCTCC    22149
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  SCAMP-4  3'  ACTGCAACCTCTGCCTCC    54388
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  SCRG1    5'  GCTACCAGAGTCTGCCTCC   23463        GG   CA
                                GGAGGTAGA  TTG  GTAGC
                                |||||||||  |||  |||||
                                CCTCCGTCT  GAC  CATCG
                                      GA   __
GAM487  SCYA16   3'  ACTGTAACCTCCACCTCC    15953       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCAATGTCA
                                    C
GAM487  SCYB11   3'  CTACCACAACCTTTCT      87443    T      CA
                                GG AGAGGTTG  GTAG
                                || ||||||||  ||||
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                                TC TTTCCAAC  CATC
                                 _      AC
GAM487  SDC3     3'  GCTTCACCCCTACCTGC     27756   G     A  T  C
                                G AGGTAG GG TG AGT
                                | |||||| || || |||
                                C TCCATC CC AC TCG
                                 G     _ C  T
GAM487  SERF1B   3'  ACTGCAACCTCCGCCTCC    43407       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  SIRPB1   3'  ACTGCAACCCCCCGCCTCC    20239       AGA
                                GGAGGT   GGTTGCAGT
                                ||||||   |||||||||
                                CCTCCG   CCAACGTCA
                                    CCC
GAM487  SLC2A10  3'  ACTGCAACCTCCACTTCC     47815       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTTCA CTCCAACGTCA
                                    C
GAM487  SP2      3'  GCCACAACCTCTCCTCC      11892       T       CA
                                GGAGG AGAGGTTG  GT
                                ||||| ||||||||  ||
                                CCTCC TCTCCAAC  CG
                                   _       AC
GAM487  SSB-4    3'  CTGCTGCTGCCACCTCT      55100       AGA   T
                                GGAGGT   GGT GCAGTAG
                                ||||||   ||| |||||||
                                TCTCCA   CCG CGTCGTC
                                    ___   T
GAM487  STAF65(gamma) 3'  ACTGCAACCTCTGCCTCC    29423
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  SUN1     3'  ACTGCAGCCTCCACCTCC     47153       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                    C
GAM487  SYT13    3'  ACTGCAACCTCCGCCTCC     93447       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  TEKT3    5'  GCTGCGACCCCTTCCTCC     49106       T  A
                                GGAGG AG GGTTGCAGT
                                ||||| || |||||||||
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                                CCTCC TC CCAGCGTCG
                                   T  C
GAM487  TRIM5    3'  ACTGCAACCTCCACCTCT    52291       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                TCTCCA CTCCAACGTCA
                                   C
GAM487  TRIM6    3'  ACTGCAACCTCTGCCTCC    54129
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  TSPAN-2  3'  CTACTGCAACCCTCACATCC  19164    G  _  A
                                GGA GT AG GGTTGCAGTAG
                                ||| || || ||||||||||
                                CCT CA TC CCAACGTCATC
                                  A  C  _
GAM487  TU12B1-TY 3'  ACTGCAACCTCTGCCTCC    33367
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  TUBB5    3'  CTTTGACCTCTGCCCC     20301    A        C
                                GG GGTAGAGGTTG AG
                                || ||||||||||| ||
                                CC CCGTCTCCAGT TC
                                  _         T
GAM487  TUCAN    3'  ACTGCAACCTCTGCCTCC    30267
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  TUSP     3'  CACTGCCCACCTCC       39626       AGA  TT    A
                                GGAGGT   GG  GCAGT G
                                ||||||   ||  ||||| |
                                CCTCCA   CC  CGTCA C
                                   ___  __    C
GAM487  UBF-fl   3'  ACTGCAACCTCTGCCTCC    51547
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  USP22    3'  GCTCACTGCAACCTCCACCTCC 68016       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  VCX-8r   3'  CTACTCCCCTATCTCC     33055        A  TTGC
                                GGAGGTAG GG    AGTAG
                                |||||||| ||    |||||
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                                CCTCTATC CC    TCATC
                                    C ____
GAM487  VDU1     3'  ACTGCAGCCTCCACCTCC    30408       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487  VPS33A   3'  ACTGCAACCTCCACCTCC    43331       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCAACGTCA
                                   C
GAM487  WBSCR20A 5'  ACCGCAACCTCTGCCTCC    49646             A
                                GGAGGTAGAGGTTGC GT
                                |||||||||||||| ||
                                CCTCCGTCTCCAACG CA
                                        C
GAM487  ZTL1     3'  ACTGCAACCTCTGCCTCC    43909
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  LOC112724 5' GCTCACTGCAACCTCCACCTCC 56500       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  LOC113675 5' ACTGCAACCTCCGCCTCC    56568       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                  GC
GAM487  LOC115219 5' ACTGCAACCTCCGCCTCC    73293       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                  GC
GAM487  LOC120114 3' GCTCACTGCAATCTCCACCTCC 75533       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCTAACGTCA TCG
                                   C         C
GAM487  LOC120939 3' ACTGTAACCTCCACCTCC    76244       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCAATGTCA
                                   C
GAM487  LOC122886 3' CTACCAGTGCTTACCTCC    75583        GA   TGCA
                                GGAGGTA  GGT   GTAG
                                |||||||  |||   ||||
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                                CCTCCAT  TCG    CATC
                                   __   TGAC
GAM487   LOC126364 3'  ACTGCAACCTCCGCCTCC    75680      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487   LOC126661 3'  ACTGCAACCTCCGCCTCC    74542      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487   LOC126661 3'  GCTACCATGCCTAGCCCC    74553    A  AG   TGCA
                                GG GGT  AGGT   GTAGC
                                || |||  ||||   |||||
                                CC CCG  TCCG   CATCG
                                 _  A_   TAC_
GAM487   LOC128077 3'  ACTGCAACCTCCGCCTCC    74701      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487   LOC128077 3'  ACTGCAACCTCTGCCTCC    74704
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487   LOC128387 3'  ACTGCAACCTCCACTTCC    74746      A
                                GGAGGT GAGGTTGCAGT
                                ||||||  ||||||||||
                                CCTTCA CTCCAACGTCA
                                   C
GAM487   LOC128989 3'  ACTGCAACCTCCGCCTCC    74803      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487   LOC130813 3'  ACCGCAACCTCCGCCTCC    75760      TA      A
                                GGAGG  GAGGTTGC GT
                                |||||  ||||||| ||
                                CCTCC  CTCCAACG CA
                                   GC       C
GAM487   LOC132625 3'  GCTCACTGCAACCTCCACCTCC 75910       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487   LOC133686 3'  GCTCTGCAACCTCCATCTCC   75123       A        T
                                GGAGGT GAGGTTGCAG AGC
                                |||||| ||||||||| |||
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                                CCTCTA CTCCAACGTC TCG
                                   C       _
GAM487  LOC135293 3'  ACTGCAACCTCTGCCTCC    76173
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  LOC135763 3'  ACTGCAACCTCCGCCTCC    56784      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC139673 3'  GCCGAATAGACCTCTACATCC  75976    G       GCAGTA
                                GGA GTAGAGGTT     GC
                                |||  |||||||||     ||
                                CCT CATCTCCAG     CG
                                  A       ATAAGC
GAM487  LOC142913 5'  ACTGCAGCCTCCACCTCC    76412      A
                                GGAGGT GAGGTTGCAGT
                                ||||||  ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487  LOC143187 3'  GCTCACTGCAACCTCCACCTCC 59099       A       _
                                GGAGGT GAGGTTGCAGT AGC
                                ||||||  |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  LOC143241 5'  ACTGCAACCTCTGCCTCC    57172
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  LOC143458 3'  ACTGCAACGTCACCT       76571      A  G
                                AGGT GA GTTGCAGT
                                ||||  ||  ||||||||
                                TCCA CT CAACGTCA
                                  _  G
GAM487  LOC144017 5'  GCCACCGCAGCTGCCTCC    83004      AGA     A  A
                                GGAGGT   GGTTGC GT GC
                                ||||||   ||||||  ||  ||
                                CCTCCG   TCGACG CA CG
                                   ___      C  C
GAM487  LOC144248 5'  GCTCACTGCAACCTCCACCTCC 76740       A       _
                                GGAGGT GAGGTTGCAGT AGC
                                ||||||  |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  LOC144317 5'  ACTGCAACCTCTTCCTCC    76783      T
                                GGAGG AGAGGTTGCAGT
                                |||||  ||||||||||||
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                                CCTCC TCTCCAACGTCA
                                   T
GAM487   LOC144524 5'  GCTCACTGCAACCTCCACCTCC 83132       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487   LOC144594 3'  ACTGTGAAATACCTCTACCTCC 76898           ____
                                GGAGGTAGAGGT    TGCAGT
                                ||||||||||||    ||||||
                                CCTCCATCTCCA    GTGTCA
                                      TAAA
GAM487   LOC145725 3'  ACTGCAGCCTCCACCTCC     77398       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487   LOC145732 3'  ACTGCAGCCTCCACCTCC     77420       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487   LOC145757 5'  GCTCACTACAACCTCTGCCTCC 77465           C  _
                                GGAGGTAGAGGTTG AGT AGC
                                |||||||||||||| ||| |||
                                CCTCCGTCTCCAAC TCA TCG
                                      A  C
GAM487   LOC146229 3'  GCTCACTGCAACCTCCACCTCC 77755       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487   LOC146229 3'  GCTCCCTGCAACCTCCACCTCC 77757       A        T_
                                GGAGGT GAGGTTGCAG  AGC
                                |||||| ||||||||||  |||
                                CCTCCA CTCCAACGTC  TCG
                                   C          CC
GAM487   LOC146784 5'  GCTCACTGCAACCTCCACCTCC 78120       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487   LOC146909 3'  ACTGCAACCTCCGCCTCC     78164       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487   LOC146952 5'  GCTCACTGCAACCTCCACCTCT 83870       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
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                                TCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  LOC147071 5'  ACTGCAACCTCTGCCTCC    72992
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  LOC147407 3'  ACTGCAACCTCCGCCTCC    76321      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC147817 3'  GCTCACTGCAACCTCCACCTCC 78501       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  LOC148189 5'  GCTCACTGCAACCTCCACCTCC 78713       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  LOC148198 3'  GCTCACTGCAACCTCCATCTCC 70685       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCTA CTCCAACGTCA TCG
                                   C         C
GAM487  LOC148479 5'  GCCACTCTCCCGCCTCTACCGC 78870    A       TGC__   A
          C                      GG GGTAGAGGT     AGT GC
                                || |||||||||     ||| ||
                                CC CCATCTCCG     TCA CG
                                 G        CCCTC   C
GAM487  LOC148760 3'  CTACTGCAGGATGACCTC    84204      AGAGG
                                GAGGT     TTGCAGTAG
                                |||||     |||||||||
                                CTCCA     GACGTCATC
                                   GTAG_
GAM487  LOC148918 5'  ACTGCAGCCTCCACCTCC    79058       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487  LOC149506 3'  ACTGCAACTTCCACCTCC    84449       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTTCAACGTCA
                                   C
GAM487  LOC149506 3'  ACTGCAACCTCTGCCTCC    84445
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
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                                CCTCCGTCTCCAACGTCA

GAM487   LOC149692 3'  ACTGTAACCTCTGCCTCC    84580
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAATGTCA

GAM487   LOC150407 3'  GCCATGGACCCCACCTCC    79825       AGA   G  GTA
                                GGAGGT   GGTT CA   GC
                                ||||||   |||| ||   ||
                                CCTCCA   CCAG GT   CG
                                   CC_    _  AC_
GAM487   LOC150696 3'  ACTGCAGCCTCCACCTCC    58476       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487   LOC150933 5'  CTACCCCTCTACCTGC      85159    G       TTGCA
                                G AGGTAGAGG    GTAG
                                | |||||||||    ||||
                                C TCCATCTCC    CATC
                                 G       C____
GAM487   LOC150960 3'  GCTGCAACCTCCGCCTCC    80067      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCG
                                   GC
GAM487   LOC151057 3'  ACTGCAACCTCTGCCTCC    85204
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487   LOC151201 3'  GCTCACTGCAACCTCCACCTCC 85285       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487   LOC151475 5'  ACTGCAACCTCTGCCTCC    85386
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487   LOC151475 5'  GCTCACTGCAACCTCCACCTCC 85410       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487   LOC151826 3'  ACTGCAACCTCCGCCTCC    80352      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
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                                CCTCC  CTCCAACGTCA
                                   GC
GAM487   LOC152445 3'  ACTGCAACCTCTGCCTCC    85740
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487   LOC152582 5'  ACCGCAACCTCTGCCTCC    85787            A
                                GGAGGTAGAGGTTGC GT
                                |||||||||||||| ||
                                CCTCCGTCTCCAACG CA
                                      C
GAM487   LOC152620 3'  GCTCACTACAACCTCTGCCTCC 60083           C  _
                                GGAGGTAGAGGTTG AGT AGC
                                |||||||||||||| ||| |||
                                CCTCCGTCTCCAAC TCA TCG
                                      A  C
GAM487   LOC152687 5'  GCCACAGCCTCTGCCTCC    80639           CA
                                GGAGGTAGAGGTTG  GT
                                ||||||||||||||  ||
                                CCTCCGTCTCCGAC  CG
                                      AC
GAM487   LOC152719 5'  ACTGCAACCTCTGCCTCC    85845
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487   LOC152794 5'  ACTGCAACCTCTACCTCC    80671
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCATCTCCAACGTCA

GAM487   LOC152925 3'  ACTCCAACCTCTGCCTCC    80734           C
                                GGAGGTAGAGGTTG AGT
                                |||||||||||||| |||
                                CCTCCGTCTCCAAC TCA
                                      C
GAM487   LOC153077 3'  ACTGCAACCTCCGCCTCC    85903      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487   LOC153516 3'  GCTACTCTGTAGCCACCCC   56709    A  AGA     __
                                GG GGT   GGTTGCA  GTAGC
                                || |||   |||||||  |||||
                                CC CCA   CCGATGT  CATCG
                                 _  ____     CT
GAM487   LOC153688 3'  GCTCACTGCAACCTCCACCTCC 86114       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
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                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  LOC154075 3'  ACTGCAACCTCCGCCTCC    81042       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC154282 5'  GCTCACTGCAACCTCCACCTCC 86203        A        _
                                GGAGGT GAGGTTGCAGT AGC
                                ||||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  LOC154790 5'  GCCACCCTTTTACCTCC     81151          __  T
                                GGAGGTAGA  GGT GC
                                |||||||||  ||| ||
                                CCTCCATTT  CCA CG
                                      TC   C
GAM487  LOC154877 3'  GCTCACTGCAACCTCTACCTCC 86300                _
                                GGAGGTAGAGGTTGCAGT AGC
                                |||||||||||||||||| |||
                                CCTCCATCTCCAACGTCA TCG
                                            C
GAM487  LOC157247 5'  GCTCACTGCAACCTCCACCCC  81371    A   A        _
                                GG GGT GAGGTTGCAGT AGC
                                || ||| |||||||||| |||
                                CC CCA CTCCAACGTCA TCG
                                 _  C          C
GAM487  LOC157798 5'  ACTGCAACCTCCGCCTCC    86545       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC157858 5'  ACTGCAACCTCTGCCTCC    86580
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  LOC158263 5'  GCCACCTCCGTTTACCTCC    81848         ____     T
                                GGAGGTA    GAGGT GC
                                |||||||    ||||| ||
                                CCTCCAT    CTCCA CG
                                     TTGC     C
GAM487  LOC158402 5'  ACTGTAACCTCTGCCTCC    86799
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAATGTCA

GAM487  LOC158476 3'  ACTGCAACCTCCGCCCC     86835    A  TA
                                GG GG  GAGGTTGCAGT
                                || ||  ||||||||||
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                                CC CC  CTCCAACGTCA
                                 _ GC
GAM487  LOC158549 5' ACTGTGACCTCCGCCTCC    86864     TA    TG
                                GGAGG  GAGGT  CAGT
                                |||||  |||||  ||||
                                CCTCC  CTCCA  GTCA
                                   GC    GT
GAM487  LOC158668 3' ACTGCAACCTCTGCCTCC    69362
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  LOC158865 5' ACTGCAACCTCTGCCTCC    86929
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  LOC159121 5' CTCCTTCATCCCCTACCTCC   86995       A  T  C  T
                                GGAGGTAG GG TG AG AG
                                ||||||||  || || || ||
                                CCTCCATC CC AC TC TC
                                     C  T  T  C
GAM487  LOC161829 3' ACTGCAACCTCCGCCTCC    82310     TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC162952 5' ACTCAGGTCTACCTC       82377       GG   C
                                GAGGTAGA  TTG AGT
                                ||||||||  ||| |||
                                CTCCATCT  GAC TCA
                                     G_  _
GAM487  LOC196047 5' ACTGCAACCTCCGCCTCC    89589     TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC196264 3' ACTGCAACCTCTGCCTCC    87600
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  LOC196411 3' ACTGCAACCTCCGCCTCC    87664     TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC196463 3' GCCACCGGACTTCTAACTCC  87713      G      GCA  A
                                GGAG TAGAGGTT   GT GC
                                ||||  ||||||||   || ||
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                                CCTC ATCTTCAG   CA CG
                                  A       GC_  C
GAM487   LOC196529 3'  GCTCACTGCAACCTCCACCTC  87776       A          _
                                GAGGT GAGGTTGCAGT AGC
                                ||||| |||||||||||| |||
                                CTCCA CTCCAACGTCA TCG
                                   C          C
GAM487   LOC196957 3'  ACTGCAGCCTCCACCTCC     87815       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487   LOC196961 3'  ACTGCAGCCTCCACCTCC     87836       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487   LOC197083 3'  GCCCCCACCTGCTACCTCC    87881         _    T___
                                GGAGGTAG AGGT    GC
                                |||||||| ||||    ||
                                CCTCCATC TCCA    CG
                                     G    CCCC
GAM487   LOC197138 3'  ACTGCAGCCTCCACCTCC     87909       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCGACGTCA
                                   C
GAM487   LOC197342 3'  CACTGCCTACCTCC         87991         AGGTT     A
                                GGAGGTAG     GCAGT G
                                ||||||||     ||||| |
                                CCTCCATC     CGTCA C
                                     _____     C
GAM487   LOC199786 3'  ACTGCAACCTCCGCCTCC     88364       TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487   LOC200014 3'  GCTCGCTGCAACCCCCACCTCC 88533        AGA        _
                                GGAGGT   GGTTGCAGT AGC
                                ||||||   ||||||||| |||
                                CCTCCA   CCAACGTCG TCG
                                   CCC        C
GAM487   LOC200169 5'  ACTGCAACCTCTGCCTCC     89940
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487   LOC200169 3'  GCTGCAACTCCACCCC       89952     A   A   G
                                GG GGT GAG TTGCAGT
                                || ||| ||| |||||||
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                                CC CCA CTC AACGTCG
                                  _  C  _
GAM487  LOC200268 3'  ACTGCAACCTCTGCCTCC    88673
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  LOC200310 3'  GCTCACTACAACCTCTGCCTCC 65740            C  _
                                GGAGGTAGAGGTTG AGT AGC
                                |||||||||||||| ||| |||
                                CCTCCGTCTCCAAC TCA TCG
                                         A  C
GAM487  LOC200314 3'  GCTCACTGCAACCTCCACCTCC 90012       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  LOC200339 3'  ACTGCAACCTCTGCCTCC    90028
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  LOC200731 3'  GCTACTGCACTCCAGCCCC   90122    A  A_  GT
                                GG GGT  GAG  TGCAGTAGC
                                || |||  |||  |||||||||
                                CC CCG  CTC  ACGTCATCG
                                  _  AC  __
GAM487  LOC200860 3'  ACTGCAACCTCCACCTCC    90157       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCAACGTCA
                                   C
GAM487  LOC201173 5'  ACTGCAACCTCTGCCTCC    87322
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  LOC201220 5'  ACTGCAACCTCTGCCTCC    87342
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  LOC201294 3'  ACTGCAACCTCCGCCTCC    88199      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC201294 3'  ACTGCAACCTCCGCCTCC    88200      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
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                                CCTCC  CTCCAACGTCA
                                   GC
GAM487   LOC201411 3'  ACTGCAACCTCTGCCTCC    62950
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487   LOC201626 3'  ACTGCAACCTCCGCCCC     88985    A  TA
                                GG GG  GAGGTTGCAGT
                                || ||  ||||||||||
                                CC CC  CTCCAACGTCA
                                 _  GC
GAM487   LOC201627 3'  GCTGACTGCAACCTCCACCTCC 89017       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                    C         G
GAM487   LOC202025 3'  ACTGCAACCTCCGCCTCC    90279      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487   LOC202934 3'  GCTCACTACAACCTCTGCCTCC 90417            C  _
                                GGAGGTAGAGGTTG AGT AGC
                                |||||||||||||| ||| |||
                                CCTCCGTCTCCAAC TCA TCG
                                        A  C
GAM487   LOC203297 5'  ACTGCAACCTCTGCCTCC    75347
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487   LOC203350 3'  ACTGCAACCTCCGCCTCC    90559      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487   LOC204804 3'  GCTCACTGCAACCTCGACCTCC 89477       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                    G         C
GAM487   LOC219513 3'  GCAGTACCTCTACCTCC     94330          __
                                GGAGGTAGAGGT  TGC
                                ||||||||||||  |||
                                CCTCCATCTCCA  ACG
                                       TG
GAM487   LOC219735 3'  ACTGCAACCTCTGCCTCC    93104
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
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                                CCTCCGTCTCCAACGTCA

GAM487  LOC219842 5'  GCCAGGCCCCTCTGCCTCC   93268          TT  AGTA
                      GGAGGTAGAGG  GC   GC
                      ||||||||||  ||   ||
                      CCTCCGTCTCC  CG   CG
                            C_  GAC_
GAM487  LOC219920 3'  ACTACAGCCCCAGCCTCC    93297       AGA    C
                      GGAGGT   GGTTG AGT
                      ||||||   ||||| |||
                      CCTCCG   CCGAC TCA
                         ACC    A
GAM487  LOC219942 3'  CTACTGTGGCCTCCACTTCC  93344       A    TG
                      GGAGGT GAGGT  CAGTAG
                      |||||| |||||  ||||||
                      CCTTCA CTCCG  GTCATC
                         C    GT
GAM487  LOC220045 5'  GCCAGCCCTCTGCCCC      93408    A      _  _
                      GG GGTAGAGG TTG C
                      || ||||||||  ||| |
                      CC CCGTCTCC GAC G
                       _      C  C
GAM487  LOC220064 3'  ACTGTAACCTCCGCCTCC    93422      TA
                      GGAGG  GAGGTTGCAGT
                      |||||  ||||||||||
                      CCTCC  CTCCAATGTCA
                         GC
GAM487  LOC220662 3'  ACTGCAACCTCCACCTCC    91159       A
                      GGAGGT GAGGTTGCAGT
                      |||||| ||||||||||
                      CCTCCA CTCCAACGTCA
                         C
GAM487  LOC220662 3'  ACTGCAACCTCCACTTCC    91162       A
                      GGAGGT GAGGTTGCAGT
                      |||||| ||||||||||
                      CCTTCA CTCCAACGTCA
                         C
GAM487  LOC221035 3'  GCTCACTACAACCTCTGCCTCC 93166           C  _
                      GGAGGTAGAGGTTG AGT AGC
                      |||||||||||||| ||| |||
                      CCTCCGTCTCCAAC TCA TCG
                            A  C
GAM487  LOC221174 5'  ACTGCGACCTCCACCTCC    93496       A
                      GGAGGT GAGGTTGCAGT
                      |||||| ||||||||||
                      CCTCCA CTCCAGCGTCA
                         C
GAM487  LOC221271 3'  ACTGCAACCTCTGCCTCC    91842
                      GGAGGTAGAGGTTGCAGT
                      ||||||||||||||||||
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                                CCTCCGTCTCCAACGTCA

GAM487  LOC221296 3'  GCTCACTGCAACCTCCACCTCC 91966       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  LOC221663 5'  GCTCACTGCAACCTCCACCTCC 93819       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  LOC221773 3'  ACTGTGACCTCCGCCTCC    91035      TA    TG
                                GGAGG  GAGGT  CAGT
                                |||||  |||||  ||||
                                CCTCC  CTCCA  GTCA
                                   GC     GT
GAM487  LOC222070 5'  ACTGCAACCTCTGCCTCC    94148
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  LOC222865 3'  GCCACTGCCACAAGCCCCTCC  92862      TAGAG  T    A
                                GGAGG    GT GCAGT GC
                                |||||    || ||||| ||
                                CCTCC    CA CGTCA CG
                                   CCGAA  C    C
GAM487  LOC253612 5'  ACTGCAACCTCCGCCTCC    96738      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC253666 5'  ACTGCAACCTCCGCCTCC    95058      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC253842 3'  GCTACTCTTACTCCCCTGCCTC 97389       A  TTGC__
           C                     GGAGGTAG GG     AGTAGC
                                |||||||| ||     ||||||
                                CCTCCGTC CC     TCATCG
                                     C  TCATTC
GAM487  LOC253866 5'  GCAGTAGCACCCTGACCTCTAC 95587         T_________  AGTA
           CTTC                   AGGTAGAGGT       GC    GC
                                ||||||||||       ||    ||
                                TCCATCTCCA       CG    CG
                                     GTCCCAIII  ATGA
GAM487  LOC254013 3'  ACTGTAGCCTCCACCTCC    94876      A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
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                                CCTCCA CTCCGATGTCA
                                   C
GAM487  LOC254018 5'  GCCACTGTGCCCAGCCTCC   96967      AGA  TT    A
                                GGAGGT   GG  GCAGT GC
                                ||||||   ||  ||||| ||
                                CCTCCG   CC  TGTCA CG
                                   A__  CG    C
GAM487  LOC254672 3'  ACTGAAACCTCTGCCTCC    94638          G
                                GGAGGTAGAGGTT CAGT
                                |||||||||||| ||||
                                CCTCCGTCTCCAA GTCA
                                      A
GAM487  LOC255497 3'  ACTGCAACCTCCGCCTCC    97185      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC255736 3'  GCTCCCCACCCCCTACCTCC   95333       A  T  CAGT
                                GGAGGTAG GG TG    AGC
                                ||||||| || ||    |||
                                CCTCCATC CC AC    TCG
                                     C  C  CCC_
GAM487  LOC255855 3'  GCCGAATAGACCTCTACATCC  96226     G       GCAGTA
                                GGA GTAGAGGTT     GC
                                ||| |||||||||     ||
                                CCT CATCTCCAG     CG
                                  A        ATAAGC
GAM487  LOC255913 3'  ACTGTTTGACCTCCTCCCC    96124    A  TA     __
                                GG GG  GAGGTT  GCAGT
                                || ||  ||||||  |||||
                                CC CC  CTCCAG  TGTCA
                                 _  TC     TT
GAM487  LOC256267 3'  ACTGCAACCTCCGCCTCC    96795      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC256267 3'  GCCCACCTCTGCCTCC      96802          T_
                                GGAGGTAGAGGT  GC
                                ||||||||||||  ||
                                CCTCCGTCTCCA  CG
                                      CC
GAM487  LOC256306 3'  GCTCACTGCAACCTCCACCTCC 96694       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  LOC51200  3'  GCTCACCACAACCTCTGCCTCC 32999           CA  _
                                GGAGGTAGAGGTTG  GT AGC
                                |||||||||||||  || |||
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                                CCTCCGTCTCCAAC  CA TCG
                                      AC  C
GAM487  LOC51219  5' ACCGCAACCTCCGCCTCC    33110      TA      A
                                GGAGG  GAGGTTGC GT
                                |||||  |||||||| ||
                                CCTCC  CTCCAACG CA
                                   GC       C
GAM487  LOC51696  3' ACTGCAACCTCTGCCTCC    32541
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM487  LOC54505  5' CACTATTTCACCTCC       67838       A    TGC   A
                                GGAGGT GAGGT   AGT G
                                |||||| |||||   ||| |
                                CCTCCA CTTTA   TCA C
                                   _    ___   C
GAM487  LOC57107  3' ACTGCAACCTCCGCCTCC    39825      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC57146  3' GCTCACTGCAACCTCCAACTCC 39924     GTA        _
                                GGAG   GAGGTTGCAGT AGC
                                ||||   |||||||||| |||
                                CCTC   CTCCAACGTCA TCG
                                  AAC          C
GAM487  LOC81034  3' GCTCACTGCAACCTCCACCTCC 47855       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  LOC89932  3' GCTCACTGCAACCTCCACCTCC 60805       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C          C
GAM487  LOC90288  3' ACTGCAACCTCCACCTCC    62076       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
                                CCTCCA CTCCAACGTCA
                                   C
GAM487  LOC90333  3' ACTGCAACCTCCTCCTCC    62279      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   TC
GAM487  LOC90333  5' ACTGCAACCTCCACTTCC    62277       A
                                GGAGGT GAGGTTGCAGT
                                |||||| ||||||||||
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                                CCTTCA CTCCAACGTCA
                                   C
GAM487  LOC90371  5' GCTCACTGCAACCTCCACCTCC 62501       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  LOC90408  5' GCTCACTGCAACCTCTACCTCC 62662                  _
                                GGAGGTAGAGGTTGCAGT AGC
                                |||||||||||||||||| |||
                                CCTCCATCTCCAACGTCA TCG
                                          C
GAM487  LOC90459  3' ACTGCAACCTCCGCCTCC    62879      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC90485  3' ACTGCAACCTCCGCCTCC    63006      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC90957  3' GCAGAACCTCTACCTC      64465        __
                                GAGGTAGAGGT  TGC
                                ||||||||||  |||
                                CTCCATCTCCA  ACG
                                      AG
GAM487  LOC91115  3' GCTCACTGCAACCTCCACCTCC 64941       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  LOC91115  3' ACTGCAACCTCCGCCTCC    64920      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC91263  3' GCCACTGCTCCTAGCCCC    65381    A  AG  TT   A
                                GG GGT  AGG  GCAGT GC
                                || |||  |||  ||||| ||
                                CC CCG  TCC  CGTCA CG
                                  _  A_  T_    C
GAM487  LOC92267  3' GCTCACTGCAACCTCCACCTCC 68619       A        _
                                GGAGGT GAGGTTGCAGT AGC
                                |||||| |||||||||| |||
                                CCTCCA CTCCAACGTCA TCG
                                   C         C
GAM487  LOC92466  3' ACTGCAACCTCCGCCTCC    69420      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
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                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC92466  3'  GCCCACCTCTGCCTCC     69427          T_
                                GGAGGTAGAGGT  GC
                                ||||||||||||  ||
                                CCTCCGTCTCCA  CG
                                      CC
GAM487  LOC92689  3'  ACTGCAACCTCCGCCTCC    70213      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC92697  5'  ACCGCAACCTCCGCCTCC    70259      TA       A
                                GGAGG  GAGGTTGC GT
                                |||||  |||||||| ||
                                CCTCC  CTCCAACG CA
                                   GC       C
GAM487  LOC92841  3'  ACCGCAACCTCCTCCTCC    70704      TA       A
                                GGAGG  GAGGTTGC GT
                                |||||  |||||||| ||
                                CCTCC  CTCCAACG CA
                                   TC       C
GAM487  LOC93132  5'  ACTGCAACCTCCGCCTCC    71479      TA
                                GGAGG  GAGGTTGCAGT
                                |||||  ||||||||||
                                CCTCC  CTCCAACGTCA
                                   GC
GAM487  LOC93349  3'  ACTGCAACCTCTGCCTCC    56449
                                GGAGGTAGAGGTTGCAGT
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTCA

GAM488  FBXL3A    3'  TGAGAAGAAAAAAGGCTTA   24068       __    C
                                TAAGCT  TTTTC TCTCG
                                ||||||  ||||| |||||
                                ATTCGG  AAAAG AGAGT
                                    AA    A
GAM488  LOC146988 5'  ACGTAGAAAGAAAAAAGCTTA  83890          CC   CGC
                                TAAGCTTTTT  TCT   CTACGT
                                ||||||||||  |||   ||||||
                                ATTCGAAAAA  AGA   GATGCA
                                      __   AA_
GAM489  AIPL1     3'  CCTGTCTCCCCATTTTGG     59850        AAA  CAA
                                CCAAAATG   GA   ACAGG
                                ||||||||   ||   |||||
                                GGTTTTAC   CT   TGTCC
                                     CC_  C__
GAM489  DVL3      3'  TCTGCAACCCCCATTTTGGGA  15376          AAAGACAAA
                                TCCCAAAATG       CAGG
                                ||||||||||       ||||
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                                AGGGTTTTAC       GTCT
                                     CCCCAAC__
GAM489  EIF4EBP2  3'  CCTGTTTGTGAATATATTTT  14589      AAAG_
                                AAAATG    ACAAACAGG
                                ||||||    |||||||||
                                TTTTAT    TGTTTGTCC
                                   ATAAG
GAM489  GAS11     3'  CCTGGACACCTTTCTTTTGGGA 7623        T    ACAAA
                                TCCCAAAA GAAAG    CAGG
                                |||||||| |||||    ||||
                                AGGGTTTT CTTTC    GTCC
                                     _    CACAG
GAM489  GNRHR     5'  TCCTGTTTTGTTCATTTCAGG  4643    CA     AGAC
                                CC  AAATGAA   AAACAGGA
                                ||  |||||||   ||||||||
                                GG  TTTACTT   TTTGTCCT
                                  AC      GT__
GAM489  GPR48     3'  CCTATTCTCATCTTTCATCTGG 37502     AA      CAAAC__
              GA                  TCCCA  ATGAAAGA     AGG
                                |||||  ||||||||      |||
                                AGGGT  TACTTTCT     TCC
                                   C_       ACTCTTA
GAM489  HLCS      5'  CCTGGGGTCTTTCACTCCCGGA 4663     CAAAA      AAA
                                TCC    TGAAAGAC   CAGG
                                |||    ||||||||   ||||
                                AGG    ACTTTCTG   GTCC
                                  CCCTC       GG_
GAM489  HLCS      5'  TCCTGTTTGCCTTTATCCACTG 4678     AAATG_   A
              G                   CCA     AAAG CAAACAGGA
                                |||     |||| |||||||||
                                GGT     TTTC GTTTGTCCT
                                  CACCTA    C
GAM489  ICAM1     3'  TCCTGTTTGCATTTCACTGGGA 71579      AAA    GA
                                TCCCA   TGAAA  CAAACAGGA
                                |||||   |||||  |||||||||
                                AGGGT   ACTTT  GTTTGTCCT
                                   C__     AC
GAM489  KCNK10    5'  TCCCACCTGTCTTTTTCTGGGG 56340      AAAT      AACA
                                TCCCA    GAAAGACA    GGA
                                |||||    ||||||||    |||
                                GGGGT    TTTTCTGT    CCT
                                   CT__       CCAC
GAM489  MHC2TA    3'  CCTGTTACCATTTTGGGG    4171          AAAGACA
                                TCCCAAAATG      AACAGG
                                ||||||||||      ||||||
                                GGGGTTTTAC      TTGTCC
                                     CA_____
GAM489  SLC25A12  3'  TCCTAGTTTGTTTTCCATTCTG 13526     A   A       _
              G                   CCA AATG AAGACAAAC AGGA
                                ||| |||| ||||||||| ||||
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                                GGT TTAC TTTTGTTTG TCCT
                                  C   C       A
GAM489  SLC7A6   3'  CCTCCTTTCATTTTTGGA   14300    C       ACAAAC
                                TCC AAAATGAAAG    AGG
                                ||| ||||||||||    |||
                                AGG TTTTACTTTC    TCC
                                  T       C_____
GAM489  SLC9A1   3'  TCCTGTTTTTAAAACATTTTG  70412       AAAGAC
                                CAAAATG    AAACAGGA
                                |||||||    ||||||||
                                GTTTTAC    TTTGTCCT
                                    AAAATT
GAM489  SNX15    3'  CCTGCCTGTCTTTTTGGGG   73735      AAAT      AA
                                TCCCA   GAAAGACA  CAGG
                                |||||   ||||||||  ||||
                                GGGGT   TTTTCTGT  GTCC
                                  _____      CC
GAM489  STIM1    3'  CCTGCCATACCTTTATCCTGGG 60147      AA    AGACAAA
            A                    TCCCA  ATGAA     CAGG
                                |||||  |||||     ||||
                                AGGGT  TATTT     GTCC
                                  CC    CCATACC
GAM489  USP1     3'  TCCTGTGGTTTTTCA      12560       AA
                                TGAAAGAC  ACAGGA
                                ||||||||  ||||||
                                ACTTTTTG  TGTCCT
                                    G_
GAM489  ZNF267   5'  TCCGAGTCTTTCGTTCTGGGA  12736      A       AAACA
                                TCCCA AATGAAAGAC    GGA
                                ||||| ||||||||||    |||
                                AGGGT TTGCTTTCTG    CCT
                                  C       AG___
GAM489  ATE1     3'  TCCTGTTTGTATTTTGT    72613   TG  G
                                A  AAA ACAAACAGGA
                                |  ||| ||||||||||
                                T  TTT TGTTTGTCCT
                                 GT   A
GAM489  C21orf109 3'  TCCTGTTTTATATACTTTCATT 57267   CCA       AC____
           TGAGA                  C   AAATGAAAG     AAACAGGA
                                |   |||||||||     ||||||||
                                G   TTTACTTTC     TTTGTCCT
                                 AG_       ATATAT
GAM489  CNOT3    3'  CTATTTTCATTTTGG      27218          ACAAAC
                                CCAAAATGAAAG     AG
                                ||||||||||||     ||
                                GGTTTTACTTTT     TC
                                      A_____
GAM489  CTNNBIP1  3'  TCCTGAGGCCTCATTTTGGGG  39669          AAGACAAA
                                TCCCAAAATGA       CAGGA
                                ||||||||||       |||||
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                                GGGGTTTTACT       GTCCT
                                      CCGGA___
GAM489  DKFZP564I122 3'  CCTGTAATCCCACCATTTTGGG 63173          AAAGACAA
           A                    TCCCAAAATG       ACAGG
                                ||||||||||       |||||
                                AGGGTTTTAC       TGTCC
                                     CACCCTAA
GAM489  DKFZP566J091 3'  CCTTTGCTTTCATTTCAGG   48120    CA       A   AC
                                CC  AAATGAAAG CAA  AGG
                                ||  ||||||||| |||  |||
                                GG  TTTACTTTC GTT  TCC
                                 AC       _  __
GAM489  FASTK    3'  CCGTTGTGAATCTCAGTTTTGG 46987        GAA   CAA  __
           GA                    TCCCAAAAT   AGA   ACA  GG
                                 |||||||||   |||   |||  ||
                                 AGGGTTTTG   TCT   TGT  CC
                                      AC_   AAG   TG
GAM489  FASTK    3'  CCGTTGTGAATCTCAGTTTTGG 52246        GAA   CAA  __
           GA                    TCCCAAAAT   AGA   ACA  GG
                                 |||||||||   |||   |||  ||
                                 AGGGTTTTG   TCT   TGT  CC
                                      AC_   AAG   TG
GAM489  FHR5     3'  TCCTGTTTGTCTCAAATTATAG 47903     CAA   GAA
           GA                    TCC   AAT   AGACAAACAGGA
                                 |||   |||   ||||||||||||
                                 AGG   TTA   TCTGTTTGTCCT
                                   ATA   AAC
GAM489  FLJ10895  3'  TCCTGTAGGTTTATTTTGG    38849         AAG  AA
                                 CCAAAATGA   AC  ACAGGA
                                 |||||||||   ||  ||||||
                                 GGTTTTATT   TG  TGTCCT
                                      ___  GA
GAM489  FLJ14824  3'  CCTGTTCATTTTATTTTAGGG  51642     _       GACA
                                 CCC AAAATGAAA    AACAGG
                                 |||  |||||||||    ||||||
                                 GGG TTTTATTTT    TTGTCC
                                   A        AC__
GAM489  FLJ32312  3'  TCCTTAATTCTTTCATTT     58497          CAAAC
                                 AAATGAAAGA     AGGA
                                 ||||||||||     ||||
                                 TTTACTTTCT     TCCT
                                      TAAT_
GAM489  FLJ32926  3'  CCTGTTTGCCTTGTGGG      58022      AAATGA   A
                                 CCCA      AAG CAAACAGG
                                 ||||      ||| ||||||||
                                 GGGT      TTC GTTTGTCC
                                   G_____   C
GAM489  KIAA0210  5'  CCTGGCCTGCTTTCATTTT    28475          A  AA_
                                 AAAATGAAAG CA   CAGG
                                 |||||||||| ||   ||||
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                                TTTTACTTTC GT   GTCC
                                      _ CCG
GAM489  KIAA0711  3' TGTGGCTTTCATTTTGGGA   29530          ACAA
                                TCCCAAAATGAAAG   ACA
                                |||||||||||||   |||
                                AGGGTTTTACTTTC   TGT
                                     GG__
GAM489  KIAA0923  3' CCTGTTTGTGGCTATTTT   25834      AAAG
                                AAAATG   ACAAACAGG
                                ||||||   |||||||||
                                TTTTAT   TGTTTGTCC
                                   CGG_
GAM489  KIAA0997  3' CCTAGAGTTACTCTCTTTTGGG 30189       T_ AA  AAAC
          A                     TCCCAAAA GA GAC   AGG
                                ||||||||  ||  |||   |||
                                AGGGTTTT  CT  TTG   TCC
                                    CT  CA  AGA_
GAM489  KIAA1163  3' TCCTGTATTTTCATTTCTG   78905   _      ACAA
                                CA AAATGAAAG   ACAGGA
                                || |||||||||   ||||||
                                GT TTTACTTTT   TGTCCT
                                 C       A___
GAM489  KIAA1233  3' TCCTGAGAACTTTATTTTGG  63083        AGACAAA
                                CCAAAATGAA     CAGGA
                                ||||||||||     |||||
                                GGTTTTATTT     GTCCT
                                     CAAGA__
GAM489  KIAA1508  5' TCTTTGTGTCTTTCAT     61894         AAC
                                ATGAAAGACA   AGGA
                                ||||||||||   ||||
                                TACTTTCTGT   TTCT
                                     GT_
GAM489  KIAA1719  3' CCTGCCTGCCTATGCATTTTGG 68158        AA_  A  AA
          GA                    TCCCAAAATG   AG CA  CAGG
                                ||||||||||   || ||  ||||
                                AGGGTTTTAC   TC GT  GTCC
                                     GTA  C  CC
GAM489  KIAA1750  3' TCCTACTTGTCTTTAACATGG  68257    AAATG      AC
                                CCA    AAAGACAA  AGGA
                                |||    ||||||||  ||||
                                GGT    TTTCTGTT  TCCT
                                  ACAA_      CA
GAM489  KIAA1940  3' TCCTGCCAACTTTCATTTGG   79992     A     ACAAA
                                CCAAA TGAAAG    CAGGA
                                |||||  ||||||    |||||
                                GGTTT ACTTTC    GTCCT
                                   _    AACC_
GAM489  MDS018    3' CTGTCTCATTTTGGGA     41533          AAGACAA
                                TCCCAAAATGA     ACAG
                                ||||||||||      ||||
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                                AGGGTTTTACT      TGTC
                                      C_______
GAM489  MGC10977  5'  TTGTCTCTCATTTTGGG     51061          A
                                CCCAAAATGA AGACAA
                                |||||||||| ||||||
                                GGGTTTTACT TCTGTT
                                      C
GAM489  MGC26655  3'  TCCTGCCATTTTTCATTTT   56291          CAAA
                                AAAATGAAAGA   CAGGA
                                ||||||||||    |||||
                                TTTTACTTTTT   GTCCT
                                      ACC_
GAM489  MGC26914  3'  TCCTGTTTCTCACTTTTGG   58668       _   AAGAC
                                CCAAAA TGA    AAACAGGA
                                |||||| |||    ||||||||
                                GGTTTT ACT    TTTGTCCT
                                   C   C____
GAM489  NYD-SP15  3'  TCCTGTTTATCACAGACTTTGG 48112       ATGAAA  C
           G                     CCCAAA     GA AAACAGGA
                                ||||||     || ||||||||
                                GGGTTT     CT TTTGTCCT
                                   CAGACA  A
GAM489  PTK6      3'  TCCTGTTTGTCTTGTGTCTTGA 19941    C   A   A
           GA                     TC CAA ATG AAGACAAACAGGA
                                || ||| ||| ||||||||||||
                                AG GTT TGT TTCTGTTTGTCCT
                                 A   C   G
GAM489  SEC15B    3'  TCCTGTACTCTTTCGTTTT   66687          CAA
                                AAAATGAAAGA   ACAGGA
                                ||||||||||   ||||||
                                TTTTGCTTTCT   TGTCCT
                                      CA_
GAM489  SEC3      5'  CCATCCGGTCTCCGTTTTGG  36812        AA   AAACA
                                CCAAAATG  AGAC    GG
                                ||||||||  ||||    ||
                                GGTTTTGC  TCTG    CC
                                     C_   GCCTA
GAM489  Spir-1    3'  TCCTGTTTAAGAGCTTTCA   64703       AC___
                                TGAAAG    AAACAGGA
                                ||||||    ||||||||
                                ACTTTC    TTTGTCCT
                                   GAGAA
GAM489  LOC113523 3'  TCCTGTCTCTTTCCATTT    73051      _    CAA
                                AAATG AAAGA   ACAGGA
                                ||||| |||||   ||||||
                                TTTAC TTTCT   TGTCCT
                                   C    C__
GAM489  LOC139221 3'  CCTGAAATTCCATTTTTGGGA  75823        TGAAA  CAAA
                                TCCCAAAA    GA   CAGG
                                ||||||||    ||   ||||
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                                AGGGTTTT    CT   GTCC
                                    TAC__  TAAA
GAM489  LOC143680 5'  TCTTGAGATCTTTTATTTTGG  82989          CAAA
                                CCAAAATGAAAGA   CAGGA
                                ||||||||||||   |||||
                                GGTTTTATTTTCT   GTTCT
                                    AGA_
GAM489  LOC143719 5'  TTGTCTCTCATTTTGGG    60624         A
                                CCCAAAATGA AGACAA
                                |||||||||| ||||||
                                GGGTTTTACT TCTGTT
                                    C
GAM489  LOC144147 5'  TTGTCTCTCATTTTGGG    71733         A
                                CCCAAAATGA AGACAA
                                |||||||||| ||||||
                                GGGTTTTACT TCTGTT
                                    C
GAM489  LOC145719 3'  TCCTGTAACTTTTTCAT    83457        CAA
                                ATGAAAGA   ACAGGA
                                ||||||||   ||||||
                                TACTTTTT   TGTCCT
                                    CAA
GAM489  LOC145720 3'  TCCTGTAACTTTTTCAT    83439        CAA
                                ATGAAAGA   ACAGGA
                                ||||||||   ||||||
                                TACTTTTT   TGTCCT
                                    CAA
GAM489  LOC148758 5'  TCCATGAGTCTTTCAGGG   78976    AAAA      AAA  _
                                CCC   TGAAAGAC   CA GGA
                                |||   ||||||||   || |||
                                GGG   ACTTTCTG   GT CCT
                                  _____      A__  A
GAM489  LOC149111 3'  CCTGTTTGTCAATCTTTGG   79182      AT  AA
                                CCAAA  GA  GACAAACAGG
                                |||||  ||  ||||||||||
                                GGTTT  CT  CTGTTTGTCC
                                   __  AA
GAM489  LOC150407 3'  CCTGTTTGTCCCTTTCAGTGGG 79823      AAA    __
                                CCCA   TGAAA  GACAAACAGG
                                ||||   |||||  ||||||||||
                                GGGT   ACTTT  CTGTTTGTCC
                                  G__    CC
GAM489  LOC150538 3'  GTCTTTCATTCGGGA      79939      AA
                                TCCC  AATGAAAGAC
                                ||||  ||||||||||
                                AGGG  TTACTTTCTG
                                  C_
GAM489  LOC152860 5'  CCTGTTTGTCTGTGGGTCCTGG 80700      AA  GAA_
            G                    CCCA  AT    AGACAAACAGG
                                ||||  ||   ||||||||||
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                                GGGT  TG    TCTGTTTGTCC
                                  CC  GGTG
GAM489   LOC159053 3'  TCCTGTTTTCTTCATTT     86983        A  C
                                AAATGAA GA AAACAGGA
                                ||||||| || ||||||||
                                TTTACTT CT TTTGTCCT
                                   _ _
GAM489   LOC197117 3'  TCCTGTAACTTTTTCAT     89725         CAA
                                ATGAAAGA   ACAGGA
                                ||||||||   ||||||
                                TACTTTTT   TGTCCT
                                    CAA
GAM489   LOC201915 5'  TCCTGTTTGCCCTCGTCTGCCG 89105     CAAA_   AAGA
           GA                     TCC    ATGA   CAAACAGGA
                                |||    ||||   |||||||||
                                AGG    TGCT   GTTTGTCCT
                                  CCGTC   CCC_
GAM489   LOC203197 3'  CTGTTTGACTTGAGGA      89288     _ AAATGAA  A
                                TCC CA      AG CAAACAG
                                ||| ||      || |||||||
                                AGG GT      TC GTTTGTC
                                  A ________  A
GAM489   LOC221662 3'  CCTGTTTCAATTTTGGGA     92402         GAAAGAC
                                TCCCAAAAT      AAACAGG
                                |||||||||      |||||||
                                AGGGTTTTA      TTTGTCC
                                    AC_____
GAM489   LOC223117 5'  TCCATGCAGTCTTTCATTTTG  94382            AAA  _
                                CAAAATGAAAGAC   CA GGA
                                ||||||||||||   || |||
                                GTTTTACTTTCTG   GT CCT
                                      AC_  A
GAM489   LOC253228 3'  TCCTGTTTGTCTTCTCCCCAGG 95942     AAAAT  _
           G                     CCC    GA AAGACAAACAGGA
                                |||    || ||||||||||||||
                                GGG    CT TTCTGTTTGTCCT
                                  ACCC_  C
GAM489   LOC254107 3'  CCTGTTTGTAAATATTCTGTGG 94385     _ A   AAAG
           A                      TCC CA AATG   ACAAACAGG
                                ||| || ||||   |||||||||
                                AGG GT TTAT   TGTTTGTCC
                                  T  C   AAA_
GAM489   LOC254685 5'  CCTTCCATCCATTTTGGGA   96485          AAA  CAAAC
                                TCCCAAAATG   GA    AGG
                                ||||||||||   ||    |||
                                AGGGTTTTAC   CT    TCC
                                     ____  ACCT_
GAM489   LOC255527 5'  TCCTGGGTCCTTTTTGGGA   96856         TGAAA   AAA
                                TCCCAAAA    GAC   CAGGA
                                ||||||||    |||   |||||
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                                AGGGTTTT    CTG   GTCCT
                                    TC___   G__
GAM489  LOC257109 3'  TTGTCTTTCATCTGGGA     95573      AA
                                TCCCA  ATGAAAGACAA
                                |||||  ||||||||||
                                AGGGT  TACTTTCTGTT
                                  C_
GAM489  LOC91097  5'  CCTGTTTGCCATCTCGGGG   64835     AAA   AAAGA
                                TCCC   ATG    CAAACAGG
                                ||||   |||    ||||||||
                                GGGG   TAC    GTTTGTCC
                                  CTC   C____
GAM489  LOC91145  3'  TCCTGTTTCTTTTCATCTCTAG 65058     CAAA_      AC
          GA                      TCC    ATGAAAG  AAACAGGA
                                |||    |||||||  ||||||||
                                AGG    TACTTTT  TTTGTCCT
                                  ATCTC      C_
GAM490  PCTP     3'  CCAATGTCTCTGGAAGTGCCAC 41095          AGTT
                                GTGGCATTTC    GACATTGG
                                ||||||||||    ||||||||
                                CACCGTGAAG    CTGTAACC
                                     GTCT
GAM490  PROCR    3'  TCCCCAACTGAAACACCA    21136     CA       ACATT
                                TGG  TTTCAGTTG    GGA
                                |||  |||||||||    |||
                                ACC  AAAGTCAAC    CCT
                                  AC        C____
GAM490  LOC145845 3'  GTCAACTCAAATGCCAC     83555         C
                                GTGGCATTT AGTTGAC
                                ||||||||| |||||||
                                CACCGTAAA TCAACTG
                                     C
GAM490  LOC158056 5'  TTCTCTGCCACCCGAAATGCCA 81690          AGT  A  TT
          C                      GTGGCATTTC   TG CA  GGA
                                ||||||||||   || ||  |||
                                CACCGTAAAG   AC GT  CTT
                                     CCC  C  CT
GAM491  ACPT     3'  GTGCCAGGGATCCTGCTGA    54990        T    ATTGA
                                TCAGCAGG ATTT     AC
                                |||||||| ||||     ||
                                AGTCGTCC TAGG     TG
                                    _    GACCG
GAM491  ADAMTS5  3'  GTGTTCAATAGATACC      22894
                                GGTATTTATTGAACAC
                                ||||||||||||||||
                                CCATAGATAACTTGTG

GAM491  AGL      5'  TGTTTACTATACTTGCT     5372          TTAT
                                AGCAGGTAT    TGAACA
                                |||||||||    ||||||
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                                TCGTTCATA   ATTTGT
                                     TC__
GAM491  APOA4    3'  TTCAATAAAGCTGCTGA    4907       GTA
                                TCAGCAG   TTTATTGAA
                                |||||||   |||||||||
                                AGTCGTC   AAATAACTT
                                    G__
GAM491  ARHGAP6  3'  TTTACCGAGTACCTGCTGA   25519          AT
                                TCAGCAGGTATTT  TGAA
                                ||||||||||||  ||||
                                AGTCGTCCATGAG  ATTT
                                       CC
GAM491  ARHGAP6  3'  TTTACCGAGTACCTGCTGA   20411          AT
                                TCAGCAGGTATTT  TGAA
                                ||||||||||||  ||||
                                AGTCGTCCATGAG  ATTT
                                       CC
GAM491  C21orf33 3'  TTCAGACCTGCTGA       16199        ATTTA
                                TCAGCAGGT    TTGAA
                                |||||||||    |||||
                                AGTCGTCCA    GACTT
                                     _____
GAM491  CLASP1   3'  TGTCTTGTACAGCCTGCTGA  65313        ATT   TGA
                                TCAGCAGGT   TAT   ACA
                                |||||||||   |||   |||
                                AGTCGTCCG   ATG   TGT
                                     AC_   TTC
GAM491  CYP46    3'  TGCTCAATAAATGTGTGTTGA 21898      GG       A
                                TCAGCA  TATTTATTGA CA
                                ||||||  |||||||||| ||
                                AGTTGT  GTAAATAACT GT
                                   GT        C
GAM491  DVL3     3'  GTGCTCAATAAATGGTAGCT   15374     AGG       A
                                AGC   TATTTATTGA CAC
                                |||   |||||||||| |||
                                TCG   GTAAATAACT GTG
                                  ATG        C
GAM491  EIF2B1   3'  CAAGAAACACTTGCTGA     59657        A   A
                                TCAGCAGGT TTT TTG
                                ||||||||| ||| |||
                                AGTCGTTCA AAA AAC
                                     C   G
GAM491  GALK1    3'  GTGCTCAATAAACTTGT     3850       AT     A
                                GCAGGT  TTATTGA CAC
                                ||||||  ||||||| |||
                                TGTTCA  AATAACT GTG
                                   __      C
GAM491  GDI1     3'  GTGTTCTGTGGTACTTGCTGA 59980          TATT
                                TCAGCAGGTATT   GAACAC
                                ||||||||||||   ||||||
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                                AGTCGTTCATGG   CTTGTG
                                       TGT_
GAM491  GUCY1B3  3'  CAATAAATATTTGTTGA    5965
                                TCAGCAGGTATTTATTG
                                ||||||||||||||||
                                AGTTGTTTATAAATAAC

GAM491  IDH3B    3'  GTGTTCAATAAAGAACATG   22578   G  A_
                                CA GT  TTTATTGAACAC
                                || ||  ||||||||||||
                                GT CA  AAATAACTTGTG
                                 A  AG
GAM491  MEF2D    3'  GTGCTCAATAAATGAATG    96916   GG       A
                                CA  TATTTATTGA CAC
                                ||  |||||||||| |||
                                GT  GTAAATAACT GTG
                                 AA        C
GAM491  MEF2D    3'  TCAATAAATGCTGA       96918      GGTA
                                TCAGCA   TTTATTGA
                                ||||||   ||||||||
                                AGTCGT   AAATAACT
                                   ____
GAM491  MKI67    3'  TCATAAATACTTGCTGA     10049           T
                                TCAGCAGGTATTTAT GA
                                |||||||||||||| ||
                                AGTCGTTCATAAATA CT
                                      _
GAM491  MT3      3'  GTGTTCCCTTTCCCTGCTGA  19881       TATTTATT
                                TCAGCAGG      GAACAC
                                ||||||||      ||||||
                                AGTCGTCC      CTTGTG
                                    CTTTCC__
GAM491  NCOA6    5'  TGCTCAATAAATATTAGCTG  25980     AG        A
                                CAGC  GTATTTATTGA CA
                                ||||  |||||||||| ||
                                GTCG  TATAAATAACT GT
                                  AT         C
GAM491  NCOA6    5'  TTCTGGAATACCTACTG     25983     C      ATT
                                CAG AGGTATTT   GAA
                                ||| ||||||||   |||
                                GTC TCCATAAG   CTT
                                  A       GT_
GAM491  NKX2E    5'  GTGCTCAGCGCTACCTGCTG  15244        TTTA   A
                                CAGCAGGTA    TTGA CAC
                                |||||||||    |||| |||
                                GTCGTCCAT    GACT GTG
                                     CGC_    C
GAM491  PLA2G2D  3'  GTGCTCAATTCATGCCTGT   24799        TT    A
                                GCAGGTAT  ATTGA CAC
                                ||||||||  ||||| |||
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                                TGTCCGTA  TAACT GTG
                                    CT    C
GAM491  PLA2G4C  3'  GTGCTCAATAAATGCTTGCTGA 73416              A
                                TCAGCAGGTATTTATTGA CAC
                                |||||||||||||||||| |||
                                AGTCGTTCGTAAATAACT GTG
                                          C
GAM491  PTGFRN   3'  GTGTTCAGAGAGCTGCTGA   67192       GTA  A
                                TCAGCAG   TTT TTGAACAC
                                |||||||   ||| ||||||||
                                AGTCGTC   GAG GACTTGTG
                                   ___  A
GAM491  PX19     3'  TCAATAAATACTTGTTGA    25088
                                TCAGCAGGTATTTATTGA
                                ||||||||||||||||||
                                AGTTGTTCATAAATAACT

GAM491  RABGGTB  3'  TGTTCAATAACTGAGCT     15930     A_  ATT
                                AGC  GGT   TATTGAACA
                                |||  |||   |||||||||
                                TCG  TCA   ATAACTTGT
                                  AG  ___
GAM491  RNMT     3'  GTGTTCAATATGTATTGCTGA  13724       G   T
                                TCAGCAG TAT TATTGAACAC
                                ||||||| ||| ||||||||||
                                AGTCGTT ATG ATAACTTGTG
                                   _  T
GAM491  RPLP1    3'  TGTTCAATAAAAAGCTGA    6402       AGGTA
                                TCAGC    TTTATTGAACA
                                |||||    ||||||||||
                                AGTCG    AAATAACTTGT
                                  AA___
GAM491  SAA4     3'  GTGTTCAATAAATGTTTGT   21493     GG
                                GCA  TATTTATTGAACAC
                                |||  ||||||||||||||
                                TGT  GTAAATAACTTGTG
                                  TT
GAM491  SLC17A5  3'  GTGTTCAACACTACGTGT    24893     G   TTTA
                                GCA GTA    TTGAACAC
                                ||| |||    ||||||||
                                TGT CAT    AACTTGTG
                                  G   CAC_
GAM491  SLC18A1  3'  TGTTCATACTTGCT       11751        TTTAT
                                AGCAGGTA    TGAACA
                                ||||||||    ||||||
                                TCGTTCAT    ACTTGT
                                     _____
GAM491  SLC1A4   3'  TGTTTTTCCAATTACCTGCTGA 11719          TTTATT_
                                TCAGCAGGTA      GAACA
                                ||||||||||      |||||
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                                AGTCGTCCAT      TTTGT
                                      TAACCTT
GAM491  SLC20A2  3'  TTCAATAAATCTTGT      22177      T
                                GCAGG ATTTATTGAA
                                ||||| ||||||||||
                                TGTTC TAAATAACTT
                                  _
GAM491  SLC8A1   3'  TGTTCACTTACCTGCTGA    40840          TTTAT
                                TCAGCAGGTA    TGAACA
                                ||||||||||    ||||||
                                AGTCGTCCAT    ACTTGT
                                      TC___
GAM491  SOD3     5'  CAATAAACATTTGTTG      11860        A
                                CAGCAGGT TTTATTG
                                |||||||| |||||||
                                GTTGTTTA AAATAAC
                                     C
GAM491  SPAG11   3'  GTGTTCAATAAATATTTGTTGA 54244
                                TCAGCAGGTATTTATTGAACAC
                                ||||||||||||||||||||||
                                AGTTGTTTATAAATAACTTGTG

GAM491  SPAG11   3'  GTGTTCAATAAATATTTGTTGA 54250
                                TCAGCAGGTATTTATTGAACAC
                                ||||||||||||||||||||||
                                AGTTGTTTATAAATAACTTGTG

GAM491  SPAG11   3'  GTGTTCAATAAATATTTGTTGA 54252
                                TCAGCAGGTATTTATTGAACAC
                                ||||||||||||||||||||||
                                AGTTGTTTATAAATAACTTGTG

GAM491  SPAG11   3'  GTGTTCAATAAATATTTGTTGA 33259
                                TCAGCAGGTATTTATTGAACAC
                                ||||||||||||||||||||||
                                AGTTGTTTATAAATAACTTGTG

GAM491  WDR8     3'  AATAAATACTTGCTGA      35158
                                TCAGCAGGTATTTATT
                                ||||||||||||||||
                                AGTCGTTCATAAATAA

GAM491  YWHAZ    3'  TGCTCAATAAATATTGATGA   12707     GCA          A
                                TCA   GGTATTTATTGA CA
                                |||   |||||||||||| ||
                                AGT   TTATAAATAACT GT
                                  AG_          C
GAM491  Z39IG    3'  GTGCTCAATAAATATCT     23436            A
                                AGGTATTTATTGA CAC
                                |||||||||||| |||
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                                TCTATAAATAACT GTG
                                      C
GAM491  ZNF2     3'  GTGCTCAATAAATATTTATATG 40807     GC_          A
              A                  TCA   AGGTATTTATTGA CAC
                                 |||   |||||||||||||| |||
                                 AGT   TTTATAAATAACT GTG
                                   ATA           C
GAM491  AFAP     3'  TGTTCAATAAATATAGTT    41310     AG
                                 AGC  GTATTTATTGAACA
                                 |||  ||||||||||||||
                                 TTG  TATAAATAACTTGT
                                   A_
GAM491  AKAP6    3'  TTCAATAAAAATTTACTGA   14998      C   A
                                 TCAG AGGT TTTATTGAA
                                 |||| |||| |||||||||
                                 AGTC TTTA AAATAACTT
                                    A   A
GAM491  ARHGEF9  3'  GTGTTCAATGGGACCTGCTG  30819         A
                                 CAGCAGGT TTTATTGAACAC
                                 ||||||||| ||||||||||||
                                 GTCGTCCA GGGTAACTTGTG
                                       _
GAM491  cerk     3'  TGTTCAATAAGAAACC      42854     A_
                                 GGT  TTTATTGAACA
                                 |||  ||||||||||
                                 CCA  GAATAACTTGT
                                   AA
GAM491  DCLRE1A  5'  GTGTTTGGGATACCTGTT    69166          TA TG
                                 AGCAGGTATT  T  AACAC
                                 ||||||||||  |  |||||
                                 TTGTCCATAG  G  TTGTG
                                       __ GT
GAM491  DKFZp434E0519 5'  GTAACATACCTGCTGA      49992           _
                                 TCAGCAGGTAT TTAT
                                 |||||||||| ||||
                                 AGTCGTCCATA AATG
                                       C
GAM491  DKFZp547O146 3'  GTGTTGCCAAAGATACCTGCTG 39567            A  __
              A                  TCAGCAGGTATTT TTG  AACAC
                                 |||||||||||| |||  |||||
                                 AGTCGTCCATAGA AAC  TTGTG
                                       _  CG
GAM491  DKFZp761O17121 3'  GTGTTCAACAGTGCATGT    50143     G    TA
                                 GCA GTATT  TTGAACAC
                                 ||| |||||  ||||||||
                                 TGT CGTGA  AACTTGTG
                                   A    C_
GAM491  E2F6     3'  GTGCTCAATAAATGTCTG    8716      GT       A
                                 CAG  ATTTATTGA CAC
                                 |||  ||||||||| |||
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                                GTC  TAAATAACT GTG
                                  TG       C
GAM491  ERO1L    3'  CAATAAATATTTGTTGG    27429
                                TCAGCAGGTATTTATTG
                                |||||||||||||||||
                                GGTTGTTTATAAATAAC

GAM491  FLJ10314 5'  GTGTTCAAGGCTACCCAGTGA  36015    GCA   TTTA
                                TCA   GGTA   TTGAACAC
                                |||   ||||   ||||||||
                                AGT   CCAT   AACTTGTG
                                  GAC   CGG_
GAM491  FLJ11164 3'  CAGAAAACTCCTGCTGA    37122       TA   A
                                TCAGCAGG  TTT TTG
                                ||||||||  ||| |||
                                AGTCGTCC  AAA GAC
                                     TC   A
GAM491  FLJ13340 3'  GTTTTTTATCCTGCTGA    54110       TATT  TT
                                TCAGCAGG   TA  GAAC
                                ||||||||   ||  ||||
                                AGTCGTCC   AT  TTTG
                                     T___  TT
GAM491  FLJ14050 3'  GTGCTCAATAAACGATAACTGC 60328     G   ___    A
                                GCAG TATT   TATTGA CAC
                                |||| ||||   |||||| |||
                                CGTC ATAG   ATAACT GTG
                                  A   CAA    C
GAM491  FLJ14437 3'  TTCAATAAATATTTGCTGG   50831
                                TCAGCAGGTATTTATTGAA
                                ||||||||||||||||||
                                GGTCGTTTATAAATAACTT

GAM491  FLJ14675 3'  CATTGGAAAACCTGCTGA    51518       A   AT_
                                TCAGCAGGT TTT   TG
                                ||||||||| |||   ||
                                AGTCGTCCA AAG   AC
                                     A   GTT
GAM491  FLJ20132 3'  GTGCTCAATAAATTGCT    34607     GGT       A
                                AGCA   ATTTATTGA CAC
                                ||||   ||||||||| |||
                                TCGT   TAAATAACT GTG
                                  ___        C
GAM491  GOA      3'  TGCTCAATAAACACTTGTTGA  78077       A      A
                                TCAGCAGGT TTTATTGA CA
                                ||||||||| |||||||| ||
                                AGTTGTTCA AAATAACT GT
                                     C      C
GAM491  GREAT    5'  TCAGAACTCCTGCTGA     55484       TA   AT
                                TCAGCAGG  TTT  TGA
                                ||||||||  |||  |||
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                                AGTCGTCC  AAG  ACT
                                    TC  __
GAM491  KIAA0014  3'  GTGCCCAGCTGGTTCCTGCTGA 27850        T  TA  AA
                                TCAGCAGG ATT  TTG  CAC
                                |||||||| |||  |||  |||
                                AGTCGTCC TGG  GAC  GTG
                                    T  TC  CC
GAM491  KIAA0227  3'  GTGTTCAACAAATGCTTGT   60701          A
                                GCAGGTATTT TTGAACAC
                                |||||||||| ||||||||
                                TGTTCGTAAA AACTTGTG
                                     C
GAM491  KIAA0322  3'  CAAGAAAACACCTGCTG    92750        A  A_
                                CAGCAGGT TTT  TTG
                                |||||||| |||  |||
                                GTCGTCCA AAA  AAC
                                    C  AG
GAM491  KIAA0377  3'  GTGCTCAATAAATATAAACT  27797    CAG        A
                                AG  GTATTTATTGA CAC
                                ||  |||||||||||| |||
                                TC  TATAAATAACT GTG
                                 AAA         C
GAM491  KIAA0637  3'  GTTCAATGACACGCTGA    29239      AG  ATT
                                TCAGC  GT  TATTGAAC
                                |||||  ||  ||||||||
                                AGTCG  CA  GTAACTTG
                                   CA  ____
GAM491  KIAA1077  3'  GTTTTTAAATACCAGCT    72910    A      TT
                                AGC GGTATTTA  GAAC
                                ||| ||||||||  ||||
                                TCG CCATAAAT  TTTG
                                  A       T_
GAM491  KIAA1077  5'  TGTTCTGAATACCTCTGA    72912    C       TT
                                TCAG AGGTATTTA  GAACA
                                |||| |||||||||  |||||
                                AGTC TCCATAAGT  CTTGT
                                   _       __
GAM491  KIAA1524  5'  TTCAGTTGACCTACTGA    73456    C   ATTT
                                TCAG AGGT   ATTGAA
                                |||| ||||   ||||||
                                AGTC TCCA   TGACTT
                                  A  GT__
GAM491  MGC11316  3'  GTGCCATTAAATACCAACTGA  51942    CA      T  A_
                                TCAG  GGTATTTA TG  AC
                                ||||  |||||||| ||  ||
                                AGTC  CCATAAAT AC  TG
                                  AA       T  CG
GAM491  MGC12679  3'  TCAATAAATATTGAATGA    51207    GCA
                                TCA  GGTATTTATTGA
                                |||  ||||||||||||
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                                AGT   TTATAAATAACT
                                  AAG
GAM491  MGC13071 3'  GTTCAATAAACATTAGC     51089    AG  A
                                GC  GT TTTATTGAAC
                                ||  || ||||||||||
                                CG  TA AAATAACTTG
                                 AT  C
GAM491  MGC26590 3'  TGTTCAATAAAAGTTTTGC    56288      TA_
                                GCAGG   TTTATTGAACA
                                |||||   ||||||||||||
                                CGTTT   AAATAACTTGT
                                   TGA
GAM491  MGC2747  3'  TTCAGTGTTACTTGCTGA    44091         TT
                                TCAGCAGGTA  TATTGAA
                                ||||||||||  |||||||
                                AGTCGTTCAT  GTGACTT
                                      T_
GAM491  MGC3248  3'  GTGTTCAATAAAGAACC     50656     A_
                                GGT  TTTATTGAACAC
                                |||  ||||||||||||
                                CCA  AAATAACTTGTG
                                  AG
GAM491  MGC4606  3'  TGTCCGTACCTGCTGG      44510          TTATT A
                                TCAGCAGGTAT    G ACA
                                ||||||||||     | |||
                                GGTCGTCCATG    C TGT
                                      _____ C
GAM491  MYT1     3'  GTGCTCAATGAGGGCCGCTGA  15781      A  A      A
                                TCAGC GGT TTTATTGA CAC
                                ||||| ||| |||||||| |||
                                AGTCG CCG GAGTAACT GTG
                                   _  G       C
GAM491  NTSR2    3'  TGCTCAATAAATTTTTGCTGG  24718        T       A
                                TCAGCAGG ATTTATTGA CA
                                |||||||| ||||||||| ||
                                GGTCGTTT TAAATAACT GT
                                     T       C
GAM491  NXP-2    3'  TGTTTTGAAATACCTGT     71110          ATT
                                GCAGGTATTT   GAACA
                                ||||||||||   |||||
                                TGTCCATAAA   TTTGT
                                     GT_
GAM491  PELI1    5'  GTGTTCAAGAGGACTGCTGA  40279       GTA  A
                                TCAGCAG   TTT TTGAACAC
                                |||||||   ||| ||||||||
                                AGTCGTC   GAG AACTTGTG
                                   AG_  _
GAM491  PRSC     3'  TGCTCAATCGTGCACTGC    21673     _   TT    A
                                GCAG GTAT  ATTGA CA
                                |||| ||||  ||||| ||
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                                CGTC CGTG  TAACT GT
                                  A   C_    C
GAM491  SC65     3'  GTGCTCAATAAATGTTTGT   21295     GG        A
                                GCA  TATTTATTGA CAC
                                |||  |||||||||| |||
                                TGT  GTAAATAACT GTG
                                  TT        C
GAM491  SPAG7    3'  TTCAATAAATACTGTT      16885      G
                                AGCAG TATTTATTGAA
                                ||||| ||||||||||
                                TTGTC ATAAATAACTT
                                  _
GAM491  TBDN100  3'  GTTTTTTATCCTGCTGA     46959        TATT  TT
                                TCAGCAGG    TA  GAAC
                                ||||||||    ||  ||||
                                AGTCGTCC    AT  TTTG
                                     T___  TT
GAM491  TBX19    3'  GTGCCCAATAAACATTTGCTGA 17652         A      AA
                                TCAGCAGGT TTTATTG  CAC
                                |||||||||| |||||||  |||
                                AGTCGTTTA AAATAAC  GTG
                                     C      CC
GAM491  TIP-1    3'  TCAATAAAAATGCTGG      27506       GGTA
                                TCAGCA    TTTATTGA
                                ||||||    ||||||||
                                GGTCGT    AAATAACT
                                   AA__
GAM491  TRIM26   3'  GTGCTCAATAAAGACTTGTTGA 12893         A       A
                                TCAGCAGGT TTTATTGA CAC
                                |||||||||| |||||||| |||
                                AGTTGTTCA AAATAACT GTG
                                     G       C
GAM491  TRPC3    3'  GTGCTCAATAAATGTTGA    12396       GGTA      A
                                TCAGCA    TTTATTGA CAC
                                ||||||    |||||||| |||
                                AGTTGT    AAATAACT GTG
                                   ____       C
GAM491  VPS33B   3'  GTGTCCACCAACTACCTGCT   37906        T  AT  A
                                AGCAGGTA TT  TG ACAC
                                |||||||| ||  || ||||
                                TCGTCCAT AA  AC TGTG
                                     C  CC  C
GAM491  ZFP95    3'  TGCCCAATAAATATTTGTTGA  27382             AA
                                TCAGCAGGTATTTATTG  CA
                                ||||||||||||||||  ||
                                AGTTGTTTATAAATAAC  GT
                                          CC
GAM491  ZFP95    3'  TGCCCAATAAATATTTGTTGA  59026             AA
                                TCAGCAGGTATTTATTG  CA
                                ||||||||||||||||  ||
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                                AGTTGTTTATAAATAAC  GT
                                          CC
GAM491   LOC126364 3'  GTGCTCAATAAATGCTT     75696           A
                                AGGTATTTATTGA CAC
                                |||||||||||| |||
                                TTCGTAAATAACT GTG
                                      C
GAM491   LOC142893 5'  GTGATTAAAATACCTGT     82878         AT   A
                                GCAGGTATTT  TGA CAC
                                ||||||||||  ||| |||
                                TGTCCATAAA  ATT GTG
                                      __  A
GAM491   LOC142955 5'  GTGTTCAATAAATAATTTTTGA 76448     CAGG
                                TCAG    TATTTATTGAACAC
                                ||||    ||||||||||||||
                                AGTT    ATAAATAACTTGTG
                                  TTTA
GAM491   LOC145622 5'  TGCTCAATAGGATTACGCTGA  77317      AG  __      A
                                TCAGC  GTA  TTTATTGA CA
                                |||||  |||  |||||||| ||
                                AGTCG  CAT  GGATAACT GT
                                   __  TA       C
GAM491   LOC145660 5'  GTGTTCAATAAACATCTCT    77324    C    A
                                AG AGGT TTTATTGAACAC
                                || |||| ||||||||||||
                                TC TCTA AAATAACTTGTG
                                 _   C
GAM491   LOC145739 3'  TCAATAAATATTGCT       77442       G
                                AGCAG TATTTATTGA
                                ||||| ||||||||||
                                TCGTT ATAAATAACT
                                  _
GAM491   LOC146714 5'  TTCATTGAGCACCTGCTG    83744         A   T
                                CAGCAGGT TTTA TGAA
                                |||||||| |||| ||||
                                GTCGTCCA GAGT ACTT
                                     C   T
GAM491   LOC146802 3'  TGTTCAACACCTCTGA      78138      C   ATTTA
                                TCAG AGGT    TTGAACA
                                |||| ||||    |||||||
                                AGTC TCCA    AACTTGT
                                  _   C____
GAM491   LOC147040 3'  GTGTCTGTGGTATACCTGT   78237        _   T  A
                                GCAGGTAT TTAT GA CAC
                                |||||||| |||| || |||
                                TGTCCATA GGTG CT GTG
                                     T   T  _
GAM491   LOC148936 3'  TCAATAAATATTGGTT      84302     AG
                                AGC  GTATTTATTGA
                                |||  ||||||||||
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                                TTG  TATAAATAACT
                                  GT
GAM491   LOC148938 3'  TCAATAAATATTGGTT      84283      AG
                                AGC  GTATTTATTGA
                                |||  ||||||||||
                                TTG  TATAAATAACT
                                  GT
GAM491   LOC150035 5'  GTGTCCAACTGAAACCTGT    84810        A  TA   A
                                GCAGGT TT  TTG ACAC
                                |||||| ||  ||| ||||
                                TGTCCA AG  AAC TGTG
                                    A  TC   C
GAM491   LOC150142 5'  GTGTTGGAATAGCTGCTGA    79579        G     ATTG
                                TCAGCAG TATTT    AACAC
                                ||||||| |||||    |||||
                                AGTCGTC ATAAG    TTGTG
                                     G     G___
GAM491   LOC150630 3'  GTGCTCAATAAATACTGAGTGA 85110      GCA          A
                                TCA   GGTATTTATTGA CAC
                                |||   |||||||||||| |||
                                AGT   TCATAAATAACT GTG
                                  GAG           C
GAM491   LOC150978 3'  GTGTTCAATAAAAAGCTGA    80086       AGGTA
                                TCAGC     TTTATTGAACAC
                                |||||     ||||||||||||
                                AGTCG     AAATAACTTGTG
                                   AA___
GAM491   LOC151465 3'  TGTTCAATGTCCTCTGA      62780      C   TATT
                                TCAG AGG    TATTGAACA
                                |||| |||    |||||||||
                                AGTC TCC    GTAACTTGT
                                  _   T___
GAM491   LOC152225 5'  GTGCTCAATAAAAGCTTGTT   85595        A       A
                                AGCAGGT TTTATTGA CAC
                                ||||||| |||||||| |||
                                TTGTTCG AAATAACT GTG
                                     A       C
GAM491   LOC152453 3'  GTGTTGGTGCATACCTGT     80603         T   TG A
                                GCAGGTAT TAT  A CAC
                                |||||||| |||  | |||
                                TGTCCATA GTG  T GTG
                                     C   GT _
GAM491   LOC154562 3'  TCAATAAATACTTGTT       81093
                                AGCAGGTATTTATTGA
                                ||||||||||||||||
                                TTGTTCATAAATAACT

GAM491   LOC154739 5'  TCAGCGGGCCACTTGCTGA    86240         A_  TA
                                TCAGCAGGT  TT  TTGA
                                |||||||||  ||  ||||
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                                AGTCGTTCA  GG  GACT
                                     CC  GC
GAM491   LOC157660 3'  TCAACAAATATTTGTTGA    86511           A
                                TCAGCAGGTATTT TTGA
                                |||||||||||| ||||
                                AGTTGTTTATAAA AACT
                                     C
GAM491   LOC158310 3'  GTGCTCAATAAATATCTGCCGA 86761    A          A
                                TC GCAGGTATTTATTGA CAC
                                || ||||||||||||||| |||
                                AG CGTCTATAAATAACT GTG
                                 C           C
GAM491   LOC163404 3'  GTGTTCAACAAAAATGTGATGA 82129    G  G  A   A
                                TCA CA GT TTT TTGAACAC
                                ||| || || ||| ||||||||
                                AGT GT TA AAA AACTTGTG
                                  A  G  A   C
GAM491   LOC197407 3'  CATTCAATACTTGTTGA     88058          TAT
                                TCAGCAGGTATT   TG
                                ||||||||||||   ||
                                AGTTGTTCATAA   AC
                                     CTT
GAM491   LOC197408 5'  CATTCAATACTTGTTGA     89748          TAT
                                TCAGCAGGTATT   TG
                                ||||||||||||   ||
                                AGTTGTTCATAA   AC
                                     CTT
GAM491   LOC203068 3'  TCAATAAATACTTGTT      89256
                                AGCAGGTATTTATTGA
                                ||||||||||||||||
                                TTGTTCATAAATAACT

GAM491   LOC203286 3'  TGTCCAAGTCCCTGCTGG    90505        TATTTA   A
                                TCAGCAGG     TTG ACA
                                ||||||||     ||| |||
                                GGTCGTCC     AAC TGT
                                     CTG___   C
GAM491   LOC220430 5'  TTCAAAATACCTGC        94337          AT
                                GCAGGTATTT  TGAA
                                |||||||||  ||||
                                CGTCCATAAA  ACTT
                                     __
GAM491   LOC220930 5'  GTGCTCAATAAATTTATGCT   93133      GGT       A
                                AGCA   ATTTATTGA CAC
                                ||||   ||||||||| |||
                                TCGT   TAAATAACT GTG
                                  ATT        C
GAM491   LOC222681 5'  TCTGTTGATCCTGCTGA     92854        T   T  T
                                TCAGCAGG ATT AT GA
                                |||||||| ||| || ||
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                                AGTCGTCC TAG TG CT
                                     _  T  T
GAM491  LOC253681 3'  GTGTCTGTGGTATACCTGT   95134        _   T  A
                                GCAGGTAT TTAT GA CAC
                                |||||||| |||| || |||
                                TGTCCATA GGTG CT GTG
                                     T   T  _
GAM491  LOC253805 3'  GTGTTGAGATAATACCTGT   96434        TA  G
                                GCAGGTATT  TT AACAC
                                |||||||||  || |||||
                                TGTCCATAA  GA TTGTG
                                     TA  G
GAM491  LOC255104 3'  TGGTGAATACATGCTGA     95400       G
                                TCAGCA GTATTTATTG
                                |||||| ||||||||||
                                AGTCGT CATAAGTGGT
                                   A
GAM491  LOC256087 3'  GTGTTCAATAAATGTTT     95116   GG
                                A  TATTTATTGAACAC
                                |  ||||||||||||||
                                T  GTAAATAACTTGTG
                                 TT
GAM491  LOC256338 3'  TCAATAAATAATTGTTGA    94611       G
                                TCAGCAG TATTTATTGA
                                ||||||| ||||||||||
                                AGTTGTT ATAAATAACT
                                     A
GAM491  LOC257494 3'  GTGCTCAATAAAGACTTGTTGA 97797        A      A
                                TCAGCAGGT TTTATTGA CAC
                                ||||||||| |||||||| |||
                                AGTTGTTCA AAATAACT GTG
                                     G       C
GAM491  LOC257507 5'  TCTGTTGATCCTGCTGA     97776        T  T  T
                                TCAGCAGG ATT AT GA
                                |||||||| ||| || ||
                                AGTCGTCC TAG TG CT
                                     _  T  T
GAM491  LOC257625 5'  TCTGTTGATCCTGCTGA     97907        T  T  T
                                TCAGCAGG ATT AT GA
                                |||||||| ||| || ||
                                AGTCGTCC TAG TG CT
                                     _  T  T
GAM491  LOC50999  3'  GTGCAAGTAATCCTGCTGA   32102        T  TA  A
                                TCAGCAGG ATT  TTG AC
                                |||||||| |||  ||| ||
                                AGTCGTCC TAA  AAC TG
                                     _  TG  G
GAM491  LOC91628  3'  GTGCTCAATAAATTGTAGCTG  66761     AGGT       A
                                CAGC   ATTTATTGA CAC
                                ||||   ||||||||| |||
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                                GTCG   TAAATAACT GTG
                                  ATGT       C
GAM491  LOC91907  3'  GTGTGGCAATATCTGCTGA   67496          TATTGA
                                TCAGCAGGTATT     ACAC
                                ||||||||||||     ||||
                                AGTCGTCTATAA     TGTG
                                      CGG___
GAM491  LOC92755  3'  TCAATAAATACTTGTT     70502
                                AGCAGGTATTTATTGA
                                ||||||||||||||||
                                TTGTTCATAAATAACT

GAM492  DBT      3'  TCAGCCAGGTGTGATG     8612         CA  CT
                                CATCACACC  GC  TGA
                                |||||||||  ||  |||
                                GTAGTGTGG  CG  ACT
                                     AC  __
GAM492  DBT      3'  CCAAAAAGCCAAGTGTGGTG  8609         CCA  C  GA
                                CATCACAC   GC TT  GG
                                ||||||||   || ||  ||
                                GTGGTGTG   CG AA  CC
                                     AAC  A  AA
GAM492  DDX3     3'  CCTTGGCACACAGGTGTGAT  7223         CA___  TT
                                ATCACACC    GCC  GAGG
                                ||||||||    |||  ||||
                                TAGTGTGG    CGG  TTCC
                                     ACACA  __
GAM492  DGKI     5'  AAATCAATTCAGGCCAAGTGTG 16340        CCA   T  __
            GTG                   CATCACAC   GCCT GAG  GATTT
                                ||||||||   |||| |||  |||||
                                GTGGTGTG   CGGA CTT  CTAAA
                                     AAC   _  AA
GAM492  EFG2     5'  TTCAAGGCCAGGCATGGTG   50479      CA  CA
                                CATCA  CC  GCCTTGAG
                                |||||  ||  ||||||||
                                GTGGT  GG  CGGAACTT
                                   AC  AC
GAM492  LPP      3'  TAAGGCCAGGTGTGGTG     18750        CA
                                CATCACACC  GCCTTG
                                |||||||||  ||||||
                                GTGGTGTGG  CGGAAT
                                     AC
GAM492  RANBP2L1 3'  TTTCAAGGCCAGGTGTGGTG  17316        CA
                                CATCACACC  GCCTTGAGG
                                |||||||||  |||||||||
                                GTGGTGTGG  CGGAACTTT
                                     AC
GAM492  SIGLEC11 3'  AAGGCTGGGCATGGTG     53541      CA
                                CATCA  CCCAGCCTT
                                |||||  |||||||||
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                                GTGGT  GGGTCGGAA
                                   AC
GAM492  SLC14A1  3'  AGGGCTGAGTGTGGTG      31835         C
                                CATCACAC CAGCCTT
                                |||||||| |||||||
                                GTGGTGTG GTCGGGA
                                     A
GAM492  SLC16A2  3'  AAATCCTCAAGGAGTTTGG   21496     ___
                                CCAG   CCTTGAGGATTT
                                ||||   ||||||||||||
                                GGTT   GGAACTCCTAAA
                                   TGA
GAM492  ATP1B4   3'  AAATCTGCCTAAGCCGGGTGTG 23810          A  CTTGA_
           GTG                    CATCACACCC GC     GGATTT
                                |||||||||| ||     ||||||
                                GTGGTGTGGG CG     TCTAAA
                                      C  AATCCG
GAM492  C20orf121 3'  TGAGGCTGGATGAAATG     44278     CA  C
                                CAT  CA CCAGCCTTG
                                |||  || |||||||||
                                GTA  GT GGTCGGAGT
                                  AA  A
GAM492  C22orf19  3'  AAATAAGATGGGCTGGGCACAG 13416     A___       TGAGG
           TG                    CAC    CCCAGCCT    ATTT
                                |||    ||||||||    ||||
                                GTG    GGGTCGGG    TAAA
                                  ACAC       TAGAA
GAM492  C22orf19  3'  TCAGCCAGGTGTGGTG      13433         CA  CT
                                CATCACACC  GC  TGA
                                |||||||||  ||  |||
                                GTGGTGTGG  CG  ACT
                                     AC  __
GAM492  CFLAR    3'  CCAAAAGGCTGGGCGTAGTG   13928     C  A       GA
                                CAT AC CCCAGCCTT  GG
                                ||| || |||||||||  ||
                                GTG TG GGGTCGGAA  CC
                                  A  C        AA
GAM492  DKFZP564M182 3'  TGAGGCTGGGCGTGGTG     78044       A
                                CATCAC CCCAGCCTTG
                                |||||| ||||||||||
                                GTGGTG GGGTCGGAGT
                                   C
GAM492  ET       3'  AAATAGCAAAGCTGGGTGTGGT 44219           C   AGG
           G                     CATCACACCCAGC TTG   ATTT
                                |||||||||||| |||   ||||
                                GTGGTGTGGGTCG AAC   TAAA
                                      A   GA_
GAM492  FLJ00060  3'  TTCAAGGCTGGGTGCGGTG   61107      A
                                CATC CACCCAGCCTTGAG
                                |||| ||||||||||||
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                                GTGG GTGGGTCGGAACTT
                                  C
GAM492  FLJ10738 3' AAATCCTTTTCTGGACATGA  36526    CAC   CCTT
                                TCA  CCAG   GAGGATTT
                                |||  ||||   ||||||||
                                AGT  GGTC   TTCCTAAA
                                  ACA   TT__
GAM492  FLJ13153 5' AAATCCTCAGGGGAACTGATG 45554      CACCCAG
                                CATCA     CCTTGAGGATTT
                                |||||     ||||||||||||
                                GTAGT     GGGACTCCTAAA
                                   CAAG___
GAM492  FLJ13193 3' TTTTCAAGCTGGGCGTAGTG  49777    C A    C
                                CAT AC CCCAGC TTGAGGA
                                ||| || |||||| |||||||
                                GTG TG GGGTCG AACTTTT
                                  A C    _
GAM492  FLJ13448 3' CTTTGGGCTGGGCACAGTG   47136    A___      T
                                CAC   CCCAGCCT GAG
                                |||   |||||||| |||
                                GTG   GGGTCGGG TTC
                                  ACAC      T
GAM492  FLJ13842 3' AAATCCTCAATGAGTGTGATG 44981       C GCC
                                CATCACAC CA  TTGAGGATTT
                                |||||||| ||  ||||||||||
                                GTAGTGTG GT  AACTCCTAAA
                                    A ___
GAM492  FLJ14117 3' TCAGCTGGGTGTGGTG     42916          CT
                                CATCACACCCAGC  TGA
                                ||||||||||||  |||
                                GTGGTGTGGGTCG  ACT
                                       __
GAM492  FLJ20059 3' AAATATTTCAGGCTGGGCGTGG 34445      A      T  _
          TG                    CATCAC CCCAGCCT GAGG ATTT
                                |||||| |||||||| |||| ||||
                                GTGGTG GGGTCGGA CTTT TAAA
                                   C      _   A
GAM492  FLJ23499 3' AAATCTTGGTGGGCTGGGTACG 42815     AC      TG_
          GTG                    CATC  ACCCAGCCT   AGGATTT
                                ||||  |||||||||   |||||||
                                GTGG  TGGGTCGGG   TTCTAAA
                                  CA       TGG
GAM492  FLJ25012 3' GAGGCCAGGTGTGATG     58091        CA
                                CATCACACC  GCCTT
                                |||||||||  |||||
                                GTAGTGTGG  CGGAG
                                     AC
GAM492  FLJ30681 3' CCTCTTGGCCGGGTGTGGT   91785        A   TT
                                ATCACACCC GCC  GAGG
                                |||||||| |||  ||||
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                                TGGTGTGGG CGG  CTCC
                                      C   TT
GAM492  JAM1     3' CTGGAGGCTGGGCGCAGTG   57926    A___      G
                                CAC    CCCAGCCTT AG
                                |||    ||||||||| ||
                                GTG    GGGTCGGAG TC
                                  ACGC       G
GAM492  JAM1     3' CTGGAGGCTGGGCGCAGTG   57952    A___      G
                                CAC    CCCAGCCTT AG
                                |||    ||||||||| ||
                                GTG    GGGTCGGAG TC
                                  ACGC       G
GAM492  JAM1     3' CTGGAGGCTGGGCGCAGTG   57897    A___      G
                                CAC    CCCAGCCTT AG
                                |||    ||||||||| ||
                                GTG    GGGTCGGAG TC
                                  ACGC       G
GAM492  JAM1     3' CTGGAGGCTGGGCGCAGTG   33759    A___      G
                                CAC    CCCAGCCTT AG
                                |||    ||||||||| ||
                                GTG    GGGTCGGAG TC
                                  ACGC       G
GAM492  KIAA0336 3' TTTCAAGGCCAGGTGTGGTG  27591        CA
                                CATCACACC  GCCTTGAGG
                                |||||||||  |||||||||
                                GTGGTGTGG  CGGAACTTT
                                     AC
GAM492  KIAA0355 3' GAGGCTGGGCGTGGTG     28027      A
                                CATCAC CCCAGCCTT
                                |||||| |||||||||
                                GTGGTG GGGTCGGAG
                                   C
GAM492  KIAA0447 3' AAGACTGGGTGTGGTG     71661          C
                                CATCACACCCAG CTT
                                |||||||||||| |||
                                GTGGTGTGGGTC GAA
                                       A
GAM492  KIAA0530 3' AAATCCTTTGTGAATGTGAT  70864      CC  GCCTT
                                ATCACA  CA    GAGGATTT
                                ||||||  ||    ||||||||
                                TAGTGT  GT    TTCCTAAA
                                   AA  GT___
GAM492  KIAA1277 3' CTCTGGCTGGGTGTG      64453         TT
                                CACACCCAGCC  GAG
                                ||||||||||  |||
                                GTGTGGGTCGG  CTC
                                       T_
GAM492  KIAA1649 5' CCACAATTAGCCAGGTGTGGTG 50250        CA  C__   A
                                CATCACACC  GC   TTG GG
                                |||||||||  ||   ||| ||
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                                GTGGTGTGG  CG   AAC CC
                                     AC  ATT   A
GAM492  KIAA1715  3'  GGGGCCAGGTGTGGTG     68124         CA
                                CATCACACC  GCCTT
                                |||||||||  |||||
                                GTGGTGTGG  CGGGG
                                     AC
GAM492  KIAA1879  3'  CCAGGCCAAGTGTGGTG     73564         CCA   TGA
                                CATCACAC   GCCT   GG
                                ||||||||   ||||   ||
                                GTGGTGTG   CGGA   CC
                                     AAC   ___
GAM492  KIAA1975  5'  AAATCCTTGTTAGGTTTGATG  73966      C   C   CTT
                                CATCA ACC AGC   GAGGATTT
                                ||||| ||| |||   ||||||||
                                GTAGT TGG TTG   TTCCTAAA
                                   T   A  ___
GAM492  LIM       3'  AGGGCCAGGTGTGGTG      21301         CA
                                CATCACACC  GCCTT
                                |||||||||  |||||
                                GTGGTGTGG  CGGGA
                                     AC
GAM492  MGC12538  3'  AAATCTTCAAGCTGAGTG    51239     C   C
                                CAC CAGC TTGAGGATTT
                                ||| |||| ||||||||||
                                GTG GTCG AACTTCTAAA
                                  A   _
GAM492  MGC13053  3'  TTTAAGGCCGGGCACGGTG   51135      ACA   A
                                CATC   CCC GCCTTGAG
                                ||||   ||| ||||||||
                                GTGG   GGG CGGAATTT
                                   CAC   C
GAM492  MGC39350  3'  CCAGGCCAGGTGTGATG     58653         CA   TGA
                                CATCACACC  GCCT   GG
                                |||||||||  ||||   ||
                                GTAGTGTGG  CGGA   CC
                                     AC   ___
GAM492  OS4       3'  AAATCCTCAAAGCGTGGACGTG 19174       __  _  C
            TG                    CACAC  CCA GC TTGAGGATTT
                                |||||  ||| || ||||||||||
                                GTGTG  GGT CG AACTCCTAAA
                                   CA   G  A
GAM492  OSBPL11   3'  AAATCCTCAAAATGAGT     42889     C  GCC
                                AC CA   TTGAGGATTT
                                || ||   ||||||||||
                                TG GT   AACTCCTAAA
                                 A  AA_
GAM492  PAFAH2    3'  AAGGCTGGGCGTGGTG      4757         A
                                CATCAC CCCAGCCTT
                                |||||| |||||||||
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                                GTGGTG GGGTCGGAA
                                   C
GAM492  PRO0233  3' AATCCTCTTAGGATGTGTG  26114     CCAG  T_
                                CACAC   CCT  GAGGATT
                                |||||   |||  |||||||
                                GTGTG   GGA  CTCCTAA
                                   TA__  TT
GAM492  PRO2730  3' CCTCAAGGCTGGGCGCGGTG  47413    ACA
                                CATC  CCCAGCCTTGAGG
                                ||||  ||||||||||||
                                GTGG  GGGTCGGAACTCC
                                  CGC
GAM492  Rpo1-2   3' AAGGCTGGGTGTGGTG     38695
                                CATCACACCCAGCCTT
                                ||||||||||||||||
                                GTGGTGTGGGTCGGAA

GAM492  SCIN    3' TTAAGGCTGGGCGCGGTG    52427     ACA
                                CATC  CCCAGCCTTGA
                                ||||  ||||||||||
                                GTGG  GGGTCGGAATT
                                  CGC
GAM492  TTY7    5' AAATCCCCCATGCCCAGGTGTG 49175        CA_  CT  A_
           GTG                   CATCACACC  GC  TG  GGATTT
                                |||||||||  ||  ||  ||||||
                                GTGGTGTGG  CG  AC  CCTAAA
                                     ACC  T_  CC
GAM492  TXNL2    3' AAGTGCCAGGCTGGG      21547        TGA  _
                                CCCAGCCT  GG ATTT
                                ||||||||  || ||||
                                GGGTCGGA  CC TGAA
                                    ___  G
GAM492  ust3     3' CAAGGCTGGGTGCGGTG    93227     A
                                CATC CACCCAGCCTTG
                                |||| ||||||||||||
                                GTGG GTGGGTCGGAAC
                                  C
GAM492  LOC144501 3' AAATCCTCAGTGGG      83102     GCC
                                CCCA  TTGAGGATTT
                                ||||  ||||||||||
                                GGGT  GACTCCTAAA
                                   ___
GAM492  LOC146958 3' AAATCCTCCAATGGGCTGGG  83880       T___
                                CCCAGCCT   GAGGATTT
                                ||||||||   ||||||||
                                GGGTCGGG   CTCCTAAA
                                    TAAC
GAM492  LOC148293 3' TCAGGCCAGGTGTGGTG    78784        CA   T
                                CATCACACC  GCCT GA
                                |||||||||  |||| ||
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                                GTGGTGTGG  CGGA CT
                                     AC   _
GAM492  LOC149086 5'  CAGGGCTGGGCATGAT     84336     CA
                                ATCA  CCCAGCCTTG
                                ||||  ||||||||||
                                TAGT  GGGTCGGGAC
                                  AC
GAM492  LOC150519 3'  TCCTCAAGGTAGGCATGATG   79923      CAC  A
                                CATCA   CC GCCTTGAGGA
                                |||||   || ||||||||||
                                GTAGT   GG TGGAACTCCT
                                   AC_  A
GAM492  LOC150577 3'  CTTAGCTGGGTGTGGTG     85074          CT
                                CATCACACCCAGC  TGAG
                                ||||||||||||  ||||
                                GTGGTGTGGGTCG  ATTC
                                       __
GAM492  LOC151068 3'  CTTAGCTGGGTGTGGTG     85220          CT
                                CATCACACCCAGC  TGAG
                                ||||||||||||  ||||
                                GTGGTGTGGGTCG  ATTC
                                       __
GAM492  LOC151446 3'  TCAGCCGGGTGTGGTG      85378         A  CT
                                CATCACACCC GC  TGA
                                ||||||||||  ||  |||
                                GTGGTGTGGG CG  ACT
                                     C  __
GAM492  LOC152348 3'  AAATCCTAATCCCCAGTGTGAT 85690        CCAGCCTTG
          G                      CATCACAC       AGGATTT
                                ||||||||       |||||||
                                GTAGTGTG       TCCTAAA
                                    ACCCCTAA_
GAM492  LOC153218 5'  CTCAAGGCTAGTTGTGA     80777      CCC
                                TCACA   AGCCTTGAG
                                |||||   |||||||||
                                AGTGT   TCGGAACTC
                                   TGA
GAM492  LOC153218 5'  CTCAAGGCTAGTTGTGA     80776      CCC
                                TCACA   AGCCTTGAG
                                |||||   |||||||||
                                AGTGT   TCGGAACTC
                                   TGA
GAM492  LOC154877 3'  CCTCTCTTGGCTGGGTGTGGTG 86290           TT__
                                CATCACACCCAGCC    GAGG
                                ||||||||||||||   ||||
                                GTGGTGTGGGTCGG    CTCC
                                        TTCT
GAM492  LOC158677 5'  AAATTTTAGCTGGGTGTTATG  86887     C       CTTG
                                CAT ACACCCAGC    AGGATTT
                                ||| |||||||||    |||||||
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                                GTA TGTGGGTCG    TTTTAAA
                                  T       A___
GAM492   LOC167555 3'  TCAGCCAGGTGTGATG      82680         CA  CT
                                CATCACACC  GC  TGA
                                |||||||||  ||  |||
                                GTAGTGTGG  CG  ACT
                                     AC  __
GAM492   LOC197201 3'  AAGGCTGGGTGTGATG      87927
                                CATCACACCCAGCCTT
                                ||||||||||||||||
                                GTAGTGTGGGTCGGAA

GAM492   LOC219406 3'  CAAGGCTGGGTGCAGTG     93556     CA
                                CAT  CACCCAGCCTTG
                                |||  ||||||||||||
                                GTG  GTGGGTCGGAAC
                                  AC
GAM492   LOC220001 3'  CCCAAGGCTGGATGT       91633     C       A
                                ACA CCAGCCTTG GG
                                ||| |||||||||  ||
                                TGT GGTCGGAAC CC
                                  A       _
GAM492   LOC220692 3'  TTTCAAGGCCAGGTGTGGTG   91223         CA
                                CATCACACC  GCCTTGAGG
                                |||||||||  |||||||||
                                GTGGTGTGG  CGGAACTTT
                                     AC
GAM492   LOC221263 3'  AAATCCTCAGTGAGTG      93611     C  GCC
                                CAC CA   TTGAGGATTT
                                ||| ||   ||||||||||
                                GTG GT   GACTCCTAAA
                                  A  ___
GAM492   LOC221787 3'  CAAAGCCAGGTGTGGTG     92467         CA  C
                                CATCACACC  GC TTG
                                |||||||||  || |||
                                GTGGTGTGG  CG AAC
                                     AC  A
GAM492   LOC257095 5'  CCAGGCTGGGTGCAATG     96936     CA        TGA
                                CAT  CACCCAGCCT   GG
                                |||  ||||||||||   ||
                                GTA  GTGGGTCGGA   CC
                                  AC        ___
GAM492   LOC91250  5'  AAATCAAGAATAGGCTAGGTGT 65318         C     TGAG__
           GGTG                    CATCACACC AGCCT     GATTT
                                |||||||||  |||||     |||||
                                GTGGTGTGG TCGGA     CTAAA
                                     A    TAAGAA
GAM492   LOC91565  3'  AAGGCTGGGTGCAGTG      66457     CA
                                CAT  CACCCAGCCTT
                                |||  ||||||||||
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                                GTG  GTGGGTCGGAA
                                  AC
GAM492  LOC93132  5'  TCAGCCGGGTGTGGTG     71502          A  CT
                                CATCACACCC GC  TGA
                                |||||||||| ||  |||
                                GTGGTGTGGG CG  ACT
                                     C  __
GAM493  AIPL1     3'  CCTGTCTCCCCATTTTGG    59850        AAA  CAA
                                CCAAAATG   GA   ACAGG
                                ||||||||   ||   |||||
                                GGTTTTAC   CT   TGTCC
                                    CC_  C__
GAM493  DVL3      3'  TCTGCAACCCCCATTTTGGGA  15376          AAAGACAAA
                                TCCCAAAATG        CAGG
                                ||||||||||        ||||
                                AGGGTTTTAC        GTCT
                                     CCCCAAC__
GAM493  EIF4EBP2  3'  CCTGTTTGTGAATATATTTT   14589       AAAG_
                                AAAATG     ACAAACAGG
                                ||||||     |||||||||
                                TTTTAT     TGTTTGTCC
                                   ATAAG
GAM493  GAS11     3'  CCTGGACACCTTTCTTTTGGGA 7623          T     ACAAA
                                TCCCAAAA GAAAG     CAGG
                                |||||||| |||||     ||||
                                AGGGTTTT CTTTC     GTCC
                                     _    CACAG
GAM493  GNRHR     5'  TCCTGTTTTGTTCATTTCAGG  4643     CA      AGAC
                                CC  AAATGAA    AAACAGGA
                                ||  |||||||    ||||||||
                                GG  TTTACTT    TTTGTCCT
                                 AC      GT__
GAM493  GPR48     3'  CCTATTCTCATCTTTCATCTGG 37502      AA       CAAAC__
            GA                    TCCCA  ATGAAAGA      AGG
                                |||||  ||||||||      |||
                                AGGGT  TACTTTCT      TCC
                                   C_       ACTCTTA
GAM493  HLCS      5'  CCTGGGGTCTTTCACTCCCGGA 4663      CAAAA       AAA
                                TCC    TGAAAGAC   CAGG
                                |||    ||||||||   ||||
                                AGG    ACTTTCTG   GTCC
                                  CCCTC       GG_
GAM493  HLCS      5'  TCCTGTTTGCCTTTATCCACTG 4678      AAATG_   A
            G                     CCA      AAAG CAAACAGGA
                                |||     |||| |||||||||
                                GGT     TTTC GTTTGTCCT
                                  CACCTA    C
GAM493  ICAM1     3'  TCCTGTTTGCATTTCACTGGGA 71579       AAA     GA
                                TCCCA   TGAAA  CAAACAGGA
                                |||||   |||||  |||||||||
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                                AGGGT  ACTTT  GTTTGTCCT
                                  C__    AC
GAM493  KCNK10   5'  TCCCACCTGTCTTTTTCTGGGG 56340      AAAT      AACA
                                TCCCA   GAAAGACA   GGA
                                |||||   ||||||||   |||
                                GGGGT   TTTTCTGT   CCT
                                  CT__      CCAC
GAM493  MHC2TA   3'  CCTGTTACCATTTTGGGG   4171         AAAGACA
                                TCCCAAAATG     AACAGG
                                ||||||||||     ||||||
                                GGGGTTTTAC     TTGTCC
                                     CA_____
GAM493  SLC25A12 3'  TCCTAGTTTGTTTTCCATTCTG 13526    A   A      _
           G                     CCA AATG AAGACAAAC AGGA
                                ||| |||| ||||||||| ||||
                                GGT TTAC TTTTGTTTG TCCT
                                  C   C       A
GAM493  SLC7A6   3'  CCTCCTTTCATTTTTGGA   14300    C       ACAAAC
                                TCC AAAATGAAAG     AGG
                                ||| ||||||||||     |||
                                AGG TTTTACTTTC     TCC
                                  T        C_____
GAM493  SLC9A1   3'  TCCTGTTTTTAAAACATTTTG  70412       AAAGAC
                                CAAAATG     AAACAGGA
                                |||||||     ||||||||
                                GTTTTAC     TTTGTCCT
                                    AAAATT
GAM493  SNX15    3'  CCTGCCTGTCTTTTTGGGG   73735      AAAT      AA
                                TCCCA   GAAAGACA  CAGG
                                |||||   ||||||||  ||||
                                GGGGT   TTTTCTGT  GTCC
                                  _____      CC
GAM493  STIM1    3'  CCTGCCATACCTTTATCCTGGG 60147      AA    AGACAAA
           A                     TCCCA  ATGAA      CAGG
                                |||||  |||||      ||||
                                AGGGT  TATTT      GTCC
                                  CC    CCATACC
GAM493  USP1     3'  TCCTGTGGTTTTTCA      12560        AA
                                TGAAAGAC  ACAGGA
                                ||||||||  ||||||
                                ACTTTTTG  TGTCCT
                                    G_
GAM493  ZNF267   5'  TCCGAGTCTTTCGTTCTGGGA  12736      A        AAACA
                                TCCCA AATGAAAGAC    GGA
                                ||||| ||||||||||    |||
                                AGGGT TTGCTTTCTG    CCT
                                  C        AG___
GAM493  ATE1     3'  TCCTGTTTGTATTTTGT    72613   TG  G
                                A  AAA ACAAACAGGA
                                |  ||| ||||||||||
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                                T  TTT TGTTTGTCCT
                                 GT   A
GAM493  C21orf109 3'  TCCTGTTTTATATACTTTCATT 57267    CCA       AC____
           TGAGA                  C   AAATGAAAG     AAACAGGA
                                |  |||||||||     ||||||||
                                G  TTTACTTTC     TTTGTCCT
                                 AG_       ATATAT
GAM493  CNOT3    3'  CTATTTTCATTTTGG      27218           ACAAAC
                                CCAAAATGAAAG     AG
                                ||||||||||||     ||
                                GGTTTTACTTTT     TC
                                      A_____
GAM493  CTNNBIP1  3'  TCCTGAGGCCTCATTTTGGGG  39669          AAGACAAA
                                TCCCAAAATGA       CAGGA
                                ||||||||||       |||||
                                GGGGTTTTACT       GTCCT
                                      CCGGA___
GAM493  DKFZP564I122 3'  CCTGTAATCCCACCATTTTGGG 63173          AAAGACAA
           A                     TCCCAAAATG       ACAGG
                                ||||||||||       |||||
                                AGGGTTTTAC       TGTCC
                                      CACCCTAA
GAM493  DKFZP566J091 3'  CCTTTGCTTTCATTTCAGG    48120    CA       A   AC
                                CC  AAATGAAAG CAA  AGG
                                ||  ||||||||| |||  |||
                                GG  TTTACTTTC GTT  TCC
                                 AC       _  __
GAM493  FASTK    3'  CCGTTGTGAATCTCAGTTTTGG 52246        GAA   CAA  __
           GA                    TCCCAAAAT   AGA   ACA  GG
                                |||||||||   |||   |||  ||
                                AGGGTTTTG   TCT   TGT  CC
                                     AC_   AAG   TG
GAM493  FASTK    3'  CCGTTGTGAATCTCAGTTTTGG 46987        GAA   CAA  __
           GA                    TCCCAAAAT   AGA   ACA  GG
                                |||||||||   |||   |||  ||
                                AGGGTTTTG   TCT   TGT  CC
                                     AC_   AAG   TG
GAM493  FHR5     3'  TCCTGTTTGTCTCAAATTATAG 47903     CAA   GAA
           GA                    TCC   AAT   AGACAAACAGGA
                                |||   |||   ||||||||||||
                                AGG   TTA   TCTGTTTGTCCT
                                  ATA   AAC
GAM493  FLJ10895  3'  TCCTGTAGGTTTATTTTGG    38849        AAG  AA
                                CCAAAATGA   AC  ACAGGA
                                |||||||||   ||  ||||||
                                GGTTTTATT   TG  TGTCCT
                                     ___  GA
GAM493  FLJ14824  3'  CCTGTTCATTTTATTTTAGGG  51642     _       GACA
                                CCC AAAATGAAA    AACAGG
                                ||| |||||||||    ||||||
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                                GGG TTTTATTTT   TTGTCC
                                  A       AC__
GAM493  FLJ32312  3' TCCTTAATTCTTTCATTT    58497         CAAAC
                                AAATGAAAGA    AGGA
                                ||||||||||    ||||
                                TTTACTTTCT    TCCT
                                     TAAT_
GAM493  FLJ32926  3' CCTGTTTGCCTTGTGGG    58022     AAATGA  A
                                CCCA     AAG CAAACAGG
                                ||||     ||| ||||||||
                                GGGT     TTC GTTTGTCC
                                  G_____  C
GAM493  KIAA0210  5' CCTGGCCTGCTTTCATTTT   28475         A  AA_
                                AAAATGAAAG CA   CAGG
                                |||||||||| ||   ||||
                                TTTTACTTTC GT   GTCC
                                     _ CCG
GAM493  KIAA0711  3' TGTGGCTTTCATTTTGGGA   29530           ACAA
                                TCCCAAAATGAAAG   ACA
                                ||||||||||||||   |||
                                AGGGTTTTACTTTC   TGT
                                       GG__
GAM493  KIAA0923  3' CCTGTTTGTGGCTATTTT    25834       AAAG
                                AAAATG   ACAAACAGG
                                ||||||   |||||||||
                                TTTTAT   TGTTTGTCC
                                   CGG_
GAM493  KIAA0997  3' CCTAGAGTTACTCTCTTTTGGG 30189        T_  AA   AAAC
            A                    TCCCAAAA  GA  GAC    AGG
                                ||||||||  ||  |||   |||
                                AGGGTTTT  CT  TTG    TCC
                                     CT  CA   AGA_
GAM493  KIAA1163  3' TCCTGTATTTTCATTTCTG   78905    _       ACAA
                                CA AAATGAAAG    ACAGGA
                                || |||||||||   ||||||
                                GT TTTACTTTT    TGTCCT
                                  C       A___
GAM493  KIAA1233  3' TCCTGAGAACTTTATTTTGG   63083         AGACAAA
                                CCAAAATGAA      CAGGA
                                ||||||||||      |||||
                                GGTTTTATTT      GTCCT
                                     CAAGA__
GAM493  KIAA1508  5' TCTTTGTGTCTTTCAT     61894          AAC
                                ATGAAAGACA   AGGA
                                ||||||||||   ||||
                                TACTTTCTGT   TTCT
                                     GT_
GAM493  KIAA1719  3' CCTGCCTGCCTATGCATTTTGG 68158          AA_  A  AA
            GA                    TCCCAAAATG   AG CA  CAGG
                                ||||||||||   || ||  ||||
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                                AGGGTTTTAC  TC GT  GTCC
                                      GTA  C  CC
GAM493  KIAA1750  3'  TCCTACTTGTCTTTAACATGG  68257    AAATG      AC
                                CCA    AAAGACAA  AGGA
                                |||    ||||||||  ||||
                                GGT    TTTCTGTT  TCCT
                                  ACAA_      CA
GAM493  KIAA1940  3'  TCCTGCCAACTTTCATTTGG  79992     A     ACAAA
                                CCAAA TGAAAG    CAGGA
                                ||||| ||||||    |||||
                                GGTTT ACTTTC    GTCCT
                                   _    AACC_
GAM493  MDS018    3'  CTGTCTCATTTTGGGA     41533          AAGACAA
                                TCCCAAAATGA     ACAG
                                ||||||||||      ||||
                                AGGGTTTTACT     TGTC
                                      C_______
GAM493  MGC10977  5'  TTGTCTCTCATTTTGGG    51061          A
                                CCCAAAATGA AGACAA
                                |||||||||| ||||||
                                GGGTTTTACT TCTGTT
                                      C
GAM493  MGC26655  3'  TCCTGCCATTTTTCATTTT   56291          CAAA
                                AAAATGAAAGA   CAGGA
                                ||||||||||   |||||
                                TTTTACTTTTT   GTCCT
                                      ACC_
GAM493  MGC26914  3'  TCCTGTTTCTCACTTTTGG   58668       _  AAGAC
                                CCAAAA TGA    AAACAGGA
                                |||||| |||    ||||||||
                                GGTTTT ACT    TTTGTCCT
                                   C  C____
GAM493  NYD-SP15  3'  TCCTGTTTATCACAGACTTTGG 48112       ATGAAA  C
           G                     CCCAAA     GA AAACAGGA
                                ||||||     || ||||||||
                                GGGTTT     CT TTTGTCCT
                                   CAGACA  A
GAM493  PTK6      3'  TCCTGTTTGTCTTGTGTCTTGA 19941    C   A   A
           GA                     TC CAA ATG AAGACAAACAGGA
                                || ||| ||| ||||||||||||||
                                AG GTT TGT TTCTGTTTGTCCT
                                 A  C  G
GAM493  SEC15B    3'  TCCTGTACTCTTTCGTTTT   66687          CAA
                                AAAATGAAAGA   ACAGGA
                                ||||||||||   ||||||
                                TTTTGCTTTCT   TGTCCT
                                      CA_
GAM493  SEC3      5'  CCATCCGGTCTCCGTTTTGG  36812        AA   AAACA
                                CCAAAATG  AGAC    GG
                                ||||||||  ||||    ||
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                                GGTTTTGC  TCTG    CC
                                    C_    GCCTA
GAM493   Spir-1    3'  TCCTGTTTAAGAGCTTTCA   64703       AC___
                                TGAAAG    AAACAGGA
                                ||||||    ||||||||
                                ACTTTC    TTTGTCCT
                                   GAGAA
GAM493   LOC113523 3'  TCCTGTCTCTTTCCATTT    73051      _    CAA
                                AAATG AAAGA   ACAGGA
                                ||||| |||||   ||||||
                                TTTAC TTTCT   TGTCCT
                                  C    C__
GAM493   LOC139221 3'  CCTGAAATTCCATTTTTGGGA  75823        TGAAA  CAAA
                                TCCCAAAA    GA    CAGG
                                ||||||||    ||    ||||
                                AGGGTTTT    CT    GTCC
                                    TAC__  TAAA
GAM493   LOC143680 5'  TCTTGAGATCTTTTATTTTGG  82989           CAAA
                                CCAAAATGAAAGA    CAGGA
                                ||||||||||||    |||||
                                GGTTTTATTTTCT    GTTCT
                                      AGA_
GAM493   LOC143719 5'  TTGTCTCTCATTTTGGG     60624          A
                                CCCAAAATGA AGACAA
                                |||||||||| ||||||
                                GGGTTTTACT TCTGTT
                                   C
GAM493   LOC144147 5'  TTGTCTCTCATTTTGGG     71733          A
                                CCCAAAATGA AGACAA
                                |||||||||| ||||||
                                GGGTTTTACT TCTGTT
                                   C
GAM493   LOC145719 3'  TCCTGTAACTTTTTCAT     83457        CAA
                                ATGAAAGA   ACAGGA
                                ||||||||   ||||||
                                TACTTTTT   TGTCCT
                                    CAA
GAM493   LOC145720 3'  TCCTGTAACTTTTTCAT     83439        CAA
                                ATGAAAGA   ACAGGA
                                ||||||||   ||||||
                                TACTTTTT   TGTCCT
                                    CAA
GAM493   LOC148758 5'  TCCATGAGTCTTTCAGGG    78976     AAAA      AAA  _
                                CCC    TGAAAGAC   CA GGA
                                |||    ||||||||   || |||
                                GGG    ACTTTCTG   GT CCT
                                  _____       A__  A
GAM493   LOC149111 3'  CCTGTTTGTCAATCTTTGG   79182      AT  AA
                                CCAAA  GA  GACAAACAGG
                                |||||  ||  ||||||||||
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                                GGTTT  CT  CTGTTTGTCC
                                  __  AA
GAM493  LOC150407 3'  CCTGTTTGTCCCTTTCAGTGGG 79823     AAA   __
                                CCCA  TGAAA  GACAAACAGG
                                ||||  |||||  ||||||||||
                                GGGT  ACTTT  CTGTTTGTCC
                                  G__   CC
GAM493  LOC150538 3'  GTCTTTCATTCGGGA      79939     AA
                                TCCC  AATGAAAGAC
                                ||||  ||||||||||
                                AGGG  TTACTTTCTG
                                  C_
GAM493  LOC152860 5'  CCTGTTTGTCTGTGGGTCCTGG 80700     AA  GAA_
          G                      CCCA  AT   AGACAAACAGG
                                ||||  ||   ||||||||||
                                GGGT  TG   TCTGTTTGTCC
                                  CC  GGTG
GAM493  LOC159053 3'  TCCTGTTTTCTTCATTT     86983       A  C
                                AAATGAA GA AAACAGGA
                                ||||||| || ||||||||
                                TTTACTT CT TTTGTCCT
                                   _ _
GAM493  LOC197117 3'  TCCTGTAACTTTTTCAT     89725        CAA
                                ATGAAAGA  ACAGGA
                                ||||||||  ||||||
                                TACTTTTT  TGTCCT
                                    CAA
GAM493  LOC201915 5'  TCCTGTTTGCCCTCGTCTGCCG 89105     CAAA_   AAGA
          GA                    TCC    ATGA   CAAACAGGA
                                |||    ||||   |||||||||
                                AGG    TGCT   GTTTGTCCT
                                  CCGTC   CCC_
GAM493  LOC203197 3'  CTGTTTGACTTGAGGA      89288    _  AAATGAA  A
                                TCC CA      AG CAAACAG
                                ||| ||      || |||||||
                                AGG GT      TC GTTTGTC
                                  A ________  A
GAM493  LOC221662 3'  CCTGTTTCAATTTTGGGA    92402        GAAAGAC
                                TCCCAAAAT      AAACAGG
                                |||||||||      |||||||
                                AGGGTTTTA      TTTGTCC
                                    AC_____
GAM493  LOC223117 5'  TCCATGCAGTCTTTCATTTTG  94382          AAA  _
                                CAAAATGAAAGAC   CA GGA
                                ||||||||||||||  || |||
                                GTTTTACTTTCTG   GT CCT
                                      AC_  A
GAM493  LOC253228 3'  TCCTGTTTGTCTTCTCCCCAGG 95942     AAAAT  _
          G                     CCC    GA AAGACAAACAGGA
                                |||    || ||||||||||||||
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                                GGG    CT TTCTGTTTGTCCT
                                  ACCC_  C
GAM493  LOC254107 3'  CCTGTTTGTAAATATTCTGTGG 94385    _ A   AAAG
           A                     TCC CA AATG   ACAAACAGG
                                 ||| || ||||   |||||||||
                                 AGG GT TTAT   TGTTTGTCC
                                   T  C   AAA_
GAM493  LOC254685 5'  CCTTCCATCCATTTTGGGA   96485        AAA  CAAAC
                                 TCCCAAAATG  GA   AGG
                                 ||||||||||  ||   |||
                                 AGGGTTTTAC  CT   TCC
                                       ____ ACCT_
GAM493  LOC255527 5'  TCCTGGGTCCTTTTTGGGA   96856       TGAAA  AAA
                                 TCCCAAAA   GAC  CAGGA
                                 ||||||||   |||  |||||
                                 AGGGTTTT   CTG  GTCCT
                                      TC___  G__
GAM493  LOC257109 3'  TTGTCTTTCATCTGGGA    95573      AA
                                 TCCCA  ATGAAAGACAA
                                 |||||  ||||||||||||
                                 AGGGT  TACTTTCTGTT
                                   C_
GAM493  LOC91097  5'  CCTGTTTGCCATCTCGGGG   64835     AAA  AAAGA
                                 TCCC  ATG   CAAACAGG
                                 ||||  |||   ||||||||
                                 GGGG  TAC   GTTTGTCC
                                   CTC  C____
GAM493  LOC91145  3'  TCCTGTTTCTTTTCATCTCTAG 65058    CAAA_     AC
           GA                    TCC    ATGAAAG  AAACAGGA
                                 |||    |||||||  ||||||||
                                 AGG    TACTTTT  TTTGTCCT
                                   ATCTC     C_
GAM494  CNGA1    3'  CAACTGATAATGTGCAAA    59507         GC  A
                                 TTTGCACATTA  TAG TTG
                                 ||||||||||  ||| |||
                                 AAACGTGTAAT  GTC AAC
                                       A_  _
GAM494  ESRRG    3'  TGGCAGTCTTATGTGCAAA   66396        TAGCT
                                 TTTGCACAT    AGATTGCCA
                                 |||||||||    |||||||||
                                 AAACGTGTA    TCTGACGGT
                                      T_____
GAM494  KCNJ3    3'  GCAATAATGTGCAAA      9525          GCTAGA
                                 TTTGCACATTA     TTGC
                                 ||||||||||     ||||
                                 AAACGTGTAAT     AACG
                                                _______
GAM494  SDC2     3'  GCAAATTAATGTGTAAA     67132          CTAGA
                                 TTTGCACATTAG    TTGC
                                 ||||||||||||    ||||
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                                AAATGTGTAATT    AACG
                                      A____
GAM494  USP9X    3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
              A                  TTTGCACATTAGC     GCCAT
                                 ||||||||||||     |||||
                                 AAATGTGTAATCG     CGGTA
                                       TAGTC_
GAM494  AMOTL1   3'  GGCAAGTAATGTGCAAA    73650         G  AGAT
                                 TTTGCACATTA CT    TGCC
                                 |||||||||| ||    ||||
                                 AAACGTGTAAT GA    ACGG
                                      _ ____
GAM494  BCAR3    3'  AGTAATAATGTGCAAA     13098         __
                                 TTTGCACATTA  GCT
                                 |||||||||| |||
                                 AAACGTGTAAT  TGA
                                       AA
GAM494  DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930        AGCTA    C
                                 TTTGCACATT    GATTG CA
                                 |||||||||    ||||| ||
                                 AGACGTGTAA    TTAAC GT
                                      A____    A
GAM494  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                 TTTGCACATTAG  AGA TG CAT
                                 |||||||||||  ||| || |||
                                 AGACGTGTAATC  TTT AC GTA
                                       __  T  A
GAM494  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
              AA                   TTTGCACATTAGCTAGATTGCCAT
                                   ||||||||||||||||||||||||
                                   AAACGTGTAATCGATCTAACGGTA

GAM495  ARNT2    3'  AAACAACCCGTGCATCCCTGC  29450    A   TTTTA
                                 GTA GGAT    GGGTTGTTT
                                 ||| ||||    |||||||||
                                 CGT CCTA    CCCAACAAA
                                   C   CGTG_
GAM495  LCT      3'  AACCGTAAAAATCCTT     9697          G
                                 AAGGATTTTTA GGTT
                                 |||||||||| ||||
                                 TTCCTAAAAAT CCAA
                                       G
GAM495  RPL15    3'  AAACAACCCTAAAAATCCTTAC 11382
                                 GTAAGGATTTTTAGGGTTGTTT
                                 |||||||||||||||||||||||
                                 CATTCCTAAAAATCCCAACAAA

GAM495  FBXO30   3'  AACTAAAAAAATCCTGAC    49573    A       AG
                                 GT AGGATTTTT  GGTT
                                 || |||||||||  ||||
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                                CA TCCTAAAAA  TCAA
                                 G        AA
GAM495  KIAA0494  3'  AACAACCCTTACTTAC      28736       GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                  AT_____
GAM495  PRO0641   5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                  ___    C
GAM495  SMT3H2    3'  AACAACATAAAAATCCTTGC   22670           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM495  LOC120103 3'  AACCTATGAAAAATCCTTGC   74002           A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
                                CGTTCCTAAAAA   TCCAA
                                       GTA
GAM495  LOC129831 3'  AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM495  LOC133088 5'  AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                      GTA GGATTTTT     TTGTTT
                                ||| ||||||||     ||||||
                                CGT CCTAAAAA     AACAAA
                                  C       GATAA
GAM495  LOC148089 3'  GGCCCTAAAAATTCCTAC     78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM495  LOC154547 3'  AACAACATAAAAATCCTTGC   76050           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM495  LOC158104 3'  ACAGCCAAAAATCCTTA     60313          AG
                                TAAGGATTTTT  GGTTGT
                                ||||||||||  ||||||
                                ATTCCTAAAAA  CCGACA
                                       __
GAM495  LOC205880 5'  AAACAACCATCATCCTGAC    90709     A    TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
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                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM495  LOC221561 3'  AACAACATAAAAATCCTTGC  92130          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM495  LOC257591 3'  AACAACATAAAAATCCTTGC  97840          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM495  LOC51145  3'  AGCTAAAATCCTTAC      32393          TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
                                CATTCCTAAAA   TCGA
                                       ___
GAM496  DDEF1    3'  GAGCTTTAGCAGCCTC      59564    A   AGATAC      A
                                GA GCT     CTAAAGCT C
                                || |||     |||||||| |
                                CT CGA     GATTTCGA G
                                 C   C_____       C
GAM496  DDX3     3'  GAGCCTTAGGTATTTG      43759          A   A
                                TAGATACCTAA GCT C
                                |||||||||| ||| |
                                GTTTATGGATT CGA G
                                       C   C
GAM496  GRAF     3'  GGTAACTCCCTCCCTAGCTTC  30573        ATACCTAA  C
                                GAAGCTAG       AG TACC
                                ||||||||       || ||||
                                CTTCGATC       TC ATGG
                                     CCTCCC__  A
GAM496  MAT1A    3'  AGCTTTAGAATCCCAGC     90825     A_   AC
                                GCT  GAT  CTAAAGCT
                                |||  |||  ||||||||
                                CGA  CTA  GATTTCGA
                                  CC   A_
GAM496  MYLK     3'  AGCTTCAGACATTTGGTT    97018        AC  A
                                AGCTAGAT  CT AAGCT
                                ||||||||  || |||||
                                TTGGTTTA  GA TTCGA
                                     CA  C
GAM496  RGL      3'  GTAGCTAAAACTTAGCTTCA  30736         ATACCTAA
                                TGAAGCTAG       AGCTAC
                                |||||||||       ||||||
                                ACTTCGATT       TCGATG
                                     CAAAA___
GAM496  ZFP93    3'  GTAGCCTTAATAACGTTAGTTT 14887         ATACC_   A
             CA                   TGAAGCTAG     TAA GCTAC
                                |||||||||     ||| |||||
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                                ACTTTGATT     ATT CGATG
                                      GCAATA   C
GAM496  C3orf4   3'  AGCATTGACACATAGCTTCA  39118        GATACC   A
                                TGAAGCTA     TAA GCT
                                ||||||||     ||| |||
                                ACTTCGAT     GTT CGA
                                     ACACA_   A
GAM496  D2S448   3'  GGCAGGAGTCCTAGCTTCA   73527         _  A   AAA
                                TGAAGCTAG AT CCT   GCT
                                ||||||||| || |||   |||
                                ACTTCGATC TG GGA   CGG
                                      C  A  ___
GAM496  FLJ12604 3'  AGCTTTAGTATTGACTTCA   64436      CTA    C
                                TGAAG   GATAC TAAAGCT
                                |||||   ||||| |||||||
                                ACTTC   TTATG ATTTCGA
                                   AG_    _
GAM496  FLJ14280 5'  GGTAGCTCCTGGCCAGCTCA   45999     A   AGATA  TAA
                                TGA GCT    CC   AGCTACC
                                |||  |||    ||   |||||||
                                ACT CGA    GG   TCGATGG
                                  _   CC___  TCC
GAM496  H2AFJ    3'  GTTGTCAAGTTTCTAGCTTCA  36842         T  CTAA_
                                TGAAGCTAGA AC     AGC
                                |||||||||| ||     |||
                                ACTTCGATCT TG     TTG
                                      T  AACTG
GAM496  KIAA0441 3'  TAGCTTTGTTAATCTAGCCTC  28960    A      ACC
                                GA GCTAGAT   TAAAGCTA
                                || |||||||   ||||||||
                                CT CGATCTA   GTTTCGAT
                                 C      ATT
GAM496  KIAA1128 3'  TAGCTTTATGTGCAGCTTGCA  68483    _    AGA   C
                                TG AAGCT   TAC TAAAGCTA
                                || |||||   ||| ||||||||
                                AC TTCGA   GTG ATTTCGAT
                                 G    C__   T
GAM496  KIAA1750 3'  TAGCCCCAGGAGTGGGCTTTA  68254       AG  A   AAA
                                TGAAGCT  AT CCT   GCTA
                                |||||||  || |||   ||||
                                ATTTCGG  TG GGA   CGAT
                                     G_  A   CCC
GAM496  KPNA5    3'  GGTAGCTTCAGGTAACT     9629     A    A
                                AG TACCT AAGCTACC
                                || ||||| ||||||||
                                TC ATGGA TTCGATGG
                                 A    C
GAM496  MAGEH1   5'  GGTAGCTTCAGCGGCAGCAGCT 25924       AGATAC_  A
            TC                    GAAGCT      CT AAGCTACC
                                |||||||      || ||||||||
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                                CTTCGA      GA TTCGATGG
                                   CGACGGC  C
GAM496  MGC12921  3'  AGCCCTATTTAGCTTC      63774          CCTAAA
                                GAAGCTAGATA     GCT
                                ||||||||||      |||
                                CTTCGATTTAT     CGA
                                      CC____
GAM496  MGC30052  3'  AGCTTTAGAATAGCTTC     58532        GATAC
                                GAAGCTA    CTAAAGCT
                                |||||||    ||||||||
                                CTTCGAT    GATTTCGA
                                   AA___
GAM496  RNF34     3'  AGCAAGGGCTGCATCTAGCTTC 47094         A___   AAA
                                GAAGCTAGAT    CCT   GCT
                                ||||||||||    |||   |||
                                CTTCGATCTA    GGG   CGA
                                      CGTC   AA_
GAM496  TNFRSF19L 3'  GTAGCTTTTATCCCAGC     51779     A_    CCT
                                GCT  GATA   AAAGCTAC
                                |||  ||||   ||||||||
                                CGA  CTAT   TTTCGATG
                                  CC    ___
GAM496  LOC121536 3'  AGCAAATCACATTTAGCTTCA  74082          ACCTAAA
                                TGAAGCTAGAT      GCT
                                ||||||||||       |||
                                ACTTCGATTTA      CGA
                                      CACTAAA
GAM496  LOC255452 3'  TAGGTACCTACCTTCA      97544       C   A
                                TGAAG TAG TACCTA
                                |||||  |||  ||||||
                                ACTTC ATC ATGGAT
                                   C   C
GAM496  LOC257396 3'  GGCAGCTTTAGGCTTAACTT   97139     C   ATA       A
                                AAG TAG   CCTAAAGCT CC
                                |||  |||   |||||||||  ||
                                TTC ATT   GGATTTCGA GG
                                  A   C__        C
GAM496  LOC92710  3'  GTACAAGGCATCTAGCTT     70359         A   AAAGC
                                AAGCTAGAT CCT     TAC
                                |||||||||  |||     |||
                                TTCGATCTA GGA     ATG
                                      C   AC___
GAM497  D12S2489E 3'  GGAATTTTGCCTCTGAA      23744      C    GCCT
                                TTCA AGGT    GAAATTCC
                                ||||  ||||    ||||||||
                                AAGT TCCG    TTTTAAGG
                                  C    _____
GAM497  FZD6      3'  AGGAATTTCACAGATCT      13041      GCC
                                AGGT   TGAAATTCCT
                                ||||   ||||||||||
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                                TCTA  ACTTTAAGGA
                                  GAC
GAM497  GAD1     5' AGGCGGTCAGGCACCTG    5873          AATT
                                CAGGTGCCTGA   CCT
                                ||||||||||   |||
                                GTCCACGGACT   GGA
                                     GGC_
GAM497  GRINL1A  3' AGTTGTTCCAGGCACCT    69512        A  TC
                                AGGTGCCTG AAT  CT
                                ||||||||| ||| ||
                                TCCACGGAC TTG  GA
                                    C  TT
GAM497  ITGA1    3' GAATTTCAGGTTTG       63531     GT
                                CAG  GCCTGAAATTC
                                |||  ||||||||||
                                GTT  TGGACTTTAAG
                                 __
GAM497  ITGA5    3' AGGAATTTCCCAGGACCCTG  61277     TG  __
                                CAGG  CCT  GAAATTCCT
                                ||||  |||  |||||||||
                                GTCC  GGA  CTTTAAGGA
                                  CA  CC
GAM497  MAP3K7IP1 3' AGGAAGAGGCGCCCTGTGAA  20376        _    GAAA
                                TTCACAGG TGCCT   TTCCT
                                |||||||| |||||   |||||
                                AAGTGTCC GCGGA   AAGGA
                                    C    G___
GAM497  POLH     3' GTTCCAGGCACCTGTGA    21466          A
                                TCACAGGTGCCTG AAT
                                |||||||||||| |||
                                AGTGTCCACGGAC TTG
                                       C
GAM497  RAG1     3' AGGAATTTCAATATGTAGAA  4811     _  GGTGCC
                                TTC ACA     TGAAATTCCT
                                ||| |||     ||||||||||
                                AAG TGT     ACTTTAAGGA
                                  A  ATA___
GAM497  SIRT1    3' GAATTTCAGGATTATTGT    24265     GTG_
                                ACAG   CCTGAAATTC
                                ||||   ||||||||||
                                TGTT   GGACTTTAAG
                                  ATTA
GAM497  TSN      3' AGAAATTTCAGGTTGTTGGTGA 16101     AGGT_       C
                                TCAC    GCCTGAAATT CT
                                ||||    |||||||||| ||
                                AGTG    TGGACTTTAA GA
                                  GTTGT        A
GAM497  APOARGC  3' AGGAATCCAGATCCTGTGGA  44415       TGC  AA
                                TTCACAGG  CTG  ATTCCT
                                ||||||||  |||  ||||||
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                                AGGTGTCC  GAC  TAAGGA
                                    TA_  C_
GAM497  ARHGAP11A 3'  AGGAATTTCAAATCATC    28793     CC_
                                GGTG  TGAAATTCCT
                                ||||  ||||||||||
                                CTAC  ACTTTAAGGA
                                  TAA
GAM497  ATP9A    3'  GAATTTCAGAGGTGTGA    62043     GGTGC
                                TCACA   CTGAAATTC
                                |||||   |||||||||
                                AGTGT   GACTTTAAG
                                  GGA__
GAM497  CL683    3'  AGGATGAAATACCTGTGAA   31649         CCTGAAAT
                                TTCACAGGTG      TCCT
                                ||||||||||      ||||
                                AAGTGTCCAT      AGGA
                                     AAAGT___
GAM497  DDX21    3'  AGGAATTTCACATGTAT    16384     C__
                                GTGC  TGAAATTCCT
                                ||||  ||||||||||
                                TATG  ACTTTAAGGA
                                  TAC
GAM497  DJ971N18.2 3'  AGGCTGCAGGCCCTGTGAA   40957        T    AAATT
                                TTCACAGG GCCTG    CCT
                                |||||||| |||||    |||
                                AAGTGTCC CGGAC    GGA
                                    _    GTC__
GAM497  FLJ14957  3'  AGGAATTTCAGGGAGC     51738    G_
                                GT  CCTGAAATTCCT
                                ||  ||||||||||||
                                CG  GGACTTTAAGGA
                                 AG
GAM497  FLJ22169  3'  AGGAATTTGGGGCCTAGGAA   43998     ACA  T    G
                                TTC   GG GCCT AAATTCCT
                                |||   || |||| ||||||||
                                AAG   TC CGGG TTTAAGGA
                                  GA_  _    G
GAM497  FLJ25059  5'  AGGAATTTCAGACCTG     58681      GC
                                CAGGT  CTGAAATTCCT
                                |||||  ||||||||||
                                GTCCA  GACTTTAAGGA
                                   __
GAM497  KIAA0057  3'  AGTGGCAGGCACCTGT     24416          AA
                                ACAGGTGCCTG  ATT
                                ||||||||||  |||
                                TGTCCACGGAC  TGA
                                     GG
GAM497  KIAA0133  3'  AGGAATTTTTTTTTCCTATG   28765    C   TGCCT
                                CA AGG    GAAATTCCT
                                || |||    |||||||||
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                                GT TCC    TTTTAAGGA
                                 A  TTTTT
GAM497  KIAA0495  5'  GGGAGTAAACCCTGTGAA   62597       TGCCTGAA
                                TTCACAGG      ATTCCT
                                ||||||||      ||||||
                                AAGTGTCC      TGAGGG
                                    CAAA____
GAM497  KIAA0789  3'  AGGAACCTCAGGCACC     63679        AA
                                GGTGCCTGA  TTCCT
                                |||||||||  |||||
                                CCACGGACT  AAGGA
                                     CC
GAM497  KIAA0984  3'  GAACACAGCACCTGTGA    65529         C  AAA
                                TCACAGGTGC TG   TTC
                                |||||||||| ||   |||
                                AGTGTCCACG AC   AAG
                                     _  AC_
GAM497  KIAA1789  5'  AGTTCCAGCACCTGT      67098        C  A
                                ACAGGTGC TG AATT
                                |||||||| || ||||
                                TGTCCACG AC TTGA
                                    _ C
GAM497  KIAA1954  5'  GGAATTTATCCTGGAA     77721     A   TGCCTG
                                TTC CAGG     AAATTCC
                                ||| ||||     |||||||
                                AAG GTCC     TTTAAGG
                                  _   TA____
GAM497  LRMP      5'  AGGAATTTCCTCACTATGA   20466     CA   CCT
                                TCA  GGTG   GAAATTCCT
                                |||  ||||   |||||||||
                                AGT  TCAC   CTTTAAGGA
                                  A_   TC_
GAM497  MGC12972  3'  AGGAACCTCATGCGACCTGTGA 51077        _  C   AA
                                TCACAGGT GC TGA  TTCCT
                                |||||||| || |||  |||||
                                AGTGTCCA CG ACT  AAGGA
                                    G  T   CC
GAM497  MGC13033  3'  GAATTGTACCTGTG       48752        CTGA
                                CACAGGTGC    AATTC
                                |||||||||    |||||
                                GTGTCCATG    TTAAG
                                     ____
GAM497  TSPEAR    3'  GGGTCAGCACCTGTGAA     58723         C   AAT
                                TTCACAGGTGC TGA   TCC
                                |||||||||||| |||   |||
                                AAGTGTCCACG ACT   GGG
                                     _  ___
GAM497  WBSCR23   3'  ATTTCTAAGACACCTGTGAA  46753         C  __
                                TTCACAGGTG CT  GAAAT
                                |||||||||| ||  |||||
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                                AAGTGTCCAC GA  CTTTA
                                      A  AT
GAM497   LOC122727 5'  GGAGAGACACTTGTGAA     74149          C  GAAA
                                TTCACAGGTG CT    TTCC
                                |||||||||| ||    ||||
                                AAGTGTTCAC GA    GAGG
                                      A  _____
GAM497   LOC124460 3'  AGGAATTTATTATCTGT     76037        CCTG
                                ACAGGTG    AAATTCCT
                                |||||||    ||||||||
                                TGTCTAT    TTTAAGGA
                                   TA__
GAM497   LOC149619 3'  CTAGGAATTTCAGTCAACAGCA 84528   _  _______         III
            GCCTGTGAA                 G TGC     CTGAAATTCCT   AG
                                | |||     ||||||||||   ||
                                C ACG     GACTTTAAGGA   TC
                                 G   ACAACT         III
GAM497   LOC150538 3'  GAATTTCAAACTTGGAA     79934     A    GCC
                                TTC CAGGT   TGAAATTC
                                ||| |||||   ||||||||
                                AAG GTTCA   ACTTTAAG
                                  _    A__
GAM497   LOC158431 3'  AGAAATTTCAGGAAAACC    86828     G__       C
                                GGT   CCTGAAATT CT
                                |||   ||||||||| ||
                                CCA   GGACTTTAA GA
                                  AAA        A
GAM497   LOC199926 3'  GAATTTCAGGTTGGAA      89879     A  GGT
                                TTC CA   GCCTGAAATTC
                                ||| ||   ||||||||||
                                AAG GT   TGGACTTTAAG
                                  _ ___
GAM497   LOC200251 5'  AGTGGCAGGCACCTGT      88663          AA
                                ACAGGTGCCTG  ATT
                                ||||||||||  |||
                                TGTCCACGGAC  TGA
                                       GG
GAM497   LOC200609 5'  GAATCTCAGGAATTGAGAA    90099     A   GTG    A
                                TTC CAG   CCTGA ATTC
                                ||| |||   ||||| ||||
                                AAG GTT   GGACT TAAG
                                  A   AA_    C
GAM497   LOC201689 3'  AGGTTGAGGCTCCTGTGAA    67141        T    G  ATT
                                TTCACAGG GCCT AA   CCT
                                |||||||| |||| ||   |||
                                AAGTGTCC CGGA TT   GGA
                                     T   G  ___
GAM497   LOC202025 5'  GGATCAACACCTGTGGA     90295          CC   AAT
                                TTCACAGGTG  TGA   TCC
                                |||||||||  |||   |||
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                                AGGTGTCCAC  ACT   AGG
                                     A_  ___
GAM497  LOC202316 3'  GAATTTCAGGTTGGAA     90339     A  GGT
                                TTC CA   GCCTGAAATTC
                                ||| ||   ||||||||||
                                AAG GT   TGGACTTTAAG
                                  _ ___
GAM497  LOC202460 5'  GGAAACACTTGTGAA      89184         CCTGAAA
                                TTCACAGGTG      TTCC
                                ||||||||||      ||||
                                AAGTGTTCAC      AAGG
                                     A______
GAM497  LOC222178 3'  AGGACTGAGGCAGCCTGTGAA 94172        _    GAAAT
                                TTCACAGG TGCCT    TCCT
                                |||||||| |||||    ||||
                                AAGTGTCC ACGGA    AGGA
                                     G    GTC__
GAM497  LOC255645 3'  GAATGGGGGCACCTATGGA   96651     C       GAA
                                TTCA AGGTGCCT   ATTC
                                |||| ||||||||   ||||
                                AGGT TCCACGGG   TAAG
                                  A       GG_
GAM497  LOC256158 5'  AGGAACATACACCTGTGAA   97644         CC  AAA
                                TTCACAGGTG  TG   TTCCT
                                ||||||||||  ||   |||||
                                AAGTGTCCAC  AC   AAGGA
                                     AT  ___
GAM498  PMX1     3'  TAATACTTACCTACCTCA    22595           C
                                TGAGGTAGGTAAGT ATTG
                                |||||||||||||| ||||
                                ACTCCATCCATTCA TAAT
                                          _
GAM498  PMX1     3'  TAATACTTACCTACCTCA    42662           C
                                TGAGGTAGGTAAGT ATTG
                                |||||||||||||| ||||
                                ACTCCATCCATTCA TAAT
                                          _
GAM498  WIG1     3'  GTGACCTACCTACCCCA     94469    A      A
                                TG GGTAGGTA GTCAT
                                || |||||||| |||||
                                AC CCATCCAT CAGTG
                                 C       C
GAM498  ABCF2     5'  TGAAACAACAGTAACCTACC   19099       AAGTCA
                                GGTAGGT     TTGTTTCA
                                |||||||     ||||||||
                                CCATCCA     AACAAAGT
                                    ATGAC_
GAM498  CTPS2     3'  AAACCCATACTACTACCTCA   39081       GTA   CATT
                                TGAGGTAG   AGT    GTTT
                                ||||||||   |||    ||||
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                                ACTCCATC  TCA   CAAA
                                    A__   TACC
GAM498  CYP4F8   3' CAGTGACCCACCCACCT    23409     A  AA
                                AGGT GGT  GTCATTG
                                |||| |||  |||||||
                                TCCA CCA  CAGTGAC
                                  C   CC
GAM498  DKFZp761N1114 3' AGTACCTACCCTACCTCA    79013        TA  TC
                                TGAGGTAGG  AG  ATT
                                |||||||||  ||  |||
                                ACTCCATCC  TC  TGA
                                     CA  CA
GAM498  FLJ11082 3' TGAAACAATAACTCTGCACCA  37036    AG   GTA  C
                                TG  GTAG   AGT ATTGTTTCA
                                ||  ||||   ||| |||||||||
                                AC  CGTC   TCA TAACAAAGT
                                 CA   ___  A
GAM498  FLJ11560 3' AGACTCTGACCCACCTACCTCA 47215         AA   TT
                                TGAGGTAGGT  GTCA  GTTT
                                ||||||||||  ||||  ||||
                                ACTCCATCCA  CAGT  CAGA
                                     CC    CT
GAM498  FLJ20485 3' CAGTGACTCTCCCACCTCA   38765      A  TA
                                TGAGGT GG  AGTCATTG
                                ||||||  ||  ||||||||
                                ACTCCA CC  TCAGTGAC
                                   C  TC
GAM498  FLJ20511 3' AAACAATGAATGAGCCACCTTA 35316      A  AAG_
                                TGAGGT GGT   TCATTGTTT
                                ||||||  |||   |||||||||
                                ATTCCA CCG   AGTAACAAA
                                   _  AGTA
GAM498  KIAA0557 3' TGACTTCCTACCTCA      78011        T
                                TGAGGTAGG AAGTCA
                                |||||||||  ||||||
                                ACTCCATCC TTCAGT
                                          _
GAM498  KIAA1274 3' TAATACTTGCCTACCT     91369          C
                                AGGTAGGTAAGT ATTG
                                ||||||||||||  ||||
                                TCCATCCGTTCA TAAT
                                          _
GAM498  KIAA1297 3' TGACTCTCCTACCTCA     72188        TA
                                TGAGGTAGG  AGTCA
                                |||||||||  |||||
                                ACTCCATCC  TCAGT
                                     TC
GAM498  KIAA1571 5' TAGTGACTGACCCACCTCA   60959      A  A
                                TGAGGT GGT AGTCATTG
                                ||||||  ||| ||||||||
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                                ACTCCA CCA TCAGTGAT
                                   C   G
GAM498  ZNF396    3'  GAAACAACAAGTGCCTCA    75668       GGTAAGTCA
                                TGAGGTA       TTGTTTC
                                |||||||       |||||||
                                ACTCCGT       AACAAAG
                                   GAAC_____
GAM498  LOC130576 5'  AAACAATAACTGCCTA      74953       A  C
                                TAGGTA GT ATTGTTT
                                |||||| || |||||||
                                ATCCGT CA TAACAAA
                                   _  A
GAM498  LOC153339 3'  TGATTACCTACCTCA       86015          G
                                TGAGGTAGGTAA TCA
                                |||||||||||| |||
                                ACTCCATCCATT AGT
                                          _
GAM498  LOC158563 3'  TAATTGCCCTACCTACCTCA  81952          A_  C
                                TGAGGTAGGTA  GT ATTG
                                ||||||||||  || ||||
                                ACTCCATCCAT  CG TAAT
                                      CC  T
GAM498  LOC200942 3'  TGAAACCTTCCTACCCTACCTA 88949          A_  CATT__
          CCTCA                   TGAGGTAGGTA  GT     GTTTCA
                                ||||||||||  ||     ||||||
                                ACTCCATCCAT  CA     CAAAGT
                                      CC  TCCTTC
GAM498  LOC255349 3'  GAAATCATACCTACCTCA    95612          AGTCAT  _
                                TGAGGTAGGTA     TG TTTC
                                ||||||||||      || ||||
                                ACTCCATCCAT     AC AAAG
                                      _______  T
GAM499  ADH1B     3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM499  AHR       3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM499  FDFT1     3'  TAGGAAAGTGAAATG       15518          A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM499  JTB       3'  ATCTCAGACAGTGAAAGTGAAA 21959
          TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
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                                GTAAAGTGAAAGTGACAGACTCTA

GAM499  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM499  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM499  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM499  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM499  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_   CG_
GAM499  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM499  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                |||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM499  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                 ||||||        |||||||||
                                 GTAAAG        CAGACTCTA
                                    AAACATTT_
GAM499  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                    C__
GAM499  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
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                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM499  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM499  NIR3     3'  GCAGTGAAAGTGCAAT      66242      T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM499  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM499  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM499  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__   TT
GAM499  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM499  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM499  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM499  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM499  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
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                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM499  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                        _
GAM500  DDX19    3'  AACTACCTACCTCACTT     23383       TGTT   C
                                GAGTG    GGG AGGTAGTT
                                |||||    ||| ||||||||
                                TTCAC    TCC TCCATCAA
                                   _____  A
GAM500  CDC42BPB  3'  ACCCACCCAACACACTC     20098           CA
                                GAGTGTGTTGGG  GGT
                                ||||||||||||  |||
                                CTCACACAACCC  CCA
                                      AC
GAM500  COTL1    3'  AAACCACCTGTTCCCACCCTCT 87951       T   TT       A
              T                  AAGAG GTG  GGGCAGGT GTTT
                                ||||| |||  |||||||| ||||
                                TTCTC CAC  CTTGTCCA CAAA
                                   C   C_       C
GAM500  FLJ11126  3'  AACTACCTACCTCACTT     37082       TGTT   C
                                GAGTG    GGG AGGTAGTT
                                |||||    ||| ||||||||
                                TTCAC    TCC TCCATCAA
                                   _____  A
GAM500  NAV3     3'  AAACCACCTGCCCACTC     29769      GTGTT       A
                                GAGT     GGGCAGGT GTTT
                                ||||     |||||||| ||||
                                CTCA     CCCGTCCA CAAA
                                   ______       C
GAM500  RAI17    3'  ACCTACCCAACACACTTTT    91273            C
                                AAGAGTGTGTTGGG AGGT
                                |||||||||||||| ||||
                                TTTTCACACAACCC TCCA
                                      A
GAM500  LOC124460 3'  AAACTACCCCCCCACCACCCTC 76035     T   T    CA
                                GAG GTG TGGG  GGTAGTTT
                                ||| ||| ||||  ||||||||
                                CTC CAC ACCC  CCATCAAA
                                  C   C    CC
GAM500  LOC157867 3'  AACTAAGCAACACACTT     86554          GGCAGG
                                GAGTGTGTTG      TAGTT
                                ||||||||||      |||||
                                TTCACACAAC      ATCAA
                                      GA____
GAM501  ACVR1    5'  ATGTGACCAAGAGCCTGCATTA 6602             CT
                                TAATGCAGGCTCTT  TCACAT
                                ||||||||||||||  ||||||
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                                ATTACGTCCGAGAA  AGTGTA
                                       CC
GAM501  ARHGAP6  5' ATGTCCGCGCAGAGCCTGCTCC 6759     AAT       TCTTC_
           ACA                   TGT   GCAGGCTCT     ACAT
                                |||   |||||||||     ||||
                                ACA   CGTCCGAGA     TGTA
                                  CCT       CGCGCC
GAM501  ATP11B   3' AGTAGGCCTGCATTACA     80314          T  T
                                TGTAATGCAGGC CT CT
                                |||||||||||| || ||
                                ACATTACGTCCG GA GA
                                       _  T
GAM501  CALCR    3' ATGTGAAGAAAAAGACCTGCA  8217       _  C_
                                TGCAGG CT  TTCTTCACAT
                                |||||| ||  ||||||||||
                                ACGTCC GA  AAGAAGTGTA
                                   A  AA
GAM501  DUSP5    3' ATGTGAAGAAAAGCAGTAT   15350     AG   C
                                ATGC  GCT TTCTTCACAT
                                ||||  ||| ||||||||||
                                TATG  CGA AAGAAGTGTA
                                  A_   A
GAM501  FOXO1A   3' ATGCGAACAGACCAACCTGGCA 8904        _  C___   TC   A
           TTACA                 GTAATGC AGG    TCT  TTC CAT
                                ||||||| |||    |||  ||| |||
                                CATTACG TCC    AGA  AAG GTA
                                   G   AACC   C_  C
GAM501  SYT4     3' ATGTAAAGAAAATGTATTACA  62434         GGCTC    C
                                TGTAATGCA    TTCTT ACAT
                                |||||||||    ||||| ||||
                                ACATTATGT    AAGAA TGTA
                                     AA___     A
GAM501  C1orf24  3' AAGTGCCTTGCATTACA     53699         _  T
                                TGTAATGCA GGC CTT
                                ||||||||| ||| |||
                                ACATTACGT CCG GAA
                                     T   T
GAM501  FLJ10546 3' GGAAACCTGTATTACA      59478          CTC
                                TGTAATGCAGG   TTCT
                                ||||||||||   ||||
                                ACATTATGTCC   AAGG
                                      A__
GAM501  FLJ22174 3' ATGTGCGGGGGAGGCCCACACT 41674      A  CA  _     T
           ACA                   TGTA TG  GGC TCTTCT CACAT
                                |||| ||  ||| |||||| |||||
                                ACAT AC  CCG AGGGGG GTGTA
                                  C  AC   G     C
GAM501  MGC2217  5' ATGTGAAGAAACTCATGCA   44175     GGCTC
                                TGCA    TTCTTCACAT
                                ||||    ||||||||||
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                                ACGT    AAGAAGTGTA
                                  ACTCA
GAM501  LOC149992 5'  ATGCGAAGAAGAGGACTGCTCT 79556     AT   G_      A
           ACA                    TGTA  GCAG  CTCTTCTTC CAT
                                |||| |||| ||||||||| |||
                                ACAT  CGTC  GAGAAGAAG GTA
                                  CT   AG       C
GAM501  LOC255452 5'  GAAGAAGGGACCTCCA     97535    C  _
                                TG AGG CTCTTCTTC
                                || ||| |||||||||
                                AC TCC GGGAAGAAG
                                 C  A
GAM502  ABCC3    3'  GGCCCCTGTCATCCTCATGCTG 39160     TCA      CTT_
                                CAGC   AGGATGAC   GCC
                                ||||  ||||||||   |||
                                GTCG   TCCTACTG   CGG
                                  TAC      TCCC
GAM502  ACCN2    3'  GGGCAAGGGACCTCAGGCTG   39170     CA   ATGA
                                CAGCT  AGG   CCTTGCCC
                                |||||  |||   ||||||||
                                GTCGG  TCC   GGAACGGG
                                  AC   AG__
GAM502  ACTR1B   3'  GGACAGGAGCCTTGAGCTG   70822        ATGA   TG
                                CAGCTCAAGG   CCT  CC
                                ||||||||||   |||  ||
                                GTCGAGTTCC   GGA  GG
                                     GA__   CA
GAM502  ARG2     3'  GTGCATCCTTGAACTG     6754     C       _
                                CAG TCAAGGATG AC
                                ||| ||||||||| ||
                                GTC AGTTCCTAC TG
                                  A       G
GAM502  AXIN1    3'  GGGCAAGGTCCCGAGGCT    60858     CAA  AT
                                AGCT   GG  GACCTTGCCC
                                ||||   ||  ||||||||||
                                TCGG   CC  CTGGAACGGG
                                  AG_  __
GAM502  CLTCL1   3'  CATGGTGCTTGAGCTG     63669        GATG   T
                                CAGCTCAAG    ACC TG
                                |||||||||    ||| ||
                                GTCGAGTTC    TGG AC
                                     G___    T
GAM502  DLG5     5'  AGGTCATCTCTGAGCTG     82910       AG
                                CAGCTCA  GATGACCT
                                |||||||  ||||||||
                                GTCGAGT  CTACTGGA
                                    CT
GAM502  E2F1     3'  GGGCAGGGGTCCCTGAGCTG  84800       A   GA
                                CAGCTCA GGAT  CCTTGCCC
                                ||||||| ||||  ||||||||
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                                GTCGAGT CCTG  GGGACGGG
                                    C   __
GAM502  FMOD    3'  GGGCAAGGTTGGGACAAAGC  8932     CAAGGA
                                GCT     TGACCTTGCCC
                                |||     ||||||||||
                                CGA     GTTGGAACGGG
                                  AACAGG
GAM502  FUT6    5'  GGGCAAGGTCATGCATGACTG 3815     C  AGG
                                CAG TCA  ATGACCTTGCCC
                                ||| |||  ||||||||||||
                                GTC AGT  TACTGGAACGGG
                                  _  ACG
GAM502  GGA3    3'  GGCCACACTTGAGCTG     25743        GA  ACCTT
                                CAGCTCAAG  TG    GCC
                                |||||||||  ||    |||
                                GTCGAGTTC  AC    CGG
                                     AC  _____
GAM502  GGA3    3'  GGCCACACTTGAGCTG     56827        GA  ACCTT
                                CAGCTCAAG  TG    GCC
                                |||||||||  ||    |||
                                GTCGAGTTC  AC    CGG
                                     AC  _____
GAM502  GRB10   5'  GCGGTGCATTCTTGA      17980        _  TT
                                TCAAGGATG ACC  GC
                                |||||||||  |||  ||
                                AGTTCTTAC TGG  CG
                                     G  __
GAM502  HOXD4   5'  GGATTCATTCTCCCTTGAGCTG 27527         AT  CCTTG_
                                CAGCTCAAGG  GA     CC
                                ||||||||||  ||     ||
                                GTCGAGTTCC  CT     GG
                                     CT  TACTTA
GAM502  IL17    3'  GCATGTCTTTGAGT       9332          ACCT
                                GCTCAAGGATG    TGC
                                ||||||||||    |||
                                TGAGTTTCTGT    ACG
                                      ____
GAM502  IL1RAPL2 5'  GGGCAAGGCTGCTCCGAAGC  33795    CAA  _ GA
                                GCT   GGA T  CCTTGCCC
                                |||   ||| |  ||||||||
                                CGA   CCT G  GGAACGGG
                                  AG_   C TC
GAM502  IL21R   3'  CAAGGTCACCTGGGCTG    41425       A  A
                                CAGCTCA GG TGACCTTG
                                ||||||| || ||||||||
                                GTCGGGT CC ACTGGAAC
                                     _ _
GAM502  INHBB   3'  GGTGGCATTCTTGAACTG   9341     C       A  TT
                                CAG TCAAGGATG CC  GCC
                                ||| |||||||| ||  |||
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                                GTC AGTTCTTAC GG  TGG
                                  A       _ __
GAM502  IRS2     3'  GGCAAGGTCACCTGC      59720    TCA   A
                                GC   AGG TGACCTTGCC
                                ||   ||| ||||||||||
                                CG   TCC ACTGGAACGG
                                 ____   _
GAM502  JAK2     3'  GTCATCCTTTGAGCTG      17127         _
                                CAGCTCAA GGATGAC
                                |||||||| |||||||
                                GTCGAGTT CCTACTG
                                     T
GAM502  MAP3K5   5'  GCGCGGCGCCCTTGAGCTG   19803          A  A  T
                                CAGCTCAAGG TG CC TGC
                                |||||||||| || || |||
                                GTCGAGTTCC GC GG GCG
                                      C  _  C
GAM502  MEST     3'  GCATGTCTCTCTTGAGCT    69899         AT   CT
                                AGCTCAAGG  GAC  TGC
                                |||||||||  |||  |||
                                TCGAGTTCT  CTG  ACG
                                     CT   T_
GAM502  MEST     5'  GGCAAGGTCTTACCTGA     69900     A  AT_
                                TCA GG   GACCTTGCC
                                ||| ||   |||||||||
                                AGT CC   CTGGAACGG
                                  _  ATT
GAM502  MGST2    5'  GCAAAGGTCATTCAGC      10033     CAA        _
                                GCT   GGATGACCTT GC
                                |||   |||||||||| ||
                                CGA   CTTACTGGAA CG
                                  ___         A
GAM502  PACSIN3  5'  GGACACCCGGGTCCTTGAAGT  32585     _      GA  T__  _
                                GCT CAAGGAT  CC   TG CC
                                ||| |||||||  ||   || ||
                                TGA GTTCCTG  GG   AC GG
                                  A      __  CCC  A
GAM502  PFKL     5'  GGGCAAGGCCATCGGC      10520     CAAG    A
                                GCT    GATG CCTTGCCC
                                |||    |||| ||||||||
                                CGG    CTAC GGAACGGG
                                  _____    C
GAM502  POU4F1   3'  GGGCATAGTCTTTGAGCT    20664          GACCT
                                AGCTCAAGGAT    TGCCC
                                ||||||||||     |||||
                                TCGAGTTTCTG    ACGGG
                                      AT___
GAM502  PPP2R5C  3'  GCAAAATCATTTTGAGTT    10759         G    CC
                                AGCTCAAG ATGA  TTGC
                                |||||||| ||||  ||||
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                                TTGAGTTT TACT  AACG
                                    _   AA
GAM502  RPA3    5'  GGGCAAGGCCCAGGAATCTG  11381    C_  AA  ATGA
                                CAG  TC  GG   CCTTGCCC
                                |||  ||  ||   ||||||||
                                GTC  AG  CC   GGAACGGG
                                  TA  GA  C___
GAM502  RRM2    3'  GGGCAAGGAGCTTCTTAAGTT  6409     C    TGA
                                AGCT AAGGA   CCTTGCCC
                                |||| |||||   ||||||||
                                TTGA TTCTT   GGAACGGG
                                  A    CGA
GAM502  SF1     3'  GGCAAGGGCTTTGGC      16146    T    ATGA
                                GC CAAGG   CCTTGCC
                                || |||||   |||||||
                                CG GTTTC   GGAACGG
                                 _    G___
GAM502  SLC16A2  3'  GGCAGGGTCATCCCCGGGC   21502     AA
                                GCTC  GGATGACCTTGCC
                                ||||  ||||||||||||
                                CGGG  CCTACTGGGACGG
                                  CC
GAM502  SPTBN2   3'  GGCAAGGTCCCAGGC      22706     CAA  AT
                                GCT   GG  GACCTTGCC
                                |||   ||  |||||||||
                                CGG   CC  CTGGAACGG
                                  A__  __
GAM502  STK6    3'  GGCAAGGTTCGACTGCAGC   13189     CA  GAT
                                GCT  AG   GACCTTGCC
                                |||  ||   |||||||||
                                CGA  TC   TTGGAACGG
                                  CG  AGC
GAM502  TEM7    3'  GGACAAGGTTGTAGCTG     39887      CAAGG TG    _
                                CAGCT    A  ACCTTG CC
                                |||||    |  |||||| ||
                                GTCGA    T  TGGAAC GG
                                   _____ GT     A
GAM502  XPC     3'  GCCCACTCACCCTTTGAGCT   16135       _  A   CCTT
                                AGCTCAA GG TGA   GC
                                ||||||| || |||   ||
                                TCGAGTT CC ACT   CG
                                    T  C   CACC
GAM502  AKAP12   5'  GGGCAGGGACCCGCTAAGCTG  57844      CAA_  ATGA
                                CAGCT   GG   CCTTGCCC
                                |||||   ||   ||||||||
                                GTCGA   CC   GGGACGGG
                                  ATCG  CA__
GAM502  AKAP3   5'  CAAGATCTTGAGCTG      21209          ATGAC
                                CAGCTCAAGG    CTTG
                                ||||||||||    ||||
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                                GTCGAGTTCT    GAAC
                                     A____
GAM502  ARHGEF16 3'  GGACAAGAAGGGCCTTGAGT  27071       ATGAC  _
                                GCTCAAGG    CTTG CC
                                ||||||||    |||| ||
                                TGAGTTCC    GAAC GG
                                    GGGAA   A
GAM502  BMF      3'  GGGCAAGGCCATCAGCT    53162     CAAG   A
                                AGCT   GATG CCTTGCCC
                                ||||   |||| ||||||||
                                TCGA   CTAC GGAACGGG
                                  ____   C
GAM502  C1QR1    3'  GGACAACCTGTCTTTGAGC   23842         ACC  _
                                GCTCAAGGATG   TTG CC
                                ||||||||||   ||| ||
                                CGAGTTTCTGT   AAC GG
                                      CC_   A
GAM502  C20orf177 5'  GCAAGAATATTTTGAGC    62149       G   AC
                                GCTCAAG ATG  CTTGC
                                ||||||| |||  |||||
                                CGAGTTT TAT  GAACG
                                   _  AA
GAM502  C20orf97  3'  GGCATCCTTGAGCTG      40964          A
                                CAGCTCAAGGATG CC
                                |||||||||||| ||
                                GTCGAGTTCCTAC GG
                                          _
GAM502  CBCIP2   3'  GGCAAGGTCATTGGC      51591     CAAG
                                GCT   GATGACCTTGCC
                                |||   ||||||||||||
                                CGG   TTACTGGAACGG
                                  _____
GAM502  CRR9     3'  GGTCACCTTGAGCTG      47880         A
                                CAGCTCAAGG TGACC
                                |||||||||| |||||
                                GTCGAGTTCC ACTGG
                                         _
GAM502  CSMD1    5'  GGACAAGGTCATCAAGCT   73125     CAAG       _
                                AGCT   GATGACCTTG CC
                                ||||   |||||||||| ||
                                TCGA   CTACTGGAAC GG
                                  A___        A
GAM502  DDX17    5'  CAAGTCCTGAGTTG       48038       A  TGAC
                                CAGCTCA GGA   CTTG
                                ||||||| |||   ||||
                                GTTGAGT CCT   GAAC
                                   _  _____
GAM502  DKFZP434N161 3'  GGCAAGAGCTTGAGCT     78521       GATGAC
                                AGCTCAAG     CTTGCC
                                ||||||||     ||||||
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                                TCGAGTTC     GAACGG
                                    GA____
GAM502  DKFZP564I122 3'  GCAAAAGGTTTTGAGT      63174       GGAT    __
                                GCTCAA   GACCT  TGC
                                ||||||   |||||  |||
                                TGAGTT   TTGGA  ACG
                                   ____    AA
GAM502  DMRTC2   3'  GGCATTTCCTTGGCTG      61824      T     TGACCT
                                CAGC CAAGGA     TGCC
                                |||| ||||||     ||||
                                GTCG GTTCCT     ACGG
                                  _     TT____
GAM502  FLJ00001  3'  GGCGCTCACCCCTGAGC     81818       A  A   CCT
                                GCTCA GG TGA   TGCC
                                ||||| || |||   ||||
                                CGAGT CC ACT   GCGG
                                   C  C   C__
GAM502  FLJ10101  3'  GGACAGAGTCTTGAGCTG    45267        GGAT   C   _
                                CAGCTCAA    GAC TTG CC
                                ||||||||    ||| ||| ||
                                GTCGAGTT    CTG GAC GG
                                    ____   A   A
GAM502  FLJ10781  3'  GCAGGGTCCCTGAG        36632      A  AT
                                CTCA GG  GACCTTGC
                                ||||  ||  ||||||||
                                GAGT CC  CTGGGACG
                                  _  __
GAM502  FLJ11850  3'  CAAGGTCATGCCGTGACTG    42718     C   A  _
                                CAG TCA GG ATGACCTTG
                                ||| ||| ||  |||||||||
                                GTC AGT CC TACTGGAAC
                                  _   G  G
GAM502  FLJ12294  5'  GGGCAAATCACTTGAGCT     47019        _   GACC
                                AGCTCAAG GAT    TTGCCC
                                ||||||||  |||    ||||||
                                TCGAGTTC CTA    AACGGG
                                    A   ____
GAM502  FLJ14888  3'  GGGCAGATTGCTTGAGCTG    51684         _   GACC
                                CAGCTCAAG GAT    TTGCCC
                                |||||||||  |||    ||||||
                                GTCGAGTTC TTA    GACGGG
                                     G   ____
GAM502  FLJ20085  3'  GGCAAGACCTCAATTCTTGGCT 34518      T      _  C__
          G                      CAGC CAAGGAT GA   CTTGCC
                                ||||  |||||||  ||   ||||||
                                GTCG GTTCTTA CT   GAACGG
                                  _      A  CCA
GAM502  FLJ21302  3'  GCAAGGTCAAATATGAGCTG   43215        AGGA
                                CAGCTCA    TGACCTTGC
                                |||||||    |||||||||
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                                GTCGAGT   ACTGGAACG
                                   ATAA
GAM502  FLJ21438  5'  GGCAGGGCCCTGAGC      61524      A  ATGA
                                GCTCA GG   CCTTGCC
                                ||||| ||   |||||||
                                CGAGT CC   GGGACGG
                                  C  ____
GAM502  FLJ22593  5'  GCCTTGTCACCCATTGAGCTG  45226       _  A   CTT
                                CAGCTCAA GG TGAC  GC
                                |||||||| || ||||  ||
                                GTCGAGTT CC ACTG  CG
                                    A  C   TTC
GAM502  FLJ22729  5'  AGGTCATCCCTGTACTG    45186    CT  A
                                CAG  CA GGATGACCT
                                |||  || |||||||||
                                GTC  GT CCTACTGGA
                                  AT  C
GAM502  FLJ25012  3'  GGCAAATCTCTTGAGC     58092       _  GACC
                                GCTCAAG GAT   TTGCC
                                ||||||| |||   |||||
                                CGAGTTC CTA   AACGG
                                   T  _____
GAM502  FLJ32894  3'  GCACCTGGTTCCTTGGGCTG  58339         TG  T__
                                CAGCTCAAGGA  ACC  TGC
                                ||||||||||  |||  |||
                                GTCGGGTTCCT  TGG  ACG
                                     __  TCC
GAM502  GTPBP5    3'  GGGCAAGGACAGCTCAGCTG  65360     CAA  A  A
                                CAGCT   GG TG CCTTGCCC
                                |||||   || || ||||||||
                                GTCGA   TC AC GGAACGGG
                                  C__  G  A
GAM502  H2AV      3'  GCAAGATTCTTGATCTG     56853    C      GAC
                                CAG TCAAGGAT   CTTGC
                                ||| ||||||||   |||||
                                GTC AGTTCTTA   GAACG
                                  T       ___
GAM502  HIG2      3'  GGGCAAGGCCTGTTTAGGC   25295    CA___   ATGA
                                GCT    AGG   CCTTGCCC
                                |||    |||   ||||||||
                                CGG    TCC   GGAACGGG
                                  ATTTG  ____
GAM502  HSPB7     3'  GGCAAGGCCACGTGGGGTTG  27028      AAGGA  A
                                CAGCTC    TG CCTTGCC
                                ||||||    || |||||||
                                GTTGGG    AC GGAACGG
                                   GTGC_  C
GAM502  KIAA0014  3'  GGCAGGGTGCCTGAGCTG   27849       A  ATG
                                CAGCTCA GG   ACCTTGCC
                                ||||||| ||   ||||||||
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                                GTCGAGT CC   TGGGACGG
                                   _ G__
GAM502  KIAA0062  3' GGCAAGGTTCATCCTGA     70242     A     _
                                TCA GGATGA CCTTGCC
                                ||| |||||| |||||||
                                AGT CCTACT GGAACGG
                                  _     T
GAM502  KIAA0534  5' GGACAAGGTCGGGAGACTG    71431     _  AAGGAT      _
                                CAG CTC     GACCTTG CC
                                ||| |||     ||||||| ||
                                GTC GAG     CTGGAAC GG
                                  A  GG____      A
GAM502  KIAA0537  5' GGGCAAGGTCCGTGAGTCA    29253    A    AGGAT
                                C GCTCA     GACCTTGCCC
                                | |||||     ||||||||||
                                A TGAGT     CTGGAACGGG
                                 C    GC___
GAM502  KIAA0889  3' GGGCAGATCACTTGAGCTG    31144         _  GACC
                                CAGCTCAAG GAT    TTGCCC
                                ||||||||| |||    ||||||
                                GTCGAGTTC CTA    GACGGG
                                     A  _____
GAM502  KIAA0937  3' GGGCTACCTCATCCTCGTGCTG 91588      TCA      CCTT
                                CAGC   AGGATGA    GCCC
                                ||||   |||||||    ||||
                                GTCG   TCCTACT    CGGG
                                  TGC      CCAT
GAM502  KIAA0940  3' GCATTCACCCTTGGGCTG    29871         A   CCT
                                CAGCTCAAGG TGA   TGC
                                |||||||||| |||   |||
                                GTCGGGTTCC ACT   ACG
                                     C   T__
GAM502  KIAA1054  5' GGCGAACACTTGAGCTG     68444         GATGACC
                                CAGCTCAAG      TTGCC
                                |||||||||      |||||
                                GTCGAGTTC      AGCGG
                                     ACA____
GAM502  KIAA1102  3' AAGCTCTATCTCTGAGCT    69008       AG  _  C
                                AGCTCA  GAT GA CTT
                                ||||||  ||| || |||
                                TCGAGT  CTA CT GAA
                                   CT   T  C
GAM502  KIAA1196  3' GGCTTCATCCTTGGGC      61474           CCTT
                                GCTCAAGGATGA    GCC
                                ||||||||||||    |||
                                CGGGTTCCTACT    CGG
                                      T___
GAM502  KIAA1321  3' AGGCATCCTTGAGCT       62222           A
                                AGCTCAAGGATG CCT
                                |||||||||||| |||
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                                TCGAGTTCCTAC GGA
                                           _
GAM502  KIAA1464  3'  GGACAGAGGCCCTTGAGT    68269        ATGA  _ _
                                GCTCAAGG   CCT TG CC
                                ||||||||   ||| || ||
                                TGAGTTCC   GGA AC GG
                                    C___   G  A
GAM502  KIAA1484  3'  GGGCAGGGCCCCCTGACACTG  69977     CTCA  ATGA
                                CAG   AGG   CCTTGCCC
                                |||   |||   ||||||||
                                GTC   TCC   GGGACGGG
                                  ACAG  CCC_
GAM502  KIAA1831  3'  GGGCAAGGCACTGGCTGAGCTG 63784       A__  A  A
                                CAGCTCA  GG TG CCTTGCCC
                                |||||||  || || ||||||||
                                GTCGAGT  TC AC GGAACGGG
                                    CGG  _ _
GAM502  KIAA1856  3'  GGGCAAGGCCCGCAAGCT    92666     CAA  ATGA
                                AGCT  GG   CCTTGCCC
                                ||||  ||   ||||||||
                                TCGA  CC   GGAACGGG
                                  ACG  C___
GAM502  MGC10966  5'  GCAAGGTTGTCTTGGCTG    48894      CA   TG
                                CAGCT  AGGA  ACCTTGC
                                |||||  ||||  |||||||
                                GTCGG  TTCT  TGGAACG
                                  __   GT
GAM502  MGC10981  3'  GGGCTTTTTACCCTTGAGCTG  51022        A  CCTT
                                CAGCTCAAGG TGA   GCCC
                                |||||||||| |||   ||||
                                GTCGAGTTCC ATT   CGGG
                                     C  TTT_
GAM502  MGC22014  3'  GGCAAGTTCCTGAGCT      64496       A  TGAC
                                AGCTCA GGA   CTTGCC
                                |||||| |||   ||||||
                                TCGAGT CCT   GAACGG
                                   _  T___
GAM502  MGC2562   3'  GCAAATCACTTGAGCT      50440        _  GACC
                                AGCTCAAG GAT   TTGC
                                |||||||| |||   ||||
                                TCGAGTTC CTA   AACG
                                   A  ____
GAM502  MGC29667  3'  GGCTGGTTCATCCTTGA     58334         _ TT
                                TCAAGGATGA CC  GCC
                                |||||||||| ||  |||
                                AGTTCCTACT GG  CGG
                                     T  T_
GAM502  MYH7B     3'  GCAAGGTCAAGAGCT       70531       AAGGA
                                AGCTC    TGACCTTGC
                                |||||    |||||||||
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                                TCGAG    ACTGGAACG
                                  A____
GAM502  NIR3     3'  GAGCAATCCTTGGCTG      66240      T      GAC
                                CAGC CAAGGAT   CTT
                                |||| |||||||   |||
                                GTCG GTTCCTA   GAG
                                  _      AC_
GAM502  NPTXR    3'  GGGCAAGGTTCAAGGC      54186     CAAG  TG
                                GCT   GA  ACCTTGCCC
                                |||   ||  |||||||||
                                CGG   CT  TGGAACGGG
                                 AA__  __
GAM502  NPTXR    3'  GGGCAAGGTTCAAGGC      26650     CAAG  TG
                                GCT   GA  ACCTTGCCC
                                |||   ||  |||||||||
                                CGG   CT  TGGAACGGG
                                 AA__  __
GAM502  NYD-SP16 3'  GCAAGGTCTTCAAGCT      49219      CAA   T
                                AGCT   GGA GACCTTGC
                                ||||   ||| ||||||||
                                TCGA   CTT CTGGAACG
                                  A__   _
GAM502  PJA1     3'  GGCAAAATCATTTTTG       42325         CC
                                CAAGGATGA  TTGCC
                                |||||||||  |||||
                                GTTTTTACT  AACGG
                                     AA
GAM502  PRO1992  3'  GCACTCCTCTTGAGCTG     26057         AT  CCT
                                CAGCTCAAGG  GA   TGC
                                ||||||||||  ||   |||
                                GTCGAGTTCT  CT   ACG
                                     C_  C__
GAM502  RIS1     3'  GCAAGGTTTGTGCTG       80581      T  AGGAT
                                CAGC CA    GACCTTGC
                                |||| ||    ||||||||
                                GTCG GT    TTGGAACG
                                  T  _____
GAM502  RPL34    5'  GCAGTCCTTTGAGCTG      53246         AT   CT
                                CAGCTCAAGG  GAC  TGC
                                |||||||||  |||  |||
                                GTCGAGTTTC  CTG  ACG
                                          __   __
GAM502  SCYA13   3'  GCAAGGCCTTGAGC        18258         ATGA
                                GCTCAAGG   CCTTGC
                                ||||||||   ||||||
                                CGAGTTCC   GGAACG
                                           ____
GAM502  SEPT3    3'  CAGGGATCCTTGGCT       38887     T      GA
                                AGC CAAGGAT  CCTTG
                                ||| |||||||  |||||
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                                TCG GTTCCTA  GGGAC
                                  _     __
GAM502  TIMM22   3'  GGGCAAGGCGGACTGATGC   78313    TCA  GA  A
                                GC   AG  TG CCTTGCCC
                                ||   ||  || ||||||||
                                CG   TC  GC GGAACGGG
                                 TAG  AG  _
GAM502  UBE2C    3'  GGACTCTTTATCTTGAGCTG   22818        G    CCTTG
                                CAGCTCAAG ATGA    CC
                                ||||||||| ||||    ||
                                GTCGAGTTC TATT    GG
                                     _   TCTCA
GAM502  VRP      5'  GGGCAAGGAACTTAAACTTG   22948     GA   ___
                                CAAG  TGA   CCTTGCCC
                                ||||  |||   ||||||||
                                GTTC  ATT   GGAACGGG
                                  AA   CAA
GAM502  WBSCR16  3'  GGGCAAGGTCCCTCTCCAGCTG 94512      CA   AT
                                CAGCT  AGG  GACCTTGCCC
                                |||||  |||  ||||||||||
                                GTCGA  TCT  CTGGAACGGG
                                   CC   CC
GAM502  LOC115219 5' GGGCAAGGCGGGTTCTAGCTG  73315      CA    GA_
                                CAGCT  AGGAT   CCTTGCCC
                                |||||  |||||   ||||||||
                                GTCGA  TCTTG   GGAACGGG
                                   __    GGC
GAM502  LOC124912 5' GGACATCTTGAGCTG       74352         G   A
                                CAGCTCAAG ATG CC
                                ||||||||| ||| ||
                                GTCGAGTTC TAC GG
                                     _   A
GAM502  LOC126536 3' GGACAACAAGCCTTGAGCTG   74539          ATGACC  _
                                CAGCTCAAGG     TTG CC
                                ||||||||||     ||| ||
                                GTCGAGTTCC     AAC GG
                                     GAAC__   A
GAM502  LOC130074 3' GGGCAAGGCAGCTGGGC     76136       A GA  A
                                GCTCA G  TG CCTTGCCC
                                ||||| |  || ||||||||
                                CGGGT C  AC GGAACGGG
                                  _ G_  _
GAM502  LOC134637 3' CAAGTGCTTGAGTTG       75201          G TGAC
                                CAGCTCAAG A    CTTG
                                ||||||||| |    ||||
                                GTTGAGTTC T    GAAC
                                     G _____
GAM502  LOC139709 3' GGCAACTCCTTGGCTG      75382      T     TGACC
                                CAGC CAAGGA    TTGCC
                                |||| ||||||    |||||
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                                GTCG GTTCCT    AACGG
                                  _    C____
GAM502  LOC144289 3'  GGGCAAGGCTGGTTTAGAACTG 83027    C  A   ATGA
                                CAG TC AGG   CCTTGCCC
                                ||| || |||   ||||||||
                                GTC AG TTT   GGAACGGG
                                  A  A   GGTC
GAM502  LOC144845 5'  GGGCAAGGTGGGGGTGAAGT   56662    _  AGGATG
                                GCT CA     ACCTTGCCC
                                ||| ||     |||||||||
                                TGA GT     TGGAACGGG
                                  A  GGGGG_
GAM502  LOC145333 3'  GGCCAACACCTTGAGCTG    83329         A  ACCTT
                                CAGCTCAAGG TG    GCC
                                |||||||||| ||    |||
                                GTCGAGTTCC AC    CGG
                                      _  AAC__
GAM502  LOC145815 5'  GGGCAAGGTTTTGAACTTG   83520     GAT__
                                CAAG    GACCTTGCCC
                                ||||    ||||||||||
                                GTTC    TTGGAACGGG
                                  AAGTT
GAM502  LOC145988 5'  GGGCAAGTTGCTTGAGCT    77611        GAT   C
                                AGCTCAAG   GAC TTGCCC
                                ||||||||   ||| ||||||
                                TCGAGTTC   TTG AACGGG
                                    G__   _
GAM502  LOC146272 5'  GGACGTCATCCTCGAACTG   77790    C  A      CTTG
                                CAG TC AGGATGAC   CC
                                ||| || ||||||||   ||
                                GTC AG TCCTACTG   GG
                                  A  C       CA__
GAM502  LOC146445 3'  GGGCAAGGCCACCAAAGC    83681    CAA  A  A
                                GCT   GG TG CCTTGCCC
                                |||   || || ||||||||
                                CGA   CC AC GGAACGGG
                                  AA_  _  C
GAM502  LOC148936 5'  GGCAAGGTAGAGCTTGGGCTG  84296        GATG
                                CAGCTCAAG   ACCTTGCC
                                |||||||||   ||||||||
                                GTCGGGTTC   TGGAACGG
                                    GAGA
GAM502  LOC148938 5'  GGCAAGGTAGAGCTTGGGCTG  84278        GATG
                                CAGCTCAAG   ACCTTGCC
                                |||||||||   ||||||||
                                GTCGGGTTC   TGGAACGG
                                    GAGA
GAM502  LOC149837 5'  GCAAGCTGGGCCTTGGGCTG   84739        ATGAC
                                CAGCTCAAGG    CTTGC
                                ||||||||||    |||||
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                                GTCGGGTTCC    GAACG
                                     GGGTC
GAM502  LOC151162 5'  GGACATGTTCTTGAGC      85245          ACCT  _
                                GCTCAAGGATG   TG CC
                                ||||||||||   || ||
                                CGAGTTCTTGT   AC GG
                                     ____  A
GAM502  LOC152317 3'  GGCTAAAGTCATCCTGAACTG  85646    C   A     C  _
                                CAG TCA GGATGAC TT GCC
                                ||| ||| ||||||| || |||
                                GTC AGT CCTACTG AA CGG
                                  A  _     A  T
GAM502  LOC152319 3'  AAGTTCATCCTTGGACTG    80532    CT       C
                                CAG  CAAGGATGA CTT
                                |||  ||||||||| |||
                                GTC  GTTCCTACT GAA
                                  AG        T
GAM502  LOC155064 3'  GGGCAAGAGGCTTTGAGTTG   81249          ATGAC
                                CAGCTCAAGG    CTTGCCC
                                ||||||||||    |||||||
                                GTTGAGTTTC    GAACGGG
                                     GGA__
GAM502  LOC155370 5'  CAAGGTCGTCGGCTG       72061       CAAG
                                CAGCT    GATGACCTTG
                                |||||   ||||||||||
                                GTCGG    CTGCTGGAAC
                                   ____
GAM502  LOC157688 5'  GGGCATCCCTCCCCTTGAGCTG 87283          ATGACCT
                                CAGCTCAAGG      TGCCC
                                ||||||||||      |||||
                                GTCGAGTTCC      ACGGG
                                     CCTCCCT
GAM502  LOC158230 3'  GCAACTCTGTCCTTGAGC    81799          ACC
                                GCTCAAGGATG   TTGC
                                ||||||||||   ||||
                                CGAGTTCCTGT   AACG
                                      CTC
GAM502  LOC170082 3'  GGACAAGTGTCCTTGAG     82562         GAC   _
                                CTCAAGGAT   CTTG CC
                                |||||||||   |||| ||
                                GAGTTCCTG   GAAC GG
                                     T__    A
GAM502  LOC197408 5'  GGGCAAGGCCCCTCAAGC    89751     CA  ATGA
                                GCT  AGG    CCTTGCCC
                                |||  |||    ||||||||
                                CGA  TCC    GGAACGGG
                                  AC   CC__
GAM502  LOC200470 5'  GAGCTTGCTCCTTGAGCTG   90063          _  C
                                CAGCTCAAGGA TGA CTT
                                |||||||||| ||| |||
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                                GTCGAGTTCCT GTT GAG
                                      C   C
GAM502   LOC200942 5'  GGCAAGGTCCCTGGACTG    88948    CT  A  AT
                                CAG  CA GG  GACCTTGCC
                                |||  || ||  |||||||||
                                GTC  GT CC  CTGGAACGG
                                  AG  _ __
GAM502   LOC203377 5'  GGACATGTTCTTGAGC      90583         ACCT  _
                                GCTCAAGGATG    TG CC
                                ||||||||||    || ||
                                CGAGTTCTTGT    AC GG
                                      ____ A
GAM502   LOC220370 3'  GGGCAGGGGTCCTCAAAGC   92833    CA_    GA
                                GCT   AGGAT  CCTTGCCC
                                |||   |||||  ||||||||
                                CGA   TCCTG  GGGACGGG
                                  AAC    __
GAM502   LOC220776 3'  GGCTCCATCCCTGGCTG     68395     T  A    ACCTT
                                CAGC CA GGATG    GCC
                                |||| || |||||    |||
                                GTCG GT CCTAC    CGG
                                  _ C    CT___
GAM502   LOC221486 3'  GGCAAGGGGCTGGCTG      91013      CAA  ATGA
                                CAGCT   GG    CCTTGCC
                                |||||   ||    |||||||
                                GTCGG   TC    GGAACGG
                                   ___  GG__
GAM502   LOC221560 3'  GGGCAAGGGAGACTTGGCTG  93774     T    GATGA
                                CAGC CAAG     CCTTGCCC
                                |||| ||||     ||||||||
                                GTCG GTTC     GGAACGGG
                                  _   AGAG_
GAM502   LOC221760 3'  GGCAAGATCTTAATTTTGAGT  93789        AT__  C
                                GCTCAAGG    GA CTTGCC
                                ||||||||    || ||||||
                                TGAGTTTT    CT GAACGG
                                     AATT  A
GAM502   LOC254419 5'  GCAAGGGCATTCAAGCT     97508     CAA    A
                                AGCT   GGATG CCTTGC
                                ||||   ||||| ||||||
                                TCGA   CTTAC GGAACG
                                  A__     G
GAM502   LOC254439 3'  GGCAAGGACCACAGCTG     94748      CAA  ATGA
                                CAGCT   GG    CCTTGCC
                                |||||   ||    |||||||
                                GTCGA   CC    GGAACGG
                                   CA_  A___
GAM502   LOC255995 5'  GGACAATCTATTTCTTGAGC   96976        TGACC  _
                                GCTCAAGGA     TTG CC
                                |||||||||     ||| ||
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                                CGAGTTCTT    AAC GG
                                     TATCT   A
GAM502  LOC257426 3'  GGGCAAGGCCACCAGACCTG  66646    C  AA  A  A
                                CAG TC  GG TG CCTTGCCC
                                ||| ||  || || ||||||||
                                GTC AG  CC AC GGAACGGG
                                  C  A_  _  C
GAM502  LOC257535 3'  GGGCAAGGGAGACTTGGCTG  97779     T   GATGA
                                CAGC CAAG    CCTTGCCC
                                |||| ||||    ||||||||
                                GTCG GTTC    GGAACGGG
                                  _   AGAG_
GAM502  LOC257595 3'  GGGCAAGGGAGACTTGGCTG  97943     T   GATGA
                                CAGC CAAG    CCTTGCCC
                                |||| ||||    ||||||||
                                GTCG GTTC    GGAACGGG
                                  _   AGAG_
GAM502  LOC84524  3'  GCAAGGTTAGGCTGAGT     50670      A GA
                                GCTCA G  TGACCTTGC
                                ||||| |  |||||||||
                                TGAGT C  ATTGGAACG
                                  _ GG
GAM502  LOC88745  3'  GGCAAGGATCACAGCTG     92267      CAAG   GA
                                CAGCT    GAT  CCTTGCC
                                |||||    |||  |||||||
                                GTCGA    CTA  GGAACGG
                                   CA__   __
GAM502  LOC89953  5'  GGGCAAGGTCCCCCAGGC    56377     CAA  AT
                                GCT   GG  GACCTTGCCC
                                |||   ||  ||||||||||
                                CGG   CC  CTGGAACGGG
                                  A__  CC
GAM502  LOC90019  3'  GGGCAGGGGCCCTTGGCTG   56766     T    ATGA
                                CAGC CAAGG   CCTTGCCC
                                |||| |||||   ||||||||
                                GTCG GTTCC   GGGACGGG
                                  _    CG__
GAM502  LOC90092  5'  GGACAAGGTCATCTAGC     61411     CAA        _
                                GCT   GGATGACCTTG CC
                                |||   |||||||||||  ||
                                CGA   TCTACTGGAAC GG
                                  ___         A
GAM502  LOC90141  3'  GCAAGCCTTGAGCTG       61628          ATGAC
                                CAGCTCAAGG    CTTGC
                                ||||||||||    |||||
                                GTCGAGTTCC    GAACG
                                              _____
GAM502  LOC90297  5'  GGTGCCCTCATCCTTGGCTG  62159      T       CCT
                                CAGC CAAGGATGA   TGCC
                                |||| |||||||||   ||||
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                                GTCG GTTCCTACT   GTGG
                                  _       CCC
GAM502  LOC90333  3'  GGCAAGGTCTTCAGTCAAGCT  62293     CAAG_  T
                                AGCT    GA GACCTTGCC
                                ||||    || |||||||||
                                TCGA    CT CTGGAACGG
                                  ACTGA  T
GAM502  LOC90719  3'  GGGCAAGGGCCCCTAAGACTG  63886    _  CA   ATGA
                                CAG CT  AGG    CCTTGCCC
                                ||| ||  |||    ||||||||
                                GTC GA  TCC    GGAACGGG
                                 A  A_   CCG_
GAM502  LOC91450  5'  GGGCATGTGCCCTTGGGC    66075        AT ACCT
                                GCTCAAGG  G    TGCCC
                                ||||||||  |    |||||
                                CGGGTTCC  T    ACGGG
                                     CG GT__
GAM503  MBD4      3'  GTACAACCAACCACCTT     14090      CA  A
                                AAGG  GT GGTTGTAT
                                ||||  || ||||||||
                                TTCC  CA CCAACATG
                                  AC  A
GAM503  FLJ13782  3'  GACACAGGCAACCTACCCCT   46168     CA       ATA_
                                AGG  GTAGGTTGT    GTT
                                |||  |||||||||    |||
                                TCC  CATCCAACG    CAG
                                 C_        GACA
GAM503  SLC2A12   3'  GACATCAACCTCCGCCTT    59081      AGT     T  A
                                AAGGC   AGGTTG AT GTT
                                |||||   |||||| || |||
                                TTCCG   TCCAAC TA CAG
                                  CC_     _ _
GAM503  LOC91363  3'  ATAACTGCCCACCACCCCC   65775    CA  A   T TA
                                GG  GT GGT G  TAGTTAT
                                ||  || ||| |  |||||||
                                CC  CA CCA C  GTCAATA
                                 CC  _   _ CC
GAM504  GALC      3'  ATGGCAGTAACTTGATCA    3845            T
                                TGATCAAGTTACT GCTGT
                                |||||||||||| |||||
                                ACTAGTTCAATGA CGGTA
                                                _
GAM504  HOXD4     3'  TGGAAAGTAACTTAATCA    27532      C       G
                                TGAT AAGTTACTT CTG
                                |||| ||||||||| |||
                                ACTA TTCAATGAA GGT
                                  A       A
GAM504  INPP5B    3'  CACAGCAAGCAAACAGGTCA  95523      AAG  A
                                TGATC   TT CTTGCTGTG
                                |||||   || |||||||||
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                                ACTGG   AA GAACGACAC
                                   ACA  C
GAM504  CYP-M    3'  TGCACAGTATATTGATCA    40339       GTTACT
                                TGATCAA     TGCTGTGCA
                                |||||||     |||||||||
                                ACTAGTT     ATGACACGT
                                    AT_____
GAM504  FPGT     3'  TAGAAGTAACTTGTCCA     13848    AT       G
                                TG  CAAGTTACTT CTG
                                ||  |||||||||| |||
                                AC  GTTCAATGAA GAT
                                 CT        _
GAM504  HSD17B12 3'  ACTGCATTGTAACTTGGCCA  32340    AT      T_  T
                                TG  CAAGTTAC  TGC GT
                                ||  ||||||||  ||| ||
                                AC  GTTCAATG  ACG CA
                                 CG       TT  T
GAM504  KIAA0285 3'  ATTGTAGCAAAAAACTCAATCA 29012     CA   AC    GT
                                TGAT  AGTT  TTGCT  GCAAT
                                ||||  ||||  |||||  |||||
                                ACTA  TCAA  AACGA  TGTTA
                                  AC    AA    __
GAM504  KIAA1764 5'  CACAGCAAAACCGTGAT    69287     A_  AC
                                ATCA  GTT  TTGCTGTG
                                ||||  |||  ||||||||
                                TAGT  CAA  AACGACAC
                                  GC  __
GAM504  POPX1    3'  CACAGCAGTGTTAACTCA    29797   A    _ _
                                C AGTTA C TTGCTGTG
                                | |||||  | ||||||||
                                A TCAAT G GACGACAC
                                 C    T T
GAM504  LOC112817 3'  CAGCTTAAGAAACTTGATCA   56507         A  __
                                TGATCAAGTT CTT  GCTG
                                |||||||||| |||  ||||
                                ACTAGTTCAA GAA  CGAC
                                      A   TT
GAM504  LOC154739 5'  GCAGCTAAGTAACCTGACCA   86231    A  A     _
                                TG TCA GTTACTT GCTGT
                                || ||| ||||||| |||||
                                AC AGT CAATGAA CGACG
                                 C  C      T
GAM504  LOC167147 5'  ATTGCACAAGAGAAAACTAATC 82671     CA   A_  GC
           A                     TGAT  AGTT  CTT  TGTGCAAT
                                ||||  ||||  |||  ||||||||
                                ACTA  TCAA  GAG  ACACGTTA
                                  A_   AA  A_
GAM505  BRCA1    5'  CGAGGGAAGCGCTGAGGATCAG 23526     CA      AC__  GG
           GA                    TCC  ATCCTCAG   TCC  TG
                                |||  ||||||||   |||  ||
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                                AGG  TAGGAGTC   AGG  GC
                                  AC       GCGA   GA
GAM505  CAV2    3'  CCCAGGTCTGGAGATTGGGA  6942        CT     CC
                                TCCCAATC  CAGACT  GG
                                ||||||||  ||||||  ||
                                AGGGTTAG  GTCTGG  CC
                                    AG     AC
GAM505  CHRNA4  3'  CAGCGAGTCTGGAGACCAGGA  5614      CAA  CT      C G
                                TCC   TC  CAGACTC G TG
                                |||   ||  |||||||  | ||
                                AGG   AG  GTCTGAG C AC
                                  ACC  AG      _ G
GAM505  FBXL7   5'  CACCGGAGGGGATCGGGG   24543     A    CAGA
                                TCCC ATCCT    CTCCGGTG
                                ||||  |||||    ||||||||
                                GGGG TAGGG    GAGGCCAC
                                  C    _____
GAM505  HMGCL   3'  CCAGACCTGAGGAGTGAGA   3954     C  A      AC  C
                                TC CA TCCTCAG  TC GG
                                ||  ||  |||||||  ||  ||
                                AG GT AGGAGTC  AG CC
                                 A  G      C_  A
GAM505  LMAN1   3'  TTCGATGATCTGAGGATT    18736         C  CGG
                                AATCCTCAGA TC   TGAA
                                ||||||||||  ||   ||||
                                TTAGGAGTCT AG   GCTT
                                     _  TA_
GAM505  NTSR1   3'  CTGGAGTCTGAGGCCTGGGA   10292      AT
                                TCCCA  CCTCAGACTCCGG
                                |||||  ||||||||||||
                                AGGGT  GGAGTCTGAGGTC
                                   CC
GAM505  PARG    3'  CCAAAGTTTGAGAACTGGGA   13269      ATC      CC
                                TCCCA   CTCAGACT  GG
                                |||||   ||||||||  ||
                                AGGGT   GAGTTTGA  CC
                                   CAA       AA
GAM505  PRDM4   3'  TCACCACAGAATGGATTGGGA  24826         TCAGA  CC
                                TCCCAATCC    CT  GGTGA
                                |||||||||    ||  |||||
                                AGGGTTAGG    GA  CCACT
                                     TAA__  CA
GAM505  PRG2    5'  TCACCAACCTGCAGATTGGGA  10783        CT   ACTCC
                                TCCCAATC  CAG    GGTGA
                                ||||||||  |||    |||||
                                AGGGTTAG  GTC    CCACT
                                    AC   CAA__
GAM505  RAD9    3'  TCAGCCCTGGGGATCAGA    15936    CCA      ACTCC  _
                                TC   ATCCTCAG    GG TGA
                                ||   ||||||||    || |||
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                                AG   TAGGGGTC    CC ACT
                                 AC_       _____  G
GAM505  RXRA     3'  TTGGAATCTGAGAACCCGGA  11420     CAATC     C
                                TCC    CTCAGA TCCGG
                                |||    |||||| |||||
                                AGG    GAGTCT AGGTT
                                  CCCAA     A
GAM505  SMT3H1   3'  TCGGGGTCTGAGGCCCAGGA  59961     CAAT
                                TCC    CCTCAGACTCCGG
                                |||    ||||||||||||
                                AGG    GGAGTCTGGGGCT
                                  ACCC
GAM505  ABHD1    5'  GGAGCCTGAGGGTCGG      50881    A       A
                                CC ATCCTCAG CTCC
                                || |||||||| ||||
                                GG TGGGAGTC GAGG
                                 C       C
GAM505  AMOTL1   3'  TCTGAGCCTGAGGATGG     73656     A      A   C
                                CCA TCCTCAG CTC GG
                                ||| ||||||| ||| ||
                                GGT AGGAGTC GAG CT
                                  _      C   T
GAM505  C9orf7   3'  CATCTGCGTCTGAGGCTGGGA  34166      AT       TCC
                                TCCCA  CCTCAGAC   GGTG
                                |||||  ||||||||   ||||
                                AGGGT  GGAGTCTG   CTAC
                                   C_       CGT
GAM505  CALN1    3'  TCACCACTGTCCCCTTAGGATT 48876        CA___   TCC
           GG                     CCAATCCT    GAC   GGTGA
                                |||||||     |||   |||||
                                GGTTAGGA    CTG   CCACT
                                     TTCCC   TCA
GAM505  CNNM1    3'  CACAGCATAGTCTGGGACTGG  39768     A   T     CCG__
                                CCA TCC CAGACT     GTG
                                ||| ||| ||||||     |||
                                GGT AGG GTCTGA     CAC
                                  C   _      TACGA
GAM505  CSE-C    3'  TTGTGGGAATCTCAGGATTGG  91484        C   C   G TG
                                CCAATCCT AGA TCC G  A
                                |||||||| ||| ||| |  |
                                GGTTAGGA TCT AGG T  T
                                     C   A   G GT
GAM505  DCTD     3'  TTCAATCTCCAGAAGATTGGGA 8623          C  AGACTCCGG
                                TCCCAATC TC        TGAA
                                |||||||| ||        ||||
                                AGGGTTAG AG        ACTT
                                     A  ACCTCTA__
GAM505  DKFZp434A1520 5'  CCGGTCTGGGACTGG       61116     A   T    CT
                                CCA TCC CAGA  CCGG
                                ||| ||| ||||  ||||
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                                GGT AGG GTCT  GGCC
                                  C  _   __
GAM505  FLJ11320  3'  CACATCACTCTGAGGACAGGGA 37241      AA       CTCCG
                                TCCC  TCCTCAGA    GTG
                                ||||  ||||||||    |||
                                AGGG  AGGAGTCT    CAC
                                  AC       CACTA
GAM505  KIAA0350  3'  TTCACCATCGCGTGGGATTGGG 61177         T  GACTCC
          A                      TCCCAATCC CA     GGTGAA
                                |||||||||  ||     ||||||
                                AGGGTTAGG GT     CCACTT
                                     _  GCGCTA
GAM505  KIAA0652  3'  CACCCCTGAAGGTCGGGA    28458      A   C    ACTCC
                                TCCC ATC TCAG    GGTG
                                |||| ||| ||||    ||||
                                AGGG TGG AGTC    CCAC
                                  C   A   C____
GAM505  KIAA0980  3'  CTGGGACATCTGAGGATTGGGA 47203            C__
                                TCCCAATCCTCAGA   TCCGG
                                ||||||||||||||  |||||
                                AGGGTTAGGAGTCT   GGGTC
                                        ACA
GAM505  MGC10540  3'  CCAGTCCTGAAGGCTGGGA   50380      AT C   _   CC
                                TCCCA  C TCAG ACT  GG
                                |||||  | |||| |||  ||
                                AGGGT  G AGTC TGA  CC
                                   CG A    C  __
GAM505  NPC1L1    3'  CCAGGAGTCTGAAGGCTGGGA  25413      AT C       _
                                TCCCA  C TCAGACTCC GG
                                |||||  | |||||||||  ||
                                AGGGT  G AGTCTGAGG CC
                                   CG A        A
GAM505  TIP-1     3'  TCCTGGACACCGAGGATTGG   27507        AGAC    T
                                CCAATCCTC    TCCGG GA
                                |||||||||    |||||  ||
                                GGTTAGGAG    AGGTC CT
                                     CCAC    _
GAM505  YAP       3'  GAGTCTGGAGACTGGGA     57457      A  CT
                                TCCCA TC  CAGACTC
                                |||||  ||  |||||||
                                AGGGT AG  GTCTGAG
                                   C  AG
GAM505  YAP       3'  GAGTCTGGAGACTGGGA     36788      A  CT
                                TCCCA TC  CAGACTC
                                |||||  ||  |||||||
                                AGGGT AG  GTCTGAG
                                   C  AG
GAM505  YAP       3'  GAGTCTGGAGACTGGGA     57465      A  CT
                                TCCCA TC  CAGACTC
                                |||||  ||  |||||||
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                                AGGGT AG  GTCTGAG
                                   C  AG
GAM505  YAP      3'  GAGTCTGGAGACTGGGA     57463      A  CT
                                TCCCA TC  CAGACTC
                                ||||| ||  |||||||
                                AGGGT AG  GTCTGAG
                                   C  AG
GAM505  YAP      3'  GAGTCTGGAGACTGGGA     57459      A  CT
                                TCCCA TC  CAGACTC
                                ||||| ||  |||||||
                                AGGGT AG  GTCTGAG
                                   C  AG
GAM505  ZNF212   5'  TCACCGAGCAGGAATGGGA   24308      A   CAGA   C
                                TCCCA TCCT   CTC GGTGA
                                ||||| ||||   ||| |||||
                                AGGGT AGGA   GAG CCACT
                                   A   C___  _
GAM505  ZNF396   5'  TTCACCTCCTTGAGGATT    75672        ACTCC
                                AATCCTCAG    GGTGAA
                                |||||||||    ||||||
                                TTAGGAGTT    CCACTT
                                     CCT__
GAM505  LOC138389 3'  GGAGTCTGAGGATGGGA     76229      A
                                TCCCA TCCTCAGACTCC
                                ||||| ||||||||||||
                                AGGGT AGGAGTCTGAGG
                                   _
GAM505  LOC146669 5'  CTGAAATCTGAGGGTTGG    78056          CTC
                                CCAATCCTCAGA  CGG
                                ||||||||||||  |||
                                GGTTGGGAGTCT  GTC
                                      AAA
GAM505  LOC148753 3'  CCAGTCCTGAGGATGGGA    84212      A     _  CC
                                TCCCA TCCTCAG ACT  GG
                                ||||| ||||||| |||  ||
                                AGGGT AGGAGTC TGA  CC
                                   _     C  __
GAM505  LOC152441 5'  TGGAGTCCAAGGAATGAGA   85736   C  A   CA
                                TC CA TCCT  GACTCCG
                                || || ||||  |||||||
                                AG GT AGGA  CTGAGGT
                                 A  A   AC
GAM505  LOC157773 3'  TTCACAGATTTGAGGA      81611        C  CG
                                TCCTCAGA TC  GTGAA
                                |||||||| ||  |||||
                                AGGAGTTT AG  CACTT
                                     _ A_
GAM505  LOC221271 3'  TTCACCATGCTTTGGGGATT  91884          CTCC
                                AATCCTCAGA   GGTGAA
                                ||||||||||   ||||||
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                                TTAGGGGTTT    CCACTT
                                      CGTA
GAM505   LOC221663 5'  TCATGCTAAGGACTGGGA    93824      A    C  ACTCCG
                                TCCCA TCCT AG     GTGA
                                ||||| |||| ||     ||||
                                AGGGT AGGA TC     TACT
                                   C    A  G_____
GAM505   LOC253675 5'  TTCACTTCACTGGGATTAGGA  96775     C     T   ACTCC
                                TCC AATCC CAG     GGTGAA
                                ||| ||||| |||     ||||||
                                AGG TTAGG GTC     TCACTT
                                  A     _   ACT__
GAM505   LOC253955 3'  TCCTGGGTCTGAGCATT     94433     C      T    T
                                AAT CTCAGAC CCGG GA
                                ||| ||||||| |||| ||
                                TTA GAGTCTG GGTC CT
                                  C      _    _
GAM505   LOC254058 5'  AGTATGAGGATTGAGA      97324     C       G
                                TC CAATCCTCA ACT
                                || |||||||| |||
                                AG GTTAGGAGT TGA
                                 A        A
GAM505   LOC256230 5'  CTGGAGAATCTGGGGATTGGGA 97452            __
                                TCCCAATCCTCAGA  CTCCGG
                                ||||||||||||||  ||||||
                                AGGGTTAGGGGTCT  GAGGTC
                                      AA
GAM505   LOC256231 5'  CTGGAGAATCTGGGGATTGGGA 97453            __
                                TCCCAATCCTCAGA  CTCCGG
                                ||||||||||||||  ||||||
                                AGGGTTAGGGGTCT  GAGGTC
                                      AA
GAM505   LOC257444 3'  CTGAAATCTAAGGATTGG    81112        C   CTC
                                CCAATCCT AGA   CGG
                                |||||||| |||   |||
                                GGTTAGGA TCT   GTC
                                     A   AAA
GAM505   LOC65243  5'  TCACCGGAATCTGTACCGGGA  43538      AATCCT    C
                                TCCC     CAGA TCCGGTGA
                                ||||     |||| ||||||||
                                AGGG     GTCT AGGCCACT
                                  CCAT__    A
GAM505   LOC93349  3'  TCACACAGTCACCCGGGATTGG 56463         CA__    CCG
                                CCAATCCT    GACT   GTGA
                                ||||||||    ||||   ||||
                                GGTTAGGG    CTGA   CACT
                                     CCCA    CA_
GAM506   ATP10C    5'  ATGGAGCAGGCGGGGAGCTCGC 44407     AT       AA   C
            A                    TGC  GCTCCCTGT  TGC CCAT
                                ||| |||||||||  ||| ||||
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                                ACG  CGAGGGGCG  ACG GGTA
                                  CT       G_  A
GAM506  AVPR1A   5'  GGGTAATAAATAGCATGCA   5540        CCCTG  A
                                TGCATGCT    TA TGCCC
                                ||||||||    || |||||
                                ACGTACGA    AT ATGGG
                                    TAA__  A
GAM506  CYP24    3'  ATGGGACAAGTGTAAAGCATGC 5767        CCCTGTAA  C
          A                      TGCATGCT       TG CCCAT
                                ||||||||       || |||||
                                ACGTACGA       AC GGGTA
                                    AATGTGA_  A
GAM506  SNTB2    3'  GGGCATTGAGATGCA      55613      G   CCTGT
                                TGCAT CTC    AATGCCC
                                ||||| |||    |||||||
                                ACGTA GAG    TTACGGG
                                  _  ______
GAM506  SORCS3   3'  ATGTAGCTGCAGAAAGCATGCA 30371       CC    AT  CC
                                TGCATGCT  CTGTA  GC  CAT
                                ||||||||  |||||  ||  |||
                                ACGTACGA  GACGT  CG  GTA
                                    AA    __  AT
GAM506  BNIP-S   3'  ATGGAGCGATGTAGAAGCATGC 56272       CC    A   C
          A                      TGCATGCT  CTGTA TGC CCAT
                                ||||||||  ||||| ||| ||||
                                ACGTACGA  GATGT GCG GGTA
                                    A_    A   A
GAM506  C2F      5'  GCGGTGGGGAGCAGGCA    20929     A      TG AA
                                TGC TGCTCCC  T  TGC
                                ||| |||||||  |  |||
                                ACG ACGAGGG  G  GCG
                                  G      GT __
GAM506  CIP29    3'  CAGAACAAGAAAGCATGTA   50401        CC  _  AA
                                TGCATGCT  CT GT  TG
                                ||||||||  || ||  ||
                                ATGTACGA  GA CA  AC
                                    AA  A  AG
GAM506  DKFZp547D155 3'  ATGAGGTTCAAGGGAGCGTGCA 70433          GTAAT   C
                                TGCATGCTCCCT    GCC CAT
                                ||||||||||||    ||| |||
                                ACGTGCGAGGGA    TGG GTA
                                    ACT__   A
GAM506  DNAJC6   3'  ATGAGGAGAGAATACAAAAAGC 28843        CCC    ATG___  C
          ATGCA                  TGCATGCT   TGTA     CC CAT
                                ||||||||   ||||     || |||
                                ACGTACGA   ACAT     GG GTA
                                    AAA    AAGAGA  A
GAM506  FLJ20130 3'  CGTCACGAGGAGCATGCA    34605         C   A
                                TGCATGCTCC TGT ATG
                                |||||||||| ||| |||
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                                ACGTACGAGG GCA TGC
                                      A   C
GAM506  G4      3' GGTGACAGGGAGCCTGCA    90995     T       AA
                                TGCA GCTCCCTGT  TGCC
                                |||| |||||||||  ||||
                                ACGT CGAGGGACA  GTGG
                                  C       __
GAM506  GREB1   3' ATGGGACATTATGGACA     72405    C   CT     C
                                TG TCC  GTAATG CCCAT
                                || |||  |||||| |||||
                                AC AGG  TATTAC GGGTA
                                 _  __     A
GAM506  KIAA0705 3' GGCACCAAGGCCTGGGAGCATG 24534         T_  AA___
                                CATGCTCCC  GT    TGCC
                                |||||||||  ||    ||||
                                GTACGAGGG  CG    ACGG
                                      TC  GAACC
GAM506  KIAA1580 5' ATGTGCACACAGGGAGCATTCA 69442    C        AA   CC
                                TG ATGCTCCCTGT  TGC  CAT
                                || ||||||||||  |||  |||
                                AC TACGAGGGACA  ACG  GTA
                                 T         C_   T_
GAM506  KIAA1951 3' GGCTCTGCCCACAGGAGGCATG 73764       TC    AAT____
           CA                    TGCATGC  CCTGT      GCC
                                |||||||  |||||      |||
                                ACGTACG  GGACA      CGG
                                    GA    CCCGTCT
GAM506  MGC10715 3' GCCACAGGGAGCTGCA      44248      T       AAT
                                TGCA GCTCCCTGT   GC
                                |||| |||||||||   ||
                                ACGT CGAGGGACA   CG
                                  _       C__
GAM506  MGC14407 3' ATGGAAGCCTCAGGGAGC    51875        TAAT  C_
                                GCTCCCTG    GC  CCAT
                                ||||||||    ||  ||||
                                CGAGGGAC    CG  GGTA
                                      TC__  AA
GAM506  MGC20460 5' GTGCTACAGGGAACATGC    53848      C       AT
                                GCATG TCCCTGTA  GC
                                ||||| ||||||||  ||
                                CGTAC AGGGACAT  TG
                                   A       CG
GAM506  RBM14    3' ATGGGGCACCACAGGGAG    20908        AA
                                CTCCCTGT  TGCCCCAT
                                ||||||||  ||||||||
                                GAGGGACA  ACGGGGTA
                                      CC
GAM506  SFRS12   3' TTACAGAAAGTATGCA      57529        CC
                                TGCATGCT  CTGTAA
                                ||||||||  ||||||
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                                ACGTATGA  GACATT
                                    AA
GAM506  LOC146445 3'  CATCACAGGGAGACGCA     83677     ATG       A
                                TGC   CTCCCTGT ATG
                                |||   |||||||| |||
                                ACG   GAGGGACA TAC
                                  CA_       C
GAM506  LOC150225 3'  GGGCAAGGAGGAGCTGCA    85006      T    _  GTAA
                                TGCA GCTCC CT    TGCCC
                                |||| ||||| ||    |||||
                                ACGT CGAGG GG    ACGGG
                                  _     A  A___
GAM506  LOC201102 3'  GGCTCCAGAAAGTATGCA    88095        CC   TAAT
                                TGCATGCT  CTG    GCC
                                ||||||||  |||    |||
                                ACGTATGA  GAC    CGG
                                    AA   CT__
GAM506  LOC201304 3'  CAGAACCTGGGAACATGTA   88229       C    T_  AA
                                TGCATG TCCC  GT  TG
                                ||||||| ||||  ||  ||
                                ATGTAC AGGG  CA  AC
                                   A    TC  AG
GAM506  LOC220776 3'  GGTAGAGCAGCATGCA      68396        CCCT  AA
                                TGCATGCT    GT  TGCC
                                ||||||||    ||  ||||
                                ACGTACGA    CG  ATGG
                                    _____  AG
GAM506  LOC221964 3'  TGGGGCCCAAGAGTATGCA   93984         CC  TAAT
                                TGCATGCTC  TG    GCCCCA
                                |||||||||  ||    ||||||
                                ACGTATGAG  AC    CGGGGT
                                    A_  C___
GAM506  LOC222008 3'  ATGGGATGAAGGGAGCA     94004        GTA  GC
                                TGCTCCCT    AT  CCCAT
                                ||||||||    ||  |||||
                                ACGAGGGA    TA  GGGTA
                                    AG_  __
GAM506  LOC257554 3'  GGTGACAGGGAGCCTGCA    97696     T       AA
                                TGCA GCTCCCTGT  TGCC
                                |||| |||||||||  ||||
                                ACGT CGAGGGACA  GTGG
                                  C       __
GAM506  LOC51308  3'  ATGGGGGAAAGGGAGCA     33491        GTAATG
                                TGCTCCCT     CCCCAT
                                ||||||||     ||||||
                                ACGAGGGA     GGGGTA
                                    AAG___
GAM507  ABCA4     3'  CGGGCCATCCCACTAGCAGCT  67092          AA_  A
                                AGCTGCTAGTGG   GG CTG
                                ||||||||||||   || |||
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                                TCGACGATCACC  CC GGC
                                      CTA  G
GAM507  CORO2A   3'  AACACAGTAGAAAACTAGAGCT 53399     G    GGAAGG
                                AGCT CTAGT     ACTGTGTT
                                |||| |||||     ||||||||
                                TCGA GATCA     TGACACAA
                                  _    AAAGA_
GAM507  CORO2A   3'  AACACAGTAGAAAACTAGAGCT 12643     G    GGAAGG
                                AGCT CTAGT     ACTGTGTT
                                |||| |||||     ||||||||
                                TCGA GATCA     TGACACAA
                                  _    AAAGA_
GAM507  HBD      5'  ACAGTGTTCACTAGCA      4970          AGG
                                TGCTAGTGGA   ACTGT
                                ||||||||||   |||||
                                ACGATCACTT   TGACA
                                      G__
GAM507  KIAA0442 3'  ACACAGTCGGCTAAAGCT    31466     GC   GGAAG
                                AGCT  TAGT    GACTGTGT
                                ||||  ||||    ||||||||
                                TCGA  ATCG    CTGACACA
                                  A_   G____
GAM507  MNAT1    3'  AACACAGTCCTTCCACTAGCAG 10100
           CT                    AGCTGCTAGTGGAAGGACTGTGTT
                                ||||||||||||||||||||||||
                                TCGACGATCACCTTCCTGACACAA

GAM507  CASPR3   3'  AACACAGTCCTCCAC       53349      A
                                GTGGA GGACTGTGTT
                                ||||| ||||||||||
                                CACCT CCTGACACAA
                                  _
GAM507  FLJ10199 5'  GGCCCTTCCACCGCAGC     71235      TA      A
                                GCTGC  GTGGAAGG CT
                                |||||  |||||||| ||
                                CGACG  CACCTTCC GG
                                   C_      C
GAM507  KIAA0406 5'  AACTGAGCCTCCCTAGCAGCT  61327        T  A  A  GT
                                AGCTGCTAG GGA GG CT  GTT
                                ||||||||| ||| || ||  |||
                                TCGACGATC CCT CC GA  CAA
                                      _  _ _ GT
GAM507  KIAA0674 5'  TCCTTCCACCACAGCT     60618      CTA
                                AGCTG   GTGGAAGGA
                                |||||   |||||||||
                                TCGAC   CACCTTCCT
                                   AC_
GAM507  MYH7B    3'  AACACAGTCCTAGGGACAAAAG 70528     AG  GA___
           C                     GCT  TG    AGGACTGTGTT
                                |||  ||    ||||||||||
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                                CGA  AC    TCCTGACACAA
                                  AA  AGGGA
GAM507  PTD012   3'  ACACAAACATTAGCAACT    25888    C      GAAGGAC
                                AG TGCTAGTG      TGTGT
                                || ||||||||      |||||
                                TC ACGATTAC      ACACA
                                 A       AA_____
GAM507  USP8     5'  AACGCCTTTCCTTCCACCAGCT 17664     T   A       CT_
           GCT                    AGC GCT GTGGAAGGA   GTGTT
                                ||| ||| |||||||||   |||||
                                TCG CGA CACCTTCCT   CGCAA
                                  T   C        TTC
GAM507  LOC254938 3'  AACACAGTCCTCCAATTAGGAG 97056      G    _   A
           CT                     AGCT CTAGT GGA GGACTGTGTT
                                |||| ||||| ||| ||||||||||
                                TCGA GATTA CCT CCTGACACAA
                                  G    A   _
GAM507  LOC255055 3'  ACACAGTGTACCTACAGC    94869     A    AAGG
                                GCT GTGG    ACTGTGT
                                ||| ||||    |||||||
                                CGA CATC    TGACACA
                                  _    CATG
GAM508  AVPR1A   5'  CAGGAAGCAGGACTCCAGA    5536        TCC     CA
                                TCTGGA   GTCTT  CTTCCTG
                                ||||||   |||||  |||||||
                                AGACCT   CAGGA  GAAGGAC
                                   ____     C_
GAM508  SFTPA2   3'  GGCAAAGACTGGATCCA     22649        _     CA
                                TGGATCC GTCTT  CT
                                ||||||| |||||  ||
                                ACCTAGG CAGAA  GG
                                    T    AC
GAM508  SLC25A15  3'  ACAGGAAGTAAACTGCTTCAGA 26506        TCC  CTTC
                                TCTGGA   GT    ACTTCCTGT
                                ||||||   ||    |||||||||
                                AGACTT   CA    TGAAGGACA
                                   CGT  AA__
GAM508  CABYR    3'  TGAAAACTGATCCAGA      24112         C  C
                                TCTGGATC GT TTCA
                                |||||||| || ||||
                                AGACCTAG CA AAGT
                                     T  A
GAM508  DKFZP566D193 3'  ACAAGAAATGAAGTGGACAGA  85566      GA   T    C   C
                                TCTG  TCCG CTTCA TTC TGT
                                ||||  |||| ||||| ||| |||
                                AGAC  AGGT GAAGT AAG ACA
                                  __   _    A  A
GAM508  FLJ11726  3'  ACAGGAAGTAAAAAGGCCCA   46405     ATCC    C__
                                TGG    GTCTT   ACTTCCTGT
                                |||    |||||   |||||||||
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                                ACC   CGGAA  TGAAGGACA
                                 ____    AAA
GAM508  KIAA0367  3'  ACAGGAAGTAATGAAAAATCCA 67290      CCG  TTC
            G                    CTGGAT  TC  ACTTCCTGT
                                 ||||||  ||  |||||||||
                                 GACCTA  AG  TGAAGGACA
                                    AAA  TAA
GAM508  ROBO4    3'  ACAGGAAGTGGAGGAGCCAGA  38788     ATCCG
                                 TCTGG   TCTTCACTTCCTGT
                                 |||||   ||||||||||||||
                                 AGACC   GGAGGTGAAGGACA
                                   GA___
GAM508  LOC139673 5'  ACAGGAAGTGAGTCATCGCAGA 75975    _  CCGTC
                                 TCTG GAT   TTCACTTCCTGT
                                 |||| |||   ||||||||||||
                                 AGAC CTA   GAGTGAAGGACA
                                   G  CT___
GAM508  LOC152024 5'  CAGAGAAGACGGATCCA    80434          ACTTC
                                 TGGATCCGTCTTC   CTG
                                 ||||||||||||    |||
                                 ACCTAGGCAGAAG   GAC
                                        A____
GAM508  LOC159036 3'  CAGAAAGTTGGATTCAGA   86970        TCTTC   C
                                 TCTGGATCCG    ACTT CTG
                                 |||||||||    |||| |||
                                 AGACTTAGGT    TGAA GAC
                                       _____   A
GAM508  LOC222112 5'  ACAGGAAGCACTTTGGTCCAGA 92802      T  TCTTCA
                                 TCTGGA CCG    CTTCCTGT
                                 |||||| |||    ||||||||
                                 AGACCT GGT    GAAGGACA
                                   _  TTCAC_
GAM509  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                 ATTT ACTTT  TGTCTGAG
                                 |||| |||||  ||||||||
                                 TAAA TGAAA  ACAGATTC
                                   A    T__
GAM509  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875      CAC  C  T
                                 CATTT  TTT AC GTCTGAGAT
                                 |||||  ||| || |||||||||
                                 GTAAA  AAA TG TAGACTCTA
                                    TA_  T  _
GAM509  FDFT1    3'  TAGGAAAGTGAAATG      15518          A
                                 CATTTCACTTTC CTG
                                 |||||||||||| |||
                                 GTAAAGTGAAAG GAT
                                              _
GAM509  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                   CATTTCACTTTCACTGTCTGAGAT
                                 |||||||||||||||||||||||||
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                                GTAAAGTGAAAGTGACAGACTCTA

GAM509  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM509  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM509  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM509  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM509  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_   CG_
GAM509  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM509  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM509  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||         |||||||||
                                GTAAAG         CAGACTCTA
                                   AAACATTT_
GAM509  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM509  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
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                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM509  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM509  NIR3     3'  GCAGTGAAAGTGCAAT      66242      T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM509  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM509  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM509  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__   TT
GAM509  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM509  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM509  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM509  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM509  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
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                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM509  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM510  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM510  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM510  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM510  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
           TG                     CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM510  KLF4     3'  TCCCAGACAGTGGATATG     14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM510  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM510  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM510  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM510  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
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                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM510  CG012    5' CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                     CT  __
GAM510  EIF2C2   3' ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM510  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM510  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM510  KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM510  KLHL6    3' ATCTCAGAGCAGGAAA      55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM510  NIR3     3' GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM510  PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM510  PP35     3' ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM510  PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148         TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
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                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM510  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                      A    TC
GAM510  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941        CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                      AAAGG
GAM510  LOC149703 3' ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM510  LOC154007 3' ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                     TTTCC_  A
GAM510  LOC155004 3' TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM510  LOC222134 5' ACAGTGAAGTGAAATG       94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM511  ARNT2    3'  AAACAACCCGTGCATCCCTGC  29450     A    TTTTA
                                GTA GGAT     GGGTTGTTT
                                ||| ||||     |||||||||
                                CGT CCTA     CCCAACAAA
                                  C    CGTG_
GAM511  LCT      3'  AACCGTAAAAATCCTT      9697           G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
                                TTCCTAAAAAT CCAA
                                      G
GAM511  RPL15    3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM511  FBXO30   3'  AACTAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
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                                CA TCCTAAAAA  TCAA
                                 G        AA
GAM511  KIAA0494  3'  AACAACCCTTACTTAC      28736       GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                  AT_____
GAM511  PRO0641   5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                  ___    C
GAM511  SMT3H2    3'  AACAACATAAAAATCCTTGC   22670           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM511  LOC120103 3'  AACCTATGAAAAATCCTTGC   74002           A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
                                CGTTCCTAAAAA   TCCAA
                                       GTA
GAM511  LOC129831 3'  AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM511  LOC133088 5'  AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                      GTA GGATTTTT     TTGTTT
                                ||| ||||||||     ||||||
                                CGT CCTAAAAA     AACAAA
                                  C       GATAA
GAM511  LOC148089 3'  GGCCCTAAAAATTCCTAC     78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM511  LOC154547 3'  AACAACATAAAAATCCTTGC   76050           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM511  LOC158104 3'  ACAGCCAAAAATCCTTA     60313          AG
                                TAAGGATTTTT  GGTTGT
                                ||||||||||  ||||||
                                ATTCCTAAAAA  CCGACA
                                       __
GAM511  LOC205880 5'  AAACAACCATCATCCTGAC    90709     A    TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
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                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM511  LOC221561 3'  AACAACATAAAAATCCTTGC  92130          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM511  LOC257591 3'  AACAACATAAAAATCCTTGC  97840          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM511  LOC51145  3'  AGCTAAAATCCTTAC      32393          TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
                                CATTCCTAAAA   TCGA
                                      ___
GAM512  ABCB11    3'  TGTTGATTTATGCTTTA     13619
                                TAAAGCATAGATCAACA
                                |||||||||||||||||
                                ATTTCGTATTTAGTTGT

GAM512  FGA       3'  ACTAAGTATGATCTATGCT   4960           _  AA
                                AGCATAGATCA AC  AGT
                                ||||||||||| ||  |||
                                TCGTATCTAGT TG  TCA
                                       A  AA
GAM512  GPR81     3'  GCTCAGTCAATCAATGCTTTA 50763        A   CA  AA
                                TAAAGCAT GAT  AC  AGT
                                |||||||| |||  ||  |||
                                ATTTCGTA CTA  TG  TCG
                                     A   AC  AC
GAM512  MPP5      3'  CTACTTTGTTAGGCTT      42485      ATAGATC
                                AAGC      AACAAAGTAG
                                ||||      ||||||||||
                                TTCG      TTGTTTCATC
                                  GA_____
GAM512  MS4A3     3'  CTACTTTGTCGGTTGCT      20431      TAG   A
                                AGCA   ATC ACAAAGTAG
                                ||||   ||| |||||||||
                                TCGT   TGG TGTTTCATC
                                  ___   C
GAM512  PRPS1     3'  CTACTTTGTATGTGAATGCTT  10898       AGAT  _
                                AAGCAT    CA ACAAAGTAG
                                ||||||    || |||||||||
                                TTCGTA    GT TGTTTCATC
                                   AGT_  A
GAM512  PTPRD     3'  CTGCTGACCTGTGCTT      11103        A   ACAAA
                                AAGCATAG TCA    GTAG
                                |||||||| |||    ||||
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                                TTCGTGTC AGT    CGTC
                                    C  _____
GAM512  PTPRD    3'  CTGCTGACCTGTGCTT     55227        A  ACAAA
                                AAGCATAG TCA    GTAG
                                |||||||| |||    ||||
                                TTCGTGTC AGT    CGTC
                                    C  _____
GAM512  PTPRD    3'  CTGCTGACCTGTGCTT     55228        A  ACAAA
                                AAGCATAG TCA    GTAG
                                |||||||| |||    ||||
                                TTCGTGTC AGT    CGTC
                                    C  _____
GAM512  PTPRD    3'  CTGCTGACCTGTGCTT     55229        A  ACAAA
                                AAGCATAG TCA    GTAG
                                |||||||| |||    ||||
                                TTCGTGTC AGT    CGTC
                                    C  _____
GAM512  ABLIM    3'  GCCACTTTATTATCATGCTTTG 22032        A  C C    A
                                TAAAGCAT GAT AA AAAGT GC
                                |||||||| ||| || ||||| ||
                                GTTTCGTA CTA TT TTTCA CG
                                    _  _ A    C
GAM512  ABLIM    3'  GCCACTTTATTATCATGCTTTG 9771         A  C C    A
                                TAAAGCAT GAT AA AAAGT GC
                                |||||||| ||| || ||||| ||
                                GTTTCGTA CTA TT TTTCA CG
                                    _  _ A    C
GAM512  ARF4     3'  GCTACTTTACTGATACCTTTA  82813      CATAG   AC
                                TAAAG    ATCA  AAAGTAGC
                                |||||    ||||  ||||||||
                                ATTTC    TAGT  TTTCATCG
                                   CA___   CA
GAM512  C8orf17  5'  GCTACTCTCCGGATGATTTATG 39602          ACAA___
            CTT                   AAGCATAGATCA      AGTAGC
                                |||||||||||      ||||||
                                TTCGTATTTAGT      TCATCG
                                      AGGCCTC
GAM512  KIAA0555 3'  GCTACTTTGTACAATGCT    60115      AGATCA
                                AGCAT     ACAAAGTAGC
                                |||||     ||||||||||
                                TCGTA     TGTTTCATCG
                                   ACA___
GAM512  KIAA1434 3'  GCATTGTTGATCTATGC     69612           A
                                GCATAGATCAACAA GT
                                |||||||||||||| ||
                                CGTATCTAGTTGTT CG
                                      A
GAM512  KIAA1671 3'  GCTGCTTTGTTGATCTATGCTT 65681
            TA                  TAAAGCATAGATCAACAAAGTAGC
                                |||||||||||||||||||||||||
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                                ATTTCGTATCTAGTTGTTTCGTCG

GAM512  KIF13B   3'  GCTACTTTATTTGGTGC     30910      _   CAAC
                                GCAT AGAT    AAAGTAGC
                                |||| ||||    ||||||||
                                CGTG TTTA    TTTCATCG
                                  G   _____
GAM512  KIF13B   3'  GCTACTTTATTTGGTGC     82824      _   CAAC
                                GCAT AGAT    AAAGTAGC
                                |||| ||||    ||||||||
                                CGTG TTTA    TTTCATCG
                                  G   _____
GAM512  KRTAP3-2 3'  GCTACTTTGCTCAGTGC     49231      A  TCAA
                                GCAT GA    CAAAGTAGC
                                |||| ||    |||||||||
                                CGTG CT    GTTTCATCG
                                  A  C____
GAM512  KRTAP3-3 3'  GCTACTTTGCTCAGTGC     52594      A  TCAA
                                GCAT GA    CAAAGTAGC
                                |||| ||    |||||||||
                                CGTG CT    GTTTCATCG
                                  A  C____
GAM512  MAL2     3'  CTACTTTGGTTTTCCTAGCT   53552      A   ATCAA_
                                AGC TAG     CAAAGTAG
                                ||| |||     ||||||||
                                TCG ATC     GTTTCATC
                                  _  CTTTTG
GAM512  LOC147429 3' GCTACTTTGTCAAATAAAGCTT 78361      ATAGATCA
                                AAGC       ACAAAGTAGC
                                ||||       ||||||||||
                                TTCG       TGTTTCATCG
                                  AAATAAAC
GAM512  LOC149711 3' GCTACTTTTTCTATGCT     84682        TCAAC
                                AGCATAGA    AAAGTAGC
                                ||||||||    ||||||||
                                TCGTATCT    TTTCATCG
                                     T_____
GAM512  LOC203232 3' GCTACTTTGCTGACTGGTT   71412     A  A  A
                                AGC TAG TCA CAAAGTAGC
                                ||| ||| ||| |||||||||
                                TTG GTC AGT GTTTCATCG
                                  _  _  C
GAM512  LOC90459  3' ACTTTTATTCTATGCTT     62881        TCAAC
                                AAGCATAGA    AAAGT
                                |||||||||    |||||
                                TTCGTATCT    TTTCA
                                     TAT__
GAM513  CABC1    5'  GCAGCACAAACAGACGCTC   39656      T A
                                GGGC G CTGTTTGTGCTGC
                                |||| | ||||||||||||
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                                CTCG C GACAAACACGACG
                                  _ A
GAM513  CAST    5' GCAGCAGTCAATCCTCC    8256      GC     TTG
                                GGAGG  TGACTGT   TGC
                                |||||  |||||||   |||
                                CCTCC  ACTGACG   ACG
                                   TA     ___
GAM513  DDX3    3' CAGCAATGACCAGCCCTC    7221        ACT   TG
                                GAGGGCTG   GTT  TGCTG
                                ||||||||   |||  |||||
                                CTCCCGAC   CAG  ACGAC
                                     ___   TA
GAM513  GNAZ    3' CAGCACTAACCAGACCTCC   9064      G   ACT   T
                                GGAGG CTG   GTT GTGCTG
                                |||||  |||   |||  ||||||
                                CCTCC GAC   CAA CACGAC
                                   A   ___   T
GAM513  HCN4    5' CAGACGGACAGCCAGCCCTCC  18488        A      G
                                GGAGGGCTG CTGTTTGT CTG
                                |||||||||  ||||||||  |||
                                CCTCCCGAC GACAGGCA GAC
                                     C       _
GAM513  INS     3' GCAGCCCGCAGGCAGCCCCCC  3979    A     A    TTGT
                                GG GGGCTG CTGT    GCTGC
                                ||  ||||||  ||||    |||||
                                CC CCCGAC GACG    CGACG
                                 C     G    CC__
GAM513  KCNE1L  3' CAGCACGCTCCAGCCCTCTG   24402         ACT  TT
                                CGGAGGGCTG   GT  GTGCTG
                                ||||||||||   ||  ||||||
                                GTCTCCCGAC   CG  CACGAC
                                      CT_  __
GAM513  KCNQ4   3' GCAGCACACGGCCAGCCCCGCG 16288    GA     A    TT
                                CG  GGGCTG CTGT  GTGCTGC
                                ||  ||||||  ||||  |||||||
                                GC  CCCGAC GGCA  CACGACG
                                 GC     C    __
GAM513  NRAS    3' CAGCACAAACACACCTC     10268      GCTGAC
                                GAGG     TGTTTGTGCTG
                                ||||     ||||||||||
                                CTCC     ACAAACACGAC
                                  AC_____
GAM513  PPP2R5D 3' GCAGCACAAATAGGCCCCCC   20718    A    TGA
                                GG GGGC   CTGTTTGTGCTGC
                                || ||||   ||||||||||||
                                CC CCCG   GATAAACACGACG
                                 C    ____
GAM513  SLC2A8  3' GCAGACCTGCGGTCAGCCCTCC 27422            TT  G
                                GGAGGGCTGACTGT  GT CTGC
                                ||||||||||||||  || ||||
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                                CCTCCCGACTGGCG  CA GACG
                                       TC  _
GAM513  C22orf2   3'  GCAGCAAGCACCAGCCTTCC   94456        AC    TG
                                GGAGGGCTG  TGTT  TGCTGC
                                |||||||||  ||||  ||||||
                                CCTTCCGAC  ACGA  ACGACG
                                     C_   __
GAM513  C7orf13   5'  GCAGCACGCTCCTCAGCCGCCC 50932     AG     CTGTT
          G                      CGG  GGCTGA    TGTGCTGC
                                |||  ||||||    ||||||||
                                GCC  CCGACT    GCACGACG
                                  CG     CCTC_
GAM513  DKFZP761D0211 3'  GCAGCAGCCTTACCAGTCCTCC 49354         ACTGTTTG
                                GGAGGGCTG       TGCTGC
                                |||||||||       ||||||
                                CCTCCTGAC       ACGACG
                                     CATTCCG_
GAM513  FBP17     3'  CAGCTCAGTCAGCCCTC     72784          TTTGT
                                GAGGGCTGACTG     GCTG
                                ||||||||||||    ||||
                                CTCCCGACTGAC     CGAC
                                       T_____
GAM513  FLJ13614  3'  CAACACAAACAGTAATCTCTCC 57449       CTG        C
                                GGAGGG   ACTGTTTGTG TG
                                ||||||   ||||||||||| ||
                                CCTCTC   TGACAAACAC AC
                                   TAA         A
GAM513  FLJ20232  3'  CAGACCCAACAGCCAGCCCTTC 38669         A     TGTG
                                GGAGGGCTG CTGTT    CTG
                                ||||||||| |||||    |||
                                CTTCCCGAC GACAA    GAC
                                     C     CCCA
GAM513  KIAA0638  3'  ACAGGCTGCCAGCCCCCC    72393    A     ACT
                                GG GGGCTG   GTTTGT
                                || ||||||   ||||||
                                CC CCCGAC   CGGACA
                                 C     CGT
GAM513  KIAA1075  3'  GCAGGAGAACGTCAGCCCTCC  61718          T    GTG
                                GGAGGGCTGAC GTTT   CTGC
                                |||||||||| ||||   ||||
                                CCTCCCGACTG CAAG   GACG
                                      _    AG_
GAM513  KIAA1280  5'  GCAACTGCACCCAGACCAGCCC 69718         A_   TTT    ___
          TCCG                    GGAGGGCTG  CTG   GTGC   TGC
                                |||||||||  |||   ||||   |||
                                CCTCCCGAC  GAC   CACG   ACG
                                     CA   C__    TCA
GAM513  KIAA1510  5'  GCAGCCTGCCCAGCCCTCCG   61358         ACT  TTGT
                                CGGAGGGCTG   GT    GCTGC
                                ||||||||||   ||    |||||
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                                GCCTCCCGAC  CG   CGACG
                                      C__  TC__
GAM513  LGALS8   5' GCCTGGAACAGCCAGCCGCCC 21449   AG   A    GT_
                                GG  GGCTG CTGTTT  GC
                                ||  ||||| ||||||  ||
                                CC  CCGAC GACAAG  CG
                                 CG    C     GTC
GAM513  MGC35570 3' GCAGAGGCCCAGCCAGCCCTCT 58116        A  TTT  G_
          G                      CGGAGGGCTG CTG  GT  CTGC
                                ||||||||||  |||  ||  ||||
                                GTCTCCCGAC GAC  CG  GACG
                                      C  C__  GA
GAM513  PEX12    5' CAGCTGGAGTCAGCCCTC   4296          GTTTGT
                                GAGGGCTGACT    GCTG
                                ||||||||||     ||||
                                CTCCCGACTGA    CGAC
                                       GGT___
GAM513  LOC130813 3' CAGCACCAGTCAGCTCCCC   75765   A       TTT
                                GG GGGCTGACTG  GTGCTG
                                || ||||||||||  ||||||
                                CC CTCGACTGAC  CACGAC
                                 C       ___
GAM513  LOC152274 3' ACAGCAGCCAGCCCTC     80497       A   T
                                GAGGGCTG CTGTT GT
                                |||||||| ||||| ||
                                CTCCCGAC GACGA CA
                                     C   _
GAM513  LOC202052 3' ACAGGCAGGCAGCCCTCC    90303        A
                                GGAGGGCTG CTGTTTGT
                                ||||||||| ||||||||
                                CCTCCCGAC GACGGACA
                                      G
GAM513  LOC222112 3' GCAGCATCGGATGTCAGCCCCC 92804    A      T   _
                                GG GGGCTGAC GTTTG TGCTGC
                                || |||||||| ||||| ||||||
                                CC CCCGACTG TAGGC ACGACG
                                 _      _    T
GAM513  LOC253256 5' CAGCACAGGCCCAGCCCT    96243       ACT
                                AGGGCTG  GTTTGTGCTG
                                |||||||  ||||||||||
                                TCCCGAC  CGGACACGAC
                                    C__
GAM513  LOC254219 3' CAGAGACCACTGCCAGCCCTCC 96546        ACT  TTGTG
                                GGAGGGCTG  GT   CTG
                                |||||||||  ||   |||
                                CCTCCCGAC  CA   GAC
                                      CGT  CCAGA
GAM513  LOC256306 5' CAGCACAAAGAGTCCCCC    96681    CT   G
                                GGG  GACT TTTGTGCTG
                                |||  |||| |||||||||
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                                CCC  CTGA AAACACGAC
                                  C_   G
GAM513  LOC90668  3'  CAACACCCTCCTCAGCCCTC   82268        CTGTTT   C
                                GAGGGCTGA     GTG TG
                                |||||||||     ||| ||
                                CTCCCGACT     CAC AC
                                     CCTCC_   A
GAM513  LOC92840  3'  GCAACATCCCCACGCAGCCCCC 56432    A     AC  TTT   C
            C                    GG GGGCTG  TG   GTG TGC
                                || ||||||  ||   ||| |||
                                CC CCCGAC  AC   TAC ACG
                                 C     GC  CCC   A
GAM514  EIF1A    3'  TCTTGATTGTATAGAGTCA   88605        CAC   T    CT
                                TGACTCTA   ACA TCAA  GA
                                ||||||||   ||| ||||  ||
                                ACTGAGAT   TGT AGTT  CT
                                     A__   T    __
GAM514  EXTL1    5'  TCAGTTGAGGGCAAGGTCA   15496     T  ACACACA
                                TGAC CT      TTCAACTGA
                                ||||  ||      |||||||||
                                ACTG GA      GAGTTGACT
                                  _  ACGG___
GAM514  IL1F5    3'  CAGTTGAGCCTTATAGGGTCA  24378        CACACA
                                TGACTCTA     TTCAACTG
                                ||||||||     ||||||||
                                ACTGGGAT     GAGTTGAC
                                     ATTCC_
GAM514  MPP2     3'  CAGGAATGTGTCAGAGTCA    59817       AC       AA
                                TGACTCT  ACACATTC  CTG
                                |||||||  ||||||||  |||
                                ACTGAGA  TGTGTAAG  GAC
                                     C_       __
GAM514  PLS1     3'  TTGAATGTGCATATAGTCA    10667      C  CA
                                TGACT TA  CACATTCAA
                                |||||  ||  |||||||||
                                ACTGA AT  GTGTAAGTT
                                   T  AC
GAM514  FLJ13449  3'  TGTATGTGTGTAAAATCA    44620     CTC       T
                                TGA   TACACACAT CA
                                |||   ||||||||| ||
                                ACT   ATGTGTGTA GT
                                  AAA        T
GAM514  FLJ20489  3'  TGAGTGTGCTAGAGCCA     35254    A    CA
                                TG CTCTA  CACATTCA
                                || |||||  ||||||||
                                AC GAGAT  GTGTGAGT
                                 C    C_
GAM514  FLJ21709  3'  CTCAGCCAGGAGCACGTAGAGT 77919         ACACA   AA_
            CA                    TGACTCTAC    TTC   CTGAG
                                |||||||||    |||   |||||
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                                ACTGAGATG    AGG  GACTC
                                     CACG_  ACC
GAM514  KIAA0972  3'  CAGTTGAACATTATGTGAGCA  30008   A  T  CACA_
                                TG CTC ACA    TTCAACTG
                                || ||| |||    ||||||||
                                AC GAG TGT    AAGTTGAC
                                 _  _  ATTAC
GAM514  KIAA1753  3'  CAGCGACACGGTAGAGTCA   64879       ACACAT  AA
                                TGACTCTAC     TC  CTG
                                |||||||||     ||  |||
                                ACTGAGATG     AG  GAC
                                     GCAC__  C_
GAM514  RALGPS1A  3'  CTCAGTTGAACATGTTTTGTCA 27600     TCTAC  CA
                                TGAC    ACA  TTCAACTGAG
                                ||||    |||  ||||||||||
                                ACTG    TGT  AAGTTGACTC
                                  TTT__  AC
GAM514  UPLC1    3'  CAGCCAAATTGTAGAGTCA   34721       CAC  CAA
                                TGACTCTACA  ATT  CTG
                                ||||||||||  |||  |||
                                ACTGAGATGT  TAA  GAC
                                     ___  ACC
GAM514  LOC123096 3'  CTCATGCCCACACTGTAGAGTC 74200        CACATTCAAC
           A                     TGACTCTACA        TGAG
                                ||||||||||        ||||
                                ACTGAGATGT        ACTC
                                     CACACCCGT_
GAM514  LOC126661 3'  CTCAGTTGAACTTGGAAAGT  74548    CTACA  CA
                                ACT    CA  TTCAACTGAG
                                |||    ||  ||||||||||
                                TGA    GT  AAGTTGACTC
                                  AAG__  TC
GAM514  LOC130888 3'  CAGTGCCTTGCTAGAGTCA   74990       CACA  TTCA
                                TGACTCTA   CA   ACTG
                                ||||||||   ||   ||||
                                ACTGAGAT   GT   TGAC
                                     C___  TCCG
GAM514  LOC150935 3'  TGAATGGTATAGAGTCA     80039       C  A
                                TGACTCTA AC CATTCA
                                |||||||| || ||||||
                                ACTGAGAT TG GTAAGT
                                     A  _
GAM514  LOC90538  3'  CTCAGTTGGAAATGCAGAAATC 63191     C_  A  CACA
           A                     TGA  TCT CA   TTCAACTGAG
                                |||  ||| ||   ||||||||||
                                ACT  AGA GT   AGGTTGACTC
                                  AA  C  AA__
GAM514  LOC90631  3'  CAGGGATGTGTGAAGTCA   63633      CTA       AA
                                TGACT   CACACATTC  CTG
                                |||||   |||||||||  |||
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                                ACTGA  GTGTGTAGG  GAC
                                  A__      __
GAM515  AGTR1    5'  TCAGAGTGTGGCTGTACCA   49432    CAT     AGAG
                                TGG  CAGCCACA   TGA
                                |||  ||||||||   |||
                                ACC  GTCGGTGT   ACT
                                  AT_      GAG_
GAM515  ALDH3A2  3'  CTCTTGTGACTAATGTCA    69273      C  C
                                TGGCAT AG CACAAGAG
                                |||||| || ||||||||
                                ACTGTA TC GTGTTCTC
                                   A  A
GAM515  ATP2B3   5'  TCCCTAGCTGTGGCTGAGCCA  41693     A       AG_  T
                                TGGC TCAGCCACA   AG GA
                                |||| |||||||||   || ||
                                ACCG AGTCGGTGT   TC CT
                                  _       CGA  C
GAM515  B4GALT6  3'  TTTGGTGCACTGATGCCA    59869        C_  A
                                TGGCATCAG  CAC AGA
                                |||||||||  ||| |||
                                ACCGTAGTC  GTG TTT
                                     AC   G
GAM515  BAALC    3'  CATGCTTGTGGCCAATGC    45663     CA      A
                                GCAT  GCCACAAG GTG
                                ||||  |||||||| |||
                                CGTA  CGGTGTTC TAC
                                  AC       G
GAM515  CHC1L    3'  ATTCAGCTGGCTGATACCA    7013     C      CAA
                                TGG ATCAGCCA   GAGT
                                ||| ||||||||   ||||
                                ACC TAGTCGGT   CTTA
                                  A       CGA
GAM515  CMAR     3'  TTCCCAGTGTGGCTGAGGCCA  17780     A       AGAGT
                                TGGC TCAGCCACA    GAA
                                |||| |||||||||    |||
                                ACCG AGTCGGTGT    CTT
                                  G       GACC_
GAM515  FLNB     3'  GCTTTGTGGTTGATGCCA    62179           A
                                TGGCATCAGCCACA GAGT
                                |||||||||||||| ||||
                                ACCGTAGTTGGTGT TTCG
                                                _
GAM515  HEPH     3'  TTTCACTTTGAACTGAGGCCA  28967     A   CCACA
                                TGGC TCAG    AGAGTGAAA
                                |||| ||||    |||||||||
                                ACCG AGTC    TTTCACTTT
                                  G   AAG__
GAM515  HEPH     3'  TTTCACTTTGAACTGAGGCCA  57035     A   CCACA
                                TGGC TCAG    AGAGTGAAA
                                |||| ||||    |||||||||
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                                ACCG AGTC    TTTCACTTT
                                  G   AAG__
GAM515  PDE7A   3'  GTTTCCAAGTGAGTGATGCCA  65523       GC  AAGAGT
                                TGGCATCA  CAC    GAAAC
                                |||||||  |||    |||||
                                ACCGTAGT  GTG    CTTTG
                                    GA  AAC___
GAM515  PTPN23  5'  GCTCGTGGCTGAGCCA     63729     A      AA
                                TGGC TCAGCCAC  GAGT
                                |||| ||||||||  ||||
                                ACCG AGTCGGTG  CTCG
                                  _      __
GAM515  SPG7    3'  TTCCCAGTGTGGCTGAGGCCA  11906     A       AGAGT
                                TGGC TCAGCCACA    GAA
                                |||| |||||||||    |||
                                ACCG AGTCGGTGT    CTT
                                  G       GACC_
GAM515  TCF12   3'  CACTCAGCTGATGCCA      12178         CACAA
                                TGGCATCAGC    GAGTG
                                ||||||||||    |||||
                                ACCGTAGTCG    CTCAC
                                     A____
GAM515  TEM8    3'  TTTCACTCCCGCCCCATGCCA  36333      CA_  CACAA
                                TGGCAT   GC    GAGTGAAA
                                ||||||   ||    ||||||||
                                ACCGTA   CG    CTCACTTT
                                   CCC  CC___
GAM515  TNFAIP1  3'  ACTCTTATGATAGCTGATGCCA 40914         ___  C
                                TGGCATCAGC   CA AAGAGT
                                ||||||||||   || ||||||
                                ACCGTAGTCG   GT TTCTCA
                                     ATA  A
GAM515  C1orf34  3'  CAAGGTGGGCTGATGCCA    60664         A  AGAG
                                TGGCATCAGCC CA    TG
                                ||||||||||| ||    ||
                                ACCGTAGTCGG GT    AC
                                     _  GGA_
GAM515  C1QTNF7  3'  CACTCTTGCTTGTGTCA     49156       C   CAC
                                TGGCAT AGC   AAGAGTG
                                ||||||  |||   |||||||
                                ACTGTG TCG   TTCTCAC
                                   T  ___
GAM515  FLJ00024 3'  TCACTGTGCTGATGCC      63768         C   AGA
                                GGCATCAGC ACA   GTGA
                                |||||||| |||   ||||
                                CCGTAGTCG TGT   CACT
                                     _  ___
GAM515  FLJ13391 5'  CTCTACTGGCTGATGCCA    49790          CA
                                TGGCATCAGCCA  AGAG
                                ||||||||||||  ||||
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                                ACCGTAGTCGGT  TCTC
                                      CA
GAM515  FLJ14642  3'  CACTCTTGTAGCATGG      51495     _  C
                                TCA GC ACAAGAGTG
                                ||| || |||||||||
                                GGT CG TGTTCTCAC
                                  A  A
GAM515  FLJ14721  3'  CACCCTGTGCCTGCTGATGCC  51577          ___    A A
                                GGCATCAGC   CACA G GTG
                                |||||||||   |||| | |||
                                CCGTAGTCG   GTGT C CAC
                                      TCC    _ C
GAM515  FLJ14753  5'  GCCTATGTAGCTGATGTCA    50776          C   _  A
                                TGGCATCAGC ACA AG GT
                                |||||||||| ||| || ||
                                ACTGTAGTCG TGT TC CG
                                      A   A  _
GAM515  FLJ20127  3'  TACATTATGGCTGATCCA     34593     C       C  GA
                                TGG ATCAGCCA AA  GTG
                                ||| ||||||| ||  |||
                                ACC TAGTCGGT TT  CAT
                                  _       A  A_
GAM515  FLJ20847  5'  ACTCCAGTAGCTGATGTCA    94827          C  AA
                                TGGCATCAGC AC  GAGT
                                |||||||||| ||  ||||
                                ACTGTAGTCG TG  CTCA
                                      A  AC
GAM515  FLJ21562  3'  TTTCACTGATGCTGAGCCA    47079      A    CACAAG
                                TGGC TCAGC      AGTGAAA
                                |||| |||||      |||||||
                                ACCG AGTCG      TCACTTT
                                  _     TAG___
GAM515  GNG3      3'  ACCTTTGTGGCCGACCCCA    24191     CA  A       A
                                TGG  TC GCCACAAG GT
                                |||  || |||||||| ||
                                ACC  AG CGGTGTTT CA
                                  CC  C       C
GAM515  KIAA0140  3'  CACACTGGCAATGATGCCA    27805          __    CAA A
                                TGGCATCA  GCCA   G GTG
                                ||||||||  ||||   | |||
                                ACCGTAGT  CGGT   C CAC
                                     AA    ___ A
GAM515  KIAA0417  3'  TCGATCTGTGCTGATGCCA    71245          C   A  G
                                TGGCATCAGC ACA GA TGA
                                |||||||||| ||| || |||
                                ACCGTAGTCG TGT CT GCT
                                      _   _  A
GAM515  KIAA0831  3'  TCCTTACGGCTGATGCTA     29983          ACAA   T
                                TGGCATCAGCC    GAG GA
                                ||||||||||     ||| ||
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```
                                ATCGTAGTCGG   TTC CT
                                    CA__  _
GAM515  KIF13B   3' TTCGTGGTGGCTGAGCCA   30915     A      AA_
                                TGGC TCAGCCAC  GAG
                                |||| ||||||||  |||
                                ACCG AGTCGGTG  CTT
                                  _      GTG
GAM515  KIF13B   3' TTCGTGGTGGCTGAGCCA   82828     A      AA_
                                TGGC TCAGCCAC  GAG
                                |||| ||||||||  |||
                                ACCG AGTCGGTG  CTT
                                  _      GTG
GAM515  MAP2K6   3' GCTGTTGTGACTGCTGCCA   49245     T  C   G
                                TGGCA CAG CACAA AGT
                                ||||| ||| ||||| |||
                                ACCGT GTC GTGTT TCG
                                   C  A   G
GAM515  MAP2K6   3' GCTGTTGTGACTGCTGCCA   10871     T  C   G
                                TGGCA CAG CACAA AGT
                                ||||| ||| ||||| |||
                                ACCGT GTC GTGTT TCG
                                   C  A   G
GAM515  MESDC2   3' TCATGCCGTGGCTGAACCA   72500    CA     AAGA
                                TGG  TCAGCCAC   GTGA
                                |||  ||||||||   ||||
                                ACC  AGTCGGTG   TACT
                                  A_      CCG_
GAM515  MGC11335 3' TCCTCATGGTGATGCCA    48020       G  CAA  T
                                TGGCATCA CCA  GAG GA
                                |||||||| |||  ||| ||
                                ACCGTAGT GGT  CTC CT
                                    _  A__  _
GAM515  MGC14480 3' CTCAGCCGTGGCTGAGGCCA  58747     A      AA__
                                TGGC TCAGCCAC   GAG
                                |||| ||||||||   |||
                                ACCG AGTCGGTG   CTC
                                  G      CCGA
GAM515  MGC2376  3' ACTCCATTGCAACTGATGCCA 43701       CCA  __
                                TGGCATCAG  CAA  GAGT
                                |||||||||  |||  ||||
                                ACCGTAGTC  GTT  CTCA
                                     AAC  AC
GAM515  NDRG4    3' ATTCCAGTGTGGTGATGCCA  43286       G   A__
                                TGGCATCA CCACA  GAGT
                                |||||||| |||||  ||||
                                ACCGTAGT GGTGT  CTTA
                                    _   GAC
GAM515  NDRG4    3' ATTCCAGTGTGGTGATGCCA  39983       G   A__
                                TGGCATCA CCACA  GAGT
                                |||||||| |||||  ||||
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                                ACCGTAGT GGTGT  CTTA
                                     _    GAC
GAM515  NYD-SP11  3'  TCACTCTTACAGCTGACCCA  49215    CA    CAC
                                TGG  TCAGC  AAGAGTGA
                                |||  |||||  ||||||||
                                ACC  AGTCG  TTCTCACT
                                  C_    ACA
GAM515  PCBP4     5'  TTGTTCGCAGCTGATGTCA   52234        CACAA  TG
                                TGGCATCAGC    GAG  A
                                ||||||||||    |||  |
                                ACTGTAGTCG    CTT  T
                                      ACG__   GT
GAM515  PDE8A     3'  TTACCTGTGGTGATGCCA    62639       G    A A
                                TGGCATCA CCACA G GTGA
                                |||||||| ||||| | ||||
                                ACCGTAGT GGTGT C CATT
                                     _    _ _
GAM515  SDS3      3'  GTTTCACTCTTGTGGCTGATGC 69233
              CA                  TGGCATCAGCCACAAGAGTGAAAC
                                ||||||||||||||||||||||||
                                ACCGTAGTCGGTGTTCTCACTTTG

GAM515  SEMA5A    3'  TCACAGGTGATGCCA      14261        G  ACAAGA
                                TGGCATCA CC     GTGA
                                |||||||| ||     ||||
                                ACCGTAGT GG     CACT
                                     _ A_____
GAM515  SFRS12    3'  TTTCCATGGTGGCTGACACA  57530    GCA      AAGAGT
                                TG   TCAGCCAC     GAAA
                                ||   ||||||||     ||||
                                AC   AGTCGGTG     CTTT
                                 AC_      GTAC__
GAM515  VMP       3'  TTTTGTGGCTGTCACCA     54906     CAT
                                TGG   CAGCCACAAGA
                                |||   ||||||||||
                                ACC   GTCGGTGTTTT
                                  ACT
GAM515  LOC118738 3'  TTTCACTCTCCCTGTGTGCCA  75497       _  CCACA
                                TGGCAT CAG    AGAGTGAAA
                                |||||| |||    |||||||||
                                ACCGTG GTC    TCTCACTTT
                                   T   CC___
GAM515  LOC138399 5'  CAAGCTGTGGCTGCTACCA    75324     CAT      A AG
                                TGG   CAGCCACA G  TG
                                |||   |||||||| |  ||
                                ACC   GTCGGTGT C  AC
                                  ATC       _ GA
GAM515  LOC149302 5'  GCTTCGGTAACTGATGCC     79270        CC  AA
                                GGCATCAG  AC  GAGT
                                ||||||||  ||  ||||
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                                CCGTAGTC  TG  TTCG
                                     AA  GC
GAM515  LOC150279 3'  TTTCATTTAGCTGCTGCCA   79670      T   CACAA
                                TGGCA CAGC    GAGTGAAA
                                ||||| ||||    ||||||||
                                ACCGT GTCG    TTTACTTT
                                   C   A____
GAM515  LOC150319 3'  TCCCTTCTGTGGCTGACACC   79661    CA       AG  T
                                GG  TCAGCCACA  AG GA
                                ||  |||||||||  || ||
                                CC  AGTCGGTGT  TC CT
                                 AC        CT  C
GAM515  LOC196410 5'  CACTCCTGCAGCTGCTGGTGCT 87658         CA___  A
                                GGCATCAGC    CA GAGTG
                                |||||||||    || |||||
                                TCGTGGTCG    GT CTCAC
                                      TCGAC  C
GAM515  LOC202865 5'  TTACTTATGGTGATGCCA    59257        G   CAA
                                TGGCATCA CCA   GAGTGA
                                |||||||| |||   ||||||
                                ACCGTAGT GGT   TTCATT
                                     _   A__
GAM515  LOC219920 5'  CTCCTGCGGCTGAGCCA     93309      A     A  A
                                TGGC TCAGCC CA GAG
                                |||| |||||| || |||
                                ACCG AGTCGG GT CTC
                                   _     C  C
GAM515  LOC255177 3'  TTTCACTCTCGTTGCC      96611      TCAGCC  A
                                GGCA     AC AGAGTGAAA
                                ||||     || |||||||||
                                CCGT     TG TCTCACTTT
                                   _______  C
GAM515  LOC257052 3'  CACCCCCTGGCTGATGCCA   96269          CAAGA
                                TGGCATCAGCCA    GTG
                                ||||||||||||    |||
                                ACCGTAGTCGGT    CAC
                                      CCCC_
GAM515  LOC90625  3'  TCACTTGGGGCTGATGCCA   63615          ACAA
                                TGGCATCAGCC    GAGTGA
                                ||||||||||    ||||||
                                ACCGTAGTCGG    TTCACT
                                      GG__
GAM515  LOC91266  5'  CACTCTCCCCTCCTGATGCTA  65409        CCACA_
                                TGGCATCAG     AGAGTG
                                |||||||||     ||||||
                                ATCGTAGTC     TCTCAC
                                     CTCCCC
GAM515  LOC91344  5'  GCTCTGTGGCTGTCACCA    65616     CAT       A
                                TGG   CAGCCACA GAGT
                                |||   |||||||| ||||
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                                ACC   GTCGGTGT CTCG
                                  ACT       _
GAM515  LOC92017  5'  CATGGCTGTAGCTGATGC    67885        C   AGA
                                GCATCAGC ACA   GTG
                                |||||||| |||   |||
                                CGTAGTCG TGT   TAC
                                    A   CGG
GAM516  CCR2      3'  CAATCTCTGATTCTGTCA    5386         CG    GG
                                TGACAGAA  AGAG  TG
                                ||||||||  ||||  ||
                                ACTGTCTT  TCTC  AC
                                    AG    TA
GAM516  CYP51     5'  AGCTTCTCTCGTTCCGTC    5779      A         T
                                GAC GAACGAGAGGG GCT
                                ||| |||||||||| |||
                                CTG CTTGCTCTCTT CGA
                                  C         _
GAM516  GABRP     3'  TCAGAGAGTCGCTGTCATTCTG 26402         C  G  _  TG
          TCA                     TGACAGAA GA AG GG  CTCTGA
                                |||||||| || || ||  ||||||
                                ACTGTCTT CT TC CT  GAGACT
                                    A  G  G  GA
GAM516  GMPS      5'  GGCACCCTCCCGCCCCGTC   13918     AGAA  A
                                GAC    CG GAGGGTGCT
                                |||    || |||||||||
                                CTG    GC CTCCCACGG
                                  CCCC  C
GAM516  LIMD1     3'  GGGGACCCTCTCTTCCCATCA  26463     CA_  C       G
                                TGA   GAA GAGAGGGT CTC
                                |||   ||| |||||||| |||
                                ACT   CTT CTCTCCCA GGG
                                  ACC   _       G
GAM516  OCRL      3'  CACTCCCCTCGTTCTGTCA    7825           A  _
                                TGACAGAACGAG GG GTG
                                |||||||||||| || |||
                                ACTGTCTTGCTC CC CAC
                                      C  T
GAM516  OCRL      3'  CACTCCCCTCGTTCTGTCA    4259           A  _
                                TGACAGAACGAG GG GTG
                                |||||||||||| || |||
                                ACTGTCTTGCTC CC CAC
                                      C  T
GAM516  PYGO2     3'  GCTCCCTCTCGCTCTCTCA    63987     C   A       T
                                TGA AGA CGAGAGGG GC
                                ||| ||| |||||||| ||
                                ACT TCT GCTCTCCC CG
                                  C   C       T
GAM516  TCFL4     3'  TCAAAATCACCCTTTCTGTCA  63465        ACGA      CTC_
                                TGACAGA    GAGGGTG    TGA
                                |||||||    |||||||    |||
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                                ACTGTCT   TTCCCAC   ACT
                                   ____      TAAA
GAM516  BIRC1    3'  CAGTCTCTCCCATTCTGT    15787      C__     G
                                ACAGAA   GAGAGG TG
                                ||||||   |||||| ||
                                TGTCTT   CTCTCT AC
                                   ACC     G
GAM516  CHERP    3'  AGCGCCTTCCACTCCATCA   21096    CA  ACGA
                                TGA  GA   GAGGGTGCT
                                |||  ||   |||||||||
                                ACT  CT   CTTCCGCGA
                                  AC  CAC_
GAM516  DKFZP564K2062 3'  TCAGAAGTCTCAGTTCTGTCA  31238        GA   GTGC
                                TGACAGAAC  GAGG   TCTGA
                                |||||||||  ||||   |||||
                                ACTGTCTTG  CTCT   AGACT
                                     A_   GA__
GAM516  FLJ10482  3'  TCAGAGTGATCTGTCCTGCCA  36165    A   AAC  G  GG
                                TG CAG   GA AG  TGCTCTGA
                                || |||   || ||  ||||||||
                                AC GTC   CT TC  GTGAGACT
                                 C   ___  G  TA
GAM516  FLJ13848  3'  CAGAAGGACTTCTCGTTCCTCA 45461     CA        GTGC
                                TGA  GAACGAGAGG   TCTG
                                |||  ||||||||||   ||||
                                ACT  CTTGCTCTTC   AGAC
                                  C_        AGGA
GAM516  FLJ21802  3'  CAGAGCACCAACTTCATC    44980    AC   AG
                                GA  GAG  GGTGCTCTG
                                ||  |||  |||||||||
                                CT  TTC  CCACGAGAC
                                 AC   AA
GAM516  KIAA1458  3'  CAGGACCTCCATTCTGTCA   69002        CGA   GTGC
                                TGACAGAA   GAGG   TCTG
                                ||||||||   ||||   ||||
                                ACTGTCTT   CTCC   GGAC
                                     AC_   A___
GAM516  MGC10500  3'  GTCCCCCTCGTTCTGT     48935         A   TG
                                ACAGAACGAG GGG  C
                                |||||||||| |||  |
                                TGTCTTGCTC CCC  G
                                      _  CT
GAM516  NDP52    3'  CATCCTCTCACCTGTCA     19526       AAC
                                TGACAG   GAGAGGGTG
                                ||||||   |||||||||
                                ACTGTC   CTCTCCTAC
                                   CA_
GAM516  SEC24C   3'  TCAAGTATCCTGCCACTCTGTC 17000        ACGAG       C
            A                    TGACAGA    AGGGTGCT TGA
                                |||||||    |||||||| |||
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                                ACTGTCT    TCCTATGA ACT
                                   CACCG      _
GAM516  SNRPD3   5' CAGAGCCGAACTCTCTTCCTGC 14800    A   AAC      ___
            CA                   TG CAG   GAGAGGGT   GCTCTG
                                || |||   ||||||||   ||||||
                                AC GTC   TTCTCTCA   CGAGAC
                                 C   C__       AGC
GAM516  LOC152328 3' CAAGTGCCCTCCCCTATCA   80523    C  AACGA    TG  C
                                TGA AG    GAGGG  CT TG
                                ||| ||    |||||  || ||
                                ACT TC    CTCCC  GA AC
                                  A  CC___    GT  _
GAM516  LOC158835 3' CATCCCTCTCATTCCATC    82009    CA   C     _
                                GA  GAA GAGAGGG TG
                                ||  ||| ||||||| ||
                                CT  CTT CTCTCCC AC
                                 AC   A      T
GAM516  LOC197003 3' CAGACCTTCTCACACTGCCA   87871    A   AAC     TGC
                                TG CAG   GAGAGGG   TCTG
                                || |||   |||||||   ||||
                                AC GTC   CTCTTCC   AGAC
                                 C   ACA     ___
GAM516  LOC257443 3' CAGGACCTCCATTCTGTCA    95846       CGA    GTGC
                                TGACAGAA   GAGG    TCTG
                                ||||||||   ||||    ||||
                                ACTGTCTT   CTCC    GGAC
                                     AC_    A___
GAM516  LOC257451 3' GCTCCCTCTCGCTCTCTCA    95557    C   A      T
                                TGA AGA CGAGAGGG GC
                                ||| ||| |||||||| ||
                                ACT TCT GCTCTCCC CG
                                  C   C       T
GAM516  LOC92609  5' CAAAGTCTCTCGTTC       72844         GGT   C
                                GAACGAGAG   GCT TG
                                |||||||||   ||| ||
                                CTTGCTCTC   TGA AC
                                     ___   A
GAM517  CD34     3' CCAACCCTTCCCCACTGCACAC 8340     A   A  TTATC
                                GTG GCA TG    AGGGTTGG
                                ||| ||| ||    ||||||||
                                CAC CGT AC    TCCCAACC
                                  A   C  CCCT_
GAM517  MYO15A   3' CCAACCCCAGACCCCCATCAC  32670     GCAAT   ATCA
                                GTGA    GTT    GGGTTGG
                                ||||    |||    |||||||
                                CACT    CAG    CCCAACC
                                  ACCCC   AC__
GAM517  SLC6A12  3' CCTTTGCTGATAACACCACCAC 11733     AGCAA       GGTT
                                GTG    TGTTATCAG    GG
                                |||    |||||||||    ||
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                                CAC    ACAATAGTC   CC
                                  CACC_       GTTT
GAM517  XYLB    3'  TCCAACCCTGACTGCCCAC   17561    A   ATGTTA
                                GTG GCA     TCAGGGTTGGA
                                ||| |||     ||||||||||
                                CAC CGT     AGTCCCAACCT
                                  C   C_____
GAM517  CTNNBIP1  3'  CCAACCCTGCCCTGCCCCAC   39661    A_   ATGTTAT
                                GTG  GCA     CAGGGTTGG
                                |||  |||     |||||||||
                                CAC  CGT     GTCCCAACC
                                  CC   CCC____
GAM517  DVS27   3'  TCCTGATAACACTGCTTAC   53082       A
                                GTGAGCA TGTTATCAGGG
                                ||||||| ||||||||||
                                CATTCGT ACAATAGTCCT
                                    C
GAM517  KIAA1554  3'  CCAACCCTTTATTCATCCTCAC 95148      CA   TTATC
                                GTGAG  ATG    AGGGTTGG
                                |||||  |||    ||||||||
                                CACTC  TAC    TCCCAACC
                                  C_   TTATT
GAM517  LOC115129 3'  CCAACCTTTAATCACTCAC   73228      CAAT   TC
                                GTGAG   GTTA  AGGGTTGG
                                |||||   ||||  ||||||||
                                CACTC   TAAT  TTCCAACC
                                  AC__   __
GAM517  LOC143188 5'  TCCAACCCCAGAACTGCCCAC  82902    A   AT   ATCA
                                GTG GCA  GTT   GGGTTGGA
                                ||| |||  |||   ||||||||
                                CAC CGT  CAA   CCCAACCT
                                  C   __   GAC_
GAM517  LOC146713 3'  CCAACCCCCATTACCCAC    83723    AGC   TTATCA
                                GTG   AATG    GGGTTGG
                                |||   ||||    |||||||
                                CAC   TTAC    CCCAACC
                                  CCA   C_____
GAM517  LOC148894 5'  CCAACCCCAGCTCTCTCTGCTC 84256       ATGTTATCA_
            AC                  GTGAGCA       GGGTTGG
                                |||||||       |||||||
                                CACTCGT       CCCAACC
                                    CTCTCTCGAC
GAM517  LOC158267 3'  CCAACCCTGGCACTGTCAC   81826     G  A   TAT
                                GTGA CA TGT   CAGGGTTGG
                                |||| || |||   |||||||||
                                CACT GT ACG   GTCCCAACC
                                  _  C   ___
GAM518  ADH1B   3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
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                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM518  AHR     3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM518  FDFT1   3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                        _
GAM518  JTB     3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM518  KLF4    3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM518  PHYH    3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM518  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                       T__    _
GAM518  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM518  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_    CG_
GAM518  CG012   5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM518  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
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                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM518  FLJ23462  3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
            G                     CATTTC        GTCTGAGAT
                                  ||||||        |||||||||
                                  GTAAAG        CAGACTCTA
                                     AAACATTT_
GAM518  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                  CATTTCA   TCACTGTCTGAGAT
                                  |||||||   ||||||||||||||
                                  GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM518  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                  TTCA TTTCACTG  TGAG
                                  |||| ||||||||  ||||
                                  AAGT AAAGTGAC  GTTT
                                    A       CT
GAM518  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                  TTTC CTG TCTGAGAT
                                  |||| ||| ||||||||
                                  AAAG GAC AGACTCTA
                                    _  G
GAM518  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                  ATT CACTTTCACTGT
                                  ||| ||||||||||||
                                  TAA GTGAAAGTGACG
                                   C
GAM518  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                  TTCACTTT  CT TCTGAGAT
                                  ||||||||  || ||||||||
                                  AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM518  PP35      3'  ATCTCAGACTGAAA       22814      CT
                                  TTTCA  GTCTGAGAT
                                  |||||  |||||||||
                                  AAAGT  CAGACTCTA
                                     __
GAM518  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148         TCAC  C_
                                  CATTTCACTT   TGT  TGAG
                                  ||||||||||   |||  ||||
                                  GTAAAGTGAA   ACG  ACTC
                                       TA__   TT
GAM518  SEP15     3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                  TTTCACTTT ACTGT  GA
                                  ||||||||| |||||  ||
                                  AAAGTGAGA TGACA  CT
                                       A    TC
GAM518  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                  TTTCACTTT    TCTGAG
                                  |||||||||    ||||||
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                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM518  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM518  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM518  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226     A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM518  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM519  BTG1     3'  CATCTGATGATGATCCA     8189     A        C
                                TG ATCATTATCAG ATG
                                || ||||||||||| |||
                                AC TAGTAGTAGTC TAC
                                 C         _
GAM519  CD47     3'  CATGGCCTTGATGATTCA    8349          TCAG
                                TGAATCATTA    CATG
                                ||||||||||    ||||
                                ACTTAGTAGT    GTAC
                                      TCCG
GAM519  GALC     3'  CATCATGTTGTATGATTTA   3846         TAT
                                TGAATCAT   CAGCATGATG
                                ||||||||   ||||||||||
                                ATTTAGTA   GTTGTACTAC
                                     T__
GAM519  GCN1L1   3'  CAGATGAAAATGATTCA     69753         A   GCA
                                TGAATCATT TCA   TG
                                ||||||||| |||   ||
                                ACTTAGTAA AGT   AC
                                     A   AG_
GAM519  NLGN2    5'  CATCATGCTGCCTGTGTGGTTC 88155        TAT__
          A                      TGAATCAT    CAGCATGATG
                                 ||||||||    ||||||||||
                                 ACTTGGTG    GTCGTACTAC
                                      TGTCC
GAM519  NVL      5'  TATTCTGATGATGATTCA    10302           C
                                TGAATCATTATCAG ATG
                                |||||||||||||| |||
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                                ACTTAGTAGTAGTC TAT
                                       T
GAM519  OLFM1    3'  CATGTTGATAATAATCA     26553     ATC
                                TGA   ATTATCAGCATG
                                |||   ||||||||||||
                                ACT   TAATAGTTGTAC
                                  AA_
GAM519  PTHLH    3'  CATCATGTCATAAACGATTC   11012      A_   CA
                                GAATC  TTAT  GCATGATG
                                |||||  ||||  ||||||||
                                CTTAG  AATA  TGTACTAC
                                   CA   C_
GAM519  SLC1A1   3'  GCATCATAAATAGTAAATAATG 14793        CA _____     III
            ATTCA                  ATCATTAT  GC    ATGATG   C
                                |||||||| ||    ||||||  |
                                TAGTAATA  TG    TACTAC   G
                                     AA  ATAAA     III
GAM519  SLC35A3  3'  CATCATGCTGAATCTGATCA  24271     A   TTA
                                TGA TCA   TCAGCATGATG
                                ||| |||   ||||||||||
                                ACT AGT   AGTCGTACTAC
                                  _   CTA
GAM519  TCF2     3'  ATCATGCTTGATTGA      21374     TT   _
                                TCA  ATCA GCATGAT
                                |||  |||| |||||||
                                AGT  TAGT CGTACTA
                                  __    T
GAM519  ADAMDEC1 3'  CATCATGTCGAGAATGATTCA 27132         A  A
                                TGAATCATT TC GCATGATG
                                ||||||||| || ||||||||
                                ACTTAGTAA AG TGTACTAC
                                      G  C
GAM519  CLIC4    3'  ATCATTTAATGATTCA      25631          TCAGC
                                TGAATCATTA    ATGAT
                                ||||||||||    |||||
                                ACTTAGTAAT    TACTA
                                      T____
GAM519  GR6      3'  CATCATGGGTGGATGATTC   23728         ATCAG
                                GAATCATT    CATGATG
                                ||||||||    |||||||
                                CTTAGTAG    GTACTAC
                                     GTGG_
GAM519  KIAA1301 3'  CATCATGCTAATATGTATC   66341    AT   T  C
                                GA  CAT AT AGCATGATG
                                ||  ||| || |||||||||
                                CT  GTA TA TCGTACTAC
                                 AT   _  A
GAM519  KR18     3'  CATTCTGATAATGTTCA     52743      T       C
                                TGAA CATTATCAG ATG
                                |||| ||||||||| |||
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                                ACTT GTAATAGTC TAC
                                  _       T
GAM519  STK3     3'  CATCATGTTCCTGATGAT    73719       TC
                                ATCATTA  AGCATGATG
                                |||||||  |||||||||
                                TAGTAGT  TTGTACTAC
                                    CC
GAM519  TCF-3    3'  CATTGAGTAGTAATGATTCA  48424         CA  A
                                TGAATCATTAT  GC TGATG
                                ||||||||||  || |||||
                                ACTTAGTAATG  TG GTTAC
                                      A_  A
GAM519  LOC147172 3'  CATTTATTTGATAATGATTTA  78295           CAT
                                TGAATCATTATCAG   GATG
                                ||||||||||||||   ||||
                                ATTTAGTAATAGTT   TTAC
                                         TAT
GAM520  ZNF207   3'  ACATTATCTTCCCACATACCA  12915         A    TCTGT
                                TGGTATGTGG GAAG    ATGT
                                |||||||||| ||||    ||||
                                ACCATACACC CTTC    TACA
                                      _   TAT__
GAM520  BM-002   3'  ACATACAGACTTCAAAATACC  33522      GTGGA
                                GGTAT    GAAGTCTGTATGT
                                |||||    ||||||||||||
                                CCATA    CTTCAGACATACA
                                   AAA__
GAM520  FLJ21290  3'  TAGAATCTTCTCCACATACCA  46744            __
                                TGGTATGTGGAGAAG  TCTG
                                ||||||||||||||  ||||
                                ACCATACACCTCTTC  AGAT
                                         TA
GAM520  HEMK     3'  ACAGCCTCCCCACCACCA    32424     AT   A  A T
                                TGGT  GTGG GA G CTGT
                                ||||  |||| || | ||||
                                ACCA  CACC CT C GACA
                                  C_   C  C _
GAM520  KIAA1211  3'  ACACACCCACCCACACACCA  68889     A    AGAA  C
                                TGGT TGTGG   GT TGT
                                |||| |||||   || |||
                                ACCA ACACC   CA ACA
                                  C    CACC  C
GAM520  OSBPL3   3'  ACATACAGTTTATTCCACACAG 31433    A_     A  T
          C                      GT  TGTGGAG AG CTGTATGT
                                ||  ||||||| || ||||||||
                                CG  ACACCTT TT GACATACA
                                 AC      A  T
GAM520  LOC147054 5'  ACACACAAACATGCACACATAC 83917       GAGAA  C   A
                                GTATGTG    GT TGT TGT
                                |||||||    || ||| |||
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                                CATACAC    CA ACA ACA
                                    ACGTA  A   C
GAM520  LOC221814 5'  ACAGCCCCTCCCCCACATAC  93941        A_  AGT_
                                GTATGTGG  GA    CTGT
                                ||||||||  ||    ||||
                                CATACACC  CT    GACA
                                    CC  CCCC
GAM520  LOC51075  3'  ATACTCCCCACACCCA     31987     TA    A  AGTCT
                                TGG  TGTGG GA    GTAT
                                |||  ||||| ||    ||||
                                ACC  ACACC CT    CATA
                                  C_    C  _____
GAM521  ARNT2     3'  AAACAACCCGTGCATCCCTGC  29450     A    TTTTA
                                GTA GGAT    GGGTTGTTT
                                ||| ||||    |||||||||
                                CGT CCTA    CCCAACAAA
                                  C   CGTG_
GAM521  LCT       3'  AACCGTAAAAATCCTT      9697           G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
                                TTCCTAAAAAT CCAA
                                      G
GAM521  RPL15     3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM521  FBXO30    3'  AACTAAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                 G        AA
GAM521  KIAA0494  3'  AACAACCCTTACTTAC      28736      GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM521  PRO0641   5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                  ___    C
GAM521  SMT3H2    3'  AACAACATAAAAATCCTTGC  22670          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM521  LOC120103 3'  AACCTATGAAAAATCCTTGC  74002          A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
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                                CGTTCCTAAAAA  TCCAA
                                      GTA
GAM521  LOC129831 3'  AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM521  LOC133088 5'  AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                      GTA GGATTTTT    TTGTTT
                                ||| ||||||||    ||||||
                                CGT CCTAAAAA    AACAAA
                                  C       GATAA
GAM521  LOC148089 3'  GGCCCTAAAAATTCCTAC    78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM521  LOC154547 3'  AACAACATAAAAATCCTTGC   76050           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM521  LOC158104 3'  ACAGCCAAAAATCCTTA     60313          AG
                                TAAGGATTTTT  GGTTGT
                                ||||||||||  ||||||
                                ATTCCTAAAAA  CCGACA
                                      __
GAM521  LOC205880 5'  AAACAACCATCATCCTGAC    90709    A    TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM521  LOC221561 3'  AACAACATAAAAATCCTTGC   92130           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM521  LOC257591 3'  AACAACATAAAAATCCTTGC   97840           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM521  LOC51145  3'  AGCTAAAATCCTTAC       32393          TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
                                CATTCCTAAAA   TCGA
                                      ___
GAM522  ADH4      3'  TAAAAAGATTTTTACTGGA    5408         CGT
                                TCCAGTGG   TCTTTTTA
                                ||||||||   ||||||||
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                                AGGTCATT  AGAAAAAT
                                    TTT
GAM522  B4GALT2  3'  AGTAAAAAACGTGAATGGA  47580     GTG   CT
                                TCCA  GCGTT  TTTTACT
                                ||||  |||||  |||||||
                                AGGT  TGCAA  AAAATGA
                                  AAG   __
GAM522  CTBP1    3'  AAAAAGAAAACCTGAAGGAG  67941     AGT_  CG
                                CTCC   GG  TTCTTTTT
                                ||||   ||  ||||||||
                                GAGG   CC  AAGAAAAA
                                  AAGT  AA
GAM522  ENPP3    3'  TAAAAAGAACAGCAGAGAG   17226     CAGTG  _
                                CTC    GC GTTCTTTTTA
                                |||    || ||||||||||
                                GAG    CG CAAGAAAAAT
                                  AGA__  A
GAM522  F8       3'  TAAAAAAATAAGTCAGGAGGA  3732       AG   GTTC_
                                TCCTCC  TGGC    TTTTTA
                                ||||||  ||||    ||||||
                                AGGAGG  ACTG    AAAAAT
                                   __   AATAA
GAM522  GK       3'  AGCAAAAAGAATGCTAT     3911          A
                                GTGGCGTTCTTTTT CT
                                |||||||||||||| ||
                                TATCGTAAGAAAAA GA
                                      C
GAM522  ID4      3'  GAAAAAAAGCCACCGGAGGA   7755       A    GTTC
                                TCCTCC GTGGC    TTTTT
                                |||||| |||||    |||||
                                AGGAGG CACCG    AAAAG
                                   C    AAA_
GAM522  PITX1    3'  GAAAAAGACGTCGGAG      10599     AGT    T     A
                                CTCC   GGCGT CTTTTT C
                                ||||   ||||| |||||| |
                                GAGG   CTGCA GAAAAA G
                                  ___    _     C
GAM522  TDG      3'  GAAAAAGATGCTGGAG      12191        GCGT      A
                                CTCCAGTG    TCTTTTT C
                                ||||||||    ||||||| |
                                GAGGTCGT    AGAAAAA G
                                     _____       C
GAM522  XRCC2    3'  AGCAAAAAGAACAAAGCTGGAG 18318         GGC       A
          G                      CCTCCAGT   GTTCTTTTT CT
                                ||||||||   ||||||||| ||
                                GGAGGTCG   CAAGAAAAA GA
                                     AAA        C
GAM522  DKFZP727M111 5'  AAAAGGAAAAGCCCTGAAG   31401    C   T   G_
                                CT CAG GGC  TTCTTTTT
                                || ||| |||  ||||||||
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                                GA GTC CCG  AAGGAAAA
                                 A  _  AA
GAM522  ELKS     3'  AGTGGTCAACGCCCTGGAAGA  30501    C    T    CTTT
                                TC TCCAG GGCGTT   TTACT
                                || ||||| ||||||   |||||
                                AG AGGTC CCGCAA   GGTGA
                                 A    _    CT__
GAM522  FLJ10648  3'  AGCAAAAAGAACAAAGTCCTGG 36378        T  ___       A
           AGGA                    TCCTCCAG GGC   GTTCTTTTT CT
                                ||||||||| |||   ||||||||| ||
                                AGGAGGTC CTG   CAAGAAAAA GA
                                     _  AAA       C
GAM522  FLJ20151  3'  AAAGACCCTGGAGGA      34648        T  CGT
                                TCCTCCAG GG   TCTTT
                                |||||||| ||   |||||
                                AGGAGGTC CC   AGAAA
                                     _ ___
GAM522  FLJ20435  3'  TAAAAAGAGCCATCTGGAGGA  35162        _   GT
                                TCCTCCAG TGGC  TCTTTTTA
                                |||||||| ||||  ||||||||
                                AGGAGGTC ACCG  AGAAAAAT
                                     T   __
GAM522  MDS024   3'  AAAAAGAATTGCCAAGGA    41522     AG    _
                                TCC  TGGCG TTCTTTTT
                                |||  ||||| ||||||||
                                AGG  ACCGT AAGAAAAA
                                  A_    T
GAM522  ShrmL    5'  AGAGCGCCACTGAAGGA     40463      C
                                TCCT CAGTGGCGTTCT
                                |||| ||||||||||||
                                AGGA GTCACCGCGAGA
                                   A
GAM522  SIAT8C   5'  TAAAAAAGCCCCACAGAGGA   31883      CA   C   C
                                TCCTC  GTGG GTT TTTTTA
                                |||||  |||| ||| ||||||
                                AGGAG  CACC CGA AAAAAT
                                   A_   C   _
GAM522  VEST1    5'  AAAAAGATGCACTGGGGA    53678     T    G   T
                                TCC CCAGTG CGT CTTTTT
                                ||| |||||| ||| ||||||
                                AGG GGTCAC GTA GAAAAA
                                     _    _  _
GAM522  ZFD25    5'  AAAAAGAGCCCTGGA       32573      T   GT
                                TCCAG GGC  TCTTTTT
                                ||||| |||  |||||||
                                AGGTC CCG  AGAAAAA
                                     _  __
GAM522  LOC124626 3'  AGTAAGACCAAACCACTGGA   74313        CGTTCT
                                TCCAGTGG     TTTTACT
                                ||||||||     |||||||
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                                AGGTCACC     AGAATGA
                                     AAACC_
GAM522  LOC144577 3'  TAAAAAGAAGCCACAAAGAG  76902     CA_    G
                                CTC   GTGGC TTCTTTTTA
                                |||   ||||| |||||||||
                                GAG   CACCG AAGAAAAAT
                                  AAA    _
GAM522  LOC145837 5'  AGCAAAAAGAACCAAAGAGGA  83542      CAG   CG      A
                                TCCTC   TGG  TTCTTTTT CT
                                |||||   |||  |||||||| ||
                                AGGAG   ACC  AAGAAAAA GA
                                   AA_  __       C
GAM522  LOC151194 3'  TAAAAAAACTGGGGA      59215     T    GGCGTTC
                                TCC CCAGT      TTTTTA
                                ||| |||||      ||||||
                                AGG GGTCA      AAAAAT
                                  _    A_______
GAM522  LOC154789 5'  AGTAAAATCTCAGGCCACTAGA 81131     C     GTTCT_
          G                      CTC AGTGGC     TTTTACT
                                ||| ||||||     |||||||
                                GAG TCACCG     AAAATGA
                                  A     GACTCT
GAM522  LOC197322 3'  AAAGACTCCACTGGAGGA    89736          C  T
                                TCCTCCAGTGG GT CTTT
                                |||||||||| || ||||
                                AGGAGGTCACC CA GAAA
                                       T  _
GAM522  LOC221596 3'  TAAAAACCTCACACTGGAGAGA 91980    _      GCGTTC
                                TC CTCCAGTG     TTTTTA
                                || ||||||||     ||||||
                                AG GAGGTCAC     AAAAAT
                                  A       ACTCC_
GAM522  LOC91796  3'  AGCAAAAAGAACAAGGCTGGA  67208       GGC       A
                                TCCAGT   GTTCTTTTT CT
                                ||||||   |||||||| ||
                                AGGTCG   CAAGAAAAA GA
                                    GAA       C
GAM522  LOC92539  5'  TAAAAAGTGTCACTG       69638         TT
                                CAGTGGCG  CTTTTTA
                                ||||||||  |||||||
                                GTCACTGT  GAAAAAT
                                          __
GAM523  ARNT2     3'  AAACAACCCGTGCATCCCTGC  29450     A    TTTTA
                                GTA GGAT     GGGTTGTTT
                                ||| ||||     |||||||||
                                CGT CCTA     CCCAACAAA
                                  C    CGTG_
GAM523  LCT       3'  AACCGTAAAAATCCTT      9697           G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
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                                TTCCTAAAAAT CCAA
                                      G
GAM523  RPL15    3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM523  FBXO30   3'  AACTAAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                  G        AA
GAM523  KIAA0494 3'  AACAACCCTTACTTAC      28736      GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM523  PRO0641  5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                   ___    C
GAM523  SMT3H2   3'  AACAACATAAAAATCCTTGC   22670           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM523  LOC120103 3' AACCTATGAAAAATCCTTGC   74002           A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
                                CGTTCCTAAAAA   TCCAA
                                      GTA
GAM523  LOC129831 3' AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM523  LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                      GTA GGATTTTT     TTGTTT
                                ||| ||||||||     ||||||
                                CGT CCTAAAAA     AACAAA
                                  C       GATAA
GAM523  LOC148089 3' GGCCCTAAAAATTCCTAC    78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM523  LOC154547 3' AACAACATAAAAATCCTTGC   76050           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
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                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM523  LOC158104 3'  ACAGCCAAAAATCCTTA     60313          AG
                                TAAGGATTTTT  GGTTGT
                                |||||||||||  ||||||
                                ATTCCTAAAAA  CCGACA
                                       __
GAM523  LOC205880 5'  AAACAACCATCATCCTGAC   90709    A    TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM523  LOC221561 3'  AACAACATAAAAATCCTTGC  92130          GG
                                GTAAGGATTTTTA  GTTGTT
                                |||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM523  LOC257591 3'  AACAACATAAAAATCCTTGC  97840          GG
                                GTAAGGATTTTTA  GTTGTT
                                |||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM523  LOC51145  3'  AGCTAAAATCCTTAC       32393          TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
                                CATTCCTAAAA   TCGA
                                       ___
GAM524  AIM1      3'  CTCACTGCAGCCTCTACCTCC  91822     AATTAAAA  __
                                GGAG       AGG  GTAGTGAG
                                ||||       |||  ||||||||
                                CCTC       TCC  CGTCACTC
                                  CATC_____   GA
GAM524  ASGR1     5'  CACCCCCATTCTCCA       8031         TAAAAA   TA
                                TGGAGAAT     GGG  GTG
                                ||||||||     |||  |||
                                ACCTCTTA     CCC  CAC
                                     _______  C_
GAM524  CRYZ      5'  CACGCAGATTTTAATTCCCA  8544      A       AGG  A
                                TGG GAATTAAAA   GT GTG
                                ||| |||||||||   || |||
                                ACC CTTAATTTT   CG CAC
                                  _       AGA  _
GAM524  GPX3      3'  CCCTTTCTCTCCAGTTCTCCA  9119         AA_____
                                TGGAGAATT     AAAGGG
                                |||||||||     ||||||
                                ACCTCTTGA     TTTCCC
                                     CCTCTC
GAM524  MEF2D     3'  TCCTCTTCCCCCATTCTCCA   96919        TAAAAA   T  T_
                                TGGAGAAT     GGG AG  GA
                                ||||||||     ||| ||  ||
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                                ACCTCTTA     CCC TC  CT
                                    C_____   T  TC
GAM524  MYO1D    3'  ACCCTTTCTCATTCTCCA    71763        TAA
                                TGGAGAAT   AAAGGGT
                                ||||||||   |||||||
                                ACCTCTTA   TTTCCCA
                                    CTC
GAM524  PIK3R2   3'  CTTCCCTCCCCCATTCTCCA   17257        TAAAA   T
                                TGGAGAAT    AGGG AG
                                ||||||||    |||| ||
                                ACCTCTTA    TCCC TC
                                    CCCCC   T
GAM524  PPP2R5A  3'  CCCTTCCTCTGCAATTCTCCA  20707         AAA____
                                TGGAGAATT      AAGGG
                                |||||||||      |||||
                                ACCTCTTAA      TTCCC
                                     CGTCTCC
GAM524  PTN      5'  TCATCCCTCCCATTCTCCA    82716        TAAAA   TA
                                TGGAGAAT    AGGG  GTGA
                                ||||||||    ||||  ||||
                                ACCTCTTA    TCCC  TACT
                                    CCC__   __
GAM524  SAR1     3'  CTCATTTTTATTCTCCA     39323         T   A
                                TGGAGAAT AAAA GGG
                                |||||||| |||| |||
                                ACCTCTTA TTTT CTC
                                    T   A
GAM524  STXBP1   3'  CTCAGCAGCTCTCATTCTCCA  12046        TAAAA    A _
                                TGGAGAAT    AGGGT G TGAG
                                ||||||||    ||||| | ||||
                                ACCTCTTA    TCTCG C ACTC
                                    C____    A G
GAM524  TEGT     3'  ACCCCTGTTAACTCTCCA    64621        A   AAA
                                TGGAGA TTAA   GGGT
                                ||||||  ||||  ||||
                                ACCTCT AATT   CCCA
                                   C   GTC
GAM524  ANKRD6   3'  TCAAATTCGTAATTCTCCA   30090         AA  GGGTAG
                                TGGAGAATTA  AA     TGA
                                ||||||||||  ||     |||
                                ACCTCTTAAT  TT     ACT
                                     GC  AA____
GAM524  ARHGEF4  3'  CTGCCCTCTAGTTCTCCA    52214         AAA
                                TGGAGAATTA   AGGGTAG
                                ||||||||||   |||||||
                                ACCTCTTGAT   TCCCGTC
                                     C__
GAM524  CEP3     3'  CTCACCATAGCGAATTCTCCA 21249         AAAAAGG  A
                                TGGAGAATT      GT GTGAG
                                |||||||||      || |||||
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                                ACCTCTTAA      TA CACTC
                                     GCGA___  C
GAM524  DAPK2    3'  CAAAGCTCTTAATTCTCCA   26735         AAA    AG
                                TGGAGAATTA   AGGGT  TG
                                ||||||||||   |||||  ||
                                ACCTCTTAAT   TCTCG  AC
                                     ___     AA
GAM524  EDR1     3'  CCCAGGTCTTAATTCTCCA   15381         AAA__
                                TGGAGAATTAA    GGG
                                ||||||||||     |||
                                ACCTCTTAATT    CCC
                                      CTGGA
GAM524  FLJ12969 5'  CTGCCTTTCCCACTCTCCA   43111       ATTAAA
                                TGGAGA     AAGGGTAG
                                ||||||     ||||||||
                                ACCTCT     TTTCCGTC
                                   CACCC_
GAM524  FLJ13941 3'  TCTGCTCCCCGATTCTCCA   45841        AAAAA  T  _
                                TGGAGAATT    GGG AGT GA
                                |||||||||    ||| ||| ||
                                ACCTCTTAG    CCC TCG CT
                                     _____  C   T
GAM524  FLJ13984 5'  CTCACTGCAGTTTCAACCTCC  45447     AATTA  AGG
                                GGAG    AAA   GTAGTGAG
                                ||||    |||   ||||||||
                                CCTC    TTT   CGTCACTC
                                  CAAC_  GA_
GAM524  KIAA0628 3'  CACTACCCTGAAGTCATCCA   28864     GA   AAAA
                                TGGA  ATT    AGGGTAGTG
                                ||||  |||    |||||||||
                                ACCT  TGA    TCCCATCAC
                                  AC   AG__
GAM524  KIAA0865 3'  CTCACTGTATATCCTCAACCCT 61249     AATTAAAA    ____
           CC                     GGAG      AGGGT    AGTGAG
                                ||||      |||||   ||||||
                                CCTC      TCCTA    TCACTC
                                  CCAAC___     TATG
GAM524  KIAA1037 3'  CACCACCCTTTTTTTTCATTTC 30434      ATT__       A
           C                     GGAGA    AAAAAGGGT GTG
                                |||||    ||||||||| |||
                                CCTTT    TTTTTCCCA CAC
                                   ACTTT       C
GAM524  KIAA1829 3'  CTCACTGCAGCCTCAACTTCCC 61946     A   TTAAAA  __
           A                      TGG GAA     AGG  GTAGTGAG
                                ||| |||     |||  ||||||||
                                ACC CTT     TCC  CGTCACTC
                                  _  CAAC__   GA
GAM524  KIAA1894 3'  CTACCCTCCCAATTCCCC    73844    A    AAAA
                                GG GAATT    AGGGTAG
                                || |||||    |||||||
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                                CC CTTAA   TCCCATC
                                 C    CCC_
GAM524  MAFB     3'  CCCTTCAATTCTTCA      18411         AAA
                                TGGAGAATT   AAGGG
                                |||||||||   |||||
                                ACTTCTTAA   TTCCC
                                     C__
GAM524  MGC10200 3'  CTCACTGCAGCCTCAACCTCC  58985     AATTAAAA  __
                                GGAG       AGG  GTAGTGAG
                                ||||       |||  ||||||||
                                CCTC       TCC  CGTCACTC
                                  CAAC____   GA
GAM524  MGC13008 5'  CTTAGTGGCCTCTTTAATTCTC 51080          A   G  G
           CA                     TGGAGAATTAAA AGG TA TGAG
                                ||||||||||| ||| || ||||
                                ACCTCTTAATTT TCC GT ATTC
                                       C   G  G
GAM524  P2RXL1   3'  TGCTGCCTCTCAATCTCCA   18385       ATTAAAAA
                                TGGAGA       GGGTAGTG
                                ||||||       ||||||||
                                ACCTCT       TCCGTCGT
                                   AACTC___
GAM524  PHRET1   3'  CTCCCTACCCTTAATCCCCA  41058     A  A   AAA     T
                                TGG GA TTA   AGGGTAG GAG
                                ||| || |||   ||||||| |||
                                ACC CT AAT   TCCCATC CTC
                                  C  _  ___      C
GAM524  WIT-1    3'  CTTACTGTCCTAACTCTCC   31826      A  AAAA   GT
                                GGAGA TT    AGG  AGTGAG
                                ||||| ||    |||  ||||||
                                CCTCT AA    TCC  TCATTC
                                  C  _____   TG
GAM524  LOC143310 3'  CATGACCTCTTTAATTCTC   76528         A   GTA
                                GAGAATTAAA AGG   GTG
                                |||||||||| |||   |||
                                CTCTTAATTT TCC   TAC
                                      C   AG_
GAM524  LOC144438 3'  TCTGCTACTTAATTCTCCA   76837         AAAAG     _
                                TGGAGAATTA    GGTAGT GA
                                ||||||||||    |||||| ||
                                ACCTCTTAAT    TCATCG CT
                                      ______     T
GAM524  LOC147093 5'  CTCACTACCCCCAGCTTCCCA  83942     A   TTAAAAA
                                TGG GAA      GGGTAGTGAG
                                ||| |||      ||||||||||
                                ACC CTT      CCCATCACTC
                                  _  CGACC__
GAM524  LOC147180 5'  CACTGCCCCCTCATATTCCCCA 83984     A    TAAAAA
                                TGG GAAT     GGGTAGTG
                                ||| ||||     ||||||||
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                                ACC CTTA     CCCGTCAC
                                  C    TACTCC
GAM524   LOC152343 5'  CCCATTTTTTAATCTCC     80560       A      __
                                GGAGA TTAAAAA  GGG
                                ||||| |||||||  |||
                                CCTCT AATTTTT  CCC
                                   _      TA
GAM524   LOC153811 3'  CTCACTGCAGCCTCAACTTCCA 80949       AATTAAAA  __
                                TGGAG       AGG  GTAGTGAG
                                |||||       |||  ||||||||
                                ACCTT       TCC  CGTCACTC
                                   CAAC____   GA
GAM524   LOC158014 5'  CATTTCCTCATTCTCCA     81645        TAAAA    T
                                TGGAGAAT     AGGG AGTG
                                ||||||||     |||| ||||
                                ACCTCTTA     TCCT TTAC
                                     C____   _
GAM524   LOC221662 3'  CTCTTTCCCTCCCAATTTTCCA 92403         AAAA    TAGT
                                TGGAGAATT    AGGG    GAG
                                |||||||||    ||||    |||
                                ACCTTTTAA    TCCC    CTC
                                     CCC_    TTT_
GAM524   LOC221756 3'  CATCCCTTTTCATTCTCCA    92137        TA      TA
                                TGGAGAAT  AAAAGGG  GTG
                                ||||||||  |||||||  |||
                                ACCTCTTA  TTTTCCC  TAC
                                     C_      __
GAM524   LOC221773 3'  CCCTGTCTTCTTAATTCTCCA  91042          AA____
                                TGGAGAATTAA      AGGG
                                ||||||||||      ||||
                                ACCTCTTAATT      TCCC
                                      CTTCTG
GAM524   LOC255707 3'  CTCACTGCAGCCTCAATCTTCC 96958      GA   AAAA  __
            A                    TGGA  ATT    AGG  GTAGTGAG
                                ||||  |||    |||  ||||||||
                                ACCT  TAA    TCC  CGTCACTC
                                  TC   C___   GA
GAM524   LOC256310 5'  GCCTTTCCAGATTCTCCA     96348         AAA
                                TGGAGAATT   AAGGGT
                                |||||||||   ||||||
                                ACCTCTTAG   TTTCCG
                                     ACC
GAM524   LOC51086  3'  TTGTCCTATTTAATTCCCCA   32010     A       A   GT
                                TGG GAATTAAA AGG  AG
                                ||| |||||||| |||  ||
                                ACC CTTAATTT TCC  TT
                                  C       A   TG
GAM524   LOC57146  3'  CTCACTGCAACCTCCAACTCC  39920      AATTAAAA  __
                                GGAG       AGG  GTAGTGAG
                                ||||       |||  ||||||||
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                                CCTC      TCC  CGTCACTC
                                  AACC____   AA
GAM524  LOC92568  3'  CTCCTCTTTTTAATTTTCCA  69771            T
                                TGGAGAATTAAAAAGGG AG
                                |||||||||||||||| ||
                                ACCTTTTAATTTTTCTC TC
                                          C
GAM524  LOC93259  5'  CTCAGTGTCCCCCAGTTCTCCA 71815        AAAAA  _  G
                                TGGAGAATT    GGG TA TGAG
                                |||||||||    ||| || ||||
                                ACCTCTTGA    CCC GT ACTC
                                     CC___  T  G
GAM525  ADRA1A   3'  GCACAAATCCAACATG     52784      AAGCC  A
                                CATGT    TG ATTTGTGC
                                |||||    || ||||||||
                                GTACA    AC TAAACACG
                                  _____ C
GAM525  AEGL1    5'  GCACAAATACACTACAT     6679       AGCC  A
                                ATGTA   TG ATTTGTGC
                                |||||   || ||||||||
                                TACAT   AC TAAACACG
                                  C___  A
GAM525  CDH2     3'  GCACAAATGTTTTACAT     8377        CCTGA
                                ATGTAAG    ATTTGTGC
                                |||||||    ||||||||
                                TACATTT    TAAACACG
                                    TG___
GAM525  CHRNE    3'  GCCCTCAGGCCCACAGGT    3586     A  AA     ATTTGT
                                ACC TGT  GCCTGA     GC
                                ||| |||  ||||||     ||
                                TGG ACA  CGGACT     CG
                                  _  CC     CC____
GAM525  COL4A3   3'  GGCCATGGCTCACATGGT    3622        A   TGAATT  T
                                ACCATGT AGCC     TG GCC
                                ||||||| ||||     || |||
                                TGGTACA TCGG     AC CGG
                                    C   T_____  _
GAM525  COL4A3   3'  GGCCATGGCTCACATGGT    48557       A   TGAATT  T
                                ACCATGT AGCC     TG GCC
                                ||||||| ||||     || |||
                                TGGTACA TCGG     AC CGG
                                    C   T_____  _
GAM525  COL4A3   3'  GGCCATGGCTCACATGGT    48568       A   TGAATT  T
                                ACCATGT AGCC     TG GCC
                                ||||||| ||||     || |||
                                TGGTACA TCGG     AC CGG
                                    C   T_____  _
GAM525  CYP3A4   3'  ACAAGCCTGGCCTACATGGT  33923        A  TGAA
                                ACCATGTA GCC    TTTGT
                                |||||||| |||    |||||
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                                TGGTACAT CGG    GAACA
                                     C   TCC_
GAM525  HIVEP3   5'  GGCACAAACCCAGCAGCCTCA  44439    TAA __   AA
                                TG   GC  CTG  TTTGTGCC
                                ||   ||  |||  ||||||||
                                AC   CG  GAC  AAACACGG
                                 TC_  AC   CC
GAM525  RECK     3'  GCAACAGGCTCACTGGT     40869      T  A     AAT
                                ACCA GT AGCCTG   TTGT
                                |||| || ||||||   ||||
                                TGGT CA TCGGAC   AACG
                                  _ C     ___
GAM525  TNFSF8   3'  GCACAAATTTAATACA      6966       AGCC
                                TGTA    TGAATTTGTGC
                                ||||    ||||||||||
                                ACAT    ATTTAAACACG
                                  A___
GAM525  ADAR3    3'  CACAAATTCAGAACGTG     38018       AAGC
                                CATGT    CTGAATTTGTG
                                |||||    ||||||||||
                                GTGCA    GACTTAAACAC
                                   A___
GAM525  BIVM     3'  CACAAATTCACTTA        34667      CC
                                TAAG  TGAATTTGTG
                                ||||  ||||||||||
                                ATTC  ACTTAAACAC
                                   __
GAM525  C20orf160 3'  GCAGTTACAGGATTACATGGT  54648          G    AAT
                                ACCATGTAA CCTG   TTGT
                                ||||||||| ||||   ||||
                                TGGTACATT GGAC   GACG
                                     A    ATT
GAM525  EPHA7    3'  CACAAATTTGCTGCACA     15433     A_   CT
                                TGT  AGC  GAATTTGTG
                                |||  |||  |||||||||
                                ACA  TCG  TTTAAACAC
                                  CG  __
GAM525  FLJ12783  3'  AGTTCAGGCTCACTG       48675     T  A
                                CA GT AGCCTGAATT
                                || || ||||||||||
                                GT CA TCGGACTTGA
                                 _ C
GAM525  HSC3     3'  CACAGGTTCAGACTACA      59067      A C
                                TGTA G CTGAATTTGTG
                                |||| | ||||||||||
                                ACAT C GACTTGGACAC
                                  _ A
GAM525  KIAA0316  3'  GCACAAATGCTCTTCACAGTGG 69674      _   _   CCTGA
             T                   ACCA TGT AAG     ATTTGTGC
                                ||||  ||| |||     ||||||||
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                                TGGT ACA TTC     TAAACACG
                                  G   C   TCG__
GAM525  KIAA0453  3'  GCACAAGTAGCTACATAGT   69047    C     A  CTGA
                                AC ATGTA GC    ATTTGTGC
                                || ||||| ||    ||||||||
                                TG TACAT CG    TGAACACG
                                 A     _  A___
GAM525  KIAA1423  3'  AATTCAAGTTTACATG      61719         C
                                CATGTAAGC TGAATT
                                ||||||||| ||||||
                                GTACATTTG ACTTAA
                                      A
GAM525  KIAA1691  3'  GCACAAATGCTGTCCATGG   92556      TA_   CTGA
                                CCATG   AGC    ATTTGTGC
                                |||||   |||    ||||||||
                                GGTAC   TCG    TAAACACG
                                   CTG   _____
GAM525  PPP1R3B   3'  GCCAGGTTCAGATTACA     44820      GC        T
                                TGTAA  CTGAATTTG GC
                                |||||  ||||||||| ||
                                ACATT  GACTTGGAC CG
                                   A_        _
GAM525  SFXN2     3'  GCAGCAGAGTTACATGGT    73946         GC   AATTTG
                                ACCATGTAA  CTG     TGC
                                |||||||||  |||     |||
                                TGGTACATT  GAC     ACG
                                     GA   G_____
GAM525  TBC1D2    5'  TAAATTCAGACCTACTGGT   37321     T   AGC
                                ACCA GTA   CTGAATTTG
                                ||||| |||   |||||||||
                                TGGT CAT   GACTTAAAT
                                  _   CCA
GAM525  ZNF347    3'  GGCTTTATTCAGGCCTCACA  50848     AA_       TTGT
                                TGT   GCCTGAAT    GCC
                                |||   ||||||||    |||
                                ACA   CGGACTTA    CGG
                                  CTC       TTT_
GAM525  LOC134147 3'  CACAAATTCAGTAGGACGT   57158     AAGC
                                ATGT    CTGAATTTGTG
                                ||||    ||||||||||
                                TGCA    GACTTAAACAC
                                  GGAT
GAM525  LOC151195 5'  GCACAAATTTATTTACA     80169       CC
                                TGTAAG  TGAATTTGTGC
                                ||||||  ||||||||||
                                ACATTT  ATTTAAACACG
                                        __
GAM525  LOC152860 3'  AATTCCAGCTTACATGG     80695          CT
                                CCATGTAAGC  GAATT
                                |||||||||  |||||
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                                GGTACATTCG  CTTAA
                                      AC
GAM525  LOC200382 3'  ACAGGGGCCAGACTTACATG   88801        C   AA_
                                CATGTAAG CTG   TTTGT
                                |||||||| |||   |||||
                                GTACATTC GAC   GGACA
                                     A   CGG
GAM525  LOC93622  3'  ACAGTCATTCCAGGCTTAGATG 56929     G      _  __
                                CAT TAAGCCTG AAT  TTGT
                                ||| |||||||| |||  ||||
                                GTA ATTCGGAC TTA  GACA
                                  G       C   CT
GAM526  MYO10     3'  AACCAACACTAATCGACCGTA  24699     A   GA    CA
                                TGC GTTG  ATTAG  TTGGTT
                                ||| ||||  |||||  ||||||
                                ATG CAGC  TAATC  AACCAA
                                  C   __     AC
GAM526  FLJ10719  3'  AACCCACTGAATTCAACTGCAC 62540          A    CATT
                                GTGCAGTTGGA TTAG    GGTT
                                |||||||||||| ||||    ||||
                                CACGTCAACTT AGTC    CCAA
                                      A    AC__
GAM526  MGC10981  3'  GCTATTCCAACCGCAC      51020      A       T
                                GTGC GTTGGAAT AGC
                                |||| |||||||| |||
                                CACG CAACCTTA TCG
                                  C       _
GAM526  MYO5C     3'  AACCTAAGAATCCCAATTGCAC 38103          A   AGCATT
                                GTGCAGTTGG ATT      GGTT
                                |||||||||| |||      ||||
                                CACGTTAACC TAA      CCAA
                                      C   GAAT__
GAM526  Rabip4R   3'  TGCAATTCCAACTATAC     35792     C        A
                                GTG AGTTGGAATT GCA
                                ||| |||||||||| |||
                                CAT TCAACCTTAA CGT
                                  A         _
GAM526  LOC203052 3'  ACCACCATTTCAACTGCAC    90449            TAGCAT
                                GTGCAGTTGGAAT     TGGT
                                ||||||||||||      ||||
                                CACGTCAACTTTA     ACCA
                                      CC_____
GAM526  LOC221344 5'  TGCCAACTCCAACTGC      93653          A  A
                                GCAGTTGGA TT GCA
                                ||||||||| || |||
                                CGTCAACCT AA CGT
                                      C  C
GAM527  ADORA3    5'  CTGAATGAATGAACTCTG    5441      GC       CC
                                CAG  TTCATTCA  CAG
                                |||  ||||||||  |||
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                                GTC  AAGTAAGT  GTC
                                  TC       AA
GAM527  ARHGEF7  3' GGAAGCAGAAGCCTGGTGG   14008          ATTCA
                                CCACCAGGCTTC    CC
                                ||||||||||||    ||
                                GGTGGTCCGAAG    GG
                                      ACGAA
GAM527  BAIAP3   3' CTGGGTGGCCAACTTGGCAGGA 14124    CA    CTTCAT
                                TCC  CCAGG     TCACCCAG
                                |||  |||||     ||||||||
                                AGG  GGTTC     GGTGGGTC
                                  AC    AACC__
GAM527  CDK10    3' GGTGGGCCTGGCAGGA     13405    CA     TCATT
                                TCC  CCAGGCT    CACC
                                |||  |||||||    ||||
                                AGG  GGTCCGG    GTGG
                                  AC     ______
GAM527  CDK10    3' GGTGGGCCTGGCAGGA     53772    CA     TCATT
                                TCC  CCAGGCT    CACC
                                |||  |||||||    ||||
                                AGG  GGTCCGG    GTGG
                                  AC     ______
GAM527  CDK10    3' GGTGGGCCTGGCAGGA     53781    CA     TCATT
                                TCC  CCAGGCT    CACC
                                |||  |||||||    ||||
                                AGG  GGTCCGG    GTGG
                                  AC     ______
GAM527  CHST6    3' TGGACAAGCCTGGAAGGA    41235    CA      CA
                                TCC  CCAGGCTT  TTCA
                                |||  ||||||||  ||||
                                AGG  GGTCCGAA  AGGT
                                  AA       C_
GAM527  COX10    3' GGTCTTGAAGCTTGACAGGA   7124     CAC       TTC
                                TCC   CAGGCTTCA   ACC
                                |||   |||||||||   |||
                                AGG   GTTCGAAGT   TGG
                                  ACA       TC_
GAM527  CPNE7    3' GAGAAAGCCTGGGGGA     27039     A      CA
                                TCCC CCAGGCTT  TTC
                                ||||  ||||||||  |||
                                AGGG GGTCCGAA  GAG
                                   _       A_
GAM527  CYLN2    3' TGAGACCCAGGCCTGGCAGGA  12639    CA      CA__
                                TCC  CCAGGCTT   TTCA
                                |||  ||||||||   ||||
                                AGG  GGTCCGGA   GAGT
                                  AC       CCCA
GAM527  DGKG     5' AGTGTTGCCTGGTGAGG     7203     _      TT
                                CC CACCAGGC  CATT
                                ||  ||||||||  ||||
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                                GG GTGGTCCG  GTGA
                                 A       TT
GAM527  FCN2     3'  GGCTGCACACCTGGTGGGA   31742          CTTCATT  C
                                TCCCACCAGG      CA CC
                                ||||||||||      || ||
                                AGGGTGGTCC      GT GG
                                      ACAC___  C
GAM527  FLRT1    5'  GGTGCAAGGCCTGGTAGGA   59612     C       CATT
                                TCC ACCAGGCTT   CACC
                                ||| |||||||||   ||||
                                AGG TGGTCCGGA   GTGG
                                  A       AC__
GAM527  GALNT2   3'  GTGGAAGCCTGGCTGG      15600     _       ATT
                                CCA CCAGGCTTC   CAC
                                ||| |||||||||   |||
                                GGT GGTCCGAAG   GTG
                                  C       ___
GAM527  GNAI3    3'  CTGGAAATGAGACCTGGTGG   21443        CT    CAC
                                CCACCAGG  TCATT   CCAG
                                ||||||||  |||||   ||||
                                GGTGGTCC  AGTAA   GGTC
                                     AG    A__
GAM527  JAM3     3'  GGTGAAAGGCCTGGCGGGG   51426     A       CA
                                TCCC CCAGGCTT  TTCACC
                                |||| ||||||||  ||||||
                                GGGG GGTCCGGA  AAGTGG
                                  C       __
GAM527  JRK      5'  GGTGTGTGGAGCCTGG      86536          T
                                CCAGGCTTCAT CACC
                                |||||||||||| ||||
                                GGTCCGAGGTG GTGG
                                       T
GAM527  LYPLA1   5'  TGAGCGTGCGCCCGGTGGGG   20926        A   TT   __
                                TCCCACC GGC  CAT  TCA
                                ||||||| |||  |||  |||
                                GGGGTGG CCG  GTG  AGT
                                     C   C_   CG
GAM527  MEOX1    3'  CTGGACACCACCTGGCCTGGTG 15756          TCATTCAC_
            GGA                    TCCCACCAGGCT        CCAG
                                   ||||||||||||        ||||
                                   AGGGTGGTCCGG        GGTC
                                         TCCACCACA
GAM527  MEOX1    3'  CTGGACACCACCTGGCCTGGTG 25730          TCATTCAC_
            GGA                    TCCCACCAGGCT        CCAG
                                   ||||||||||||        ||||
                                   AGGGTGGTCCGG        GGTC
                                         TCCACCACA
GAM527  N33      3'  AATGAAGCCAAGTGGGA     22222        CA
                                TCCCAC  GGCTTCATT
                                ||||||  |||||||||
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                                AGGGTG  CCGAAGTAA
                                   AA
GAM527  NUMA1    3'  TGGGTCTGACCTGGTGGGA   93441        CT   TTC
                                TCCCACCAGG  TCA   ACCCA
                                ||||||||||  |||   |||||
                                AGGGTGGTCC  AGT   TGGGT
                                      __   C__
GAM527  PAX5     3'  TGGGTGACCCTGGCAGG    33638    CA    CTTCAT
                                CC  CCAGG     TCACCCA
                                ||  |||||     |||||||
                                GG  GGTCC     AGTGGGT
                                 AC    C_____
GAM527  PIK3R3   3'  GGCAAATGGAGTGGGG     61060     ACCAG      CA
                                TCCC    GCTTCATT  CC
                                ||||    ||||||||  ||
                                GGGG    TGAGGTAA  GG
                                  _____       AC
GAM527  PLAU     3'  TGGACTGAAGCCTGCAGGA   68968    CAC       TTCAC
                                TCC   CAGGCTTCA    CCA
                                |||   |||||||||    |||
                                AGG   GTCCGAAGT    GGT
                                  AC_       CA___
GAM527  PSCDBP   3'  GATCCCAGCTTGGTGGGA    15021          TCAT
                                TCCCACCAGGCT    TC
                                ||||||||||||    ||
                                AGGGTGGTTCGA    AG
                                       CCCT
GAM527  PTPRE    5'  CTGGGTGGCTGGGCCTGG    55236       T  TT
                                CCAGGCT CA  CACCCAG
                                |||||||  ||  |||||||
                                GGTCCGG GT  GTGGGTC
                                    _  CG
GAM527  RANBP3   5'  CTGAAGAGGAAGCCTGTGAGA  23633    C   C      A   ACC
                                TC CAC AGGCTTC TTC   CAG
                                ||  ||| |||||||  |||   |||
                                AG GTG TCCGAAG GAG   GTC
                                 A   _      _   AA_
GAM527  SCP2     3'  CTGGGTGAATAGAGCCTGATGG  11442     C     TC
                                CCA CAGGCT  ATTCACCCAG
                                |||  ||||||  ||||||||||
                                GGT GTCCGA  TAAGTGGGTC
                                  A     GA
GAM527  SLC19A2  3'  GATGCTTGGCCTGGTGGGA    68978          T__
                                TCCCACCAGGCT   CATT
                                ||||||||||||   ||||
                                AGGGTGGTCCGG   GTAG
                                       TTC
GAM527  SLC4A7   3'  CTGGATGAATGGGGTTGTG    13226     CA         C
                                CAC  GGCTTCATTCA CCAG
                                |||  |||||||||| ||||
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                                GTG  TTGGGGTAAGT GGTC
                                  __         A
GAM527  TUFT1    3'  TGGCAAGGCCTGGTGAGA    39267    C        CATTCAC
                                TC CACCAGGCTT      CCA
                                || ||||||||||      |||
                                AG GTGGTCCGGA      GGT
                                 A         AC_____
GAM527  VIPR1    3'  TGGGTCAGTCTGGTGGGA    16117           TCATTC
                                TCCCACCAGGCT     ACCCA
                                ||||||||||||     |||||
                                AGGGTGGTCTGA     TGGGT
                                       C_____
GAM527  ABLIM    5'  TGAACTTGAAGCCTGGAGG   22039    A        __
                                CC CCAGGCTTCA  TTCA
                                || ||||||||||  ||||
                                GG GGTCCGAAGT  AAGT
                                 A         TC
GAM527  B3GNT5   3'  TGAGTCAAACCTGGATG     49429    _    C  C
                                CA CCAGG TT ATTCA
                                || ||||| || |||||
                                GT GGTCC AA TGAGT
                                 A    A  C
GAM527  BCCIP    3'  GGATGAATGAAGCCAATAGGA  54306     CACCA         C
                                TCC     GGCTTCATTCA CC
                                |||     |||||||||||| ||
                                AGG     CCGAAGTAAGT GG
                                  ATAA_          A
GAM527  C21orf55 3'  TGGATGAATCTGTGG       35223      C   C
                                CCAC AGG TTCATTCA
                                |||| ||| ||||||||
                                GGTG TCT AAGTAGGT
                                  _  _
GAM527  C21orf61 3'  TGAGTGAACTGGTG        88711       GC
                                CACCAG  TTCATTCA
                                ||||||  ||||||||
                                GTGGTC  AAGTGAGT
                                   __
GAM527  DKFZP566I1024 3'  CTGGATGTCATGGGGCC     70102         T_  C
                                GGCTTCAT  CA CCAG
                                ||||||||  || ||||
                                CCGGGGTA  GT GGTC
                                     CT  A
GAM527  DXS9879E 3'  TGGGCAAATGGAGCGAGG    20032    AG       CA
                                CC  GCTTCATT  CCCA
                                ||  ||||||||  ||||
                                GG  CGAGGTAA  GGGT
                                 AG       AC
GAM527  EPN2     3'  CTGGGCAGCTTGCCTGGTGG   30324          TTCATTCA
                                CCACCAGGC       CCCAG
                                |||||||||       |||||
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                                GGTGGTCCG      GGGTC
                                     TTCGAC__
GAM527  ET      3'  CTGGACACAGAGCTTGGTGG  44220         CATTCAC
                                CCACCAGGCTT     CCAG
                                ||||||||||      ||||
                                GGTGGTTCGAG     GGTC
                                     ACACA__
GAM527  FARP1   3'  CTGTATTAATGAAGCCTGGT  19280          CACC
                                ACCAGGCTTCATT   CAG
                                ||||||||||||   |||
                                TGGTCCGAAGTAA   GTC
                                      TTAT
GAM527  FLJ14810 3' GGGCAAATGGGGTCGGGGGGA 51628     A A      CA
                                TCCC CC GGCTTCATT  CCC
                                |||| || |||||||||  |||
                                AGGG GG CTGGGGTAA  GGG
                                  _ G       AC
GAM527  FLJ21596 3' TGAGTGAATCAGAGGGA    45703     ACCA  C
                                TCCC   GG TTCATTCA
                                ||||   || ||||||||
                                AGGG   CT AAGTGAGT
                                  AGA_ _
GAM527  FLJ21870 3' GGAGATCAAGAACCTGGTGGGA 43462         C   AT__  A
                                TCCCACCAGG TTC   TC CC
                                |||||||||| |||   || ||
                                AGGGTGGTCC AAG   AG GG
                                     _  AACT  A
GAM527  FLJ22160 3' CTGGGCATTTGGGCCTGGTGG  44733         T  TTCA
                                CCACCAGGCT CA   CCCAG
                                |||||||||| ||   |||||
                                GGTGGTCCGG GT   GGGTC
                                     _ TTAC
GAM527  GPS2    5'  TGGATGAATTCAACAATGGGG  87164      CCA__ GC
                                TCCCA    G  TTCATTCA
                                |||||    |  ||||||||
                                GGGGT    C  AAGTAGGT
                                   AACAA TT
GAM527  IBTK    3'  CTGGAAGGTAAGCCTGG     67488        C   CAC
                                CCAGGCTT ATT   CCAG
                                |||||||| |||   ||||
                                GGTCCGAA TGG   GGTC
                                     _  AA_
GAM527  IMAGE:4907098 3' GTGGAGAAAGGCTGGTGGGA  91666        G   CA
                                TCCCACCAG CTT  TTCAC
                                ||||||||| |||  |||||
                                AGGGTGGTC GAA  AGGTG
                                     G  AG
GAM527  JM11    3'  CTGGGTGGGATGCCTG     53257      T  AT
                                CAGGC TC  TCACCCAG
                                ||||| ||  ||||||||
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                                GTCCG AG  GGTGGGTC
                                  T __
GAM527  KIAA0368 3' TGAGTGAGCTTAATGG     65167     CC    T
                                CCA  AGGCT CATTCA
                                |||  ||||| ||||||
                                GGT  TTCGA GTGAGT
                                  AA    _
GAM527  KIAA0471 3' TGAATGAAGCCTTGTG      29402     C
                                CAC AGGCTTCATTCA
                                ||| ||||||||||||
                                GTG TCCGAAGTAAGT
                                  T
GAM527  KIAA0821 3' CTGGGCAGGGCTCTGGTGGGA  29944         _   CATTCA
                                TCCCACCAG GCTT     CCCAG
                                |||||||| ||||     |||||
                                AGGGTGGTC CGGG     GGGTC
                                      T   AC____
GAM527  KIAA0945 3' TGGGCCAAGCCTGAGGGA    30218     AC     CATTCA
                                TCCC  CAGGCTT     CCCA
                                ||||  |||||||     ||||
                                AGGG  GTCCGAA     GGGT
                                  A_      CC____
GAM527  KIAA1198 3' TGAATGGAGCTGGTGAGA    63342    C     G
                                TC CACCAG CTTCATTCA
                                || |||||| |||||||||
                                AG GTGGTC GAGGTAAGT
                                 A     _
GAM527  KIAA1522 3' TGAAGCCTGAGTGAGA      64978    C  _
                                TC CAC CAGGCTTCA
                                || ||| |||||||||
                                AG GTG GTCCGAAGT
                                 A  A
GAM527  KIAA1804 5' CTGGGCACGACCATGGTGGGA  69789        _ CT  ATTCA
                                TCCCACCA GG  TC    CCCAG
                                |||||||| ||  ||    |||||
                                AGGGTGGT CC  AG    GGGTC
                                     A  __  CAC__
GAM527  KIAA1854 3' GGCAAATATGTTTGGTGGG   71745         TTC   CA
                                CCCACCAGGC   ATT  CC
                                ||||||||||   |||  ||
                                GGGTGGTTTG   TAA  GG
                                      TA_   AC
GAM527  KIAA1866 3' GTGGACAGCCTGGATG      60935    _     TCA
                                CA CCAGGCT   TTCAC
                                || |||||||   |||||
                                GT GGTCCGA   AGGTG
                                 A      C__
GAM527  KIAA1908 5' TGGATGAACGTTTGTGG     73404      C   _
                                CCAC AGGC TTCATTCA
                                |||| |||| ||||||||
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                                GGTG TTTG AAGTAGGT
                                  _   C
GAM527  KIF1C    3'  CTGGGCAGAGGGCCTGGTGGGG 61223          TCA  A_
                                TCCCACCAGGCT  TTC  CCCAG
                                ||||||||||||  |||  |||||
                                GGGGTGGTCCGG  GAG  GGGTC
                                      ___  AC
GAM527  KRT6IRS  3'  CTGGATGACCAAGCTTGGTG  53087        CAT  C
                                CACCAGGCTT  TCA CCAG
                                ||||||||||  ||| ||||
                                GTGGTTCGAA  AGT GGTC
                                      CC_  A
GAM527  KRTAP2-4  3'  TGGATACAGCCTGGTG     52591        TC
                                CACCAGGCT  ATTCA
                                |||||||||  |||||
                                GTGGTCCGA  TAGGT
                                     CA
GAM527  LGI3     3'  GGGTGGGGGCTGGTGGGA    57747        G  TCAT
                                TCCCACCAG CT   TCACCC
                                ||||||||| ||   ||||||
                                AGGGTGGTC GG   GGTGGG
                                     G _____
GAM527  MAP1LC3A  3'  TGGGTGCTGGCTGGTGGGA   50709        G  TCATT
                                TCCCACCAG CT   CACCCA
                                ||||||||| ||   ||||||
                                AGGGTGGTC GG   GTGGGT
                                     _ TC___
GAM527  MGC11082  3'  TGAATGAACAGCTGGGA    51102      CCAG  __
                                TCCCA   GCT  TCATTCA
                                |||||   |||  |||||||
                                AGGGT   CGA  AGTAAGT
                                   _____  CA
GAM527  MGC15619  3'  CTGGGTGGACACAGCCTTGTGG 50421     C    TCA
                                CCAC AGGCT   TTCACCCAG
                                |||| |||||  |||||||||
                                GGTG TCCGA   AGGTGGGTC
                                  T    CAC
GAM527  MGC20460  5'  TGAGTGAACCTCCAGGGA    53850     ACC  C
                                TCCC   AGG TTCATTCA
                                ||||   ||| ||||||||
                                AGGG   TCC AAGTGAGT
                                  ACC  _
GAM527  NR5A1    3'  TGGGCAGGGCCTGGCGG     17105    A      CATTCA
                                CC CCAGGCTT     CCCA
                                || ||||||||     ||||
                                GG GGTCCGGG     GGGT
                                 C       AC_____
GAM527  OBTP     5'  GGGTGAGGGGCCTGACGG    34248    AC      AT
                                CC  CAGGCTTC  TCACCC
                                ||  ||||||||  ||||||
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                                GG  GTCCGGGG  AGTGGG
                                 CA       __
GAM527  PCYT2    3'  GAATAAAGCCTGGTGG      11170          C
                                CCACCAGGCTT ATTC
                                |||||||||| ||||
                                GGTGGTCCGAA TAAG
                                      A
GAM527  PLCE1    3'  CTGATGAATGAAGCCCAGGGGA 32964      ACCA         CC
                                TCCC    GGCTTCATTCA  CAG
                                ||||    ||||||||||  |||
                                AGGG    CCGAAGTAAGT  GTC
                                  GAC_         A_
GAM527  PRO2605  3'  AATGAATTGCGGTGGG      94855       AG __
                                CCCACC  GC  TTCATT
                                ||||||  ||  ||||||
                                GGGTGG  CG  AAGTAA
                                   __  TT
GAM527  REC8     5'  GAACGGGGATCTGGTGG      17618         _   A
                                CCACCAGG CTTC TTC
                                |||||||| |||| |||
                                GGTGGTCT GGGG AAG
                                     A   C
GAM527  REM      3'  GATCCAAGCCTGGGGGA      25807      A       CAT
                                TCCC CCAGGCTT   TC
                                |||| ||||||||   ||
                                AGGG GGTCCGAA   AG
                                  _       CCT
GAM527  RER1     3'  GGCGGGTGGAGCCCATGGGA   22865       CCA        A
                                TCCCA   GGCTTCATTC CC
                                |||||   |||||||||| ||
                                AGGGT   CCGAGGTGGG GG
                                   AC_        C
GAM527  S164     5'  CTGGATGAATGGAAAGC      60778     __      C
                                GCT  TCATTCA CCAG
                                |||  ||||||| ||||
                                CGA  GGTAAGT GGTC
                                  AA       A
GAM527  SPINT1   3'  GATGGACCTGCCTGCATAGGA  62650     CAC_    ___
                                TCC    CAGGC   TTCATT
                                |||    |||||   ||||||
                                AGG    GTCCG   AGGTAG
                                  ATAC     TCC
GAM527  SREC     3'  CTGGGCAGAGACCCTGTAGG   13501    AC    CT  A  CA
                                CC  CAGG  TC TT  CCCAG
                                ||  ||||  || ||  |||||
                                GG  GTCC  AG AG  GGGTC
                                 AT    C_  _  AC
GAM527  SRp25    3'  GTGGGAAGCCTGATGGG      33560      C       AT
                                CCCA CAGGCTTC  TCAC
                                |||| ||||||||  ||||
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                                GGGT GTCCGAAG  GGTG
                                  A      __
GAM527  SRp25    3'  GTGGGAAGCCTGATGGG     37981      C       AT
                                CCCA CAGGCTTC  TCAC
                                |||| ||||||||  ||||
                                GGGT GTCCGAAG  GGTG
                                  A      __
GAM527  STX3A    3'  TGGATGAATACTGGGAGA    14807    CCA    GC
                                TC   CCAG  TTCATTCA
                                ||   ||||  ||||||||
                                AG   GGTC  AAGTAGGT
                                 AG_    AT
GAM527  SYT12    3'  GGTGGCTGAGGCCTGATGGGA  94738      C       TT
                                TCCCA CAGGCTTCA  CACC
                                ||||| |||||||||  ||||
                                AGGGT GTCCGGAGT  GTGG
                                   A        CG
GAM527  TMPRSS5  3'  GATGAAGCCTATGGGA      47784      CC
                                TCCCA  AGGCTTCATT
                                |||||  ||||||||||
                                AGGGT  TCCGAAGTAG
                                   A_
GAM527  ZD52F10  5'  GGGAATGAAGCCCGCGGGA    52820      ACCA        A
                                TCCC    GGCTTCATTC CC
                                ||||    |||||||||| ||
                                AGGG    CCGAAGTAAG GG
                                  CGC_         _
GAM527  ZNF228   3'  GAATGTAAGCTTGGTG      59923          _
                                CACCAGGCTT CATTC
                                |||||||||| |||||
                                GTGGTTCGAA GTAAG
                                      T
GAM527  LOC112840 3'  GGGAGAGACCTGGTGGGA    54728          CT  ATTCA
                                TCCCACCAGG  TC    CCC
                                ||||||||||  ||    |||
                                AGGGTGGTCC  AG    GGG
                                      AG  A____
GAM527  LOC131583 5'  GGGCCGAGCCTGGCAGGG    75865     A_      CATTCA
                                CCC  CCAGGCTT     CCC
                                |||  ||||||||     |||
                                GGG  GGTCCGAG     GGG
                                  AC       CC____
GAM527  LOC131744 5'  GACAGACCTGGATGGGA     75870       _    _ _
                                TCCCA CCAGG CT TC
                                ||||| ||||| || ||
                                AGGGT GGTCC GA AG
                                   A    A  C
GAM527  LOC148764 5'  TGAGTGAATGGGATGG      78990     GG  T      C
                                CCA  CT CATTCAC CA
                                |||  || |||||| ||
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                                GGT  GG GTAAGTG GT
                                  A_ _      A
GAM527   LOC149076 3'  CTGGGTGGCGGGCCCAGGGA   79150      ACCA    CAT
                                TCCC    GGCTT   TCACCCAG
                                ||||    |||||   ||||||||
                                AGGG    CCGGG   GGTGGGTC
                                  AC__    C__
GAM527   LOC149373 3'  TGAGCACAGCCTGGTAGGG    79315    _      TCA
                                CCC ACCAGGCT   TTCA
                                ||| ||||||||   ||||
                                GGG TGGTCCGA   GAGT
                                  A       CAC
GAM527   LOC149704 3'  TGAGTGAATAAAGGATGG    84694     GG   C     C
                                CCA  CTT ATTCAC CA
                                |||  ||| |||||| ||
                                GGT  GAA TAAGTG GT
                                  AG   A     A
GAM527   LOC150421 3'  GGGCAGGGGGCCTGAGCGGGA  85039      AC_      ATTCA
                                TCCC   CAGGCTTC    CCC
                                ||||   ||||||||    |||
                                AGGG   GTCCGGGG    GGG
                                  CGA       GAC__
GAM527   LOC151658 5'  GTGAGAGAGAGCCTGGCTG    85480    _     _ A
                                CA CCAGGCT TC TTCAC
                                || ||||||| || |||||
                                GT GGTCCGA AG GAGTG
                                 C      G  A
GAM527   LOC151904 5'  CTGAGTCCTGGAGCCTGATGAG 80389    _ C       TTC  C
           G                     CC CA CAGGCTTCA   AC CAG
                                || || |||||||||   || |||
                                GG GT GTCCGAGGT   TG GTC
                                 A  A       CC_  A
GAM527   LOC152274 3'  TGGGGGAAACCCAGTGGGG    80511       CA  C   ATT A
                                TCCCAC  GG TTC   C CCCA
                                ||||||  || |||   | ||||
                                GGGGTG  CC AAG   G GGGT
                                    AC  A   ___ _
GAM527   LOC153577 5'  TGAGTAAAGCCTGGTGG     86062          C
                                CCACCAGGCTT ATTCA
                                |||||||||| |||||
                                GGTGGTCCGAA TGAGT
                                       A
GAM527   LOC157858 5'  CTGGGACAAGCCTGGGTGGA   86590     CA       CATTCA
                                TCC  CCAGGCTT     CCCAG
                                |||  ||||||||     |||||
                                AGG  GGTCCGAA     GGGTC
                                  TG       CA____
GAM527   LOC161357 5'  CTGGACAGCAGCGCTGGTGGGA 82272         _   TCATTCAC
                                TCCCACCAG GCT       CCAG
                                ||||||||| |||       ||||
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                                AGGGTGGTC CGA       GGTC
                                     G   CGACA___
GAM527  LOC165257 5'  GAGCGGAGCCTGGCGGGA    82481      A        A
                                TCCC CCAGGCTTC TTC
                                |||| ||||||||| |||
                                AGGG GGTCCGAGG GAG
                                  C        C
GAM527  LOC197201 3'  GGGCTTGGGAGCCTGGGGGA   87946      A        ATTCA
                                TCCC CCAGGCTTC     CCC
                                |||| |||||||||     |||
                                AGGG GGTCCGAGG     GGG
                                  _        GTTC_
GAM527  LOC203248 3'  TGGAAAGCCTGGGG        89313     A       CA
                                CC CCAGGCTT  TTCA
                                || ||||||||  ||||
                                GG GGTCCGAA  AGGT
                                 _       __
GAM527  LOC253502 3'  GAGAAAGCCTGGGGGA      94579      A       CA
                                TCCC CCAGGCTT  TTC
                                |||| ||||||||  |||
                                AGGG GGTCCGAA  GAG
                                  _       A_
GAM527  LOC51195  3'  CTGGGTGAGGTTTCCTGG    32943       CTTCA
                                CCAGG     TTCACCCAG
                                |||||     |||||||||
                                GGTCC     GAGTGGGTC
                                   TTTG_
GAM527  LOC90850  3'  GGTAAGGCCTGGTGAGG     64214     _        CATTC
                                CC CACCAGGCTT     ACC
                                || ||||||||||     |||
                                GG GTGGTCCGGA     TGG
                                 A         A____
GAM527  LOC96597  5'  TGGATGACCTGACAGGG     66921     AC_    CT
                                CCC   CAGG  TCATTCA
                                |||   ||||  |||||||
                                GGG   GTCC  AGTAGGT
                                  ACA   __
GAM528  GGA1      3'  CCATAACTCGGGGGCCATGCTG 25345         AGA___     AGC
            GA                    TCCAGTAT     TGAGT   TATGG
                                |||||||      |||||   |||||
                                AGGTCGTA     GCTCA   ATACC
                                     CCGGGG    ___
GAM528  DKFZp434A2417 3'  CCACCTCTCTCATCTAGAC    66098     A       T  CTA
                                GT TAGATGAG AG   TGG
                                || |||||||| ||   |||
                                CA ATCTACTC TC   ACC
                                 G       _ TCC
GAM528  MGC13040  3'  CCATAATAAAATCTATAC     51938         GAG  GC
                                GTATAGAT   TA  TATGG
                                ||||||||   ||  |||||
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                                CATATCTA  AT  ATACC
                                    AA_  A_
GAM528  MGC3020   3'  CCATAACCGCCCCAGTACTGGA 43893       AGA  A_  AGC
                                TCCAGTAT  TG  GT  TATGG
                                ||||||||  ||  ||  |||||
                                AGGTCATG  AC  CG  ATACC
                                    ___  CC  CCA
GAM528  SLC5A7   3'  CCATAGCTACTATATGC    41508     GATG
                                GTATA   AGTAGCTATGG
                                |||||   ||||||||||
                                CGTAT   TCATCGATACC
                                  A___
GAM528  LOC138050 5'  CTACTCATCCATAATG     75296    G  A
                                CA TAT GATGAGTAG
                                || ||| |||||||||
                                GT ATA CTACTCATC
                                 A  C
GAM528  LOC148753 3'  CCATAGCTACTGCTGTCACTG  84213     _   ATG
                                CAGT ATAG  AGTAGCTATGG
                                |||| ||||  ||||||||||
                                GTCA TGTC  TCATCGATACC
                                  C   G__
GAM529  ALDH1B1   3'  AAACATCCCAAATGTCCATC  5483      AAA  C
                                GGTG  ATT GGGATGTTT
                                ||||  ||| |||||||||
                                CTAC  TAA CCCTACAAA
                                  CTG  A
GAM529  NDN     3'  ACAACCCCACCGTGA      10190       AAAATTC  A
                                TCACGGTG     GGG TGT
                                ||||||||     ||| |||
                                AGTGCCAC     CCC ACA
                                    _______  A
GAM529  RFX2    3'  CCAATTTTCACCATGA     5306     C       C
                                TCA GGTGAAAATT GG
                                ||| |||||||||| ||
                                AGT CCACTTTTAA CC
                                  A       _
GAM529  C7orf3   5'  AAACTGATTGGAACTTTCACCG 71476       A  G  AT_
                                CGGTGAAA TTC GG  GTTT
                                |||||||| ||| ||  ||||
                                GCCACTTT AAG TT  CAAA
                                    C  G  AGT
GAM529  FLJ13920  3'  TCGAAATTTCCATCGTGA   44656       _  A
                                TCACGGTG AAA TTCGG
                                |||||||| ||| |||||
                                AGTGCTAC TTT AAGCT
                                    C  A
GAM529  GW112   3'  AAACATTTTCTCTTTCACC   21182       ATTC
                                GGTGAAA   GGGATGTTT
                                |||||||   |||||||||
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                                CCACTTT    TTTTACAAA
                                    CTC_
GAM529  KIAA1508 3'  AAACATCCATGGATTTCCC   61870    T   A   _
                                GG GAAA TTCG GGATGTTT
                                || |||| |||| ||||||||
                                CC CTTT AGGT CCTACAAA
                                 _   _    A
GAM529  KIAA1872 3'  AAACATTCTGCCCCCACC    62916     AAAATT
                                GGTG     CGGGATGTTT
                                ||||     ||||||||||
                                CCAC     GTCTTACAAA
                                  CCCC__
GAM529  LOC195977 3'  AACACCTGCCCCACTGTGA   87534        AAAATT   A
                                TCACGGTG     CGGG TGTT
                                ||||||||     |||| ||||
                                AGTGTCAC     GTCC ACAA
                                     CCC____   _
GAM530  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM530  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM530  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM530  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM530  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM530  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                       A
GAM530  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
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                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM530  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM530  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM530  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM530  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM530  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||         |||||||||
                                GTAAAG         CAGACTCTA
                                   AAACATTT_
GAM530  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281         CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM530  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM530  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM530  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM530  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598         CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
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                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM530  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM530  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                     TA__    TT
GAM530  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A     TC
GAM530  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                     AAAGG
GAM530  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM530  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM530  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM530  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM531  ARNT2    3'  AAACAACCCGTGCATCCCTGC  29450     A    TTTTA
                                GTA GGAT     GGGTTGTTT
                                ||| ||||     |||||||||
                                CGT CCTA     CCCAACAAA
                                  C    CGTG_
GAM531  LCT      3'  AACCGTAAAAATCCTT      9697           G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
```

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                                TTCCTAAAAAT CCAA
                                      G
GAM531  RPL15    3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM531  FBXO30   3'  AACTAAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                  G        AA
GAM531  KIAA0494 3'  AACAACCCTTACTTAC      28736      GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM531  PRO0641  5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                   ___    C
GAM531  SMT3H2   3'  AACAACATAAAAATCCTTGC   22670           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM531  LOC120103 3' AACCTATGAAAAATCCTTGC   74002           A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
                                CGTTCCTAAAAA   TCCAA
                                      GTA
GAM531  LOC129831 3' AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM531  LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                      GTA GGATTTTT     TTGTTT
                                ||| ||||||||     ||||||
                                CGT CCTAAAAA     AACAAA
                                  C       GATAA
GAM531  LOC148089 3' GGCCCTAAAAATTCCTAC    78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM531  LOC154547 3' AACAACATAAAAATCCTTGC   76050           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
```

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                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM531  LOC158104 3'  ACAGCCAAAAATCCTTA     60313          AG
                                TAAGGATTTTT  GGTTGT
                                |||||||||||  ||||||
                                ATTCCTAAAAA  CCGACA
                                      __
GAM531  LOC205880 5'  AAACAACCATCATCCTGAC   90709    A    TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM531  LOC221561 3'  AACAACATAAAAATCCTTGC  92130          GG
                                GTAAGGATTTTTA  GTTGTT
                                |||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM531  LOC257591 3'  AACAACATAAAAATCCTTGC  97840          GG
                                GTAAGGATTTTTA  GTTGTT
                                |||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM531  LOC51145  3'  AGCTAAAATCCTTAC       32393          TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
                                CATTCCTAAAA   TCGA
                                      ___
GAM532  BNIP3L    3'  CTGTTGTTTAGAAATTTGCAA  15081        CACCAA   TG
                                TTGCAAATT     GAG  ACAG
                                |||||||||     |||  ||||
                                AACGTTTAA     TTT  TGTC
                                     AGA___   GT
GAM532  LDHB      5'  CTGCCACTCTTGGTGA      9711           A
                                TCACCAAGAGTG CAG
                                |||||||||||| |||
                                AGTGGTTCTCAC GTC
                                      C
GAM532  MAT2A     3'  TGTCAGCATGAATTTGTAA   19790          CCAAGAG
                                TTGCAAATTCA      TGACA
                                ||||||||||       |||||
                                AATGTTTAAGT      ACTGT
                                      ACG____
GAM532  SLC38A2   3'  CAAGAATTGGCAAATTTGCA  38589        CA   GAG_
                                TGCAAATT  CCAA   TG
                                ||||||||  ||||   ||
                                ACGTTTAA  GGTT   AC
                                     AC   AAGA
GAM532  DKFZp547I014 5'  CATTCAGTGAATTTACAA   39545    C       CAA
                                TTG AAATTCAC   GAGTG
                                ||| ||||||||   |||||
```

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                                AAC TTTAAGTG   CTTAC
                                  A       A__
GAM532  ESM1     3'  CTGTGACTTCGGTGAATTTTCA 22879     C       AA    G
              A                   TTG AAATTCACC  GAGT ACAG
                                  ||| |||||||||  |||| ||||
                                  AAC TTTAAGTGG  TTCA TGTC
                                    T       C_    G
GAM532  FLJ10511 3'  TGTCAAGTGCAATTTGCAA    36206         _  CAAGAG
                                  TTGCAAATT CAC     TGACA
                                  ||||||||| |||     |||||
                                  AACGTTTAA GTG     ACTGT
                                        C   A_____
GAM532  FLJ10738 3'  CTGTGCTTCATCGAATTTGCAA 36530          ACCAA    G
                                  TTGCAAATTC    GAGT ACAG
                                  ||||||||||    |||| ||||
                                  AACGTTTAAG    TTCG TGTC
                                        CTAC_   _
GAM532  KIAA0040 5'  CTGCCACTCTTGGTGA      27785           A
                                  TCACCAAGAGTG CAG
                                  |||||||||||| |||
                                  AGTGGTTCTCAC GTC
                                         C
GAM532  KIAA0276 3'  TACAGATTGGTGAATTTGC    70968           GA_
                                  GCAAATTCACCAA   GTG
                                  ||||||||||||   |||
                                  CGTTTAAGTGGTT   CAT
                                          AGA
GAM532  KIAA0455 3'  CTGCTGTGAATTTGCAA     72469           CA_
                                  TTGCAAATTCAC   AG
                                  ||||||||||||   ||
                                  AACGTTTAAGTG   TC
                                         TCG
GAM532  KIAA0523 5'  CGTCTCTTGGTGAACTTG    67734     A         _
                                  CAA TTCACCAAGAG TG
                                  ||| |||||||||| ||
                                  GTT AAGTGGTTCTC GC
                                    C          T
GAM532  MGC4655  3'  CACTCTGCTGGATTTGGAA    52799    G       CCA
                                  TT CAAATTCA   AGAGTG
                                  || ||||||||   ||||||
                                  AA GTTTAGGT   TCTCAC
                                   G       CG_
GAM532  SYNJ2    3'  CTGTCACTCTCGTGTAGTTTAC 61767     C    _   CA
              AA                    TTG AAATT CAC  AGAGTGACAG
                                  ||| ||||| |||  ||||||||||
                                  AAC TTTGA GTG  TCTCACTGTC
                                    A    T   C_
GAM532  LOC136319 3'  TGTCACTCTCTATCTGC     75261     A  TCACCA
                                  GCA AT      AGAGTGACA
                                  ||| ||      |||||||||
```

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                                CGT TA     TCTCACTGT
                                  C  TC____
GAM532  LOC154789 5'  CACTCTTGTTGGCCTGTCAA  81132    _ AAT   C
                                TTG CA   TCA CAAGAGTG
                                ||| ||   ||| ||||||||
                                AAC GT   GGT GTTCTCAC
                                  T  CC_   T
GAM532  LOC96810  3'  CACTCCATCTGATTTGCA    70562       T  CCAA
                                TGCAAAT CA    GAGTG
                                ||||||| ||    |||||
                                ACGTTTA GT    CTCAC
                                    _ CTAC
GAM533  AIM1      3'  ATATCAAGATTTCAAGACTGTG 91815        _  T
                                CACAGTCT GG GTCTTGATAT
                                |||||||| || ||||||||||
                                GTGTCAGA CT TAGAACTATA
                                     A  T
GAM533  KCNAB2    3'  ACACCACACTGTGATG      13299         C
                                CATCACAGT TGGTGT
                                ||||||||| ||||||
                                GTAGTGTCA ACCACA
                                     C
GAM533  PUNC      5'  CAGTGCACCAGACCGCGGTG  89653     ACA       C
                                CATC   GTCTGGTGT TTG
                                ||||   ||||||||| |||
                                GTGG   CAGACCACG GAC
                                  CGC        T
GAM533  DKFZp762L0311 3'  ACACCAAGACAGTGTG     38050    T   A   _
                                CA CAC GTCT GGTGT
                                || ||| |||| |||||
                                GT GTG CAGA CCACA
                                 _  A   A
GAM533  FLJ11715  3'  ACCCCAGACTGTGCTG     44665    T       T
                                CA CACAGTCTGG GT
                                || |||||||||| ||
                                GT GTGTCAGACC CA
                                 C        C
GAM533  KIAA1280  5'  ACACCAGCTACAAACTGGATG  69708     A   _______
                                CATC CAGT     CTGGTGT
                                |||| ||||     |||||||
                                GTAG GTCA     GACCACA
                                  _   AACATC
GAM533  MGC13102  3'  ATCAAATGGGACTGTGGTG   50313         G  GTC
                                CATCACAGTCT GT   TTGAT
                                |||||||||| ||   |||||
                                GTGGTGTCAGG TA   AACTA
                                       G ____
GAM533  SLC6A14   3'  ATATCAAGGAAAACTGTGA   23346       CTGGTG
                                TCACAGT     TCTTGATAT
                                |||||||     |||||||||
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                                AGTGTCA     GGAACTATA
                                    AAA___
GAM533  UNC5D    3'  AGATTCACCAGACTGT      55132          __
                                ACAGTCTGGTG  TCT
                                ||||||||||  |||
                                TGTCAGACCAC  AGA
                                     TT
GAM533  LOC90643 3'  ATCAAGACCCTGACTGGA    63688    A    T  T
                                TC CAGTC GG GTCTTGAT
                                || ||||| || ||||||||
                                AG GTCAG CC CAGAACTA
                                 _    T  _
GAM533  LOC91818 5'  ATCAAGACCCTGACTGGA    67269    A    T  T
                                TC CAGTC GG GTCTTGAT
                                || ||||| || ||||||||
                                AG GTCAG CC CAGAACTA
                                 _    T  _
GAM533  LOC93052 5'  AGAACCAAACTGTGATG     71257         C    G
                                CATCACAGT TGGT TCT
                                ||||||||| |||| |||
                                GTAGTGTCA ACCA AGA
                                     A   _
GAM534  ADAM19   3'  CAGGAAGAAGACTGGCCATTAT 52703       C    CTGAG
          G                      CATGA GGCT    TTCTTCCTG
                                ||||| ||||    |||||||||
                                GTATT CCGG    AAGAAGGAC
                                   A   TCAG_
GAM534  FACL5    5'  CAGGAAGAACTCAGAGCCG   64186
                                CGGCTCTGAGTTCTTCCTG
                                ||||||||||||||||||
                                GCCGAGACTCAAGAAGGAC

GAM534  GNAL     5'  CAGGAAAGAGAGGAGCCGTCG  9058          GAG TC
                                TGACGGCTCT   T  TTCCTG
                                ||||||||||   |  ||||||
                                GCTGCCGAGG   A  AAGGAC
                                     AG_ GA
GAM534  KAL1     3'  CAGGAAGAACTTCTGTCA    4013        CTCT
                                TGACGG   GAGTTCTTCCTG
                                ||||||   ||||||||||||
                                ACTGTC   TTCAAGAAGGAC
                                   ____
GAM534  MYO1E    3'  CAGGAGGACAAAACCACCATG  17187     AC  CTC  AGT
                                CATG  GG   TG   TCTTCCTG
                                ||||  ||   ||   ||||||||
                                GTAC  CC   AC   AGGAGGAC
                                  CA  AAA  ___
GAM534  PRKAR2B  3'  CAGAAAGAACTCAGATGT    10804    _         C
                                GC TCTGAGTTCTT CTG
                                || ||||||||||| |||
```

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                                TG AGACTCAAGAA GAC
                                 T         A
GAM534  PUM2     3'  AGGATCAAAGCTGTCATG    31014         C   GTTCT
                                CATGACGGCT TGA    TCCT
                                |||||||||| |||    ||||
                                GTACTGTCGA ACT    AGGA
                                      A  _____
GAM534  SKI      3'  CAGGAAGTGCAGAGCCGCA   11701    A      AGTT
                                TG CGGCTCTG   CTTCCTG
                                || ||||||||   |||||||
                                AC GCCGAGAC   GAAGGAC
                                 _      GT__
GAM534  TEM8     3'  AGGAAGATGCAACCCCATG   36326     AC  CTC  AGT
                                CATG  GG   TG   TCTTCCT
                                ||||  ||   ||   |||||||
                                GTAC  CC   AC   AGAAGGA
                                  C_  A__  GT_
GAM534  ARHGEF4  5'  AGAAAAAACTCAGGGC     52207         C  C
                                GCTCTGAGTT TT CT
                                |||||||||| || ||
                                CGGGACTCAA AA GA
                                      A  A
GAM534  FLJ31978 3'  CAGGAAGGAACAAGCGCC   58348     T  GAG
                                GGC CT   TTCTTCCTG
                                ||| ||   |||||||||
                                CCG GA   AGGAAGGAC
                                  C  ACA
GAM534  HSU24186 5'  AGAACTCAAAGCCGTC     25324        C
                                GACGGCT TGAGTTCT
                                ||||||| ||||||||
                                CTGCCGA ACTCAAGA
                                    A
GAM534  KCNT1    3'  AGCTCCCAGGGCCGCCA     61825    A     __
                                TG CGGCTCT  GAGTT
                                || |||||||  |||||
                                AC GCCGGGA  CTCGA
                                 C      CC
GAM534  KIAA1867 3'  CAGGAAGAACCCAAGAGCTCAT 94822     CG    GA_
                                ATGA  GCTCT   GTTCTTCCTG
                                ||||  |||||   ||||||||||
                                TACT  CGAGA   CAAGAAGGAC
                                  __    ACC
GAM534  KIAA1878 3'  AATTCAGAGAATCGTCATG   91707        __
                                CATGACGG  CTCTGAGTT
                                ||||||||  |||||||||
                                GTACTGCT  GAGACTTAA
                                      AA
GAM534  MFN1     3'  CAGGAAGAACTCATGA      35541    _
                                TC TGAGTTCTTCCTG
                                || ||||||||||||
```

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                                AG ACTCAAGAAGGAC
                                 T
GAM534  MIDORI   3'  CAGGGCCCTTCCAGAGCCTGTC 73784       _      AGTTCT
            ATG                   CATGAC GGCTCTG     TCCTG
                                |||||| |||||||      |||||
                                GTACTG CCGAGAC     GGGAC
                                   T      CTTCCC
GAM534  MYH7B    3'  CAGGAAGAACCTGGCTCGCATG 70530      A _  CTGA
                                CATG CG GCT    GTTCTTCCTG
                                |||| || |||    ||||||||||
                                GTAC GC CGG    CAAGAAGGAC
                                  _ T  TC__
GAM534  RNAHP    3'  AGAAAGCAGCAGCCGTCAT   23761         _  AG
                                ATGACGGCT CTG  TTCT
                                ||||||||| |||  ||||
                                TACTGCCGA GAC  AAGA
                                     C  GA
GAM534  SLC37A1  3'  AGACGGAGCTCAGACCC     38561    C       TC
                                GG TCTGAGTTCT  CT
                                || ||||||||||  ||
                                CC AGACTCGAGG  GA
                                 C         CA
GAM534  LOC116236 3'  CAGGAAAAGCACAAACCTCAT  73809     C  CTC  A   C
                                ATGA GG   TG GTT TTCCTG
                                |||| ||   || ||| ||||||
                                TACT CC   AC CGA AAGGAC
                                  _ AA_  A   A
GAM534  LOC124801 3'  CAGGAAGAACTCTCTTGCATG  74336     A   CTCT
                                CATG CGG    GAGTTCTTCCTG
                                |||| |||    ||||||||||||
                                GTAC GTT    CTCAAGAAGGAC
                                  _   CT__
GAM534  LOC222160 5'  AGGAAGAACTCACCCC      94117    CTC
                                GG   TGAGTTCTTCCT
                                ||   ||||||||||||
                                CC   ACTCAAGAAGGA
                                 CC_
GAM534  LOC51094  3'  CAGGAAGAATAAAGCC      32045      CTGA
                                GGCT    GTTCTTCCTG
                                ||||    ||||||||||
                                CCGA    TAAGAAGGAC
                                  AA__
GAM534  LOC92078  3'  CAGGAAGAAGAATCGACCGTC  67977      C  T  G__
                                GACGG TC GA   TTCTTCCTG
                                ||||| || ||   |||||||||
                                CTGCC AG CT   AAGAAGGAC
                                  _ _  AAG
GAM535  MDM4     3'  ATGCATTTATTCAGTTCAC    9978        CAAAGTTT
                                GTGAAC       TAGGTGCAT
                                ||||||       |||||||||
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                                CACTTG       ATTTACGTA
                                   ACTT____
GAM535  DKFZP564I1171 3'  TACTGAACTTTGGCCTAC    71591     AA        TA
                                GTG  CCAAAGTTT  GGTG
                                |||  |||||||||  ||||
                                CAT  GGTTTCAAG  TCAT
                                  CC        __
GAM535  FLJ11068  3'  CAGTTAAAACTTTGATTC    37025     C         G
                                GAA CAAAGTTTTAG TG
                                ||| ||||||||||| ||
                                CTT GTTTCAAAATT AC
                                  A         G
GAM535  KIAA1577  3'  TACCAACTTTGGTT        64482          TTA
                                AACCAAAGTT   GGTG
                                ||||||||||   ||||
                                TTGGTTTCAA   CCAT
                                      ___
GAM535  ZNF226    5'  CACTACTCAAACTGTGGTTCAC 33187         A     TA__
                                GTGAACCA AGTTT    GGTG
                                |||||||| |||||    ||||
                                CACTTGGT TCAAA    TCAC
                                     G    CTCA
GAM535  LOC159090 3'  CGCAGAGAACTTTGATCCAT   82085     AAC       AG
                                GTG   CAAAGTTTT  GTG
                                |||   |||||||||  |||
                                TAC   GTTTCAAGA  CGC
                                  CTA        GA
GAM535  LOC221178 3'  ATTCAAAATTTGGTTCAC    93529          G    AG
                                GTGAACCAAA TTTT  GT
                                |||||||||| ||||  ||
                                CACTTGGTTT AAAA  TA
                                      _   CT
GAM535  LOC255520 3'  TTTAAAAATTTGGTTCAC    95868          G
                                GTGAACCAAA TTTTAGG
                                |||||||||| |||||||
                                CACTTGGTTT AAAATTT
                                     A
GAM536  DMRT2     3'  CACAACAAGCAACAAGAACA   21614      CTATC_
                                TGTTC     CTTGTTGTG
                                |||||     |||||||||
                                ACAAG     GAACAACAC
                                   AACAAC
GAM536  F8        3'  CACAACAAAAATGTAACAGGG  3725     G   CC   CC
                                CCC TGTT  TAT  TTGTTGTG
                                ||| ||||  |||  ||||||||
                                GGG ACAA  GTA  AACAACAC
                                  _   T_   AA
GAM536  GJB3      3'  TAAGAGACAGGAACACAGG    43770    C      A  _
                                CC GTGTTCCT TC CTTG
                                || |||||||| || ||||
```

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                                GG CACAAGGA AG GAAT
                                 A       C  A
GAM536  SH3BP2   3'  CAAGGACAGGAACACTGGT   11593     C       A
                                ACC GTGTTCCT TCCTTG
                                ||| |||||||| ||||||
                                TGG CACAAGGA AGGAAC
                                  T       C
GAM536  TEM8     3'  CACCCAGGGATAAAAACA    49851     CC      TT
                                TGTT  TATCCTTG  GTG
                                ||||  ||||||||  |||
                                ACAA  ATAGGGAC  CAC
                                  AA       C_
GAM536  ZNF216   3'  CACAGATAATAGGAACA     20018         CCTTG
                                TGTTCCTAT    TTGTG
                                |||||||||    |||||
                                ACAAGGATA    GACAC
                                      ATA__
GAM536  C20orf142 3'  AAGGAGCAGAAACACAGGT   74763     C    C  A_
                                ACC GTGTT CT  TCCTT
                                ||| ||||| ||  |||||
                                TGG CACAA GA  AGGAA
                                  A    A  CG
GAM536  C20orf59  3'  CACACGAGCAGAGAGGAACAC  41991        A  __    T
                                GTGTTCCT TC  CTTGT GTG
                                |||||||| ||  ||||| |||
                                CACAAGGA AG  GAGCA CAC
                                     G  AC    _
GAM536  CLSTN2   3'  CACAACAAGGACAACAAGGACA 42126     T   A____
          C                      GTGT CCT    TCCTTGTTGTG
                                |||| |||    ||||||||||
                                CACA GGA    AGGAACAACAC
                                  _  ACAAC
GAM536  CLSTN2   3'  CACAACAAGGACAGTCACAAC  42127    _  TC  A
                                GT GT  CT TCCTTGTTGTG
                                || ||  || ||||||||||
                                CA CA  GA AGGAACAACAC
                                 A  CT  C
GAM536  CLSTN2   3'  CACAACAAGGACAGTCACAACA 42128    CG__   TC  A
          AGG                     CC    TGT  CT TCCTTGTTGTG
                                ||   |||  || ||||||||||
                                GG   ACA  GA AGGAACAACAC
                                 AACA   CT  C
GAM536  FLJ10101  5'  CGGGGAGACAGGAACACGGG   45264         A__
                                CCCGTGTTCCT   TCCTTG
                                ||||||||||   ||||||
                                GGGCACAAGGA   AGGGGC
                                      CAG
GAM536  HEYL     3'  CACTCAGGACAGGAACAAGG   27391    G      A    T TT
                                CC TGTTCCT TCCT G  GTG
                                || ||||||| |||| |  |||
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                                GG ACAAGGA AGGA C  CAC
                                 A      C    _ T_
GAM536  INPP4B   3'  TAATAAACAGGAACAC      13915        ATCC
                                GTGTTCCT    TTGTTG
                                ||||||||    ||||||
                                CACAAGGA    AATAAT
                                     CA__
GAM536  KIAA0391 3'  CAAGAGACAGGAACAC      27906        A  _
                                GTGTTCCT TC CTTG
                                |||||||| || ||||
                                CACAAGGA AG GAAC
                                     C  A
GAM536  KIAA1376 3'  CACAACAAGGAACAAAACA   63621      CCTA
                                TGTT    TCCTTGTTGTG
                                ||||    ||||||||||
                                ACAA    AGGAACAACAC
                                  AACA
GAM536  KIAA1494 3'  CACAACAAAGTAGCAC      68457      C  ATCC
                                GTGTT CT    TTGTTGTG
                                ||||| ||    ||||||||
                                CACGA GA    AACAACAC
                                   T _____
GAM536  LOC147639 3'  CACAATAACAGGGACAC    78378        ATCC
                                GTGTTCCT    TTGTTGTG
                                ||||||||    ||||||||
                                CACAGGGA    AATAACAC
                                     C___
GAM536  LOC219529 3'  ACAGGATAACAGGAACAC   92964         ___    T
                                GTGTTCCT   ATCCT GT
                                ||||||||   ||||| ||
                                CACAAGGA   TAGGA CA
                                     CAA    _
GAM537  ADAM20   5'  GCACTGCAGCTCTGA       13767     A       AT
                                TCA AGCTGCAG  TGC
                                ||| ||||||||  |||
                                AGT TCGACGTC  ACG
                                  C       __
GAM537  ANXA9    5'  CACAGGCAATCTACCAGGC    13102     GC__
                                GCT    AGATTGCCTGTG
                                |||    ||||||||||||
                                CGG    TCTAACGGACAC
                                  ACCA
GAM537  E2F1     3'  CAATCTGCACTTTGA       84795       C
                                TCAAAG TGCAGATTG
                                |||||| |||||||||
                                AGTTTC ACGTCTAAC
                                       _
GAM537  E2F1     3'  CACCTTGTCTCTGCAGCCCTGG 84796     AA       TTGCCT
                                TCA  GCTGCAGA     GTG
                                |||  ||||||||     |||
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                                GGT  CGACGTCT     CAC
                                  CC       CTGTTC
GAM537  FPRL1    5'  CACTGCATTTGCAGCCTTGA   7590      A       T  CT
                                TCAA GCTGCAGAT GC  GTG
                                |||| ||||||||| ||  |||
                                AGTT CGACGTTTA CG  CAC
                                  C        _  T_
GAM537  FSHPRH1  5'  CACGGCTCTCTGCAGC     22114        TT   T
                                GCTGCAGA  GCC GTG
                                ||||||||  ||| |||
                                CGACGTCT  CGG CAC
                                     CT  _
GAM537  IL10RA   3'  CACAGGCATGGAAGCTGTGA   59641     A   GCAGAT
                                TCA AGCT     TGCCTGTG
                                ||| ||||     ||||||||
                                AGT TCGA     ACGGACAC
                                  G    AGGT__
GAM537  ITGA6    3'  CACAGGTGCAACAGACTTGA   3983      AG   CAGATT
                                TCAA  CTG     GCCTGTG
                                ||||  |||     |||||||
                                AGTT  GAC     TGGACAC
                                  CA   AACG__
GAM537  ITPKA    3'  CATGTGGACCTGCAGCTTTG   9415          ATTG  _
                                CAAAGCTGCAG    CC TGTG
                                ||||||||||    || ||||
                                GTTTCGACGTC    GG GTAC
                                      CA__  T
GAM537  LILRB4   3'  CAGGACCTGCAGCTTTG     22431          ATTG
                                CAAAGCTGCAG    CCTG
                                ||||||||||    ||||
                                GTTTCGACGTC    GGAC
                                      CA__
GAM537  MBD3     3'  CACAGGCACCCAGCTTTGG    14093         CAGAT
                                TCAAAGCTG    TGCCTGTG
                                |||||||||    ||||||||
                                GGTTTCGAC    ACGGACAC
                                     CC___
GAM537  MPP3     3'  CACAGGCAAGCTGACCCT    8635     CTG   A
                                AG   CAG TTGCCTGTG
                                ||   ||| |||||||||
                                TC   GTC AACGGACAC
                                 CCA   G
GAM537  NR1I2    3'  CAAACTGCAGCTGTGA      13963     A      A
                                TCA AGCTGCAG TTG
                                ||| |||||||| |||
                                AGT TCGACGTC AAC
                                  G       A
GAM537  NR1I2    3'  CAAACTGCAGCTGTGA      41826     A      A
                                TCA AGCTGCAG TTG
                                ||| |||||||| |||
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                                AGT TCGACGTC AAC
                                  G       A
GAM537  OCM      3'  CACAGGCAATGCCTCT     20546    CT   GA
                                AG  GCA  TTGCCTGTG
                                ||  |||  |||||||||
                                TC  CGT  AACGGACAC
                                 TC   __
GAM537  OGDH     3'  CACAGAAAGGGCAGCTT     91105        AGA  GC
                                AAGCTGC   TT  CTGTG
                                |||||||   ||  |||||
                                TTCGACG   AA  GACAC
                                    GG_  A_
GAM537  PACE4    3'  GGGAATCCACAGCTCTGG    56348     A    CA   G
                                TCA AGCTG  GATT CC
                                ||| |||||  |||| ||
                                GGT TCGAC  CTAA GG
                                  C    AC   G
GAM537  PACE4    3'  GGGAATCCACAGCTCTGG    10403     A    CA   G
                                TCA AGCTG  GATT CC
                                ||| |||||  |||| ||
                                GGT TCGAC  CTAA GG
                                  C    AC   G
GAM537  PIGK     3'  GGAATCCTGCAGCTTT      66701          _  G
                                AAAGCTGCAG ATT CC
                                |||||||||| ||| ||
                                TTTCGACGTC TAA GG
                                     C  _
GAM537  STARD4   3'  CACAGCTCACTGCAGCTTTGA  57510           ATT  C
                                TCAAAGCTGCAG   GC TGTG
                                ||||||||||||   || ||||
                                AGTTTCGACGTC   CG ACAC
                                       ACT  _
GAM537  UBE4A    3'  CACAAGCAAGTGTGTAGCTT   16561        G  _  C
                                AAGCTGCA ATT GC TGTG
                                |||||||| ||| || ||||
                                TTCGATGT TGA CG ACAC
                                    G   A  A
GAM537  BIRC8    5'  CAGGTTTATCCGCAGCTTT    52904        A   T_
                                AAAGCTGC GAT  GCCTG
                                |||||||| |||  |||||
                                TTTCGACG CTA  TGGAC
                                    C   TT
GAM537  C11orf9  3'  CACTCATTCTCAGCTTTGA    25207         C   T  CCT
                                TCAAAGCTG AGA TG   GTG
                                ||||||||| ||| ||   |||
                                AGTTTCGAC TCT AC   CAC
                                     _  T  T__
GAM537  C20orf98 3'  CACAGGCAATTACTAGC     71512      CA
                                GCTG  GATTGCCTGTG
                                ||||  ||||||||||
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                                CGAT  TTAACGGACAC
                                  CA
GAM537  C6orf5   3'  GCTCACTGCAGCTTTGA    31354          ATT
                                TCAAAGCTGCAG  GC
                                ||||||||||||  ||
                                AGTTTCGACGTC  CG
                                      ACT
GAM537  CHST3    3'  ACAGACAATCTGCCGT     14963    T      C
                                GC GCAGATTG CTGT
                                || |||||||| ||||
                                TG CGTCTAAC GACA
                                 C       A
GAM537  DKFZP434B103 3'  CACAGGCAGAGGGCAGCT    31588       AGA
                                AGCTGC  TTGCCTGTG
                                ||||||  |||||||||
                                TCGACG  GACGGACAC
                                   GGA
GAM537  FLJ10813  3'  TAATCTGCCACTTTGA     36686       CT
                                TCAAAG  GCAGATTG
                                ||||||  ||||||||
                                AGTTTC  CGTCTAAT
                                   AC
GAM537  FLJ12168  3'  CACAGGCACTTTAGC      45184     C  AT
                                GCTG AG  TGCCTGTG
                                |||| ||  ||||||||
                                CGAT TC  ACGGACAC
                                  T  __
GAM537  FLJ12331  3'  CAATCAGTGCAGTTTGA     46475      G    __
                                TCAAA CTGCA  GATTG
                                ||||| |||||  |||||
                                AGTTT GACGT  CTAAC
                                   _    GA
GAM537  FLJ12650  3'  CACAGGCATGGAGCT       44524     G  GAT
                                AGCT CA   TGCCTGTG
                                |||| ||   ||||||||
                                TCGA GT   ACGGACAC
                                  G  ___
GAM537  FLJ14082  5'  CACATGGAGAGCTGCAGCT   46670        ATTG  _
                                AGCTGCAG    CC TGTG
                                ||||||||    || ||||
                                TCGACGTC    GG ACAC
                                     GAGA  T
GAM537  FLJ14326  5'  CATCCTGCCCCAGCTTTGA   49804        ___   AT
                                TCAAAGCT   GCAG  TG
                                ||||||||   ||||  ||
                                AGTTTCGA   CGTC  AC
                                     CCC    CT
GAM537  FLJ20249  3'  CACAGTCCTTTCTGCAGCTT   79424         TTGC_
                                AAGCTGCAGA    CTGTG
                                ||||||||||    |||||
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                                TTCGACGTCT    GACAC
                                      TTCCT
GAM537  FLJ20436  3' CACAGGCAACCCAGACT    35167   _  CAGA
                                AG CTG   TTGCCTGTG
                                || |||   |||||||||
                                TC GAC   AACGGACAC
                                 A  CC__
GAM537  FLJ21945  3' ACAGGCAATGTCTGCA     47313       __
                                TGCAGAT  TGCCTGT
                                |||||||  |||||||
                                ACGTCTG  ACGGACA
                                    TA
GAM537  FLJ22037  5' CACAAGTTCCTGCAGCT    93913       ATT  C
                                AGCTGCAG   GC TGTG
                                ||||||||   || ||||
                                TCGACGTC   TG ACAC
                                     CT_  A
GAM537  FLJ23185  3' CACAGGCCACCGGCTCCAGCTT 46828        C  ATT___
           TGA                    TCAAAGCTG AG     GCCTGTG
                                |||||||||  ||     |||||||
                                AGTTTCGAC TC     CGGACAC
                                      C  GGCCAC
GAM537  FLJ23563  5' CACGGTCACCCACAGCTTTGA  67590        CAGAT  C
                                TCAAAGCTG    TG CTGTG
                                |||||||||    || |||||
                                AGTTTCGAC    AC GGCAC
                                      ACCC_  T
GAM537  KIAA0544  3' CACAAGCTGCGTGCAGCTCTGG 70888    A     GATT  C
                                TCA AGCTGCA   GC TGTG
                                ||| |||||||   || ||||
                                GGT TCGACGT   CG ACAC
                                  C      GCGT  A
GAM537  KIAA0557  3' CAGACATCTGTAGCCCTGA   77991    AA       T C
                                TCA  GCTGCAGAT G CTG
                                |||  ||||||||| | |||
                                AGT  CGATGTCTA C GAC
                                  CC        _ A
GAM537  KIAA0844  3' CACAGGCAAGCACCT      30198   C   AGA
                                AG TGC   TTGCCTGTG
                                || |||   |||||||||
                                TC ACG   AACGGACAC
                                 C  ___
GAM537  KIAA1348  3' CACAAAAATCTGCAAATTTGA  68574      GC      GCC
                                TCAAA  TGCAGATT   TGTG
                                |||||  ||||||||   ||||
                                AGTTT  ACGTCTAA   ACAC
                                   AA       AA_
GAM537  KIAA1579  3' CACAAATTGCTGCAGTCTGA   36604    AA     ATTGCC
                                TCA  GCTGCAG     TGTG
                                |||  |||||||     ||||
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                                AGT  TGACGTC     ACAC
                                  C_      GTTAA_
GAM537  KIAA1712  5'  CACAGAGAAGCTCCCAGCTTTG 67532          C_  A  GC
              A                    TCAAAGCTG  AG TT  CTGTG
                                   |||||||||  || ||  |||||
                                   AGTTTCGAC  TC AA  GACAC
                                        CC  G  GA
GAM537  MGC20258  5'  CAGGAATCTGCAGCCTGGA   58150    AAA        G
                                   TC   GCTGCAGATT CCTG
                                   ||   |||||||||| ||||
                                   AG   CGACGTCTAA GGAC
                                    GTC         _
GAM537  MGC5528   3'  CACAGGCAATGCTCACT     44043    C  C  _
                                   AG TG AG ATTGCCTGTG
                                   || || || ||||||||||
                                   TC AC TC TAACGGACAC
                                    _  _  G
GAM537  MIC2L1    3'  CACTGGAATCTGCAGC      48820          G  T
                                   GCTGCAGATT CC GTG
                                   |||||||||| || |||
                                   CGACGTCTAA GG CAC
                                         _  T
GAM537  MYO5C     3'  ACAGGTGACAGCTGTGA     38104     A    CAGA TG
                                   TCA AGCTG    T  CCTGT
                                   ||| |||||    |  |||||
                                   AGT TCGAC    A  GGACA
                                     G     _____ GT
GAM537  OSR2      3'  CAGCCGCACCTGCAGCT     53805         AT   __
                                   AGCTGCAG  TGC  CTG
                                   ||||||||  |||  |||
                                   TCGACGTC  ACG  GAC
                                        C_   CC
GAM537  PLSCR3    3'  CACAGGCATATCAGCTTT    90759        CAGAT
                                   AAAGCTG    TGCCTGTG
                                   |||||||    ||||||||
                                   TTTCGAC    ACGGACAC
                                        TAT__
GAM537  PLSCR3    3'  CACAGGCATATCAGCTTT    39792        CAGAT
                                   AAAGCTG    TGCCTGTG
                                   |||||||    ||||||||
                                   TTTCGAC    ACGGACAC
                                        TAT__
GAM537  STATI2    3'  CACAGGCCTCACTGCAATTTGA 13920       GC    ATT_
                                   TCAAA  TGCAG    GCCTGTG
                                   |||||  |||||    |||||||
                                   AGTTT  ACGTC    CGGACAC
                                     A_     ACTC
GAM537  STATI2    3'  CACAGGCCTCACTGCAATTTGA 94550       GC    ATT_
                                   TCAAA  TGCAG    GCCTGTG
                                   |||||  |||||    |||||||
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                                AGTTT  ACGTC    CGGACAC
                                  A_     ACTC
GAM537   TRIM11    3'  CACAGTTCCTGCAGCTTTG    72830          ATTGC
                                CAAAGCTGCAG     CTGTG
                                ||||||||||     |||||
                                GTTTCGACGTC     GACAC
                                     CTT__
GAM537   LOC115574 3'  CACAGGTCATGTCTGCAGC    73464          _ _
                                GCTGCAGAT TG CCTGTG
                                ||||||||| || ||||||
                                CGACGTCTG AC GGACAC
                                     T  T
GAM537   LOC124976 3'  CGATCTGCAGCTTTGA      74378
                                TCAAAGCTGCAGATTG
                                ||||||||||||||||
                                AGTTTCGACGTCTAGC

GAM537   LOC130471 3'  GCACTGCAGCTCTGA       74941     A       AT
                                TCA AGCTGCAG  TGC
                                ||| ||||||||  |||
                                AGT TCGACGTC  ACG
                                  C       __
GAM537   LOC145501 3'  CACAGGAGGCTATCTGTAGC   77251          TG___
                                GCTGCAGAT     CCTGTG
                                |||||||||     ||||||
                                CGATGTCTA     GGACAC
                                     TCGGA
GAM537   LOC146819 3'  CACATTATTTTGCAGCTCTGA  78150     A       TTGCC
                                TCA AGCTGCAGA     TGTG
                                ||| |||||||||     ||||
                                AGT TCGACGTTT     ACAC
                                  C       TATT_
GAM537   LOC146821 3'  CACATTATTTTGCAGCTCTGA  78142     A       TTGCC
                                TCA AGCTGCAGA     TGTG
                                ||| |||||||||     ||||
                                AGT TCGACGTTT     ACAC
                                  C       TATT_
GAM537   LOC150005 5'  CACAGGCACCAGCTCTGA     84817     A     CAGAT
                                TCA AGCTG     TGCCTGTG
                                ||| |||||     ||||||||
                                AGT TCGAC     ACGGACAC
                                  C    C____
GAM537   LOC150005 3'  CACAGGCAGGGGTAGC       84818       AGA
                                GCTGC   TTGCCTGTG
                                |||||   |||||||||
                                CGATG   GACGGACAC
                                   GG_
GAM537   LOC151318 3'  CACAGGCAATCTACCTTCTGA  80225     _   CTGC
                                TCA AAG    AGATTGCCTGTG
                                ||| |||    ||||||||||||
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                                AGT TTC    TCTAACGGACAC
                                  C   CA__
GAM537   LOC151907 3'  CAGTTATCTAAGCTTTGA    80397        GC    TGC
                                TCAAAGCT  AGAT   CTG
                                ||||||||  ||||   |||
                                AGTTTCGA  TCTA   GAC
                                    A_    TT_
GAM537   LOC163724 5'  CACACCAGCTGCAGCTT     82152         A   CC
                                AAGCTGCAG TTG  TGTG
                                |||||||||| |||  ||||
                                TTCGACGTC GAC  ACAC
                                    _   C_
GAM537   LOC168667 3'  CACCCTCGTATCTGCAGCCTGA 92756     AA       _  CCT
                                TCA  GCTGCAGAT TG   GTG
                                |||  |||||||||| ||   |||
                                AGT  CGACGTCTA GC   CAC
                                  C_        T  TCC
GAM537   LOC201324 3'  CACATCAGCTGCAGCT      68561         A   CC
                                AGCTGCAG TTG  TGTG
                                |||||||| |||  ||||
                                TCGACGTC GAC  ACAC
                                    _   T_
GAM537   LOC219818 3'  CAGTCTTATTACAGCTTTGA   90887          C____
                                TCAAAGCTG     AGATTG
                                |||||||||     ||||||
                                AGTTTCGAC     TCTGAC
                                    ATTAT
GAM537   LOC220980 3'  ACATACTGCAGTTTGA      93141       G     ATTGCC
                                TCAAA CTGCAG     TGT
                                ||||| ||||||     |||
                                AGTTT GACGTC     ACA
                                  _     AT____
GAM537   LOC221576 3'  AATCTGCAAGCTTTGA      93700          _
                                TCAAAGCT GCAGATT
                                |||||||| |||||||
                                AGTTTCGA CGTCTAA
                                    A
GAM537   LOC254962 3'  CACAGGCAATCTTGCTTCT    96614     CT   _
                                AG  GCA GATTGCCTGTG
                                ||  ||| ||||||||||
                                TC  CGT CTAACGGACAC
                                 TT   T
GAM537   LOC255299 5'  CAACCTGGAGCTTTGA      97464         G   A
                                TCAAAGCT CAG TTG
                                |||||||| ||| |||
                                AGTTTCGA GTC AAC
                                    G   C
GAM537   LOC255545 3'  CAGTTATCTAAGCTTTGA    95706         GC    TGC
                                TCAAAGCT  AGAT   CTG
                                ||||||||  ||||   |||
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                                AGTTTCGA  TCTA   GAC
                                    A_    TT_
GAM537   LOC256940 3'  CACAGGTTTTCTGCAGT     96492        TT
                                GCTGCAGA  GCCTGTG
                                ||||||||  |||||||
                                TGACGTCT  TGGACAC
                                    TT
GAM537   LOC257319 3'  ACATGCTGCAGCTTGA      95771      A      ATTGCC
                                TCAA GCTGCAG     TGT
                                |||| |||||||     |||
                                AGTT CGACGTC     ACA
                                  _      GT_____
GAM537   LOC257515 3'  AATCTGCAAGCTTTGA      97780        _
                                TCAAAGCT GCAGATT
                                |||||||| |||||||
                                AGTTTCGA CGTCTAA
                                    A
GAM537   LOC257572 3'  AATCTGCAAGCTTTGA      97909        _
                                TCAAAGCT GCAGATT
                                |||||||| |||||||
                                AGTTTCGA CGTCTAA
                                    A
GAM537   LOC51075  3'  CACAAGCCTGAGGTGCAGCTTT 31989        GA  __  C
                                AAAGCTGCA  TT  GC TGTG
                                |||||||||  ||  || ||||
                                TTTCGACGT  AG  CG ACAC
                                     GG  TC  A
GAM537   LOC56267  3'  CACAGATTTTACAGCTTTGG   39010        C   TTGC
                                TCAAAGCTG AGA    CTGTG
                                ||||||||| |||    |||||
                                GGTTTCGAC TTT    GACAC
                                    A   TA__
GAM537   LOC90139  3'  CACAGGCGTGACAGTTCTGA   55401     A    _  GAT
                                TCA AGCTG CA   TGCCTGTG
                                ||| ||||| ||   ||||||||
                                AGT TTGAC GT   GCGGACAC
                                  C    A  ___
GAM538   CNGA1     3'  CAACTGATAATGTGCAAA     59507          GC   A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                     A_   _
GAM538   ESRRG     3'  TGGCAGTCTTATGTGCAAA    66396         TAGCT
                                TTTGCACAT     AGATTGCCA
                                |||||||||     |||||||||
                                AAACGTGTA     TCTGACGGT
                                    T_____
GAM538   KCNJ3     3'  GCAATAATGTGCAAA       9525           GCTAGA
                                TTTGCACATTA      TTGC
                                ||||||||||      ||||
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                                AAACGTGTAAT     AACG
                                        _______
GAM538  SDC2     3'  GCAAATTAATGTGTAAA     67132          CTAGA
                                TTTGCACATTAG    TTGC
                                ||||||||||||    ||||
                                AAATGTGTAATT    AACG
                                      A_____
GAM538  USP9X    3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
              A                  TTTGCACATTAGC     GCCAT
                                 |||||||||||||     |||||
                                 AAATGTGTAATCG     CGGTA
                                       TAGTC_
GAM538  AMOTL1   3'  GGCAAGTAATGTGCAAA     73650          G  AGAT
                                TTTGCACATTA CT    TGCC
                                |||||||||||  ||   ||||
                                AAACGTGTAAT GA    ACGG
                                         _ _____
GAM538  BCAR3    3'  AGTAATAATGTGCAAA      13098          __
                                TTTGCACATTA  GCT
                                ||||||||||  |||
                                AAACGTGTAAT  TGA
                                      AA
GAM538  DKFZP434B044 3'  TGACAATTAAATGTGCAGA    48930          AGCTA    C
                                TTTGCACATT     GATTG CA
                                |||||||||     ||||| ||
                                AGACGTGTAA     TTAAC GT
                                      A_____    A
GAM538  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                TTTGCACATTAG  AGA TG CAT
                                ||||||||||||  ||| || |||
                                AGACGTGTAATC  TTT AC GTA
                                       __  T  A
GAM538  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
              AA                  TTTGCACATTAGCTAGATTGCCAT
                                  ||||||||||||||||||||||||
                                  AAACGTGTAATCGATCTAACGGTA

GAM539  A1BG     3'  CAGGGTCTCACTGTGTTGC    55413        TAT_
                                GCAACACA    GGCTTTG
                                ||||||||    |||||||
                                CGTTGTGT    CTGGGAC
                                     CACT
GAM539  ACPT     3'  CACCCCGCCATATGCTGC     54980     ACA      TTT
                                GCA   CATATGGC   GTG
                                |||   ||||||||   |||
                                CGT   GTATACCG   CAC
                                  C__       CCC
GAM539  ACPT     3'  CACCCCGCCATATGCTGC     54986     ACA      TTT
                                GCA   CATATGGC   GTG
                                |||   ||||||||   |||
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                                CGT   GTATACCG   CAC
                                  C__       CCC
GAM539  AHCY     3'  CACAAAGCCCATGTGTTTTGC  5473       C       _
                                GCAA ACATATGG CTTTGTG
                                |||| |||||||| |||||||
                                CGTT TGTGTACC GAAACAC
                                  T       C
GAM539  BCL7A    3'  CAGGATTCCATTTGTGTTGCT  40638          T    CT  G
                                AGCAACACA ATGG  TT TG
                                ||||||||| ||||  || ||
                                TCGTTGTGT TACC  AG AC
                                     T    TT  G
GAM539  CDK5R2   3'  CACAAAGCCACCGCCGCTGTT  14132      ACACATA
                                AGCA      TGGCTTTGTG
                                ||||      ||||||||||
                                TTGT      ACCGAAACAC
                                  CGCCGCC
GAM539  CHC1     3'  CACAAAGCATACTCTTGC    7019       CACA    G
                                GCAA    TATG CTTTGTG
                                ||||    |||| |||||||
                                CGTT    ATAC GAAACAC
                                  CTC_   _
GAM539  CIT      3'  CACAAGGCATCTGTTGCT    69741        CATATG
                                AGCAACA     GCTTTGTG
                                |||||||     ||||||||
                                TCGTTGT     CGGAACAC
                                    CTA___
GAM539  COL6A2   5'  CAGGGCCACAGGTGCTGC    8480      A   ATA
                                GCA CAC   TGGCTTTG
                                ||| |||   ||||||||
                                CGT GTG   ACCGGGAC
                                  C   GAC
GAM539  COL6A2   5'  CAGGGCCACAGGTGCTGC    54168     A   ATA
                                GCA CAC   TGGCTTTG
                                ||| |||   ||||||||
                                CGT GTG   ACCGGGAC
                                  C   GAC
GAM539  EYA1     3'  CACAGCGTTATGTGTCTGC   4952      AC       T
                                GCA  ACATATGGC TTGTG
                                |||  ||||||||| |||||
                                CGT  TGTGTATTG GACAC
                                  C_       C
GAM539  FBN2     3'  CAAGGAACCATATGTG      8844          __
                                CACATATGG  CTTTG
                                |||||||||  |||||
                                GTGTATACC  GGAAC
                                     AA
GAM539  FMO1     3'  CACAAATGATTGTGTTGT    8924         TATGGC
                                GCAACACA     TTTGTG
                                ||||||||     ||||||
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                                TGTTGTGT     AAACAC
                                    TAGT__
GAM539  GALNT2   3'  CACAAAGCCGTTCGCAGCT   15594     AACACAT
                                AGC      ATGGCTTTGTG
                                |||      ||||||||||
                                TCG      TGCCGAAACAC
                                  ACGCT__
GAM539  GALNT2   3'  CACAAAGCCGAGTCGTGT    15593     _ A
                                ACAC AT TGGCTTTGTG
                                |||| || ||||||||||
                                TGTG TG GCCGAAACAC
                                  C  A
GAM539  GPR4     3'  CAGGGTCTCACTGTGTTGC   59902       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM539  HNMT     3'  CACAAAGCCTGTGTTACT    22567    C     TAT
                                AG AACACA  GGCTTTGTG
                                || ||||||  |||||||||
                                TC TTGTGT  CCGAAACAC
                                 A    ___
GAM539  IL1RN    3'  CACAAAGCCCTTCCATGTCGC  5141     A   CATAT_
                                GC ACA     GGCTTTGTG
                                || |||     |||||||||
                                CG TGT     CCGAAACAC
                                 C  ACCTTC
GAM539  IL2RB    3'  CACAAAGTGGATGCCTGCT   6069      ACA  ATG
                                AGCA  CAT  GCTTTGTG
                                ||||  |||  ||||||||
                                TCGT  GTA  TGAAACAC
                                  CC_  GG_
GAM539  ITSN2    3'  CACAAAGCCATGCACGCT    38971     AACACA
                                AGC     TATGGCTTTGTG
                                |||     ||||||||||||
                                TCG     GTACCGAAACAC
                                  CAC___
GAM539  JRK      3'  CAGGGTCTCACTGTGTTGC   86524       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM539  LANCL1   3'  CACAATTTTATATGTATGCT  20210     AC      CT
                                AGCA ACATATGG  TTGTG
                                ||||  ||||||||  |||||
                                TCGT  TGTATATT  AACAC
                                  A_       TT
GAM539  LGR6     5'  GGCCATCGTGTTGCT      84200       AT
                                AGCAACAC  ATGGCT
                                ||||||||  ||||||
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                                TCGTTGTG  TACCGG
                                    C_
GAM539  LRRC2    3'  CAAGGCACCATGTGTTACT   44465    C      ATG
                                AG AACACAT   GCTTTG
                                || |||||||   ||||||
                                TC TTGTGTA   CGGAAC
                                 A      CCA
GAM539  MYBL2    3'  CAGGGCCATGTGCTGC      10154     ACA
                                GCA   CATATGGCTTTG
                                |||   ||||||||||||
                                CGT   GTGTACCGGGAC
                                  C__
GAM539  OCLN     3'  CACAAAGTTTTGGTTGCT    10314       A  TAT
                                AGCAAC CA   GGCTTTGTG
                                |||||| ||   |||||||||
                                TCGTTG GT   TTGAAACAC
                                   _  T__
GAM539  OSR1     3'  CACAAAGTAATATGTG      17566       G
                                CACATAT GCTTTGTG
                                ||||||| ||||||||
                                GTGTATA TGAAACAC
                                    A
GAM539  PCDH9    5'  CACAAAGTGACAGTGCTGGCT  82794     AA_   ATATG
                                AGC   CAC    GCTTTGTG
                                |||   |||    ||||||||
                                TCG   GTG    TGAAACAC
                                  GTC   ACAG_
GAM539  PRDM2    5'  CACAAAGCCACATCCTGC    31847     ACAC  A
                                GCA    AT TGGCTTTGTG
                                |||    || ||||||||||
                                CGT    TA ACCGAAACAC
                                  CC__  C
GAM539  PRDM2    5'  CACAAAGCCACATCCTGC    24246     ACAC  A
                                GCA    AT TGGCTTTGTG
                                |||    || ||||||||||
                                CGT    TA ACCGAAACAC
                                  CC__  C
GAM539  PRG4     3'  CACAAAGCTTTATCGTGTTGT  19415        _   T
                                GCAACAC ATA GGCTTTGTG
                                ||||||| ||| |||||||||
                                TGTTGTG TAT TCGAAACAC
                                    C   T
GAM539  RXRB     3'  CACAAAGCACTGGCCTTGC    41757      CA_  TATG
                                GCAA   CA    GCTTTGTG
                                ||||   ||    ||||||||
                                CGTT   GT    CGAAACAC
                                  CCG  CA__
GAM539  SMARCD1  3'  CACAAAGTTCCCATGTG     57429        ___
                                CATATGG   CTTTGTG
                                |||||||   |||||||
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```
                                GTGTACC  GAAACAC
                                   CTT
GAM539  SMARCD1  3'  CACAAAGTTCCCATGTG    11811       ___
                                CATATGG  CTTTGTG
                                |||||||  |||||||
                                GTGTACC  GAAACAC
                                   CTT
GAM539  SMURF1   3'  CACGTGTGATCTGTGTTGC   92448       T  G  TT
                                GCAACACA AT GC  TGTG
                                |||||||| || ||  ||||
                                CGTTGTGT TA TG  GCAC
                                    C  G  T_
GAM539  STX7     3'  CACCAAGATGTGTGTTACT   13108    C      GG   T
                                AG AACACATAT  CTT GTG
                                || |||||||||  ||| |||
                                TC TTGTGTGTA  GAA CAC
                                 A        __  C
GAM539  TAF4B    3'  CACAAAGCATTGTTGC     87167      CATATG
                                GCAACA    GCTTTGTG
                                ||||||    ||||||||
                                CGTTGT    CGAAACAC
                                   TA_____
GAM539  TF       3'  CACAGCTCTGTGTTGC     6512        TAT   T
                                GCAACACA  GGCT TG
                                ||||||||  |||| ||
                                CGTTGTGT  TCGA AC
                                    C__   C
GAM539  TLR4     5'  CACAGGGCCACTGCTGCT   56736     A  CATA
                                AGCA CA   TGGCTTTGTG
                                |||| ||   ||||||||||
                                TCGT GT   ACCGGGACAC
                                  C  C___
GAM539  TLR4     5'  CACAGGGCCACTGCTGCT   12317     A  CATA
                                AGCA CA   TGGCTTTGTG
                                |||| ||   ||||||||||
                                TCGT GT   ACCGGGACAC
                                  C  C___
GAM539  TLR4     5'  CACAGGGCCACTGCTGCT   56727     A  CATA
                                AGCA CA   TGGCTTTGTG
                                |||| ||   ||||||||||
                                TCGT GT   ACCGGGACAC
                                  C  C___
GAM539  TLR4     5'  CACAGGGCCACTGCTGCT   56732     A  CATA
                                AGCA CA   TGGCTTTGTG
                                |||| ||   ||||||||||
                                TCGT GT   ACCGGGACAC
                                  C  C___
GAM539  VIPR2    3'  CACAGTCTCCATGTGTGTGC  12605     A      CT_
                                GCA CACATATGG  TTGTG
                                ||| |||||||||  |||||
```

```
                                CGT GTGTGTACC  GACAC
                                  _      TCT
GAM539  ANKT    3' CAGGGTCTCACTGTGTTGC  33024       TAT_
                                GCAACACA  GGCTTTG
                                ||||||||  |||||||
                                CGTTGTGT  CTGGGAC
                                    CACT
GAM539  ATP9A   3' CACAAAGCCAGTGGCTGTT  62039    A_  ATA
                                AGCA CAC  TGGCTTTGTG
                                ||||  |||  ||||||||||
                                TTGT GTG  ACCGAAACAC
                                  CG  ___
GAM539  CETN2   3' CACATGTTACACCTGTGTTGC 15093       TA GCTT_
                                GCAACACA TG   TGTG
                                |||||||| ||   ||||
                                CGTTGTGT AC   ACAC
                                    CC ATTGT
GAM539  CYLD    3' CACAAGGTTTTATACTGCT  30883    ACAC  TG
                                AGCA  ATA GCTTTGTG
                                ||||  ||| ||||||||
                                TCGT  TAT TGGAACAC
                                  CA__  TT
GAM539  DKFZP586A0522 3' CAGGGTCTCACTGTGTTGC  25871       TAT_
                                GCAACACA  GGCTTTG
                                ||||||||  |||||||
                                CGTTGTGT  CTGGGAC
                                    CACT
GAM539  DKFZp762K222 3' ACAGATGCGTGTTGCT    71116       ATATG _
                                AGCAACAC   GC TTTGT
                                ||||||||   || |||||
                                TCGTTGTG   CG AGACA
                                    _____ T
GAM539  FLJ10297  3' CAGGGCTTCACTGTGTTGC  35979       TAT_
                                GCAACACA  GGCTTTG
                                ||||||||  |||||||
                                CGTTGTGT  TCGGGAC
                                    CACT
GAM539  FLJ10511  3' CACATGTGTATGTGCAGCT  36204    AA     G TT
                                AGC  CACATATG C  TGTG
                                |||  |||||||| |  ||||
                                TCG  GTGTATGT G  ACAC
                                  AC      _ T_
GAM539  FLJ11029  5' CACTAGCACCTGTGTTGCT  60973       TATG  TT
                                AGCAACACA  GCT  GTG
                                |||||||||  |||  |||
                                TCGTTGTGT  CGA  CAC
                                    CCA_  T_
GAM539  FLJ11117  3' CACAAAGCTTGTATGTG    37073       _
                                CACATATG GCTTTGTG
                                |||||||| ||||||||
```

```
                                GTGTATGT CGAAACAC
                                     T
GAM539  FLJ11715  3'  CAGGGTCTCCATATGTTGC   44668      C  AT_
                                GCAACA AT   GGCTTTG
                                |||||| ||   |||||||
                                CGTTGT TA   CTGGGAC
                                   A  CCT
GAM539  FLJ20275  3'  CACAAAGGGCTTTATGTGTCAG 34819    A_     T   __
          CT                     AGC  ACACATA GGCT  TTGTG
                                |||  ||||||| ||||  |||||
                                TCG  TGTGTAT TCGG  AACAC
                                  AC      T   GA
GAM539  FLJ20413  3'  CAGAGCCGCATGCACTGCT   35131     ACA   A
                                AGCA   CAT TGGCTTTG
                                ||||   ||| ||||||||
                                TCGT   GTA GCCGAGAC
                                  CAC   C
GAM539  FLJ20450  3'  CACCTGGGACCTGTGTTGCT   35192        TAT  _   T_
                                AGCAACACA   GG CTT  GTG
                                |||||||||   || |||  |||
                                TCGTTGTGT   CC GGG  CAC
                                     ___  A   TC
GAM539  FLJ20671  3'  CAATTCAAATGTGTTGC     35516         A   CT
                                GCAACACAT TGG  TTG
                                ||||||||| |||  |||
                                CGTTGTGTA ACT  AAC
                                      A   T_
GAM539  FLJ23598  3'  CACAAAGAGAGGCTGTGCTGC  45521     A    TATGG_
                                GCA CACA     CTTTGTG
                                ||| ||||     |||||||
                                CGT GTGT     GAAACAC
                                  C    CGGAGA
GAM539  FRSB      3'  CATAGGCCATACATGTTACT   19090    C    CA      T
                                AG AACA  TATGGCTT GTG
                                || ||||  |||||||| |||
                                TC TTGT  ATACCGGA TAC
                                 A    AC      _
GAM539  H2AV      3'  CACAGCCATATGTATTGTT    56845      C        T
                                AGCAA ACATATGGCT TG
                                ||||| |||||||||| ||
                                TTGTT TGTATACCGA AC
                                   A         C
GAM539  HIC2      3'  CACAAAGTCTGTACCGC     65256    AAC   TAT
                                GC   ACA   GGCTTTGTG
                                ||   |||   |||||||||
                                CG   TGT   CTGAAACAC
                                 CCA  ___
GAM539  KIAA0140  3'  CACATGGCCATGTCTTGC    27806     CAC      T
                                GCAA   ATATGGCT TGTG
                                ||||   |||||||| ||||
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                                CGTT  TGTACCGG ACAC
                                  C__     T
GAM539  KIAA0215 3' CAAATTCCATATGTAATGC  28416   AC     C_
                                GCA  ACATATGG  TTTG
                                |||  ||||||||  ||||
                                CGT  TGTATACC  AAAC
                                  AA      TT
GAM539  KIAA0254 3' AGCCACCTGTGTTGCT    28595       TA
                                AGCAACACA  TGGCT
                                |||||||||  |||||
                                TCGTTGTGT  ACCGA
                                     CC
GAM539  KIAA0618 3' CACAAAAACATGTGTTGT   29162       TA  GC
                                GCAACACA  TG  TTTGTG
                                ||||||||  ||  ||||||
                                TGTTGTGT  AC  AAACAC
                                    __  AA
GAM539  KIAA0953 3' AGCTTTCATAGTGTTGCT   66778       A   ___
                                AGCAACAC TATG  GCT
                                |||||||| ||||  |||
                                TCGTTGTG ATAC  CGA
                                    _   TTT
GAM539  KIAA1193 3' CACAGAGCCATATACCTCGCT 67630    AACAC
                                AGC    ATATGGCTTTGTG
                                |||    |||||||||||||
                                TCG    TATACCGAGACAC
                                  CTCCA
GAM539  KIAA1281 3' CACAGAGTAACAAATGTTGCT 89151      CATATG
                                AGCAACA    GCTTTGTG
                                |||||||    ||||||||
                                TCGTTGT    TGAGACAC
                                   AAACAA
GAM539  KIAA1466 5' AGCCATATGTGCGCT     71913    AA
                                AGC  CACATATGGCT
                                |||  ||||||||||
                                TCG  GTGTATACCGA
                                  C_
GAM539  KIAA1821 3' CAGGGTCTCACTGTGTTGC  71780       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM539  KIF13B   3' CACAAAGTCCGTGGTGC    82820    A  ATAT
                                GCA CAC   GGCTTTGTG
                                ||| |||   |||||||||
                                CGT GTG   CTGAAACAC
                                  G  C___
GAM539  KIF13B   3' CACAAAGTCCGTGGTGC    30904    A  ATAT
                                GCA CAC   GGCTTTGTG
                                ||| |||   |||||||||
```

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                              CGT GTG   CTGAAACAC
                                G  C___
GAM539  MGC12921  3'  CACAAAGGCCGTTATTGC   63775    CACAT   _
                              GCAA   ATGGC TTTGTG
                              ||||   ||||| ||||||
                              CGTT   TGCCG AAACAC
                                AT___   G
GAM539  MGC14836  5'  CACAAAGCTATCATCCTGC   53035   ACACAT
                              GCA    ATGGCTTTGTG
                              |||    ||||||||||
                              CGT    TATCGAAACAC
                                CCTAC_
GAM539  MGC15429  3'  CACATTGTCATGTGCAGCT   51249   AACA     TT
                              AGC   CATATGGC  TGTG
                              |||   ||||||||  ||||
                              TCG   GTGTACTG  ACAC
                                AC__      TT
GAM539  MGC15875  3'  CGAGGCCATAATGCT     51908    ACACA
                              AGCA   TATGGCTTTG
                              ||||   ||||||||||
                              TCGT   ATACCGGAGC
                                A____
GAM539  MGC16279  5'  GAAGCCATCGTGTCGCT    51888    A   AT
                              AGC ACAC  ATGGCTTT
                              ||| ||||  ||||||||
                              TCG TGTG  TACCGAAG
                                C   C_
GAM539  MGC27434  3'  CACAATAAGTATGTGTT    58947       GGCT
                              AACACATAT   TTGTG
                              |||||||||   |||||
                              TTGTGTATG   AACAC
                                   AAT_
GAM539  MGC3048   3'  CACAAAGCATGAATGTT    43899    CA   G
                              AACA  TATG CTTTGTG
                              ||||  |||| |||||||
                              TTGT  GTAC GAAACAC
                                AA   _
GAM539  MIG-6     3'  CACAAGCTGGCCTTGTGTTGCT 38486       TAT   ___
                              AGCAACACA   GGCT   TTGTG
                              |||||||||   ||||   |||||
                              TCGTTGTGT   CCGG   AACAC
                                   T__    TCG
GAM539  MUC17     3'  CACTGCCCCATATGTGTCCCT  94271    CA       CTTT
                              AG  ACACATATGG   GTG
                              ||  ||||||||||   |||
                              TC  TGTGTATACC   CAC
                               CC        CCGT
GAM539  MYO3B     3'  CACTCTCCCACATGTGTTGT   57301       A   CTTT
                              GCAACACAT TGG   GTG
                              ||||||||| |||   |||
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                                TGTTGTGTA ACC   CAC
                                     C  CTCT
GAM539  NS1-BP   3'  CACAAAGCTTTTGCATATTGC  72542     CA__  TAT
                                GCAA   CA  GGCTTTGTG
                                ||||   ||  |||||||||
                                CGTT   GT  TCGAAACAC
                                  ATAC  TT_
GAM539  OR51E2   3'  CACAGGTTTTATGTGTTCT   47791    C      TG   T
                                AG AACACATA  GCTT GTG
                                || ||||||||  |||| |||
                                TC TTGTGTAT  TGGA CAC
                                 _      TT   _
GAM539  PRDM11   3'  CAGGTGCTCCATGTGTTGC   39581        AT  _
                                GCAACACAT  GGC TTTG
                                |||||||||  ||| ||||
                                CGTTGTGTA  TCG GGAC
                                     CC  T
GAM539  PRO0943  5'  CACAAAAGTGTTATATGTG   37701         ___
                                CACATATGGC  TTTGTG
                                ||||||||||  ||||||
                                GTGTATATTG  AAACAC
                                     TGA
GAM539  SULT1C2  5'  CACAACGCAGCCATATGCTG  21674   _      ___
                                CA CATATGGCT  TTGTG
                                || |||||||||  |||||
                                GT GTATACCGA  AACAC
                                 C       CGC
GAM539  VEST1    3'  CACCTGCCATACATGTTGT   53685      CA    TTT
                                GCAACA  TATGGC  GTG
                                ||||||  ||||||  |||
                                TGTTGT  ATACCG  CAC
                                   AC    TC_
GAM539  ZFP100   3'  AGTCACCTGTGTTGCT     70049        TA
                                AGCAACACA  TGGCT
                                |||||||||  |||||
                                TCGTTGTGT  ACTGA
                                     CC
GAM539  ZNF363   5'  AGCCATATTGTCGCT      73452    A  C
                                AGC ACA ATATGGCT
                                ||| ||| ||||||||
                                TCG TGT TATACCGA
                                  C  _
GAM539  LOC118611 5'  CACAGAGCATTTGCGTTACT  75469   C  A  TATG
                                AG AAC CA   GCTTTGTG
                                || ||| ||   ||||||||
                                TC TTG GT   CGAGACAC
                                 A  C  TTA_
GAM539  LOC120526 3'  CAGGGCCATTGCACTGCT   74015    ACA  T
                                AGCA  CA ATGGCTTTG
                                ||||  || |||||||||
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                                TCGT   GT TACCGGGAC
                                  CAC  _
GAM539   LOC126669 3'  CACAAAGTTCCATATGT     75399         __
                                ACATATGG  CTTTGTG
                                ||||||||  |||||||
                                TGTATACC  GAAACAC
                                    TT
GAM539   LOC139840 5'  CACAAGAGCCATGGGT      76266    A       _
                                AC TATGGCTTT GTG
                                || |||||||| |||
                                TG GTACCGAGA CAC
                                 G       A
GAM539   LOC143465 5'  CACATGCACATATGTG      82962         _  TT
                                CACATATG GC  TGTG
                                |||||||| ||  ||||
                                GTGTATAC CG  ACAC
                                    A  T_
GAM539   LOC146774 3'  CACTGACATGTGTGTGC     78094     A       GCTTT
                                GCA CACATATG    GTG
                                ||| ||||||||    |||
                                CGT GTGTGTAC    CAC
                                  _       AGT__
GAM539   LOC147407 5'  CACAAAGCTATCATCCTGC    76322     ACACAT
                                GCA     ATGGCTTTGTG
                                |||     ||||||||||
                                CGT     TATCGAAACAC
                                  CCTAC_
GAM539   LOC151057 3'  ACAGAGCACATACTGT      85199     _   _
                                ACA TATG GCTTTGT
                                ||| |||| |||||||
                                TGT ATAC CGAGACA
                                  C   A
GAM539   LOC151473 3'  CACAACAACCTATGTGTT     80254         T  CT_
                                AACACATA GG   TTGTG
                                |||||||| ||   |||||
                                TTGTGTAT CC   AACAC
                                    _ AAC
GAM539   LOC154739 5'  CACAAAGTTCAAATGTATGC   86227     AC    A   _
                                GCA  ACAT TGG CTTTGTG
                                |||  |||| ||| |||||||
                                CGT  TGTA ACT GAAACAC
                                  A_   A  T
GAM539   LOC157507 5'  CACAGCTGTGTATGTGTGCT   81454      A      __    T
                                AGCA CACATAT  GGCT TG
                                |||| |||||||  |||| ||
                                TCGT GTGTATG  TCGA AC
                                  _      TG   C
GAM539   LOC161734 3'  CACAAACATTTAGTGTTGCT   87097         AT_   GC
                                AGCAACAC   ATG  TTTGTG
                                ||||||||   |||  ||||||
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                                TCGTTGTG  TAC  AAACAC
                                   ATT  __
GAM539  LOC196410 3'  CACAAAAGTCATGGTG     87657     A       _
                                CAC TATGGCTTT GTG
                                ||| ||||||||| |||
                                GTG GTACTGAAA CAC
                                  _       A
GAM539  LOC196485 3'  CACAAAAACCTGTGTTGT    87730        TAT  C_
                                GCAACACA  GG  TTTGTG
                                ||||||||  ||  ||||||
                                TGTTGTGT  CC  AAACAC
                                   ___  AA
GAM539  LOC196529 3'  CAGGGTCTCACTGTGTTGC   87771        TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                   CACT
GAM539  LOC197003 5'  CACAAAGCTCCATGCTGT    87870    _  AT
                                ACA CAT  GGCTTTGTG
                                ||| |||  |||||||||
                                TGT GTA  TCGAAACAC
                                  C  CC
GAM539  LOC202025 5'  CACAGTTGTATGGTTGCT    90281      A   TG  T
                                AGCAAC CATA  GCT TG
                                |||||| ||||  ||| ||
                                TCGTTG GTAT  TGA AC
                                   _  GT  C
GAM539  LOC203276 3'  CACAAAGTTCAAGTGTATGC  90475    _  ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM539  LOC203292 3'  CAGGGTTTCATATGTGTT    90509        __
                                AACACATATG  GCTTTG
                                ||||||||||  ||||||
                                TTGTGTATAC  TGGGAC
                                     TT
GAM539  LOC203305 3'  CACAAAGTTCAAGTGTATGC  90519    _  ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM539  LOC221354 3'  CACAAAAACATGTGTTGT    92409       TA  GC
                                GCAACACA  TG  TTTGTG
                                ||||||||  ||  ||||||
                                TGTTGTGT  AC  AAACAC
                                   __  AA
GAM539  LOC254243 3'  CACAAAGTTCAAGTGTATGC  97404    _  ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
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                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM539  LOC255870 3'  CACAACTGGCCATGTCCTGC  94657    ACAC     __
                                GCA   ATATGGCT  TTGTG
                                |||   ||||||||  |||||
                                CGT   TGTACCGG  AACAC
                                  CC__      TC
GAM539  LOC90038  3'  CACAAAGTTCAAGTGTATGC  61148    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM539  LOC90321  3'  CACAAATGGATTGTGTGTGC  62262    A    TGGC_
                                GCA CACATA    TTTGTG
                                ||| ||||||    ||||||
                                CGT GTGTGT    AAACAC
                                  _     TAGGT
GAM539  LOC90750  3'  CACAAAGTTAAGATTGCT   63917     CACATA
                                AGCAA     TGGCTTTGTG
                                |||||     ||||||||||
                                TCGTT     ATTGAAACAC
                                   AGA___
GAM539  LOC91069  3'  GAAGCCATCGTGTCACT    64778   CA   AT
                                AG  ACAC  ATGGCTTT
                                ||  ||||  ||||||||
                                TC  TGTG  TACCGAAG
                                 AC   C_
GAM539  LOC92539  3'  CACAAAGCCACTGTAGC    69630   A  CATA
                                GC ACA   TGGCTTTGTG
                                || |||   ||||||||||
                                CG TGT   ACCGAAACAC
                                 A  C___
GAM540  CLCN5     5'  TGAAATACCTAAGCTGCTCCAA 3595        _______
                                TTGGAGCAG      GTTTCA
                                |||||||||      ||||||
                                AACCTCGTC      TAAAGT
                                     GAATCCA
GAM540  FLRT2     5'  ATTGAAAAATGAGGTCTGC   25056    GT    CTC
                                GCAG  TTCATT   CAAT
                                ||||  ||||||   ||||
                                CGTC  GAGTAA   GTTA
                                  TG     AAA
GAM540  IL17      3'  TGGGGAAAATGAAACCCTCC  9333     CA     __
                                GGAG  GGTTTCAT  TCTCCA
                                ||||  ||||||||  ||||||
                                CCTC  CCAAAGTA  AGGGGT
                                  __       AA
GAM540  NLGN1     5'  TGAAGATGCTGCTCCAA    30026       G__
                                TTGGAGCAG   TTTCA
                                |||||||||   |||||
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                                AACCTCGTC  GAAGT
                                     GTA
GAM540  POLG     3'  GTGATAAACCTGCTCCAA   10682          __
                                TTGGAGCAGGTT  TCAT
                                ||||||||||||  ||||
                                AACCTCGTCCAA  AGTG
                                      AT
GAM540  TPK1     3'  GGAGAACCTGTCCAA      42384      G    TTCAT
                                TTGGA CAGGT    TCTCC
                                ||||| |||||    |||||
                                AACCT GTCCA    AGAGG
                                  _   ______
GAM540  C1orf8   5'  GAGAATGAAACCCTC      16832     CA
                                GAG  GGTTTCATTCTC
                                |||  ||||||||||||
                                CTC  CCAAAGTAAGAG
                                  __
GAM540  CLIC6    3'  TGGAGAACATGTTCCAA     82536       G  TTCAT
                                TTGGAGCA GT    TCTCCA
                                |||||||| ||    ||||||
                                AACCTTGT CA    AGAGGT
                                     A  ______
GAM540  CLIPR-59 3'  TGGAGAATTTCAATGCCCCGA  31374     A   GGTTTC
                                TTGG GCA     ATTCTCCA
                                |||| |||     ||||||||
                                AGCC CGT     TAAGAGGT
                                  C   AACTT_
GAM540  DKFZP547L112 3'  TGGAGAACTCTTGCTCCA    66532         TTTCA
                                TGGAGCAGG    TTCTCCA
                                |||||||||    |||||||
                                ACCTCGTTC    AAGAGGT
                                     TC___
GAM540  EPS8R3   5'  GGACCACCTGCTCCAA     55701          TTCATTC
                                TTGGAGCAGGT     TCC
                                ||||||||||      |||
                                AACCTCGTCCA     AGG
                                     CC_____
GAM540  EPS8R3   5'  GGACCACCTGCTCCAA     57404          TTCATTC
                                TTGGAGCAGGT     TCC
                                ||||||||||      |||
                                AACCTCGTCCA     AGG
                                     CC_____
GAM540  FLJ20552 3'  AGAACAAAACTGCTCCAA    35389        G   CA
                                TTGGAGCAG TTT  TTCT
                                ||||||||| |||  ||||
                                AACCTCGTC AAA  AAGA
                                     _  AC
GAM540  FLJ22865 5'  TGGAGAAAACTGCTCTAA    47071         GTTTCA
                                TTGGAGCAG    TTCTCCA
                                |||||||||    |||||||
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                                AATCTCGTC     AAGAGGT
                                    AA____
GAM540  KIAA0372  5'  ATTGAAATTTGTTACCTACTCC 27663       C   TT  TTCTC
            AA                    TTGGAG AGGT  CA    CAAT
                                  |||||| ||||  ||    ||||
                                  AACCTC TCCA  GT    GTTA
                                     A   TT  TTAAA
GAM540  PRO0132   5'  ATGAAACCACTCCAA      26101       CA
                                  TTGGAG  GGTTTCAT
                                  ||||||  ||||||||
                                  AACCTC  CCAAAGTA
                                     A_
GAM540  TEX27     3'  AGAGTGGAACCCGCTGCAA   41658     G   A
                                  TTG AGC GGTTTCATTCT
                                  ||| ||| ||||||||||
                                  AAC TCG CCAAGGTGAGA
                                    G   C
GAM540  LOC149373 3'  ATTGGGGTGATGATACCCACCC 79312      AGCA   T    _
            CAA                     TTGG    GGT TCATT CTCCAAT
                                  ||||    ||| ||||| |||||||
                                  AACC    CCA AGTAG GGGGTTA
                                    CCAC   T    T
GAM540  LOC152687 3'  TTGGAGAATATTGCTCC     80643        GTTTC
                                  GGAGCAG     ATTCTCCAA
                                  |||||||     |||||||||
                                  CCTCGTT     TAAGAGGTT
                                      A____
GAM540  LOC51202  3'  ATTGGAGAATGAAACCTGCTCC 33017
            AA                    TTGGAGCAGGTTTCATTCTCCAAT
                                  ||||||||||||||||||||||||
                                  AACCTCGTCCAAAGTAAGAGGTTA

GAM541  ADD2      3'  TGGGTCCCTGCCCTGCTCGTC  33937     A       A T  TA
                                  GAC AGCAGGGCA G GA  CA
                                  ||| ||||||||| | ||  ||
                                  CTG TCGTCCCGT C CT  GT
                                    C        _ C  GG
GAM541  ADD2      3'  TGGGTCCCTGCCCTGCTCGTC  33948     A       A T  TA
                                  GAC AGCAGGGCA G GA  CA
                                  ||| ||||||||| | ||  ||
                                  CTG TCGTCCCGT C CT  GT
                                    C        _ C  GG
GAM541  ADD2      3'  TGGGTCCCTGCCCTGCTCGTC  33954     A       A T  TA
                                  GAC AGCAGGGCA G GA  CA
                                  ||| ||||||||| | ||  ||
                                  CTG TCGTCCCGT C CT  GT
                                    C        _ C  GG
GAM541  ADD2      3'  TGGGTCCCTGCCCTGCTCGTC  33965     A       A T  TA
                                  GAC AGCAGGGCA G GA  CA
                                  ||| ||||||||| | ||  ||
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                                CTG TCGTCCCGT C CT  GT
                                  C       _ C  GG
GAM541  ARNT2    3'  CACCCTCGCCCTGCTTGCCC  29454    A       AA__
                                GG CAAGCAGGGC   GTG
                                || ||||||||||   |||
                                CC GTTCGTCCCG   CAC
                                 C        CTCC
GAM541  ATP2A3   3'  CACTCGCCCACTTGCCCA   17721    A   CA   A
                                TGG CAAG  GGGC AGTG
                                ||| ||||  |||| ||||
                                ACC GTTC  CCCG TCAC
                                  C   A_   C
GAM541  CD34     3'  CACAGCCCTGCTTACCA    8339     AC       AA
                                TGG  AAGCAGGGC  GTG
                                |||  |||||||||  |||
                                ACC  TTCGTCCCG  CAC
                                  A_       A_
GAM541  CHRNB1   3'  GTACCACTTGCCCCCTCCA  60537     CAAGCA       A
                                TGGA     GGGCAAGTG TAC
                                ||||     ||||||||| |||
                                ACCT     CCCGTTCAC ATG
                                  CC____        C
GAM541  CRAT     3'  CATCTGTACCCTGCTTCCCA  5658     AC      __  AG
                                TGG  AAGCAGGG  CA  TG
                                |||  ||||||||  ||  ||
                                ACC  TTCGTCCC  GT  AC
                                  C_       AT  CT
GAM541  CRAT     3'  CATCTGTACCCTGCTTCCCA  14350    AC      __  AG
                                TGG  AAGCAGGG  CA  TG
                                |||  ||||||||  ||  ||
                                ACC  TTCGTCCC  GT  AC
                                  C_       AT  CT
GAM541  DAP      3'  ACTGTCCTGCTCACCCA    72551    ACA       A
                                TGG   AGCAGGGCA GT
                                |||   |||||||||  ||
                                ACC   TCGTCCTGT CA
                                  CAC       _
GAM541  DAZ      3'  GCTTACTCTGCTTATCCA    82114     C       C
                                TGGA AAGCAGGG AAGT
                                |||| |||||||| ||||
                                ACCT TTCGTCTC TTCG
                                   A       A
GAM541  EXTL3    3'  TACTTATCCCTGCTCTCC    7536     CA      C_
                                GGA  AGCAGGG  AAGTG
                                |||  |||||||  |||||
                                CCT  TCGTCCC  TTCAT
                                  C_       TA
GAM541  GLUL     3'  TGGGTTTCTGCCCTGCCCACCC 9048     ACAA       A T  TA
                                GG    GCAGGGCA G GA  CA
                                ||    |||||||| | ||  ||
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                                CC   CGTCCCGT C TT  GT
                                 CACC       _ T  GG
GAM541  GYS1    3'  CACTCCCCGCCTGTCC      88398      A  A   CA
                                GGACA GC GGG  AGTG
                                ||||| || |||  ||||
                                CCTGT CG CCC  TCAC
                                  C  C  __
GAM541  KHK     3'  TCCTCTGCCCTGCCCACCA   4033     ACAA       _  T
                                TGG   GCAGGGCA AG GA
                                |||   |||||||| || ||
                                ACC   CGTCCCGT TC CT
                                 ACC_       C  _
GAM541  KHK     3'  TCCTCTGCCCTGCCCACCA   21403     ACAA       _  T
                                TGG   GCAGGGCA AG GA
                                |||   |||||||| || ||
                                ACC   CGTCCCGT TC CT
                                 ACC_       C  _
GAM541  MAT1A   3'  CACCTGCCCTACCTGCCCCA  90827     ACA  C_     A
                                TGG   AG  AGGGCA GTG
                                |||   ||  |||||| |||
                                ACC   TC  TCCCGT CAC
                                 CCG  CA     C
GAM541  MAT1A   3'  TACCTGCCCCACTTGTCC    90836       CA     A
                                GGACAAG  GGGCA GTG
                                |||||||  ||||| |||
                                CCTGTTC  CCCGT CAT
                                    AC     C
GAM541  MCL1    3'  ACTGCCCTGCCTGCCCA     41712     A  A      A
                                TGG CA GCAGGGCA GT
                                ||| || |||||||| ||
                                ACC GT CGTCCCGT CA
                                 C  C       _
GAM541  PDGFB   3'  CACCCCTCCCTGCTTGCACA  10495    GA       CAA_
                                TG  CAAGCAGGG   GTG
                                ||  |||||||||   |||
                                AC  GTTCGTCCC   CAC
                                 AC        TCCC
GAM541  PFKFB4  3'  TGTAATCGGGTGCCCTGCTGTC 15875       A      AG   _
           CA                    TGGACA GCAGGGCA  TGAT ACA
                                ||||||  ||||||||  |||| |||
                                ACCTGT CGTCCCGT  GCTA TGT
                                   _       GG    A
GAM541  RAI14   3'  TCATCACCCTGCTTATC     31482    C       CAA
                                GA AAGCAGGG   GTGA
                                || ||||||||   ||||
                                CT TTCGTCCC   TACT
                                 A       AC_
GAM541  SFRP1   3'  ACTTTACCCTTCTTGTCCA   11563        C    C_
                                TGGACAAG AGGG  AAGT
                                |||||||| ||||  ||||
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                                ACCTGTTC TCCC  TTCA
                                    T   AT
GAM541  SLA2     3'  CTTGCCCTGTTGCCCA     49898     ACA
                                TGG  AGCAGGGCAAG
                                |||  ||||||||||
                                ACC  TTGTCCCGTTC
                                  CG_
GAM541  SLC25A11 3'  GCTTGCCCTGCTCGTCC     13091      A
                                GGAC AGCAGGGCAAGT
                                |||| ||||||||||||
                                CCTG TCGTCCCGTTCG
                                  C
GAM541  SLC7A4   3'  CACTTGCCCCGCCCTCC     65203     CAA  A
                                GGA  GC GGGCAAGTG
                                |||  || |||||||||
                                CCT  CG CCCGTTCAC
                                  CC_  C
GAM541  TEAD3    3'  ATCACCCTGCTCTGCCCA     12207     ACAA       A_
                                TGG   GCAGGGCA  GTGAT
                                |||   ||||||||  |||||
                                ACC   CGTCTCGT  CACTA
                                  ____       CC
GAM541  TFE3     3'  TGCCCTGCTCTGCCCA      21513     A  _
                                TGG CA AGCAGGGCA
                                ||| || |||||||||
                                ACC GT TCGTCCCGT
                                  C  C
GAM541  TRPM6    3'  TGCTTGCCCTGCCTGCCA     34550     A  A
                                TGG CA GCAGGGCAAGTG
                                ||| || ||||||||||||
                                ACC GT CGTCCCGTTCGT
                                  _  C
GAM541  VDR      3'  TGCAGGCCCCGCTTGTCCA    4573          A   AA
                                TGGACAAGC GGGC  GTG
                                ||||||||| ||||  |||
                                ACCTGTTCG CCCG  CGT
                                      C   GA
GAM541  VIPR1    3'  GCTGCCCTCCTTGTCCA      16114         C     A
                                TGGACAAG AGGGCA GT
                                |||||||| |||||| ||
                                ACCTGTTC TCCCGT CG
                                     C     _
GAM541  AP3D1    3'  CGCATCCCCTGCTTGCCA     14136     A       CAA
                                TGG CAAGCAGGG   GTG
                                ||| |||||||||   |||
                                ACC GTTCGTCCC   CGC
                                  _       CTA
GAM541  ATP9A    3'  GCCAGCCCTGCTTATCCA     62044      C       AA
                                TGGA AAGCAGGGC  GT
                                |||| |||||||||  ||
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                                ACCT TTCGTCCCG  CG
                                  A        AC
GAM541  B3GNT7   3'  CGCACCCTGCTTCTCCA     71127      C       CAA
                                TGGA AAGCAGGG   GTG
                                |||| ||||||||   |||
                                ACCT TTCGTCCC   CGC
                                  C       A__
GAM541  BAGE     3'  CACATCTTCCTGCTTTGTCCA  6807         _     CAA_
                                TGGACAA GCAGGG    GTG
                                |||||||  ||||||    |||
                                ACCTGTT CGTCCT    CAC
                                    T     TCTA
GAM541  BCAN     3'  CACTGCCCTGTCACCCA     41689     ACAA       A
                                TGG    GCAGGGCA GTG
                                |||    ||||||||  |||
                                ACC    TGTCCCGT CAC
                                  CAC_       _
GAM541  BLP2     3'  ATCACTTGTATCTCCAGCCCA  47115     ACAA  A  ____
                                TGG    GC GG    GCAAGTGAT
                                |||    || ||    |||||||||
                                ACC    CG CC    TGTTCACTA
                                  ____  A  TCTA
GAM541  BLP2     3'  ATCACTTGTATCTCCAGCCCA  54333     ACAA  A  ____
                                TGG    GC GG    GCAAGTGAT
                                |||    || ||    |||||||||
                                ACC    CG CC    TGTTCACTA
                                  ____  A  TCTA
GAM541  BTBD3    3'  ATCTAGCTCCCTTACTTGTCCA 30305         C_    CAAGT
                                TGGACAAG  AGGG     GAT
                                ||||||||  ||||     |||
                                ACCTGTTC  TCCC     CTA
                                    AT    TCGAT
GAM541  C19orf7  3'  CACACCCTGCTTGCCCA     61126     A       CAA
                                TGG CAAGCAGGG   GTG
                                ||| |||||||||   |||
                                ACC GTTCGTCCC   CAC
                                  C       A__
GAM541  C9orf16  3'  CACTTGCCTGCCCACCCA    44114     ACAA    G
                                TGG    GCAGG CAAGTG
                                |||    ||||| ||||||
                                ACC    CGTCC GTTCAC
                                  CACC    _
GAM541  CENTB5   3'  CGCGGCCCTGCTCGCCCA    95484     ACA       AA
                                TGG   AGCAGGGC  GTG
                                |||   ||||||||  |||
                                ACC   TCGTCCCG  CGC
                                  CGC       G_
GAM541  CXYorf1  5'  TCTCTGCCCTGCTGCCCA    82054     ACA       A T
                                TGG   AGCAGGGCA G GA
                                |||   ||||||||| | ||
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                                ACC   TCGTCCCGT C CT
                                  CG_       _ T
GAM541  CYP2C18   3'  GTATCACTTGTATTGACCA   5750     ACAAG   G
                                TGG    CAG GCAAGTGATAC
                                |||    ||| ||||||||||
                                ACC    GTT TGTTCACTATG
                                  A____   A
GAM541  DCOHM     3'  TGCCTGCCCTGCCCACCA    49615    ACAA      A
                                TGG    GCAGGGCA GTG
                                |||    |||||||| |||
                                ACC    CGTCCCGT CGT
                                  ACC_      C
GAM541  DKFZp547E052 3'  GTACCAGCCACTTGTCC     50099       CAG   AAG  A
                                GGACAAG   GGC   TG TAC
                                |||||||   |||   || |||
                                CCTGTTC   CCG   AC ATG
                                    A__   ___  C
GAM541  DKFZp547O146 3'  CGCCTGTCCTGCCCGCCCA   39566    ACAA      A
                                TGG    GCAGGGCA GTG
                                |||    |||||||| |||
                                ACC    CGTCCTGT CGC
                                  CGCC      C
GAM541  DKFZP564O0423 3'  CGCTTTGGCCTGCTTGTCCA   91683          G   _
                                TGGACAAGCAGG CAA GTG
                                |||||||||||| ||| |||
                                ACCTGTTCGTCC GTT CGC
                                       G   T
GAM541  DKFZP566N034 3'  CACACCACTGCTTGCCC     80139    A     _  CAA
                                GG CAAGCAG GG   GTG
                                || ||||||| ||   |||
                                CC GTTCGTC CC   CAC
                                 C      A  A__
GAM541  ERF       3'  TGCCTGCCCTGCCCCTCCA   21439     CAA      A
                                TGGA   GCAGGGCA GTG
                                ||||   |||||||| |||
                                ACCT   CGTCCCGT CGT
                                  CCC      C
GAM541  FBXO29    3'  TACGGTCCCTGCTTAGCCA   76758    AC      CAA
                                TGG  AAGCAGGG   GTG
                                |||  ||||||||   |||
                                ACC  TTCGTCCC   CAT
                                  GA       TGG
GAM541  FIBL-6    5'  ATCCCTGCCCTGCCCA     72914    ACAA      A T
                                TGG    GCAGGGCA G GAT
                                |||    |||||||| | |||
                                ACC    CGTCCCGT C CTA
                                  _____       _ C
GAM541  FLJ14810  3'  CACCCTCTGCCCTGCCCGGCCA 51623    ACAA      A___
                                TGG    GCAGGGCA    GTG
                                |||    ||||||||    |||
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                                ACC   CGTCCCGT   CAC
                                  GGCC      CTCC
GAM541  FLJ20542  3'  TGTCACCTGCCTGCCCA    49787    ACAA    G  A
                                TGG   GCAGG CA GTGATA
                                |||   ||||| || ||||||
                                ACC   CGTCC GT CACTGT
                                  ____    _ C
GAM541  FLJ22955  5'  CACTTGCCCTGCTCTCCA    95117     CA
                                TGGA  AGCAGGGCAAGTG
                                ||||  ||||||||||||
                                ACCT  TCGTCCCGTTCAC
                                  C_
GAM541  GAL3ST2   3'  GTCCTGCCCTGCCCTCC     52313     CAA      A T
                                GGA   GCAGGGCA G GAT
                                |||   |||||||| | |||
                                CCT   CGTCCCGT C CTG
                                  CC_      _ _
GAM541  HSA250839 3'  GTCTCTGCCCTGCCCACCCA   37260     ACAA      A T
                                TGG   GCAGGGCA G GAT
                                |||   |||||||| | |||
                                ACC   CGTCCCGT C CTG
                                  CACC      _ T
GAM541  IRO039700 3'  CACACAGCCCTGCTTGGCCA   37909     A        AA_
                                TGG CAAGCAGGGC   GTG
                                ||| ||||||||||   |||
                                ACC GTTCGTCCCG   CAC
                                  G         ACA
GAM541  KIAA0427  3'  CACAGCCCTGCTCCCCA     28718     ACA      AA
                                TGG   AGCAGGGC  GTG
                                |||   ||||||||  |||
                                ACC   TCGTCCCG  CAC
                                  CC_       A_
GAM541  KIAA0495  3'  TGGAGTCTTGCCCTGTCACCCA 62600     ACAA       TGATA
                                TGG   GCAGGGCAAG    CA
                                |||   ||||||||||    ||
                                ACC   TGTCCCGTTC    GT
                                  CAC_        TGAG_
GAM541  KIAA1041  3'  TGGAGTCTTGCCCTGTTGCCCA 30144     ACA        TGATA
                                TGG   AGCAGGGCAAG    CA
                                |||   ||||||||||    ||
                                ACC   TTGTCCCGTTC    GT
                                  CG_         TGAG_
GAM541  KIAA1111  3'  TCACCCCAGCTTGCCCA     96208     A    A   CAA
                                TGG CAAGC GGG   GTGA
                                ||| ||||| |||   ||||
                                ACC GTTCG CCC   CACT
                                  C    A  ___
GAM541  KIAA1321  3'  TGTATCACTTCTCTGTCTGTCC 62228       AG    C
            A                    TGGACA  CAGGG AAGTGATACA
                                ||||||  ||||| ||||||||||
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                                ACCTGT  GTCTC TTCACTATGT
                                   CT    _
GAM541  KIAA1437  3'  TGCCTGCCCTGCCTCTCCA   60595     CAA      A
                                TGGA   GCAGGGCA GTG
                                ||||   |||||||| |||
                                ACCT   CGTCCCGT CGT
                                  CTC       C
GAM541  KIAA1464  3'  GGAGCTGCCCTGCCCTCCA   68271     CAA      A  GATA
                                TGGA   GCAGGGCA GT    C
                                ||||   |||||||| ||    |
                                ACCT   CGTCCCGT CG    G
                                  CC_       _ AG__
GAM541  KIAA1560  3'  CACTCTGCCCTGCCTGTC    64174     A      _
                                GACA GCAGGGCA AGTG
                                |||| |||||||| ||||
                                CTGT CGTCCCGT TCAC
                                  C       C
GAM541  KIAA1881  3'  CGCGGGGTCGCCCTGCTCTGTC 95338       _      AA____
          CA                      TGGACA AGCAGGGC     GTG
                                |||||| ||||||||     |||
                                ACCTGT TCGTCCCG     CGC
                                   C       CTGGGG
GAM541  LASP1     3'  TGTGATTTTGCCCTCCTGCCCA 20464     ACA  C       TGA
                                TGG   AG AGGGCAAG   TACA
                                |||   || ||||||||   ||||
                                ACC   TC TCCCGTTT   GTGT
                                  CG_  C       TA_
GAM541  MGC3130   3'  TGGTTGCTCTGCTCATCCA   43822     CA       G
                                TGGA  AGCAGGGCAA TG
                                ||||  |||||||||| ||
                                ACCT  TCGTCTCGTT GT
                                  AC         G
GAM541  RAB1B     3'  CACCTGTGCCCTGCCCTCCA   48284     CAA      A__
                                TGGA   GCAGGGCA   GTG
                                ||||   ||||||||   |||
                                ACCT   CGTCCCGT   CAC
                                  CC_       GTC
GAM541  VI        3'  TGTATCACCTGGGTTCTGTCC  25560       _  AG  CAA
                                GGACA AGC  GG   GTGATACA
                                ||||| |||  ||   ||||||||
                                CCTGT TTG  TC   CACTATGT
                                   C   GG  ___
GAM541  LOC128977 3'  TGCTAGCCCTACTTGCCCA   74829     A   C    A
                                TGG CAAG AGGGC AGTG
                                ||| |||| ||||| ||||
                                ACC GTTC TCCCG TCGT
                                  C   A    A
GAM541  LOC132671 3'  TGCTTTCTACCCTGCCTGGCCA 59172     A  A     C___
                                TGG CA GCAGGG    AAGTG
                                ||| || ||||||    |||||
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                                ACC GT CGTCCC    TTCGT
                                  G  C     ATCT
GAM541   LOC143153 3'  GTAGCAGCTGTCCTGCTCACCC 76468     ACA       A  GA_
             A                    TGG   AGCAGGGCA GT   TAC
                                  |||   ||||||||| ||   |||
                                  ACC   TCGTCCTGT CG   ATG
                                    CAC       _  ACG
GAM541   LOC144583 3'  TGTCTGCCCTGCTCTCC     76896     CA       AGT
                                  GGA  AGCAGGGCA   GATA
                                  |||  |||||||||   ||||
                                  CCT  TCGTCCCGT   CTGT
                                    C_       ___
GAM541   LOC145333 5'  CATTCTCCCACTTGTCCA    83324        CA   CA
                                  TGGACAAG  GGG  AGTG
                                  ||||||||  |||  ||||
                                  ACCTGTTC  CCC  TTAC
                                       A_   TC
GAM541   LOC147975 3'  TACAGTCCCTGCTTATTCA    84085      C       CAA
                                  TGGA AAGCAGGG   GTG
                                  |||| ||||||||   |||
                                  ACTT TTCGTCCC   CAT
                                    A       TGA
GAM541   LOC148137 3'  ATGGCTCTGCCCTGCCCCCCA  58420     ACAA      _   G
                                  TGG    GCAGGGCA AGT AT
                                  |||    |||||||| ||| ||
                                  ACC    CGTCCCGT TCG TA
                                    CCC_       C   G
GAM541   LOC151405 5'  TGTATCACTGTTTAATGTTACC 85340     ACA   __    A
             CA                     TGG   AGCA  GGGCA GTGATACA
                                    |||   ||||  ||||| ||||||||
                                    ACC   TTGT  TTTGT CACTATGT
                                      CA_    AA    _
GAM541   LOC152271 3'  CATCTGCCCTGCCTGCCCA    80514     A  A      AG
                                  TGG CA GCAGGGCA  TG
                                  ||| || ||||||||  ||
                                  ACC GT CGTCCCGT  AC
                                    C  C       CT
GAM541   LOC152282 5'  CTTGCCCTGTTGCCCA      80552     ACA
                                  TGG   AGCAGGGCAAG
                                  |||   ||||||||||
                                  ACC   TTGTCCCGTTC
                                    CG_
GAM541   LOC154547 5'  CGCACCCTCTCCCCTTGTCCA  76052        C____   CAA
                                  TGGACAAG    AGGG   GTG
                                  ||||||||    ||||   |||
                                  ACCTGTTC    TCCC   CGC
                                       CCCTC    A__
GAM541   LOC158629 3'  TATCACTTACTATATGTC    86884      AGCAG  C
                                  GACA    GG AAGTGATA
                                  ||||    || ||||||||
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                                CTGT    TC TTCACTAT
                                  ATA__  A
GAM541  LOC200093 5'  GTCTCTGCCCTGCTGCCCA   63098    ACA       A T
                                TGG   AGCAGGGCA G GAT
                                |||   ||||||||| | |||
                                ACC   TCGTCCCGT C CTG
                                  CG_       _ T
GAM541  LOC200470 5'  CACCTCCTCACTTGTCCA    90057        CA   CAA
                                TGGACAAG  GGG   GTG
                                ||||||||  |||   |||
                                ACCTGTTC  TCC   CAC
                                     AC   TC_
GAM541  LOC219295 5'  GTAGCAGCTGTCCTGCTCGCCC 92995     ACA       A  GA_
           A                     TGG   AGCAGGGCA GT   TAC
                                |||   ||||||||| ||   |||
                                ACC   TCGTCCTGT CG   ATG
                                  CGC       _  ACG
GAM541  LOC221466 5'  TGTATCACCTGGTGACTTGTC  93697       _  GGG  A
                                GACAAG CA   CA GTGATACA
                                |||||| ||   || ||||||||
                                CTGTTC GT   GT CACTATGT
                                   A  G__  C
GAM541  LOC221561 5'  CGCACCCTCTCCCCTTGTCCA  92132        C____    CAA
                                TGGACAAG    AGGG   GTG
                                ||||||||    ||||   |||
                                ACCTGTTC    TCCC   CGC
                                     CCCTC    A__
GAM541  LOC222066 5'  CACCTGCCCTGCCTGTT     92742      A       A
                                GACA GCAGGGCA GTG
                                |||| |||||||| |||
                                TTGT CGTCCCGT CAC
                                  C       C
GAM541  LOC253187 5'  TATCCTCTTGCTTACCCA    97116     AC      GCA  T
                                TGG  AAGCAGG   AG GATA
                                |||  |||||||   || ||||
                                ACC  TTCGTTC   TC CTAT
                                  CA      ___  _
GAM541  LOC253558 5'  GCGTGCCCTGCTTGTC      95673           A
                                GACAAGCAGGGCA GT
                                |||||||||||| ||
                                CTGTTCGTCCCGT CG
                                       G
GAM541  LOC257591 5'  CGCACCCTCTCCCCTTGTCCA  97842        C____    CAA
                                TGGACAAG    AGGG   GTG
                                ||||||||    ||||   |||
                                ACCTGTTC    TCCC   CGC
                                     CCCTC    A__
GAM541  LOC90139  3'  ATCACATTCCCTTGTCCA    55398       AGC    CAA
                                TGGACA   AGGG   GTGAT
                                ||||||   ||||   |||||
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                                ACCTGT  TCCC  CACTA
                                   ___   TTA
GAM541  LOC90750  3'  CACAGCCCTGCCCTGCC    63918   A  A_     AA
                                GG CA  GCAGGGC  GTG
                                || ||  |||||||  |||
                                CC GT  CGTCCCG  CAC
                                 _ CC      A_
GAM541  LOC91040  5'  GTCTCTGCCCTGCTGCCCA   64722    ACA       A T
                                TGG   AGCAGGGCA G GAT
                                |||   ||||||||| | |||
                                ACC   TCGTCCCGT C CTG
                                  CG_       _ T
GAM541  LOC91574  3'  CACTGCACTCCACCTGTCCA  66519      AGCA_ _   A
                                TGGACA    GG GCA GTG
                                ||||||    || ||| |||
                                ACCTGT    TC CGT CAC
                                   CCACC  A  _
GAM542  ARHGEF12  3'  GCCTGTAATTAATTTTCCTGTC 31000       TAACTGGC
           A                     TGACAGG       TTACAGGC
                                |||||||       ||||||||
                                ACTGTCC       AATGTCCG
                                    TTTTAATT
GAM542  CDKN2B    3'  GCCTGTAAGCCTGCAAGCCTGT 54355       AACT_
           C                     GACAGGT    GGCTTACAGGC
                                |||||||    ||||||||||
                                CTGTCCG    CCGAATGTCCG
                                    AACGT
GAM542  HSF2BP    3'  CCTGTAGGTTCACCT      22860     AACT
                                AGGT   GGCTTACAGG
                                ||||   ||||||||||
                                TCCA   TTGGATGTCC
                                  C___
GAM542  LHCGR     3'  CCTGTAAAAAAAAATTACCTGT 4070        CTGGC__
                                ACAGGTAA      TTACAGG
                                ||||||||      |||||||
                                TGTCCATT      AATGTCC
                                    AAAAAAA
GAM542  NOS1      5'  GCCTTGTCAGCACCTGTCA   5250        AA    TTAC
                                TGACAGGT  CTGGC   AGGC
                                |||||||  |||||   ||||
                                ACTGTCCA  GACTG   TCCG
                                    C_    T___
GAM542  ARHGEF3   3'  GCCTGCATCTTACCTGT    38956       CTG  TTAC
                                ACAGGTAA   GC   AGGC
                                ||||||||   ||   ||||
                                TGTCCATT   CG   TCCG
                                    CTA  ____
GAM542  C9orf16   3'  GGCCTACCTGGGCCAGCCCCC  44115    TAA      C__
                                GG   CTGGCTTA   AGGCC
                                ||   ||||||||   |||||
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                                CC  GACCGGGT  TCCGG
                                 CCC      CCA
GAM542  DKFZP434H132 3'  GGCCTGCTGTGAGCCACCTGCC 31321      AC       ___
           T                      AGGTA  TGGCTTACA  GGCC
                                  |||||  |||||||||  ||||
                                  TCCGT  ACCGAGTGT  CCGG
                                    CC       CGT
GAM542  FLJ10193  3'  CCTGTAGCCACCTGTCA    35883       AACT   T
                                  TGACAGGT   GGCT ACAGG
                                  ||||||||   |||| |||||
                                  ACTGTCCA   CCGA TGTCC
                                       ____   _
GAM542  FLJ14816  3'  CCGGTCCAATTGCCTGTCA   51634        C  CTT  A
                                  TGACAGGTAA TGG  AC GG
                                  ||||||||||| |||  || ||
                                  ACTGTCCGTT ACC  TG CC
                                        A  ___  G
GAM542  FLJ20313  3'  CCTGTAAAATGGATCTGTCA  34931       AA  GC
                                  TGACAGGT  CTG  TTACAGG
                                  ||||||||  |||  |||||||
                                  ACTGTCTA  GGT  AATGTCC
                                       __  AA
GAM542  FLJ20507  3'  CCTGTAAGCCTCCTGT    35281      TAACT
                                  ACAGG    GGCTTACAGG
                                  |||||    ||||||||||
                                  TGTCC    CCGAATGTCC
                                    T____
GAM542  FLJ20507  3'  CCTGTAAGCCTCCTGT    60216      TAACT
                                  ACAGG    GGCTTACAGG
                                  |||||    ||||||||||
                                  TGTCC    CCGAATGTCC
                                    T____
GAM542  KIAA1266  3'  CCACCGGGTCAGTCCCCTGCCA 66115    A   TA      ACA
                                  TG CAGG  ACTGGCTT   GG
                                  || ||||  ||||||||   ||
                                  AC GTCC  TGACTGGG   CC
                                   C   CC       CCA
GAM542  RAI1     3'  GGCCCGGGCCAGTCCCTGCCA  60326    A   TA      ACA
                                  TG CAGG  ACTGGCTT   GGCC
                                  || ||||  ||||||||   ||||
                                  AC GTCC  TGACCGGG   CCGG
                                   C   C_       C__
GAM542  SEC14L1   3'  GGCCTGTGCTGTGATCACCTG  11504      A___  T   TT
                                  CAGGT    AC GGC  ACAGGCC
                                  |||||    || |||  |||||||
                                  GTCCA    TG TCG  TGTCCGG
                                    CTAG  _   __
GAM542  LOC121793 5'  CCTGATGCCAGCCATCTGTCA  74113        AA    TTA
                                  TGACAGGT  CTGGC   CAGG
                                  ||||||||  |||||   ||||
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                                ACTGTCTA  GACCG   GTCC
                                    CC    TA_
GAM542  LOC145955 5'  GCCTGTGAAGAGCACCTGTCA  83593       AACTG   ___
                                TGACAGGT    GCTT   ACAGGC
                                ||||||||    ||||  ||||||
                                ACTGTCCA    CGAG   TGTCCG
                                    _____   AAG
GAM542  LOC150960 5'  GCCTGAGATAAACCACCTGTCA 80063       AACT  C  ___
                                TGACAGGT    GG TTA   CAGGC
                                ||||||||    || |||   |||||
                                ACTGTCCA    CC AAT   GTCCG
                                    ____  A   AGA
GAM542  LOC220038 5'  GGCTTGAGCCATATCACCTGTC 91722       AAC_    TA
          A                      TGACAGGT    TGGCT  CAGGCC
                                ||||||||    |||||  ||||||
                                ACTGTCCA    ACCGA  GTTCGG
                                    CTAT    __
GAM542  LOC222161 5'  CCTGTACAGTGAGGTACCTGTC 92795        A  G  _
          A                      TGACAGGTA CT GCT TACAGG
                                |||||||||  || ||| ||||||
                                ACTGTCCAT GA TGA ATGTCC
                                     G  G   C
GAM542  LOC91115  3'  GCCTATAACAACCTGTCA    64938        AAC  GC   C
                                TGACAGGT   TG  TTA AGGC
                                ||||||||   ||  ||| ||||
                                ACTGTCCA   AC  AAT TCCG
                                    ___  __   A
GAM543  AQP3      3'  ATCCACTGACTGTCCAAGGGC  59588     ATTTA  AA_
                                GCCC    GA   TCAGTGGAT
                                ||||    ||   |||||||||
                                CGGG    CT   AGTCACCTA
                                  AAC__  GTC
GAM543  CADPS     3'  ATCCACTGATTTCCTGATG   65206     TA
                                CATT  GAAATCAGTGGAT
                                ||||  ||||||||||||
                                GTAG  CTTTAGTCACCTA
                                  TC
GAM543  RALB      3'  TCCACCGATTTTTTGGGT    11246      TTT      A
                                GCCCA   AGAAATC GTGGA
                                |||||   ||||||| |||||
                                TGGGT   TTTTTAG CACCT
                                   ___      C
GAM543  SH3BP2    3'  TCACCCCTAAGTGGGCTG    11611          AAATCA
                                CAGCCCATTTAG     GTGG
                                ||||||||||||     ||||
                                GTCGGGTGAATC     CACT
                                      CC____
GAM543  SOCS5     3'  CCAGATTTTCTAAATAGGC   25796     C       TCAG
                                GCC ATTTAGAAA    TGG
                                ||| |||||||||    |||
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                                CGG TAAATCTTT   ACC
                                  A       TAG_
GAM543  C20orf175 5'  TTTACCTCTAAATGAGGT   55068    _      AATCA
                                GCC CATTTAGA   GTGGA
                                ||| ||||||||    |||||
                                TGG GTAAATCT   CATTT
                                  A       C____
GAM543  DKFZP434O047 5'  CCACTGATTTGAAAACTG   31509    CCCA  AG
                                CAG   TTT  AAATCAGTGG
                                |||   |||  ||||||||||
                                GTC   AAA  TTTAGTCACC
                                  _____  AG
GAM543  DKFZp586H0623 3'  CCACTGATTCAGAAATG    34068      AGA
                                CATTT   AATCAGTGG
                                |||||   |||||||||
                                GTAAA   TTAGTCACC
                                   GAC
GAM543  DNAJA3   3'  TCCACTGGAAACTAGGC    60487    CATT   AAA
                                GCC   TAG   TCAGTGGA
                                |||   |||   ||||||||
                                CGG   ATC   GGTCACCT
                                  _____  AAA
GAM543  KIAA0256  3'  CTGATTTCTAAATAAGCTG   64419     CC
                                CAGC  ATTTAGAAATCAG
                                ||||  ||||||||||||
                                GTCG  TAAATCTTTAGTC
                                  AA
GAM543  KIAA1199  3'  ATCCACTGATATCCATGATGCT 72509     C_   TTA  A
           G                     CAGC  CAT   GA ATCAGTGGAT
                                ||||  |||   || ||||||||||
                                GTCG  GTA   CT TAGTCACCTA
                                  TA   C__  A
GAM543  KIAA1671  3'  CCATTCTAAATGGAGT      65668    _      AATCA
                                GC CCATTTAGA    GTGG
                                || |||||||||    ||||
                                TG GGTAAATCT    TACC
                                 A       _____
GAM543  LGI2     3'  TGTATTTCCAAATGGGC     36401         A    _
                                GCCCATTT GAAAT CA
                                |||||||| ||||| ||
                                CGGGTAAA CTTTA GT
                                     C    T
GAM543  PCDH19   3'  ATCCACTGATCTCTAA      63696      A
                                TTAGA ATCAGTGGAT
                                ||||| ||||||||||
                                AATCT TAGTCACCTA
                                   C
GAM543  PDE4DIP   3'  ATCTCATCTCCTAAATGGACTG 27688     C       AAATCA  _
                                CAG CCATTTAG     GTG GAT
                                ||| ||||||||     ||| |||
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                                GTC GGTAAATC     TAC CTA
                                  A       CTC___   T
GAM543  LOC150481 3'  ATCCACTGACCCTGGGGC    79881     ATT   AAA
                                GCCC   TAG   TCAGTGGAT
                                ||||   |||   |||||||||
                                CGGG   GTC   AGTCACCTA
                                  ___   CC_
GAM543  LOC157247 5'  CCACCCCTAAATGGAGC     81361    _      AAATCA
                                GC CCATTTAG     GTGG
                                || ||||||||     ||||
                                CG GGTAAATC     CACC
                                 A       CC____
GAM543  LOC158191 3'  ATCCACTGACCCTGGGGC    81771     ATT   AAA
                                GCCC   TAG   TCAGTGGAT
                                ||||   |||   |||||||||
                                CGGG   GTC   AGTCACCTA
                                  ___   CC_
GAM543  LOC253962 5'  TCCCCTCCAGATGGGCTG    96660         A  AATCA T
                                CAGCCCATTT GA     G GGA
                                |||||||||| ||     | |||
                                GTCGGGTAGA CT     C CCT
                                      C  _____ C
GAM543  LOC55885  3'  CCAGCTATTTTAAATGAGCTG  37815     C        ATC  _
                                CAGC CATTTAGAA   AG TGG
                                |||| |||||||||   || |||
                                GTCG GTAAATTTT   TC ACC
                                  A        A__  G
GAM543  LOC90190  3'  ATCCTGTGCCCTAAGTGGGC   61773         AAAT  GT
                                GCCCATTTAG    CA  GGAT
                                ||||||||||    ||  ||||
                                CGGGTGAATC    GT  CCTA
                                      CC__  GT
GAM544  B4GALT1   3'  CTTCGGTCCTAAAGCCT     7670       GCC  _
                                AGGCT   AGG TCGAAG
                                |||||   ||| ||||||
                                TCCGA   TCC GGCTTC
                                   AA_   T
GAM544  CASP8     5'  ACTTCTTCCTGGGAGCCTT    52918       G     TCG
                                AAGGCT CCAGG   AAGAAGT
                                |||||| |||||   |||||||
                                TTCCGA GGTCC   TTCTTCA
                                   G    ___
GAM544  CASP8     5'  ACTTCTTCCTGGGAGCCTT    52941       G     TCG
                                AAGGCT CCAGG   AAGAAGT
                                |||||| |||||   |||||||
                                TTCCGA GGTCC   TTCTTCA
                                   G    ___
GAM544  GPR30     5'  GGACCCCTTCGGCCTGGACAGC 7695        _         AA
            C                    GGCTG CCAGGTCGAAG  GTCC
                                |||||| ||||||||||  ||||
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                                CCGAC GGTCCGGCTTC  CAGG
                                   A          CC
GAM544  ICA1     3'  ACTTCTCACACTATGGCAGCC  42254         _  CGA
                                GGCTGCCA GGT   AGAAGT
                                |||||||| |||   ||||||
                                CCGACGGT TCA   TCTTCA
                                    A   CAC
GAM544  ITGA11   3'  GGACTCCCGGAGCCTGTGCAGC 24205         _    CGAAGA
              CTT                  AAGGCTGC CAGGT     AGTCC
                                |||||||| |||||     |||||
                                TTCCGACG GTCCG     TCAGG
                                    T     AGGCCC
GAM544  JPH2     5'  GGACTTCTTGGAAGGCAGACTT 94450     G    AGG  G
                                AAG CTGCC   TC AAGAAGTCC
                                ||| |||||   || |||||||||
                                TTC GACGG   AG TTCTTCAGG
                                  A    A__  G
GAM544  LBX1     3'  GGACTCGGCTCCTGGCAGCC   21632          TCGAA  A
                                GGCTGCCAGG    GA GTCC
                                ||||||||||    || ||||
                                CCGACGGTCC    CT CAGG
                                     TCGG_  _
GAM544  NRXN3    5'  GAACTCTTCCACCTGCAGCC   57278       C   C    AG
                                GGCTGC AGGT GAAGA  TC
                                |||||| |||| |||||  ||
                                CCGACG TCCA CTTCT  AG
                                   _   C    CA
GAM544  PIK3R3   5'  GACTTCTCCGGCCGGCCC    61058    CT  A    A
                                GG  GCC GGTCG AGAAGTC
                                ||  ||| ||||| |||||||
                                CC  CGG CCGGC TCTTCAG
                                 __  _    C
GAM544  PLXNA2   3'  GACCAGACACCTGGCAGCC   47209          CGAAGAA
                                GGCTGCCAGGT      GTC
                                ||||||||||      |||
                                CCGACGGTCCA      CAG
                                      CAGAC__
GAM544  PSMD9    3'  ACTCTATTTGACCTGACAGCC  10979      C        GA_
                                GGCTG CAGGTCGAA   AGT
                                ||||| |||||||||   |||
                                CCGAC GTCCAGTTT   TCA
                                   A        ATC
GAM544  ZNF10    3'  ACTACGAGGAACATGGCAGCCT 31175         GG_  GAAGA
                                AGGCTGCCA   TC    AGT
                                |||||||||   ||    |||
                                TCCGACGGT   AG    TCA
                                     ACA  GAGCA
GAM544  ZNF180   5'  ACTTAACCCCCAGCGGCCTT   25135        CA  TCGAAG
                                AAGGCTGC  GG     AAGT
                                ||||||||  ||     ||||
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                                TTCCGGCG  CC     TTCA
                                    AC  CCAA__
GAM544  ART5     3'  GGACCCAGCCCTAGCAGCCTT  53815        C   TCGAAGAA
                                AAGGCTGC AGG       GTCC
                                |||||||| |||       ||||
                                TTCCGACG TCC       CAGG
                                    A   CGACC___
GAM544  DKFZp434I1117 5'  ACTTCCGACTCTGGCAGC    62156        _   AA
                                GCTGCCAG GTCG  GAAGT
                                |||||||| ||||  |||||
                                CGACGGTC CAGC  CTTCA
                                    T   __
GAM544  FLJ14327  3'  GACCCGGCATGACAGCC     46137      C  G    AAGAA
                                GGCTG CA GTCG     GTC
                                ||||| || ||||     |||
                                CCGAC GT CGGC     CAG
                                   A  A    C____
GAM544  FLJ22357  5'  GACCCCCGGCGGCGGCAGCCT  42391        AG    AAGAA_
                                AGGCTGCC  GTCG     GTC
                                ||||||||  ||||     |||
                                TCCGACGG  CGGC     CAG
                                    __    GGCCCC
GAM544  FXYD3     5'  GACTCCGCCTGGCAGCC     41586          T  AAGA
                                GGCTGCCAGG CG    AGTC
                                |||||||||| ||    ||||
                                CCGACGGTCC GC    TCAG
                                     _  C___
GAM544  FXYD3     5'  GACTCCGCCTGGCAGCC     19926          T  AAGA
                                GGCTGCCAGG CG    AGTC
                                |||||||||| ||    ||||
                                CCGACGGTCC GC    TCAG
                                     _  C___
GAM544  KIAA0275  3'  GGCTCCCAACCTGGCAGTC   28682          CGAA  A
                                GGCTGCCAGGT    GA GTC
                                ||||||||||    || |||
                                CTGACGGTCCA    CT CGG
                                      ACC_  _
GAM544  KIAA0934  3'  GACTTCTCACAGCAGCC     64220       CAG  C  A
                                GGCTGC   GT GA GAAGTC
                                ||||||   || || ||||||
                                CCGACG   CA CT CTTCAG
                                   A__  _  _
GAM544  KLK7      5'  TCCTCGCCTGGCAGCC      57739          T   A
                                GGCTGCCAGG CGA GA
                                |||||||||| ||| ||
                                CCGACGGTCC GCT CT
                                     _  C
GAM544  KLK7      5'  TCCTCGCCTGGCAGCC      17299          T   A
                                GGCTGCCAGG CGA GA
                                |||||||||| ||| ||
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                                CCGACGGTCC GCT CT
                                      _  C
GAM544  NLI-IF   3'  GACTTCTGCCTTAACCAGCC  41048     CC__   CGA
                                GGCTG   AGGT  AGAAGTC
                                |||||   ||||  |||||||
                                CCGAC   TCCG  TCTTCAG
                                  CAAT   ___
GAM544  PABPC5   3'  ACTTCTTCGAAGAACACCTT  55069     C  CCAGG
                                AAGG TG    TCGAAGAAGT
                                |||| ||    ||||||||||
                                TTCC AC    AGCTTCTTCA
                                  _ AAGA_
GAM544  PB1      3'  GACTTCTTTGGGGAGCCT    36370      G  AGGT
                                AGGCT CC    CGAAGAAGTC
                                ||||| ||    ||||||||||
                                TCCGA GG    GTTTCTTCAG
                                  G ____
GAM544  PPP1R16B 3'  GACCTGCTCCCCGCAGCCTT  61386       _______
                                AAGGCTGC     CAGGTC
                                ||||||||     ||||||
                                TTCCGACG     GTCCAG
                                    CCCCTC
GAM544  PSK      3'  GGACCTCTAGACAGGCAGCCT  32362        AG   GA   A
                                AGGCTGCC  GTC  AGA GTCC
                                ||||||||  |||  ||| ||||
                                TCCGACGG  CAG  TCT CAGG
                                    A_   A_   C
GAM544  RES4-22  3'  GACTCCTTCGATTGTAGCT   13517       CA       A
                                GGCTGC  GGTCGAAG AGTC
                                ||||||  |||||||| ||||
                                TCGATG  TTAGCTTC TCAG
                                   __       C
GAM544  SLC21A12 3'  ACTTCTATTTGACCTGCAACCT 33013     C   C      __
          T                      AAGG TGC AGGTCGA  AGAAGT
                                 |||| ||| |||||||  ||||||
                                 TTCC ACG TCCAGTT  TCTTCA
                                   A  _      TA
GAM544  LOC124402 3'  ACTTCAGAGACCACGCAGCCTT 59147        CA    GAA
                                AAGGCTGC  GGTC   GAAGT
                                ||||||||  ||||   |||||
                                TTCCGACG  CCAG   CTTCA
                                    CA    AGA
GAM544  LOC148775 5'  GGACTCAGTGCCAGGCAGCCTT 84223         A  T  AA  A
                                AAGGCTGCC GG CG  GA GTCC
                                ||||||||| || ||  || ||||
                                TTCCGACGG CC GT  CT CAGG
                                    A  _  GA  _
GAM544  LOC149297 3'  GACCTCTCGGTTTGCCAGCCTT 84394       C   GT   A  A
                                AAGGCTG CAG  CGA GA GTC
                                ||||||| |||  ||| || |||
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                                TTCCGAC GTT  GCT CT CAG
                                    C   TG   _ C
GAM544   LOC149606 3'  GACCCTGCCTGGCAGGCCT   79452     _      CGA  AA
                                AGGC TGCCAGGT   AG  GTC
                                |||| ||||||||   ||  |||
                                TCCG ACGGTCCG   TC  CAG
                                  G       ___  C_
GAM544   LOC152762 3'  CTTCCGCCGGCAGCTT     80650        A   C
                                AGGCTGCC GGT GAAG
                                |||||||| ||| ||||
                                TTCGACGG CCG CTTC
                                    _  C
GAM544   LOC155435 3'  GGCCTCACCTGGCAGCC    81353          CGAA  A
                                GGCTGCCAGGT    GA GTC
                                ||||||||||    || |||
                                CCGACGGTCCA    CT CGG
                                      ____  C
GAM544   LOC163231 5'  ACTTCTTCATTCTCAACC    82433    C  CC   TC
                                GG TG  AGG  GAAGAAGT
                                || ||  |||  ||||||||
                                CC AC  TCT  CTTCTTCA
                                 A  __   TA
GAM544   LOC200058 3'  GGACCTCCCACCTCACAGCT   88558      CC    CGAA  A
                                GGCTG  AGGT    GA GTCC
                                |||||  ||||    || ||||
                                TCGAC  TCCA    CT CAGG
                                   AC    CC__  C
GAM544   LOC256586 5'  GCTCCCCGACCCGGCGGCCT   94946        A    AA  A
                                AGGCTGCC GGTCG  GA GT
                                |||||||| |||||  || ||
                                TCCGGCGG CCAGC  CT CG
                                    C    CC  _
GAM544   LOC256764 5'  GGACTTCTCTAAACAGCC    94947      CCA  TCGA
                                GGCTG   GG    AGAAGTCC
                                |||||   ||    ||||||||
                                CCGAC   TC    TCTTCAGG
                                   AAA  ____
GAM544   LOC90768  5'  GACTTCCTTACCAGCC      63955      CC   TCGAA
                                GGCTG  AGG     GAAGTC
                                |||||  |||     ||||||
                                CCGAC  TTC     CTTCAG
                                   CA   _____
GAM544   LOC93589  3'  ACTTCTTTACAAAGCC      72667      GCCAG  C
                                GGCT     GT GAAGAAGT
                                ||||     || ||||||||
                                CCGA     CA TTTCTTCA
                                  AA___  _
GAM545   CLIPR-59  3'  CACAGGCACCAGGAAACCCCAC 31368     A       A___    A
            A                    TGT GGGTTTCT    GTTT TG
                                ||| ||||||||    |||| ||
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                                ACA CCCAAAGG   CGGA AC
                                  C      ACCA   C
GAM545  KIAA1323  3'  GAACAAAAAACCCTACA    63042        CTA
                                TGTAGGGTTT  GTTT
                                ||||||||||  ||||
                                ACATCCCAAA  CAAG
                                      AAA
GAM545  KIAA1511  3'  GACCAGAAACCCCACA     70165    A     A
                                TGT GGGTTTCT GTT
                                ||| |||||||| |||
                                ACA CCCAAAGA CAG
                                  C      C
GAM545  ZNF33A    3'  CATACTACAAAAAACCCTACA  91346       CTA  T_
                                TGTAGGGTTT  GT  TATG
                                ||||||||||  ||  ||||
                                ACATCCCAAA  CA  ATAC
                                      AAA  TC
GAM545  LOC255030 5'  AAACAAAAAACCCTACA    97266        CTA
                                TGTAGGGTTT  GTTT
                                ||||||||||  ||||
                                ACATCCCAAA  CAAA
                                      AAA
GAM545  LOC90317  5'  TGGACAGAAACCCTACA    62256         A
                                TGTAGGGTTTCT GTTTA
                                |||||||||||| |||||
                                ACATCCCAAAGA CAGGT
                                           _
GAM546  BAALC     3'  GACCGTCTTACCTGGCAGCA  45664       ATA    T
                                TGCTGCCAG  AGGAC GTC
                                |||||||||  ||||| |||
                                ACGACGGTC  TTCTG CAG
                                     CA_    C
GAM546  CYP39A1   3'  GCACTACCCCACCTGGCAGCA 33446       ATAA  ACT  C
                                TGCTGCCAG   GG  GT GC
                                |||||||||   ||  || ||
                                ACGACGGTC   CC  CA CG
                                     CACC  AT_  _
GAM546  DSCR4     3'  ACAGCCATAATGGCAGCAT   19637       GA  A  A
                                ATGCTGCCA  TA GG CTGT
                                |||||||||  || || ||||
                                TACGACGGT  AT CC GACA
                                     A_  A  _
GAM546  EGLN2     5'  ACAGCTCATGTGGCAGCA    34092       G  AA GA
                                TGCTGCCA AT  G  CTGT
                                |||||||| ||  |  ||||
                                ACGACGGT TA  C  GACA
                                    G  __ TC
GAM546  EVC       3'  GCAGGCCCTCTGGCAGCA    27297        TAA  A
                                TGCTGCCAGA  GG CTGT
                                ||||||||||  || ||||
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                                ACGACGGTCT   CC GACG
                                     C__  G
GAM546  NCALD    3'  GCAGCCCATTGACAGCAT    49374       C   ATAA  A
                                ATGCTG CAG    GG CTGT
                                |||||| |||    || ||||
                                TACGAC GTT    CC GACG
                                   A   AC__  _
GAM546  NFIA     3'  CCTATCTGGCATCAT      70367     C       A
                                ATG TGCCAGATA GG
                                ||| ||||||||| ||
                                TAC ACGGTCTAT CC
                                  T       _
GAM546  PFN2     3'  CCTTATCTGGCAACAT      53825     C
                                ATG TGCCAGATAAGG
                                ||| ||||||||||||
                                TAC ACGGTCTATTCC
                                  A
GAM546  PFN2     3'  CCTTATCTGGCAACAT      10526     C
                                ATG TGCCAGATAAGG
                                ||| ||||||||||||
                                TAC ACGGTCTATTCC
                                  A
GAM546  PSD      5'  GCTCGGCCCTACCTGGCAGC   10930        A  A  A   TC
                                GCTGCCAG TA GG CTG  GC
                                |||||||| || || |||  ||
                                CGACGGTC AT CC GGC  CG
                                     C  C  _   T_
GAM546  RUNX3    3'  ACACTCCCCATCAGGCAGCAT  15108        A   AA   C
                                ATGCTGCC GAT  GGA TGT
                                |||||||| |||  ||| |||
                                TACGACGG CTA  CCT ACA
                                     A   CC   C
GAM546  CAPN6    3'  GCGACAGTCCTATCTAGACATC 26606     C  CC_    A
           AT                     ATG TG   AGATA GGACTGTCGC
                                ||| ||   ||||| ||||||||||
                                TAC AC   TCTAT CCTGACAGCG
                                  T  AGA    _
GAM546  CITED1   5'  ACAGCTCCAGCTGGCAGCAT   14728          ATAA   _
                                ATGCTGCCAG    GGA CTGT
                                ||||||||||    ||| ||||
                                TACGACGGTC    CCT GACA
                                     GA__   C
GAM546  CNNM4    3'  GCGCTGTAGCTTATCTGACAAC 39481    C  C       G_  T T
           G                      TG TG CAGATAAG  AC G CGC
                                || || ||||||||  || | |||
                                GC AC GTCTATTC  TG C GCG
                                 A  A       GA  T _
GAM546  FLJ12132 3'  CCTTGCCTTCCCGGCAGCAT   46468         _____  A
                                ATGCTGCC    AG TAAGG
                                ||||||||    || |||||
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                                TACGACGG   TC GTTCC
                                    CCCT  C
GAM546  FLJ32430  3'  GATGTTTCTGGCAGCA     58324         TAAG   T
                                TGCTGCCAGA   GAC GTC
                                ||||||||||   ||| |||
                                ACGACGGTCT   TTG TAG
                                     _____  _
GAM546  HSC3    3'  CGACAGTCCGGGTAACAT    59068    C   AGATAA
                                ATG TGCC     GGACTGTCG
                                ||| ||||     |||||||||
                                TAC ATGG     CCTGACAGC
                                  A   G_____
GAM546  KIAA0964  3'  CGACAGTCCAAGGGCAGC    29761       AGATAA
                                GCTGCC     GGACTGTCG
                                ||||||     |||||||||
                                CGACGG     CCTGACAGC
                                   GAA___
GAM546  KIAA1229  3'  GCAACCTGTCTTTATCTAAAGC 62066      GCC        T_  C
            AT                    ATGCT   AGATAAGGAC  GT GC
                                |||||   ||||||||||  || ||
                                TACGA   TCTATTTCTG  CA CG
                                   AA_        TC  A
GAM546  KIAA1941  3'  GCAGCTACATCTGGCAGCA   74839          AA  A
                                TGCTGCCAGAT  GG CTGT
                                ||||||||||  || ||||
                                ACGACGGTCTA  TC GACG
                                      CA  _
GAM546  NGEF    5'  TCCTCTCTGGCAGCA      69164          TA
                                TGCTGCCAGA  AGGA
                                |||||||||  ||||
                                ACGACGGTCT  TCCT
                                      C_
GAM546  SLC12A5   3'  GTCCCCATCTGGCAGC     40387          AA
                                GCTGCCAGAT  GGAC
                                |||||||||  ||||
                                CGACGGTCTA  CCTG
                                      CC
GAM546  LOC144512 3'  GCAATCTTTATCTAGCTACA   83116    CT  C       C
                                TG  GC AGATAAGGA TGT
                                ||  || |||||||| |||
                                AC  CG TCTATTTCT ACG
                                  AT  A       A
GAM546  LOC148764 5'  GTCCTCCTCATTCTGGCAGCA  78989          TA____
                                TGCTGCCAGA     AGGAC
                                ||||||||||     |||||
                                ACGACGGTCT     TCCTG
                                      TACTCC
GAM546  LOC152627 5'  AGTTTATTGGCAGCAT      80626          ATAA
                                ATGCTGCCAG    GGACT
                                ||||||||||    |||||
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                                TACGACGGTT    TTTGA
                                     A___
GAM546  LOC157931 3'  GTCACAGTCCTCATCTGACAGC 86666     C    A      C
                                GCTG CAGAT AGGACTGT GC
                                |||| ||||| |||||||| ||
                                CGAC GTCTA TCCTGACA TG
                                  A    C       C
GAM546  LOC168512 5'  ACAGCCTCTCTGGCAGC     82711         TA   A
                                GCTGCCAGA  AGG CTGT
                                |||||||||  ||| ||||
                                CGACGGTCT  TCC GACA
                                     C_  _
GAM546  LOC200531 3'  GCAGCTCTTCCTGGCAGCA   88822         AT   GA
                                TGCTGCCAG  AAG  CTGT
                                |||||||||  |||  ||||
                                ACGACGGTC  TTC  GACG
                                     C_  TC
GAM546  LOC219612 5'  GCATTCCCTGGCAGTA      94280         ATAA   C
                                TGCTGCCAG    GGA TGT
                                |||||||||    ||| |||
                                ATGACGGTC    CCT ACG
                                     ____  T
GAM546  LOC254143 3'  GCAATCTTTATCTAGCTACA   96498    CT  C       C
                                TG  GC AGATAAGGA TGT
                                ||  || |||||||| |||
                                AC  CG TCTATTTCT ACG
                                 AT  A       A
GAM546  LOC254967 5'  GCGACAGTGGCCTCACAGCA   96265      CCAGATA   __
                                TGCTG      AGG  ACTGTCGC
                                |||||      |||  ||||||||
                                ACGAC      TCC  TGACAGCG
                                   AC_____   GG
GAM546  LOC93589  3'  GCAACAACCCTGTGAGGGCAGT 72670        AGATA   AC   C
            AT                    ATGCTGCC     AGG  TGT GC
                                |||||||     |||  ||| ||
                                TATGACGG     TCC  ACA CG
                                     GAGTG   CA   A
GAM547  AGL      5'  CCCAGCTGCCTCGGCGCT    5347     A    GA
                                AG TGCTG  GCAGCTGGG
                                || |||||  |||||||||
                                TC GCGGC  CGTCGACCC
                                 _    TC
GAM547  AOAH     5'  GCCTCAGCTCCAGCATC     91117          AGCT
                                GATGCTGGAGC    GGGC
                                ||||||||||    ||||
                                CTACGACCTCG    TCCG
                                      AC__
GAM547  ARCN1    3'  CCCAGCTGCTCCTTTATT     7977       CT
                                GATG  GGAGCAGCTGGG
                                ||||  ||||||||||||
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                                TTAT  CCTCGTCGACCC
                                  TT
GAM547  BCL11A   3'  CCCTACATTCCAGCATCTT   43161          CAGCT
                                AAGATGCTGGAG    GGG
                                ||||||||||||    |||
                                TTCTACGACCTT    CCC
                                      ACAT_
GAM547  CACNB1   3'  GCCCCTCCCCAGCATC     5572        AGC  CT
                                GATGCTGG  AG  GGGC
                                ||||||||  ||  ||||
                                CTACGACC  TC  CCCG
                                    CC_  __
GAM547  CDKN2D   5'  GCCCGGCTCCCAGCCCCT   8396    AT    AGC
                                AG  GCTGG  AGCTGGGC
                                ||  |||||  ||||||||
                                TC  CGACC  TCGGCCCG
                                 CC    C__
GAM547  CLDN5    3'  CTCACTCCAGCATCT      12345         CAGC
                                AGATGCTGGAG   TGGG
                                ||||||||||    ||||
                                TCTACGACCTC   ACTC
                                      ____
GAM547  COL9A2   3'  GCCCAGCTACAGTTCCA    8488       ___
                                TGGAGC  AGCTGGGC
                                ||||||  ||||||||
                                ACCTTG  TCGACCCG
                                   ACA
GAM547  CSTA     5'  CTTTGGTTCCAGCATCCTGTC  17806     A        AGCT
                                GACA GATGCTGGAGC   GG
                                |||| ||||||||||   ||
                                CTGT CTACGACCTTG   TC
                                  C         GTT_
GAM547  EPHA8    3'  GCCCAGCTGCCCAGC      40061      A
                                GCTGG GCAGCTGGGC
                                ||||| ||||||||||
                                CGACC CGTCGACCCG
                                   _
GAM547  ISL1     5'  GCCACAGCTCCAGCATC     9366          AGC  _
                                GATGCTGGAGC  TG GGC
                                ||||||||||  || |||
                                CTACGACCTCG  AC CCG
                                     ___  A
GAM547  MXI1     3'  CCCAGCTGCCACCTCTCCATC  19901     CT__  A_
                                GATG   GG  GCAGCTGGG
                                ||||   ||  |||||||||
                                CTAC   CC  CGTCGACCC
                                  CTCT  AC
GAM547  MXI1     3'  CCCAGCTGCCACCTCTCCATC  55262     CT__  A_
                                GATG   GG  GCAGCTGGG
                                ||||   ||  |||||||||
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                                CTAC   CC  CGTCGACCC
                                  CTCT  AC
GAM547  NEU3     3'  GCCCAGCTACTCCTTTACCTGT 21849     A A  CT   C
                                ACA G TG  GGAG AGCTGGGC
                                ||| | ||  |||| ||||||||
                                TGT C AT  CCTC TCGACCCG
                                  _ C  TT   A
GAM547  NTSR1    3'  GCCTGGTCTCCAGCACCT    10295    A      CA  TG
                                AG TGCTGGAG  GC  GGC
                                || ||||||||  ||  |||
                                TC ACGACCTC  TG  CCG
                                 C       __ GT
GAM547  PRODH    3'  CCCTTAGCCTCCAGCA      32924        CA  __
                                TGCTGGAG  GCT  GGG
                                ||||||||  |||  |||
                                ACGACCTC  CGA  CCC
                                     __  TT
GAM547  ROM1     5'  GCTGACTCAGCATCCTG     4383     A      AG
                                CA GATGCTGG  CAGC
                                || ||||||||  ||||
                                GT CTACGACT  GTCG
                                 C       CA
GAM547  SERPINI1 5'  GCTCCAGCATCCCGTC      17232     AA
                                GAC  GATGCTGGAGC
                                |||  ||||||||||
                                CTG  CTACGACCTCG
                                  CC
GAM547  SPN      3'  CCAGCCTCCAGCACCTT     11919     A      CA
                                AAG TGCTGGAG  GCTGG
                                ||| ||||||||  |||||
                                TTC ACGACCTC  CGACC
                                  C       __
GAM547  TAGLN    3'  CCCAGCCTGCCCCCTATC    59634     CT  A   _
                                GATG  GG GCAG CTGGG
                                ||||  || |||| |||||
                                CTAT  CC CGTC GACCC
                                   CC  _   C
GAM547  TBX2     3'  GCCCAGCTGCTCCCCTGC    19993    T__
                                GC   GGAGCAGCTGGGC
                                ||   ||||||||||||
                                CG   CCTCGTCGACCCG
                                  TCC
GAM547  USP11    5'  CCAGGACTCCAGCACCTT    16202     A      CAG
                                AAG TGCTGGAG   CTGG
                                ||| ||||||||   ||||
                                TTC ACGACCTC   GACC
                                  C       AG_
GAM547  C20orf140 3'  CAGAAGCTCCAGCATTT     58243           AG
                                AGATGCTGGAGC  CTG
                                ||||||||||||  |||
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                                TTTACGACCTCG  GAC
                                      AA
GAM547  CRA      3'  CTGCTCCAACTCTTGTC     21971        TGC
                                GACAAGA   TGGAGCAG
                                |||||||   ||||||||
                                CTGTTCT   ACCTCGTC
                                    CA_
GAM547  DDX12    3'  GCCCAGCTGTTTGCATCCTGC  59699   A  A    TG
                                G CA GATGC  GAGCAGCTGGGC
                                | || |||||  ||||||||||||
                                C GT CTACG  TTTGTCGACCCG
                                 _ C    __
GAM547  DKFZP434O047 5'  GCCCAGATGGCAGCATCT    31513        GAG  G
                                AGATGCTG   CA CTGGGC
                                ||||||||   || ||||||
                                TCTACGAC   GT GACCCG
                                     G__  A
GAM547  DKFZP761I2123 3'  CCCAGCCTGCTTCTTGTC    48760        TGCTGG    _
                                GACAAGA     AGCAG CTGGG
                                |||||||     ||||| |||||
                                CTGTTCT     TCGTC GACCC
                                    _______    C
GAM547  FLJ10079  3'  CCTCCTCCCCATCATCTTGTC  60201         C   AGC  CT
                                GACAAGATG TGG   AG  GG
                                ||||||||| |||   ||  ||
                                CTGTTCTAC ACC   TC  CC
                                      T   CC_  CT
GAM547  FLJ10110  5'  CCCCCTCCAGCGTCCTGTC   35819     A        CAGCT
                                GACA GATGCTGGAG    GGG
                                |||| ||||||||||    |||
                                CTGT CTGCGACCTC    CCC
                                  C        C____
GAM547  FLJ12650  3'  CTCTTCGCCCAGCATCCTG   44525    A      A  AGCT
                                CA GATGCTGG GC    GGG
                                || ||||||| ||    |||
                                GT CTACGACC CG    CTC
                                 C       _ CTT_
GAM547  FLJ12788  3'  CTTGGGCTCCAGCATCTGTC   42547     A         AG TG
                                GACA GATGCTGGAGC  C  GG
                                |||| ||||||||||  |  ||
                                CTGT CTACGACCTCG  G  TC
                                  _         __ GT
GAM547  FLJ13590  5'  CCCAGCCACATTTATCCATC   45784     C_   GCA_
                                GATG  TGGA    GCTGGG
                                ||||  ||||    ||||||
                                CTAC  ATTT    CGACCC
                                  CT    ACAC
GAM547  FLJ14327  3'  CCCAGCTGCCCTCAGC     46132      _ A
                                GCTG G GCAGCTGGG
                                |||| | |||||||||
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                                CGAC C CGTCGACCC
                                  T C
GAM547  FLJ22362  3'  CCCAGCTGCCCCACATCTTG  43075       C  A
                                CAAGATG TGG GCAGCTGGG
                                ||||||| ||| |||||||||
                                GTTCTAC ACC CGTCGACCC
                                   _  C
GAM547  KIAA0773  3'  CCCAGGCTTCAGCATCT    28051          AG
                                AGATGCTGGAGC  CTGGG
                                ||||||||||||  |||||
                                TCTACGACTTCG  GACCC
                                       __
GAM547  KIAA1872  3'  GCCCAGCTGCCACGATTTGTC  62933       A  C  GA
                                GACAAG TG TG  GCAGCTGGGC
                                ||||||  ||  ||  ||||||||||
                                CTGTTT GC AC  CGTCGACCCG
                                   A  _  __
GAM547  MGC4707  3'  CCCAGCCTCCTCTCCAGCACCT 44120     A      CA___
           TG                     CAAG TGCTGGAG    GCTGGG
                                ||||  ||||||||    ||||||
                                GTTC ACGACCTC    CGACCC
                                  C       TCCTC
GAM547  MMP24   3'  CCCAGCTGCCAGCCTTCTGTC  21943     AG T   GA
                                GACA  A GCTG  GCAGCTGGG
                                ||||  | ||||  |||||||||
                                CTGT  T CGAC  CGTCGACCC
                                  CT C   __
GAM547  NMT1    3'  GCAAAGGCCCCAGCATCT    40784        A  AG  GG
                                AGATGCTGG GC  CT  GC
                                |||||||||  ||  ||  ||
                                TCTACGACC CG  GA  CG
                                     C  __  AA
GAM547  PHYHIP   3'  GCCCAGCTGCCCTCCCCTC   28611    TGCT_  A
                                GA    GG GCAGCTGGGC
                                ||    || ||||||||||
                                CT    CC CGTCGACCCG
                                 CCCCT  _
GAM547  RASSF2   3'  CCCAGCTGACAGCCTGTC    28432     AGAT   GAG
                                GACA   GCTG   CAGCTGGG
                                ||||   ||||  ||||||||
                                CTGT   CGAC   GTCGACCC
                                  C___   A__
GAM547  SES2    3'  CCCATCCCAGTATCTCATC   48808    CA       AGCAGC
                                GA  AGATGCTGG     TGGG
                                ||  |||||||||     ||||
                                CT  TCTATGACC     ACCC
                                 AC        CT____
GAM547  SLC2A10  3'  CCATCTCCAGCATCCTG    47819    A        CAGC
                                CA GATGCTGGAG    TGG
                                || ||||||||||    |||
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                                GT CTACGACCTC    ACC
                                 C         T___
GAM547  UBF-fl   3'  CCCAGCCACTGTTAGTGTC   51558         _ CA
                                GATGCTGG AG  GCTGGG
                                |||||||| ||  ||||||
                                CTGTGATT TC  CGACCC
                                    G  AC
GAM547  ZNF213   3'  GCCCAGCCACGGCACATCCTG  65100    A __    GAGCA
                                CA GA  TGCTG    GCTGGGC
                                || ||  |||||    |||||||
                                GT CT  ACGGC    CGACCCG
                                 C  AC    AC___
GAM547  LOC116150 3'  CCCAGCTACTTCCCTATT    56632      CT    C
                                GATG  GGAG AGCTGGG
                                ||||  |||| |||||||
                                TTAT  CTTC TCGACCC
                                  CC    A
GAM547  LOC128954 5'  CCCAGCTGCTCCCATC      75795      CT
                                GATG  GGAGCAGCTGGG
                                ||||  ||||||||||||
                                CTAC  CCTCGTCGACCC
                                  __
GAM547  LOC130951 3'  GCCCAGCTGCCCAGC       57144       A
                                GCTGG GCAGCTGGGC
                                ||||| ||||||||||
                                CGACC CGTCGACCCG
                                  _
GAM547  LOC144373 3'  GCCCAGCTGTTTGCATCCTGC  76820    A  A    TG
                                G CA GATGC  GAGCAGCTGGGC
                                | || |||||  ||||||||||||
                                C GT CTACG  TTTGTCGACCCG
                                 _  C    __
GAM547  LOC145501 3'  GCCCAGCTGCCCGTGTGCCT   77256    AT  _   A
                                AG  GC TGG GCAGCTGGGC
                                ||  || ||| ||||||||||
                                TC  TG GCC CGTCGACCCG
                                 CG  T   _
GAM547  LOC145676 5'  CATTGCTCCAGCATCTTTC    77337    C            C
                                A AAGATGCTGGAGCAG TG
                                | ||||||||||||||| ||
                                C TTCTACGACCTCGTT AC
                                 T             _
GAM547  LOC146712 5'  GCCCAGCTGCTCGGCTCCCTC  83719    CAA  T    G
                                GA   GA GCTG AGCAGCTGGGC
                                ||   || |||| ||||||||||
                                CT   CT CGGC TCGTCGACCCG
                                 CC_  _    _
GAM547  LOC147515 3'  CCCAGCTGCTCCAAGC       84020      _
                                GCT GGAGCAGCTGGG
                                ||| ||||||||||||
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                                CGA CCTCGTCGACCC
                                  A
GAM547   LOC148479 5'  GCCCCGCTCCAGCATC      78871          AGCT
                                GATGCTGGAGC   GGGC
                                ||||||||||   ||||
                                CTACGACCTCG   CCCG
                                      C___
GAM547   LOC148697 3'  CCCAGCTGCCTTACCTT     78922     ATGCT  A
                                AAG    GG GCAGCTGGG
                                |||    || |||||||||
                                TTC    TC CGTCGACCC
                                  CAT__  _
GAM547   LOC148709 5'  GCCCAGCTACTGCTTCACCA   78944    C      ___
                                TG TGGAGCA   GCTGGGC
                                || |||||||   |||||||
                                AC ACTTCGT   CGACCCG
                                 C      CAT
GAM547   LOC149426 3'  CCCAGCTGCCCCTGGCCTCT   84416     T  _  A
                                AGA GCT GG GCAGCTGGG
                                ||| ||| || |||||||||
                                TCT CGG CC CGTCGACCC
                                  C   T  C
GAM547   LOC149461 3'  GCCCCCTTGCCCAGCATC     79404        A    CT
                                GATGCTGG GCAG  GGGC
                                |||||||| ||||  ||||
                                CTACGACC CGTT  CCCG
                                     _    CC
GAM547   LOC149935 5'  GCCCAGCTGCTGTCTGGATC   60300     G TG  __
                                GAT C  GA  GCAGCTGGGC
                                ||| |  ||  ||||||||||
                                CTA G  CT  CGTCGACCCG
                                  _ GT  GT
GAM547   LOC149995 3'  CCCAGCTGCTCCAAGC      84842     _
                                GCT GGAGCAGCTGGG
                                ||| ||||||||||||
                                CGA CCTCGTCGACCC
                                  A
GAM547   LOC150421 3'  CCCGTTCCCAGCATC       85037        AGC   T
                                GATGCTGG   AGC GGG
                                ||||||||   ||| |||
                                CTACGACC   TTG CCC
                                     C__   _
GAM547   LOC151512 5'  CCTGCCTCCAGCATCT      85428          CA  T
                                AGATGCTGGAG  GC GG
                                ||||||||||  || ||
                                TCTACGACCTC  CG CC
                                       __ T
GAM547   LOC153346 5'  CCCAGCTGCTGACCTTGTT    86023       ATGCTGG
                                GACAAG      AGCAGCTGGG
                                ||||||      ||||||||||
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                                TTGTTC      TCGTCGACCC
                                   CAG____
GAM547  LOC154313 5'  GCCCAACTGCTCCGACCGTC  81064     C_      C
                                GATG  TGGAGCAG TGGGC
                                ||||  |||||||| |||||
                                CTGC  GCCTCGTC ACCCG
                                  CA       A
GAM547  LOC158061 3'  GCCCAGCTGCAGAAGGACCTC 81671    TG_  GGA_
                                GA   CT    GCAGCTGGGC
                                ||   ||    ||||||||||
                                CT   GG    CGTCGACCCG
                                 CCA  AAGA
GAM547  LOC158434 5'  GCCTCCTGCTCCAGCTC     86822    T        CT
                                GA GCTGGAGCAG  GGGC
                                || ||||||||||  ||||
                                CT CGACCTCGTC  TCCG
                                 _         C_
GAM547  LOC196985 5'  GCCCAGCTGCCTTTGTGATC  89663     _  T_  A
                                GAT GC  GG GCAGCTGGGC
                                ||| ||  || ||||||||||
                                CTA TG  TC CGTCGACCCG
                                  G  TT  _
GAM547  LOC196986 5'  GCCCAGCTGCCTTTGTGATC  89658     _  T_  A
                                GAT GC  GG GCAGCTGGGC
                                ||| ||  || ||||||||||
                                CTA TG  TC CGTCGACCCG
                                  G  TT  _
GAM547  LOC199986 5'  CCCGAAGCTCCAGCACCT    89902    A        AGC
                                AG TGCTGGAGC   TGGG
                                || |||||||||   ||||
                                TC ACGACCTCG   GCCC
                                 C        AA_
GAM547  LOC200575 5'  CCCAACTACTCGGGCCTC    88828    T   G   C  C
                                GA GCT GAG AG TGGG
                                || ||| ||| || ||||
                                CT CGG CTC TC ACCC
                                 C   G   A  A
GAM547  LOC220021 3'  CCACTCTCCAGCATCT      93392          C  C
                                AGATGCTGGAG AG TGG
                                |||||||||| || |||
                                TCTACGACCTC TC ACC
                                      _ _
GAM547  LOC220739 3'  GCTTCACTCCAGCACCCTGTC  92933      AGA       C__
                                GACA   TGCTGGAG   AGC
                                ||||   ||||||||   |||
                                CTGT   ACGACCTC   TCG
                                  CCC       ACT
GAM547  LOC221927 5'  GCCCAGCTGCTCCCGGCTCT   92650     T    _
                                AGA GCTGG AGCAGCTGGGC
                                ||| ||||| ||||||||||
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                                TCT CGGCC TCGTCGACCCG
                                  _    C
GAM547  LOC254439 3'  CCCAACTGCCCTTCTTGTC   94746       TGCT  A   C
                                GACAAGA   GG GCAG TGGG
                                |||||||   || |||| ||||
                                CTGTTCT   CC CGTC ACCC
                                    T___  _   A
GAM547  LOC255031 5'  CCCAGCTGTGCATC       97233      TGGA
                                GATGC   GCAGCTGGG
                                |||||   |||||||||
                                CTACG   TGTCGACCC
                                  ____
GAM547  LOC255170 3'  CCCAGCTGCCACCCCTATCT  97519      CT  A_
                                AGATG  GG  GCAGCTGGG
                                |||||  ||  |||||||||
                                TCTAT  CC  CGTCGACCC
                                   CC  AC
GAM547  LOC56961  5'  GCCCCCCTCCCCAGCGTC    62908       AGC  CT
                                GATGCTGG   AG  GGGC
                                ||||||||   ||  ||||
                                CTGCGACC   TC  CCCG
                                     CC_  CC
GAM547  LOC89919  3'  CTGAGCCACCCCAGCATCCTGC 60721    A  A      AGCA   G
                                G CA GATGCTGG    GCT GG
                                | || ||||||||    ||| ||
                                C GT CTACGACC    CGA TC
                                _ C       CCAC   G
GAM547  LOC92080  3'  CCCGACTCAGCATCCTGTC    68043     A     GAGC  C
                                GACA GATGCTG    AG TGGG
                                |||| |||||||    || ||||
                                CTGT CTACGAC    TC GCCC
                                  C      _____  A
GAM548  CHD2      3'  GGCTGGGTAATTTATAGA    7031         CCTA   AAA
                                TCTATAAA    TGC   CAGCC
                                ||||||||    |||   |||||
                                AGATATTT    ATG   GTCGG
                                     A___   G__
GAM548  GLUL      3'  GTCCACATAGGTTTAGAGA   9044      A        CAA
                                TCT TAAACCTATG   AC
                                ||| ||||||||||   ||
                                AGA ATTTGGATAC   TG
                                  G         ACC
GAM548  LCT       3'  GGCTGTTTTAAGTTTCAGA   9698      AT    C  TGC
                                TCT  AAAC TA   AAACAGCC
                                |||  |||| ||   ||||||||
                                AGA  TTTG AT   TTTGTCGG
                                  C_   A  ___
GAM548  PAICS     3'  GCCTATCCATGGTTTATAGA   21256         T   CAAACA
                                TCTATAAACC ATG     GC
                                |||||||||| |||     ||
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                                AGATATTTGG TAC     CG
                                      _  CTATC_
GAM548  PUM2     3'  GCACAACAGGTTTATAGA    31015          A___
                                TCTATAAACCT    TGC
                                ||||||||||    |||
                                AGATATTTGGA    ACG
                                     CAAC
GAM548  TCF3     3'  GGACTGTCTTGGGTTTA     70732        TGCAA   _
                                TAAACCTA     ACAG CC
                                ||||||||     |||| ||
                                ATTTGGGT     TGTC GG
                                    TC___    A
GAM548  ALDH5A1  3'  GCACTGGGTTTACAGA      6549      A       _
                                TCT TAAACCTA TGC
                                ||| |||||||| |||
                                AGA ATTTGGGT ACG
                                  C       C
GAM548  CG018    3'  TTTACATAGGTTCATAGA     53396       A       C
                                TCTAT AACCTATG AAA
                                ||||| |||||||| |||
                                AGATA TTGGATAC TTT
                                   C       A
GAM548  CLL-1    5'  GGTACAGTAGGTTTATA      56366           GCAAACA
                                TATAAACCTAT      GCC
                                ||||||||||       |||
                                ATATTTGGATG      TGG
                                      ACA____
GAM548  DKFZP434N093 3'  GCTGCTTGTCATTTATGGA    79945         CCTAT    A
                                TCTATAAA     GCAA CAGC
                                ||||||||     |||| ||||
                                AGGTATTT     TGTT GTCG
                                    AC___    C
GAM548  KIAA1434  3'  GGCTGTTTGTAGGCGTTT     69615      _  A
                                AAAC CT TGCAAACAGCC
                                |||| || ||||||||||
                                TTTG GG ATGTTTGTCGG
                                  C  _
GAM548  KIAA1668  3'  TTGCAGAGGTTTATTGA      66485     T       A
                                TC ATAAACCT TGCAA
                                || |||||||| |||||
                                AG TATTTGGA ACGTT
                                  T       G
GAM548  ZFD25    3'  GGCTGTTTGTGTTTAACTTATA 32582       ACCT_
                                TATAA     ATGCAAACAGCC
                                |||||     ||||||||||||
                                ATATT     TGTGTTTGTCGG
                                   CAATT
GAM548  LOC146784 5'  GGGCTATTTGTACTTTTTTATA 78123          CCTA      C
           GA                     TCTATAAA    TGCAAA AGCCC
                                |||||||    |||||| |||||
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                                AGATATTT   ATGTTT TCGGG
                                    TTTC     A
GAM548  LOC150157 5'  GGGCCACGGGACGGTTTATAGA 84879          TATGCAAACA
                                TCTATAAACC         GCCC
                                ||||||||||         ||||
                                AGATATTTGG         CGGG
                                     CAGGGCAC__
GAM548  LOC158237 3'  GGTTGCTCAGGTTTATA     60454          AT   AACA
                                TATAAACCT  GCA    GCC
                                |||||||||  |||    |||
                                ATATTTGGA  CGT    TGG
                                    CT   ____
GAM548  LOC196890 5'  GGGCCACGGGATGGTTTATAGA 89649          TATGCAAACA
                                TCTATAAACC         GCCC
                                ||||||||||         ||||
                                AGATATTTGG         CGGG
                                     TAGGGCAC__
GAM548  LOC221300 3'  GCTTTGAAAGGTTTATA     91927          ATG   AC
                                TATAAACCT   CAA  AGC
                                |||||||||   |||  |||
                                ATATTTGGA   GTT  TCG
                                    AA_   __
GAM548  LOC254085 5'  CTGCCAAAGTATAGGTTATAGA 96118        A      AAA__
                                TCTATAA CCTATGC     CAG
                                ||||||| |||||||     |||
                                AGATATT GGATATG     GTC
                                   _      AAACC
GAM548  LOC257017 5'  GCTGTTTGAATTATAGA     97376        ACCTATG
                                TCTATAA      CAAACAGC
                                |||||||      ||||||||
                                AGATATT      GTTTGTCG
                                   AA_____
GAM548  LOC92465  5'  GGTCACATAGTTTATAGA    69411          C    CAAACA
                                TCTATAAAC TATG     GCC
                                ||||||||| ||||     |||
                                AGATATTTG ATAC     TGG
                                    _   AC____
GAM549  CABC1     5'  GCACAAACAGACGCTC      39654      CTGGC
                                GAGC     TCTGTTTGTGC
                                ||||     ||||||||||||
                                CTCG     AGACAAACACG
                                  C____
GAM549  CEACAM5   3'  AACAGAGCAAGACTCCA     15153       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                  A  A
GAM549  F2R       3'  AACAGAGCAAGACTCCA     8831        C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  A
GAM549  FGFR2   3'  GACAGAGCGAGACTCCA     43377      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM549  FGFR2   3'  GACAGAGCGAGACTCCA     43383      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM549  FUT6    3'  GACAGAGCAAGACTCCA     3812       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  GCLM    5'  GGCGCAGACCAGGCTCCA    9026          C    TTGT  _
                                TGGAGCCTGG TCTGT   GC C
                                |||||||||| |||||   || |
                                ACCTCGGACC AGACG   CG G
                                      _   ____  A
GAM549  GPC1    3'  GGCTGCAGAGCCCGGCCCCA  9103     A  T      TTGT
                                TGG GCC GGCTCTGT   GCC
                                ||| ||| ||||||||   |||
                                ACC CGG CCGAGACG   CGG
                                  C  C      T___
GAM549  HPSE    3'  CAAACAGGCCAGGCTCCA    21890          T
                                TGGAGCCTGGC CTGTTTG
                                |||||||||| |||||||
                                ACCTCGGACCG GACAAAC
                                      _
GAM549  IFIT4   3'  AACAGAGCAAGACTCCA     70918      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM549  KCNJ5   3'  GACAGAGCGAGACTCCA     6091       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM549  LY94    3'  GACAGAGCGAGACTCCA     16705      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM549  LZTS1   3'  ACAGAGCCTGGCCCCA     40676    A  T
                                TGG GCC GGCTCTGT
                                ||| ||| ||||||||
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                                ACC CGG CCGAGACA
                                  C   T
GAM549  MSH3    3' AACAGAGCAAGACTCCA    10116      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM549  POLH    3' AACAGAGCGAGACTCCA    21461      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM549  PRKAB1  3' GCACACCACCAGGCTCCA   20736         CTC  TT
                                TGGAGCCTGG  TG  TGTGC
                                ||||||||||  ||  |||||
                                ACCTCGGACC  AC  ACACG
                                     ___  C_
GAM549  SIGLEC6 3' AACAGAGCGAGACTCCA    59925      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM549  SLC10A2 5' AGCAGAGCCAGGGCCCA    4840      AG
                                TGG  CCTGGCTCTGTT
                                |||  ||||||||||||
                                ACC  GGACCGAGACGA
                                  CG
GAM549  SNRPN   5' CAAGCAAAAACCAGGCTCCA  42991         CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM549  SNRPN   5' CAAGCAAAAACCAGGCTCCA  42998         CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM549  SNRPN   5' CAAGCAAAAACCAGGCTCCA  43005         CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM549  SNRPN   5' CAAGCAAAAACCAGGCTCCA  43013         CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM549  TNFSF11 5' CAGGAGCCAAAGCCGGGCTCCA 13512           CT_   G
                                TGGAGCCTGGCT  GTTT TG
                                ||||||||||||  |||| ||
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                                ACCTCGGGCCGA  CGAG AC
                                      AAC   G
GAM549  TSNAX    3'  GGTAACAGAGCAAGACTCCA  20002     C  G     TTG
                                TGGAG CT GCTCTGT  TGCC
                                ||||| || |||||||  ||||
                                ACCTC GA CGAGACA  ATGG
                                   A  A     ___
GAM549  UBE2L3   3'  GCCTTTGCAGAGTCAAGCTCCA 12503       C       TTGT
                                TGGAGC TGGCTCTGT   GC
                                |||||| |||||||||   ||
                                ACCTCG ACTGAGACG   CG
                                   A       TTTC
GAM549  ZNF264   3'  AACAGAGCGAGACTCCA    12738      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM549  ARNTL2   3'  GACAGAGCGAGACTCCA    39466      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM549  C22orf5  3'  GGATCAGAGCCAGACACCA   24344     AGC       TTTGTG
                                TGG  CTGGCTCTG    CC
                                |||  |||||||||    ||
                                ACC  GACCGAGAC    GG
                                  ACA       TA____
GAM549  DKFZp547C176 3'  GACAGAGCAAGACTCCA    67223      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  DKFZp564K142 3'  AACAGAGCGAGACTCCA    49522      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM549  FADS1    3'  GACAGAGCAAGACTCCA    25477      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  FLJ12298 3'  AACAGAGCGAGACTCCA    49664      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM549  FLJ14117 3'  AACAGAGCAAGACTCCA    42896      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  A
GAM549  FLJ14251  3' GGTAACAGAGCGAGACTCCA  45977      C  G     TTG
                                TGGAG CT GCTCTGT  TGCC
                                ||||| || |||||||  ||||
                                ACCTC GA CGAGACA  ATGG
                                   A  G     ___
GAM549  FLJ14327  3' AACAGAGCTAGACTCCA     46127      C
                                TGGAG CTGGCTCTGTT
                                ||||| ||||||||||
                                ACCTC GATCGAGACAA
                                   A
GAM549  FLJ14566  5' GGCCACAGAGCCAGCCCCA   51446     A  C       TT T
                                TGG GC TGGCTCTGT  G GCC
                                ||| || |||||||||  | |||
                                ACC CG ACCGAGACA  C CGG
                                  C  _       __ _
GAM549  FLJ20084  3' AACAGAGCGAGACTCCA     34511      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM549  FLJ20306  3' GACAGAGCAAGACTCCA     34917      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  FLJ20456  3' GGTAACAGAGCTAGACTCCA  35215      C       TTG
                                TGGAG CTGGCTCTGT  TGCC
                                ||||| ||||||||||  ||||
                                ACCTC GATCGAGACA  ATGG
                                   A        ___
GAM549  FLJ22054  3' AACAGAGCAAGACTCCA     94391      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM549  FLJ22393  5' AGCAGGAACCAGGCTCCA    47058         C_
                                TGGAGCCTGG  TCTGTT
                                ||||||||||  ||||||
                                ACCTCGGACC  GGACGA
                                      AA
GAM549  FLJ23598  3' GCCAAGAGCCAGCTCCA     45522       C     GTT  T
                                TGGAGC TGGCTCT  TG GC
                                |||||| |||||||  || ||
                                ACCTCG ACCGAGA  AC CG
                                   _     ___  _
GAM549  FLJ31168  3' GACAGAGCGAGACTCCA     58502      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAG
                                   A  G
GAM549  GP5       3'  GACAGAGCGAGACTCCA     15646       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM549  GTPBP5    3'  GACAGAGCAAGACTCCA     65357       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  HIC       3'  AACAGAGCGAGACTCCA     67444       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM549  ING1-like 3'  GACAGAGCGAGACTCCA     54156       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM549  KBRAS2    3'  AACAGAGCAAGACTCCA     34191       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM549  KIAA0189  3'  CAGGAGCAGAGCCAGGCCCA  28273       A          G
                                TGG GCCTGGCTCTGTTT TG
                                ||| |||||||||||||| ||
                                ACC CGGACCGAGACGAG AC
                                  _           G
GAM549  KIAA0472  3'  AGCAGAGCAAGACTCCA     71853       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACGA
                                   A  A
GAM549  KIAA0563  3'  GACAGAGCAAGACTCCA     29188       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  KIAA0565  3'  GACAGAGCAAGACTCCA     66890       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  KIAA0648  3'  CAAACAGAAGCAGGCTCCA   82651           GC
                                TGGAGCCTG  TCTGTTTG
                                |||||||||  ||||||||
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                                ACCTCGGAC  AGACAAAC
                                     GA
GAM549  KIAA0924  3'  AACAGAGCGAGACTCCA     29712      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM549  KIAA1028  3'  CAGAGCACAGGCTCCA      91934        _
                                TGGAGCCTG GCTCTG
                                ||||||||| ||||||
                                ACCTCGGAC CGAGAC
                                     A
GAM549  KIAA1719  3'  GGCCAGGGCCAGGCCCCA    68169     A        TTTGT
                                TGG GCCTGGCTCTG    GCC
                                ||| ||||||||||     |||
                                ACC CGGACCGGGAC    CGG
                                  C        _____
GAM549  KIAA1940  3'  GGTCTCAGAACCAAGGCTCCA  79988       _ C    TTTGT
                                TGGAGCCT GG TCTG    GCC
                                |||||||| || ||||    |||
                                ACCTCGGA CC AGAC    TGG
                                     A A   TC___
GAM549  LGI2      3'  CAAATCAAAGCCAGGCTC    36397        C _
                                GAGCCTGGCT TG TTTG
                                |||||||||| || ||||
                                CTCGGACCGA AC AAAC
                                     A  T
GAM549  MGC10200  3'  AACAGAGCGAGACTCCA     58980      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM549  MGC2705   5'  GCACCAAGCCAGGCTCC     51113         C  TTT
                                GGAGCCTGGCT TG  GTGC
                                |||||||||| ||  ||||
                                CCTCGGACCGA AC  CACG
                                     _  ___
GAM549  MGC4562   3'  AACAGAGCGAGACTCCA     55908      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM549  MGC4663   3'  AACAGAGCCAGACTCC      44501      C
                                GGAG CTGGCTCTGTT
                                |||| ||||||||||
                                CCTC GACCGAGACAA
                                  A
GAM549  NPTXR     3'  AACAGAGCAAGACTCCA     54171      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  A
GAM549  NPTXR    3'  AACAGAGCAAGACTCCA     26635      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM549  OR7C1    5'  AACAGAGCCAAGTCCA      82428      G C
                                TGGA C TGGCTCTGTT
                                |||| | ||||||||||
                                ACCT G ACCGAGACAA
                                  _ A
GAM549  POFUT1   3'  AACAGAGCGAGACTCCA     70462      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM549  PTK6     3'  GACAGAGCGAGACTCCA     19936      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM549  RASGRF2  3'  GCACGAAGCCAGGCTCC     61042          CTGT
                                GGAGCCTGGCT    TTGTGC
                                ||||||||||    ||||||
                                CCTCGGACCGA    AGCACG
                                           ____
GAM549  SC65     3'  GACAGAGCGAGACTCCA     21289      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM549  SNURF    3'  CAAGCAAAAACCAGGCTCCA  19052          CTC_
                                TGGAGCCTGG    TGTTTG
                                ||||||||||    ||||||
                                ACCTCGGACC    ACGAAC
                                      AAAA
GAM549  TMG4     3'  GACAGAGCAAGACTCCA     43989      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  WBSCR23  3'  GACAGAGCAAGACTCCA     46762      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  WIRE     3'  GACAGAGCCAGACTCC      78305      C
                                GGAG CTGGCTCTGTT
                                |||| ||||||||||
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                                CCTC GACCGAGACAG
                                  A
GAM549  WSB1      3'  AACAGAGCGAGACTCCA     56138      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM549  WSB1      3'  AACAGAGCGAGACTCCA     56144      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM549  LOC115704 3'  CAGCCAGAGCCAGGCCCC    73541    A        T
                                GG GCCTGGCTCTG TTG
                                || |||||||||| |||
                                CC CGGACCGAGAC GAC
                                 C         C
GAM549  LOC124220 5'  GGCACAACCAGACGCC      59146    _   T
                                GGC TCTG TTGTGCC
                                ||| |||| |||||||
                                CCG AGAC AACACGG
                                  C   C
GAM549  LOC127262 3'  GACAGAGCGAGACTCCA     76110      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM549  LOC129563 3'  AGCAGAGCAGGCCCCA      74878    A    G
                                TGG GCCTG CTCTGTT
                                ||| ||||| |||||||
                                ACC CGGAC GAGACGA
                                  C   _
GAM549  LOC129880 3'  AACAGAGCAAGACTCCA     74900      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM549  LOC143196 3'  AACAGAGCGAGACTCCA     82903      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM549  LOC144319 3'  GGCACAAACAGGCGCCCC    83057    A  CTG  T
                                GG GC   GC CTGTTTGTGCC
                                || ||   || ||||||||||
                                CC CG   CG GACAAACACGG
                                 C ___  _
GAM549  LOC145216 3'  GACAGAGCAAGACTCCA     83267      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAG
                                   A  A
GAM549  LOC145820 3'  GACAGAGCAAGACTCCA     77514      C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  LOC146227 3'  GGTCAGAGCCAGACCCC     77711    AGC       TTTGT
                                GG   CTGGCTCTG    GCC
                                ||   |||||||||    |||
                                CC   GACCGAGAC    TGG
                                 CCA       _____
GAM549  LOC146713 3'  AACAGAGCAAGACTCCA     83720      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM549  LOC147071 3'  GACAGAGCAAGACTCCA     72999      C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  LOC147649 3'  GACAGAGCGAGACTCCA     78414      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM549  LOC148936 3'  AACAGAGCAAGACTCCA     84286      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM549  LOC149803 5'  CAGGCAGAGCAAGCTCCA    79538       CTG
                                TGGAGC   GCTCTGTTTG
                                ||||||   ||||||||||
                                ACCTCG   CGAGACGGAC
                                   AA_
GAM549  LOC150299 3'  GACAGAGCAAGACTCCA     84970      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  LOC151429 3'  GACAGAGCAAGACTCCA     85353      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  LOC151904 3'  AACAGAGCGAGACTCCA     80382      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  G
GAM549  LOC158292 5'  GACAGAGCGAGACTCCA     86730      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM549  LOC162137 5'  CAAGCAGGCCAAGCCCCA    87111     A  C   T
                                TGG GC TGGC CTGTTTG
                                ||| || |||| |||||||
                                ACC CG ACCG GACGAAC
                                  C  A   _
GAM549  LOC163033 5'  CGACCAGGACCAAGCCCCA   82396     A  C   CT   T
                                TGG GC TGG  CTG TTG
                                ||| || |||  ||| |||
                                ACC CG ACC  GAC AGC
                                  C  A   AG   C
GAM549  LOC163682 3'  ACACTCAAAGCCGGGCTCCA  87020           C  TT
                                TGGAGCCTGGCT TG  TGT
                                ||||||||||| ||  |||
                                ACCTCGGGCCGA AC  ACA
                                       A  TC
GAM549  LOC200261 3'  GCACAAACCTCTGGAGGCCCA 88655     A   GGCTCT
                                TGG GCCT     GTTTGTGC
                                ||| ||||     ||||||||
                                ACC CGGA     CAAACACG
                                  _   GGTCTC
GAM549  LOC201173 3'  GACAGAGCAAGACTCCA     87329      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  LOC201182 5'  AACAGAGCAAGACTCCA     89760      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM549  LOC219627 3'  GACAGAGCGAGACTCCA     92178      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM549  LOC221543 5'  GACAGAGCAAGACTCCA     93742      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  LOC221943 5'  GACAGAGCAAGACTCCA     93989      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAG
                                   A  A
GAM549  LOC222160 5'  GACAGAGCAAGACTCCA     94127      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  LOC253039 5'  GGCTCCAAAACCAGGCTCTA   96159          CTCTG   T_
                                TGGAGCCTGG    TTTG  GCC
                                ||||||||||    ||||  |||
                                ATCTCGGACC    AAAC  CGG
                                      A____   CT
GAM549  LOC254659 3'  AAACAGAGCAAGACTCCA     95109      C  G
                                TGGAG CT GCTCTGTTT
                                ||||| || |||||||||
                                ACCTC GA CGAGACAAA
                                   A  A
GAM549  LOC256158 5'  AACATCGAGCCAGGCCCA     97639     A       __
                                TGG GCCTGGCTC  TGTT
                                ||| |||||||||  ||||
                                ACC CGGACCGAG  ACAA
                                  _       CT
GAM549  LOC256207 3'  GACAGAGCAAGACTCCA     95169      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  LOC257596 5'  GACAGAGCAAGACTCCA     97935      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM549  LOC56963  3'  GCACAAAGCCAGGCTTCA     71455          CTGT
                                TGGAGCCTGGCT   TTGTGC
                                ||||||||||||   ||||||
                                ACTTCGGACCGA   AACACG
                                      ____
GAM549  LOC91149  3'  GCTGAACCAGAGCCAGACTCCA 65079      C       _   T
                                TGGAG CTGGCTCTG TTTG GC
                                ||||| ||||||||| |||| ||
                                ACCTC GACCGAGAC AAGT CG
                                   A       C   _
GAM549  LOC91409  3'  AGGCAAGGCCAGGCCCCA     65951     A      TC
                                TGG GCCTGGC  TGTTT
                                ||| |||||||  |||||
                                ACC CGGACCG  ACGGA
                                  C      GA
GAM549  LOC91862  3'  GGTGACAGAGCGAGACTCCA   53470      C  G      TGT
                                TGGAG CT GCTCTGTT   GCC
                                ||||| || ||||||||   |||
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                                ACCTC GA CGAGACAG   TGG
                                  A  G      ___
GAM549  LOC92482  3'  AACAGAGCAAGACTCCA     69485       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                  A  A
GAM550  ADAMTS3   3'  AAGAAAAGAAACAC        26476     CT
                                GTG  TTTCTTTTCTT
                                |||  ||||||||||
                                CAC  AAAGAAAAGAA
                                 __
GAM550  ANK3      3'  AAAGAAAAGAAAACCAC     40627     C
                                GTG TTTTCTTTTCTTT
                                ||| ||||||||||||
                                CAC AAAAGAAAAGAAA
                                  C
GAM550  CCNT2     3'  AAAGAAAAGATTACTGACTGTG 54264    T     GCTTT_
           CA                     TG CACAGT     TCTTTTCTTT
                                || ||||||     ||||||||||
                                AC GTGTCA     AGAAAAGAAA
                                 _     GTCATT
GAM550  CEACAM5   3'  AAGAAAAGAAAAGAAGAC    15154     ACAGTG
                                GTC     CTTTTCTTTTCTT
                                |||     ||||||||||||
                                CAG     GAAAAGAAAAGAA
                                  AA____
GAM550  DUSP4     3'  AAAGAAAAGAAAAAGAC     7333      GC
                                GT  TTTTCTTTTCTTT
                                ||  ||||||||||||
                                CA  AAAAGAAAAGAAA
                                 GA
GAM550  DUSP4     3'  AAAGAAAAGAAAAAGAC     54051     GC
                                GT  TTTTCTTTTCTTT
                                ||  ||||||||||||
                                CA  AAAAGAAAAGAAA
                                 GA
GAM550  IRS1      3'  AAAAAAAAATGCACTGTGACA  18661          _   C
                                TGTCACAGTGC TTTT TTTT
                                |||||||||| |||| ||||
                                ACAGTGTCACG AAAA AAAA
                                       T    A
GAM550  KCNA7     3'  AAAGAAAAGAAAAAGC      49043       _
                                GCTTTT CTTTTCTTT
                                |||||| |||||||||
                                CGAAAA GAAAAGAAA
                                   A
GAM550  LILRB1    5'  AAAGAAAAGAAAAAGTGGGA  21899    G    AGTGC
                                T TCAC     TTTTCTTTTCTTT
                                | ||||     ||||||||||||
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                                A GGTG    AAAAGAAAAGAAA
                                 G   A____
GAM550  LY64     3'  AAAGAAAAGAAAAGCAT     18754
                                GTGCTTTTCTTTTCTTT
                                ||||||||||||||||
                                TACGAAAAGAAAAGAAA

GAM550  PAPPA    5'  AAAGAAAAGAAAAAAGCAAGTG 10421      AG    __
              A                  TCAC  TGCTTT  TCTTTTCTTT
                                 ||||  ||||||  ||||||||||
                                 AGTG  ACGAAA  AGAAAAGAAA
                                   A_     AA
GAM550  PAX5     5'  AAAGAAAAAAAAAAGGCAC    33632        C_
                                 GTGCTTTT  TTTTCTTT
                                 ||||||||  ||||||||
                                 CACGGAAA  AAAAGAAA
                                       AA
GAM550  RAD9     3'  AAAGAAAAGAAAAATAC     15931     C
                                 GTG TTTTCTTTTCTTT
                                 ||| ||||||||||||
                                 CAT AAAAGAAAAGAAA
                                   A
GAM550  SLC25A15 3'  AAAAGAAAAGCAATTGTAC   26505    C    _
                                 GT ACAGT GCTTTTCTTTT
                                 || ||||| ||||||||||
                                 CA TGTTA CGAAAAGAAAA
                                  _    A
GAM550  TPX1     3'  AAAGAAGAAGACTGTAACA   12377     C    GC
                                 TGT ACAGT  TTTTCTTT
                                 ||| |||||  ||||||||
                                 ACA TGTCA  AGAAGAAA
                                   A    GA
GAM550  WSX1     3'  AAAGAAAAGAAAAAAC      16729    GC
                                 GT  TTTTCTTTTCTTT
                                 ||  ||||||||||||
                                 CA  AAAAGAAAAGAAA
                                  A_
GAM550  WSX1     3'  AAAGAAAAGAAAAAACACTG   16730      C_
                                 CAGTG  TTTTCTTTTCTTT
                                 |||||  ||||||||||||
                                 GTCAC  AAAAGAAAAGAAA
                                    AA
GAM550  ANP32B   3'  AAAAAAAAGGTAGCTGTGATA  21132        _     C
                                 TGTCACAG TGCTTTT TTTT
                                 |||||||| ||||||| ||||
                                 ATAGTGTC ATGGAAA AAAA
                                       G      A
GAM550  ARHGAP5  3'  AAAGAAAAAATACACTTGACA  77067      C   CT   CT
                                 TGTCA AGTG  TTT  TTTCTTT
                                 ||||| ||||  |||  |||||||
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                                ACAGT TCAC  AAA  AAAGAAA
                                  _   AT  __
GAM550  ARNTL2   3'  AAAGAAAAGAAAAGTCT    39451    T
                                AG GCTTTTCTTTTCTTT
                                || ||||||||||||||
                                TC TGAAAAGAAAAGAAA
                                 _
GAM550  BCoR     3'  AAAGAAAGGACACTATTACA   34861     CAC   _
                                TGT   AGTG CTTTTCTTT
                                |||   |||| |||||||||
                                ACA   TCAC GGAAAGAAA
                                  TTA   A
GAM550  C20orf172 3'  AAAGAGAAGCATGCAACA    46208     CACA
                                TGT   GTGCTTTTCTTT
                                |||   ||||||||||||
                                ACA   TACGAAGAGAAA
                                  ACG_
GAM550  CENTA2   3'  AAAGAAAAAAAAATTAGCTGGA 37262      A   GC_   C
           CA                     TGTC CAGT   TTTT TTTTCTTT
                                |||| ||||   |||| ||||||||
                                ACAG GTCG   AAAA AAAAGAAA
                                  _   ATT   A
GAM550  CNNM1    3'  AAAGAAAAGAAAAGCAACCACA 39764     CACAG
                                TGT    TGCTTTTCTTTTCTTT
                                |||    ||||||||||||||||
                                ACA    ACGAAAAGAAAAGAAA
                                  CCA__
GAM550  CYorf14   3'  AGAAAAGAAAATAACT     37606     GC
                                AGT  TTTTCTTTTCT
                                |||  ||||||||||
                                TCA  AAAAGAAAAGA
                                  AT
GAM550  DKFZP434B172 3'  AAAATAGAAGCATATGACA   70034      CA      C
                                TGTCA  GTGCTTTT TTTT
                                |||||  |||||||| ||||
                                ACAGT  TACGAAGA AAAA
                                   A_      T
GAM550  DKFZp434D0513 5'  AAAGAAAGTCCACCCTGTGACA 61861        __   C_
                                TGTCACA  GTG  TTTTCTTT
                                |||||||  |||  ||||||||
                                ACAGTGT  CAC  GAAAGAAA
                                    CC   CT
GAM550  DKFZp547J036 5'  AAAAGAAAATATTTTGGCA   50124      C   C
                                TGTCA AGTG TTTTCTTTT
                                ||||| |||| |||||||||
                                ACGGT TTAT AAAAGAAAA
                                   T   _
GAM550  EFA6R    3'  AAAAAAAAAGTCTGTGACA   30976        T     C
                                TGTCACAG GCTTTT TTTT
                                |||||||| |||||| ||||
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                                ACAGTGTC TGAAAA AAAA
                                    _     A
GAM550  FLJ11996  3'  AAGAAAAGAAAACAC      46432     C
                                GTG TTTTCTTTTCTT
                                ||| ||||||||||||
                                CAC AAAAGAAAAGAA
                                 _
GAM550  KEAP1     3'  AAAGAAAAGACAGCACTG    24450       TT
                                CAGTGCT  TCTTTTCTTT
                                |||||||  ||||||||||
                                GTCACGA  AGAAAAGAAA
                                    C_
GAM550  KIAA0202  3'  AAAAGTCTGCTTTGTGACA   64365       T  TTTT
                                TGTCACAG GC    CTTTT
                                |||||||| ||    |||||
                                ACAGTGTT CG    GAAAA
                                     T  TCT_
GAM550  KIAA0871  3'  AAGAAAAGAAAAAGCA      30296       _
                                TGCTTTT CTTTTCTT
                                ||||||| ||||||||
                                ACGAAAA GAAAAGAA
                                    A
GAM550  KIAA0940  3'  AAAGAAAAGAAAAAAGGCAT   29860      ___
                                GTGCT   TTTCTTTTCTTT
                                |||||   ||||||||||||
                                TACGG   AAAGAAAAGAAA
                                   AAA
GAM550  KIAA1006  3'  AAAGAAAAAAAAAGCATGTTGTG 69870       __      C
           ATA                    TGTCACA  GTGCTTTT TTTTCTTT
                                |||||||  |||||||| ||||||||
                                ATAGTGT  TACGAAAA AAAAGAAA
                                    TG      _
GAM550  KIAA1389  3'  AAAAAAAAAAGCACTGT      69764          C
                                ACAGTGCTTTT TTTT
                                |||||||||||| ||||
                                TGTCACGAAAA AAAA
                                      A
GAM550  KIAA1674  3'  AAAGAAAGGACACTGTGA     68767       _
                                TCACAGTG CTTTTCTTT
                                |||||||| |||||||||
                                AGTGTCAC GGAAAGAAA
                                    A
GAM550  KIAA1872  3'  AAAGAAAAGAAAAGAATGGACA 62918     A  GTG
                                TGTC CA   CTTTTCTTTTCTTT
                                |||| ||   ||||||||||||||
                                ACAG GT   GAAAAGAAAAGAAA
                                   _  AA_
GAM550  MAPK6     3'  AAAGAAATGCACTAAGACA   10832     AC    T
                                TGTC  AGTGC TTTCTTT
                                ||||  ||||| |||||||
```

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                                ACAG  TCACG AAAGAAA
                                  AA    T
GAM550  MGC13198  5'  AAGAAAAAAAAGAAGTAC    51093        C__
                                GTGCTTTT   TTTTCTT
                                ||||||||   |||||||
                                CATGAAGA   AAAAGAA
                                    AAA
GAM550  NUCKS     3'  AAAGAAAAGAAAATGC      42696    _
                                GC TTTTCTTTTCTTT
                                || ||||||||||||
                                CG AAAAGAAAAGAAA
                                 T
GAM550  PCDH17    3'  AAAGAAAAAAAAAAAGGCATTG 27086      CA       C___
           GCA                    TGTCA  GTGCTTTT    TTTTCTTT
                                |||||  ||||||||    ||||||||
                                ACGGT  TACGGAAA    AAAAGAAA
                                  __       AAAA
GAM550  SCN12A    3'  AAGAAAAGAAAAGAAAC     26220    G_
                                GT  CTTTTCTTTTCTT
                                ||  ||||||||||||
                                CA  GAAAAGAAAAGAA
                                 AA
GAM550  STIP-1    3'  AAAAGAAAAAACTGGGAC    69660     A    GC
                                GTC CAGT  TTTTCTTTT
                                ||| ||||  |||||||||
                                CAG GTCA  AAAAGAAAA
                                  G    A_
GAM550  LOC113612 3'  AAAGAAAAGAAAATTAC     73083     C
                                GTG TTTTCTTTTCTTT
                                ||| ||||||||||||
                                CAT AAAAGAAAAGAAA
                                  T
GAM550  LOC115442 5'  AAAGAATTTGAGACACTGCAAC 72674     CA    _   TTCTT
           A                     TGT  CAGTG CTT     TTCTTT
                                |||  ||||| |||    ||||||
                                ACA  GTCAC GAG     AAGAAA
                                  AC    A   TTT__
GAM550  LOC125434 3'  AAAGAAAAAAAAAAAAGGTGAC 74405       AGTGC    C
           A                     TGTCAC     TTTT TTTTCTTT
                                ||||||     |||| ||||||||
                                ACAGTG     AAAA AAAAGAAA
                                   GAAA_    A
GAM550  LOC135293 3'  AAAGAAAAGAAAAGACAC     76167     _
                                GTG CTTTTCTTTTCTTT
                                ||| ||||||||||||||
                                CAC GAAAAGAAAAGAAA
                                  A
GAM550  LOC142955 3'  AAAGAAAAAAAAAGTAC      76438        C
                                GTGCTTTT TTTTCTTT
                                |||||||| ||||||||
```

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                                CATGAAAA AAAAGAAA
                                    A
GAM550  LOC157507 5'  AAAGAAAATGAGTTACACTGTA 81448    C     CTT  _
          AC                    GT ACAGTG   TTC TTTTCTTT
                                || ||||||   ||| ||||||||
                                CA TGTCAC   GAG AAAAGAAA
                                 A     ATT   T
GAM550  LOC158677 5'  AAAAAAAGGGGGCTGTACA   86886    C    G    C
                                TGT ACAGT CTTTT TTTT
                                ||| ||||| ||||| ||||
                                ACA TGTCG GGGAA AAAA
                                  _    G    A
GAM550  LOC170372 3'  AAAGAAATGCACTAAGACA   76360     AC    T
                                TGTC  AGTGC TTTCTTT
                                ||||  ||||| |||||||
                                ACAG  TCACG AAAGAAA
                                   AA    T
GAM550  LOC219627 3'  AAAAGAAAAGACAGTAGCA   92174    TC  A  G
                                TG  AC GT CTTTTCTTTT
                                ||  || || ||||||||||
                                AC  TG CA GAAAAGAAAA
                                 GA  A  _
GAM550  LOC221042 3'  AAAGAAAAGAGCTATGGCA   93178      C   G
                                TGTCA AGT CTTTTCTTT
                                ||||| ||| |||||||||
                                ACGGT TCG GAAAAGAAA
                                   A   A
GAM550  LOC51290  3'  AAAGAAAAGAAAACAC     69189     C
                                GTG TTTTCTTTTCTTT
                                ||| ||||||||||||
                                CAC AAAAGAAAAGAAA
                                  _
GAM551  FBXL11    3'  TTCAACAGGAAACCGATCTTCC 24578        _  GG  ATAC
          C                     GGGAAGAT GGT  CT    TGAA
                                |||||||| |||  ||    ||||
                                CCCTTCTA CCA  GG    ACTT
                                     G   AA  ACA_
GAM551  GRINL1A   3'  GTTCAGTATGTGAAACCACCAT 69517     A      C____
          TTCCC                   GGA GATGGTGG     TATACTGAAC
                                ||| ||||||||    ||||||||||
                                CCT TTACCACC     GTATGACTTG
                                  _      AAAGT
GAM551  HD        3'  TCAACATAGAGTTTGTCTTCCT 9191         TG TGG    AC
                                GGGAAGA  G   CTAT  TGA
                                |||||||  |   ||||  |||
                                TCCTTCT  T   GATA  ACT
                                    GT TGA    CA
GAM551  IL8       3'  TAGCCACCATCTTACC      94480    G
                                GG AAGATGGTGGCTA
                                || ||||||||||||
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                                CC TTCTACCACCGAT
                                 A
GAM551  LASS1    3'  TCCCTGCGGCCACCACCTCCT  41200      A A      TA  CT
                                GGGA G TGGTGGC  TA  GA
                                |||| | |||||||  ||  ||
                                TCCT C ACCACCG  GT  CT
                                  _ C      GC  CC
GAM551  PNUTL1   3'  TCAGCACCACCCCCTCCC    10675      A AT    CTATA
                                GGGA G  GGTGG    CTGA
                                |||| |  |||||    ||||
                                CCCT C  CCACC    GACT
                                  _ CC    AC___
GAM551  SUFU     3'  GTTCAGCACATCACACACCATC 32413     AA      GCTATA___
           CCC                    GGG  GATGGTG       CTGAAC
                                |||  |||||||       ||||||
                                CCC  CTACCAC       GACTTG
                                  __      ACACTACAC
GAM551  UBE4A    3'  TTCAATATTTATCATCCTCCT  16567      A       C   AC
                                GGGA GATGGTGG TAT  TGAA
                                |||| |||||||| |||  ||||
                                TCCT CTACTATT ATA  ACTT
                                  C       T  __
GAM551  VARS2    5'  AGTCTGACCATCTCCC      20848      A     __
                                GGGA GATGGT  GGCT
                                |||| ||||||  ||||
                                CCCT CTACCA  CTGA
                                  _     GT
GAM551  XK       3'  GGAGTAGCCACCAGCCTCCC   40801      AGA        A
                                GGGA   TGGTGGCTAT CT
                                ||||   |||||||||| ||
                                CCCT   ACCACCGATG GG
                                  CCG         A
GAM551  APM2     3'  CGGGCAGCCACCACCTCCT    22406      A A       ATA
                                GGGA G TGGTGGCT   CTG
                                |||| | |||||||   |||
                                TCCT C ACCACCGA   GGC
                                  _ C       CG_
GAM551  ARPP-19  3'  TCAGCACACACTGCCAGTCTTC 21803        _   TG CTATA_
           CC                     GGGAAGA TGG  G     CTGA
                                ||||||| |||  |     ||||
                                CCCTTCT ACC  C     GACT
                                   G   GT ACACAC
GAM551  DEPP     3'  TCAGTGCTACCATCCCC     22824     AA       TAT
                                GGG  GATGGTGGC   ACTGA
                                |||  |||||||||   |||||
                                CCC  CTACCATCG   TGACT
                                  __       ____
GAM551  FLJ00058 5'  CAGACCCCACCATCTCCC    78763      A       CTATA
                                GGGA GATGGTGG     CTG
                                |||| ||||||||     |||
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                                CCCT CTACCACC    GAC
                                  _      CCA__
GAM551  FLJ14810  3'  AGCACGCTGTCATCCC     51620     A     _
                                GGGA GATGGTG GCT
                                |||| ||||||| |||
                                CCCT CTGTCGC CGA
                                  A      A
GAM551  GPS1      3'  CAGTGGCACCATTTCCC     14678     A     G  AT
                                GGGA GATGGTG CT  ACTG
                                |||| ||||||| ||  ||||
                                CCCT TTACCAC GG  TGAC
                                  _     _ __
GAM551  GTPBP1    3'  TAGAACCCCATCTTCCC     15017         T  __
                                GGGAAGATGG GG  CTA
                                |||||||||| ||  |||
                                CCCTTCTACC CC  GAT
                                      _ AA
GAM551  GTPBP1    3'  TAGAACCCCATCTTCCC     15018         T  __
                                GGGAAGATGG GG  CTA
                                |||||||||| ||  |||
                                CCCTTCTACC CC  GAT
                                      _ AA
GAM551  KIAA0552  3'  AGCACATCATCTTCCT     28306         _
                                GGGAAGATGGTG GCT
                                |||||||||||| |||
                                TCCTTCTACTAC CGA
                                       A
GAM551  KIAA1344  3'  TTCAGCATTCTGCCATCTCCT  72453     A    TG CT  A
                                GGGA GATGG  G  AT CTGAA
                                |||| |||||  |  || |||||
                                TCCT CTACC  C  TA GACTT
                                  _    GT T_  C
GAM551  KIAA1464  3'  TTCAGTGAACATCTCCC     68277     A   GTGGCTA
                                GGGA GATG      TACTGAA
                                |||| ||||      |||||||
                                CCCT CTAC      GTGACTT
                                  _   AA_____
GAM551  MGC2452   5'  TAGCCACCACTTCCC      50989      A
                                GGGAAG TGGTGGCTA
                                |||||| |||||||||
                                CCCTTC ACCACCGAT
                                  _
GAM551  NCBP2     3'  CAGTATAATTTTCCC      23746        GGTGGC
                                GGGAAGAT     TATACTG
                                ||||||||     |||||||
                                CCCTTTTA     ATATGAC
                                     _______
GAM551  PLSCR3    3'  TATAGCCACCGCCCCCC     39794     AAGA
                                GGG    TGGTGGCTATA
                                |||    ||||||||||
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                                CCC   GCCACCGATAT
                                  CCC_
GAM551  PLSCR3   3'  TATAGCCACCGCCCCCC    90761    AAGA
                                GGG   TGGTGGCTATA
                                |||   ||||||||||
                                CCC   GCCACCGATAT
                                  CCC_
GAM551  POLR2D   3'  ATAACACCACCTTCCC     16654      A    GC
                                GGGAAG TGGTG  TAT
                                |||||| |||||  |||
                                CCCTTC ACCAC  ATA
                                   C    A_
GAM551  RPH3A    3'  TTCAGTAACACACCCTCCC   30247    AGAT   GCTA
                                GGGA   GGTG   TACTGAA
                                ||||   ||||   |||||||
                                CCCT   CCAC   ATGACTT
                                  C___   ACA_
GAM551  SLC5A6   3'  TTCAACATAGCCATAGTCCT  40835    AGATG     AC
                                GGGA   GTGGCTAT  TGAA
                                ||||   ||||||||  ||||
                                TCCT   TACCGATA  ACTT
                                  GA___      CA
GAM551  LOC132946 5' CAGTGTGGCACCCACCC    75073    AAGA  TG
                                GGG   TGG  GCTATACTG
                                |||   |||  |||||||||
                                CCC   ACC  CGGTGTGAC
                                  _____  CA
GAM551  LOC139422 5' TCAGTATAGCCTAGAACTCCT  75847    AGATGGT
                                GGGA     GGCTATACTGA
                                ||||     ||||||||||
                                TCCT     CCGATATGACT
                                  CAAGAT_
GAM551  LOC146822 3' TCTCCATGCCACCACCTGCCC  78154    A  A     TATACT
                                GGG AG TGGTGGC     GA
                                ||| || |||||||     ||
                                CCC TC ACCACCG     CT
                                  G  C     TACCT_
GAM551  LOC151816 5' GTCCAGCCACCATCTTCCT   85499           AT
                                GGGAAGATGGTGGCT  AC
                                ||||||||||||||  ||
                                TCCTTCTACCACCGA  TG
                                         CC
GAM551  LOC221712 5' GTTCAGGGGCCACCATCCCCC 93626    AA       ATA
                                GGG  GATGGTGGCT   CTGAAC
                                |||  ||||||||||   ||||||
                                CCC  CTACCACCGG   GACTTG
                                  C_        G__
GAM551  LOC253430 5' CAGAGCCACCATCCCCCC    96236    AA       ATA
                                GGG  GATGGTGGCT   CTG
                                |||  ||||||||||   |||
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                                CCC  CTACCACCGA   GAC
                                  CC        ___
GAM551  LOC253715 3'  TTCAGTATCCAACCATCCTCTC 96928      A     _  CT
                                GGGA GATGGT GG  ATACTGAA
                                |||| |||||| ||  ||||||||
                                CTCT CTACCA CC  TATGACTT
                                  C     A  __
GAM551  LOC90190  3'  CAGTCCATCCCACCATCACCCC 61775     AA       CTAT_
                                GGG  GATGGTGG     ACTG
                                |||  ||||||||     ||||
                                CCC  CTACCACC     TGAC
                                  CA       CTACC
GAM552  HSPA5     3'  TTGTTATTTACACTGGTCTA   18083     C     A      TG
                                TAG ACCAGT TAAATAG  A
                                ||| |||||| |||||||  |
                                ATC TGGTCA ATTTATT  T
                                  _     C       GT
GAM552  LDB3      3'  ACTACTTTATACTAGTG     76403     C      _
                                CAC AGTATAAA TAGT
                                ||| |||||||| ||||
                                GTG TCATATTT ATCA
                                  A       C
GAM552  RFX1      3'  AAATCACTATTTTGTGTGCT   11307      _  GTAT
                                AGCAC CA    AAATAGTGATTT
                                ||||| ||    ||||||||||||
                                TCGTG GT    TTTATCACTAAA
                                  T  _____
GAM552  DKFZP564D172 3'  AAATCACTATTTAATTGCCTCT 49382     CAC    A
            A                     TAG   CAGT TAAATAGTGATTT
                                |||   |||| ||||||||||||||
                                ATC   GTTA ATTTATCACTAAA
                                  TCC   _
GAM552  DKFZP586I2223 3'  ACTGTCTTCCACACTGGTGCTA 54908          ATAA___
                                TAGCACCAGT      ATAGT
                                ||||||||||      |||||
                                ATCGTGGTCA      TGTCA
                                      CACCTTC
GAM552  DKFZP586I2223 3'  ACTGTCTTCCACACTGGTGCTA 54916          ATAA___
                                TAGCACCAGT      ATAGT
                                ||||||||||      |||||
                                ATCGTGGTCA      TGTCA
                                      CACCTTC
GAM552  DKFZP586I2223 3'  ACTGTCTTCCACACTGGTGCTA 31266          ATAA___
                                TAGCACCAGT      ATAGT
                                ||||||||||      |||||
                                ATCGTGGTCA      TGTCA
                                      CACCTTC
GAM552  ELF2      3'  TCACTTAACTGGTGCTA     22501          ATAAAT
                                TAGCACCAGT     AGTGA
                                ||||||||||     |||||
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                                ATCGTGGTCA     TCACT
                                     AT_____
GAM552  FLJ20139  3'  TCACTCTGGTGCTA       34630        TATAAAT
                                TAGCACCAG      AGTGA
                                |||||||||      |||||
                                ATCGTGGTC      TCACT
                                          ________
GAM552  KIAA1622  3'  TTATTTGTACTAATGCTA    54262      CC
                                TAGCA  AGTATAAATAG
                                |||||  ||||||||||
                                ATCGT  TCATGTTTATT
                                   AA
GAM552  p25       3'  TATTTATACTGGACTA     22855     CA
                                TAG  CCAGTATAAATA
                                |||  ||||||||||||
                                ATC  GGTCATATTTAT
                                  A_
GAM552  TRAF6     3'  AAATCACTACCGCCTTGTGCTA 16093       C  TATAAA
                                TAGCAC AG     TAGTGATTT
                                |||||| ||     |||||||||
                                ATCGTG TC     ATCACTAAA
                                   T  CGCC__
GAM552  ZFP91     3'  AAATCACTACAATAGCCTAGTG 53816      C  TA  AA_
           CT                     AGCAC AG  TA   TAGTGATTT
                                |||||  ||  ||   |||||||||
                                TCGTG TC  AT   ATCACTAAA
                                   A  CG  AAC
GAM552  LOC151273 3'  TCACTTAACTGGTGCTA     67018          ATAAAT
                                TAGCACCAGT     AGTGA
                                ||||||||||     |||||
                                ATCGTGGTCA     TCACT
                                     AT_____
GAM552  LOC81034  3'  AAATCACTTATTACAGATGCTA 47838      CCA   TAAAT
                                TAGCA   GTA    AGTGATTT
                                |||||   |||    ||||||||
                                ATCGT   CAT    TCACTAAA
                                   AGA   TAT__
GAM553  ADORA1    3'  TGAGCCCTCCTTCTTGCCCTG  5429        CATTTTAAA
                                CAGGGTA        AGGGCTCA
                                |||||||        ||||||||
                                GTCCCGT        TCCCGAGT
                                    TCTTCC___
GAM553  COG5      3'  AGTTATAACATGTACCCTG    20953         T   AAAG
                                CAGGGTACAT TTA    GGCT
                                |||||||||| |||    ||||
                                GTCCCATGTA AAT    TTGA
                                     C   A___
GAM553  COL4A1    3'  GAACCCTAGAAATATATCCTG  8462        C    AAA   C
                                CAGGGTA ATTTT   AGGG TC
                                ||||||| |||||   |||| ||
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                                GTCCTAT TAAAG   TCCC AG
                                    A    A__    A
GAM553  DISC1    3'  AGCCCTTTACAGTCATATCCT  37870       CATTTTA
                                AGGGTA      AAAGGGCT
                                ||||||      ||||||||
                                TCCTAT      TTTCCCGA
                                   ACTGACA
GAM553  DLEU2    3'  TGAACCCTTTTAATGAAGACCT 20061      ACATT       C
                                GGGT    TTAAAAGGG TCA
                                ||||    ||||||||| |||
                                TCCA    AATTTTCCC AGT
                                  GAAGT       A
GAM553  EGFL4    3'  TGAGCCCTTCCTGGCACCCCTG 61821      TACATTTTAA
                                CAGGG        AAGGGCTCA
                                |||||        |||||||||
                                GTCCC        TTCCCGAGT
                                   CACGGTCC__
GAM553  MCP      3'  CTTTTTAAAACATCCCT     9965      TACA
                                AGGG   TTTTAAAAGG
                                ||||   ||||||||||
                                TCCC   AAAATTTTTC
                                  TAC_
GAM553  MKI67    3'  GTCCCCCAAAATGTGCCCTG   10048          AAAA
                                CAGGGTACATTTT   GGGC
                                ||||||||||||   ||||
                                GTCCCGTGTAAAA   CCTG
                                       CCC_
GAM553  MPV17    3'  CTCTAAAATGTACACTG     70511     G       AAA
                                CAG GTACATTTT   AGGG
                                ||| |||||||||   ||||
                                GTC CATGTAAAA   TCTC
                                  A       ___
GAM553  PACE     3'  TGAGCCCCCCCAACACTGTGCC 10400         TTTTAAAA_
            CTG                    CAGGGTACA       GGGCTCA
                                |||||||||       |||||||
                                GTCCCGTGT       CCCGAGT
                                     CACAACCCC
GAM553  PCDHA1   3'  TGAGCCCTCTTAGAGACCTCA  38186   A   ACA     A
                                C GGGT   TTTTAA AGGGCTCA
                                | ||||   |||||| ||||||||
                                A TCCA   GAGATT TCCCGAGT
                                 C   ___     C
GAM553  PCDHA1   3'  TGAGCCCTCTTAGAGACCTCA  48597   A   ACA     A
                                C GGGT   TTTTAA AGGGCTCA
                                | ||||   |||||| ||||||||
                                A TCCA   GAGATT TCCCGAGT
                                 C   ___     C
GAM553  PCDHA10  3'  TGAGCCCTCTTAGAGACCTCA  38194   A   ACA     A
                                C GGGT   TTTTAA AGGGCTCA
                                | ||||   |||||| ||||||||
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                                A TCCA  GAGATT TCCCGAGT
                                 C   ___    C
GAM553  PCDHA10  3' TGAGCCCTCTTAGAGACCTCA 49030  A  ACA   A
                                C GGGT  TTTTAA AGGGCTCA
                                | ||||  |||||| ||||||||
                                A TCCA  GAGATT TCCCGAGT
                                 C   ___    C
GAM553  PCDHA11  3' TGAGCCCTCTTAGAGACCTCA 38205  A  ACA   A
                                C GGGT  TTTTAA AGGGCTCA
                                | ||||  |||||| ||||||||
                                A TCCA  GAGATT TCCCGAGT
                                 C   ___    C
GAM553  PCDHA12  3' TGAGCCCTCTTAGAGACCTCA 38213  A  ACA   A
                                C GGGT  TTTTAA AGGGCTCA
                                | ||||  |||||| ||||||||
                                A TCCA  GAGATT TCCCGAGT
                                 C   ___    C
GAM553  PCDHA13  3' TGAGCCCTCTTAGAGACCTCA 38222  A  ACA   A
                                C GGGT  TTTTAA AGGGCTCA
                                | ||||  |||||| ||||||||
                                A TCCA  GAGATT TCCCGAGT
                                 C   ___    C
GAM553  PCDHA2   3' TGAGCCCTCTTAGAGACCTCA 38230  A  ACA   A
                                C GGGT  TTTTAA AGGGCTCA
                                | ||||  |||||| ||||||||
                                A TCCA  GAGATT TCCCGAGT
                                 C   ___    C
GAM553  PCDHA3   3' TGAGCCCTCTTAGAGACCTCA 38238  A  ACA   A
                                C GGGT  TTTTAA AGGGCTCA
                                | ||||  |||||| ||||||||
                                A TCCA  GAGATT TCCCGAGT
                                 C   ___    C
GAM553  PCDHA4   3' TGAGCCCTCTTAGAGACCTCA 38246  A  ACA   A
                                C GGGT  TTTTAA AGGGCTCA
                                | ||||  |||||| ||||||||
                                A TCCA  GAGATT TCCCGAGT
                                 C   ___    C
GAM553  PCDHA5   3' TGAGCCCTCTTAGAGACCTCA 38254  A  ACA   A
                                C GGGT  TTTTAA AGGGCTCA
                                | ||||  |||||| ||||||||
                                A TCCA  GAGATT TCCCGAGT
                                 C   ___    C
GAM553  PCDHA6   3' TGAGCCCTCTTAGAGACCTCA 38262  A  ACA   A
                                C GGGT  TTTTAA AGGGCTCA
                                | ||||  |||||| ||||||||
                                A TCCA  GAGATT TCCCGAGT
                                 C   ___    C
GAM553  PCDHA6   3' TGAGCCCTCTTAGAGACCTCA 49003  A  ACA   A
                                C GGGT  TTTTAA AGGGCTCA
                                | ||||  |||||| ||||||||
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                                A TCCA   GAGATT TCCCGAGT
                                 C   ___     C
GAM553  PCDHA7   3'  TGAGCCCTCTTAGAGACCTCA  38270   A   ACA     A
                                C GGGT   TTTTAA AGGGCTCA
                                | ||||   |||||| ||||||||
                                A TCCA   GAGATT TCCCGAGT
                                 C   ___     C
GAM553  PCDHA8   3'  TGAGCCCTCTTAGAGACCTCA  38278   A   ACA     A
                                C GGGT   TTTTAA AGGGCTCA
                                | ||||   |||||| ||||||||
                                A TCCA   GAGATT TCCCGAGT
                                 C   ___     C
GAM553  PCDHA9   3'  TGAGCCCTCTTAGAGACCTCA  49020   A   ACA     A
                                C GGGT   TTTTAA AGGGCTCA
                                | ||||   |||||| ||||||||
                                A TCCA   GAGATT TCCCGAGT
                                 C   ___     C
GAM553  PCDHAC1  3'  TGAGCCCTCTTAGAGACCTCA  38169   A   ACA     A
                                C GGGT   TTTTAA AGGGCTCA
                                | ||||   |||||| ||||||||
                                A TCCA   GAGATT TCCCGAGT
                                 C   ___     C
GAM553  PCDHAC2  3'  TGAGCCCTCTTAGAGACCTCA  38178   A   ACA     A
                                C GGGT   TTTTAA AGGGCTCA
                                | ||||   |||||| ||||||||
                                A TCCA   GAGATT TCCCGAGT
                                 C   ___     C
GAM553  ARAP3    5'  TGAGCCCTCCCTTCACCCTG  42505       ACATTTTAAA
                                CAGGGT        AGGGCTCA
                                ||||||        ||||||||
                                GTCCCA        TCCCGAGT
                                    CTTCCC____
GAM553  DKFZP566D1346 3'  TGATGTTTTTAAAATGTATCCT 48001              GG  _
          G                      CAGGGTACATTTTAAAA  GC TCA
                                 ||||||||||||||||  || |||
                                 GTCCTATGTAAAATTTT  TG AGT
                                          __  T
GAM553  FLJ10781  3'  TGAGCCCTCTCAGGAATCCTG  36637       ACA   AAA
                                CAGGGT   TTTT   AGGGCTCA
                                ||||||   ||||   ||||||||
                                GTCCTA   AGGA   TCCCGAGT
                                    ___    CTC
GAM553  KIAA0564  3'  CTTTCAAAATGTACCTT     66207           A
                                AGGGTACATTTT AAAG
                                |||||||||||| ||||
                                TTCCATGTAAAA TTTC
                                       C
GAM553  KIAA1580  5'  GGCTCCAAAATGTACCC     69446           AAAA
                                GGGTACATTTT    GGGCT
                                ||||||||||    |||||
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                                CCCATGTAAAA   CTCGG
                                      C___
GAM553  KIAA1671  3'  CCTTTAAAAATACCCTG    65671       CA   A
                                CAGGGTA  TTTT AAAGG
                                |||||||  |||| |||||
                                GTCCCAT  AAAA TTTCC
                                   __   A
GAM553  MGC5149   3'  TTTTAAAATGACCCTG     72302       A
                                CAGGGT CATTTTAAAA
                                |||||| ||||||||||
                                GTCCCA GTAAAATTTT
                                   _
GAM553  TM4SF3    3'  CCCCTTTAAAATGTTGCTTT  16066       _       A
                                AGGGTA CATTTTAAA GGG
                                |||||| ||||||||| |||
                                TTTCGT GTAAAATTT CCC
                                    T        C
GAM553  LOC112687 3'  GCCTCTAAAATGTATCCTG   72861            AAA
                                CAGGGTACATTTTA   GGGC
                                ||||||||||||||   ||||
                                GTCCTATGTAAAAT   TCCG
                                      C__
GAM553  LOC153642 3'  CCCTGGATGTACCT       80906          TAAA
                                GGGTACATTT    AGGG
                                |||||||||    ||||
                                TCCATGTAGG    TCCC
                                    _____
GAM553  LOC163682 3'  AGCCCTTTTGGTCACC     87021     ACATT
                                GGT    TTAAAAGGGCT
                                |||    ||||||||||
                                CCA    GGTTTTCCCGA
                                  CT___
GAM553  LOC200261 5'  TGAGCCCTTGGCATGTAACCC  88658     _   TTTAA
                                GGGT ACAT    AAGGGCTCA
                                |||| ||||    |||||||||
                                CCCA TGTA    TTCCCGAGT
                                   A   CGG__
GAM553  LOC200734 3'  GCTTTAAAATGTACCGTG    88864    G         AAG
                                CA GGTACATTTTAA   GGC
                                || ||||||||||||   |||
                                GT CCATGTAAAATT   TCG
                                  G          ___
GAM553  LOC205100 5'  TGAGCCCTCCCCTGGTCCCTG  90699      T  ATTTTAAA
                                CAGGG AC       AGGGCTCA
                                ||||| ||       ||||||||
                                GTCCC TG       TCCCGAGT
                                   _  GTCCCC__
GAM553  LOC83468  3'  CCCTTAAAATATTCCCTG    48516      TAC     AA
                                CAGGG   ATTTTA  AGGG
                                |||||   ||||||  ||||
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                                GTCCC  TAAAAT  TCCC
                                  TTA    __
GAM554  A1BG    3'  CAGGGTCTCACTGTGTTGC   55413       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM554  ACPT    3'  CACCCCGCCATATGCTGC   54986    ACA      TTT
                                GCA  CATATGGC  GTG
                                |||  ||||||||  |||
                                CGT  GTATACCG  CAC
                                  C__      CCC
GAM554  ACPT    3'  CACCCCGCCATATGCTGC   54980    ACA      TTT
                                GCA  CATATGGC  GTG
                                |||  ||||||||  |||
                                CGT  GTATACCG  CAC
                                  C__      CCC
GAM554  AHCY    3'  CACAAAGCCCATGTGTTTTGC  5473      C      _
                                GCAA ACATATGG CTTTGTG
                                |||| |||||||| |||||||
                                CGTT TGTGTACC GAAACAC
                                  T       C
GAM554  BCL7A   3'  CAGGATTCCATTTGTGTTGCT  40638        T   CT  G
                                AGCAACACA ATGG  TT TG
                                ||||||||| ||||  || ||
                                TCGTTGTGT TACC  AG AC
                                     T   TT  G
GAM554  CDK5R2  3'  CACAAAGCCACCGCCGCTGTT  14132     ACACATA
                                AGCA     TGGCTTTGTG
                                ||||     ||||||||||
                                TTGT     ACCGAAACAC
                                  CGCCGCC
GAM554  CHC1    3'  CACAAAGCATACTCTTGC    7019     CACA   G
                                GCAA   TATG CTTTGTG
                                ||||   |||| |||||||
                                CGTT   ATAC GAAACAC
                                  CTC_   _
GAM554  CIT     3'  CACAAGGCATCTGTTGCT    69741       CATATG
                                AGCAACA    GCTTTGTG
                                |||||||    ||||||||
                                TCGTTGT    CGGAACAC
                                   CTA___
GAM554  COL6A2  5'  CAGGGCCACAGGTGCTGC    8480     A  ATA
                                GCA CAC  TGGCTTTG
                                ||| |||  ||||||||
                                CGT GTG  ACCGGGAC
                                  C  GAC
GAM554  COL6A2  5'  CAGGGCCACAGGTGCTGC    54168    A  ATA
                                GCA CAC  TGGCTTTG
                                ||| |||  ||||||||
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                                CGT GTG   ACCGGGAC
                                  C   GAC
GAM554   EYA1     3'  CACAGCGTTATGTGTCTGC   4952      AC       T
                                GCA  ACATATGGC TTGTG
                                |||  ||||||||| |||||
                                CGT  TGTGTATTG GACAC
                                  C_       C
GAM554   FBN2     3'  CAAGGAACCATATGTG      8844          __
                                CACATATGG  CTTTG
                                |||||||||  |||||
                                GTGTATACC  GGAAC
                                     AA
GAM554   FMO1     3'  CACAAATGATTGTGTTGT    8924         TATGGC
                                GCAACACA     TTTGTG
                                ||||||||     ||||||
                                TGTTGTGT     AAACAC
                                     TAGT__
GAM554   GALNT2   3'  CACAAAGCCGTTCGCAGCT   15594     AACACAT
                                AGC      ATGGCTTTGTG
                                |||      ||||||||||
                                TCG      TGCCGAAACAC
                                  ACGCT__
GAM554   GALNT2   3'  CACAAAGCCGAGTCGTGT    15593      _  A
                                ACAC AT TGGCTTTGTG
                                |||| || ||||||||||
                                TGTG TG GCCGAAACAC
                                  C  A
GAM554   GPR4     3'  CAGGGTCTCACTGTGTTGC   59902        TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                     CACT
GAM554   HNMT     3'  CACAAAGCCTGTGTTACT    22567    C     TAT
                                AG AACACA   GGCTTTGTG
                                || ||||||   |||||||||
                                TC TTGTGT   CCGAAACAC
                                 A     ____
GAM554   IL1RN    3'  CACAAAGCCCTTCCATGTCGC  5141     A   CATAT_
                                GC ACA     GGCTTTGTG
                                || |||     |||||||||
                                CG TGT     CCGAAACAC
                                 C   ACCTTC
GAM554   IL2RB    3'  CACAAAGTGGATGCCTGCT   6069       ACA   ATG
                                AGCA   CAT   GCTTTGTG
                                ||||   |||   ||||||||
                                TCGT   GTA   TGAAACAC
                                  CC_   GG_
GAM554   ITSN2    3'  CACAAAGCCATGCACGCT    38971     AACACA
                                AGC     TATGGCTTTGTG
                                |||     ||||||||||||
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                                TCG     GTACCGAAACAC
                                  CAC___
GAM554  JRK     3'  CAGGGTCTCACTGTGTTGC   86524        TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM554  LANCL1  3'  CACAATTTTATATGTATGCT  20210     AC      CT
                                AGCA  ACATATGG  TTGTG
                                ||||  ||||||||  |||||
                                TCGT  TGTATATT  AACAC
                                  A_       TT
GAM554  LGR6    5'  GGCCATCGTGTTGCT      84200        AT
                                AGCAACAC  ATGGCT
                                ||||||||  ||||||
                                TCGTTGTG  TACCGG
                                    C_
GAM554  LRRC2   3'  CAAGGCACCATGTGTTACT   44465    C      ATG
                                AG AACACAT   GCTTTG
                                || |||||||   ||||||
                                TC TTGTGTA   CGGAAC
                                 A      CCA
GAM554  MYBL2   3'  CAGGGCCATGTGCTGC     10154     ACA
                                GCA   CATATGGCTTTG
                                |||   ||||||||||||
                                CGT   GTGTACCGGGAC
                                  C__
GAM554  OCLN    3'  CACAAAGTTTTGGTTGCT    10314       A  TAT
                                AGCAAC CA   GGCTTTGTG
                                ||||||  ||   |||||||||
                                TCGTTG GT   TTGAAACAC
                                   _  T__
GAM554  OSR1    3'  CACAAAGTAATATGTG      17566        G
                                CACATAT GCTTTGTG
                                |||||||  ||||||||
                                GTGTATA TGAAACAC
                                    A
GAM554  PCDH9   5'  CACAAAGTGACAGTGCTGGCT  82794     AA_   ATATG
                                AGC   CAC    GCTTTGTG
                                |||   |||    ||||||||
                                TCG   GTG    TGAAACAC
                                  GTC   ACAG_
GAM554  PRDM2   5'  CACAAAGCCACATCCTGC    24246     ACAC  A
                                GCA    AT TGGCTTTGTG
                                |||    || ||||||||||
                                CGT    TA ACCGAAACAC
                                  CC__  C
GAM554  PRDM2   5'  CACAAAGCCACATCCTGC    31847     ACAC  A
                                GCA    AT TGGCTTTGTG
                                |||    || ||||||||||
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                                CGT    TA ACCGAAACAC
                                  CC__  C
GAM554  PRG4     3'  CACAAAGCTTTATCGTGTTGT  19415        _  T
                                GCAACAC ATA GGCTTTGTG
                                ||||||| ||| |||||||||
                                TGTTGTG TAT TCGAAACAC
                                    C   T
GAM554  RXRB     3'  CACAAAGCACTGGCCTTGC   41757     CA_  TATG
                                GCAA   CA    GCTTTGTG
                                ||||   ||    ||||||||
                                CGTT   GT    CGAAACAC
                                  CCG  CA__
GAM554  SMARCD1  3'  CACAAAGTTCCCATGTG     11811       ___
                                CATATGG   CTTTGTG
                                |||||||   |||||||
                                GTGTACC   GAAACAC
                                    CTT
GAM554  SMARCD1  3'  CACAAAGTTCCCATGTG     57429       ___
                                CATATGG   CTTTGTG
                                |||||||   |||||||
                                GTGTACC   GAAACAC
                                    CTT
GAM554  SMURF1   3'  CACGTGTGATCTGTGTTGC   92448        T  G  TT
                                GCAACACA AT GC  TGTG
                                |||||||| || ||  ||||
                                CGTTGTGT TA TG  GCAC
                                     C  G  T_
GAM554  STX7     3'  CACCAAGATGTGTGTTACT   13108    C       GG   T
                                AG AACACATAT  CTT GTG
                                || |||||||||  ||| |||
                                TC TTGTGTGTA  GAA CAC
                                 A        __  C
GAM554  TAF4B    3'  CACAAAGCATTGTTGC      87167       CATATG
                                GCAACA     GCTTTGTG
                                ||||||     ||||||||
                                CGTTGT     CGAAACAC
                                    TA____
GAM554  TF       3'  CACAGCTCTGTGTTGC      6512         TAT   T
                                GCAACACA   GGCT TG
                                ||||||||   |||| ||
                                CGTTGTGT   TCGA AC
                                     C__    C
GAM554  TLR4     5'  CACAGGGCCACTGCTGCT    56736     A  CATA
                                AGCA CA    TGGCTTTGTG
                                |||| ||    ||||||||||
                                TCGT GT    ACCGGGACAC
                                  C  C___
GAM554  TLR4     5'  CACAGGGCCACTGCTGCT    12317     A  CATA
                                AGCA CA    TGGCTTTGTG
                                |||| ||    ||||||||||
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                                TCGT GT   ACCGGGACAC
                                  C  C___
GAM554  TLR4    5'  CACAGGGCCACTGCTGCT   56727     A  CATA
                                AGCA CA   TGGCTTTGTG
                                |||| ||   ||||||||||
                                TCGT GT   ACCGGGACAC
                                  C  C___
GAM554  TLR4    5'  CACAGGGCCACTGCTGCT   56732     A  CATA
                                AGCA CA   TGGCTTTGTG
                                |||| ||   ||||||||||
                                TCGT GT   ACCGGGACAC
                                  C  C___
GAM554  VIPR2   3'  CACAGTCTCCATGTGTGTGC  12605    A       CT_
                                GCA CACATATGG  TTGTG
                                ||| |||||||||  |||||
                                CGT GTGTGTACC  GACAC
                                  _       TCT
GAM554  ANKT    3'  CAGGGTCTCACTGTGTTGC   33024       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM554  ATP9A   3'  CACAAAGCCAGTGGCTGTT   62039     A_  ATA
                                AGCA  CAC  TGGCTTTGTG
                                ||||  |||  ||||||||||
                                TTGT  GTG  ACCGAAACAC
                                  CG  ___
GAM554  CETN2   3'  CACATGTTACACCTGTGTTGC 15093       TA  GCTT_
                                GCAACACA  TG    TGTG
                                ||||||||  ||    ||||
                                CGTTGTGT  AC    ACAC
                                    CC  ATTGT
GAM554  CYLD    3'  CACAAGGTTTTATACTGCT   30883     ACAC  TG
                                AGCA   ATA  GCTTTGTG
                                ||||   |||  ||||||||
                                TCGT   TAT  TGGAACAC
                                  CA__   TT
GAM554  DKFZP586A0522 3'  CAGGGTCTCACTGTGTTGC   25871       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM554  DKFZp762K222 3'  ACAGATGCGTGTTGCT     71116       ATATG  _
                                AGCAACAC    GC TTTGT
                                ||||||||    || |||||
                                TCGTTGTG    CG AGACA
                                    _____  T
GAM554  FLJ10297  3'  CAGGGCTTCACTGTGTTGC   35979       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
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                                CGTTGTGT   TCGGGAC
                                    CACT
GAM554  FLJ10511  3' CACATGTGTATGTGCAGCT   36204    AA      G TT
                                AGC  CACATATG C  TGTG
                                |||  |||||||| |  ||||
                                TCG  GTGTATGT G  ACAC
                                  AC      _ T_
GAM554  FLJ11029  5' CACTAGCACCTGTGTTGCT   60973       TATG   TT
                                AGCAACACA   GCT  GTG
                                |||||||||   |||  |||
                                TCGTTGTGT   CGA  CAC
                                    CCA_   T_
GAM554  FLJ11117  3' CACAAAGCTTGTATGTG    37073       _
                                CACATATG GCTTTGTG
                                |||||||| ||||||||
                                GTGTATGT CGAAACAC
                                    T
GAM554  FLJ11715  3' CAGGGTCTCCATATGTTGC   44668      C  AT_
                                GCAACA AT   GGCTTTG
                                |||||| ||   |||||||
                                CGTTGT TA   CTGGGAC
                                   A  CCT
GAM554  FLJ20275  3' CACAAAGGGCTTTATGTGTCAG 34819    A_     T   __
          CT                      AGC  ACACATA GGCT  TTGTG
                                |||  ||||||| ||||  |||||
                                TCG  TGTGTAT TCGG  AACAC
                                  AC      T   GA
GAM554  FLJ20413  3' CAGAGCCGCATGCACTGCT   35131    ACA   A
                                AGCA   CAT TGGCTTTG
                                ||||   ||| ||||||||
                                TCGT   GTA GCCGAGAC
                                  CAC   C
GAM554  FLJ20450  3' CACCTGGGACCTGTGTTGCT   35192       TAT  _   T_
                                AGCAACACA   GG CTT  GTG
                                |||||||||   || |||  |||
                                TCGTTGTGT   CC GGG  CAC
                                    ___  A   TC
GAM554  FLJ20671  3' CAATTCAAATGTGTTGC    35516       A   CT
                                GCAACACAT TGG  TTG
                                ||||||||| |||  |||
                                CGTTGTGTA ACT  AAC
                                    A   T_
GAM554  FLJ23598  3' CACAAAGAGAGGCTGTGCTGC  45521    A   TATGG_
                                GCA CACA     CTTTGTG
                                ||| ||||     |||||||
                                CGT GTGT     GAAACAC
                                  C   CGGAGA
GAM554  FRSB     3' CATAGGCCATACATGTTACT   19090    C   CA      T
                                AG AACA  TATGGCTT GTG
                                || ||||  |||||||| |||
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                                TC TTGT  ATACCGGA TAC
                                 A   AC      _
GAM554  H2AV     3' CACAGCCATATGTATTGTT   56845      C        T
                                AGCAA ACATATGGCT TG
                                ||||| |||||||||| ||
                                TTGTT TGTATACCGA AC
                                   A        C
GAM554  HIC2     3' CACAAAGTCTGTACCGC    65256    AAC   TAT
                                GC   ACA   GGCTTTGTG
                                ||   |||   |||||||||
                                CG   TGT   CTGAAACAC
                                 CCA  ___
GAM554  KIAA0140 3' CACATGGCCATGTCTTGC    27806     CAC       T
                                GCAA   ATATGGCT TGTG
                                ||||   |||||||| ||||
                                CGTT   TGTACCGG ACAC
                                  C__       T
GAM554  KIAA0215 3' CAAATTCCATATGTAATGC   28416    AC       C_
                                GCA  ACATATGG  TTTG
                                |||  ||||||||  ||||
                                CGT  TGTATACC  AAAC
                                  AA       TT
GAM554  KIAA0254 3' AGCCACCTGTGTTGCT     28595         TA
                                AGCAACACA  TGGCT
                                |||||||||  |||||
                                TCGTTGTGT  ACCGA
                                     CC
GAM554  KIAA0618 3' CACAAAAACATGTGTTGT    29162        TA  GC
                                GCAACACA  TG  TTTGTG
                                ||||||||  ||  ||||||
                                TGTTGTGT  AC  AAACAC
                                    __  AA
GAM554  KIAA0953 3' AGCTTTCATAGTGTTGCT    66778        A   ___
                                AGCAACAC TATG   GCT
                                |||||||| ||||   |||
                                TCGTTGTG ATAC   CGA
                                    _   TTT
GAM554  KIAA1193 3' CACAGAGCCATATACCTCGCT 67630     AACAC
                                AGC    ATATGGCTTTGTG
                                |||    ||||||||||||||
                                TCG    TATACCGAGACAC
                                  CTCCA
GAM554  KIAA1281 3' CACAGAGTAACAAATGTTGCT 89151       CATATG
                                AGCAACA     GCTTTGTG
                                |||||||     ||||||||
                                TCGTTGT     TGAGACAC
                                   AAACAA
GAM554  KIAA1466 5' AGCCATATGTGCGCT      71913     AA
                                AGC  CACATATGGCT
                                |||  ||||||||||
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                              TCG  GTGTATACCGA
                                C_
GAM554  KIAA1821  3'  CAGGGTCTCACTGTGTTGC   71780       TAT_
                              GCAACACA   GGCTTTG
                              ||||||||   |||||||
                              CGTTGTGT   CTGGGAC
                                  CACT
GAM554  KIF13B    3'  CACAAAGTCCGTGGTGC    30904    A  ATAT
                              GCA CAC   GGCTTTGTG
                              ||| |||   |||||||||
                              CGT GTG   CTGAAACAC
                                G  C___
GAM554  KIF13B    3'  CACAAAGTCCGTGGTGC    82820    A  ATAT
                              GCA CAC   GGCTTTGTG
                              ||| |||   |||||||||
                              CGT GTG   CTGAAACAC
                                G  C___
GAM554  MGC12921  3'  CACAAAGGCCGTTATTGC   63775    CACAT   _
                              GCAA   ATGGC TTTGTG
                              ||||   ||||| ||||||
                              CGTT   TGCCG AAACAC
                                AT___   G
GAM554  MGC14836  5'  CACAAAGCTATCATCCTGC  53035    ACACAT
                              GCA    ATGGCTTTGTG
                              |||    ||||||||||
                              CGT    TATCGAAACAC
                                CCTAC_
GAM554  MGC15429  3'  CACATTGTCATGTGCAGCT  51249    AACA     TT
                              AGC   CATATGGC  TGTG
                              |||   ||||||||  ||||
                              TCG   GTGTACTG  ACAC
                                AC__      TT
GAM554  MGC15875  3'  CGAGGCCATAATGCT     51908    ACACA
                              AGCA   TATGGCTTTG
                              ||||   ||||||||||
                              TCGT   ATACCGGAGC
                                A____
GAM554  MGC16279  5'  GAAGCCATCGTGTCGCT    51888    A  AT
                              AGC ACAC  ATGGCTTT
                              ||| ||||  ||||||||
                              TCG TGTG  TACCGAAG
                                C  C_
GAM554  MGC27434  3'  CACAATAAGTATGTGTT    58947       GGCT
                              AACACATAT   TTGTG
                              |||||||||   |||||
                              TTGTGTATG   AACAC
                                   AAT_
GAM554  MGC3048   3'  CACAAAGCATGAATGTT    43899    CA  G
                              AACA  TATG CTTTGTG
                              ||||  |||| |||||||
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                                TTGT  GTAC GAAACAC
                                  AA   _
GAM554  MIG-6    3'  CACAAGCTGGCCTTGTGTTGCT 38486        TAT   ___
                                AGCAACACA   GGCT   TTGTG
                                |||||||||   ||||   |||||
                                TCGTTGTGT   CCGG   AACAC
                                    T__    TCG
GAM554  MUC17    3'  CACTGCCCCATATGTGTCCCT  94271    CA       CTTT
                                AG  ACACATATGG    GTG
                                ||  ||||||||||    |||
                                TC  TGTGTATACC    CAC
                                 CC        CCGT
GAM554  MYO3B    3'  CACTCTCCCACATGTGTTGT   57301        A   CTTT
                                GCAACACAT TGG    GTG
                                ||||||||| |||    |||
                                TGTTGTGTA ACC    CAC
                                    C   CTCT
GAM554  NS1-BP   3'  CACAAAGCTTTTGCATATTGC  72542     CA__  TAT
                                GCAA    CA   GGCTTTGTG
                                ||||    ||   |||||||||
                                CGTT    GT   TCGAAACAC
                                  ATAC  TT_
GAM554  OR51E2   3'  CACAGGTTTTATGTGTTCT   47791    C      TG    T
                                AG AACACATA  GCTT GTG
                                || ||||||||  |||| |||
                                TC TTGTGTAT  TGGA CAC
                                 _       TT    _
GAM554  PRDM11   3'  CAGGTGCTCCATGTGTTGC   39581        AT   _
                                GCAACACAT  GGC TTTG
                                |||||||||  ||| ||||
                                CGTTGTGTA  TCG GGAC
                                    CC   T
GAM554  PRO0943  5'  CACAAAAGTGTTATATGTG   37701         ___
                                CACATATGGC   TTTGTG
                                ||||||||||   ||||||
                                GTGTATATTG   AAACAC
                                     TGA
GAM554  SULT1C2  5'  CACAACGCAGCCATATGCTG  21674    _      ___
                                CA CATATGGCT   TTGTG
                                || |||||||||   |||||
                                GT GTATACCGA   AACAC
                                 C       CGC
GAM554  VEST1    3'  CACCTGCCATACATGTTGT   53685      CA     TTT
                                GCAACA  TATGGC   GTG
                                ||||||  ||||||   |||
                                TGTTGT  ATACCG   CAC
                                   AC     TC_
GAM554  ZFP100   3'  AGTCACCTGTGTTGCT     70049         TA
                                AGCAACACA  TGGCT
                                |||||||||  |||||
```

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                                TCGTTGTGT  ACTGA
                                     CC
GAM554  ZNF363    5'  AGCCATATTGTCGCT      73452     A   C
                                AGC ACA ATATGGCT
                                ||| ||| ||||||||
                                TCG TGT TATACCGA
                                  C   _
GAM554  LOC118611 5'  CACAGAGCATTTGCGTTACT   75469    C   A  TATG
                                AG AAC CA    GCTTTGTG
                                || ||| ||    ||||||||
                                TC TTG GT    CGAGACAC
                                 A   C  TTA_
GAM554  LOC120526 3'  CAGGGCCATTGCACTGCT    74015      ACA  T
                                AGCA   CA ATGGCTTTG
                                ||||   || |||||||||
                                TCGT   GT TACCGGGAC
                                   CAC  _
GAM554  LOC126669 3'  CACAAAGTTCCATATGT     75399         __
                                ACATATGG  CTTTGTG
                                ||||||||  |||||||
                                TGTATACC  GAAACAC
                                     TT
GAM554  LOC139840 5'  CACAAGAGCCATGGGT      76266     A        _
                                AC TATGGCTTT GTG
                                || |||||||| |||
                                TG GTACCGAGA CAC
                                 G        A
GAM554  LOC143465 5'  CACATGCACATATGTG      82962         _  TT
                                CACATATG GC  TGTG
                                |||||||| ||  ||||
                                GTGTATAC CG  ACAC
                                     A  T_
GAM554  LOC146774 3'  CACTGACATGTGTGTGC     78094     A       GCTTT
                                GCA CACATATG     GTG
                                ||| ||||||||     |||
                                CGT GTGTGTAC     CAC
                                  _       AGT__
GAM554  LOC147407 5'  CACAAAGCTATCATCCTGC   76322     ACACAT
                                GCA      ATGGCTTTGTG
                                |||      ||||||||||||
                                CGT      TATCGAAACAC
                                  CCTAC_
GAM554  LOC151057 3'  ACAGAGCACATACTGT      85199     _   _
                                ACA TATG GCTTTGT
                                ||| |||| |||||||
                                TGT ATAC CGAGACA
                                  C    A
GAM554  LOC151473 3'  CACAACAACCTATGTGTT    80254         T  CT_
                                AACACATA GG   TTGTG
                                |||||||| ||   |||||
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                                TTGTGTAT CC   AACAC
                                     _ AAC
GAM554   LOC154739 5'  CACAAAGTTCAAATGTATGC   86227     AC    A  _
                                GCA  ACAT TGG CTTTGTG
                                |||  |||| ||| |||||||
                                CGT  TGTA ACT GAAACAC
                                  A_   A  T
GAM554   LOC157507 5'  CACAGCTGTGTATGTGTGCT   81454      A      __    T
                                AGCA CACATAT  GGCT TG
                                |||| |||||||  |||| ||
                                TCGT GTGTATG  TCGA AC
                                  _     TG   C
GAM554   LOC161734 3'  CACAAACATTTAGTGTTGCT   87097        AT_  GC
                                AGCAACAC   ATG  TTTGTG
                                ||||||||   |||  ||||||
                                TCGTTGTG   TAC  AAACAC
                                     ATT  __
GAM554   LOC196410 3'  CACAAAAGTCATGGTG      87657     A       _
                                CAC TATGGCTTT GTG
                                ||| ||||||||| |||
                                GTG GTACTGAAA CAC
                                  _       A
GAM554   LOC196485 3'  CACAAAAACCTGTGTTGT    87730        TAT  C_
                                GCAACACA   GG  TTTGTG
                                ||||||||   ||  ||||||
                                TGTTGTGT   CC  AAACAC
                                     ___  AA
GAM554   LOC196529 3'  CAGGGTCTCACTGTGTTGC   87771        TAT_
                                GCAACACA    GGCTTTG
                                ||||||||    |||||||
                                CGTTGTGT    CTGGGAC
                                     CACT
GAM554   LOC197003 5'  CACAAAGCTCCATGCTGT    87870     _  AT
                                ACA CAT  GGCTTTGTG
                                ||| |||  |||||||||
                                TGT GTA  TCGAAACAC
                                  C   CC
GAM554   LOC202025 5'  CACAGTTGTATGGTTGCT    90281       A   TG   T
                                AGCAAC CATA  GCT TG
                                ||||||  ||||  ||| ||
                                TCGTTG GTAT  TGA AC
                                   _   GT   C
GAM554   LOC203276 3'  CACAAAGTTCAAGTGTATGC   90475     _   ATAT
                                GCA ACAC    GGCTTTGTG
                                ||| ||||    |||||||||
                                CGT TGTG    TTGAAACAC
                                  A   AAC_
GAM554   LOC203292 3'  CAGGGTTTCATATGTGTT    90509          __
                                AACACATATG  GCTTTG
                                ||||||||||  ||||||
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                                TTGTGTATAC  TGGGAC
                                      TT
GAM554  LOC203305 3'  CACAAAGTTCAAGTGTATGC   90519    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM554  LOC221354 3'  CACAAAAACATGTGTTGT    92409       TA  GC
                                GCAACACA  TG  TTTGTG
                                ||||||||  ||  ||||||
                                TGTTGTGT  AC  AAACAC
                                     __ AA
GAM554  LOC254243 3'  CACAAAGTTCAAGTGTATGC   97404    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM554  LOC255870 3'  CACAACTGGCCATGTCCTGC   94657    ACAC      __
                                GCA   ATATGGCT  TTGTG
                                |||   ||||||||  |||||
                                CGT   TGTACCGG  AACAC
                                  CC__      TC
GAM554  LOC90038  3'  CACAAAGTTCAAGTGTATGC   61148    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM554  LOC90321  3'  CACAAATGGATTGTGTGTGC   62262    A    TGGC_
                                GCA CACATA    TTTGTG
                                ||| ||||||    ||||||
                                CGT GTGTGT    AAACAC
                                  _     TAGGT
GAM554  LOC90750  3'  CACAAAGTTAAGATTGCT    63917     CACATA
                                AGCAA     TGGCTTTGTG
                                |||||     ||||||||||
                                TCGTT     ATTGAAACAC
                                   AGA___
GAM554  LOC91069  3'  GAAGCCATCGTGTCACT    64778   CA   AT
                                AG  ACAC  ATGGCTTT
                                ||  ||||  ||||||||
                                TC  TGTG  TACCGAAG
                                 AC   C_
GAM554  LOC92539  3'  CACAAAGCCACTGTAGC    69630   A   CATA
                                GC ACA   TGGCTTTGTG
                                || |||   ||||||||||
                                CG TGT   ACCGAAACAC
                                 A  C___
GAM555  ADAM11    3'  GGGATGCCCCCAGGCAGC    9969      A   AA
                                GCTGC CTG  GGCATCTT
                                ||||| |||  ||||||||
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                                CGACG GAC  CCGTAGGG
                                  _  CC
GAM555  ADAM11   3'  GGGATGCCCCCAGGCAGC    41217      A   AA
                                GCTGC CTG  GGCATCTT
                                ||||| |||  ||||||||
                                CGACG GAC  CCGTAGGG
                                  _  CC
GAM555  AXIN1    3'  GAGTGCCTTCAACACAGC    60852      CAC      T
                                GCTG   TGAAGGCA CTT
                                ||||   |||||||| |||
                                CGAC   ACTTCCGT GAG
                                  ACA      _
GAM555  BMP6     3'  AAATGAGGGTGCCCAGC     8163       CACTGAA    _
                                GCTG      GGCATC TTATTT
                                ||||      |||||| ||||||
                                CGAC      CCGTGG AGTAAA
                                  _______    G
GAM555  CDH13    5'  ATGCTCAGTGCAGC       6993          AG
                                GCTGCACTGA  GCAT
                                ||||||||||  ||||
                                CGACGTGACT  CGTA
                                     __
GAM555  DNCI1    3'  GAAATGAGCCACCCCCACTGCA 91063       C  AA  CAT
           GC                     GCTGCA TG  GG   CTTATTTC
                                ||||||  ||  ||   ||||||||
                                CGACGT AC  CC   GAGTAAAG
                                   C  CC  ACC
GAM555  LIFR     3'  GAATTGATTGCCTTCAGCACAG 9745      CA       TC   T
           C                     GCTG  CTGAAGGCA  TTA TTC
                                ||||  |||||||||  ||| |||
                                CGAC  GACTTCCGT  AGT AAG
                                  AC       T_   T
GAM555  PTPN13   3'  AAATAAGATCACAGAGCAGC   54774      A   AAGGC
                                GCTGC CTG    ATCTTATTT
                                ||||| |||    |||||||||
                                CGACG GAC    TAGAATAAA
                                  A   AC___
GAM555  CSRP2BP  3'  GAGATGCCTTCAGCCAGC    70113      CA
                                GCTG  CTGAAGGCATCTT
                                ||||  ||||||||||||
                                CGAC  GACTTCCGTAGAG
                                  C_
GAM555  FLJ22029 3'  AGATCCTCAGTGCAGC      46329          A  C
                                GCTGCACTGA GG ATCT
                                |||||||||| || ||||
                                CGACGTGACT CC TAGA
                                     _  _
GAM555  FLJ22938 5'  ATGCCTTCAGTCAGC       45158      C
                                GCTG ACTGAAGGCAT
                                |||| ||||||||||
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                                CGAC TGACTTCCGTA
                                   _
GAM555  KIAA0016 3' AAATAATGTATTAGTGCA    28641        AG   CT
                                TGCACTGA GCAT TATTT
                                |||||||| |||| |||||
                                ACGTGATT TGTA ATAAA
                                    A_  __
GAM555  KIAA0830 3' GAAATAAGTACCCAGCACAGT 69697     CA  AA CAT
                                GCTG CTG GG  CTTATTTC
                                |||| ||| ||  ||||||||
                                TGAC GAC CC  GAATAAAG
                                  AC  __ AT_
GAM555  KIAA1853 3' GGATGCCACCCAGTGCAGC   69397        AA_
                                GCTGCACTG  GGCATCT
                                |||||||||  |||||||
                                CGACGTGAC  CCGTAGG
                                     CCA
GAM555  LGP1     5' AGAGCTCAGTGCAGC      50649         AG A
                                GCTGCACTGA GC TCT
                                |||||||||| || |||
                                CGACGTGACT CG AGA
                                    __ _
GAM555  MOST2    5' GAAATAAACCAGACAGTGCAGC 39685        AA_ CATC
                                GCTGCACTG  GG   TTATTTC
                                |||||||||  ||   |||||||
                                CGACGTGAC  CC   AATAAAG
                                     AGA A___
GAM555  PPP1R3B  3' GACGCACATCTCCAGTGCAGC 44819        A ____ A
                                GCTGCACTG AG   GC TC
                                ||||||||| ||   || ||
                                CGACGTGAC TC   CG AG
                                     C TACA C
GAM555  LOC134145 3' AAATAAGATGCCAATAG    75143    AA
                                CTG GGCATCTTATTT
                                ||| ||||||||||||
                                GAT CCGTAGAATAAA
                                  AA
GAM555  LOC143188 5' GAAGTGGCACCTTCAGGCAGC 82897     A     CATC
                                GCTGC CTGAAGG   TTATTTC
                                ||||| |||||||   |||||||
                                CGACG GACTTCC   GGTGAAG
                                   _     AC__
GAM555  LOC170370 5' GGAGGCCTTCAGTACAGC    82840     C       A
                                GCTG ACTGAAGGC TCT
                                |||| ||||||||| |||
                                CGAC TGACTTCCG AGG
                                  A       G
GAM555  LOC195977 3' GAGCTGCCTTCAACCCAGC   87539     CAC      T
                                GCTG  TGAAGGCA CTT
                                ||||  |||||||| |||
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                                CGAC   ACTTCCGT GAG
                                  CCA       C
GAM555  LOC51063  3'  AAGTGGCCTCCAGTGCAGC   31917         A   AT
                                GCTGCACTG AGGC  CTT
                                ||||||||| ||||  |||
                                CGACGTGAC TCCG  GAA
                                    C   GT
GAM556  ADH4      3'  TAAAAAGATTTTTACTGGA   5408         CGT
                                TCCAGTGG   TCTTTTTA
                                ||||||||   ||||||||
                                AGGTCATT   AGAAAAAT
                                    TTT
GAM556  B4GALT2   3'  AGTAAAAAAACGTGAATGGA   47580     GTG    CT
                                TCCA   GCGTT  TTTTACT
                                ||||   |||||  |||||||
                                AGGT   TGCAA  AAAATGA
                                  AAG    __
GAM556  CTBP1     3'  AAAAAGAAAACCTGAAGGAG   67941     AGT_  CG
                                CTCC    GG  TTCTTTTT
                                ||||    ||  ||||||||
                                GAGG    CC  AAGAAAAA
                                  AAGT  AA
GAM556  ENPP3     3'  TAAAAAGAACAGCAGAGAG   17226     CAGTG  _
                                CTC     GC GTTCTTTTTA
                                |||     || ||||||||||
                                GAG     CG CAAGAAAAAT
                                  AGA__  A
GAM556  F8        3'  TAAAAAAATAAGTCAGGAGGA  3732       AG    GTTC_
                                TCCTCC  TGGC    TTTTTA
                                ||||||  ||||    ||||||
                                AGGAGG  ACTG    AAAAAT
                                   __    AATAA
GAM556  GK        3'  AGCAAAAAGAATGCTAT     3911           A
                                GTGGCGTTCTTTTT CT
                                |||||||||||||| ||
                                TATCGTAAGAAAAA GA
                                       C
GAM556  ID4       3'  GAAAAAAAGCCACCGGAGGA   7755        A    GTTC
                                TCCTCC GTGGC    TTTTT
                                |||||| |||||    |||||
                                AGGAGG CACCG    AAAAG
                                   C     AAA_
GAM556  PITX1     3'  GAAAAAGACGTCGGAG      10599      AGT    T     A
                                CTCC   GGCGT CTTTTT C
                                ||||   ||||| |||||| |
                                GAGG   CTGCA GAAAAA G
                                  ____    _     C
GAM556  TDG       3'  GAAAAAGATGCTGGAG      12191        GCGT      A
                                CTCCAGTG    TCTTTTT C
                                ||||||||    ||||||| |
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                                GAGGTCGT    AGAAAAA G
                                    ____        C
GAM556  XRCC2     3'  AGCAAAAAGAACAAAGCTGGAG 18318         GGC        A
              G                    CCTCCAGT   GTTCTTTTT CT
                                   ||||||||   |||||||||  ||
                                   GGAGGTCG   CAAGAAAAA GA
                                       AAA        C
GAM556  DKFZP727M111 5'  AAAAGGAAAAGCCCTGAAG    31401    C   T   G_
                                   CT CAG GGC  TTCTTTTT
                                   || ||| |||  ||||||||
                                   GA GTC CCG  AAGGAAAA
                                    A   _   AA
GAM556  ELKS      3'  AGTGGTCAACGCCCTGGAAGA  30501    C     T     CTTT
                                   TC TCCAG GGCGTT    TTACT
                                   || ||||| ||||||    |||||
                                   AG AGGTC CCGCAA    GGTGA
                                    A     _      CT__
GAM556  FLJ10648  3'  AGCAAAAAGAACAAAGTCCTGG 36378         T   ___        A
              AGGA                     TCCTCCAG GGC   GTTCTTTTT CT
                                   ||||||||| |||   |||||||||  ||
                                   AGGAGGTC CTG   CAAGAAAAA GA
                                       _   AAA        C
GAM556  FLJ20151  3'  AAAGACCCTGGAGGA       34648         T  CGT
                                   TCCTCCAG GG   TCTTT
                                   |||||||| ||   |||||
                                   AGGAGGTC CC   AGAAA
                                       _  ___
GAM556  FLJ20435  3'  TAAAAAGAGCCATCTGGAGGA  35162         _    GT
                                   TCCTCCAG TGGC  TCTTTTTA
                                   |||||||| ||||  ||||||||
                                   AGGAGGTC ACCG  AGAAAAAT
                                        T    __
GAM556  MDS024    3'  AAAAAGAATTGCCAAGGA     41522      AG     _
                                   TCC  TGGCG TTCTTTTT
                                   |||  ||||| ||||||||
                                   AGG  ACCGT AAGAAAAA
                                    A_     T
GAM556  ShrmL     5'  AGAGCGCCACTGAAGGA      40463       C
                                   TCCT CAGTGGCGTTCT
                                   |||| ||||||||||||
                                   AGGA GTCACCGCGAGA
                                     A
GAM556  SIAT8C    5'  TAAAAAAGCCCCACAGAGGA   31883       CA    C   C
                                   TCCTC  GTGG GTT TTTTTA
                                   |||||  |||| ||| ||||||
                                   AGGAG  CACC CGA AAAAAT
                                     A_    C   _
GAM556  VEST1     5'  AAAAAGATGCACTGGGGA     53678      T     G   T
                                   TCC CCAGTG CGT CTTTTT
                                   ||| |||||| ||| ||||||
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                                AGG GGTCAC GTA GAAAAA
                                  _     _  _
GAM556  ZFD25     5'  AAAAAGAGCCCTGGA       32573       T   GT
                                TCCAG GGC  TCTTTTT
                                ||||| |||  |||||||
                                AGGTC CCG  AGAAAAA
                                  _  ___
GAM556  LOC124626 3'  AGTAAGACCAAACCACTGGA   74313         CGTTCT
                                TCCAGTGG     TTTTACT
                                ||||||||     |||||||
                                AGGTCACC     AGAATGA
                                     AAACC_
GAM556  LOC144577 3'  TAAAAAGAAGCCACAAAGAG   76902     CA_    G
                                CTC   GTGGC TTCTTTTTA
                                |||   ||||| |||||||||
                                GAG   CACCG AAGAAAAAT
                                  AAA    _
GAM556  LOC145837 5'  AGCAAAAAGAACCAAAGAGGA  83542       CAG   CG       A
                                TCCTC   TGG  TTCTTTTT CT
                                |||||   |||  |||||||| ||
                                AGGAG   ACC  AAGAAAAA GA
                                   AA_  __       C
GAM556  LOC151194 3'  TAAAAAAACTGGGGA       59215     T    GGCGTTC
                                TCC CCAGT       TTTTTA
                                ||| |||||       ||||||
                                AGG GGTCA       AAAAAT
                                  _     A_______
GAM556  LOC154789 5'  AGTAAAATCTCAGGCCACTAGA 81131     C     GTTCT_
          G                      CTC AGTGGC      TTTTACT
                                ||| ||||||      |||||||
                                GAG TCACCG      AAAATGA
                                  A      GACTCT
GAM556  LOC197322 3'  AAAGACTCCACTGGAGGA    89736          C  T
                                TCCTCCAGTGG GT CTTT
                                |||||||||| || ||||
                                AGGAGGTCACC CA GAAA
                                       T  _
GAM556  LOC221596 3'  TAAAAACCTCACACTGGAGAGA 91980    _       GCGTTC
                                TC CTCCAGTG      TTTTTA
                                || ||||||||      ||||||
                                AG GAGGTCAC      AAAAAT
                                  A       ACTCC_
GAM556  LOC91796  3'  AGCAAAAAGAACAAGGCTGGA  67208       GGC       A
                                TCCAGT   GTTCTTTTT CT
                                ||||||   ||||||||| ||
                                AGGTCG   CAAGAAAAA GA
                                    GAA        C
GAM556  LOC92539  5'  TAAAAAGTGTCACTG       69638         TT
                                CAGTGGCG  CTTTTTA
                                ||||||||  |||||||
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                                GTCACTGT  GAAAAAT
                                    __
GAM557  ACVR1    5'  TTCTACTCTCCGAGTACCCCA  6613     A   G  A  TATTT
                                TG GGTA TC GG    GTAGAA
                                || |||| || ||    ||||||
                                AC CCAT AG CC    CATCTT
                                 C   G  _  TCT__
GAM557  ADORA1   3'  CACCTGCCTGACCATCCCA   5423     A  A      TT
                                TG GGT GTCAGGTA  TG
                                || ||| ||||||||  ||
                                AC CTA CAGTCCGT  AC
                                 C  C       CC
GAM557  CRIM1    3'  TTCTACAAAATAGAAACTACTT 33182         CAGGTA
           CA                     TGAGGTAGT     TTTGTAGAA
                                |||||||||     |||||||||
                                ACTTCATCA     AAACATCTT
                                      AAGATA
GAM557  EEF1A1   3'  AATACCTGCCACCCCA      7386     A   A T
                                TG GGT G CAGGTATT
                                || ||| | ||||||||
                                AC CCA C GTCCATAA
                                 C  C _
GAM557  GYG2     3'  TCTACCCTCACTACCTCA    14050         C   TATTT
                                TGAGGTAGT AGG    GTAGA
                                ||||||||| |||    |||||
                                ACTCCATCA TCC    CATCT
                                      C  _____
GAM557  SAG      5'  CTACAAATTCCCCACATC    5023      A  CA  T
                                GGT GT  GG ATTTGTAG
                                ||| ||  || ||||||||
                                CTA CA  CC TAAACATC
                                  _  CC  T
GAM557  STS      3'  TCTACAAATACCTGGGGC    4455     AG
                                GT  TCAGGTATTTGTAGA
                                ||  ||||||||||||||
                                CG  GGTCCATAAACATCT
                                 G_
GAM557  TMPRSS2  3'  TCTACACATTGCTACCTCA   18968        T   GTATT
                                TGAGGTAG CAG    TGTAGA
                                |||||||| |||    ||||||
                                ACTCCATC GTT    ACATCT
                                      _   AC___
GAM557  C20orf54  3'  TTCCAGTAAGTACCAACTACCT 53010         CA      TA_
           CA                     TGAGGTAGT  GGTATTTG   GAA
                                |||||||||  ||||||||   |||
                                ACTCCATCA  CCATGAAT   CTT
                                      A_       GAC
GAM557  C3F      5'  TTCTACAAGGAGACCTACCTCA 19301         _  AGGTA
                                TGAGGTAG TC    TTTGTAGAA
                                |||||||| ||    |||||||||
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                                ACTCCATC AG    GAACATCTT
                                    C  AG___
GAM557  CCR7     3'  AATCCCAGCTACCTCA     8450         CA  T
                                TGAGGTAGT  GG ATT
                                |||||||||  || |||
                                ACTCCATCG  CC TAA
                                    AC  _
GAM557  DDM36    3'  TCTAACAACGTGACTACCTCA  40579          G  ATTTG
                                TGAGGTAGTCA GT    TAGA
                                ||||||||||| ||    ||||
                                ACTCCATCAGT CA    ATCT
                                     G  ACA__
GAM557  FLJ11560 3'  TCTGACCCACCTACCTCA    47221        TCA   ATTTG
                                TGAGGTAG   GGT    TAGA
                                ||||||||   |||    ||||
                                ACTCCATC   CCA    GTCT
                                    CAC  _____
GAM557  FLJ31153 3'  TCTACAAAACACCCCTCA    58132      TAGTCA   A_
                                TGAGG     GGT  TTTGTAGA
                                |||||     |||  ||||||||
                                ACTCC     CCA  AAACATCT
                                  _______  CA
GAM557  KIAA0318 3'  TTCTATAGTATACCAACCACCC 68960    A   A  CA    _
           CA                     TG GGT GT  GGTAT TTGTAGAA
                                || ||| ||  ||||| ||||||||
                                AC CCA CA  CCATA GATATCTT
                                 C   C  A_    T
GAM557  NMU2R    3'  TTCCACTATCCTAACTGCCTCA 39402         C   TATTT  A
                                TGAGGTAGT AGG     GT GAA
                                ||||||||| |||     || |||
                                ACTCCGTCA TCC     CA CTT
                                     A   TAT__  C
GAM557  PRO1914  3'  TCTACAGGAATGACTACCTTA  26047          GGTA
                                TGAGGTAGTCA    TTTGTAGA
                                ||||||||||    ||||||||
                                ATTCCATCAGT    GGACATCT
                                     AA__
GAM557  LOC145098 5'  CTCCAGCCCTGACTATCCCA   76990    A        TAT   T
                                TG GGTAGTCAGG   TTG AG
                                || ||||||||||   ||| ||
                                AC CTATCAGTCC   GAC TC
                                 C         C__   C
GAM557  LOC146823 3'  CTACAAATACCTCCAGCCCCTC 83795      TAGTC_
                                GAGG     AGGTATTTGTAG
                                ||||     ||||||||||||
                                CTCC     TCCATAAACATC
                                  CCGACC
GAM557  LOC148371 3'  AATACCTGCCACCCCA      78804    A   A T
                                TG GGT G CAGGTATT
                                || ||| | ||||||||
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                                AC CCA C GTCCATAA
                                 C   C _
GAM557   LOC149620 5'  TCTACAAATACCCGACTGACAC 79459     ___    A
                C                GGT   AGTC GGTATTTGTAGA
                                 |||   |||| ||||||||||||
                                 CCA   TCAG CCATAAACATCT
                                   CAG    C
GAM557   LOC151318 3'  TCCACAAACACCCTGAGTGCC  80229     G    TA_    A
                                 GGTA TCAGG   TTTGT GA
                                 |||| |||||   ||||| ||
                                 CCGT AGTCC   AAACA CT
                                   G    CAC    C
GAM557   LOC161589 3'  AATACCTGCCACCCCA      82281    A   A T
                                 TG GGT G CAGGTATT
                                 || ||| | ||||||||
                                 AC CCA C GTCCATAA
                                  C   C _
GAM557   LOC196283 3'  TCTACAAAGCATACCTCA    87621       GTCAGGTA
                                 TGAGGTA       TTTGTAGA
                                 |||||||       ||||||||
                                 ACTCCAT       AAACATCT
                                     ACG_____
GAM557   LOC200942 3'  CTACCCTACCTACCTCA     88946       TC   TATTT
                                 TGAGGTAG  AGG    GTAG
                                 ||||||||  |||    ||||
                                 ACTCCATC  TCC    CATC
                                      CA  _____
GAM557   LOC221838 3'  AATACCTGCCACCCCA      92542    A   A T
                                 TG GGT G CAGGTATT
                                 || ||| | ||||||||
                                 AC CCA C GTCCATAA
                                  C   C _
GAM557   LOC221839 3'  AATACCTGCCACCCCA      92494    A   A T
                                 TG GGT G CAGGTATT
                                 || ||| | ||||||||
                                 AC CCA C GTCCATAA
                                  C   C _
GAM558   ADH1B    3'  CTTAGACATAAAGTAAAAT    72644     C    CAC
                                 ATTT ACTTT   TGTCTGAG
                                 |||| |||||   ||||||||
                                 TAAA TGAAA   ACAGATTC
                                   A    T__
GAM558   AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                 CATTT   TTT AC GTCTGAGAT
                                 |||||   ||| || |||||||||
                                 GTAAA   AAA TG TAGACTCTA
                                    TA_   T  _
GAM558   FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                 CATTTCACTTTC CTG
                                 |||||||||||| |||
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                                GTAAAGTGAAAG GAT
                                             _
GAM558  JTB     3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                  CATTTCACTTTCACTGTCTGAGAT
                                  ||||||||||||||||||||||||
                                  GTAAAGTGAAAGTGACAGACTCTA

GAM558  KLF4    3'  TCCCAGACAGTGGATATG    14891    CT        A
                                  CA  TTCACTGTCTG GA
                                  ||  ||||||||||| ||
                                  GT  AGGTGACAGAC CT
                                   AT         C
GAM558  PHYH    3'  ACAGTAAAAGTGAAAT     20608          C
                                  ATTTCACTTT ACTGT
                                  |||||||||| |||||
                                  TAAAGTGAAA TGACA
                                        A
GAM558  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                  TTTCACTTTCA   TCTG GA
                                  ||||||||||   |||| ||
                                  AAAGTGAAAGT   GGAC CT
                                         T__   _
GAM558  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                  TTTCA TTTCACTGTCT
                                  ||||| ||||||||||
                                  AAAGT AAAGTGACGGG
                                     A
GAM558  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                  TTTCACTTT  CTGT   AGAT
                                  |||||||||  ||||   ||||
                                  AAAGTGAAA  GACA   TCTA
                                       C_    CG_
GAM558  CG012   5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                  TTCACTTTCA  GT  GAG
                                  ||||||||||  ||  |||
                                  AAGTGAAAGT  CA  CTC
                                        CT  __
GAM558  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                  CTTTCACT TC  GAGAT
                                  |||||||| ||  |||||
                                  GAAAGTGA AG  TTCTA
                                       G  TC
GAM558  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
              G                    CATTTC        GTCTGAGAT
                                   ||||||        |||||||||
                                   GTAAAG        CAGACTCTA
                                      AAACATTT_
GAM558  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                  CATTTCA   TCACTGTCTGAGAT
                                  |||||||   ||||||||||||||
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                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM558  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM558  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM558  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM558  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM558  PP35      3'  ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM558  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148       TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__   TT
GAM558  SEP15     3'  TCCTACAGTAAGAGTGAAA   14934       C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                      A    TC
GAM558  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA  73941       CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM558  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM558  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015      TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
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                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM558  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                   _       ATTT
GAM558  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                      _
GAM559  ARNT2    3'  AAACAACCCGTGCATCCCTGC  29450     A    TTTTA
                                GTA GGAT    GGGTTGTTT
                                ||| ||||    |||||||||
                                CGT CCTA    CCCAACAAA
                                  C   CGTG_
GAM559  LCT      3'  AACCGTAAAAATCCTT      9697           G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
                                TTCCTAAAAAT CCAA
                                      G
GAM559  RPL15    3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM559  FBXO30   3'  AACTAAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                 G        AA
GAM559  KIAA0494  3'  AACAACCCTTACTTAC      28736       GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM559  PRO0641   5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                   ___    C
GAM559  SMT3H2   3'  AACAACATAAAAATCCTTGC   22670           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM559  LOC120103 3'  AACCTATGAAAAATCCTTGC   74002           A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
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                                CGTTCCTAAAAA  TCCAA
                                      GTA
GAM559  LOC129831 3'  AAACAACCCCAATGTCC     74889     TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM559  LOC133088 5'  AAACAAAATAGAAAAATCCCTG 75075     A      AGGG_
          C                      GTA GGATTTTT    TTGTTT
                                ||| ||||||||    ||||||
                                CGT CCTAAAAA    AACAAA
                                  C       GATAA
GAM559  LOC148089 3'  GGCCCTAAAAATTCCTAC    78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM559  LOC154547 3'  AACAACATAAAAATCCTTGC   76050          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM559  LOC158104 3'  ACAGCCAAAAATCCTTA     60313          AG
                                TAAGGATTTTT  GGTTGT
                                ||||||||||  ||||||
                                ATTCCTAAAAA  CCGACA
                                      __
GAM559  LOC205880 5'  AAACAACCATCATCCTGAC    90709    A    TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM559  LOC221561 3'  AACAACATAAAAATCCTTGC   92130          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM559  LOC257591 3'  AACAACATAAAAATCCTTGC   97840          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM559  LOC51145  3'  AGCTAAAATCCTTAC       32393          TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
                                CATTCCTAAAA   TCGA
                                      ___
GAM560  ABCG1     3'  CCTAGAACCGCGTTGGGTT   16982       TAGATCA
                                AACCCG      GTTCTAGG
                                ||||||      ||||||||
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                                TTGGGT      CAAGATCC
                                   TGCGC__
GAM560  ADORA2A  3'  CCTAGACTCTCCTAGGGTT   5433       G   ATC   T
                                AACCC TAG   AGT CTAGG
                                ||||| |||   ||| |||||
                                TTGGG ATC   TCA GATCC
                                  _  CTC   _
GAM560  AIM1     3'  CCCAGGCTGATCTCG      91819    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTAGTCG GA CC
                                 _      _ C
GAM560  B4GALT5  3'  CCCAGGCTGGTCTCG      16495    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM560  CBFA2T2  3'  CCCAGAGGCTGATCTGC     17460          _  A
                                GTAGATCAGT TCT GG
                                |||||||||| ||| ||
                                CGTCTAGTCG AGA CC
                                      G   C
GAM560  CBFB     3'  CCCAGGCTGGTCTCG      8274     T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM560  CBFB     3'  CCCAGGCTGGTCTCG      43141    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM560  CIT      3'  CCTAGGGCTAGACCTA     69745    A  _
                                TAG TC AGTTCTAGG
                                ||| || |||||||||
                                ATC AG TCGGGATCC
                                  C  A
GAM560  CRLF1    3'  CCTAGAACCCCTGCCAGGG   16452     __   ATCA
                                CCC  GTAG   GTTCTAGG
                                |||  ||||   ||||||||
                                GGG  CGTC   CAAGATCC
                                  AC   CC__
GAM560  DMPK     3'  CCTAGAACTGTCTTCG      15323    T   T
                                CG AGA CAGTTCTAGG
                                || ||| ||||||||||
                                GC TCT GTCAAGATCC
                                 T  _
GAM560  EDAR     5'  CCCAGAACTGGATGG       42265     AGA      A
                                CCGT   TCAGTTCT GG
                                ||||   |||||||| ||
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                                GGTA   GGTCAAGA CC
                                  ___        C
GAM560  EPHB3    5'  CCTAGAGCTGCCACGG      15455      AGAT
                                CCGT    CAGTTCTAGG
                                ||||    ||||||||||
                                GGCA    GTCGAGATCC
                                  CC__
GAM560  GAB2     3'  CCCAGAACTCTGGAGCTACAGG 24492    C    A ___     A
                                CC GTAG TC   AGTTCT GG
                                || |||| ||   |||||| ||
                                GG CATC AG   TCAAGA CC
                                 A    G  GTC     C
GAM560  GAB2     3'  CCCAGAACTCTGGAGCTACAGG 54449    C    A ___     A
                                CC GTAG TC   AGTTCT GG
                                || |||| ||   |||||| ||
                                GG CATC AG   TCAAGA CC
                                 A    G  GTC     C
GAM560  GRM6     3'  CCCAGGCTGGTCTCG       5929     T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _  C
GAM560  ITGAL    3'  CCCAGAACTGGACTCAGG     9389     GT  A       A
                                CC  AG TCAGTTCT GG
                                ||  || |||||||| ||
                                GG  TC GGTCAAGA CC
                                 AC  A       C
GAM560  MIPOL1   5'  CCCAGACTGGTCTCG       77066    T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCA GA CC
                                 _       _  C
GAM560  MTR      3'  CCTAAAATTGATCTATGG     4208             C
                                CCGTAGATCAGTT TAGG
                                |||||||||||| ||||
                                GGTATCTAGTTAA ATCC
                                          A
GAM560  NGFR     3'  CCTAGAATCAGCCTAGGGGT   10224      G   ATCA
                                ACCC TAG    GTTCTAGG
                                |||| |||    ||||||||
                                TGGG ATC    TAAGATCC
                                  G   CGAC
GAM560  RFXANK   3'  CCCAGAACTGACTTCAAAGG   13561    GT___  A       A
                                CC     AG TCAGTTCT GG
                                ||     || |||||||| ||
                                GG     TC AGTCAAGA CC
                                 AAACT  _       C
GAM560  RFXANK   3'  CCCAGAACTGACTTCAAAGG   56239    GT___  A       A
                                CC     AG TCAGTTCT GG
                                ||     || |||||||| ||
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                                GG    TC AGTCAAGA CC
                                 AAACT _       C
GAM560  SLC3A2   5' CCCAGACTGGTCTCG      9983    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCA GA CC
                                 _      _ C
GAM560  TEM5     3' CCAAGGTCTGACCTAGGGTT  51318      G   A   TT  A
                                AACCC TAG TCAG  CT GG
                                ||||| ||| ||||  || ||
                                TTGGG ATC AGTC  GA CC
                                   _  C   TG  A
GAM560  WHSC1    5' CCCAGGCTGGTCTCG      55825    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM560  WHSC1    5' CCCAGGCTGGTCTCG      55842    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM560  WHSC1    5' CCCAGGCTGGTCTCG      29907    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM560  WHSC1    5' CCCAGGCTGGTCTCG      23656    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM560  ZFX      5' CCCAGGCTGGTCTCG      12717    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM560  ALDH9    5' CCTAGAACCGATCCCGTGG   5512     _ TA   A
                                CC CG  GATC GTTCTAGG
                                || ||  |||| ||||||||
                                GG GC  CTAG CAAGATCC
                                 T  C_   C
GAM560  C22orf19 3' CCCAGGCTGGTCTCG      13418    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM560  CBX6     3' CTAGAAACTAGGGTT      26612      G  ATCAG
                                AACCC TAG    TTCTAG
                                ||||| |||    ||||||
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                                TTGGG ATC     AAGATC
                                  _  A____
GAM560  CHL1     3'  CCTAGAGAACTGTCCAAGGGTT 21745      GTA  T   __
                                AACCC   GA CAGT  TCTAGG
                                |||||   || ||||  ||||||
                                TTGGG   CT GTCA  AGATCC
                                   AAC  _    AG
GAM560  CIP29    3'  CCCAGGCTGGTCTCG      50402    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM560  FLJ10483 3'  CCTAGAACCTCTACAGGT    36168     C    TCA
                                ACC GTAGA   GTTCTAGG
                                ||| |||||   ||||||||
                                TGG CATCT   CAAGATCC
                                  A    C__
GAM560  FLJ10815 3'  CTGGAATCCACGGGT       36694       A   CAGT
                                ACCCGT GAT    TCTAG
                                |||||| |||    |||||
                                TGGGCA CTA    AGGTC
                                   C   _____
GAM560  FLJ10898 5'  CCCAGAGGTAGATCGACAGGTT 59427      C  A   AG_   A
                                AACC GT GATC   TTCT GG
                                |||| || ||||   |||| ||
                                TTGG CA CTAG   GAGA CC
                                  A  G    ATG    C
GAM560  FLJ11715 3'  CCCAGGCTGGTCTCG       44669    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM560  FLJ12448 3'  CCTAGAACTGTCTGAGG     43176    G    T
                                CC TAGA CAGTTCTAGG
                                || |||| ||||||||||
                                GG GTCT GTCAAGATCC
                                 A   _
GAM560  FLJ20147 3'  CCCAGACTGGTCTCG       34637    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCA GA CC
                                 _       _ C
GAM560  FLJ30532 3'  CCTCAGATGATCTAC       58543        GT   _
                                GTAGATCA  TCT AGG
                                ||||||||  ||| |||
                                CATCTAGT  AGA TCC
                                     __  C
GAM560  FLJ32334 3'  CCCAGGCTGGTCTCG       57981    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
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                                GC TCTGGTCG GA CC
                                 _       _ C
GAM560  KIAA0205 3' CCTGAATAATCTATGGGTT   29579          CA   T
                                AACCCGTAGAT  GTTC AGG
                                ||||||||||  |||| |||
                                TTGGGTATCTA  TAAG TCC
                                      A_   _
GAM560  KIAA0268 3' CCCAGAACTGAAGATGG     70001      AGA      A
                                CCGT   TCAGTTCT GG
                                ||||   |||||||| ||
                                GGTA   AGTCAAGA CC
                                  GA_       C
GAM560  KIAA0318 3' CCTACGTCATCTATGGGTT   68950          CAGTTC
                                AACCCGTAGAT     TAGG
                                ||||||||||      ||||
                                TTGGGTATCTA     ATCC
                                      CTGC__
GAM560  KIAA0552 3' CCTAGAACCTGGGCCTAGG   28311    G   A_   _
                                CC TAG  TCAG TTCTAGG
                                || |||  |||| |||||||
                                GG ATC  GGTC AAGATCC
                                 _  CG   C
GAM560  KIAA0710 3' CCCAGAACTGGGAGATGG    29566      AGA      A
                                CCGT   TCAGTTCT GG
                                ||||   |||||||| ||
                                GGTA   GGTCAAGA CC
                                  GAG       C
GAM560  KIAA0907 3' CCCAGAACTGGTTGC       30172     G       A
                                GTA ATCAGTTCT GG
                                ||| ||||||||| ||
                                CGT TGGTCAAGA CC
                                 _       C
GAM560  KIAA1157 3' AGCTTATCTACGGGTT      72237          C
                                AACCCGTAGAT AGTT
                                |||||||||| ||||
                                TTGGGCATCTA TCGA
                                      T
GAM560  KIAA1671 3' CCCAGGCTGGTCTCG       65669    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM560  KIAA1715 3' CCTGAGCATGATCTAC      68118        _   T
                                GTAGATCA GTTC AGG
                                |||||||| |||| |||
                                CATCTAGT CGAG TCC
                                     A   _
GAM560  KIAA1814 3' CCTAGAGCAGTCTCCAGGG   70360     GT_   CA
                                CCC   AGAT  GTTCTAGG
                                |||   ||||  ||||||||
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                                GGG  TCTG  CGAGATCC
                                  ACC   A_
GAM560  LIECG3   3'  CCCAGGCTGGTCTCG      87409   T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM560  MGC10812 3'  CCTAGAACTTTTGCCAGT   48666   CC    TC
                                AC  GTAGA  AGTTCTAGG
                                ||  |||||  |||||||||
                                TG  CGTTT  TCAAGATCC
                                 AC    __
GAM560  PELI1    5'  CCCAGGCTGGTCTCG      40258   T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM560  PGGT1B   5'  AGTGCTGATCTAGGG      17230    G       T
                                CCC TAGATCAGT CT
                                ||| |||||||||  ||
                                GGG ATCTAGTCG GA
                                  _       T
GAM560  PIP3-E   3'  CCTAGAACTGGGAGATG    66803    AGA
                                CGT   TCAGTTCTAGG
                                |||   ||||||||||
                                GTA   GGTCAAGATCC
                                  GAG
GAM560  PIP5K2B  3'  CCTCAGAACTGAGCCACAGG  13070   C  AGA      _
                                CC GT   TCAGTTCT AGG
                                || ||   |||||||| |||
                                GG CA   AGTCAAGA TCC
                                 A  CCG       C
GAM560  PTDSS1   3'  CCTAGAACTGAGAGGG     28571    GTAGA
                                CCC    TCAGTTCTAGG
                                |||    ||||||||||
                                GGG    AGTCAAGATCC
                                  AG___
GAM560  PYPAF3   3'  CCTGGGATCGCTCTACG    57539       TCA
                                CGTAGA   GTTCTAGG
                                ||||||   ||||||||
                                GCATCT   TAGGGTCC
                                   CGC
GAM560  SDS3     3'  CCCAGAGGCTGATCTGC     69226         _  A
                                GTAGATCAGT TCT GG
                                |||||||||| ||| ||
                                CGTCTAGTCG AGA CC
                                      G   C
GAM560  SRF      3'  CCCAGAACTGGCTGGG      11943    GT  A      A
                                CCC  AG TCAGTTCT GG
                                |||  || |||||||| ||
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                                GGG  TC GGTCAAGA CC
                                  __ _      C
GAM560  TRIM2    5' CCCAGTTGTCTGCGGG     30941       T  TT  A
                                CCCGTAGA CAG  CT GG
                                |||||||| |||  || ||
                                GGGCGTCT GTT  GA CC
                                    _  __ C
GAM560  TSPEAR   3' CCTAGGGCATCCCGGG     58719     TA  CA
                                CCCG  GAT  GTTCTAGG
                                ||||  |||  ||||||||
                                GGGC  CTA  CGGGATCC
                                  C_  __
GAM560  LOC113026 3' CCCAGGCTGGTCTCG      55899    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM560  LOC125144 3' CCCAGGCTGGTCTCAGG    74393    GT      T  A
                                CC  AGATCAGT CT GG
                                ||  |||||||| || ||
                                GG  TCTGGTCG GA CC
                                 AC       _ C
GAM560  LOC126549 5' CCTAGAACTGGCTGC      75708     A
                                GTAG TCAGTTCTAGG
                                |||| ||||||||||
                                CGTC GGTCAAGATCC
                                  _
GAM560  LOC126661 3' CCCAGGCTGGTCTCG      74547    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM560  LOC127702 3' CCTGGGACACCTACAGG    75458    C   ATCA
                                CC GTAG   GTTCTAGG
                                || ||||   ||||||||
                                GG CATC   CAGGGTCC
                                 A   CA__
GAM560  LOC143920 3' CCCAGAGTCCTATCTAGGGT  76624     G   C __   A
                                ACCC TAGAT AG  TTCT GG
                                |||| ||||| ||  |||| ||
                                TGGG ATCTA TC  GAGA CC
                                  _   _ CT   C
GAM560  LOC145725 3' CCCAGGCTGGTCTCG      77403    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM560  LOC145732 3' CCCAGGCTGGTCTCG      77425    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
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                                GC TCTGGTCG GA CC
                                 _       _ C
GAM560   LOC146733 3'  CCTGGCTTGATCTACAGGT   83759     C       TT
                                ACC GTAGATCAG  CTAGG
                                ||| |||||||||  |||||
                                TGG CATCTAGTT  GGTCC
                                  A       C_
GAM560   LOC154877 3'  CCCAGGCTGGTCTCG       86286    T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM560   LOC154881 3'  CCCAGAACAGAAGAAGGGTT   81170       GTAGA  A     A
                                AACCC     TC GTTCT GG
                                |||||     || ||||| ||
                                TTGGG     AG CAAGA CC
                                   AAGA_  A     C
GAM560   LOC163998 5'  CCCAGAACTGGATGG       87053      AGA       A
                                CCGT   TCAGTTCT GG
                                ||||   |||||||| ||
                                GGTA   GGTCAAGA CC
                                  ___       C
GAM560   LOC170261 3'  CTGCAGCCTACGGGT       82582         ATCA   C
                                ACCCGTAG    GTT TAG
                                ||||||||    ||| |||
                                TGGGCATC    CGA GTC
                                    _____   C
GAM560   LOC196463 3'  CCTAGAGTGGGTCACG      87710     A    AG
                                CGT GATC  TTCTAGG
                                ||| ||||  |||||||
                                GCA CTGG  GAGATCC
                                  _    GT
GAM560   LOC196957 3'  CCCAGGCTGGTCTCG       87820    T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM560   LOC196961 3'  CCCAGGCTGGTCTCG       87841    T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM560   LOC197138 3'  CCCAGGCTGGTCTCG       87914    T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM560   LOC197423 5'  CCCAGAACTGATAGTGC     77857     G_        A
                                GTA  ATCAGTTCT GG
                                |||  ||||||||| ||
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                                CGT  TAGTCAAGA CC
                                  GA        C
GAM560   LOC200268 3'  CCCAGGCTGGTCTCG       88681    T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _  C
GAM560   LOC200339 3'  AACTGATCTACAGGTT       90022      C
                                AACC GTAGATCAGTT
                                |||| ||||||||||
                                TTGG CATCTAGTCAA
                                  A
GAM560   LOC219653 3'  CCCAGAACTGAACACTAGGT   91292     CG   A__       A
                                ACC  TAG   TCAGTTCT GG
                                |||  |||   |||||||| ||
                                TGG  ATC   AGTCAAGA CC
                                  __   ACA       C
GAM560   LOC220565 5'  CCCAGAACTGATAGTGC     90748     G_        A
                                GTA  ATCAGTTCT GG
                                |||  ||||||||| ||
                                CGT  TAGTCAAGA CC
                                  GA        C
GAM560   LOC221895 3'  CCTATTGATATCTGCGG     92524         __     TCT
                                CCGTAGA  TCAGT   AGG
                                |||||||  |||||   |||
                                GGCGTCT  AGTTA   TCC
                                    AT    ___
GAM560   LOC221960 3'  CCCAGGCTGGTCTCG       91081    T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _  C
GAM560   LOC253228 3'  CTAGTGCTGACCTACGGG     95940         A    T
                                CCCGTAG TCAGT CTAG
                                ||||||| ||||| ||||
                                GGGCATC AGTCG GATC
                                    C    T
GAM560   LOC254181 5'  CCCAGAACTGGCTCAGG      97583    GT  A       A
                                CC  AG TCAGTTCT GG
                                ||  || |||||||| ||
                                GG  TC GGTCAAGA CC
                                 AC  _       C
GAM560   LOC257051 3'  CTGCAGCCTACGGGT        96316         ATCA   C
                                ACCCGTAG    GTT TAG
                                ||||||||    ||| |||
                                TGGGCATC    CGA GTC
                                     _____  C
GAM560   LOC51226  3'  CCCAGAACTGACTCCTAAGG   33150    G   A__       A
                                CC TAG   TCAGTTCT GG
                                || |||   |||||||| ||
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                                GG ATC   AGTCAAGA CC
                                 A  CTC       C
GAM560  LOC51622  3' CCCAGGCTGGTCTCG      31566    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM560  LOC90139  3' CCCAGAACTGAGGCTTGG    55402     T  A_      A
                                CCG AG  TCAGTTCT GG
                                ||| ||  |||||||| ||
                                GGT TC  AGTCAAGA CC
                                  _ GG       C
GAM560  LOC90979  3' CCTGCAGGCTGATCCAGGG   64525     GTA      C_
                                CCC   GATCAGTT  TAGG
                                |||   ||||||||  ||||
                                GGG   CTAGTCGG  GTCC
                                  AC_       AC
GAM560  LOC91012  5' CCCAGGCTGGTCTCGG     64639     T      T  A
                                CCG AGATCAGT CT GG
                                ||| |||||||| || ||
                                GGC TCTGGTCG GA CC
                                  _       _ C
GAM560  LOC92568  5' CTGGAGATTCTACGGG     69772        TCAG
                                CCCGTAGA    TTCTAG
                                ||||||||    ||||||
                                GGGCATCT    GAGGTC
                                     TA__
GAM560  LOC93550  5' CCTAGAACTGGAATAC     72584     GA
                                GTA  TCAGTTCTAGG
                                |||  ||||||||||
                                CAT  GGTCAAGATCC
                                  AA
GAM560  LOC93550  5' GGTGCTGATCTCCGAGT     72586    C  T      T
                                AC CG AGATCAGT CT
                                || || |||||||| ||
                                TG GC TCTAGTCG GG
                                 A  C       T
GAM561  ALDH3B1   3' CACACCTGTAATCCCAGCACTT 91522         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| |||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  ALOX5     3' CACACCCAGCTCAGCATTT    90851        TGA   CA
                                AAGTGCTG   TTG  GGTGTG
                                ||||||||   |||  ||||||
                                TTTACGAC   GAC  CCACAC
                                     TC_   ___
GAM561  AREG      5' CACACCTGGGTGCCAGCGC    7995        TG   G
                                GTGCTG  ATT CAGGTGTG
                                ||||||  ||| ||||||||
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                                CGCGAC  TGG GTCCACAC
                                   CG  _
GAM561  ATM      3'  CACACCTATAATCCCAGCACTT 56299          T    C
              T                    AAAGTGCTG GATTG AGGTGTG
                                   ||||||||| ||||| |||||||
                                   TTTCACGAC CTAAT TCCACAC
                                        C    A
GAM561  BHMT2    3'  CACACCTGCAATCCCAGCACTT 34308          T
              T                    AAAGTGCTG GATTGCAGGTGTG
                                   ||||||||| |||||||||||||
                                   TTTCACGAC CTAACGTCCACAC
                                        C
GAM561  BPHL     3'  CACAGCTATAATCTCAGCACTT 15083          T    C  G
              T                    AAAGTGCTG GATTG AG TGTG
                                   ||||||||| ||||| || ||||
                                   TTTCACGAC CTAAT TC ACAC
                                        T    A  G
GAM561  C1orf1   3'  CACCTGTAATCCCAACACTTT  6857         C  T
                                   AAAGTG TG GATTGCAGGTG
                                   |||||| || ||||||||||
                                   TTTCAC AC CTAATGTCCAC
                                      A  C
GAM561  C21orf5  3'  CACACCTGTAATCTCAGCACTT 17610          T
              T                    AAAGTGCTG GATTGCAGGTGTG
                                   ||||||||| |||||||||||||
                                   TTTCACGAC CTAATGTCCACAC
                                        T
GAM561  CASP6    3'  CACACCTGTAATCCCAGCACTT 52201          T
              T                    AAAGTGCTG GATTGCAGGTGTG
                                   ||||||||| |||||||||||||
                                   TTTCACGAC CTAATGTCCACAC
                                        C
GAM561  CASP6    3'  CACACCTGTAATCCCAGCACTT 6908           T
              T                    AAAGTGCTG GATTGCAGGTGTG
                                   ||||||||| |||||||||||||
                                   TTTCACGAC CTAATGTCCACAC
                                        C
GAM561  CHRNA5   3'  CACACCTGTAATCCCAGCACTT 59754          T
              T                    AAAGTGCTG GATTGCAGGTGTG
                                   ||||||||| |||||||||||||
                                   TTTCACGAC CTAATGTCCACAC
                                        C
GAM561  CPM      3'  CACACCTTGTAATCCCAGCACT 59675          T    _
              TT                    AAAGTGCTG GATTGCA GGTGTG
                                   ||||||||| ||||||| ||||||
                                   TTTCACGAC CTAATGT CCACAC
                                        C      T
GAM561  CRACC    3'  CACACCTGTAATCCCAGCACTT 41003          T
              T                    AAAGTGCTG GATTGCAGGTGTG
                                   ||||||||| |||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  CTMP     3'  CACACCTGTAATCCCAGCACTT 53875          T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  CYP4F3   3'  CACACCTGTAATCCCAGCACTT 6110           T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  DCLRE1C  3'  CACACTTGTAATCCCAGCACTT 42526          T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTTCACAC
                                      C
GAM561  DMC1     3'  CACACCTGTAATCCCAGCACTT 22971          T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  DNASE2   3'  CACATCTGTAACCCCAGCACTT 7264          TGA
           T                   AAAGTGCTG   TTGCAGGTGTG
                               |||||||||   ||||||||||
                               TTTCACGAC   AATGTCTACAC
                                      CCC
GAM561  EHHADH   3'  CACACCTGTAATCCCAGCACTT 8749          T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  ESRRB    5'  ACACCTGCCCTAGCCCT     67316    T    TGATT
                               AG GCTG     GCAGGTGT
                               || ||||     ||||||||
                               TC CGAT     CGTCCACA
                                C    CC___
GAM561  F2RL3    3'  CACACCTGCAATCCCAGCACTT 14171          T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAACGTCCACAC
                                      C
GAM561  FANCC    3'  CACACCTGTGATCCCAGCACTT 70519          T   TG
           T                   AAAGTGCTG GAT  CAGGTGTG
                               ||||||||| |||  ||||||||
                               TTTCACGAC CTA  GTCCACAC
                                      C   GT
GAM561  FANCD2   3'  CACACCTGTAATCCCAGCACTT 52354          T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  FPGS    3'  CACACCTGCAGTGCCAGC    17081      TG
                                GCTG  ATTGCAGGTGTG
                                ||||  ||||||||||||
                                CGAC  TGACGTCCACAC
                                  CG
GAM561  FUT6    3'  CACACCTGTAATCCCAGCACTT 3808          T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||||  ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  GRM6    3'  CACACCTGTAATCCCAGCACTT 5928          T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||||  ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  HIP1    3'  CACACGTTTAATCCCAGCACTT 18057         T    CAG
           T                     AAAGTGCTG GATTG   GTGTG
                                 |||||||||  |||||   |||||
                                 TTTCACGAC CTAAT   CACAC
                                      C    TTG
GAM561  HUNK    3'  CACACCTGTAATCCCAGCACTT 27443         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||||  ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  IFNAR1  3'  CACACCTGTAATCCCAGCACTT 5282          T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||||  ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  KCNK3   3'  CACACCTGTATTCCCAACACTT 9548        C  T  T
           T                     AAAGTG TG GA TGCAGGTGTG
                                 ||||||  ||  ||  ||||||||||
                                 TTTCAC AC CT ATGTCCACAC
                                    A  C  T
GAM561  KLF8    5'  CACACCTGTAATCTCAGCACTT 23403         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||||  ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                      T
GAM561  LRRC2   3'  CACACCTGTAATCCCAGCACTT 44466         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||||  ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  LUZP1   3'  CACACCTGTAATCCCAGCACTT 53297         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||||  ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  MAFF    3'  CACATCTGTAATCCCAGCACTT 24642        T
                T                AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCTACAC
                                      C
GAM561  MAPK4   3'  CACCCTAACCACAGCGC    10823        A   CA
                                 GTGCTGTG TTG  GGTG
                                 |||||||| |||  ||||
                                 CGCGACAC AAT  CCAC
                                      C   C_
GAM561  MCM4    3'  CACACCTGTAATCCCAGCACTT 61902        T
                T                AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  MRC1    3'  CACAGCACCACAGCAC     10113        AT   AG
                                 GTGCTGTG  TGC  GTG
                                 ||||||||  |||  |||
                                 CACGACAC  ACG  CAC
                                      C_   A_
GAM561  MTNR1A  3'  CACACCTGTAATCTCAGCACTT 19888        T
                T                AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                      T
GAM561  NOV     3'  CACACCTACAGAGCAC     10241       G  ATTGC
                                 GTGCT TG    AGGTGTG
                                 ||||| ||    |||||||
                                 CACGA AC    TCCACAC
                                    G  A____
GAM561  PAICS   3'  CACACCTACGATCACAGCACTT 21254            C
                                 AAGTGCTGTGATTG AGGTGTG
                                 |||||||||||||| |||||||
                                 TTCACGACACTAGC TCCACAC
                                           A
GAM561  PCDH11X 3'  CACACCTGTAATCCCAGCACTT 52006        T
                T                AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  PDE4A   3'  CACACTCTGATCACAGC    20580        TG  _
                                 GCTGTGAT  CAG GTGTG
                                 ||||||||  ||| |||||
                                 CGACACTA  GTC CACAC
                                      __  T
GAM561  PSD     5'  CTGCAATCCCAGCACTTT    10928        T
                                 AAAGTGCTG GATTGCAG
                                 ||||||||| ||||||||
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                                TTTCACGAC CTAACGTC
                                      C
GAM561  PSMB9    3'  CACACCTATAATCCCAGCACTT 10958         T    C
           T                   AAAGTGCTG GATTG AGGTGTG
                               ||||||||| ||||| |||||||
                               TTTCACGAC CTAAT TCCACAC
                                      C    A
GAM561  PSMB9    3'  CTGTAATCACAGCACTTT    10961
                               AAAGTGCTGTGATTGCAG
                               ||||||||||||||||||
                               TTTCACGACACTAATGTC

GAM561  PTAFR    3'  CACACCTGTAATCCCAGCACTT 6293          T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  PTHLH    3'  ACACCTGGGCAAACTTT     11011      GC   GATTG
                               AAAGT  TGT    CAGGTGT
                               |||||  |||    |||||||
                               TTTCA  ACG    GTCCACA
                                  A_   G____
GAM561  RAB7L1   3'  CACACCTGTAATCCCAGCACTT 14105         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  RARB     5'  CACACCTAGAGGATAAGCACTT 6372         GTGA_  GC
           T                   AAAGTGCT    TT  AGGTGTG
                               ||||||||    ||  |||||||
                               TTTCACGA    AG  TCCACAC
                                    ATAGG  A_
GAM561  SEPX1    3'  CACACCTGCAGGGAGGCCCTT  32914     T   GTGA
                               AAG GCT    TTGCAGGTGTG
                               ||| |||    ||||||||||
                               TTC CGG    GACGTCCACAC
                                 C   AGG_
GAM561  SIM2     3'  CACACCTGTAATCCCAGCACTT 23782         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  SUV39H2  3'  CACACCTGTGATCCCAGCACTT 45135         T   TG
           T                   AAAGTGCTG GAT  CAGGTGTG
                               ||||||||| |||  ||||||||
                               TTTCACGAC CTA  GTCCACAC
                                      C   GT
GAM561  TNFSF15  3'  CACACCTGTAATCCCAACACTT 17590       C  T
           T                   AAAGTG TG GATTGCAGGTGTG
                               |||||| || ||||||||||||
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                                TTTCAC AC CTAATGTCCACAC
                                   A  C
GAM561  UBE2G2   3'  CACGCCTGCAATCCCAGCACTT 64851          T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAACGTCCGCAC
                                    C
GAM561  XRCC3    3'  CACACTGTGCCCCACAAAACTT 18335      GC    ATT  _
                                AAGT  TGTG   GCA GGTGTG
                                ||||  ||||   ||| ||||||
                                TTCA  ACAC   CGT TCACAC
                                  AA   CC_   G
GAM561  ZNF136   3'  CACACCTGTAATCCCAGCACTT 59886          T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                    C
GAM561  ZNF137   3'  CACACCTGTAATCCCAGCACTT 12859          T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                    C
GAM561  AAK1     3'  CACACTTGTAACCACAGGACTT 29842       G     A
            T                   AAAGT CTGTG TTGCAGGTGTG
                                ||||| ||||| ||||||||||
                                TTTCA GACAC AATGTTCACAC
                                   G    C
GAM561  AF020591 3'  CACCTGTAATCCCAGCAC    27137        T
                                GTGCTG GATTGCAGGTG
                                |||||| ||||||||||
                                CACGAC CTAATGTCCAC
                                   C
GAM561  BIRC1    3'  CACACCTGTAATCCCAGCACTT 15786          T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                    C
GAM561  C13orf1  3'  CACACCTGTAATCCCAGCACTT 39965          T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                    C
GAM561  C1orf24  3'  CACCTATAATCCCAGCACTTT  53708          T    C
                                AAAGTGCTG GATTG AGGTG
                                ||||||||| ||||| |||||
                                TTTCACGAC CTAAT TCCAC
                                    C    A
GAM561  C22orf20 3'  CACGGCTGTAATCCCAGCACTT 47428          T       G
            T                   AAAGTGCTG GATTGCAG TGTG
                                ||||||||| |||||||| ||||
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                                TTTCACGAC CTAATGTC GCAC
                                     C       G
GAM561  C6orf5   3'  CACACCTGTAATCCCAGCACTT 31339         T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                   C
GAM561  C8orf2   3'  CACACCTGTAATCCCAGCACTT 23159         T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                   C
GAM561  C9orf5   3'  CACATCTGTAATCCCAGCACTT 49273         T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCTACAC
                                   C
GAM561  CALN1    3'  CACACCTATAATCCCAGCACTT 48856         T    C
           T                  AAAGTGCTG GATTG AGGTGTG
                              ||||||||| ||||| |||||||
                              TTTCACGAC CTAAT TCCACAC
                                   C    A
GAM561  CAMKK2   5'  CACACCTGTAATCCCAGCACTT 21577          T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                   C
GAM561  CFLAR    3'  CACACCTGTAATCCCAGCACTT 13927         T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                   C
GAM561  CYorf14  3'  CACACCCTGTAATCCCAGCACT 37607         T      _
           TT                  AAAGTGCTG GATTGCAGG TGTG
                              ||||||||| ||||||||| ||||
                              TTTCACGAC CTAATGTCC ACAC
                                   C       C
GAM561  D21S2056E 3'  CACACCTGTAATCCCAGCACTT 13468          T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                   C
GAM561  dJ383J4.3 3'  CACACCTGTAATTCCAGCACTT 66943         TG
           T                  AAAGTGCTG  ATTGCAGGTGTG
                              |||||||||  ||||||||||||
                              TTTCACGAC  TAATGTCCACAC
                                   CT
GAM561  DKFZp434E0519 3'  CACACCTATAATCCCAGCACTT 49982         T    C
           T                  AAAGTGCTG GATTG AGGTGTG
                              ||||||||| ||||| |||||||
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                                TTTCACGAC CTAAT TCCACAC
                                      C     A
GAM561   DKFZp434E0519 3'  CACACTTATAATCCCAGCACTT 49983          T     C
            T                  AAAGTGCTG GATTG AGGTGTG
                               ||||||||| ||||| |||||||
                               TTTCACGAC CTAAT TTCACAC
                                      C     A
GAM561   DKFZP434F1735 3'  CACATTTGTAATCCCAGCACTT 31497          T
            T                  AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| |||||||||||||
                               TTTCACGAC CTAATGTTTACAC
                                      C
GAM561   DKFZp547C176 3'  CACACCTGTAATCCCAGCACTT 67220          T
            T                  AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| |||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561   DKFZp547I094 3'  CACACCTGTAATCCCAGCACTT 49632          T
            T                  AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| |||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561   DKFZP586D2223 3'  CACACCTGTAATTCCAACACTT 37680       C  TG
            T                  AAAGTG TG  ATTGCAGGTGTG
                               |||||| ||  ||||||||||||
                               TTTCAC AC  TAATGTCCACAC
                                  A  CT
GAM561   DKFZp761O132 5'  CACACCTGCCCACCCTGCACTC 50196    A     T__   ATT
            C                  A AGTGC   GTG   GCAGGTGTG
                               | |||||   |||   |||||||||
                               C TCACG   CAC   CGTCCACAC
                               C     TCC   C__
GAM561   DRF1     3'  CACACCTGTAATCCCAGCACTT 47025          T
            T                  AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| |||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561   EIF2S1    3'  CACACAGTAGCTCCAACACTTT 14583        C  T  _    AG
                               AAAGTG TG GA TTGC  GTGTG
                               |||||| || || ||||  |||||
                               TTTCAC AC CT GATG  CACAC
                                  A  _  C    A_
GAM561   FBXO26    3'  CACACCTGTGGAATCCCAGCAC 46093         T    __
            TT                  AAGTGCTG GATT  GCAGGTGTG
                               |||||||| ||||  |||||||||
                               TTCACGAC CTAA  TGTCCACAC
                                     C    GG
GAM561   FLJ10043  3'  CACACCTGTAATCCCAGCACTT 35755          T
            T                  AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| |||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  FLJ10460 3' CACACCTGTAATCCCAACACTT 36126       C  T
           T                  AAAGTG TG GATTGCAGGTGTG
                              |||||| || ||||||||||||||
                              TTTCAC AC CTAATGTCCACAC
                                 A  C
GAM561  FLJ10547 3' CACACCTGTAATCCCAGCACTT 36266        T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  FLJ10650 3' CACACCTGTAATCCCAGCACTT 36380        T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  FLJ10803 3' CACACCGGTAATCCCAGCACTT 36661        T     A
           T                  AAAGTGCTG GATTGC GGTGTG
                              ||||||||| |||||| ||||||
                              TTTCACGAC CTAATG CCACAC
                                     C     G
GAM561  FLJ10803 3' CACACCTGTAATCCCAGCACTT 36662        T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  FLJ10830 3' CACACCTATAATCGAGCACTTT 36719        G     C
                              AAAGTGCT TGATTG AGGTGTG
                              |||||||| |||||| |||||||
                              TTTCACGA GCTAAT TCCACAC
                                 _     A
GAM561  FLJ10989 3' CACACCTGTAATCCCAGCACTT 36945        T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  FLJ11029 3' CACACCTGTAATCCCAGCACTT 60971        T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  FLJ11149 3' CACACCGGTAATCCCAGCACTT 37108        T     A
           T                  AAAGTGCTG GATTGC GGTGTG
                              ||||||||| |||||| ||||||
                              TTTCACGAC CTAATG CCACAC
                                     C     G
GAM561  FLJ11259 3' CACACCTGTATTCCCAGCACTT 37185        T  T
           T                  AAAGTGCTG GA TGCAGGTGTG
                              ||||||||| || ||||||||||
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                                TTTCACGAC CT ATGTCCACAC
                                     C  T
GAM561  FLJ11700  3'  CACACCTGTAATCCCAGCACTT 46035        T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                   C
GAM561  FLJ11726  3'  CACACCTGTAATCCCAGCACTT 46407        T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                   C
GAM561  FLJ11800  3'  CACACTTGTAATCACTGCACTT 46423       T
           T                  AAAGTGC GTGATTGCAGGTGTG
                              ||||||| |||||||||||||||
                              TTTCACG CACTAATGTTCACAC
                                  T
GAM561  FLJ11996  3'  CACACCTGTAATTCCAGCACTT 46435        TG
           T                  AAAGTGCTG  ATTGCAGGTGTG
                              |||||||||  ||||||||||||
                              TTTCACGAC  TAATGTCCACAC
                                   CT
GAM561  FLJ12078  3'  CACACTAGTAATCACAGCCTCC 46452   A  T        A
                              A AG GCTGTGATTGC GGTGTG
                              | || |||||||||| ||||||
                              C TC CGACACTAATG TCACAC
                               C _         A
GAM561  FLJ12294  5'  CACACCTGTAAACCCAGCACTT 47008        TGA
           T                  AAAGTGCTG   TTGCAGGTGTG
                              |||||||||   ||||||||||
                              TTTCACGAC   AATGTCCACAC
                                   CCA
GAM561  FLJ12363  3'  CACACCTGTAATCCCAGCACTT 49673        T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                   C
GAM561  FLJ12985  3'  CACACCTGTAATCCCAGCACTT 46238        T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                   C
GAM561  FLJ13193  3'  CACACCTGCAATCCCAACACTT 49759       C  T
           T                  AAAGTG TG GATTGCAGGTGTG
                              |||||| || ||||||||||||
                              TTTCAC AC CTAACGTCCACAC
                                 A  C
GAM561  FLJ13193  3'  CACACCTGTAATCCCAGCACTT 49760        T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  FLJ13352 3' CACACCTGTTAATCCCAGCACT 44752        T   _
           T                  AAGTGCTG GATTG CAGGTGTG
                              |||||||| ||||| ||||||||
                              TTCACGAC CTAAT GTCCACAC
                                   C    T
GAM561  FLJ13390 3' CACACCTGAAATCCCAGCACTT 42537        T   G
           T                  AAAGTGCTG GATT CAGGTGTG
                              ||||||||| |||| ||||||||
                              TTTCACGAC CTAA GTCCACAC
                                   C   A
GAM561  FLJ13544 3' CACACCTGTCATCCCAGCACTT 46575        T  T
           T                  AAAGTGCTG GAT GCAGGTGTG
                              ||||||||| ||| |||||||||
                              TTTCACGAC CTA TGTCCACAC
                                   C  C
GAM561  FLJ13659 3' CACACCTGTAATCCCAGCACTT 47244        T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                   C
GAM561  FLJ13848 3' CACCTGTAATCCCAGCACTTT  45460        T
                              AAAGTGCTG GATTGCAGGTG
                              ||||||||| ||||||||||
                              TTTCACGAC CTAATGTCCAC
                                   C
GAM561  FLJ13984 3' CACCTGTAATCCCAGCACTTT  45446        T
                              AAAGTGCTG GATTGCAGGTG
                              ||||||||| ||||||||||
                              TTTCACGAC CTAATGTCCAC
                                   C
GAM561  FLJ14011 3' CACCTGTAACCCCAGCACTTT  42063        TGA
                              AAAGTGCTG  TTGCAGGTG
                              |||||||||  |||||||||
                              TTTCACGAC  AATGTCCAC
                                   CCC
GAM561  FLJ14117 3' CACACTTGTAATCCCAGCACTT 42902        T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTTCACAC
                                   C
GAM561  FLJ14117 3' CACACTTGTAATCCCAGCACTT 42903        T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTTCACAC
                                   C
GAM561  FLJ14251 3' CACACCTGTAATCCCAGCACTT 45966        T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  FLJ14346  3'  CACACCTGTAATCCCAGCACTT 46708         T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  FLJ14397  3'  CACACCTATAATCCCAGCACTT 51324         T    C
           T                  AAAGTGCTG GATTG AGGTGTG
                              ||||||||| ||||| |||||||
                              TTTCACGAC CTAAT TCCACAC
                                     C    A
GAM561  FLJ14642  3'  CACACCTGTAATCCCAGCACTT 51494         T
                              AAGTGCTG GATTGCAGGTGTG
                              |||||||| ||||||||||||
                              TTCACGAC CTAATGTCCACAC
                                     C
GAM561  FLJ14957  3'  CACTGAGACCAATCACAGCCT  51740    T       CA___
                              AG GCTGTGATTG    GGTG
                              || ||||||||||    ||||
                              TC CGACACTAAC    TCAC
                               _        CAGAG
GAM561  FLJ20045  3'  CACACCTCTAATCCCAGCACTT 34414         T    C
           T                  AAAGTGCTG GATTG AGGTGTG
                              ||||||||| ||||| |||||||
                              TTTCACGAC CTAAT TCCACAC
                                     C    C
GAM561  FLJ20139  3'  CACACCTGTAATCCCAACACTT 34622       C  T
           T                  AAAGTG TG GATTGCAGGTGTG
                              |||||| || ||||||||||||
                              TTTCAC AC CTAATGTCCACAC
                                  A  C
GAM561  FLJ20280  3'  CACACCTGTAATCCCAGCACTT 34848         T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  FLJ20340  3'  CACACCCGTAATCCCAGCACTT 34973         T    A
           T                  AAAGTGCTG GATTGC GGTGTG
                              ||||||||| |||||| ||||||
                              TTTCACGAC CTAATG CCACAC
                                     C    C
GAM561  FLJ20519  3'  CACACCTGCAATGATTACT   35345     CT  G
                              AGTG  GT ATTGCAGGTGTG
                              ||||  || ||||||||||||
                              TCAT  TA TAACGTCCACAC
                                __  G
GAM561  FLJ20808  3'  CACACCCATAATCCCAGCACTT 35672         T    CA
           T                  AAAGTGCTG GATTG  GGTGTG
                              ||||||||| |||||  ||||||
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                                TTTCACGAC CTAAT  CCACAC
                                      C     AC
GAM561  FLJ22054  3'  CACACCTGTAATCCCAGCACTT 94392          T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  FLJ23499  3'  CACACCTAATCCCAGCACTTT  42818          T   GC
                               AAAGTGCTG GATT  AGGTGTG
                               ||||||||| ||||  |||||||
                               TTTCACGAC CTAA  TCCACAC
                                      C   __
GAM561  FLJ30092  3'  CACACCTGTAATCCCAGCACTT 58686          T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  FLJ31300  3'  CACACCCGCACTACCTGCACTT 58284        T_  AT   A
                               AAGTGC  GTG  TGC GGTGTG
                               ||||||  |||  ||| ||||||
                               TTCACG  CAT  ACG CCACAC
                                   TC   C_   C
GAM561  FUSIP1    3'  CACACCTGTAATCCCAGCACTT 53956          T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  GCN2      3'  CACACCTTTAATCCCAGCACTT 62769          T    C
           T                   AAAGTGCTG GATTG AGGTGTG
                               ||||||||| ||||| |||||||
                               TTTCACGAC CTAAT TCCACAC
                                      C    T
GAM561  GIT2      3'  ACACCTGGAGCAGCCT      54074    T    GAT G
                               AG GCTGT   T CAGGTGT
                               || |||||   | |||||||
                               TC CGACG   A GTCCACA
                                _    ___ G
GAM561  GIT2      3'  ACACCTGGAGCAGCCT      54087    T    GAT G
                               AG GCTGT   T CAGGTGT
                               || |||||   | |||||||
                               TC CGACG   A GTCCACA
                                _    ___ G
GAM561  GIT2      3'  ACACCTGGAGCAGCCT      28752    T    GAT G
                               AG GCTGT   T CAGGTGT
                               || |||||   | |||||||
                               TC CGACG   A GTCCACA
                                _    ___ G
GAM561  IRF7      5'  CACACCTGCAGTCACA      14439
                               TGTGATTGCAGGTGTG
                               ||||||||||||||||
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                                ACACTGACGTCCACAC

GAM561  IRF7     5' CACACCTGCAGTCACA      14441
                                TGTGATTGCAGGTGTG
                                ||||||||||||||||
                                ACACTGACGTCCACAC

GAM561  IRF7     5' CACACCTGCAGTCACA      7814
                                TGTGATTGCAGGTGTG
                                ||||||||||||||||
                                ACACTGACGTCCACAC

GAM561  IRF7     5' CACACCTGCAGTCACA      14445
                                TGTGATTGCAGGTGTG
                                ||||||||||||||||
                                ACACTGACGTCCACAC

GAM561  KATII    3' CACACCTATAATCCCAGCACTT 32643          T    C
              T                  AAAGTGCTG GATTG AGGTGTG
                                 ||||||||| ||||| |||||||
                                 TTTCACGAC CTAAT TCCACAC
                                       C    A
GAM561  KIAA0184 3' CACCTGTAATCCCAGCACTTT  65193          T
                                 AAAGTGCTG GATTGCAGGTG
                                 ||||||||| ||||||||||
                                 TTTCACGAC CTAATGTCCAC
                                       C
GAM561  KIAA0226 3' CACACCTGTAATCCCAGCACTT 63512          T
              T                  AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                       C
GAM561  KIAA0266 3' CACACCTGTAATCCCAGCACTT 41327          T
              T                  AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                       C
GAM561  KIAA0266 3' CACACCTGTAATCCCAGCACTT 41328          T
              T                  AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                       C
GAM561  KIAA0391 3' CACACCTACAGTTCCAGCACTT 27907          TG   C
              T                  AAAGTGCTG  ATTG AGGTGTG
                                 ||||||||| |||| |||||||
                                 TTTCACGAC  TGAC TCCACAC
                                       CT   A
GAM561  KIAA0471 3' CACATCTGTAATCCCAGCACTT 29388          T
              T                  AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCTACAC
                                      C
GAM561  KIAA0596 3' CACACCTACCTGCACAGCAC  62825        ATTGC
                                GTGCTGTG    AGGTGTG
                                ||||||||    |||||||
                                CACGACAC    TCCACAC
                                    GTCCA
GAM561  KIAA0798 3' CACCTGTAATCCCAGCACTTT 27718         T
                                AAAGTGCTG GATTGCAGGTG
                                ||||||||| ||||||||||
                                TTTCACGAC CTAATGTCCAC
                                      C
GAM561  KIAA0912 3' CACACCTGTAATCCCAGCACTT 64408         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  KIAA0939 3' CACACCTGGCCTCACACTTT  62007      GCT   TTG
                                AAAGT  GTGA  CAGGTGTG
                                |||||  ||||  ||||||||
                                TTTCA  CACT  GTCCACAC
                                   ___   CCG
GAM561  KIAA1001 3' CACACCTGTAGTCCCAGCACTT 30289         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTGATGTCCACAC
                                      C
GAM561  KIAA1086 3' CACACCTATAATCCCAGCACTT 70741         T   C
           T                     AAAGTGCTG GATTG AGGTGTG
                                ||||||||| ||||| |||||||
                                TTTCACGAC CTAAT TCCACAC
                                      C    A
GAM561  KIAA1204 3' CACATCTGTAATCCCAACACTT 69216       C  T
           T                     AAAGTG TG GATTGCAGGTGTG
                                |||||| || ||||||||||||
                                TTTCAC AC CTAATGTCTACAC
                                   A  C
GAM561  KIAA1423 3' CACATCTGTAATCTCAACACTT 61724       C  T
           T                     AAAGTG TG GATTGCAGGTGTG
                                |||||| || ||||||||||||
                                TTTCAC AC CTAATGTCTACAC
                                   A  T
GAM561  KIAA1456 3' CACACCTGTACTCCCAGCACTT 66991         T  T
                                AAGTGCTG GA TGCAGGTGTG
                                |||||||| || ||||||||||
                                TTCACGAC CT ATGTCCACAC
                                      C  C
GAM561  KIAA1456 5' CACCTGTAATCCCAGCACTTT  66992         T
                                AAAGTGCTG GATTGCAGGTG
                                ||||||||| ||||||||||
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                                TTTCACGAC CTAATGTCCAC
                                      C
GAM561  KIAA1559 3'  CACACCTGTAATCCCAGCACTT 73059         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  KIAA1586 5'  CACACCTGTAATCCCAGCACTT 92328         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  KIAA1855 3'  CACACCACCTCCCTCAGCACTT 92336        TGATTGCA
                               AAGTGCTG       GGTGTG
                               ||||||||       ||||||
                               TTCACGAC       CCACAC
                                    TCCCTCCA
GAM561  KIAA1941 3'  CACACCTGTAATCCCAGCACTT 74836         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  KIAA1954 3'  CACACCTGTAATCCCAGCACTT 77716         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  KIAA1979 3'  CACACCTGGCACAACAT     88275     C    ATTG
                               GTG TGTG    CAGGTGTG
                               ||| ||||    ||||||||
                               TAC ACAC    GTCCACAC
                                 A    G___
GAM561  KR18     3'  CACACCTGTGATCCCAGCACTT 52740         T   TG
           T                   AAAGTGCTG GAT  CAGGTGTG
                               ||||||||| |||  ||||||||
                               TTTCACGAC CTA  GTCCACAC
                                      C   GT
GAM561  MACF1    3'  CACACCTGTAATCCCAGCACTT 52315         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  MGC10814 3'  CACACCTGTAATCCCAGCACTT 51037         T
                               AAGTGCTG GATTGCAGGTGTG
                               |||||||| ||||||||||||
                               TTCACGAC CTAATGTCCACAC
                                     C
GAM561  MGC14407 3'  CACACCTGTAATCTCAGCACTT 51876         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                      T
GAM561  MGC14817 3' CACACCTGTAATCCCAGCACTT 50335        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  MGC2562  3' CACACCTGTAATCCCAGCACTT 50434        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  MGC29762 3' CACACCTGTAATCCCAGCACTT 58468        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  MGC29891 3' CACACCTGTAATCCCAACACTT 58200      C  T
           T                   AAAGTG TG GATTGCAGGTGTG
                               |||||| || ||||||||||||
                               TTTCAC AC CTAATGTCCACAC
                                  A  C
GAM561  MGC3079  3' CACCTGTAATCCCAGCACTTT  50949        T
                               AAAGTGCTG GATTGCAGGTG
                               ||||||||| |||||||||||
                               TTTCACGAC CTAATGTCCAC
                                      C
GAM561  MGC3207  3' CACACCTGTAATCCCAGCACTT 62557        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  MGC39350 3' CACACCTGTAATCCCCAGCACT 58652        T_
           TT                   AAAGTGCTG  GATTGCAGGTGTG
                               |||||||||  ||||||||||||
                               TTTCACGAC  CTAATGTCCACAC
                                      CC
GAM561  MGC4248  3' CACACCTGTAATCCCAGCACTT 50326        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  MGC4400  3' CACACCTGTAATCTCAGCACTT 51052        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      T
GAM561  MGC4840  3' CACACCTGTAATTCCAGCACTT 71565        TG
           T                   AAAGTGCTG  ATTGCAGGTGTG
                               |||||||||  ||||||||||||
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                                TTTCACGAC  TAATGTCCACAC
                                     CT
GAM561  MGC5457  3'  CACACCTTAATCCCAGCACTTT 50944        T    C
                                AAAGTGCTG GATTG AGGTGTG
                                ||||||||| ||||| |||||||
                                TTTCACGAC CTAAT TCCACAC
                                     C    _
GAM561  MOST2    5'  CACACCTGTAATCCCAGCACTT 39675        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  NMNAT    3'  CACACCTGTAATCCCAGCACTT 42955        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  OSBPL2   3'  CACACCTGTGACGGAAGCACTT 57854       G_  A TG
                                AAGTGCT  TG T  CAGGTGTG
                                |||||||  || |  ||||||||
                                TTCACGA  GC A  GTCCACAC
                                    AG  _ GT
GAM561  OSBPL2   3'  CACACCTGTGACGGAAGCACTT 29203       G_  A TG
                                AAGTGCT  TG T  CAGGTGTG
                                |||||||  || |  ||||||||
                                TTCACGA  GC A  GTCCACAC
                                    AG  _ GT
GAM561  PB1      3'  CACACCTGTAATCCCAGCACTT 37020        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  PIWIL2   3'  CACACCTGTAATCCAAGCACTT 36053        GT
           T                     AAAGTGCT  GATTGCAGGTGTG
                                ||||||||  ||||||||||||
                                TTTCACGA  CTAATGTCCACAC
                                    AC
GAM561  PP591    5'  CACACCTATAATTCCAGCACTT 47366        TG   C
           T                     AAAGTGCTG  ATTG AGGTGTG
                                |||||||||  |||| |||||||
                                TTTCACGAC  TAAT TCCACAC
                                     CT    A
GAM561  PRO0478  5'  CACACCTGTAATCCCAGCACTT 26184        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  PRO1048  5'  CACATCTGTAATCCCAGCACTT 37510        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCTACAC
                                      C
GAM561  PRO2730  3'  CACACCTGTAATCCCAGCACTT 47411          T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  PSR      3'  CACACCTGTAATCCCAGCACTT 65176          T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  RNF24    3'  CTTGTGACAACCAAAGCACTTT 23317         ___  GA TG
                               AAAGTGCT   GT  T  CAGG
                               ||||||||   ||  |  ||||
                               TTTCACGA   CA  A  GTTC
                                    AAC  AC GT
GAM561  RPL13    3'  CACAGCTGTAATCCCAGCACTT 52679          T      G
           T                   AAAGTGCTG GATTGCAG TGTG
                               ||||||||| |||||||| ||||
                               TTTCACGAC CTAATGTC ACAC
                                      C       G
GAM561  RPL13    3'  CACAGCTGTAATCCCAGCACTT 6387           T      G
           T                   AAAGTGCTG GATTGCAG TGTG
                               ||||||||| |||||||| ||||
                               TTTCACGAC CTAATGTC ACAC
                                      C       G
GAM561  SCIN     3'  CACACCTGTAATCCCAGCACTT 52423          T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  SEC24B   3'  CAAGATGCAACGCACAGCACT  20897          A_    GG_
                               AGTGCTGTG  TTGCA   TG
                               |||||||||  |||||   ||
                               TCACGACAC  AACGT   AC
                                     GC     AGA
GAM561  SPTLC2   3'  CACCTGTAATCCCAACACTTT  16798        C  T
                               AAAGTG TG GATTGCAGGTG
                               |||||| || ||||||||||
                               TTTCAC AC CTAATGTCCAC
                                  A  C
GAM561  STX12    3'  CACACTTGTAATCCCAACACTT 66349        C  T
           T                   AAAGTG TG GATTGCAGGTGTG
                               |||||| || ||||||||||||
                               TTTCAC AC CTAATGTTCACAC
                                  A  C
GAM561  TIP47    3'  CACACCTGTAATCCCAGCACTT 19478          T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                    C
GAM561  TP53INP1  3'  CTGAACAATACAGCACTTT   52725          A  __
                                AAAGTGCTGTG TTG  CAG
                                |||||||||| ||| |||
                                TTTCACGACAT AAC  GTC
                                    _  AA
GAM561  TP53INP1  3'  CTGAACAATACAGCACTTT   72952          A  __
                                AAAGTGCTGTG TTG  CAG
                                |||||||||| ||| |||
                                TTTCACGACAT AAC  GTC
                                    _  AA
GAM561  UBF-fl   3'  CACACCTGTAATCCCAGCACTT 51553         T
          T                      AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  WBSCR22  3'  CACACCTGTAATCCCAGCAC   34034       T
                                 GTGCTG GATTGCAGGTGTG
                                 |||||| ||||||||||||
                                 CACGAC CTAATGTCCACAC
                                    C
GAM561  YME1L1   3'  CACATCTGTAATCCCAGCACTT 26526         T
          T                      AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCTACAC
                                     C
GAM561  YME1L1   3'  CACATCTGTAATCCCAGCACTT 57776         T
          T                      AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCTACAC
                                     C
GAM561  ZNF297B  5'  CACACCTGTAATCCCAGCACTT 25776         T
          T                      AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  LOC112687 3'  CACACCTATAATCCCAGCACTT 72856         T   C
          T                      AAAGTGCTG GATTG AGGTGTG
                                 ||||||||| ||||| |||||||
                                 TTTCACGAC CTAAT TCCACAC
                                     C   A
GAM561  LOC116236 3'  CACACCTATAATCTCAGCACTT 73808         T   C
          T                      AAAGTGCTG GATTG AGGTGTG
                                 ||||||||| ||||| |||||||
                                 TTTCACGAC CTAAT TCCACAC
                                     T   A
GAM561  LOC126282 3'  CACACCTGTAATCCCAGCACTT 74470         T
          T                      AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561   LOC130535 3'  CACACTTGTAATCCCAGCACTT 76148        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTTCACAC
                                      C
GAM561   LOC130951 3'  CACACCTGTAATCCCAACACTT 57142       C  T
            T                   AAAGTG TG GATTGCAGGTGTG
                                |||||| || ||||||||||||
                                TTTCAC AC CTAATGTCCACAC
                                   A  C
GAM561   LOC138428 3'  CACACCTATAATCCCAGCACTT 75332        T    C
            T                   AAAGTGCTG GATTG AGGTGTG
                                ||||||||| ||||| |||||||
                                TTTCACGAC CTAAT TCCACAC
                                      C    A
GAM561   LOC143162 3'  CACAGTACTAATCACAGCAT   76495          CAGG
                                GTGCTGTGATTG    TGTG
                                ||||||||||||    ||||
                                TACGACACTAAT    ACAC
                                     CATG
GAM561   LOC143465 3'  CACACCTGTAATCTCAGCACTT 82961        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      T
GAM561   LOC144289 3'  CACATCTGTAATCCCAGCACTT 83023        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCTACAC
                                      C
GAM561   LOC144558 3'  CACCTGTAATCCCAGCACTTT  83146        T
                                AAAGTGCTG GATTGCAGGTG
                                ||||||||| ||||||||||
                                TTTCACGAC CTAATGTCCAC
                                      C
GAM561   LOC145387 3'  CACCTGTAATCCCAGCACTTT  83352        T
                                AAAGTGCTG GATTGCAGGTG
                                ||||||||| ||||||||||
                                TTTCACGAC CTAATGTCCAC
                                      C
GAM561   LOC146272 5'  CACACCTGTAATCCCAGCACTT 77786        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561   LOC146540 3'  CACACCTGTAATCCCAGCACTT 77971        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  LOC146656 3'  CACACCTGTGATCCCCCCAGCA 78072        T___  TG
          CTTT                  AAAGTGCTG   GAT  CAGGTGTG
                                |||||||||   |||  ||||||||
                                TTTCACGAC   CTA  GTCCACAC
                                     CCCC   GT
GAM561  LOC146923 3'  CACACCTGTAATCCCAGCACTT 78191        T
          T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  LOC146975 5'  CACACCTATAATCCCAGCACTT 78222        T    C
          T                     AAAGTGCTG GATTG AGGTGTG
                                ||||||||| ||||| |||||||
                                TTTCACGAC CTAAT TCCACAC
                                     C    A
GAM561  LOC147669 3'  CACACCTGTAATCCCAGCACTT 84058        T
          T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  LOC148936 3'  CACACCTGTAATCCCAGCACTT 84288        T
          T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  LOC148938 3'  CACACCTGTAATCCCAGCACTT 84267        T
          T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  LOC149705 3'  CACACCTGTAATCCCAACACTT 84622       C  T
          T                     AAAGTG TG GATTGCAGGTGTG
                                |||||| || ||||||||||||
                                TTTCAC AC CTAATGTCCACAC
                                    A  C
GAM561  LOC150481 3'  CACACCTGTAATCCCAGCACTT 79882        T
          T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  LOC151429 3'  CACACCTGTAATCCCAGCACTT 85346        T
          T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  LOC151614 3'  CACACCTGTAATCCCAGCACTT 80302        T
          T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  LOC151623 3'  CACCTGTAATCCCAGCACTTT  85457        T
                                AAAGTGCTG GATTGCAGGTG
                                ||||||||| ||||||||||
                                TTTCACGAC CTAATGTCCAC
                                      C
GAM561  LOC151632 3'  CACACCTGTGATCTCAGCAC   85464      T  TG
                                GTGCTG GAT  CAGGTGTG
                                |||||| |||  ||||||||
                                CACGAC CTA  GTCCACAC
                                   T  GT
GAM561  LOC152263 3'  CACACCTGTAATCCCAGCACTT 85672        T
          T                      AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  LOC152317 3'  CACACCTGTAACCCCAACACTT 85637      C  TGA
          T                      AAAGTG TG   TTGCAGGTGTG
                                |||||| ||   ||||||||||
                                TTTCAC AC   AATGTCCACAC
                                   A  CCC
GAM561  LOC152860 3'  CACACCTATAATCCCAGCACTT 80697        T    C
          T                      AAAGTGCTG GATTG AGGTGTG
                                ||||||||| ||||| |||||||
                                TTTCACGAC CTAAT TCCACAC
                                      C    A
GAM561  LOC153260 3'  CACACCTGTAATCCCAGCACTT 80802        T
          T                      AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  LOC154092 3'  CACATCTGTAATCCCAGCACTT 86159        T
          T                      AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCTACAC
                                      C
GAM561  LOC154992 3'  CACATTCGTAATCCCAGCACTT 81211        T    AG
          T                      AAAGTGCTG GATTGC  GTGTG
                                ||||||||| ||||||  |||||
                                TTTCACGAC CTAATG  TACAC
                                      C     CT
GAM561  LOC155072 3'  CACACCTGTAATCCCAGCACTT 86372        T
          T                      AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  LOC155376 3'  CACACTTGTAATCCCAGCACTT 81335        T
          T                      AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTTCACAC
                                      C
GAM561  LOC157278 3'  CACACCTGTAATCCCAGCACTT 86422         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  LOC158288 3'  CTGTAATCACAGCACTTT     86713
                               AAAGTGCTGTGATTGCAG
                               ||||||||||||||||||
                               TTTCACGACACTAATGTC

GAM561  LOC158819 5'  CACACCTGTAATCCCAGCACTT 86902         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM561  LOC158863 3'  CACACCTGTAATCCCAACACTT 86922       C  T
           T                   AAAGTG TG GATTGCAGGTGTG
                               |||||| || ||||||||||||
                               TTTCAC AC CTAATGTCCACAC
                                  A  C
GAM561  LOC158987 3'  CACACCTGTTATCCCAGCACTT 86959         T   T
           T                   AAAGTGCTG GAT GCAGGTGTG
                               ||||||||| ||| |||||||||
                               TTTCACGAC CTA TGTCCACAC
                                      C   T
GAM561  LOC167555 3'  CACACCCGTAATCCCAGCACTT 82678         T     A
           T                   AAAGTGCTG GATTGC GGTGTG
                               ||||||||| |||||| ||||||
                               TTTCACGAC CTAATG CCACAC
                                      C     C
GAM561  LOC196027 3'  CACACCTGTAATCTCAGCACTT 87547         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      T
GAM561  LOC196415 5'  CACCTGTAATCCCAGCACTTT  89630         T
                               AAAGTGCTG GATTGCAGGTG
                               ||||||||| ||||||||||
                               TTTCACGAC CTAATGTCCAC
                                      C
GAM561  LOC196528 3'  CACCTATAATCCCAGCACTTT  87763         T    C
                               AAAGTGCTG GATTG AGGTG
                               ||||||||| ||||| |||||
                               TTTCACGAC CTAAT TCCAC
                                      C    A
GAM561  LOC196738 3'  CACAGTACTAATCACAGCAT   87503           CAGG
                               GTGCTGTGATTG    TGTG
                               ||||||||||||    ||||
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                                TACGACACTAAT    ACAC
                                      CATG
GAM561   LOC197319 3'  CACACCTGTAATCCCAGCACTT 87967         T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                       C
GAM561   LOC199786 3'  CACACCTGTAATCCCAGCACTT 88368         T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                       C
GAM561   LOC200301 3'  CACACCTTGCCACAGCACT    88737        ATT  _
                                 AGTGCTGTG   GCA GGTGTG
                                 |||||||||   ||| ||||||
                                 TCACGACAC   CGT CCACAC
                                       ___   T
GAM561   LOC200904 3'  CACACCTGTGATCTCAGCAC   90185       T   TG
                                 GTGCTG GAT  CAGGTGTG
                                 |||||| |||  ||||||||
                                 CACGAC CTA  GTCCACAC
                                     T   GT
GAM561   LOC200918 3'  CACAGCTGTAATCCCAGCACT  88938        T       G
                                 AGTGCTG GATTGCAG TGTG
                                 ||||||| |||||||| ||||
                                 TCACGAC CTAATGTC ACAC
                                      C       G
GAM561   LOC201685 3'  CACACCTGTAATCCCAGCACTT 90240         T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                       C
GAM561   LOC201689 3'  CACACCTGTAATCCCAGCACTT 67142         T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                       C
GAM561   LOC201895 3'  CACACCTGTAATCCCAGCACTT 89086         T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                       C
GAM561   LOC202868 3'  CACACCTGTAATCCCAGCACTT 90370         T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                       C
GAM561   LOC203083 3'  CACACCTGTGATCTCAGCAC   90461       T   TG
                                 GTGCTG GAT  CAGGTGTG
                                 |||||| |||  ||||||||
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                                CACGAC CTA  GTCCACAC
                                   T   GT
GAM561   LOC219406 3'  CACACCTGCAATCCCAGCTACT 93558     _   T
                                AGT GCTG GATTGCAGGTGTG
                                ||| |||| |||||||||||||
                                TCA CGAC CTAACGTCCACAC
                                  T   C
GAM561   LOC219722 5'  CACACCTGTAATCCCAGCACTT 93080         T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| |||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561   LOC220506 3'  CACACCTATAATCCCAGCACTT 74075         T    C
            T                    AAAGTGCTG GATTG AGGTGTG
                                ||||||||| ||||| |||||||
                                TTTCACGAC CTAAT TCCACAC
                                      C    A
GAM561   LOC220575 3'  CACACTTGTAATCACTGCACTT 76307        T
            T                    AAAGTGC GTGATTGCAGGTGTG
                                ||||||| ||||||||||||||||
                                TTTCACG CACTAATGTTCACAC
                                   T
GAM561   LOC220662 3'  CACACCTGTAATCCCAGCACTT 91163         T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| |||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561   LOC221271 3'  CACACCTGTAATCCCAGCACTT 91849         T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| |||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561   LOC221410 3'  CACACCTGTAATCCAAGCACTT 92056        GT
            T                    AAAGTGCT  GATTGCAGGTGTG
                                ||||||||  ||||||||||||||
                                TTTCACGA  CTAATGTCCACAC
                                     AC
GAM561   LOC221489 3'  CACACCTGTAATCCCAGCACTT 93638         T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| |||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561   LOC221543 5'  CACACCTGTAATCCCAGCACT  93736        T
                                AGTGCTG GATTGCAGGTGTG
                                ||||||| |||||||||||||
                                TCACGAC CTAATGTCCACAC
                                   C
GAM561   LOC221543 3'  CACACCTGTAATCCCAGCACTT 93737         T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| |||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561   LOC221641 3'  CACACTTATCATCTCAGCACTT 93725        T   TGC
           T                   AAAGTGCTG GAT   AGGTGTG
                               ||||||||| |||   |||||||
                               TTTCACGAC CTA   TTCACAC
                                     T   CTA
GAM561   LOC221795 3'  CACACCTGTGATCTCAGCAC   92475      T   TG
                               GTGCTG GAT  CAGGTGTG
                               |||||| |||  ||||||||
                               CACGAC CTA  GTCCACAC
                                   T   GT
GAM561   LOC221954 5'  CACACCTGTAATCCCAGCACTT 93998        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                     C
GAM561   LOC221962 3'  CACACCTGTAATCCCAGCACTT 92679        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                     C
GAM561   LOC253532 3'  CACACTTGTAATCCCAGCACTT 96027        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTTCACAC
                                     C
GAM561   LOC254176 3'  CACACCTGTGATCTCAGCAC   97338      T   TG
                               GTGCTG GAT  CAGGTGTG
                               |||||| |||  ||||||||
                               CACGAC CTA  GTCCACAC
                                   T   GT
GAM561   LOC254531 5'  CACACCTGTAATCCCAGCACTT 94982        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                     C
GAM561   LOC254875 3'  CACACTTGTAATCCCAGCACTT 96057        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTTCACAC
                                     C
GAM561   LOC255177 3'  CACACCTGTAATCCCAGCACTT 96601        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                     C
GAM561   LOC255231 3'  CACACCTGTAATCCCAGCACTT 95372        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561   LOC255461 3'  CACACCTGTAATCCCAGCACTT 97317         T
           T                    AAAGTGCTG GATTGCAGGTGTG
                                |||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561   LOC255516 3'  CACACCTGTAATCCCAGCACTT 97330         T
           T                    AAAGTGCTG GATTGCAGGTGTG
                                |||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561   LOC255624 3'  CACACCTGTAATCCCAGCACTT 94521         T
           T                    AAAGTGCTG GATTGCAGGTGTG
                                |||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561   LOC255671 3'  CACATCTGTAATCCCAGCACTT 97252         T
           T                    AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCTACAC
                                      C
GAM561   LOC256515 3'  CACACCTGTGATCTCAGCAC   96460       T   TG
                                GTGCTG GAT  CAGGTGTG
                                |||||| |||  ||||||||
                                CACGAC CTA  GTCCACAC
                                    T   GT
GAM561   LOC257596 5'  CACACCTGTAATCCCAGCACT  97929        T
                                AGTGCTG GATTGCAGGTGTG
                                ||||||| ||||||||||||
                                TCACGAC CTAATGTCCACAC
                                     C
GAM561   LOC257596 3'  CACACCTGTAATCCCAGCACTT 97930         T
           T                    AAAGTGCTG GATTGCAGGTGTG
                                |||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM561   LOC90072  3'  CACACCTGCAATCCCACCACTT 61291       C  T
           T                    AAAGTG TG GATTGCAGGTGTG
                                |||||| || ||||||||||||
                                TTTCAC AC CTAACGTCCACAC
                                    C  C
GAM561   LOC90092  3'  CACACCTGTAATCCCAGCACTT 61400         T
                                AAGTGCTG GATTGCAGGTGTG
                                |||||||| ||||||||||||
                                TTCACGAC CTAATGTCCACAC
                                      C
GAM561   LOC90092  3'  CACACCTGTAATCCCAGCACTT 61401         T
           T                    AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  LOC90141  3' CATGCCTACAATCCCAGCACTT 61626        T    C
             T                   AAAGTGCTG GATTG AGGTGTG
                                 ||||||||| ||||| |||||||
                                 TTTCACGAC CTAAC TCCGTAC
                                     C    A
GAM561  LOC90538  3' CACATCTGTAATCCCAGCACTT 63187        T
             T                   AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCTACAC
                                     C
GAM561  LOC90639  3' CACGCCTGCAATCCCAGCACTT 63652        T
             T                   AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAACGTCCGCAC
                                     C
GAM561  LOC90979  3' CACACCTGTAATCCCAGCACTT 64524        T
             T                   AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  LOC91574  3' CACATCTGTAATCCCAGCACTT 66518        T
             T                   AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCTACAC
                                     C
GAM561  LOC91862  3' CACACCTGTAACCCCAGCACTT 53464        TGA
             T                   AAAGTGCTG  TTGCAGGTGTG
                                 |||||||||  ||||||||||
                                 TTTCACGAC  AATGTCCACAC
                                     CCC
GAM561  LOC92078  3' CACACCTATAATCCCAGCACTT 67974        T    C
             T                   AAAGTGCTG GATTG AGGTGTG
                                 ||||||||| ||||| |||||||
                                 TTTCACGAC CTAAT TCCACAC
                                     C    A
GAM561  LOC92267  3' CACACCTGTAATCCCAGCACTT 68605        T
             T                   AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  LOC92299  3' CACACCTGTAATCTCAGCACTT 68807        T
             T                   AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     T
GAM561  LOC92573  5' CACACCTGTAATCCCAGCACTT 69802        T
             T                   AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM561  LOC93132  5'  CACACCTGTAATCCCAGCACTT 71483          T
           T                    AAAGTGCTG GATTGCAGGTGTG
                                |||||||||  ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM562  AOAH     5'  ACCACAGACTCCCTCCAGCTCT 91115       CGC  A_ _  CA
           T                    AAGAGC  GAG  AG CTG  GT
                                ||||||  |||  || |||  ||
                                TTCTCG  CTC  TC GAC  CA
                                   AC_  CC  A  AC
GAM562  ATP11A   3'  ACTGCAGCTCCGCCCGC     77016    C_  A  A
                                GC  GCG GA GCTGCAGT
                                ||  ||| || ||||||||
                                CG  CGC CT CGACGTCA
                                 CC  _ _
GAM562  CGA      3'  TACTGCAGCTTTACTGC     5596     A_
                                GCG  GAAGCTGCAGTA
                                |||  ||||||||||||
                                CGT  TTTCGACGTCAT
                                  CA
GAM562  CMAR     3'  GCACTTCCTCTCGCGGCCCT   17774    A       ___  C
                                AG GCCGCGAGA  AG TGC
                                || |||||||||  || |||
                                TC CGGCGCTCT  TC ACG
                                 C       CCT  _
GAM562  CRYAA    3'  CTGGGCTCTCGCGGCCTCT   4617      _      A  G
                                AGAG CCGCGAGA GCT CAG
                                |||| |||||||| ||| |||
                                TCTC GGCGCTCT CGG GTC
                                  C      _  _
GAM562  CTF1     3'  ACTGCAGCCTCAACCTC     7180     CCGC  AA
                                GAG   GAG  GCTGCAGT
                                |||   |||  ||||||||
                                CTC   CTC  CGACGTCA
                                  CAA_  __
GAM562  EPB49    3'  ACTGCAGCTTCCTGCTCCTCT  8781      CC  A
                                AGAG  GCG GAAGCTGCAGT
                                ||||  ||| ||||||||||
                                TCTC  CGT CTTCGACGTCA
                                  CT  C
GAM562  FBXL2    5'  GGCTCGCTCGCGGCTCTT    24066          A_
                                AAGAGCCGCGAG  AGCT
                                ||||||||||||  ||||
                                TTCTCGGCGCTC  TCGG
                                       GC
GAM562  FBXL4    5'  GCCGCTCCTCGCGGCCTC    24072    _     A  T
                                GAG CCGCGAG AGC GC
                                ||| ||||||| ||| ||
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                                CTC GGCGCTC TCG CG
                                  C      C   C
GAM562  G1P3    3' ACTGCAGCCTCCAACTC    43149    CCGC   AA
                                GAG   GAG  GCTGCAGT
                                |||   |||  ||||||||
                                CTC   CTC  CGACGTCA
                                  AAC_  __
GAM562  G1P3    3' ACTGCAGCCTCCAACTC    43151    CCGC   AA
                                GAG   GAG  GCTGCAGT
                                |||   |||  ||||||||
                                CTC   CTC  CGACGTCA
                                  AAC_  __
GAM562  G1P3    3' ACTGCAGCCTCCAACTC    8974     CCGC   AA
                                GAG   GAG  GCTGCAGT
                                |||   |||  ||||||||
                                CTC   CTC  CGACGTCA
                                  AAC_  __
GAM562  GNA11   5' ACCGCAGCCCCCTGTGGCT   76093       AGAA    A
                                AGCCGCG   GCTGC GT
                                |||||||   ||||| ||
                                TCGGTGT   CGACG CA
                                    CCCC    C
GAM562  MN1     3' TACTGCATAGCAAACTCTT   10096      CC_  GAGAAGC
                                AAGAG  GC     TGCAGTA
                                |||||  ||     |||||||
                                TTCTC  CG     ACGTCAT
                                   AAA  AT_____
GAM562  MPP2    3' ACTGCAGCTCCCAGCTC    59816     CGCGA  A
                                GAGC    GA GCTGCAGT
                                ||||    || ||||||||
                                CTCG    CT CGACGTCA
                                  ACC__  _
GAM562  MYB     5' GCGGTCCCCGCGGCTCT    59540        AGAA
                                AGAGCCGCG   GCTGC
                                |||||||||   |||||
                                TCTCGGCGC   TGGCG
                                     CCC_
GAM562  NR3C2   3' ACTGCGGTGTCTGCAGCTC  6131     C  G   A
                                GAGC GC AGA GCTGCAGT
                                |||| || ||| ||||||||
                                CTCG CG TCT TGGCGTCA
                                  A  _   G
GAM562  NTRK3   5' ACTAGGGCCTCTCGCGGCTC  10283         A   GC
                                GAGCCGCGAGA GCT  AGT
                                |||||||||||| |||  |||
                                CTCGGCGCTCT CGG  TCA
                                      C   GA
GAM562  OSCAR   3' ACTGCAGCCCGAGACTTCC   55668   A   CCG  AGAA
                                A GAG   CG   GCTGCAGT
                                | |||   ||   ||||||||
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                                C TTC   GC    CGACGTCA
                                 C   AGA  C___
GAM562  OSCAR    3'  ACTGCAGCCCGAGACTTCC   55371   A   CCG  AGAA
                                A GAG   CG    GCTGCAGT
                                | |||   ||    ||||||||
                                C TTC   GC    CGACGTCA
                                 C   AGA  C___
GAM562  OSCAR    3'  ACTGCAGCCCGAGACTTCC   55664   A   CCG  AGAA
                                A GAG   CG    GCTGCAGT
                                | |||   ||    ||||||||
                                C TTC   GC    CGACGTCA
                                 C   AGA  C___
GAM562  PDE4A    5'  GCCCAGGCCCCTCCGCGGCTC  20586         _  AA   ___
                                GAGCCGCG AG  GCT   GC
                                |||||||| ||  |||   ||
                                CTCGGCGC TC  CGG   CG
                                     C  CC   ACC
GAM562  PPP2R5E  5'  GCTCCAGCTCCTGCGGCTC   20726        G  A    C
                                GAGCCGC AG AGCTG AGT
                                ||||||| || ||||| |||
                                CTCGGCG TC TCGAC TCG
                                    _ C    C
GAM562  SPG7     3'  GCACTTCCTCTCGCGGCCCT  11903    A       ___  C
                                AG GCCGCGAGA   AG TGC
                                || |||||||||   || |||
                                TC CGGCGCTCT   TC ACG
                                 C        CCT  _
GAM562  SRD5A1   3'  AGCTCCTCGTGGCCCTT     6454     A       A
                                AAG GCCGCGAG AGCT
                                ||| |||||||| ||||
                                TTC CGGTGCTC TCGA
                                  C       C
GAM562  WNT3A    3'  GCACCGGCCGCGGCTC      52432        AGAA   CA
                                GAGCCGCG    GCTG  GT
                                ||||||||    ||||  ||
                                CTCGGCGC    CGGC  CG
                                     _____    CA
GAM562  WNT6     5'  ACTGAAGCCCGGGCCCT     21514    A  G  AGAA  G
                                AG GCC CG    GCT CAGT
                                || ||| ||    ||| ||||
                                TC CGG GC    CGA GTCA
                                 C   _  C___   A
GAM562  ZNF219   5'  GCCGCCTCTCGCGGCTC     33133          A  T
                                GAGCCGCGAGA GC GC
                                |||||||||| || ||
                                CTCGGCGCTCT CG CG
                                       C  C
GAM562  BICD2    3'  ACTGCAGCCCCTTCCCCTTC  70386    CCGC   AA
                                GAG   GAG  GCTGCAGT
                                |||   |||  ||||||||
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                                CTT   TTC  CGACGTCA
                                  CCCC   CC
GAM562  C20orf149 5'  GCGGCTTCCCGCGGTCTT    44173     G    A
                                AAGA CCGCG GAAGCTGC
                                |||| ||||| ||||||||
                                TTCT GGCGC CTTCGGCG
                                  _    C
GAM562  EFS2    5'  GCGGCTTCTCCCAGCCCT    19622    A  CGC
                                AG GC   GAGAAGCTGC
                                || ||   ||||||||||
                                TC CG   CTCTTCGGCG
                                 C  ACC
GAM562  FLJ10640  5'  ACTGCAGCCTTGACCTC    38719    CCG   AA
                                GAG   CGAG  GCTGCAGT
                                |||   ||||  ||||||||
                                CTC   GTTC  CGACGTCA
                                  CA_   __
GAM562  FLJ10737  3'  ACTGCAGCTCCCCGCTCCTGC  36519    C___   AGA
                                GC   GCG   AGCTGCAGT
                                ||   |||   |||||||||
                                CG   CGC   TCGACGTCA
                                 TCCT   CCC
GAM562  FLJ10743  3'  GCAGGACTTCTCGCTGCCCTT  36549     A  C      __
                                AAG GC GCGAGAAG  CTGC
                                ||| || ||||||||  ||||
                                TTC CG CGCTCTTC  GACG
                                  C  T       AG
GAM562  FLJ10847  3'  GTACTGCAGCCTCAACCTC   36753    CCGC   AA
                                GAG   GAG  GCTGCAGTAC
                                |||   |||  ||||||||||
                                CTC   CTC  CGACGTCATG
                                  CAA_   __
GAM562  FLJ14146  3'  GCTGAGCTTCTCACATCTCT   45244     CCGC      G
                                AGAG   GAGAAGCT CAGT
                                ||||   |||||||| ||||
                                TCTC   CTCTTCGA GTCG
                                  TACA      _
GAM562  FLJ20485  3'  ACTGCAGCCTCGACCTC    38762    CCG   AA
                                GAG   CGAG  GCTGCAGT
                                |||   ||||  ||||||||
                                CTC   GCTC  CGACGTCA
                                  CA_   __
GAM562  FLJ20793  5'  GTCAGCTTCTGCAGCTCT    91807     C  G     _
                                AGAGC GC AGAAGCTG C
                                ||||| || |||||||| |
                                TCTCG CG TCTTCGAC G
                                   A  _       T
GAM562  HRIHFB2436 5'  GCCTCGGGCCCGTCGCGGCTC  26793        GAA  ____
                                GAGCCGCGA   GCT   GC
                                |||||||||   |||   ||
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                                CTCGGCGCT  CGG   CG
                                     GCC  GCTC
GAM562  HSPC111  5' GTACCACCGGGTTCTCGCGGGT 33067     G      G  CA_
           CTT                   AAGA CCGCGAGAA CTG  GTAC
                                |||| ||||||||| |||  ||||
                                TTCT GGCGCTCTT GGC  CATG
                                  G       G  CAC
GAM562  KIAA0337 3' TGGCTTCTCCCGACCCTC   28838    C__ C
                                GAG  CG GAGAAGCTG
                                |||  || |||||||||
                                CTC  GC CTCTTCGGT
                                 CCA  C
GAM562  KIAA0513 3' ACTGCAGCCTGAACTC     28336    CCG G  AA
                                GAG  C AG  GCTGCAGT
                                |||  | ||  ||||||||
                                CTC  G TC  CGACGTCA
                                 AA_ _  __
GAM562  KIAA0766 5' GCGCTTCTCAGGCTC      29005     GC     T
                                GAGCC  GAGAAGC GC
                                |||||  ||||||| ||
                                CTCGG  CTCTTCG CG
                                  A_     _
GAM562  KIAA1396 3' ACTGCAGAGCGGTCTT     62983     G   GAGAAG
                                AAGA CCGC    CTGCAGT
                                |||| ||||    |||||||
                                TTCT GGCG    GACGTCA
                                  _   A_____
GAM562  LANCL2   3' ACTGCAGCTCTGTCAGGGC   37992    ___ G  A
                                GCC  GC AGA GCTGCAGT
                                |||  || ||| ||||||||
                                CGG  TG TCT CGACGTCA
                                 GAC  _  _
GAM562  MCM10    3' ACTGCAGCCTTGGCTTCC    37568   A   GC  AA
                                A GAGCC  GAG  GCTGCAGT
                                | |||||  |||  ||||||||
                                C TTCGG  TTC  CGACGTCA
                                 C    __  __
GAM562  MGC10966 5' GTACTACAGCTTCTTCG     48899   C      C
                                CG GAGAAGCTG AGTAC
                                || |||||||| |||||
                                GC TTCTTCGAC TCATG
                                 _       A
GAM562  MGC10981 3' ACTGCAGCCCTGCCACTT    51012    CC  G  AA
                                GAG  GC AG  GCTGCAGT
                                |||  || ||  ||||||||
                                TTC  CG TC  CGACGTCA
                                 AC  _  C_
GAM562  MGC4827  5' GTACTGCAGCGAATGAGCTC  44124     CG  AGAA
                                GAGC  CG   GCTGCAGTAC
                                ||||  ||   ||||||||||
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                                CTCG  GT   CGACGTCATG
                                  A_  AAG_
GAM562  NUP54    5'  GCTGCAGCCACCGCGGC    60100      AGAA
                                GCCGCG   GCTGCAGT
                                ||||||   ||||||||
                                CGGCGC   CGACGTCG
                                   CAC_
GAM562  PDGFC    5'  GCTGGGGACTTCTCGCCGCTC  32499     C      _  G
                                GAGC GCGAGAAG CT CAGT
                                |||| |||||||| || ||||
                                CTCG CGCTCTTC GG GTCG
                                  C       A  G
GAM562  PIR      5'  GCACTCGCTCCCGGCGGCTCTT 13356        ___   A_  C
                                AAGAGCCGC   GAG  AG TGC
                                |||||||||   |||  || |||
                                TTCTCGGCG   CTC  TC ACG
                                     GCC   GC  _
GAM562  PP1628   5'  GCTGAGCCCCCTGCAGCTC   47301     C   AGAA   G
                                GAGC GCG   GCT CAGT
                                |||| |||   ||| ||||
                                CTCG CGT   CGA GTCG
                                  A   CCCC   _
GAM562  PPM1G    3'  ACTGCAGCCGGGAGCCTCT   10707     CC  GAGAA
                                AGAG  GC    GCTGCAGT
                                ||||  ||    ||||||||
                                TCTC  CG    CGACGTCA
                                  __  AGGGC
GAM562  PTDSS1   3'  ACCACAGCTTCTCCCCAGCTT  28570     CGC_       CA
                                GAGC   GAGAAGCTG  GT
                                ||||   |||||||||  ||
                                TTCG   CTCTTCGAC  CA
                                  ACCC       AC
GAM562  SLC12A5  3'  GCAACCTCTTCTCATCGGCTCT 40381        C_     C___
           T                     AAGAGCCG  GAGAAG   TGC
                                |||||||  ||||||   |||
                                TTCTCGGC  CTCTTC   ACG
                                     TA     TCCA
GAM562  TXI1     5'  GTACCACAGCTTCTCGTCCGCT 37372     C_         CA
           T                     GAGC  GCGAGAAGCTG  GTAC
                                ||||  ||||||||||  ||||
                                TTCG  TGCTCTTCGAC  CATG
                                  CC         AC
GAM562  USP22    3'  ACTGCAGCCTCCCTGGGC    67999     G  A_  A
                                GCC CG  GA GCTGCAGT
                                ||| ||  || ||||||||
                                CGG GT  CT CGACGTCA
                                  _  CC  C
GAM562  VMP      3'  ACTGCAGCCTTGAACTC     54896     CCG   AA
                                GAG   CGAG  GCTGCAGT
                                |||   ||||  ||||||||
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                                CTC   GTTC  CGACGTCA
                                  AA_   __
GAM562  WBSCR17   3'  ACTGCAGCTCTGGACTTTT   81295     _ GCG   A
                                AAGAG CC   AGA GCTGCAGT
                                |||||| ||   ||| ||||||||
                                TTTTC GG   TCT CGACGTCA
                                  A ____  _
GAM562  LOC126520 5'  TACTGCAGCCGCCAGTCTT   74525    GCC   AGAA
                                AAGA   GCG    GCTGCAGTA
                                ||||   |||    |||||||||
                                TTCT   CGC    CGACGTCAT
                                  GAC  _____
GAM562  LOC130471 3'  ACTGCAGCTCTGACAGGGC   74937    GCG__   A
                                GCC     AGA GCTGCAGT
                                |||     ||| ||||||||
                                CGG     TCT CGACGTCA
                                  GACAG  _
GAM562  LOC130497 3'  GCAGCCCCCTCCCAGCTCTT   74947      CGC   AA_
                                AAGAGC   GAG   GCTGC
                                ||||||   |||   |||||
                                TTCTCG   CTC   CGACG
                                   ACC   CCC
GAM562  LOC138050 5'  GCTGGCCCCCGGCGGCTCTT   75298        GAGAA   _
                                AAGAGCCGC     GCT GC
                                |||||||||     ||| ||
                                TTCTCGGCG     CGG CG
                                     GCCCC   T
GAM562  LOC139046 5'  GCACATCCTCTCGCGGCCCT   75812    A       AGC__
                                AG GCCGCGAGA     TGC
                                || |||||||||     |||
                                TC CGGCGCTCT     ACG
                                 C        CCTAC
GAM562  LOC146455 3'  TACTGCTGTTCACAGCTTTT   77908      CGC   AAGCT
                                AAGAGC   GAG    GCAGTA
                                ||||||   |||    ||||||
                                TTTTCG   CTT    CGTCAT
                                   ACA   GT___
GAM562  LOC151568 5'  ACTGCAGCCTCCGCCGACTC   56689     C  _  A  A
                                GAG CG CG GA GCTGCAGT
                                ||| || || || ||||||||
                                CTC GC GC CT CGACGTCA
                                  A  C  _  C
GAM562  LOC157919 3'  GTACTGTAACTCACGACTGTT  81636    G  C  C   AAGC
                                AA AG CG GAG    TGCAGTAC
                                || || || |||    ||||||||
                                TT TC GC CTC    ATGTCATG
                                 G  A  A   A___
GAM562  LOC245757 3'  TACTGGTCTGCAGCTC      90776      C  G   AGCTG
                                GAGC GC AGA     CAGTA
                                |||| || |||     |||||
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                                CTCG CG TCT    GTCAT
                                  A  _  G____
GAM562  LOC253070 5'  GCAGAGCTTCTCCGGC     97008     C      __
                                GCCG GAGAAGCT  GC
                                |||| ||||||||  ||
                                CGGC CTCTTCGA  CG
                                  _      GA
GAM562  LOC254013 3'  ACTGCAGCCTTGAACTCT    94875     CCG    AA
                                AGAG   CGAG  GCTGCAGT
                                ||||   ||||  ||||||||
                                TCTC   GTTC  CGACGTCA
                                  AA_   __
GAM562  LOC256691 3'  TACTGACTCAGGGCTCTT    96200       GC   AAGCTG
                                AAGAGCC  GAG     CAGTA
                                |||||||  |||     |||||
                                TTCTCGG  CTC     GTCAT
                                    GA   A_____
GAM562  LOC57805  3'  GCACCTCTTTCCCGTGGCTC  40987       A    C___
                                GAGCCGCG GAAG    TGC
                                |||||||| ||||    |||
                                CTCGGTGC CTTT    ACG
                                     C    CTCC
GAM562  LOC91496  5'  GTACTGCAGCTTCTTGTCTCT  66224     CC
                                AGAG  GCGAGAAGCTGCAGTAC
                                ||||  ||||||||||||||||
                                TCTC  TGTTCTTCGACGTCATG
                                  __
GAM563  GJB3      5'  CAAAGCACATCTTTCCACC    43764      T  TT
                                GGTGG AG  GTGTGCTTTG
                                ||||| ||  ||||||||||
                                CCACC TT  TACACGAAAC
                                  _  TC
GAM563  DKFZP566M114 5'  AAAACCCACCCACCCTAA    49541        TAGTT   TGC
                                TTAGGGTGG    GTG   TTT
                                |||||||||    |||   |||
                                AATCCCACC    CAC   AAA
                                     _____  CCA
GAM563  HSPB7     5'  CAAAACACACAATAAACCC    27023     GGTA      C
                                GGGT    GTTGTGTG TTTG
                                ||||    |||||||| ||||
                                CCCA    TAACACAC AAAC
                                  AA__       A
GAM564  ADH1B     3'  CTTAGACATAAAGTAAAAT    72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM564  AHR       3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
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                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM564  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                                _
GAM564  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                  CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM564  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||  ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM564  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM564  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM564  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM564  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_    CG_
GAM564  CG012    5'  CTCACTCTGAAAGTGAA     83218          CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM564  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM564  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
              G                   CATTTC        GTCTGAGAT
                                ||||||        |||||||||
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                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM564  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA  TCACTGTCTGAGAT
                                |||||||  ||||||||||||||
                                GTAAAGT  AGTGACAGACTCTA
                                   C__
GAM564  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM564  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM564  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                 C
GAM564  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM564  PP35      3'  ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM564  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148        TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM564  SEP15     3'  TCCTACAGTAAGAGTGAAA   14934       C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM564  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA  73941       CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM564  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
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                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM564  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM564  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM564  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA

                                        _
GAM565  ABCB9    3'  TCCCCACACCCGCCCCTGTG   39038     TGAT   AAA  A
                                CAC    GGG   GT TGGGGA
                                |||    |||   || ||||||
                                GTG    CCC   CA ACCCCT
                                  TC__   GCC  C
GAM565  ACK1     3'  TCCATGTTTTCCCACCAG    19346     A
                                CTG TGGGAAAGTATGGG
                                ||| ||||||||||||||
                                GAC ACCCTTTTGTACCT
                                  C
GAM565  ADCY9    3'  CCCCATTGCCCACCCGCA    6656     A    AAA   _
                                TG TGGG   GTA TGGGG
                                || ||||   ||| |||||
                                AC GCCC   CGT ACCCC
                                  _    ACC   T
GAM565  ADRBK1   3'  CCCCATCCTGGCCCATCAGTGT 7867           AA  T
                                ACACTGATGGG  AG ATGGGG
                                ||||||||||  || ||||||
                                TGTGACTACCC  TC TACCCC
                                       GG  C
GAM565  AKAP13   3'  TCCCCATACTGTTTCCA     89687        _
                                TGGGAA AGTATGGGGA
                                |||||| ||||||||||
                                ACCTTT TCATACCCCT
                                   G
GAM565  AP2M1    3'  CCCCACCACACATCAGTGT    14514         GGAAAGTA
                                ACACTGATG       TGGGG
                                |||||||||       |||||
                                TGTGACTAC       ACCCC
                                     ACACC____
GAM565  AQP6     5'  CCCCACATCCCACCCCATCAG  7943         AAA__  A
                                CTGATGGG    GT TGGGG
                                ||||||||    || |||||
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                                GACTACCC    TA ACCCC
                                    CACCC  C
GAM565  AQP6    5'  CCCCACATCCCACCCCATCAG  53916       AAA__  A
                                CTGATGGG    GT TGGGG
                                ||||||||    || |||||
                                GACTACCC    TA ACCCC
                                    CACCC  C
GAM565  ARHG    3'  TCCTACCCCCATCAG      8018        AAA  T
                                CTGATGGG  GTA GGG
                                ||||||||  ||| |||
                                GACTACCC  CAT CCT
                                    C__  _
GAM565  BCL11B  5'  CCCCGGCTCCCCCCCATCAGTG  56800       AA_  A
                                CACTGATGGG  AGT TGGGG
                                ||||||||||  ||| |||||
                                GTGACTACCC  TCG GCCCC
                                     CCC  _
GAM565  BCL11B  5'  CCCCGGCTCCCCCCCATCAGTG  43186       AA_  A
                                CACTGATGGG  AGT TGGGG
                                ||||||||||  ||| |||||
                                GTGACTACCC  TCG GCCCC
                                     CCC  _
GAM565  ESRRA   3'  CCAGGGCTTCCCCATCAG   15481       A   A_
                                CTGATGGG AAGT  TGG
                                |||||||| ||||  |||
                                GACTACCC TTCG  ACC
                                    C   GG
GAM565  HLA-C   3'  CCCCACACTGACCTGTGTT   92103     TGAT  AA  A
                                AACAC   GGG  AGT TGGGG
                                |||||   |||  ||| |||||
                                TTGTG   TCC  TCA ACCCC
                                   _____  AG  C
GAM565  HMG20A  3'  CCCAGTCTTCTCCCATCATTG  36537   C     _  TA
                                CA TGATGGGA AAG  TGGG
                                || |||||||| |||  ||||
                                GT ACTACCCT TTC  ACCC
                                 T      C  TG
GAM565  HOXB5   3'  CCCCTCCCCATCTGTGTT    9265      T    AAAGTAT
                                AACAC GATGGG     GGGG
                                ||||| ||||||     ||||
                                TTGTG CTACCC     CCCC
                                   T    CT_____
GAM565  IDH3B   3'  TCCCCATACCCTTCAGTGCAGT 22579      ATGG  A_
          GT                    ACACTG   GAA  GTATGGGGA
                                ||||||   |||  |||||||||
                                TGTGAC   CTT  CATACCCCT
                                   GTGA  CC
GAM565  IL1R1   3'  CCCATGCTTTCCCACCAG   6056    A
                                CTG TGGGAAAGTATGGG
                                ||| ||||||||||||||
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                                GAC ACCCTTTCGTACCC
                                  C
GAM565  ITGA3   3'  CCCCTCCTCCCCCAGTGT   9376       AT   AAGTAT
                                ACACTG  GGGA    GGGG
                                ||||||  ||||    ||||
                                TGTGAC  CCCT    CCCC
                                   C_   CCT___
GAM565  ITGA3   3'  CCCCTCCTCCCCCAGTGT   18538      AT   AAGTAT
                                ACACTG  GGGA    GGGG
                                ||||||  ||||    ||||
                                TGTGAC  CCCT    CCCC
                                   C_   CCT___
GAM565  LIMD1   3'  CCCTCTCTTCCCATCA     26456        A TAT
                                TGATGGGAA G  GGGG
                                |||||||||  |  ||||
                                ACTACCCTT C  TCCC
                                     _ TC_
GAM565  MAZ     3'  CCCCTCTTTTCCCACCA    73387    A      TAT
                                TG TGGGAAAG  GGGG
                                ||  ||||||||  ||||
                                AC ACCCTTTT  CCCC
                                 C      CT_
GAM565  MFAP4   3'  TCCCCATACCCTCTGGGTGTT  69257      GAT   AAA
                                AACACT  GGG  GTATGGGGA
                                ||||||  |||  |||||||||
                                TTGTGG  TCC  CATACCCCT
                                   GTC  ___
GAM565  MKI67   3'  CCTGGAACTTTCCCACCAG   10042    A      A_
                                CTG TGGGAAAGT  TGGG
                                |||  |||||||||  ||||
                                GAC ACCCTTTCA  GTCC
                                  C       AG
GAM565  MPL     3'  TCCCCACACTTCCCATT     18157        A  A
                                GATGGGAA GT TGGGGA
                                ||||||||  ||  ||||||
                                TTACCCTT CA ACCCCT
                                     _  C
GAM565  PIG3    5'  TCCCGCCGTTCCCATCTGTGTT 16878      T      AGTA
                                AACAC GATGGGAA   TGGGG
                                |||||  ||||||||   |||||
                                TTGTG CTACCCTT   GCCCT
                                   T      GCC_
GAM565  PODXL   3'  TCCCGGGGCCCCCCATCAG   18239       AAA  A_
                                CTGATGGG  GT  TGGGG
                                ||||||||  ||  |||||
                                GACTACCC  CG  GCCCT
                                     CC_  GG
GAM565  RORA    5'  CCCCATACTCCTCCCCATCA  56135       AA__
                                TGATGGG   AGTATGGGG
                                |||||||   |||||||||
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                                ACTACCC   TCATACCCC
                                   CTCC
GAM565  RORA    5'  CCCCATACTCCTCCCCATCA  11376       AA__
                                TGATGGG   AGTATGGGG
                                |||||||   |||||||||
                                ACTACCC   TCATACCCC
                                   CTCC
GAM565  RTN4R   3'  CCCCATCTCCACCCCATCATGT 43431     C     AA__  T
          T                     AACA TGATGGG   AG ATGGGG
                                |||| |||||||   || ||||||
                                TTGT ACTACCC   TC TACCCC
                                  _     CACC  _
GAM565  SIAT1   3'  TCTATCTCTCCCATCAG    11664         A  T
                                CTGATGGGA AG ATGGG
                                ||||||||| || |||||
                                GACTACCCT TC TATCT
                                     C  _
GAM565  SPARC   3'  TCCCCTTCGTGTTTCCCCCAAT 11899     C  AT    GTAT__
          GTT                     AACA TG  GGGAAA    GGGGA
                                |||| ||  ||||||     |||||
                                TTGT AC  CCCTTT    CCCCT
                                  A  C_    GTGCTT
GAM565  TCF2    3'  TCCATACTTTCCCACAG    21385    A
                                CTG TGGGAAAGTATGGG
                                ||| ||||||||||||||
                                GAC ACCCTTTCATACCT
                                  _
GAM565  TEGT    3'  TCCGCTTTCCCACCAG     64626    A       AT
                                CTG TGGGAAAGT  GGG
                                ||| |||||||||  |||
                                GAC ACCCTTTCG  CCT
                                  C       __
GAM565  THY1    3'  CCCCTCGCCCATCAGTG    20810         AAAGTAT
                                CACTGATGGG     GGGG
                                ||||||||||     ||||
                                GTGACTACCC     CCCC
                                     GCT_____
GAM565  TMOD2   3'  CTTCTTCCCCATCAG      27248        A   TATG
                                CTGATGGG AAG   GGG
                                ||||||| |||   |||
                                GACTACCC TTC   TTC
                                     C  _____
GAM565  VDR     3'  CCCCACCCCCTTCAGTG    4568       T   AAAGTA
                                CACTGA GGG    TGGGG
                                |||||| |||    |||||
                                GTGACT CCC    ACCCC
                                   T  CC_____
GAM565  ZNF137  3'  TCCTCTATTTCCCATCA    12867         GTAT
                                TGATGGGAAA   GGGGA
                                ||||||||||   |||||
```

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                                ACTACCCTTT   CTCCT
                                     AT__
GAM565  ACAA2    5'  TCCCTGTGTACCTCCCTCAG  91769     T   AA   __
                                CTGA GGGA  GTAT  GGGGA
                                |||| ||||  ||||  |||||
                                GACT CCCT  CATG  TCCCT
                                  _   C_   TG
GAM565  BRD4     3'  TTCCTTCCCACCTGTGTT    54279      TGA     AGTAT
                                AACAC   TGGGAA    GGGG
                                |||||   ||||||    ||||
                                TTGTG   ACCCTT    CCTT
                                  TCC     _____
GAM565  C20orf112 3'  TCCCCATACCTAACATTCCAT  54646       AA____
                                ATGGGA     GTATGGGGA
                                ||||||     |||||||||
                                TACCTT     CATACCCCT
                                   ACAATC
GAM565  CDC37    3'  CTGCAGCCCCCCATCAG     22957        AAA  A  G
                                CTGATGGG   GT TG GG
                                ||||||||   || || ||
                                GACTACCC   CG AC TC
                                     CC_  _  G
GAM565  CDH22    3'  CCCCAGGTTTCCCCCATCAGAG 41155     A      A_   TA
          TT                     AAC CTGATGGG  AAG  TGGGG
                                ||| ||||||||  |||  |||||
                                TTG GACTACCC  TTT  ACCCC
                                  A       CC   GG
GAM565  CRR9     3'  TCCCAAGTTCCCATCACGT   47881    _       AGTA
                                AC TGATGGGAA    TGGGG
                                || |||||||||    |||||
                                TG ACTACCCTT    ACCCT
                                 C        GA__
GAM565  CXYorf1  3'  CCGCTTTCTCATCAGTG     82044             AT
                                CACTGATGGGAAAGT  GG
                                ||||||||||||||  ||
                                GTGACTACTCTTTCG  CC
                                          __
GAM565  DCTN3    3'  CCCTCCCCCCCAATCAGTGTT  44309         _   AAAGTAT
                                AACACTGAT GGG      GGGG
                                ||||||||| |||      ||||
                                TTGTGACTA CCC      TCCC
                                     A   CCC_____
GAM565  DCTN3    3'  CCCTCCCCCCCAATCAGTGTT  23373         _   AAAGTAT
                                AACACTGAT GGG      GGGG
                                ||||||||| |||      ||||
                                TTGTGACTA CCC      TCCC
                                     A   CCC_____
GAM565  DKFZP434H132 5'  TCCCTGTACCCCCCCAGCA   73610    A    AAA
                                TG TGGG   GTATGGGGA
                                || ||||   |||||||||
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                                AC ACCC   CATGTCCCT
                                 G    CCC
GAM565  DKFZP434J1813 5'  TCCACGCCTTTCCCACAATG   61791    C  A     _ TA
                                CA TG TGGGAAA G  TGGG
                                || || ||||||| |  ||||
                                GT AC ACCCTTT C  ACCT
                                 A  _      C GC
GAM565  DKFZP566G1424 5'  TCCCCATACCTAACATTCCAT  84790       AA____
                                ATGGGA     GTATGGGGA
                                ||||||     |||||||||
                                TACCTT     CATACCCCT
                                   ACAATC
GAM565  EIF4B    3'  CCCTTCTCCCATCAGT      75967          AAGTAT
                                ACTGATGGGA     GGGG
                                ||||||||||     ||||
                                TGACTACCCT     TCCC
                                      CT____
GAM565  FLJ13993  3'  TCCAAGACCTTTCCCATCCATG 60465    CT        TATGG
                                CA  GATGGGAAAG    GGA
                                ||  ||||||||||    |||
                                GT  CTACCCTTTC    CCT
                                 AC         CAGAA
GAM565  FLJ14665  3'  TCCTGCTTCCCTCCCATCA    51512         ___    T
                                TGATGGGA   AAGTA GGG
                                ||||||||   ||||| |||
                                ACTACCCT   TTCGT CCT
                                     CCC    _
GAM565  FLJ30473  5'  TCCGACAGCTCCCCATCTGTG  58465     T     AA   A  G_
                                CAC GATGGG  AGT TG  GGA
                                ||| ||||||  ||| ||  |||
                                GTG CTACCC  TCG AC  CCT
                                  T     C_  _  AG
GAM565  HEMK     3'  TCCCAAGGCCCCATCAGTG   32440          AAA  ATG
                                CACTGATGGG   GT   GGGA
                                ||||||||||   ||   ||||
                                GTGACTACCC   CG   CCCT
                                      ___  GAA
GAM565  HSA9947   3'  CCCCAGCTCCCCTCAGTG    42021       T   AA  A
                                CACTGA GGGA  GT TGGGG
                                |||||| ||||  || |||||
                                GTGACT CCCT  CG ACCCC
                                   C   __ _
GAM565  HUMAGCGB  5'  CCCCACACCTTCTGTACTCAG  25229      TG__   A  A
                                CTGA    GGAA GT TGGGG
                                ||||    |||| || |||||
                                GACT    TCTT CA ACCCC
                                  CATG    C  C
GAM565  JDD1     3'  CCCCATACCTTGGGAG      63217    GA    AAA
                                CT  TGGG   GTATGGGG
                                ||  ||||   ||||||||
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                              GA  GTTC   CATACCCC
                               GG   ___
GAM565  KIAA0254  3'  TCCCCATACCTTCCCCTCATGT 28601     _  T    A
              GT                  ACAC TGA GGGAA GTATGGGGA
                                  |||| ||| ||||| |||||||||
                                  TGTG ACT CCCTT CATACCCCT
                                    T  C    C
GAM565  KIAA0450  5'  CCCCATGTGTCCCCAGTG    27628      AT    AAG
                                  CACTG  GGGA   TATGGGG
                                  |||||  ||||   |||||||
                                  GTGAC  CCCT   GTACCCC
                                     __   GT_
GAM565  KIAA0470  3'  CCCCTTGACCCCATCAGT    29055        AAA  AT_
                                  ACTGATGGG   GT   GGGG
                                  |||||||||   ||   ||||
                                  TGACTACCC   CA   CCCC
                                       ___  GTT
GAM565  KIAA1055  3'  CCCTTCCATCAGTGT      66060          AAGTAT
                                  ACACTGATGGGA     GGG
                                  ||||||||||||     |||
                                  TGTGACTACCTT     CCC
                                                 _______
GAM565  KIAA1297  3'  CCCCACACCCCCGTCAGT    72174        AAA  A
                                  ACTGATGGG   GT TGGGG
                                  |||||||||   || |||||
                                  TGACTGCCC   CA ACCCC
                                       C__  C
GAM565  KIAA1319  3'  TCCCCATACCCCTCCAGT    40409     AT   AAA
                                  ACTG  GGG   GTATGGGGA
                                  ||||  |||   |||||||||
                                  TGAC  CCC   CATACCCCT
                                    CT   ___
GAM565  KIAA1467  3'  TCCTTATTCTTTCCCACCTGT  71616    TGA      T
                                  AC   TGGGAAAG ATGGGGA
                                  ||   |||||||| |||||||
                                  TG   ACCCTTTC TATTCCT
                                   TCC       T
GAM565  KIAA1821  3'  TCGTGCACTCCCCCATCCATG  71797    CT     AAA__
                                  CA  GATGGG    GTATGG
                                  ||  ||||||    ||||||
                                  GT  CTACCC    CGTGCT
                                   AC     CCTCA
GAM565  KIAA1879  5'  CCTGCCCTCCCATCAGTGT   73567          AA   T
                                  ACACTGATGGGA  GTA GG
                                  ||||||||||||  ||| ||
                                  TGTGACTACCCT  CGT CC
                                         CC  _
GAM565  LAT1-3TM  5'  CCCTCCTCCATCAGTGT     68599          AAAGTAT
                                  ACACTGATGGG      GGGG
                                  ||||||||||       ||||
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                                TGTGACTACCT      TCCC
                                      CC_____
GAM565  LAT1-3TM  3'  CCCTCCTCCATCAGTGT     48314          AAAGTAT
                                ACACTGATGGG      GGGG
                                ||||||||||       ||||
                                TGTGACTACCT      TCCC
                                      CC_____
GAM565  MAP2K5    3'  CCCCATACCTTCTGGTT     10863     G    A
                                GAT GGAA GTATGGGG
                                ||| |||| ||||||||
                                TTG TCTT CATACCCC
                                  G    C
GAM565  MGC15437  3'  CCCCATACACCAGTGTT     51780       ATGGGAAA
                                AACACTG       GTATGGGG
                                |||||||       ||||||||
                                TTGTGAC       CATACCCC
                                    CA_______
GAM565  MRPS34    3'  TCCCTTTCCCCCATTAGTG   43740          AAAGTAT
                                CACTGATGGG      GGGGA
                                ||||||||||      |||||
                                GTGATTACCC      TCCCT
                                      CCTT____
GAM565  NCOA2     3'  CCCCATACTCCCTATT      21545       AA
                                GATGGG  AGTATGGGG
                                ||||||  |||||||||
                                TTATCC  TCATACCCC
                                   C_
GAM565  PI4KII    3'  TCCATCTCCCATCAGTG     37347          AA T
                                CACTGATGGGA  G ATGGG
                                ||||||||||  | |||||
                                GTGACTACCCT  C TACCT
                                       __ _
GAM565  PIG11     3'  CCCCAAGCTGCCATCAATGT   61612     C     GAA   A
                                ACA TGATGG   AGT TGGGG
                                ||| ||||||   ||| |||||
                                TGT ACTACC   TCG ACCCC
                                  A     G__   A
GAM565  RAI15     3'  CCCCAACCCCCACCAG      66666     A   AAA  A
                                CTG TGGG   GT TGGGG
                                ||| ||||   || |||||
                                GAC ACCC   CA ACCCC
                                  C    C__  _
GAM565  TP53TG3   3'  ACTTTCCCACCAGTGT      31101       A
                                ACACTG TGGGAAAGT
                                |||||| |||||||||
                                TGTGAC ACCCTTTCA
                                   C
GAM565  LOC116113 3'  TCCCCATGTATTCCCCACCTGT 92221       TGAT_    AG
            GTT                   AACAC    GGGAA  TATGGGGA
                                |||||    |||||  ||||||||
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                                TTGTG    CCCTT  GTACCCCT
                                   TCCAC    AT
GAM565  LOC128954 5'  CCCAGCTGCTCCCATCAG    75796        A_  A
                                CTGATGGGA  AGT TGGG
                                |||||||||  ||| ||||
                                GACTACCCT  TCG ACCC
                                     CG  _
GAM565  LOC129138 3'  TCCTGTGCCTCTCACCAG    57125    A    AA
                                CTG TGGGA  GTATGGGG
                                ||| |||||  ||||||||
                                GAC ACTCT  CGTGTCCT
                                  C    C_
GAM565  LOC144114 5'  TCCAGCTTTCCCCTCAATG    82211    C  T      A
                                CA TGA GGGAAAGT TGGG
                                || ||| |||||||| ||||
                                GT ACT CCCTTTCG ACCT
                                 A  C      _
GAM565  LOC145622 3'  TCCACTTTACCATCAGTGTT   77315         G    AT
                                AACACTGATGG AAAGT  GGG
                                |||||||||| |||||  |||
                                TTGTGACTACC TTTCA  CCT
                                      A    __
GAM565  LOC145719 3'  TCCCCATGAAATCCACCAGGTG 83456      GATG   AAG
          T                      ACACT   GGA   TATGGGGA
                                |||||   |||  ||||||||
                                TGTGG   CCT   GTACCCCT
                                   ACCA   AAA
GAM565  LOC145720 3'  TCCCCATGAAATCCACCAGGTG 83438      GATG   AAG
          T                      ACACT   GGA   TATGGGGA
                                |||||   |||  ||||||||
                                TGTGG   CCT   GTACCCCT
                                   ACCA   AAA
GAM565  LOC146176 5'  TCCATGCCTTCGCATCAATG   77698    C    G  A
                                CA TGATG GAA GTATGGG
                                || ||||| ||| |||||||
                                GT ACTAC CTT CGTACCT
                                 A    G  C
GAM565  LOC149301 5'  TCTGCACCTTCCCCATCAG    79252        A  TA  G
                                CTGATGGG AAG  TG GGA
                                |||||||| |||  || |||
                                GACTACCC TTC  AC TCT
                                     C  C_  G
GAM565  LOC149478 3'  TCCCCAGCTCTGCCCCCATCGT 79383      T     AA_  TA_
          GTT                     AACAC GATGGG   AG   TGGGGA
                                |||||  ||||||   ||   ||||||
                                TTGTG CTACCC   TC   ACCCCT
                                   _     CCG  TCG
GAM565  LOC149506 3'  CCCCTCCCCATCAGTGT     84457          AAAGTAT
                                ACACTGATGGG      GGGG
                                ||||||||||      ||||
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                                TGTGACTACCC      CCCC
                                      CT_____
GAM565  LOC157737 5'  CCCCACACCAGTGTTCATCAGT 86540         AAA__  A
                                ACTGATGGG    GT TGGGG
                                |||||||||    || |||||
                                TGACTACTT    CA ACCCC
                                     GTGAC  C
GAM565  LOC161244 3'  CCCCAGATCTCCCCGTCAG   87079        AA  TA_
                                CTGATGGG  AG   TGGGG
                                ||||||||  ||   |||||
                                GACTGCCC  TC   ACCCC
                                     C_  TAG
GAM565  LOC161244 3'  CCCCAGATCTCCCCGTCAG   87080        AA  TA_
                                CTGATGGG  AG   TGGGG
                                ||||||||  ||   |||||
                                GACTGCCC  TC   ACCCC
                                     C_  TAG
GAM565  LOC163944 5'  TCCCCGGGCTCCCATCAGTG   87048         AA  A
                                CACTGATGGGA  GT TGGGGA
                                ||||||||||  || ||||||
                                GTGACTACCCT  CG GCCCCT
                                      __  G
GAM565  LOC197114 3'  TCCCCATGAAATCCACCAGGTG 89709      GATG   AAG
          T                      ACACT    GGA   TATGGGGA
                                 |||||    |||   ||||||||
                                 TGTGG    CCT   GTACCCCT
                                    ACCA   AAA
GAM565  LOC197117 3'  TCCCCATAAAATCCACCAGGTG 89724      GATG   AAG
          T                      ACACT    GGA   TATGGGGA
                                 |||||    |||   ||||||||
                                 TGTGG    CCT   ATACCCCT
                                    ACCA   AAA
GAM565  LOC197363 5'  CCCCACAGTCACCTGTGTT    88056      TGAT  _  AAGTA
                                AACAC    GG GA    TGGGG
                                |||||    || ||    |||||
                                TTGTG    CC CT    ACCCC
                                   T___  A  GAC__
GAM565  LOC197423 5'  CCCTCCTCCATCAGTGT     77858          AAAGTAT
                                ACACTGATGGG      GGGG
                                ||||||||||       ||||
                                TGTGACTACCT      TCCC
                                      CC_____
GAM565  LOC201633 3'  TACTCTCCATCAGTG       90238          AA
                                CACTGATGGG  AGTA
                                ||||||||||  ||||
                                GTGACTACCT  TCAT
                                      C_
GAM565  LOC219754 3'  TCCTGCTTCCCCCCCATCAG   91354        A__    T
                                CTGATGGG   AAGTA GGG
                                ||||||||   ||||| |||
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                                GACTACCC   TTCGT CCT
                                     CCC    _
GAM565  LOC220469 3'  TCCTGTCCCTCCCATCAG    76387        AAGT
                                CTGATGGGA   ATGGGG
                                |||||||||   ||||||
                                GACTACCCT   TGTCCT
                                     CCC_
GAM565  LOC220565 5'  CCCTCCTCCATCAGTGT     90749         AAAGTAT
                                ACACTGATGGG     GGGG
                                ||||||||||      ||||
                                TGTGACTACCT     TCCC
                                      CC_____
GAM565  LOC220766 3'  CCCCTTGACCCCATCAGT    90795        AAA  AT_
                                ACTGATGGG   GT   GGGG
                                |||||||||   ||   ||||
                                TGACTACCC   CA   CCCC
                                     ___  GTT
GAM565  LOC221399 5'  TCCCCATACTGAATCAGCTGT  93851     _    GGGAA
                                ACA CTGAT    AGTATGGGGA
                                ||| |||||    ||||||||||
                                TGT GACTA    TCATACCCCT
                                  C    AG___
GAM565  LOC221463 3'  CCACCTGCCCATCAGCGT    92068    A      AAAGTAT  _
                                AC CTGATGGG      GG GG
                                || ||||||||      || ||
                                TG GACTACCC      CC CC
                                 C       GT_____  A
GAM565  LOC253148 5'  CCCCACACCTCCCATCA     96875        AA  A
                                TGATGGGA  GT TGGGG
                                ||||||||  || |||||
                                ACTACCCT  CA ACCCC
                                     C_  C
GAM565  LOC256273 3'  TCAGGGCCTTTCCCACCTGTG  96408     TGA      TA__
                                CAC   TGGGAAAG   TGG
                                |||   ||||||||   |||
                                GTG   ACCCTTTC   ACT
                                  TCC       CGGG
GAM565  LOC51008  3'  TCCCCATAGATTCACCATT    31972      _  AG
                                GATGG GAA  TATGGGGA
                                ||||| |||  ||||||||
                                TTACC CTT  ATACCCCT
                                   A   AG
GAM565  LOC56834  5'  CCGGCTCTCCCATCAG      39341        A   A
                                CTGATGGGA AGT TGG
                                ||||||||| ||| |||
                                GACTACCCT TCG GCC
                                     C   _
GAM565  LOC85414  3'  CCCCAACTTTCCCCACCAG   52396     AT_      A
                                CTG   GGGAAAGT TGGGG
                                |||   |||||||| |||||
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                                GAC   CCCTTTCA ACCCC
                                  CAC      _
GAM565  LOC90462  3' CCACCTTTCCCATCAGT     62901          TA
                                ACTGATGGGAAAG  TGG
                                |||||||||||||  |||
                                TGACTACCCTTTC  ACC
                                       C_
GAM565  LOC90841  3' TCCATTTTCCCCCAG      64203     AT     GT
                                CTG  GGGAAA  ATGGG
                                |||  ||||||  |||||
                                GAC  CCCTTT  TACCT
                                  C_     __
GAM565  LOC91040  3' CCGCTTTCTCATCAGTG     64714           AT
                                CACTGATGGGAAAGT  GG
                                ||||||||||||||  ||
                                GTGACTACTCTTTCG  CC
                                                __
GAM565  LOC91301  3' CCCCACCGCCCCCCATCAG   65540       AAA  A_
                                CTGATGGG   GT  TGGGG
                                ||||||||   ||  |||||
                                GACTACCC   CG  ACCCC
                                     CC_  CC
GAM565  LOC93380  3' TCCCTGCCCCCCATTAGT     72202        AAA   T
                                ACTGATGGG   GTA GGGG
                                |||||||||   ||| ||||
                                TGATTACCC   CGT CCCT
                                      C__   _
GAM566  ADH1B     3' CTTAGACATAAAGTAAAAT   72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A     T__
GAM566  AHR       3' ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM566  FDFT1     3' TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                                _
GAM566  JTB       3' ATCTCAGACAGTGAAAGTGAAA 21959
              TG                  CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM566  KLF4      3' TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
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                                GT  AGGTGACAGAC CT
                                 AT         C
GAM566  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM566  PKD2     3'  TCCAGGTTGAAAGTGAAA     60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM566  WRN      3'  GGGCAGTGAAAATGAAA      5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM566  ZNF216   3'  ATCTGCACAGCAAAGTGAAA   20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM566  CG012    5'  CTCACTCTGAAAGTGAA      83218          CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM566  EIF2C2   3'  ATCTTCTGAGAGTGAAAG     71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM566  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM566  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281         CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM566  KIAA0984 3'  TTTGTCCAGTGAAAATGAA    65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM566  KLHL6    3'  ATCTCAGAGCAGGAAA       55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
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                                AAAG GAC AGACTCTA
                                  _  G
GAM566  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM566  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM566  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM566  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148         TCAC   C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM566  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM566  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM566  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM566  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM566  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||   |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM566  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
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                                GTAAAGTGAA GTGACA
                                          _
GAM567  DLC1     3'  AAGCAACGCAACCGCTTCCACC 20335     ATCAAT       A
              AC                  GTG     GTGGTTGC TTGCTT
                                  |||     |||||||| ||||||
                                  CAC     CGCCAACG AACGAA
                                    CACCTT       C
GAM567  GABRR2   3'  GCAGCAGCTACTGGACCAC   8982      A  AAT       AT
                                  GTG TC   GTGGTTGC  TGC
                                  ||| ||   ||||||||  |||
                                  CAC AG   CATCGACG  ACG
                                    C  GT_       __
GAM567  LDHA     3'  CAATGCAACCAACTATC     18720     CAATG
                                  GAT     TGGTTGCATTG
                                  |||     ||||||||||
                                  CTA     ACCAACGTAAC
                                    TCA__
GAM567  PPP2R5E  3'  CAATACAACCATGAAATTGATC 20723          ___      C
              AC                  GTGATCAAT   GTGGTTG ATTG
                                  |||||||||   ||||||| ||||
                                  CACTAGTTA   TACCAAC TAAC
                                       AAG      A
GAM567  RECK     3'  AAGCAACAGGCTCACTGGTCAC 40868        AT  _  GCA
                                  GTGATCA  GTG GTT   TTGCTT
                                  |||||||  ||| |||   ||||||
                                  CACTGGT  CAC CGG   AACGAA
                                       __   T   AC_
GAM567  APOBEC3G 3'  AAGCAATGCACTCCTGACCA   41526    A   ATGT  T_
                                  TG TCA    GG  TGCATTGCTT
                                  || |||    ||  ||||||||||
                                  AC AGT    CC  ACGTAACGAA
                                   C   _____  TC
GAM567  LOC145676 5'  CAACCACATTCATCAC      77335       C
                                  GTGAT AATGTGGTTG
                                  ||||| ||||||||||
                                  CACTA TTACACCAAC
                                     C
GAM567  LOC203378 3'  AAGCAACGGCCACCAGTGATCA 90587        AT_      CA
              C                    GTGATCA   GTGGTTG  TTGCTT
                                   |||||||   |||||||  ||||||
                                   CACTAGT   CACCGGC  AACGAA
                                       GAC      __
GAM568  KHK      3'  CTGGATTCAAATCTGCCA    4032       CA
                                  TGGCA  ATTTGAATTCAG
                                  |||||  ||||||||||||
                                  ACCGT  TAAACTTAGGTC
                                     C_
GAM568  KHK      3'  CTGGATTCAAATCTGCCA    21402      CA
                                  TGGCA  ATTTGAATTCAG
                                  |||||  ||||||||||||
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                                ACCGT  TAAACTTAGGTC
                                  C_
GAM568  NRXN3    5'  GCTGGAATTCAAACTGCC    57280      CAA       _
                                GGCA   TTTGAATTC AGT
                                ||||   ||||||||| |||
                                CCGT   AAACTTAAG TCG
                                  C__       G
GAM568  PRSS16   3'  CTGGTTCAAATTCTGCCA    19629      C       T
                                TGGCA AATTTGAAT CAG
                                ||||| ||||||||| |||
                                ACCGT TTAAACTTG GTC
                                  C       _
GAM568  PXF      3'  ATTCAAGATTGTGCCA      11149          _
                                TGGCACAATTT GAAT
                                |||||||||||| ||||
                                ACCGTGTTAGA CTTA
                                       A
GAM568  RAG1     3'  TTACTGAAACATTTTGCCA   4819       C   TTGAA
                                TGGCA AAT    TTCAGTAA
                                ||||| |||    ||||||||
                                ACCGT TTA    AAGTCATT
                                   T  CA___
GAM568  SLC25A15 3'  ACTGAAATTGTGCCA       26507          TGAAT
                                TGGCACAATT    TCAGT
                                ||||||||||    |||||
                                ACCGTGTTAA    AGTCA
                                      _____
GAM568  TPM1     3'  CTGGTTCAAATGTGCCA     4526        A      T
                                TGGCACA TTTGAAT CAG
                                ||||||| ||||||| |||
                                ACCGTGT AAACTTG GTC
                                   _     _
GAM568  DKFZP434E2135 5'  TTACTGAGATCAGCCA      47959      ACAATT   A
                                TGGC     TGA TTCAGTAA
                                ||||     ||| ||||||||
                                ACCG     ACT GAGTCATT
                                  ______  A
GAM568  FLJ10824 3'  ACTGAATTCTGAGGGTGCC   72574      AA  T
                                GGCAC  TT GAATTCAGT
                                |||||  || |||||||||
                                CCGTG  AG CTTAAGTCA
                                   GG  T
GAM568  FLJ22282 3'  TGGACCAAATTGTGCC      45594          AA
                                GGCACAATTTG  TTCA
                                ||||||||||  ||||
                                CCGTGTTAAAC  AGGT
                                       C_
GAM568  H2AV     3'  CTAGATTCAAATTATGC     56848     C       TC
                                GCA AATTTGAAT  AG
                                ||| |||||||||  ||
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                                CGT TTAAACTTA  TC
                                  A       GA
GAM568  HPCL2    3'  TACTGTTAAAATTGTGC     24323         GAATT
                                GCACAATTT    CAGTA
                                |||||||||    |||||
                                CGTGTTAAA    GTCAT
                                     ATT__
GAM568  KIAA0256 3'  TTTACTGAACTCATTGGGACTA 64425     CA_   TT   A
                                TGG   CAA  TGA TTCAGTAAA
                                |||   |||  ||| |||||||||
                                ATC   GTT  ACT AAGTCATTT
                                  AGG   __   C
GAM568  KIAA0265 3'  TTAGGTTCAAATTATGCCA    69888       C        TC
                                TGGCA AATTTGAAT  AG
                                ||||| |||||||||  ||
                                ACCGT TTAAACTTG  TT
                                   A        GA
GAM568  KRTAP2-4 3'  TTTTACTGCTCAAACTGTCACC 52592     C_   A    ATT
             A                   TGG  ACA TTTGA   CAGTAAAA
                                |||  ||| |||||   ||||||||
                                ACC  TGT AAACT   GTCATTTT
                                  AC   C    C__
GAM568  SGKL     3'  ACTGAAATTGTGCCA       25139          TGAAT
                                TGGCACAATT    TCAGT
                                ||||||||||    |||||
                                ACCGTGTTAA    AGTCA
                                      _____
GAM568  Spir-1   5'  TACTGAATCAGATGCACCA    64702     CACA     A
                                TGG    ATTTGA TTCAGTA
                                |||    |||||| |||||||
                                ACC    TAGACT AAGTCAT
                                  ACG_     _
GAM568  LOC149566 3'  TTGGTTTAAATTATGCCA     84498       C        T
                                TGGCA AATTTGAAT CAG
                                ||||| ||||||||| |||
                                ACCGT TTAAATTTG GTT
                                   A       _
GAM568  LOC158490 3'  TTTACTGAAAATCCTGCCA    81936       CA    GAAT
                                TGGCA  ATTT    TCAGTAAA
                                |||||  ||||    ||||||||
                                ACCGT  TAAA    AGTCATTT
                                   CC    _____
GAM568  LOC201183 5'  TTTACTGCTGAATTGTCCA    89759     C       AATT
                                TGG ACAATTTG    CAGTAAA
                                ||| ||||||||    |||||||
                                ACC TGTTAAGT    GTCATTT
                                  _       C___
GAM568  LOC253725 3'  ACTGAATTCTGAGGGTGCC    94700       AA  T
                                GGCAC  TT GAATTCAGT
                                |||||  || |||||||||
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                                CCGTG  AG CTTAAGTCA
                                   GG  T
GAM568  LOC254268 3'  GAATTCAAATTAACCA      95408     CAC
                                TGG   AATTTGAATTC
                                |||   ||||||||||
                                ACC   TTAAACTTAAG
                                  AA_
GAM568  LOC51133  3'  TTTACTGAATTTCAGT       32286     T
                                ATT GAATTCAGTAAA
                                ||| ||||||||||||
                                TGA TTTAAGTCATTT
                                  C
GAM568  LOC54466  3'  TTACTGAACTCAGGTACAGC   38656    ACA     A
                                GC   ATTTGA TTCAGTAA
                                ||   |||||| ||||||||
                                CG   TGGACT AAGTCATT
                                  ACA     C
GAM569  AXL       3'  AATGCATTAGGGATGCCTCCT  8092     A  _      G
                                AG AGG ATTTTTG ATGCATT
                                || ||| ||||||| |||||||
                                TC TCC TAGGGAT TACGTAA
                                 C  G      _
GAM569  AXL       3'  AATGCATTAGGGATGCCTCCT  41589    A  _      G
                                AG AGG ATTTTTG ATGCATT
                                || ||| ||||||| |||||||
                                TC TCC TAGGGAT TACGTAA
                                 C  G      _
GAM569  CNTNAP2   3'  AATGCATCCAAAAAATCTTTTT 26227            _
                                AGAAGGATTTTT GGATGCATT
                                |||||||||||| |||||||||
                                TTTTTCTAAAAA CCTACGTAA
                                       A
GAM569  FMO4      3'  AATGCATCTTCTACCCTGCT   8926     A   ATTTTT
                                AG AGG     GGATGCATT
                                || |||     |||||||||
                                TC TCC     TCTACGTAA
                                 G   CATCT_
GAM569  MSR1      3'  ATCTAAAAATCCTTTT      56951
                                AGAAGGATTTTTGGAT
                                ||||||||||||||||
                                TTTTCCTAAAAATCTA

GAM569  MSR1      3'  ATCTAAAAATCCTTTT      56959
                                AGAAGGATTTTTGGAT
                                ||||||||||||||||
                                TTTTCCTAAAAATCTA

GAM569  POLK      3'  AGTGCAATAATCCTTC      32564         TTTGGA
                                GAAGGATT     TGCATT
                                ||||||||     ||||||
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                                CTTCCTAA     ACGTGA
                                     TA____
GAM569  RAB23    3'  AATGCATTAAGAAACCCATC  32780    A A    G
                                GA GG TTTTT GATGCATT
                                || || ||||| ||||||||
                                CT CC AAAGA TTACGTAA
                                 A C    A
GAM569  RS1      3'  GCCCCAAACATCCTTCT     4395         T    AT
                                AGAAGGAT TTTGG  GC
                                |||||||| |||||  ||
                                TCTTCCTA AAACC  CG
                                     C    C_
GAM569  TRIM9    3'  AATGCATCTTACTTCT      30741       GATTTTT
                                AGAAG      GGATGCATT
                                |||||      |||||||||
                                TCTTC      TCTACGTAA
                                   AT_____
GAM569  ACTR2    3'  CATTTAAAAATCCTTT      19149
                                GAAGGATTTTTGGATG
                                ||||||||||||||||
                                TTTCCTAAAAATTTAC

GAM569  FLJ13955 3'  TAATGCTATCAAAGTCCTCCT  45408    A       TG  _
                                AG AGGATTTT  GAT GCATTA
                                || ||||||||  ||| ||||||
                                TC TCCTGAAA  CTA CGTAAT
                                 C       __  T
GAM569  FLJ20298 3'  AATGCATCATTCCTTT      34899       TTTTTG
                                GAAGGA     GATGCATT
                                ||||||     ||||||||
                                TTTCCT     CTACGTAA
                                   TA____
GAM569  FLJ21551 3'  GCTCCAAAAAGCCTTC      45631       A       T
                                GAAGG TTTTTGGA GC
                                ||||| |||||||| ||
                                CTTCC AAAAACCT CG
                                   G       _
GAM569  KIAA1674 3'  TAATGCATCTTCTTCCCTC    68794    A   TTTTT
                                GA GGA     GGATGCATTA
                                || |||     ||||||||||
                                CT CCT     TCTACGTAAT
                                 C  TCT__
GAM569  MGC5139  5'  TAATGATTGAAAATCCTT     74110         TG ATG
                                AAGGATTTT  G   CATTA
                                |||||||||  |   |||||
                                TTCCTAAAA  T   GTAAT
                                     GT A__
GAM569  NY-REN-60 3'  ATTCAGAACAAATCCTTCT   67107          ___
                                AGAAGGATT   TTTGGAT
                                |||||||||   |||||||
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                                TCTTCCTAA   AGACTTA
                                     ACA
GAM569  PRO2214   5'  AATGCAAATGATCCTTCT    37565        TTTGGA
                                AGAAGGATT     TGCATT
                                |||||||||     ||||||
                                TCTTCCTAG     ACGTAA
                                     TAA___
GAM569  STRN      3'  AATGCATCATCTTCACCTTCT  12039       ATTTTTG
                                AGAAGG      GATGCATT
                                ||||||      ||||||||
                                TCTTCC      CTACGTAA
                                   ACTTCTA
GAM569  LOC116411 5'  TATCCTCAAATCGTTCT     73872      G     TT
                                AGAA GATTT  GGATG
                                |||| |||||  |||||
                                TCTT CTAAA  CCTAT
                                  G     CT
GAM569  LOC130507 3'  TAATGCATCTTTTTTCCTCT   74952     A   TTTTT
                                AGA GGA     GGATGCATTA
                                ||| |||     ||||||||||
                                TCT CCT     TCTACGTAAT
                                  _   TTTT_
GAM569  LOC149821 3'  TAATGCATTTTGCTAATCACTC 84767    A _    TTT_
           CT                     AG AG GATT    GGATGCATTA
                                || || ||||    ||||||||||
                                TC TC CTAA    TTTACGTAAT
                                 C  A    TCGT
GAM569  LOC150596 5'  CACTCAAGCAAAATCCTTC    79950          ___  GA
                                GAAGGATTTT   TG  TG
                                ||||||||||   ||  ||
                                CTTCCTAAAA   AC  AC
                                     CGA  TC
GAM569  LOC200197 3'  AATGCATCCGTCCTTC      88610        TTTT
                                GAAGGAT    GGATGCATT
                                |||||||    |||||||||
                                CTTCCTG    CCTACGTAA
                                     _____
GAM570  AMY2B     5'  CTGACTATATACACCATGTTT  40605      GTAA   GC_
                                AGATA    GTG   ATAGTCAG
                                |||||    |||   ||||||||
                                TTTGT    CAC   TATCAGTC
                                   AC__   ATA
GAM570  DTNA      3'  CTGACTATTCACGTCCCATCTT 7327       AGTAA    C
           T                     AAAGAT     GTGG ATAGTCAG
                                ||||||     |||| |||||||||
                                TTTCTA     CACT TATCAGTC
                                   CCCTG    _
GAM570  DTNA      3'  CTGACTATTCACGTCCCATCTT 52132      AGTAA    C
           T                     AAAGAT     GTGG ATAGTCAG
                                ||||||     |||| |||||||||
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                                TTTCTA    CACT TATCAGTC
                                   CCCTG   _
GAM570  DTNA    3'  CTGACTATTCACGTCCCATCTT 52129       AGTAA   C
              T                    AAAGAT    GTGG ATAGTCAG
                                   ||||||    |||| ||||||||
                                   TTTCTA    CACT TATCAGTC
                                      CCCTG   _
GAM570  DTNA    3'  CTGACTATTCACGTCCCATCTT 52135       AGTAA   C
              T                    AAAGAT    GTGG ATAGTCAG
                                   ||||||    |||| ||||||||
                                   TTTCTA    CACT TATCAGTC
                                      CCCTG   _
GAM570  PBX3    3'  GTGCTCACTTACTACCT    20567    A       _
                                   AG TAGTAAGTG GCAT
                                   || |||||||| ||||
                                   TC ATCATTCAC CGTG
                                    C        T
GAM570  XPC     3'  CTGCAGGCCACTTACCTTC   16134    TA       ATA T
                                   GA  GTAAGTGGC   G CAG
                                   ||  |||||||||   | |||
                                   CT  CATTCACCG   C GTC
                                    TC        GA_ _
GAM570  ATP5D   3'  CTGACGGGCCGCTTACCATC   8072     A       ATA
                                   GAT GTAAGTGGC   GTCAG
                                   ||| |||||||||   |||||
                                   CTA CATTCGCCG   CAGTC
                                     C        GG_
GAM570  BY55    3'  CTGACTATGGCTTAGTATCTTT 59344       G    GG
                                   AAAGATA TAAGT  CATAGTCAG
                                   ||||||| |||||  |||||||||
                                   TTTCTAT ATTCG  GTATCAGTC
                                       G    __
GAM570  C20orf35 3'  CTGACCACGCTGGCTATT    37480       A   GCATA
                                   GATAGT AGTG    GTCAG
                                   |||||| ||||    |||||
                                   TTATCG TCGC    CAGTC
                                      G   AC___
GAM570  CYorf14  5'  CTGACTATGTCCTTTACCTTCT 37608    TA    T
                                   AGA  GTAAG GGCATAGTCAG
                                   |||  ||||| ||||||||||
                                   TCT  CATTT CTGTATCAGTC
                                     TC    C
GAM570  FLJ20276 3'  TGACCAGCTTACTATTTT    34831          GGCATA
                                   AAGATAGTAAGT     GTCA
                                   ||||||||||||     ||||
                                   TTTTATCATTCG     CAGT
                                          AC____
GAM570  FLJ32334 3'  ACTATGCCACATTCTCTTT   57979      T   AA
                                   AAAGA AGT  GTGGCATAGT
                                   ||||| |||  ||||||||||
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                                TTTCT TTA  CACCGTATCA
                                  C  __
GAM570  GGTLA1   5'  CTGACCATCTTTCTCTTACTGT 14660        T  C__  A
            C                    GATAGTAAG GG   AT GTCAG
                                 ||||||||| ||   || |||||
                                 CTGTCATTC CT   TA CAGTC
                                      T  TTC  C
GAM570  HSN44A4A 5'  GGCGCCACTTACTAGCT     31114    A        ATA
                                 AG TAGTAAGTGGC   GTC
                                 || ||||||||||   |||
                                 TC ATCATTCACCG   CGG
                                  G        ____
GAM570  KIAA0596 3'  CTGACTGTTGCCTCACTTCCTT 62830     AT   AAGT   _
                                 AAG  AGT    GGCA TAGTCAG
                                 |||  |||    |||| |||||||
                                 TTC  TCA    CCGT GTCAGTC
                                   CT   CT__    T
GAM570  SEPT6    3'  TGACCATGACCACCTACT    30698      A   _  A
                                 AGTA GTGG CAT GTCA
                                 |||| |||| ||| ||||
                                 TCAT CACC GTA CAGT
                                   C    A   C
GAM570  SLC2A13   3'  CTGACTCTGCACACTATCTTT  53548         AA   G  T
                                 AAAGATAGT  GTG CA AGTCAG
                                 |||||||||  ||| || ||||||
                                 TTTCTATCA  CAC GT TCAGTC
                                       __  _ C
GAM570  LOC145314 3'  TGACCACTGACCATCTT     77089       A  A    _
                                 AAGAT GT AGTGG CA
                                 ||||| || ||||| ||
                                 TTCTA CA TCACC GT
                                    C  G    A
GAM570  LOC153077 3'  ACTATGCCATGCTATTCTT    85900      _    AA
                                 AAGA TAGT  GTGGCATAGT
                                 |||| ||||  ||||||||||
                                 TTCT ATCG  TACCGTATCA
                                   T   __
GAM570  LOC255290 5'  CTGACCATCTTTCTCTTACTGT 95610         T  C__  A
            C                    GATAGTAAG GG   AT GTCAG
                                 ||||||||| ||   || |||||
                                 CTGTCATTC CT   TA CAGTC
                                      T  TTC  C
GAM571  ADAMTS8   5'  TCGGGCCGCCAGCACCTG    22886    _      ATAAG
                                 CAG TGCTGGC    CTGA
                                 ||| |||||||    ||||
                                 GTC ACGACCG    GGCT
                                   C      CCG__
GAM571  BAP1     3'  TCAGGGACCCAGCACTGG    16219          CATAAG
                                 CCAGTGCTGG     CTGA
                                 ||||||||||     ||||
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                                GGTCACGACC     GACT
                                      CAGG__
GAM571  BF      5'  TTCAGCTTGGACACTG     8140       CTGGCA
                                CAGTG     TAAGCTGAA
                                |||||     |||||||||
                                GTCAC     GTTCGACTT
                                   AG_____
GAM571  C1QB    3'  TTCAACTCTGTGTCCCAGCACT 4923    A        __   _ C
           GGC                     G CCAGTGCTGG  CATA AG TGAA
                                | ||||||||||  |||| || ||||
                                C GGTCACGACC  GTGT TC ACTT
                                _         CT    C  A
GAM571  CHC1    3'  CAGCCCTGAGCACTGTGTC    7020     _      __ CATAA
                                GAC CAGTGCT  GG     GCTG
                                ||| |||||||  ||     ||||
                                CTG GTCACGA  CC     CGAC
                                  T       GT  _____
GAM571  CMRF35  5'  CAGAGCTGTCAGCACCGG    21929    A        TAAG
                                CC GTGCTGGCA    CTG
                                || |||||||||    |||
                                GG CACGACTGT    GAC
                                 C        CGA_
GAM571  EPHB6   3'  TCAGCCCTGGACACTGGTC    15466         _ TG CATAA
                                GACCAGTG C  G     GCTGA
                                |||||||| |  |     |||||
                                CTGGTCAC G  C     CGACT
                                      A GT C____
GAM571  EVPL    5'  CAGCCTGAGCCAGCACT     8803          A  A
                                AGTGCTGGC TA GCTG
                                ||||||||| || ||||
                                TCACGACCG GT CGAC
                                      A  C
GAM571  GARP    3'  CAGCCCAGCACTGG        18594          CATAA
                                CCAGTGCTGG    GCTG
                                ||||||||||    ||||
                                GGTCACGACC    CGAC
                                      _____
GAM571  GJB5    3'  CAGCTCGACGGCACTGG     17945          GCATA
                                CCAGTGCTG     AGCTG
                                |||||||||     |||||
                                GGTCACGGC     TCGAC
                                      AGC__
GAM571  GPR81   3'  CTTACCAGCATTAGTC      50757     C       CA
                                GAC AGTGCTGG  TAAG
                                ||| ||||||||  ||||
                                CTG TTACGACC  ATTC
                                  A       __
GAM571  IFI16   5'  AGCAAGCCAGCACTAGTC    71221     C        ATAA
                                GAC AGTGCTGGC    GCT
                                ||| |||||||||    |||
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                                CTG TCACGACCG    CGA
                                  A       AA__
GAM571  KRT4     3'  CAGCTGGGCCCAGCACTGGT  9635          _ ATA
                                ACCAGTGCTGG C   AGCTG
                                |||||||||||  |   |||||
                                TGGTCACGACC G   TCGAC
                                      C GG_
GAM571  MAP3K9   3'  TTCAGCTTCCCAAACACCAGT  60709    CA   C_   CAT
                                AC  GTG  TGG   AAGCTGAA
                                ||  |||  |||   ||||||||
                                TG  CAC  ACC   TTCGACTT
                                 AC   AA   C__
GAM571  MGAT5    5'  TCAGCTTACAGTTCCTG     10028     T_    GCA
                                CAG  GCTG   TAAGCTGA
                                |||  ||||   ||||||||
                                GTC  TGAC   ATTCGACT
                                  CT   ____
GAM571  MOCS1    3'  TTCAGCTTAACAGTTGCCCGGT 92037      A_   _   GCA
           C                     GACC  GTG CTG   TAAGCTGAA
                                ||||  ||| |||   |||||||||
                                CTGG  CGT GAC   ATTCGACTT
                                  CC   T   A__
GAM571  P23      3'  TCAGCTTATACCCGGGCT    21719     G    C_
                                AGT CTGG  ATAAGCTGA
                                ||| ||||  |||||||||
                                TCG GGCC  TATTCGACT
                                  _    CA
GAM571  PFKFB4   3'  TCAGCCACATGCAACACTGTGT 15874     _     CTG    AA_
           C                     GAC CAGTG   GCAT   GCTGA
                                ||| |||||   ||||   |||||
                                CTG GTCAC   CGTA   CGACT
                                  T    AA_    CAC
GAM571  PTPRK    3'  TTCAGCCTGTGGCCCAGCACTG 11125           __    A
           GTC                     GACCAGTGCTGG  CATA GCTGAA
                                ||||||||||||  |||| ||||||
                                CTGGTCACGACC  GTGT CGACTT
                                      CG    C
GAM571  RNPEPL1  3'  CGGATGCCAGCACCTG      36676     _       AAG
                                CAG TGCTGGCAT   CTG
                                |||  |||||||||   |||
                                GTC ACGACCGTA   GGC
                                  C       ___
GAM571  UBE2L3   3'  TCAGCCCTGGCACTGGC     12507    A      TG CATAA
                                G CCAGTGC  G    GCTGA
                                | |||||||  |    |||||
                                C GGTCACG  C    CGACT
                                 _      GT C____
GAM571  APXL2    5'  CAGCCTCAGCACTCATC     75185    CC       CATAA
                                GA  AGTGCTGG    GCTG
                                ||  ||||||||    ||||
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                                CT  TCACGACT    CGAC
                                 AC       C____
GAM571  ARHGEF9  3'  TTCAGCTTACCAAGCA     30824      _  CA
                                TGCT GG  TAAGCTGAA
                                |||| ||  |||||||||
                                ACGA CC  ATTCGACTT
                                  A  __
GAM571  CEGP1    3'  TTCAGCTTCCTCTAGCCCGG   40589    AGT    CAT
                                CC   GCTGG   AAGCTGAA
                                ||   |||||   ||||||||
                                GG   CGATC   TTCGACTT
                                 CC_    TCC
GAM571  DKFZp547D155 3'  CAGCCCTGAGACCACTGGTC   70435        CTGG  TAA
                                GACCAGTG    CA   GCTG
                                ||||||||    ||   ||||
                                CTGGTCAC    GT   CGAC
                                     CAGA  CC_
GAM571  DKFZP727G051 3'  TTCAGCCCATCAACCAGCATTG 69483           CATAA__
           GTC                    GACCAGTGCTGG      GCTGAA
                                ||||||||||||      ||||||
                                CTGGTTACGACC      CGACTT
                                      AACTACC
GAM571  DUSP14   5'  CACTGTCACCAGCACTGCTC   22834    C       CATA  C
                                GA CAGTGCTGG    AG TG
                                || |||||||||    || ||
                                CT GTCACGACC    TC AC
                                 C       ACTG  _
GAM571  FLJ10206  5'  CAGCTTATGCCAGGAGTC    35898     CAGTG
                                GAC    CTGGCATAAGCTG
                                |||    ||||||||||||||
                                CTG    GACCGTATTCGAC
                                  AG___
GAM571  FLJ20967  5'  GGCGCCCAGCACTGGTT     41962          CATAA
                                GACCAGTGCTGG    GCT
                                ||||||||||||    |||
                                TTGGTCACGACC    CGG
                                      CG___
GAM571  FLJ22569  3'  TTCAGCTTACTAAACTG     43679      GC   CA
                                CAGT  TGG  TAAGCTGAA
                                ||||  |||  |||||||||
                                GTCA  ATC  ATTCGACTT
                                  A_  __
GAM571  FOXN4    3'  TTCAGCTTGGACACACTGG    75574       C  GCA
                                CCAGTG TG   TAAGCTGAA
                                |||||| ||   |||||||||
                                GGTCAC AC   GTTCGACTT
                                   _ AG_
GAM571  GW112    3'  TTCAACTGAAGCCAGCACTGGT 21194           ATA  C
           T                    GACCAGTGCTGGC   AG TGAA
                                ||||||||||||||   || ||||
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                                TTGGTCACGACCG  TC ACTT
                                      AAG  A
GAM571  HOOK2    3'  CAGCTCACATGGCGCCCAGCAC 25256        _____  A__
            TGG                  CCAGTGCTGG   CAT  AGCTG
                                 ||||||||||   |||  |||||
                                 GGTCACGACC   GTA  TCGAC
                                      CGCG  CAC
GAM571  jdp2     3'  TTCAGCACAGCCAGCAT    55327       ATAA
                                 GTGCTGGC   GCTGAA
                                 ||||||||   ||||||
                                 TACGACCG   CGACTT
                                     ACA_
GAM571  KIAA0767 3'  TCTGCTGCCAGCACAGG    60632    A      TAA  T
                                 CC GTGCTGGCA  GC GA
                                 || |||||||||  || ||
                                 GG CACGACCGT  CG CT
                                  A       ___  T
GAM571  KIAA0923 3'  TCAGCTTGATGCATGGTC    25838     G   TGGCA
                                 GACCA TGC    TAAGCTGA
                                 ||||| |||    ||||||||
                                 CTGGT ACG    GTTCGACT
                                    _  TA___
GAM571  KIAA0982 3'  TTCACTGTTTGCCAGCAC    25852       TA_  C
                                 GTGCTGGCA  AG TGAA
                                 |||||||||  || ||||
                                 CACGACCGT  TC ACTT
                                      TTG  _
GAM571  KIAA1000 3'  TTCAGCTTTGCAAAGTACTGG  65281       G_   T
                                 CCAGTGCT  GCA AAGCTGAA
                                 ||||||||  ||| ||||||||
                                 GGTCATGA  CGT TTCGACTT
                                     AA  _
GAM571  MAP3K3   3'  TCAGCCTGGGCGCTGGTC    9999        GG  TAA
                                 GACCAGTGCT  CA  GCTGA
                                 ||||||||||  ||  |||||
                                 CTGGTCGCGG  GT  CGACT
                                      __  C__
GAM571  MGC16037 5'  CTTGTCCAGCACTAGTC    51821    C      C
                                 GAC AGTGCTGG ATAAG
                                 ||| |||||||| |||||
                                 CTG TCACGACC TGTTC
                                   A      _
GAM571  MIDORI   3'  TCAGCTTATCCTGCAACT    73792    _  T  C
                                 AGT GC GG ATAAGCTGA
                                 ||| || || |||||||||
                                 TCA CG CC TATTCGACT
                                   A  T  _
GAM571  MtFMT    5'  CAGTGGCGAGCACTGG      57651       G  ATAA
                                 CCAGTGCT GC   GCTG
                                 |||||||| ||   ||||
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                                GGTCACGA CG    TGAC
                                    G  G___
GAM571  PCDH16    5'  TCAGTTCCAACCACTGG     72826       C_   CATA
                                CCAGTG  TGG    AGCTGA
                                ||||||  |||    ||||||
                                GGTCAC  ACC    TTGACT
                                   CA   _____
GAM571  QKI       3'  CAGCTTATCAACTCGTC     65439     C   GCTGGC
                                GAC AGT     ATAAGCTG
                                ||| |||     ||||||||
                                CTG TCA     TATTCGAC
                                  C   AC____
GAM571  TNRC6     3'  CAACTTTTAGCACTG       70506         CAT   C
                                CAGTGCTGG   AAG TG
                                |||||||||   ||| ||
                                GTCACGATT   TTC AC
                                    ___   A
GAM571  TOB2      3'  CAGCCCAGGCCAGCACTG    95618          ATAA
                                CAGTGCTGGC    GCTG
                                ||||||||||    ||||
                                GTCACGACCG    CGAC
                                     GACC
GAM571  TU12B1-TY 3'  TCAGCCCACAGCACTGTC    33406     C      GCATAA
                                GAC AGTGCTG     GCTGA
                                ||| |||||||     |||||
                                CTG TCACGAC     CGACT
                                  _      ACC___
GAM571  TUSP      3'  TCAGCCTAAGAGCGCAGCACTG 39641         _  A__  A
                                CAGTGCTG GC   TA GCTGA
                                |||||||| ||   || |||||
                                GTCACGAC CG   AT CGACT
                                    G  AGA  C
GAM571  USP19     3'  TCAGCTTATGCATCTGGT    88959       TGCTG
                                ACCAG    GCATAAGCTGA
                                |||||    ||||||||||
                                TGGTC    CGTATTCGACT
                                   TA___
GAM571  ZD52F10   3'  CAGCCTGTGCCAGCCCTGG    52819     T       A
                                CCAG GCTGGCATA GCTG
                                |||| ||||||||| ||||
                                GGTC CGACCGTGT CGAC
                                   C       C
GAM571  LOC145268 3'  TCAGCTTACAAGAGCCACTG   77062      _ GGCA
                                CAGTG CT    TAAGCTGA
                                ||||| ||    ||||||||
                                GTCAC GA    ATTCGACT
                                   C  GAAC
GAM571  LOC149296 5'  CAGCTTATGGGCAGCA      79256       G_
                                TGCTG  CATAAGCTG
                                |||||  |||||||||
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                                ACGAC  GTATTCGAC
                                   GG
GAM571  LOC161877 5'  TCAGGGCAGGCCAGCGCTGG  82326          ATAAG
                                CCAGTGCTGGC    CTGA
                                ||||||||||    ||||
                                GGTCGCGACCG    GACT
                                     GACGG
GAM571  LOC163115 5'  TCAGCCCCTGACAGCACTGG  82413        G  TAA
                                CCAGTGCTG CA   GCTGA
                                ||||||||| ||   |||||
                                GGTCACGAC GT   CGACT
                                     A  CCC
GAM571  LOC196500 3'  TCAGCTCACTCAGTGGTC    87744     AGT    CATA
                                GACC   GCTGG   AGCTGA
                                ||||   |||||   ||||||
                                CTGG   TGACT   TCGACT
                                  ___    CAC_
GAM571  LOC197287 3'  TCAGCTCATGTGTTTTGCACTG 60865       T_    __
                                CAGTGC  GGCATA  AGCTGA
                                ||||||  ||||||  ||||||
                                GTCACG  TTGTGT  TCGACT
                                   TT     AC
GAM571  LOC200470 5'  TCAGCCTGCGGCGCTGG     90069        G  TAA
                                CCAGTGCTG CA   GCTGA
                                ||||||||| ||   |||||
                                GGTCGCGGC GT   CGACT
                                     _ C__
GAM571  LOC221584 3'  CAGCTTATGTGGCAC       93828       G
                                GTGCTG CATAAGCTG
                                |||||| |||||||||
                                CACGGT GTATTCGAC
                                  _
GAM571  LOC51716  3'  CAGCTCATGGCCCTAGCA    32787       ___  A
                                TGCTGG   CAT AGCTG
                                ||||||   ||| |||||
                                ACGATC   GTA TCGAC
                                   CCG   C
GAM571  LOC92196  5'  CAGAGCACCAGCACTGGC    68456   A       CATAAG
                                G CCAGTGCTGG     CTG
                                | ||||||||||     |||
                                C GGTCACGACC     GAC
                                _        ACGA__
GAM572  CASP7    5'  CAGCAGAGATCAATGAGATCAG 52895    AA    TA_  CTC
           A                     TC  ATCTC   GA   CTCTGCTG
                                 ||  |||||   ||   ||||||||
                                 AG  TAGAG   CT   GAGACGAC
                                  AC    TAA  A__
GAM572  GABRA2   3'  AGAAAAACTAGAGATTTGA   5862          ACTCC
                                TCAAATCTCTAG    TCT
                                ||||||||||||    |||
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                                AGTTTAGAGATC    AGA
                                      AAAA_
GAM572  HRH1     3'  CAGCAGAGAGATTGAACTTTGA 5983       TC  TAGA   C
                                TCAAA  TC    CTC TCTGCTG
                                |||||  ||    ||| |||||||
                                AGTTT  AG    GAG AGACGAC
                                   CA  TTA_   _
GAM572  SIGLEC7  3'  CAGCAAAGGAGTCTGAGGCTGA 26894     AA    T      C
                                TCA  TCTC AGACTCCT TGCTG
                                |||  |||| |||||||| |||||
                                AGT  GGAG TCTGAGGA ACGAC
                                  C_   _      A
GAM572  SIGLEC7  3'  CAGCAAAGGAGTCTGAGGCTGA 33304     AA    T      C
                                TCA  TCTC AGACTCCT TGCTG
                                |||  |||| |||||||| |||||
                                AGT  GGAG TCTGAGGA ACGAC
                                  C_   _      A
GAM572  ZFP93    3'  CAGCAGAAAAGTCTTGTCGGA  14886     CT__    CC
                                TCT    AGACT  TCTGCTG
                                |||    |||||  |||||||
                                AGG    TCTGA  AGACGAC
                                  CTGT     AA
GAM572  FLJ10961 3'  CAGAGGAGGGATCATGA     63486     A_    CTAGA
                                TCA  ATCT     CTCCTCTG
                                |||  ||||     ||||||||
                                AGT  TAGG     GAGGAGAC
                                  AC    ______
GAM572  KIAA0752 3'  CAGCAGAGGTCAGGAGTTTGA  67049      T    A  CT
                                TCAAA CTCT GA  CCTCTGCTG
                                ||||| |||| ||  |||||||||
                                AGTTT GAGG CT  GGAGACGAC
                                   _    A  __
GAM572  MGC13168 5'  CGGGGGAGCCCGAAATTTGA   51210       C  TAGA
                                TCAAAT TC    CTCCTCTG
                                |||||| ||    ||||||||
                                AGTTTA AG    GAGGGGGC
                                   A  CCC_
GAM572  NPD009   5'  CAGCAGAGAAGTATTATTTGG  95046       CTCTAG   C
                                TCAAAT     ACT CTCTGCTG
                                ||||||     ||| ||||||||
                                GGTTTA     TGA GAGACGAC
                                   TTA___   A
GAM572  LOC115939 3'  GAGAAAATCTAGAGACATGA   73663     AA      CTC_
                                TCA  TCTCTAGA    CTC
                                |||  ||||||||    |||
                                AGT  AGAGATCT    GAG
                                  AC       AAAA
GAM572  LOC127255 3'  CAGACAGTGCAGAGATTTGA   59163          AG   CC
                                TCAAATCTCT  ACT  TCTG
                                ||||||||||  |||  ||||
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                                AGTTTAGAGA  TGA  AGAC
                                      CG   C_
GAM572  LOC150225 3'  CAGCAGAGGAGCCTGG      84984      A
                                CTAG CTCCTCTGCTG
                                |||| ||||||||||
                                GGTC GAGGAGACGAC
                                  C
GAM572  LOC152220 3'  CAGCAGAGGCAGTAAGAGATGT 85578     A     AG  _
          GA                      TCA ATCTCT  ACT CCTCTGCTG
                                ||| ||||||  ||| |||||||||
                                AGT TAGAGA  TGA GGAGACGAC
                                  G     A_  C
GAM572  LOC196527 3'  CAGCAAAGGAAAACTCAGATTT 87755       CTAGAC   C
                                AAATCT     TCCT TGCTG
                                ||||||     |||| |||||
                                TTTAGA     AGGA ACGAC
                                    CTCAAA    A
GAM572  LOC255065 3'  CAGCAGATCTCCAGAGA     96581      A  CTCC
                                TCTCT GA    TCTGCTG
                                ||||| ||    |||||||
                                AGAGA CT    AGACGAC
                                   C  CT__
GAM572  LOC257235 3'  GAGTCTGAGATTTGA       97060         T
                                TCAAATCTC AGACTC
                                ||||||||| ||||||
                                AGTTTAGAG TCTGAG
                                          _
GAM573  BCL11A   3'  AGAGAGAGAAAAAGAC      43157       G
                                GTCTTTT TCTCTCTCT
                                ||||||| |||||||||
                                CAGAAAA AGAGAGAGA
                                          _
GAM573  DXF68S1E  3'  CTTGACGGTTGAGACAAAA   60005         TC  T
                                TTTTGTCTC  TC TCAAG
                                |||||||||  || |||||
                                AAAACAGAG  GG AGTTC
                                      TT  C
GAM573  GFRA2    5'  AAGGGAGAAAGACAAAA     7657         __
                                TTTTGTC  TCTCTCTT
                                |||||||  ||||||||
                                AAAACAG  AGAGGGAA
                                    AA
GAM573  KCNA5    3'  TTGAAGAAAGGCAAATCTG   59709     TCT      CTC
                                CAG   TTTGTCT   TCTTCAA
                                |||   |||||||   |||||||
                                GTC   AAACGGA   AGAAGTT
                                  T__      A__
GAM573  LRRC2    3'  TTGAAGAAACAAAGGCTG    44481         T  CTCTC
                                CAGTCTTT GT    TCTTCAA
                                |||||||| ||    |||||||
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                                GTCGGAAA CA     AGAAGTT
                                     _  A_____
GAM573  NIPSNAP1  3'  AGAGATGACAAAAGAC      13289          _
                                GTCTTTTGTC TCTCT
                                |||||||||| |||||
                                CAGAAAACAG AGAGA
                                      T
GAM573  PDE4B     3'  CTTGAAAATGGAAGACACAAAA 10478      C  T     CT TC_
           CTG                    CAGT TT TGTCT  C   TTCAAG
                                |||| || |||||  |   ||||||
                                GTCA AA ACAGA  G   AAGTTC
                                  A  C     AG TAA
GAM573  SPAG9     5'  CTTGAAGAAAGAGAAGCAGAAC 14273      _  TTTG     C
           TG                     CAGT CT    TCTCT TCTTCAAG
                                |||| ||    ||||| ||||||||
                                GTCA GA    AGAGA AGAAGTTC
                                  A  CGA_    A
GAM573  TEC       3'  TGAAGAGAAGAAAGTCT     12223    T   TTG   C
                                AG CTT   TCT TCTCTTCA
                                || |||   ||| ||||||||
                                TC GAA   AGA AGAGAAGT
                                 T   ___   _
GAM573  ALDH9     3'  CTTGAAGAAAAAAAACAAAAAA 5513     C     CTCTC_
           C                      GT TTTTGT     TCTTCAAG
                                || ||||||     ||||||||
                                CA AAAACA     AGAAGTTC
                                 A     AAAAAA
GAM573  CDC10     3'  CTTGAAGAGAAAAAAGTCA   91112    T  C___
                                TG CT    TCTCTTCAAG
                                || ||    ||||||||||
                                AC GA    AGAGAAGTTC
                                 T  AAAA
GAM573  CLECSF9   5'  AGAGAGAAACAAAAAAC     26836    C     C
                                GT TTTTGT TCTCTCT
                                || |||||| |||||||
                                CA AAAACA AGAGAGA
                                 A     A
GAM573  FLJ22843  3'  CTTAAAGAGAGATGTGAAGAT  47226       TGTC       C
                                GTCTTT    TCTCTCTT AAG
                                ||||||    |||||||| |||
                                TAGAAG    AGAGAGAA TTC
                                   TGT_       A
GAM573  KIAA0061  3'  CTTAAAGAGAGAAATCATGGAC 68291      TT  TC_      C
                                GTCT  TG   TCTCTCTT AAG
                                ||||  ||   |||||||| |||
                                CAGG  AC   AGAGAGAA TTC
                                  T_  TAA       A
GAM573  KIAA1854  3'  TGAAAACTCTCAAAAGACTG   71747          TCTCTCTC
                                CAGTCTTTTG       TTCA
                                ||||||||||       ||||
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                                GTCAGAAAAC       AAGT
                                      TCTCAA__
GAM573  MGC10067  3'  GAGAAACAGAAGACTG      58936          C
                                CAGTCTTTTGT TCTC
                                |||||||||||| ||||
                                GTCAGAAGACA AGAG
                                       A
GAM573  MGC12217  3'  CTTGACATGAAAACAAAGACTG 51311        T  CTC  TCT
                                CAGTCTTT GT   TC   TCAAG
                                |||||||| ||   ||   |||||
                                GTCAGAAA CA   AG   AGTTC
                                     _  AA_  TAC
GAM573  MY014    5'  TGAAGAGAGAGTTTGCCAACT  48144     CTTTTGT
                                AGT      CTCTCTCTTCA
                                |||      ||||||||||
                                TCA      GAGAGAGAAGT
                                  ACCGTTT
GAM573  NXPH3    5'  GAAAAGAGAAGGGGAGAGC   65759   T    G   _    C
                                G CTTTT TCT CTCT TTC
                                | ||||| ||| |||| |||
                                C GAGAG GGA GAGA AAG
                                 _    G   A   A
GAM573  P15-2    5'  CTTGAAGAGAAAAGAGCCAGA  38008     T   ___
                                TTTG CTC   TCTCTTCAAG
                                |||| |||   ||||||||||
                                AGAC GAG   AGAGAAGTTC
                                  C   AAA
GAM573  RASSF2   3'  TTGTGTAAAGGACAAAAGAC   28447         T  CTCTT
                                GTCTTTTGTC CT    CAA
                                |||||||||| ||    |||
                                CAGAAAACAG GA    GTT
                                     _  AATGT
GAM573  RGS11    3'  TGAAGAGAGGTGAGAC      13829      TTGTC
                                GTCTT    TCTCTCTTCA
                                |||||    ||||||||||
                                CAGAG    GGAGAGAAGT
                                   T____
GAM573  SLC5A7   3'  AAGTAGGTATACAAAAGACT   41502         CT_  CT
                                AGTCTTTTGT   CT  CTT
                                ||||||||||   ||  |||
                                TCAGAAAACA   GG  GAA
                                      TAT  AT
GAM573  SYNJ2BP  3'  AAGAGAGAAAGATTG       37197       TTGTC
                                CAGTCTT    TCTCTCTT
                                |||||||    ||||||||
                                GTTAGAA    AGAGAGAA
                                     _____
GAM573  WBSCR20A 3'  AAGAGAAAGAAGAGAC      35957       TG   C
                                GTCTTT  TCT TCTCTT
                                ||||||  ||| ||||||
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                                CAGAGA  AGA AGAGAA
                                   __   A
GAM573  ZNF11B    5'  GAAGAGAGAGTGAGCTG     73984     T   TTGT
                                CAG CTT    CTCTCTCTTC
                                ||| |||    ||||||||||
                                GTC GAG    GAGAGAGAAG
                                  _   T___
GAM573  LOC158219 3'  TGAATAAGAGACAAAA      81793          CTC
                                TTTTGTCTCT   TTCA
                                ||||||||||   ||||
                                AAAACAGAGA   AAGT
                                      AT_
GAM573  LOC199796 5'  CTTGAAGAGAGAACGGAACAC  74453    C     C
                                GT TTTTGT TCTCTCTTCAAG
                                || |||||| ||||||||||||
                                CA AAGGCA AGAGAGAAGTTC
                                 C     _
GAM573  LOC199837 5'  CTTGAAGAGAAAGAAGAC     88407     TTTG   C
                                GTCT    TCT TCTCTTCAAG
                                ||||    ||| ||||||||||
                                CAGA    AGA AGAGAAGTTC
                                   _____   A
GAM573  LOC199838 5'  CTTGAAGAGAAAGAAGAC     88408     TTTG   C
                                GTCT    TCT TCTCTTCAAG
                                ||||    ||| ||||||||||
                                CAGA    AGA AGAGAAGTTC
                                   _____   A
GAM573  LOC221092 5'  TGAAGAAGAGGCAAAAGAT    93242           C
                                GTCTTTTGTCTCT TCTTCA
                                |||||||||||| ||||||
                                TAGAAAACGGAGA AGAAGT
                                             _
GAM573  LOC253039 3'  CTTGAAGAAAGAGAAGGAAGAC 96156       TG    C
                                GTCTTT  TCTCT TCTTCAAG
                                ||||||  ||||| ||||||||
                                CAGAAG  AGAGA AGAAGTTC
                                    GA     A
GAM573  LOC253981 3'  CTTGAAGAGCTCTAAGAGACTG 95830          TCTCT
                                CAGTCTTTTG     CTCTTCAAG
                                ||||||||||     |||||||||
                                GTCAGAGAAT     GAGAAGTTC
                                      CTC__
GAM573  LOC254120 3'  TGAAGAGAGAAACAGAG      97396       C
                                TTTTGT TCTCTCTTCA
                                |||||| ||||||||||
                                GAGACA AGAGAGAAGT
                                    A
GAM573  LOC255056 5'  AAGAGAGAGACCACAGGAACTG 97627      _   TT_
                                CAGT CTT   GTCTCTCTCTT
                                |||| |||   ||||||||||
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                                GTCA GGA   CAGAGAGAGAA
                                  A   CAC
GAM573  LOC257235 3'  CTTGGGTCAGAGACAAAAGACT 97059            CT  T
                                AGTCTTTTGTCTCT  CT CAAG
                                |||||||||||||  || ||||
                                TCAGAAAACAGAGA  GG GTTC
                                       CT  _
GAM573  LOC257455 5'  TTGAAAAGCAAAGGACT     78750         TCTCT  C
                                AGTCTTTTG    CT TTCAA
                                |||||||||    || |||||
                                TCAGGAAAC    GA AAGTT
                                     _____ A
GAM573  LOC90784  5'  TTGAAATAGAAAAGACTG    64007        TGTC   CTC
                                CAGTCTTT    TCT   TTCAA
                                ||||||||    |||   |||||
                                GTCAGAAA    AGA   AAGTT
                                    _____  TA_
GAM574  ADAMTS8   5'  TCGGGCCGCCAGCACCTG    22886    _      ATAAG
                                CAG TGCTGGC    CTGA
                                ||| |||||||    ||||
                                GTC ACGACCG    GGCT
                                  C      CCG__
GAM574  BAP1      3'  TCAGGGACCCAGCACTGG     16219          CATAAG
                                CCAGTGCTGG     CTGA
                                ||||||||||     ||||
                                GGTCACGACC     GACT
                                      CAGG__
GAM574  BF        5'  TTCAGCTTGGACACTG      8140        CTGGCA
                                CAGTG     TAAGCTGAA
                                |||||     |||||||||
                                GTCAC     GTTCGACTT
                                   AG____
GAM574  C1QB      3'  TTCAACTCTGTGTCCCAGCACT 4923     A        __   _ C
            GGC                   G CCAGTGCTGG  CATA AG TGAA
                                | ||||||||||  |||| || ||||
                                C GGTCACGACC  GTGT TC ACTT
                                _         CT    C  A
GAM574  CHC1      3'  CAGCCCTGAGCACTGTGTC    7020      _      __ CATAA
                                GAC CAGTGCT  GG     GCTG
                                ||| |||||||  ||     ||||
                                CTG GTCACGA  CC     CGAC
                                  T      GT  _____
GAM574  CMRF35    5'  CAGAGCTGTCAGCACCGG    21929    A       TAAG
                                CC GTGCTGGCA    CTG
                                || |||||||||    |||
                                GG CACGACTGT    GAC
                                 C        CGA_
GAM574  EPHB6     3'  TCAGCCCTGGACACTGGTC    15466         _ TG CATAA
                                GACCAGTG C  G    GCTGA
                                |||||||| |  |    |||||
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                                CTGGTCAC G  C    CGACT
                                    A GT C____
GAM574  EVPL    5'  CAGCCTGAGCCAGCACT    8803         A  A
                                AGTGCTGGC TA GCTG
                                ||||||||| || ||||
                                TCACGACCG GT CGAC
                                    A  C
GAM574  GARP    3'  CAGCCCAGCACTGG       18594         CATAA
                                CCAGTGCTGG    GCTG
                                ||||||||||    ||||
                                GGTCACGACC    CGAC
                                      _____
GAM574  GJB5    3'  CAGCTCGACGGCACTGG     17945         GCATA
                                CCAGTGCTG    AGCTG
                                |||||||||    |||||
                                GGTCACGGC    TCGAC
                                    AGC__
GAM574  GPR81   3'  CTTACCAGCATTAGTC     50757     C       CA
                                GAC AGTGCTGG  TAAG
                                ||| ||||||||  ||||
                                CTG TTACGACC  ATTC
                                  A       __
GAM574  IFI16   5'  AGCAAGCCAGCACTAGTC    71221     C       ATAA
                                GAC AGTGCTGGC    GCT
                                ||| |||||||||    |||
                                CTG TCACGACCG    CGA
                                  A       AA__
GAM574  KRT4    3'  CAGCTGGGCCCAGCACTGGT   9635           _ ATA
                                ACCAGTGCTGG C   AGCTG
                                |||||||||||  |   |||||
                                TGGTCACGACC G   TCGAC
                                      C GG_
GAM574  MAP3K9  3'  TTCAGCTTCCCAAACACCAGT  60709    CA   C_   CAT
                                AC  GTG  TGG   AAGCTGAA
                                ||  |||  |||   ||||||||
                                TG  CAC  ACC   TTCGACTT
                                 AC   AA   C__
GAM574  MGAT5   5'  TCAGCTTACAGTTCCTG     10028     T_   GCA
                                CAG  GCTG   TAAGCTGA
                                |||  ||||   ||||||||
                                GTC  TGAC   ATTCGACT
                                  CT    ____
GAM574  MOCS1   3'  TTCAGCTTAACAGTTGCCCGGT 92037      A_   _   GCA
            C                    GACC  GTG CTG   TAAGCTGAA
                                ||||  ||| |||   |||||||||
                                CTGG  CGT GAC   ATTCGACTT
                                  CC   T   A__
GAM574  P23     3'  TCAGCTTATACCCGGGCT    21719     G   C_
                                AGT CTGG  ATAAGCTGA
                                ||| ||||  |||||||||
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                                TCG GGCC  TATTCGACT
                                  _   CA
GAM574  PFKFB4   3'  TCAGCCACATGCAACACTGTGT 15874    _    CTG   AA_
            C                    GAC CAGTG  GCAT  GCTGA
                                 ||| |||||  ||||  |||||
                                 CTG GTCAC  CGTA  CGACT
                                   T    AA_   CAC
GAM574  PTPRK    3'  TTCAGCCTGTGGCCCAGCACTG 11125          __   A
            GTC                    GACCAGTGCTGG  CATA GCTGAA
                                 ||||||||||||  |||| ||||||
                                 CTGGTCACGACC  GTGT CGACTT
                                       CG   C
GAM574  RNPEPL1  3'  CGGATGCCAGCACCTG     36676    _       AAG
                                 CAG TGCTGGCAT   CTG
                                 ||| |||||||||   |||
                                 GTC ACGACCGTA   GGC
                                   C       ___
GAM574  UBE2L3   3'  TCAGCCCTGGCACTGGC     12507   A     TG CATAA
                                 G CCAGTGC  G    GCTGA
                                 | |||||||  |    |||||
                                 C GGTCACG  C    CGACT
                                  _      GT C____
GAM574  APXL2    5'  CAGCCTCAGCACTCATC     75185   CC      CATAA
                                 GA  AGTGCTGG    GCTG
                                 ||  ||||||||    ||||
                                 CT  TCACGACT    CGAC
                                   AC       C____
GAM574  ARHGEF9  3'  TTCAGCTTACCAAGCA     30824     _ CA
                                 TGCT GG  TAAGCTGAA
                                 |||| ||  |||||||||
                                 ACGA CC  ATTCGACTT
                                   A  __
GAM574  CEGP1    3'  TTCAGCTTCCTCTAGCCCGG   40589    AGT    CAT
                                 CC   GCTGG   AAGCTGAA
                                 ||   |||||   ||||||||
                                 GG   CGATC   TTCGACTT
                                  CC_    TCC
GAM574  DKFZp547D155 3'  CAGCCCTGAGACCACTGGTC   70435        CTGG  TAA
                                 GACCAGTG    CA   GCTG
                                 ||||||||    ||   ||||
                                 CTGGTCAC    GT   CGAC
                                      CAGA  CC_
GAM574  DKFZP727G051 3'  TTCAGCCCATCAACCAGCATTG 69483           CATAA__
            GTC                    GACCAGTGCTGG      GCTGAA
                                 ||||||||||||      ||||||
                                 CTGGTTACGACC      CGACTT
                                       AACTACC
GAM574  DUSP14   5'  CACTGTCACCAGCACTGCTC   22834    C       CATA  C
                                 GA CAGTGCTGG    AG TG
                                 || |||||||||    || ||
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                                CT GTCACGACC    TC AC
                                 C        ACTG  _
GAM574  FLJ10206  5'  CAGCTTATGCCAGGAGTC    35898     CAGTG
                                GAC    CTGGCATAAGCTG
                                |||    ||||||||||||
                                CTG    GACCGTATTCGAC
                                  AG___
GAM574  FLJ20967  5'  GGCGCCCAGCACTGGTT     41962          CATAA
                                GACCAGTGCTGG    GCT
                                ||||||||||||    |||
                                TTGGTCACGACC    CGG
                                      CG___
GAM574  FLJ22569  3'  TTCAGCTTACTAAACTG     43679     GC   CA
                                CAGT  TGG  TAAGCTGAA
                                ||||  |||  |||||||||
                                GTCA  ATC  ATTCGACTT
                                  A_  __
GAM574  FOXN4     3'  TTCAGCTTGGACACACTGG    75574       C  GCA
                                CCAGTG TG   TAAGCTGAA
                                |||||| ||   |||||||||
                                GGTCAC AC   GTTCGACTT
                                   _ AG_
GAM574  GW112     3'  TTCAACTGAAGCCAGCACTGGT 21194           ATA  C
           T                     GACCAGTGCTGGC   AG TGAA
                                ||||||||||||   || ||||
                                TTGGTCACGACCG   TC ACTT
                                      AAG  A
GAM574  HOOK2     3'  CAGCTCACATGGCGCCCAGCAC 25256         _____  A__
           TGG                    CCAGTGCTGG    CAT   AGCTG
                                ||||||||||    |||   |||||
                                GGTCACGACC    GTA   TCGAC
                                     CGCG   CAC
GAM574  jdp2      3'  TTCAGCACAGCCAGCAT     55327        ATAA
                                GTGCTGGC    GCTGAA
                                ||||||||    ||||||
                                TACGACCG    CGACTT
                                    ACA_
GAM574  KIAA0767  3'  TCTGCTGCCAGCACAGG     60632    A       TAA  T
                                CC GTGCTGGCA   GC GA
                                || |||||||||   || ||
                                GG CACGACCGT   CG CT
                                 A        ___  T
GAM574  KIAA0923  3'  TCAGCTTGATGCATGGTC    25838      G   TGGCA
                                GACCA TGC    TAAGCTGA
                                ||||| |||    ||||||||
                                CTGGT ACG    GTTCGACT
                                   _  TA___
GAM574  KIAA0982  3'  TTCACTGTTTGCCAGCAC    25852         TA_  C
                                GTGCTGGCA   AG TGAA
                                |||||||||   || ||||
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                                CACGACCGT   TC ACTT
                                     TTG  _
GAM574  KIAA1000  3'  TTCAGCTTTGCAAAGTACTGG  65281        G_   T
                                CCAGTGCT  GCA AAGCTGAA
                                ||||||||  ||| ||||||||
                                GGTCATGA  CGT TTCGACTT
                                    AA  _
GAM574  MAP3K3    3'  TCAGCCTGGGCGCTGGTC    9999          GG  TAA
                                GACCAGTGCT  CA   GCTGA
                                ||||||||||  ||   |||||
                                CTGGTCGCGG  GT   CGACT
                                     __  C__
GAM574  MGC16037  5'  CTTGTCCAGCACTAGTC     51821     C       C
                                GAC AGTGCTGG ATAAG
                                ||| |||||||| |||||
                                CTG TCACGACC TGTTC
                                  A       _
GAM574  MIDORI    3'  TCAGCTTATCCTGCAACT    73792     _  T  C
                                AGT GC GG ATAAGCTGA
                                ||| || || |||||||||
                                TCA CG CC TATTCGACT
                                  A  T  _
GAM574  MtFMT     5'  CAGTGGCGAGCACTGG      57651         G  ATAA
                                CCAGTGCT GC    GCTG
                                |||||||| ||    ||||
                                GGTCACGA CG    TGAC
                                     G  G___
GAM574  PCDH16    5'  TCAGTTCCAACCACTGG     72826       C_   CATA
                                CCAGTG  TGG    AGCTGA
                                ||||||  |||    ||||||
                                GGTCAC  ACC    TTGACT
                                   CA  _____
GAM574  QKI       3'  CAGCTTATCAACTCGTC     65439     C   GCTGGC
                                GAC AGT      ATAAGCTG
                                ||| |||      ||||||||
                                CTG TCA      TATTCGAC
                                  C   AC_____
GAM574  TNRC6     3'  CAACTTTTAGCACTG       70506         CAT   C
                                CAGTGCTGG   AAG TG
                                |||||||||   ||| ||
                                GTCACGATT   TTC AC
                                     ___   A
GAM574  TOB2      3'  CAGCCCAGGCCAGCACTG    95618          ATAA
                                CAGTGCTGGC    GCTG
                                ||||||||||    ||||
                                GTCACGACCG    CGAC
                                      GACC
GAM574  TU12B1-TY 3'  TCAGCCCACAGCACTGTC    33406     C      GCATAA
                                GAC AGTGCTG     GCTGA
                                ||| |||||||     |||||
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                                CTG TCACGAC     CGACT
                                  _     ACC___
GAM574  TUSP     3'  TCAGCCTAAGAGCGCAGCACTG 39641       _ A__  A
                                CAGTGCTG GC   TA GCTGA
                                |||||||| ||   || |||||
                                GTCACGAC CG   AT CGACT
                                     G  AGA  C
GAM574  USP19    3'  TCAGCTTATGCATCTGGT    88959      TGCTG
                                ACCAG    GCATAAGCTGA
                                |||||    ||||||||||
                                TGGTC    CGTATTCGACT
                                   TA___
GAM574  ZD52F10  3'  CAGCCTGTGCCAGCCCTGG   52819     T       A
                                CCAG GCTGGCATA GCTG
                                |||| ||||||||| ||||
                                GGTC CGACCGTGT CGAC
                                   C       C
GAM574  LOC145268 3' TCAGCTTACAAGAGCCACTG  77062      _ GGCA
                                CAGTG CT    TAAGCTGA
                                ||||| ||    ||||||||
                                GTCAC GA    ATTCGACT
                                   C  GAAC
GAM574  LOC149296 5' CAGCTTATGGGCAGCA      79256      G_
                                TGCTG  CATAAGCTG
                                |||||  |||||||||
                                ACGAC  GTATTCGAC
                                   GG
GAM574  LOC161877 5' TCAGGGCAGGCCAGCGCTGG  82326          ATAAG
                                CCAGTGCTGGC    CTGA
                                ||||||||||     ||||
                                GGTCGCGACCG    GACT
                                      GACGG
GAM574  LOC163115 5' TCAGCCCCTGACAGCACTGG  82413        G  TAA
                                CCAGTGCTG CA   GCTGA
                                |||||||| ||   |||||
                                GGTCACGAC GT   CGACT
                                     A  CCC
GAM574  LOC196500 3' TCAGCTCACTCAGTGGTC    87744     AGT    CATA
                                GACC   GCTGG    AGCTGA
                                ||||   |||||    ||||||
                                CTGG   TGACT    TCGACT
                                  ___    CAC_
GAM574  LOC197287 3' TCAGCTCATGTGTTTTGCACTG 60865       T_     __
                                CAGTGC  GGCATA  AGCTGA
                                ||||||  ||||||  ||||||
                                GTCACG  TTGTGT  TCGACT
                                   TT     AC
GAM574  LOC200470 5' TCAGCCTGCGGCGCTGG     90069         G  TAA
                                CCAGTGCTG CA   GCTGA
                                |||||||| ||   |||||
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                                GGTCGCGGC GT   CGACT
                                     _ C__
GAM574  LOC221584 3'  CAGCTTATGTGGCAC       93828       G
                                GTGCTG CATAAGCTG
                                |||||| |||||||||
                                CACGGT GTATTCGAC
                                   _
GAM574  LOC51716  3'  CAGCTCATGGCCCTAGCA    32787       ___   A
                                TGCTGG   CAT AGCTG
                                ||||||   ||| |||||
                                ACGATC   GTA TCGAC
                                   CCG   C
GAM574  LOC92196  5'  CAGAGCACCAGCACTGGC    68456   A       CATAAG
                                G CCAGTGCTGG     CTG
                                | ||||||||||     |||
                                C GGTCACGACC     GAC
                                _        ACGA__
GAM575  PRO0659   3'  CATGTATGTAAATGTTGCAATA 26218         TTCACTAAT
                                TATTGCAAC        TGCATG
                                |||||||||        ||||||
                                ATAACGTTG        ATGTAC
                                     TAAATGT__
GAM576  TNFAIP1   3'  CATCAGCTGAGGACAGCAAACT 40917     AG     G
           CC                     GGA  TTGCTG CTTCAGCTGATG
                                |||  |||||| ||||||||||||
                                CCT  AACGAC GGAGTCGACTAC
                                  CA     A
GAM576  C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 21681     AA      _ ____
           CCC                    GG  GTTGCTGG CT   TCAGCTG
                                ||  |||||||| ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM576  C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 94622     AA      _ ____
           CCC                    GG  GTTGCTGG CT   TCAGCTG
                                ||  |||||||| ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM576  C20orf59  3'  CATCCCTAGCCAGCAGCTCC   41992     A       TC  CT
                                GGA GTTGCTGGCT  AG  GATG
                                ||| ||||||||||  ||  ||||
                                CCT CGACGACCGA  TC  CTAC
                                  _        __ C_
GAM576  FLJ20079  3'  CATTCTGGTAAACCAGCAGCCT 34490     A      CT__   CT
           CC                     GGA GTTGCTGG    TCAG  GATG
                                ||| ||||||||    ||||  ||||
                                CCT CGACGACC    GGTC  TTAC
                                  C       AAAT   __
GAM576  SSAT2     3'  CATCAGCTGAAGCACTCTTC   56041      TTGCTG
                                GAAG     GCTTCAGCTGATG
                                ||||     ||||||||||||
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                                CTTC     CGAAGTCGACTAC
                                  TCA___
GAM576  SYNJ2    3'  ATCAGCTTAAGCAATTCC    61763     GTTGCTG   C
                                GGAA      GCTT AGCTGAT
                                ||||      |||| |||||||
                                CCTT      CGAA TCGACTA
                                  AA_____   T
GAM576  LOC162333 5'  CTGAAGCCAGCAATTCC     87131      G
                                GGAA TTGCTGGCTTCAG
                                |||| ||||||||||||
                                CCTT AACGACCGAAGTC
                                  _
GAM576  LOC222060 5'  CACCTCCCACCAGCAACCCCC  94104    AA       CTTC  C
                                GG  GTTGCTGG    AG TG
                                ||  ||||||||    || ||
                                CC  CAACGACC    TC AC
                                 CC       ACCC  C
GAM576  LOC255650 3'  CATCAGCCCCAGGCAACTTCC  96711         _  CTTCA
                                GGAAGTTGC TGG     GCTGATG
                                ||||||||| |||     |||||||
                                CCTTCAACG ACC     CGACTAC
                                     G   C____
GAM577  CCNT2    3'  GGTGGTTGTGCTACTGTAT    54266         A
                                ATACAGTAG ACAACCATT
                                ||||||||| |||||||||
                                TATGTCATC TGTTGGTGG
                                     G
GAM577  D8S2298E  3'  ATGTTTATTCTGCTGTAT     19035          C  C
                                ATACAGTAGAA AA CAT
                                |||||||||||| || |||
                                TATGTCGTCTT TT GTA
                                      A  T
GAM577  ERBB2IP   3'  TGGTTATTGTACTGTAT     37988         G  C
                                ATACAGTA AA AACCA
                                |||||||| || |||||
                                TATGTCAT TT TTGGT
                                     G  A
GAM577  ICMT     3'  TCAATGAAATCTGTACTGTAT  24819         GAACAAC
                                ATACAGTA      CATTGA
                                ||||||||      ||||||
                                TATGTCAT      GTAACT
                                     GTCTAAA
GAM577  PLGL     3'  ATGTAATCGTTGTTATACTGTA 10636         G     C    A
              T                  ATACAGTA AACAAC ATTG CAT
                                ||||||||| |||||| |||| |||
                                TATGTCAT TTGTTG TAAT GTA
                                     A     C   _
GAM577  PTPRC    3'  ATGTCCTCCTTGTTCTACT    11100          CCATT
                                AGTAGAACAA     GACAT
                                ||||||||||     |||||
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                                TCATCTTGTT    CTGTA
                                      CCTC_
GAM577  PTPRC    3'  ATGTCCTCCTTGTTCTACT   55165        CCATT
                                AGTAGAACAA    GACAT
                                ||||||||||    |||||
                                TCATCTTGTT    CTGTA
                                      CCTC_
GAM577  TGFBR1   3'  GTCAGTTGTTCTAC       16051         CAT
                                GTAGAACAAC   TGAC
                                ||||||||||   ||||
                                CATCTTGTTG   ACTG
                                      ___
GAM577  TLL1     3'  ATGTCAATATAGATTACTGTAT 24948        AACAACC
                                ATACAGTAG     ATTGACAT
                                |||||||||     ||||||||
                                TATGTCATT     TAACTGTA
                                      AGATA__
GAM577  TMOD2    3'  TCAGAAGTGTTCTACTG     27252         ACCA
                                CAGTAGAACA    TTGA
                                ||||||||||    ||||
                                GTCATCTTGT    GACT
                                      GAA_
GAM577  ZK1      3'  ATGCAAATAGTTGTTCTATTGT 19462           C   GA
           AT                     ATACAGTAGAACAAC ATT  CAT
                                ||||||||||||||| |||  |||
                                TATGTTATCTTGTTG TAA  GTA
                                        A   AC
GAM577  BTBD3    3'  ATGTTGAATGTTATTGTACTGT 30306       G  C   CA TG
           AT                     ATACAGTA AA AAC  T  ACAT
                                |||||||| || |||  |  ||||
                                TATGTCAT TT TTG  A  TGTA
                                     G  A   TA GT
GAM577  FLJ14054 3'  TGTTTATTGTTCTAATGTA   44663     G      CCATT
                                TACA TAGAACAA    GACA
                                |||| ||||||||    ||||
                                ATGT ATCTTGTT    TTGT
                                  A       AT___
GAM577  HSU84971 3'  ATGTAGTGGTTTTCCTACT   25252      AAC       A
                                AGTAG   AACCATTG CAT
                                |||||   |||||||| |||
                                TCATC   TTGGTGAT GTA
                                   CTT       _
GAM577  KIAA0716 3'  GTGGTATCTACTGTAT      28165         ACA
                                ATACAGTAGA   ACCAT
                                ||||||||||   |||||
                                TATGTCATCT   TGGTG
                                      A__
GAM577  KIAA1344 3'  TGGTGCTCTACTGTAT      72451         ACA
                                ATACAGTAGA   ACCA
                                ||||||||||   ||||
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                                TATGTCATCT   TGGT
                                     CG_
GAM577  NIP30    3'  GTGTTGTTTGGTTCTACTG   46325        AACCAT
                                CAGTAGAAC     TGACAT
                                |||||||||     ||||||
                                GTCATCTTG     GTTGTG
                                     GTTT__
GAM577  PRKCBP1  5'  ATGGTCCGTTTTACTATAT   24833    C       A_
                                ATA AGTAGAAC  ACCAT
                                ||| ||||||||  |||||
                                TAT TCATTTTG  TGGTA
                                  A       CC
GAM577  PSMD10   3'  TGTTGAGATTGTTCTACTGT   10995          CCA TG
                                ACAGTAGAACAA   T  ACA
                                ||||||||||||   |  |||
                                TGTCATCTTGTT   A  TGT
                                       AG_ GT
GAM577  TUCAN    3'  ATGTCTTTTCTATTCTACTGT  30270        CAACCATT
                                ACAGTAGAA       GACAT
                                |||||||||       |||||
                                TGTCATCTT       CTGTA
                                     ATCTTTT_
GAM577  LOC115827 3'  ATGTCAATGGCTCGTAC     56621     _  ACAA
                                GTA GA    CCATTGACAT
                                ||| ||    ||||||||||
                                CAT CT    GGTAACTGTA
                                  G  C___
GAM577  LOC146227 3'  TGTCTGTTGTACTGTAT     77714        G    ACCATT
                                ATACAGTA AACA     GACA
                                |||||||| ||||     ||||
                                TATGTCAT TTGT     CTGT
                                     G   _______
GAM577  LOC147219 3'  TGTCATTTTACTGTAT      83992          CAACCAT
                                ATACAGTAGAA      TGACA
                                ||||||||||      |||||
                                TATGTCATTTT      ACTGT
                                                 _______
GAM577  LOC150054 3'  TCTGTGATCATTCTACTGTTC  84838   T       CAAC   T
                                A ACAGTAGAA    CAT GA
                                | |||||||||    ||| ||
                                C TGTCATCTT    GTG CT
                                 T       ACTA   T
GAM577  LOC152667 3'  GTGTTGTTTGGTTCTACTG   80638        AACCAT
                                CAGTAGAAC     TGACAT
                                |||||||||     ||||||
                                GTCATCTTG     GTTGTG
                                     GTTT__
GAM577  LOC196424 3'  TGGTTTATTTCTACTGTA    87704         C__
                                TACAGTAGAA   AACCA
                                ||||||||||   |||||
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                                ATGTCATCTT   TTGGT
                                     TAT
GAM577  LOC199907 3'  ATGTCACAAAGCTACTTACTGT 88462        AACAACCAT
            A                    TACAGTAG       TGACAT
                                 ||||||||       ||||||
                                 ATGTCATT       ACTGTA
                                     CATCGAAAC
GAM577  LOC203369 3'  ATGTCAATAGTTATAACCTAC  89336     AAC__   C
                                 GTAG    AAC ATTGACAT
                                 ||||    ||| ||||||||
                                 CATC    TTG TAACTGTA
                                   CAATA   A
GAM577  LOC90576  3'  ATGCAAATAGTTGTTCTATTGT 63344            C   GA
            AT                    ATACAGTAGAACAAC ATT  CAT
                                  |||||||||||||| |||  |||
                                  TATGTTATCTTGTTG TAA  GTA
                                           A   AC
GAM577  LOC93496  3'  ATGTCACTTAAATCGTACTGTA 72430        _  ACAACCAT
            T                     ATACAGTA GA       TGACAT
                                  |||||||| ||       ||||||
                                  TATGTCAT CT       ACTGTA
                                      G  AAATTC__
GAM578  AQP3    3'  TTCACGATCCACCCTTTC    59593     T_   _
                                 GAAA  GTGG TCGTGAA
                                 ||||  |||| |||||||
                                 CTTT  CACC AGCACTT
                                   CC    T
GAM578  ARSB    3'  TCACGACTCTTGTC       3502        AATGTG
                                 GACAAGA     GTCGTGA
                                 |||||||     |||||||
                                 CTGTTCT     CAGCACT
                                      _______
GAM578  B4GALT5  3'  TTTTCACAAAAATAGTCCTTTG 16519       AAA_  GGTC
            TCA                    TGACAAG    TGT    GTGAAAA
                                   |||||||    |||    |||||||
                                   ACTGTTT    ATA    CACTTTT
                                       CCTG   AAAA
GAM578  CHRNA3   3'  TCGTTACCCATTTCTT     5610         T   CG
                                 AAGAAATG GGT  TGA
                                 |||||||| |||  |||
                                 TTCTTTAC CCA  GCT
                                      _   TT
GAM578  DRD1    3'  TTACAACCACATTTCTGGCCA  5840     ACA         C
                                 TG   AGAAATGTGGT GTGA
                                 ||   |||||||||||| ||||
                                 AC   TCTTTACACCA CATT
                                  CGG         A
GAM578  FUT1    3'  TCTGATCACATCCCCTGTC   3798      AGAA        T
                                 GACA    ATGTGGTCG GA
                                 ||||    ||||||||| ||
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                                CTGT    TACACTAGT CT
                                  CCCC       _
GAM578  IRF1     3'  GCCACATTTCTGATCA     64345     CA
                                TGA  AGAAATGTGGT
                                |||  ||||||||||
                                ACT  TCTTTACACCG
                                  AG
GAM578  MAP3K8   5'  TCACGACCACCTCATG      17791    A  AAT
                                CA GA   GTGGTCGTGA
                                || ||   ||||||||||
                                GT CT   CACCAGCACT
                                 A  C__
GAM578  NGFR     3'  TTCTGACCACACTTCCTGTC   10231      A   A       T
                                GACA GAA TGTGGTCG GAA
                                |||| ||| |||||||| |||
                                CTGT CTT ACACCAGT CTT
                                  C   C       _
GAM578  OLR1     3'  TTCACAACAGTTCTTGTTA    10341         ATGTG  C
                                TGACAAGAA    GT GTGAA
                                |||||||||    || |||||
                                ATTGTTCTT    CA CACTT
                                     GA___  A
GAM578  POU4F1   3'  CACTGAAAACATTTTTGTCA   20660         A   GG  _
                                TGACAAGAA TGT  TC GTG
                                ||||||||| |||  || |||
                                ACTGTTTTT ACA  AG CAC
                                     _  AA  T
GAM578  SMP1     3'  TTTCACATGAATAATTTTTGTC 26705         A   GGTC
           A                     TGACAAGAA TGT    GTGAAA
                                |||||||||| |||    ||||||
                                ACTGTTTTT ATA    CACTTT
                                     A   AGTA
GAM578  ZNF264   3'  TTCTATTAACATTTCTTTTCA  12769     C        GGTCGT
                                TGA AAGAAATGT     GAA
                                ||| |||||||||     |||
                                ACT TTCTTTACA     CTT
                                  T       ATTAT_
GAM578  C20orf175 3'  CGAGCTCCACGTTTCCTGCCA  55063    A  A       ___
                                TG CA GAAATGTGG   TCG
                                || || |||||||||   |||
                                AC GT CTTTGCACC   AGC
                                 C  C        TCG
GAM578  CAPNS2   3'  TTTCACAACCCTACATATTTCT 50323     CA       ____  C
           GATCA                   TGA  AGAAATGT    GGT GTGAAA
                                |||  ||||||||   ||| ||||||
                                ACT  TCTTTATA    CCA CACTTT
                                  AG       CATC   A
GAM578  CLDN6    3'  TTTACACTCACATTTTTATCA  41041     CA       _  C
                                TGA  AGAAATGTG GT GTGAA
                                |||  ||||||||| || |||||
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                                ACT  TTTTTACAC CA CATTT
                                  A_       T  _
GAM578  DKFZP564L0864 3'  GCACCAATTTCTTGCCA     72555    A      G   C
                                TG CAAGAAAT TGGT GT
                                || |||||||| |||| ||
                                AC GTTCTTTA ACCA CG
                                 C      _   _
GAM578  DKFZP566B183 3'  TTTCCATAAACATTTCTTTTCA 31330     C       GGTCGT
                                TGA AAGAAATGT     GAAA
                                ||| |||||||||     ||||
                                ACT TTCTTTACA     CTTT
                                  T       AATAC_
GAM578  GTF2E1   3'  TACAGACCTCTTGTCA      18616        AATGT   _
                                TGACAAGA    GGTC GTG
                                ||||||||    |||| |||
                                ACTGTTCT    CCAG CAT
                                    _____   A
GAM578  KIAA0089  3'  TTTTAATTCACATTTCTT    69967          TCG
                                AAGAAATGTGG   TGAAA
                                ||||||||||   |||||
                                TTCTTTACACT   ATTTT
                                      TA_
GAM578  KIAA0373  5'  TTTTCAAAGTAACATTTCTT   28015         GGTCG
                                AAGAAATGT    TGAAAA
                                |||||||||    ||||||
                                TTCTTTACA    ACTTTT
                                     ATGAA
GAM578  KIAA1813  3'  TTTTCACACTGTAAATTTCTTG 70314         __ TG  C
           T                     ACAAGAAAT  G  GT GTGAAAA
                                |||||||||  |  || |||||||
                                TGTTCTTTA  T  CA CACTTTT
                                     AA GT  _
GAM578  KIAA1951  3'  TTCCAGGCTTCTCTTGTCA   73766        AATGT   GT
                                TGACAAGA    GGTC  GAA
                                ||||||||    ||||  |||
                                ACTGTTCT    TCGG  CTT
                                    CT___    AC
GAM578  MGC4170   3'  TTCACCATTTCTTGTC      44227          TGGTC
                                GACAAGAAATG    GTGAA
                                ||||||||||    |||||
                                CTGTTCTTTAC    CACTT
                                      _____
GAM578  NRN1     3'  CACTGCACATTTCTCCTCA   33432     CA       GTC
                                TGA  AGAAATGTG   GTG
                                |||  |||||||||  |||
                                ACT  TCTTTACAC   CAC
                                  CC        GT_
GAM578  PLA2G12   3'  TTTTCACAACCACATTT     48028         C
                                AAATGTGGT GTGAAAA
                                ||||||||| |||||||
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                                TTTACACCA CACTTTT
                                     A
GAM578  PPY2     3'  CACTCCACATTCCTGGCCA   40819    ACA  A      TC
                                TG   AG AATGTGG  GTG
                                ||   || |||||||  |||
                                AC   TC TTACACC  CAC
                                 CGG  C      T_
GAM578  ZNF31    3'  TTTGTAGACCACATTTCCTGTT 64992       A         _ TG
             A                   TGACA GAAATGTGGTC G  AA
                                 ||||| |||||||||||  |  ||
                                 ATTGT CTTTACACCAG T  TT
                                    C          A GT
GAM578  LOC115219 3' CACGACAACGGGTCCTCA    73295     CAA  AA   G
                                 TGA   GA  TGT GTCGTG
                                 |||   ||  ||| ||||||
                                 ACT   CT  GCA CAGCAC
                                   C__  GG   A
GAM578  LOC120376 5' TTCAGAGCATTTCTTTCA    75986     C       GG  G
                                 TGA AAGAAATGT  TC TGAA
                                 ||| |||||||||  || ||||
                                 ACT TTCTTTACG  AG ACTT
                                   _        __ _
GAM578  LOC133418 3' TTTCATATACATTTTTTGCCA  75094    A         GTC
                                 TG CAAGAAATGTG   GTGAAA
                                 || ||||||||||   ||||||
                                 AC GTTTTTTACAT   TACTTT
                                  C          A__
GAM578  LOC151199 3' TTAAAACCACAGCTCTTGCCA  80174    A    AA     CG
                                 TG CAAGA  TGTGGT  TGA
                                 || |||||  ||||||  |||
                                 AC GTTCT  ACACCA  ATT
                                  C    CG     AA
GAM578  LOC152317 5' TCACACTGACTTTTGTCA    85649        AATG   C
                                 TGACAAGA    TGGT GTGA
                                 ||||||||    |||| ||||
                                 ACTGTTTT    GTCA CACT
                                      CA__    _
GAM578  LOC152674 3' TTCAACCCACCCTCTTGTCA   85841        AAT    TCG
                                 TGACAAGA   GTGG   TGAA
                                 ||||||||   ||||   ||||
                                 ACTGTTCT   CACC   ACTT
                                      CC_    CA_
GAM578  LOC152845 5' CATGACCACATTTTTCA     60330     CAA
                                 TGA   GAAATGTGGTCGTG
                                 |||   ||||||||||||||
                                 ACT   TTTTACACCAGTAC
                                   ____
GAM578  LOC154743 3' TTTAGTCCACATTGTCTTGTCA 81118         _      TCG
                                 TGACAAGA AATGTGG   TGAA
                                 |||||||| |||||||   ||||
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                                ACTGTTCT TTACACC   ATTT
                                     G      TG_
GAM578  LOC165476 5'  TTCACGGCACCTTCT      87201      AT   G
                                AGAA  GTG TCGTGAA
                                ||||  ||| |||||||
                                TCTT  CAC GGCACTT
                                  C_  _
GAM578  LOC254266 5'  TTTTCGGTCACACATCTTATCA 97356     C    AA    GT  T
                                TGA AAGA  TGTG  CG GAA
                                ||| ||||  ||||  || |||
                                ACT TTCT  ACAC  GC TTT
                                  A   AC    TG  T
GAM578  LOC255919 3'  TTTCATTCTTACATTTCTAATC 95043     CA        TC
            A                    TGA  AGAAATGTGG  GTGAAA
                                |||  ||||||||||  ||||||
                                ACT  TCTTTACATT  TACTTT
                                  AA         CT
GAM578  LOC51754  5'  CACGGCCACATCTCTGTCA    71027      A  A
                                TGACA GA ATGTGGTCGTG
                                ||||| || ||||||||||
                                ACTGT CT TACACCGGCAC
                                   _  C
GAM578  LOC55862  3'  ACCTCATTTCTTGCCA      37485    A       T
                                TG CAAGAAATG GGT
                                || |||||||| |||
                                AC GTTCTTTAC CCA
                                 C        T
GAM578  LOC55954  3'  CACGTGGTCACTTTTCTCATCA 38877     CA    T   GT __
                                TGA  AGAAA GTG  C  GTG
                                |||  ||||| |||  |  |||
                                ACT  TCTTT CAC  G  CAC
                                  AC    T   TG TG
GAM579  ABP1     5'  AGGGCAAAGGCTGG        63109          TACTCT
                                CCAGTCTTTG     CCCT
                                ||||||||||     ||||
                                GGTCGGAAAC     GGGA
                                       _______
GAM579  AP2B1    3'  AGGGTCCATGACTAAGACTGG  7057         T  ACTCT_
                                CCAGTCTT GT     CCCT
                                |||||||| ||     ||||
                                GGTCAGAA CA     GGGA
                                     T  GTACCT
GAM579  ED1      3'  GGAAAGCACAAGACTGG     7373         T  A  C
                                CCAGTCTT GT CT TCC
                                |||||||| || || |||
                                GGTCAGAA CA GA AGG
                                     _  C  A
GAM579  EEF1A1   3'  TTTAGTAGTAAAAGACTGG   7390          G   CTCC
                                CCAGTCTTT TACT   CTAAA
                                ||||||||| ||||   |||||
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                                GGTCAGAAA ATGA   GATTT
                                      _   T___
GAM579  EPHB4   5'  AGGGAGAGTCAGACCTGG   15460     TC   T
                                CCAG  TTTG ACTCTCCCT
                                ||||  |||| |||||||||
                                GGTC  AGAC TGAGAGGGA
                                  C_   _
GAM579  GARP    3'  TTAGGAAGAGAATGAAACT   18604     C  TG A   C
                                AGT TT  T CTCT CCTAA
                                ||| ||  | |||| |||||
                                TCA AA  A GAGA GGATT
                                  _ GT A   A
GAM579  ID3     3'  GTTTAGGGAAACTGAGGC    79048      T  ACTC
                                GTCTT GT   TCCCTAAAC
                                ||||| ||   |||||||||
                                CGGAG CA   AGGGATTTG
                                   T  A___
GAM579  ITGA11  3'  AGGGAGGAAGACTG       24203       GTACT
                                CAGTCTTT    CTCCCT
                                ||||||||    ||||||
                                GTCAGAAG    GAGGGA
                                      _____
GAM579  ITGB1   3'  AGGGAAGCCAAAAGATTGG   53368        GTA  C
                                CCAGTCTTT   CT TCCCT
                                |||||||||   || |||||
                                GGTTAGAAA   GA AGGGA
                                     ACC  _
GAM579  KCNA7   3'  AGGGAGAGGGAGAC       49047       GTA
                                GTCTTT   CTCTCCCT
                                ||||||   ||||||||
                                CAGAGG   GAGAGGGA
                                     ___
GAM579  LTA     3'  GGAGAAACAGAGACAGG     5177     A      AC
                                CC GTCTTTGT  TCTCC
                                || ||||||||  |||||
                                GG CAGAGACA  AGAGG
                                 A       A_
GAM579  MAFF    3'  TTTAGGGAAAGCCGGAGA    24656       TA  C
                                TCTTTG  CT TCCCTAAA
                                ||||||  || ||||||||
                                AGAGGC  GA AGGGATTT
                                   C_  A
GAM579  MYCL1   3'  GAGAGGACAATACTGG      18165      CT   A
                                CCAGT  TTGT CTCTC
                                |||||  |||| |||||
                                GGTCA  AACA GAGAG
                                   T_   G
GAM579  NEU1    3'  AGGGAACTGGGGAAGGCTG   4740        GTA  ___
                                CAGTCTTT   CTC   TCCCT
                                ||||||||   |||   |||||
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                                GTCGGAAG  GGG  AGGGA
                                    ___  TCA
GAM579  NQO1    3'  AGAGAAGGTAAAAGACTG    6151        G  TC  C
                                CAGTCTTT TAC  TC CT
                                |||||||| |||  || ||
                                GTCAGAAA ATG  AG GA
                                    _  GA  A
GAM579  PEA15   3'  TAGGGAGGTTGAAGAATG    13655    G    T  T
                                CA TCTTTG AC CTCCCTA
                                || |||||| || |||||||
                                GT AGAAGT TG GAGGGAT
                                 A    _ _
GAM579  PPP1R11  3'  TTTAGGATTTCTGACAAAGCTG 41709     T    ACTCTC_
          G                      CCAG CTTTGT      CCTAAA
                                |||| ||||||      ||||||
                                GGTC GAAACA      GGATTT
                                  _     GTCTTTA
GAM579  PRKG2   3'  AGGGAGAGGCAAGATTG    20752       T  A
                                CAGTCTT GT CTCTCCCT
                                ||||||| || ||||||||
                                GTTAGAA CG GAGAGGGA
                                    _ _
GAM579  PTCRA   3'  TTTAGGGAGCAGATGACTG   56317     _   TACT
                                CAGTC TTTG   CTCCCTAAA
                                ||||| ||||   |||||||||
                                GTCAG AGAC   GAGGGATTT
                                  T   ____
GAM579  RNMT    3'  TTCAGGGAGAGGAGCTGG    13726     T  TGTA      A
                                CCAG CTT   CTCTCCCT AA
                                |||| |||   |||||||| ||
                                GGTC GAG   GAGAGGGA TT
                                  _  ____       C
GAM579  RNPEPL1  3'  AGGGAGAGTGTGGGGACAGG  36674    A    TG
                                CC GTCTT  TACTCTCCCT
                                || |||||  ||||||||||
                                GG CAGGG  GTGAGAGGGA
                                 A    GT
GAM579  SLC5A5   5'  AGGGAGAGGGACAGAC     4843      TT  A_
                                GTCT  GT  CTCTCCCT
                                ||||  ||  ||||||||
                                CAGA  CA  GAGAGGGA
                                  __  GG
GAM579  SOST    3'  AGAGCACAAGACTGG      47466        T  A
                                CCAGTCTT GT CTCT
                                |||||||| || ||||
                                GGTCAGAA CA GAGA
                                    _ C
GAM579  SURF4   3'  TTTAGGGACACCCAAAGAATG  52548    G    TACTC
                                CA TCTTTG    TCCCTAAA
                                || ||||||    ||||||||
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                                GT AGAAAC    AGGGATTT
                                 A     CCAC_
GAM579  C22orf4   3'  TAGGGCTGACAAAGACAGG   60644    A      ACTCT
                                CC GTCTTTGT    CCCTA
                                || ||||||||    |||||
                                GG CAGAAACA    GGGAT
                                 A       GTC__
GAM579  C9orf5    3'  GGGAGATACAAAGACTG     49281          C
                                CAGTCTTTGTA TCTCCC
                                |||||||||||| ||||||
                                GTCAGAAACAT AGAGGG
                                                _
GAM579  DKFZP564O0423 3'  TTAGGGAGAGAGGATTGG    91706        TGTA
                                CCAGTCTT    CTCTCCCTAA
                                ||||||||    ||||||||||
                                GGTTAGGA    GAGAGGGATT
                                             _____
GAM579  FLJ20718  3'  AGAGTGGAAGAGTGG       35606     G    G
                                CCA TCTTT TACTCT
                                ||| ||||| ||||||
                                GGT AGAAG GTGAGA
                                  G    _
GAM579  FLJ22028  3'  AGGGAAGCCAAAAGATTGG    45851         GTA  C
                                CCAGTCTTT   CT TCCCT
                                |||||||||   || |||||
                                GGTTAGAAA   GA AGGGA
                                      ACC  _
GAM579  FLJ22028  3'  AGGGAAGCCAAAAGATTGG    45852         GTA  C
                                CCAGTCTTT   CT TCCCT
                                |||||||||   || |||||
                                GGTTAGAAA   GA AGGGA
                                      ACC  _
GAM579  FLJ30681  3'  TTTAGGGAAGAAGATT       91792        GTACTC
                                AGTCTTT     TCCCTAAA
                                |||||||     ||||||||
                                TTAGAAG     AGGGATTT
                                    A_____
GAM579  FLJ32356  3'  AGGGAGAACCTCGGGGCTGG   58357         TGTAC
                                CCAGTCTT    TCTCCCT
                                ||||||||    |||||||
                                GGTCGGGG    AGAGGGA
                                     CTCCA
GAM579  KIAA0261  3'  TTTAGGGAAAGGGACAGA    68185       A_  C
                                TTTGT  CT TCCCTAAA
                                |||||  || ||||||||
                                AGACA  GA AGGGATTT
                                   GG  A
GAM579  KIAA0318  5'  AGGGAGAGTATCTCCTG     68947     TCTTT
                                CAG    GTACTCTCCCT
                                |||    ||||||||||
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                                GTC    TATGAGAGGGA
                                  CTC__
GAM579  KIAA0630  3'  TTAGGGAGTATGTAAA     89399       CT
                                TTTGTA  CTCCCTAA
                                ||||||  ||||||||
                                AAATGT  GAGGGATT
                                   AT
GAM579  KIAA0753  3'  AGGGAGAGCACAGTCTGG    28996     T  TT  A
                                CCAG CT  GT CTCTCCCT
                                ||||  ||  ||  ||||||||
                                GGTC GA  CA GAGAGGGA
                                  T  __  C
GAM579  KIAA0798  5'  AGAGGAGACAAAGAC      27715       TAC    _
                                GTCTTTG   TCTCC CT
                                |||||||   |||||  ||
                                CAGAAAC   AGAGG GA
                                   ___    A
GAM579  KIAA1754  3'  GTTCAGAGAAAGTTGCAGAGAT 63240         _  C  C  A
                                GTCTTTGTA CT TC CT AAC
                                |||||||||  ||  ||  ||  |||
                                TAGAGACGT GA AG GA TTG
                                     T  A  A  C
GAM579  MGC10540  3'  AGTGTCCCCCAAAGACTGG   50379         _____
                                CCAGTCTTTG    TACT
                                ||||||||||    ||||
                                GGTCAGAAAC    GTGA
                                     CCCCT
GAM579  MUC13    3'  AGAGTGTTTAGAAAGACTG   52327        G ____
                                CAGTCTTT T    ACTCT
                                ||||||||  |   |||||
                                GTCAGAAA A    TGAGA
                                     G TTTG
GAM579  PLAGL2   3'  TTTAAAGAGAAAAGTACAAGAC 70461      T   ___   CC
                                GTCTT GTAC   TCTC  TAAA
                                |||||  ||||   ||||  ||||
                                CAGAA CATG   AGAG  ATTT
                                   _    AAA    AA
GAM579  RHOBTB1  3'  GAAAGCACAAAGCTGG     91440     T     A  C
                                CCAG CTTTGT CT TC
                                ||||  ||||||  ||  ||
                                GGTC GAAACA GA AG
                                   _     C  A
GAM579  SCAND2   3'  AGGGTGGCTCACAAAGAC    53314        AC_  T
                                GTCTTTGT   TC CCCT
                                ||||||||   ||  ||||
                                CAGAAACA   GG GGGA
                                     CTC  T
GAM579  SEC15B   3'  AGGTAATTAGTACAAAGAC   66684          CTC__
                                GTCTTTGTACT    CCT
                                ||||||||||    |||
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                                CAGAAACATGA    GGA
                                      TTAAT
GAM579  TCL6    3'  TTAGGGAGGGTGAAAACTCA  40152   C   C   G
                                C AGT TTT TACTCTCCCTAA
                                | ||| ||| ||||||||||||
                                A TCA AAA GTGGGAGGGATT
                                 C  _  _
GAM579  TCL6    3'  TTAGGGAGGGTGAAAACTCA  40119   C   C   G
                                C AGT TTT TACTCTCCCTAA
                                | ||| ||| ||||||||||||
                                A TCA AAA GTGGGAGGGATT
                                 C  _  _
GAM579  LOC112840 3'  TAGGGAGAGACCTGG      54729     TCTTT  A
                                CCAG    GT CTCTCCCTA
                                ||||    || |||||||||
                                GGTC    CA GAGAGGGAT
                                  _____  _
GAM579  LOC121838 5'  TTTAGGAAACAAAGATGG    76005    G     ACTCTC
                                CCA TCTTTGT     CCTAAA
                                ||| |||||||     ||||||
                                GGT AGAAACA     GGATTT
                                  _     AA____
GAM579  LOC124817 5'  AGGGTGTGGCAGAAGACTGG  74342       _   ACTCT
                                CCAGTCT TTGT    CCCT
                                ||||||| ||||    ||||
                                GGTCAGA GACG    GGGA
                                    A   GTGT_
GAM579  LOC126208 3'  AGGGAGAAGCGGACGG     74462    A   TT  AC
                                CC GTCT  GT  TCTCCCT
                                || ||||  ||  |||||||
                                GG CAGG  CG  AGAGGGA
                                 _   __  A_
GAM579  LOC134266 3'  TAGGGAAAAGGGAAGACTGG  75168        GTACTC
                                CCAGTCTTT     TCCCTA
                                |||||||||     ||||||
                                GGTCAGAAG     AGGGAT
                                      GGAAA_
GAM579  LOC143465 5'  GTTTAGAAAACTAAAAAAGACT 82970       GTACTCTCC
            G                    CAGTCTTT       CTAAAC
                                 ||||||||       ||||||
                                 GTCAGAAA       GATTTG
                                      AAATCAAAA
GAM579  LOC144681 3'  TTTAAAGAGAAGTTGCAAAGAT 83177        _ _  CC
                                GTCTTTGTA CT CTC  TAAA
                                ||||||||| || |||  ||||
                                TAGAAACGT GA GAG  ATTT
                                      T  A   AA
GAM579  LOC147650 5'  AGAGAGAGAGGAAGATGG    78385    G    GTA    C
                                CCA TCTTT   CTCTC CT
                                ||| |||||   ||||| ||
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                                GGT AGAAG   GAGAG GA
                                  _    GA_    A
GAM579   LOC148371 3'  TTTAGTAGTAAAAGACTGG   78811        G   CTCC
                                CCAGTCTTT TACT   CTAAA
                                ||||||||| ||||   |||||
                                GGTCAGAAA ATGA   GATTT
                                     _   T___
GAM579   LOC152503 3'  AGAGGACAGAAGACTGG    85767       _   A
                                CCAGTCT TTGT CTCT
                                ||||||| |||| ||||
                                GGTCAGA GACA GAGA
                                    A   G
GAM579   LOC157503 3'  TAGGGAGAGTCGATGA     86469    T  T
                                TC TTG ACTCTCCCTA
                                || ||| ||||||||||
                                AG AGC TGAGAGGGAT
                                 T  _
GAM579   LOC161589 3'  TTTAGTAGTAAAAGACTGG   82284        G   CTCC
                                CCAGTCTTT TACT   CTAAA
                                ||||||||| ||||   |||||
                                GGTCAGAAA ATGA   GATTT
                                     _   T___
GAM579   LOC161978 5'  GAGGACACAAAGACTG     82327         AC
                                CAGTCTTTGT  TCTC
                                ||||||||||  ||||
                                GTCAGAAACA  GGAG
                                      CA
GAM579   LOC196510 3'  AGGAAGAGTAGGACTGG    87745       TTG    C
                                CCAGTCT   TACTCT CCT
                                |||||||   |||||| |||
                                GGTCAGG   ATGAGA GGA
                                   ___     A
GAM579   LOC200220 3'  AGGAAGAGTAGGACTGG    88635       TTG    C
                                CCAGTCT   TACTCT CCT
                                |||||||   |||||| |||
                                GGTCAGG   ATGAGA GGA
                                   ___     A
GAM579   LOC204285 3'  AGGGAGCAGCAAGAGTGG   89456    G   T  ACT
                                CCA TCTT GT   CTCCCT
                                ||| |||| ||   ||||||
                                GGT AGAA CG   GAGGGA
                                  G   _  AC_
GAM579   LOC221271 3'  AGGGAGAGAAGGAT       91845       GTA
                                GTCTTT   CTCTCCCT
                                ||||||   ||||||||
                                TAGGAA   GAGAGGGA
                                    ___
GAM579   LOC221838 3'  TTTAGTAGTAAAAGACTGG   92548        G   CTCC
                                CCAGTCTTT TACT   CTAAA
                                ||||||||| ||||   |||||
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                                GGTCAGAAA ATGA    GATTT
                                      _   T___
GAM579  LOC253776 3'  AGGAAGATGGCTGAAGACT   97429       _ AC   C
                                AGTCTTT GT  TCT CCT
                                ||||||| ||  ||| |||
                                TCAGAAG CG  AGA GGA
                                    T  GT   A
GAM579  LOC253805 3'  TAGGGAGAGTACTAGGACT   96436       T
                                AGTCTT GTACTCTCCCTA
                                |||||| ||||||||||||
                                TCAGGA CATGAGAGGGAT
                                   T
GAM579  LOC256861 3'  AGGAAGATGCCAAGAC      96787      T   C   C
                                GTCTT GTA TCT CCT
                                ||||| ||| ||| |||
                                CAGAA CGT AGA GGA
                                  C   _   A
GAM579  LOC51145  3'  TTAGGAAGAGACTGG       32401       TTTGTAC   C
                                CCAGTC      TCT CCTAA
                                ||||||      ||| |||||
                                GGTCAG      AGA GGATT
                                   ________  A
GAM579  LOC56891  5'  GAGATTCACACAGAAGACTGG  39277        ___   AC_
                                CCAGTCTT   TGT   TCTC
                                ||||||||   |||   ||||
                                GGTCAGAA   ACA   AGAG
                                     GAC   CTT
GAM580  CYB5     3'  GGAAACTCTTATCAC       8594       G
                                GTGA TAAGAGTTTCC
                                |||| ||||||||||
                                CACT ATTCTCAAAGG
                                  _
GAM580  FGFR2    3'  TGCTTTGGAAACACCCACTCAC 43363       AAGA
                                GTGAGT    GTTTCCGGAGTA
                                ||||||    ||||||||||||
                                CACTCA    CAAAGGTTTCGT
                                   CCCA
GAM580  FGFR2    3'  TGCTTTGGAAACACCCACTCAC 3767        AAGA
                                GTGAGT    GTTTCCGGAGTA
                                ||||||    ||||||||||||
                                CACTCA    CAAAGGTTTCGT
                                   CCCA
GAM580  FGFR2    3'  TGCTTTGGAAACACCCACTCAC 43375       AAGA
                                GTGAGT    GTTTCCGGAGTA
                                ||||||    ||||||||||||
                                CACTCA    CAAAGGTTTCGT
                                   CCCA
GAM580  FGFR2    3'  TGCTTTGGAAACACCCACTCAC 43486       AAGA
                                GTGAGT    GTTTCCGGAGTA
                                ||||||    ||||||||||||
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                                CACTCA   CAAAGGTTTCGT
                                   CCCA
GAM580  FGFR2    3'  TGCTTTGGAAACACCCACTCAC 43496      AAGA
                                GTGAGT   GTTTCCGGAGTA
                                ||||||   ||||||||||||
                                CACTCA   CAAAGGTTTCGT
                                   CCCA
GAM580  FGFR2    3'  TGCTTTGGAAACACCCACTCAC 43506      AAGA
                                GTGAGT   GTTTCCGGAGTA
                                ||||||   ||||||||||||
                                CACTCA   CAAAGGTTTCGT
                                   CCCA
GAM580  FLJ13262 3'  ACTTAACTCTTACCTAC    46154    A      TCCG
                                GTG GTAAGAGTT   GAGT
                                ||| |||||||||   ||||
                                CAT CATTCTCAA   TTCA
                                  C      _____
GAM580  KLK7     3'  TACACCGAGACCCTTATTCAC  17294       A   C  A
                                GTGAGTAAG GTTTC GG GTA
                                ||||||||| ||||| || |||
                                CACTTATTC CAGAG CC CAT
                                     C    _  A
GAM580  KLK7     3'  TACACCGAGACCCTTATTCAC  57734       A   C  A
                                GTGAGTAAG GTTTC GG GTA
                                ||||||||| ||||| || |||
                                CACTTATTC CAGAG CC CAT
                                     C    _  A
GAM580  MGC15875 3'  TGTACTCCAGAAGAAACTC   51911       C___
                                GAGTTTC   GGAGTACA
                                |||||||   ||||||||
                                CTCAAAG   CCTCATGT
                                   AAGA
GAM580  LOC143287 3' ACTCCTCGCCTTGCTCAC    82927        A  TTCC
                                GTGAGTAAG GT   GGAGT
                                ||||||||| ||   |||||
                                CACTCGTTC CG   CCTCA
                                     _ CT__
GAM580  LOC170261 5' GTACCCCGGAGAGGAGCTTTCT 82586      T  AG__     A
           CAC                    GTGAG AAG   TTTCCGG GTAC
                                |||||  |||   ||||||| ||||
                                CACTC TTC   AGAGGCC CATG
                                   T  GAGG     C
GAM580  LOC205106 5' ACACTGGACTCCCACTC    90700     AA  TT   A
                                GAGT  GAG  TCCGG GT
                                ||||  |||  ||||| ||
                                CTCA  CTC  AGGTC CA
                                  CC  __    A
GAM580  LOC257051 5' GTACCCCGGAGAGGAGCTTTCT 96320      T  AG__     A
           CAC                    GTGAG AAG   TTTCCGG GTAC
                                |||||  |||   ||||||| ||||
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                                CACTC TTC    AGAGGCC CATG
                                   T   GAGG      C
GAM580  LOC90334  3'  CCAAAACCCTTACTCAC     62311          A    CC
                                GTGAGTAAG GTTT  GG
                                ||||||||| ||||  ||
                                CACTCATTC CAAA  CC
                                     C    A_
GAM581  ACP2      3'  AGAAAGTTCTAGACTG      7851       GC  TC
                                CAGT  CT  AGAACTTTCT
                                ||||  ||  ||||||||||
                                GTCA  GA  TCTTGAAAGA
                                  __  __
GAM581  APTX      5'  AAGAGAAAGAGATCAGGCA   34655       TCAGAA
                                TGCCT     CTTTCTCTT
                                |||||     |||||||||
                                ACGGA     GAAAGAGAA
                                   CTAGA_
GAM581  BCL7A     3'  AGGCTGTCTCCTTAAGGCACTG 40637          C  A__  TT
                                CAGTGCCTT AG   AC  TCT
                                ||||||||| ||   ||  |||
                                GTCACGGAA TC   TG  GGA
                                     T  CTC  TC
GAM581  CLC       3'  AAGAGAAAATACTGAAAGCACA 25105    A    C     AAC
           GG                     CC GTGC TTCAG   TTTCTCTT
                                || |||| |||||   ||||||||
                                GG CACG AAGTC   AAAGAGAA
                                 A   A    ATA
GAM581  CNK       3'  AAGCCCTGAAGGCCTG      14517     T       AA
                                CAG GCCTTCAG  CTT
                                ||| ||||||||  |||
                                GTC CGGAAGTC  GAA
                                  _       CC
GAM581  COL4A3    3'  AAGTGCAGGTTCTGAGGGCACC 48549    A            TCT
           GG                     CC GTGCCTTCAGAACTT   CTT
                                || ||||||||||||||   |||
                                GG CACGGGAGTCTTGGA   GAA
                                 C            CGT
GAM581  CSPG4     3'  AAGAGAGACCTGGAGACAC    8570      C      AAC
                                GTG CTTCAG   TTTCTCTT
                                ||| ||||||   ||||||||
                                CAC GAGGTC   AGAGAGAA
                                  A     C__
GAM581  CYP1B1    3'  AAGAGAAAAGAGAGAAACACTG 3651        CC   AGAAC
                                CAGTG  TTC    TTTCTCTT
                                |||||  |||    ||||||||
                                GTCAC  AAG    AAAGAGAA
                                   A_   AGAGA
GAM581  DLG3      3'  AAGAGAAAAGAGGAGGACTG   40880      G     AGAAC
                                CAGT CCTTC    TTTCTCTT
                                |||| |||||    ||||||||
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                                GTCA GGAGG    AAAGAGAA
                                  _    AGA__
GAM581  DLG5    5'  AGGCAGACTCTGAAGGC    82909        A_  T
                                GCCTTCAGA  CT TCT
                                |||||||||  || |||
                                CGGAAGTCT  GA GGA
                                     CA  C
GAM581  FLT1    3'  AAGAGAAACCGGGAGAAGGCAT 8910        AGAAC_
                                GTGCCTTC    TTTCTCTT
                                ||||||||    ||||||||
                                TACGGAAG    AAAGAGAA
                                    AGGGCC
GAM581  GRB10   3'  AGAGAAAATGGCACCTGG    17971    _   TTCAGAAC
                                CCAG TGCC      TTTCTCT
                                |||| ||||      |||||||
                                GGTC ACGG      AAAGAGA
                                  C   TA_______
GAM581  LFG     3'  AAGAGAAAAGGAGCCAAGAACT 76711     GC   CAGAA   _
           GG                     CCAGT  CTT    CTTT CTCTT
                                |||||  |||    |||| |||||
                                GGTCA  GAA    GAAA GAGAA
                                  A_   CCGAG   A
GAM581  MAN2A2  3'  AAGAGAAAGTTCATTCAC    20391    CCTTCA
                                GTG    GAACTTTCTCTT
                                |||    ||||||||||||
                                CAC    CTTGAAAGAGAA
                                 TTA___
GAM581  NLGN3   3'  AAGAAAAGTTCTTAAAACACT  38596    CC  C      C
                                AGTG  TT AGAACTTT TCTT
                                ||||  || |||||||| ||||
                                TCAC  AA TCTTGAAA AGAA
                                  AA  T      _
GAM581  NPAS1   5'  AAGGTCTCCCGAGGGCACT   59879        A_  _
                                AGTGCCTTC  GA ACTTT
                                |||||||||  || |||||
                                TCACGGGAG  CT TGGAA
                                     CC  C
GAM581  PLAG1   3'  AGTGTGTTCCAAAGGCATT   10605        CA   TTT
                                AGTGCCTT  GAAC   CT
                                ||||||||  ||||   ||
                                TTACGGAA  CTTG   GA
                                    AC    TGT
GAM581  PLXNA1  3'  AGAAAATGAAGGCAGTGG    72309    G      GAAC
                                CCA TGCCTTCA    TTTCT
                                ||| ||||||||    |||||
                                GGT ACGGAAGT    AAAGA
                                  G       A___
GAM581  PPP4R1  3'  AAGAGAAAGTACAGTAAACACT 17620     CCTTCAGA
                                AGTG       ACTTTCTCTT
                                ||||       ||||||||||
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                                TCAC       TGAAAGAGAA
                                  AAATGACA
GAM581  ACYP2    3'  AAGAGAAAAATTGTAACACACT 56612      CC  _   AAC
            G                    CAGTG  TT CAG   TTTCTCTT
                                 ||||||  || |||   ||||||||
                                 GTCAC  AA GTT   AAAGAGAA
                                   AC  T   AA_
GAM581  B3GNT6   3'  AGAAATCAGATGAAGGCAT   22503        GAAC_
                                 GTGCCTTCA    TTTCT
                                 |||||||||    |||||
                                 TACGGAAGT    AAAGA
                                      AGACT
GAM581  BAG5     3'  AAGAGAAGGGATAAAGGAC   16835    G   CAGAA
                                 GT CCTT    CTTTCTCTT
                                 || ||||    |||||||||
                                 CA GGAA    GGAAGAGAA
                                  _   ATAG_
GAM581  BIVM     3'  AAGAGAAAAGACTCAAGAAACT 34665     GC   C  AAC
            G                    CAGT  CTT AG   TTTCTCTT
                                 ||||  ||| ||   ||||||||
                                 GTCA  GAA TC   AAAGAGAA
                                   AA   C  AGA
GAM581  C15orf5  3'  AGAGAAAAGAAAGCAC     48195      C   AGAAC
                                 GTGC TTC    TTTCTCT
                                 |||| |||    |||||||
                                 CACG AAG    AAAGAGA
                                   A   A____
GAM581  C20orf80  5'  AAGAGAAGAAGATGAAGAAAC  65282    GC    GAAC
                                 GT  CTTCA   TTTCTCTT
                                 ||  |||||   ||||||||
                                 CA  GAAGT   GAAGAGAA
                                  AA    AGAA
GAM581  CLSTN1   3'  AGTTCTGAGGACACTGG     30103       C
                                 CCAGTG CTTCAGAACT
                                 |||||| ||||||||||
                                 GGTCAC GGAGTCTTGA
                                    A
GAM581  DKFZP434P0111 3'  AAGAGAAAGTTTCTGCAC    67368     CTTCA
                                 GTGC    GAACTTTCTCTT
                                 ||||    ||||||||||||
                                 CACG    TTTGAAAGAGAA
                                   TC___
GAM581  DORFIN   5'  AGAATTCTCTGAAGGAAC    31257    G      ACT
                                 GT CCTTCAGA   TTCT
                                 || ||||||||   ||||
                                 CA GGAAGTCT   AAGA
                                  A       CTT
GAM581  FLJ10300  5'  AAGAGAAAGATGAAGACTCTG  35997    TGC    GAA
                                 CAG   CTTCA   CTTTCTCTT
                                 |||   |||||   |||||||||
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                                GTC   GAAGT   GAAAGAGAA
                                  TCA    A__
GAM581  FLJ20373  3'  AAGAGAAGAAGGAAAGGCACAG 35070    A     _ AGAAC
            G                    CC GTGCCTT C    TTTCTCTT
                                || ||||||| |    ||||||||
                                GG CACGGAA G    GAAGAGAA
                                 A      A GAA__
GAM581  FLJ23511  5'  AGAGAAAAACAAGGCAT    49956       CAGAAC
                                GTGCCTT     TTTCTCT
                                |||||||     |||||||
                                TACGGAA     AAAGAGA
                                    CAA___
GAM581  FLJ30681  3'  AGAGAAGAAAGACCACTGG   91782      CCT  AGAAC
                                CCAGTG   TC    TTTCTCT
                                ||||||   ||    |||||||
                                GGTCAC   AG    GAAGAGA
                                   C__  AAA__
GAM581  HDAC11    3'  GAGCTATAGGCACTGG      45717       TC  AACTTT
                                CCAGTGCCT  AG     CTC
                                |||||||||  ||     |||
                                GGTCACGGA  TC     GAG
                                     TA  _______
GAM581  IKKE      5'  AGTGAGCCCTGAAAGCTCTGG  25745     T  C    AA   T
                                CCAG GC TTCAG  CTT CT
                                |||| || |||||  ||| ||
                                GGTC CG AAGTC  GAG GA
                                  T  A    CC   T
GAM581  KIAA0680  3'  AGAGAAAATTGAAGCAT     28232     C    AAC
                                GTGC TTCAG   TTTCTCT
                                |||| |||||   |||||||
                                TACG AAGTT   AAAGAGA
                                  _    A__
GAM581  KIAA1228  3'  AGGGGGTGATTCTGAGGCACTG 65035       T   ___   TT
                                CAGTGCCT CAGA   ACT  CT
                                |||||||| ||||   |||  ||
                                GTCACGGA GTCT   TGG  GA
                                     _   TAG   GG
GAM581  KIAA1300  5'  AGGAACCCTGAAGGCA      62860       AAC
                                TGCCTTCAG   TTTCT
                                |||||||||   |||||
                                ACGGAAGTC   AAGGA
                                     CC_
GAM581  KIAA1805  3'  AAGAGAAAGTAGAAGCAGCA   79966    __   AGA
                                TGC  CTTC   ACTTTCTCTT
                                |||  ||||   ||||||||||
                                ACG  GAAG   TGAAAGAGAA
                                  AC    A__
GAM581  LENG1     5'  AAGAGAAAGCTCTGGGCATCCT 84074    __   TT   A
            G                    CAG  TGCC  CAGA CTTTCTCTT
                                |||  ||||  |||| |||||||||
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                                GTC  ACGG  GTCT GAAAGAGAA
                                  CT    __    C
GAM581  LHX6     3'  AAGAGAAAACTCTGGGGTCA  26854    C      AC
                                TG CTTCAGA  TTTCTCTT
                                || |||||||  ||||||||
                                AC GGGGTCT  AAAGAGAA
                                 T      CA
GAM581  N4BP3    3'  AGCTCCAGAAGGCACTGG    66250          A_  A
                                CCAGTGCCTTC  GA CT
                                ||||||||||  || ||
                                GGTCACGGAAG  CT GA
                                       AC  C
GAM581  NASP     3'  AGAGGGTGAAGAAACTG     67966     GC   AGA
                                CAGT  CTTC   ACTTTCT
                                ||||  ||||   |||||||
                                GTCA  GAAG   TGGGAGA
                                  AA   ___
GAM581  SMARCF1  3'  AAAATTCTGAAGGAC       57480    G       C
                                GT CCTTCAGAA TTT
                                || |||||||| |||
                                CA GGAAGTCTT AAA
                                 _       A
GAM581  SMARCF1  3'  AAAATTCTGAAGGAC       37430    G       C
                                GT CCTTCAGAA TTT
                                || |||||||| |||
                                CA GGAAGTCTT AAA
                                 _       A
GAM581  SMARCF1  3'  AAAATTCTGAAGGAC       20034    G       C
                                GT CCTTCAGAA TTT
                                || |||||||| |||
                                CA GGAAGTCTT AAA
                                 _       A
GAM581  TED      3'  AAGAGAAAGTCCAGGGACTGG  31630      G   TCA  A
                                CCAGT CCT   GA CTTTCTCTT
                                ||||| |||   || |||||||||
                                GGTCA GGA   CT GAAAGAGAA
                                   G   C__  _
GAM581  TGIF2    3'  AGAAGGGTGCTGAAGGC     41447         AA_
                                GCCTTCAG   CTTTCT
                                ||||||||   ||||||
                                CGGAAGTC   GGAAGA
                                     GTG
GAM581  WBSCR20A 3'  AAGAGAAAGAAGAGACAGCA  35958     CT  AGAA
                                TGC  TC    CTTTCTCTT
                                |||  ||    |||||||||
                                ACG  AG    GAAAGAGAA
                                  AC  AGAA
GAM581  LOC115273 3'  AGAAAGTTCTGATGGCCAGG  73356    AGT   T
                                CC   GCC TCAGAACTTTCT
                                ||   ||| ||||||||||||
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                                GG   CGG AGTCTTGAAAGA
                                 AC_   T
GAM581   LOC145761 5'  AAGAGAAAGTGGAAGGCATGG  83472     G      AGA
                                CCA TGCCTTC   ACTTTCTCTT
                                ||| |||||||   ||||||||||
                                GGT ACGGAAG   TGAAAGAGAA
                                  _      G__
GAM581   LOC146179 5'  AGAAAGTTTTGGGCCT      77700     T   TT
                                AG GCC  CAGAACTTTCT
                                || |||  ||||||||||
                                TC CGG  GTTTTGAAAGA
                                 _  __
GAM581   LOC147072 3'  AAGAGAAAGTGAGAAGAAACTG 60407      GC    AGA
                                CAGT  CTTC   ACTTTCTCTT
                                ||||  ||||   ||||||||||
                                GTCA  GAAG   TGAAAGAGAA
                                  AA    AG_
GAM581   LOC148758 5'  AGAAAGTTCTGAGAAAC     78962     GCC
                                GT   TTCAGAACTTTCT
                                ||   |||||||||||||
                                CA   GAGTCTTGAAAGA
                                 AA_
GAM581   LOC148932 3'  AGGAATCTGAAGGCACTGG    79103            AC
                                CCAGTGCCTTCAGA  TTTCT
                                ||||||||||||||  |||||
                                GGTCACGGAAGTCT  AAGGA
                                              __
GAM581   LOC149386 5'  AAGTTTTGAAAGCACT      84400       C
                                AGTGC TTCAGAACTT
                                ||||| ||||||||||
                                TCACG AAGTTTTGAA
                                   A
GAM581   LOC150139 3'  AGAAAATAGAAAAAGGCGCTGG 79583          CAGAAC_
                                CCAGTGCCTT      TTTCT
                                ||||||||||      |||||
                                GGTCGCGGAA      AAAGA
                                      AAAGATA
GAM581   LOC152756 3'  AAGATGCAGTTCTGAAAACCTG 85871     TGCC        TTC
                                CAG    TTCAGAACT   TCTT
                                |||    |||||||||   ||||
                                GTC    AAGTCTTGA   AGAA
                                  CAA_        CGT
GAM581   LOC162333 5'  AAGAGAAAGCGATGACACTG   87114      CCT   GAA
                                CAGTG   TCA   CTTTCTCTT
                                |||||   |||   |||||||||
                                GTCAC   AGT   GAAAGAGAA
                                   ____  AGC
GAM581   LOC199221 3'  AAGAGAAGCTCGAAAGCATGG  80347     G   C   A  A   T
                                CCA TGC TTC GA CTT CTCTT
                                ||| ||| ||| || ||| |||||
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                                GGT ACG AAG CT GAA GAGAA
                                  _  A  _ C  _
GAM581  LOC203339 3'  AGAGAAAATTGGGCCTG    90542    T   TCAGAAC
                                CAG GCCT     TTTCTCT
                                ||| ||||     |||||||
                                GTC CGGG     AAAGAGA
                                  _   TTA____
GAM581  LOC255017 3'  AGAAAGAGGAACTGG      94624      G   TCAGAA
                                CCAGT CCT    CTTTCT
                                ||||| |||    ||||||
                                GGTCA GGA    GAAAGA
                                   A  _______
GAM581  LOC256021 3'  AAGAGAAACAAAGACAACACTG 96512       CCT  AGAAC
           G                     CCAGTG   TC    TTTCTCTT
                                ||||||  ||    ||||||||
                                GGTCAC   AG    AAAGAGAA
                                   AAC  AAAC_
GAM581  LOC90139  3'  AGAATCCCGAAGGCAT     55396        A_  ACT
                                GTGCCTTC  GA   TTCT
                                ||||||||  ||   ||||
                                TACGGAAG  CT   AAGA
                                    CC  ___
GAM582  CDK7    3'  GGGAAAACTTAATAAAAATTAT 8394          ATAG   C
           TA                    TAATGATTTT   GGG TTTCCC
                                ||||||||||   ||| ||||||
                                ATTATTAAAA   TTC AAAGGG
                                     ATAA   A
GAM582  EFNB2    3'  AAAGCCCCTCTTCATT     14568      TTTTAT
                                AATGA     AGGGGCTTT
                                |||||     |||||||||
                                TTACT     TCCCCGAAA
                                  TC____
GAM582  OXTR    3'  GTTTCCCGAAACTATAAAATC  6216          ________  CTTT
                                GATTTTATAG     GGG   C
                                ||||||||||     |||   |
                                CTAAAATATC     CCC   G
                                     AAAGIII   TTTC
GAM582  SLC13A1   3'  GGAAAGCTGAACACTATAAAAC 42381      A      G____
           TATTA                  TAATG TTTTATAG    GGCTTTCC
                                ||||| ||||||||    ||||||||
                                ATTAT AAAATATC    TCGAAAGG
                                  C       ACAAG
GAM582  C20orf45  3'  GGCTTTCCCAAAAAAATAAAGT 32107        AG_________  CTT
           CATTA                  TGATTTTAT       GGG   TC
                                |||||||||       |||   ||
                                ACTGAAATA       CCT   GG
                                     AAAAAAIIIC   TTC
GAM582  GA17    3'  AAAGCCCTAAATCAT      64206       TATA
                                ATGATTT   GGGGCTTT
                                |||||||   ||||||||
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                                TACTAAA   TCCCGAAA
                                     ____
GAM582  KIAA0326 3' GAAAAACCCTATAAACCAT   64327    AT      GC
                                ATG  TTTATAGGG  TTTC
                                |||  |||||||||  ||||
                                TAC  AAATATCCC  AAAG
                                  C_       AA
GAM582  KIAA0570 3' GGTTTCTCCTTATAAAACCAT  28180    A       CTTT
                                ATG TTTTATAGGGG   CC
                                ||| ||||||||||   ||
                                TAC AAAATATTCCT   GG
                                  C        CTTT
GAM582  KIAA1069 3' GGAAAACCCCTGTCCCAGCA  67938   ATTTT    C
                                TG    ATAGGGG TTTCC
                                ||    ||||||| |||||
                                AC    TGTCCCC AAAGG
                                 GACCC      A
GAM582  KIAA1940 3' GGAAAGCCCCTCAGTC     79986     TTAT
                                GATT   AGGGGCTTTCC
                                ||||   ||||||||||
                                CTGA   TCCCCGAAAGG
                                  C___
GAM582  MRPL3    3' GGAAAGACAATAAAATCAT   23286        AGGGG
                                ATGATTTTAT    CTTTCC
                                ||||||||||    ||||||
                                TACTAAAATA    GAAAGG
                                      ACA__
GAM582  P311     3' GGAAAACAAGGTCTACAAAATC 16488       ATAG   _____
           AT                    ATGATTTT   GGGCT    TTCC
                                ||||||||   |||||    ||||
                                TACTAAAA   TCTGG    AAGG
                                    CA__    AACAA
GAM582  PAK2     5' AAAGCCCAGGCATAAAATCAT  66533        AG__
                                ATGATTTTAT   GGGCTTT
                                ||||||||||   |||||||
                                TACTAAAATA   CCCGAAA
                                      CGGA
GAM582  PGRMC2   3' GGGAAAGCCCCTATAATGAATT 20892    TT___
           CA                    TGA    TTATAGGGGCTTTCCC
                                |||    ||||||||||||||||
                                ACT    AATATCCCCGAAAGGG
                                  TAAGT
GAM582  LOC144453 3' AAGCCTCCTACAGAATCAT   76842       A  _
                                ATGATTTT TAGG GGCTT
                                |||||||| |||| |||||
                                TACTAAGA ATCC CCGAA
                                    C   T
GAM582  LOC196337 3' GTTTCCCGAGACTATAAAATC  87651        _______  CTTT
                                GATTTTATAG     GGG   C
                                ||||||||||     |||   |
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                                CTAAAATATC      CCC    G
                                     AGAGIII   TTTC
GAM582  LOC203335 3'  GGCTTTCCCAAAAGCTATAAAA 89334          _________  CTTT
           TCAT                   GATTTTATAG       GGG    CC
                                  ||||||||||       |||    ||
                                  CTAAAATATC       CCC    GG
                                       GAAAAIII   TTTC
GAM582  LOC254345 5'  GGAAAGCCCCTCTCTTCA    97631     TTTTAT
                                  TGA     AGGGGCTTTCC
                                  |||     ||||||||||||
                                  ACT     TCCCCGAAAGG
                                    TCTC__
GAM582  LOC257101 5'  GGAAAGCCCATGATCA      96908       TTATAG
                                  TGATT     GGGCTTTCC
                                  |||||     |||||||||
                                  ACTAG     CCCGAAAGG
                                     TA____
GAM582  LOC54516  3'  GGGCTGCATCCCTATAAACCCA 38761     AT       __ TTT
           T                       ATG  TTTATAGGG  GC   CCC
                                  |||  |||||||||  ||   |||
                                  TAC  AAATATCCC  CG   GGG
                                    CC        TA  TC_
GAM582  LOC89985  3'  AGAGCCTCCCATAAAATCA    61017         A  _
                                  TGATTTTAT GG GGCTTT
                                  |||||||||  || ||||||
                                  ACTAAAATA CC CCGAGA
                                       C  T
GAM582  LOC90155  3'  GAGAGCCCCTTATAAAACCAT  61695     A      _
                                  ATG TTTTATA GGGGCTTTC
                                  ||| |||||||  |||||||||
                                  TAC AAAATAT CCCCGAGAG
                                    C      T
GAM583  FLJ22672  3'  AACCAGGCCGAGAGGCCAC    46066        ___
                                  GTGGTC   CGGCCTGGTT
                                  ||||||   ||||||||||
                                  CACCGG   GCCGGACCAA
                                      AGA
GAM583  RBT1      3'  AACCAGGCCGGACCACGTGCAA 25348
           TA                       TATTGCACGTGGTCCGGCCTGGTT
                                  ||||||||||||||||||||||||
                                  ATAACGTGCACCAGGCCGGACCAA

GAM584  ATRN      3'  TTAATGGGTGCAGCACAC     23833          C  TT
                                  GTGTGCTGT TT  TTAA
                                  |||||||||  ||  ||||
                                  CACACGACG GG  AATT
                                       T  GT
GAM584  ATRN      3'  TTAATGGGTGCAGCACAC     57809          C  TT
                                  GTGTGCTGT TT  TTAA
                                  |||||||||  ||  ||||
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                                CACACGACG GG  AATT
                                     T  GT
GAM584  BHLHB3   3'  TTAAAAAAGACATAATGGATG  47769       GTGTGC
                                CATCCA     TGTCTTTTTTAA
                                ||||||     ||||||||||||
                                GTAGGT     ACAGAAAAAATT
                                   AAT___
GAM584  MLLT2    3'  TAAAAAAGAAGCACCACGAGAT 19851      CA  _   G
           G                     CATC  GTG TGCT TCTTTTTTA
                                ||||  ||| |||| |||||||||
                                GTAG  CAC ACGA AGAAAAAAT
                                  AG  C   _
GAM584  MTMR2    3'  AAAGAACACACTGCATG     32379     C      CTG
                                CAT CAGTGTG   TCTTT
                                ||| |||||||   |||||
                                GTA GTCACAC   AGAAA
                                  C      A__
GAM584  SCN3A    3'  AAGGAAACACACTGGAT     22627          CTG
                                ATCCAGTGTG   TCTTT
                                ||||||||||   |||||
                                TAGGTCACAC   AGGAA
                                     AA_
GAM584  SOX9     3'  TAAAAAAGACAGCAAACT    4440      G
                                AGT TGCTGTCTTTTTTA
                                ||| ||||||||||||||
                                TCA ACGACAGAAAAAAT
                                  A
GAM584  CNOT7    3'  TAAAAAAGACAAGAAACT    25333     GTG  _
                                AGT   CT GTCTTTTTTA
                                |||   || ||||||||||
                                TCA   GA CAGAAAAAAT
                                  AA_  A
GAM584  DKFZp762K2015 3'  AAAAAAGAAGCCAC       72472     T   G
                                GTG GCT TCTTTTTT
                                ||| ||| ||||||||
                                CAC CGA AGAAAAAA
                                  _  _
GAM584  FUBP3    3'  TTAAAAAAGACAATTGGA    63735       GTGC
                                TCCAGT    TGTCTTTTTTAA
                                ||||||    ||||||||||||
                                AGGTTA    ACAGAAAAAATT
                                     ____
GAM584  GOLPH3   3'  TTAAATTGAAACAGCACA    42116        C  T_
                                TGTGCTGT TT  TTTAA
                                |||||||| ||  |||||
                                ACACGACA AG  AAATT
                                     A  TT
GAM584  KIAA1001 3'  AAAAAAGACTTTGCCTGG    30286     T   CT
                                CCAG GTG  GTCTTTTTT
                                |||| |||  |||||||||
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                                GGTC CGT  CAGAAAAAA
                                  _   TT
GAM584  KIAA1466  3'  AAAAAAGACATAGAC      71912    G  C
                                GT TG TGTCTTTTTT
                                || || ||||||||||
                                CA AT ACAGAAAAAA
                                 G  _
GAM584  KIAA1468  3'  TAAAAAAGACATTGGCTG    91776     GTGC
                                CAGT   TGTCTTTTTTA
                                ||||   |||||||||||
                                GTCG   ACAGAAAAAAT
                                  GTT_
GAM584  KIAA1883  3'  TAAAAAAGACAAAAACA     73420     GC_
                                TGT   TGTCTTTTTTA
                                |||   |||||||||||
                                ACA   ACAGAAAAAAT
                                  AAA
GAM584  MEGF10    3'  TTAAAAAAGAAAATCTGGA   50587      TGTGCTG
                                TCCAG      TCTTTTTTAA
                                |||||      ||||||||||
                                AGGTC      AGAAAAAATT
                                   TAAA___
GAM584  MOST2     5'  TAAAAAAGACAGGAGGA     39690     AGTGTG
                                TCC     CTGTCTTTTTTA
                                |||     ||||||||||||
                                AGG     GACAGAAAAAAT
                                  AG____
GAM584  PPP1R16B  3'  TTAAAAAAAACAGTCGCT    61394      T    C
                                AGTG GCTGT TTTTTTAA
                                |||| ||||| ||||||||
                                TCGC TGACA AAAAAATT
                                  _    A
GAM584  SLC11A2   3'  AAAAGCGCAGACTGGATG    5230         G   T T
                                CATCCAGT TGC G CTTTT
                                |||||||| ||| | |||||
                                GTAGGTCA ACG C GAAAA
                                     G  _ _
GAM584  LOC124783 5'  AAAGAGCACACTGGA       74334          TG
                                TCCAGTGTGC  TCTTT
                                ||||||||||  |||||
                                AGGTCACACG  AGAAA
                                            __
GAM584  LOC144248 5'  TAAAAAAGACAAACA       76743     GC
                                TGT  TGTCTTTTTTA
                                |||  ||||||||||
                                ACA  ACAGAAAAAAT
                                  A_
GAM584  LOC146712 5'  AAGGCCAGCACACAGGA     83712     A       _
                                TCC GTGTGCTG TCTT
                                ||| |||||||| ||||
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                                AGG CACACGAC GGAA
                                  A       C
GAM584   LOC146723 3'  AAAAAAGACACTTGTACAC    78081       ___
                                GTGTGC   TGTCTTTTTT
                                ||||||   ||||||||||
                                CACATG   ACAGAAAAAA
                                   TTC
GAM584   LOC151040 3'  TTAATGGGTGCAGCACAC     80105         C  TT
                                GTGTGCTGT TT  TTAA
                                |||||||||  ||  ||||
                                CACACGACG GG  AATT
                                      T  GT
GAM584   LOC153606 5'  TTAAAACAAAACAAACACTGGA 86077         GC   C  _
                                TCCAGTGT  TGT TT TTTTAA
                                ||||||||  ||| || ||||||
                                AGGTCACA  ACA AA AAAATT
                                     A_   A  C
GAM584   LOC157697 5'  GACAGCACACAGATG       81549      CA
                                CATC  GTGTGCTGTC
                                ||||  ||||||||||
                                GTAG  CACACGACAG
                                  A_
GAM584   LOC220906 3'  AAAAAGACCCACACCGGA    91395     A    CT
                                TCC GTGTG  GTCTTTTT
                                ||| |||||  ||||||||
                                AGG CACAC  CAGAAAAA
                                  C    C_
GAM584   LOC222252 3'  TTAATGGGTGCAGCACAC    94310         C  TT
                                GTGTGCTGT TT  TTAA
                                |||||||||  ||  ||||
                                CACACGACG GG  AATT
                                      T  GT
GAM584   LOC222697 3'  TAAAAAAACACACTGGA     94354         CTGTC
                                TCCAGTGTG    TTTTTTA
                                |||||||||    |||||||
                                AGGTCACAC    AAAAAAT
                                     A____
GAM584   LOC90317  5'  AAAGGAGTCACACTGGA     62248         _  G
                                TCCAGTGTG CT TCTTT
                                |||||||||  ||  |||||
                                AGGTCACAC GA GGAAA
                                      T  _
GAM584   LOC90829  3'  TTAATGGGTGCAGCACAC    64101         C  TT
                                GTGTGCTGT TT  TTAA
                                |||||||||  ||  ||||
                                CACACGACG GG  AATT
                                      T  GT
GAM584   LOC92876  3'  TTAATGGGTGCAGCACAC    70806         C  TT
                                GTGTGCTGT TT  TTAA
                                |||||||||  ||  ||||
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                                CACACGACG GG  AATT
                                      T  GT
GAM585  FOXM1    3'  AGTATCTGATTCCTCTGCTGT  41703     C   TT   A
                                GCA CAG  GAA TCAGATACT
                                ||| |||  ||| |||||||||
                                TGT GTC  CTT AGTCTATGA
                                  C   TC  _
GAM585  LAMP2    3'  CTATTCCAACTGGGC       25711    A      A   C
                                GC CCAGTTG AAT AG
                                || ||||||| ||| ||
                                CG GGTCAAC TTA TC
                                  _      C   _
GAM585  LHX4     3'  TTTGCTCCAACTGGTGTGT   52909            AAAT
                                ACGCACCAGTTG    CAGA
                                ||||||||||||    ||||
                                TGTGTGGTCAAC    GTTT
                                        CTC_
GAM585  MAPK4    3'  GACCTCAATGGTGCGT      10829         G    AA
                                ACGCACCA TTGA  TC
                                |||||||| ||||  ||
                                TGCGTGGT AACT  AG
                                     _   CC
GAM585  NAB1     3'  ATCTGGTTATCAATGC      19907     CCAG   _
                                GCA    TTGA AATCAGAT
                                |||    |||| ||||||||
                                CGT    AACT TTGGTCTA
                                  _____    A
GAM585  OPHN1    3'  AGCATCTAATTTCAATTATAGT 10352      ACC        C    A
          GT                      ACGC   AGTTGAAAT AGAT CT
                                ||||   ||||||||| |||| ||
                                TGTG   TTAACTTTA TCTA GA
                                  ATA        A    C
GAM585  ORC1L    3'  AGCATCTGATTTTGGAAGT    14735     CAG TG        A
                                AC   T  AAATCAGAT CT
                                ||   |  ||||||||| ||
                                TG   G  TTTAGTCTA GA
                                 AA_ GT        C
GAM585  RAB7L1   3'  ATCTGATTCTGGAATGC     14104      __    TTGA
                                GCA  CCAG    AATCAGAT
                                |||  ||||    ||||||||
                                CGT  GGTC    TTAGTCTA
                                  AA   _____
GAM585  ZNF137   3'  AGCATCTGATTTCAAACTCTTA 12858     ACC_   _        A
          GC                      GC    AGTT GAAATCAGAT CT
                                ||    |||| |||||||||| ||
                                CG    TCAA CTTTAGTCTA GA
                                 ATTC    A        C
GAM585  ABCA8    3'  AGTATCTGATATCAAT      23149       A
                                GTTGA ATCAGATACT
                                ||||| ||||||||||
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                                TAACT TAGTCTATGA
                                   A
GAM585  DKFZP434L187 5'  AGTATCTGATAAAGTGG     68801     G  GAA
                                CCA TT   ATCAGATACT
                                ||| ||   ||||||||||
                                GGT AA   TAGTCTATGA
                                  G  A__
GAM585  FLJ12568  3'  AGTATCTGATTTTAGATG    46498    G
                                CA TTGAAATCAGATACT
                                || ||||||||||||||
                                GT GATTTTAGTCTATGA
                                 A
GAM585  FLJ31153  3'  TATCTGATTACATTGATG    58129    C    T A
                                CA CAGT G AATCAGATA
                                || |||| | |||||||||
                                GT GTTA C TTAGTCTAT
                                 A    _ A
GAM585  GREAT    3'  ATCTGATTCCAGTGTG      55480      CAGT  A
                                CGCAC    TG AATCAGAT
                                ||||||    || ||||||||
                                GTGTG    AC TTAGTCTA
                                   _____  C
GAM585  KIAA1323  3'  GTATCTATTAACTGG       63044        AATC
                                CCAGTTGA    AGATAC
                                ||||||||    ||||||
                                GGTCAATT    TCTATG
                                     A___
GAM585  SLC19A3   3'  CTGATTTTTAAATGGTAGC    47487    _    GTT_
                                GC ACCA    GAAATCAG
                                || ||||    ||||||||
                                CG TGGT    TTTTAGTC
                                 A    AAAT
GAM585  VEST1     5'  TATCTGATTTTTTGAGC     53688     AC   TT
                                GC  CAG  GAAATCAGATA
                                ||  |||  ||||||||||||
                                CG  GTT  TTTTAGTCTAT
                                 A_  __
GAM585  LOC221935 3'  GTATCTGACCAGTGC       92626      CAGT  AAA
                                GCAC    TG   TCAGATAC
                                ||||    ||   ||||||||
                                CGTG    AC   AGTCTATG
                                   _____  C__
GAM585  LOC256515 5'  TACCTGATTGGTCCGT      96465     C    GTTGAA    A
                                ACG ACCA      ATCAG TA
                                ||| ||||      ||||| ||
                                TGC TGGT      TAGTC AT
                                  C    _______     C
GAM586  AIRE      5'  GCTCTCAGCTGGGCCCGTGGGT 5397         AA    T
              G                  CACCCAT  GGTTC GCTGAGAGC
                                 |||||||  ||||| |||||||||
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                                GTGGGTG  CCGGG CGACTCTCG
                                   C_    T
GAM586  ATP1A2   3'  TGGTCAGAACCTTTGG     5530     T      _
                                CCA AAGGTTCTG CTG
                                ||| ||||||||| |||
                                GGT TTCCAAGAC GGT
                                  _       T
GAM586  ATSV     3'  GCTCCCAGCAGAGGCTGTG   15057     A G      A
                                CATA G TTCTGCTG GAGC
                                |||| | |||||||| ||||
                                GTGT C GAGACGAC CTCG
                                  _ G       C
GAM586  DEDD     3'  GCCCTCAGCAGAACTT     52225           A
                                AGGTTCTGCTGAG GC
                                |||||||||||| ||
                                TTCAAGACGACTC CG
                                        C
GAM586  ED1      3'  CTCCCAGAACCTCTAAGTG   7369     CCATA      CT
                                CAC    AGGTTCTG  GAG
                                |||    ||||||||  |||
                                GTG    TCCAAGAC  CTC
                                  AATC_      C_
GAM586  GRLF1    3'  TCTCAGCACTGGGTG      78565      TAAGGTTC
                                CACCCA      TGCTGAGA
                                ||||||      ||||||||
                                GTGGGT      ACGACTCT
                                   C________
GAM586  HTR1E    3'  CTTTTTCCAGAGCCTCATGAGT 6014     C   A      CT
          G                      CAC CAT AGGTTCTG  GAGAG
                                ||| ||| ||||||||  |||||
                                GTG GTA TCCGAGAC  TTTTC
                                  A  C       CT
GAM586  ITGB3    3'  CTCTCAGCAGCTATGG     3995      AGGTT
                                CCATA    CTGCTGAGAG
                                |||||    ||||||||||
                                GGTAT    GACGACTCTC
                                   C_____
GAM586  LDB1     5'  CAGCAGAGGGGCCCGGTG    13982     CATAA  ___
                                CACC    GGT   TCTGCTG
                                ||||    |||   |||||||
                                GTGG    CCG   AGACGAC
                                  C_____   GGG
GAM586  LMAN1    3'  GCCTAAAAAACCTTGTGGGTG  18734          CTGCTG  A
                                CACCCATAAGGTT     AG GC
                                ||||||||||||     || ||
                                GTGGGTGTTCCAA     TC CG
                                        AAAA__  _
GAM586  MMP19    3'  CTCAGTAGAACCTTGCAGGTG  42970     CA
                                CACC  TAAGGTTCTGCTGAG
                                ||||  ||||||||||||||
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                                GTGG GTTCCAAGATGACTC
                                  AC
GAM586  MMP19   3' CTCAGTAGAACCTTGCAGGTG 10082    CA
                                CACC TAAGGTTCTGCTGAG
                                |||| ||||||||||||||
                                GTGG GTTCCAAGATGACTC
                                  AC
GAM586  MMP19   3' CTCAGTAGAACCTTGCAGGTG 42979    CA
                                CACC TAAGGTTCTGCTGAG
                                |||| ||||||||||||||
                                GTGG GTTCCAAGATGACTC
                                  AC
GAM586  MMP19   3' CTCAGTAGAACCTTGCAGGTG 42984    CA
                                CACC TAAGGTTCTGCTGAG
                                |||| ||||||||||||||
                                GTGG GTTCCAAGATGACTC
                                  AC
GAM586  PCSK1   3' CTCTCAGTCCCCATGG     4771     AA TTCT
                                CCAT GG   GCTGAGAG
                                |||| ||   ||||||||
                                GGTA CC   TGACTCTC
                                  CC _____
GAM586  PLS1    3' CTGTCTAAAACCTTATGG    10660        CTGCT G
                                CCATAAGGTT    GA AG
                                ||||||||||    || ||
                                GGTATTCCAA    CT TC
                                      AAT__ G
GAM586  SLC22A2 5' GCTCTCAGCCTCGCTCCGGG 59534    ATAA TCT
                                CCC   GGT  GCTGAGAGC
                                |||   |||  |||||||||
                                GGG   TCG  CGACTCTCG
                                  CC__  CTC
GAM586  SLC7A6  3' GCATGTGGCAGAACCTCATGG 14309     A        AGA
                                CCAT AGGTTCTGCTG  GC
                                |||| ||||||||||  ||
                                GGTA TCCAAGACGGT  CG
                                  C         GTA
GAM586  SON     3' CCTCAGAGCCTGTGG      54201      A    GCT  A
                                CCATA GGTTCT  GAG G
                                ||||| ||||||  ||| |
                                GGTGT CCGAGA  CTC C
                                  _     ___  C
GAM586  TNNI2   3' GCTCCCAGCAGAACATACTAGG 12350    ATAAG_       A
          G                      CCC     GTTCTGCTG GAGC
                                |||     ||||||||| ||||
                                GGG     CAAGACGAC CTCG
                                  ATCATA       C
GAM586  ZNF124  3' CTCCAGATTGACCTTAT    12824       CTG  A
                                ATAAGGTT  CTG GAG
                                ||||||||  ||| |||
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                                TATTCCAG   GAC CTC
                                    TTA  _
GAM586  C21orf6  3' CTCTCAGTGGCCTCAGG    33745    ATA    CT
                                CC   AGGTT  GCTGAGAG
                                ||   |||||  ||||||||
                                GG   TCCGG  TGACTCTC
                                 AC_    __
GAM586  CECR6    3' CTCAACAGGATGTGG      49085     AAG     C
                                CCAT   GTTCTG TGAG
                                ||||   |||||| ||||
                                GGTG   TAGGAC ACTC
                                  ___     A
GAM586  FLJ10520 5' GCTCTCAGCATTACGCTGTGGG 36213       AG  TC
                                CCCATA  GT  TGCTGAGAGC
                                ||||||  ||  ||||||||||
                                GGGTGT  CA  ACGACTCTCG
                                    CG  TT
GAM586  FLJ13265 3' GCTCCAGCCAGAACTTTACAGG 45928      CA        _  A
           TG                     CACC  TAAGGTTCTG CTG GAGC
                                ||||  |||||||||| ||| ||||
                                GTGG  ATTTCAAGAC GAC CTCG
                                  AC         C  _
GAM586  FLJ20344 3' CGGAGAGAAACCTTATG     35009          _ G_
                                CATAAGGTT CT  CTG
                                |||||||| ||  |||
                                GTATTCCAA GA  GGC
                                     A  GA
GAM586  FLJ22054 3' CTCATGTTCAGAACCTTGT   94394           C___
                                ATAAGGTTCTG   TGAG
                                ||||||||||    ||||
                                TGTTCCAAGAC   ACTC
                                      TTGT
GAM586  FLJ23584 3' CTCCCAGCAGAGTGAGG     44738    _  AAGGT      A
                                CC CAT    TCTGCTG GAG
                                || |||    ||||||| |||
                                GG GTG    AGACGAC CTC
                                 A  _____      C
GAM586  KIAA0227 3' GCCTCTCAGAACCTCAT     60698    A      CT   A
                                AT AGGTTCTG  GAG GC
                                || ||||||||  ||| ||
                                TA TCCAAGAC  CTC CG
                                 C       T_  _
GAM586  KIAA0522 3' CAGCAGTTGCCATGGG      71965      AA   T_
                                CCCAT  GGT  CTGCTG
                                |||||  |||  ||||||
                                GGGTA  CCG  GACGAC
                                   __  TT
GAM586  KIAA0945 3' CTCTCAGCTTGGCCCAAGGT   30210     CATAA    CT
                                ACC    GGTT  GCTGAGAG
                                |||    ||||  ||||||||
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                                TGG    CCGG  CGACTCTC
                                  AAC__    TT
GAM586  KIAA1191  5'  TCACAGAACCTCTGG      39961     TA      C
                                CCA  AGGTTCTG TGA
                                |||  |||||||| |||
                                GGT  TCCAAGAC ACT
                                  C_       _
GAM586  KIAA1956  3'  CAGGACCTTATGAGTG      78433     C
                                CAC CATAAGGTTCTG
                                ||| ||||||||||||
                                GTG GTATTCCAGGAC
                                  A
GAM586  KLHL4     3'  CTCTCAGCATGCATCATG    38922     AAG  TC
                                CAT   GT  TGCTGAGAG
                                |||   ||  |||||||||
                                GTA   CG  ACGACTCTC
                                  CTA  T_
GAM586  LOXL4     3'  GCTCTCAGTTTCTTAGGG    49869     A    TTCT
                                CCC TAAGG    GCTGAGAGC
                                ||| |||||    |||||||||
                                GGG ATTCT    TGACTCTCG
                                  _    T____
GAM586  MGC11324  3'  GCCAGAGGCAGAACCTACAGGT 51167      CATA        GAGA
           G                     CACC    AGGTTCTGCT    GC
                                ||||    ||||||||||    ||
                                GTGG    TCCAAGACGG    CG
                                  ACA_         AGAC
GAM586  MGC11352  3'  GCTCCCAGCAGAGCAGAGAGGG 64803       ATAAG        A
           TG                     CACCC     GTTCTGCTG GAGC
                                |||||     ||||||||| ||||
                                GTGGG     CGAGACGAC CTCG
                                   AGAGA        C
GAM586  MGC2647   3'  CTCCCAGCAGAGGCGGGG    73702     ATAAGG       A
                                CCC      TTCTGCTG GAG
                                |||      |||||||| |||
                                GGG      GAGACGAC CTC
                                  GCG___       C
GAM586  MGC29762  5'  CTCTCAGAGCTGCTTTCGGG   58471     AT    TCTG
                                CCC  AAGGT    CTGAGAG
                                |||  |||||    |||||||
                                GGG  TTTCG    GACTCTC
                                  C_    TCGA
GAM586  PRPF8     3'  GCTCTCATTGGCCTTATG    61192         CTGC
                                CATAAGGTT    TGAGAGC
                                |||||||||    |||||||
                                GTATTCCGG    ACTCTCG
                                      TT__
GAM586  Rpo1-2    3'  GCTCTCAGCAGGCAGTGAGTG  49878     C   AAG  T
                                CAC CAT   GT CTGCTGAGAGC
                                ||| |||   || ||||||||||
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                                GTG GTG   CG GACGACTCTCG
                                  A   A__  _
GAM586  Rpo1-2    3'  GCTCTCAGCAGGCAGTGAGTG  38703     C   AAG  T
                                CAC CAT   GT CTGCTGAGAGC
                                ||| |||   || ||||||||||
                                GTG GTG   CG GACGACTCTCG
                                  A   A__  _
GAM586  ZNF226    5'  CAGCAGAACCCCATGGG     33188       AA
                                CCCAT  GGTTCTGCTG
                                |||||  ||||||||||
                                GGGTA  CCAAGACGAC
                                   CC
GAM586  LOC123643 5'  GCCCTCAGCAGCATCACAGG   76018    ATAA   T       A
                                CC    GGT CTGCTGAG GC
                                ||    ||| |||||||| ||
                                GG    CTA GACGACTC CG
                                 ACA_   C       C
GAM586  LOC143310 3'  CTTTGCCAACCTTATG      76534         CT  T
                                CATAAGGTT  GC GAG
                                |||||||||  || |||
                                GTATTCCAA  CG TTC
                                      C_  T
GAM586  LOC143970 5'  CTCAGCTATGGGTG        83000         AGGTTCT
                                CACCCATA      GCTGAG
                                ||||||||      ||||||
                                GTGGGTAT      CGACTC
                                      _______
GAM586  LOC147685 3'  GCTCCCAGAGAACCTTATGG   78444           G   A
                                CCATAAGGTTCT CTG GAGC
                                |||||||||||| ||| ||||
                                GGTATTCCAAGA GAC CTCG
                                       _   C
GAM586  LOC149296 5'  CTCTCAGCAGAACACCTATGGG 79257        AG_
                                CCCATA   GTTCTGCTGAGAG
                                ||||||   ||||||||||||||
                                GGGTAT   CAAGACGACTCTC
                                   CCA
GAM586  LOC149506 3'  CTCTCAGTTCTCCAGGTG    84462      CATAA  TTCT
                                CACC    GG    GCTGAGAG
                                ||||    ||    ||||||||
                                GTGG    CC    TGACTCTC
                                  A_____  TCT_
GAM586  LOC155061 3'  CTCTCAGCAGAGCTGGG     81267      TAAG
                                CCCA    GTTCTGCTGAGAG
                                ||||    ||||||||||||||
                                GGGT    CGAGACGACTCTC
                                  _____
GAM586  LOC161823 3'  GCTCTCAGGTGCTTACTGGGTG 82303        TA    TCTG
                                CACCCA  AGGT    CTGAGAGC
                                ||||||  ||||    ||||||||
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                                GTGGGT  TTCG    GACTCTCG
                                   CA    TG__
GAM586  LOC221540 3'  GCCCTCAGCAGAGAATTA    93838     GG        A
                                TAA  TTCTGCTGAG GC
                                |||  |||||||||| ||
                                ATT  GAGACGACTC CG
                                  AA         C
GAM586  LOC221596 3'  CTATAGAAAAACCTTATG    91978         CTG  _
                                CATAAGGTT   CTG AG
                                |||||||||   ||| ||
                                GTATTCCAA   GAT TC
                                      AAA   A
GAM586  LOC253868 3'  GCTCCCAGCAGAGGACTGAGG  95584    ATA  G_      A
                                CC   AG  TTCTGCTG GAGC
                                ||   ||  |||||||| ||||
                                GG   TC  GAGACGAC CTCG
                                 AG_  AG       C
GAM586  LOC254494 5'  GCCCTCAGCAGGTGCTGACGGG 97620      ATAA  _       A
           T                     ACCC    GGT TCTGCTGAG GC
                                ||||    ||| |||||||||| ||
                                TGGG    TCG GGACGACTC CG
                                  CAG_  T        C
GAM586  LOC256112 3'  CAGGAGAAAAAACCTTATG    96364         ___  G
                                CATAAGGT   TCT CTG
                                ||||||||   ||| |||
                                GTATTCCA   AGA GAC
                                     AAA   G
GAM586  LOC256581 5'  GCCAGAAGACAGAACCTCTAAG 97573     CCATA      _  GAGA
           TG                     CAC     AGGTTCTG CT    GC
                                |||     |||||||| ||    ||
                                GTG     TCCAAGAC GA    CG
                                  AATC_       A  AGAC
GAM586  LOC257437 3'  GCTCCCAGCAGAGCAGAGAGGG 91269       ATAAG        A
           TG                     CACCC     GTTCTGCTG GAGC
                                |||||     ||||||||| ||||
                                GTGGG     CGAGACGAC CTCG
                                   AGAGA        C
GAM586  LOC257545 3'  GCCCTCAGCAGAGAATTA    97806     GG        A
                                TAA  TTCTGCTGAG GC
                                |||  |||||||||| ||
                                ATT  GAGACGACTC CG
                                  AA         C
GAM586  LOC257598 3'  GCCCTCAGCAGAGAATTA    97921     GG        A
                                TAA  TTCTGCTGAG GC
                                |||  |||||||||| ||
                                ATT  GAGACGACTC CG
                                  AA         C
GAM586  LOC55893  3'  GCCCTCAGCAGAAACC      37862      _       A
                                GGTT CTGCTGAG GC
                                |||| |||||||| ||
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                                CCAA GACGACTC CG
                                  A       C
GAM586  LOC90784  5'  GCTCTCAGTTTTGGACCTTA  64002        T__
                                TAAGGTTC  GCTGAGAGC
                                ||||||||  |||||||||
                                ATTCCAGG  TGACTCTCG
                                    TTT
GAM586  LOC93082  3'  GCTCCCAACACCCATGCCATGG 56445      AA  TC___  C  A
          G                      CCCAT  GGT    TG TG GAGC
                                |||||  |||    || || ||||
                                GGGTA  CCG    AC AC CTCG
                                  __  TACCC  A  C
GAM587  ADAM19   3'  CAGGAAGAAGACTGGCCATTAT 52703      C   CTGAG
          G                      CATGA GGCT    TTCTTCCTG
                                ||||| ||||    |||||||||
                                GTATT CCGG    AAGAAGGAC
                                  A   TCAG_
GAM587  FACL5    5'  CAGGAAGAACTCAGAGCCG   64186
                                CGGCTCTGAGTTCTTCCTG
                                ||||||||||||||||||
                                GCCGAGACTCAAGAAGGAC

GAM587  GNAL     5'  CAGGAAAGAGAGGAGCCGTCG  9058         GAG TC
                                TGACGGCTCT  T  TTCCTG
                                ||||||||||  |  ||||||
                                GCTGCCGAGG  A  AAGGAC
                                    AG_ GA
GAM587  KAL1     3'  CAGGAAGAACTTCTGTCA    4013       CTCT
                                TGACGG   GAGTTCTTCCTG
                                ||||||   ||||||||||||
                                ACTGTC   TTCAAGAAGGAC
                                  ____
GAM587  MYO1E    3'  CAGGAGGACAAAACCACCATG  17187     AC  CTC  AGT
                                CATG  GG  TG  TCTTCCTG
                                ||||  ||  ||  ||||||||
                                GTAC  CC  AC  AGGAGGAC
                                  CA  AAA  ___
GAM587  PRKAR2B  3'  CAGAAAGAACTCAGATGT    10804   _        C
                                GC TCTGAGTTCTT CTG
                                || ||||||||||| |||
                                TG AGACTCAAGAA GAC
                                 T         A
GAM587  PUM2     3'  AGGATCAAAGCTGTCATG    31014         C  GTTCT
                                CATGACGGCT TGA    TCCT
                                |||||||||| |||    ||||
                                GTACTGTCGA ACT    AGGA
                                    A  _____
GAM587  SKI      3'  CAGGAAGTGCAGAGCCGCA   11701    A      AGTT
                                TG CGGCTCTG   CTTCCTG
                                || ||||||||   |||||||
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                                AC GCCGAGAC    GAAGGAC
                                 _       GT__
GAM587  TEM8     3'  AGGAAGATGCAACCCCATG   36326      AC  CTC  AGT
                                CATG  GG   TG   TCTTCCT
                                ||||  ||   ||   |||||||
                                GTAC  CC   AC   AGAAGGA
                                  C_  A__  GT_
GAM587  ARHGEF4  5'  AGAAAAAACTCAGGGC      52207          C  C
                                GCTCTGAGTT TT CT
                                |||||||||| || ||
                                CGGGACTCAA AA GA
                                      A  A
GAM587  FLJ31978 3'  CAGGAAGGAACAAGCGCC    58348     T  GAG
                                GGC CT   TTCTTCCTG
                                ||| ||   |||||||||
                                CCG GA   AGGAAGGAC
                                  C  ACA
GAM587  HSU24186 5'  AGAACTCAAAGCCGTC      25324        C
                                GACGGCT TGAGTTCT
                                ||||||| ||||||||
                                CTGCCGA ACTCAAGA
                                    A
GAM587  KCNT1    3'  AGCTCCCAGGGCCGCCA     61825    A      __
                                TG CGGCTCT  GAGTT
                                || |||||||  |||||
                                AC GCCGGGA  CTCGA
                                 C      CC
GAM587  KIAA1867 3'  CAGGAAGAACCCAAGAGCTCAT 94822      CG     GA_
                                ATGA  GCTCT   GTTCTTCCTG
                                ||||  |||||   ||||||||||
                                TACT  CGAGA   CAAGAAGGAC
                                  __    ACC
GAM587  KIAA1878 3'  AATTCAGAGAATCGTCATG   91707         __
                                CATGACGG  CTCTGAGTT
                                ||||||||  |||||||||
                                GTACTGCT  GAGACTTAA
                                    AA
GAM587  MFN1     3'  CAGGAAGAACTCATGA      35541    _
                                TC TGAGTTCTTCCTG
                                || ||||||||||||
                                AG ACTCAAGAAGGAC
                                 T
GAM587  MIDORI   3'  CAGGGCCCTTCCAGAGCCTGTC 73784        _      AGTTCT
           ATG                    CATGAC GGCTCTG     TCCTG
                                ||||||| |||||||      |||||
                                GTACTG CCGAGAC      GGGAC
                                   T      CTTCCC
GAM587  MYH7B    3'  CAGGAAGAACCTGGCTCGCATG 70530      A  _  CTGA
                                CATG CG GCT    GTTCTTCCTG
                                |||| || |||    ||||||||||
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                                GTAC GC CGG    CAAGAAGGAC
                                  _ T   TC__
GAM587  RNAHP     3'  AGAAAGCAGCAGCCGTCAT   23761         _   AG
                                ATGACGGCT CTG  TTCT
                                ||||||||| |||  ||||
                                TACTGCCGA GAC  AAGA
                                     C   GA
GAM587  SLC37A1   3'  AGACGGAGCTCAGACCC     38561    C        TC
                                GG TCTGAGTTCT  CT
                                || ||||||||||  ||
                                CC AGACTCGAGG  GA
                                 C         CA
GAM587  LOC116236 3'  CAGGAAAAGCACAAACCTCAT  73809     C  CTC  A   C
                                ATGA GG   TG GTT TTCCTG
                                |||| ||   || ||| ||||||
                                TACT CC   AC CGA AAGGAC
                                  _ AA_  A   A
GAM587  LOC124801 3'  CAGGAAGAACTCTCTTGCATG  74336     A   CTCT
                                CATG CGG    GAGTTCTTCCTG
                                |||| |||    ||||||||||||
                                GTAC GTT    CTCAAGAAGGAC
                                  _   CT__
GAM587  LOC222160 5'  AGGAAGAACTCACCCC      94117    CTC
                                GG   TGAGTTCTTCCT
                                ||   ||||||||||||
                                CC   ACTCAAGAAGGA
                                 CC_
GAM587  LOC51094  3'  CAGGAAGAATAAAGCC      32045      CTGA
                                GGCT    GTTCTTCCTG
                                ||||    ||||||||||
                                CCGA    TAAGAAGGAC
                                  AA__
GAM587  LOC92078  3'  CAGGAAGAAGAATCGACCGTC  67977      C  T  G__
                                GACGG TC GA   TTCTTCCTG
                                ||||| || ||   |||||||||
                                CTGCC AG CT   AAGAAGGAC
                                   _ _  AAG
GAM588  FACL6     3'  ACACAGCTGAAAATGAATA    30919        C  GTCC
                                TATTCAT TT    CGGCTGTGT
                                ||||||| ||    |||||||||
                                ATAAGTA AA    GTCGACACA
                                    A _____
GAM588  LY9       3'  ACACATGACACAAGATG      71681         CC  GC
                                CATCTTGT  CG  TGTGT
                                ||||||||  ||  |||||
                                GTAGAACA  GT  ACACA
                                     CA  __
GAM588  PLS1      3'  ATGGTTCAAAAAAGATGAATA  10657          GTCCC
                                TATTCATCTT    GGCTGT
                                ||||||||||    ||||||
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                                ATAAGTAGAA    TTGGTA
                                      AAAAC
GAM588  AQP9     3'  ACTGCAGGAGACAAGATGAAT  40606          _  G  T
                                ATTCATCTTGTC CC GC GT
                                |||||||||||| || || ||
                                TAAGTAGAACAG GG CG CA
                                      A  A  T
GAM588  CXYorf1  3'  ACACAGCCAGGACAAGCTG   82035    T      C
                                CA CTTGTCC GGCTGTGT
                                || ||||||| ||||||||
                                GT GAACAGG CCGACACA
                                 C      A
GAM588  EIF2S1   3'  ACAGCAGGGACAAGAT      14582          G
                                ATCTTGTCCC GCTGT
                                |||||||||| |||||
                                TAGAACAGGG CGACA
                                      A
GAM588  FLJ00007 3'  ACACAGCCAAAAGCTGGA    71270      T   GTCCC
                                TTCA CTT    GGCTGTGT
                                |||| |||    ||||||||
                                AGGT GAA    CCGACACA
                                  C   AA___
GAM588  FLJ23590 3'  ACACAGTTTGTAACAAGA    45013       CC  _
                                TCTTGT  CGG CTGTGT
                                ||||||  ||| ||||||
                                AGAACA  GTT GACACA
                                    AT   T
GAM588  HDAC9-PENDING 3'  ACACAGTAACAGGATGAATA  28174          CCCG
                                TATTCATCTTGT   GCTGTGT
                                ||||||||||||   |||||||
                                ATAAGTAGGACA   TGACACA
                                      A___
GAM588  HEY2     3'  CCAAAACAAGATGAATG     24316          CCC
                                TATTCATCTTGT   GG
                                ||||||||||||   ||
                                GTAAGTAGAACA   CC
                                      AAA
GAM588  KIAA0391 3'  GGAACACAGATGAATA      27917         _   C
                                TATTCATCT TGT CC
                                ||||||||| ||| ||
                                ATAAGTAGA ACA GG
                                     C   A
GAM588  KIAA1056 3'  ACTTGAGGGAAAGATGAATA  29689         G   GGCT
                                TATTCATCTT TCCC   GT
                                |||||||||| ||||   ||
                                ATAAGTAGAA AGGG   CA
                                      _   AGTT
GAM588  MSTP032  3'  ACACAGCCAGGAGAATGAA   47437      CT G   C
                                TTCAT  T TCC GGCTGTGT
                                |||||  | ||| ||||||||
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                                AAGTA  A AGG CCGACACA
                                  __ G   A
GAM588  NIFU     5'  CACAGCCAGGAAGGA      67312      G   C
                                TCTT TCC GGCTGTG
                                |||| ||| |||||||
                                AGGA AGG CCGACAC
                                  _   A
GAM588  PRO1600  3'  ACACAGCCAGCAAATGAA    26031      C    CCC
                                TTCAT TTGT   GGCTGTGT
                                ||||| ||||   ||||||||
                                AAGTA AACG   CCGACACA
                                  _    A__
GAM588  SIAT4A   5'  CACAGCCGATGACAGA      11668     T   C_
                                TCT GTC  CGGCTGTG
                                ||| |||  ||||||||
                                AGA CAG  GCCGACAC
                                  _   TA
GAM588  SNAP91   3'  ACACAGCCGTGAAAGTGAA   29265      T   G  C
                                TTCA CTT TC CGGCTGTGT
                                |||| ||| || |||||||||
                                AAGT GAA AG GCCGACACA
                                  _   _ T
GAM588  LOC147991 5'  ACACAGCCAGAGATCAAT    78601     C    GTCCC
                                ATT ATCTT    GGCTGTGT
                                ||| |||||    ||||||||
                                TAA TAGAG    CCGACACA
                                  C    A_____
GAM588  LOC149296 5'  ACACAGCCAACTAGTTATGA   79255      __  T  CCC
                                TCAT  CT GT   GGCTGTGT
                                ||||  || ||   ||||||||
                                AGTA  GA CA   CCGACACA
                                  TT  T  A__
GAM588  LOC200093 3'  ACACAGCCAGGACAAGCTG    63085    T      C
                                CA CTTGTCC GGCTGTGT
                                || ||||||| ||||||||
                                GT GAACAGG CCGACACA
                                 C      A
GAM588  LOC91040  3'  ACACAGCCAGGACAAGCTG    64707    T      C
                                CA CTTGTCC GGCTGTGT
                                || ||||||| ||||||||
                                GT GAACAGG CCGACACA
                                 C      A
GAM589  GPR56    3'  CCACCTGCCCATGTGATGAA   19068    G   T   AAA   A
                                TT ATCA CGTG   GCAG TGG
                                || |||| ||||   |||| |||
                                AA TAGT GTAC   CGTC ACC
                                 G   _   C__   C
GAM589  KAL1     3'  TCCAGTATTATTCAAATGATCA 4017         CG   AGCAGA
            A                    TTGATCAT  TGAA     TGGA
                                ||||||||  ||||     ||||
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                                AACTAGTA  ACTT     ACCT
                                    A_    ATTATG
GAM589  FLJ14107  3'  GCTTCCAGGATGATCAA     46695         G  A
                                TTGATCATC TG AAGC
                                ||||||||| || ||||
                                AACTAGTAG AC TTCG
                                    G  C
GAM589  PRO2325   5'  CCATCTGCCTCAGTCTGGGCCA 37588     AT ATCG_   AA
          A                      TTG  C    TGA  GCAGATGG
                                ||| |    |||  ||||||||
                                AAC  G    ACT  CGTCTACC
                                  CG GTCTG   C_
GAM589  LOC119369 3'  CCAAAGGCCTTCAAATGATCAA 75510         CG    A  AGA
                                TTGATCAT  TGAA GC   TGG
                                ||||||||  |||| ||   |||
                                AACTAGTA  ACTT CG   ACC
                                    A_    C  GAA
GAM590  CSNK1G2   3'  GGCCCAGCCCTGCAGGT     7170         AAC   ACTT
                                ACCTGTAG   CTG    GGCC
                                ||||||||   |||    ||||
                                TGGACGTC   GAC    CCGG
                                    CC_   ____
GAM590  PCDH11X   3'  CAATCATATTCTACAG      27238         CC   C
                                CTGTAGAA  TGA TTG
                                ||||||||  ||| |||
                                GACATCTT  ACT AAC
                                    AT   _
GAM590  SFTPA2    3'  GGTCAGGCTCTCCAGGTG    22650       T   A
                                CACCTG AGA CCTGACT
                                |||||| ||| |||||||
                                GTGGAC TCT GGACTGG
                                   C   C
GAM590  TBX5      5'  CCAAGTCCTATAGGTG      3956          AACCT
                                CACCTGTAG    GACTTGG
                                |||||||||    |||||||
                                GTGGATATC    CTGAACC
                                             _____
GAM590  TBX5      5'  CCAAGTCCTATAGGTG      54888         AACCT
                                CACCTGTAG    GACTTGG
                                |||||||||    |||||||
                                GTGGATATC    CTGAACC
                                             _____
GAM590  ZNF132    3'  GCCAAGTCAAACTTCATGCAG  12826      _  CC_
                                CTGTA GAA   TGACTTGGC
                                ||||| |||   |||||||||
                                GACGT CTT   ACTGAACCG
                                   A   CAA
GAM590  C9orf14   5'  GCCAAGTCCATCTAAAGTG   86676     CTG   ACCT
                                CAC   TAGA   GACTTGGC
                                |||   ||||   ||||||||
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                                GTG   ATCT    CTGAACCG
                                  AA_    AC__
GAM590  DKFZP434J037 3' GCCCGGTCAGGCTCTCAG    48213     T   A      T
                                CTG AGA CCTGACT GGC
                                ||| ||| ||||||| |||
                                GAC TCT GGACTGG CCG
                                  _  C      C
GAM590  ELOVL2   3' GCCTAGGTTATACAG       34959      G     ACTT
                                CTGTA AACCTG    GGC
                                ||||| ||||||    |||
                                GACAT TTGGAT    CCG
                                   A     _____
GAM590  FLJ11996 3' TTAGGTGCCTACAGGT      46447         A_
                                ACCTGTAG  ACCTGA
                                ||||||||  ||||||
                                TGGACATC  TGGATT
                                     CG
GAM590  FLJ13265 3' GCCAGAACTTTACAGGTG    45926          ACCTGAC
                                CACCTGTAGA      TTGGC
                                ||||||||||      |||||
                                GTGGACATTT      GACCG
                                      CAA_____
GAM590  FLJ20038 5' CCAAGTCAGAACTGCG      34402       AAC
                                TGTAG   CTGACTTGG
                                |||||   |||||||||
                                GCGTC   GACTGAACC
                                   AA_
GAM590  FLJ20972 3' GCCAAGTCAGTTCCTGGTG   46725      TGTA    C
                                CACC    GAAC TGACTTGGC
                                ||||    |||| |||||||||
                                GTGG    CTTG ACTGAACCG
                                  TC__    _
GAM590  KIAA0061 3' GCCAAGTTCTACATGTG     68292     C     ACCTG
                                CAC TGTAGA    ACTTGGC
                                ||| ||||||    |||||||
                                GTG ACATCT    TGAACCG
                                  T     ______
GAM590  KIAA0141 3' CGGGAGTTCAGGTTCCCAAG  28732    GTA       _   GG
                                CT   GAACCTGA CTT  CCG
                                ||   |||||||| |||  |||
                                GA   CTTGGACT GAG  GGC
                                 ACC       T   __
GAM590  KIAA1260 3' GTCAGGTTGCACAGGTG     60029        AG
                                CACCTGT  AACCTGAC
                                |||||||  ||||||||
                                GTGGACA  TTGGACTG
                                     CG
GAM590  KIAA1301 3' GCCTATGGGTTTACAGG     66342         A    ACTT
                                CCTGTAGA CCTG    GGC
                                |||||||| ||||    |||
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                                GGACATTT GGGT   CCG
                                    _   AT__
GAM590  KIAA1485  3'  GGCTGCCAGGCTCTGCAGG   89262       A   ACT
                                CCTGTAGA CCTG  TGGCC
                                |||||||| ||||  |||||
                                GGACGTCT GGAC  GTCGG
                                    C   C__
GAM590  KIAA1546  3'  CAGGCAAACACCTACAGGT   67904       AACC_  A
                                ACCTGTAG    TG CTTG
                                ||||||||    || ||||
                                TGGACATC    AC GGAC
                                    CACAA  _
GAM590  KIAA1643  3'  CACCTCAGGTTCCCAGGTG   64548      TA      CT
                                CACCTG  GAACCTGA  TG
                                ||||||  ||||||||  ||
                                GTGGAC  CTTGGACT  AC
                                   C_       CC
GAM590  MGC10981  3'  CTGAGTCGATCCCACAGGTG   51017      A_  ACC    TG
                                CACCTGT  GA   TGACT  G
                                |||||||  ||   |||||  |
                                GTGGACA  CT   GCTGA  C
                                    CC  A__    GT
GAM590  MGC11324  3'  AGGCAGAACCTACAGGTG    51164       AAC   A
                                CACCTGTAG   CTG CTT
                                |||||||||   ||| |||
                                GTGGACATC   GAC GGA
                                     CAA  _
GAM590  MOST2     5'  CGGCCAAGCCTGTGCCTACGGT 39682     T    A_  CTGA
          G                      CACC GTAG  AC    CTTGGCCG
                                |||| ||||  ||    ||||||||
                                GTGG CATC  TG    GAACCGGC
                                  _    CG  TCC_
GAM590  PADI3     3'  CGGCCAAGCTCCTGC      32657      AACCT  _
                                GTAG    GA CTTGGCCG
                                ||||    || ||||||||
                                CGTC    CT GAACCGGC
                                  _____  C
GAM590  phospho1  5'  CAGAGTCCCTACAGGTG     82367        A_  _
                                CACCTGTAG  AC CTG
                                |||||||||  || |||
                                GTGGACATC  TG GAC
                                     CC  A
GAM590  RAB3D     3'  TGGCTGCCAGGTTCCTCAGG   15010     TA      ACT
                                CCTG  GAACCTG   TGGCCG
                                ||||  |||||||   ||||||
                                GGAC  CTTGGAC   GTCGGT
                                  TC      C__
GAM590  LOC122955 5'  GCTGTCAGTTCTACAG      75585        C    TT
                                CTGTAGAAC TGAC  GGC
                                ||||||||| ||||  |||
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                                GACATCTTG ACTG  TCG
                                      _   __
GAM590  LOC149386 5'  CAAGTCAGGTCCACA       84404     A  A
                                TGT GA CCTGACTTG
                                ||| || |||||||||
                                ACA CT GGACTGAAC
                                  C  _
GAM590  LOC150197 5'  GCCAGGTCCTACGG        79598       AACCT
                                CTGTAG    GACTTGGC
                                ||||||    ||||||||
                                GGCATC    CTGGACCG
                                     _____
GAM590  LOC151878 5'  CTAGTTCAGACTCTAAGG    80374     G    AC    C
                                CCT TAGA  CTGA TTGG
                                ||| ||||  |||| ||||
                                GGA ATCT  GACT GATC
                                  _    CA    T
GAM590  LOC153146 5'  GCCAGAGCCTACAGGT      85929        AAC  GAC
                                ACCTGTAG   CT   TTGGC
                                ||||||||   ||   |||||
                                TGGACATC   GA   GACCG
                                     C__  ___
GAM590  LOC221931 3'  AAGTTGCAGGTTCTTCAG    93992     T       __
                                CTG AGAACCTG  ACTT
                                ||| ||||||||  ||||
                                GAC TCTTGGAC  TGAA
                                  T       GT
GAM590  LOC254848 5'  CGGCAGGCACAGGTTCTCCA  97090    T      A_   G
                                TG AGAACCTG  CTTG CCG
                                || ||||||||  |||| |||
                                AC TCTTGGAC  GGAC GGC
                                 C       AC   _
GAM591  ADCY7     3'  TTGAAAGTCAACCTAACTGTA  6648        _  T  GGATA
                                TACAGT AG GT    ACTTTCAA
                                |||||| || ||    ||||||||
                                ATGTCA TC CA    TGAAAGTT
                                    A  _  AC___
GAM591  CALM2     3'  AAAGTTGCACTATTG       8225          GGAT
                                CAGTAGTGT    AACTTT
                                |||||||||    ||||||
                                GTTATCACG    TTGAAA
                                     _____
GAM591  MMP16     3'  TTGAAAACAACAAAACACTACT 42590         GGATAAC_
                                AGTAGTGT       TTTCAA
                                ||||||||       ||||||
                                TCATCACA       AAAGTT
                                     AAACAACA
GAM591  MSL3L1    3'  GAGTTGCCCACATACTG     22309      G    A
                                CAGTA TGTGG TAACTT
                                ||||| ||||| ||||||
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                                GTCAT ACACC GTTGAG
                                   _    C
GAM591  MSL3L1   3' AAAGTCATCCCAGTGC     54358    G  T   A
                                GTA TG GGAT ACTTT
                                ||| || |||| |||||
                                CGT AC CCTA TGAAA
                                  G  _   C
GAM591  MSL3L1   3' GAGTTGCCCACATACTG     54372     G    A
                                CAGTA TGTGG TAACTT
                                ||||| ||||| ||||||
                                GTCAT ACACC GTTGAG
                                   _    C
GAM591  MSL3L1   3' GAGTTGCCCACATACTG     54374     G    A
                                CAGTA TGTGG TAACTT
                                ||||| ||||| ||||||
                                GTCAT ACACC GTTGAG
                                   _    C
GAM591  TBX6     3' AAAGCCATCCATGCTCA     16036   T      AA
                                G AGTGTGGAT  CTTT
                                | |||||||||  ||||
                                A TCGTACCTA  GAAA
                                 C       CC
GAM591  ZFHX1B   3' AAGGTGCCCGCACTAC      28919        ATA
                                GTAGTGTGG   ACTTT
                                |||||||||   |||||
                                CATCACGCC   TGGAA
                                     CG_
GAM591  ACYP2    3' TGAAAGCTAAGCGACTGTA   56614      A  G   ATAA
                                TACAGT GT TGG    CTTTCA
                                |||||| || |||    ||||||
                                ATGTCA CG ATC    GAAAGT
                                   G  A  ____
GAM591  DKFZP564D1378 3'  TTGAAAACTAAATTTTCTACTG 49529        TGTGGATAAC
           TA                   TACAGTAG        TTTCAA
                                ||||||||        ||||||
                                ATGTCATC        AAAGTT
                                     TTTTAAATCA
GAM591  FLJ10724  3' AAAGTCATCCTCCTACTCA   36498   C    TGT   A
                                A AGTAG   GGAT ACTTT
                                | |||||   |||| |||||
                                A TCATC   CCTA TGAAA
                                 C    CT_   C
GAM591  FLJ10846  3' TGAAAGCCAGGTACAACTACTG 36745       _  GATAA
                                CAGTAGT GTG    CTTTCA
                                ||||||| |||    ||||||
                                GTCATCA CAT    GAAAGT
                                    A  GGACC
GAM591  FLJ14100  3' GAGATCACACTACTG      46681          ATAAC
                                CAGTAGTGTGG    TTTC
                                ||||||||||    ||||
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                                GTCATCACACT    AGAG
                                           _____
GAM591  HH114    3'  GAAACCACTACTGTA      50687         TGGATAAC
                                TACAGTAGTG      TTTC
                                ||||||||||      ||||
                                ATGTCATCAC      AAAG
                                     C_______
GAM591  IPLA2(GAMMA) 3'  GAAAGCTATATTGTACTGTG   60691       __    ATAA
                                TACAGTA  GTGTGG   CTTTC
                                |||||||  ||||||   |||||
                                GTGTCAT  TATATC   GAAAG
                                   GT    _____
GAM591  KIAA1210  3'  GAAAACATTTGCACTGCTGTA  96330         TG   AAC
                                TACAGTAGTG  GAT   TTTC
                                ||||||||||  |||   ||||
                                ATGTCGTCAC  TTA   AAAG
                                     GT   CA_
GAM591  KIAA1363  3'  TTGAAAGTTACTTTCTACCACT 69267      _   ___
           AT                    GTAGTG TGGA   TAACTTTCAA
                                 ||||||  ||||   ||||||||||
                                 TATCAC ATCT   ATTGAAAGTT
                                    C    TTC
GAM591  NXP-2    3'  TGAAAACCATAATCTTTACTGT 71109        ____    ATAAC
           A                     TACAGTAG    TGTGG    TTTCA
                                 ||||||||    |||||    |||||
                                 ATGTCATT    ATACC    AAAGT
                                      TCTA    A____
GAM591  PPP1R10   3'  TGAAAGTCACACTAC       10738        GATA
                                GTAGTGTG    ACTTTCA
                                ||||||||    |||||||
                                CATCACAC    TGAAAGT
                                           _____
GAM591  SEZ6     3'  TGAAAGCCACTTTGTACATGTA 74367      _  GT__   ATAA
                                TACA GTA    GTGG    CTTTCA
                                |||| |||    ||||    ||||||
                                ATGT CAT    CACC    GAAAGT
                                  A  GTTT   _____
GAM591  SLC38A1   3'  TGAAAGTTATAGGGCACTGC   47725        GG_
                                GTAGTGT   ATAACTTTCA
                                |||||||   ||||||||||
                                CGTCACG   TATTGAAAGT
                                    GGA
GAM591  SPANXB1   5'  AAAGCTCCAAAAACCTACTGTA 50606         TG___   TAA
                                TACAGTAG    TGGA   CTTT
                                ||||||||    ||||   ||||
                                ATGTCATC    ACCT   GAAA
                                     CAAAA    C__
GAM591  LOC113146 5'  TTGAAAGTCAAGAGGTCACTAT 72975        TGGATA__
                                GTAGTG       ACTTTCAA
                                ||||||       ||||||||
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                                TATCAC       TGAAAGTT
                                   TGGAGAAC
GAM591   LOC129868 5'  GAAAGCTACCAGCACTGC    57128       _  A  A
                                GTAGTG TGG TA CTTTC
                                |||||| ||| || |||||
                                CGTCAC ACC AT GAAAG
                                   G  _  C
GAM591   LOC130633 5'  GAAAGCTACCAGCACTGC    74964       _  A  A
                                GTAGTG TGG TA CTTTC
                                |||||| ||| || |||||
                                CGTCAC ACC AT GAAAG
                                   G  _  C
GAM591   LOC202559 3'  TTGAAAACAAGCAGCTACTGTA 89199        _  GGATAAC
                                TACAGTAG TGT      TTTCAA
                                |||||||| |||      ||||||
                                ATGTCATC ACG      AAAGTT
                                     G  AACA___
GAM591   LOC221035 3'  TTGAAAACCAGGTATCCACAC  93173        A  ____
                                GTGTGGATA CT    TTCAA
                                ||||||||| ||    |||||
                                CACACCTAT GA    AAGTT
                                     G  CCAA
GAM591   LOC222161 5'  TTGAAAGTGCAACATTACTGTA 92801         GGATA
                                TACAGTAGTGT    ACTTTCAA
                                ||||||||||    ||||||||
                                ATGTCATTACA    TGAAAGTT
                                      ACG__
GAM592   AMPD3    3'  CTGGATTTCCTTATTCC     4897      CTA  A
                                GGA  GAG GAAATCCAG
                                |||  ||| |||||||||
                                CCT  TTC CTTTAGGTC
                                  TA_  _
GAM592   CDK10    3'  CTGAGCTGGATCCCTGCTC    13401     _  AA
                                GAG AG  ATCCAGCTCAG
                                ||| ||  ||||||||||
                                CTC TC  TAGGTCGAGTC
                                  G  CC
GAM592   CDK10    3'  CTGAGCTGGATCCCTGCTC    53768     _  AA
                                GAG AG  ATCCAGCTCAG
                                ||| ||  ||||||||||
                                CTC TC  TAGGTCGAGTC
                                  G  CC
GAM592   CDK10    3'  CTGAGCTGGATCCCTGCTC    53777     _  AA
                                GAG AG  ATCCAGCTCAG
                                ||| ||  ||||||||||
                                CTC TC  TAGGTCGAGTC
                                  G  CC
GAM592   CLTCL1   3'  CTGAGCTGGCCATCCTCTACTC 63671     C    A  AAT
            C                    GGA TAGAG GA   CCAGCTCAG
                                ||| ||||| ||   |||||||||
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                                CCT ATCTC CT   GGTCGAGTC
                                  C    _ ACC
GAM592  MCL1    3'  CTGAACTCTTTCTAGCC    41717   A      AATC
                                GG CTAGAGAGA   CAG
                                || |||||||||   |||
                                CC GATCTTTCT   GTC
                                  _       CAA_
GAM592  MDM1    3'  CTGAGCTGACTTCTACCTAGCC 39271   A   AG   ATC
                                GG CTAG  AGAA  CAGCTCAG
                                || ||||  ||||  ||||||||
                                CC GATC  TCTT  GTCGAGTC
                                  _   CA   CA_
GAM592  PML     3'  CTGAGCTGCCTCCTCCAGCCC  52661   A A  A AATC
                                GG CT GAG GA   CAGCTCAG
                                || || ||| ||   ||||||||
                                CC GA CTC CT   GTCGAGTC
                                  C  C  _ CC__
GAM592  PML     3'  CTGAGCTGCCTCCTCCAGCCC  52667   A A  A AATC
                                GG CT GAG GA   CAGCTCAG
                                || || ||| ||   ||||||||
                                CC GA CTC CT   GTCGAGTC
                                  C  C  _ CC__
GAM592  PML     3'  CTGAGCTGCCTCCTCCAGCCC  52673   A A  A AATC
                                GG CT GAG GA   CAGCTCAG
                                || || ||| ||   ||||||||
                                CC GA CTC CT   GTCGAGTC
                                  C  C  _ CC__
GAM592  SHOX    3'  TGAGCTGAACTGTAGATCC   4839    _  G AGAAATC
                                GGA CTA AG     CAGCTCA
                                ||| ||| ||     |||||||
                                CCT GAT TC     GTCGAGT
                                  A  G AA_____
GAM592  TRPM1   5'  CTGAGCTGTGCCCTCTCCATTC 10057   CTA   AAATC
          C                      GGA  GAGAG   CAGCTCAG
                                |||  |||||   ||||||||
                                CCT  CTCTC   GTCGAGTC
                                  TAC   CCGT_
GAM592  ELOVL1  5'  GGACTTCTCTCTGGCC    43062   A      A
                                GG CTAGAGAGAA TCC
                                || |||||||||| |||
                                CC GGTCTCTCTT AGG
                                  _       C
GAM592  FLJ20296 5' CTGACGCGTTTCTCTCCATTCC 34890   CTA      CCA _
                                GGA  GAGAGAAAT  GC TCAG
                                |||  |||||||||  || ||||
                                CCT  CTCTCTTTG  CG AGTC
                                  TAC       ___ C
GAM592  FLJ20721 3' GACTTCTCTCTAGTGC    35609  G       A
                                G ACTAGAGAGAA TC
                                | ||||||||||| ||
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                                C TGATCTCTCTT AG
                                 G         C
GAM592  KIAA0265  3'  AGCGACCTCTTCTCTAGTCC   69874          _  AA  CA
                                GGACTAGAGA GA  TC  GCT
                                |||||||||| ||  ||  |||
                                CCTGATCTCT CT  AG  CGA
                                      T  CC  __
GAM592  KIAA0285  3'  GCTAGATGCCCTCTCTAGTCC  29018           AA_  C
                                GGACTAGAGAG   ATC AGC
                                ||||||||||   ||| |||
                                CCTGATCTCTC   TAG TCG
                                       CCG   A
GAM592  KIAA0820  3'  CTGAGCTGAATCTTAAAAAGCC 69023    ACTAGA    AATC
                                GG     GAGA    CAGCTCAG
                                ||     ||||    ||||||||
                                CC     TTCT    GTCGAGTC
                                 GAAAAA    AA__
GAM592  KIAA1274  3'  GGCATCTCTCTCTGTCC     91367      T      A  _
                                GGAC AGAGAGA AT CC
                                |||| ||||||| || ||
                                CCTG TCTCTCT TA GG
                                  _      C  C
GAM592  KIAA1831  3'  CTGAGCTGCTGTGGCTCCCTAG 63782    A    A   AA  C_
          CC                      GG CTAG GAG  AT  CAGCTCAG
                                || |||| |||  ||  ||||||||
                                CC GATC CTC  TG  GTCGAGTC
                                 _   C   GG  TC
GAM592  MGC2560   5'  CTGAGCTGGATTGACATAGCC  48781    A   GAGAGA
                                GG CTA     AATCCAGCTCAG
                                || |||     ||||||||||||
                                CC GAT     TTAGGTCGAGTC
                                 _  ACAG__
GAM592  Rab11-FIP3 3'  CTGAGCTGGATTCGGGACTC   28125     AGA__
                                GAG    AATCCAGCTCAG
                                |||    ||||||||||||
                                CTC    TTAGGTCGAGTC
                                  AGGGC
GAM592  UGT2B10   3'  CTGAGCTGGAGCCTCCATGCC  6541     ACTAGA   AAA
                                GG     GAG   TCCAGCTCAG
                                ||     |||   ||||||||||
                                CC     CTC   AGGTCGAGTC
                                 GTAC__   CG_
GAM592  LOC145815 5'  GGATTTCTCCCTGACCC     83519    AC   A
                                GG  TAG GAGAAATCC
                                ||  ||| |||||||||
                                CC  GTC CTCTTTAGG
                                 CA   C
GAM592  LOC146745 5'  TGAGCTGAGGCTGCAGTCC    78091       AG  AGAAATC
                                GGACT  AG      CAGCTCA
                                |||||  ||      |||||||
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                                CCTGA  TC      GTCGAGT
                                  CG  GGA____
GAM592  LOC201243 5'  TGAGCTGAGGCTGCAGTCC   88163       AG  AGAAATC
                                GGACT  AG      CAGCTCA
                                |||||  ||      |||||||
                                CCTGA  TC      GTCGAGT
                                  CG  GGA____
GAM592  LOC221929 3'  CTGAGCTGGACTTCCTCCTCC  92675     CTA   A   A
                                GGA   GAG GAA TCCAGCTCAG
                                |||   ||| ||| ||||||||||
                                CCT   CTC CTT AGGTCGAGTC
                                  C__   _   C
GAM592  LOC51042  5'  GAGCGCACTCTCTAGCC     31854     A       AAATCCA
                                GG CTAGAGAG      GCTC
                                || ||||||||      ||||
                                CC GATCTCTC      CGAG
                                 _       ACG____
GAM592  LOC56912  3'  TGAGCTGGCCCCTCTGCC    39337    AC    AGAAAT
                                GG  TAGAG     CCAGCTCA
                                ||  |||||     ||||||||
                                CC  GTCTC     GGTCGAGT
                                 __     CCC___
GAM593  TNFAIP1   3'  CATCAGCTGAGGACAGCAAACT 40917     AG     G
                   CC                GGA  TTGCTG CTTCAGCTGATG
                                |||  |||||| ||||||||||||
                                CCT  AACGAC GGAGTCGACTAC
                                  CA     A
GAM593  C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 21681     AA       _ ___
                   CCC                GG  GTTGCTGG CT   TCAGCTG
                                ||  |||||||| ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM593  C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 94622     AA       _ ___
                   CCC                GG  GTTGCTGG CT   TCAGCTG
                                ||  |||||||| ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM593  C20orf59  3'  CATCCCTAGCCAGCAGCTCC   41992     A        TC  CT
                                GGA GTTGCTGGCT  AG  GATG
                                ||| ||||||||||  ||  ||||
                                CCT CGACGACCGA  TC  CTAC
                                  _        __ C_
GAM593  FLJ20079  3'  CATTCTGGTAAACCAGCAGCCT 34490     A       CT__    CT
                   CC                GGA GTTGCTGG    TCAG  GATG
                                ||| ||||||||    ||||  ||||
                                CCT CGACGACC    GGTC  TTAC
                                  C       AAAT   __
GAM593  SSAT2     3'  CATCAGCTGAAGCACTCTTC   56041      TTGCTG
                                GAAG     GCTTCAGCTGATG
                                ||||     ||||||||||||
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                                CTTC     CGAAGTCGACTAC
                                  TCA___
GAM593  SYNJ2    3'  ATCAGCTTAAGCAATTCC    61763     GTTGCTG   C
                                GGAA      GCTT AGCTGAT
                                ||||      |||| |||||||
                                CCTT      CGAA TCGACTA
                                  AA_____   T
GAM593  LOC162333 5'  CTGAAGCCAGCAATTCC     87131      G
                                GGAA TTGCTGGCTTCAG
                                |||| ||||||||||||
                                CCTT AACGACCGAAGTC
                                  _
GAM593  LOC222060 5'  CACCTCCCACCAGCAACCCCC  94104    AA      CTTC  C
                                GG  GTTGCTGG    AG TG
                                ||  ||||||||    || ||
                                CC  CAACGACC    TC AC
                                 CC       ACCC  C
GAM593  LOC255650 3'  CATCAGCCCCAGGCAACTTCC  96711         _  CTTCA
                                GGAAGTTGC TGG     GCTGATG
                                ||||||||| |||     |||||||
                                CCTTCAACG ACC     CGACTAC
                                     G   C____
GAM594  BCAT2    3'  TCACCTGAAGTGCAATA     6815          GTC    TT
                                TATTGCACT   TCAG  TGA
                                |||||||||   ||||  |||
                                ATAACGTGA   AGTC  ACT
                                    ___    C_
GAM594  BLTR2    5'  CAAACTAAGACAGTGC      39039         C
                                GCACTGTCT AGTTTG
                                ||||||||| ||||||
                                CGTGACAGA TCAAAC
                                     A
GAM594  FZD10    3'  TCAAACGATGTGCAATA     23242         T   TCA
                                TATTGCAC GTC   GTTTGA
                                |||||||| |||   ||||||
                                ATAACGTG TAG   CAAACT
                                    _  ___
GAM594  NR2E1    3'  GGTCCAAACTCGTGGTGCAG   12326       TG CTC     A
                                TTGCAC  T   AGTTTG ACC
                                ||||||  |   |||||| |||
                                GACGTG  G   TCAAAC TGG
                                   GT C__      C
GAM594  RELA     3'  GGCTGAAGGAAACAGTGCAA   41755         ___  _
                                TTGCACTGT   CT CAGTT
                                |||||||||   || |||||
                                AACGTGACA   GA GTCGG
                                     AAG  A
GAM594  SLC38A2  3'  AGCTAGGGAAAACAGTGCAA   38587         ___    _
                                TTGCACTG   TCTC AGTT
                                ||||||||   |||| ||||
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                                AACGTGAC   AGGG TCGA
                                     AAA    A
GAM594  TLL2     3'  TTCAAACTGCATTTGCAA    24967      CTGTCT
                                TTGCA     CAGTTTGAA
                                |||||     |||||||||
                                AACGT     GTCAAACTT
                                   TTAC__
GAM594  DKFZP434J1813 3'  AGCCGAGAAACAGTGCAG    61784        __   A
                                TTGCACTG  TCTC GTT
                                ||||||||  |||| |||
                                GACGTGAC  AGAG CGA
                                     AA    C
GAM594  FLJ14298  3'  TTCAAACTGCTACTTGTCAATA 45431      _  CT  CT
                                TATTG CA  GT  CAGTTTGAA
                                ||||| ||  ||  |||||||||
                                ATAAC GT  CA  GTCAAACTT
                                   T  T_  TC
GAM594  G2       3'  GGTTCAAACTGTCAATGCA    66662     C  TCT
                                TGCA TG   CAGTTTGAACC
                                |||| ||   ||||||||||
                                ACGT AC   GTCAAACTTGG
                                  A  T__
GAM594  HSU47926  3'  TCAGAGGACAGTGCA      26523         CAG
                                TGCACTGTCT   TTTGA
                                ||||||||||   |||||
                                ACGTGACAGG   AGACT
                                             ___
GAM594  IL1RAPL1  3'  TTCAGAGAACAGTGCAA     26548         _  AGTT
                                TTGCACTGT CTC    TGAA
                                ||||||||| |||    ||||
                                AACGTGACA GAG    ACTT
                                     A  _____
GAM594  KIAA0329  3'  TTGAGTCAGTGCAATA      29283         T
                                TATTGCACTG CTCAG
                                |||||||||| |||||
                                ATAACGTGAC GAGTT
                                      T
GAM594  KIAA0478  3'  GTAAGTGAGACAGCAA      29554      AC      G  TGA
                                TTGC  TGTCTCA TT   AC
                                ||||  ||||||| ||   ||
                                AACG  ACAGAGT AA   TG
                                  __       G  ___
GAM594  KIAA1145  3'  TTCAAATTAAGTGCAATA    65631         GTCTCA
                                TATTGCACT     GTTTGAA
                                |||||||||     |||||||
                                ATAACGTGA     TAAACTT
                                      AT_____
GAM594  MMD      3'  GGTTGTAAAAGTCAGTGCAATA 59810          T  CAG   _
                                TATTGCACTG CT   TTTG AACC
                                |||||||||| ||   |||| ||||
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                                ATAACGTGAC GA   AAAT TTGG
                                      T ___    G
GAM594  PRPF8    3'  AATTGAGACAGTACAA      61180     C
                                TTG ACTGTCTCAGTT
                                ||| ||||||||||||
                                AAC TGACAGAGTTAA
                                  A
GAM594  ROBO2    3'  GACTCTAAACAGTGCAATG    62487          CTC_
                                TATTGCACTGT    AGTT
                                ||||||||||    ||||
                                GTAACGTGACA    TCAG
                                      AATC
GAM594  SEMA3C   3'  CAAACTGATAGACAGT      21060       __
                                ACTGTC  TCAGTTTG
                                ||||||  ||||||||
                                TGACAG  AGTCAAAC
                                   AT
GAM594  ZNF226   5'  GACTGAGTACAGTGCAA     33189         _
                                TTGCACTGT CTCAGTT
                                ||||||||| |||||||
                                AACGTGACA GAGTCAG
                                      T
GAM594  ZNF287   3'  CTGAAGAAGTGCAATA      40297         G  _
                                TATTGCACT TCT CAG
                                ||||||||| ||| |||
                                ATAACGTGA AGA GTC
                                      _  A
GAM594  LOC139221 5'  TTGGAAAGACAGTGCAA     75828          CAG  TG
                                TTGCACTGTCT   TT  A
                                ||||||||||   ||  |
                                AACGTGACAGA   AG  T
                                      A__  GT
GAM594  LOC148166 5'  GGTCCAACCAGACAGTGGAATA 78696      G       CA   T  A
                                TATT CACTGTCT  GTT GA CC
                                |||| ||||||||  ||| || ||
                                ATAA GTGACAGA  CAA CT GG
                                  G       C_  C  _
GAM594  LOC201689 5'  GGCTCAAACTGAGAAGTGC   67148      G         A
                                GCACT TCTCAGTTTGA CC
                                ||||| |||||||||||  ||
                                CGTGA AGAGTCAAACT GG
                                  _         C
GAM595  ADAM19   3'  CAGGAAGAAGACTGGCCATTAT 52703      C    CTGAG
          G                      CATGA GGCT     TTCTTCCTG
                                ||||| ||||    |||||||||
                                GTATT CCGG     AAGAAGGAC
                                  A   TCAG_
GAM595  FACL5    5'  CAGGAAGAACTCAGAGCCG   64186
                                CGGCTCTGAGTTCTTCCTG
                                ||||||||||||||||||
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                                GCCGAGACTCAAGAAGGAC

GAM595  GNAL     5' CAGGAAAGAGAGGAGCCGTCG 9058          GAG TC
                                TGACGGCTCT   T TTCCTG
                                ||||||||||  | ||||||
                                GCTGCCGAGG  A AAGGAC
                                     AG_ GA
GAM595  KAL1     3' CAGGAAGAACTTCTGTCA    4013       CTCT
                                TGACGG   GAGTTCTTCCTG
                                ||||||   ||||||||||||
                                ACTGTC   TTCAAGAAGGAC
                                   ____
GAM595  MYO1E    3' CAGGAGGACAAAACCACCATG 17187     AC CTC AGT
                                CATG GG  TG  TCTTCCTG
                                ||||  ||  ||  ||||||||
                                GTAC CC  AC  AGGAGGAC
                                  CA AAA ___
GAM595  PRKAR2B  3' CAGAAAGAACTCAGATGT    10804   _       C
                                GC TCTGAGTTCTT CTG
                                || ||||||||||| |||
                                TG AGACTCAAGAA GAC
                                 T         A
GAM595  PUM2     3' AGGATCAAAGCTGTCATG    31014        C  GTTCT
                                CATGACGGCT TGA    TCCT
                                |||||||||| |||    ||||
                                GTACTGTCGA ACT    AGGA
                                     A  _____
GAM595  SKI      3' CAGGAAGTGCAGAGCCGCA   11701   A     AGTT
                                TG CGGCTCTG   CTTCCTG
                                || ||||||||   |||||||
                                AC GCCGAGAC   GAAGGAC
                                 _      GT__
GAM595  TEM8     3' AGGAAGATGCAACCCCATG   36326    AC CTC AGT
                                CATG GG  TG  TCTTCCT
                                ||||  ||  ||  |||||||
                                GTAC CC  AC  AGAAGGA
                                  C_ A__ GT_
GAM595  ARHGEF4  5' AGAAAAAACTCAGGGC     52207        C C
                                GCTCTGAGTT TT CT
                                |||||||||| || ||
                                CGGGACTCAA AA GA
                                     A  A
GAM595  FLJ31978 3' CAGGAAGGAACAAGCGCC   58348    T GAG
                                GGC CT   TTCTTCCTG
                                ||| ||   |||||||||
                                CCG GA   AGGAAGGAC
                                  C  ACA
GAM595  HSU24186 5' AGAACTCAAAGCCGTC     25324       C
                                GACGGCT TGAGTTCT
                                ||||||| ||||||||
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                                CTGCCGA ACTCAAGA
                                    A
GAM595  KCNT1    3'  AGCTCCCAGGGCCGCCA     61825    A     __
                                TG CGGCTCT  GAGTT
                                || |||||||  |||||
                                AC GCCGGGA  CTCGA
                                 C      CC
GAM595  KIAA1867 3'  CAGGAAGAACCCAAGAGCTCAT 94822     CG    GA_
                                ATGA  GCTCT   GTTCTTCCTG
                                ||||  |||||   ||||||||||
                                TACT  CGAGA   CAAGAAGGAC
                                  __    ACC
GAM595  KIAA1878 3'  AATTCAGAGAATCGTCATG   91707        __
                                CATGACGG  CTCTGAGTT
                                ||||||||  |||||||||
                                GTACTGCT  GAGACTTAA
                                     AA
GAM595  MFN1     3'  CAGGAAGAACTCATGA      35541    _
                                TC TGAGTTCTTCCTG
                                || ||||||||||||
                                AG ACTCAAGAAGGAC
                                 T
GAM595  MIDORI   3'  CAGGGCCCTTCCAGAGCCTGTC 73784       _      AGTTCT
           ATG                    CATGAC GGCTCTG     TCCTG
                                ||||||| |||||||      |||||
                                GTACTG CCGAGAC     GGGAC
                                   T      CTTCCC
GAM595  MYH7B    3'  CAGGAAGAACCTGGCTCGCATG 70530     A _  CTGA
                                CATG CG GCT    GTTCTTCCTG
                                |||| || |||    ||||||||||
                                GTAC GC CGG    CAAGAAGGAC
                                  _ T  TC__
GAM595  RNAHP    3'  AGAAAGCAGCAGCCGTCAT   23761        _  AG
                                ATGACGGCT CTG  TTCT
                                ||||||||| |||  ||||
                                TACTGCCGA GAC  AAGA
                                     C   GA
GAM595  SLC37A1  3'  AGACGGAGCTCAGACCC     38561    C       TC
                                GG TCTGAGTTCT  CT
                                || ||||||||||  ||
                                CC AGACTCGAGG  GA
                                 C         CA
GAM595  LOC116236 3'  CAGGAAAAGCACAAACCTCAT  73809     C  CTC  A   C
                                ATGA GG   TG GTT TTCCTG
                                |||| ||   || ||| ||||||
                                TACT CC   AC CGA AAGGAC
                                  _ AA_  A   A
GAM595  LOC124801 3'  CAGGAAGAACTCTCTTGCATG  74336     A   CTCT
                                CATG CGG    GAGTTCTTCCTG
                                |||| |||    ||||||||||||
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                                GTAC GTT    CTCAAGAAGGAC
                                  _   CT__
GAM595  LOC222160 5'  AGGAAGAACTCACCCC      94117     CTC
                                GG   TGAGTTCTTCCT
                                ||   ||||||||||||
                                CC   ACTCAAGAAGGA
                                 CC_
GAM595  LOC51094  3'  CAGGAAGAATAAAGCC      32045      CTGA
                                GGCT    GTTCTTCCTG
                                ||||    ||||||||||
                                CCGA    TAAGAAGGAC
                                  AA__
GAM595  LOC92078  3'  CAGGAAGAAGAATCGACCGTC  67977       C  T  G__
                                GACGG TC GA   TTCTTCCTG
                                ||||| || ||   |||||||||
                                CTGCC AG CT   AAGAAGGAC
                                  _ _  AAG
GAM596  ADH1B     3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A     T__
GAM596  AHR       3'  ATCTCAGATGTTAAAATAAATG 7875        CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM596  FDFT1     3'  TAGGAAAGTGAAATG       15518            A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM596  JTB       3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                  CATTTCACTTTCACTGTCTGAGAT
                                ||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM596  KLF4      3'  TCCCAGACAGTGGATATG     14891     CT         A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM596  PHYH      3'  ACAGTAAAAGTGAAAT       20608           C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                       A
GAM596  PKD2      3'  TCCAGGTTGAAAGTGAAA     60096           CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
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                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM596  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM596  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM596  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM596  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM596  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||         |||||||||
                                GTAAAG         CAGACTCTA
                                   AAACATTT_
GAM596  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM596  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM596  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM596  NIR3     3'  GCAGTGAAAGTGCAAT      66242      T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM596  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598         CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
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                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM596  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM596  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                     TA__   TT
GAM596  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM596  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM596  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM596  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM596  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM596  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                     _
GAM597  ATP2B2   3'  GCTTAAATTGCTCT       8067          TAACAG
                                AGAGCAATTT     AGGC
                                ||||||||||     ||||
                                TCTCGTTAAA     TTCG
                                    _______
GAM597  AXIN1    3'  AGGGCCTCTGTCAATTGT    60849       TTA
                                GCAATT   ACAGAGGCCCT
                                ||||||   ||||||||||||
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                                TGTTAA  TGTCTCCGGGA
                                   C__
GAM597  CRP     3'  GGCCATTAGAATTGC      71629         CAGA
                                GCAATTTTAA   GGCC
                                ||||||||||   ||||
                                CGTTAAGATT   CCGG
                                     A___
GAM597  DACH    3'  AGGACCTATGAAAATTGTCT  54968    G     AACAG  C
                                AGA CAATTTT    AGG CCT
                                ||| |||||||    ||| |||
                                TCT GTTAAAA    TCC GGA
                                  _     GTA__  A
GAM597  FPGS    3'  AGGGCCTCTGCCTGGGACACTG 17080    A__    A_
          C                      GCA  TTTTA  CAGAGGCCCT
                                |||   |||||  ||||||||||
                                CGT   AGGGT  GTCTCCGGGA
                                  CAC    CC
GAM597  HLA-E   3'  GGGCCTCTGAATCTGTCTG   91025     G  AT  TAA
                                CAGA CA  TT   CAGAGGCCC
                                |||| ||  ||   |||||||||
                                GTCT GT  AA   GTCTCCGGG
                                  _ CT  ___
GAM597  HOXB3   5'  TTGTTAAAATTGCTTTG    9264
                                CAGAGCAATTTTAACAG
                                |||||||||||||||||
                                GTTTCGTTAAAATTGTT

GAM597  HOXC5   3'  AGGGCCCCCACAGTTGCTCT  38490        TTAACAGA
                                AGAGCAATT      GGCCCT
                                |||||||||      ||||||
                                TCTCGTTGA      CCGGGA
                                     CACCC___
GAM597  IHPK1   3'  GGGCCTCTGGTGGCTCTG   95760      AATTTTAA
                                CAGAGC      CAGAGGCCC
                                ||||||      |||||||||
                                GTCTCG      GTCTCCGGG
                                   GTG_____
GAM597  IL22RA2 3'  CCCATGAAAATTGCTC     53690         AA  GA
                                GAGCAATTTT  CA  GG
                                |||||||||  ||  ||
                                CTCGTTAAAA  GT  CC
                                     __ AC
GAM597  LY64    3'  GCTTAGCAAAATTGCTCT    18756         AACAG
                                AGAGCAATTTT    AGGC
                                ||||||||||    ||||
                                TCTCGTTAAAA    TTCG
                                     CGA__
GAM597  MASP1   3'  AGGGCCTCTGCATTGTTGCTC  57469       TTTAA
                                GAGCAAT    CAGAGGCCCT
                                |||||||    ||||||||||
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                                CTCGTTG    GTCTCCGGGA
                                    TTAC_
GAM597  MYO1D    3'  AGGGCCTCTGACCACCGCTCTG 71765       AATTTTAA
                                CAGAGC      CAGAGGCCCT
                                ||||||      ||||||||||
                                GTCTCG      GTCTCCGGGA
                                   CCACCA__
GAM597  PFKFB4   3'  AGGGCCTCTACCATCCTCTCTG 15865      CAATTTTAAC
                                CAGAG       AGAGGCCCT
                                |||||       |||||||||
                                GTCTC       TCTCCGGGA
                                  TCCTACCA__
GAM597  PPP2R4   3'  GCCTCTGTTTTGCACCTG    60559    A_   TTTT
                                CAG  GCAA   AACAGAGGC
                                |||  ||||   |||||||||
                                GTC  CGTT   TTGTCTCCG
                                  CA   _____
GAM597  RPL15    3'  TCTGTTAAAACTAGTCTG    11385     GCAA
                                CAGA   TTTTAACAGA
                                ||||   ||||||||||
                                GTCT   AAAATTGTCT
                                  GATC
GAM597  SRD5A1   3'  TTGTTAAAATTCTCT      6461      C
                                AGAG AATTTTAACAG
                                |||| ||||||||||
                                TCTC TTAAAATTGTT
                                  _
GAM597  XYLB     3'  AGGGCCTCTCTTACTTGC    17557     TTT  C
                                GCAA  TAA AGAGGCCCT
                                ||||  ||| |||||||||
                                CGTT  ATT TCTCCGGGA
                                  C__  C
GAM597  ZNF267   5'  GACCTCTGTTGCTCTG      12735       ATTTTA     CC
                                CAGAGCA     ACAGAGG  C
                                |||||||     |||||||  |
                                GTCTCGT     TGTCTCC  G
                                   _______     AA
GAM597  ARTS-1   3'  CTCTTTTAAAATTGCTCTG   33184            C
                                CAGAGCAATTTTAA AGAG
                                |||||||||||||| ||||
                                GTCTCGTTAAAATT TCTC
                                        T
GAM597  C1orf25  3'  GGCTCACATGTTAAAATGACCC 72536    AGCA       GA__
          TG                    CAG   ATTTTAACA   GGCC
                                |||   |||||||||   ||||
                                GTC   TAAAATTGT   TCGG
                                  CCAG       ACAC
GAM597  C22orf5  3'  AGGGCCCCTGGGCACCGCTTCT 24339     _ AATTTTAA  A
          G                     CAGA GC       CAG GGCCCT
                                |||| ||       ||| ||||||
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                                GTCT CG       GTC CCGGGA
                                  T  CCACGG__   C
GAM597  CD109    3'  AGGAGCATACTGAAAATTGCCC 56045     A      AA   AG_ _
             TG                    CAG GCAATTTT  CAG   GC CCT
                                   ||| ||||||||  |||   || |||
                                   GTC CGTTAAAA  GTC   CG GGA
                                     C       __   ATA  A
GAM597  FKHL18   3'  AGGGCCTCTTGGGATTTACTCT 79553      C_     AC
             G                     CAGAG  AATTTTA  AGAGGCCCT
                                   |||||  |||||||  |||||||||
                                   GTCTC  TTAGGGT  TCTCCGGGA
                                     AT      __
GAM597  FLJ22054 3'  CCATCTGTTAAAATTACCTG  94393     AGC         _
                                   CAG   AATTTTAACAGA GG
                                   |||   ||||||||||||| ||
                                   GTC   TTAAAATTGTCT CC
                                     CA_          A
GAM597  FLJ23074 3'  GCCTTAGAAAATTGCCTG    46818     A       AACA
                                   CAG GCAATTTT    GAGGC
                                   ||| ||||||||    |||||
                                   GTC CGTTAAAA    TTCCG
                                     _       GA__
GAM597  FLJ30473 3'  GGCCTCTGCTGCCACTG     58463     A_   ATTTTAA
                                   CAG  GCA      CAGAGGCC
                                   |||  |||      ||||||||
                                   GTC  CGT      GTCTCCGG
                                     AC   C_______
GAM597  FOXJ1    3'  GGCCTCTGGGGTCTTTGCCTG  7574      A    TTTTAA
                                   CAG GCAA     CAGAGGCC
                                   ||| ||||     ||||||||
                                   GTC CGTT     GTCTCCGG
                                     _    TCTGGG
GAM597  KIAA0514 3'  GCCTAAAATTGCACT       28086     A       AACAG
                                   AG GCAATTTT     AGGC
                                   || ||||||||     ||||
                                   TC CGTTAAAA     TCCG
                                    A       ______
GAM597  KIAA0543 3'  AGAGCCCCCAGAGGCATTGTTC 68931          TTTAACAGA   C
             TG                    CAGAGCAAT        GGC CT
                                   |||||||||        ||| ||
                                   GTCTTGTTA        CCG GA
                                        CGGAGACCC   A
GAM597  KIAA1546 3'  GGCCTCTGGATTTTGCTC    67909        TTTTAA
                                   GAGCAA     CAGAGGCC
                                   ||||||     ||||||||
                                   CTCGTT     GTCTCCGG
                                      TTAG__
GAM597  KRTHB2   3'  AGGGCCTCTGCCCTGAACATCT 52285      GCAATTTTAA
             G                     CAGA         CAGAGGCCCT
                                   ||||         ||||||||||
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                                GTCT        GTCTCCGGGA
                                  ACAAGTCCC_
GAM597  LIPI     3'  CTCATGTTAAAATCACTT    79566     CA       _
                                GAG  ATTTTAACA GAG
                                |||  |||||||| |||
                                TTC  TAAAATTGT CTC
                                  AC        A
GAM597  MGC15606 5'  AGGACCTCTGGTCAAAATTGCC 58874     A       AA_     C
             TG                   CAG GCAATTTT   CAGAGG CCT
                                |||  |||||||   ||||||  |||
                                GTC CGTTAAAA   GTCTCC GGA
                                  _       CTG     A
GAM597  MGC20255 3'  GCCTCTGCTACGGAGCGCTTCT 53443      _ AA   _  A
             G                    CAGA GC  TTT TA CAGAGGC
                                |||| ||  ||| || |||||||
                                GTCT CG  AGG AT GTCTCCG
                                  T  CG   C  C
GAM597  MGC2742  5'  AGGGCCTCTGTCTCCATCTCTG 43744       CAATTTTA
                                CAGAG       ACAGAGGCCCT
                                |||||       ||||||||||
                                GTCTC       TGTCTCCGGGA
                                  TACCTC__
GAM597  NLP_1    3'  TGTTTAAAATTGCTTTG     23710           _
                                CAGAGCAATTTTAA CA
                                |||||||||||||| ||
                                GTTTCGTTAAAATT GT
                                       T
GAM597  PIK4CA   3'  AGGGCCTCTGCCCCATGTGCCC 10592    A   ATTTTAA
             T                    AG GCA      CAGAGGCCCT
                                || |||      ||||||||||
                                TC CGT      GTCTCCGGGA
                                 C   GTACCCC
GAM597  PIK4CA   3'  AGGGCCTCTGCCCCATGTGCCC 54123    A   ATTTTAA
             T                    AG GCA      CAGAGGCCCT
                                || |||      ||||||||||
                                TC CGT      GTCTCCGGGA
                                 C   GTACCCC
GAM597  SLC21A14 5'  TTGTTCAAAATTGCTGTG    33833    G       _
                                CA AGCAATTTT AACAG
                                || |||||||| |||||
                                GT TCGTTAAAA TTGTT
                                 G        C
GAM597  TSGA14   3'  GCCCACTGAAAATTGCCTG   38047     A       AA   A_
                                CAG GCAATTTT  CAG  GGC
                                ||| ||||||||  |||  |||
                                GTC CGTTAAAA  GTC  CCG
                                  _       __  AC
GAM597  LOC124411 5'  GACCTCTGTTACTCTG      74284       CAATTT        CC
                                CAGAG     TAACAGAGG  C
                                |||||     |||||||||  |
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                                GTCTC     ATTGTCTCC  G
                                  _______       AA
GAM597   LOC139221 3'  TGTTAAAATTGCACTG      75827     A
                                CAG GCAATTTTAACA
                                ||| ||||||||||||
                                GTC CGTTAAAATTGT
                                  A
GAM597   LOC144501 3'  AGGGCCTCTGTTCTCCTCT    83103      CAATTTT
                                AGAG      AACAGAGGCCCT
                                ||||      ||||||||||||
                                TCTC      TTGTCTCCGGGA
                                  CTC____
GAM597   LOC148183 3'  GGGCCCCTGTGTTCTCTG     84121      C   TTTA    A
                                CAGAG AAT    ACAG GGCCC
                                ||||| |||    |||| |||||
                                GTCTC TTG    TGTC CCGGG
                                  _  ____    C
GAM597   LOC149134 5'  GGGCCTCTGTCAGCACTG     84363     A  AATTTTA
                                CAG GC       ACAGAGGCCC
                                ||| ||       ||||||||||
                                GTC CG       TGTCTCCGGG
                                  A  AC_____
GAM597   LOC149910 3'  AGGGCCTCTGCCCAGGCTCT   79528       AATTTTAA
                                AGAGC        CAGAGGCCCT
                                |||||        ||||||||||
                                TCTCG        GTCTCCGGGA
                                   GACCC___
GAM597   LOC160156 5'  AGGGCCTCCGTTCCCTGAGCTC 82206      AATTTT   A
                                GAGC     AAC GAGGCCCT
                                ||||     ||| ||||||||
                                CTCG     TTG CTCCGGGA
                                  AGTCCC   C
GAM597   LOC160414 5'  GCCAAAATTGTTCTG       87067           AACAGA
                                CAGAGCAATTTT     GGC
                                ||||||||||||     |||
                                GTCTTGTTAAAA     CCG
                                         _______
GAM597   LOC162952 5'  AGGGCCTCTACACCTGCTC    82378       ATTTTAAC
                                GAGCA        AGAGGCCCT
                                |||||        |||||||||
                                CTCGT        TCTCCGGGA
                                   CCACA___
GAM597   LOC196214 5'  AGGGCTTATGCAAAATTGT    89615        AA  G
                                GCAATTTT  CA AGGCCCT
                                ||||||||  || |||||||
                                TGTTAAAA  GT TTCGGGA
                                     C_  A
GAM597   LOC220686 3'  AGGGCCTCTGCCCCATGTGCCC 92920     A   ATTTTAA
            T                    AG GCA       CAGAGGCCCT
                                || |||       ||||||||||
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                                TC CGT      GTCTCCGGGA
                                 C  GTACCCC
GAM597  LOC257476 3'  GGGCCTCTGGTGGCTCTG    61255       AATTTTAA
                                CAGAGC      CAGAGGCCC
                                ||||||      |||||||||
                                GTCTCG      GTCTCCGGG
                                   GTG_____
GAM597  LOC257539 3'  GGGCCTCTGAATCTGTCTG    97703     G  AT  TAA
                                CAGA CA  TT   CAGAGGCCC
                                |||| ||  ||   |||||||||
                                GTCT GT  AA   GTCTCCGGG
                                  _ CT  ___
GAM597  LOC257578 3'  GGGCCTCTGAATCTGTCTG    97823     G  AT  TAA
                                CAGA CA  TT   CAGAGGCCC
                                |||| ||  ||   |||||||||
                                GTCT GT  AA   GTCTCCGGG
                                  _ CT  ___
GAM597  LOC90092  5'  GGCACCAAGTCAAAGTTACTCT 61412      C     A  AGAG_
          G                      CAGAG AATTTT AC     GCC
                                |||||| |||||| ||     |||
                                GTCTC TTGAAA TG     CGG
                                   A     C  AACCA
GAM598  ARAF1    5'  ATTTTGTCCCCTGCCA      63935    A   A
                                TG CAG GGACAAAGT
                                || ||| |||||||||
                                AC GTC CCTGTTTTA
                                 C   C
GAM598  CCNG1    5'  GGAGCTGCAGTCTCTGTCA    14485         ACAAA T
                                TGACAGAGG    G CAGCTCC
                                |||||||||    | |||||||
                                ACTGTCTCT    C GTCGAGG
                                     GA___ _
GAM598  DNAH5    5'  GAGCTGACTCCAGCCTGTC    7258       A__   CAAA
                                GACAG   GGA   GTCAGCTC
                                |||||   |||   ||||||||
                                CTGTC   CCT   CAGTCGAG
                                   CGA  _____
GAM598  EIF2AK3  3'  AGCTGACTCCATTTTTGTC    16710        ACAA
                                GACAGAGG    AGTCAGCT
                                ||||||||    ||||||||
                                CTGTTTTT    TCAGTCGA
                                     ACC_
GAM598  FXYD2    3'  GACCTTTGTCCCCGTCA     41210      AGA      _
                                TGAC   GGACAAAG TC
                                ||||   |||||||| ||
                                ACTG   CCTGTTTC AG
                                  CC_       C
GAM598  FXYD2    3'  GACCTTTGTCCCCGTCA     8061       AGA      _
                                TGAC   GGACAAAG TC
                                ||||   |||||||| ||
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                                ACTG   CCTGTTTC AG
                                  CC_       C
GAM598  GPR56    3'  AGGGCACTCTGCATCCTCTGTC 19065          CAA  TCA  T
            A                    TGACAGAGGA   AG   GC CCT
                                 ||||||||||   ||   || |||
                                 ACTGTCTCCT   TC   CG GGA
                                      ACG  TCA  _
GAM598  HLALS    3'  AGGAGCCATGTTATCCTCTGTC 7736          C  AGTCA
                                 GACAGAGGA AA    GCTCCT
                                 |||||||||  ||    ||||||
                                 CTGTCTCCT TT    CGAGGA
                                      A  GTAC_
GAM598  ISLR     5'  AGGAGCTGGGGTCCTCTTC   18668    C      AAAG
                                 GA AGAGGAC    TCAGCTCCT
                                 || |||||||    |||||||||
                                 CT TCTCCTG    GGTCGAGGA
                                  _      G___
GAM598  KCND2    3'  GAGCTAATAATTATCCCTCTGT 24398          ACAAA__  C
            CA                     TGACAGAGG      GT AGCTC
                                   |||||||||      || |||||
                                   ACTGTCTCC      TA TCGAG
                                        CTATTAA  A
GAM598  PKIA     3'  GACTTTTCCCTACCTCTGTCA  22384          AC____
                                   TGACAGAGG     AAAGTC
                                   |||||||||     ||||||
                                   ACTGTCTCC     TTTCAG
                                        ATCCCT
GAM598  PSCD4    3'  GGCCCTGCCTCTGTCA      25407          A  AA
                                   TGACAGAGG CA  GTC
                                   |||||||||  ||  |||
                                   ACTGTCTCC GT  CGG
                                        _  CC
GAM598  PXF      3'  AGAAGTCTGCCCGCTGCCCTCT 11147          ACAA  ___  _  C
            GTCA                     GACAGAGG   AGT   CAG CT CT
                                     ||||||||   |||   ||| || ||
                                     CTGTCTCC   TCG   GTC GA GA
                                          CG__   CCC   T  A
GAM598  RALBP1   3'  GACTCTTCCTCTGTCA      22296          CAA
                                   TGACAGAGGA   AGTC
                                   |||||||||   ||||
                                   ACTGTCTCCT   TCAG
                                        TC_
GAM598  RBBP2    5'  GATGCGCTTCGGCCTCTGTCA  17322          ACA   CA  _
                                   TGACAGAGG   AAGT  GC TC
                                   |||||||||   ||||  || ||
                                   ACTGTCTCC   TTCG  CG AG
                                        GGC    __  T
GAM598  RFX5     3'  GACCTACTTTGTCCTCT     4823           C  C
                                   AGAGGACAAAGT AG TC
                                   |||||||||||| || ||
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                                TCTCCTGTTTCA TC AG
                                      _  C
GAM598  RNMT    3'  CTGACTTTCTGTTGTC     13720      A   CA
                                GACAG GGA  AAGTCAG
                                |||||| |||  |||||||
                                CTGTT TCT  TTCAGTC
                                  G   __
GAM598  SAR1    3'  AGAAGCCAAGAGTCTCTGTCA  39321         ACAAAGTCA   C
                                TGACAGAGG       GCT CT
                                |||||||||       ||| ||
                                ACTGTCTCT       CGA GA
                                     GAGAAC___   A
GAM598  SLC4A1  3'  AGGTCCGAGCTCTGTCCTCTGT 4423          A   CAGCT
           CA                     TGACAGAGGACA AGT    CCT
                                ||||||||||||| |||    |||
                                ACTGTCTCCTGT TCG    GGA
                                      C   AGCCT
GAM598  STK9    5'  AGGAGCTGTGGGGTCCCCTG   12035    A   AAAGT
                                CAG GGAC    CAGCTCCT
                                ||| ||||    ||||||||
                                GTC CCTG    GTCGAGGA
                                  C   GGGT_
GAM598  TRIM9   3'  AGCTGGTCCTCTGCA      30748    A      AAAGT
                                TG CAGAGGAC    CAGCT
                                || ||||||||    |||||
                                AC GTCTCCTG    GTCGA
                                _      _____
GAM598  AMOTL2  3'  AGGAGCTGAGCTCCCTCTG   32480      ACAA  _
                                CAGAGG   AG TCAGCTCCT
                                ||||||   || |||||||||
                                GTCTCC   TC AGTCGAGGA
                                   C___  G
GAM598  C1orf24 3'  GGAGATTCTCCTCTGTCA    53724        CAAAGTCAG
                                TGACAGAGGA       CTCC
                                ||||||||||       ||||
                                ACTGTCTCCT       GAGG
                                     CTTA_____
GAM598  C20orf42 3'  AGGAACCAACTTTGTTTT    34581        CAGC
                                AGGACAAAGT   TCCT
                                ||||||||||   ||||
                                TTTTGTTTCA   AGGA
                                     ACCA
GAM598  FLJ14297 3'  GGATGTCCACCCTCTGTC    46086       ACAAA  CA  _
                                GACAGAGG    GT  GC TCC
                                ||||||||    ||  || |||
                                CTGTCTCC    CA  TG AGG
                                     _____  CC  T
GAM598  FLJ22329 3'  GAGTAGAGTCTGTCTCTGTCA  45069       G   AAG  A
                                TGACAGAG ACA   TC GCTC
                                |||||||| |||   || ||||
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                                ACTGTCTC TGT   AG TGAG
                                     _  CTG  A
GAM598  FLJ32865  3'  AGAAGCTGACTTTGGCC     58165    A        C
                                GG CAAAGTCAGCT CT
                                || |||||||||| ||
                                CC GTTTCAGTCGA GA
                                 G         A
GAM598  KIAA0173  3'  AGGAAGGGTCACCCTCTGTCA  27666        ACAAAG  AGC
                                TGACAGAGG     TC   TCCT
                                |||||||||     ||   ||||
                                ACTGTCTCC     GG   AGGA
                                     CACT__  GA_
GAM598  KIAA0226  3'  TGACTCTGTCCTCTGTTA    63525          A
                                TGACAGAGGACA AGTCA
                                |||||||||||| |||||
                                ATTGTCTCCTGT TCAGT
                                       C
GAM598  KIAA0318  3'  AGGAGCGGTTGCTCTCTGTCA  68946       GA   AGTCA
                                TGACAGAG  CAA    GCTCCT
                                ||||||||  |||    ||||||
                                ACTGTCTC  GTT    CGAGGA
                                     TC   GG___
GAM598  KIAA0495  3'  AGGACACTTTCTACCCTCTGTC 62574        AC__    CAGC
          A                  TGACAGAGG    AAAGT    TCCT
                             |||||||||    |||||    ||||
                             ACTGTCTCC    TTTCA    AGGA
                                  CATC    C___
GAM598  KIAA0555  3'  AGGAGCTGAGGCTGCCCT    60111     A  AAG
                                AGG CA   TCAGCTCCT
                                ||| ||   |||||||||
                                TCC GT   AGTCGAGGA
                                  C  CGG
GAM598  KIAA0674  3'  GAGTCCTGTCCTCTGCCA    60613    A       AAGTCA
                                TG CAGAGGACA     GCTC
                                || |||||||||     ||||
                                AC GTCTCCTGT     TGAG
                                 C        CC____
GAM598  KIAA1196  3'  AGGTGCACTTTGTCCTT     61459          CA  T
                                GAGGACAAAGT  GC CCT
                                ||||||||||  || |||
                                TTCCTGTTTCA  CG GGA
                                      __  T
GAM598  KIAA1617  3'  GCTCTGTCCTCTGTTA      91431          A
                                TGACAGAGGACA AGT
                                |||||||||||| |||
                                ATTGTCTCCTGT TCG
                                       C
GAM598  KIAA1956  3'  AGCCTTCTGCCTTCTGTCA    78429         A  _   TCA
                                TGACAGAGG CA AAG   GCT
                                ||||||||| || |||   |||
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                                ACTGTCTTC GT TTC   CGA
                                      C  C  ___
GAM598  MGC5139  5' AGGACGTTTTGTCCGCTATCA 74103    C  A     GTCA _
                                TGA AG GGACAAA   GC TCCT
                                ||| || |||||||   || ||||
                                ACT TC CCTGTTT   TG AGGA
                                  A  G      ____  C
GAM598  MGC5139  5' AGGAGACCCTGCCCTTTGTCA 74104        A  AA   AGC
                                TGACAGAGG CA  GTC   TCCT
                                ||||||||| ||  |||   ||||
                                ACTGTTTCC GT  CAG   AGGA
                                      C  CC  ___
GAM598  NLI-IF   3' GGCCCTGTCCTCTGTC     41051          AA
                                GACAGAGGACA  GTC
                                ||||||||||  |||
                                CTGTCTCCTGT  CGG
                                       CC
GAM598  PP1628   5' AGGAGCTGGTGACCCTCT   47291      ACAAA
                                AGAGG    GTCAGCTCCT
                                |||||    ||||||||||
                                TCTCC    TGGTCGAGGA
                                   CAG__
GAM598  RNAC     3' GGCTTCCTCAGCCCTCTGTCA 19313        ACAA  TC
                                TGACAGAGG    AG  AGCT
                                |||||||||    ||  ||||
                                ACTGTCTCC    TC  TCGG
                                      CGAC  CT
GAM598  LOC124977 5' GGAGCCCTTGTCCTCCGT    76061    A       A TCA
                                AC GAGGACAA G   GCTCC
                                || |||||||| |   |||||
                                TG CTCCTGTT C   CGAGG
                                 C       _ C__
GAM598  LOC149464 5' GAGCTGACTCAGCTGTC     84430      AG  CAAA      C
                                GACAG  GA    GTCAGCT C
                                |||||  ||    ||||||| |
                                CTGTC  CT    CAGTCGA G
                                   GA  ____      A
GAM598  LOC151904 5' AGGAGCTAACTTTGTCC     80384         C
                                GGACAAAGT AGCTCCT
                                ||||||||| |||||||
                                CCTGTTTCA TCGAGGA
                                      A
GAM598  LOC158427 3' TTGACCTTGTCCTTTATCA   57682     C        A
                                TGA AGAGGACAA GTCAG
                                ||| ||||||||| |||||
                                ACT TTTCCTGTT CAGTT
                                  A        C
GAM598  LOC201283 3' GAGCTGCTCCCCTCTGTTA   60414         ACAA  T
                                TGACAGAGG    AG CAGCTC
                                |||||||||    || ||||||
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                                ATTGTCTCC   TC GTCGAG
                                     CC__  _
GAM598  LOC201685 3'  GAGCCAAGTCATCTCTGTCA  90242        __  AAAGTCA
                                TGACAGAG  GAC      GCTC
                                ||||||||  |||      ||||
                                ACTGTCTC  CTG      CGAG
                                     TA   AAC____
GAM598  LOC219843 5'  AGGAATATGCTGTTCTCTATCA 91507     C       AA T  GC_
                                TGA AGAGGACA  G CA   TCCT
                                ||| ||||||||  | ||   ||||
                                ACT TCTCTTGT  C GT   AGGA
                                  A       __ _  ATA
GAM598  LOC255126 5'  AGGAGCTGCTCACCCTC     97471      ACAA  T
                                GAGG    AG CAGCTCCT
                                ||||    || ||||||||
                                CTCC    TC GTCGAGGA
                                   CAC_  _
GAM598  LOC255739 3'  GGGACTCTGTCCTCTATTA    96187     C       A    AGCT
                                TGA AGAGGACA AGTC    CC
                                ||| |||||||| ||||    ||
                                ATT TCTCCTGT TCAG    GG
                                  A       C    ____
GAM598  LOC90982  3'  AGTTGTCCTGCCCTCTGTCA   64536         A  AAGT
                                TGACAGAGG CA    CAGCT
                                |||||||||  ||    |||||
                                ACTGTCTCC GT    GTTGA
                                     C  CCT_
GAM598  LOC91149  3'  CTGAACTTCATCCTTTGTCA   65074         CA   _
                                TGACAGAGGA  AAGT CAG
                                ||||||||||  |||| |||
                                ACTGTTTCCT  TTCA GTC
                                      AC    A
GAM599  DDEF1     3'  GAGCTTTAGCAGCCTC      59564     A   AGATAC       A
                                GA GCT      CTAAAGCT C
                                || |||      |||||||| |
                                CT CGA      GATTTCGA G
                                 C   C_____        C
GAM599  DDX3      3'  GAGCCTTAGGTATTTG       43759           A   A
                                TAGATACCTAA GCT C
                                |||||||||||  ||| |
                                GTTTATGGATT CGA G
                                      C   C
GAM599  GRAF      3'  GGTAACTCCCTCCCTAGCTTC  30573         ATACCTAA  C
                                GAAGCTAG       AG TACC
                                ||||||||       || ||||
                                CTTCGATC       TC ATGG
                                     CCTCCC__  A
GAM599  MAT1A     3'  AGCTTTAGAATCCCAGC      90825     A_   AC
                                GCT  GAT  CTAAAGCT
                                |||  |||  ||||||||
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                                CGA  CTA  GATTTCGA
                                  CC   A_
GAM599  MYLK     3'  AGCTTCAGACATTTGGTT    97018        AC  A
                                AGCTAGAT  CT AAGCT
                                ||||||||  || |||||
                                TTGGTTTA  GA TTCGA
                                    CA  C
GAM599  RGL      3'  GTAGCTAAAACTTAGCTTCA  30736         ATACCTAA
                                TGAAGCTAG       AGCTAC
                                |||||||||       ||||||
                                ACTTCGATT       TCGATG
                                    CAAAA___
GAM599  ZFP93    3'  GTAGCCTTAATAACGTTAGTTT 14887         ATACC_  A
           CA                     TGAAGCTAG     TAA GCTAC
                                |||||||||     ||| |||||
                                ACTTTGATT     ATT CGATG
                                    GCAATA   C
GAM599  C3orf4   3'  AGCATTGACACATAGCTTCA  39118        GATACC   A
                                TGAAGCTA     TAA GCT
                                ||||||||     ||| |||
                                ACTTCGAT     GTT CGA
                                    ACACA_   A
GAM599  D2S448   3'  GGCAGGAGTCCTAGCTTCA   73527         _  A   AAA
                                TGAAGCTAG AT CCT   GCT
                                |||||||| || |||   |||
                                ACTTCGATC TG GGA   CGG
                                    C  A  ___
GAM599  FLJ12604 3'  AGCTTTAGTATTGACTTCA   64436      CTA    C
                                TGAAG   GATAC TAAAGCT
                                |||||   ||||| |||||||
                                ACTTC   TTATG ATTTCGA
                                  AG_    _
GAM599  FLJ14280 5'  GGTAGCTCCTGGCCAGCTCA  45999     A   AGATA  TAA
                                TGA GCT    CC   AGCTACC
                                ||| |||    ||   |||||||
                                ACT CGA    GG   TCGATGG
                                  _  CC___  TCC
GAM599  H2AFJ    3'  GTTGTCAAGTTTCTAGCTTCA 36842         T  CTAA_
                                TGAAGCTAGA AC    AGC
                                |||||||||| ||    |||
                                ACTTCGATCT TG    TTG
                                    T  AACTG
GAM599  KIAA0441 3'  TAGCTTTGTTAATCTAGCCTC  28960    A      ACC
                                GA GCTAGAT   TAAAGCTA
                                || |||||||   ||||||||
                                CT CGATCTA   GTTTCGAT
                                 C      ATT
GAM599  KIAA1128 3'  TAGCTTTATGTGCAGCTTGCA  68483    _    AGA   C
                                TG AAGCT   TAC TAAAGCTA
                                || |||||   ||| ||||||||
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                                AC TTCGA   GTG ATTTCGAT
                                 G    C__   T
GAM599  KIAA1750  3'  TAGCCCCAGGAGTGGGCTTTA  68254       AG  A   AAA
                                TGAAGCT  AT CCT   GCTA
                                |||||||  || |||   ||||
                                ATTTCGG  TG GGA   CGAT
                                    G_  A   CCC
GAM599  KPNA5     3'  GGTAGCTTCAGGTAACT     9629     A     A
                                AG TACCT AAGCTACC
                                || ||||| ||||||||
                                TC ATGGA TTCGATGG
                                 A    C
GAM599  MAGEH1    5'  GGTAGCTTCAGCGGCAGCAGCT 25924       AGATAC_  A
              TC                   GAAGCT      CT AAGCTACC
                                |||||||      || ||||||||
                                CTTCGA      GA TTCGATGG
                                   CGACGGC  C
GAM599  MGC12921  3'  AGCCCTATTTAGCTTC      63774          CCTAAA
                                GAAGCTAGATA     GCT
                                ||||||||||      |||
                                CTTCGATTTAT     CGA
                                      CC____
GAM599  MGC30052  3'  AGCTTTAGAATAGCTTC     58532        GATAC
                                GAAGCTA    CTAAAGCT
                                |||||||    ||||||||
                                CTTCGAT    GATTTCGA
                                    AA___
GAM599  RNF34     3'  AGCAAGGGCTGCATCTAGCTTC 47094         A___   AAA
                                GAAGCTAGAT    CCT   GCT
                                ||||||||||    |||   |||
                                CTTCGATCTA    GGG   CGA
                                      CGTC   AA_
GAM599  TNFRSF19L 3'  GTAGCTTTTATCCCAGC     51779     A_    CCT
                                GCT  GATA   AAAGCTAC
                                |||  ||||   ||||||||
                                CGA  CTAT   TTTCGATG
                                  CC    ___
GAM599  LOC121536 3'  AGCAAATCACATTTAGCTTCA  74082          ACCTAAA
                                TGAAGCTAGAT      GCT
                                ||||||||||      |||
                                ACTTCGATTTA      CGA
                                      CACTAAA
GAM599  LOC255452 3'  TAGGTACCTACCTTCA      97544       C   A
                                TGAAG TAG TACCTA
                                ||||| ||| ||||||
                                ACTTC ATC ATGGAT
                                   C   C
GAM599  LOC257396 3'  GGCAGCTTTAGGCTTAACTT   97139     C   ATA       A
                                AAG TAG   CCTAAAGCT CC
                                ||| |||   ||||||||| ||
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                                TTC ATT   GGATTTCGA GG
                                  A   C__       C
GAM599  LOC92710  3'  GTACAAGGCATCTAGCTT    70359         A   AAAGC
                                AAGCTAGAT CCT     TAC
                                ||||||||| |||     |||
                                TTCGATCTA GGA     ATG
                                     C   AC___
GAM600  AQP3      3'  TTCACGATCCACCCTTTC    59593      T_   _
                                GAAA  GTGG TCGTGAA
                                ||||  |||| |||||||
                                CTTT  CACC AGCACTT
                                  CC    T
GAM600  ARSB      3'  TCACGACTCTTGTC        3502         AATGTG
                                GACAAGA     GTCGTGA
                                |||||||     |||||||
                                CTGTTCT     CAGCACT

                                   _______
GAM600  B4GALT5   3'  TTTTCACAAAAATAGTCCTTTG 16519        AAA_   GGTC
           TCA                    TGACAAG    TGT    GTGAAAA
                                |||||||    |||    |||||||
                                ACTGTTT    ATA    CACTTTT
                                    CCTG   AAAA
GAM600  CHRNA3    3'  TCGTTACCCATTTCTT      5610         T   CG
                                AAGAAATG GGT  TGA
                                |||||||| |||  |||
                                TTCTTTAC CCA  GCT
                                    _  TT
GAM600  DRD1      3'  TTACAACCACATTTCTGGCCA  5840     ACA         C
                                TG   AGAAATGTGGT GTGA
                                ||   |||||||||||| ||||
                                AC   TCTTTACACCA CATT
                                  CGG         A
GAM600  FUT1      3'  TCTGATCACATCCCCTGTC    3798       AGAA        T
                                GACA    ATGTGGTCG GA
                                ||||    ||||||||| ||
                                CTGT    TACACTAGT CT
                                  CCCC        _
GAM600  IRF1      3'  GCCACATTTCTGATCA      64345     CA
                                TGA  AGAAATGTGGT
                                |||  ||||||||||
                                ACT  TCTTTACACCG
                                  AG
GAM600  MAP3K8    5'  TCACGACCACCTCATG      17791     A  AAT
                                CA GA   GTGGTCGTGA
                                || ||   ||||||||||
                                GT CT   CACCAGCACT
                                  A  C__
GAM600  NGFR      3'  TTCTGACCACACTTCCTGTC   10231      A   A       T
                                GACA GAA TGTGGTCG GAA
                                |||| ||| |||||||| |||
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                                CTGT CTT ACACCAGT CTT
                                  C  C      _
GAM600  OLR1     3'  TTCACAACAGTTCTTGTTA   10341        ATGTG  C
                                TGACAAGAA    GT GTGAA
                                |||||||||    || |||||
                                ATTGTTCTT    CA CACTT
                                     GA___  A
GAM600  POU4F1   3'  CACTGAAAACATTTTTGTCA  20660        A  GG  _
                                TGACAAGAA TGT  TC GTG
                                ||||||||| |||  || |||
                                ACTGTTTTT ACA  AG CAC
                                     _  AA  T
GAM600  SMP1     3'  TTTCACATGAATAATTTTTGTC 26705        A  GGTC
           A                     TGACAAGAA TGT   GTGAAA
                                |||||||||| |||   ||||||
                                ACTGTTTTT ATA   CACTTT
                                     A  AGTA
GAM600  ZNF264   3'  TTCTATTAACATTTCTTTTCA  12769    C       GGTCGT
                                TGA AAGAAATGT     GAA
                                ||| |||||||||     |||
                                ACT TTCTTTACA     CTT
                                  T       ATTAT_
GAM600  C20orf175 3'  CGAGCTCCACGTTTCCTGCCA  55063    A  A       ___
                                TG CA GAAATGTGG   TCG
                                || || |||||||||   |||
                                AC GT CTTTGCACC   AGC
                                 C  C        TCG
GAM600  CAPNS2   3'  TTTCACAACCCTACATATTTCT 50323     CA      ____  C
           GATCA                    TGA  AGAAATGT    GGT GTGAAA
                                |||  ||||||||   ||| ||||||
                                ACT  TCTTTATA    CCA CACTTT
                                  AG       CATC   A
GAM600  CLDN6    3'  TTTACACTCACATTTTTATCA  41041     CA       _  C
                                TGA  AGAAATGTG GT GTGAA
                                |||  ||||||||| || |||||
                                ACT  TTTTTACAC CA CATTT
                                  A_       T  _
GAM600  DKFZP564L0864 3'  GCACCAATTTCTTGCCA     72555    A      G   C
                                TG CAAGAAAT TGGT GT
                                || |||||||| |||| ||
                                AC GTTCTTTA ACCA CG
                                 C       _   _
GAM600  DKFZP566B183 3'  TTTCCATAAACATTTCTTTTCA 31330     C       GGTCGT
                                TGA AAGAAATGT     GAAA
                                ||| |||||||||     ||||
                                ACT TTCTTTACA     CTTT
                                  T       AATAC_
GAM600  GTF2E1   3'  TACAGACCTCTTGTCA      18616        AATGT   _
                                TGACAAGA    GGTC GTG
                                ||||||||    |||| |||
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                                ACTGTTCT    CCAG CAT
                                    _____   A
GAM600  KIAA0089  3'  TTTTAATTCACATTTCTT    69967         TCG
                                AAGAAATGTGG   TGAAA
                                ||||||||||   |||||
                                TTCTTTACACT   ATTTT
                                     TA_
GAM600  KIAA0373  5'  TTTTCAAAGTAACATTTCTT   28015        GGTCG
                                AAGAAATGT    TGAAAA
                                |||||||||    ||||||
                                TTCTTTACA    ACTTTT
                                     ATGAA
GAM600  KIAA1813  3'  TTTTCACACTGTAAATTTCTTG 70314        __ TG  C
          T                      ACAAGAAAT  G  GT GTGAAAA
                                |||||||||  |  || |||||||
                                TGTTCTTTA  T  CA CACTTTT
                                     AA GT  _
GAM600  KIAA1951  3'  TTCCAGGCTTCTCTTGTCA   73766        AATGT   GT
                                TGACAAGA    GGTC  GAA
                                ||||||||    ||||  |||
                                ACTGTTCT    TCGG  CTT
                                    CT___    AC
GAM600  MGC4170   3'  TTCACCATTTCTTGTC     44227         TGGTC
                                GACAAGAAATG    GTGAA
                                ||||||||||    |||||
                                CTGTTCTTTAC    CACTT
                                    _____
GAM600  NRN1      3'  CACTGCACATTTCTCCTCA   33432     CA       GTC
                                TGA  AGAAATGTG   GTG
                                |||  |||||||||   |||
                                ACT  TCTTTACAC   CAC
                                  CC        GT_
GAM600  PLA2G12   3'  TTTTCACAACCACATTT     48028         C
                                AAATGTGGT GTGAAAA
                                ||||||||| |||||||
                                TTTACACCA CACTTTT
                                     A
GAM600  PPY2      3'  CACTCCACATTCCTGGCCA   40819    ACA  A      TC
                                TG   AG AATGTGG  GTG
                                ||   || |||||||  |||
                                AC   TC TTACACC  CAC
                                  CGG  C      T_
GAM600  ZNF31     3'  TTTGTAGACCACATTTCCTGTT 64992       A         _ TG
          A                      TGACA GAAATGTGGTC G  AA
                                |||||  ||||||||||| |  ||
                                ATTGT CTTTACACCAG T  TT
                                   C          A GT
GAM600  LOC115219 3'  CACGACAACGGGTCCTCA    73295     CAA  AA   G
                                TGA   GA  TGT GTCGTG
                                |||   ||  ||| ||||||
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                                ACT   CT  GCA CAGCAC
                                  C__  GG   A
GAM600   LOC120376 5'  TTCAGAGCATTTCTTTCA    75986     C       GG  G
                                TGA AAGAAATGT  TC TGAA
                                ||| |||||||||  || ||||
                                ACT TTCTTTACG  AG ACTT
                                  _       __ _
GAM600   LOC133418 3'  TTTCATATACATTTTTTGCCA  75094    A        GTC
                                TG CAAGAAATGTG   GTGAAA
                                || ||||||||||   ||||||
                                AC GTTTTTTACAT   TACTTT
                                 C         A__
GAM600   LOC151199 3'  TTAAAACCACAGCTCTTGCCA  80174    A    AA     CG
                                TG CAAGA  TGTGGT  TGA
                                || |||||  ||||||  |||
                                AC GTTCT  ACACCA  ATT
                                 C    CG     AA
GAM600   LOC152317 5'  TCACACTGACTTTTGTCA    85649        AATG   C
                                TGACAAGA    TGGT GTGA
                                ||||||||    |||| ||||
                                ACTGTTTT    GTCA CACT
                                     CA__    _
GAM600   LOC152674 3'  TTCAACCCACCCTCTTGTCA   85841        AAT    TCG
                                TGACAAGA   GTGG   TGAA
                                ||||||||   ||||   ||||
                                ACTGTTCT   CACC   ACTT
                                     CC_    CA_
GAM600   LOC152845 5'  CATGACCACATTTTTCA     60330     CAA
                                TGA   GAAATGTGGTCGTG
                                |||   ||||||||||||||
                                ACT   TTTTACACCAGTAC
                                  ___
GAM600   LOC154743 3'  TTTAGTCCACATTGTCTTGTCA 81118         _      TCG
                                TGACAAGA AATGTGG   TGAA
                                |||||||| |||||||   ||||
                                ACTGTTCT TTACACC   ATTT
                                     G      TG_
GAM600   LOC165476 5'  TTCACGGCACCTTCT      87201      AT   G
                                AGAA  GTG TCGTGAA
                                ||||  ||| |||||||
                                TCTT  CAC GGCACTT
                                  C_  _
GAM600   LOC254266 5'  TTTTCGGTCACACATCTTATCA 97356     C    AA    GT  T
                                TGA AAGA  TGTG  CG GAA
                                ||| ||||  ||||  || |||
                                ACT TTCT  ACAC  GC TTT
                                  A   AC    TG  T
GAM600   LOC255919 3'  TTTCATTCTTACATTTCTAATC 95043     CA        TC
           A                     TGA  AGAAATGTGG  GTGAAA
                                ||| ||||||||||  ||||||
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                                ACT  TCTTTACATT  TACTTT
                                  AA         CT
GAM600  LOC51754  5'  CACGGCCACATCTCTGTCA   71027      A  A
                                TGACA GA ATGTGGTCGTG
                                ||||| || ||||||||||
                                ACTGT CT TACACCGGCAC
                                   _  C
GAM600  LOC55862  3'  ACCTCATTTCTTGCCA     37485    A       T
                                TG CAAGAAATG GGT
                                || |||||||| |||
                                AC GTTCTTTAC CCA
                                 C        T
GAM600  LOC55954  3'  CACGTGGTCACTTTTCTCATCA 38877    CA    T   GT __
                                TGA  AGAAA GTG  C  GTG
                                |||  ||||| |||  |  |||
                                ACT  TCTTT CAC  G  CAC
                                  AC     T   TG TG
GAM601  GPRK7    3'  CCCTAAAAAGGAGTGGATTAC  57627    TAA  T  G   CC
                                GT   CC CT CTT  TAGGG
                                ||   || || |||  |||||
                                CA   GG GA GAA  ATCCC
                                 TTA  T  G   AA
GAM601  PAH      5'  CCCTAGTGCGAGGTTAA     4266          T  TTC
                                TTAACCTC GC   CTAGGG
                                |||||||| ||   ||||||
                                AATTGGAG CG   GATCCC
                                     _  T__
GAM601  FLJ11017  3'  TCCCCAGGAAACAAAGGGTTAG 36988        C_  C    A
                                TTAACCT  TG TTCCT GGGA
                                |||||||  || ||||| ||||
                                GATTGGG  AC AAGGA CCCT
                                    AA  A    C
GAM601  FLJ11726  3'  TCCCTGAGGAGCAGAGGCCAAC 46419     AA        C
                                GTT  CCTCTGCTTC TAGGGA
                                |||  |||||||||| ||||||
                                CAA  GGAGACGAGG GTCCCT
                                  CC         A
GAM601  KIAA0907  3'  TCCCTAGGAAACAGTGGAAC   30182     AA  T   C
                                GTT  CC CTG TTCCTAGGGA
                                |||  || ||| ||||||||||
                                CAA  GG GAC AAGGATCCCT
                                  __  T   A
GAM601  KIAA1775  3'  CCCCAGGACAGAAGTCATAC   52377    TA_  C    CT    A
                                GT   AC TCTG  TCCT GGG
                                ||   || ||||  |||| |||
                                CA   TG AGAC  AGGA CCC
                                 TAC  A    __    C
GAM601  MGC13071  3'  CCCCAGGAAGCAGAGAGCG   51087      AAC         A
                                CGTT   CTCTGCTTCCT GGG
                                ||||   |||||||||| |||
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                                GCGA   GAGACGAAGGA CCC
                                  ___          C
GAM601  SPARCL1   5'  GAAGCAGAGCTAACGA      16263        AC
                                TCGTTA  CTCTGCTTC
                                ||||||  |||||||||
                                AGCAAT  GAGACGAAG
                                   C_
GAM601  LOC152860 3'  TCCCTGTGTGAGCAGAGGTAAA 80704     A        CC_
          C                     GTT ACCTCTGCTT   TAGGGA
                                ||| ||||||||||   ||||||
                                CAA TGGAGACGAG   GTCCCT
                                  A        TGT
GAM602  CLCN5     5'  TGAAATACCTAAGCTGCTCCAA 3595          ________
                                TTGGAGCAG      GTTTCA
                                |||||||||      ||||||
                                AACCTCGTC      TAAAGT
                                     GAATCCA
GAM602  FLRT2     5'  ATTGAAAAATGAGGTCTGC   25056      GT     CTC
                                GCAG  TTCATT   CAAT
                                ||||  ||||||   ||||
                                CGTC  GAGTAA   GTTA
                                  TG     AAA
GAM602  IL17      3'  TGGGGAAAATGAAACCCTCC   9333       CA      __
                                GGAG  GGTTTCAT  TCTCCA
                                ||||  ||||||||  ||||||
                                CCTC  CCAAAGTA  AGGGGT
                                  __       AA
GAM602  NLGN1     5'  TGAAGATGCTGCTCCAA     30026         G__
                                TTGGAGCAG   TTTCA
                                |||||||||   |||||
                                AACCTCGTC   GAAGT
                                     GTA
GAM602  POLG      3'  GTGATAAACCTGCTCCAA    10682           __
                                TTGGAGCAGGTT  TCAT
                                ||||||||||||  ||||
                                AACCTCGTCCAA  AGTG
                                      AT
GAM602  TPK1      3'  GGAGAACCTGTCCAA       42384       G    TTCAT
                                TTGGA CAGGT    TCTCC
                                ||||| |||||    |||||
                                AACCT GTCCA    AGAGG
                                  _    ______
GAM602  C1orf8    5'  GAGAATGAAACCCTC       16832     CA
                                GAG  GGTTTCATTCTC
                                |||  ||||||||||||
                                CTC  CCAAAGTAAGAG
                                  __
GAM602  CLIC6     3'  TGGAGAACATGTTCCAA     82536         G  TTCAT
                                TTGGAGCA GT    TCTCCA
                                |||||||| ||    ||||||
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                                AACCTTGT CA    AGAGGT
                                   A _____
GAM602  CLIPR-59 3'  TGGAGAATTTCAATGCCCCGA 31374     A  GGTTTC
                                TTGG GCA     ATTCTCCA
                                |||| |||     ||||||||
                                AGCC CGT     TAAGAGGT
                                  C  AACTT_
GAM602  DKFZP547L112 3'  TGGAGAACTCTTGCTCCA   66532        TTTCA
                                TGGAGCAGG    TTCTCCA
                                |||||||||    |||||||
                                ACCTCGTTC    AAGAGGT
                                     TC___
GAM602  EPS8R3   5'  GGACCACCTGCTCCAA     55701          TTCATTC
                                TTGGAGCAGGT     TCC
                                ||||||||||      |||
                                AACCTCGTCCA     AGG
                                      CC_____
GAM602  EPS8R3   5'  GGACCACCTGCTCCAA     57404          TTCATTC
                                TTGGAGCAGGT     TCC
                                ||||||||||      |||
                                AACCTCGTCCA     AGG
                                      CC_____
GAM602  FLJ20552 3'  AGAACAAAACTGCTCCAA   35389        G  CA
                                TTGGAGCAG TTT  TTCT
                                ||||||||| |||  ||||
                                AACCTCGTC AAA  AAGA
                                     _  AC
GAM602  FLJ22865 5'  TGGAGAAAACTGCTCTAA   47071        GTTTCA
                                TTGGAGCAG     TTCTCCA
                                |||||||||     |||||||
                                AATCTCGTC     AAGAGGT
                                      AA____
GAM602  KIAA0372 5'  ATTGAAATTTGTTACCTACTCC 27663      C   TT  TTCTC
           AA                    TTGGAG AGGT  CA    CAAT
                                |||||| ||||  ||    ||||
                                AACCTC TCCA  GT    GTTA
                                   A   TT  TTAAA
GAM602  PRO0132  5'  ATGAAACCACTCCAA      26101       CA
                                TTGGAG  GGTTTCAT
                                ||||||  ||||||||
                                AACCTC  CCAAAGTA
                                   A_
GAM602  TEX27    3'  AGAGTGGAACCCGCTGCAA   41658     G  A
                                TTG AGC GGTTTCATTCT
                                ||| ||| ||||||||||
                                AAC TCG CCAAGGTGAGA
                                  G  C
GAM602  LOC149373 3'  ATTGGGGTGATGATACCCACCC 79312     AGCA  T   _
           CAA                    TTGG   GGT TCATT CTCCAAT
                                ||||   ||| ||||| |||||||
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                                AACC    CCA AGTAG GGGGTTA
                                  CCAC   T    T
GAM602  LOC152687 3'  TTGGAGAATATTGCTCC     80643        GTTTC
                                GGAGCAG    ATTCTCCAA
                                |||||||    |||||||||
                                CCTCGTT    TAAGAGGTT
                                   A____
GAM602  LOC51202  3'  ATTGGAGAATGAAACCTGCTCC 33017
           AA                    TTGGAGCAGGTTTCATTCTCCAAT
                                |||||||||||||||||||||||
                                AACCTCGTCCAAAGTAAGAGGTTA

GAM603  ALK      3'  CAATGGCTCCTTCAC       73381         ACTC
                                GTGAAGGA   CTGTTG
                                ||||||||   ||||||
                                CACTTCCT   GGTAAC
                                    C___
GAM603  ARAF1    5'  CAACAGGAGGGCCTGAGC    63936    GA   AA
                                GT  AGG  CTCCTGTTG
                                ||  |||  |||||||||
                                CG  TCC  GAGGACAAC
                                 AG   GG
GAM603  KIF3C    3'  ACGGAAGTCCCTCCACTGG    9597        A   A   C
                                TCAGTG AGG ACT CTGT
                                |||||| ||| ||| ||||
                                GGTCAC TCC TGA GGCA
                                   C   C   A
GAM603  MAP2     3'  CAACAGGAAGACACTGG     48995       AAGGAAC
                                TCAGTG      TCCTGTTG
                                ||||||      ||||||||
                                GGTCAC      AGGACAAC
                                   AGA____
GAM603  PPP2R5A  3'  CAACCTGTCCTTCACCTAGT   20706     CA       ACTCCT
                                ACT  GTGAAGGA     GTTG
                                |||  ||||||||     ||||
                                TGA  CACTTCCT     CAAC
                                  TC       GTC___
GAM603  SHANK2   3'  ACAGGCTCCTGTCACTGAG    24582         _    ACT
                                CTCAGTGA AGGA   CCTGT
                                |||||||| ||||   |||||
                                GAGTCACT TCCT   GGACA
                                    G    C__
GAM603  SYNGR1   3'  AGGTGGGCTCTTCACTGAG    16309          AA  _
                                CTCAGTGAAGG  CT CCT
                                ||||||||||  || |||
                                GAGTCACTTCT  GG GGA
                                      CG  T
GAM603  TDE1     3'  CAAAGGTCTCCTTCACCGA    22341    A       ACT   G
                                TC GTGAAGGA   CCT TTG
                                || ||||||||   ||| |||
```

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                                AG CACTTCCT   GGA AAC
                                 C       CT_  _
GAM603  TGFB3    3'  CAACAAACCTCACTGAG     12258        A  AACTCC
                                CTCAGTGA GG     TGTTG
                                |||||||| ||     |||||
                                GAGTCACT CC     ACAAC
                                    _  AA_____
GAM603  TRAF5    3'  CAACAGGAATATACTGA     16074       AAGGAAC
                                TCAGTG      TCCTGTTG
                                ||||||      ||||||||
                                AGTCAT      AGGACAAC
                                   ATA____
GAM603  ZNF24    3'  CAACAGGAATTACAAAGT    22726     CA   AGGAAC
                                ACT  GTGA     TCCTGTTG
                                |||  ||||     ||||||||
                                TGA  CATT     AGGACAAC
                                  AA   A_____
GAM603  ADAMTSL1 3'  ACAAAAGACTCTTCACTGAG  57685          AA  CC
                                CTCAGTGAAGG  CT  TGT
                                ||||||||||  ||  |||
                                GAGTCACTTCT  GA  ACA
                                      CA  AA
GAM603  C1QTNF7  3'  GCACCTTGTTCTTCACTGA   49160          ACTCC
                                TCAGTGAAGGA    TGT
                                ||||||||||    |||
                                AGTCACTTCTT    ACG
                                      GTTCC
GAM603  DGS-A    3'  GCAACAGGGAGATTCC      84899      _   _
                                GGAA CTCC TGTTGC
                                |||| |||| ||||||
                                CCTT GAGG ACAACG
                                  A   G
GAM603  FLJ10607 3'  CAACAGAAATCCTTCAC     77106        ACTC
                                GTGAAGGA   CTGTTG
                                ||||||||   ||||||
                                CACTTCCT   GACAAC
                                    AAA_
GAM603  FLJ13340 3'  GCACTGGATTCTTTCACTGAG  54104           C   T  T
                                CTCAGTGAAGGAA TCC GT GC
                                |||||||||||| ||| || ||
                                GAGTCACTTTCTT AGG CA CG
                                      _   T  _
GAM603  FLJ14721 3'  GCAGGAGTCCCCTCACGAAGT  51583     CA   A  A
                                ACT  GTGA GG ACTCCTGT
                                |||  |||| || ||||||||
                                TGA  CACT CC TGAGGACG
                                  AG   C  C
GAM603  FLJ25359 5'  GGAGTTCCTCCACTCAG     58075    C    A
                                CT AGTG AGGAACTCC
                                || |||| |||||||||
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                                GA TCAC TCCTTGAGG
                                 C   C
GAM603  FLJ31547  3'  GCAACAAGATTTCTTCA     58831        C  C
                                TGAAGGAA TC TGTTGC
                                |||||||| || ||||||
                                ACTTCTTT AG ACAACG
                                     _  A
GAM603  FYCO1     3'  GCAACAAGAACCACCATTCACT 44495          _  AAC_  C
           GAGT                    ACTCAGTGAA GG    TC TGTTGC
                                |||||||||| ||    || ||||||
                                TGAGTCACTT CC    AG ACAACG
                                      A  ACCA  A
GAM603  KIAA1323  5'  GCAACAGGAATCCTGGTGGA   63043    AGTGA    AC
                                TC    AGGA  TCCTGTTGC
                                ||    ||||  |||||||||
                                AG    TCCT  AGGACAACG
                                 GTGG_    A_
GAM603  MGC12538  3'  CAACAAAAGCTTTGCTGG    51242     TG   GAA  CC
                                TCAG  AAG   CT  TGTTG
                                ||||  |||   ||  |||||
                                GGTC  TTC   GA  ACAAC
                                  GT   ___  AA
GAM603  MGC29761  5'  CAACAGGACGCCGCCGAGT    58326      A  GAA  AAC
                                ACTC GT   GG   TCCTGTTG
                                |||| ||   ||   ||||||||
                                TGAG CG   CC   AGGACAAC
                                  C  ___  GC_
GAM603  SCOP      3'  CAACTCACCCTCACTTCACTGA 91778          _  ACTCCT
                                TCAGTGAAG GA     GTTG
                                |||||||||  ||     ||||
                                AGTCACTTC CT     CAAC
                                     A  CCCACT
GAM603  SNAP29    3'  CAACAGGTCTTCCACTGG     16538        A    ACT
                                TCAGTG AGGA   CCTGTTG
                                |||||| ||||   |||||||
                                GGTCAC TTCT   GGACAAC
                                   C   ___
GAM603  TBDN100   3'  GCACTGGATTCTTTCACTGAG  46953            C   T  T
                                CTCAGTGAAGGAA TCC GT GC
                                |||||||||||||  ||| || ||
                                GAGTCACTTTCTT AGG CA CG
                                      _   T  _
GAM603  UBE4B     3'  CAGCATCCCTTCATGA      20163     G     AACTCC
                                TCA TGAAGG     TGTTG
                                ||| ||||||     |||||
                                AGT ACTTCC     ACGAC
                                  _     CT_____
GAM603  LOC145438 3'  GCAAAAACGCCCTCACTGAG   83338         A  AACTCCTG
                                CTCAGTGA GG       TTGC
                                ||||||||  ||       ||||
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                                GAGTCACT CC       AACG
                                    C  GCAAA___
GAM603   LOC148764 5'  CAACAACCTGTCACTGAGT    78982          _   AACTCC
                                ACTCAGTGA AGG     TGTTG
                                ||||||||| |||     |||||
                                TGAGTCACT TCC     ACAAC
                                   G   A_____
GAM603   LOC151623 5'  ACATGGACCCCCTCACTGG    85454        A  AAC   _
                                TCAGTGA GG   TCC TGT
                                ||||||| ||   ||| |||
                                GGTCACT CC   AGG ACA
                                    C  CC_   T
GAM603   LOC158696 3'  GGAGCTCCCCCACAGAGT    81973      A   AA   A
                                ACTC GTG  GGA CTCC
                                |||| |||  ||| ||||
                                TGAG CAC  CCT GAGG
                                  A   CC   C
GAM603   LOC199837 5'  CAACAAGAAAATTGACTTCACT 88406           GAAC___  C
           GAGT                   ACTCAGTGAAG      TC TGTTG
                                ||||||||||      || |||||
                                TGAGTCACTTC      AG ACAAC
                                     AGTTAAA  A
GAM603   LOC200261 3'  AGTTGCTCCACTGAGT      88652         A  G
                                ACTCAGTG AG AACT
                                |||||||| || ||||
                                TGAGTCAC TC TTGA
                                    C  G
GAM603   LOC219735 3'  GCAACAAGAATTCCTTTA     93109         C  C
                                TGAAGGAA TC TGTTGC
                                |||||||| || ||||||
                                ATTTCCTT AG ACAACG
                                    A  A
GAM603   LOC220370 3'  GCAAGTCACTCACCTCACTGAG 92827         A  AACTCCTG
                                CTCAGTGA GG       TTGC
                                |||||||| ||       ||||
                                GAGTCACT CC       AACG
                                    _  ACTCACTG
GAM603   LOC220686 3'  GCAACAGGAGCCGGACCTACA  92921     A   AA___
                                TG AGG    CTCCTGTTGC
                                || |||    ||||||||||
                                AC TCC    GAGGACAACG
                                 A   AGGCC
GAM603   LOC245757 3'  CAACAAGGGAGCTCACTGAGT  90775         AGGAA    __
                                ACTCAGTGA    CTCCT  GTTG
                                |||||||||    |||||  ||||
                                TGAGTCACT    GAGGG  CAAC
                                    C____    AA
GAM603   LOC51651  3'  CAACAAAAGCTGAATTTCTTCA 32182          _____  CC
           C                    GTGAAGGAA    CT  TGTTG
                                |||||||||    ||  |||||
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                                CACTTCTTT    GA  ACAAC
                                     AAGTC  AA
GAM603  LOC91137  3'  GGTTCCTTCACTGAGT     57066
                                ACTCAGTGAAGGAACT
                                ||||||||||||||||
                                TGAGTCACTTCCTTGG

GAM604  ARHGEF6  3'  CAAACTTGAAGCCAGGC     68197       ACCA
                                GCCTGG   CAAGTTTG
                                ||||||   ||||||||
                                CGGACC   GTTCAAAC
                                   GAA_
GAM604  CNTN2    3'  GTCACAACCCAGGTGA      17411        ACCACAA  _
                                TCGCCTGG      GTT TGAC
                                ||||||||      ||| ||||
                                AGTGGACC      CAA ACTG
                                    ________  C
GAM604  CORO2A   3'  AAACTGTGGTCCAGAGA     53398    GC        A
                                TC  CTGGACCACA GTTT
                                ||  ||||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM604  CORO2A   3'  AAACTGTGGTCCAGAGA     12642    GC        A
                                TC  CTGGACCACA GTTT
                                ||  ||||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM604  GRLF1    3'  AGGTCAGAAAGTGGCCCAGG   78551      A   AAG
                                CCTGG CCAC   TTTGACCT
                                |||||| ||||  ||||||||
                                GGACC GGTG   AGACTGGA
                                   C   AA_
GAM604  LAPTM5   3'  AGGCTTGTGGTCAAGC      22199    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCGGA
                                 AA_
GAM604  POU2AF1  3'  AGATTTACAGTCCAGGC     20647        CAC
                                GCCTGGAC   AAGTTT
                                ||||||||   ||||||
                                CGGACCTG   TTTAGA
                                     ACA
GAM604  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  54574         C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM604  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  6355         C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
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                                GACCTGGT TTC     CTG
                                    A   TGTCCT
GAM604  TRIM34   5'  AGGTCAAGTTGAGCCCAG    55224     ACCA   G
                                CTGG    CAA TTTGACCT
                                ||||    ||| ||||||||
                                GACC    GTT GAACTGGA
                                  CGA_   _
GAM604  TRIM9    5'  AGGCCAGGCAAGTCCAGGC    30749       CACAA    A
                                GCCTGGAC    GTTTG CCT
                                ||||||||    ||||| |||
                                CGGACCTG    CGGAC GGA
                                    AA___    C
GAM604  ABLIM    5'  GATATGTAACCCAGGCGG    22030       ACC   A
                                TCGCCTGG   ACA GTT
                                ||||||||   ||| |||
                                GGCGGACC   TGT TAG
                                    CAA   A
GAM604  AMOT     3'  AGGCATCTTCATGGTCCAGGGA 55716    G       C_   TT  A
                                TC CCTGGACCA  AAG  TG CCT
                                || |||||||||  |||  || |||
                                AG GGACCTGGT  TTC  AC GGA
                                 _       AC   T_ _
GAM604  DKFZp434D177 5'  TTAGACCCAGGCGA       50056       ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                    ________
GAM604  DKFZp434D177 5'  TTAGACCCAGGCGA       79443       ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                    ________
GAM604  FLJ23420  3'  CAAGTGGGTCCAGGC       46845         A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                    _  __
GAM604  HSA249128 5'  GGCGCGGTCCAGGCGG      34152          ACAA
                                TCGCCTGGACC    GTT
                                ||||||||||    |||
                                GGCGGACCTGG    CGG
                                      CG__
GAM604  MGC15668  5'  AGACCCGGTGGTCCAGACG   51277    C       AA_
                                CG CTGGACCAC   GTTT
                                || |||||||||   ||||
                                GC GACCTGGTG   CAGA
                                 A        GCC
GAM604  MGC22014  3'  AGGTCCCGAGTGTAACCCAGGT 64486        ACC   AGTTT
           GA                    TCGCCTGG   ACA    GACCT
                                ||||||||   |||    |||||
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                                AGTGGACC  TGT   CTGGA
                                    CAA  GAGCC
GAM604  SDCCAG10  5'  AGAGTTGTGGTCCAAAGA   19641   GCC       G
                                TC  TGGACCACAA TTT
                                ||  |||||||||| |||
                                AG  ACCTGGTGTT AGA
                                 AA_       G
GAM604  LOC115442 3'  AGGTCAGGGATGGTCCAG   72676       CAAG
                                CTGGACCA   TTTGACCT
                                ||||||||   ||||||||
                                GACCTGGT   GGACTGGA
                                    AG__
GAM604  LOC129011 5'  AGACCTGCGGTCCAGGC    74862        A  A
                                GCCTGGACC CA GTTT
                                ||||||||| || ||||
                                CGGACCTGG GT CAGA
                                     C  C
GAM604  LOC130536 5'  GCAAAGTCCAGGCG       75746        CACAAG   A
                                CGCCTGGAC    TTTG C
                                |||||||||     |||| |
                                GCGGACCTG    AAAC G
                                     _______  C
GAM604  LOC149108 3'  AGACTTCACTGTGGTCCA   84357        ____
                                TGGACCACA   AGTTT
                                |||||||||   |||||
                                ACCTGGTGT   TCAGA
                                     CACT
GAM604  LOC221688 5'  AGACTCGGGCCCAGACGA   93674    C   A  ACA
                                TCG CTGG CC  AGTTT
                                ||| |||| ||  |||||
                                AGC GACC GG  TCAGA
                                  A   C  GC_
GAM604  LOC256228 5'  AGACTTGTGGTCAAAGC    96233   CTG
                                GC  GACCACAAGTTT
                                ||  ||||||||||||
                                CG  CTGGTGTTCAGA
                                 AAA
GAM604  LOC257441 5'  TTAGACCCAGGCGA       95566        ACCACAA
                                TCGCCTGG     GTTTGA
                                ||||||||     ||||||
                                AGCGGACC     CAGATT
                                     _______
GAM604  LOC91960  3'  AGGTGCCTCTCGTGGTCCAAGC 67657   C      A  TTTG
                                GC TGGACCAC AG   ACCT
                                || |||||||| ||   ||||
                                CG ACCTGGTG TC   TGGA
                                 A      C  TCCG
GAM604  LOC92840  3'  GTCCCTCGGGTCCAGGC    56435        ACA  TTT
                                GCCTGGACC  AG  GAC
                                |||||||||  ||  |||
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                                CGGACCTGG  TC  CTG
                                     GC_ C__
GAM605  MSL3L1   3' AGCAGGCGCCAAGCACCCAA  54362      A AGACA
                                TTGGGT CT    TGTTTGCT
                                |||||| ||    ||||||||
                                AACCCA GA    GCGGACGA
                                   C ACC__
GAM605  STAF65(gamma) 3' AGCAAACATTGAGTACC    29424      AGAC
                                GGTACT   ATGTTTGCT
                                ||||||   |||||||||
                                CCATGA   TACAAACGA
                                   GT__
GAM605  LOC162083 5' AGCAAACACAGGCTGCACCCAG 82333      AC  ACA_
                                TTGGGT  TAG   TGTTTGCT
                                ||||||  |||   ||||||||
                                GACCCA  GTC   ACAAACGA
                                   C_  GGAC
GAM605  LOC253596 5' AGCCTCCTACTAGTACCCAA  95478        ACATGTTT
                                TTGGGTACTAG      GCT
                                ||||||||||       |||
                                AACCCATGATC      CGA
                                      ATCCTC__
GAM605  LOC51652  3' GGTACTAAGCCTAGTACCCAA 32195        ACATGTT
                                TTGGGTACTAG     TGCT
                                ||||||||||      ||||
                                AACCCATGATC     ATGG
                                      CGAATC_
GAM606  CDC42    3' AACAAAAACCCTTCA     8369      CCT
                                TGGGG  GGTTTTTGTT
                                |||||  ||||||||||
                                ACTTC  CCAAAAACAA
                                  ___
GAM606  CERD4    3' AACAAAAAGCTCCCAC     23848     _ CTGG
                                GTGGG GC   TTTTTGTT
                                ||||| ||   ||||||||
                                CACCC CG   AAAAACAA
                                   T ____
GAM606  COL5A3   3' TGAACAAAAGCCCCCCCAC  31697      CCT
                                GTGGGG  GGTTTTTGTTCA
                                ||||||  ||||||||||||
                                CACCCC  CCGAAAACAAGT
                                   C__
GAM606  DPYSL2   3' GAACAAGCAGCCCCCA     7297      C  GTT
                                TGGGG CTG  TTTGTTC
                                ||||| |||  |||||||
                                ACCCC GAC  GAACAAG
                                   C ___
GAM606  DRPLA    3' AACAAAAACATCCTCACA    8664       CCTG
                                TGTGGGG   GTTTTTGTT
                                |||||||   |||||||||
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                                ACACTCC   CAAAAACAA
                                   TA__
GAM606  E48     3' GACTTGGAGCAGGCCCCACA  13506         G  TT
                                TGTGGGGCCTG TTT  GTT
                                |||||||||| |||  |||
                                ACACCCCGGAC AGG  CAG
                                   G  TT
GAM606  FUT1    3' GCCAACAAGCCCCACA     3789        C  GTTT  TT
                                TGTGGGGC TG   TTG  C
                                |||||||| ||   |||  |
                                ACACCCCG AC   AAC  G
                                   A  ____  CT
GAM606  GCK     5' TGAAGGACACTAAGCCCCACA 3871        C   TT  G
                                TGTGGGGC TGGT  TT TTCA
                                |||||||| ||||  || ||||
                                ACACCCCG ATCA  AG AAGT
                                   A   C_  G
GAM606  ITSN2   3' AGAAACCAAACCCCATA    38970       CC
                                TGTGGGG  TGGTTTTT
                                |||||||  ||||||||
                                ATACCCC  ACCAAAGA
                                   AA
GAM606  MAPK4   3' AACAGCAGACCCTACA     10822       C  GTTT
                                TGTGGGG CTG   TTGTT
                                ||||||| |||   |||||
                                ACATCCC GAC   GACAA
                                   A  ____
GAM606  MEF2A   3' AACAAAAAAGCCCCACA    18775       CTGG
                                TGTGGGGC   TTTTTGTT
                                ||||||||   ||||||||
                                ACACCCCG   AAAAACAA
                                   A___
GAM606  MMP16   3' AACAAAAAACCCACA      19876      GCCTGG
                                TGTGGG     TTTTTGTT
                                ||||||     ||||||||
                                ACACCC     AAAAACAA
                                   A_____
GAM606  RALBP1  3' CGAAAACAAACCCCACA    22295       CCTG
                                TGTGGGG   GTTTTTG
                                |||||||   |||||||
                                ACACCCC   CAAAAGC
                                   AAA_
GAM606  SFTPA2  3' TGAACAAATCTGCACCCCAC  22652      CC  TT
                                GTGGGG  TGG  TTTGTTCA
                                ||||||  |||  ||||||||
                                CACCCC  GTC  AAACAAGT
                                   AC  T_
GAM606  SLA2    3' CATTAACCAGGCCCCAC    49895         TT
                                GTGGGGCCTGGTT  TG
                                ||||||||||||  ||
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                                CACCCCGGACCAA  AC
                                       TT
GAM606  SSPN     3'  TGAAAGCCAAGCACCACA    17446      G  C
                                TGTGG GC TGGTTTTTG
                                ||||| || |||||||||
                                ACACC CG ACCGAAAGT
                                   A  A
GAM606  XKRY     5'  AACAAAAACATGCCCACACA  60012     _   CTG
                                TGTG GGGC   GTTTTTGTT
                                |||| ||||   |||||||||
                                ACAC CCCG   CAAAAACAA
                                  A    TA_
GAM606  XKRY     5'  AACAAAAACATGCCCACACA  16251     _   CTG
                                TGTG GGGC   GTTTTTGTT
                                |||| ||||   |||||||||
                                ACAC CCCG   CAAAAACAA
                                  A    TA_
GAM606  ZNF253   3'  AACAGAAGCCCTACA       40734        CTGGT
                                TGTGGGGC    TTTTGTT
                                ||||||||    |||||||
                                ACATCCCG    AAGACAA
                                            ______
GAM606  AP4S1    3'  TAGAATCCAGGCCCCACA    22997          T
                                TGTGGGGCCTGG TTTTG
                                |||||||||||| |||||
                                ACACCCCGGACC AAGAT
                                       T
GAM606  BRDG1    5'  AGAAACCAAACCACACA     23992      G  CC
                                TGTG GG  TGGTTTTT
                                |||| ||  ||||||||
                                ACAC CC  ACCAAAGA
                                  A  AA
GAM606  C22orf2  3'  TGAAAACCAGACCGCACA    94458      G  C
                                TGTG GG CTGGTTTTTG
                                |||| || ||||||||||
                                ACAC CC GACCAAAAGT
                                  G  A
GAM606  DKFZP566G1424 3'  AACAAAAACCTCTCAC      84772       CCT
                                GTGGGG   GGTTTTTGTT
                                ||||||   ||||||||||
                                CACTCT   CCAAAAACAA
                                         ___
GAM606  DKFZP667O116 3'  GAAAACCAAACCCAACA     94282     G   CC
                                TGT GGG  TGGTTTTT
                                ||| |||  ||||||||
                                ACA CCC  ACCAAAAG
                                  A   AA
GAM606  FLJ10420  3'  AACACAAGCCCCCCA       36102       CCT    T
                                TGGGG   GGTTT TGTT
                                |||||   ||||| ||||
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                                ACCCC  CCGAA ACAA
                                  ___    C
GAM606  FLJ10815  3'  AAACTCAGGCCCCACA     36691          _
                                TGTGGGGCCTG GTTT
                                |||||||||||| ||||
                                ACACCCCGGAC CAAA
                                      T
GAM606  FLJ13782  3'  CAAGGGACAGGCCCCACA   46162          GT
                                TGTGGGGCCTG  TTTTG
                                ||||||||||  |||||
                                ACACCCCGGAC  GGAAC
                                      AG
GAM606  FLJ14596  5'  TGAACTCATCCAGCCCCACA  51464        C  TTTTT
                                TGTGGGGC TGG    GTTCA
                                |||||||| |||    |||||
                                ACACCCCG ACC    CAAGT
                                    _  TACT_
GAM606  FLJ21562  3'  TGAACAAAAATATGACCCCA  47077      CCTG
                                TGGGG   GTTTTTGTTCA
                                |||||   ||||||||||
                                ACCCC   TAAAAACAAGT
                                  AGTA
GAM606  FLJ22029  3'  GAACAAAAACCAGCCT     46330      C
                                GGGC TGGTTTTTGTTC
                                |||| ||||||||||||
                                TCCG ACCAAAAACAAG
                                  _
GAM606  FLJ22938  5'  CAAACACCCGAGGCCCCA   45159        __  T
                                TGGGGCCT  GGT TTTG
                                ||||||||  ||| ||||
                                ACCCCGGA  CCA AAAC
                                    GC  C
GAM606  FLJ22969  3'  TAAAGCCCAGGCCCCAC    68659          T
                                GTGGGGCCTGG TTTTG
                                |||||||||| |||||
                                CACCCCGGACC GAAAT
                                      C
GAM606  FLJ23191  5'  TGGAAACCAAGCCCCAC    44710       C     TT
                                GTGGGGC TGGTTT  G
                                ||||||| ||||||  |
                                CACCCCG ACCAAA  T
                                    A     GG
GAM606  GNG10     3'  AACAAAAACCTTACCAC     14674      GGCCT
                                GTGG    GGTTTTTGTT
                                ||||    ||||||||||
                                CACC    CCAAAAACAA
                                  ATT__
GAM606  KIAA0663  3'  AACAAAAATACCCAC       29123      GCCTG
                                GTGGG    GTTTTTGTT
                                |||||    |||||||||
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                                CACCC    TAAAAACAA
                                  A____
GAM606  KIAA0676 3' AAAACCAGACCCCCA      30447    T   C
                                TG GGGG CTGGTTTT
                                || |||| ||||||||
                                AC CCCC GACCAAAA
                                 _   A
GAM606  KIAA0802 3' TGAACAAAACTCTGCCCAACA 62568     G   CT    T
                                TGT GGGC  GGTTTT GTTCA
                                ||| ||||  |||||| |||||
                                ACA CCCG  TCAAAA CAAGT
                                  A   TC    _
GAM606  KIAA0945 3' CAGGAACCAGACCCAACA    30208     G   C
                                TGT GGG CTGGTTTTTG
                                ||| ||| ||||||||||
                                ACA CCC GACCAAGGAC
                                  A   A
GAM606  KIAA1260 3' AACAAAAACCACAAACA     60021     GGGGCC
                                TGT     TGGTTTTTGTT
                                |||     ||||||||||||
                                ACA     ACCAAAAACAA
                                  AAC___
GAM606  KIAA1321 3' CAAACCCAGACCCCAC      62223       C   TT
                                GTGGGG CTGG  TTTG
                                |||||| ||||  ||||
                                CACCCC GACC  AAAC
                                   A   C_
GAM606  KIAA1627 3' TGAACAAAAACTCTTCCCA   80755      CCT
                                TGGGG   GGTTTTTGTTCA
                                |||||   ||||||||||||
                                ACCCT   TCAAAAACAAGT
                                  TC_
GAM606  KIAA1856 3' ACTTAACCAGGCCCCA      92660          TTT
                                TGGGGCCTGGTT   GT
                                ||||||||||||   ||
                                ACCCCGGACCAA   CA
                                       TT_
GAM606  KIAA1937 3' AACATCACAGGCCCCCA     73690    T      GTTTT
                                TG GGGGCCTG     TGTT
                                || ||||||||     ||||
                                AC CCCCGGAC     ACAA
                                 _       ACT__
GAM606  MGC3178  3' GAAGCCAGAGCCCACA     47986       GC
                                TGTGGG  CTGGTTTT
                                ||||||  ||||||||
                                ACACCC  GACCGAAG
                                   GA
GAM606  NKX2C    5' CAAAACCCAGACCCCCA     59217    T   C   T
                                TG GGGG CTGG TTTTG
                                || |||| |||| |||||
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                                AC CCCC GACC AAAAC
                                 _   A   C
GAM606  P114-RHO-GEF 3'  CGGGAACCAGAGCCCCACA   31021        _
                                TGTGGGGC CTGGTTTTTG
                                |||||||| ||||||||||
                                ACACCCCG GACCAAGGGC
                                    A
GAM606  TReP-132  5'  AGAACCAGGCCCCCA      37288    T
                                TG GGGGCCTGGTTTT
                                || ||||||||||||
                                AC CCCCGGACCAAGA

                                 _
GAM606  TReP-132  5'  AGAACCAGGCCCCCA      53145    T
                                TG GGGGCCTGGTTTT
                                || ||||||||||||
                                AC CCCCGGACCAAGA

                                 _
GAM606  TReP-132  5'  AGAACCAGGCCCCCA      53135    T
                                TG GGGGCCTGGTTTT
                                || ||||||||||||
                                AC CCCCGGACCAAGA

                                 _
GAM606  LOC124599 3'  AGGGACCAAGACCCACA    75651      GCC
                                TGTGGG  TGGTTTTT
                                ||||||  ||||||||
                                ACACCC  ACCAGGGA
                                   AGA
GAM606  LOC126208 3'  GAGTGGCGACCAGGCCCCA  74463          T TG
                                TGGGGCCTGGTT T  TTC
                                |||||||||||| |  |||
                                ACCCCGGACCAG G  GAG
                                      C GT
GAM606  LOC138389 3'  GAACACAAAGCCCCGCA    76224       CTGG  T
                                TGTGGGGC   TTT TGTTC
                                ||||||||   ||| |||||
                                ACGCCCCG   AAA ACAAG
                                    ____  C
GAM606  LOC145439 5'  GAGACCAGAGCCCACA     77208      GC
                                TGTGGG  CTGGTTTT
                                ||||||  ||||||||
                                ACACCC  GACCAGAG
                                   GA
GAM606  LOC147817 5'  TGAACAGACAAACCCCACA  78508      CC  GTT
                                TGTGGGG  TG  TTTGTTCA
                                |||||||  ||  ||||||||
                                ACACCCC  AC  AGACAAGT
                                   AA  ___
GAM606  LOC150407 3'  AACAAAAAAAACCCCATA   79815      CCTGG
                                TGTGGGG   TTTTTGTT
                                |||||||   ||||||||
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                                ATACCCC    AAAAACAA
                                    AAA__
GAM606  LOC157226 5'  CGAAGGCCAGGCCCAACA    63932     G
                                TGT GGGCCTGGTTTTTG
                                ||| |||||||||||||
                                ACA CCCGGACCGGAAGC
                                  A
GAM606  LOC164382 3'  TAGAAACCAAACCGCACA    87204     G  CC
                                TGTG GG  TGGTTTTTG
                                |||| ||  |||||||||
                                ACAC CC  ACCAAAGAT
                                  G  AA
GAM606  LOC199958 3'  CAAACTCCGGGCCCCACA    89884          TT
                                TGTGGGGCCTGG  TTTG
                                ||||||||||||  ||||
                                ACACCCCGGGCC  AAAC
                                       TC
GAM606  LOC219621 3'  TGAAAGGAAAACCAAGCCCCAC 91460       C      G_
                                GTGGGGC TGGTTTTT  TTCA
                                ||||||| ||||||||  ||||
                                CACCCCG ACCAAAAG  AAGT
                                    A       GA
GAM606  LOC253019 3'  AACAAAAATACCCAC      95363      GCCTG
                                GTGGG    GTTTTTGTT
                                |||||    |||||||||
                                CACCC    TAAAAACAA
                                  A____
GAM606  LOC253975 3'  AACAAAAATACCCAC      95993      GCCTG
                                GTGGG    GTTTTTGTT
                                |||||    |||||||||
                                CACCC    TAAAAACAA
                                  A____
GAM606  LOC254413 5'  GAACAAAAAAAGCCACA    97123      GGC  GG
                                TGTGG   CT  TTTTTGTTC
                                |||||   ||  |||||||||
                                ACACC   GA  AAAAACAAG
                                  ___  A_
GAM606  LOC90829  3'  CAAAAACCAAACACCACA    64098      GGCC
                                TGTGG    TGGTTTTTG
                                |||||    |||||||||
                                ACACC    ACCAAAAAC
                                  ACAA
GAM606  LOC92689  3'  TAGGAACCAGGCCACACA    70227     G
                                TGTG GGCCTGGTTTTTG
                                |||| ||||||||||||
                                ACAC CCGGACCAAGGAT
                                  A
GAM607  ADAM17    3'  GGCTCATGCCTGTAATCCCAG  41557       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  ADAM17   3'  GGCTCATGCCTGTAATCCCAG  12083      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  ADCY2    3'  GGCACGTGCCTGTAGTCCCAG  65020         A TG  A
                                CTGGGACTACA G  TG GCC
                                |||||||||||  |  || |||
                                GACCCTGATGT C  GC CGG
                                      C GT  A
GAM607  AICDA    3'  GGCTCACGCCTGTAATCCCAG  40330      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  AK1      3'  GGCTCATGCCTGTAATCCCAG  4886       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  ALDH3A2  3'  GGCTCATGCCTGTAATCCCAG  69274      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  ALDH3B1  3'  GGCTCACACCTGTAATCCCAG  91531      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  ANKH     3'  GGCTCATGCCTGTAATCCCA   53991      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGTACTCGG
                                   A   C
GAM607  AOC3     5'  CACCCTTAGTCCCAGG      13584         CA  T
                                CCTGGGACTA  AG GTG
                                ||||||||||  || |||
                                GGACCCTGAT  TC CAC
                                      __  C
GAM607  APG5L    3'  GCTTTATTACTCTAATCCCAGG 16761        C  CA   T__
          TA                      TACCTGGGA TA  AGTG   GAGC
                                |||||||||  ||  ||||   ||||
                                ATGGACCCT AT  TCAT   TTCG
                                     A  C_    TAT
GAM607  APOC4    3'  GGCGGGTGCCTGTAGTCCCAG  7916          A TG GA
                                CTGGGACTACA G  T  GCC
                                |||||||||||  |  |  |||
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                                GACCCTGATGT C  G  CGG
                                      C GT GG
GAM607  ARHGEF6  3' GGCCCACACCTGTGGTCCCAG 68204          A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGGTGT CACAC CGG
                                      C    C
GAM607  ATF5     3' GGCTTATGCTTGTAATCCCAG 23807       C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCGTATTCGG
                                   A
GAM607  ATM      3' GCACCTGTAGTCCCAG     3512          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  ATM      3' GGCTCACGCCTGTAATCCCAG 3513       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  ATM      3' GGCTCACGCCTGTAATCCCAG 56296      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  ATM      3' GCTCACACCTATAATCCCAG  56306      C CAA
                                CTGGGA TA   GTGTGAGC
                                |||||| ||   ||||||||
                                GACCCT AT   CACACTCG
                                   A  ATC
GAM607  ATP1A2   3' GGCTCATGCCTGTAATCCCAG 5527       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  ATP6V1G2 3' CTCTCTTATAATTCCAGGTA  56279       C C  TGT
                                TACCTGGGA TA AAG  GAG
                                ||||||||| || |||  |||
                                ATGGACCTT AT TTC  CTC
                                      A A  T__
GAM607  ATP6V1G2 3' CTCTCTTATAATTCCAGGTA  55319       C C  TGT
                                TACCTGGGA TA AAG  GAG
                                ||||||||| || |||  |||
                                ATGGACCTT AT TTC  CTC
                                      A A  T__
GAM607  BCAS1    3' GGCACACACCTGTAGTCCCAG 13340         A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
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                                GACCCTGATGT CACAC CGG
                                      C    A
GAM607  BMP1    3' GCATCATTAGTCCCAG     20422        CAAGT  _
                                CTGGGACTA    GTGA GC
                                |||||||||    |||| ||
                                GACCCTGAT    TACT CG
                                     _____   A
GAM607  BRCA1   3' ACACCTGTAATCCCAG     23515      C   A
                                CTGGGA TACA GTGT
                                |||||| |||| ||||
                                GACCCT ATGT CACA
                                   A   C
GAM607  BRCA1   3' GGCTCACGCCTGTAATCCCAG 23522      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  BRCA1   3' ACACCTGTAATCCCAG     23523      C   A
                                CTGGGA TACA GTGT
                                |||||| |||| ||||
                                GACCCT ATGT CACA
                                   A   C
GAM607  BRCA1   3' GGCTCACGCCTGTAATCCCAG 23532      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  BRCA1   3' ACACCTGTAATCCCAG     23533      C   A
                                CTGGGA TACA GTGT
                                |||||| |||| ||||
                                GACCCT ATGT CACA
                                   A   C
GAM607  BRCA1   3' GGCTCACGCCTGTAATCCCAG 23539      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  BRCA1   3' ACACCTGTAATCCCAG     23540      C   A
                                CTGGGA TACA GTGT
                                |||||| |||| ||||
                                GACCCT ATGT CACA
                                   A   C
GAM607  BRCA1   3' GGCTCACGCCTGTAATCCCAG 23547      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  BRCA1   3' ACACCTGTAATCCCAG     23548      C   A
                                CTGGGA TACA GTGT
                                |||||| |||| ||||
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                                GACCCT ATGT CACA
                                   A   C
GAM607  BRCA1   3' GGCTCACGCCTGTAATCCCAG 23555      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  BRCA1   3' ACACCTGTAATCCCAG     23556      C   A
                                CTGGGA TACA GTGT
                                |||||| |||| ||||
                                GACCCT ATGT CACA
                                   A   C
GAM607  BRCA1   3' GGCTCACGCCTGTAATCCCAG 23563      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  BRCA1   3' ACACCTGTAATCCCAG     23564      C   A
                                CTGGGA TACA GTGT
                                |||||| |||| ||||
                                GACCCT ATGT CACA
                                   A   C
GAM607  BRCA1   3' GGCTCACGCCTGTAATCCCAG 23572      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  BRCA1   3' ACACCTGTAATCCCAG     23573      C   A
                                CTGGGA TACA GTGT
                                |||||| |||| ||||
                                GACCCT ATGT CACA
                                   A   C
GAM607  BRCA1   3' GGCTCACGCCTGTAATCCCAG 23580      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  BRCA1   3' ACACCTGTAATCCCAG     23581      C   A
                                CTGGGA TACA GTGT
                                |||||| |||| ||||
                                GACCCT ATGT CACA
                                   A   C
GAM607  BRCA1   3' GGCTCACGCCTGTAATCCCAG 23588      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  BRCA1   3' ACACCTGTAATCCCAG     23589      C   A
                                CTGGGA TACA GTGT
                                |||||| |||| ||||
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                                GACCCT ATGT CACA
                                   A   C
GAM607  BRCA1    3' GGCTCACGCCTGTAATCCCAG 23596      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  BRCA2    3' GGCTCATGCCTGTAATCCCA  3549       C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGTACTCGG
                                  A   C
GAM607  C1orf1   3' GGCTTACACCTGTAATCCCA  6864       C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CACATTCGG
                                  A   C
GAM607  C1orf1   3' GGTGTGTGCTTGTAGTCCCAG 6865           TG  A
                                CTGGGACTACAAG  TG GCC
                                |||||||||||||  || |||
                                GACCCTGATGTTC  GT TGG
                                      GT  G
GAM607  C21orf5  3' GGCTCACACCTGTAATCTCAG  17612      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACTCT ATGT CACACTCGG
                                   A   C
GAM607  C5R1     3' GGCTCACGCCTGTAATCCCAG  8208       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  CASP8    3' GGCTCATGTCTATAATCCCAG  6918       C  CAA TG
                                CTGGGA TA   G  TGAGCC
                                |||||| ||   |  ||||||
                                GACCCT AT   T  ACTCGG
                                   A  ATC GT
GAM607  CASP8    3' GGCTCATGTCTATAATCCCAG  52950      C  CAA TG
                                CTGGGA TA   G  TGAGCC
                                |||||| ||   |  ||||||
                                GACCCT AT   T  ACTCGG
                                   A  ATC GT
GAM607  CASP8    3' GGCTCATGTCTATAATCCCAG  52924      C  CAA TG
                                CTGGGA TA   G  TGAGCC
                                |||||| ||   |  ||||||
                                GACCCT AT   T  ACTCGG
                                   A  ATC GT
GAM607  CASP8    3' GGCTCATGTCTATAATCCCAG  52935      C  CAA TG
                                CTGGGA TA   G  TGAGCC
                                |||||| ||   |  ||||||
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                                GACCCT AT   T  ACTCGG
                                   A  ATC GT
GAM607  CD28     3'  GGCTCATGCTTGTAATCCCAG  20440       C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCGTACTCGG
                                   A
GAM607  CD68     3'  GGCTCATGCCTGTAATCCCAG  59799       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  CEACAM5  3'  GGCGCGCACCTGTAGTCCCAG  15160           A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CACGC CGG
                                      C    G
GAM607  CHRNA5   3'  GGCTCACACCTGTAATCCCAG  59757       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  CHST5    3'  GGCTCATGCCTGTAATCCCAG  24029       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  COG7     3'  GGCTCACGCCTGTAATCCCAG  67623       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  COPA     3'  GGCTCATACCTGTAATCCCAG  15188       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CATACTCGG
                                   A   C
GAM607  CORO2A   3'  GGCTCATGCCTGTAATCCCAG  12646       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  CORO2A   3'  GGCTCATGCCTGTAATCCCAG  53402       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  CPM      3'  GGCTCACACCTTGTAATCCCAG 59677       C   _
                                CTGGGA TACAAG TGTGAGCC
                                |||||| |||||| ||||||||
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                                GACCCT ATGTTC ACACTCGG
                                   A     C
GAM607  CPT2    3'  GGCTCATGCCTGTAATCCCAG  3642       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  CRACC   3'  GGCTCACACCTGTAATCCCAG  41009      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  CRSP9   3'  GGCTCACACTTATAATCCTAG  14960      C  C
                                CTGGGA TA AAGTGTGAGCC
                                |||||| || ||||||||||
                                GATCCT AT TTCACACTCGG
                                   A  A
GAM607  CTMP    3'  GGCGTACGCCTGTAGTCCCAG  53880         A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CGCAT CGG
                                      C    G
GAM607  CTMP    3'  GGCTCACACCTGTAATCCCAG  53881      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  CTSS    3'  GGCTCACGCCTGTAATCCCAG  14544      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  CYB561  3'  GCGCCTGTAGTCCCAG      8602          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  CYP4F3  3'  GCTCACACCTGTAATCCCAG  6118       C    A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
                                GACCCT ATGT CACACTCG
                                   A    C
GAM607  DAPP1   3'  GGCTCATGCCTGTAATCCCAGG 26919      C    A
                                CCTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GGACCCT ATGT CGTACTCGG
                                    A    C
GAM607  DBT     3'  GGCTCACGCCTGTAATCCCAG  8611       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  DCLRE1C  3' GGCTCACACTTGTAATCCCAG 42528      C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCACACTCGG
                                   A
GAM607  DCLRE1C  3' GGCTCATGCCTGTAATCCCAG 42529      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  DDOST    3' GCACCTGTAGTCCCAG     17817         A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  DDOST    3' GGCTCATGCCTGTAATCCCAG 17818      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  DFFA     3' GGCTCACGCCTGTAATCCCAG 15304      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  DGKI     5' GGTGCACACCTGTAGTCCCAG 16346        A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CACAC TGG
                                      C    G
GAM607  DHFR     3' GGCCCATGCCTGTAGTCCCAG 5810         A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CGTAC CGG
                                      C    C
GAM607  DHFR     5' GGCCCTGCCCAGTCCCAG    5811        ACAA  TGA
                                CTGGGACT   GTG  GCC
                                ||||||||   |||  |||
                                GACCCTGA   CGT  CGG
                                     CC__  CC_
GAM607  DHFR     3' GGCTCACACCTGTAATCCCAG 5812       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  DMC1     3' GGCATGTGCTTGTAATCCCAG 22976      C    TG  A
                                CTGGGA TACAAG  TG GCC
                                |||||| ||||||  || |||
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                                GACCCT ATGTTC  GT CGG
                                   A     GT  A
GAM607  DMC1     3'  GGCTCACACCTGTAATCCCAG  22977       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  DNASE1   5'  GGCTCACATTTGCCCCAGG   17825       ACTA
                                CCTGGG   CAAGTGTGAGCC
                                ||||||   ||||||||||||
                                GGACCC   GTTTACACTCGG
                                   C___
GAM607  DNASE2   3'  ATGCCTGTAGTCCCAG      7262           A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGTA
                                      C
GAM607  DNASE2   3'  GGCTCACATCTGTAACCCCAG  7266       AC   AG
                                CTGGG  TACA  TGTGAGCC
                                |||||  ||||  ||||||||
                                GACCC  ATGT  ACACTCGG
                                   CA   CT
GAM607  DNASE2   3'  GGCTCACGTATGTAATCCCAG  7267       C    AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  GCACTCGG
                                   A    AT
GAM607  DVL3     3'  GGCTCACGTCTGTAATCCCAG  15371      C    AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  GCACTCGG
                                   A    CT
GAM607  EFG2     5'  GGCTCACGCCTGTAATCCCAG  50477      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  EGFL5    3'  GGCTCACGCCTGTAATCCCAG  86624      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  EHHADH   3'  GGCTCACACCTGTAATCCCAG  8752       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  EPHB2    3'  CAGGTCTGCAGCTCCAGGTA   15442      GA  A  AG G
                                TACCTGG  CT CA  T TG
                                |||||||  || ||  | ||
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                                ATGGACC  GA GT  G AC
                                    TC  C  CT G
GAM607  EPHB2    3'  CAGGTCTGCAGCTCCAGGTA  33885       GA  A  AG G
                                TACCTGG  CT CA  T TG
                                |||||||  || ||  | ||
                                ATGGACC  GA GT  G AC
                                    TC  C  CT G
GAM607  F2R      3'  GCACCTGTAGTCCCAG     8840          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  F2R      3'  GGCTCACGCCTGTAATCCCAG  8841       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  F2RL3    3'  GGCTCACACCTGCAATCCCAG  14189      CTA  A
                                CTGGGA   CA GTGTGAGCC
                                ||||||   || |||||||||
                                GACCCT   GT CACACTCGG
                                   AAC  C
GAM607  F2RL3    3'  GGCTCACGCCTGTAATCCCAG  14190      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  F2RL3    3'  GGCATGCGCCTATAGTCCCAG  14188        CAA    A
                                CTGGGACTA   GTGTG GCC
                                |||||||||   ||||| |||
                                GACCCTGAT   CGCGT CGG
                                     ATC    A
GAM607  FANCC    3'  GGCTCACACCTGTGATCCCAG  70525      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT GTGT CACACTCGG
                                   A    C
GAM607  FANCD2   3'  GGCTCACACCTGTAATCCCAG  52357      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  FCMD     3'  GGCTCACACCTGTAATACCAG  22094     GAC    A
                                CTGG   TACA GTGTGAGCC
                                ||||   |||| |||||||||
                                GACC   ATGT CACACTCGG
                                  ATA    C
GAM607  FGFR1    3'  GCACCTGTAGTCCCAG      43616          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
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                                GACCCTGATGT CACG
                                      C
GAM607  FGFR1   3' GCACCTGTAGTCCCAG     43623          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  FGFR2   3' GGCTCATGCCTGTAATCCCAG 43380      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FGFR2   3' GGCTCATGCCTGTAATCCCAG 43386      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FKRP    3' GGCTCACGCCTGTAATCCCAG 44187      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FUT6    3' GGCTCACACCTGTAATCCCAG 3814       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  FUT6    3' GCTCCTGCAGTCCCAG     3813        ACAA  T
                                CTGGGACT   GTG GAGC
                                ||||||||   ||| ||||
                                GACCCTGA   CGT CTCG
                                     ____  C
GAM607  GGCX    3' GGCTCACGCCTGTAATCCCAG 5880       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  GGT2    5' GCTCGGAGCAGTCCCAG    73711       ACAA  G_
                                CTGGGACT   GT  TGAGC
                                ||||||||   ||  |||||
                                GACCCTGA   CG  GCTCG
                                     ____  AG
GAM607  GNE     3' GGCTCACGCCTGTAATCCCAG 18483      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  GP2     3' GGCTCATGCCTGTAATCCCAG 7682       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  GRAF    3' GCGCCTGTAGTCCCAG     30563         A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  GRAF    3' GGCTCACGCCTATAATCCCAG 30572      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGCACTCGG
                                   A  ATC
GAM607  GRM6    3' GGCTCACACCTGTAATCCCAG 5938       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  GTF2F1  3' GCGCCTGCAGTCCCAG     9152        A  A
                                CTGGGACT CA GTGT
                                |||||||| || ||||
                                GACCCTGA GT CGCG
                                    C  C
GAM607  HIP1    3' GGCTCACGCCTGTAATCCCAG 18062      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  HLA-E   3' GCTCATGCCTGTAATCCCAG  91024      C    A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
                                GACCCT ATGT CGTACTCG
                                   A   C
GAM607  HUNK    3' GGCTCACACCTGTAATCCCAG 27458      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  IAPP    3' GGCTCTTGCCTGTAGTCCCGG 4695         A   T
                                CTGGGACTACA GTG GAGCC
                                |||||||||||| ||| |||||
                                GGCCCTGATGT CGT CTCGG
                                      C   T
GAM607  IFIT4   3' GGCTCATGCCTGTAATCCCAG 70924      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  IFIT4   3' GGCTGGCACCTGTAGTCCCAG 70925        A   G
                                CTGGGACTACA GTGT AGCC
                                |||||||||||| |||| ||||
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                                GACCCTGATGT CACG TCGG
                                      C   G
GAM607  IFNAR1   3' GGCTCACACCTGTAATCCCAG 5285       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  IL10     3' GGCTCACGCCTGTAATCCCAG 5129       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  IL12RB2  3' GCTCATGCCTGTAATCCCAG  7770       C   A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
                                GACCCT ATGT CGTACTCG
                                   A   C
GAM607  IL13RA1  3' GGCTCACGCCTGTAATCCCAG 7776       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  IL17R    3' GGCTCACGCCTGTAATCCCAG 26779      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  IL1R1    3' GGCTCACGCCTATAATCCCAG 6063       C CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGCACTCGG
                                   A ATC
GAM607  IL4R     5' GGCTCATGCCTATAATCCCAG 4703       C CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGTACTCGG
                                   A ATC
GAM607  IPP      3' GGCTCACGCCTGTAGTCCCAG 19728        A
                                CTGGGACTACA GTGTGAGCC
                                |||||||||||| |||||||||
                                GACCCTGATGT CGCACTCGG
                                      C
GAM607  IRAK1    3' GGCTCACGCCTGTAATCCCAG 7811       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  IRAK4    3' ACACCTGTAGTCCCAG     61197        A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
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                                GACCCTGATGT CACA
                                      C
GAM607  ITGAL   3' GGCACACACCTGTAGTCCCAG 9393          A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CACAC CGG
                                      C    A
GAM607  JRK     3' GGCTCACGCCTGTAATCCCAG 86534      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  KAI1    3' GCACCTGTAGTCCCAG     9500          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  KCNA7   3' GCACCTGTAGTCCCAG     49052          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  KCNA7   3' GGCTCATGCCTGTAACCCCAG 49056      AC   A
                                CTGGG  TACA GTGTGAGCC
                                |||||  |||| |||||||||
                                GACCC  ATGT CGTACTCGG
                                   CA   C
GAM607  KCNJ5   3' GGCAGGTGCCTGTAGTCCCAG 6095          A TG GA
                                CTGGGACTACA G  T  GCC
                                |||||||||| |  |  |||
                                GACCCTGATGT C  G  CGG
                                      C GT GA
GAM607  KCNJ5   3' GGCTCACACCTGTGATCCCAG 6096       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT GTGT CACACTCGG
                                   A   C
GAM607  KCNK3   3' GGCTCACACCTGTATTCCCA  9551      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CACACTCGG
                                   T   C
GAM607  KCNK4   3' CACGCTGTCCCAGG       33504        TACA
                                CCTGGGAC   AGTGTG
                                ||||||||   ||||||
                                GGACCCTG   TCGCAC
                                     ____
GAM607  KCNK4   5' TCACCCGGTAGTCCCAG    52809         AAGT
                                CTGGGACTAC   GTGA
                                |||||||||   ||||
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                                GACCCTGATG   CACT
                                     GCC_
GAM607  KIF1B   3'  GGCTCACGCCTGTAATCCAAG  30590   G  C   A
                                CT GGA TACA GTGTGAGCC
                                || ||| |||| |||||||||
                                GA CCT ATGT CGCACTCGG
                                 A  A   C
GAM607  KLF8    5'  GGCTCACACCTGTAATCTCAG  23405      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACTCT ATGT CACACTCGG
                                   A   C
GAM607  KLRD1   3'  CTCACACTGCCCAGG      23678      ACTA  A
                                CCTGGG   CA GTGTGAG
                                ||||||   || |||||||
                                GGACCC   GT CACACTC
                                   ____  _
GAM607  KLRD1   3'  CTCACACTGCCCAGG      9619       ACTA  A
                                CCTGGG   CA GTGTGAG
                                ||||||   || |||||||
                                GGACCC   GT CACACTC
                                   ____  _
GAM607  KNSL1   3'  GGCTCATGCCTGTAATCCCAG  15749      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  LAMP2   3'  GGCTCACGCCTGTAATCCCAG  25715      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LDLR    3'  GCACCTGTAGTCCCAG     4988          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  LEP     3'  GCGCCTGTAGTCCCAG     4051          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  LEP     3'  GGCTCACGCCTGTAATCCCAG  4053       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LPP     3'  CTCACACTTGTAATCCCAG   18746      C
                                CTGGGA TACAAGTGTGAG
                                |||||| ||||||||||||
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                                GACCCT ATGTTCACACTC
                                   A
GAM607  LRRC2   3' GGCTCACACCTATAATCCCAG 44474      C CAA
                                CTGGGA TA  GTGTGAGCC
                                |||||| ||  |||||||||
                                GACCCT AT  CACACTCGG
                                   A ATC
GAM607  LRRC2   3' GGCTCACACCTGTAATCCCAG 44475      C  A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A  C
GAM607  LUZP1   3' GGCTCACACCTGTAATCCCAG 53301      C  A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A  C
GAM607  MAFF    3' GGCTCACATCTGTAATCCCAG 24650      C  AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  ACACTCGG
                                   A  CT
GAM607  MAFF    3' GGCTCATGCCTGTAGTCCCAG 24651        A
                                CTGGGACTACA GTGTGAGCC
                                |||||||||||| |||||||||
                                GACCCTGATGT CGTACTCGG
                                      C
GAM607  MCC     3' GGTGTTACTTACAGTCCCAG  9960       AC   TGA
                                CTGGGACT  AAGTG  GCC
                                ||||||||  |||||  |||
                                GACCCTGA  TTCAT  TGG
                                    CA    TG_
GAM607  MCM4    3' GGCTCACACCTGTAATCCCAG 61905      C  A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A  C
GAM607  MLLT4   3' GGCTCACACCTGTAATCCCAG 72486      C  A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A  C
GAM607  MOG     3' GGCTCACGCCTGTAATCCCAG 10105      C  A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A  C
GAM607  MS4A1   3' GGCAGTCACCTGTAGTCCCAG 3749        A  TGA
                                CTGGGACTACA GTG  GCC
                                |||||||||| |||  |||
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                                GACCCTGATGT CAC   CGG
                                      C   TGA
GAM607  MSH3    3' GGCGCACACCTGTAGTCCCAG  10121          A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CACAC CGG
                                      C    G
GAM607  MSH3    3' GGCTCATGCCTGTAATCCCAG  10122       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  MTMR8   3' GCGCCTGTAGTCCCAG      31294          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  MTMR8   3' GGCTTACGCCTGTAATCCCAG  31295       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCATTCGG
                                   A   C
GAM607  MTMR8   3' GGTGTGTGCCTATAGTCCCAG  31296         CAA TG  A
                                CTGGGACTA   G  TG GCC
                                |||||||||   |  || |||
                                GACCCTGAT   C  GT TGG
                                      ATC GT  G
GAM607  MYO1B   3' GGCTCACACCTATAATCCCA   24234      C  CAA
                                TGGGA TA   GTGTGAGCC
                                ||||| ||   |||||||||
                                ACCCT AT   CACACTCGG
                                   A  ATC
GAM607  MYO1C   3' GGCTCACGCCTGTAACCCCAG  61211       AC   A
                                CTGGG  TACA GTGTGAGCC
                                |||||  |||| |||||||||
                                GACCC  ATGT CGCACTCGG
                                   CA   C
GAM607  NFKBIL2 3' GGCTCACGCCTGTAATCCCA   25527      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                   A   C
GAM607  NPHP1   3' GGCTCACGCCTGTAATCCCA   62481      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                   A   C
GAM607  NPHS1   3' GGCGCATGCCTGTAGTCCCAG  16193          A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
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                                GACCCTGATGT CGTAC CGG
                                      C     G
GAM607  Nrap     3'  GGCTCATGCTTGTAATCCCA   57636       C
                                TGGGA TACAAGTGTGAGCC
                                ||||| ||||||||||||||
                                ACCCT ATGTTCGTACTCGG
                                   A
GAM607  NT5C2    3'  GGCTCACGCCTGTAATCCCAG  24240       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  OASL     3'  GCTCACACCTGTAATCCCAG   13579       C    A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
                                GACCCT ATGT CACACTCG
                                   A    C
GAM607  OPTN     3'  GGCTCATGCCTGTAATCCCAG  41769       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  PA2G4    3'  GGCTCACGCCTGTAATCCCAG  71301       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  PAICS    3'  GGCTCACACCTACGATCACAG  21258     G  CTACAA
                                CTG GA     GTGTGAGCC
                                ||| ||     |||||||||
                                GAC CT     CACACTCGG
                                  A  AGCATC
GAM607  PCDH11X  3'  GCGCCTGTAGTCCCAG      52010          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  PCDH11X  3'  GGCTCACACCTGTAATCCCAG  52011       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  PCDH11X  3'  GGCTCACGCCTGTAATCCCAG  52012       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  PCDH11Y  3'  GCGCCTGTAGTCCCAG      52063          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
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                                GACCCTGATGT CGCG
                                      C
GAM607  PCDH11Y  3'  GGCTCATACCTGTAATCCCAG  52064       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CATACTCGG
                                   A    C
GAM607  PCDH11Y  3'  GCGCCTGTAGTCCCAG      52069           A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  PCDH11Y  3'  GGCTCATACCTGTAATCCCAG  52070       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CATACTCGG
                                   A    C
GAM607  PCDHB9   3'  GGCACATGCTTGTAATCCCAG  38944       C        A
                                CTGGGA TACAAGTGTG GCC
                                |||||| |||||||||| |||
                                GACCCT ATGTTCGTAC CGG
                                   A         A
GAM607  PDE4C    3'  GGCTTATGCCTGTAATCCCGGT 6235       T    C    A
           A                     TACC GGGA TACA GTGTGAGCC
                                |||| |||| |||| |||||||||
                                ATGG CCCT ATGT CGTATTCGG
                                  _   A    C
GAM607  PIK3CG   3'  GGTATGTGCCTGTAGTCCCAGG 10588             A TG  A
           TA                     TACCTGGGACTACA G  TG GCC
                                |||||||||||||| |  || |||
                                ATGGACCCTGATGT C  GT TGG
                                       C GT  A
GAM607  PIK3R2   3'  GGCTCATGCCTGTAATCCCAG  17259       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  PKD2     3'  GGCTCACGCCTGTAATCCCAG  60094       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  PLA2G2D  3'  GGCTCATGCCTGTAATCCCA   24797       C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGTACTCGG
                                  A    C
GAM607  POLK     3'  GGCTCACACCTGTAATGCCAG  32568      GAC    A
                                CTGG   TACA GTGTGAGCC
                                ||||   |||| |||||||||
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                                GACC   ATGT CACACTCGG
                                  GTA    C
GAM607   POLL     3'  GGCTGGTTTGAAGCCCCAGGTA 25180        A  A    TG G
                                TACCTGGG CT CAAG  T AGCC
                                |||||||| || ||||  | ||||
                                ATGGACCC GA GTTT  G TCGG
                                     C  A    __ G
GAM607   PSD      5'  GGCGCACGCCTGTAGTCCCAG  10932          A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CGCAC CGG
                                       C    G
GAM607   PSMB2    3'  GGCTCATGCCTGTAATCCCAG  10952       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   PSMB9    3'  GGCTCACACCTATAATCCCAG  10963       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACACTCGG
                                   A  ATC
GAM607   PTAFR    3'  GGCTCACACCTGTAATCCCAG  6299        C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   PTAFR    3'  GGCACACGCCTGTAGTCCCAG  6297          A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CGCAC CGG
                                       C    A
GAM607   PTGS1    3'  GCTCACACTCCAGTGGCAG   6353     GG   ACA
                                CTG  ACT   AGTGTGAGC
                                |||  |||   |||||||||
                                GAC  TGA   TCACACTCG
                                  GG   CC_
GAM607   PTGS1    3'  GCTCACACTCCAGTGGCAG   54572    GG   ACA
                                CTG  ACT   AGTGTGAGC
                                |||  |||   |||||||||
                                GAC  TGA   TCACACTCG
                                  GG   CC_
GAM607   RAB3B    3'  GGCTCACGCCTGTAATCCCAG  11186       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   RAB7L1   3'  GGCTCATGCCTGTAATCCCAG  14109       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  RAB7L1   3' GGCTCACACCTGTAATCCCAG 14108      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  RANBP9   3' GCTCACACTTATATTGTGG  18522     _____
                                CTACA    AGTGTGAGC
                                |||||    |||||||||
                                GGTGT    TCACACTCG
                                  TATAT
GAM607  RBBP9    3' GGCTCATGCCTGTAATCCCAG 70136      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  RPS6KA2  3' ACACCCACGTCCCAGGTA   40904        TACAA
                                TACCTGGGAC   GTGT
                                ||||||||||   ||||
                                ATGGACCCTG   CACA
                                     CACC_
GAM607  RRAD     3' GGCTCATATGCGTCCCA    14786      TACAA
                                TGGGAC   GTGTGAGCC
                                ||||||   |||||||||
                                ACCCTG   TATACTCGG
                                   CG___
GAM607  SCAP2    3' GTTCACCTGCAGTCCCAG   14111       ACA  T
                                CTGGGACT  AG GTGAGC
                                ||||||||  || ||||||
                                GACCCTGA  TC CACTTG
                                    CG_ _
GAM607  SIM2     3' GGCTCACACCTGTAATCCCAG 23786      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  SLC11A3  3' GCCCACACTTGTGAAGGT   27435     GGGAC       A
                                ACCT    TACAAGTGTG GC
                                ||||    |||||||||| ||
                                TGGA    GTGTTCACAC CG
                                  A____        C
GAM607  SLC14A2  3' GGCTCACGCCTGTAATCCCAG 23137      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  SLC17A5  3' GGCTCATGCCTGTAGTCCCAG 24892         A
                                CTGGGACTACA GTGTGAGCC
                                |||||||||| |||||||||
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                                GACCCTGATGT CGTACTCGG
                                      C
GAM607  SLC25A15 3' GGCACGTGCCTGTAGTCCCAG 26511         A TG  A
                                CTGGGACTACA G  TG GCC
                                |||||||||||  |  || |||
                                GACCCTGATGT C  GC CGG
                                      C GT  A
GAM607  SLC26A4  3' GCGCCTGTAGTCCCAG     4786          A
                                CTGGGACTACA GTGT
                                |||||||||||  ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  SLC26A4  3' GGCTCATGCCTGTAATCCCAG 4787       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  SLC28A2  3' GCGACTGTAGTCCCAG     14870         AGT  GA
                                CTGGGACTACA   GT  GC
                                ||||||||||   ||  ||
                                GACCCTGATGT   CA  CG
                                      ___  G_
GAM607  SLC2A3   3' GGCTCACGCCTGTAATCCCAG 22664       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  SLC2A6   3' GGCTCACGCCTGTAATCCCAG 34159       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  SMG1     3' GCGCCTGTAGTCCCAG     30653         A
                                CTGGGACTACA GTGT
                                |||||||||||  ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  SMG1     3' GGCTCACGCCTGTAATCCCAG 30654       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  STAT3    3' GCGCCTGTAGTCCCAG     12000         A
                                CTGGGACTACA GTGT
                                |||||||||||  ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  STAT3    3' GGCTCACGCCTGTAATCCCAG 12001       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  STAT3    3' GCGCCTGTAGTCCCAG     57715          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  STAT3    3' GGCTCACGCCTGTAATCCCAG 57716       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  SULT1A3  3' GGCACTTACCTGTAGTCCCAG 12054         A  TGA
                                CTGGGACTACA GTG  GCC
                                |||||||||| |||  |||
                                GACCCTGATGT CAT  CGG
                                      C  TCA
GAM607  SULT1C1  3' CTTTTCTTTTAGTCCCA    6467        C  TGT
                                TGGGACTA AAG  GAG
                                |||||||| |||  |||
                                ACCCTGAT TTC  TTC
                                     T  TT_
GAM607  SULT2A1  3' GGCTCATGTCTGTAATCCCAG 71754      C   AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  GTACTCGG
                                   A   CT
GAM607  SUV39H2  3' GGCTCACACCTGTGATCCCAG 45140      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT GTGT CACACTCGG
                                   A   C
GAM607  SUV39H2  3' GGCACACGCCTGTAGTCCCAG 45138        A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CGCAC CGG
                                      C    A
GAM607  SWAP70   3' GGCTCACGCCTGTAATCCCAG 71352      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  TBX6     3' GGCTCACGCATGTAATCCCAG 54966      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   A
GAM607  TCTA     3' GGCTCACGCCTGTAATCCCA  42240      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
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                                ACCCT ATGT CGCACTCGG
                                  A   C
GAM607  TEM7    3' GGCTCACGCCTGTAATCCCAG 39890      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  TEM7    3' GGCTCACGCCTGTAGTCCCAGG 39891          A
           TA                    TACCTGGGACTACA GTGTGAGCC
                                |||||||||||||| |||||||||
                                ATGGACCCTGATGT CGCACTCGG
                                       C
GAM607  TEM7    3' GGTGCACCTGTAGTCCCAG   39894        A   GA
                                CTGGGACTACA GTGT  GCC
                                |||||||||| ||||  |||
                                GACCCTGATGT CACG  TGG
                                      C   __
GAM607  TEP1    3' GGCTCACGCTTGTAATCCCAG 23044      C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCGCACTCGG
                                   A
GAM607  TM7SF3  3' GGCTCACACCTGTAATCCCA  59668     C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CACACTCGG
                                  A   C
GAM607  TNFRSF10A 3' GGCTCATGCCTGTAATCCCAG 13887      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  TNFRSF10D 3' GGCTCATGCCTGTAATCCCAG 13861      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  TNFRSF6B  5' GCTCACACTCGAGCAG     33167    GGA  ACA
                                CTG   CT   AGTGTGAGC
                                |||   ||   |||||||||
                                GAC   GA   TCACACTCG
                                  ___  GC_
GAM607  TNFSF10   3' GGCACATGCCTGTAGTCCCAG 13750         A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CGTAC CGG
                                      C    A
GAM607  TNFSF10   3' GGCTCACACCTGTAATCCCA  13751      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
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                                ACCCT ATGT CACACTCGG
                                  A    C
GAM607  TNFSF15  3'  GGCTCACACCTGTAATCCCA  17596      C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CACACTCGG
                                  A    C
GAM607  TPM4     3'  GCCTGCCTGTAGTCCCAG    12372          A T  GA
                                CTGGGACTACA G GT  GC
                                |||||||||||| | ||  ||
                                GACCCTGATGT C CG  CG
                                      _ _  TC
GAM607  TSN      3'  GGCTCACACCTGTAATCCCAG  16110       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  TSNAX    3'  GGCTCACGCCTGTAATCCCAG  20001       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  TTF2     3'  GGCTCATGCCTGTAATCCCG   13175      C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                GCCCT ATGT CGTACTCGG
                                  A    C
GAM607  UBE2B    3'  GGCTCCCACCTGTAGTCCCAG  12475          A   T
                                CTGGGACTACA GTG GAGCC
                                |||||||||||| ||| |||||
                                GACCCTGATGT CAC CTCGG
                                      C   C
GAM607  UBE2G2   3'  GCGCCTGTAGTCCCAG      64861          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  UBE2G2   3'  GGCTCACGCCTGCAATCCCAG  64863       CTA  A
                                CTGGGA   CA GTGTGAGCC
                                ||||||   || |||||||||
                                GACCCT   GT CGCACTCGG
                                   AAC  C
GAM607  UC28     3'  GGCTCACGCCTGTAATCCCAG  41292       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  UPK1B    3'  GGCTCATGCCTGTAATCCCAG  22720       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  UQCRC1   5' ACTTGTGGTCCCAGGTA    12552
                                TACCTGGGACTACAAGT
                                |||||||||||||||||
                                ATGGACCCTGGTGTTCA

GAM607  USP14    3' GGCTCACGCCTGTAATCCCAG 17661      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  VDR      3' GGCTCACGCCTGTAATCCCAG 4570       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  VHL      3' GCGCCTGTAGTCCCAG      5072          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  VHL      3' GGCTCATGCCTGTAATCCCAG 5076       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  VHL      3' GGCTCATGCCTGTAATCCCAG 5077       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  WIG1     3' GGCTCACGCCTGTAATCCCAG 94468      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  WSX1     3' GGCTCACGCCTGTAATCCCAG 16737      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  ZNF136   3' GGCTCACACCTGTAATCCCAG 59889      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  ZNF137   3' GGCTCACACCTGTAATCCCAG 12866      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  ZNF14    3' GGCTCATGCCTATAGTCCCAG 40716        CAA
                                CTGGGACTA  GTGTGAGCC
                                |||||||||  |||||||||
                                GACCCTGAT  CGTACTCGG
                                     ATC
GAM607  ZNF36    3' GGCTCACGCCTGTAATCCCAG 93966      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  ZNF74    3' GGCTCACACCTGTAATCTTA  12802      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ATTCT ATGT CACACTCGG
                                   A   C
GAM607  ZNF91    3' GCGCCTGTAGTCCCAG     12821          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  AAK1     3' GGCTCACACTTGTAACCACAGG 29852     _ AC
                                CCTG GG  TACAAGTGTGAGCC
                                |||| ||  ||||||||||||||
                                GGAC CC  ATGTTCACACTCGG
                                  A  A_
GAM607  AF020591 3' GCTCCTGTAGTCCCAG     27142          AGTGT
                                CTGGGACTACA    GAGC
                                ||||||||||    ||||
                                GACCCTGATGT    CTCG
                                      C____
GAM607  AF020591 3' GGCGCATACCTGTAGTCCCAG 27143         A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CATAC CGG
                                      C    G
GAM607  AF020591 3' GGCTCATGCCTGTAATCCCAG 27144      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  AF020591 3' CTCACACCTGTAATCCCAG   27138      C   A
                                CTGGGA TACA GTGTGAG
                                |||||| |||| |||||||
                                GACCCT ATGT CACACTC
                                   A   C
GAM607  AGMAT    3' GCTCACGCCTGTAATCCCAGG 45405       C   A
                                CCTGGGA TACA GTGTGAGC
                                ||||||| |||| ||||||||
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                                GGACCCT ATGT CGCACTCG
                                    A    C
GAM607  AKR1D1   3'  GGCTCATGCCTATAATCCCAG  19977      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGTACTCGG
                                    A  ATC
GAM607  ALOX15B  3'  GGCTCATGCCCATAATCCCAG  6691       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGTACTCGG
                                    A  ACC
GAM607  AP1GBP1  3'  GCACCTGTAGTCCCAG      54532          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CACG
                                       C
GAM607  AP1GBP1  3'  GGCTCACACCTGTAATCTCA  54534      C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACTCT ATGT CACACTCGG
                                   A    C
GAM607  AP4S1    3'  GGCTCACGCCAGTAATCCCAG  22995      C   AA
                                CTGGGA TAC  GTGTGAGCC
                                |||||| |||  |||||||||
                                GACCCT ATG  CGCACTCGG
                                    A   AC
GAM607  AP4S1    3'  GGTGTGTGCCTATAGTCCCA   22996       CAA TG  A
                                TGGGACTA   G  TG GCC
                                ||||||||   |  || |||
                                ACCCTGAT   C  GT TGG
                                     ATC GT  G
GAM607  APOF     3'  GGCTCACGCCTGTAATCCCAG  7912       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                    A    C
GAM607  APXL2    3'  GGCTCACGCCTGTAATCCCAG  75192      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                    A    C
GAM607  ARNTL2   3'  GGCTCATGCCTGTAATCCCAG  39469      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                    A    C
GAM607  BIA2     3'  GGCTCACGCCTGTAATCCCAG  71283      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  BIRC1    3' GGCACATGCCTGTAGTCCCAG 15790         A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CGTAC CGG
                                      C    A
GAM607  BIRC1    3' GGCTCACACCTGTAATCCCAG 15791      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  BIRC3    3' GGTATGTGCCTGTAGTCCCAGG 67198         A TG  A
                                CCTGGGACTACA G  TG GCC
                                |||||||||||| |  || |||
                                GGACCCTGATGT C  GT TGG
                                      C GT  A
GAM607  BLOV1    3' GGCTCACGCCTGTAATCCCAG 76283      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  BNIP-S   3' GGCTCACGTCTGTAATCCCAG 56273      C   AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  GCACTCGG
                                   A   CT
GAM607  BTN3A2   3' GCACCTGTAGTCCCAG     22911         A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  C13orf1  3' GGCTCACACCTGTAATCCCAG 39973      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  C1orf24  3' GCTTACACCTATAATCCCAG  53723      C  CAA
                                CTGGGA TA   GTGTGAGC
                                |||||| ||   ||||||||
                                GACCCT AT   CACATTCG
                                   A  ATC
GAM607  C1orf33  3' GGCATGTGCCTGTAGTCCCAG 32460         A TG  A
                                CTGGGACTACA G  TG GCC
                                |||||||||||| |  || |||
                                GACCCTGATGT C  GT CGG
                                      C GT  A
GAM607  C1QTNF2  3' GCTCATGCCTATAATCCCAGG 49130      C  CAA
                                CCTGGGA TA   GTGTGAGC
                                ||||||| ||   ||||||||
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                                  GGACCCT AT   CGTACTCG
                                      A  ATC
GAM607   C20orf108 3'  GGCACACGCCTGTAGTCCCAG  55048          A    A
                                  CTGGGACTACA GTGTG GCC
                                  |||||||||||| ||||| |||
                                  GACCCTGATGT CGCAC CGG
                                        C    A
GAM607   C20orf108 3'  GGCTCACGCCTGTAATCCCAG  55049       C    A
                                  CTGGGA TACA GTGTGAGCC
                                  |||||| |||| |||||||||
                                  GACCCT ATGT CGCACTCGG
                                     A    C
GAM607   C20orf12  3'  GGCTTACGCCTGTAATCCCAG  36325       C    A
                                  CTGGGA TACA GTGTGAGCC
                                  |||||| |||| |||||||||
                                  GACCCT ATGT CGCATTCGG
                                     A    C
GAM607   C20orf142 3'  GGCTCACACCTATAATCCTGG  74782   TG   C  CAA
                                  C  GGA TA   GTGTGAGCC
                                  |  ||| ||   |||||||||
                                  G  CCT AT   CACACTCGG
                                   GT   A  ATC
GAM607   C20orf142 3'  GGCTCACACCTGTAATCCTAG  74783       C    A
                                  CTGGGA TACA GTGTGAGCC
                                  |||||| |||| |||||||||
                                  GATCCT ATGT CACACTCGG
                                     A    C
GAM607   C20orf175 3'  GGCTCACGCCTGTAATCCCA   55066      C    A
                                  TGGGA TACA GTGTGAGCC
                                  ||||| |||| |||||||||
                                  ACCCT ATGT CGCACTCGG
                                     A    C
GAM607   C20orf177 3'  GGCTCACGCCTGTAATCCCAG  62152       C    A
                                  CTGGGA TACA GTGTGAGCC
                                  |||||| |||| |||||||||
                                  GACCCT ATGT CGCACTCGG
                                     A    C
GAM607   C20orf183 3'  GGCTCACGCCTGTAATCCCAG  47808       C    A
                                  CTGGGA TACA GTGTGAGCC
                                  |||||| |||| |||||||||
                                  GACCCT ATGT CGCACTCGG
                                     A    C
GAM607   C20orf29  3'  GGCTCACGCCTGTAATCCCAG  37127       C    A
                                  CTGGGA TACA GTGTGAGCC
                                  |||||| |||| |||||||||
                                  GACCCT ATGT CGCACTCGG
                                     A    C
GAM607   C21orf108 3'  GGCTCACGCCTATAATCCCAG  88724       C  CAA
                                  CTGGGA TA   GTGTGAGCC
                                  |||||| ||   |||||||||
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                                GACCCT AT   CGCACTCGG
                                   A  ATC
GAM607  C22orf19  3'  GGCTCACGTCTGTAATCCCAG  13427       C    AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  GCACTCGG
                                   A    CT
GAM607  C2F       3'  GGCTCACGCCTGTAATCCCAG  20932       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  C6orf5    3'  GCGCCTGTAGTCCCAG      31351           A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  C6orf5    3'  GGCTCACACCTGTAATCCCAG  31358       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  C8orf17   3'  GGCACATGCCTGTAGTCCCAG  39604           A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CGTAC CGG
                                      C    A
GAM607  C8orf2    3'  GGCTCACACCTGTAATCCCAG  23167       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  C9orf5    3'  GGCTCACATCTGTAATCCCAG  49280       C    AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  ACACTCGG
                                   A    CT
GAM607  CALN1     3'  GGCTCACACCTATAATCCCAG  48872       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACACTCGG
                                   A  ATC
GAM607  CCR6      3'  GGCTCACACCTGTAATCCCAG  48588       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  CCR6      3'  GGCTCACACCTGTAATCCCAG  15172       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  CDT1    3'  GGCTCACGCCTGTAACCCCAG  77674      AC   A
                                CTGGG  TACA GTGTGAGCC
                                |||||  |||| |||||||||
                                GACCC  ATGT CGCACTCGG
                                   CA   C
GAM607  CENTA2  3'  ATGCCTGTAGTCCCAG      37264          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGTA
                                      C
GAM607  cerk    3'  GGCTCACGCCTGTAATCCCAG  42851       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  CES2    3'  GGCCCATACTTGTAATCCCAG  13917       C        A
                                CTGGGA TACAAGTGTG GCC
                                |||||| |||||||||| |||
                                GACCCT ATGTTCATAC CGG
                                   A        C
GAM607  CFLAR   3'  GGCTCACACCTGTAATCCCAG  13930       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  CG012   5'  GGCTCATGCCTGTAATCCCA   83225       C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGTACTCGG
                                   A   C
GAM607  CGRP-RCP 3' CTCATGCTTGTAATCCCAG   27129       C
                                CTGGGA TACAAGTGTGAG
                                |||||| ||||||||||||
                                GACCCT ATGTTCGTACTC
                                   A
GAM607  CHRFAM7A 3' ATGCTTGTAATCCCAG      95016       C
                                CTGGGA TACAAGTGT
                                |||||| |||||||||
                                GACCCT ATGTTCGTA
                                   A
GAM607  CHST3   3'  GGCTCATACCTGTAATCCCAG  14978       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CATACTCGG
                                   A   C
GAM607  CLDN15  3'  GGCTCATGCCTGTAATCCCAG  56562       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  CLONE24922 3'  GCACTTGTAATCCCAG      31623       C
                                CTGGGA TACAAGTGT
                                |||||| |||||||||
                                GACCCT ATGTTCACG
                                   A
GAM607  CNNM1    3'  GGCTCACACCTGTAATCCCA   39775      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CACACTCGG
                                  A   C
GAM607  CPR2     3'  GGCTCACGTCTGTAATCCCAG  48101      C   AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  GCACTCGG
                                   A   CT
GAM607  CREB-H   5'  GCTTGCCCAGCCCCAGGTA   50885        A  ACAAGT TG
                                TACCTGGG CT     G  AGC
                                |||||||| ||     |  |||
                                ATGGACCC GA     C  TCG
                                     C  CC_____ GT
GAM607  CRTAM    3'  GCACCTGTAGTCTCAG      38982          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACTCTGATGT CACG
                                      C
GAM607  CSAD     3'  GGCTCACGCCTGTAATCCCAG  32032       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  CYorf14  3'  GCTCACACCCTGTAATCCCAG  37609       C   A_
                                CTGGGA TACA  GTGTGAGC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  CACACTCG
                                   A   CC
GAM607  D21S2056E 3'  GGCTCACACCTGTAATCCCAG  13473       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  DDO      3'  CATGCCTATAGTCCCAG     14448         CAA
                                CTGGGACTA   GTGTG
                                |||||||||   |||||
                                GACCCTGAT   CGTAC
                                     ATC
GAM607  DDO      3'  CATGCCTATAGTCCCAG     13325         CAA
                                CTGGGACTA   GTGTG
                                |||||||||   |||||
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                                GACCCTGAT   CGTAC
                                      ATC
GAM607   DDX34    3'  GCGCCTGTAGTCCCAG      27984          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                       C
GAM607   DDX34    3'  GGCTTACGCCTGTAATCCCAG  27987       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCATTCGG
                                   A    C
GAM607   DEGS     3'  GGCTCATGCCTATAATCCCAG  13413       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGTACTCGG
                                   A  ATC
GAM607   DJ122O8.2 3'  GGCTCATGCTTGTAATCCCAG  39992       C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCGTACTCGG
                                   A
GAM607   dJ383J4.3 3'  GGCTCACACCTGTAATTCCAG  66945       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCTT ATGT CACACTCGG
                                   A    C
GAM607   DKFZP434B168 3'  GCGCCTGTAGTCCCAG      31255          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                       C
GAM607   DKFZP434C171 3'  GCGCCTGTAGTCCCAG      31556          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                       C
GAM607   DKFZP434C171 3'  GGCTCACGCCTGTAATCCCAG  31558       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607   DKFZP434C1715 3'  GGCACACACCTGTAGTCCCAG  86150          A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CACAC CGG
                                       C    A
GAM607   DKFZp434E0519 3'  GGCTCACACTTATAATCCCAG  49990       C  C
                                CTGGGA TA AAGTGTGAGCC
                                |||||| || ||||||||||
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                                GACCCT AT TTCACACTCGG
                                   A  A
GAM607   DKFZp434E0519 3'  GGCTCACACCTATAATCCCAG  49989       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACACTCGG
                                   A  ATC
GAM607   DKFZp434E169 3'  GCGCCTGTAGTCCCAG      50063          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   DKFZp434E2220 5'  GGCGCGTGCTTGTAATCCCAG  34299       C     TG  A
                                CTGGGA TACAAG  TG GCC
                                |||||| ||||||  || |||
                                GACCCT ATGTTC  GC CGG
                                   A     GT  G
GAM607   DKFZP434F1735 3'  GGCACACACCTGTAGTCCCAG  31499          A     A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CACAC CGG
                                      C     A
GAM607   DKFZp434G171 3'  GGCTCACGCTTGTAATCCCAG  79436       C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCGCACTCGG
                                   A
GAM607   DKFZp434G171 3'  GGCTCATGCCTGTAATCCCAG  79437       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607   DKFZP434N1511 3'  GCGCCTGTAGTCCCAG      91418          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   DKFZP434N1511 3'  GGCTCATGCCTGTAATCCCAG  91419       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607   DKFZp547C176 3'  GGCTCACACCTGTAATCCCAG  67229       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607   DKFZp547I014 5'  GGCTCCATCCTGTAGTCCCA   39546          A_   T
                                TGGGACTACA  GTG GAGCC
                                ||||||||||  ||| |||||
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                                ACCCTGATGT  TAC CTCGG
                                      CC  _
GAM607  DKFZp547I094 3'  GGCTCACACCTGTAATCCCAG  49642       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  DKFZP564A022 3'  GCGCCTGTAGTCCCAG      48228          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  DKFZP564B1023 3'  GGCATGCACCTGTAGTCCCAG  48540          A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CACGT CGG
                                      C    A
GAM607  DKFZP564B1023 3'  GGCTCACGCCTGTAATCCCAG  48541       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  DKFZP564I052 3'  GGCTCACGCCTGTAATCCCAG  66714       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  DKFZP564M182 3'  GGCTCACATCTGTAATCCCAG  78040       C    AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  ACACTCGG
                                   A   CT
GAM607  DKFZP564M182 3'  GGCTCACGCCTGTAATCCCAG  78041       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  DKFZP564O0463 3'  GCAGTTTAGTCCCAG       26279          C  G
                                CTGGGACTA AA TGT
                                ||||||||| || |||
                                GACCCTGAT TT ACG
                                     _  G
GAM607  DKFZp566H0824 3'  GGCTCACGCCTGTAATCCCAG  34056       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  DKFZP566J2046 3'  GCGCCTGTAGTCCCAG      48309          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
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                                GACCCTGATGT CGCG
                                      C
GAM607  DKFZP586D2223 3'  GGCTCACACCTGTAATCCTAG  37684       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GATCCT ATGT CACACTCGG
                                   A   C
GAM607  DKFZP586D2223 3'  GGCTCACACCTGTAATTCCA   37685      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCTT ATGT CACACTCGG
                                  A   C
GAM607  DKFZP586D2223 3'  GCACTGGTAATCCCAGGTA    37683        C  A
                                TACCTGGGA TAC AGTGT
                                ||||||||| ||| |||||
                                ATGGACCCT ATG TCACG
                                     A  G
GAM607  DKFZP586M1120 3'  GGCTCACGCCTGTAATCCCAG  48466       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  DKFZP667O116 3'  GGCTCATGCCTATAATCCCGG  94284       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GGCCCT AT   CGTACTCGG
                                   A  ATC
GAM607  DKFZp727G131 3'  GGCTTACGCCTGTAATCCCAG  59033       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCATTCGG
                                   A   C
GAM607  DKFZp727G131 3'  GGCACATGCCTGCAGTCCCAG  59032        A A   A
                                CTGGGACT CA GTGTG GCC
                                |||||||| || ||||| |||
                                GACCCTGA GT CGTAC CGG
                                     C C    A
GAM607  DKFZP761E2110 3'  GGCTCATGCCTGTAATCCCAG  48225       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  DKFZP761G1913 3'  GGCTCATGCCTGTAATCCCAG  48916       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  DKFZp761J139 5'  GGCTCACGCCTGTAATCCCAG  50114       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  DOCK3   3'  GCTCGCGTATCCCAACCCCAGG 66503       ACTACAAG_
              TA                 TACCTGGG       TGTGAGC
                                 ||||||||       |||||||
                                 ATGGACCC       GCGCTCG
                                    CAACCCTAT
GAM607  DRF1    3'  GGCTCACACCTGTAATCCCAG  47034      C   A
                                 CTGGGA TACA GTGTGAGCC
                                 |||||| |||| |||||||||
                                 GACCCT ATGT CACACTCGG
                                   A   C
GAM607  DRF1    3'  GGCTCACGCCTATAATCCCAG  47035      C  CAA
                                 CTGGGA TA   GTGTGAGCC
                                 |||||| ||   |||||||||
                                 GACCCT AT   CGCACTCGG
                                   A  ATC
GAM607  FADS1   3'  GGCTCATGCCTGTAATCCCA   25481      C   A
                                 TGGGA TACA GTGTGAGCC
                                 ||||| |||| |||||||||
                                 ACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FAM3A   3'  GGCTCACACCCCACACCCGGG  41441      ACTACAA
                                 CCTGGG      GTGTGAGCC
                                 ||||||      |||||||||
                                 GGGCCC      CACACTCGG
                                   ACACCC_
GAM607  FBXO27  3'  GGCTCACACCTGTAATCCC    74512     C   A
                                 GGGA TACA GTGTGAGCC
                                 |||| |||| |||||||||
                                 CCCT ATGT CACACTCGG
                                   A   C
GAM607  FBXO27  3'  GGCTCATGCCTGTAATCCCAG  74513      C   A
                                 CTGGGA TACA GTGTGAGCC
                                 |||||| |||| |||||||||
                                 GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FBXO6   3'  GCGCCTGTAGTCCCAG       37385          A
                                 CTGGGACTACA GTGT
                                 |||||||||||| ||||
                                 GACCCTGATGT CGCG
                                       C
GAM607  FBXO6   3'  GGCTCACGCCTGTAATCCCAG  37386      C   A
                                 CTGGGA TACA GTGTGAGCC
                                 |||||| |||| |||||||||
                                 GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FBXO9   3'  GGCATGCACCTGTAGTCCCAG  53103          A   A
                                 CTGGGACTACA GTGTG GCC
                                 |||||||||||| ||||| |||
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                                GACCCTGATGT CACGT CGG
                                      C     A
GAM607  FBXO9    3' GGCTCATGCCTATAATCCCAG  53104       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGTACTCGG
                                   A  ATC
GAM607  FKBP14   3' GGCTCATGCCTGTAATCCCAG  35627       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| ||||  |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  FKBP14   3' GGCTCATGCCTGTAATCCCAG  35628       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| ||||  |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  FKBP14   3' GGTGCACACCTGTAGTCCCAG  35629            A     A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||  |||||  |||
                                GACCCTGATGT CACAC TGG
                                      C     G
GAM607  FLJ00060 3' GGCTCATGTCTGTAATCCCAG  61102       C    AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  GTACTCGG
                                   A    CT
GAM607  FLJ00060 3' GGCGGGTGCCTGTAGTCCCAG  61101            A TG GA
                                CTGGGACTACA G  T  GCC
                                ||||||||||| |  |  |||
                                GACCCTGATGT C  G  CGG
                                      C GT GG
GAM607  FLJ10008 3' GCGCCTGTAGTCCCAG       35727           A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  FLJ10008 3' GGCTCACGTCTGTAATCCCAG  35728       C    AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  GCACTCGG
                                   A    CT
GAM607  FLJ10058 3' GGCACACACCTATAGTCCCAG  35786          CAA    A
                                CTGGGACTA   GTGTG GCC
                                |||||||||   ||||| |||
                                GACCCTGAT   CACAC CGG
                                      ATC     A
GAM607  FLJ10139 3' GGCTCACACCTATAATCCTAGG 35841       C  CAA
                                CCTGGGA TA   GTGTGAGCC
                                |||||||  ||   |||||||||
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                                GGATCCT AT   CACACTCGG
                                    A  ATC
GAM607  FLJ10460 3' GGCTCACACCTGTAATCCCA  36132      C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CACACTCGG
                                   A    C
GAM607  FLJ10460 3' GGCTCACACCTGTAATCCTA  36133      C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ATCCT ATGT CACACTCGG
                                   A    C
GAM607  FLJ10460 3' GGCTCACGCCTGTAATCCCAG 36134      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                    A    C
GAM607  FLJ10547 3' GGCTCACACCTGTAATCCCAG 36268      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                    A    C
GAM607  FLJ10607 3' GGCTCACGCCTGTAATCCCAG 77122      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                    A    C
GAM607  FLJ10613 3' GGCTCACGTCTGTAATCCCAG 38824      C    AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  GCACTCGG
                                    A    CT
GAM607  FLJ10650 3' GGCTCACACCTGTAATCCCAG 36383      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                    A    C
GAM607  FLJ10704 3' GGCTCACACCTGTAATCCCAG 36458      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                    A    C
GAM607  FLJ10781 3' GGCTCACGCCTGTAATCCCAG 36635      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                    A    C
GAM607  FLJ10803 3' GGCTCACACCGGTAATCCCAG 36667      C   AA
                                CTGGGA TAC  GTGTGAGCC
                                |||||| |||  |||||||||
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                                GACCCT ATG  CACACTCGG
                                   A   GC
GAM607  FLJ10803 3' GGCTCACACCTGTAATCCCAG 36668      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  FLJ10826 3' GGCTCACGCCTGTAATCCCAG 36703      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  FLJ10932 3' GGCTCGCGCCTGTAATCCCAG 36894      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCGCTCGG
                                   A    C
GAM607  FLJ10989 3' GCATCTGTAGTCCCAG      36950          AG
                                CTGGGACTACA  TGT
                                ||||||||||  |||
                                GACCCTGATGT  ACG
                                      CT
GAM607  FLJ10989 3' GGCTCACACCTGTAATCCCAG 36951      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  FLJ11029 3' GGCTCACACCTGTAATCCCAG 60976      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  FLJ11042 3' GGCATGTGGCTGTAGTCCCAG 37007          AG GT A
                                CTGGGACTACA  T  G GCC
                                ||||||||||  |  | |||
                                GACCCTGATGT  G  T CGG
                                      CG TG A
GAM607  FLJ11042 3' GGCTCATGCCTGTAATCCCAG 37008      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  FLJ11106 3' GCACCTGTAGTCCCAG      37054          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  FLJ11126 3' GGCGCACGCCTGTAGTCCCAG 37085          A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
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                                GACCCTGATGT CGCAC CGG
                                      C    G
GAM607  FLJ11126 3' GGCTCATGCCTATAATCCCAG 37086      C CAA
                                CTGGGA TA  GTGTGAGCC
                                |||||| ||  |||||||||
                                GACCCT AT  CGTACTCGG
                                   A ATC
GAM607  FLJ11136 3' GGCTCACGCCTGTAATCCCAG 37094      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ11151 3' GGCTTACGCCTGTAATCCCAG 67882      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCATTCGG
                                   A   C
GAM607  FLJ11259 3' GGCTCACACCTGTATTCCCAG 37189      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   T   C
GAM607  FLJ11267 3' GGCTCATGCCTGTAATCCCAG 39004      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FLJ11370 3' GGCTCATACCTGTAATCCCAG 46372      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CATACTCGG
                                   A   C
GAM607  FLJ11506 3' GGCTCACACCCCTCCAG    45111      ACTACAA
                                CTGGG     GTGTGAGCC
                                |||||     |||||||||
                                GACCT     CACACTCGG
                                  CCC____
GAM607  FLJ11577 3' GGCTCACGCCTGTAATCCCAG 47179      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ11637 3' GGCTCACGCCTGTAATCCCAG 46381      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ11700 3' GGCTCACACCTGTAATCCCAG 46040      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  FLJ11722 3' GGCTCATGCCTGTAATCCCAGG 46396       C   A
                                CCTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GGACCCT ATGT CGTACTCGG
                                    A   C
GAM607  FLJ11726 3' GGCTCACACCTGTAATCCCAG  46417      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  FLJ11800 3' GCTCACACTTGTAATCACT    46429    _ C
                                GG GA TACAAGTGTGAGC
                                || || ||||||||||||
                                TC CT ATGTTCACACTCG
                                 A  A
GAM607  FLJ11996 3' GGCTCACACCTGTAATTCCAG  46439      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCTT ATGT CACACTCGG
                                   A   C
GAM607  FLJ11996 3' GGCTCATGCCTGTAGTCCCAG  46440          A
                                CTGGGACTACA GTGTGAGCC
                                |||||||||| |||||||||
                                GACCCTGATGT CGTACTCGG
                                      C
GAM607  FLJ12056 3' GGCTCATGCCTATAATCCCA   46256      C  CAA
                                TGGGA TA   GTGTGAGCC
                                ||||| ||   |||||||||
                                ACCCT AT   CGTACTCGG
                                   A  ATC
GAM607  FLJ12132 3' GGCTTGTACCCGTAATCCCAG  46473      C   AA   TG
                                CTGGGA TAC  GTG  AGCC
                                |||||| |||  |||  ||||
                                GACCCT ATG  CAT  TCGG
                                   A   CC   GT
GAM607  FLJ12178 3' GGCTCACGTCTGTAATCCCAG  47102      C   AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  GCACTCGG
                                   A   CT
GAM607  FLJ12294 5' GCTCACACCTGTAAACCCAG   47015      AC   A
                                CTGGG  TACA GTGTGAGC
                                |||||  |||| ||||||||
                                GACCC  ATGT CACACTCG
                                   AA   C
GAM607  FLJ12294 5' GGCGGGTGCCTGTAGTCCCAG  47017          A TG GA
                                CTGGGACTACA G  T  GCC
                                |||||||||| |  |  |||
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                                GACCCTGATGT C  G  CGG
                                      C GT GG
GAM607  FLJ12294 3' GGCTCACGCCTGTAATCCCAG 47018      C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  FLJ12331 3' GGCTCACGCCTATAATCCCAG 46479      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                ||||||| ||   |||||||||
                                GACCCT AT   CGCACTCGG
                                   A  ATC
GAM607  FLJ12363 3' GGCTCACACCTGTAATCCCAG 49688      C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  FLJ12409 3' GGCAGACACCTGTAGTCCCAG 47050          A    GA
                                CTGGGACTACA GTGT  GCC
                                |||||||||||| ||||  |||
                                GACCCTGATGT CACA  CGG
                                      C    GA
GAM607  FLJ12409 3' GGCTCACACCTGTAACCCCAG 47051      AC    A
                                CTGGG  TACA GTGTGAGCC
                                |||||  |||| |||||||||
                                GACCC  ATGT CACACTCGG
                                   CA    C
GAM607  FLJ12448 3' GGCTCATGCCTGTAATCCAAG 43179    G  C    A
                                CT GGA TACA GTGTGAGCC
                                || ||| |||| |||||||||
                                GA CCT ATGT CGTACTCGG
                                 A  A    C
GAM607  FLJ12547 3' GGCTCACGCCTGTAATCCCAG 46493      C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  FLJ12606 3' GGCTTACGCCTGTAATCCCAG 45643      C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GACCCT ATGT CGCATTCGG
                                   A    C
GAM607  FLJ12660 3' GGCTCACGCCTGTAATCCCAG 47145      C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  FLJ12666 3' GGCTCACGCCTGTAATCCCAG 44770      C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ12671  3'  GGCTCACGCCTGTAGTCCCA  48281        A
                                TGGGACTACA GTGTGAGCC
                                |||||||||| |||||||||
                                ACCCTGATGT CGCACTCGG
                                     C
GAM607  FLJ12800  3'  GGCTCACGCCTGTAATCCCAG  43234      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ12921  3'  GCGCCTGTAGTCCCAG      45913          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  FLJ12921  3'  GGCTCACGCCGGTAATCCCAG  45914      C   AA
                                CTGGGA TAC  GTGTGAGCC
                                |||||| |||  |||||||||
                                GACCCT ATG  CGCACTCGG
                                   A   GC
GAM607  FLJ12949  3'  CATGCCTGTAGTCCCAG     43443          A
                                CTGGGACTACA GTGTG
                                |||||||||| |||||
                                GACCCTGATGT CGTAC
                                      C
GAM607  FLJ12985  3'  GGCTCACACCTGTAATCCCAG  46241      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  FLJ13117  3'  GGCTCATGCCTGTAATCCCAG  43546      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FLJ13153  3'  GGCTCACACCTGTGAGCACAG  45558    GGAC   A
                                CTG   TACA GTGTGAGCC
                                |||   |||| |||||||||
                                GAC   GTGT CACACTCGG
                                  ACGA   C
GAM607  FLJ13162  3'  GGCTCACGCCTGTAATCCCAG  46560      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ13193  3'  GGCGCATGCCTGTAGTCCCA   49770        A   A
                                TGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
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                                ACCCTGATGT CGTAC CGG
                                      C     G
GAM607  FLJ13193 3' GGCTCACACCTGTAATCCCAG 49771       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  FLJ13193 3' GGCTCACGCCTGTAATCCCA  49772       C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                  A    C
GAM607  FLJ13193 3' GGCTCATGTGTGTAATCCCAG 49773       C    A TG
                                CTGGGA TACA G  TGAGCC
                                |||||| |||| |  ||||||
                                GACCCT ATGT T  ACTCGG
                                   A    G GT
GAM607  FLJ13305 3' GGCTCATGCCTGTAATCCCAG 90131       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  FLJ13315 3' CACATCCCTGTAGTCCCAG   46567         A__
                                CTGGGACTACA   GTGTG
                                ||||||||||   |||||
                                GACCCTGATGT   TACAC
                                      CCC
GAM607  FLJ13330 3' GGCTCACACCTGTAATCTCAG 46976       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACTCT ATGT CACACTCGG
                                   A    C
GAM607  FLJ13352 3' GGCACATGCCTGTAGTCCCAG 44755         A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CGTAC CGG
                                      C     A
GAM607  FLJ13352 3' GGCTCACACCTGTTAATCCCAG 44756       CT_  A
                                CTGGGA   ACA GTGTGAGCC
                                ||||||   ||| |||||||||
                                GACCCT   TGT CACACTCGG
                                   AAT   C
GAM607  FLJ13390 3' GGCTCACACCTGAAATCCCAG  42539       CTA  A
                                CTGGGA   CA GTGTGAGCC
                                ||||||   || |||||||||
                                GACCCT   GT CACACTCGG
                                   AAA  C
GAM607  FLJ13448 3' GGCTCACACCTGTAATCCCAG  47139       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  FLJ13456 3' GGCTCACGCCTGTAATCCCAG 65943      C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ13456 3' GGCTCATGCTTGTAATCCCAG 65944      C
                                CTGGGA TACAAGTGTGAGCC
                                ||||||| ||||||||||||||
                                GACCCT ATGTTCGTACTCGG
                                   A
GAM607  FLJ13544 3' GGCTCACACCTGTCATCCCAG 46577      CT  A
                                CTGGGA  ACA GTGTGAGCC
                                ||||||  ||| |||||||||
                                GACCCT  TGT CACACTCGG
                                   AC  C
GAM607  FLJ13614 3' GGCTCACACCTGTAATCCCAG 57454      C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  FLJ13621 3' GCGCCTGTAGTCCCAG      46582          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  FLJ13621 3' GGCATGTGCCTATGGTCCCAGG 46583          CAA TG  A
           TA                    TACCTGGGACTA   G  TG GCC
                                |||||||||||||   |  || |||
                                ATGGACCCTGGT   C  GT CGG
                                      ATC GT  A
GAM607  FLJ13659 3' GGCTCACACCTGTAATCCCAG 47248      C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  FLJ13769 3' GGCTCACGCCTGTAATCCCAG 46618      C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ13769 3' GGCTCATGCCTATAATCCCAG 46619      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||||  ||  |||||||||
                                GACCCT AT   CGTACTCGG
                                   A  ATC
GAM607  FLJ13769 3' GGTGCACACTTGTAGTCCCA  46621           A
                                TGGGACTACAAGTGTG GCC
                                |||||||||||||||| |||
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                                ACCCTGATGTTCACAC TGG
                                      G
GAM607  FLJ13848 3' GGCTTACACCTGTAATCCCAG 45470      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACATTCGG
                                   A   C
GAM607  FLJ13984 3' GGCTCGCACCTGTAATCCCAG 45452      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACGCTCGG
                                   A   C
GAM607  FLJ14011 3' GGCTTACACCTGTAACCCCAG 42065     AC   A
                                CTGGG  TACA GTGTGAGCC
                                |||||  |||| |||||||||
                                GACCC  ATGT CACATTCGG
                                  CA   C
GAM607  FLJ14082 3' GGCTCATGCCCGTAATCCCAG 46674      C  AA
                                CTGGGA TAC  GTGTGAGCC
                                |||||| |||  |||||||||
                                GACCCT ATG  CGTACTCGG
                                   A  CC
GAM607  FLJ14100 3' GCGCCTGTAGTCCCAG     46684         A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  FLJ14100 3' GGCTCACGCCTGTAATCCCAG 46685      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ14107 3' GGCTCATGCCTGTAATCCCAG 46696      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FLJ14117 3' CATGCCTGTAGTCCCAG     42904         A
                                CTGGGACTACA GTGTG
                                |||||||||||| |||||
                                GACCCTGATGT CGTAC
                                      C
GAM607  FLJ14117 3' GGCTCACACTTGTAATCCCAG 42912      C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCACACTCGG
                                   A
GAM607  FLJ14117 3' GGCTCACACTTGTAATCCCAG 42913      C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
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                                GACCCT ATGTTCACACTCGG
                                   A
GAM607  FLJ14117 3' GGCTCACGCCTGTAATCCCAG 42914      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ14225 3' GGCTCACGCCTGTAATCCCAG 45905      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ14251 3' GGCTCACACCTGTAATCCCAG 45976      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  FLJ14326 3' GGCTCACGCCTGTAATCCCAG 49814      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ14326 3' GGCTCATGCCTGTAATCCCAG 49815      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FLJ14327 3' GCTCATGCCTGTAATCCCAG  46142      C   A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
                                GACCCT ATGT CGTACTCG
                                   A   C
GAM607  FLJ14345 3' GGCTCACGCCTGTAATCCCAG 45338      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ14346 3' GGCAGGTGCCTGTAGTCCCAG 46715          A TG GA
                                CTGGGACTACA G  T  GCC
                                |||||||||||| |  |  |||
                                GACCCTGATGT C  G  CGG
                                      C GT GA
GAM607  FLJ14346 3' GGCTCACACCTGTAATCCCAG 46716      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  FLJ14346 3' GGCTCACGCCTGTAATCCCAG 46717      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ14397 3' GGCGGGTGCCTGTAGTCCCAG 51327          A TG GA
                                CTGGGACTACA G  T  GCC
                                |||||||||||| |  |  |||
                                GACCCTGATGT C  G  CGG
                                      C GT GG
GAM607  FLJ14397 3' GGCTCACACCTATAATCCCAG 51328       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACACTCGG
                                   A  ATC
GAM607  FLJ14457 3' GCGCCTGTAGTCCCAG      51384          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  FLJ14466 3' GGCGCATGCTTGTAATCCCAG 51394       C         A
                                CTGGGA TACAAGTGTG GCC
                                |||||| |||||||||| |||
                                GACCCT ATGTTCGTAC CGG
                                   A         G
GAM607  FLJ14621 3' GGCACGCGCCTGTAGTCCCAG 51475          A     A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CGCGC CGG
                                      C     A
GAM607  FLJ14621 3' GGCTCACGCCTGTAATCCCAG 51476       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ14641 3' GGCTCACACCTGTAATCCCA  51489       C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CACACTCGG
                                   A   C
GAM607  FLJ14642 3' GGCTCACACCTGTAATCCCAG 51504       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  FLJ14642 3' GGCTCATGCCTGTAATCCCAG 51505       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FLJ14888 3' GGCTCATGCCTGTAATCCCAG 51683       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FLJ20006 3' GGCTCACGCCTGTAATCCCAG 34323      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ20013 3' GGCACACACCTGTAGTCCCAG 34333         A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CACAC CGG
                                      C   A
GAM607  FLJ20013 3' GGCTCACACCTGTAATCCTA  34336     C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ATCCT ATGT CACACTCGG
                                   A   C
GAM607  FLJ20034 3' GGCTCACGCCTGTAATCCCAG 34378      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ20045 3' GCGCTTGTAATCCCAG      34421      C
                                CTGGGA TACAAGTGT
                                |||||| |||||||||
                                GACCCT ATGTTCGCG
                                   A
GAM607  FLJ20045 3' GGCTCACACCTCTAATCCCAG 34426      C CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACACTCGG
                                   A CTC
GAM607  FLJ20055 3' GGCTCACGCCTGTAATCCCAG 34443      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ20139 3' GGCATGCACCTGTAGTCCCAG 34626         A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CACGT CGG
                                      C   A
GAM607  FLJ20139 3' GGTTCACACCTGTAATCCCA  34629     C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CACACTTGG
                                   A   C
GAM607  FLJ20211 3' GGCTCACGCCTGTAATCCCAG 34752      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ20241  3' GCGCCTGTAGTCCCAG      34779          A
                                CTGGGACTACA GTGT
                                |||||||||||  ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  FLJ20280  3' GGCTCACACCTGTAATCCCAG  34852       C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  FLJ20337  3' GCTCACACCCACCGCCCAGGT  34967        ACTACAA
                                ACCTGGG      GTGTGAGC
                                |||||||      ||||||||
                                TGGACCC      CACACTCG
                                   GCCACC_
GAM607  FLJ20340  3' GGCTCACACCCGTAATCCCAG  34976       C  AA
                                CTGGGA TAC  GTGTGAGCC
                                ||||||  |||  |||||||||
                                GACCCT ATG  CACACTCGG
                                   A   CC
GAM607  FLJ20340  3' GGCTCATGCCTGTAATCCCAG  34977       C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FLJ20359  3' GGCTCATGCCTGTAATCCCAG  35044       C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FLJ20456  3' GGCTTACGCTTGTAGTCCCAG  35214
                                CTGGGACTACAAGTGTGAGCC
                                |||||||||||||||||||||
                                GACCCTGATGTTCGCATTCGG

GAM607  FLJ20464  3' GGCTCATGCCTGTAATCCCAG  35235       C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FLJ20546  3' GGCTCACGTCTGTAATCCCAG  35370       C   AG
                                CTGGGA TACA  TGTGAGCC
                                ||||||  ||||  ||||||||
                                GACCCT ATGT  GCACTCGG
                                   A   CT
GAM607  FLJ20671  3' GCACCTGTAGTCCCAG      35525          A
                                CTGGGACTACA GTGT
                                |||||||||||  ||||
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                                GACCCTGATGT CACG
                                      C
GAM607  FLJ20700 3' GCACCTGTAGTCCCAG      35576          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  FLJ20700 3' GGCTCATGCCTGTAATCCCAG 35582       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  FLJ20783 3' GGCTCACGCCTGTAATCCCAG 35664       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  FLJ20802 3' GCACCTGTAGTCCCAG      35670          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  FLJ20808 3' GGCTCACACCCATAATCCCAG 35673       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACACTCGG
                                   A  ACC
GAM607  FLJ20825 3' GGCTCACGCCTGTAATCCCAG 35701       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  FLJ20972 3' GGCTCACGCTTGTAATCCCAG 46727       C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCGCACTCGG
                                   A
GAM607  FLJ21106 3' GGCTTACGCCTGTAATCCCAG 46998       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCATTCGG
                                   A    C
GAM607  FLJ21144 3' GGCGTGCGCCTGTAGTCCCAG 42879            A   GA
                                CTGGGACTACA GTGT  GCC
                                |||||||||||| ||||  |||
                                GACCCTGATGT CGCG  CGG
                                      C    TG
GAM607  FLJ21162 3' GGCTCATGCCTATAATCCCAG 45895       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
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                                GACCCT AT   CGTACTCGG
                                   A  ATC
GAM607  FLJ21272  3' GGCTCATGCCTGTAATCCCAG  46739      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  FLJ21657  3' GGCTCACGCCTGTAATCCCA   42513      C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                  A    C
GAM607  FLJ21687  3' GGCTCACGCCTGTAATCCCAG  45859      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  FLJ21870  3' GGCTCATGCCTGTAATCCCAG  43463      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  FLJ22054  3' GGCTCACACCTGTAATCCCAG  94397      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  FLJ22167  3' GGCTCATGCCTGTAATCCCAG  44581      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  FLJ22313  3' GGCTCACGTCTGTAATCCCAG  42342      C    AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  GCACTCGG
                                   A    CT
GAM607  FLJ22389  3' CTCACACTCGGAATCCCAG    46235      CTACA
                                CTGGGA    AGTGTGAG
                                ||||||    ||||||||
                                GACCCT    TCACACTC
                                   AAGGC
GAM607  FLJ22474  3' GGCTCACGCTTATGTAGTCCCA 45277          __
          G                      CTGGGACTACA  AGTGTGAGCC
                                ||||||||||  ||||||||||
                                GACCCTGATGT  TCGCACTCGG
                                      AT
GAM607  FLJ22474  3' GGCTCACGCCTGCAGTCCCAG  45276       A  A
                                CTGGGACT CA GTGTGAGCC
                                |||||||| || |||||||||
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                                GACCCTGA GT CGCACTCGG
                                     C  C
GAM607  FLJ22692  3'  GCGCCTGTAGTCCCAG      46806          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  FLJ22692  3'  GGCTCACGCCTGTAATCCCAG  46807       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  FLJ22692  3'  GGTGTGTGCCTGTAGTCCCAG  46808           A TG  A
                                CTGGGACTACA G  TG GCC
                                |||||||||||  |  || |||
                                GACCCTGATGT C  GT TGG
                                      C GT  G
GAM607  FLJ22814  3'  GCGCCTGTAGTCCCAG      46176          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  FLJ23040  3'  GGCTCACGCTTATAATCCCAG  47200       C  C
                                CTGGGA TA AAGTGTGAGCC
                                |||||| || ||||||||||
                                GACCCT AT TTCGCACTCGG
                                   A  A
GAM607  FLJ23042  3'  GGCTCACGCCTGTAATCCCAG  47174       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  FLJ23235  3'  GGCTCATGCCTGTAATCCCAG  46308       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  FLJ23360  3'  GCACCTGTAGTCCCAG       43569          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  FLJ23447  3'  GGCACATGCCTGTAGTCCCAG  45714           A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CGTAC CGG
                                      C    A
GAM607  FLJ23447  3'  GGCTCATGCCTGTAATCCCAG  45715       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FLJ23476 3' GGCTCATGCCTGTAATCCCA  44961     C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FLJ23499 3' GGCTCATGCCTGTAATCCCAG 42827      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FLJ23499 3' GGCTCACACCTAATCCCAG   42824      C CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACACTCGG
                                   A  C__
GAM607  FLJ23499 3' GGCTCACGCCTGTAATCCCAG 42825      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ23499 3' GGCTCATGCCTGTAATCCCAG 42826      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FLJ23878 3' GGCTCACGCTTGTAATCCCAG 58711      C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCGCACTCGG
                                   A
GAM607  FLJ25012 3' GGCTCACGCCTGTAATCCCAG 58093      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ25179 3' GGCTCATGCCTGTAATCCCAG 58356      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  FLJ25461 3' CTCACACTTCCCCAG      58633      ACTAC
                                CTGGG    AAGTGTGAG
                                |||||    |||||||||
                                GACCC    TTCACACTC
                                   C____
GAM607  FLJ30092 3' CATATCTGTAGTCCCAG     58687          AG
                                CTGGGACTACA  TGTG
                                ||||||||||  ||||
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                                GACCCTGATGT  ATAC
                                      CT
GAM607  FLJ30092  3'  GGCTCACACCTGTAATCCCAG  58690      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  FLJ31168  3'  GGCTCACACCTGTAATCCTAG  58508      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GATCCT ATGT CACACTCGG
                                   A   C
GAM607  FLJ31455  3'  GGCGCATACCTGTAGTCCCAG  58628         A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CATAC CGG
                                      C    G
GAM607  FLJ31455  3'  GGCTCACGCCTGTAATCCCAG  58629      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  FLJ31737  3'  GGCTTACGCCTGTAATCCCAG  58696      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCATTCGG
                                   A   C
GAM607  FLJ31952  3'  GGCTCACACCTGTAATCCCAG  58385      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  FUSIP1    3'  GGCTCACACCTGTAATCCCAG  53960      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  GALNT6    3'  GGCACGCACCTGCAGTCCCAG  23294       A A   A
                                CTGGGACT CA GTGTG GCC
                                |||||||| || ||||| |||
                                GACCCTGA GT CACGC CGG
                                     C C    A
GAM607  GALNT6    3'  GGCTCACACCTGTAATCCTAG  23295      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GATCCT ATGT CACACTCGG
                                   A   C
GAM607  GCN2      3'  GGCACATGCCTGTAGTCCCAG  62773        A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
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                                GACCCTGATGT CGTAC CGG
                                      C     A
GAM607  GCN2    3' GGCTCACACCTTTAATCCCAG 62774       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACACTCGG
                                   A  TTC
GAM607  GGA2    3' GGCTCACGCCTGTAGTCCCAG 56889          A
                                CTGGGACTACA GTGTGAGCC
                                |||||||||||| |||||||||
                                GACCCTGATGT CGCACTCGG
                                      C
GAM607  GGA2    3' GGCTCACGCCTGTAGTCCCAG 30475          A
                                CTGGGACTACA GTGTGAGCC
                                |||||||||||| |||||||||
                                GACCCTGATGT CGCACTCGG
                                      C
GAM607  GLTP    3' GGCTCACGCCTGTAATCCCAG 33163       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  GNB4    3' GGCTTACACCTATAATCCCAG 41270       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACATTCGG
                                   A  ATC
GAM607  GP5     3' GCTCACGCCTGTAATCCCAG  15649       C    A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
                                GACCCT ATGT CGCACTCG
                                   A    C
GAM607  GP5     3' GGCAGGTGCCTGTAGTCCCAG 15654          A TG GA
                                CTGGGACTACA G  T  GCC
                                |||||||||||| |  |  |||
                                GACCCTGATGT C  G  CGG
                                      C GT GA
GAM607  GSG2    3' GGCGTGCGCCTGTAGTCCCAG 49237          A    GA
                                CTGGGACTACA GTGT  GCC
                                |||||||||||| ||||  |||
                                GACCCTGATGT CGCG  CGG
                                      C    TG
GAM607  GTPBP5  3' GGCTCATGCCTGTAGTCCCAG 65359          A
                                CTGGGACTACA GTGTGAGCC
                                |||||||||||| |||||||||
                                GACCCTGATGT CGTACTCGG
                                      C
GAM607  GTPBP5  3' GGCGGTCACCTGTAGTCCCAG 65358          A   TGA
                                CTGGGACTACA GTG   GCC
                                |||||||||||| |||   |||
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                                GACCCTGATGT CAC   CGG
                                      C   TGG
GAM607   HES2     3'  GGCTCACGCCTGTAATCCCAG  38856       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607   HSA250303 3'  GGCACACACCTGTAGTCCCAGG 37411             A     A
            TA                    TACCTGGGACTACA GTGTG GCC
                                ||||||||||||||| ||||| |||
                                ATGGACCCTGATGT CACAC CGG
                                      C     A
GAM607   HSC3     3'  GCACCTGTAGTCCCAG      59069           A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607   HSC3     3'  GGCTCACACCTGTAATCCTAG  59070       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GATCCT ATGT CACACTCGG
                                   A    C
GAM607   HSH2     3'  GGCTCATGCCTGTAGTCCCAG  51677           A
                                CTGGGACTACA GTGTGAGCC
                                |||||||||||| |||||||||
                                GACCCTGATGT CGTACTCGG
                                      C
GAM607   HSMPP8   3'  GGCTCACACCTATAATCCCAG  93480       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACACTCGG
                                   A  ATC
GAM607   HTCD37   3'  CATATCTGCAGTCCCAG     67672         A  AG
                                CTGGGACT CA  TGTG
                                |||||||| ||  ||||
                                GACCCTGA GT  ATAC
                                     C  CT
GAM607   IL-23R   3'  GGCAGGTGCTTGTAATCCCAG  58455       C     TG GA
                                CTGGGA TACAAG  T  GCC
                                |||||| ||||||  |  |||
                                GACCCT ATGTTC  G  CGG
                                   A     GT GA
GAM607   IL-23R   3'  GGCTCATGCTTGTAATCCCAG  58456       C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCGTACTCGG
                                   A
GAM607   IMAGE:4907098 3'  GGCTCACGCCTGTAATCCCAG  91662       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                  GACCCT ATGT CGCACTCGG
                                     A   C
GAM607  ING1-like 3'  GCGCCTGTAGTCCCAG      54158          A
                                  CTGGGACTACA GTGT
                                  |||||||||||| ||||
                                  GACCCTGATGT CGCG
                                        C
GAM607  ING1-like 3'  GGCTCACGCCTGTAATCCCAG  54159       C   A
                                  CTGGGA TACA GTGTGAGCC
                                  |||||| |||| |||||||||
                                  GACCCT ATGT CGCACTCGG
                                     A   C
GAM607  JDD1     3'  GGCATGTGCTTGTAGTCCCAG  63219           TG  A
                                  CTGGGACTACAAG  TG GCC
                                  ||||||||||||  || |||
                                  GACCCTGATGTTC  GT CGG
                                           GT  A
GAM607  KALI     3'  GGCTCACACCTGTAATCCCAG  53594       C   A
                                  CTGGGA TACA GTGTGAGCC
                                  |||||| |||| |||||||||
                                  GACCCT ATGT CACACTCGG
                                     A   C
GAM607  KIAA0042 3'  GGCTCACGCCTGTAATCCCAG  29613       C   A
                                  CTGGGA TACA GTGTGAGCC
                                  |||||| |||| |||||||||
                                  GACCCT ATGT CGCACTCGG
                                     A   C
GAM607  KIAA0159 3'  GGCTCACGCCTGTAATCCCAG  29509       C   A
                                  CTGGGA TACA GTGTGAGCC
                                  |||||| |||| |||||||||
                                  GACCCT ATGT CGCACTCGG
                                     A   C
GAM607  KIAA0184 3'  GCGCCTGTAGTCCCAG      65197          A
                                  CTGGGACTACA GTGT
                                  |||||||||||| ||||
                                  GACCCTGATGT CGCG
                                        C
GAM607  KIAA0184 3'  GGCTTACACCTGTAATCCCAG  65199       C   A
                                  CTGGGA TACA GTGTGAGCC
                                  |||||| |||| |||||||||
                                  GACCCT ATGT CACATTCGG
                                     A   C
GAM607  KIAA0226 3'  GGCTCACACCTGTAATCCCAG  63521       C   A
                                  CTGGGA TACA GTGTGAGCC
                                  |||||| |||| |||||||||
                                  GACCCT ATGT CACACTCGG
                                     A   C
GAM607  KIAA0252 3'  GCTCACGCCTGTAATCCCAG   62795       C   A
                                  CTGGGA TACA GTGTGAGC
                                  |||||| |||| ||||||||
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                                GACCCT ATGT CGCACTCG
                                   A   C
GAM607  KIAA0355 3' GGCGTGCGCCTGTAGTCCCAG  28030          A   GA
                                CTGGGACTACA GTGT  GCC
                                |||||||||||| ||||  |||
                                GACCCTGATGT CGCG  CGG
                                      C   TG
GAM607  KIAA0355 3' GGCTCACGCCTGTAATCCCAG  28031       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  KIAA0391 3' GGCCCACACCTACAGTTCCAG  27918        ACAA    A
                                CTGGGACT   GTGTG GCC
                                ||||||||   ||||| |||
                                GACCTTGA   CACAC CGG
                                     CATC    C
GAM607  KIAA0418 3' GCATCTTGCCACCCCAGGTA   27557        ACTA   _
                                TACCTGGG   CAAG TGT
                                ||||||||   |||| |||
                                ATGGACCC   GTTC ACG
                                     CACC   T
GAM607  KIAA0419 3' GGCTCACACCTGTACTCCCAG  28192       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   C   C
GAM607  KIAA0420 3' GGCTCATGCCTATAATCCCA   63361      C  CAA
                                TGGGA TA   GTGTGAGCC
                                ||||| ||   |||||||||
                                ACCCT AT   CGTACTCGG
                                   A  ATC
GAM607  KIAA0441 3' GGCTCATGCCTGTAATCCCAG  28958       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  KIAA0445 5' GGCTCACGCCTGTAATCCCAG  27954       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  KIAA0446 5' GCGCCTGTAGTCCCAG      68871          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  KIAA0471 3' GGCTCACATCTGTAATCCCAG  29396       C   AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
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                                GACCCT ATGT  ACACTCGG
                                   A    CT
GAM607  KIAA0475 3' GGCATGCGCCTGTAGTCCCAG  29502          A     A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| |||||| |||
                                GACCCTGATGT CGCGT CGG
                                      C     A
GAM607  KIAA0514 3' GGCTCATGCCTGTAATCCCAG  28091       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  KIAA0547 3' GGTGTGTGCTTGTAATCCCAG  28913       C      TG  A
                                CTGGGA TACAAG  TG GCC
                                |||||| ||||||  || |||
                                GACCCT ATGTTC  GT TGG
                                   A     GT  G
GAM607  KIAA0557 3' GGCACGTGCCTGTAGTCCCAG  78001           A TG  A
                                CTGGGACTACA G  TG GCC
                                |||||||||||| |  || |||
                                GACCCTGATGT C  GC CGG
                                      C GT  A
GAM607  KIAA0557 3' GGCTCACGCTTGTAATCCCAG  78002       C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCGCACTCGG
                                   A
GAM607  KIAA0557 3' GGTGTGCCTGTAGTCCCAG    78005          A TG GA
                                CTGGGACTACA G  T  GCC
                                |||||||||||| |  |  |||
                                GACCCTGATGT C  G  TGG
                                      C GT __
GAM607  KIAA0563 3' GGCTCACGCCTGTAATCCCAG  29191       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  KIAA0635 3' GGCTCACGCCTGTAATCCCAG  27697       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  KIAA0694 3' GCTCACGCCTGTAATCCCAG   72581       C    A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
                                GACCCT ATGT CGCACTCG
                                   A    C
GAM607  KIAA0752 3' GGCTCACGCCTGTAATCCCAG  67050       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  KIAA0794 3' GGCTCATGCCTGTAATCCCA  80413     C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGTACTCGG
                                   A   C
GAM607  KIAA0795 3' GGCTCACGCCTATAATCCCAG 46594      C CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGCACTCGG
                                   A ATC
GAM607  KIAA0798 3' GGCTCACGCTTGTAATCCCAG 27727      C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCGCACTCGG
                                   A
GAM607  KIAA0798 3' GGCTTGCACCTGTAATCCCAG 27728      C   A  TG
                                CTGGGA TACA GTG  AGCC
                                |||||| |||| |||  ||||
                                GACCCT ATGT CAC  TCGG
                                   A   C  GT
GAM607  KIAA0825 3' GGCTCACGCCTGTAATCCCAG 61026      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  KIAA0831 3' GGCTCACGCCTGTAATCCCGG 29980      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GGCCCT ATGT CGCACTCGG
                                   A   C
GAM607  KIAA0852 5' GGCTCACGCCTGTAATCCCAG 30080      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  KIAA0872 3' GCGCCTGTAGTCCCAG      30066          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  KIAA0872 3' GGCTCACGCCTGTAATCCCAG 30067      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  KIAA0872 3' GGCTTATGCCTGTAATCCCAG 30068      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGTATTCGG
                                   A   C
GAM607  KIAA0889 3' GGCTCATGCCTGTAATCCCAG 31143      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  KIAA0892 3' GGCGCATGCCTGTAGTCCCAG 71014         A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CGTAC CGG
                                      C   G
GAM607  KIAA0894 3' GGCTCACGCCTGTAATCCCAG 29705      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  KIAA0907 3' GGCTCACGCCTGTAATCCCAG 30179      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  KIAA0907 3' GGCTCACGCCTGTAATCCCAG 30180      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  KIAA0912 3' GGCTCACACCTGTAATCCCAG 64412      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  KIAA0930 3' GGCTCACGCCTGTAATCCCAG 70547      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  KIAA0953 3' GGCTCACACCTGTGATCCCA 66788     C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT GTGT CACACTCGG
                                  A   C
GAM607  KIAA0953 3' TGCACCTGTGGTCCCAGGTA 66790          A
                                TACCTGGGACTACA GTGTG
                                |||||||||||||| |||||
                                ATGGACCCTGGTGT CACGT
                                        C
GAM607  KIAA0961 3' GGCTCGTGCCTGTAGTCCCAG 29738         A TG
                                CTGGGACTACA G  TGAGCC
                                |||||||||| |  ||||||
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                                GACCCTGATGT C  GCTCGG
                                      C GT
GAM607  KIAA0981 3' GGCATATACCTGTAACCCCA  61421     AC   A    A
                                TGGG  TACA GTGTG GCC
                                |||| |||| ||||| |||
                                ACCC  ATGT CATAT CGG
                                  CA   C    A
GAM607  KIAA1001 3' GGCTCACACCTGTAGTCCCAG 30294         A
                                CTGGGACTACA GTGTGAGCC
                                |||||||||| |||||||||
                                GACCCTGATGT CACACTCGG
                                      C
GAM607  KIAA1056 3' GGCTCACGCCTGTAATCCCAG 29698      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  KIAA1086 3' GCACCTGTAGTCCCAG      70746         A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  KIAA1086 3' GGCCCAAGCCTGTAGTCCCAG 70750         A  G  A
                                CTGGGACTACA GT TG GCC
                                |||||||||| || || |||
                                GACCCTGATGT CG AC CGG
                                      C  A  C
GAM607  KIAA1086 3' GGCTCACACCTATAATCCCAG 70751      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACACTCGG
                                   A  ATC
GAM607  KIAA1117 3' GCTCACACCTGTAATCCTAG  61120      C   A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
                                GATCCT ATGT CACACTCG
                                   A   C
GAM607  KIAA1130 3' GGCTCATGCCTGTAATCCCAG 62424      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  KIAA1143 3' GGCTCATGCTTGTAATCCCA  68685      C
                                TGGGA TACAAGTGTGAGCC
                                ||||| ||||||||||||||
                                ACCCT ATGTTCGTACTCGG
                                   A
GAM607  KIAA1155 3' GGCTGCTGCAAACCCCAGGTA 62237       ACTACA  GTG
                                TACCTGGG    AGT  AGCC
                                ||||||||    |||  ||||
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                                ATGGACCC     TCG   TCGG
                                    CAAACG   ___
GAM607  KIAA1160 3' GGCTCACGCCTGTAACCCCAG  40373      AC    A
                                CTGGG  TACA GTGTGAGCC
                                |||||  |||| |||||||||
                                GACCC  ATGT CGCACTCGG
                                   CA    C
GAM607  KIAA1164 3' GGCTCACGCCTGTAATCCCA   69506      C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                   A    C
GAM607  KIAA1191 3' GCGCCTGTAGTCCCAG      39957           A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  KIAA1191 3' GGCTCACGCCTGTAATCCCAG  39959       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  KIAA1228 3' GCGCACGCCTGTAGTCCCAG   65043          A    A
                                CTGGGACTACA GTGTG GC
                                |||||||||| ||||| ||
                                GACCCTGATGT CGCAC CG
                                      C    G
GAM607  KIAA1228 3' GGCTCACGCCTGTAATCCCAG  65047       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  KIAA1244 3' GGCTCACGCCTGTAATCCCAG  71992       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  KIAA1257 3' GCACCTGTAGTCCCAG       62741           A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  KIAA1271 3' GGCTCACGCCTGTAATCCCAG  69550       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  KIAA1276 3' GGCGTGTGCCTGTGGTCCCAGG 66434             A TG GA
           TA                     TACCTGGGACTACA G  T  GCC
                                |||||||||||||| |  |  |||
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                                ATGGACCCTGGTGT C  G  CGG
                                      C GT TG
GAM607  KIAA1277 3' GGCTCATGCCTATAATCCCAG  64459      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGTACTCGG
                                   A  ATC
GAM607  KIAA1328 3' GGCTTACACCTGTAATCCCAGG 61653       C    A
                                CCTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GGACCCT ATGT CACATTCGG
                                   A    C
GAM607  KIAA1364 3' GGCTCATGCCTGTAATCCCAG  63596      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  KIAA1377 3' GGCATGCACCTGTAGTCCCAG  67175          A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CACGT CGG
                                      C    A
GAM607  KIAA1377 3' GGCTTATGCCTGTAATCCCAG  67177      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTATTCGG
                                   A    C
GAM607  KIAA1404 3' GGCTTACGCCTGTAATCCCAG  61991      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCATTCGG
                                   A    C
GAM607  KIAA1423 3' CATGCCCATAGTCCCAG     61725        CAA
                                CTGGGACTA   GTGTG
                                |||||||||   |||||
                                GACCCTGAT   CGTAC
                                      ACC
GAM607  KIAA1456 3' GGCTCATGCCTGTAATCCCAG  67001      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  KIAA1456 5' GGCTTGCACCTGTAATCCCAG  67002      C    A   TG
                                CTGGGA TACA GTG  AGCC
                                |||||| |||| |||  ||||
                                GACCCT ATGT CAC  TCGG
                                   A    C   GT
GAM607  KIAA1473 3' GGCTCACGCCTGTAATCCCAG  70671      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   KIAA1486 3' GCGCCTGTAGTCCCAG      67381          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                     C
GAM607   KIAA1486 3' GGCTCACGCCTGTAATCCCAG 67383      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   KIAA1559 3' GGCACACACCTGTAGTCCCAGG 73068         A   A
                                CCTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GGACCCTGATGT CACAC CGG
                                     C   A
GAM607   KIAA1559 3' GGCTCATGCCTGTAATCCCAG  73070      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   KIAA1586 5' GGCTCACACCTGTAATCCCAG  92334      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   KIAA1614 3' GGCTCATGCCTGTAATCCCAG  70120      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   KIAA1649 3' GCGCTTGTAATCCCAG      50268      C
                                CTGGGA TACAAGTGT
                                |||||| |||||||||
                                GACCCT ATGTTCGCG
                                   A
GAM607   KIAA1656 5' GGCTCACGCCTGTAATCCCAG  65801      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   KIAA1674 3' GGCTCACGCCTGTAATCCCAG  68785      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   KIAA1715 3' GGCTCACGCCTGTAATCCCAG  68123      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  KIAA1735 3' GGCACACACCTGTAGTCCCAG 87629         A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CACAC CGG
                                      C    A
GAM607  KIAA1751 3' GCGCCTGTAATCCCAG     71696      C   A
                                CTGGGA TACA GTGT
                                |||||| |||| ||||
                                GACCCT ATGT CGCG
                                   A   C
GAM607  KIAA1751 3' GGCTCATGCCTGTAATCCCAG 71703      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  KIAA1841 3' GGCATACACCTGTAGTCCCAG 80048         A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CACAT CGG
                                      C    A
GAM607  KIAA1841 3' GGCTCACGCCAGTAATCCCAG 80050      C  AA
                                CTGGGA TAC  GTGTGAGCC
                                |||||| |||  |||||||||
                                GACCCT ATG  CGCACTCGG
                                   A  AC
GAM607  KIAA1871 3' CACGCCTGTAGTCCCAGGTA  61230          A
                                TACCTGGGACTACA GTGTG
                                |||||||||||||| |||||
                                ATGGACCCTGATGT CGCAC
                                      C
GAM607  KIAA1872 3' GGCGCGCACCTGTAGTCCCAG 62941         A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CACGC CGG
                                      C    G
GAM607  KIAA1872 3' GGCTCACGCCTATAATCCCAG 62942      C CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||  |||||||||
                                GACCCT AT   CGCACTCGG
                                   A ATC
GAM607  KIAA1872 3' GGCTCACGCCTGTAATCCCAG 62943      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  KIAA1872 3' GGCTCATGCCTGTAATCCCAG 62944      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  KIAA1941 3' GGCTCACACCTGTAATCCCAG 74842      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  KIAA1948 3' GCGCCTGTAGTCCCAG     82405         A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  KIAA1948 5' GGCACATGCCTATAATCCCAG 82406      C CAA   A
                                CTGGGA TA   GTGTG GCC
                                |||||| ||   ||||| |||
                                GACCCT AT   CGTAC CGG
                                   A ATC    A
GAM607  KIAA1951 3' GGCTCACGCCTGTAATCCCAG 73763      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  KIAA1954 3' CTCACACCTGTAATCCCAG   77718      C   A
                                CTGGGA TACA GTGTGAG
                                |||||| |||| |||||||
                                GACCCT ATGT CACACTC
                                   A   C
GAM607  KIAA1958 3' GGCTCACGCCTATAATCCCAG 81908      C CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGCACTCGG
                                   A ATC
GAM607  KIAA1979 3' GGCTCACGCCTGTAATCCCAG 88287      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  KR18     3' GGCTCACACCTGTAATCCCAG 52750      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  KR18     3' GGCTCACACCTGTGATCCCAG 52751      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT GTGT CACACTCGG
                                   A   C
GAM607  LANO     3' GCGCCTGTAGTCCCAG     47190         A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
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                                GACCCTGATGT CGCG
                                      C
GAM607  LHFPL2   3'  GGCTCACACTTATTTTTCTA  69952      CTAC
                                TGGGA   AAGTGTGAGCC
                                |||||   ||||||||||
                                ATCTT   TTCACACTCGG
                                   TTTA
GAM607  LIAS     3'  GGCTCACGCCTGTAATCCCAG  70637      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LIM      3'  GGCTCACGCCTGTAATCCCAG  21307      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LIM      3'  GGCGTGCCTGTAGTCCCATGTA 21306     C       A TG GA
                                TAC TGGGACTACA G  T  GCC
                                ||| ||||||||| |  |  |||
                                ATG ACCCTGATGT C  G  CGG
                                  T        C GT __
GAM607  LRG      3'  GCACCTGTAGTCCCAG      53751          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  LRG      3'  GGCTCACGCCTGTAATCCCAG  53752      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LY6G5B   5'  ACCCGGTAGTGCCCAGGTA   41128       _   AA_
                                TACCTGGG ACTAC   GT
                                |||||||| |||||   ||
                                ATGGACCC TGATG   CA
                                     G    GCC
GAM607  LYSAL1   3'  GGCTCACGCCTGTAATCCCAG  16919      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  MACF1    3'  GCTCACACCTGTAATCCCAG  52318      C   A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
                                GACCCT ATGT CACACTCG
                                   A   C
GAM607  MACF1    3'  GGCACGCACCTATAGTCCCAG  52319       CAA   A
                                CTGGGACTA   GTGTG GCC
                                |||||||||   ||||| |||
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                                GACCCTGAT   CACGC CGG
                                     ATC    A
GAM607  MACF1    3'  GGCGGGTGCCTGTAGTCCCAG  52320          A TG GA
                                CTGGGACTACA G  T  GCC
                                |||||||||||  |  |  |||
                                GACCCTGATGT C  G  CGG
                                      C GT GG
GAM607  MAWBP    3'  GGCTCATGCCTGTAATCCCAG  42108       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  MCAM     3'  GGCTCACGCCTGTAATCCCAG  21457       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  MESDC2   3'  GGCTCACGCCTGTAATCCCAG  72496       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  MGC10765 3'  GGCTCATGCCTGTAATCCCAG  44303       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  MGC10771 3'  GGCTCATGCCTGTAATCCCAG  44452       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  MGC10814 3'  GGCTCACACCTGTAATCCCAG  51041       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  MGC10814 5'  GGCTCATGCCTGTAATCCCAG  51042       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  MGC11287 5'  GGCTCACGTCTATAATCCCAG  48833       C  CA  _
                                CTGGGA TA  AG TGTGAGCC
                                ||||||  ||  ||  ||||||||
                                GACCCT AT  TC GCACTCGG
                                   A  A_  T
GAM607  MGC11352 3'  GGCGGGTGCCTGTAGTCCCAG  64804          A TG GA
                                CTGGGACTACA G  T  GCC
                                |||||||||||  |  |  |||
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                                GACCCTGATGT C  G  CGG
                                      C GT GG
GAM607  MGC11386 3' GGCTCACGCCTATAATCCCAG  51956      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGCACTCGG
                                   A  ATC
GAM607  MGC13053 3' GGCTCACGCCTGTAATCCCAG  51134      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  MGC14126 3' GGCTCACGCCTGTAATCCCAG  51856      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  MGC14407 3' GGCTCACACCTGTAATCTCAG  51880      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACTCT ATGT CACACTCGG
                                   A    C
GAM607  MGC14817 3' GGCTCACACCTGTAATCCCAG  50338      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  MGC15397 3' GGCTCACGCCTGTAATCCCAG  54681      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  MGC16142 3' GGCTCATGCCTATAATCCCAG  51293      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGTACTCGG
                                   A  ATC
GAM607  MGC16332 3' GGCTCATGCCTGTAATCCCA   56778      C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGTACTCGG
                                   A    C
GAM607  MGC16332 3' GGTGTGTGCCTGTAGTCCCAG  56779          A TG  A
                                CTGGGACTACA G  TG GCC
                                |||||||||||| |  || |||
                                GACCCTGATGT C  GT TGG
                                      C GT  G
GAM607  MGC16385 3' GGCTCACGCCTGTAATCCCAG  58888      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  MGC16703 3' GGCTCATGCCTGTAATCCCAG 73102      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  MGC20235 3' ATACCTGTAGTCCCAG     58892         A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CATA
                                      C
GAM607  MGC20235 3' GGCTTACACCTGTAATCCCAG 58901      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACATTCGG
                                   A   C
GAM607  MGC23244 3' GGCTCACGCCTGTAATCCCAG 58189      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  MGC2562  3' GGCTCACACCTGTAATCCCAG 50446      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  MGC2562  3' GGCTCACGCCTATAATCCCAG 50447      C CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGCACTCGG
                                   A ATC
GAM607  MGC2562  3' GCATGCGCCTGTAGTCCCAG  50441        A   A
                                CTGGGACTACA GTGTG GC
                                |||||||||||| ||||| ||
                                GACCCTGATGT CGCGT CG
                                      C   A
GAM607  MGC2731  3' GGCTCACGCTTGTAATCCCAG 43952      C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCGCACTCGG
                                   A
GAM607  MGC29762 3' GGCTCACACCTGTAATCCCAG 58473      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  MGC29891 3' GGCACACGCCTGTAGTCCCAG 58209        A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
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                                GACCCTGATGT CGCAC CGG
                                      C     A
GAM607  MGC29891 3' GGCTCACACCTGTAATCCCA  58210      C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CACACTCGG
                                   A    C
GAM607  MGC29891 3' GGCTCACGCCTGTAATCCCAG 58211       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  MGC29891 3' GGCTCACGCCTGTAGTCCCA  58212         A
                                TGGGACTACA GTGTGAGCC
                                |||||||||| |||||||||
                                ACCCTGATGT CGCACTCGG
                                      C
GAM607  MGC29937 3' GGCTCATGCCTGTAATCCCAG 58114       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  MGC3207  3' GCACCTGCAGTCCCAG      62560        A  A
                                CTGGGACT CA GTGT
                                |||||||| || ||||
                                GACCCTGA GT CACG
                                     C  C
GAM607  MGC3207  3' GGCTCACACCTGTAATCCCAG 62562       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  MGC39350 3' GGCTCACACCTGTAATCCCCAG 58655       AC_    A
                                CTGGG   TACA GTGTGAGCC
                                |||||   |||| |||||||||
                                GACCC   ATGT CACACTCGG
                                   CTA    C
GAM607  MGC4248  3' GCACCTGTAGTCCCAG      50329          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  MGC4248  3' GGCTCACACCTGTAATCCCAG 50331       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  MGC4400  3' GGCTCACACCTGTAATCTCAG 51055       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACTCT ATGT CACACTCGG
                                   A   C
GAM607  MGC4562  3' GGCATGCGCCTGTAGTCCCAG  55910         A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CGCGT CGG
                                      C    A
GAM607  MGC4562  3' GGCTCACGCCTGTAACCCCAG  55911      AC   A
                                CTGGG  TACA GTGTGAGCC
                                |||||  |||| |||||||||
                                GACCC  ATGT CGCACTCGG
                                  CA   C
GAM607  MGC4663  3' GCACCTGTAGTCCCAG      44506          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  MGC4663  3' GGCTCACGCCTATAATCCCAG  44507      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGCACTCGG
                                   A  ATC
GAM607  MGC4840  3' GGCTCACACCTGTAATTCCAG  71569      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCTT ATGT CACACTCGG
                                   A   C
GAM607  MGC5254  3' GGCTCACGCCTGTAATCCCAG  50411      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  MGC5384  3' GCGCCTGTAGTCCCAG      48271          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  MGC5384  3' GGCTCATGCCTGTAATCCCAG  48272      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  MGC5457  3' GGCTCACACCTTAATCCCAG   50946      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACACTCGG
                                   A  TC_
GAM607  MIDORI   3' GCATTCTGTAGTCCCAGG    73787          _
                                CCTGGGACTACA AGTGT
                                |||||||||||| |||||
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                                GGACCCTGATGT TTACG
                                      C
GAM607  MKRN4   3' GCGCCTGTAGTCCCAG     47748          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  MKRN4   3' GGCTCACGCCTGTAATCCCAG 47753      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  MOST2   5' GGCACATGCCTGTAGTCCCAG 39687         A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CGTAC CGG
                                      C   A
GAM607  MOST2   5' GGCTCACACCTGTAATCCCAG 39688      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  MRP63   3' GGCTCACGCCTGTAATCCCA  43810      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                   A   C
GAM607  MRPL56  3' GGCTCACGCCTGTAATCCCA  51690      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                   A   C
GAM607  MRPS10  3' GGCTCACGCCTGTAATCCCAG 36297      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  MT-ACT48 3' GCACCTGTAGTCCCAG     24688          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  MT-ACT48 3' GGCTCATGCCTGTAATCCCAG 24691      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  My015   3' GCACCTGCAGTCCCAG     66654        A  A
                                CTGGGACT CA GTGT
                                |||||||| || ||||
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                                GACCCTGA GT CACG
                                    C  C
GAM607  NBR2    3'  GGCTCATGCCTGTAGTCCCAG  19490          A
                                CTGGGACTACA GTGTGAGCC
                                |||||||||||  |||||||||
                                GACCCTGATGT CGTACTCGG
                                      C
GAM607  NCBP2   3'  GGCTCACACGTGTAATCCCA  23748      C   A
                                TGGGA TACA GTGTGAGCC
                                |||||  ||||  |||||||||
                                ACCCT ATGT CACACTCGG
                                  A   G
GAM607  NDUFC2  3'  GGCTCATGCCTGTAATCCCAG  15841      C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  NMNAT   3'  GGCTCACGCCTGTAGTCCCAG  42960          A
                                CTGGGACTACA GTGTGAGCC
                                |||||||||||  |||||||||
                                GACCCTGATGT CGCACTCGG
                                      C
GAM607  NMNAT   3'  GCTCCTGTAGTCCCAG      42958          AGTGT
                                CTGGGACTACA    GAGC
                                ||||||||||     ||||
                                GACCCTGATGT    CTCG
                                      C____
GAM607  NMNAT   3'  GGCTCACACCTGTAATCCCAG  42959      C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  NMT2    3'  GGCTCACGCCTGTAATCCCAG  16667      C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  NPTXR   3'  GGCTCACGCCTGTAATCCCAG  54185      C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  NPTXR   3'  GGCTCACGCCTGTAATCCCAG  26649      C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  OCLM    5'  GGCTCATGCCTATAATCCCAG  42350      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                ||||||  ||   |||||||||
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                                GACCCT AT   CGTACTCGG
                                   A  ATC
GAM607  ORC6L    3'  GGCTCACGCCTGTAATCCCAG  26725       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  PAFAH2   3'  GGCTCATGCCTGTAATCCCAG  4766        C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  PB1      3'  GGCTCACACCTGTAATCCCAG  37024       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  PDCD7    3'  GGCTCACGCCTGTAATCCCA   72140       C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                  A    C
GAM607  PDCD7    3'  GGTGCACACCTGTAGTCCCAG  72141           A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CACAC TGG
                                      C    G
GAM607  phorbolin-1 3'  GCGCCTGTAGTCCCAG      88780           A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  phorbolin-1 3'  GGCTCACGCCTGTAATCCCAG  88781       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  POFUT1   3'  GGCTCATGCCTGTAATCCCAG  70473       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  POLYDOM  3'  GGCTCACGCCTGTAATCCCAG  44427       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  PP591    5'  GGCACGCGCCTGTAGTCCCAG  47370           A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
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                                GACCCTGATGT CGCGC CGG
                                      C     A
GAM607  PP591    5' GGCTCACACCTATAATTCCAG 47371      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCTT AT   CACACTCGG
                                   A  ATC
GAM607  PPP1R3B  3' GCGCCTGTAGTCCCAG     44823         A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  PPP1R3B  3' GGCTTATGCCTGTAATCCCAG 44824      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTATTCGG
                                   A    C
GAM607  PRO0038  3' GGCTCATGCCTATAATCCCA  26093     C  CAA
                                TGGGA TA   GTGTGAGCC
                                ||||| ||   |||||||||
                                ACCCT AT   CGTACTCGG
                                   A  ATC
GAM607  PRO0478  3' GCTCACACCTGTAATCCCAG  26191      C    A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
                                GACCCT ATGT CACACTCG
                                   A    C
GAM607  PRO0478  5' GGCTCACACCTGTAATCCCAG 26193      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  PRO0478  3' GGCTCATGCCTGTAATCCCAG 26194      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  PRO0478  5' GTGCACACCTGTAATCCCAGGT 26196        C    A    A
          A                      TACCTGGGA TACA GTGTG GC
                                |||||||| |||| ||||| ||
                                ATGGACCCT ATGT CACAC TG
                                     A    C    G
GAM607  PRO0611  3' GGCTCATGCCTGTAATCCCAG 26012      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  PRO0628  3' GGCTCACGCATGTAATCCCAG 26207      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   A
GAM607  PRO1048  5' GGCATGTGCCTGTAGTCCCAG 37521          A TG  A
                                CTGGGACTACA G  TG GCC
                                |||||||||||  |  || |||
                                GACCCTGATGT C  GT CGG
                                      C GT  A
GAM607  PRO1048  3' GGCTCACACCTGTAATCCTAG 37522       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GATCCT ATGT CACACTCGG
                                   A   C
GAM607  PRO1386  3' CTCACCCATAGTCCCAG    48380        CAAGT
                                CTGGGACTA    GTGAG
                                |||||||||    |||||
                                GACCCTGAT    CACTC
                                      ACC__
GAM607  PRO1496  3' GGCATGTGCCTGTAGTCCCAG 37760          A TG  A
                                CTGGGACTACA G  TG GCC
                                |||||||||||  |  || |||
                                GACCCTGATGT C  GT CGG
                                      C GT  A
GAM607  PRO1777  3' GGCTCATGCCTGTAATCCCAG 37763       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  PRO1853  3' GGCTCATGCCTGTAATCCCAG 37774       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  PRO2015  3' GGCTCACGCCTGTAATCCCAG 37561       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  PRO2198  5' GGCTCACGCCTGTAATCCCGG 37793       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GGCCCT ATGT CGCACTCGG
                                   A   C
GAM607  PRO2730  3' GGCTCACACCTGTAATCCCAG 47418       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  PRO2859  3' GCACTTGTAGTCCCAG      37615
                                CTGGGACTACAAGTGT
                                ||||||||||||||||
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                                GACCCTGATGTTCACG

GAM607  PRO2859  3' GGCTCATGCCTGTAATCCCAG 37616      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  PRO2949  3' GGCTCATGCCTGTAATCCCAG 37622      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  PRO2964  3' GCACCTGTAGTCCCAG     37655         A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  PRO2964  3' GGCTCACGCCTGTAATCCCAG 37656      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  PSR      3' GGCACATGCCTGTAGTCCCAG 65185        A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CGTAC CGG
                                      C   A
GAM607  PSR      3' GGCTCACACCTGTAATCCCAG 65186      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  PTD012   3' GGCTCATGCCTATAATCCCAG 25894      C CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGTACTCGG
                                   A  ATC
GAM607  PTK6     3' GGCTCATGCCTGTAATCCCAG 19939      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  PTRF     3' GGCTTATGCCTGTAACCCCAG 63506     AC   A
                                CTGGG  TACA GTGTGAGCC
                                |||||  |||| |||||||||
                                GACCC  ATGT CGTATTCGG
                                  CA   C
GAM607  RAB4B    5' GGCTCATGCCTGTAATCCCAG 32378      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  RASGRP4  3'  GCCCATTCAGTCCCAGG     53654        ACAAGT   A
                                CCTGGGACT      GTG GC
                                |||||||||      ||| ||
                                GGACCCTGA      TAC CG
                                   CT_____    C
GAM607  RES4-25  3'  GGCACGCACCTGTAGTCCCA   64651         A    A
                                TGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                ACCCTGATGT CACGC CGG
                                   C     A
GAM607  RFX4     3'  GGCTCACACCTGTAGTCCCAG  11317         A
                                CTGGGACTACA GTGTGAGCC
                                |||||||||| |||||||||
                                GACCCTGATGT CACACTCGG
                                   C
GAM607  RNO2     5'  GGCTCACGCCTGTAATCCCAG  52774       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  RNO2     5'  GGCTCATGCCTGTAGTCCCAG  52775         A
                                CTGGGACTACA GTGTGAGCC
                                |||||||||| |||||||||
                                GACCCTGATGT CGTACTCGG
                                   C
GAM607  RoXaN    3'  GGCGGGTGCCTGTAGTCCCAG  46650          A TG GA
                                CTGGGACTACA G  T  GCC
                                |||||||||| |  |  |||
                                GACCCTGATGT C  G  CGG
                                   C GT GG
GAM607  RoXaN    3'  GGCTCACACCTATAATCCCAG  46652       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                ||||||  ||   |||||||||
                                GACCCT AT   CACACTCGG
                                   A  ATC
GAM607  RoXaN    3'  GGCTCACGCCAGTAATCCCAG  46653       C   AA
                                CTGGGA TAC  GTGTGAGCC
                                ||||||  |||  |||||||||
                                GACCCT ATG  CGCACTCGG
                                   A   AC
GAM607  RoXaN    3'  GGCTCATGCCTGTAATCCCAG  46654       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  Rpo1-2   3'  GGCACACCCCTGTAGTCCCAG  38704          AGT   A
                                CTGGGACTACA   GTG GCC
                                ||||||||||   ||| |||
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                                GACCCTGATGT   CAC CGG
                                      CCC   A
GAM607   Rpo1-2   3'  GGCTCACACCCATAATCCCA   38706      C  CAA
                                TGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                ACCCT AT   CACACTCGG
                                   A  ACC
GAM607   RRP4     3'  GGCTCACGCCTATAATCCCAG  26565       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGCACTCGG
                                   A  ATC
GAM607   RRP4     3'  GCACCTGTAGTCCCAG      26564          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607   SAC2     3'  GGCTCACACCTATAATCCCA   30056      C  CAA
                                TGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                ACCCT AT   CACACTCGG
                                   A  ATC
GAM607   SAMHD1   3'  GGCGTGTGCCTGTAGTCCCAG  61317          A TG GA
                                CTGGGACTACA G  T  GCC
                                |||||||||||| |  |  |||
                                GACCCTGATGT C  G  CGG
                                      C GT TG
GAM607   SAMHD1   3'  GGTGTGTGCTTGTAATCCCAG  61318       C     TG  A
                                CTGGGA TACAAG  TG GCC
                                |||||| ||||||  || |||
                                GACCCT ATGTTC  GT TGG
                                   A     GT  G
GAM607   SC65     3'  GGCTCACACCTGTAATCCCAG  21291       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607   SC65     3'  GGCTCACGCCTGTAATCCCAG  21292       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607   SCIN     3'  GGCTCACACCTGTAATCCCAG  52425       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607   SCYA5    3'  GCGCCTGTAGTCCCAG      11453          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
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                                GACCCTGATGT CGCG
                                      C
GAM607  SEMA3E   3'  GGCTCACGCCTGTAATCCCAG  24884      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  SEMA3E   3'  GCGCCTGTAGTCCCAG     24883         A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  SEMA4G   5'  GCAACTGCAGTCCCAGG    94682         A  AG
                                CCTGGGACT CA  TGT
                                ||||||||| ||  |||
                                GGACCCTGA GT  ACG
                                     C  CA
GAM607  SEMA5A   3'  GGCTCATGCCTATAATCCCAG  14259      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGTACTCGG
                                   A  ATC
GAM607  SIAT4A   3'  GGCACACACTTGTAGCCCCAG  11672      A        A
                                CTGGG CTACAAGTGTG GCC
                                ||||| |||||||||| |||
                                GACCC GATGTTCACAC CGG
                                   C         A
GAM607  SIAT4A   3'  GGCTCACACCTGTAATCT    11673     C   A
                                GGA TACA GTGTGAGCC
                                ||| |||| |||||||||
                                TCT ATGT CACACTCGG
                                  A   C
GAM607  SLC19A3  3'  GGCTCACACCTGTAATCCCAG  47495      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  SLC7A11  3'  GGCTTACATCTGTAATCCCAG  26755      C   AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  ACATTCGG
                                   A   CT
GAM607  SMAP-5   3'  GCGCCTGTAGTCCCAG     47933         A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  SMAP-5   3'  GCTCACGCCTGTAATCCCAG  47934      C   A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
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                                GACCCT ATGT CGCACTCG
                                   A   C
GAM607  SPTLC2   3' GGCTCACACCTGTAATCCTAG 16804      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GATCCT ATGT CACACTCGG
                                   A   C
GAM607  SRF     3' CTTGCGCTGTCCCAGG     11947       TACA   TG
                                CCTGGGAC   AGTG  AG
                                ||||||||   ||||  ||
                                GGACCCTG   TCGC  TC
                                     ____   GT
GAM607  STX12   3' GGCTCACACTTGTAATCCCA  66353     C
                                TGGGA TACAAGTGTGAGCC
                                ||||| ||||||||||||||
                                ACCCT ATGTTCACACTCGG
                                   A
GAM607  SYAP1   3' GCACCTGTAATCCCAGGTA   51403       C   A
                                TACCTGGGA TACA GTGT
                                ||||||||| |||| ||||
                                ATGGACCCT ATGT CACG
                                     A   C
GAM607  SYT12   3' GGTGTCCCGCAGTCCCAGG   94739       ACAA  T _
                                CCTGGGACT   GTG GA GCC
                                |||||||||   ||| || |||
                                GGACCCTGA   CGC CT TGG
                                     ____  C  G
GAM607  TA-LRRP 3' GGCTCATGCCTATAATCCCAG 31071     C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGTACTCGG
                                   A  ATC
GAM607  TACTILE 3' GCACCTGTAGTCCCAG     19472        A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  TACTILE 3' GGCTCACGCCTGTAATCCCAG 19474     C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  THEA    3' GGCTCACGCCTGTAATCCCAG 66295     C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  TIP47   3' GGCTCACACCTGTAATCCCAG 19482     C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  TMG4    3'  GGCTCATGCCTGTAATCCCAG  43991      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  TRIAD3  3'  GGCGCATGCCTATAATCCCAGG 94506        C  CAA    A
          TA                     TACCTGGGA TA   GTGTG GCC
                                |||||||||  ||   ||||| |||
                                ATGGACCCT AT   CGTAC CGG
                                     A  ATC    G
GAM607  TRIM38  3'  GGCTCACGCCTGTAATCCCAG  20988      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  TXNL2   3'  GGCTCGTGCTTGTAATCCCAG  21552      C    TG
                                CTGGGA TACAAG  TGAGCC
                                |||||| ||||||  ||||||
                                GACCCT ATGTTC  GCTCGG
                                   A     GT
GAM607  UBF-fl  3'  GGCTCACACCTGTAATCCCAG  51568      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  ust3    3'  GGCTCACGCCTGTAATCCCAG  93229      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  VIT1    5'  GGCTCATGCCTGTAACCCCAG  37977     AC   A
                                CTGGG  TACA GTGTGAGCC
                                |||||  |||| |||||||||
                                GACCC  ATGT CGTACTCGG
                                   CA   C
GAM607  VMP     3'  CTCACACTTGCTCAGTTCAGG  54898     G  A__
                                CCTGG ACT   CAAGTGTGAG
                                ||||| |||  ||||||||||
                                GGACT TGA   GTTCACACTC
                                   _  CTC
GAM607  VPS4B   3'  GGCTTATGCCTGTAATCCCAG  16823      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTATTCGG
                                   A   C
GAM607  WBSCR22 3'  GGCTCACACCTGTAATCCCAG  34036      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  WBSCR23  3'  GGCGCATGCCTATAGTCCCAG  46767        CAA    A
                                CTGGGACTA   GTGTG GCC
                                |||||||||   ||||| |||
                                GACCCTGAT   CGTAC CGG
                                   ATC    G
GAM607  YEA      3'  GGCTCACACCTGTAATCCCAG  51532       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  YME1L1   3'  GGCTCACATCTGTAATCCCAG  26530       C   AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  ACACTCGG
                                   A   CT
GAM607  YME1L1   3'  GGCTCACATCTGTAATCCCAG  57780       C   AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  ACACTCGG
                                   A   CT
GAM607  ZAK      3'  GCACACACCTGTAGTCCCAG   56127         A    A
                                CTGGGACTACA GTGTG GC
                                |||||||||||| ||||| ||
                                GACCCTGATGT CACAC CG
                                      C    A
GAM607  ZAK      3'  GGCTCACGCCTGTAATCCCAG  56131       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  ZFP106   3'  GGCTCACACCTGTAATCCCAG  42474       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  ZFP106   3'  GGCTCACGCCTGTAATCCCAG  42475       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  ZNF197   3'  GGCTCACTCCTGTAGTCCCAGG 22764          AGT
                                CCTGGGACTACA  GTGAGCC
                                ||||||||||||  |||||||
                                GGACCCTGATGT  CACTCGG
                                      CCT
GAM607  ZNF197   3'  GGCTCATGCCTGTAATCCCAG  22765       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  ZNF271   3'  GCGCCTGTAGTCCCAG      95254          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  ZNF271   3'  GGCTCACGCCTGTAATCCCA  95255      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                   A   C
GAM607  ZNF297B  5'  GGCTCACACCTGTAATCCCAG 25787       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  ZNF297B  3'  GGCTCACGCCTGTAATCCCAG 25788       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  ZNF31    5'  ACAGCTGAGTCCCAGGTA    64980          A  AG
                                TACCTGGGACT CA  TGT
                                |||||||||| ||  |||
                                ATGGACCCTGA GT  ACA
                                      _ CG
GAM607  ZNF339   3'  GGTGTGTACCTGTAGTCCCAG 41126          A   TGA
                                CTGGGACTACA GTG   GCC
                                |||||||||| |||   |||
                                GACCCTGATGT CAT   TGG
                                      C   GTG
GAM607  ZNF347   3'  GGCTCATGCCTGTAATCCCA  50847      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGTACTCGG
                                   A   C
GAM607  LOC112687 3' GGCTCACACCTATAATCCCAG 72865       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACACTCGG
                                   A  ATC
GAM607  LOC115129 3' GGCACACACCCGTAATCCCAG 73236       C   AA    A
                                CTGGGA TAC  GTGTG GCC
                                |||||| |||  ||||| |||
                                GACCCT ATG  CACAC CGG
                                   A   CC    A
GAM607  LOC115129 5' GGCACACGCCTGTAATCCCAGG 73237          C   A    A
           TA                     TACCTGGGA TACA GTGTG GCC
                                |||||||||| |||| ||||| |||
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                                ATGGACCCT ATGT CGCAC CGG
                                    A   C    A
GAM607  LOC115129 3'  GGCTCACACCTATAATCCCAG  73239      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACACTCGG
                                   A  ATC
GAM607  LOC115129 5'  GGCTCACGCCTATAATCCCAG  73240      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGCACTCGG
                                   A  ATC
GAM607  LOC115129 5'  GGCTTACACCTGTAATCCCAG  73241      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACATTCGG
                                   A   C
GAM607  LOC115757 3'  ATACCTGTAGTCCCAG      73574          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CATA
                                      C
GAM607  LOC115761 3'  GGCATGTGCCTGTAGTCCCAG  91739          A TG  A
                                CTGGGACTACA G  TG GCC
                                |||||||||||  |  || |||
                                GACCCTGATGT C  GT CGG
                                      C GT  A
GAM607  LOC115761 3'  GGCTCATGCCTGTAATCCCAG  91740      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  LOC116228 3'  GGCTCATACCTGTAATCCCAG  73802      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CATACTCGG
                                   A   C
GAM607  LOC116349 3'  GGCTCACGCCTGTAATCCCAG  73834      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LOC119504 5'  GGCTCACGCCTGTAATCCCAG  73992      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LOC121457 3'  GGCTCACACCTGTAATCCTAG  74072      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GATCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC122704 3'  GGCTCACGCCTGTAATCCCAG  74141      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC122970 3'  GGCTCACACCTGTAATCCCAG  74182      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC122970 3'  GGTACACACCTGTAGTCCCAG  74183        A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CACAC TGG
                                      C    A
GAM607   LOC123016 3'  GCATGTGCCTATAGTCCCAG   58106       CAA TG  A
                                CTGGGACTA   G  TG GC
                                |||||||||   |  || ||
                                GACCCTGAT   C  GT CG
                                     ATC GT  A
GAM607   LOC126282 3'  GGCACATGCCTGTAGTCCCAG  74477        A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CGTAC CGG
                                      C    A
GAM607   LOC126282 3'  GGCTCACACCTGTAATCCCAG  74478      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC126282 3'  GGCTCACGCCTGTAATCCCAG  74479      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC126669 3'  GGCTCATGCACGTAATCCCA   75411      C  AA
                                TGGGA TAC  GTGTGAGCC
                                ||||| |||  |||||||||
                                ACCCT ATG  CGTACTCGG
                                  A   CA
GAM607   LOC127262 3'  GGCTCATGCCTGTAATCCCAG  76112      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC127294 3'  GGCTCACGCCTGTAATCCCAG  74658      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC130026 3'  GGCTCACGCTTGTAATCCCAG  56650       C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCGCACTCGG
                                   A
GAM607   LOC130026 3'  GGCACGTGCCTGTAGTCCCAG  56649          A TG  A
                                CTGGGACTACA G  TG GCC
                                |||||||||||  |  || |||
                                GACCCTGATGT C  GC CGG
                                      C GT  A
GAM607   LOC130162 3'  GCTCATGTCTGTAATCCCAG   74911       C   AG
                                CTGGGA TACA  TGTGAGC
                                |||||| ||||  |||||||
                                GACCCT ATGT  GTACTCG
                                   A   CT
GAM607   LOC130535 3'  GGCACACGCCTGTAGTCCCAG  76155          A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||  |||||  |||
                                GACCCTGATGT CGCAC CGG
                                      C    A
GAM607   LOC130535 3'  GGCTCATGCCTGTAATCCCAG  76156       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC130535 3'  CTCACACTTGTAATCCCAG    76150       C
                                CTGGGA TACAAGTGTGAG
                                |||||| ||||||||||||
                                GACCCT ATGTTCACACTC
                                   A
GAM607   LOC130589 3'  GGCTCACGCCTGTAATCCCAG  57133       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC130951 3'  GGCTCACACCTGTAATCCCA   57146      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CACACTCGG
                                  A   C
GAM607   LOC131744 3'  GGCTCATGCCTGTAATCCCAG  75871       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC131965 3'  GGCTCATGCCTATAACCCCAG  75032      ACTACAA
                                CTGGG      GTGTGAGCC
                                |||||      |||||||||
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                                GACCC      CGTACTCGG
                                   CAATATC
GAM607   LOC131965 3'  GGCTCATGCCTGTAATCCCAG  75033       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                    A    C
GAM607   LOC133926 3'  GCGCCTGTAGTCCCAG      75134          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                       C
GAM607   LOC134147 3'  GGCTCACGCCTGTAATCCCAG  57164       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                    A    C
GAM607   LOC137362 3'  GGCTCATGCCTGTAATCCCA   75266      C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGTACTCGG
                                   A    C
GAM607   LOC138241 3'  GGCTCACGCCTGTAATCCCA   75309      C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                   A    C
GAM607   LOC138428 3'  GGCTCACACCTATAATCCCAG  75338      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACACTCGG
                                    A  ATC
GAM607   LOC139422 3'  GGCTCACACCTGTAATCCTAG  75844      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GATCCT ATGT CACACTCGG
                                    A    C
GAM607   LOC142927 3'  CAGGCTATAATCCCAGGTA    76420        C  CA   G
                                TACCTGGGA TA  AGT TG
                                ||||||||| ||  ||| ||
                                ATGGACCCT AT  TCG AC
                                      A  A_   G
GAM607   LOC142927 3'  GGCTCATGCTTGTAATCCCAG  76429      C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCGTACTCGG
                                    A
GAM607   LOC142948 3'  GCGCCTGTAGTCCCAG      82890          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
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                                GACCCTGATGT CGCG
                                      C
GAM607  LOC143196 3'  GGCTCGTGCCTGTAATCCCAG  82906      C   A TG
                                CTGGGA TACA G  TGAGCC
                                |||||| |||| |  ||||||
                                GACCCT ATGT C  GCTCGG
                                   A   C GT
GAM607  LOC143310 3'  GGCTCACGCCTGTAATCCCAG  76537      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LOC143465 3'  GGCTCACACCTGTAATCTCAG  82965      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACTCT ATGT CACACTCGG
                                   A   C
GAM607  LOC143888 3'  GGCTCACGCCTGTAATCCCAG  76660      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LOC144465 3'  GGCTCATGCCTGTAATCCCA   76856      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGTACTCGG
                                   A   C
GAM607  LOC144481 3'  GCTCATGCCTGTAATCCCA   83099      C   A
                                TGGGA TACA GTGTGAGC
                                ||||| |||| ||||||||
                                ACCCT ATGT CGTACTCG
                                   A   C
GAM607  LOC144486 3'  GGCTCACGCCTGTAATCCCAG  83086      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LOC144524 5'  GGCTCACATGTGTAATCCCAG  83134      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT TACACTCGG
                                   A   G
GAM607  LOC144583 3'  GGCTCACACCTGTAATCCTAG  76894      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GATCCT ATGT CACACTCGG
                                   A   C
GAM607  LOC144817 3'  GGCTCACGCCTGTAATCCCAG  76972      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC145216 3'  GGCTCACGCCTGTAATCCCAG  83268      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC145231 3'  GGCTCATGCCTATAATCCCAG  83292      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGTACTCGG
                                   A  ATC
GAM607   LOC145299 3'  GCGCCTGTAGTCCCAG      83316          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   LOC145299 3'  GGCTCACGCCTGTAATCCCAG  83317      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC145333 3'  GCGCCTGTAGTCCCAG      83328          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   LOC145333 3'  GGCTCACGCCTGTAATCCCAG  83330      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC145387 3'  GGCTTACACCTGTAATCCCAG  83358      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACATTCGG
                                   A   C
GAM607   LOC145438 3'  GCGCCTGTAGTCCCAG      83341          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   LOC145438 3'  GGCTCACGCCTGTAATCCCAG  83342      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC145453 3'  GGCTCACACCTGTAATCTGAG  77145   G  C   A
                                CT GGA TACA GTGTGAGCC
                                || ||| |||| |||||||||
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                                GA TCT ATGT CACACTCGG
                                 G  A   C
GAM607  LOC145483 3'  GGCTCACGCCTGTAATCCCA  77246      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LOC145663 3'  GGCTCACGCCTGTAATCCCAG 83415      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LOC145663 3'  GGCTCATGCTTGTAATCCCAG 83416      C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCGTACTCGG
                                   A
GAM607  LOC145757 3'  GGCTCATGCCTGTAATCCCAG 77469      C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  LOC145820 3'  GCGCCTGTAGTCCCAG      77516          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  LOC145820 3'  GGCTCACGCCTGTAATCCCAG 77517      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LOC145824 3'  GGCTCATGCCTGTAATCCCAG 77526      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  LOC145955 3'  GGCTCACACTTGTAATCCCAG 83596      C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| |||||||||||||||
                                GACCCT ATGTTCACACTCGG
                                   A
GAM607  LOC145955 3'  GGCTCATGCCTGTAATCCCA  83597      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGTACTCGG
                                   A   C
GAM607  LOC146059 3'  GGCTCATGCCTGTAATCCCAG 77622      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC146159 3'  GGCTCACACCTGGAATCCCAG  77683      CTA  A
                                CTGGGA   CA GTGTGAGCC
                                ||||||   || |||||||||
                                GACCCT   GT CACACTCGG
                                   AAG  C
GAM607   LOC146227 3'  ACGCTGCAGGCCCCAGGTA   77710       A  ACA
                                TACCTGGG CT   AGTGT
                                |||||||| ||   |||||
                                ATGGACCC GG   TCGCA
                                    C  ACG
GAM607   LOC146229 3'  GGCTCACGCCTGTAATCCCAG  77767      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC146272 5'  GGCTCACACCTGTAATCCCAG  77792      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC146332 3'  GGCTCACGCCTGTAATCCCA   77828     C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                  A   C
GAM607   LOC146540 3'  GGCTCACACCTGTGATCCCAG  77979      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT GTGT CACACTCGG
                                   A   C
GAM607   LOC146540 3'  GGCACATGCCTGTAGTCCCAG  77977         A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CGTAC CGG
                                      C    A
GAM607   LOC146540 3'  GGCTCACACCTGTAATCCCAG  77978      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC146667 3'  GGCTCATGCCTGTAATCCCAG  83705      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC146701 3'  GGCTCACACCTGTAATCCCAG  83711      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC146713 3'  GGCGGGTGCCTGTAGTCCCAG  83731          A TG GA
                                CTGGGACTACA G  T  GCC
                                |||||||||||  |  |  |||
                                GACCCTGATGT C  G  CGG
                                      C GT GG
GAM607   LOC146713 3'  GGCTCACGCCTGTAATCCCAG  83732       C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC146728 3'  GGCTCACGCCTATAATCCCA   83751       C  CAA
                                TGGGA TA   GTGTGAGCC
                                |||||  ||   |||||||||
                                ACCCT AT   CGCACTCGG
                                   A  ATC
GAM607   LOC146756 3'  GCGCCTGTAGTCCCAG      83781          A
                                CTGGGACTACA GTGT
                                ||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   LOC146756 3'  GGCTCACGCCTGTAATCCCAG  83783       C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC146756 3'  GGCTCACGCCTGTAATCCCAG  83784       C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC146923 3'  GCACCTGTAGTCCCAG      78193          A
                                CTGGGACTACA GTGT
                                ||||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607   LOC146923 3'  GGCTCACACCTGTAATCCCAG  78194       C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC146975 5'  GGCTCACACCTATAATCCCAG  78224       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                ||||||  ||   |||||||||
                                GACCCT AT   CACACTCGG
                                   A  ATC
GAM607   LOC147054 5'  GGCTCACACCTGTAGGACA   83924    GGA    A
                                TG   CTACA GTGTGAGCC
                                ||   |||||  |||||||||
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                                AC   GATGT CACACTCGG
                                 AG_     C
GAM607   LOC147057 3'  GGCGCGCGCCTGTAGTCCCAG  83911          A     A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CGCGC CGG
                                      C     G
GAM607   LOC147057 3'  GGCTCATGCCTGTAATCCCAG  83912       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607   LOC147071 3'  GGCTCACGCCTGTAATCCCAG  73003       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607   LOC147180 5'  GGCATGTGCCTGTAGTCCCAG  83988          A TG  A
                                CTGGGACTACA G  TG GCC
                                |||||||||||  |  || |||
                                GACCCTGATGT C  GT CGG
                                      C GT  A
GAM607   LOC147599 3'  GGCACGTGCCTATAGTCCCAG  84042         CAA TG  A
                                CTGGGACTA   G  TG GCC
                                |||||||||   |  || |||
                                GACCCTGAT   C  GC CGG
                                     ATC GT  A
GAM607   LOC147599 3'  GGCTCATGCCTGTAATCCCAG  84043       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607   LOC147649 3'  GCGCCTGTAGTCCCAG       78416           A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   LOC147664 3'  GGCTCACGCCTGTAATCCCA   78410       C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                   A    C
GAM607   LOC147700 3'  GGCTCACGCCTGTAATCCCA   59199       C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                   A    C
GAM607   LOC147727 5'  GGCTCACGCTTGTAATCCCAG  78471       C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
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                                GACCCT ATGTTCGCACTCGG
                                   A
GAM607   LOC147727 5'  GGCTCACGTTTGTAATCCCAG  78472       C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTTGCACTCGG
                                   A
GAM607   LOC147837 3'  GGCTCACGCCTGTAATCCCAG  78517       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607   LOC148089 3'  GCACGGGCGCAGTCCCAGG    78633         ACAA  G  A
                                CCTGGGACT    GT TG GC
                                |||||||||    || || ||
                                GGACCCTGA    CG GC CG
                                      CG__  G  A
GAM607   LOC148089 3'  GGCTGCCCTGAGTCCCAGG    78638         A  A T  G
                                CCTGGGACT CA G GT AGCC
                                ||||||||| || | || ||||
                                GGACCCTGA GT C CG TCGG
                                     _ _ C  _
GAM607   LOC148147 3'  GCGCCTGTAGTCCCAG       78682           A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   LOC148147 3'  GGCTCACGCCTGTAATCCCAG  78686       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607   LOC148166 3'  GGCTCACACCTGTAATCTCAG  78695       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACTCT ATGT CACACTCGG
                                   A    C
GAM607   LOC148198 3'  GGCTCACGCCTGTAATCCCAG  70687       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607   LOC148293 3'  GGCATGCACCTGTAGTCCCAG  78782           A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CACGT CGG
                                      C    A
GAM607   LOC148397 3'  GGCTCACGCCTGTAATCCCGG  78820       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GGCCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC148534 3'  GGCTCATGCCTGTAATCCCAG  78896      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC148734 3'  GGCTCACGCCTGTAATCCCAG  78957      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC148749 3'  GGCTCACGCCTGTAATCCCAG  78961      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC148758 5'  GGCTCATGCCTGTAATCCCAG  78972      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC148809 5'  GGCTCACGCCTGTAATCCCAG  79004      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC148823 3'  GGTGCACACCTGTAGTCCCAGG 59209          A   A
            TA                    TACCTGGGACTACA GTGTG GCC
                                |||||||||||||| ||||| |||
                                ATGGACCCTGATGT CACAC TGG
                                      C   G
GAM607   LOC148918 5'  GGCTCACACCTGTAACCCTAG  79079      AC   A
                                CTGGG  TACA GTGTGAGCC
                                |||||  |||| |||||||||
                                GATCC  ATGT CACACTCGG
                                   CA   C
GAM607   LOC148918 5'  GGCTCACGCCTGTAATCCCAG  79080      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC148936 3'  GGCTCACACCTGTAATCCCAG  84298      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC148938 3'  GGCTCACACCTGTAATCCCAG  84280      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC149073 3'  GGCTCACGCCTATAATCCCAG  84327      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGCACTCGG
                                   A  ATC
GAM607   LOC149113 3'  GGCTCACGCCTGTAATCCCAG  79168      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC149175 3'  GCGCCTGTAGTCCCAG      79211          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   LOC149194 5'  GGCTCACGTCTGTAATCCCAG  79228      C   AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  GCACTCGG
                                   A   CT
GAM607   LOC149271 5'  GCCCACAGGGTGGTCCCAGG   79243         AAG   A
                                CCTGGGACTAC   TGTG GC
                                ||||||||||   |||| ||
                                GGACCCTGGTG   ACAC CG
                                      GG_   C
GAM607   LOC149271 3'  GGCTCACGCCTGTAATCCCAG  79245      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC149319 3'  GGCTCACGTCTGTAATCCCAG  79299      C   AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  GCACTCGG
                                   A   CT
GAM607   LOC149460 3'  GGCTCACGCTTGTAATCCCAG  84441      C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCGCACTCGG
                                   A
GAM607   LOC149579 5'  GGCTCACGCCTGTAATCCCAG  71136      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC149628 3'  GGCTTACGCCTATAATCCCAG  79465      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
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                                GACCCT AT   CGCATTCGG
                                   A  ATC
GAM607   LOC149628 3'  GGCTCACGCCTGTAATCCCAG  79464       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607   LOC149705 3'  GGCTCACACCTGTAATCCCA   84626      C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CACACTCGG
                                   A    C
GAM607   LOC149711 5'  GCTCACACCTATAATCCTAG   84683      C  CAA
                                CTGGGA TA   GTGTGAGC
                                |||||| ||   ||||||||
                                GATCCT AT   CACACTCG
                                   A  ATC
GAM607   LOC150185 3'  GGCTCATGCCTGTAATCCCA   84908      C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGTACTCGG
                                   A    C
GAM607   LOC150225 3'  ACGCCTGTAGTCCCAG      84976          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCA
                                      C
GAM607   LOC150245 3'  GGCTCACACCGGTAATCCCA   84936      C   AA
                                TGGGA TAC  GTGTGAGCC
                                ||||| |||  |||||||||
                                ACCCT ATG  CACACTCGG
                                   A   GC
GAM607   LOC150299 3'  GCACCTGTAGTCCCAG      84971          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607   LOC150319 3'  GGCTCATGCCTGTAATCCCAG  79660       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607   LOC150343 5'  GGCTCACACCCAAATCAGG    79674      GACTACAA
                                CCTGG       GTGTGAGCC
                                |||||       |||||||||
                                GGACT       CACACTCGG
                                   AAACC___
GAM607   LOC150343 3'  GGCTCACGCCTGTAATCCCAG  79675       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC150358 3'  GCACCTGTAGTCCCAG      84923          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607   LOC150358 3'  GGCGGACACCTGTAATCCCAGG 84924         C   A   GA
           TA                    TACCTGGGA TACA GTGT  GCC
                                |||||||||| |||| ||||  |||
                                ATGGACCCT ATGT CACA  CGG
                                     A   C   GG
GAM607   LOC150358 3'  GGCTCATGCCTATAATCCCAG  84925       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGTACTCGG
                                   A  ATC
GAM607   LOC150358 3'  GGCTCATGCCTGTAATCCCAG  84926       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC150372 3'  GGCACGCACCTGTAGTCCCAG  79803          A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CACGC CGG
                                      C    A
GAM607   LOC150372 3'  GGCTTATGCCTGTAATCCCAG  79805       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTATTCGG
                                   A   C
GAM607   LOC150465 3'  GCTCATGCTTGTAATCCCAG   79872       C
                                CTGGGA TACAAGTGTGAGC
                                |||||| ||||||||||||
                                GACCCT ATGTTCGTACTCG
                                   A
GAM607   LOC150481 3'  GGTTCACACCTGTAATCCCAG  79896       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTTGG
                                   A   C
GAM607   LOC150622 3'  GGCTCACGCCTGTAATCCCA   79963       C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                  A   C
GAM607   LOC150630 3'  GGCTCATGCCTGTAATCCCAG  85109       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC150889 3'  GCACTTGTAATCCCAG      80026       C
                                CTGGGA TACAAGTGT
                                |||||| |||||||||
                                GACCCT ATGTTCACG
                                   A
GAM607   LOC150889 3'  GGCTCATGCCTGTAATCCCAG  80028       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC150960 3'  GGCATGCACCTGTAGTCCCAG  80069           A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CACGT CGG
                                      C    A
GAM607   LOC151196 3'  GGCTCACGCCTGTAATCCCAG  85269       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC151248 3'  GCGCCTGTAGTCCCAG      80190           A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   LOC151248 3'  GGCTCACGCCTGTAATCCCAG  80191       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC151429 3'  GCGCCTGTAGTCCCAG      85356           A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   LOC151429 3'  GGCTCACACCTGTAATCCCAG  85357       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC151446 3'  GGCTCATGCCCGTAATCCCAG  85377       C   AA
                                CTGGGA TAC  GTGTGAGCC
                                |||||| |||  |||||||||
                                GACCCT ATG  CGTACTCGG
                                   A   CC
GAM607   LOC151556 3'  GGCTCACGCCTGTAATCCCAG  80281       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC151602 3'  GGCTCACGCCTGTAATCCCA  80299      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC151614 3'  GGCTCACACCTGTAATCCCAG 80307      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC151632 3'  GGCTCACACCTGTGATCTCAG 85471      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACTCT GTGT CACACTCGG
                                   A   C
GAM607   LOC151720 3'  GCACCTGTAGTCCCAG      80340          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607   LOC151904 3'  GGCTCACGCCTGTAATCCCAG 80393      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC152106 3'  GCCTGCCTGTAGTCCCAG    70062          A T  GA
                                CTGGGACTACA G GT  GC
                                |||||||||||| | ||  ||
                                GACCCTGATGT C CG  CG
                                      _ _  TC
GAM607   LOC152263 3'  GGCTCACACCTGTAATCCCAG 85675      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC152271 3'  GGCTCACACCTATGATCTCAG 80520      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACTCT GT   CACACTCGG
                                   A  ATC
GAM607   LOC152275 3'  GCTCACATGTAAATCCAGGTA 85618       AC   AG
                                TACCTGGG  TACA  TGTGAGC
                                ||||||||  ||||  |||||||
                                ATGGACCT  ATGT  ACACTCG
                                    AA   __
GAM607   LOC152313 3'  GCGCCTGTAGTCCCAG      85666          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
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                                GACCCTGATGT CGCG
                                      C
GAM607   LOC152313 3'  GGCTCGTGCTTGTAATCCCAG  85667       C     TG
                                CTGGGA TACAAG  TGAGCC
                                |||||| ||||||  ||||||
                                GACCCT ATGTTC  GCTCGG
                                   A     GT
GAM607   LOC152316 3'  GGCATGTGCCTGTAGTCCCAG  85614          A TG  A
                                CTGGGACTACA G  TG GCC
                                |||||||||||| |  || |||
                                GACCCTGATGT C  GT CGG
                                      C GT  A
GAM607   LOC152317 3'  GGCTCACACCTGTAACCCCA   85647      AC    A
                                TGGG  TACA GTGTGAGCC
                                ||||  |||| |||||||||
                                ACCC  ATGT CACACTCGG
                                  CA    C
GAM607   LOC152426 3'  GCTCACGCCTGTAATCCCAG   85716       C    A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
                                GACCCT ATGT CGCACTCG
                                   A    C
GAM607   LOC152426 3'  GGCGGGTGCCTGTAGTCCCAG  85718          A TG GA
                                CTGGGACTACA G  T  GCC
                                |||||||||||| |  |  |||
                                GACCCTGATGT C  G  CGG
                                      C GT GG
GAM607   LOC152445 3'  GGCTCACACCTGTAATCCCAG  85758       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607   LOC152453 3'  GGCTCACGCCTGTAATCCCA   80602       C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                  A    C
GAM607   LOC152627 5'  GGCTCATACCTGTAATCCCAG  80631       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CATACTCGG
                                   A    C
GAM607   LOC152804 3'  GGCTCACGCTTGTAATCCCAG  85887       C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCGCACTCGG
                                   A
GAM607   LOC152860 3'  GGCTCACACCTATAATCCCAG  80703       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
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                                GACCCT AT   CACACTCGG
                                   A  ATC
GAM607   LOC152897 3'  GGCACGTGCTTGTAGTCCCAG  80729          TG  A
                                CTGGGACTACAAG  TG GCC
                                ||||||||||||  || |||
                                GACCCTGATGTTC  GC CGG
                                      GT  A
GAM607   LOC152926 3'  GGCTCATGCCTGTAATCCCAG  80746      C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC153077 3'  GGCTCACGTCTGTAATCCCAG  85913      C   AG
                                CTGGGA TACA  TGTGAGCC
                                ||||||| ||||  ||||||||
                                GACCCT ATGT  GCACTCGG
                                   A   CT
GAM607   LOC153260 3'  GGCTCACACCTGTAATCCCAG  80806      C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC153561 3'  GGCTCATGCCTGTAATCCCAG  80889      C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC153579 3'  GGCATGTGCCTGTAGTCCCAG  80897         A TG  A
                                CTGGGACTACA G  TG GCC
                                ||||||||||| |  || |||
                                GACCCTGATGT C  GT CGG
                                      C GT  A
GAM607   LOC153579 3'  GGCTCACACCTGTAATCCCAG  80898      C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC153642 3'  GGCTCACACCTGTAATCCCAGG 80911       C   A
                                CCTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GGACCCT ATGT CACACTCGG
                                    A   C
GAM607   LOC153682 3'  GGCAGGTGCCTGTAGTCCCAG  86086         A TG GA
                                CTGGGACTACA G  T  GCC
                                ||||||||||| |  |  |||
                                GACCCTGATGT C  G  CGG
                                      C GT GA
GAM607   LOC153682 3'  GGCTCATGCCTGTAATCCCAG  86087      C   A
                                CTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
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                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC153733 3'  GGCTCATGCTTGTAATCCCAG  80923      C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCGTACTCGG
                                   A
GAM607   LOC154089 3'  GGCTCGTGCCTGTAATCCCAG  81040      C   A TG
                                CTGGGA TACA G  TGAGCC
                                |||||| |||| |  ||||||
                                GACCCT ATGT C  GCTCGG
                                   A   C GT
GAM607   LOC154791 3'  GGCTCACGCCTGTAATCCCAG  81160      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC154881 3'  CATGTCTGTAGTCCCAG     81169          AG
                                CTGGGACTACA  TGTG
                                ||||||||||  ||||
                                GACCCTGATGT  GTAC
                                      CT
GAM607   LOC154992 3'  GGCTCACATTCGTAATCCCAG  81218      C   A
                                CTGGGA TAC AGTGTGAGCC
                                |||||| ||| ||||||||||
                                GACCCT ATG TTACACTCGG
                                   A   C
GAM607   LOC155006 3'  GGCTCATGCCTGTAATCCCAG  81240      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC155006 3'  GGCTCATGCCTGTAATCCCAG  81241      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC155072 3'  GCGCCTGTAGTCCCAG     86380          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   LOC155072 3'  GCGCCTGTAGTCCCAG     86381          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   LOC155072 3'  GGCTCACACCTGTAATCCCAG  86383      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC155072 3'  GGCTCACGCCTGTAATCCCAG  86384      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC155376 3'  GGCTCACACTTGTAATCCCAG  81338      C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCACACTCGG
                                   A
GAM607   LOC155438 3'  GGCTCACACCTGTAATCCCAG  86395      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC157464 5'  GGCTCACGCCTGTAATCCCAG  86450      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC157657 3'  GCTCACGCCTGTAATCCCAG   81519      C   A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
                                GACCCT ATGT CGCACTCG
                                   A   C
GAM607   LOC157660 3'  GGCTCACGCCTGTAATCCCAG  86510      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC157931 5'  GCTCTGGACGTGTCCCAGG   86665       TACAA  G _
                                CCTGGGAC    GT T GAGC
                                ||||||||    || | ||||
                                GGACCCTG    CA G CTCG
                                     TG___  G T
GAM607   LOC158088 3'  GCACCTGTAGTCCCAG      86682          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607   LOC158187 3'  GGCACACGCCTGTAGTCCCAG  86693          A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CGCAC CGG
                                      C    A
GAM607   LOC158191 3'  GGCACACACCTGTAGTCCCAG  81780          A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
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                                GACCCTGATGT CACAC CGG
                                      C     A
GAM607   LOC158267 3'  GGCTCACACTTATCCTAG    81835       CTAC
                                CTGGGA    AAGTGTGAGCC
                                ||||||    ||||||||||
                                GATCCT    TTCACACTCGG
                                   A___
GAM607   LOC158310 3'  GGCTCACACCTGTAATCCCAG  86758       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607   LOC158382 5'  GGCTCACACCTATAGTCCCAG  86788         CAA
                                CTGGGACTA   GTGTGAGCC
                                |||||||||   |||||||||
                                GACCCTGAT   CACACTCGG
                                      ATC
GAM607   LOC158819 5'  GGCTCACACCTGTAATCCCAG  86910       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607   LOC158863 3'  GGCTCACACCTGTAATCCCA   86925       C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CACACTCGG
                                   A    C
GAM607   LOC158987 3'  GCATGTGCCTGTAATCCCAGGT 86964         C    A TG  A
           A                     TACCTGGGA TACA G  TG GC
                                |||||||||| |||| |  || ||
                                ATGGACCCT ATGT C  GT CG
                                      A    C GT  A
GAM607   LOC158987 3'  GGCTCACACCTGTTATCCCAG  86966       CT   A
                                CTGGGA  ACA GTGTGAGCC
                                ||||||  ||| |||||||||
                                GACCCT  TGT CACACTCGG
                                   AT   C
GAM607   LOC158987 3'  GGCTCACGCCTGTAATCCCA   86967       C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                   A    C
GAM607   LOC159036 3'  GGCTCATGCCTGTAATCCCAG  86973       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607   LOC159053 3'  GCGCCTGTAGTCCCAG       86980           A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
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                                GACCCTGATGT CGCG
                                      C
GAM607   LOC159053 3'  GGCTCACGCCTGTAATCCCA   86981      C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                   A    C
GAM607   LOC159053 3'  GGCTTACGCCTGTAATCCCAGG 86982       C    A
                                CCTGGGA TACA GTGTGAGCC
                                ||||||| |||| |||||||||
                                GGACCCT ATGT CGCATTCGG
                                    A    C
GAM607   LOC160646 3'  GGCTCACACCTGTAATCTCAG  82230       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACTCT ATGT CACACTCGG
                                   A    C
GAM607   LOC161823 3'  GGCTCATGCCTGTAATCCCAG  82305       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607   LOC161823 3'  GGTACACACCTGTAGTCCCAG  82306          A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CACAC TGG
                                      C    A
GAM607   LOC163255 5'  CTCACACTTGGTTC       82448      TA
                                GGAC  CAAGTGTGAG
                                ||||  ||||||||||
                                CTTG  GTTCACACTC
                                  __
GAM607   LOC163748 5'  GGCTCACACTCTTGCCCA    87044      ACTACA
                                TGGG     AGTGTGAGCC
                                ||||     ||||||||||
                                ACCC     TCACACTCGG
                                  GTTC__
GAM607   LOC167555 3'  GGCTCACACCCGTAATCCCAG  82679       C   AA
                                CTGGGA TAC  GTGTGAGCC
                                |||||| |||  |||||||||
                                GACCCT ATG  CACACTCGG
                                   A   CC
GAM607   LOC170395 3'  GGCACACGCCTGCAGTCCCAG  76375        A A    A
                                CTGGGACT CA GTGTG GCC
                                |||||||| || ||||| |||
                                GACCCTGA GT CGCAC CGG
                                    C C    A
GAM607   LOC170395 3'  GGCTCACGCCTGTAATCCCAG  76376       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC196027 3'  GGCTCACACCTGTAATCTCAG  87549      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACTCT ATGT CACACTCGG
                                   A   C
GAM607   LOC196027 3'  GGCTCATGCTTGTAATCCCGG  87550      C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GGCCCT ATGTTCGTACTCGG
                                   A
GAM607   LOC196047 5'  GGCGTGCACCTGTAGTCCCAG  89605         A   GA
                                CTGGGACTACA GTGT  GCC
                                |||||||||| ||||  |||
                                GACCCTGATGT CACG  CGG
                                      C   TG
GAM607   LOC196047 5'  GGCTCACGCCTGTAATCCCAG  89606      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC196528 3'  GGCTTACACCTATAATCCCAG  87765      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACATTCGG
                                   A  ATC
GAM607   LOC196529 3'  GTGCCTGTAATCCCAGGTA   87778        C   A TG
                                TACCTGGGA TACA G  T
                                ||||||||| |||| |  |
                                ATGGACCCT ATGT C  G
                                     A   C GT
GAM607   LOC196540 3'  ATGCCTGTAGTCCCAG      89634          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGTA
                                      C
GAM607   LOC197196 3'  GGCTCACGCCTGTAATCCCAG  89735      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC197201 3'  GGCTCACGCCTGTAATCCCAG  87943      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC197201 3'  GGCTCACGCCTGTAATCCCAG  87944      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC197319 3'  GGCTCACACCTGTAATCCCAG  87973      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC199858 3'  GCTCCTGTAGTCCCAG      88420          AGTGT
                                CTGGGACTACA    GAGC
                                ||||||||||    ||||
                                GACCCTGATGT    CTCG
                                      C____
GAM607   LOC200470 3'  GGCTCACGCCTGTAATCCCA   90066      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC200728 3'  GCACCTGTAGTCCCAG      90116          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607   LOC200728 3'  GGCTCACGCCTGTAATCCCAG  90117      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC200731 3'  GGCTCACACCTGTAATCCCAG  90123      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC200904 3'  GGCTCACACCTGTGATCTCAG  90188      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACTCT GTGT CACACTCGG
                                   A   C
GAM607   LOC201164 3'  GGTTTGCATTCCCAGGTA    88122          CTACAA   TG
                                TACCTGGGA     GTG  AGCC
                                |||||||||     |||  ||||
                                ATGGACCCT     TAC  TTGG
                                      _______  GT
GAM607   LOC201173 3'  GGCTCACGCCTGTAATCCCAG  87333      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC201220 3'  GGCTCACGCCTGTAATCCCAG  87354      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC201252 3'  GGCTCACGCCTGTAATCCCAG  88170      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC201685 3'  GGCTCACACCTGTAATCCCAG  90247      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC201689 3'  GGCTCACACCTGTAATCCCAG  67149      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC201689 3'  GGTACACACCTGTAGTCCCAG  67150          A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CACAC TGG
                                     C   A
GAM607   LOC201868 3'  GGCTCACGCCTGTAATCCCAG  89080      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC201895 3'  GGCTCACACCTGTAATCCCAG  89090      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC201911 3'  GGCTCACGCCTGTAATCCCAG  90263      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC201931 3'  GCACCTGTAGTCCCAG      89113          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CACG
                                     C
GAM607   LOC202020 3'  GGCTCACGCCTGTAATCCCAG  89137      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC202052 3'  GGCACATGCCTGTAGTCCCAG  90310          A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
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                                GACCCTGATGT CGTAC CGG
                                      C     A
GAM607   LOC202781 3'  GGCACGCGCCTGTAGTCCCAG  90367          A     A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||  |||||  |||
                                GACCCTGATGT CGCGC CGG
                                      C     A
GAM607   LOC202868 3'  GCGCCTGTAGTCCCAG      90378          A
                                CTGGGACTACA GTGT
                                |||||||||||  ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   LOC202868 3'  GCGCCTGTAGTCCCAG      90379          A
                                CTGGGACTACA GTGT
                                |||||||||||  ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   LOC202868 3'  GGCTCACACCTGTAATCCCAG  90381       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607   LOC202868 3'  GGCTCACGCCTGTAATCCCAG  90382       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607   LOC203025 3'  GGCTCATGCCTGTAATCCCA   89252       C    A
                                TGGGA TACA GTGTGAGCC
                                |||||  ||||  |||||||||
                                ACCCT ATGT CGTACTCGG
                                  A    C
GAM607   LOC203083 3'  GGCTCACACCTGTGATCTCAG  90464       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACTCT GTGT CACACTCGG
                                   A    C
GAM607   LOC203246 3'  GCGCCTGTAGTCCCAG      89306          A
                                CTGGGACTACA GTGT
                                |||||||||||  ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   LOC203246 3'  GGCTCACGCCTGTAATCCCAG  89308       C    A
                                CTGGGA TACA GTGTGAGCC
                                ||||||  ||||  |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607   LOC203378 3'  GGCATGTACCTGTAACCCCAGG 90612         AC    A  GT A
            TA                    TACCTGGG  TACA GT  G GCC
                                ||||||||  ||||  ||  |  |||
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                                ATGGACCC  ATGT CA  T CGG
                                    CA    C  TG A
GAM607   LOC203378 3'  GGCTCACACCTGTAATCCCGG  90613       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GGCCCT ATGT CACACTCGG
                                   A    C
GAM607   LOC219627 3'  GGCTCATGCCTGTAATCCCA   92183       C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGTACTCGG
                                  A    C
GAM607   LOC219627 3'  GGCGCGTGCCTGTAGTCCCAG  92181            A TG  A
                                CTGGGACTACA G  TG GCC
                                |||||||||||  |  || |||
                                GACCCTGATGT C  GC CGG
                                      C GT  G
GAM607   LOC219627 3'  GGCTCACGCCTGTAATCCCAG  92182       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607   LOC219649 3'  GCGCCTGTAGTCCCAG       92958           A
                                CTGGGACTACA GTGT
                                |||||||||||  ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   LOC219649 3'  GGCTCATGCCTATAATCCCAG  92959       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGTACTCGG
                                   A  ATC
GAM607   LOC219672 5'  GGCTCATGCCTGTAATCCCAG  91331       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607   LOC219672 3'  GTTCACACCTGTAGTCCCAG   91333           A
                                CTGGGACTACA GTGTGAGC
                                ||||||||||| ||||||||
                                GACCCTGATGT CACACTTG
                                      C
GAM607   LOC219673 3'  GGCTCACGCCTGTAATCCCAG  93036       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607   LOC219722 5'  GGCTCACACCTGTAATCCCAG  93085       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC219919 3'  GGCTCACACCTGTGATCTCAG  93294       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACTCT GTGT CACACTCGG
                                   A   C
GAM607   LOC220070 3'  GGTGCACACCTGTAGTCCCAG  59263          A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CACAC TGG
                                      C    G
GAM607   LOC220370 3'  GGCTCATGCCTGTAATCCCA   92831      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC220506 3'  GGCGTGTGCCTGTAGTCCCAG  74079          A TG GA
                                CTGGGACTACA G  T  GCC
                                |||||||||||  |  |  |||
                                GACCCTGATGT C  G  CGG
                                      C GT TG
GAM607   LOC220506 3'  GGCTCACACCTATAATCCCAG  74080       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACACTCGG
                                   A  ATC
GAM607   LOC220575 3'  GCTCACACTTGTAATCACT    76314    _  C
                                GG GA TACAAGTGTGAGC
                                || || ||||||||||||
                                TC CT ATGTTCACACTCG
                                 A  A
GAM607   LOC220662 3'  GGCTCACGCCTGTAATCCCAG  91175       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC220662 3'  GGCTCACACCTGTAATCCCAG  91174       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC220906 3'  GGCTCATGCCTGTAATCCCA   91400      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC220992 3'  GGCATATGCCTGTAGTCCCAG  91471          A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
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                                GACCCTGATGT CGTAT CGG
                                      C     A
GAM607   LOC221178 3'  GGCTCATGCCTGTAATCCCAG  93536       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607   LOC221271 3'  GGCTCACACCTGTAATCCCAG  91867       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607   LOC221271 3'  GGCTCACACCTGTAATCCCAG  91868       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607   LOC221271 3'  GCACCTGTAGTCCCAG       91858           A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607   LOC221271 3'  GGCGGGTGCCTGTAGTCCCAG  91866           A TG GA
                                CTGGGACTACA G  T  GCC
                                |||||||||||| |  |  |||
                                GACCCTGATGT C  G  CGG
                                      C GT GG
GAM607   LOC221288 3'  GCGCCTGTAGTCCCAG       93616           A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   LOC221410 3'  GGCACACGCCTGTAGTCCCAG  92061           A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||||| ||||| |||
                                GACCCTGATGT CGCAC CGG
                                      C     A
GAM607   LOC221477 3'  GGCTCACACCTGTAATTGCAG  92159     G  C    A
                                CTG GA TACA GTGTGAGCC
                                ||| || |||| |||||||||
                                GAC TT ATGT CACACTCGG
                                  G  A    C
GAM607   LOC221489 3'  GGCTCACACCTGTAATCCCAG  93642       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607   LOC221490 3'  GGCACGCTCCTGTAGTCCCAG  93664           AGT   A
                                CTGGGACTACA   GTG GCC
                                ||||||||||   ||| |||
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                                GACCCTGATGT   CGC CGG
                                      CCT   A
GAM607   LOC221490 3'  GGCTCACGCCTGTAATCCCAG  93665      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC221543 3'  GCTCACACCTGTAATCCCAG   93743      C   A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
                                GACCCT ATGT CACACTCG
                                   A   C
GAM607   LOC221543 5'  GGCTCACACCTGTAATCCCAG  93744      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC221585 3'  GGCTCACGCCTGCAGTCCCAG  93631       A  A
                                CTGGGACT CA GTGTGAGCC
                                |||||||| || |||||||||
                                GACCCTGA GT CGCACTCGG
                                    C  C
GAM607   LOC221641 3'  GGCTCACACTTATCATCTCAG  93729      CTAC
                                CTGGGA   AAGTGTGAGCC
                                ||||||   ||||||||||
                                GACTCT   TTCACACTCGG
                                   ACTA
GAM607   LOC221787 3'  GGCTCACACCTCCAGTCCCAG  92469       ACAA
                                CTGGGACT   GTGTGAGCC
                                ||||||||   |||||||||
                                GACCCTGA   CACACTCGG
                                    CCTC
GAM607   LOC221795 3'  GGCTCACACCTGTGATCTCAG  92479      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACTCT GTGT CACACTCGG
                                   A   C
GAM607   LOC221931 3'  GGCTCATGCCTGTAATCCCAG  93995      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC221946 3'  GGCTCATACGTGTAATCCCAG  93977      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CATACTCGG
                                   A   G
GAM607   LOC221954 5'  GGCTCACACCTGTAATCCCAG  94001      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC222066 3'  GGCTCACACCTGTAATCCCAG  92745      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC222066 3'  GGCTCACACCTGTGATCCCAG  92746      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT GTGT CACACTCGG
                                   A   C
GAM607   LOC222160 3'  CATGCCTGTAGTCCCAG     94122          A
                                CTGGGACTACA GTGTG
                                |||||||||| |||||
                                GACCCTGATGT CGTAC
                                      C
GAM607   LOC222865 3'  GGCTCACGCCTGTAATCCCAG  92865      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC253003 3'  GGCGGGTGCCTGTAGTCCCAG  96893          A TG GA
                                CTGGGACTACA G  T  GCC
                                |||||||||| |  |  |||
                                GACCCTGATGT C  G  CGG
                                      C GT GG
GAM607   LOC253039 3'  GGCACGCACCTGTAGTCCCAG  96158          A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CACGC CGG
                                      C    A
GAM607   LOC253532 3'  GGCTCACACTTGTAATCCCAG  96030      C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
                                GACCCT ATGTTCACACTCGG
                                   A
GAM607   LOC253612 3'  GGCTCACGCCTGTAATCCCA   96754      C   A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                  A   C
GAM607   LOC253639 3'  GGCTCGTGCCTGTAATCCCAG  95821      C   A TG
                                CTGGGA TACA G  TGAGCC
                                |||||| |||| |  ||||||
                                GACCCT ATGT C  GCTCGG
                                   A   C GT
GAM607   LOC253786 3'  GGCTCACGCCTGTAGTCCCAG  97043          A
                                CTGGGACTACA GTGTGAGCC
                                |||||||||| |||||||||
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                                GACCCTGATGT CGCACTCGG
                                      C
GAM607   LOC253840 3'  GGCTTGTGCCTGTAATCCCAG  96188       C   A   TG
                                CTGGGA TACA GTG  AGCC
                                |||||| |||| |||  ||||
                                GACCCT ATGT CGT  TCGG
                                   A   C   GT
GAM607   LOC253927 3'  GGCTCATGCCTGTAATCCCAG  95024       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC254045 3'  GCTCATGCCTGTAATCCCA   96508       C   A
                                TGGGA TACA GTGTGAGC
                                ||||| |||| ||||||||
                                ACCCT ATGT CGTACTCG
                                   A   C
GAM607   LOC254100 3'  GGCTCACGCCTGTAACCCCAG  96414       AC   A
                                CTGGG  TACA GTGTGAGCC
                                |||||  |||| |||||||||
                                GACCC  ATGT CGCACTCGG
                                   CA   C
GAM607   LOC254176 3'  GGCTCACACCTGTGATCTCAG  97341       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACTCT GTGT CACACTCGG
                                   A   C
GAM607   LOC254266 3'  GGCTGGTGCCTGTAGTCCCAG  97354           A TG G
                                CTGGGACTACA G  T AGCC
                                |||||||||||| |  | ||||
                                GACCCTGATGT C  G TCGG
                                      C GT G
GAM607   LOC254531 5'  GGCTCACACCTGTAATCCCAG  94987       C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC254635 3'  ACATTTCTGTAGTCCCAG    94390          __
                                CTGGGACTACA  AGTGT
                                ||||||||||  |||||
                                GACCCTGATGT  TTACA
                                      CT
GAM607   LOC254808 3'  GCGCCTGTAGTCCCAG      97024          A
                                CTGGGACTACA GTGT
                                |||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607   LOC254875 3'  GGCTCACACTTGTAATCCCAG  96060       C
                                CTGGGA TACAAGTGTGAGCC
                                |||||| ||||||||||||||
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                                GACCCT ATGTTCACACTCGG
                                   A
GAM607   LOC255042 3'  GGCTCACGCCTGTAATCCCAG  95321      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC255042 3'  GGCTCACGCCTGTAATCCCAG  95322      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC255177 3'  GGCTCACACCTGTAATCCCAG  96609      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC255196 3'  GGCTCATGCCTATAATCCCAG  97173      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGTACTCGG
                                   A  ATC
GAM607   LOC255196 5'  GGCTTACGCCTGTAATCCCAG  97174      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCATTCGG
                                   A   C
GAM607   LOC255231 3'  GCATCTGTAGTCCCAG      95376          AG
                                CTGGGACTACA  TGT
                                ||||||||||  |||
                                GACCCTGATGT  ACG
                                      CT
GAM607   LOC255231 3'  GGTTCACACCTGTAATCCCAG  95378      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTTGG
                                   A   C
GAM607   LOC255252 3'  GGCTCATGCCTATAATCCCAG  95009      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGTACTCGG
                                   A  ATC
GAM607   LOC255326 3'  GGCTCACGCCTGTAATCCCAG  96378      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC255624 3'  GGCTCACACCTGTAATCCCAG  94524      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC255671 3'  GGCTCACATCTGTAATCCCAG  97260      C   AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
                                GACCCT ATGT  ACACTCGG
                                   A   CT
GAM607   LOC255798 3'  GGCTCATGCCTATAATCCAAG  97006    G  C  CAA
                                CT GGA TA   GTGTGAGCC
                                || ||| ||   |||||||||
                                GA CCT AT   CGTACTCGG
                                 A  A ATC
GAM607   LOC255937 3'  GGCTCACACCTGTAATCCCAG  95991      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607   LOC255971 3'  GGCTTACGCCTATAATCCCAG  96535      C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGCATTCGG
                                   A  ATC
GAM607   LOC255971 3'  GGCGTACGCCTATAGTCCCAG  96534        CAA   A
                                CTGGGACTA   GTGTG GCC
                                |||||||||   ||||| |||
                                GACCCTGAT   CGCAT CGG
                                     ATC    G
GAM607   LOC256267 3'  GGCTCATGCCTGTAATCCCAG  96806      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607   LOC256277 3'  GGCTCACGCCTGTAATCCCAG  94699      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607   LOC256515 3'  GGCTCACACCTGTGATCTCAG  96464      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACTCT GTGT CACACTCGG
                                   A   C
GAM607   LOC256594 3'  GGCTCACACCTGTGTTCTCAG  97080      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACTCT GTGT CACACTCGG
                                   T   C
GAM607   LOC256980 3'  GGCTTACATCTGTAATCCCAG  95222      C   AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
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                                GACCCT ATGT  ACATTCGG
                                   A    CT
GAM607   LOC257115 3'  GGCCTGCACCTGTAGTCCCAG  96524          A    GA
                                CTGGGACTACA GTGT  GCC
                                |||||||||||| ||||  |||
                                GACCCTGATGT CACG  CGG
                                      C    TC
GAM607   LOC257180 3'  GGCGTGCACTGTAGTCCCAG   95575          A    GA
                                CTGGGACTACA GTGT  GCC
                                |||||||||||| ||||  |||
                                GACCCTGATGT CACG  CGG
                                      _    TG
GAM607   LOC257354 3'  GGCTCATGCCTATAATCCCA   95094       C  CAA
                                TGGGA TA   GTGTGAGCC
                                ||||| ||   |||||||||
                                ACCCT AT   CGTACTCGG
                                   A  ATC
GAM607   LOC257358 5'  GCTCATCAGTCCCAG       97102         ACAAGT
                                CTGGGACT     GTGAGC
                                ||||||||     ||||||
                                GACCCTGA     TACTCG
                                     C_____
GAM607   LOC257480 3'  GGCTCACGCCTGTAATCCCAG  77870       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607   LOC257539 3'  GCTCATGCCTGTAATCCCAG   97702       C    A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
                                GACCCT ATGT CGTACTCG
                                   A    C
GAM607   LOC257578 3'  GCTCATGCCTGTAATCCCAG   97822       C    A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
                                GACCCT ATGT CGTACTCG
                                   A    C
GAM607   LOC257596 3'  GCTCACACCTGTAATCCCAG   97936       C    A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
                                GACCCT ATGT CACACTCG
                                   A    C
GAM607   LOC257596 5'  GGCTCACACCTGTAATCCCAG  97937       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607   LOC51279  3'  CGTGCCTGTAGTCCCAG     33312          A TG
                                CTGGGACTACA G  TG
                                |||||||||||  |  ||
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                                GACCCTGATGT C  GC
                                      C GT
GAM607  LOC51279 3' GGCTCACGCCTGTAATCCCA  33316      C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                   A    C
GAM607  LOC51336 3' GGCTCACACCTGTAATTTCAG 33579     GG C    A
                                CTG  A TACA GTGTGAGCC
                                |||  | |||| |||||||||
                                GAC  T ATGT CACACTCGG
                                  TT A    C
GAM607  LOC54518 3' GCTCACACCTGTAGTCCCGG  38771          A
                                CTGGGACTACA GTGTGAGC
                                |||||||||| ||||||||
                                GGCCCTGATGT CACACTCG
                                      C
GAM607  LOC55974 3' GGCTCACGCCTGTAATCCCAG 38133      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  LOC57118 3' GGCTCACGCCTGTAATCCCA  39868      C    A
                                TGGGA TACA GTGTGAGCC
                                ||||| |||| |||||||||
                                ACCCT ATGT CGCACTCGG
                                   A    C
GAM607  LOC57333 3' GCAGATGCAGTCCCAGG     73715         ACAA    GA
                                CCTGGGACT    GTGT  GC
                                |||||||||    ||||  ||
                                GGACCCTGA    CGTA  CG
                                     ____    GA
GAM607  LOC64167 3' GGCAGGTGCCTGTAGTCCCAG 42281           A TG GA
                                CTGGGACTACA G  T  GCC
                                |||||||||| |  |  |||
                                GACCCTGATGT C  G  CGG
                                      C GT GA
GAM607  LOC64167 3' GGCTCACGCCTGTAATCCCAG 42282      C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  LOC90072 3' GGCTCACACCTGCAATCCCA  61301      CTA  A
                                TGGGA   CA GTGTGAGCC
                                |||||   || |||||||||
                                ACCCT   GT CACACTCGG
                                   AAC  C
GAM607  LOC90072 5' GGTGCACACCTGTAGTCCCAG 61302           A    A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
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                                GACCCTGATGT CACAC TGG
                                      C     G
GAM607  LOC90092 3' GCTCACACCTGTAATCCCAG  61409       C    A
                                CTGGGA TACA GTGTGAGC
                                |||||| |||| ||||||||
                                GACCCT ATGT CACACTCG
                                   A    C
GAM607  LOC90092 3' GGCTCACACCTGTAATCCCAG 61414       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A    C
GAM607  LOC90141 3' GGCTCATGCCTACAATCCCAG 61630       CTACAA
                                CTGGGA     GTGTGAGCC
                                ||||||     |||||||||
                                GACCCT     CGTACTCGG
                                   AACATC
GAM607  LOC90141 3' GGTGTGTACCTGTAGTCCCAG 61631           A   TGA
                                CTGGGACTACA GTG   GCC
                                |||||||||||| |||   |||
                                GACCCTGATGT CAT   TGG
                                      C   GTG
GAM607  LOC90233 3' GCATGCGCCTATAGTCCCAG  56382         CAA    A
                                CTGGGACTA   GTGTG GC
                                |||||||||   ||||| ||
                                GACCCTGAT   CGCGT CG
                                     ATC    A
GAM607  LOC90321 3' GGCTCACACCTGTAATCCTAG 62265       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GATCCT ATGT CACACTCGG
                                   A    C
GAM607  LOC90393 5' GCACCTGTAGTCCCAG      62623           A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CACG
                                      C
GAM607  LOC90408 5' GGCTCATGCCTGTAATCCCAG 62664       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  LOC90509 3' GGCTCACGCCTGTAATCCCAG 63106       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  LOC90538 3' GGCTCACATCTGTAATCCCAG 63193       C    AG
                                CTGGGA TACA  TGTGAGCC
                                |||||| ||||  ||||||||
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                                GACCCT ATGT  ACACTCGG
                                   A    CT
GAM607  LOC90591  3' GCGCCTGTAGTCCCAG      63431          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  LOC90591  3' GGCGCGTGCCTGTAGTCCCAG  63437          A TG  A
                                CTGGGACTACA G  TG GCC
                                |||||||||||| |  || |||
                                GACCCTGATGT C  GC CGG
                                      C GT  G
GAM607  LOC90591  3' GGCTCACGCCTGTAATCCCAG  63438       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A    C
GAM607  LOC90624  3' GCGCCTGTAGTCCCAG      63605          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
                                GACCCTGATGT CGCG
                                      C
GAM607  LOC90624  3' GGCTCACACCTGTAATCCC    63606      C    A
                                GGGA TACA GTGTGAGCC
                                |||| |||| |||||||||
                                CCCT ATGT CACACTCGG
                                  A    C
GAM607  LOC90639  3' GGCTCACGCCTGCAATCCCAG  63660       CTA  A
                                CTGGGA   CA GTGTGAGCC
                                ||||||   || |||||||||
                                GACCCT   GT CGCACTCGG
                                   AAC  C
GAM607  LOC90784  5' GGCTCACGCTTACAGTCCCAG  64005        AC
                                CTGGGACT  AAGTGTGAGCC
                                ||||||||  ||||||||||
                                GACCCTGA  TTCGCACTCGG
                                     CA
GAM607  LOC91035  3' GGCTCACGCCTATAATCCCAG  64673       C  CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CGCACTCGG
                                   A  ATC
GAM607  LOC91056  3' GGCTCATGCCTGTAATCCCAG  94760       C    A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A    C
GAM607  LOC91064  3' GCACCTGTAGTCCCAG      64763          A
                                CTGGGACTACA GTGT
                                |||||||||||| ||||
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                                GACCCTGATGT CACG
                                      C
GAM607  LOC91397 3' GGCTCATGCCTGTAGTCCCAG 65913         A
                                CTGGGACTACA GTGTGAGCC
                                |||||||||| |||||||||
                                GACCCTGATGT CGTACTCGG
                                      C
GAM607  LOC91522 3' GCTCACACCTGTACAG     66315    GGAC   A
                                CTG   TACA GTGTGAGC
                                |||   |||| |||||||||
                                GAC   ATGT CACACTCG
                                  ____  C
GAM607  LOC91565 3' GGCATACTCCTGTAGTCCCAG 66463         AGT  A
                                CTGGGACTACA  GTG GCC
                                ||||||||||  ||| |||
                                GACCCTGATGT  CAT CGG
                                      CCT  A
GAM607  LOC91664 3' GGCTCACGCCTGTAATCCCAG 66874      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LOC91750 3' GGCTCACGCCTGTAATCCCAG 67062      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LOC91796 5' GGCTTATGCCTGTAATCCCAG 67213      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTATTCGG
                                   A   C
GAM607  LOC91862 3' GGCTCACACCTGTAACCCCAG 53469      AC   A
                                CTGGG  TACA GTGTGAGCC
                                |||||  |||| |||||||||
                                GACCC  ATGT CACACTCGG
                                  CA   C
GAM607  LOC92078 3' GGCTCACACCTATAATCCCAG 67985      C CAA
                                CTGGGA TA   GTGTGAGCC
                                |||||| ||   |||||||||
                                GACCCT AT   CACACTCGG
                                   A  ATC
GAM607  LOC92223 3' GGCTCACACCTGTAATCCC   68523     C   A
                                GGGA TACA GTGTGAGCC
                                |||| |||| |||||||||
                                CCCT ATGT CACACTCGG
                                  A   C
GAM607  LOC92228 3' GGCTCACGCCTGTAATCCCAG 68543      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LOC92267 3' GGCTCACACCTGTAATCCCAG 68622      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  LOC92270 5' GGCTCACGCCTGTAATCCCAG 68633      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LOC92283 3' GGCTCATGCCTGTAATCCCAG 68748      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  LOC92299 3' GGCTCACACCTGTAATCTCAG 68814      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACTCT ATGT CACACTCGG
                                   A   C
GAM607  LOC92299 3' GGCTCACGCCTGTAATCCCAG 68815      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LOC92465 3' GGCTCACGCCTGTAATCCCAG 69409      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LOC92465 5' GGCTCATGCCTGTAATCCCAG 69410      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  LOC92466 3' GGCTCATGCCTGTAATCCCAG 69431      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGTACTCGG
                                   A   C
GAM607  LOC92482 3' GGCTCACGCCTGTAATCCCAG 69492      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LOC92573 5' GGCTCACACCTGTAATCCCAG 69809      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
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                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  LOC92736  3'  GGCTCACGCCTGTAATCCCAG  70430      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CGCACTCGG
                                   A   C
GAM607  LOC92771  3'  GGCTCACACCTGTAATCCCAG  53077      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  LOC93132  5'  GGCATGCACCTGTAGTCCCAG  71494         A   A
                                CTGGGACTACA GTGTG GCC
                                |||||||||| ||||| |||
                                GACCCTGATGT CACGT CGG
                                      C    A
GAM607  LOC93132  5'  GGCTCACACCTGTAATCCCAG  71496      C   A
                                CTGGGA TACA GTGTGAGCC
                                |||||| |||| |||||||||
                                GACCCT ATGT CACACTCGG
                                   A   C
GAM607  LOC93259  5'  CCGTCACCCCAGGTA      71812        ACTACAA  _  A
                                TACCTGGG     GTG TG G
                                ||||||||     ||| || |
                                ATGGACCC     CAC GC C
                                   ________  T  C
GAM608  CALU    3'  GATCCCTTTGCTCTA      6887         TGTTTCA
                                TAGAGCAAA     GGATC
                                |||||||||     |||||
                                ATCTCGTTT     CCTAG
                                   C_______
GAM608  CCND2   3'  GGAATCCTGGATTTTGCCCT  8296    A    TGT     _
                                AG GCAAA  TTCAGGAT CC
                                || |||||  |||||||| ||
                                TC CGTTT  AGGTCCTA GG
                                 C    T__      A
GAM608  CTLA4   5'  GGATCCTGAAAGGTTTTGCTCT 17808         _ G
            AC                    GTAGAGCAAA T TTTCAGGATCC
                                |||||||||| | ||||||||||
                                CATCTCGTTT G AAAGTCCTAGG
                                     T G
GAM608  CYP1A1  3'  GGATCCTGCCTGCCCCTAC  4945     A_  AATGTTT
                                GTAG  GCA     CAGGATCC
                                ||||  |||     ||||||||
                                CATC  CGT     GTCCTAGG
                                  CC  CC_____
GAM608  ETF1    3'  CCTGAAGCTGATGCTTCAC  16394    AG   AAT
                                GT  AGCA  GTTTCAGG
                                ||  ||||  ||||||||
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                                CA  TCGT   CGAAGTCC
                                 CT    AGT
GAM608  HDAC4    3'  GGGATCCTGCCACCTGCCCT  20115    A   AA  TTT
                                AG GCA  TG   CAGGATCCC
                                || |||  ||   |||||||||
                                TC CGT  AC   GTCCTAGGG
                                 C   CC  C__
GAM608  PIGA     3'  GAAACACATTGCTCTAC     40013        A_
                                GTAGAGCAA  TGTTTC
                                |||||||||  ||||||
                                CATCTCGTT  ACAAAG
                                      AC
GAM608  PIGA     3'  GAAACACATTGCTCTAC     40004        A_
                                GTAGAGCAA  TGTTTC
                                |||||||||  ||||||
                                CATCTCGTT  ACAAAG
                                      AC
GAM608  PIGA     3'  GAAACACATTGCTCTAC     10552        A_
                                GTAGAGCAA  TGTTTC
                                |||||||||  ||||||
                                CATCTCGTT  ACAAAG
                                      AC
GAM608  PLCB2    3'  GGGATCCTGGCCCCACTCTGC  15894       CAAA  TT_
                                GTAGAG   TG   TCAGGATCCC
                                ||||||   ||   ||||||||||
                                CGTCTC   AC   GGTCCTAGGG
                                   _____  CCC
GAM608  STK6     3'  GGAACACGTGCTCTAC      13187        AA
                                GTAGAGCA  TGTTTC
                                ||||||||  ||||||
                                CATCTCGT  ACAAGG
                                      GC
GAM608  TMOD2    5'  GGGATCCTGGCCCCGCTCCAC  27251    A    AAATGTT
                                GT GAGC      TCAGGATCCC
                                || ||||      ||||||||||
                                CA CTCG      GGTCCTAGGG
                                 C   CCCC___
GAM608  DKFZP434K1421 3'  GGAAAATTTGCTCCAC      49553    A       G
                                GT GAGCAAAT TTTC
                                || |||||||| ||||
                                CA CTCGTTTA AAGG
                                 C       A
GAM608  DKFZP434N178 5'  GGGATCCTTGCCTCTCTGCCCT 71908      A   AATGTTTC
           GC                    GTAG GCA       AGGATCCC
                                ||||| |||       ||||||||
                                CGTC CGT       TCCTAGGG
                                  C   CTCTCCGT
GAM608  EST-YD1  3'  GACCTCGACATTTGCTC     41080          TC   A
                                GAGCAAATGTT  AGG TC
                                ||||||||||  ||| ||
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                                CTCGTTTACAG  TCC AG
                                      C_  _
GAM608  FLJ11026  5'  GGATCACCAGTTTGCTCCAC  36993    A      GTTTCAG
                                GT GAGCAAAT      GATCC
                                || ||||||||      |||||
                                CA CTCGTTTG      CTAGG
                                 C       ACCA___
GAM608  FLJ13769  3'  GACCCTGAAACACTCAGC    46609    A   CAAA       A
                                GT GAG    TGTTTCAGG TC
                                || |||    ||||||||| ||
                                CG CTC    ACAAAGTCC AG
                                 A  _____        C
GAM608  FLJ20294  3'  GGATCCTGCTGCACCCCTCCAC 34879    A   CAAA   TT
                                GT GAG    TGT  CAGGATCC
                                || |||    |||  ||||||||
                                CA CTC    ACG  GTCCTAGG
                                 C   CCC_   TC
GAM608  FLJ21918  3'  GATCCCAATGTTCTAC      46289        AA  TTTCA
                                GTAGAGCA  TG    GGATC
                                ||||||||  ||    |||||
                                CATCTTGT  AC    CCTAG
                                     A_ ______
GAM608  GAB1      3'  GAAACATTTGTTCCAC      8977     A
                                GT GAGCAAATGTTTC
                                || ||||||||||||
                                CA CTTGTTTACAAAG
                                 C
GAM608  HSMPP8    3'  TCTAAAACATTTGCTT      93486           C
                                GAGCAAATGTTT AGG
                                |||||||||||| |||
                                TTCGTTTACAAA TCT
                                       A
GAM608  KIAA0143  3'  GAAACACAAACTTTGCTCTAC  64785          _____
                                GTAGAGCAAA     TGTTTC
                                ||||||||||     ||||||
                                CATCTCGTTT     ACAAAG
                                       CAAAC
GAM608  KIAA0759  3'  GATCCTGGGCCAGCCCCTCCAC 67323    A   CAAA  TT
                                GT GAG    TG  TCAGGATC
                                || |||    ||  ||||||||
                                CA CTC    AC  GGTCCTAG
                                 C   CCCG  CG
GAM608  KIAA1211  3'  GTCCAAAACATTTACTCTAC   68896       C       CA
                                GTAGAG AAATGTTT  GGAT
                                |||||| ||||||||  ||||
                                CATCTC TTTACAAA  CCTG
                                    A       A_
GAM608  KIAA1373  3'  GGGATCCTGATTAATGCTCTA  70948        AATGTT
                                TAGAGCA     TCAGGATCCC
                                |||||||     ||||||||||
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                                ATCTCGT     AGTCCTAGGG
                                    AATT__
GAM608  KIAA1511  3'  GGGCACTGAAACATTTGT    70169           GA
                                GCAAATGTTTCAG  TCC
                                ||||||||||||  |||
                                TGTTTACAAAGTC  GGG
                                      AC
GAM608  KIAA1586  5'  GATCATGCCATTGTGCTCTAC  92330        _   TTT  G
                                GTAGAGCA AATG   CA GATC
                                |||||||| ||||   || ||||
                                CATCTCGT TTAC   GT CTAG
                                     G   C__  A
GAM608  MGC9753   5'  GGGATCCTGCCCCCGCCCTGC  53056      A  AAATGTTT
                                GTAG GC       CAGGATCCC
                                |||| ||       |||||||||
                                CGTC CG       GTCCTAGGG
                                  C  CCCCC___
GAM608  NFKBIE    3'  GGACCCTGAAACACCGTTGTTT 15851       A__       A
                                GAGCAA   TGTTTCAGG TCC
                                ||||||   ||||||||| |||
                                TTTGTT   ACAAAGTCC AGG
                                    GCC        C
GAM608  LOC123435 5'  GGGACCCTGGGATTTTGCTCT  74208        T  TT    A
                                AGAGCAAA GT  CAGG TCCC
                                |||||||| ||  |||| ||||
                                TCTCGTTT TA  GTCC AGGG
                                    _ GG    C
GAM608  LOC136895 5'  GGACCCTATTTGCTCTGC    57170          GTTTC   A
                                GTAGAGCAAAT     AGG TCC
                                ||||||||||     ||| |||
                                CGTCTCGTTTA     TCC AGG
                                      _____  C
GAM608  LOC144248 5'  GGAATCCACCCTTATTTGCTCT 76741          TTTCA   _
                                AGAGCAAATG     GGAT CC
                                ||||||||||     |||| ||
                                TCTCGTTTAT     CCTA GG
                                     TCCCA    A
GAM608  LOC148189 5'  GGATCCGCACCGCCCTAC    78716      A  AAA   TTCA
                                GTAG GC   TGT    GGATCC
                                |||| ||   |||    ||||||
                                CATC CG   ACG    CCTAGG
                                  C  CC_   ____
GAM608  LOC149711 5'  ATCCACTATCTGCTCTAC    84670        A   TTTCA
                                GTAGAGCA ATG     GGAT
                                |||||||| |||     ||||
                                CATCTCGT TAT     CCTA
                                    C   CA___
GAM608  LOC165693 3'  GACCCTGAAACAGCTC      82597      AAA        A
                                GAGC   TGTTTCAGG TC
                                ||||   ||||||||| ||
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                                CTCG   ACAAAGTCC AG
                                  ___        C
GAM608  LOC253985 5'  ATCCACCATGCTCTAC      96482         AAT  TTCA
                                GTAGAGCA   GT    GGAT
                                ||||||||   ||    ||||
                                CATCTCGT   CA    CCTA
                                    AC_  ____
GAM608  LOC256568 3'  GATCAGACACATTGCTCTAC   94843          A   T  AG
                                GTAGAGCAA TGT TC  GATC
                                ||||||||| ||| ||  ||||
                                CATCTCGTT ACA AG  CTAG
                                     _  C  A_
GAM608  LOC91266  5'  CCTGAAACATGTTC       65412       AA
                                GAGCA  TGTTTCAGG
                                |||||  |||||||||
                                CTTGT  ACAAAGTCC

                                  __
GAM609  AQP3      3'  TTCACGATCCACCCTTTC     59593      T_   _
                                GAAA  GTGG TCGTGAA
                                ||||  |||| |||||||
                                CTTT  CACC AGCACTT
                                  CC    T
GAM609  ARSB      3'  TCACGACTCTTGTC        3502         AATGTG
                                GACAAGA     GTCGTGA
                                |||||||     |||||||
                                CTGTTCT     CAGCACT

                                  _______
GAM609  B4GALT5   3'  TTTTCACAAAAATAGTCCTTTG 16519        AAA_   GGTC
           TCA                    TGACAAG    TGT    GTGAAAA
                                |||||||    |||    |||||||
                                ACTGTTT    ATA    CACTTTT
                                    CCTG   AAAA
GAM609  CHRNA3    3'  TCGTTACCCATTTCTT      5610          T   CG
                                AAGAAATG GGT  TGA
                                |||||||| |||  |||
                                TTCTTTAC CCA  GCT
                                    _  TT
GAM609  DRD1      3'  TTACAACCACATTTCTGGCCA  5840      ACA         C
                                TG   AGAAATGTGGT GTGA
                                ||   |||||||||||| ||||
                                AC   TCTTTACACCA CATT
                                 CGG         A
GAM609  FUT1      3'  TCTGATCACATCCCCTGTC    3798       AGAA        T
                                GACA    ATGTGGTCG GA
                                ||||    ||||||||| ||
                                CTGT    TACACTAGT CT
                                  CCCC        _
GAM609  IRF1      3'  GCCACATTTCTGATCA      64345      CA
                                TGA  AGAAATGTGGT
                                |||  ||||||||||
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                                ACT  TCTTTACACCG
                                  AG
GAM609  MAP3K8   5'  TCACGACCACCTCATG      17791    A  AAT
                                CA GA   GTGGTCGTGA
                                || ||   ||||||||||
                                GT CT   CACCAGCACT
                                 A  C__
GAM609  NGFR     3'  TTCTGACCACACTTCCTGTC   10231      A   A       T
                                GACA GAA TGTGGTCG GAA
                                |||| ||| |||||||| |||
                                CTGT CTT ACACCAGT CTT
                                  C   C       _
GAM609  OLR1     3'  TTCACAACAGTTCTTGTTA    10341          ATGTG  C
                                TGACAAGAA     GT GTGAA
                                |||||||||     || |||||
                                ATTGTTCTT     CA CACTT
                                      GA___  A
GAM609  POU4F1   3'  CACTGAAAACATTTTTGTCA   20660          A   GG  _
                                TGACAAGAA TGT  TC GTG
                                ||||||||| |||  || |||
                                ACTGTTTTT ACA  AG CAC
                                      _  AA  T
GAM609  SMP1     3'  TTTCACATGAATAATTTTTGTC 26705          A   GGTC
           A                     TGACAAGAA TGT    GTGAAA
                                ||||||||| |||    ||||||
                                ACTGTTTTT ATA    CACTTT
                                      A   AGTA
GAM609  ZNF264   3'  TTCTATTAACATTTCTTTTCA  12769     C       GGTCGT
                                TGA AAGAAATGT      GAA
                                ||| |||||||||      |||
                                ACT TTCTTTACA      CTT
                                  T        ATTAT_
GAM609  C20orf175 3'  CGAGCTCCACGTTTCCTGCCA  55063    A  A       ___
                                TG CA GAAATGTGG   TCG
                                || || |||||||||   |||
                                AC GT CTTTGCACC   AGC
                                 C  C        TCG
GAM609  CAPNS2   3'  TTTCACAACCCTACATATTTCT 50323     CA       ____  C
           GATCA                    TGA  AGAAATGT    GGT GTGAAA
                                |||  ||||||||    ||| ||||||
                                ACT  TCTTTATA    CCA CACTTT
                                  AG       CATC   A
GAM609  CLDN6    3'  TTTACACTCACATTTTTATCA  41041     CA       _  C
                                TGA  AGAAATGTG GT GTGAA
                                |||  ||||||||| || |||||
                                ACT  TTTTTACAC CA CATTT
                                  A_        T  _
GAM609  DKFZP564L0864 3'  GCACCAATTTCTTGCCA     72555    A       G    C
                                TG CAAGAAAT TGGT GT
                                || |||||||| |||| ||
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                                AC GTTCTTTA ACCA CG
                                 C      _   _
GAM609  DKFZP566B183 3'  TTTCCATAAACATTTCTTTTCA 31330     C       GGTCGT
                                TGA AAGAAATGT     GAAA
                                ||| |||||||||     ||||
                                ACT TTCTTTACA     CTTT
                                  T       AATAC_
GAM609  GTF2E1   3'  TACAGACCTCTTGTCA      18616        AATGT   _
                                TGACAAGA    GGTC GTG
                                ||||||||    |||| |||
                                ACTGTTCT    CCAG CAT
                                     _____   A
GAM609  KIAA0089 3'  TTTTAATTCACATTTCTT    69967          TCG
                                AAGAAATGTGG   TGAAA
                                ||||||||||   |||||
                                TTCTTTACACT   ATTTT
                                       TA_
GAM609  KIAA0373 5'  TTTTCAAAGTAACATTTCTT   28015         GGTCG
                                AAGAAATGT    TGAAAA
                                |||||||||    ||||||
                                TTCTTTACA    ACTTTT
                                     ATGAA
GAM609  KIAA1813 3'  TTTTCACACTGTAAATTTCTTG 70314         __ TG  C
           T                     ACAAGAAAT  G  GT GTGAAAA
                                |||||||||  |  || |||||||
                                TGTTCTTTA  T  CA CACTTTT
                                     AA GT  _
GAM609  KIAA1951 3'  TTCCAGGCTTCTCTTGTCA   73766        AATGT   GT
                                TGACAAGA    GGTC  GAA
                                ||||||||    ||||  |||
                                ACTGTTCT    TCGG  CTT
                                     CT___    AC
GAM609  MGC4170  3'  TTCACCATTTCTTGTC      44227          TGGTC
                                GACAAGAAATG    GTGAA
                                ||||||||||    |||||
                                CTGTTCTTTAC    CACTT
                                      _____
GAM609  NRN1     3'  CACTGCACATTTCTCCTCA   33432     CA       GTC
                                TGA  AGAAATGTG   GTG
                                |||  |||||||||   |||
                                ACT  TCTTTACAC   CAC
                                  CC        GT_
GAM609  PLA2G12  3'  TTTTCACAACCACATTT     48028         C
                                AAATGTGGT GTGAAAA
                                ||||||||| |||||||
                                TTTACACCA CACTTTT
                                     A
GAM609  PPY2     3'  CACTCCACATTCCTGGCCA   40819    ACA  A      TC
                                TG   AG AATGTGG  GTG
                                ||   || |||||||  |||
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                                AC   TC TTACACC  CAC
                                 CGG  C      T_
GAM609  ZNF31     3'  TTTGTAGACCACATTTCCTGTT 64992       A         _ TG
           A                     TGACA GAAATGTGGTC G  AA
                                 |||||| |||||||||||| |  ||
                                 ATTGT CTTTACACCAG T  TT
                                    C          A GT
GAM609  LOC115219 3'  CACGACAACGGGTCCTCA    73295     CAA  AA   G
                                 TGA   GA  TGT GTCGTG
                                 |||   ||  ||| ||||||
                                 ACT   CT  GCA CAGCAC
                                  C__  GG   A
GAM609  LOC120376 5'  TTCAGAGCATTTCTTTCA    75986     C       GG  G
                                 TGA AAGAAATGT  TC TGAA
                                 ||| |||||||||  || ||||
                                 ACT TTCTTTACG  AG ACTT
                                   _       __ _
GAM609  LOC133418 3'  TTTCATATACATTTTTTGCCA  75094    A         GTC
                                 TG CAAGAAATGTG   GTGAAA
                                 || ||||||||||   ||||||
                                 AC GTTTTTTACAT   TACTTT
                                  C          A__
GAM609  LOC151199 3'  TTAAAACCACAGCTCTTGCCA  80174    A    AA     CG
                                 TG CAAGA  TGTGGT  TGA
                                 || |||||  ||||||  |||
                                 AC GTTCT  ACACCA  ATT
                                  C    CG     AA
GAM609  LOC152317 5'  TCACACTGACTTTTGTCA    85649        AATG   C
                                 TGACAAGA    TGGT GTGA
                                 ||||||||    |||| ||||
                                 ACTGTTTT    GTCA CACT
                                      CA__    _
GAM609  LOC152674 3'  TTCAACCCACCCTCTTGTCA   85841        AAT    TCG
                                 TGACAAGA   GTGG   TGAA
                                 ||||||||   ||||   ||||
                                 ACTGTTCT   CACC   ACTT
                                      CC_    CA_
GAM609  LOC152845 5'  CATGACCACATTTTTCA     60330     CAA
                                 TGA   GAAATGTGGTCGTG
                                 |||   ||||||||||||||
                                 ACT   TTTTACACCAGTAC
                                   ____
GAM609  LOC154743 3'  TTTAGTCCACATTGTCTTGTCA 81118         _      TCG
                                 TGACAAGA AATGTGG   TGAA
                                 |||||||| |||||||   ||||
                                 ACTGTTCT TTACACC   ATTT
                                      G       TG_
GAM609  LOC165476 5'  TTCACGGCACCTTCT       87201      AT   G
                                 AGAA  GTG TCGTGAA
                                 ||||  ||| |||||||
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                                TCTT  CAC GGCACTT
                                  C_  _
GAM609  LOC254266 5'  TTTTCGGTCACACATCTTATCA 97356     C    AA    GT  T
                                TGA AAGA  TGTG  CG GAA
                                ||| ||||  ||||  || |||
                                ACT TTCT  ACAC  GC TTT
                                  A    AC    TG  T
GAM609  LOC255919 3'  TTTCATTCTTACATTTCTAATC 95043     CA        TC
           A                     TGA  AGAAATGTGG  GTGAAA
                                |||  ||||||||||  ||||||
                                ACT  TCTTTACATT  TACTTT
                                  AA         CT
GAM609  LOC51754  5'  CACGGCCACATCTCTGTCA    71027      A  A
                                TGACA GA ATGTGGTCGTG
                                ||||| || ||||||||||
                                ACTGT CT TACACCGGCAC
                                   _ C
GAM609  LOC55862  3'  ACCTCATTTCTTGCCA      37485     A       T
                                TG CAAGAAATG GGT
                                || |||||||| |||
                                AC GTTCTTTAC CCA
                                 C        T
GAM609  LOC55954  3'  CACGTGGTCACTTTTCTCATCA 38877     CA    T   GT __
                                TGA  AGAAA GTG  C  GTG
                                |||  ||||| |||  |  |||
                                ACT  TCTTT CAC  G  CAC
                                  AC     T   TG TG
GAM610  CASP3     3'  ACATACTCCTTCCATCA     15095     C     A
                                TG ATGGAA GAGTATGT
                                || |||||| ||||||||
                                AC TACCTT CTCATACA
                                 _     C
GAM610  CASP3     3'  ACATACTCCTTCCATCA     52191     C     A
                                TG ATGGAA GAGTATGT
                                || |||||| ||||||||
                                AC TACCTT CTCATACA
                                 _     C
GAM610  MSL3L1    3'  AAGAATACTCAGATTTCCAT   54359        GAGTAT
                                ATGGAAA     GTATTCTT
                                |||||||     ||||||||
                                TACCTTT     CATAAGAA
                                    AGACT_
GAM610  SACM1L    3'  GCATACTTTTCCACACA     25824     CA    A
                                TG  TGGAA GAGTATGT
                                ||  ||||| ||||||||
                                AC  ACCTT TTCATACG
                                 AC    _
GAM610  SURF6     3'  TAAGAATACATACTCTTTCCAT 22192                  III
           GCA                    GCATGGAAAGAGTATGTATTCTT   A
                                ||||||||||||||||||||||  |
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                                CGTACCTTTCTCATACATAAGAA  T
                                                        III
GAM610  UCHL1    3'  AATATATACCCCCCCATGCA  14814       AAAGA
                                TGCATGG    GTATGTATT
                                |||||||    |||||||||
                                ACGTACC    CATATATAA
                                    CCCC_
GAM610  DYRK4    5'  AAGAATACGGTAAGCTTCCCA  64225    A  AG  _
                                TGG AAG  TAT GTATTCTT
                                ||| |||  ||| ||||||||
                                ACC TTC  ATG CATAAGAA
                                  C  GA  G
GAM610  FLJ10276 3'  ACATACTCTGTCCATACA    35961    C    A
                                TG ATGGA AGAGTATGT
                                || ||||| |||||||||
                                AC TACCT TCTCATACA
                                 A    G
GAM610  KIAA0678 3'  AAGAATATTTCCCTCTCCTGCA 66851     T  AA  TAT_
                                TGCA GGA  GAG   GTATTCTT
                                |||| |||  |||   ||||||||
                                ACGT CCT  CTC   TATAAGAA
                                  _  __  CCTT
GAM610  SGKL     3'  AAGAACAAGCATCCCTTCCATG 25138        A_ _ A  AT
           TA                    TGCATGGAA  GA GT TGT  TCTT
                                |||||||||  || || |||  ||||
                                ATGTACCTT  CT CG ACA  AGAA
                                     CC  A  A  __
GAM610  LOC148638 3'  CACTCTCTTTCCACGCA    78919    A      TA
                                TGC TGGAAAGAG  TG
                                ||| |||||||||  ||
                                ACG ACCTTTCTC  AC
                                  C       TC
GAM610  LOC196385 3'  ATCTCTTTCCATACA      87654    C      T
                                TG ATGGAAAGAG AT
                                || |||||||||| ||
                                AC TACCTTTCTC TA
                                 A       _
GAM610  LOC221178 3'  ATACTCCTTCATGCA      93526       AA
                                TGCATGGA  GAGTAT
                                ||||||||  ||||||
                                ACGTACTT  CTCATA
                                    C_
GAM610  LOC221405 3'  AGAATTGCTTTCCATGCA   93880         AGTATGT
                                TGCATGGAAAG     ATTCT
                                ||||||||||      |||||
                                ACGTACCTTTC     TAAGA
                                      GT_____
GAM611  ALDH3B1  3'  CACACCTGTAATCCCAGCACTT 91522        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                |||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  ALOX5   3'  CACACCCAGCTCAGCATTT   90851       TGA   CA
                                AAGTGCTG  TTG  GGTGTG
                                ||||||||  |||  ||||||
                                TTTACGAC  GAC  CCACAC
                                    TC_  __
GAM611  AREG    5'  CACACCTGGGTGCCAGCGC   7995       TG  G
                                GTGCTG  ATT CAGGTGTG
                                ||||||  ||| ||||||||
                                CGCGAC  TGG GTCCACAC
                                   CG  _
GAM611  ATM     3'  CACACCTATAATCCCAGCACTT 56299        T    C
           T                     AAAGTGCTG GATTG AGGTGTG
                                ||||||||| ||||| |||||||
                                TTTCACGAC CTAAT TCCACAC
                                     C    A
GAM611  BHMT2   3'  CACACCTGCAATCCCAGCACTT 34308        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||||
                                TTTCACGAC CTAACGTCCACAC
                                     C
GAM611  BPHL    3'  CACAGCTATAATCTCAGCACTT 15083        T    C  G
           T                     AAAGTGCTG GATTG AG TGTG
                                ||||||||| ||||| || ||||
                                TTTCACGAC CTAAT TC ACAC
                                     T    A  G
GAM611  C1orf1  3'  CACCTGTAATCCCAACACTTT  6857       C  T
                                AAAGTG TG GATTGCAGGTG
                                |||||| || ||||||||||
                                TTTCAC AC CTAATGTCCAC
                                   A  C
GAM611  C21orf5 3'  CACACCTGTAATCTCAGCACTT 17610        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     T
GAM611  CASP6   3'  CACACCTGTAATCCCAGCACTT 6908         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  CASP6   3'  CACACCTGTAATCCCAGCACTT 52201        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  CHRNA5  3'  CACACCTGTAATCCCAGCACTT 59754        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  CPM      3'  CACACCTTGTAATCCCAGCACT 59675          T      _
            TT                    AAAGTGCTG GATTGCA GGTGTG
                                |||||||||  |||||||  ||||||
                                TTTCACGAC CTAATGT CCACAC
                                     C      T
GAM611  CRACC    3'  CACACCTGTAATCCCAGCACTT 41003          T
            T                     AAAGTGCTG GATTGCAGGTGTG
                                |||||||||  ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  CTMP     3'  CACACCTGTAATCCCAGCACTT 53875          T
            T                     AAAGTGCTG GATTGCAGGTGTG
                                |||||||||  ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  CYP4F3   3'  CACACCTGTAATCCCAGCACTT 6110           T
            T                     AAAGTGCTG GATTGCAGGTGTG
                                |||||||||  ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  DCLRE1C  3'  CACACTTGTAATCCCAGCACTT 42526          T
            T                     AAAGTGCTG GATTGCAGGTGTG
                                |||||||||  ||||||||||||
                                TTTCACGAC CTAATGTTCACAC
                                     C
GAM611  DMC1     3'  CACACCTGTAATCCCAGCACTT 22971          T
            T                     AAAGTGCTG GATTGCAGGTGTG
                                |||||||||  ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  DNASE2   3'  CACATCTGTAACCCCAGCACTT 7264          TGA
            T                     AAAGTGCTG   TTGCAGGTGTG
                                |||||||||   ||||||||||
                                TTTCACGAC   AATGTCTACAC
                                     CCC
GAM611  EHHADH   3'  CACACCTGTAATCCCAGCACTT 8749           T
            T                     AAAGTGCTG GATTGCAGGTGTG
                                |||||||||  ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  ESRRB    5' ACACCTGCCCTAGCCCT     67316    T   TGATT
                                AG GCTG     GCAGGTGT
                                || ||||     ||||||||
                                TC CGAT     CGTCCACA
                                 C   CC___
GAM611  F2RL3    3'  CACACCTGCAATCCCAGCACTT 14171          T
            T                     AAAGTGCTG GATTGCAGGTGTG
                                |||||||||  ||||||||||||
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                                TTTCACGAC CTAACGTCCACAC
                                      C
GAM611  FANCC    3'  CACACCTGTGATCCCAGCACTT 70519         T  TG
           T                   AAAGTGCTG GAT  CAGGTGTG
                               ||||||||| |||  ||||||||
                               TTTCACGAC CTA  GTCCACAC
                                      C  GT
GAM611  FANCD2   3'  CACACCTGTAATCCCAGCACTT 52354         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  FPGS     3'  CACACCTGCAGTGCCAGC    17081      TG
                               GCTG  ATTGCAGGTGTG
                               ||||  ||||||||||||
                               CGAC  TGACGTCCACAC
                                 CG
GAM611  FUT6     3'  CACACCTGTAATCCCAGCACTT 3808          T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  GRM6     3'  CACACCTGTAATCCCAGCACTT 5928          T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  HIP1     3'  CACACGTTTAATCCCAGCACTT 18057         T    CAG
           T                   AAAGTGCTG GATTG   GTGTG
                               ||||||||| |||||   |||||
                               TTTCACGAC CTAAT   CACAC
                                      C    TTG
GAM611  HUNK     3'  CACACCTGTAATCCCAGCACTT 27443         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  IFNAR1   3'  CACACCTGTAATCCCAGCACTT 5282          T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  KCNK3    3'  CACACCTGTATTCCCAACACTT 9548        C  T  T
           T                   AAAGTG TG GA TGCAGGTGTG
                               |||||| || || ||||||||||
                               TTTCAC AC CT ATGTCCACAC
                                  A  C  T
GAM611  KLF8     5'  CACACCTGTAATCTCAGCACTT 23403         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                      T
GAM611  LRRC2    3'  CACACCTGTAATCCCAGCACTT 44466          T
                T                      AAAGTGCTG GATTGCAGGTGTG
                                       ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  LUZP1    3'  CACACCTGTAATCCCAGCACTT 53297          T
                T                      AAAGTGCTG GATTGCAGGTGTG
                                       ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  MAFF     3'  CACATCTGTAATCCCAGCACTT 24642          T
                T                      AAAGTGCTG GATTGCAGGTGTG
                                       ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCTACAC
                                      C
GAM611  MAPK4    3'  CACCCTAACCACAGCGC     10823          A   CA
                                GTGCTGTG TTG  GGTG
                                |||||||| |||  ||||
                                CGCGACAC AAT  CCAC
                                     C   C_
GAM611  MCM4     3'  CACACCTGTAATCCCAGCACTT 61902          T
                T                      AAAGTGCTG GATTGCAGGTGTG
                                       ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  MRC1     3'  CACAGCACCACAGCAC      10113          AT   AG
                                GTGCTGTG  TGC  GTG
                                ||||||||  |||  |||
                                CACGACAC  ACG  CAC
                                     C_   A_
GAM611  MTNR1A   3'  CACACCTGTAATCTCAGCACTT 19888          T
                T                      AAAGTGCTG GATTGCAGGTGTG
                                       ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      T
GAM611  NOV      3'  CACACCTACAGAGCAC      10241       G  ATTGC
                                GTGCT TG     AGGTGTG
                                ||||| ||     |||||||
                                CACGA AC     TCCACAC
                                   G  A____
GAM611  PAICS    3'  CACACCTACGATCACAGCACTT 21254             C
                                AAGTGCTGTGATTG AGGTGTG
                                |||||||||||||| |||||||
                                TTCACGACACTAGC TCCACAC
                                         A
GAM611  PCDH11X  3'  CACACCTGTAATCCCAGCACTT 52006          T
                T                      AAAGTGCTG GATTGCAGGTGTG
                                       ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  PDE4A   3'  CACACTCTGATCACAGC    20580       TG  _
                                GCTGTGAT  CAG GTGTG
                                |||||||| ||| |||||
                                CGACACTA  GTC CACAC
                                    __  T
GAM611  PSD     5'  CTGCAATCCCAGCACTTT    10928       T
                                AAAGTGCTG GATTGCAG
                                ||||||||| ||||||||
                                TTTCACGAC CTAACGTC
                                      C
GAM611  PSMB9   3'  CACACCTATAATCCCAGCACTT 10958       T   C
          T                     AAAGTGCTG GATTG AGGTGTG
                                ||||||||| ||||| |||||||
                                TTTCACGAC CTAAT TCCACAC
                                      C    A
GAM611  PSMB9   3'  CTGTAATCACAGCACTTT    10961
                                AAAGTGCTGTGATTGCAG
                                ||||||||||||||||||
                                TTTCACGACACTAATGTC

GAM611  PTAFR   3'  CACACCTGTAATCCCAGCACTT 6293        T
          T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  PTHLH   3'  ACACCTGGGCAAACTTT    11011     GC  GATTG
                                AAAGT  TGT   CAGGTGT
                                |||||  |||   |||||||
                                TTTCA  ACG   GTCCACA
                                   A_  G____
GAM611  RAB7L1  3'  CACACCTGTAATCCCAGCACTT 14105       T
          T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  RARB    5'  CACACCTAGAGGATAAGCACTT 6372        GTGA_  GC
          T                     AAAGTGCT   TT  AGGTGTG
                                ||||||||   ||  |||||||
                                TTTCACGA   AG  TCCACAC
                                     ATAGG  A_
GAM611  SEPX1   3'  CACACCTGCAGGGAGGCCCTT  32914    T  GTGA
                                AAG GCT   TTGCAGGTGTG
                                ||| |||   ||||||||||
                                TTC CGG   GACGTCCACAC
                                  C  AGG_
GAM611  SIM2    3'  CACACCTGTAATCCCAGCACTT 23782       T
          T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  SUV39H2  3'  CACACCTGTGATCCCAGCACTT 45135        T  TG
           T                   AAAGTGCTG GAT  CAGGTGTG
                               ||||||||| |||  ||||||||
                               TTTCACGAC CTA  GTCCACAC
                                     C  GT
GAM611  TNFSF15  3'  CACACCTGTAATCCCAACACTT 17590      C  T
           T                   AAAGTG TG GATTGCAGGTGTG
                               |||||| || ||||||||||||
                               TTTCAC AC CTAATGTCCACAC
                                  A  C
GAM611  UBE2G2   3'  CACGCCTGCAATCCCAGCACTT 64851        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAACGTCCGCAC
                                     C
GAM611  XRCC3    3'  CACACTGTGCCCCACAAAACTT 18335     GC   ATT  _
                               AAGT  TGTG   GCA GGTGTG
                               ||||  ||||   ||| ||||||
                               TTCA  ACAC   CGT TCACAC
                                 AA   CC_   G
GAM611  ZNF136   3'  CACACCTGTAATCCCAGCACTT 59886        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  ZNF137   3'  CACACCTGTAATCCCAGCACTT 12859        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  AAK1     3'  CACACTTGTAACCACAGGACTT 29842      G    A
           T                   AAAGT CTGTG TTGCAGGTGTG
                               ||||| ||||| ||||||||||
                               TTTCA GACAC AATGTTCACAC
                                  G    C
GAM611  AF020591 3'  CACCTGTAATCCCAGCAC    27137       T
                               GTGCTG GATTGCAGGTG
                               |||||| ||||||||||
                               CACGAC CTAATGTCCAC
                                  C
GAM611  BIRC1    3'  CACACCTGTAATCCCAGCACTT 15786        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  C13orf1  3'  CACACCTGTAATCCCAGCACTT 39965        T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                    C
GAM611  C1orf24   3'  CACCTATAATCCCAGCACTTT  53708        T    C
                                AAAGTGCTG GATTG AGGTG
                                ||||||||| ||||| |||||
                                TTTCACGAC CTAAT TCCAC
                                    C    A
GAM611  C22orf20  3'  CACGGCTGTAATCCCAGCACTT 47428         T      G
           T                     AAAGTGCTG GATTGCAG TGTG
                                ||||||||| |||||||| ||||
                                TTTCACGAC CTAATGTC GCAC
                                    C       G
GAM611  C6orf5    3'  CACACCTGTAATCCCAGCACTT 31339         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                    C
GAM611  C8orf2    3'  CACACCTGTAATCCCAGCACTT 23159         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                    C
GAM611  C9orf5    3'  CACATCTGTAATCCCAGCACTT 49273         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCTACAC
                                    C
GAM611  CALN1     3'  CACACCTATAATCCCAGCACTT 48856         T    C
           T                     AAAGTGCTG GATTG AGGTGTG
                                ||||||||| ||||| |||||||
                                TTTCACGAC CTAAT TCCACAC
                                    C    A
GAM611  CAMKK2    5'  CACACCTGTAATCCCAGCACTT 21577          T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                    C
GAM611  CFLAR     3'  CACACCTGTAATCCCAGCACTT 13927          T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                    C
GAM611  CYorf14   3'  CACACCCTGTAATCCCAGCACT 37607         T       _
           TT                     AAAGTGCTG GATTGCAGG TGTG
                                ||||||||| ||||||||| ||||
                                TTTCACGAC CTAATGTCC ACAC
                                    C        C
GAM611  D21S2056E 3'  CACACCTGTAATCCCAGCACTT 13468          T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  dJ383J4.3 3'  CACACCTGTAATTCCAGCACTT 66943          TG
          T                    AAAGTGCTG  ATTGCAGGTGTG
                               |||||||||  ||||||||||||
                               TTTCACGAC  TAATGTCCACAC
                                      CT
GAM611  DKFZp434E0519 3'  CACACCTATAATCCCAGCACTT 49982          T    C
          T                    AAAGTGCTG GATTG AGGTGTG
                               ||||||||| ||||| |||||||
                               TTTCACGAC CTAAT TCCACAC
                                      C    A
GAM611  DKFZp434E0519 3'  CACACTTATAATCCCAGCACTT 49983          T    C
          T                    AAAGTGCTG GATTG AGGTGTG
                               ||||||||| ||||| |||||||
                               TTTCACGAC CTAAT TTCACAC
                                      C    A
GAM611  DKFZP434F1735 3'  CACATTTGTAATCCCAGCACTT 31497          T
          T                    AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTTTACAC
                                      C
GAM611  DKFZp547C176 3'  CACACCTGTAATCCCAGCACTT 67220          T
          T                    AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  DKFZp547I094 3'  CACACCTGTAATCCCAGCACTT 49632          T
          T                    AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  DKFZP586D2223 3'  CACACCTGTAATTCCAACACTT 37680        C  TG
          T                    AAAGTG TG  ATTGCAGGTGTG
                               |||||| ||  ||||||||||||
                               TTTCAC AC  TAATGTCCACAC
                                  A  CT
GAM611  DKFZp761O132 5'  CACACCTGCCCACCCTGCACTC 50196    A    T__   ATT
          C                    A AGTGC   GTG   GCAGGTGTG
                               | |||||   |||   |||||||||
                               C TCACG   CAC   CGTCCACAC
                               C    TCC   C__
GAM611  DRF1     3'  CACACCTGTAATCCCAGCACTT 47025          T
          T                    AAAGTGCTG GATTGCAGGTGTG
                               |||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  EIF2S1   3'  CACACAGTAGCTCCAACACTTT 14583        C  T  _   AG
                               AAAGTG TG GA TTGC  GTGTG
                               |||||| || || ||||  |||||
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                                TTTCAC AC CT GATG  CACAC
                                   A  _  C    A_
GAM611  FBXO26   3'  CACACCTGTGGAATCCCAGCAC 46093        T   __
                TT                  AAGTGCTG GATT  GCAGGTGTG
                                    |||||||| ||||  |||||||||
                                    TTCACGAC CTAA  TGTCCACAC
                                       C    GG
GAM611  FLJ10043 3'  CACACCTGTAATCCCAGCACTT 35755         T
                T                   AAAGTGCTG GATTGCAGGTGTG
                                    ||||||||| ||||||||||||
                                    TTTCACGAC CTAATGTCCACAC
                                       C
GAM611  FLJ10460 3'  CACACCTGTAATCCCAACACTT 36126       C  T
                T                   AAAGTG TG GATTGCAGGTGTG
                                    |||||| || ||||||||||||
                                    TTTCAC AC CTAATGTCCACAC
                                       A  C
GAM611  FLJ10547 3'  CACACCTGTAATCCCAGCACTT 36266         T
                T                   AAAGTGCTG GATTGCAGGTGTG
                                    ||||||||| ||||||||||||
                                    TTTCACGAC CTAATGTCCACAC
                                       C
GAM611  FLJ10650 3'  CACACCTGTAATCCCAGCACTT 36380         T
                T                   AAAGTGCTG GATTGCAGGTGTG
                                    ||||||||| ||||||||||||
                                    TTTCACGAC CTAATGTCCACAC
                                       C
GAM611  FLJ10803 3'  CACACCGGTAATCCCAGCACTT 36661         T     A
                T                   AAAGTGCTG GATTGC GGTGTG
                                    ||||||||| |||||| ||||||
                                    TTTCACGAC CTAATG CCACAC
                                       C     G
GAM611  FLJ10803 3'  CACACCTGTAATCCCAGCACTT 36662         T
                T                   AAAGTGCTG GATTGCAGGTGTG
                                    ||||||||| ||||||||||||
                                    TTTCACGAC CTAATGTCCACAC
                                       C
GAM611  FLJ10830 3'  CACACCTATAATCGAGCACTTT 36719        G     C
                                    AAAGTGCT TGATTG AGGTGTG
                                    |||||||| |||||| |||||||
                                    TTTCACGA GCTAAT TCCACAC
                                       _     A
GAM611  FLJ10989 3'  CACACCTGTAATCCCAGCACTT 36945         T
                T                   AAAGTGCTG GATTGCAGGTGTG
                                    ||||||||| ||||||||||||
                                    TTTCACGAC CTAATGTCCACAC
                                       C
GAM611  FLJ11029 3'  CACACCTGTAATCCCAGCACTT 60971         T
                T                   AAAGTGCTG GATTGCAGGTGTG
                                    ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  FLJ11149  3'  CACACCGGTAATCCCAGCACTT 37108        T     A
            T                    AAAGTGCTG GATTGC GGTGTG
                                 ||||||||| |||||| ||||||
                                 TTTCACGAC CTAATG CCACAC
                                     C     G
GAM611  FLJ11259  3'  CACACCTGTATTCCCAGCACTT 37185        T  T
            T                    AAAGTGCTG GA TGCAGGTGTG
                                 ||||||||| || ||||||||||
                                 TTTCACGAC CT ATGTCCACAC
                                     C  T
GAM611  FLJ11700  3'  CACACCTGTAATCCCAGCACTT 46035        T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  FLJ11726  3'  CACACCTGTAATCCCAGCACTT 46407        T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  FLJ11800  3'  CACACTTGTAATCACTGCACTT 46423       T
            T                    AAAGTGC GTGATTGCAGGTGTG
                                 ||||||| ||||||||||||||
                                 TTTCACG CACTAATGTTCACAC
                                    T
GAM611  FLJ11996  3'  CACACCTGTAATTCCAGCACTT 46435        TG
            T                    AAAGTGCTG  ATTGCAGGTGTG
                                 |||||||||  ||||||||||||
                                 TTTCACGAC  TAATGTCCACAC
                                     CT
GAM611  FLJ12078  3'  CACACTAGTAATCACAGCCTCC 46452    A  T        A
                                 A AG GCTGTGATTGC GGTGTG
                                 | || |||||||||| ||||||
                                 C TC CGACACTAATG TCACAC
                                  C _         A
GAM611  FLJ12294  5'  CACACCTGTAAACCCAGCACTT 47008        TGA
            T                    AAAGTGCTG   TTGCAGGTGTG
                                 |||||||||   ||||||||||
                                 TTTCACGAC   AATGTCCACAC
                                     CCA
GAM611  FLJ12363  3'  CACACCTGTAATCCCAGCACTT 49673        T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  FLJ12985  3'  CACACCTGTAATCCCAGCACTT 46238        T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  FLJ13193 3' CACACCTGCAATCCCAACACTT 49759      C  T
            T                    AAAGTG TG GATTGCAGGTGTG
                                 |||||| || ||||||||||||
                                 TTTCAC AC CTAACGTCCACAC
                                    A  C
GAM611  FLJ13193 3' CACACCTGTAATCCCAGCACTT 49760       T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  FLJ13352 3' CACACCTGTTAATCCCAGCACT 44752       T   _
            T                    AAGTGCTG GATTG CAGGTGTG
                                 |||||||| ||||| ||||||||
                                 TTCACGAC CTAAT GTCCACAC
                                      C    T
GAM611  FLJ13390 3' CACACCTGAAATCCCAGCACTT 42537       T   G
            T                    AAAGTGCTG GATT CAGGTGTG
                                 ||||||||| |||| ||||||||
                                 TTTCACGAC CTAA GTCCACAC
                                     C    A
GAM611  FLJ13544 3' CACACCTGTCATCCCAGCACTT 46575       T  T
            T                    AAAGTGCTG GAT GCAGGTGTG
                                 ||||||||| ||| |||||||||
                                 TTTCACGAC CTA TGTCCACAC
                                     C   C
GAM611  FLJ13659 3' CACACCTGTAATCCCAGCACTT 47244       T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  FLJ13848 3' CACCTGTAATCCCAGCACTTT  45460       T
                                 AAAGTGCTG GATTGCAGGTG
                                 ||||||||| ||||||||||
                                 TTTCACGAC CTAATGTCCAC
                                     C
GAM611  FLJ13984 3' CACCTGTAATCCCAGCACTTT  45446       T
                                 AAAGTGCTG GATTGCAGGTG
                                 ||||||||| ||||||||||
                                 TTTCACGAC CTAATGTCCAC
                                     C
GAM611  FLJ14011 3' CACCTGTAACCCCAGCACTTT  42063       TGA
                                 AAAGTGCTG   TTGCAGGTG
                                 |||||||||   |||||||||
                                 TTTCACGAC   AATGTCCAC
                                     CCC
GAM611  FLJ14117 3' CACACTTGTAATCCCAGCACTT 42902       T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTTCACAC
                                     C
GAM611  FLJ14117  3'  CACACTTGTAATCCCAGCACTT 42903        T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTTCACAC
                                     C
GAM611  FLJ14251  3'  CACACCTGTAATCCCAGCACTT 45966        T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  FLJ14346  3'  CACACCTGTAATCCCAGCACTT 46708        T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  FLJ14397  3'  CACACCTATAATCCCAGCACTT 51324        T    C
            T                    AAAGTGCTG GATTG AGGTGTG
                                 ||||||||| ||||| |||||||
                                 TTTCACGAC CTAAT TCCACAC
                                     C    A
GAM611  FLJ14642  3'  CACACCTGTAATCCCAGCACTT 51494        T
                                 AAGTGCTG GATTGCAGGTGTG
                                 |||||||| ||||||||||||
                                 TTCACGAC CTAATGTCCACAC
                                     C
GAM611  FLJ14957  3'  CACTGAGACCAATCACAGCCT  51740    T       CA___
                                 AG GCTGTGATTG    GGTG
                                 || ||||||||||    ||||
                                 TC CGACACTAAC    TCAC
                                  _       CAGAG
GAM611  FLJ20045  3'  CACACCTCTAATCCCAGCACTT 34414        T    C
            T                    AAAGTGCTG GATTG AGGTGTG
                                 ||||||||| ||||| |||||||
                                 TTTCACGAC CTAAT TCCACAC
                                     C    C
GAM611  FLJ20139  3'  CACACCTGTAATCCCAACACTT 34622       C  T
            T                    AAAGTG TG GATTGCAGGTGTG
                                 |||||| || ||||||||||||
                                 TTTCAC AC CTAATGTCCACAC
                                    A  C
GAM611  FLJ20280  3'  CACACCTGTAATCCCAGCACTT 34848        T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  FLJ20340  3'  CACACCCGTAATCCCAGCACTT 34973        T    A
            T                    AAAGTGCTG GATTGC GGTGTG
                                 ||||||||| |||||| ||||||
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                                TTTCACGAC CTAATG CCACAC
                                      C     C
GAM611  FLJ20519  3'  CACACCTGCAATGATTACT   35345     CT  G
                                AGTG  GT ATTGCAGGTGTG
                                ||||  || ||||||||||||
                                TCAT  TA TAACGTCCACAC
                                  __  G
GAM611  FLJ20808  3'  CACACCCATAATCCCAGCACTT 35672         T    CA
           T                     AAAGTGCTG GATTG  GGTGTG
                                ||||||||| |||||  ||||||
                                TTTCACGAC CTAAT  CCACAC
                                      C     AC
GAM611  FLJ22054  3'  CACACCTGTAATCCCAGCACTT 94392         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  FLJ23499  3'  CACACCTAATCCCAGCACTTT  42818         T   GC
                                AAAGTGCTG GATT  AGGTGTG
                                ||||||||| ||||  |||||||
                                TTTCACGAC CTAA  TCCACAC
                                      C   __
GAM611  FLJ30092  3'  CACACCTGTAATCCCAGCACTT 58686         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  FLJ31300  3'  CACACCCGCACTACCTGCACTT 58284       T_  AT   A
                                AAGTGC  GTG  TGC GGTGTG
                                ||||||  |||  ||| ||||||
                                TTCACG  CAT  ACG CCACAC
                                    TC   C_   C
GAM611  FUSIP1    3'  CACACCTGTAATCCCAGCACTT 53956         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  GCN2      3'  CACACCTTTAATCCCAGCACTT 62769         T    C
           T                     AAAGTGCTG GATTG AGGTGTG
                                ||||||||| ||||| |||||||
                                TTTCACGAC CTAAT TCCACAC
                                      C     T
GAM611  GIT2      3'  ACACCTGGAGCAGCCT      54074     T    GAT G
                                AG GCTGT   T CAGGTGT
                                || |||||   | |||||||
                                TC CGACG   A GTCCACA
                                 _    ___ G
GAM611  GIT2      3'  ACACCTGGAGCAGCCT      54087     T    GAT G
                                AG GCTGT   T CAGGTGT
                                || |||||   | |||||||
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                                TC CGACG   A GTCCACA
                                 _    ___ G
GAM611  GIT2    3'  ACACCTGGAGCAGCCT      28752    T    GAT G
                                AG GCTGT   T CAGGTGT
                                || |||||   | |||||||
                                TC CGACG   A GTCCACA
                                 _    ___ G
GAM611  IRF7    5'  CACACCTGCAGTCACA      14441
                                TGTGATTGCAGGTGTG
                                ||||||||||||||||
                                ACACTGACGTCCACAC

GAM611  IRF7    5'  CACACCTGCAGTCACA      14445
                                TGTGATTGCAGGTGTG
                                ||||||||||||||||
                                ACACTGACGTCCACAC

GAM611  IRF7    5'  CACACCTGCAGTCACA      14439
                                TGTGATTGCAGGTGTG
                                ||||||||||||||||
                                ACACTGACGTCCACAC

GAM611  IRF7    5'  CACACCTGCAGTCACA      7814
                                TGTGATTGCAGGTGTG
                                ||||||||||||||||
                                ACACTGACGTCCACAC

GAM611  KATII   3'  CACACCTATAATCCCAGCACTT 32643          T    C
            T                    AAAGTGCTG GATTG AGGTGTG
                                ||||||||| ||||| |||||||
                                TTTCACGAC CTAAT TCCACAC
                                      C    A
GAM611  KIAA0184 3'  CACCTGTAATCCCAGCACTTT  65193         T
                                AAAGTGCTG GATTGCAGGTG
                                ||||||||| ||||||||||
                                TTTCACGAC CTAATGTCCAC
                                      C
GAM611  KIAA0226 3'  CACACCTGTAATCCCAGCACTT 63512         T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  KIAA0266 3'  CACACCTGTAATCCCAGCACTT 41327         T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  KIAA0266 3'  CACACCTGTAATCCCAGCACTT 41328         T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  KIAA0391 3' CACACCTACAGTTCCAGCACTT 27907         TG   C
           T                  AAAGTGCTG  ATTG AGGTGTG
                              |||||||||  |||| |||||||
                              TTTCACGAC  TGAC TCCACAC
                                   CT    A
GAM611  KIAA0471 3' CACATCTGTAATCCCAGCACTT 29388         T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              |||||||||  |||||||||||||
                              TTTCACGAC CTAATGTCTACAC
                                     C
GAM611  KIAA0596 3' CACACCTACCTGCACAGCAC   62825        ATTGC
                              GTGCTGTG    AGGTGTG
                              ||||||||    |||||||
                              CACGACAC    TCCACAC
                                   GTCCA
GAM611  KIAA0798 3' CACCTGTAATCCCAGCACTTT  27718         T
                              AAAGTGCTG GATTGCAGGTG
                              |||||||||  ||||||||||
                              TTTCACGAC CTAATGTCCAC
                                     C
GAM611  KIAA0912 3' CACACCTGTAATCCCAGCACTT 64408         T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              |||||||||  |||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  KIAA0939 3' CACACCTGGCCTCACACTTT   62007      GCT   TTG
                              AAAGT   GTGA   CAGGTGTG
                              |||||   ||||   ||||||||
                              TTTCA   CACT   GTCCACAC
                                 ___    CCG
GAM611  KIAA1001 3' CACACCTGTAGTCCCAGCACTT 30289         T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              |||||||||  |||||||||||||
                              TTTCACGAC CTGATGTCCACAC
                                     C
GAM611  KIAA1086 3' CACACCTATAATCCCAGCACTT 70741         T    C
           T                  AAAGTGCTG GATTG AGGTGTG
                              |||||||||  |||||  |||||||
                              TTTCACGAC CTAAT TCCACAC
                                     C    A
GAM611  KIAA1204 3' CACATCTGTAATCCCAACACTT 69216       C  T
           T                  AAAGTG TG GATTGCAGGTGTG
                              ||||||  ||  |||||||||||||
                              TTTCAC AC CTAATGTCTACAC
                                 A  C
GAM611  KIAA1423 3' CACATCTGTAATCTCAACACTT 61724       C  T
           T                  AAAGTG TG GATTGCAGGTGTG
                              ||||||  ||  |||||||||||||
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                                TTTCAC AC CTAATGTCTACAC
                                   A  T
GAM611  KIAA1456 3'  CACACCTGTACTCCCAGCACTT 66991        T  T
                                AAGTGCTG GA TGCAGGTGTG
                                |||||||| || ||||||||||
                                TTCACGAC CT ATGTCCACAC
                                     C  C
GAM611  KIAA1456 5'  CACCTGTAATCCCAGCACTTT  66992         T
                                AAAGTGCTG GATTGCAGGTG
                                ||||||||| ||||||||||
                                TTTCACGAC CTAATGTCCAC
                                     C
GAM611  KIAA1559 3'  CACACCTGTAATCCCAGCACTT 73059         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  KIAA1586 5'  CACACCTGTAATCCCAGCACTT 92328         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  KIAA1855 3'  CACACCACCTCCCTCAGCACTT 92336        TGATTGCA
                                AAGTGCTG       GGTGTG
                                ||||||||       ||||||
                                TTCACGAC       CCACAC
                                     TCCCTCCA
GAM611  KIAA1941 3'  CACACCTGTAATCCCAGCACTT 74836         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  KIAA1954 3'  CACACCTGTAATCCCAGCACTT 77716         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  KIAA1979 3'  CACACCTGGCACAACAT     88275     C    ATTG
                                GTG TGTG    CAGGTGTG
                                ||| ||||    ||||||||
                                TAC ACAC    GTCCACAC
                                  A   G___
GAM611  KR18     3'  CACACCTGTGATCCCAGCACTT 52740         T   TG
           T                     AAAGTGCTG GAT  CAGGTGTG
                                ||||||||| |||  ||||||||
                                TTTCACGAC CTA  GTCCACAC
                                     C   GT
GAM611  MACF1    3'  CACACCTGTAATCCCAGCACTT 52315         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  MGC10814  3'  CACACCTGTAATCCCAGCACTT 51037        T
                                AAGTGCTG GATTGCAGGTGTG
                                |||||||| ||||||||||||
                                TTCACGAC CTAATGTCCACAC
                                      C
GAM611  MGC14407  3'  CACACCTGTAATCTCAGCACTT 51876        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                       T
GAM611  MGC14817  3'  CACACCTGTAATCCCAGCACTT 50335        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                       C
GAM611  MGC2562   3'  CACACCTGTAATCCCAGCACTT 50434        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                       C
GAM611  MGC29762  3'  CACACCTGTAATCCCAGCACTT 58468        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                       C
GAM611  MGC29891  3'  CACACCTGTAATCCCAACACTT 58200      C  T
           T                     AAAGTG TG GATTGCAGGTGTG
                                 |||||| || ||||||||||||
                                 TTTCAC AC CTAATGTCCACAC
                                    A  C
GAM611  MGC3079   3'  CACCTGTAATCCCAGCACTTT  50949        T
                                AAAGTGCTG GATTGCAGGTG
                                ||||||||| ||||||||||
                                TTTCACGAC CTAATGTCCAC
                                      C
GAM611  MGC3207   3'  CACACCTGTAATCCCAGCACTT 62557        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                       C
GAM611  MGC39350  3'  CACACCTGTAATCCCCAGCACT 58652        T_
           TT                     AAAGTGCTG  GATTGCAGGTGTG
                                  |||||||||  ||||||||||||
                                  TTTCACGAC  CTAATGTCCACAC
                                        CC
GAM611  MGC4248   3'  CACACCTGTAATCCCAGCACTT 50326        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  MGC4400  3'  CACACCTGTAATCTCAGCACTT 51052         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      T
GAM611  MGC4840  3'  CACACCTGTAATTCCAGCACTT 71565         TG
           T                   AAAGTGCTG  ATTGCAGGTGTG
                               |||||||||  ||||||||||||
                               TTTCACGAC  TAATGTCCACAC
                                      CT
GAM611  MGC5457  3'  CACACCTTAATCCCAGCACTTT 50944         T    C
                               AAAGTGCTG GATTG AGGTGTG
                               ||||||||| ||||| |||||||
                               TTTCACGAC CTAAT TCCACAC
                                      C    _
GAM611  MOST2    5'  CACACCTGTAATCCCAGCACTT 39675         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  NMNAT    3'  CACACCTGTAATCCCAGCACTT 42955         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  OSBPL2   3'  CACACCTGTGACGGAAGCACTT 57854        G_  A TG
                               AAGTGCT  TG T  CAGGTGTG
                               |||||||  || |  ||||||||
                               TTCACGA  GC A  GTCCACAC
                                   AG  _ GT
GAM611  OSBPL2   3'  CACACCTGTGACGGAAGCACTT 29203        G_  A TG
                               AAGTGCT  TG T  CAGGTGTG
                               |||||||  || |  ||||||||
                               TTCACGA  GC A  GTCCACAC
                                   AG  _ GT
GAM611  PB1      3'  CACACCTGTAATCCCAGCACTT 37020         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  PIWIL2   3'  CACACCTGTAATCCAAGCACTT 36053        GT
           T                   AAAGTGCT  GATTGCAGGTGTG
                               ||||||||  ||||||||||||
                               TTTCACGA  CTAATGTCCACAC
                                      AC
GAM611  PP591    5'  CACACCTATAATTCCAGCACTT 47366         TG   C
           T                   AAAGTGCTG  ATTG AGGTGTG
                               |||||||||  |||| |||||||
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                                TTTCACGAC  TAAT TCCACAC
                                     CT    A
GAM611  PRO0478  5'  CACACCTGTAATCCCAGCACTT 26184         T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  PRO1048  5'  CACATCTGTAATCCCAGCACTT 37510         T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCTACAC
                                     C
GAM611  PRO2730  3'  CACACCTGTAATCCCAGCACTT 47411         T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  PSR      3'  CACACCTGTAATCCCAGCACTT 65176         T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  RNF24    3'  CTTGTGACAACCAAAGCACTTT 23317         ___  GA TG
                              AAAGTGCT   GT  T  CAGG
                              ||||||||   ||  |  ||||
                              TTTCACGA   CA  A  GTTC
                                   AAC  AC GT
GAM611  RPL13    3'  CACAGCTGTAATCCCAGCACTT 6387          T      G
           T                  AAAGTGCTG GATTGCAG TGTG
                              ||||||||| |||||||| ||||
                              TTTCACGAC CTAATGTC ACAC
                                     C       G
GAM611  RPL13    3'  CACAGCTGTAATCCCAGCACTT 52679         T      G
           T                  AAAGTGCTG GATTGCAG TGTG
                              ||||||||| |||||||| ||||
                              TTTCACGAC CTAATGTC ACAC
                                     C       G
GAM611  SCIN     3'  CACACCTGTAATCCCAGCACTT 52423         T
           T                  AAAGTGCTG GATTGCAGGTGTG
                              ||||||||| ||||||||||||
                              TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  SEC24B   3'  CAAGATGCAACGCACAGCACT  20897         A_    GG_
                              AGTGCTGTG  TTGCA   TG
                              |||||||||  |||||   ||
                              TCACGACAC  AACGT   AC
                                     GC    AGA
GAM611  SPTLC2   3'  CACCTGTAATCCCAACACTTT  16798       C  T
                              AAAGTG TG GATTGCAGGTG
                              |||||| || ||||||||||
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                                TTTCAC AC CTAATGTCCAC
                                   A  C
GAM611  STX12    3'  CACACTTGTAATCCCAACACTT 66349       C  T
           T                    AAAGTG TG GATTGCAGGTGTG
                                |||||| || ||||||||||||||
                                TTTCAC AC CTAATGTTCACAC
                                   A  C
GAM611  TIP47    3'  CACACCTGTAATCCCAGCACTT 19478         T
           T                    AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  TP53INP1 3'  CTGAACAATACAGCACTTT    52725          A  __
                                AAAGTGCTGTG TTG  CAG
                                |||||||||| |||  |||
                                TTTCACGACAT AAC  GTC
                                     _  AA
GAM611  TP53INP1 3'  CTGAACAATACAGCACTTT    72952          A  __
                                AAAGTGCTGTG TTG  CAG
                                |||||||||| |||  |||
                                TTTCACGACAT AAC  GTC
                                     _  AA
GAM611  UBF-fl   3'  CACACCTGTAATCCCAGCACTT 51553         T
           T                    AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  WBSCR22  3'  CACACCTGTAATCCCAGCAC   34034       T
                                GTGCTG GATTGCAGGTGTG
                                |||||| ||||||||||||||
                                CACGAC CTAATGTCCACAC
                                   C
GAM611  YME1L1   3'  CACATCTGTAATCCCAGCACTT 26526         T
           T                    AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||||
                                TTTCACGAC CTAATGTCTACAC
                                     C
GAM611  YME1L1   3'  CACATCTGTAATCCCAGCACTT 57776         T
           T                    AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||||
                                TTTCACGAC CTAATGTCTACAC
                                     C
GAM611  ZNF297B  5'  CACACCTGTAATCCCAGCACTT 25776         T
           T                    AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611  LOC112687 3' CACACCTATAATCCCAGCACTT 72856         T    C
           T                    AAAGTGCTG GATTG AGGTGTG
                                ||||||||| ||||| |||||||
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                                TTTCACGAC CTAAT TCCACAC
                                    C    A
GAM611  LOC116236 3'  CACACCTATAATCTCAGCACTT 73808        T    C
          T                      AAAGTGCTG GATTG AGGTGTG
                                 ||||||||| ||||| |||||||
                                 TTTCACGAC CTAAT TCCACAC
                                    T    A
GAM611  LOC126282 3'  CACACCTGTAATCCCAGCACTT 74470        T
          T                      AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                    C
GAM611  LOC130535 3'  CACACTTGTAATCCCAGCACTT 76148        T
          T                      AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||||
                                 TTTCACGAC CTAATGTTCACAC
                                    C
GAM611  LOC130951 3'  CACACCTGTAATCCCAACACTT 57142       C  T
          T                      AAAGTG TG GATTGCAGGTGTG
                                 |||||| || ||||||||||||||
                                 TTTCAC AC CTAATGTCCACAC
                                   A  C
GAM611  LOC138428 3'  CACACCTATAATCCCAGCACTT 75332        T    C
          T                      AAAGTGCTG GATTG AGGTGTG
                                 ||||||||| ||||| |||||||
                                 TTTCACGAC CTAAT TCCACAC
                                    C    A
GAM611  LOC143162 3'  CACAGTACTAATCACAGCAT   76495          CAGG
                                 GTGCTGTGATTG    TGTG
                                 ||||||||||||    ||||
                                 TACGACACTAAT    ACAC
                                       CATG
GAM611  LOC143465 3'  CACACCTGTAATCTCAGCACTT 82961        T
          T                      AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                    T
GAM611  LOC144289 3'  CACATCTGTAATCCCAGCACTT 83023        T
          T                      AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||||
                                 TTTCACGAC CTAATGTCTACAC
                                    C
GAM611  LOC144558 3'  CACCTGTAATCCCAGCACTTT  83146        T
                                 AAAGTGCTG GATTGCAGGTG
                                 ||||||||| |||||||||||
                                 TTTCACGAC CTAATGTCCAC
                                    C
GAM611  LOC145387 3'  CACCTGTAATCCCAGCACTTT  83352        T
                                 AAAGTGCTG GATTGCAGGTG
                                 ||||||||| |||||||||||
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                                TTTCACGAC CTAATGTCCAC
                                      C
GAM611   LOC146272 5'  CACACCTGTAATCCCAGCACTT 77786        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC146540 3'  CACACCTGTAATCCCAGCACTT 77971        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC146656 3'  CACACCTGTGATCCCCCCAGCA 78072        T___  TG
            CTTT                  AAAGTGCTG   GAT  CAGGTGTG
                                ||||||||    |||  ||||||||
                                TTTCACGAC   CTA  GTCCACAC
                                      CCCC   GT
GAM611   LOC146923 3'  CACACCTGTAATCCCAGCACTT 78191        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC146975 5'  CACACCTATAATCCCAGCACTT 78222        T   C
            T                   AAAGTGCTG GATTG AGGTGTG
                                ||||||||| ||||| |||||||
                                TTTCACGAC CTAAT TCCACAC
                                      C    A
GAM611   LOC147669 3'  CACACCTGTAATCCCAGCACTT 84058        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC148936 3'  CACACCTGTAATCCCAGCACTT 84288        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC148938 3'  CACACCTGTAATCCCAGCACTT 84267        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC149705 3'  CACACCTGTAATCCCAACACTT 84622       C  T
            T                   AAAGTG TG GATTGCAGGTGTG
                                |||||| || ||||||||||||
                                TTTCAC AC CTAATGTCCACAC
                                   A  C
GAM611   LOC150481 3'  CACACCTGTAATCCCAGCACTT 79882        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC151429 3'  CACACCTGTAATCCCAGCACTT 85346         T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC151614 3'  CACACCTGTAATCCCAGCACTT 80302         T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC151623 3'  CACCTGTAATCCCAGCACTTT  85457         T
                                AAAGTGCTG GATTGCAGGTG
                                ||||||||| ||||||||||
                                TTTCACGAC CTAATGTCCAC
                                      C
GAM611   LOC151632 3'  CACACCTGTGATCTCAGCAC   85464       T  TG
                                GTGCTG GAT  CAGGTGTG
                                |||||| |||  ||||||||
                                CACGAC CTA  GTCCACAC
                                   T  GT
GAM611   LOC152263 3'  CACACCTGTAATCCCAGCACTT 85672         T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC152317 3'  CACACCTGTAACCCCAACACTT 85637       C  TGA
            T                   AAAGTG TG   TTGCAGGTGTG
                                |||||| ||   ||||||||||
                                TTTCAC AC   AATGTCCACAC
                                   A  CCC
GAM611   LOC152860 3'  CACACCTATAATCCCAGCACTT 80697         T    C
            T                   AAAGTGCTG GATTG AGGTGTG
                                ||||||||| ||||| |||||||
                                TTTCACGAC CTAAT TCCACAC
                                      C    A
GAM611   LOC153260 3'  CACACCTGTAATCCCAGCACTT 80802         T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC154092 3'  CACATCTGTAATCCCAGCACTT 86159         T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCTACAC
                                      C
GAM611   LOC154992 3'  CACATTCGTAATCCCAGCACTT 81211         T    AG
            T                   AAAGTGCTG GATTGC  GTGTG
                                ||||||||| ||||||  |||||
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                                TTTCACGAC CTAATG  TACAC
                                    C     CT
GAM611   LOC155072 3'  CACACCTGTAATCCCAGCACTT 86372        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM611   LOC155376 3'  CACACTTGTAATCCCAGCACTT 81335        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTTCACAC
                                     C
GAM611   LOC157278 3'  CACACCTGTAATCCCAGCACTT 86422        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM611   LOC158288 3'  CTGTAATCACAGCACTTT    86713
                                 AAAGTGCTGTGATTGCAG
                                 ||||||||||||||||||
                                 TTTCACGACACTAATGTC

GAM611   LOC158819 5'  CACACCTGTAATCCCAGCACTT 86902        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM611   LOC158863 3'  CACACCTGTAATCCCAACACTT 86922      C  T
           T                     AAAGTG TG GATTGCAGGTGTG
                                 |||||| || ||||||||||||
                                 TTTCAC AC CTAATGTCCACAC
                                    A  C
GAM611   LOC158987 3'  CACACCTGTTATCCCAGCACTT 86959        T  T
           T                     AAAGTGCTG GAT GCAGGTGTG
                                 ||||||||| ||| |||||||||
                                 TTTCACGAC CTA TGTCCACAC
                                     C   T
GAM611   LOC167555 3'  CACACCCGTAATCCCAGCACTT 82678        T    A
           T                     AAAGTGCTG GATTGC GGTGTG
                                 ||||||||| |||||| ||||||
                                 TTTCACGAC CTAATG CCACAC
                                     C     C
GAM611   LOC196027 3'  CACACCTGTAATCTCAGCACTT 87547        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     T
GAM611   LOC196415 5'  CACCTGTAATCCCAGCACTTT  89630        T
                                 AAAGTGCTG GATTGCAGGTG
                                 ||||||||| ||||||||||
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                                TTTCACGAC CTAATGTCCAC
                                      C
GAM611  LOC196528 3'  CACCTATAATCCCAGCACTTT  87763        T    C
                                AAAGTGCTG GATTG AGGTG
                                ||||||||| ||||| |||||
                                TTTCACGAC CTAAT TCCAC
                                      C    A
GAM611  LOC196738 3'  CACAGTACTAATCACAGCAT   87503          CAGG
                                GTGCTGTGATTG   TGTG
                                ||||||||||||   ||||
                                TACGACACTAAT   ACAC
                                       CATG
GAM611  LOC197319 3'  CACACCTGTAATCCCAGCACTT 87967        T
          T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  LOC199786 3'  CACACCTGTAATCCCAGCACTT 88368        T
          T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  LOC200301 3'  CACACCTTGCCACAGCACT    88737        ATT  _
                                AGTGCTGTG   GCA GGTGTG
                                |||||||||   ||| ||||||
                                TCACGACAC   CGT CCACAC
                                      ___   T
GAM611  LOC200904 3'  CACACCTGTGATCTCAGCAC   90185      T   TG
                                GTGCTG GAT  CAGGTGTG
                                |||||| |||  ||||||||
                                CACGAC CTA  GTCCACAC
                                    T  GT
GAM611  LOC200918 3'  CACAGCTGTAATCCCAGCACT  88938       T      G
                                AGTGCTG GATTGCAG TGTG
                                ||||||| |||||||| ||||
                                TCACGAC CTAATGTC ACAC
                                     C       G
GAM611  LOC201685 3'  CACACCTGTAATCCCAGCACTT 90240        T
          T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  LOC201689 3'  CACACCTGTAATCCCAGCACTT 67142        T
          T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  LOC201895 3'  CACACCTGTAATCCCAGCACTT 89086        T
          T                     AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611   LOC202868 3'  CACACCTGTAATCCCAGCACTT 90370        T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM611   LOC203083 3'  CACACCTGTGATCTCAGCAC  90461      T  TG
                                 GTGCTG GAT  CAGGTGTG
                                 |||||| |||  ||||||||
                                 CACGAC CTA  GTCCACAC
                                    T  GT
GAM611   LOC219406 3'  CACACCTGCAATCCCAGCTACT 93558    _  T
                                 AGT GCTG GATTGCAGGTGTG
                                 ||| |||| ||||||||||||
                                 TCA CGAC CTAACGTCCACAC
                                   T   C
GAM611   LOC219722 5'  CACACCTGTAATCCCAGCACTT 93080        T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM611   LOC220506 3'  CACACCTATAATCCCAGCACTT 74075        T   C
            T                    AAAGTGCTG GATTG AGGTGTG
                                 ||||||||| ||||| |||||||
                                 TTTCACGAC CTAAT TCCACAC
                                     C    A
GAM611   LOC220575 3'  CACACTTGTAATCACTGCACTT 76307       T
            T                    AAAGTGC GTGATTGCAGGTGTG
                                 ||||||| ||||||||||||||||
                                 TTTCACG CACTAATGTTCACAC
                                    T
GAM611   LOC220662 3'  CACACCTGTAATCCCAGCACTT 91163        T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM611   LOC221271 3'  CACACCTGTAATCCCAGCACTT 91849        T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                     C
GAM611   LOC221410 3'  CACACCTGTAATCCAAGCACTT 92056       GT
            T                    AAAGTGCT  GATTGCAGGTGTG
                                 ||||||||  ||||||||||||
                                 TTTCACGA  CTAATGTCCACAC
                                     AC
GAM611   LOC221489 3'  CACACCTGTAATCCCAGCACTT 93638        T
            T                    AAAGTGCTG GATTGCAGGTGTG
                                 ||||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                     C
GAM611   LOC221543 5'  CACACCTGTAATCCCAGCACT  93736       T
                                AGTGCTG GATTGCAGGTGTG
                                ||||||| |||||||||||||
                                TCACGAC CTAATGTCCACAC
                                     C
GAM611   LOC221543 3'  CACACCTGTAATCCCAGCACTT 93737        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||||| |||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC221641 3'  CACACTTATCATCTCAGCACTT 93725        T  TGC
           T                     AAAGTGCTG GAT   AGGTGTG
                                 |||||||||| |||   |||||||
                                 TTTCACGAC CTA   TTCACAC
                                       T  CTA
GAM611   LOC221795 3'  CACACCTGTGATCTCAGCAC   92475      T  TG
                                GTGCTG GAT  CAGGTGTG
                                |||||| |||  ||||||||
                                CACGAC CTA  GTCCACAC
                                    T  GT
GAM611   LOC221954 5'  CACACCTGTAATCCCAGCACTT 93998        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||||| |||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC221962 3'  CACACCTGTAATCCCAGCACTT 92679        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||||| |||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC253532 3'  CACACTTGTAATCCCAGCACTT 96027        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||||| |||||||||||||
                                 TTTCACGAC CTAATGTTCACAC
                                      C
GAM611   LOC254176 3'  CACACCTGTGATCTCAGCAC   97338      T  TG
                                GTGCTG GAT  CAGGTGTG
                                |||||| |||  ||||||||
                                CACGAC CTA  GTCCACAC
                                    T  GT
GAM611   LOC254531 5'  CACACCTGTAATCCCAGCACTT 94982        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||||| |||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC254875 3'  CACACTTGTAATCCCAGCACTT 96057        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||||| |||||||||||||
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                                TTTCACGAC CTAATGTTCACAC
                                      C
GAM611   LOC255177 3'  CACACCTGTAATCCCAGCACTT 96601        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC255231 3'  CACACCTGTAATCCCAGCACTT 95372        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC255461 3'  CACACCTGTAATCCCAGCACTT 97317        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC255516 3'  CACACCTGTAATCCCAGCACTT 97330        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC255624 3'  CACACCTGTAATCCCAGCACTT 94521        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC255671 3'  CACATCTGTAATCCCAGCACTT 97252        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCTACAC
                                      C
GAM611   LOC256515 3'  CACACCTGTGATCTCAGCAC  96460      T  TG
                                GTGCTG GAT  CAGGTGTG
                                |||||| |||  ||||||||
                                CACGAC CTA  GTCCACAC
                                    T  GT
GAM611   LOC257596 3'  CACACCTGTAATCCCAGCACTT 97930        T
            T                   AAAGTGCTG GATTGCAGGTGTG
                                ||||||||| ||||||||||||
                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC257596 5'  CACACCTGTAATCCCAGCACT  97929       T
                                AGTGCTG GATTGCAGGTGTG
                                ||||||| ||||||||||||
                                TCACGAC CTAATGTCCACAC
                                      C
GAM611   LOC90072  3'  CACACCTGCAATCCCACCACTT 61291      C  T
            T                   AAAGTG TG GATTGCAGGTGTG
                                |||||| || ||||||||||||
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                                TTTCAC AC CTAACGTCCACAC
                                   C  C
GAM611  LOC90092  3'  CACACCTGTAATCCCAGCACTT 61400        T
                                AAGTGCTG GATTGCAGGTGTG
                                |||||||| ||||||||||||
                                TTCACGAC CTAATGTCCACAC
                                   C
GAM611  LOC90092  3'  CACACCTGTAATCCCAGCACTT 61401        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                    C
GAM611  LOC90141  3'  CATGCCTACAATCCCAGCACTT 61626        T    C
           T                     AAAGTGCTG GATTG AGGTGTG
                                 |||||||| ||||| |||||||
                                 TTTCACGAC CTAAC TCCGTAC
                                    C    A
GAM611  LOC90538  3'  CACATCTGTAATCCCAGCACTT 63187        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCTACAC
                                    C
GAM611  LOC90639  3'  CACGCCTGCAATCCCAGCACTT 63652         T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||| ||||||||||||
                                 TTTCACGAC CTAACGTCCGCAC
                                    C
GAM611  LOC90979  3'  CACACCTGTAATCCCAGCACTT 64524        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCCACAC
                                    C
GAM611  LOC91574  3'  CACATCTGTAATCCCAGCACTT 66518        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||| ||||||||||||
                                 TTTCACGAC CTAATGTCTACAC
                                    C
GAM611  LOC91862  3'  CACACCTGTAACCCCAGCACTT 53464        TGA
           T                     AAAGTGCTG   TTGCAGGTGTG
                                 |||||||||   ||||||||||
                                 TTTCACGAC   AATGTCCACAC
                                    CCC
GAM611  LOC92078  3'  CACACCTATAATCCCAGCACTT 67974        T    C
           T                     AAAGTGCTG GATTG AGGTGTG
                                 |||||||| ||||| |||||||
                                 TTTCACGAC CTAAT TCCACAC
                                    C    A
GAM611  LOC92267  3'  CACACCTGTAATCCCAGCACTT 68605        T
           T                     AAAGTGCTG GATTGCAGGTGTG
                                 |||||||| ||||||||||||
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                                TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  LOC92299  3'  CACACCTGTAATCTCAGCACTT 68807         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      T
GAM611  LOC92573  5'  CACACCTGTAATCCCAGCACTT 69802         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM611  LOC93132  5'  CACACCTGTAATCCCAGCACTT 71483         T
           T                   AAAGTGCTG GATTGCAGGTGTG
                               ||||||||| ||||||||||||
                               TTTCACGAC CTAATGTCCACAC
                                      C
GAM612  AF1Q     3'  TCTGACTCGACATCTTGTCCC  22369            CGCATG
                               GGGACAAGATGTTG     CAGA
                               ||||||||||||||     ||||
                               CCCTGTTCTACAGC     GTCT
                                        TCA___
GAM612  EN2      5'  CTGCATGCGCGCAGCTCTCGCC 7461      ACA  T __
           C                    GGG  AGA GT  TGCGCATGCAG
                               |||  ||| ||  ||||||||||
                               CCC  TCT CG  GCGCGTACGTC
                                 GC_  _  AC
GAM612  SLC22A12  3'  CGCACTGCCACTTGTCCC    58068        ATGT  C  _  A
                               GGGACAAG    TG GCA TGC G
                               ||||||||    || ||| ||| |
                               CCCTGTTC    AC CGT ACG C
                                    ____ _  C  C
GAM612  ZNF76    3'  TCTGCATGGCCACTCTTGCCC  12813     A    T  T  G
                               GGG CAAGA GT GC CATGCAGA
                               ||| ||||| || || ||||||||
                               CCC GTTCT CA CG GTACGTCT
                                 _    _ C  _
GAM612  C9orf7   3'  CTGGGTCAGCAGCATCCCACCC 34171     ACAA      GC  G
                               GGG   GATGTTGC  AT CAG
                               |||   ||||||||  || |||
                               CCC   CTACGACG  TG GTC
                                 ACC_       AC  G
GAM612  CAMK2G   3'  CTGCATGCAGCCCTCCCGCCC  68964     ACAA  TGTT  _
                               GGG   GA   GC GCATGCAG
                               |||   ||   || ||||||||
                               CCC   CT   CG CGTACGTC
                                 GCC_  CC__  A
GAM612  DDX34    3'  CTGCATGCGCCCCTCACGCCC  27981     ACAA  TGTT
                               GGG   GA   GCGCATGCAG
                               |||   ||   ||||||||||
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                                CCC   CT   CGCGTACGTC
                                  GCA_  CCC_
GAM612  DKFZp547E052 3'  TCTGCTATAACACATCTTGCCC 50100     A      TGCGCAT
                                GGG CAAGATGT      GCAGA
                                ||| ||||||||      |||||
                                CCC GTTCTACA      CGTCT
                                  _       CAATAT_
GAM612  FBXO21   3'  TCTGCATGCAGTATTCTCACCC 53242     ACA   TGT   _
                                GGG   AGA   TGC GCATGCAGA
                                |||   |||   ||| |||||||||
                                CCC   TCT   ATG CGTACGTCT
                                  AC_   T__   A
GAM612  FEM-2    3'  CTGCATGCCCAGCCTTACCCC  27578     AC   AT   C
                                GGG  AAG  GTTG GCATGCAG
                                |||  |||  |||| ||||||||
                                CCC  TTC  CGAC CGTACGTC
                                  CA   __   C
GAM612  FLJ12681  3'  CAGGCCAACCCTTGTCCC    42872        AT   C  A
                                GGGACAAG  GTTG GC TG
                                ||||||||  |||| || ||
                                CCCTGTTC  CAAC CG AC
                                     C_   _  G
GAM612  GNB4     3'  CTGCATCTGAACATCTTTCCC  41268      C       G  C
                                GGGA AAGATGTT CG ATGCAG
                                |||| |||||||| || ||||||
                                CCCT TTCTACAA GT TACGTC
                                  _       _ C
GAM612  HSJ1     3'  TCTGCATGCTGAGCCCCATC   22138      TT  ___
                                GATG  GC   GCATGCAGA
                                ||||  ||   |||||||||
                                CTAC  CG   CGTACGTCT
                                  CC  AGT
GAM612  NYD-SP17  5'  TCTGTTTTCCAACACCTTGCCT 50879     A   A    CGCAT
                                GGG CAAG TGTTG    GCAGA
                                ||| |||| |||||    |||||
                                TCC GTTC ACAAC    TGTCT
                                  _   C    CTTT_
GAM612  SLC17A6   3'  GCACAACATCTCATCCT     39744      CA      C
                                GGGA  AGATGTTG GC
                                ||||  |||||||| ||
                                TCCT  TCTACAAC CG
                                  AC       A
GAM612  TRPV5    5'  CTGCATGCACACACACCACC   39047    GACAAGA  _  C
                                GG      TGT TG GCATGCAG
                                ||      ||| || ||||||||
                                CC      ACA AC CGTACGTC
                                 ACC_____   C  A
GAM612  LOC148987 3'  TGGGCAGCATCCTATCCC    79122      CAA      G
                                GGGA   GATGTTGC CA
                                ||||   |||||||| ||
```

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                                CCCT   CTACGACG GT
                                  ATC       G
GAM612  LOC152641 5'  TCTGCATGCGCATTCCTCGCGC 80635    ACAA  TGT_
          C                     GG    GA    TGCGCATGCAGA
                                ||    ||    ||||||||||||
                                CC    CT    ACGCGTACGTCT
                                 GCG_  CCTT
GAM612  LOC253980 3'  GCCAACACTTGTCCC       95072         A    C
                                GGGACAAG TGTTG GC
                                |||||||| ||||| ||
                                CCCTGTTC ACAAC CG
                                      _    _
GAM612  LOC254556 3'  TGCCTAACATCTGCCC      94619     A  A      C
                                GGG CA GATGTTG GCA
                                ||| || ||||||| |||
                                CCC GT CTACAAT CGT
                                 _ _      C
GAM613  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A     T__
GAM613  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875        CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM613  FDFT1    3'  TAGGAAAGTGAAATG       15518            A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                      _
GAM613  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM613  KLF4     3'  TCCCAGACAGTGGATATG     14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM613  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                       A
GAM613  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
```

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                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM613  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM613  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM613  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM613  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM613  FLJ23462  3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM613  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM613  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM613  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM613  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM613  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598         CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
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                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM613  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM613  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG 48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                     TA__    TT
GAM613  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A     TC
GAM613  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                     AAAGG
GAM613  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM613  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM613  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM613  LOC222134 5'  ACAGTGAAGTGAAATG       94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                      _
GAM614  NFIA     3'  ACTACTACTACTACTGTTC    70366     G       C
                                GAA TAGTAGTAG AGTAGT
                                ||| ||||||||| ||||||
                                CTT GTCATCATC TCATCA
                                  _       A
GAM614  RDX      3'  ACTACCTCACTACTACATCT   11276     A      _  CA
                                AGA GTAGTAGT AG  GTAGT
                                ||| |||||||| ||  |||||
```

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                                TCT CATCATCA TC  CATCA
                                  A       C  __
GAM614  RRM2B    3'  ACTACTACTGTTAGCACCACTA 67823       A  ___
            CT                    AGTAGT GT   AGCAGTAGTAGT
                                  |||||| ||   ||||||||||||
                                  TCATCA CA   TTGTCATCATCA
                                    C  CGA
GAM614  STATH    3'  TATCACACTACTACCACTTTT  12028       A      CA  A
                                  AGAAGT GTAGTAG  GT GTA
                                  |||||| |||||||  || |||
                                  TTTTCA CATCATC  CA TAT
                                     C      A_  C
GAM614  TM4SF4   3'  ACTGCCATACTACTTCT     16068          GTA
                                  AGAAGTAGTA   GCAGT
                                  ||||||||||   |||||
                                  TCTTCATCAT   CGTCA
                                        AC_
GAM614  BIKE     3'  ACTCTGCTACTACTGC      34182            T
                                  GTAGTAGTAGCAG AGT
                                  |||||||||||||| |||
                                  CGTCATCATCGTC TCA
                                                _
GAM614  C3IP1    3'  ACTACTACACTATTACACTTC  41279       A      CA
                                  GAAGT GTAGTAG  GTAGTAGT
                                  ||||| |||||||  ||||||||
                                  CTTCA CATTATC  CATCATCA
                                     _      A_
GAM614  FLJ10482 3'  GCTGCTACTCTACCACTTC    36163       A  __
                                  GAAGT GT  AGTAGCAGT
                                  ||||| ||  |||||||||
                                  CTTCA CA  TCATCGTCG
                                     C  TC
GAM614  FLJ14399 3'  ACTACTACTGGACTACTAGCCT 51330     A  _     AG
            C                      GA GT AGTAGT  CAGTAGTAGT
                                  || || ||||||  ||||||||||
                                  CT CG TCATCA  GTCATCATCA
                                   C  A     G_
GAM614  HSNOV1   3'  TGCTATTACTACTTCT      34016
                                  AGAAGTAGTAGTAGCA
                                  ||||||||||||||||
                                  TCTTCATCATTATCGT

GAM614  KIAA1244 3'  ACTTAAACTACTACTACTGTCT 71985     _         CAGT
                                  AGA AGTAGTAGTAG    AGT
                                  ||| ||||||||||    |||
                                  TCT TCATCATCATC    TCA
                                    G          AAAT
GAM614  KIAA1866 3'  ACTACCATGCAGCCCACCACTA 60931       A  A_  A  __
            CT                     AGTAGT GT  GC GTA  GTAGT
                                  ||||||  ||  ||  |||  |||||
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                                TCATCA CA  CG CGT  CATCA
                                   C  CC  A   AC
GAM614  PROL3    3'  ACTACCCTTGTAACTACTGCTT 21934          A    TA
             CT                   AGAAGTAGTAGT GCAG  GTAGT
                                  |||||||||||| ||||  |||||
                                  TCTTCGTCATCA TGTT  CATCA
                                         A    CC
GAM614  LOC153937 5'  CTGCTACTACTCCTCT      81006     A T
                                  AGA G AGTAGTAGCAG
                                  ||| | ||||||||||
                                  TCT C TCATCATCGTC
                                    _ C
GAM614  LOC203378 5'  ACTGCTACCACCACTTT     90591       A  A
                                  GAAGT GT GTAGCAGT
                                  ||||| || ||||||||
                                  TTTCA CA CATCGTCA
                                     C  C
GAM614  LOC206012 5'  ACTACTCAAACTACTACTACT  89523          CAGT
                                  AGTAGTAGTAG    AGTAGT
                                  ||||||||||    ||||||
                                  TCATCATCATC    TCATCA
                                         AAAC
GAM614  LOC90342  5'  TACTACCAGCTCTTCT     62362      TAGTAGT   A_
                                  AGAAG      AGC  GTAGTA
                                  |||||      |||  ||||||
                                  TCTTC      TCG  CATCAT
                                     ________  AC
GAM615  ACADVL    3'  CCAGTTATGTGCCTTCCCTCAA 3413     G   A      ____
             G                     CT GAG GAAGGCAC    TTGG
                                  || ||| ||||||||    ||||
                                  GA CTC CTTCCGTG    GACC
                                   A   C       TATT
GAM615  ALDH3B1   3'  TCCCTCTTCTCTCCAG      91533           CACTT
                                  CTGGAGAGAAGG     GGA
                                  ||||||||||||     |||
                                  GACCTCTCTTCT     CCT
                                         C____
GAM615  ALPPL2    3'  CCCTGCTCCCCACCTCCAGTC  68840        AGAA__    CTT
                                  GACTGGAG     GGCA   GG
                                  ||||||||     ||||   ||
                                  CTGACCTC     TCGT   CC
                                       CACCCC    C__
GAM615  APOD      5'  TCCAGGTCCCTTCTCCAG    7918         GA   C
                                  CTGGAGA  AGG ACTTGGA
                                  |||||||  ||| |||||||
                                  GACCTCT  TCC TGGACCT
                                     __   C
GAM615  APXL      3'  TTCCTCCTCCTCTCCAG     7933         A   CACTT
                                  CTGGAGAG AGG    GGAA
                                  |||||||| |||    ||||
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                                GACCTCTC TCC    CCTT
                                    C   T____
GAM615  AR      5'  TTCCCCCCCTCCCCCGTC    3497     T  A   AA  CACTT
                                GAC GG GAG  GG    GGAA
                                ||| || |||  ||    ||||
                                CTG CC CTC  CC    CCTT
                                  C  C   CC  _____
GAM615  ARHGEF1  3'  CCAAGTGCCTTCGCTC     16299     A
                                GAG GAAGGCACTTGG
                                ||| ||||||||||||
                                CTC CTTCCGTGAACC
                                  G
GAM615  ASIC4    3'  TTCCTGCCCCTCTCCAG     37923        AA   CTT
                                CTGGAGAG  GGCA   GGAA
                                ||||||||  ||||   ||||
                                GACCTCTC  CCGT   CCTT
                                    C_    ___
GAM615  BCL6     5'  CCACTTCCTTCCCTCCAGTC   57221        A    CACT
                                GACTGGAG GAAGG    TGG
                                |||||||| |||||    |||
                                CTGACCTC CTTCC    ACC
                                    C     TTC_
GAM615  CABC1    5'  TCCACAGACTTCTCTTCAG    39659          GCACT
                                CTGGAGAGAAG     TGGA
                                ||||||||||     ||||
                                GACTTCTCTTC     ACCT
                                     AGAC_
GAM615  CACNA2D2  3'  TCCAAGTGCCCCCTCACCTCTC 20088    CT  A   AA
                                GA  GG GAG  GGCACTTGGA
                                ||  || |||  ||||||||||
                                CT  CC CTC  CCGTGAACCT
                                 CT  A   CC
GAM615  CALCR    3'  TCCAAATCTCCAGTC       8222          GAAGGCAC
                                GACTGGAGA       TTGGA
                                |||||||||       |||||
                                CTGACCTCT       AACCT
                                    A________
GAM615  CD3E     3'  CCCAGGTCTCCTCTCCAGTC   5589          A   A  T
                                GACTGGAGAG AGGC CT GG
                                |||||||||| |||| || ||
                                CTGACCTCTC TCTG GA CC
                                     C    _  C
GAM615  CDH5     3'  CCAACCCCTCTCCAG       8385         AA  CAC
                                CTGGAGAG  GG   TTGG
                                ||||||||  ||   ||||
                                GACCTCTC  CC   AACC
                                    C_   ___
GAM615  CENTD2   3'  TTCAGCCTTCCTTCCAGTC   57559        A     ACT
                                GACTGGAG GAAGGC   TGGA
                                |||||||| ||||||   ||||
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                                CTGACCTT CTTCCG   ACTT
                                     C     ___
GAM615  CENTD2   3'  TTCAGCCTTCCTTCCAGTC   30878        A     ACT
                                GACTGGAG GAAGGC   TGGA
                                |||||||| ||||||   ||||
                                CTGACCTT CTTCCG   ACTT
                                     C     ___
GAM615  CGTHBA   3'  CCTACGCTTCCCTCCAGTC   23861        A   G ACTT
                                GACTGGAG GAAG C    GG
                                |||||||| |||| |    ||
                                CTGACCTC CTTC G    CC
                                     C    _ CAT_
GAM615  CLCN4    5'  CTTCCAGGGTCTTCCCCCCA  8444      AGA     A
                                TGG   GAAGGC CTTGGAAG
                                |||   |||||| ||||||||
                                ACC   CTTCTG GGACCTTC
                                  CCC     _
GAM615  COL1A1   3'  TTCCACCCTCTCTCCA      3610         A  CACT
                                TGGAGAGA GG    TGGAA
                                |||||||| ||    |||||
                                ACCTCTCT CC    ACCTT
                                     C  _____
GAM615  DIRC1    3'  CCTCTTGCACTTTCTCTCCAGT 53666          _ _   CTT
              C                  GACTGGAGAGAA G GCA   GG
                                ||||||||||||| | |||   ||
                                CTGACCTCTCTT C CGT   CC
                                       T A   TCT
GAM615  EGFL3    3'  CCGTGGAGCCCGCCTCTCCAGT 62614          AA_   A  _
              C                  GACTGGAGAG   GGC CT TGG
                                ||||||||||   ||| || |||
                                CTGACCTCTC   CCG GG GCC
                                      CGC   A  T
GAM615  EPB49    3'  CTTCCAAGCCTTTTGCTCCAG  8786        _      AC
                                CTGGAG AGAAGGC  TTGGAAG
                                ||||||  |||||||  |||||||
                                GACCTC TTTTCCG  AACCTTC
                                   G      __
GAM615  EPHA2    3'  CCAAGCCGACCTTCCCTCC    15402      A    CA__
                                GGAG GAAGG    CTTGG
                                |||| |||||    |||||
                                CCTC CTTCC    GAACC
                                  C     AGCC
GAM615  FGR      3'  TCCCTCACTTCTCTCCTATC   17897    CT       GCACTT
                                GA  GGAGAGAAG     GGA
                                ||  |||||||||     |||
                                CT  CCTCTCTTC     CCT
                                 AT        ACTC__
GAM615  GPR86    3'  TCCAAACACCTTCTCACATTC  43652    C  GA      CAC
                                GA TG  GAGAAGG   TTGGA
                                || ||  |||||||   |||||
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                                CT AC  CTCTTCC   AACCT
                                 T  A_      ACA
GAM615  GRAF    3'  CTTTCAGGTACCCCCTCCCCAG 30559      A   AA  C
                                CTGG GAG  GG ACTTGGAAG
                                |||| |||  || |||||||||
                                GACC CTC  CC TGGACTTTC
                                  C   CC  A
GAM615  GSTT2   3'  CCCAGTCCCTTCTCTCCAG   5959           C   T
                                CTGGAGAGAAGG ACT GG
                                |||||||||||| ||| ||
                                GACCTCTCTTCC TGA CC
                                       C   C
GAM615  KRT5    3'  CTTCCAAGTGCAGCAACCCAG  4711      AGAGAAG
                                CTGG      GCACTTGGAAG
                                ||||      ||||||||||
                                GACC      CGTGAACCTTC
                                  CAACGA_
GAM615  LOXL2   3'  CTTCCAATGAAACCCTCCAGTC 9795         AGAAGG  C
                                GACTGGAG     CA TTGGAAG
                                ||||||||     || |||||||
                                CTGACCTC     GT AACCTTC
                                    CCAAA_  _
GAM615  LY95    5'  CCAATTCCCTCTCCCCAGTC   16703       A   A  CAC
                                GACTGG GAGA GG   TTGG
                                |||||| |||| ||   ||||
                                CTGACC CTCT CC   AACC
                                   C    C  TT_
GAM615  MAF     5'  CCCCTCCCTCTCCTCCAGTC   18098        _  A  CACTT
                                GACTGGAG AGA GG    GG
                                |||||||| ||| ||    ||
                                CTGACCTC TCT CC    CC
                                    C   C  TCC__
GAM615  MGAT1   3'  TCCTGCCCTTCTCTCCTGTC   10012     T       _ CTT
                                GAC GGAGAGAAGG CA   GGA
                                ||| |||||||||| ||   |||
                                CTG CCTCTCTTCC GT   CCT
                                  T        C  ___
GAM615  MPP1    5'  TCCCGCCTTCTCCGCAG     10112     GA      ACTT
                                CTG  GAGAAGGC    GGA
                                |||  ||||||||    |||
                                GAC  CTCTTCCG    CCT
                                  GC       C___
GAM615  NOS1    3'  CCAAAGGCTTTCTTTCCAATC  5246     C         AC
                                GA TGGAGAGAAGGC  TTGG
                                || ||||||||||||  ||||
                                CT ACCTTTCTTTCG  AACC
                                 A          GA
GAM615  NPM1    5'  TCCGTCCGCCTTCTCTCC    10252          ACT
                                GGAGAGAAGGC   TGGA
                                ||||||||||   ||||
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                                CCTCTCTTCCG  GCCT
                                     CCT
GAM615  NRXN3   5'  TCCTCTTTCCCTCCAGTC   57281       A   CACTT
                                GACTGGAG GAAGG   GGA
                                |||||||| |||||    |||
                                CTGACCTC CTTTC   CCT
                                    C    T____
GAM615  OTP     3'  CCGCCGCCTCCCCTCCGGTC  49495       AGA   ACT
                                GACTGGAG  AGGC  TGG
                                ||||||||  ||||  |||
                                CTGGCCTC  TCCG  GCC
                                    CCC   CC_
GAM615  PES1    3'  TCCTCCTTTCTCCAG      26672        A  CACTT
                                CTGGAGAGA GG   GGA
                                ||||||||| ||   |||
                                GACCTCTTT CC   CCT
                                     _ T____
GAM615  PGM1    3'  AGTGCCTTCTGTCCAATC   10537   C   G
                                GA TGGA AGAAGGCACT
                                || |||| ||||||||||
                                CT ACCT TCTTCCGTGA
                                 A   G
GAM615  PKIG    3'  CCAACACCTCCTCTCCAG   22959       A  CAC
                                CTGGAGAG AGG  TTGG
                                |||||||| |||  ||||
                                GACCTCTC TCC  AACC
                                    C  AC_
GAM615  PKLR    3'  CCATCCCTTCCTCCCCAGTC  4315       A  _   CACT
                                GACTGG GAG AAGG   TGG
                                |||||| ||| ||||   |||
                                CTGACC CTC TTCC   ACC
                                   C  C   CT__
GAM615  PRDM1   5'  CCAAGTGTAACTCCAGC    6826   A    AGAAG
                                G CTGGAG   GCACTTGG
                                | ||||||   ||||||||
                                C GACCTC   TGTGAACC
                                _     AA___
GAM615  RARA    3'  CCCAGTTCTCCTCCTCAG   6365    GA  A  C  T
                                CTG  GAG AGG ACT GG
                                |||  ||| ||| ||| ||
                                GAC  CTC TCT TGA CC
                                  TC  C  _  C
GAM615  RFX1    3'  CCCAGCGTCTTCTCCCCAG  11309    A     A  T
                                CTGG GAGAAGGC CT GG
                                |||| |||||||| || ||
                                GACC CTCTTCTG GA CC
                                  C      C  C
GAM615  RORB    5'  TTCCTCCTCCTCCTCAGTC  22612    GA  A  CACTT
                                GACTG  GAG AGG   GGAA
                                |||||  ||| |||   ||||
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                                CTGAC  CTC TCC    CCTT
                                  TC   C   T____
GAM615  SAC     5'  CCGGCCTCCTCTCCTGTC    37313    T    A   ACT
                                GAC GGAGAG AGGC   TGG
                                ||| |||||| ||||   |||
                                CTG CCTCTC TCCG   GCC
                                  T     C   ___
GAM615  SEPN1   3'  CAGGCTGCCCCCTCCCCAG   66364     A   AA   _
                                CTGG GAG  GGCA CTTG
                                |||| |||  |||| ||||
                                GACC CTC  CCGT GGAC
                                  C   CC    C
GAM615  SNAI2   3'  CTTCCAAGTGCCTTTTT     11775
                                GAGAAGGCACTTGGAAG
                                |||||||||||||||||
                                TTTTTCCGTGAACCTTC

GAM615  SNRP70   5'  CCACCCCCTGCTCCAGTC    78547        _  AA  CACT
                                GACTGGAG AG  GG    TGG
                                |||||||| ||  ||    |||
                                CTGACCTC TC  CC    ACC
                                     G  CC  ____
GAM615  SOX13   3'  CCACTTCTCTCCAG        19081          GCACT
                                CTGGAGAGAAG     TGG
                                ||||||||||     |||
                                GACCTCTCTTC     ACC
                                          _____
GAM615  SOX13   3'  CCCCGTCTTCTCTCCATC    19082    C         ACTT
                                GA TGGAGAGAAGGC    GG
                                || ||||||||||||    ||
                                CT ACCTCTCTTCTG    CC
                                 _          CC__
GAM615  TBL3    3'  TCCGGCCTCTCTCCAGTC    21267          A   ACT
                                GACTGGAGAGA GGC   TGGA
                                |||||||||| |||   ||||
                                CTGACCTCTCT CCG   GCCT
                                          _  ___
GAM615  TNFAIP1  5'  CTTCCAAGCCTACCTCC     40920      AGA    AC
                                GGAG   AGGC  TTGGAAG
                                ||||   ||||  |||||||
                                CCTC   TCCG  AACCTTC
                                  CA_   __
GAM615  UBE2L3   3'  CCACACCCCTCCTCCAGTC   12499        A  A  CACT
                                GACTGGAG GA GG    TGG
                                |||||||| || ||    |||
                                CTGACCTC CT CC    ACC
                                     _  C  CAC_
GAM615  UBE4A    3'  CCATGCTGCCTCCAGTC     16562        AGAA    CT
                                GACTGGAG    GGCA  TGG
                                ||||||||    ||||  |||
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                                CTGACCTC   TCGT  ACC
                                    CG__   __
GAM615  ALOXE3   3'  CTTCCAAGCCTAGAGCCACCAG 41264     AGAGA__   AC
                                CTGG      AGGC  TTGGAAG
                                ||||      ||||  |||||||
                                GACC      TCCG  AACCTTC
                                  ACCGAGA   __
GAM615  AMOT     3'  TTCCAAGTGCCATCCA      55730      GAGAA
                                TGGA    GGCACTTGGAA
                                ||||    ||||||||||
                                ACCT    CCGTGAACCTT
                                  A____
GAM615  ARHGAP4  3'  CCCCTTGCTTCTCTCCAG    8019          G  CTT
                                CTGGAGAGAAG CA   GG
                                |||||||||| ||   ||
                                GACCTCTCTTC GT   CC
                                      _  TCC
GAM615  ART5     3'  CCTAGCAGCCTTCTCCCCA   53814     A      A_  T
                                TGG GAGAAGGC  CT GG
                                ||| ||||||||  || ||
                                ACC CTCTTCCG  GA CC
                                  C       AC  T
GAM615  ASB16    3'  TTCAGACCCTCTCTCCAGC   55111   A       A  CAC
                                G CTGGAGAGA GG   TTGGA
                                | |||||||| ||   |||||
                                C GACCTCTCT CC   GACTT
                                _       C  A__
GAM615  C20orf142 3'  TTGATGCCCCTCTCTCCAATC  74790    C      A_   C TG
                                GA TGGAGAGA  GGCA T  G
                                || ||||||||  |||| |  |
                                CT ACCTCTCT  CCGT A  T
                                 A       CC    _ GT
GAM615  DKFZP434H132 5'  TCCCAGCACCCTCTCCAG    73609        AA  CA  T
                                CTGGAGAG  GG  CT GGA
                                |||||||  ||  || |||
                                GACCTCTC  CC  GA CCT
                                     __  AC  C
GAM615  DKFZP566H073 3'  CCGTCGTCTTCCCTCCAGTC   31381        A     ACT
                                GACTGGAG GAAGGC   TGG
                                ||||||| ||||||   |||
                                CTGACCTC CTTCTG   GCC
                                     C     CT_
GAM615  E1B-AP5  3'  TCCCACTGCCTCCTCTCCAGT  22904         A    CTT
                                ACTGGAGAG AGGCA   GGA
                                ||||||||| |||||   |||
                                TGACCTCTC TCCGT   CCT
                                      C     CAC
GAM615  E1B-AP5  3'  TCCCACTGCCTCCTCTCCAGT  58570         A    CTT
                                ACTGGAGAG AGGCA   GGA
                                ||||||||| |||||   |||
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                                TGACCTCTC TCCGT   CCT
                                     C    CAC
GAM615  E2IG4    3' CCAAGTGCCTTCCCTC     90909    A
                                GAG GAAGGCACTTGG
                                ||| ||||||||||||
                                CTC CTTCCGTGAACC
                                  C
GAM615  EPN2     3' CTGAGGCCGCCCTCTCCAGTC 30323        AA_  A  TG
                                GACTGGAGAG  GGC CT  G
                                ||||||||||  ||| ||  |
                                CTGACCTCTC  CCG GA  C
                                      CCG  _ GT
GAM615  EPN2     3' CTTCCAAGGCAGGCCCCTC  30325    AA  A___
                                GAG  GGC   CTTGGAAG
                                |||  |||   ||||||||
                                CTC  CCG   GAACCTTC
                                  C_  GACG
GAM615  FLJ10700 3' CCTCTCGTCCTCCCCTCCAGC 36427   A    A_ A  ACTT
                                G CTGGAG  GA GGC   GG
                                | ||||||  || |||   ||
                                C GACCTC  CT CTG   CC
                                 _    CC  C  CTCT
GAM615  FLJ11320 3' CCCCTCCCTCTCCAGTC    37244        A_  CACTT
                                GACTGGAGAG  AGG   GG
                                ||||||||||  |||   ||
                                CTGACCTCTC  TCC   CC
                                      CC  _____
GAM615  FLJ12595 3' TCCCACTGTTCTCTCCACTC  46507   C     AG  CTT
                                GA TGGAGAGA  GCA  GGA
                                || ||||||||  |||  |||
                                CT ACCTCTCT  TGT  CCT
                                 C      __  CAC
GAM615  FLJ12650 3' TTCCTCTCTTCTCCAG     44531      GA  CACTT
                                CTGGAGA  AGG   GGAA
                                |||||||  |||   ||||
                                GACCTCT  TCT   CCTT
                                    TC  _____
GAM615  FLJ14100 5' CCTCGCCCTCTCCAGTC    46677        AA  ACTT
                                GACTGGAGAG  GGC   GG
                                ||||||||||  |||   ||
                                CTGACCTCTC  CCG   CC
                                      __  CT__
GAM615  FLJ14827 3' CTAAGATGCCTCTCTCCAG  51652        A  _
                                CTGGAGAGA GGCA CTTGG
                                ||||||||| |||| |||||
                                GACCTCTCT CCGT GAATC
                                      _  A
GAM615  FLJ21034 3' CCATGCCACCTCCCTTCCAGTC 46293       ___  AA  CT
                                GACTGGA  GAG  GGCA  TGG
                                |||||||  |||  ||||  |||
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                                CTGACCT  CTC  CCGT  ACC
                                   TCC  CA   __
GAM615  FLJ22596  5'  CCACCTTCTCTCCA      46960         CACT
                                TGGAGAGAAGG   TGG
                                ||||||||||   |||
                                ACCTCTCTTCC   ACC
                                      ____
GAM615  GEMIN7   3'  TCCTCTCTTCTCTCCAG    45236         CACTT
                                CTGGAGAGAAGG    GGA
                                ||||||||||||    |||
                                GACCTCTCTTCT    CCT
                                      CT___
GAM615  ITGB8    5'  CTTGCAGAGCCCTCTCTCCAGT 9406          A  A  T G
          C                      GACTGGAGAGA GGC CT G AAG
                                ||||||||||| ||| || | |||
                                CTGACCTCTCT CCG GA C TTC
                                      C  A  _ G
GAM615  KIAA0321  3'  TCCTGCTTCCCTTCAGTC    62398       A   G  CTT
                                GACTGGAG GAAG CA  GGA
                                |||||||| |||| ||  |||
                                CTGACTTC CTTC GT  CCT
                                   C   _ ___
GAM615  KIAA0436  3'  TCCAGGCCTCCCTTCCAGTC  60057       AGA   A  T
                                GACTGGAG  AGGC CT GGA
                                ||||||||  |||| || |||
                                CTGACCTT  TCCG GA CCT
                                   CCC   _ _
GAM615  KIAA0574  3'  CCCAGAGCCTTCCTCCAGTC  69280       A    A  T
                                GACTGGAG GAAGGC CT GG
                                |||||||| |||||| || ||
                                CTGACCTC CTTCCG GA CC
                                   _    A  C
GAM615  KIAA1049  5'  CTTCCTTCTCCCTCTCTCCAG 30365       A  CACTT
                                CTGGAGAGA GG   GGAAG
                                ||||||||| ||   |||||
                                GACCTCTCT CC   CCTTC
                                   C  TCTT_
GAM615  KIAA1128  3'  TCCCCCATCTCCAGTC     68484       GAA  CACTT
                                GACTGGAGA  GG   GGA
                                |||||||||  ||   |||
                                CTGACCTCT  CC   CCT
                                   AC_  _____
GAM615  KIAA1183  3'  CTGGGTGCCCCCTCTCCAGT  62533       AA    TG
                                ACTGGAGAG  GGCACT  G
                                |||||||||  ||||||  |
                                TGACCTCTC  CCGTGG  C
                                   CC    GT
GAM615  KIAA1190  3'  CCAAGTGCCCCCCCTTTCT   71099      AA__
                                GGAGAG   GGCACTTGG
                                ||||||   |||||||||
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                                TCTTTC   CCGTGAACC
                                   CCCC
GAM615  KIAA1271 3' CCTGTGGAGCTCCTCTCCAG  69541       A  G__  TT
                                CTGGAGAG AG   CAC  GG
                                |||||||| ||   |||  ||
                                GACCTCTC TC   GTG  CC
                                    C  GAG   T_
GAM615  KIAA1538 3' TTCCATCCCTTCTCCAG    71562       GA   CACT
                                CTGGAGA  AGG   TGGAA
                                |||||||  |||   |||||
                                GACCTCT  TCC   ACCTT
                                   __  CT__
GAM615  KIAA1656 3' CCACTTCCTTCCAGTC     65787       A   GCACT
                                GACTGGAG GAAG    TGG
                                |||||||| ||||    |||
                                CTGACCTT CTTC    ACC
                                    C   _____
GAM615  KIAA1762 5' TCCAGCCCCATCTCCAGTC  63791        GAA  ACT
                                GACTGGAGA  GGC  TGGA
                                |||||||||  |||  ||||
                                CTGACCTCT  CCG  ACCT
                                    ACC  ___
GAM615  KIAA1762 5' CCAACCCCCTTCTCCAG    63789       GA  CAC
                                CTGGAGA  AGG  TTGG
                                |||||||  |||  ||||
                                GACCTCT  TCC  AACC
                                   __  CCC
GAM615  KIAA1817 5' CCAACCCATCTCTCCA     68224       A  CAC
                                TGGAGAGA GG   TTGG
                                |||||||| ||   ||||
                                ACCTCTCT CC   AACC
                                    A  C__
GAM615  KIAA1855 3' TCCGACCCCTTTCCAG     92347       AA  CAC
                                CTGGAGAG  GG   TTGGA
                                |||||||  ||   |||||
                                GACCTTTC  CC   AGCCT
                                    C_  ___
GAM615  KIAA1881 3' CTTCCCAAGCCTTCTCCTCAG 95341    GA      ACTT
                                CTG  GAGAAGGC   GGAAG
                                |||  ||||||||   |||||
                                GAC  CTCTTCCG   CCTTC
                                  TC      AAC_
GAM615  KIAA1887 5' CCAAGGGGCAATGCCCCCTCTC 76772        AA   _______
           CAG                  CTGGAGAG  GGCA    CTTGG
                                |||||||| ||||    |||||
                                GACCTCTC  CCGT    GAACC
                                    CC   AACGGG
GAM615  KLHL6   3' CCTCTCACCCTCCTCCAGTC  55301        A  A  CACTT
                                GACTGGAG GA GG    GG
                                |||||||| || ||    ||
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                                CTGACCTC CT CC    CC
                                     _ C  ACTCT
GAM615  LIP8     5'  CCTCCCTTCTCCCAAGTC    88149     _ A     CACTT
                                GACT GG GAGAAGG    GG
                                |||| || |||||||    ||
                                CTGA CC CTCTTCC    CC
                                  A _     CT___
GAM615  MAPK8IP2 3'  CTTCCAAGTGATGCCCTCC   33156    AGAAGG
                                GGAG    CACTTGGAAG
                                ||||    ||||||||||
                                CCTC    GTGAACCTTC
                                  CCGTA_
GAM615  MAPK8IP2 3'  CTTCCAAGTGATGCCCTCC   24657    AGAAGG
                                GGAG    CACTTGGAAG
                                ||||    ||||||||||
                                CCTC    GTGAACCTTC
                                  CCGTA_
GAM615  MAPK8IP2 3'  CTTCCAAGTGATGCCCTCC   57466    AGAAGG
                                GGAG    CACTTGGAAG
                                ||||    ||||||||||
                                CCTC    GTGAACCTTC
                                  CCGTA_
GAM615  MGC4707  3'  CCAGCCTCCTCTCCAGC    44117   A     A   ACT
                                G CTGGAGAG AGGC   TGG
                                | |||||||| ||||   |||
                                C GACCTCTC TCCG   ACC
                                _       C    ____
GAM615  MGC5457  5'  TCCTTGCTCCTTTCCAGTC   50948        AA   CTT
                                GACTGGAGAG  GGCA   GGA
                                ||||||||||  ||||   |||
                                CTGACCTTTC  TCGT   CCT
                                      C_    T__
GAM615  MGC5590  3'  TCCCATCTCTCTCCCAGTC   43928      A   AG CACTT
                                GACTGG GAGA  G    GGA
                                |||||| ||||  |    |||
                                CTGACC CTCT  C    CCT
                                   _    CT TAC__
GAM615  MUC16    3'  CCTGGGGTGCCTTTCCCCCAG  60528    AGA       __
                                CTGG   GAAGGCACTT  GG
                                ||||   ||||||||||  ||
                                GACC   TTTCCGTGGG  CC
                                  CCC        GT
GAM615  PP1201   3'  TTGAGGCCCATCTCTCCAG   42195       A_   A  TG
                                CTGGAGAGA  GGC CT  G
                                |||||||||  ||| ||  |
                                GACCTCTCT  CCG GA  T
                                      AC   _  GT
GAM615  RGS11    3'  CCAAGTGCCTCACCAGTC    13824      A  GAA
                                GACTGG GA   GGCACTTGG
                                ||||||  ||   |||||||||
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                                CTGACC CT   CCGTGAACC
                                   A ___
GAM615  RIP5    3'  CCAAGTGCTCCCTATCCAGTC  38124       G  AA
                                GACTGGA AG  GGCACTTGG
                                ||||||| ||  |||||||||
                                CTGACCT TC  TCGTGAACC
                                   A  CC
GAM615  SAE1    3'  TTCCAAGCACCCCTCTGCC   18536   _   AA  CA
                                GG AGAG  GG  CTTGGAA
                                || ||||  ||  |||||||
                                CC TCTC  CC  GAACCTT
                                 G   C_  AC
GAM615  SCYD1   3'  CTGAGGCCCTTCTCTCCAG   90930         CA  TG
                                CTGGAGAGAAGG  CT  G
                                ||||||||||||  ||  |
                                GACCTCTCTTCC  GA  C
                                      CG  GT
GAM615  SEC24B  5'  CTTCCTCTCTCCTCTCCGG   20898       A   CACTT
                                CTGGAGAG AGG    GGAAG
                                |||||||| |||    |||||
                                GGCCTCTC TCT    CCTTC
                                   C   CT___
GAM615  SLC12A5  3'  CTTCCCACCCTCCTCTCCAGTC 40380        A   CACTT
                                GACTGGAGAG AGG    GGAAG
                                |||||||||| |||    |||||
                                CTGACCTCTC TCC    CCTTC
                                     C   CAC__
GAM615  SNTA1   3'  CTTCCTGCTGCCCCCCTCCA  11858     AGAA   CTT
                                TGGAG   GGCA   GGAAG
                                |||||   ||||   |||||
                                ACCTC   CCGT   CCTTC
                                  CCC_   CGT
GAM615  TESK2   3'  CCAGACCCTCTCCAGT     63180        AA  CAC
                                ACTGGAGAG  GG   TTGG
                                |||||||||  ||   ||||
                                TGACCTCTC  CC   GACC
                                     __ A__
GAM615  TRIM5   3'  TCCCAGTTTTCTCTCAAGTC  52363     G       ACTT
                                GACT GAGAGAAGGC   GGA
                                |||| ||||||||||   |||
                                CTGA CTCTCTTTTG   CCT
                                  A        AC__
GAM615  WBSCR23  3'  CCGTGCACCTCCACCTCCAG  46755      A__  AG_   TT
                                CTGGAG   GA   GCAC  GG
                                ||||||   ||   ||||  ||
                                GACCTC   CT   CGTG  CC
                                   CAC  CCA   __
GAM615  ZDHHC7   5'  TCGCACCGCCCCGCTCTCCAG  34846       AA_   ACT  _
                                CTGGAGAG   GGC   TG GA
                                ||||||||   |||   || ||
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                                GACCTCTC  CCG  AC CT
                                    GCC  CC_  G
GAM615  LOC112476 3'  TCCCTGCACTTCTTCCAG   59116     G   _  CTT
                                CTGGA AGAAG GCA  GGA
                                ||||| ||||| |||  |||
                                GACCT TCTTC CGT  CCT
                                  _   A  C__
GAM615  LOC120425 5'  TCCCCGCTCCACTCCAGTC   74010      AGAA  ACTT
                                GACTGGAG   GGC   GGA
                                ||||||||   |||   |||
                                CTGACCTC   TCG   CCT
                                    ACC_  CC__
GAM615  LOC126123 5'  TCCGCCCTCATCCCCAGTC   74437      A _ A  ACTT
                                GACTGG GA GA GGC   GGA
                                |||||| || || |||   |||
                                CTGACC CT CT CCG   CCT
                                   C  A  C  _____
GAM615  LOC144147 3'  CTTCTCACCTCCTCTCTAG   71730      A  CACTT
                                CTGGAGAG AGG    GGAAG
                                |||||||| |||    |||||
                                GATCTCTC TCC    TCTTC
                                    C  AC___
GAM615  LOC145725 5'  CCACAGCCCCACTCTCCAG   77401      AA_  ACT
                                CTGGAGAG  GGC  TGG
                                ||||||||  |||  |||
                                GACCTCTC  CCG  ACC
                                    ACC  AC_
GAM615  LOC145732 5'  CCACAGCCCCACTCTCCAG   77423      AA_  ACT
                                CTGGAGAG  GGC  TGG
                                ||||||||  |||  |||
                                GACCTCTC  CCG  ACC
                                    ACC  AC_
GAM615  LOC145813 5'  TCCAACATTCTCCCAATC    83513   C  A   GGCAC
                                GA TGG GAGAA    TTGGA
                                || ||| |||||    |||||
                                CT ACC CTCTT    AACCT
                                 A  _    AC___
GAM615  LOC146733 5'  CTTCCAAGATTCTTCCCTCCAT 83763   C    A    CA
          TC                     GA TGGAG GAAGG  CTTGGAAG
                                || ||||| |||||  ||||||||
                                CT ACCTC CTTCT  GAACCTTC
                                 T    C    TA
GAM615  LOC149132 5'  TCCCAGCCTTCTCTCCAG    79179          ACTT
                                CTGGAGAGAAGGC   GGA
                                ||||||||||||   |||
                                GACCTCTCTTCCG   CCT
                                       AC__
GAM615  LOC149606 3'  CTTCCATTCCTCTCTCTA    79451       A  CACT
                                TGGAGAGA GG   TGGAAG
                                |||||||| ||   ||||||
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                                ATCTCTCT CC    ACCTTC
                                    _ TT__
GAM615  LOC150793 3'  TCCCTTTCCCCCTCTCTCCAG  80014        A  CACTT_
                                CTGGAGAGA GG     GGA
                                ||||||||| ||     |||
                                GACCTCTCT CC     CCT
                                    C  CCTTTC
GAM615  LOC151996 5'  GAGCACCTTCCTCTCCAG    85533        _   CA
                                CTGGAGAG AAGG  CTT
                                |||||||| ||||  |||
                                GACCTCTC TTCC  GAG
                                    C    AC
GAM615  LOC158364 5'  CTTCCCTACACTTCTCTCCA   81876        GCACTT
                                TGGAGAGAAG     GGAAG
                                ||||||||||     |||||
                                ACCTCTCTTC     CCTTC
                                    ACATC_
GAM615  LOC158856 5'  CCACACCCCTCCCCAGTC    86913      A   AA  CACT
                                GACTGG GAG  GG    TGG
                                |||||| |||  ||    |||
                                CTGACC CTC  CC    ACC
                                   C   C_  AC__
GAM615  LOC162427 3'  CCAAGGGAGGCTTCTCTCCA   82349        GCA__
                                TGGAGAGAAG    CTTGG
                                ||||||||||    |||||
                                ACCTCTCTTC    GAACC
                                    GGAGG
GAM615  LOC196478 5'  CCACGGGCCCTCCCCCA     87725     A_  AA  A  _
                                TGG  GAG  GGC CT TGG
                                |||  |||  ||| || |||
                                ACC  CTC  CCG GG ACC
                                  CC   __   _  C
GAM615  LOC196957 5'  CCACAGCCCCACTCTCCAG   87818       AA_  ACT
                                CTGGAGAG   GGC   TGG
                                ||||||||   |||   |||
                                GACCTCTC   CCG   ACC
                                    ACC   AC_
GAM615  LOC196961 5'  CCACAGCCCCACTCTCCAG   87839       AA_  ACT
                                CTGGAGAG   GGC   TGG
                                ||||||||   |||   |||
                                GACCTCTC   CCG   ACC
                                    ACC   AC_
GAM615  LOC197138 5'  CCACAGCCCCACTCTCCAG   87912       AA_  ACT
                                CTGGAGAG   GGC   TGG
                                ||||||||   |||   |||
                                GACCTCTC   CCG   ACC
                                    ACC   AC_
GAM615  LOC200312 3'  TTTGGGACCTTCTCTGCAATC  89998    C  G      CA  TG
                                GA TG AGAGAAGG  CT  GA
                                || || ||||||||  ||  ||
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                                CT AC TCTCTTCC  GG  TT
                                 A  G       A_  GT
GAM615  LOC203504 5'  TCCCACACCCCTCCCCAGTC   90643       A   AA  CACTT
                                GACTGG GAG  GG     GGA
                                |||||| |||  ||     |||
                                CTGACC CTC  CC     CCT
                                   C   C_  ACAC_
GAM615  LOC220739 3'  AGTGCCTTCCTCCAG       92924       A
                                CTGGAG GAAGGCACT
                                ||||||| |||||||||
                                GACCTC CTTCCGTGA
                                  _
GAM615  LOC220954 5'  CCAGCCACCTTGTCTCCAGTC  93140         G    CAC
                                GACTGGAGA AAGG   TTGG
                                ||||||||| ||||   ||||
                                CTGACCTCT TTCC   GACC
                                     G    ACC
GAM615  LOC221922 5'  CCATGCCTCTCCAG       92689       GAA    CT
                                CTGGAGA   GGCA  TGG
                                |||||||   ||||  |||
                                GACCTCT   CCGT  ACC
                                  ___    __
GAM615  LOC254263 3'  CCCAGGCTCTTTCTCCAG    94716         AG  A  T
                                CTGGAGAGA  GC CT GG
                                |||||||||  || || ||
                                GACCTCTTT  CG GA CC
                                     CT  _  C
GAM615  LOC255975 5'  TCCCAGCCTTCTCTCCAG    95899           ACTT
                                CTGGAGAGAAGGC   GGA
                                ||||||||||||    |||
                                GACCTCTCTTCCG   CCT
                                       AC__
GAM615  LOC51762  5'  TCCCCGCCTCTCTCCA      33270        A   ACTT
                                TGGAGAGA GGC    GGA
                                |||||||| |||    |||
                                ACCTCTCT CCG    CCT
                                    _   CC__
GAM615  LOC58486  5'  TCCCCTCCCCCTCCAGTC    41083        AGA_   CACTT
                                GACTGGAG    AGG    GGA
                                ||||||||    |||    |||
                                CTGACCTC    TCC    CCT
                                    CCCC   _____
GAM615  LOC90591  3'  CCGGCCTTCTCCCCATTC    63419    C   A      ACT
                                GA TGG GAGAAGGC   TGG
                                || ||| ||||||||   |||
                                CT ACC CTCTTCCG   GCC
                                 T   C      ___
GAM615  LOC91373  3'  TCCTGCCTTCTCCCCA      65845     A       CTT
                                TGG GAGAAGGCA   GGA
                                ||| |||||||||   |||
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                                ACC CTCTTCCGT   CCT
                                  C       ____
GAM616  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM616  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM616  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT

                                          _
GAM616  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
             TG                   CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM616  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM616  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM616  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                       T__    _
GAM616  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM616  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_    CG_
GAM616  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
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```
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM616  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                |||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM616  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
          G                      CATTTC       GTCTGAGAT
                                 ||||||       |||||||||
                                 GTAAAG       CAGACTCTA
                                    AAACATTT_
GAM616  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281       CTT
                                 CATTTCA   TCACTGTCTGAGAT
                                 |||||||   ||||||||||||||
                                 GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM616  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM616  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM616  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM616  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM616  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM616  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148         TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__    TT
GAM616  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
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                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM616  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM616  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM616  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                     TTTCC_  A
GAM616  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM616  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                                _
GAM617  ATRN     3'  TAGCATCTATTACACTC     57803    A    C
                                GA TGTAA AGATGTTG
                                || ||||| ||||||||
                                CT ACATT TCTACGAT
                                 C    A
GAM617  DYRK1A   3'  GATTACAACATCTGTTACATTC 7353
           TA                     TAGAATGTAACAGATGTTGTAATC
                                |||||||||||||||||||||||
                                ATCTTACATTGTCTACAACATTAG

GAM617  DYRK1A   3'  GATTACAACATCTGTTACATTC 55204
           TA                     TAGAATGTAACAGATGTTGTAATC
                                |||||||||||||||||||||||
                                ATCTTACATTGTCTACAACATTAG

GAM617  DYRK1A   3'  GATTACAACATCTGTTACATTC 55244
           TA                     TAGAATGTAACAGATGTTGTAATC
                                |||||||||||||||||||||||
                                ATCTTACATTGTCTACAACATTAG

GAM617  IFI16    5'  GATTACAACATCCTGCGGTTC  71223      _   ACA
                                GAAT GTA   GATGTTGTAATC
                                |||| |||   ||||||||||||
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                                CTTG CGT   CTACAACATTAG
                                  G  C__
GAM617  PMCHL1   3'  GATTATTCATTCTGTTATACTC 49073     A       TGTT
            TA                    TAGA TGTAACAGA    GTAATC
                                |||| |||||||||    ||||||
                                ATCT ATATTGTCT    TATTAG
                                  C        TACT
GAM617  RAB4A    3'  ACTCCGTTTACTACATTCTA  15919        AC    TT
                                TAGAATGTA  AGATG  GT
                                |||||||||  |||||  ||
                                ATCTTACAT  TTTGC  CA
                                     CA    CT
GAM617  ARHE     3'  ATTACAACACTCAGTTCTA   17712      GTAAC  A
                                TAGAAT    AG TGTTGTAAT
                                ||||||    || |||||||||
                                ATCTTG    TC ACAACATTA
                                   AC___  _
GAM617  CTCFL    3'  ATTGCCCTGGTTACATTC    82503        AGATGTT
                                GAATGTAAC      GTAAT
                                |||||||||      |||||
                                CTTACATTG      CGTTA
                                     GTCC___
GAM617  DKFZp434J1015 3'  ACACACCTGCTACATTTTA   92630        A  A  T
                                TAGAATGTA CAG TGT GT
                                ||||||||| ||| ||| ||
                                ATTTTACAT GTC ACA CA
                                     C  C  _
GAM617  DKFZp761D0614 3'  ACCACTACTGTTACATTTTA  87555          AT  T
                                TAGAATGTAACAG  GT GT
                                ||||||||||||  || ||
                                ATTTTACATTGTC  CA CA
                                       AT  C
GAM617  HUMGT198A 3'  GATTACAACGTCACACTC    25235    A  AACA
                                GA TGT    GATGTTGTAATC
                                || |||    ||||||||||||
                                CT ACA    CTGCAACATTAG
                                 C  _____
GAM617  KIAA0410  3'  GATTACAAAGTACCCACATTC  28775      AACAG  G
                                GAATGT    AT TTGTAATC
                                ||||||    || ||||||||
                                CTTACA    TG AACATTAG
                                   CCCA_  A
GAM617  KIAA0648  3'  GATTACCAAGTGTTACATC   82655    A     GA  TT
                                GA TGTAACA  TG  GTAATC
                                || |||||||  ||  ||||||
                                CT ACATTGT  AC  CATTAG
                                 _     GA  __
GAM617  KIAA0971  3'  ATTACTGATGTACATTCTA   30003        A  GATGTT
                                TAGAATGTA CA     GTAAT
                                ||||||||| ||     |||||
```

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                                ATCTTACAT GT     CATTA
                                     _ AGT___
GAM617  KIAA0981  3'  ATTACACCATTGCATTC     61418       AACA    T
                                GAATGT    GATG TGTAAT
                                ||||||    |||| ||||||
                                CTTACG    TTAC ACATTA
                                    ____    C
GAM617  MGC26744  5'  ACAGAGTTATCTGTGACATTC  58310       A      ___
                                GAATGT ACAGATG   TTGT
                                |||||| |||||||   ||||
                                CTTACA TGTCTAT   GACA
                                   G      TGA
GAM617  P1P373C6  3'  GATGAGTTATCTTCTACATTCT 38902         AC     TTGTA
           A                     TAGAATGTA  AGATG     ATC
                                |||||||||  |||||     |||
                                ATCTTACAT  TCTAT     TAG
                                     CT     TGAG_
GAM617  RNF24     3'  GATTACAACACCTGCTAT    23318     A   A
                                GTA CAG TGTTGTAATC
                                ||| ||| ||||||||||
                                TAT GTC ACAACATTAG
                                  C   C
GAM617  ZAP128    3'  AACATCTGCCACATTT      22373       AA
                                GAATGT  CAGATGTT
                                ||||||  ||||||||
                                TTTACA  GTCTACAA
                                   CC
GAM617  LOC150630 3'  GATCATGGCATCTGCCACACTT 85105     A   AA      TG A
                                GA TGT  CAGATGT  T ATC
                                || |||  |||||||  | |||
                                TT ACA  GTCTACG  A TAG
                                 C   CC      GT C
GAM617  LOC152179 3'  ACATGGATCTGTTACAATTCTA 85556       _       GT_
                                TAGAAT GTAACAGAT   TGT
                                |||||| |||||||||   |||
                                ATCTTA CATTGTCTA   ACA
                                   A        GGT
GAM617  LOC203232 3'  ACAGCCATCTGTGACAT     71410      A     _
                                ATGT ACAGATG TTGT
                                |||| ||||||| ||||
                                TACA TGTCTAC GACA
                                  G      C
GAM617  LOC253386 3'  AACATCTGCCACATTT      94937       AA
                                GAATGT  CAGATGTT
                                ||||||  ||||||||
                                TTTACA  GTCTACAA
                                   CC
GAM617  LOC253612 5'  ATTACACCATTGCATTC     96740       AACA    T
                                GAATGT    GATG TGTAAT
                                ||||||    |||| ||||||
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                                CTTACG    TTAC ACATTA
                                   ____    C
GAM617  LOC254672 3'  GATTATTCATTCTGTTATACTC 94646      A        TGTT
          TA                     TAGA TGTAACAGA    GTAATC
                                |||| |||||||||    ||||||
                                ATCT ATATTGTCT    TATTAG
                                  C        TACT
GAM617  LOC91517  3'  GGCCTTTTGCTACATTCTA    66310         A    T_
                                TAGAATGTA CAGA  GTT
                                ||||||||| ||||  |||
                                ATCTTACAT GTTT  CGG
                                     C    TC
GAM618  CNGA1     3'  CAACTGATAATGTGCAAA     59507          GC   A
                                TTTGCACATTA  TAG TTG
                                |||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                      A_   _
GAM618  ESRRG     3'  TGGCAGTCTTATGTGCAAA    66396         TAGCT
                                TTTGCACAT    AGATTGCCA
                                |||||||||    |||||||||
                                AAACGTGTA    TCTGACGGT
                                     T_____
GAM618  KCNJ3     3'  GCAATAATGTGCAAA       9525           GCTAGA
                                TTTGCACATTA     TTGC
                                ||||||||||      ||||
                                AAACGTGTAAT     AACG
                                      _______
GAM618  SDC2      3'  GCAAATTAATGTGTAAA     67132           CTAGA
                                TTTGCACATTAG    TTGC
                                ||||||||||||    ||||
                                AAATGTGTAATT    AACG
                                      A_____
GAM618  USP9X     3'  ATGGCCTGATGCTAATGTGTAA 16206           TAGATT
          A                      TTTGCACATTAGC     GCCAT
                                |||||||||||||     |||||
                                AAATGTGTAATCG     CGGTA
                                       TAGTC_
GAM618  AMOTL1    3'  GGCAAGTAATGTGCAAA     73650          G  AGAT
                                TTTGCACATTA CT    TGCC
                                |||||||||| ||    ||||
                                AAACGTGTAAT GA    ACGG
                                      _  _____
GAM618  BCAR3     3'  AGTAATAATGTGCAAA      13098          __
                                TTTGCACATTA  GCT
                                ||||||||||  |||
                                AAACGTGTAAT  TGA
                                      AA
GAM618  DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930          AGCTA    C
                                TTTGCACATT    GATTG CA
                                |||||||||     ||||| ||
```

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                                AGACGTGTAA    TTAAC GT
                                     A____    A
GAM618  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                TTTGCACATTAG  AGA TG CAT
                                |||||||||||  ||| || |||
                                AGACGTGTAATC  TTT AC GTA
                                      __  T  A
GAM618  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
           AA                    TTTGCACATTAGCTAGATTGCCAT
                                 ||||||||||||||||||||||||
                                 AAACGTGTAATCGATCTAACGGTA

GAM619  LTA      3'  GCGCACAAGGCTGACCAAG   5176        T  GTCC  AC
                                CTTGGTCG GTC   TGC  GC
                                |||||||| |||   |||  ||
                                GAACCAGT CGG   ACG  CG
                                     _  AAC_  __
GAM619  RASD1    3'  CGCGCTGGCGACACAACC    32221    C      CT  A
                                GGT GTGTCGTC  GC CG
                                ||| ||||||||  || ||
                                CCA CACAGCGG  CG GC
                                  A       T_  C
GAM619  BC002942 3'  AGGAAAACACGACCAAG     65461          CG
                                CTTGGTCGTGT  TCCT
                                ||||||||||  ||||
                                GAACCAGCACA  AGGA
                                      AA
GAM619  MGC15438 5'  GCACAGCAACATGACCAAG   51790          C  CC
                                CTTGGTCGTGT GT  TGC
                                |||||||||| ||  |||
                                GAACCAGTACA CG  ACG
                                      A  AC
GAM619  MYH7B    3'  GCATGCAGGACCTGGTGGACAA 70532     GT  TGTC      C
           G                     CTTG  CG   GTCCTGCA GC
                                 ||||  ||   |||||||| ||
                                 GAAC  GT   CAGGACGT CG
                                   AG  GGTC       A
GAM619  PSKH1    3'  TGCAGCACGACCCAG      68243    T     TCGTC
                                CT GGTCGTG    CTGCA
                                || |||||||    |||||
                                GA CCAGCAC    GACGT
                                 C     _____
GAM620  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM620  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
```

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                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T _
GAM620  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM620  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                  CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM620  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||  ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM620  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM620  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM620  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM620  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_   CG_
GAM620  CG012    5'  CTCACTCTGAAAGTGAA     83218          CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM620  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM620  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
              G                   CATTTC        GTCTGAGAT
                                ||||||        |||||||||
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                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM620  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA  TCACTGTCTGAGAT
                                |||||||  ||||||||||||||
                                GTAAAGT  AGTGACAGACTCTA
                                   C__
GAM620  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM620  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM620  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                 C
GAM620  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM620  PP35      3'  ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM620  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148        TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM620  SEP15     3'  TCCTACAGTAAGAGTGAAA   14934       C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM620  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA  73941       CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM620  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
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                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM620  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM620  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM620  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA

                                          _
GAM621  ALK      3'  CTATTTTGAAGTACCACCAA   73382          C   TG
                                TTGGTGGTAC TTA  GTAG
                                |||||||||| |||  ||||
                                AACCACCATG AGT  TATC
                                     A   TT
GAM621  OCRL     3'  AGCATATCCAAGGCACCACCAG 4257          A    AT    GA
          T                      ATTGGTGGT CCTT  GGTA  CT
                                |||||||| ||||  ||||  ||
                                TGACCACCA GGAA  CTAT  GA
                                     C    C_    AC
GAM621  OCRL     3'  AGCATATCCAAGGCACCACCAG 7823          A    AT    GA
          T                      ATTGGTGGT CCTT  GGTA  CT
                                |||||||| ||||  ||||  ||
                                TGACCACCA GGAA  CTAT  GA
                                     C    C_    AC
GAM621  POU4F1   3'  CTACCAACCACCAA       20663         ACCTTA
                                TTGGTGGT     TGGTAG
                                ||||||||     ||||||
                                AACCACCA     ACCATC

                                _______
GAM621  RNMT     5'  ATCAGATAGGCACCACCAA   13709         A   TA_
                                TTGGTGGT CCT   TGGT
                                |||||||| |||   ||||
                                AACCACCA GGA   ACTA
                                     C   TAG
GAM621  DNAJC6   3'  AGTCCAGTGATTACCACCAA   28842         CC    GGTA
                                TTGGTGGTA  TTAT   GACT
                                |||||||||  ||||   ||||
                                AACCACCAT  AGTG   CTGA
                                     T_    AC__
GAM621  FLJ12747 3'  GTTGTAAGACTCCACCAAT   49722         TAC    GG
                                ATTGGTGG   CTTAT  T
                                ||||||||   |||||  |
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                                TAACCACC  GAATG  G
                                    TCA    TT
GAM621  KIAA1143  3'  GTCTACCACTTCCACCAA    68687       TACCTTA
                                TTGGTGG     TGGTAGAC
                                |||||||     ||||||||
                                AACCACC     ACCATCTG
                                   TTC____
GAM621  POPX1     3'  GTAAGATACCACCAGT     29800         C
                                ATTGGTGGTA CTTAT
                                |||||||||| |||||
                                TGACCACCAT GAATG
                                      A
GAM621  VIT1      5'  ACCTAAATACCACCAA     37970         CC  T
                                TTGGTGGTA  TTA GGT
                                |||||||||  ||| |||
                                AACCACCAT  AAT CCA
                                      A_  _
GAM621  LOC147670 3'  ATCATTAAGATGCCACCAA   84068         C   _
                                TTGGTGGTA CTTA TGGT
                                |||||||||| |||| ||||
                                AACCACCGT GAAT ACTA
                                      A   T
GAM621  LOC152179 5'  ACCATTCAAAAGACCACCAAT  85557         ACCTT__
                                ATTGGTGGT     ATGGT
                                |||||||||     |||||
                                TAACCACCA     TACCA
                                      GAAAACT
GAM621  LOC254381 5'  CACAAGATACCACCAA     97459         C  A
                                TTGGTGGTA CTT TG
                                |||||||||| ||| ||
                                AACCACCAT GAA AC
                                      A  C
GAM622  ABCB10    3'  TTTACGAAATTGCATTTCATTG 23889     _     TG __     AA
           TTA                    ACAA GAAATG  G  TCGTGAA
                                |||| ||||||  |  |||||||
                                TGTT CTTTAC  T  AGCATTT
                                  A     GT AA
GAM622  BMPR1A    3'  TTTTTGTGGTTATTATTTTTGT 15080        AT  GT  TG
           CA                     TGACAAGAA  GTG  CG  AAAA
                                |||||||||  |||  ||  ||||
                                ACTGTTTTT  TAT  GT  TTTT
                                      AT   TG  GT
GAM622  CACNA2D2  3'  ATGTCATGTTGCTTGTC     20078       A     T
                                GACAAG AATGTGG CGT
                                |||||| ||||||| |||
                                CTGTTC TTGTACT GTA
                                   G     _
GAM622  CALCR     3'  TGACCGCTTGTTTCTTGTTA   8224          __
                                TGACAAGAAAT  GTGGTCG
                                ||||||||||  |||||||
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                                ATTGTTCTTTG  CGCCAGT
                                      TT
GAM622  CBFB    3'  TTTTCATGGTCACATTT    8279       GT
                                AAATGTG  CGTGAAAA
                                |||||||  ||||||||
                                TTTACAC  GTACTTTT
                                   TG
GAM622  CBFB    3'  TTTTCATGGTCACATTT    43146      GT
                                AAATGTG  CGTGAAAA
                                |||||||  ||||||||
                                TTTACAC  GTACTTTT
                                   TG
GAM622  CD164   3'  TTTACCTCACATTTTTTGTT  20052          TC
                                GACAAGAAATGTGG  GTGAA
                                ||||||||||||||  |||||
                                TTGTTTTTTACACT  CATTT
                                         C_
GAM622  CDK2    3'  TTTTTATGATTTGTCTCTGTCA 8393      _  AATGT
                                TGACA AGA    GGTCGTGAAAA
                                ||||| |||    ||||||||||
                                ACTGT TCT    TTAGTATTTTT
                                  C  GT___
GAM622  CHAC    3'  TTGTAATTGTATTTCTTG    52796       TG  CG
                                CAAGAAATG  GT  TGA
                                |||||||||  ||  |||
                                GTTCTTTAT  TA  GTT
                                     GT  AT
GAM622  CLOCK   3'  TGATTGCATATTTTGTTA    16913       A  TG
                                TGACAAGA ATG  GTCG
                                |||||||| |||  ||||
                                ATTGTTTT TAC  TAGT
                                     A  GT
GAM622  CPO     3'  TTTTTGTGGAACCATTGTTTGT 3640       AAAT   __ TG
           TA                    TGACAAG   GTGGT  CG  AAAA
                                |||||||   |||||  ||  ||||
                                ATTGTTT   TACCA  GT  TTTT
                                   GT__    AG  GT
GAM622  CTNNA1  3'  TTCTAGCTGTATTTTTTGT   65922        TG  CGT
                                ACAAGAAATG  GT   GAA
                                ||||||||||  ||   |||
                                TGTTTTTTAT  CG   CTT
                                     GT  AT_
GAM622  DDX20   5'  TCCTCAGGCCACATTTTTTGT  23274          G   AAA
                                ACAAGAAATGTGGTC TGA
                                ||||||||||||||| |||
                                TGTTTTTTACACCGG ACT
                                         _  CCTT
GAM622  DEK     3'  TTTTCACAGGTTTGTTTCTTG  12958        TGGTC
                                CAAGAAATG    GTGAAAA
                                |||||||||    |||||||
```

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                                GTTCTTTGT    CACTTTT
                                     TTGGA
GAM622  EPS8    3'  TTTTTGGAAACACAATTTTTGT 15471         A   G_ G
           CA                    TGACAAGAA TGTG  TC TGAAAA
                                 ||||||||| ||||  || ||||||
                                 ACTGTTTTT ACAC  AG GTTTTT
                                      A   AA  _
GAM622  ESRRBL1  3'  TATATCAAACTATATTTCATGT 35850     A        CG   AAA
           T                     GACA GAAATGTGGT  TGA
                                 |||| ||||||||||  |||
                                 TTGT CTTTATATCA  ACT
                                   A        A_   ATATT
GAM622  ESRRBL1  3'  TTTCATGGCTGTTGTCA     35851      AGAAAT TG
                                 TGACA     G  GTCGTGAAA
                                 |||||     |  |||||||||
                                 ACTGT     T  CGGTACTTT
                                   _______ GT
GAM622  FOXE1    3'  TGTCCACTGTTTCTTGTCA    15561          _   T
                                 TGACAAGAAAT GTGG CG
                                 |||||||||||| |||| ||
                                 ACTGTTCTTTG CACC GT
                                       T   T
GAM622  GHR      3'  TAGCACAGGCTAATTTTTTGTT 3886          G    _   AAAA
                                 GACAAGAAAT TGGTC GTG
                                 |||||||||| ||||| |||
                                 TTGTTTTTTA ATCGG CAC
                                      _    A   GAT
GAM622  GNAO1    3'  TTTTCATGACCAATCCTATGTC 90969       AGAAATG
           A                     TGACA      TGGTCGTGAAAA
                                 |||||      ||||||||||||
                                 ACTGT      ACCAGTACTTTT
                                   ATCCTA_
GAM622  GNAZ     3'  TTTTCAAAACATATTTTTTTTC 9066      C        GTCG
           A                     TGA AAGAAATGTG    TGAAAA
                                 ||| ||||||||||    ||||||
                                 ACT TTTTTTATAC    ACTTTT
                                   T        AAA_
GAM622  GPM6B    3'  TTTTTATGATCACATGGTTC   67078     __
                                 GAA  ATGTGGTCGTGAAAA
                                 |||  |||||||||||||||
                                 CTT  TACACTAGTATTTTT
                                   GG
GAM622  GRPR     5'  TTTTTGTGGCTAAGTTTTGTT  18003       AATG     TG
                                 GACAAGA    TGGTCG  AAAA
                                 |||||||    ||||||  ||||
                                 TTGTTTT    ATCGGT  TTTT
                                      GA__      GT
GAM622  HEM1     5'  TTGCAGAGCTACTTTTCTTGTT 18054          T    CG  AAAA
                                 GACAAGAAA GTGGT  TG
                                 |||||||| |||||  ||
```

```
                                TTGTTCTTT CATCG  AC
                                     T    AG  GTT
GAM622  HSF2BP   3'  TTTTAGTTCTATATTTTTTGT  22861           TCG
                                ACAAGAAATGTGG   TGAAA
                                ||||||||||||   |||||
                                TGTTTTTTATATC   ATTTT
                                      TTG
GAM622  IL1RAP   3'  TTTTTACTGGAATGTTTTTGTG 9315      _      GG  _
           TCA                    GACA AGAAATGT  TC GTGAAAA
                                ||||| ||||||||  || |||||||
                                CTGT TTTTTGTA  GG CATTTTT
                                  G       A_  T
GAM622  IMMT     3'  TTTTCATAAAGTCATATTTCAT 22420      A       TC__
           GTCA                    GACA GAAATGTGG    GTGAAAA
                                ||||| |||||||||    |||||||
                                CTGT CTTTATACT    TACTTTT
                                  A        GAAA
GAM622  IPP      3'  TTTTTGCTTGCTCATATTTTTT 19730           _  C_ TG
           GTC                    GACAAGAAATGTG GT  G  AAAA
                                ||||||||||||| ||  |  ||||
                                CTGTTTTTTATAC CG  C  TTTT
                                      T  TT GT
GAM622  ITPR1    3'  TGGTTTTATTTCTTGTCA    9442           T GT
                                TGACAAGAAATG G  CG
                                ||||||||||| |  ||
                                ACTGTTCTTTAT T  GT
                                      T TG
GAM622  KCNA7    3'  TTTTCGTGGCCACAGCGAGTTG 49066     GAAA_
                                CAA    TGTGGTCGTGAAAA
                                |||    ||||||||||||||
                                GTT    ACACCGGTGCTTTT
                                  GAGCG
GAM622  KLRD1    3'  TTTTTAATTTTTAATTTTTTGT 9624          GTGGTCG
           CA                     TGACAAGAAAT      TGAAAA
                                ||||||||||      ||||||
                                ACTGTTTTTTA      ATTTTT
                                      ATTTTTA
GAM622  KLRD1    3'  TTTTTAATTTTTAATTTTTTGT 23683         GTGGTCG
           CA                     TGACAAGAAAT      TGAAAA
                                ||||||||||      ||||||
                                ACTGTTTTTTA      ATTTTT
                                      ATTTTTA
GAM622  LDB2     3'  TTTTTATAGTATATTTCTTGT  7095           GTC
                                ACAAGAAATGTG   GTGAAAA
                                ||||||||||||   |||||||
                                TGTTCTTTATAT   TATTTTT
                                      GA_
GAM622  LFNG     3'  CCCGTGGGCTGTGTTTCTTGTT 92639          TG   GTGAAAA
                                GACAAGAAATG  GTC
                                ||||||||||  |||
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                                TTGTTCTTTGT  CGG
                                      GT   GTGCCCT
GAM622  MEN1     5'  TTTTTATGATTACAAAACTCTT 93388       AA__
             G                    CAAGA   TGTGGTCGTGAAAA
                                  |||||   ||||||||||||||
                                  GTTCT   ACATTAGTATTTTT
                                     CAAA
GAM622  NAP1L3   3'  TGGTCATGTTTCTGTTA     15797      A      GT
                                  TGACA GAAATGTG  CG
                                  ||||| ||||||||  ||
                                  ATTGT CTTTGTAC  GT
                                     _       TG
GAM622  NAPB     3'  TTTTATGTCCTTTTTGTT     70196        ATGT  T
                                  GACAAGAA    GG CGTGAAA
                                  ||||||||    || |||||||
                                  TTGTTTTT    CC GTATTTT
                                        ____  T
GAM622  NOS1     3'  TTTTTATGATGACATTTTGGTT 5256      AA      G
                                  GAC  GAAATGT GTCGTGAAAA
                                  |||  ||||||| ||||||||||
                                  TTG  TTTTACA TAGTATTTTT
                                    G_      G
GAM622  NOVA1    3'  TTTTTGTTGTTCATTTGTTTCT 21414         __    TC_ TG
             TGTCA                  CAAGAAAT  GTGG   G  AAAA
                                    ||||||||  ||||   |  ||||
                                    GTTCTTTG  TACT   T  TTTT
                                         TT    TGT GT
GAM622  PCDHB16  3'  TCCTATGTTACATTTCTT    40557          T    AAAA
                                  AAGAAATGTGG CGTG
                                  |||||||||||| ||||
                                  TTCTTTACATT GTAT
                                         _    CCTT
GAM622  PCDHB6   3'  TTTTTGTGACTATAGACTTTA  38440    C   AAA       TG
                                  A AAG   TGTGGTCG  AAAA
                                  | |||   ||||||||  ||||
                                  A TTC   ATATCAGT  TTTT
                                   T   AG_       GT
GAM622  PDCL     3'  TGTCATATTTCTAGTCA     18220      A        T
                                  TGAC AGAAATGTGG CG
                                  |||| ||||||||||  ||
                                  ACTG TCTTTATACT GT
                                     A        _
GAM622  PLXNA2   3'  TTTTTGCTACTGTTTTTTGTT  47212          GT   C TG
                                  GACAAGAAAT  GGT G  AAAA
                                  ||||||||||  ||| |  ||||
                                  TTGTTTTTTG  TCA C  TTTT
                                         __   T GT
GAM622  PPP1R8   3'  TTTACCTGTTTTTCTTGTCA   56744          T TG TC
                                  TGACAAGAAA G  G  GTGAA
                                  |||||||||| |  |  |||||
```

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                                ACTGTTCTTT T  C  CATTT
                                     T GT __
GAM622  PPP1R8   3'  TTTACCTGTTTTTCTTGTCA  26069          T TG TC
                                TGACAAGAAA G  G  GTGAA
                                |||||||||| |  |  |||||
                                ACTGTTCTTT T  C  CATTT
                                     T GT __
GAM622  PPP1R8   3'  TTTACCTGTTTTTCTTGTCA  10728          T TG TC
                                TGACAAGAAA G  G  GTGAA
                                |||||||||| |  |  |||||
                                ACTGTTCTTT T  C  CATTT
                                     T GT __
GAM622  PRDM2    3'  TTTACATTTCACTTTTTTTGTT 31852          T   TC_    AA
                                GACAAGAAA GTGG   GTGAA
                                ||||||||| ||||   |||||
                                TTGTTTTTT CACT   CATTT
                                     T   TTA
GAM622  PYCS     3'  TTTTCGCGTTTTATTTCTTTCA 11169     C       TG T
                                TGA AAGAAATG  G CGTGAAAA
                                ||| ||||||||  | ||||||||
                                ACT TTCTTTAT  T GCGCTTTT
                                  _       TT _
GAM622  RELN     3'  ACTGTATTTACTTGTTA     94301        _    TG
                                TGACAAG AAATG  GT
                                ||||||| |||||  ||
                                ATTGTTC TTTAT  CA
                                    A     GT
GAM622  RPL15    3'  TTTTCAAGTGGCTGCGTTTTTT 11388         TG   __
                                AAGAAATG  GTCG  TGAAAA
                                ||||||||  ||||  ||||||
                                TTTTTTGC  CGGT  ACTTTT
                                     GT   GA
GAM622  SEL1L    3'  TTTTACTTTGCATTTCTTTTT  17368    C       TG TC
                                GA AAGAAATG  G  GTGAAA
                                || ||||||||  |  ||||||
                                TT TTCTTTAC  T  CATTTT
                                  T       GT T_
GAM622  SPON1    3'  TTTTCTTCCTGCATTTATTGTT 62461       G    TG TCGT
                                GACAA AAATG  G    GAAAA
                                ||||| |||||  |    |||||
                                TTGTT TTTAC  C    CTTTT
                                   A     GT CTT_
GAM622  SYT4     3'  TTTTTATGACTATGCCTAATGT 62442     AGAAAT
                                ACA      GTGGTCGTGAAAA
                                |||      |||||||||||||
                                TGT      TATCAGTATTTTT
                                  AATCCG
GAM622  TAF4B    3'  TTAAATTGGCCACATTTTTTTT 87169    C           TGAAAA
           T                     GA AAGAAATGTGGTCG
                                || ||||||||||||||
```

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                                TT TTTTTTACACCGGT
                                 T           TAAATTT
GAM622  TIRAP    3'  TTTTCTTCTGTATTTCTTTTCA 53573     C       TG TCGT
                                TGA AAGAAATG  G    GAAAA
                                ||| ||||||||  |    |||||
                                ACT TTCTTTAT  C    CTTTT
                                  T       GT TT__
GAM622  TMOD2    3'  GCAGATGATTGCATTTTTTG   27249         TG    GAAAA
                                CAAGAAATG  GTCGT
                                |||||||||  |||||
                                GTTTTTTAC  TAGTA
                                     GT    GACGT
GAM622  TNFRSF11A 3'  TTTTATGACTATCCTGTT    13858      A  AATG
                                GACA GA    TGGTCGTGAAA
                                |||| ||    ||||||||||
                                TTGT CT    ATCAGTATTTT
                                  C  ____
GAM622  TRAF5    3'  TTGTGATGTTTCTTGTCA    16092          GTG    TG
                                TGACAAGAAAT   GTCG  A
                                ||||||||||   ||||  |
                                ACTGTTCTTTG   TAGT  T
                                      ___    GT
GAM622  TRHDE    3'  TTTTCATGGCTGTGTGTTGTGT 25392     AGAA   TG
                                ACA    ATG  GTCGTGAAAA
                                |||    |||  ||||||||||
                                TGT    TGT  CGGTACTTTT
                                  GTTG   GT
GAM622  UBL3     3'  TTTTTATTTCTTGTATTTTTTG 23036          TG TC_
            TT                   GACAAGAAATG  G   GTGAAAA
                                ||||||||||  |  |||||||
                                TTGTTTTTTAT  T   TATTTTT
                                      GT CTT
GAM622  WHSC1    3'  TTTTATGGCCTTTTCTT     29922       TGT
                                AAGAAA   GGTCGTGAAA
                                ||||||   ||||||||||
                                TTCTTT   CCGGTATTTT
                                   T__
GAM622  WHSC1    3'  TTTTATGGCCTTTTCTT     55840       TGT
                                AAGAAA   GGTCGTGAAA
                                ||||||   ||||||||||
                                TTCTTT   CCGGTATTTT
                                   T__
GAM622  WHSC1    3'  TTTTATGGCCTTTTCTT     55857       TGT
                                AAGAAA   GGTCGTGAAA
                                ||||||   ||||||||||
                                TTCTTT   CCGGTATTTT
                                   T__
GAM622  ZNF124   3'  TTTAATCACTACAGTTTTTGTC 12825         A     CG_   AA
            A                    TGACAAGAA TGTGGT   TGAA
                                |||||||| ||||||   ||||
```

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                                ACTGTTTTT ACATCA   ATTT
                                     G     CTA
GAM622  ZNF216   3'  TTTTCATGTGCATCTTTTGTC  20023       A   GGT
                                GACAAGA ATGT   CGTGAAAA
                                ||||||| ||||   ||||||||
                                CTGTTTT TACG   GTACTTTT
                                    C   T__
GAM622  ZNF236   3'  TTTTCCTTCATGTTTCTGGTTA 23723     A        TCGT
                                TGAC AGAAATGTGG    GAAAA
                                |||| ||||||||||    |||||
                                ATTG TCTTTGTACT    CTTTT
                                  G        TC__
GAM622  ANKRD6   3'  TTTTCATGGTTATGCCTTGTT  30095      AAA   GT
                                GACAAG   TGTG  CGTGAAAA
                                ||||||   ||||  ||||||||
                                TTGTTC   GTAT  GTACTTTT
                                   C__   TG
GAM622  ARHGEF9  3'  TTCATTGCTTTTCTTGTTA   30825        TGT   C
                                TGACAAGAAA   GGT GTGAA
                                ||||||||||   ||| |||||
                                ATTGTTCTTT   TCG TACTT
                                     ___   T
GAM622  BRD4     3'  TTTTCTATATATATTTTTTGTT 54280          GTCGT
                                GACAAGAAATGTG    GAAAA
                                ||||||||||||     |||||
                                TTGTTTTTTATAT    CTTTT
                                       ATAT_
GAM622  BRDG1    3'  ACCACATTTTTTGTTA     23991
                                TGACAAGAAATGTGGT
                                ||||||||||||||||
                                ATTGTTTTTTACACCA

GAM622  C1orf26  3'  TTTTATGATCAAACTGTCA   34583      AGAAATG
                                TGACA      TGGTCGTGAAA
                                |||||      ||||||||||
                                ACTGT      ACTAGTATTTT
                                   CAA____
GAM622  C21orf91 3'  TTTTTATGGTCATTAAATTTGC 33883    A   AAAT   GT
           CA                    TG CAAG    GTG  CGTGAAAA
                                || ||||    |||  ||||||||
                                AC GTTT    TAC  GTATTTTT
                                 C    AAAT   TG
GAM622  C4S-2    3'  TTTTTATGACCTACGATTTTGC 37821    A    AA  _
           A                     TG CAAGA  TGT GGTCGTGAAAA
                                || |||||  ||| ||||||||||
                                AC GTTTT  GCA CCAGTATTTTT
                                 _    A_   T
GAM622  C9orf5   3'  TTTTATTAGTTTCTTGTC    49286          GTGGTC
                                GACAAGAAAT     GTGAAA
                                ||||||||||     ||||||
```

```
                                CTGTTCTTTG     TATTTT
                                      AT____
GAM622  CDW92    3'  TTTTTATGCTTATTTTTGTCA  54508         ATGT  T
                                TGACAAGAA    GG CGTGAAAA
                                |||||||||    || ||||||||
                                ACTGTTTTT    TC GTATTTTT
                                      AT__  _
GAM622  CYorf15B  3'  TTTTACATATATTCTCTTGTCA 50822         _     GTC
                                TGACAAGA AATGTG   GTGAAA
                                |||||||| ||||||   ||||||
                                ACTGTTCT TTATAT   CATTTT
                                     C     A__
GAM622  DJ122O8.2 3'  TTTTCAAAGTCTCCATGTGTTT 39995       A     TCG___
           TGTT                    CAAGA ATGTGG     TGAAAA
                                |||||| ||||||     ||||||
                                GTTTT TGTACC     ACTTTT
                                   G     TCTGAA
GAM622  DKFZp434A171 3'  TTTTTATGACCATGTAATGTT  50013     AGAA
                                GACA    ATGTGGTCGTGAAAA
                                ||||    ||||||||||||||||
                                TTGT    TGTACCAGTATTTTT
                                  AA__
GAM622  DKFZP434C171 3'  TTTCATGAAGCTTTTTGCA    31564    A     AT  GG
                                TG CAAGAA  GT  TCGTGAAA
                                || ||||||  ||  ||||||||
                                AC GTTTTT  CG  AGTACTTT
                                 _     __  A_
GAM622  DKFZp434K2435 3'  TTTTGCGTATGTGTTTTTTGTT 50037          TG  GT  TG   A
                                GACAAGAAA  TG  CG  AAA
                                |||||||||  ||  ||  |||
                                TTGTTTTTT  GT  GC  TTT
                                      GT  AT  GT
GAM622  DKFZP434L187 3'  TTTACATTTACATTTATTGTCA 68806       G       TC
                                TGACAA AAATGTGG  GTGAA
                                ||||||| ||||||||  |||||
                                ACTGTT TTTACATT  CATTT
                                    A       TA
GAM622  DKFZp547A023 3'  TTTTTATGGCTCACATCTTTTT 72618       _    _
                                AAGAA ATGTG GTCGTGAAAA
                                ||||| ||||| ||||||||||
                                TTTTT TACAC CGGTATTTTT
                                   C    T
GAM622  DKFZP727C091 3'  TTTTTGTTTCCATGTTTTCTTG 66213          _    TC TG
           TCA                    TGACAAGAAA TGTGG  G  AAAA
                                |||||||||| |||||  |  ||||
                                ACTGTTCTTT GTACC  T  TTTT
                                      T    TT GT
GAM622  DKFZp761F2014 3'  TTTCATGATCAACTTGT     39544       AAATG
                                ACAAG    TGGTCGTGAAA
                                |||||    ||||||||||
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                                TGTTC    ACTAGTACTTT
                                  A____
GAM622  FER1L4   3' GGCTACATTTTTTTCA     47359    C
                                TGA AAGAAATGTGGTC
                                ||| ||||||||||||
                                ACT TTTTTTACATCGG
                                  _
GAM622  FKBP5    3' TTTTTATGAAATATTTCTT   14655       GG
                                AAGAAATGT  TCGTGAAAA
                                |||||||||  |||||||||
                                TTCTTTATA  AGTATTTTT
                                     A_
GAM622  FLJ10055 3' TGAATTGTATTTCTTGT    35777        TG _
                                ACAAGAAATG  GT CG
                                ||||||||||  || ||
                                TGTTCTTTAT  TA GT
                                      GT  A
GAM622  FLJ10199 5' TTTAGCATCCACGTTTTTTG  71238         TC  GAAAA
                                CAAGAAATGTGG  GT
                                ||||||||||||  ||
                                GTTTTTTGCACC  CG
                                       TA  ATTT
GAM622  FLJ10242 3' TTGTGTGCTATATTTCTTGT  35938          _ TG
                                ACAAGAAATGTGGT CG  A
                                |||||||||||||| ||  |
                                TGTTCTTTATATCG GT  T
                                       T  GT
GAM622  FLJ10540 3' TTCAATACTGTATTTTCTGTTA 36261     AG    TG  CG
                                TGACA  AAATG  GT  TGAA
                                |||||  |||||  ||  ||||
                                ATTGT  TTTAT  CA  ACTT
                                   CT    GT  TA
GAM622  FLJ10715 3' GCCATATTTCTTTTCA     36477    C
                                TGA AAGAAATGTGGT
                                ||| ||||||||||||
                                ACT TTCTTTATACCG
                                  T
GAM622  FLJ11186 5' GCTACTTTCTTGTCA      37143        T
                                TGACAAGAAA GTGGT
                                |||||||||| |||||
                                ACTGTTCTTT CATCG
                                       _
GAM622  FLJ11703 3' TTTTTATGATCATGACTGATCA 46386    CA  AAA
                                TGA  AG   TGTGGTCGTGAAAA
                                |||  ||   ||||||||||||||
                                ACT  TC   GTACTAGTATTTTT
                                  AG  A__
GAM622  FLJ13621 3' TTCTGCATTGACTGCATTTTTT 46584       TG   _ AAAA
                                AAGAAATG  GTCG TG
                                ||||||||  |||| ||
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```
                                TTTTTTAC  CAGT AC
                                    GT    T  GTCTTT
GAM622  FLJ14753  5'  TTCTCGGTCACGTTTTCTGTTA 50778      AG      GT  T
                                TGACA  AAATGTG  CG GAA
                                |||||  |||||||  || |||
                                ATTGT  TTTGCAC  GC CTT
                                   CT      TG  T
GAM622  FLJ20032  3'  GCTTACATTTTTTGTCA     67898           _
                                TGACAAGAAATGTG GT
                                |||||||||||||| ||
                                ACTGTTTTTTACAT CG
                                          T
GAM622  FLJ20035  3'  TTTTTAAACATACATTTTGTGT 34396      A       GTCG
          T                      GACA GAAATGTG    TGAAAA
                                |||| ||||||||    ||||||
                                TTGT TTTTACAT    ATTTTT
                                  G       ACAA
GAM622  FLJ20152  3'  TTTTTGTGATTGCTTATGTCA  38649      AGAAAT TG    TG
                                TGACA     G  GTCG  AAAA
                                |||||     |  ||||  ||||
                                ACTGT     C  TAGT  TTTT
                                   ATT___ GT    GT
GAM622  FLJ20273  3'  ACCATGTTTCTTGCA       38725    A
                                TG CAAGAAATGTGGT
                                || ||||||||||||
                                AC GTTCTTTGTACCA
                                 _
GAM622  FLJ20456  3'  TGTCCATGTTTATTGTTA     35217       G       T
                                TGACAA AAATGTGG CG
                                |||||| |||||||| ||
                                ATTGTT TTTGTACC GT
                                   A       T
GAM622  FLJ21615  3'  TTTTTGCGGCCTTATATTTTG  49841      A   T    TG
                                CAAGA ATG GGTCG  AAAA
                                ||||| ||| |||||  ||||
                                GTTTT TAT CCGGC  TTTT
                                   A   T    GT
GAM622  FLJ21941  3'  TTTTACCTCATATTTTCTGTCA 46747      AG       TC
                                TGACA  AAATGTGG  GTGAAA
                                |||||  ||||||||  ||||||
                                ACTGT  TTTATACT  CATTTT
                                   CT       C_
GAM622  FLJ23556  3'  TTTTCATGATCACCAAAGTGTT 45964      AGAAAT
                                GACA     GTGGTCGTGAAAA
                                ||||     ||||||||||||||
                                TTGT     CACTAGTACTTTT
                                  GAAAC_
GAM622  FLJ23563  3'  TTACATTTTCTTGTCA      67605           _
                                TGACAAGAAA TGTGG
                                |||||||||| |||||
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```
                                ACTGTTCTTT ACATT
                                      T
GAM622  FLJ25442  3'  TTTTCCAGTTGATGTTTTTTGT 58842           GGTCGT
            CA                    TGACAAGAAATGT     GAAAA
                                  ||||||||||||||     |||||
                                  ACTGTTTTTTGTA     CTTTT
                                        GTTGAC
GAM622  FLJ30046  3'  TTTTTGTGCCTATTTCTTTTTA 58104     C       T  T  TG
                                  TGA AAGAAATG GG CG  AAAA
                                  ||| |||||||| || ||  ||||
                                  ATT TTCTTTAT CC GT  TTTT
                                    T       _ _ GT
GAM622  FLJ31153  3'  TTTTTACGAAGTATTTTTTGTT 58134          TGG
                                  GACAAGAAATG   TCGTGAAAA
                                  ||||||||||||  |||||||||
                                  TTGTTTTTTTAT   AGCATTTTT
                                        GA_
GAM622  FPGT      3'  TTTTCATCTTATTTTTTGTC   13850          TGGTC
                                  GACAAGAAATG    GTGAAAA
                                  ||||||||||||    |||||||
                                  CTGTTTTTTTAT    TACTTTT
                                        TC___
GAM622  GTF2F2    3'  TAAACAGGTGATCACGTTTCTT 14680     C           GAAAA
            TTCA                    TGA AAGAAATGTGGTCGT
                                  ||| ||||||||||||||
                                  ACT TTCTTTGCACTAGTG
                                    T           GACAAATT
GAM622  GTF3C2    3'  TTTTGTGACCACTTGT      7725      GAAAT      TG
                                  ACAA    GTGGTCG  AAA
                                  ||||    |||||||  |||
                                  TGTT    CACCAGT  TTT
                                    _____      GT
GAM622  HARC      3'  TTTTTGTGGCTACTAAATTTG  35486      AAAT      TG
                                  CAAG    GTGGTCG  AAAA
                                  ||||    |||||||  ||||
                                  GTTT    CATCGGT  TTTT
                                     AAAT      GT
GAM622  HERC1     3'  TTTTCCCTCCATATTTTTGGTC 14068      A        TCGT
            A                     TGAC AGAAATGTGG    GAAAA
                                  ||||||||||||||    |||||
                                  ACTG TTTTTATACC    CTTTT
                                    G         TCC_
GAM622  HGRG8     3'  TTTTTATGAAGAATTTTTGTC  32744         ATGTGG
                                  GACAAGAA     TCGTGAAAA
                                  ||||||||     |||||||||
                                  CTGTTTTT     AGTATTTTT
                                       AAGA__
GAM622  HSPC152   3'  TCTTGTTATGACTGTGTATTTT 33085         _  TG      AAA
            TGTT                    GACAAGAA ATG  GTCGTGA
                                  ||||||||| |||  |||||||
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                                TTGTTTTT TGT  CAGTATT
                                    A  GT      GTTCTT
GAM622  HSPC152  3'  TCTTGTTATGACTGTGTATTTT 94519        _  TG      AAA
            TGTT                  GACAAGAA ATG  GTCGTGA
                                |||||||| |||  |||||||
                                TTGTTTTT TGT  CAGTATT
                                    A  GT      GTTCTT
GAM622  HSPC195  3'  TTTTTATATATATATTTTTTGT 80968           GTC
            T                   GACAAGAAATGTG  GTGAAAA
                                |||||||||||||  |||||||
                                TTGTTTTTTATAT  TATTTTT
                                       ATA
GAM622  IMPACT   3'  TTATAACTATATTTTATGTT  37395     A       CG
                                GACA GAAATGTGGT  TGA
                                |||| ||||||||||  |||
                                TTGT TTTTATATCA  ATT
                                  A        AT
GAM622  JWA      3'  TTTACCTTGCACATTTTTTGTT 21142          GTC_    AA
                                GACAAGAAATGTG   GTGAA
                                ||||||||||||    |||||
                                TTGTTTTTTACAC   CATTT
                                       GTTC
GAM622  KIAA0095 3'  TTTCTGTATTATGTATTTTTGT 90921        _     _ T   A
            CA                    TGACAAGAA ATGTGGT CG GAAA
                                |||||||| ||||||| || ||||
                                ACTGTTTTT TGTATTA GT CTTT
                                     A      T _
GAM622  KIAA0164 3'  TTTCATGACCCTTTTATTG   28454     G   TGT
                                CAA AAA   GGTCGTGAAA
                                ||| |||   ||||||||||
                                GTT TTT   CCAGTACTTT
                                  A  TC_
GAM622  KIAA0212 3'  TTTATGTTGCATTTTTAGTCA  27946      A      TG T
                                TGAC AGAAATG  G CGTGAA
                                |||| |||||||  | ||||||
                                ACTG TTTTTAC  T GTATTT
                                  A      GT _
GAM622  KIAA0240 3'  TTTATTTTTATTTCTTGTCA   92444          TGGTC
                                TGACAAGAAATG    GTGAA
                                ||||||||||||    |||||
                                ACTGTTCTTTAT    TATTT
                                       TTT__
GAM622  KIAA0293 3'  TTATGCCGTTTACGTTTTTTGT 60609          _____ T    AAA
            T                   ACAAGAAATGT    GG CGTGA
                                ||||||||||||    || |||||
                                TGTTTTTTGCA    CC GTATT
                                       TTTG  _
GAM622  KIAA0447 3'  TGGCTATTTTTTTGTT      71679          T
                                GACAAGAAA GTGGTCG
                                ||||||||| |||||||
```

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                              TTGTTTTTT TATCGGT
                                    _
GAM622  KIAA0453 3' TGGCTTGTGGTTTTTGTCA   69057        ATGT_
                              TGACAAGAA    GGTCG
                              |||||||||    |||||
                              ACTGTTTTT    TCGGT
                                   GGTGT
GAM622  KIAA0680 3' TTTCAAAATTGCATTTCTTGT 28235         TG  CG
                              ACAAGAAATG  GT  TGAAA
                              ||||||||||  ||  |||||
                              TGTTCTTTAC  TA  ACTTT
                                    GT  AA
GAM622  KIAA0831 3' TTTTCAGCTCACGTGTCTTGTC 29986        A    _  CG
           A                   TGACAAGA ATGTG GT  TGAAAA
                              ||||||||| ||||| ||  ||||||
                              ACTGTTCT TGCAC CG  ACTTTT
                                   G    T  __
GAM622  KIAA0892 3' TTTTCATGACCACCCTGTTA   71017      A AAAT
                              TGACA G    GTGGTCGTGAAAA
                              ||||| |    ||||||||||||
                              ATTGT C    CACCAGTACTTTT
                                 _ C___
GAM622  KIAA0976 3' TTTGTGAATTGCATTTTTGTGT 29899     _      TG  _  TG  AA
           T                   GACA AGAAATG  GT CG  AA
                              |||| |||||||  || ||  ||
                              TTGT TTTTTAC  TA GT  TT
                                G      GT  A  GT
GAM622  KIAA1025 3' TTTTTGTGACTTTATTTTTTTA 63980    C      T    TG
                              A AAGAAATG GGTCG  AAAA
                              | ||||||||| |||||  ||||
                              A TTTTTTAT TCAGT  TTTT
                               T       T    GT
GAM622  KIAA1058 3' TTTTTGTGACTAGTTTTTG    82258       ATG     TG
                              CAAGAA   TGGTCG  AAAA
                              ||||||   ||||||  ||||
                              GTTTTT   ATCAGT  TTTT
                                 G__     GT
GAM622  KIAA1185 3' TTTTCACCCCAGTTTTTTTGTT 62613         TG   TC
                              GACAAGAAA  TGG  GTGAAAA
                              |||||||||  |||  |||||||
                              TTGTTTTTT  ACC  CACTTTT
                                    TG   C_
GAM622  KIAA1254 3' TTTTTATGATTTGATGAGTTTC 70029        GT____
           TTGT                AAGAAAT     GGTCGTGAAAA
                              |||||||     ||||||||||||
                              TTCTTTG     TTAGTATTTTT
                                 AGTAGT
GAM622  KIAA1320 3' ACCACGTTTCTTTTCA      69290     C
                              TGA AAGAAATGTGGT
                              ||| ||||||||||||
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                                ACT TTCTTTGCACCA
                                  T
GAM622  KIAA1348 3' TTTTTGTGATTATGCTTGT   68578      AAA      TG
                                ACAAG  TGTGGTCG  AAAA
                                |||||  ||||||||  ||||
                                TGTTC  GTATTAGT  TTTT
                                  ___      GT
GAM622  KIAA1349 3' TTTTTATGATTTTATTTTTT  70762       TG
                                AAGAAATG  GTCGTGAAAA
                                ||||||||  ||||||||||
                                TTTTTTAT  TAGTATTTTT
                                    TT
GAM622  KIAA1456 5' ATTATATTTCTTGTTA     66990
                                TGACAAGAAATGTGGT
                                ||||||||||||||||
                                ATTGTTCTTTATATTA

GAM622  KIAA1462 3' TAACAAAGTGACTATATTTCTT 91388    C         GTGAAAA
           TTTA                   TGA AAGAAATGTGGTC
                                ||| ||||||||||||
                                ATT TTCTTTATATCAG
                                  T          TGAAACAATT
GAM622  KIAA1786 3' TTGGTGTATTACATTTTTTGTT 66044           CGTGAAAA
           A                     TGACAAGAAATGTGGT
                                ||||||||||||||||
                                ATTGTTTTTTACATTA
                                        TGTGGTT
GAM622  KRTAP9-2 3' TTTTCATGATAAATTTGTGTT  49233     AG   GTG
                                GACA  AAAT   GTCGTGAAAA
                                ||||  ||||   ||||||||||
                                TTGT  TTTA   TAGTACTTTT
                                  G_    AA_
GAM622  LNX      3' TTTCAAATACCATGTTATTTGT 50923       A      CG_    A
           TA                     TGACAAG AATGTGGT   TGAAA
                                |||||||  ||||||||   |||||
                                ATTGTTT TTGTACCA   ACTTT
                                    A       TAA
GAM622  MADP-1   3' TTTTGTCATCATATTTCTTGT  52411           C TG   A
                                ACAAGAAATGTGGT G  AAA
                                ||||||||||||| |  |||
                                TGTTCTTTATACTA T  TTT
                                        C GT
GAM622  MGC12466 3' TTTTTATGGGAAAACTACTTTT 52633      T    _____
           TTGTT                   AGAAA GTGGT    CGTGAAAA
                                ||||| |||||    ||||||||
                                TTTTT CATCA    GTATTTTT
                                  _    AAAGG
GAM622  MGC12466 3' TTTTTATGGGAAAACTACTTTT 79039      T    _____
           TTGTT                   AGAAA GTGGT    CGTGAAAA
                                ||||| |||||    ||||||||
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                                TTTTT CATCA    GTATTTTT
                                   _    AAAGG
GAM622  MGC14844  3'  TTTTCCTGCTGCATTTCTTGT  50342         TG T  T
                                ACAAGAAATG  G CG GAAAA
                                ||||||||||  | || |||||
                                TGTTCTTTAC  C GT CTTTT
                                     GT _  C
GAM622  MGC3329   3'  TTTTTGTGGCTTCACTTGT   44021      AAA  T    TG
                                ACAAG   TG GGTCG  AAAA
                                |||||   || |||||  ||||
                                TGTTC   AC TCGGT  TTTT
                                   ___  T    GT
GAM622  MGC5395   3'  TTTTGTGACCGTTCTTTG    43935   C    ATG     TG
                                A AAGAA   TGGTCG  AAA
                                | |||||   ||||||  |||
                                G TTCTT   GCCAGT  TTT
                                 T    ____     GT
GAM622  MKI67IP   3'  TTTTCAATGTATTATATTTCTT 50498          _  _
                                AAGAAATGTGGT CGT GAAAA
                                |||||||||||| ||| |||||
                                TTCTTTATATTA GTA CTTTT
                                      T   A
GAM622  MO25      3'  TTTTGCACCACTTTTTTGTTA  32818          T    C TG
                                TGACAAGAAA GTGGT G  AAA
                                |||||||||| ||||| |  |||
                                ATTGTTTTTT CACCA C  TTT
                                      _    _ GT
GAM622  OSBPL3    3'  CTATACTTTCTTGTTA      31436          _
                                TGACAAGAAA TGTGG
                                |||||||||| |||||
                                ATTGTTCTTT ATATC
                                      C
GAM622  PAPSS2    3'  TTTTTATGATTAGATGCTTTGT 59598       AA  G
                                ACAAG  AT TGGTCGTGAAAA
                                |||||  || ||||||||||||
                                TGTTT  TA ATTAGTATTTTT
                                   CG  G
GAM622  PCDH19    3'  TTTTTATGACTAATAGTTTTTT 63714         G__
            G                    CAAGAAAT   TGGTCGTGAAAA
                                 ||||||||   ||||||||||||
                                 GTTTTTTG   ATCAGTATTTTT
                                      ATA
GAM622  PEF       3'  TTTTTAATTTGCATTTTTTTTC 24755     C       TG TCG
            A                    TGA AAGAAATG  G   TGAAAA
                                 ||| ||||||||  |   ||||||
                                 ACT TTTTTTAC  T   ATTTTT
                                   T       GT TA_
GAM622  PIG7      3'  TTTTATGACCTCCTTTTG    16796       AATGT
                                CAAGA    GGTCGTGAAA
                                |||||    ||||||||||
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                                GTTTT    CCAGTATTTT
                                  CCT__
GAM622  PLEKHA3  3'  TTTTTATGTATTTATTTTCTTG 38865        TGT  _
            TT                  GACAAGAAA  GGT CGTGAAAA
                                |||||||||  ||| ||||||||
                                TTGTTCTTT  TTA GTATTTTT
                                    TAT  T
GAM622  PRDM15   3'  TGGCTGTATTTCCTGTCA   61714     A    TG
                                TGACA GAAATG  GTCG
                                ||||| ||||||  ||||
                                ACTGT CTTTAT  CGGT
                                  C     GT
GAM622  PRRG1    3'  TTTTCTTTAGTTTTGTTTCTTG 6289          TGGTCGT_
            TTA                   TGACAAGAAATG      GAAAA
                                ||||||||||||       |||||
                                ATTGTTCTTTGT       CTTTT
                                      TTTGATTT
GAM622  RGS18    3'  TGATTATATTCTTGTTA     55394         A
                                TGACAAGAA TGTGGTCG
                                ||||||||| ||||||||
                                ATTGTTCTT ATATTAGT
                                    _
GAM622  RNPC2    3'  TTTCAAAATTATATTTCTTG   16923          CG    A
                                CAAGAAATGTGGT  TGAAA
                                ||||||||||||  |||||
                                GTTCTTTATATTA  ACTTT
                                     AA
GAM622  SEC15B   3'  TTTTCATTGACCTTTGCATTTT 66692        ____   _
            TTTCA                  AAGAAATGT   GGTCG TGAAAA
                                |||||||||   ||||| ||||||
                                TTTTTTACG   CCAGT ACTTTT
                                    TTT    T
GAM622  SOX6     3'  TTTTCATGAACTTGAGTTTTTT 52829         GT_  _
            GTT                    GACAAGAAAT   GGT CGTGAAAA
                                ||||||||||   ||| ||||||||
                                TTGTTTTTTG   TCA GTACTTTT
                                    AGT   A
GAM622  Spir-1   3'  ACTATCATTTTTTGTT      64694          _
                                GACAAGAAATG TGGT
                                |||||||||| ||||
                                TTGTTTTTTAC ATCA
                                     T
GAM622  TIX1     3'  CGGCTACGTTTCATGTCA    61741       A
                                TGACA GAAATGTGGTCG
                                ||||| ||||||||||||
                                ACTGT CTTTGCATCGGC
                                  A
GAM622  TOB2     3'  TTTTTATTTTTTACATTTTTTG 95628          TC_
                                CAAGAAATGTGG   GTGAAAA
                                ||||||||||||   |||||||
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                                GTTTTTTACATT   TATTTTT
                                      TTT
GAM622  TOPK     3'  TTTGAGGACCATAGTTTCTTGT 37507          _      GTGAAAA
            TA                    TGACAAGAAA TGTGGTC
                                  |||||||||| |||||||
                                  ATTGTTCTTT ATACCAG
                                       G      GAGTTT
GAM622  ZNF238   3'  TTTTCAATATATTTTTTGTC  20977           GTCG
                                  GACAAGAAATGTG    TGAAAA
                                  ||||||||||||    ||||||
                                  CTGTTTTTTATAT    ACTTTT
                                        A___
GAM622  ZNF31    3'  TTTGTAGACCACATTTCCTGTT 64993       A         GTGAAAA
            A                     TGACA GAAATGTGGTC
                                  ||||| ||||||||||
                                  ATTGT CTTTACACCAG
                                     C         ATGTTT
GAM622  LOC114932 3'  TTTTTGTGGTCACGTTTATTCT 72717        ___    GT  TG
            TGTTA                   CAAGAA   ATGTG  CG  AAAA
                                  ||||||   |||||  ||  ||||
                                  GTTCTT   TGCAC  GT  TTTT
                                     ATT    TG  GT
GAM622  LOC115294 3'  ATTTTCATGATCATTGCATATT 73012         _____
            TCTTGTCA                GAAATGTG    GTCGTGAAAA   T
                                  ||||||||    ||||||||||  |
                                  CTTTATAC    TAGTACTTTT   A
                                       GTTAC
GAM622  LOC122525 3'  TTTATATGAGCATATTTTATGT 76009      A       G     AAAA
            T                     GACA GAAATGTG TCGTG
                                  |||| |||||||| |||||
                                  TTGT TTTTATAC AGTAT
                                    A       G     ATTTT
GAM622  LOC144203 3'  TTGCAGTGGGCTATGGTTTCTT 76709          _     GTGAAAA
            GTCA                    GACAAGAAAT GTGGTC
                                  |||||||||| ||||||
                                  CTGTTCTTTG TATCGG
                                        G      GTGACGTTT
GAM622  LOC145645 3'  TTTTAATAATTCATATTTCATG 77327      A       TCG__     A
            TT                     GACA GAAATGTGG     TGAAA
                                  |||| |||||||||     |||||
                                  TTGT CTTTATACT     ATTTT
                                    A        TAATA
GAM622  LOC146381 5'  TTTTGCGGCCACCATTGT     77868      GAAAT      TG
                                  ACAA     GTGGTCG  AAA
                                  ||||     |||||||  |||
                                  TGTT     CACCGGC  TTT
                                    AC___       GT
GAM622  LOC146839 5'  TTGTTATTATTATATTTTTGTC 83819          A     C    AAA
            A                     TGACAAGAA TGTGGT GTGA
                                  ||||||||| |||||| ||||
```

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                                ACTGTTTTT ATATTA TATT
                                      _     T   GTTT
GAM622  LOC147671 3'  TTTTTATTTTTTACATTTTTTG 78464          TC_
                                CAAGAAATGTGG  GTGAAAA
                                |||||||||||  |||||||
                                GTTTTTTACATT  TATTTTT
                                    TTT
GAM622  LOC149628 3'  TTTTCACACACCATATTTCTTT 79466    C         C_
          CA                     TGA AAGAAATGTGGT  GTGAAAA
                                ||| ||||||||||||  |||||||
                                ACT TTCTTTATACCA  CACTTTT
                                  _         CA
GAM622  LOC150280 3'  TTTTTGCTCAATTTTTTTTGTC 79714         TG_  TC TG
          A                     TGACAAGAAA  TGG  G  AAAA
                                ||||||||||  |||  |  ||||
                                ACTGTTTTTT  ACT  C  TTTT
                                    TTA  __ GT
GAM622  LOC150482 3'  TTTTTATGACCACGTAATGTT  63076     AGAA
                                GACA   ATGTGGTCGTGAAAA
                                ||||   ||||||||||||||
                                TTGT   TGCACCAGTATTTTT
                                  AA__
GAM622  LOC150886 3'  TTTTCATGATTGCATTTT    85155      TG
                                GAAATG  GTCGTGAAAA
                                ||||||  ||||||||||
                                TTTTAC  TAGTACTTTT
                                   GT
GAM622  LOC151188 3'  ATTTTCATGTATGTACTACATT 80157         _____
          TTTTG                   GAAATGTGGT   CGTGAAAA  T
                                ||||||||||    ||||||||  |
                                TTTTACATCA    GTACTTTT  A
                                    TGTAT
GAM622  LOC151201 3'  TTTTCATGATTGCTTTTTGTT  85301       AT TG
                                GACAAGAA  G  GTCGTGAAAA
                                ||||||||  |  ||||||||||
                                TTGTTTTT  C  TAGTACTTTT
                                    __ GT
GAM622  LOC151470 3'  TTTTGTTATTACCTTTTTTGTT 80262        T    C TG  A
                                GACAAGAAA GTGGT G  AAA
                                |||||||| ||||| |  |||
                                TTGTTTTTT CATTA T  TTT
                                    C    T GT
GAM622  LOC152215 3'  TGTCACATTTTTTTGTTA    80492         _    T
                                TGACAAGAAA TGTGG CG
                                |||||||||| ||||| ||
                                ATTGTTTTTT ACACT GT
                                    T    _
GAM622  LOC152313 3'  GCCAATGGTCACAATTTTTGTT 85664        A   GT  GAAAA
                                GACAAGAA TGTG  CGT
                                |||||||| ||||  |||
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                                TTGTTTTT ACAC  GTA
                                    A   TG   ACCGT
GAM622   LOC153279 3'  GATTTTATTTTTTGTTA     80807          TG
                                TGACAAGAAATG  GTC
                                ||||||||||||  |||
                                ATTGTTTTTTAT  TAG
                                     TT
GAM622   LOC153346 5'  GGCTGTATTTTTGGTCA     86024      A      TG
                                TGAC AGAAATG  GTC
                                |||| |||||||  |||
                                ACTG TTTTTAT  CGG
                                  G      GT
GAM622   LOC154743 3'  TTTAGTCCACATTGTCTTGTCA 81118         _      TCG
                                TGACAAGA AATGTGG   TGAA
                                |||||||| |||||||   ||||
                                ACTGTTCT TTACACC   ATTT
                                     G      TG_
GAM622   LOC154743 3'  TTTCATAACTTTCTTGTT    81119        ATGT   CG
                                GACAAGAA    GGT  TGAAA
                                ||||||||    |||  |||||
                                TTGTTCTT    TCA  ACTTT
                                     _____   AT
GAM622   LOC155061 3'  TTTTCAGGGCGTGCATTTCTGT 81273       A       _   G
           CA                     TGACA GAAATGTG GTC TGAAAA
                                |||||| |||||||| ||| ||||||
                                ACTGT CTTTACGT CGG ACTTTT
                                  _       G   G
GAM622   LOC157708 3'  GGAAGATGCCACATTTTTTGTT 81560             T   GAAAA
           A                      TGACAAGAAATGTGG CGT
                                |||||||||||||| |||
                                ATTGTTTTTTACACC GTA
                                       _   GAAGGG
GAM622   LOC196812 3'  TTTTATGTTTTGTTTTTTGTCA 89580           TG T
                                TGACAAGAAATG  G CGTGAAA
                                ||||||||||||  | |||||||
                                ACTGTTTTTTGT  T GTATTTT
                                       TT _
GAM622   LOC197439 5'  TTTTGCGGCCACCATTGT    88076      GAAAT      TG
                                ACAA    GTGGTCG  AAA
                                ||||    |||||||  |||
                                TGTT    CACCGGC  TTT
                                  AC___      GT
GAM622   LOC200728 3'  ACATATGACCATGTTTCTTG   90113              AAAA
                                CAAGAAATGTGGTCGTG
                                |||||||||||||||||
                                GTTCTTTGTACCAGTAT
                                       ACAT
GAM622   LOC200853 3'  TAGTACACCGTGTTTCTGTT   88917      A   TG   C   AAAA
                                GACA GAAA  TGGT GTG
                                |||| ||||  |||| |||
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                                TTGT CTTT  GCCA CAT
                                  _   GT   _  GATT
GAM622  LOC201484 3'  TTTTCATGGTCACAGATTGT  89787     GAAA   GT
                                ACAA   TGTG  CGTGAAAA
                                ||||   ||||  ||||||||
                                TGTT   ACAC  GTACTTTT
                                  AG__   TG
GAM622  LOC202025 3'  TTCAGATTGCATCTTTTGTC  90300       A  TG  G
                                GACAAGA ATG  GTC TGAA
                                ||||||| |||  ||| ||||
                                CTGTTTT TAC  TAG ACTT
                                    C  GT  _
GAM622  LOC202451 3'  TGTCCTACATTTCTTTCA    90356    C       _ T
                                TGA AAGAAATGT GG CG
                                ||| |||||||| || ||
                                ACT TTCTTTACA CC GT
                                  _       T  T
GAM622  LOC202986 3'  TTTTGCTCACATGTTTTTTGTT 90446          GTC TG  A
                                GACAAGAAATGTG  G  AAA
                                ||||||||||||  |  |||
                                TTGTTTTTTGTAC  C  TTT
                                       ACT GT
GAM622  LOC219914 3'  GCGGCCGTGTTTTCTGTT   93327     AG  TG
                                GACA  AAA  TGGTCGT
                                ||||  |||  |||||||
                                TTGT  TTT  GCCGGCG
                                  CT  GT
GAM622  LOC220930 5'  TTTATGCTTATAATTTTTGTCA 93134        A    T
                                TGACAAGAA TGTGG CGTGAA
                                ||||||||| ||||| ||||||
                                ACTGTTTTT ATATT GTATTT
                                     A   C
GAM622  LOC221354 3'  TTTTGCTCACATGTTTTTTG  92415         GTC TG  A
                                CAAGAAATGTG  G  AAA
                                ||||||||||  |  |||
                                GTTTTTTGTAC  C  TTT
                                       ACT GT
GAM622  LOC221763 3'  TTTTTAAACCATTTTTTCTTG  93799       T_   CG
                                CAAGAAA  GTGGT  TGAAAA
                                |||||||  |||||  ||||||
                                GTTCTTT  TACCA  ATTTTT
                                    TT   A_
GAM622  LOC253233 5'  TGGACAGACTGCATTGCTTGTT 95635      A   TG  _  GAAAA
                                GACAAG AATG  GTC GT
                                |||||| ||||  ||| ||
                                TTGTTC TTAC  CAG CA
                                   G   GT  A  GGT
GAM622  LOC254778 3'  TTTCATGGCCATTTG      96132    GAAAT
                                CAA    GTGGTCGTGAAA
                                |||    ||||||||||||
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                                GTT     TACCGGTACTTT
                                  _____
GAM622   LOC255308 3'  TTTGGCCCCATATTTTATGTT  94539      A        TC  G
                                GACA GAAATGTGG  GT AAA
                                |||| |||||||||  || |||
                                TTGT TTTTATACC  CG TTT
                                  A        C_  G
GAM622   LOC255324 3'  TTTCACTCTGGGTTTTTTGTT  95876          G   TC
                                GACAAGAAAT TGG  GTGAAA
                                |||||||||| |||  ||||||
                                TTGTTTTTTG GTC  CACTTT
                                      G   T_
GAM622   LOC256730 3'  CATTGCGACTGTGTTTCTGTTA 95229       A     TG    TG AAA
                                TGACA GAAATG  GTCG  A
                                ||||| ||||||  ||||  |
                                ATTGT CTTTGT  CAGC  T
                                  _     GT    GT ACA
GAM622   LOC257277 5'  TTTCATGATCACTATTT     95263      _
                                AAAT GTGGTCGTGAAA
                                |||| ||||||||||||
                                TTTA CACTAGTACTTT
                                  T
GAM622   LOC257465 3'  TTTTTACCAGTTTTATTTTCTT 81604         T    TC___
           GTCA                   ACAAGAAA GTGG     GTGAAAA
                                |||||||| ||||     |||||||
                                TGTTCTTT TATT     CATTTTT
                                    _    TTGAC
GAM622   LOC51313  3'  TTTTCACGGTTACGTCTGTTA  33515      A  AA    GT
                                TGACA GA  TGTG  CGTGAAAA
                                ||||| ||  ||||  ||||||||
                                ATTGT CT  GCAT  GCACTTTT
                                  _ __    TG
GAM622   LOC90509  3'  TTTTCATGGTAACATTTTTCA  63108    A       GG
                                C AGAAATGT  TCGTGAAAA
                                | ||||||||  |||||||||
                                A TTTTTACA  GGTACTTTT
                                 C        AT
GAM622   LOC90670  3'  TAGGATTTATTTTTTGTCA    63742           T   G
                                TGACAAGAAATG GGTC TG
                                |||||||||||| |||| ||
                                ACTGTTTTTTAT TTAG AT
                                      _    G
GAM622   LOC92405  3'  TTCCTAGGCCAGTTTCTTGTT  69195          G    GT_
                                GACAAGAAAT TGGTC   GAA
                                |||||||||| |||||   |||
                                TTGTTCTTTG ACCGG   CTT
                                      _     ATC
GAM623   AHCY      3'  GCCACAGGGAACCATGAGC    5475     _          A
                                GC CATGGTTCCCTGT GC
                                || ||||||||||||| ||
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                                CG GTACCAAGGGACA CG
                                 A          C
GAM623  BAP1    3'  CTACAGGGTCCTAGCT     16215    CA   TT
                                GGC  TGG  CCCTGTAG
                                |||  |||  ||||||||
                                TCG  ATC  GGGACATC
                                  __   CT
GAM623  CACNG6   5'  TCTGAGCCCAAGGGAACCCCGG 49104     AT      GTA  _
            CC                    GGCC  GGTTCCCT   GC CAGA
                                |||| ||||||||  || ||||
                                CCGG  CCAAGGGA   CG GTCT
                                  CC       ACC  A
GAM623  CD47    3'  TTCTGTTTAAGCACCATGGCC  8350         TCC  G   C
                                GGCCATGGT   CT TAG CAGAA
                                |||||||||   || ||| |||||
                                CCGGTACCA   GA ATT GTCTT
                                     C__  _   T
GAM623  CML66    5'  TTCTGGGATGGGAACCACGCC  68234     CA      T  AG
                                GGC  TGGTTCCC GT  CCAGAA
                                |||  |||||||| ||  ||||||
                                CCG  ACCAAGGG TA  GGTCTT
                                  C_       _ G_
GAM623  CTSB    3'  CTGGCTACATCCCAGCC     64727     CA   TTCCC
                                GGC  TGG    TGTAGCCAG
                                |||  |||    |||||||||
                                CCG  ACC    ACATCGGTC
                                  __   CT___
GAM623  DPYSL2   3'  TACAGGGAACCACACC      7302     CCA
                                GG   TGGTTCCCTGTA
                                ||   ||||||||||||
                                CC   ACCAAGGGACAT
                                 AC_
GAM623  HTR2A    3'  GCTACAGGGGAGGCT       5258      ATGG
                                GGCC    TTCCCTGTAGC
                                ||||    ||||||||||
                                TCGG    AGGGGACATCG
                                  ____
GAM623  ICMT    3'  GGCCAAGGGGACCATGGCC    24818           GTA
                                GGCCATGGTTCCCT   GCC
                                ||||||||||||||   |||
                                CCGGTACCAGGGGA   CGG
                                       AC_
GAM623  IFI27    3'  CTGCAGAGAAGAGAACCATGCC 18647     C      C_____
                                GGC ATGGTTC     CTGTAG
                                ||| |||||||     ||||||
                                CCG TACCAAG     GACGTC
                                  _      AGAAGA
GAM623  MAP3K14  3'  GGCTCACAGTGGGAACCAGGGC 14208      A       __   _
            C                     GGCC TGGTTCCC  TGT AGCC
                                |||| ||||||||  ||| ||||
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                                CCGG ACCAAGGG  ACA TCGG
                                  G       TG   C
GAM623  OVOL1    5'  TCTAGCTACAGCATGGCC    15860        GTTCC      C
                                GGCCATG    CTGTAGC AGA
                                |||||||    ||||||| |||
                                CCGGTAC    GACATCG TCT
                                    _____      A
GAM623  PCTK3    3'  TCTGGCTTGAACCATGGCT    72968          CCTGT
                                GGCCATGGTTC    AGCCAGA
                                ||||||||||    |||||||
                                TCGGTACCAAG    TCGGTCT
                                      T____
GAM623  PDGFRB   3'  TCTGGGGACTCAGGAACCATGC 65981     C       CT_  AG
              C                  GGC ATGGTTCC   GT  CCAGA
                                ||| ||||||||   ||  |||||
                                CCG TACCAAGG   CA  GGTCT
                                  _       ACT  GG
GAM623  PLP2     3'  TCTGACTGAACCATGCC     10655     C      CCTGT  C
                                GGC ATGGTTC    AG CAGA
                                ||| |||||||    || ||||
                                CCG TACCAAG    TC GTCT
                                  _      _____ A
GAM623  RFNG     3'  GGCGCGGGGAACCAGAGCC    88178     CA         A
                                GGC  TGGTTCCCTGT GCC
                                |||  ||||||||||| |||
                                CCG  ACCAAGGGGCG CGG
                                  AG          _
GAM623  TM7SF2   5'  TCCGGCGGAGCGGAGACCATGG 12332          _  _  GTA   A
              CC                   GGCCATGGT TCC CT   GCC GA
                                ||||||||| ||| ||   ||| ||
                                CCGGTACCA AGG GA   CGG CT
                                     G   C  GG_   C
GAM623  TSC      3'  ACATGGAAACCATGGCC     35445          _  C
                                GGCCATGGTT CC TGT
                                |||||||||| || |||
                                CCGGTACCAA GG ACA
                                      A  T
GAM623  ARHGEF16 5'  TCTGGCTGAGGAACCCAGCC   27072     CAT     CTG
                                GGC   GGTTCC   TAGCCAGA
                                |||   ||||||   ||||||||
                                CCG   CCAAGG   GTCGGTCT
                                  AC_     A__
GAM623  C12orf5  3'  CTCCAGTGGAACCATAGCC    39810     C       _   T
                                GGC ATGGTTCC CTG AG
                                ||| |||||||| ||| ||
                                CCG TACCAAGG GAC TC
                                  A       T   C
GAM623  CRA      3'  CTGGCTCCCTAGACCACAGCC  21973     CA     CCCTGT
                                GGC  TGGTT     AGCCAG
                                |||  |||||     ||||||
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                                CCG  ACCAG     TCGGTC
                                  AC    ATCCC_
GAM623  DKFZP547L112 5'  TCTGGCATGGGGGAACCCGGCC 66531      AT      GTA
                                GGCC  GGTTCCCT   GCCAGA
                                ||||  ||||||||   ||||||
                                CCGG  CCAAGGGG   CGGTCT
                                  C_       GTA
GAM623  DNAL4    3'  GCAGGGAACCCTGGCC      19216      T
                                GGCCA GGTTCCCTGT
                                ||||| ||||||||||
                                CCGGT CCAAGGGACG
                                   C
GAM623  FLJ11186 3'  CTGGCTACAAGTGATCCGCC   37141     CAT  T  C  _
                                GGC   GG TC CT GTAGCCAG
                                |||   || || || ||||||||
                                CCG   CC AG GA CATCGGTC
                                  ___  T  T  A
GAM623  HTMP10   3'  CTGACCACAGGGAAGCACC    52610    CCA  G      AGC
                                GG   TG TTCCCTGT   CAG
                                ||   || ||||||||   |||
                                CC   AC AAGGGACA   GTC
                                 ___  G       CCA
GAM623  KIAA1026 3'  TCTGGCTACAGGGCGAC     71214     _
                                GTT CCCTGTAGCCAGA
                                ||| ||||||||||||
                                CAG GGGACATCGGTCT
                                  C
GAM623  KIAA1219 3'  TCTGGGGGGAAACCAGGACC   61372    _  A    _   GTAG
                                GG CC TGGTT CCCT    CCAGA
                                || || ||||| ||||    |||||
                                CC GG ACCAA GGGG    GGTCT
                                 A  _    A   _____
GAM623  KIAA1858 3'  TCTGACCACAGGGTCATGCC   67138     C    TT     AGC
                                GGC ATGG  CCCTGT   CAGA
                                ||| ||||  ||||||   ||||
                                CCG TACT  GGGACA   GTCT
                                  _   __      CCA
GAM623  KIAA1858 3'  TCTGACCACAGGGTCATGCC   67139     C    TT     AGC
                                GGC ATGG  CCCTGT   CAGA
                                ||| ||||  ||||||   ||||
                                CCG TACT  GGGACA   GTCT
                                  _   __      CCA
GAM623  MGC2477  5'  GCAAGGAATCCATGGCC     44064         _   C
                                GGCCATGG TTCC TGT
                                |||||||| |||| |||
                                CCGGTACC AAGG ACG
                                     T   A
GAM623  MGC2647  3'  GCCACAGGCTGTGGCT      73705         TTC    A
                                GGCCATGG   CCTGT GC
                                ||||||||   ||||| ||
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                                TCGGTGTC  GGACA CG
                                   ___    C
GAM623  MGC26766 5'  TCCGCACTTGAAATCCATGGCC 58821       __  CCT  A  CA
                                GGCCATGG  TTC  GT GC  GA
                                ||||||||  |||  || ||  ||
                                CCGGTACC  AAG  CA CG  CT
                                    TA  TT_  _  C_
GAM623  MIDORI   3'  TCTGGCTACAGCAAGACC    73795     CC_
                                GGTT  CTGTAGCCAGA
                                ||||  ||||||||||
                                CCAG  GACATCGGTCT
                                  AAC
GAM623  MKRN2    3'  CTAGGGGAACCAAGCC     72413     CA       G
                                GGC  TGGTTCCCT TAG
                                |||  ||||||||| |||
                                CCG  ACCAAGGGG ATC
                                  A_       _
GAM623  PTD008   3'  CTGGATAGAGGGAACCTGGCC  32349      T      G  G
                                GGCCA GGTTCCCT TA CCAG
                                ||||| |||||||| || ||||
                                CCGGT CCAAGGGA AT GGTC
                                   _       G  A
GAM623  SIAT9    3'  CTGGGCTACAGAAACCACAGTC 13990     CA    CC      _
                                GGC  TGGTT  CTGTAGCC AG
                                |||  |||||  |||||||| ||
                                CTG  ACCAA  GACATCGG TC
                                  AC    A_      G
GAM623  ZDHHC4   5'  CTGGAAGAACCATGTCC     36156    C      CCTGTAG
                                GG CATGGTTC      CCAG
                                || ||||||||      ||||
                                CC GTACCAAG      GGTC
                                 T       AA_____
GAM623  LOC139197 5'  CTGCCCAGGGAACCTCAGCC   75821     CAT       TA  C
                                GGC   GGTTCCCTG  GC AG
                                |||   |||||||||  || ||
                                CCG   CCAAGGGAC  CG TC
                                  ACT       C_  _
GAM623  LOC143381 3'  CTGAGTATAGGGAACCAGGGCC 76547      A         GC
                                GGCC TGGTTCCCTGTA  CAG
                                |||| ||||||||||||  |||
                                CCGG ACCAAGGGATAT  GTC
                                   G          GA
GAM623  LOC143425 3'  CTGGTGGAGAAACGATGACC   87636    C   G   _ _  TGTA
                                GG CAT GTT C CC    GCCAG
                                || ||| ||| | ||    |||||
                                CC GTA CAA G GG    TGGTC
                                 A   G   A A  _____
GAM623  LOC147341 3'  CTGGCTTAAGTGGGAGCCATGG 83993            TGT__
             CC                   GGCCATGGTTCCC     AGCCAG
                                ||||||||||||     ||||||
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                                CCGGTACCGAGGG    TCGGTC
                                      TGAAT
GAM623  LOC148397 5'  TCTGGAGGAGCCATGGCC    78824          CTGTAG
                                GGCCATGGTTCC    CCAGA
                                ||||||||||||    |||||
                                CCGGTACCGAGG    GGTCT
                                      A_____
GAM623  LOC149670 3'  CTGAGATTGGGAACCACC    79488    CCA      T  AGC
                                GG   TGGTTCCC GT   CAG
                                ||   |||||||| ||   |||
                                CC   ACCAAGGG TA   GTC
                                 ___      T  GA_
GAM623  LOC151146 5'  CTGGCTACAGTTTCAGGCC    80136     A   TTCC
                                GGCC TGG    CTGTAGCCAG
                                |||| |||    ||||||||||
                                CCGG ACT    GACATCGGTC
                                  _   TT__
GAM623  LOC152190 5'  CTGGCTACTCCATGATC     69656    GC    TTCCCT
                                G  CATGG     GTAGCCAG
                                |  |||||     ||||||||
                                C  GTACC     CATCGGTC
                                 TA    T_____
GAM623  LOC153454 3'  GGCATAGGAGCCATAGCC    80834     C      C   A
                                GGC ATGGTTCC TGT GCC
                                ||| |||||||| ||| |||
                                CCG TACCGAGG ATA CGG
                                  A      _   _
GAM623  LOC153577 5'  CTACAGGGACCACGGCC     86057     A    T
                                GGCC TGGT CCCTGTAG
                                |||| |||| ||||||||
                                CCGG ACCA GGGACATC
                                  C    _
GAM623  LOC200473 3'  CTACAGGAAAGGAACCATCGCC 90075     C       ____
                                GGC ATGGTTCC    CTGTAG
                                ||| ||||||||    ||||||
                                CCG TACCAAGG    GACATC
                                  C       AAAG
GAM623  LOC200953 5'  GTGGGGAACCATGGTC      90211           TG
                                GGCCATGGTTCCC  T
                                ||||||||||||  |
                                CTGGTACCAAGGG  G
                                      GT
GAM623  LOC201500 5'  TCTGGCTGAGAACATGGCC    89788       G   CCTG
                                GGCCATG TTC    TAGCCAGA
                                |||||||  |||    ||||||||
                                CCGGTAC AAG    GTCGGTCT
                                    _   A___
GAM623  LOC219621 5'  GGCGGGAACCACGCC       91459     CA       TGTA
                                GGC  TGGTTCCC    GCC
                                |||  ||||||||    |||
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                                CCG ACCAAGGG  CGG
                                  C_     ____
GAM623  LOC255452 3' CTACAGGGAACAGGCT    97531    ATG
                                GGCC GTTCCCTGTAG
                                |||| ||||||||||
                                TCGG CAAGGGACATC
                                  A__
GAM623  LOC89944  3' CTGGCAGAAGCCATGGCC   91546      CC GTA
                                GGCCATGGTT CT GCCAG
                                |||||||||| || |||||
                                CCGGTACCGA GA CGGTC
                                     A_ ___
GAM623  LOC89944  3' CTGGCAGAAGCCATGGCC   91547      CC GTA
                                GGCCATGGTT CT GCCAG
                                |||||||||| || |||||
                                CCGGTACCGA GA CGGTC
                                     A_ ___
GAM623  LOC89944  3' CTGGCAGAAGCCATGGCC   91548      CC GTA
                                GGCCATGGTT CT GCCAG
                                |||||||||| || |||||
                                CCGGTACCGA GA CGGTC
                                     A_ ___
GAM623  LOC90379  3' TCCAACTACCTCCGTGGCC   62538     TTCCCT  CCA
                                GGCCATGG   GTAG GA
                                |||||||    |||| ||
                                CCGGTGCC   CATC CT
                                    TC____  AAC
GAM624  CNGA1     3' CAACTGATAATGTGCAAA   59507      GC  A
                                TTTGCACATTA TAG TTG
                                |||||||||| ||| |||
                                AAACGTGTAAT GTC AAC
                                     A_  _
GAM624  ESRRG     3' TGGCAGTCTTATGTGCAAA  66396      TAGCT
                                TTTGCACAT   AGATTGCCA
                                |||||||||   |||||||||
                                AAACGTGTA   TCTGACGGT
                                    T____
GAM624  KCNJ3     3' GCAATAATGTGCAAA     9525       GCTAGA
                                TTTGCACATTA    TTGC
                                ||||||||||     ||||
                                AAACGTGTAAT    AACG
                                      _______
GAM624  SDC2      3' GCAAATTAATGTGTAAA   67132       CTAGA
                                TTTGCACATTAG   TTGC
                                ||||||||||||   ||||
                                AAATGTGTAATT   AACG
                                     A____
GAM624  USP9X     3' ATGGCCTGATGCTAATGTGTAA 16206       TAGATT
          A                     TTTGCACATTAGC    GCCAT
                                ||||||||||||     |||||
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                                AAATGTGTAATCG     CGGTA
                                      TAGTC_
GAM624  AMOTL1   3'  GGCAAGTAATGTGCAAA     73650          G  AGAT
                                TTTGCACATTA CT    TGCC
                                |||||||||| ||    ||||
                                AAACGTGTAAT GA    ACGG
                                      _ ____
GAM624  BCAR3    3'  AGTAATAATGTGCAAA      13098          __
                                TTTGCACATTA  GCT
                                |||||||||| |||
                                AAACGTGTAAT  TGA
                                      AA
GAM624  DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930          AGCTA    C
                                TTTGCACATT    GATTG CA
                                |||||||||     ||||| ||
                                AGACGTGTAA    TTAAC GT
                                      A____    A
GAM624  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                TTTGCACATTAG  AGA TG CAT
                                |||||||||||  ||| || |||
                                AGACGTGTAATC  TTT AC GTA
                                      __  T  A
GAM624  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
          AA                    TTTGCACATTAGCTAGATTGCCAT
                                ||||||||||||||||||||||||
                                AAACGTGTAATCGATCTAACGGTA

GAM625  RUNX3    3'  CAGGCTGCATGGATTCTCACA  15111     CA       T_
                                TGTG  AATCCATGC  TCTG
                                ||||  |||||||||  ||||
                                ACAC  TTAGGTACG  GGAC
                                  TC       TC
GAM625  TACR1    3'  CCATCAGAAACACCCTCACA   6471      CAAATCCA  C
                                TGTG       TG TTCTGATGG
                                ||||       || |||||||||
                                ACAC       AC AAGACTACC
                                  TCCC____  A
GAM625  CPR2     3'  CATCACCACAATTTGCACA   48093         CCA  CTTC
                                TGTGCAAAT   TG   TGATG
                                |||||||||   ||   |||||
                                ACACGTTTA   AC   ACTAC
                                      ___  ACC_
GAM625  FXYD5    3'  CCATCAGAAACAGGAGCTGACA 26342     G  AA   A  C
                                TGT CA  TCC TG TTCTGATGG
                                ||| ||  ||| || |||||||||
                                ACA GT  AGG AC AAGACTACC
                                  _  CG   _  A
GAM625  KIAA0674 3'  AAGCATGATTTTGCACA     60611         TC
                                TGTGCAAA  CATGCTT
                                ||||||||  |||||||
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                                ACACGTTT  GTACGAA
                                    TA
GAM625  KIAA0903  3'  CCTGTGAAATAGATTTGCACA  71406        C  GC   TGAT
                                TGTGCAAATC AT  TTC   GG
                                |||||||||| ||  |||   ||
                                ACACGTTTAG TA  AAG   CC
                                     A  __   TGT_
GAM625  KLHL4    3'  CCATCAGAATAGAGACCTGCA  38921     AA  CA  C
                                TGCA  TC  TG TTCTGATGG
                                ||||  ||  || |||||||||
                                ACGT  AG  AT AAGACTACC
                                  CC  AG  _
GAM625  RoXaN    3'  CAGGAGCACAGCCTGCACA   46639      AATCCA
                                TGTGCA     TGCTTCTG
                                ||||||     ||||||||
                                ACACGT     ACGAGGAC
                                   CCGAC_
GAM625  STARD7   3'  CAGGGACATGAATTTGTACA  57696        C   CT
                                TGTGCAAAT CATG  TCTG
                                ||||||||| ||||  ||||
                                ACATGTTTA GTAC  GGAC
                                     A   AG
GAM625  STARD7   3'  CAGGGACATGAATTTGTACA  39329        C   CT
                                TGTGCAAAT CATG  TCTG
                                ||||||||| ||||  ||||
                                ACATGTTTA GTAC  GGAC
                                     A   AG
GAM625  LOC143173 5'  GGAAGCTAAATTTGCACA   60376        CCAT
                                TGTGCAAAT   GCTTCT
                                |||||||||   ||||||
                                ACACGTTTA   CGAAGG
                                     AAT_
GAM625  LOC145173 3'  AAGCAAAATTTGCACA     77040        CCA
                                TGTGCAAAT  TGCTT
                                |||||||||  |||||
                                ACACGTTTA  ACGAA
                                     AA_
GAM625  LOC148932 3'  CCATCAGATGGACGATCTGAAC 79105    G  A   CATG  _
           A                     TGT CA ATC   CT TCTGATGG
                                ||| || |||   || ||||||||
                                ACA GT TAG   GG AGACTACC
                                  A  C   CA__  T
GAM625  LOC150157 5'  CCATCAGGACGAGACCTCACA  84874     CAAA  CA  C
                                TGTG   TC  TG TTCTGATGG
                                ||||   ||  || |||||||||
                                ACAC   AG  GC AGGACTACC
                                  TCC_  A_  _
GAM625  LOC221288 3'  GAAGCATAGATTCACA     93614      CA   C
                                TGTG  AATC ATGCTTC
                                ||||  |||| |||||||
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                                ACAC  TTAG TACGAAG
                                  __   A
GAM626  EVC     3'  CAGCCCCTCTCACCACAG    27288    CAT      A
                                CTG   TGAGAGGG GTTG
                                |||   |||||||| ||||
                                GAC   ACTCTCCC CGAC
                                  ACC       _
GAM626  EVC     3'  CCATCCCCTCTCACCACAG   27291    CAT      AGTT
                                CTG   TGAGAGGG   GTGG
                                |||   ||||||||   ||||
                                GAC   ACTCTCCC   TACC
                                  ACC       C___
GAM626  EVC     3'  CAGCCCCTCTCACCACAG    27286    CAT      A
                                CTG   TGAGAGGG GTTG
                                |||   |||||||| ||||
                                GAC   ACTCTCCC CGAC
                                  ACC       _
GAM626  HIVEP3   5'  CTCCCTCCAACACAGT     44436     CA   A
                                ACTG  TTG GAGGGAG
                                ||||  ||| |||||||
                                TGAC  AAC CTCCCTC
                                  AC  _
GAM626  KIR2DL1  3'  GGCTCCCTCTTAACGCAG    26425     A
                                CTGC TTGAGAGGGAGTT
                                |||| ||||||||||||
                                GACG AATTCTCCCTCGG
                                  C
GAM626  KIR2DL2  3'  GGCTCCCTCTTAACGCAG    26427     A
                                CTGC TTGAGAGGGAGTT
                                |||| ||||||||||||
                                GACG AATTCTCCCTCGG
                                  C
GAM626  KIR2DS2  3'  GGCTCCCTCTTAACACAG    24599     CA
                                CTG  TTGAGAGGGAGTT
                                |||  ||||||||||||
                                GAC  AATTCTCCCTCGG
                                  AC
GAM626  MAFF     5'  CCCACAACAAAACTCAGCGCAG 24646      A    AGGGA
                                CTGC TTGAG    GTTGTGGG
                                |||| |||||    ||||||||
                                GACG GACTC    CAACACCC
                                  C    AAAA_
GAM626  PES1     3'  CCACAGCCCCCTCCCACACAGT 26671      CAT  A    A
                                ACTG   TG GAGGG GTTGTGG
                                ||||   || ||||| |||||||
                                TGAC   AC CTCCC CGACACC
                                  AC_  C    C
GAM626  RAD9     3'  CCACAACCCCCAGCCAAT    15933      AGA   A
                                ATTG   GGG GTTGTGG
                                ||||   ||| |||||||
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                                TAAC   CCC CAACACC
                                  CGA   C
GAM626  SPON1    3'  CCCAAAGCCCCCCCAATGCA   62448       AGA   A   G
                                TGCATTG   GGG GTT TGGG
                                |||||||   ||| ||| ||||
                                ACGTAAC   CCC CGA ACCC
                                    CC_   _   A
GAM626  DCTN3    3'  CCCACCCTCCCCCCAATCAGT  23372     C    AGA    TT
                                ACTG ATTG   GGGAG  GTGGG
                                |||| ||||   |||||  |||||
                                TGAC TAAC   CCCTC  CACCC
                                  _   CC_    C_
GAM626  DCTN3    3'  CCCACCCTCCCCCCAATCAGT  44308     C    AGA    TT
                                ACTG ATTG   GGGAG  GTGGG
                                |||| ||||   |||||  |||||
                                TGAC TAAC   CCCTC  CACCC
                                  _   CC_    C_
GAM626  FLJ22035 3'  CTATTTTCTCCCTCTCATCACA 44536     CAT       TT_
           GT                    ACTG   TGAGAGGGAG   GTGG
                                ||||   ||||||||||   ||||
                                TGAC   ACTCTCCCTC   TATC
                                  ACT        TTT
GAM626  KIAA0471 5'  CCTGGCTCCCCTCCCACCGCAG 29392      ATT__   A      T
           T                     ACTGC    GAG GGGAGTTG GG
                                |||||    ||| |||||||| ||
                                TGACG    CTC CCCTCGGT CC
                                  CCACC   _      _
GAM626  KIAA0551 3'  CCCTCCGCCCCTCCCAGTACAG 66838     C    A    A  TGT
           T                     ACTG ATTG GAGGG GT   GGG
                                |||| |||| ||||| ||   |||
                                TGAC TGAC CTCCC CG   CCC
                                  A   C    _ CCT
GAM626  MGC17303 3'  CCCACAACCCCCTCTCCTTTCT 57500     CATT____      A
           TTCAGT                   CTG       GAGAGGG GTTGTGGG
                                |||       ||||||| ||||||||
                                GAC       CTCTCCC CAACACCC
                                  TTTCTTTC      C
GAM626  LOC145739 3'  CCACAGTTCCCACCACAGT   77440     CAT  AGA   GT
                                ACTG   TG   GGGA  TGTGG
                                ||||   ||   ||||  |||||
                                TGAC   AC   CCCT  ACACC
                                  ___  CA_    TG
GAM626  LOC149952 3'  CCACAACTTCCCACACAGT   79555     CAT  AGA
                                ACTG   TG   GGGAGTTGTGG
                                ||||   ||   ||||||||||
                                TGAC   AC   CCTTCAACACC
                                  ___  AC_
GAM626  LOC200317 5'  CCCACGTTTTCCCTCCCAACAC 88792    CA   A      T_
           A                     TG  TTG GAGGGAG  TGTGGG
                                ||  ||| |||||||  ||||||
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                                AC  AAC CTCCCTT  GCACCC
                                 AC   C      TT
GAM626  LOC51125  3'  CCCACAGAATTTTCTCATATAC 32248     CAT_      AG
            AGT                   ACTG   TGAGAGGG  TTGTGGG
                                ||||   ||||||||  |||||||
                                TGAC   ACTCTTTT  GACACCC
                                  ATAT       AA
GAM626  LOC91409  3'  CCAAGCCTCTCATGCAGT    65953       T     GAGTTG
                                ACTGCAT GAGAGG     TGG
                                |||||||  ||||||     |||
                                TGACGTA CTCTCC     ACC
                                   _     GA____
GAM627  DACH      3'  TGAGAATGTTTGTAAATGTACA 54974      CATCC   CT
                                TGTACA    ACA  CATTCTCA
                                ||||||    |||  ||||||||
                                ACATGT    TGT  GTAAGAGT
                                   AAA__   TT
GAM627  IL11RA    3'  GGAACGTGTGTAATGTGTACA  15712        C_    TCA
                                TGTACACAT  CACAC   TTCT
                                |||||||||  |||||   ||||
                                ACATGTGTA  GTGTG   AAGG
                                     AT    C__
GAM627  LYPLA1    3'  AGAATGAGGTGGTATTACA   20922     CACAT    A
                                TGTA    CCAC CTCATTCT
                                ||||    |||| ||||||||
                                ACAT    GGTG GAGTAAGA
                                  TAT__   _
GAM627  NAPB      3'  GAGAATGAATGTATGT     70183     CC   C
                                ACAT  ACA TCATTCTC
                                ||||  ||| ||||||||
                                TGTA  TGT AGTAAGAG
                                  __   A
GAM627  NRF1      3'  GAATATATGTATATGTGTACA  60120        CC   CTC
                                TGTACACAT  ACA   ATTC
                                |||||||||  |||   ||||
                                ACATGTGTA  TGT   TAAG
                                     TA   ATA
GAM627  PRKAB1    3'  AGAGGGAATGGACTGTACA   20734      CA   CA   AT
                                TGTACA  TCCA  CTC  TCT
                                ||||||  ||||  |||  |||
                                ACATGT  AGGT  GGG  AGA
                                   C_    AA   __
GAM627  PTGFR     3'  TGAGAGAGATGTGTACA     6319         CACA
                                TGTACACATC    CTCA
                                ||||||||||    ||||
                                ACATGTGTAG    GAGT
                                     AGA_
GAM627  RBBP5     3'  AGATTGGATAGATGTGTACA  17327         CACAC   T
                                TGTACACATC    TCA TCT
                                ||||||||||    ||| |||
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                                ACATGTGTAG    GGT AGA
                                     ATA__   T
GAM627  SAT     3'  TGAGTCATTTAAATGTGTACA  11436        CCAC___
                                TGTACACAT      ACTCA
                                |||||||||      |||||
                                ACATGTGTA      TGAGT
                                     AATTTAC
GAM627  TMP21   3'  AATGGTGATGGATGTGACA   22399     A      _   T
                                TGT CACATCCA CAC CATT
                                ||| |||||||| ||| ||||
                                ACA GTGTAGGT GTG GTAA
                                  _      A   _
GAM627  UBE2V1  3'  TGAAATGTGGATGCATAC    41797     CA      C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
                                CAT  GTAGGTGT  AGT
                                  AC       AA
GAM627  UBE2V1  3'  TGAAATGTGGATGCATAC    42374     CA      C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
                                CAT  GTAGGTGT  AGT
                                  AC       AA
GAM627  UBE2V1  3'  TGAAATGTGGATGCATAC    12522     CA      C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
                                CAT  GTAGGTGT  AGT
                                  AC       AA
GAM627  ZIC1    3'  AGAATGTTCTAGTAAATGTGTA 12720        CC  ACT__
           C                     GTACACAT  AC    CATTCT
                                |||||||| ||    ||||||
                                CATGTGTA  TG    GTAAGA
                                     AA  ATCTT
GAM627  AF038169  5'  TGAAAATGAGTGCTGTAGATG  25255     __ _      C
                                CATC  CA CACTCATT TCA
                                ||||  || |||||||| |||
                                GTAG  GT GTGAGTAA AGT
                                  AT  C       A
GAM627  CDC14A  3'  AGAAGTGGATGTATATA     13391     C       ACTCA
                                TGTA ACATCCAC     TTCT
                                |||| ||||||||     ||||
                                ATAT TGTAGGTG     AAGA
                                  A      _____
GAM627  DKFZP564I052 3'  GATGATCATGTGATGTGTACA  66710          C   C__
                                TGTACACATC ACA   TCATT
                                |||||||||| |||   |||||
                                ACATGTGTAG TGT   AGTAG
                                     _  ACT
GAM627  DKFZP761F241 3'  TGAGAATGAGTGAGGTTTCGTA 48800       ACAT  A
           CA                     TGTAC    CC CACTCATTCTCA
                                |||||    || ||||||||||||
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                                ACATG   GG GTGAGTAAGAGT
                                   CTTT  A
GAM627  FLJ11101  3'  AGAAGTGTTGAGTGTGTACA  37049       TC  _   CAT
                                TGTACACA  CA CACT   TCT
                                ||||||||  || ||||   |||
                                ACATGTGT  GT GTGA   AGA
                                     GA  T   ___
GAM627  FLJ14642  3'  AGTATGGGTGTGTACA     51492          C
                                TGTACACATCCA ACT
                                |||||||||||| |||
                                ACATGTGTGGGT TGA
                                       A
GAM627  FLJ20399  3'  GGTGGCTGTGGATGCCACA   35125    ACA      CT
                                TGT   CATCCACA  CATT
                                |||   ||||||||  ||||
                                ACA   GTAGGTGT  GTGG
                                  CC_      CG
GAM627  GFPT1     3'  GAAGATGGGATGTGTACA    9022         A  C  A
                                TGTACACATCC CA TC TTC
                                |||||||||||| || || |||
                                ACATGTGTAGG GT AG AAG
                                       _  _  _
GAM627  KIAA0450  3'  GAGGGCAGTGTGGATG     27640         CA
                                CATCCACACT  TTCTC
                                ||||||||||  |||||
                                GTAGGTGTGA  GGGAG
                                       C_
GAM627  KIAA0530  3'  GATGGTATGAAAATGTGTACA  70867        C__  C  T
                                TGTACACAT   CA AC CATT
                                |||||||||   || || ||||
                                ACATGTGTA   GT TG GTAG
                                     AAA  A  _
GAM627  KIAA0753  3'  GGGGAGTTAAATGTGTACA   28999        CCAC    ATT
                                TGTACACAT   ACTC   CTC
                                |||||||||   ||||   |||
                                ACATGTGTA   TGAG   GGG
                                     AAT_   ___
GAM627  KIAA0788  3'  TGAATTAGGAATGTGTACA   71339        _  ACAC
                                TGTACACAT CC    TCA
                                |||||||||  ||    |||
                                ACATGTGTA GG    AGT
                                     A  ATTA
GAM627  KIAA0855  3'  AGAATGAGCAGTGTAC      30400       ATCCACA
                                GTACAC      CTCATTCT
                                ||||||      ||||||||
                                CATGTG      GAGTAAGA
                                   AC_____
GAM627  KIAA0865  5'  GAGCAAGTGGAATGTGTACA  61250         _   A__
                                TGTACACAT CCAC   CTC
                                |||||||||  ||||   |||
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                                ACATGTGTA GGTG   GAG
                                     A    AAC
GAM627  KIAA0992  3'  GGAAGTGTGGAGCACACA    32207     ACACA       CAT
                                TGT    TCCACACT   TCT
                                |||    ||||||||   |||
                                ACA    AGGTGTGA   AGG
                                  CACG_      ____
GAM627  MGC16037  5'  TGAGGTGTAGATATGTATA    51822       C  C   _
                                TGTACA ATC ACAC TCA
                                |||||| ||| |||| |||
                                ATATGT TAG TGTG AGT
                                   A  A   G
GAM627  OSRF      3'  TGAAAATGCACACAAATGTGTA 59525         CCACACT    C
           CA                     TGTACACAT      CATT TCA
                                |||||||||      |||| |||
                                ACATGTGTA      GTAA AGT
                                     AACACAC    A
GAM627  RAB3-GAP150 3'  TGAGAATCAGAGATGTGTA    24839        CACA  C
                                TACACATC    CT ATTCTCA
                                ||||||||    || |||||||
                                ATGTGTAG    GA TAAGAGT
                                     A___  C
GAM627  RAP140    3'  GATGGGTAAATGTGTACA     30844         CCAC
                                TGTACACAT    ACTCATT
                                |||||||||    |||||||
                                ACATGTGTA    TGGGTAG
                                     AA__
GAM627  TACTILE   5'  GAGTGCATGTGTACA       19471         CCA
                                TGTACACAT   CACTC
                                |||||||||   |||||
                                ACATGTGTA   GTGAG
                                     C__
GAM627  LOC131873 3'  GATGTATGCATATGTGTACA  75880         CCA  CT
                                TGTACACAT   CA  CATT
                                |||||||||   ||  ||||
                                ACATGTGTA   GT  GTAG
                                     TAC  AT
GAM627  LOC134145 3'  AGCTGTATATGTGTACA     75144         CC  _
                                TGTACACAT  ACA CT
                                |||||||||  ||| ||
                                ACATGTGTA  TGT GA
                                     TA   C
GAM627  LOC145482 3'  AATGGTATGATGTGTACA    77226          CAC  T
                                TGTACACATC   AC CATT
                                ||||||||||   || ||||
                                ACATGTGTAG   TG GTAA
                                      TA_  _
GAM627  LOC148195 3'  GAAAAGGTGGATGTGTCA    84129    T        A  CA
                                TG ACACATCCAC CT  TTC
                                || ||||||||||  ||  |||
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                                AC TGTGTAGGTG GA  AAG
                                 _       _ A_
GAM627  LOC152633 5'  TGAGCTGTACATGTAGAGTGTA 85826       A  C   CT__  TT
           CA                    TGTACAC TC ACA    CA  CTCA
                                 ||||||| || |||   ||  ||||
                                 ACATGTG AG TGT    GT  GAGT
                                    _ A   ACAT  C_
GAM627  LOC153630 5'  AATGAGTGTGCGTAC      86079      ACATC
                                 GTAC    CACACTCATT
                                 ||||    ||||||||||
                                 CATG    GTGTGAGTAA
                                   C____
GAM627  LOC221662 3'  AGAATGAGGGGAATGGGCA   92399    TA  CA   ACA
                                 TG  CA  TCC   CTCATTCT
                                 ||  ||  |||   ||||||||
                                 AC  GT  AGG   GAGTAAGA
                                  GG  A_   G__
GAM627  LOC254659 5'  GAGAATGGAGATGCTACA    95113     CA   CACAC
                                 TGTA  CATC    TCATTCTC
                                 ||||  ||||    ||||||||
                                 ACAT  GTAG    GGTAAGAG
                                   C_   A____
GAM627  LOC83693  3'  AGGGTGTGTGGATGGCACA   48830     ACA       TC
                                 TGT   CATCCACAC  ATTCT
                                 |||   |||||||||  |||||
                                 ACA   GTAGGTGTG  TGGGA
                                   CG_        __
GAM627  LOC90981  3'  AATGGTGATGGATGTGACA   64532     A      _   T
                                 TGT CACATCCA CAC CATT
                                 ||| |||||||| ||| ||||
                                 ACA GTGTAGGT GTG GTAA
                                   _       A   _
GAM628  ADAMTS8   5'  TCGGGCCGCCAGCACCTG    22886     _      ATAAG
                                 CAG TGCTGGC    CTGA
                                 ||| |||||||    ||||
                                 GTC ACGACCG    GGCT
                                   C      CCG__
GAM628  BAP1      3'  TCAGGGACCCAGCACTGG    16219          CATAAG
                                 CCAGTGCTGG     CTGA
                                 ||||||||||     ||||
                                 GGTCACGACC     GACT
                                      CAGG__
GAM628  BF        5'  TTCAGCTTGGACACTG      8140       CTGGCA
                                 CAGTG     TAAGCTGAA
                                 |||||     |||||||||
                                 GTCAC     GTTCGACTT
                                   AG_____
GAM628  C1QB      3'  TTCAACTCTGTGTCCCAGCACT 4923     A        __    _  C
           GGC                     G CCAGTGCTGG  CATA AG TGAA
                                 | ||||||||||  |||| || ||||
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                                C GGTCACGACC  GTGT TC ACTT
                                _        CT    C  A
GAM628  CHC1     3'  CAGCCCTGAGCACTGTGTC    7020      _      __  CATAA
                                GAC CAGTGCT  GG     GCTG
                                ||| |||||||  ||     ||||
                                CTG GTCACGA  CC     CGAC
                                  T      GT  _____
GAM628  CMRF35   5'  CAGAGCTGTCAGCACCGG    21929    A        TAAG
                                CC GTGCTGGCA    CTG
                                || |||||||||    |||
                                GG CACGACTGT    GAC
                                 C        CGA_
GAM628  EPHB6    3'  TCAGCCCTGGACACTGGTC    15466         _ TG CATAA
                                GACCAGTG C  G    GCTGA
                                |||||||| |  |    |||||
                                CTGGTCAC G  C    CGACT
                                     A GT C____
GAM628  EVPL     5'  CAGCCTGAGCCAGCACT     8803          A  A
                                AGTGCTGGC TA GCTG
                                ||||||||| || ||||
                                TCACGACCG GT CGAC
                                     A  C
GAM628  GARP     3'  CAGCCCAGCACTGG        18594          CATAA
                                CCAGTGCTGG    GCTG
                                ||||||||||    ||||
                                GGTCACGACC    CGAC
                                              _____
GAM628  GJB5     3'  CAGCTCGACGGCACTGG     17945         GCATA
                                CCAGTGCTG    AGCTG
                                |||||||||    |||||
                                GGTCACGGC    TCGAC
                                     AGC__
GAM628  GPR81    3'  CTTACCAGCATTAGTC      50757     C       CA
                                GAC AGTGCTGG  TAAG
                                ||| ||||||||  ||||
                                CTG TTACGACC  ATTC
                                  A       __
GAM628  IFI16    5'  AGCAAGCCAGCACTAGTC    71221     C        ATAA
                                GAC AGTGCTGGC    GCT
                                ||| |||||||||    |||
                                CTG TCACGACCG    CGA
                                  A        AA__
GAM628  KRT4     3'  CAGCTGGGCCCAGCACTGGT   9635           _ ATA
                                ACCAGTGCTGG C   AGCTG
                                |||||||||||| |   |||||
                                TGGTCACGACC G   TCGAC
                                       C GG_
GAM628  MAP3K9   3'  TTCAGCTTCCCAAACACCAGT  60709    CA   C_   CAT
                                AC  GTG  TGG   AAGCTGAA
                                ||  |||  |||   ||||||||
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                                TG  CAC  ACC   TTCGACTT
                                 AC   AA   C__
GAM628  MGAT5    5'  TCAGCTTACAGTTCCTG     10028     T_   GCA
                                CAG  GCTG   TAAGCTGA
                                |||  ||||   ||||||||
                                GTC  TGAC   ATTCGACT
                                  CT   ___
GAM628  MOCS1    3'  TTCAGCTTAACAGTTGCCCGGT 92037      A_  _   GCA
            C                    GACC  GTG CTG   TAAGCTGAA
                                ||||  ||| |||   |||||||||
                                CTGG  CGT GAC   ATTCGACTT
                                  CC   T   A__
GAM628  P23      3'  TCAGCTTATACCCGGGCT    21719     G   C_
                                AGT CTGG  ATAAGCTGA
                                |||  ||||  |||||||||
                                TCG GGCC  TATTCGACT
                                  _    CA
GAM628  PFKFB4   3'  TCAGCCACATGCAACACTGTGT 15874     _    CTG    AA_
            C                    GAC CAGTG   GCAT   GCTGA
                                |||  |||||   ||||   |||||
                                CTG GTCAC   CGTA   CGACT
                                  T    AA_    CAC
GAM628  PTPRK    3'  TTCAGCCTGTGGCCCAGCACTG 11125           __    A
            GTC                    GACCAGTGCTGG  CATA GCTGAA
                                ||||||||||||  ||||  ||||||
                                CTGGTCACGACC  GTGT CGACTT
                                       CG    C
GAM628  RNPEPL1  3'  CGGATGCCAGCACCTG      36676     _       AAG
                                CAG TGCTGGCAT   CTG
                                |||  |||||||||   |||
                                GTC ACGACCGTA   GGC
                                  C       ___
GAM628  UBE2L3   3'  TCAGCCCTGGCACTGGC     12507    A      TG CATAA
                                G CCAGTGC  G    GCTGA
                                |  |||||||  |    |||||
                                C GGTCACG  C    CGACT
                                 _      GT C____
GAM628  APXL2    5'  CAGCCTCAGCACTCATC     75185    CC       CATAA
                                GA  AGTGCTGG    GCTG
                                ||  ||||||||    ||||
                                CT  TCACGACT    CGAC
                                  AC       C____
GAM628  ARHGEF9  3'  TTCAGCTTACCAAGCA      30824     _ CA
                                TGCT GG  TAAGCTGAA
                                ||||  ||  |||||||||
                                ACGA CC  ATTCGACTT
                                  A  __
GAM628  CEGP1    3'  TTCAGCTTCCTCTAGCCCGG   40589    AGT    CAT
                                CC   GCTGG   AAGCTGAA
                                ||   |||||   ||||||||
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                                GG  CGATC  TTCGACTT
                                 CC_    TCC
GAM628  DKFZp547D155 3' CAGCCCTGAGACCACTGGTC  70435       CTGG  TAA
                                GACCAGTG   CA  GCTG
                                ||||||||   ||  ||||
                                CTGGTCAC   GT  CGAC
                                    CAGA  CC_
GAM628  DKFZP727G051 3' TTCAGCCCATCAACCAGCATTG 69483          CATAA__
          GTC                    GACCAGTGCTGG     GCTGAA
                                ||||||||||||     ||||||
                                CTGGTTACGACC     CGACTT
                                      AACTACC
GAM628  DUSP14   5' CACTGTCACCAGCACTGCTC  22834    C       CATA  C
                                GA CAGTGCTGG   AG TG
                                || |||||||||   || ||
                                CT GTCACGACC   TC AC
                                 C       ACTG  _
GAM628  FLJ10206 5' CAGCTTATGCCAGGAGTC   35898    CAGTG
                                GAC    CTGGCATAAGCTG
                                |||    ||||||||||||
                                CTG    GACCGTATTCGAC
                                 AG___
GAM628  FLJ20967 5' GGCGCCCAGCACTGGTT    41962          CATAA
                                GACCAGTGCTGG    GCT
                                ||||||||||||    |||
                                TTGGTCACGACC    CGG
                                      CG___
GAM628  FLJ22569 3' TTCAGCTTACTAAACTG    43679     GC  CA
                                CAGT  TGG  TAAGCTGAA
                                ||||  |||  |||||||||
                                GTCA  ATC  ATTCGACTT
                                  A_  __
GAM628  FOXN4    3' TTCAGCTTGGACACACTGG   75574       C  GCA
                                CCAGTG TG   TAAGCTGAA
                                |||||| ||   |||||||||
                                GGTCAC AC   GTTCGACTT
                                   _  AG_
GAM628  GW112    3' TTCAACTGAAGCCAGCACTGGT 21194           ATA  C
          T                     GACCAGTGCTGGC   AG TGAA
                                ||||||||||||   || ||||
                                TTGGTCACGACCG   TC ACTT
                                      AAG  A
GAM628  HOOK2    3' CAGCTCACATGGCGCCCAGCAC 25256         _____  A__
          TGG                    CCAGTGCTGG    CAT   AGCTG
                                ||||||||||    |||   |||||
                                GGTCACGACC    GTA   TCGAC
                                     CGCG   CAC
GAM628  jdp2     3' TTCAGCACAGCCAGCAT     55327        ATAA
                                GTGCTGGC    GCTGAA
                                ||||||||    ||||||
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                                TACGACCG   CGACTT
                                    ACA_
GAM628  KIAA0767  3'  TCTGCTGCCAGCACAGG    60632    A       TAA  T
                                CC GTGCTGGCA   GC GA
                                || |||||||||   || ||
                                GG CACGACCGT   CG CT
                                 A       ___  T
GAM628  KIAA0923  3'  TCAGCTTGATGCATGGTC    25838     G   TGGCA
                                GACCA TGC    TAAGCTGA
                                ||||| |||    ||||||||
                                CTGGT ACG    GTTCGACT
                                   _  TA___
GAM628  KIAA0982  3'  TTCACTGTTTGCCAGCAC    25852       TA_  C
                                GTGCTGGCA   AG TGAA
                                |||||||||   || ||||
                                CACGACCGT   TC ACTT
                                    TTG  _
GAM628  KIAA1000  3'  TTCAGCTTTGCAAAGTACTGG  65281       G_   T
                                CCAGTGCT  GCA AAGCTGAA
                                ||||||||  ||| ||||||||
                                GGTCATGA  CGT TTCGACTT
                                    AA  _
GAM628  MAP3K3    3'  TCAGCCTGGGCGCTGGTC    9999         GG  TAA
                                GACCAGTGCT  CA   GCTGA
                                ||||||||||  ||   |||||
                                CTGGTCGCGG  GT   CGACT
                                    __  C__
GAM628  MGC16037  5'  CTTGTCCAGCACTAGTC    51821    C      C
                                GAC AGTGCTGG ATAAG
                                ||| |||||||| |||||
                                CTG TCACGACC TGTTC
                                  A       _
GAM628  MIDORI    3'  TCAGCTTATCCTGCAACT    73792    _  T  C
                                AGT GC GG ATAAGCTGA
                                ||| || || |||||||||
                                TCA CG CC TATTCGACT
                                  A  T  _
GAM628  MtFMT     5'  CAGTGGCGAGCACTGG      57651       G  ATAA
                                CCAGTGCT GC    GCTG
                                |||||||| ||    ||||
                                GGTCACGA CG    TGAC
                                    G  G___
GAM628  PCDH16    5'  TCAGTTCCAACCACTGG     72826      C_  CATA
                                CCAGTG  TGG    AGCTGA
                                ||||||  |||    ||||||
                                GGTCAC  ACC    TTGACT
                                   CA  _____
GAM628  QKI       3'  CAGCTTATCAACTCGTC     65439    C  GCTGGC
                                GAC AGT     ATAAGCTG
                                ||| |||     ||||||||
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                                CTG TCA     TATTCGAC
                                  C  AC____
GAM628  TNRC6    3'  CAACTTTTAGCACTG       70506         CAT  C
                                CAGTGCTGG  AAG TG
                                |||||||||  ||| ||
                                GTCACGATT  TTC AC
                                     ___  A
GAM628  TOB2     3'  CAGCCCAGGCCAGCACTG    95618          ATAA
                                CAGTGCTGGC   GCTG
                                ||||||||||   ||||
                                GTCACGACCG   CGAC
                                     GACC
GAM628  TU12B1-TY 3'  TCAGCCCACAGCACTGTC    33406     C      GCATAA
                                GAC AGTGCTG     GCTGA
                                ||| |||||||     |||||
                                CTG TCACGAC     CGACT
                                  _      ACC___
GAM628  TUSP     3'  TCAGCCTAAGAGCGCAGCACTG 39641         _  A__  A
                                CAGTGCTG GC   TA GCTGA
                                |||||||| ||   || |||||
                                GTCACGAC CG   AT CGACT
                                     G  AGA  C
GAM628  USP19    3'  TCAGCTTATGCATCTGGT    88959      TGCTG
                                ACCAG    GCATAAGCTGA
                                |||||    ||||||||||
                                TGGTC    CGTATTCGACT
                                   TA___
GAM628  ZD52F10  3'  CAGCCTGTGCCAGCCCTGG   52819     T       A
                                CCAG GCTGGCATA GCTG
                                |||| ||||||||| ||||
                                GGTC CGACCGTGT CGAC
                                  C        C
GAM628  LOC145268 3'  TCAGCTTACAAGAGCCACTG  77062      _ GGCA
                                CAGTG CT    TAAGCTGA
                                ||||| ||    ||||||||
                                GTCAC GA    ATTCGACT
                                   C  GAAC
GAM628  LOC149296 5'  CAGCTTATGGGCAGCA      79256      G_
                                TGCTG  CATAAGCTG
                                |||||  |||||||||
                                ACGAC  GTATTCGAC
                                   GG
GAM628  LOC161877 5'  TCAGGGCAGGCCAGCGCTGG  82326          ATAAG
                                CCAGTGCTGGC    CTGA
                                ||||||||||     ||||
                                GGTCGCGACCG    GACT
                                     GACGG
GAM628  LOC163115 5'  TCAGCCCCTGACAGCACTGG  82413         G  TAA
                                CCAGTGCTG CA   GCTGA
                                |||||||| ||   |||||
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                                GGTCACGAC GT   CGACT
                                     A  CCC
GAM628  LOC196500 3'  TCAGCTCACTCAGTGGTC    87744     AGT    CATA
                                GACC   GCTGG    AGCTGA
                                ||||   |||||    ||||||
                                CTGG   TGACT    TCGACT
                                  ___    CAC_
GAM628  LOC197287 3'  TCAGCTCATGTGTTTTGCACTG 60865       T_     __
                                CAGTGC  GGCATA  AGCTGA
                                ||||||  ||||||  ||||||
                                GTCACG  TTGTGT  TCGACT
                                   TT     AC
GAM628  LOC200470 5'  TCAGCCTGCGGCGCTGG     90069         G  TAA
                                CCAGTGCTG CA   GCTGA
                                ||||||||| ||   |||||
                                GGTCGCGGC GT   CGACT
                                     _ C__
GAM628  LOC221584 3'  CAGCTTATGTGGCAC       93828       G
                                GTGCTG CATAAGCTG
                                |||||| |||||||||
                                CACGGT GTATTCGAC
                                  _
GAM628  LOC51716  3'  CAGCTCATGGCCCTAGCA    32787       ___  A
                                TGCTGG   CAT AGCTG
                                ||||||   ||| |||||
                                ACGATC   GTA TCGAC
                                   CCG   C
GAM628  LOC92196  5'  CAGAGCACCAGCACTGGC    68456   A        CATAAG
                                G CCAGTGCTGG     CTG
                                | ||||||||||     |||
                                C GGTCACGACC     GAC
                                _        ACGA__
GAM629  CABC1     5'  GCACAAACAGACGCTC      39654      CTGGC
                                GAGC     TCTGTTTGTGC
                                ||||     ||||||||||||
                                CTCG     AGACAAACACG
                                  C_____
GAM629  CEACAM5   3'  AACAGAGCAAGACTCCA      15153       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM629  F2R       3'  AACAGAGCAAGACTCCA      8831        C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM629  FGFR2     3'  GACAGAGCGAGACTCCA      43377       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAG
                                   A  G
GAM629  FGFR2   3'  GACAGAGCGAGACTCCA     43383       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM629  FUT6    3'  GACAGAGCAAGACTCCA     3812        C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM629  GCLM    5'  GGCGCAGACCAGGCTCCA    9026           C    TTGT _
                                TGGAGCCTGG TCTGT   GC C
                                |||||||||| |||||   || |
                                ACCTCGGACC AGACG   CG G
                                      _   _____ A
GAM629  GPC1    3'  GGCTGCAGAGCCCGGCCCCA  9103      A  T      TTGT
                                TGG GCC GGCTCTGT   GCC
                                ||| ||| ||||||||   |||
                                ACC CGG CCGAGACG   CGG
                                  C  C       T___
GAM629  HPSE    3'  CAAACAGGCCAGGCTCCA    21890          T
                                TGGAGCCTGGC CTGTTTG
                                |||||||||| |||||||
                                ACCTCGGACCG GACAAAC
                                          _
GAM629  IFIT4   3'  AACAGAGCAAGACTCCA     70918       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM629  KCNJ5   3'  GACAGAGCGAGACTCCA     6091        C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM629  LY94    3'  GACAGAGCGAGACTCCA     16705       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM629  LZTS1   3'  ACAGAGCCTGGCCCCA      40676     A  T
                                TGG GCC GGCTCTGT
                                ||| ||| ||||||||
                                ACC CGG CCGAGACA
                                  C  T
GAM629  MSH3    3'  AACAGAGCAAGACTCCA     10116       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  A
GAM629  POLH     3'  AACAGAGCGAGACTCCA     21461       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM629  PRKAB1   3'  GCACACCACCAGGCTCCA    20736          CTC  TT
                                TGGAGCCTGG  TG  TGTGC
                                ||||||||||  ||  |||||
                                ACCTCGGACC  AC  ACACG
                                      ___  C_
GAM629  SIGLEC6  3'  AACAGAGCGAGACTCCA     59925       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM629  SLC10A2  5'  AGCAGAGCCAGGGCCCA     4840      AG
                                TGG  CCTGGCTCTGTT
                                |||  ||||||||||||
                                ACC  GGACCGAGACGA
                                  CG
GAM629  SNRPN    5'  CAAGCAAAAACCAGGCTCCA   42991          CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM629  SNRPN    5'  CAAGCAAAAACCAGGCTCCA   42998          CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM629  SNRPN    5'  CAAGCAAAAACCAGGCTCCA   43005          CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM629  SNRPN    5'  CAAGCAAAAACCAGGCTCCA   43013          CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM629  TNFSF11  5'  CAGGAGCCAAAGCCGGGCTCCA 13512            CT_   G
                                TGGAGCCTGGCT  GTTT TG
                                ||||||||||||  |||| ||
                                ACCTCGGGCCGA  CGAG AC
                                      AAC   G
GAM629  TSNAX    3'  GGTAACAGAGCAAGACTCCA   20002      C  G     TTG
                                TGGAG CT GCTCTGT  TGCC
                                ||||| || |||||||  ||||
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                                ACCTC GA CGAGACA   ATGG
                                  A  A      ___
GAM629  UBE2L3    3'  GCCTTTGCAGAGTCAAGCTCCA 12503       C       TTGT
                                TGGAGC TGGCTCTGT    GC
                                |||||| |||||||||    ||
                                ACCTCG ACTGAGACG    CG
                                   A        TTTC
GAM629  ZNF264    3'  AACAGAGCGAGACTCCA     12738      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                  A  G
GAM629  ARNTL2    3'  GACAGAGCGAGACTCCA     39466      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                  A  G
GAM629  C22orf5   3'  GGATCAGAGCCAGACACCA   24344     AGC       TTTGTG
                                TGG   CTGGCTCTG     CC
                                |||   |||||||||     ||
                                ACC   GACCGAGAC     GG
                                  ACA       TA____
GAM629  DKFZp547C176 3'  GACAGAGCAAGACTCCA     67223      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                  A  A
GAM629  DKFZp564K142 3'  AACAGAGCGAGACTCCA     49522      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                  A  G
GAM629  FADS1     3'  GACAGAGCAAGACTCCA     25477      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                  A  A
GAM629  FLJ12298  3'  AACAGAGCGAGACTCCA     49664      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                  A  G
GAM629  FLJ14117  3'  AACAGAGCAAGACTCCA     42896      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                  A  A
GAM629  FLJ14251  3'  GGTAACAGAGCGAGACTCCA  45977      C  G     TTG
                                TGGAG CT GCTCTGT   TGCC
                                ||||| || |||||||   ||||
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                                ACCTC GA CGAGACA   ATGG
                                  A  G      ___
GAM629  FLJ14327  3'  AACAGAGCTAGACTCCA     46127       C
                                TGGAG CTGGCTCTGTT
                                ||||| ||||||||||
                                ACCTC GATCGAGACAA
                                  A
GAM629  FLJ14566  5'  GGCCACAGAGCCAGCCCCA   51446     A  C        TT T
                                TGG GC TGGCTCTGT  G GCC
                                ||| || |||||||||  | |||
                                ACC CG ACCGAGACA  C CGG
                                 C  _       __ _
GAM629  FLJ20084  3'  AACAGAGCGAGACTCCA     34511       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                  A  G
GAM629  FLJ20306  3'  GACAGAGCAAGACTCCA     34917       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                  A  A
GAM629  FLJ20456  3'  GGTAACAGAGCTAGACTCCA  35215       C        TTG
                                TGGAG CTGGCTCTGT   TGCC
                                ||||| ||||||||||   ||||
                                ACCTC GATCGAGACA   ATGG
                                  A        ___
GAM629  FLJ22054  3'  AACAGAGCAAGACTCCA     94391       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                  A  A
GAM629  FLJ22393  5'  AGCAGGAACCAGGCTCCA    47058          C_
                                TGGAGCCTGG  TCTGTT
                                ||||||||||  ||||||
                                ACCTCGGACC  GGACGA
                                     AA
GAM629  FLJ23598  3'  GCCAAGAGCCAGCTCCA     45522        C      GTT  T
                                TGGAGC TGGCTCT   TG GC
                                |||||| |||||||   || ||
                                ACCTCG ACCGAGA   AC CG
                                  _      ___  _
GAM629  FLJ31168  3'  GACAGAGCGAGACTCCA     58502       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                  A  G
GAM629  GP5       3'  GACAGAGCGAGACTCCA     15646       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAG
                                   A  G
GAM629  GTPBP5    3' GACAGAGCAAGACTCCA     65357      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM629  HIC       3' AACAGAGCGAGACTCCA     67444      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM629  ING1-like 3' GACAGAGCGAGACTCCA     54156      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM629  KBRAS2    3' AACAGAGCAAGACTCCA     34191      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM629  KIAA0189  3' CAGGAGCAGAGCCAGGCCCA  28273      A          G
                                TGG GCCTGGCTCTGTTT TG
                                ||| |||||||||||||| ||
                                ACC CGGACCGAGACGAG AC
                                _           G
GAM629  KIAA0472  3' AGCAGAGCAAGACTCCA     71853      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACGA
                                   A  A
GAM629  KIAA0563  3' GACAGAGCAAGACTCCA     29188      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM629  KIAA0565  3' GACAGAGCAAGACTCCA     66890      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM629  KIAA0648  3' CAAACAGAAGCAGGCTCCA   82651         GC
                                TGGAGCCTG  TCTGTTTG
                                |||||||||  ||||||||
                                ACCTCGGAC  AGACAAAC
                                     GA
GAM629  KIAA0924  3' AACAGAGCGAGACTCCA     29712      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  G
GAM629  KIAA1028  3'  CAGAGCACAGGCTCCA      91934          _
                                TGGAGCCTG GCTCTG
                                ||||||||| ||||||
                                ACCTCGGAC CGAGAC
                                     A
GAM629  KIAA1719  3'  GGCCAGGGCCAGGCCCCA    68169     A         TTTGT
                                TGG GCCTGGCTCTG    GCC
                                ||| ||||||||||     |||
                                ACC CGGACCGGGAC    CGG
                                  C         _____
GAM629  KIAA1940  3'  GGTCTCAGAACCAAGGCTCCA  79988         _  C    TTTGT
                                TGGAGCCT GG TCTG    GCC
                                |||||||| || ||||    |||
                                ACCTCGGA CC AGAC    TGG
                                     A  A    TC___
GAM629  LGI2      3'  CAAATCAAAGCCAGGCTC     36397          C  _
                                GAGCCTGGCT TG TTTG
                                |||||||||| || ||||
                                CTCGGACCGA AC AAAC
                                     A  T
GAM629  MGC10200  3'  AACAGAGCGAGACTCCA      58980       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM629  MGC2705   5'  GCACCAAGCCAGGCTCC      51113           C  TTT
                                GGAGCCTGGCT TG   GTGC
                                |||||||||| ||   ||||
                                CCTCGGACCGA AC   CACG
                                          _  ___
GAM629  MGC4562   3'  AACAGAGCGAGACTCCA      55908       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM629  MGC4663   3'  AACAGAGCCAGACTCC       44501      C
                                GGAG CTGGCTCTGTT
                                |||| ||||||||||
                                CCTC GACCGAGACAA
                                  A
GAM629  NPTXR     3'  AACAGAGCAAGACTCCA      54171       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM629  NPTXR     3'  AACAGAGCAAGACTCCA      26635       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  A
GAM629  OR7C1    5'  AACAGAGCCAAGTCCA      82428      G C
                                TGGA C TGGCTCTGTT
                                |||| | ||||||||||
                                ACCT G ACCGAGACAA
                                  _ A
GAM629  POFUT1   3'  AACAGAGCGAGACTCCA     70462       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM629  PTK6     3'  GACAGAGCGAGACTCCA     19936       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM629  RASGRF2  3'  GCACGAAGCCAGGCTCC     61042           CTGT
                                GGAGCCTGGCT   TTGTGC
                                ||||||||||    ||||||
                                CCTCGGACCGA   AGCACG
                                      ____
GAM629  SC65     3'  GACAGAGCGAGACTCCA     21289       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM629  SNURF    3'  CAAGCAAAAACCAGGCTCCA  19052           CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM629  TMG4     3'  GACAGAGCAAGACTCCA     43989       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM629  WBSCR23  3'  GACAGAGCAAGACTCCA     46762       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM629  WIRE     3'  GACAGAGCCAGACTCC      78305       C
                                GGAG CTGGCTCTGTT
                                |||| ||||||||||
                                CCTC GACCGAGACAG
                                  A
GAM629  WSB1     3'  AACAGAGCGAGACTCCA     56144       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  G
GAM629  WSB1      3'  AACAGAGCGAGACTCCA     56138       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM629  LOC115704 3'  CAGCCAGAGCCAGGCCCC     73541     A         T
                                GG GCCTGGCTCTG TTG
                                || |||||||||| |||
                                CC CGGACCGAGAC GAC
                                 C          C
GAM629  LOC124220 5'  GGCACAACCAGACGCC       59146     _    T
                                GGC TCTG TTGTGCC
                                ||| |||| |||||||
                                CCG AGAC AACACGG
                                  C    C
GAM629  LOC127262 3'  GACAGAGCGAGACTCCA      76110       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM629  LOC129563 3'  AGCAGAGCAGGCCCCA       74878     A    G
                                TGG GCCTG CTCTGTT
                                ||| ||||| |||||||
                                ACC CGGAC GAGACGA
                                  C    _
GAM629  LOC129880 3'  AACAGAGCAAGACTCCA      74900       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM629  LOC143196 3'  AACAGAGCGAGACTCCA      82903       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM629  LOC144319 3'  GGCACAAACAGGCGCCCC     83057     A  CTG  T
                                GG GC   GC CTGTTTGTGCC
                                || ||   || ||||||||||
                                CC CG   CG GACAAACACGG
                                 C ____ _
GAM629  LOC145216 3'  GACAGAGCAAGACTCCA      83267       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM629  LOC145820 3'  GACAGAGCAAGACTCCA      77514       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAG
                                   A  A
GAM629  LOC146227 3'  GGTCAGAGCCAGACCCC    77711    AGC       TTTGT
                                GG  CTGGCTCTG    GCC
                                ||  |||||||||    |||
                                CC  GACCGAGAC    TGG
                                 CCA       _____
GAM629  LOC146713 3'  AACAGAGCAAGACTCCA    83720      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM629  LOC147071 3'  GACAGAGCAAGACTCCA    72999      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM629  LOC147649 3'  GACAGAGCGAGACTCCA    78414      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM629  LOC148936 3'  AACAGAGCAAGACTCCA    84286      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM629  LOC149803 5'  CAGGCAGAGCAAGCTCCA    79538       CTG
                                TGGAGC  GCTCTGTTTG
                                ||||||  ||||||||||
                                ACCTCG  CGAGACGGAC
                                   AA_
GAM629  LOC150299 3'  GACAGAGCAAGACTCCA    84970      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM629  LOC151429 3'  GACAGAGCAAGACTCCA    85353      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM629  LOC151904 3'  AACAGAGCGAGACTCCA    80382      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM629  LOC158292 5'  GACAGAGCGAGACTCCA    86730      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAG
                                   A  G
GAM629  LOC162137 5'  CAAGCAGGCCAAGCCCCA    87111     A  C    T
                                TGG GC TGGC CTGTTTG
                                ||| || |||| |||||||
                                ACC CG ACCG GACGAAC
                                  C  A   _
GAM629  LOC163033 5'  CGACCAGGACCAAGCCCCA   82396     A  C   CT   T
                                TGG GC TGG  CTG TTG
                                ||| || |||  ||| |||
                                ACC CG ACC  GAC AGC
                                  C  A   AG   C
GAM629  LOC163682 3'  ACACTCAAAGCCGGGCTCCA  87020           C  TT
                                TGGAGCCTGGCT TG  TGT
                                ||||||||||| ||  |||
                                ACCTCGGGCCGA AC  ACA
                                       A  TC
GAM629  LOC200261 3'  GCACAAACCTCTGGAGGCCCA 88655     A   GGCTCT
                                TGG GCCT     GTTTGTGC
                                ||| ||||     ||||||||
                                ACC CGGA     CAAACACG
                                  _   GGTCTC
GAM629  LOC201173 3'  GACAGAGCAAGACTCCA     87329      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM629  LOC201182 5'  AACAGAGCAAGACTCCA     89760      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM629  LOC219627 3'  GACAGAGCGAGACTCCA     92178      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM629  LOC221543 5'  GACAGAGCAAGACTCCA     93742      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM629  LOC221943 5'  GACAGAGCAAGACTCCA     93989      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM629  LOC222160 5'  GACAGAGCAAGACTCCA     94127      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAG
                                   A  A
GAM629  LOC253039 5'  GGCTCCAAAACCAGGCTCTA  96159        CTCTG   T_
                                TGGAGCCTGG    TTTG  GCC
                                ||||||||||    ||||  |||
                                ATCTCGGACC    AAAC  CGG
                                      A____   CT
GAM629  LOC254659 3'  AAACAGAGCAAGACTCCA    95109     C  G
                                TGGAG CT GCTCTGTTT
                                ||||| || |||||||||
                                ACCTC GA CGAGACAAA
                                   A  A
GAM629  LOC256158 5'  AACATCGAGCCAGGCCCA    97639     A      __
                                TGG GCCTGGCTC  TGTT
                                ||| |||||||||  ||||
                                ACC CGGACCGAG  ACAA
                                  _       CT
GAM629  LOC256207 3'  GACAGAGCAAGACTCCA     95169     C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM629  LOC257596 5'  GACAGAGCAAGACTCCA     97935     C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM629  LOC56963  3'  GCACAAAGCCAGGCTTCA    71455         CTGT
                                TGGAGCCTGGCT   TTGTGC
                                ||||||||||||   ||||||
                                ACTTCGGACCGA   AACACG
                                      _____
GAM629  LOC91149  3'  GCTGAACCAGAGCCAGACTCCA 65079     C      _   T
                                TGGAG CTGGCTCTG TTTG GC
                                ||||| ||||||||| |||| ||
                                ACCTC GACCGAGAC AAGT CG
                                   A       C   _
GAM629  LOC91409  3'  AGGCAAGGCCAGGCCCCA    65951     A     TC
                                TGG GCCTGGC  TGTTT
                                ||| |||||||  |||||
                                ACC CGGACCG  ACGGA
                                  C      GA
GAM629  LOC91862  3'  GGTGACAGAGCGAGACTCCA  53470     C  G      TGT
                                TGGAG CT GCTCTGTT   GCC
                                ||||| || ||||||||   |||
                                ACCTC GA CGAGACAG   TGG
                                   A  G      ___
GAM629  LOC92482  3'  AACAGAGCAAGACTCCA     69485     C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                  A  A
GAM630  CDH6     3'  ACACTTGAACCTAATACC    17026        TG  T_
                                GGTATTAGGT  TCA  TGT
                                ||||||||||  |||  |||
                                CCATAATCCA  AGT  ACA
                                      __  TC
GAM630  CDH6     3'  ACACTTGAACCTAATACC    17026        TG  T_
                                GGTATTAGGT  TCA  TGT
                                ||||||||||  |||  |||
                                CCATAATCCA  AGT  ACA
                                      __  TC
GAM630  SH3BP2   3'  CATAAATGCACAACCTAACAC  11597    A      _   G
                                GT TTAGGTTGT CATT TATG
                                || ||||||||| |||| ||||
                                CA AATCCAACA GTAA ATAC
                                 C       C   _
GAM630  SH3BP2   3'  CATAAATGCACAACCTAACAC  11597    A      _   G
                                GT TTAGGTTGT CATT TATG
                                || ||||||||| |||| ||||
                                CA AATCCAACA GTAA ATAC
                                 C       C   _
GAM630  DKFZP434I116 5'  CATACAATGATCCAACAACCT  31322     ATTA  TT
                                AGGT   GG  GTCATTGTATG
                                ||||   ||  ||||||||||
                                TCCA   CC  TAGTAACATAC
                                  ACAA  __
GAM630  DKFZP434I116 5'  CATACAATGATCCAACAACCT  31322     ATTA  TT
                                AGGT   GG  GTCATTGTATG
                                ||||   ||  ||||||||||
                                TCCA   CC  TAGTAACATAC
                                  ACAA  __
GAM630  LOC145844 3'  ATAGGTACAACCTAACAC    77537    A      CA
                                GT TTAGGTTGT  TTGT
                                || |||||||||  ||||
                                CA AATCCAACA  GATA
                                 C       TG
GAM630  LOC145844 3'  ATAGGTACAACCTAACAC    77537    A      CA
                                GT TTAGGTTGT  TTGT
                                || |||||||||  ||||
                                CA AATCCAACA  GATA
                                 C       TG
GAM630  LOC146952 5'  CATATGCCTCAACCTAACACTT 83863      A      TCATT
                                AGGT TTAGGTTG    GTATG
                                |||| ||||||||    |||||
                                TTCA AATCCAAC    TATAC
                                  C      TCCG_
GAM630  LOC146952 5'  CATATGCCTCAACCTAACACTT 83863      A      TCATT
                                AGGT TTAGGTTG    GTATG
                                |||| ||||||||    |||||
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                                TTCA AATCCAAC    TATAC
                                  C      TCCG_
GAM631  ACCN2    3'  CCAGCTGCCTCCTCACATC   39166     CT_   _
                                GATG  GGAG CAGCTGG
                                ||||  |||| |||||||
                                CTAC  CCTC GTCGACC
                                  ACT   C
GAM631  ADAMTS8  5'  CCAGCTGCTCGCGCTC     22883    T  TG
                                GA GC  GAGCAGCTGG
                                || ||  ||||||||||
                                CT CG  CTCGTCGACC
                                 _ CG
GAM631  ADARB1   3'  CGGTTGTCCCCAGCATCT    31721        A_
                                AGATGCTGG  GCAGCTG
                                |||||||||  |||||||
                                TCTACGACC  TGTTGGC
                                     CC
GAM631  ADARB1   3'  CGGTTGTCCCCAGCATCT    6631         A_
                                AGATGCTGG  GCAGCTG
                                |||||||||  |||||||
                                TCTACGACC  TGTTGGC
                                     CC
GAM631  AGL      5'  CCAGCTGCCTCGGCGCT     5346    A    GA
                                AG TGCTG  GCAGCTGG
                                || |||||  ||||||||
                                TC GCGGC  CGTCGACC
                                 _    TC
GAM631  AP1M1    3'  CCAGCTGCAGGTGGCATCT   50666       GA_
                                AGATGCTG   GCAGCTGG
                                ||||||||   ||||||||
                                TCTACGGT   CGTCGACC
                                     GGA
GAM631  ARCN1    3'  CAGCTGCTCCTTTATT      7974      CT
                                GATG  GGAGCAGCTG
                                ||||  ||||||||||
                                TTAT  CCTCGTCGAC
                                  TT
GAM631  CAPN10   3'  CTGTCCCCAGCACCTTCC    43601   C  A    A_
                                A AAG TGCTGG  GCAG
                                | ||| ||||||  ||||
                                C TTC ACGACC  TGTC
                                 C  C     CC
GAM631  CAPN10   3'  CTGTCCCCAGCACCTTCC    43595   C  A    A_
                                A AAG TGCTGG  GCAG
                                | ||| ||||||  ||||
                                C TTC ACGACC  TGTC
                                 C  C     CC
GAM631  CDC25A   3'  CGGGCTCCAGCATCT       8364          AG
                                AGATGCTGGAGC  CTG
                                ||||||||||||  |||
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                                TCTACGACCTCG  GGC
                                           __
GAM631  CLCN6   3'  CCAGCCTTTTCAGCATCT   7075          CA
                                AGATGCTGGAG  GCTGG
                                ||||||||||  |||||
                                TCTACGACTTT  CGACC
                                      TC
GAM631  CLCN6   3'  CCAGCCTTTTCAGCATCT   41397         CA
                                AGATGCTGGAG  GCTGG
                                ||||||||||  |||||
                                TCTACGACTTT  CGACC
                                      TC
GAM631  CLCN6   3'  CCAGCCTTTTCAGCATCT   41382         CA
                                AGATGCTGGAG  GCTGG
                                ||||||||||  |||||
                                TCTACGACTTT  CGACC
                                      TC
GAM631  CPT1B   3'  CCAGCTGCCCTTTCGTC    15198     CT_  A
                                GATG   GG GCAGCTGG
                                ||||   || ||||||||
                                CTGC   CC CGTCGACC
                                  TTT  _
GAM631  CSF3R   3'  CCAGTCACCAGCATCT     5668        AGCA
                                AGATGCTGG   GCTGG
                                |||||||||   |||||
                                TCTACGACC   TGACC
                                     AC__
GAM631  DDX11   3'  CAGCTGTGCACTTTG      47648     A   TGGA
                                CAAG TGC   GCAGCTG
                                |||| |||   |||||||
                                GTTT ACG   TGTCGAC
                                  C  ____
GAM631  DLEC1   3'  CAGCTGCCTCGTTGTC     23697     GATGC  GA
                                GACAA   TG  GCAGCTG
                                |||||   ||  |||||||
                                CTGTT   GC  CGTCGAC
                                   _____  TC
GAM631  DR1     5'  CCAGCTGCTCCTCCGTT    59371     CT
                                GATG  GGAGCAGCTGG
                                ||||  ||||||||||
                                TTGC  CCTCGTCGACC
                                  CT
GAM631  ECHS1   3'  CCAGCTGCCCCTGCTTC    14566    T  T  A
                                GA GC GG GCAGCTGG
                                || || || ||||||||
                                CT CG CC CGTCGACC
                                 T  T  C
GAM631  EIF2C1  3'  CCAGCTGCCACCCCCCCACCT  24169    A  CT  A__
                                AG TG  GG   GCAGCTGG
                                || ||  ||   ||||||||
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                                TC AC  CC   CGTCGACC
                                 C  CC  CAC
GAM631  EPB49    3'  CCAGCTGCTTTCCTCACCT   8784     A  CT   __
                                AG TG  GGA  GCAGCTGG
                                || ||  |||  ||||||||
                                TC AC  CCT  CGTCGACC
                                 C  T_   TT
GAM631  GLUL     5'  CCAGCTGCTTCGGCTTCGTC   9041      AA  T
                                GAC  GA GCTGGAGCAGCTGG
                                |||  || ||||||||||||||
                                CTG  CT CGGCTTCGTCGACC
                                  __  T
GAM631  GRIK3    3'  CCAGCTGCTTGGGCTTC     5886     T   G
                                GA GCT GAGCAGCTGG
                                || ||| ||||||||||
                                CT CGG TTCGTCGACC
                                 T   G
GAM631  GRLF1    3'  CCAGCTGCAGTGACTTGTC   78555       A   GGA
                                GACAAG TGCT   GCAGCTGG
                                |||||| ||||   ||||||||
                                CTGTTC GTGA   CGTCGACC
                                   A   ___
GAM631  GUCY2F   5'  CTCTCCAGTATCTCGTC     7726      A        C
                                GAC AGATGCTGGAG AG
                                ||| ||||||||||| ||
                                CTG TCTATGACCTC TC
                                  C        _
GAM631  HK2      3'  CCAGCTGTCGCATCT       3950        TGGA
                                AGATGC    GCAGCTGG
                                ||||||    ||||||||
                                TCTACG    TGTCGACC
                                   C___
GAM631  ICOS     3'  CCAAGGACCAGCATCTGTC   23904      A      AGCAGC
                                GACA GATGCTGG     TGG
                                |||| ||||||||     |||
                                CTGT CTACGACC     ACC
                                  _       AGGA__
GAM631  ISL1     5'  CCACAGCTCCAGCATC      9364           AGC
                                GATGCTGGAGC   TGG
                                ||||||||||   |||
                                CTACGACCTCG   ACC
                                      AC_
GAM631  LPIN2    3'  CCAGCTGCTCAGGCTC      27706    T   G
                                GA GCT GAGCAGCTGG
                                || ||| ||||||||||
                                CT CGG CTCGTCGACC
                                 _  A
GAM631  MUC4     3'  CCAGCTGCCTTCCAACTTC   56323    TGC   __
                                GA   TGGA  GCAGCTGG
                                ||   ||||  ||||||||
```

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                                CT   ACCT  CGTCGACC
                                 TCA   TC
GAM631  MXI1    3'  CCAGCTGCCACCTCTCCATC  55261     CT__  A_
                                GATG   GG  GCAGCTGG
                                ||||   ||  ||||||||
                                CTAC   CC  CGTCGACC
                                  CTCT  AC
GAM631  MXI1    3'  CCAGCTGCCACCTCTCCATC  19900     CT__  A_
                                GATG   GG  GCAGCTGG
                                ||||   ||  ||||||||
                                CTAC   CC  CGTCGACC
                                  CTCT  AC
GAM631  MYO1D   5'  CCAGCCGCTGCCGTCTCCGTC  71767     A_   GCT  _  A
                                GAC  AGAT   GG AGC GCTGG
                                |||  ||||   || ||| |||||
                                CTG  TCTG   CC TCG CGACC
                                  CC   ___  G   C
GAM631  NEDD4   3'  CCAGCTGCAGACCTTCATC   70009     CT  A__
                                GATG  GG   GCAGCTGG
                                ||||  ||   ||||||||
                                CTAC  CC   CGTCGACC
                                  TT  AGA
GAM631  NOVA1   3'  CCAGCTGCTCCTTTCTGT    10246     A  TGCT
                                ACA GA    GGAGCAGCTGG
                                ||| ||    ||||||||||
                                TGT CT    CCTCGTCGACC
                                  _  TT__
GAM631  NOVA1   3'  CCAGCTGCTCCTTTCTGT    21408     A  TGCT
                                ACA GA    GGAGCAGCTGG
                                ||| ||    ||||||||||
                                TGT CT    CCTCGTCGACC
                                  _  TT__
GAM631  OGDH    3'  CCAGCTGCCCCTCATTTATC  91106    CA    CT  A
                                GA  AGATG  GG GCAGCTGG
                                ||  |||||  || ||||||||
                                CT  TTTAC  CC CGTCGACC
                                 A_    TC  _
GAM631  PIGA    3'  CAGCTGCTACCCTGTC      40012      A ATGCT  _
                                GACA G     GG AGCAGCTG
                                |||| |     || ||||||||
                                CTGT C     CC TCGTCGAC
                                  _ _____  A
GAM631  PIGA    3'  CAGCTGCTACCCTGTC      40003      A ATGCT  _
                                GACA G     GG AGCAGCTG
                                |||| |     || ||||||||
                                CTGT C     CC TCGTCGAC
                                  _ _____  A
GAM631  PIGA    3'  CAGCTGCTACCCTGTC      10551      A ATGCT  _
                                GACA G     GG AGCAGCTG
                                |||| |     || ||||||||
```

```
                                CTGT C    CC TCGTCGAC
                                  _ _____ A
GAM631  PLA2G2D  3' CCAACTGCTCCAATCTGCCTC 24788   CA_   GC      C
                                GA  AGAT  TGGAGCAG TGG
                                ||  ||||  |||||||| |||
                                CT  TCTA  ACCTCGTC ACC
                                 CCG   __      A
GAM631  POLR2E   3' CCAGCTGCTCCTCACT     59916    A  CT
                                AG TG  GGAGCAGCTGG
                                || ||  ||||||||||
                                TC AC  CCTCGTCGACC
                                 _ T_
GAM631  PRKACA   3' CCAGCTGCTCCCCCTCATC   10788     CT__
                                GATG   GGAGCAGCTGG
                                ||||   ||||||||||
                                CTAC   CCTCGTCGACC
                                  TCCC
GAM631  RFX5     3' CCAGGTGGCAGCATCTTGTC  4822          GAG  G
                                GACAAGATGCTG  CA CTGG
                                ||||||||||||  || ||||
                                CTGTTCTACGAC  GT GACC
                                      G__  G
GAM631  SCGB1A1  3' CCAACTGCTCCAGCCTCT    12538    T       C
                                AGA GCTGGAGCAG TGG
                                ||| |||||||||| |||
                                TCT CGACCTCGTC ACC
                                 C        A
GAM631  SEMA3F   3' CCAGCTGCCTGTGCCT     14820    AT  T  A
                                AG  GC GG GCAGCTGG
                                ||  || || ||||||||
                                TC  TG TC CGTCGACC
                                 CG  _  _
GAM631  SERPINI1 5' GCTCCAGCATCCCGTC     17233     AA
                                GAC  GATGCTGGAGC
                                |||  ||||||||||
                                CTG  CTACGACCTCG
                                  CC
GAM631  SLC13A1  3' CCAGCTGTTACTGACCTTGTC 42377       ATGCTGG
                                GACAAG      AGCAGCTGG
                                ||||||      |||||||||
                                CTGTTC      TTGTCGACC
                                   CAGTCA_
GAM631  SLC25A19 3' CCAGCTGCCCCAAGCGGGGT  41377    AAGA   _  A
                                AC    TGCT GG GCAGCTGG
                                ||    |||| || ||||||||
                                TG    GCGA CC CGTCGACC
                                 GG__    A  C
GAM631  SMARCD3  3' CCGGGCCCCAGCATTTTG    11829          A  AG
                                CAAGATGCTGG GC  CTGG
                                |||||||||| ||  ||||
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                                GTTTTACGACC CG  GGCC
                                      C  __
GAM631  TEM7     3'  TTGCTCCAACTCCTTGTC    39899       ATGC
                                GACAAG    TGGAGCAG
                                ||||||    ||||||||
                                CTGTTC    ACCTCGTT
                                   CTCA
GAM631  TMP21    3'  CAAAGTCAGCATTTGTC     22401      A       AGCAGC
                                GACA GATGCTGG     TG
                                |||| ||||||||     ||
                                CTGT TTACGACT     AC
                                  _       GAA___
GAM631  USP11    5'  CCAGGACTCCAGCACCTT    16203     A       CAG
                                AAG TGCTGGAG   CTGG
                                ||| ||||||||   ||||
                                TTC ACGACCTC   GACC
                                  C       AG_
GAM631  VAT1     5'  CCAGCTGTGCGCTCTCGTC   21045     A   T  TGGA
                                GAC AGA GC    GCAGCTGG
                                ||| ||| ||    ||||||||
                                CTG TCT CG    TGTCGACC
                                  C   _  CG__
GAM631  VTN      5'  CCAGCTACTGGGCATTTTGTC  5314           GG  C
                                GACAAGATGCT  AG AGCTGG
                                ||||||||||  || ||||||
                                CTGTTTTACGG  TC TCGACC
                                      G_  A
GAM631  XPC      3'  GCTCCAGCCCTTGTC       16137       AT
                                GACAAG  GCTGGAGC
                                ||||||  ||||||||
                                CTGTTC  CGACCTCG
                                   C_
GAM631  ARHGDIG  3'  CCAGCTGCCAGGGGCATC    6777        GGA_
                                GATGCT    GCAGCTGG
                                ||||||    ||||||||
                                CTACGG    CGTCGACC
                                   GGAC
GAM631  BG1      5'  CCAGCTGCCCACAGCTTC    87308    T    GA_
                                GA GCTG   GCAGCTGG
                                || ||||   ||||||||
                                CT CGAC   CGTCGACC
                                 T    ACC
GAM631  C20orf140 3'  CAGAAGCTCCAGCATTT     58244           AG
                                AGATGCTGGAGC  CTG
                                ||||||||||||  |||
                                TTTACGACCTCG  GAC
                                      AA
GAM631  C20orf55  5'  CCAGCTGCCTACTTTCT     48659     TGC   A
                                AGA   TGG GCAGCTGG
                                |||   ||| ||||||||
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```
                                TCT   ATC CGTCGACC
                                  TTC   _
GAM631  C20orf97  3'  CCAGCTGCCTTTGTATCTTGT  40963         T_  A
                                ACAAGATGC  GG GCAGCTGG
                                |||||||||  || ||||||||
                                TGTTCTATG  TC CGTCGACC
                                     TT  _
GAM631  C4S-2    3'  CCAGCTGTTCCCATACTGTC  37819     AG   CT
                                GACA  ATG  GGAGCAGCTGG
                                ||||  |||  ||||||||||
                                CTGT  TAC  CCTTGTCGACC
                                  CA  __
GAM631  CAP350   3'  CCAGCTGCTCCCAGAATC    29044     G   _
                                GAT CTGG AGCAGCTGG
                                ||| |||| |||||||||
                                CTA GACC TCGTCGACC
                                  A   C
GAM631  CGB7     5'  CCAGCTCACTCCAGCATC    52471         C_
                                GATGCTGGAG  AGCTGG
                                ||||||||||  ||||||
                                CTACGACCTC  TCGACC
                                     AC
GAM631  CRA      3'  CTGCTCCAACTCTTGTC     21972        TGC
                                GACAAGA   TGGAGCAG
                                |||||||   ||||||||
                                CTGTTCT   ACCTCGTC
                                    CA_
GAM631  CSEN     3'  CCAGCTGCTGGATGTC      25529      _  GG
                                GATG CT  AGCAGCTGG
                                |||| ||  |||||||||
                                CTGT GG  TCGTCGACC
                                  A  __
GAM631  DDX12    3'  CCAGCTGTTTGCATCCTGC   59696   A  A    TG
                                G CA GATGC  GAGCAGCTGG
                                | || |||||  ||||||||||
                                C GT CTACG  TTTGTCGACC
                                 _  C    __
GAM631  DKFZP434H0820 3'  CCAGCTGCCGCAGCCCTGGTC  63847     A  AT   GA
                                GAC AG  GCTG  GCAGCTGG
                                ||| ||  ||||  ||||||||
                                CTG TC  CGAC  CGTCGACC
                                  G  C_   GC
GAM631  DKFZP434H132 5'  CCAGCTGCCGGACATTT     31316      _  GA
                                AGATG CTG  GCAGCTGG
                                |||||  |||  ||||||||
                                TTTAC GGC  CGTCGACC
                                  A  __
GAM631  DKFZp434I099 5'  CCAGCTGCGCTACCACT     50081    A  C   A
                                AG TG TGG GCAGCTGG
                                || || ||| ||||||||
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                                TC AC ATC CGTCGACC
                                 _ C   G
GAM631  DKFZP434O047 5' CCAGATGGCAGCATCT     31511        GAG  G
                                AGATGCTG   CA CTGG
                                ||||||||   || ||||
                                TCTACGAC   GT GACC
                                     G__  A
GAM631  DKFZP761I2123 3' CAGCCTGCTTCTTGTC     48756        TGCTGG   _
                                GACAAGA     AGCAG CTG
                                |||||||     ||||| |||
                                CTGTTCT     TCGTC GAC
                                    _______    C
GAM631  DMWD     3' CCAGCTGCCCTTGCTATTGTC  60877      GAT  T_  A
                                GACAA   GC  GG GCAGCTGG
                                |||||   ||  || ||||||||
                                CTGTT   CG  CC CGTCGACC
                                   AT_  TT  _
GAM631  FLJ00007  3' CCAGCTGCCACGCTCT      71274     T  T GA
                                AGA GC G  GCAGCTGG
                                ||| || |  ||||||||
                                TCT CG C  CGTCGACC
                                 _  _ AC
GAM631  FLJ00024  3' CAGCTGCTCACTCTTTC     63754   C    TGCTG
                                A AAGA     GAGCAGCTG
                                | ||||     |||||||||
                                C TTCT     CTCGTCGAC
                                 T    CA___
GAM631  FLJ11722  3' CAGCTGCTGTCACTGTC     46390     GC   _
                                GAT  TGG AGCAGCTG
                                |||  ||| ||||||||
                                CTG  ACT TCGTCGAC
                                  TC   G
GAM631  FLJ12270  3' CCAGCTGCTATCCCTTG     47571      ATGCT   __
                                CAAG    GGA  GCAGCTGG
                                ||||    |||  ||||||||
                                GTTC    CCT  CGTCGACC
                                  _____  AT
GAM631  FLJ12331  3' AGCAATCAGCATCTTTC     46474   C        AGCA
                                A AAGATGCTGG    GCT
                                | ||||||||||    |||
                                C TTCTACGACT    CGA
                                 T         AA__
GAM631  FLJ12788  3' GCTCCAGCATCTGTC       42548      A
                                GACA GATGCTGGAGC
                                |||| ||||||||||
                                CTGT CTACGACCTCG
                                  _
GAM631  FLJ12891  3' CCAGCTGCACTGTGCCCCTGTC 46338      A AT  _   A
                                GACA G  GC TGG GCAGCTGG
                                |||| |  || ||| ||||||||
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                                CTGT C  CG GTC CGTCGACC
                                  _ CC  T   A
GAM631  FLJ13769  3'  CAGCCACCATCTTGT      46605        C  GAGCA
                                ACAAGATG TG    GCTG
                                |||||||| ||    ||||
                                TGTTCTAC AC    CGAC
                                    C _____
GAM631  FLJ13855  3'  CCAGCTGCTCTTGTCACTGTC  43583     A A  _ T
                                GACA G TG C GGAGCAGCTGG
                                |||| | || | ||||||||||
                                CTGT C AC G TCTCGTCGACC
                                  _ _  T T
GAM631  FLJ14810  5'  CCAGCTGCCCCGGCTGCTG   51625    AGAT    A
                                CA   GCTGG GCAGCTGG
                                ||   ||||| ||||||||
                                GT   CGGCC CGTCGACC
                                 CGT_    C
GAM631  FLJ20034  3'  CCAGGGGCCCAGCATC      34364        A  AG
                                GATGCTGG GC  CTGG
                                |||||||| ||  ||||
                                CTACGACC CG  GACC
                                     _ GG
GAM631  FLJ20320  5'  CCAGCTGCCCCAGTGGCT    34939    AT    A
                                AG  GCTGG GCAGCTGG
                                ||  ||||| ||||||||
                                TC  TGACC CGTCGACC
                                 GG    C
GAM631  FLJ20542  3'  CCAGCTGCGCTTCACCT     49783    A  CT  A
                                AG TG  GG GCAGCTGG
                                || ||  || ||||||||
                                TC AC  TC CGTCGACC
                                 C  T_  G
GAM631  FLJ22362  3'  CCAGCTGCCCCACATCTTG   43073       C   A
                                CAAGATG TGG GCAGCTGG
                                ||||||| ||| ||||||||
                                GTTCTAC ACC CGTCGACC
                                    _  C
GAM631  FLJ23511  5'  CCAAAGTTCCAGCATC      49959          AGC
                                GATGCTGGAGC   TGG
                                ||||||||||   |||
                                CTACGACCTTG   ACC
                                      AA_
GAM631  GMEB2     3'  CCAGCTGCTTCCCTTTGTC   24728       ATGCT
                                GACAAG    GGAGCAGCTGG
                                ||||||    ||||||||||
                                CTGTTT    CTTCGTCGACC
                                   CC___
GAM631  HCC-4     5'  CCAACTTGTCTCAGCATC    56818       GA  _ C
                                GATGCTG  GCA G TGG
                                |||||||  ||| | |||
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                                CTACGAC  TGT C ACC
                                    TC   T A
GAM631  HSU79266 3' CCGTCTGCTCCAGACCCT    25249    ATG       C
                                AG   CTGGAGCAG TGG
                                ||   ||||||||| |||
                                TC   GACCTCGTC GCC
                                 CCA        T
GAM631  IL14     5' CCAGCCAGGTCAGAACATCCTG 95431    A   __    AGCA
                                CA GATG  CTGG    GCTGG
                                || ||||  ||||    |||||
                                GT CTAC  GACT    CGACC
                                 C    AA    GGAC
GAM631  KBRAS2   3' CCAGCTGCCCCAGACA      34194    _   A
                                TG CTGG GCAGCTGG
                                || |||| ||||||||
                                AC GACC CGTCGACC
                                 A   C
GAM631  KIAA0140 3' CCAGCCGCTCTAGTCTCT    27807     T       A
                                AGA GCTGGAGC GCTGG
                                ||| |||||||| |||||
                                TCT TGATCTCG CGACC
                                  C       C
GAM631  KIAA0399 3' CCAGCTGCTTCTGCCCTGT   30671     AGAT  T
                                ACA    GC GGAGCAGCTGG
                                |||    || ||||||||||
                                TGT    CG CTTCGTCGACC
                                  CC__  T
GAM631  KIAA0481 3' CCAGCTGTTGTGCACCTTCC   71846   C   A   T G
                                A AAG TGC G AGCAGCTGG
                                | ||| ||| | |||||||||
                                C TTC ACG T TTGTCGACC
                                 C   C   _ G
GAM631  KIAA0557 3' CCAGCTGCCCGTTTC       77992    T  T  A
                                GA GC GG GCAGCTGG
                                || || || ||||||||
                                CT TG CC CGTCGACC
                                 T  _  _
GAM631  KIAA0748 5' CCAGCTACTTGATCTTG     28936       GCTG   C
                                CAAGAT    GAG AGCTGG
                                ||||||    ||| ||||||
                                GTTCTA    TTC TCGACC
                                    G___   A
GAM631  KIAA0889 3' CCAGAGACTGCCAGCATC    31131         _ CAG
                                GATGCTGG AG   CTGG
                                |||||||| ||   ||||
                                CTACGACC TC   GACC
                                     G  AGA
GAM631  KIAA0892 3' CCAGCCACCTTCCCCCATCTTG 71009         CT    CA__
           T                     ACAAGATG  GGAG    GCTGG
                                ||||||||  ||||    |||||
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                                TGTTCTAC  CCTT    CGACC
                                     CC    CCAC
GAM631  KIAA1054  3'  CCAGCATCTCAGCATCCTG   68431    A      G  CA
                                CA GATGCTG AG  GCTGG
                                || ||||||| ||  |||||
                                GT CTACGAC TC  CGACC
                                 C      _  TA
GAM631  KIAA1266  3'  CAGCCCAACATCTTGT      66114         C   AGCA
                                ACAAGATG TGG    GCTG
                                |||||||| |||    ||||
                                TGTTCTAC ACC    CGAC
                                     A  ____
GAM631  KIAA1548  3'  CTCTCCAGCATTCCGTC     40503     AA         C
                                GAC  GATGCTGGAG AG
                                |||  ||||||||||| ||
                                CTG  TTACGACCTC TC
                                  CC         _
GAM631  KIAA1655  3'  CCAGCTGCCTCAGCCTC     66602    T    GA
                                GA GCTG  GCAGCTGG
                                || ||||  ||||||||
                                CT CGAC  CGTCGACC
                                 C    TC
GAM631  KIAA1753  3'  CCAGCTGCCCCCAGCTCT    64880     T     A_
                                AGA GCTGG  GCAGCTGG
                                ||| |||||  ||||||||
                                TCT CGACC  CGTCGACC
                                  _     CC
GAM631  KIAA1862  3'  CCAGCTGTAAGCCTCCTGTC   68926      A  T   GGA
                                GACA GA GCT   GCAGCTGG
                                |||| || |||   ||||||||
                                CTGT CT CGA   TGTCGACC
                                  C  C   A__
GAM631  KIAA1872  3'  CCAGCTGCCACGATTTGTC    62926       A  C  GA
                                GACAAG TG TG  GCAGCTGG
                                |||||| || ||  ||||||||
                                CTGTTT GC AC  CGTCGACC
                                   A  _  __
GAM631  KIAA1884  3'  CCAGCTGCCAGAAACCCTGTT  73335      AGATG_   GA
                                GACA     CTG  GCAGCTGG
                                ||||     |||  ||||||||
                                TTGT     GAC  CGTCGACC
                                  CCCAAA   __
GAM631  KIAA1909  5'  CCAGCTGCCCCTGCCGTCT    73837       _ T  A
                                AGATG C GG GCAGCTGG
                                ||||| | || ||||||||
                                TCTGC G CC CGTCGACC
                                   C T  C
GAM631  KRTAP4-13 3'  CCAGCTGCTGCCAGCCTTC    52596    T_     _
                                GA  GCTGG AGCAGCTGG
                                ||  ||||| |||||||||
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                                CT  CGACC TCGTCGACC
                                 TC     G
GAM631  KRTAP4-4  3'  CCAGCTGCTGCCAGCCTTC    50718    T_    _
                                GA  GCTGG AGCAGCTGG
                                ||  ||||| |||||||||
                                CT  CGACC TCGTCGACC
                                 TC     G
GAM631  LGALS9    3'  CCAGCTGCTGGAATC       23789     G  GG
                                GAT CT  AGCAGCTGG
                                |||  ||  |||||||||
                                CTA GG  TCGTCGACC
                                  A  __
GAM631  LGALS9    3'  CCAGCTGCTGGAATC       9721      G  GG
                                GAT CT  AGCAGCTGG
                                |||  ||  |||||||||
                                CTA GG  TCGTCGACC
                                  A  __
GAM631  MGC12760  3'  CCGCGGTTTCCAGCATC     51174          _ A  T
                                GATGCTGGAG C GC GG
                                |||||||||| | || ||
                                CTACGACCTT G CG CC
                                      T G  _
GAM631  MGC20470  3'  CCAGCTGCAGCTATCCTG    58962    A  _   GGA
                                CA GAT GCT   GCAGCTGG
                                || ||| |||   ||||||||
                                GT CTA CGA   CGTCGACC
                                 C   T  ___
GAM631  MGC4707   3'  CCAGCCTCCTCTCCAGCACCTT 44119      A       CA___
           G                     CAAG TGCTGGAG     GCTGG
                                |||| ||||||||     |||||
                                GTTC ACGACCTC     CGACC
                                  C       TCCTC
GAM631  MGC5309   3'  CCAGCTGTTCCAGCAGCTTGTC 80813        A
                                GACAAG TGCTGGAGCAGCTGG
                                |||||| ||||||||||||||||
                                CTGTTC ACGACCTTGTCGACC
                                   G
GAM631  MMP24     3'  CCAGCTGCCAGCCTTCTGTC   21942      AG T    GA
                                GACA  A GCTG  GCAGCTGG
                                ||||  | ||||  ||||||||
                                CTGT  T CGAC  CGTCGACC
                                  CT C   __
GAM631  NT5C1B    5'  CAGCTGCCCCGGTCGCT     71226    AT    A
                                AG  GCTGG GCAGCTG
                                ||  ||||| |||||||
                                TC  TGGCC CGTCGAC
                                 GC     C
GAM631  NXPH3     3'  CCAGCTGCCAGTGGCACCTTGT 65755       A    GA_
                                ACAAG TGCTG   GCAGCTGG
                                ||||| |||||   ||||||||
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                                TGTTC ACGGT   CGTCGACC
                                   C    GAC
GAM631  OPRL1    3'  CCAGCTGCCTTCAGCCCTGT  6196     AGAT     _
                                ACA   GCTGGAG CAGCTGG
                                |||   ||||||| |||||||
                                TGT   CGACTTC GTCGACC
                                  CC__      C
GAM631  OR1F2    5'  CCAGCAGCAGCATCTCCTC   65108    CA     GGA  A
                                GA  AGATGCT   GC GCTGG
                                ||  |||||||   || |||||
                                CT  TCTACGA   CG CGACC
                                 CC       ___  A
GAM631  OS4      3'  CCAGCTGCCCCATTCTT     19178     TGC   A
                                AAGA   TGG GCAGCTGG
                                ||||   ||| ||||||||
                                TTCT   ACC CGTCGACC
                                  T__   C
GAM631  PIB5PA   3'  CCAGCTGTATCTGCACCT    66052    A   T  A
                                AG TGC GG GCAGCTGG
                                || ||| || ||||||||
                                TC ACG CT TGTCGACC
                                 C   T  A
GAM631  PIP5K1C  3'  GCCAGCCGCGTGGCTCCCAGCA 70763        _  A_____    III
           TC                    GATGCTGG AGC     GCTGG   C
                                |||||||| |||     |||||   |
                                CTACGACC TCG     CGACC   G
                                     C   GTGCGC    III
GAM631  PP1201   3'  CCAGCATGGAACAGCATCT   42190        GAG  _
                                AGATGCTG   CA GCTGG
                                ||||||||   || |||||
                                TCTACGAC   GT CGACC
                                     AAG  A
GAM631  PP1665   3'  GCTCCAGCCCCTTGTC      47917       AT
                                GACAAG  GCTGGAGC
                                ||||||  ||||||||
                                CTGTTC  CGACCTCG
                                   CC
GAM631  PPP1R1B  3'  CCAGCTGCTCTGCCCCTTTC  49826    C   AT  T
                                GA AAG  GC GGAGCAGCTGG
                                || |||  || ||||||||||
                                CT TTC  CG TCTCGTCGACC
                                 _   CC  _
GAM631  PRPF8    3'  CCAGCTGCCCCAGCAT      61187       A
                                ATGCTGG GCAGCTGG
                                ||||||| ||||||||
                                TACGACC CGTCGACC
                                     C
GAM631  RNF24    3'  CCAGCTGCCACTTCTTTTG   23315      TGCT  A_
                                CAAGA   GG  GCAGCTGG
                                |||||   ||  ||||||||
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                                GTTTT   TC  CGTCGACC
                                  CT__  AC
GAM631  SARM     3'  CTTTTCCAGCATCCTGT     30606     A        C
                                ACA GATGCTGGAG AG
                                ||| |||||||||| ||
                                TGT CTACGACCTT TC
                                  C         T
GAM631  SEPT3    3'  CCAGCTGCTGGTCTC       38890    T   GG
                                GA GCT  AGCAGCTGG
                                || |||  |||||||||
                                CT TGG  TCGTCGACC
                                 C  __
GAM631  SIAT4A   3'  CCAGCCCCAGCATCTTG     11669          AGCA
                                CAAGATGCTGG   GCTGG
                                ||||||||||    |||||
                                GTTCTACGACC   CGACC
                                      C___
GAM631  SLC26A9  3'  CCAGCTGCCTCAACTCTGTC  53619     A  TGC  GA
                                GACA GA   TG  GCAGCTGG
                                |||| ||   ||  ||||||||
                                CTGT CT   AC  CGTCGACC
                                  _  CA_  TC
GAM631  SLC26A9  3'  CCAGCTGCCTCAACTCTGTC  56180     A  TGC  GA
                                GACA GA   TG  GCAGCTGG
                                |||| ||   ||  ||||||||
                                CTGT CT   AC  CGTCGACC
                                  _  CA_  TC
GAM631  SLC2A10  3'  CCATCTCCAGCATCCTG     47820    A        CAGC
                                CA GATGCTGGAG    TGG
                                || ||||||||||    |||
                                GT CTACGACCTC    ACC
                                 C         T___
GAM631  STRAIT11499 5'  CCAGCTGCTCCAATC       41141     GC
                                GAT  TGGAGCAGCTGG
                                |||  ||||||||||||
                                CTA  ACCTCGTCGACC
                                  __
GAM631  UBCE7IP5  3'  CTCTCCAGAATCTTGTC     30151        G     C
                                GACAAGAT CTGGAG AG
                                |||||||| |||||| ||
                                CTGTTCTA GACCTC TC
                                     A     _
GAM631  UBF-fl   3'  CCAGCCACTGTTAGTGTC     51557        _  CA
                                GATGCTGG AG  GCTGG
                                |||||||| ||  |||||
                                CTGTGATT TC  CGACC
                                     G  AC
GAM631  ZNF213   3'  CCAGCCACGGCACATCCTG   65094    A  __    GAGCA
                                CA GA  TGCTG    GCTGG
                                || ||  |||||    |||||
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                                GT CT  ACGGC    CGACC
                                 C  AC    AC___
GAM631   LOC112476 3'  CTGCTCCTGCATCTTG     59112        T
                                CAAGATGC GGAGCAG
                                |||||||| |||||||
                                GTTCTACG CCTCGTC
                                     T
GAM631   LOC123096 3'  CCAGCTGCTGCCACTCCTG   74199    A  TGC  _
                                CA GA   TGG AGCAGCTGG
                                || ||   ||| |||||||||
                                GT CT   ACC TCGTCGACC
                                 C  C__   G
GAM631   LOC128954 5'  CAGCTGCTCCCATC       75792      CT
                                GATG  GGAGCAGCTG
                                ||||  ||||||||||
                                CTAC  CCTCGTCGAC
                                  __
GAM631   LOC144348 5'  CCAGCCAGCAGTATCTCATC   76805    CA      GAGCA
                                GA  AGATGCTG    GCTGG
                                ||  ||||||||    |||||
                                CT  TCTATGAC    CGACC
                                 AC       GAC__
GAM631   LOC144373 3'  CCAGCTGTTTGCATCCTGC    76818    A  A    TG
                                G CA GATGC  GAGCAGCTGG
                                | || |||||  ||||||||||
                                C GT CTACG  TTTGTCGACC
                                 _ C    __
GAM631   LOC145501 3'  CCAGCTGCCCGTGTGCCT    77253    AT  _   A
                                AG  GC TGG GCAGCTGG
                                ||  || ||| ||||||||
                                TC  TG GCC CGTCGACC
                                 CG  T   _
GAM631   LOC145608 5'  CCAGCTGCTCTGCTGGCTTG   83383      AT_  T
                                CAAG   GC GGAGCAGCTGG
                                ||||   || ||||||||||
                                GTTC   CG TCTCGTCGACC
                                   GGT  _
GAM631   LOC145676 5'  CATTGCTCCAGCATCTTTC    77338    C           C
                                A AAGATGCTGGAGCAG TG
                                | |||||||||||||| ||
                                C TTCTACGACCTCGTT AC
                                 T           _
GAM631   LOC145741 5'  CCAGCCGCTAAGCGCCT     83459    A    GG   A
                                AG TGCT  AGC GCTGG
                                || ||||  ||| |||||
                                TC GCGA  TCG CGACC
                                 C    A_   C
GAM631   LOC145871 5'  CCAGCCCTGGCTCAGCATCTAG 83562     A       G   A___
            TC                    GAC AGATGCTG AGC    GCTGG
                                ||| |||||||| |||    |||||
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                                CTG TCTACGAC TCG    CGACC
                                  A       _  GTCC
GAM631   LOC145946 5'  CCAGCCCATGCATCTTGTT    83569          _  AGCA
                                GACAAGATGC TGG    GCTGG
                                |||||||||| |||    |||||
                                TTGTTCTACG ACC    CGACC
                                     T  ____
GAM631   LOC146712 5'  CCAGCTGCTCGGCTCCCTC    83716    CAA  T    G
                                GA   GA GCTG AGCAGCTGG
                                ||   || |||| |||||||||
                                CT   CT CGGC TCGTCGACC
                                 CC_ _    _
GAM631   LOC146823 3'  CCAGCTGCTGGCGTGCTGTC   83792      AG    GG
                                GACA  ATGCT  AGCAGCTGG
                                ||||  |||||  |||||||||
                                CTGT  TGCGG  TCGTCGACC
                                  CG    __
GAM631   LOC147124 3'  CCAGCTGCTGGAATC       76300     G  GG
                                GAT CT  AGCAGCTGG
                                ||| ||  |||||||||
                                CTA GG  TCGTCGACC
                                  A  __
GAM631   LOC147649 5'  CCAGCTGCTGTGCACTGCTGTC 78413      __  A   T G
                                GACA  AG TGC G AGCAGCTGG
                                ||||  || ||| | |||||||||
                                CTGT  TC ACG T TCGTCGACC
                                  CG  _   _ G
GAM631   LOC148418 5'  CTGCCCAGATCTTGTC      78848         G    A
                                GACAAGAT CTGG GCAG
                                |||||||| |||| ||||
                                CTGTTCTA GACC CGTC

                                    _    _
GAM631   LOC148709 5'  CCAGCTACTGCTTCACCA    78938    C      ___
                                TG TGGAGCA   GCTGG
                                || |||||||   |||||
                                AC ACTTCGT   CGACC
                                 C      CAT
GAM631   LOC148753 5'  CCAGCTGTTTCACGTC      84211      C
                                GATG TGGAGCAGCTGG
                                |||| ||||||||||||
                                CTGC ACTTTGTCGACC

                                  _
GAM631   LOC148887 3'  CCAGCCGCTCCAGTTGGGCT   84231    AT__       A
                                AG    GCTGGAGC GCTGG
                                ||    |||||||| |||||
                                TC    TGACCTCG CGACC
                                 GGGT       C
GAM631   LOC149267 3'  CCAGCCTAGAACATCCTG    56676    A   __   AGCA
                                CA GATG  CTGG    GCTGG
                                || ||||  ||||    |||||
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                                GT CTAC  GATC    CGACC
                                 C    AA   ____
GAM631   LOC149426 3'  CCAGCTGCCCCTGGCCTCT    84415     T   _  A
                                AGA GCT GG GCAGCTGG
                                ||| ||| || ||||||||
                                TCT CGG CC CGTCGACC
                                  C   T  C
GAM631   LOC149577 3'  CAGCTGCCCGCCCTGT      84504     AGAT  T  A
                                ACA    GC GG GCAGCTG
                                |||    || || |||||||
                                TGT    CG CC CGTCGAC
                                  CC__  _  _
GAM631   LOC149935 5'  CCAGCTGCTGTCTGGATC     60297     G TG  __
                                GAT C  GA  GCAGCTGG
                                ||| |  ||  ||||||||
                                CTA G  CT  CGTCGACC
                                  _ GT  GT
GAM631   LOC150245 3'  CCAGCTGCTCCGGCTC      84933     T
                                GA GCTGGAGCAGCTGG
                                || ||||||||||||||
                                CT CGGCCTCGTCGACC
                                 _
GAM631   LOC151571 5'  CCAGCTGCTCCTCCGCG     85444     T__
                                TGC   GGAGCAGCTGG
                                |||   ||||||||||
                                GCG   CCTCGTCGACC
                                  CCT
GAM631   LOC153346 5'  CAGCTGCTGACCTTGTT     86020       ATGCTGG
                                GACAAG      AGCAGCTG
                                ||||||      ||||||||
                                TTGTTC      TCGTCGAC
                                   CAG_____
GAM631   LOC154313 5'  CCAACTGCTCCGACCGTC     81063      C_       C
                                GATG  TGGAGCAG TGG
                                ||||  |||||||| |||
                                CTGC  GCCTCGTC ACC
                                  CA       A
GAM631   LOC158226 3'  CCAGCTGCTCGCTTC       81795     T  TG
                                GA GC  GAGCAGCTGG
                                || ||  ||||||||||
                                CT CG  CTCGTCGACC
                                 T  __
GAM631   LOC158267 3'  CCAGGGACAGCGTCTTATC    81828     C        GAGCAG
                                GA AAGATGCTG     CTGG
                                || |||||||||     ||||
                                CT TTCTGCGAC     GACC
                                 A        AGG___
GAM631   LOC158434 5'  CCAGCTGCTCCTGATTCCTGC  86820    A  A  TGCT
                                G CA GA    GGAGCAGCTGG
                                | || ||    ||||||||||
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                                C GT CT   CCTCGTCGACC
                                 _ C  TAGT
GAM631  LOC159121 5'  CCAGCTGCTCCACTCT     86993     TGC
                                AGA  TGGAGCAGCTGG
                                |||  ||||||||||||
                                TCT  ACCTCGTCGACC
                                  C__
GAM631  LOC162461 3'  CCAGCTGCCTCTCTTGTC    82358       TGCT GA
                                GACAAGA   G  GCAGCTGG
                                |||||||   |  ||||||||
                                CTGTTCT   C  CGTCGACC
                                    ____ TC
GAM631  LOC163782 5'  CCAGCTGCTGAGCTCCCTC   82155    CAA  T   GG
                                GA   GA GCT  AGCAGCTGG
                                ||   || |||  |||||||||
                                CT   CT CGA  TCGTCGACC
                                 CC_  _   G_
GAM631  LOC165552 3'  CAGCTGCGGACCGCATC     82484      T  A__
                                GATGC GG   GCAGCTG
                                ||||| ||   |||||||
                                CTACG CC   CGTCGAC
                                   _ AGG
GAM631  LOC196418 5'  CCAGCCAGCAGTATCTCATC  87694    CA      GAGCA
                                GA  AGATGCTG    GCTGG
                                ||  ||||||||    |||||
                                CT  TCTATGAC    CGACC
                                 AC       GAC__
GAM631  LOC196463 3'  CTGTTCCAGCACCCTT     87712     A_
                                AAG  TGCTGGAGCAG
                                |||  ||||||||||
                                TTC  ACGACCTTGTC
                                  CC
GAM631  LOC196985 5'  CCAGCTGCCTTTGTGATC    89662     _  T_  A
                                GAT GC  GG GCAGCTGG
                                ||| ||  || ||||||||
                                CTA TG  TC CGTCGACC
                                  G  TT  _
GAM631  LOC196986 5'  CCAGCTGCCTTTGTGATC    89657     _  T_  A
                                GAT GC  GG GCAGCTGG
                                ||| ||  || ||||||||
                                CTA TG  TC CGTCGACC
                                  G  TT  _
GAM631  LOC199986 5'  CCGAAGCTCCAGCACCT     89904    A       AGC
                                AG TGCTGGAGC   TGG
                                || |||||||||   |||
                                TC ACGACCTCG   GCC
                                 C        AA_
GAM631  LOC200940 5'  CCAGCTGCTCCGCCTGTC    88952      AGAT  T
                                GACA    GC GGAGCAGCTGG
                                ||||    || ||||||||||
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                                CTGT    CG CCTCGTCGACC
                                  C___  _
GAM631   LOC221178 3'  CCAGCTGAACCAGCATTTTATC 93531    C        AG
                                GA AAGATGCTGG  CAGCTGG
                                || ||||||||||  |||||||
                                CT TTTTACGACC  GTCGACC
                                 A         AA
GAM631   LOC221927 5'  CCAGCTGCTCCCGGCTCT    92649     T    _
                                AGA GCTGG AGCAGCTGG
                                ||| ||||| |||||||||
                                TCT CGGCC TCGTCGACC
                                  _    C
GAM631   LOC253216 3'  CCAGCTGCCCACCGTC      94956     C   A
                                GATG TGG GCAGCTGG
                                |||| ||| ||||||||
                                CTGC ACC CGTCGACC
                                  C   _
GAM631   LOC254439 3'  CCAACTGCCCTTCTTGTC    94745       TGCT  A    C
                                GACAAGA    GG GCAG TGG
                                |||||||    || |||| |||
                                CTGTTCT    CC CGTC ACC
                                    T___  _    A
GAM631   LOC255121 5'  CCAGCTGCCCCCACCGCCTTCC 97560   C   A  C   A_
                                A AAG TG TGG  GCAGCTGG
                                | ||| || |||  ||||||||
                                C TTC GC ACC  CGTCGACC
                                 C   C  C   CC
GAM631   LOC255170 3'  CCAGCTGCCACCCCTATCT    97518      CT  A_
                                AGATG  GG  GCAGCTGG
                                |||||  ||  ||||||||
                                TCTAT  CC  CGTCGACC
                                   CC  AC
GAM631   LOC255575 5'  CCAGCCGTGGGCTCAGCATCTT 97442         G   A____
                                AAGATGCTG AGC     GCTGG
                                |||||||| |||     |||||
                                TTCTACGAC TCG     CGACC
                                     _   GGTGC
GAM631   LOC255988 5'  CCAGCTGCAGGGCCTCTTG    97609      T   GGA
                                CAAGA GCT   GCAGCTGG
                                ||||| |||   ||||||||
                                GTTCT CGG   CGTCGACC
                                   C   GA_
GAM631   LOC256158 5'  CCAGCTGCTCCCAGGC      97652     __
                                GCT  GGAGCAGCTGG
                                |||  ||||||||||
                                CGG  CCTCGTCGACC
                                  AC
GAM631   LOC56961  5'  CCAGCTGCCGCGGCCTC     62905    T   GA
                                GA GCTG  GCAGCTGG
                                || ||||  ||||||||
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                                CT CGGC  CGTCGACC
                                 C   GC
GAM631  LOC56961  5' CCAGCTGCTCCCCACCT    62906    A  CT
                                AG TG  GGAGCAGCTGG
                                || ||  ||||||||||
                                TC AC  CCTCGTCGACC
                                 C  C_
GAM631  LOC89919  3' AGCCACCCCAGCATCCTGC   60716   A  A      AGCA
                                G CA GATGCTGG    GCT
                                | || ||||||||    |||
                                C GT CTACGACC    CGA
                                 _ C       CCAC
GAM631  LOC90620  5' CCAGCTGCCCCACTAGATTG  63570    GA  C   A
                                CAA  TG TGG GCAGCTGG
                                |||  || ||| ||||||||
                                GTT  AT ACC CGTCGACC
                                  AG  C   C
GAM631  LOC90719  3' CCAGCTGCCAAGCATC     63882       GGA
                                GATGCT   GCAGCTGG
                                ||||||   ||||||||
                                CTACGA   CGTCGACC
                                   AC_
GAM631  LOC90981  3' CAAAGTCAGCATTTGTC    64534     A       AGCAGC
                                GACA GATGCTGG     TG
                                |||| ||||||||     ||
                                CTGT TTACGACT     AC
                                  _       GAA___
GAM631  LOC91301  5' CCAGCTGCCTGGTCTTTGTC  65539       AT  TG A
                                GACAAG  GC  G GCAGCTGG
                                ||||||  ||  | ||||||||
                                CTGTTT  TG  C CGTCGACC
                                   C_  GT _
GAM631  LOC91355  5' CCAGCTGTGTCCAGCCTGTC  65711     AGAT     _
                                GACA    GCTGGA GCAGCTGG
                                ||||    |||||| ||||||||
                                CTGT    CGACCT TGTCGACC
                                  C___      G
GAM631  LOC91373  3' CCAGCTGCCCCAGGGTTCTTCC 65835   C    _ G    A
                                A AAGA T CTGG GCAGCTGG
                                | |||| | |||| ||||||||
                                C TTCT G GACC CGTCGACC
                                 C    T G    C
GAM631  LOC91409  3' CCAACTGCTCTGCCCCT     65952    AT  T      C
                                AG  GC GGAGCAG TGG
                                ||  || ||||||| |||
                                TC  CG TCTCGTC ACC
                                 CC  _      A
GAM631  LOC91974  5' CCAGCTGCTAAGATC       67753     G  GG
                                GAT CT  AGCAGCTGG
                                ||| ||  |||||||||
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                                CTA GA  TCGTCGACC
                                  _ A_
GAM631  LOC92335  3'  CCAGCTGCCCTGGTGCTTTC  68971   C   A   TG A
                                A AAG TGC  G GCAGCTGG
                                | ||| |||  | ||||||||
                                C TTC GTG  C CGTCGACC
                                 T  _  GT C
GAM632  ADH1B   3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM632  AHR     3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM632  FDFT1   3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM632  JTB     3'  ATCTCAGACAGTGAAAGTGAAA 21959
           TG                     CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM632  KLF4    3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM632  PHYH    3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM632  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG   A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM632  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM632  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017         CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
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                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM632  CG012    5' CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                     CT  __
GAM632  EIF2C2   3' ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM632  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC       GTCTGAGAT
                                ||||||       |||||||||
                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM632  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM632  KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM632  KLHL6    3' ATCTCAGAGCAGGAAA      55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM632  NIR3     3' GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM632  PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM632  PP35     3' ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM632  PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148         TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
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                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM632  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM632  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941        CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM632  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM632  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM632  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226     A      GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM632  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM633  ADAM19   3'  CAGGAAGAAGACTGGCCATTAT 52703     C    CTGAG
           G                     CATGA GGCT     TTCTTCCTG
                                |||||| ||||    |||||||||
                                GTATT CCGG     AAGAAGGAC
                                  A    TCAG_
GAM633  FACL5    5'  CAGGAAGAACTCAGAGCCG   64186
                                CGGCTCTGAGTTCTTCCTG
                                ||||||||||||||||||
                                GCCGAGACTCAAGAAGGAC

GAM633  GNAL     5'  CAGGAAAGAGAGGAGCCGTCG  9058          GAG TC
                                TGACGGCTCT   T  TTCCTG
                                ||||||||||   |  ||||||
                                GCTGCCGAGG   A  AAGGAC
                                     AG_ GA
GAM633  KAL1     3'  CAGGAAGAACTTCTGTCA    4013        CTCT
                                TGACGG    GAGTTCTTCCTG
                                ||||||    ||||||||||||
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                                ACTGTC   TTCAAGAAGGAC
                                     ____
GAM633  MYO1E    3' CAGGAGGACAAAACCACCATG 17187     AC  CTC  AGT
                                CATG  GG   TG   TCTTCCTG
                                ||||  ||   ||   ||||||||
                                GTAC  CC   AC   AGGAGGAC
                                  CA  AAA  ___
GAM633  PRKAR2B  3' CAGAAAGAACTCAGATGT    10804    _        C
                                GC TCTGAGTTCTT CTG
                                || ||||||||||| |||
                                TG AGACTCAAGAA GAC
                                 T         A
GAM633  PUM2     3' AGGATCAAAGCTGTCATG    31014         C   GTTCT
                                CATGACGGCT TGA    TCCT
                                |||||||||| |||    ||||
                                GTACTGTCGA ACT    AGGA
                                      A  _____
GAM633  SKI      3' CAGGAAGTGCAGAGCCGCA   11701    A      AGTT
                                TG CGGCTCTG   CTTCCTG
                                || ||||||||   |||||||
                                AC GCCGAGAC   GAAGGAC
                                 _      GT__
GAM633  TEM8     3' AGGAAGATGCAACCCCATG   36326     AC  CTC  AGT
                                CATG  GG   TG   TCTTCCT
                                ||||  ||   ||   |||||||
                                GTAC  CC   AC   AGAAGGA
                                  C_  A__  GT_
GAM633  ARHGEF4  5' AGAAAAAACTCAGGGC      52207         C  C
                                GCTCTGAGTT TT CT
                                |||||||||| || ||
                                CGGGACTCAA AA GA
                                      A  A
GAM633  FLJ31978 3' CAGGAAGGAACAAGCGCC    58348     T  GAG
                                GGC CT   TTCTTCCTG
                                ||| ||   |||||||||
                                CCG GA   AGGAAGGAC
                                  C  ACA
GAM633  HSU24186 5' AGAACTCAAAGCCGTC      25324        C
                                GACGGCT TGAGTTCT
                                ||||||| ||||||||
                                CTGCCGA ACTCAAGA
                                    A
GAM633  KCNT1    3' AGCTCCCAGGGCCGCCA     61825    A     __
                                TG CGGCTCT  GAGTT
                                || |||||||  |||||
                                AC GCCGGGA  CTCGA
                                 C      CC
GAM633  KIAA1867 3' CAGGAAGAACCCAAGAGCTCAT 94822      CG    GA_
                                ATGA  GCTCT   GTTCTTCCTG
                                ||||  |||||   ||||||||||
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                                TACT  CGAGA   CAAGAAGGAC
                                  __    ACC
GAM633  KIAA1878  3'  AATTCAGAGAATCGTCATG   91707        __
                                CATGACGG  CTCTGAGTT
                                ||||||||  |||||||||
                                GTACTGCT  GAGACTTAA
                                     AA
GAM633  MFN1      3'  CAGGAAGAACTCATGA      35541    _
                                TC TGAGTTCTTCCTG
                                || ||||||||||||
                                AG ACTCAAGAAGGAC
                                 T
GAM633  MIDORI    3'  CAGGGCCCTTCCAGAGCCTGTC 73784       _      AGTTCT
            ATG                    CATGAC GGCTCTG     TCCTG
                                |||||| |||||||     |||||
                                GTACTG CCGAGAC     GGGAC
                                    T      CTTCCC
GAM633  MYH7B     3'  CAGGAAGAACCTGGCTCGCATG 70530     A  _   CTGA
                                CATG CG GCT    GTTCTTCCTG
                                |||| || |||    ||||||||||
                                GTAC GC CGG    CAAGAAGGAC
                                  _ T   TC__
GAM633  RNAHP     3'  AGAAAGCAGCAGCCGTCAT    23761         _  AG
                                ATGACGGCT CTG  TTCT
                                |||||||| |||  ||||
                                TACTGCCGA GAC  AAGA
                                     C   GA
GAM633  SLC37A1   3'  AGACGGAGCTCAGACCC     38561    C        TC
                                GG TCTGAGTTCT  CT
                                || ||||||||||  ||
                                CC AGACTCGAGG  GA
                                 C         CA
GAM633  LOC116236 3'  CAGGAAAAGCACAAACCTCAT  73809     C  CTC  A   C
                                ATGA GG   TG GTT TTCCTG
                                |||| ||   || ||| ||||||
                                TACT CC   AC CGA AAGGAC
                                  _ AA_  A   A
GAM633  LOC124801 3'  CAGGAAGAACTCTCTTGCATG  74336     A   CTCT
                                CATG CGG    GAGTTCTTCCTG
                                |||| |||    ||||||||||||
                                GTAC GTT    CTCAAGAAGGAC
                                  _   CT__
GAM633  LOC222160 5'  AGGAAGAACTCACCCC      94117    CTC
                                GG   TGAGTTCTTCCT
                                ||   ||||||||||||
                                CC   ACTCAAGAAGGA
                                 CC_
GAM633  LOC51094  3'  CAGGAAGAATAAAGCC      32045      CTGA
                                GGCT    GTTCTTCCTG
                                ||||    ||||||||||
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                                CCGA   TAAGAAGGAC
                                  AA__
GAM633  LOC92078  3'  CAGGAAGAAGAATCGACCGTC  67977      C  T  G__
                                GACGG TC GA   TTCTTCCTG
                                ||||| || ||   |||||||||
                                CTGCC AG CT   AAGAAGGAC
                                  _ _  AAG
GAM634  ADAM19    3'  CAGGAAGAAGACTGGCCATTAT 52703      C    CTGAG
          G                      CATGA GGCT    TTCTTCCTG
                                ||||| ||||    |||||||||
                                GTATT CCGG    AAGAAGGAC
                                  A   TCAG_
GAM634  ADAM19    3'  CAGGAAGAAGACTGGCCATTAT 52703      C    CTGAG
          G                      CATGA GGCT    TTCTTCCTG
                                ||||| ||||    |||||||||
                                GTATT CCGG    AAGAAGGAC
                                  A   TCAG_
GAM634  FACL5     5'  CAGGAAGAACTCAGAGCCG   64186
                                CGGCTCTGAGTTCTTCCTG
                                ||||||||||||||||||
                                GCCGAGACTCAAGAAGGAC

GAM634  FACL5     5'  CAGGAAGAACTCAGAGCCG   64186
                                CGGCTCTGAGTTCTTCCTG
                                ||||||||||||||||||
                                GCCGAGACTCAAGAAGGAC

GAM634  GNAL      5'  CAGGAAAGAGAGGAGCCGTCG  9058         GAG TC
                                TGACGGCTCT   T  TTCCTG
                                ||||||||||   |  ||||||
                                GCTGCCGAGG   A  AAGGAC
                                     AG_ GA
GAM634  GNAL      5'  CAGGAAAGAGAGGAGCCGTCG  9058         GAG TC
                                TGACGGCTCT   T  TTCCTG
                                ||||||||||   |  ||||||
                                GCTGCCGAGG   A  AAGGAC
                                     AG_ GA
GAM634  KAL1      3'  CAGGAAGAACTTCTGTCA    4013       CTCT
                                TGACGG   GAGTTCTTCCTG
                                ||||||   ||||||||||||
                                ACTGTC   TTCAAGAAGGAC
                                  ____
GAM634  KAL1      3'  CAGGAAGAACTTCTGTCA    4013       CTCT
                                TGACGG   GAGTTCTTCCTG
                                ||||||   ||||||||||||
                                ACTGTC   TTCAAGAAGGAC
                                  ____
GAM634  MYO1E     3'  CAGGAGGACAAAACCACCATG  17187      AC  CTC  AGT
                                CATG GG  TG  TCTTCCTG
                                ||||  ||  ||  ||||||||
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                              GTAC  CC   AC   AGGAGGAC
                                CA  AAA  ___
GAM634  MYO1E    3'  CAGGAGGACAAAACCACCATG  17187     AC  CTC  AGT
                              CATG  GG   TG   TCTTCCTG
                              ||||  ||   ||   ||||||||
                              GTAC  CC   AC   AGGAGGAC
                                CA  AAA  ___
GAM634  PRKAR2B  3'  CAGAAAGAACTCAGATGT    10804    _        C
                              GC TCTGAGTTCTT CTG
                              || ||||||||||| |||
                              TG AGACTCAAGAA GAC
                               T         A
GAM634  PRKAR2B  3'  CAGAAAGAACTCAGATGT    10804    _        C
                              GC TCTGAGTTCTT CTG
                              || ||||||||||| |||
                              TG AGACTCAAGAA GAC
                               T         A
GAM634  PUM2     3'  AGGATCAAAGCTGTCATG    31014         C   GTTCT
                              CATGACGGCT TGA    TCCT
                              |||||||||| |||    ||||
                              GTACTGTCGA ACT    AGGA
                                    A  _____
GAM634  PUM2     3'  AGGATCAAAGCTGTCATG    31014         C   GTTCT
                              CATGACGGCT TGA    TCCT
                              |||||||||| |||    ||||
                              GTACTGTCGA ACT    AGGA
                                    A  _____
GAM634  SKI      3'  CAGGAAGTGCAGAGCCGCA   11701    A      AGTT
                              TG CGGCTCTG   CTTCCTG
                              || ||||||||   |||||||
                              AC GCCGAGAC   GAAGGAC
                               _      GT__
GAM634  SKI      3'  CAGGAAGTGCAGAGCCGCA   11701    A      AGTT
                              TG CGGCTCTG   CTTCCTG
                              || ||||||||   |||||||
                              AC GCCGAGAC   GAAGGAC
                               _      GT__
GAM634  TEM8     3'  AGGAAGATGCAACCCCATG   36326     AC  CTC  AGT
                              CATG  GG   TG   TCTTCCT
                              ||||  ||   ||   |||||||
                              GTAC  CC   AC   AGAAGGA
                                C_  A__  GT_
GAM634  TEM8     3'  AGGAAGATGCAACCCCATG   36326     AC  CTC  AGT
                              CATG  GG   TG   TCTTCCT
                              ||||  ||   ||   |||||||
                              GTAC  CC   AC   AGAAGGA
                                C_  A__  GT_
GAM634  ARHGEF4  5'  AGAAAAAACTCAGGGC     52207         C  C
                              GCTCTGAGTT TT CT
                              |||||||||| || ||
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                                CGGGACTCAA AA GA
                                      A  A
GAM634  ARHGEF4   5' AGAAAAAACTCAGGGC     52207          C  C
                                GCTCTGAGTT TT CT
                                |||||||||| || ||
                                CGGGACTCAA AA GA
                                      A  A
GAM634  FLJ31978  3' CAGGAAGGAACAAGCGCC    58348     T  GAG
                                GGC CT   TTCTTCCTG
                                ||| ||   |||||||||
                                CCG GA   AGGAAGGAC
                                  C  ACA
GAM634  FLJ31978  3' CAGGAAGGAACAAGCGCC    58348     T  GAG
                                GGC CT   TTCTTCCTG
                                ||| ||   |||||||||
                                CCG GA   AGGAAGGAC
                                  C  ACA
GAM634  HSU24186  5' AGAACTCAAAGCCGTC      25324        C
                                GACGGCT TGAGTTCT
                                ||||||| ||||||||
                                CTGCCGA ACTCAAGA
                                    A
GAM634  HSU24186  5' AGAACTCAAAGCCGTC      25324        C
                                GACGGCT TGAGTTCT
                                ||||||| ||||||||
                                CTGCCGA ACTCAAGA
                                    A
GAM634  KCNT1     3' AGCTCCCAGGGCCGCCA     61825    A     __
                                TG CGGCTCT  GAGTT
                                || |||||||  |||||
                                AC GCCGGGA  CTCGA
                                 C      CC
GAM634  KCNT1     3' AGCTCCCAGGGCCGCCA     61825    A     __
                                TG CGGCTCT  GAGTT
                                || |||||||  |||||
                                AC GCCGGGA  CTCGA
                                 C      CC
GAM634  KIAA1867  3' CAGGAAGAACCCAAGAGCTCAT 94822     CG    GA_
                                ATGA  GCTCT   GTTCTTCCTG
                                ||||  |||||   ||||||||||
                                TACT  CGAGA   CAAGAAGGAC
                                  __    ACC
GAM634  KIAA1867  3' CAGGAAGAACCCAAGAGCTCAT 94822     CG    GA_
                                ATGA  GCTCT   GTTCTTCCTG
                                ||||  |||||   ||||||||||
                                TACT  CGAGA   CAAGAAGGAC
                                  __    ACC
GAM634  KIAA1878  3' AATTCAGAGAATCGTCATG   91707        __
                                CATGACGG  CTCTGAGTT
                                ||||||||  |||||||||
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                                GTACTGCT  GAGACTTAA
                                    AA
GAM634  KIAA1878 3'  AATTCAGAGAATCGTCATG   91707       __
                                CATGACGG  CTCTGAGTT
                                ||||||||  |||||||||
                                GTACTGCT  GAGACTTAA
                                    AA
GAM634  MFN1     3'  CAGGAAGAACTCATGA     35541    _
                                TC TGAGTTCTTCCTG
                                || ||||||||||||
                                AG ACTCAAGAAGGAC
                                 T
GAM634  MFN1     3'  CAGGAAGAACTCATGA     35541    _
                                TC TGAGTTCTTCCTG
                                || ||||||||||||
                                AG ACTCAAGAAGGAC
                                 T
GAM634  MIDORI   3'  CAGGGCCCTTCCAGAGCCTGTC 73784      _     AGTTCT
          ATG                     CATGAC GGCTCTG     TCCTG
                                ||||||| |||||||     |||||
                                GTACTG CCGAGAC     GGGAC
                                   T      CTTCCC
GAM634  MIDORI   3'  CAGGGCCCTTCCAGAGCCTGTC 73784      _     AGTTCT
          ATG                     CATGAC GGCTCTG     TCCTG
                                ||||||| |||||||     |||||
                                GTACTG CCGAGAC     GGGAC
                                   T      CTTCCC
GAM634  MYH7B    3'  CAGGAAGAACCTGGCTCGCATG 70530     A _  CTGA
                                CATG CG GCT    GTTCTTCCTG
                                ||||  ||  |||    ||||||||||
                                GTAC GC CGG    CAAGAAGGAC
                                  _  T   TC__
GAM634  MYH7B    3'  CAGGAAGAACCTGGCTCGCATG 70530     A _  CTGA
                                CATG CG GCT    GTTCTTCCTG
                                ||||  ||  |||    ||||||||||
                                GTAC GC CGG    CAAGAAGGAC
                                  _  T   TC__
GAM634  RNAHP    3'  AGAAAGCAGCAGCCGTCAT    23761        _  AG
                                ATGACGGCT CTG  TTCT
                                |||||||||  |||  ||||
                                TACTGCCGA GAC  AAGA
                                     C   GA
GAM634  RNAHP    3'  AGAAAGCAGCAGCCGTCAT    23761        _  AG
                                ATGACGGCT CTG  TTCT
                                |||||||||  |||  ||||
                                TACTGCCGA GAC  AAGA
                                     C   GA
GAM634  SLC37A1  3'  AGACGGAGCTCAGACCC     38561    C       TC
                                GG TCTGAGTTCT  CT
                                ||  ||||||||||  ||
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                                CC AGACTCGAGG  GA
                                 C         CA
GAM634  SLC37A1   3'  AGACGGAGCTCAGACCC     38561    C        TC
                                GG TCTGAGTTCT  CT
                                || ||||||||||  ||
                                CC AGACTCGAGG  GA
                                 C         CA
GAM634  LOC116236 3'  CAGGAAAAGCACAAACCTCAT  73809     C  CTC  A   C
                                ATGA GG   TG GTT TTCCTG
                                |||| ||   || ||| ||||||
                                TACT CC   AC CGA AAGGAC
                                  _  AA_  A   A
GAM634  LOC116236 3'  CAGGAAAAGCACAAACCTCAT  73809     C  CTC  A   C
                                ATGA GG   TG GTT TTCCTG
                                |||| ||   || ||| ||||||
                                TACT CC   AC CGA AAGGAC
                                  _  AA_  A   A
GAM634  LOC124801 3'  CAGGAAGAACTCTCTTGCATG  74336     A   CTCT
                                CATG CGG    GAGTTCTTCCTG
                                |||| |||    ||||||||||||
                                GTAC GTT    CTCAAGAAGGAC
                                  _   CT__
GAM634  LOC124801 3'  CAGGAAGAACTCTCTTGCATG  74336     A   CTCT
                                CATG CGG    GAGTTCTTCCTG
                                |||| |||    ||||||||||||
                                GTAC GTT    CTCAAGAAGGAC
                                  _   CT__
GAM634  LOC222160 5'  AGGAAGAACTCACCCC      94117    CTC
                                GG   TGAGTTCTTCCT
                                ||   ||||||||||||
                                CC   ACTCAAGAAGGA
                                 CC_
GAM634  LOC222160 5'  AGGAAGAACTCACCCC      94117    CTC
                                GG   TGAGTTCTTCCT
                                ||   ||||||||||||
                                CC   ACTCAAGAAGGA
                                 CC_
GAM634  LOC51094  3'  CAGGAAGAATAAAGCC      32045     CTGA
                                GGCT    GTTCTTCCTG
                                ||||    ||||||||||
                                CCGA    TAAGAAGGAC
                                  AA__
GAM634  LOC51094  3'  CAGGAAGAATAAAGCC      32045     CTGA
                                GGCT    GTTCTTCCTG
                                ||||    ||||||||||
                                CCGA    TAAGAAGGAC
                                  AA__
GAM634  LOC92078  3'  CAGGAAGAAGAATCGACCGTC  67977      C  T  G__
                                GACGG TC GA   TTCTTCCTG
                                ||||| || ||   |||||||||
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                                CTGCC AG CT   AAGAAGGAC
                                  _ _ AAG
GAM634  LOC92078 3' CAGGAAGAAGAATCGACCGTC 67977      C T G__
                                GACGG TC GA   TTCTTCCTG
                                ||||| || ||   |||||||||
                                CTGCC AG CT   AAGAAGGAC
                                  _ _ AAG
GAM635  B3GNT3   3' CCCACCTGGTACTGTT      26517         TACTAA A
                                AACAGTATC     AG TGGG
                                |||||||||     || ||||
                                TTGTCATGG     TC ACCC
                                      _______ C
GAM635  CSPG3    3' AGCCCATTGACTTAGAAACTGT 15227       A    CTAAA
           T                     AACAGT TCTA     GATGGGCT
                                ||||||| ||||     ||||||||
                                TTGTCA AGAT     TTACCCGA
                                   A   TCAG_
GAM635  EVA1     3' AGCCCATCTCTAATGAGGACT  58572     A   AC_ A
                                AGT TCT   TA AGATGGGCT
                                ||| |||   || |||||||||
                                TCA GGA   AT TCTACCCGA
                                  _   GTA  C
GAM635  ID4      3' CTTTAATAGATACTGT      7754          C
                                ACAGTATCTA TAAAG
                                |||||||||| |||||
                                TGTCATAGAT ATTTC
                                      A
GAM635  RAD51C   3' TTTAGAGATACTGTT       54255         A
                                AACAGTATCT CTAAA
                                |||||||||| |||||
                                TTGTCATAGA GATTT
                                      _
GAM635  RHO      3' AGCCCATCTTCAGCAGTTGCT  5018       T  A  A
                                AGTA CT CT AAGATGGGCT
                                |||| || || ||||||||||
                                TCGT GA GA TTCTACCCGA
                                  T  C  C
GAM635  STAR     3' CTCATTAGTAGACATGTT    4445      GTA      AAG
                                AACA   TCTACTA   ATGGG
                                ||||   |||||||   |||||
                                TTGT   AGATGAT   TACTC
                                  AC_      ___
GAM635  CD109    3' AGTGGTCTCAGTAGATACT   56046         AA   GG
                                AGTATCTACT  AGAT  GCT
                                ||||||||||  ||||  |||
                                TCATAGATGA  TCTG  TGA
                                      C_   G_
GAM635  FLJ00024 3' AGCCCATCCCTGGGACCTGC  63747    TCTA  AA
                                GTA   CTA  GATGGGCT
                                |||   |||  ||||||||
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                                CGT   GGT  CTACCCGA
                                  CCAG   CC
GAM635  FLJ20666  3'  GCTTACCACAGATACTGTT   35510        ACTAAAGA
                                AACAGTATCT      TGGGC
                                ||||||||||      |||||
                                TTGTCATAGA      ATTCG
                                     CACC____
GAM635  FLJ20666  3'  GCTTACCACAGATACTGTT   37089        ACTAAAGA
                                AACAGTATCT      TGGGC
                                ||||||||||      |||||
                                TTGTCATAGA      ATTCG
                                     CACC____
GAM635  FLJ22969  3'  GGCTCAGCAGATGCTGT    68657        ACTAAAGA
                                ACAGTATCT      TGGGCT
                                |||||||||      ||||||
                                TGTCGTAGA      ACTCGG
                                     CG______
GAM635  GGTLA1    5'  AGCCCATCTCTGTCCCATTGT  14657      ATCT  TAA
                                ACAGT   AC   AGATGGGCT
                                |||||   ||   |||||||||
                                TGTTA   TG   TCTACCCGA
                                   CCC_  TC_
GAM635  KIAA0240  3'  TTTAGTAGATTCTGTT     92443      T
                                AACAG ATCTACTAAA
                                ||||| ||||||||||
                                TTGTC TAGATGATTT
                                   T
GAM635  KIAA1028  3'  TTTATTAGATACTGTT     91952          C
                                AACAGTATCTA TAAA
                                |||||||||||| ||||
                                TTGTCATAGAT ATTT
                                      T
GAM635  KIAA1332  3'  CATCAAAAGATACTGTT    71163         ACTAAA
                                AACAGTATCT    GATG
                                ||||||||||    ||||
                                TTGTCATAGA    CTAC
                                     AAA___
GAM635  KIAA1497  3'  ATCTTTAGTAGACACT     67503    A
                                AGT TCTACTAAAGAT
                                ||| ||||||||||||
                                TCA AGATGATTTCTA
                                  C
GAM635  KIAA1858  3'  AGCCCATCTCTAGCACACCTTG 67133    TATCTA   A
                                CAG     CTA AGATGGGCT
                                |||     ||| |||||||||
                                GTT     GAT TCTACCCGA
                                  CCACAC   C
GAM635  p25       3'  GCCCATCCAGGACACTCC    22851   C   A   ACTAAA
                                A AGT TCT     GATGGGC
                                | ||| |||     |||||||
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                                C TCA AGG     CTACCCG
                                 C   C   AC____
GAM635  PME-1     3'  AGCCCATCTTTTCTGTGACTGT 32351      ATCTACT
                                ACAGT      AAAGATGGGCT
                                |||||      ||||||||||
                                TGTCA      TTTCTACCCGA
                                   GTGTCT_
GAM635  PRO0628   3'  AGCCCATCTTCTGTACTGCT   26205     TC   TA
                                AGTA  TAC  AAGATGGGCT
                                ||||  |||  ||||||||||
                                TCGT  ATG  TTCTACCCGA
                                  C_   TC
GAM635  LOC122728 3'  AGCCCATCTGCTGTATTACTG  74150      TC   TAA
                                CAGTA  TAC   AGATGGGCT
                                |||||  |||   |||||||||
                                GTCAT  ATG   TCTACCCGA
                                   T_   TCG
GAM635  LOC130507 3'  ATCTCTAGTAAATACTGTT    74948        C    A
                                AACAGTAT TACTA AGAT
                                |||||||| ||||| ||||
                                TTGTCATA ATGAT TCTA
                                     A    C
GAM635  LOC144110 3'  AGCCTGGGGCAGCAGGTACTG  76672        A  AAAGA
                                CAGTATCT CT    TGGGCT
                                |||||||| ||    ||||||
                                GTCATGGA GA    GTCCGA
                                     C  CGGG_
GAM635  LOC145368 3'  AGCCCATCTGCTGTATTACTG  77092      TC   TAA
                                CAGTA  TAC   AGATGGGCT
                                |||||  |||   |||||||||
                                GTCAT  ATG   TCTACCCGA
                                   T_   TCG
GAM635  LOC149830 3'  CCCATCTCTAAGGCAGGATGCT 84724        A__  AA_
            G                    CAGTATCT   CT   AGATGGG
                                |||||||   ||   |||||||
                                GTCGTAGG   GA   TCTACCC
                                     ACG  ATC
GAM635  LOC150236 5'  AGCCCATCCCCCAGTTCACT   79680    ATCT   AAA_
                                AGT    ACT    GATGGGCT
                                |||    |||    ||||||||
                                TCA    TGA    CTACCCGA
                                  CT__   CCCC
GAM635  LOC150279 3'  CCCATGAGGCTCAGATGCTGTT 79667         ACTAAAG
                                AACAGTATCT      ATGGG
                                ||||||||||      |||||
                                TTGTCGTAGA      TACCC
                                     CTCGGAG
GAM635  LOC150423 3'  AGCCCATCTCCTGTATTACTG  79863      TC   TAA
                                CAGTA  TAC   AGATGGGCT
                                |||||  |||   |||||||||
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                                GTCAT  ATG   TCTACCCGA
                                  T_   TCC
GAM635  LOC151405 5'  AGATGGGCTTTAGTAAAGACTG 85334      ATC      ATGGG
          T                    ACAGT   TACTAAAG    CT
                               |||||  ||||||||    ||
                               TGTCA  ATGATTTC    GA
                                  GAA      GGGTA
GAM635  LOC151473 3'  AGCCCATCTCTAGACTCTCGT  80250    _ TA   CTAA
                               AC AG  TCTA   AGATGGGCT
                               || ||  ||||   |||||||||
                               TG TC  AGAT   TCTACCCGA
                                C  TC   C___
GAM635  LOC153196 5'  AGCCCATCCTTGGGACCCTACT 85953     TCTA_   A
                               AGTA    CTAA GATGGGCT
                               ||||    |||| ||||||||
                               TCAT    GGTT CTACCCGA
                                  CCCAG   C
GAM635  LOC221002 3'  AGCCCATTCAGATAAAACTG   91475     ___   ACTAAA
                               CAGT   ATCT    GATGGGCT
                               ||||  ||||    ||||||||
                               GTCA   TAGA    TTACCCGA
                                  AAA   C_____
GAM635  LOC255290 5'  AGCCCATCTCTGTCCCATTGT  95607     ATCT  TAA
                               ACAGT   AC   AGATGGGCT
                               |||||   ||  |||||||||
                               TGTTA   TG   TCTACCCGA
                                  CCC_  TC_
GAM635  LOC91907  3'  ATCTTTAGTAGACACT     67493    A
                               AGT TCTACTAAAGAT
                               ||| ||||||||||||
                               TCA AGATGATTTCTA
                                 C
GAM636  ABCC12    3'  CTTGGGGTTGGTTCTGGGT   52645     TA    TT
                               ACCCG  GATCAG  CTAGG
                               |||||  ||||||  |||||
                               TGGGT  TTGGTT  GGTTC
                                  C_    GG
GAM636  ABCG1     3'  CCTAGAACCGCGTTGGGTT   16982     TAGATCA
                               AACCCG     GTTCTAGG
                               ||||||     ||||||||
                               TTGGGT     CAAGATCC
                                  TGCGC__
GAM636  ACAA1     5'  CTGGTGGCTGGTCTGCAGGGTT 7838      _       _   G
                               AACCC GTAGATCAGTT CTAG
                               ||||| |||||||||| ||||
                               TTGGG CGTCTGGTCGG GGTC
                                  A         T
GAM636  ACATN     5'  CTGGGACTGGACGG       16406     AGA
                               CCGT   TCAGTTCTAG
                               ||||   ||||||||||
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                              GGCA  GGTCAGGGTC
                                ___
GAM636  ACLY    3' TTAGAAACTGTGGGT      65062      TAGAT   _
                              ACCCG    CAGTT CTAG
                              |||||    ||||| ||||
                              TGGGT    GTCAA GATT
                                _____    A
GAM636  ACP1    3' CCTAGGGCCTTTTGTGG    23019       TCA
                              CCGTAGA  GTTCTAGG
                              |||||||  ||||||||
                              GGTGTTT  CGGGATCC
                                  TC_
GAM636  ACP1    3' CCTAGGGCCTTTTGTGG    15031       TCA
                              CCGTAGA  GTTCTAGG
                              |||||||  ||||||||
                              GGTGTTT  CGGGATCC
                                  TC_
GAM636  ACTN2   3' TTAGGGCTGGATGG       6595      AGA
                              CCGT  TCAGTTCTAG
                              ||||  ||||||||||
                              GGTA  GGTCGGGATT
                                ___
GAM636  ADAT1   3' TCTGGAGCTGTAAGGGT    23901     GTAGAT
                              ACCC    CAGTTCTAGG
                              ||||    ||||||||||
                              TGGG    GTCGAGGTCT
                                AAT___
GAM636  ADCY6   3' CTTGAACTGTCTGGGGTT   30930     G   T    T
                              AACCC TAGA CAGTTC AG
                              ||||| |||| |||||| ||
                              TTGGG GTCT GTCAAG TC
                                _  _     T
GAM636  ADCY6   3' CTTGAACTGTCTGGGGTT   40618     G   T    T
                              AACCC TAGA CAGTTC AG
                              ||||| |||| |||||| ||
                              TTGGG GTCT GTCAAG TC
                                _  _     T
GAM636  AGPAT2  3' CCTGGAAGACTCTGTGGG   21154       _ AG
                              CCCGTAGA TC  TTCTAGG
                              |||||||| ||  |||||||
                              GGGTGTCT AG  AAGGTCC
                                  C __
GAM636  AGPAT2  3' CCTGGAAGACTCTGTGGG   65821       _ AG
                              CCCGTAGA TC  TTCTAGG
                              |||||||| ||  |||||||
                              GGGTGTCT AG  AAGGTCC
                                  C __
GAM636  AHCY    3' TCTGGGGCTGATCAC      5477    A
                              GT GATCAGTTCTAGG
                              || ||||||||||||
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                                CA CTAGTCGGGGTCT
                                  _
GAM636  AKAP13   3'  TTTGGAACAATACGAGGTT   89692     _   GATCA
                                AACC CGTA    GTTCTAGG
                                |||| ||||    ||||||||
                                TTGG GCAT    CAAGGTTT
                                  A   AA___
GAM636  AOX1     3'  TCTGGAGCTGATTTAAAGT   6723     CCG
                                AC   TAGATCAGTTCTAGG
                                ||   ||||||||||||||
                                TG   ATTTAGTCGAGGTCT
                                 AA_
GAM636  AP2M1    3'  CTGGAGTGGGAGGGTT     14516      GTAGA   G
                                AACCC     TCA TTCTAG
                                |||||     ||| ||||||
                                TTGGG     GGT GAGGTC
                                   AG___   _
GAM636  APPBP2   3'  CTTGGAGTAGTCTGTGGGT   21076         CAG
                                ACCCGTAGAT   TTCTAGG
                                ||||||||||   |||||||
                                TGGGTGTCTG   GAGGTTC
                                      AT_
GAM636  APTX     5'  CTTAGAGTGATGATGCGGGT   34658       G_   G
                                ACCCGTA  ATCA TTCTAGG
                                |||||||  |||| |||||||
                                TGGGCGT  TAGT GAGATTC
                                    AG   _
GAM636  ARVCF    3'  TTGGGGCTGGTGGG       8030     GTAG
                                CCC    ATCAGTTCTAG
                                |||    ||||||||||
                                GGG    TGGTCGGGGTT
                                  _____
GAM636  ASTN     3'  TCTGGGTTGGTCTGTGG     69338          TT T
                                CCGTAGATCAG  C AGG
                                ||||||||||  | |||
                                GGTGTCTGGTT  G TCT
                                      GG _
GAM636  ATF4     5'  CCTGGGGCCGGCGCGGGTT   8035        AGA  A
                                AACCCGT   TC GTTCTAGG
                                |||||||   || ||||||||
                                TTGGGCG   GG CGGGGTCC
                                    C__  C
GAM636  ATP8B2   3'  TTTGGAGCTGGGAGTGGGT   65241      TAGA
                                ACCCG    TCAGTTCTAGG
                                |||||    ||||||||||
                                TGGGT    GGTCGAGGTTT
                                   GAG_
GAM636  ATSV     3'  CTTGGGGCTAGCACACGGGT   15054       AGATC
                                ACCCGT    AGTTCTAGG
                                ||||||    |||||||||
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                                TGGGCA    TCGGGGTTC
                                   CACGA
GAM636  BCL11B   3'  TCTGGAATGGATATATTGGTT  43195     C   G   A
                                AACC GTA ATC GTTCTAGG
                                |||| ||| ||| ||||||||
                                TTGG TAT TAG TAAGGTCT
                                  T   A   G
GAM636  BCL6     5'  CTTGGAGCCGATGGG      57222     GTAG   A
                                CCC    ATC GTTCTAGG
                                |||    ||| ||||||||
                                GGG    TAG CGAGGTTC
                                  _____  C
GAM636  C21orf2  3'  CTTGGGACTGTGGAGTGGGT   17010      TAGAT
                                ACCCG    CAGTTCTAGG
                                |||||    ||||||||||
                                TGGGT    GTCAGGGTTC
                                   GAGGT
GAM636  CARKL    3'  CCTGACACCATCTGTGGGT   25188         CA  TC
                                ACCCGTAGAT  GT  TAGG
                                ||||||||||  ||  ||||
                                TGGGTGTCTA  CA  GTCC
                                     C_  CA
GAM636  CBFA2T2  3'  TCTAGGGCAGTGCTGGGTT   17478      _   GATCA
                                AACCC GTA    GTTCTAGG
                                ||||| |||    ||||||||
                                TTGGG CGT    CGGGATCT
                                   T   GA___
GAM636  CCND2    3'  TCTGGGACTGAAAGGTT     8299      CGTAGA
                                AACC     TCAGTTCTAGG
                                ||||     ||||||||||
                                TTGG     AGTCAGGGTCT
                                  AA_____
GAM636  CDS2     3'  CTTGGAGCTGCAGAAGGGTT  13777      GTAGAT
                                AACCC     CAGTTCTAGG
                                |||||     ||||||||||
                                TTGGG     GTCGAGGTTC
                                   AAGAC_
GAM636  CELSR3   3'  CCTAGGACTGATGCTGTG    7397       _
                                CGTAG ATCAGTTCTAGG
                                ||||| ||||||||||||
                                GTGTC TAGTCAGGATCC
                                   G
GAM636  CETN1    3'  CCTGGAGCACATGAGGTT    95259     _  AGATCA
                                AACC CGT     GTTCTAGG
                                |||| |||     ||||||||
                                TTGG GTA     CGAGGTCC
                                  A  CA_____
GAM636  CHD2     3'  TTTGAACTTCTTGGATCTGTGG 7039          _____    TAGG
            GTT                   CCCGTAGATC    AGTTC
                                ||||||||||    |||||
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                                GGGTGTCTAG    TCAAG
                                      GTTCT    TTT
GAM636  CHD2    3'  TCTGGAGCTTTGTTATGAGTT  7034     C    ATC
                                AAC CGTAG   AGTTCTAGG
                                ||| |||||   |||||||||
                                TTG GTATT   TCGAGGTCT
                                  A    GTT
GAM636  CHRNA2  5'  CCTGGGGCCAGGCTTGGGTT  5602       T  ATCA
                                AACCCG AG   GTTCTAGG
                                |||||| ||   ||||||||
                                TTGGGT TC   CGGGGTCC
                                   _ GGAC
GAM636  CKTSF1B1 3'  CTTAGGATTGATCTAAGG   25366    G
                                CC TAGATCAGTTCTAGG
                                || ||||||||||||||
                                GG ATCTAGTTAGGATTC
                                 A
GAM636  COG7    5'  CCTGGCGTTTCTGGGGTT    67621      G   TCAGTT
                                AACCC TAGA     CTAGG
                                ||||| ||||     |||||
                                TTGGG GTCT     GGTCC
                                   _    TTGC__
GAM636  COL1A1  3'  CTGGGGACCTGGGGTT      3605       G  A  AGT
                                AACCC TAG TC   TCTAG
                                ||||| ||| ||   |||||
                                TTGGG GTC AG   GGGTC
                                   _  C  ___
GAM636  COX10   3'  TCTGGAGTCACTACTGTGGGT  7126        ATCAG_
                                ACCCGTAG     TTCTAGG
                                ||||||||     |||||||
                                TGGGTGTC     GAGGTCT
                                     ATCACT
GAM636  CPNE7   3'  TCTGCCTGGCCTGTGGGTT   27040        AT   TTC
                                AACCCGTAG  CAG   TAGG
                                |||||||||  |||   ||||
                                TTGGGTGTC  GTC   GTCT
                                     CG   C__
GAM636  CRY2    3'  CCTGGAGCTCCATGG      72207     A  TCA
                                CCGT GA   GTTCTAGG
                                |||| ||   ||||||||
                                GGTA CT   CGAGGTCC
                                  C  ___
GAM636  CSNK1E  3'  CCTGGAGTCAGGGCTGGGTT  95629      _  AGATCAG
                                AACCC GT      TTCTAGG
                                ||||| ||      |||||||
                                TTGGG CG      GAGGTCC
                                   T  GGACT__
GAM636  CSPG4   3'  CCTGGAGCTGGTTTGGG     8571      TA
                                CCCG  GATCAGTTCTAGG
                                ||||  ||||||||||||
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                                GGGT  TTGGTCGAGGTCC
                                  __
GAM636  CTNNB1   3'  TTTGGGATATGTATGGGT    8582        G  CA
                                ACCCGTA AT  GTTCTAGG
                                ||||||| ||  ||||||||
                                TGGGTAT TA  TAGGGTTT
                                   G  __
GAM636  CTSZ     5'  TCTGGGACTCGGAGCGGG    62117      AGA  _
                                CCCGT   TC AGTTCTAGG
                                |||||   || |||||||||
                                GGGCG   GG TCAGGGTCT
                                  A__  C
GAM636  CYP1B1   3'  CTAGTATTTATGGGT      3653          CAGTT
                                ACCCGTAGAT    CTAG
                                ||||||||||    ||||
                                TGGGTATTTA    GATC
                                     T_____
GAM636  CYP27B1  3'  CCTAGCCTGGTTTACGG     5775           TT
                                CCGTAGATCAG  CTAGG
                                ||||||||||  |||||
                                GGCATTTGGTC  GATCC
                                     C_
GAM636  DAG1     3'  TCTGGAATTACACTGGGGTT   15283      G   ATC
                                AACCC TAG   AGTTCTAGG
                                ||||| |||   ||||||||||
                                TTGGG GTC   TTAAGGTCT
                                  _  ACA
GAM636  DAZ      3'  CTTAGAACTGGTGATG      14550     AG
                                CGT  ATCAGTTCTAGG
                                |||  ||||||||||||
                                GTA  TGGTCAAGATTC
                                  G_
GAM636  DNAJB9   3'  CTTAGTATGGATTTATGTGTT  24680     C       AGTT
                                AAC CGTAGATC    CTAGG
                                ||| ||||||||    |||||
                                TTG GTATTTAG    GATTC
                                  T       GTAT
GAM636  DPYSL2   3'  TCTGGTTGGGGTTTTGGGTT   7304        T    AGTT
                                AACCCG AGATC    CTAGG
                                ||||||| |||||   |||||
                                TTGGGT TTTGG    GGTCT
                                   _    GGTT
GAM636  DPYSL2   3'  CCTACACATCTATGGGT     7294          CA  TC
                                ACCCGTAGAT  GT  TAGG
                                ||||||||||  ||  ||||
                                TGGGTATCTA  CA  ATCC
                                     __  C_
GAM636  EEF1B2   5'  TCTAGGGCTGGTTCCCG     40882    TA
                                CG  GATCAGTTCTAGG
                                ||  ||||||||||||
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                                GC  TTGGTCGGGATCT
                                 CC
GAM636  EGFL3   5'  CTTAGGGCGCAGCGCGGTT   62615     _  AGATCA
                                AACC CGT     GTTCTAGG
                                |||| |||     ||||||||
                                TTGG GCG     CGGGATTC
                                  C   ACG___
GAM636  EGR2    3'  CTTGGGACTGATTTGGGG    4628     G
                                CCC TAGATCAGTTCTAGG
                                ||| ||||||||||||||
                                GGG GTTTAGTCAGGGTTC
                                  _
GAM636  EGR4    3'  CAAGAGATGGGTTTATGGGTT  8743          AG_   AGG
                                AACCCGTAGATC   TTCT
                                ||||||||||||   ||||
                                TTGGGTATTTGG   GAGA
                                       GTA    AC
GAM636  ELK1    3'  TTGGGACCTGGGGGTT      17848      G  ATCA
                                AACCC TAG    GTTCTAG
                                ||||| |||    |||||||
                                TTGGG GTC    CAGGGTT
                                  G  _____
GAM636  ESR1    3'  TCTAGCACAATTATGGGTT   3711         ATCA  T
                                AACCCGTAG    GT CTAGG
                                |||||||||    || |||||
                                TTGGGTATT    CA GATCT
                                     AA__  C
GAM636  EVA1    5'  TCTGGGGCCAAGGCTGGGTT  58573      _  AGATCA
                                AACCC GT     GTTCTAGG
                                ||||| ||     ||||||||
                                TTGGG CG     CGGGGTCT
                                  T  GAAC__
GAM636  EVA1    5'  TCTGGGGCCAAGGCTGGGTT  19398      _  AGATCA
                                AACCC GT     GTTCTAGG
                                ||||| ||     ||||||||
                                TTGGG CG     CGGGGTCT
                                  T  GAAC__
GAM636  EZH1    3'  CCTCAAGCTGGACTGTGGGTT  8817         A     CT
                                AACCCGTAG TCAGTT  AGG
                                ||||||||| ||||||  |||
                                TTGGGTGTC GGTCGA  TCC
                                     A     AC
GAM636  FANCC    3'  TCTGGAATTGTATTGGTT    70527     C   GAT
                                AACC GTA   CAGTTCTAGG
                                |||| |||   ||||||||||
                                TTGG TAT   GTTAAGGTCT
                                  T  ___
GAM636  FBLN1   3'  CTTAGAACCTTCCATGG     21396      A  TCA
                                CCGT GA   GTTCTAGG
                                |||| ||   ||||||||
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                                GGTA CT   CAAGATTC
                                  C  TC_
GAM636  FBXL11   3'  TTAGAGGTGAGGGTT      24577      GTAGA   G
                                AACCC     TCA TTCTAG
                                |||||     ||| ||||||
                                TTGGG     AGT GAGATT
                                  _____   G
GAM636  FBXL4    3'  TTTGGGATTGGTTTTGGGTT   24073       T
                                AACCCG AGATCAGTTCTAGG
                                |||||| ||||||||||||||
                                TTGGGT TTTGGTTAGGGTTT
                                  _
GAM636  FCRH3    3'  CCTGTGCCTGATCTGTGTGTT  53631     C        TTC
                                AAC CGTAGATCAG   TAGG
                                ||| ||||||||||   ||||
                                TTG GTGTCTAGTC   GTCC
                                  T         CGT
GAM636  FKBP10   3'  TTGGGGCTGAGGGGT      41650      GTAGA
                                ACCC     TCAGTTCTAG
                                ||||     ||||||||||
                                TGGG     AGTCGGGGTT
                                  G____
GAM636  FOXE3    3'  CTTAGGACTTATTGGGTT    24104      GTA   C
                                AACCC   GAT AGTTCTAGG
                                |||||   ||| |||||||||
                                TTGGG   TTA TCAGGATTC
                                  ___   T
GAM636  G2A      3'  CCTGGGGCCAGCAATGTGGTT  25319     _   AGATCA
                                AACC CGT     GTTCTAGG
                                |||| |||     ||||||||
                                TTGG GTA     CGGGGTCC
                                  T   ACGAC_
GAM636  GABRE    5'  CCTGGATGGCTGTCTGTGGGT  41804         T   __
                                ACCCGTAGA CAGT  TCTAGG
                                ||||||||| ||||  ||||||
                                TGGGTGTCT GTCG  AGGTCC
                                     _    GT
GAM636  GALGT    3'  TCTGGGGCTGGGGTGAGGG   7617      G  GA
                                CCC TA  TCAGTTCTAGG
                                ||| ||  ||||||||||
                                GGG GT  GGTCGGGGTCT
                                  A  GG
GAM636  GCK      3'  CCTAAGATTGTGTGGGTT    53178       TAGAT    TC
                                AACCCG    CAGT  TAGG
                                ||||||    ||||  ||||
                                TTGGGT    GTTA  ATCC
                                   GT___    GA
GAM636  GCK      3'  CCTAAGATTGTGTGGGTT    3868        TAGAT    TC
                                AACCCG    CAGT  TAGG
                                ||||||    ||||  ||||
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                                TTGGGT    GTTA  ATCC
                                   GT___    GA
GAM636  GCK     3'  CCTAAGATTGTGTGGGTT    53173      TAGAT   TC
                                AACCCG    CAGT  TAGG
                                ||||||    ||||  ||||
                                TTGGGT    GTTA  ATCC
                                   GT___    GA
GAM636  GFRA2    5'  TTTGGGGCTGATTAC      7663     A
                                GT GATCAGTTCTAGG
                                || ||||||||||||
                                CA TTAGTCGGGGTTT
                                 _
GAM636  GNA15    3'  TCTGGGACCCTCTGTGGGT   59911        TCA
                                ACCCGTAGA  GTTCTAGG
                                |||||||||  ||||||||
                                TGGGTGTCT  CAGGGTCT
                                     CC_
GAM636  GPR44    3'  CCTGGTGTTCTGTGGG     16527       T  GTT
                                CCCGTAGA CA   CTAGG
                                |||||||| ||   |||||
                                GGGTGTCT GT   GGTCC
                                     T  ___
GAM636  GSTM5    3'  TCTAGAACTGGCATGG     5957      AGA
                                CCGT   TCAGTTCTAGG
                                ||||   ||||||||||
                                GGTA   GGTCAAGATCT
                                  C__
GAM636  GYG2     5'  CTCTGCTCTGCGGGTT     14049        T   TTCT
                                AACCCGTAGA CAG    AG
                                |||||||||| |||    ||
                                TTGGGCGTCT GTC    TC
                                     C  _____
GAM636  HIVEP2   3'  TTGGACTCTGAGGGTT     22121      GTAGA   T_
                                AACCC    TCAG  TCTAG
                                |||||    ||||  |||||
                                TTGGG    AGTC  AGGTT
                                   ______   TC
GAM636  HNMT     3'  TTTGGAATCATATGGG     22569      GATCA
                                CCCGTA    GTTCTAGG
                                ||||||    ||||||||
                                GGGTAT    TAAGGTTT
                                   AC___
GAM636  HOXD4    3'  CTGGACTTTCTGGGTT     27522      GT   TC   T
                                AACCC  AGA  AGT CTAG
                                |||||  |||  ||| ||||
                                TTGGG  TCT  TCA GGTC
                                   __   T_  _
GAM636  HTR1D    3'  TTTGGAGCCAGGATGGGT    6006       AGATCA
                                ACCCGT     GTTCTAGG
                                ||||||     ||||||||
```

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                                TGGGTA     CGAGGTTT
                                   GGAC__
GAM636  HUS1     3'  CCTGGGGCCAGTTTTGGGTT  91101       T   CA
                                AACCCG AGAT  GTTCTAGG
                                |||||| ||||  ||||||||
                                TTGGGT TTTG  CGGGGTCC
                                   _   AC
GAM636  IHPK2    3'  CCTGGAGCTGATGTGC      61860     G
                                GTA ATCAGTTCTAGG
                                ||| ||||||||||||
                                CGT TAGTCGAGGTCC
                                  G
GAM636  INHBB    3'  TCTAGGACTGGTTTGGGG    9343      G
                                CCC TAGATCAGTTCTAGG
                                ||| ||||||||||||||
                                GGG GTTTGGTCAGGATCT
                                 _
GAM636  IRTA2    5'  CTTGGAGCTGGTGTGC      48404     G
                                GTA ATCAGTTCTAGG
                                ||| ||||||||||||
                                CGT TGGTCGAGGTTC
                                  G
GAM636  ITSN1    3'  CCTAGAGCTGATCACTCGG   11617     TA_
                                CCG   GATCAGTTCTAGG
                                |||   ||||||||||||
                                GGC   CTAGTCGAGATCC
                                  TCA
GAM636  KCNK6    3'  CTGGGACTGAGGGGT       16692     GTAGA
                                ACCC    TCAGTTCTAG
                                ||||    ||||||||||
                                TGGG    AGTCAGGGTC
                                  G_____
GAM636  KIFAP3   3'  CTTAGAAGAAATCTGTGTGGGT 30363       __    CAG
           T                     AACCCG  TAGAT   TTCTAGG
                                ||||||  |||||   |||||||
                                TTGGGT  GTCTA   AAGATTC
                                   GT    AAG
GAM636  KLHL3    3'  TCTACCTGGCTGTGGGTT    87467        A   TTC
                                AACCCGTAG TCAG   TAGG
                                |||||||| ||||   ||||
                                TTGGGTGTC GGTC   ATCT
                                      _   C__
GAM636  KPNB2    3'  TCTGGAGCCTTTGTGGGT    9632         TCA
                                ACCCGTAGA   GTTCTAGG
                                |||||||||   ||||||||
                                TGGGTGTTT   CGAGGTCT
                                     C__
GAM636  LAF4     3'  CCTGGGGCCAGAGTGGG     9658      TAGA  A_
                                CCCG   TC  GTTCTAGG
                                ||||   ||  ||||||||
```

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                                GGGT   AG  CGGGGTCC
                                  G___  AC
GAM636  LARGE    3'  CCTGGAGGTGGGGTTGATGGGT 56108       AGA__  G
              T                   AACCCGT    TCA TTCTAGG
                                  |||||||    ||| |||||||
                                  TTGGGTA    GGT GAGGTCC
                                     GTTGG   G
GAM636  LARGE    3'  CCTGGAGGTGGGGTTGATGGGT 16434       AGA__  G
              T                   AACCCGT    TCA TTCTAGG
                                  |||||||    ||| |||||||
                                  TTGGGTA    GGT GAGGTCC
                                     GTTGG   G
GAM636  LFG      3'  CCTGGGAGGCATTTGGGGTT   76716      G    CAG
                                  AACCC TAGAT   TTCTAGG
                                  ||||| |||||   |||||||
                                  TTGGG GTTTA   AGGGTCC
                                    _    CGG
GAM636  LIFR     3'  TCTGGAGTGATTGTGGTT    9747      CGTA    G
                                  AACC    GATCA TTCTAGG
                                  ||||    ||||| |||||||
                                  TTGG    TTAGT GAGGTCT
                                    TG__    _
GAM636  LIMD1    3'  CCTGGGGTGGAAGTGGGGT    26457     G  GA  A TT
                                  ACCC TA  TC G  CTAGG
                                  |||| ||  || |  |||||
                                  TGGG GT  AG T  GGTCC
                                    _ GA  G GG
GAM636  LNK      3'  TCTAGAATTTCCTTGGG     18473     TA  TC
                                  CCCG  GA  AGTTCTAGG
                                  ||||  ||  |||||||||
                                  GGGT  CT  TTAAGATCT
                                    TC  __
GAM636  LPIN2    3'  TCTGGAGCTGGTCCCGC     27711    A_
                                  GT  GATCAGTTCTAGG
                                  ||  ||||||||||||
                                  CG  CTGGTCGAGGTCT
                                   CC
GAM636  LPIN2    3'  CCTGGGATCCCTCCTTTGTGGG 27707         TCA___
              T                   ACCCGTAGA     GTTCTAGG
                                  |||||||||     ||||||||
                                  TGGGTGTTT     TAGGGTCC
                                       CCTCCC
GAM636  LPIN2    3'  CCTGGGGCTGGAGGCCTGGG   27708     TAGA_
                                  CCCG    TCAGTTCTAGG
                                  ||||    ||||||||||
                                  GGGT    GGTCGGGGTCC
                                    CCGGA
GAM636  MADH6    5'  CCTGGGACCTGAGACGGCGTT  18765     _   AGA   _
                                  AAC CCGT   TCAG TTCTAGG
                                  ||| ||||   |||| |||||||
```

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                                TTG GGCA   AGTC AGGGTCC
                                  C   G__   C
GAM636  MAGEB3   3'  TTTAGGATTGATACTGGT   9889     C   GA
                                ACC GTA  TCAGTTCTAGG
                                ||| |||  ||||||||||
                                TGG CAT  AGTTAGGATTT
                                  T  __
GAM636  MAN2A2   3'  CCTATGTACTGATTTGTGGG  20393          TC_
                                CCCGTAGATCAGT   TAGG
                                ||||||||||||   ||||
                                GGGTGTTTAGTCA   ATCC
                                       TGT
GAM636  MAP4     3'  CTTGGAGCGTGGACTGGTT   48060     C  AGATCA
                                AACC GT     GTTCTAGG
                                |||| ||     ||||||||
                                TTGG CA     CGAGGTTC
                                  T  GGTG__
GAM636  MAP4     3'  CTTGGAGCGTGGACTGGTT   9908      C  AGATCA
                                AACC GT     GTTCTAGG
                                |||| ||     ||||||||
                                TTGG CA     CGAGGTTC
                                  T  GGTG__
GAM636  MCL1     3'  CCTGGGATTGAGAGGTT    41715     CGTAGA
                                AACC     TCAGTTCTAGG
                                ||||     ||||||||||
                                TTGG     AGTTAGGGTCC
                                  AG____
GAM636  MGAT5    5'  TCTAGAATTGAGAGGTT    10029     CGTAGA
                                AACC     TCAGTTCTAGG
                                ||||     ||||||||||
                                TTGG     AGTTAAGATCT
                                  AG____
GAM636  MID2     5'  CCTGGGAACGCTATGGGT   53388       ATCAG
                                ACCCGTAG    TTCTAGG
                                ||||||||    |||||||
                                TGGGTATC    AGGGTCC
                                    GCA__
GAM636  MID2     5'  CCTGGGAACGCTATGGGT   24223       ATCAG
                                ACCCGTAG    TTCTAGG
                                ||||||||    |||||||
                                TGGGTATC    AGGGTCC
                                    GCA__
GAM636  MLF2     3'  TTTGGGGTGAGCTCTGGGTT  18375      T  A  G
                                AACCCG AG TCA TTCTAGG
                                |||||| || ||| |||||||
                                TTGGGT TC AGT GGGGTTT
                                   C  G  _
GAM636  MLLT7    3'  TTTAGAGCTAGGGTGGGGT   19870     GTAGA  _
                                ACCC    TC AGTTCTAGG
                                ||||    || |||||||||
```

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                                TGGG    GG TCGAGATTT
                                  GTG__  A
GAM636  MMP25   3'  TCTAGAGTGAGGGGTGGGT   42447      AGA  G
                                ACCCGT  TCA TTCTAGG
                                ||||||  ||| |||||||
                                TGGGTG  AGT GAGATCT
                                   GGG  _
GAM636  MNT     3'  CCTGGCGGCCTGTGGGTT    39710        AT AGTT
                                AACCCGTAG  C   CTAGG
                                |||||||||  |   |||||
                                TTGGGTGTC  G   GGTCC
                                     CG C___
GAM636  MTF1    3'  CCTAGAGTGAACTTGTGG    19882   _  T  A  G
                                CC CG AG TCA TTCTAGG
                                || || || ||| |||||||
                                GG GT TC AGT GAGATCC
                                 T  _  A  _
GAM636  MTR     3'  CCTAAAATTGATCTATGG    4208          C
                                CCGTAGATCAGTT TAGG
                                |||||||||||| ||||
                                GGTATCTAGTTAA ATCC
                                       A
GAM636  MTR     5'  CCTAGGGCGCTGCGGG     4209        ATCA
                                CCCGTAG   GTTCTAGG
                                |||||||   ||||||||
                                GGGCGTC   CGGGATCC
                                   G___
GAM636  NAT1    3'  CCTAGAAAAGTTTTATGGGT  5405        TCAG
                                ACCCGTAGA   TTCTAGG
                                |||||||||   |||||||
                                TGGGTATTT   AAGATCC
                                     TGAA
GAM636  NEURL   3'  CTGGGGCTGATGGT       14859    CGTAG
                                ACC    ATCAGTTCTAG
                                |||    ||||||||||
                                TGG    TAGTCGGGGTC
                                 _____
GAM636  NOLA1   3'  CCTGGCACTCTGTGGGT    52205        TCA  T
                                ACCCGTAGA  GT CTAGG
                                |||||||||  || |||||
                                TGGGTGTCT  CA GGTCC
                                     ___  C
GAM636  NR1I2   3'  CCTGGGGCTGGAATGCTGGGT  13967    _  GA
                                ACCC GTA  TCAGTTCTAGG
                                ||||  |||  ||||||||||
                                TGGG CGT  GGTCGGGGTCC
                                  T  AA
GAM636  NR1I2   3'  CCTGGGGCTGGAATGCTGGGT  41827    _  GA
                                ACCC GTA  TCAGTTCTAGG
                                ||||  |||  ||||||||||
```

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                                TGGG CGT  GGTCGGGGTCC
                                  T  AA
GAM636  NRIP1    3'  TCTGGACATGACGTCTGTGG  59954       __  GT
                                CCGTAGA  TCA  TCTAGG
                                |||||||  |||  ||||||
                                GGTGTCT  AGT  AGGTCT
                                   GC   AC
GAM636  NYX      3'  CCTGGGGTCTGAGATGTG    42598     GA  _
                                CGTA  TCAG TTCTAGG
                                ||||  |||| |||||||
                                GTGT  AGTC GGGGTCC
                                  AG   T
GAM636  OTOF     3'  CCTGTCCTGCCTGTGGGTT   16641       AT  TTC
                                AACCCGTAG  CAG  TAGG
                                |||||||||  |||  ||||
                                TTGGGTGTC  GTC  GTCC
                                     C_  CT_
GAM636  P2RY2    3'  TCTGGAGCTGAGCTACCTGGG  10381    __  A
                                CCC  GTAG TCAGTTCTAGG
                                |||  |||| ||||||||||
                                GGG  CATC AGTCGAGGTCT
                                  TC   G
GAM636  PACE     5'  CTGGAGCTGGATGG       10391     AGA
                                CCGT  TCAGTTCTAG
                                ||||  ||||||||||
                                GGTA  GGTCGAGGTC
                                  ___
GAM636  PAG      3'  CTGGACCCTGCGGGT       37403       ATCA  T
                                ACCCGTAG   GT CTAG
                                ||||||||   || ||||
                                TGGGCGTC   CA GGTC
                                     C___  _
GAM636  PCDH11X  5'  AGGTTTGGTCAGTGTTGTGCGG 52016      _______    TTCTAGG
          GTT                   CCGTA     GATCAG
                                |||||     ||||||
                                GGCGT     CTGGTT
                                   GTTGTGA    T  GGAT
GAM636  PCDH11X  5'  AGGTTTGGTCAGTGTTGTGCGG 52038      _______    TTCTAGG
          GTT                   CCGTA     GATCAG
                                |||||     ||||||
                                GGCGT     CTGGTT
                                   GTTGTGA    T  GGAT
GAM636  PCDH11X  5'  AGGTTTGGTCAGTGTTGTGCGG 27237      _______    TTCTAGG
          GTT                   CCGTA     GATCAG
                                |||||     ||||||
                                GGCGT     CTGGTT
                                   GTTGTGA    T  GGAT
GAM636  PCTK1    3'  CCTGGGGCCCTGAAATGGG   52262     AGA  __
                                CCCGT  TCA  GTTCTAGG
                                |||||  |||  ||||||||
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                                GGGTA  AGT  CGGGGTCC
                                  A__  CC
GAM636  PCTK1    3'  CCTGGGGCCCTGAAATGGG   52267     AGA  __
                                CCCGT  TCA  GTTCTAGG
                                |||||  |||  ||||||||
                                GGGTA  AGT  CGGGGTCC
                                  A__  CC
GAM636  PCTK1    3'  CCTGGGGCCCTGAAATGGG   20578     AGA  __
                                CCCGT  TCA  GTTCTAGG
                                |||||  |||  ||||||||
                                GGGTA  AGT  CGGGGTCC
                                  A__  CC
GAM636  PIGA     3'  TTTAGAAACAGTCTTTGTGGGT 40009     T__  CAG
                                ACCCG  AGAT  TTCTAGG
                                |||||  ||||  |||||||
                                TGGGT  TCTG  AAGATTT
                                  GTT  ACA
GAM636  PIGA     3'  TTTAGAAACAGTCTTTGTGGGT 10556     T__  CAG
                                ACCCG  AGAT  TTCTAGG
                                |||||  ||||  |||||||
                                TGGGT  TCTG  AAGATTT
                                  GTT  ACA
GAM636  PIGA     3'  TTTAGAAACAGTCTTTGTGGGT 40018     T__  CAG
                                ACCCG  AGAT  TTCTAGG
                                |||||  ||||  |||||||
                                TGGGT  TCTG  AAGATTT
                                  GTT  ACA
GAM636  PIK3R2   3'  TCTGGCTCTTGTTTGGGGTT  17260     G   C  TT
                                AACCC TAGAT AG  CTAGG
                                ||||| ||||| ||  |||||
                                TTGGG GTTTG TC  GGTCT
                                  _   T  TC
GAM636  PIWIL1   3'  TTTGGAACTGGGACATG    72824    AGA
                                CGT  TCAGTTCTAGG
                                |||  ||||||||||
                                GTA  GGTCAAGGTTT
                                 CAG
GAM636  PMP22    3'  CCTAGAGCTTGGCTGGGT    4324     GT  A  _
                                ACCC  AG TCA GTTCTAGG
                                ||||  || ||| ||||||||
                                TGGG  TC GGT CGAGATCC
                                  __  _  T
GAM636  POU2AF1  3'  CCTGGAATTGAGCCCCAGGTT  20649     CGTAGA
                                AACC    TCAGTTCTAGG
                                ||||    ||||||||||
                                TTGG    AGTTAAGGTCC
                                  ACCCCG
GAM636  PPP1R12A 3'  CCTGGAACTGAATTGC     10178     A
                                GTAG TCAGTTCTAGG
                                |||| ||||||||||
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                                CGTT AGTCAAGGTCC
                                  A
GAM636  PROC    3'  CCTAGAGCAACTCTGTGGG   4343        TCA
                                CCCGTAGA  GTTCTAGG
                                ||||||||  ||||||||
                                GGGTGTCT  CGAGATCC
                                    CAA
GAM636  PSAP    3'  TTTGGGGTTCTGTGGGTT    69360        TCA TT
                                AACCCGTAGA  G CTAGG
                                ||||||||||  | |||||
                                TTGGGTGTCT  T GGTTT
                                    ___ GG
GAM636  PSD     3'  TTTGGGGCTGAGCTGGTT    10936     C AGA
                                AACC GT  TCAGTTCTAGG
                                |||| ||  ||||||||||
                                TTGG CG  AGTCGGGGTTT
                                  T ___
GAM636  PSMD9   3'  CTTGGGACTGGTTTTGC    10984     _
                                GTAGA TCAGTTCTAGG
                                ||||| ||||||||||
                                CGTTT GGTCAGGGTTC
                                  T
GAM636  PTK7    3'  CTTGGGATGAGCTGGGTT    11017      TAGA  G
                                AACCCG   TCA TTCTAGG
                                ||||||   ||| |||||||
                                TTGGGT   AGT AGGGTTC
                                  CG__  _
GAM636  PTPN7   3'  CCTGGGGCTGACAAAAGGGT  54549     GTAGA
                                ACCC    TCAGTTCTAGG
                                ||||    ||||||||||
                                TGGG    AGTCGGGGTCC
                                  AAAAC
GAM636  PTPN7   3'  CCTGGGGCTGACAAAAGGGT  11067     GTAGA
                                ACCC    TCAGTTCTAGG
                                ||||    ||||||||||
                                TGGG    AGTCGGGGTCC
                                  AAAAC
GAM636  PTPN7   3'  CCTGGGGCTGACAAAAGGGT  54560     GTAGA
                                ACCC    TCAGTTCTAGG
                                ||||    ||||||||||
                                TGGG    AGTCGGGGTCC
                                  AAAAC
GAM636  RAD17   5'  CTTAGAACAGATTTATGG    55867        A
                                CCGTAGATC GTTCTAGG
                                ||||||||| ||||||||
                                GGTATTTAG CAAGATTC
                                    A
GAM636  RAD51L1 3'  TCTAGAGTTGATGGGGGT    56063     G AG   GT
                                ACCC T  ATCA  TCTAGG
                                |||| |  ||||  ||||||
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                                TGGG G  TAGT  AGATCT
                                  G __   TG
GAM636  RBBP2   3'  CATGGACTCTGTGGGTT    17320        TCA   TAGG
                                AACCCGTAGA  GTTC
                                ||||||||||  ||||
                                TTGGGTGTCT  CAGG
                                     ___   TACG
GAM636  RDS     3'  TCTGGAGTGAACCACGGGTT  4365       AGA  G
                                AACCCGT  TCA TTCTAGG
                                |||||||  ||| |||||||
                                TTGGGCA  AGT GAGGTCT
                                   CCA  _
GAM636  REGL    3'  TCTAGAATTGGTCTACCAGTT  21487    CC
                                AAC  GTAGATCAGTTCTAGG
                                |||  ||||||||||||||||
                                TTG  CATCTGGTTAAGATCT
                                  AC
GAM636  ROR2    3'  GATCTGGTCTGTTGGTT    15853    CG      T
                                AACC  TAGATCAG TC
                                ||||  |||||||| ||
                                TTGG  GTCTGGTC AG
                                  TT      T
GAM636  RPL38   5'  TCTAGGGTGATACGTGGGT   6397      TAG   G
                                ACCCG  ATCA TTCTAGG
                                |||||  |||| |||||||
                                TGGGT  TAGT GGGATCT
                                  GCA  _
GAM636  RPP30   3'  AACTGTTCTGCGGGTT     21158         T
                                AACCCGTAGA CAGTT
                                |||||||||| |||||
                                TTGGGCGTCT GTCAA
                                      T
GAM636  RRP22   3'  TCTGGGACCTCAATGGGT   21359      A  TCA
                                ACCCGT GA  GTTCTAGG
                                |||||| ||  ||||||||
                                TGGGTA CT  CAGGGTCT
                                   A  C__
GAM636  RXRA    3'  CCTGGAGCTGCAGGAGTT    11408    _  GTAGAT
                                AAC CC     CAGTTCTAGG
                                ||| ||     ||||||||||
                                TTG GG     GTCGAGGTCC
                                  A  AC_____
GAM636  SHC1    3'  TTTGGGAGTGTTCTGTGGG   11655       T  G
                                CCCGTAGA CA TTCTAGG
                                |||||||| || |||||||
                                GGGTGTCT GT AGGGTTT
                                     T  G
GAM636  SLC17A2 5'  TCTAGGGCTTAAAATACTGGTT 19545     C  GATC_
                                AACC GTA    AGTTCTAGG
                                |||| |||    |||||||||
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                                TTGG CAT    TCGGGATCT
                                  T  AAAAT
GAM636  SLC19A1  5'  CTTGGAGCAGCTGTGGGT   11757       ATCA
                                ACCCGTAG   GTTCTAGG
                                ||||||||   ||||||||
                                TGGGTGTC   CGAGGTTC
                                    GA__
GAM636  SLC7A6   3'  TTTGGAATTGGTCAAC     14317    A
                                GT GATCAGTTCTAGG
                                || ||||||||||||
                                CA CTGGTTAAGGTTT
                                 A
GAM636  SMURF1   3'  TCTGGGATCCCGCTGTGGGT  92461       ATCA
                                ACCCGTAG   GTTCTAGG
                                ||||||||   ||||||||
                                TGGGTGTC   TAGGGTCT
                                    GCCC
GAM636  SORCS2   3'  CTTAGTTATCTGTGGGTT    40417        CAGTT
                                AACCCGTAGAT    CTAGG
                                ||||||||||    |||||
                                TTGGGTGTCTA    GATTC
                                      TT___
GAM636  SRRM1    3'  CCTAGAATTCCCAGAGGGGTT  19552      GTAGATC
                                AACCC      AGTTCTAGG
                                |||||      |||||||||
                                TTGGG      TTAAGATCC
                                  GAGACCC
GAM636  STAT4    5'  TCTAGAATAGAGTGGGT     12006      TAGA  A
                                ACCCG   TC GTTCTAGG
                                |||||   || ||||||||
                                TGGGT   AG TAAGATCT
                                  G___  A
GAM636  SUFU     3'  CTTGGGACTGGGGTTTCGG   32411     TAGA_
                                CCG    TCAGTTCTAGG
                                |||    ||||||||||
                                GGC    GGTCAGGGTTC
                                 TTTGG
GAM636  SUFU     3'  TTTGGAGTTCCTCTCGGGTT  32418      T   TC GT
                                AACCCG AGA  A  TCTAGG
                                |||||| |||  |  ||||||
                                TTGGGC TCT  T  AGGTTT
                                   _  CC TG
GAM636  SWAP70   3'  TCTGTGAAATCTATGGG    71354       CAG  _
                                CCCGTAGAT   TTC TAGG
                                |||||||||   ||| ||||
                                GGGTATCTA   AAG GTCT
                                     ___  T
GAM636  TAGLN    3'  CCTGGAATATTTTTGGGGTT  59636      G   TCA
                                AACCC TAGA   GTTCTAGG
                                ||||| ||||   ||||||||
```

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                                TTGGG GTTT   TAAGGTCC
                                  _    TTA
GAM636  TARBP2   3'  TCTGGTACCCTCTGTGGGT   56170        TCA  T
                                ACCCGTAGA   GT CTAGG
                                |||||||||   || |||||
                                TGGGTGTCT   CA GGTCT
                                     CC_  T
GAM636  TARBP2   3'  TCTGGTACCCTCTGTGGGT   56162        TCA  T
                                ACCCGTAGA   GT CTAGG
                                |||||||||   || |||||
                                TGGGTGTCT   CA GGTCT
                                     CC_  T
GAM636  TARBP2   3'  TCTGGTACCCTCTGTGGGT   14810        TCA  T
                                ACCCGTAGA   GT CTAGG
                                |||||||||   || |||||
                                TGGGTGTCT   CA GGTCT
                                     CC_  T
GAM636  TBL1X    3'  CCTAGAGTGTTTGGTCGGGTT  18928      TA_  T  G
                                AACCCG   GA CA TTCTAGG
                                ||||||   || || |||||||
                                TTGGGC   TT GT GAGATCC
                                   TGG  T  _
GAM636  TBX1     3'  CCTGGAGCCACCGCGGGT    54672      AGATCA
                                ACCCGT     GTTCTAGG
                                ||||||     ||||||||
                                TGGGCG     CGAGGTCC
                                   CCAC__
GAM636  TBXA2R   5'  GCCTGGGACTGGTCAGTGGAGT 6492      _   TA
          T                      AAC CCG  GATCAGTTCTAGG   C
                                 ||| |||  ||||||||||||||  |
                                 TTG GGT  CTGGTCAGGGTCC   G
                                   A   GA
GAM636  TCEB1L   3'  GAATAAAACTGAACTGTGGGTT 12147        A     CTAGG
                                AACCCGTAG TCAGTT
                                ||||||||| ||||||
                                TTGGGTGTC AGTCAA
                                     A     AATAAGT
GAM636  TCL1B    3'  CTTGGATGCCCTGTGGGT    16984        AT  GT
                                ACCCGTAG  CA  TCTAGG
                                ||||||||  ||  ||||||
                                TGGGTGTC  GT  AGGTTC
                                     CC  __
GAM636  TGFA     3'  CTTGGGCCAGATATGTGGGTT  12251        G   A_   T  G
                                AACCCGTA ATC  GTTC AG
                                |||||||| |||  |||| ||
                                TTGGGTGT TAG  CGGG TC
                                     A   AC    T
GAM636  TGFB3    3'  CTTGGGGCATTATGGGT     12260        ATCA
                                ACCCGTAG    GTTCTAGG
                                ||||||||    ||||||||
```

```
                              TGGGTATT   CGGGGTTC
                                 A___
GAM636  THOP1   3'  CCTGGGACTGGCAGGGT    73376     GTAGA
                              ACCC    TCAGTTCTAGG
                              ||||    ||||||||||
                              TGGG    GGTCAGGGTCC
                                AC___
GAM636  TJP1    3'  TTTAGAGTTGATACTAC     12302     _   GT
                              GTAG ATCA  TCTAGG
                              |||| ||||  ||||||
                              CATC TAGT  AGATTT
                                A   TG
GAM636  TLL2    3'  CTTGGAATTCCATGGG      24963      A  TCA
                              CCCGT GA   GTTCTAGG
                              ||||| ||   ||||||||
                              GGGTA CT   TAAGGTTC
                                 C  ___
GAM636  TNFRSF1B 3'  CTGGAGCCCTTGGGTT     6522       T  ATCA
                              AACCCG AG    GTTCTAG
                              |||||| ||    |||||||
                              TTGGGT TC    CGAGGTC
                                 _ C___
GAM636  TNFRSF6B 3'  CTTGGGGTCTGGGGTGGGTT   33165       TAGA   _
                              AACCCG    TCAG TTCTAGG
                              ||||||    |||| |||||||
                              TTGGGT    GGTC GGGGTTC
                                 GG__   T
GAM636  TNFRSF6B 3'  CTTGGGGTCTGGGGTGGGTT   31604       TAGA   _
                              AACCCG    TCAG TTCTAGG
                              ||||||    |||| |||||||
                              TTGGGT    GGTC GGGGTTC
                                 GG__   T
GAM636  TPM4    3'  TCTGGAGCTCCGTGGGT     12373      TA  TCA
                              ACCCG  GA   GTTCTAGG
                              |||||  ||   ||||||||
                              TGGGT  CT   CGAGGTCT
                                 GC  ___
GAM636  TPP2    3'  CCTAGGACTTCGAGTTGGGTT  12374       TA__  TC
                              AACCCG    GA  AGTTCTAGG
                              ||||||    ||  ||||||||||
                              TTGGGT    CT  TCAGGATCC
                                 TGAG  __
GAM636  TRADD   3'  CCTGGATGGCCTTAGGGTT   13697      GT  AT  GT
                              AACCC  AG  CA  TCTAGG
                              |||||  ||  ||  ||||||
                              TTGGG  TC  GT  AGGTCC
                                 AT  CG  __
GAM636  TRAF1   3'  CCTAGAGCTACAGGGGTT    18973      GTAGATC
                              AACCC      AGTTCTAGG
                              |||||      |||||||||
```

```
                                TTGGG      TCGAGATCC
                                  GACA___
GAM636  TRPM8    3'  CTGGGACTGGAGGTT      43984      CGTAGA
                                AACC     TCAGTTCTAG
                                ||||     ||||||||||
                                TTGG     GGTCAGGGTC
                                  A_____
GAM636  TRPS1    3'  TCTAGAATTTGAAAGGGTT   26081      GTAGA  _
                                AACCC    TCAG TTCTAGG
                                |||||    |||| |||||||
                                TTGGG    AGTT AAGATCT
                                  AA___    T
GAM636  TXNIP    3'  TCTAGAGCTGATTTGATGG   21353     _
                                CCGT AGATCAGTTCTAGG
                                |||| ||||||||||||||
                                GGTA TTTAGTCGAGATCT
                                  G
GAM636  TXNIP    3'  CTTGGAATTGATTCTAAGGT  21350     CG  _
                                ACC  TAGA TCAGTTCTAGG
                                |||  |||| ||||||||||
                                TGG  ATCT AGTTAAGGTTC
                                  A_   T
GAM636  UBE2G2   3'  CCTGGAGTGTTGAGGGGGTT  64853      GTAGA  __
                                AACCC    TCAG  TTCTAGG
                                |||||    ||||  |||||||
                                TTGGG    AGTT  GAGGTCC
                                  GG___    GT
GAM636  UROS     5'  CCTGGGGCCCAGCGCGGGT   4561       AGATCA
                                ACCCGT     GTTCTAGG
                                ||||||     ||||||||
                                TGGGCG     CGGGGTCC
                                   CGACC_
GAM636  VIPR2    3'  CCTGGAATTGGAGTCGTGTT   12608     C  TAGA
                                AAC CG    TCAGTTCTAGG
                                ||| ||    ||||||||||
                                TTG GC    GGTTAAGGTCC
                                  T  TGA_
GAM636  VSX1     3'  TCTAGAATGGAAACGG      27470      AGA  A
                                CCGT   TC GTTCTAGG
                                ||||   || ||||||||
                                GGCA   AG TAAGATCT
                                  A__  G
GAM636  WDR4     3'  TCTAGGAGCATCTGTGGG    37907        CAG
                                CCCGTAGAT   TTCTAGG
                                |||||||||   |||||||
                                GGGTGTCTA   AGGATCT
                                     CG_
GAM636  WDR4     3'  TCTAGGAGCATCTGTGGG    53360        CAG
                                CCCGTAGAT   TTCTAGG
                                |||||||||   |||||||
```

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                                GGGTGTCTA  AGGATCT
                                     CG_
GAM636  WHSC1   5' TGGAGACTGCGGGTT     23673       A  AGT
                                AACCCGTAG TC  TCTA
                                ||||||||| ||  ||||
                                TTGGGCGTC AG  AGGT
                                     _  ___
GAM636  WHSC1   5' TGGAGACTGCGGGTT     55855       A  AGT
                                AACCCGTAG TC  TCTA
                                ||||||||| ||  ||||
                                TTGGGCGTC AG  AGGT
                                     _  ___
GAM636  WHSC1   5' TGGAGACTGCGGGTT     55838       A  AGT
                                AACCCGTAG TC  TCTA
                                ||||||||| ||  ||||
                                TTGGGCGTC AG  AGGT
                                     _  ___
GAM636  WHSC1   5' TGGAGACTGCGGGTT     29920       A  AGT
                                AACCCGTAG TC  TCTA
                                ||||||||| ||  ||||
                                TTGGGCGTC AG  AGGT
                                     _  ___
GAM636  YWHAH   3' TTTGGAATTCAATGGGT    12698      A  TCA
                                ACCCGT GA  GTTCTAGG
                                |||||| ||  ||||||||
                                TGGGTA CT  TAAGGTTT
                                   A  ___
GAM636  ZNF136  3' TCTGGCTCTGTGGCTTTGTGGG 59893        T___  TT
          TT                    AACCCGTAGA  CAG  CTAGG
                                ||||||||||  |||  |||||
                                TTGGGTGTTT  GTC  GGTCT
                                     CGGT  TC
GAM636  ZNF26   3' CCTGCTTCTCTGATCTGTGTGT 72979    C       TTC__
          T                     AAC CGTAGATCAG    TAGG
                                ||| ||||||||||    ||||
                                TTG GTGTCTAGTC    GTCC
                                  T       TCTTC
GAM636  ABLIM   3' TCTACATTTTGGTTTGGGGTT 22038     G      TTC_
                                AACCC TAGATCAG   TAGG
                                ||||| ||||||||   ||||
                                TTGGG GTTTGGTT   ATCT
                                   _      TTAC
GAM636  ABLIM   3' TCTACATTTTGGTTTGGGGTT 9777      G      TTC_
                                AACCC TAGATCAG   TAGG
                                ||||| ||||||||   ||||
                                TTGGG GTTTGGTT   ATCT
                                   _      TTAC
GAM636  ABTB1   3' CCTGGGGTGGGGGTGGG    50728     AGA  G
                                CCCGT  TCA TTCTAGG
                                |||||  ||| |||||||
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                                GGGTG   GGT GGGGTCC
                                  GG_  _
GAM636  ADIR     3'  TTTGGGACTGTGAGGTGTT   42333     _ GTAGAT
                                AAC CC     CAGTTCTAGG
                                ||| ||     ||||||||||
                                TTG GG     GTCAGGGTTT
                                  T  AGT___
GAM636  ALS2CR2  5'  CCTGGGGCTGGTGC       37705    AG
                                GT  ATCAGTTCTAGG
                                ||  ||||||||||||
                                CG  TGGTCGGGGTCC
                                 __
GAM636  AMOT     3'  CTTAGATAATCTTTTGGG    55719     T_   CAGT
                                CCCG  AGAT    TCTAGG
                                ||||  ||||    ||||||
                                GGGT  TCTA    AGATTC
                                  TT    AT__
GAM636  APXL2    5'  CCTGGGACTGGTCCTAC     75186     _
                                GTAG ATCAGTTCTAGG
                                |||| ||||||||||||
                                CATC TGGTCAGGGTCC
                                  C
GAM636  ARF4     3'  TCTGGGACTGGTTTGGG     82816     TA
                                CCCG  GATCAGTTCTAGG
                                ||||  ||||||||||||
                                GGGT  TTGGTCAGGGTCT
                                 __
GAM636  ARFRP1   3'  TCTGGGGCTGATCTTGC     12245     _
                                GTA GATCAGTTCTAGG
                                ||| ||||||||||||
                                CGT CTAGTCGGGGTCT
                                  T
GAM636  ARHGEF4  3'  TCTGGGGTTGGTGTAGGG    52218     G  G    TT
                                CCC TA ATCAG  CTAGG
                                ||| || |||||  |||||
                                GGG AT TGGTT  GGTCT
                                  _ G    GG
GAM636  ASTN2    3'  CCTGGGGCCTGGGTGGG     73184     TAGA   _
                                CCCG    TCAG TTCTAGG
                                ||||    |||| |||||||
                                GGGT    GGTC GGGGTCC
                                  G___    C
GAM636  ATP6V1D  3'  CCTAGATGTCTATTTATGGG  32040         CAGT_
                                CCCGTAGAT    TCTAGG
                                |||||||||    ||||||
                                GGGTATTTA    AGATCC
                                     TCTGT
GAM636  BG1      5'  TCTGGAGCTGGATACGG     87312      GA
                                CCGTA  TCAGTTCTAGG
                                |||||  ||||||||||
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                                GGCAT  GGTCGAGGTCT
                                  A_
GAM636  BHLHB2   3'  TTGGGAGCTGGGTCTGTGG   13382        _    AGG
                                CCGTAGATC AGTTCT
                                ||||||||| ||||||
                                GGTGTCTGG TCGAGG
                                     G     GTTT
GAM636  BLCAP    5'  CTGGAGAGTGAGGGTT     21980     GTAGA   G_
                                AACCC    TCA  TTCTAG
                                |||||    |||  |||||||
                                TTGGG    AGT  GAGGTC
                                  _____  GA
GAM636  BOP      5'  CCTGGAGTTGGTTTTG     85050    T     GT
                                CG AGATCA  TCTAGG
                                || ||||||  ||||||
                                GT TTTGGT  AGGTCC
                                 _     TG
GAM636  BRD2     3'  TTTGGGGCCCTGGGGGTT    17540      G   ATCA
                                AACCC TAG    GTTCTAGG
                                ||||| |||    ||||||||
                                TTGGG GTC    CGGGGTTT
                                  G   C___
GAM636  BRD2     5'  CTTGGAGATGTGGCGGGTT   17535       AGAT  G
                                AACCCGT    CA TTCTAGG
                                |||||||    || |||||||
                                TTGGGCG    GT GAGGTTC
                                    GT__  A
GAM636  C11orf23 3'  TTTAGAACTGGTTTGTG     37018
                                CGTAGATCAGTTCTAGG
                                ||||||||||||||||
                                GTGTTTGGTCAAGATTT

GAM636  C15orf15 3'  TTTGGAAAGTAGAATTTATGGG 32836         _ AG__
          T                      ACCCGTAGAT C    TTCTAGG
                                 |||||||||| |    |||||||
                                 TGGGTATTTA G    AAGGTTT
                                       A ATGA
GAM636  C17orf26 3'  TTTGGAATCTGCTGTGGGT   57546        AT  _
                                ACCCGTAG  CAG TTCTAGG
                                ||||||||  ||| |||||||
                                TGGGTGTC  GTC AAGGTTT
                                    __   T
GAM636  C1orf27  3'  CCTGGGGCTGGGAGGG     35264     GTAGA
                                CCC    TCAGTTCTAGG
                                |||    ||||||||||
                                GGG    GGTCGGGGTCC
                                  AG___
GAM636  C1QR1    3'  CTTGGGGCTACAGTAGTGGGT  23839      TAGATC_
                                ACCCG      AGTTCTAGG
                                |||||      |||||||||
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                                TGGGT      TCGGGGTTC
                                  GATGACA
GAM636  C1QTNF7   3'  GATTGAATCTGGGGTT     49159      G    _
                                AACCC TAGAT CAGTT
                                ||||| ||||| |||||
                                TTGGG GTCTA GTTAG
                                  _    A
GAM636  C20orf108 3'  TTTGGATTGGTTTTAGGGTT   55053      GT        TAGG
                                AACCC  AGATCAGTTC
                                |||||  ||||||||||
                                TTGGG  TTTGGTTAGG
                                  AT        TTT
GAM636  C20orf108 3'  TTTGGCGAGGGTCTGTGGGT   55054          AGTT
                                ACCCGTAGATC    CTAGG
                                ||||||||||    |||||
                                TGGGTGTCTGG    GGTTT
                                      GAGC
GAM636  C20orf108 3'  TTTAGGGTTTTAGGGTTGTAGG 55052     GTA    ____  TT
           GTT                    ACCC   GATC    AG  CTAGG
                                ||||   ||||    ||  |||||
                                TGGG   TTGG    TT  GATTT
                                  ATG    GATT  GG
GAM636  C20orf20  3'  TCTGGAGCAGCTGTGG      36855       ATCA
                                CCGTAG    GTTCTAGG
                                ||||||    ||||||||
                                GGTGTC    CGAGGTCT
                                   GA__
GAM636  C2F      3'  CCTGGTTGTTTTGGGGTT    20927      G    T   TT
                                AACCC TAGA CAG  CTAGG
                                ||||| |||| |||  |||||
                                TTGGG GTTT GTT  GGTCC
                                  _    T   __
GAM636  C4.4A    3'  GCTGCGCTGGTTTGCGG     26946          TC   G
                                CCGTAGATCAGT  TAG
                                ||||||||||||  |||
                                GGCGTTTGGTCG  GTC
                                      C_   GT
GAM636  C4.4A    3'  TTTGGAGCGTGGGGTGGGT    26948      TAGA   _
                                ACCCG    TCA GTTCTAGG
                                |||||    ||| ||||||||
                                TGGGT    GGT CGAGGTTT
                                  GG__   G
GAM636  C5orf3   3'  TCTGGAATAAAATCTATGG    37964        CA_
                                CCGTAGAT   GTTCTAGG
                                ||||||||   ||||||||
                                GGTATCTA   TAAGGTCT
                                    AAA
GAM636  CACNG4   3'  CCTACTACTGGTTTTGGGTT   26952       T      TC
                                AACCCG AGATCAGT  TAGG
                                |||||| ||||||||  ||||
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                                TTGGGT TTTGGTCA  ATCC
                                   _       TC
GAM636  CASP9    5'  CCTGGGGCGGGGGCGGGT    6925        AGA  A
                                ACCCGT   TC GTTCTAGG
                                ||||||   || ||||||||
                                TGGGCG   GG CGGGGTCC
                                   GG_  _
GAM636  CBX1     3'  CCTGTCACATCTGACTGTGGGT 22327         A    TTC___
          T                      AACCCGTAG TCAG     TAGG
                                |||||||||  ||||     ||||
                                TTGGGTGTC AGTC     GTCC
                                      _   TACACT
GAM636  CBX6     3'  CTAGAAACTAGGGTT       26612       G   ATCAG
                                AACCC TAG    TTCTAG
                                |||||  |||    ||||||
                                TTGGG ATC    AAGATC
                                   _  A____
GAM636  CDW92    3'  TGGGGGTGGGTTTGGGGTT    54506       G     A TT  AGG
                                AACCC TAGATC G  CT
                                |||||  ||||||  |  ||
                                TTGGG GTTTGG T  GG
                                   _     G GG  GTT
GAM636  CEACAM4  3'  CTGGGAGCTGCTCTTGTGGGTT 8426        GT_  T      AGG
                                AACCC   AGA CAGTTCT
                                |||||   |||  |||||||
                                TTGGG   TCT GTCGAGG
                                   TGT   C      GTCT
GAM636  CECR6    3'  CCTGGGGTGAGGACGG      49084      AGA   G
                                CCGT   TCA TTCTAGG
                                ||||   |||  |||||||
                                GGCA   AGT GGGGTCC
                                  GG_  _
GAM636  CENTG2   5'  CCTAGGGCTGGAAGGCGG    29878      AGA
                                CCGT   TCAGTTCTAGG
                                ||||   ||||||||||
                                GGCG   GGTCGGGATCC
                                  GAA
GAM636  CEP3     3'  GAACTTTATGGGTT        21250          ATC
                                AACCCGTAG   AGTTC
                                |||||||||   |||||
                                TTGGGTATT   TCAAG
                                      ___
GAM636  cerk     3'  TCTGTACGCATCTGCGGGTT  42853           CA  TC
                                AACCCGTAGAT  GT  TAGG
                                ||||||||||  ||  ||||
                                TTGGGCGTCTA  CA  GTCT
                                      CG  T_
GAM636  CHCR     3'  TTTAGAATATTTCTGTAGGTT  37239      CG    TCA
                                AACC  TAGA   GTTCTAGG
                                ||||  ||||   ||||||||
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                                TTGG  GTCT   TAAGATTT
                                  AT   TTA
GAM636  CHRAC1   3'  TTTAGAGCCCTCTATGG    33882       TCA
                                CCGTAGA  GTTCTAGG
                                |||||||  ||||||||
                                GGTATCT  CGAGATTT
                                   CC_
GAM636  CHST3    3'  TCTGGAATCTGGGTGGGT    14981      TAGA  _
                                ACCCG   TCAG TTCTAGG
                                |||||   |||| |||||||
                                TGGGT   GGTC AAGGTCT
                                  G___   T
GAM636  CRR9     3'  TTTGGAGCTGGTAGCG     47882     AG
                                CGT  ATCAGTTCTAGG
                                |||  ||||||||||||
                                GCG  TGGTCGAGGTTT
                                  A_
GAM636  CUGBP2   3'  CCTAGAGCTTCAGTGTGTT   21629     C  TA  TC
                                AAC CG  GA  AGTTCTAGG
                                ||| ||  ||  |||||||||
                                TTG GT  CT  TCGAGATCC
                                  T  GA  __
GAM636  CUGBP2   3'  CAAGTTTGATTTCGGGTT    21627       T      TT  AGG
                                AACCCG AGATCAG  CT
                                |||||| |||||||  ||
                                TTGGGC TTTAGTT  GA
                                   _      T_  ACT
GAM636  CUGBP2   3'  TTTAGAATTGGTTTAC      21630
                                GTAGATCAGTTCTAGG
                                ||||||||||||||||
                                CATTTGGTTAAGATTT

GAM636  D123     5'  TTTAGGGCGAAGACGGAGTT   20069     _   AGA  A
                                AAC CCGT   TC GTTCTAGG
                                ||| ||||   || ||||||||
                                TTG GGCA   AG CGGGATTT
                                  A   GA_  _
GAM636  DAZAP1   3'  TTTGGAGCGGCTGTGGGT    38538       ATCA
                                ACCCGTAG   GTTCTAGG
                                ||||||||   ||||||||
                                TGGGTGTC   CGAGGTTT
                                   GG__
GAM636  DDX18    3'  TTTGGAGCAAAAACTATGGGTT 22265        ATCA_
                                AACCCGTAG    GTTCTAGG
                                |||||||||    ||||||||
                                TTGGGTATC    CGAGGTTT
                                     AAAAA
GAM636  DKFZp434C0328 5'  TCTGGAGCTGGAGTGGGTT   34136       TAGA
                                AACCCG   TCAGTTCTAGG
                                ||||||   ||||||||||
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                                TTGGGT   GGTCGAGGTCT
                                   GA__
GAM636  DKFZP434G156 5'  CTGGAACAGCGGGTT      69780       AGATCA
                                AACCCGT     GTTCTAG
                                |||||||     |||||||
                                TTGGGCG     CAAGGTC
                                   A_____
GAM636  DKFZP434I2117 3'  TCTGGGGCTGATGGCTGGGGTT 48936      G  __
                                AACCC TAG  ATCAGTTCTAGG
                                ||||| |||  ||||||||||||
                                TTGGG GTC  TAGTCGGGGTCT
                                   _  GG
GAM636  DKFZp434J0226 5'  CCTGGGACATGTGGG      72332      TAGAT  _
                                CCCG    CA GTTCTAGG
                                ||||    || ||||||||
                                GGGT    GT CAGGGTCC
                                  _____  A
GAM636  DKFZP434L0718 3'  CCTAGAGCTACACGTATATGGG 49547        GATC___
                TT                AACCCGTA      AGTTCTAGG
                                |||||||||     |||||||||
                                TTGGGTAT      TCGAGATCC
                                    ATGCACA
GAM636  DKFZP547E1010 5'  CTTAGGATTGATTAAGGTT   31541     CGTA
                                AACC   GATCAGTTCTAGG
                                ||||   ||||||||||||
                                TTGG   TTAGTTAGGATTC
                                  AA__
GAM636  DKFZP547E1010 5'  CTTAGGATTGATTAAGGTT   66934     CGTA
                                AACC   GATCAGTTCTAGG
                                ||||   ||||||||||||
                                TTGG   TTAGTTAGGATTC
                                  AA__
GAM636  DKFZP564B1023 3'  TTTGGGGCTGACAATGG     48544     AGA
                                CCGT   TCAGTTCTAGG
                                ||||   ||||||||||
                                GGTA   AGTCGGGGTTT
                                  AC_
GAM636  DKFZP564D172 3'  CCTGTTGATTATGGGTT     49387       A     TTC
                                AACCCGT GATCAG   TAGG
                                ||||||| ||||||   ||||
                                TTGGGTA TTAGTT   GTCC
                                   _     ___    A
GAM636  DKFZP564L0864 3'  CTTGGAACACTCACTATGG   72554       ATCA_
                                CCGTAG    GTTCTAGG
                                ||||||    ||||||||
                                GGTATC    CAAGGTTC
                                   ACTCA
GAM636  DKFZP572C163 5'  CCTGGAACTTATGTGGG     61164       GATC
                                CCCGTA   AGTTCTAGG
                                ||||||   |||||||||
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                                GGGTGT   TCAAGGTCC
                                   AT__
GAM636  DKFZP586A011 3'  CTTAGGACTGATCCAC     31218    A
                                GT GATCAGTTCTAGG
                                || ||||||||||||
                                CA CTAGTCAGGATTC
                                 C
GAM636  DKFZP761C169 5'  TTTGGGACTGAGACTGGTT   67812     C  AGA
                                AACC GT   TCAGTTCTAGG
                                |||| ||   ||||||||||
                                TTGG CA   AGTCAGGGTTT
                                  T  G__
GAM636  DKFZP761G1913 3'  CCTGGGGTTGACTGGGTT    48911      GT  A    TT
                                AACCC  AG TCAG  CTAGG
                                |||||  || ||||  |||||
                                TTGGG  TC AGTT  GGTCC
                                   __ _   GG
GAM636  DKFZp761J139 5'  CCTGGAATCCGCCTGTGGGT   50107        ATCA
                                ACCCGTAG   GTTCTAGG
                                ||||||||   ||||||||
                                TGGGTGTC   TAAGGTCC
                                     CGCC
GAM636  DKFZp761O0113 5'  CCTGGAGTTGGTGGTTGGTGT  37276   _  TAG   GT
                                AC CCG   ATCA  TCTAGG
                                || |||   ||||  ||||||
                                TG GGT   TGGT  AGGTCC
                                 T   TGG   TG
GAM636  DNAJC5   3'  CTAGACCTTGTGGGT      61453       GATC  T
                                ACCCGTA    AG TCTAG
                                |||||||    || |||||
                                TGGGTGT    TC AGATC
                                    ____  C
GAM636  DNAM-1   3'  TCTAGAGCTGAGAAGCAGGGT  21640     _  AGA
                                ACCC GT   TCAGTTCTAGG
                                |||| ||   ||||||||||
                                TGGG CG   AGTCGAGATCT
                                  A  AAG
GAM636  DORFIN   3'  TTTGGAGCTGGTTGAAC     31264    A_
                                GT  GATCAGTTCTAGG
                                ||  ||||||||||||
                                CA  TTGGTCGAGGTTT
                                 AG
GAM636  E2IG5    3'  CTTAGAATTCTCAACTGGG   26853    _ A  TC
                                CCC GT GA  AGTTCTAGG
                                ||| || ||  |||||||||
                                GGG CA CT  TTAAGATTC
                                  T  A  C_
GAM636  EFS2     5'  TTTGGGAAGTTTTGTGGGTT   19627         TCAG
                                AACCCGTAGA    TTCTAGG
                                |||||||||    |||||||
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                                TTGGGTGTTT   AGGGTTT
                                     TGA_
GAM636  EIF4ENIF1 3'  CCTGCTTCATCTCGGGTT   39050      T   C_  TCT
                                AACCCG AGAT  AGT   AGG
                                |||||| ||||  |||   |||
                                TTGGGC TCTA  TCG   TCC
                                   _   CT  ___
GAM636  EIF4ENIF1 3'  TCTCGGGTTGGTTTATGGG   39052          TT T
                                CCCGTAGATCAG  C AGG
                                ||||||||||||  | |||
                                GGGTATTTGGTT  G TCT
                                      GG C
GAM636  EMR2    3'  CTAGTTCTACGGGTT      25582         TCAGTT
                                AACCCGTAGA     CTAG
                                ||||||||||     ||||
                                TTGGGCATCT     GATC
                                     T_____
GAM636  EPS8R1   5'  TCTAGGATTGACACTGG     57603    C  AGA
                                CC GT   TCAGTTCTAGG
                                || ||   ||||||||||||
                                GG CA   AGTTAGGATCT
                                 T  C__
GAM636  EZFIT    3'  CCTAGAGCTGGGACAGGT    41106     C  AGA
                                ACC GT   TCAGTTCTAGG
                                ||| ||   ||||||||||||
                                TGG CA   GGTCGAGATCC
                                  A  G__
GAM636  FADS1    3'  TTAGAATTGAGGAGTT      25486     _ GTAGA
                                AAC CC     TCAGTTCTAG
                                ||| ||     ||||||||||
                                TTG GG     AGTTAAGATT
                                  A  _____
GAM636  FBXW2    3'  TTTGGGTGCCGGGGCTGCGGGT 24086         A_  A  _
           T                     AACCCGTAG  TC GT TCTAGG
                                 |||||||||  || || ||||||
                                 TTGGGCGTC  GG CG GGGTTT
                                      GG  C  T
GAM636  FEM-2    3'  CCTAGAACGCTGTGGGT     27573        ATCA
                                ACCCGTAG    GTTCTAGG
                                ||||||||    ||||||||
                                TGGGTGTC    CAAGATCC
                                    G___
GAM636  FJX1     3'  TCTGGGGCTGGGGTATGG    26789      GA
                                CCGTA  TCAGTTCTAGG
                                |||||  ||||||||||||
                                GGTAT  GGTCGGGGTCT
                                   GG
GAM636  FLJ10620 3'  TTTAGAATTGGTCCTATG    36361      _
                                CGTAG ATCAGTTCTAGG
                                ||||| ||||||||||||
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                                GTATC TGGTTAAGATTT
                                   C
GAM636  FLJ10737 3' TCTGGAGCAGATTGCGGGTT  36525        A  A
                                AACCCGTAG TC GTTCTAGG
                                ||||||||| || ||||||||
                                TTGGGCGTT AG CGAGGTCT
                                     _ A
GAM636  FLJ10815 3' CTGGAATCCACGGGT      36694       A  CAGT
                                ACCCGT GAT   TCTAG
                                |||||| |||   |||||
                                TGGGCA CTA   AGGTC
                                   C  ____
GAM636  FLJ11275 3' TCTAGAAAAGACTTGTTGGTT 37207     CG  A  AG
                                AACC  TAG TC  TTCTAGG
                                ||||  ||| ||  |||||||
                                TTGG  GTT AG  AAGATCT
                                  TT  C  AA
GAM636  FLJ11362 3' CCTGGGGCTGAGTGGT     41679     CGTAGA
                                ACC     TCAGTTCTAGG
                                |||     ||||||||||
                                TGG     AGTCGGGGTCC
                                 TG____
GAM636  FLJ11539 5' CTGTGACTGTGGGTT      45377       TAGAT    C
                                AACCCG    CAGTT TAG
                                ||||||    ||||| |||
                                TTGGGT    GTCAG GTC
                                    _____   T
GAM636  FLJ11715 3' TGGAGATTGGTCTGAGGGTT  44679      G       _   GG
                                AACCC TAGATCAGT TCTA
                                ||||| ||||||||| ||||
                                TTGGG GTCTGGTTA AGGT
                                   A       G
GAM636  FLJ11726 3' TTTGGGACTGTATTTGTGG   46420       _
                                CCGTAGAT CAGTTCTAGG
                                |||||||| ||||||||||
                                GGTGTTTA GTCAGGGTTT
                                     T
GAM636  FLJ11726 3' CCTGGGACTTTGTTAGGTT   46409     CG  ATC
                                AACC  TAG  AGTTCTAGG
                                ||||  |||  |||||||||
                                TTGG  ATT  TCAGGGTCC
                                  __  GTT
GAM636  FLJ12229 5' CTTGGAGTTCCCACGGGT    45916      A_  TCAG
                                ACCCGT  GA   TTCTAGG
                                ||||||  ||   |||||||
                                TGGGCA  CT   GAGGTTC
                                   CC  T___
GAM636  FLJ12229 5' TGGGGGACTGGCTGTGGG    45920       A      AGG
                                CCCGTAG TCAGTTCT
                                ||||||| ||||||||
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                              GGGTGTC GGTCAGGG
                                 _      GGTT
GAM636  FLJ12294  3' CCTGGGGCTGACAATGGG    47010      AGA
                              CCCGT   TCAGTTCTAGG
                              |||||   ||||||||||
                              GGGTA   AGTCGGGGTCC
                                 AC_
GAM636  FLJ12294  3' CCTGGGGCTGGGCCTGGGG   47011    G   A_
                              CCC TAG  TCAGTTCTAGG
                              ||| |||  ||||||||||
                              GGG GTC  GGTCGGGGTCC
                                _  CG
GAM636  FLJ12888  3' AATTGATTTACTGGTT     46315     C
                              AACC GTAGATCAGTT
                              |||| ||||||||||
                              TTGG CATTTAGTTAA
                                T
GAM636  FLJ12895  5' CCTGCAGGCAGGTCTGTGGGTT 43681          A   C_
                              AACCCGTAGATC GTT  TAGG
                              |||||||||||| |||  ||||
                              TTGGGTGTCTGG CGG  GTCC
                                    A   AC
GAM636  FLJ13114  3' CCTGGGGCTGTGCTTGG    44596    T  AT
                              CCG AG  CAGTTCTAGG
                              ||| ||  ||||||||||
                              GGT TC  GTCGGGGTCC
                                _ GT
GAM636  FLJ13114  3' TTTGGAGCTGGTGGCAAGTT   44606    CC  AG
                              AAC  GT  ATCAGTTCTAGG
                              |||  ||  ||||||||||||
                              TTG  CG  TGGTCGAGGTTT
                                AA  G_
GAM636  FLJ13181  5' CCTGAGTAGATCTGTGGGT   47239         AG   T
                              ACCCGTAGATC  TTC AGG
                              ||||||||||  ||| |||
                              TGGGTGTCTAG  GAG TCC
                                    AT  _
GAM636  FLJ13204  3' CCTGCTCTGATCTGTGG    45416         TTC
                              CCGTAGATCAG   TAGG
                              ||||||||||   ||||
                              GGTGTCTAGTC   GTCC
                                    TC_
GAM636  FLJ13441  3' GAGCTTTATGGGTT      43663        ATC
                              AACCCGTAG   AGTTC
                              |||||||||   |||||
                              TTGGGTATT   TCGAG
                                 ____
GAM636  FLJ13449  3' TTTGGGGTTGGTTGGTTGGTT 44622     CGTA     TT
                              AACC   GATCAG  CTAGG
                              ||||   ||||||  |||||
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                                TTGG   TTGGTT  GGTTT
                                  TTGG     GG
GAM636  FLJ13576  5'  TTTGGAACTGACTCCGAGGGTT 42516      GTA  _
                                AACCC   GA TCAGTTCTAGG
                                |||||   || ||||||||||
                                TTGGG   CT AGTCAAGGTTT
                                   AGC  C
GAM636  FLJ13848  3'  TCTGGAGTCCTGGGTCTGGGGT 45474      G    _ __
          T                      AACCC TAGATC AG  TTCTAGG
                                |||||  |||||| ||  |||||||
                                TTGGG GTCTGG TC  GAGGTCT
                                   _     G  CT
GAM636  FLJ13902  3'  TTGGGGCTGGTTTCTG     45046    T
                                CG AGATCAGTTCTAG
                                ||  ||||||||||||
                                GT TTTGGTCGGGGTT
                                 C
GAM636  FLJ13910  3'  CCTGGGAGAGCTGGGGTT    42926      G   A  AG
                                AACCC TAG TC  TTCTAGG
                                |||||  |||  ||  |||||||
                                TTGGG GTC AG  AGGGTCC
                                   _  G  __
GAM636  FLJ14327  3'  CCTGGAGTTGGGCTGTCGGGT  46133      _  AT  GT
                                ACCCG TAG  CA  TCTAGG
                                |||||  |||  ||  ||||||
                                TGGGC GTC  GT  AGGTCC
                                   T   GG  TG
GAM636  FLJ14743  3'  TCTGGGGTGGGGGTGGGGT   68068     G  GA  A TT
                                ACCC TA  TC G  CTAGG
                                ||||  ||  ||  |  |||||
                                TGGG GT  GG T  GGTCT
                                  _  GG  G GG
GAM636  FLJ14768  3'  CCTGGAATGAGTGTGGGT    51599       GA   G
                                ACCCGTA  TCA TTCTAGG
                                |||||||  |||  |||||||
                                TGGGTGT  AGT AAGGTCC
                                    G_  _
GAM636  FLJ20084  3'  CTAGGGTGTGCTGGTT      34512      C   G   AGTT
                                AACC GTA ATC    CTAG
                                ||||  |||  |||    ||||
                                TTGG CGT TGG    GATC
                                  T   G   _____
GAM636  FLJ20184  5'  CCTGGAGTGAAGCGG       34694      AGA   G
                                CCGT   TCA TTCTAGG
                                ||||   |||  |||||||
                                GGCG   AGT GAGGTCC
                                  A__   _
GAM636  FLJ20208  3'  TTGGGAACGGGGTTGATGGGTT 34748        A   A_    AGG
                                AACCCGT GATC  GTTCT
                                |||||||  ||||  |||||
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                              TTGGGTA TTGG  CAAGG
                                 G   GG    GTTT
GAM636  FLJ20281 3' TCTGAACAGAGCTATGGGTT  90985        A A   T
                              AACCCGTAG TC GTTC AGG
                              ||||||||| || |||| |||
                              TTGGGTATC AG CAAG TCT
                                 G A   _
GAM636  FLJ20315 3' CTTGGTTCCTCTGGGGGTT  34934     G   TCAGTT
                              AACCC TAGA    CTAGG
                              ||||| ||||    |||||
                              TTGGG GTCT    GGTTC
                                 G   CCTT__
GAM636  FLJ20345 3' CTTGGGGCTTGCTGAGGTT  35022     CG  ATC
                              AACC  TAG   AGTTCTAGG
                              ||||  |||   |||||||||
                              TTGG  GTC   TCGGGGTTC
                                A_  GT_
GAM636  FLJ20519 3' TTTAGAGCAACAAGCTGGGTT 35349      TAGATCA
                              AACCCG     GTTCTAGG
                              ||||||     ||||||||
                              TTGGGT     CGAGATTT
                                 CGAACAA
GAM636  FLJ20666 3' TCTAGGATTGGCAATGG    35511     AGA
                              CCGT   TCAGTTCTAGG
                              ||||   ||||||||||
                              GGTA   GGTTAGGATCT
                                AC_
GAM636  FLJ20671 3' CTTGGAACTGGTAGCAGGT   35524    C  AG
                              ACC GT  ATCAGTTCTAGG
                              ||| ||  ||||||||||||
                              TGG CG  TGGTCAAGGTTC
                               A  A_
GAM636  FLJ20856 3' TTTAGAATCGAGGTATTGGTT 47120     C   GA  A
                              AACC GTA  TC GTTCTAGG
                              |||| |||  || ||||||||
                              TTGG TAT  AG TAAGATTT
                                T   GG  C
GAM636  FLJ21290 3' CTTAGGATGCCTCATTGGGTT 46742      TA  TCA
                              AACCCG  GA   GTTCTAGG
                              ||||||  ||   ||||||||
                              TTGGGT  CT   TAGGATTC
                                 TA  CCG
GAM636  FLJ21615 3' TTTAGAACTGATAGAC     49840    AG
                              GT  ATCAGTTCTAGG
                              ||  ||||||||||||
                              CA  TAGTCAAGATTT
                               GA
GAM636  FLJ21709 3' CTTGGAGCTGAGAAGGGT    77920     GTAGA
                              ACCC    TCAGTTCTAGG
                              ||||    ||||||||||
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                              TGGG    AGTCGAGGTTC
                                AAG__
GAM636  FLJ21977  3' CCTAGAGCTGCTAGG      49884    G   AT
                              CC TAG  CAGTTCTAGG
                              || |||  ||||||||||
                              GG ATC  GTCGAGATCC
                               _  __
GAM636  FLJ22037  5' TCTGGGGCTGGTGG       93916    GTAG
                              CC    ATCAGTTCTAGG
                              ||    ||||||||||||
                              GG    TGGTCGGGGTCT
                               ____
GAM636  FLJ22282  3' CCTGGGACAATCATTGTGGGT  45589       __   CA
                              ACCCGTA  GAT  GTTCTAGG
                              |||||||  |||  ||||||||
                              TGGGTGT  CTA  CAGGGTCC
                                  TA   A_
GAM636  FLJ22693  3' TCTAGATACAATTTTATGG    42764       TCA  _
                              CCGTAGA   GT TCTAGG
                              |||||||   || ||||||
                              GGTATTT   CA AGATCT
                                  TAA  T
GAM636  FLJ22794  5' TCTGGGACAGTGCAACTACGGG 91614         AT_  __
          TT                   AACCCGTAG   CA  GTTCTAGG
                              |||||||||   ||  ||||||||
                              TTGGGCATC   GT  CAGGGTCT
                                   AAC  GA
GAM636  FLJ23510  3' TTTAGAACGAGCGTTGGGTT   45293       TAGA  A
                              AACCCG    TC GTTCTAGG
                              ||||||    || ||||||||
                              TTGGGT    AG CAAGATTT
                                 TGCG  _
GAM636  FLJ31168  3' CCTGGGATGGGAGTGGGGT    58501      GTAGA  A_
                              ACCC     TC  GTTCTAGG
                              ||||     ||  ||||||||
                              TGGG     AG  TAGGGTCC
                                GTG__  GG
GAM636  FLJ32332  3' CTTGGAGTTGGCTGGGT     58305      GT  A   GT
                              ACCC  AG TCA  TCTAGG
                              ||||  || |||  ||||||
                              TGGG  TC GGT  AGGTTC
                                __  _   TG
GAM636  FLJ32356  3' TCTGGGGCATGGGAGGGGTT   58368       GTAGA  _
                              AACCC     TCA GTTCTAGG
                              |||||     ||| ||||||||
                              TTGGG     GGT CGGGGTCT
                                 GAG__   A
GAM636  FLJ32926  3' CCTGGCTCTCTGTGGG      58020        TCA TT
                              CCCGTAGA   G  CTAGG
                              ||||||||   |  |||||
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                                GGGTGTCT  C  GGTCC
                                   ___ TC
GAM636  GMEB2    5'  TCTGGGACTCAAGGGTGGGT  24739      AGATC
                                ACCCGT    AGTTCTAGG
                                ||||||    |||||||||
                                TGGGTG    TCAGGGTCT
                                   GGAAC
GAM636  GP5      3'  TGGGAGTTGGTTTCTGGGTT  15659      T    GT  AGG
                                AACCCG AGATCA  TCT
                                |||||| ||||||  |||
                                TTGGGT TTTGGT  AGG
                                   C     TG  GTT
GAM636  GPT2     3'  CCTGGGGCTGAGAAAGGGT   55955     GTAGA
                                ACCC    TCAGTTCTAGG
                                ||||    ||||||||||
                                TGGG    AGTCGGGGTCC
                                  AAAG_
GAM636  GPT2     3'  TCTGGAAAGTTCATTTGGGGTT 55959     G    CAG__
                                AACCC TAGAT    TTCTAGG
                                ||||| |||||    |||||||
                                TTGGG GTTTA    AAGGTCT
                                  _    CTTGA
GAM636  GRID1    3'  CCTGGGGCTGAGGAGGT    68495    CGTAGA
                                ACC     TCAGTTCTAGG
                                |||     ||||||||||
                                TGG     AGTCGGGGTCC
                                  AGG___
GAM636  GRP3     3'  CTTGGGACACTGTGGG     31118      ATCA
                                CCCGTAG   GTTCTAGG
                                |||||||   ||||||||
                                GGGTGTC   CAGGGTTC
                                   A___
GAM636  GTF3C4   3'  TTTGGAACTGCCTTCGGG   24198     T  AT
                                CCCG AG  CAGTTCTAGG
                                |||| ||  ||||||||||
                                GGGC TC  GTCAAGGTTT
                                  T  C_
GAM636  H105E3   5'  CCTGGAGTTCAGTGGGT    31928     TA  TCAG
                                ACCCG  GA   TTCTAGG
                                |||||  ||   |||||||
                                TGGGT  CT   GAGGTCC
                                   GA  T___
GAM636  H2BFQ    3'  TTTGGAGCTGATGGCAGGG   59362    _  AG
                                CCC GT  ATCAGTTCTAGG
                                |||  ||  ||||||||||||
                                GGG CG  TAGTCGAGGTTT
                                  A  G_
GAM636  HDAC9-PENDING 3'  CCTAGAATCTTTGTGAGGTT  28175     _    TCA
                                AACC CGTAGA   GTTCTAGG
                                |||| ||||||   ||||||||
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                                TTGG GTGTTT   TAAGATCC
                                  A     C__
GAM636  HIC2     3'  CCTGGGGCTGGGGGAGGG    65260     GTAGA
                                CCC     TCAGTTCTAGG
                                |||     ||||||||||
                                GGG     GGTCGGGGTCC
                                  AGGG_
GAM636  HSA249128 3'  TTTGGGTGAATTCTGCAGGTT  34154      C     TCAGT
                                AACC GTAGA     TCTAGG
                                |||| |||||     ||||||
                                TTGG CGTCT     GGGTTT
                                  A     TAAGT
GAM636  HSRNAFEV  3'  CCTGGGACCTGAGCAGGTT   34020      C  AGA   _
                                AACC GT   TCAG TTCTAGG
                                |||| ||   |||| |||||||
                                TTGG CG   AGTC AGGGTCC
                                  A ___    C
GAM636  HYA22    3'  CTTAGTCCTCTGTGGGTT    19426          TCA TT
                                AACCCGTAGA   G  CTAGG
                                ||||||||||   |  |||||
                                TTGGGTGTCT   C  GATTC
                                      ___ CT
GAM636  HYA22    3'  TCTGGAATCCTACGTGTT    19430     C    ATCA
                                AAC CGTAG    GTTCTAGG
                                ||| |||||    ||||||||
                                TTG GCATC    TAAGGTCT
                                  T    C___
GAM636  HYA22    3'  CCTACGTGTTGGTCTGTGG    19422          TTC_
                                CCGTAGATCAG    TAGG
                                ||||||||||    ||||
                                GGTGTCTGGTT    ATCC
                                      GTGC
GAM636  ING3     3'  CTTGAATTTTATGGGTT     38834          TCA    T
                                AACCCGTAGA   GTTC AG
                                ||||||||||   |||| ||
                                TTGGGTATTT   TAAG TC
                                      ___    T
GAM636  ISL2     3'  TCTGGGACTTACCAGGGTT    70841      GTAGATC
                                AACCC      AGTTCTAGG
                                |||||      |||||||||
                                TTGGG      TCAGGGTCT
                                   ACCAT__
GAM636  KBRAS2   3'  CCTGGGGCAGTTGTGGGT    34195        ATCA
                                ACCCGTAG    GTTCTAGG
                                ||||||||    ||||||||
                                TGGGTGTT    CGGGGTCC
                                     GA__
GAM636  KIAA0152 3'  CCTGGGGCTGGTCAC       28298     A
                                GT GATCAGTTCTAGG
                                || ||||||||||||
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                              CA CTGGTCGGGGTCC
                                 _
GAM636  KIAA0153 3' CCTGGGGCTGGGGCTG     30702     A_
                              TAG  TCAGTTCTAGG
                              |||  ||||||||||
                              GTC  GGTCGGGGTCC
                                GG
GAM636  KIAA0205 3' CCTGAATAATCTATGGGTT   29579         CA    T
                              AACCCGTAGAT  GTTC AGG
                              ||||||||||  |||| |||
                              TTGGGTATCTA  TAAG TCC
                                    A_   _
GAM636  KIAA0265 3' TCTAGGGTGGATGAGGGTT   69885      GTAG   A TT
                              AACCC    ATC G  CTAGG
                              |||||    ||| |  |||||
                              TTGGG    TAG T  GATCT
                                 AG__   G GG
GAM636  KIAA0265 3' TCTAGGACTTCCGTGTGCG   69884     G  C__
                              CGTA AT   AGTTCTAGG
                              |||| ||   |||||||||
                              GCGT TG   TCAGGATCT
                                G  CCT
GAM636  KIAA0268 3' TTTAGGACTGTGAGGGTT    70006      GTAGAT
                              AACCC     CAGTTCTAGG
                              |||||     ||||||||||
                              TTGGG     GTCAGGATTT
                                 AGT___
GAM636  KIAA0286 3' TTTGGGCAGATGCTATGGGTT 68331         _  A    TAGG
                              AACCCGTAG ATC GTTC
                              ||||||||| ||| ||||
                              TTGGGTATC TAG CGGG
                                    G   A    TTT
GAM636  KIAA0318 3' CCTACGTCATCTATGGGTT   68950         CAGTTC
                              AACCCGTAGAT     TAGG
                              ||||||||||     ||||
                              TTGGGTATCTA     ATCC
                                    CTGC__
GAM636  KIAA0326 3' CCTGGAGCCCTCCAGGGTT   64325      GTA  TCA
                              AACCC   GA   GTTCTAGG
                              |||||   ||   ||||||||
                              TTGGG   CT   CGAGGTCC
                                 AC_  CC_
GAM636  KIAA0354 3' CTTGGGACACAGTGGGTT    29569      TAGATCA
                              AACCCG      GTTCTAGG
                              ||||||      ||||||||
                              TTGGGT      CAGGGTTC
                                 GACA___
GAM636  KIAA0376 3' CTTAGGACACTGTGGG      65600       ATCA
                              CCCGTAG    GTTCTAGG
                              |||||||    ||||||||
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                                GGGTGTC   CAGGATTC
                                   A___
GAM636  KIAA0391  5'  TCTGTCCCCTGGTTTGCGG   27927         TTC_
                                CCGTAGATCAG   TAGG
                                ||||||||||   ||||
                                GGCGTTTGGTC   GTCT
                                     CCCT
GAM636  KIAA0408  3'  CTTAGAACTGGTGGGCGCGGT  28134    _  AG
                                ACC CGT  ATCAGTTCTAGG
                                ||| |||  ||||||||||||
                                TGG GCG  TGGTCAAGATTC
                                  C  GG
GAM636  KIAA0408  3'  TCTGGTATGATCTGTGG    28139        GTT
                                CCGTAGATCA  CTAGG
                                ||||||||||  |||||
                                GGTGTCTAGT  GGTCT
                                     AT_
GAM636  KIAA0420  3'  CCTGGGACCATGTGGG     63355      GATCA
                                CCCGTA    GTTCTAGG
                                ||||||    ||||||||
                                GGGTGT    CAGGGTCC
                                   AC___
GAM636  KIAA0429  5'  CCTAGGGCTGGCCGGGT    28554      TAGA
                                ACCCG   TCAGTTCTAGG
                                |||||   ||||||||||
                                TGGGC   GGTCGGGATCC
                                  C___
GAM636  KIAA0441  3'  CCTGAAAATGTTGATCTACGTG 28954   C       ____  T
          TT                    AC CGTAGATCAG   TTC AGG
                                || ||||||||||   ||| |||
                                TG GCATCTAGTT   AAG TCC
                                 T       GTAA  _
GAM636  KIAA0450  5'  CCTGGCCCCTCTGTGGGT   27634        TCAGTT
                                ACCCGTAGA     CTAGG
                                |||||||||     |||||
                                TGGGTGTCT     GGTCC
                                     CCCC__
GAM636  KIAA0495  3'  CCGGGTTGATTGTGCGGGTT  62576       _    TT TAGG
                                AACCCGTA GATCAG  C
                                |||||||| ||||||  |
                                TTGGGCGT TTAGTT  G
                                   G     GG CC
GAM636  KIAA0495  3'  CTGGGTTGATTGTGTGGGTT  62583      TA_    TT T  G
                                AACCCG   GATCAG  C AG
                                ||||||   ||||||  | ||
                                TTGGGT   TTAGTT  G TC
                                   GTG     GG _
GAM636  KIAA0495  3'  CTGGGTTGATTGTGTGGGTT  62584      TA_    TT T  G
                                AACCCG   GATCAG  C AG
                                ||||||   ||||||  | ||
```

```
                                TTGGGT   TTAGTT  G TC
                                   GTG     GG _
GAM636  KIAA0495 3' CCGGGTTGATTGTGCGGGTT   62577        _     TT TAGG
                                AACCCGTA GATCAG  C
                                |||||||| ||||||  |
                                TTGGGCGT TTAGTT  G
                                   G     GG CC
GAM636  KIAA0495 3' CTGGGTTGATTGTACGGGTT   62581        _     TT T  G
                                AACCCGTA GATCAG  C AG
                                |||||||| ||||||  | ||
                                TTGGGCAT TTAGTT  G TC
                                   G     GG _
GAM636  KIAA0495 3' CTGGGTTGATTGTGTGGGTT   62585       TA_     TT T  G
                                AACCCG   GATCAG  C AG
                                ||||||   ||||||  | ||
                                TTGGGT   TTAGTT  G TC
                                   GTG     GG _
GAM636  KIAA0495 3' CTGGGTTGATTCTGCGGGTT   62580         _   TT T  G
                                AACCCGTAGA TCAG  C AG
                                |||||||||| ||||  | ||
                                TTGGGCGTCT AGTT  G TC
                                    T   GG _
GAM636  KIAA0495 3' CTGGGTTGATTGTGTGGGTT   62586       TA_     TT T  G
                                AACCCG   GATCAG  C AG
                                ||||||   ||||||  | ||
                                TTGGGT   TTAGTT  G TC
                                   GTG     GG _
GAM636  KIAA0495 3' CTGGGTTGATTGTATGGGTT   62582        _     TT T  G
                                AACCCGTA GATCAG  C AG
                                |||||||| ||||||  | ||
                                TTGGGTAT TTAGTT  G TC
                                   G     GG _
GAM636  KIAA0495 3' CTGGGTTGATTGTGTGGGTT   62587       TA_     TT T  G
                                AACCCG   GATCAG  C AG
                                ||||||   ||||||  | ||
                                TTGGGT   TTAGTT  G TC
                                   GTG     GG _
GAM636  KIAA0514 3' TTTGGAGCGTTTGTTGGGTT   28103       TAGATCA
                                AACCCG      GTTCTAGG
                                ||||||      ||||||||
                                TTGGGT      CGAGGTTT
                                   TGTTTG_
GAM636  KIAA0560 5' CTTGGGCTGTTGTACGGGTT   61502        GAT     T  G
                                AACCCGTA   CAGTTC AG
                                ||||||||   |||||| ||
                                TTGGGCAT   GTCGGG TC
                                    GTT     T
GAM636  KIAA0618 3' TTTGGGGCTGGGCTGGGT    29176      GT  AT
                                ACCC  AG  CAGTTCTAGG
                                ||||  ||  ||||||||||
```

```
                                TGGG  TC  GTCGGGGTTT
                                  __  GG
GAM636  KIAA0630  3'  TTTAGGACTGGTTCTGTG    89402       _
                                CGTAGA TCAGTTCTAGG
                                |||||| ||||||||||
                                GTGTCT GGTCAGGATTT
                                   T
GAM636  KIAA0649  3'  CTCGAGCTGTGGGTT       29048       TAGAT     T
                                AACCCG    CAGTTC AG
                                ||||||    |||||| ||
                                TTGGGT    GTCGAG TC
                                  _____     C
GAM636  KIAA0737  3'  CTGGAATTAGAGGGTT      29136       GTAGA  _
                                AACCC    TC AGTTCTAG
                                |||||    || ||||||||
                                TTGGG    AG TTAAGGTC
                                  _____  A
GAM636  KIAA0806  3'  CCTGGGATTCTTCAGTGG    29059     TA  TC
                                CCG  GA  AGTTCTAGG
                                |||  ||  |||||||||
                                GGT  CT  TTAGGGTCC
                                  GA  TC
GAM636  KIAA0819  3'  CTGAGGCTTGTGGGTT      63577       GATC   TC
                                AACCCGTA   AGT  TAG
                                ||||||||   |||  |||
                                TTGGGTGT   TCG  GTC
                                   _____   GA
GAM636  KIAA0843  3'  TCTATGCCTCTGGTCTGTGGG  30116          TTC__
                                CCCGTAGATCAG    TAGG
                                ||||||||||||    ||||
                                GGGTGTCTGGTC    ATCT
                                      TCCGT
GAM636  KIAA0844  3'  CCTGGAAGCACTGCGGGT    30200        ATCAG
                                ACCCGTAG    TTCTAGG
                                ||||||||    |||||||
                                TGGGCGTC    AAGGTCC
                                    ACG__
GAM636  KIAA0872  3'  CTTGGGACTGGCCTGAGGGT   30063     G   AT
                                ACCC TAG  CAGTTCTAGG
                                |||| |||  ||||||||||
                                TGGG GTC  GTCAGGGTTC
                                  A   CG
GAM636  KIAA0884  3'  CCTAATTTTCTGGTTTGTGG   70203          TTC__
                                CCGTAGATCAG    TAGG
                                ||||||||||    ||||
                                GGTGTTTGGTC    ATCC
                                      TTTTA
GAM636  KIAA0976  3'  CTTAGAATGCAATGGGT     29891       AGATCA
                                ACCCGT     GTTCTAGG
                                ||||||     ||||||||
```

```
                              TGGGTA     TAAGATTC
                                 ACG___
GAM636  KIAA0992  3'  GCTGATTTGCTGGGTT     32206      _
                              AACCC GTAGATCAGT
                              ||||| ||||||||||
                              TTGGG CGTTTAGTCG
                                 T
GAM636  KIAA1014  3'  TCTAGAACTGGTAGCTCGG   65354     TAG_
                              CCG   ATCAGTTCTAGG
                              |||   ||||||||||||
                              GGC   TGGTCAAGATCT
                                TCGA
GAM636  KIAA1023  3'  CTAGAGCTTTGGGTT      34258       TAGATC
                              AACCCG     AGTTCTAG
                              ||||||     ||||||||
                              TTGGGT     TCGAGATC
                                 T_____
GAM636  KIAA1029  3'  TCTGGGGTTGGGGATGGGTT  23481       AGA   TT
                              AACCCGT   TCAG  CTAGG
                              |||||||   ||||  |||||
                              TTGGGTA   GGTT  GGTCT
                                 GG_   GG
GAM636  KIAA1036  3'  CTAGGCACCTGGGGTT     29817      G   ATCA  _
                              AACCC TAG    GT TCTAG
                              ||||| |||    || |||||
                              TTGGG GTC    CA GGATC
                                _  _____  C
GAM636  KIAA1068  3'  CCTGGGAAGTCTTCTGTGGGT  31030        TCAG_
                              ACCCGTAGA    TTCTAGG
                              |||||||||    |||||||
                              TGGGTGTCT    AGGGTCC
                                   TCTGA
GAM636  KIAA1115  5'  CTAGGATGGGATGGTT     30019     CGTAG   A_
                              AACC    ATC  GTTCTAG
                              ||||    |||  |||||||
                              TTGG    TAG  TAGGATC
                                _____  GG
GAM636  KIAA1157  3'  AGCTTATCTACGGGTT     72237          C
                              AACCCGTAGAT AGTT
                              |||||||||| ||||
                              TTGGGCATCTA TCGA
                                    T
GAM636  KIAA1181  3'  TCTGGACTCCCTACGGGT    68378        ATC   T
                              ACCCGTAG   AGT CTAGG
                              ||||||||   ||| |||||
                              TGGGCATC   TCA GGTCT
                                 CC_  _
GAM636  KIAA1238  3'  TTTGGGATTGGGGGTGGGTT  71082       AGA
                              AACCCGT   TCAGTTCTAGG
                              |||||||   ||||||||||
```

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                                TTGGGTG  GGTTAGGGTTT
                                   GG_
GAM636  KIAA1239 3' CCTGGAGTTGATTATATGAGT 71329   C  _   GT
                                AC CGTA GATCA  TCTAGG
                                || |||| |||||  ||||||
                                TG GTAT TTAGT  AGGTCC
                                 A   A    TG
GAM636  KIAA1240 3' TTTAGAGTTGGCTATGG    66742      A  GT
                                CCGTAG TCA  TCTAGG
                                |||||| |||  ||||||
                                GGTATC GGT  AGATTT
                                   _  TG
GAM636  KIAA1246 5' CCTGGGAATGCCTGGGGTT  92054     G  AT  G
                                AACCC TAG  CA TTCTAGG
                                ||||| |||  || |||||||
                                TTGGG GTC  GT AGGGTCC
                                   _  C_  A
GAM636  KIAA1266 3' CTTGGAGCTGTGCTGGGT   66118    _  GAT
                                ACCC GTA   CAGTTCTAGG
                                |||| |||   ||||||||||
                                TGGG CGT   GTCGAGGTTC
                                  T  ___
GAM636  KIAA1300 3' CCTAGGATGGGGTGGG     62862    TAGA  G
                                CCCG   TCA TTCTAGG
                                ||||   ||| |||||||
                                GGGT   GGT AGGATCC
                                  GG__  _
GAM636  KIAA1328 3' CTTAGGAAATTTGTGGGTT  61647       CAG
                                AACCCGTAGAT   TTCTAGG
                                ||||||||||   |||||||
                                TTGGGTGTTTA   AGGATTC
                                      A__
GAM636  KIAA1340 3' TCTAGTATGTTTAGGGTT   69185     G   T  GTT
                                AACCC TAGA CA   CTAGG
                                ||||| |||| ||   |||||
                                TTGGG ATTT GT   GATCT
                                   _   _  AT_
GAM636  KIAA1404 3' CTTGGAGCTGTTCCCTGGGT  61988     TA  T
                                ACCCG  GA CAGTTCTAGG
                                |||||  || ||||||||||
                                TGGGT  CT GTCGAGGTTC
                                   CC  T
GAM636  KIAA1463 3' CTTAGATGGTGTTTGTGGG   72275       CAGT
                                CCCGTAGAT   TCTAGG
                                |||||||||   ||||||
                                GGGTGTTTG   AGATTC
                                      TGGT
GAM636  KIAA1467 3' TTTGGAAGTCATCTGTGGGT  71621       CAG
                                ACCCGTAGAT   TTCTAGG
                                |||||||||   |||||||
```

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                              TGGGTGTCTA  AAGGTTT
                                   CTG
GAM636  KIAA1509 3' TTTAGGAGTGTTTGGGGTT  61619     G   T G
                              AACCC TAGA CA TTCTAGG
                              ||||| |||| || |||||||
                              TTGGG GTTT GT AGGATTT
                                _   _ G
GAM636  KIAA1554 3' TCTGGGACTGAAACG     95156    AGA
                              CGT  TCAGTTCTAGG
                              |||  ||||||||||
                              GCA  AGTCAGGGTCT
                               A__
GAM636  KIAA1602 3' CCTGGAAGGGACTGGGGGTT  64627     G  A  AG
                              AACCC TAG TC  TTCTAGG
                              ||||| ||| ||  |||||||
                              TTGGG GTC AG  AAGGTCC
                                 G  _ GG
GAM636  KIAA1615 3' CTTAGGACTGCTGACTTGGTT 68710    C_ AGAT
                              AACC  GT   CAGTTCTAGG
                              ||||  ||   ||||||||||
                              TTGG  CA   GTCAGGATTC
                                TT  GTC_
GAM636  KIAA1649 3' TCTGGAGCTGGTGCTATAGGT 50280    CG  _
                              ACC  TAG ATCAGTTCTAGG
                              |||  ||| ||||||||||||
                              TGG  ATC TGGTCGAGGTCT
                               AT  G
GAM636  KIAA1649 3' TCTGGAGCTGGTGCTATAGGT 66984    CG  _
                              ACC  TAG ATCAGTTCTAGG
                              |||  ||| ||||||||||||
                              TGG  ATC TGGTCGAGGTCT
                               AT  G
GAM636  KIAA1655 5' TCTGGAACTGGGTGTGGGTT  66635      GA
                              AACCCGTA  TCAGTTCTAGG
                              ||||||||  ||||||||||
                              TTGGGTGT  GGTCAAGGTCT
                                   G_
GAM636  KIAA1677 3' TTTAGAGTTGGTTTGGG    67074    TA   GT
                              CCCG  GATCA  TCTAGG
                              ||||  |||||  ||||||
                              GGGT  TTGGT  AGATTT
                                __    TG
GAM636  KIAA1681 3' CTGGTTGTATATGGGTT    61070      ___
                              AACCCGTA   GATCAG
                              ||||||||   ||||||
                              TTGGGTAT   TTGGTC
                                   ATG
GAM636  KIAA1755 3' CCTGGAGCCAGAGGCCGGTT  61342    C  AGATCA
                              AACC GT    GTTCTAGG
                              |||| ||    ||||||||
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                                TTGG CG     CGAGGTCC
                                  C  GAGAC_
GAM636  KIAA1814  3'  CCTGGGGGCTGATGGGTT    70361      GTAG       _
                                AACCC    ATCAGTTCT AGG
                                |||||    ||||||||| |||
                                TTGGG    TAGTCGGGG TCC
                                  _____        G
GAM636  KIAA1843  3'  TTTGGAACAATATGGGT     62193       GATCA
                                ACCCGTA    GTTCTAGG
                                |||||||    ||||||||
                                TGGGTAT    CAAGGTTT
                                   AA___
GAM636  KIAA1853  3'  CCTGGAACACCCTGGGGTT   69391      G   ATCA
                                AACCC TAG    GTTCTAGG
                                ||||| |||    ||||||||
                                TTGGG GTC    CAAGGTCC
                                  _  CCA_
GAM636  KIAA1867  3'  TCTGGTCTCTCTGTGGG     94824       TC  TT
                                CCCGTAGA  AG  CTAGG
                                ||||||||  ||  |||||
                                GGGTGTCT  TC  GGTCT
                                    C_  T_
GAM636  KIAA1878  3'  CTTGGAAGTGTCTGTGGG    91711        T  G
                                CCCGTAGA CA TTCTAGG
                                |||||||| || |||||||
                                GGGTGTCT GT AAGGTTC
                                   _  G
GAM636  KIAA1879  5'  CCTAGAGCTGGGAAGGG     73566     GTAGA
                                CCC     TCAGTTCTAGG
                                |||     ||||||||||
                                GGG     GGTCGAGATCC
                                  AAG__
GAM636  KIAA1909  5'  CCTGGGGCTGGTTGTCCTGGT  73838     CGTA_
                                ACC     GATCAGTTCTAGG
                                |||     ||||||||||||
                                TGG     TTGGTCGGGGTCC
                                  TCCTG
GAM636  KIAA1915  3'  CCTGGAATTGATGTTGC     73279      _
                                GTAG ATCAGTTCTAGG
                                |||| ||||||||||||
                                CGTT TAGTTAAGGTCC
                                  G
GAM636  KIAA1950  3'  CTTGGACCTTTTGTGGGT    92590        TC  T
                                ACCCGTAGA  AG TCTAGG
                                |||||||||  || ||||||
                                TGGGTGTTT  TC AGGTTC
                                    __ C
GAM636  KIAA1985  3'  TCTGGAGCCTTTACCGGTT   44715      C     TCA
                                AACC GTAGA   GTTCTAGG
                                |||| |||||   ||||||||
```

```
                                TTGG CATTT   CGAGGTCT
                                  C    C__
GAM636  KIF13B   3'  TTTGGTGCCAGGTTTGTGGG  30917         A_  T
                                CCCGTAGATC  GT CTAGG
                                ||||||||||  || |||||
                                GGGTGTTTGG  CG GGTTT
                                      AC  T
GAM636  KIF13B   3'  TTTGGTGCCAGGTTTGTGGG  82830         A_  T
                                CCCGTAGATC  GT CTAGG
                                ||||||||||  || |||||
                                GGGTGTTTGG  CG GGTTT
                                      AC  T
GAM636  KLHL6    3'  CCTGGTTAGAAGGTCTAGGGTT 55302       G     AGTT__
                                AACCC TAGATC     CTAGG
                                |||||  ||||||      |||||
                                TTGGG ATCTGG     GGTCC
                                  _     AAGATT
GAM636  LIP8     5'  CTTAGGGCGTGACTGAGGGTT  88150       G   A   _
                                AACCC TAG TCA GTTCTAGG
                                |||||  |||  |||  ||||||||
                                TTGGG GTC AGT CGGGATTC
                                   A   _   G
GAM636  LNX      3'  CCTAGAAACTACACTATGGGT  50918         ATC    _
                                ACCCGTAG   AGTT CTAGG
                                ||||||||   ||||  |||||
                                TGGGTATC   TCAA GATCC
                                     ACA    A
GAM636  MAD4     3'  CTGGGGCAGGTGGGT      21276      GTAG   A
                                ACCC    ATC GTTCTAG
                                ||||    |||  |||||||
                                TGGG    TGG CGGGGTC
                                  ____   A
GAM636  MAP2K6   3'  CCTACTGTGGATTGGTGGGTT  10869       TA    AG TC
                                AACCCG  GATC  T  TAGG
                                ||||||  ||||  |  ||||
                                TTGGGT  TTAG  G  ATCC
                                   GG    GT TC
GAM636  MAP2K6   3'  CCTACTGTGGATTGGTGGGTT  49242       TA    AG TC
                                AACCCG  GATC  T  TAGG
                                ||||||  ||||  |  ||||
                                TTGGGT  TTAG  G  ATCC
                                   GG    GT TC
GAM636  MDS018   3'  TTTGGAGCTGAGGCTGAGG   41538    G   A_
                                CC TAG  TCAGTTCTAGG
                                ||  |||  ||||||||||
                                GG GTC  AGTCGAGGTTT
                                 A  GG
GAM636  MFN2     3'  TTTGGGATTGTTACTGGTT   29607      C    AT
                                AACC GTAG  CAGTTCTAGG
                                ||||  ||||  ||||||||||
```

```
                                TTGG CATT  GTTAGGGTTT
                                  T   __
GAM636  MGC10812 3' CTGGGGCCTGGGGGTT     48667      G   ATCA
                                AACCC TAG    GTTCTAG
                                ||||| |||    |||||||
                                TTGGG GTC    CGGGGTC
                                  G  ____
GAM636  MGC13016 3' CCTGGGGCTGCCACGTGTT   50350     C   AGAT
                                AAC CGT    CAGTTCTAGG
                                ||| |||    ||||||||||
                                TTG GCA    GTCGGGGTCC
                                  T  CC__
GAM636  MGC13064 3' CCTGTTCGCGGTGTTTATGGGT 50352          CA_  TC_
           T                     AACCCGTAGAT   GT   TAGG
                                ||||||||||   ||   ||||
                                TTGGGTATTTG   CG   GTCC
                                      TGG  CTT
GAM636  MGC17330 3' CCTGGAACTGAACCAGGG    53527     GTAGA
                                CCC    TCAGTTCTAGG
                                |||    ||||||||||
                                GGG    AGTCAAGGTCC
                                  ACCA_
GAM636  MGC2217  3' CCTAGAATCTCAGGTGGGT   44177       AGATCA
                                ACCCGT     GTTCTAGG
                                ||||||     ||||||||
                                TGGGTG     TAAGATCC
                                   GACTC_
GAM636  MGC23280 3' CCTGGACACTGACGGGTT    58394       TAGA    _
                                AACCCG    TCAGT TCTAGG
                                ||||||    ||||| ||||||
                                TTGGGC    AGTCA AGGTCC
                                   ____     C
GAM636  MGC2705  3' CCTGGAATGGGGTTGGTT    51112     CGTA    A_
                                AACC    GATC  GTTCTAGG
                                ||||    ||||  ||||||||
                                TTGG    TTGG  TAAGGTCC
                                  ____   GG
GAM636  MGC2721  3' CCTGGAGTTGGTCTGTG     51218        GT
                                CGTAGATCA  TCTAGG
                                |||||||||  ||||||
                                GTGTCTGGT  AGGTCC
                                     TG
GAM636  MGC29956 3' CCTGGGGTTGGTCTGC      58279        TT
                                GTAGATCAG  CTAGG
                                |||||||||  |||||
                                CGTCTGGTT  GGTCC
                                     GG
GAM636  MGC3113  3' CTTGGAGCTGAGCCCTGGG   43846     TAGA
                                CCCG    TCAGTTCTAGG
                                ||||    ||||||||||
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                                GGGT   AGTCGAGGTTC
                                  CCCG
GAM636  MGC3329  3' TTTGGAGTGGCCTGTGGG   44020       AT  G
                                CCCGTAG  CA TTCTAGG
                                |||||||  || |||||||
                                GGGTGTC  GT GAGGTTT
                                   CG  _
GAM636  MGC5338  5' CTGGGATTGGCAGGT      43939     C  AGAT
                                ACC GT   CAGTTCTAG
                                ||| ||   |||||||||
                                TGG CG   GTTAGGGTC
                                 A  ____
GAM636  MGC5457  5' CCTGGGAGGCTGAGATTTATGG 50945         __    __
          GT                    ACCCGTAGA  TCAGT  TCTAGG
                                |||||||||  |||||  ||||||
                                TGGGTATTT  AGTCG  GGGTCC
                                     AG    GA
GAM636  MGC5590  3' TCTGTCTCTGATTTAGGGTT  43929      G      TTC
                                AACCC TAGATCAG   TAGG
                                ||||| ||||||||   ||||
                                TTGGG ATTTAGTC   GTCT
                                  _      TCT
GAM636  MRF2     3' CCTACTAGGCTGCGGGTT    76518        A  _   TCT
                                AACCCGTAG TC AGT   AGG
                                ||||||||| || |||   |||
                                TTGGGCGTC GG TCA   TCC
                                    _ A   ___
GAM636  MRPL41   5' CTTGGAGCTCGTGTGGGGT   50647     G  G  C
                                ACCC TA AT AGTTCTAGG
                                |||| || || |||||||||
                                TGGG GT TG TCGAGGTTC
                                  _  G  C
GAM636  MSP      3' CCTGGGATGGATCGTGGGTT  49415      GTA   A
                                AACCC   GATC GTTCTAGG
                                |||||   |||| ||||||||
                                TTGGG   CTAG TAGGGTCC
                                   TG_   G
GAM636  MVD      3' CTGGGACATGTGGGT      10142      TAGAT  _
                                ACCCG    CA GTTCTAG
                                |||||    || |||||||
                                TGGGT    GT CAGGGTC
                                  _____  A
GAM636  MYT1L    5' CCTGGACTATGGGTT      66823        ATCAGT
                                AACCCGTAG     TCTAGG
                                |||||||||     ||||||
                                TTGGGTATC     AGGTCC
                                    _______    C
GAM636  NPC1L1   3' CTTGGGGCTGGGCTGGT    25415     C  AGA
                                ACC GT   TCAGTTCTAGG
                                ||| ||   ||||||||||
```

```
                                TGG CG   GGTCGGGGTTC
                                  T ___
GAM636  OS4      3'  CCTGGGGTGGGTGGGGTT    19179      GTAG   A TT
                                AACCC    ATC G  CTAGG
                                |||||    ||| |  |||||
                                TTGGG    TGG T  GGTCC
                                   G___   G GG
GAM636  OS4      3'  CTTAGAGCCAGCTGTGG     19183       ATCA
                                CCGTAG    GTTCTAGG
                                ||||||    ||||||||
                                GGTGTC    CGAGATTC
                                   GAC_
GAM636  OSBPL8   3'  TTTAGAGCAAATGTTATGGGTT 40462         ATCA_
                                AACCCGTAG    GTTCTAGG
                                |||||||||    ||||||||
                                TTGGGTATT    CGAGATTT
                                     GTAAA
GAM636  P101-PI3K 3'  CTGGGGCCTCAGGGTT      26678      GT  ATCA
                                AACCC  AG    GTTCTAG
                                |||||  ||    |||||||
                                TTGGG  TC    CGGGGTC
                                   AC _____
GAM636  p25      3'  CCTAGGCCACGCCTGTGGGTT  22850         ATCAGT
                                AACCCGTAG     TCTAGG
                                |||||||||     ||||||
                                TTGGGTGTC     GGATCC
                                     CGCACC
GAM636  P2RX1    3'  CCTGGAGCCCTGGTGGGT    67169     GTAG   __
                                ACCC    ATCA  GTTCTAGG
                                ||||    ||||  ||||||||
                                TGGG    TGGT  CGAGGTCC
                                  _____    CC
GAM636  PANK     3'  TTTAGGGTAAGTCATGGGTT   56336       A   CA TT
                                AACCCGT GAT  G  CTAGG
                                ||||||| |||  |  |||||
                                TTGGGTA CTG  T  GATTT
                                   _   AA GG
GAM636  PCQAP    3'  CTTAGAGAGCCTGGGGTT    31896      G   ATCAG
                                AACCC TAG    TTCTAGG
                                ||||| |||    |||||||
                                TTGGG GTC    GAGATTC
                                   _   CGA__
GAM636  PILR(BETA) 5'  CCTGGAGGTGTACTGGTT    25553     C   G   AGT
                                AACC GTA ATC   TCTAGG
                                |||| ||| |||   ||||||
                                TTGG CAT TGG   AGGTCC
                                  T   G   ___
GAM636  PLK      3'  TCTGGGGCCCATACTGGTT    17268     C   GATCA
                                AACC GTA    GTTCTAGG
                                |||| |||    ||||||||
```

```
                                TTGG CAT    CGGGGTCT
                                  T  ACC__
GAM636  POFUT1   3'  CCTAGAACTCTCTGTGG    70467       TC
                                CCGTAGA  AGTTCTAGG
                                |||||||  |||||||||
                                GGTGTCT  TCAAGATCC
                                    C_
GAM636  PP1628   3'  CCTGGGGCCTGGTGGGT    47295     GTAG   _
                                ACCC   ATCAG TTCTAGG
                                ||||   ||||| |||||||
                                TGGG   TGGTC GGGGTCC
                                  ____   C
GAM636  PRO1777  3'  TTTGGAACTGGTCAC      37765    A
                                GT GATCAGTTCTAGG
                                || ||||||||||||
                                CA CTGGTCAAGGTTT
                                 _
GAM636  PRO2015  3'  CTTAGCAATGTTTACGGG    37558       T  GTT
                                CCCGTAGA CA   CTAGG
                                |||||||| ||   |||||
                                GGGCATTT GT   GATTC
                                    _ AAC
GAM636  PRO2435  5'  CCTGGAACTGATTCGTG     37591    TA
                                CG  GATCAGTTCTAGG
                                ||  ||||||||||||
                                GT  TTAGTCAAGGTCC
                                 GC
GAM636  PRO2730  5'  CCTAGGGCTGGAAGGTT     47412     CGTAGA
                                AACC     TCAGTTCTAGG
                                ||||     ||||||||||
                                TTGG     GGTCGGGATCC
                                  AA____
GAM636  PRO2730  3'  TTGGAACCATGGGTT       47423       AGATCA
                                AACCCGT     GTTCTAG
                                |||||||     |||||||
                                TTGGGTA     CAAGGTT
                                    C_____
GAM636  PRO2949  3'  TCTGGGGCCTATGCTGGTT   37627     C   GATCA
                                AACC GTA    GTTCTAGG
                                |||| |||    ||||||||
                                TTGG CGT    CGGGGTCT
                                  T  ATC__
GAM636  PTK6     3'  TCTGGAGGTTCTATTTACGGGT 19943          C  ___
          T                      AACCCGTAGAT AG   TTCTAGG
                                ||||||||||| ||   |||||||
                                TTGGGCATTTA TC   GAGGTCT
                                      _ TTG
GAM636  PTK6     5'  TCTGGAGCGCCTGTGGGT    19942        ATCA
                                ACCCGTAG   GTTCTAGG
                                ||||||||   ||||||||
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                                TGGGTGTC   CGAGGTCT
                                    CG__
GAM636  RAB1B   3'  CCTGGGGCATTTGAGTCTGTGG 48286       _  ___
                                CCGTAGA TCA  GTTCTAGG
                                ||||||| |||  ||||||||
                                GGTGTCT AGT  CGGGGTCC
                                    G  TTA
GAM636  RAB35   3'  CTTGGGACTGTCCTGGTT   22479     CGT  AT
                                AACC  AG  CAGTTCTAGG
                                ||||  ||  ||||||||||
                                TTGG  TC  GTCAGGGTTC
                                  ___ CT
GAM636  RACGAP1  3'  TTTAGAACTGATTTCCG    25203    T
                                CG AGATCAGTTCTAGG
                                || ||||||||||||||
                                GC TTTAGTCAAGATTT
                                 C
GAM636  RDH-E2   3'  TCTGGAATCCACTATGG    57274      ATCA
                                CCGTAG   GTTCTAGG
                                ||||||   ||||||||
                                GGTATC   TAAGGTCT
                                   ACC_
GAM636  REG1B   3'  TCTAGAACTGGTCCTGC    21483     _
                                GTAG ATCAGTTCTAGG
                                |||| ||||||||||||
                                CGTC TGGTCAAGATCT
                                  C
GAM636  RES4-25  3'  GTCTGGGATCGGGAATGGTCTG 64652        _______
           TGTGTT               CGTAGATCA    GTTCTAGG  T
                                |||||||||    ||||||||  |
                                GTGTCTGGT    TAGGGTCT  G
                                     AAGGGC
GAM636  RFT1    3'  CCTGGACCAGCTATGGGT   53472       ATCAGT
                                ACCCGTAG    TCTAGG
                                ||||||||    ||||||
                                TGGGTATC    AGGTCC
                                    GACC__
GAM636  RNASE7   3'  CTTGGGGCTGTTCCCTGG   50811    TA  T
                                CCG  GA CAGTTCTAGG
                                |||  || ||||||||||
                                GGT  CT GTCGGGGTTC
                                  CC  T
GAM636  RNF38   3'  TTTGGAGTTGAGAGGGTT   42941     GTAGA  GT
                                AACCC   TCA  TCTAGG
                                |||||   |||  ||||||
                                TTGGG   AGT  AGGTTT
                                  AG___  TG
GAM636  RRN3    3'  GACTGTTTTACGGGTT    37356         T
                                AACCCGTAGA CAGTT
                                |||||||||| |||||
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                                TTGGGCATTT GTCAG
                                      T
GAM636  SBB103   3'  CTTGGAGCTGTATAGCTGGGT  19357      TAG  _
                                ACCCG   AT CAGTTCTAGG
                                |||||   || ||||||||||
                                TGGGT   TA GTCGAGGTTC
                                   CGA  T
GAM636  SDC3     3'  CCTGGTCTCTCTGGGGTT    27748      G   TC  TT
                                AACCC TAGA  AG  CTAGG
                                ||||| ||||  ||  |||||
                                TTGGG GTCT  TC  GGTCC
                                   _   C_  T_
GAM636  SDS3     3'  TCTGGGTAATCTTTTACGGGT  69234        TCAGT_
                                ACCCGTAGA     TCTAGG
                                |||||||||     ||||||
                                TGGGCATTT     GGGTCT
                                      TCTAAT
GAM636  SEC14L1  3'  TCTGGGGCAGCTATGG      11527       ATCA
                                CCGTAG    GTTCTAGG
                                ||||||    ||||||||
                                GGTATC    CGGGGTCT
                                   GA__
GAM636  SEF      3'  TTTAGTTTGGATTTAGGGTT   69469      G     AGTT
                                AACCC TAGATC    CTAGG
                                ||||| ||||||    |||||
                                TTGGG ATTTAG    GATTT
                                   _     GTTT
GAM636  SERP1    3'  TCTGGAATTGAATGG       27066      AGA
                                CCGT   TCAGTTCTAGG
                                ||||   ||||||||||||
                                GGTA   AGTTAAGGTCT
                                      ___
GAM636  SES2     3'  CCTGGGGCTTAAGTGGGTT    48809       TAGATC
                                AACCCG     AGTTCTAGG
                                ||||||     |||||||||
                                TTGGGT     TCGGGGTCC
                                   GAAT__
GAM636  SFXN5    3'  CCTGGAGTTGGGCTGGTT    58034      C  AGA   GT
                                AACC GT   TCA  TCTAGG
                                |||| ||   |||  ||||||
                                TTGG CG   GGT  AGGTCC
                                  T  ___   TG
GAM636  SFXN5    3'  TCTGGGGCTGAGAGTGGG    58039      TAGA
                                CCCG    TCAGTTCTAGG
                                ||||    ||||||||||||
                                GGGT    AGTCGGGGTCT
                                  GAG_
GAM636  SHANK3   3'  AGCTGGTCTGGGGTT       65488       G
                                AACCC TAGATCAGTT
                                ||||| ||||||||||
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                                TTGGG GTCTGGTCGA
                                   _
GAM636  SHANK3   5'  CTGGGGCCCTCGGGTT     65496      T  ATCA
                                AACCCG AG   GTTCTAG
                                |||||| ||   |||||||
                                TTGGGC TC   CGGGGTC
                                   _ C___
GAM636  SHAPY    3'  TTTGGAACTGTGCCTGGGTT  57116      TAGAT
                                AACCCG    CAGTTCTAGG
                                ||||||    ||||||||||
                                TTGGGT    GTCAAGGTTT
                                   CCGT_
GAM636  SIMRP7   3'  TCTGGAACGCCAGGTGGGTT  92373      AGATCA
                                AACCCGT    GTTCTAGG
                                |||||||    ||||||||
                                TTGGGTG    CAAGGTCT
                                    GACCG_
GAM636  SLC11A2  3'  CTTAGAACTGGATTAGGGT   5236     G   A
                                ACCC TAG TCAGTTCTAGG
                                |||| ||| ||||||||||
                                TGGG ATT GGTCAAGATTC
                                  _  A
GAM636  SLC2A10  3'  CCTGGAATTCTGGAACTGTGG  47821      A ___
                                CCGTAG TC   AGTTCTAGG
                                |||||| ||   ||||||||
                                GGTGTC AG   TTAAGGTCC
                                   A  GTC
GAM636  SLC4A11  5'  CCTAGGGTGGCGTGGGTT    49339      TAGA   G
                                AACCCG    TCA TTCTAGG
                                ||||||    ||| |||||||
                                TTGGGT    GGT GGGATCC
                                   GC__   _
GAM636  SNPH     3'  CCTGGGGCCTTCGATGGG    28241      A  TCA
                                CCCGT GA   GTTCTAGG
                                ||||| ||   ||||||||
                                GGGTA CT   CGGGGTCC
                                  G  TC_
GAM636  SNX11    3'  CCTACCCTGTCTGTGGG     25267       T   TTC
                                CCCGTAGA CAG   TAGG
                                |||||||| |||   ||||
                                GGGTGTCT GTC   ATCC
                                   _   CC_
GAM636  SSI-1    3'  CCTGGAACCATGTGGGT     13627       GATCA
                                ACCCGTA    GTTCTAGG
                                |||||||    ||||||||
                                TGGGTGT    CAAGGTCC
                                   AC____
GAM636  STAB2    3'  TCTCTGGCTGATCTGGGGGTT  34115      G        CT
                                AACCC TAGATCAGTT  AGG
                                ||||| ||||||||||  |||
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                                TTGGG GTCTAGTCGG  TCT
                                   G         TC
GAM636  STAB2    3'  CTGGGGGTTGTTTCTGTGGGT  34113         T_  TT  AGG
                                ACCCGTAGA  CAG  CT
                                |||||||||  |||  ||
                                TGGGTGTCT  GTT  GG
                                     TT   GG  GTCT
GAM636  STAT5A   3'  TCTAGGATATGGTGGGT     12016      GTAG   _
                                ACCC    ATCA GTTCTAGG
                                ||||    |||| ||||||||
                                TGGG    TGGT TAGGATCT
                                  ____    A
GAM636  STK29    3'  TCTGGGGCGGCTGTGGG     87580        ATCA
                                CCCGTAG    GTTCTAGG
                                |||||||    ||||||||
                                GGGTGTC    CGGGGTCT
                                    GG__
GAM636  TAS1R1   3'  TTTGGGCATCGCGGTCTGGGGT 56921       G     A ____
           T                     AACCC TAGATC GT    TCTAGG
                                |||||| |||||| ||    ||||||
                                TTGGG GTCTGG CG    GGGTTT
                                  _     _ CTAC
GAM636  TCEA3    5'  TTTGGGGCCCGCGCGGGTT    88509        AGATCA
                                AACCCGT     GTTCTAGG
                                |||||||     ||||||||
                                TTGGGCG     CGGGGTTT
                                    CGCC__
GAM636  TCL6     5'  ATGCAAGGCTGGTTTATGAGTT 40154     C          CTAGG
                                AAC CGTAGATCAGTT
                                ||| ||||||||||||
                                TTG GTATTTGGTCGG
                                  A          AACGTAT
GAM636  TCL6     5'  ATGCAAGGCTGGTTTATGAGTT 40123     C          CTAGG
                                AAC CGTAGATCAGTT
                                ||| ||||||||||||
                                TTG GTATTTGGTCGG
                                  A          AACGTAT
GAM636  TEX27    3'  CTTAGAGCTGGGGGGGGT    41662      GTAGA
                                ACCC    TCAGTTCTAGG
                                ||||    ||||||||||
                                TGGG    GGTCGAGATTC
                                  GGG__
GAM636  TFB2M    3'  AACTGATTTACTGGTT      42307      C
                                AACC GTAGATCAGTT
                                |||| ||||||||||
                                TTGG CATTTAGTCAA
                                  T
GAM636  TGOLN2   3'  TCTAGAATTTAGTGGCGGGT   64050        AGATC
                                ACCCGT    AGTTCTAGG
                                ||||||    |||||||||
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                                TGGGCG    TTAAGATCT
                                   GTGAT
GAM636  THEA     3' TCTGGAAGGTTGTGGGTT    66302      GTA   AG
                                AACCC   GATC  TTCTAGG
                                |||||   ||||  |||||||
                                TTGGG   TTGG  AAGGTCT
                                   TG_   __
GAM636  TIP120B  3' TTTGGAAGATGATACGGGTT  72419       GA  G_
                                AACCCGTA  TCA  TTCTAGG
                                ||||||||  |||  |||||||
                                TTGGGCAT  AGT  AAGGTTT
                                     __  AG
GAM636  TNKS2    3' TTTAGAACTGCAGCGG     47456     AGAT
                                CCGT    CAGTTCTAGG
                                ||||    ||||||||||
                                GGCG    GTCAAGATTT
                                  AC__
GAM636  TOB2     3' CCTGGAGCTGATGTCTGTG   95620       __
                                CGTAGA  TCAGTTCTAGG
                                ||||||  ||||||||||
                                GTGTCT  AGTCGAGGTCC
                                   GT
GAM636  TOB2     3' CCTGGAGTTGAGACTTTGGG  95621     T  A_  GT
                                CCCG AG  TCA  TCTAGG
                                |||| ||  |||  ||||||
                                GGGT TC  AGT  AGGTCC
                                  T  AG   TG
GAM636  TOPK     3' CTTGGAATTGTACTGGGTT   37505      _  GAT
                                AACCC GTA   CAGTTCTAGG
                                ||||| |||   ||||||||||
                                TTGGG CAT   GTTAAGGTTC
                                   T  ____
GAM636  TRIM35   3' CCTGGAGCTTCCTGGGT    60838      TA  TC
                                ACCCG  GA  AGTTCTAGG
                                |||||  ||  |||||||||
                                TGGGT  CT  TCGAGGTCC
                                   C_  __
GAM636  TRIP-Br2 3' CCTAGAGCTTTCCCTGTGTT  28580     C  TA  TC
                                AAC CG  GA  AGTTCTAGG
                                ||| ||  ||  |||||||||
                                TTG GT  CT  TCGAGATCC
                                  T  CC  T_
GAM636  TTTY2    5' GTCTGGAAAACTCCTGGTTTGA 87007    G      _____
           GGGTT                 CC TAGATCAG    TTCTAGG   T
                                || ||||||||    |||||||  |
                                GG GTTTGGTC    AAGGTCT   G
                                 A       CTCAA
GAM636  TXNL2    3' TCTAGGGCTGGGAGCTGGG   21554     TAGA
                                CCCG    TCAGTTCTAGG
                                ||||    ||||||||||
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                                GGGT   GGTCGGGATCT
                                  CGAG
GAM636  Ubc6p    3'  CTTGGAGCTCCTGGCGCGTT  54152    C  AGATC
                                AAC CGT    AGTTCTAGG
                                ||| |||    |||||||||
                                TTG GCG    TCGAGGTTC
                                  C  GTCC_
GAM636  UBCE7IP5  3'  TTTAGAGATCTGGGTTTGGGGT 30166     G    AG___
          T                      AACCC TAGATC    TTCTAGG
                                ||||| ||||||    |||||||
                                TTGGG GTTTGG    GAGATTT
                                  _    GTCTA
GAM636  UNC5D    3'  CTTGGAATCCACATTTGGGTT  55137      TAGATCA
                                AACCCG      GTTCTAGG
                                ||||||      ||||||||
                                TTGGGT      TAAGGTTC
                                   TTACACC
GAM636  UPLC1    3'  GCCTGGAGACCTGACTGGTCTG 34725         _______
          TGG                     CGTAGATCAGT     TCTAGG  C
                                ||||||||||     ||||||  |
                                GTGTCTGGTCA     AGGTCC  G
                                     GTCCAG
GAM636  USP16    3'  TCTGGAAACACATTTATGG   21243       CAG_
                                CCGTAGAT   TTCTAGG
                                ||||||||   |||||||
                                GGTATTTA   AAGGTCT
                                     CACA
GAM636  VEST1    3'  AACTTGTCTAGGGTT      53680      G   C
                                AACCC TAGAT AGTT
                                ||||| ||||| ||||
                                TTGGG ATCTG TCAA
                                  _    T
GAM636  WBSCR17  3'  TCTGGGACTGGCAGGGT    81306     GTAGA
                                ACCC    TCAGTTCTAGG
                                ||||    ||||||||||
                                TGGG    GGTCAGGGTCT
                                  AC___
GAM636  WIT-1    3'  CCTGGAGCCGCTGGGGTT   31824      G  ATCA
                                AACCC TAG   GTTCTAGG
                                ||||| |||   |||||||
                                TTGGG GTC   CGAGGTCC
                                  _  GC__
GAM636  YF13H12  5'  TTTAGGGCTGGACTCTTGGGT  26664      T  __
                                ACCCG AGA  TCAGTTCTAGG
                                ||||| |||  ||||||||||
                                TGGGT TCT  GGTCGGGATTT
                                  _  CA
GAM636  ZFP100   3'  CCTGGAGTTCTGCTGGTT   70052     C   TCAG
                                AACC GTAGA   TTCTAGG
                                |||| |||||   |||||||
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                                TTGG CGTCT    GAGGTCC
                                  T    T___
GAM636  ZFP106   3'  AACTGTTCTGTGGGTT      42459          T
                                AACCCGTAGA CAGTT
                                |||||||||| |||||
                                TTGGGTGTCT GTCAA
                                     T
GAM636  ZFP106   3'  TCTGGGCAGCTCTATGGG    42480        TCA  T
                                CCCGTAGA   GT CTAGG
                                ||||||||   || |||||
                                GGGTATCT   CG GGTCT
                                    CGA  _
GAM636  ZNF258   3'  TCTGGAACTGCTGGCTGGGTT  23147       _  AGAT
                                AACCC GT    CAGTTCTAGG
                                ||||| ||    ||||||||||
                                TTGGG CG    GTCAAGGTCT
                                   T  GTC_
GAM636  ZNF297B  3'  CCTAGGATGAGAAATTGGTT   81807     C  AGA   G
                                AACC GT   TCA TTCTAGG
                                |||| ||   ||| |||||||
                                TTGG TA   AGT AGGATCC
                                  T  AAG   _
GAM636  ZNF297B  3'  CCTAGGATGAGAAATTGGTT   25779     C  AGA   G
                                AACC GT   TCA TTCTAGG
                                |||| ||   ||| |||||||
                                TTGG TA   AGT AGGATCC
                                  T  AAG   _
GAM636  LOC114984 3'  TCTGGGGCCAAATGGGT     73170       AGATCA
                                ACCCGT     GTTCTAGG
                                ||||||     ||||||||
                                TGGGTA     CGGGGTCT
                                   AAC___
GAM636  LOC115509 3'  TCTGGGGCTGGACTTG      73460    T  A
                                CG AG TCAGTTCTAGG
                                || || ||||||||||
                                GT TC GGTCGGGGTCT
                                 _  A
GAM636  LOC115648 3'  TTTGGGATGCCCTCTGGGTT   59305       T  ATCA
                                AACCCG AG    GTTCTAGG
                                |||||| ||    ||||||||
                                TTGGGT TC    TAGGGTTT
                                   C  CCG_
GAM636  LOC118487 3'  TTTGGAATCATAGTATGGGT   73921       GATCA
                                ACCCGTA    GTTCTAGG
                                |||||||    ||||||||
                                TGGGTAT    TAAGGTTT
                                    GATAC
GAM636  LOC118738 3'  CCTAAGTCGTGAGTCTGTGGGT 75489          _  GTT  _
           T                     AACCCGTAGA TCA   CT AGG
                                ||||||||| |||   || |||
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                                TTGGGTGTCT AGT   GA TCC
                                      G   GCT  A
GAM636   LOC120856 3'  CTTAGAACAGATGGGTT     74028        AGATCA
                                AACCCGT     GTTCTAGG
                                |||||||     ||||||||
                                TTGGGTA     CAAGATTC
                                   GA____
GAM636   LOC122830 3'  TTTGGAATGAGTTCTGTGGGTT 74172          TCA_
                                AACCCGTAGA    GTTCTAGG
                                ||||||||||    ||||||||
                                TTGGGTGTCT    TAAGGTTT
                                      TGAG
GAM636   LOC123876 3'  CTTGGAACTGTCAGGGT     74246      GTA  T
                                ACCC   GA CAGTTCTAGG
                                ||||   || ||||||||||
                                TGGG   CT GTCAAGGTTC
                                  A__  _
GAM636   LOC124222 3'  TCTGGGGCTCAGGTTGGGT    74274      TAGATC
                                ACCCG     AGTTCTAGG
                                |||||     |||||||||
                                TGGGT     TCGGGGTCT
                                   TGGAC_
GAM636   LOC126353 3'  TTTGGGACTGTTGGGTT     74501       TAGAT
                                AACCCG     CAGTTCTAGG
                                ||||||     ||||||||||
                                TTGGGT     GTCAGGGTTT
                                   T_____
GAM636   LOC126669 3'  TCTGGGGTTGGTCATTTGGGT  75420      TA_     TT
                                ACCCG   GATCAG  CTAGG
                                |||||   ||||||  |||||
                                TGGGT   CTGGTT  GGTCT
                                   TTA     GG
GAM636   LOC126917 3'  TTGGGGCAGGTGGGT       74599      GTAG   A
                                ACCC    ATC GTTCTAG
                                ||||    ||| |||||||
                                TGGG    TGG CGGGGTT
                                  _____  A
GAM636   LOC126917 3'  CCTGGGCCTTTGCGGGT     74581        ATC  TT
                                ACCCGTAG   AG  CTAGG
                                ||||||||   ||  |||||
                                TGGGCGTT   TC  GGTCC
                                     ___  CG
GAM636   LOC127281 3'  CCTGGGGACCACTGTGGGTT   74646         ATCAG
                                AACCCGTAG     TTCTAGG
                                |||||||||     |||||||
                                TTGGGTGTC     GGGGTCC
                                     ACCA_
GAM636   LOC127702 3'  TCTAAAATGTTTATGGG     75462         CA   C
                                CCCGTAGAT  GTT TAGG
                                |||||||||  ||| ||||
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                                GGGTATTTG  TAA ATCT
                                    __  A
GAM636  LOC130074 3'  TCTCCAGCTGACTCTGTGGGTT 76141          _     CT
                                AACCCGTAGA TCAGTT  AGG
                                |||||||||| ||||||  |||
                                TTGGGTGTCT AGTCGA  TCT
                                     C     CC
GAM636  LOC130074 3'  TTTGGGGTTGATGTGGGTT   76144       TAG    TT
                                AACCCG   ATCAG  CTAGG
                                ||||||   |||||  |||||
                                TTGGGT   TAGTT  GGTTT
                                   G__    GG
GAM636  LOC131965 5'  CCTCAGAATTGGTTTAGGGTT  75029      G         _
                                AACCC TAGATCAGTTCT AGG
                                ||||| |||||||||||| |||
                                TTGGG ATTTGGTTAAGA TCC
                                  _         C
GAM636  LOC132954 5'  CCTGGAGAAGGCTGCGGGT   75071        A  AG
                                ACCCGTAG TC  TTCTAGG
                                |||||||| ||  |||||||
                                TGGGCGTC GG  GAGGTCC
                                    _ AA
GAM636  LOC138311 3'  CCTGGAGCTGGCCAGGT    76211     CGTAGA
                                ACC     TCAGTTCTAGG
                                |||     ||||||||||
                                TGG     GGTCGAGGTCC
                                  ACC___
GAM636  LOC138649 5'  TTTGGGGCTGGGTGGGGGT   75360     G  GA
                                ACCC TA  TCAGTTCTAGG
                                |||| ||  ||||||||||
                                TGGG GT  GGTCGGGGTTT
                                  G  G_
GAM636  LOC140380 5'  CTTGGGGCTGAGCTACGGG   75959       A
                                CCCGTAG TCAGTTCTAGG
                                ||||||| ||||||||||
                                GGGCATC AGTCGGGGTTC
                                    G
GAM636  LOC142927 3'  CCTGGACAGTTCTCTGTGGG  76424       TCAGT_
                                CCCGTAGA     TCTAGG
                                ||||||||     ||||||
                                GGGTGTCT     AGGTCC
                                     CTTGAC
GAM636  LOC143872 3'  TTGAATTTGGCTTATGGGTT  76651       AT  _  TAGG
                                AACCCGTAG  CAG TTC
                                |||||||||  ||| |||
                                TTGGGTATT  GTT AAG
                                     CG  T  TT
GAM636  LOC143941 5'  CCTGGAGCTGCAGGGGGT    76662     GTAGAT
                                ACCC     CAGTTCTAGG
                                ||||     ||||||||||
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                                TGGG     GTCGAGGTCC
                                  GGAC__
GAM636  LOC144161 3' CTGGTAGTCTGGGGTT     83007      G    CAGTT
                                AACCC TAGAT     CTAG
                                ||||| |||||     ||||
                                TTGGG GTCTG     GGTC
                                  _    AT___
GAM636  LOC144348 3' GATTGATTTGTTGGTT     76807     CG
                                AACC  TAGATCAGTT
                                ||||  ||||||||||
                                TTGG  GTTTAGTTAG
                                  TT
GAM636  LOC145098 3' TTTGGGGCTGATTAAC     76997    A
                                GT GATCAGTTCTAGG
                                || ||||||||||||
                                CA TTAGTCGGGGTTT
                                 A
GAM636  LOC145225 3' CCTGGGATGCAGACAGGTT   83303     C  AGATCA
                                AACC GT     GTTCTAGG
                                |||| ||     ||||||||
                                TTGG CA     TAGGGTCC
                                  A  GACG__
GAM636  LOC145333 3' TTCAGTTCTGGTTTAGGGGTT  83332      G       TT  AGG
                                AACCC TAGATCAG  CT
                                ||||| ||||||||  ||
                                TTGGG ATTTGGTC  GA
                                   G       TT  CTTT
GAM636  LOC145608 3' TCTGGAATTGTCCTTGG     83387     TA  T
                                CCG  GA CAGTTCTAGG
                                |||  || ||||||||||
                                GGT  CT GTTAAGGTCT
                                  TC  _
GAM636  LOC147622 3' CCTATTCTGTCTAGGGTT    84045      G    T   TTC
                                AACCC TAGA CAG   TAGG
                                ||||| |||| |||   ||||
                                TTGGG ATCT GTC   ATCC
                                  _    _   TT_
GAM636  LOC148343 3' TTTGGGATGCCAAGGCGGGT   78797       AGATCA
                                ACCCGT     GTTCTAGG
                                ||||||     ||||||||
                                TGGGCG     TAGGGTTT
                                   GAACCG
GAM636  LOC148398 3' CCTGGAACTGGGAACTGGT    78825     C  AGA
                                ACC GT   TCAGTTCTAGG
                                ||| ||   ||||||||||
                                TGG CA   GGTCAAGGTCC
                                  T  AG_
GAM636  LOC148479 3' CTTGGAACTGTGCCGAGTT    78868     C  TAGAT
                                AAC CG     CAGTTCTAGG
                                ||| ||     ||||||||||
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                                TTG GC    GTCAAGGTTC
                                  A  CGT__
GAM636  LOC149319 3'  CCTGGAGCTTGGCTGTGG    79292       A  _
                                CCGTAG TCA GTTCTAGG
                                ||||||| ||| ||||||||
                                GGTGTC GGT CGAGGTCC
                                   _  T
GAM636  LOC149373 3'  CTTAGAGCTGGGCTTCAGGGTT 79313      GT_  AT
                                AACCC   AG  CAGTTCTAGG
                                |||||   ||  ||||||||||
                                TTGGG   TC  GTCGAGATTC
                                   ACT  GG
GAM636  LOC149401 3'  CCTAATGTAGATTATGGGTT   79332       A    AG TC
                                AACCCGT GATC  T  TAGG
                                ||||||| ||||  |  ||||
                                TTGGGTA TTAG  G  ATCC
                                    _   AT TA
GAM636  LOC149478 5'  CTTGGGACTGGTCGTGC     79377     _
                                GTA GATCAGTTCTAGG
                                ||| ||||||||||||
                                CGT CTGGTCAGGGTTC
                                  G
GAM636  LOC149483 3'  CCTGGGGCTGGCCTGGT     79386     CGT  AT
                                ACC   AG  CAGTTCTAGG
                                |||   ||  ||||||||||
                                TGG   TC  GTCGGGGTCC
                                  ___  CG
GAM636  LOC149563 3'  CCTGGAGCTGGTATTTTTGGG  84526     TAG__
                                CCCG    ATCAGTTCTAGG
                                ||||    ||||||||||||
                                GGGT    TGGTCGAGGTCC
                                  TTTTA
GAM636  LOC149570 3'  CTTGGGGCCTTTATGGG     84500        TCA
                                CCCGTAGA   GTTCTAGG
                                ||||||||   ||||||||
                                GGGTATTT   CGGGGTTC
                                    C__
GAM636  LOC149668 3'  CTTGGGCTTGGGTCTGTGGGT  84540          __    T  G
                                ACCCGTAGATC  AGTTC AG
                                ||||||||||  ||||| ||
                                TGGGTGTCTGG  TCGGG TC
                                      GT    T
GAM636  LOC149706 3'  CTGGGGCCCTTGGGTT      84640       T  ATCA
                                AACCCG AG    GTTCTAG
                                |||||| ||    |||||||
                                TTGGGT TC    CGGGGTC
                                   _ C___
GAM636  LOC150054 3'  CTGGAATACTAGGGTT      84831       G   ATCA
                                AACCC TAG    GTTCTAG
                                ||||| |||    |||||||
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                                TTGGG ATC    TAAGGTC
                                  _  A___
GAM636  LOC150245 3'  CCTGGACACGTCTGTGGGT   84934         CA  _
                                ACCCGTAGAT  GT TCTAGG
                                ||||||||||  || ||||||
                                TGGGTGTCTG  CA AGGTCC
                                    __  C
GAM636  LOC150407 3'  CCTGGAGCCCTGTCTGGGGTT  79822      G    CA_
                                AACCC TAGAT   GTTCTAGG
                                ||||| |||||   ||||||||
                                TTGGG GTCTG   CGAGGTCC
                                  _    TCC
GAM636  LOC150951 5'  TTTAGGATTGGGAGGGT     85170      GTAGA
                                ACCC     TCAGTTCTAGG
                                ||||     ||||||||||
                                TGGG     GGTTAGGATTT
                                  AG___
GAM636  LOC151201 3'  TTTGGAACTGATAATAGGT    85300     CGTAG
                                ACC     ATCAGTTCTAGG
                                |||     ||||||||||||
                                TGG     TAGTCAAGGTTT
                                 ATAA_
GAM636  LOC151201 3'  CTTAATTGTCTACGG       85277        T    CT
                                CCGTAGA CAGTT  AG
                                ||||||| |||||  ||
                                GGCATCT GTTAA  TC
                                   _    T_
GAM636  LOC151457 5'  CTTGAATTGGATTTGTTGGTT  80244      CG    _    T  G
                                AACC  TAGATC AGTTC AG
                                ||||  |||||| ||||| ||
                                TTGG  GTTTAG TTAAG TC
                                  TT     G    T
GAM636  LOC151475 5'  CCTGTCAGGACTGTGGGTT    85400       TAGAT     ___
                                AACCCG    CAGTTCT   AGG
                                ||||||    |||||||   |||
                                TTGGGT    GTCAGGA   TCC
                                   _____      CTG
GAM636  LOC151516 5'  CCGACACTGCTCTGTGGGTT   80269         T   TCTA
                                AACCCGTAGA CAGT    GG
                                |||||||||| ||||    ||
                                TTGGGTGTCT GTCA    CC
                                     C    CAG_
GAM636  LOC151701 5'  TCTGGAGCCAAGGCTGTGGGT  85491        ATCA_
                                ACCCGTAG    GTTCTAGG
                                ||||||||    ||||||||
                                TGGGTGTC    CGAGGTCT
                                   GGAAC
GAM636  LOC152048 3'  TTTGGGAAAAGTGCGGGTT    85550        GATCAG
                                AACCCGTA     TTCTAGG
                                ||||||||     |||||||
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                                TTGGGCGT     AGGGTTT
                                     GAAA__
GAM636  LOC152441 5'  CCTGGGACAGGGTGGGTT    85733      GTAG  A_
                                AACCC    ATC  GTTCTAGG
                                |||||    |||  ||||||||
                                TTGGG    TGG  CAGGGTCC
                                   _____   GA
GAM636  LOC152445 5'  TCTGTTTCTGTCTATGG     85765       T   TTC
                                CCGTAGA CAG   TAGG
                                ||||||| |||   ||||
                                GGTATCT GTC   GTCT
                                    _  TTT
GAM636  LOC152633 5'  CCTGGGATTTCTGTGTGTT    85808     C     TC
                                AAC CGTAGA  AGTTCTAGG
                                ||| ||||||  |||||||||
                                TTG GTGTCT  TTAGGGTCC
                                  T     __
GAM636  LOC152790 5'  CTTGGGATTGAAGGATTGGGTT 85875       TAGA_
                                AACCCG     TCAGTTCTAGG
                                ||||||     ||||||||||
                                TTGGGT     AGTTAGGGTTC
                                    TAGGA
GAM636  LOC152860 5'  CCTGTTTGTCTGTGGGT     80699        T   TTC
                                ACCCGTAGA CAG   TAGG
                                ||||||||| |||   ||||
                                TGGGTGTCT GTT   GTCC
                                     _  T__
GAM636  LOC152926 3'  CTTAGGCAGCTATGGGTT    80745        ATCA  T
                                AACCCGTAG    GT CTAGG
                                |||||||||    || |||||
                                TTGGGTATC    CG GATTC
                                     GA__  _
GAM636  LOC153811 3'  CCTGCGAAGCTGTGGGTT    80945       TAGAT    _ _
                                AACCCG     CAGTT C TAGG
                                ||||||     ||||| | ||||
                                TTGGGT     GTCGA G GTCC
                                   _____     A C
GAM636  LOC153839 5'  CTTGGAGCTGGAGCTGGGGT   80969      G   A_
                                ACCC TAG  TCAGTTCTAGG
                                |||| |||  ||||||||||
                                TGGG GTC  GGTCGAGGTTC
                                   _   GA
GAM636  LOC154007 3'  CTTAGAACACCACCTGCGG    81019       ATCA_
                                CCGTAG     GTTCTAGG
                                ||||||     ||||||||
                                GGCGTC     CAAGATTC
                                    CACCA
GAM636  LOC154323 5'  CCTAGGACACAACACAGGTT   86213      C  AGATCA
                                AACC GT      GTTCTAGG
                                |||| ||      ||||||||
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                                TTGG CA     CAGGATCC
                                  A  CAACA_
GAM636   LOC154449 5'  TCTGGAGCTGGTCAGCG     81088     A
                                CGT GATCAGTTCTAGG
                                ||| ||||||||||||
                                GCG CTGGTCGAGGTCT
                                  A
GAM636   LOC154739 5'  CCTGGGGCTGAGGATCGG     86230     TAGA
                                CCG    TCAGTTCTAGG
                                |||    ||||||||||
                                GGC    AGTCGGGGTCC
                                  TAGG
GAM636   LOC155006 3'  CCTGGAGCTGGTGCTG      81236     _
                                TAG ATCAGTTCTAGG
                                ||| ||||||||||||
                                GTC TGGTCGAGGTCC
                                  G
GAM636   LOC155008 5'  CCTGGGATGAGAGCGGGT     81227       AGA   G
                                ACCCGT   TCA TTCTAGG
                                ||||||   ||| |||||||
                                TGGGCG   AGT AGGGTCC
                                   AG_   _
GAM636   LOC155072 5'  TCTGGAGTTGATTTGC      86387        GT
                                GTAGATCA  TCTAGG
                                ||||||||  ||||||
                                CGTTTAGT  AGGTCT
                                     TG
GAM636   LOC157292 3'  CCTAGAACTCCCTGTGGAGTT  86412     _     ATC
                                AAC CCGTAG   AGTTCTAGG
                                ||| ||||||   |||||||||
                                TTG GGTGTC   TCAAGATCC
                                  A     CC_
GAM636   LOC157349 3'  TCTGGGGCTGTTTGGG      81424      TAGAT
                                CCCG     CAGTTCTAGG
                                ||||     ||||||||||
                                GGGT     GTCGGGGTCT
                                  TT___
GAM636   LOC157531 5'  CTTAGGGTGATCGTGGGTT    86472      GTA    G
                                AACCC   GATCA TTCTAGG
                                |||||   ||||| |||||||
                                TTGGG   CTAGT GGGATTC
                                   TG_    _
GAM636   LOC157556 3'  CCTGGGGTGCGAACGGGT     86483       AGA  A_ TT
                                ACCCGT   TC  G  CTAGG
                                ||||||   ||  |  |||||
                                TGGGCA   AG  T  GGTCC
                                   ___  CG GG
GAM636   LOC157638 5'  CCTGGAGTTGGTTTCG      81511     T     GT
                                CG AGATCA  TCTAGG
                                || ||||||  ||||||
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                                GC TTTGGT  AGGTCC
                                 _     TG
GAM636  LOC158428 5'  CTGGATTCTAGGGTT      70559      G    TCAGT
                                AACCC TAGA    TCTAG
                                ||||| ||||    |||||
                                TTGGG ATCT    AGGTC
                                  _   T____
GAM636  LOC159148 5'  GTCTGGAAAACTCCTGGTTTGA 87016    G      _____
                GGGTT                  CC TAGATCAG    TTCTAGG   T
                                || ||||||||    |||||||  |
                                GG GTTTGGTC    AAGGTCT   G
                                 A       CTCAA
GAM636  LOC164397 5'  CCTGCTCACAGGTTTGCGGG   82523          A  TC_
                                CCCGTAGATC GT   TAGG
                                |||||||||| ||   ||||
                                GGGCGTTTGG CA   GTCC
                                      A  CTC
GAM636  LOC166042 5'  TCTGGGAAAGCGTCAATGGGTT 82610        A   CAG_
                                AACCCGT GAT    TTCTAGG
                                ||||||| |||    |||||||
                                TTGGGTA CTG    AGGGTCT
                                   A   CGAA
GAM636  LOC196027 3'  TTTAGAAACTAAGATGTATGGG 87554        G   __   _
                TT                  AACCCGTA ATC  AGTT CTAGG
                                ||||||||| |||  |||| |||||
                                TTGGGTAT TAG  TCAA GATTT
                                     G   AA    A
GAM636  LOC196418 3'  GATTGATTTGTTGGTT      87697      CG
                                AACC  TAGATCAGTT
                                ||||  ||||||||||
                                TTGG  GTTTAGTTAG
                                  TT
GAM636  LOC196418 5'  TCTGGAATGTCTTGGGGGTT   87699      G  _   CA
                                AACCC TA GAT  GTTCTAGG
                                ||||| || |||  ||||||||
                                TTGGG GT CTG  TAAGGTCT
                                   G  T   __
GAM636  LOC196463 3'  CCTGGAGCTGGTGAGC      87711    AG
                                GT  ATCAGTTCTAGG
                                ||  ||||||||||||
                                CG  TGGTCGAGGTCC
                                 AG
GAM636  LOC196463 3'  TCTGGGGCTCCCATGGG     87716      AGATC
                                CCCGT    AGTTCTAGG
                                |||||    |||||||||
                                GGGTA    TCGGGGTCT
                                   CCC__
GAM636  LOC199695 3'  CCTAGGGCTGCCCGAGGGTT   88318      GTAGAT
                                AACCC     CAGTTCTAGG
                                |||||     ||||||||||
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                                TTGGG     GTCGGGATCC
                                   AGCCC_
GAM636   LOC199986 5'  CCTGGAGCCCTGCAGGTT    89905      C    ATCA
                                AACC GTAG    GTTCTAGG
                                |||| ||||    ||||||||
                                TTGG CGTC    CGAGGTCC
                                  A    C___
GAM636   LOC200010 3'  TCTGGAGCTGGTTCTGTGGG   89924         _
                                CCCGTAGA TCAGTTCTAGG
                                |||||||| ||||||||||
                                GGGTGTCT GGTCGAGGTCT
                                     T
GAM636   LOC200059 3'  TTTGGGATTGGGTGGGGGT    88554      G  GA
                                ACCC TA  TCAGTTCTAGG
                                |||| ||  ||||||||||
                                TGGG GT  GGTTAGGGTTT
                                  G  G_
GAM636   LOC200339 3'  AACTGATCTACAGGTT       90023      C
                                AACC GTAGATCAGTT
                                |||| ||||||||||
                                TTGG CATCTAGTCAA
                                  A
GAM636   LOC200471 3'  TGAAGGAGGCTGATTTAAGGGT 90055       G        _   AGG
      T                          AACCC TAGATCAGT TCT
                                ||||| |||||||| |||
                                TTGGG ATTTAGTCG AGG
                                   A        G   AAGTT
GAM636   LOC201895 3'  TTTGGGGTTGTCTGGG      89096     GT   T   TT
                                CCC  AGA CAG  CTAGG
                                |||  ||| |||  |||||
                                GGG  TCT GTT  GGTTT
                                  __  _  GG
GAM636   LOC202868 5'  TCTGGAGTTGATTTGC      90385         GT
                                GTAGATCA  TCTAGG
                                ||||||||  ||||||
                                CGTTTAGT  AGGTCT
                                     TG
GAM636   LOC203235 5'  CCTGGGACTCCTGTGGGT    90467         ATC
                                ACCCGTAG   AGTTCTAGG
                                ||||||||   |||||||||
                                TGGGTGTC   TCAGGGTCC
                                     C__
GAM636   LOC203276 3'  CCTGGGGCTGATGATCGG    90482     TAG
                                CCG   ATCAGTTCTAGG
                                |||   ||||||||||||
                                GGC   TAGTCGGGGTCC
                                  TAG
GAM636   LOC203305 3'  CCTGGGGCTGATGATCGG    90526     TAG
                                CCG   ATCAGTTCTAGG
                                |||   ||||||||||||
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                                GGC   TAGTCGGGGTCC
                                  TAG
GAM636   LOC219594 3'  GAATAAAACTGAACTGTGGGTT 90779         A     CTAGG
                                AACCCGTAG TCAGTT
                                ||||||||| ||||||
                                TTGGGTGTC AGTCAA
                                     A     AATAAGT
GAM636   LOC219700 3'  GGACGTCTAGGGTT       93065      G    CA
                                AACCC TAGAT  GTTC
                                ||||| |||||  ||||
                                TTGGG ATCTG  CAGG
                                  _    __
GAM636   LOC219731 5'  CCTAGGAGAGCTGGTGGGTT   93092      GTAG       ___
                                AACCC    ATCAGTTCT   AGG
                                |||||    |||||||||   |||
                                TTGGG    TGGTCGAGA   TCC
                                  ____        GGA
GAM636   LOC219920 5'  CCTGGGTGCTCGCTGTGGGT   93307        ATC   _
                                ACCCGTAG   AGT TCTAGG
                                ||||||||   ||| ||||||
                                TGGGTGTC   TCG GGGTCC
                                     GC_   T
GAM636   LOC220032 3'  CTTGGAACTGGTTGC       91669     G
                                GTA ATCAGTTCTAGG
                                ||| ||||||||||||
                                CGT TGGTCAAGGTTC
                                  _
GAM636   LOC220164 3'  CCTGGACCCGTCTGTGGG    91797         CA  T
                                CCCGTAGAT  GT CTAGG
                                |||||||||  || |||||
                                GGGTGTCTG  CA GGTCC
                                     CC  _
GAM636   LOC220705 3'  GCCGGGAACTTGCGGGTT    91228        GATC     A
                                AACCCGTA    AGTTCT GG
                                ||||||||    |||||| ||
                                TTGGGCGT    TCAAGG CC
                                     _____     G  GG
GAM636   LOC221061 3'  TCTGGAATCCTATGGG      93222        ATCA
                                CCCGTAG    GTTCTAGG
                                |||||||    ||||||||
                                GGGTATC    TAAGGTCT
                                   C___
GAM636   LOC221477 3'  CCTGTTTGTCTATGGG      92150         T   TTC
                                CCCGTAGA CAG   TAGG
                                |||||||| |||   ||||
                                GGGTATCT GTT   GTCC
                                     _   T__
GAM636   LOC221683 3'  TCTAGAACTCTTTGTAGGTT   93718      CG    TC
                                AACC  TAGA  AGTTCTAGG
                                ||||  ||||  |||||||||
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                                TTGG  GTTT  TCAAGATCT
                                  AT    C_
GAM636   LOC221683 3'  TTTGGGATGTGATTAGGGTT   93721      GTA    _
                                AACCC   GATCA GTTCTAGG
                                |||||   ||||| ||||||||
                                TTGGG   TTAGT TAGGGTTT
                                  A__    G
GAM636   LOC221922 5'  TTTGGAGCCCGATGGGT     92708       AGATCA
                                ACCCGT     GTTCTAGG
                                ||||||     ||||||||
                                TGGGTA     CGAGGTTT
                                   GCC___
GAM636   LOC222183 3'  TCTGGGGTCTGGTCCGGGTT   94169       TA     _
                                AACCCG  GATCAG TTCTAGG
                                ||||||  |||||| |||||||
                                TTGGGC  CTGGTC GGGGTCT
                                   __     T
GAM636   LOC253502 3'  TCTGCCTGGCCTGTGGGTT    94582        AT   TTC
                                AACCCGTAG  CAG   TAGG
                                |||||||||  |||   ||||
                                TTGGGTGTC  GTC   GTCT
                                     CG   C__
GAM636   LOC253868 3'  CTTAGGGCTCTCTCGGG     95582     T   TC
                                CCCG AGA  AGTTCTAGG
                                |||| |||  |||||||||
                                GGGC TCT  TCGGGATTC
                                  _   C_
GAM636   LOC254050 3'  TTGTGATACTTATCTGTGGGTT 94890          C   _  TAGG
                                AACCCGTAGAT AGT TC
                                |||||||||||| ||| ||
                                TTGGGTGTCTA TCA AG
                                      T   T  TGTTT
GAM636   LOC254394 3'  TTTGGAATTGAGAAGGGT    95985     GTAGA
                                ACCC    TCAGTTCTAGG
                                ||||    ||||||||||
                                TGGG    AGTTAAGGTTT
                                  AAG__
GAM636   LOC255328 3'  CTTGGCCTTTTTATGGGT    96559        TC  TT T
                                ACCCGTAGA  AG  C AG
                                |||||||||  ||  | ||
                                TGGGTATTT  TC  G TC
                                     T_  CG T
GAM636   LOC255465 3'  TTTGGCCCTTGGTCTGTGG   97311         _ TT
                                CCGTAGATCA G  CTAGG
                                ||||||||||  |  |||||
                                GGTGTCTGGT C  GGTTT
                                      T CC
GAM636   LOC256073 3'  TCTGGGGCTGAAGGCTGGG   96668     _  AGA
                                CCC GT   TCAGTTCTAGG
                                ||| ||   ||||||||||
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                                GGG CG   AGTCGGGGTCT
                                  T  GA_
GAM636   LOC256158 5'  CCTGGAGCCGGTGGAGTT    97659     _ GTAG   A
                                AAC CC    ATC GTTCTAGG
                                ||| ||    ||| ||||||||
                                TTG GG    TGG CGAGGTCC
                                  A _____   C
GAM636   LOC256394 3'  CCTGGGGCTGCTATGTGGTT   94941      _    AT
                                AACC CGTAG  CAGTTCTAGG
                                |||| |||||  ||||||||||
                                TTGG GTATC  GTCGGGGTCC
                                  T    __
GAM636   LOC256581 5'  TTTGGGGCTGGGCTGGT     97574     C  AGA
                                ACC GT   TCAGTTCTAGG
                                ||| ||   ||||||||||
                                TGG CG   GGTCGGGGTTT
                                  T  ___
GAM636   LOC256878 5'  CCTGGAGCTGGGCGG      96901     AGA
                                CCGT   TCAGTTCTAGG
                                ||||   ||||||||||
                                GGCG   GGTCGAGGTCC
                                   ___
GAM636   LOC256980 3'  CCTGGAGCTCAGATGGGT    95218       AGATC
                                ACCCGT    AGTTCTAGG
                                ||||||    ||||||||
                                TGGGTA    TCGAGGTCC
                                   GAC__
GAM636   LOC257041 5'  TCTGGGGCTGGCAGAGCGG   97495     AGA_
                                CCGT    TCAGTTCTAGG
                                ||||    ||||||||||
                                GGCG    GGTCGGGGTCT
                                  AGAC
GAM636   LOC257222 5'  TCTGGAGCTCCTCTGTGG    97594       TC
                                CCGTAGA  AGTTCTAGG
                                |||||||  ||||||||
                                GGTGTCT  TCGAGGTCT
                                    CC
GAM636   LOC257354 3'  CCTGGGACCATGTGGG      95088       GATCA
                                CCCGTA    GTTCTAGG
                                ||||||    ||||||||
                                GGGTGT    CAGGGTCC
                                   AC___
GAM636   LOC51019  5'  TCTGGGAGGGGTTTGTGGGT  32128         AG
                                ACCCGTAGATC  TTCTAGG
                                ||||||||||  |||||||
                                TGGGTGTTTGG  AGGGTCT
                                      GG
GAM636   LOC51068  5'  TCTATTTTGTTGCGGGTT    31948        AT   TTC
                                AACCCGTAG  CAG   TAGG
                                |||||||||  |||   ||||
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                              TTGGGCGTT  GTT   ATCT
                                 __   TT_
GAM636  LOC51149  3' TCTGGGACTGGCAGGTT    32446     C  AGAT
                              AACC GT    CAGTTCTAGG
                              |||| ||    ||||||||||
                              TTGG CG    GTCAGGGTCT
                                A  ____
GAM636  LOC51161  3' TCTAATGAGGATCTGGGGTT  32518      G     AGTTC
                              AACCC TAGATC     TAGG
                              ||||| ||||||     ||||
                              TTGGG GTCTAG     ATCT
                                 _     GAGTA
GAM636  LOC51177  3' TCTGGAACTTGTCGGGTT    32775      GTA   C
                              AACCC   GAT AGTTCTAGG
                              |||||   ||| |||||||||
                              TTGGG   CTG TCAAGGTCT
                                 ___   T
GAM636  LOC51657  3' CCTGGGGGGCATTTTGTGGGT  32226         TCAG
                              ACCCGTAGA    TTCTAGG
                              |||||||||    |||||||
                              TGGGTGTTT    GGGGTCC
                                   TACG
GAM636  LOC51716  3' CCTGGGGCTGGACGAGGTT   32790     _  AGA
                              AACC CGT   TCAGTTCTAGG
                              |||| |||   ||||||||||
                              TTGG GCA   GGTCGGGGTCC
                                A  ___
GAM636  LOC63923  3' CTTGGGGCGGGGTGGGT     67120     GTAG  A_
                              ACCC    ATC  GTTCTAGG
                              ||||    |||  ||||||||
                              TGGG    TGG  CGGGGTTC
                                 _____  GG
GAM636  LOC83468  5' TTTGGGACTTCCAATGGG    48519      A_  TC
                              CCCGT  GA  AGTTCTAGG
                              |||||  ||  |||||||||
                              GGGTA  CT  TCAGGGTTT
                                 AC  __
GAM636  LOC89985  5' CTGGGAGCTACTCTGTGGG   61018         TC     AGG
                              CCCGTAGA  AGTTCT
                              ||||||||  ||||||
                              GGGTGTCT  TCGAGG
                                   CA     GTCT
GAM636  LOC90488  3' CTTAGAATCATCTATGG     63033         CA
                              CCGTAGAT  GTTCTAGG
                              ||||||||  ||||||||
                              GGTATCTA  TAAGATTC
                                   C_
GAM636  LOC90785  3' CTGGAGCTGCTGGTT       64016      C TAGAT
                              AACC G     CAGTTCTAG
                              |||| |     |||||||||
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                              TTGG C    GTCGAGGTC
                                T _____
GAM636  LOC91010  3' CCTGGAATTGGCCAAGGG   64614    GTAGA
                              CCC    TCAGTTCTAGG
                              |||    ||||||||||
                              GGG    GGTTAAGGTCC
                                AACC_
GAM636  LOC91064  5' TCTGGGTTCTGTGTGGGTT   64767      TAGAT  T_
                              AACCCG    CAG  TCTAGG
                              ||||||    |||  ||||||
                              TTGGGT    GTC  GGGTCT
                                 GT___   TT
GAM636  LOC91133  3' CTTAGGCCCATCTGTGGGTT  65011         CA  T
                              AACCCGTAGAT  GT CTAGG
                              ||||||||||  || |||||
                              TTGGGTGTCTA  CG GATTC
                                    CC  _
GAM636  LOC91301  5' TCTAGGAGTGTATCTGGGGTT 65549     G    _ G
                              AACCC TAGAT CA TTCTAGG
                              ||||| ||||| || |||||||
                              TTGGG GTCTA GT AGGATCT
                                 _    T  G
GAM636  LOC91397  5' CCTGGGGCTGAGAGGTT    65908     CGTAGA
                              AACC     TCAGTTCTAGG
                              ||||     ||||||||||
                              TTGG     AGTCGGGGTCC
                                AG____
GAM636  LOC91768  3' CCTGGGGCGTGTGGGT     67112     TAGAT  _
                              ACCCG    CA GTTCTAGG
                              |||||    || ||||||||
                              TGGGT    GT CGGGGTCC
                                 _____  G
GAM636  LOC92126  5' CCTGGAAAAAATATGGGTT   68221       GATCAG
                              AACCCGTA     TTCTAGG
                              ||||||||     |||||||
                              TTGGGTAT     AAGGTCC
                                   AAAA__
GAM636  LOC92162  3' TCTGGGGCTGGGGGGCGGG   68364     AGA
                              CCCGT   TCAGTTCTAGG
                              |||||   ||||||||||
                              GGGCG   GGTCGGGGTCT
                                 GGG
GAM636  LOC92230  5' TCTGGGGCCTGACACGAGTT  68547    C   AGA   _
                              AAC CGT   TCAG TTCTAGG
                              ||| |||   |||| |||||||
                              TTG GCA   AGTC GGGGTCT
                                A   C__    C
GAM636  LOC92360  5' CCTAGGATTCTAGGATATGGGT 69071       GATC__
           T                   AACCCGTA     AGTTCTAGG
                              ||||||||     |||||||||
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                                TTGGGTAT     TTAGGATCC
                                     AGGATC
GAM636  LOC92539  5' CTTAGAACTGGGGGCATGGTT  69635     C_  AGA
                                AACC  GT   TCAGTTCTAGG
                                ||||  ||   ||||||||||
                                TTGG  CG   GGTCAAGATTC
                                  TA  GG_
GAM636  LOC92714  3' CCTGGGGCTGGGGTGGGGGT   70374     G  GA
                                ACCC TA  TCAGTTCTAGG
                                |||| ||  ||||||||||
                                TGGG GT  GGTCGGGGTCC
                                  G  GG
GAM636  LOC93017  3' CCTGGAGTGTGCTGCGGGTT   71153        AT  G
                                AACCCGTAG  CA TTCTAGG
                                |||||||||  || |||||||
                                TTGGGCGTC  GT GAGGTCC
                                     GT  _
GAM636  LOC96573  3' CTTGGAGCACTGCTGGTT    63171     C    ATCA
                                AACC GTAG    GTTCTAGG
                                |||| ||||    ||||||||
                                TTGG CGTC    CGAGGTTC
                                  T    A___
GAM637  AKAP13    3' GGAAGCACTCACCCCCCA    89684    AA  T     TCTGT  _
                                TG  GG GTGAGT    GCT CC
                                ||  || ||||||    ||| ||
                                AC  CC CACTCA    CGA GG
                                 CC  _     _____   A
GAM637  H3F3B     3' AGGAGCACAAAACTCCAGCC   18019     GT    C
                                GGT  GAGTT TGTGCTCCT
                                |||  ||||| |||||||||
                                CCG  CTCAA ACACGAGGA
                                  AC    A
GAM637  RASD1     3' AGGAACACAAAACAAAACTTGC 32220    A   GTGA  C   C
           A                     TG AGGT    GTT TGTG TCCT
                                || ||||    ||| |||| ||||
                                AC TTCA    CAA ACAC AGGA
                                 G   AAA_   A   A
GAM637  SLC6A3    5' GAGCACAGAATTCCTCA     6449     T_        C
                                TG  GAGTTCTGTGCT C
                                ||  ||||||||||| |
                                AC  CTTAAGACACGA G
                                 TC          A
GAM637  SLC9A6    3' GAGCACAGAACAATTTCTCA   21004     A  T  GA
                                TGA GG GT  GTTCTGTGCTC
                                ||| || ||  ||||||||||
                                ACT CT TA  CAAGACACGAG
                                  _  T  A_
GAM637  AF311304  3' ACAAAACTCACACTCTCA    48329     AG       C
                                TGA  GTGTGAGTT TGT
                                |||  ||||||||| |||
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                                ACT  CACACTCAA ACA
                                  CT        A
GAM637  DKFZp434O0320 3'  AGGAGCACAGAAAGGTTTACAT 83692          ___
            C                      GGTGTGAG   TTCTGTGCTCCT
                                   ||||||||   ||||||||||||
                                   CTACATTT   AAGACACGAGGA
                                       GGA
GAM637  FLJ11125  3'  CATCTGTGCCACCACCTTCA   59579         _ A  TCT_
                                   TGAAGGTG TG GT    GTG
                                   |||||||| || ||    |||
                                   ACTTCCAC AC CG    TAC
                                       C  _  TGTC
GAM637  FLJ11286  3'  AGGAACACAGAGTCACAGCTTC 37215       G    G      C
            A                      TGAAG TGTGA TTCTGTG TCCT
                                   ||||| ||||| ||||||| ||||
                                   ACTTC ACACT GAGACAC AGGA
                                      G     _      A
GAM637  FLJ13110  3'  AGGAGCACCTGTGGCTCACACC 43297            CT__
            TTC                      GAAGGTGTGAGTT    GTGCTCCT
                                   ||||||||||||||    ||||||||
                                   CTTCCACACTCGG    CACGAGGA
                                          TGTC
GAM637  FLJ13912  3'  GAACACAGAATGGCTCCTCA   42861     A  T  GA       C
                                   TGA GG GT  GTTCTGTG TC
                                   ||| || ||  |||||||| ||
                                   ACT CC CG  TAAGACAC AG
                                     _  T  G_       A
GAM637  FLJ20013  3'  AGGAGCACAGAACAGGGCCT   34328      GTGA
                                   AGGT    GTTCTGTGCTCCT
                                   ||||    ||||||||||||||
                                   TCCG    CAAGACACGAGGA
                                     GGA_
GAM637  KIAA0182  3'  GAGCCCACACCTTCA       72027          AGTTCTGT
                                   TGAAGGTGTG       GCTC
                                   ||||||||||       ||||
                                   ACTTCCACAC       CGAG
                                         C________
GAM637  KIAA1666  3'  AGAAGCAAGCGTTCAGACCCTC 65248     A   G    TT  G    C
            A                      TGA GGT TGAG  CT TGCT CT
                                   ||| ||| ||||  || |||| ||
                                   ACT CCA ACTT  GA ACGA GA
                                     C   G    GC  _    A
GAM637  MFN2      3'  GAGCTGGCTCATACCCCCA   29600     AA        CTGT
                                   TG  GGTGTGAGTT    GCTC
                                   ||  ||||||||||    ||||
                                   AC  CCATACTCGG    CGAG
                                    CC         T___
GAM637  SCYA11    5'  GCCAAAGCTCACACCTTCA   11455             C  T
                                   TGAAGGTGTGAGTT TG GC
                                   |||||||||||||| || ||
```

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                                ACTTCCACACTCGA AC CG
                                       A  _
GAM637  SIRPB1   3'  AGAAACTCTCACACTCTCA   20240     AG      ___
                                TGA  GTGTGAG   TTCT
                                |||  |||||||   ||||
                                ACT  CACACTC   AAGA
                                  CT       TCA
GAM637  TREX1    5'  AGAAGCACAGAACCTGGCATTC 53275     AG   G  _       C
           A                     TGA  GTGT AG TTCTGTGCT CT
                                |||  |||| || |||||||||  ||
                                ACT  TACG TC AAGACACGA GA
                                  __   G  C        A
GAM637  TREX1    5'  AGAAGCACAGAACCTGGCATTC 53286     AG   G  _       C
           A                     TGA  GTGT AG TTCTGTGCT CT
                                |||  |||| || |||||||||  ||
                                ACT  TACG TC AAGACACGA GA
                                  __   G  C        A
GAM637  LOC120105 5'  AGCACAGGTCACCATCA     75512     A    TGAGT
                                TGA GGTG    TCTGTGCT
                                |||  ||||    ||||||||
                                ACT CCAC    GGACACGA
                                  A   T____
GAM637  LOC146443 5'  AGGGGCACCACCCCCA      77881     AA    TGAGTTCT
                                TG  GGTG       GTGCTCCT
                                ||  ||||       ||||||||
                                AC  CCAC       CACGGGGA
                                 CC   _________
GAM637  LOC150095 5'  AGGAGGCAGCCACCCACACCTT 84853          A  T_   G
           C                     GAAGGTGTG GT  CTGT CTCCT
                                |||||||||  ||  |||| |||||
                                CTTCCACAC CA  GACG GAGGA
                                     C  CC   _
GAM637  LOC150221 3'  AGAAGCAAGCGTTCAGACCCTC 65274     A   G    TT  G    C
           A                     TGA GGT TGAG  CT TGCT CT
                                |||  ||| ||||  ||  |||| ||
                                ACT CCA ACTT  GA ACGA GA
                                  C   G    GC  _   A
GAM637  LOC221263 3'  AGAGCCCCACCACCTTCA     93612         _  A_
                                TGAAGGTG TG  GTTCT
                                ||||||||  ||  |||||
                                ACTTCCAC AC  CGAGA
                                     C  CC
GAM637  LOC257396 5'  GGAGCATCTCAGACCTTCA    97138        G    TTCT
                                TGAAGGT TGAG    GTGCTCC
                                |||||||  ||||    |||||||
                                ACTTCCA ACTC    TACGAGG
                                    G   _____
GAM637  LOC54516  3'  AGAACCTCACACTCCCA     38758     AA      _
                                TG  GGTGTGAG TTCT
                                ||  ||||||||  ||||
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                                AC  TCACACTC AAGA
                                 CC       C
GAM637  LOC96652  3'  AGCTCAGAACTCCACCTCCA  65463    A    T      T
                                TG AGGTG GAGTTCTG GCT
                                || ||||| |||||||| |||
                                AC TCCAC CTCAAGAC CGA
                                 C    _       T
GAM638  ARNT2     3'  AAACAACCCGTGCATCCCTGC  29450    A   TTTTA
                                GTA GGAT    GGGTTGTTT
                                ||| ||||    |||||||||
                                CGT CCTA    CCCAACAAA
                                  C   CGTG_
GAM638  LCT       3'  AACCGTAAAAATCCTT      9697          G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
                                TTCCTAAAAAT CCAA
                                       G
GAM638  RPL15     3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM638  FBXO30    3'  AACTAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                 G        AA
GAM638  KIAA0494  3'  AACAACCCTTACTTAC      28736      GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM638  PRO0641   5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                   ___    C
GAM638  SMT3H2    3'  AACAACATAAAAATCCTTGC   22670          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM638  LOC120103 3'  AACCTATGAAAAATCCTTGC   74002          A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
                                CGTTCCTAAAAA   TCCAA
                                       GTA
GAM638  LOC129831 3'  AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
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                                CCTG  AA CCCAACAAA
                                  T_  C
GAM638  LOC133088 5'  AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                        GTA GGATTTTT     TTGTTT
                                   ||| ||||||||     ||||||
                                   CGT CCTAAAAA     AACAAA
                                     C       GATAA
GAM638  LOC148089 3'  GGCCCTAAAAATTCCTAC     78637     A
                                   GTA GGATTTTTAGGGTT
                                   ||| ||||||||||||||
                                   CAT CTTAAAAATCCCGG
                                     C
GAM638  LOC154547 3'  AACAACATAAAAATCCTTGC   76050           GG
                                   GTAAGGATTTTTA  GTTGTT
                                   ||||||||||||  ||||||
                                   CGTTCCTAAAAAT  CAACAA
                                          A_
GAM638  LOC158104 3'  ACAGCCAAAAATCCTTA      60313           AG
                                   TAAGGATTTTT  GGTTGT
                                   ||||||||||  ||||||
                                   ATTCCTAAAAA  CCGACA
                                          __
GAM638  LOC205880 5'  AAACAACCATCATCCTGAC    90709    A    TTTTAG
                                   GT AGGAT     GGTTGTTT
                                   || |||||     ||||||||
                                   CA TCCTA     CCAACAAA
                                    G    CTA___
GAM638  LOC221561 3'  AACAACATAAAAATCCTTGC   92130           GG
                                   GTAAGGATTTTTA  GTTGTT
                                   ||||||||||||  ||||||
                                   CGTTCCTAAAAAT  CAACAA
                                          A_
GAM638  LOC257591 3'  AACAACATAAAAATCCTTGC   97840           GG
                                   GTAAGGATTTTTA  GTTGTT
                                   ||||||||||||  ||||||
                                   CGTTCCTAAAAAT  CAACAA
                                          A_
GAM638  LOC51145  3'  AGCTAAAATCCTTAC        32393           TAG
                                   GTAAGGATTTT   GGTT
                                   ||||||||||   ||||
                                   CATTCCTAAAA   TCGA
                                          ___
GAM639  CNGA1     3'  CAACTGATAATGTGCAAA     59507          GC   A
                                   TTTGCACATTA  TAG TTG
                                   ||||||||||  ||| |||
                                   AAACGTGTAAT  GTC AAC
                                          A_  _
GAM639  ESRRG     3'  TGGCAGTCTTATGTGCAAA    66396         TAGCT
                                   TTTGCACAT    AGATTGCCA
                                   |||||||||    |||||||||
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                                AAACGTGTA    TCTGACGGT
                                     T____
GAM639  KCNJ3    3'  GCAATAATGTGCAAA      9525          GCTAGA
                                TTTGCACATTA     TTGC
                                ||||||||||     ||||
                                AAACGTGTAAT     AACG
                                      _______
GAM639  SDC2     3'  GCAAATTAATGTGTAAA     67132          CTAGA
                                TTTGCACATTAG    TTGC
                                ||||||||||||    ||||
                                AAATGTGTAATT    AACG
                                     A____
GAM639  USP9X    3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
              A                  TTTGCACATTAGC     GCCAT
                                ||||||||||||     |||||
                                AAATGTGTAATCG     CGGTA
                                      TAGTC_
GAM639  AMOTL1   3'  GGCAAGTAATGTGCAAA     73650          G  AGAT
                                TTTGCACATTA CT    TGCC
                                |||||||||| ||    ||||
                                AAACGTGTAAT GA    ACGG
                                      _ ____
GAM639  BCAR3    3'  AGTAATAATGTGCAAA      13098          __
                                TTTGCACATTA  GCT
                                ||||||||||  |||
                                AAACGTGTAAT  TGA
                                      AA
GAM639  DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930          AGCTA    C
                                TTTGCACATT    GATTG CA
                                |||||||||     ||||| ||
                                AGACGTGTAA    TTAAC GT
                                     A____    A
GAM639  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                TTTGCACATTAG  AGA TG CAT
                                ||||||||||  ||| || |||
                                AGACGTGTAATC  TTT AC GTA
                                      __  T  A
GAM639  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
              AA                  TTTGCACATTAGCTAGATTGCCAT
                                ||||||||||||||||||||||||
                                AAACGTGTAATCGATCTAACGGTA

GAM640  MS4A4A   3'  CTCCATGCAAAACACATA    43781        GTCG   GGTA
                                TATGTGTT   TGCA   GAG
                                ||||||||   ||||   |||
                                ATACACAA   ACGT   CTC
                                     A___    AC__
GAM640  PPP2R5D  3'  CCCTACCTGCTCCTCACCCACA 20716      T_  TCGT      A
                                TGTG  TG   GCAGGTAG GG
                                ||||  ||   |||||||| ||
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                                ACAC  AC    CGTCCATC CC
                                  CC  TCCT      _
GAM640  FLJ00058  5'  ACCCACGCACACACACA     78762       _  _    CA
                                TGTGT TGT CGTG  GGT
                                ||||| ||| ||||  |||
                                ACACA ACA GCAC  CCA
                                   C  C   __
GAM640  KIAA0397  3'  TCTACCCCAACACATG      61678         TCGTGCA
                                TATGTGTTG      GGTAGA
                                |||||||||      ||||||
                                GTACACAAC      CCATCT
                                     C_______
GAM640  KIAA0544  3'  CTCTCCCCAACAACACA     70902         CG  CA  T
                                TGTGTTGT  TG  GG AGAG
                                ||||||||  ||  || ||||
                                ACACAACA  AC  CC TCTC
                                    __  C_  _
GAM640  RAB4B     5'  CCTGGCCCACAACAACACA   32375         C   CA   AG
                                TGTGTTGT GTG  GGT  AGG
                                ||||||| |||  |||  |||
                                ACACAACA CAC  CCG  TCC
                                    A   __   G_
GAM640  SR-BP1    3'  CTTTTACACACACACAACACAT 19633          C   CAG
          A                      TATGTGTTGT GTG   GTAGAGG
                                ||||||||| |||   |||||||
                                ATACACAACA CAC   CATTTTC
                                     _   ACA
GAM640  LOC147463 3'  CTCTACCCAAGAACCATA    78371      T   GTCG  CA
                                TATG GTT    TG  GGTAGAG
                                |||| |||    ||  |||||||
                                ATAC CAA    AC  CCATCTC
                                  _   GA__  __
GAM640  LOC219513 3'  CTCTACCTGTTCAACAACA   94327        CGT
                                TGTTGT   GCAGGTAGAG
                                ||||||   ||||||||||
                                ACAACA   TGTCCATCTC
                                   ACT
GAM640  LOC253609 3'  CCTCCACCTTCTAAACACATA  96760         GTCGTGC   A
                                TATGTGTT      AGGT GAGG
                                ||||||||      |||| ||||
                                ATACACAA      TCCA CTCC
                                    ATCT___    C
GAM640  LOC51336  3'  CCTCTACTAAAAACACACACAC 33577       _  C  GCA_
          A                      TGTGT TGT GT    GGTAGAGG
                                ||||| ||| ||    ||||||||
                                ACACA ACA CA    TCATCTCC
                                  C   _  AAAA
GAM640  LOC91782  3'  GCCACACAACAACACA      67155         C   CA
                                TGTGTTGT GTG  GGT
                                |||||||| |||  |||
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                                ACACAACA CAC  CCG
                                    A  A_
GAM641  ALS2    3'  AACATAGGTGCTCTTCCTCA  40504       T  TGGAT
                                TGAGGAAGA GT    TGTT
                                ||||||||| ||    ||||
                                ACTCCTTCT CG    ACAA
                                    _ TGGAT
GAM641  CTGF    3'  AATAGTCTATCTTCCCCA   8573    A     GTT
                                TG GGAAGAT  GGATTGTT
                                || |||||||  ||||||||
                                AC CCTTCTA  TCTGATAA
                                 C     ___
GAM641  DNAJB9  3'  AACTGGTTGACTCTTCCTCA  24676       T  TG ATT
                                TGAGGAAGA GT  G  GTT
                                ||||||||| ||  |  |||
                                ACTCCTTCT CA  T  CAA
                                    _ GT GGT
GAM641  EPO     3'  ATCCACCACCTCCCTCA    5853      A  A  T
                                TGAGG AG TG TGGAT
                                ||||| || || |||||
                                ACTCC TC AC ACCTA
                                   C  C  C
GAM641  FGF23   3'  AACAACAGCTTCTTCCCA   40191   A    T   GA
                                TG GGAAGA GTTG  TTGTT
                                || |||||| ||||  |||||
                                AC CCTTCT CGAC  AACAA
                                 _     T   __
GAM641  GCS1    3'  AATTCAAACCTTCCTCA    20867       ATG
                                TGAGGAAG  TTGGATT
                                ||||||||  |||||||
                                ACTCCTTC  AACTTAA
                                    CA_
GAM641  GPR48   3'  TCCATACATCTTCCCCA    37504   A      _
                                TG GGAAGATGT TGGA
                                || ||||||||| ||||
                                AC CCTTCTACA ACCT
                                 C       T
GAM641  HNRPH2  3'  AACAATTTTTAGCTTTCCTCA  38975       ATGTT
                                TGAGGAAG    GGATTGTT
                                ||||||||    ||||||||
                                ACTCCTTT    TTTAACAA
                                    CGATT
GAM641  IL17    3'  AACATTTTTCTCTTCCTCA   9328        TGTT  T
                                TGAGGAAGA   GGA TGTT
                                |||||||||   ||| ||||
                                ACTCCTTCT   TTT ACAA
                                    CT__  T
GAM641  KIT     3'  AACAAAAAACTCCCCTTCCTCA 4038       AT__  GGA
                                TGAGGAAG   GTT  TTGTT
                                ||||||||   |||  |||||
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                                ACTCCTTC   CAA  AACAA
                                    CCCT  AA_
GAM641  MAPT     3' ATCCAACATTTCCTCA     33705      A
                                TGAGGA GATGTTGGAT
                                |||||| ||||||||||
                                ACTCCT TTACAACCTA
                                   _
GAM641  MAPT     3' ATCCAACATTTCCTCA     19775      A
                                TGAGGA GATGTTGGAT
                                |||||| ||||||||||
                                ACTCCT TTACAACCTA
                                   _
GAM641  MAPT     3' ATCCAACATTTCCTCA     33686      A
                                TGAGGA GATGTTGGAT
                                |||||| ||||||||||
                                ACTCCT TTACAACCTA
                                   _
GAM641  MAPT     3' ATCCAACATTTCCTCA     33695      A
                                TGAGGA GATGTTGGAT
                                |||||| ||||||||||
                                ACTCCT TTACAACCTA
                                   _
GAM641  NR5A2    3' AATTCAAATCTTCCCCA    13788    A     G
                                TG GGAAGAT TTGGATT
                                || ||||||| |||||||
                                AC CCTTCTA AACTTAA
                                 C     _
GAM641  PIK3CG   5' TCCAACATCTTCTCA      10589    G
                                TGAG AAGATGTTGGA
                                |||| ||||||||||
                                ACTC TTCTACAACCT
                                   _
GAM641  PPP2R2B  3' AACAATCCATCAACCTC    15903     AA  TGT
                                GAGG  GA   TGGATTGTT
                                ||||  ||   |||||||||
                                CTCC  CT   ACCTAACAA
                                  AA  ____
GAM641  RBM8A    3' AACAATCCTGCTTTCTCA    17541       ATGTT
                                TGAGGAAG    GGATTGTT
                                ||||||||    ||||||||
                                ACTCTTTC    CCTAACAA
                                    GT____
GAM641  SLA2     3' AACAATTCTCCTGCCTCA    49888     A  ATGTT
                                TGAGG AG    GGATTGTT
                                ||||| ||    ||||||||
                                ACTCC TC    CTTAACAA
                                  G  CT____
GAM641  XPR1     3' AACAAATTATACTTCCTCA   16423       A   TGGA
                                TGAGGAAG TGT    TTGTT
                                |||||||| |||    |||||
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                                ACTCCTTC ATA    AACAA
                                     _  TTA_
GAM641  YWHAE    3' AACAATCCGTGGCTGCTCA   22193     GA  ATGT
                                TGAG  AG   TGGATTGTT
                                ||||  ||   |||||||||
                                ACTC  TC   GCCTAACAA
                                  G_  GGT_
GAM641  ALTE     3' AACAATCCTTTGCTTTTCCTCA 16386        T  T__
                                TGAGGAAGA GT   GGATTGTT
                                ||||||||| ||   ||||||||
                                ACTCCTTTT CG   CCTAACAA
                                     _ TTT
GAM641  AQP10    3' AACAGTCATTCTTCCTC     54428        TGTTG
                                GAGGAAGA    GATTGTT
                                ||||||||    |||||||
                                CTCCTTCT    CTGACAA
                                    TA___
GAM641  ARHGEF9  3' TCCAACATCCTCTCA      30821      AA
                                TGAGG  GATGTTGGA
                                |||||  |||||||||
                                ACTCT  CTACAACCT
                                  C_
GAM641  BTN3A1   3' AACAATTCTCCTGCCTCA    22913      A  ATGTT
                                TGAGG AG    GGATTGTT
                                ||||| ||    ||||||||
                                ACTCC TC    CTTAACAA
                                  G  CT___
GAM641  CL683    3' AACAATCCAAACAATACCTCA  31648      AAGATG
                                TGAGG     TTGGATTGTT
                                |||||     ||||||||||
                                ACTCC     AACCTAACAA
                                  ATAACA
GAM641  FLJ11539 3' TTCAACATTTCCTCA       45383       A
                                TGAGGA GATGTTGGA
                                |||||| |||||||||
                                ACTCCT TTACAACTT
                                     _
GAM641  FLJ12476 3' AACAATCCCTTCTTCTTC    42947        TGTT
                                GAGGAAGA   GGATTGTT
                                ||||||||   ||||||||
                                CTTCTTCT   CCTAACAA
                                    TC__
GAM641  FLJ25415 3' ACAATCCAACGGCTCT      58493     AGA
                                GGA   TGTTGGATTGT
                                |||   ||||||||||
                                TCT   GCAACCTAACA
                                  CG_
GAM641  FYCO1    3' ACACTGCTCTTCCTCA      44483        T  TGGAT
                                TGAGGAAGA GT    TGT
                                ||||||||| ||    |||
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                                ACTCCTTCT CG    ACA
                                     _ TC___
GAM641  KIAA0854 3' AACAATAAGATCTTCCT    30096       G GG
                                AGGAAGAT TT  ATTGTT
                                |||||||| ||  ||||||
                                TCCTTCTA AA  TAACAA
                                    G __
GAM641  KIAA1026 3' AACAATTCTCCTGCCTCA    71185     A ATGTT
                                TGAGG AG    GGATTGTT
                                ||||| ||    ||||||||
                                ACTCC TC    CTTAACAA
                                  G CT___
GAM641  KRTAP4-12 3' TCCAACATCCTCCCA      49010    A  A
                                TG GGA GATGTTGGA
                                || ||| |||||||||
                                AC CCT CTACAACCT
                                 _  C
GAM641  LY117    3' CCAGACACCTTCCTCA      92351       A  _
                                TGAGGAAG TGT TGG
                                |||||||| ||| |||
                                ACTCCTTC ACA ACC
                                    C  G
GAM641  LY117    3' CCAGACACCTTCCTCA      97745       A  _
                                TGAGGAAG TGT TGG
                                |||||||| ||| |||
                                ACTCCTTC ACA ACC
                                    C  G
GAM641  LY117    3' CCAGACACCTTCCTCA      97846       A  _
                                TGAGGAAG TGT TGG
                                |||||||| ||| |||
                                ACTCCTTC ACA ACC
                                    C  G
GAM641  MEF-2    3' AACAATTCTCCTGCCTCA    64373     A ATGTT
                                TGAGG AG    GGATTGTT
                                ||||| ||    ||||||||
                                ACTCC TC    CTTAACAA
                                  G CT___
GAM641  MGC10200 3' AACAATCCACCCTCCTCA    58979      AGAT  T
                                TGAGGA   GT GGATTGTT
                                ||||||   || ||||||||
                                ACTCCT   CA CCTAACAA
                                   CC__  _
GAM641  MYH10    3' AACAGATGCCATCTTCCT    69137       TT GA
                                AGGAAGATG  G  TTGTT
                                |||||||||  |  |||||
                                TCCTTCTAC  T  GACAA
                                     CG A_
GAM641  MYO5C    3' AACAATTCTCCTGCCTCA    38102     A ATGTT
                                TGAGG AG    GGATTGTT
                                ||||| ||    ||||||||
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                                ACTCC TC    CTTAACAA
                                   G  CT___
GAM641  PAK6     3'  AACAAAAGCATCTTCC     39403         GGA
                                GGAAGATGTT   TTGTT
                                ||||||||||  |||||
                                CCTTCTACGA   AACAA
                                     A__
GAM641  PRO0628  5'  AACAAATACTCATCTTCCCA  26204    A      TTGGA
                                TG GGAAGATG    TTGTT
                                || ||||||||    |||||
                                AC CCTTCTAC    AACAA
                                 _      TCATA
GAM641  PRO1600  3'  AACAATTTAACCTTCC     26030      AT
                                GGAAG  GTTGGATTGTT
                                |||||  ||||||||||
                                CCTTC  CAATTTAACAA

                                  __
GAM641  SKIL     5'  AATGTAACTCTTCCCCA     18280    A     T   G
                                TG GGAAGA GTTG ATT
                                || |||||| |||| |||
                                AC CCTTCT CAAT TAA
                                 C     _   G
GAM641  SLC2A13  3'  AATCACTACACCTTCCTCA   53545        A  TG_
                                TGAGGAAG TGT   GATT
                                |||||||| |||   ||||
                                ACTCCTTC ACA   CTAA
                                     C   TCA
GAM641  LOC115219 5'  AACAATTCTCCTGCCTCA    73289      A  ATGTT
                                TGAGG AG    GGATTGTT
                                ||||| ||    ||||||||
                                ACTCC TC    CTTAACAA
                                   G  CT___
GAM641  LOC138311 3'  GGTCCAACCCTCCCTCA     76212      A  AT
                                TGAGG AG  GTTGGATT
                                ||||| ||  ||||||||
                                ACTCC TC  CAACCTGG
                                   C  C_
GAM641  LOC149628 5'  AACAATCCTCATTTCCTACA  79461    _   A   TT
                                TG AGGA GATG  GGATTGTT
                                || |||| ||||  ||||||||
                                AC TCCT TTAC  CCTAACAA
                                 A   _   T_
GAM641  LOC150406 3'  AACAACATGAGCATCCTCCTC  79855      A    _ GA
                                GAGGA GATGTT G  TTGTT
                                ||||| |||||| |  |||||
                                CTCCT CTACGA T  AACAA
                                   C     G AC
GAM641  LOC152282 5'  AACAATCCTTCTTCCTC     80550        TGTT
                                GAGGAAGA   GGATTGTT
                                ||||||||   ||||||||
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                                CTCCTTCT    CCTAACAA
                                     T___
GAM641   LOC169436 5'  AACCCTCCAACATCATCCTCA  82737       A       TT
                                TGAGGA GATGTTGGA  GTT
                                |||||| |||||||||  |||
                                ACTCCT CTACAACCT  CAA
                                    A        CC
GAM641   LOC206012 5'  TCCACCATCTTCCTCA      89525          T
                                TGAGGAAGATG TGGA
                                |||||||||||| ||||
                                ACTCCTTCTAC ACCT
                                       C
GAM641   LOC206012 5'  TCCACCATCTTCCTCA      89526          T
                                TGAGGAAGATG TGGA
                                |||||||||||| ||||
                                ACTCCTTCTAC ACCT
                                       C
GAM641   LOC221830 3'  AACAATTTTAGCCTTTCTCA   92504        AT     _
                                TGAGGAAG  GTTGGA TTGTT
                                ||||||||  |||||| |||||
                                ACTCTTTC  CGATTT AACAA
                                     __      T
GAM641   LOC256683 5'  AACAATCTTCTTGTCTTCCCA  96279    A       TT_
                                TG GGAAGATG   GGATTGTT
                                || ||||||||   ||||||||
                                AC CCTTCTGT   TCTAACAA
                                 _       TCT
GAM641   LOC256895 3'  AACAGTATTCATCTCCTC     96860      A    TTGG
                                GAGGA GATG    ATTGTT
                                ||||| ||||    ||||||
                                CTCCT CTAC    TGACAA
                                   _    TTA_
GAM641   LOC257465 3'  AACAATTCTCCTGCCTCA     81588      A  ATGTT
                                TGAGG AG     GGATTGTT
                                ||||| ||     ||||||||
                                ACTCC TC     CTTAACAA
                                   G  CT___
GAM642   ACN       5'  AACACCCAAGCGCCCC      30367      AAA T  ATCA
                                GGGGC   G CT    GGTGTT
                                |||||   | ||   ||||||
                                CCCCG   C GA    CCACAA
                                   ____ _  AC__
GAM642   CLCN6     3'  AAACACCTCTCTCTCCCC    41379      CAA  TCTATC
                                GGGG   AG     AGGTGTTT
                                ||||   ||     ||||||||
                                CCCC   TC     TCCACAAA
                                   ___  TCTC__
GAM642   CLCN6     3'  AAACACCTCTCTCTCCCC    41394      CAA  TCTATC
                                GGGG   AG     AGGTGTTT
                                ||||   ||     ||||||||
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                                CCCC  TC    TCCACAAA
                                  ___ TCTC__
GAM642  CLCN6   3' AAACACCTCTCTCTCCCC   7072     CAA  TCTATC
                                GGGG  AG    AGGTGTTT
                                ||||  ||    ||||||||
                                CCCC  TC    TCCACAAA
                                  ___ TCTC__
GAM642  CNTN3   3' TATCTGATCAGACTTTGCCCC  66698          _
                                GGGGCAAAGTCT ATCAGGTG
                                |||||||||||| ||||||||
                                CCCCGTTTCAGA TAGTCTAT
                                       C
GAM642  CSRP1   3' CAAACACCTTTCCCTTTGCCCT 14526        TCTATC
                                GGGGCAAAG    AGGTGTTTG
                                |||||||||    |||||||||
                                TCCCGTTTC    TCCACAAAC
                                     CCTT__
GAM642  MYCL2   3' TGATAGATTTTGCCCC     18191
                                GGGGCAAAGTCTATCA
                                ||||||||||||||||
                                CCCCGTTTTAGATAGT

GAM642  NTSR1   3' ACTTCCTGCCAAACTTTGCCCC 10284         CTAT   T_
                                GGGGCAAAGT   CAGG  GT
                                ||||||||||   ||||  ||
                                CCCCGTTTCA   GTCC  CA
                                     AACC    TT
GAM642  RAB26   3' CAAGTGGACAGACTTTGCC   26822         A  AGG_
                                GGCAAAGTCT TC    TG
                                |||||||||| ||    ||
                                CCGTTTCAGA AG    AC
                                     C  GTGA
GAM642  STK10   3' CCTGATAGACCTGCCCC    19984       AA
                                GGGGCA  GTCTATCAGG
                                ||||||  ||||||||||
                                CCCCGT  CAGATAGTCC
                                   C_
GAM642  TCTA    3' CAAACACCCACATACCTGGCCC 42234     AAA  CTATCA
                                GGGC   GT    GGTGTTTG
                                ||||   ||    ||||||||
                                CCCG   CA    CCACAAAC
                                  GTC  TACAC_
GAM642  ELKS    3' CAAACACTACAAACTTCATCCC 30502     CA   CTATCA
                                GGGG  AAGT    GGTGTTTG
                                ||||  ||||    ||||||||
                                CCCT  TTCA    TCACAAAC
                                  AC    AACA__
GAM642  FLJ23537 3' CAAACACCTGCCTCTCTTCAAC 46023    GCA   TCTAT
           CC                   GGG   AAG    CAGGTGTTTG
                                |||   |||    ||||||||||
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                                CCC  TTC    GTCCACAAAC
                                  AAC  TCTCC
GAM642  KIAA0433  5'  CAAACACCTCACCCCTGCCTC  30835      AAGTCTATC
                                GGGGCA       AGGTGTTTG
                                ||||||       |||||||||
                                CTCCGT       TCCACAAAC
                                   CCCCAC___
GAM642  KIAA0450  3'  CACTGCTGATGACTTTGCCCC  27620         T   __
                                GGGGCAAAGTC ATCAG  GTG
                                |||||||||||  |||||  |||
                                CCCCGTTTCAG TAGTC  CAC
                                      _    GT
GAM642  LEAP-2    5'  AAATATAAACTTTGCCCC    53739         CTATCAG
                                GGGGCAAAGT     GTGTTT
                                ||||||||||     ||||||
                                CCCCGTTTCA     TATAAA
                                     AA_____
GAM642  LOC147077 3'  CACCTCCTAATAGACTTAGCCC 78249      A      C___
          C                      GGGGC AAGTCTAT   AGGTG
                                |||||  ||||||||   |||||
                                CCCCG TTCAGATA   TCCAC
                                   A       ATCC
GAM643  ANXA2     3'  CCTGTCTAGTCTCTCCTGT   14458     AAGC   TG
                                ACAG   AGAG  TAGACAGG
                                ||||   ||||  ||||||||
                                TGTC   TCTC  ATCTGTCC
                                  C___   TG
GAM643  BAK1      5'  CTGCCCTCTGCTTCTG      91990         T
                                CAGAAGCAGAG GTAG
                                ||||||||||| ||||
                                GTCTTCGTCTC CGTC
                                      C
GAM643  CHST6     3'  CTGCACTTTCTGCTTCT     41224         __
                                AGAAGCAGA  GTGTAG
                                |||||||||  ||||||
                                TCTTCGTCT  CACGTC
                                     TT
GAM643  DIO3      3'  CCTGGGACTCTGCTTCTGT   7243           GTAGA
                                ACAGAAGCAGAGT    CAGG
                                ||||||||||||    ||||
                                TGTCTTCGTCTCA    GTCC
                                       GG___
GAM643  DNM1      3'  CCTGCCTGGACGGCTGTTCTGT 15320       G   A_  G   A
          GA                     TCACAGAA CAG  GT TAG CAGG
                                ||||||||  |||  || ||| ||||
                                AGTGTCTT GTC  CA GTC GTCC
                                     _  GG  G   C
GAM643  DPP6      3'  CCGCCCACACTAGCCTCTGTG  55446      A  AG    AGACA
                                CACAGA GC  AGTGT    GG
                                ||||||  ||  |||||    ||
```

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                                GTGTCT CG  TCACA    CC
                                   C  A_    CCCG_
GAM643  DPYSL3   3'  CTATCATGCTGCTTCTG     7316          A  _
                                CAGAAGCAG GTG TAG
                                ||||||||| ||| |||
                                GTCTTCGTC TAC ATC
                                     G   T
GAM643  EIF2C1   3'  CCTGCCTGTCTGCCTATGTGA 24171      GAA    GTG   A
                                TCACA   GCAGA   TAG CAGG
                                |||||   |||||   ||| ||||
                                AGTGT   CGTCT   GTC GTCC
                                   ATC    ___   C
GAM643  FOXM1    3'  CTGCCCTTGCCCCTGTG     41704      AA   G  T
                                CACAG  GCA AG GTAG
                                |||||  ||| || ||||
                                GTGTC  CGT TC CGTC
                                   CC   _  C
GAM643  GCNT3    5'  CTGTCTCCCATTCTGT      16456        T_
                                GCAGAGTG  AGACAG
                                ||||||||  ||||||
                                TGTCTTAC  TCTGTC
                                     CC
GAM643  HPN      3'  CCTGTCTAGGTGCCCCTGATGA 9275      _  AA   GAG G
                                TCA CAG  GCA   T TAGACAGG
                                ||| |||  |||   | ||||||||
                                AGT GTC  CGT   G ATCTGTCC
                                  A   CC   ___ G
GAM643  LENG4    3'  CCGCCTACACTCCTACGTG    44163     AGA  CA       ACA
                                CAC   AG  GAGTGTAG   GG
                                |||   ||  ||||||||   ||
                                GTG   TC  CTCACATC   CC
                                  CA_  __       CG_
GAM643  MAGEA12  3'  CTCACTCTATTCTGT       18111        GC     T
                                ACAGAA  AGAGTG AG
                                ||||||  |||||| ||
                                TGTCTT  TCTCAC TC
                                   A_     _
GAM643  PRX      3'  CCCGTCCCTACACTCCTGTT   40526       _     __   A
                                AGCAG AGTGTA  GAC GG
                                ||||| ||||||  ||| ||
                                TTGTC TCACAT  CTG CC
                                   C     CC   C
GAM643  PTPN7    3'  CCTATCAGTGACTCTGCTCCCT 11066     A_       _ TA  C
           G                     CAG  AGCAGAGT G  GA AGG
                                |||  |||||||| |  || |||
                                GTC  TCGTCTCA T  CT TCC
                                  CC       G GA  A
GAM643  PTPN7    3'  CCTATCAGTGACTCTGCTCCCT 54548     A_       _ TA  C
           G                     CAG  AGCAGAGT G  GA AGG
                                |||  |||||||| |  || |||
```

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                                GTC  TCGTCTCA T  CT TCC
                                  CC       G GA  A
GAM643  PTPN7    3'  CCTATCAGTGACTCTGCTCCCT 54559     A_       _ TA  C
              G                    CAG  AGCAGAGT G  GA AGG
                                |||  |||||||| |  || |||
                                GTC  TCGTCTCA T  CT TCC
                                  CC       G GA  A
GAM643  RAP1GA1  3'  CTACCCTGCTTCTTGA      11252     C       AGT
                                TCA AGAAGCAG   GTAG
                                |||  |||||||   ||||
                                AGT TCTTCGTC   CATC
                                  _       C__
GAM643  SHB      3'  CTGCCCTGCTCTGTGA      11640        A    AGT
                                TCACAGA GCAG   GTAG
                                |||||||  ||||   ||||
                                AGTGTCT CGTC   CGTC
                                    _    C__
GAM643  SOX12    3'  CTGTCTAGGCCTCTATGT    22697     GA  C  A  G
                                ACA  AG AG GT TAGACAG
                                |||  || || || |||||||
                                TGT  TC TC CG ATCTGTC
                                  A_  _  _  G
GAM643  SYT1     3'  CATTCACTTCTGTGA       18898         CA
                                TCACAGAAG  GAGTG
                                |||||||||  |||||
                                AGTGTCTTC  CTTAC
                                     A_
GAM643  WBSCR1   3'  CCTGTCAGCTTCTCTGCTTCTG 42226     A         T_  A
              AGA                    TC CAGAAGCAGAG  GT GACAGG
                                ||  ||||||||||  ||  ||||||
                                AG GTCTTCGTCTC  CG CTGTCC
                                 A          TT  A
GAM643  WBSCR1   3'  CCTGTCAGCTTCTCTGCTTCTG 49258     A         T_  A
              AGA                    TC CAGAAGCAGAG  GT GACAGG
                                ||  ||||||||||  ||  ||||||
                                AG GTCTTCGTCTC  CG CTGTCC
                                 A          TT  A
GAM643  C6orf31  3'  CCTGTAAACGCTCTGT      47641          AG
                                GCAGAGTGT  ACAGG
                                |||||||||  |||||
                                TGTCTCGCA  TGTCC
                                     AA
GAM643  CAC-1    3'  CCTGCAAGCAACTCTGCTCTGT 53167        A      _  AGA
              GA                     TCACAGA GCAGAGT GT   CAGG
                                |||||||  |||||||  ||   ||||
                                AGTGTCT CGTCTCA CG   GTCC
                                    _      A  AAC
GAM643  CLSTN2   3'  CCTGTCTGGGCACCTGCT    42130       A   __
                                AGCAG GTGT  AGACAGG
                                |||||  ||||  |||||||
```

```
                                TCGTC CACG  TCTGTCC
                                  _   GG
GAM643  CUL2     5'  CCTGCCCCTTGCCCTGCTTCTG 13169        A   TAGA_
                                CAGAAGCAG GTG    CAGG
                                ||||||||| |||    ||||
                                GTCTTCGTC CGT    GTCC
                                     C   TCCCC
GAM643  DKFZp434I099 3'  CCTGTTTGTTCCTGCTTCTCAT 50082    C_      AGTG
           GA                    TCA  AGAAGCAG   TAGACAGG
                                ||| ||||||||   ||||||||
                                AGT  TCTTCGTC   GTTTGTCC
                                  AC       CTT_
GAM643  FHX      3'  CCTTTTTCCCATTCTGC     37303        T_  C
                                GCAGAGTG  AGA AGG
                                ||||||||  ||| |||
                                CGTCTTAC  TTT TCC
                                     CC   T
GAM643  FLJ12704  5'  TGTTTCCCTTCTGTGA     46537        CA  GTGTA
                                TCACAGAAG  GA    GACA
                                |||||||||  ||    ||||
                                AGTGTCTTC  CT    TTGT
                                     C_  _____
GAM643  FLJ20793  3'  CCTGTCCGTGTCTGCTTC    91805        G  TA
                                GAAGCAGA TG  GACAGG
                                |||||||| ||  ||||||
                                CTTCGTCT GT  CTGTCC
                                     _  GC
GAM643  FLJ21777  3'  CCTGTCTGGTTCTGCTTCTGTG 49863          GTG
           G                     TCACAGAAGCAGA   TAGACAGG
                                ||||||||||||   ||||||||
                                GGTGTCTTCGTCT   GTCTGTCC
                                       TG_
GAM643  FLJ23584  3'  CCTGATTCTACTCTGCCTC    44736    A      T  A
                                GA GCAGAGTG AG CAGG
                                || |||||||| || ||||
                                CT CGTCTCAT TT GTCC
                                 C       C  A
GAM643  FLJ32332  3'  CCTGTAGTAGCCTGCCTCT    58302    A    A  GTAG
                                AGA GCAG GT    ACAGG
                                ||| |||| ||    |||||
                                TCT CGTC CG    TGTCC
                                  C    _  ATGA
GAM643  GMPPB     3'  CCTGCCTTCTGCTCTGCCCCTG 95728     AA      GT_  A
                                CAG  GCAGAGT   AG CAGG
                                |||  |||||||   || ||||
                                GTC  CGTCTCG   TC GTCC
                                  CC      TCT  C
GAM643  KIAA0229  3'  CCGGTGCGCCTCTGCTTCT    92425         T  AG  A
                                AGAAGCAGAG GT  AC GG
                                ||||||||| ||  || ||
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                                TCTTCGTCTC CG  TG CC
                                     _ CG  G
GAM643  KIAA0775  3'  CTACATTTCCTCTGTGA     28279        AGCA
                                TCACAGA   GAGTGTAG
                                |||||||   ||||||||
                                AGTGTCT   TTTACATC
                                    CC__
GAM643  MGC15437  3'  CCTATCCCCCCTCCTTGCTTCT 51781          __  TGTA  C
           GTGA                  TCACAGAAGCA  GAG   GA AGG
                                |||||||||||  |||   || |||
                                AGTGTCTTCGT  CTC   CT TCC
                                      TC   CCCC  A
GAM643  MGC2641   3'  CTGCCTAATTTCTGTGA     50942        CAG  T
                                TCACAGAAG   AG GTAG
                                |||||||||   || ||||
                                AGTGTCTTT   TC CGTC
                                     AA_  _
GAM643  MGC4737   3'  CTGCACCCATTTCTGTGA    48848         CAGA
                                TCACAGAAG   GTGTAG
                                |||||||||   ||||||
                                AGTGTCTTT   CACGTC
                                     ACC_
GAM643  NFKBIE    3'  CTAGGCTCTGTTCCATGA    92022     CA  G     G
                                TCA  GAA CAGAGT TAG
                                |||  ||| |||||| |||
                                AGT  CTT GTCTCG ATC
                                  AC  _     G
GAM643  OPN4      3'  ACACTCTGCGTCTGTGA     52716        A
                                TCACAGA GCAGAGTGT
                                ||||||| |||||||||
                                AGTGTCT CGTCTCACA
                                    G
GAM643  OXCT2     5'  CGCCCTGCTCTGTGA       42092        A   A
                                TCACAGA GCAG GTG
                                ||||||| |||| |||
                                AGTGTCT CGTC CGC
                                    _   C
GAM643  PDE10A    3'  CTGCCAATCTCTTCTGTGA   21863         C  GT_
                                TCACAGAAG AGA   GTAG
                                ||||||||| |||   ||||
                                AGTGTCTTC TCT   CGTC
                                     _  AAC
GAM643  PPP4R1L   5'  CCTGCTACTCCCCCGATTCTGT 79500         GCAGAGT_   A
           GA                    TCACAGAA       GTAG CAGG
                                ||||||||       |||| ||||
                                AGTGTCTT       CATC GTCC
                                    AGCCCCCT   _
GAM643  REM       3'  CCCATCTACACTTGACTGTAGA 25806    _   AAGCA       CA
                                TC ACAG    GAGTGTAGA  GG
                                || ||||    |||||||||  ||
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```
                                AG TGTC    TTCACATCT  CC
                                 A   AG___       AC
GAM643  RODH-4   5' CCTGTCTGTGTCTGTCCTCTG 13531     A_   A TG
                                CAGA  GCAG G  TAGACAGG
                                |||| |||| |  ||||||||
                                GTCT  TGTC T  GTCTGTCC
                                  CC   _ GT
GAM643  Rpo1-2   3' CCTTCTACCCTGTTTCTATGA 49876    C      AGT    C
                                TCA AGAAGCAG   GTAGA AGG
                                ||| ||||||||   ||||| |||
                                AGT TCTTTGTC   CATCT TCC
                                  A       C__    _
GAM643  Rpo1-2   3' CCTTCTACCCTGTTTCTATGA 38700    C      AGT    C
                                TCA AGAAGCAG   GTAGA AGG
                                ||| ||||||||   ||||| |||
                                AGT TCTTTGTC   CATCT TCC
                                  A       C__    _
GAM643  TED      3' TCTTACCCTGCCTCTGTG    31645       A   A   T
                                CACAGA GCAG GTG AGA
                                |||||| |||| ||| |||
                                GTGTCT CGTC CAT TCT
                                   C   C   _
GAM643  TEX27    3' CTGCAGTATCTGTTCTGTGA   41661       G   G__
                                TCACAGAA CAGA   TGTAG
                                |||||||| ||||   |||||
                                AGTGTCTT GTCT   ACGTC
                                     _   ATG
GAM643  TNKS1BP1  5' CCTGTCCCACACTCTGCCTCTG 53005      A       A_
          T                      ACAGA GCAGAGTGT  GACAGG
                                |||||| |||||||||  ||||||
                                TGTCT CGTCTCACA  CTGTCC
                                  C        CC
GAM643  LOC123855 5' CCTGTGTGCTCTGCTACCATGA 75627     CAGA      TG AG
                                TCA   AGCAGAG  T  ACAGG
                                |||   |||||||  |  |||||
                                AGT   TCGTCTC  G  TGTCC
                                  ACCA      GT __
GAM643  LOC124935 5' CTGCCTGTGCTTCAGTGA    74370     A     G  T
                                TCAC GAAGCA AG GTAG
                                |||| |||||| || ||||
                                AGTG CTTCGT TC CGTC
                                  A     G  _
GAM643  LOC126133 3' CTAGCTGTGCTTCTGCGA    74441    A      G   G
                                TC CAGAAGCA AGT TAG
                                || |||||||| ||| |||
                                AG GTCTTCGT TCG ATC
                                 C       G   _
GAM643  LOC126767 3' ACCTACTCTTCTGTGA      75431         C  _  T
                                TCACAGAAG AG AG GT
                                |||||||| || || ||
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                                AGTGTCTTC TC TC CA
                                    _ A _
GAM643  LOC144438 3'  CCTGGAGCCTCAGCTTCTGT  76834       A  T  AGA
                                ACAGAAGC GAG GT  CAGG
                                |||||||| ||| ||  ||||
                                TGTCTTCG CTC CG  GTCC
                                    A  _ AG_
GAM643  LOC145225 3'  CCTGCCCCACTTTGTCCTGTGA 83302      AA      TAGA
                                TCACAG  GCAGAGTG  CAGG
                                ||||||  ||||||||  ||||
                                AGTGTC  TGTTTCAC  GTCC
                                  C_      CCC_
GAM643  LOC146733 3'  CTGTGACCACTTCTGTGA  83762      AGCAG  TAG
                                TCACAGA  AGTG  ACAG
                                |||||||  ||||  ||||
                                AGTGTCT  TCAC  TGTC
                                    _____  CAG
GAM643  LOC148046 3'  CCCATCGTTCCCTGGTTCTGTG 84105       G  AGTGTA  CA
            A                    TCACAGAA CAG    GA  GG
                                |||||||| |||    ||  ||
                                AGTGTCTT GTC    CT  CC
                                    G  CCTTG_  AC
GAM643  LOC148223 3'  CACCCTGCACTTCTGTG  78733       __  A
                                CACAGAA  GCAG GTG
                                |||||||  |||| |||
                                GTGTCTT  CGTC CAC
                                    CA  C
GAM643  LOC149657 3'  CTGCCCGTTGCTTCTGTG  84572        AGT
                                CACAGAAGCAG  GTAG
                                ||||||||||  ||||
                                GTGTCTTCGTT  CGTC
                                      GCC
GAM643  LOC150005 3'  CTGTGTCTGTTTCTG  84819        GTGTAG
                                CAGAAGCAGA  ACAG
                                ||||||||||  ||||
                                GTCTTTGTCT  TGTC
                                    G_____
GAM643  LOC152343 5'  CCTTTCTACTCTGCCTCCATGA 80561  CA  A  GT  C
                                TCA  GA GCAGAGT  AGA AGG
                                |||  || |||||||  ||| |||
                                AGT  CT CGTCTCA  TCT TCC
                                  AC  C    __  T
GAM643  LOC158972 3'  CCTTCTTGCTGCTTCTGTG  86948        AGTGT  C
                                CACAGAAGCAG  AGA AGG
                                ||||||||||  ||| |||
                                GTGTCTTCGTC  TCT TCC
                                    GT___  _
GAM643  LOC160777 3'  CCTGCCTGTGTTCCTGCCTCCT 82239  AA_  _ TG  A
            G                    CAG  GCAG AG  TAG CAGG
                                |||  |||| ||  ||| ||||
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                                GTC   CGTC TT  GTC GTCC
                                  CTC    C  GT   C
GAM643   LOC164945 5'  CTGCCTCCTGCCTCTGTG    87185       A    _  T
                                CACAGA GCAG AG GTAG
                                |||||| |||| || ||||
                                GTGTCT CGTC TC CGTC
                                   C    C  _
GAM643   LOC197319 3'  CTGTTTCCACTTTTGTGA    87971       AGCAG    T
                                TCACAGA    AGTG AGACAG
                                |||||||    |||| ||||||
                                AGTGTTT    TCAC TTTGTC
                                    _____   C
GAM643   LOC200895 5'  CCTGTGCGGCCCCTGCTTCTGC 88918    A       AGT  AG_
           GG                     TC CAGAAGCAG   GT   ACAGG
                                || |||||||||   ||   |||||
                                GG GTCTTCGTC   CG   TGTCC
                                 C        CC_  GCG
GAM643   LOC219700 3'  ACCTCTGTTTATTCTGT     93058       ___     T
                                ACAGAA   GCAGAG GT
                                ||||||   |||||| ||
                                TGTCTT   TGTCTC CA
                                   ATT     _
GAM643   LOC219701 3'  ACCTCTGTTTATTCTGT     93057       ___     T
                                ACAGAA   GCAGAG GT
                                ||||||   |||||| ||
                                TGTCTT   TGTCTC CA
                                   ATT     _
GAM643   LOC221025 3'  CCTGTCTAGTCTCTCCTGT   93176     AAGC    TG
                                ACAG    AGAG  TAGACAGG
                                ||||    ||||  ||||||||
                                TGTC    TCTC  ATCTGTCC
                                  C___    TG
GAM643   LOC221692 3'  CCTAGTATTCTGTGCTTCTGT  92238         G  TGTAG  _
                                ACAGAAGCA AG     AC AGG
                                ||||||||| ||     || |||
                                TGTCTTCGT TC     TG TCC
                                     G  TTA__  A
GAM643   LOC254359 3'  CCGCCTACACTCCTACGTG   94781     AGA  CA      ACA
                                CAC   AG  GAGTGTAG   GG
                                |||   ||  ||||||||   ||
                                GTG   TC  CTCACATC   CC
                                  CA_  __       CG_
GAM643   LOC255126 5'  CCTGTCTACAGCATCAGCTTCT 97472          A  _ _
           GTGA                   TCACAGAAGC GA G TGTAGACAGG
                                |||||||||| || | ||||||||||
                                AGTGTCTTCG CT C ACATCTGTCC
                                     A  A G
GAM643   LOC255515 3'  TGTCTATGCCTCCTG       96100     AAGC  A
                                CAG    AG GTGTAGACA
                                |||    || |||||||||
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                                GTC    TC CGTATCTGT
                                 C___  _
GAM643  LOC257020 5'  CTGCGGCTGCCCCGGTTCTGTG 97490        _____   AG
            A                    TCACAGAA    GCAG  TGTAG
                                 ||||||||    ||||  |||||
                                 AGTGTCTT    CGTC  GCGTC
                                     GGCCC    G_
GAM643  LOC56834  3'  CCTGCCACCTCTGCTTC     39342         T  AGA
                                 GAAGCAGAG GT   CAGG
                                 |||||||||  ||   ||||
                                 CTTCGTCTC CA   GTCC
                                      _  CC_
GAM643  LOC91496  5'  CTACCAGATCTGCTTTATGA   66221     CA       GT__
                                 TCA  GAAGCAGA    GTAG
                                 |||  ||||||||    ||||
                                 AGT  TTTCGTCT    CATC
                                   A_       AGAC
GAM643  LOC91661  3'  CTGAGCTCTGCCTTCTGTGA   56400         _     G
                                 TCACAGAAG CAGAGT TAG
                                 |||||||||  ||||||  |||
                                 AGTGTCTTC GTCTCG GTC
                                      C     A
GAM643  LOC92691  5'  CCCATCTAGGAAGAAGTTCTGT 56422         GCAGAGTG    CA
            GA                     TCACAGAA       TAGA  GG
                                 ||||||||       ||||  ||
                                 AGTGTCTT       ATCT  CC
                                     GAAGAAGG    AC
GAM644  CASQ2     3'  CTGATGCCCTGAGGCACTG    6936          AGATTC
                                 CAGTGCCTCA     TCAG
                                 ||||||||||     ||||
                                 GTCACGGAGT     AGTC
                                      CCCGT_
GAM644  LMAN1     3'  AGAACTAAGACATTGTGAA    18732         C  CA  A
                                 TTCACAGTG CT  AG TTCT
                                 |||||||||  ||  ||  ||||
                                 AAGTGTTAC GA  TC AAGA
                                      A  A_  _
GAM644  MUTYH     3'  CTGAGAATCCTGTTGTTAGT   24232     AGT  CT  A
                                 AC   GC  CA GATTCTCAG
                                 ||   ||  ||  |||||||||
                                 TG   TG  GT CTAAGAGTC
                                  AT_  TT  C
GAM644  PDE4C     3'  CTGAGAATCCCAGCTACTCAGA 6233      AC    C  CAA
            A                      TTC  AGTG CT   GATTCTCAG
                                 |||  ||||  ||   |||||||||
                                 AAG  TCAT GA   CTAAGAGTC
                                   AC    C  CC_
GAM644  TIMP3     3'  TGAGTGTGAGGCACCTGAA    4520       CA       AGATT
                                 TTCA  GTGCCTCA    CTCA
                                 ||||  ||||||||    ||||
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                                AAGT  CACGGAGT    GAGT
                                  C_      GT___
GAM644  TRPS1    3'  GGTCTTGAGACCTGTGAA    26076       TGC
                                TTCACAG   CTCAAGATT
                                |||||||   |||||||||
                                AAGTGTC   GAGTTCTGG
                                    CA_
GAM644  XKRY     3'  CTGAAAATCATCCAGAAGCACT 60017        C  AA___   C
           GTGA                   TCACAGTGC TC    GATT TCAG
                                |||||||||  ||    |||| ||||
                                AGTGTCACG AG    CTAA AGTC
                                     A  ACCTA    A
GAM644  XKRY     3'  CTGAAAATCATCCAGAAGCACT 16256        C  AA___   C
           GTGA                   TCACAGTGC TC    GATT TCAG
                                |||||||||  ||    |||| ||||
                                AGTGTCACG AG    CTAA AGTC
                                     A  ACCTA    A
GAM644  DKFZP727M111 3'  TGGGCTGAGGCATATGAA    31415     CA      AGATT
                                TTCA  GTGCCTCA    CTCA
                                ||||  ||||||||    ||||
                                AAGT  TACGGAGT    GGGT
                                  A_      C____
GAM644  DKFZp761D221 3'  CTGAGAATTATCCAGCATATGA 50163     CA    CTCAA
           A                    TTCA  GTGC    GATTCTCAG
                                ||||  ||||    |||||||||
                                AAGT  TACG    TTAAGAGTC
                                  A_   ACCTA
GAM644  FLJ12704  3'  CTGATTGTTAGAAACACTGTGA 46534        CC  AA   TC
           A                    TTCACAGTG  TC  GAT  TCAG
                                |||||||||  ||  |||  ||||
                                AAGTGTCAC  AG  TTG  AGTC
                                     AA  A_   TT
GAM644  FLJ14213  3'  CTGAGAATTTCTAGCATGTGAA 45794       G   CTCA
                                TTCACA TGC    AGATTCTCAG
                                ||||||  |||   ||||||||||
                                AAGTGT ACG    TTTAAGAGTC
                                    _   ATC_
GAM644  GOLPH2   3'  GAATACTGAAAACTGTGAA   33321        GCC   AG
                                TTCACAGT   TCA  ATTC
                                ||||||||   |||  ||||
                                AAGTGTCA   AGT  TAAG
                                     AA_   CA
GAM644  KIAA0326  3'  GAGTCTGGAAGGCACTGTG   64328         _ A
                                CACAGTGCCT C AGATTC
                                ||||||||||  | ||||||
                                GTGTCACGGA G TCTGAG
                                      A G
GAM644  KIAA0757  3'  GAATCCTGAGGCCACTGTGAA  20131         _    A
                                TTCACAGTG CCTCA GATTC
                                |||||||||  |||||  |||||
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                                AAGTGTCAC GGAGT CTAAG
                                     C    C
GAM644  OSBPL6   5'  CTGAGGATAAATCACTGTGAA  50715        CCTCAAG
                                TTCACAGTG      ATTCTCAG
                                |||||||||      ||||||||
                                AAGTGTCAC      TAGGAGTC
                                     TAAA___
GAM644  SEC15B   3'  TCTGAAACACTGTGAA      66688        CC   A
                                TTCACAGTG  TCA GA
                                |||||||||  ||| ||
                                AAGTGTCAC  AGT CT
                                     AA  _
GAM644  TDP1     3'  AATCTTGAGGCACTGTGAA   37043
                                TTCACAGTGCCTCAAGATT
                                ||||||||||||||||||
                                AAGTGTCACGGAGTTCTAA

GAM644  LOC148823 5'  CTGAGAAACCGAGTCACTGTGA 59208         C   AAGA
           A                   TTCACAGTG CTC    TTCTCAG
                               |||||||||  |||    |||||||
                               AAGTGTCAC GAG    AAGAGTC
                                    T   CCA_
GAM644  LOC157858 3'  CTGAAAATCCTGGCACAGCTGT 86589        ___   TCAA    C
           GAA                   TTCACAGT   GCC    GATT TCAG
                                 ||||||||   |||    |||| ||||
                                 AAGTGTCG   CGG    CTAA AGTC
                                      ACA   TC__    A
GAM644  LOC163509 5'  TGAGAATCCTCATCATGAA    82142      CA   CCTCAA
                                TTCA  GTG     GATTCTCA
                                ||||  |||     ||||||||
                                AAGT  TAC     CTAAGAGT
                                  AC   TC____
GAM644  LOC220980 5'  ATCACTGAGGCACTGTGA     93144           A_
                                TCACAGTGCCTCA  GAT
                                ||||||||||||  |||
                                AGTGTCACGGAGT  CTA
                                       CA
GAM644  LOC54499  3'  GACTCTCAAGGCACTGTG     70631         CA   T
                                CACAGTGCCT  AGA TC
                                ||||||||||  ||| ||
                                GTGTCACGGA  TCT AG
                                      AC   C
GAM644  LOC58512  3'  AGCGTCGAGGTCACTGTGAA   64656         _   AA   T
                                TTCACAGTG CCTC  GAT CT
                                ||||||||| ||||  ||| ||
                                AAGTGTCAC GGAG  CTG GA
                                      T    __   C
GAM645  CDH10     3'  TAGTTCTCCCTTAAGCAACCT  22058     CG   CAGTGT  A
                                AGG  GCT     GA GAACTA
                                |||  |||     || ||||||
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                              TCC  CGA     CT CTTGAT
                                AA   ATTCC_  _
GAM645  CDH10    3'  TAGTTCTCCCTTAAGCAACCT  22058     CG   CAGTGT  A
                              AGG  GCT     GA GAACTA
                              |||  |||     || |||||||
                              TCC  CGA     CT CTTGAT
                                AA   ATTCC_  _
GAM645  DACH     3'  TAGTTCTTCCATAACCACCT   54971     C  CTCA   T
                              AGG GG    GTG GAAGAACTA
                              ||| ||    ||| |||||||||
                              TCC CC    TAC CTTCTTGAT
                                A  AA__   _
GAM645  DACH     3'  TAGTTCTTCCATAACCACCT   54971     C  CTCA   T
                              AGG GG    GTG GAAGAACTA
                              ||| ||    ||| |||||||||
                              TCC CC    TAC CTTCTTGAT
                                A  AA__   _
GAM645  HPS1     3'  TCTTCCAGAGCTGCCT      3969          AG  T
                              AGGCGGCTC  TG GAAGA
                              |||||||||  || |||||
                              TCCGTCGAG  AC CTTCT
                                         __  _
GAM645  HPS1     3'  TCTTCCAGAGCTGCCT      3969          AG  T
                              AGGCGGCTC  TG GAAGA
                              |||||||||  || |||||
                              TCCGTCGAG  AC CTTCT
                                         __  _
GAM645  PCTK1    5'  TCTTCAGGCTGCCT        52264         CAGTG
                              AGGCGGCT    TGAAGA
                              ||||||||    ||||||
                              TCCGTCGG    ACTTCT
                                         ______
GAM645  PCTK1    5'  TCTTCAGGCTGCCT        52264         CAGTG
                              AGGCGGCT    TGAAGA
                              ||||||||    ||||||
                              TCCGTCGG    ACTTCT
                                         ______
GAM645  RORB     5'  AGCTCTTCGCCGACCACCT   22606     C  C  AGT     A
                              AGG GG TC   GTGAAGA CT
                              ||| || ||   ||||||| ||
                              TCC CC AG   CGCTTCT GA
                                A  _  C__       C
GAM645  RORB     5'  AGCTCTTCGCCGACCACCT   22606     C  C  AGT     A
                              AGG GG TC   GTGAAGA CT
                              ||| || ||   ||||||| ||
                              TCC CC AG   CGCTTCT GA
                                A  _  C__       C
GAM645  SPTBN4   3'  AGTCCCCATGGCCGCCT     47386        CAGT   AA  A
                              AGGCGGCT    GTG  GA CT
                              ||||||||    |||  || ||
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                              TCCGCCGG   TAC  CT GA
                                 _____  CC  _
GAM645  SPTBN4   3' AGTCCCCATGGCCGCCT    47386       CAGT  AA  A
                              AGGCGGCT   GTG  GA CT
                              ||||||||   |||  || ||
                              TCCGCCGG   TAC  CT GA
                                 _____  CC  _
GAM645  ZNF200   3' GTAGTTCTGAATTCCCAAGCTG 12909       CAGT_  GA
           CCT                  AGGCGGCT    GT  AGAACTAC
                              ||||||||    ||  ||||||||
                              TCCGTCGA    TA  TCTTGATG
                                 ACCCT  AG
GAM645  ZNF200   3' GTAGTTCTGAATTCCCAAGCTG 12909       CAGT_  GA
           CCT                  AGGCGGCT    GT  AGAACTAC
                              ||||||||    ||  ||||||||
                              TCCGTCGA    TA  TCTTGATG
                                 ACCCT  AG
GAM645  BTN2A1   3' GTAATTCTCAGTGTGTGAGCTG 54342        _ TG GA   C
           CCT                  AGGCGGCTCA G  T  AGAA TAC
                              ||||||||||| |  |  |||| |||
                              TCCGTCGAGT T  G  TCTT ATG
                                 G GT AC   A
GAM645  BTN2A1   3' GTAATTCTCAGTGTGTGAGCTG 54342        _ TG GA   C
           CCT                  AGGCGGCTCA G  T  AGAA TAC
                              ||||||||||| |  |  |||| |||
                              TCCGTCGAGT T  G  TCTT ATG
                                 G GT AC   A
GAM645  CFP1     3' TAGCTCCGTCAAGCTGCCT   58771       CAGTG  A_  A
                              AGGCGGCT    TGA  GA CTA
                              ||||||||    |||  || |||
                              TCCGTCGA    ACT  CT GAT
                                 ______  GC  C
GAM645  CFP1     3' TAGCTCCGTCAAGCTGCCT   58771       CAGTG  A_  A
                              AGGCGGCT    TGA  GA CTA
                              ||||||||    |||  || |||
                              TCCGTCGA    ACT  CT GAT
                                 ______  GC  C
GAM645  FENS-1   3' TGGGAGTCACACAAGCCGCCT  40445       CA    AGAA
                              AGGCGGCT  GTGTGA   CTA
                              ||||||||  ||||||   |||
                              TCCGCCGA  CACACT   GGT
                                 A_     GAG_
GAM645  FENS-1   3' TGGGAGTCACACAAGCCGCCT  40445       CA    AGAA
                              AGGCGGCT  GTGTGA   CTA
                              ||||||||  ||||||   |||
                              TCCGCCGA  CACACT   GGT
                                 A_     GAG_
GAM645  FLJ14082 3' AGTTCTTCCTAAGGCACCC   46668    CG   CAG  T
                              GG  GCT   TG GAAGAACT
                              ||  |||   || ||||||||
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                                CC  CGG   AT CTTCTTGA
                                 CA   A__  C
GAM645  FLJ14082  3'  AGTTCTTCCTAAGGCACCC   46668    CG   CAG  T
                                GG  GCT   TG GAAGAACT
                                ||  |||   || ||||||||
                                CC  CGG   AT CTTCTTGA
                                 CA   A__  C
GAM645  FLJ20539  5'  TGGGGCCACCTGAGCCGCC   35363         T   AAGAA
                                GGCGGCTCAG GTG    CTA
                                |||||||||| |||    |||
                                CCGCCGAGTC CAC    GGT
                                      _   CGG__
GAM645  FLJ20539  5'  TGGGGCCACCTGAGCCGCC   35363         T   AAGAA
                                GGCGGCTCAG GTG    CTA
                                |||||||||| |||    |||
                                CCGCCGAGTC CAC    GGT
                                      _   CGG__
GAM645  FLJ22301  3'  AGCCCTTCACGTAGCCTCCT   45756    C   CAG      AA
                                AGG GGCT   TGTGAAG  CT
                                |||  ||||   |||||||  ||
                                TCC CCGA   GCACTTC  GA
                                  T    T__      CC
GAM645  FLJ22301  3'  AGCCCTTCACGTAGCCTCCT   45756    C   CAG      AA
                                AGG GGCT   TGTGAAG  CT
                                |||  ||||   |||||||  ||
                                TCC CCGA   GCACTTC  GA
                                  T    T__      CC
GAM645  HEMGN     5'  TAGAGAAAAAAACTGAGCCACC 37380     C       GTGAAGAA
           T                     AGG GGCTCAGT       CTA
                                |||  ||||||||       |||
                                TCC CCGAGTCA       GAT
                                  A       AAAAAAGA
GAM645  HEMGN     5'  TAGAGAAAAAAACTGAGCCACC 37380     C       GTGAAGAA
           T                     AGG GGCTCAGT       CTA
                                |||  ||||||||       |||
                                TCC CCGAGTCA       GAT
                                  A       AAAAAAGA
GAM645  KIAA0379  3'  GTAGTTCTTGCGAATGCCACC  68150    C   TCAG   G
                                GG GGC    TGT AAGAACTAC
                                ||  |||    ||| |||||||||
                                CC CCG    GCG TTCTTGATG
                                 A   TAA_   _
GAM645  KIAA0379  3'  GTAGTTCTTGCGAATGCCACC  68150    C   TCAG   G
                                GG GGC    TGT AAGAACTAC
                                ||  |||    ||| |||||||||
                                CC CCG    GCG TTCTTGATG
                                 A   TAA_   _
GAM645  KIAA0494  3'  TCTCACACTGACCACC      28750    C  C        A
                                GG GG TCAGTGTGA GA
                                ||  ||  |||||||||  ||
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                                CC CC AGTCACACT CT
                                 A  _       _
GAM645  KIAA0494  3'  TCTCACACTGACCACC     28750    C  C       A
                                GG GG TCAGTGTGA GA
                                || || ||||||||| ||
                                CC CC AGTCACACT CT
                                 A  _       _
GAM645  LACE1     3'  CTTCACATTAAACCACCT    91837    C  CTC
                                AGG GG   AGTGTGAAG
                                ||| ||   |||||||||
                                TCC CC   TTACACTTC
                                  A  AAA
GAM645  LACE1     3'  CTTCACATTAAACCACCT    91837    C  CTC
                                AGG GG   AGTGTGAAG
                                ||| ||   |||||||||
                                TCC CC   TTACACTTC
                                  A  AAA
GAM645  NAPG      3'  TAGTTCTTCAGGTAGCACCT  96730    CG   CAG G
                                AGG  GCT   T TGAAGAACTA
                                |||  |||   | ||||||||||
                                TCC  CGA   G ACTTCTTGAT
                                  A_   T__ G
GAM645  NAPG      3'  TAGTTCTTCAGGTAGCACCT  96730    CG   CAG G
                                AGG  GCT   T TGAAGAACTA
                                |||  |||   | ||||||||||
                                TCC  CGA   G ACTTCTTGAT
                                  A_   T__ G
GAM645  PRO2405   5'  AGGAGCACATTAAGCCGCCT  37798        C     AAGAA
                                AGGCGGCT AGTGTG    CT
                                |||||||| ||||||    ||
                                TCCGCCGA TTACAC    GA
                                     A     GAG__
GAM645  PRO2405   5'  AGGAGCACATTAAGCCGCCT  37798        C     AAGAA
                                AGGCGGCT AGTGTG    CT
                                |||||||| ||||||    ||
                                TCCGCCGA TTACAC    GA
                                     A     GAG__
GAM645  LOC121219 5'  AGTCCTCAGCGAAGCCGCCT  74040        CA  G   A  A
                                AGGCGGCT  GT TGA GA CT
                                ||||||||  || ||| || ||
                                TCCGCCGA  CG ACT CT GA
                                     AG  _   C  _
GAM645  LOC121219 5'  AGTCCTCAGCGAAGCCGCCT  74040        CA  G   A  A
                                AGGCGGCT  GT TGA GA CT
                                ||||||||  || ||| || ||
                                TCCGCCGA  CG ACT CT GA
                                     AG  _   C  _
GAM645  LOC146990 3'  CTTCACACCCAGCCGCCT    83886        CA
                                AGGCGGCT  GTGTGAAG
                                ||||||||  ||||||||
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                                TCCGCCGA  CACACTTC
                                    CC
GAM645  LOC146990 3'  CTTCACACCCAGCCGCCT    83886        CA
                                AGGCGGCT  GTGTGAAG
                                ||||||||  ||||||||
                                TCCGCCGA  CACACTTC
                                    CC
GAM645  LOC148371 5'  TTCCACTGAGCCACC       78809    C       T
                                GG GGCTCAGTG GAA
                                || ||||||||| |||
                                CC CCGAGTCAC CTT
                                 A       _
GAM645  LOC148371 5'  TTCCACTGAGCCACC       78809    C       T
                                GG GGCTCAGTG GAA
                                || ||||||||| |||
                                CC CCGAGTCAC CTT
                                 A       _
GAM645  LOC152274 3'  AGTCCCTGCAGGAGCAGCCT   80498     G   AG   AA  A
                                AGGC GCTC  TGTG  GA CT
                                |||| ||||  ||||  || ||
                                TCCG CGAG  ACGT  CT GA
                                  A   G_   CC  _
GAM645  LOC152274 3'  AGTCCCTGCAGGAGCAGCCT   80498     G   AG   AA  A
                                AGGC GCTC  TGTG  GA CT
                                |||| ||||  ||||  || ||
                                TCCG CGAG  ACGT  CT GA
                                  A   G_   CC  _
GAM645  LOC200261 3'  AGTTGCTCCACTGAGTCACC   88653    C       T  AG
                                GG GGCTCAGTG GA  AACT
                                || |||||||| ||  ||||
                                CC CTGAGTCAC CT  TTGA
                                 A       _ CG
GAM645  LOC200261 3'  AGTTGCTCCACTGAGTCACC   88653    C       T  AG
                                GG GGCTCAGTG GA  AACT
                                || |||||||| ||  ||||
                                CC CTGAGTCAC CT  TTGA
                                 A       _ CG
GAM645  LOC201562 5'  GTAGTCCGGCCCGAGCCGCT   88975        AGT  GAA  A
                                GGCGGCTC   GT   GA CTAC
                                ||||||||   ||   || ||||
                                TCGCCGAG   CG   CT GATG
                                    CC_  GC_  _
GAM645  LOC201562 5'  GTAGTCCGGCCCGAGCCGCT   88975        AGT  GAA  A
                                GGCGGCTC   GT   GA CTAC
                                ||||||||   ||   || ||||
                                TCGCCGAG   CG   CT GATG
                                    CC_  GC_  _
GAM645  LOC202347 3'  TCATGGCAGAGCCGCCT     90349        A  _
                                AGGCGGCTC GT GTGA
                                ||||||||| || ||||
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                                TCCGCCGAG CG TACT
                                     A  G
GAM645  LOC202347 3'  TCATGGCAGAGCCGCCT     90349          A  _
                                AGGCGGCTC GT GTGA
                                ||||||||| || ||||
                                TCCGCCGAG CG TACT
                                     A  G
GAM645  LOC220370 3'  TCACCTCACTGAGCCACCT    92834     C       ___
                                AGG GGCTCAGT   GTGA
                                ||| ||||||||   ||||
                                TCC CCGAGTCA   CACT
                                  A       CTC
GAM645  LOC220370 3'  TCACCTCACTGAGCCACCT    92834     C       ___
                                AGG GGCTCAGT   GTGA
                                ||| ||||||||   ||||
                                TCC CCGAGTCA   CACT
                                  A       CTC
GAM645  LOC221838 5'  TTCCACTGAGCCACC       92546    C       T
                                GG GGCTCAGTG GAA
                                || ||||||||| |||
                                CC CCGAGTCAC CTT
                                 A       _
GAM645  LOC221838 5'  TTCCACTGAGCCACC       92546    C       T
                                GG GGCTCAGTG GAA
                                || ||||||||| |||
                                CC CCGAGTCAC CTT
                                 A       _
GAM645  LOC51716  3'  AGTTCCACACTGAGCGCCT    32786      G       AA
                                AGGCG CTCAGTGTG  GAACT
                                ||||| |||||||||  |||||
                                TCCGC GAGTCACAC  CTTGA
                                   _       __
GAM645  LOC51716  3'  AGTTCCACACTGAGCGCCT    32786      G       AA
                                AGGCG CTCAGTGTG  GAACT
                                ||||| |||||||||  |||||
                                TCCGC GAGTCACAC  CTTGA
                                   _       __
GAM645  LOC89919  3'  CTTCCACTGAGCCACC       60722    C       T
                                GG GGCTCAGTG GAAG
                                || ||||||||| ||||
                                CC CCGAGTCAC CTTC
                                 A       _
GAM645  LOC89919  3'  CTTCCACTGAGCCACC       60722    C       T
                                GG GGCTCAGTG GAAG
                                || ||||||||| ||||
                                CC CCGAGTCAC CTTC
                                 A       _
GAM645  LOC91947  3'  TAGTTCTTTCATTGTAAGCCGC 67614          __     T
           T                     GGCGGCT  CAGTG GAAGAACTA
                                ||||||| ||||| |||||||||
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                                TCGCCGA  GTTAC TTTCTTGAT
                                   AT    _
GAM645  LOC91947  3'  TAGTTCTTTCATTGTAAGCCGC 67614       __    T
             T                   GGCGGCT  CAGTG GAAGAACTA
                                 |||||||  ||||| |||||||||
                                TCGCCGA  GTTAC TTTCTTGAT
                                   AT    _
GAM646  ACRV1    5'  CTGGAAGCTTTTGCTC     39181
                                GAGCAAAAGCTTTTAG
                                ||||||||||||||||
                                CTCGTTTTCGAAGGTC

GAM646  ACRV1    5'  CTGGAAGCTTTTGCTC     39206
                                GAGCAAAAGCTTTTAG
                                ||||||||||||||||
                                CTCGTTTTCGAAGGTC

GAM646  ACRV1    5'  CTGGAAGCTTTTGCTC     7860
                                GAGCAAAAGCTTTTAG
                                ||||||||||||||||
                                CTCGTTTTCGAAGGTC

GAM646  ACRV1    5'  CTGGAAGCTTTTGCTC     39176
                                GAGCAAAAGCTTTTAG
                                ||||||||||||||||
                                CTCGTTTTCGAAGGTC

GAM646  ACRV1    5'  CTGGAAGCTTTTGCTC     39201
                                GAGCAAAAGCTTTTAG
                                ||||||||||||||||
                                CTCGTTTTCGAAGGTC

GAM646  ACRV1    5'  CTGGAAGCTTTTGCTC     39196
                                GAGCAAAAGCTTTTAG
                                ||||||||||||||||
                                CTCGTTTTCGAAGGTC

GAM646  ACRV1    5'  CTGGAAGCTTTTGCTC     39216
                                GAGCAAAAGCTTTTAG
                                ||||||||||||||||
                                CTCGTTTTCGAAGGTC

GAM646  ACRV1    5'  CTGGAAGCTTTTGCTC     39191
                                GAGCAAAAGCTTTTAG
                                ||||||||||||||||
                                CTCGTTTTCGAAGGTC

GAM646  ACRV1    5'  CTGGAAGCTTTTGCTC     39186
                                GAGCAAAAGCTTTTAG
                                ||||||||||||||||
```

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                                CTCGTTTTCGAAGGTC

GAM646  ACRV1    5'  CTGGAAGCTTTTGCTC      39211
                                GAGCAAAAGCTTTTAG
                                ||||||||||||||||
                                CTCGTTTTCGAAGGTC

GAM646  CALB1    5'  ACACGCTGAGCTTTTGCTCA  17021          TT  _
                                TGAGCAAAAGCTT  AG GTGT
                                ||||||||||||  || ||||
                                ACTCGTTTTCGAG  TC CACA
                                       __  G
GAM646  CALCRL   5'  ACATTGCAAAGCTTTCACTC  19386    CA      TA
                                GAG  AAAGCTTT  GGTGT
                                |||  ||||||||  |||||
                                CTC  TTTCGAAA  TTACA
                                  AC       CG
GAM646  CCNF     3'  ACACCACTTGAGCCCCTGCCCA 8310    A   AAA   TTA_
                                TG GCA   GCTT   GGTGT
                                || |||   ||||   |||||
                                AC CGT   CGAG   CCACA
                                 C   CCC    TTCA
GAM646  CD59     3'  ACACCAGGAGAGCTTCTC    5211     CAA      A_
                                GAG   AAGCTTTT  GGTGT
                                |||   ||||||||  |||||
                                CTC   TTCGAGAG  CCACA
                                  ____       GA
GAM646  CYP27A1  3'  ACACCCTGAGCTTTTGCCA   5772    A       TTA
                                TG GCAAAAGCTT   GGTGT
                                || ||||||||||   |||||
                                AC CGTTTTCGAG   CCACA
                                 _        TC_
GAM646  DSC3     3'  ACACCCACTGTGTTTTGCTCA  44336        _  TTTTA
                                TGAGCAAAA GC    GGTGT
                                |||||||| ||    |||||
                                ACTCGTTTT TG    CCACA
                                      G  TCAC_
GAM646  DSC3     3'  ACACCCACTGTGTTTTGCTCA  8673         _  TTTTA
                                TGAGCAAAA GC    GGTGT
                                |||||||| ||    |||||
                                ACTCGTTTT TG    CCACA
                                      G  TCAC_
GAM646  FUT6     5'  ACCGGAGGAAGCTTCTGCCA  3804    A  A     TA__
                                TG GCA AAGCTTT    GGT
                                || ||| |||||||    |||
                                AC CGT TTCGAAG    CCA
                                 _  C      GAGG
GAM646  MOCS1    3'  CACCTGGCCCTGTTCA     92032      AAA   TTT
                                TGAGCA   GCT   AGGTG
                                ||||||   |||   |||||
```

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                              ACTTGT  CGG  TCCAC
                                 CC_  ___
GAM646  PCDH11X  3' ACCTAAACTTTTGTTCA    52035       CT
                              TGAGCAAAAG  TTTAGGT
                              ||||||||||  |||||||
                              ACTTGTTTTC  AAATCCA
                                          __
GAM646  PCDH11X  3' ACCTAAACTTTTGTTCA    52013       CT
                              TGAGCAAAAG  TTTAGGT
                              ||||||||||  |||||||
                              ACTTGTTTTC  AAATCCA
                                          __
GAM646  PCDH11Y  3' ACCTAAACTTTTGTTCA    52071       CT
                              TGAGCAAAAG  TTTAGGT
                              ||||||||||  |||||||
                              ACTTGTTTTC  AAATCCA
                                          __
GAM646  PRDX3    3' ACATTGAAAGCTTCTGATCA  73350    G  A      G
                              TGA CA AAGCTTTTAG TGT
                              ||| || |||||||||| |||
                              ACT GT TTCGAAAGTT ACA
                                A  C       _
GAM646  PRKACB   3' ACATCTGAGCTCACACTCA   10794     CAAA    TT
                              TGAG   AGCTT  AGGTGT
                              ||||   |||||  ||||||
                              ACTC   TCGAG  TCTACA
                                ACAC    __
GAM646  RELN     3' ACCTGAAAGCCCTTCTCA    94300     C  AA
                              TGAG AA  GCTTTTAGGT
                              |||| ||  ||||||||||
                              ACTC TT  CGAAAGTCCA
                                 _  CC
GAM646  RNGTT    3' ACGAAAGCAAGCTTTTGCCA  13728    A       TTAGG
                              TG GCAAAAGCTT    TGT
                              || ||||||||||    |||
                              AC CGTTTTCGAA    GCA
                               _       CGAAA
GAM646  RNH      5' ACACCCTGGTCGGTTTTGCTCA 11358        ___  TTTA
                              TGAGCAAAA  GCT   GGTGT
                              |||||||||  |||   |||||
                              ACTCGTTTT  TGG   CCACA
                                   GGC  TC__
GAM646  RNH      5' ACACCCTGGTCGGTTTTGCTCA 59613        ___  TTTA
                              TGAGCAAAA  GCT   GGTGT
                              |||||||||  |||   |||||
                              ACTCGTTTT  TGG   CCACA
                                   GGC  TC__
GAM646  SCN3A    3' TAAAATTTTTGCTCA      22632         C
                              TGAGCAAAAG TTTTA
                              |||||||||| |||||
```

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                                ACTCGTTTTT AAAAT
                                      _
GAM646  SERPIND1  3'  ACACCTGACTCTGTCACTCA  3942      CAAA  CTT
                                TGAG   AG   TTAGGTGT
                                ||||   ||   ||||||||
                                ACTC   TC   AGTCCACA
                                  ACTG  TC_
GAM646  SH2D1A    3'  ACACCTGGTCCCTGCTC    9846      AAA   TTT
                                GAGCA   GCT   AGGTGT
                                ||||||  |||   ||||||
                                CTCGT   TGG   TCCACA
                                  CCC   ____
GAM646  SPRR3     3'  CTATAAAGCTTTTGTTCA    95497          _
                                TGAGCAAAAGCTTT TAG
                                |||||||||||||| |||
                                ACTTGTTTTCGAAA ATC
                                       T
GAM646  ZNF136    3'  ACATGGGAAAGCTTTCAATCA  59883    GCA       AG
                                TGA   AAAGCTTTT  GTGT
                                |||   |||||||||  ||||
                                ACT   TTTCGAAAG  TACA
                                  AAC       GG
GAM646  ZNF36     3'  ACACCTAAGAGGCACTCA    93956     CAAAAG
                                TGAG     CTTTTAGGTGT
                                ||||     ||||||||||
                                ACTC     GAGAATCCACA
                                  ACG____
GAM646  AWP1      5'  ACAGGACAGCTGTTTGCTCA  38662       _   T  AG
                                TGAGCAAA AGCT TT  GT
                                |||||||| |||| ||  ||
                                ACTCGTTT TCGA AG  CA
                                     G   C  GA
GAM646  BCMP1     3'  ACCTTAAAGCTTTTGCTC    48729          T
                                GAGCAAAAGCTTT AGGT
                                |||||||||||| ||||
                                CTCGTTTTCGAAA TCCA
                                       T
GAM646  C21orf61  3'  ACACCTAGCCTGCTTGCTTA  88709      AA   TT_
                                TGAGCA  AGC   TTAGGTGT
                                ||||||  |||   ||||||||
                                ATTCGT  TCG   GATCCACA
                                   __   TCC
GAM646  C9orf7    3'  ACACCTGGAGTCCTCTGCTC  34162      AAA_    T
                                GAGCA    GCTTT AGGTGT
                                |||||    ||||| ||||||
                                CTCGT    TGAGG TCCACA
                                  CTCC    _
GAM646  CMG2      3'  GCTTGAAACTTTTGCTCA    54163         C
                                TGAGCAAAAG TTTTAGGT
                                |||||||||| ||||||||
```

```
                                ACTCGTTTTC AAAGTTCG
                                          _
GAM646  DKFZP762D096 3'  ACACCTAGACTCGCCCTGCCA  65574    A   AAA  T__
                                TG GCA   GC   TTTAGGTGT
                                || |||   ||   |||||||||
                                AC CGT   CG   AGATCCACA
                                 _   CC_  CTC
GAM646  FBXL3B   5'  AAAAGCATTTTGCTCA      24069         _
                                TGAGCAAAA GCTTTT
                                ||||||||| ||||||
                                ACTCGTTTT CGAAAA
                                      A
GAM646  FLJ12700  3'  CTGGGAGCCTCTGCTCA     46117       AAA
                                TGAGCA   GCTTTTAG
                                ||||||   ||||||||
                                ACTCGT   CGAGGGTC
                                    CTC
GAM646  FLJ12892  5'  ACCTAATGAAGCTTCTGCT    67852      A     __
                                AGCA AAGCTTT  TAGGT
                                |||| |||||||  |||||
                                TCGT TTCGAAG  ATCCA
                                  C      TA
GAM646  FLJ13110  3'  AGAAGCTGTTTGCTCA      43296         _
                                TGAGCAAA AGCTTTT
                                |||||||| |||||||
                                ACTCGTTT TCGAAGA
                                      G
GAM646  FLJ20209  3'  AAAAGCTCTTTGCTCA      85515         _
                                TGAGCAAA AGCTTTT
                                |||||||| |||||||
                                ACTCGTTT TCGAAAA
                                      C
GAM646  FLJ23519  5'  ACACCCTGGTCGGTTTTGCTCA 69196          ___   TTTA
                                TGAGCAAAA   GCT    GGTGT
                                |||||||||   |||    |||||
                                ACTCGTTTT   TGG    CCACA
                                      GGC   TC__
GAM646  FYCO1    3'  ACACCCAAAGGGATGCTC    44482      AAAG    A
                                GAGCA    CTTTT GGTGT
                                |||||    ||||| |||||
                                CTCGT    GGAAA CCACA
                                   AG__     C
GAM646  HMP19    3'  ACACCTGGATACTGCCCA    87470    A   AAA CT
                                TG GCA   G  TTTAGGTGT
                                || |||   |  |||||||||
                                AC CGT   C  AGGTCCACA
                                 C   ___ AT
GAM646  HSPC014  3'  ACACCTGAGAATTTCTGCTCA  31939       A   C
                                TGAGCA AAG TTTTAGGTGT
                                |||||| ||| ||||||||||
```

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                                ACTCGT TTT AGAGTCCACA
                                   C   A
GAM646  KIAA0275  3'  ACTTGAAACTTCTGCTC    28671      A   C
                                GAGCA AAG TTTTAGGT
                                ||||| ||| ||||||||
                                CTCGT TTC AAAGTTCA
                                   C   _
GAM646  KIAA0625  3'  ACACCTGAGCCTCTGGTCA   30479    G  AAA   TT
                                TGA CA   GCTT  AGGTGT
                                ||| ||   ||||  ||||||
                                ACT GT   CGAG  TCCACA
                                  G  CTC   __
GAM646  KIAA0630  3'  ACACCTCTGTTTTGCTCA    89385        G TTTT
                                TGAGCAAAA C    AGGTGT
                                ||||||||| |    ||||||
                                ACTCGTTTT G    TCCACA
                                      _ TC__
GAM646  KIAA1340  3'  ACAATAAAAGCTTCTGCCA   69178    A  A       GG
                                TG GCA AAGCTTTTA  TGT
                                || ||| |||||||||  |||
                                AC CGT TTCGAAAAT  ACA
                                 _  C        A_
GAM646  MCM10     3'  CTGAAGTTTTTGCCCA     37572    A        T
                                TG GCAAAAGCTTT AG
                                || ||||||||||| ||
                                AC CGTTTTTGAAG TC
                                 C          _
GAM646  MSTP033   3'  ACACTTGACTTCTGCTCA    50780      A   CTT
                                TGAGCA AAG   TTAGGTGT
                                |||||| |||   ||||||||
                                ACTCGT TTC   AGTTCACA
                                   C   ____
GAM646  SLC26A9   5'  ACACCTGCAGCCCTGCCCA   53614    A   AAA   TT
                                TG GCA   GCT  TAGGTGT
                                || |||   |||  |||||||
                                AC CGT   CGA  GTCCACA
                                 C   CC_   C_
GAM646  SLC26A9   5'  ACACCTGCAGCCCTGCCCA   56175    A   AAA   TT
                                TG GCA   GCT  TAGGTGT
                                || |||   |||  |||||||
                                AC CGT   CGA  GTCCACA
                                 C   CC_   C_
GAM646  TRAF3     3'  ACAGGGGAGCCCTTTGCTCA  59731        A_     AG
                                TGAGCAAA  GCTTTT  GT
                                ||||||||  ||||||  ||
                                ACTCGTTT  CGAGGG  CA
                                     CC     GA
GAM646  UBN1      3'  ACACCTAGGGTGTGCTCA    33727       AAA    T
                                TGAGCA   GCTTT AGGTGT
                                ||||||   ||||| ||||||
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                                ACTCGT   TGGGA TCCACA
                                   G__    _
GAM646  ULK2     3'  ACACCTACAGATTTTCTCA   27999     C   G  TT
                                TGAG AAAA CT  TAGGTGT
                                |||| |||| ||  |||||||
                                ACTC TTTT GA  ATCCACA
                                  _   A  C_
GAM646  LOC115400 5' GCTTTAAAGCCCTGCTCA    73443       AAA    T
                                TGAGCA   GCTTT AGGT
                                ||||||   ||||| ||||
                                ACTCGT   CGAAA TTCG
                                   CC_    T
GAM646  LOC143677 5' CTAGAGGCCTTTGCTCA     82976        A
                                TGAGCAAA GCTTTTAG
                                |||||||| ||||||||
                                ACTCGTTT CGGAGATC
                                     C
GAM646  LOC146515 3' CTAAAAGCTTTCACTC      77964     CA
                                GAG  AAAGCTTTTAG
                                |||  ||||||||||
                                CTC  TTTCGAAAATC
                                 AC
GAM646  LOC146853 3' ACACCTGACTCTGTCCGCTCA  59181      AAA_  CTT
                                TGAGC    AG   TTAGGTGT
                                |||||    ||   ||||||||
                                ACTCG    TC   AGTCCACA
                                   CCTG  TC_
GAM646  LOC149010 3' ACAATTAAAAGCTTTTGC    79126           G
                                GCAAAAGCTTTTAG TGT
                                |||||||||||||| |||
                                CGTTTTCGAAAATT ACA
                                        A
GAM646  LOC200531 3' ACACCTAAGGCGCCCTGCTC  88820      AAA_    T
                                GAGCA    GCTTT AGGTGT
                                |||||    ||||| ||||||
                                CTCGT    CGGAA TCCACA
                                   CCCG    _
GAM646  LOC200609 5' ACTTAAGCCCTTTGCTCA    90094        A_   TT
                                TGAGCAAA  GCT  TAGGT
                                ||||||||  |||  |||||
                                ACTCGTTT  CGA  ATTCA
                                     CC  __
GAM646  LOC219402 5' ACAGAAGAGCTTCTCCTCA   93571     CAA      AG
                                TGAG   AAGCTTTT  GT
                                ||||   ||||||||  ||
                                ACTC   TTCGAGAA  CA
                                  CTC       GA
GAM646  LOC220992 5' ACACCTGGATGCTGCTCA    91467       AAA  T
                                TGAGCA   GC TTTAGGTGT
                                ||||||   || |||||||||
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                                ACTCGT   CG AGGTCCACA
                                   ___  T
GAM646  LOC221415 3'  ACACCTAAGTGCCTC      93871     CAAAA  T
                                GAG    GC TTTAGGTGT
                                |||    || |||||||||
                                CTC    CG GAATCCACA
                                 _____  T
GAM646  LOC254611 5'  ACATTTAAAGCTTTTGTCCA  97605    AG        T
                                TG  CAAAAGCTTT AGGTGT
                                ||  |||||||||| ||||||
                                AC  GTTTTCGAAA TTTACA
                                 CT        _
GAM646  LOC51580  3'  ACACAGTGCTTTTGTTCA    31858          TTTTAG
                                TGAGCAAAAGC     GTGT
                                ||||||||||      ||||
                                ACTTGTTTTCG     CACA
                                      TGA___
GAM646  LOC91149  3'  ACATAGCATGCTTTTGCTCA  65065          TTTTAG
                                TGAGCAAAAGC     GTGT
                                ||||||||||      ||||
                                ACTCGTTTTCG     TACA
                                      TACGA_
GAM646  LOC91170  5'  ACCTCAAGCCCTTGCTTA    65134       AA    TT
                                TGAGCAA  GCTT  AGGT
                                |||||||  ||||  ||||
                                ATTCGTT  CGAA  TCCA
                                    CC    C_
GAM646  LOC91660  5'  ACCTAAAGTCTCTGCTCA    66866       AA  C
                                TGAGCA  AG TTTTAGGT
                                ||||||  || ||||||||
                                ACTCGT  TC GAAATCCA
                                   C_  T
GAM647  AQP3      3'  TTCACGATCCACCCTTTC    59593      T_   _
                                GAAA  GTGG TCGTGAA
                                ||||  |||| |||||||
                                CTTT  CACC AGCACTT
                                  CC    T
GAM647  ARSB      3'  TCACGACTCTTGTC        3502         AATGTG
                                GACAAGA     GTCGTGA
                                |||||||     |||||||
                                CTGTTCT     CAGCACT
                                            _______
GAM647  B4GALT5   3'  TTTTCACAAAAATAGTCCTTTG 16519        AAA_   GGTC
           TCA                    TGACAAG    TGT    GTGAAAA
                                |||||||    |||    |||||||
                                ACTGTTT    ATA    CACTTTT
                                    CCTG   AAAA
GAM647  CHRNA3    3'  TCGTTACCCATTTCTT      5610          T   CG
                                AAGAAATG GGT  TGA
                                |||||||| |||  |||
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                                TTCTTTAC CCA  GCT
                                     _  TT
GAM647  DRD1    3'  TTACAACCACATTTCTGGCCA  5840    ACA        C
                                TG  AGAAATGTGGT GTGA
                                ||  |||||||||| ||||
                                AC  TCTTTACACCA CATT
                                 CGG         A
GAM647  FUT1    3'  TCTGATCACATCCCCTGTC   3798     AGAA       T
                                GACA   ATGTGGTCG GA
                                ||||   ||||||||| ||
                                CTGT   TACACTAGT CT
                                  CCCC       _
GAM647  IRF1    3'  GCCACATTTCTGATCA     64345    CA
                                TGA  AGAAATGTGGT
                                |||  ||||||||||
                                ACT  TCTTTACACCG
                                  AG
GAM647  MAP3K8  5'  TCACGACCACCTCATG     17791    A  AAT
                                CA GA   GTGGTCGTGA
                                || ||   ||||||||||
                                GT CT   CACCAGCACT
                                 A  C__
GAM647  NGFR    3'  TTCTGACCACACTTCCTGTC  10231     A  A      T
                                GACA GAA TGTGGTCG GAA
                                |||| ||| |||||||| |||
                                CTGT CTT ACACCAGT CTT
                                  C  C      _
GAM647  OLR1    3'  TTCACAACAGTTCTTGTTA   10341        ATGTG  C
                                TGACAAGAA    GT GTGAA
                                |||||||||    || |||||
                                ATTGTTCTT    CA CACTT
                                     GA___  A
GAM647  POU4F1  3'  CACTGAAAACATTTTTGTCA  20660        A  GG  _
                                TGACAAGAA TGT  TC GTG
                                ||||||||| |||  || |||
                                ACTGTTTTT ACA  AG CAC
                                     _  AA  T
GAM647  SMP1    3'  TTTCACATGAATAATTTTTGTC 26705        A  GGTC
           A                     TGACAAGAA TGT   GTGAAA
                                |||||||| |||   ||||||
                                ACTGTTTTT ATA   CACTTT
                                     A  AGTA
GAM647  ZNF264  3'  TTCTATTAACATTTCTTTTCA  12769    C      GGTCGT
                                TGA AAGAAATGT     GAA
                                ||| |||||||||     |||
                                ACT TTCTTTACA     CTT
                                  T       ATTAT_
GAM647  C20orf175 3'  CGAGCTCCACGTTTCCTGCCA  55063    A  A      ___
                                TG CA GAAATGTGG   TCG
                                || || |||||||||   |||
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                                AC GT CTTTGCACC   AGC
                                 C  C        TCG
GAM647  CAPNS2   3'  TTTCACAACCCTACATATTTCT 50323     CA      ____  C
            GATCA                   TGA  AGAAATGT    GGT GTGAAA
                                ||| ||||||||   ||| ||||||
                                ACT  TCTTTATA    CCA CACTTT
                                  AG       CATC   A
GAM647  CLDN6    3'  TTTACACTCACATTTTTATCA  41041     CA       _  C
                                TGA  AGAAATGTG GT GTGAA
                                |||  ||||||||| || |||||
                                ACT  TTTTTACAC CA CATTT
                                  A_       T  _
GAM647  DKFZP564L0864 3'  GCACCAATTTCTTGCCA     72555    A      G   C
                                TG CAAGAAAT TGGT GT
                                || |||||||| |||| ||
                                AC GTTCTTTA ACCA CG
                                 C      _   _
GAM647  DKFZP566B183 3'  TTTCCATAAACATTTCTTTTCA 31330     C       GGTCGT
                                TGA AAGAAATGT     GAAA
                                ||| |||||||||     ||||
                                ACT TTCTTTACA     CTTT
                                  T       AATAC_
GAM647  GTF2E1   3'  TACAGACCTCTTGTCA      18616        AATGT   _
                                TGACAAGA    GGTC GTG
                                ||||||||    |||| |||
                                ACTGTTCT    CCAG CAT
                                     _____   A
GAM647  KIAA0089  3'  TTTTAATTCACATTTCTT    69967          TCG
                                AAGAAATGTGG   TGAAA
                                ||||||||||   |||||
                                TTCTTTACACT   ATTTT
                                      TA_
GAM647  KIAA0373  5'  TTTTCAAAGTAACATTTCTT   28015         GGTCG
                                AAGAAATGT    TGAAAA
                                |||||||||    ||||||
                                TTCTTTACA    ACTTTT
                                     ATGAA
GAM647  KIAA1813  3'  TTTTCACACTGTAAATTTCTTG 70314         __ TG  C
            T                    ACAAGAAAT  G  GT GTGAAAA
                                |||||||||  |  || |||||||
                                TGTTCTTTA  T  CA CACTTTT
                                     AA GT  _
GAM647  KIAA1951  3'  TTCCAGGCTTCTCTTGTCA   73766        AATGT   GT
                                TGACAAGA    GGTC  GAA
                                ||||||||    ||||  |||
                                ACTGTTCT    TCGG  CTT
                                     CT___    AC
GAM647  MGC4170   3'  TTCACCATTTCTTGTC      44227          TGGTC
                                GACAAGAAATG    GTGAA
                                ||||||||||     |||||
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                                CTGTTCTTTAC    CACTT
                                      _____
GAM647  NRN1     3'  CACTGCACATTTCTCCTCA   33432    CA      GTC
                                TGA  AGAAATGTG   GTG
                                |||  |||||||||   |||
                                ACT  TCTTTACAC   CAC
                                  CC       GT_
GAM647  PLA2G12  3'  TTTTCACAACCACATTT    48028        C
                                AAATGTGGT GTGAAAA
                                ||||||||| |||||||
                                TTTACACCA CACTTTT
                                     A
GAM647  PPY2     3'  CACTCCACATTCCTGGCCA   40819    ACA  A     TC
                                TG   AG AATGTGG  GTG
                                ||   || |||||||  |||
                                AC   TC TTACACC  CAC
                                 CGG  C      T_
GAM647  ZNF31    3'  TTTGTAGACCACATTTCCTGTT 64992      A        _ TG
              A                  TGACA GAAATGTGGTC G  AA
                                 |||||| |||||||||||  |  ||
                                 ATTGT CTTTACACCAG T  TT
                                    C          A GT
GAM647  LOC115219 3'  CACGACAACGGGTCCTCA    73295     CAA  AA   G
                                TGA   GA  TGT GTCGTG
                                |||   ||  ||| ||||||
                                ACT   CT  GCA CAGCAC
                                  C__  GG   A
GAM647  LOC120376 5'  TTCAGAGCATTTCTTTCA    75986     C       GG  G
                                TGA AAGAAATGT  TC TGAA
                                ||| |||||||||  || ||||
                                ACT TTCTTTACG  AG ACTT
                                  _       __ _
GAM647  LOC133418 3'  TTTCATATACATTTTTTGCCA  75094    A        GTC
                                TG CAAGAAATGTG   GTGAAA
                                || ||||||||||   ||||||
                                AC GTTTTTTACAT   TACTTT
                                 C         A__
GAM647  LOC151199 3'  TTAAAACCACAGCTCTTGCCA  80174    A    AA     CG
                                TG CAAGA  TGTGGT  TGA
                                || |||||  ||||||  |||
                                AC GTTCT  ACACCA  ATT
                                 C    CG     AA
GAM647  LOC152317 5'  TCACACTGACTTTTGTCA    85649        AATG   C
                                TGACAAGA    TGGT GTGA
                                ||||||||    |||| ||||
                                ACTGTTTT    GTCA CACT
                                     CA__    _
GAM647  LOC152674 3'  TTCAACCCACCCTCTTGTCA   85841        AAT    TCG
                                TGACAAGA   GTGG   TGAA
                                ||||||||   ||||   ||||
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                                ACTGTTCT  CACC  ACTT
                                    CC_   CA_
GAM647  LOC152845 5'  CATGACCACATTTTTCA    60330    CAA
                                TGA  GAAATGTGGTCGTG
                                |||  ||||||||||||||
                                ACT  TTTTACACCAGTAC
                                  ____
GAM647  LOC154743 3'  TTTAGTCCACATTGTCTTGTCA 81118       _     TCG
                                TGACAAGA AATGTGG  TGAA
                                |||||||| |||||||  ||||
                                ACTGTTCT TTACACC  ATTT
                                    G     TG_
GAM647  LOC165476 5'  TTCACGGCACCTTCT     87201     AT  G
                                AGAA  GTG TCGTGAA
                                ||||  ||| |||||||
                                TCTT  CAC GGCACTT
                                  C_  _
GAM647  LOC254266 5'  TTTTCGGTCACACATCTTATCA 97356    C   AA   GT  T
                                TGA AAGA  TGTG  CG GAA
                                ||| ||||  ||||  || |||
                                ACT TTCT  ACAC  GC TTT
                                  A   AC   TG  T
GAM647  LOC255919 3'  TTTCATTCTTACATTTCTAATC 95043    CA       TC
          A                      TGA  AGAAATGTGG  GTGAAA
                                |||  ||||||||||  ||||||
                                ACT  TCTTTACATT  TACTTT
                                  AA        CT
GAM647  LOC51754  5'  CACGGCCACATCTCTGTCA   71027     A  A
                                TGACA GA ATGTGGTCGTG
                                ||||| || ||||||||||
                                ACTGT CT TACACCGGCAC
                                   _ C
GAM647  LOC55862  3'  ACCTCATTTCTTGCCA     37485    A       T
                                TG CAAGAAATG GGT
                                || |||||||| |||
                                AC GTTCTTTAC CCA
                                 C        T
GAM647  LOC55954  3'  CACGTGGTCACTTTTCTCATCA 38877    CA    T   GT __
                                TGA  AGAAA GTG  C  GTG
                                |||  ||||| |||  |  |||
                                ACT  TCTTT CAC  G  CAC
                                  AC    T   TG TG
GAM648  ABCC1    3'  ACCTCTTTTCTTTCCCTCTCA  17177    GA  A      TTTGT
                                TG  AG GAAAGAAG    AGGT
                                ||  || ||||||||    ||||
                                AC  TC CTTTCTTT    TCCA
                                 TC  C       TC___
GAM648  ABCC1    3'  ACCTCTTTTCTTTCCCTCTCA  39130    GA  A      TTTGT
                                TG  AG GAAAGAAG    AGGT
                                ||  || ||||||||    ||||
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                                AC  TC CTTTCTTT    TCCA
                                 TC  C      TC___
GAM648  ABCC1    3'  ACCTCTTTTCTTTCCCTCTCA  39122    GA  A      TTTGT
                                TG  AG GAAAGAAG    AGGT
                                ||  || ||||||||    ||||
                                AC  TC CTTTCTTT    TCCA
                                 TC  C      TC___
GAM648  B4GALT3  3'  ACCCCAAGCCCCTCCCTCTTCC 13675       AA  AA    TA
            A                    TGGAAGAG  AG  GTTTG  GGT
                                ||||||||  ||  |||||  |||
                                ACCTTCTC  TC  CGAAC  CCA
                                     CC  CC    C_
GAM648  CBFA2T3  3'  ACCGCAGCTACTCCCCTTTCTT 17754        A___  A   T  A
            CCA                     TGGAAGAGA    AG AGTT GT GGT
                                ||||||||||    || |||| || |||
                                ACCTTCTTT    TC TCGA CG CCA
                                     CCCC  A   _  _
GAM648  CSRP1    3'  ACCCAAGACCCTGCCTCTTCCA 14524       AA  AA    GTA
                                TGGAAGAG  AG  GTTT   GGT
                                ||||||||  ||  ||||   |||
                                ACCTTCTC  TC  CAGA   CCA
                                     CG  C_    AC_
GAM648  DCN      5'  ACCTACCCCCTCCTCCTTTCCA 8615       A  AA A  TTT
                                TGGAAG GA  G AG   GTAGGT
                                ||||||  ||  | ||   ||||||
                                ACCTTT CT  C TC   CATCCA
                                    C  __ C  CCC
GAM648  EHD4     3'  CTAGATGACTTCTTTCACCTCC 57691      AGA        TG_
            A                    TGGA   GAAAGAAGTT   TAG
                                ||||   ||||||||||   |||
                                ACCT   CTTTCTTCAG   ATC
                                  CCA        TAG
GAM648  GCK      3'  ACCCCCAGAGACCTTTTCTCTC 53176     A      AAG_   TA
            CCA                     TGG AGAGAAAG    TTTG  GGT
                                ||| ||||||||    ||||  |||
                                ACC TCTCTTTT    AGAC  CCA
                                  C       CCAG    CC
GAM648  GCK      3'  ACCCCCAGAGACCTTTTCTCTC 53171     A      AAG_   TA
            CCA                     TGG AGAGAAAG    TTTG  GGT
                                ||| ||||||||    ||||  |||
                                ACC TCTCTTTT    AGAC  CCA
                                  C       CCAG    CC
GAM648  IRF1     5'  TCTGCCTTCTTCCCTCTTCCA  64348        A_     TTT
                                TGGAAGAG  AAGAAG   GTAGG
                                ||||||||  ||||||   |||||
                                ACCTTCTC  TTCTTC   CGTCT
                                     CC     ___
GAM648  KCNMB1   3'  ACCTGCCCTCCCACTCTTCCA  14707        AAA  A TTT
                                TGGAAGAG   GA G   GTAGGT
                                ||||||||   || |   ||||||
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                                ACCTTCTC  CT C  CGTCCA
                                    ACC  _ C__
GAM648  LOH11CR2A 3'  ACCTACATGTCTTTTCTTCCA  27536        A  AGTT
                                TGGAAGAGAA GA   TGTAGGT
                                |||||||||| ||   |||||||
                                ACCTTCTTTT CT   ACATCCA
                                     _  GT__
GAM648  LPHH1    5'  ACAGACGTTCTTTCTCCTCCA  24535     A      _
                                TGGA GAGAAAGAA GTTTGT
                                |||| ||||||||| ||||||
                                ACCT CTCTTTCTT CAGACA
                                  C       G
GAM648  MYCL2    3'  CCCAGCTCTCTCTCTTCC    18179       A  A  TGTA
                                GGAAGAGA AGA GTT   GG
                                |||||||| ||| |||   ||
                                CCTTCTCT TCT CGA   CC
                                    C  _  C___
GAM648  MYL1     5'  ACCCAACCACCATCCTCTTCCA 54376       AAAGAAGT  TA
                                TGGAAGAG      TTG  GGT
                                ||||||||      |||  |||
                                ACCTTCTC      AAC  CCA
                                    CTACCACC  __
GAM648  OGT      5'  CCTCCTCCTCCTCTTCCA    13202       AA  A  TTTGT
                                TGGAAGAG  AG AG    AGG
                                ||||||||  || ||    |||
                                ACCTTCTC  TC TC    TCC
                                    C_  C  C_____
GAM648  PCDHA1   3'  ACCCAAGTTTCCTTTCTCCTCC 48590    A     _ GT  TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| |||||||  ||  |||  |||
                                CCT CTCTTTC TT  AAC  CCA
                                  C      C  TG  __
GAM648  PCDHA1   3'  ACCCAAGTTTCCTTTCTCCTCC 38179    A     _ GT  TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| |||||||  ||  |||  |||
                                CCT CTCTTTC TT  AAC  CCA
                                  C      C  TG  __
GAM648  PCDHA10  3'  ACCCAAGTTTCCTTTCTCCTCC 49023    A     _ GT  TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| |||||||  ||  |||  |||
                                CCT CTCTTTC TT  AAC  CCA
                                  C      C  TG  __
GAM648  PCDHA10  3'  ACCCAAGTTTCCTTTCTCCTCC 38187    A     _ GT  TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| |||||||  ||  |||  |||
                                CCT CTCTTTC TT  AAC  CCA
                                  C      C  TG  __
GAM648  PCDHA11  3'  ACCCAAGTTTCCTTTCTCCTCC 38196    A     _ GT  TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| |||||||  ||  |||  |||
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                                CCT CTCTTTC TT  AAC  CCA
                                  C     C  TG  __
GAM648  PCDHA12  3' ACCCAAGTTTCCTTTCTCCTCC 38206    A    _ GT  TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| ||||||| ||  |||  |||
                                CCT CTCTTTC TT  AAC  CCA
                                  C     C  TG  __
GAM648  PCDHA13  3' ACCCAAGTTTCCTTTCTCCTCC 38215    A    _ GT  TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| ||||||| ||  |||  |||
                                CCT CTCTTTC TT  AAC  CCA
                                  C     C  TG  __
GAM648  PCDHA2   3' ACCCAAGTTTCCTTTCTCCTCC 38223    A    _ GT  TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| ||||||| ||  |||  |||
                                CCT CTCTTTC TT  AAC  CCA
                                  C     C  TG  __
GAM648  PCDHA3   3' ACCCAAGTTTCCTTTCTCCTCC 38231    A    _ GT  TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| ||||||| ||  |||  |||
                                CCT CTCTTTC TT  AAC  CCA
                                  C     C  TG  __
GAM648  PCDHA4   3' ACCCAAGTTTCCTTTCTCCTCC 38239    A    _ GT  TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| ||||||| ||  |||  |||
                                CCT CTCTTTC TT  AAC  CCA
                                  C     C  TG  __
GAM648  PCDHA5   3' ACCCAAGTTTCCTTTCTCCTCC 38247    A    _ GT  TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| ||||||| ||  |||  |||
                                CCT CTCTTTC TT  AAC  CCA
                                  C     C  TG  __
GAM648  PCDHA6   3' ACCCAAGTTTCCTTTCTCCTCC 48996    A    _ GT  TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| ||||||| ||  |||  |||
                                CCT CTCTTTC TT  AAC  CCA
                                  C     C  TG  __
GAM648  PCDHA6   3' ACCCAAGTTTCCTTTCTCCTCC 38255    A    _ GT  TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| ||||||| ||  |||  |||
                                CCT CTCTTTC TT  AAC  CCA
                                  C     C  TG  __
GAM648  PCDHA7   3' ACCCAAGTTTCCTTTCTCCTCC 38263    A    _ GT  TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| ||||||| ||  |||  |||
                                CCT CTCTTTC TT  AAC  CCA
                                  C     C  TG  __
GAM648  PCDHA8   3' ACCCAAGTTTCCTTTCTCCTCC 38271    A    _ GT  TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| ||||||| ||  |||  |||
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                                CCT CTCTTTC TT  AAC  CCA
                                  C      C  TG  __
GAM648  PCDHA9   3'  ACCCAAGTTTCCTTTCTCCTCC 49011     A     _  GT   TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| ||||||| ||  |||  |||
                                CCT CTCTTTC TT  AAC  CCA
                                  C      C  TG  __
GAM648  PCDHAC1  3'  ACCCAAGTTTCCTTTCTCCTCC 38160     A     _  GT   TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| ||||||| ||  |||  |||
                                CCT CTCTTTC TT  AAC  CCA
                                  C      C  TG  __
GAM648  PCDHAC2  3'  ACCCAAGTTTCCTTTCTCCTCC 38171     A     _  GT   TA
                                GGA GAGAAAG AA  TTG  GGT
                                ||| ||||||| ||  |||  |||
                                CCT CTCTTTC TT  AAC  CCA
                                  C      C  TG  __
GAM648  PTGFRN   3'  ACTGCTCTCTCTTCCA      67181         A  A
                                TGGAAGAGA AG AGT
                                ||||||||| || |||
                                ACCTTCTCT TC TCA
                                     C  G
GAM648  RING1    3'  ACCCCAGCTTCTTTGTCCCCCA 11345     AA  G       TGTA
                                TGG  GA AAAGAAGTT    GGT
                                |||  || |||||||||    |||
                                ACC  CT TTTCTTCGA    CCA
                                  CC  G        CC__
GAM648  RPL29    5'  ACCGCAGCCCCTTTCTCTTCC  6392           AA   T  A
                                GGAAGAGAAAG  GTT GT GGT
                                ||||||||||  ||| || |||
                                CCTTCTCTTTC  CGA CG CCA
                                      CC  _ _
GAM648  SELP     3'  ACCTACCACCCCTTCCTGTCC  11534     AG  A   AA  TT
                                GGA  AG AAG  GT  GTAGGT
                                |||  || |||  ||  ||||||
                                CCT  TC TTC  CA  CATCCA
                                  G_  C   CC  C_
GAM648  SHANK2   3'  ACCTGCCCCTCTTTCTC     24583         A TTT
                                GAGAAAGA G   GTAGGT
                                ||||||||  |   ||||||
                                CTCTTTCT C   CGTCCA
                                     _ CC_
GAM648  STAU     3'  CCACTGCTTTCTCTTCCA    33899           A   TTGTA
                                TGGAAGAGAAAG AGT    GG
                                ||||||||||||  |||    ||
                                ACCTTCTCTTTC TCA    CC
                                      G  _____
GAM648  STAU     3'  CCACTGCTTTCTCTTCCA    33906           A   TTGTA
                                TGGAAGAGAAAG AGT    GG
                                ||||||||||||  |||    ||
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                                ACCTTCTCTTTC TCA    CC
                                      G  _____
GAM648  STAU    3'  CCACTGCTTTCTCTTCCA   15998         A  TTGTA
                                TGGAAGAGAAAG AGT    GG
                                |||||||||||| |||    ||
                                ACCTTCTCTTTC TCA    CC
                                      G  _____
GAM648  STAU    3'  CCACTGCTTTCTCTTCCA   33893         A  TTGTA
                                TGGAAGAGAAAG AGT    GG
                                |||||||||||| |||    ||
                                ACCTTCTCTTTC TCA    CC
                                      G  _____
GAM648  UBE4A   3'  CCTGCTATTTCTCTTCCA   16563         GAAGTTT
                                TGGAAGAGAAA     GTAGG
                                ||||||||||      |||||
                                ACCTTCTCTTT     CGTCC
                                      AT_____
GAM648  WAS     3'  CCTCCACTCTCCTCTTCCA   4581        AA  AGTT  T
                                TGGAAGAG  AGA   TG AGG
                                ||||||||  |||   || |||
                                ACCTTCTC  TCT   AC TCC
                                    C_  C___  C
GAM648  C12orf22 3'  AAGCCCTTTCTCTCCCA    47972    A      AA
                                TGG AGAGAAAG  GTTT
                                ||| ||||||||  ||||
                                ACC TCTCTTTC  CGAA
                                  C       C_
GAM648  C17orf31 3'  CCTGCTCCCTTTCTCCTC   34121    A     AAGTTT
                                GA GAGAAAG     GTAGG
                                || |||||||     |||||
                                CT CTCTTTC     CGTCC
                                 C      CCT___
GAM648  C20orf150 3'  ACCTGGCCCTCCTCCTTTTCCA 65386       AA  A  TTTG
                                TGGAAGAG  AG AG   TAGGT
                                ||||||||  || ||   |||||
                                ACCTTTTC  TC TC   GTCCA
                                    C_  C  CCG_
GAM648  C3F     5'  ACCTACCTCATCCACCTCTTCC 19282       AAA  AGTTT
          A                      TGGAAGAG  GA    GTAGGT
                                 ||||||||  ||    ||||||
                                 ACCTTCTC  CT    CATCCA
                                    CAC  ACTC_
GAM648  CAMK1G  3'  AACTCCTCTGCTCTTCCA    39946       AA_  A
                                TGGAAGAG   AG AGTT
                                ||||||||   || ||||
                                ACCTTCTC   TC TCAA
                                    GTC  C
GAM648  CX46.6  3'  ACCTGCGACCCCTTCTCCTC  39940     AA    T__
                                GAG  AGAAG   TTGTAGGT
                                |||  |||||   ||||||||
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                                CTC  TCTTC   AGCGTCCA
                                  C_    CCC
GAM648  EHM2     3'  CCAGCACCCTCTTCCTCTTCTA 38914        A    A TT   A
                                TGGAAGAG AAGA G  TGT GG
                                |||||||| |||| |  ||| ||
                                ATCTTCTC TTCT C  ACG CC
                                     C    _ CC   A
GAM648  FLJ11539 3'  CCTTCCCTCTCTCTTCTA    45374         A  AAGTTTGT
                                TGGAAGAGA AG       AGG
                                |||||||||  ||       |||
                                ATCTTCTCT TC       TCC
                                      C  CCT_____
GAM648  FLJ11726 3'  CCCACAGGCTCCTCTTCCA    46408        AAA  A     A
                                TGGAAGAG   GA GTTTGT GG
                                ||||||||   || |||||| ||
                                ACCTTCTC   CT CGGACA CC
                                     ___  _     C
GAM648  FLJ14641 3'  ACCTTTTTTCTTCCTCTTCC   51481        A     TTTGT
                                GGAAGAG AAGAAG    AGGT
                                ||||||| ||||||    ||||
                                CCTTCTC TTCTTT    TCCA
                                     C     TT___
GAM648  GABARAPL1 3'  ACTTCTTTTCTCCCA       48599     A     A
                                TGG AGAGAA GAAGT
                                ||| |||||| |||||
                                ACC TCTTTT CTTCA
                                  C     _
GAM648  GABARAPL3 3'  ACTTCTTTTCTCCCA       50799     A     A
                                TGG AGAGAA GAAGT
                                ||| |||||| |||||
                                ACC TCTTTT CTTCA
                                  C     _
GAM648  HSPBP1   3'  ACCTACAAGGCCCTCTCCCA   24358     A   AAAGAAG
                                TGG AGAG      TTTGTAGGT
                                ||| ||||      |||||||||
                                ACC TCTC      GAACATCCA
                                  C    CCG____
GAM648  KIAA0335 3'  ACCCCCATTCCCTCTCTTCT   28990        AA   GTT  TA
                                GGAAGAGA  GAA   TG  GGT
                                ||||||||  |||   ||  |||
                                TCTTCTCT  CTT   AC  CCA
                                     CC   ___  CC
GAM648  KIAA0427 3'  CCTGCCTTCTTCCTCCCTCCA  28719     A_   A     TTT
                                TGGA  GAG AAGAAG   GTAGG
                                ||||  ||| ||||||   |||||
                                ACCT  CTC TTCTTC   CGTCC
                                  CC   C     ___
GAM648  KIAA0721 5'  GAACTCTCCCTCTCCCA     95968     A    AA   A
                                TGG AGAG  AGA GTTT
                                ||| ||||  ||| ||||
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                                ACC TCTC  TCT CAAG
                                  C    CC  _
GAM648  KIAA1887  5'  ACCTTCAGACCCTCCTCTCTTC 76770         AA  A_    T
            CA                    TGGAAGAGA  GA  GTTTG AGGT
                                  |||||||||  ||  ||||| ||||
                                  ACCTTCTCT  CT  CAGAC TCCA
                                       C_  CC    T
GAM648  KIAA1979  3'  TTGTCAAGTTCCTTCTCTTCCA 88295          A   G  TG
                                  TGGAAGAGAA GAA TT  TAG
                                  |||||||||| ||| ||  |||
                                  ACCTTCTCTT CTT AA  GTT
                                        C   G  CT
GAM648  PRO0233   5'  CTGTAATTCTTCCTCTTCCA   26116         A    GT
                                  TGGAAGAG AAGAA  TTGTAG
                                  ||||||||| |||||  ||||||
                                  ACCTTCTC TTCTT  AATGTC
                                       C    __
GAM648  PTPN9     3'  ACCTCCCTCCTCCTTTCTCCCG 11075     AA_      A  TTTGT
            CCA                     TGG   GAGAAAG AG    AGGT
                                  |||   ||||||| ||    ||||
                                  ACC   CTCTTTC TC    TCCA
                                    GCC      C  CTCCC
GAM648  STX5A     3'  CCTCTTTCTTCCTCTTTCA    12042         A     TTTGT
                                  TGGAAGAG AAGAAG    AGG
                                  |||||||| ||||||    |||
                                  ACTTTCTC TTCTTT    TCC
                                       C     C____
GAM648  SUPT4H1   3'  ACCTGCCTTGCCTCCCTCTTCC 12058         AAA  A  TT_
            A                     TGGAAGAG   GA GT   GTAGGT
                                  ||||||||   || ||   ||||||
                                  ACCTTCTC   CT CG   CGTCCA
                                       C__  C  TTC
GAM648  TEB4      3'  ACCCACATCCTCTCTTTTCCA  60653         AA  A TT   A
                                  TGGAAGAGA  GA G  TGT GGT
                                  |||||||||  || |  ||| |||
                                  ACCTTTTCT  CT C  ACA CCA
                                       __  _ CT   C
GAM648  THTPA     3'  ACAGTGACTCCTCTCTCTCCA  44257      A    A  A   __
                                  TGGA GAGA AG AGTT  TGT
                                  |||| |||| || ||||  |||
                                  ACCT CTCT TC TCAG  ACA
                                    _    C  C    TG
GAM648  UBE3B     3'  AAACTTCATTTCTCTTCCA    76918           _
                                  TGGAAGAGAAA GAAGTTT
                                  |||||||||| |||||||
                                  ACCTTCTCTTT CTTCAAA
                                         A
GAM648  VELI1     5'  ACCCACCCAAGCTTTCTTCTCC 16234      AG     AAGTTT  A
            A                     TGGA  AGAAAG     GT GGT
                                  ||||  ||||||     || |||
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                                ACCT  TCTTTC     CA CCA
                                  CT     GAACC_  C
GAM648  ZDHHC3    3'  ACCCCATCTCCCTCTCTTCC  33456        AA  A TT  TA
                                GGAAGAGA  GA G  TG  GGT
                                ||||||||  || |  ||  |||
                                CCTTCTCT  CT C  AC  CCA
                                    CC  _ T_  C_
GAM648  LOC136015 3'  CCTAGATCTTTCTCTCCCA   76202     A       AGTTTG
                                TGG AGAGAAAGA     TAGG
                                ||| |||||||||     ||||
                                ACC TCTCTTTCT     ATCC
                                  C        AG____
GAM648  LOC143310 5'  GTAGACTTTCCTCTCTCCCA  76539     A     AA
                                TGG AGAGA  GAAGTTTGT
                                ||| |||||  |||||||||
                                ACC TCTCT  TTTCAGATG
                                  C     CC
GAM648  LOC144473 3'  ACCTCATTCTCTCCCCCTCTTC 83065        AAA  _  TT  T
          TA                      TGGAAGAG   GA AG  TG AGGT
                                ||||||||   || ||  || ||||
                                ATCTTCTC   CT TC  AC TCCA
                                    CCC  C  TT  _
GAM648  LOC146243 3'  ACTCTCCTCTCTTCCA      83639         A_  A
                                TGGAAGAGA  AGA GT
                                |||||||||  ||| ||
                                ACCTTCTCT  TCT CA
                                     CC  _
GAM648  LOC150319 3'  ACCCCTTTCTTCTTCCA     79644        _    AA
                                TGGAAGA GAAAG  GT
                                |||||||| |||||  ||
                                ACCTTCT CTTTC  CA
                                    T     CC
GAM648  LOC152137 5'  ACCTGCAGCTCCCCCTCCCCCA 80477     AA   AAA  A   T
                                TGG  GAG   GA GTT GTAGGT
                                |||  |||   || ||| ||||||
                                ACC  CTC   CT CGA CGTCCA
                                  CC   CCC  _  _
GAM648  LOC152926 5'  ACAGACTTCTCCCTCTCCA   80742     A   AA
                                TGGA GAG  AGAAGTTTGT
                                |||| |||  ||||||||||
                                ACCT CTC  TCTTCAGACA
                                   _   CC
GAM648  LOC154788 3'  CCTAGATCTTTCTCTCCCA   86246     A       AGTTTG
                                TGG AGAGAAAGA     TAGG
                                ||| |||||||||     ||||
                                ACC TCTCTTTCT     ATCC
                                  C        AG____
GAM648  LOC157421 5'  ACCCCCTCCTTCCTTCTTCCA  86441        AAA    TTTGTA
                                TGGAAGAG   GAAG     GGT
                                ||||||||   ||||     |||
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                                ACCTTCTT  CTTC     CCA
                                    C__   CTCCC_
GAM648  LOC157627 5'  CTGAGGACTTCTTTCCTCTCCA 81504     A  _       TG
                                TGGA GAG AAAGAAGTT  TAG
                                |||| ||| |||||||||  |||
                                ACCT CTC TTTCTTCAG  GTC
                                  _  C       GA
GAM648  LOC157931 3'  ACCTTCCCTCCTTTCCTCTTCC 86654       _   A  TTTGT
          A                    TGGAAGAG AAAG AG    AGGT
                               |||||||| |||| ||    ||||
                               ACCTTCTC TTTC TC    TCCA
                                   C   C  CCT__
GAM648  LOC221876 5'  AAACTTCCCTTCTTCCA    93917       AAA
                               TGGAAGAG  GAAGTTT
                               ||||||||  |||||||
                               ACCTTCTT  CTTCAAA
                                   CC_
GAM648  LOC254824 3'  ACCAGCCCCCTCCCTGCTCTTC 96613       AAAGA  TTT  A
          CA                   TGGAAGAG    AG  GT GGT
                               ||||||||    ||  || |||
                               ACCTTCTC    TC  CG CCA
                                   GTCCC  CCC  A
GAM648  LOC255862 3'  ACCTGCGTTCTCCTACCTCTTC 94484       AA  A  TT
          CA                   TGGAAGAG  AG AG  TGTAGGT
                               ||||||||  || ||  |||||||
                               ACCTTCTC  TC TC  GCGTCCA
                                   CA  C  TT
GAM648  LOC93190  3'  ACCCACAGGTTCCTTTCTTTTC 71657         A  TT   A
          CA                   TGGAAGAGAAAG AG  TGT GGT
                               ||||||||||||| ||  ||| |||
                               ACCTTTTCTTTC TT  ACA CCA
                                     C  GG   C
GAM649  KIAA1908  5'  AGCACACAGCCCTGA      73392       A  CGTTT
                               TTAGGGCT GT    GTGCT
                               |||||||| ||    |||||
                               AGTCCCGA CA    CACGA
                                  _ ______
GAM649  LOC124739 5'  AGCACAGTGGCAGCCCTGA   74324       A   GTT
                               TTAGGGCT GTC   TGTGCT
                               |||||||| |||   ||||||
                               AGTCCCGA CGG   ACACGA
                                   _   TG_
GAM649  LOC145988 5'  CACACACAACCCAGCCCTAA   77607       A_  C  T
                               TTAGGGCT  GT GT TGTG
                               ||||||||  || || ||||
                               AATCCCGA  CA CA ACAC
                                   CC  A  C
GAM649  LOC219654 3'  AGTCCAACGACTAACCCTGA   91298      C       T TG
                               TTAGGG TAGTCGTT G  CT
                               |||||| |||||||| |  ||
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                                AGTCCC ATCAGCAA C  GA
                                   A       _ CT
GAM650  FUS1     3'  CTACAGCACTTTACAAGC    23448    CG  T
                                GC  GT GAAGTGCTGTAG
                                ||  || ||||||||||||
                                CG  CA TTTCACGACATC
                                 AA  _
GAM650  LNK      3'  CAGGCCCCAGCCGGCAACT    18460    C       AA  G
                                AG TGCCGGTTG  GT CTG
                                || |||||||||  || |||
                                TC ACGGCCGAC  CG GAC
                                 A        CC  _
GAM650  MRPL49   3'  GCCACAGCAAGGAGCCCGACAC 69569    C  C   TTGAAG     A
           T                     AG TG CGG     TGCTGT GC
                                || || |||     |||||| ||
                                TC AC GCC     ACGACA CG
                                 _ A   CGAGGA     C
GAM650  PHLDA3   5'  CACCTCACCGGCAGC       24764         T  A
                                GCTGCCGGT GA GTG
                                ||||||||| || |||
                                CGACGGCCA CT CAC
                                      _ C
GAM650  TCFL4    3'  CTACAACACCTCACACTGGTCA 63463      _    _  A   C
           GCT                    AGCTG CCGGT TGA GTG TGTAG
                                ||||| ||||| ||| ||| |||||
                                TCGAC GGTCA ACT CAC ACATC
                                   T    C   C   A
GAM650  WNT5A    3'  GCCACGTTTCCAAACGGCAGCT 12667        G   AAGT  T  A
                                AGCTGCCG TTG    GC GT GC
                                |||||||| |||    || || ||
                                TCGACGGC AAC    TG CA CG
                                     A   CTT_  _  C
GAM650  C17orf31 3'  TACAGCAACAGCAGCT     34128       CG  TGAAG
                                AGCTGC  GT    TGCTGTA
                                ||||||  ||    |||||||
                                TCGACG  CA    ACGACAT
                                   A_ ______
GAM650  DKFZp547M072 3'  CTACAGCAAGCCAACAGGT    61079     G    AAG
                                GCC GTTG   TGCTGTAG
                                ||| ||||   ||||||||
                                TGG CAAC   ACGACATC
                                  A    CGA
GAM650  FLJ10898 5'  CTACAGCACCTGCTGGATCAGC 59429       __     TGAA
           T                     AGCTG  CCGGT    GTGCTGTAG
                                |||||  |||||   |||||||||
                                TCGAC  GGTCG    CACGACATC
                                   TA    TC__
GAM650  FLJ13262 3'  GCCACCCCCTTCTACCGGCAGC 46158         T   TGCT  A
                                GCTGCCGGT GAAG    GT GC
                                |||||||| ||||    || ||
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                                CGACGGCCA CTTC    CA CG
                                     T    CCC_  C
GAM650  FLJ13841  3'  GCTACAACACCTCTGAACTGGC 45223    C       __  A   C
            ACT                    AG TGCCGGTT  GA GTG TGTAGC
                                || ||||||||  || ||| ||||||
                                TC ACGGTCAA  CT CAC ACATCG
                                 _       GT  C   A
GAM650  FLJ20154  5'  TACAGCAGCAGCAGCT      72933       CG  TGAAG
                                AGCTGC  GT    TGCTGTA
                                ||||||  ||    |||||||
                                TCGACG  CG    ACGACAT
                                   A_  ______
GAM650  KCNS1     3'  TACAGCACCCAGCACT      9583     C   C  TTGAA
                                AG TGC GG     GTGCTGTA
                                || ||| ||     ||||||||
                                TC ACG CC     CACGACAT
                                 _   A  ______
GAM650  KIAA0420  3'  GCTGTAGCACTTGCTCCAACCA 63360    C     A  T________  TGTA
            GCAGC                    GC GGTTG AG       GC    GC
                                || ||||| ||       ||    ||
                                CG CCAAC TC       CG    CG
                                 A    C  GTTCAIII  ATGT
GAM650  KIAA1879  5'  GCCACAGCACTGACCAGGCATG 73570    _   _   GA       A
            C                     GC TGCC GGTT  AGTGCTGT GC
                                || |||| ||||  |||||||| ||
                                CG ACGG CCAG  TCACGACA CG
                                 T    A    __       C
GAM650  PP1628    3'  GCCTTCCCCCACCAGCAGC    47300      C   T___    T
                                GCTGC GGT    GAAG GC
                                ||||| |||    |||| ||
                                CGACG CCA    CTTC CG
                                   A   CCCC    _
GAM650  LOC146488 5'  GCTACAACCGCTTCAACAACAA 70814    C  CCG       C_
            CT                     AG TG   GTTGAAGTG  TGTAGC
                                || ||   |||||||||  ||||||
                                TC AC   CAACTTCGC  ACATCG
                                 A  AA_        CA
GAM650  LOC159199 3'  GCCACAGCCAACACCAGCAGCT 82182       C   TGAAGT    A
                                AGCTGC GGT     GCTGT GC
                                |||||| |||     ||||| ||
                                TCGACG CCA     CGACA CG
                                   A   CAAC__     C
GAM650  LOC199923 5'  CACAGCACTCGCAGCT      88497       CGGTT  A      A
                                AGCTGC     GA GTGCTGT G
                                ||||||     || ||||||| |
                                TCGACG     CT CACGACA C
                                   _____  _      C
GAM650  LOC201799 5'  CAGTGCTTCAACAGCAACT    89055    C   CG      TG
                                AG TGC  GTTGAAG  CTG
                                || |||  |||||||  |||
```

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                                TC ACG  CAACTTC  GAC
                                 A  A_      GT
GAM650  LOC220739 3'  GCCACCCTGCCAGCCAGCAGCT 92930       C    AA  CT  A
                                AGCTGC GGTTG  GTG  GT GC
                                |||||| |||||  |||  || ||
                                TCGACG CCGAC  CGT  CA CG
                                   A    __   CC  C
GAM650  LOC254221 5'  GCCAGTTCCCACCGGCAGC   97601         T_  G  _
                                GCTGCCGGT  GAA TG C
                                |||||||||  ||| || |
                                CGACGGCCA  CTT AC G
                                     CC   G  C
GAM650  LOC257354 3'  GCTGTAGCACTTGCTCCAACCA 95093    C    A  T________  TGTA
           GCAGC                  GC GGTTG AG       GC    GC
                                || ||||| ||       ||    ||
                                CG CCAAC TC       CG    CG
                                 A    C  GTTCAIII  ATGT
GAM650  LOC92578  5'  GCTACAGCTCTACAACCAGCAG 69828      C    A  T
           C                     GCTGC GGTTG AG GCTGTAGC
                                ||||| ||||| || ||||||||
                                CGACG CCAAC TC CGACATCG
                                   A    A  T
GAM651  COL11A1   3'  CATTTTGTGCCACATGCAA   8494       CTA      C
                                TTGCAT   GCACAAAA TG
                                ||||||   |||||||| ||
                                AACGTA   CGTGTTTT AC
                                   CAC      _
GAM651  COL11A1   3'  CATTTTGTGCCACATGCAA   8494       CTA      C
                                TTGCAT   GCACAAAA TG
                                ||||||   |||||||| ||
                                AACGTA   CGTGTTTT AC
                                   CAC      _
GAM651  COL11A1   3'  CATTTTGTGCCACATGCAA   54653      CTA      C
                                TTGCAT   GCACAAAA TG
                                ||||||   |||||||| ||
                                AACGTA   CGTGTTTT AC
                                   CAC      _
GAM651  COL11A1   3'  CATTTTGTGCCACATGCAA   54653      CTA      C
                                TTGCAT   GCACAAAA TG
                                ||||||   |||||||| ||
                                AACGTA   CGTGTTTT AC
                                   CAC      _
GAM651  DBY       3'  TTTTGTGGCCAGATGCAA    16230        A  _
                                TTGCATCT GC ACAAAA
                                |||||||| || ||||||
                                AACGTAGA CG TGTTTT
                                     C  G
GAM651  DBY       3'  TTTTGTGGCCAGATGCAA    16230        A  _
                                TTGCATCT GC ACAAAA
                                |||||||| || ||||||
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                                AACGTAGA CG TGTTTT
                                     C  G
GAM651  NONO     3'  TAATCAGTTCTGTGTGGTGCA  82021       TA    A
                                TGCATC  GCACA AACTGATTA
                                ||||||  ||||| |||||||||
                                ACGTGG  TGTGT TTGACTAAT
                                   __    C
GAM651  NONO     3'  TAATCAGTTCTGTGTGGTGCA  82021       TA    A
                                TGCATC  GCACA AACTGATTA
                                ||||||  ||||| |||||||||
                                ACGTGG  TGTGT TTGACTAAT
                                   __    C
GAM651  NUFIP1   3'  TAATCAGTTTCTGAAATGTAA  24721       CTAG  CA
                                TTGCAT   CA  AAACTGATTA
                                ||||||   ||  ||||||||||
                                AATGTA   GT  TTTGACTAAT
                                   AA__  C_
GAM651  NUFIP1   3'  TAATCAGTTTCTGAAATGTAA  24721       CTAG  CA
                                TTGCAT   CA  AAACTGATTA
                                ||||||   ||  ||||||||||
                                AATGTA   GT  TTTGACTAAT
                                   AA__  C_
GAM651  COE2     3'  AATCAGTTTTCTAGAAGAAGCA 64246      A___    CAC
          A                      TTGC   TCTAG   AAAACTGATT
                                 ||||   |||||  ||||||||||
                                 AACG   AGATC   TTTTGACTAA
                                   AAGA   ___
GAM651  COE2     3'  AATCAGTTTTCTAGAAGAAGCA 64246      A___    CAC
          A                      TTGC   TCTAG   AAAACTGATT
                                 ||||   |||||  ||||||||||
                                 AACG   AGATC   TTTTGACTAA
                                   AAGA   ___
GAM651  HSPC043  3'  TTGTGACTAGATGCAA     67724         _
                                TTGCATCTAG CACAA
                                |||||||||| |||||
                                AACGTAGATC GTGTT
                                      A
GAM651  HSPC043  3'  TTGTGACTAGATGCAA     67724         _
                                TTGCATCTAG CACAA
                                |||||||||| |||||
                                AACGTAGATC GTGTT
                                      A
GAM651  KIAA0553 3'  TTTTCTGCTAGATGCAA     69896          C
                                TTGCATCTAGCA AAAA
                                |||||||||||| ||||
                                AACGTAGATCGT TTTT
                                      C
GAM651  KIAA0553 3'  TTTTCTGCTAGATGCAA     69896          C
                                TTGCATCTAGCA AAAA
                                |||||||||||| ||||
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                                AACGTAGATCGT TTTT
                                      C
GAM651  KIAA1041 3'  TTTTGTGCAGATACAA     30148    C   A
                                TTG ATCT GCACAAAA
                                ||| |||| ||||||||
                                AAC TAGA CGTGTTTT
                                  A   _
GAM651  KIAA1041 3'  TTTTGTGCAGATACAA     30148    C   A
                                TTG ATCT GCACAAAA
                                ||| |||| ||||||||
                                AAC TAGA CGTGTTTT
                                  A   _
GAM651  LRMP     5'  GTCCTGCGCAGATGCAA     20467       A  A  AA
                                TTGCATCT GC CA  AC
                                |||||||| || ||  ||
                                AACGTAGA CG GT  TG
                                     _  C  CC
GAM651  LRMP     5'  GTCCTGCGCAGATGCAA     20467       A  A  AA
                                TTGCATCT GC CA  AC
                                |||||||| || ||  ||
                                AACGTAGA CG GT  TG
                                     _  C  CC
GAM651  MAL2     3'  TTTTGTCCAGATGCAA      53561       AGC
                                TTGCATCT   ACAAAA
                                ||||||||   ||||||
                                AACGTAGA   TGTTTT
                                     CC_
GAM651  MAL2     3'  TTTTGTCCAGATGCAA      53561       AGC
                                TTGCATCT   ACAAAA
                                ||||||||   ||||||
                                AACGTAGA   TGTTTT
                                     CC_
GAM651  RAB14    3'  CAGCGCTTGTGCTGATACAA  32869    C  T     AA_
                                TTG ATC AGCACAA   CTG
                                ||| ||| |||||||   |||
                                AAC TAG TCGTGTT   GAC
                                  A  _      CGC
GAM651  RAB14    3'  CAGCGCTTGTGCTGATACAA  32869    C  T     AA_
                                TTG ATC AGCACAA   CTG
                                ||| ||| |||||||   |||
                                AAC TAG TCGTGTT   GAC
                                  A  _      CGC
GAM651  SPAF     3'  AATCAGTTTTACCTGGA     82634      CAC
                                TCTAG   AAAACTGATT
                                |||||   ||||||||||
                                AGGTC   TTTTGACTAA
                                   CA_
GAM651  SPAF     3'  AATCAGTTTTACCTGGA     82634      CAC
                                TCTAG   AAAACTGATT
                                |||||   ||||||||||
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```
                                AGGTC   TTTTGACTAA
                                   CA_
GAM651   LOC146455 3'  TAATCAGTTCTGTGTGGTGCA  77907       TA    A
                                TGCATC  GCACA AACTGATTA
                                ||||||  ||||| |||||||||
                                ACGTGG  TGTGT TTGACTAAT
                                   __    C
GAM651   LOC146455 3'  TAATCAGTTCTGTGTGGTGCA  77907       TA    A
                                TGCATC  GCACA AACTGATTA
                                ||||||  ||||| |||||||||
                                ACGTGG  TGTGT TTGACTAAT
                                   __    C
GAM651   LOC157653 5'  AGTACCATGTTAGATGCAA    81521          CAAA
                                TTGCATCTAGCA    ACT
                                ||||||||||||    |||
                                AACGTAGATTGT    TGA
                                      ACCA
GAM651   LOC157653 5'  AGTACCATGTTAGATGCAA    81521          CAAA
                                TTGCATCTAGCA    ACT
                                ||||||||||||    |||
                                AACGTAGATTGT    TGA
                                      ACCA
GAM651   LOC158427 3'  AATCAGTTTTATTTGCTA     57675       C__
                                TAGCA   AAAACTGATT
                                |||||   ||||||||||
                                ATCGT   TTTTGACTAA
                                   TTA
GAM651   LOC158427 3'  AATCAGTTTTATTTGCTA     57675       C__
                                TAGCA   AAAACTGATT
                                |||||   ||||||||||
                                ATCGT   TTTTGACTAA
                                   TTA
GAM652   ARHGEF6   3'  CAAACTTGAAGCCAGGC      68197        ACCA
                                GCCTGG    CAAGTTTG
                                ||||||    ||||||||
                                CGGACC    GTTCAAAC
                                   GAA_
GAM652   CNTN2     3'  GTCACAACCCAGGTGA       17411         ACCACAA   _
                                TCGCCTGG       GTT TGAC
                                ||||||||       ||| ||||
                                AGTGGACC       CAA ACTG
                                     _______   C
GAM652   CORO2A    3'  AAACTGTGGTCCAGAGA      12642     GC        A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_         _
GAM652   CORO2A    3'  AAACTGTGGTCCAGAGA      53398     GC        A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
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                                AG  GACCTGGTGT CAAA
                                 A_       _
GAM652  GRLF1    3'  AGGTCAGAAAGTGGCCCAGG   78551      A    AAG
                                CCTGG CCAC   TTTGACCT
                                ||||| ||||   ||||||||
                                GGACC GGTG   AGACTGGA
                                   C    AA_
GAM652  LAPTM5   3'  AGGCTTGTGGTCAAGC     22199    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCGGA
                                 AA_
GAM652  POU2AF1  3'  AGATTTACAGTCCAGGC     20647        CAC
                                GCCTGGAC   AAGTTT
                                ||||||||   ||||||
                                CGGACCTG   TTTAGA
                                     ACA
GAM652  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  6355         C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM652  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  54574        C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM652  TRIM34   5'  AGGTCAAGTTGAGCCCAG    55224     ACCA   G
                                CTGG    CAA TTTGACCT
                                ||||    ||| ||||||||
                                GACC    GTT GAACTGGA
                                  CGA_   _
GAM652  TRIM9    5'  AGGCCAGGCAAGTCCAGGC   30749        CACAA    A
                                GCCTGGAC    GTTTG CCT
                                ||||||||    ||||| |||
                                CGGACCTG    CGGAC GGA
                                     AA___     C
GAM652  ABLIM    5'  GATATGTAACCCAGGCGG    22030        ACC   A
                                TCGCCTGG   ACA GTT
                                ||||||||   ||| |||
                                GGCGGACC   TGT TAG
                                     CAA   A
GAM652  AMOT     3'  AGGCATCTTCATGGTCCAGGGA 55716    G       C_   TT  A
                                TC CCTGGACCA  AAG  TG CCT
                                || |||||||||  |||  || |||
                                AG GGACCTGGT  TTC  AC GGA
                                  _       AC   T_  _
GAM652  DKFZp434D177 5'  TTAGACCCAGGCGA       50056        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
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                                AGCGGACC      CAGATT
                                        _______
GAM652  DKFZp434D177 5'  TTAGACCCAGGCGA       79443        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                        _______
GAM652  FLJ23420  3'  CAAGTGGGTCCAGGC       46845         A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                      _ __
GAM652  HSA249128 5'  GGCGCGGTCCAGGCGG      34152          ACAA
                                TCGCCTGGACC    GTT
                                ||||||||||    |||
                                GGCGGACCTGG    CGG
                                      CG__
GAM652  MGC15668  5'  AGACCCGGTGGTCCAGACG   51277    C       AA_
                                CG CTGGACCAC   GTTT
                                || |||||||||   ||||
                                GC GACCTGGTG   CAGA
                                 A        GCC
GAM652  MGC22014  3'  AGGTCCCGAGTGTAACCCAGGT 64486        ACC   AGTTT
          GA                     TCGCCTGG   ACA    GACCT
                                ||||||||   |||    |||||
                                AGTGGACC   TGT    CTGGA
                                     CAA   GAGCC
GAM652  SDCCAG10  5'  AGAGTTGTGGTCCAAAGA    19641    GCC        G
                                TC   TGGACCACAA TTT
                                ||   |||||||||| |||
                                AG   ACCTGGTGTT AGA
                                 AA_         G
GAM652  LOC115442 3'  AGGTCAGGGATGGTCCAG    72676        CAAG
                                CTGGACCA    TTTGACCT
                                ||||||||    ||||||||
                                GACCTGGT    GGACTGGA
                                     AG__
GAM652  LOC129011 5'  AGACCTGCGGTCCAGGC     74862         A  A
                                GCCTGGACC CA GTTT
                                ||||||||| || ||||
                                CGGACCTGG GT CAGA
                                      C  C
GAM652  LOC130536 5'  GCAAAGTCCAGGCG        75746         CACAAG    A
                                CGCCTGGAC     TTTG C
                                |||||||||     |||| |
                                GCGGACCTG     AAAC G
                                      _______   C
GAM652  LOC149108 3'  AGACTTCACTGTGGTCCA    84357         _____
                                TGGACCACA    AGTTT
                                |||||||||    |||||
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                                ACCTGGTGT   TCAGA
                                     CACT
GAM652  LOC221688 5'  AGACTCGGGCCCAGACGA   93674    C   A  ACA
                                TCG CTGG CC   AGTTT
                                ||| |||| ||   |||||
                                AGC GACC GG   TCAGA
                                  A   C  GC_
GAM652  LOC256228 5'  AGACTTGTGGTCAAAGC    96233    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCAGA
                                 AAA
GAM652  LOC257441 5'  TTAGACCCAGGCGA       95566        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                              _______
GAM652  LOC91960  3'  AGGTGCCTCTCGTGGTCCAAGC 67657    C      A  TTTG
                                GC TGGACCAC AG    ACCT
                                || |||||||| ||    ||||
                                CG ACCTGGTG TC    TGGA
                                 A       C  TCCG
GAM652  LOC92840  3'  GTCCCTCGGGTCCAGGC     56435        ACA  TTT
                                GCCTGGACC   AG   GAC
                                |||||||||   ||   |||
                                CGGACCTGG   TC   CTG
                                     GC_  C__
GAM653  ATRN      3'  TTAATGGGTGCAGCACAC    57809        C  TT
                                GTGTGCTGT TT  TTAA
                                ||||||||| ||  ||||
                                CACACGACG GG  AATT
                                     T  GT
GAM653  ATRN      3'  TTAATGGGTGCAGCACAC    23833        C  TT
                                GTGTGCTGT TT  TTAA
                                ||||||||| ||  ||||
                                CACACGACG GG  AATT
                                     T  GT
GAM653  BHLHB3    3'  TTAAAAAAGACATAATGGATG  47769       GTGTGC
                                CATCCA     TGTCTTTTTTAA
                                ||||||     ||||||||||||
                                GTAGGT     ACAGAAAAAATT
                                   AAT___
GAM653  MLLT2     3'  TAAAAAAGAAGCACCACGAGAT 19851      CA  _   G
          G                      CATC  GTG TGCT TCTTTTTTA
                                ||||  ||| |||| |||||||||
                                GTAG  CAC ACGA AGAAAAAAT
                                  AG  C   _
GAM653  MTMR2     3'  AAAGAACACACTGCATG     32379     C      CTG
                                CAT CAGTGTG   TCTTT
                                ||| |||||||   |||||
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                                GTA GTCACAC   AGAAA
                                  C      A__
GAM653  SCN3A    3'  AAGGAAACACACTGGAT     22627          CTG
                                ATCCAGTGTG   TCTTT
                                ||||||||||   |||||
                                TAGGTCACAC   AGGAA
                                     AA_
GAM653  SOX9     3'  TAAAAAAGACAGCAAACT    4440      G
                                AGT TGCTGTCTTTTTTA
                                ||| ||||||||||||||
                                TCA ACGACAGAAAAAAT
                                  A
GAM653  CNOT7    3'  TAAAAAAGACAAGAAACT    25333     GTG  _
                                AGT   CT GTCTTTTTTA
                                |||   || ||||||||||
                                TCA   GA CAGAAAAAAT
                                  AA_  A
GAM653  DKFZp762K2015 3'  AAAAAAGAAGCCAC       72472     T   G
                                GTG GCT TCTTTTTT
                                ||| ||| ||||||||
                                CAC CGA AGAAAAAA
                                  _  _
GAM653  FUBP3    3'  TTAAAAAAGACAATTGGA    63735       GTGC
                                TCCAGT    TGTCTTTTTTAA
                                ||||||    ||||||||||||
                                AGGTTA    ACAGAAAAAATT
                                     ____
GAM653  GOLPH3   3'  TTAAATTGAAACAGCACA    42116        C  T_
                                TGTGCTGT TT  TTTAA
                                |||||||| ||  |||||
                                ACACGACA AG  AAATT
                                     A  TT
GAM653  KIAA1001 3'  AAAAAAGACTTTGCCTGG    30286      T   CT
                                CCAG GTG  GTCTTTTTT
                                |||| |||  |||||||||
                                GGTC CGT  CAGAAAAAA
                                  _   TT
GAM653  KIAA1466 3'  AAAAAAGACATAGAC       71912     G  C
                                GT TG TGTCTTTTTT
                                || || ||||||||||
                                CA AT ACAGAAAAAA
                                 G  _
GAM653  KIAA1468 3'  TAAAAAAGACATTGGCTG    91776      GTGC
                                CAGT    TGTCTTTTTTA
                                ||||    ||||||||||
                                GTCG    ACAGAAAAAAT
                                  GTT_
GAM653  KIAA1883 3'  TAAAAAAGACAAAAACA     73420     GC_
                                TGT   TGTCTTTTTTA
                                |||   ||||||||||
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                                ACA   ACAGAAAAAAT
                                  AAA
GAM653  MEGF10   3'  TTAAAAAAGAAAATCTGGA   50587      TGTGCTG
                                TCCAG      TCTTTTTTAA
                                |||||      ||||||||||
                                AGGTC      AGAAAAAATT
                                   TAAA___
GAM653  MOST2    5'  TAAAAAAGACAGGAGGA     39690     AGTGTG
                                TCC     CTGTCTTTTTTA
                                |||     ||||||||||||
                                AGG     GACAGAAAAAAT
                                  AG____
GAM653  PPP1R16B 3'  TTAAAAAAAACAGTCGCT    61394      T    C
                                AGTG GCTGT TTTTTTAA
                                |||| ||||| ||||||||
                                TCGC TGACA AAAAAATT
                                  _    A
GAM653  SLC11A2  3'  AAAAGCGCAGACTGGATG    5230         G   T T
                                CATCCAGT TGC G CTTTT
                                |||||||| ||| | |||||
                                GTAGGTCA ACG C GAAAA
                                     G  _ _
GAM653  LOC124783 5'  AAAGAGCACACTGGA       74334          TG
                                TCCAGTGTGC  TCTTT
                                ||||||||||  |||||
                                AGGTCACACG  AGAAA
                                           __
GAM653  LOC144248 5'  TAAAAAAGACAAACA       76743     GC
                                TGT  TGTCTTTTTTA
                                |||  ||||||||||
                                ACA  ACAGAAAAAAT
                                  A_
GAM653  LOC146712 5'  AAGGCCAGCACACAGGA     83712     A      _
                                TCC GTGTGCTG TCTT
                                ||| |||||||| ||||
                                AGG CACACGAC GGAA
                                  A       C
GAM653  LOC146723 3'  AAAAAAGACACTTGTACAC   78081       ___
                                GTGTGC   TGTCTTTTTT
                                ||||||   ||||||||||
                                CACATG   ACAGAAAAAA
                                    TTC
GAM653  LOC151040 3'  TTAATGGGTGCAGCACAC    80105         C  TT
                                GTGTGCTGT TT  TTAA
                                |||||||||  ||  ||||
                                CACACGACG GG  AATT
                                      T  GT
GAM653  LOC153606 5'  TTAAAACAAAACAAACACTGGA 86077         GC   C  _
                                TCCAGTGT  TGT TT TTTTAA
                                ||||||||  ||| || ||||||
```

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                                AGGTCACA  ACA AA AAAATT
                                    A_   A  C
GAM653   LOC157697 5'  GACAGCACACAGATG       81549      CA
                                CATC  GTGTGCTGTC
                                ||||  ||||||||||
                                GTAG  CACACGACAG
                                  A_
GAM653   LOC220906 3'  AAAAAGACCCACACCGGA    91395     A    CT
                                TCC GTGTG  GTCTTTTT
                                ||| |||||  ||||||||
                                AGG CACAC  CAGAAAAA
                                  C    C_
GAM653   LOC222252 3'  TTAATGGGTGCAGCACAC    94310         C  TT
                                GTGTGCTGT TT  TTAA
                                |||||||||  ||  ||||
                                CACACGACG GG  AATT
                                    T  GT
GAM653   LOC222697 3'  TAAAAAAACACACTGGA     94354         CTGTC
                                TCCAGTGTG    TTTTTTA
                                |||||||||    |||||||
                                AGGTCACAC    AAAAAAT
                                    A____
GAM653   LOC90317  5'  AAAGGAGTCACACTGGA     62248         _  G
                                TCCAGTGTG CT TCTTT
                                |||||||||  ||  |||||
                                AGGTCACAC GA GGAAA
                                    T  _
GAM653   LOC90829  3'  TTAATGGGTGCAGCACAC    64101         C  TT
                                GTGTGCTGT TT  TTAA
                                |||||||||  ||  ||||
                                CACACGACG GG  AATT
                                    T  GT
GAM653   LOC92876  3'  TTAATGGGTGCAGCACAC    70806         C  TT
                                GTGTGCTGT TT  TTAA
                                |||||||||  ||  ||||
                                CACACGACG GG  AATT
                                    T  GT
GAM654   PBX3      3'  GCGAACTCATACAAACCA    20564     ATCC       G
                                TGG   GTATGAGTT GC
                                |||   |||||||||  ||
                                ACC   CATACTCAA CG
                                  AAA_       G
GAM654   DKFZp434P2235 3'  AAGCCAACCATGCCCA      50038     ATCC    A
                                TGG   GTATG GTTGGCTT
                                |||   ||||| ||||||||
                                ACC   CGTAC CAACCGAA
                                  _____   _
GAM654   GAB3      3'  AAGCCAAGACCCAGAGTCCA   54622       CCGTA  A  __
                                TGGAT    TG GT  TGGCTT
                                |||||    ||  ||  ||||||
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                                ACCTG    AC CA  ACCGAA
                                  AG___  C  GA
GAM654  KIAA0923  3'  ATGAAGCTCCTGATAAAGATCC 25833       CG   G  TT
            A                    TGGATC  TAT AG  GGCTTCAT
                                 ||||||  ||| ||  ||||||||
                                 ACCTAG  ATA TC  TCGAAGTA
                                    AA   G  C_
GAM654  PRPF8     3'  AACCATACGAATTCA      61178      C     A
                                 TGGAT CGTATG GTT
                                 ||||| |||||| |||
                                 ACTTA GCATAC CAA
                                   A     _
GAM654  SYNJ2     3'  TGAAACCTCACGGATCC     61769        AT  GTT  C
                                 GGATCCGT  GA   GG TTCA
                                 ||||||||  ||   || ||||
                                 CCTAGGCA  CT   CC AAGT
                                     __  ___  A
GAM654  WIT-1     5'  CGACCCCAACGGATCCA     31825         A  A_
                                 TGGATCCGT TG  GTTG
                                 |||||||||  ||  ||||
                                 ACCTAGGCA AC  CAGC
                                       _  CC
GAM654  LOC146782 3'  AAGCCAACCATGCCCA      76289     ATCC     A
                                 TGG    GTATG GTTGGCTT
                                 |||    ||||| ||||||||
                                 ACC    CGTAC CAACCGAA
                                   _____    _
GAM654  LOC219562 3'  AAGCCAACCATGCCCA      90766     ATCC     A
                                 TGG    GTATG GTTGGCTT
                                 |||    ||||| ||||||||
                                 ACC    CGTAC CAACCGAA
                                   _____    _
GAM654  LOC257181 3'  AAGCCAACCATGCCCA      94588     ATCC     A
                                 TGG    GTATG GTTGGCTT
                                 |||    ||||| ||||||||
                                 ACC    CGTAC CAACCGAA
                                   _____    _
GAM655  ARNT2     3'  AAACAACCCGTGCATCCCTGC  29450     A    TTTTA
                                 GTA GGAT     GGGTTGTTT
                                 ||| ||||     |||||||||
                                 CGT CCTA     CCCAACAAA
                                   C    CGTG_
GAM655  LCT       3'  AACCGTAAAAATCCTT      9697            G
                                 AAGGATTTTTA GGTT
                                 |||||||||||  ||||
                                 TTCCTAAAAAT CCAA
                                        G
GAM655  RPL15     3'  AAACAACCCTAAAAATCCTTAC 11382
                                 GTAAGGATTTTTAGGGTTGTTT
                                 |||||||||||||||||||||
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                                CATTCCTAAAAATCCCAACAAA

GAM655  FBXO30    3'  AACTAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                  G        AA
GAM655  KIAA0494  3'  AACAACCCTTACTTAC      28736      GATTTTT
                                GTAAG      AGGGTTGTT
                                ||||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM655  PRO0641   5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                   ___    C
GAM655  SMT3H2    3'  AACAACATAAAAATCCTTGC   22670          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                        A_
GAM655  LOC120103 3'  AACCTATGAAAAATCCTTGC   74002          A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
                                CGTTCCTAAAAA   TCCAA
                                        GTA
GAM655  LOC129831 3'  AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM655  LOC133088 5'  AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                      GTA GGATTTTT     TTGTTT
                                ||| ||||||||     ||||||
                                CGT CCTAAAAA     AACAAA
                                  C       GATAA
GAM655  LOC148089 3'  GGCCCTAAAAATTCCTAC    78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM655  LOC154547 3'  AACAACATAAAAATCCTTGC   76050          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                        A_
GAM655  LOC158104 3'  ACAGCCAAAAATCCTTA     60313          AG
                                TAAGGATTTTT  GGTTGT
                                ||||||||||  ||||||
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                                ATTCCTAAAAA  CCGACA
                                   __
GAM655  LOC205880 5'  AAACAACCATCATCCTGAC   90709    A    TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM655  LOC221561 3'  AACAACATAAAAATCCTTGC   92130          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM655  LOC257591 3'  AACAACATAAAAATCCTTGC   97840          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM655  LOC51145  3'  AGCTAAAATCCTTAC       32393          TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
                                CATTCCTAAAA   TCGA
                                   ___
GAM656  GARP      3'  TATAACCTACCTGAATGTATTA 18601
           AA                    TTTAATACATTCAGGTAGGTTATA
                                 ||||||||||||||||||||||
                                 AAATTATGTAAGTCCATCCAATAT

GAM656  GARP      3'  TATAACCTACCTGAATGTATTA 18601
           AA                    TTTAATACATTCAGGTAGGTTATA
                                 ||||||||||||||||||||||
                                 AAATTATGTAAGTCCATCCAATAT

GAM656  RANBP2    3'  CTCCTGACGTATTAAA      20765        AT    T
                                TTTAATAC  TCAGG AG
                                ||||||||  ||||| ||
                                AAATTATG  AGTCC TC
                                     C_    _
GAM656  RANBP2    3'  CTCCTGACGTATTAAA      20765        AT    T
                                TTTAATAC  TCAGG AG
                                ||||||||  ||||| ||
                                AAATTATG  AGTCC TC
                                     C_    _
GAM656  SPTB      3'  TTACCTGAATGTAATAAA    4442       A
                                TTTA TACATTCAGGTAG
                                |||| ||||||||||||
                                AAAT ATGTAAGTCCATT
                                  A
GAM656  SPTB      3'  TTACCTGAATGTAATAAA    4442       A
                                TTTA TACATTCAGGTAG
                                |||| ||||||||||||
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                                AAAT ATGTAAGTCCATT
                                  A
GAM656  TACC1   3' ACTTTCCCAAATGTGTTAAA  20790        CA  T
                                TTTAATACATT  GG AGGT
                                ||||||||||  || ||||
                                AAATTGTGTAA  CC TTCA
                                      AC  T
GAM656  TACC1   3' ACTTTCCCAAATGTGTTAAA  20790        CA  T
                                TTTAATACATT  GG AGGT
                                ||||||||||  || ||||
                                AAATTGTGTAA  CC TTCA
                                      AC  T
GAM656  BANK    3' ATAACCTACCTTTGTATTAAG  35594       TTC
                                TTTAATACA  AGGTAGGTTAT
                                |||||||||  ||||||||||
                                GAATTATGT  TCCATCCAATA
                                     T__
GAM656  BANK    3' ATAACCTACCTTTGTATTAAG  35594       TTC
                                TTTAATACA  AGGTAGGTTAT
                                |||||||||  ||||||||||
                                GAATTATGT  TCCATCCAATA
                                     T__
GAM656  FLJ11151 3' ACCTGATTGTATTAAA     67869        T
                                TTTAATACA TCAGGT
                                ||||||||| ||||||
                                AAATTATGT AGTCCA
                                     T
GAM656  FLJ11151 3' ACCTGATTGTATTAAA     67869        T
                                TTTAATACA TCAGGT
                                ||||||||| ||||||
                                AAATTATGT AGTCCA
                                     T
GAM656  SAC2    3' TCTACTTGAACACATTAAA   30059      ACA
                                TTTAAT  TTCAGGTAGG
                                ||||||  ||||||||||
                                AAATTA  AAGTTCATCT
                                   CAC
GAM656  SAC2    3' TCTACTTGAACACATTAAA   30059      ACA
                                TTTAAT  TTCAGGTAGG
                                ||||||  ||||||||||
                                AAATTA  AAGTTCATCT
                                   CAC
GAM656  WAC     3' ATAACCTACTTGTTTGTAT   55185     TT
                                ATACA  CAGGTAGGTTAT
                                |||||  ||||||||||||
                                TATGT  GTTCATCCAATA
                                  TT
GAM656  WAC     3' ATAACCTACTTGTTTGTAT   55185     TT
                                ATACA  CAGGTAGGTTAT
                                |||||  ||||||||||||
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                                TATGT GTTCATCCAATA
                                   TT
GAM656  WAC     3' ATAACCTACTTGTTTGTAT  55191     TT
                                ATACA CAGGTAGGTTAT
                                ||||| ||||||||||||
                                TATGT GTTCATCCAATA
                                   TT
GAM656  WAC     3' ATAACCTACTTGTTTGTAT  55191     TT
                                ATACA CAGGTAGGTTAT
                                ||||| ||||||||||||
                                TATGT GTTCATCCAATA
                                   TT
GAM656  WAC     3' ATAACCTACTTGTTTGTAT  33551     TT
                                ATACA CAGGTAGGTTAT
                                ||||| ||||||||||||
                                TATGT GTTCATCCAATA
                                   TT
GAM656  WAC     3' ATAACCTACTTGTTTGTAT  33551     TT
                                ATACA CAGGTAGGTTAT
                                ||||| ||||||||||||
                                TATGT GTTCATCCAATA
                                   TT
GAM656  ZFR     3' TATAATGACTTAAATGTATTA 32256       C   AG
                                TAATACATT AGGT GTTATA
                                ||||||||| |||| ||||||
                                ATTATGTAA TTCA TAATAT
                                     A   G_
GAM656  ZFR     3' TATAATGACTTAAATGTATTA 32256       C   AG
                                TAATACATT AGGT GTTATA
                                ||||||||| |||| ||||||
                                ATTATGTAA TTCA TAATAT
                                     A   G_
GAM656  LOC147947 5' AATGTAACGAATGTATTAAA  78581        AGG G
                                TTTAATACATTC  TA GTT
                                |||||||||||  || |||
                                AAATTATGTAAG  AT TAA
                                      CA_ G
GAM656  LOC147947 5' AATGTAACGAATGTATTAAA  78581        AGG G
                                TTTAATACATTC  TA GTT
                                |||||||||||  || |||
                                AAATTATGTAAG  AT TAA
                                      CA_ G
GAM657  ACP2    3' CCATTAGACTCAGACAGA   7853         CT_
                                TCTGTCTGAGTT  TGG
                                |||||||||||  |||
                                AGACAGACTCAG  ACC
                                      ATT
GAM657  GFRA2   5' ACCCAAGGGAGAAAGACA   7658      GAG_
                                TGTCT   TTCTTGGGT
                                |||||   |||||||||
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                                ACAGA   GGGAACCCA
                                  AAGA
GAM657  SERPINA5  3'  ACCCAAGAACTCCTGA     5267    T_
                                TC  GAGTTCTTGGGT
                                ||  ||||||||||||
                                AG  CTCAAGAACCCA
                                 TC
GAM657  TNFSF8    3'  AGAAGTCAGACAGAGA     6963          G
                                TCTCTGTCTGA TTCT
                                |||||||||||| ||||
                                AGAGACAGACT AAGA
                                      G
GAM657  C6orf26   3'  ACCCCAGCCTCAGACAGA   47508         TT  T
                                TCTGTCTGAG  CT GGGT
                                ||||||||||  || ||||
                                AGACAGACTC  GA CCCA
                                      C_  C
GAM657  CLIC5     3'  ACCCAAGAATGGGTCAAAAATG 33715    CTC  T  GA
                                CAT   TG CT  GTTCTTGGGT
                                |||   || ||  ||||||||||
                                GTA   AC GG  TAAGAACCCA
                                  AAA  T  G_
GAM657  CNNM1     3'  ACCCAACTGGGAGCCAGAGATG 39766       __   G   TCT
                                CATCTCTG  TCT AGT   TGGGT
                                ||||||||  ||| |||   |||||
                                GTAGAGAC  AGG TCA   ACCCA
                                     CG   G   ___
GAM657  DKFZp761O0113 5'  ACCCATAGCCAGACAGGA    37273    T     A   CT
                                TC CTGTCTG GTT  TGGGT
                                || |||||| |||  |||||
                                AG GACAGAC CGA  ACCCA
                                 _      _   T_
GAM657  FLJ13912  3'  ACCCAAGAACCCATGGCCAAG  42860    CT  _  A
                                CT  GTC TG GTTCTTGGGT
                                ||  ||| || ||||||||||
                                GA  CGG AC CAAGAACCCA
                                 AC   T  C
GAM657  FLJ14957  3'  ACCCAAGAACTTTGGGAG    51732     GTCT
                                CTCT   GAGTTCTTGGGT
                                ||||   ||||||||||||
                                GAGG   TTCAAGAACCCA
                                  GT__
GAM657  KIAA0014  3'  CCGTGGCCCAGACAGAGA    27840         A   CT
                                TCTCTGTCTG GTT  TGG
                                |||||||||| |||  |||
                                AGAGACAGAC CGG  GCC
                                      C   T_
GAM657  KIAA0368  3'  ACCCAAGAAACTTCCAAGATG  65162      C  TCT   _
                                CATCT TG   GAGTT CTTGGGT
                                ||||| ||   ||||| |||||||
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                                GTAGA AC   TTCAA GAACCCA
                                  _ C__     A
GAM657  KIAA0446 5'  CCAGGGCCCAGACAGAGG    68860          A  T
                                TCTCTGTCTG GT CTTGG
                                |||||||||| || |||||
                                GGAGACAGAC CG GGACC
                                     C  _
GAM657  KIAA0930 3'  ACCCAAAGAGGACTAGAGATG  70534        _   GAGT   _
                                CATCTCT GTCT   TCTT GGGT
                                ||||||| ||||   |||| ||||
                                GTAGAGA CAGG   AGAA CCCA
                                    T   _____   A
GAM657  KIAA1219 3'  ACCCAGGAACAGATCAGAAATG 61363     C   _  GA
                                CAT TCTG TCT  GTTCTTGGGT
                                ||| |||| |||  ||||||||||
                                GTA AGAC AGA  CAAGGACCCA
                                  A   T  __
GAM657  POLD4    3'  CCCAAGAACCTCAGGACA    40985     _   _
                                TGTC TGAG TTCTTGGG
                                |||| |||| ||||||||
                                ACAG ACTC AAGAACCC
                                  G   C
GAM657  RPS6KA4  3'  ACCCCACTCCCAGACAGAG   14142        __   TCTT
                                CTCTGTCT  GAGT   GGGT
                                ||||||||  ||||   ||||
                                GAGACAGA  CTCA   CCCA
                                     CC   C___
GAM657  SLC39A2  3'  ACCCTGGACTAAGACAAAGAT  27420     C    G    TT
                                ATCT TGTCT AGTTC  GGGT
                                |||| ||||| |||||  ||||
                                TAGA ACAGA TCAGG  CCCA
                                  A    A    T_
GAM657  SQV7L    5'  CCATGCCCAGCCAGAGATG   70571        T   A  TCT
                                CATCTCTG CTG GT   TGG
                                |||||||| ||| ||   |||
                                GTAGAGAC GAC CG   ACC
                                     C   C  T__
GAM657  USP22    3'  AATTCAAACAGAGATG      67995         C
                                CATCTCTGT TGAGTT
                                ||||||||| ||||||
                                GTAGAGACA ACTTAA
                                     A
GAM657  LOC145497 5'  ACCTCTCCCAGACAGAGTTG   77212    T       AGTTCTT
                                CA CTCTGTCTG      GGGT
                                || |||||||||      ||||
                                GT GAGACAGAC      TCCA
                                 T       CCTC___
GAM657  LOC150519 3'  ACCCAAATATTATAGGCAGAAA 79911     C      _   TC
           TG                    CAT TCTGTCTG AGT  TTGGGT
                                ||| |||||||| |||  ||||||
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                                GTA AGACGGAT TTA  AACCCA
                                  A       A  TA
GAM657  LOC220954 3'  ACCCACCTTCAGACAGA     93138          TTCT
                                TCTGTCTGAG    TGGGT
                                ||||||||||    |||||
                                AGACAGACTT    ACCCA
                                     CC__
GAM657  LOC81569  3'  ACCCAAGGGGGAAGACAAGATG 61985      C     GAG
                                CATCT TGTCT   TTCTTGGGT
                                ||||| |||||   |||||||||
                                GTAGA ACAGA   GGGAACCCA
                                   _    AGG
GAM658  CDH13     3'  CGTCTGAAGCTTGACTC     6994        C       GT
                                GAGTCA AGCTTCAG  G
                                |||||| ||||||||  |
                                CTCAGT TCGAAGTC  C
                                   _       TG
GAM658  CHD2      3'  TCTGAAGCTGCACCCTC     7033      A  CA
                                GAG GT  CAGCTTCAGG
                                ||| ||  ||||||||||
                                CTC CA  GTCGAAGTCT
                                  C  C_
GAM658  CIT       3'  CACGAAACTGTGACTTTC     69742           C   AG
                                GAGAGTCACAG TTC  GTG
                                |||||||||| |||  |||
                                CTTTCAGTGTC AAG  CAC
                                      A  __
GAM658  POU3F1    3'  CAAACACCCGGACGACCCTC   59308     A   ACAGC   A
                                GAG GTC     TTC GGTGTTTG
                                ||| |||     ||| ||||||||
                                CTC CAG     AGG CCACAAAC
                                  C   C_____   C
GAM658  SMURF1    3'  CCCAAAGCTGTGACCTC     92450     A        CA
                                GAG GTCACAGCTT  GG
                                ||| ||||||||||  ||
                                CTC CAGTGTCGAA  CC
                                  _        AC
GAM658  TAT       3'  GTCTGAAGCTCAACTCTC    4474        CAC
                                GAGAGT   AGCTTCAGGT
                                ||||||   ||||||||||
                                CTCTCA   TCGAAGTCTG
                                   AC_
GAM658  FLJ20359  3'  ACCCCTGAAGCTGCACTC    35034      CA        T
                                GAGT  CAGCTTCAGG GT
                                ||||  |||||||||| ||
                                CTCA  GTCGAAGTCC CA
                                  C_         C
GAM658  GPR105    5'  AAATGAGTGAAGCATGACTCTC 29652         CA     GG
                                GAGAGTCA  GCTTCA  TGTTT
                                ||||||||  ||||||  |||||
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                                CTCTCAGT  CGAAGT  GTAAA
                                    A_     GA
GAM658  TRIM11   5'  AGGATGTGAAGCTGCAGC    72829    CA      G  G
                                GT  CAGCTTCA GT TT
                                ||  |||||||| || ||
                                CG  GTCGAAGT TA GA
                                 AC       G  G
GAM658  LOC150837 3'  AAACACCAGTGCCACCCTC   80015    A  CACA   TCA
                                GAG GT    GCT   GGTGTTT
                                ||| ||    |||   |||||||
                                CTC CA    TGA   CCACAAA
                                 C  CCG_  ___
GAM658  LOC165246 5'  CAAACACCTTCAGTGGCTC   82478       AGCTTC
                                GAGTCAC     AGGTGTTTG
                                |||||||     |||||||||
                                CTCGGTG     TCCACAAAC
                                    ACT___
GAM659  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A     T__
GAM659  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM659  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                       _
GAM659  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM659  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM659  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                       A
GAM659  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
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                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM659  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM659  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM659  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM659  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM659  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||         |||||||||
                                GTAAAG         CAGACTCTA
                                   AAACATTT_
GAM659  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM659  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM659  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM659  NIR3     3'  GCAGTGAAAGTGCAAT      66242      T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM659  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598         CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
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                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM659  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM659  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                     TA__    TT
GAM659  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A     TC
GAM659  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                     AAAGG
GAM659  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC       CTGTCTGAGAT
                                ||||       ||||||||||
                                AAAG       GACAGACTCTA
                                  GTTTGCC
GAM659  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT      GT TGAGAT
                                |||||||      || ||||||
                                AAAGTGA      CA ACTCTA
                                    TTTCC_  A
GAM659  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM659  LOC222134 5'  ACAGTGAAGTGAAATG       94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                     _
GAM660  BIN3     3'  CACCCTCCAGCAGGCAGCCCAG 37955         C     AT  CA
          CA                      TGCTGGGCT CCTGC  GA  GTG
                                |||||||||| |||||  ||  |||
                                ACGACCCGA GGACG  CT  CAC
                                     C     AC  CC
GAM660  BIN3     3'  CACCCTCCAGCAGGCAGCCCAG 37955         C     AT  CA
          CA                      TGCTGGGCT CCTGC  GA  GTG
                                |||||||||| |||||  ||  |||
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                                ACGACCCGA GGACG  CT  CAC
                                      C    AC  CC
GAM660  CRSP8   3'  CACGCAGGAAGCCCACA    80963   C    C   A
                                TG TGGGCT CCTGC TG
                                || |||||| ||||| ||
                                AC ACCCGA GGACG AC
                                 _    A    C
GAM660  CRSP8   3'  CACGCAGGAAGCCCACA    80963   C    C   A
                                TG TGGGCT CCTGC TG
                                || |||||| ||||| ||
                                AC ACCCGA GGACG AC
                                 _    A    C
GAM660  ENG     5'  CACTGCCATCCATTGGAGCCCA 3687          C_  C   A
           GCA                    TGCTGGGCTCC  TG ATG CAGTG
                                ||||||||||  || ||| |||||
                                ACGACCCGAGG  AC TAC GTCAC
                                      TT  C   C
GAM660  ENG     5'  CACTGCCATCCATTGGAGCCCA 3687          C_  C   A
           GCA                    TGCTGGGCTCC  TG ATG CAGTG
                                ||||||||||  || ||| |||||
                                ACGACCCGAGG  AC TAC GTCAC
                                      TT  C   C
GAM660  HD      3'  CACTGTTAGTGACAGAGCCCAG 9181          CC  _  _
           CA                     TGCTGGGCTC  TG CA TGACAGTG
                                |||||||||  || || ||||||||
                                ACGACCCGAG  AC GT ATTGTCAC
                                     __  A  G
GAM660  HD      3'  CACTGTTAGTGACAGAGCCCAG 9181          CC  _  _
           CA                     TGCTGGGCTC  TG CA TGACAGTG
                                |||||||||  || || ||||||||
                                ACGACCCGAG  AC GT ATTGTCAC
                                     __  A  G
GAM660  IGLL1   5'  CACTCTCTAGGGAGCCCACA  39174   C       CAT  C
                                TG TGGGCTCCCTG   GA AGTG
                                || ||||||||||   || ||||
                                AC ACCCGAGGGAT   CT TCAC
                                 _        ___  C
GAM660  IGLL1   5'  CACTCTCTAGGGAGCCCACA  39174   C       CAT  C
                                TG TGGGCTCCCTG   GA AGTG
                                || ||||||||||   || ||||
                                AC ACCCGAGGGAT   CT TCAC
                                 _        ___  C
GAM660  THBD    3'  CACTGCCACACAGGGTCTGCA  4494    T   CT   CA  A
                                TGC GGG  CCCTG  TG CAGTG
                                ||| |||  |||||  || |||||
                                ACG TCT  GGGAC  AC GTCAC
                                  _  __    AC  C
GAM660  THBD    3'  CACTGCCACACAGGGTCTGCA  4494    T   CT   CA  A
                                TGC GGG  CCCTG  TG CAGTG
                                ||| |||  |||||  || |||||
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                                ACG TCT  GGGAC  AC GTCAC
                                  _  __    AC  C
GAM660  ARHGEF16 3'  CACCGTGTCCCAGGGAGCCCAG 27069          CAT  __
           C                     GCTGGGCTCCCTG  GACA  GTG
                                 ||||||||||||  ||||  |||
                                 CGACCCGAGGGAC  CTGT  CAC
                                       C__   GC
GAM660  ARHGEF16 3'  CACCGTGTCCCAGGGAGCCCAG 27069          CAT  __
           C                     GCTGGGCTCCCTG  GACA  GTG
                                 ||||||||||||  ||||  |||
                                 CGACCCGAGGGAC  CTGT  CAC
                                       C__   GC
GAM660  CABIN1   3'  ACCACATGGGAGCCCAG    24479        TGC  ACA
                                 CTGGGCTCCC  ATG  GT
                                 |||||||||  |||  ||
                                 GACCCGAGGG  TAC  CA
                                      ___  AC_
GAM660  CABIN1   3'  ACCACATGGGAGCCCAG    24479        TGC  ACA
                                 CTGGGCTCCC  ATG  GT
                                 |||||||||  |||  ||
                                 GACCCGAGGG  TAC  CA
                                      ___  AC_
GAM660  FLJ10232 3'  ACTGTCAGGAACCCAG     35920     C  CTGCA
                                 CTGGG TCC   TGACAGT
                                 |||||  |||   |||||||
                                 GACCC AGG   ACTGTCA
                                   A  _____
GAM660  FLJ10232 3'  ACTGTCAGGAACCCAG     35920     C  CTGCA
                                 CTGGG TCC   TGACAGT
                                 |||||  |||   |||||||
                                 GACCC AGG   ACTGTCA
                                   A  _____
GAM660  FLJ20154 5'  GCCTTCAGGCCCAGCA     72927        CCCTGCA  CA
                                 TGCTGGGCT     TGA  GT
                                 |||||||||     |||  ||
                                 ACGACCCGG     ACT  CG
                                      _______  TC
GAM660  FLJ20154 5'  GCCTTCAGGCCCAGCA     72927        CCCTGCA  CA
                                 TGCTGGGCT     TGA  GT
                                 |||||||||     |||  ||
                                 ACGACCCGG     ACT  CG
                                      _______  TC
GAM660  FLJ21865 3'  CACCGCCATGCAGGGCTCGC  42805   T   TC     ACA
                                 GC GGGC  CCTGCATG  GTG
                                 ||  ||||  ||||||||  |||
                                 CG CTCG  GGACGTAC  CAC
                                   _   __      CGC
GAM660  FLJ21865 3'  CACCGCCATGCAGGGCTCGC  42805   T   TC     ACA
                                 GC GGGC  CCTGCATG  GTG
                                 ||  ||||  ||||||||  |||
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                                CG CTCG  GGACGTAC   CAC
                                 _   __       CGC
GAM660  IRF7     3'  CACCGCGGTGCAAGAGCCCAGC 14443        CC    GACA
                                GCTGGGCTC  TGCAT   GTG
                                |||||||||  |||||   |||
                                CGACCCGAG  ACGTG   CAC
                                     A_    GCGC
GAM660  IRF7     3'  CACCGCGGTGCAAGAGCCCAGC 14443        CC    GACA
                                GCTGGGCTC  TGCAT   GTG
                                |||||||||  |||||   |||
                                CGACCCGAG  ACGTG   CAC
                                     A_    GCGC
GAM660  KIAA0864 3'  CACTGTCAGTATTAAGGCCCAG 63247        CCC_  A
             CA                   TGCTGGGCT   TGC TGACAGTG
                                |||||||||   ||| ||||||||
                                ACGACCCGG   ATG ACTGTCAC
                                     AATT  _
GAM660  KIAA0864 3'  CACTGTCAGTATTAAGGCCCAG 63247        CCC_  A
             CA                   TGCTGGGCT   TGC TGACAGTG
                                |||||||||   ||| ||||||||
                                ACGACCCGG   ATG ACTGTCAC
                                     AATT  _
GAM660  MFN2     3'  ACAAGGCAGGGGCCCAGCA   29595        T     ATGACA
                                TGCTGGGC CCCTGC     GT
                                |||||||| ||||||     ||
                                ACGACCCG GGGACG     CA
                                     _     GAA___
GAM660  MFN2     3'  ACAAGGCAGGGGCCCAGCA   29595        T     ATGACA
                                TGCTGGGC CCCTGC     GT
                                |||||||| ||||||     ||
                                ACGACCCG GGGACG     CA
                                     _     GAA___
GAM660  MGC3101  3'  GTCACACAGAGCCCAGCA   43883         CC  CA
                                TGCTGGGCTC  TG  TGAC
                                ||||||||||  ||  ||||
                                ACGACCCGAG  AC  ACTG
                                      __  AC
GAM660  MGC3101  3'  GTCACACAGAGCCCAGCA   43883         CC  CA
                                TGCTGGGCTC  TG  TGAC
                                ||||||||||  ||  ||||
                                ACGACCCGAG  AC  ACTG
                                      __  AC
GAM660  SCYB11   3'  CACTGCCCAAAGGAGTCCAACA 87442    C       CTGCATGA
                                TG TGGGCTCC       CAGTG
                                || ||||||||       |||||
                                AC ACCTGAGG       GTCAC
                                 A       AAACCC__
GAM660  SCYB11   3'  CACTGCCCAAAGGAGTCCAACA 87442    C       CTGCATGA
                                TG TGGGCTCC       CAGTG
                                || ||||||||       |||||
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                                AC ACCTGAGG       GTCAC
                                 A       AAACCC__
GAM660  TIX1     3'  CATGTAAGGAGCCCAGCA    61739          C
                                TGCTGGGCTCC TGCATG
                                |||||||||| ||||||
                                ACGACCCGAGG ATGTAC
                                       A
GAM660  TIX1     3'  CATGTAAGGAGCCCAGCA    61739          C
                                TGCTGGGCTCC TGCATG
                                |||||||||| ||||||
                                ACGACCCGAGG ATGTAC
                                       A
GAM660  UBP1     3'  CTGCCATAGCCAAGCA     27224     G   CCCTGC   A
                                TGCT GGCT     ATG CAG
                                |||| ||||      ||| |||
                                ACGA CCGA     TAC GTC
                                  A   _______   C
GAM660  UBP1     3'  CTGCCATAGCCAAGCA     27224     G   CCCTGC   A
                                TGCT GGCT     ATG CAG
                                |||| ||||      ||| |||
                                ACGA CCGA     TAC GTC
                                  A   _______   C
GAM660  LOC123242 3'  ACCATTAAGCAGCCCAGCA   75589        CCCT  A   CA
                                TGCTGGGCT   GC TGA  GT
                                |||||||||   || |||  ||
                                ACGACCCGA   CG ATT  CA
                                      ____  A   AC
GAM660  LOC123242 3'  ACCATTAAGCAGCCCAGCA   75589        CCCT  A   CA
                                TGCTGGGCT   GC TGA  GT
                                |||||||||   || |||  ||
                                ACGACCCGA   CG ATT  CA
                                      ____  A   AC
GAM660  LOC144058 5'  CTGGATGCAGGGCACCCAACA  76666    C   CT      GA
                                TG TGGG  CCCTGCAT  CAG
                                || ||||  ||||||||  |||
                                AC ACCC  GGGACGTA  GTC
                                 A   AC       G_
GAM660  LOC144058 5'  CTGGATGCAGGGCACCCAACA  76666    C   CT      GA
                                TG TGGG  CCCTGCAT  CAG
                                || ||||  ||||||||  |||
                                AC ACCC  GGGACGTA  GTC
                                 A   AC       G_
GAM660  LOC147160 5'  CACAGGGGAGCCCAGCA     83958          GCA
                                TGCTGGGCTCCCT   TG
                                ||||||||||||   ||
                                ACGACCCGAGGGG   AC
                                       AC_
GAM660  LOC147160 5'  CACAGGGGAGCCCAGCA     83958          GCA
                                TGCTGGGCTCCCT   TG
                                ||||||||||||   ||
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                                ACGACCCGAGGGG  AC
                                      AC_
GAM660  LOC148870 5'  CACTGCTCCCAGGAGCCCACA  79041    C      C  CAT  _
                                TG TGGGCTCC TG   GA CAGTG
                                || |||||||| ||   || |||||
                                AC ACCCGAGG AC   CT GTCAC
                                 _       _ C__  C
GAM660  LOC148870 5'  CACTGCTCCCAGGAGCCCACA  79041    C      C  CAT  _
                                TG TGGGCTCC TG   GA CAGTG
                                || |||||||| ||   || |||||
                                AC ACCCGAGG AC   CT GTCAC
                                 _       _ C__  C
GAM660  LOC149421 5'  CACTGCCAACGTAGAGGGCCCA 79355          C    A_  A
           GCA                    TGCTGGGCTC CTGC  TG CAGTG
                                ||||||||||| ||||  || |||||
                                ACGACCCGGG GATG  AC GTCAC
                                      A   CA  C
GAM660  LOC149421 5'  CACTGCCAACGTAGAGGGCCCA 79355          C    A_  A
           GCA                    TGCTGGGCTC CTGC  TG CAGTG
                                ||||||||||| ||||  || |||||
                                ACGACCCGGG GATG  AC GTCAC
                                      A   CA  C
GAM660  LOC151360 3'  CACTGTCACACCGTAGCCCACA 85311    C     CCCTGCA
                                TG TGGGCT      TGACAGTG
                                || ||||||      ||||||||
                                AC ACCCGA      ACTGTCAC
                                 _     TGCCAC_
GAM660  LOC151360 3'  CACTGTCACACCGTAGCCCACA 85311    C     CCCTGCA
                                TG TGGGCT      TGACAGTG
                                || ||||||      ||||||||
                                AC ACCCGA      ACTGTCAC
                                 _     TGCCAC_
GAM660  LOC151361 3'  CACTGTCACACCGTAGCCCACA 85320    C     CCCTGCA
                                TG TGGGCT      TGACAGTG
                                || ||||||      ||||||||
                                AC ACCCGA      ACTGTCAC
                                 _     TGCCAC_
GAM660  LOC151361 3'  CACTGTCACACCGTAGCCCACA 85320    C     CCCTGCA
                                TG TGGGCT      TGACAGTG
                                || ||||||      ||||||||
                                AC ACCCGA      ACTGTCAC
                                 _     TGCCAC_
GAM660  LOC152286 3'  CACTAGACAGCCAGGAGCCCAG 85626          CT  A  AC_
           CA                     TGCTGGGCTCC  GC TG   AGTG
                                ||||||||||  || ||   ||||
                                ACGACCCGAGG  CG AC   TCAC
                                      AC  _  AGA
GAM660  LOC152286 3'  CACTAGACAGCCAGGAGCCCAG 85626          CT  A  AC_
           CA                     TGCTGGGCTCC  GC TG   AGTG
                                ||||||||||  || ||   ||||
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                                ACGACCCGAGG  CG AC   TCAC
                                      AC  _  AGA
GAM660  LOC152674 3'  CACTGTCACCTGGAAGCCCAG  85834       C  TGCA
                                CTGGGCT CC    TGACAGTG
                                ||||||| ||    ||||||||
                                GACCCGA GG    ACTGTCAC
                                   A  TCC_
GAM660  LOC152674 3'  CACTGTCACCTGGAAGCCCAG  85834       C  TGCA
                                CTGGGCT CC    TGACAGTG
                                ||||||| ||    ||||||||
                                GACCCGA GG    ACTGTCAC
                                   A  TCC_
GAM660  LOC253001 3'  ACCATTAAGCAGCCCAGCA   96249        CCCT  A   CA
                                TGCTGGGCT    GC TGA  GT
                                |||||||||    || |||  ||
                                ACGACCCGA    CG ATT  CA
                                     ____  A   AC
GAM660  LOC253001 3'  ACCATTAAGCAGCCCAGCA   96249        CCCT  A   CA
                                TGCTGGGCT    GC TGA  GT
                                |||||||||    || |||  ||
                                ACGACCCGA    CG ATT  CA
                                     ____  A   AC
GAM660  LOC255030 3'  ACTGAGAAGAAGCCCAGC    97267        CC  GCATGA
                                GCTGGGCT  CT     CAGT
                                ||||||||  ||     ||||
                                CGACCCGA  GA     GTCA
                                    A_  AGA___
GAM660  LOC255030 3'  ACTGAGAAGAAGCCCAGC    97267        CC  GCATGA
                                GCTGGGCT  CT     CAGT
                                ||||||||  ||     ||||
                                CGACCCGA  GA     GTCA
                                    A_  AGA___
GAM660  LOC51131  3'  ACTGTCACACTCCCAGCA    32277       CTCCC  CA
                                TGCTGGG    TG  TGACAGT
                                |||||||    ||  |||||||
                                ACGACCC    AC  ACTGTCA
                                   TC___  __
GAM660  LOC51131  3'  ACTGTCACACTCCCAGCA    32277       CTCCC  CA
                                TGCTGGG    TG  TGACAGT
                                |||||||    ||  |||||||
                                ACGACCC    AC  ACTGTCA
                                   TC___  __
GAM661  FOXM1    3'  AGTATCTGATTCCTCTGCTGT  41703     C   TT   A
                                GCA CAG  GAA TCAGATACT
                                ||| |||  ||| |||||||||
                                TGT GTC  CTT AGTCTATGA
                                  C   TC  _
GAM661  LAMP2    3'  CTATTCCAACTGGGC       25711     A     A   C
                                GC CCAGTTG AAT AG
                                || ||||||| ||| ||
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                                CG GGTCAAC TTA TC
                                 _      C   _
GAM661  LHX4     3'  TTTGCTCCAACTGGTGTGT   52909           AAAT
                                ACGCACCAGTTG    CAGA
                                ||||||||||||    ||||
                                TGTGTGGTCAAC    GTTT
                                       CTC_
GAM661  MAPK4    3'  GACCTCAATGGTGCGT      10829         G    AA
                                ACGCACCA TTGA  TC
                                |||||||| ||||  ||
                                TGCGTGGT AACT  AG
                                     _   CC
GAM661  NAB1     3'  ATCTGGTTATCAATGC      19907     CCAG   _
                                GCA    TTGA AATCAGAT
                                |||    |||| ||||||||
                                CGT    AACT TTGGTCTA
                                 _____   A
GAM661  OPHN1    3'  AGCATCTAATTTCAATTATAGT 10352      ACC        C    A
           GT                     ACGC   AGTTGAAAT AGAT CT
                                ||||   ||||||||| |||| ||
                                TGTG   TTAACTTTA TCTA GA
                                  ATA        A    C
GAM661  ORC1L    3'  AGCATCTGATTTTGGAAGT    14735     CAG TG        A
                                AC   T  AAATCAGAT CT
                                ||   |  ||||||||| ||
                                TG   G  TTTAGTCTA GA
                                 AA_ GT        C
GAM661  RAB7L1   3'  ATCTGATTCTGGAATGC     14104     __    TTGA
                                GCA  CCAG    AATCAGAT
                                |||  ||||    ||||||||
                                CGT  GGTC    TTAGTCTA
                                  AA   _____
GAM661  ZNF137   3'  AGCATCTGATTTCAAACTCTTA 12858     ACC_   _        A
           GC                     GC    AGTT GAAATCAGAT CT
                                ||    |||| |||||||||| ||
                                CG    TCAA CTTTAGTCTA GA
                                 ATTC    A         C
GAM661  ABCA8    3'  AGTATCTGATATCAAT      23149       A
                                GTTGA ATCAGATACT
                                ||||| ||||||||||
                                TAACT TAGTCTATGA
                                   A
GAM661  DKFZP434L187 5'  AGTATCTGATAAAGTGG     68801     G  GAA
                                CCA TT   ATCAGATACT
                                ||| ||   ||||||||||
                                GGT AA   TAGTCTATGA
                                  G  A__
GAM661  FLJ12568 3'  AGTATCTGATTTTAGATG    46498    G
                                CA TTGAAATCAGATACT
                                || ||||||||||||||
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                                GT GATTTTAGTCTATGA
                                 A
GAM661  FLJ31153  3'  TATCTGATTACATTGATG    58129    C    T A
                                CA CAGT G AATCAGATA
                                || |||| | |||||||||
                                GT GTTA C TTAGTCTAT
                                 A   _ A
GAM661  GREAT     3'  ATCTGATTCCAGTGTG      55480      CAGT  A
                                CGCAC   TG AATCAGAT
                                ||||||   || ||||||||
                                GTGTG   AC TTAGTCTA
                                   _____ C
GAM661  KIAA1323  3'  GTATCTATTAACTGG       63044        AATC
                                CCAGTTGA   AGATAC
                                ||||||||   ||||||
                                GGTCAATT   TCTATG
                                     A___
GAM661  SLC19A3   3'  CTGATTTTTAAATGGTAGC   47487   _   GTT_
                                GC ACCA   GAAATCAG
                                || ||||   ||||||||
                                CG TGGT   TTTTAGTC
                                 A   AAAT
GAM661  VEST1     5'  TATCTGATTTTTTGAGC     53688    AC   TT
                                GC  CAG  GAAATCAGATA
                                ||  |||  ||||||||||
                                CG  GTT  TTTTAGTCTAT
                                 A_  __
GAM661  LOC221935 3'  GTATCTGACCAGTGC       92626     CAGT  AAA
                                GCAC   TG   TCAGATAC
                                ||||   ||   ||||||||
                                CGTG   AC   AGTCTATG
                                  _____ C__
GAM661  LOC256515 5'  TACCTGATTGGTCCGT      96465    C   GTTGAA    A
                                ACG ACCA     ATCAG TA
                                ||| ||||     ||||| ||
                                TGC TGGT     TAGTC AT
                                  C   _______    C
GAM662  ADRA1A    3'  GCACAAATCCAACATG      52784      AAGCC  A
                                CATGT    TG ATTTGTGC
                                |||||    || ||||||||
                                GTACA    AC TAAACACG
                                   _____ C
GAM662  AEGL1     5'  GCACAAATACACTACAT     6679       AGCC  A
                                ATGTA   TG ATTTGTGC
                                |||||   || ||||||||
                                TACAT   AC TAAACACG
                                   C___  A
GAM662  CDH2      3'  GCACAAATGTTTTACAT     8377        CCTGA
                                ATGTAAG    ATTTGTGC
                                |||||||    ||||||||
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                                TACATTT    TAAACACG
                                   TG___
GAM662  CHRNE   3' GCCCTCAGGCCCACAGGT   3586     A  AA    ATTTGT
                                ACC TGT  GCCTGA    GC
                                ||| |||  ||||||     ||
                                TGG ACA  CGGACT    CG
                                  _  CC     CC____
GAM662  COL4A3  3' GGCCATGGCTCACATGGT   3622       A   TGAATT  T
                                ACCATGT AGCC    TG GCC
                                ||||||| ||||     || |||
                                TGGTACA TCGG    AC CGG
                                   C   T_____ _
GAM662  COL4A3  3' GGCCATGGCTCACATGGT   48557      A   TGAATT  T
                                ACCATGT AGCC    TG GCC
                                ||||||| ||||     || |||
                                TGGTACA TCGG    AC CGG
                                   C   T_____ _
GAM662  COL4A3  3' GGCCATGGCTCACATGGT   48568      A   TGAATT  T
                                ACCATGT AGCC    TG GCC
                                ||||||| ||||     || |||
                                TGGTACA TCGG    AC CGG
                                   C   T_____ _
GAM662  CYP3A4  3' ACAAGCCTGGCCTACATGGT  33923       A  TGAA
                                ACCATGTA GCC   TTTGT
                                |||||||| |||   |||||
                                TGGTACAT CGG   GAACA
                                    C  TCC_
GAM662  HIVEP3  5' GGCACAAACCCAGCAGCCTCA 44439   TAA __  AA
                                TG  GC  CTG  TTTGTGCC
                                ||  ||  |||  ||||||||
                                AC  CG  GAC  AAACACGG
                                 TC_  AC  CC
GAM662  RECK    3' GCAACAGGCTCACTGGT    40869     T  A    AAT
                                ACCA GT AGCCTG  TTGT
                                |||| || ||||||  ||||
                                TGGT CA TCGGAC  AACG
                                  _  C     ___
GAM662  TNFSF8  3' GCACAAATTTAATACA     6966      AGCC
                                TGTA   TGAATTTGTGC
                                ||||   ||||||||||
                                ACAT   ATTTAAACACG
                                  A___
GAM662  ADAR3   3' CACAAATTCAGAACGTG    38018     AAGC
                                CATGT   CTGAATTTGTG
                                |||||   ||||||||||
                                GTGCA   GACTTAAACAC
                                  A___
GAM662  BIVM    3' CACAAATTCACTTA       34667     CC
                                TAAG  TGAATTTGTG
                                ||||  ||||||||||
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                                ATTC  ACTTAAACAC
                                  __
GAM662  C20orf160 3'  GCAGTTACAGGATTACATGGT  54648         G    AAT
                                ACCATGTAA CCTG   TTGT
                                ||||||||| ||||   ||||
                                TGGTACATT GGAC   GACG
                                     A    ATT
GAM662  EPHA7    3'  CACAAATTTGCTGCACA     15433     A_   CT
                                TGT  AGC  GAATTTGTG
                                |||  |||  |||||||||
                                ACA  TCG  TTTAAACAC
                                  CG  __
GAM662  FLJ12783  3'  AGTTCAGGCTCACTG       48675     T  A
                                CA GT AGCCTGAATT
                                || || ||||||||||
                                GT CA TCGGACTTGA
                                 _  C
GAM662  HSC3     3'  CACAGGTTCAGACTACA     59067      A C
                                TGTA G CTGAATTTGTG
                                |||| | ||||||||||
                                ACAT C GACTTGGACAC
                                  _ A
GAM662  KIAA0316  3'  GCACAAATGCTCTTCACAGTGG 69674      _  _   CCTGA
           T                     ACCA TGT AAG     ATTTGTGC
                                |||| ||| |||     ||||||||
                                TGGT ACA TTC     TAAACACG
                                  G   C   TCG__
GAM662  KIAA0453  3'  GCACAAGTAGCTACATAGT    69047    C     A  CTGA
                                AC ATGTA GC    ATTTGTGC
                                || ||||| ||    ||||||||
                                TG TACAT CG    TGAACACG
                                 A     _  A___
GAM662  KIAA1423  3'  AATTCAAGTTTACATG       61719          C
                                CATGTAAGC TGAATT
                                ||||||||| ||||||
                                GTACATTTG ACTTAA
                                     A
GAM662  KIAA1691  3'  GCACAAATGCTGTCCATGG    92556       TA_   CTGA
                                CCATG   AGC    ATTTGTGC
                                |||||   |||    ||||||||
                                GGTAC   TCG    TAAACACG
                                  CTG   _____
GAM662  PPP1R3B   3'  GCCAGGTTCAGATTACA     44820       GC        T
                                TGTAA  CTGAATTTG GC
                                |||||  ||||||||| ||
                                ACATT  GACTTGGAC CG
                                  A_        _
GAM662  SFXN2     3'  GCAGCAGAGTTACATGGT     73946          GC   AATTTG
                                ACCATGTAA  CTG     TGC
                                |||||||||  |||     |||
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                                TGGTACATT  GAC     ACG
                                    GA   G_____
GAM662  TBC1D2   5'  TAAATTCAGACCTACTGGT   37321     T   AGC
                                ACCA GTA   CTGAATTTG
                                |||| |||   |||||||||
                                TGGT CAT   GACTTAAAT
                                  _   CCA
GAM662  ZNF347   3'  GGCTTTATTCAGGCCTCACA  50848     AA_      TTGT
                                TGT   GCCTGAAT   GCC
                                |||   ||||||||   |||
                                ACA   CGGACTTA   CGG
                                  CTC       TTT_
GAM662  LOC134147 3'  CACAAATTCAGTAGGACGT   57158     AAGC
                                ATGT   CTGAATTTGTG
                                ||||   ||||||||||
                                TGCA   GACTTAAACAC
                                  GGAT
GAM662  LOC151195 5'  GCACAAATTTATTTACA     80169       CC
                                TGTAAG  TGAATTTGTGC
                                ||||||  ||||||||||
                                ACATTT  ATTTAAACACG
                                   __
GAM662  LOC152860 3'  AATTCCAGCTTACATGG     80695         CT
                                CCATGTAAGC  GAATT
                                |||||||||  |||||
                                GGTACATTCG  CTTAA
                                      AC
GAM662  LOC200382 3'  ACAGGGGCCAGACTTACATG  88801         C   AA_
                                CATGTAAG CTG   TTTGT
                                |||||||| |||   |||||
                                GTACATTC GAC   GGACA
                                    A   CGG
GAM662  LOC93622  3'  ACAGTCATTCCAGGCTTAGATG 56929     G      _   __
                                CAT TAAGCCTG AAT  TTGT
                                ||| |||||||| |||  ||||
                                GTA ATTCGGAC TTA  GACA
                                  G       C   CT
GAM663  C1orf6    3'  GGAACATAGTCTTCCATCT   39284         TACT
                                AGATGGAAGG   TGTTCC
                                ||||||||||   ||||||
                                TCTACCTTCT   ACAAGG
                                      GAT_
GAM663  CDH16     3'  AAGCCCCTCCATCTGC      14495         A  TA
                                GCAGATGGA GG  CTT
                                ||||||||| ||  |||
                                CGTCTACCT CC  GAA
                                      _ CC
GAM663  DAG1      3'  GAACATCCGTCCGTCCATCTGC 15279          A  TACT_
              AT                    ATGCAGATGGA GG    TGTTC
                                ||||||||||| ||    |||||
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                                TACGTCTACCT CC    ACAAG
                                      G  TGCCT
GAM663  DMPK    3'  AAGGCCCTCCATCTGC     15321        A  TA
                                GCAGATGGA GG  CTT
                                |||||||||  ||  |||
                                CGTCTACCT CC  GAA
                                     _  CG
GAM663  GNAO1   3'  AACAAACATACCCATCTGCA  90965        AAG  AC
                                TGCAGATGG   GT  TTGTT
                                |||||||||   ||  |||||
                                ACGTCTACC   TA  AACAA
                                     CA_  CA
GAM663  GRM7    3'  AACAAGTACATCTGTA     5942        GGAAG
                                TGCAGAT    GTACTTGTT
                                |||||||    |||||||||
                                ATGTCTA    CATGAACAA

                                ______
GAM663  GTF2H1  5'  GAGTTGTAGCTTCCACCTGCA  18007      A     G   TTG
                                TGCAG TGGAAG TAC   TTC
                                ||||| ||||||  |||   |||
                                ACGTC ACCTTC ATG   GAG
                                   C     G   TT_
GAM663  MDM4    3'  AACAAGAGATTTCTTCCATGCA 9975      GA      TA___
                                TGCA  TGGAAGG    CTTGTT
                                ||||  |||||||    ||||||
                                ACGT  ACCTTCT    GAACAA
                                  __      TTAGA
GAM663  PODXL   3'  GAACAAAGATTCCATTTGCA   18233          GGTAC
                                TGCAGATGGAA    TTGTTC
                                ||||||||||     ||||||
                                ACGTTTACCTT    AACAAG
                                      AGA__
GAM663  RING1   3'  AACACGCCCCCATCTGC     11344        AA   ACT
                                GCAGATGG  GGT   TGTT
                                ||||||||  |||   ||||
                                CGTCTACC  CCG   ACAA
                                     C_   C__
GAM663  TRPM6   3'  AACAAATACCCTTCCAT     34523        _  C
                                ATGGAAGG TA TTGTT
                                |||||||| || |||||
                                TACCTTCC AT AACAA
                                     C  A
GAM663  TXNRD1  3'  AACAAGTACATCTGCG      12453        GGAAG
                                TGCAGAT    GTACTTGTT
                                |||||||    |||||||||
                                GCGTCTA    CATGAACAA

                                ______
GAM663  AFAP    3'  GAACAAGCACCCCTTGC     41305      AT  AA   A
                                GCAG  GG  GGT CTTGTTC
                                ||||  ||  ||| |||||||
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                                CGTT  CC  CCA GAACAAG
                                  __ __   C
GAM663  CENTB1   5' AAGTGCCTCCACCTGCAT    28201       A   A
                                ATGCAG TGGA GGTACTT
                                ||||||| |||| |||||||
                                TACGTC ACCT CCGTGAA
                                   C   _
GAM663  CNOT8    3' GTACCTACCATCTGCAT     16530         A
                                ATGCAGATGG AGGTAC
                                |||||||||| ||||||
                                TACGTCTACC TCCATG
                                     A
GAM663  FLJ20174 3' AACACTTGCTCCTTCCATCTGC 34683           TACT__
           A                     TGCAGATGGAAGG     TGTT
                                ||||||||||||||     ||||
                                ACGTCTACCTTCC     ACAA
                                      TCGTTC
GAM663  FLJ21290 5' GGAACCCAGCTCCCATCTGC   46743        AA   ACTT
                                GCAGATGG  GGT   GTTCC
                                ||||||||  |||   |||||
                                CGTCTACC  TCG   CAAGG
                                    C_   ACC_
GAM663  HSD17B12 3' AACAAATAGCCATCTGC     32339        AAG  AC
                                GCAGATGG   GT  TTGTT
                                ||||||||   ||  |||||
                                CGTCTACC   TA  AACAA
                                    GA_  __
GAM663  KIAA0121 3' AACACTGCATCTGCAT      72651        GA  GTACT
                                ATGCAGATG  AG    TGTT
                                |||||||||  ||    ||||
                                TACGTCTAC  TC    ACAA
                                    G_  _____
GAM663  KIAA0406 3' AGTTCCCCTCCATCTGCAT   61329          A  T_
                                ATGCAGATGGA GG  ACT
                                |||||||||||  ||  |||
                                TACGTCTACCT CC  TGA
                                      C  CT
GAM663  KIAA1674 3' AGGTCCCTCCCATCTGC     68771        A   T
                                GCAGATGG AGG ACTT
                                |||||||| ||| ||||
                                CGTCTACC TCC TGGA
                                    C   C
GAM663  PDE8A    3' GAACAGCCCCCGATCTGCAT   62634         _ AA   ACT
                                ATGCAGAT GG  GGT   TGTTC
                                |||||||| ||  |||   |||||
                                TACGTCTA CC  CCG   ACAAG
                                    G  C_   ___
GAM663  PPAP2A   3' AACAGTGCCCCACCTGTAT   67832       A  AA     T
                                ATGCAG TGG  GGTACT GTT
                                |||||| |||  |||||| |||
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                                TATGTC ACC  CCGTGA CAA
                                   C  __    _
GAM663  RNF36    5'  AACAAGCTACATCTGCA     54957        GA  GTA
                                TGCAGATG  AG   CTTGTT
                                ||||||||  ||   ||||||
                                ACGTCTAC  TC   GAACAA
                                    A_  ___
GAM663  LOC113230 5'  GAAGCCCCCCACCTGCGT    72986       A   AA   ACTTG
                                ATGCAG TGG  GGT    TTC
                                |||||| |||  |||    |||
                                TGCGTC ACC  CCG    AAG
                                   C   CC  _____
GAM663  LOC145980 5'  GGAAGCCCACCCCCACACCTGC 83605       A__   AA   ACTTG
           AT                    ATGCAG   TGG  GGT    TTCC
                                ||||||   |||  |||    ||||
                                TACGTC   ACC  CCA    AAGG
                                   CAC   C_   CCCG_
GAM663  LOC148254 3'  GAACAAATACCTTCCTC     78759    T       C
                                GA GGAAGGTA TTGTTC
                                || |||||||| ||||||
                                CT CCTTCCAT AACAAG
                                 _       A
GAM663  LOC148266 3'  AACAAGGTATCTTCCATCAGCA 78768      A          _
           T                     ATGC GATGGAAGGTAC TTGTT
                                |||| |||||||||||| |||||
                                TACG CTACCTTCTATG AACAA
                                  A          G
GAM663  LOC148936 5'  GGAACCCACCCCTTCCATCTGC 84294             TACTT
           AT                    ATGCAGATGGAAGG    GTTCC
                                ||||||||||||||    |||||
                                TACGTCTACCTTCC    CAAGG
                                       CCACC
GAM663  LOC148938 5'  GGAACCCACCCCTTCCATCTGC 84276             TACTT
           GT                    ATGCAGATGGAAGG    GTTCC
                                ||||||||||||||    |||||
                                TGCGTCTACCTTCC    CAAGG
                                       CCACC
GAM664  ARNT2    3'  AAACAACCCGTGCATCCCTGC  29450    A   TTTTA
                                GTA GGAT    GGGTTGTTT
                                ||| ||||    |||||||||
                                CGT CCTA    CCCAACAAA
                                  C   CGTG_
GAM664  LCT      3'  AACCGTAAAAATCCTT      9697           G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
                                TTCCTAAAAAT CCAA
                                       G
GAM664  RPL15    3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
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                                CATTCCTAAAAATCCCAACAAA

GAM664  FBXO30   3'  AACTAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                  G        AA
GAM664  KIAA0494  3'  AACAACCCTTACTTAC      28736      GATTTTT
                                GTAAG      AGGGTTGTT
                                ||||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM664  PRO0641   5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                   ___    C
GAM664  SMT3H2    3'  AACAACATAAAAATCCTTGC   22670          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                        A_
GAM664  LOC120103 3'  AACCTATGAAAAATCCTTGC   74002          A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
                                CGTTCCTAAAAA   TCCAA
                                        GTA
GAM664  LOC129831 3'  AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM664  LOC133088 5'  AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                      GTA GGATTTTT     TTGTTT
                                ||| ||||||||     ||||||
                                CGT CCTAAAAA     AACAAA
                                  C       GATAA
GAM664  LOC148089 3'  GGCCCTAAAAATTCCTAC    78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM664  LOC154547 3'  AACAACATAAAAATCCTTGC   76050          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                        A_
GAM664  LOC158104 3'  ACAGCCAAAAATCCTTA     60313          AG
                                TAAGGATTTTT  GGTTGT
                                ||||||||||  ||||||
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                                ATTCCTAAAAA  CCGACA
                                      __
GAM664  LOC205880 5'  AAACAACCATCATCCTGAC   90709    A    TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM664  LOC221561 3'  AACAACATAAAAATCCTTGC   92130          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM664  LOC257591 3'  AACAACATAAAAATCCTTGC   97840          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM664  LOC51145  3'  AGCTAAAATCCTTAC       32393          TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
                                CATTCCTAAAA   TCGA
                                      ___
GAM665  ACT       5'  CAGGAAGAAGCGGCTTTAA   40040         CAACGG  C
                                TTAAAGCTGC     CT CCTG
                                |||||||||     || ||||
                                AATTTCGGCG     GA GGAC
                                     AA____  A
GAM665  ATP11A    3'  AGGCCACGCCGGCAGCTT    77017        AAC   TC__
                                AAGCTGCC   GGC    CCT
                                ||||||||   |||    |||
                                TTCGACGG   CCG    GGA
                                     ___   CACC
GAM665  CLASP2    3'  CAGGAATGCTTAAAGCTTTAA  64592        GCCAAC   TC_
                                TTAAAGCT     GGC   CCTG
                                ||||||||     |||   ||||
                                AATTTCGA     TCG   GGAC
                                     AAT___   TAA
GAM665  LTB4R     3'  GCTCCCACAGGCAGCTTTAA   5648          AAC___
                                TTAAAGCTGCC     GGC
                                ||||||||||     |||
                                AATTTCGACGG     TCG
                                      ACACCC
GAM665  POU3F1    3'  GCAGGAAATAGCCAAAGCTTTA 59310        GCCAAC    C___
          A                      TTAAAGCT     GGCT    CCTGC
                                 ||||||||     ||||    |||||
                                 AATTTCGA     CCGA    GGACG
                                      AA____    TAAA
GAM665  RAP1B     3'  CAGGGAGCCACAGTATTTAA   31598      _    CCAAC
                                TTAAA GCTG    GGCTCCCTG
                                ||||| ||||    |||||||||
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                                AATTT TGAC    CCGAGGGAC
                                  A   A____
GAM665  RBBP2    3'  GCAAGGAGCCGTTTTTTGGCTT 17323        CC_      C
            TGA                   TTAAAGCTG  AACGGCTCC TGC
                                  |||||||||  ||||||||| |||
                                  AGTTTCGGT  TTGCCGAGG ACG
                                      TTT       A
GAM665  SLC21A9  3'  CAGGGAGCCACCAGCAGT    23418      CAAC
                                  GCTGC   GGCTCCCTG
                                  ||||||  |||||||||
                                  TGACG   CCGAGGGAC
                                    ACCA
GAM665  UCP2     5'  AGCCACTGGCAGCTTTGA    12531          AC
                                  TTAAAGCTGCCA  GGCT
                                  ||||||||||||  ||||
                                  AGTTTCGACGGT  CCGA
                                        CA
GAM665  CDC42BPB 3'  CAGAAGACGGCAGTTTTAA   20099         AACGG  CC
                                  TTAAAGCTGCC    CT  CTG
                                  ||||||||||     ||  |||
                                  AATTTTGACGG    GA  GAC
                                        CA___  A_
GAM665  CLDN4    3'  GCAGGGAGGAGGGGACAGCTT  7137       _  AACGG
                                  AAGCTG CC     CTCCCTGC
                                  |||||| ||    ||||||||
                                  TTCGAC GG     GAGGGACG
                                     A  GGAG_
GAM665  CXYorf1  3'  CAGGGAGCCACCGGTCGC    82038    T   AAC
                                  GC GCC   GGCTCCCTG
                                  || |||   |||||||||
                                  CG TGG   CCGAGGGAC
                                   C   CCA
GAM665  DKFZP434J193 3'  CAGAAGCCTGGCAGCT      71001        AC    CC
                                  AGCTGCCA  GGCT  CTG
                                  ||||||||  ||||  |||
                                  TCGACGGT  CCGA  GAC
                                       __    A_
GAM665  DKFZp586H0623 3'  CAGGGAGCAGAGACTGCTTTAA 34066        TGCCAACG
                                  TTAAAGC       GCTCCCTG
                                  |||||||       ||||||||
                                  AATTTCG       CGAGGGAC
                                      TCAGAGA_
GAM665  FLJ20034  3'  CAGGGAGCCCGGTCAGCT    34362      _  AAC
                                  AGCTG CC   GGCTCCCTG
                                  ||||| ||   |||||||||
                                  TCGAC GG   CCGAGGGAC
                                     T  C__
GAM665  FLJ22031  3'  CAGGGAGACAGCTTTAG     46886         CCAACGG
                                  TTAAAGCTG      CTCCCTG
                                  |||||||||      |||||||
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                                GATTTCGAC      GAGGGAC
                                     A_______
GAM665  GOLPH2   3' GCAAAGTAGCAACAGCTTTAA 33322        CCAACG   CCC_
                                TTAAAGCTG     GCT    TGC
                                |||||||||     |||    |||
                                AATTTCGAC     CGA    ACG
                                     AA_____   TGAA
GAM665  GPR      3' GCAGGGAGCAGGAGC      23333     G  AACG
                                GCT CC    GCTCCCTGC
                                ||| ||    |||||||||
                                CGA GG    CGAGGGACG
                                  _ A___
GAM665  KIAA0335 3' GCAGTAGATGGGCAGCTT    28992        AACGG  CC
                                AAGCTGCC    CT  CTGC
                                ||||||||    ||  ||||
                                TTCGACGG    GA  GACG
                                     GTA__  T_
GAM665  KIAA0355 3' CAAGGGTGGTTGGCAGCT    28023         G  T  C
                                AGCTGCCAAC GC CC TG
                                |||||||||| || || ||
                                TCGACGGTTG TG GG AC
                                     G  _  A
GAM665  KIAA1211 3' AGGGACTTGGCAGTTT      68890         AC  C
                                AAGCTGCCA  GG TCCCT
                                |||||||||  || |||||
                                TTTGACGGT  TC AGGGA
                                          __  _
GAM665  MGC4251  3' CAGGGAGCCACTGAGGGT    50456     GC  AC
                                GCT  CA  GGCTCCCTG
                                |||  ||  |||||||||
                                TGG  GT  CCGAGGGAC
                                  GA  CA
GAM665  SFRS10   5' GCAAGAGGTTGGCAGCTTCGA 15977   TA        GG   CC
                                T  AAGCTGCCAAC  CTC  TGC
                                |  ||||||||||  |||  |||
                                A  TTCGACGGTTG  GAG  ACG
                                 GC          __   A_
GAM665  TFPT     5' AGAAAGACGTTGGCAACT    25318    C      G  CC
                                AG TGCCAACG CT  CT
                                || |||||||| ||  ||
                                TC ACGGTTGC GA  GA
                                 A       A  AA
GAM665  LOC146669 5' CAGAGAGAGCAGCTTT      78054        CAACGG   C
                                AAAGCTGC     CTC CTG
                                ||||||||     ||| |||
                                TTTCGACG     GAG GAC
                                     A_____   A
GAM665  LOC149076 3' GCAGAGGGGTGCGGCAGCTT  79153         AACG    _
                                AAGCTGCC    GCTCC CTGC
                                ||||||||    ||||| ||||
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                                TTCGACGG   TGGGG GACG
                                    CG__    A
GAM665  LOC151475 5'  AGACATTGACAGCTTTAA   85388        C  CGG
                                TTAAAGCTG CAA  CT
                                ||||||||| |||  ||
                                AATTTCGAC GTT  GA
                                    A  ACA
GAM665  LOC153416 3'  CAGGGAGCCACAGTATTTAA  60539     _  CCAAC
                                TTAAA GCTG   GGCTCCCTG
                                ||||| ||||   |||||||||
                                AATTT TGAC   CCGAGGGAC
                                  A  A____
GAM665  LOC153768 3'  CCCCTGCACAGTGTTGGCAGCT 56714         G_______  TCCCT
          T                    AAGCTGCCAAC      GC    G
                               ||||||||||       ||    |
                               TTCGACGGTTG      CG    C
                                    TGACAIII  TCCCT
GAM665  LOC51760  3'  CAGGGAAGGCAGCTTT     33265        AACGGC
                                AAAGCTGCC    TCCCTG
                                |||||||||    ||||||
                                TTTCGACGG    AGGGAC
                                    A_____
GAM665  LOC91040  3'  CAGGGAGCCACCGGTCGC   64709   T  AAC
                                GC GCC  GGCTCCCTG
                                || |||  |||||||||
                                CG TGG  CCGAGGGAC
                                 C  CCA
GAM665  LOC92181  3'  CAAAGAGCCAGGCTTTGA   68401       GCCAAC   CC
                                TTAAAGCT    GGCTC  TG
                                ||||||||    |||||  ||
                                AGTTTCGG    CCGAG  AC
                                    A_____    AA
GAM666  DACH    3'  TGAGAATGTTTGTAAATGTACA 54974      CATCC  CT
                                TGTACA   ACA  CATTCTCA
                                ||||||   |||  ||||||||
                                ACATGT   TGT  GTAAGAGT
                                   AAA__  TT
GAM666  IL11RA  3'  GGAACGTGTGTAATGTGTACA  15712       C_   TCA
                                TGTACACAT  CACAC  TTCT
                                |||||||||  |||||  ||||
                                ACATGTGTA  GTGTG  AAGG
                                    AT   C__
GAM666  LYPLA1  3'  AGAATGAGGTGGTATTACA   20922    CACAT   A
                                TGTA   CCAC CTCATTCT
                                ||||   |||| ||||||||
                                ACAT   GGTG GAGTAAGA
                                  TAT__  _
GAM666  NAPB    3'  GAGAATGAATGTATGT     70183     CC  C
                                ACAT  ACA TCATTCTC
                                ||||  ||| ||||||||
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                                TGTA  TGT AGTAAGAG
                                  __  A
GAM666  NRF1    3'  GAATATATGTATATGTGTACA  60120       CC  CTC
                                TGTACACAT  ACA  ATTC
                                |||||||||  |||  ||||
                                ACATGTGTA  TGT  TAAG
                                     TA  ATA
GAM666  PRKAB1  3'  AGAGGGAATGGACTGTACA   20734     CA  CA  AT
                                TGTACA  TCCA  CTC  TCT
                                ||||||  ||||  |||  |||
                                ACATGT  AGGT  GGG  AGA
                                   C_   AA  __
GAM666  PTGFR   3'  TGAGAGAGATGTGTACA     6319        CACA
                                TGTACACATC   CTCA
                                ||||||||||   ||||
                                ACATGTGTAG   GAGT
                                     AGA_
GAM666  RBBP5   3'  AGATTGGATAGATGTGTACA  17327       CACAC  T
                                TGTACACATC    TCA TCT
                                ||||||||||    ||| |||
                                ACATGTGTAG    GGT AGA
                                     ATA__  T
GAM666  SAT     3'  TGAGTCATTTAAATGTGTACA  11436       CCAC___
                                TGTACACAT     ACTCA
                                |||||||||     |||||
                                ACATGTGTA     TGAGT
                                     AATTTAC
GAM666  TMP21   3'  AATGGTGATGGATGTGACA   22399    A     _  T
                                TGT CACATCCA CAC CATT
                                ||| |||||||| ||| ||||
                                ACA GTGTAGGT GTG GTAA
                                  _     A  _
GAM666  UBE2V1  3'  TGAAATGTGGATGCATAC    41797    CA     C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
                                CAT  GTAGGTGT  AGT
                                  AC      AA
GAM666  UBE2V1  3'  TGAAATGTGGATGCATAC    42374    CA     C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
                                CAT  GTAGGTGT  AGT
                                  AC      AA
GAM666  UBE2V1  3'  TGAAATGTGGATGCATAC    12522    CA     C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
                                CAT  GTAGGTGT  AGT
                                  AC      AA
GAM666  ZIC1    3'  AGAATGTTCTAGTAAATGTGTA 12720       CC  ACT__
           C                     GTACACAT  AC    CATTCT
                                ||||||||  ||    ||||||
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                                CATGTGTA TG    GTAAGA
                                     AA ATCTT
GAM666  AF038169 5' TGAAAATGAGTGCTGTAGATG 25255     __ _      C
                                CATC CA CACTCATT TCA
                                |||| || |||||||| |||
                                GTAG GT GTGAGTAA AGT
                                  AT C       A
GAM666  CDC14A   3' AGAAGTGGATGTATATA     13391     C      ACTCA
                                TGTA ACATCCAC    TTCT
                                |||| ||||||||    ||||
                                ATAT TGTAGGTG    AAGA
                                  A      _____
GAM666  DKFZP564I052 3' GATGATCATGTGATGTGTACA 66710         C  C__
                                TGTACACATC ACA   TCATT
                                |||||||||| |||   |||||
                                ACATGTGTAG TGT   AGTAG
                                      _  ACT
GAM666  DKFZP761F241 3' TGAGAATGAGTGAGGTTTCGTA 48800      ACAT  A
           CA                     TGTAC    CC CACTCATTCTCA
                                |||||    || ||||||||||||
                                ACATG    GG GTGAGTAAGAGT
                                   CTTT  A
GAM666  FLJ11101  3' AGAAGTGTTGAGTGTGTACA  37049       TC  _   CAT
                                TGTACACA  CA CACT   TCT
                                ||||||||  || ||||   |||
                                ACATGTGT  GT GTGA   AGA
                                     GA  T   ___
GAM666  FLJ14642  3' AGTATGGGTGTGTACA     51492          C
                                TGTACACATCCA ACT
                                |||||||||||| |||
                                ACATGTGTGGGT TGA
                                       A
GAM666  FLJ20399  3' GGTGGCTGTGGATGCCACA   35125    ACA      CT
                                TGT   CATCCACA  CATT
                                |||   ||||||||  ||||
                                ACA   GTAGGTGT  GTGG
                                  CC_      CG
GAM666  GFPT1    3' GAAGATGGGATGTGTACA    9022          A  C  A
                                TGTACACATCC CA TC TTC
                                |||||||||| || || |||
                                ACATGTGTAGG GT AG AAG
                                        _  _  _
GAM666  KIAA0450  3' GAGGGCAGTGTGGATG     27640         CA
                                CATCCACACT  TTCTC
                                ||||||||||  |||||
                                GTAGGTGTGA  GGGAG
                                      C_
GAM666  KIAA0530  3' GATGGTATGAAAATGTGTACA  70867        C__  C  T
                                TGTACACAT   CA AC CATT
                                |||||||||   || || ||||
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                                ACATGTGTA  GT TG GTAG
                                     AAA  A  _
GAM666  KIAA0753  3'  GGGGAGTTAAATGTGTACA   28999        CCAC   ATT
                                TGTACACAT   ACTC  CTC
                                |||||||||   ||||  |||
                                ACATGTGTA   TGAG  GGG
                                     AAT_   ___
GAM666  KIAA0788  3'  TGAATTAGGAATGTGTACA   71339        _  ACAC
                                TGTACACAT CC   TCA
                                ||||||||| ||   |||
                                ACATGTGTA GG   AGT
                                     A  ATTA
GAM666  KIAA0855  3'  AGAATGAGCAGTGTAC     30400       ATCCACA
                                GTACAC     CTCATTCT
                                ||||||     ||||||||
                                CATGTG     GAGTAAGA
                                   AC_____
GAM666  KIAA0865  5'  GAGCAAGTGGAATGTGTACA  61250        _   A__
                                TGTACACAT CCAC  CTC
                                ||||||||| ||||  |||
                                ACATGTGTA GGTG  GAG
                                     A   AAC
GAM666  KIAA0992  3'  GGAAGTGTGGAGCACACA    32207    ACACA      CAT
                                TGT    TCCACACT  TCT
                                |||    ||||||||  |||
                                ACA    AGGTGTGA  AGG
                                  CACG_      ___
GAM666  MGC16037  5'  TGAGGTGTAGATATGTATA   51822      C  C   _
                                TGTACA ATC ACAC TCA
                                |||||| ||| |||| |||
                                ATATGT TAG TGTG AGT
                                   A  A   G
GAM666  OSRF      3'  TGAAAATGCACACAAATGTGTA 59525       CCACACT   C
           CA                     TGTACACAT      CATT TCA
                                |||||||||      |||| |||
                                ACATGTGTA      GTAA AGT
                                     AACACAC   A
GAM666  RAB3-GAP150 3'  TGAGAATCAGAGATGTGTA   24839       CACA  C
                                TACACATC   CT ATTCTCA
                                ||||||||   || |||||||
                                ATGTGTAG   GA TAAGAGT
                                     A___  C
GAM666  RAP140    3'  GATGGGTAAATGTGTACA    30844       CCAC
                                TGTACACAT   ACTCATT
                                |||||||||   |||||||
                                ACATGTGTA   TGGGTAG
                                     AA__
GAM666  TACTILE   5'  GAGTGCATGTGTACA       19471       CCA
                                TGTACACAT   CACTC
                                |||||||||   |||||
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                                ACATGTGTA  GTGAG
                                     C__
GAM666  LOC131873 3'  GATGTATGCATATGTGTACA  75880       CCA  CT
                                TGTACACAT  CA  CATT
                                |||||||||  ||  ||||
                                ACATGTGTA  GT  GTAG
                                     TAC  AT
GAM666  LOC134145 3'  AGCTGTATATGTGTACA    75144       CC  _
                                TGTACACAT  ACA CT
                                |||||||||  ||| ||
                                ACATGTGTA  TGT GA
                                     TA  C
GAM666  LOC145482 3'  AATGGTATGATGTGTACA   77226       CAC  T
                                TGTACACATC  AC CATT
                                ||||||||||  || ||||
                                ACATGTGTAG  TG GTAA
                                      TA_  _
GAM666  LOC148195 3'  GAAAAGGTGGATGTGTCA   84129   T       A  CA
                                TG ACACATCCAC CT  TTC
                                || ||||||||||  ||  |||
                                AC TGTGTAGGTG GA  AAG
                                 _       _ A_
GAM666  LOC152633 5'  TGAGCTGTACATGTAGAGTGTA 85826      A  C  CT__  TT
          CA                    TGTACAC TC ACA   CA  CTCA
                                |||||||  || |||   ||  ||||
                                ACATGTG AG TGT   GT  GAGT
                                    _ A  ACAT  C_
GAM666  LOC153630 5'  AATGAGTGTGCGTAC      86079     ACATC
                                GTAC    CACACTCATT
                                ||||    ||||||||||
                                CATG    GTGTGAGTAA
                                  C_____
GAM666  LOC221662 3'  AGAATGAGGGGAATGGGCA   92399   TA  CA  ACA
                                TG  CA  TCC  CTCATTCT
                                ||  ||  |||  ||||||||
                                AC  GT  AGG  GAGTAAGA
                                 GG  A_  G__
GAM666  LOC254659 5'  GAGAATGGAGATGCTACA    95113     CA   CACAC
                                TGTA  CATC    TCATTCTC
                                ||||  ||||    ||||||||
                                ACAT  GTAG    GGTAAGAG
                                  C_   A_____
GAM666  LOC83693  3'  AGGGTGTGTGGATGGCACA   48830    ACA      TC
                                TGT   CATCCACAC  ATTCT
                                |||   |||||||||  |||||
                                ACA   GTAGGTGTG  TGGGA
                                  CG_       __
GAM666  LOC90981  3'  AATGGTGATGGATGTGACA   64532    A      _  T
                                TGT CACATCCA CAC CATT
                                ||| |||||||| ||| ||||
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                                ACA GTGTAGGT GTG GTAA
                                  _       A   _
GAM667  ADAM19   3'  CAGGAAGAAGACTGGCCATTAT 52703      C    CTGAG
              G                   CATGA GGCT     TTCTTCCTG
                                  ||||| ||||     |||||||||
                                  GTATT CCGG     AAGAAGGAC
                                    A    TCAG_
GAM667  FACL5    5'  CAGGAAGAACTCAGAGCCG   64186
                                  CGGCTCTGAGTTCTTCCTG
                                  ||||||||||||||||||
                                  GCCGAGACTCAAGAAGGAC

GAM667  GNAL     5'  CAGGAAAGAGAGGAGCCGTCG  9058          GAG TC
                                  TGACGGCTCT   T  TTCCTG
                                  ||||||||||   |  ||||||
                                  GCTGCCGAGG   A  AAGGAC
                                        AG_ GA
GAM667  KAL1     3'  CAGGAAGAACTTCTGTCA    4013        CTCT
                                  TGACGG    GAGTTCTTCCTG
                                  ||||||    ||||||||||||
                                  ACTGTC    TTCAAGAAGGAC
                                      ____
GAM667  MYO1E    3'  CAGGAGGACAAAACCACCATG  17187      AC  CTC  AGT
                                  CATG  GG   TG   TCTTCCTG
                                  ||||  ||   ||   ||||||||
                                  GTAC  CC   AC   AGGAGGAC
                                    CA  AAA  ___
GAM667  PRKAR2B  3'  CAGAAAGAACTCAGATGT    10804    _         C
                                  GC TCTGAGTTCTT CTG
                                  || ||||||||||| |||
                                  TG AGACTCAAGAA GAC
                                   T         A
GAM667  PUM2     3'  AGGATCAAAGCTGTCATG    31014          C   GTTCT
                                  CATGACGGCT TGA     TCCT
                                  |||||||||| |||     ||||
                                  GTACTGTCGA ACT     AGGA
                                        A  _____
GAM667  SKI      3'  CAGGAAGTGCAGAGCCGCA   11701    A       AGTT
                                  TG CGGCTCTG    CTTCCTG
                                  || ||||||||    |||||||
                                  AC GCCGAGAC    GAAGGAC
                                   _       GT__
GAM667  TEM8     3'  AGGAAGATGCAACCCCATG   36326     AC  CTC  AGT
                                  CATG  GG   TG   TCTTCCT
                                  ||||  ||   ||   |||||||
                                  GTAC  CC   AC   AGAAGGA
                                    C_  A__  GT_
GAM667  ARHGEF4  5'  AGAAAAAACTCAGGGC      52207          C  C
                                  GCTCTGAGTT TT CT
                                  |||||||||| || ||
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                                CGGGACTCAA AA GA
                                      A  A
GAM667  FLJ31978  3'  CAGGAAGGAACAAGCGCC    58348     T  GAG
                                GGC CT   TTCTTCCTG
                                ||| ||   |||||||||
                                CCG GA   AGGAAGGAC
                                  C  ACA
GAM667  HSU24186  5'  AGAACTCAAAGCCGTC      25324        C
                                GACGGCT TGAGTTCT
                                ||||||| ||||||||
                                CTGCCGA ACTCAAGA
                                    A
GAM667  KCNT1     3'  AGCTCCCAGGGCCGCCA     61825    A      __
                                TG CGGCTCT  GAGTT
                                || |||||||  |||||
                                AC GCCGGGA  CTCGA
                                 C      CC
GAM667  KIAA1867  3'  CAGGAAGAACCCAAGAGCTCAT 94822      CG     GA_
                                ATGA  GCTCT   GTTCTTCCTG
                                ||||  |||||   ||||||||||
                                TACT  CGAGA   CAAGAAGGAC
                                  __    ACC
GAM667  KIAA1878  3'  AATTCAGAGAATCGTCATG   91707         __
                                CATGACGG  CTCTGAGTT
                                ||||||||  |||||||||
                                GTACTGCT  GAGACTTAA
                                     AA
GAM667  MFN1      3'  CAGGAAGAACTCATGA      35541    _
                                TC TGAGTTCTTCCTG
                                || ||||||||||||
                                AG ACTCAAGAAGGAC
                                 T
GAM667  MIDORI    3'  CAGGGCCCTTCCAGAGCCTGTC 73784        _      AGTTCT
            ATG                   CATGAC GGCTCTG     TCCTG
                                |||||| |||||||     |||||
                                GTACTG CCGAGAC     GGGAC
                                   T      CTTCCC
GAM667  MYH7B     3'  CAGGAAGAACCTGGCTCGCATG 70530      A  _  CTGA
                                CATG CG GCT    GTTCTTCCTG
                                |||| || |||    ||||||||||
                                GTAC GC CGG    CAAGAAGGAC
                                  _ T   TC__
GAM667  RNAHP     3'  AGAAAGCAGCAGCCGTCAT    23761         _  AG
                                ATGACGGCT CTG  TTCT
                                ||||||||| |||  ||||
                                TACTGCCGA GAC  AAGA
                                      C   GA
GAM667  SLC37A1   3'  AGACGGAGCTCAGACCC     38561    C        TC
                                GG TCTGAGTTCT  CT
                                || ||||||||||  ||
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                                CC AGACTCGAGG  GA
                                 C         CA
GAM667  LOC116236 3'  CAGGAAAAGCACAAACCTCAT  73809      C  CTC  A   C
                                ATGA GG   TG GTT TTCCTG
                                |||| ||   || ||| ||||||
                                TACT CC   AC CGA AAGGAC
                                  _  AA_  A   A
GAM667  LOC124801 3'  CAGGAAGAACTCTCTTGCATG  74336      A   CTCT
                                CATG CGG    GAGTTCTTCCTG
                                |||| |||    ||||||||||||
                                GTAC GTT    CTCAAGAAGGAC
                                  _   CT__
GAM667  LOC222160 5'  AGGAAGAACTCACCCC      94117     CTC
                                GG   TGAGTTCTTCCT
                                ||   ||||||||||||
                                CC   ACTCAAGAAGGA
                                 CC_
GAM667  LOC51094  3'  CAGGAAGAATAAAGCC      32045      CTGA
                                GGCT    GTTCTTCCTG
                                ||||    ||||||||||
                                CCGA    TAAGAAGGAC
                                  AA__
GAM667  LOC92078  3'  CAGGAAGAAGAATCGACCGTC  67977      C  T  G__
                                GACGG TC GA   TTCTTCCTG
                                ||||| || ||   |||||||||
                                CTGCC AG CT   AAGAAGGAC
                                  _ _  AAG
GAM668  DACH      3'  TGAGAATGTTTGTAAATGTACA 54974       CATCC   CT
                                TGTACA    ACA  CATTCTCA
                                ||||||    |||  ||||||||
                                ACATGT    TGT  GTAAGAGT
                                   AAA__   TT
GAM668  IL11RA    3'  GGAACGTGTGTAATGTGTACA  15712        C_    TCA
                                TGTACACAT  CACAC   TTCT
                                |||||||||  |||||   ||||
                                ACATGTGTA  GTGTG   AAGG
                                     AT    C__
GAM668  LYPLA1    3'  AGAATGAGGTGGTATTACA    20922      CACAT   A
                                TGTA    CCAC CTCATTCT
                                ||||    |||| ||||||||
                                ACAT    GGTG GAGTAAGA
                                  TAT__   _
GAM668  NAPB      3'  GAGAATGAATGTATGT      70183      CC   C
                                ACAT  ACA TCATTCTC
                                ||||  ||| ||||||||
                                TGTA  TGT AGTAAGAG
                                  __  A
GAM668  NRF1      3'  GAATATATGTATATGTGTACA  60120         CC   CTC
                                TGTACACAT  ACA   ATTC
                                |||||||||  |||   ||||
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                                ACATGTGTA TGT  TAAG
                                     TA  ATA
GAM668  PRKAB1   3' AGAGGGAATGGACTGTACA  20734     CA  CA  AT
                                TGTACA TCCA CTC TCT
                                |||||| |||| ||| |||
                                ACATGT AGGT GGG AGA
                                   C_   AA  __
GAM668  PTGFR    3' TGAGAGAGATGTGTACA    6319        CACA
                                TGTACACATC   CTCA
                                ||||||||||   ||||
                                ACATGTGTAG   GAGT
                                     AGA_
GAM668  RBBP5    3' AGATTGGATAGATGTGTACA  17327       CACAC  T
                                TGTACACATC    TCA TCT
                                ||||||||||    ||| |||
                                ACATGTGTAG    GGT AGA
                                     ATA__  T
GAM668  SAT      3' TGAGTCATTTAAATGTGTACA 11436       CCAC___
                                TGTACACAT     ACTCA
                                |||||||||     |||||
                                ACATGTGTA     TGAGT
                                     AATTTAC
GAM668  TMP21    3' AATGGTGATGGATGTGACA   22399    A     _  T
                                TGT CACATCCA CAC CATT
                                ||| |||||||| ||| ||||
                                ACA GTGTAGGT GTG GTAA
                                  _      A  _
GAM668  UBE2V1   3' TGAAATGTGGATGCATAC   41797    CA     C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
                                CAT  GTAGGTGT  AGT
                                  AC      AA
GAM668  UBE2V1   3' TGAAATGTGGATGCATAC   42374    CA     C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
                                CAT  GTAGGTGT  AGT
                                  AC      AA
GAM668  UBE2V1   3' TGAAATGTGGATGCATAC   12522    CA     C_
                                GTA  CATCCACA  TCA
                                |||  ||||||||  |||
                                CAT  GTAGGTGT  AGT
                                  AC      AA
GAM668  ZIC1     3' AGAATGTTCTAGTAAATGTGTA 12720      CC  ACT__
           C                     GTACACAT  AC    CATTCT
                                |||||||| ||    ||||||
                                CATGTGTA  TG    GTAAGA
                                     AA  ATCTT
GAM668  AF038169 5' TGAAAATGAGTGCTGTAGATG 25255     __ _     C
                                CATC  CA CACTCATT TCA
                                ||||  || |||||||| |||
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                                GTAG  GT GTGAGTAA AGT
                                  AT  C       A
GAM668  CDC14A    3'  AGAAGTGGATGTATATA     13391      C       ACTCA
                                TGTA ACATCCAC     TTCT
                                |||| ||||||||     ||||
                                ATAT TGTAGGTG     AAGA
                                  A       _____
GAM668  DKFZP564I052 3'  GATGATCATGTGATGTGTACA  66710          C   C__
                                TGTACACATC ACA   TCATT
                                |||||||||| |||   |||||
                                ACATGTGTAG TGT   AGTAG
                                      _  ACT
GAM668  DKFZP761F241 3'  TGAGAATGAGTGAGGTTTCGTA 48800       ACAT  A
           CA                     TGTAC    CC CACTCATTCTCA
                                |||||    || ||||||||||||
                                ACATG    GG GTGAGTAAGAGT
                                   CTTT  A
GAM668  FLJ11101  3'  AGAAGTGTTGAGTGTGTACA   37049        TC  _    CAT
                                TGTACACA  CA CACT   TCT
                                ||||||||  || ||||   |||
                                ACATGTGT  GT GTGA   AGA
                                     GA  T   ___
GAM668  FLJ14642  3'  AGTATGGGTGTGTACA      51492           C
                                TGTACACATCCA ACT
                                |||||||||||| |||
                                ACATGTGTGGGT TGA
                                       A
GAM668  FLJ20399  3'  GGTGGCTGTGGATGCCACA   35125     ACA       CT
                                TGT   CATCCACA  CATT
                                |||   ||||||||  ||||
                                ACA   GTAGGTGT  GTGG
                                  CC_       CG
GAM668  GFPT1     3'  GAAGATGGGATGTGTACA    9022           A  C  A
                                TGTACACATCC CA TC TTC
                                |||||||||| || || |||
                                ACATGTGTAGG GT AG AAG
                                       _  _  _
GAM668  KIAA0450  3'  GAGGGCAGTGTGGATG      27640          CA
                                CATCCACACT  TTCTC
                                |||||||||  |||||
                                GTAGGTGTGA  GGGAG
                                     C_
GAM668  KIAA0530  3'  GATGGTATGAAAATGTGTACA  70867         C__  C  T
                                TGTACACAT   CA AC CATT
                                |||||||||   || || ||||
                                ACATGTGTA   GT TG GTAG
                                     AAA  A  _
GAM668  KIAA0753  3'  GGGGAGTTAAATGTGTACA   28999         CCAC    ATT
                                TGTACACAT    ACTC   CTC
                                |||||||||    ||||   |||
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                                ACATGTGTA   TGAG  GGG
                                     AAT_   ___
GAM668  KIAA0788 3'  TGAATTAGGAATGTGTACA   71339        _ ACAC
                                TGTACACAT CC   TCA
                                ||||||||| ||   |||
                                ACATGTGTA GG   AGT
                                     A  ATTA
GAM668  KIAA0855 3'  AGAATGAGCAGTGTAC     30400      ATCCACA
                                GTACAC     CTCATTCT
                                ||||||     ||||||||
                                CATGTG     GAGTAAGA
                                   AC_____
GAM668  KIAA0865 5'  GAGCAAGTGGAATGTGTACA  61250        _   A__
                                TGTACACAT CCAC  CTC
                                ||||||||| ||||  |||
                                ACATGTGTA GGTG  GAG
                                     A   AAC
GAM668  KIAA0992 3'  GGAAGTGTGGAGCACACA    32207    ACACA      CAT
                                TGT    TCCACACT  TCT
                                |||    ||||||||  |||
                                ACA    AGGTGTGA  AGG
                                  CACG_     ___
GAM668  MGC16037 5'  TGAGGTGTAGATATGTATA   51822      C  C   _
                                TGTACA ATC ACAC TCA
                                |||||| ||| |||| |||
                                ATATGT TAG TGTG AGT
                                   A  A   G
GAM668  OSRF     3'  TGAAAATGCACACAAATGTGTA 59525        CCACACT   C
           CA                    TGTACACAT     CATT TCA
                                |||||||||     |||| |||
                                ACATGTGTA     GTAA AGT
                                     AACACAC   A
GAM668  RAB3-GAP150 3'  TGAGAATCAGAGATGTGTA   24839       CACA  C
                                TACACATC   CT ATTCTCA
                                ||||||||   || |||||||
                                ATGTGTAG   GA TAAGAGT
                                     A___  C
GAM668  RAP140   3'  GATGGGTAAATGTGTACA    30844       CCAC
                                TGTACACAT   ACTCATT
                                |||||||||   |||||||
                                ACATGTGTA   TGGGTAG
                                     AA__
GAM668  TACTILE  5'  GAGTGCATGTGTACA       19471       CCA
                                TGTACACAT  CACTC
                                |||||||||  |||||
                                ACATGTGTA  GTGAG
                                     C__
GAM668  LOC131873 3'  GATGTATGCATATGTGTACA  75880       CCA  CT
                                TGTACACAT  CA  CATT
                                |||||||||  ||  ||||
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                                ACATGTGTA  GT  GTAG
                                     TAC  AT
GAM668  LOC134145 3'  AGCTGTATATGTGTACA    75144        CC  _
                                TGTACACAT  ACA CT
                                |||||||||  ||| ||
                                ACATGTGTA  TGT GA
                                     TA   C
GAM668  LOC145482 3'  AATGGTATGATGTGTACA    77226        CAC  T
                                TGTACACATC   AC CATT
                                ||||||||||   || ||||
                                ACATGTGTAG   TG GTAA
                                      TA_  _
GAM668  LOC148195 3'  GAAAAGGTGGATGTGTCA    84129    T       A  CA
                                TG ACACATCCAC CT  TTC
                                || ||||||||||  ||  |||
                                AC TGTGTAGGTG GA  AAG
                                 _       _ A_
GAM668  LOC152633 5'  TGAGCTGTACATGTAGAGTGTA 85826       A  C   CT__  TT
           CA                    TGTACAC TC ACA    CA  CTCA
                                |||||||  || |||    ||  ||||
                                ACATGTG AG TGT    GT  GAGT
                                    _ A   ACAT  C_
GAM668  LOC153630 5'  AATGAGTGTGCGTAC      86079      ACATC
                                GTAC    CACACTCATT
                                ||||    ||||||||||
                                CATG    GTGTGAGTAA
                                  C____
GAM668  LOC221662 3'  AGAATGAGGGGAATGGGCA   92399    TA  CA   ACA
                                TG  CA  TCC   CTCATTCT
                                ||  ||  |||   ||||||||
                                AC  GT  AGG   GAGTAAGA
                                 GG  A_   G__
GAM668  LOC254659 5'  GAGAATGGAGATGCTACA    95113     CA    CACAC
                                TGTA  CATC    TCATTCTC
                                ||||  ||||    ||||||||
                                ACAT  GTAG    GGTAAGAG
                                  C_   A____
GAM668  LOC83693  3'  AGGGTGTGTGGATGGCACA   48830     ACA       TC
                                TGT   CATCCACAC  ATTCT
                                |||   |||||||||  |||||
                                ACA   GTAGGTGTG  TGGGA
                                  CG_       __
GAM668  LOC90981  3'  AATGGTGATGGATGTGACA   64532     A      _  T
                                TGT CACATCCA CAC CATT
                                ||| |||||||| ||| ||||
                                ACA GTGTAGGT GTG GTAA
                                  _      A  _
GAM669  AQP6      3'  TCTCAAACTCCTGACCT     53945
                                AGGTCAGGAGTTTGAGA
                                |||||||||||||||||
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                                TCCAGTCCTCAAACTCT

GAM669  AQP6     3'  TCTCAAACTCCTGACCT     7965
                                AGGTCAGGAGTTTGAGA
                                |||||||||||||||||
                                TCCAGTCCTCAAACTCT

GAM669  ARSF     5'  TCTCGAACTCCCGACCTCA    64605        A
                                TGAGGTC GGAGTTTGAGA
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAGCTCT
                                    C
GAM669  ATP1B2   3'  TCTCGAACTCCCGACCTCA    8057         A
                                TGAGGTC GGAGTTTGAGA
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAGCTCT
                                    C
GAM669  ATP7A    3'  TCTTAAACTCCTAACCTCA    3531         C
                                TGAGGT AGGAGTTTGAGA
                                |||||| ||||||||||||
                                ACTCCA TCCTCAAATTCT
                                   A
GAM669  AXL      3'  TCTAAAACTCCTGACCTCA    8110             G
                                TGAGGTCAGGAGTTT AGA
                                |||||||||||||| |||
                                ACTCCAGTCCTCAAA TCT
                                       A
GAM669  AXL      3'  TCTAAAACTCCTGACCTCA    41607            G
                                TGAGGTCAGGAGTTT AGA
                                |||||||||||||| |||
                                ACTCCAGTCCTCAAA TCT
                                       A
GAM669  C7       3'  TCTCCAACTCCTGACCTCA    5167             T
                                TGAGGTCAGGAGTT GAGA
                                |||||||||||||| ||||
                                ACTCCAGTCCTCAA CTCT
                                       C
GAM669  CBFA2T2  3'  TCTCAAACCCCGGACCTCA    17479        A  A
                                TGAGGTC GG GTTTGAGA
                                ||||||| || ||||||||
                                ACTCCAG CC CAAACTCT
                                    G  C
GAM669  CHRNB4   3'  TTTCGAACTCCTGACCTCA    5637
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTTT

GAM669  CLECSF12 3'  AGTCCCGAACTCCTGACCTCA  76683              A
                                TGAGGTCAGGAGTTTG GACT
                                |||||||||||||||| ||||
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                                ACTCCAGTCCTCAAGC CTGA
                                        C
GAM669  CORO2B   3'  ACCTCTAACCTCCTGACCTCA  64567          TTTG  CT
                                TGAGGTCAGGAG   AGA  GGT
                                ||||||||||||   |||  |||
                                ACTCCAGTCCTC   TCT  CCA
                                      CAA_  __
GAM669  CYP1A2   3'  ACTAGTCTCAAACTCCTGACCT 69090
            CA                    TGAGGTCAGGAGTTTGAGACTGGT
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGATCA

GAM669  CYP1A2   3'  TCTCGAACTCCTGACCCCA   69131    A
                                TG GGTCAGGAGTTTGAGA
                                || ||||||||||||||||
                                AC CCAGTCCTCAAGCTCT
                                 C
GAM669  CYP1A2   3'  ACTAGTCTCAAACTCCTGACCT 5671
            CA                    TGAGGTCAGGAGTTTGAGACTGGT
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGATCA

GAM669  CYP1A2   3'  TCTCGAACTCCTGACCCCA   5711     A
                                TG GGTCAGGAGTTTGAGA
                                || ||||||||||||||||
                                AC CCAGTCCTCAAGCTCT
                                 C
GAM669  DFFB     3'  TCTCAAACTCCTGACCTCA   87400
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  DFFB     3'  TCTCGAACTCCTGACCTCA   87401
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  DISC1    3'  GGTCTCAAACTCCTGACCTCA  37887
                                TGAGGTCAGGAGTTTGAGACT
                                |||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGG

GAM669  DSP      3'  TACCAGCCCCCCTCTCAAACCC 15341   A  A      _______    III
            CCAACCCA                GG GTTTGAGA     CTGGT   A
                                 || ||||||||     |||||  |
                                 CC CAAACTCT     GACCA   T
                                C  C       CCCCCC    III
GAM669  EVC      3'  TCTCGAACTCCTGACCTCA   27301
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCT

GAM669  FCAR    3'  TCTCGAACTCCTGACCTCA   8859
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  FCAR    3'  TCTCGAACTCCTGACCTCA   55787
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  FCAR    3'  TCTCGAACTCCCGACCTCA   55806       A
                                TGAGGTC GGAGTTTGAGA
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAGCTCT
                                     C
GAM669  FCAR    3'  TCTCGAACTCCTGACCTCA   55754
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  FCAR    3'  TCTCGAACTCCTGACCTCA   55765
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  FCAR    3'  TCTCGAACTCCTGACCTCA   55776
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  FZD4    3'  TCTCGAACTCCTGACCTCA   24153
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  G6PC    3'  TCTCGAACTCCTGACCTCA   3836
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  GRAF    3'  TCTCGAACTCCTGACCTCA   30578
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  HCS     3'  TCTCAAACTCCTGAGCTCA   38482       G
                                TGAG TCAGGAGTTTGAGA
                                |||| ||||||||||||||
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                                ACTC AGTCCTCAAACTCT
                                  G
GAM669  IFNAR2   3'  TCTCGAACTCCTGACCTCA   6046
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  JAK3     3'  TCTCGAACTCCTAACCTCA   4007        C
                                TGAGGT AGGAGTTTGAGA
                                |||||| ||||||||||||
                                ACTCCA TCCTCAAGCTCT
                                   A
GAM669  KMO      3'  AGTCTCAAACTCCTGGCCTCA  13445
                                TGAGGTCAGGAGTTTGAGACT
                                |||||||||||||||||||||
                                ACTCCGGTCCTCAAACTCTGA

GAM669  MAK      3'  TCTCAAACTCCTGACCTCA   19769
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  MEFV     3'  TCTCAAACTCCTGACCTCA   4156
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  MEFV     3'  TCTCGAACTCCTGACCTCA   4157
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  MFI2     3'  TCTCAAACCCCCAGCCTCA   52818       CA  A
                                TGAGGT  GG GTTTGAGA
                                ||||||  || ||||||||
                                ACTCCG  CC CAAACTCT
                                   AC  C
GAM669  MICB     3'  CCAGTTTCAAACTCCTGACCTC 19824
                  A              TGAGGTCAGGAGTTTGAGACTGG
                                ||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTTTGACC

GAM669  MLANA    3'  TCTCAAACTCCTGACCTCA   18590
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  NCOA6    5'  TCTCAAACTCCTGACCTCA   25979
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAACTCT

GAM669  NDRG3    3'  TCTCAAACTCCTGACCTCA   49308
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  NQO1     3'  TCTCAAACTCCTGACCTCA   6171
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  PDE6B    3'  TCTCGAACTCCTGACCTCA   4291
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  PDE6D    3'  ACCAGACTAAACTCCCAACCCC 10486    A   CA      G  A
              A                  TG GGT  GGAGTTT AG CTGGT
                                || |||  ||||||| || |||||
                                AC CCA  CCTCAAA TC GACCA
                                 C   AC      _  A
GAM669  PER2     3'  TCTCGAACTCCTGACCTCA   43048
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  PIK3CD   3'  TCTCGAACTCCTGACCTCA   17251
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  PRKR     3'  TCTCAAACTCCTGACCTCA   10889
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  RHD      3'  TCTCAAACTCCTGACCTCA   32321
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  RHD      3'  TCTCAAACTCCTGACCTCA   32630
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  RP2      3'  TCTCGAACTCCTGACCTCA   22621
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCT

GAM669  RPP30    3'  TGGTCTCAATCTCCTGACCTCA 21176          T
                                TGAGGTCAGGAG TTGAGACTG
                                |||||||||||| |||||||||
                                ACTCCAGTCCTC AACTCTGGT
                                       T
GAM669  SAS      3'  TCTCGAACTCCTGACCTCA   19961
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  SCML2    3'  TCTCAAACTCCTGACCTCA   20325
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  SH3BP2   3'  TCTCGAACTCCTGACCTCA   11614
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  SHOX     3'  TCTCGAACTCCTGACCTCA   22548
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  SIL      3'  TCTCAAACTCCCGACCTCA   11700       A
                                TGAGGTC GGAGTTTGAGA
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAACTCT
                                     C
GAM669  SLC6A12  3'  CAAACCCCTGACTTCA     11731         A
                                TGAGGTCAGG GTTTG
                                |||||||||| |||||
                                ACTTCAGTCC CAAAC
                                       C
GAM669  SNX15    3'  TCTCGAACTCCTGACCTCA   73752
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  SPN      3'  TCTCAAACTCCTGACCTCA   11930
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  SULT2B1  5'  TCTCAAACTCCTGACCTCA   16034
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||||
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                                ACTCCAGTCCTCAAACTCT

GAM669  TAT     3'  TCTCAAACTCCTGACCTCA   4478
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  TES     3'  TCTCAAACTCCTGACCTCA   72011
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  TIM3    3'  TCTCAAACTCCTGACCTCA   51350
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  TMPRSS3  3'  TCTCAAACCCCTGACCTCA   43800        A
                                TGAGGTCAGG GTTTGAGA
                                |||||||||| ||||||||
                                ACTCCAGTCC CAAACTCT
                                      C
GAM669  TMPRSS3  3'  TCTCAAACCCCTGACCTCA   50511        A
                                TGAGGTCAGG GTTTGAGA
                                |||||||||| ||||||||
                                ACTCCAGTCC CAAACTCT
                                      C
GAM669  TMPRSS3  3'  TCTCAAACCCCTGACCTCA   50532        A
                                TGAGGTCAGG GTTTGAGA
                                |||||||||| ||||||||
                                ACTCCAGTCC CAAACTCT
                                      C
GAM669  TNFRSF10B 3'  TCTCGAACTCCTGACCTCA   13882
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  TRAF5   3'  TCTCAAACTCCTGACCTCA   16091
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  TRPM6   3'  TCTCAAACTCCTGACCTCA   34548
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  TRPV1   3'  TCTCGAACTCCTGACCTCA   38100
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCT

GAM669  TRPV1    3'  TCTCGAACTCCTGACCTCA   54818
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  TRPV1    3'  TCTCGAACTCCTGACCTCA   54850
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  TRPV1    3'  TCTCGAACTCCTGACCTCA   54883
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  XRCC2    3'  TCTCGAACTCCTGACCTCA   18332
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  ZNF157   3'  TCTCTAACTCCTGACCTCA   12882          T
                                TGAGGTCAGGAGTT GAGA
                                |||||||||||| ||||
                                ACTCCAGTCCTCAA CTCT
                                      T
GAM669  AAK1     3'  TCTCGAACTCCTGACCTCA   29856
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  ATP1B4   3'  TCTCGAACTCCTGACCTCA   23830
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  BA108L7.2 3'  AGTCTCGAACTCCTGACCTCA  48255
                                TGAGGTCAGGAGTTTGAGACT
                                |||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGA

GAM669  C13orf1  3'  TCTCAAACTCCTGACCTCA   39979
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  C20orf142 3'  TCTCAAACTCCTGACCGCA   74789    A
                                TG GGTCAGGAGTTTGAGA
                                || ||||||||||||||
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                                AC CCAGTCCTCAAACTCT
                                 G
GAM669  C21orf25  3'  TCTCGAACTCCTGACCTCA   63557
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  C9orf9    3'  TGGTCTCAATCTCCTGACCTCA 38533          T
                                TGAGGTCAGGAG TTGAGACTG
                                |||||||||||| |||||||||
                                ACTCCAGTCCTC AACTCTGGT
                                       T
GAM669  CDC14B    3'  TCTCGAACTCCTGACCTCA   52862
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  CHRAC1    3'  TCTCAAACTCCTAACCTCA   33880      C
                                TGAGGT AGGAGTTTGAGA
                                |||||| ||||||||||||
                                ACTCCA TCCTCAAACTCT
                                    A
GAM669  CPSF2     3'  CTCAAACTCCCGACCTCA    61581       A
                                TGAGGTC GGAGTTTGAG
                                ||||||| |||||||||
                                ACTCCAG CCTCAAACTC
                                     C
GAM669  CPSF2     3'  TCTCAAACTCCTGACCTCA   61602
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  CSL4      3'  TCTCAAACTCCTGGCCTCA   32115
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCGGTCCTCAAACTCT

GAM669  DBR1      3'  TCTCCAACTCCTGACCTCA   32539          T
                                TGAGGTCAGGAGTT GAGA
                                |||||||||||||| ||||
                                ACTCCAGTCCTCAA CTCT
                                       C
GAM669  DCOHM     3'  TCTCAAACTCCTGGCCTCA   49613
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCGGTCCTCAAACTCT

GAM669  DKFZp434A2417 3'  TCTCAAACTCCCAACCTCA   66111      CA
                                TGAGGT  GGAGTTTGAGA
                                ||||||  ||||||||||
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                                ACTCCA  CCTCAAACTCT
                                   AC
GAM669  DKFZP434J037 3'  TCTCAAACTCCCGACCTCA   48222       A
                                TGAGGTC GGAGTTTGAGA
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAACTCT
                                    C
GAM669  DKFZP564O0423 3'  TCTCAAACTCCTGGCCTCA   91700
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCGGTCCTCAAACTCT

GAM669  EVI5    3'  TCTCGAACTCCTAACCTCA   19016       C
                                TGAGGT AGGAGTTTGAGA
                                |||||| ||||||||||||
                                ACTCCA TCCTCAAGCTCT
                                   A
GAM669  EVI5    3'  TCTCAAACTTCTGACCTCA   19015
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCTTCAAACTCT

GAM669  FBP17   3'  TCTCAAACTCCTGACCTCA   72811
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  FLJ10232  3'  TCCCGAACTCCTGACCTCA   35931           A
                                TGAGGTCAGGAGTTTG GA
                                |||||||||||||||| ||
                                ACTCCAGTCCTCAAGC CT
                                          C
GAM669  FLJ10298  3'  TCTCAAACTCCTGACCT    35995
                                AGGTCAGGAGTTTGAGA
                                |||||||||||||||||
                                TCCAGTCCTCAAACTCT

GAM669  FLJ10607  3'  TCTCAAACTCCTGAGCTCA   77130     G
                                TGAG TCAGGAGTTTGAGA
                                |||| ||||||||||||||
                                ACTC AGTCCTCAAACTCT
                                  G
GAM669  FLJ10901  3'  TCTCGAACTCCTGACCTCA   36833
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  FLJ12363  3'  TCTCAAACTCCTGACCTCA   49693
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAACTCT

GAM669  FLJ12668 3' TCTCAAACTCCTGACCTCA   46527
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  FLJ12687 3' TCTCAAACTCCTGACCTCA   46204
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  FLJ12787 3' TCTAAAACTCCTGACCTCA   49754           G
                                TGAGGTCAGGAGTTT AGA
                                ||||||||||||||| |||
                                ACTCCAGTCCTCAAA TCT
                                          A
GAM669  FLJ12975 3' TCTCGAACTCCTGACCTCA   69595
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  FLJ13072 5' TCTCGAACTCCTGACCTCA   89830
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  FLJ13102 3' TCTCGAACTCCTGACCTCA   46018
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  FLJ20034 3' TCTCAAACTCCCGACCTCA   34387       A
                                TGAGGTC GGAGTTTGAGA
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAACTCT
                                     C
GAM669  FLJ20419 3' CAAACTCCCGCCTCA       35139       CA
                                TGAGGT  GGAGTTTG
                                ||||||  ||||||||
                                ACTCCG  CCTCAAAC
                                   C_
GAM669  FLJ20452 3' TCTCGAACTCCTGACCTCA   35207
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  FLJ20700 3' TCTCGAACTCCTGACCTCA   35588
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCT

GAM669  FLJ20813  3'  TCTCAAACTCCTGACCTCA   35691
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  FLJ21324  5'  TCTCAAACTCCTGACCTCA   91211
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  FLJ21459  3'  TCTCGAACTCCTGACCTCA   44520
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  FLJ22329  3'  ACTGGTCTCGAACTCCTGACCT 45061              TG
          CA                      TGAGGTCAGGAGTTTGAGAC  GT
                                  ||||||||||||||||||||  ||
                                  ACTCCAGTCCTCAAGCTCTG  CA
                                                GT
GAM669  FLJ22529  3'  AGTCTCAAACCCCTGACCTTA  45564         A
                                TGAGGTCAGG GTTTGAGACT
                                |||||||||| ||||||||||
                                ATTCCAGTCC CAAACTCTGA
                                      C
GAM669  FLJ22529  3'  TCTCGAACTCCTGACCTCA   45578
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  FLJ22684  3'  ACTGGTCTCAAACTCCTGACCT 46786              TG
          CA                      TGAGGTCAGGAGTTTGAGAC  GT
                                  ||||||||||||||||||||  ||
                                  ACTCCAGTCCTCAAACTCTG  CA
                                                GT
GAM669  FLJ23392  3'  TCTCAAATTCCTGACCCCA   45550    A
                                TG GGTCAGGAGTTTGAGA
                                || ||||||||||||||||
                                AC CCAGTCCTTAAACTCT
                                  C
GAM669  FLJ23556  3'  TCTCGAACTCCTGACCTCA   45959
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  FLJ25416  5'  TCTCAAACTCCCTACCTCA   58813       CA
                                TGAGGT  GGAGTTTGAGA
                                ||||||  ||||||||||
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                                ACTCCA  CCTCAAACTCT
                                    TC
GAM669  FLJ30532  3'  TCTCAAGCTCCTGACCTCA   58554
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCGAACTCT

GAM669  FLJ32865  3'  TCTCAAACCCCTGACCTCA   58186          A
                                TGAGGTCAGG GTTTGAGA
                                |||||||||| ||||||||
                                ACTCCAGTCC CAAACTCT
                                      C
GAM669  GGA2      3'  TCTCGAACTCCTGACCTCA   56891
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  GGA2      3'  TCTCGAACTCCTGACCTCA   30477
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  GNG4      3'  TCTCAAACTCCTGACCTC    15627
                                GAGGTCAGGAGTTTGAGA
                                |||||||||||||||||
                                CTCCAGTCCTCAAACTCT

GAM669  GTF2H3    3'  TCTCAAACTCCTGAGCTCA   7708       G
                                TGAG TCAGGAGTTTGAGA
                                |||| |||||||||||||
                                ACTC AGTCCTCAAACTCT
                                  G
GAM669  H2AV      3'  ACTGGTCTCAAACTCCTGACCT 56843                TG
            CA                    TGAGGTCAGGAGTTTGAGAC  GT
                                ||||||||||||||||||  ||
                                ACTCCAGTCCTCAAACTCTG  CA
                                          GT
GAM669  HSPC065   3'  TCTCGAACTCCTGACCTCA   26330
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  JAM1      3'  TCTCAAACTCCTGACCTC    57905
                                GAGGTCAGGAGTTTGAGA
                                |||||||||||||||||
                                CTCCAGTCCTCAAACTCT

GAM669  JAM1      3'  TCTCAAACTCCTGACCTC    57936
                                GAGGTCAGGAGTTTGAGA
                                |||||||||||||||||
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                                CTCCAGTCCTCAAACTCT

GAM669  JAM1     3'  TCTCAAACTCCTGACCTC    57960
                                GAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                CTCCAGTCCTCAAACTCT

GAM669  JAM1     3'  TCTCAAACTCCTGACCTC    33767
                                GAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                CTCCAGTCCTCAAACTCT

GAM669  KIAA0022 3'  TCTCAAACTCCTGACCTCA   29674
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  KIAA0063 3'  TCTCAAACTCCCGACCTCA   29645       A
                                TGAGGTC GGAGTTTGAGA
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAACTCT
                                     C
GAM669  KIAA0161 3'  TCTCAAACTCCTGACCTCA   28515
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  KIAA0186 3'  TCTCAAACTCCTGGCCTCA   40765
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCGGTCCTCAAACTCT

GAM669  KIAA0205 3'  CTCGAACTCCTGACCTCA    29582
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM669  KIAA0391 3'  TCTCAAACTCCTGACCTCA   27926
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  KIAA0513 3'  TCTCGAACTCCTGACCTCA   28379
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  KIAA0555 3'  TCTCGAACTCCTGACCTCA   28889
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCT

GAM669  KIAA0561 3' TCTCGAACTCCTGACCTCA   65899
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  KIAA0720 3' TCTCGAACTCCTGACCCCA   62332    A
                                TG GGTCAGGAGTTTGAGA
                                || ||||||||||||||||
                                AC CCAGTCCTCAAGCTCT
                                 C
GAM669  KIAA0737 3' TCTCGAACTCCTGACCTCA   29149
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  KIAA0841 3' ACTGGTCTCGAACTCCTGACCT 71370                TG
          CA                    TGAGGTCAGGAGTTTGAGAC  GT
                                |||||||||||||||||||  ||
                                ACTCCAGTCCTCAAGCTCTG  CA
                                             GT
GAM669  KIAA0889 3' TCTCGAACTCCCGACCTCA   31147       A
                                TGAGGTC GGAGTTTGAGA
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAGCTCT
                                     C
GAM669  KIAA0961 3' TCTCAACTCCTGACCTCA    29740            T
                                TGAGGTCAGGAGTT GAGA
                                |||||||||||||| ||||
                                ACTCCAGTCCTCAA CTCT
                                              _
GAM669  KIAA1054 3' TCTCGAACTCCTGACCTCA   68454
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  KIAA1128 3' TCTCGAACTCCTGACCTCA   68486
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  KIAA1143 3' TGGTCTCAATCTCCTGACCTCA 68692           T
                                TGAGGTCAGGAG TTGAGACTG
                                |||||||||||| |||||||||
                                ACTCCAGTCCTC AACTCTGGT
                                        T
GAM669  KIAA1145 3' ACCAGTCCCACCCTGATCTCA  65617          A  TT A
                                TGAGGTCAGG GT  G GACTGGT
                                |||||||||| ||  | |||||||
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                                ACTCTAGTCC CA  C CTGACCA
                                      _ __ C
GAM669  KIAA1161 5' AGTCTCAAACTCCTGACCT   81735
                                AGGTCAGGAGTTTGAGACT
                                ||||||||||||||||||
                                TCCAGTCCTCAAACTCTGA

GAM669  KIAA1170 3' CTCAAACTCCTGACCTCA    69850
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM669  KIAA1198 3' TCTCAAACTCCTGACCTCA   63340
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  KIAA1200 3' TCTCGAACTCCTGACCTCA   62383
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  KIAA1257 3' TCTCAAACTCCCGACTTCA   62762       A
                                TGAGGTC GGAGTTTGAGA
                                ||||||| ||||||||||
                                ACTTCAG CCTCAAACTCT
                                     C
GAM669  KIAA1493 3' TCTCAAACTCCTGACCTCA   64166
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  KIAA1497 5' TCTCGAACTCCTGACCTCA   67523
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  KIAA1615 3' TCTCAAACTCCCGACCTCA   68737       A
                                TGAGGTC GGAGTTTGAGA
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAACTCT
                                     C
GAM669  KIAA1655 3' TCTCAAACTCCTGACCTC    66633
                                GAGGTCAGGAGTTTGAGA
                                |||||||||||||||||
                                CTCCAGTCCTCAAACTCT

GAM669  KIAA1712 3' TCTCAAACTCCTGACCTCA   67542
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAACTCT

GAM669  KIAA1737 3' TCTCGAACTCCTGACCTCA   67365
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  KIAA1862 3' CCAGCCGTTCCTGATCTCA   68925          TT  AGA
                                TGAGGTCAGGAG  TG   CTGG
                                ||||||||||||  ||   ||||
                                ACTCTAGTCCTT  GC   GACC
                                       __  C__
GAM669  KIAA1922 5' TCTCGAACTCCTGACCTCA   73644
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  MAP-1    3' AGTTTCGAACTCCTGACCTCA 42177
                                TGAGGTCAGGAGTTTGAGACT
                                |||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTTTGA

GAM669  MCLC     3' TCTCGAACTCCTGACCTCA   30696
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  MEF-2    3' TCTCAAACTCCTGACCTC    64398
                                GAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                CTCCAGTCCTCAAACTCT

GAM669  MGC:13379 3' ACCAGTCCCCTGCTGACCTCA 33242          G  TTTGA
                                TGAGGTCAG AG    GACTGGT
                                |||||||| ||    |||||||
                                ACTCCAGTC TC    CTGACCA
                                      G  CC___
GAM669  MGC13204 3' TCTCAAAATCCTGACCTCA   48840          G
                                TGAGGTCAGGA TTTGAGA
                                |||||||||| |||||||
                                ACTCCAGTCCT AAACTCT
                                       A
GAM669  MKRN4    3' TCTCGAACTCCTGACCTCA   47756
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  moblak   3' TCTCAAACTCCTGACTTCA   55516
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
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                                ACTTCAGTCCTCAAACTCT

GAM669  MRPS27   3'  TCTCAACCTCCTGACCTCA   30646          T
                                TGAGGTCAGGAG TTGAGA
                                |||||||||||| ||||||
                                ACTCCAGTCCTC AACTCT
                                       C
GAM669  NAPG     5'  TCTCAAACTCCTAAGCTCA   96732     GTC
                                TGAG  AGGAGTTTGAGA
                                ||||  ||||||||||||
                                ACTC  TCCTCAAACTCT
                                  GAA
GAM669  NXN      3'  TCTCGAACTCCTGACCTCA   42427
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  OPN4     3'  CTCAAAACTCCTGCCCCA    52718    A  T       _
                                TG GG CAGGAGTTT GAG
                                || || ||||||||| |||
                                AC CC GTCCTCAAA CTC
                                 C  _       A
GAM669  OSBPL2   3'  TCTCAAACTCCCGACCTCA   57874        A
                                TGAGGTC GGAGTTTGAGA
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAACTCT
                                     C
GAM669  OSBPL2   3'  TCTCAAACTCCCGACCTCA   29223        A
                                TGAGGTC GGAGTTTGAGA
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAACTCT
                                     C
GAM669  PELI1    5'  TCTCAAACTCCCAACCTCA   40291       CA
                                TGAGGT  GGAGTTTGAGA
                                ||||||  ||||||||||
                                ACTCCA  CCTCAAACTCT
                                    AC
GAM669  PRO0245  5'  AGTCTCAAACTCCCGAGCCCA  26124    A  _  A
                                TG GG TC GGAGTTTGAGACT
                                || || || |||||||||||||
                                AC CC AG CCTCAAACTCTGA
                                 _  G  C
GAM669  PRO0529  5'  TCTCAAACTCCTGACCTCA   26001
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  PRO2955  3'  TCTCAAACTCCTGACCTCA   37650
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAACTCT

GAM669  PSTPIP2  3'  TCTCAAACTCCTGACCTCA   44401
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  RAI     5'  TCTCAAACTCCTGATCTCA   21888
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCTAGTCCTCAAACTCT

GAM669  SC4MOL   3'  TCTCAAACTTCTGACCTCA   22165
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCTTCAAACTCT

GAM669  SCAMP-4  3'  TCTCGAACTCCTGACCTCA   54403
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  SFXN2    3'  ACTGGTCTCGAACTCCTGACCT 73937                TG
          CA                      TGAGGTCAGGAGTTTGAGAC  GT
                                ||||||||||||||||||  ||
                                ACTCCAGTCCTCAAGCTCTG  CA
                                        GT
GAM669  SLC19A3  3'  TCTCAAACTCCTGACTTCA   47498
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTTCAGTCCTCAAACTCT

GAM669  STAF65(gamma) 3'  TCTCAAAACTCCTGACCTCA   29447          _
                                TGAGGTCAGGAGTTT GAGA
                                |||||||||||||| ||||
                                ACTCCAGTCCTCAAA CTCT
                                        A
GAM669  TBCC     3'  TCTCGAACTCCTGACCTCA   12143
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  TCL6     3'  TCTCAAACTCCTGAGCTCA   40117      G
                                TGAG TCAGGAGTTTGAGA
                                |||| ||||||||||||||
                                ACTC AGTCCTCAAACTCT
                                  G
GAM669  TCL6     3'  TCTCAAACTCCTGAGCTCA   40147      G
                                TGAG TCAGGAGTTTGAGA
                                |||| ||||||||||||||
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                                ACTC AGTCCTCAAACTCT
                                  G
GAM669  THEA     3'  TCTCAAACTCCTGACTTCA   66301
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTTCAGTCCTCAAACTCT

GAM669  TRIM16   3'  TCTCAAACTCCTGACCTC    21346
                                GAGGTCAGGAGTTTGAGA
                                |||||||||||||||||
                                CTCCAGTCCTCAAACTCT

GAM669  TU12B1-TY 3'  TCTCAAACTCCTAGCCTCA   33408      TC
                                TGAGG AGGAGTTTGAGA
                                |||||  ||||||||||||
                                ACTCC  TCCTCAAACTCT
                                   GA
GAM669  TU12B1-TY 3'  TCTCGAACTCCTGACCTCA   33409
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  UBF-fl   3'  TCTCAAACTCCTGACCTCA   51573
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  USP22    3'  ACCATGTCTCAAACTCCTGACC 67996                _
           TCA                    TGAGGTCAGGAGTTTGAGAC TGGT
                                ||||||||||||||||||| ||||
                                ACTCCAGTCCTCAAACTCTG ACCA
                                             T
GAM669  VDU1     3'  AGTCTCAAACTCCTGACCTCA  30411
                                TGAGGTCAGGAGTTTGAGACT
                                |||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGA

GAM669  VPS33A   3'  TCTCAAACTCCTGACCTCA   43345
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  WBSCR23  3'  TCTCAAACTCCTGACCTCA   46773
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  ZNF17    3'  TCTCAAACTCCCGACCTCA   82395        A
                                TGAGGTC GGAGTTTGAGA
                                |||||||  ||||||||||
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                                ACTCCAG CCTCAAACTCT
                                    C
GAM669  LOC112687 3'  TCCCAAACTCCTGACCTCA   72868              A
                                TGAGGTCAGGAGTTTG GA
                                |||||||||||||||| ||
                                ACTCCAGTCCTCAAAC CT
                                        C
GAM669  LOC115648 3'  TCTCGAACTCCTGACCTCA   59303
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  LOC119392 3'  TCTCGAACTCCTGACCTCA   59139
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  LOC120114 3'  TCTCAAACTCCTGACCTC    75541
                                GAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                CTCCAGTCCTCAAACTCT

GAM669  LOC120224 5'  TCTCGAACTCCTGACCTCA   57106
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  LOC124216 3'  CCAGTCTCAAACTCCTGACCTC 74260
                                GAGGTCAGGAGTTTGAGACTGG
                                |||||||||||||||||||||||
                                CTCCAGTCCTCAAACTCTGACC

GAM669  LOC126364 3'  TCTCGAACTCCTGACCTCA   75702
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  LOC126669 3'  TCTCAAACTCCTGACCTCA   75419
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  LOC130639 5'  CTCGAACTCCTGACCTCA    74971
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM669  LOC132625 3'  AGTCTCAAACTCCTGACCTC  75897
                                GAGGTCAGGAGTTTGAGACT
                                ||||||||||||||||||||
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                                CTCCAGTCCTCAAACTCTGA

GAM669   LOC135154 3'  TCTCGAACTCCTGACCTCA   75224
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669   LOC135293 3'  TCTCGAACTCCTGACCTCA   76193
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669   LOC143916 3'  TCTCAAACTTCTGACCTCA   76647
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCTTCAAACTCT

GAM669   LOC144317 5'  TCTCGAACTCCTGACCTCA   76802
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669   LOC144524 5'  TCTCAAACTCCTGAACTCA   83140     G
                                TGAG TCAGGAGTTTGAGA
                                |||| ||||||||||||
                                ACTC AGTCCTCAAACTCT
                                   A
GAM669   LOC145453 5'  TCTCAAACTCCTGACCTCA   77147
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669   LOC146050 3'  TCTCAAACTCCCGACCTCA   77653       A
                                TGAGGTC GGAGTTTGAGA
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAACTCT
                                     C
GAM669   LOC146229 3'  TCTCAAACTCCTGACCTCA   77778
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669   LOC146229 3'  TCTCAAACTCCTGACCTCA   77779
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669   LOC146229 3'  TCTCAAACTCCTGACTTCA   77780
                                TGAGGTCAGGAGTTTGAGA
                                |||||||||||||||||
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                                ACTTCAGTCCTCAAACTCT

GAM669  LOC146901 3'  TCTCGAACTCCTGACCTCA   83850
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  LOC146952 5'  TCTCAAACTCCTGACCTCA   83876
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669  LOC147178 5'  ACCAGCCCCAGCACTGACCTC  61321        GA   TGAGA
                                GAGGTCAG  GTT    CTGGT
                                ||||||||  |||    |||||
                                CTCCAGTC  CGA    GACCA
                                     A_   CCCC_
GAM669  LOC147817 3'  TCTCAAACTCCTGACCTTA   78507
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ATTCCAGTCCTCAAACTCT

GAM669  LOC148709 3'  AGTCTCAAACTCCCGACCTTA  78933        A
                                TGAGGTC GGAGTTTGAGACT
                                ||||||| ||||||||||||
                                ATTCCAG CCTCAAACTCTGA
                                     C
GAM669  LOC148918 5'  TCTCGAACTCCTGACCTCA   79087
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  LOC149577 3'  ACTGGTCTCGAACTCCTGACCT 84503                TG
          CA                      TGAGGTCAGGAGTTTGAGAC  GT
                                ||||||||||||||||||  ||
                                ACTCCAGTCCTCAAGCTCTG  CA
                                                GT
GAM669  LOC149692 3'  GGTCTCAAAGTCCTGACCTCA  84593          G
                                TGAGGTCAGGA TTTGAGACT
                                |||||||||| |||||||||
                                ACTCCAGTCCT AAACTCTGG
                                      G
GAM669  LOC149692 3'  TCTCGAACTCCTGACCTCA   84596
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  LOC149711 3'  TCACAAACTCCTGACCTCA   84689             A
                                TGAGGTCAGGAGTTTG GA
                                |||||||||||||||| ||
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                                ACTCCAGTCCTCAAAC CT
                                        A
GAM669   LOC150225 3'  TCTCAAACTCCTGACCTCA    85014
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669   LOC150290 3'  ACTGGTCTCAAACTCCTGGCCT 79766                  TG
           CA                    TGAGGTCAGGAGTTTGAGAC  GT
                                ||||||||||||||||||  ||
                                ACTCCGGTCCTCAAACTCTG  CA
                                        GT
GAM669   LOC150960 3'  TCTCAAATTCCTGACCTCA    80075
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTTAAACTCT

GAM669   LOC151475 5'  AGTTTCAAACTCCTGACCTTA  85390
                                TGAGGTCAGGAGTTTGAGACT
                                |||||||||||||||||||
                                ATTCCAGTCCTCAAACTTTGA

GAM669   LOC151701 3'  TCTCGAACTCCTGACCTCA    85490
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669   LOC152137 3'  TCTCGAACCCCCTGACCTCA    80484          A
                                TGAGGTCAGG GTTTGAGA
                                |||||||||| ||||||||
                                ACTCCAGTCC CAAGCTCT
                                      C
GAM669   LOC153688 3'  TCTCGAACTCCCAACCTCA    86125        CA
                                TGAGGT  GGAGTTTGAGA
                                ||||||  ||||||||||
                                ACTCCA  CCTCAAGCTCT
                                    AC
GAM669   LOC153811 3'  TCTCAAACTCCTGACCTCA    80957
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669   LOC157247 5'  TCTCGAACTCCTGACCTCA    81380
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669   LOC157858 5'  TCTCAAACTCCTGACCTC     86605
                                GAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
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                                CTCCAGTCCTCAAACTCT

GAM669   LOC158014 5'  TCTCGAACTCCTGACCTCA    81659
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669   LOC162427 3'  TCTCAAACTCCTGACCTCA    82353
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669   LOC169611 3'  CCAGTCTCAAACTCCTGACCTC 82760
           A                     TGAGGTCAGGAGTTTGAGACTGG
                                ||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGACC

GAM669   LOC196047 5'  AGTCTCAAACTCCTGACCTCA  89591
                                TGAGGTCAGGAGTTTGAGACT
                                |||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGA

GAM669   LOC196707 3'  ACCAGCCCCAGGCTTCCATCCT 87524      TCA      AGA
           CA                    TGAGG  GGAGTTTG  CTGGT
                                |||||  ||||||||  |||||
                                ACTCC  CTTCGGAC  GACCA
                                   TAC      CCC
GAM669   LOC197358 3'  TCTCGAACTCCTGACCTCA    88052
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669   LOC199699 3'  TCTCAAACTCCTGGCCTCA    88316
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCGGTCCTCAAACTCT

GAM669   LOC199906 3'  TCTCAAACTCCTGACCTCA    88489
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669   LOC200014 3'  TCTCGAACTCCTGACCTCA    88543
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669   LOC200314 3'  TCTCGAACTCCTGACCTCA    90019
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCT

GAM669   LOC200407 3'  TCTCAAACTCCTGACCTCA   90046
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669   LOC201164 3'  TCTCAAACTCCTGACCTCA   88126
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669   LOC201627 3'  TCTCAAACTCCCGACCTCA   89028       A
                                TGAGGTC GGAGTTTGAGA
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAACTCT
                                     C
GAM669   LOC219529 5'  CAGCCTCAAACTCCTGAGCCCA 92967    A _         A
                                TG GG TCAGGAGTTTGAG CTG
                                || || |||||||||||| |||
                                AC CC AGTCCTCAAACTC GAC
                                 _ G          C
GAM669   LOC219673 5'  TCTCAAACGCCTGACCTCA   93046         A
                                TGAGGTCAGG GTTTGAGA
                                |||||||||| ||||||||
                                ACTCCAGTCC CAAACTCT
                                      G
GAM669   LOC220074 3'  TCTCAAACTCCTGACCTCA   59286
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669   LOC221060 3'  TCTCGAACTCCTGACCTCA   93217
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669   LOC221271 3'  TCTCAAACTCCTGATCTCA   91879
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCTAGTCCTCAAACTCT

GAM669   LOC221418 3'  CAAACCCTGACCTCA      93635         A
                                TGAGGTCAGG GTTTG
                                |||||||||| |||||
                                ACTCCAGTCC CAAAC
                                          _
GAM669   LOC245771 5'  TCTCGAACTCCTGACCTCA   92898
                                TGAGGTCAGGAGTTTGAGA
                                |||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCT

GAM669   LOC253765 3'  CCAGTCTCAAAGACCTGA    95029      AG
                                TCAGG  TTTGAGACTGG
                                |||||  ||||||||||
                                AGTCC  AAACTCTGACC
                                   AG
GAM669   LOC253805 3'  TCTCGAACTCCTGACCTCA    96439
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669   LOC254268 3'  TCTCAAACTCCTGACCTCA    95415
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669   LOC254532 5'  TCTCAAACTCCTGACCTCA    96646
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669   LOC254655 3'  TCTCGAACTCCTGACCTCA    95476
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669   LOC255065 5'  TCTCAAACTCCTGACCTCA    96586
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM669   LOC255104 3'  ACCAGCTCTCCCCTGGCCTCA  95393          AGTTT   A
                                TGAGGTCAGG    GAG CTGGT
                                ||||||||||    ||| |||||
                                ACTCCGGTCC    CTC GACCA
                                      CCT__   _
GAM669   LOC255193 5'  CCAACCTCAGGCTGACCT    95353       GGA      AC
                                AGGTCA   GTTTGAG  TGG
                                ||||||   |||||||  |||
                                TCCAGT   CGGACTC  ACC
                                   ___       CA
GAM669   LOC255497 3'  TCTCGAACTCCTGACCTCA    97196
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669   LOC51200  3'  TCTCAAACTCCCAACCTCA    33004       CA
                                TGAGGT  GGAGTTTGAGA
                                ||||||  ||||||||||
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                                ACTCCA  CCTCAAACTCT
                                   AC
GAM669  LOC51219  5' TCTCGAACTCCCGACCTCA   33130       A
                                TGAGGTC GGAGTTTGAGA
                                ||||||| |||||||||||
                                ACTCCAG CCTCAAGCTCT
                                   C
GAM669  LOC57107  3' AGTCTCGAACTCCTGACCTCA  39828
                                TGAGGTCAGGAGTTTGAGACT
                                ||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGA

GAM669  LOC57146  3' AGTCTCAAACTCCTGACCTCA  39913
                                TGAGGTCAGGAGTTTGAGACT
                                ||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGA

GAM669  LOC90072  3' TCTCGAACTCCCGACCTCA   61304       A
                                TGAGGTC GGAGTTTGAGA
                                ||||||| |||||||||||
                                ACTCCAG CCTCAAGCTCT
                                   C
GAM669  LOC90591  3' TCTCGAACTCCTGACCTCA   63447
                                TGAGGTCAGGAGTTTGAGA
                                |||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  LOC90918  3' TCTCAAACTCCTGACCTTA   64363
                                TGAGGTCAGGAGTTTGAGA
                                |||||||||||||||||||
                                ATTCCAGTCCTCAAACTCT

GAM669  LOC91115  3' ACTGGTCTCCAACTCCTGACCT 64921           T    TG
          CA                      TGAGGTCAGGAGTT GAGAC  GT
                                ||||||||||||| ||||| ||
                                ACTCCAGTCCTCAA CTCTG  CA
                                        C    GT
GAM669  LOC91561  5' TCTCGAACTCCTGACCTCA   66455
                                TGAGGTCAGGAGTTTGAGA
                                |||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  LOC91963  3' TCTCAAACTCCTGAGCTCA   67700     G
                                TGAG TCAGGAGTTTGAGA
                                |||| |||||||||||||
                                ACTC AGTCCTCAAACTCT
                                  G
GAM669  LOC92267  3' TCTCAAACTCCTGACCTCA   68626
                                TGAGGTCAGGAGTTTGAGA
                                |||||||||||||||||||
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                                ACTCCAGTCCTCAAACTCT

GAM669  LOC92697  5'  TCTCGAACTCCCAACCTCA   70284       CA
                                TGAGGT  GGAGTTTGAGA
                                ||||||  ||||||||||
                                ACTCCA  CCTCAAGCTCT
                                   AC
GAM669  LOC93349  3'  TCTCGAACTCCTGACCTCA   56468
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM669  LOC93408  5'  TCTCAAACTCCTGGCCTCA   56485
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCGGTCCTCAAACTCT

GAM670  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM670  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM670  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                        _
GAM670  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                ||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM670  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM670  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM670  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
```

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                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM670  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM670  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM670  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM670  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM670  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM670  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM670  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM670  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM670  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM670  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598         CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
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                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM670  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM670  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__    TT
GAM670  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                      A     TC
GAM670  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                      AAAGG
GAM670  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM670  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM670  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM670  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM671  BACH2    3'  ACCTTCACAATGGTGCTA    41480          _   ATC
                                TAGCACCATT TGAA   GGT
                                |||||||||| ||||   |||
                                ATCGTGGTAA ACTT   CCA
                                      C    ___
GAM671  CEACAM6  3'  AGCCCCAAATGGTGGTA     10184    G       AAATC
                                TA CACCATTTG     GGTT
                                || |||||||||     ||||
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                                AT GTGGTAAAC    CCGA
                                 G       C____
GAM671  HCS     3'  AACCAGTCATGGTGCTA    38451       TT   AATC
                                TAGCACCA  TGA   GGTT
                                ||||||||  |||   ||||
                                ATCGTGGT  ACT   CCAA
                                    __   GA__
GAM671  METTL1  3'  TAACCGATGTGCTGGAGCTA  43512     A   TTTGAA
                                TAGC CCA     ATCGGTTA
                                |||| |||     ||||||||
                                ATCG GGT     TAGCCAAT
                                  A  CGTG__
GAM671  NMI     3'  GTTTCAAATGGTGCTG     16266
                                TAGCACCATTTGAAAT
                                ||||||||||||||||
                                GTCGTGGTAAACTTTG

GAM671  RNTRE   3'  TAACCACTTAATGGTGCT   28038       TGAAATC
                                AGCACCATT      GGTTA
                                |||||||||      |||||
                                TCGTGGTAA      CCAAT
                                     TTCA___
GAM671  TCL1A   3'  TGGTCTCACATGGTGCTA   41740       T   A
                                TAGCACCAT TGA ATCG
                                ||||||||| ||| ||||
                                ATCGTGGTA ACT TGGT
                                     C   C
GAM671  TCTEL1  3'  ATTTCAAAGGTGCTA      21508       A
                                TAGCACC TTTGAAAT
                                ||||||| ||||||||
                                ATCGTGG AAACTTTA
                                   _
GAM671  WISP1   3'  TAACCATTCAAATGACGC   13943   AC      ATC
                                GC  CATTTGAA  GGTTA
                                ||  ||||||||  |||||
                                CG  GTAAACTT  CCAAT
                                 CA      A__
GAM671  FIBL-6  3'  TGATCCCAAATGGTGCT    72916         AA
                                AGCACCATTTG  ATCG
                                ||||||||||  ||||
                                TCGTGGTAAAC  TAGT
                                     CC
GAM671  LENG9   3'  AGCTTCCAAATGGTGCT    74519         AAATC
                                AGCACCATTTG    GGTT
                                ||||||||||     ||||
                                TCGTGGTAAAC    TCGA
                                     CT___
GAM671  PCDH19  3'  GTTTCAAATGGTGTTA     63707
                                TAGCACCATTTGAAAT
                                ||||||||||||||||
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                                ATTGTGGTAAACTTTG

GAM671  PTD012   3'  AACTCTCTAATGGTGCTA    25886         T  AATC
                                TAGCACCATT GA    GGTT
                                |||||||||| ||    ||||
                                ATCGTGGTAA CT    TCAA
                                      T  C___
GAM671  RAP2B    3'  TAACCGATTTTAATG       95822      T
                                CATT GAAATCGGTTA
                                |||| ||||||||||
                                GTAA TTTTAGCCAAT
                                  _
GAM671  LOC145622 3'  AACTTGATTCAAATGATGTTA  77285       C       A  _
                                TAGCA CATTTGAA TCG GTT
                                ||||| |||||||| ||| |||
                                ATTGT GTAAACTT AGT CAA
                                   A       _  T
GAM671  LOC151473 3'  ATTTTAAATGGTGCTA      80253
                                TAGCACCATTTGAAAT
                                ||||||||||||||||
                                ATCGTGGTAAATTTTA

GAM671  LOC202460 5'  ATTTCAAACGTGCTA       89178       CA
                                TAGCAC  TTTGAAAT
                                ||||||  ||||||||
                                ATCGTG  AAACTTTA
                                   C_
GAM671  LOC50999  3'  AACCGATTTCCATAATG     32099      T__
                                CATT   GAAATCGGTT
                                ||||   ||||||||||
                                GTAA   CTTTAGCCAA
                                  TAC
GAM671  LOC51194  3'  AGCTGTTCAGATGATGCTA   32932       C       AT
                                TAGCA CATTTGAA  CGGTT
                                ||||| ||||||||  |||||
                                ATCGT GTAGACTT  GTCGA
                                   A       __
GAM672  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM672  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875        CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM672  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
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                                GTAAAGTGAAAG GAT
                                           _
GAM672  JTB     3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                  CATTTCACTTTCACTGTCTGAGAT
                                  ||||||||||||||||||||||||
                                  GTAAAGTGAAAGTGACAGACTCTA

GAM672  KLF4    3'  TCCCAGACAGTGGATATG    14891    CT        A
                                  CA  TTCACTGTCTG GA
                                  ||  ||||||||||| ||
                                  GT  AGGTGACAGAC CT
                                   AT         C
GAM672  PHYH    3'  ACAGTAAAAGTGAAAT     20608          C
                                  ATTTCACTTT ACTGT
                                  |||||||||| |||||
                                  TAAAGTGAAA TGACA
                                        A
GAM672  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                  TTTCACTTTCA   TCTG GA
                                  ||||||||||   |||| ||
                                  AAAGTGAAAGT   GGAC CT
                                         T__   _
GAM672  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                  TTTCA TTTCACTGTCT
                                  ||||| ||||||||||
                                  AAAGT AAAGTGACGGG
                                     A
GAM672  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                  TTTCACTTT  CTGT   AGAT
                                  |||||||||  ||||   ||||
                                  AAAGTGAAA  GACA   TCTA
                                       C_   CG_
GAM672  CG012   5'  CTCACTCTGAAAGTGAA     83218          CT  CT
                                  TTCACTTTCA  GT  GAG
                                  ||||||||||  ||  |||
                                  AAGTGAAAGT  CA  CTC
                                        CT  __
GAM672  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                  CTTTCACT TC  GAGAT
                                  |||||||| ||  |||||
                                  GAAAGTGA AG  TTCTA
                                       G  TC
GAM672  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
              G                    CATTTC        GTCTGAGAT
                                   ||||||        |||||||||
                                   GTAAAG        CAGACTCTA
                                      AAACATTT_
GAM672  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                  CATTTCA   TCACTGTCTGAGAT
                                  |||||||   ||||||||||||||
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                                GTAAAGT  AGTGACAGACTCTA
                                   C__
GAM672  KIAA0984 3'  TTTGTCCAGTGAAAATGAA  65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM672  KLHL6    3'  ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM672  NIR3     3'  GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM672  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM672  PP35     3'  ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM672  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148        TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM672  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                      A    TC
GAM672  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941        CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM672  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM672  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
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                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM672  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM672  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                      _
GAM673  ABP1     5'  AGGGCAAAGGCTGG        63109          TACTCT
                                CCAGTCTTTG     CCCT
                                ||||||||||     ||||
                                GGTCGGAAAC     GGGA
                                      _______
GAM673  AP2B1    3'  AGGGTCCATGACTAAGACTGG  7057         T  ACTCT_
                                CCAGTCTT GT     CCCT
                                |||||||| ||     ||||
                                GGTCAGAA CA     GGGA
                                     T  GTACCT
GAM673  ED1      3'  GGAAAGCACAAGACTGG     7373         T  A  C
                                CCAGTCTT GT CT TCC
                                |||||||| || || |||
                                GGTCAGAA CA GA AGG
                                     _  C  A
GAM673  EEF1A1   3'  TTTAGTAGTAAAAGACTGG   7390          G    CTCC
                                CCAGTCTTT TACT    CTAAA
                                ||||||||| ||||    |||||
                                GGTCAGAAA ATGA    GATTT
                                      _    T___
GAM673  EPHB4    5'  AGGGAGAGTCAGACCTGG    15460      TC    T
                                CCAG  TTTG ACTCTCCCT
                                ||||  |||| |||||||||
                                GGTC  AGAC TGAGAGGGA
                                  C_    _
GAM673  GARP     3'  TTAGGAAGAGAATGAAACT   18604     C  TG A    C
                                AGT TT  T CTCT CCTAA
                                ||| ||  | |||| |||||
                                TCA AA  A GAGA GGATT
                                  _  GT A    A
GAM673  ID3      3'  GTTTAGGGAAACTGAGGC    79048       T  ACTC
                                GTCTT GT    TCCCTAAAC
                                ||||| ||    |||||||||
                                CGGAG CA    AGGGATTTG
                                   T  A___
GAM673  ITGA11   3'  AGGGAGGAAGACTG        24203         GTACT
                                CAGTCTTT    CTCCCT
                                ||||||||    ||||||
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                                GTCAGAAG    GAGGGA
                                        _____
GAM673  ITGB1    3'  AGGGAAGCCAAAAGATTGG   53368        GTA  C
                                CCAGTCTTT   CT TCCCT
                                |||||||||   || |||||
                                GGTTAGAAA   GA AGGGA
                                     ACC  _
GAM673  KCNA7    3'  AGGGAGAGGGAGAC       49047       GTA
                                GTCTTT   CTCTCCCT
                                ||||||   ||||||||
                                CAGAGG   GAGAGGGA
                                       ___
GAM673  LTA      3'  GGAGAAACAGAGACAGG     5177     A      AC
                                CC GTCTTTGT  TCTCC
                                || ||||||||  |||||
                                GG CAGAGACA  AGAGG
                                 A       A_
GAM673  MAFF     3'  TTTAGGGAAAGCCGGAGA    24656       TA  C
                                TCTTTG  CT TCCCTAAA
                                ||||||  || ||||||||
                                AGAGGC  GA AGGGATTT
                                   C_  A
GAM673  MYCL1    3'  GAGAGGACAATACTGG      18165      CT   A
                                CCAGT  TTGT CTCTC
                                |||||  |||| |||||
                                GGTCA  AACA GAGAG
                                  T_   G
GAM673  NEU1     3'  AGGGAACTGGGGAAGGCTG   4740        GTA  ___
                                CAGTCTTT   CTC   TCCCT
                                ||||||||   |||   |||||
                                GTCGGAAG   GGG   AGGGA
                                     ___   TCA
GAM673  NQO1     3'  AGAGAAGGTAAAAGACTG    6151        G   TC  C
                                CAGTCTTT TAC  TC CT
                                |||||||| |||  || ||
                                GTCAGAAA ATG  AG GA
                                     _   GA  A
GAM673  PEA15    3'  TAGGGAGGTTGAAGAATG    13655    G     T  T
                                CA TCTTTG AC CTCCCTA
                                || |||||| || |||||||
                                GT AGAAGT TG GAGGGAT
                                 A     _ _
GAM673  PPP1R11  3'  TTTAGGATTTCTGACAAAGCTG 41709     T     ACTCTC_
          G                      CCAG CTTTGT      CCTAAA
                                 |||| ||||||      ||||||
                                 GGTC GAAACA      GGATTT
                                   _     GTCTTTA
GAM673  PRKG2    3'  AGGGAGAGGCAAGATTG     20752       T  A
                                CAGTCTT GT CTCTCCCT
                                ||||||| || ||||||||
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                                GTTAGAA CG GAGAGGGA
                                    _ _
GAM673  PTCRA    3'  TTTAGGGAGCAGATGACTG   56317      _   TACT
                                CAGTC TTTG   CTCCCTAAA
                                ||||| ||||   |||||||||
                                GTCAG AGAC   GAGGGATTT
                                  T  _____
GAM673  RNMT     3'  TTCAGGGAGAGGAGCTGG    13726     T  TGTA      A
                                CCAG CTT   CTCTCCCT AA
                                |||| |||   |||||||| ||
                                GGTC GAG   GAGAGGGA TT
                                  _  _____       C
GAM673  RNPEPL1  3'  AGGGAGAGTGTGGGGACAGG  36674    A    TG
                                CC GTCTT  TACTCTCCCT
                                || |||||  ||||||||||
                                GG CAGGG  GTGAGAGGGA
                                 A    GT
GAM673  SLC5A5   5'  AGGGAGAGGGACAGAC     4843      TT  A_
                                GTCT  GT  CTCTCCCT
                                ||||  ||  ||||||||
                                CAGA  CA  GAGAGGGA
                                  __ GG
GAM673  SOST     3'  AGAGCACAAGACTGG      47466       T  A
                                CCAGTCTT GT CTCT
                                |||||||| || ||||
                                GGTCAGAA CA GAGA
                                     _ C
GAM673  SURF4    3'  TTTAGGGACACCCAAAGAATG  52548    G     TACTC
                                CA TCTTTG    TCCCTAAA
                                || ||||||    ||||||||
                                GT AGAAAC    AGGGATTT
                                 A     CCAC_
GAM673  C22orf4  3'  TAGGGCTGACAAAGACAGG   60644    A      ACTCT
                                CC GTCTTTGT    CCCTA
                                || ||||||||    |||||
                                GG CAGAAACA    GGGAT
                                 A       GTC__
GAM673  C9orf5   3'  GGGAGATACAAAGACTG     49281          C
                                CAGTCTTTGTA TCTCCC
                                |||||||||| ||||||
                                GTCAGAAACAT AGAGGG
                                    _
GAM673  DKFZP564O0423 3'  TTAGGGAGAGAGGATTGG    91706        TGTA
                                CCAGTCTT   CTCTCCCTAA
                                ||||||||   ||||||||||
                                GGTTAGGA   GAGAGGGATT
                                    _____
GAM673  FLJ20718 3'  AGAGTGGAAGAGTGG      35606     G    G
                                CCA TCTTT TACTCT
                                ||| ||||| ||||||
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                                GGT AGAAG GTGAGA
                                  G    _
GAM673  FLJ22028  3' AGGGAAGCCAAAAGATTGG   45851        GTA  C
                                CCAGTCTTT   CT TCCCT
                                |||||||||   || |||||
                                GGTTAGAAA   GA AGGGA
                                     ACC  _
GAM673  FLJ22028  3' AGGGAAGCCAAAAGATTGG   45852        GTA  C
                                CCAGTCTTT   CT TCCCT
                                |||||||||   || |||||
                                GGTTAGAAA   GA AGGGA
                                     ACC  _
GAM673  FLJ30681  3' TTTAGGGAAGAAGATT      91792        GTACTC
                                AGTCTTT     TCCCTAAA
                                |||||||     ||||||||
                                TTAGAAG     AGGGATTT
                                   A_____
GAM673  FLJ32356  3' AGGGAGAACCTCGGGGCTGG   58357        TGTAC
                                CCAGTCTT    TCTCCCT
                                ||||||||    |||||||
                                GGTCGGGG    AGAGGGA
                                     CTCCA
GAM673  KIAA0261  3' TTTAGGGAAAGGGACAGA    68185      A_  C
                                TTTGT  CT TCCCTAAA
                                |||||  || ||||||||
                                AGACA  GA AGGGATTT
                                   GG  A
GAM673  KIAA0318  5' AGGGAGAGTATCTCCTG     68947     TCTTT
                                CAG    GTACTCTCCCT
                                |||    ||||||||||
                                GTC    TATGAGAGGGA
                                  CTC__
GAM673  KIAA0630  3' TTAGGGAGTATGTAAA      89399       CT
                                TTTGTA  CTCCCTAA
                                ||||||  ||||||||
                                AAATGT  GAGGGATT
                                   AT
GAM673  KIAA0753  3' AGGGAGAGCACAGTCTGG    28996      T  TT  A
                                CCAG CT  GT CTCTCCCT
                                |||| ||  || ||||||||
                                GGTC GA  CA GAGAGGGA
                                  T  __  C
GAM673  KIAA0798  5' AGAGGAGACAAAGAC       27715       TAC    _
                                GTCTTTG   TCTCC CT
                                |||||||   ||||| ||
                                CAGAAAC   AGAGG GA
                                     ___    A
GAM673  KIAA1754  3' GTTCAGAGAAAGTTGCAGAGAT 63240         _  C  C  A
                                GTCTTTGTA CT TC CT AAC
                                ||||||||| || || || |||
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                                TAGAGACGT GA AG GA TTG
                                     T  A  A  C
GAM673  MGC10540  3'  AGTGTCCCCCAAAGACTGG   50379          _____
                                CCAGTCTTTG    TACT
                                ||||||||||    ||||
                                GGTCAGAAAC    GTGA
                                      CCCCT
GAM673  MUC13    3'  AGAGTGTTTAGAAAGACTG   52327        G ____
                                CAGTCTTT T    ACTCT
                                ||||||||  |   |||||
                                GTCAGAAA A    TGAGA
                                     G TTTG
GAM673  PLAGL2   3'  TTTAAAGAGAAAAGTACAAGAC 70461       T   ___   CC
                                GTCTT GTAC   TCTC  TAAA
                                ||||| ||||   ||||  ||||
                                CAGAA CATG   AGAG  ATTT
                                   _   AAA    AA
GAM673  RHOBTB1  3'  GAAAGCACAAAGCTGG     91440     T     A  C
                                CCAG CTTTGT CT TC
                                |||| ||||||  || ||
                                GGTC GAAACA GA AG
                                   _     C  A
GAM673  SCAND2   3'  AGGGTGGCTCACAAAGAC    53314        AC_  T
                                GTCTTTGT   TC CCCT
                                ||||||||   || ||||
                                CAGAAACA   GG GGGA
                                     CTC  T
GAM673  SEC15B   3'  AGGTAATTAGTACAAAGAC   66684          CTC__
                                GTCTTTGTACT    CCT
                                ||||||||||    |||
                                CAGAAACATGA    GGA
                                      TTAAT
GAM673  TCL6     3'  TTAGGGAGGGTGAAAACTCA  40119   C   C   G
                                C AGT TTT TACTCTCCCTAA
                                | ||| ||| ||||||||||||
                                A TCA AAA GTGGGAGGGATT
                                 C  _  _
GAM673  TCL6     3'  TTAGGGAGGGTGAAAACTCA  40152   C   C   G
                                C AGT TTT TACTCTCCCTAA
                                | ||| ||| ||||||||||||
                                A TCA AAA GTGGGAGGGATT
                                 C  _  _
GAM673  LOC112840 3'  TAGGGAGAGACCTGG      54729      TCTTT  A
                                CCAG    GT CTCTCCCTA
                                ||||    || |||||||||
                                GGTC    CA GAGAGGGAT
                                     _____  _
GAM673  LOC121838 5'  TTTAGGAAACAAAGATGG    76005     G      ACTCTC
                                CCA TCTTTGT     CCTAAA
                                ||| |||||||     ||||||
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                                GGT AGAAACA     GGATTT
                                  _     AA____
GAM673  LOC124817 5'  AGGGTGTGGCAGAAGACTGG  74342       _   ACTCT
                                CCAGTCT TTGT    CCCT
                                ||||||| ||||    ||||
                                GGTCAGA GACG    GGGA
                                    A   GTGT_
GAM673  LOC126208 3'  AGGGAGAAGCGGACGG     74462    A   TT  AC
                                CC GTCT  GT  TCTCCCT
                                || ||||  ||  |||||||
                                GG CAGG  CG  AGAGGGA
                                 _   __ A_
GAM673  LOC134266 3'  TAGGGAAAAGGGAAGACTGG  75168        GTACTC
                                CCAGTCTTT     TCCCTA
                                |||||||||     ||||||
                                GGTCAGAAG     AGGGAT
                                     GGAAA_
GAM673  LOC143465 5'  GTTTAGAAAACTAAAAAAGACT 82970        GTACTCTCC
          G                      CAGTCTTT       CTAAAC
                                |||||||        ||||||
                                GTCAGAAA       GATTTG
                                    AAATCAAAA
GAM673  LOC144681 3'  TTTAAAGAGAAGTTGCAAAGAT 83177        _ _  CC
                                GTCTTTGTA CT CTC  TAAA
                                ||||||||| || |||  ||||
                                TAGAAACGT GA GAG  ATTT
                                     T  A   AA
GAM673  LOC147650 5'  AGAGAGAGAGGAAGATGG    78385    G    GTA    C
                                CCA TCTTT   CTCTC CT
                                ||| |||||   ||||| ||
                                GGT AGAAG   GAGAG GA
                                  _    GA_    A
GAM673  LOC148371 3'  TTTAGTAGTAAAAGACTGG   78811        G   CTCC
                                CCAGTCTTT TACT   CTAAA
                                ||||||||| ||||   |||||
                                GGTCAGAAA ATGA   GATTT
                                     _   T___
GAM673  LOC152503 3'  AGAGGACAGAAGACTGG     85767       _   A
                                CCAGTCT TTGT CTCT
                                ||||||| |||| ||||
                                GGTCAGA GACA GAGA
                                    A   G
GAM673  LOC157503 3'  TAGGGAGAGTCGATGA     86469    T  T
                                TC TTG ACTCTCCCTA
                                || ||| ||||||||||
                                AG AGC TGAGAGGGAT
                                 T  _
GAM673  LOC161589 3'  TTTAGTAGTAAAAGACTGG   82284        G   CTCC
                                CCAGTCTTT TACT   CTAAA
                                ||||||||| ||||   |||||
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                                GGTCAGAAA ATGA    GATTT
                                      _   T___
GAM673   LOC161978 5'  GAGGACACAAAGACTG      82327          AC
                                CAGTCTTTGT  TCTC
                                ||||||||||  ||||
                                GTCAGAAACA  GGAG
                                     CA
GAM673   LOC196510 3'  AGGAAGAGTAGGACTGG     87745        TTG     C
                                CCAGTCT   TACTCT CCT
                                |||||||   |||||| |||
                                GGTCAGG   ATGAGA GGA
                                   ___      A
GAM673   LOC200220 3'  AGGAAGAGTAGGACTGG     88635        TTG     C
                                CCAGTCT   TACTCT CCT
                                |||||||   |||||| |||
                                GGTCAGG   ATGAGA GGA
                                   ___      A
GAM673   LOC204285 3'  AGGGAGCAGCAAGAGTGG    89456     G    T  ACT
                                CCA TCTT GT   CTCCCT
                                ||| |||| ||   ||||||
                                GGT AGAA CG   GAGGGA
                                  G    _  AC_
GAM673   LOC221271 3'  AGGGAGAGAAGGAT        91845        GTA
                                GTCTTT   CTCTCCCT
                                ||||||   ||||||||
                                TAGGAA   GAGAGGGA
                                   ___
GAM673   LOC221838 3'  TTTAGTAGTAAAAGACTGG   92548          G    CTCC
                                CCAGTCTTT TACT    CTAAA
                                |||||||| ||||    |||||
                                GGTCAGAAA ATGA    GATTT
                                      _   T___
GAM673   LOC253776 3'  AGGAAGATGGCTGAAGACT   97429         _  AC   C
                                AGTCTTT GT  TCT CCT
                                ||||||| ||  ||| |||
                                TCAGAAG CG  AGA GGA
                                     T  GT   A
GAM673   LOC253805 3'  TAGGGAGAGTACTAGGACT   96436        T
                                AGTCTT GTACTCTCCCTA
                                |||||| ||||||||||||
                                TCAGGA CATGAGAGGGAT
                                    T
GAM673   LOC256861 3'  AGGAAGATGCCAAGAC      96787       T   C   C
                                GTCTT GTA TCT CCT
                                ||||| ||| ||| |||
                                CAGAA CGT AGA GGA
                                   C   _   A
GAM673   LOC51145  3'  TTAGGAAGAGACTGG       32401        TTTGTAC   C
                                CCAGTC      TCT CCTAA
                                ||||||      ||| |||||
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                                GGTCAG      AGA GGATT
                                   _______  A
GAM673  LOC56891  5'  GAGATTCACACAGAAGACTGG  39277        ___   AC_
                                CCAGTCTT   TGT   TCTC
                                ||||||||   |||   ||||
                                GGTCAGAA   ACA   AGAG
                                     GAC   CTT
GAM674  KHK       3'  CTGGATTCAAATCTGCCA    4032       CA
                                TGGCA  ATTTGAATTCAG
                                |||||  ||||||||||||
                                ACCGT  TAAACTTAGGTC
                                   C_
GAM674  KHK       3'  CTGGATTCAAATCTGCCA    21402      CA
                                TGGCA  ATTTGAATTCAG
                                |||||  ||||||||||||
                                ACCGT  TAAACTTAGGTC
                                   C_
GAM674  NRXN3     5'  GCTGGAATTCAAACTGCC    57280      CAA       _
                                GGCA   TTTGAATTC AGT
                                ||||   ||||||||| |||
                                CCGT   AAACTTAAG TCG
                                   C__        G
GAM674  PRSS16    3'  CTGGTTCAAATTCTGCCA    19629      C       T
                                TGGCA AATTTGAAT CAG
                                ||||| ||||||||| |||
                                ACCGT TTAAACTTG GTC
                                   C       _
GAM674  PXF       3'  ATTCAAGATTGTGCCA      11149          _
                                TGGCACAATTT GAAT
                                |||||||||||  ||||
                                ACCGTGTTAGA CTTA
                                      A
GAM674  RAG1      3'  TTACTGAAACATTTTGCCA   4819       C   TTGAA
                                TGGCA AAT    TTCAGTAA
                                ||||| |||    ||||||||
                                ACCGT TTA    AAGTCATT
                                   T   CA___
GAM674  SLC25A15  3'  ACTGAAATTGTGCCA       26507          TGAAT
                                TGGCACAATT    TCAGT
                                ||||||||||    |||||
                                ACCGTGTTAA    AGTCA
                                      ______
GAM674  TPM1      3'  CTGGTTCAAATGTGCCA     4526        A      T
                                TGGCACA TTTGAAT CAG
                                ||||||| ||||||| |||
                                ACCGTGT AAACTTG GTC
                                      _     _
GAM674  DKFZP434E2135 5'  TTACTGAGATCAGCCA      47959      ACAATT   A
                                TGGC     TGA TTCAGTAA
                                ||||     ||| ||||||||
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                                ACCG     ACT GAGTCATT
                                  _____  A
GAM674  FLJ10824  3'  ACTGAATTCTGAGGGTGCC   72574      AA  T
                                GGCAC  TT GAATTCAGT
                                ||||||  || |||||||||
                                CCGTG  AG CTTAAGTCA
                                   GG  T
GAM674  FLJ22282  3'  TGGACCAAATTGTGCC     45594          AA
                                GGCACAATTTG  TTCA
                                ||||||||||  ||||
                                CCGTGTTAAAC  AGGT
                                      C_
GAM674  H2AV    3'  CTAGATTCAAATTATGC    56848    C       TC
                                GCA AATTTGAAT  AG
                                ||| |||||||||  ||
                                CGT TTAAACTTA  TC
                                  A       GA
GAM674  HPCL2   3'  TACTGTTAAAATTGTGC    24323        GAATT
                                GCACAATTT    CAGTA
                                |||||||||    |||||
                                CGTGTTAAA    GTCAT
                                     ATT__
GAM674  KIAA0256  3'  TTTACTGAACTCATTGGGACTA 64425    CA_   TT   A
                                TGG   CAA  TGA TTCAGTAAA
                                |||   |||  ||| |||||||||
                                ATC   GTT  ACT AAGTCATTT
                                  AGG   __   C
GAM674  KIAA0265  3'  TTAGGTTCAAATTATGCCA   69888      C       TC
                                TGGCA AATTTGAAT  AG
                                |||||  |||||||||  ||
                                ACCGT TTAAACTTG  TT
                                   A       GA
GAM674  KRTAP2-4  3'  TTTTACTGCTCAAACTGTCACC 52592    C_   A    ATT
           A                     TGG  ACA TTTGA   CAGTAAAA
                                |||  |||  |||||   ||||||||
                                ACC  TGT AAACT   GTCATTTT
                                  AC   C    C__
GAM674  SGKL    3'  ACTGAAATTGTGCCA      25139          TGAAT
                                TGGCACAATT    TCAGT
                                ||||||||||    |||||
                                ACCGTGTTAA    AGTCA
                                      _____
GAM674  Spir-1   5'  TACTGAATCAGATGCACCA   64702    CACA     A
                                TGG    ATTTGA TTCAGTA
                                |||    |||||| |||||||
                                ACC    TAGACT AAGTCAT
                                  ACG_     _
GAM674  LOC149566 3'  TTGGTTTAAATTATGCCA    84498      C       T
                                TGGCA AATTTGAAT CAG
                                ||||| ||||||||| |||
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                                ACCGT TTAAATTTG GTT
                                  A       _
GAM674  LOC158490 3'  TTTACTGAAAATCCTGCCA   81936      CA   GAAT
                                TGGCA  ATTT   TCAGTAAA
                                |||||  ||||   ||||||||
                                ACCGT  TAAA   AGTCATTT
                                  CC   _____
GAM674  LOC201183 5'  TTTACTGCTGAATTGTCCA   89759     C      AATT
                                TGG ACAATTTG   CAGTAAA
                                ||| ||||||||   |||||||
                                ACC TGTTAAGT   GTCATTT
                                  _      C___
GAM674  LOC253725 3'  ACTGAATTCTGAGGGTGCC   94700      AA  T
                                GGCAC  TT GAATTCAGT
                                |||||  || |||||||||
                                CCGTG  AG CTTAAGTCA
                                   GG  T
GAM674  LOC254268 3'  GAATTCAAATTAACCA     95408     CAC
                                TGG   AATTTGAATTC
                                |||   ||||||||||||
                                ACC   TTAAACTTAAG
                                  AA_
GAM674  LOC51133  3'  TTTACTGAATTTCAGT     32286     T
                                ATT GAATTCAGTAAA
                                ||| ||||||||||||
                                TGA TTTAAGTCATTT
                                  C
GAM674  LOC54466  3'  TTACTGAACTCAGGTACAGC  38656    ACA     A
                                GC   ATTTGA TTCAGTAA
                                ||   |||||| ||||||||
                                CG   TGGACT AAGTCATT
                                 ACA     C
GAM675  ADORA2A   5'  AAGCTGGGCTGAGCCA      5431
                                TGGCTCAGTCCAGCTT
                                ||||||||||||||||
                                ACCGAGTCGGGTCGAA

GAM675  ADORA2A   5'  AAGCTGGGCTGAGCCA      5431
                                TGGCTCAGTCCAGCTT
                                ||||||||||||||||
                                ACCGAGTCGGGTCGAA

GAM675  AP2B1     3'  GCTGACCTGACTGAGCCA    7063          ____
                                TGGCTCAGTC   CAGC
                                ||||||||||   ||||
                                ACCGAGTCAG   GTCG
                                      TCCA
GAM675  AP2B1     3'  GCTGACCTGACTGAGCCA    7063          ____
                                TGGCTCAGTC   CAGC
                                ||||||||||   ||||
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                                ACCGAGTCAG   GTCG
                                     TCCA
GAM675  ATP11B   3' CTTCCAGACCTGAGCCA    80316       _ CAGCT  A
                                TGGCTCAG TC    TG AAG
                                |||||||| ||    || |||
                                ACCGAGTC AG    AC TTC
                                    C _____  C
GAM675  ATP11B   3' CTTCCAGACCTGAGCCA    80316       _ CAGCT  A
                                TGGCTCAG TC    TG AAG
                                |||||||| ||    || |||
                                ACCGAGTC AG    AC TTC
                                    C _____  C
GAM675  B3GALT5  3' CTTCCCAAGCCTGAGCCA   52557       TCCA    A_
                                TGGCTCAG   GCTTG  AAG
                                ||||||||   |||||  |||
                                ACCGAGTC   CGAAC  TTC
                                     ____   CC
GAM675  B3GALT5  3' CTTCCCAAGCCTGAGCCA   52577       TCCA    A_
                                TGGCTCAG   GCTTG  AAG
                                ||||||||   |||||  |||
                                ACCGAGTC   CGAAC  TTC
                                     ____   CC
GAM675  B3GALT5  3' CTTCCCAAGCCTGAGCCA   52570       TCCA    A_
                                TGGCTCAG   GCTTG  AAG
                                ||||||||   |||||  |||
                                ACCGAGTC   CGAAC  TTC
                                     ____   CC
GAM675  B3GALT5  5' GCTCTTGGTCTTGGACTGAGCC 20221          C_ TG A
          A                      TGGCTCAGTCCAG  T  A AGC
                                ||||||||||||| |  | |||
                                ACCGAGTCAGGTT  G  T TCG
                                      CT GT C
GAM675  B3GALT5  3' CTTCCCAAGCCTGAGCCA   20219       TCCA    A_
                                TGGCTCAG   GCTTG  AAG
                                ||||||||   |||||  |||
                                ACCGAGTC   CGAAC  TTC
                                     ____   CC
GAM675  B3GALT5  3' CTTCCCAAGCCTGAGCCA   20219       TCCA    A_
                                TGGCTCAG   GCTTG  AAG
                                ||||||||   |||||  |||
                                ACCGAGTC   CGAAC  TTC
                                     ____   CC
GAM675  B3GALT5  3' CTTCCCAAGCCTGAGCCA   52577       TCCA    A_
                                TGGCTCAG   GCTTG  AAG
                                ||||||||   |||||  |||
                                ACCGAGTC   CGAAC  TTC
                                     ____   CC
GAM675  B3GALT5  5' GCTCTTGGTCTTGGACTGAGCC 52579          C_ TG A
          A                      TGGCTCAGTCCAG  T  A AGC
                                ||||||||||||| |  | |||
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                                ACCGAGTCAGGTT  G  T TCG
                                      CT GT C
GAM675  B3GALT5  5' GCTCTTGGTCTTGGACTGAGCC 52572          C_ TG A
           A                   TGGCTCAGTCCAG  T  A AGC
                               |||||||||||||  |  | |||
                               ACCGAGTCAGGTT  G  T TCG
                                      CT GT C
GAM675  B3GALT5  3' CTTCCCAAGCCTGAGCCA    52562        TCCA    A_
                               TGGCTCAG   GCTTG  AAG
                               ||||||||   |||||  |||
                               ACCGAGTC   CGAAC  TTC
                                   ____    CC
GAM675  B3GALT5  3' CTTCCCAAGCCTGAGCCA    52557        TCCA    A_
                               TGGCTCAG   GCTTG  AAG
                               ||||||||   |||||  |||
                               ACCGAGTC   CGAAC  TTC
                                   ____    CC
GAM675  B3GALT5  5' GCTCTTGGTCTTGGACTGAGCC 52572          C_ TG A
           A                   TGGCTCAGTCCAG  T  A AGC
                               |||||||||||||  |  | |||
                               ACCGAGTCAGGTT  G  T TCG
                                      CT GT C
GAM675  B3GALT5  5' GCTCTTGGTCTTGGACTGAGCC 52564          C_ TG A
           A                   TGGCTCAGTCCAG  T  A AGC
                               |||||||||||||  |  | |||
                               ACCGAGTCAGGTT  G  T TCG
                                      CT GT C
GAM675  B3GALT5  5' GCTCTTGGTCTTGGACTGAGCC 52564          C_ TG A
           A                   TGGCTCAGTCCAG  T  A AGC
                               |||||||||||||  |  | |||
                               ACCGAGTCAGGTT  G  T TCG
                                      CT GT C
GAM675  B3GALT5  5' GCTCTTGGTCTTGGACTGAGCC 52579          C_ TG A
           A                   TGGCTCAGTCCAG  T  A AGC
                               |||||||||||||  |  | |||
                               ACCGAGTCAGGTT  G  T TCG
                                      CT GT C
GAM675  B3GALT5  3' CTTCCCAAGCCTGAGCCA    52570        TCCA    A_
                               TGGCTCAG   GCTTG  AAG
                               ||||||||   |||||  |||
                               ACCGAGTC   CGAAC  TTC
                                   ____    CC
GAM675  B3GALT5  3' CTTCCCAAGCCTGAGCCA    52562        TCCA    A_
                               TGGCTCAG   GCTTG  AAG
                               ||||||||   |||||  |||
                               ACCGAGTC   CGAAC  TTC
                                   ____    CC
GAM675  B3GALT5  5' GCTCTTGGTCTTGGACTGAGCC 20221          C_ TG A
           A                   TGGCTCAGTCCAG  T  A AGC
                               |||||||||||||  |  | |||
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                                ACCGAGTCAGGTT  G  T TCG
                                      CT GT C
GAM675  CALCR   3'  GCTCCTTGTCAATACTGAGCCA 8220        CCA_  TTGAA
                                TGGCTCAGT   GC    AGC
                                |||||||||   ||    |||
                                ACCGAGTCA   TG    TCG
                                     TAAC  TTCC_
GAM675  CALCR   3'  GCTCCTTGTCAATACTGAGCCA 8220        CCA_  TTGAA
                                TGGCTCAGT   GC    AGC
                                |||||||||   ||    |||
                                ACCGAGTCA   TG    TCG
                                     TAAC  TTCC_
GAM675  CBR1    5'  CTCCCGGGCCTGAGCCA    8283        TCCA    AA
                                TGGCTCAG   GCTTG  AG
                                ||||||||   |||||  ||
                                ACCGAGTC   CGGGC  TC
                                     ____    CC
GAM675  CBR1    5'  CTCCCGGGCCTGAGCCA    8283        TCCA    AA
                                TGGCTCAG   GCTTG  AG
                                ||||||||   |||||  ||
                                ACCGAGTC   CGGGC  TC
                                     ____    CC
GAM675  CCR2    3'  CTCCCAAGCTGGACTATGGCT  5381      C_        AA
                                GGCT  AGTCCAGCTTG  AG
                                ||||  ||||||||||  ||
                                TCGG  TCAGGTCGAAC  TC
                                  TA        CC
GAM675  CCR2    3'  CTCCCAAGCTGGACTATGGCT  5381      C_        AA
                                GGCT  AGTCCAGCTTG  AG
                                ||||  ||||||||||  ||
                                TCGG  TCAGGTCGAAC  TC
                                  TA        CC
GAM675  CISH    3'  GCTTCATTATACTGAGCCA   59017       CCAGCT   A
                                TGGCTCAGT    TGAA GC
                                |||||||||    |||| ||
                                ACCGAGTCA    ACTT CG
                                     TATT__   _
GAM675  CISH    3'  GCTTCATTATACTGAGCCA   25280       CCAGCT   A
                                TGGCTCAGT    TGAA GC
                                |||||||||    |||| ||
                                ACCGAGTCA    ACTT CG
                                     TATT__   _
GAM675  CISH    3'  GCTTCATTATACTGAGCCA   59017       CCAGCT   A
                                TGGCTCAGT    TGAA GC
                                |||||||||    |||| ||
                                ACCGAGTCA    ACTT CG
                                     TATT__   _
GAM675  CISH    3'  GCTTCATTATACTGAGCCA   25280       CCAGCT   A
                                TGGCTCAGT    TGAA GC
                                |||||||||    |||| ||
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                                ACCGAGTCA     ACTT CG
                                     TATT__   _
GAM675  CNN1    3' GCTCTTGGCTGGACCCAGCCA 7115      CA      TGAA
                                TGGCT  GTCCAGCT   AGC
                                |||||  ||||||||   |||
                                ACCGA  CAGGTCGG   TCG
                                   CC       TTC_
GAM675  CNN1    3' GCTCTTGGCTGGACCCAGCCA 7115      CA      TGAA
                                TGGCT  GTCCAGCT   AGC
                                |||||  ||||||||   |||
                                ACCGA  CAGGTCGG   TCG
                                   CC       TTC_
GAM675  CNP     3' AGGCTGGGCCAAGCCA     52442     CA
                                TGGCT  GTCCAGCTT
                                |||||  |||||||||
                                ACCGA  CGGGTCGGA
                                   AC
GAM675  CNP     3' AGGCTGGGCCAAGCCA     52442     CA
                                TGGCT  GTCCAGCTT
                                |||||  |||||||||
                                ACCGA  CGGGTCGGA
                                   AC
GAM675  COX10   3' TTCCTGGTGACTGAGCCA   7128        CA  T_
                                TGGCTCAGTC  GCT  GAA
                                ||||||||||  |||  |||
                                ACCGAGTCAG  TGG  CTT
                                     __   TC
GAM675  COX10   3' TTCCTGGTGACTGAGCCA   7128        CA  T_
                                TGGCTCAGTC  GCT  GAA
                                ||||||||||  |||  |||
                                ACCGAGTCAG  TGG  CTT
                                     __   TC
GAM675  CSK     3' CGAGCCTGAACTGAGCC    15218       C  _
                                GGCTCAGT CAG CTTG
                                ||||||||  ||| ||||
                                CCGAGTCA GTC GAGC
                                     A   C
GAM675  CSK     3' CGAGCCTGAACTGAGCC    15218       C  _
                                GGCTCAGT CAG CTTG
                                ||||||||  ||| ||||
                                CCGAGTCA GTC GAGC
                                     A   C
GAM675  CTNS    5' CTCCGGGGGACTGAGC     17040       AG   AA
                                GCTCAGTCC  CTTG  AG
                                |||||||||  ||||  ||
                                CGAGTCAGG  GGGC  TC
                                     __    C_
GAM675  CTNS    5' CTCCGGGGGACTGAGC     17040       AG   AA
                                GCTCAGTCC  CTTG  AG
                                |||||||||  ||||  ||
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                                CGAGTCAGG  GGGC  TC
                                    __    C_
GAM675  DLG5    5'  TGAGCCTGGACCTGAGCCA   82924        _    _
                                TGGCTCAG TCCAG CTTG
                                |||||||| ||||| ||||
                                ACCGAGTC AGGTC GAGT
                                    C     C
GAM675  DLG5    5'  TGAGCCTGGACCTGAGCCA   82924        _    _
                                TGGCTCAG TCCAG CTTG
                                |||||||| ||||| ||||
                                ACCGAGTC AGGTC GAGT
                                    C     C
GAM675  EBAF    3'  TCCTCTGGAGACTGAGCC    65427        __    CTT
                                GGCTCAG  TCCAG   GA
                                |||||||  |||||   ||
                                CCGAGTC  AGGTC   CT
                                    AG    TC_
GAM675  EBAF    3'  TCCTCTGGAGACTGAGCC    65427        __    CTT
                                GGCTCAG  TCCAG   GA
                                |||||||  |||||   ||
                                CCGAGTC  AGGTC   CT
                                    AG    TC_
GAM675  ELF3    3'  CTTGAAAGCACACTTGGACTGA 15421         A_________  TGAA
          GCCA                  GCTCAGTCC       GCT    AG
                                |||||||||       |||    ||
                                CGAGTCAGG       CGA    TC
                                    TTCACAIII   AAGT
GAM675  ELF3    3'  CTTGAAAGCACACTTGGACTGA 15421         A_________  TGAA
          GCCA                  GCTCAGTCC       GCT    AG
                                |||||||||       |||    ||
                                CGAGTCAGG       CGA    TC
                                    TTCACAIII   AAGT
GAM675  EZH1    3'  TCAAGCTGGACTGTGG      8826     _
                                CT CAGTCCAGCTTGA
                                || ||||||||||||
                                GG GTCAGGTCGAACT
                                 T
GAM675  EZH1    3'  TCAAGCTGGACTGTGG      8826     _
                                CT CAGTCCAGCTTGA
                                || ||||||||||||
                                GG GTCAGGTCGAACT
                                 T
GAM675  FGF18   5'  GCTGTCCCCGGACTGAGCC   13911         AGCTT  A
                                GGCTCAGTCC    GA AGC
                                ||||||||||    || |||
                                CCGAGTCAGG    CT TCG
                                    CCC__  G
GAM675  FGF18   5'  GCTGTCCCCGGACTGAGCC   13911         AGCTT  A
                                GGCTCAGTCC    GA AGC
                                ||||||||||    || |||
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                                CCGAGTCAGG    CT TCG
                                     CCC__  G
GAM675  FGF18   5'  GCTGTCCCCGGACTGAGCC   53346        AGCTT  A
                                GGCTCAGTCC    GA AGC
                                ||||||||||    || |||
                                CCGAGTCAGG    CT TCG
                                     CCC__  G
GAM675  FGF18   5'  GCTGTCCCCGGACTGAGCC   53346        AGCTT  A
                                GGCTCAGTCC    GA AGC
                                ||||||||||    || |||
                                CCGAGTCAGG    CT TCG
                                     CCC__  G
GAM675  FUS2    5'  TCCAGCCTGGCACTGAGCCA  24117        _   _  T
                                TGGCTCAGT CCAG CT GA
                                ||||||||| |||| || ||
                                ACCGAGTCA GGTC GA CT
                                     C   C  C
GAM675  FUS2    5'  TCCAGCCTGGCACTGAGCCA  24117        _   _  T
                                TGGCTCAGT CCAG CT GA
                                ||||||||| |||| || ||
                                ACCGAGTCA GGTC GA CT
                                     C   C  C
GAM675  GATA2   3'  CAGGCTGGGCTGAGCCA     8997
                                TGGCTCAGTCCAGCTTG
                                |||||||||||||||||
                                ACCGAGTCGGGTCGGAC

GAM675  GATA2   3'  CAGGCTGGGCTGAGCCA     8997
                                TGGCTCAGTCCAGCTTG
                                |||||||||||||||||
                                ACCGAGTCGGGTCGGAC

GAM675  KCNH5   3'  GCTTTCAAGATGATGACCA   57790    C   G  CAG
                                TGG TCA TC   CTTGAAAGC
                                ||| ||| ||   |||||||||
                                ACC AGT AG   GAACTTTCG
                                  _  _  TA_
GAM675  KCNH5   3'  GCTTTCAAGATGATGACCA   57790    C   G  CAG
                                TGG TCA TC   CTTGAAAGC
                                ||| ||| ||   |||||||||
                                ACC AGT AG   GAACTTTCG
                                  _  _  TA_
GAM675  KIR2DS1 3'  CTTCCAAATGCTGAGCC     27208       CCAGC  A
                                GGCTCAGT     TTG AAG
                                ||||||||     ||| |||
                                CCGAGTCG     AAC TTC
                                     TA___   C
GAM675  KIR2DS1 3'  CTTCCAAATGCTGAGCC     27208       CCAGC  A
                                GGCTCAGT     TTG AAG
                                ||||||||     ||| |||
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                              CCGAGTCG    AAC TTC
                                  TA___   C
GAM675  KIR2DS2  3' CTTCCAAATGCTGAGCC    24597       CCAGC  A
                              GGCTCAGT    TTG AAG
                              ||||||||    ||| |||
                              CCGAGTCG    AAC TTC
                                  TA___   C
GAM675  KIR2DS2  3' CTTCCAAATGCTGAGCC    24597       CCAGC  A
                              GGCTCAGT    TTG AAG
                              ||||||||    ||| |||
                              CCGAGTCG    AAC TTC
                                  TA___   C
GAM675  KIR2DS4  3' CTTCCAAATGCTGAGCC    24600       CCAGC  A
                              GGCTCAGT    TTG AAG
                              ||||||||    ||| |||
                              CCGAGTCG    AAC TTC
                                  TA___   C
GAM675  KIR2DS4  3' CTTCCAAATGCTGAGCC    24600       CCAGC  A
                              GGCTCAGT    TTG AAG
                              ||||||||    ||| |||
                              CCGAGTCG    AAC TTC
                                  TA___   C
GAM675  KLHL1    3' GCTTTTTTAACACACTGAGCCA 40490        CCAGCTT
                              TGGCTCAGT     GAAAGC
                              |||||||||     ||||||
                              ACCGAGTCA     TTTTCG
                                  CACAATT
GAM675  KLHL1    3' GCTTTTTTAACACACTGAGCCA 40490        CCAGCTT
                              TGGCTCAGT     GAAAGC
                              |||||||||     ||||||
                              ACCGAGTCA     TTTTCG
                                  CACAATT
GAM675  LARGE    3' GCCTTCAAATTCAAAATTGAGC 56110        CCAGC__    A
           CA                   TGGCTCAGT     TTGAA GC
                              |||||||||     ||||| ||
                              ACCGAGTTA     AACTT CG
                                  AAACTTA    C
GAM675  LARGE    3' GCCTTCAAATTCAAAATTGAGC 56110        CCAGC__    A
           CA                   TGGCTCAGT     TTGAA GC
                              |||||||||     ||||| ||
                              ACCGAGTTA     AACTT CG
                                  AAACTTA    C
GAM675  LARGE    3' GCCTTCAAATTCAAAATTGAGC 16436        CCAGC__    A
           CA                   TGGCTCAGT     TTGAA GC
                              |||||||||     ||||| ||
                              ACCGAGTTA     AACTT CG
                                  AAACTTA    C
GAM675  LARGE    3' GCCTTCAAATTCAAAATTGAGC 16436        CCAGC__    A
           CA                   TGGCTCAGT     TTGAA GC
                              |||||||||     ||||| ||
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                                ACCGAGTTA      AACTT CG
                                     AAACTTA    C
GAM675  LIMK1    3'  AGGTCCCCGACTGAGCCA    33641         CA__
                                TGGCTCAGTC   GCTT
                                ||||||||||   ||||
                                ACCGAGTCAG   TGGA
                                     CCCC
GAM675  LIMK1    3'  AGGTCCCCGACTGAGCCA    33641         CA__
                                TGGCTCAGTC   GCTT
                                ||||||||||   ||||
                                ACCGAGTCAG   TGGA
                                     CCCC
GAM675  LNK      3'  TTTACAGTCTGAGCCA      18474         TCCA  _
                                TGGCTCAG   GCT TGAA
                                ||||||||   ||| ||||
                                ACCGAGTC   TGA ATTT
                                     ____  C
GAM675  LNK      3'  TTTACAGTCTGAGCCA      18474         TCCA  _
                                TGGCTCAG   GCT TGAA
                                ||||||||   ||| ||||
                                ACCGAGTC   TGA ATTT
                                     ____  C
GAM675  MEA      3'  CTTGAAAGCACCTATGTACTGA 27545        C A_________  TGAA
           GCCA                    GCTCAGT C       GCT   AG
                                ||||||| |       |||   ||
                                CGAGTCA G       CGA   TC
                                    T TATCCAIII  AAGT
GAM675  MEA      3'  CTTGAAAGCACCTATGTACTGA 27545        C A_________  TGAA
           GCCA                    GCTCAGT C       GCT   AG
                                ||||||| |       |||   ||
                                CGAGTCA G       CGA   TC
                                    T TATCCAIII  AAGT
GAM675  MMP14    3'  CTTCCAAGGAAGGAGCCTGAGC 17170        __  AG_   A
           CA                     TGGCTCAG  TCC   CTTG AAG
                                ||||||||  |||   |||| |||
                                ACCGAGTC  AGG   GAAC TTC
                                    CG   AAG   C
GAM675  MMP14    3'  CTTCCAAGGAAGGAGCCTGAGC 17170        __  AG_   A
           CA                     TGGCTCAG  TCC   CTTG AAG
                                ||||||||  |||   |||| |||
                                ACCGAGTC  AGG   GAAC TTC
                                    CG   AAG   C
GAM675  MPO      3'  GCCTTGGAGGGATAAGCCA   4202       CA   AG   G  A
                                TGGCT  GTCC  CTT AA GC
                                |||||  ||||  ||| || ||
                                ACCGA  TAGG  GAG TT CG
                                  A_   __   G  C
GAM675  MPO      3'  GCCTTGGAGGGATAAGCCA   4202       CA   AG   G  A
                                TGGCT  GTCC  CTT AA GC
                                |||||  ||||  ||| || ||
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                                ACCGA  TAGG  GAG TT CG
                                  A_   __   G  C
GAM675  NPR1    3'  CTTACAGGCTGAGCCA      87369          CAGCT  A
                                TGGCTCAGTC    TG AAG
                                ||||||||||    || |||
                                ACCGAGTCGG    AC TTC
                                      _____ A
GAM675  NPR1    3'  CTTACAGGCTGAGCCA      87369          CAGCT  A
                                TGGCTCAGTC    TG AAG
                                ||||||||||    || |||
                                ACCGAGTCGG    AC TTC
                                      _____ A
GAM675  NPTX1   3'  GCTAGGGTCTGAGCCA      10263          _  _
                                TGGCTCAG TCC AGC
                                |||||||| ||| |||
                                ACCGAGTC GGG TCG
                                     T   A
GAM675  NPTX1   3'  GCTAGGGTCTGAGCCA      10263          _  _
                                TGGCTCAG TCC AGC
                                |||||||| ||| |||
                                ACCGAGTC GGG TCG
                                     T   A
GAM675  NPY2R   3'  CTTTTAACCTGAGCCA      6186         TCCAGC
                                TGGCTCAG    TTGAAAG
                                ||||||||    |||||||
                                ACCGAGTC    AATTTTC
                                     C_____
GAM675  NPY2R   5'  CTTTTAACCTGAGCCA      6185         TCCAGC
                                TGGCTCAG    TTGAAAG
                                ||||||||    |||||||
                                ACCGAGTC    AATTTTC
                                     C_____
GAM675  NPY2R   3'  CTTTTAACCTGAGCCA      6186         TCCAGC
                                TGGCTCAG    TTGAAAG
                                ||||||||    |||||||
                                ACCGAGTC    AATTTTC
                                     C_____
GAM675  NPY2R   5'  CTTTTAACCTGAGCCA      6185         TCCAGC
                                TGGCTCAG    TTGAAAG
                                ||||||||    |||||||
                                ACCGAGTC    AATTTTC
                                     C_____
GAM675  NRAS    3'  CTTTCAAGCTGCACTGA      10271        C
                                TCAGT CAGCTTGAAAG
                                ||||| ||||||||||
                                AGTCA GTCGAACTTTC
                                   C
GAM675  NRAS    3'  CTTTCAAGCTGCACTGA      10271        C
                                TCAGT CAGCTTGAAAG
                                ||||| ||||||||||
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                              AGTCA GTCGAACTTTC
                                C
GAM675  PKIG    3'  CTTTCAAGACACTGTAACCA  22960    CT_   CCAG
                              TGG  CAGT   CTTGAAAG
                              |||  ||||   ||||||||
                              ACC  GTCA   GAACTTTC
                                AAT   CA__
GAM675  PKIG    3'  CTTTCAAGACACTGTAACCA  22960    CT_   CCAG
                              TGG  CAGT   CTTGAAAG
                              |||  ||||   ||||||||
                              ACC  GTCA   GAACTTTC
                                AAT   CA__
GAM675  PMP2    3'  GCTCCCACTGGCCAAACTTGAG 10673       _ ____   CT  AA
           CCA                  TGGCTCA GT   CCAG  TG  AGC
                              |||||||  ||   ||||  ||  |||
                              ACCGAGT CA   GGTC  AC  TCG
                                 T  AACC   __  CC
GAM675  PMP2    3'  GCTCCCACTGGCCAAACTTGAG 10673       _ ____   CT  AA
           CCA                  TGGCTCA GT   CCAG  TG  AGC
                              |||||||  ||   ||||  ||  |||
                              ACCGAGT CA   GGTC  AC  TCG
                                 T  AACC   __  CC
GAM675  PRSS8   3'  TCCGGAGGACTGAGCC     10918        AG  T
                              GGCTCAGTCC  CT GA
                              ||||||||||  || ||
                              CCGAGTCAGG  GG CT
                                   A_  C
GAM675  PRSS8   3'  TCCGGAGGACTGAGCC     10918        AG  T
                              GGCTCAGTCC  CT GA
                              ||||||||||  || ||
                              CCGAGTCAGG  GG CT
                                   A_  C
GAM675  PTGER1  3'  CTTGAAAGCGCCCAACGACTAA 6301     C   CA_________  TGAA
           GCCA                 GCT AGTC       GCT   AG
                              |||  ||||       |||   ||
                              CGA TCAG       CGA   TC
                                A   CAACCCGIII  AAGT
GAM675  PTGER1  3'  CTTGAAAGCGCCCAACGACTAA 6301     C   CA_________  TGAA
           GCCA                 GCT AGTC       GCT   AG
                              |||  ||||       |||   ||
                              CGA TCAG       CGA   TC
                                A   CAACCCGIII  AAGT
GAM675  PXN     3'  CTTCCAAGCTGGCTTTTCCCA  11162    CTC_  T      A
                              TGG   AG CCAGCTTG AAG
                              |||   || ||||||||  |||
                              ACC   TC GGTCGAAC TTC
                                CTTT  _       C
GAM675  PXN     3'  CTTCCAAGCTGGCTTTTCCCA  11162    CTC_  T      A
                              TGG   AG CCAGCTTG AAG
                              |||   || ||||||||  |||
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                                ACC   TC GGTCGAAC TTC
                                  CTTT _      C
GAM675  RAB36   3' GCCCTCAAGCTGTAGGCC   16965     CAGTC      AA
                                GGCT    CAGCTTGA  GC
                                ||||    ||||||||  ||
                                CCGG    GTCGAACT  CG
                                  AT___       CC
GAM675  RAB36   3' GCCCTCAAGCTGTAGGCC   16965     CAGTC      AA
                                GGCT    CAGCTTGA  GC
                                ||||    ||||||||  ||
                                CCGG    GTCGAACT  CG
                                  AT___       CC
GAM675  RDS     3' TGAGTCTGGAGTGAACCA   4366     C  G   _
                                TGG TCA TCCAG CTTG
                                ||| ||| ||||| ||||
                                ACC AGT AGGTC GAGT
                                  A  G    T
GAM675  RDS     3' TGAGTCTGGAGTGAACCA   4366     C  G   _
                                TGG TCA TCCAG CTTG
                                ||| ||| ||||| ||||
                                ACC AGT AGGTC GAGT
                                  A  G    T
GAM675  RNPEPL1  3' TCCTTGCAGGGATCTGAGCCA 36680       _  A_  TT_
                                TGGCTCAG TCC  GC   GA
                                |||||||| |||  ||   ||
                                ACCGAGTC AGG  CG   CT
                                     T   GA  TTC
GAM675  RNPEPL1  3' TCCTTGCAGGGATCTGAGCCA 36680       _  A_  TT_
                                TGGCTCAG TCC  GC   GA
                                |||||||| |||  ||   ||
                                ACCGAGTC AGG  CG   CT
                                     T   GA  TTC
GAM675  SLC19A2  3' TTTTCATAAACTGAGCC    68984       CCAGCT
                                GGCTCAGT    TGAAAG
                                ||||||||    ||||||
                                CCGAGTCA    ACTTTT
                                     AAT___
GAM675  SLC19A2  3' TTTTCATAAACTGAGCC    68984       CCAGCT
                                GGCTCAGT    TGAAAG
                                ||||||||    ||||||
                                CCGAGTCA    ACTTTT
                                     AAT___
GAM675  TH1L    3' CTTTTTGAGACTGAGC     33076       _ GCTT
                                GCTCAGTC CA   GAAAG
                                |||||||| ||   |||||
                                CGAGTCAG GT   TTTTC
                                     A _____
GAM675  TH1L    3' CTTTTTGAGACTGAGC     33076       _ GCTT
                                GCTCAGTC CA   GAAAG
                                |||||||| ||   |||||
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                                CGAGTCAG GT    TTTTC
                                    A _____
GAM675  TNP2    5'  GCTTTGTCTTGGCTGAGCCA   18298        T   CTTG
                                TGGCTCAG CCAG    AAAGC
                                |||||||| ||||    |||||
                                ACCGAGTC GGTT    TTTCG
                                    _   CTG_
GAM675  TNP2    5'  GCTTTGTCTTGGCTGAGCCA   18298        T   CTTG
                                TGGCTCAG CCAG    AAAGC
                                |||||||| ||||    |||||
                                ACCGAGTC GGTT    TTTCG
                                    _   CTG_
GAM675  TRPV1   5'  GCCTTCAAGCTCACAAGC    38085     CA  CC      A
                                GCT  GT  AGCTTGAA GC
                                |||  ||  |||||||| ||
                                CGA  CA  TCGAACTT CG
                                  A_  C_       C
GAM675  TRPV1   5'  TCTTCTGGACTGAGCCA     54884           CTT
                                TGGCTCAGTCCAG   GA
                                ||||||||||||   ||
                                ACCGAGTCAGGTC   CT
                                      TT_
GAM675  TRPV1   5'  GCCTTCAAGCTCACAAGC    38085     CA  CC      A
                                GCT  GT  AGCTTGAA GC
                                |||  ||  |||||||| ||
                                CGA  CA  TCGAACTT CG
                                  A_  C_       C
GAM675  TRPV1   5'  TCTTCTGGACTGAGCCA     54884           CTT
                                TGGCTCAGTCCAG   GA
                                ||||||||||||   ||
                                ACCGAGTCAGGTC   CT
                                      TT_
GAM675  ZNF214  5'  CTCTCAGGAGGACTGAGCCA   25116         AG    A
                                TGGCTCAGTCC  CTTGA AG
                                ||||||||||  ||||| ||
                                ACCGAGTCAGG  GGACT TC
                                      A_    C
GAM675  ZNF214  5'  CTCTCAGGAGGACTGAGCCA   25116         AG    A
                                TGGCTCAGTCC  CTTGA AG
                                ||||||||||  ||||| ||
                                ACCGAGTCAGG  GGACT TC
                                      A_    C
GAM675  ZNF289  3'  CTTGAAAGCGCCTGTGGACTGA 65332         A_________  TGAA
            GCC                   GCTCAGTCC       GCT   AG
                                |||||||||       |||   ||
                                CGAGTCAGG       CGA   TC
                                    TGTCCGIII   AAGT
GAM675  ZNF289  3'  CTTGAAAGCGCCTGTGGACTGA 65332         A_________  TGAA
            GCC                   GCTCAGTCC       GCT   AG
                                |||||||||       |||   ||
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                                CGAGTCAGG       CGA   TC
                                    TGTCCGIII   AAGT
GAM675  ARNTL2   3' CTTTTTAGGGGACTGAACCA  39465    C     AG  T
                                TGG TCAGTCC  CT GAAAG
                                ||| |||||||  || |||||
                                ACC AGTCAGG  GA TTTTC
                                  A      G_  T
GAM675  ARNTL2   3' CTTTTTAGGGGACTGAACCA  39465    C     AG  T
                                TGG TCAGTCC  CT GAAAG
                                ||| |||||||  || |||||
                                ACC AGTCAGG  GA TTTTC
                                  A      G_  T
GAM675  ATP5D    3' GCTCTGGGGACTGGGCCA    8073          ____
                                TGGCTCAGTCC    AGC
                                ||||||||||    |||
                                ACCGGGTCAGG    TCG
                                      GGTC
GAM675  ATP5D    3' GCTCTGGGGACTGGGCCA    8073          ____
                                TGGCTCAGTCC    AGC
                                ||||||||||    |||
                                ACCGGGTCAGG    TCG
                                      GGTC
GAM675  BAG3     5' TTCTCTGGACTGGACCA     15004     CT      CTT
                                TGG  CAGTCCAG   GAA
                                |||  ||||||||   |||
                                ACC  GTCAGGTC   CTT
                                  AG       T__
GAM675  BAG3     5' TTCTCTGGACTGGACCA     15004     CT      CTT
                                TGG  CAGTCCAG   GAA
                                |||  ||||||||   |||
                                ACC  GTCAGGTC   CTT
                                  AG       T__
GAM675  BTN2A2   3' GCTTTCAGACTTAAACTGAGCC 22778         CC_  CT
            A                    TGGCTCAGT   AG  TGAAAGC
                                |||||||||   ||  |||||||
                                ACCGAGTCA   TC  ACTTTCG
                                     AAT  AG
GAM675  BTN2A2   3' GCTTTCAGACTTAAACTGAGCC 22778         CC_  CT
            A                    TGGCTCAGT   AG  TGAAAGC
                                |||||||||   ||  |||||||
                                ACCGAGTCA   TC  ACTTTCG
                                     AAT  AG
GAM675  C20orf43 3' GCCTTCAAGCTGGTGTGGCCA 59937     T  GT        A
                                TGGC CA  CCAGCTTGAA GC
                                |||| ||  |||||||||| ||
                                ACCG GT  GGTCGAACTT CG
                                  _  GT        C
GAM675  C20orf43 3' GCCTTCAAGCTGGTGTGGCCA 59937     T  GT        A
                                TGGC CA  CCAGCTTGAA GC
                                |||| ||  |||||||||| ||
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                                ACCG GT  GGTCGAACTT CG
                                  _ GT        C
GAM675  C20orf44  3'  CTTGAAAGCAAACCAGAGCTGA 36761       CCA_________  TGAA
          GCCA                    GCTCAGT         GCT    AG
                                |||||||         |||    ||
                                CGAGTCG         CGA    TC
                                   AGACCAAAIII   AAGT
GAM675  C20orf44  3'  CTTGAAAGCAAACCAGAGCTGA 36761       CCA_________  TGAA
          GCCA                    GCTCAGT         GCT    AG
                                |||||||         |||    ||
                                CGAGTCG         CGA    TC
                                   AGACCAAAIII   AAGT
GAM675  CDC14B   3'  GCTCTCAAGCTGAATGAC    52834     ___      A
                                GTC   CAGCTTGA AGC
                                |||   |||||||| |||
                                CAG   GTCGAACT TCG
                                  TAA       C
GAM675  CDC14B   3'  GCTCTCAAGCTGAATGAC    13387     ___      A
                                GTC   CAGCTTGA AGC
                                |||   |||||||| |||
                                CAG   GTCGAACT TCG
                                  TAA       C
GAM675  CDC14B   3'  GCTCTCAAGCTGAATGAC    13387     ___      A
                                GTC   CAGCTTGA AGC
                                |||   |||||||| |||
                                CAG   GTCGAACT TCG
                                  TAA       C
GAM675  CDC14B   3'  GCTCTCAAGCTGAATGAC    52834     ___      A
                                GTC   CAGCTTGA AGC
                                |||   |||||||| |||
                                CAG   GTCGAACT TCG
                                  TAA       C
GAM675  DKFZP564O0423 3'  CTTTCAAGCTCTCAGC      91689     C  TCC
                                GCT AG   AGCTTGAAAG
                                ||| ||   ||||||||||
                                CGA TC   TCGAACTTTC
                                  C  ___
GAM675  DKFZP564O0423 3'  CTTTCAAGCTCTCAGC      91689     C  TCC
                                GCT AG   AGCTTGAAAG
                                ||| ||   ||||||||||
                                CGA TC   TCGAACTTTC
                                  C  ___
GAM675  DKFZP564O043 5'  TTCAAGCTGGCGGGAGC     92492      A_ T
                                GCTC  G CCAGCTTGAA
                                ||||  | ||||||||||
                                CGAG  C GGTCGAACTT
                                   GG _
GAM675  DKFZP564O043 5'  TTCAAGCTGGCGGGAGC     92492      A_ T
                                GCTC  G CCAGCTTGAA
                                ||||  | ||||||||||
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                                CGAG  C GGTCGAACTT
                                  GG _
GAM675  DKFZP586J1624 5'  GCCTTTGGGCTGGACCAGCCA  31393      CA       TG  A
                                TGGCT  GTCCAGCT  AA GC
                                |||||  ||||||||  || ||
                                ACCGA  CAGGTCGG  TT CG
                                   C_       GT  C
GAM675  DKFZP586J1624 5'  GCCTTTGGGCTGGACCAGCCA  31393      CA       TG  A
                                TGGCT  GTCCAGCT  AA GC
                                |||||  ||||||||  || ||
                                ACCGA  CAGGTCGG  TT CG
                                   C_       GT  C
GAM675  DKFZP762N2316 3'  GCTTTTTAGGACTGAACA    67128    GC      AGCTT
                                TG  TCAGTCC    GAAAGC
                                ||  |||||||    ||||||
                                AC  AGTCAGG    TTTTCG
                                 A_      AT___
GAM675  DKFZP762N2316 3'  GCTTTTTAGGACTGAACA    67128    GC      AGCTT
                                TG  TCAGTCC    GAAAGC
                                ||  |||||||    ||||||
                                AC  AGTCAGG    TTTTCG
                                 A_      AT___
GAM675  EDG1     3'  GCTTTGATTTTGCACTGAGCCA 59328         C   CTTG
                                TGGCTCAGT CAG    AAAGC
                                |||||||||| |||    |||||
                                ACCGAGTCA GTT    TTTCG
                                     C   TTAG
GAM675  EDG1     3'  GCTTTGATTTTGCACTGAGCCA 59328         C   CTTG
                                TGGCTCAGT CAG    AAAGC
                                |||||||||| |||    |||||
                                ACCGAGTCA GTT    TTTCG
                                     C   TTAG
GAM675  ESDN     3'  TTCTGTTGGCCTGAGCCA    55182         T    TT
                                TGGCTCAG CCAGC  GAA
                                ||||||||| |||||  |||
                                ACCGAGTC GGTTG  CTT
                                    C    T_
GAM675  ESDN     3'  TTCTGTTGGCCTGAGCCA    55182         T    TT
                                TGGCTCAG CCAGC  GAA
                                ||||||||| |||||  |||
                                ACCGAGTC GGTTG  CTT
                                    C    T_
GAM675  ET       5'  TCCGGCAGAGCTGAGCCA    44221         CCA  T
                                TGGCTCAGT   GCT GA
                                |||||||||   ||| ||
                                ACCGAGTCG   CGG CT
                                     AGA   C
GAM675  ET       5'  TCCGGCAGAGCTGAGCCA    44221         CCA  T
                                TGGCTCAGT   GCT GA
                                |||||||||   ||| ||
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                              ACCGAGTCG  CGG CT
                                   AGA  C
GAM675  FBXO8    5' AGTTCCCGGCTGAGCCA    24098        C__
                              TGGCTCAGTC  AGCT
                              ||||||||||  ||||
                              ACCGAGTCGG  TTGA
                                   CCC
GAM675  FBXO8    5' AGTTCCCGGCTGAGCCA    24098        C__
                              TGGCTCAGTC  AGCT
                              ||||||||||  ||||
                              ACCGAGTCGG  TTGA
                                   CCC
GAM675  FLJ10697 3' TTAAGCACTGAGCCA      36421        CCA
                              TGGCTCAGT  GCTTGA
                              |||||||||  ||||||
                              ACCGAGTCA  CGAATT
                                         ___
GAM675  FLJ10697 3' TTAAGCACTGAGCCA      36421        CCA
                              TGGCTCAGT  GCTTGA
                              |||||||||  ||||||
                              ACCGAGTCA  CGAATT
                                         ___
GAM675  FLJ13111 3' AGGCTGGACTGAGCCA     46936
                              TGGCTCAGTCCAGCTT
                              ||||||||||||||||
                              ACCGAGTCAGGTCGGA

GAM675  FLJ13111 3' AGGCTGGACTGAGCCA     46936
                              TGGCTCAGTCCAGCTT
                              ||||||||||||||||
                              ACCGAGTCAGGTCGGA

GAM675  FLJ13902 3' CAAGCTGGGCTGAGCCA    45039
                              TGGCTCAGTCCAGCTTG
                              |||||||||||||||||
                              ACCGAGTCGGGTCGAAC

GAM675  FLJ13902 3' CAAGCTGGGCTGAGCCA    45039
                              TGGCTCAGTCCAGCTTG
                              |||||||||||||||||
                              ACCGAGTCGGGTCGAAC

GAM675  FLJ14001 5' GCTTTCCTCGGCCTGAGCCA  45168        T _ CTT
                              TGGCTCAG CC AG  GAAAGC
                              ||||||||  ||  ||  ||||||
                              ACCGAGTC GG TC  CTTTCG
                                   C  C  ___
GAM675  FLJ14001 5' GCTTTCCTCGGCCTGAGCCA  45168        T _ CTT
                              TGGCTCAG CC AG  GAAAGC
                              ||||||||  ||  ||  ||||||
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                              ACCGAGTC GG TC   CTTTCG
                                  C  C  ___
GAM675  FLJ20170 5' CTTTCAAGCAGAAGTCA    34671      CAG  CA
                              TGGCT   TC  GCTTGAAAG
                              |||||   ||  |||||||||
                              ACTGA   AG  CGAACTTTC
                                 ___  A_
GAM675  FLJ20170 5' CTTTCAAGCAGAAGTCA    34671      CAG  CA
                              TGGCT   TC  GCTTGAAAG
                              |||||   ||  |||||||||
                              ACTGA   AG  CGAACTTTC
                                 ___  A_
GAM675  FLJ20208 3' CAGGCCTGAACTGAGCTA    34743        C  _
                              TGGCTCAGT CAG CTTG
                              |||||||||  |||  ||||
                              ATCGAGTCA GTC GGAC
                                   A   C
GAM675  FLJ20208 3' CAGGCCTGAACTGAGCTA    34743        C  _
                              TGGCTCAGT CAG CTTG
                              |||||||||  |||  ||||
                              ATCGAGTCA GTC GGAC
                                   A   C
GAM675  FLJ20533 3' TCAGTATTGAGCCA        35358        CCA  T
                              TGGCTCAGT   GCT GA
                              |||||||||   |||  ||
                              ACCGAGTTA   TGA CT
                                  ___   _
GAM675  FLJ20533 3' TCAGTATTGAGCCA        35358        CCA  T
                              TGGCTCAGT   GCT GA
                              |||||||||   |||  ||
                              ACCGAGTTA   TGA CT
                                  ___   _
GAM675  FLJ20752 5' GCTCCTTCAGGGCTGAGCCA  38779          AGCT  __
                              TGGCTCAGTCC   TGAA  AGC
                              ||||||||||    ||||  |||
                              ACCGAGTCGGG   ACTT  TCG
                                   ____   CC
GAM675  FLJ20752 5' GCTCCTTCAGGGCTGAGCCA  38779          AGCT  __
                              TGGCTCAGTCC   TGAA  AGC
                              ||||||||||    ||||  |||
                              ACCGAGTCGGG   ACTT  TCG
                                   ____   CC
GAM675  FLJ22529 3' GCTCCTGGGGCTGAGCCA    45574          ____
                              TGGCTCAGTCC   AGC
                              ||||||||||    |||
                              ACCGAGTCGGG   TCG
                                    GTCC
GAM675  FLJ22529 3' GCTCCTGGGGCTGAGCCA    45574          ____
                              TGGCTCAGTCC   AGC
                              ||||||||||    |||
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                                ACCGAGTCGGG   TCG
                                      GTCC
GAM675  FLJ23093  3'  GCTCCCAAGGTGGCTGAGC   44978      T  G   AA
                                GCTCAG CCA CTTG  AGC
                                |||||| ||| ||||  |||
                                CGAGTC GGT GAAC  TCG
                                   _  G   CC
GAM675  FLJ23093  3'  GCTCCCAAGGTGGCTGAGC   44978      T  G   AA
                                GCTCAG CCA CTTG  AGC
                                |||||| ||| ||||  |||
                                CGAGTC GGT GAAC  TCG
                                   _  G   CC
GAM675  GREB1     3'  CTCCCAAGTTCTGGGCCA    27870      TCC    AA
                                TGGCTCAG  AGCTTG AG
                                ||||||||  ||||||  ||
                                ACCGGGTC  TTGAAC  TC
                                    ___     CC
GAM675  GREB1     3'  CTCCCAAGTTCTGGGCCA    27870      TCC    AA
                                TGGCTCAG  AGCTTG AG
                                ||||||||  ||||||  ||
                                ACCGGGTC  TTGAAC  TC
                                    ___     CC
GAM675  HS322B1A  3'  CTTAGCAATCTGAGCCA     31111      TCCA  TGA
                                TGGCTCAG   GCT  AAG
                                ||||||||   |||  |||
                                ACCGAGTC   CGA  TTC
                                    TAA_  ___
GAM675  HS322B1A  3'  CTTAGCAATCTGAGCCA     31111      TCCA  TGA
                                TGGCTCAG   GCT  AAG
                                ||||||||   |||  |||
                                ACCGAGTC   CGA  TTC
                                    TAA_  ___
GAM675  HSPC065   3'  GCTCTCGCAGTTTGGACTGAGA 26309    G      _ _  A
          CA                      TG CTCAGTCCAG CT TGA AGC
                                || |||||||||| || ||| |||
                                AC GAGTCAGGTT GA GCT TCG
                                 A        T  C  C
GAM675  HSPC065   3'  GCTCTCGCAGTTTGGACTGAGA 26309    G      _ _  A
          CA                      TG CTCAGTCCAG CT TGA AGC
                                || |||||||||| || ||| |||
                                AC GAGTCAGGTT GA GCT TCG
                                 A        T  C  C
GAM675  ITPK1     3'  CAAGCACTGAGCCA       26408        CCA
                                TGGCTCAGT  GCTTG
                                |||||||||  |||||
                                ACCGAGTCA  CGAAC
                                    ___
GAM675  ITPK1     3'  CAAGCACTGAGCCA       26408        CCA
                                TGGCTCAGT  GCTTG
                                |||||||||  |||||
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                                ACCGAGTCA  CGAAC
                                    ___
GAM675  KIAA0258 3' GCTAGAGGCTGGGCTGAGCCA 28819          GAA
                                TGGCTCAGTCCAGCTT  AGC
                                |||||||||||||||  |||
                                ACCGAGTCGGGTCGGA  TCG
                                      GA_
GAM675  KIAA0258 3' GCTAGAGGCTGGGCTGAGCCA 28819          GAA
                                TGGCTCAGTCCAGCTT  AGC
                                |||||||||||||||  |||
                                ACCGAGTCGGGTCGGA  TCG
                                      GA_
GAM675  KIAA0285 3' AAGCTGGCCTGAGCCA     29009       T
                                TGGCTCAG CCAGCTT
                                |||||||| |||||||
                                ACCGAGTC GGTCGAA
                                     C
GAM675  KIAA0285 3' AAGCTGGCCTGAGCCA     29009       T
                                TGGCTCAG CCAGCTT
                                |||||||| |||||||
                                ACCGAGTC GGTCGAA
                                     C
GAM675  KIAA0450 3' TCCCGCAGACTGAGCCA    27649        CA  TT
                                TGGCTCAGTC  GC  GA
                                ||||||||||  ||  ||
                                ACCGAGTCAG  CG  CT
                                      A_  CC
GAM675  KIAA0450 3' TCCCGCAGACTGAGCCA    27649        CA  TT
                                TGGCTCAGTC  GC  GA
                                ||||||||||  ||  ||
                                ACCGAGTCAG  CG  CT
                                      A_  CC
GAM675  KIAA0523 3' TTCAGCCTGAGCCA       67745       TCCA  T
                                TGGCTCAG   GCT GAA
                                ||||||||   ||| |||
                                ACCGAGTC   CGA CTT
                                    _____  _
GAM675  KIAA0523 3' TTCAGCCTGAGCCA       67745       TCCA  T
                                TGGCTCAG   GCT GAA
                                ||||||||   ||| |||
                                ACCGAGTC   CGA CTT
                                    _____  _
GAM675  KIAA0669 5' CGAGCTGGACTGACCA     28787    C
                                TGG TCAGTCCAGCTTG
                                ||| ||||||||||||
                                ACC AGTCAGGTCGAGC
                                  _
GAM675  KIAA0669 5' CGAGCTGGACTGACCA     28787    C
                                TGG TCAGTCCAGCTTG
                                ||| ||||||||||||
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                                ACC AGTCAGGTCGAGC
                                  _
GAM675  KIAA1024 3' TCGAGGCTGGACCAAACCA   69066    CTCA      _
                                TGG   GTCCAGCTT GA
                                |||   ||||||||| ||
                                ACC   CAGGTCGGA CT
                                  AAAC       G
GAM675  KIAA1024 3' TCGAGGCTGGACCAAACCA   69066    CTCA      _
                                TGG   GTCCAGCTT GA
                                |||   ||||||||| ||
                                ACC   CAGGTCGGA CT
                                  AAAC       G
GAM675  KIAA1032 3' GGCTGGAGCTGAGCCA      66158      _
                                TGGCTCAG TCCAGCT
                                |||||||| |||||||
                                ACCGAGTC AGGTCGG
                                     G
GAM675  KIAA1032 3' GGCTGGAGCTGAGCCA      66158      _
                                TGGCTCAG TCCAGCT
                                |||||||| |||||||
                                ACCGAGTC AGGTCGG
                                     G
GAM675  KIAA1068 3' CAAGCCTATGCCCTGAGCCA  31028      TC ___
                                TGGCTCAG  CA  GCTTG
                                ||||||||  ||  |||||
                                ACCGAGTC  GT  CGAAC
                                     CC  ATC
GAM675  KIAA1068 3' CAAGCCTATGCCCTGAGCCA  31028      TC ___
                                TGGCTCAG  CA  GCTTG
                                ||||||||  ||  |||||
                                ACCGAGTC  GT  CGAAC
                                     CC  ATC
GAM675  KIAA1163 5' TCCCTGCTGCTGAGCCA     78904      TC  TT_
                                TGGCTCAG  CAGC  GA
                                ||||||||  ||||  ||
                                ACCGAGTC  GTCG  CT
                                     __   TCC
GAM675  KIAA1163 5' TCCCTGCTGCTGAGCCA     78904      TC  TT_
                                TGGCTCAG  CAGC  GA
                                ||||||||  ||||  ||
                                ACCGAGTC  GTCG  CT
                                     __   TCC
GAM675  KIAA1189 3' GCTTTCAAACTGAATTAAACC 72044   CTC  C  C
                                GG  AGT CAG TTGAAAGC
                                ||  ||| ||| ||||||||
                                CC  TTA GTC AACTTTCG
                                 AAA  A  A
GAM675  KIAA1189 3' GCTTTCAAACTGAATTAAACC 72044   CTC  C  C
                                GG  AGT CAG TTGAAAGC
                                ||  ||| ||| ||||||||
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                                CC   TTA GTC AACTTTCG
                                 AAA  A  A
GAM675  KIAA1246 3'  TCAAATGCCGGACTGAGCC   92055        A __
                                GGCTCAGTCC GC  TTGA
                                |||||||||| ||  ||||
                                CCGAGTCAGG CG  AACT
                                     C  TA
GAM675  KIAA1246 3'  TCAAATGCCGGACTGAGCC   92055        A __
                                GGCTCAGTCC GC  TTGA
                                |||||||||| ||  ||||
                                CCGAGTCAGG CG  AACT
                                     C  TA
GAM675  KIAA1533 5'  CAAGCCGGCCCCCACCTGAGCC 73755       T_____ A
           A                     TGGCTCAG      CC GCTTG
                                |||||||       || |||||
                                ACCGAGTC      GG CGAAC
                                     CACCCCC  C
GAM675  KIAA1533 5'  CAAGCCGGCCCCCACCTGAGCC 73755       T_____ A
           A                     TGGCTCAG      CC GCTTG
                                |||||||       || |||||
                                ACCGAGTC      GG CGAAC
                                     CACCCCC  C
GAM675  KIAA1602 3'  TTCAGGCTGAGCCA       64636        CAGCT
                                TGGCTCAGTC    TGAA
                                ||||||||||    ||||
                                ACCGAGTCGG    ACTT
                                      _____
GAM675  KIAA1602 3'  TTCAGGCTGAGCCA       64636        CAGCT
                                TGGCTCAGTC    TGAA
                                ||||||||||    ||||
                                ACCGAGTCGG    ACTT
                                      _____
GAM675  KIF13B   3'  TTCGTGGTGGCTGAGCCA    30915        T  GCT
                                TGGCTCAG CCA  TGAA
                                |||||||| |||  ||||
                                ACCGAGTC GGT  GCTT
                                     _  GGT
GAM675  KIF13B   3'  TTCGTGGTGGCTGAGCCA    82828        T  GCT
                                TGGCTCAG CCA  TGAA
                                |||||||| |||  ||||
                                ACCGAGTC GGT  GCTT
                                     _  GGT
GAM675  KIF13B   3'  TTCGTGGTGGCTGAGCCA    82828        T  GCT
                                TGGCTCAG CCA  TGAA
                                |||||||| |||  ||||
                                ACCGAGTC GGT  GCTT
                                     _  GGT
GAM675  KIF13B   3'  TTCGTGGTGGCTGAGCCA    30915        T  GCT
                                TGGCTCAG CCA  TGAA
                                |||||||| |||  ||||
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                                ACCGAGTC GGT   GCTT
                                    _  GGT
GAM675  KIR3DS1  3' CTTCCAAATGCTGAGCC    27211       CCAGC   A
                                GGCTCAGT    TTG AAG
                                ||||||||    ||| |||
                                CCGAGTCG    AAC TTC
                                    TA___   C
GAM675  KIR3DS1  3' CTTCCAAATGCTGAGCC    27211       CCAGC   A
                                GGCTCAGT    TTG AAG
                                ||||||||    ||| |||
                                CCGAGTCG    AAC TTC
                                    TA___   C
GAM675  KRTAP1-3 3' CTTGAAAGCACCTTGAAACTGA 48238      C_ A_______  TGAA
           GCC                  GCTCAGT  C      GCT   AG
                                |||||||  |      |||   ||
                                CGAGTCA  G      CGA   TC
                                    AA TTCCAIII  AAGT
GAM675  KRTAP1-3 3' CTTGAAAGCACCTTGAAACTGA 48238      C_ A_______  TGAA
           GCC                  GCTCAGT  C      GCT   AG
                                |||||||  |      |||   ||
                                CGAGTCA  G      CGA   TC
                                    AA TTCCAIII  AAGT
GAM675  MDN1     3' GCTTTCAAGCTGGACTGAGCCA 62680
                                TGGCTCAGTCCAGCTTGAAAGC
                                |||||||||||||||||||||
                                ACCGAGTCAGGTCGAACTTTCG

GAM675  MDN1     3' GCTTTCAAGCTGGACTGAGCCA 62680
                                TGGCTCAGTCCAGCTTGAAAGC
                                |||||||||||||||||||||
                                ACCGAGTCAGGTCGAACTTTCG

GAM675  MGC12679 3' GCTTCCAAGCTGGCCGGCC   51206     CA T      A
                                GGCT  G CCAGCTTG AAGC
                                ||||  | ||||||| ||||
                                CCGG  C GGTCGAAC TTCG
                                  C_ _      C
GAM675  MGC12679 3' GCTTCCAAGCTGGCCGGCC   51206     CA T      A
                                GGCT  G CCAGCTTG AAGC
                                ||||  | ||||||| ||||
                                CCGG  C GGTCGAAC TTCG
                                  C_ _      C
GAM675  MGC16175 3' AAGCCGAGACTGAGCCA     51299       CA_
                                TGGCTCAGTC   GCTT
                                ||||||||||   ||||
                                ACCGAGTCAG   CGAA
                                      AGC
GAM675  MGC16175 3' AAGCCGAGACTGAGCCA     51299       CA_
                                TGGCTCAGTC   GCTT
                                ||||||||||   ||||
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                                ACCGAGTCAG  CGAA
                                      AGC
GAM675  MGC2306  3' CAGGCTGGGCTGAGCCA    50957
                                TGGCTCAGTCCAGCTTG
                                ||||||||||||||||
                                ACCGAGTCGGGTCGGAC

GAM675  MGC2306  3' CAGGCTGGGCTGAGCCA    50957
                                TGGCTCAGTCCAGCTTG
                                ||||||||||||||||
                                ACCGAGTCGGGTCGGAC

GAM675  MGC2721  5' CTTGAAAGCACACCAAAACTGA 51219      CCA_________  TGAA
           GCCA                 GCTCAGT        GCT   AG
                                |||||||        |||   ||
                                CGAGTCA        CGA   TC
                                    AAACCACAIII  AAGT
GAM675  MGC2721  5' CTTGAAAGCACACCAAAACTGA 51219      CCA_________  TGAA
           GCCA                 GCTCAGT        GCT   AG
                                |||||||        |||   ||
                                CGAGTCA        CGA   TC
                                    AAACCACAIII  AAGT
GAM675  MGC4796  3' GCTGTCTCTGGACTGAGC   61492       CTT  A
                                GCTCAGTCCAG  GA AGC
                                ||||||||||  || |||
                                CGAGTCAGGTC  CT TCG
                                      T__  G
GAM675  MGC4796  3' GCTGTCTCTGGACTGAGC   61492       CTT  A
                                GCTCAGTCCAG  GA AGC
                                ||||||||||  || |||
                                CGAGTCAGGTC  CT TCG
                                      T__  G
GAM675  MIG2     3' TCTAATGCCTGGACTGGCCA  72426    T     _ TT__
                                TGGC CAGTCCAG C   GA
                                |||| |||||||| |   ||
                                ACCG GTCAGGTC G   CT
                                  _      C TAAT
GAM675  MIG2     3' TCTAATGCCTGGACTGGCCA  72426    T     _ TT__
                                TGGC CAGTCCAG C   GA
                                |||| |||||||| |   ||
                                ACCG GTCAGGTC G   CT
                                  _      C TAAT
GAM675  MKP-7    3' TTAGCGCTGAGACTGAGCCA  66424       _  _
                                TGGCTCAGTC CAGC TTGA
                                |||||||||| |||| ||||
                                ACCGAGTCAG GTCG GATT
                                      A   C
GAM675  MKP-7    3' TTAGCGCTGAGACTGAGCCA  66424       _  _
                                TGGCTCAGTC CAGC TTGA
                                |||||||||| |||| ||||
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                                ACCGAGTCAG GTCG GATT
                                     A   C
GAM675  N4BP3   3'  GCTCATCCAGGCTGGACAAACC 66266    CTCA       AA__
          A                   TGG   GTCCAGCTTG   AGC
                              |||   ||||||||||   |||
                              ACC   CAGGTCGGAC   TCG
                                AAA_       CTAC
GAM675  N4BP3   3'  GCTCATCCAGGCTGGACAAACC 66266    CTCA       AA__
          A                   TGG   GTCCAGCTTG   AGC
                              |||   ||||||||||   |||
                              ACC   CAGGTCGGAC   TCG
                                AAA_       CTAC
GAM675  NCKX3   3'  TAACTGGCCTGAGCCA     40355       T   C
                              TGGCTCAG CCAG TTG
                              |||||||| |||| |||
                              ACCGAGTC GGTC AAT
                                   C   _
GAM675  NCKX3   3'  TAACTGGCCTGAGCCA     40355       T   C
                              TGGCTCAG CCAG TTG
                              |||||||| |||| |||
                              ACCGAGTC GGTC AAT
                                   C   _
GAM675  NPD002  3'  CTTCTGAACTGAGCC      25914       C  CTTGA
                              GGCTCAGT CAG    AAG
                              |||||||| |||    |||
                              CCGAGTCA GTC    TTC
                                   A  _____
GAM675  NPD002  3'  CTTCTGAACTGAGCC      25914       C  CTTGA
                              GGCTCAGT CAG    AAG
                              |||||||| |||    |||
                              CCGAGTCA GTC    TTC
                                   A  _____
GAM675  NR6A1   3'  TTCAGCAGTGGACTGGCCA   52876     T    __  T
                              TGGC CAGTCCA  GCT GAA
                              |||| |||||||  ||| |||
                              ACCG GTCAGGT  CGA CTT
                                _      GA  _
GAM675  NR6A1   3'  TTCAGCAGTGGACTGGCCA   52888     T    __  T
                              TGGC CAGTCCA  GCT GAA
                              |||| |||||||  ||| |||
                              ACCG GTCAGGT  CGA CTT
                                _      GA  _
GAM675  NR6A1   3'  TTCAGCAGTGGACTGGCCA   52888     T    __  T
                              TGGC CAGTCCA  GCT GAA
                              |||| |||||||  ||| |||
                              ACCG GTCAGGT  CGA CTT
                                _      GA  _
GAM675  NR6A1   3'  TTCAGCAGTGGACTGGCCA   7651      T    __  T
                              TGGC CAGTCCA  GCT GAA
                              |||| |||||||  ||| |||
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                                ACCG GTCAGGT  CGA CTT
                                  _      GA  _
GAM675  NR6A1    3' TTCAGCAGTGGACTGGCCA   52876     T      __  T
                                TGGC CAGTCCA  GCT GAA
                                |||| |||||||  ||| |||
                                ACCG GTCAGGT  CGA CTT
                                  _      GA  _
GAM675  NR6A1    3' TTCAGCAGTGGACTGGCCA   7651      T      __  T
                                TGGC CAGTCCA  GCT GAA
                                |||| |||||||  ||| |||
                                ACCG GTCAGGT  CGA CTT
                                  _      GA  _
GAM675  NUDEL    3' GCTCCGGGGTGGACTGAACA  47969    GC      G   AA
                                TG  TCAGTCCA CTTG  AGC
                                ||  |||||||| ||||  |||
                                AC  AGTCAGGT GGGC  TCG
                                 A_      G   C_
GAM675  NUDEL    3' GCTCCGGGGTGGACTGAACA  47969    GC      G   AA
                                TG  TCAGTCCA CTTG  AGC
                                ||  |||||||| ||||  |||
                                AC  AGTCAGGT GGGC  TCG
                                 A_      G   C_
GAM675  PIP5K2B  3' CCTCAGAACTGAGCCA     13069        CCAGC   AA
                                TGGCTCAGT    TTGA  G
                                |||||||||    ||||  |
                                ACCGAGTCA    GACT  C
                                     A____   CC
GAM675  PIP5K2B  3' CCTCAGAACTGAGCCA     13069        CCAGC   AA
                                TGGCTCAGT    TTGA  G
                                |||||||||    ||||  |
                                ACCGAGTCA    GACT  C
                                     A____   CC
GAM675  PLA2G3   5' GCTTTGTCTGACTGGACTGGGC 31685          CTT  __
          CA                      TGGCTCAGTCCAG   GA  AAGC
                                |||||||||||||   ||  ||||
                                ACCGGGTCAGGTC   CT  TTCG
                                       AGT  GT
GAM675  PLA2G3   5' GCTTTGTCTGACTGGACTGGGC 31685          CTT  __
          CA                      TGGCTCAGTCCAG   GA  AAGC
                                |||||||||||||   ||  ||||
                                ACCGGGTCAGGTC   CT  TTCG
                                       AGT  GT
GAM675  PSKH1    3' GCTTTCCCAGAGGCCTGAGCCA 68241        T  AGCTT
                                TGGCTCAG CC    GAAAGC
                                ||||||||  ||    ||||||
                                ACCGAGTC GG    CTTTCG
                                     C  AGACC
GAM675  PSKH1    3' GCTTTCCCAGAGGCCTGAGCCA 68241        T  AGCTT
                                TGGCTCAG CC    GAAAGC
                                ||||||||  ||    ||||||
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                                ACCGAGTC GG    CTTTCG
                                    C  AGACC
GAM675  RAB4B   3'  GCTTTGGGGCAAGACTGAGCCA 32377        CA   G
                                TGGCTCAGTC  GCTT AAAGC
                                ||||||||||  |||| |||||
                                ACCGAGTCAG  CGGG TTTCG
                                     AA   G
GAM675  RAB4B   3'  GCTTTGGGGCAAGACTGAGCCA 32377        CA   G
                                TGGCTCAGTC  GCTT AAAGC
                                ||||||||||  |||| |||||
                                ACCGAGTCAG  CGGG TTTCG
                                     AA   G
GAM675  RAI16   5'  GCTTTCAAACTCCCGCAAAGCC 42758     CA  CC_  C
                                GGCT  GT   AG TTGAAAGC
                                ||||  ||   || ||||||||
                                CCGA  CG   TC AACTTTCG
                                  AA  CCC  A
GAM675  RAI16   5'  GCTTTCAAACTCCCGCAAAGCC 42758     CA  CC_  C
                                GGCT  GT   AG TTGAAAGC
                                ||||  ||   || ||||||||
                                CCGA  CG   TC AACTTTCG
                                  AA  CCC  A
GAM675  SELB    3'  CAAGCTTGGTGCTGAGCC    61913        _   _
                                GGCTCAGT CCA GCTTG
                                |||||||| ||| |||||
                                CCGAGTCG GGT CGAAC
                                     T   T
GAM675  SELB    3'  CAAGCTTGGTGCTGAGCC    61913        _   _
                                GGCTCAGT CCA GCTTG
                                |||||||| ||| |||||
                                CCGAGTCG GGT CGAAC
                                     T   T
GAM675  SEMA4B  3'  GCTCCTTATGTAAACTGAGCC  69037       CCA  T   A_
                                GGCTCAGT   GC TGA  AGC
                                ||||||||   || |||  |||
                                CCGAGTCA   TG ATT  TCG
                                     AA_  T   CC
GAM675  SEMA4B  3'  GCTCCTTATGTAAACTGAGCC  69037       CCA  T   A_
                                GGCTCAGT   GC TGA  AGC
                                ||||||||   || |||  |||
                                CCGAGTCA   TG ATT  TCG
                                     AA_  T   CC
GAM675  TOR2A   3'  GCTCCTCCCCGCACTGAGCCA  55314       CCA  TT_  A_
                                TGGCTCAGT   GC   GA  AGC
                                |||||||||   ||   ||  |||
                                ACCGAGTCA   CG   CT  TCG
                                     ___  CCC  CC
GAM675  TOR2A   3'  GCTCCTCCCCGCACTGAGCCA  55314       CCA  TT_  A_
                                TGGCTCAGT   GC   GA  AGC
                                |||||||||   ||   ||  |||
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                                ACCGAGTCA  CG  CT  TCG
                                    ___  CCC  CC
GAM675  LOC114971 3'  GCTGCAGACTGAGCCA     73149          __
                                TGGCTCAGTC  CAGC
                                ||||||||||  ||||
                                ACCGAGTCAG  GTCG
                                     AC
GAM675  LOC114971 3'  GCTGCAGACTGAGCCA     73149          __
                                TGGCTCAGTC  CAGC
                                ||||||||||  ||||
                                ACCGAGTCAG  GTCG
                                     AC
GAM675  LOC116113 3'  CAACCTGAGACAGAACCA    92211     C  A  _  C
                                TGG TC GTC CAG TTG
                                ||| || ||| ||| |||
                                ACC AG CAG GTC AAC
                                  A  A   A   C
GAM675  LOC116113 3'  CAACCTGAGACAGAACCA    92211     C  A  _  C
                                TGG TC GTC CAG TTG
                                ||| || ||| ||| |||
                                ACC AG CAG GTC AAC
                                  A  A   A   C
GAM675  LOC116411 5'  TAGGCTGGACTGACCA      73871     C
                                TGG TCAGTCCAGCTTG
                                ||| ||||||||||||
                                ACC AGTCAGGTCGGAT
                                  _
GAM675  LOC116411 5'  TAGGCTGGACTGACCA      73871     C
                                TGG TCAGTCCAGCTTG
                                ||| ||||||||||||
                                ACC AGTCAGGTCGGAT
                                  _
GAM675  LOC118987 3'  GCTTTCAAACCACCTGTGCCA  73957     T  TCCAGC
                                TGGC CAG     TTGAAAGC
                                |||| |||     ||||||||
                                ACCG GTC     AACTTTCG
                                  T  CACCA_
GAM675  LOC118987 3'  GCTTTCAAACCACCTGTGCCA  73957     T  TCCAGC
                                TGGC CAG     TTGAAAGC
                                |||| |||     ||||||||
                                ACCG GTC     AACTTTCG
                                  T  CACCA_
GAM675  LOC126917 3'  GCCTTCTCCCTTAAGCTGAGCC 74587        CC_  CTT  A
          A                      TGGCTCAGT  AG  GAA GC
                                 |||||||||  ||  ||| ||
                                 ACCGAGTCG  TC  CTT CG
                                      AAT  CCT  C
GAM675  LOC126917 3'  GCCTTCTCCCTTAAGCTGAGCC 74587        CC_  CTT  A
          A                      TGGCTCAGT  AG  GAA GC
                                 |||||||||  ||  ||| ||
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                                ACCGAGTCG  TC  CTT CG
                                     AAT  CCT  C
GAM675  LOC127281 3'  GCTTTCAGTTACACCAAGCTA  74647     CA  CC   T
                                TGGCT  GT  AGCT GAAAGC
                                |||||  ||  |||| ||||||
                                ATCGA  CA  TTGA CTTTCG
                                   AC  CA   _
GAM675  LOC127281 3'  GCTTTCAGTTACACCAAGCTA  74647     CA  CC   T
                                TGGCT  GT  AGCT GAAAGC
                                |||||  ||  |||| ||||||
                                ATCGA  CA  TTGA CTTTCG
                                   AC  CA   _
GAM675  LOC143310 5'  CTTGAAAGCACTTTTGGCCTGA 76533      T  A________  TGAA
           GCCA                  GCTCAG CC       GCT   AG
                                |||||| ||       |||   ||
                                CGAGTC GG       CGA   TC
                                   C  TTTTCAIII  AAGT
GAM675  LOC143310 5'  CTTGAAAGCACTTTTGGCCTGA 76533      T  A________  TGAA
           GCCA                  GCTCAG CC       GCT   AG
                                |||||| ||       |||   ||
                                CGAGTC GG       CGA   TC
                                   C  TTTTCAIII  AAGT
GAM675  LOC145195 3'  TCAACTCTGAGCCA       83274        TCC  C
                                TGGCTCAG   AG TTGA
                                ||||||||   || ||||
                                ACCGAGTC   TC AACT
                                    ___  _
GAM675  LOC145195 3'  TCAACTCTGAGCCA       83274        TCC  C
                                TGGCTCAG   AG TTGA
                                ||||||||   || ||||
                                ACCGAGTC   TC AACT
                                    ___  _
GAM675  LOC145371 3'  CTCCCAGGCGGAGGACTGAGCC 77152         A__   AA
                                GGCTCAGTCC  GCTTG  AG
                                ||||||||||  |||||  ||
                                CCGAGTCAGG  CGGAC  TC
                                     AGG   CC
GAM675  LOC145371 3'  CTCCCAGGCGGAGGACTGAGCC 77152         A__   AA
                                GGCTCAGTCC  GCTTG  AG
                                ||||||||||  |||||  ||
                                CCGAGTCAGG  CGGAC  TC
                                     AGG   CC
GAM675  LOC146823 3'  GCCTTCAAGTTTCCTAGCCTGA 83800       TCC____      A
           GCCA                  TGGCTCAG      AGCTTGAA GC
                                ||||||||      |||||||| ||
                                ACCGAGTC      TTGAACTT CG
                                   CGATCCT       C
GAM675  LOC146823 3'  GCCTTCAAGTTTCCTAGCCTGA 83800       TCC____      A
           GCCA                  TGGCTCAG      AGCTTGAA GC
                                ||||||||      |||||||| ||
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                                ACCGAGTC      TTGAACTT CG
                                     CGATCCT       C
GAM675  LOC148823 3'  AGGCTGAACTGAGCCA      59205         C
                                TGGCTCAGT CAGCTT
                                ||||||||| ||||||
                                ACCGAGTCA GTCGGA
                                     A
GAM675  LOC148823 3'  AGGCTGAACTGAGCCA      59205         C
                                TGGCTCAGT CAGCTT
                                ||||||||| ||||||
                                ACCGAGTCA GTCGGA
                                     A
GAM675  LOC148936 3'  TTTGGGACTTGGACTGAGCCA  84305           _ _  TG
                                TGGCTCAGTCCA G CT  AA
                                |||||||||||| | ||  ||
                                ACCGAGTCAGGT C GG  TT
                                      T A  GT
GAM675  LOC148936 3'  TTTGGGACTTGGACTGAGCCA  84305           _ _  TG
                                TGGCTCAGTCCA G CT  AA
                                |||||||||||| | ||  ||
                                ACCGAGTCAGGT C GG  TT
                                      T A  GT
GAM675  LOC148938 3'  GCTTTGGGACTTGGACTGAGCC 84275           _ CT G
          A                      TGGCTCAGTCCA G  T AAAGC
                                ||||||||||||  |  | |||||
                                ACCGAGTCAGGT C  G TTTCG
                                      T AG G
GAM675  LOC148938 3'  GCTTTGGGACTTGGACTGAGCC 84275           _ CT G
          A                      TGGCTCAGTCCA G  T AAAGC
                                ||||||||||||  |  | |||||
                                ACCGAGTCAGGT C  G TTTCG
                                      T AG G
GAM675  LOC149194 3'  CTTTCAAGGCACTGAACA    79226    GC    CCAG
                                TG  TCAGT    CTTGAAAG
                                ||  |||||    ||||||||
                                AC  AGTCA    GAACTTTC
                                 A_     CG__
GAM675  LOC149194 3'  CTTTCAAGGCACTGAACA    79226    GC    CCAG
                                TG  TCAGT    CTTGAAAG
                                ||  |||||    ||||||||
                                AC  AGTCA    GAACTTTC
                                 A_     CG__
GAM675  LOC149271 5'  TTCAAGCTTTCAGCC       79248      C  TCC
                                GGCT AG   AGCTTGAA
                                ||||  ||   ||||||||
                                CCGA TT   TCGAACTT
                                  C  ___
GAM675  LOC149271 5'  TTCAAGCTTTCAGCC       79248      C  TCC
                                GGCT AG   AGCTTGAA
                                ||||  ||   ||||||||
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                                CCGA TT   TCGAACTT
                                  C ___
GAM675  LOC149577 3'  CTTTCTCTAGACTGAGC     84513        C  CTT
                                GCTCAGTC AG   GAAAG
                                |||||||| ||   |||||
                                CGAGTCAG TC   CTTTC
                                    A  T__
GAM675  LOC149577 3'  CTTTCTCTAGACTGAGC     84513        C  CTT
                                GCTCAGTC AG   GAAAG
                                |||||||| ||   |||||
                                CGAGTCAG TC   CTTTC
                                    A  T__
GAM675  LOC149951 3'  CTTGAAAGCACTTCCTAACTGA 84804        CCA_________  TGAA
          GCCA                    GCTCAGT        GCT    AG
                                |||||||         |||    ||
                                CGAGTCA         CGA    TC
                                    ATCCTTCAIII   AAGT
GAM675  LOC149951 3'  CTTGAAAGCACTTCCTAACTGA 84804        CCA_________  TGAA
          GCCA                    GCTCAGT        GCT    AG
                                |||||||         |||    ||
                                CGAGTCA         CGA    TC
                                    ATCCTTCAIII   AAGT
GAM675  LOC150113 5'  TGAAAGCACTTTGGACTGGCCA 87216      T     A________  TGAA
                                TGGC CAGTCC       GCT    A
                                |||| ||||||       |||    |
                                ACCG GTCAGG       CGA    T
                                  _     TTTCAIII   AAGT
GAM675  LOC150113 5'  TGAAAGCACTTTGGACTGGCCA 87216      T     A________  TGAA
                                TGGC CAGTCC       GCT    A
                                |||| ||||||       |||    |
                                ACCG GTCAGG       CGA    T
                                  _     TTTCAIII   AAGT
GAM675  LOC150819 3'  CTTGAAAGCACTTATCAACTGA 85119        CCA_________  TGAA
          GCCA                    GCTCAGT        GCT    AG
                                |||||||         |||    ||
                                CGAGTCA         CGA    TC
                                    ACTATTCAIII   AAGT
GAM675  LOC150819 3'  CTTGAAAGCACTTATCAACTGA 85119        CCA_________  TGAA
          GCCA                    GCTCAGT        GCT    AG
                                |||||||         |||    ||
                                CGAGTCA         CGA    TC
                                    ACTATTCAIII   AAGT
GAM675  LOC151571 5'  GCCTTCAAGCTTCAAGCC    85445     CAGTCC       A
                                GGCT     AGCTTGAA GC
                                ||||     |||||||| ||
                                CCGA     TCGAACTT CG
                                  ACT___       C
GAM675  LOC151571 5'  GCCTTCAAGCTTCAAGCC    85445     CAGTCC       A
                                GGCT     AGCTTGAA GC
                                ||||     |||||||| ||
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                                CCGA     TCGAACTT CG
                                  ACT___       C
GAM675  LOC155060 5'  CGAGCCAGGCTGAGCCA     86329          CA
                                TGGCTCAGTC  GCTTG
                                ||||||||||  |||||
                                ACCGAGTCGG  CGAGC
                                      AC
GAM675  LOC155060 5'  CGAGCCAGGCTGAGCCA     86329          CA
                                TGGCTCAGTC  GCTTG
                                ||||||||||  |||||
                                ACCGAGTCGG  CGAGC
                                      AC
GAM675  LOC157292 3'  CTTTCAAGTTAAGGCCA     86414       CAGTCC
                                TGGCT     AGCTTGAAAG
                                |||||     ||||||||||
                                ACCGG     TTGAACTTTC
                                  AA____
GAM675  LOC157292 3'  CTTTCAAGTTAAGGCCA     86414       CAGTCC
                                TGGCT     AGCTTGAAAG
                                |||||     ||||||||||
                                ACCGG     TTGAACTTTC
                                  AA____
GAM675  LOC158333 3'  TGAAAGCGCATTGGACTGAGCC 86781           A________   TGAA
          A                      TGGCTCAGTCC       GCT    A
                                 ||||||||||        |||    |
                                 ACCGAGTCAGG       CGA    T
                                       TTACGIII   AAGT
GAM675  LOC158333 3'  TGAAAGCGCATTGGACTGAGCC 86781           A________   TGAA
          A                      TGGCTCAGTCC       GCT    A
                                 ||||||||||        |||    |
                                 ACCGAGTCAGG       CGA    T
                                       TTACGIII   AAGT
GAM675  LOC168448 3'  GCTCTCAAGCTGAATGAC     82699     ___       A
                                GTC   CAGCTTGA AGC
                                |||   |||||||| |||
                                CAG   GTCGAACT TCG
                                  TAA       C
GAM675  LOC168448 3'  GCTCTCAAGCTGAATGAC     82699     ___       A
                                GTC   CAGCTTGA AGC
                                |||   |||||||| |||
                                CAG   GTCGAACT TCG
                                  TAA       C
GAM675  LOC170396 3'  CTTCAAAACTGAGTCA      82843         CCAGC     A
                                TGGCTCAGT     TTGAA G
                                |||||||||     ||||| |
                                ACTGAGTCA     AACTT C
                                      A____     C
GAM675  LOC170396 3'  CTTCAAAACTGAGTCA      82843         CCAGC     A
                                TGGCTCAGT     TTGAA G
                                |||||||||     ||||| |
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                                ACTGAGTCA    AACTT C
                                     A____    C
GAM675  LOC196955 5' GAGCTAGCTGAGCCA      77378       CC
                                TGGCTCAGT  AGCTT
                                |||||||||  |||||
                                ACCGAGTCG  TCGAG
                                     A_
GAM675  LOC196955 5' GAGCTAGCTGAGCCA      77378       CC
                                TGGCTCAGT  AGCTT
                                |||||||||  |||||
                                ACCGAGTCG  TCGAG
                                     A_
GAM675  LOC200298 3' GCTGGAAGCTGGACTGAGACA 89975   G         GAA
                                TG CTCAGTCCAGCTT   AGC
                                || ||||||||||||   |||
                                AC GAGTCAGGTCGAA   TCG
                                 A          GG_
GAM675  LOC200298 3' GCTGGAAGCTGGACTGAGACA 89975   G         GAA
                                TG CTCAGTCCAGCTT   AGC
                                || ||||||||||||   |||
                                AC GAGTCAGGTCGAA   TCG
                                 A          GG_
GAM675  LOC203052 3' TAAGGTGGGCTGAGCCA     90459         G
                                TGGCTCAGTCCA CTTG
                                |||||||||||| ||||
                                ACCGAGTCGGGT GAAT
                                      G
GAM675  LOC203052 3' TAAGGTGGGCTGAGCCA     90459         G
                                TGGCTCAGTCCA CTTG
                                |||||||||||| ||||
                                ACCGAGTCGGGT GAAT
                                      G
GAM675  LOC221486 3' GCTTCCCGGGATAAACTGAGCC 91012       CCAG   A_
                                GGCTCAGT   CTTG  AAGC
                                ||||||||   ||||  ||||
                                CCGAGTCA   GGGC  TTCG
                                     AATA   CC
GAM675  LOC221486 3' GCTTCCCGGGATAAACTGAGCC 91012       CCAG   A_
                                GGCTCAGT   CTTG  AAGC
                                ||||||||   ||||  ||||
                                CCGAGTCA   GGGC  TTCG
                                     AATA   CC
GAM675  LOC221490 5' GCTAGATCTAGGCTGAGCCA  93663        C  C  GAA
                                TGGCTCAGTC AG TT   AGC
                                |||||||||| || ||   |||
                                ACCGAGTCGG TC AG   TCG
                                      A  T  A__
GAM675  LOC221490 5' GCTAGATCTAGGCTGAGCCA  93663        C  C  GAA
                                TGGCTCAGTC AG TT   AGC
                                |||||||||| || ||   |||
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                                ACCGAGTCGG TC AG   TCG
                                     A  T  A__
GAM675  LOC245771 3'  TGAAAGCGCCTTGTACTGAGCC 92900        C A_______  TGAA
          A                    TGGCTCAGT C       GCT    A
                               ||||||||| |       |||    |
                               ACCGAGTCA G       CGA    T
                                    T TTCCGIII   AAGT
GAM675  LOC245771 3'  TGAAAGCGCCTTGTACTGAGCC 92900        C A_______  TGAA
          A                    TGGCTCAGT C       GCT    A
                               ||||||||| |       |||    |
                               ACCGAGTCA G       CGA    T
                                    T TTCCGIII   AAGT
GAM675  LOC254778 3'  TTCAGGATTGAAACTGAGCCA  96131        C_  _
                               TGGCTCAGT  CAG CTTGAA
                               |||||||||  ||| ||||||
                               ACCGAGTCA  GTT GGACTT
                                    AA   A
GAM675  LOC254778 3'  TTCAGGATTGAAACTGAGCCA  96131        C_  _
                               TGGCTCAGT  CAG CTTGAA
                               |||||||||  ||| ||||||
                               ACCGAGTCA  GTT GGACTT
                                    AA   A
GAM675  LOC256401 3'  GCTCTCAAGCTGAATGAC    96019    ___      A
                               GTC   CAGCTTGA AGC
                               |||   |||||||| |||
                               CAG   GTCGAACT TCG
                                 TAA       C
GAM675  LOC256401 3'  GCTCTCAAGCTGAATGAC    96019    ___      A
                               GTC   CAGCTTGA AGC
                               |||   |||||||| |||
                               CAG   GTCGAACT TCG
                                 TAA       C
GAM675  LOC257422 5'  GCTTTCAGTATTACAGAGCCA  96576      A  CCA   T
                               TGGCTC GT   GCT GAAAGC
                               |||||| ||   ||| ||||||
                               ACCGAG CA   TGA CTTTCG
                                  A  TTA   _
GAM675  LOC257422 5'  GCTTTCAGTATTACAGAGCCA  96576      A  CCA   T
                               TGGCTC GT   GCT GAAAGC
                               |||||| ||   ||| ||||||
                               ACCGAG CA   TGA CTTTCG
                                  A  TTA   _
GAM675  LOC51162  3'  CAGGCTGGACTGAGCC      32520
                               GGCTCAGTCCAGCTTG
                               ||||||||||||||||
                               CCGAGTCAGGTCGGAC

GAM675  LOC51162  3'  CAGGCTGGACTGAGCC      65818
                               GGCTCAGTCCAGCTTG
                               ||||||||||||||||
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                                CCGAGTCAGGTCGGAC

GAM675  LOC51162  3'  CAGGCTGGACTGAGCC      65818
                                GGCTCAGTCCAGCTTG
                                ||||||||||||||||
                                CCGAGTCAGGTCGGAC

GAM675  LOC51162  3'  CAGGCTGGACTGAGCC      32520
                                GGCTCAGTCCAGCTTG
                                ||||||||||||||||
                                CCGAGTCAGGTCGGAC

GAM675  LOC64150  5'  GAGCGCCCGAACTGAGCCA    67282         _ CA__
                                TGGCTCAGT C    GCTT
                                |||||||||  |    ||||
                                ACCGAGTCA G    CGAG
                                      A CCCG
GAM675  LOC64150  5'  GAGCGCCCGAACTGAGCCA    67282         _ CA__
                                TGGCTCAGT C    GCTT
                                |||||||||  |    ||||
                                ACCGAGTCA G    CGAG
                                      A CCCG
GAM675  LOC91759  3'  GCTGCCTGGCACTGAGCCA    67088         _   CTTGAA
                                TGGCTCAGT CCAG     AGC
                                |||||||||  ||||     |||
                                ACCGAGTCA GGTC     TCG
                                      C    CG____
GAM675  LOC91759  3'  GCTGCCTGGCACTGAGCCA    67088         _   CTTGAA
                                TGGCTCAGT CCAG     AGC
                                |||||||||  ||||     |||
                                ACCGAGTCA GGTC     TCG
                                      C    CG____
GAM675  LOC92231  3'  CAGGCTGGCCTGAGCCA      68550         T
                                TGGCTCAG CCAGCTTG
                                ||||||||  ||||||||
                                ACCGAGTC GGTCGGAC
                                      C
GAM675  LOC92231  3'  CAGGCTGGCCTGAGCCA      68550         T
                                TGGCTCAG CCAGCTTG
                                ||||||||  ||||||||
                                ACCGAGTC GGTCGGAC
                                      C
GAM676  C20orf7   3'  CCTAATATCACATCTATAGTA  44143       TA       _  C
                                TACTA  TAGGTGTG TA TAGG
                                |||||  ||||||||  ||  ||||
                                ATGAT  ATCTACAC AT ATCC
                                   __       T  A
GAM676  CCR5      3'  CCTAGTACAAGGCAACATATA  5149        AG_  G_
                                TATAT   GT  TGTACTAGG
                                |||||   ||  |||||||||
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                                ATATA   CG  ACATGATCC
                                   CAA  GA
GAM676  DKFZP434B0335 5'  GCCCCCCCCACACACCTACATG  92464     A        ACTA_
                                TAT TAGGTGTGT     GGC
                                ||| |||||||||     |||
                                GTA ATCCACACA     CCG
                                  C        CCCCC
GAM676  DKFZP564O0423 3'  GCCTAACCCTGTGCCTATGTA  91691         TG GTAC_
                                TATATAGG  T     TAGGC
                                ||||||||  |     |||||
                                ATGTATCC  G     ATCCG
                                     GT TCCCA
GAM676  FLJ21615  3'  CCTATATATCACCTATA     49835         _   C
                                TATAGGTG TGTA TAGG
                                |||||||| |||| ||||
                                ATATCCAC ATAT ATCC
                                     T   _
GAM676  KIAA0102  3'  CCTAGCAGTACTTTATATAGTA 28566           T   TA_
                                TACTATATAGG GTG   CTAGG
                                |||||||||||| |||   |||||
                                ATGATATATTT CAT   GATCC
                                       _  GAC
GAM676  KIAA0436  3'  GCCTAACACGAGGTATACAGTA 60056      A   GG_    AC
                                TACT TATA   TGTGT  TAGGC
                                |||| ||||   |||||  |||||
                                ATGA ATAT   GCACA  ATCCG
                                  C   GGA    __
GAM676  KIAA1280  5'  GCCTAATACATATTTATTGTA  69721     TAT         C
                                TAC   ATAGGTGTGTA TAGGC
                                |||   ||||||||||| |||||
                                ATG   TATTTATACAT ATCCG
                                  T__         A
GAM676  RAB33B    3'  ACACACCTAATAGTA       48481       A
                                TACTAT TAGGTGTGT
                                |||||| |||||||||
                                ATGATA ATCCACACA
                                       _
GAM676  LOC144231 5'  GCCCAGCACACACCTATG    83016           A  A
                                TATAGGTGTGT CT GGC
                                |||||||||||  || |||
                                GTATCCACACA GA CCG
                                       C  C
GAM676  LOC151657 5'  GCCTAGTAAATATTATTTAG   85476    T   G   G
                                CTA ATAG TGT TACTAGGC
                                ||| |||| ||| ||||||||
                                GAT TATT ATA ATGATCCG
                                  T   _  A
GAM676  LOC256905 3'  GCCTATGTATACCTATGTA    96867            C
                                TATATAGGTGTGTA TAGGC
                                ||||||||||||| |||||
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                                ATGTATCCATATGT ATCCG
                                                _
GAM676  LOC257428 3'  GCCTCACACACCTGTACAG   94278    A        ACT
                                CT TATAGGTGTGT   AGGC
                                || ||||||||||   ||||
                                GA ATGTCCACACA   TCCG
                                 C         C__
GAM676  LOC90777  3'  CCTAGTAAATACTCAGTA    63966     ATATA    G
                                TACT    GGTGT TACTAGG
                                ||||    ||||| |||||||
                                ATGA    TCATA ATGATCC
                                  C____    A
GAM677  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM677  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM677  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                                _
GAM677  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM677  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM677  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM677  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG   A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                       T__   _
GAM677  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
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                                AAAGT AAAGTGACGGG
                                   A
GAM677  ZNF216   3' ATCTGCACAGCAAAGTGAAA  20017        CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM677  CG012    5' CTCACTCTGAAAGTGAA    83218        CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM677  EIF2C2   3' ATCTTCTGAGAGTGAAAG   71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM677  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||         |||||||||
                                GTAAAG         CAGACTCTA
                                   AAACATTT_
GAM677  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM677  KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM677  KLHL6    3' ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM677  NIR3     3' GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM677  PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM677  PP35     3' ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
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                                AAAGT  CAGACTCTA
                                  __
GAM677  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148          TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM677  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM677  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM677  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM677  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM677  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226     A      GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM677  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM678  ALDH3A1   3'  CACCATTCCAAGTCTCCAC    5482     A        TAT
                                GT GAGACTTGGG   GTG
                                || ||||||||||   |||
                                CA CTCTGAACCT   CAC
                                 C         TAC
GAM678  E48      3'  TATTTTGTACTCAAATCTCTAC 13507         C        T
           A                     TGTAGAGA TTGGGTATG GATA
                                 |||||||| ||||||||| ||||
                                 ACATCTCT AACTCATGT TTAT
                                      A        T
GAM678  MPV17    3'  CACATACTAGGCACTCCATA   70510     A   ACTTG
                                TGT GAG    GGTATGTG
                                ||| |||    ||||||||
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                                ATA CTC    TCATACAC
                                  C  ACGGA
GAM678  TSPY    3'  ACCAGCAAGTCTCTGCA    82103          __
                                TGTAGAGACTTG  GGT
                                ||||||||||||  |||
                                ACGTCTCTGAAC  CCA
                                      GA
GAM678  C1QTNF7  3'  TATCCCTTCCAAGTCTCACA  49163    A       TATGT
                                TGT GAGACTTGGG    GATA
                                ||| ||||||||||    ||||
                                ACA CTCTGAACCT    CTAT
                                  _       TCC__
GAM678  ERF     3'  CATGGGCCACAAATCTCTACA  21436       C  _  A
                                TGTAGAGA TTG GGT TGTG
                                |||||||| ||| ||| ||||
                                ACATCTCT AAC CCG GTAC
                                     A  A  G
GAM678  FLJ11125  3'  TACCCCAGATCTCTACA    59584       _ T
                                TGTAGAGA CT GGGTA
                                |||||||| || |||||
                                ACATCTCT GA CCCAT
                                     A  C
GAM678  FLJ21195  3'  TATCACACACAAAGGTCTCTAT 42453         GG  A
          A                      TGTAGAGACTT  GT TGTGATA
                                ||||||||||  || |||||||
                                ATATCTCTGGA  CA ACACTAT
                                      AA  C
GAM678  KIAA0449  3'  CACCCCAAATCTCTA     34198      C    TAT
                                TAGAGA TTGGG   GTG
                                ||||||  |||||   |||
                                ATCTCT AACCC   CAC
                                   A   ___
GAM678  MGC15435  3'  TATCACACCATGTGCCTATA  50420     AG  T   GTA
                                TGTAG  AC TGG   TGTGATA
                                |||||  ||  |||   |||||||
                                ATATC  TG ACC   ACACTAT
                                   CG  T  ___
GAM678  MGC32043  3'  CACATCCAATCTCTCA     58044    T    C   GT
                                TG AGAGA TTGG  ATGTG
                                ||  |||||  ||||  |||||
                                AC TCTCT AACC  TACAC
                                  _    _   __
GAM678  MSP     3'  CATCCCCCAAGTCACTACA   49412      A      TAT
                                TGTAG GACTTGGG   GTG
                                |||||  ||||||||   |||
                                ACATC CTGAACCC   TAC
                                   A      CC_
GAM678  RGS13    3'  TATCACATGTATCTTCTACA  58576       GACTT    __
                                TGTAGA    GGGTA  TGTGATA
                                ||||||    |||||  |||||||
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                                ACATCT    TCTAT  ACACTAT
                                   _____    GT
GAM678  RGS13    3'  TATCACATGTATCTTCTACA  11339      GACTT    __
                                TGTAGA    GGGTA  TGTGATA
                                ||||||    |||||  |||||||
                                ACATCT    TCTAT  ACACTAT
                                   _____    GT
GAM678  SLC2A13  3'  CATGCCCAAATCACTACA    53547      A  C
                                TGTAG GA TTGGGTATG
                                ||||| || |||||||||
                                ACATC CT AACCCGTAC
                                   A  A
GAM678  LOC125268 3'  CACATCAGGGTCTCCAC     76070    A      GGGT
                                GT GAGACTT    ATGTG
                                || |||||||    |||||
                                CA CTCTGGG    TACAC
                                 C      AC__
GAM678  LOC142779 3'  CACCCCAAGTCCTTACA     76393      A       TAT
                                TGTAG GACTTGGG   GTG
                                ||||| ||||||||   |||
                                ACATT CTGAACCC   CAC
                                   C      ___
GAM678  LOC150113 5'  ATCAATACCCAACCCCCTACA  87210      AGAC      G
                                TGTAG    TTGGGTAT TGAT
                                |||||    |||||||| ||||
                                ACATC    AACCCATA ACTA
                                   CCCC      _
GAM678  LOC197379 3'  CACACTAAGTCTCCAC      89741    A       GTA
                                GT GAGACTTGG   TGTG
                                || |||||||||   ||||
                                CA CTCTGAATC   ACAC
                                 C       ___
GAM678  LOC220776 3'  CATCGTGCCCAAGTCTTACA   68387     A          _
                                TGT GAGACTTGGGTATG TG
                                ||| ||||||||||||| ||
                                ACA TTCTGAACCCGTGC AC
                                  _           T
GAM678  LOC92379  3'  ATCACATACCGAACCCTTACA  69146     A  AC  G
                                TGT GAG  TT GGTATGTGAT
                                ||| |||  || ||||||||||
                                ACA TTC  AA CCATACACTA
                                  _  CC  G
GAM679  BAZ2A    3'  GCAGAGAGCTGAGGCAT     25604         AC_
                                ATGCCTCAGC   CTGC
                                ||||||||||   ||||
                                TACGGAGTCG   GACG
                                      AGA
GAM679  BUB1B    5'  GCAGCAGGACGAGGACCTGA   6855     AATG   AGCA
                                TCA   CCTC   CCTGCTGC
                                |||   ||||   ||||||||
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                                AGT   GGAG   GGACGACG
                                  CCA_   CA__
GAM679  CASQ1    3'  GCTGGGTGCTGAGACACTGA  6931     AA  C       _
                                TCA  TG CTCAGCACCT GC
                                |||  || |||||||||| ||
                                AGT  AC GAGTCGTGGG CG
                                  C_  A        T
GAM679  COL5A3   3'  GCATTTGGTGCTGAGGCTTTGA 31694      T        TGC
                                TCAAA GCCTCAGCACC   TGC
                                ||||| ||||||||||   |||
                                AGTTT CGGAGTCGTGG   ACG
                                   _        TTT
GAM679  FBN2     3'  CAGCCAGTCTGCAGAAGCATTT 8845        C  A   C_  _
              GA                  TCAAATGC TC GCA  CTG CTG
                                |||||||| || |||  ||| |||
                                AGTTTACG AG CGT  GAC GAC
                                     A  A   CT   C
GAM679  GPR44    3'  CAGCAGGTGCTGAGCA     16525     C
                                TGC TCAGCACCTGCTG
                                ||| ||||||||||||
                                ACG AGTCGTGGACGAC
                                  _
GAM679  GPR91    3'  GCAACAAGTTGTCTGCATTTGA 52332        CT_   ACC_
                                TCAAATGC   CAGC   TGC
                                ||||||||   ||||   |||
                                AGTTTACG   GTTG   ACG
                                     TCT    AACA
GAM679  GUCY1A3  5'  GCAGCAGGGTAAGAGACA    63489    C   A_  A
                                TG CTC  GC CCTGCTGC
                                || |||  || ||||||||
                                AC GAG  TG GGACGACG
                                 A   AA  _
GAM679  GYPC     3'  CAGCAGGTGCCAGAGC      33652    _  CA
                                GC CT  GCACCTGCTG
                                || ||  ||||||||||
                                CG GA  CGTGGACGAC
                                 A  C_
GAM679  GYPC     3'  CAGCAGGTGCCAGAGC      9162     _  CA
                                GC CT  GCACCTGCTG
                                || ||  ||||||||||
                                CG GA  CGTGGACGAC
                                 A  C_
GAM679  LIPA     3'  CAGCAGGTGCATAGTCA     4080     C  CA
                                TG CT  GCACCTGCTG
                                || ||  ||||||||||
                                AC GA  CGTGGACGAC
                                 T  TA
GAM679  NAB2     5'  GCAGCAGGCGCCGAGCGC    19915    _  A  A
                                GC CTC GC CCTGCTGC
                                || ||| || ||||||||
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                                CG GAG CG GGACGACG
                                 C   C  C
GAM679  PDHA1    5'  GCGTCTGCTGGGGCACCTGA  4294      AA        CC
                                TCA  TGCCTCAGCA  TGC
                                |||  ||||||||||  |||
                                AGT  ACGGGGTCGT  GCG
                                  CC         CT
GAM679  PLCG1    3'  GCAGCAGGTGCTGTGCGCCTTG 10621     A_   CT
                                CAA  TGC  CAGCACCTGCTGC
                                |||  |||  |||||||||||||
                                GTT  GCG  GTCGTGGACGACG
                                  CC   T_
GAM679  SCAMP1   3'  CAACAGGTGCTAGTTTTGA   53404      TGC  C       C
                                TCAAA   CT AGCACCTG TG
                                |||||   || ||||||||  ||
                                AGTTT   GA TCGTGGAC AC
                                   T__  _       A
GAM679  SERPINA4 3'  CAGCAGGTGCTGGC       20610     TC
                                GCC  AGCACCTGCTG
                                |||  ||||||||||
                                CGG  TCGTGGACGAC
                                  __
GAM679  SLC9A6   3'  GCAACGAGCTGATGGCATTTGA 21005          _    ACC_
                                TCAAATGCC TCAGC    TGC
                                |||||||| |||||    |||
                                AGTTTACGG AGTCG    ACG
                                      T    AGCA
GAM679  SORBS1   3'  GCAAAACTGAGGCACCTGA   31155     AA      CACC
                                TCA  TGCCTCAG    TGC
                                |||  ||||||||    |||
                                AGT  ACGGAGTC    ACG
                                  CC       AAA_
GAM679  TRIM9    3'  GCTGGTGCCAAAGCATTCTGA  53759     _    CTCA    T
                                TCA AATGC    GCACC GC
                                ||| |||||    ||||| ||
                                AGT TTACG    CGTGG CG
                                  C    AAAC    T
GAM679  WISP2    3'  GCAGCAGGTGCTGGGC      13934     T
                                GCC CAGCACCTGCTGC
                                ||| |||||||||||||
                                CGG GTCGTGGACGACG
                                  _
GAM679  C11orf16 3'  CAGCAGGAAGGCACCTG     40217    AA    CAGCA
                                CA  TGCCT    CCTGCTG
                                ||  |||||    |||||||
                                GT  ACGGA    GGACGAC
                                 CC    A____
GAM679  C17orf31 3'  CAGCCCAGCCTGAGGCATT   34118          CACCT
                                AATGCCTCAG    GCTG
                                ||||||||||    ||||
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                                TTACGGAGTC    CGAC
                                      CGACC
GAM679  DKFZp434N2435 5'  GCAGCAGCGGCAGAAGTATTTG 96339        C  A  AC
          A                     TCAAATGC TC GC  CTGCTGC
                                |||||||| || ||  |||||||
                                AGTTTATG AG CG  GACGACG
                                     A  A  GC
GAM679  FLJ10120  3'  GCAGCAGGAAGTAAAGGCATCT 35831    A     CA  A_
          G                     CA ATGCCT  GC  CCTGCTGC
                                || ||||||  ||  ||||||||
                                GT TACGGA  TG  GGACGACG
                                 C     AA  AA
GAM679  FLJ11252  3'  GCAACAGGTGCTAGAG      67608     _      C
                                CTC AGCACCTG TGC
                                ||| |||||||| |||
                                GAG TCGTGGAC ACG
                                  A       A
GAM679  FLJ20485  3'  AGCAGGAGTATTTGA       38763        CTCAGCA
                                TCAAATGC      CCTGCT
                                ||||||||      ||||||
                                AGTTTATG      GGACGA
                                     A_______
GAM679  FLJ22127  3'  CAGCAGGTGCTGCCAT      42882     CCT
                                ATG   CAGCACCTGCTG
                                |||   ||||||||||||
                                TAC   GTCGTGGACGAC
                                  C__
GAM679  FLJ31952  5'  CAGCAGGCGGTGGGCATT    58382       CA  A_
                                AATGCCT  GC  CCTGCTG
                                |||||||  ||  |||||||
                                TTACGGG  TG  GGACGAC
                                     __  GC
GAM679  KIAA0350  3'  CAGCAGGTGAACATTT      61168      CCTCAG
                                AAATG     CACCTGCTG
                                |||||     |||||||||
                                TTTAC     GTGGACGAC
                                   AA____
GAM679  KIAA0779  5'  GCAGCAGGCGCTGTAGT     85727    CT    A
                                GC  CAGC CCTGCTGC
                                ||  |||| ||||||||
                                TG  GTCG GGACGACG
                                 AT    C
GAM679  KIAA1046  3'  GCAGCAGGATGCTGGCATCTG  29997    A     TC    _
                                CA ATGCC  AGCA CCTGCTGC
                                || |||||  |||| ||||||||
                                GT TACGG  TCGT GGACGACG
                                 C     __    A
GAM679  KIAA1706  3'  GCAGCAGGGTTAGCATT     92787      CTC   A
                                AATGC   AGC CCTGCTGC
                                |||||   ||| ||||||||
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                                TTACG   TTG GGACGACG
                                  A__   _
GAM679  MGC10854  3'  CAAGGGATGCTGAGGCTTCTGA 50203     AAT       _   GC
                                TCA   GCCTCAGCA CCT  TG
                                |||   ||||||||| |||  ||
                                AGT   CGGAGTCGT GGG  AC
                                  CTT       A   A_
GAM679  MGC15631  3'  GCAGCAGGAGGGGGCCCTGA   51265     AAT    AGCA
                                TCA   GCCTC    CCTGCTGC
                                |||   |||||    ||||||||
                                AGT   CGGGG    GGACGACG
                                  CC_    GA__
GAM679  MGC2752   5'  GCAACAAGTGCTGAGATCAGCG 78448     _____      C  C
                                TGC    CTCAGCAC TG TGC
                                |||    |||||||| || |||
                                GCG    GAGTCGTG AC ACG
                                  ACTA       A  A
GAM679  MGC2752   5'  GCGATTACTGAGGCATCTGG   78449     A       CACC
                                TCA ATGCCTCAG    TGC
                                ||| |||||||||    |||
                                GGT TACGGAGTC    GCG
                                  C        ATTA
GAM679  MSTP032   5'  GCAGAACTAACTGAGGCATTT  47441          CACCTG
                                AAATGCCTCAG     CTGC
                                ||||||||||      ||||
                                TTTACGGAGTC     GACG
                                      AATCAA
GAM679  OIP5      3'  CAACAGGTGCTGCTTAGTCAT  62783     C ___       C
                                ATG CT   CAGCACCTG TG
                                ||| ||   ||||||||| ||
                                TAC GA   GTCGTGGAC AC
                                  T  TTC        A
GAM679  PNMA5     3'  CAGCAGGGACATTTGA      73594        CCTCAGCA
                                TCAAATG       CCTGCTG
                                |||||||       |||||||
                                AGTTTAC       GGACGAC
                                    AG_______
GAM679  PPP1R15A  5'  GCTTGTCGCCACGGCACTTGA  59895     A   TCA  _  CT
                                TCAA TGCC   GC AC  GC
                                |||| ||||   || ||  ||
                                AGTT ACGG   CG TG  CG
                                  C    CAC  C  TT
GAM679  QKI       3'  GCAGCGAGCTGAGGCACTTG   65443     A       ACC
                                CAA TGCCTCAGC   TGCTGC
                                ||| |||||||||   ||||||
                                GTT ACGGAGTCG   GCGACG
                                  C        A__
GAM679  LOC128402 3'  GCTTTGCTGAGGCCCTGA    75783     AAT       CCT
                                TCA   GCCTCAGCA   GC
                                |||   |||||||||   ||
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                                AGT   CGGAGTCGT   CG
                                  CC_       TT_
GAM679   LOC147172 3'  GCAGCAGGAAGCAAAGGCATTG 78296      A    CA  A_
            A                      TCAA TGCCT  GC  CCTGCTGC
                                   |||| |||||  ||  ||||||||
                                   AGTT ACGGA  CG  GGACGACG
                                     _    AA  AA
GAM679   LOC148166 5'  GCAGGACGCTGAGGCTCTGA   78691     AAT      A_
                                   TCA   GCCTCAGC  CCTGC
                                   |||   ||||||||  |||||
                                   AGT   CGGAGTCG  GGACG
                                     CT_      CA
GAM679   LOC149570 3'  GCAGTGGCGCTGAGGCCCTGA  84501     AAT      A  T
                                   TCA   GCCTCAGC CC GCTGC
                                   |||   |||||||| || |||||
                                   AGT   CGGAGTCG GG TGACG
                                     CC_      C  _
GAM679   LOC155006 5'  GCAGCAGGCACTCGGCA     81238     TC  CA
                                   TGCC  AG  CCTGCTGC
                                   ||||  ||  ||||||||
                                   ACGG  TC  GGACGACG
                                     C_  AC
GAM679   LOC155438 3'  CAGCAGGTGTCCTTGCGTCTGA 86392     A    CTCA
                                   TCA ATGC    GCACCTGCTG
                                   ||| ||||    ||||||||||
                                   AGT TGCG    TGTGGACGAC
                                     C    TTCC
GAM679   LOC219541 5'  GCGGTGCCTGAGGCAT      91568         _   T
                                   ATGCCTCAG CACC GC
                                   ||||||||| |||| ||
                                   TACGGAGTC GTGG CG
                                        C   _
GAM679   LOC253039 3'  GTATAACTGAAGCATTTGA    96160        C    CACC
                                   TCAAATGC TCAG    TGC
                                   |||||||| ||||    |||
                                   AGTTTACG AGTC    ATG
                                        A   AAT_
GAM679   LOC51125  5'  GCAGCAGGCGCCGGTGTCCGGA 32249    AA_    TCA  A
                                   TC   ATGCC   GC CCTGCTGC
                                   ||   |||||   || ||||||||
                                   AG   TGTGG   CG GGACGACG
                                    GCC    C__  C
GAM680   AQP3     3'  TTCACGATCCACCCTTTC     59593      T_   _
                                   GAAA  GTGG TCGTGAA
                                   ||||  |||| |||||||
                                   CTTT  CACC AGCACTT
                                     CC    T
GAM680   ARSB     3'  TCACGACTCTTGTC        3502         AATGTG
                                   GACAAGA     GTCGTGA
                                   |||||||     |||||||
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                                CTGTTCT     CAGCACT
                                        ______
GAM680  B4GALT5  3'  TTTTCACAAAAATAGTCCTTTG 16519       AAA_  GGTC
            TCA                   TGACAAG   TGT   GTGAAAA
                                  |||||||   |||   |||||||
                                  ACTGTTT   ATA   CACTTTT
                                      CCTG  AAAA
GAM680  CHRNA3   3'  TCGTTACCCATTTCTT     5610        T  CG
                                  AAGAAATG GGT  TGA
                                  ||||||||| |||  |||
                                  TTCTTTAC CCA  GCT
                                       _  TT
GAM680  DRD1     3'  TTACAACCACATTTCTGGCCA  5840     ACA        C
                                  TG  AGAAATGTGGT GTGA
                                  ||  |||||||||||| ||||
                                  AC  TCTTTACACCA CATT
                                   CGG         A
GAM680  FUT1     3'  TCTGATCACATCCCCTGTC   3798      AGAA       T
                                  GACA   ATGTGGTCG GA
                                  ||||   ||||||||| ||
                                  CTGT   TACACTAGT CT
                                    CCCC       _
GAM680  IRF1     3'  GCCACATTTCTGATCA     64345     CA
                                  TGA  AGAAATGTGGT
                                  |||  ||||||||||
                                  ACT  TCTTTACACCG
                                    AG
GAM680  MAP3K8   5'  TCACGACCACCTCATG     17791    A  AAT
                                  CA GA   GTGGTCGTGA
                                  || ||   ||||||||||
                                  GT CT   CACCAGCACT
                                   A  C__
GAM680  NGFR     3'  TTCTGACCACACTTCCTGTC   10231     A  A      T
                                  GACA GAA TGTGGTCG GAA
                                  |||| ||| |||||||| |||
                                  CTGT CTT ACACCAGT CTT
                                    C   C      _
GAM680  OLR1     3'  TTCACAACAGTTCTTGTTA    10341        ATGTG  C
                                  TGACAAGAA    GT GTGAA
                                  |||||||||    || |||||
                                  ATTGTTCTT    CA CACTT
                                       GA___  A
GAM680  POU4F1   3'  CACTGAAAACATTTTTGTCA   20660        A  GG  _
                                  TGACAAGAA TGT  TC GTG
                                  ||||||||| |||  || |||
                                  ACTGTTTTT ACA  AG CAC
                                       _  AA  T
GAM680  SMP1     3'  TTTCACATGAATAATTTTTGTC 26705        A  GGTC
            A                     TGACAAGAA TGT   GTGAAA
                                  ||||||||| |||   ||||||
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                                ACTGTTTTT ATA    CACTTT
                                     A   AGTA
GAM680  ZNF264    3'  TTCTATTAACATTTCTTTTCA  12769     C       GGTCGT
                                TGA AAGAAATGT     GAA
                                ||| |||||||||     |||
                                ACT TTCTTTACA     CTT
                                  T       ATTAT_
GAM680  C20orf175 3'  CGAGCTCCACGTTTCCTGCCA  55063     A  A       ___
                                TG CA GAAATGTGG   TCG
                                || || |||||||||   |||
                                AC GT CTTTGCACC   AGC
                                 C  C       TCG
GAM680  CAPNS2    3'  TTTCACAACCCTACATATTTCT 50323     CA       ____   C
           GATCA                    TGA  AGAAATGT    GGT GTGAAA
                                |||  ||||||||    ||| ||||||
                                ACT  TCTTTATA    CCA CACTTT
                                  AG       CATC   A
GAM680  CLDN6     3'  TTTACACTCACATTTTTATCA  41041     CA       _  C
                                TGA  AGAAATGTG GT GTGAA
                                |||  |||||||||| || |||||
                                ACT  TTTTTACAC CA CATTT
                                  A_       T  _
GAM680  DKFZP564L0864 3'  GCACCAATTTCTTGCCA     72555     A       G    C
                                TG CAAGAAAT TGGT GT
                                || |||||||| |||| ||
                                AC GTTCTTTA ACCA CG
                                 C       _    _
GAM680  DKFZP566B183 3'  TTTCCATAAACATTTCTTTTCA 31330     C       GGTCGT
                                TGA AAGAAATGT     GAAA
                                ||| |||||||||     ||||
                                ACT TTCTTTACA     CTTT
                                  T       AATAC_
GAM680  GTF2E1    3'  TACAGACCTCTTGTCA      18616        AATGT    _
                                TGACAAGA    GGTC GTG
                                ||||||||    |||| |||
                                ACTGTTCT    CCAG CAT
                                     _____   A
GAM680  KIAA0089  3'  TTTTAATTCACATTTCTT    69967          TCG
                                AAGAAATGTGG   TGAAA
                                ||||||||||   |||||
                                TTCTTTACACT   ATTTT
                                      TA_
GAM680  KIAA0373  5'  TTTTCAAAGTAACATTTCTT   28015        GGTCG
                                AAGAAATGT    TGAAAA
                                |||||||||    ||||||
                                TTCTTTACA    ACTTTT
                                     ATGAA
GAM680  KIAA1813  3'  TTTTCACACTGTAAATTTCTTG 70314        __ TG  C
           T                     ACAAGAAAT  G  GT GTGAAAA
                                |||||||||  |  || |||||||
```

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                                TGTTCTTTA  T  CA CACTTTT
                                     AA GT  _
GAM680  KIAA1951  3'  TTCCAGGCTTCTCTTGTCA   73766       AATGT   GT
                                TGACAAGA    GGTC  GAA
                                ||||||||    ||||  |||
                                ACTGTTCT    TCGG  CTT
                                    CT___    AC
GAM680  MGC4170   3'  TTCACCATTTCTTGTC     44227         TGGTC
                                GACAAGAAATG    GTGAA
                                ||||||||||    |||||
                                CTGTTCTTTAC    CACTT
                                     _____
GAM680  NRN1      3'  CACTGCACATTTCTCCTCA   33432     CA       GTC
                                TGA  AGAAATGTG   GTG
                                |||  |||||||||   |||
                                ACT  TCTTTACAC   CAC
                                  CC        GT_
GAM680  PLA2G12   3'  TTTTCACAACCACATTT     48028         C
                                AAATGTGGT GTGAAAA
                                ||||||||| |||||||
                                TTTACACCA CACTTTT
                                     A
GAM680  PPY2      3'  CACTCCACATTCCTGGCCA   40819    ACA  A      TC
                                TG   AG AATGTGG  GTG
                                ||   || |||||||  |||
                                AC   TC TTACACC  CAC
                                  CGG  C      T_
GAM680  ZNF31     3'  TTTGTAGACCACATTTCCTGTT 64992       A         _ TG
            A                    TGACA GAAATGTGGTC G  AA
                                |||||  |||||||||||  |  ||
                                ATTGT CTTTACACCAG T  TT
                                   C          A GT
GAM680  LOC115219 3'  CACGACAACGGGTCCTCA    73295     CAA  AA   G
                                TGA   GA  TGT GTCGTG
                                |||   ||  |||  ||||||
                                ACT   CT  GCA CAGCAC
                                  C__  GG   A
GAM680  LOC120376 5'  TTCAGAGCATTTCTTTCA    75986     C       GG  G
                                TGA AAGAAATGT  TC TGAA
                                |||  |||||||||  ||  ||||
                                ACT TTCTTTACG  AG ACTT
                                  _        __  _
GAM680  LOC133418 3'  TTTCATATACATTTTTTGCCA  75094    A         GTC
                                TG CAAGAAATGTG   GTGAAA
                                || ||||||||||   ||||||
                                AC GTTTTTTACAT   TACTTT
                                  C          A__
GAM680  LOC151199 3'  TTAAAACCACAGCTCTTGCCA  80174    A    AA     CG
                                TG CAAGA  TGTGGT  TGA
                                || |||||  ||||||  |||
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                                AC GTTCT  ACACCA  ATT
                                 C    CG     AA
GAM680  LOC152317 5'  TCACACTGACTTTTGTCA    85649        AATG   C
                                TGACAAGA   TGGT GTGA
                                ||||||||   |||| ||||
                                ACTGTTTT   GTCA CACT
                                    CA__   _
GAM680  LOC152674 3'  TTCAACCCACCCTCTTGTCA   85841        AAT   TCG
                                TGACAAGA   GTGG   TGAA
                                ||||||||   ||||   ||||
                                ACTGTTCT   CACC   ACTT
                                    CC_    CA_
GAM680  LOC152845 5'  CATGACCACATTTTTCA     60330     CAA
                                TGA   GAAATGTGGTCGTG
                                |||   ||||||||||||||
                                ACT   TTTTACACCAGTAC

                                 ___
GAM680  LOC154743 3'  TTTAGTCCACATTGTCTTGTCA 81118         _      TCG
                                TGACAAGA AATGTGG   TGAA
                                |||||||| |||||||   ||||
                                ACTGTTCT TTACACC   ATTT
                                    G      TG_
GAM680  LOC165476 5'  TTCACGGCACCTTCT       87201      AT   G
                                AGAA  GTG TCGTGAA
                                ||||  ||| |||||||
                                TCTT  CAC GGCACTT
                                  C_   _
GAM680  LOC254266 5'  TTTTCGGTCACACATCTTATCA 97356     C    AA    GT  T
                                TGA AAGA  TGTG  CG GAA
                                ||| ||||  ||||  || |||
                                ACT TTCT  ACAC  GC TTT
                                  A    AC    TG  T
GAM680  LOC255919 3'  TTTCATTCTTACATTTCTAATC 95043     CA         TC
           A                     TGA  AGAAATGTGG  GTGAAA
                                |||  ||||||||||  ||||||
                                ACT  TCTTTACATT  TACTTT
                                  AA         CT
GAM680  LOC51754  5'  CACGGCCACATCTCTGTCA    71027       A  A
                                TGACA GA ATGTGGTCGTG
                                ||||| || ||||||||||
                                ACTGT CT TACACCGGCAC
                                   _ C
GAM680  LOC55862  3'  ACCTCATTTCTTGCCA      37485     A        T
                                TG CAAGAAATG GGT
                                || |||||||| |||
                                AC GTTCTTTAC CCA
                                 C        T
GAM680  LOC55954  3'  CACGTGGTCACTTTTCTCATCA 38877     CA     T   GT __
                                TGA  AGAAA GTG  C  GTG
                                |||  ||||| |||  |  |||
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                                ACT  TCTTT CAC  G  CAC
                                  AC    T   TG TG
GAM681  IL21R    3'  ATGTGCACAAGTGTGCAC    41423       C___
                                GTGCAT   GTGCACAT
                                ||||||   ||||||||
                                CACGTG   CACGTGTA
                                   TGAA
GAM681  MUC4     3'  GCCCATGTGCACCTGCCC    56328    T  TC      AA
                                GG GCA  GTGCACAT  GC
                                || |||  ||||||||  ||
                                CC CGT  CACGTGTA  CG
                                 _  C_      CC
GAM681  PLXNA2   3'  GCTTTATCTACCACACACCTGT 47211        CATC   CACAT__
           A                     TACAGGTG   GTG      AAGC
                                ||||||||   |||      ||||
                                ATGTCCAC   CAC      TTCG
                                     A___   CATCTAT
GAM681  ARNTL2   3'  CTAATGGCACACACCTGTA   39461        CATC   A  A
                                TACAGGTG   GTGC CAT AG
                                ||||||||   |||| ||| ||
                                ATGTCCAC   CACG GTA TC
                                     A___   _  A
GAM681  C1QTNF2  3'  CTTATGTGCACACTCTG     49126    _ GCATC
                                CAG GT    GTGCACATAAG
                                ||| ||    ||||||||||
                                GTC CA    CACGTGTATTC
                                 T _____
GAM681  KIAA0596 3'  GCTTATGTGGAACACCT     62833      CA  GTG
                                AGGTG  TC   CACATAAGC
                                |||||  ||   |||||||||
                                TCCAC  AG   GTGTATTCG
                                  A_  ___
GAM681  KIAA0923 3'  GCTTACATGCACTCACCCTGT  25836      _  CATC    CA
                                ACAGG TG   GTGCA  TAAGC
                                ||||| ||   |||||  |||||
                                TGTCC AC   CACGT  ATTCG
                                   C  T___    AC
GAM681  NTN4     3'  GCTCATTTGCAATGCACTTGTA 62915          CG   C  A
                                TACAGGTGCAT  TGCA AT AGC
                                ||||||||||  |||| || |||
                                ATGTTCACGTA  ACGT TA TCG
                                      __   T  C
GAM681  RPL32    3'  GCTCATGTGCACGTTTTCTGT  6394       TGCAT       A
                                ACAGG    CGTGCACAT AGC
                                |||||    ||||||||| |||
                                TGTCT    GCACGTGTA TCG
                                   TTT__       C
GAM681  LOC51236 3'  TATGTGCATCCCTCACCTG   33204       CATC
                                CAGGTG   GTGCACATA
                                ||||||   |||||||||
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                                GTCCAC    TACGTGTAT
                                   TCCC
GAM682  ARNT2    3'  AAACAACCCGTGCATCCCTGC  29450     A    TTTTA
                                GTA GGAT     GGGTTGTTT
                                ||| ||||     |||||||||
                                CGT CCTA     CCCAACAAA
                                  C    CGTG_
GAM682  LCT      3'  AACCGTAAAAATCCTT      9697           G
                                AAGGATTTTTA GGTT
                                |||||||||||| ||||
                                TTCCTAAAAAT CCAA
                                       G
GAM682  RPL15    3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM682  FBXO30   3'  AACTAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                  G        AA
GAM682  KIAA0494 3'  AACAACCCTTACTTAC      28736       GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM682  PRO0641  5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                   ___    C
GAM682  SMT3H2   3'  AACAACATAAAAATCCTTGC   22670           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM682  LOC120103 3'  AACCTATGAAAAATCCTTGC   74002           A__
                                GTAAGGATTTTTT   GGGTT
                                ||||||||||||   |||||
                                CGTTCCTAAAAA   TCCAA
                                       GTA
GAM682  LOC129831 3'  AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM682  LOC133088 5'  AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
           C                     GTA GGATTTTT     TTGTTT
                                ||| ||||||||     ||||||
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                                CGT CCTAAAAA     AACAAA
                                  C       GATAA
GAM682   LOC148089 3'  GGCCCTAAAAATTCCTAC    78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM682   LOC154547 3'  AACAACATAAAAATCCTTGC   76050           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM682   LOC158104 3'  ACAGCCAAAAATCCTTA     60313          AG
                                TAAGGATTTTT  GGTTGT
                                ||||||||||  ||||||
                                ATTCCTAAAAA  CCGACA

                                       __
GAM682   LOC205880 5'  AAACAACCATCATCCTGAC    90709    A    TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM682   LOC221561 3'  AACAACATAAAAATCCTTGC   92130           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM682   LOC257591 3'  AACAACATAAAAATCCTTGC   97840           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM682   LOC51145  3'  AGCTAAAATCCTTAC       32393           TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
                                CATTCCTAAAA   TCGA

                                       ___
GAM683   BIN3     3'  CACCCTCCAGCAGGCAGCCCAG 37955         C    AT  CA
            CA                    TGCTGGGCT CCTGC  GA  GTG
                                ||||||||| |||||  ||  |||
                                ACGACCCGA GGACG  CT  CAC
                                     C    AC  CC
GAM683   CRSP8    3'  CACGCAGGAAGCCCACA     80963    C     C    A
                                TG TGGGCT CCTGC TG
                                || |||||| ||||| ||
                                AC ACCCGA GGACG AC
                                 _     A    C
GAM683   ENG      5'  CACTGCCATCCATTGGAGCCCA 3687           C_  C   A
            GCA                    TGCTGGGCTCC  TG ATG CAGTG
                                ||||||||||  || ||| |||||
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                                ACGACCCGAGG  AC TAC GTCAC
                                      TT  C   C
GAM683  HD      3'  CACTGTTAGTGACAGAGCCCAG 9181          CC  _  _
            CA                    TGCTGGGCTC  TG CA TGACAGTG
                                  ||||||||||  || || ||||||||
                                  ACGACCCGAG  AC GT ATTGTCAC
                                       __  A  G
GAM683  IGLL1    5'  CACTCTCTAGGGAGCCCACA  39174    C        CAT  C
                                  TG TGGGCTCCCTG   GA AGTG
                                  || ||||||||||   || ||||
                                  AC ACCCGAGGGAT   CT TCAC
                                   _         ___  C
GAM683  THBD     3'  CACTGCCACACAGGGTCTGCA  4494     T   CT    CA  A
                                  TGC GGG  CCCTG  TG CAGTG
                                  ||| |||  |||||  || |||||
                                  ACG TCT  GGGAC  AC GTCAC
                                    _  __    AC  C
GAM683  ARHGEF16 3'  CACCGTGTCCCAGGGAGCCCAG 27069           CAT   __
            C                      GCTGGGCTCCCTG   GACA  GTG
                                   ||||||||||||   ||||  |||
                                   CGACCCGAGGGAC   CTGT  CAC
                                          C__    GC
GAM683  CABIN1   3'  ACCACATGGGAGCCCAG     24479         TGC   ACA
                                  CTGGGCTCCC   ATG   GT
                                  |||||||||   |||   ||
                                  GACCCGAGGG   TAC   CA
                                       ___   AC_
GAM683  FLJ10232 3'  ACTGTCAGGAACCCAG      35920      C   CTGCA
                                  CTGGG TCC    TGACAGT
                                  ||||| |||    |||||||
                                  GACCC AGG    ACTGTCA
                                    A  _____
GAM683  FLJ20154 5'  GCCTTCAGGCCCAGCA      72927         CCCTGCA   CA
                                  TGCTGGGCT      TGA  GT
                                  |||||||||      |||  ||
                                  ACGACCCGG      ACT  CG
                                       _______  TC
GAM683  FLJ21865 3'  CACCGCCATGCAGGGCTCGC   42805    T   TC      ACA
                                  GC GGGC  CCTGCATG   GTG
                                  || ||||  ||||||||   |||
                                  CG CTCG  GGACGTAC   CAC
                                   _   __       CGC
GAM683  IRF7     3'  CACCGCGGTGCAAGAGCCCAGC 14443         CC    GACA
                                  GCTGGGCTC  TGCAT   GTG
                                  |||||||||  |||||   |||
                                  CGACCCGAG  ACGTG   CAC
                                       A_    GCGC
GAM683  KIAA0864 3'  CACTGTCAGTATTAAGGCCCAG 63247         CCC_  A
            CA                     TGCTGGGCT    TGC TGACAGTG
                                   |||||||||    ||| ||||||||
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                                ACGACCCGG   ATG ACTGTCAC
                                     AATT  _
GAM683  MFN2     3'  ACAAGGCAGGGGCCCAGCA   29595       T    ATGACA
                                TGCTGGGC CCCTGC     GT
                                |||||||| ||||||     ||
                                ACGACCCG GGGACG     CA
                                     _     GAA___
GAM683  MGC3101  3'  GTCACACAGAGCCCAGCA    43883         CC  CA
                                TGCTGGGCTC  TG  TGAC
                                ||||||||||  ||  ||||
                                ACGACCCGAG  AC  ACTG
                                      __ AC
GAM683  SCYB11   3'  CACTGCCCAAAGGAGTCCAACA 87442    C      CTGCATGA
                                TG TGGGCTCC       CAGTG
                                || ||||||||       |||||
                                AC ACCTGAGG       GTCAC
                                 A       AAACCC__
GAM683  TIX1     3'  CATGTAAGGAGCCCAGCA    61739          C
                                TGCTGGGCTCC TGCATG
                                |||||||||| ||||||
                                ACGACCCGAGG ATGTAC
                                      A
GAM683  UBP1     3'  CTGCCATAGCCAAGCA      27224      G   CCCTGC   A
                                TGCT GGCT     ATG CAG
                                |||| ||||     ||| |||
                                ACGA CCGA     TAC GTC
                                  A   _______   C
GAM683  LOC123242 3'  ACCATTAAGCAGCCCAGCA   75589        CCCT  A   CA
                                TGCTGGGCT   GC TGA  GT
                                |||||||||   || |||  ||
                                ACGACCCGA   CG ATT  CA
                                     ____  A   AC
GAM683  LOC144058 5'  CTGGATGCAGGGCACCCAACA  76666    C   CT      GA
                                TG TGGG  CCCTGCAT  CAG
                                || ||||  ||||||||  |||
                                AC ACCC  GGGACGTA  GTC
                                 A   AC       G_
GAM683  LOC147160 5'  CACAGGGGAGCCCAGCA     83958          GCA
                                TGCTGGGCTCCCT   TG
                                ||||||||||||   ||
                                ACGACCCGAGGGG   AC
                                       AC_
GAM683  LOC148870 5'  CACTGCTCCCAGGAGCCCACA  79041    C      C  CAT  _
                                TG TGGGCTCC TG   GA CAGTG
                                || ||||||||  ||   || |||||
                                AC ACCCGAGG AC   CT GTCAC
                                 _       _  C__  C
GAM683  LOC149421 5'  CACTGCCAACGTAGAGGGCCCA 79355         C   A_  A
           GCA                    TGCTGGGCTC CTGC  TG CAGTG
                                |||||||||| ||||  || |||||
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                                ACGACCCGGG GATG  AC GTCAC
                                      A    CA  C
GAM683  LOC151360 3'  CACTGTCACACCGTAGCCCACA 85311    C     CCCTGCA
                                TG TGGGCT      TGACAGTG
                                || ||||||      ||||||||
                                AC ACCCGA      ACTGTCAC
                                 _     TGCCAC_
GAM683  LOC151361 3'  CACTGTCACACCGTAGCCCACA 85320    C     CCCTGCA
                                TG TGGGCT      TGACAGTG
                                || ||||||      ||||||||
                                AC ACCCGA      ACTGTCAC
                                 _     TGCCAC_
GAM683  LOC152286 3'  CACTAGACAGCCAGGAGCCCAG 85626          CT  A  AC_
           CA                     TGCTGGGCTCC  GC TG   AGTG
                                ||||||||||  || ||   ||||
                                ACGACCCGAGG  CG AC   TCAC
                                      AC  _  AGA
GAM683  LOC152674 3'  CACTGTCACCTGGAAGCCCAG  85834       C  TGCA
                                CTGGGCT CC    TGACAGTG
                                ||||||| ||    ||||||||
                                GACCCGA GG    ACTGTCAC
                                    A  TCC_
GAM683  LOC253001 3'  ACCATTAAGCAGCCCAGCA   96249        CCCT  A   CA
                                TGCTGGGCT    GC TGA  GT
                                |||||||||    || |||  ||
                                ACGACCCGA    CG ATT  CA
                                     _____  A   AC
GAM683  LOC255030 3'  ACTGAGAAGAAGCCCAGC    97267        CC  GCATGA
                                GCTGGGCT  CT     CAGT
                                ||||||||  ||     ||||
                                CGACCCGA  GA     GTCA
                                    A_  AGA___
GAM683  LOC51131  3'  ACTGTCACACTCCCAGCA    32277        CTCCC  CA
                                TGCTGGG    TG  TGACAGT
                                |||||||    ||  |||||||
                                ACGACCC    AC  ACTGTCA
                                    TC___  __
GAM684  ACP2     3'  AGAAAGTTCTAGACTG      7851       GC  TC
                                CAGT  CT  AGAACTTTCT
                                ||||  ||  ||||||||||
                                GTCA  GA  TCTTGAAAGA
                                      __  __
GAM684  APTX     5'  AAGAGAAAGAGATCAGGCA   34655       TCAGAA
                                TGCCT     CTTTCTCTT
                                |||||     |||||||||
                                ACGGA     GAAAGAGAA
                                   CTAGA_
GAM684  BCL7A    3'  AGGCTGTCTCCTTAAGGCACTG 40637         C  A__  TT
                                CAGTGCCTT AG   AC  TCT
                                |||||||| ||   ||  |||
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                                GTCACGGAA TC   TG  GGA
                                     T  CTC  TC
GAM684  CLC     3'  AAGAGAAAATACTGAAAGCACA 25105    A   C    AAC
           GG                   CC GTGC TTCAG   TTTCTCTT
                                || |||| |||||   ||||||||
                                GG CACG AAGTC   AAAGAGAA
                                 A   A    ATA
GAM684  CNK     3'  AAGCCCTGAAGGCCTG     14517     T      AA
                                CAG GCCTTCAG  CTT
                                ||| ||||||||  |||
                                GTC CGGAAGTC  GAA
                                  _       CC
GAM684  COL4A3  3'  AAGTGCAGGTTCTGAGGGCACC 48549    A           TCT
           GG                   CC GTGCCTTCAGAACTT   CTT
                                || ||||||||||||||   |||
                                GG CACGGGAGTCTTGGA   GAA
                                 C            CGT
GAM684  CSPG4   3'  AAGAGAGACCTGGAGACAC    8570     C     AAC
                                GTG CTTCAG   TTTCTCTT
                                ||| ||||||   ||||||||
                                CAC GAGGTC   AGAGAGAA
                                  A     C__
GAM684  CYP1B1  3'  AAGAGAAAAGAGAGAAACACTG 3651       CC   AGAAC
                                CAGTG  TTC    TTTCTCTT
                                |||||  |||    ||||||||
                                GTCAC  AAG    AAAGAGAA
                                   A_   AGAGA
GAM684  DLG3    3'  AAGAGAAAAGAGGAGGACTG   40880     G    AGAAC
                                CAGT CCTTC    TTTCTCTT
                                |||| |||||    ||||||||
                                GTCA GGAGG    AAAGAGAA
                                  _    AGA__
GAM684  DLG5    5'  AGGCAGACTCTGAAGGC     82909         A_  T
                                GCCTTCAGA  CT TCT
                                |||||||||  || |||
                                CGGAAGTCT  GA GGA
                                     CA  C
GAM684  FLT1    3'  AAGAGAAACCGGGAGAAGGCAT 8910         AGAAC_
                                GTGCCTTC     TTTCTCTT
                                ||||||||     ||||||||
                                TACGGAAG     AAAGAGAA
                                   AGGGCC
GAM684  GRB10   3'  AGAGAAAATGGCACCTGG    17971     _   TTCAGAAC
                                CCAG TGCC       TTTCTCT
                                |||| ||||       |||||||
                                GGTC ACGG       AAAGAGA
                                  C   TA_______
GAM684  LFG     3'  AAGAGAAAAGGAGCCAAGAACT 76711      GC   CAGAA   _
           GG                   CCAGT  CTT    CTTT CTCTT
                                |||||  |||    |||| |||||
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                                GGTCA  GAA    GAAA GAGAA
                                  A_   CCGAG   A
GAM684  MAN2A2   3'  AAGAGAAAGTTCATTCAC    20391    CCTTCA
                                GTG     GAACTTTCTCTT
                                |||     ||||||||||||
                                CAC     CTTGAAAGAGAA
                                  TTA___
GAM684  NLGN3    3'  AAGAAAAGTTCTTAAAACACT  38596     CC  C      C
                                AGTG  TT AGAACTTT TCTT
                                ||||  || |||||||| ||||
                                TCAC  AA TCTTGAAA AGAA
                                  AA  T      _
GAM684  NPAS1    5'  AAGGTCTCCCGAGGGCACT   59879        A_  _
                                AGTGCCTTC  GA ACTTT
                                |||||||||  || |||||
                                TCACGGGAG  CT TGGAA
                                     CC  C
GAM684  PLAG1    3'  AGTGTGTTCCAAAGGCATT   10605       CA    TTT
                                AGTGCCTT  GAAC   CT
                                ||||||||  ||||   ||
                                TTACGGAA  CTTG   GA
                                    AC    TGT
GAM684  PLXNA1   3'  AGAAAATGAAGGCAGTGG    72309    G      GAAC
                                CCA TGCCTTCA    TTTCT
                                ||| ||||||||    |||||
                                GGT ACGGAAGT    AAAGA
                                  G       A___
GAM684  PPP4R1   3'  AAGAGAAAGTACAGTAAACACT 17620     CCTTCAGA
                                AGTG       ACTTTCTCTT
                                ||||       ||||||||||
                                TCAC       TGAAAGAGAA
                                  AAATGACA
GAM684  ACYP2    3'  AAGAGAAAAATTGTAACACACT 56612      CC  _   AAC
           G                     CAGTG  TT CAG   TTTCTCTT
                                |||||  || |||   ||||||||
                                GTCAC  AA GTT   AAAGAGAA
                                   AC  T   AA_
GAM684  B3GNT6   3'  AGAAATCAGATGAAGGCAT   22503        GAAC_
                                GTGCCTTCA     TTTCT
                                |||||||||     |||||
                                TACGGAAGT     AAAGA
                                     AGACT
GAM684  BAG5     3'  AAGAGAAGGGATAAAGGAC   16835    G   CAGAA
                                GT CCTT     CTTTCTCTT
                                || ||||     |||||||||
                                CA GGAA     GGAAGAGAA
                                 _    ATAG_
GAM684  BIVM     3'  AAGAGAAAAGACTCAAGAAACT 34665     GC   C  AAC
           G                     CAGT  CTT AG   TTTCTCTT
                                ||||  ||| ||   ||||||||
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                                GTCA  GAA TC   AAAGAGAA
                                  AA   C  AGA
GAM684  C15orf5   3'  AGAGAAAAGAAAGCAC      48195      C   AGAAC
                                GTGC TTC     TTTCTCT
                                |||| |||     |||||||
                                CACG AAG     AAAGAGA
                                  A   A____
GAM684  C20orf80  5'  AAGAGAAGAAGATGAAGAAAC  65282    GC     GAAC
                                GT  CTTCA    TTTCTCTT
                                ||  |||||    ||||||||
                                CA  GAAGT    GAAGAGAA
                                 AA     AGAA
GAM684  CLSTN1    3'  AGTTCTGAGGACACTGG     30103       C
                                CCAGTG CTTCAGAACT
                                |||||| ||||||||||
                                GGTCAC GGAGTCTTGA
                                   A
GAM684  DKFZP434P0111 3'  AAGAGAAAGTTTCTGCAC     67368      CTTCA
                                GTGC     GAACTTTCTCTT
                                ||||     ||||||||||||
                                CACG     TTTGAAAGAGAA
                                  TC___
GAM684  DORFIN    5'  AGAATTCTCTGAAGGAAC     31257     G       ACT
                                GT CCTTCAGA   TTCT
                                || ||||||||   ||||
                                CA GGAAGTCT   AAGA
                                 A       CTT
GAM684  FLJ10300  5'  AAGAGAAAGATGAAGACTCTG  35997     TGC     GAA
                                CAG   CTTCA   CTTTCTCTT
                                |||   |||||   |||||||||
                                GTC   GAAGT   GAAAGAGAA
                                  TCA    A__
GAM684  FLJ20373  3'  AAGAGAAGAAGGAAAGGCACAG 35070     A      _ AGAAC
          G                      CC GTGCCTT C     TTTCTCTT
                                || ||||||| |     ||||||||
                                GG CACGGAA G     GAAGAGAA
                                 A      A GAA__
GAM684  FLJ23511  5'  AGAGAAAAACAAGGCAT     49956        CAGAAC
                                GTGCCTT      TTTCTCT
                                |||||||      |||||||
                                TACGGAA      AAAGAGA
                                   CAA___
GAM684  FLJ30681  3'  AGAGAAGAAAGACCACTGG   91782       CCT  AGAAC
                                CCAGTG   TC     TTTCTCT
                                ||||||   ||     |||||||
                                GGTCAC   AG     GAAGAGA
                                   C__  AAA__
GAM684  HDAC11    3'  GAGCTATAGGCACTGG      45717         TC  AACTTT
                                CCAGTGCCT  AG      CTC
                                |||||||||  ||     |||
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                                GGTCACGGA  TC     GAG
                                     TA _______
GAM684  IKKE     5'  AGTGAGCCCTGAAAGCTCTGG  25745      T  C    AA   T
                                CCAG GC TTCAG  CTT CT
                                |||| || |||||  ||| ||
                                GGTC CG AAGTC  GAG GA
                                  T A    CC   T
GAM684  KIAA0680 3'  AGAGAAAATTGAAGCAT     28232      C    AAC
                                GTGC TTCAG   TTTCTCT
                                |||| |||||   |||||||
                                TACG AAGTT   AAAGAGA
                                  _    A__
GAM684  KIAA1228 3'  AGGGGGTGATTCTGAGGCACTG 65035        T   ___   TT
                                CAGTGCCT CAGA   ACT  CT
                                |||||||| ||||   |||  ||
                                GTCACGGA GTCT   TGG  GA
                                     _   TAG   GG
GAM684  KIAA1300 5'  AGGAACCCTGAAGGCA      62860         AAC
                                TGCCTTCAG   TTTCT
                                |||||||||   |||||
                                ACGGAAGTC   AAGGA
                                     CC_
GAM684  KIAA1805 3'  AAGAGAAAGTAGAAGCAGCA   79966     __    AGA
                                TGC  CTTC   ACTTTCTCTT
                                |||  ||||   ||||||||||
                                ACG  GAAG   TGAAAGAGAA
                                  AC    A__
GAM684  LENG1    5'  AAGAGAAAGCTCTGGGCATCCT 84074     __    TT    A
           G                     CAG  TGCC  CAGA CTTTCTCTT
                                |||  ||||  |||| |||||||||
                                GTC  ACGG  GTCT GAAAGAGAA
                                  CT    __    C
GAM684  LHX6     3'  AAGAGAAAACTCTGGGGTCA   26854    C      AC
                                TG CTTCAGA  TTTCTCTT
                                || |||||||  ||||||||
                                AC GGGGTCT  AAAGAGAA
                                 T      CA
GAM684  N4BP3    3'  AGCTCCAGAAGGCACTGG     66250          A_  A
                                CCAGTGCCTTC  GA CT
                                ||||||||||  || ||
                                GGTCACGGAAG  CT GA
                                      AC  C
GAM684  NASP     3'  AGAGGGTGAAGAAACTG     67966      GC    AGA
                                CAGT  CTTC   ACTTTCT
                                ||||  ||||   |||||||
                                GTCA  GAAG   TGGGAGA
                                  AA   ___
GAM684  SMARCF1  3'  AAAATTCTGAAGGAC       57480    G       C
                                GT CCTTCAGAA TTT
                                || |||||||| |||
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                                CA GGAAGTCTT AAA
                                 _       A
GAM684  SMARCF1  3'  AAAATTCTGAAGGAC      20034    G       C
                                GT CCTTCAGAA TTT
                                || ||||||||| |||
                                CA GGAAGTCTT AAA
                                 _       A
GAM684  SMARCF1  3'  AAAATTCTGAAGGAC      37430    G       C
                                GT CCTTCAGAA TTT
                                || ||||||||| |||
                                CA GGAAGTCTT AAA
                                 _       A
GAM684  TED      3'  AAGAGAAAGTCCAGGGACTGG  31630      G   TCA  A
                                CCAGT CCT   GA CTTTCTCTT
                                ||||| |||   || |||||||||
                                GGTCA GGA   CT GAAAGAGAA
                                   G   C__ _
GAM684  TGIF2    3'  AGAAGGGTGCTGAAGGC     41447        AA_
                                GCCTTCAG   CTTTCT
                                ||||||||   ||||||
                                CGGAAGTC   GGAAGA
                                     GTG
GAM684  WBSCR20A  3'  AAGAGAAAGAAGAGACAGCA   35958     CT  AGAA
                                TGC  TC    CTTTCTCTT
                                |||  ||    |||||||||
                                ACG  AG    GAAAGAGAA
                                  AC  AGAA
GAM684  LOC115273 3'  AGAAAGTTCTGATGGCCAGG   73356    AGT   T
                                CC   GCC TCAGAACTTTCT
                                ||   ||| ||||||||||||
                                GG   CGG AGTCTTGAAAGA
                                 AC_   T
GAM684  LOC145761 5'  AAGAGAAAGTGGAAGGCATGG  83472     G      AGA
                                CCA TGCCTTC   ACTTTCTCTT
                                ||| |||||||   ||||||||||
                                GGT ACGGAAG   TGAAAGAGAA
                                  _      G__
GAM684  LOC146179 5'  AGAAAGTTTTGGGCCT      77700    T   TT
                                AG GCC  CAGAACTTTCT
                                || |||  ||||||||||
                                TC CGG  GTTTTGAAAGA
                                  _  __
GAM684  LOC147072 3'  AAGAGAAAGTGAGAAGAAACTG 60407      GC    AGA
                                CAGT  CTTC   ACTTTCTCTT
                                ||||  ||||   ||||||||||
                                GTCA  GAAG   TGAAAGAGAA
                                  AA    AG_
GAM684  LOC148758 5'  AGAAAGTTCTGAGAAAC     78962    GCC
                                GT   TTCAGAACTTTCT
                                ||   ||||||||||||
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                                CA   GAGTCTTGAAAGA
                                 AA_
GAM684   LOC148932 3'  AGGAATCTGAAGGCACTGG   79103            AC
                                CCAGTGCCTTCAGA  TTTCT
                                ||||||||||||||  |||||
                                GGTCACGGAAGTCT  AAGGA
                                        __
GAM684   LOC149386 5'  AAGTTTTGAAAGCACT      84400       C
                                AGTGC TTCAGAACTT
                                ||||| ||||||||||
                                TCACG AAGTTTTGAA
                                   A
GAM684   LOC150139 3'  AGAAAATAGAAAAAGGCGCTGG 79583          CAGAAC_
                                CCAGTGCCTT      TTTCT
                                ||||||||||      |||||
                                GGTCGCGGAA      AAAGA
                                      AAAGATA
GAM684   LOC152756 3'  AAGATGCAGTTCTGAAAACCTG 85871     TGCC        TTC
                                CAG    TTCAGAACT   TCTT
                                |||    |||||||||   ||||
                                GTC    AAGTCTTGA   AGAA
                                  CAA_        CGT
GAM684   LOC162333 5'  AAGAGAAAGCGATGACACTG   87114      CCT   GAA
                                CAGTG   TCA   CTTTCTCTT
                                |||||   |||   |||||||||
                                GTCAC   AGT   GAAAGAGAA
                                   ___   AGC
GAM684   LOC199221 3'  AAGAGAAGCTCGAAAGCATGG  80347     G   C   A A   T
                                CCA TGC TTC GA CTT CTCTT
                                ||| ||| ||| || ||| |||||
                                GGT ACG AAG CT GAA GAGAA
                                  _   A   _  C   _
GAM684   LOC203339 3'  AGAGAAAATTGGGCCTG     90542     T   TCAGAAC
                                CAG GCCT      TTTCTCT
                                ||| ||||      |||||||
                                GTC CGGG      AAAGAGA
                                  _    TTA____
GAM684   LOC255017 3'  AGAAAGAGGAACTGG       94624       G   TCAGAA
                                CCAGT CCT     CTTTCT
                                ||||| |||     ||||||
                                GGTCA GGA     GAAAGA
                                   A  _______
GAM684   LOC256021 3'  AAGAGAAACAAAGACAACACTG 96512       CCT  AGAAC
            G                    CCAGTG   TC    TTTCTCTT
                                ||||||  ||    ||||||||
                                GGTCAC   AG    AAAGAGAA
                                   AAC  AAAC_
GAM684   LOC90139  3'  AGAATCCCGAAGGCAT      55396         A_  ACT
                                GTGCCTTC  GA   TTCT
                                ||||||||  ||   ||||
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                                TACGGAAG CT   AAGA
                                    CC ___
GAM685  ADRA1A   3' GCACAAATCCAACATG     52784      AAGCC A
                                CATGT    TG ATTTGTGC
                                |||||    || ||||||||
                                GTACA    AC TAAACACG
                                   _____ C
GAM685  AEGL1    5' GCACAAATACACTACAT     6679       AGCC A
                                ATGTA    TG ATTTGTGC
                                |||||    || ||||||||
                                TACAT    AC TAAACACG
                                   C___ A
GAM685  CDH2     3' GCACAAATGTTTTACAT     8377        CCTGA
                                ATGTAAG    ATTTGTGC
                                |||||||    ||||||||
                                TACATTT    TAAACACG
                                    TG___
GAM685  CHRNE    3' GCCCTCAGGCCCACAGGT    3586     A  AA     ATTTGT
                                ACC TGT  GCCTGA     GC
                                ||| |||  ||||||     ||
                                TGG ACA  CGGACT     CG
                                  _  CC     CC____
GAM685  COL4A3   3' GGCCATGGCTCACATGGT    3622        A   TGAATT  T
                                ACCATGT AGCC     TG GCC
                                ||||||| ||||     || |||
                                TGGTACA TCGG     AC CGG
                                    C   T_____ _
GAM685  COL4A3   3' GGCCATGGCTCACATGGT    48557       A   TGAATT  T
                                ACCATGT AGCC     TG GCC
                                ||||||| ||||     || |||
                                TGGTACA TCGG     AC CGG
                                    C   T_____ _
GAM685  COL4A3   3' GGCCATGGCTCACATGGT    48568       A   TGAATT  T
                                ACCATGT AGCC     TG GCC
                                ||||||| ||||     || |||
                                TGGTACA TCGG     AC CGG
                                    C   T_____ _
GAM685  CYP3A4   3' ACAAGCCTGGCCTACATGGT  33923        A  TGAA
                                ACCATGTA GCC    TTTGT
                                |||||||| |||    |||||
                                TGGTACAT CGG    GAACA
                                    C   TCC_
GAM685  HIVEP3   5' GGCACAAACCCAGCAGCCTCA 44439    TAA __   AA
                                TG   GC  CTG  TTTGTGCC
                                ||   ||  |||  ||||||||
                                AC   CG  GAC  AAACACGG
                                 TC_  AC   CC
GAM685  RECK     3' GCAACAGGCTCACTGGT     40869     T  A     AAT
                                ACCA GT AGCCTG   TTGT
                                |||| || ||||||   ||||
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                                TGGT CA TCGGAC   AACG
                                  _ C     ___
GAM685  TNFSF8   3'  GCACAAATTTAATACA      6966      AGCC
                                TGTA   TGAATTTGTGC
                                ||||   ||||||||||
                                ACAT   ATTTAAACACG
                                  A___
GAM685  ADAR3    3'  CACAAATTCAGAACGTG     38018      AAGC
                                CATGT   CTGAATTTGTG
                                |||||   ||||||||||
                                GTGCA   GACTTAAACAC
                                  A___
GAM685  BIVM     3'  CACAAATTCACTTA       34667      CC
                                TAAG  TGAATTTGTG
                                ||||  ||||||||||
                                ATTC  ACTTAAACAC
                                  __
GAM685  C20orf160 3'  GCAGTTACAGGATTACATGGT  54648         G    AAT
                                ACCATGTAA CCTG   TTGT
                                ||||||||| ||||   ||||
                                TGGTACATT GGAC   GACG
                                     A    ATT
GAM685  EPHA7    3'  CACAAATTTGCTGCACA     15433     A_   CT
                                TGT  AGC  GAATTTGTG
                                |||  |||  |||||||||
                                ACA  TCG  TTTAAACAC
                                  CG   __
GAM685  FLJ12783  3'  AGTTCAGGCTCACTG       48675     T  A
                                CA GT AGCCTGAATT
                                || || ||||||||||
                                GT CA TCGGACTTGA
                                  _  C
GAM685  HSC3     3'  CACAGGTTCAGACTACA     59067      A C
                                TGTA G CTGAATTTGTG
                                |||| | ||||||||||
                                ACAT C GACTTGGACAC
                                  _ A
GAM685  KIAA0316  3'  GCACAAATGCTCTTCACAGTGG 69674      _  _  CCTGA
           T                     ACCA TGT AAG     ATTTGTGC
                                ||||| ||| |||     ||||||||
                                TGGT ACA TTC     TAAACACG
                                  G   C   TCG__
GAM685  KIAA0453  3'  GCACAAGTAGCTACATAGT    69047     C     A  CTGA
                                AC ATGTA GC    ATTTGTGC
                                || ||||| ||    ||||||||
                                TG TACAT CG    TGAACACG
                                 A     _  A___
GAM685  KIAA1423  3'  AATTCAAGTTTACATG       61719          C
                                CATGTAAGC TGAATT
                                ||||||||| ||||||
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                                GTACATTTG ACTTAA
                                     A
GAM685  KIAA1691  3'  GCACAAATGCTGTCCATGG   92556      TA_  CTGA
                                CCATG  AGC   ATTTGTGC
                                |||||  |||   ||||||||
                                GGTAC  TCG   TAAACACG
                                  CTG  ____
GAM685  PPP1R3B  3'  GCCAGGTTCAGATTACA    44820      GC       T
                                TGTAA  CTGAATTTG GC
                                |||||  ||||||||| ||
                                ACATT  GACTTGGAC CG
                                  A_       _
GAM685  SFXN2    3'  GCAGCAGAGTTACATGGT    73946        GC   AATTTG
                                ACCATGTAA  CTG     TGC
                                |||||||||  |||     |||
                                TGGTACATT  GAC     ACG
                                     GA   G_____
GAM685  TBC1D2   5'  TAAATTCAGACCTACTGGT   37321     T   AGC
                                ACCA GTA   CTGAATTTG
                                ||||  |||   |||||||||
                                TGGT CAT   GACTTAAAT
                                  _   CCA
GAM685  ZNF347   3'  GGCTTTATTCAGGCCTCACA  50848     AA_      TTGT
                                TGT   GCCTGAAT   GCC
                                |||   ||||||||   |||
                                ACA   CGGACTTA   CGG
                                  CTC       TTT_
GAM685  LOC134147 3'  CACAAATTCAGTAGGACGT   57158     AAGC
                                ATGT   CTGAATTTGTG
                                ||||   ||||||||||
                                TGCA   GACTTAAACAC
                                  GGAT
GAM685  LOC151195 5'  GCACAAATTTATTTACA     80169       CC
                                TGTAAG  TGAATTTGTGC
                                ||||||  ||||||||||
                                ACATTT  ATTTAAACACG
                                      __
GAM685  LOC152860 3'  AATTCCAGCTTACATGG     80695         CT
                                CCATGTAAGC  GAATT
                                |||||||||  |||||
                                GGTACATTCG  CTTAA
                                     AC
GAM685  LOC200382 3'  ACAGGGGCCAGACTTACATG   88801        C   AA_
                                CATGTAAG CTG   TTTGT
                                ||||||||  |||   |||||
                                GTACATTC GAC   GGACA
                                     A   CGG
GAM685  LOC93622  3'  ACAGTCATTCCAGGCTTAGATG 56929     G      _   __
                                CAT TAAGCCTG AAT  TTGT
                                |||  ||||||||  |||  ||||
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                                GTA ATTCGGAC TTA  GACA
                                  G       C   CT
GAM686  PRO2900  3'  TGTGCGCATCTCAATCA     37808         CC
                                TGATTGAG  GCGCACG
                                ||||||||  |||||||
                                ACTAACTC  CGCGTGT
                                    TA
GAM687  ADAMTS4  3'  TCTTGAACTCCTGACCTCA   17522            TG
                                TGAGGTCAGGAGTT  AGA
                                ||||||||||||||  |||
                                ACTCCAGTCCTCAA  TCT
                                        GT
GAM687  AQP6     3'  GTCTCAAACTCCTGACCT    7959
                                AGGTCAGGAGTTTGAGAC
                                ||||||||||||||||||
                                TCCAGTCCTCAAACTCTG

GAM687  AQP6     3'  GTCTCAAACTCCTGACCT    53939
                                AGGTCAGGAGTTTGAGAC
                                ||||||||||||||||||
                                TCCAGTCCTCAAACTCTG

GAM687  ARSF     5'  GCTGGTCTCGAACTCCCGACCT 64601         A
          CA                      TGAGGTC GGAGTTTGAGACTAGC
                                ||||||| ||||||||||||||||
                                ACTCCAG CCTCAAGCTCTGGTCG
                                    C
GAM687  ATP1B2   3'  GCTGGTCTCGAACTCCCGACCT 8053         A
          CA                      TGAGGTC GGAGTTTGAGACTAGC
                                ||||||| ||||||||||||||||
                                ACTCCAG CCTCAAGCTCTGGTCG
                                    C
GAM687  ATP7A    3'  CTGGTCTTAAACTCCTAACCTC 3522         C
          A                       TGAGGT AGGAGTTTGAGACTAG
                                ||||||| ||||||||||||||||
                                ACTCCA TCCTCAAATTCTGGTC
                                    A
GAM687  AXL      3'  GCTGGTCTAAAACTCCTGACCT 8103             G
          CA                      TGAGGTCAGGAGTTT AGACTAGC
                                ||||||||||||||| ||||||||
                                ACTCCAGTCCTCAAA TCTGGTCG
                                        A
GAM687  AXL      3'  GCTGGTCTAAAACTCCTGACCT 41600            G
          CA                      TGAGGTCAGGAGTTT AGACTAGC
                                ||||||||||||||| ||||||||
                                ACTCCAGTCCTCAAA TCTGGTCG
                                        A
GAM687  C7       3'  GTCTCCAACTCCTGACCTCA  5166             T
                                TGAGGTCAGGAGTT GAGAC
                                ||||||||||||| |||||
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                                ACTCCAGTCCTCAA CTCTG
                                        C
GAM687  CBFA2T2  3'  GCTGGTCTCAAACCCCGGACCT 17473       A  A
           CA                    TGAGGTC GG GTTTGAGACTAGC
                                 ||||||| || ||||||||||||
                                 ACTCCAG CC CAAACTCTGGTCG
                                    G  C
GAM687  CCNF     3'  GCTAGTCTCGAACTCATGACCT 8320         G
           CA                    TGAGGTCA GAGTTTGAGACTAGC
                                 |||||||| ||||||||||||||
                                 ACTCCAGT CTCAAGCTCTGATCG
                                    A
GAM687  CHRNB4   3'  GCTGATTTCGAACTCCTGACCT 5633              C
           CA                    TGAGGTCAGGAGTTTGAGA TAGC
                                 |||||||||||||||||| ||||
                                 ACTCCAGTCCTCAAGCTTT GTCG
                                          A
GAM687  CLECSF12 3'  TAGTCCCGAACTCCTGACCTCA 76699            A
                                 TGAGGTCAGGAGTTTG GACTA
                                 |||||||||||||||| |||||
                                 ACTCCAGTCCTCAAGC CTGAT
                                        C
GAM687  CORO2B   3'  CTCTAACCTCCTGACCTCA   64571          _  T
                                 TGAGGTCAGGAG TT GAG
                                 |||||||||||| || |||
                                 ACTCCAGTCCTC AA CTC
                                       C  T
GAM687  CYP1A2   3'  CTAGTCTCAAACTCCTGACCTC 69107
           A                     TGAGGTCAGGAGTTTGAGACTAG
                                 |||||||||||||||||||||||
                                 ACTCCAGTCCTCAAACTCTGATC

GAM687  CYP1A2   3'  GCTTGTCTCGAACTCCTGACCC 69118    A           T
           CA                    TG GGTCAGGAGTTTGAGAC AGC
                                 || ||||||||||||||| |||
                                 AC CCAGTCCTCAAGCTCTG TCG
                                  C            T
GAM687  CYP1A2   3'  CTAGTCTCAAACTCCTGACCTC 5687
           A                     TGAGGTCAGGAGTTTGAGACTAG
                                 |||||||||||||||||||||||
                                 ACTCCAGTCCTCAAACTCTGATC

GAM687  CYP1A2   3'  GCTTGTCTCGAACTCCTGACCC 5698    A           T
           CA                    TG GGTCAGGAGTTTGAGAC AGC
                                 || ||||||||||||||| |||
                                 AC CCAGTCCTCAAGCTCTG TCG
                                  C            T
GAM687  DFFB     3'  GCTGGTCTCAAACTCCTGACCT 87391
           CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                 |||||||||||||||||||||||
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                                ACTCCAGTCCTCAAACTCTGGTCG

GAM687  DFFB    3'  GCTGTTCTCGAACTCCTGACCT 87392                C
             CA                  TGAGGTCAGGAGTTTGAGA TAGC
                                 |||||||||||||||||| ||||
                                 ACTCCAGTCCTCAAGCTCT GTCG
                                           T
GAM687  DISC1   3'  GTCTCAAACTCCTGACCTCA  37890
                                 TGAGGTCAGGAGTTTGAGAC
                                 ||||||||||||||||||||
                                 ACTCCAGTCCTCAAACTCTG

GAM687  DSP     3'  TCTCAAACCCCCAACCCA   15342   A  CA  A
                                 TG GGT  GG GTTTGAGA
                                 || |||  || ||||||||
                                 AC CCA  CC CAAACTCT
                                  _  AC  C
GAM687  EPB72   3'  GCTAGTCACGAACTCCTAACCT 14605       C       A
             CA                  TGAGGT AGGAGTTTG GACTAGC
                                 |||||| ||||||||| |||||||
                                 ACTCCA TCCTCAAGC CTGATCG
                                    A       A
GAM687  EVC     3'  TCTCGAACTCCTGACCTCA   27300
                                 TGAGGTCAGGAGTTTGAGA
                                 ||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTCT

GAM687  FCAR    3'  GCTGGTCTCGAACTCCTGACCT 55751
             CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  FCAR    3'  GCTGGTCTCGAACTCCTGACCT 55762
             CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  FCAR    3'  GCTGGTCTCGAACTCCTGACCT 55773
             CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  FCAR    3'  GCTGGTCTCGAACTCCTGACCT 55784
             CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  FCAR    3'  GCTGGTCTCGAACTCCCGACCT 55802       A
             CA                  TGAGGTC GGAGTTTGAGACTAGC
                                 ||||||| ||||||||||||||||
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                                ACTCCAG CCTCAAGCTCTGGTCG
                                    C
GAM687  FCAR    3'  GCTGGTCTCGAACTCCTGACCT 8856
                CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                    ||||||||||||||||||||||||
                                    ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  FZD4    3'  GCTGGTCTCGAACTCCTGACCT 24145
                CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                    ||||||||||||||||||||||||
                                    ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  G6PC    3'  GCTGGTCTCGAACTCCTGACCT 3830
                CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                    ||||||||||||||||||||||||
                                    ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  GRAF    3'  GCTGATCTCGAACTCCTGACCT 30565              C
                CA                  TGAGGTCAGGAGTTTGAGA TAGC
                                    |||||||||||||||||| ||||
                                    ACTCCAGTCCTCAAGCTCT GTCG
                                              A
GAM687  HCN4    3'  GCCAGTCCCAGCCTGACCTC  18490        AGT  A   A
                                    GAGGTCAGG  TTG GACT GC
                                    |||||||||  ||| |||| ||
                                    CTCCAGTCC  GAC CTGA CG
                                         ___  C   C
GAM687  HCS     3'  GCTGGTCTCAAACTCCTGAGCT 38477     G
                CA                  TGAG TCAGGAGTTTGAGACTAGC
                                    |||| ||||||||||||||||||
                                    ACTC AGTCCTCAAACTCTGGTCG
                                      G
GAM687  HSPA5   3'  CTAGTCTTCCCTTACCTCA   18081      C  AGTTT
                                    TGAGGT AGG    GAGACTAG
                                    ||||||| |||    ||||||||
                                    ACTCCA TCC    TTCTGATC
                                       T  C_____
GAM687  IFNAR2  3'  GCTGGTCTCGAACTCCTGACCT 6044
                CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                    ||||||||||||||||||||||||
                                    ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  IL11    3'  GCTGGTTTCGAACTCCTGACCT 5329
                CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                    ||||||||||||||||||||||||
                                    ACTCCAGTCCTCAAGCTTTGGTCG

GAM687  JAK3    3'  GCTGATCTCGAACTCCTAACCT 4005        C          C
                CA                  TGAGGT AGGAGTTTGAGA TAGC
                                    ||||||  |||||||||||| ||||
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                                ACTCCA TCCTCAAGCTCT GTCG
                                   A          A
GAM687  KMO      3'  GCCAGTCTCAAACTCCTGGCCT 13450                A
             CA                   TGAGGTCAGGAGTTTGAGACT GC
                                  |||||||||||||||||||| ||
                                  ACTCCGGTCCTCAAACTCTGA CG
                                                C
GAM687  MAK      3'  GCTGGTCTCAAACTCCTGACCT 19763
             CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                  |||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  MEFV     3'  GCCGGTCTCAAACTCCTGACCT 4139                 TA
             CA                   TGAGGTCAGGAGTTTGAGAC  GC
                                  |||||||||||||||||||  ||
                                  ACTCCAGTCCTCAAACTCTG  CG
                                                GC
GAM687  MEFV     3'  GCTGGTCTCGAACTCCTGACCT 4148
             CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                  |||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  MFI2     3'  GCTGGTCTCAAACCCCCAGCCT 52817       CA  A
             CA                   TGAGGT  GG GTTTGAGACTAGC
                                  ||||||  ||  ||||||||||||
                                  ACTCCG  CC CAAACTCTGGTCG
                                     AC  C
GAM687  MICB     3'  GCCCAGTTTCAAACTCCTGACC 19827                A_
             TCA                   TGAGGTCAGGAGTTTGAGACT  GC
                                  |||||||||||||||||||  ||
                                  ACTCCAGTCCTCAAACTTTGA  CG
                                                CC
GAM687  MLANA    3'  GCTGGTCTCAAACTCCTGACCT 18588
             CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                  |||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  NCOA6    5'  GCTAGTCTGGAACTCCTGAGCT 25970      G        G
             CA                   TGAG TCAGGAGTTT AGACTAGC
                                  |||| |||||||||| ||||||||
                                  ACTC AGTCCTCAAG TCTGATCG
                                     G         G
GAM687  NCOA6    5'  GCTGGTCTCAAACTCCTGACCT 25975
             CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                  |||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  NDRG3    3'  GCTGGTCTCAAACTCCTGACCT 49301
             CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                  |||||||||||||||||||||||
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                                ACTCCAGTCCTCAAACTCTGGTCG

GAM687  NQO1     3'  GCTGGTCTCAAACTCCTGACCT 6163
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  PDE6B    3'  GCTGGTCTCGAACTCCTGACCT 4287
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  PER2     3'  GCTGGTCTCGAACTCCTGACCT 43038
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  PIK3CD   3'  GCTGGTCTCGAACTCCTGACCT 17248
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  PRKR     3'  GCTGGTCTCAAACTCCTGACCT 10885
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  RAP1GA1  3'  CAGCCTCCTGGCCCCA     11250    A       T
                                  TG GGTCAGGAG TTG
                                  || |||||||| |||
                                  AC CCGGTCCTC GAC
                                    C       C
GAM687  RGS9     5'  GCTAGCCTCAAACTCCTGGGCT 13834      G          A
                CA                TGAG TCAGGAGTTTGAG CTAGC
                                  |||| |||||||||||| |||||
                                  ACTC GGTCCTCAAACTC GATCG
                                    G          C
GAM687  RHD      3'  GCTGATCTCAAACTCCTGACCT 32310               C
                CA                TGAGGTCAGGAGTTTGAGA TAGC
                                  |||||||||||||||||| ||||
                                  ACTCCAGTCCTCAAACTCT GTCG
                                                     A
GAM687  RHD      3'  GCTGATCTCAAACTCCTGACCT 32619               C
                CA                TGAGGTCAGGAGTTTGAGA TAGC
                                  |||||||||||||||||| ||||
                                  ACTCCAGTCCTCAAACTCT GTCG
                                                     A
GAM687  RP2      3'  GCTGGTCTCGAACTCCTGACCT 22620
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  RPP30    3'  GTCTCAATCTCCTGACCTCA  21170          T
                                TGAGGTCAGGAG TTGAGAC
                                |||||||||||| |||||||
                                ACTCCAGTCCTC AACTCTG
                                       T
GAM687  SAS      3'  GCTGGTCTCGAACTCCTGACCT 19957
              CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  SCML2    3'  GCTGGTCTCAAACTCCTGACCT 20321
              CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  SEDL     3'  GCTGGTTTCAAACTCCTGACCT 27350
              CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTTTGGTCG

GAM687  SFRP1    3'  CAGTCTCAGATGCCCC      11564    TCA  A        A
                                GG   GG GTTTGAGACT G
                                ||   || |||||||||| |
                                CC   CC TAGACTCTGA C
                                  ___  G         C
GAM687  SH3BP2   3'  GCTGGTCTCGAACTCCTGACCT 11607
              CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  SHOX     3'  GCTGGTCTCGAACTCCTGACCT 22541
              CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  SIL      3'  GCTGGTCTCAAACTCCCGACCT 11694         A
              CA                  TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
                                  ACTCCAG CCTCAAACTCTGGTCG
                                      C
GAM687  SLA2     3'  GCTGGTGTCGAACTCCTGACCT 49903               G
              CA                  TGAGGTCAGGAGTTTGA ACTAGC
                                  |||||||||||||||| ||||||
                                  ACTCCAGTCCTCAAGCT TGGTCG
                                             G
GAM687  SLC6A12  3'  CAAACCCCTGACTTCA      11731          A
                                TGAGGTCAGG GTTTG
                                |||||||||| |||||
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                                ACTTCAGTCC CAAAC
                                      C
GAM687  SNX15    3'  GCTGGTCTCGAACTCCTGACCT 73746
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  SPN      3'  GCTGGTCTCAAACTCCTGACCT 11924
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  SULT2B1  5'  GCTGGTCTCAAACTCCTGACCT 16028
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  TAT      3'  GCTGGTCTCAAACTCCTGACCT 4472
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  TCOF1    3'  AGCTCCCATGACCTCA      4484          __
                                  TGAGGTCA  GGAGTT
                                  ||||||||  ||||||
                                  ACTCCAGT  CCTCGA
                                        AC
GAM687  TES      3'  GCTGGTCTCAAACTCCTGACCT 72009
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  TIM3     3'  GTCTCAAACTCCTGACCTCA   51347
                                  TGAGGTCAGGAGTTTGAGAC
                                  ||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTG

GAM687  TMPRSS3  3'  GCTGCTCTCAAACCCCTGACCT 43797          A       C
            CA                    TGAGGTCAGG GTTTGAGA TAGC
                                  |||||||||| |||||||| ||||
                                  ACTCCAGTCC CAAACTCT GTCG
                                        C       C
GAM687  TMPRSS3  3'  GCTGCTCTCAAACCCCTGACCT 50508          A       C
            CA                    TGAGGTCAGG GTTTGAGA TAGC
                                  |||||||||| |||||||| ||||
                                  ACTCCAGTCC CAAACTCT GTCG
                                        C       C
GAM687  TMPRSS3  3'  GCTGCTCTCAAACCCCTGACCT 50529          A       C
            CA                    TGAGGTCAGG GTTTGAGA TAGC
                                  |||||||||| |||||||| ||||
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                                ACTCCAGTCC CAAACTCT GTCG
                                      C       C
GAM687  TNFRSF10B 3'  GCTGGTCTCGAACTCCTGACCT 13874
           CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  TRAF5    3'  GCTGATCTCAAACTCCTGACCT 16083                C
           CA                   TGAGGTCAGGAGTTTGAGA TAGC
                                |||||||||||||||||| ||||
                                ACTCCAGTCCTCAAACTCT GTCG
                                           A
GAM687  TRPM6    3'  GCTGGTCTCAAACTCCTGACCT 34543
           CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM687  TRPV1    3'  GCTGGTCTCGAACTCCTGACCT 38091
           CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  TRPV1    3'  GCTGGTCTCGAACTCCTGACCT 54809
           CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  TRPV1    3'  GCTGGTCTCGAACTCCTGACCT 54842
           CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  TRPV1    3'  GCTGGTCTCGAACTCCTGACCT 54875
           CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  VHL      3'  GCTGGTTTCAAACTCCTGACCT 5075
           CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTTTGGTCG

GAM687  XRCC2    3'  GCTGGTCTCGAACTCCTGACCT 18328
           CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  ZNF157   3'  GCTGGTCTCTAACTCCTGACCT 12879             T
           CA                   TGAGGTCAGGAGTT GAGACTAGC
                                |||||||||||||| |||||||||
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                                ACTCCAGTCCTCAA CTCTGGTCG
                                       T
GAM687  AAK1     3'  GCTGGTCTCGAACTCCTGACCT 29851
           CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  ARHGAP5  5'  GCTGGTGTCGAACTCCCAACCT 77077       CA        G
           CA                    TGAGGT  GGAGTTTGA ACTAGC
                                 ||||||  ||||||||| ||||||
                                 ACTCCA  CCTCAAGCT TGGTCG
                                   AC        G
GAM687  ATP1B4   3'  GCTGGTCTCGAACTCCTGACCT 23824
           CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  BA108L7.2 3'  GCTAGTCTCGAACTCCTGACCT 48264
           CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTCTGATCG

GAM687  C13orf1   3'  GCTGGTCTCAAACTCCTGACCT 39972
           CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCCAGTCCTCAAACTCTGGTCG

GAM687  C20orf142 3'  GCTGGTCTCAAACTCCTGACCG 74779     A
           CA                    TG GGTCAGGAGTTTGAGACTAGC
                                 || ||||||||||||||||||||
                                 AC CCAGTCCTCAAACTCTGGTCG
                                  G
GAM687  C21orf25  3'  GCTGGTCTCGAACTCCTGACCT 63551
           CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  C9orf9    3'  GTCTCAATCTCCTGACCTCA   38522           T
                                 TGAGGTCAGGAG TTGAGAC
                                 ||||||||||| |||||||
                                 ACTCCAGTCCTC AACTCTG
                                        T
GAM687  CDC14B    3'  GCTGGTCTCGAACTCCTGACCT 52857
           CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  CHRAC1    3'  GCTTGTCTCAAACTCCTAACCT 33875       C          T
           CA                    TGAGGT AGGAGTTTGAGAC AGC
                                 |||||| |||||||||||| |||
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                                ACTCCA TCCTCAAACTCTG TCG
                                   A          T
GAM687  CPSF2    3'  GCTGGCCTCAAACTCCCGACCT 61590       A       A
           CA                    TGAGGTC GGAGTTTGAG CTAGC
                                 ||||||| |||||||||| |||||
                                 ACTCCAG CCTCAAACTC GGTCG
                                    C        C
GAM687  CPSF2    3'  GCTGGTCTCAAACTCCTGACCT 61594
           CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCCAGTCCTCAAACTCTGGTCG

GAM687  CSL4     3'  GCTGTCTCAAACTCCTGGCCTC 32114              T
           A                     TGAGGTCAGGAGTTTGAGAC AGC
                                 |||||||||||||||||| |||
                                 ACTCCGGTCCTCAAACTCTG TCG
                                                 _
GAM687  DBR1     3'  GTCTCCAACTCCTGACCTCA  32536           T
                                 TGAGGTCAGGAGTT GAGAC
                                 |||||||||||||| |||||
                                 ACTCCAGTCCTCAA CTCTG
                                       C
GAM687  DCOHM    3'  GCTGATCTCAAACTCCTGGCCT 49606             C
           CA                    TGAGGTCAGGAGTTTGAGA TAGC
                                 |||||||||||||||||| ||||
                                 ACTCCGGTCCTCAAACTCT GTCG
                                          A
GAM687  DKFZp434A2417 3'  GCTGATCTCAAACTCCCAACCT 66105      CA       C
           CA                    TGAGGT  GGAGTTTGAGA TAGC
                                 ||||||  |||||||||| ||||
                                 ACTCCA  CCTCAAACTCT GTCG
                                    AC        A
GAM687  DKFZP434J037 3'  GCTGGTCTCAAACTCCCGACCT 48217       A
           CA                    TGAGGTC GGAGTTTGAGACTAGC
                                 ||||||| ||||||||||||||||
                                 ACTCCAG CCTCAAACTCTGGTCG
                                    C
GAM687  DKFZP564O0423 3'  GCTGTTCTCAAACTCCTGGCCT 91695             C
           CA                    TGAGGTCAGGAGTTTGAGA TAGC
                                 |||||||||||||||||| ||||
                                 ACTCCGGTCCTCAAACTCT GTCG
                                          T
GAM687  DSCR6    3'  TTTGAACTCCTGACCTCA    38555          TG
                                 TGAGGTCAGGAGTT  AG
                                 |||||||||||||  ||
                                 ACTCCAGTCCTCAA  TT
                                       GT
GAM687  EVI5     3'  GCTGATCTCAAACTTCTGACCT 19002            C
           CA                    TGAGGTCAGGAGTTTGAGA TAGC
                                 |||||||||||||||||| ||||
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                                ACTCCAGTCTTCAAACTCT GTCG
                                                    A
GAM687  EVI5    3'  GCTGGTCTCGAACTCCTAACCT 19004       C
            CA                    TGAGGT AGGAGTTTGAGACTAGC
                                  |||||| ||||||||||||||||||
                                  ACTCCA TCCTCAAGCTCTGGTCG
                                    A
GAM687  FBP17   3'  GCTGGTCTCAAACTCCTGACCT 72799
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  FLJ10232 3' GCTGGTCCCGAACTCCTGACCT 35928              A
            CA                    TGAGGTCAGGAGTTTG GACTAGC
                                  |||||||||||||||| |||||||
                                  ACTCCAGTCCTCAAGC CTGGTCG
                                              C
GAM687  FLJ10298 3' GCTGGTCTCAAACTCCTGACCT 35992
                                  AGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  TCCAGTCCTCAAACTCTGGTCG

GAM687  FLJ10607 3' GCCGGTCTCAAACTCCTGAGCT 77116      G           TA
            CA                    TGAG TCAGGAGTTTGAGAC  GC
                                  |||| ||||||||||||||  ||
                                  ACTC AGTCCTCAAACTCTG  CG
                                    G             GC
GAM687  FLJ10901 3' GCTGGTCTCGAACTCCTGACCT 36831
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  FLJ12363 3' GCTGGTCTCAAACTCCTGACCT 49687
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  FLJ12649 3' GCTAGTCTCGAAATCCTGGCCT 44779          G
            CA                    TGAGGTCAGGA TTTGAGACTAGC
                                  |||||||||| ||||||||||
                                  ACTCCGGTCCT AAGCTCTGATCG
                                        A
GAM687  FLJ12668 3' GCTGGTCTCAAACTCCTGACCT 46519
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  FLJ12687 3' GCTGGTCTCAAACTCCTGACCT 46200
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAACTCTGGTCG

GAM687  FLJ12787  3'  GCTGGTCTAAAACTCCTGACCT 49750            G
            CA                  TGAGGTCAGGAGTTT AGACTAGC
                                |||||||||||||| ||||||||
                                ACTCCAGTCCTCAAA TCTGGTCG
                                          A
GAM687  FLJ12975  3'  TCTCGAACTCCTGACCTCA   69594
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCT

GAM687  FLJ13072  5'  GCTGGTCTCGAACTCCTGACCT 89819
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  FLJ13102  3'  GCTGGTCTCGAACTCCTGACCT 46014
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  FLJ14351  3'  GCCAGTCTTGAACTCCTGAGCT 45325     G       TG    A
            CA                  TGAG TCAGGAGTT  AGACT GC
                                |||| |||||||||  ||||| ||
                                ACTC AGTCCTCAA  TCTGA CG
                                  G       GT    C
GAM687  FLJ20034  3'  GCTGGTCTCAAACTCCCGACCT 34376       A
            CA                  TGAGGTC GGAGTTTGAGACTAGC
                                |||||||| ||||||||||||||||
                                ACTCCAG CCTCAAACTCTGGTCG
                                    C
GAM687  FLJ20034  3'  GTCTCAAACTCCCGACCTCA   34382       A
                                TGAGGTC GGAGTTTGAGAC
                                |||||||| ||||||||||||
                                ACTCCAG CCTCAAACTCTG
                                    C
GAM687  FLJ20419  3'  CAAACTCCCGCCTCA       35139       CA
                                TGAGGT  GGAGTTTG
                                ||||||  ||||||||
                                ACTCCG  CCTCAAAC
                                   C_
GAM687  FLJ20452  3'  GCTGGTCTCGAACTCCTGACCT 35205
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  FLJ20700  3'  GCTGGTCTCGAACTCCTGACCT 35580
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  FLJ20813  3'  GCTGGTCTCAAACTCCTGACCT 35687
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM687  FLJ21324  5'  GCTGGTCTCAAACTCCTGACCT 91206
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM687  FLJ21459  3'  GCTGGTCTCGAACTCCTGACCT 44519
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  FLJ22329  3'  CTGGTCTCGAACTCCTGACCTC 45068
            A                   TGAGGTCAGGAGTTTGAGACTAG
                                |||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTC

GAM687  FLJ22529  3'  GCTAGTCTCAAACCCCTGACCT 45572          A
            TA                  TGAGGTCAGG GTTTGAGACTAGC
                                |||||||||| ||||||||||||
                                ATTCCAGTCC CAAACTCTGATCG
                                      C
GAM687  FLJ22529  3'  GCTGGTCTCGAACTCCTGACCT 45576
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  FLJ22684  3'  CTGGTCTCAAACTCCTGACCTC 46794
            A                   TGAGGTCAGGAGTTTGAGACTAG
                                |||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTC

GAM687  FLJ23392  3'  GCTGGTCTCAAATTCCTGACCC 45543    A
            CA                  TG GGTCAGGAGTTTGAGACTAGC
                                || ||||||||||||||||||||
                                AC CCAGTCCTTAAACTCTGGTCG
                                  C
GAM687  FLJ23556  3'  GCTGGTCTCGAACTCCTGACCT 45955
            CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  FLJ25416  5'  GCTGGTCTCAAACTCCCTACCT 58812       CA
            CA                  TGAGGT  GGAGTTTGAGACTAGC
                                ||||||  ||||||||||||||||
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                                ACTCCA  CCTCAAACTCTGGTCG
                                   TC
GAM687  FLJ30532  3'  GTCTCAAGCTCCTGACCTCA   58550
                                TGAGGTCAGGAGTTTGAGAC
                                ||||||||||||||||||||
                                ACTCCAGTCCTCGAACTCTG

GAM687  FLJ32865  3'  GCTGGTCTCAAACCCCTGACCT 58179          A
           CA                     TGAGGTCAGG GTTTGAGACTAGC
                                ||||||||||| ||||||||||||
                                ACTCCAGTCC CAAACTCTGGTCG
                                      C
GAM687  GGA2      3'  GCTGGTCTCGAACTCCTGACCT 56887
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  GGA2      3'  GCTGGTCTCGAACTCCTGACCT 30473
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  GNG4      3'  GCTGGTCTCAAACTCCTGACCT 15621
           C                       GAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                CTCCAGTCCTCAAACTCTGGTCG

GAM687  GTF2H3    3'  GTCTCAAACTCCTGAGCTCA   7707       G
                                TGAG TCAGGAGTTTGAGAC
                                |||| ||||||||||||||
                                ACTC AGTCCTCAAACTCTG
                                  G
GAM687  H2AV      3'  CTGGTCTCAAACTCCTGACCTC 56851
           A                       TGAGGTCAGGAGTTTGAGACTAG
                                |||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTC

GAM687  HSPC065   3'  GCTGGTCTCGAACTCCTGACCT 26315
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  HSPC232   3'  GCTAGTCTCTAACTCCTGGCCT 33232            T
           CA                     TGAGGTCAGGAGTT GAGACTAGC
                                |||||||||||||| |||||||||
                                ACTCCGGTCCTCAA CTCTGATCG
                                         T
GAM687  JAM1      3'  GCTGGTCTCAAACTCCTGACCT 33765
           C                       GAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
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                                CTCCAGTCCTCAAACTCTGGTCG

GAM687  JAM1     3'  GCTGGTCTCAAACTCCTGACCT 57903
                C                GAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||
                                 CTCCAGTCCTCAAACTCTGGTCG

GAM687  JAM1     3'  GCTGGTCTCAAACTCCTGACCT 57932
                C                GAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||
                                 CTCCAGTCCTCAAACTCTGGTCG

GAM687  JAM1     3'  GCTGGTCTCAAACTCCTGACCT 57958
                C                GAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||
                                 CTCCAGTCCTCAAACTCTGGTCG

GAM687  KIAA0022 3'  GCTGGTCTCAAACTCCTGACCT 29668
                CA                 TGAGGTCAGGAGTTTGAGACTAGC
                                   ||||||||||||||||||||||
                                   ACTCCAGTCCTCAAACTCTGGTCG

GAM687  KIAA0063 3'  GCTGGTCTCAAACTCCCGACCT 29635       A
                CA                 TGAGGTC GGAGTTTGAGACTAGC
                                   ||||||| ||||||||||||||
                                   ACTCCAG CCTCAAACTCTGGTCG
                                       C
GAM687  KIAA0161 3'  GCTACTCTCAAACTCCTGACCT 28507              C
                CA                 TGAGGTCAGGAGTTTGAGA TAGC
                                   |||||||||||||||||| ||||
                                   ACTCCAGTCCTCAAACTCT ATCG
                                              C
GAM687  KIAA0186 3'  GCTGGTCTCAAACTCCTGGCCT 40759
                CA                 TGAGGTCAGGAGTTTGAGACTAGC
                                   ||||||||||||||||||||||
                                   ACTCCGGTCCTCAAACTCTGGTCG

GAM687  KIAA0186 3'  GCTGGTTTCAAACTCCTGACCT 40760
                CA                 TGAGGTCAGGAGTTTGAGACTAGC
                                   ||||||||||||||||||||||
                                   ACTCCAGTCCTCAAACTTTGGTCG

GAM687  KIAA0186 3'  GTTTCAAACTCCTGACCTCA  40763
                                   TGAGGTCAGGAGTTTGAGAC
                                   ||||||||||||||||||||
                                   ACTCCAGTCCTCAAACTTTG

GAM687  KIAA0205 3'  CTCGAACTCCTGACCTCA    29581
                                   TGAGGTCAGGAGTTTGAG
                                   ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTC

GAM687  KIAA0391 3' TCTCAAACTCCTGACCTCA   27925
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM687  KIAA0513 3' GCTGGTCTCGAACTCCTGACCT 28365
              CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  KIAA0515 3' TTTCAAACCCCCATCCTCA   63819      TCA  A
                                TGAGG   GG GTTTGAGA
                                |||||   || ||||||||
                                ACTCC   CC CAAACTTT
                                   TAC  C
GAM687  KIAA0555 3' GCTGGTCTCGAACTCCTGACCT 28886
              CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  KIAA0561 3' GCTGGTCTCGAACTCCTGACCT 65894
              CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  KIAA0720 3' GCTGGTCTCGAACTCCTGACCC 62324    A
              CA                  TG GGTCAGGAGTTTGAGACTAGC
                                  || ||||||||||||||||||||
                                  AC CCAGTCCTCAAGCTCTGGTCG
                                   C
GAM687  KIAA0737 3' GCTGGTCTCGAACTCCTGACCT 29144
              CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  KIAA0841 3' CTGGTCTCGAACTCCTGACCTC 71384
              A                    TGAGGTCAGGAGTTTGAGACTAG
                                   |||||||||||||||||||||||
                                   ACTCCAGTCCTCAAGCTCTGGTC

GAM687  KIAA0889 3' GCTGGTCTCGAACTCCCGACCT 31142        A
              CA                  TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
                                  ACTCCAG CCTCAAGCTCTGGTCG
                                      C
GAM687  KIAA0961 3' GCTGGTCTCAACTCCTGACCTC 29737             T
              A                    TGAGGTCAGGAGTT GAGACTAGC
                                   |||||||||||||| |||||||||
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                                ACTCCAGTCCTCAA CTCTGGTCG
                                        _
GAM687  KIAA1026 3' GTCTTCAACTCCTGACCTCA  71203           T
                                TGAGGTCAGGAGTT GAGAC
                                |||||||||||||| |||||
                                ACTCCAGTCCTCAA TTCTG
                                        C
GAM687  KIAA1054 3' GCTGGTCTCGAACTCCTGACCT 68443
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  KIAA1128 3' GCTGGTCTCGAACTCCTGACCT 68482
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  KIAA1143 3' GTCTCAATCTCCTGACCTCA  68688           T
                                TGAGGTCAGGAG TTGAGAC
                                |||||||||||| |||||||
                                ACTCCAGTCCTC AACTCTG
                                        T
GAM687  KIAA1145 3' AGTCCCACCCTGATCTCA    65619          A  TT A
                                TGAGGTCAGG GT  G GACT
                                |||||||||| ||  | ||||
                                ACTCTAGTCC CA  C CTGA
                                        _ __ C
GAM687  KIAA1161 5' GCTAGTCTCAAACTCCTGACCT 81754
                                AGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||
                                TCCAGTCCTCAAACTCTGATCG

GAM687  KIAA1170 3' GCTGACCTCAAACTCCTGACCT 69855               AC
           CA                     TGAGGTCAGGAGTTTGAG  TAGC
                                |||||||||||||||||  ||||
                                ACTCCAGTCCTCAAACTC  GTCG
                                        CA
GAM687  KIAA1198 3' GCTGGTCTCAAACTCCTGACCT 63325
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM687  KIAA1200 3' GCTGGTCTCGAACTCCTGACCT 62379
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                |||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  KIAA1257 3' GCTGGTCTCAAACTCCCGACTT 62750        A
           CA                     TGAGGTC GGAGTTTGAGACTAGC
                                ||||||| ||||||||||||||||
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                                ACTTCAG CCTCAAACTCTGGTCG
                                    C
GAM687  KIAA1467 3' GCTGGTCACGAACTCCTGACCT 71612            A
           CA                     TGAGGTCAGGAGTTTG GACTAGC
                                  ||||||||||||||| |||||||
                                  ACTCCAGTCCTCAAGC CTGGTCG
                                           A
GAM687  KIAA1493 3' GCTGGTCTCAAACTCCTGACCT 64163
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  KIAA1497 5' GTCTCGAACTCCTGACCTCA  67515
                                  TGAGGTCAGGAGTTTGAGAC
                                  ||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTG

GAM687  KIAA1615 3' GTCTCAAACTCCCGACCTCA  68721       A
                                  TGAGGTC GGAGTTTGAGAC
                                  ||||||| ||||||||||||
                                  ACTCCAG CCTCAAACTCTG
                                      C
GAM687  KIAA1617 3' GCTAGTCTTGAACTCCCAACCT 91428      CA    TG
           CA                     TGAGGT  GGAGTT  AGACTAGC
                                  ||||||  ||||||  ||||||||
                                  ACTCCA  CCTCAA  TCTGATCG
                                     AC     GT
GAM687  KIAA1655 3' GCTGGTCTCAAACTCCTGACCT 66620
           C                       GAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  CTCCAGTCCTCAAACTCTGGTCG

GAM687  KIAA1712 3' GCTGGTCTCAAACTCCTGACCT 67540
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  KIAA1737 3' GCTGGTCTCGAACTCCTGACCT 67359
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  KIAA1862 3' CAGCCGTTCCTGATCTCA    68924          T__
                                  TGAGGTCAGGAG   TTG
                                  |||||||||||   |||
                                  ACTCTAGTCCTT   GAC
                                         GCC
GAM687  KIAA1922 5' GCTGGTCTCGAACTCCTGACCT 73634
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  KIAA1985 3'  CAGACTCTGACCCCA      44713    A     G
                                TG GGTCAG AGTTTG
                                || |||||| ||||||
                                AC CCAGTC TCAGAC
                                 C    _
GAM687  LY117    5'  GCCAGTCCCTGATCCCTGACCT 92352        AG  TGA   A
                                AGGTCAGG  TT   GACT GC
                                ||||||||  ||   |||| ||
                                TCCAGTCC  AG   CTGA CG
                                     CT  TCC    C
GAM687  LY117    5'  GCCAGTCCCTGATCCCTGACCT 97746        AG  TGA   A
                                AGGTCAGG  TT   GACT GC
                                ||||||||  ||   |||| ||
                                TCCAGTCC  AG   CTGA CG
                                     CT  TCC    C
GAM687  LY117    5'  GCCAGTCCCTGATCCCTGACCT 97847        AG  TGA   A
                                AGGTCAGG  TT   GACT GC
                                ||||||||  ||   |||| ||
                                TCCAGTCC  AG   CTGA CG
                                     CT  TCC    C
GAM687  MAP-1    3'  GCTAGTTTCGAACTCCTGACCT 42181
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTTTGATCG

GAM687  MCLC     3'  GCTGGTCTCGAACTCCTGACCT 30689
           CA                     TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  MEF-2    3'  GCTGGTCTCAAACTCCTGACCT 64391
           C                       GAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                CTCCAGTCCTCAAACTCTGGTCG

GAM687  MGC:13379 3'  AGTCCCCTGCTGACCTCA     33244         G  TTTGA
                                TGAGGTCAG AG     GACT
                                |||||||| ||     ||||
                                ACTCCAGTC TC     CTGA
                                     G  CC___
GAM687  MGC13204  3'  GCTGGTCTCAAAATCCTGACCT 48839           G
           CA                     TGAGGTCAGGA TTTGAGACTAGC
                                |||||||||| ||||||||||
                                ACTCCAGTCCT AAACTCTGGTCG
                                       A
GAM687  MGC21738  3'  TCGAACTCCTGACCTCA     58921
                                TGAGGTCAGGAGTTTGA
                                |||||||||||||||
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                                ACTCCAGTCCTCAAGCT

GAM687  MKRN4    3'  GCTGGTCTCGAACTCCTGACCT 47752
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  moblak   3'  GCTGGTCTCAAACTCCTGACTT 55507
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  ACTTCAGTCCTCAAACTCTGGTCG

GAM687  MRPL44   3'  CTAGTCTTGAACTCCTGACCTC 43318          TG
                A                 TGAGGTCAGGAGTT  AGACTAG
                                  ||||||||||||||  |||||||
                                  ACTCCAGTCCTCAA  TCTGATC
                                        GT
GAM687  MRPS27   3'  GCTGGTCTCAACCTCCTGACCT 30640          T
                CA                TGAGGTCAGGAG TTGAGACTAGC
                                  |||||||||||| ||||||||||
                                  ACTCCAGTCCTC AACTCTGGTCG
                                        C
GAM687  NAPG     5'  GCTGTTCTCAAACTCCTAAGCT 96727     GTC        C
                CA                TGAG   AGGAGTTTGAGA TAGC
                                  ||||   |||||||||||| ||||
                                  ACTC   TCCTCAAACTCT GTCG
                                    GAA          T
GAM687  NXN      3'  GCTGGTCTCGAACTCCTGACCT 42421
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  OPN4     3'  CTCAAAACTCCTGCCCCA    52718    A  T      _
                                  TG GG CAGGAGTTT GAG
                                  || || ||||||||| |||
                                  AC CC GTCCTCAAA CTC
                                   C  _        A
GAM687  OSBPL2   3'  GCTGGTCTCAAACTCCCGACCT 57868        A
                CA                TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
                                  ACTCCAG CCTCAAACTCTGGTCG
                                      C
GAM687  OSBPL2   3'  GCTGGTCTCAAACTCCCGACCT 29217        A
                CA                TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
                                  ACTCCAG CCTCAAACTCTGGTCG
                                      C
GAM687  PELI1    5'  GCTGGTCTCAAACTCCCAACCT 40275       CA
                CA                TGAGGT  GGAGTTTGAGACTAGC
                                  ||||||  ||||||||||||||||
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                                ACTCCA  CCTCAAACTCTGGTCG
                                   AC
GAM687  PIP3-E   3'  GCTGGTTTCAAACTCCTGACCT 66808
            CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCCAGTCCTCAAACTTTGGTCG

GAM687  PRIC285  3'  GCCAGCCTGCCTCCTGGCCTCA 61436          TTTG  A  A
                                 TGAGGTCAGGAG    AG CT GC
                                 ||||||||||||    || || ||
                                 ACTCCGGTCCTC    TC GA CG
                                        CG__  C  C
GAM687  PRO0245  5'  GCTAGTCTCAAACTCCCGAGCC 26132    A  _  A
            CA                   TG GG TC GGAGTTTGAGACTAGC
                                 || || || ||||||||||||||||
                                 AC CC AG CCTCAAACTCTGATCG
                                  _  G  C
GAM687  PRO0529  5'  GCTGGTCTCAAACTCCTGACCT 25995
            CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCCAGTCCTCAAACTCTGGTCG

GAM687  PRO2955  3'  GCTGGTCTCAAACTCCTGACCT 37642
            CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCCAGTCCTCAAACTCTGGTCG

GAM687  PSTPIP2  3'  GCTGGTCTCAAACTCCTGACCT 44394
            CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCCAGTCCTCAAACTCTGGTCG

GAM687  RAI      5'  GCTGGTCTCAAACTCCTGATCT 21885
            CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCTAGTCCTCAAACTCTGGTCG

GAM687  SC4MOL   3'  GCTGGTCTCAAACTTCTGACCT 22159
            CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCCAGTCTTCAAACTCTGGTCG

GAM687  SCAMP-4  3'  GCTGGTCTCGAACTCCTGACCT 54397
            CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                 ||||||||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  SFXN2    3'  CTGGTCTCGAACTCCTGACCTC 73944
            A                    TGAGGTCAGGAGTTTGAGACTAG
                                 |||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCTGGTC

GAM687  SIRPB1    3'  CTAGTCTTGAACTCCCGACCTC 20248        A     TG
                A                TGAGGTC GGAGTT  AGACTAG
                                 ||||||| ||||||  |||||||
                                 ACTCCAG CCTCAA  TCTGATC
                                     C     GT
GAM687  SLC19A3   3'  GCTGGTCTCAAACTCCTGACTT 47494
                CA                 TGAGGTCAGGAGTTTGAGACTAGC
                                   ||||||||||||||||||||||||
                                   ACTTCAGTCCTCAAACTCTGGTCG

GAM687  STAF65(gamma) 3'  GCTGGTCTCAAAACTCCTGACC 29439                _
                TCA                 TGAGGTCAGGAGTTT GAGACTAGC
                                    |||||||||||||| |||||||||
                                    ACTCCAGTCCTCAAA CTCTGGTCG
                                          A
GAM687  TBCC      3'  TCTCGAACTCCTGACCTCA    12142
                                   TGAGGTCAGGAGTTTGAGA
                                   ||||||||||||||||||
                                   ACTCCAGTCCTCAAGCTCT

GAM687  TCL6      3'  GCTGGTCTCAAACTCCTGAGCT 40108       G
                CA                 TGAG TCAGGAGTTTGAGACTAGC
                                   |||| ||||||||||||||||||
                                   ACTC AGTCCTCAAACTCTGGTCG
                                     G
GAM687  TCL6      3'  GCTGGTCTCAAACTCCTGAGCT 40141       G
                CA                 TGAG TCAGGAGTTTGAGACTAGC
                                   |||| ||||||||||||||||||
                                   ACTC AGTCCTCAAACTCTGGTCG
                                     G
GAM687  THEA      3'  GCTGGTCTCAAACTCCTGACTT 66293
                CA                 TGAGGTCAGGAGTTTGAGACTAGC
                                   ||||||||||||||||||||||||
                                   ACTTCAGTCCTCAAACTCTGGTCG

GAM687  TRIM16    3'  GCAGATCTCAAACTCCTGACCT 21339                _ A
                C                   GAGGTCAGGAGTTTGAGA CT GC
                                    |||||||||||||||| || ||
                                    CTCCAGTCCTCAAACTCT GA CG
                                          A _
GAM687  TU12B1-TY 3'  GCTGGTCTCAAACTCCTAGCCT 33395       TC
                CA                 TGAGG  AGGAGTTTGAGACTAGC
                                   |||||  ||||||||||||||||
                                   ACTCC  TCCTCAAACTCTGGTCG
                                     GA
GAM687  TU12B1-TY 3'  GCTGGTCTCGAACTCCTGACCT 33396
                CA                 TGAGGTCAGGAGTTTGAGACTAGC
                                   ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  UBF-fl   3'  GCTGGTCTCAAACTCCTGACCT 51567
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  USP22    3'  GTCTCAAACTCCTGACCTCA  68020
                                  TGAGGTCAGGAGTTTGAGAC
                                  ||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTG

GAM687  VDU1     3'  GCTAGTCTCAAACTCCTGACCT 30420
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGATCG

GAM687  VPS33A   3'  GCTGGTCTCAAACTCCTGACCT 43341
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  WBSCR23  3'  GCTGGTCTCAAACTCCTGACCT 46766
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  ZNF17    3'  GCTGGTCTCAAACTCCCGACCT 82393        A
            CA                    TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
                                  ACTCCAG CCTCAAACTCTGGTCG
                                      C
GAM687  LOC112687 3'  GCTGGTCCCAAACTCCTGACCT 72864              A
            CA                    TGAGGTCAGGAGTTTG GACTAGC
                                  ||||||||||||||| |||||||
                                  ACTCCAGTCCTCAAAC CTGGTCG
                                             C
GAM687  LOC115219 5'  GCTAGTCTCAAACTCCTGACGT 73309    G
            C                      GA GTCAGGAGTTTGAGACTAGC
                                   || ||||||||||||||||||
                                   CT CAGTCCTCAAACTCTGATCG
                                    G
GAM687  LOC115648 3'  GCTGGGTCTCGAACTCCTGACC 59302                  _
            TCA                     TGAGGTCAGGAGTTTGAGACT AGC
                                    |||||||||||||||||||| |||
                                    ACTCCAGTCCTCAAGCTCTGG TCG
                                               G
GAM687  LOC119392 3'  GCTGGTCTCGAACTCCTGACCT 59137
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687   LOC120114 3'  GCTGGTCTCAAACTCCTGACCT 75535
                 C                GAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  CTCCAGTCCTCAAACTCTGGTCG

GAM687   LOC120224 5'  GCTTATCTCGAACTCCTGACCT 57103              CT
                 CA                 TGAGGTCAGGAGTTTGAGA  AGC
                                    ||||||||||||||||||  |||
                                    ACTCCAGTCCTCAAGCTCT  TCG
                                                AT
GAM687   LOC124216 3'  GCCAGTCTCAAACTCCTGACCT 74263               A
                 C                GAGGTCAGGAGTTTGAGACT GC
                                  |||||||||||||||||| ||
                                  CTCCAGTCCTCAAACTCTGA CG
                                              C
GAM687   LOC126364 3'  GCTGGTCTCGAACTCCTGACCT 75695
                 CA                 TGAGGTCAGGAGTTTGAGACTAGC
                                    ||||||||||||||||||||||
                                    ACTCCAGTCCTCAAGCTCTGGTCG

GAM687   LOC126669 3'  GCTGGTCTCAAACTCCTGACCT 75410
                 CA                 TGAGGTCAGGAGTTTGAGACTAGC
                                    ||||||||||||||||||||||
                                    ACTCCAGTCCTCAAACTCTGGTCG

GAM687   LOC130639 5'  CTCGAACTCCTGACCTCA    74970
                                    TGAGGTCAGGAGTTTGAG
                                    |||||||||||||||||
                                    ACTCCAGTCCTCAAGCTC

GAM687   LOC132625 3'  GCTAGTCTCAAACTCCTGACCT 75908
                 C                GAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  CTCCAGTCCTCAAACTCTGATCG

GAM687   LOC135154 3'  GCTGGTCTCGAACTCCTGACCT 75219
                 CA                 TGAGGTCAGGAGTTTGAGACTAGC
                                    ||||||||||||||||||||||
                                    ACTCCAGTCCTCAAGCTCTGGTCG

GAM687   LOC135293 3'  GCTGGTCTCGAACTCCTGACCT 76187
                 CA                 TGAGGTCAGGAGTTTGAGACTAGC
                                    ||||||||||||||||||||||
                                    ACTCCAGTCCTCAAGCTCTGGTCG

GAM687   LOC142927 5'  GCTGGTGTCAAACTCCTGGCCT 76428              G
                 CA                 TGAGGTCAGGAGTTTGA ACTAGC
                                    |||||||||||||||| ||||||
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                                ACTCCGGTCCTCAAACT TGGTCG
                                       G
GAM687   LOC143916 3'  GCTGGTCTCAAACTTCTGACCT 76644
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  ACTCCAGTCTTCAAACTCTGGTCG

GAM687   LOC144317 5'  GCTGGTCTCGAACTCCTGACCT 76796
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687   LOC144519 3'  GCTAGTCTCGAACTCCTGACCT 76872
                                  AGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||
                                  TCCAGTCCTCAAGCTCTGATCG

GAM687   LOC144524 5'  GCTGGTCTCAAACTCCTGAACT 83133      G
                CA                TGAG TCAGGAGTTTGAGACTAGC
                                  |||| ||||||||||||||||||
                                  ACTC AGTCCTCAAACTCTGGTCG
                                    A
GAM687   LOC145453 5'  CTGGTCTCAAACTCCTGACCTC 77139
                A                  TGAGGTCAGGAGTTTGAGACTAG
                                   |||||||||||||||||||||
                                   ACTCCAGTCCTCAAACTCTGGTC

GAM687   LOC146050 3'  GCTGGTCTCAAACTCCCGACCT 77645        A
                CA                TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
                                  ACTCCAG CCTCAAACTCTGGTCG
                                      C
GAM687   LOC146229 3'  GCTGGTCTCAAACTCCTGACCT 77762
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687   LOC146229 3'  GCTGGTCTCAAACTCCTGACCT 77763
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687   LOC146229 3'  GCTGGTCTCAAACTCCTGACTT 77764
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  ACTTCAGTCCTCAAACTCTGGTCG

GAM687   LOC146901 3'  GCTGGTCTCGAACTCCTGACCT 83844
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687   LOC146952 5'  GCTGGTCTCAAACTCCTGACCT 83872
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687   LOC147817 3'  GCTGGTCTCAAACTCCTGACCT 78502
                TA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ATTCCAGTCCTCAAACTCTGGTCG

GAM687   LOC148709 3'  GCTAGTCTCAAACTCCCGACCT 78945      A
                TA                TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
                                  ATTCCAG CCTCAAACTCTGATCG
                                      C
GAM687   LOC148918 5'  GCTGGTCTCGAACTCCTGACCT 79075
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687   LOC149577 3'  CTGGTCTCGAACTCCTGACCTC 84512
                A                 TGAGGTCAGGAGTTTGAGACTAG
                                  |||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTC

GAM687   LOC149692 3'  GCTGGTCTCGAACTCCTGACCT 84591
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687   LOC149692 3'  GTCTCAAAGTCCTGACCTCA  84594          G
                                  TGAGGTCAGGA TTTGAGAC
                                  |||||||||| ||||||||
                                  ACTCCAGTCCT AAACTCTG
                                        G
GAM687   LOC149711 3'  GCTGGTCACAAACTCCTGACCT 84685             A
                CA                TGAGGTCAGGAGTTTG GACTAGC
                                  |||||||||||||| |||||||
                                  ACTCCAGTCCTCAAAC CTGGTCG
                                           A
GAM687   LOC150225 3'  GCTGGTCTCAAACTCCTGACCT 85001
                CA                TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687   LOC150290 3'  CTGGTCTCAAACTCCTGGCCTC 79774
                A                 TGAGGTCAGGAGTTTGAGACTAG
                                  |||||||||||||||||||||||
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                                ACTCCGGTCCTCAAACTCTGGTC

GAM687  LOC150960 3'  GCTGGTCTCAAATTCCTGACCT 80068
              CA                TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                ACTCCAGTCCTTAAACTCTGGTCG

GAM687  LOC151475 5'  GCTAGTTTCAAACTCCTGACCT 85408
              TA                TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                ATTCCAGTCCTCAAACTTTGATCG

GAM687  LOC151701 3'  GCTGGTCTCGAACTCCTGACCT 85486
              CA                TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  LOC151979 5'  GCTAGTGTCGATCTCCTGACCT 80423          T   G
              CA                TGAGGTCAGGAG TTGA ACTAGC
                                |||||||||||| |||| ||||||
                                ACTCCAGTCCTC AGCT TGATCG
                                      T   G
GAM687  LOC152137 3'  GCTGGTCTCGAACCCCTGACCT 80482         A
              CA                TGAGGTCAGG GTTTGAGACTAGC
                                |||||||||| ||||||||||||
                                ACTCCAGTCC CAAGCTCTGGTCG
                                     C
GAM687  LOC152794 5'  GCTAGTCTTGAACTCCTGACCT 80679           TG
              CA                TGAGGTCAGGAGTT  AGACTAGC
                                |||||||||||||  ||||||||
                                ACTCCAGTCCTCAA  TCTGATCG
                                      GT
GAM687  LOC153688 3'  GCTGGTCTCGAACTCCCAACCT 86115       CA
              CA                TGAGGT  GGAGTTTGAGACTAGC
                                ||||||  ||||||||||||||||
                                ACTCCA  CCTCAAGCTCTGGTCG
                                   AC
GAM687  LOC153811 3'  GCTAGCCTCAAACTCCTGGGCT 80951     G          A
              C                  GAG TCAGGAGTTTGAG CTAGC
                                 ||| |||||||||||| |||||
                                 CTC GGTCCTCAAACTC GATCG
                                   G           C
GAM687  LOC153811 3'  GCTGGTCTCAAACTCCTGACCT 80954
              CA                TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM687  LOC154877 3'  GCTGGTTTCGAACTCCCGACCT 86303        A
              CA                TGAGGTC GGAGTTTGAGACTAGC
                                |||||||| ||||||||||||||||
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                                ACTCCAG CCTCAAGCTTTGGTCG
                                    C
GAM687  LOC155372 3'  GTCCCCAACTCCTGACCTCA  81343           TGA
                                TGAGGTCAGGAGTT  GAC
                                |||||||||||||  |||
                                ACTCCAGTCCTCAA  CTG
                                      CCC
GAM687  LOC157247 5'  GCTGGTCTCGAACTCCTGACCT 81373
          CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  LOC157858 5'  GCTGGTCTCAAACTCCTGACCT 86596
          C                     GAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||
                                CTCCAGTCCTCAAACTCTGGTCG

GAM687  LOC158014 5'  GCTGGTCTCGAACTCCTGACCT 81652
          CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  LOC158402 5'  GCTAGTCTCGAGCTCGTGACCT 86807       G
          CA                    TGAGGTCA GAGTTTGAGACTAGC
                                ||||||||| ||||||||||||||
                                ACTCCAGT CTCGAGCTCTGATCG
                                    G
GAM687  LOC158629 5'  GCTAGCCCCAAACTCCTGGGCT 86877     G       AGA
          CA                    TGAG TCAGGAGTTTG  CTAGC
                                |||| ||||||||||  |||||
                                ACTC GGTCCTCAAAC  GATCG
                                  G         CCC
GAM687  LOC162427 3'  GCTGGTCTCAAACTCCTGACCT 82352
          CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGGTCG

GAM687  LOC169611 3'  GCCAGTCTCAAACTCCTGACCT 82767                A
          CA                    TGAGGTCAGGAGTTTGAGACT GC
                                |||||||||||||||||||| ||
                                ACTCCAGTCCTCAAACTCTGA CG
                                      C
GAM687  LOC196047 5'  GCTAGTCTCAAACTCCTGACCT 89603
          CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTGATCG

GAM687  LOC196955 5'  TAAGCTCCTGCCCCCA     77387    A  T
                                TG GG CAGGAGTTTG
                                || || ||||||||||
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                                AC CC GTCCTCGAAT
                                 C  C
GAM687   LOC197358 3'  GCTGGTCTCGAACTCCTGACCT 88044
             CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687   LOC199699 3'  GCTGGTCTCAAACTCCTGGCCT 88311
             CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  ACTCCGGTCCTCAAACTCTGGTCG

GAM687   LOC199906 3'  GCTGGTCTCAAACTCCTGACCT 88485
             CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687   LOC200014 3'  GCTGGTCTCGAACTCCTGACCT 88536
             CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687   LOC200314 3'  CTGGTCTCGAACTCCTGACCTC 90010
             A                    TGAGGTCAGGAGTTTGAGACTAG
                                  |||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTC

GAM687   LOC200339 3'  GCTAGTCATGAACTCCTGGCCT 90035              A
             CA                   TGAGGTCAGGAGTTTG GACTAGC
                                  |||||||||||||||| |||||||
                                  ACTCCGGTCCTCAAGT CTGATCG
                                            A
GAM687   LOC200407 3'  GCTGGTCTCAAACTCCTGACCT 90045
             CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687   LOC201164 3'  GCTGGTCTCAAACTCCTGACCT 88120
             CA                   TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687   LOC201627 3'  GCTGGTCTCAAACTCCCGACCT 89020        A
             CA                   TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
                                  ACTCCAG CCTCAAACTCTGGTCG
                                      C
GAM687   LOC219529 5'  CTCAAACTCCTGAGCCCA    92970    A  _
                                  TG GG TCAGGAGTTTGAG
                                  || || ||||||||||||
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                                AC CC AGTCCTCAAACTC
                                 _  G
GAM687  LOC219673 5'  GCTGGTCTCAAACGCCTGACCT 93034          A
           CA                    TGAGGTCAGG GTTTGAGACTAGC
                                 |||||||||| ||||||||||||
                                 ACTCCAGTCC CAAACTCTGGTCG
                                       G
GAM687  LOC220074 3'  GCTGGTCTCAAACTCCTGACCT 59279
           CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                 |||||||||||||||||||||||
                                 ACTCCAGTCCTCAAACTCTGGTCG

GAM687  LOC220739 3'  CTGGTCTCCCTGCCCCA     92929    A  T    AGTTT
                                 TG GG CAGG     GAGACTAG
                                 || || ||||     ||||||||
                                 AC CC GTCC     CTCTGGTC
                                  C  _   _____
GAM687  LOC221060 3'  GCTGGTCTCGAACTCCTGACCT 93213
           CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                 |||||||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  LOC221271 3'  GCTGATCTCAAACTCCTGATCT 91865                C
           CA                    TGAGGTCAGGAGTTTGAGA TAGC
                                 |||||||||||||||||| ||||
                                 ACTCTAGTCCTCAAACTCT GTCG
                                           A
GAM687  LOC221418 3'  CAAACCCTGACCTCA       93635          A
                                 TGAGGTCAGG GTTTG
                                 |||||||||| |||||
                                 ACTCCAGTCC CAAAC
                                       _
GAM687  LOC245771 5'  GCTGGTCTCGAACTCCTGACCT 92896
           CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                 |||||||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  LOC253765 3'  AGTCTCAAAGACCTGA      95028       AG
                                 TCAGG  TTTGAGACT
                                 |||||  |||||||||
                                 AGTCC  AAACTCTGA
                                    AG
GAM687  LOC253805 3'  GCTGGTCTCGAACTCCTGACCT 96432
           CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                 |||||||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  LOC254268 3'  GCTGGTCTCAAACTCCTGACCT 95412
           CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                 |||||||||||||||||||||||
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                                ACTCCAGTCCTCAAACTCTGGTCG

GAM687   LOC254532 5'  GTCTCAAACTCCTGACCTCA   96643
                                TGAGGTCAGGAGTTTGAGAC
                                ||||||||||||||||||||
                                ACTCCAGTCCTCAAACTCTG

GAM687   LOC254655 3'  GCTGGTCTCGAACTCCTGACCT 95474
              CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687   LOC255065 5'  TCTCAAACTCCTGACCTCA    96585
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM687   LOC255065 5'  TCTCAAACTCCTGACCTCA    96586
                                TGAGGTCAGGAGTTTGAGA
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTCT

GAM687   LOC255104 3'  AGCTCTCCCCTGGCCTCA     95394          AGTTT   A
                                TGAGGTCAGG     GAG CT
                                ||||||||||     ||| ||
                                ACTCCGGTCC     CTC GA
                                       CCT__   _
GAM687   LOC255308 3'  CAGTCTCTCCTGACCTCA     94532          GTTT     A
                                TGAGGTCAGGA    GAGACT G
                                ||||||||||    |||||| |
                                ACTCCAGTCCT    CTCTGA C
                                      ____      C
GAM687   LOC255497 3'  GCTGGTCTCGAACTCCTGACCT 97193
              CA                  TGAGGTCAGGAGTTTGAGACTAGC
                                ||||||||||||||||||||||||
                                ACTCCAGTCCTCAAGCTCTGGTCG

GAM687   LOC256364 5'  GCTGGTCACAAACTCCTGGCCT 94802              A
              CA                  TGAGGTCAGGAGTTTG GACTAGC
                                ||||||||||||||| |||||||
                                ACTCCGGTCCTCAAAC CTGGTCG
                                         A
GAM687   LOC51193  3'  GCCAGTCTCAAACTCCTGGACT 32907      GT           A
              CA                  TGAG  CAGGAGTTTGAGACT GC
                                ||||  |||||||||||||| ||
                                ACTC  GTCCTCAAACTCTGA CG
                                  AG            C
GAM687   LOC51200  3'  GCTGGTCTCAAACTCCCAACCT 33001       CA
              CA                  TGAGGT  GGAGTTTGAGACTAGC
                                ||||||  ||||||||||||||||
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                                ACTCCA  CCTCAAACTCTGGTCG
                                   AC
GAM687  LOC51219  5'  GCTGGTCTCGAACTCCCGACCT 33124        A
            CA                    TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
                                  ACTCCAG CCTCAAGCTCTGGTCG
                                     C
GAM687  LOC57107  3'  GCTAGTCTCGAACTCCTGACCT 39838
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGATCG

GAM687  LOC57146  3'  GCTAGTCTCAAACTCCTGACCT 39922
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGATCG

GAM687  LOC90072  3'  GCTGGTCTCGAACTCCCGACCT 61299        A
            CA                    TGAGGTC GGAGTTTGAGACTAGC
                                  ||||||| ||||||||||||||||
                                  ACTCCAG CCTCAAGCTCTGGTCG
                                     C
GAM687  LOC90591  3'  GTCTCGAACTCCTGACCTCA   63439
                                  TGAGGTCAGGAGTTTGAGAC
                                  ||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTG

GAM687  LOC90918  3'  GCTGGTCTCAAACTCCTGACCT 64359
            TA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ATTCCAGTCCTCAAACTCTGGTCG

GAM687  LOC91115  3'  GTCTCCAACTCCTGACCTCA   64947              T
                                  TGAGGTCAGGAGTT GAGAC
                                  |||||||||||||| |||||
                                  ACTCCAGTCCTCAA CTCTG
                                           C
GAM687  LOC91291  5'  GCTGGTCTCAAACTCCTGAC   65483
                                  GTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||
                                  CAGTCCTCAAACTCTGGTCG

GAM687  LOC91561  5'  GCTGGTCTCGAACTCCTGACCT 66454
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  LOC91963  3'  TCTCAAACTCCTGAGCTCA    67699      G
                                  TGAG TCAGGAGTTTGAGA
                                  |||| ||||||||||||||
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                                ACTC AGTCCTCAAACTCT
                                  G
GAM687  LOC92267  3'  GCTGGTCTCAAACTCCTGACCT 68621
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAACTCTGGTCG

GAM687  LOC92697  5'  GCTGGTCTCGAACTCCCAACCT 70277       CA
            CA                    TGAGGT  GGAGTTTGAGACTAGC
                                  ||||||  ||||||||||||||||
                                  ACTCCA  CCTCAAGCTCTGGTCG
                                    AC
GAM687  LOC92841  3'  GCTGGTCACGAACTCCTGACCT 70715              A
            CA                    TGAGGTCAGGAGTTTG GACTAGC
                                  |||||||||||||||| |||||||
                                  ACTCCAGTCCTCAAGC CTGGTCG
                                           A
GAM687  LOC93349  3'  GCTGGTCTCGAACTCCTGACCT 56462
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTCTGGTCG

GAM687  LOC93408  5'  GCTGGTCTCAAACTCCTGGCCT 56481
            CA                    TGAGGTCAGGAGTTTGAGACTAGC
                                  ||||||||||||||||||||||||
                                  ACTCCGGTCCTCAAACTCTGGTCG

GAM688  CHRNE    3'  AGGCCTGGCCGCAGTCCAGGGG 3582          CACAA   TGA
                                  CCCCTGGAC    GTT   CCT
                                  |||||||||    |||  |||
                                  GGGGACCTG    CGG   GGA
                                       ACGC_   TCC
GAM688  CYLN2     3'  AAGCTTGTGACAGGTCCAGG   12628         ____
                                  CCTGGACC    ACAAGTTT
                                  ||||||||    ||||||||
                                  GGACCTGG    TGTTCGAA
                                       ACAG
GAM688  FLT1      3'  AGGTCAATAAGGTCAAGGG    8913       G    ACAAGT
                                  CCCT GACC     TTGACCT
                                  |||| ||||     |||||||
                                  GGGA CTGG     AACTGGA
                                    A    AAT___
GAM688  GALNT2    3'  GTCAAACTTCGGCAAGG     15599     GGA  AC
                                  CCT   CC  AAGTTTGAC
                                  |||   ||  |||||||||
                                  GGA   GG  TTCAAACTG
                                    AC_   C_
GAM688  GHR       3'  AGGTGGCTTTTGCGGTTCAGG  3877         A    TTTG
                                  CCTGGACC CAAG    ACCT
                                  |||||||| ||||    ||||
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                                GGACTTGG GTTT   TGGA
                                    C   TCGG
GAM688  GRLF1   3'  AGGTCAGAAAGTGGCCCAGG  78551     A   AAG
                                CCTGG CCAC  TTTGACCT
                                ||||| ||||  ||||||||
                                GGACC GGTG  AGACTGGA
                                   C   AA_
GAM688  HNF3G   3'  AACTCTGGTCCAGGAGA    72340   C      CA
                                TC CCTGGACCA  AGTT
                                || |||||||||  ||||
                                AG GGACCTGGT  TCAA
                                 A       C_
GAM688  ILK     5'  AGGCTTCCCCAATCCAGGGGA  15724       CCAC__
                                TCCCCTGGA    AAGTTT
                                |||||||||    ||||||
                                AGGGGACCT    TTCGGA
                                     AACCCC
GAM688  LIF     3'  AGACAGCAGGGCCCAGGGGA  9724        A  ACAA_
                                TCCCCTGG CC    GTTT
                                |||||||| ||    ||||
                                AGGGGACC GG    CAGA
                                    C  GACGA
GAM688  LMO2    3'  AAGCTTTGGACCCAAGGGA   18738    C  A_  C
                                TCCC TGG  CCA AAGTTT
                                |||| |||  ||| ||||||
                                AGGG ACC  GGT TTCGAA
                                  A  CA  _
GAM688  MMP19   3'  CTTGCTGCCCAGGGGA     10084       AC  _
                                TCCCCTGG  CA CAAG
                                ||||||||  || ||||
                                AGGGGACC  GT GTTC
                                    C_  C
GAM688  MMP19   3'  CTTGCTGCCCAGGGGA     42972       AC  _
                                TCCCCTGG  CA CAAG
                                ||||||||  || ||||
                                AGGGGACC  GT GTTC
                                    C_  C
GAM688  PAP     5'  ACTTTAGTCCTAGGGGA    57238       _   CAC
                                TCCCCT GGAC   AAGT
                                |||||| ||||  ||||
                                AGGGGA CCTG   TTCA
                                   T   AT_
GAM688  PCSK5   5'  AGGTCCCGGCAGCCCCAGGG  20573      ACCACAA  T_
                                CCCTGG     GTT  GACCT
                                ||||||     |||  |||||
                                GGGACC     CGG  CTGGA
                                   CCGA___   CC
GAM688  PRX     3'  GGTCAAGGTGCCCAAGGGA   40536    C  AC  AAG
                                TCCC TGG  CAC   TTTGACC
                                |||| |||  |||   |||||||
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                                AGGG ACC  GTG   GAACTGG
                                  A  C_  ____
GAM688  PTGIS    3' AGGCTGGGTCCAGGGGA     6324          A  A
                                TCCCCTGGACC CA GTTT
                                |||||||||||  || ||||
                                AGGGGACCTGG GT CGGA
                                       _  _
GAM688  PTGS1    3' GTCTCCTGTCTTATGGTCCAG  6355        C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM688  PTGS1    3' GTCTCCTGTCTTATGGTCCAG  54574       C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM688  RCV1     5' AGCCTGCGGCCAGGGGA     11274        A  A  A
                                TCCCCTGG CC CA GTT
                                |||||||| || || |||
                                AGGGGACC GG GT CGA
                                     _  C  C
GAM688  ROBO1    3' CAAACTTGTTCATTTAG     11373      CC_
                                CTGGA   ACAAGTTTG
                                |||||   |||||||||
                                GATTT   TGTTCAAAC
                                   ACT
GAM688  ROBO1    3' CAAACTTGTTCATTTAG     56086      CC_
                                CTGGA   ACAAGTTTG
                                |||||   |||||||||
                                GATTT   TGTTCAAAC
                                   ACT
GAM688  SNX9     3' AGGTCAAGTGTTGCGGTCCGGG 32590        A   GT_
                                CCTGGACC CAA   TTGACCT
                                |||||||| |||   |||||||
                                GGGCCTGG GTT   AACTGGA
                                     C   GTG
GAM688  SOX13    3' GGGCTTATGGCCAGGGGA    19085        A   C
                                TCCCCTGG CCA AAGTTT
                                |||||||| ||| ||||||
                                AGGGGACC GGT TTCGGG
                                     _   A
GAM688  STAT3    3' AGACCCATGATCAGGGGA    11996        AC  CAA
                                TCCCCTGG  CA   GTTT
                                ||||||||  ||   ||||
                                AGGGGACT  GT   CAGA
                                     A_  ACC
GAM688  STAT3    3' AGACCCATGATCAGGGGA    57711        AC  CAA
                                TCCCCTGG  CA   GTTT
                                ||||||||  ||   ||||
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                                AGGGGACT GT   CAGA
                                    A_ ACC
GAM688  TAZ      3' AGGGCATCTTGGTCCAGG    31305        CA TT A
                                CCTGGACCA AG TG CCT
                                ||||||||| || || |||
                                GGACCTGGT TC AC GGA
                                    __ T_ G
GAM688  TRIM34   5' AGGTCAAGTTGAGCCCAG    55224     ACCA G
                                CTGG   CAA TTTGACCT
                                ||||   ||| ||||||||
                                GACC   GTT GAACTGGA
                                  CGA_ _
GAM688  AMOT     3' AGGCATCTTCATGGTCCAGGG 55715        C_ TT A
                                CCCTGGACCA AAG TG CCT
                                |||||||||| ||| || |||
                                GGGACCTGGT TTC AC GGA
                                    AC T_ _
GAM688  ARPP-21  3' GGTTTACCTGAGCCCAGGGGA 32829       ACCA A TT
                                TCCCCTGG   CA GT GACC
                                ||||||||   || ||  ||||
                                AGGGGACC   GT CA TTGG
                                    CGA_ C T_
GAM688  BLR1     3' AGGGTGGCTGGGTCCAGGGGA 8157         A A TGA
                                TCCCCTGGACC CA GTT  CCT
                                |||||||||| || |||  |||
                                AGGGGACCTGG GT CGG  GGA
                                    _ _  TG_
GAM688  BLR1     3' AGGGTGGCTGGGTCCAGGGGA 52002        A A TGA
                                TCCCCTGGACC CA GTT  CCT
                                |||||||||| || |||  |||
                                AGGGGACCTGG GT CGG  GGA
                                    _ _  TG_
GAM688  C20orf108 3' GGTCAAAGGATCAGGG    55050      A ACAAG
                                CCCTGG CC   TTTGACC
                                |||||| ||   |||||||
                                GGGACT GG   AAACTGG
                                  A _____
GAM688  DKFZp547O146 5' AGGCACTGACTGTAATCCAGGG 39563       CC A __ A
          GG                    TCCCCTGGA ACA GTT TG CCT
                                ||||||||| ||| |||  || |||
                                GGGGGACCT TGT CAG AC GGA
                                    AA _ TC _
GAM688  FLJ13449 3' ACTTGCATTCCAGGGGA    44615       CCA
                                TCCCCTGGA  CAAGT
                                |||||||||  |||||
                                AGGGGACCT  GTTCA
                                    TAC
GAM688  FLJ23058 3' AGGCCAGCAGTGCTGTGGCCAG 45200      A  A ____ A
          GGGA                  CCCCTGG CCACA GT   TTG CCT
                                ||||||| ||||| ||   ||| |||
```

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                                GGGGACC GGTGT CG    GAC GGA
                                   _    _ TGAC   C
GAM688  GAB3     3' GGTCCTGGGGTCCAGGAGA   54633    C      ACA  TTT
                                TC CCTGGACC   AG   GACC
                                || ||||||||   ||   ||||
                                AG GGACCTGG   TC   CTGG
                                 A       GG_  ____
GAM688  GMEB2    5' GGGAGCCTGCGTCCAGGG    24736        CA  A    GA
                                CCCTGGAC  CA GTTT  CC
                                ||||||||  || ||||  ||
                                GGGACCTG  GT CGAG  GG
                                     C_  C    __
GAM688  HEMGN    3' AAGTTGTGGTCCAATGGA    37375     CC        G
                                TCC  TGGACCACAA TT
                                |||  ||||||||||  ||
                                AGG  ACCTGGTGTT AA
                                  TA         G
GAM688  KCNK13   3' AGGATGATTGCCGCCCAGGGGA 41904        ACCACA    TGA
                                TCCCCTGG     AGTT   CCT
                                ||||||||     ||||   |||
                                AGGGGACC     TTAG   GGA
                                     CGCCG_    TA_
GAM688  KIAA0323 3' AGGTCCCCGATGTGTATCCAGG 63254         C_    AGTTT
           GGA                    TCCCCTGGA  CACA    GACCT
                                ||||||||||  ||||    |||||
                                AGGGGACCT  GTGT    CTGGA
                                      AT    AGCCC
GAM688  KIAA0354 3' AGGCCAAGTGTGCGTCCAGGGG 29567          _    AG    A
           A                     TCCCCTGGAC CACA  TTTG CCT
                                ||||||||||  ||||  ||||  |||
                                AGGGGACCTG GTGT  GAAC GGA
                                      C    __    C
GAM688  KIAA1193 5' AGCCTGTGCCCAGGGGA     67629         AC    A
                                TCCCCTGG  CACA GTT
                                ||||||||  ||||  |||
                                AGGGGACC  GTGT CGA
                                     C_    C
GAM688  MDS028   3' AGGCTTTAGGCCCAGGGGA    37462         A  AC
                                TCCCCTGG CC  AAGTTT
                                ||||||||  ||  ||||||
                                AGGGGACC GG  TTCGGA
                                     C  AT
GAM688  MGC16153 5' AGGCCCGGGTCCAGGGGA    51295          ACAA
                                TCCCCTGGACC    GTTT
                                ||||||||||    ||||
                                AGGGGACCTGG    CGGA
                                       GCC_
GAM688  MGC4771  3' GGTCAAACACCCAGAAGGA    51032     C_    ACCACAA
                                TCC  CTGG      GTTTGACC
                                |||  ||||      ||||||||
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                                AGG  GACC      CAAACTGG
                                  AA    CA_____
GAM688  PLPL     3'  AGGTCACTCTGTGGTCCAAAAG 39429    CC_       A TT
              G                    CC   TGGACCACA G  TGACCT
                                ||   |||||||||| |  ||||||
                                GG   ACCTGGTGT C  ACTGGA
                                  AAA        _ TC
GAM688  SCYA17   3'  GCCTGGGTCCAGGGGA      11457          A  A
                                TCCCCTGGACC CA GT
                                |||||||||||  || ||
                                AGGGGACCTGG GT CG
                                       _  C
GAM688  SE57-1   5'  GGTCCGATCGCCCAGGGGA   47398        ACCACAA   T
                                TCCCCTGG      GTT GACC
                                ||||||||      ||| ||||
                                AGGGGACC      TAG CTGG
                                     CGC____   C
GAM688  SGK2     5'  AAGTCTGGGTCCAGGGGA    32776          A  AG
                                TCCCCTGGACC CA  TTT
                                ||||||||||  ||  |||
                                AGGGGACCTGG GT  GAA
                                       _  CT
GAM688  VRP      3'  AAACTGTGGCCAGGGGA     22944         A    A
                                TCCCCTGG CCACA GTTT
                                |||||||| ||||| ||||
                                AGGGGACC GGTGT CAAA
                                       _    _
GAM688  ZNF185   3'  GAGCTTGTGAATCCAGG     23112       C_
                                CCTGGA  CACAAGTTT
                                ||||||  |||||||||
                                GGACCT  GTGTTCGAG
                                   AA
GAM688  LOC115399 3'  AGACCTGCAGTCCAGGGGG   73422          CA  A
                                TCCCCTGGAC  CA GTTT
                                ||||||||||  ||  ||||
                                GGGGGACCTG  GT CAGA
                                      AC  C
GAM688  LOC115442 3'  AGGTCAGGGATGGTCCAG    72676        CAAG
                                CTGGACCA    TTTGACCT
                                ||||||||    ||||||||
                                GACCTGGT    GGACTGGA
                                     AG__
GAM688  LOC124997 3'  AGGCTGGCCGTGGTCCAGG   74386          AA   TGA
                                CCTGGACCAC  GTT   CCT
                                ||||||||||  |||   |||
                                GGACCTGGTG  CGG   GGA
                                      C_   TC_
GAM688  LOC130888 3'  AGGTCAAATCATGGCCCGAGG  74989     _  A   CAA
                                CCT GG CCA   GTTTGACCT
                                ||| || |||   |||||||||
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                                GGA CC GGT   TAAACTGGA
                                  G  C   AC_
GAM688   LOC145608 5'  CAGAGTTTGTGGCACAGG    83382      GA      _
                                CCTG  CCACAAG TTTG
                                ||||  ||||||| ||||
                                GGAC  GGTGTTT AGAC
                                  AC      G
GAM688   LOC146774 3'  GGGCGTTGGGATCCAGGGGA   78099         _ A   _
                                TCCCCTGGA CC CAA GTTT
                                ||||||||| || ||| ||||
                                AGGGGACCT GG GTT CGGG
                                     A  _   G
GAM688   LOC147118 5'  CAGGCGGAGTCCAGGGGA    83950          CACAA
                                TCCCCTGGAC    GTTTG
                                ||||||||||    |||||
                                AGGGGACCTG    CGGAC
                                      AGG__
GAM688   LOC147136 3'  GGTGCTCAGGTCCAGGGGA   78269          ACA   TTG
                                TCCCCTGGACC   AGT   ACC
                                ||||||||||   |||   |||
                                AGGGGACCTGG   TCG   TGG
                                      AC_   ___
GAM688   LOC148231 5'  AGACCCAGGCCCAGGGGA    78751        A  ACAA
                                TCCCCTGG CC    GTTT
                                |||||||| ||    ||||
                                AGGGGACC GG    CAGA
                                     C  ACC_
GAM688   LOC149127 3'  AGGCCTGTGGTCCCAGGAGA   84343    C    _     A
                                TC CCTGG ACCACA GTTT
                                || ||||| |||||| ||||
                                AG GGACC TGGTGT CGGA
                                  A    C     C
GAM688   LOC150370 3'  AGGCCAAGCTGCCATCCCAGGG 84940        ACCACA     A
            GA                    TCCCCTGG     AGTTTG CCT
                                |||||||     |||||| |||
                                AGGGGACC     TCGAAC GGA
                                     CTACCG     C
GAM688   LOC151318 3'  AGGTCAAACGTTTTCAGG    80224       CCACAA
                                CCTGGA     GTTTGACCT
                                ||||||     |||||||||
                                GGACTT     CAAACTGGA
                                   TTG___
GAM688   LOC153139 3'  GGGTGTCTTAGGTCCAGGAGA  85926    C       AC   TTTG
                                TC CCTGGACC  AAG    ACCT
                                || ||||||||  |||    ||||
                                AG GGACCTGG  TTC    TGGG
                                  A       A_   TG__
GAM688   LOC154184 3'  GGGTGTCTTAGGTCCAGGAGA  86180    C       AC   TTTG
                                TC CCTGGACC  AAG    ACCT
                                || ||||||||  |||    ||||
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                                AG GGACCTGG  TTC    TGGG
                                 A       A_   TG__
GAM688   LOC155081 3'  GAACACCGGACCCAGGGGA   81292        A_  ACAA
                                TCCCCTGG  CC    GTTT
                                ||||||||  ||    ||||
                                AGGGGACC  GG    CAAG
                                     CA  CCA_
GAM688   LOC157567 5'  GGGCTGTGGTCCGGGG      81482           A
                                CCCTGGACCACA GTTT
                                |||||||||||| ||||
                                GGGGCCTGGTGT CGGG
                                          _
GAM688   LOC163994 5'  TCAATCACGGTCCAGGGGA   87051          ACAAGT
                                TCCCCTGGACC      TTGA
                                ||||||||||      ||||
                                AGGGGACCTGG      AACT
                                      CACT__
GAM688   LOC196540 3'  GGACCTGTCAGGCCCAGGGGA  89635        A __  A
                                TCCCCTGG CC  ACA GTTT
                                |||||||| ||  ||| ||||
                                AGGGGACC GG  TGT CAGG
                                     C  AC   C
GAM688   LOC196955 5'  AGACTCCTCTGGGGCCCAGGGG 77359        A  A  ____
           A                     TCCCCTGG CC CA    AGTTT
                                |||||||| || ||    |||||
                                AGGGGACC GG GT    TCAGA
                                     C  G  CTCC
GAM688   LOC199986 5'  AGGCAGTTTCAGCCCAGGGGA  89898        ACCACAAGT   A
                                TCCCCTGG        TTG CCT
                                ||||||||        ||| |||
                                AGGGGACC        GAC GGA
                                     CGACTTT__   _
GAM688   LOC202802 3'  GAACACCGGACCCAGGGGA   89206        A_  ACAA
                                TCCCCTGG  CC    GTTT
                                ||||||||  ||    ||||
                                AGGGGACC  GG    CAAG
                                     CA  CCA_
GAM688   LOC220776 5'  AGGTCGAGGTGATCGAG     68382    G  C   AAG
                                CT GA CAC   TTTGACCT
                                || || |||   ||||||||
                                GA CT GTG   GAGCTGGA
                                 G  A  ___
GAM688   LOC221337 3'  CGCACCTGCAGCCAGGGGA   92109        ACCA  A  T
                                TCCCCTGG    CA GT TG
                                ||||||||    || || ||
                                AGGGGACC    GT CA GC
                                     GAC_  C  C
GAM688   LOC221415 5'  GGTCGAGTGGCGCAGAGGA   93876     C   GA    AAGT
                                TCC CTG  CCAC    TTGACC
                                ||| |||  ||||    ||||||
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                                AGG GAC  GGTG   AGCTGG
                                  A  GC   ____
GAM688  LOC221601 3'  GGGTGTCTTAGGTCCAGGAGA  93648   C      AC  TTTG
                                TC CCTGGACC  AAG   ACCT
                                || ||||||||  |||   ||||
                                AG GGACCTGG  TTC   TGGG
                                 A      A_  TG__
GAM688  LOC222161 3'  TGAACCTGACCCAGGGGA   92800       ACCA  A
                                TCCCCTGG   CA GTTTG
                                ||||||||   || |||||
                                AGGGGACC   GT CAAGT
                                     CA__  C
GAM688  LOC222228 3'  CGGACTTGCAGTCCAGGAGG  94294   _     CA
                                CC CCTGGAC  CAAGTTTG
                                || |||||||  ||||||||
                                GG GGACCTG  GTTCAGGC
                                 A      AC
GAM688  LOC222228 3'  GAACACTGGACCCAGGGGA   94297       A_  CAA
                                TCCCCTGG  CCA  GTTT
                                ||||||||  |||  ||||
                                AGGGGACC  GGT  CAAG
                                     CA  CA_
GAM688  LOC222233 3'  GAACACCGGACCCAGGGGA   94253       A_  ACAA
                                TCCCCTGG  CC   GTTT
                                ||||||||  ||   ||||
                                AGGGGACC  GG   CAAG
                                     CA  CCA_
GAM688  LOC222233 3'  CGGACTTGCAGTCCAGGAGG  94252   _     CA
                                CC CCTGGAC  CAAGTTTG
                                || |||||||  ||||||||
                                GG GGACCTG  GTTCAGGC
                                 A      AC
GAM688  LOC222662 5'  CGGACTTGCAGCCCACGGGA  92842    C  ACCA
                                TCCC TGG   CAAGTTTG
                                |||| |||   ||||||||
                                AGGG ACC   GTTCAGGC
                                  C  CGAC
GAM688  LOC254876 3'  GAACACCGGACCCAGGGGA   96051       A_  ACAA
                                TCCCCTGG  CC   GTTT
                                ||||||||  ||   ||||
                                AGGGGACC  GG   CAAG
                                     CA  CCA_
GAM688  LOC255265 5'  AGATCAAACCACAAACCAGGGG 95348       ACCACAA    C
          A                      TCCCCTGG      GTTTGA CT
                                 ||||||||      |||||| ||
                                 AGGGGACC      CAAACT GA
                                      AAACAC_     A
GAM688  LOC256414 3'  AATTTGTGGCCAAAGGA    96826    CC  A
                                TCC  TGG CCACAAGTT
                                |||  ||| |||||||||
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                                AGG  ACC GGTGTTTAA
                                  AA  _
GAM688  LOC257444 3'  GAATCTGTGGTCCAGGAGG   81113    _        AG
                                CC CCTGGACCACA  TTT
                                || ||||||||||  |||
                                GG GGACCTGGTGT  AAG
                                 A         CT
GAM688  LOC84549  3'  GAACAGCGGTCCAGGAGA    50700    C      ACAA
                                TC CCTGGACC    GTTT
                                || ||||||||    ||||
                                AG GGACCTGG    CAAG
                                 A       CGA_
GAM688  LOC89932  5'  AGCCTGGGCCAGGGGA      60788         A  A  A
                                TCCCCTGG CC CA GTT
                                |||||||| || || |||
                                AGGGGACC GG GT CGA
                                     _ _  C
GAM688  LOC90139  3'  AGGCCATCAGAGATGGCCAGGA 55397    C    A   CAAG    ___
              GA                  TC CCTGG CCA    TTTGA   CCT
                                || ||||| |||    |||||   |||
                                AG GGACC GGT    AGACT   GGA
                                 A    _  AG__     ACC
GAM688  LOC91373  3'  AGGCTTCGGGTTGGGGCCCAAG 65832     C   A  A   G TT  _
              GGA                   TCCC TGG CC CAA T  GA CCT
                                |||| ||| || ||| |  || |||
                                AGGG ACC GG GTT G  TT GGA
                                  A  C  G   G GC  C
GAM689  CLCN5     5'  TGAAATACCTAAGCTGCTCCAA 3595          ________
                                TTGGAGCAG      GTTTCA
                                |||||||||      ||||||
                                AACCTCGTC      TAAAGT
                                     GAATCCA
GAM689  FLRT2     5'  ATTGAAAAATGAGGTCTGC   25056     GT     CTC
                                GCAG  TTCATT   CAAT
                                ||||  ||||||   ||||
                                CGTC  GAGTAA   GTTA
                                  TG     AAA
GAM689  IL17      3'  TGGGGAAAATGAAACCCTCC   9333      CA      __
                                GGAG  GGTTTCAT  TCTCCA
                                ||||  ||||||||  ||||||
                                CCTC  CCAAAGTA  AGGGGT
                                  __       AA
GAM689  NLGN1     5'  TGAAGATGCTGCTCCAA     30026         G__
                                TTGGAGCAG   TTTCA
                                |||||||||   |||||
                                AACCTCGTC   GAAGT
                                     GTA
GAM689  POLG      3'  GTGATAAACCTGCTCCAA    10682           __
                                TTGGAGCAGGTT  TCAT
                                ||||||||||||  ||||
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                                AACCTCGTCCAA  AGTG
                                      AT
GAM689  TPK1     3'  GGAGAACCTGTCCAA      42384      G    TTCAT
                                TTGGA CAGGT    TCTCC
                                ||||| |||||    |||||
                                AACCT GTCCA    AGAGG
                                  _    _____
GAM689  C1orf8   5'  GAGAATGAAACCCTC      16832     CA
                                GAG  GGTTTCATTCTC
                                |||  ||||||||||||
                                CTC  CCAAAGTAAGAG
                                  __
GAM689  CLIC6    3'  TGGAGAACATGTTCCAA     82536        G  TTCAT
                                TTGGAGCA GT    TCTCCA
                                |||||||| ||    ||||||
                                AACCTTGT CA    AGAGGT
                                    A _____
GAM689  CLIPR-59 3'  TGGAGAATTTCAATGCCCCGA 31374     A   GGTTTC
                                TTGG GCA     ATTCTCCA
                                |||| |||     ||||||||
                                AGCC CGT     TAAGAGGT
                                  C   AACTT_
GAM689  DKFZP547L112 3'  TGGAGAACTCTTGCTCCA    66532         TTTCA
                                TGGAGCAGG    TTCTCCA
                                |||||||||    |||||||
                                ACCTCGTTC    AAGAGGT
                                     TC___
GAM689  EPS8R3   5'  GGACCACCTGCTCCAA      55701          TTCATTC
                                TTGGAGCAGGT      TCC
                                ||||||||||       |||
                                AACCTCGTCCA      AGG
                                     CC_____
GAM689  EPS8R3   5'  GGACCACCTGCTCCAA      57404          TTCATTC
                                TTGGAGCAGGT      TCC
                                ||||||||||       |||
                                AACCTCGTCCA      AGG
                                     CC_____
GAM689  FLJ20552 3'  AGAACAAAACTGCTCCAA    35389         G   CA
                                TTGGAGCAG TTT  TTCT
                                ||||||||| |||  ||||
                                AACCTCGTC AAA  AAGA
                                     _  AC
GAM689  FLJ22865 5'  TGGAGAAAACTGCTCTAA    47071         GTTTCA
                                TTGGAGCAG     TTCTCCA
                                |||||||||     |||||||
                                AATCTCGTC     AAGAGGT
                                     AA____
GAM689  KIAA0372 5'  ATTGAAATTTGTTACCTACTCC 27663       C    TT  TTCTC
           AA                     TTGGAG AGGT  CA    CAAT
                                |||||| ||||  ||    ||||
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                                AACCTC TCCA  GT    GTTA
                                   A   TT  TTAAA
GAM689  PRO0132  5'  ATGAAACCACTCCAA      26101       CA
                                TTGGAG  GGTTTCAT
                                ||||||  ||||||||
                                AACCTC  CCAAAGTA
                                   A_
GAM689  TEX27    3'  AGAGTGGAACCCGCTGCAA   41658     G   A
                                TTG AGC GGTTTCATTCT
                                ||| ||| ||||||||||
                                AAC TCG CCAAGGTGAGA
                                  G   C
GAM689  LOC149373 3'  ATTGGGGTGATGATACCCACCC 79312      AGCA   T    _
           CAA                    TTGG    GGT TCATT CTCCAAT
                                ||||    ||| ||||| |||||||
                                AACC    CCA AGTAG GGGGTTA
                                   CCAC   T    T
GAM689  LOC152687 3'  TTGGAGAATATTGCTCC     80643       GTTTC
                                GGAGCAG    ATTCTCCAA
                                |||||||    |||||||||
                                CCTCGTT    TAAGAGGTT
                                   A____
GAM689  LOC51202  3'  ATTGGAGAATGAAACCTGCTCC 33017
           AA                    TTGGAGCAGGTTTCATTCTCCAAT
                                ||||||||||||||||||||||||
                                AACCTCGTCCAAAGTAAGAGGTTA

GAM690  APPBP2   3'  AAGTAGTCTGGCCCACATTTT  21066        ACA   _
                                AAAATGTGG   AGGC ACTT
                                |||||||||   |||| ||||
                                TTTTACACC   TCTG TGAA
                                     CGG    A
GAM690  BTC      5'  AAGTGCCTTGCTCATTTG    96340     AAT   GA
                                CAA   GTG  CAAGGCACTT
                                |||   |||  ||||||||||
                                GTT   TAC  GTTCCGTGAA
                                  ___   TC
GAM690  CACNA1C  3'  AAGTGCCTCACTGTTCTCGT   5555      T    ___
                                ATG GGACA   AGGCACTT
                                ||| |||||   ||||||||
                                TGC CTTGT   TCCGTGAA
                                  T    CAC
GAM690  COL4A1   3'  AAGTGCCTTATAGGAATTTGCG 8459        ATGTGGAC
                                CGCAAA       AAGGCACTT
                                ||||||       |||||||||
                                GCGTTT       TTCCGTGAA
                                   AAGGATA_
GAM690  DDX3     3'  TGCCTCTGCCACTTTG      7229       AT    A  _
                                CAAA  GTGG CA AGGCA
                                ||||  |||| || |||||
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                                GTTT  CACC GT TCCGT
                                  __   _ C
GAM690  ING1L    3' AGGCCATCCACATTTT     7796          CAA   A
                                AAAATGTGGA   GGC CT
                                ||||||||||   ||| ||
                                TTTTACACCT   CCG GA
                                     A__   _
GAM690  PIR51    3' TTGTCCACATTTCATGA    21366     CA
                                TCG  AAATGTGGACAA
                                |||  ||||||||||||
                                AGT  TTTACACCTGTT
                                  AC
GAM690  RNASE2   3' AAGTGCCTTGTGAACCCTGC   11352     AAAT  GG
                                GCA   GT  ACAAGGCACTT
                                |||   ||  ||||||||||
                                CGT   CA  TGTTCCGTGAA
                                  CC__  AG
GAM690  C20orf16 3' AAGTGCCTTCAATACTTTGC   38720      AT   GAC
                                GCAAA  GTG   AAGGCACTT
                                |||||  |||   |||||||||
                                CGTTT  CAT   TTCCGTGAA
                                   __   AAC
GAM690  C7orf11  3' AAGTACCTACCACATTTTAGA  56936    GC       ACA   C
                                TC  AAAATGTGG   AGG ACTT
                                ||  |||||||||   ||| ||||
                                AG  TTTTACACC   TCC TGAA
                                 A_       A__   A
GAM690  FEM-2    3' AAGTGCCTTACACAGCTTTG   27569     A_   GAC
                                CAAA  TGTG   AAGGCACTT
                                ||||  ||||   |||||||||
                                GTTT  ACAC   TTCCGTGAA
                                  CG    A__
GAM690  FLJ10044 3' AAGTCCTGCTGTCCACA     35764        __   C
                                TGTGGACA  AGG ACTT
                                ||||||||  ||| ||||
                                ACACCTGT  TCC TGAA
                                     CG   _
GAM690  KIAA0172 3' AAGTGCCTTAGACTCTTGC   64966     AAT  GGAC
                                GCAA   GT    AAGGCACTT
                                ||||   ||    |||||||||
                                CGTT   CA    TTCCGTGAA
                                  CT_  GA__
GAM690  KIAA0947 3' AAGTGCCTTGACACATTTTG  61528         GA
                                CAAAATGTG  CAAGGCACTT
                                |||||||||  ||||||||||
                                GTTTTACAC  GTTCCGTGAA
                                     A_
GAM690  KIAA0987 3' GCCATCCACATTTCAGA     24564    GCA       CAA
                                TC   AAATGTGGA   GGC
                                ||   |||||||||   |||
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                                AG  TTTACACCT  CCG
                                 AC_       A__
GAM690  KIAA0992 3'  TGCCTTGTCTTTGC      32210     AATGT
                                GCAA    GGACAAGGCA
                                ||||    ||||||||||
                                CGTT    TCTGTTCCGT
                                  _____
GAM690  MAP      3'  AGGTACCCACATTTTG     43053         ACAAG  A
                                CAAAATGTGG    GC CT
                                ||||||||||    || ||
                                GTTTTACACC    TG GA
                                     CA___  _
GAM690  PPM1A    3'  TGCCTTGTTTCTTTGC     40660     ATGT
                                GCAAA   GGACAAGGCA
                                |||||   ||||||||||
                                CGTTT   TTTGTTCCGT
                                  C___
GAM690  SSH2     5'  TGCCTTGTGCACTGC      62216    AAAT   G
                                GCA   GTG ACAAGGCA
                                |||   ||| ||||||||
                                CGT   CAC TGTTCCGT
                                 _____  G
GAM690  VAMP3    3'  CCCCGTCCACATTTTGC    16534           AA
                                GCAAAATGTGGAC  GG
                                ||||||||||||  ||
                                CGTTTTACACCTG  CC
                                      CC
GAM690  YAP1     3'  GTATTCTCCACATTTT     20354         C  G
                                AAAATGTGGA AA GC
                                |||||||||| || ||
                                TTTTACACCT TT TG
                                     C  A
GAM690  LOC146224 5'  AAGTGGTTCCATATTTT    77705         CAA G
                                AAAATGTGGA   G CACTT
                                ||||||||||   | |||||
                                TTTTATACCT   T GTGAA
                                     ___ G
GAM691  ABR      3'  CCCATCATTTGCACAA     41722    _        A
                                TTG GTAAATGATGG G
                                ||| ||||||||||| |
                                AAC CGTTTACTACC C
                                  A         C
GAM691  ABR      3'  CCCATCATTTGCACAA     6570     _        A
                                TTG GTAAATGATGG G
                                ||| ||||||||||| |
                                AAC CGTTTACTACC C
                                  A         C
GAM691  AIM1     3'  CAAATTTACCAACTTTGTG   91817     C         GA
                                CACA AGTTGGTAAAT  TG
                                |||| ||||||||||  ||
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                                GTGT TCAACCATTTA  AC
                                  T         A_
GAM691  ANKRD3   3'  GCTCCATCATCGATCTAGGC  40198     __  AA
                                GTT  GGT  ATGATGGAGC
                                |||  |||  ||||||||||
                                CGG  CTA  TACTACCTCG
                                  AT   GC
GAM691  BCL2L11  3'  GCTCCATCACCCAGCT     56834       TAAA
                                AGTTGG    TGATGGAGC
                                ||||||    |||||||||
                                TCGACC    ACTACCTCG
                                   C___
GAM691  CX3CR1   3'  CCATCATTCATGCTACTG    70644     T   __
                                CAGT GGTA  AATGATGG
                                |||| ||||  ||||||||
                                GTCA TCGT  TTACTACC
                                  _   AC
GAM691  FLT1     3'  CCTATTTCACAACTGTGT    8916        GT    AT
                                ACACAGTTG  AAATG  GG
                                |||||||||  |||||  ||
                                TGTGTCAAC  TTTAT  CC
                                     AC    __
GAM691  GNPI     3'  CTCCATCATTTTGATGTCTG  18445     TTGGT_
                                CAG     AAATGATGGAG
                                |||     ||||||||||
                                GTC     TTTACTACCTC
                                  TGTAGT
GAM691  IL9R     5'  CTCACGTCACCAACTGCTG   9316    _      AAAT   _
                                CA CAGTTGGT    GATG GAG
                                || ||||||||    |||| |||
                                GT GTCAACCA    CTGC CTC
                                 C       ____    A
GAM691  OXTR     3'  CCAAATGTCTACCAACTG    6205         A  GA_
                                CAGTTGGTA AT   TGG
                                ||||||||| ||   |||
                                GTCAACCAT TG   ACC
                                     C  TAA
GAM691  PLS1     3'  CAGTTAATTTACCAACTG    10659          GA__
                                CAGTTGGTAAAT   TG
                                ||||||||||||   ||
                                GTCAACCATTTA   AC
                                       ATTG
GAM691  BDG-29   5'  CTCCATCATCCACAACT     72353      GTAA
                                AGTTG   ATGATGGAG
                                |||||   |||||||||
                                TCAAC   TACTACCTC
                                  ACC_
GAM691  BSMAP    3'  GCCCCATCACTGCCAACTG   23994        AA     A
                                CAGTTGGTA  TGATGG GC
                                |||||||||  |||||| ||
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                                GTCAACCGT  ACTACC CG
                                     C_     C
GAM691  C9orf9   3'  GCCCCACCACCAGCCCCAACTG 38515        TAAA__  A   A
           T                    ACAGTTGG     TG TGG GC
                                ||||||||     || ||| ||
                                TGTCAACC     AC ACC CG
                                     CCGACC  C   C
GAM691  CHERP    3'  CTCCATCATTTCATTTCAC   21099    T_  _
                                GT  GGT AAATGATGGAG
                                ||  ||| ||||||||||||
                                CA  TTA TTTACTACCTC
                                 CT   C
GAM691  DGKD     3'  CTCCATCATTCGATGAC     59403      GTA
                                GTTG   AATGATGGAG
                                ||||   ||||||||||
                                CAGT   TTACTACCTC
                                  AGC
GAM691  DKFZp547A023 3'  CTCCAAACTTTCCAACTGTGT  72616          T   TGA
                                ACACAGTTGG AAA   TGGAG
                                |||||||||| |||   |||||
                                TGTGTCAACC TTT   ACCTC
                                      _  CAA
GAM691  DKFZP566B183 3'  GCTCCATCACCCTCTTGTGTG  31326        TT  TAAA
                                CACACAG  GG   TGATGGAGC
                                |||||||  ||   |||||||||
                                GTGTGTT  CC   ACTACCTCG
                                     CT  C___
GAM691  FLJ10607  3'  TCCATCACCCAGGCTG      77129      _  TAAA
                                CAGT TGG   TGATGGA
                                |||| |||   |||||||
                                GTCG ACC   ACTACCT
                                  G   C___
GAM691  FLJ10876  3'  CCATCATTATACCAGTG     36791     AGT    _
                                CAC   TGGTA AATGATGG
                                |||   ||||| ||||||||
                                GTG   ACCAT TTACTACC
                                  ___     A
GAM691  FLJ23040  3'  GCTCCATCACCCAAGCCAGAGT 47198     AG    AAA__
           G                     CAC  TTGGT    TGATGGAGC
                                |||  |||||    |||||||||
                                GTG  GACCG    ACTACCTCG
                                 A_    AACCC
GAM691  FLJ23119  3'  CCATCCCCCAACTGCTG     45036    _     TAAAT
                                CA CAGTTGG    GATGG
                                || |||||||    |||||
                                GT GTCAACC    CTACC
                                 C      CC___
GAM691  GP5      3'  GCTCTACCACTTACTAACTG   15652          A  A
                                CAGTTGGTAA TG TGGAGC
                                |||||||||| || ||||||
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                              GTCAATCATT AC ATCTCG
                                    C  C
GAM691  KIAA0515  3'  GCTCCACCAGGGCCACCAATGT 63809      GT__   AAA  A
          GT                  ACACA   TGGT   TG TGGAGC
                              |||||   ||||  || ||||||
                              TGTGT   ACCG   AC ACCTCG
                                AACC   GG_  C
GAM691  KIAA0747  3'  GCTCCATCACCGCCTCAATGTG 30966     GTT_  AAA
                              CACA   GGT   TGATGGAGC
                              ||||   |||  |||||||||
                              GTGT   CCG   ACTACCTCG
                                AACT   CC_
GAM691  KIAA1076  3'  CTCCATCATCCATATGT    65515    GT   TAA
                              ACA  TGG   ATGATGGAG
                              |||  |||  |||||||||
                              TGT  ACC   TACTACCTC
                                AT  ___
GAM691  KIAA1321  3'  GCCCCATCATATTAACTGTCA  62226   C       AA    A
                              A ACAGTTGGTA  TGATGG GC
                              | ||||||||||  |||||| ||
                              A TGTCAATTAT  ACTACC CG
                               C        __     C
GAM691  MGC2376   3'  CTCCATCAATAAACCACTTG   43704    T   AAA_
                              CAG TGGT   TGATGGAG
                              ||| ||||   ||||||||
                              GTT ACCA   ACTACCTC
                                C   AATA
GAM691  MGC2647   3'  GCCCTGGCCACCCACTGTGTG  73706       T  AAATGAT  A
                              CACACAGT GGT      GG GC
                              |||||||| |||      || ||
                              GTGTGTCA CCA      CC CG
                                  C  CCGGT__ _
GAM691  MGC2747   3'  GCTGAATCCCACAACTGTGTG  44086        GTAAAT   GG
                              CACACAGTTG     GAT  AGC
                              ||||||||||     |||  |||
                              GTGTGTCAAC     CTA  TCG
                                    ACC___   AG
GAM691  PIGQ     3'  CTCCATCACTGGCACTG     14848     TG  AAA
                              CAGT  GT   TGATGGAG
                              ||||  ||   ||||||||
                              GTCA  CG   ACTACCTC
                                __ GTC
GAM691  POLR3F   3'  GCTCCATCACCCCTTCTG    59940    TT  TAAA
                              CAG  GG   TGATGGAGC
                              |||  ||   |||||||||
                              GTC  CC   ACTACCTCG
                                TT  CC__
GAM691  SHC3     5'  GCTCCATCAGAGGCAACTATG  33714    C    G AAA
                              CA AGTTG T   TGATGGAGC
                              || ||||| |   |||||||||
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                                GT TCAAC G   ACTACCTCG
                                 A    _ GAG
GAM691  SLC26A7  3' GCTCTTGTCTTTACCAACTG  53418         T   _
                                CAGTTGGTAAA GATG GAGC
                                |||||||||||| |||| ||||
                                GTCAACCATTT CTGT CTCG
                                      _   T
GAM691  SSB-3    3' CTCCATCATTGGCGTGC    55094    TG  A
                                GT  GT AATGATGGAG
                                ||  || ||||||||||
                                CG  CG TTACTACCTC
                                 TG  G
GAM691  ST7L     3' GCTCCATCATTCTCAGC    57000      TA
                                GTTGG  AATGATGGAGC
                                |||||  ||||||||||
                                CGACT  TTACTACCTCG
                                   C_
GAM691  ST7L     3' GCTCCATCATTCTCAGC    34856      TA
                                GTTGG  AATGATGGAGC
                                |||||  ||||||||||
                                CGACT  TTACTACCTCG
                                   C_
GAM691  ST7L     3' GCTCCATCATTCTCAGC    57577      TA
                                GTTGG  AATGATGGAGC
                                |||||  ||||||||||
                                CGACT  TTACTACCTCG
                                   C_
GAM691  TAF9L    3' GCTCCATCATTTACCAACTGTG 32005
            TG                    CACACAGTTGGTAAATGATGGAGC
                                ||||||||||||||||||||||||
                                GTGTGTCAACCATTTACTACCTCG

GAM691  TRPM3    3' GCTCCATCACTGGTGACTG   64909       G  AA
                                CAGTTG TA  TGATGGAGC
                                |||||| ||  |||||||||
                                GTCAGT GT  ACTACCTCG
                                    G  C_
GAM691  Ubc6p    3' GCTCTATAATTTACCAATTGT  54153           G
                                ACAGTTGGTAAAT ATGGAGC
                                |||||||||||| |||||||
                                TGTTAACCATTTA TATCTCG
                                       A
GAM691  ZNF213   3' CTCCATCATCACTAC      65097    T   AA
                                GT GGT  ATGATGGAG
                                || |||  |||||||||
                                CA TCA  TACTACCTC
                                 _  C_
GAM691  ZNF213   3' CTCCATCATCACTATGT    65098     GT   AA
                                ACA  TGGT  ATGATGGAG
                                |||  ||||  |||||||||
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                                TGT  ATCA  TACTACCTC
                                  __   C_
GAM691  LOC144776 5'  CTCCATCACTCAGGCTGGAGT  76959    A_    GGTAAA
                                AC  CAGTT     TGATGGAG
                                ||  |||||     ||||||||
                                TG  GTCGG     ACTACCTC
                                 AG    ACTC__
GAM691  LOC147136 3'  GCCCCGGCGCCACCAGCTG   78265        AAA  A   A
                                CAGTTGGT   TG TGG GC
                                ||||||||   || ||| ||
                                GTCGACCA   GC GCC CG
                                     CC_  G   C
GAM691  LOC147180 5'  GCCCCATCATTTTCACAGC   83986     GT_       A
                                GTTG   AAATGATGG GC
                                ||||   ||||||||| ||
                                CGAC   TTTACTACC CG
                                  ACT        C
GAM691  LOC147639 5'  GCCCATCTCACCAACTG     78382        AAAT    A
                                CAGTTGGT    GATGG GC
                                ||||||||    ||||| ||
                                GTCAACCA    CTACC CG
                                     CT__    _
GAM691  LOC149912 5'  GCTCTGCCACTTACCAGCTG   84717          A  AT
                                CAGTTGGTAA TG  GGAGC
                                |||||||||| ||  |||||
                                GTCGACCATT AC  TCTCG
                                      C  CG
GAM691  LOC150113 3'  GCTCCATCACCAAT       87214       AAAT
                                GTTGGT    GATGGAGC
                                ||||||    ||||||||
                                TAACCA    CTACCTCG
                                   ____
GAM691  LOC152078 3'  CTGTGATTTCTACCAACT    80453        __  G
                                AGTTGGTA  AAT ATGG
                                ||||||||  ||| ||||
                                TCAACCAT  TTA TGTC
                                     CT   G
GAM691  LOC157254 5'  GCCCCATCATTTGACGGTG   81385     A   GGT       A
                                CAC GTT   AAATGATGG GC
                                ||| |||   ||||||||| ||
                                GTG CAG   TTTACTACC CG
                                  G   ___       C
GAM691  LOC167147 5'  CTCCAACTCACCAACTGTG   82672          AAATGA
                                CACAGTTGGT     TGGAG
                                ||||||||||     |||||
                                GTGTCAACCA     ACCTC
                                      CTCA__
GAM691  LOC203378 3'  CCACTCACCCACTGTG      90596       T   AAAT  _
                                CACAGT GGT    GA TGG
                                |||||| |||    || |||
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                                GTGTCA CCA    CT ACC
                                   C  ____  C
GAM691  LOC221486 3'  GCCCCATCATTGCACCTGC   91011    T  A_      A
                                GT GGT  AATGATGG GC
                                || |||  |||||||| ||
                                CG CCA  TTACTACC CG
                                 T  CG       C
GAM691  LOC256861 3'  GCTCTGTCATTCACCAGCTGTG 96788           A
          TG                     CACACAGTTGGT AATGATGGAGC
                                |||||||||||| ||||||||||
                                GTGTGTCGACCA TTACTGTCTCG
                                       C
GAM691  LOC90334  5'  CTCCATCATTTCACCACTTA  62312   C  T  _
                                A AGT GGT AAATGATGGAG
                                | ||| ||| ||||||||||
                                A TCA CCA TTTACTACCTC
                                 T  _  C
GAM691  LOC91813  5'  GCCCGATCCCCGCCAACTGTG  67253         AAAT  _  A
                                CACAGTTGGT    GAT GG GC
                                ||||||||||    ||| || ||
                                GTGTCAACCG    CTA CC CG
                                      CCC_   G  _
GAM692  ACAD8     3'  GAACACATACTACCTT     26892         G  GCA
                                GAGGTAGTG GTG   TTC
                                ||||||||| |||   |||
                                TTCCATCAT CAC   AAG
                                      A  ___
GAM692  ADAM17    3'  AGAACCTAACCACTACCTT   41551         GT_  CA
                                GAGGTAGTGG   GG  TTCT
                                ||||||||||   ||  ||||
                                TTCCATCACC   CC  AAGA
                                      AAT  __
GAM692  ADAM17    3'  AGAACCTAACCACTACCTT   12079         GT_  CA
                                GAGGTAGTGG   GG  TTCT
                                ||||||||||   ||  ||||
                                TTCCATCACC   CC  AAGA
                                      AAT  __
GAM692  ADAM23    3'  AGAACACCTTTCACCACCT   13761     A    T  CA
                                AGGT GTGGG GG  TTCT
                                |||| ||||| ||  ||||
                                TCCA CACTT CC  AAGA
                                  C    T  AC
GAM692  ALX3      3'  AGAATGAGCTGCCCACCTCT  21417      AGT   TG  __
                                AGAGGT   GGG  GC  ATTCT
                                ||||||   |||  ||  |||||
                                TCTCCA   CCC  CG  TAAGA
                                   ___   GT  AG
GAM692  BAG1      3'  AGAATGGCGCCACCAGCTCT  94515     GTA   G  G
                                AGAG   GTGG TG CATTCT
                                ||||   |||| || ||||||
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                                TCTC   CACC GC GTAAGA
                                  GAC    _ G
GAM692  BRPF1    3'  GCCATCCCACCACCTCT     73087       A    _
                                AGAGGT GTGGG TGGC
                                |||||| ||||| ||||
                                TCTCCA CACCC ACCG
                                   C    T
GAM692  BTEB1    3'  AGAACACTTTCTACCTCT    6837         TG   GCA
                                AGAGGTAG  GGTG   TTCT
                                ||||||||  ||||   ||||
                                TCTCCATC  TCAC   AAGA
                                     TT   ____
GAM692  CARD4    3'  GAATGCCCTCAGCTCT      20330      GTAG   T
                                AGAG    TGGG GGCATTC
                                ||||    |||| |||||||
                                TCTC    ACTC CCGTAAG
                                  G____   _
GAM692  CELSR3   3'  AGAATGTAGGTGCCACTGCCTC 7394          GTG__
                                GAGGTAGTGG    GCATTCT
                                ||||||||||    |||||||
                                CTCCGTCACC    TGTAAGA
                                     GTGGA
GAM692  CLN5     5'  GAATGCTTCCCCCTCT      21428       TAGT   T
                                AGAGG    GGG GGCATTC
                                |||||    ||| |||||||
                                TCTCC    CCC TCGTAAG
                                  _____  T
GAM692  CRMP1    3'  AGAAGCTCGCCCCACCTC    7151        AGT    _ A
                                GAGGT   GGGTG GC TTCT
                                |||||   ||||| || ||||
                                CTCCA   CCCGC CG AAGA
                                  C__     T _
GAM692  CSF3     3'  TGTCACCCTCCACCTCT     5667        AGT
                                AGAGGT   GGGTGGCA
                                ||||||   ||||||||
                                TCTCCA   CCCACTGT
                                   CCT
GAM692  CTNNA1   3'  AGAATGCAGGAGCCTACTTCT  65916         TGGGTG
                                AGAGGTAG     GCATTCT
                                ||||||||     |||||||
                                TCTTCATC     CGTAAGA
                                     CGAGGA
GAM692  DDEF2    3'  AATGCCATCAGTTCACCTT    13949       _ TG
                                GAGGT AG  GGTGGCATT
                                ||||| ||  |||||||||
                                TTCCA TT  CTACCGTAA
                                  C  GA
GAM692  EIF4EBP2 3'  AGAATATCTGTCACTCCTCT   14586       T    GT GC
                                AGAGG AGTGG  G  ATTCT
                                ||||| |||||  |  |||||
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                                TCTCC TCACT  C  TAAGA
                                  _    GT TA
GAM692  FACL4    3'  GATGCCACTACCCCT      43400    A   AGTG
                                AG GGT    GGTGGCATT
                                || |||    |||||||||
                                TC CCA    TCACCGTAG
                                 C  _____
GAM692  FACL4    3'  GATGCCACTACCCCT      15510    A   AGTG
                                AG GGT    GGTGGCATT
                                || |||    |||||||||
                                TC CCA    TCACCGTAG
                                 C  _____
GAM692  FOSB     3'  AATGCCACTCCCTACC      22100      T
                                GGTAG GGGTGGCATT
                                ||||| ||||||||||
                                CCATC CTCACCGTAA
                                   C
GAM692  GARP     3'  AATGCCACTCTCTCC       18592    T  T
                                GG AG GGGTGGCATT
                                || || ||||||||||
                                CC TC CTCACCGTAA
                                 _ T
GAM692  GNAZ     3'  AGAATGTCCCCCACCCCT    9063     TA    T
                                AGG  GTGGG GGCATTCT
                                |||  ||||| ||||||||
                                TCC  CACCC CTGTAAGA
                                  C_    C
GAM692  GPR81    3'  AATGCCACCCCCCTTT      50746      TAGT
                                AGAGG    GGGTGGCATT
                                |||||    ||||||||||
                                TTTCC    CCCACCGTAA
                                   C___
GAM692  GRB2     3'  AATGCCAAAACTTACCT     9130       _  GGG
                                AGGTA GT   TGGCATT
                                ||||| ||   |||||||
                                TCCAT CA   ACCGTAA
                                   T  AA_
GAM692  HADHSC   3'  AGAACATTTTACTACCT     18029          _  GCA
                                AGGTAGTGGG TG   TTCT
                                |||||||||| ||   ||||
                                TCCATCATTT AC   AAGA
                                      T  ___
GAM692  HMGA2    5'  GCCACCCACTACTCT       13000      G
                                AGAG TAGTGGGTGGC
                                |||| ||||||||||
                                TCTC ATCACCCACCG
                                  _
GAM692  IL11     3'  AGAACACCACCCAGCCGCC   5322     TA _      CA
                                GG  G TGGGTGG  TTCT
                                ||  | |||||||  ||||
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                                CC  C ACCCACC  AAGA
                                 GC G      AC
GAM692  KNG      3'  AGAATGCCATTTTATCACTCT  6100      GTAGT
                                AGAG    GGGTGGCATTCT
                                ||||    ||||||||||||
                                TCTC    TTTACCGTAAGA
                                  ACTAT
GAM692  LIMK1    3'  GGGACCCACCCACCCCC     9787     TA      CA
                                GG  GTGGGTGG  TTCT
                                ||  ||||||||  ||||
                                CC  CACCCACC  AGGG
                                 CC       C_
GAM692  LIMK1    3'  GGGACCCACCCACCCCC     33649    TA      CA
                                GG  GTGGGTGG  TTCT
                                ||  ||||||||  ||||
                                CC  CACCCACC  AGGG
                                 CC       C_
GAM692  LZTS1    3'  AGAATGCCATTTCTCACGCC   40679     A    ____
                                GGT GTGGG   TGGCATTCT
                                |||  |||||   |||||||||
                                CCG CACTC   ACCGTAAGA
                                  _    TTT
GAM692  MT1G     5'  GTGCACCCACTGCCTCT     19879            G
                                AGAGGTAGTGGGTG CAT
                                |||||||||||||| |||
                                TCTCCGTCACCCAC GTG
                                                _
GAM692  OAS3     3'  AATGCCACCACTACCCCT    20536    A       G
                                AG GGTAGTGG TGGCATT
                                ||  ||||||||  |||||||
                                TC CCATCACC ACCGTAA
                                 C       _
GAM692  OAS3     3'  GAATGCCCCCTCCTC       20541      TAGT   T
                                GAGG    GGG GGCATTC
                                ||||    |||  |||||||
                                CTCC    CCC CCGTAAG
                                  T____   _
GAM692  ODF2     5'  AGAACACCCCTGTCC       10324    _   T    GCA
                                GG TAG GGGTG   TTCT
                                ||  |||  |||||   ||||
                                CC GTC CCCAC   AAGA
                                 T   _    ____
GAM692  OGDH      3'  ATGCCCCACCCACCCCTC    91104      TA     __
                                GAGG  GTGGGT  GGCAT
                                ||||  ||||||  |||||
                                CTCC  CACCCA  CCGTA
                                  C_     CC
GAM692  PRKAR2A  3'  AGAGGTTCAACCCACACCTC  14774       A     GGCA_
                                GAGGT GTGGGT    TTCT
                                |||||  ||||||     ||||
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                                CTCCA CACCCA    GAGA
                                  _     ACTTG
GAM692  PSMD9    3'  AATGCTTATTCTTCCTC     10978     TAGT    _
                                GAGG   GGGTG GCATT
                                ||||   ||||| |||||
                                CTCC   CTTAT CGTAA
                                  TT__    T
GAM692  RBP1     3'  AATGTCCAGCCACCCCT     11264     TA   G  _
                                AGG  GTGG TGG CATT
                                |||  |||| ||| ||||
                                TCC  CACC ACC GTAA
                                 C_   G  T
GAM692  SCN4A    5'  GCCACCCACCACCCT       4414     A   A
                                AG GGT GTGGGTGGC
                                || ||| |||||||||
                                TC CCA CACCCACCG
                                 _  C
GAM692  SUDD     3'  AATGTCACTACCTCT       13819          GGTG
                                AGAGGTAGTG   GCATT
                                ||||||||||   |||||
                                TCTCCATCAC   TGTAA
                                             ____
GAM692  TAL1     3'  AGAATGAACCACTGCCCCT   12101    A      GTGG
                                AG GGTAGTGG   CATTCT
                                || ||||||||   ||||||
                                TC CCGTCACC   GTAAGA
                                 C       AA__
GAM692  AP4S1    3'  GATGCCCACCAGCCCT      22994    A  AG  GT
                                AG GGT  TGG  GGCATT
                                || |||  |||  ||||||
                                TC CCG  ACC  CCGTAG
                                 _  __   AC
GAM692  BRD4     3'  GCCACCCACCACCCCT      54277    A  A
                                AG GGT GTGGGTGGC
                                || ||| |||||||||
                                TC CCA CACCCACCG
                                 C  C
GAM692  C1QTNF6  3'  GAATGCTGTCTCCTCT      49145     TAGT  TG
                                AGAGG   GGG  GCATTC
                                |||||   |||  ||||||
                                TCTCC   TCT  CGTAAG
                                   ____  GT
GAM692  CHM-I    3'  AATGCCATAACCCCTT      59724     TA  GG
                                GAGG  GT  GTGGCATT
                                ||||  ||  ||||||||
                                TTCC  CA  TACCGTAA
                                  C_  A_
GAM692  D15Wsu75e 3'  AATGCCACCCCTTCT      66648      TAGT
                                AGAGG   GGGTGGCATT
                                |||||   ||||||||||
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                                TCTTC    CCCACCGTAA
                                  ____
GAM692  D21S2056E 3'  AATGCCGCGCAGCCCT      13466    A   AG  G
                                AG GGT  TG GTGGCATT
                                || |||  || ||||||||
                                TC CCG  AC CGCCGTAA
                                 _  __  G
GAM692  DKFZp547I224 5'  AGAACGGGCAGACTGCCTC    39551         GG  GGCA
                                GAGGTAGT  GT    TTCT
                                ||||||||  ||    ||||
                                CTCCGTCA  CG    AAGA
                                     GA  GGC_
GAM692  DKFZP566C243 3'  AGAACCCCTCCCCACCTACCCC 31166    A    _    T_  CA
           T                     AG GGTAG TGGG  GG  TTCT
                                || ||||| ||||  ||  ||||
                                TC CCATC ACCC  CC  AAGA
                                 C    C    CT  CC
GAM692  DKFZp586H0623 5'  AATGTTACTACCTACT      34064       TG
                                GGTAG  GGTGGCATT
                                |||||  |||||||||
                                TCATC  TCATTGTAA
                                   CA
GAM692  DNAJC6   3'  AGAGGCCACCACCC        28841    TA   G    A
                                GG  GTGG TGGC TTCT
                                ||  |||| |||| ||||
                                CC  CACC ACCG GAGA
                                 __   _   _
GAM692  FLJ10774  3'  AGAATGCCACATCTGCGTC   45081    G    TGG
                                GA GTAG   GTGGCATTCT
                                || ||||   ||||||||||
                                CT CGTC   CACCGTAAGA
                                 G   TA_
GAM692  FLJ12668  3'  AGAATGCATTTGTCCACCTTT  46512       A_ TG    G
                                AGAGGT  G  GGTG CATTCT
                                ||||||  |  |||| ||||||
                                TTTCCA  T  TTAC GTAAGA
                                    CC GT   _
GAM692  FLJ12899  3'  AGAATGCCTTCCACTTCC    44760    T     T
                                GG AGTGGG GGCATTCT
                                || |||||| ||||||||
                                CC TCACCT CCGTAAGA
                                 T     T
GAM692  FLJ13340  3'  AGAACACTAGTCCTACCTCT   54102         T  G   CA
                                AGAGGTAG GG TGG  TTCT
                                |||||||| || |||  ||||
                                TCTCCATC CT ATC  AAGA
                                     _ G   AC
GAM692  FLJ13441  3'  GTCACCCACGACCCCT     43672    A   A
                                AG GGT GTGGGTGGC
                                || ||| |||||||||
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                                TC CCA CACCCACTG
                                 C   G
GAM692  FLJ20323  3'  AATGTTACCACCTT       38658       AGTG
                                GAGGT   GGTGGCATT
                                |||||   |||||||||
                                TTCCA   CCATTGTAA
                                  ____
GAM692  FLJ22282  3'  AGAATATTCATATTACCTC   45585         GGTGGC
                                GAGGTAGTG     ATTCT
                                |||||||||     |||||
                                CTCCATTAT     TAAGA
                                     ACTTA_
GAM692  FLJ22833  3'  AGTGGTACCCACTTCCCCT   43100    A  T      G
                                AG GG AGTGGGTG CATT
                                || || |||||||| ||||
                                TC CC TCACCCAT GTGA
                                 C  T       G
GAM692  FLJ23093  3'  AGAACTGTCATCCACCTCT   44975       AGT      _
                                AGAGGT   GGGTGGCA TTCT
                                ||||||   |||||||| ||||
                                TCTCCA   CCTACTGT AAGA
                                   ___       C
GAM692  FLJ23510  3'  AGAAAGTACCAACACCTCT   45279       A  G    G A
                                AGAGGT GT GGTG C TTCT
                                |||||| || |||| | ||||
                                TCTCCA CA CCAT G AAGA
                                   _  A    _ A
GAM692  FLJ32734  5'  AGTGCAGCCACCACCCCT    58380    A   A    G  G
                                AG GGT GTGG TG CATT
                                || ||| |||| || ||||
                                TC CCA CACC AC GTGA
                                 C   C    G  _
GAM692  FOXH1     5'  AGAATGCTCTCTGCCCCT    14070    A     T GGT
                                AG GGTAG G   GGCATTCT
                                || ||||| |   ||||||||
                                TC CCGTC C   TCGTAAGA
                                 C     T ___
GAM692  GSH-2     5'  GCCACCCACCCCTCT       55739       TA
                                AGAGG  GTGGGTGGC
                                |||||  |||||||||
                                TCTCC  CACCCACCG
                                   C_
GAM692  HT010     3'  GAATGCCCCAACCCT       37473     TA  G  T
                                AGG  GT GG GGCATTC
                                |||  || || |||||||
                                TCC  CA CC CCGTAAG
                                  __  A  _
GAM692  KIAA0373  5'  AGAATCTCATCTACCCCT    28012     TA       C
                                AGG  GTGGGTGG ATTCT
                                |||  |||||||| |||||
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                                TCC  CATCTACT TAAGA
                                  C_       C
GAM692  KIAA0417 3' AATGCCACCCATCTGC      71239      _
                                GTAG TGGGTGGCATT
                                |||| ||||||||||
                                CGTC ACCCACCGTAA
                                   T
GAM692  KIAA0435 3' AGAATGCCCTCCACCC      28968    TA    T
                                GG  GTGGG GGCATTCT
                                ||  ||||| ||||||||
                                CC  CACCT CCGTAAGA
                                 __    C
GAM692  KIAA0553 3' AGTGCTACCCACCCCTCT    69890      TA
                                AGAGG  GTGGGTGGCATT
                                |||||  ||||||||||||
                                TCTCC  CACCCATCGTGA
                                   C_
GAM692  KIAA0628 3' GCAACCCACTACCCT       28870    A        G
                                AG GGTAGTGGGT GC
                                || |||||||||| ||
                                TC CCATCACCCA CG
                                 _        A
GAM692  KIAA0789 3' AATGGACCCCCACTACCTT   63677          T __
                                GAGGTAGTGGG GG  CATT
                                |||||||||||  ||  ||||
                                TTCCATCACCC CC  GTAA
                                      _ AG
GAM692  KIAA0853 3' AATCTTACCCACCTCT      30535       AGT     C
                                AGAGGT   GGGTGG ATT
                                ||||||   |||||| |||
                                TCTCCA   CCCATT TAA
                                    ___      C
GAM692  KIAA1086 3' AGACCCCCCACCCACCTC    70740       A_    T  CAT
                                GAGGT  GTGGG GG   TCT
                                |||||  ||||| ||   |||
                                CTCCA  CACCC CC   AGA
                                   CC    _  C__
GAM692  KIAA1396 3' AGAATGCCTCTTCTCCTC    62984     T  T   T
                                GAGG AG GGG GGCATTCT
                                |||| || ||| ||||||||
                                CTCC TC TCT CCGTAAGA
                                  _ T  _
GAM692  KIAA1434 3' GCCACCCACCCACCTCT     69613       A_
                                AGAGGT  GTGGGTGGC
                                ||||||  |||||||||
                                TCTCCA  CACCCACCG
                                   CC
GAM692  KIAA1795 3' AATGTGCACACACTACCTT   72146         G  _
                                GAGGTAGTG GTG GCATT
                                ||||||||| ||| |||||
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                                TTCCATCAC CAC TGTAA
                                     A   G
GAM692  KIAA1817 5' AGAACACCACCTACTTCC    68223    T       CA
                                GG AGTGGGTGG  TTCT
                                || |||||||||  ||||
                                CC TCATCCACC  AAGA
                                 T        AC
GAM692  KIAA1855 3' AGTGTCACACCACCTCC     92335    TA   _
                                GG  GTGG GTGGCATT
                                ||  |||| ||||||||
                                CC  CACC CACTGTGA
                                 TC    A
GAM692  LTB4DH   3' AATGTATACTACCTT       81922         GGTG
                                GAGGTAGTG    GCATT
                                |||||||||    |||||
                                TTCCATCAT    TGTAA
                                     A___
GAM692  MGC11324 3' AGAATGATTGTCTCTACCTCT  51163        T   TG _
                                AGAGGTAG GGG  G CATTCT
                                |||||||| |||  | ||||||
                                TCTCCATC TCT  T GTAAGA
                                     _  GT A
GAM692  MGC15504 3' AGAATGAGCAAAACCACATCT  51253      A    GTGG___
                                AGGT GTGG      CATTCT
                                |||| ||||      ||||||
                                TCTA CACC      GTAAGA
                                  _   AAAACGA
GAM692  MGC15854 5' GGTTCCCCCACTACCTCT    58851           T  C
                                AGAGGTAGTGGG GG ATT
                                |||||||||||| || |||
                                TCTCCATCACCC CC TGG
                                       _ T
GAM692  MGC15875 3' AATGCTACCCACCCCCTC    51906     TA
                                GAGG  GTGGGTGGCATT
                                ||||  ||||||||||||
                                CTCC  CACCCATCGTAA
                                  CC
GAM692  MMP24    3' GATGTCCCCCTACC       21944      T   T
                                GGTAG GGG GGCATT
                                ||||| ||| ||||||
                                CCATC CCC CTGTAG
                                  _  _
GAM692  PRO1914  5' AGAATTTTAACCACCACCTACT 26045      TG    C____
                                GGTAG  GGTGG    ATTCT
                                |||||  |||||    |||||
                                TCATC  CCACC    TAAGA
                                  CA    AATTT
GAM692  RIN3     5' AGAACCTTCCCACTGCCCCT   45741    A       T_  CA
                                AG GGTAGTGGG  GG  TTCT
                                || |||||||||  ||  ||||
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                                TC CCGTCACCC  CC  AAGA
                                 C        TT  __
GAM692  SCYA22   3'  AGAAAGTCCCACCACCT     90938      A    TG  A
                                AGGT GTGGG  GC TTCT
                                |||| |||||  || ||||
                                TCCA CACCC  TG AAGA
                                  C    __  A
GAM692  SFXN5    3'  AGAATGCCTAGGCCAGCTCC   58033    T   G   ___
                                GG AGT GGT   GGCATTCT
                                || ||| |||   ||||||||
                                CC TCG CCG   CCGTAAGA
                                 _  A  GAT
GAM692  STX5A    3'  AGAATGACCACTGCCCCT    12041    A      GTGG
                                AG GGTAGTGG    CATTCT
                                || ||||||||    ||||||
                                TC CCGTCACC    GTAAGA
                                 C       A___
GAM692  TA-PP2C  3'  AGAATGCCTTAACTACCCT   57753    A     GGGT
                                AG GGTAGT    GGCATTCT
                                || ||||||    ||||||||
                                TC CCATCA    CCGTAAGA
                                 _     ATT_
GAM692  TBDN100  3'  AGAACACTAGTCCTACCTCT  46947        T  G   CA
                                AGAGGTAG GG TGG  TTCT
                                |||||||| || |||  ||||
                                TCTCCATC CT ATC  AAGA
                                     _ G   AC
GAM692  TSARG2   3'  GATGCCACCATCTCT       58309       AGTG
                                AGAGGT    GGTGGCATT
                                ||||||    |||||||||
                                TCTCTA    CCACCGTAG
                                   _____
GAM692  WIT-1    5'  GGTTTTACCCACCACCCCT   31829    A  A      C
                                AG GGT GTGGGTGG ATT
                                || ||| |||||||| |||
                                TC CCA CACCCATT TGG
                                 C  C       T
GAM692  ZFP100   3'  AATGCCACATTCCCTC      70048     T   GG
                                GAGG AGT  GTGGCATT
                                |||| |||  ||||||||
                                CTCC TTA  CACCGTAA
                                  C  __
GAM692  ZNF358   3'  AATCCTCCCACTGCCTC     36086          T  C
                                GAGGTAGTGGG GG ATT
                                |||||||||| || |||
                                CTCCGTCACCC CC TAA
                                       T  _
GAM692  LOC115574 3'  AATGTCCCCACTACC       73463          T
                                GGTAGTGGG GGCATT
                                ||||||||| ||||||
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                                CCATCACCC CTGTAA
                                      _
GAM692  LOC126031 5'  AGACCTTCACCCACTCCTC   74431     T       CAT
                                GAGG AGTGGGTGG   TCT
                                |||| |||||||||   |||
                                CTCC TCACCCACT   AGA
                                  _       TCC
GAM692  LOC127534 3'  AGAATGCCCTTCCCACCCCCT  75435     TA    T__
                                AGG  GTGGG   GGCATTCT
                                |||  |||||   ||||||||
                                TCC  CACCC   CCGTAAGA
                                  CC    TTC
GAM692  LOC128008 5'  AGAATGCCAGTGTTACTCC   75464    T    G__
                                GG AGTGG   TGGCATTCT
                                || |||||   |||||||||
                                CC TCATT   ACCGTAAGA
                                 _    GTG
GAM692  LOC143162 3'  AATGCCCTACCTTT       76492        TGGGT
                                AGAGGTAG    GGCATT
                                ||||||||    ||||||
                                TTTCCATC    CCGTAA
                                     _____
GAM692  LOC144348 5'  AGAATGCCAAACTGACTCT   76803     G   GGG
                                AGAG TAGT   TGGCATTCT
                                |||| ||||   |||||||||
                                TCTC GTCA   ACCGTAAGA
                                  A   A__
GAM692  LOC145231 3'  TGCCACCCACCTCCTC      83296     TA
                                GAGG  GTGGGTGGCA
                                ||||  ||||||||||
                                CTCC  CACCCACCGT
                                  TC
GAM692  LOC148696 5'  AGGGTGCCACCCCCTC      84187     TAGT
                                GAGG   GGGTGGCATTCT
                                ||||   ||||||||||||
                                CTCC   CCCACCGTGGGA
                                     ____
GAM692  LOC149465 3'  AGATTGGCCCCTACCTCT    79390       T   GG  T
                                AGAGGTAG GGGT  CA TCT
                                |||||||| ||||  || |||
                                TCTCCATC CCCG  GT AGA
                                    _   __  T
GAM692  LOC149711 5'  AATGTACCATCACTACC     84666       __   G
                                GGTAGTG  GGTG CATT
                                |||||||  |||| ||||
                                CCATCAC  CCAT GTAA
                                   TA   _
GAM692  LOC150225 3'  AGAAGGAGCCACTGCCCCT   84979    A      GTGGCA
                                AG GGTAGTGG     TTCT
                                || ||||||||     ||||
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                                TC CCGTCACC     AAGA
                                 C       GAGG__
GAM692  LOC151176 3'  AGAGTTAACCCACTGCCTC   85256          GGC
                                GAGGTAGTGGGT   ATTCT
                                ||||||||||||  |||||
                                CTCCGTCACCCA   TGAGA
                                       AT_
GAM692  LOC151878 3'  AGAAATATTCCACCTACCTCT  80372        _   TGGCA
                                AGAGGTAG TGGG    TTCT
                                |||||||| ||||    ||||
                                TCTCCATC ACCT    AAGA
                                     C    TATA_
GAM692  LOC152316 3'  GCCATGCCCCACCACCTCT   85611       A    ___
                                AGAGGT GTGGG   TGGC
                                |||||| |||||  ||||
                                TCTCCA CACCC   ACCG
                                    C    CGT
GAM692  LOC157858 5'  GTGCCACCCACCACGCCT    86600     A__
                                AGGT   GTGGGTGGCAT
                                ||||   ||||||||||||
                                TCCG   CACCCACCGTG
                                  CAC
GAM692  LOC158158 3'  AGAACGGGCAGACTGCCTC   81721        GG  GGCA
                                GAGGTAGT  GT    TTCT
                                ||||||||  ||    ||||
                                CTCCGTCA  CG    AAGA
                                     GA  GGC_
GAM692  LOC158314 5'  AATGCCACTGGTCTCCT     86766     T  _ G
                                AGG AG T GGTGGCATT
                                ||| || | |||||||||
                                TCC TC G TCACCGTAA
                                  _  T G
GAM692  LOC161734 3'  AGAACGGGCAGACTGCCTC   87094        GG  GGCA
                                GAGGTAGT  GT    TTCT
                                ||||||||  ||    ||||
                                CTCCGTCA  CG    AAGA
                                     GA  GGC_
GAM692  LOC196418 5'  AGAATGCCAAACTGACTCT    87692     G    GGG
                                AGAG TAGT   TGGCATTCT
                                |||| ||||   |||||||||
                                TCTC GTCA   ACCGTAAGA
                                  A    A__
GAM692  LOC196738 3'  AATGCCCTACCTTT       87500         TGGGT
                                AGAGGTAG    GGCATT
                                ||||||||    ||||||
                                TTTCCATC    CCGTAA
                                      _____
GAM692  LOC197358 3'  AATGTTTATTACTGCCCCT   88023    A       GT
                                AG GGTAGTGG  GGCATT
                                || ||||||||  ||||||
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                                TC CCGTCATT  TTGTAA
                                 C       AT
GAM692   LOC202460 5'  ATTCCACCCACCACCCT     89177    A  A      C
                                AG GGT GTGGGTGG AT
                                || ||| |||||||| ||
                                TC CCA CACCCACC TA
                                 _  C       T
GAM692   LOC203245 3'  AGAATGCTCAACTCCTCT     89299      T  GGGT
                                AGAGG AGT    GGCATTCT
                                ||||| |||    ||||||||
                                TCTCC TCA    TCGTAAGA
                                   _  AC__
GAM692   LOC206012 5'  TGCCCCACCCACACCTC     89527      A     __
                                GAGGT GTGGGT  GGCA
                                ||||| ||||||  ||||
                                CTCCA CACCCA  CCGT
                                   _     CC
GAM692   LOC219735 3'  AGAATGCCAATTTACTTC     93105       TGGG
                                GAGGTAG    TGGCATTCT
                                |||||||    |||||||||
                                CTTCATT    ACCGTAAGA
                                    TA__
GAM692   LOC220143 5'  AGAATGCCACCAGGCTGCC    93586       G_
                                GGTAGT  GGTGGCATTCT
                                ||||||  ||||||||||
                                CCGTCG  CCACCGTAAGA
                                    GA
GAM692   LOC253805 3'  AATGCTGTCCAACCTC      96424      AG    TG
                                GAGGT  TGGG  GCATT
                                |||||  ||||  |||||
                                CTCCA  ACCT  CGTAA
                                   __    GT
GAM692   LOC255743 5'  AGAACACCTCTACC        95916       T    GCA
                                GGTAG GGGTG   TTCT
                                ||||| |||||   ||||
                                CCATC TCCAC   AAGA
                                   _    ____
GAM692   LOC257457 5'  AGAATGCCACTGGCCCC     62626    TA  G
                                GG  GT GGTGGCATTCT
                                ||  || ||||||||||
                                CC  CG TCACCGTAAGA
                                 C_  G
GAM692   LOC92305  3'  GCTACCCACTCCCCT       56416    A  T
                                AG GG AGTGGGTGGC
                                || || ||||||||||
                                TC CC TCACCCATCG
                                 _  C
GAM693   ADAM17    3'  ATGCCTGTAATCCCAGCACTTG 12081    _  A          A
                                CA GT GCTGGGATTACAG CAT
                                || || |||||||||||| |||
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                                GT CA CGACCCTAATGTC GTA
                                 T _          C
GAM693  ADAM17   3'  ATGCCTGTAATCCCAGCACTTG 41553    _ A          A
                                CA GT GCTGGGATTACAG CAT
                                || || |||||||||||||| |||
                                GT CA CGACCCTAATGTC GTA
                                 T _          C
GAM693  ADAT1    3'  CTGTAATCCTAGCTACT     23898
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGATCCTAATGTC

GAM693  AICDA    3'  CTGTAATCCCAGCACT      40326     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693  AK1      3'  ATGCCTGTAATCCCAGCACT   4879      A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                 _          C
GAM693  ALDH3A2  3'  ATGCCTGTAATCCCAGCACT   69270     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                 _          C
GAM693  ALDH3B1  3'  ATGCCTGTAATCCCAGCTACT  91520               A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM693  ALDH3B1  3'  CTGTAATCCCAGCACT      91524     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693  ALDH8A1  3'  ATGCCTATAATCCCAGCACT   42607     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                 _         A  C
GAM693  ANKH     3'  ATGCCTGTAATCCCAACACT   53987     AGC         A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_          C
GAM693  ANKH     3'  CTGTAATCCCAGCTACT     53989
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
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                                TCATCGACCCTAATGTC

GAM693  ARHGEF6  3' CTGTGGTCCCAGCTACTCA   68202   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||||
                                A TCATCGACCCTGGTGTC
                                 C
GAM693  ATM      3' CTGTAATCCCAGCACT      56295     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  ATM      3' CTATAATCCCAGCACT      56303     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM693  ATM      3' CTGTAATCCCAGCACT      3511      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  ATP1A2   3' ATGCCTGTAATCCCAGCACT  5521      A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  ATP1A2   3' CTGTAATCTCAGCTACTCA   5524    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||||
                                A TCATCGACTCTAATGTC
                                 C
GAM693  BAAT     3' ATGTCTCCCCCAGCTGC     8112          ATTAC
                                GTAGCTGGG    AGACAT
                                |||||||||    ||||||
                                CGTCGACCC    TCTGTA
                                      CC___
GAM693  BHMT2    3' CTGCAATCCCAGCACT      34309     A       A
                                AGT GCTGGGATT CAG
                                ||| ||||||||| |||
                                TCA CGACCCTAA GTC
                                  _        C
GAM693  BRCA1    3' CTGTAATCCCAGCACT      23518     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  BRCA1    3' CTGTAATCCCAGCTACT     23519
                                AGTAGCTGGGATTACAG
                                |||||||||||||||||
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                                TCATCGACCCTAATGTC

GAM693  BRCA1   3' CTGTAATCCCAGCACT     23527    A
                           AGT GCTGGGATTACAG
                           ||| ||||||||||||
                           TCA CGACCCTAATGTC
                             _
GAM693  BRCA1   3' CTGTAATCCCAGCTACT     23528
                           AGTAGCTGGGATTACAG
                           ||||||||||||||||
                           TCATCGACCCTAATGTC

GAM693  BRCA1   3' CTGTAATCCCAGCACT     23535    A
                           AGT GCTGGGATTACAG
                           ||| ||||||||||||
                           TCA CGACCCTAATGTC
                             _
GAM693  BRCA1   3' CTGTAATCCCAGCTACT     23536
                           AGTAGCTGGGATTACAG
                           ||||||||||||||||
                           TCATCGACCCTAATGTC

GAM693  BRCA1   3' CTGTAATCCCAGCACT     23543    A
                           AGT GCTGGGATTACAG
                           ||| ||||||||||||
                           TCA CGACCCTAATGTC
                             _
GAM693  BRCA1   3' CTGTAATCCCAGCTACT     23544
                           AGTAGCTGGGATTACAG
                           ||||||||||||||||
                           TCATCGACCCTAATGTC

GAM693  BRCA1   3' CTGTAATCCCAGCACT     23551    A
                           AGT GCTGGGATTACAG
                           ||| ||||||||||||
                           TCA CGACCCTAATGTC
                             _
GAM693  BRCA1   3' CTGTAATCCCAGCTACT     23552
                           AGTAGCTGGGATTACAG
                           ||||||||||||||||
                           TCATCGACCCTAATGTC

GAM693  BRCA1   3' CTGTAATCCCAGCACT     23559    A
                           AGT GCTGGGATTACAG
                           ||| ||||||||||||
                           TCA CGACCCTAATGTC
                             _
GAM693  BRCA1   3' CTGTAATCCCAGCTACT     23560
                           AGTAGCTGGGATTACAG
                           ||||||||||||||||
```

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                                TCATCGACCCTAATGTC

GAM693  BRCA1   3' CTGTAATCCCAGCACT     23568    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  BRCA1   3' CTGTAATCCCAGCTACT     23569
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  BRCA1   3' CTGTAATCCCAGCACT     23576    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  BRCA1   3' CTGTAATCCCAGCTACT     23577
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  BRCA1   3' CTGTAATCCCAGCACT     23584    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  BRCA1   3' CTGTAATCCCAGCTACT     23585
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  BRCA1   3' CTGTAATCCCAGCACT     23592    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  BRCA1   3' CTGTAATCCCAGCTACT     23593
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  BRCA2   3' ATGCCTGTAATCCCAACACTTT 3548     TAGC_        A
          G                      CAG    TGGGATTACAG CAT
                                 |||    |||||||||||| |||
                                 GTT    ACCCTAATGTC GTA
                                   TCACA         C
GAM693  C1orf1  3' CTGTAATCCCAACACT     6859     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
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                                TCA   ACCCTAATGTC
                                  CA_
GAM693  C5R1     3'  CTGTAATCCCAGAACT      8204      AG
                                AGT  CTGGGATTACAG
                                |||  ||||||||||||
                                TCA  GACCCTAATGTC
                                  A_
GAM693  CARKL    3'  ATGCCTGTAATCCCAGCTACT  25183              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                          C
GAM693  CASP10   3'  ATGCCTGTAATCCCAGTACTCT 52098     TA_          A
           G                     CAG   GCTGGGATTACAG CAT
                                |||   |||||||||||||| |||
                                GTC   TGACCCTAATGTC GTA
                                  TCA           C
GAM693  CASP10   3'  ATGCCTGTAATCCCAGTACTCT 52116     TA_          A
           G                     CAG   GCTGGGATTACAG CAT
                                |||   |||||||||||||| |||
                                GTC   TGACCCTAATGTC GTA
                                  TCA           C
GAM693  CASP6    3'  ATGCCTGCAATCCCAGCTACTT 52200     _          A   A
           G                     CA GTAGCTGGGATT CAG CAT
                                || |||||||||||| ||| |||
                                GT CATCGACCCTAA GTC GTA
                                 T          C   C
GAM693  CASP6    3'  CTGTAATCCCAGCACT      52203     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  CASP6    3'  ATGCCTGCAATCCCAGCTACTT 6907      _          A   A
           G                     CA GTAGCTGGGATT CAG CAT
                                || |||||||||||| ||| |||
                                GT CATCGACCCTAA GTC GTA
                                 T          C   C
GAM693  CASP6    3'  CTGTAATCCCAGCACT      6910      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  CASP8    3'  ATGTCTATAATCCCAGCACT   6913      A        C
                                AGT GCTGGGATTA AGACAT
                                ||| |||||||||| ||||||
                                TCA CGACCCTAAT TCTGTA
                                  _         A
GAM693  CASP8    3'  ATGTCTATAATCCCAGCACT   52919     A        C
                                AGT GCTGGGATTA AGACAT
                                ||| |||||||||| ||||||
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                                TCA CGACCCTAAT TCTGTA
                                  _        A
GAM693  CASP8   3' ATGTCTATAATCCCAGCACT  52930    A       C
                                AGT GCTGGGATTA AGACAT
                                ||| |||||||||| ||||||
                                TCA CGACCCTAAT TCTGTA
                                  _        A
GAM693  CASP8   3' ATGTCTATAATCCCAGCACT  52942    A       C
                                AGT GCTGGGATTA AGACAT
                                ||| |||||||||| ||||||
                                TCA CGACCCTAAT TCTGTA
                                  _        A
GAM693  CD68    3' ATGCCTGTAATCCCAGCACT  59797    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  CHRNA5  3' CTGTAATCCCAGCACT     59755    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  CHST5   3' ATGCCTGTAATCCCAGCATTTT 24022    TA_         A
          G                      CAG  GCTGGGATTACAG CAT
                                |||  |||||||||||| |||
                                GTT  CGACCCTAATGTC GTA
                                  TTA          C
GAM693  CHST5   3' CTGTAATCCCAGCTACTTA   24025  C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 T
GAM693  CNGB1   3' ATGCCTATAATCCCAGTGCT  7110     G       C A
                                AGTA CTGGGATTA AG CAT
                                |||| ||||||||| || |||
                                TCGT GACCCTAAT TC GTA
                                  _        A C
GAM693  COG7    3' CTGTAATCCCAGCACT     67622    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  COL16A1 3' CTGTAATCCTAGCTATT    8500
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TTATCGATCCTAATGTC

GAM693  COPA    3' CTGTAATCCCAGCACT     15187    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  CORO2A   3'  ATGCCTGTAATCCCAGCACTCT 53400     TA_          A
           G                     CAG   GCTGGGATTACAG CAT
                                 |||   |||||||||||||| |||
                                 GTC   CGACCCTAATGTC GTA
                                   TCA           C
GAM693  CORO2A   3'  ATGCCTGTAATCCCAGCACTCT 12644     TA_          A
           G                     CAG   GCTGGGATTACAG CAT
                                 |||   |||||||||||||| |||
                                 GTC   CGACCCTAATGTC GTA
                                   TCA           C
GAM693  CPT2     3'  ATGCCTGTAATCCCAGCATTTT 3641      TA_          A
           G                     CAG   GCTGGGATTACAG CAT
                                 |||   |||||||||||||| |||
                                 GTT   CGACCCTAATGTC GTA
                                   TTA           C
GAM693  CRACC    3'  CTGTAATCCCAGCACT      41005     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                  _
GAM693  CTMP     3'  CTGTAATCCCAGCACTTTA   53876    C   A
                                 TA AGT GCTGGGATTACAG
                                 || ||| ||||||||||||
                                 AT TCA CGACCCTAATGTC
                                  T   _
GAM693  CTMP     3'  CTGTAGTCCCAGCTACTCA   53877    C
                                 A AGTAGCTGGGATTACAG
                                 | ||||||||||||||||
                                 A TCATCGACCCTGATGTC
                                  C
GAM693  CTNNB1   3'  TCTGTAATGGTACTG       8581       G  GGG
                                 CAGTA CT   ATTACAGA
                                 ||||| ||   ||||||||
                                 GTCAT GG   TAATGTCT
                                    _  ___
GAM693  CTSS     3'  ATGCCTGTAATCCCAGCTACTT 14540    _            A
           G                     CA GTAGCTGGGATTACAG CAT
                                 || |||||||||||||| |||
                                 GT CATCGACCCTAATGTC GTA
                                   T             C
GAM693  CTSS     3'  CTGTAATCCCAGTACTTG    14542    C    G
                                 A AGTA CTGGGATTACAG
                                 | |||| ||||||||||||
                                 G TCAT GACCCTAATGTC
                                  T   _
GAM693  CYP4F3   3'  CTGTAATCCCAGCACTTTA   6115     C   A
                                 TA AGT GCTGGGATTACAG
                                 || ||| ||||||||||||
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                                AT TCA CGACCCTAATGTC
                                 T  _
GAM693  DAPP1    3'  ATGCCTGTAATCCCAGGACT  26917    AG         A
                                AGT  CTGGGATTACAG CAT
                                |||  |||||||||||| |||
                                TCA  GACCCTAATGTC GTA
                                  G_         C
GAM693  DAPP1    3'  TGTAATCCCAGCTACTCA   26920   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  DBT      3'  CTGTAATCCCAGCACT     8610     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                 _
GAM693  DCLRE1C  3'  ATGCCTGTAATCCCAGCTAC  42524          A
                                GTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                CATCGACCCTAATGTC GTA
                                          C
GAM693  DDOST    3'  ATGCCTGTAATCCCAGCACT  17816    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _         C
GAM693  DFFA     3'  CTGTAATCCCAGCACTG     15302     A
                                CAGT GCTGGGATTACAG
                                |||| ||||||||||||
                                GTCA CGACCCTAATGTC

                                  _
GAM693  DHFR     3'  ATGCCTGTAGTCCCAGCTACTC 5799    C           A
          A                      A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACCCTGATGTC GTA
                                 C            C
GAM693  DHFR     3'  CTGTAATCCCAGCGCT      5803     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCG CGACCCTAATGTC

                                  _
GAM693  DMC1     3'  CTGTAATCCCAGCACT      22972    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM693  DNASE2   3'  ATGCCTGTAGTCCCAGCCACTG 7263      A         A
                                CAGT GCTGGGATTACAG CAT
                                |||| |||||||||||| |||
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                                GTCA CGACCCTGATGTC GTA
                                  C          C
GAM693  DSC1    3'  CTGTAATCCCAGCTACTCA   17059   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM693  DSC1    3'  CTGTAATCCCAGCTACTCA   44328   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM693  DVL3    3'  GTCTGTAATCCCAGCACT    15373    A
                                AGT GCTGGGATTACAGAC
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCTG

GAM693  DYRK1A  3'  ATGTCTGTAACCAATAATGTA  55198     G  GCTG  A
                                TACA TA   GG TTACAGACAT
                                |||| ||   || ||||||||||
                                ATGT AT   CC AATGTCTGTA
                                  A  AA__  _
GAM693  DYRK1A  3'  ATGTCTGTAACCAATAATGTA  55240     G  GCTG  A
                                TACA TA   GG TTACAGACAT
                                |||| ||   || ||||||||||
                                ATGT AT   CC AATGTCTGTA
                                  A  AA__  _
GAM693  DYRK1A  3'  ATGTCTGTAACCAATAATGTA  7349      G  GCTG  A
                                TACA TA   GG TTACAGACAT
                                |||| ||   || ||||||||||
                                ATGT AT   CC AATGTCTGTA
                                  A  AA__  _
GAM693  EFG2    5'  CTGTAATCCCAGCACT     50476    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

GAM693  EGFL5   3'  CTGTAATCCCAGCACT     86618    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

GAM693  EHHADH  3'  CTGTAATCCCAGCACT     8750     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

GAM693  F2R     3'  CTGTAATCCCAGCACT     8837     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
```

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                                TCA CGACCCTAATGTC
                                  _
GAM693  F2RL3    3' CTGCAATCCCAGCACT     14178    A       A
                                AGT GCTGGGATT CAG
                                ||| ||||||||| |||
                                TCA CGACCCTAA GTC
                                  _       C
GAM693  F2RL3    3' CTGTAATCCCAGCACTTTA   14179    C   A
                                TA AGT GCTGGGATTACAG
                                || ||| ||||||||||||
                                AT TCA CGACCCTAATGTC
                                 T  _
GAM693  F2RL3    3' TGTAATCCCAGCTACTCA    14197   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  FANCD2   3' CTGTAATCCCAGCACT      52355    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FCMD     3' CTATAGTCCCAGCTAC      22091          C
                                GTAGCTGGGATTA AG
                                |||||||||||| ||
                                CATCGACCCTGAT TC
                                       A
GAM693  FGFR1    3' CTGTAATCCCAGCACTTTA   43614    C   A
                                TA AGT GCTGGGATTACAG
                                || ||| ||||||||||||
                                AT TCA CGACCCTAATGTC
                                 T  _
GAM693  FGFR1    3' CTGTAATCCCAGCACTTTA   43621    C   A
                                TA AGT GCTGGGATTACAG
                                || ||| ||||||||||||
                                AT TCA CGACCCTAATGTC
                                 T  _
GAM693  FGFR2    3' ATGCCTGTAATCCCAGCACT  43376    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  FGFR2    3' ATGCCTGTAATCCCAGCACT  43382    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  FKRP     3' CTGTAATCCCAGCACT      44185    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  FLRT2   5' GTCTGTAATCCCAGCGCTCTGT 25064     TA_
                                ACAG  GCTGGGATTACAGAC
                                ||||  ||||||||||||||
                                TGTC  CGACCCTAATGTCTG
                                  TCG
GAM693  FUT6    3' CTGTAATCCCAGCACT     3811     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  GALNT7  3' CTGTAATCCCAGCTACTTG  54018    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                 T
GAM693  GNE     3' CTGTAATCCCAGCACT     18478    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  GP2     3' ATGCCTGTAATCCCAGC    7680           A
                                GCTGGGATTACAG CAT
                                |||||||||||| |||
                                CGACCCTAATGTC GTA
                                      C
GAM693  GP6     3' ATGTCTGTAATCCTAGCACTGT 33030      A
          G                      TACAGT GCTGGGATTACAGACAT
                                ||||||| ||||||||||||||||
                                GTGTCA CGATCCTAATGTCTGTA
                                   _
GAM693  GPRK7   3' TCTATAATCCCAGTTAC    57629          C
                                GTAGCTGGGATTA AGA
                                |||||||||||| |||
                                CATTGACCCTAAT TCT
                                      A
GAM693  GRAF    3' CTATAATCCCAGCACT     30556    A      C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _       A
GAM693  GRM6    3' CTGTAATCCCAGCACT     5934     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  HFE     3' CTGTAATCCCAGGGTGCTG  4651      G _
                                CAGTA C TGGGATTACAG
                                ||||| | ||||||||||
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                                GTCGT G ACCCTAATGTC
                                   G G
GAM693  HIP1    3'  ATGCCTGTAATCCCAGAACT  18055    AG         A
                                AGT  CTGGGATTACAG CAT
                                |||  |||||||||||| |||
                                TCA  GACCCTAATGTC GTA
                                  A_          C
GAM693  HIP1    3'  CTGTAATCCCAGCACT     18059    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  HIP1    3'  GTAATCCCAGCTACTCA    18065   C
                                A AGTAGCTGGGATTAC
                                | ||||||||||||||
                                A TCATCGACCCTAATG
                                 C
GAM693  HLA-E   3'  ATGCCTGTAATCCCAGCACT  91021    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  HUNK    3'  CTGTAATCCCAGCACT     27449    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  IAPP    3'  GTGCCTGTAATCCCAGCTACTC 4696   C            A
          A                      A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGACCCTAATGTC GTG
                                 C             C
GAM693  ICA1    3'  TGCAGTCCCAGCTACTCA   42257   C          A
                                A AGTAGCTGGGATT CA
                                | |||||||||||| ||
                                A TCATCGACCCTGA GT
                                 C          C
GAM693  ICMT    3'  CTGTAATCCCAAAGTGCTG  24812     GC_
                                CAGTA   TGGGATTACAG
                                |||||   ||||||||||
                                GTCGT   ACCCTAATGTC
                                   GAA
GAM693  IFIT4   3'  ATGCCTGTAATCCCAGCACT  70920    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  IFNAR1  3'  CTGTAATCCCAGCACT     5284     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
```

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                                TCA CGACCCTAATGTC
                                  _
GAM693  IL10     3'  CTGTAATCCCAGCACT     5127      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  IL12RB2  3'  ATGCCTGTAATCCCAGCACT  7768      A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  IL17R    3'  CTGTAATCCCAGCAC      26776     A
                                GT GCTGGGATTACAG
                                || ||||||||||||
                                CA CGACCCTAATGTC
                                  _
GAM693  IL1R1    3'  CTATAATCCCAGCACT     6057      A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM693  IL1R1    3'  CTGTAATCCCAGCTAC     6058
                                GTAGCTGGGATTACAG
                                ||||||||||||||||
                                CATCGACCCTAATGTC

GAM693  IL4R     5'  ATGCCTATAATCCCAGCACT  4699      A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM693  IPP      3'  ATGCCTATAATCCCAGCACT  19724     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM693  IRAK1    3'  CTGTAATCCCAGCACT     7808      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  ITGAL    3'  CTGTAATCCCAGCACT     9391      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  ITGAL    3'  CTGTAGTCCCAGCTACTCA  9392      C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
```

```
                                A TCATCGACCCTGATGTC
                                 C
GAM693  JRK     3'  CTGTAATCCCAGCACTG     86526      A
                                CAGT GCTGGGATTACAG
                                |||| ||||||||||||
                                GTCA CGACCCTAATGTC

                                 _
GAM693  KAI1    3'  CTGTAATCCCAGCACT      9499      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                 _
GAM693  KCNA7   3'  ATGCCTGTGATCCCAGCTACTC 49049    C             A
            A                    A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACCCTAGTGTC GTA
                                 C             C
GAM693  KNSL1   3'  ATGCCTGTAATCCCAGCACT   15747     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| ||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                 _          C
GAM693  LAMP2   3'  CTGTAATCCCAGCACT      25712     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                 _
GAM693  LDLR    3'  CTGTAATCCCAGCACT      4985      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                 _
GAM693  LDLR    3'  CTGTAATCCCAGCACT      4986      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                 _
GAM693  LEP     3'  CTGTAATCCCAGCACT      4048      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                 _
GAM693  LRRC2   3'  CTATAATCCCAGCACT      44467     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                 _         A
GAM693  LRRC2   3'  CTATAATCCCAGCACT      44468     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
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                                TCA CGACCCTAAT TC
                                  _        A
GAM693  LRRC2   3'  CTGTAATCCCAGCACT      44469     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LRRC2   3'  GTAATCCCAGCTACTCA     44477   C
                                A AGTAGCTGGGATTAC
                                | ||||||||||||||
                                A TCATCGACCCTAATG
                                 C
GAM693  LUZP1   3'  ATGCCTGTAATCGCAGCTACTC 53296   C       G       A
            A                    A AGTAGCTG GATTACAG CAT
                                | |||||||| |||||||| |||
                                A TCATCGAC CTAATGTC GTA
                                 C       G       C
GAM693  LUZP1   3'  CTGTAATCCCAGCACT      53299     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  MAFF    3'  TCTGTAATCCCAGCACT     24654     A
                                AGT GCTGGGATTACAGA
                                ||| |||||||||||||
                                TCA CGACCCTAATGTCT
                                  _
GAM693  MCM4    3'  CTGTAATCCCAGCACT      61903     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  MIR16   3'  ATGCCTGTATTCCCAGCTACTC 33563   C         T     A
            A                    A AGTAGCTGGGA TACAG CAT
                                | |||||||||| ||||| |||
                                A TCATCGACCCT ATGTC GTA
                                 C         T     C
GAM693  MOG     3'  CTGTAATCCCAGCACT      10102     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  MSH3    3'  ATGCCTGTAATCCCAGCACT  10118     A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  MTMR8   3'  CTGTAATCCCAGCACT      31292     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  MTNR1A   3'  CTGTAATCCCAGCTACT     19889
                                AGTAGCTGGGATTACAG
                                |||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  NFKBIL2  3'  CTGTAATCCCAACACT      25525     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693  NPHP1    3'  CTGTAATCCCAACACT      62479     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693  NPHS1    3'  CTATAATCCCAGCACT      16190     A         C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _         A
GAM693  NT5C2    3'  ATGCCTGTAATCCCATCATCTA 24237       C___          A
          CT                      AGTAG    TGGGATTACAG CAT
                                |||||    |||||||||||| |||
                                TCATC    ACCCTAATGTC GTA
                                   TACT          C
GAM693  NT5C2    3'  CTGTAATCCCAGCACT      24238     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  OASL     3'  CTGTAATCCCAGAACT      13578     AG
                                AGT  CTGGGATTACAG
                                |||  ||||||||||||
                                TCA  GACCCTAATGTC
                                  A_
GAM693  OPTN     3'  ATGCCTGTAATCCCAGCACT  41767     A           A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693  P2RX7    3'  GTCTGTAATCCCAGCGCT    10374     A
                                AGT GCTGGGATTACAGAC
                                ||| ||||||||||||||
                                TCG CGACCCTAATGTCTG
                                  _
GAM693  PA2G4    3'  CTGTAATCCCAGCACT      71299     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                              TCA CGACCCTAATGTC
                                _
GAM693  PCDH11X  3' CTGTAATCCCAGCACT     52007     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM693  PCDH11X  3' CTGTAATCCCAGCACT     52008     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM693  PCDH11Y  3' CTGTAATCCCAGCACT     52060     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM693  PCDH11Y  3' CTGTAATCCCAGCACT     52066     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM693  PDE4C    3' ATGCCTATAATCCCAGCACT   6230      A        C  A
                              AGT GCTGGGATTA AG CAT
                              ||| |||||||||| || |||
                              TCA CGACCCTAAT TC GTA
                                _         A  C
GAM693  PDE4C    3' TGCCTGTAATCCCGGTACT    6238      G         A
                              AGTA CTGGGATTACAG CA
                              |||| |||||||||||| ||
                              TCAT GGCCCTAATGTC GT
                                _          C
GAM693  PIK3R2   3' ATGCCTGTAATCCCAGCACT   17256     A          A
                              AGT GCTGGGATTACAG CAT
                              ||| |||||||||||| |||
                              TCA CGACCCTAATGTC GTA
                                _          C
GAM693  PKD2     3' CTGTAATCCCAGCACT      60092     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM693  PLA2G2D  3' ATGCCTGTAATCCCAACACT  24786     AGC        A
                              AGT   TGGGATTACAG CAT
                              |||   |||||||||| |||
                              TCA   ACCCTAATGTC GTA
                                CA_          C
GAM693  POLK     3' CTGTAATCCCAGCTACT     32566
                              AGTAGCTGGGATTACAG
                              ||||||||||||||||
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                                TCATCGACCCTAATGTC

GAM693  PSD      5'  CTGCAATCCCAGCACT      10927     A       A
                                AGT GCTGGGATT CAG
                                ||| ||||||||| |||
                                TCA CGACCCTAA GTC
                                  _       C
GAM693  PSMB2    3'  ATGCCTGTAATCCCAGCACT  10947     A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  PSMB9    3'  CTATAATCCCAGCACT      10960     A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _       A
GAM693  PSMD5    3'  CTATAATCTCAGCTACTCA   17303     C         C
                                A AGTAGCTGGGATTA AG
                                | |||||||||||||| ||
                                A TCATCGACTCTAAT TC
                                 C          A
GAM693  PTAFR    3'  CTGTAATCCCAGCACT      6294      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  PTAFR    3'  CTGTAGTCCCAGCTACTCA   6295      C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTGATGTC
                                 C
GAM693  RAB3B    3'  CTGTAATCCCAGCACT      11185     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  RAB7L1   3'  CTGTAATCCCAGCACT      14107     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  RAB7L1   3'  TGCCTGTAATCCCAGC      14110       A
                                GCTGGGATTACAG CA
                                |||||||||||| ||
                                CGACCCTAATGTC GT
                                     C
GAM693  RAD51L1  5'  CTGTAATCCCAGCGCT      56060     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCG CGACCCTAATGTC
                                  _
GAM693  RBBP5   3'  ATGCCTGTAATCCCAGCTAC  17332            A
                                GTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                CATCGACCCTAATGTC GTA
                                       C
GAM693  RBBP5   3'  CTGTAATCCCAGCACT     17334    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  RBBP9   3'  ATGCCTGTAATCCCAGCACTGT 70128      A         A
          G                      TACAGT GCTGGGATTACAG CAT
                                ||||||| |||||||||||| |||
                                GTGTCA CGACCCTAATGTC GTA
                                  _          C
GAM693  RBL1    3'  ATGCCTATAATCCCAGCTACTT 11260   _         C  A
          G                      CA GTAGCTGGGATTA AG CAT
                                || |||||||||||| || |||
                                GT CATCGACCCTAAT TC GTA
                                 T          A  C
GAM693  RBM3    3'  CTGTAATCCCAGTGACT    70487    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA TGACCCTAATGTC
                                  G
GAM693  RECQL5  3'  ATGTCTGTATTGGCTACTGT  14924       TG GAT
                                ACAGTAGC  G   TACAGACAT
                                ||||||||  |   |||||||||
                                TGTCATCG  T   ATGTCTGTA
                                     GT ___
GAM693  RFC2    3'  CTGTAATCCCAACACT     11304    AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693  RPN1    5'  ATGCCTGTAATCCCAGCTACT  11389            A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                       C
GAM693  SCD     3'  ATGTCTGTTTATTAACTACTG  17346      C   GATT
                                CAGTAG TGG    ACAGACAT
                                |||||| |||    ||||||||
                                GTCATC ATT    TGTCTGTA
                                   A   ATT_
GAM693  SCN2B   3'  CTGTAATCCCAGCACT     15938    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                              TCA CGACCCTAATGTC
                                _
GAM693  SIM2     3'  CTGTAATCCCAGCACT     23783     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM693  SLC14A1  3'  CTGTAATCCCAGCACT     31839     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM693  SLC14A2  3'  CTGTAATCCCAGCACT     23132     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM693  SLC26A4  3'  ATGCCTGTAATCCCAGCACT  4783      A          A
                              AGT GCTGGGATTACAG CAT
                              ||| |||||||||||| |||
                              TCA CGACCCTAATGTC GTA
                                _          C
GAM693  SLC28A2  3'  CTGTAATCCCAGCGCT      14869     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCG CGACCCTAATGTC
                                _
GAM693  SLC2A3   3'  CTGTAATCCCAGCACT      22660     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM693  SLC2A6   3'  CTGTAATCCCAGCACT      34157     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM693  SLC31A1  3'  ATGCCTGTAATCCCAGCACT  8511      A          A
                              AGT GCTGGGATTACAG CAT
                              ||| |||||||||||| |||
                              TCA CGACCCTAATGTC GTA
                                _          C
GAM693  SLC31A1  3'  TGTAATCCCAGCTACTCA    8515    C
                              A AGTAGCTGGGATTACA
                              | ||||||||||||||||
                              A TCATCGACCCTAATGT
                               C
GAM693  SMG1     3'  CTGTAATCCCAGCACT      30651     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  SRGAP1   5' ATGCCTGTAGTCTCAGCTACTC 72259   C            A
             A                   A AGTAGCTGGGATTACAG CAT
                                 | ||||||||||||||||| |||
                                 A TCATCGACTCTGATGTC GTA
                                  C             C
GAM693  STAT3    3' CTGTAATCCCAGCACT     57713    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                  _
GAM693  STAT3    3' CTGTAATCCCAGCACT     11998    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                  _
GAM693  SULT1A2  3' ATGTCTGCAATCCCAGCGATTT 72215    TA_      A
             G                    CAG   GCTGGGATT CAGACAT
                                 |||   ||||||||| |||||||
                                 GTT   CGACCCTAA GTCTGTA
                                   TAG       C
GAM693  SULT1A3  3' ATGTCTGCAATCCCAGCGATTT 12052    TA_      A
             G                    CAG   GCTGGGATT CAGACAT
                                 |||   ||||||||| |||||||
                                 GTT   CGACCCTAA GTCTGTA
                                   TAG       C
GAM693  SULT2A1  3' ATGCCTGTAATCCCAGCACT  71751    A         A
                                 AGT GCTGGGATTACAG CAT
                                 ||| |||||||||||| |||
                                 TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  SULT2A1  3' ATGTCTGTAATCCCAGCACT  71752    A
                                 AGT GCTGGGATTACAGACAT
                                 ||| ||||||||||||||||
                                 TCA CGACCCTAATGTCTGTA
                                  _
GAM693  SUV39H2  3' CTGTAGTCCCAGCTACTCA   45136   C
                                 A AGTAGCTGGGATTACAG
                                 | ||||||||||||||||
                                 A TCATCGACCCTGATGTC
                                  C
GAM693  SWAP70   3' CTGTAATCCCAGCACT     71348    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                  _
GAM693  TBX6     3' CTGTAATCCCAACTACTTG   54964    _   C
                                 CA GTAG TGGGATTACAG
                                 || |||| ||||||||||
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                                GT CATC ACCCTAATGTC
                                 T    A
GAM693  TCF7     3'  CTGTAATCCCAGCACT      12161     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  TCTA     3'  CTGTAATCCCAACACT      42238     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693  TEM7     3'  CTGTAATCCCAGCACT      39884     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  TKTL1    5'  ATGTCTGTCTTTCAGCCAC   24296     A    GG TT
                                GT GCTG  A  ACAGACAT
                                || ||||  |  ||||||||
                                CA CGAC  T  TGTCTGTA
                                 C    TT C_
GAM693  TM7SF3   3'  CTGTAATCCCAATACTG     59666      GC
                                CAGTA  TGGGATTACAG
                                |||||  ||||||||||
                                GTCAT  ACCCTAATGTC
                                   A_
GAM693  TNFRSF10A 3'  ATGCCTGTAATCCCAGCACT   13886     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  TNFRSF10D 3'  ATGCCTGTAATCCCAGCACT   13860     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  TNFSF15  3'  CTGTAATCCCAACACT      17592     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693  TRIM14   3'  CTGTAATCCCAGCGCT      52635     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCG CGACCCTAATGTC
                                  _
GAM693  TRIM14   3'  ATGCCTGTAATCCCAGCTACT  28851              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
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                                TCATCGACCCTAATGTC GTA
                                          C
GAM693  TRIM9    5'  ATGCCTGTAATCCCAGCTA   30752            A
                                TAGCTGGGATTACAG CAT
                                ||||||||||||||| |||
                                ATCGACCCTAATGTC GTA
                                          C
GAM693  TRPM8    3'  TGTAATCCCAGCTACTCA    43987   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  TSN      3'  CTGTAATCCCAGCACACTG   16106     A_
                                CAGT  GCTGGGATTACAG
                                ||||  ||||||||||||
                                GTCA  CGACCCTAATGTC
                                   CA
GAM693  TSN      3'  TGCCTGTAATTCAGT       16111      G     A
                                GCTGG ATTACAG CA
                                ||||| ||||||| ||
                                TGACT TAATGTC GT
                                   _      C
GAM693  TSNAX    3'  CTGTAATCCCAGCACT      19998     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  TTF2     3'  TGCCTGTAATCCCGACACT   13176     AGC        A
                                AGT   TGGGATTACAG CA
                                |||   |||||||||| ||
                                TCA   GCCCTAATGTC GT
                                  CA_         C
GAM693  UBE2G2   3'  CTGCAATCCCAGCACT      64855     A       A
                                AGT GCTGGGATT CAG
                                ||| ||||||||| |||
                                TCA CGACCCTAA GTC
                                  _        C
GAM693  UBE2G2   3'  CTGTAGTCTCAGCTACTCA   64856   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACTCTGATGTC
                                 C
GAM693  UC28     3'  ATGCCTGTAATCCCAGCTACT  41288            A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                          C
GAM693  UC28     3'  CTGTAATCCCAGCACT      41290     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
```

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                                TCA CGACCCTAATGTC
                                  _
GAM693  UPK1B   3' ATGCCTGTAATCCCAGCACT  22715    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  USP14   3' CTGTAATCCCAGCACT     17658    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  VDR     3' TGTAATCCCAGCTACTCA    4574    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  VHL     3' ATGCCTGTAATCCCAGC     5058            A
                                GCTGGGATTACAG CAT
                                |||||||||||| |||
                                CGACCCTAATGTC GTA
                                       C
GAM693  VHL     3' ATGCCTGTAATCCCAGCACT  5059    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  VHL     3' ATGCCTGTAATCCTAGCTACTC 5060   C           A
          A                      A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGATCCTAATGTC GTA
                                 C            C
GAM693  VHL     3' CTGTAATCCCAGCACT      5069    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  VHL     3' TCTGTAATCCTAGCTACT    5090
                                AGTAGCTGGGATTACAGA
                                ||||||||||||||||||
                                TCATCGATCCTAATGTCT

GAM693  VPS41   3' ATGCCTGTAATCCCAGCTACT 26921           A
                                AGTAGCTGGGATTACAG CAT
                                ||||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                       C
GAM693  WIG1    3' CTGTAATCCCAGCACT      94466    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
```

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                                TCA CGACCCTAATGTC
                                   _
GAM693  WSX1     3'  CTGTAATCCCAGCACT      16732     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                   _
GAM693  ZNF136   3'  CTGTAATCCCAGCACT      59888     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                   _
GAM693  ZNF137   3'  CTGTAATCCCAGCACT      12862     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                   _
GAM693  ZNF14    3'  ATGCCTCTAATCCCAGCTACTC 40713    C          C  A
            A                    A AGTAGCTGGGATTA AG CAT
                                | |||||||||||||| || |||
                                A TCATCGACCCTAAT TC GTA
                                 C           C  C
GAM693  ZNF36    3'  CTGTAATCCCAGCACT      93962     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                   _
GAM693  ZNF74    3'  ATGTCCCTGTGGTCCCAGCTAC 12790    C          __
            TCA                   A AGTAGCTGGGATTACA  GACAT
                                | ||||||||||||||||  |||||
                                A TCATCGACCCTGGTGT  CTGTA
                                 C             CC
GAM693  ZNF74    3'  CTGTAATCTTAACACTGTG    12795       AGC
                                TACAGT   TGGGATTACAG
                                ||||||   ||||||||||||
                                GTGTCA   ATTCTAATGTC
                                   CA_
GAM693  AF020591 3'  ATGCCTGTAATCCCAGCACTCT 27135     TA_          A
            G                    CAG   GCTGGGATTACAG CAT
                                |||   |||||||||||||| |||
                                GTC   CGACCCTAATGTC GTA
                                  TCA           C
GAM693  AF020591 3'  CTGTAATCCCAGCACT      27139     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                   _
GAM693  AF020591 3'  CTGTAGTCCCAGCTACTCA   27140    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
```

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                                A TCATCGACCCTGATGTC
                                 C
GAM693  AKAP11   3' CTGTAATCCCAGAACTCTG   57831    TAG_
                                CAG   CTGGGATTACAG
                                |||   ||||||||||||
                                GTC   GACCCTAATGTC
                                  TCAA
GAM693  AKR1D1   3' ATGCCTATAATCCCAGCACT  19972    A       C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _       A  C
GAM693  AKR1D1   3' TGTAATCCCAGCTACTCA    19978   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  APOF     3' CTGTAATCCCAGCACTGTG   7909       A
                                TACAGT GCTGGGATTACAG
                                |||||| ||||||||||||
                                GTGTCA CGACCCTAATGTC
                                   _
GAM693  APXL2    3' CTGTAATCCCAGCACT     75189    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                   _
GAM693  ARNTL2   3' ATGCCTGTAATCCCAGCACT  39454    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  ARNTL2   3' CTGTAATCCCAACTGCT     39462      C
                                AGTAG TGGGATTACAG
                                ||||| ||||||||||
                                TCGTC ACCCTAATGTC
                                   A
GAM693  ARNTL2   3' CTGTAATCCCAGTACT      39463     G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                   _
GAM693  BANP     3' ATGCCTGTAATCCCAGC     66214          A
                                GCTGGGATTACAG CAT
                                |||||||||||| |||
                                CGACCCTAATGTC GTA
                                        C
GAM693  BFAR     3' CTGTAATCCCAGCTACTTG   60771    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
```

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                                GT CATCGACCCTAATGTC
                                 T
GAM693  BIA2     3'  CTGTAATCCCAGCACT      71281     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693  BIRC1    3'  CTGTAATCCCAGCACT      15788     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693  BLOV1    3'  ATGCCTGTAATCCCAGCTACT  76277               A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                          C
GAM693  BLOV1    3'  CTGTAATCCCAGCACT      76280     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693  BLOV1    3'  CTGTAATCCCAGCTACTTG   76281     _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                 T
GAM693  BNIP-S   3'  GTCTGTAATCCCAGCACT    56274     A
                                AGT GCTGGGATTACAGAC
                                ||| |||||||||||||||
                                TCA CGACCCTAATGTCTG
                                 _
GAM693  C13orf1  3'  CTGTAATCCCAGCACT      39969     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693  C1orf24  3'  CTATAATCCCAGCACT      53714     A         C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                 _         A
GAM693  C1QTNF2  3'  ATGCCTATAATCCCAGGACT  49124     AG        C  A
                                AGT  CTGGGATTA AG CAT
                                |||  |||||||| || |||
                                TCA  GACCCTAAT TC GTA
                                  G_        A  C
GAM693  C20orf108 3' CTGTAATCCCAGCACT      55045     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
```

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                                TCA CGACCCTAATGTC
                                  _
GAM693  C20orf12  3'  ATGCCTGTAATCCCAGTTACT  36321              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATTGACCCTAATGTC GTA
                                        C
GAM693  C20orf12  3'  CTGTAATCCCAGCACT      36322     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  C20orf130 3'  GTGGCTGTCCCAGCCAC     61758     A      TTA   A
                                GT GCTGGGA   CAG CAT
                                || |||||||   ||| |||
                                CA CGACCCT   GTC GTG
                                 C       ___   G
GAM693  C20orf142 3'  CTGTAATCCCAGCTACT     74775
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  C20orf175 3'  CTGTAATCCCAACACT      55064     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693  C20orf177 3'  ATGCCTGTAATCCCAGCTACT  62143              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                        C
GAM693  C20orf177 3'  CTGTAATCCCAGCACT      62146     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  C20orf183 3'  CTGTAATCCCAGCACT      47803     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  C20orf29  3'  CTGTAATCCCAGCACT      37126     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  C21orf108 3'  CTATAATCCCAGCACT      88720     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
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                                TCA CGACCCTAAT TC
                                  _        A
GAM693  C22orf19  3'  GTCTGTAATCCCAGCACT    13429     A
                                AGT GCTGGGATTACAGAC
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCTG
                                  _
GAM693  C22orf20  3'  ATGCCTGTAATCCCAGCTATT  47425               A
                                AGTAGCTGGGATTACAG CAT
                                ||||||||||||||||| |||
                                TTATCGACCCTAATGTC GTA
                                          C
GAM693  C2F       3'  CTGTAATCCCAGCACT      20928     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  C6orf10   5'  CTGTAATCCCATCATTTGCT   22289      C___
                                AGTAG   TGGGATTACAG
                                |||||   ||||||||||
                                TCGTT   ACCCTAATGTC
                                   TACT
GAM693  C6orf5    3'  CTGTAATCCCAGCACT      31346     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  C6orf5    3'  CTGTAATCCCAGCACT      31347     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  C8orf2    3'  CTGTAATCCCAGCACT      23163     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  C9orf5    3'  TCTGTAATCCCAGCACT     49284     A
                                AGT GCTGGGATTACAGA
                                ||| |||||||||||||
                                TCA CGACCCTAATGTCT
                                  _
GAM693  CALN1     3'  CTATAATCCCAGCACT      48866     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM693  CAMKK2    5'  CTGTAATCCCAGCACT      21582     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  CBCIP2   3'  CTGTAATCCCAGCACT      51590     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  cerk     3'  CTGTAATCCCAGCACT      42846     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  CFLAR    3'  CTGTAATCCCAGCACT      13929     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  CG012    5'  ATGCCTATATTCTAGCTACTCA 83214    C          TAC  A
                                A AGTAGCTGGGAT   AG CAT
                                | ||||||||||||   || |||
                                A TCATCGATCTTA   TC GTA
                                 C          TA_  C
GAM693  CG012    5'  ATGCCTGTAATCCCAACACT   83215     AGC         A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_          C
GAM693  CG012    5'  CTGTAATCCCAGCTATTCGGCT 83219     _____
           G                     CAGT     AGCTGGGATTACAG
                                ||||     ||||||||||||||
                                GTCG     TCGACCCTAATGTC
                                   GCTTA
GAM693  CGI-203  3'  TGTAATCCCAGCTACTCA    39904    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  CHRFAM7A 3'  ATGCTTGTAATCCCAGCTACTC 95017    C            GA
           A                     A AGTAGCTGGGATTACA  CAT
                                | ||||||||||||||||  |||
                                A TCATCGACCCTAATGT  GTA
                                 C              TC
GAM693  CLDN15   3'  ATGCCTGTAATCCCAGCACT   56558     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693  CNNM4    3'  TCTGTTGTCAACTGCTGTA   39484        CTGG   T
                                TACAGTAG    GAT ACAGA
                                ||||||||    ||| |||||
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                                ATGTCGTC    CTG TGTCT
                                    AA__    T
GAM693   COE2     3'  ATGCCTGTAATCCCAGCTACTT 64247    _            A
            G                    CA GTAGCTGGGATTACAG CAT
                                 || |||||||||||||||| |||
                                 GT CATCGACCCTAATGTC GTA
                                  T             C
GAM693   COE2     3'  CTGTAATCCCAGCACT      64251     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                   _
GAM693   CPR2     3'  CTGTAATCCCAGCACT      48095     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                   _
GAM693   CPR2     3'  CTGTAATCCCAGCTACTCA   48096    C
                                 A AGTAGCTGGGATTACAG
                                 | ||||||||||||||||
                                 A TCATCGACCCTAATGTC
                                  C
GAM693   CSAD     3'  CTGTAATCCCAGCACT      32028     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                   _
GAM693   D21S2056E 3'  ATGCCTGTAATCCCAGCTACT  13467              A
                                 AGTAGCTGGGATTACAG CAT
                                 |||||||||||||||| |||
                                 TCATCGACCCTAATGTC GTA
                                             C
GAM693   D21S2056E 3'  CTGTAATCCCAGCACT      13470     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                   _
GAM693   DCOHM    3'  CTGTAATCCCTGCACT      49600     A  T
                                 AGT GC GGGATTACAG
                                 ||| || ||||||||||
                                 TCA CG CCCTAATGTC
                                   _  T
GAM693   DDX34    3'  CTGTAATCCCAGCACT      27982     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                   _
GAM693   DEGS     3'  ATGCCTATAATCCCAGCACT  13409     A        C  A
                                 AGT GCTGGGATTA AG CAT
                                 ||| |||||||||| || |||
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                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM693  DEGS     3'  ATGCCTGTAATCCCAGCTACAT 13410    _           A
           G                     CA GTAGCTGGGATTACAG CAT
                                 || |||||||||||||||| |||
                                 GT CATCGACCCTAATGTC GTA
                                  A            C
GAM693  DEGS     3'  ATGCCTGTAATCCCAGCTACAT 58613    _           A
           G                     CA GTAGCTGGGATTACAG CAT
                                 || |||||||||||||||| |||
                                 GT CATCGACCCTAATGTC GTA
                                  A            C
GAM693  DIS3     3'  ATGCCTGTAATCCCAGCTACTT 30227    _           A
           G                     CA GTAGCTGGGATTACAG CAT
                                 || |||||||||||||||| |||
                                 GT CATCGACCCTAATGTC GTA
                                  T            C
GAM693  DKFZP434B168 3'  CTGTAATCCCAGCACT      31253     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC

                                  _
GAM693  DKFZP434C171 3'  CTGTAATCCCAGCACT      31553     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC

                                  _
GAM693  DKFZP434C1715 3'  CTGTAATCCCAGCAC      86148     A
                                 GT GCTGGGATTACAG
                                 || ||||||||||||
                                 CA CGACCCTAATGTC

                                  _
GAM693  DKFZp434E0519 3'  CTATAATCCCAGCACT      49986     A        C
                                 AGT GCTGGGATTA AG
                                 ||| |||||||||| ||
                                 TCA CGACCCTAAT TC
                                   _         A
GAM693  DKFZp434E2220 5'  TGTAATCCCAGCTACTCA    34304    C
                                 A AGTAGCTGGGATTACA
                                 | ||||||||||||||||
                                 A TCATCGACCCTAATGT
                                  C
GAM693  DKFZP434F091 3'  TGTAATCCCAACTACTCA    31284    C    C
                                 A AGTAG TGGGATTACA
                                 | ||||| ||||||||||
                                 A TCATC ACCCTAATGT
                                  C    A
GAM693  DKFZp434G171 3'  ATGCCTGTAATCCCAGCACT   79431     A          A
                                 AGT GCTGGGATTACAG CAT
                                 ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  DKFZp434G171 3'  TGTAATCCCAGCTACTCA    79440   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  DKFZP434I1735 3'  CTGTAATCCCAGCTACT     87801
                                AGTAGCTGGGATTACAG
                                |||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  DKFZP434L187 5'  CTGTAATCCCAGCTACT     68804
                                AGTAGCTGGGATTACAG
                                |||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  DKFZP434N1511 3'  ATGCCTGTAATCCCAGCACT   91415     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  DKFZP434N161 3'  GTCTGTAATCCCAGCACT    78522     A
                                AGT GCTGGGATTACAGAC
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCTG
                                  _
GAM693  DKFZp547C176 3'  CTGTAATCCCAGCACT      67222     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  DKFZp547I094 3'  CTGTAATCCCAGCACT      49639     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  DKFZp547I094 3'  CTGTAGTCACAGCTACT     49640         G
                                AGTAGCTG GATTACAG
                                |||||||| ||||||||
                                TCATCGAC CTGATGTC
                                     A
GAM693  DKFZP564B1023 3'  ATGCCTGTAATCCCAGCTACT  48536              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM693  DKFZP564B1023 3'  CTGTAATCCCAGCACT      48538     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  DKFZP564I052 3'  CTGTAATCCCAGCACT      66707     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  DKFZP564M182 3'  CTGTAATCCCAGCACT      78033     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  DKFZP564M182 3'  CTGTAATCCCAGCTACT     78034
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  DKFZp566H0824 3'  CTGTAATCCCAGCACTTTA   34050    C   A
                                TA AGT GCTGGGATTACAG
                                || ||| ||||||||||||
                                AT TCA CGACCCTAATGTC
                                 T  _
GAM693  DKFZP586C1324 3'  ATGCCTGTAATCCCAGCACT  69796     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  DKFZP586M1120 3'  CTGTAATCCCAGCACT      48457     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  DKFZP667O116 3'  TGCCTATAATCCCGGCACT    94287     A        C  A
                                AGT GCTGGGATTA AG CA
                                ||| |||||||||| || ||
                                TCA CGGCCCTAAT TC GT
                                  _        A  C
GAM693  DKFZP761E2110 3'  ATGCCTGTAATCCCAGCAC   48224     A          A
                                GT GCTGGGATTACAG CAT
                                || |||||||||||| |||
                                CA CGACCCTAATGTC GTA
                                  _          C
GAM693  DKFZP761G1913 3'  ATGCCTGTAATCCCAGCACT  48909     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  DKFZP761G1913 3'  CTGTAATCCCAGCTACTTG   48913     _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
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                                GT CATCGACCCTAATGTC
                                 T
GAM693  DKFZp761J139 5'  CTGTAATCCCAGCACT      50108     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  DRF1     3'  CTATAATCCCAGCACT      47030     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM693  DRF1     3'  CTGTAATCCCAGCACT      47032     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  DRF1     3'  TGTAATCCCAGCTACTCA    47038    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  FADS1    3'  ATGCCTGTAATCCCAACACT   25473     AGC         A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_          C
GAM693  FADS1    3'  CTGTAATCCCAGCTAC      25476
                                GTAGCTGGGATTACAG
                                ||||||||||||||||
                                CATCGACCCTAATGTC

GAM693  FBXO27   3'  ATGCCTGTAATCCCAGCACT   74504     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693  FBXO27   3'  CTGTAATCCCTGCACT      74508     A  T
                                AGT GC GGGATTACAG
                                ||| || ||||||||||
                                TCA CG CCCTAATGTC
                                  _  T
GAM693  FBXO6    3'  CTGTAATCCCAGCACT      37383     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FBXO9    3'  ATGCCTATAATCCCAGCACT   53100     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
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                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM693  FBXO9    3' CTATAATCCCAATACT     53102     GC      C
                                AGTA  TGGGATTA AG
                                ||||  |||||||| ||
                                TCAT  ACCCTAAT TC
                                  A_      A
GAM693  FKBP14   3' ATGCCTGTAATCCCAGCACT  35622    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  FKBP14   3' ATGCCTGTAATCCCAGCACT  35623    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  FKSG17   3' CTGTAATCCCAGTTACTCA   49329   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATTGACCCTAATGTC
                                 C
GAM693  FLJ00060 3' ATGTCTGTAATCCCAGCACTCT 61091    TA_
          G                      CAG   GCTGGGATTACAGACAT
                                |||   ||||||||||||||||
                                GTC   CGACCCTAATGTCTGTA
                                  TCA
GAM693  FLJ10008 3' GTCTGTAATCCCAGCACT    35729    A
                                AGT GCTGGGATTACAGAC
                                ||| |||||||||||||
                                TCA CGACCCTAATGTCTG
                                  _
GAM693  FLJ10043 3' CTGTAATCCCAGCACT      35758    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ10043 3' CTGTAATCCCAGCTACT     35759
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  FLJ10058 3' ATGCCTGTAATCCCAGCACT  35782    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  FLJ10244 3' ATGCCTGTAATCCCAGCTGCT  35940              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
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                                TCGTCGACCCTAATGTC GTA
                                          C
GAM693  FLJ10460 3' CTGTAATCCCAACACT     36127     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693  FLJ10460 3' CTGTAATCCCAGCACT      36128     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ10460 3' CTGTAATCCCAGCTACTTG   36129     _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                 T
GAM693  FLJ10547 3' CTGTAATCCCAGCACT      36267     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ10607 3' CTGTAATCCCAGCACT      77113     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ10607 3' CTGTAATCCCAGCTACTCA   77114   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM693  FLJ10613 3' GTCTGTAATCCCAGCACT    38825     A
                                AGT GCTGGGATTACAGAC
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCTG
                                  _
GAM693  FLJ10650 3' CTGTAATCCCAGCACT      36382     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ10704 3' ATGCCTGTAATCCCAGCTACT 36449               A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                          C
GAM693  FLJ10781 3' CTGTAATCCCAGCACT      36631     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ10781 3' TGTAATCCCAGCTACTCA    36638   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  FLJ10803 3' CTGTAATCCCAGCACT      36664     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ10826 3' ATGCCTGTAATCCCAGCTACT  36700              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                          C
GAM693  FLJ10830 3' ATGCCTGTAGTCCCAGCCACTC 36717   C   A          A
           A                     A AGT GCTGGGATTACAG CAT
                                | ||| ||||||||||||| |||
                                A TCA CGACCCTGATGTC GTA
                                 C   C           C
GAM693  FLJ10830 3' ATGCCTGTAGTTCCAGCTACTC 36718   C             A
           A                     A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACCTTGATGTC GTA
                                 C              C
GAM693  FLJ10989 3' CTGTAATCCCAGCACT      36949     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ10997 3' TGCCTGACCACCTACTGTA    36957         C   GATTA   A
                                TACAGTAG TGG     CAG CA
                                |||||||| |||     ||| ||
                                ATGTCATC ACC     GTC GT
                                      C   A____   C
GAM693  FLJ11029 3' CTGTAATCCCAGCACT      60975     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ11036 3' CTGCGGTTCCAGCTACTCA    36998   C          TA
                                A AGTAGCTGGGAT  CAG
                                | ||||||||||||  |||
                                A TCATCGACCTTG  GTC
                                 C           GC
GAM693  FLJ11042 3' ATGCCTGTAATCCCAGCACT   37004     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  FLJ11126 3' ATGCCTATAATCCCAGCAC   37083    A       C  A
                                GT GCTGGGATTA AG CAT
                                || |||||||||| || |||
                                CA CGACCCTAAT TC GTA
                                  _        A  C
GAM693  FLJ11136 3' CTGTAATCCCAGCACT     37093    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM693  FLJ11151 3' CTGTAATCCCAGCACT     67874    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM693  FLJ11151 3' CTGTAATCCCAGCTACT    67875
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  FLJ11267 3' ATGCCTGTAATCCCAGCACT  39003    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| ||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  FLJ11370 3' ATGCCTGTAATCCCAGCTACT 46370              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM693  FLJ11637 3' CTGTAATCCCAGCACT     46380    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM693  FLJ11700 3' CTGTAATCCCAGCACT     46038    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM693  FLJ11700 3' CTGTAATCCCAGCTACTCA  46039   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM693  FLJ11710 5' ATGCCTGTAGTCCCAGCTACTC 45825   C           A
          A                      A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
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                                A TCATCGACCCTGATGTC GTA
                                 C             C
GAM693  FLJ11722 3' ATGCCTGTAATCCCAGGACT  46389    AG        A
                                AGT  CTGGGATTACAG CAT
                                |||  |||||||||||| |||
                                TCA  GACCCTAATGTC GTA
                                  G_          C
GAM693  FLJ11722 3' CTGTAATCCCAGCTACT    46391
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  FLJ11722 3' TGTAATCCCAGCTACTCA   46401   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  FLJ11726 3' CTGTAATCCCAGCACT     46411    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ11996 3' ATGCCTGTAATCCCAGCTACT 46434            A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                      C
GAM693  FLJ12056 3' ATGCCTGTAATCCCAGCTATT 46252            A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TTATCGACCCTAATGTC GTA
                                      C
GAM693  FLJ12056 3' ATGCCTATAATCCCAACACT  46251    AGC     C  A
                                AGT   TGGGATTA AG CAT
                                |||   |||||||| || |||
                                TCA   ACCCTAAT TC GTA
                                  CA_       A  C
GAM693  FLJ12122 3' CTGTAATCCCAGCACT     46462    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ12178 3' GTCTGTAATCCCAGCACT   47103    A
                                AGT GCTGGGATTACAGAC
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCTG
                                  _
GAM693  FLJ12294 3' CTATAATCCCAGCTACT    47012          C
                                AGTAGCTGGGATTA AG
                                |||||||||||||| ||
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                                TCATCGACCCTAAT TC
                                        A
GAM693  FLJ12294  3'  CTGTAATCCCAGCACT     47013     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693  FLJ12331  3'  CTATAATCCCAGCACTTTA   46478    C   A        C
                                TA AGT GCTGGGATTA AG
                                || ||| |||||||||| ||
                                AT TCA CGACCCTAAT TC
                                 T  _        A
GAM693  FLJ12363  3'  CTGTAATCCCAGCACT     49679     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693  FLJ12547  3'  CTGTAATCCCAGCACTGTG   46491       A
                                TACAGT GCTGGGATTACAG
                                |||||| ||||||||||||
                                GTGTCA CGACCCTAATGTC
                                  _
GAM693  FLJ12606  3'  CTGTAATCCCAGCACT     45640     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693  FLJ12618  3'  ATGCCTGTAATCTCAGCTACTC 45994   C             A
          A                      A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACTCTAATGTC GTA
                                 C             C
GAM693  FLJ12660  3'  CTGTAATCCCAGCACT     47141     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693  FLJ12660  3'  CTGTAATCCCAGCTACT     47142
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  FLJ12666  3'  CTGTAATCCCAGCACT     44767     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693  FLJ12800  3'  CTGTAATCCCAGCACT     43232     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ12949 3' ATGCCTGTAGTCCCAGCTACTC 43442   C           A
              A                  A AGTAGCTGGGATTACAG CAT
                                 | ||||||||||||||||| |||
                                 A TCATCGACCCTGATGTC GTA
                                  C             C
GAM693  FLJ12949 3' CTGTAATCCCAGCACT     43445    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                  _
GAM693  FLJ12985 3' CTGTAATCCCAGCACT     46240    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                  _
GAM693  FLJ13117 3' ATGCCTGTAATCCCAGCACT  43539    A         A
                                 AGT GCTGGGATTACAG CAT
                                 ||| |||||||||||| |||
                                 TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  FLJ13162 3' ATGCCTGTAATCCCAGCTACT 46550             A
                                 AGTAGCTGGGATTACAG CAT
                                 ||||||||||||||| |||
                                 TCATCGACCCTAATGTC GTA
                                             C
GAM693  FLJ13162 3' CTGTAATCCCAGCACT     46556    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                  _
GAM693  FLJ13193 3' ATGCCTATAATCCCGGCTACT 49758           C  A
                                 AGTAGCTGGGATTA AG CAT
                                 |||||||||||||| || |||
                                 TCATCGGCCCTAAT TC GTA
                                           A  C
GAM693  FLJ13193 3' CTGTAATCCCAACACTTTA   49765   C   AGC
                                 TA AGT   TGGGATTACAG
                                 || |||   ||||||||||
                                 AT TCA   ACCCTAATGTC
                                  T   CA_
GAM693  FLJ13193 3' CTGTAATCCCAGCACT     49766    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                  _
GAM693  FLJ13305 3' ATGCCTGTAATCCCAGC    90125          A
                                 GCTGGGATTACAG CAT
                                 |||||||||||| |||
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                                CGACCCTAATGTC GTA
                                        C
GAM693  FLJ13448 3' CTGTAATCCCAGTTACT    47135
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATTGACCCTAATGTC

GAM693  FLJ13456 3' CTGTAATCCCAGCACT     65936    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ13456 3' CTGTAATCCCAGCTACTCA  65937   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM693  FLJ13614 3' CTGTAATCCCAGCACT     57451    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ13659 3' ATGCCTGTAATCCCAGCTACT 47243             A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                        C
GAM693  FLJ13659 3' CTGTAATCCCAGCACT     47246    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ13769 3' ATGCCTATAATCCCAGCACT  46600    A       C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _       A  C
GAM693  FLJ13769 3' CTGTAATCCCAGCACT     46608    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ13848 3' CTGTAATCCCAGCACT     45465    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ13910 3' CTGCATTTTAGCTCTG     42927    T       TA
                                CAG AGCTGGGAT  CAG
                                ||| |||||||||  |||
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                                GTC TCGATTTTA  GTC
                                  _       C_
GAM693  FLJ13952 3' ATGCCTGTAACCCCAGCTACT 45613         A     A
                                AGTAGCTGGG TTACAG CAT
                                |||||||||| |||||| |||
                                TCATCGACCC AATGTC GTA
                                      C     C
GAM693  FLJ13952 3' ATGCCTGTAATCCCAGCACT  45614    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  FLJ13984 3' CTGTGGTCCCAGCTACTCA   45448   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTGGTGTC
                                 C
GAM693  FLJ14100 3' CTGTAATCCCAGCACT     46679    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ14107 3' ATGCCTGTAATCCCAGCACT  46689    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  FLJ14117 3' ATGCCTGTAGTCCCAGCTACTC 42901   C           A
          A                      A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACCCTGATGTC GTA
                                 C             C
GAM693  FLJ14117 3' CTGTAATACCAGCTACTCA   42907   C       G
                                A AGTAGCTGG ATTACAG
                                | ||||||||| |||||||
                                A TCATCGACC TAATGTC
                                 C       A
GAM693  FLJ14117 3' CTGTAATCCCAGCACT     42908    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ14225 3' CTGTAATCCCAGCACT     45902    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ14251 3' CTGTAATCCCAGCACT     45970    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ14326 3' ATGCCTATAATCCCAGCTACT 49799          C  A
                                AGTAGCTGGGATTA AG CAT
                                |||||||||||||| || |||
                                TCATCGACCCTAAT TC GTA
                                      A  C
GAM693  FLJ14326 3' ATGCCTGTAATCCCAGC    49800         A
                                GCTGGGATTACAG CAT
                                |||||||||||| |||
                                CGACCCTAATGTC GTA
                                      C
GAM693  FLJ14327 3' ATGCCTGTAATCCCAGCACT  46129    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _         C
GAM693  FLJ14345 3' CTGTAATCCCAGCACT     45334    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ14345 3' CTGTAATCCCAGCTACT    45335
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  FLJ14346 3' CTGTAATCCCAGCACT     46709    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ14346 3' CTGTAATCCCAGCACT     46710    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ14397 3' ATGCCTGTAACCCCAGCTACT 51323        A    A
                                AGTAGCTGGG TTACAG CAT
                                |||||||||| |||||| |||
                                TCATCGACCC AATGTC GTA
                                      C    C
GAM693  FLJ14397 3' CTATAATCCCAGCACT     51325    A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _       A
GAM693  FLJ14621 3' CTGTAATCCCAGCACT     51470    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ14642 3' ATGCCTGTAATCCCAGCACT  51493    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  FLJ14642 3' CTGTAATCCCAGCACT     51499    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ14888 3' ATGCCTGTAATCCCAGCACT  51679    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  FLJ20004 3' ATGCCTGTAATCCCAGCACT  34312    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  FLJ20004 3' CTGTAATCCCAGCACT     95292    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ20004 3' TGCCTGTAATCCCAGCTACT  95301              A
                                AGTAGCTGGGATTACAG CA
                                |||||||||||||||| ||
                                TCATCGACCCTAATGTC GT
                                           C
GAM693  FLJ20006 3' CTGTAATCCCAGCACT     34320    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ20006 3' CTGTAATCCCAGCTACT     34321
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  FLJ20034 3' CTGTAATCCCAGCACT     34371    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ20055 3' CTGAAGTCCCAGCTACTCA  34440  C         A
                                A AGTAGCTGGGATT CAG
                                | |||||||||||| |||
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                                A TCATCGACCCTGA GTC
                                 C          A
GAM693  FLJ20055 3' CTGTAATCCCAGCACTTTA   34441    C  A
                                TA AGT GCTGGGATTACAG
                                || ||| ||||||||||||
                                AT TCA CGACCCTAATGTC
                                 T  _
GAM693  FLJ20059 3' ATGCCTGTAATCCCAGCACT  34446     A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  FLJ20071 3' ATGCCTATAATCCCAGCTACTT 34479    _         C  A
          G                      CA GTAGCTGGGATTA AG CAT
                                || |||||||||||| || |||
                                GT CATCGACCCTAAT TC GTA
                                 T          A  C
GAM693  FLJ20081 3' CTGTAATCCCAGCACT     34507    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ20139 3' CTGTAATCCCAACACT     34624    AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693  FLJ20174 3' CTGTAATCCCAAAGTGCTG  34688     GC_
                                CAGTA   TGGGATTACAG
                                |||||   ||||||||||
                                GTCGT   ACCCTAATGTC
                                   GAA
GAM693  FLJ20200 3' TGCCTGTAATCCCTGCACT  34729    A  T       A
                                AGT GC GGGATTACAG CA
                                ||| || |||||||||| ||
                                TCA CG CCCTAATGTC GT
                                  _  T        C
GAM693  FLJ20211 3' CTGTAATCCCAGCACT     34751    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ20280 3' CTGTAATCCCAGCACT     34849    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ20280 3' CTGTAATCCCTGCTACT    34850      T
                                AGTAGC GGGATTACAG
                                |||||| ||||||||||
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                                TCATCG CCCTAATGTC
                                   T
GAM693  FLJ20340 3' ATGCCTGTAATCCCAGCATTTT 34972     TA_          A
              G                  CAG   GCTGGGATTACAG CAT
                                 |||   |||||||||||||| |||
                                 GTT   CGACCCTAATGTC GTA
                                   TTA           C
GAM693  FLJ20340 3' TGTAATCCCAGCTACTCA    34979    C
                                 A AGTAGCTGGGATTACA
                                 | ||||||||||||||||
                                 A TCATCGACCCTAATGT
                                  C
GAM693  FLJ20359 3' ATGCCTGTAATCCCAGCACT   35035     A          A
                                 AGT GCTGGGATTACAG CAT
                                 ||| |||||||||||| |||
                                 TCA CGACCCTAATGTC GTA
                                   _           C
GAM693  FLJ20452 3' ATGCCTGTAATCCCAGCACT   35196     A          A
                                 AGT GCTGGGATTACAG CAT
                                 ||| |||||||||||| |||
                                 TCA CGACCCTAATGTC GTA
                                   _           C
GAM693  FLJ20464 3' ATGCCTATAATCCGAGCTACT  35228       G     C  A
                                 AGTAGCT GGATTA AG CAT
                                 ||||||| |||||| || |||
                                 TCATCGA CCTAAT TC GTA
                                      G     A  C
GAM693  FLJ20464 3' ATGCCTGTAATCCCAGCACT   35229     A          A
                                 AGT GCTGGGATTACAG CAT
                                 ||| |||||||||||| |||
                                 TCA CGACCCTAATGTC GTA
                                   _           C
GAM693  FLJ20464 3' ATGCCTGTAATCTCAGCTACT  35230              A
                                 AGTAGCTGGGATTACAG CAT
                                 |||||||||||||||| |||
                                 TCATCGACTCTAATGTC GTA
                                             C
GAM693  FLJ20627 3' ATGCCTGTAATCCCAGCACT   35471     A          A
                                 AGT GCTGGGATTACAG CAT
                                 ||| |||||||||||| |||
                                 TCA CGACCCTAATGTC GTA
                                   _           C
GAM693  FLJ20627 3' GTCATCTCAGCTACTCA     35475    C          T
                                 A AGTAGCTGGGAT AC
                                 | |||||||||||  ||
                                 A TCATCGACTCTA TG
                                  C           C
GAM693  FLJ20695 3' ATGCCTGTAATCCCAGCACT   35556     A          A
                                 AGT GCTGGGATTACAG CAT
                                 ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  FLJ20700 3' ATGCCTGTAATCCCAGCACT  35570    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  FLJ20783 3' CTGTAATCCCAGCACT     35661    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ20825 3' ATGCCTGTAATCCCAACTCTTG 35693    T C       A
                                CAG AG TGGGATTACAG CAT
                                ||| || |||||||||| |||
                                GTT TC ACCCTAATGTC GTA
                                  C A         C
GAM693  FLJ20825 3' ATGCCTGTAATCCCAGCTACT 35694            A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                          C
GAM693  FLJ20825 3' CTGTAATCCCAGCACT     35696    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ20972 3' ATGCCTATAATCCCAGGTACT 46722     G       C A
                                AGTA CTGGGATTA AG CAT
                                |||| ||||||||| || |||
                                TCAT GACCCTAAT TC GTA
                                  G       A C
GAM693  FLJ21106 3' CTGTAATCCCAGCACT     46995    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ21144 3' ATGCCTGTAATCCCAGCACT  42875    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  FLJ21162 3' ATGCCTATAATCCCAGCACT  45892    A       C A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _       A C
GAM693  FLJ21162 3' CTATAAACCCAGCTACTCA   45894   C       A  C
                                A AGTAGCTGGG TTA AG
                                | |||||||||| ||| ||
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                                A TCATCGACCC AAT TC
                                 C         A  A
GAM693  FLJ21240 3' ATGCCTGTAATATCAGCTACTC 45837   C       GG      A
              A                  A AGTAGCTG  ATTACAG CAT
                                 | ||||||||  ||||||| |||
                                 A TCATCGAC  TAATGTC GTA
                                  C       TA      C
GAM693  FLJ21272 3' ATGCCTGTAATCCCAGC     46735            A
                                 GCTGGGATTACAG CAT
                                 |||||||||||||| |||
                                 CGACCCTAATGTC GTA
                                          C
GAM693  FLJ21551 3' CTGTAATCCCAGCTAC      45628
                                 GTAGCTGGGATTACAG
                                 ||||||||||||||||
                                 CATCGACCCTAATGTC

GAM693  FLJ21657 3' CTGTAATCCCAACACT      42509     AGC
                                 AGT   TGGGATTACAG
                                 |||   ||||||||||||
                                 TCA   ACCCTAATGTC
                                   CA_
GAM693  FLJ21687 3' CTGTAATCCCAGCACT      45857     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                    _
GAM693  FLJ21870 3' ATGCCTGTAATCCCAGCACT   43458     A          A
                                 AGT GCTGGGATTACAG CAT
                                 ||| |||||||||||| |||
                                 TCA CGACCCTAATGTC GTA
                                   _           C
GAM693  FLJ22054 3' CTGTAATCCAAGCTGC      94395       G
                                 GTAGCT GGATTACAG
                                 |||||| |||||||||
                                 CGTCGA CCTAATGTC
                                     A
GAM693  FLJ22054 3' CTGTAATCCCAGCACT      94396     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                    _
GAM693  FLJ22167 3' ATGCCTGTAATCCCAGCATTTT 44565     TA_          A
              G                   CAG   GCTGGGATTACAG CAT
                                 |||   |||||||||||| |||
                                 GTT   CGACCCTAATGTC GTA
                                   TTA           C
GAM693  FLJ22167 3' CTGTAATCCCAGCTACTTA    44572   C
                                 A AGTAGCTGGGATTACAG
                                 | ||||||||||||||||
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                                A TCATCGACCCTAATGTC
                                 T
GAM693  FLJ22313  3'  GTCTGTAATCCCAGCACT    42344     A
                                AGT GCTGGGATTACAGAC
                                ||| |||||||||||||||
                                TCA CGACCCTAATGTCTG
                                  _
GAM693  FLJ22692  3'  CTGTAATCCCAGCACT      46802     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ23022  3'  TGCCTGTAATCCCTGCACT   46814     A  T        A
                                AGT GC GGGATTACAG CA
                                ||| || |||||||||| ||
                                TCA CG CCCTAATGTC GT
                                  _  T         C
GAM693  FLJ23042  3'  ATGCCTGTAATCCCAGCTACT  47170              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM693  FLJ23042  3'  CTGTAATCCCAGCACT      47172     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ23120  3'  CTGTAATCCCAGCTACTCA   85148   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM693  FLJ23235  3'  ATGCCTGTAATCCCAGCACT  46305     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693  FLJ23323  3'  CTGTAATCCCAAAGTGCTG   45051      GC_
                                CAGTA   TGGGATTACAG
                                |||||   ||||||||||||
                                GTCGT   ACCCTAATGTC
                                   GAA
GAM693  FLJ23447  3'  ATGCCTGTAATCCCAGCACT  45710     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693  FLJ23476  3'  ATGCCTGTAATCCCAACATTCT 44958     TAGC_         A
            G                    CAG     TGGGATTACAG CAT
                                |||     |||||||||||| |||
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                                GTC     ACCCTAATGTC GTA
                                  TTACA          C
GAM693  FLJ23499  3'  ATGCCTGTAATCCCAGCACT   42816     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _            C
GAM693  FLJ23499  3'  ATGCCTGTAATCCCAGCACT   42817     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _            C
GAM693  FLJ23499  3'  CTGTAATCCCAGCTACT     42821
                                AGTAGCTGGGATTACAG
                                |||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  FLJ23537  3'  ATGCCTGCAATCCCAGCTACTT 46021    _          A   A
                  G              CA GTAGCTGGGATT CAG CAT
                                || ||||||||||| ||| |||
                                GT CATCGACCCTAA GTC GTA
                                 T          C   C
GAM693  FLJ25012  3'  ATGCCTGTAATCCAGTACT    58088      G   G      A
                                AGTA CTGG ATTACAG CAT
                                |||| |||| ||||||| |||
                                TCAT GACC TAATGTC GTA
                                  _   _       C
GAM693  FLJ25012  3'  CTATGGTCCCAGCTACTCA    58089    C            C
                                A AGTAGCTGGGATTA AG
                                | ||||||||||||| ||
                                A TCATCGACCCTGGT TC
                                 C           A
GAM693  FLJ25012  3'  CTGTAATCCCAGCACT       58090     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ25179  3'  ATGCCTGTAATCCCAGCACT   58354     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _            C
GAM693  FLJ30046  3'  CTGCAATGTTTGCTACTGTA   58100          TG G   A
                                TACAGTAGC  G ATT CAG
                                |||||||||  | ||| |||
                                ATGTCATCG  T TAA GTC
                                      TT G   C
GAM693  FLJ30092  3'  CTGTAATCCCAGCACT       58689     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ30681  3'  CTGTAATCCCAGCTACT     91786
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  FLJ31455  3'  CTGTAATCCCAGCACT      58623     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FLJ31737  3'  CTGTAATCCCAGCACT      58694     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  FUSIP1    3'  ATGCCTGTAATCTCAGCTACTC 53955    C              A
              A                  A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGACTCTAATGTC GTA
                                 C             C
GAM693  FUSIP1    3'  CTGTAATCCCAGCACT      53957     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  GALNT6    3'  ATGCCTGTAGTCGCAGCTACTC 23290    C       G       A
              A                  A AGTAGCTG GATTACAG CAT
                                | |||||||| |||||||| |||
                                A TCATCGAC CTGATGTC GTA
                                 C       G       C
GAM693  GCN2      3'  ATGCCTGTAGTCCCAGCTACT  62768              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTGATGTC GTA
                                          C
GAM693  GLTP      3'  CTGTAATCCCAGCACT      33159     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  GLTP      3'  CTGTAGTTCCAGCTACTCA   33160    C
                                A AGTAGCTGGGATTACAG
                                | |||||||||||||||||
                                A TCATCGACCTTGATGTC
                                 C
GAM693  GP5       3'  CTGTAATCCCAGCACT      15645     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  HES2     3'  CTGTAATCCCAGCACT      38854     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  HSD17B7  3'  TGTAGTCCCAGCTACTCA    33037    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTGATGT
                                 C
GAM693  HSH2     3'  ATGCCTGTAATCCCAGCTACTT 51671    _            A
            G                    CA GTAGCTGGGATTACAG CAT
                                || |||||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 T             C
GAM693  HSMPP8   3'  CTATAATCCCAGCGCT      93474     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCG CGACCCTAAT TC
                                  _        A
GAM693  HSPC043  3'  ATGCCTGTAATCCCAGCACT   67719     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  HSPC043  3'  CTGTAATCCCAGCTACT     67720
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  ICAM4    3'  CTGTAATCCCAGCACT      42353     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  ICAM4    3'  CTGTAATCCCAGCACT      7749      A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  IL10RB   3'  ATGCCTATAATCCCAGCTACT  5275            C  A
                                AGTAGCTGGGATTA AG CAT
                                |||||||||||| || |||
                                TCATCGACCCTAAT TC GTA
                                          A  C
GAM693  IMAGE:4907098 3'  CTGTAATCCCAGCACT      91658     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  INE1     3' CTGTAATCCCAGCTCTTTGT  13374     T_
                                ACAG  AGCTGGGATTACAG
                                ||||  ||||||||||||||
                                TGTT  TCGACCCTAATGTC
                                  TC
GAM693  ING1-like 3' CTGTAATCCCAGCACT     54155     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  JAM1     3' ATGCCTGTAATCCCAGCTGCT  33749              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCGTCGACCCTAATGTC GTA
                                      C
GAM693  JAM1     3' CTATAATCCCAGAGGCTG    33756     AG       C
                                CAGT  CTGGGATTA AG
                                ||||  ||||||||| ||
                                GTCG  GACCCTAAT TC
                                  GA        A
GAM693  JAM1     3' ATGCCTGTAATCCCAGCTGCT  57887              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCGTCGACCCTAATGTC GTA
                                      C
GAM693  JAM1     3' CTATAATCCCAGAGGCTG    57894     AG       C
                                CAGT  CTGGGATTA AG
                                ||||  ||||||||| ||
                                GTCG  GACCCTAAT TC
                                  GA        A
GAM693  JAM1     3' ATGCCTGTAATCCCAGCTGCT  57915              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCGTCGACCCTAATGTC GTA
                                      C
GAM693  JAM1     3' CTATAATCCCAGAGGCTG    57923     AG       C
                                CAGT  CTGGGATTA AG
                                ||||  ||||||||| ||
                                GTCG  GACCCTAAT TC
                                  GA        A
GAM693  JAM1     3' ATGCCTGTAATCCCAGCTGCT  57942              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCGTCGACCCTAATGTC GTA
                                      C
GAM693  JAM1     3' CTATAATCCCAGAGGCTG    57949     AG       C
                                CAGT  CTGGGATTA AG
                                ||||  ||||||||| ||
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                                GTCG  GACCCTAAT TC
                                  GA        A
GAM693  KALI     3' CTGTAATCCCAGTACT      53592      G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                  _
GAM693  KATII    3' CTATAATCCCAGCACT      32646     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM693  KBRAS2   3' ATGCCTGTAATCCCAGCTAC  34192              A
                                GTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                CATCGACCCTAATGTC GTA
                                          C
GAM693  KIAA0042 3' CTGTAATCCCAGCACT      29610     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA0090 3' ATGCCTGTAATCCCAGC     88438           A
                                GCTGGGATTACAG CAT
                                |||||||||||| |||
                                CGACCCTAATGTC GTA
                                          C
GAM693  KIAA0159 3' CTGTAATCCCAGCACT      29507     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA0159 3' TGTAATCCCAGCTACTCA    29511    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  KIAA0184 3' CTGTAATCCCAGCACT      65194     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA0226 3' CTGTAATCCCAGCACT      63514     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA0226 3' CTGTAATCCCAGCTACTTG   63515    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
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```
                                GT CATCGACCCTAATGTC
                                 T
GAM693  KIAA0252 3' CTGTAATCCCAGCACT      62791     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA0266 3' CTGTAATCCCAGCACT      41331     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA0266 3' CTGTAATCCCAGCACT      41332     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA0268 3' CTGTGTTTTAGCTAATGTA    70002      G        T
                                TACA TAGCTGGGAT ACAG
                                |||| |||||||||| ||||
                                ATGT ATCGATTTTG TGTC
                                   A       _
GAM693  KIAA0355 3' CTGTAATCCCAGCACT      28025     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA0391 3' ATGCCTGTGGTCCCAGCTACTC 27904    C             A
           A                     A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACCCTGGTGTC GTA
                                 C              C
GAM693  KIAA0420 3' ATGCCTATAATCCCAACACT   63352     AGC       C  A
                                AGT   TGGGATTA AG CAT
                                |||   |||||||| || |||
                                TCA   ACCCTAAT TC GTA
                                  CA_       A  C
GAM693  KIAA0441 3' ATGCCTGTAATCCCAGCACT   28952     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693  KIAA0445 5' CTGTAATCCCAGCACT      27953     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA0471 3' TCTGTAATCCCAGCACT     29400     A
                                AGT GCTGGGATTACAGA
                                ||| |||||||||||||
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                                TCA CGACCCTAATGTCT

                                  _
GAM693  KIAA0472 3' ATGCCTGTAATCCAAGATACTC 71859   C   G G       A
              A                  A AGTA CT GGATTACAG CAT
                                 | |||| || |||||||||| |||
                                 A TCAT GA CCTAATGTC GTA
                                  C   A A       C
GAM693  KIAA0514 3' ATGCCTGTAATCCCAGCACT  28077    A          A
                                 AGT GCTGGGATTACAG CAT
                                 ||| |||||||||||| |||
                                 TCA CGACCCTAATGTC GTA
                                   _         C
GAM693  KIAA0547 3' TGTAATCCCAGCTACTCA    28918   C
                                 A AGTAGCTGGGATTACA
                                 | ||||||||||||||||
                                 A TCATCGACCCTAATGT
                                  C
GAM693  KIAA0563 3' CTGTAATCCCAGCACT      29187    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC

                                  _
GAM693  KIAA0565 3' TCTGTAATTGCTATTG      66900       TGG
                                 CAGTAGC   GATTACAGA
                                 |||||||   |||||||||
                                 GTTATCG   TTAATGTCT

                                   ___
GAM693  KIAA0618 3' ATGCCTGTAATCCCAGC     29161           A
                                 GCTGGGATTACAG CAT
                                 |||||||||||| |||
                                 CGACCCTAATGTC GTA
                                         C
GAM693  KIAA0635 3' CTGTAATCCCAGCACT      27696    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC

                                  _
GAM693  KIAA0694 3' ATGCCTATAATCCCAATACTTT 72579   C   GC      C A
              A                   TA AGTA  TGGGATTA AG CAT
                                 || ||||  |||||||| || |||
                                 AT TCAT  ACCCTAAT TC GTA
                                  T   A_       A  C
GAM693  KIAA0694 3' CTGTAATCCCAGCACT      72580    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC

                                  _
GAM693  KIAA0752 3' ATGCCTGCAATCCCAGCTACT 67048           A  A
                                 AGTAGCTGGGATT CAG CAT
                                 |||||||||||| ||| |||
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                                TCATCGACCCTAA GTC GTA
                                      C   C
GAM693  KIAA0794 3' ATGCCTGTAATCCCAACACT  80409    AGC        A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_         C
GAM693  KIAA0794 3' CTGTAATCCCAGCTACTCA   80411   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM693  KIAA0795 3' CTATAATCCCAGCACT     46590    A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM693  KIAA0825 3' CTGTAATCCCAGCACT     61025    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA0825 3' GTGCCTGCAATCCCAGCTACTC 61027   C          A  A
          A                      A AGTAGCTGGGATT CAG CAT
                                | |||||||||||| ||| |||
                                A TCATCGACCCTAA GTC GTG
                                 C           C   C
GAM693  KIAA0831 3' CTGTAATCCCAGCTACT    29972
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  KIAA0831 3' CTGTAATCCCGGCACT     29973    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGGCCCTAATGTC
                                  _
GAM693  KIAA0852 5' CTGTAATCCCAGCACT     30077    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA0853 3' ATGTCTGTAGTCACAGCTACTC 30537   C      G
          A                      A AGTAGCTG GATTACAGACAT
                                | |||||||| ||||||||||||
                                A TCATCGAC CTGATGTCTGTA
                                 C       A
GAM693  KIAA0872 3' ATGCCTGTAATCCCAGCACT  30061    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  KIAA0872 3' CTGTAATCCCAGCACT     30062     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM693  KIAA0889 3' ATGCCTGTAATCCCAGCACT  31129     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  KIAA0907 3' CTGTAATCCCAGCACT     30173     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM693  KIAA0907 3' CTGTAATCCCAGCACT     30174     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM693  KIAA0912 3' CTGTAATCCCAGCACT     64409     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM693  KIAA0918 3' TCTGTAAGATGGGGCTACTGT  73136         GGGA_
                                ACAGTAGCT    TTACAGA
                                |||||||||    |||||||
                                TGTCATCGG    AATGTCT
                                     GGTAG
GAM693  KIAA0930 3' CTGTAATCCCAGCACT     70542     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM693  KIAA1032 3' ATGCCTGTAGTCCCAGCTACTC 66151   C              A
          A                      A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGACCCTGATGTC GTA
                                 C             C
GAM693  KIAA1056 3' CTGTAATCCCAGCACT     29695     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM693  KIAA1056 3' CTGTAATCCCAGCTGCT    29696
                                AGTAGCTGGGATTACAG
                                |||||||||||||||||
```

```
                                TCGTCGACCCTAATGTC

GAM693  KIAA1086 3' CTATAATCCCAGCACT     70744    A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _       A
GAM693  KIAA1086 3' CTGTAATCCCAGCACT     70745    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA1130 3' ATGCCTGTAATCCCAGCACT 62412    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _         C
GAM693  KIAA1130 3' ATGCCTGTAATCCCAGTGCT 62413    G         A
                                AGTA CTGGGATTACAG CAT
                                |||| |||||||||||| |||
                                TCGT GACCCTAATGTC GTA
                                  _         C
GAM693  KIAA1130 3' TGTAATCCCAGCTACTCA   62428   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  KIAA1164 3' ATGCCTGTAATCCCAGTACT 69503    G         A
                                AGTA CTGGGATTACAG CAT
                                |||| |||||||||||| |||
                                TCAT GACCCTAATGTC GTA
                                  _         C
GAM693  KIAA1191 3' CTGTAATCCCAGCACT     39954    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA1204 3' TCTGTAATCCCAACACT    69220    AGC
                                AGT   TGGGATTACAGA
                                |||   ||||||||||||
                                TCA   ACCCTAATGTCT
                                  CA_
GAM693  KIAA1228 3' CTGTAATCCCAGCACT     65041    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA1244 3' CTGTAATCCCAGCACT     71989    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
```

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                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA1244 3' CTGTAATCCCAGCTACTTA   71990   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 T
GAM693  KIAA1253 3' ATGCCTGTGGTCCCAGCTACTG 91896              A
                                CAGTAGCTGGGATTACAG CAT
                                |||||||||||||||||| |||
                                GTCATCGACCCTGGTGTC GTA
                                           C
GAM693  KIAA1271 3' CTGTAATCCCAGCACT     69542    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA1271 3' GTCTGTAATCCCAGCTATT   69551
                                AGTAGCTGGGATTACAGAC
                                ||||||||||||||||||
                                TTATCGACCCTAATGTCTG

GAM693  KIAA1276 3' CTGTAATCCCATCACT     66430    AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CT_
GAM693  KIAA1277 3' ATGCCTATAATCCCAGCACT  64450    A       C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _       A  C
GAM693  KIAA1328 3' CTGTAATCCCAGGCTTTG    61646    T  _
                                CAG AGC TGGGATTACAG
                                ||| ||| ||||||||||
                                GTT TCG ACCCTAATGTC
                                  _  G
GAM693  KIAA1348 3' ATGCCTGTAATCCCAGCTACT 68571             A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM693  KIAA1348 3' CTGTAATCCCAGCACTGTG   68575      A
                                TACAGT GCTGGGATTACAG
                                |||||| ||||||||||||
                                GTGTCA CGACCCTAATGTC
                                  _
GAM693  KIAA1364 3' ATGCCTGTAATCCCAGCACT  63586    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  KIAA1364 3' CTGTAATCCCAGCTACTTG   63593    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                 T
GAM693  KIAA1377 3' ATGCCTGTAATCCCAGCACT  67174    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  KIAA1404 3' CTGTAATCCCAGCACT      61987    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA1423 3' TAGTCCCAGCTACTCA      61728   C
                                A AGTAGCTGGGATTA
                                | ||||||||||||||
                                A TCATCGACCCTGAT
                                 C
GAM693  KIAA1456 3' ATGCCTGTAATCCCAGCACT  66988    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  KIAA1456 3' ATGCCTGTAATCCCAGCCACTT 66989   _ A          A
          G                      CA GT GCTGGGATTACAG CAT
                                || || |||||||||||||| |||
                                GT CA CGACCCTAATGTC GTA
                                 T C          C
GAM693  KIAA1473 3' ATGCCTGTAATCCCAGCTACT  70663              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM693  KIAA1473 3' CTGTAATCCCAGCACT      70667    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA1486 3' CTGTAATCCCAGCACTCTG   67379    TA_
                                CAG  GCTGGGATTACAG
                                |||  ||||||||||||
                                GTC  CGACCCTAATGTC
                                  TCA
GAM693  KIAA1554 3' CTGTAATCCCAGCTACCTG   95152    _
                                CAG TAGCTGGGATTACAG
                                ||| ||||||||||||||
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                                GTC ATCGACCCTAATGTC
                                  C
GAM693  KIAA1559 3' ATGCCTGTAATCCCAGCACT  73057    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _         C
GAM693  KIAA1559 3' ATGCCTGTAATCCCAGCTACTT 73058   _          A
                  G              CA GTAGCTGGGATTACAG CAT
                                || |||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 T           C
GAM693  KIAA1559 3' CTGTAATCCCAGCACT     73064    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA1586 5' CTGTAATCCCAGCACT     92329    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA1614 3' ATGCCTATAATCCCAGCTACTT 70117   _         C  A
                  G              CA GTAGCTGGGATTA AG CAT
                                || |||||||||||| || |||
                                GT CATCGACCCTAAT TC GTA
                                 T          A  C
GAM693  KIAA1614 3' ATGCCTGTAATCCCAGAACT  70118    AG        A
                                AGT  CTGGGATTACAG CAT
                                |||  |||||||||||| |||
                                TCA  GACCCTAATGTC GTA
                                  A_         C
GAM693  KIAA1630 3' ATGCCTGTAATCCCAGCACT  38030    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| ||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _         C
GAM693  KIAA1656 5' CTGTAATCCCAGCACT     65794    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA1674 3' CTGTAATCCCAGCACT     68777    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA1715 3' ATGCCTGTAATCCTAGCTACTC 68117   C          A
                  A              A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
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                                A TCATCGATCCTAATGTC GTA
                                 C             C
GAM693  KIAA1735 3' CTGTAGTCCCAGCTACTCA   87627   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTGATGTC
                                 C
GAM693  KIAA1751 3' ATGCCTGTAATCCCAGAACT  71688    AG         A
                                AGT  CTGGGATTACAG CAT
                                |||  |||||||||||| |||
                                TCA  GACCCTAATGTC GTA
                                  A_          C
GAM693  KIAA1811 5' CTGTAATCCCAGCACT     64796    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA1829 3' TGTAATCCCAGCTACTCA   61958   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  KIAA1872 3' ATGCCTGTAATCCCAGCACTCT 62923    TA_          A
           G                     CAG   GCTGGGATTACAG CAT
                                |||   |||||||||||| |||
                                GTC   CGACCCTAATGTC GTA
                                  TCA           C
GAM693  KIAA1872 3' ATGCCTGTAATCCCAGCTACT  62924              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM693  KIAA1872 3' CTATAATCCCAGCACT     62929    A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _         A
GAM693  KIAA1872 3' CTGTAATCCCAGACTTTG   62931    T  _
                                CAG AG CTGGGATTACAG
                                ||| || ||||||||||||
                                GTT TC GACCCTAATGTC
                                  _ A
GAM693  KIAA1941 3' CTGTAATCCCAGCACT     74838    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA1948 5' ATGCCTATAATCCCAGCTACT 82399            C  A
                                AGTAGCTGGGATTA AG CAT
                                |||||||||||||| || |||
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                                TCATCGACCCTAAT TC GTA
                                       A  C
GAM693  KIAA1951  3'  CTGTAATCCCAGCACT      73761     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA1954  3'  CTGTAATCCCAGCACT      77719     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA1958  3'  CTATAATCCCAGCACT      81902     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM693  KIAA1979  3'  CTGTAATCCCAGCACT      88278     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  KIAA1979  3'  CTGTAATCCCAGCTACTCA   88279   C
                                A AGTAGCTGGGATTACAG
                                | |||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM693  KLHL6     3'  CTGTAATCCCAGCCCTATG   55303   GTA_
                                CA   GCTGGGATTACAG
                                ||   ||||||||||||
                                GT   CGACCCTAATGTC
                                  ATCC
GAM693  KLHL8     3'  CTGTAATTCCAGCTACTCA   62854   C
                                A AGTAGCTGGGATTACAG
                                | |||||||||||||||||
                                A TCATCGACCTTAATGTC
                                 C
GAM693  KR18      3'  CTGTAATCCCAGTACT      52745     G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                  _
GAM693  KREMEN    3'  ATGCCTGTAATCCCAGCACT  49404     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  KREMEN    3'  CTGTAATCCCAGCTACT     49406
                                AGTAGCTGGGATTACAG
                                |||||||||||||||||
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                                TCATCGACCCTAATGTC

GAM693  LHPP    5'  CTGTAATCCCAGCACT     42101     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LIAS    3'  CTGTAATCCCAGCACTTTA   70635    C   A
                                TA AGT GCTGGGATTACAG
                                || ||| ||||||||||||||
                                AT TCA CGACCCTAATGTC
                                 T   _
GAM693  LIM     3'  CTGTAATCCCAGCACT      21302     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LIM     3'  CTGTAATCCCAGCTACTCA   21303    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM693  LRG     3'  CTGTAATCCCAGCACT      53750     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LRRFIP1  3'  TGCCTGTAATCTCAGTAC    16420     G         A
                                GTA CTGGGATTACAG CA
                                ||| |||||||||||| ||
                                CAT GACTCTAATGTC GT
                                  _          C
GAM693  LRRFIP1  3'  TGTAATCCCAGCCACT      16421     A
                                AGT GCTGGGATTACA
                                ||| ||||||||||||
                                TCA CGACCCTAATGT
                                  C
GAM693  LSR68    3'  TGCCTATAATCCCAGCTACTCA 37937   C           C  A
                                A AGTAGCTGGGATTA AG CA
                                | ||||||||||||| || ||
                                A TCATCGACCCTAAT TC GT
                                 C            A  C
GAM693  LYSAL1   3'  CTGTAATCCCAGCACT      16918     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  MACF1    3'  CTGTAATCCCAGCACT      52316     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
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```
                                TCA CGACCCTAATGTC
                                  _
GAM693  MAWBP    3' ATGCCTGTAATCCCAGCACT  42106    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  MCAM     3' CTGTAATCCCAGCACT     21454    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  MESDC2   3' CTGTAATCCCAGTACT     72492    G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                  _
GAM693  MESDC2   3' TGTAATCCCAGCTACTCA   72503   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  METL     3' ATGCCTGTAATCCCAGCCACT 37253    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  C          C
GAM693  MGC10765 3' ATGCCTGTAATCCCAGCACT  44299    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  MGC10765 3' CTGTAATCCCAGCTAC     44301
                                GTAGCTGGGATTACAG
                                ||||||||||||||||
                                CATCGACCCTAATGTC

GAM693  MGC10771 3' ATGCCTGTAATCCCAGCACT  44451    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  MGC10814 5' ATGCCTGTAATCCCAGCACT  51036    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  MGC10814 3' CTGTAATCCCAGCACT     51038    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  MGC10999 3' ATGCCTGTAATCCCAGCACTGT 50225       A          A
          G                  TACAGT GCTGGGATTACAG CAT
                             |||||| |||||||||||| |||
                             GTGTCA CGACCCTAATGTC GTA
                               _          C
GAM693  MGC11287 5' GTCTATAATCCCAGCACTGTG  48834       A        C
                             TACAGT GCTGGGATTA AGAC
                             |||||| |||||||||| ||||
                             GTGTCA CGACCCTAAT TCTG
                               _        A
GAM693  MGC11386 3' CTATAATCCCAGCACT      51950     A        C
                             AGT GCTGGGATTA AG
                             ||| |||||||||| ||
                             TCA CGACCCTAAT TC
                               _        A
GAM693  MGC13017 3' TCTGTAATCCCAGCTACT    54694
                             AGTAGCTGGGATTACAGA
                             ||||||||||||||||||
                             TCATCGACCCTAATGTCT

GAM693  MGC13053 3' CTGTAATCCCAGTACT      51131      G
                             AGTA CTGGGATTACAG
                             |||| ||||||||||||
                             TCAT GACCCTAATGTC
                               _
GAM693  MGC13523 3' TGCCTGTAATTTCACTA     53031     C  GG      A
                             TAG TG  ATTACAG CA
                             ||| ||  ||||||| ||
                             ATC AC  TAATGTC GT
                               _ TT      C
GAM693  MGC14126 3' CTGTAATCCCAGCACT      51854     A
                             AGT GCTGGGATTACAG
                             ||| ||||||||||||
                             TCA CGACCCTAATGTC
                               _
GAM693  MGC14817 3' CTGTAATCCCAGCACT      50336     A
                             AGT GCTGGGATTACAG
                             ||| ||||||||||||
                             TCA CGACCCTAATGTC
                               _
GAM693  MGC15397 3' CTGTAATCCCAGCACT      54679     A
                             AGT GCTGGGATTACAG
                             ||| ||||||||||||
                             TCA CGACCCTAATGTC
                               _
GAM693  MGC15631 3' ATGCCTGTAATCCCAGTGCT  51259      G          A
                             AGTA CTGGGATTACAG CAT
                             |||| |||||||||||| |||
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                                TCGT GACCCTAATGTC GTA
                                  _          C
GAM693  MGC15631 3' CTGTCATCCCAGCTAC      51263          T
                                GTAGCTGGGAT ACAG
                                |||||||||| ||||
                                CATCGACCCTA TGTC
                                       C
GAM693  MGC16142 3' ATGCCTATAATCCCAGCACT   51291     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM693  MGC16142 3' ATGCCTATAATCCCAGCTACT  51292           C  A
                                AGTAGCTGGGATTA AG CAT
                                |||||||||||||| || |||
                                TCATCGACCCTAAT TC GTA
                                         A  C
GAM693  MGC16332 3' ATGCCTGTAATCCCAACACT   56774     AGC        A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_         C
GAM693  MGC16385 3' CTGTAATCCCAGCACT       58887     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  MGC16703 3' ATGCCTGTAATCCCAGCACT   73098     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  MGC20235 3' CTGTAATCCCAGTACT       58894      G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                  _
GAM693  MGC20235 3' CTGTAGTCCCAGCTACTCA    58895    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTGATGTC
                                 C
GAM693  MGC22805 3' ATGCCTGTAATCCCAGCTACTT 58080    _            A
           G                     CA GTAGCTGGGATTACAG CAT
                                || ||||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 T             C
GAM693  MGC2396  3' ATGCCTGTAATCCCAGCTACT  53460              A
                                AGTAGCTGGGATTACAG CAT
                                ||||||||||||||| |||
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                                TCATCGACCCTAATGTC GTA
                                          C
GAM693  MGC2562  3' CTATAATCCCAGCACT     50437    A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM693  MGC2562  3' CTGTAATCCCAGCACT     50438    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  MGC26641 3' CTGTAATCCCAACTACTCA  58657  C   C
                                A AGTAG TGGGATTACAG
                                | ||||| ||||||||||
                                A TCATC ACCCTAATGTC
                                 C    A
GAM693  MGC2731  3' ATGCCTGTAATCCCAGCTACT 43948            A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                          C
GAM693  MGC29762 3' CTGTAATCCCAGCACT     58472    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  MGC29891 3' CTGTAATCCCAACACT     58204    AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693  MGC29891 3' CTGTAATCCCAGCACT     58205    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  MGC29937 3' ATGCCTGTAATCCCAGCACT 58110    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  MGC29937 3' ATGCCTGTAATCCCAGTTACTC 58111  C           A
          A                      A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATTGACCCTAATGTC GTA
                                 C             C
GAM693  MGC3207  3' CTGTAATCCCAGCACT     62558    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  MGC39350 3' CTGTAATCCCCAGCACT    58654    A    _
                                AGT GCTGGG ATTACAG
                                ||| |||||| |||||||
                                TCA CGACCC TAATGTC
                                  _    C
GAM693  MGC4248  3' CTGTAATCCCAGCACT     50327    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  MGC4663  3' CTATAATCCCAGCACTTTA   44505   C  A       C
                                TA AGT GCTGGGATTA AG
                                || ||| |||||||||| ||
                                AT TCA CGACCCTAAT TC
                                 T  _       A
GAM693  MGC5254  3' CTGTAATCCCAGCACT     50410    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  MGC5384  3' ATGCCTGTAATCCCAGCACT  48269    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _         C
GAM693  MKRN4    3' CTGTAATCCCAGCACT     47746    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  MOST2    5' ATGCCTGTAGTCCCAGCTACTC 39674   C            A
           A                     A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACCCTGATGTC GTA
                                 C             C
GAM693  MOST2    5' CTGTAATCCCAGCACT     39684    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  MRP63    3' CTGTAATCCCAACACTTTA   43807   C  AGC
                                TA AGT   TGGGATTACAG
                                || |||   ||||||||||
                                AT TCA   ACCCTAATGTC
                                 T  CA_
GAM693  MRPL56   3' CTGTAATCCCAACACT     51688    AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
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                                TCA   ACCCTAATGTC
                                  CA_
GAM693  MRPS10   3'  CTGTAATCCCAGCACT      36292     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  MRPS10   3'  GTGCCTGTAATCCCAGCTACTC 36298   C             A
           A                     A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACCCTAATGTC GTG
                                 C             C
GAM693  MT-ACT48 3'  ATGCCTGTAATCCCAGCACT   24686     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  N4BP2    3'  CTGTAATCCCAGCACT      36403     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  NDUFC2   3'  ATGCCTGTAATCCCAGCACT   15825     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  NDUFC2   3'  CTGCAATCCCAGCTACTCA    15832   C          A
                                A AGTAGCTGGGATT CAG
                                | |||||||||||| |||
                                A TCATCGACCCTAA GTC
                                 C          C
GAM693  NMNAT    3'  CTGTAATCCCAGCACT      42956     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  NMT2     3'  CTGTAATCCCAGCACT      16664     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  NPTXR    3'  CTGTAATCCCAGCACT      54178     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  NPTXR    3'  CTGTAATCCCAGCACT      26642     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  OCLM     5'  ATGCCTATAATCCCAGCACT  42347     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM693  ORC6L    3'  ATGCCTGTAATCCCAGCTCCT  26722    T          A
                                AG AGCTGGGATTACAG CAT
                                || |||||||||||||| |||
                                TC TCGACCCTAATGTC GTA
                                 C           C
GAM693  ORC6L    3'  CTGTAATCCCAGCACT      26724     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  PAFAH2   3'  ATGCCTGTAATCCCAGCACT  4760      A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  PAFAH2   3'  CTATAATCCCAGCTACTCA   4762     C          C
                                A AGTAGCTGGGATTA AG
                                | |||||||||||||| ||
                                A TCATCGACCCTAAT TC
                                 C           A
GAM693  PB1      3'  CTGTAATCCCAGCACT      37021     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  PDCD7    3'  CTGTAATCCCAACACT      72138     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693  phorbolin-1 3'  CTGTAATCCCAGCACT      88778     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  PILR(ALPHA) 3'  CTGTAATCCCAGCTACT     25546
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  PIWIL2   3'  CTGTAGTCCCAGCTACTCA   36055    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
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                                A TCATCGACCCTGATGTC
                                 C
GAM693  PNPASE    3'  ATGCCTGTAATCCTAGCTACTC 70870    C             A
                A                A AGTAGCTGGGATTACAG CAT
                                 | |||||||||||||||| |||
                                 A TCATCGATCCTAATGTC GTA
                                 C             C
GAM693  POFUT1    3'  ATGCCTGTAATCCCAGCACT   70465     A          A
                                 AGT GCTGGGATTACAG CAT
                                 ||| |||||||||||| |||
                                 TCA CGACCCTAATGTC GTA
                                   _           C
GAM693  POLYDOM   3'  ATGCCTGTAATTCCAGCTACTC 44424    C             A
                A                A AGTAGCTGGGATTACAG CAT
                                 | |||||||||||||||| |||
                                 A TCATCGACCTTAATGTC GTA
                                 C             C
GAM693  POLYDOM   3'  CTGTAATCCCAGCACT      44425     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                   _
GAM693  PPP1R3B   3'  ATGCCTGTAATCCCAGCACT   44815     A          A
                                 AGT GCTGGGATTACAG CAT
                                 ||| |||||||||||| |||
                                 TCA CGACCCTAATGTC GTA
                                   _           C
GAM693  PPP1R3B   3'  TGCCTGTAATCCCTGCACT    44826     A  T       A
                                 AGT GC GGGATTACAG CA
                                 ||| || |||||||||| ||
                                 TCA CG CCCTAATGTC GT
                                   _ T         C
GAM693  PRDM14    3'  ATGCCTGTGGTTCCAGCCACTC 44444    C  A          A
                A                A AGT GCTGGGATTACAG CAT
                                 | ||| |||||||||||| |||
                                 A TCA CGACCTTGGTGTC GTA
                                 C  C           C
GAM693  PRDM14    3'  CTGTAATCCCAGCACT      44447     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                   _
GAM693  PRO0038   3'  ATGCCTATAATCCCAACACCCT 26090     TAGC_      C  A
                G                 CAG     TGGGATTA AG CAT
                                 |||     |||||||| || |||
                                 GTC     ACCCTAAT TC GTA
                                   CCACA       A  C
GAM693  PRO0255   3'  CTGTAATCTCAGCACT      26141     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
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                                TCA CGACTCTAATGTC
                                  _
GAM693  PRO0478  3' ATGCCTGTAATCCCAGCACT  26183    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  PRO0478  5' CTGTAATCCCAGCACT     26187    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  PRO0478  3' CTGTAATCCCAGCCTG     26188    TA
                                CAG  GCTGGGATTACAG
                                |||  ||||||||||||
                                GTC  CGACCCTAATGTC
                                  __
GAM693  PRO0478  5' CTGTAATCCCAGGTACT    26189     G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                   G
GAM693  PRO0478  3' TGTAATCCCAGCTACTCA   26198   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  PRO0611  3' ATGCCTGTAATCCCAGCACT  26007    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  PRO0618  3' CTGTAATCCCAGCACTTTA   26200   C  A
                                TA AGT GCTGGGATTACAG
                                || ||| ||||||||||||
                                AT TCA CGACCCTAATGTC
                                 T  _
GAM693  PRO1048  5' TCTGTAATCCCAGCACT     37525    A
                                AGT GCTGGGATTACAGA
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCT
                                  _
GAM693  PRO1496  3' ATGCCTGTAATCCCAGCACT  37757    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  PRO1580  5' ATGCCTTGTCCCAGCTTCT   37530   T      TAC  A
                                AG AGCTGGGAT   AG CAT
                                || |||||||||   || |||
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                                TC TCGACCCTG   TC GTA
                                 T       T__  C
GAM693  PRO1777  3' ATGCCTGTAATCCCAGCATTCT 37762     TA_          A
          G                       CAG   GCTGGGATTACAG CAT
                                  |||   |||||||||||||| |||
                                  GTC   CGACCCTAATGTC GTA
                                    TTA           C
GAM693  PRO1853  3' ATGCCTGTAATCCCAGCACT   37771     A          A
                                  AGT GCTGGGATTACAG CAT
                                  ||| |||||||||||| |||
                                  TCA CGACCCTAATGTC GTA
                                    _           C
GAM693  PRO2015  3' CTGTAATCCCAGCACT      37557     A
                                  AGT GCTGGGATTACAG
                                  ||| ||||||||||||
                                  TCA CGACCCTAATGTC
                                    _
GAM693  PRO2198  5' CTGTAATCCCGGCACT      37791     A
                                  AGT GCTGGGATTACAG
                                  ||| ||||||||||||
                                  TCA CGGCCCTAATGTC
                                    _
GAM693  PRO2730  3' CTGTAATCCCAGCACT      47415     A
                                  AGT GCTGGGATTACAG
                                  ||| ||||||||||||
                                  TCA CGACCCTAATGTC
                                    _
GAM693  PRO2859  3' ATGCCTGTAATCCCAGCACT   37614     A          A
                                  AGT GCTGGGATTACAG CAT
                                  ||| |||||||||||| |||
                                  TCA CGACCCTAATGTC GTA
                                    _           C
GAM693  PRO2949  3' ATGCCTGTAATCCCAGCACT   37619     A          A
                                  AGT GCTGGGATTACAG CAT
                                  ||| |||||||||||| |||
                                  TCA CGACCCTAATGTC GTA
                                    _           C
GAM693  PSR      3' CTGTAATCCCAGCACT       65180     A
                                  AGT GCTGGGATTACAG
                                  ||| ||||||||||||
                                  TCA CGACCCTAATGTC
                                    _
GAM693  PTD012   3' ATGCCTATAATCCCAGCACT   25890     A        C  A
                                  AGT GCTGGGATTA AG CAT
                                  ||| |||||||||| || |||
                                  TCA CGACCCTAAT TC GTA
                                    _         A  C
GAM693  PTK6     3' ATGCCTGTAATCCCAGCACT   19934     A          A
                                  AGT GCTGGGATTACAG CAT
                                  ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  PTRF    3'  ATGCCTGTAATCCCAGCTACT  63497            A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM693  RAB4B   5'  ATGCCTGTAATCCCAGCACT  32372    A        A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  RAB4B   5'  ATGCCTGTAATCCCAGCTACT  32373            A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM693  RHOBTB3 3'  CTGTAATCCCAGCTACT    29744
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  RNO2    5'  CTGTAATCCCAGCACT     52769    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  RoXaN   3'  ATGCCTGTAATCCCAGC    46632          A
                                GCTGGGATTACAG CAT
                                |||||||||||| |||
                                CGACCCTAATGTC GTA
                                        C
GAM693  RoXaN   3'  CTATAATCCCAGCACTCTG   46641    TA_       C
                                CAG   GCTGGGATTA AG
                                |||   |||||||||| ||
                                GTC   CGACCCTAAT TC
                                  TCA        A
GAM693  RoXaN   3'  TCTGTAATCCCAGCTACTCA  46659   C
                                A AGTAGCTGGGATTACAGA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTCT
                                 C
GAM693  Rpo1-2  3'  ATGCCTGTAGTTCCAGCTACTC 38697   C            A
          A                      A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||| |||
                                A TCATCGACCTTGATGTC GTA
                                 C            C
GAM693  RRP4    3'  CTATAATCCCAGCACT    26563    A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
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                                TCA CGACCCTAAT TC
                                  _        A
GAM693  SAMHD1   3' ATGCCTGTAATCCCAGCACT  61308    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  SC65     3' CTGTAATCCCAGCACTG    21288     A
                                CAGT GCTGGGATTACAG
                                |||| ||||||||||||
                                GTCA CGACCCTAATGTC

                                  _
GAM693  SCIN     3' CTGTAATCCCAGCACT     52424     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM693  SCYA5    3' CTGTAATCCCAGCTACT    11450
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  SEMA3E   3' CTGTAATCCCAGCACT     24881     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM693  SEMA5A   3' ATGCCTATAATCCCAGCACT  14252    A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM693  SGKL     3' ATGCCTATAATCCCAGCTACTT 25140   _          C  A
           G                     CA GTAGCTGGGATTA AG CAT
                                || |||||||||||| || |||
                                GT CATCGACCCTAAT TC GTA
                                 T          A  C
GAM693  SGKL     3' ATGCCTTTAGTCCCAGCTACTC 25141   C          C  A
           A                     A AGTAGCTGGGATTA AG CAT
                                | ||||||||||||| || |||
                                A TCATCGACCCTGAT TC GTA
                                 C          T  C
GAM693  SGKL     3' CTGTAATCCCAGCACT     25142     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM693  SLC7A11  3' TCTGTAATCATATCTAC    26757     C  G
                                GTAG TG GATTACAGA
                                |||| || |||||||||
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                                CATC AT CTAATGTCT
                                  T  A
GAM693  SLC7A11  3'  TCTGTAATCCCAGCACT     26758     A
                                AGT GCTGGGATTACAGA
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCT
                                 _
GAM693  SMAP-5   3'  CTGTAATCCCAGCACT      47931     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693  SNAPC1   3'  ATGCCTGTAATCCCAGC     11838           A
                                GCTGGGATTACAG CAT
                                ||||||||||||| |||
                                CGACCCTAATGTC GTA
                                        C
GAM693  SPTLC2   3'  ATGCCTGTAATCCCAGCTAC  16797             A
                                GTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                CATCGACCCTAATGTC GTA
                                         C
GAM693  SS18L1   3'  CTGTAATCCCAGCACT      65344     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693  SS18L1   3'  CTGTAATCCCAGCTACT     65345
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  TA-LRRP  3'  ATGCCTATAATCCCAGCACT  31068     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                 _         A  C
GAM693  TACTILE  3'  CTGTAATCCCAGCACT      19469     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693  THEA     3'  CTGTAATCCCAGCACT      66282     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693  TIP47    3'  CTGTAATCCCAGCACT      19479     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  TMG4     3'  ATGCCTGTAATCCCAGCACT  43988     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693  TRIAD3   3'  ATGCCTATAATCCCAGGTACTC 94500   C   G       C  A
          A                      A AGTA CTGGGATTA AG CAT
                                | |||| ||||||||| || |||
                                A TCAT GACCCTAAT TC GTA
                                 C   G       A  C
GAM693  TRIM38   3'  CTGTAATCCCAGAACTATGT  20986    GTAG_
                                ACA    CTGGGATTACAG
                                |||    ||||||||||||
                                TGT    GACCCTAATGTC
                                  ATCAA
GAM693  UBF-fl   3'  CTGTAATCCCAGCACT     51564    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  VPS4B    3'  ATGCCTGTAATCCCAGCACT  16821    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693  VPS4B    3'  TGTAATCCCAGCTACTCA    16826   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  WBSCR21  3'  CTGTAATCCCAGCTACT     48476
                                AGTAGCTGGGATTACAG
                                |||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  WBSCR23  3'  CTGTAATCCCAGCACT      46759    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  WBSCR23  3'  CTGTAATCCCAGCTACT     46760
                                AGTAGCTGGGATTACAG
                                |||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  WBSCR23  3'  GTCTGTAGTCCCAGCTACTCA  46770   C
                                A AGTAGCTGGGATTACAGAC
                                | ||||||||||||||||||
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                                A TCATCGACCCTGATGTCTG
                                 C
GAM693  YEA      3'  ATGCCTGTAATCCCAGCTACTT 51528    _           A
              G                   CA GTAGCTGGGATTACAG CAT
                                  || |||||||||||||| |||
                                  GT CATCGACCCTAATGTC GTA
                                   T            C
GAM693  YME1L1   3'  CTGTAATCCCAGCACT     57778    A
                                  AGT GCTGGGATTACAG
                                  ||| ||||||||||||
                                  TCA CGACCCTAATGTC
                                   _
GAM693  YME1L1   3'  TCTGTAATCCCAGCACT    57781    A
                                  AGT GCTGGGATTACAGA
                                  ||| |||||||||||||
                                  TCA CGACCCTAATGTCT
                                   _
GAM693  YME1L1   3'  CTGTAATCCCAGCACT     26528    A
                                  AGT GCTGGGATTACAG
                                  ||| ||||||||||||
                                  TCA CGACCCTAATGTC
                                   _
GAM693  YME1L1   3'  TCTGTAATCCCAGCACT    26531    A
                                  AGT GCTGGGATTACAGA
                                  ||| |||||||||||||
                                  TCA CGACCCTAATGTCT
                                   _
GAM693  ZAK      3'  CTGTAATCCCAGCACT     56125    A
                                  AGT GCTGGGATTACAG
                                  ||| ||||||||||||
                                  TCA CGACCCTAATGTC
                                   _
GAM693  ZFP106   3'  CTGTAATCCCAGCACT     42466    A
                                  AGT GCTGGGATTACAG
                                  ||| ||||||||||||
                                  TCA CGACCCTAATGTC
                                   _
GAM693  ZFP106   3'  CTGTAATCCCAGCTCT     42467    T
                                  AG AGCTGGGATTACAG
                                  || |||||||||||||
                                  TC TCGACCCTAATGTC
                                   _
GAM693  ZIM3     3'  ATGCCTGTAATCCCAGTACT  53536     G          A
                                  AGTA CTGGGATTACAG CAT
                                  |||| |||||||||||| |||
                                  TCAT GACCCTAATGTC GTA
                                    _          C
GAM693  ZNF197   3'  ATGCCTGTAATCCCAGCACT  22763     A          A
                                  AGT GCTGGGATTACAG CAT
                                  ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  ZNF197   3' GTAATCCCAGCTACTCA     22766   C
                                A AGTAGCTGGGATTAC
                                | ||||||||||||||
                                A TCATCGACCCTAATG
                                 C
GAM693  ZNF271   3' CTGTAATCCCAACACT      95250     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693  ZNF297B  5' ATGCCTATAATCCCAACACTTT 25774    C   AGC       C  A
            A                    TA AGT   TGGGATTA AG CAT
                                || |||   |||||||| || |||
                                AT TCA   ACCCTAAT TC GTA
                                 T   CA_       A  C
GAM693  ZNF297B  5' CTGTAATCCCAGCACT      25781     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  ZNF297B  3' CTGTAATCCCAGCACT      25782     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  ZNF297B  3' CTGTAATCCCAGCTACT     25783
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  ZNF33A   3' ATGCCTGTAATCCCAGCACT  91344     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  ZNF347   3' ATGCCTGTAATCCCAACACT  50845     AGC        A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_         C
GAM693  LOC112687 3' CTATAATCCCAGCACT      72859     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM693  LOC113201 3' ATGCCTATAGTCCCAGCTACT 56549            C  A
                                AGTAGCTGGGATTA AG CAT
                                |||||||||||||| || |||
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                                TCATCGACCCTGAT TC GTA
                                       A  C
GAM693  LOC115129 5'  CTATAATCCCAGCACT      73229     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM693  LOC115129 5'  CTGTAATCCCAGCTACT     73231
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  LOC115129 5'  CTGTAATCCCAGGTACT     73232      G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                  G
GAM693  LOC115273 3'  ATGCCTGTAATCCCAGTTACT  73357              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATTGACCCTAATGTC GTA
                                       C
GAM693  LOC115761 3'  ATGCCTGTAATCCCAGCACTGT 91737       A          A
   G                             TACAGT GCTGGGATTACAG CAT
                                ||||||| |||||||||||| |||
                                GTGTCA CGACCCTAATGTC GTA
                                  _          C
GAM693  LOC116228 3'  CTGTAATCCCAGCACT      73798     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC116349 3'  CTGTAATCCCAGCACT      73830     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC119504 5'  ATGCCTGTAATCCCAGCTACT  73989              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                       C
GAM693  LOC119504 5'  CTGTAATCCCAGCACT      73990     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC122704 3'  CTGTAATCCCAGCACT      74139     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC122704 3'  TGTAATCCCAGCTACTCA    74145   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693   LOC122970 3'  CTGTAATCCCAGTACT      74178     G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                  _
GAM693   LOC126282 3'  CTGTAATCCCAGCACT      74472     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC126282 3'  CTGTAATCCCAGCACT      74473     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC127262 3'  ATGCCTGTAATCCCAGC     76107           A
                                GCTGGGATTACAG CAT
                                |||||||||||| |||
                                CGACCCTAATGTC GTA
                                       C
GAM693   LOC127428 3'  ATGCCTATAATCCCAGCGCT   74662     A       C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCG CGACCCTAAT TC GTA
                                  _       A  C
GAM693   LOC130162 3'  ATGTCTGTAATCCCAGCACT   74909     A
                                AGT GCTGGGATTACAGACAT
                                ||| ||||||||||||||||
                                TCA CGACCCTAATGTCTGTA
                                  _
GAM693   LOC130535 3'  ATGCCTGTAATCCCAGC     76147           A
                                GCTGGGATTACAG CAT
                                |||||||||||| |||
                                CGACCCTAATGTC GTA
                                       C
GAM693   LOC130535 3'  CTGTAGTCCCAGCTACTCA    76151   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTGATGTC
                                 C
GAM693   LOC130589 3'  CTGTAATCCCAGCACT      57132     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC130951 3'  CTGTAATCCCAACACTTTG   57143     TAGC_
                                CAG     TGGGATTACAG
                                |||     ||||||||||
                                GTT     ACCCTAATGTC
                                  TCACA
GAM693  LOC131744 3'  ATGCCTGTAATCCCAGCACTGT 75868        A           A
                   A                TACAGT GCTGGGATTACAG CAT
                                    |||||| |||||||||||| |||
                                    ATGTCA CGACCCTAATGTC GTA
                                       _           C
GAM693  LOC131965 3'  ATGCCTGTAATCCCAGCACT   75027     A           A
                                    AGT GCTGGGATTACAG CAT
                                    ||| |||||||||||| |||
                                    TCA CGACCCTAATGTC GTA
                                      _           C
GAM693  LOC131965 3'  TGTAATCCCAGCTACTCA     75034    C
                                    A AGTAGCTGGGATTACA
                                    | ||||||||||||||||
                                    A TCATCGACCCTAATGT
                                     C
GAM693  LOC132625 3'  ATGCCTGTAATCCCAACACTTT 75898      TAGC_         A
                   GT                 ACAG     TGGGATTACAG CAT
                                    ||||     |||||||||||| |||
                                    TGTT     ACCCTAATGTC GTA
                                      TCACA          C
GAM693  LOC132625 3'  CTGTGTTCCCAGCTACTCA    75906    C         T
                                    A AGTAGCTGGGA TACAG
                                    | |||||||||| |||||
                                    A TCATCGACCCT GTGTC
                                     C          T
GAM693  LOC133926 3'  ATGCCTGTAATCCCAGCGCT   75131     A           A
                                    AGT GCTGGGATTACAG CAT
                                    ||| |||||||||||| |||
                                    TCG CGACCCTAATGTC GTA
                                      _           C
GAM693  LOC134147 3'  CTGTAATCCCAGCACT       57161     A
                                    AGT GCTGGGATTACAG
                                    ||| ||||||||||||
                                    TCA CGACCCTAATGTC
                                      _
GAM693  LOC134147 3'  GTGCCTGTAATCCCAGCTACTC 57166    C             A
                   A                 A AGTAGCTGGGATTACAG CAT
                                    | |||||||||||||||| |||
                                    A TCATCGACCCTAATGTC GTG
                                     C              C
GAM693  LOC137362 3'  ATGCCTGTAATCCCAACACTTT 75263     TAGC_         A
                   G                  CAG     TGGGATTACAG CAT
                                    |||     |||||||||| |||
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                                GTT     ACCCTAATGTC GTA
                                  TCACA          C
GAM693   LOC138241 3'  CTGTAATCCCAACACT      75308     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693   LOC138428 3'  ATGCCTGTAATCCCTGCTACT  75331       T         A
                                AGTAGC GGGATTACAG CAT
                                |||||| |||||||||| |||
                                TCATCG CCCTAATGTC GTA
                                   T         C
GAM693   LOC138428 3'  CTATAATCCCAGCACT      75335     A         C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _         A
GAM693   LOC143310 3'  CTGTAATCCCAGCACT      76532     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC143888 3'  CTGTAATCCCAGCACT      76659     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC143943 3'  ATGCCTGTAATCCCAGCACT   82994     A           A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693   LOC144289 3'  CTGTAATCCCAGCTACT     83024
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693   LOC144289 3'  TCTGTAATCCCAGCACT     83029     A
                                AGT GCTGGGATTACAGA
                                ||| ||||||||||||
                                TCA CGACCCTAATGTCT
                                  _
GAM693   LOC144465 3'  ATGCCTGTAATCCCAAAACT   76852     AGC         A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  AA_         C
GAM693   LOC144465 3'  ATGCCTGTAATCCCAGCTACT  76853               A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
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                                TCATCGACCCTAATGTC GTA
                                          C
GAM693   LOC144465 3'  TGTAATCCCAGCTACTCA    76857    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693   LOC144481 3'  ATGCCTGTAATCCCAATACT   83093      GC          A
                                AGTA  TGGGATTACAG CAT
                                ||||  |||||||||| |||
                                TCAT  ACCCTAATGTC GTA
                                  A_          C
GAM693   LOC144481 3'  ATGCCTGTAATCCCAGCTACT  83094                 A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                          C
GAM693   LOC144486 3'  CTGTAATCCCAGCACGCTG    83083      A_
                                CAGT  GCTGGGATTACAG
                                ||||  ||||||||||||
                                GTCG  CGACCCTAATGTC
                                  CA
GAM693   LOC144524 3'  ATGCCTGTAGTCCCAGCTACTT 83121    C              A
           A                     A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACCCTGATGTC GTA
                                 T              C
GAM693   LOC144817 3'  CTGTAATCCCAGCACT      76967     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC145216 3'  CTGTAATCCCAGCACT      83265     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC145216 3'  CTGTAATCCCAGCTACTCA    83266    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM693   LOC145231 3'  ATGCCTATAATCCCAGCACT   83278     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _         A  C
GAM693   LOC145231 3'  ATGCCTGTAATCCCAGCACT   83279     A           A
                                AGT GCTGGGATTACAG CAT
                                ||| ||||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  LOC145231 3'  ATGCCTGTAATCCCAGCTACTT 83280    _           A
                G                  CA GTAGCTGGGATTACAG CAT
                                   || |||||||||||||| |||
                                   GT CATCGACCCTAATGTC GTA
                                    T            C
GAM693  LOC145299 3'  CTGTAATCCCAGCACT     83314     A
                                   AGT GCTGGGATTACAG
                                   ||| ||||||||||||
                                   TCA CGACCCTAATGTC
                                     _
GAM693  LOC145333 3'  CTGTAATCCCAGCACT     83326     A
                                   AGT GCTGGGATTACAG
                                   ||| ||||||||||||
                                   TCA CGACCCTAATGTC
                                     _
GAM693  LOC145387 3'  CTGTAATCCCAGCACT     83354     A
                                   AGT GCTGGGATTACAG
                                   ||| ||||||||||||
                                   TCA CGACCCTAATGTC
                                     _
GAM693  LOC145438 3'  ATGCCTGTAGCCCCAGCTACTC 83334   C        AT    A
                A                   A AGTAGCTGGG  TACAG CAT
                                   | |||||||||  ||||| |||
                                   A TCATCGACCC  ATGTC GTA
                                    C         CG    C
GAM693  LOC145438 3'  CTGTAATCCCAGCACT     83336     A
                                   AGT GCTGGGATTACAG
                                   ||| ||||||||||||
                                   TCA CGACCCTAATGTC
                                     _
GAM693  LOC145453 3'  CTGTAATCTGAGCAC      77140    A   G
                                   GT GCT GGATTACAG
                                   || ||| |||||||||
                                   CA CGA TCTAATGTC
                                    _   G
GAM693  LOC145482 3'  CTGTAATCCCAGCTACT    77229
                                   AGTAGCTGGGATTACAG
                                   ||||||||||||||||
                                   TCATCGACCCTAATGTC

GAM693  LOC145483 3'  CTGTAATCCCAACACT     77242     AGC
                                   AGT   TGGGATTACAG
                                   |||   ||||||||||
                                   TCA   ACCCTAATGTC
                                     CA_
GAM693  LOC145663 3'  CTGTAATCCCAGCAATTG   83413      A
                                   CAGT GCTGGGATTACAG
                                   |||| ||||||||||||
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                                GTTA CGACCCTAATGTC
                                  A
GAM693   LOC145757 3'  ATGCCTGTAATCCCAGCACT   77454     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693   LOC145757 3'  GTAGTCCCAGCTACTCA     77470    C
                                A AGTAGCTGGGATTAC
                                | ||||||||||||||
                                A TCATCGACCCTGATG
                                 C
GAM693   LOC145820 3'  CTGTAATCCCAGCACT      77513     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC145824 3'  ATGCCTGTAATCCCAGCACT   77523     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693   LOC145955 3'  ATGCCTGTAATCCCAACACT   83588     AGC        A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_         C
GAM693   LOC146059 3'  ATGCCTGTAATCCCAGCACT   77619     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693   LOC146059 3'  TGTAATCCCAGCTACTCA     77623    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693   LOC146229 3'  CTGTAATCCCAGCACTCTG    77751     TA_
                                CAG   GCTGGGATTACAG
                                |||   ||||||||||||
                                GTC   CGACCCTAATGTC
                                  TCA
GAM693   LOC146272 5'  CTGTAATCCCAGCACT      77787     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC146332 3'  CTGTAATCCCAACACT      77824     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
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                                TCA   ACCCTAATGTC
                                  CA_
GAM693   LOC146540 3'  ATGCCTGTAGTCCCAGCTACTC 77970    C            A
                A                  A AGTAGCTGGGATTACAG CAT
                                   | ||||||||||||||||| |||
                                   A TCATCGACCCTGATGTC GTA
                                    C             C
GAM693   LOC146540 3'  CTGTAATCCCAGCACT      77974     A
                                   AGT GCTGGGATTACAG
                                   ||| ||||||||||||
                                   TCA CGACCCTAATGTC
                                     _
GAM693   LOC146667 3'  ATGCCTGTAATCCCAGCACT   83702     A          A
                                   AGT GCTGGGATTACAG CAT
                                   ||| |||||||||||| |||
                                   TCA CGACCCTAATGTC GTA
                                     _           C
GAM693   LOC146669 3'  CTGTAATCCAGCACTGTG     78058       A    G
                                   TACAGT GCTGG ATTACAG
                                   |||||| ||||| |||||||
                                   GTGTCA CGACC TAATGTC
                                      _    _
GAM693   LOC146713 3'  CTGTAATCCCAGCACT      83725     A
                                   AGT GCTGGGATTACAG
                                   ||| ||||||||||||
                                   TCA CGACCCTAATGTC
                                     _
GAM693   LOC146723 3'  CTGTAATCCCAGCTACT     78083
                                   AGTAGCTGGGATTACAG
                                   ||||||||||||||||
                                   TCATCGACCCTAATGTC

GAM693   LOC146728 3'  ATGCCTGTGGTCCCAGCTACTC 83746    C            A
                A                  A AGTAGCTGGGATTACAG CAT
                                   | ||||||||||||||||| |||
                                   A TCATCGACCCTGGTGTC GTA
                                    C             C
GAM693   LOC146756 3'  CTGTAATCCCAGCACT      83776     A
                                   AGT GCTGGGATTACAG
                                   ||| ||||||||||||
                                   TCA CGACCCTAATGTC
                                     _
GAM693   LOC146756 3'  CTGTAATCCCAGCACT      83777     A
                                   AGT GCTGGGATTACAG
                                   ||| ||||||||||||
                                   TCA CGACCCTAATGTC
                                     _
GAM693   LOC146780 3'  ATGCCTGTAATCCCTGCACTTA 83786    C   A  T        A
                                   A AGT GC GGGATTACAG CAT
                                   | ||| || |||||||||| |||
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                                A TCA CG CCCTAATGTC GTA
                                 T  _ T       C
GAM693  LOC146901 3'  ATGCCTATAATCCCAGCTACT  83829           C  A
                                AGTAGCTGGGATTA AG CAT
                                |||||||||||||| || |||
                                TCATCGACCCTAAT TC GTA
                                        A  C
GAM693  LOC146901 3'  CTGTAATCCCCGCACT     83839     A  T
                                AGT GC GGGATTACAG
                                ||| || ||||||||||
                                TCA CG CCCTAATGTC
                                  _  C
GAM693  LOC146923 3'  CTGTAATCCCAGCACT     78192     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC146975 5'  CTATAATCCCAGCACT     78223     A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _       A
GAM693  LOC147057 3'  ATGCCTGTAATCCCAGCACT  83909     A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _         C
GAM693  LOC147071 3'  CTGTAATCCCAGCACT     72998     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC147599 3'  ATGCCTGTAATCCCAGCACCCT 84040     TA_         A
          G                      CAG   GCTGGGATTACAG CAT
                                |||   |||||||||||| |||
                                GTC   CGACCCTAATGTC GTA
                                  CCA          C
GAM693  LOC147660 3'  CTGTAATCCCAGCAC      78392     A
                                GT GCTGGGATTACAG
                                || ||||||||||||
                                CA CGACCCTAATGTC
                                  _
GAM693  LOC147664 3'  ATGCCTGTAATCCCAGCTACTT 78403    _           A
          G                      CA GTAGCTGGGATTACAG CAT
                                || ||||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 T            C
GAM693  LOC147664 3'  CTGTAATCCCAACACT     78408     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
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                                TCA   ACCCTAATGTC
                                  CA_
GAM693   LOC147669 3'  CTGTAATCCCAGCACT      84061     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC147700 3'  ATGCCTGTAATCCCAGCTACT  59193             A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                        C
GAM693   LOC147700 3'  CTGTAATCCCAACACT      59197     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693   LOC147727 5'  CTATAATCCCAGCTACTCA    78467    C          C
                                A AGTAGCTGGGATTA AG
                                | |||||||||||||| ||
                                A TCATCGACCCTAAT TC
                                 C           A
GAM693   LOC147837 3'  ATGCCTGTAATCCCAGCTACT  78512             A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                        C
GAM693   LOC147837 3'  CTGTAATCCCAGCACT      78515     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC147990 3'  CTGTAATCCCAGCACT      84092     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC147990 3'  CTGTAATCTCAGCTACTCA    84093    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACTCTAATGTC
                                 C
GAM693   LOC148147 3'  CTGTAATCCCAGCACT      78680     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC148198 3'  ATGCCTGTAATCCCAGCTACT  70676             A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
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                                TCATCGACCCTAATGTC GTA
                                          C
GAM693   LOC148198 3'  CTGTAATCCCAGCACT      70681     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC148254 3'  TGCCTGTAATCCCTGCACT    78760     A  T        A
                                AGT GC GGGATTACAG CA
                                ||| || |||||||||| ||
                                TCA CG CCCTAATGTC GT
                                  _ T         C
GAM693   LOC148343 3'  TGCCTGTAATCCCCGCACT    78796     A  T        A
                                AGT GC GGGATTACAG CA
                                ||| || |||||||||| ||
                                TCA CG CCCTAATGTC GT
                                  _ C         C
GAM693   LOC148397 3'  ATGCCTGTAATCCTAGCTATT  78812               A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TTATCGATCCTAATGTC GTA
                                          C
GAM693   LOC148397 3'  CTGTAATCCCGGCACTGTG    78817       A
                                TACAGT GCTGGGATTACAG
                                |||||| ||||||||||||
                                GTGTCA CGGCCCTAATGTC
                                  _
GAM693   LOC148534 3'  ATGCCTGTAATCCCAGCACT   78894     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693   LOC148734 3'  CTGTAATCCCAGCACT      78954     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC148749 3'  CTGTAATCCCAGCACT      78960     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC148758 5'  ATGCCTATAATCCCAGCTACTT 78965    _          C  A
           G                     CA GTAGCTGGGATTA AG CAT
                                || |||||||||||| || |||
                                GT CATCGACCCTAAT TC GTA
                                 T           A  C
GAM693   LOC148758 5'  ATGCCTGTAATCCCAGAACT   78966     AG         A
                                AGT  CTGGGATTACAG CAT
                                |||  |||||||||||| |||
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                                TCA  GACCCTAATGTC GTA
                                  A_          C
GAM693   LOC148809 3'  ATGCCTATAATCCCAGCTTCT  79000    T        C  A
                                AG AGCTGGGATTA AG CAT
                                || |||||||||| || |||
                                TC TCGACCCTAAT TC GTA
                                 T          A  C
GAM693   LOC148809 5'  CTGTAATCCCAGCACT      79003     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC148918 5'  CTGTAATCCCAGCACT      79071     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC148936 3'  CTGTAATCCCAGCACT      84290     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC148938 3'  CTGTAATCCCAGCACT      84270     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC149073 3'  CTATAATCCCAGCACT      84324     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM693   LOC149073 3'  GTGCCTGTAATCCCAGCTACTC 84331    C             A
                   A                A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGACCCTAATGTC GTG
                                 C             C
GAM693   LOC149113 3'  CTGTAATCCCAGAACTTTA    79164    C   AG
                                TA AGT  CTGGGATTACAG
                                || |||  ||||||||||||
                                AT TCA  GACCCTAATGTC
                                 T   A_
GAM693   LOC149113 3'  CTGTAATCCCAGCACT      79165     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC149194 5'  CTGTAATCCCAGCTACTCA    79225    C
                                A AGTAGCTGGGATTACAG
                                | |||||||||||||||||
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                                A TCATCGACCCTAATGTC
                                 C
GAM693   LOC149194 5'  GTCTGTAATCCCAGCACT    79229     A
                                AGT GCTGGGATTACAGAC
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCTG
                                  _
GAM693   LOC149271 3'  CTGTAATCCCAGCACT      79240     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC149319 3'  GTCTGTAATCCCAGCACT    79301     A
                                AGT GCTGGGATTACAGAC
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCTG
                                  _
GAM693   LOC149579 5'  CTGTAATCCCAGCACT      71133     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC149606 3'  GTCTGTAGTCCCAGCTACTCA  79455    C
                                A AGTAGCTGGGATTACAGAC
                                | ||||||||||||||||||
                                A TCATCGACCCTGATGTCTG
                                 C
GAM693   LOC149628 3'  CTATAATCCCAGCTACT      79462             C
                                AGTAGCTGGGATTA AG
                                |||||||||||||| ||
                                TCATCGACCCTAAT TC
                                          A
GAM693   LOC149628 3'  CTGTAATCCCAGCACT      79463     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC149668 3'  ATGCCTGTAATCCCAGCACT   84534     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693   LOC149705 3'  CTGTAATCCCAACACTTTG    84623     TAGC_
                                CAG     TGGGATTACAG
                                |||     ||||||||||
                                GTT     ACCCTAATGTC
                                  TCACA
GAM693   LOC149837 3'  TGGAAATCCCAGCTAT       84747           A_
                                GTAGCTGGGATT  CA
                                ||||||||||  ||
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                                TATCGACCCTAA  GT
                                      AG
GAM693   LOC150139 3'  ATGCCTGTAATCCCAGCTG    79584            A
                                TAGCTGGGATTACAG CAT
                                |||||||||||||| |||
                                GTCGACCCTAATGTC GTA
                                      C
GAM693   LOC150185 3'  ATGCCTGTAATCCCAACACT   84905     AGC        A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_         C
GAM693   LOC150319 3'  ATGCCTGTAATCCCAGCACT   79647     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693   LOC150319 3'  ATGCCTGTAATCCCAGTTACTC 79648    C             A
           A                     A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||| |||
                                A TCATTGACCCTAATGTC GTA
                                 C             C
GAM693   LOC150343 3'  CTGTAATCCCAGCACT      79672     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC150358 3'  ATGCCTATAATCCCAGCACT   84920     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _         A  C
GAM693   LOC150358 3'  ATGCCTGTAATCCCAGCACT   84921     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| ||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693   LOC150358 3'  CTGTAATCCCAGGTACTCA    84922    C    G
                                A AGTA CTGGGATTACAG
                                | |||| ||||||||||||
                                A TCAT GACCCTAATGTC
                                 C    G
GAM693   LOC150372 3'  ATGCCTGTAATCCCAGC      79786            A
                                GCTGGGATTACAG CAT
                                |||||||||||| |||
                                CGACCCTAATGTC GTA
                                      C
GAM693   LOC150481 3'  CTGTAATCCCAGCACT      79884     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC150622 3'  CTGTAATCCCAACACT      79958     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693   LOC150630 3'  ATGCCTATAATCCCAGCTACT  85099           C  A
                                AGTAGCTGGGATTA AG CAT
                                |||||||||||||| || |||
                                TCATCGACCCTAAT TC GTA
                                         A  C
GAM693   LOC150630 3'  ATGCCTGTAATCCCAGCACT   85100     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| ||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693   LOC150889 3'  ATGCCTGTAATCCCAGCACT   80024     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| ||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693   LOC150935 3'  ATGCCTGTAATCCCAGCGCT   80031     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| ||||||||||||| |||
                                TCG CGACCCTAATGTC GTA
                                  _          C
GAM693   LOC150998 3'  CTGTGGTCCCAGCTAC      85183
                                GTAGCTGGGATTACAG
                                ||||||||||||||||
                                CATCGACCCTGGTGTC

GAM693   LOC151196 3'  CTGTAACCCCAGCTACTCA    85265    C         A
                                A AGTAGCTGGG TTACAG
                                | |||||||||| ||||||
                                A TCATCGACCC AATGTC
                                 C         C
GAM693   LOC151196 3'  CTGTAATCCCAGCACT      85266     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC151248 3'  CTGTAATCCCAGCACT      80186     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC151248 3'  TGTAATCCCAGCTACTCA    80193    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
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                                A TCATCGACCCTAATGT
                                 C
GAM693   LOC151429 3'  ATGCCTGTAATCCCAGC     85344            A
                                GCTGGGATTACAG CAT
                                ||||||||||||| |||
                                CGACCCTAATGTC GTA
                                        C
GAM693   LOC151429 3'  CTGTAATCCCAGCACT      85352     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC151446 3'  ATGCCTGTAATCCCAGCTACTG 85375               A
                                CAGTAGCTGGGATTACAG CAT
                                |||||||||||||||||| |||
                                GTCATCGACCCTAATGTC GTA
                                           C
GAM693   LOC151556 3'  CTGTAATCCCAGTACT      80274      G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                  _
GAM693   LOC151556 3'  TGTAATCCCAGCTACTCA    80283    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693   LOC151602 3'  CTGTAATCCCAACACT      80294     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693   LOC151602 3'  CTGTAATCCCAGCTACTCA    80295    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM693   LOC151614 3'  CTGTAATCCCAGCACT      80304     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC151623 3'  ATGCCTGTGGTCTCAGCTACTC 85456    C              A
            A                    A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGACTCTGGTGTC GTA
                                 C             C
GAM693   LOC151904 3'  CTGTAATCCCAGCACT      80390     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC152263 3'  CTGTAATCCCAGCACT      85674     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC152263 3'  TCCATAATCCTAGCTGCT     85676            CA
                                AGTAGCTGGGATTA  GA
                                ||||||||||||||  ||
                                TCGTCGATCCTAAT  CT
                                        AC
GAM693   LOC152316 3'  ATGCCTGTAATCCCAGCACTTT 85609    C  A          A
            A                    TA AGT GCTGGGATTACAG CAT
                                || ||| |||||||||||||| |||
                                AT TCA CGACCCTAATGTC GTA
                                 T  _           C
GAM693   LOC152426 3'  CTGTAATCCCAGCACT      85714     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC152445 3'  ATGCCTGTAATCCCAACTACT  85746       C         A
                                AGTAG TGGGATTACAG CAT
                                ||||| |||||||||| |||
                                TCATC ACCCTAATGTC GTA
                                   A          C
GAM693   LOC152453 3'  ATGCCTGTAATCCCAGCACT   80592     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693   LOC152453 3'  ATGCCTGTAATCCCAGCTACT  80593              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                        C
GAM693   LOC152453 3'  CTGTAATCCCAACACT      80595     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693   LOC152453 3'  CTGTAATCCCAGCACT      80596     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC152453 3'  CTGTAATCCCAGTTACTCA    80597    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
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                                A TCATTGACCCTAATGTC
                                 C
GAM693   LOC152627 5'  TGTAATCCCAGCTACTCA    80632   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693   LOC152804 3'  ATGCCTGTAATCCCAGCTACT  85878             A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                          C
GAM693   LOC152860 3'  ATGTCTGTAATCCCAGCTACTG 80696
                                CAGTAGCTGGGATTACAGACAT
                                |||||||||||||||||||||
                                GTCATCGACCCTAATGTCTGTA

GAM693   LOC152860 3'  CTATAATCCCAGCACT      80701     A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _       A
GAM693   LOC152926 3'  ATGCCTGTAATCCCAGCACT   80744     A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693   LOC153077 3'  CTATAATCCCAGCTACTCA    85909   C         C
                                A AGTAGCTGGGATTA AG
                                | |||||||||||||| ||
                                A TCATCGACCCTAAT TC
                                 C          A
GAM693   LOC153260 3'  CTGTAATCCCAGCACT      80804     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC153561 3'  ATGCCTGTAATCCCAGCACT   80888     A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693   LOC153579 3'  CTGTAATCCCAGTACT      80895     G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                   _
GAM693   LOC153642 3'  CTATAGTCTCAGCTACTCA    80907   C         C
                                A AGTAGCTGGGATTA AG
                                | |||||||||||||| ||
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                                A TCATCGACTCTGAT TC
                                 C           A
GAM693   LOC153642 3'  CTGTAATCCCAGGACT     80908     AG
                                AGT  CTGGGATTACAG
                                |||  ||||||||||||
                                TCA  GACCCTAATGTC
                                  G_
GAM693   LOC153682 3'  ATGCCTGTAATCCCAGCACT   86084     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693   LOC153688 3'  ATGCCTATAATCCCAGCACT   86095     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| ||||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM693   LOC154092 3'  TCTGTAATCCCAGCACT     86161     A
                                AGT GCTGGGATTACAGA
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCT
                                  _
GAM693   LOC154215 3'  ATGTCTGTAATATACACACAC  81053    AGC  GG_
                                GT   TG   ATTACAGACAT
                                ||   ||   ||||||||||||
                                CA   AC   TAATGTCTGTA
                                 CAC  ATA
GAM693   LOC154403 3'  CTGTAATCCCAGAACTTTA    81071    C   AG
                                TA AGT  CTGGGATTACAG
                                || |||  ||||||||||||
                                AT TCA  GACCCTAATGTC
                                 T   A_
GAM693   LOC154739 5'  ATGTCTATAATTCCAGCTACTC 86225    C          C
           A                     A AGTAGCTGGGATTA AGACAT
                                | |||||||||||||| ||||||
                                A TCATCGACCTTAAT TCTGTA
                                 C           A
GAM693   LOC154791 3'  ATGCCTGTAATCCCAGCTACT  81154              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM693   LOC154791 3'  CTGTAATCCCAGCACT      81156     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC154992 3'  CTGTAATCCCAGAACTTTA    81215    C   AG
                                TA AGT  CTGGGATTACAG
                                || |||  ||||||||||||
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                                AT TCA  GACCCTAATGTC
                                 T   A_
GAM693   LOC155006 3'  ATGCCTGTAATCCCAGCACT   81229     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693   LOC155006 3'  ATGCCTGTAATCCCAGCACT   81230     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693   LOC155006 3'  CTGTAATCCCAGCTACTTG    81237    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                 T
GAM693   LOC155072 3'  CTGTAATCCCAGCACT      86375     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC155072 3'  CTGTAATCCCAGCACT      86376     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC155438 3'  CTGTAATCCCAGTACCT     86393     TA
                                AG  GCTGGGATTACAG
                                ||  ||||||||||||||
                                TC  TGACCCTAATGTC
                                 CA
GAM693   LOC157278 3'  CTGTAATCCCAGCACT      86423     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC157292 5'  CTGTAATCTCAGTTACTCA    86413    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATTGACTCTAATGTC
                                 C
GAM693   LOC157464 5'  CTGTAATCCCAGCACT      86448     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC157657 3'  ATGCCTGTAATCCCAACTACT  81516       C          A
                                AGTAG TGGGATTACAG CAT
                                ||||| |||||||||| |||
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                                TCATC ACCCTAATGTC GTA
                                   A          C
GAM693   LOC157657 3'  CTGTAATCCCAGCACT      81518     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693   LOC157660 3'  CTGTAATCCCAGCACT      86507     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693   LOC158160 3'  TGTAGTCCCAACTACTCA     73082     C     C
                                A AGTAG TGGGATTACA
                                | ||||| ||||||||||
                                A TCATC ACCCTGATGT
                                 C     A
GAM693   LOC158187 3'  CTGTAGTCCCAGCTAC       86691
                                GTAGCTGGGATTACAG
                                ||||||||||||||||
                                CATCGACCCTGATGTC

GAM693   LOC158191 3'  CTGTAATCCCAGCACT      81775     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693   LOC158292 5'  ATGCCTGTAATCCCAGCACT   86728     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                 _           C
GAM693   LOC158292 5'  TGTAATCCCAGCTACTCA     86732     C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693   LOC158310 3'  CTGTAATCCCAGCACT      86753     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM693   LOC158819 5'  ATGCCTGTAATCCCAGCTTCT  86901     T          A
                                AG AGCTGGGATTACAG CAT
                                || |||||||||||||| |||
                                TC TCGACCCTAATGTC GTA
                                 T           C
GAM693   LOC158819 3'  CTGTAATCCCAGCACT      86903     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC158819 5'  CTGTAATCCCAGCACT      86904     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC158863 3'  CTGTAATCCCAACACT      86923     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693   LOC158987 3'  CTGTAATCCCAACACT      86961     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693   LOC159036 3'  ATGCCTGTAATCCCAGCACT   86969     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693   LOC159053 3'  CTGTAATCCCAGGACT      86978     AG
                                AGT  CTGGGATTACAG
                                |||  ||||||||||
                                TCA  GACCCTAATGTC
                                  G_
GAM693   LOC161823 3'  ATGCCTGTAATCCCAGCACT   82300     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693   LOC170395 3'  CTGCAGTCCCAGCTACTCA    76368    C          A
                                A AGTAGCTGGGATT CAG
                                | |||||||||||| |||
                                A TCATCGACCCTGA GTC
                                 C          C
GAM693   LOC170395 3'  CTGTAATCCCAGCACT      76369     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC196047 5'  CTGTAATCCCAGTACT      89600     G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                  _
GAM693   LOC196528 3'  CTATAATCCCAGCACT      87764     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
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                                TCA CGACCCTAAT TC
                                  _        A
GAM693   LOC197196 3'  CTGTAATCCCAGCACT      89733     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC197201 3'  ATGCCTGTAATCTCAGCTACTC 87933    C              A
                  A                A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACTCTAATGTC GTA
                                 C              C
GAM693   LOC197201 3'  CTGTAATCCCAGCACT      87936     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC197319 3'  CTGTAATCCCAGCACT      87969     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC197319 3'  CTGTAATCCCAGCTCCT     87970     T
                                AG AGCTGGGATTACAG
                                || ||||||||||||
                                TC TCGACCCTAATGTC
                                 C
GAM693   LOC199733 3'  CTGAAATCCCAGCTACTG    89849             A
                                CAGTAGCTGGGATT CAG
                                |||||||||||||| |||
                                GTCATCGACCCTAA GTC
                                          A
GAM693   LOC199786 3'  CTGTAATCCCAGCACT      88380     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC200014 3'  CTGTAATCCCACCACT      88526     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CC_
GAM693   LOC200251 5'  CTGTAATCCCAGCTACTCA   88665    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM693   LOC200317 3'  CTGTAATCCCAGCTACTTG   88794    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
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                                GT CATCGACCCTAATGTC
                                 T
GAM693   LOC200470 3'  CTGTAATCCCAACACT      90062     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM693   LOC200728 3'  CTGTAATCCCAGCACT      90115     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC200803 3'  ATGCCTGTAATCCTAGCTACTC 88879    C             A
              A                  A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGATCCTAATGTC GTA
                                 C              C
GAM693   LOC200803 3'  TGCCTGTAATCCCACCACT    88881     AGC         A
                                AGT   TGGGATTACAG CA
                                |||   |||||||||| ||
                                TCA   ACCCTAATGTC GT
                                  CC_          C
GAM693   LOC200918 3'  TGTAATCCCAGCTACTTA     88943    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 T
GAM693   LOC200940 3'  ATGCCTGTAATCCCAGCTACTT 88950     _             A
              G                  CA GTAGCTGGGATTACAG CAT
                                || |||||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 T              C
GAM693   LOC201173 3'  CTGTAATCCCAGCACT      87328     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC201182 5'  ATGCCTGTAATCCCAGCTAC   89763              A
                                GTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                CATCGACCCTAATGTC GTA
                                           C
GAM693   LOC201220 3'  CTGTAATCCCAGCACT      87349     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC201252 3'  ATGCCTGTAATCCCAACTACT  88165       C          A
                                AGTAG TGGGATTACAG CAT
                                ||||| |||||||||| |||
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                                TCATC ACCCTAATGTC GTA
                                   A         C
GAM693   LOC201252 3'  CTGTAATCCCAGAACT      88168     AG
                                AGT  CTGGGATTACAG
                                |||  ||||||||||||
                                TCA  GACCCTAATGTC
                                 A_
GAM693   LOC201564 3'  ATGCCTGTAATCCCAGCTACTT 80435    _             A
           G                     CA GTAGCTGGGATTACAG CAT
                                || ||||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 T             C
GAM693   LOC201685 3'  ATGTCTATGGTCCCAGCTACTC 90239   C             C
           A                     A AGTAGCTGGGATTA AGACAT
                                | ||||||||||||| ||||||
                                A TCATCGACCCTGGT TCTGTA
                                 C             A
GAM693   LOC201685 3'  CTGTAATCCCAGCACT      90241     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC201689 3'  CTGTAATCCCAGCACT      67144     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC201868 3'  CTGTAATCCCAGCACT      89077     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC201868 3'  TGTAATCCCAGCTACTCA    89084    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693   LOC201895 3'  CTGTAATCCCAGCACT      89087     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC201895 3'  GTGCCTGTAATCCCAGCTACTC 89091   C             A
           A                     A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGACCCTAATGTC GTG
                                 C             C
GAM693   LOC201911 3'  CTGTAATCCCAGCACT      90261     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC202868 3'  CTGTAATCCCAGCACT      90373     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC202868 3'  CTGTAATCCCAGCACT      90374     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC203025 3'  ATGCCTGTAATCCCAACACTTT 89249     TAGC_         A
           G                     CAG     TGGGATTACAG CAT
                                |||     |||||||||| |||
                                GTT     ACCCTAATGTC GTA
                                  TCACA          C
GAM693   LOC203246 3'  CTGTAATCCCAGCACT      89304     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC203276 3'  GTCTATAATTCCAGCTACTCA  90487    C           C
                                A AGTAGCTGGGATTA AGAC
                                | |||||||||||| ||||
                                A TCATCGACCTTAAT TCTG
                                 C            A
GAM693   LOC203305 3'  GTCTATAATTCCAGCTACTCA  90531    C           C
                                A AGTAGCTGGGATTA AGAC
                                | |||||||||||| ||||
                                A TCATCGACCTTAAT TCTG
                                 C            A
GAM693   LOC203350 3'  ATGCCTGTAATCCCAGCACT   90560     A           A
                                AGT GCTGGGATTACAG CAT
                                ||| ||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693   LOC203350 3'  ATGCCTGTAGTTGCAGCTACTC 90561    C       G       A
           A                     A AGTAGCTG GATTACAG CAT
                                | |||||||| |||||||| |||
                                A TCATCGAC TTGATGTC GTA
                                 C       G       C
GAM693   LOC203378 3'  CTGTAATCCCGGCACT      90602     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGGCCCTAATGTC
                                  _
GAM693   LOC203378 3'  CTGTAGTTCCAGCTACTG    90603
                                CAGTAGCTGGGATTACAG
                                ||||||||||||||||||
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                                GTCATCGACCTTGATGTC

GAM693   LOC219406 3'  CTGCAATCCCAGCTACT     93559            A
                                AGTAGCTGGGATT CAG
                                |||||||||||| |||
                                TCATCGACCCTAA GTC
                                      C
GAM693   LOC219406 3'  CTGTAATCCCAGCACT      93560     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC219540 3'  CTGTAATCCCAGCTACTTG   93598    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                 T
GAM693   LOC219627 3'  ATGCCTGTAATCCCAACACT  92175     AGC         A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_         C
GAM693   LOC219627 3'  CTGTAATCCCAGCACT      92177     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC219627 3'  GTGCCTGTAATCCCAGCTACTC 92185    C             A
            A                    A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGACCCTAATGTC GTG
                                 C              C
GAM693   LOC219649 3'  ATGCCTATAATCCCAGC      92950          C  A
                                GCTGGGATTA AG CAT
                                |||||||||| || |||
                                CGACCCTAAT TC GTA
                                      A  C
GAM693   LOC219649 3'  CTGTAATCCCAGCTACT      92956
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693   LOC219649 3'  GTCTGTAATCCCAGCACT     92961     A
                                AGT GCTGGGATTACAGAC
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCTG
                                  _
GAM693   LOC219672 5'  ATGCCTGTAATCCCAGCACT   91328     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693   LOC219673 3'  CTGTAATCCCAGCACT      93031     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC219722 5'  CTGTAATCCCAGCACT      93081     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC220370 3'  ATGCCTGTAATCCCAACACTCT 92824     T  C__          A
            G                    CAG AG   TGGGATTACAG CAT
                                ||| ||   |||||||||| |||
                                GTC TC   ACCCTAATGTC GTA
                                  _ ACA          C
GAM693   LOC220506 3'  CTATAATCCCAGCACTTTA    74077     C   A        C
                                TA AGT GCTGGGATTA AG
                                || ||| |||||||||| ||
                                AT TCA CGACCCTAAT TC
                                 T   _         A
GAM693   LOC220662 3'  CTGTAATCCCAGCTACTTG    91171     _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                 T
GAM693   LOC220662 3'  CTGTCATCCCAGCTACTCA    91172    C          T
                                A AGTAGCTGGGAT ACAG
                                | |||||||||||| ||||
                                A TCATCGACCCTA TGTC
                                 C           C
GAM693   LOC220662 3'  CTGTAATCCCAGCACT      91169     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC220662 3'  CTGTAATCCCAGCACT      91170     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC220906 3'  ATGCCTGTAATCCCAACACT   91396     AGC         A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_          C
GAM693   LOC221042 3'  CTGTAATCCCAGCGCT      93185     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCG CGACCCTAATGTC
                                  _
GAM693  LOC221178 3'  ATGCCTGTAATCCCAGCACT  93527    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  LOC221178 3'  ATGCCTGTAATCCCAGCTACTG 93528               A
                                CAGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                GTCATCGACCCTAATGTC GTA
                                           C
GAM693  LOC221271 3'  CTGTAATCCCAGCACT     91856    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC221271 3'  CTGTAATCCCAGCTACT    91857
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693  LOC221474 3'  CTGTAATCCCAGCACT     92381    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC221474 3'  TGTAATCCCAGCTACTCA   92389    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  LOC221477 3'  CTGTAATCCCAGCTAC     92152
                                GTAGCTGGGATTACAG
                                ||||||||||||||||
                                CATCGACCCTAATGTC

GAM693  LOC221489 3'  CTGTAATCCCAGCACT     93641    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC221490 3'  CTGTAATCCCAGCACT     93658    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC221543 3'  CTGTAATCCCAGCACT     93740    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC221543 5'  CTGTAATCCCAGCACTCTG   93741     TA_
                                CAG   GCTGGGATTACAG
                                |||   ||||||||||||||
                                GTC   CGACCCTAATGTC
                                  TCA
GAM693   LOC221931 3'  ATGCCTGTAATCCCAGCACT   93993     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693   LOC221954 5'  CTGTAATCCCAGCACT      94000     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC221962 3'  CTGTAATCCCAGCACT      92681     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC222066 3'  CTGTAATCCCAGCTATT     92744
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TTATCGACCCTAATGTC

GAM693   LOC222160 5'  ATGCCTGTAATCCCAGCACT   94118     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693   LOC222160 3'  CTGTAATCCCAGCTACT     94125
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM693   LOC222182 3'  CTGTAATCCCTTAGCTACTCA  94189    C      __
                                A AGTAGCT  GGGATTACAG
                                | |||||||  ||||||||||
                                A TCATCGA  CCCTAATGTC
                                 C      TT
GAM693   LOC222865 3'  CTGTAATCCCAGCACT      92860     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC253612 3'  CTGTAATCCCAACACT      96748     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
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                                TCA   ACCCTAATGTC
                                  CA_
GAM693   LOC253612 3'  GTCTGTAATCCCAGCTACT    96755
                                AGTAGCTGGGATTACAGAC
                                ||||||||||||||||||
                                TCATCGACCCTAATGTCTG

GAM693   LOC253639 3'  ATGCCTGTAATCCCAGCTACT  95818              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM693   LOC253927 3'  ATGCCTGTAATCCCAGCACT   95023     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| ||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693   LOC254045 3'  ATGCCTGTAATCCCAATACT   96502     GC         A
                                AGTA  TGGGATTACAG CAT
                                ||||  |||||||||||| |||
                                TCAT  ACCCTAATGTC GTA
                                   A_         C
GAM693   LOC254045 3'  ATGCCTGTAATCCCAGCTACT  96503              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM693   LOC254243 3'  GTCTATAATTCCAGCTACTCA  97416   C          C
                                A AGTAGCTGGGATTA AGAC
                                | ||||||||||||| ||||
                                A TCATCGACCTTAAT TCTG
                                 C           A
GAM693   LOC254249 5'  TGCTTGTCCCAGCTACTG    95449           TAC  A
                                CAGTAGCTGGGAT   AG CA
                                ||||||||||||   || ||
                                GTCATCGACCCTG   TC GT
                                        T__  _
GAM693   LOC254531 5'  ATGCCTGTAATCCCAGCTACTT 94980    _           A
           G                     CA GTAGCTGGGATTACAG CAT
                                || ||||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                  T            C
GAM693   LOC254531 5'  CTGTAATCCCAGCACT      94985     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC255042 3'  ATGCCTGTAATCCTAGCTACTC 95312   C            A
           A                     A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
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                                A TCATCGATCCTAATGTC GTA
                                 C             C
GAM693   LOC255042 3'  CTGTAATCCCAGCACT     95315     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC255042 3'  CTGTAATCCCAGCACT     95316     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC255177 3'  CTGTAATCCCAGCACT     96605     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC255196 3'  ATGCCTATAATCCCAGCACT  97164     A       C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _       A  C
GAM693   LOC255196 5'  CTGTAATCCCAGCACT     97169     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC255231 3'  CTGTAATCCCAGCACT     95373     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC255252 3'  ATGCCTATAATCCCAGCACT  95006     A       C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _       A  C
GAM693   LOC255326 3'  CTGTAATCCCAGACTGTG    96376      AG
                                TACAGT  CTGGGATTACAG
                                ||||||  ||||||||||||
                                GTGTCA  GACCCTAATGTC
                                  __
GAM693   LOC255328 3'  ATGTCTGTAATCCCAGCACT  96557     A
                                AGT GCTGGGATTACAGACAT
                                ||| ||||||||||||||||
                                TCA CGACCCTAATGTCTGTA
                                  _
GAM693   LOC255461 3'  CTGTAATCCCAGCACT     97319     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC255516 3'  CTGTAATCCCAGCACT      97332     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC255624 3'  CTGTAATCCCAGCACT      94523     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC255671 3'  CTGTAATCCCAGCTGCT     97255
                                AGTAGCTGGGATTACAG
                                |||||||||||||||||
                                TCGTCGACCCTAATGTC

GAM693   LOC255671 3'  TCTGTAATCCCAGCACT     97264     A
                                AGT GCTGGGATTACAGA
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCT
                                  _
GAM693   LOC255937 3'  ATGCCTGTAATCCCAGCTACT  95987               A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                      C
GAM693   LOC255937 3'  CTGTAATCCCAGCTCT      95988     T
                                AG AGCTGGGATTACAG
                                || ||||||||||||||
                                TC TCGACCCTAATGTC
                                  _
GAM693   LOC255971 3'  CTATAATCCCAGCACT      96533     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _         A
GAM693   LOC256073 3'  CTGTAATCCCAATGCT      96664      GC
                                AGTA  TGGGATTACAG
                                ||||  ||||||||||||
                                TCGT  ACCCTAATGTC
                                   A_
GAM693   LOC256207 3'  TCTGTAATTGCTATTG      95179        TGG
                                CAGTAGC   GATTACAGA
                                |||||||   |||||||||
                                GTTATCG   TTAATGTCT
                                    ___
GAM693   LOC256267 3'  ATGCCTGTAATCCCAGCACT   96797     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693   LOC256277 3'  CTGTAATCCCAGCACT     94698     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC256520 3'  TGTAATCCCAGCTACTCA    95981    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693   LOC256980 3'  TCTGTAATCCCAGCACTCTG   95223     TA_
                                CAG   GCTGGGATTACAGA
                                |||   ||||||||||||||
                                GTC   CGACCCTAATGTCT
                                  TCA
GAM693   LOC257354 3'  ATGCCTATAATCCCAACACT   95085     AGC       C  A
                                AGT   TGGGATTA AG CAT
                                |||   |||||||| || |||
                                TCA   ACCCTAAT TC GTA
                                  CA_       A  C
GAM693   LOC257480 3'  CTGTAATCCCAGCACT      77869     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC257539 3'  ATGCCTGTAATCCCAGCACT   97699     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693   LOC257578 3'  ATGCCTGTAATCCCAGCACT   97819     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693   LOC257596 3'  CTGTAATCCCAGCACT      97933     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693   LOC257596 5'  CTGTAATCCCAGCACTCTG    97934     TA_
                                CAG   GCTGGGATTACAG
                                |||   ||||||||||||
                                GTC   CGACCCTAATGTC
                                  TCA
GAM693   LOC51145  3'  TGTAATCCCAGCTACTCA     32400    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
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                                A TCATCGACCCTAATGT
                                 C
GAM693  LOC51333 3' CTGTAATCCCAGCACT     33567     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC51333 3' CTGTAATCCCAGCTACTG    33568
                                CAGTAGCTGGGATTACAG
                                ||||||||||||||||||
                                GTCATCGACCCTAATGTC

GAM693  LOC51652 3' ATGCCTATAATCCCAGTGCT  32191     G       C  A
                                AGTA CTGGGATTA AG CAT
                                |||| ||||||||| || |||
                                TCGT GACCCTAAT TC GTA
                                  _       A  C
GAM693  LOC51716 3' TGCCTGTAATCCCTGC      32795    T       A
                                GC GGGATTACAG CA
                                || ||||||||| ||
                                CG CCCTAATGTC GT
                                 T        C
GAM693  LOC51759 3' ATGCCTGTAATCCCAGCTGCT  72812             A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCGTCGACCCTAATGTC GTA
                                    C
GAM693  LOC55974 3' ATGCCTGTAATCCCAGATACT  38130     G         A
                                AGTA CTGGGATTACAG CAT
                                |||| |||||||||||| |||
                                TCAT GACCCTAATGTC GTA
                                  A          C
GAM693  LOC55974 3' CTGTAATCCCAGCACT      38131     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC57118 3' CTGTAATCCCAACACT      39867     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                 CA_
GAM693  LOC63929 3' ATGCCTGTAATCCTGGCTACT  42041       TG       A
                                AGTAGC  GGATTACAG CAT
                                ||||||  ||||||||| |||
                                TCATCG  CCTAATGTC GTA
                                   GT       C
GAM693  LOC64167 3' CTGTAATCCCAGCACT      42279     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                              TCA CGACCCTAATGTC
                                _
GAM693  LOC89890  3' CTGTAATCCCAGCTAC     60578
                              GTAGCTGGGATTACAG
                              ||||||||||||||||
                              CATCGACCCTAATGTC

GAM693  LOC90038  3' GTCTATAATTCCAGCTACTCA 61159   C          C
                              A AGTAGCTGGGATTA AGAC
                              | |||||||||||||| ||||
                              A TCATCGACCTTAAT TCTG
                               C           A
GAM693  LOC90092  3' CTGTAATCCCAGCACT     61405    A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM693  LOC90092  3' CTGTAATCCCAGCACT     61406    A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM693  LOC90141  3' ATGCCTACAATCCCAGCACT  61625    A       AC  A
                              AGT GCTGGGATT  AG CAT
                              ||| |||||||||  || |||
                              TCA CGACCCTAA  TC GTA
                                _       CA  C
GAM693  LOC90155  5' ATGCCTGTAATCCCAGCACT  61691    A          A
                              AGT GCTGGGATTACAG CAT
                              ||| |||||||||||||| |||
                              TCA CGACCCTAATGTC GTA
                                _          C
GAM693  LOC90321  3' ATGCCTATAATCTCAGCAC   62260    A       C  A
                              GT GCTGGGATTA AG CAT
                              || |||||||||| || |||
                              CA CGACTCTAAT TC GTA
                                _        A  C
GAM693  LOC90321  3' ATGCCTGCAATCCCAGCTACT 62261          A   A
                              AGTAGCTGGGATT CAG CAT
                              |||||||||||| ||| |||
                              TCATCGACCCTAA GTC GTA
                                       C   C
GAM693  LOC90408  5' ATGCCTGTAATCCCAGCACT  62656    A          A
                              AGT GCTGGGATTACAG CAT
                              ||| |||||||||||||| |||
                              TCA CGACCCTAATGTC GTA
                                _          C
GAM693  LOC90509  3' CTGTAATCCCAGCACT     63104    A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC90538  3'  TCTGTAATCCCAGCACT     63196     A
                                AGT GCTGGGATTACAGA
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCT
                                  _
GAM693  LOC90580  3'  ATGTCTGTAATCCCAGC      63371
                                GCTGGGATTACAGACAT
                                |||||||||||||||||
                                CGACCCTAATGTCTGTA

GAM693  LOC90591  3'  ATGCCTGTAATCCCAGCTACAT 63414    _            A
              G                  CA GTAGCTGGGATTACAG CAT
                                || |||||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 A             C
GAM693  LOC90591  3'  CTGTAATCCCAGCACT      63423     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC90591  3'  CTGTAATCCCAGCACT      63424     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC90624  3'  CTGTAATCCCGCACT       63603     A  T
                                AGT GC GGGATTACAG
                                ||| || ||||||||||
                                TCA CG CCCTAATGTC
                                  _ _
GAM693  LOC90639  3'  CTGCAATCCCAGCACTTTA   63656    C  A       A
                                TA AGT GCTGGGATT CAG
                                || ||| ||||||||| |||
                                AT TCA CGACCCTAA GTC
                                 T  _        C
GAM693  LOC90777  3'  CTATAATCTCAGCAC       63967    A        C
                                GT GCTGGGATTA AG
                                || |||||||||| ||
                                CA CGACTCTAAT TC
                                  _         A
GAM693  LOC90918  5'  ATGCCTGTAATCCCAGCTACT  64350              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                            C
GAM693  LOC90979  3'  CTGTAATCCCAGCACT      64526     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC90982  5' ATGTCTCTTTCCAGCTCT    64537    T      TTAC
                                AG AGCTGGGA    AGACAT
                                || ||||||||    ||||||
                                TC TCGACCTT    TCTGTA
                                  _       TC__
GAM693  LOC91035  3' CTATAATCCCAGCACT      64669     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM693  LOC91056  3' ATGCCTGTAATCCCAGCACT  94756     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  LOC91250  5' CTGTAATCCCAGTTACT     65323
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATTGACCCTAATGTC

GAM693  LOC91250  5' TCTGTAATCCCCGCACT     65330     A  T
                                AGT GC GGGATTACAGA
                                ||| || ||||||||||
                                TCA CG CCCTAATGTCT
                                  _ C
GAM693  LOC91286  3' ATGCCTGTAATCCTAGCCACT  65451     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGATCCTAATGTC GTA
                                  C          C
GAM693  LOC91380  3' CTGTAATCCCAACTAC      65860     C
                                GTAG TGGGATTACAG
                                |||| ||||||||||
                                CATC ACCCTAATGTC
                                   A
GAM693  LOC91380  3' TGCCTGTAATCCCGGCACT   65864     A          A
                                AGT GCTGGGATTACAG CA
                                ||| |||||||||||| ||
                                TCA CGGCCCTAATGTC GT
                                  _          C
GAM693  LOC91380  3' TGTAATCCCAGCTACTCA    65865   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  LOC91574  3' TCTGTAATCCCAGCACT     66521     A
                                AGT GCTGGGATTACAGA
                                ||| ||||||||||||||
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                                TCA CGACCCTAATGTCT
                                  _
GAM693  LOC91664  3' CTGTAATCCCAGCACT      66872     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC91750  3' CTGTAATCCCAGCACT      67061     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC91796  5' ATGCCTGTAATCCCAGCACT   67210     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM693  LOC91812  3' GTGCCTGTAATCCCAGCTACTC 67242    C             A
          A                      A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGACCCTAATGTC GTG
                                 C             C
GAM693  LOC91813  3' GTGCCTGTAATCCCAGCTACTC 67259    C             A
          A                      A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGACCCTAATGTC GTG
                                 C             C
GAM693  LOC91963  5' CTGTAATCCCAGCTACTTG    67694    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                  T
GAM693  LOC92078  3' CTATAATCCCAGCACT      67980     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _         A
GAM693  LOC92078  3' TGTAATCCCAACTACTCA     67990    C    C
                                A AGTAG TGGGATTACA
                                | ||||| ||||||||||
                                A TCATC ACCCTAATGT
                                 C    A
GAM693  LOC92228  3' CTGTAATCCCAGCACT      68541     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC92267  3' CTGTAATCCCAGCACT      68613     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                              TCA CGACCCTAATGTC
                                _
GAM693  LOC92270 5' CTGTAATCCCAGCACT     68630     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM693  LOC92270 5' TGTAATCCCAGCTACTCA    68637    C
                              A AGTAGCTGGGATTACA
                              | ||||||||||||||||
                              A TCATCGACCCTAATGT
                               C
GAM693  LOC92283 3' ATGCCTGTAATCCCAGCACT  68744     A          A
                              AGT GCTGGGATTACAG CAT
                              ||| |||||||||||| |||
                              TCA CGACCCTAATGTC GTA
                                _          C
GAM693  LOC92299 3' CTGTAATCCCAGCACT      68809     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM693  LOC92405 3' ATGTCTGTAATCCCAGCTACT 69192
                              AGTAGCTGGGATTACAGACAT
                              |||||||||||||||||||||
                              TCATCGACCCTAATGTCTGTA

GAM693  LOC92421 3' ATGCCTATAATCCCAGCACT  69212     A        C  A
                              AGT GCTGGGATTA AG CAT
                              ||| |||||||||| || |||
                              TCA CGACCCTAAT TC GTA
                                _        A  C
GAM693  LOC92465 5' ATGCCTGTAATCCCAGCACT  69402     A          A
                              AGT GCTGGGATTACAG CAT
                              ||| |||||||||||| |||
                              TCA CGACCCTAATGTC GTA
                                _          C
GAM693  LOC92465 3' ATGTCTGTAGTCCCAGCCACTC 69403   C   A
           A                   A AGT GCTGGGATTACAGACAT
                              | ||| ||||||||||||||||
                              A TCA CGACCCTGATGTCTGTA
                               C   C
GAM693  LOC92465 3' CTGTAATCCCAGCACT      69406     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM693  LOC92465 5' TGTAATCCCAGCTACTCA    69415    C
                              A AGTAGCTGGGATTACA
                              | ||||||||||||||||
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                                A TCATCGACCCTAATGT
                                 C
GAM693  LOC92466 3' ATGCCTGTAATCCCAGCACT  69422    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  LOC92482 3' CTGTAATCCCAGCACT     69488    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC92573 5' CTGTAATCCCAGCACT     69805    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC92573 5' TCTGTAATCCCAGCTTCT   69811    T
                                AG AGCTGGGATTACAGA
                                || |||||||||||||
                                TC TCGACCCTAATGTCT
                                 T
GAM693  LOC92661 5' ATGCCTATAATCCCAGC    70078        C  A
                                GCTGGGATTA AG CAT
                                |||||||||| || |||
                                CGACCCTAAT TC GTA
                                      A  C
GAM693  LOC92771 3' TGTAATCCCAGCTACTCA   53078   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM693  LOC93132 5' CTGTAATCCCAGCACT     71488    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM693  LOC93613 3' ATGCCTGTAATCCCAGCACT  72694    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM693  LOC93613 3' CTGTAATCCCAGCTATT    72698
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TTATCGACCCTAATGTC

GAM693  LOC96597 5' CTGTAATCCCAGCTACTCA  66913   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
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```
                                A TCATCGACCCTAATGTC
                                 C
GAM694  ADAT1   3'  GGCATGGTGGCGCACACCTGTA 23900        CA   G    A
                                TACAGGTG  CGT ATCAT CC
                                ||||||||  ||| ||||| ||
                                ATGTCCAC  GCG TGGTA GG
                                     AC   G    C
GAM694  AICDA   3'  GGTAGCAGGCACCTGTA     40331         AC  G
                                TACAGGTGC  GT ATC
                                |||||||||  || |||
                                ATGTCCACG  CG TGG
                                     GA  A
GAM694  ANKH    3'  GTAGCACATACCTGTA      53992        CAC   ATCA
                                TACAGGTG   GTG   TAC
                                ||||||||   |||   |||
                                ATGTCCAT   CAC   ATG
                                     A__   G___
GAM694  ANKH    3'  GTGGTGTGCATCTGTAGT    39063          GTG
                                ACTACAGGTGCAC   ATCAT
                                ||||||||||||   |||||
                                TGATGTCTACGTG   TGGTG
                                                ___
GAM694  ATM     3'  ATGGTGGCGGGCACCTGTA   56293         A   G
                                TACAGGTGC CGT ATCAT
                                ||||||||| ||| |||||
                                ATGTCCACG GCG TGGTA
                                     G   G
GAM694  ATM     3'  ATGGTGGCGGGCACCTGTAGT  3510          A   G
                                ACTACAGGTGC CGT ATCAT
                                |||||||||||| ||| |||||
                                TGATGTCCACG GCG TGGTA
                                      G   G
GAM694  BCAS1   3'  GGCATGGTGGCACACACCTGTA 13341         CAC  G    A
          GT                      ACTACAGGTG   GT ATCAT CC
                                ||||||||||   || ||||| ||
                                TGATGTCCAC   CG TGGTA GG
                                     ACA  G    C
GAM694  CASP6   3'  GGTTACTCACACCTGTA     6911         CAC
                                TACAGGTG   GTGATC
                                ||||||||   ||||||
                                ATGTCCAC   CATTGG
                                     ACT
GAM694  CASP6   3'  GGTTACTCACACCTGTA     52204        CAC
                                TACAGGTG   GTGATC
                                ||||||||   ||||||
                                ATGTCCAC   CATTGG
                                     ACT
GAM694  COL16A1 3'  GGTACAGGGGCATATACCTGTA 8502         CAC   AT A__
                                TACAGGTG   GTG  C   TACC
                                ||||||||   |||  |   ||||
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                                ATGTCCAT  TAC  G  ATGG
                                    A__  GG GAC
GAM694  CRACC   3'  GGCATGGTGGCTCACACCTGTA 41008      CAC  G   A
                                TACAGGTG  GT ATCAT CC
                                ||||||||  || ||||| ||
                                ATGTCCAC  CG TGGTA GG
                                    ACT  G   C
GAM694  CST2    3'  GGTCTCCCCATGCACCTGCAG  7172    A     CGT___
                                CT CAGGTGCA    GATC
                                || ||||||||    ||||
                                GA GTCCACGT    CTGG
                                 C      ACCCCT
GAM694  CTMP    3'  GGCATGGTGGCGTACGCCTGTA 53879       C   G   A
          GT                     ACTACAGGTG ACGT ATCAT CC
                                ||||||||||  |||| ||||| ||
                                TGATGTCCGC TGCG TGGTA GG
                                    A   G   C
GAM694  CYP7A1  3'  GGTAGCAGGCACCTGTAGT   5763         AC  G
                                ACTACAGGTGC  GT ATC
                                ||||||||||  || |||
                                TGATGTCCACG  CG TGG
                                     GA  A
GAM694  DGKB    3'  GTATAAATGGGTACCTGTA   92533       A  GATC
                                TACAGGTGC CGT   ATAC
                                |||||||| |||   ||||
                                ATGTCCATG GTA   TATG
                                    G  AA__
GAM694  DHFR    3'  GGCACAGTGGCTCACACCTGTA 5808       _____  _  A
                                TACAGGTG    CAC GTG TC
                                ||||||||    ||| ||| ||
                                ATGTCCAC    GTG CAC GG
                                    ACTCG  A  _
GAM694  DHFR    3'  GGCATTGTGGCGCACACCTGTA 5809       CA  G  C  A
                                TACAGGTG  CGT AT AT CC
                                ||||||||  ||| || || ||
                                ATGTCCAC  GCG TG TA GG
                                    AC  G  T  C
GAM694  EGFL4   3'  GGCATGGTGGCACACACTTGTA 61816       CAC  G   A
          GT                     ACTACAGGTG  GT ATCAT CC
                                ||||||||||  || ||||| ||
                                TGATGTTCAC  CG TGGTA GG
                                     ACA  G   C
GAM694  EHHADH  3'  GGCACAGTGGCTCACACCTGTA 8751       _____  _  A
                                TACAGGTG    CAC GTG TC
                                ||||||||    ||| ||| ||
                                ATGTCCAC    GTG CAC GG
                                    ACTCG  A  _
GAM694  GALNT7  3'  GGCATGGTGGCGCATACCTGTA 54019      CA  G   A
                                TACAGGTG  CGT ATCAT CC
                                ||||||||  ||| ||||| ||
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                                ATGTCCAT  GCG TGGTA GG
                                    AC  G    C
GAM694  GRM6    3'  GGCATGGTGGCTCACACCTGTA 5937        CAC  G    A
                                TACAGGTG  GT ATCAT CC
                                ||||||||  || ||||| ||
                                ATGTCCAC  CG TGGTA GG
                                    ACT  G    C
GAM694  IL10    3'  GGCATGGTGGCGCGCACCTGTA 5128        A  G    A
                                TACAGGTGC CGT ATCAT CC
                                ||||||||| ||| ||||| ||
                                ATGTCCACG GCG TGGTA GG
                                     C  G    C
GAM694  IL1R1   3'  GGCATGGTGGCACACGCCTGTA 6062        CAC  G    A
                                TACAGGTG  GT ATCAT CC
                                ||||||||  || ||||| ||
                                ATGTCCGC  CG TGGTA GG
                                    ACA  G    C
GAM694  KLRG1   3'  GGCATGCTGGTGTGTACCTGTA 19438          TGAT  A
          GT                      ACTACAGGTGCACG   CAT CC
                                ||||||||||||||   ||| ||
                                TGATGTCCATGTGT   GTA GG
                                       GGTC  C
GAM694  LZTS1   3'  GGCATGATCATAGCTCACTGCA 40694   A  GT_ AC     A
          G                      CT CAG  GC  GTGATCAT CC
                                || |||  ||  |||||||| ||
                                GA GTC  CG  TACTAGTA GG
                                 C  ACT  A_      C
GAM694  MHC2TA  3'  GGTATGATCACGGCTCACTGCA 4181    A  GT_ A
          G                      CT CAG  GC CGTGATCATACC
                                || |||  || ||||||||||||
                                GA GTC  CG GCACTAGTATGG
                                 C  ACT  _
GAM694  MSH3    3'  GGCATGGTGGCGCACACCTGTA 10120        CA  G    A
          GT                      ACTACAGGTG  CGT ATCAT CC
                                ||||||||||  ||| ||||| ||
                                TGATGTCCAC  GCG TGGTA GG
                                      AC  G    C
GAM694  MSL3L1  3'  GATGATGTGCACCTATAGT   54367     C       G
                                ACTA AGGTGCACGT ATC
                                |||| |||||||||| |||
                                TGAT TCCACGTGTA TAG
                                  A        G
GAM694  MTNR1A  3'  GGCATGGTGCACACGCCTGTA  19892       CAC  _    A
                                TACAGGTG  GTG ATCAT CC
                                ||||||||  ||| ||||| ||
                                ATGTCCGC  CAC TGGTA GG
                                    A__  G    C
GAM694  OASL    3'  GTAGCTCACACCTGTA     13580       GCAC   TCA
                                TACAGGT   GTGA  TAC
                                |||||||   ||||  |||
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                                ATGTCCA   CACT   ATG
                                   ____   CG_
GAM694  P2RX7    3' ATGGTGGCATGCACCTG    10372       C  G
                                CAGGTGCA GT ATCAT
                                |||||||| || |||||
                                GTCCACGT CG TGGTA
                                    A  G
GAM694  PAICS    3' GATGACAGGCACCTGTA    21255       AC  G
                                TACAGGTGC  GT ATC
                                |||||||||  || |||
                                ATGTCCACG  CA TAG
                                     GA  G
GAM694  PCDHGA1  3' ATGATCACCATCCCCATGGT  38281    CA  TGCAC
                                ACTA  GG   GTGATCAT
                                ||||  ||   ||||||||
                                TGGT  CC   CACTAGTA
                                  AC  CTAC_
GAM694  PCDHGA10 3' ATGATCACCATCCCCATGGT  38288    CA  TGCAC
                                ACTA  GG   GTGATCAT
                                ||||  ||   ||||||||
                                TGGT  CC   CACTAGTA
                                  AC  CTAC_
GAM694  PCDHGA11 3' ATGATCACCATCCCCATGGT  38295    CA  TGCAC
                                ACTA  GG   GTGATCAT
                                ||||  ||   ||||||||
                                TGGT  CC   CACTAGTA
                                  AC  CTAC_
GAM694  PCDHGA11 3' ATGATCACCATCCCCATGGT  49459    CA  TGCAC
                                ACTA  GG   GTGATCAT
                                ||||  ||   ||||||||
                                TGGT  CC   CACTAGTA
                                  AC  CTAC_
GAM694  PCDHGA12 3' ATGATCACCATCCCCATGGT  13591    CA  TGCAC
                                ACTA  GG   GTGATCAT
                                ||||  ||   ||||||||
                                TGGT  CC   CACTAGTA
                                  AC  CTAC_
GAM694  PCDHGA2  3' ATGATCACCATCCCCATGGT  38303    CA  TGCAC
                                ACTA  GG   GTGATCAT
                                ||||  ||   ||||||||
                                TGGT  CC   CACTAGTA
                                  AC  CTAC_
GAM694  PCDHGA3  3' ATGATCACCATCCCCATGGT  38312    CA  TGCAC
                                ACTA  GG   GTGATCAT
                                ||||  ||   ||||||||
                                TGGT  CC   CACTAGTA
                                  AC  CTAC_
GAM694  PCDHGA4  3' ATGATCACCATCCCCATGGT  38319    CA  TGCAC
                                ACTA  GG   GTGATCAT
                                ||||  ||   ||||||||
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                                TGGT CC   CACTAGTA
                                  AC CTAC_
GAM694  PCDHGA5  3' ATGATCACCATCCCCATGGT 38326    CA TGCAC
                                ACTA GG   GTGATCAT
                                |||| ||   ||||||||
                                TGGT CC   CACTAGTA
                                  AC CTAC_
GAM694  PCDHGA6  3' ATGATCACCATCCCCATGGT 38333    CA TGCAC
                                ACTA GG   GTGATCAT
                                |||| ||   ||||||||
                                TGGT CC   CACTAGTA
                                  AC CTAC_
GAM694  PCDHGA7  3' ATGATCACCATCCCCATGGT 38340    CA TGCAC
                                ACTA GG   GTGATCAT
                                |||| ||   ||||||||
                                TGGT CC   CACTAGTA
                                  AC CTAC_
GAM694  PCDHGA8  3' ATGATCACCATCCCCATGGT 49451    CA TGCAC
                                ACTA GG   GTGATCAT
                                |||| ||   ||||||||
                                TGGT CC   CACTAGTA
                                  AC CTAC_
GAM694  PCDHGA9  3' ATGATCACCATCCCCATGGT 38347    CA TGCAC
                                ACTA GG   GTGATCAT
                                |||| ||   ||||||||
                                TGGT CC   CACTAGTA
                                  AC CTAC_
GAM694  PCDHGB1  3' ATGATCACCATCCCCATGGT 38354    CA TGCAC
                                ACTA GG   GTGATCAT
                                |||| ||   ||||||||
                                TGGT CC   CACTAGTA
                                  AC CTAC_
GAM694  PCDHGB2  3' ATGATCACCATCCCCATGGT 38361    CA TGCAC
                                ACTA GG   GTGATCAT
                                |||| ||   ||||||||
                                TGGT CC   CACTAGTA
                                  AC CTAC_
GAM694  PCDHGB3  3' ATGATCACCATCCCCATGGT 38368    CA TGCAC
                                ACTA GG   GTGATCAT
                                |||| ||   ||||||||
                                TGGT CC   CACTAGTA
                                  AC CTAC_
GAM694  PCDHGB4  3' ATGATCACCATCCCCATGGT 13598    CA TGCAC
                                ACTA GG   GTGATCAT
                                |||| ||   ||||||||
                                TGGT CC   CACTAGTA
                                  AC CTAC_
GAM694  PCDHGB5  3' ATGATCACCATCCCCATGGT 38375    CA TGCAC
                                ACTA GG   GTGATCAT
                                |||| ||   ||||||||
```

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                                TGGT CC   CACTAGTA
                                  AC CTAC_
GAM694  PCDHGB6  3' ATGATCACCATCCCCATGGT 38382    CA TGCAC
                                ACTA GG   GTGATCAT
                                |||| ||   ||||||||
                                TGGT CC   CACTAGTA
                                  AC CTAC_
GAM694  PCDHGB7  3' ATGATCACCATCCCCATGGT 38389    CA TGCAC
                                ACTA GG   GTGATCAT
                                |||| ||   ||||||||
                                TGGT CC   CACTAGTA
                                  AC CTAC_
GAM694  PCDHGC3  3' ATGATCACCATCCCCATGGT 10452    CA TGCAC
                                ACTA GG   GTGATCAT
                                |||| ||   ||||||||
                                TGGT CC   CACTAGTA
                                  AC CTAC_
GAM694  PCDHGC3  3' ATGATCACCATCCCCATGGT 50515    CA TGCAC
                                ACTA GG   GTGATCAT
                                |||| ||   ||||||||
                                TGGT CC   CACTAGTA
                                  AC CTAC_
GAM694  PCDHGC4  3' ATGATCACCATCCCCATGGT 38396    CA TGCAC
                                ACTA GG   GTGATCAT
                                |||| ||   ||||||||
                                TGGT CC   CACTAGTA
                                  AC CTAC_
GAM694  PCDHGC5  3' ATGATCACCATCCCCATGGT 38403    CA TGCAC
                                ACTA GG   GTGATCAT
                                |||| ||   ||||||||
                                TGGT CC   CACTAGTA
                                  AC CTAC_
GAM694  PKD2     3' GGTATGACGGCTCACGCCTGTA 60095      CAC GA
                                TACAGGTG  GT TCATACC
                                |||||||| || |||||||
                                ATGTCCGC  CG AGTATGG
                                    ACT GC
GAM694  POLH     3' GGTACAATGGCTCACGCCTGTA 21465      CAC G CA
                                TACAGGTG  GT AT TACC
                                |||||||| || || ||||
                                ATGTCCGC  CG TA ATGG
                                    ACT G AC
GAM694  POLK     3' ATGGCTCACACCTGTA    32565      GCAC _
                                TACAGGT  GTGA TCAT
                                |||||||  |||| ||||
                                ATGTCCA  CACT GGTA
                                   ____  C
GAM694  PTAFR    3' GGCATGGTGGCACACGCCTGTA 6298       CAC G   A
          GT                  ACTACAGGTG  GT ATCAT CC
                              |||||||||| || ||||| ||
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                                TGATGTCCGC   CG TGGTA GG
                                     ACA  G    C
GAM694  RABIF    3'  GGCATAGTGGTGTATACCTGTA 11207         C   TG  C  A
           GT                     ACTACAGGTG ACG  AT AT CC
                                  |||||||||| |||  || || ||
                                TGATGTCCAT TGT  TG TA GG
                                     A   GG  A  C
GAM694  RBBP9    3'  GGCATGGTGGTGCACACCTGTA 70135         CA  TG    A
           GT                     ACTACAGGTG  CG  ATCAT CC
                                  ||||||||||  ||  ||||| ||
                                TGATGTCCAC  GT  TGGTA GG
                                     AC  GG    C
GAM694  RBM3     3'  GGCATGGTGGTGTACGCCTGTA 70489        C   TG    A
                                TACAGGTG ACG  ATCAT CC
                                |||||||| |||  ||||| ||
                                ATGTCCGC TGT  TGGTA GG
                                     A   GG    C
GAM694  SCN2B    3'  GGCACAGTGGCTACGCCTGTA  15942        ____  _  A
                                TACAGGTG    CAC GTG TC
                                ||||||||    ||| ||| ||
                                ATGTCCGC    GTG CAC GG
                                     ATCG   A  _
GAM694  SIM2     3'  GGCATGGTGGTGAGCACCTGTA 23785         A  TG    A
                                TACAGGTGC CG  ATCAT CC
                                ||||||||| ||  ||||| ||
                                ATGTCCACG GT  TGGTA GG
                                     A  GG    C
GAM694  SRGAP1   3'  GGCATGGTGGTGCACACCTGTA 72264        CA  TG    A
                                TACAGGTG  CG  ATCAT CC
                                ||||||||  ||  ||||| ||
                                ATGTCCAC  GT  TGGTA GG
                                     AC  GG    C
GAM694  STARD4   3'  GGTATGATCACAGCTCACTGCA 57514    A  GT_  AC
           G                     CT CAG   GC  GTGATCATACC
                                 || |||   ||  ||||||||||
                                GA GTC   CG  CACTAGTATGG
                                 C   ACT  A_
GAM694  STAT6    3'  CATGCCTGCACCTGCAG     12020    A      __
                                CT CAGGTGCA  CGTG
                                || ||||||||  ||||
                                GA GTCCACGT  GTAC
                                 C       CC
GAM694  TM7SF3   3'  ATGGTGGCTCACACCTGTA    59665        CAC  G
                                TACAGGTG   GT ATCAT
                                ||||||||   || |||||
                                ATGTCCAC   CG TGGTA
                                     ACT  G
GAM694  TNFRSF1B 3'  GTGACGTGCACCTGTA      6525            G
                                TACAGGTGCACGT AT
                                |||||||||||| ||
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                                ATGTCCACGTGCA TG
                                      G
GAM694  VHL      3'  ATGGCGGCACACATCTGTA   5061       ____   A  G
                                TACAG   GTGC CGT AT
                                |||||   |||| ||| ||
                                ATGTC   CACG GCG TA
                                   TACA   _  G
GAM694  WSX1     3'  GGCATGATGGCACACACCTGTA 16736        CAC  G    A
           GT                    ACTACAGGTG   GT ATCAT CC
                                |||||||||||   || ||||| ||
                                TGATGTCCAC   CG TAGTA GG
                                      ACA  G    C
GAM694  ZNF36    3'  GGCATGATGGTGGGCACCTGTA 93964        A  TG    A
                                TACAGGTGC CG  ATCAT CC
                                |||||||||| ||  ||||| ||
                                ATGTCCACG GT  TAGTA GG
                                      G  GG    C
GAM694  20D7-FC4 5'  GGTATGATCACAGCATC     60907      AC
                                GGTGC  GTGATCATACC
                                |||||  ||||||||||||
                                CTACG  CACTAGTATGG
                                   A_
GAM694  AF020591 3'  ATGGTGGCGCATACCTGTAGT  27136         CA   G
                                ACTACAGGTG  CGT ATCAT
                                ||||||||||  ||| |||||
                                TGATGTCCAT  GCG TGGTA
                                      AC   G
GAM694  ANKRD6   3'  GGCATGATCACACCTCACTGCA 30086    A  GTGCAC      A
           G                     CT CAG     GTGATCAT CC
                                || |||     |||||||| ||
                                GA GTC     CACTAGTA GG
                                 C  ACTCCA       C
GAM694  AP1GBP1  3'  GGCATGATGGTGTGCACCTGTA 54533           TG    A
           GT                    ACTACAGGTGCACG  ATCAT CC
                                ||||||||||||||  ||||| ||
                                TGATGTCCACGTGT  TAGTA GG
                                        GG    C
GAM694  BTN3A2   3'  GGCATGGTGACGGGCACCTGTA 22912          A  G    A
           GT                    ACTACAGGTGC CGT ATCAT CC
                                |||||||||||| ||| ||||| ||
                                TGATGTCCACG GCA TGGTA GG
                                      G  G    C
GAM694  C20orf142 3' GGCATGGTGGCTCACACCTGTA 74780        CAC  G    A
                                TACAGGTG   GT ATCAT CC
                                ||||||||   || ||||| ||
                                ATGTCCAC   CG TGGTA GG
                                     ACT  G    C
GAM694  C21orf108 3' GGCATGGTAGCGCACACCTGTA 88723        CA   G    A
                                TACAGGTG  CGT ATCAT CC
                                ||||||||  ||| ||||| ||
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                                ATGTCCAC  GCG TGGTA GG
                                    AC  A    C
GAM694  C6orf5   3'  GGCATGGTGGTGTGCACCTGTA 31357          TG    A
                                TACAGGTGCACG  ATCAT CC
                                ||||||||||||  |||||  ||
                                ATGTCCACGTGT  TGGTA GG
                                      GG    C
GAM694  C8orf2   3'  GGCATGGTGTCAGGCACCTGTA 23166        ACGTG    A
                                TACAGGTGC    ATCAT CC
                                |||||||||    |||||  ||
                                ATGTCCACG    TGGTA GG
                                    GACTG    C
GAM694  CAMKK1   3'  GGTACATGCATCTGTA     50175         C  G
                                TACAGGTGCA GT ATC
                                ||||||||||  ||  |||
                                ATGTCTACGT CA TGG
                                     A  _
GAM694  CCR6     3'  GGCATGGTGGCTCACACCTGTA 48587       CAC  G    A
                                TACAGGTG   GT ATCAT CC
                                ||||||||   ||  |||||  ||
                                ATGTCCAC   CG TGGTA GG
                                    ACT  G    C
GAM694  CCR6     3'  GGCATGGTGGCTCACACCTGTA 15171       CAC  G    A
                                TACAGGTG   GT ATCAT CC
                                ||||||||   ||  |||||  ||
                                ATGTCCAC   CG TGGTA GG
                                    ACT  G    C
GAM694  CPR2     3'  GGCATGATGACAGGCACCTGTA 48099        AC  G    A
                                TACAGGTGC  GT ATCAT CC
                                |||||||||  ||  |||||  ||
                                ATGTCCACG  CA TAGTA GG
                                    GA  G    C
GAM694  CRYGN    3'  GACATGTAAATGCACCTG    58558        ____    A
                                CAGGTGC    ACGTG TC
                                |||||||    |||||  ||
                                GTCCACG    TGTAC AG
                                   TAAA    _
GAM694  D21S2056E 3'  GGCACAGTGGCTCACACCTGTA 13472       _____  _  A
                                TACAGGTG    CAC GTG TC
                                ||||||||    |||  |||  ||
                                ATGTCCAC    GTG CAC GG
                                    ACTCG   A  _
GAM694  DKFZP434C1715 3'  ATGGCACACACCTGTAGT    86144         CAC   A
                                ACTACAGGTG   GTG TCAT
                                ||||||||||   |||  ||||
                                TGATGTCCAC   CAC GGTA
                                     A__   _
GAM694  DKFZP434L0718 3'  GGTTACTACACGTGCACCTGTA 49549            ATCAT
          G                      CTACAGGTGCACGTG    ACC
                                ||||||||||||||||    |||
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                                GATGTCCACGTGCAC    TGG
                                      ATCAT
GAM694  DKFZp547I094 3'  GGTAGCGCACACCTGTAGT   49643         CA  G
                                ACTACAGGTG  CGT ATC
                                ||||||||||  ||| |||
                                TGATGTCCAC  GCG TGG
                                     AC   A
GAM694  DKFZP564D166 3'  GTGATTGTGCACCTGTG    47680         GT
                                TACAGGTGCAC  GATCAT
                                ||||||||||  ||||||
                                GTGTCCACGTG  TTAGTG
                                          __
GAM694  DKFZP564I122 3'  TGTGGCGCTCACCTGTA    63178        CAC  A
                                TACAGGTG   GTG TCATA
                                ||||||||   ||| |||||
                                ATGTCCAC   CGC GGTGT
                                     T__  _
GAM694  DKFZP564K0322 3'  GGCATGATCATAACTCACTGCA 49362    A  GTGCAC      A
          G                      CT CAG     GTGATCAT CC
                                || |||     |||||||| ||
                                GA GTC     TACTAGTA GG
                                 C  ACTCAA       C
GAM694  DKFZP564M182 3'  GGCATGGTGGGAGGCACCTGTA 78038         ACGTG    A
                                TACAGGTGC    ATCAT CC
                                |||||||||    ||||| ||
                                ATGTCCACG    TGGTA GG
                                     GAGGG    C
GAM694  DKFZP564M182 3'  GGCATGGTGGTGGACACCTGTA 78039        CA  TG    A
                                TACAGGTG  CG  ATCAT CC
                                ||||||||  ||  ||||| ||
                                ATGTCCAC  GT  TGGTA GG
                                     AG  GG    C
GAM694  DKFZP761G1913 3'  GGTATGGTGGTGAACACCTGTA 48918        CA  TG
                                TACAGGTG  CG  ATCATACC
                                ||||||||  ||  ||||||||
                                ATGTCCAC  GT  TGGTATGG
                                     AA  GG
GAM694  FBXO27   3'  GGTACAGTAGTACACACCTGTA 74514          CACGTG  CA
          GT                     ACTACAGGTG     AT  TACC
                                ||||||||||     ||  ||||
                                TGATGTCCAC     TG  ATGG
                                     ACATGA  AC
GAM694  FKSG17   3'  GGCATGGTGGTGCACACCTGTA 49331        CA  TG    A
                                TACAGGTG  CG  ATCAT CC
                                ||||||||  ||  ||||| ||
                                ATGTCCAC  GT  TGGTA GG
                                     AC  GG    C
GAM694  FLJ10043  3'  GGCATGGTAGTGCACGCCTGTA 35762        __   GTG    A
                                TACAGGT  GCAC   ATCAT CC
                                |||||||  ||||   ||||| ||
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                                ATGTCCG  CGTG   TGGTA GG
                                    CA   A__    C
GAM694  FLJ11151  3'  GGCATGCTGGTGCACACCTGTA 67881       __   GTGAT   A
                                TACAGGT  GCAC    CAT CC
                                |||||||  ||||    ||| ||
                                ATGTCCA  CGTG    GTA GG
                                    CA   GTC__   C
GAM694  FLJ11703  5'  GACACGTGCACCTGCAG    46383    A        A
                                CT CAGGTGCACGTG TC
                                || ||||||||||| ||
                                GA GTCCACGTGCAC AG
                                 C        _
GAM694  FLJ11726  3'  GGCACAGTGGCTCACACCTGTA 46416       _____  _  A
                                TACAGGTG    CAC GTG TC
                                ||||||||    ||| ||| ||
                                ATGTCCAC    GTG CAC GG
                                     ACTCG   A  _
GAM694  FLJ11996  3'  GGTGACATGCACCTGTA    46443         C  G
                                TACAGGTGCA GT ATC
                                |||||||||| || |||
                                ATGTCCACGT CA TGG
                                      A  G
GAM694  FLJ11996  3'  GTGGCTCACACCTGTA     46445       GCAC   _
                                TACAGGT   GTGA TCAT
                                |||||||   |||| ||||
                                ATGTCCA   CACT GGTG
                                    ____   C
GAM694  FLJ12409  3'  ATGGTGGCAGACACCTGTAGT  47042         CAC  G
                                ACTACAGGTG   GT ATCAT
                                ||||||||||   || |||||
                                TGATGTCCAC   CG TGGTA
                                      AGA  G
GAM694  FLJ12934  3'  GTATGATCAGTTAACCT    43201      GC  G
                                AGGT  AC TGATCATAC
                                ||||  || |||||||||
                                TCCA  TG ACTAGTATG
                                  AT  _
GAM694  FLJ13330  3'  GTGGCTCACACCTGTA     46978       GCAC   _
                                TACAGGT   GTGA TCAT
                                |||||||   |||| ||||
                                ATGTCCA   CACT GGTG
                                    ____   C
GAM694  FLJ13448  3'  GGCACAGTGGCTCACACCTGTA 47138       _____  _  A
                                TACAGGTG    CAC GTG TC
                                ||||||||    ||| ||| ||
                                ATGTCCAC    GTG CAC GG
                                     ACTCG   A  _
GAM694  FLJ13614  3'  GGCACAGTGGCTCACACCTGTA 57453       _____  _  A
                                TACAGGTG    CAC GTG TC
                                ||||||||    ||| ||| ||
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                                ATGTCCAC    GTG CAC GG
                                    ACTCG   A  _
GAM694  FLJ13769  3' GGTAGTGGCATGCGCCTGTA   46620         C  G  CA
                                TACAGGTGCA GT AT  TACC
                                |||||||||| || ||  ||||
                                ATGTCCGCGT CG TG  ATGG
                                    A  G  __
GAM694  FLJ13984  3' GGCATGGTGGCACACACCTGTG 45451         CAC  G    A
          GT                  ACTACAGGTG   GT ATCAT CC
                              |||||||||   || ||||| ||
                              TGGTGTCCAC   CG TGGTA GG
                                   ACA  G    C
GAM694  FLJ14251  3' GGCACAGTGGCTCACACCTGTA 45975        _____  _  A
                              TACAGGTG    CAC GTG TC
                              ||||||||    ||| ||| ||
                              ATGTCCAC    GTG CAC GG
                                   ACTCG   A  _
GAM694  FLJ20006  3' GGTAGCGCACGCCTGTA    34326        CA   G
                              TACAGGTG  CGT ATC
                              ||||||||  ||| |||
                              ATGTCCGC  GCG TGG
                                   AC   A
GAM694  FLJ20013  3' GGCACAGTGGCTCACACCTGTA 34334        _____  _  A
                              TACAGGTG    CAC GTG TC
                              ||||||||    ||| ||| ||
                              ATGTCCAC    GTG CAC GG
                                   ACTCG   A  _
GAM694  FLJ20013  3' GGCATGGTGGCACACACCTGTA 34335         CAC  G    A
          GT                  ACTACAGGTG   GT ATCAT CC
                              |||||||||   || ||||| ||
                              TGATGTCCAC   CG TGGTA GG
                                   ACA  G    C
GAM694  FLJ20139  3' GGCATGGTGGCATGCACTTGTA 34627          C  G    A
          GT                  ACTACAGGTGCA GT ATCAT CC
                              |||||||||||| || ||||| ||
                              TGATGTTCACGT CG TGGTA GG
                                    A  G    C
GAM694  FLJ20139  3' GGTGACTCGCACCTGTA    34628         AC  G
                              TACAGGTGC  GT ATC
                              |||||||||  || |||
                              ATGTCCACG  CA TGG
                                   CT  G
GAM694  FLJ20147  3' ATGATCATAGCTCACTGCAG  34635    A  GT_ AC
                              CT CAG   GC  GTGATCAT
                              || |||   ||  ||||||||
                              GA GTC   CG  TACTAGTA
                               C   ACT  A_
GAM694  FLJ20280  3' GGCATGGTGGCTCACACCTGTA 34851        CAC  G    A
                              TACAGGTG   GT ATCAT CC
                              ||||||||   || ||||| ||
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                                ATGTCCAC   CG TGGTA GG
                                    ACT  G    C
GAM694  FLJ20671  3'  GGCATGGTGGTGTGCACCTGTA 35529          TG    A
            GT                    ACTACAGGTGCACG  ATCAT CC
                                  ||||||||||||||  ||||| ||
                                  TGATGTCCACGTGT  TGGTA GG
                                        GG    C
GAM694  FLJ21551  3'  GGCATGGTGGCATGCGCCTGTA 45632        C  G    A
                                  TACAGGTGCA GT ATCAT CC
                                  |||||||||| || ||||| ||
                                  ATGTCCGCGT CG TGGTA GG
                                      A  G    C
GAM694  FLJ22814  3'  GGCATGATGGCAGGCGCCTGTA 46178        AC  G    A
            GT                    ACTACAGGTGC  GT ATCAT CC
                                  ||||||||||  || ||||| ||
                                  TGATGTCCGCG  CG TAGTA GG
                                      GA  G    C
GAM694  FLJ23040  3'  GGCATGGTGGCGGGCACCTGTA 47199        A   G    A
            GT                    ACTACAGGTGC CGT ATCAT CC
                                  |||||||||| ||| ||||| ||
                                  TGATGTCCACG GCG TGGTA GG
                                      G   G    C
GAM694  FLJ31168  3'  GGCATGGTGGCTCACACCTGTA 58506       CAC  G    A
                                  TACAGGTG   GT ATCAT CC
                                  ||||||||   || ||||| ||
                                  ATGTCCAC   CG TGGTA GG
                                      ACT  G    C
GAM694  FLJ31168  3'  GGCATGGTGTTGTGCACCT   58507        TG    A
                                  AGGTGCACG  ATCAT CC
                                  |||||||||  ||||| ||
                                  TCCACGTGT  TGGTA GG
                                      TG    C
GAM694  FLJ32915  5'  GGCATGGTGGCACGCGCCTGTA 58791        AC  G    A
                                  TACAGGTGC  GT ATCAT CC
                                  |||||||||  || ||||| ||
                                  ATGTCCGCG  CG TGGTA GG
                                      CA  G    C
GAM694  GALNT6    3'  GGCACAGTGGCTCACACCTGTA 23293        _____  _  A
                                  TACAGGTG    CAC GTG TC
                                  ||||||||    ||| ||| ||
                                  ATGTCCAC    GTG CAC GG
                                      ACTCG   A  _
GAM694  GLTP      3'  GGCATGGTGGCGCACGCCTGTA 33162        CA   G    A
            GT                    ACTACAGGTG  CGT ATCAT CC
                                  ||||||||||  ||| ||||| ||
                                  TGATGTCCGC  GCG TGGTA GG
                                      AC   G    C
GAM694  HSPC031   3'  GGCACAGTGTCGCGCCTGTA   32253        _  ___  A
                                  TACAGGTGC AC   GTG TC
                                  |||||||||  ||   ||| ||
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                                ATGTCCGCG TG   CAC GG
                                     C  TGA   _
GAM694  IMPACT   3' GGCATGATCATGGCTCACTGCA 37393    A  GT_ A       A
           G                    CT CAG   GC CGTGATCAT CC
                                || |||   || ||||||||| ||
                                GA GTC   CG GTACTAGTA GG
                                 C   ACT  _       C
GAM694  KALI     3' GGCATGGTGGCTCACACCTGTA 53593        CAC  G    A
                                TACAGGTG   GT ATCAT CC
                                ||||||||   || ||||| ||
                                ATGTCCAC   CG TGGTA GG
                                     ACT  G    C
GAM694  KIAA0141 3' CATATTGACCTGTAGT      28731         G  C_
                                ACTACAGGT CA  GTG
                                ||||||||| ||  |||
                                TGATGTCCA GT  TAC
                                     _  TA
GAM694  KIAA0226 3' GGCACAGTGGCTCACACCTGTA 63519        _____  _  A
                                TACAGGTG    CAC GTG TC
                                ||||||||    ||| ||| ||
                                ATGTCCAC    GTG CAC GG
                                     ACTCG   A  _
GAM694  KIAA0475 3' GGTGGCATGCGCCTGTAGT   29503          C  G
                                ACTACAGGTGCA GT ATC
                                |||||||||||| || |||
                                TGATGTCCGCGT CG TGG
                                       A  G
GAM694  KIAA0514 3' GGCATGGTGGTGTGCATCTGTA 28088          TG    A
           G                    CTACAGGTGCACG  ATCAT CC
                                |||||||||||||  ||||| ||
                                GATGTCTACGTGT  TGGTA GG
                                       GG    C
GAM694  KIAA0565 3' GGCATGGTGGTGTGCGCCTGCA 66893    A        TG    A
           GT                     ACT CAGGTGCACG  ATCAT CC
                                ||| ||||||||||  ||||| ||
                                TGA GTCCGCGTGT  TGGTA GG
                                  C        GG    C
GAM694  KIAA0565 3' GTGGCACACACCTGTAGT    66894         CAC   A
                                ACTACAGGTG   GTG TCAT
                                |||||||||   ||| ||||
                                TGATGTCCAC   CAC GGTG
                                     A__  _
GAM694  KIAA0680 3' ATCATGACACCTGTA      28233        CA
                                TACAGGTG  CGTGAT
                                ||||||||  ||||||
                                ATGTCCAC  GTACTA
                                     A_
GAM694  KIAA0694 3' GGTAGCATACACCTGTAGT   72582         CAC  G
                                ACTACAGGTG   GT ATC
                                |||||||||   || |||
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                                TGATGTCCAC   CG TGG
                                     ATA  A
GAM694  KIAA0798 3' GGCATGGTGGCTTGCACCTGTA 27726         C  G    A
                                TACAGGTGCA GT ATCAT CC
                                |||||||||| || ||||| ||
                                ATGTCCACGT CG TGGTA GG
                                     T  G    C
GAM694  KIAA0889 3' GTGGTGGTCACCTGTAGT    31145         C  GTG
                                ACTACAGGTG AC   ATCAT
                                |||||||||| ||   |||||
                                TGATGTCCAC TG   TGGTG
                                     _  G__
GAM694  KIAA0912 3' ATCATGGCTCACACCTGTA   64407        CA___
                                TACAGGTG    CGTGAT
                                ||||||||    ||||||
                                ATGTCCAC    GTACTA
                                    ACTCG
GAM694  KIAA0930 3' ATGGTGGCAGGCACCTGTA   70539         AC  G
                                TACAGGTGC  GT ATCAT
                                |||||||||  || |||||
                                ATGTCCACG  CG TGGTA
                                     GA  G
GAM694  KIAA0953 3' GGCATGGTGACGTGCACCTGTG 66787            G    A
          GT                  ACTACAGGTGCACGT ATCAT CC
                              |||||||||||||| ||||| ||
                              TGGTGTCCACGTGCA TGGTA GG
                                     G    C
GAM694  KIAA0961 3' GGTCACATGCGCCTGTA     29739         C
                                TACAGGTGCA GTGATC
                                |||||||||| ||||||
                                ATGTCCGCGT CACTGG
                                     A
GAM694  KIAA0981 3' GGCATGGTGGCATATACCTGTA 61422        CAC  G    A
                                TACAGGTG   GT ATCAT CC
                                ||||||||   || ||||| ||
                                ATGTCCAT   CG TGGTA GG
                                    ATA  G    C
GAM694  KIAA1001 3' GGCATGGTGGCGCTCACCTGTA 30293        CA   G    A
                                TACAGGTG  CGT ATCAT CC
                                ||||||||  ||| ||||| ||
                                ATGTCCAC  GCG TGGTA GG
                                    TC   G    C
GAM694  KIAA1117 3' GTAGCTCACACCTGTA      61121       GCAC    TCA
                                TACAGGT    GTGA   TAC
                                |||||||    ||||   |||
                                ATGTCCA    CACT   ATG
                                    _____    CG_
GAM694  KIAA1143 3' GACACACACCTGTAGT      68679         CAC   A
                                ACTACAGGTG   GTG TC
                                ||||||||||   ||| ||
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                              TGATGTCCAC   CAC AG
                                   A__   _
GAM694  KIAA1257 3' GGCATGTTGTCGGGCACCTGTA 62752          A  TGAT   A
            GT                  ACTACAGGTGC CG    CAT CC
                                |||||||||| ||    ||| ||
                                TGATGTCCACG GC    GTA GG
                                     G  TGTT   C
GAM694  KIAA1320 5' ATGATCACAGCTCACTGTAG   69295       GT_  AC
                                CTACAG   GC  GTGATCAT
                                ||||||   ||  ||||||||
                                GATGTC   CG  CACTAGTA
                                   ACT  A_
GAM694  KIAA1364 3' GGCATGGTGGTGCACACCTGTA 63595        CA  TG    A
                                TACAGGTG  CG  ATCAT CC
                                ||||||||  ||  ||||| ||
                                ATGTCCAC  GT  TGGTA GG
                                     AC  GG    C
GAM694  KIAA1377 3' GGCATGGTGGCATGCACCTGTA 67176          C  G    A
            GT                  ACTACAGGTGCA GT ATCAT CC
                                |||||||||||| || ||||| ||
                                TGATGTCCACGT CG TGGTA GG
                                      A  G    C
GAM694  KIAA1456 3' GGTACGATGACTCACACCTGTA 67004        CAC  G   A
                                TACAGGTG   GT ATC TACC
                                ||||||||   || ||| ||||
                                ATGTCCAC   CA TAG ATGG
                                     ACT  G   C
GAM694  KIAA1456 5' GTGGCTTGCACCTGTA      67005          C  G
                                TACAGGTGCA GT AT
                                |||||||||| || ||
                                ATGTCCACGT CG TG
                                      T  G
GAM694  KIAA1559 3' GGCATGGTGGCACACACCTGTA 73069         CAC  G    A
            GT                  ACTACAGGTG   GT ATCAT CC
                                ||||||||||   || ||||| ||
                                TGATGTCCAC   CG TGGTA GG
                                     ACA  G    C
GAM694  KIAA1586 5' GGCATGGTGGCTCACACCTGTA 92333        CAC  G    A
                                TACAGGTG   GT ATCAT CC
                                ||||||||   || ||||| ||
                                ATGTCCAC   CG TGGTA GG
                                     ACT  G    C
GAM694  KIAA1649 5' GGCATGGTGGTACACGCCTGTA 50275         CACG G    A
            GT                  ACTACAGGTG    T ATCAT CC
                                ||||||||||    | ||||| ||
                                TGATGTCCGC    G TGGTA GG
                                     ACAT G    C
GAM694  KIAA1821 3' GGTATGATCATAGCTCACC    71792      CAC_
                                GGTG    GTGATCATACC
                                ||||    ||||||||||
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                                CCAC    TACTAGTATGG
                                  TCGA
GAM694  KIAA1841  3'  GGCATGGTGGCATACACCTGTA 80049         CAC  G    A
              GT                  ACTACAGGTG   GT ATCAT CC
                                  ||||||||||   || ||||| ||
                                  TGATGTCCAC   CG TGGTA GG
                                       ATA  G    C
GAM694  KIAA1871  3'  GGCATGGTGGGGCACGCCTGTA 61235         CACGTG    A
              GT                  ACTACAGGTG     ATCAT CC
                                  ||||||||||     ||||| ||
                                  TGATGTCCGC     TGGTA GG
                                       ACGGGG    C
GAM694  KIAA1941  3'  GGCATGGTGGCTCACACCTGTA 74841         CAC  G    A
                                  TACAGGTG   GT ATCAT CC
                                  ||||||||   || ||||| ||
                                  ATGTCCAC   CG TGGTA GG
                                       ACT  G    C
GAM694  KIAA1954  3'  GGTATGGTGTCTCACACCTGTA 77722         CACGTG
                                  TACAGGTG     ATCATACC
                                  ||||||||     ||||||||
                                  ATGTCCAC     TGGTATGG
                                       ACTCTG
GAM694  KIAA1979  3'  ATGGTGGCATGCGCCTGTA    88273         C  G
                                  TACAGGTGCA GT ATCAT
                                  |||||||||| || |||||
                                  ATGTCCGCGT CG TGGTA
                                       A  G
GAM694  KIAA1979  3'  GGCATGGCTCACGCCTGTA    88286       TGCA    _    A
                                  TACAGG    CGTGA TCAT CC
                                  ||||||    ||||| |||| ||
                                  ATGTCC    GCACT GGTA GG
                                       ____     C    C
GAM694  KREMEN    3'  GGCATGGTGGCACACACCTGTA 49408         CAC  G    A
                                  TACAGGTG   GT ATCAT CC
                                  ||||||||   || ||||| ||
                                  ATGTCCAC   CG TGGTA GG
                                       ACA  G    C
GAM694  MGC14407  3'  GGCACAGTGGCTCACACCTGTA 51879         _____  _   A
                                  TACAGGTG    CAC GTG TC
                                  ||||||||    ||| ||| ||
                                  ATGTCCAC    GTG CAC GG
                                       ACTCG   A  _
GAM694  MGC14817  3'  GGCATGGTGGCTCACACCTGTA 50337         CAC  G    A
                                  TACAGGTG   GT ATCAT CC
                                  ||||||||   || ||||| ||
                                  ATGTCCAC   CG TGGTA GG
                                       ACT  G    C
GAM694  MGC2562   3'  GGCATGGTAGCATGCGCCTGTA 50445          C  G    A
              GT                  ACTACAGGTGCA GT ATCAT CC
                                  |||||||||||| || ||||| ||
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                                TGATGTCCGCGT CG TGGTA GG
                                      A A    C
GAM694  MGC26641  3'  GGCATGGTGGCATGCACCTGTA 58658         C  G    A
                                TACAGGTGCA GT ATCAT CC
                                |||||||||| || ||||| ||
                                ATGTCCACGT CG TGGTA GG
                                      A  G    C
GAM694  MGC29891  3'  GTGGCACACGCCTGTAGT    58215         CAC   A
                                ACTACAGGTG   GTG TCAT
                                ||||||||||   ||| ||||
                                TGATGTCCGC   CAC GGTG
                                      A__  _
GAM694  MGC3079   3'  GGTGACTTGCACCTGTA     50953         C  G
                                TACAGGTGCA GT ATC
                                |||||||||| || |||
                                ATGTCCACGT CA TGG
                                      T  G
GAM694  MGC4400   3'  GGCACAGTGGCTCACACCTGTA 51054        _____  _  A
                                TACAGGTG    CAC GTG TC
                                ||||||||    ||| ||| ||
                                ATGTCCAC    GTG CAC GG
                                     ACTCG   A  _
GAM694  MT-ACT48  3'  ATGGTGGTGTGCACCTGTAGT  24687           TG
                                ACTACAGGTGCACG  ATCAT
                                ||||||||||||||  |||||
                                TGATGTCCACGTGT  TGGTA
                                       GG
GAM694  PILR(ALPHA) 3'  GGTACAGTGGCGCACACCTGTA 25548        CA   G  CA
                                TACAGGTG  CGT AT  TACC
                                ||||||||  ||| ||  ||||
                                ATGTCCAC  GCG TG  ATGG
                                     AC   G  AC
GAM694  PRC1      3'  GGCATGTATACCTGTA      14290        C    A
                                TACAGGTG ACGTG TC
                                |||||||| ||||| ||
                                ATGTCCAT TGTAC GG
                                     A    _
GAM694  PRDM14    3'  ATGACTCACGCCTGTA      44443       TGCA   _
                                TACAGG   CGTGA TCAT
                                ||||||   ||||| ||||
                                ATGTCC   GCACT AGTA
                                    ____    C
GAM694  PRO2893   3'  GGCATGGTAGCACACGCCTGTA 37803        CAC  G    A
                                TACAGGTG   GT ATCAT CC
                                ||||||||   || ||||| ||
                                ATGTCCGC   CG TGGTA GG
                                     ACA  A    C
GAM694  RFX4      3'  TGGCTCACACCTGTAGT     11320         GCAC   _
                                ACTACAGGT   GTGA TCA
                                |||||||||   |||| |||
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                                TGATGTCCA   CACT GGT
                                    ____    C
GAM694  RNAH    3'  TATGATCACATGTAGAAGTAG  61960     AGG   C
                                CTAC   TGCA GTGATCATA
                                ||||   |||| |||||||||
                                GATG   ATGT CACTAGTAT
                                  AAG   A
GAM694  RoXaN   3'  GACACTTGTGCACCCCAGT   46644     ACA     __  A
                                ACT   GGTGCAC  GTG TC
                                |||   |||||||  ||| ||
                                TGA   CCACGTG  CAC AG
                                  CC_     TT  _
GAM694  Rpo1-2  3'  GGCATGGTGCTGTGCATCTATA 49879     C       TG    A
          GT                      ACTA AGGTGCACG  ATCAT CC
                                |||| |||||||||  ||||| ||
                                TGAT TCTACGTGT  TGGTA GG
                                  A       CG    C
GAM694  Rpo1-2  3'  GGCATGGTGCTGTGCATCTATA 38705     C       TG    A
          GT                      ACTA AGGTGCACG  ATCAT CC
                                |||| |||||||||  ||||| ||
                                TGAT TCTACGTGT  TGGTA GG
                                  A       CG    C
GAM694  Rpo1-2  3'  GTGGCACACCCCTGTAGT    38708       TGCAC   A
                                ACTACAGG    GTG TCAT
                                ||||||||    ||| ||||
                                TGATGTCC    CAC GGTG
                                    CCA__   _
GAM694  SC65    3'  GGCATGGTGGCACACACCTGTA 21290       CAC  G    A
                                TACAGGTG   GT ATCAT CC
                                ||||||||   || ||||| ||
                                ATGTCCAC   CG TGGTA GG
                                    ACA  G    C
GAM694  SCN12A  3'  GGCATGGTTGCGTGCGCCTGTA 26224           TG    A
          GT                      ACTACAGGTGCACG  ATCAT CC
                                |||||||||||||  ||||| ||
                                TGATGTCCGCGTGC  TGGTA GG
                                      GT    C
GAM694  SEMA4G  3'  GTAACACACACCTGTA     35437       CAC   ATCA
                                TACAGGTG   GTG   TAC
                                ||||||||   |||   |||
                                ATGTCCAC   CAC   ATG
                                    A__   A___
GAM694  SEMA4G  3'  GTAACACACACCTGTA     94684       CAC   ATCA
                                TACAGGTG   GTG   TAC
                                ||||||||   |||   |||
                                ATGTCCAC   CAC   ATG
                                    A__   A___
GAM694  SIAT4A  3'  GTGGCACACACTTGTAG     11675        CAC   A
                                CTACAGGTG   GTG TCAT
                                |||||||||   ||| ||||
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```
                                GATGTTCAC   CAC GGTG
                                     A__  _
GAM694  SS18L1   3'  GGTATGGTGGTGCATACCTGTA 65347       __   GTG
                                TACAGGT  GCAC   ATCATACC
                                |||||||  ||||   ||||||||
                                ATGTCCA  CGTG   TGGTATGG
                                    TA   G__
GAM694  SYAP1    3'  GGCATGGTGGCAGGCACCTGTA 51404        AC  G    A
                                TACAGGTGC  GT ATCAT CC
                                |||||||||  || ||||| ||
                                ATGTCCACG  CG TGGTA GG
                                     GA  G    C
GAM694  WDR7     3'  ATGACGTGACACCTGTA     30956        _    G
                                TACAGGTG CACGT AT
                                |||||||| ||||| ||
                                ATGTCCAC GTGCA TA
                                     A    G
GAM694  ZAK      3'  GGCATGGTAGCACACACCTGTA 56130         CAC  G    A
           GT                     ACTACAGGTG   GT ATCAT CC
                                |||||||||||   || ||||| ||
                                TGATGTCCAC   CG TGGTA GG
                                     ACA  A    C
GAM694  ZIM3     3'  GGCATAGTTGTGGGCACCTGTA 53538         A  TG  C  A
                                TACAGGTGC CG  AT AT CC
                                |||||||||  ||  || || ||
                                ATGTCCACG GT  TG TA GG
                                     G  GT  A  C
GAM694  ZNF323   3'  TATGAAACCTGTAGT      48081         GCACGTGA
                                ACTACAGGT       TCATA
                                |||||||||       |||||
                                TGATGTCCA       AGTAT
                                     A________
GAM694  ZNF339   3'  GGCATGATCATGGCTCACTG   41123     GT_  A       A
                                CAG   GC CGTGATCAT CC
                                |||   || ||||||||| ||
                                GTC   CG GTACTAGTA GG
                                  ACT  _       C
GAM694  ZNF339   3'  GGCATGGTGGTGTGTACCTGTA 41124            TG    A
           GT                     ACTACAGGTGCACG  ATCAT CC
                                |||||||||||||  ||||| ||
                                TGATGTCCATGTGT  TGGTA GG
                                       GG    C
GAM694  LOC115129 5'  GGCATGGTGGCACACGCCTGTA 73238         CAC  G    A
                                TACAGGTG   GT ATCAT CC
                                ||||||||   || ||||| ||
                                ATGTCCGC   CG TGGTA GG
                                     ACA  G    C
GAM694  LOC115757 3'  ATGGTGGTGCATACCTGTAGT  73575         __   GTG
                                ACTACAGGT  GCAC   ATCAT
                                |||||||||  ||||   |||||
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                                TGATGTCCA  CGTG   TGGTA
                                     TA    G__
GAM694   LOC122970 3'  ATGGTACACACCTGTAGT    74176         CAC  G
                                ACTACAGGTG   GT ATCAT
                                ||||||||||   || |||||
                                TGATGTCCAC   CA TGGTA
                                     A__  _
GAM694   LOC122970 3'  GTACAGTGGCTCACACCTGTA  74185        CAC  G  CA
                                TACAGGTG   GT AT  TAC
                                ||||||||   || ||  |||
                                ATGTCCAC   CG TG  ATG
                                     ACT  G  AC
GAM694   LOC124602 3'  GGCACAGTGACTCACACCTGTA 74308         _____  _  A
                                TACAGGTG    CAC GTG TC
                                ||||||||    ||| ||| ||
                                ATGTCCAC    GTG CAC GG
                                     ACTCA   A  _
GAM694   LOC126669 3'  GGTGGCGGGCACCTGTAGT   75413          A   G
                                ACTACAGGTGC CGT ATC
                                |||||||||||| ||| |||
                                TGATGTCCACG GCG TGG
                                      G   G
GAM694   LOC127428 3'  TATGATGGCAGGCGCCTGTA   74673        AC  G
                                TACAGGTGC  GT ATCATA
                                |||||||||  || ||||||
                                ATGTCCGCG  CG TAGTAT
                                     GA  G
GAM694   LOC130589 3'  GTAGCACGCACCCGTAGT    57135      A    AC   ATCA
                                ACTAC GGTGC  GTG   TAC
                                ||||| |||||  |||   |||
                                TGATG CCACG  CAC   ATG
                                   C    __  G___
GAM694   LOC130951 3'  GTGGCTCACACCTGTA      57147        GCAC   _
                                TACAGGT   GTGA TCAT
                                |||||||   |||| ||||
                                ATGTCCA   CACT GGTG
                                     ____   C
GAM694   LOC144583 3'  CACAGTGGCTCACACCTGTA   76893         _____  _
                                TACAGGTG    CAC GTG
                                ||||||||    ||| |||
                                ATGTCCAC    GTG CAC
                                     ACTCG   A
GAM694   LOC144817 3'  GGCATGGTGGCGCACACCTGTA 76971         CA   G    A
                                TACAGGTG  CGT ATCAT CC
                                ||||||||  ||| ||||| ||
                                ATGTCCAC  GCG TGGTA GG
                                     AC   G    C
GAM694   LOC145082 5'  GTGACACGCACCTGTAGT    83247          AC   A
                                ACTACAGGTGC  GTG TCAT
                                ||||||||||  ||| ||||
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                                TGATGTCCACG  CAC AGTG
                                   __  _
GAM694  LOC145134 5'  GGCATGGCTTAGCACACCTGTG 83256       CAC  GA__   A
                                TACAGGTG   GT    TCAT CC
                                ||||||||   ||    |||| ||
                                GTGTCCAC   CG    GGTA GG
                                    A__  ATTC    C
GAM694  LOC145453 3'  GGCATGGTGGCAGTCACCTGTA 77144       C  _  G    A
                                TACAGGTG AC GT ATCAT CC
                                |||||||| || || ||||| ||
                                ATGTCCAC TG CG TGGTA GG
                                    _  A  G    C
GAM694  LOC145955 3'  GGCATGGCAACGTGCACCTGTA 83595           GA   A
          GT                      ACTACAGGTGCACGT  TCAT CC
                                |||||||||||||||  |||| ||
                                TGATGTCCACGTGCA  GGTA GG
                                      AC    C
GAM694  LOC146540 3'  GGTACAGTGGCTCACACCTGTA 77980       CAC  G  CA
                                TACAGGTG   GT AT  TACC
                                ||||||||   || ||  ||||
                                ATGTCCAC   CG TG  ATGG
                                    ACT  G  AC
GAM694  LOC146895 5'  GGCATGATCATTGCTCACT   83826    GT_  C      A
                                AG   GCA GTGATCAT CC
                                ||   ||| |||||||| ||
                                TC   CGT TACTAGTA GG
                                  ACT  _       C
GAM694  LOC146923 3'  ATGGTGGCAGGCACCTGTAGT  78190         AC  G
                                ACTACAGGTGC  GT ATCAT
                                ||||||||||  || |||||
                                TGATGTCCACG  CG TGGTA
                                      GA  G
GAM694  LOC147660 3'  GGCATGGTGGTGGGCACCTGTA 78395         A  TG    A
          GT                      ACTACAGGTGC CG  ATCAT CC
                                ||||||||||  ||  ||||| ||
                                TGATGTCCACG GT  TGGTA GG
                                      G  GG    C
GAM694  LOC147669 3'  GGCATGGTGACCCACACCTGTA 84064       CAC  G    A
                                TACAGGTG   GT ATCAT CC
                                ||||||||   || ||||| ||
                                ATGTCCAC   CA TGGTA GG
                                    ACC  G    C
GAM694  LOC147990 3'  GGCATGGTGACACACACCTGTA 84098       CAC  G    A
                                TACAGGTG   GT ATCAT CC
                                ||||||||   || ||||| ||
                                ATGTCCAC   CA TGGTA GG
                                    ACA  G    C
GAM694  LOC148166 3'  CACAGTGGCTCACACCTGTA   78690       _____  _
                                TACAGGTG    CAC GTG
                                ||||||||    ||| |||
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                                ATGTCCAC    GTG CAC
                                    ACTCG   A
GAM694   LOC148918 5'  GGCACAGTGGCTCACACCTGTA 79078       _____  _  A
                                TACAGGTG    CAC GTG TC
                                ||||||||    ||| ||| ||
                                ATGTCCAC    GTG CAC GG
                                    ACTCG   A  _
GAM694   LOC148936 3'  GGCACAGTGGCTCACACCTGTA 84297       _____  _  A
                                TACAGGTG    CAC GTG TC
                                ||||||||    ||| ||| ||
                                ATGTCCAC    GTG CAC GG
                                    ACTCG   A  _
GAM694   LOC148938 3'  GGCACAGTGGCTCACACCTGTA 84279       _____  _  A
                                TACAGGTG    CAC GTG TC
                                ||||||||    ||| ||| ||
                                ATGTCCAC    GTG CAC GG
                                    ACTCG   A  _
GAM694   LOC150299 3'  GGCATGGTGGCGGGCACCTGTA 84973         A  G    A
           GT                     ACTACAGGTGC CGT ATCAT CC
                                ||||||||||| ||| ||||| ||
                                TGATGTCCACG GCG TGGTA GG
                                     G  G    C
GAM694   LOC151196 3'  GGCATGGTAGCAGGCACCTGTA 85268        AC  G    A
                                TACAGGTGC  GT ATCAT CC
                                |||||||||  || ||||| ||
                                ATGTCCACG  CG TGGTA GG
                                     GA  A    C
GAM694   LOC151602 3'  GGCATGGTGGCACGCGCCTGTA 80298        AC  G    A
                                TACAGGTGC  GT ATCAT CC
                                |||||||||  || ||||| ||
                                ATGTCCGCG  CG TGGTA GG
                                     CA  G    C
GAM694   LOC152263 3'  CACAGTGGCTCACACCTGTA   85673       _____  _
                                TACAGGTG    CAC GTG
                                ||||||||    ||| |||
                                ATGTCCAC    GTG CAC
                                    ACTCG   A
GAM694   LOC152283 3'  GGCATGGTGGTGTGCACCTGTA 85685         TG    A
                                TACAGGTGCACG  ATCAT CC
                                ||||||||||||  ||||| ||
                                ATGTCCACGTGT  TGGTA GG
                                      GG    C
GAM694   LOC152316 5'  ATGATCACGTGCCTG      85608     GT
                                CAG  GCACGTGATCAT
                                |||  ||||||||||||
                                GTC  CGTGCACTAGTA
                                  __
GAM694   LOC152804 3'  GGCATGGTGGCAGGCACCTGTA 85886        AC  G    A
                                TACAGGTGC  GT ATCAT CC
                                |||||||||  || ||||| ||
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                                ATGTCCACG  CG TGGTA GG
                                    GA  G    C
GAM694   LOC153338 3'  GTATGGTGGCGGTCACCTGTA  86000       CA   G
                                TACAGGTG  CGT ATCATAC
                                ||||||||  ||| |||||||
                                ATGTCCAC  GCG TGGTATG
                                    TG   G
GAM694   LOC153642 3'  GGCACAGTGGCTCACACCTGTA 80910       _____  _  A
                                TACAGGTG    CAC GTG TC
                                ||||||||    ||| ||| ||
                                ATGTCCAC    GTG CAC GG
                                    ACTCG   A  _
GAM694   LOC153688 3'  GGCATGGTGGTGCACGCCTGTA 86116        CA  TG    A
           GT                    ACTACAGGTG  CG  ATCAT CC
                                ||||||||||  ||  ||||| ||
                                TGATGTCCGC  GT  TGGTA GG
                                     AC  GG    C
GAM694   LOC154739 5'  GGCATGTTGGTGTGCACCTGTA 86237          TGAT   A
                                TACAGGTGCACG    CAT CC
                                ||||||||||||    ||| ||
                                ATGTCCACGTGT    GTA GG
                                     GGTT   C
GAM694   LOC155072 3'  GGCACAGTGGCTCACACCTGTA 86382       _____  _  A
                                TACAGGTG    CAC GTG TC
                                ||||||||    ||| ||| ||
                                ATGTCCAC    GTG CAC GG
                                    ACTCG   A  _
GAM694   LOC155376 3'  GGCATTATGGCAGGCACCTGTA 81337       AC  G  C  A
                                TACAGGTGC  GT AT AT CC
                                |||||||||  || || || ||
                                ATGTCCACG  CG TA TA GG
                                    GA  G  T  C
GAM694   LOC157278 3'  GTGACTCACACCTGTA     86426       GCAC   _
                                TACAGGT    GTGA TCAT
                                |||||||    |||| ||||
                                ATGTCCA    CACT AGTG
                                   ____    C
GAM694   LOC157292 5'  GGCATGATGGCACACACCTGTA 86418       CAC  G    A
                                TACAGGTG   GT ATCAT CC
                                ||||||||   || ||||| ||
                                ATGTCCAC   CG TAGTA GG
                                    ACA  G    C
GAM694   LOC158187 3'  GGCATGGTGGCACACGCCTGTA 86694        CAC  G    A
           GT                    ACTACAGGTG   GT ATCAT CC
                                ||||||||||   || ||||| ||
                                TGATGTCCGC   CG TGGTA GG
                                     ACA  G    C
GAM694   LOC158310 3'  GGTACAGTGGCTCACACCTGTA 86759       CAC  G  CA
                                TACAGGTG   GT AT  TACC
                                ||||||||   || ||  ||||
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                                ATGTCCAC   CG TG  ATGG
                                     ACT  G  AC
GAM694   LOC158402 3'  TATGGTTGGTACCACCTGTAGT 86812          C_  G
                                ACTACAGGTG  AC TGATCATA
                                ||||||||||  || ||||||||
                                TGATGTCCAC  TG GTTGGTAT
                                     CA  _
GAM694   LOC158863 3'  GGCATGGTGGCTCACACCTGTA 86924         CAC  G    A
                                TACAGGTG   GT ATCAT CC
                                ||||||||   || ||||| ||
                                ATGTCCAC   CG TGGTA GG
                                     ACT  G    C
GAM694   LOC161823 3'  GGCACGGTGGTACACACCTGTA 82304          _____  _  A
            GT                    ACTACAGGTG    CAC GTG TC
                                ||||||||||    ||| ||| ||
                                TGATGTCCAC    GTG CAC GG
                                     ACATG   G  _
GAM694   LOC196027 3'  GTGGCTCACACCTGTA     87552        GCAC   _
                                TACAGGT    GTGA TCAT
                                |||||||    |||| ||||
                                ATGTCCA    CACT GGTG
                                     ____   C
GAM694   LOC197379 3'  GGTATGATCCCCGTTGTGCACC 89743          T____
            TG                    CAGGTGCACG    GATCATACC
                                ||||||||||    |||||||||
                                GTCCACGTGT    CTAGTATGG
                                     TGCCC
GAM694   LOC199733 3'  GGTATGGTGGCACGCACCTGTA 89850          AC  G
            GT                    ACTACAGGTGC  GT ATCATACC
                                ||||||||||||  || ||||||||
                                TGATGTCCACG  CG TGGTATGG
                                     CA  G
GAM694   LOC200317 3'  GTAGCACACGCCTGTA     88798        CAC   ATCA
                                TACAGGTG   GTG   TAC
                                ||||||||   |||   |||
                                ATGTCCGC   CAC   ATG
                                     A__   G___
GAM694   LOC200772 3'  GACACGTGTGCACCTGTG    90136          __  A
                                TACAGGTGCAC  GTG TC
                                ||||||||||||  ||| ||
                                GTGTCCACGTG  CAC AG
                                     TG  _
GAM694   LOC201627 3'  GGCATGGTGGCACGCGCCTGTA 89022         AC  G    A
                                TACAGGTGC  GT ATCAT CC
                                |||||||||  || ||||| ||
                                ATGTCCGCG  CG TGGTA GG
                                     CA  G    C
GAM694   LOC201689 3'  GGCATGGTGGTACACACCTGTA 67147          CACG G    A
            GT                    ACTACAGGTG    T ATCAT CC
                                ||||||||||    | ||||| ||
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                                TGATGTCCAC    G TGGTA GG
                                      ACAT G     C
GAM694   LOC201931 3'  ATGGTGGCGGGCACCTGTAGT  89109          A   G
                                ACTACAGGTGC CGT ATCAT
                                |||||||||||  ||| |||||
                                TGATGTCCACG GCG TGGTA
                                      G   G
GAM694   LOC202868 3'  GGCACAGTGGCTCACACCTGTA 90380        _____  _  A
                                TACAGGTG     CAC GTG TC
                                ||||||||     ||| ||| ||
                                ATGTCCAC     GTG CAC GG
                                     ACTCG   A  _
GAM694   LOC202934 3'  GGCATGATCATAGCTCACTGCA 90421    A  GT_ AC      A
           G                     CT CAG   GC  GTGATCAT CC
                                || |||   ||  |||||||| ||
                                GA GTC   CG  TACTAGTA GG
                                 C   ACT  A_       C
GAM694   LOC203378 3'  ATGGTGGCTTACACCTGTA   90593        CAC  G
                                TACAGGTG   GT ATCAT
                                ||||||||   || |||||
                                ATGTCCAC   CG TGGTA
                                     ATT  G
GAM694   LOC203397 3'  GGCACAGTGACTCACACCTGTA 89352        _____  _  A
                                TACAGGTG     CAC GTG TC
                                ||||||||     ||| ||| ||
                                ATGTCCAC     GTG CAC GG
                                     ACTCA   A  _
GAM694   LOC219540 3'  GGCATGGTGGTACACACCTGTA 93601        CACG G    A
                                TACAGGTG    T ATCAT CC
                                ||||||||    | ||||| ||
                                ATGTCCAC    G TGGTA GG
                                     ACAT G     C
GAM694   LOC220070 3'  GGTATGGTGGTGCACACCTGTA 59262         CA  TG
           GT                     ACTACAGGTG  CG  ATCATACC
                                ||||||||||  ||  ||||||||
                                TGATGTCCAC  GT  TGGTATGG
                                      AC  GG
GAM694   LOC221271 3'  ATGATGGCTCACACCTGTA   91846        CAC  G
                                TACAGGTG   GT ATCAT
                                ||||||||   || |||||
                                ATGTCCAC   CG TAGTA
                                     ACT  G
GAM694   LOC221477 3'  GGCATGGTGGCTCACACCTGTA 92158        CAC  G    A
                                TACAGGTG   GT ATCAT CC
                                ||||||||   || ||||| ||
                                ATGTCCAC   CG TGGTA GG
                                     ACT  G     C
GAM694   LOC253532 3'  GGCATTATGGCAGGCACCTGTA 96029         AC  G  C  A
                                TACAGGTGC  GT AT AT CC
                                |||||||||  || || || ||
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                                ATGTCCACG  CG TA TA GG
                                    GA  G  T  C
GAM694   LOC254875 3'  GGCATTATGGCAGGCACCTGTA 96059         AC  G  C  A
                                TACAGGTGC  GT AT AT CC
                                |||||||||  || || || ||
                                ATGTCCACG  CG TA TA GG
                                    GA  G  T  C
GAM694   LOC255231 3'  GGCACAGTGGTTCACACCTGTA 95377         _____  _  A
                                TACAGGTG    CAC GTG TC
                                ||||||||    ||| ||| ||
                                ATGTCCAC    GTG CAC GG
                                    ACTTG   A  _
GAM694   LOC255231 3'  TGTGGAAGTGACCTGTAG    95379        G   GTGA
                                CTACAGGT CAC    TCATA
                                |||||||| |||   |||||
                                GATGTCCA GTG    GGTGT
                                    _   AA__
GAM694   LOC255461 3'  GTGACTCACACCTGTA      97321        GCAC   _
                                TACAGGT   GTGA TCAT
                                |||||||   |||| ||||
                                ATGTCCA   CACT AGTG
                                    ____   C
GAM694   LOC255465 3'  GGCATGATCATAGCTCACTGCA 97297    A  GT_  AC       A
         G                       CT CAG   GC  GTGATCAT CC
                                || |||   ||  |||||||| ||
                                GA GTC   CG  TACTAGTA GG
                                 C   ACT  A_       C
GAM694   LOC255516 3'  GTGACTCACACCTGTA      97334        GCAC   _
                                TACAGGT   GTGA TCAT
                                |||||||   |||| ||||
                                ATGTCCA   CACT AGTG
                                    ____   C
GAM694   LOC255671 3'  GTGACACACGCCTGTA      97262        CAC   A
                                TACAGGTG   GTG TCAT
                                ||||||||   ||| ||||
                                ATGTCCGC   CAC AGTG
                                    A__   _
GAM694   LOC256073 3'  GGCACAGTGGCTTACACCTGTA 96666         _____  _  A
                                TACAGGTG    CAC GTG TC
                                ||||||||    ||| ||| ||
                                ATGTCCAC    GTG CAC GG
                                    ATTCG   A  _
GAM694   LOC256207 3'  GGCATGGTGGTGTGCGCCTGCA 95172     A        TG    A
         GT                      ACT CAGGTGCACG  ATCAT CC
                                ||| ||||||||||  ||||| ||
                                TGA GTCCGCGTGT  TGGTA GG
                                  C         GG    C
GAM694   LOC256207 3'  GTGGCACACACCTGTAGT    95174         CAC   A
                                ACTACAGGTG   GTG TCAT
                                ||||||||||   ||| ||||
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                                TGATGTCCAC   CAC GGTG
                                     A__   _
GAM694  LOC256594 5'  GGCATGGTGGCATGCACCTG   97079        C  G    A
                                CAGGTGCA GT ATCAT CC
                                |||||||| || ||||| ||
                                GTCCACGT CG TGGTA GG
                                     A  G    C
GAM694  LOC51008  5'  GACGACTGCACCTGCAG     31964    A      C  GA
                                CT CAGGTGCA GT  TC
                                || |||||||| ||  ||
                                GA GTCCACGT CA  AG
                                 C       _ GC
GAM694  LOC51336  3'  GGCATGGTGGCTCACACCTGTA 33578        CAC  G    A
                                TACAGGTG   GT ATCAT CC
                                ||||||||   || ||||| ||
                                ATGTCCAC   CG TGGTA GG
                                     ACT  G    C
GAM694  LOC54518  3'  GTAGCTCACACCTGTAGT    38772        GCAC    TCA
                                ACTACAGGT    GTGA   TAC
                                |||||||||    ||||  |||
                                TGATGTCCA    CACT   ATG
                                     _____    CG_
GAM694  LOC54550  3'  GTAGGAGTCATGCCCCTGTAGT 77690        T   CG    CA_
                                ACTACAGG GCA  TGAT   TAC
                                |||||||| |||  ||||   |||
                                TGATGTCC CGT  ACTG   ATG
                                     C   __    AGG
GAM694  LOC90092  3'  GTAGCTCACACCTGTA      61416       GCAC    TCA
                                TACAGGT    GTGA   TAC
                                |||||||    ||||  |||
                                ATGTCCA    CACT   ATG
                                     _____    CG_
GAM694  LOC90979  3'  GGCATGGTGGTGCACGCCTGTA 64529         CA  TG    A
           GT                     ACTACAGGTG  CG  ATCAT CC
                                |||||||||  ||  ||||| ||
                                TGATGTCCGC  GT  TGGTA GG
                                     AC  GG    C
GAM694  LOC91064  3'  GGCATGGTGGTGTGCACCTGTA 64764           TG    A
           GT                     ACTACAGGTGCACG  ATCAT CC
                                ||||||||||||||  ||||| ||
                                TGATGTCCACGTGT  TGGTA GG
                                       GG    C
GAM694  LOC91963  5'  GTGGCACACGCCTGTA      67698        CAC   A
                                TACAGGTG   GTG TCAT
                                ||||||||   ||| ||||
                                ATGTCCGC   CAC GGTG
                                     A__   _
GAM694  LOC92223  3'  GGCATGGTGGCTCACACCTGTA 68522        CAC  G    A
                                TACAGGTG   GT ATCAT CC
                                ||||||||   || ||||| ||
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                                ATGTCCAC   CG TGGTA GG
                                     ACT  G    C
GAM694  LOC92421  3'  ATGGTGGCAGGCACCTGTA   69213         AC  G
                                TACAGGTGC  GT ATCAT
                                |||||||||  || |||||
                                ATGTCCACG  CG TGGTA
                                     GA  G
GAM694  LOC92482  3'  GGCATGGTGGCATGCGCCTGTA 69491          C  G    A
                                TACAGGTGCA GT ATCAT CC
                                |||||||||| || ||||| ||
                                ATGTCCGCGT CG TGGTA GG
                                      A  G    C
GAM694  LOC93132  5'  GGCATGGTGGCGTGCACCTGTA 71495           G    A
                                TACAGGTGCACGT ATCAT CC
                                |||||||||||| ||||| ||
                                ATGTCCACGTGCG TGGTA GG
                                        G    C
GAM694  LOC93613  3'  GGTGATGCACACCTGTA     72700        CA   G
                                TACAGGTG  CGT ATC
                                ||||||||  ||| |||
                                ATGTCCAC  GTA TGG
                                     AC   G
GAM694  LOC96597  5'  GGTGGCGGGCACCTGTA     66918         A   G
                                TACAGGTGC CGT ATC
                                ||||||||| ||| |||
                                ATGTCCACG GCG TGG
                                     G   G
GAM695  AKR1B1    3'  GTCCCCAAGTGACCTATACC   7891     C       AAA    A
                                GG ATAGGTCAC   TGGG GAC
                                || |||||||||   |||| |||
                                CC TATCCAGTG   ACCC CTG
                                  A        A__   _
GAM695  CD28      3'  GTCTCCCACTCATGAAATGAGC 20441      A  GG   CAAA
            CA                    TGGC TA  TCA    TGGGAGAC
                                |||| ||  |||   ||||||||
                                ACCG GT  AGT    ACCCTCTG
                                   A  AA   ACTC
GAM695  DRD3      3'  CCCTGTGATCTATACCA     53355     C        AAT
                                TGG ATAGGTCACA   GGG
                                ||| ||||||||||   |||
                                ACC TATCTAGTGT   CCC
                                  A        ___
GAM695  DRD3      3'  CCCTGTGATCTATACCA     53357     C        AAT
                                TGG ATAGGTCACA   GGG
                                ||| ||||||||||   |||
                                ACC TATCTAGTGT   CCC
                                  A        ___
GAM695  EXTL3     3'  TCTCCCATCCTCCCCAGCGCCA 7537       ATA  TCACAA
                                TGGC   GG     ATGGGAGA
                                ||||   ||     ||||||||
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                                ACCG  CC    TACCCTCT
                                  CGA CCTCC_
GAM695  GUCY1B2  3' TCTCCCACTTCGGCAGCCA  14687    ATAG  ACAAA
                                TGGC   GTC   TGGGAGA
                                ||||   |||   |||||||
                                ACCG   CGG   ACCCTCT
                                  A___  CTTC_
GAM695  RHO      3' TCTCCCATCCCCTACACC   5021    CA   TCACAA
                                GG TAGG    ATGGGAGA
                                || ||||    ||||||||
                                CC ATCC    TACCCTCT
                                 AC   CC____
GAM695  SOX10    3' CCCATGCCACCTATGCCA   22684        CACAA
                                TGGCATAGGT   ATGGG
                                ||||||||||   |||||
                                ACCGTATCCA   TACCC
                                      CCG__
GAM695  SOX10    3' TCTGACATGCCCATGCCA   22689      A  CACAA  GG
                                TGGCAT GGT   ATG  AGA
                                |||||| |||   |||  |||
                                ACCGTA CCG   TAC  TCT
                                   C  _____  AG
GAM695  SSX3     3' TCTCCCATCTGCTTTTCCCATT 40670     TA_  TCA__  A
           GCCA                  TGGCA  GG   CA ATGGGAGA
                                |||||  ||   || ||||||||
                                ACCGT  CC   GT TACCCTCT
                                   TAC  TTTTC  C
GAM695  WNT4     3' TCTCCCACCACCTACCCCA  47762    CA   CACAAA
                                TGG  TAGGT    TGGGAGA
                                |||  |||||    |||||||
                                ACC  ATCCA    ACCCTCT
                                  CC   CC____
GAM695  CORO1A   3' CTCCCATTCCCAGCCA    22988    ATA  TCACA
                                TGGC  GG   AATGGGAG
                                ||||  ||   ||||||||
                                ACCG  CC   TTACCCTC
                                  AC_ _____
GAM695  DDR2     3' TCACCCATGCCTATGCCA   20524        CACAA   A
                                TGGCATAGGT   ATGGG GA
                                ||||||||||   ||||| ||
                                ACCGTATCCG   TACCC CT
                                      _____    A
GAM695  DKFZP434G1411 3' CTTCTGTAACCTATGC    92104       C  AATG
                                GCATAGGT ACA   GGAG
                                |||||||| |||   ||||
                                CGTATCCA TGT   CTTC
                                    A  ____
GAM695  FLJ10726 3' TCCCCCATTTGCACTACTGGCC 36508    A  GTCA_     A
           A                    TGGC TAG   CAAATGGG GA
                                |||| |||   |||||||| ||
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                                ACCG GTC    GTTTACCC CT
                                  _  ATCAC       C
GAM695  ILF2     3'  GTCTCCCATTTGTGACCTATGC 66941
              CA                  TGGCATAGGTCACAAATGGGAGAC
                                  ||||||||||||||||||||||||
                                  ACCGTATCCAGTGTTTACCCTCTG

GAM695  KIAA0222 3'  CTCCCACCTGTGACCTGGCC  27681    A       AA
                                GGC TAGGTCACA  TGGGAG
                                ||| |||||||||  ||||||
                                CCG GTCCAGTGT  ACCCTC
                                  _       CC
GAM695  KIAA0556 3'  CTCTTGTGACCCAAACCA    69083    CATA     AATG
                                TGG   GGTCACA   GGAG
                                |||   |||||||   ||||
                                ACC   CCAGTGT   TCTC
                                  AAAC     _____
GAM695  KIAA0836 3'  TTTATCTGTGACCTATATCA  64566    GC       A
                                TG  ATAGGTCACA ATGGG
                                ||  ||||||||||| |||||
                                AC  TATCCAGTGT TATTT
                                  TA        C
GAM695  KIAA1396 3'  TCCCCCTTGGGTGCCTATGCCA 62995         T   AAAT   A
                                TGGCATAGG CAC    GGG GA
                                ||||||||| |||   ||| ||
                                ACCGTATCC GTG    CCC CT
                                      _  GGTT   C
GAM695  MRPL45   3'  GTCTCCCATTCCCCTCATGCTA 50375       _   TCACA
                                TGGCAT AGG     AATGGGAGAC
                                |||||| |||    ||||||||||
                                ATCGTA TCC     TTACCCTCTG
                                   C   CC___
GAM695  SIRPB1   3'  TCATTCTGTGACCTTTACCA   20264     CAT      _
                                TGG   AGGTCACA AATGG
                                |||   |||||||| |||||
                                ACC   TCCAGTGT TTACT
                                  ATT       C
GAM695  SNAP29   3'  CCCATGTGACCTTTGCCA     16539      T       AA
                                TGGCA AGGTCACA  TGGG
                                ||||| ||||||||  ||||
                                ACCGT TCCAGTGT  ACCC
                                   T       __
GAM695  TRIM29   3'  TCTCCCATTCACATGGCCCACC 23961    CATA    CA__
                                GG    GGTCA    AATGGGAGA
                                ||    |||||    |||||||||
                                CC    CCGGT    TTACCCTCT
                                  AC__     ACAC
GAM695  UPK1A    3'  CTCCCATTCACAGATACC    22796    C  AG  CACA
                                GG AT  GT    AATGGGAG
                                || ||  ||    ||||||||
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                                CC TA  CA    TTACCCTC
                                 A  GA  C___
GAM695  LOC115294 3'  TTTGGGACCTATGCCA      73020          A
                                TGGCATAGGTC CAAA
                                |||||||||| ||||
                                ACCGTATCCAG GTTT
                                      G
GAM695  LOC143458 3'  CCCAGCATCACCTATGCCA    76572          CACAAA
                                TGGCATAGGT     TGGG
                                |||||||||     ||||
                                ACCGTATCCA     ACCC
                                     CTACG_
GAM695  LOC146138 3'  GTCTCCCACTCGATCCCTTCGC 83616      AT   TCACAAA
           CA                     TGGC  AGG      TGGGAGAC
                                |||| |||      ||||||||
                                ACCG  TCC      ACCCTCTG
                                  CT   CTAGCTC
GAM695  LOC146784 5'  CTCCCATTTATGTGATC     78111        __
                                GGTCACA  AATGGGAG
                                |||||||  ||||||||
                                CTAGTGT  TTACCCTC
                                    AT
GAM695  LOC201220 5'  CCTATGCCTATGCCA       87346          CACAA
                                TGGCATAGGT    ATGGG
                                |||||||||    |||||
                                ACCGTATCCG    TATCC
                                              _____
GAM695  LOC202460 5'  CTCCCATTTATGACTTA     89182        C
                                TAGGTCA AAATGGGAG
                                ||||||| |||||||||
                                ATTCAGT TTTACCCTC
                                    A
GAM695  LOC90408  3'  TCTCTGTGACCCATACC     62670    C  A      AAT
                                GG AT GGTCACA   GGGA
                                || || |||||||   ||||
                                CC TA CCAGTGT   CTCT
                                 A  C     ___
GAM695  LOC90917  3'  TCCTCTTGCAGCCTACGCCA   64340     A    CA   AT
                                TGGC TAGGT  CAA  GGGA
                                |||| |||||  |||  ||||
                                ACCG ATCCG  GTT  TCCT
                                  C    AC   C_
GAM696  ALS2      3'  CTGTGAATGGCAGCCTGAGGAA 40506        AC  _  GAGTGA
                                TTCCTCAG  CT CCA     AG
                                ||||||||  || |||     ||
                                AAGGAGTC  GA GGT     TC
                                    C_  C   AAGTG_
GAM696  ALS2      3'  CTGTGAATGGCAGCCTGAGGAA 40506        AC  _  GAGTGA
                                TTCCTCAG  CT CCA     AG
                                ||||||||  || |||     ||
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                              AAGGAGTC  GA GGT     TC
                                  C_  C  AAGTG_
GAM696  BCLG    3'  CTCCATTGAGAACCTGAGGAA  47779       AC_  CAG   A
                              TTCCTCAG  CTC  AGTG AG
                              ||||||||  |||  |||| ||
                              AAGGAGTC  GAG  TTAC TC
                                  CAA  ___   C
GAM696  BCLG    3'  CTCCATTGAGAACCTGAGGAA  47779       AC_  CAG   A
                              TTCCTCAG  CTC  AGTG AG
                              ||||||||  |||  |||| ||
                              AAGGAGTC  GAG  TTAC TC
                                  CAA  ___   C
GAM696  BCLG    3'  CTCCATTGAGAACCTGAGGAA  56975       AC_  CAG   A
                              TTCCTCAG  CTC  AGTG AG
                              ||||||||  |||  |||| ||
                              AAGGAGTC  GAG  TTAC TC
                                  CAA  ___   C
GAM696  BCLG    3'  CTCCATTGAGAACCTGAGGAA  56975       AC_  CAG   A
                              TTCCTCAG  CTC  AGTG AG
                              ||||||||  |||  |||| ||
                              AAGGAGTC  GAG  TTAC TC
                                  CAA  ___   C
GAM696  BCLG    3'  CTCCATTGAGAACCTGAGGAA  56981       AC_  CAG   A
                              TTCCTCAG  CTC  AGTG AG
                              ||||||||  |||  |||| ||
                              AAGGAGTC  GAG  TTAC TC
                                  CAA  ___   C
GAM696  BCLG    3'  CTCCATTGAGAACCTGAGGAA  56981       AC_  CAG   A
                              TTCCTCAG  CTC  AGTG AG
                              ||||||||  |||  |||| ||
                              AAGGAGTC  GAG  TTAC TC
                                  CAA  ___   C
GAM696  CIT     3'  CACTCTGGGATGGGGAA    69744       GACC
                              TTCCTCA   TCCAGAGTG
                              |||||||   |||||||||
                              AAGGGGT   GGGTCTCAC
                                  A___
GAM696  CIT     3'  CACTCTGGGATGGGGAA    69744       GACC
                              TTCCTCA   TCCAGAGTG
                              |||||||   |||||||||
                              AAGGGGT   GGGTCTCAC
                                  A___
GAM696  CSRP1   3'  CTCAGAGTAAGCCTGAGGAG  14530       AC___  CA
                              TTCCTCAG   CTC  GAG
                              ||||||||   |||  |||
                              GAGGAGTC   GAG  CTC
                                  CGAAT  A_
GAM696  CSRP1   3'  CTCAGAGTAAGCCTGAGGAG  14530       AC___  CA
                              TTCCTCAG   CTC  GAG
                              ||||||||   |||  |||
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                                GAGGAGTC    GAG  CTC
                                    CGAAT   A_
GAM696  DDX6    3'  TTCTAAAAGTTTGAGGAA    15292        CTCC
                                TTCCTCAGAC    AGAG
                                ||||||||||    ||||
                                AAGGAGTTTG    TCTT
                                     AAAA
GAM696  DDX6    3'  TTCTAAAAGTTTGAGGAA    15292        CTCC
                                TTCCTCAGAC    AGAG
                                ||||||||||    ||||
                                AAGGAGTTTG    TCTT
                                     AAAA
GAM696  ED1     3'  TCTTCACTCTGGCTTC     7375     CCT
                                GA   CCAGAGTGAAGA
                                ||   ||||||||||||
                                CT   GGTCTCACTTCT
                                 TC_
GAM696  ED1     3'  TCTTCACTCTGGCTTC     7375     CCT
                                GA   CCAGAGTGAAGA
                                ||   ||||||||||||
                                CT   GGTCTCACTTCT
                                 TC_
GAM696  FSTL3   3'  CTGGAAGGACTGAGGAA     19608        A  _
                                TTCCTCAG CCT CCAG
                                |||||||| ||| ||||
                                AAGGAGTC GGA GGTC
                                     A   A
GAM696  FSTL3   3'  CTGGAAGGACTGAGGAA     19608        A  _
                                TTCCTCAG CCT CCAG
                                |||||||| ||| ||||
                                AAGGAGTC GGA GGTC
                                     A   A
GAM696  HDAC4   3'  TTCTGAAGTCTGAGGAA     20124         CTC
                                TTCCTCAGAC   CAGAG
                                ||||||||||   |||||
                                AAGGAGTCTG   GTCTT
                                     AA_
GAM696  HDAC4   3'  TTCTGAAGTCTGAGGAA     20124         CTC
                                TTCCTCAGAC   CAGAG
                                ||||||||||   |||||
                                AAGGAGTCTG   GTCTT
                                     AA_
GAM696  MAGEA8  3'  TCTTCACTCTGTGTTTGAAGAG 18108     C     CTC
                                TTC TCAGAC   CAGAGTGAAGA
                                ||| ||||||   ||||||||||||
                                GAG AGTTTG   GTCTCACTTCT
                                  A     T__
GAM696  MAGEA8  3'  TCTTCACTCTGTGTTTGAAGAG 18108     C     CTC
                                TTC TCAGAC   CAGAGTGAAGA
                                ||| ||||||   ||||||||||||
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                                GAG AGTTTG   GTCTCACTTCT
                                  A     T__
GAM696  PBP     3'  TCTTTAAGGGAGGTTT      10385        AGAG
                                AGACCTCC    TGAAGA
                                ||||||||    ||||||
                                TTTGGAGG    ATTTCT
                                    GA__
GAM696  PBP     3'  TCTTTAAGGGAGGTTT      10385        AGAG
                                AGACCTCC    TGAAGA
                                ||||||||    ||||||
                                TTTGGAGG    ATTTCT
                                    GA__
GAM696  PLSCR1  3'  CTTCACTCTAAAACTCTGG    40857      CCTCC
                                TCAGA    AGAGTGAAG
                                |||||    |||||||||
                                GGTCT    TCTCACTTC
                                   CAAAA
GAM696  PLSCR1  3'  CTTCACTCTAAAACTCTGG    40857      CCTCC
                                TCAGA    AGAGTGAAG
                                |||||    |||||||||
                                GGTCT    TCTCACTTC
                                   CAAAA
GAM696  PPEF2   5'  CTCTGTAGGTCTGAAGAA    20669     C      C
                                TTC TCAGACCT CAGAG
                                ||| |||||||| |||||
                                AAG AGTCTGGA GTCTC
                                  A       T
GAM696  PPEF2   5'  CTCTGTAGGTCTGAAGAA    20669     C      C
                                TTC TCAGACCT CAGAG
                                ||| |||||||| |||||
                                AAG AGTCTGGA GTCTC
                                  A       T
GAM696  PUM2    3'  TTTTTACTAGAGATCTGCAGAA 31019     CT    C   CAG
                                TTC  CAGA CTC   AGTGAAGA
                                |||  |||| |||   ||||||||
                                AAG  GTCT GAG   TCATTTTT
                                  AC    A   A__
GAM696  PUM2    3'  TTTTTACTAGAGATCTGCAGAA 31019     CT    C   CAG
                                TTC  CAGA CTC   AGTGAAGA
                                |||  |||| |||   ||||||||
                                AAG  GTCT GAG   TCATTTTT
                                  AC    A   A__
GAM696  RAB13   3'  CACCCCGGAAGCTGAACCTGAG 11201        ACC_____   AGA
            GGA                   TTCCTCAG       TCC   GTG
                                ||||||||       |||   |||
                                AGGGAGTC       AGG   CAC
                                    CAAGTCGA   CCC
GAM696  RAB13   3'  CACCCCGGAAGCTGAACCTGAG 11201        ACC_____   AGA
            GGA                   TTCCTCAG       TCC   GTG
                                ||||||||       |||   |||
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                                AGGGAGTC      AGG  CAC
                                    CAAGTCGA  CCC
GAM696  RFC4    5' TCGCGGAAACCTGAGGAA   11306       ACC  AGA
                                TTCCTCAG  TCC  GTGA
                                ||||||||  |||  ||||
                                AAGGAGTC  AGG  CGCT
                                    CAA  ___
GAM696  RFC4    5' TCGCGGAAACCTGAGGAA   11306       ACC  AGA
                                TTCCTCAG  TCC  GTGA
                                ||||||||  |||  ||||
                                AAGGAGTC  AGG  CGCT
                                    CAA  ___
GAM696  SF1     3' TCTTCACTGGTTTATCTGCAGA 16147    CT   CCT_  GA
          A                      TTC  CAGA   CCA  GTGAAGA
                                |||  ||||   |||  |||||||
                                AAG  GTCT   GGT  CACTTCT
                                  AC   ATTT  __
GAM696  SF1     3' TCTTCACTGGTTTATCTGCAGA 16147    CT   CCT_  GA
          A                      TTC  CAGA   CCA  GTGAAGA
                                |||  ||||   |||  |||||||
                                AAG  GTCT   GGT  CACTTCT
                                  AC   ATTT  __
GAM696  SHOX    3' CTGCAAGAGGCCTGAGGAG   4835        A   ___
                                TTCCTCAG CCTC  CAG
                                |||||||| ||||  |||
                                GAGGAGTC GGAG  GTC
                                    C   AAC
GAM696  SHOX    3' CTGCAAGAGGCCTGAGGAG   4835        A   ___
                                TTCCTCAG CCTC  CAG
                                |||||||| ||||  |||
                                GAGGAGTC GGAG  GTC
                                    C   AAC
GAM696  TAF6    5' CTCCACTGATCTGAGGAG    18905       CC  CAG   A
                                TTCCTCAGA  TC  AGTG AG
                                |||||||||  ||  |||| ||
                                GAGGAGTCT  AG  TCAC TC
                                    __ ___   C
GAM696  TAF6    5' CTCCACTGATCTGAGGAG    18905       CC  CAG   A
                                TTCCTCAGA  TC  AGTG AG
                                |||||||||  ||  |||| ||
                                GAGGAGTCT  AG  TCAC TC
                                    __ ___   C
GAM696  TAGLN   5' CTTCCTGCGAGCCCTGAGGAA  59637       AC  _  AGT
                                TTCCTCAG  CTC CAG  GAAG
                                ||||||||  ||| |||  ||||
                                AAGGAGTC  GAG GTC  CTTC
                                    CC  C  ___
GAM696  TAGLN   5' CTTCCTGCGAGCCCTGAGGAA  59637       AC  _  AGT
                                TTCCTCAG  CTC CAG  GAAG
                                ||||||||  ||| |||  ||||
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                                AAGGAGTC  GAG GTC   CTTC
                                    CC   C   ___
GAM696  TEC     3'  CTTCACTCTGACCCTGGAGAA  12219    CT   ACCTC
                                TTC  CAG    CAGAGTGAAG
                                |||  |||    ||||||||||
                                AAG  GTC    GTCTCACTTC
                                  AG   CCA__
GAM696  TEC     3'  CTTCACTCTGACCCTGGAGAA  12219    CT   ACCTC
                                TTC  CAG    CAGAGTGAAG
                                |||  |||    ||||||||||
                                AAG  GTC    GTCTCACTTC
                                  AG   CCA__
GAM696  TGFA    3'  CTTTGGAAACCAGCAGGTCTGA 12252        _________
                                TCAGACC       TCCAGAG
                                |||||||       |||||||
                                AGTCTGG       AGGTTTC
                                    ACGACCAA
GAM696  TGFA    3'  CTTTGGAAACCAGCAGGTCTGA 12252        _________
                                TCAGACC       TCCAGAG
                                |||||||       |||||||
                                AGTCTGG       AGGTTTC
                                    ACGACCAA
GAM696  TGFB1   3'  CATTTTAAAGGTTGAGGAA   5400         A   CC
                                TTCCTCAG CCT  AGAGTG
                                |||||||| |||  ||||||
                                AAGGAGTT GGA  TTTTAC
                                    _   AA
GAM696  TGFB1   3'  CATTTTAAAGGTTGAGGAA   5400         A   CC
                                TTCCTCAG CCT  AGAGTG
                                |||||||| |||  ||||||
                                AAGGAGTT GGA  TTTTAC
                                    _   AA
GAM696  ZNF261  3'  TCTTGCATTGGAGGTCCCAG  17498    CA       A  G
                                CT  GACCTCCAG GT AAGA
                                ||  ||||||||| || ||||
                                GA  CTGGAGGTT CG TTCT
                                  CC        A  _
GAM696  ZNF261  3'  TCTTGCATTGGAGGTCCCAG  17498    CA       A  G
                                CT  GACCTCCAG GT AAGA
                                ||  ||||||||| || ||||
                                GA  CTGGAGGTT CG TTCT
                                  CC        A  _
GAM696  ABCA5   3'  TCAATATAGAGATTTGAGGAA  37916        C   CAGAG
                                TTCCTCAGA CTC    TGA
                                |||||||| |||    |||
                                AAGGAGTTT GAG    ACT
                                    A   ATATA
GAM696  ABCA5   3'  TCAATATAGAGATTTGAGGAA  37916        C   CAGAG
                                TTCCTCAGA CTC    TGA
                                |||||||| |||    |||
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                                AAGGAGTTT GAG    ACT
                                    A  ATATA
GAM696  ATIP1    3'  TCTGAGACTGGAAGTCTGGAGG 40395      _  C    AGTGA
            AA                   TTCCTC AGAC TCCAG    AGA
                                 |||||| |||| |||||    |||
                                 AAGGAG TCTG AGGTC    TCT
                                    G   A    AGAG_
GAM696  ATIP1    3'  TCTGAGACTGGAAGTCTGGAGG 40395      _  C    AGTGA
            AA                   TTCCTC AGAC TCCAG    AGA
                                 |||||| |||| |||||    |||
                                 AAGGAG TCTG AGGTC    TCT
                                    G   A    AGAG_
GAM696  C1QR1    3'  CACAGATAATCTGAGGAA    23837        CC_ CAGA
                                 TTCCTCAGA  TC   GTG
                                 |||||||||  ||   |||
                                 AAGGAGTCT  AG   CAC
                                      AAT  A___
GAM696  C1QR1    3'  CACAGATAATCTGAGGAA    23837        CC_ CAGA
                                 TTCCTCAGA  TC   GTG
                                 |||||||||  ||   |||
                                 AAGGAGTCT  AG   CAC
                                      AAT  A___
GAM696  C20orf160 3'  TTCTGGAGGCTGAGGAA    54651        A
                                 TTCCTCAG CCTCCAGAG
                                 |||||||| |||||||||
                                 AAGGAGTC GGAGGTCTT
                                        _
GAM696  C20orf160 3'  TTCTGGAGGCTGAGGAA    54651        A
                                 TTCCTCAG CCTCCAGAG
                                 |||||||| |||||||||
                                 AAGGAGTC GGAGGTCTT
                                        _
GAM696  CAMK2G   5'  CTGAGGTCTTGAGGAA     68963        _    C
                                 TTCCTCA GACCTC AG
                                 ||||||| |||||| ||
                                 AAGGAGT CTGGAG TC
                                     T    _
GAM696  CAMK2G   5'  CTGAGGTCTTGAGGAA     68963        _    C
                                 TTCCTCA GACCTC AG
                                 ||||||| |||||| ||
                                 AAGGAGT CTGGAG TC
                                     T    _
GAM696  DKFZP564O0463 3'  TTGGAGGTCAGAAGAA     26284    C  A
                                 TTC TC GACCTCCAG
                                 ||| || |||||||||
                                 AAG AG CTGGAGGTT
                                   A  A
GAM696  DKFZP564O0463 3'  TTGGAGGTCAGAAGAA     26284    C  A
                                 TTC TC GACCTCCAG
                                 ||| || |||||||||
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                                AAG AG CTGGAGGTT
                                  A  A
GAM696  DKFZp586I021 3'  CTCCACTCTGGCCGGAGGAA  50089      AGACCT      A
                                TTCCTC     CCAGAGTG AG
                                ||||||     |||||||| ||
                                AAGGAG     GGTCTCAC TC
                                   GCC___       C
GAM696  DKFZp586I021 3'  CTCCACTCTGGCCGGAGGAA  50089      AGACCT      A
                                TTCCTC     CCAGAGTG AG
                                ||||||     |||||||| ||
                                AAGGAG     GGTCTCAC TC
                                   GCC___       C
GAM696  EFA6R    3'  CTTTGAAGGCTGAGGAA     30984        A   C
                                TTCCTCAG CCT CAGAG
                                |||||||| ||| |||||
                                AAGGAGTC GGA GTTTC
                                     _   A
GAM696  EFA6R    3'  CTTTGAAGGCTGAGGAA     30984        A   C
                                TTCCTCAG CCT CAGAG
                                |||||||| ||| |||||
                                AAGGAGTC GGA GTTTC
                                     _   A
GAM696  FLJ10154  3'  TCTATATTAGTGGTCTGAGGAA 35856          TCCAG    A
                                TTCCTCAGACC    AGTG AGA
                                ||||||||||     |||| |||
                                AAGGAGTCTGG    TTAT TCT
                                      TGA__    A
GAM696  FLJ10154  3'  TCTATATTAGTGGTCTGAGGAA 35856          TCCAG    A
                                TTCCTCAGACC    AGTG AGA
                                ||||||||||     |||| |||
                                AAGGAGTCTGG    TTAT TCT
                                      TGA__    A
GAM696  FLJ10201  3'  CTGAGAGCCTGAGGAA     35893        AC   _
                                TTCCTCAG  CTC CAG
                                ||||||||  ||| |||
                                AAGGAGTC  GAG GTC
                                     C_   A
GAM696  FLJ10201  3'  CTGAGAGCCTGAGGAA     35893        AC   _
                                TTCCTCAG  CTC CAG
                                ||||||||  ||| |||
                                AAGGAGTC  GAG GTC
                                     C_   A
GAM696  FLJ10829  3'  TCTTCACGAAGTCAGTCCTGAG 36714        AC  CCAGA_
          GAA                     TTCCTCAG  CT     GTGAAGA
                                ||||||||  ||     |||||||
                                AAGGAGTC  GA     CACTTCT
                                     CT  CTGAAG
GAM696  FLJ10829  3'  TCTTCACGAAGTCAGTCCTGAG 36714        AC  CCAGA_
          GAA                     TTCCTCAG  CT     GTGAAGA
                                ||||||||  ||     |||||||
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                                AAGGAGTC  GA     CACTTCT
                                    CT  CTGAAG
GAM696  FLJ12517  3'  TCCTCACCTGGGCCTGAGGGA  43439        ACC    A   A
                                TTCCTCAG   TCCAG GTGA GA
                                ||||||||   ||||| |||| ||
                                AGGGAGTC   GGGTC CACT CT
                                    C__    _   C
GAM696  FLJ12517  3'  TCCTCACCTGGGCCTGAGGGA  43439        ACC    A   A
                                TTCCTCAG   TCCAG GTGA GA
                                ||||||||   ||||| |||| ||
                                AGGGAGTC   GGGTC CACT CT
                                    C__    _   C
GAM696  FLJ20477  5'  CTCTGGGAGGCCTGAGGGA   35240        A   _
                                TTCCTCAG CCTCC AGAG
                                |||||||| ||||| ||||
                                AGGGAGTC GGAGG TCTC
                                    C    G
GAM696  FLJ20477  5'  CTCTGGGAGGCCTGAGGGA   35240        A   _
                                TTCCTCAG CCTCC AGAG
                                |||||||| ||||| ||||
                                AGGGAGTC GGAGG TCTC
                                    C    G
GAM696  FLJ21313  3'  CTCTGGAGGTCTCAGGAA    43682      C
                                TTCCT AGACCTCCAGAG
                                ||||| ||||||||||||
                                AAGGA TCTGGAGGTCTC
                                   C
GAM696  FLJ21313  3'  CTCTGGAGGTCTCAGGAA    43682      C
                                TTCCT AGACCTCCAGAG
                                ||||| ||||||||||||
                                AAGGA TCTGGAGGTCTC
                                   C
GAM696  FLJ25059  5'  CTTTGGGGCCCGAGGAA     58683      AGAC
                                TTCCTC   CTCCAGAG
                                ||||||   ||||||||
                                AAGGAG   GGGGTTTC
                                    CCC_
GAM696  FLJ25059  5'  CTTTGGGGCCCGAGGAA     58683      AGAC
                                TTCCTC   CTCCAGAG
                                ||||||   ||||||||
                                AAGGAG   GGGGTTTC
                                    CCC_
GAM696  GIT1    3'  CTCTGGAGGCCTGGGAA     25866     T  A
                                TTCC CAG CCTCCAGAG
                                |||| ||| |||||||||
                                AAGG GTC GGAGGTCTC
                                   _  C
GAM696  GIT1    3'  CTCTGGAGGCCTGGGAA     25866     T  A
                                TTCC CAG CCTCCAGAG
                                |||| ||| |||||||||
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                                AAGG GTC GGAGGTCTC
                                  _  C
GAM696  KIAA0140 3' CTCTGAGGGGAGACTGAGGAA 27808       A__  _
                                TTCCTCAG  CCTC CAGAG
                                ||||||||  |||| |||||
                                AAGGAGTC  GGGG GTCTC
                                    AGA   A
GAM696  KIAA0140 3' CTCTGAGGGGAGACTGAGGAA 27808       A__  _
                                TTCCTCAG  CCTC CAGAG
                                ||||||||  |||| |||||
                                AAGGAGTC  GGGG GTCTC
                                    AGA   A
GAM696  KIAA0194 3' TCTCCACCCCAAGCTTTGAGGA 65988       C  CCAGA  A
          A                      TTCCTCAGA CT    GTG AGA
                                ||||||||| ||    ||| |||
                                AAGGAGTTT GA    CAC TCT
                                    C  ACCC_  C
GAM696  KIAA0194 3' TCTCCACCCCAAGCTTTGAGGA 65988       C  CCAGA  A
          A                      TTCCTCAGA CT    GTG AGA
                                ||||||||| ||    ||| |||
                                AAGGAGTTT GA    CAC TCT
                                    C  ACCC_  C
GAM696  KIAA0451 3' TCTTCACATAAGCCTGGGGAA 29117       AC  CCAGA
                                TTCCTCAG  CT    GTGAAGA
                                ||||||||  ||    |||||||
                                AAGGGGTC  GA    CACTTCT
                                    C_  ATA__
GAM696  KIAA0451 3' TCTTCACATAAGCCTGGGGAA 29117       AC  CCAGA
                                TTCCTCAG  CT    GTGAAGA
                                ||||||||  ||    |||||||
                                AAGGGGTC  GA    CACTTCT
                                    C_  ATA__
GAM696  KIAA1432 3' TCCTCTGCAAAACTGAGGAA  66751       ACCTC    T
                                TTCCTCAG    CAGAG GA
                                ||||||||    ||||| ||
                                AAGGAGTC    GTCTC CT
                                    AAAAC    _
GAM696  KIAA1432 3' TCCTCTGCAAAACTGAGGAA  66751       ACCTC    T
                                TTCCTCAG    CAGAG GA
                                ||||||||    ||||| ||
                                AAGGAGTC    GTCTC CT
                                    AAAAC    _
GAM696  KIAA1559 3' CTCCACTGATGGTAAAATCTGA 73063       CCT__  G_   A
          GGA                     TCCTCAGA    CCA  AGTG AG
                                ||||||||    |||  |||| ||
                                AGGAGTCT    GGT  TCAC TC
                                    AAAAT   AG   C
GAM696  KIAA1559 3' CTCCACTGATGGTAAAATCTGA 73063       CCT__  G_   A
          GGA                     TCCTCAGA    CCA  AGTG AG
                                ||||||||    |||  |||| ||
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                                AGGAGTCT    GGT  TCAC TC
                                    AAAAT   AG   C
GAM696  KIAA1735  3'  CTTTGAGAAAACTGAGGAA   87628       ACC  _
                                TTCCTCAG   TC CAGAG
                                ||||||||   || |||||
                                AAGGAGTC   AG GTTTC
                                    AAA  A
GAM696  KIAA1735  3'  CTTTGAGAAAACTGAGGAA   87628       ACC  _
                                TTCCTCAG   TC CAGAG
                                ||||||||   || |||||
                                AAGGAGTC   AG GTTTC
                                    AAA  A
GAM696  KIAA1900  5'  TCTAAGGCTGAGAACCTGAGGA 73250       ACC  _  AGTGA
          A                      TTCCTCAG   TC CAG    AGA
                                ||||||||   || |||    |||
                                AAGGAGTC   AG GTC    TCT
                                    CA_  A  GGAA_
GAM696  KIAA1900  5'  TCTAAGGCTGAGAACCTGAGGA 73250       ACC  _  AGTGA
          A                      TTCCTCAG   TC CAG    AGA
                                ||||||||   || |||    |||
                                AAGGAGTC   AG GTC    TCT
                                    CA_  A  GGAA_
GAM696  KIAA1908  3'  TCAGGTCTGGAGGCCTGAG   73403     A      G_
                                CTCAG CCTCCAGA  TGA
                                ||||| ||||||||  |||
                                GAGTC GGAGGTCT  ACT
                                  C       GG
GAM696  KIAA1908  3'  TCAGGTCTGGAGGCCTGAG   73403     A      G_
                                CTCAG CCTCCAGA  TGA
                                ||||| ||||||||  |||
                                GAGTC GGAGGTCT  ACT
                                  C       GG
GAM696  LASP1     3'  CGAATGAGAGGTTGAGGAA   20452      A   _  GAG
                                TTCCTCAG CCTC CA   TG
                                |||||||| |||| ||   ||
                                AAGGAGTT GGAG GT   GC
                                    _   A  AA_
GAM696  LASP1     3'  CGAATGAGAGGTTGAGGAA   20452      A   _  GAG
                                TTCCTCAG CCTC CA   TG
                                |||||||| |||| ||   ||
                                AAGGAGTT GGAG GT   GC
                                    _   A  AA_
GAM696  MAGE-E1   3'  TCCTCGGCGATCTGAGGAA   47947       CCT  A   T
                                TTCCTCAGA   CC GAG GA
                                |||||||||   || ||| ||
                                AAGGAGTCT   GG CTC CT
                                     AGC  _   _
GAM696  MAGE-E1   3'  TCCTCGGCGATCTGAGGAA   47947       CCT  A   T
                                TTCCTCAGA   CC GAG GA
                                |||||||||   || ||| ||
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                                AAGGAGTCT   GG CTC CT
                                     AGC  _   _
GAM696  MGC13102  3'  CTTCACCTTTGGGGCCCGAG   50315     AGAC       _
                                CTC    CTCCAGAG TGAAG
                                |||    |||||||| |||||
                                GAG    GGGGTTTC ACTTC
                                  CCC_       C
GAM696  MGC13102  3'  CTTCACCTTTGGGGCCCGAG   50315     AGAC       _
                                CTC    CTCCAGAG TGAAG
                                |||    |||||||| |||||
                                GAG    GGGGTTTC ACTTC
                                  CCC_       C
GAM696  MGC2721   3'  TCTTTGTTAAAGATCTGAGGGA 51224          C  CCAG  TG
                                TTCCTCAGA CT    AG  AAGA
                                ||||||||| ||    ||  ||||
                                AGGGAGTCT GA    TT  TTCT
                                     A  AA__  GT
GAM696  MGC2721   3'  TCTTTGTTAAAGATCTGAGGGA 51224          C  CCAG  TG
                                TTCCTCAGA CT    AG  AAGA
                                ||||||||| ||    ||  ||||
                                AGGGAGTCT GA    TT  TTCT
                                     A  AA__  GT
GAM696  MIDORI    3'  TCTCCATTTAAGGTCTGG    73794        CCA    A
                                TCAGACCT   GAGTG AGA
                                ||||||||   ||||| |||
                                GGTCTGGA   TTTAC TCT
                                     A__    C
GAM696  MIDORI    3'  TCTCCATTTAAGGTCTGG    73794        CCA    A
                                TCAGACCT   GAGTG AGA
                                ||||||||   ||||| |||
                                GGTCTGGA   TTTAC TCT
                                     A__    C
GAM696  PELI2     3'  TCTTCACTATTGTACCTGTGGA 41185      T   ACCTC  _
          A                      TTCC CAG    CAG AGTGAAGA
                                |||| |||    ||| ||||||||
                                AAGG GTC    GTT TCACTTCT
                                  T  CAT__  A
GAM696  PELI2     3'  TCTTCACTATTGTACCTGTGGA 41185      T   ACCTC  _
          A                      TTCC CAG    CAG AGTGAAGA
                                |||| |||    ||| ||||||||
                                AAGG GTC    GTT TCACTTCT
                                  T  CAT__  A
GAM696  PKNOX2    3'  CTTCACTCTCTCCTGGAA    90878     TCA  CCTCC
                                TTCC   GA    AGAGTGAAG
                                ||||   ||    |||||||||
                                AAGG   CT    TCTCACTTC
                                  TC_  C____
GAM696  PKNOX2    3'  CTTCACTCTCTCCTGGAA    90878     TCA  CCTCC
                                TTCC   GA    AGAGTGAAG
                                ||||   ||    |||||||||
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                                AAGG  CT    TCTCACTTC
                                  TC_ C____
GAM696  PRDM11   3' CTTCCGGGAGACCTGAGGAG  39582       AC   AGAGT
                                TTCCTCAG CTCC    GAAG
                                |||||||| ||||    ||||
                                GAGGAGTC GAGG    CTTC
                                    CA   GC___
GAM696  PRDM11   3' CTTCCGGGAGACCTGAGGAG  39582       AC   AGAGT
                                TTCCTCAG CTCC    GAAG
                                |||||||| ||||    ||||
                                GAGGAGTC GAGG    CTTC
                                    CA   GC___
GAM696  RAI      3' CTTGGGAGGTCTGGGAA    21881     T      A
                                TTCC CAGACCTCC GAG
                                |||| ||||||||| |||
                                AAGG GTCTGGAGG TTC
                                  _       G
GAM696  RAI      3' CTTGGGAGGTCTGGGAA    21881     T      A
                                TTCC CAGACCTCC GAG
                                |||| ||||||||| |||
                                AAGG GTCTGGAGG TTC
                                  _       G
GAM696  SDC3     3' TCCTCTAAGGCTGAGGAA   27764       A  CC   T
                                TTCCTCAG CCT  AGAG GA
                                |||||||| |||  |||| ||
                                AAGGAGTC GGA  TCTC CT
                                    _  A_   _
GAM696  SDC3     3' TCCTCTAAGGCTGAGGAA   27764       A  CC   T
                                TTCCTCAG CCT  AGAG GA
                                |||||||| |||  |||| ||
                                AAGGAGTC GGA  TCTC CT
                                    _  A_   _
GAM696  SKIP     3' CTCCACCCTGCCATCTGAGGAA 33276       CCTC  A  A
                                TTCCTCAGA   CAG GTG AG
                                |||||||||   ||| ||| ||
                                AAGGAGTCT   GTC CAC TC
                                    ACC_  C  C
GAM696  SKIP     3' CTCCACCCTGCCATCTGAGGAA 33276       CCTC  A  A
                                TTCCTCAGA   CAG GTG AG
                                |||||||||   ||| ||| ||
                                AAGGAGTCT   GTC CAC TC
                                    ACC_  C  C
GAM696  SKIP     3' CTCCACCCTGCCATCTGAGGAA 55368       CCTC  A  A
                                TTCCTCAGA   CAG GTG AG
                                |||||||||   ||| ||| ||
                                AAGGAGTCT   GTC CAC TC
                                    ACC_  C  C
GAM696  SKIP     3' CTCCACCCTGCCATCTGAGGAA 55368       CCTC  A  A
                                TTCCTCAGA   CAG GTG AG
                                |||||||||   ||| ||| ||
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                                AAGGAGTCT   GTC CAC TC
                                     ACC_   C   C
GAM696  TFIP11    3'  CATGTATTGTGAAGTCTGAGGA 24054        C  _  GA__
          A                   TTCCTCAGAC TC CA   GTG
                              |||||||||| || ||   |||
                              AAGGAGTCTG AG GT   TAC
                                   A  T  TATG
GAM696  TFIP11    3'  CATGTATTGTGAAGTCTGAGGA 24054        C  _  GA__
          A                   TTCCTCAGAC TC CA   GTG
                              |||||||||| || ||   |||
                              AAGGAGTCTG AG GT   TAC
                                   A  T  TATG
GAM696  LOC114971 3'  TGCCTAAGGTCTGAG      73154        CC  A
                              CTCAGACCT  AG GTG
                              |||||||||  || |||
                              GAGTCTGGA  TC CGT
                                   A_  _
GAM696  LOC114971 3'  TGCCTAAGGTCTGAG      73154        CC  A
                              CTCAGACCT  AG GTG
                              |||||||||  || |||
                              GAGTCTGGA  TC CGT
                                   A_  _
GAM696  LOC121133 5'  TCTGGAGGTCTAGGGAA    75993     TC
                              TTCC  AGACCTCCAGA
                              ||||  ||||||||||
                              AAGG  TCTGGAGGTCT
                                GA
GAM696  LOC121133 5'  TCTGGAGGTCTAGGGAA    75993     TC
                              TTCC  AGACCTCCAGA
                              ||||  ||||||||||
                              AAGG  TCTGGAGGTCT
                                GA
GAM696  LOC126302 3'  CTGGACAAAGGTCTGAGGGA  74494         ____
                              TTCCTCAGACC   TCCAG
                              ||||||||||    |||||
                              AGGGAGTCTGG   AGGTC
                                    AAAC
GAM696  LOC126302 3'  CTGGACAAAGGTCTGAGGGA  74494         ____
                              TTCCTCAGACC   TCCAG
                              ||||||||||    |||||
                              AGGGAGTCTGG   AGGTC
                                    AAAC
GAM696  LOC144438 3'  TCTTCAGTTGAAGCTGAGGAA  76838       ACCTCCA  G
                              TTCCTCAG      GA TGAAGA
                              ||||||||      || ||||||
                              AAGGAGTC      TT ACTTCT
                                   GAAG___  G
GAM696  LOC144438 3'  TCTTCAGTTGAAGCTGAGGAA  76838       ACCTCCA  G
                              TTCCTCAG      GA TGAAGA
                              ||||||||      || ||||||
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                                AAGGAGTC      TT ACTTCT
                                    GAAG___  G
GAM696  LOC145173 3'  GCCTAAAGGCTGAGGAA     77042        A  CC  A
                                TTCCTCAG CCT  AG GT
                                |||||||| |||  || ||
                                AAGGAGTC GGA  TC CG
                                    _   AA  _
GAM696  LOC145173 3'  GCCTAAAGGCTGAGGAA     77042        A  CC  A
                                TTCCTCAG CCT  AG GT
                                |||||||| |||  || ||
                                AAGGAGTC GGA  TC CG
                                    _   AA  _
GAM696  LOC146159 5'  CTCCATTTTATACCTGAGGAA  77679        ACCTCC     A
                                TTCCTCAG     AGAGTG AG
                                ||||||||     |||||| ||
                                AAGGAGTC     TTTTAC TC
                                    CATA__     C
GAM696  LOC146159 5'  CTCCATTTTATACCTGAGGAA  77679        ACCTCC     A
                                TTCCTCAG     AGAGTG AG
                                ||||||||     |||||| ||
                                AAGGAGTC     TTTTAC TC
                                    CATA__     C
GAM696  LOC146669 5'  TTCTGAGATCTGAGGA      78061        C  C
                                TCCTCAGA CTC AGAG
                                |||||||| ||| ||||
                                AGGAGTCT GAG TCTT
                                    A  _
GAM696  LOC146669 5'  TTCTGAGATCTGAGGA      78061        C  C
                                TCCTCAGA CTC AGAG
                                |||||||| ||| ||||
                                AGGAGTCT GAG TCTT
                                    A  _
GAM696  LOC146669 5'  TTCTGAGATCTGAGGA      78062        C  C
                                TCCTCAGA CTC AGAG
                                |||||||| ||| ||||
                                AGGAGTCT GAG TCTT
                                    A  _
GAM696  LOC146669 5'  TTCTGAGATCTGAGGA      78062        C  C
                                TCCTCAGA CTC AGAG
                                |||||||| ||| ||||
                                AGGAGTCT GAG TCTT
                                    A  _
GAM696  LOC146669 5'  TTCTGAGATCTGAGGA      78063        C  C
                                TCCTCAGA CTC AGAG
                                |||||||| ||| ||||
                                AGGAGTCT GAG TCTT
                                    A  _
GAM696  LOC146669 5'  TTCTGAGATCTGAGGA      78063        C  C
                                TCCTCAGA CTC AGAG
                                |||||||| ||| ||||
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AGGAGTCT GAG TCTT
A _
GAM696 LOC146669 5' TTCTGAGATCTGAGGA 78064 C C
TCCTCAGA CTC AGAG
|||||||| ||| ||||
AGGAGTCT GAG TCTT
A _
GAM696 LOC146669 5' TTCTGAGATCTGAGGA 78064 C C
TCCTCAGA CTC AGAG
|||||||| ||| ||||
AGGAGTCT GAG TCTT
A _
GAM696 LOC146669 5' TTCTGAGATCTGAGGA 78065 C C
TCCTCAGA CTC AGAG
|||||||| ||| ||||
AGGAGTCT GAG TCTT
A _
GAM696 LOC146669 5' TTCTGAGATCTGAGGA 78065 C C
TCCTCAGA CTC AGAG
|||||||| ||| ||||
AGGAGTCT GAG TCTT
A _
GAM696 LOC146669 5' TTCTGAGATCTGAGGA 78066 C C
TCCTCAGA CTC AGAG
|||||||| ||| ||||
AGGAGTCT GAG TCTT
A _
GAM696 LOC146669 5' TTCTGAGATCTGAGGA 78066 C C
TCCTCAGA CTC AGAG
|||||||| ||| ||||
AGGAGTCT GAG TCTT
A _
GAM696 LOC146669 5' TTCTGAGATCTGAGGA 78067 C C
TCCTCAGA CTC AGAG
|||||||| ||| ||||
AGGAGTCT GAG TCTT
A _
GAM696 LOC146669 5' TTCTGAGATCTGAGGA 78067 C C
TCCTCAGA CTC AGAG
|||||||| ||| ||||
AGGAGTCT GAG TCTT
A _
GAM696 LOC146669 5' TTCTGAGATCTGAGGA 78068 C C
TCCTCAGA CTC AGAG
|||||||| ||| ||||
AGGAGTCT GAG TCTT
A _
GAM696 LOC146669 5' TTCTGAGATCTGAGGA 78068 C C
TCCTCAGA CTC AGAG
|||||||| ||| ||||

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                                AGGAGTCT GAG TCTT
                                    A  _
GAM696  LOC146669 5'  TTCTGAGATCTGAGGA     78069        C  C
                                TCCTCAGA CTC AGAG
                                |||||||| ||| ||||
                                AGGAGTCT GAG TCTT
                                    A  _
GAM696  LOC146669 5'  TTCTGAGATCTGAGGA     78069        C  C
                                TCCTCAGA CTC AGAG
                                |||||||| ||| ||||
                                AGGAGTCT GAG TCTT
                                    A  _
GAM696  LOC146669 5'  TTCTGAGATCTGAGGA     78070        C  C
                                TCCTCAGA CTC AGAG
                                |||||||| ||| ||||
                                AGGAGTCT GAG TCTT
                                    A  _
GAM696  LOC146669 5'  TTCTGAGATCTGAGGA     78070        C  C
                                TCCTCAGA CTC AGAG
                                |||||||| ||| ||||
                                AGGAGTCT GAG TCTT
                                    A  _
GAM696  LOC146669 5'  TTCTGAGGTCTGAGGA     78071          C
                                TCCTCAGACCTC AGAG
                                |||||||||||| ||||
                                AGGAGTCTGGAG TCTT
                                           _
GAM696  LOC146669 5'  TTCTGAGGTCTGAGGA     78071          C
                                TCCTCAGACCTC AGAG
                                |||||||||||| ||||
                                AGGAGTCTGGAG TCTT
                                           _
GAM696  LOC148758 3'  CTTCAGAAAGAGAAAGTCTGGG 78969          ___  CAGAG
          GAA                    TTCCTCAGAC  CTC    TGAAG
                                |||||||||  |||    |||||
                                AAGGGGTCTG  GAG    ACTTC
                                     AAA  AAAG_
GAM696  LOC148758 3'  CTTCAGAAAGAGAAAGTCTGGG 78969          ___  CAGAG
          GAA                    TTCCTCAGAC  CTC    TGAAG
                                |||||||||  |||    |||||
                                AAGGGGTCTG  GAG    ACTTC
                                     AAA  AAAG_
GAM696  LOC149911 3'  CTCCACATGGAGGTCCCAGGAA 84706      CA      GA  A
                                TTCCT  GACCTCCA  GTG AG
                                |||||  ||||||||  ||| ||
                                AAGGA  CTGGAGGT  CAC TC
                                   CC       A_  C
GAM696  LOC149911 3'  CTCCACATGGAGGTCCCAGGAA 84706      CA      GA  A
                                TTCCT  GACCTCCA  GTG AG
                                |||||  ||||||||  ||| ||
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                                AAGGA  CTGGAGGT  CAC TC
                                   CC       A_   C
GAM696  LOC150208 3'  CACTGGTCTGGGAA       84914      T     TCCAG
                                TTCC CAGACC    AGTG
                                |||| ||||||    ||||
                                AAGG GTCTGG    TCAC
                                  _     _____
GAM696  LOC150208 3'  CACTGGTCTGGGAA       84914      T     TCCAG
                                TTCC CAGACC    AGTG
                                |||| ||||||    ||||
                                AAGG GTCTGG    TCAC
                                  _     _____
GAM696  LOC152313 5'  TCTCCACTTTGGTCTAGGAA   85668      C     TCC      A
                                TTCCT AGACC   AGAGTG AGA
                                ||||| |||||   |||||| |||
                                AAGGA TCTGG   TTTCAC TCT
                                  _    ___     C
GAM696  LOC152313 5'  TCTCCACTTTGGTCTAGGAA   85668      C     TCC      A
                                TTCCT AGACC   AGAGTG AGA
                                ||||| |||||   |||||| |||
                                AAGGA TCTGG   TTTCAC TCT
                                  _    ___     C
GAM696  LOC153811 3'  TCTTCACTCTAACTTGGGGAA  80960        ACCTCC
                                TTCCTCAG     AGAGTGAAGA
                                ||||||||     ||||||||||
                                AAGGGGTT     TCTCACTTCT
                                     CAA___
GAM696  LOC153811 3'  TCTTCACTCTAACTTGGGGAA  80960        ACCTCC
                                TTCCTCAG     AGAGTGAAGA
                                ||||||||     ||||||||||
                                AAGGGGTT     TCTCACTTCT
                                     CAA___
GAM696  LOC162048 5'  TCACTCTGGGGTGAAGA     82330     C   GAC
                                TC TCA   CTCCAGAGTGA
                                || |||   ||||||||||
                                AG AGT   GGGGTCTCACT
                                 A  ___
GAM696  LOC162048 5'  TCACTCTGGGGTGAAGA     82330     C   GAC
                                TC TCA   CTCCAGAGTGA
                                || |||   ||||||||||
                                AG AGT   GGGGTCTCACT
                                 A  ___
GAM696  LOC202020 3'  TATTATGAGGCCTGAGGAA    89138        A   CAG
                                TTCCTCAG CCTC   AGTG
                                |||||||| ||||   ||||
                                AAGGAGTC GGAG   TTAT
                                     C    TA_
GAM696  LOC202020 3'  TATTATGAGGCCTGAGGAA    89138        A   CAG
                                TTCCTCAG CCTC   AGTG
                                |||||||| ||||   ||||
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                                AAGGAGTC GGAG   TTAT
                                    C    TA_
GAM696  LOC202460 5'  CTCCACCTCCTGGGTTTGAGGA 89181          CC_  A   A
          A                      TTCCTCAGACCT   AG GTG AG
                                 ||||||||||||   || ||| ||
                                 AAGGAGTTTGGG   TC CAC TC
                                       TCC  _   C
GAM696  LOC202460 5'  CTCCACCTCCTGGGTTTGAGGA 89181          CC_  A   A
          A                      TTCCTCAGACCT   AG GTG AG
                                 ||||||||||||   || ||| ||
                                 AAGGAGTTTGGG   TC CAC TC
                                       TCC  _   C
GAM696  LOC203557 5'  TCTTCTGAAAGGCCTGAGGGA  89515        A  C_    T
                                 TTCCTCAG CCT  CAGAG GA
                                 ||||||||| |||  ||||| ||
                                 AGGGAGTC GGA  GTCTT CT
                                     C   AA    _
GAM696  LOC203557 5'  TCTTCTGAAAGGCCTGAGGGA  89515        A  C_    T
                                 TTCCTCAG CCT  CAGAG GA
                                 ||||||||| |||  ||||| ||
                                 AGGGAGTC GGA  GTCTT CT
                                     C   AA    _
GAM696  LOC219404 3'  CTCCAAGGTCTGGGAA      93493      T      CCA
                                 TTCC CAGACCT   GAG
                                 |||| |||||||   |||
                                 AAGG GTCTGGA   CTC
                                   _      AC_
GAM696  LOC219404 3'  CTCCAAGGTCTGGGAA      93493      T      CCA
                                 TTCC CAGACCT   GAG
                                 |||| |||||||   |||
                                 AAGG GTCTGGA   CTC
                                   _      AC_
GAM696  LOC219654 3'  CTTCACTTGGTGTCTTAGGAA  91304      C    CT   G
                                 TTCCT AGAC  CCA AGTGAAG
                                 ||||| ||||  ||| |||||||
                                 AAGGA TCTG  GGT TCACTTC
                                   T    T_   _
GAM696  LOC219654 3'  CTTCACTTGGTGTCTTAGGAA  91304      C    CT   G
                                 TTCCT AGAC  CCA AGTGAAG
                                 ||||| ||||  ||| |||||||
                                 AAGGA TCTG  GGT TCACTTC
                                   T    T_   _
GAM696  LOC54499  3'  CTTCAAAGTGCTGAGGAA    70630        AC  CCAGAG
                                 TTCCTCAG  CT     TGAAG
                                 ||||||||  ||     |||||
                                 AAGGAGTC  GA     ACTTC
                                     GT  A_____
GAM696  LOC54499  3'  CTTCAAAGTGCTGAGGAA    70630        AC  CCAGAG
                                 TTCCTCAG  CT     TGAAG
                                 ||||||||  ||     |||||
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                                AAGGAGTC  GA     ACTTC
                                    GT  A_____
GAM696  LOC93132  5'  TCTTCACCCTGCAGACCTGAGG 71504        AC  C   A
          AA                    TTCCTCAG  CT CAG GTGAAGA
                                ||||||||  || ||| |||||||
                                AAGGAGTC  GA GTC CACTTCT
                                    CA  C   C
GAM696  LOC93132  5'  TCTTCACCCTGCAGACCTGAGG 71504        AC  C   A
          AA                    TTCCTCAG  CT CAG GTGAAGA
                                ||||||||  || ||| |||||||
                                AAGGAGTC  GA GTC CACTTCT
                                    CA  C   C
GAM696  LOC93444  5'  CTGTGATAGAGATCTGAGGAG  72386        C  ___  G
                                TTCCTCAGA CTC   CA AG
                                ||||||||| |||   || ||
                                GAGGAGTCT GAG   GT TC
                                     A   ATA  G
GAM696  LOC93444  5'  CTGTGATAGAGATCTGAGGAG  72386        C  ___  G
                                TTCCTCAGA CTC   CA AG
                                ||||||||| |||   || ||
                                GAGGAGTCT GAG   GT TC
                                     A   ATA  G
GAM697  ADAMTS8   5'  TCGGGCCGCCAGCACCTG    22886    _     ATAAG
                                CAG TGCTGGC    CTGA
                                ||| |||||||    ||||
                                GTC ACGACCG    GGCT
                                  C      CCG__
GAM697  BAP1      3'  TCAGGGACCCAGCACTGG    16219         CATAAG
                                CCAGTGCTGG     CTGA
                                ||||||||||     ||||
                                GGTCACGACC     GACT
                                     CAGG__
GAM697  BF        5'  TTCAGCTTGGACACTG      8140       CTGGCA
                                CAGTG     TAAGCTGAA
                                |||||     |||||||||
                                GTCAC     GTTCGACTT
                                   AG____
GAM697  C1QB      3'  TTCAACTCTGTGTCCCAGCACT 4923    A       __   _ C
          GGC                     G CCAGTGCTGG  CATA AG TGAA
                                | ||||||||||  |||| || ||||
                                C GGTCACGACC  GTGT TC ACTT
                                _        CT   C  A
GAM697  CHC1      3'  CAGCCCTGAGCACTGTGTC    7020     _     __ CATAA
                                GAC CAGTGCT  GG    GCTG
                                ||| |||||||  ||    ||||
                                CTG GTCACGA  CC    CGAC
                                  T      GT _____
GAM697  CMRF35    5'  CAGAGCTGTCAGCACCGG    21929    A       TAAG
                                CC GTGCTGGCA    CTG
                                || |||||||||    |||
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                                GG CACGACTGT    GAC
                                 C        CGA_
GAM697  EPHB6    3'  TCAGCCCTGGACACTGGTC    15466         _ TG CATAA
                                GACCAGTG C  G    GCTGA
                                |||||||| |  |    |||||
                                CTGGTCAC G  C    CGACT
                                    A GT C____
GAM697  EVPL     5'  CAGCCTGAGCCAGCACT     8803          A  A
                                AGTGCTGGC TA GCTG
                                ||||||||| || ||||
                                TCACGACCG GT CGAC
                                    A  C
GAM697  GARP     3'  CAGCCCAGCACTGG        18594          CATAA
                                CCAGTGCTGG    GCTG
                                ||||||||||    ||||
                                GGTCACGACC    CGAC
                                      _____
GAM697  GJB5     3'  CAGCTCGACGGCACTGG     17945          GCATA
                                CCAGTGCTG    AGCTG
                                |||||||||    |||||
                                GGTCACGGC    TCGAC
                                    AGC__
GAM697  GPR81    3'  CTTACCAGCATTAGTC      50757     C       CA
                                GAC AGTGCTGG  TAAG
                                ||| ||||||||  ||||
                                CTG TTACGACC  ATTC
                                  A       __
GAM697  IFI16    5'  AGCAAGCCAGCACTAGTC    71221     C       ATAA
                                GAC AGTGCTGGC    GCT
                                ||| |||||||||    |||
                                CTG TCACGACCG    CGA
                                  A        AA__
GAM697  KRT4     3'  CAGCTGGGCCCAGCACTGGT   9635           _ ATA
                                ACCAGTGCTGG C   AGCTG
                                |||||||||| |   |||||
                                TGGTCACGACC G   TCGAC
                                      C GG_
GAM697  MAP3K9   3'  TTCAGCTTCCCAAACACCAGT  60709    CA  C_  CAT
                                AC  GTG  TGG   AAGCTGAA
                                ||  |||  |||   ||||||||
                                TG  CAC  ACC   TTCGACTT
                                 AC   AA   C__
GAM697  MGAT5    5'  TCAGCTTACAGTTCCTG     10028     T_   GCA
                                CAG  GCTG   TAAGCTGA
                                |||  ||||   ||||||||
                                GTC  TGAC   ATTCGACT
                                  CT    ____
GAM697  MOCS1    3'  TTCAGCTTAACAGTTGCCCGGT 92037      A_  _   GCA
            C                    GACC  GTG CTG   TAAGCTGAA
                                ||||  ||| |||   |||||||||
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                                CTGG  CGT GAC   ATTCGACTT
                                  CC   T  A__
GAM697  P23     3'  TCAGCTTATACCCGGGCT    21719     G   C_
                                AGT CTGG  ATAAGCTGA
                                ||| ||||  |||||||||
                                TCG GGCC  TATTCGACT
                                  _   CA
GAM697  PFKFB4   3'  TCAGCCACATGCAACACTGTGT 15874     _    CTG   AA_
           C                     GAC CAGTG   GCAT   GCTGA
                                ||| |||||   ||||   |||||
                                CTG GTCAC   CGTA   CGACT
                                  T    AA_   CAC
GAM697  PTPRK    3'  TTCAGCCTGTGGCCCAGCACTG 11125          __   A
           GTC                    GACCAGTGCTGG  CATA GCTGAA
                                ||||||||||||  |||| ||||||
                                CTGGTCACGACC  GTGT CGACTT
                                       CG   C
GAM697  RNPEPL1  3'  CGGATGCCAGCACCTG     36676    _       AAG
                                CAG TGCTGGCAT   CTG
                                ||| |||||||||   |||
                                GTC ACGACCGTA   GGC
                                  C       ___
GAM697  UBE2L3   3'  TCAGCCCTGGCACTGGC     12507   A      TG CATAA
                                G CCAGTGC  G    GCTGA
                                | |||||||  |    |||||
                                C GGTCACG  C    CGACT
                                _      GT C____
GAM697  APXL2    5'  CAGCCTCAGCACTCATC     75185   CC      CATAA
                                GA  AGTGCTGG    GCTG
                                ||  ||||||||    ||||
                                CT  TCACGACT    CGAC
                                 AC       C____
GAM697  ARHGEF9  3'  TTCAGCTTACCAAGCA     30824     _ CA
                                TGCT GG  TAAGCTGAA
                                |||| ||  |||||||||
                                ACGA CC  ATTCGACTT
                                  A  __
GAM697  CEGP1    3'  TTCAGCTTCCTCTAGCCCGG  40589    AGT    CAT
                                CC   GCTGG   AAGCTGAA
                                ||   |||||   ||||||||
                                GG   CGATC   TTCGACTT
                                 CC_    TCC
GAM697  DKFZp547D155 3'  CAGCCCTGAGACCACTGGTC   70435        CTGG  TAA
                                GACCAGTG    CA   GCTG
                                ||||||||    ||   ||||
                                CTGGTCAC    GT   CGAC
                                     CAGA  CC_
GAM697  DKFZP727G051 3'  TTCAGCCCATCAACCAGCATTG 69483           CATAA__
           GTC                    GACCAGTGCTGG      GCTGAA
                                ||||||||||||      ||||||
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                                CTGGTTACGACC      CGACTT
                                      AACTACC
GAM697  DUSP14    5'  CACTGTCACCAGCACTGCTC  22834    C       CATA  C
                                GA CAGTGCTGG    AG TG
                                || |||||||||    || ||
                                CT GTCACGACC    TC AC
                                 C        ACTG  _
GAM697  FLJ10206  5'  CAGCTTATGCCAGGAGTC    35898    CAGTG
                                GAC    CTGGCATAAGCTG
                                |||    ||||||||||||||
                                CTG    GACCGTATTCGAC
                                  AG___
GAM697  FLJ20967  5'  GGCGCCCAGCACTGGTT     41962          CATAA
                                GACCAGTGCTGG    GCT
                                ||||||||||||    |||
                                TTGGTCACGACC    CGG
                                      CG___
GAM697  FLJ22569  3'  TTCAGCTTACTAAACTG     43679     GC   CA
                                CAGT  TGG  TAAGCTGAA
                                ||||  |||  |||||||||
                                GTCA  ATC  ATTCGACTT
                                  A_  __
GAM697  FOXN4     3'  TTCAGCTTGGACACACTGG    75574       C  GCA
                                CCAGTG TG   TAAGCTGAA
                                |||||| ||   |||||||||
                                GGTCAC AC   GTTCGACTT
                                   _  AG_
GAM697  GW112     3'  TTCAACTGAAGCCAGCACTGGT 21194           ATA  C
           T                     GACCAGTGCTGGC   AG TGAA
                                ||||||||||||||   || ||||
                                TTGGTCACGACCG   TC ACTT
                                      AAG  A
GAM697  HOOK2     3'  CAGCTCACATGGCGCCCAGCAC 25256         _____  A__
           TGG                    CCAGTGCTGG    CAT   AGCTG
                                ||||||||||    |||   |||||
                                GGTCACGACC    GTA   TCGAC
                                      CGCG   CAC
GAM697  jdp2      3'  TTCAGCACAGCCAGCAT     55327        ATAA
                                GTGCTGGC    GCTGAA
                                ||||||||    ||||||
                                TACGACCG    CGACTT
                                   ACA_
GAM697  KIAA0767  3'  TCTGCTGCCAGCACAGG     60632    A       TAA  T
                                CC GTGCTGGCA   GC GA
                                || |||||||||   || ||
                                GG CACGACCGT   CG CT
                                 A        ___  T
GAM697  KIAA0923  3'  TCAGCTTGATGCATGGTC    25838      G   TGGCA
                                GACCA TGC    TAAGCTGA
                                ||||| |||    ||||||||
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                                CTGGT ACG    GTTCGACT
                                  _  TA___
GAM697  KIAA0982  3'  TTCACTGTTTGCCAGCAC    25852        TA_  C
                                GTGCTGGCA   AG TGAA
                                |||||||||   || ||||
                                CACGACCGT   TC ACTT
                                     TTG  _
GAM697  KIAA1000  3'  TTCAGCTTTGCAAAGTACTGG  65281        G_   T
                                CCAGTGCT  GCA AAGCTGAA
                                ||||||||  ||| ||||||||
                                GGTCATGA  CGT TTCGACTT
                                     AA  _
GAM697  MAP3K3    3'  TCAGCCTGGGCGCTGGTC    9999         GG  TAA
                                GACCAGTGCT  CA   GCTGA
                                ||||||||||  ||   |||||
                                CTGGTCGCGG  GT   CGACT
                                     __  C__
GAM697  MGC16037  5'  CTTGTCCAGCACTAGTC     51821     C       C
                                GAC AGTGCTGG ATAAG
                                ||| |||||||| |||||
                                CTG TCACGACC TGTTC
                                  A       _
GAM697  MIDORI    3'  TCAGCTTATCCTGCAACT    73792     _  T  C
                                AGT GC GG ATAAGCTGA
                                ||| || || |||||||||
                                TCA CG CC TATTCGACT
                                  A  T  _
GAM697  MtFMT     5'  CAGTGGCGAGCACTGG      57651        G  ATAA
                                CCAGTGCT GC    GCTG
                                |||||||| ||    ||||
                                GGTCACGA CG    TGAC
                                     G  G___
GAM697  PCDH16    5'  TCAGTTCCAACCACTGG     72826       C_   CATA
                                CCAGTG  TGG    AGCTGA
                                ||||||  |||    ||||||
                                GGTCAC  ACC    TTGACT
                                   CA  _____
GAM697  QKI       3'  CAGCTTATCAACTCGTC     65439     C   GCTGGC
                                GAC AGT      ATAAGCTG
                                ||| |||      ||||||||
                                CTG TCA      TATTCGAC
                                  C   AC_____
GAM697  TNRC6     3'  CAACTTTTAGCACTG       70506         CAT   C
                                CAGTGCTGG   AAG TG
                                |||||||||   ||| ||
                                GTCACGATT   TTC AC
                                     ___   A
GAM697  TOB2      3'  CAGCCCAGGCCAGCACTG    95618         ATAA
                                CAGTGCTGGC    GCTG
                                ||||||||||    ||||
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                                GTCACGACCG   CGAC
                                     GACC
GAM697  TU12B1-TY 3'  TCAGCCCACAGCACTGTC    33406     C      GCATAA
                                GAC AGTGCTG     GCTGA
                                ||| |||||||     |||||
                                CTG TCACGAC     CGACT
                                  _      ACC___
GAM697  TUSP     3'  TCAGCCTAAGAGCGCAGCACTG 39641        _ A__  A
                                CAGTGCTG GC   TA GCTGA
                                |||||||| ||   || |||||
                                GTCACGAC CG   AT CGACT
                                     G  AGA  C
GAM697  USP19    3'  TCAGCTTATGCATCTGGT    88959      TGCTG
                                ACCAG    GCATAAGCTGA
                                |||||    ||||||||||
                                TGGTC    CGTATTCGACT
                                   TA___
GAM697  ZD52F10  3'  CAGCCTGTGCCAGCCCTGG   52819     T       A
                                CCAG GCTGGCATA GCTG
                                |||| ||||||||| ||||
                                GGTC CGACCGTGT CGAC
                                  C       C
GAM697  LOC145268 3'  TCAGCTTACAAGAGCCACTG   77062      _ GGCA
                                CAGTG CT    TAAGCTGA
                                ||||| ||    ||||||||
                                GTCAC GA    ATTCGACT
                                   C  GAAC
GAM697  LOC149296 5'  CAGCTTATGGGCAGCA      79256      G_
                                TGCTG  CATAAGCTG
                                |||||  |||||||||
                                ACGAC  GTATTCGAC
                                   GG
GAM697  LOC161877 5'  TCAGGGCAGGCCAGCGCTGG   82326          ATAAG
                                CCAGTGCTGGC    CTGA
                                ||||||||||     ||||
                                GGTCGCGACCG    GACT
                                      GACGG
GAM697  LOC163115 5'  TCAGCCCCTGACAGCACTGG   82413        G  TAA
                                CCAGTGCTG CA   GCTGA
                                |||||||| ||   |||||
                                GGTCACGAC GT   CGACT
                                     A  CCC
GAM697  LOC196500 3'  TCAGCTCACTCAGTGGTC    87744     AGT    CATA
                                GACC   GCTGG    AGCTGA
                                ||||   |||||    ||||||
                                CTGG   TGACT    TCGACT
                                  ___    CAC_
GAM697  LOC197287 3'  TCAGCTCATGTGTTTTGCACTG 60865       T_     __
                                CAGTGC  GGCATA  AGCTGA
                                ||||||  ||||||  ||||||
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                                GTCACG  TTGTGT  TCGACT
                                   TT     AC
GAM697  LOC200470 5'  TCAGCCTGCGGCGCTGG     90069        G  TAA
                                CCAGTGCTG CA   GCTGA
                                ||||||||| ||   |||||
                                GGTCGCGGC GT   CGACT
                                     _ C__
GAM697  LOC221584 3'  CAGCTTATGTGGCAC       93828       G
                                GTGCTG CATAAGCTG
                                |||||| |||||||||
                                CACGGT GTATTCGAC
                                   _
GAM697  LOC51716  3'  CAGCTCATGGCCCTAGCA    32787       ___  A
                                TGCTGG   CAT AGCTG
                                ||||||   ||| |||||
                                ACGATC   GTA TCGAC
                                   CCG   C
GAM697  LOC92196  5'  CAGAGCACCAGCACTGGC    68456   A       CATAAG
                                G CCAGTGCTGG     CTG
                                | ||||||||||     |||
                                C GGTCACGACC     GAC
                                 _       ACGA__
GAM698  CASP7     3'  CCCAATGTTTGACAAACA    52896     GAG  __
                                TGT   GTC  ACATTGGG
                                |||   |||  ||||||||
                                ACA   CAG  TGTAACCC
                                  AA_   TT
GAM698  CASP7     3'  CCCAATGTTTGACAAACA    52899     GAG  __
                                TGT   GTC  ACATTGGG
                                |||   |||  ||||||||
                                ACA   CAG  TGTAACCC
                                  AA_   TT
GAM698  CASP7     3'  TCCCAATGTTTGACAAAACA  52902     GAG  __
                                TGT   GTC  ACATTGGGA
                                |||   |||  |||||||||
                                ACA   CAG  TGTAACCCT
                                  AAA   TT
GAM698  CASP7     3'  TCCCAATGTTTGACAAAACA  6912      GAG  __
                                TGT   GTC  ACATTGGGA
                                |||   |||  |||||||||
                                ACA   CAG  TGTAACCCT
                                  AAA   TT
GAM698  DLG4      3'  CCCACCTGCCCCCAATGCAC  7251        TGA  T  CAT
                                GTGCATTG   GG CA   TGGG
                                ||||||||   || ||   ||||
                                CACGTAAC   CC GT   ACCC
                                     CC_  _  CC_
GAM698  BLCAP     3'  CCCAATGTGACCTGGGGCA   21978     ATTGTG
                                TGC     AGGTCACATTGGG
                                |||     ||||||||||||
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                                ACG     TCCAGTGTAACCC
                                  GGG___
GAM698  CSMD1    3'  TCCCAACATGTGAAGCACAATG 73129        AGG     __
            C                    GCATTGTG   TCACAT  TGGGA
                                 ||||||||   ||||||  |||||
                                 CGTAACAC   AGTGTA  ACCCT
                                     GA_     CA
GAM698  DKFZp434F1719 3'  TCCTGTACAACCTCACAAAACA 50004     CA       CACAT
            C                    GTG  TTGTGAGGT     TGGGA
                                 |||  |||||||||     |||||
                                 CAC  AACACTCCA     GTCCT
                                   AA        ACAT_
GAM698  FLJ10546  5'  TCCCAATGGAGGCACAACAC   59479     CA    AGG  A
                                 GTG  TTGTG   TC CATTGGGA
                                 |||  |||||   || ||||||||
                                 CAC  AACAC   AG GTAACCCT
                                   __     GG_  _
GAM698  FLJ31153  3'  TCCCAATGTTACCAAAATGCAC 58131        GTGA   C
                                 GTGCATT    GGT ACATTGGGA
                                 |||||||    ||| |||||||||
                                 CACGTAA    CCA TGTAACCCT
                                     AA__   T
GAM698  LOC116113 3'  TCCCAAGAACCCCCCACATACA 92219     CAT    A  TCACA
            C                    GTG   TGTG GG     TTGGGA
                                 |||   |||| ||    ||||||
                                 CAC   ACAC CC     AACCCT
                                   AT_    C  CCAAG
GAM698  LOC143680 3'  TCCCAATGTGAACAAATA    82988     GAGG
                                 TGT    TCACATTGGGA
                                 |||    ||||||||||
                                 ATA    AGTGTAACCCT
                                   AACA
GAM698  LOC90639  3'  CCCAGTGTCCTCACAGTGCAC  63654           TC
                                 GTGCATTGTGAGG  ACATTGGG
                                 ||||||||||||  ||||||||
                                 CACGTGACACTCC  TGTGACCC
                                                __
GAM699  ABCG1    3'  CCTAGAACCGCGTTGGGTT    16982       TAGATCA
                                 AACCCG      GTTCTAGG
                                 ||||||      ||||||||
                                 TTGGGT      CAAGATCC
                                    TGCGC__
GAM699  ADORA2A  3'  CCTAGACTCTCCTAGGGTT    5433       G   ATC   T
                                 AACCC TAG   AGT CTAGG
                                 |||||  |||   |||  |||||
                                 TTGGG ATC   TCA GATCC
                                    _   CTC   _
GAM699  AIM1     3'  CCCAGGCTGATCTCG      91819    T      T  A
                                 CG AGATCAGT CT GG
                                 ||  |||||||  ||  ||
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                                GC TCTAGTCG GA CC
                                 _      _ C
GAM699  B4GALT5  3'  CCCAGGCTGGTCTCG      16495   T     T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM699  CBFA2T2  3'  CCCAGAGGCTGATCTGC     17460         _  A
                                GTAGATCAGT TCT GG
                                |||||||||| ||| ||
                                CGTCTAGTCG AGA CC
                                      G   C
GAM699  CBFB     3'  CCCAGGCTGGTCTCG      8274    T     T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM699  CBFB     3'  CCCAGGCTGGTCTCG      43141   T     T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM699  CIT      3'  CCTAGGGCTAGACCTA     69745    A  _
                                TAG TC AGTTCTAGG
                                ||| || |||||||||
                                ATC AG TCGGGATCC
                                  C  A
GAM699  CRLF1    3'  CCTAGAACCCCTGCCAGGG   16452    __   ATCA
                                CCC  GTAG   GTTCTAGG
                                |||  ||||   ||||||||
                                GGG  CGTC   CAAGATCC
                                  AC   CC__
GAM699  DMPK     3'  CCTAGAACTGTCTTCG      15323   T  T
                                CG AGA CAGTTCTAGG
                                || ||| ||||||||||
                                GC TCT GTCAAGATCC
                                 T  _
GAM699  EDAR     5'  CCCAGAACTGGATGG       42265    AGA      A
                                CCGT   TCAGTTCT GG
                                ||||   |||||||| ||
                                GGTA   GGTCAAGA CC
                                   ___       C
GAM699  EPHB3    5'  CCTAGAGCTGCCACGG      15455    AGAT
                                CCGT   CAGTTCTAGG
                                ||||   ||||||||||
                                GGCA   GTCGAGATCC
                                  CC__
GAM699  GAB2     3'  CCCAGAACTCTGGAGCTACAGG 24492   C   A ___    A
                                CC GTAG TC   AGTTCT GG
                                || |||| ||   |||||| ||
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                                GG CATC AG   TCAAGA CC
                                 A   G  GTC     C
GAM699  GAB2    3'  CCCAGAACTCTGGAGCTACAGG 54449    C   A ___     A
                                CC GTAG TC   AGTTCT GG
                                || |||| ||   |||||| ||
                                GG CATC AG   TCAAGA CC
                                 A   G  GTC     C
GAM699  GRM6    3'  CCCAGGCTGGTCTCG      5929     T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _  C
GAM699  ITGAL   3'  CCCAGAACTGGACTCAGG    9389     GT  A      A
                                CC  AG TCAGTTCT GG
                                ||  || |||||||| ||
                                GG  TC GGTCAAGA CC
                                 AC  A       C
GAM699  MIPOL1  5'  CCCAGACTGGTCTCG      77066    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCA GA CC
                                 _      _  C
GAM699  MTR     3'  CCTAAAATTGATCTATGG    4208            C
                                CCGTAGATCAGTT TAGG
                                |||||||||||| ||||
                                GGTATCTAGTTAA ATCC
                                       A
GAM699  NGFR    3'  CCTAGAATCAGCCTAGGGGT  10224     G   ATCA
                                ACCC TAG   GTTCTAGG
                                |||| |||   ||||||||
                                TGGG ATC   TAAGATCC
                                  G   CGAC
GAM699  RFXANK  3'  CCCAGAACTGACTTCAAAGG  56239    GT___  A      A
                                CC    AG TCAGTTCT GG
                                ||    || |||||||| ||
                                GG    TC AGTCAAGA CC
                                 AAACT  _       C
GAM699  RFXANK  3'  CCCAGAACTGACTTCAAAGG  13561    GT___  A      A
                                CC    AG TCAGTTCT GG
                                ||    || |||||||| ||
                                GG    TC AGTCAAGA CC
                                 AAACT  _       C
GAM699  SLC3A2  5'  CCCAGACTGGTCTCG      9983     T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCA GA CC
                                 _      _  C
GAM699  TEM5    3'  CCAAGGTCTGACCTAGGGTT  51318      G   A   TT  A
                                AACCC TAG TCAG  CT GG
                                ||||| ||| ||||  || ||
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                                TTGGG ATC AGTC  GA CC
                                  _  C    TG  A
GAM699  WHSC1    5'  CCCAGGCTGGTCTCG      23656    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM699  WHSC1    5'  CCCAGGCTGGTCTCG      29907    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM699  WHSC1    5'  CCCAGGCTGGTCTCG      55825    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM699  WHSC1    5'  CCCAGGCTGGTCTCG      55842    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM699  ZFX      5'  CCCAGGCTGGTCTCG      12717    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM699  ALDH9    5'  CCTAGAACCGATCCCGTGG   5512     _ TA   A
                                CC CG  GATC GTTCTAGG
                                || ||  |||| ||||||||
                                GG GC  CTAG CAAGATCC
                                 T  C_   C
GAM699  C22orf19 3'  CCCAGGCTGGTCTCG      13418    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM699  CBX6     3'  CTAGAAACTAGGGTT       26612      G   ATCAG
                                AACCC TAG    TTCTAG
                                ||||| |||    ||||||
                                TTGGG ATC    AAGATC
                                  _  A_____
GAM699  CHL1     3'  CCTAGAGAACTGTCCAAGGGTT 21745      GTA  T   __
                                AACCC   GA CAGT  TCTAGG
                                |||||   || ||||  ||||||
                                TTGGG   CT GTCA  AGATCC
                                  AAC  _    AG
GAM699  CIP29    3'  CCCAGGCTGGTCTCG      50402    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
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                                GC TCTGGTCG GA CC
                                 _      _ C
GAM699  FLJ10483 3' CCTAGAACCTCTACAGGT   36168    C    TCA
                                ACC GTAGA  GTTCTAGG
                                ||| |||||  ||||||||
                                TGG CATCT  CAAGATCC
                                  A    C__
GAM699  FLJ10815 3' CTGGAATCCACGGGT      36694      A  CAGT
                                ACCCGT GAT   TCTAG
                                |||||| |||   |||||
                                TGGGCA CTA   AGGTC
                                   C  ____
GAM699  FLJ10898 5' CCCAGAGGTAGATCGACAGGTT 59427     C  A   AG_   A
                                AACC GT GATC  TTCT GG
                                |||| || ||||  |||| ||
                                TTGG CA CTAG  GAGA CC
                                  A  G   ATG   C
GAM699  FLJ11715 3' CCCAGGCTGGTCTCG      44669    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM699  FLJ12448 3' CCTAGAACTGTCTGAGG    43176    G   T
                                CC TAGA CAGTTCTAGG
                                || |||| ||||||||||
                                GG GTCT GTCAAGATCC
                                 A   _
GAM699  FLJ20147 3' CCCAGACTGGTCTCG      34637    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCA GA CC
                                 _      _ C
GAM699  FLJ30532 3' CCTCAGATGATCTAC      58543       GT  _
                                GTAGATCA  TCT AGG
                                ||||||||  ||| |||
                                CATCTAGT  AGA TCC
                                     __  C
GAM699  FLJ32334 3' CCCAGGCTGGTCTCG      57981    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM699  KIAA0205 3' CCTGAATAATCTATGGGTT   29579         CA   T
                                AACCCGTAGAT  GTTC AGG
                                ||||||||||  |||| |||
                                TTGGGTATCTA  TAAG TCC
                                      A_   _
GAM699  KIAA0268 3' CCCAGAACTGAAGATGG    70001     AGA      A
                                CCGT   TCAGTTCT GG
                                ||||   |||||||| ||
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                                GGTA   AGTCAAGA CC
                                  GA_       C
GAM699  KIAA0318  3'  CCTACGTCATCTATGGGTT   68950          CAGTTC
                                AACCCGTAGAT     TAGG
                                ||||||||||      ||||
                                TTGGGTATCTA     ATCC
                                      CTGC__
GAM699  KIAA0552  3'  CCTAGAACCTGGGCCTAGG   28311    G   A_   _
                                CC TAG  TCAG TTCTAGG
                                || |||  |||| |||||||
                                GG ATC  GGTC AAGATCC
                                 _  CG   C
GAM699  KIAA0710  3'  CCCAGAACTGGGAGATGG    29566     AGA       A
                                CCGT   TCAGTTCT GG
                                ||||   |||||||| ||
                                GGTA   GGTCAAGA CC
                                  GAG       C
GAM699  KIAA0907  3'  CCCAGAACTGGTTGC       30172     G        A
                                GTA ATCAGTTCT GG
                                ||| ||||||||| ||
                                CGT TGGTCAAGA CC
                                 _        C
GAM699  KIAA1157  3'  AGCTTATCTACGGGTT      72237          C
                                AACCCGTAGAT AGTT
                                |||||||||| ||||
                                TTGGGCATCTA TCGA
                                      T
GAM699  KIAA1671  3'  CCCAGGCTGGTCTCG       65669    T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM699  KIAA1715  3'  CCTGAGCATGATCTAC      68118         _   T
                                GTAGATCA GTTC AGG
                                |||||||| |||| |||
                                CATCTAGT CGAG TCC
                                     A   _
GAM699  KIAA1814  3'  CCTAGAGCAGTCTCCAGGG   70360     GT_   CA
                                CCC   AGAT  GTTCTAGG
                                |||   ||||  ||||||||
                                GGG   TCTG  CGAGATCC
                                  ACC   A_
GAM699  LIECG3    3'  CCCAGGCTGGTCTCG       87409    T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM699  MGC10812  3'  CCTAGAACTTTTGCCAGT    48666    CC     TC
                                AC  GTAGA  AGTTCTAGG
                                ||  |||||  |||||||||
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                                TG  CGTTT  TCAAGATCC
                                 AC    __
GAM699  PELI1    5'  CCCAGGCTGGTCTCG      40258    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _      _ C
GAM699  PGGT1B   5'  AGTGCTGATCTAGGG       17230     G       T
                                CCC TAGATCAGT CT
                                ||| ||||||||| ||
                                GGG ATCTAGTCG GA
                                  _       T
GAM699  PIP3-E   3'  CCTAGAACTGGGAGATG     66803     AGA
                                CGT   TCAGTTCTAGG
                                |||   ||||||||||
                                GTA   GGTCAAGATCC
                                  GAG
GAM699  PIP5K2B  3'  CCTCAGAACTGAGCCACAGG   13070    C  AGA      _
                                CC GT   TCAGTTCT AGG
                                || ||   |||||||| |||
                                GG CA   AGTCAAGA TCC
                                 A  CCG       C
GAM699  PTDSS1   3'  CCTAGAACTGAGAGGG      28571     GTAGA
                                CCC     TCAGTTCTAGG
                                |||     ||||||||||
                                GGG     AGTCAAGATCC
                                  AG___
GAM699  PYPAF3   3'  CCTGGGATCGCTCTACG     57539       TCA
                                CGTAGA   GTTCTAGG
                                ||||||   ||||||||
                                GCATCT   TAGGGTCC
                                   CGC
GAM699  SDS3     3'  CCCAGAGGCTGATCTGC     69226          _  A
                                GTAGATCAGT TCT GG
                                |||||||||| ||| ||
                                CGTCTAGTCG AGA CC
                                      G   C
GAM699  SRF      3'  CCCAGAACTGGCTGGG      11943     GT  A      A
                                CCC  AG TCAGTTCT GG
                                |||  || |||||||| ||
                                GGG  TC GGTCAAGA CC
                                  __ _       C
GAM699  TRIM2    5'  CCCAGTTGTCTGCGGG      30941        T   TT  A
                                CCCGTAGA CAG  CT GG
                                |||||||| |||  || ||
                                GGGCGTCT GTT  GA CC
                                     _  __ C
GAM699  TSPEAR   3'  CCTAGGGCATCCCGGG      58719      TA   CA
                                CCCG  GAT  GTTCTAGG
                                ||||  |||  ||||||||
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                                GGGC  CTA  CGGGATCC
                                  C_   __
GAM699   LOC113026 3'  CCCAGGCTGGTCTCG       55899    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _  C
GAM699   LOC125144 3'  CCCAGGCTGGTCTCAGG     74393    GT       T  A
                                CC  AGATCAGT CT GG
                                ||  |||||||| || ||
                                GG  TCTGGTCG GA CC
                                 AC        _  C
GAM699   LOC126549 5'  CCTAGAACTGGCTGC       75708      A
                                GTAG TCAGTTCTAGG
                                |||| ||||||||||
                                CGTC GGTCAAGATCC

                                  _
GAM699   LOC126661 3'  CCCAGGCTGGTCTCG       74547    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _  C
GAM699   LOC127702 3'  CCTGGGACACCTACAGG     75458    C    ATCA
                                CC GTAG    GTTCTAGG
                                || ||||    ||||||||
                                GG CATC    CAGGGTCC
                                 A    CA__
GAM699   LOC143920 3'  CCCAGAGTCCTATCTAGGGT   76624      G    C __    A
                                ACCC TAGAT AG  TTCT GG
                                |||| ||||| ||  |||| ||
                                TGGG ATCTA TC  GAGA CC
                                  _     _ CT    C
GAM699   LOC145725 3'  CCCAGGCTGGTCTCG       77403    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _  C
GAM699   LOC145732 3'  CCCAGGCTGGTCTCG       77425    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _  C
GAM699   LOC146733 3'  CCTGGCTTGATCTACAGGT    83759     C        TT
                                ACC GTAGATCAG  CTAGG
                                ||| |||||||||  |||||
                                TGG CATCTAGTT  GGTCC
                                  A        C_
GAM699   LOC154877 3'  CCCAGGCTGGTCTCG       86286    T      T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
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                                GC TCTGGTCG GA CC
                                 _       _ C
GAM699   LOC154881 3'  CCCAGAACAGAAGAAGGGTT   81170      GTAGA  A    A
                                AACCC     TC GTTCT GG
                                |||||     || ||||| ||
                                TTGGG     AG CAAGA CC
                                   AAGA_  A    C
GAM699   LOC163998 5'  CCCAGAACTGGATGG       87053      AGA       A
                                CCGT   TCAGTTCT GG
                                ||||   |||||||| ||
                                GGTA   GGTCAAGA CC
                                  ___       C
GAM699   LOC170261 3'  CTGCAGCCTACGGGT       82582         ATCA   C
                                ACCCGTAG    GTT TAG
                                ||||||||    ||| |||
                                TGGGCATC    CGA GTC
                                    _____  C
GAM699   LOC196463 3'  CCTAGAGTGGGTCACG      87710     A    AG
                                CGT GATC  TTCTAGG
                                ||| ||||  |||||||
                                GCA CTGG  GAGATCC
                                  _   GT
GAM699   LOC196957 3'  CCCAGGCTGGTCTCG       87820    T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM699   LOC196961 3'  CCCAGGCTGGTCTCG       87841    T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM699   LOC197138 3'  CCCAGGCTGGTCTCG       87914    T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM699   LOC197423 5'  CCCAGAACTGATAGTGC     77857     G_        A
                                GTA  ATCAGTTCT GG
                                |||  ||||||||| ||
                                CGT  TAGTCAAGA CC
                                  GA        C
GAM699   LOC200268 3'  CCCAGGCTGGTCTCG       88681    T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _ C
GAM699   LOC200339 3'  AACTGATCTACAGGTT      90022      C
                                AACC GTAGATCAGTT
                                |||| ||||||||||
```

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                                TTGG CATCTAGTCAA
                                  A
GAM699  LOC219653 3'  CCCAGAACTGAACACTAGGT   91292     CG   A__       A
                                ACC  TAG   TCAGTTCT GG
                                |||  |||   |||||||| ||
                                TGG  ATC   AGTCAAGA CC
                                  __   ACA       C
GAM699  LOC220565 5'  CCCAGAACTGATAGTGC     90748     G_        A
                                GTA  ATCAGTTCT GG
                                |||  ||||||||| ||
                                CGT  TAGTCAAGA CC
                                  GA        C
GAM699  LOC221895 3'  CCTATTGATATCTGCGG     92524         __     TCT
                                CCGTAGA  TCAGT   AGG
                                |||||||  |||||   |||
                                GGCGTCT  AGTTA   TCC
                                    AT    ___
GAM699  LOC221960 3'  CCCAGGCTGGTCTCG       91081     T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _  C
GAM699  LOC253228 3'  CTAGTGCTGACCTACGGG    95940         A     T
                                CCCGTAG TCAGT CTAG
                                ||||||| ||||| ||||
                                GGGCATC AGTCG GATC
                                    C     T
GAM699  LOC254181 5'  CCCAGAACTGGCTCAGG     97583     GT  A       A
                                CC  AG TCAGTTCT GG
                                ||  || |||||||| ||
                                GG  TC GGTCAAGA CC
                                 AC  _       C
GAM699  LOC257051 3'  CTGCAGCCTACGGGT       96316         ATCA   C
                                ACCCGTAG    GTT TAG
                                ||||||||    ||| |||
                                TGGGCATC    CGA GTC
                                    _____   C
GAM699  LOC51226  3'  CCCAGAACTGACTCCTAAGG   33150    G   A__       A
                                CC TAG   TCAGTTCT GG
                                || |||   |||||||| ||
                                GG ATC   AGTCAAGA CC
                                 A   CTC       C
GAM699  LOC51622  3'  CCCAGGCTGGTCTCG       31566     T       T  A
                                CG AGATCAGT CT GG
                                || |||||||| || ||
                                GC TCTGGTCG GA CC
                                 _       _  C
GAM699  LOC90139  3'  CCCAGAACTGAGGCTTGG    55402     T  A_       A
                                CCG AG  TCAGTTCT GG
                                ||| ||  |||||||| ||
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                                GGT TC  AGTCAAGA CC
                                  _ GG       C
GAM699  LOC90979  3' CCTGCAGGCTGATCCAGGG   64525    GTA      C_
                                CCC   GATCAGTT  TAGG
                                |||   ||||||||  ||||
                                GGG   CTAGTCGG  GTCC
                                  AC_       AC
GAM699  LOC91012  5' CCCAGGCTGGTCTCGG     64639    T      T  A
                                CCG AGATCAGT CT GG
                                ||| |||||||| || ||
                                GGC TCTGGTCG GA CC
                                  _       _ C
GAM699  LOC92568  5' CTGGAGATTCTACGGG     69772        TCAG
                                CCCGTAGA    TTCTAG
                                ||||||||    ||||||
                                GGGCATCT    GAGGTC
                                     TA__
GAM699  LOC93550  5' GGTGCTGATCTCCGAGT     72586    C  T      T
                                AC CG AGATCAGT CT
                                || || |||||||| ||
                                TG GC TCTAGTCG GG
                                 A  C       T
GAM699  LOC93550  5' CCTAGAACTGGAATAC      72584     GA
                                GTA  TCAGTTCTAGG
                                |||  ||||||||||
                                CAT  GGTCAAGATCC
                                  AA
GAM700  ALS2      3' AACATAGGTGCTCTTCCTCA   40504         T  TGGAT
                                TGAGGAAGA GT    TGTT
                                |||||||||  ||    ||||
                                ACTCCTTCT CG    ACAA
                                     _ TGGAT
GAM700  CTGF      3' AATAGTCTATCTTCCCCA    8573     A     GTT
                                TG GGAAGAT   GGATTGTT
                                || |||||||   ||||||||
                                AC CCTTCTA   TCTGATAA
                                 C      ___
GAM700  DNAJB9    3' AACTGGTTGACTCTTCCTCA   24676         T  TG ATT
                                TGAGGAAGA GT  G   GTT
                                |||||||||  ||  |   |||
                                ACTCCTTCT CA  T   CAA
                                     _ GT GGT
GAM700  EPO       3' ATCCACCACCTCCCTCA     5853       A  A  T
                                TGAGG AG TG TGGAT
                                |||||  ||  ||  |||||
                                ACTCC TC AC ACCTA
                                   C  C  C
GAM700  FGF23     3' AACAACAGCTTCTTCCCA    40191    A     T    GA
                                TG GGAAGA GTTG  TTGTT
                                ||  ||||||  ||||  |||||
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                                AC CCTTCT CGAC  AACAA
                                 _     T   __
GAM700  GCS1    3'  AATTCAAACCTTCCTCA     20867        ATG
                                TGAGGAAG   TTGGATT
                                ||||||||   |||||||
                                ACTCCTTC   AACTTAA
                                    CA_
GAM700  GPR48   3'  TCCATACATCTTCCCCA     37504    A       _
                                TG GGAAGATGT TGGA
                                || ||||||||| ||||
                                AC CCTTCTACA ACCT
                                 C        T
GAM700  HNRPH2  3'  AACAATTTTTAGCTTTCCTCA  38975        ATGTT
                                TGAGGAAG    GGATTGTT
                                ||||||||    ||||||||
                                ACTCCTTT    TTTAACAA
                                    CGATT
GAM700  IL17    3'  AACATTTTTCTCTTCCTCA    9328         TGTT   T
                                TGAGGAAGA   GGA TGTT
                                |||||||||   ||| ||||
                                ACTCCTTCT   TTT ACAA
                                     CT__   T
GAM700  KIT     3'  AACAAAAAACTCCCCTTCCTCA 4038         AT__   GGA
                                TGAGGAAG   GTT   TTGTT
                                ||||||||   |||   |||||
                                ACTCCTTC   CAA   AACAA
                                    CCCT   AA_
GAM700  MAPT    3'  ATCCAACATTTCCTCA      19775       A
                                TGAGGA GATGTTGGAT
                                |||||| ||||||||||
                                ACTCCT TTACAACCTA
                                  _
GAM700  MAPT    3'  ATCCAACATTTCCTCA      33686       A
                                TGAGGA GATGTTGGAT
                                |||||| ||||||||||
                                ACTCCT TTACAACCTA
                                  _
GAM700  MAPT    3'  ATCCAACATTTCCTCA      33695       A
                                TGAGGA GATGTTGGAT
                                |||||| ||||||||||
                                ACTCCT TTACAACCTA
                                  _
GAM700  MAPT    3'  ATCCAACATTTCCTCA      33705       A
                                TGAGGA GATGTTGGAT
                                |||||| ||||||||||
                                ACTCCT TTACAACCTA
                                  _
GAM700  NR5A2   3'  AATTCAAATCTTCCCCA     13788    A      G
                                TG GGAAGAT TTGGATT
                                || ||||||| |||||||
```

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                                AC CCTTCTA AACTTAA
                                 C      _
GAM700  PIK3CG   5'  TCCAACATCTTCTCA      10589      G
                                TGAG AAGATGTTGGA
                                |||| ||||||||||
                                ACTC TTCTACAACCT
                                  _
GAM700  PPP2R2B  3'  AACAATCCATCAACCTC     15903      AA  TGT
                                GAGG  GA   TGGATTGTT
                                ||||  ||   |||||||||
                                CTCC  CT   ACCTAACAA
                                  AA  ___
GAM700  RBM8A    3'  AACAATCCTGCTTTCTCA    17541        ATGTT
                                TGAGGAAG    GGATTGTT
                                ||||||||    ||||||||
                                ACTCTTTC    CCTAACAA
                                     GT___
GAM700  SLA2     3'  AACAATTCTCCTGCCTCA    49888      A  ATGTT
                                TGAGG AG    GGATTGTT
                                ||||| ||    ||||||||
                                ACTCC TC    CTTAACAA
                                   G  CT___
GAM700  XPR1     3'  AACAAATTATACTTCCTCA    16423        A   TGGA
                                TGAGGAAG TGT    TTGTT
                                |||||||| |||   |||||
                                ACTCCTTC ATA    AACAA
                                     _  TTA_
GAM700  YWHAE    3'  AACAATCCGTGGCTGCTCA    22193      GA  ATGT
                                TGAG  AG    TGGATTGTT
                                ||||  ||    |||||||||
                                ACTC  TC    GCCTAACAA
                                  G_  GGT_
GAM700  ALTE     3'  AACAATCCTTTGCTTTTCCTCA 16386         T  T__
                                TGAGGAAGA GT   GGATTGTT
                                ||||||||| ||   ||||||||
                                ACTCCTTTT CG   CCTAACAA
                                     _ TTT
GAM700  AQP10    3'  AACAGTCATTCTTCCTC     54428        TGTTG
                                GAGGAAGA    GATTGTT
                                ||||||||    |||||||
                                CTCCTTCT    CTGACAA
                                     TA___
GAM700  ARHGEF9  3'  TCCAACATCCTCTCA      30821      AA
                                TGAGG  GATGTTGGA
                                |||||  |||||||||
                                ACTCT  CTACAACCT
                                   C_
GAM700  BTN3A1   3'  AACAATTCTCCTGCCTCA    22913      A  ATGTT
                                TGAGG AG    GGATTGTT
                                ||||| ||    ||||||||
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                                ACTCC TC    CTTAACAA
                                   G  CT___
GAM700  CL683    3'  AACAATCCAAACAATACCTCA 31648      AAGATG
                                TGAGG    TTGGATTGTT
                                |||||    ||||||||||
                                ACTCC    AACCTAACAA
                                   ATAACA
GAM700  FLJ11539 3'  TTCAACATTTCCTCA      45383      A
                                TGAGGA GATGTTGGA
                                |||||| |||||||||
                                ACTCCT TTACAACTT
                                   _
GAM700  FLJ12476 3'  AACAATCCCTTCTTCTTC    42947       TGTT
                                GAGGAAGA   GGATTGTT
                                ||||||||   ||||||||
                                CTTCTTCT   CCTAACAA
                                     TC__
GAM700  FLJ25415 3'  ACAATCCAACGGCTCT     58493    AGA
                                GGA   TGTTGGATTGT
                                |||   ||||||||||
                                TCT   GCAACCTAACA
                                  CG_
GAM700  FYCO1    3'  ACACTGCTCTTCCTCA      44483       T  TGGAT
                                TGAGGAAGA GT    TGT
                                ||||||||| ||    |||
                                ACTCCTTCT CG    ACA
                                     _  TC___
GAM700  KIAA0854 3'  AACAATAAGATCTTCCT     30096       G  GG
                                AGGAAGAT TT  ATTGTT
                                |||||||| ||  ||||||
                                TCCTTCTA AA  TAACAA
                                     G  __
GAM700  KIAA1026 3'  AACAATTCTCCTGCCTCA    71185      A  ATGTT
                                TGAGG AG    GGATTGTT
                                ||||| ||    ||||||||
                                ACTCC TC    CTTAACAA
                                   G  CT___
GAM700  KRTAP4-12 3'  TCCAACATCCTCCCA      49010    A  A
                                TG GGA GATGTTGGA
                                || ||| |||||||||
                                AC CCT CTACAACCT
                                  _  C
GAM700  LY117    3'  CCAGACACCTTCCTCA      92351       A  _
                                TGAGGAAG TGT TGG
                                |||||||| ||| |||
                                ACTCCTTC ACA ACC
                                     C  G
GAM700  LY117    3'  CCAGACACCTTCCTCA      97745       A  _
                                TGAGGAAG TGT TGG
                                |||||||| ||| |||
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                                ACTCCTTC ACA ACC
                                     C   G
GAM700  LY117    3'  CCAGACACCTTCCTCA      97846        A  _
                                TGAGGAAG TGT TGG
                                |||||||| ||| |||
                                ACTCCTTC ACA ACC
                                     C   G
GAM700  MEF-2    3'  AACAATTCTCCTGCCTCA    64373      A  ATGTT
                                TGAGG AG    GGATTGTT
                                ||||| ||    ||||||||
                                ACTCC TC    CTTAACAA
                                   G  CT___
GAM700  MGC10200 3'  AACAATCCACCCTCCTCA    58979       AGAT  T
                                TGAGGA   GT GGATTGTT
                                ||||||   || ||||||||
                                ACTCCT   CA CCTAACAA
                                    CC__  _
GAM700  MYH10    3'  AACAGATGCCATCTTCCT    69137        TT GA
                                AGGAAGATG  G  TTGTT
                                |||||||||  |  |||||
                                TCCTTCTAC  T  GACAA
                                     CG A_
GAM700  MYO5C    3'  AACAATTCTCCTGCCTCA    38102      A  ATGTT
                                TGAGG AG    GGATTGTT
                                ||||| ||    ||||||||
                                ACTCC TC    CTTAACAA
                                   G  CT___
GAM700  PAK6     3'  AACAAAAGCATCTTCC      39403        GGA
                                GGAAGATGTT   TTGTT
                                ||||||||||   |||||
                                CCTTCTACGA   AACAA
                                     A__
GAM700  PRO0628  5'  AACAAATACTCATCTTCCCA  26204    A      TTGGA
                                TG GGAAGATG    TTGTT
                                || ||||||||    |||||
                                AC CCTTCTAC    AACAA
                                 _      TCATA
GAM700  PRO1600  3'  AACAATTTAACCTTCC      26030      AT
                                GGAAG  GTTGGATTGTT
                                |||||  ||||||||||
                                CCTTC  CAATTTAACAA
                                   __
GAM700  SKIL     5'  AATGTAACTCTTCCCCA     18280    A    T   G
                                TG GGAAGA GTTG ATT
                                || |||||| |||| |||
                                AC CCTTCT CAAT TAA
                                 C     _   G
GAM700  SLC2A13  3'  AATCACTACACCTTCCTCA   53545        A  TG_
                                TGAGGAAG TGT   GATT
                                |||||||| |||   ||||
```

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                                ACTCCTTC ACA   CTAA
                                     C   TCA
GAM700   LOC115219 5'  AACAATTCTCCTGCCTCA    73289      A  ATGTT
                                TGAGG AG    GGATTGTT
                                ||||| ||    ||||||||
                                ACTCC TC    CTTAACAA
                                   G  CT___
GAM700   LOC138311 3'  GGTCCAACCCTCCCTCA     76212      A  AT
                                TGAGG AG  GTTGGATT
                                ||||| ||  ||||||||
                                ACTCC TC  CAACCTGG
                                   C  C_
GAM700   LOC149628 5'  AACAATCCTCATTTCCTACA   79461    _   A    TT
                                TG AGGA GATG  GGATTGTT
                                || |||| ||||  ||||||||
                                AC TCCT TTAC  CCTAACAA
                                 A    _    T_
GAM700   LOC150406 3'  AACAACATGAGCATCCTCCTC  79855      A     _ GA
                                GAGGA GATGTT G  TTGTT
                                ||||| |||||| |  |||||
                                CTCCT CTACGA T  AACAA
                                   C     G AC
GAM700   LOC152282 5'  AACAATCCTTCTTCCTC     80550        TGTT
                                GAGGAAGA    GGATTGTT
                                ||||||||    ||||||||
                                CTCCTTCT    CCTAACAA
                                     T___
GAM700   LOC169436 5'  AACCCTCCAACATCATCCTCA  82737       A       TT
                                TGAGGA GATGTTGGA  GTT
                                |||||| |||||||||  |||
                                ACTCCT CTACAACCT  CAA
                                    A        CC
GAM700   LOC206012 5'  TCCACCATCTTCCTCA      89525          T
                                TGAGGAAGATG TGGA
                                |||||||||||| ||||
                                ACTCCTTCTAC ACCT
                                       C
GAM700   LOC206012 5'  TCCACCATCTTCCTCA      89526          T
                                TGAGGAAGATG TGGA
                                |||||||||||| ||||
                                ACTCCTTCTAC ACCT
                                       C
GAM700   LOC221830 3'  AACAATTTTAGCCTTTCTCA   92504        AT    _
                                TGAGGAAG  GTTGGA TTGTT
                                ||||||||  |||||| |||||
                                ACTCTTTC  CGATTT AACAA
                                     __     T
GAM700   LOC256683 5'  AACAATCTTCTTGTCTTCCCA  96279    A      TT_
                                TG GGAAGATG   GGATTGTT
                                || ||||||||   ||||||||
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```
                                AC CCTTCTGT   TCTAACAA
                                 _       TCT
GAM700  LOC256895 3'  AACAGTATTCATCTCCTC    96860      A   TTGG
                                GAGGA GATG    ATTGTT
                                ||||| ||||    ||||||
                                CTCCT CTAC    TGACAA
                                  _    TTA_
GAM700  LOC257465 3'  AACAATTCTCCTGCCTCA    81588      A  ATGTT
                                TGAGG AG     GGATTGTT
                                ||||| ||     ||||||||
                                ACTCC TC     CTTAACAA
                                   G  CT___
GAM701  KPNA3    3'  CAGGCTGACAACTGCA      9627     A  C
                                TG AG TGTCAGCCTG
                                || || ||||||||||
                                AC TC ACAGTCGGAC
                                 G  A
GAM701  MBL2     3'  TCAAGCAAACAGCTTCA     4118          CA  C
                                TGAAGCTGT  GC TGA
                                |||||||||  || |||
                                ACTTCGACA  CG ACT
                                      AA  A
GAM701  PAX2     3'  TCAGGCCGACAGCTTC      14328         A
                                GAAGCTGTC GCCTGA
                                ||||||||| ||||||
                                CTTCGACAG CGGACT
                                      C
GAM701  BHC80    3'  TGTTTTTCAGGCTGACAGT    33537           TCT_
                                GCTGTCAGCCTGA    CA
                                ||||||||||||    ||
                                TGACAGTCGGACT    GT
                                       TTTT
GAM701  KIAA0556 3'  CAGGCTGGCAGCTCCA      69080    A
                                TG AGCTGTCAGCCTG
                                || ||||||||||||
                                AC TCGACGGTCGGAC
                                 C
GAM701  MGC3222   3'  CATGAATGGCAAGCTGACAGCT 44293           C  ATC_
           TC                    GAAGCTGTCAGC TG    TCATG
                                ||||||||||| ||    |||||
                                CTTCGACAGTCG AC    AGTAC
                                       A  GGTA
GAM701  MMP24    3'  ATGAGGTACCACAGCTCCA    21939    A     CAGCCTG
                                TG AGCTGT      ATCTCAT
                                || ||||||      |||||||
                                AC TCGACA      TGGAGTA
                                 C     CCA_____
GAM701  LOC118491 5'  CATGAGGCCTCCAAACAGCTTC 73917          CAGCCTGA
           A                     TGAAGCTGT       TCTCATG
                                |||||||||       |||||||
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                                ACTTCGACA      GGAGTAC
                                     AACCTCC_
GAM701  LOC151475 5'  AGACATTGACAGCTTTA     85387          CC  A
                                TGAAGCTGTCAG  TG TCT
                                ||||||||||||  || |||
                                ATTTCGACAGTT  AC AGA
                                      __  _
GAM701  LOC152283 5'  AGCCCAGGCTGACTGCCCCA   85678    AA  T       AT
                                TG  GC GTCAGCCTG  CT
                                ||  || |||||||||  ||
                                AC  CG CAGTCGGAC  GA
                                 CC  T       CC
GAM701  LOC56899  5'  AGCCCAAGCTGACAGCTT    39305          C  AT
                                AAGCTGTCAGC TG  CT
                                ||||||||||| ||  ||
                                TTCGACAGTCG AC  GA
                                      A  CC
GAM701  LOC92492  5'  CATGGAGAGCCAGCAGCTTCA  69526        CA  CTGA  T
                                TGAAGCTGT  GC    TC CATG
                                |||||||||  ||    || ||||
                                ACTTCGACG  CG    AG GTAC
                                     AC  AG__  _
GAM702  DDEF1    3'  GAGCTTTAGCAGCCTC      59564    A   AGATAC      A
                                GA GCT     CTAAAGCT C
                                || |||     |||||||| |
                                CT CGA     GATTTCGA G
                                 C  C_____       C
GAM702  DDX3     3'  GAGCCTTAGGTATTTG      43759          A   A
                                TAGATACCTAA GCT C
                                |||||||||||| ||| |
                                GTTTATGGATT CGA G
                                      C   C
GAM702  GRAF     3'  GGTAACTCCCTCCCTAGCTTC  30573        ATACCTAA  C
                                GAAGCTAG       AG TACC
                                ||||||||       || ||||
                                CTTCGATC       TC ATGG
                                     CCTCCC__  A
GAM702  MAT1A    3'  AGCTTTAGAATCCCAGC     90825     A_   AC
                                GCT  GAT  CTAAAGCT
                                |||  |||  ||||||||
                                CGA  CTA  GATTTCGA
                                  CC   A_
GAM702  MYLK     3'  AGCTTCAGACATTTGGTT    97018        AC  A
                                AGCTAGAT  CT AAGCT
                                ||||||||  || |||||
                                TTGGTTTA  GA TTCGA
                                     CA  C
GAM702  RGL      3'  GTAGCTAAAACTTAGCTTCA  30736         ATACCTAA
                                TGAAGCTAG       AGCTAC
                                |||||||||       ||||||
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                                ACTTCGATT       TCGATG
                                     CAAAA___
GAM702  ZFP93    3'  GTAGCCTTAATAACGTTAGTTT 14887         ATACC_  A
            CA                    TGAAGCTAG     TAA GCTAC
                                  |||||||||     ||| |||||
                                  ACTTTGATT     ATT CGATG
                                       GCAATA   C
GAM702  C3orf4   3'  AGCATTGACACATAGCTTCA  39118        GATACC  A
                                  TGAAGCTA     TAA GCT
                                  ||||||||     ||| |||
                                  ACTTCGAT     GTT CGA
                                       ACACA_   A
GAM702  D2S448   3'  GGCAGGAGTCCTAGCTTCA   73527         _  A  AAA
                                  TGAAGCTAG AT CCT   GCT
                                  ||||||||| || |||   |||
                                  ACTTCGATC TG GGA   CGG
                                       C  A  ___
GAM702  FLJ12604 3'  AGCTTTAGTATTGACTTCA   64436      CTA    C
                                  TGAAG   GATAC TAAAGCT
                                  |||||   ||||| |||||||
                                  ACTTC   TTATG ATTTCGA
                                     AG_    _
GAM702  FLJ14280 5'  GGTAGCTCCTGGCCAGCTCA  45999     A   AGATA  TAA
                                  TGA GCT    CC   AGCTACC
                                  ||| |||    ||   |||||||
                                  ACT CGA    GG   TCGATGG
                                    _  CC___  TCC
GAM702  H2AFJ    3'  GTTGTCAAGTTTCTAGCTTCA 36842         T  CTAA_
                                  TGAAGCTAGA AC     AGC
                                  |||||||||| ||     |||
                                  ACTTCGATCT TG     TTG
                                        T  AACTG
GAM702  KIAA0441 3'  TAGCTTTGTTAATCTAGCCTC  28960    A      ACC
                                  GA GCTAGAT   TAAAGCTA
                                  || |||||||   ||||||||
                                  CT CGATCTA   GTTTCGAT
                                   C       ATT
GAM702  KIAA1128 3'  TAGCTTTATGTGCAGCTTGCA  68483    _    AGA   C
                                  TG AAGCT   TAC TAAAGCTA
                                  || |||||   ||| ||||||||
                                  AC TTCGA   GTG ATTTCGAT
                                   G    C__   T
GAM702  KIAA1750 3'  TAGCCCCAGGAGTGGGCTTTA  68254       AG  A   AAA
                                  TGAAGCT  AT CCT   GCTA
                                  |||||||  || |||   ||||
                                  ATTTCGG  TG GGA   CGAT
                                       G_  A   CCC
GAM702  KPNA5    3'  GGTAGCTTCAGGTAACT     9629     A    A
                                  AG TACCT AAGCTACC
                                  || ||||| ||||||||
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                                TC ATGGA TTCGATGG
                                 A    C
GAM702  MAGEH1    5'  GGTAGCTTCAGCGGCAGCAGCT 25924       AGATAC_ A
            TC                    GAAGCT      CT AAGCTACC
                                  ||||||      || ||||||||
                                  CTTCGA      GA TTCGATGG
                                     CGACGGC  C
GAM702  MGC12921  3'  AGCCCTATTTAGCTTC     63774          CCTAAA
                                  GAAGCTAGATA     GCT
                                  ||||||||||     |||
                                  CTTCGATTTAT     CGA
                                        CC____
GAM702  MGC30052  3'  AGCTTTAGAATAGCTTC     58532        GATAC
                                  GAAGCTA    CTAAAGCT
                                  |||||||    ||||||||
                                  CTTCGAT    GATTTCGA
                                     AA___
GAM702  RNF34     3'  AGCAAGGGCTGCATCTAGCTTC 47094         A___   AAA
                                  GAAGCTAGAT   CCT   GCT
                                  |||||||||   |||  |||
                                  CTTCGATCTA   GGG   CGA
                                        CGTC   AA_
GAM702  TNFRSF19L 3'  GTAGCTTTTATCCCAGC     51779     A_   CCT
                                  GCT  GATA   AAAGCTAC
                                  |||  ||||   ||||||||
                                  CGA  CTAT   TTTCGATG
                                    CC    ___
GAM702  LOC121536 3'  AGCAAATCACATTTAGCTTCA  74082          ACCTAAA
                                  TGAAGCTAGAT      GCT
                                  ||||||||||      |||
                                  ACTTCGATTTA      CGA
                                        CACTAAA
GAM702  LOC255452 3'  TAGGTACCTACCTTCA      97544       C   A
                                  TGAAG TAG TACCTA
                                  ||||| ||| ||||||
                                  ACTTC ATC ATGGAT
                                     C   C
GAM702  LOC257396 3'  GGCAGCTTTAGGCTTAACTT   97139     C   ATA       A
                                  AAG TAG   CCTAAAGCT CC
                                  ||| |||   ||||||||| ||
                                  TTC ATT   GGATTTCGA GG
                                    A   C__        C
GAM702  LOC92710  3'  GTACAAGGCATCTAGCTT    70359         A   AAAGC
                                  AAGCTAGAT CCT     TAC
                                  |||||||| |||     |||
                                  TTCGATCTA GGA     ATG
                                        C   AC___
GAM703  ACRV1     3'  AATAAATTTCACATGGTTA    7859        C       CG
                                  TAACCA TGTGAAAT  GTT
                                  |||||| ||||||||  |||
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                                ATTGGT ACACTTTA  TAA
                                   _      AA
GAM703  ACRV1   3' AATAAATTTCACATGGTTA  39175      C      CG
                                TAACCA TGTGAAAT  GTT
                                |||||| ||||||||  |||
                                ATTGGT ACACTTTA  TAA
                                   _      AA
GAM703  ACRV1   3' AATAAATTTCACATGGTTA  39180      C      CG
                                TAACCA TGTGAAAT  GTT
                                |||||| ||||||||  |||
                                ATTGGT ACACTTTA  TAA
                                   _      AA
GAM703  ACRV1   3' AATAAATTTCACATGGTTA  39185      C      CG
                                TAACCA TGTGAAAT  GTT
                                |||||| ||||||||  |||
                                ATTGGT ACACTTTA  TAA
                                   _      AA
GAM703  ACRV1   3' AATAAATTTCACATGGTTA  39190      C      CG
                                TAACCA TGTGAAAT  GTT
                                |||||| ||||||||  |||
                                ATTGGT ACACTTTA  TAA
                                   _      AA
GAM703  ACRV1   3' AATAAATTTCACATGGTTA  39195      C      CG
                                TAACCA TGTGAAAT  GTT
                                |||||| ||||||||  |||
                                ATTGGT ACACTTTA  TAA
                                   _      AA
GAM703  ACRV1   3' AATAAATTTCACATGGTTA  39200      C      CG
                                TAACCA TGTGAAAT  GTT
                                |||||| ||||||||  |||
                                ATTGGT ACACTTTA  TAA
                                   _      AA
GAM703  ACRV1   3' AATAAATTTCACATGGTTA  39205      C      CG
                                TAACCA TGTGAAAT  GTT
                                |||||| ||||||||  |||
                                ATTGGT ACACTTTA  TAA
                                   _      AA
GAM703  ACRV1   3' AATAAATTTCACATGGTTA  39210      C      CG
                                TAACCA TGTGAAAT  GTT
                                |||||| ||||||||  |||
                                ATTGGT ACACTTTA  TAA
                                   _      AA
GAM703  ACRV1   3' AATAAATTTCACATGGTTA  39215      C      CG
                                TAACCA TGTGAAAT  GTT
                                |||||| ||||||||  |||
                                ATTGGT ACACTTTA  TAA
                                   _      AA
GAM703  ATP6V0A4 3' GGCTGCACCTCCCACGGTGGT  40189        AAATC  _  A
                                ACCACTGTG    GGT TA CC
                                |||||||||    ||| || ||
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                                TGGTGGCAC    CCA GT GG
                                     CCT__   C  C
GAM703  ATP6V0A4  3'  GGCTGCACCTCCCACGGTGGT  55599        AAATC  _  A
                                ACCACTGTG    GGT TA CC
                                |||||||||    ||| || ||
                                TGGTGGCAC    CCA GT GG
                                     CCT__   C  C
GAM703  ATP6V0A4  3'  GGCTGCACCTCCCACGGTGGT  55600        AAATC  _  A
                                ACCACTGTG    GGT TA CC
                                |||||||||    ||| || ||
                                TGGTGGCAC    CCA GT GG
                                     CCT__   C  C
GAM703  CUL4B     3'  GACTTTTTCTCAGTGGTTA    13140        T   TC
                                TAACCACTG GAAA  GGTT
                                ||||||||| ||||  ||||
                                ATTGGTGAC CTTT  TCAG
                                     T   T_
GAM703  FPGS      3'  AACAGAACTTCACAGTG      17078        A_  G
                                CACTGTGAA  TC GTT
                                |||||||||  || |||
                                GTGACACTT  AG CAA
                                     CA  A
GAM703  GJB3      5'  GACCTCTCTAAATTTCACAGT  43768         C_____
                                ACTGTGAAAT      GGTT
                                ||||||||||      ||||
                                TGACACTTTA      CCAG
                                     AATCTCT
GAM703  GNA11     3'  GGTTTTTATTTCACAGT      9051         CGGTT
                                ACTGTGAAAT    AACC
                                ||||||||||    ||||
                                TGACACTTTA    TTGG
                                     TTT__
GAM703  GRB10     3'  ACCTCACAGTGGTTG        17970         AATC
                                TAACCACTGTGA   GGT
                                ||||||||||||   |||
                                GTTGGTGACACT   CCA
                                      ____
GAM703  ITGA6     3'  GACTGATTTCAGAGTG       3985       G
                                CACT TGAAATCGGTT
                                |||| ||||||||||
                                GTGA ACTTTAGTCAG
                                  G
GAM703  MFAP2     5'  AACTTGGTCTCACAGTGG     33920        A   _
                                CCACTGTGA ATCG GTT
                                ||||||||| |||| |||
                                GGTGACACT TGGT CAA
                                     C   T
GAM703  MGA       3'  CTGGCTCCACAGTGGTT      62808         AAA
                                AACCACTGTG   TCGG
                                ||||||||||   ||||
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                                TTGGTGACAC   GGTC
                                      CTC
GAM703  NCALD    3'  GGTCAGTTCCTCACAGTGGTT  49377          AATC  TTA__
                                AACCACTGTGA   GG    ACC
                                ||||||||||   ||    |||
                                TTGGTGACACT   CC    TGG
                                     ____  TTGAC
GAM703  NRAP     3'  GGTCCCAGTTTCACAG      20509         C  TTA
                                CTGTGAAAT GG   ACC
                                ||||||||| ||   |||
                                GACACTTTG CC   TGG
                                     A  C__
GAM703  SCG3     3'  GCTGAATTTACAGTAGTTA   25099      C       A
                                TAAC ACTGTGAA TCGGT
                                |||| |||||||| |||||
                                ATTG TGACATTT AGTCG
                                  A       A
GAM703  SFRS1    3'  GGCTAATTTGTCACAGTGCTTA 22638     C       AATC    A
                                TAA CACTGTGA   GGTTA CC
                                ||| ||||||||   ||||| ||
                                ATT GTGACACT   TTAAT GG
                                  C       GT__    C
GAM703  SNRPN    5'  CTGAAAATTCACAGTGG     43006          A__
                                CCACTGTGAA   TCGG
                                ||||||||||   ||||
                                GGTGACACTT   AGTC
                                     AAA
GAM703  ZNF36    3'  AACTGCACAGTGGT        93955         AAAT
                                ACCACTGTG   CGGTT
                                |||||||||   |||||
                                TGGTGACAC   GTCAA
                                     ____
GAM703  AD-017   5'  GATCACTTCAAAGTGGTTA   37424         G   ATC
                                TAACCACT TGAA   GGTT
                                |||||||| ||||   ||||
                                ATTGGTGA ACTT   CTAG
                                     A   CA_
GAM703  CAMKK1   3'  GTTGACCCCCACAGGGT     50176     A    AAATC
                                ACC CTGTG    GGTTAAC
                                ||| |||||    |||||||
                                TGG GACAC    CCAGTTG
                                  _    CC___
GAM703  DDX17    5'  TAACTTCACAGTGGTT      48042          AATC
                                AACCACTGTGA   GGTTA
                                ||||||||||   |||||
                                TTGGTGACACT   TCAAT
                                     ____
GAM703  ERMAP    3'  TTAACTATCACAGTG       37597         AATC
                                CACTGTGA   GGTTAA
                                ||||||||   ||||||
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                                GTGACACT   TCAATT
                                    A___
GAM703  FLJ11101  3'  GATTTCACAAGTGGTTA    37051       _
                                TAACCACT GTGAAATC
                                |||||||| ||||||||
                                ATTGGTGA CACTTTAG
                                    A
GAM703  FLJ20297  5'  ATGGATCCCACAGTGGTT    34895        AA  G
                                AACCACTGTG  ATC GT
                                ||||||||||  ||| ||
                                TTGGTGACAC  TAG TA
                                     CC   G
GAM703  FLJ22557  3'  AGCTAGATATTCCTCACAGTG  45254       A____  _
                                CACTGTGA    ATC GGTT
                                ||||||||    ||| ||||
                                GTGACACT    TAG TCGA
                                    CCTTA   A
GAM703  KIAA0644  3'  GTTATGGTCACAGTGGTTA   29063         AATCGGT
                                TAACCACTGTGA     TAAC
                                ||||||||||||     ||||
                                ATTGGTGACACT     ATTG
                                     GGT____
GAM703  KIAA1169  5'  AACTCTTCCACAGTGG     35446       A  TC
                                CCACTGTG AA  GGTT
                                |||||||| ||  ||||
                                GGTGACAC TT  TCAA
                                    C  C_
GAM703  KIAA1203  3'  TTAATTTTCACAGTGGT    71645         TCG
                                ACCACTGTGAAA  GTTAA
                                ||||||||||||  |||||
                                TGGTGACACTTT  TAATT
                                      ___
GAM703  KIAA1297  5'  AGCTGGTTCCACAATGG    72166    C   A
                                CCA TGTG AATCGGTT
                                ||| |||| ||||||||
                                GGT ACAC TTGGTCGA
                                  A   C
GAM703  KLHL6     3'  AACCAAGTTTCACAGAGG    55297    A      C_
                                CC CTGTGAAAT  GGTT
                                || |||||||||  ||||
                                GG GACACTTTG  CCAA
                                 A        AA
GAM703  MGC10646  3'  GATCATCTCACAGTG      51108       A  C
                                CACTGTGA AT GGTT
                                |||||||| || ||||
                                GTGACACT TA CTAG
                                    C  _
GAM703  MMD       3'  GGTCTCTTTCCACAGTGG    59809       A  TC  TTA
                                CCACTGTG AA  GG   ACC
                                |||||||| ||  ||   |||
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                                GGTGACAC TT  TC   TGG
                                    C  TC  ___
GAM703  MUF1     3'  GGCCAGGAGGTTACAGTGGT  95490          AA  __
                                ACCACTGTGA  TC  GGTT
                                ||||||||||  ||  ||||
                                TGGTGACATT  AG  CCGG
                                     GG  GA
GAM703  NYD-SP16 3'  GATCACTTAACAGTGGTTA   49218          GAAATC
                                TAACCACTGT     GGTT
                                ||||||||||     ||||
                                ATTGGTGACA     CTAG
                                     ATTCA_
GAM703  RNPC2    3'  AACTTTTTACACAGTGGTTA   16921          A  TC
                                TAACCACTGTG AA  GGTT
                                ||||||||||| ||  ||||
                                ATTGGTGACAC TT  TCAA
                                      A  TT
GAM703  SNAPC1   3'  AACCTGTTTCACAGTTG     11837    _       C
                                CA CTGTGAAAT GGTT
                                || |||||||| ||||
                                GT GACACTTTG CCAA
                                  T        T
GAM703  LOC126302 3'  AACTACTTCACAGTAGTTG   74487      C       ATC
                                TAAC ACTGTGAA   GGTT
                                |||| ||||||||   ||||
                                GTTG TGACACTT   TCAA
                                   A       CA_
GAM703  LOC144203 5'  TTGACCTCACAGTG        76708         AATC
                                CACTGTGA    GGTTAA
                                ||||||||    ||||||
                                GTGACACT    CCAGTT
                                      ____
GAM703  LOC146229 3'  AATATCTTTCTCAGTGGTTA   77725          T    TCG
                                TAACCACTG GAAA   GTT
                                ||||||||| ||||   |||
                                ATTGGTGAC CTTT   TAA
                                      T    CTA
GAM703  LOC148189 3'  GTGGATTTCACAATGGT     78719      C       G
                                ACCA TGTGAAATC GT
                                |||| ||||||||| ||
                                TGGT ACACTTTAG TG
                                   A        G
GAM703  LOC149506 5'  GGGTTTCACAGTGGTTA     84475           _
                                TAACCACTGTGAAA TC
                                |||||||||||||| ||
                                ATTGGTGACACTTT GG
                                        G
GAM703  LOC150311 5'  ATCTGGATTTCACAGT      79751          __
                                ACTGTGAAATC  GGT
                                ||||||||||  |||
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                                TGACACTTTAG  CTA
                                      GT
GAM703  LOC158376 5'  GGCCGCAGCTTCACGGTGG   86797        AT__
                                CCACTGTGAA   CGGTT
                                ||||||||||   |||||
                                GGTGGCACTT   GCCGG
                                     CGAC
GAM703  LOC196264 3'  GTTTACATTTCCAGTGGTTA  87610       T   CG  T
                                TAACCACTG GAAAT  GT AAC
                                ||||||||| |||||  || |||
                                ATTGGTGAC CTTTA  CA TTG
                                     _    __  T
GAM703  LOC196424 5'  AATCAATTTCACAGTGG     87700         C
                                CCACTGTGAAAT GGTT
                                |||||||||||| ||||
                                GGTGACACTTTA CTAA
                                      A
GAM703  LOC220739 5'  GGCTGGGGTCCTCACAGTGG  92935       AA___
                                CCACTGTGA    TCGGTT
                                |||||||||    ||||||
                                GGTGACACT    GGTCGG
                                     CCTGG
GAM703  LOC221756 3'  GACTTCCTCTCCAGTGGTTA  92140       T  AATC_
                                TAACCACTG GA    GGTT
                                ||||||||| ||    ||||
                                ATTGGTGAC CT    TCAG
                                     _ CTCCT
GAM703  LOC256730 3'  TTAACCTAATCACAGTG     95235       AATC
                                CACTGTGA   GGTTAA
                                ||||||||   ||||||
                                GTGACACT   CCAATT
                                     AAT_
GAM703  LOC92609  3'  GGTCATCGTCCCACAGTGG   72848       AAAT   TA
                                CCACTGTG   CGGT  ACC
                                ||||||||   ||||  |||
                                GGTGACAC   GCTA  TGG
                                     CCT_   C_
GAM704  CFL1      3'  GGAGCATCTGGCAGCCCCA   18573    AA       _
                                TG  GCTGCCAGATG TCC
                                ||  |||||||||| |||
                                AC  CGACGGTCTAC AGG
                                  CC         G
GAM704  CYLN2     3'  GGACACCCGGCAGCTTC     12635        AGA
                                GAAGCTGCC   TGTCC
                                |||||||||   |||||
                                CTTCGACGG   ACAGG
                                     CCC
GAM704  DUSP6     5'  TATCTGGGCAGCTTCA      65964        _
                                TGAAGCTGCC AGATG
                                |||||||||| |||||
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                                ACTTCGACGG TCTAT
                                      G
GAM704  EMS1    3'  GACTGTCACGCGGCAGCTTCA  56752          A___  _
                                TGAAGCTGCC   GAT GTC
                                ||||||||||   ||| |||
                                ACTTCGACGG   CTG CAG
                                      CGCA  T
GAM704  EMS1    3'  GACTGTCACGCGGCAGCTTCA  17852          A___  _
                                TGAAGCTGCC   GAT GTC
                                ||||||||||   ||| |||
                                ACTTCGACGG   CTG CAG
                                      CGCA  T
GAM704  LAIR1   3'  AAGGCCTCACATCTGGCAGCCC 9660     AA         ____
           CA                     TG  GCTGCCAGATGT   CCTT
                                ||  ||||||||||||   ||||
                                AC  CGACGGTCTACA   GGAA
                                 CC         CTCC
GAM704  LAIR1   3'  AAGGCCTCACATCTGGCAGCCC 41355    AA         ____
           CA                     TG  GCTGCCAGATGT   CCTT
                                ||  ||||||||||||   ||||
                                AC  CGACGGTCTACA   GGAA
                                 CC         CTCC
GAM704  PAX9    3'  CGTCTCCAGCAGCTTCA     20559         C__
                                TGAAGCTGC  AGATG
                                |||||||||  |||||
                                ACTTCGACG  TCTGC
                                      ACC
GAM704  SNRPN    5'  GATCAAGAACACTTAACAGCTT 42992        CC_  A  C  A
           CA                     TGAAGCTG  AG TGT CTT ATC
                                ||||||||  || ||| ||| |||
                                ACTTCGAC  TC ACA GAA TAG
                                     AAT  _  A  C
GAM704  TYK2    3'  GGGGATGTCAGCCTCA      59876     A  GCCA
                                TGA GCT   GATGTCCTT
                                |||  |||   |||||||||
                                ACT CGA   CTGTAGGGG
                                  C  ____
GAM704  WNT11    3'  GATTAAAAATAACTTGGCAGC  16122        _ A  CC
                                GCTGCCA G TGT  TTAATC
                                ||||||| | |||  ||||||
                                CGACGGT C ATA  AATTAG
                                    T A  AA
GAM704  ANGPTL4  3'  AGGGGCATGGAGCTTCA     32259        G  GA
                                TGAAGCT CCA  TGTCCTT
                                ||||||| |||  |||||||
                                ACTTCGA GGT  ACGGGGA
                                      _  __
GAM704  C20orf130 3'  ACACCTGGCAGCTTCA      61752           A
                                TGAAGCTGCCAG TGT
                                ||||||||||| |||
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                                ACTTCGACGGTC ACA
                                      C
GAM704  CENTB5   3' GATACCTGGCAGCCCCA    95486    AA      A
                                TG  GCTGCCAG TGTC
                                ||  |||||||| ||||
                                AC  CGACGGTC ATAG
                                  CC       C
GAM704  DKFZp434F142 3' GACTTCTGGCAGCCTCA    50026    A       T
                                TGA GCTGCCAGA GTC
                                ||| ||||||||| |||
                                ACT CGACGGTCT CAG
                                  C        T
GAM704  FLJ20013  3' GACTAAAGAGCTGGGAACAGCT 34332        ___    AT_____
           TCA                    TGAAGCTG   CCAG      GTC
                                ||||||||   ||||      |||
                                ACTTCGAC   GGTC      CAG
                                     AAG    GAGAAAT
GAM704  FLJ22814  3' GATTGTGACCTGCCAGCTTCA  46174        C   AT   CT
                                TGAAGCTG CAG  GTC  TAATC
                                |||||||| |||  |||  |||||
                                ACTTCGAC GTC  CAG  GTTAG
                                     C   __   T_
GAM704  LANCL2   3' GCACTGGCAGTTCCA      37998    A       A
                                TG AGCTGCCAG TGT
                                || ||||||||| |||
                                AC TTGACGGTC ACG
                                  C        _
GAM704  MGC30052  3' ATTAAAACAGCAGCTTTA    58533         CAGA   CC
                                TGAAGCTGC    TGT  TTAAT
                                |||||||||    |||  |||||
                                ATTTCGACG    ACA  AATTA
                                     _____   A_
GAM704  SDCBP    3' ATTAAGAACACTGGTTTCA    18841     GCT    A   C
                                TGAA   GCCAG TGT CTTAAT
                                ||||   ||||| ||| ||||||
                                ACTT   TGGTC ACA GAATTA
                                  ___    _   A
GAM704  TREX1    5' ATTAAGGACAAAGCTCCA    53278    A   GCCAGA
                                TG AGCT     TGTCCTTAAT
                                || ||||     ||||||||||
                                AC TCGA     ACAGGAATTA
                                  C   A_____
GAM704  TREX1    5' ATTAAGGACAAAGCTCCA    53288    A   GCCAGA
                                TG AGCT     TGTCCTTAAT
                                || ||||     ||||||||||
                                AC TCGA     ACAGGAATTA
                                  C   A_____
GAM704  ZNF271   5' GATTGGAAAGCCAGCTTCA   95252        CCAGATG   TT
                                TGAAGCTG     TCC  AATC
                                ||||||||     |||  ||||
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                                ACTTCGAC      AGG  TTAG
                                    CGAA___  __
GAM704  LOC120105 5'  GCGTTCTAACAGTTTCA     75513        CC  _
                                TGAAGCTG  AGA TGT
                                ||||||||  ||| |||
                                ACTTTGAC  TCT GCG
                                    AA   T
GAM704  LOC125061 3'  GACACTGACAGCTTCA      74391        C   A
                                TGAAGCTG CAG TGTC
                                |||||||| ||| ||||
                                ACTTCGAC GTC ACAG
                                    A  _
GAM704  LOC148753 3'  GACACTCCTCTGGCAGCCCCA  84218    AA       ____
                                TG  GCTGCCAGA    TGTC
                                ||  |||||||||    ||||
                                AC  CGACGGTCT    ACAG
                                  CC        CCTC
GAM704  LOC150157 5'  ACACTGGCAGCTTCA       84870          A
                                TGAAGCTGCCAG TGT
                                |||||||||||| |||
                                ACTTCGACGGTC ACA
                                          _
GAM704  LOC196890 5'  ACACTGGCAGCTTCA       89643          A
                                TGAAGCTGCCAG TGT
                                |||||||||||| |||
                                ACTTCGACGGTC ACA
                                          _
GAM704  LOC254892 3'  ATTAAGGGTCAAGGCAGTTCA  95527      G    AGA  _
                                TGAA CTGCC   TG TCCTTAAT
                                |||| |||||   || ||||||||
                                ACTT GACGG   AC GGGAATTA
                                  _    A__  T
GAM704  LOC84661  3'  TTAAGAGGCAGCTTTA      50814          AGATGTC
                                TGAAGCTGCC      CTTAA
                                ||||||||||      |||||
                                ATTTCGACGG      GAATT
                                    A_______
GAM705  APP       3'  TGCTTCTGCTATATTTGTG    4909           ATA
                                CACAAATATAG   AAGCA
                                ||||||||||   |||||
                                GTGTTTATATC   TTCGT
                                    GTC
GAM705  BCAT1     3'  CTTCATCTGTATTTATGGC    66203      C        A
                                GCCA AAATATAGAT AAG
                                |||| |||||||||| |||
                                CGGT TTTATGTCTA TTC
                                  A        C
GAM705  BTG2      3'  TGCTTTGTGTGTATGTGTGGC  22219        A    G
                                GCCACA ATATA ATAAAGCA
                                |||||| ||||| ||||||||
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                                CGGTGT TATGT TGTTTCGT
                                   G    G
GAM705  COG3    3'  TGCTTTATATTATTTGGC    48702     CA   TAG
                                GCCA  AATA   ATAAAGCA
                                ||||  ||||   ||||||||
                                CGGT  TTAT   TATTTCGT
                                  __   TA_
GAM705  DMD     5'  TGCTTTATCTGTGCTTGGC   14373     CAAA
                                GCCA   TATAGATAAAGCA
                                ||||   ||||||||||||
                                CGGT   GTGTCTATTTCGT
                                  TC__
GAM705  DMD     5'  TGCTTTATCTGTGCTTGGC   14381     CAAA
                                GCCA   TATAGATAAAGCA
                                ||||   ||||||||||||
                                CGGT   GTGTCTATTTCGT
                                  TC__
GAM705  DSC1    3'  TGCCTTATCTGTGGTTG     17062     A       A
                                CAA TATAGATAA GCA
                                ||| ||||||||| |||
                                GTT GTGTCTATT CGT
                                  G       C
GAM705  DSC1    3'  TGCCTTATCTGTGGTTG     44331     A       A
                                CAA TATAGATAA GCA
                                ||| ||||||||| |||
                                GTT GTGTCTATT CGT
                                  G       C
GAM705  ENTPD6  3'  TGCTGTAAACTATTTGTGGC  6972          TAGATAA
                                GCCACAAATA      AGCA
                                ||||||||||      ||||
                                CGGTGTTTAT      TCGT
                                     CAAATG_
GAM705  FACL3   3'  TGAGTTATCTATATTTGT    15500           AG
                                ACAAATATAGATAA  CA
                                ||||||||||||||  ||
                                TGTTTATATCTATT  GT
                                       GA
GAM705  FLRT2   5'  TGCTTTCATCTTTATATTTATG 25070     C     __   _
          GT                    GCCA AAATAT  AGAT AAAGCA
                                |||| ||||||  |||| ||||||
                                TGGT TTTATA  TCTA TTTCGT
                                  A     TT   C
GAM705  HDAC4   3'  TGCTCTGGTGGATTTTTGTGGC 20118       T  AG  AA_
                                GCCACAAA AT  AT   AGCA
                                |||||||| ||  ||   ||||
                                CGGTGTTT TA  TG   TCGT
                                     T  GG  GTC
GAM705  HIC1    5'  TGCTCCCCTCTTTGTGGC    87317       ATAT   TAA_
                                GCCACAA    AGA    AGCA
                                |||||||    |||    ||||
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                                CGGTGTT   TCT   TCGT
                                    ____  CCCC
GAM705  ITGB3   3'  TGCTTGCATTATATTTGT   3998         ATA
                                ACAAATATAG  AAGCA
                                ||||||||||  |||||
                                TGTTTATATT  TTCGT
                                     ACG
GAM705  JRKL    3'  TGCTCATTGTGTTTGTG    13663         ATAA
                                CACAAATATAG   AGCA
                                ||||||||||   ||||
                                GTGTTTGTGTT   TCGT
                                      AC__
GAM705  LPIN1   3'  GCTTTATCTAGCTCATGGT   67393     CAAATA
                                GCCA    TAGATAAAGC
                                ||||    ||||||||||
                                TGGT    ATCTATTTCG
                                  ACTCG_
GAM705  MS4A1   3'  TGCTTTATTTAATTGTAGG   3751    _   ATA
                                CC ACAA  TAGATAAAGCA
                                || ||||  ||||||||||
                                GG TGTT  ATTTATTTCGT
                                 A   A__
GAM705  NDUFS3  3'  GCCTTATCTATGATTG     15845    A       A
                                CAA TATAGATAA GC
                                ||| |||||||| ||
                                GTT GTATCTATT CG
                                  A       C
GAM705  POLK    3'  TTTTATTAATATTTGTG    32572         A
                                CACAAATAT GATAAAG
                                |||||||| |||||||
                                GTGTTTATA TTATTTT
                                     A
GAM705  POLQ    3'  TGCCTCTTTCTGTTTGTGGC  21693       AT    TAAA_
                                GCCACAA  ATAGA    GCA
                                |||||||  |||||    |||
                                CGGTGTT  TGTCT    CGT
                                    __    TTCTC
GAM705  PRNP    3'  CTTTATATTTTCTATATTTGT  4335          _____
                                ACAAATATAGA    TAAAG
                                ||||||||||    |||||
                                TGTTTATATCT    ATTTC
                                      TTTAT
GAM705  PTGFRN  3'  TGCCGAAGGCTAATTTGTGGC  67194        A   ATAAA_
                                GCCACAAAT TAG     GCA
                                ||||||||| |||     |||
                                CGGTGTTTA ATC     CGT
                                     _  GGAAGC
GAM705  PTPRO   3'  TGCTTTGTAATATGTGGC    47709       AATATAG
                                GCCACA      ATAAAGCA
                                ||||||      ||||||||
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                              CGGTGT     TGTTTCGT
                                 ATAA___
GAM705  PTPRO    3' TGCTTTGTAATATGTGGC   47718     AATATAG
                              GCCACA     ATAAAGCA
                              ||||||     ||||||||
                              CGGTGT     TGTTTCGT
                                 ATAA___
GAM705  PTPRO    3' TGCTTTGTAATATGTGGC   11136     AATATAG
                              GCCACA     ATAAAGCA
                              ||||||     ||||||||
                              CGGTGT     TGTTTCGT
                                 ATAA___
GAM705  PTPRO    3' TGCTTTGTAATATGTGGC   47700     AATATAG
                              GCCACA     ATAAAGCA
                              ||||||     ||||||||
                              CGGTGT     TGTTTCGT
                                 ATAA___
GAM705  PTPRO    3' TGCTTTGTAATATGTGGC   47704     AATATAG
                              GCCACA     ATAAAGCA
                              ||||||     ||||||||
                              CGGTGT     TGTTTCGT
                                 ATAA___
GAM705  RPS6KA2  3' CTTTGTAGATGCTGTGGC   40905      AA  AG
                              GCCACA  TAT  ATAAAG
                              ||||||  |||  ||||||
                              CGGTGT  GTA  TGTTTC
                                 C_   GA
GAM705  SERPINE2 3' TGTCTATATGTGCGGC    74924    A  A
                              GCC CA ATATAGATA
                              ||| || |||||||||
                              CGG GT TATATCTGT
                                C  G
GAM705  SLC25A15 3' TGCTTTATCTGAATAGGC   26513    ACAA  A
                              GCC    AT TAGATAAAGCA
                              |||    || ||||||||||
                              CGG    TA GTCTATTTCGT
                                A___   A
GAM705  SLC9A6   3' CTTTATCTGTATAGCAGGC  21003    ACAA
                              GCC    ATATAGATAAAG
                              |||    ||||||||||||
                              CGG    TATGTCTATTTC
                                ACGA
GAM705  SMPX     3' CTTTATCTTCATTTTTGGC   26760     C    AT
                              GCCA AAAT  AGATAAAG
                              |||| ||||  ||||||||
                              CGGT TTTA  TCTATTTC
                                T    CT
GAM705  STAU2    3' TGCTTTATAGTTGTTTGAGGC 26910    A     TAG
                              GCC CAAATA   ATAAAGCA
                              ||| ||||||   ||||||||
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                                CGG GTTTGT   TATTTCGT
                                  A     TGA
GAM705  TNFRSF10B 3'  TGCTTTATTTATTTATTTGGGC 13884     A     __
                                GCC CAAATA  TAGATAAAGCA
                                ||| ||||||  ||||||||||
                                CGG GTTTAT  ATTTATTTCGT
                                  _     TT
GAM705  TRIM37    3'  GCTATATATTTGTGG       30972          GATAA
                                CCACAAATATA    AGC
                                ||||||||||     |||
                                GGTGTTTATAT    TCG
                                       A____
GAM705  TRPC6     3'  TGCCCTATTTAGTTTGTGGC   16097        A     AA
                                GCCACAAAT TAGATA  GCA
                                ||||||||| ||||||  |||
                                CGGTGTTTG ATTTAT  CGT
                                     _     CC
GAM705  ARFD1     3'  TGCTTTAAAAAAATTTTGTGGC 7993         TATAGA_
                                GCCACAAA      TAAAGCA
                                ||||||||      |||||||
                                CGGTGTTT      ATTTCGT
                                    TAAAAAA
GAM705  BTBD3     3'  TGCTTTATTTACTTTTGT    30316      TA
                                ACAAA  TAGATAAAGCA
                                |||||  ||||||||||
                                TGTTT  ATTTATTTCGT
                                   TC
GAM705  C19orf7   3'  TGCTCTGTGGGATTTGTGG   61131        ATAG   A
                                CCACAAAT    ATA AGCA
                                ||||||||    ||| ||||
                                GGTGTTTA    TGT TCGT
                                    GGG_   C
GAM705  dA141H5.1 3'  TGCCCTTAGGTCTTTGTGGC   59108       ATAT    AAA___
                                GCCACAA    AGAT     GCA
                                |||||||    ||||     |||
                                CGGTGTT    TCTG     CGT
                                     _____   GATTCC
GAM705  ENPP4     3'  TGCCTATTGTATTTGTGGT   30051          ATAAA
                                GCCACAAATATAG    GCA
                                ||||||||||||     |||
                                TGGTGTTTATGTT    CGT
                                       ATC__
GAM705  FLJ10094  3'  TGCCTTTAGTTATATCTGTGGC 35809       A     A    _
                                GCCACA ATATAG TAAAG CA
                                |||||| |||||| ||||| ||
                                CGGTGT TATATT ATTTC GT
                                   C     G    C
GAM705  FLJ10716  3'  TGCTTTATCTACTTTAGGC   36488     ACA  TA
                                GCC   AA  TAGATAAAGCA
                                |||   ||  ||||||||||
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                                CGG  TT  ATCTATTTCGT
                                  A__  TC
GAM705  FLJ11726  3'  CTTTTGGGACTGTATTTGTGGC 46412          AT___
                                GCCACAAATATAG    AAAG
                                ||||||||||||    ||||
                                CGGTGTTTATGTC    TTTC
                                      AGGGT
GAM705  FLJ12994  3'  GCCATTTATATTTGTG     77477          AAA
                                CACAAATATAGAT  GC
                                ||||||||||||  ||
                                GTGTTTATATTTA  CG
                                      C__
GAM705  FLJ12994  3'  GCCATTTATATTTGTG     43127          AAA
                                CACAAATATAGAT  GC
                                ||||||||||||  ||
                                GTGTTTATATTTA  CG
                                      C__
GAM705  FLJ21106  3'  GCTTTATCGTGTGGC      46997       AATATA
                                GCCACA     GATAAAGC
                                ||||||     ||||||||
                                CGGTGT     CTATTTCG
                                   G_____
GAM705  FLJ21916  3'  TGCTATGTCTCTGTATTTGTGG 43646          __    A
          C                      GCCACAAATAT  AGATA AGCA
                                ||||||||||  ||||| ||||
                                CGGTGTTTATG  TCTGT TCGT
                                      TC    A
GAM705  FLJ22833  3'  CTTTAAATTATTTGTGG     43104         TAGA
                                CCACAAATA    TAAAG
                                |||||||||   |||||
                                GGTGTTTAT    ATTTC
                                     TAA_
GAM705  GABARAP   3'  TCTTAATGTTTGTGGC      23460          __
                                GCCACAAATAT  AGA
                                ||||||||||  |||
                                CGGTGTTTGTA  TCT
                                      AT
GAM705  GNG10     3'  GCTTTGTAGTTGTGGC      14676        ATATAG
                                GCCACAA     ATAAAGC
                                |||||||     |||||||
                                CGGTGTT     TGTTTCG
                                   GA____
GAM705  GTF2H3    3'  TGTCCATGTTTGTGGC      7709           A
                                GCCACAAATAT GATA
                                |||||||||| ||||
                                CGGTGTTTGTA CTGT
                                      C
GAM705  HMP19     3'  GCTTTATAATTTTGTGGT    87475         TATAG
                                GCCACAAA    ATAAAGC
                                ||||||||    |||||||
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                                TGGTGTTT    TATTTCG
                                    TAA__
GAM705  HRIHFB2436 3'  TGCTTTGATTGTATTTTGGC  26798     C      A
                                GCCA AAATATAG TAAAGCA
                                |||| |||||||| |||||||
                                CGGT TTTATGTT GTTTCGT
                                  _      A
GAM705  HSPC019  3'  TGCTTTATTATATTCAGGGC  25861    ACA    A
                                GCC  AATAT GATAAAGCA
                                |||  ||||| |||||||||
                                CGG  TTATA TTATTTCGT
                                  GAC   _
GAM705  KIAA0211 3'  TGCTTCTGTTATTTATGGC   27549    C    _   TAA
                                GCCA AAATA TAGA  AGCA
                                |||| ||||| ||||  ||||
                                CGGT TTTAT GTCT  TCGT
                                  A    T   ____
GAM705  KIAA0459 3'  CTTTATCTATGAAATGG    60995    CAAA
                                CCA   TATAGATAAAG
                                |||   ||||||||||
                                GGT   GTATCTATTTC
                                  AAA_
GAM705  KIAA0483 3'  TGCTTTATCTGCTCTCTGT   30793    AATA_
                                ACA    TAGATAAAGCA
                                |||    ||||||||||
                                TGT    GTCTATTTCGT
                                  CTCTC
GAM705  KIAA0537 3'  TGCTTTATTCACTTCTGTGG  29262     AATATA
                                CCACA    GATAAAGCA
                                |||||    |||||||||
                                GGTGT    TTATTTCGT
                                   CTTCAC
GAM705  KIAA1240 5'  TGCTTTATCAATTTTTG    66740     T  A
                                CAAA AT GATAAAGCA
                                |||| || |||||||||
                                GTTT TA CTATTTCGT
                                  T  A
GAM705  KIAA1336 3'  TGCTCCTTTCTATCTGTGGT  72326      AAT    TAA_
                                GCCACA  ATAGA   AGCA
                                ||||||  |||||   ||||
                                TGGTGT  TATCT   TCGT
                                   C__    TTCC
GAM705  KIAA1437 3'  TGCCTCTTCAGTATTTGTGGC 60594         A  TAAA
                                GCCACAAATAT GA   GCA
                                |||||||||| ||   |||
                                CGGTGTTTATG CT   CGT
                                      A  TCTC
GAM705  KIAA1765 3'  TGCTTTATTTGTAGTAGC   70614   C  AAA
                                GC AC  TATAGATAAAGCA
                                || ||  ||||||||||||
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                                CG TG   ATGTTTATTTCGT
                                 A ___
GAM705  MGC3178  3' TGCTGGACTATTTGTGGC    47992         TAGATAA
                                GCCACAAATA      AGCA
                                ||||||||||      ||||
                                CGGTGTTTAT      TCGT
                                     CAGG___
GAM705  P37NB    3' TGCCTGTCCATTTGTGG     19507        ATA   AA
                                CCACAAAT   GATA  GCA
                                ||||||||   ||||  |||
                                GGTGTTTA   CTGT  CGT
                                    C__    C_
GAM705  PAIP1    3' GCTTTATTTATATGGC      66925      CAAA
                                GCCA    TATAGATAAAGC
                                ||||    ||||||||||||
                                CGGT    ATATTTATTTCG
                                  _____
GAM705  PS-PLA1  3' TGCTTTATCTCCTTGGGC    31908     A   ATAT
                                GCC CAA    AGATAAAGCA
                                ||| |||    ||||||||||
                                CGG GTT    TCTATTTCGT
                                  _   CC__
GAM705  PSPH     3' CTTTATGTATATTTGTAGC    15915    C       G
                                GC ACAAATATA ATAAAG
                                || |||||||| ||||||
                                CG TGTTTATAT TATTTC
                                 A        G
GAM705  S164     5' GCGGCTGTATTTGCGGC     60781     A       ATAAA
                                GCC CAAATATAG     GC
                                ||| |||||||||     ||
                                CGG GTTTATGTC     CG
                                  C        GG___
GAM705  SCDGF-B  3' TGCTTTGTTAATGCCATGGC   52453     CAAA   A
                                GCCA    TAT GATAAAGCA
                                ||||    ||| |||||||||
                                CGGT    GTA TTGTTTCGT
                                   ACC_   A
GAM705  SCDGF-B  3' TGCTTTGTTAATGCCATGGC   47381     CAAA   A
                                GCCA    TAT GATAAAGCA
                                ||||    ||| |||||||||
                                CGGT    GTA TTGTTTCGT
                                   ACC_   A
GAM705  TRIM36   3' TGCTAAAGTCACATTTGTGGT  38017         ATA   AA_
                                GCCACAAAT   GAT   AGCA
                                |||||||||   |||   ||||
                                TGGTGTTTA   CTG   TCGT
                                     CA_   AAA
GAM705  TSPAN-2  3' CTTTACTGTGTCTGTAGC    19165    C   A     A
                                GC ACA ATATAG TAAAG
                                || ||| |||||| |||||
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                                CG TGT TGTGTC ATTTC
                                 A  C    _
GAM705  ZDHHC3   3'  TGTCTTATCTATATTT     33459          AG
                                AAATATAGATAA  CA
                                ||||||||||||  ||
                                TTTATATCTATT  GT
                                      CT
GAM705  ZDHHC8   3'  TGCTTTATGCTCTTGTGG    63908      ATAT  _
                                CCACAA   AG ATAAAGCA
                                ||||||   || ||||||||
                                GGTGTT   TC TATTTCGT
                                   C___  G
GAM705  LOC121536 3' TGCTTTATTCTGTATCTG    74091    A     _
                                CA ATATAGA TAAAGCA
                                || ||||||| |||||||
                                GT TATGTCT ATTTCGT
                                 C      T
GAM705  LOC150737 3' GCTTTATTTACCCTTTGGC   79996     CAAATA
                                GCCA     TAGATAAAGC
                                ||||     ||||||||||
                                CGGT     ATTTATTTCG
                                  TTCCC_
GAM705  LOC151126 3' TGCTACATAATTTTGTGGC   80132        TATAG  AA
                                GCCACAAA    AT  AGCA
                                ||||||||    ||  ||||
                                CGGTGTTT    TA  TCGT
                                     TAA__  CA
GAM705  LOC153505 3' TGCTGACCATCTTTGTGGC   80850       ATAT   AA__
                                GCCACAA   AGAT   AGCA
                                |||||||   ||||   ||||
                                CGGTGTT   TCTA   TCGT
                                    _____   CCAG
GAM705  LOC158730 3' TGCAGGTGTATATTTGTGGT  86891          G  AAA
                                GCCACAAATATA AT   GCA
                                ||||||||||||| ||   |||
                                TGGTGTTTATAT TG   CGT
                                       G  GA_
GAM705  LOC199675 3' TGCCCTGTCACTATCTGTGGC 88270       A   TA    AA
                                GCCACA ATA  GATA  GCA
                                |||||| |||  ||||  |||
                                CGGTGT TAT  CTGT  CGT
                                   C   CA    CC
GAM705  LOC253512 3' TGCTTCTTTATTTGTG      94914        T   TAA
                                CACAAATA AGA   AGCA
                                ||||||||| |||   ||||
                                GTGTTTAT TCT   TCGT
                                     T  ____
GAM705  LOC253805 3' TGCTTATCATATATTTGTG   96440          _    A
                                CACAAATATA GATAA GCA
                                |||||||||| ||||| |||
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```
                                GTGTTTATAT CTATT CGT
                                     A    _
GAM705  LOC255040 3'  TGCTTTGTTTATTTGGTG    96384    AAAT
                                CAC   ATAGATAAAGCA
                                |||   ||||||||||||
                                GTG   TATTTGTTTCGT
                                  GTT_
GAM705  LOC255041 3'  TGCTTTGTTTATTTGGTG    96389    AAAT
                                CAC   ATAGATAAAGCA
                                |||   ||||||||||||
                                GTG   TATTTGTTTCGT
                                  GTT_
GAM705  LOC51107  3'  TGCTTTGTCCTTTTGTG     32063      TATA
                                CACAAA   GATAAAGCA
                                ||||||   |||||||||
                                GTGTTT   CTGTTTCGT
                                   TC__
GAM705  LOC91628  3'  TCTTGGTATTTGTGGT      66763         __
                                GCCACAAATAT  AGA
                                ||||||||||  |||
                                TGGTGTTTATG  TCT
                                      GT
GAM706  ALDH3B1   3'  ATTCCTGCCCTCTCTGAGT   91521    CG    AAA
                                AC  GGAGA   GCAGGAAT
                                ||  |||||   ||||||||
                                TG  TCTCT   CGTCCTTA
                                 AG    CC_
GAM706  AOC3      3'  TCCTGCAATTTCTCCCG     13588       A_
                                CGGGAGAAA  GCAGGA
                                |||||||||  ||||||
                                GCCCTCTTT  CGTCCT
                                     AA
GAM706  AQP8      3'  ATTCCTGCTGCTCCAGGTG   6752      G   AAA
                                CACC GGAG   AGCAGGAAT
                                |||| ||||   |||||||||
                                GTGG CCTC   TCGTCCTTA
                                  A   G__
GAM706  ARF3      3'  ATTCCTGCCTTCCAGTG     7996     C    AAAA
                                CAC GGGAG    GCAGGAAT
                                ||| |||||    ||||||||
                                GTG CCTTC    CGTCCTTA
                                  A    _____
GAM706  ATP10C    3'  CCTGGGCTTTTCTCCC      44410         __
                                GGGAGAAAAGC  AGG
                                ||||||||||  |||
                                CCCTCTTTTCG  TCC
                                      GG
GAM706  ATP8A2    3'  TCTGCTCTTTCTCCCAGG    93520    _      _
                                CC GGGAGAAA AGCAGG
                                || |||||||| ||||||
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                                GG CCCTCTTT TCGTCT
                                 A       C
GAM706  ATRX     3'  TTTCTCTCTCCTGG        56250         AAA C
                                CCGGGAGA   G AGGAA
                                ||||||||   | |||||
                                GGTCCTCT   C TCTTT
                                     ___ _
GAM706  ATRX     3'  TTTCTCTCTCCTGG        4919          AAA C
                                CCGGGAGA   G AGGAA
                                ||||||||   | |||||
                                GGTCCTCT   C TCTTT
                                     ___ _
GAM706  BSND     5'  TGTCTTCTCTCCCTGTG     54112     C     A  _
                                CAC GGGAGA AAG CA
                                ||| |||||| ||| ||
                                GTG CCCTCT TTC GT
                                  T     C   T
GAM706  BTNL3    3'  ATTCCTGCCTCACAGGTG    21999      GG_   AAAA
                                CACC   GAG    GCAGGAAT
                                ||||   |||    ||||||||
                                GTGG   CTC    CGTCCTTA
                                  ACA   _____
GAM706  CAPN10   3'  CCTGCTTCCCCTTCTCGGT   43600         AA__
                                ACCGGGAG    AAGCAGG
                                ||||||||    |||||||
                                TGGCTCTT    TTCGTCC
                                     CCCC
GAM706  DLST     3'  ATTCCTGCCTTTCTTCC     8643          A
                                GGGAGAAA GCAGGAAT
                                |||||||| ||||||||
                                CCTTCTTT CGTCCTTA
                                     C
GAM706  DLST     3'  TTTTGCTTCTCCCTAGTG    8650      C_     AA
                                CAC  GGGAGA  AGCAGGA
                                |||  ||||||  |||||||
                                GTG  CCCTCT  TCGTTTT
                                  AT     __
GAM706  ETF1     3'  TCCTGACCTCCTGGTG      16400          AAAAG
                                CACCGGGAG    CAGGA
                                |||||||||    |||||
                                GTGGTCCTC    GTCCT
                                     CA___
GAM706  ETV5     3'  ATTCCTGCCTTTTTTT      15485         _
                                GAGAAAAG CAGGAAT
                                |||||||| |||||||
                                TTTTTTTC GTCCTTA
                                     C
GAM706  FCMD     3'  CCTGCTTCTTTTGG        22090         AA
                                CCGGGAGA  AGCAGG
                                ||||||||  ||||||
```

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                                GGTTTTCT  TCGTCC
                                    __
GAM706  FN1     5'  CTTGCCTCCCGGTG       54013        AAAA
                                CACCGGGAG   GCAGG
                                |||||||||   |||||
                                GTGGCCCTC   CGTTC
                                    ____
GAM706  FN1     5'  CTTGCCTCCCGGTG       8947         AAAA
                                CACCGGGAG   GCAGG
                                |||||||||   |||||
                                GTGGCCCTC   CGTTC
                                    ____
GAM706  FOXD2   3'  TCCTCAGCCTCTCCCGG    15570        AAA __
                                CCGGGAGA  GC  AGGA
                                ||||||||  ||  ||||
                                GGCCCTCT  CG  TCCT
                                     C__  AC
GAM706  FRDA    3'  ATTCCTGCTTTTGAGG     3780    GGGAG
                                CC    AAAAGCAGGAAT
                                ||    ||||||||||||
                                GG    TTTTCGTCCTTA
                                 AG___
GAM706  GAD1    5'  TCTCTCTCTTCTCCTGG     5875         A  CA
                                CCGGGAGAA AG  GGA
                                |||||||||  ||  |||
                                GGTCCTCTT TC  TCT
                                      C  TC
GAM706  GAS1    5'  TTCCCCTCCTCTCCCGG     8996         AA  CA
                                CCGGGAGA  AG  GGAA
                                ||||||||  ||  ||||
                                GGCCCTCT  TC  CCTT
                                     CC  C_
GAM706  GNAO1   3'  CCTGCCTTTGTTTCGGTG    90967      GG G   A
                                CACCG  A AAA GCAGG
                                |||||  | ||| |||||
                                GTGGC  T TTT CGTCC
                                   TT G   C
GAM706  GNLY    5'  CCTGCTCTCTCCCGG       25027        AA
                                CCGGGAGA  AGCAGG
                                ||||||||  ||||||
                                GGCCCTCT  TCGTCC
                                     C_
GAM706  HEBP1   3'  TCTCTTTTCTCACGGT      32026      G       C
                                ACCG GAGAAAAG AGG
                                ||||  |||||||| |||
                                TGGC CTCTTTTC TCT
                                  A       _
GAM706  IKBKB   3'  ATTCCTGCTCAAGCGTGTG   63202     _  GGAGAAA
                                CAC CG      AGCAGGAAT
                                ||| ||      |||||||||
```

```
                              GTG GC      TCGTCCTTA
                                T  GAAC___
GAM706  ITGAL    3'  CCAGCCTTTCTCCCAGG     9388     _      A  A
                              CC GGGAGAAA GC GG
                              || |||||||| || ||
                              GG CCCTCTTT CG CC
                               A       C  A
GAM706  ITPKB    3'  ATTCCTGCTTCCCC       9422      A  AA
                              GGG GA  AGCAGGAAT
                              ||| ||  |||||||||
                              CCC CT  TCGTCCTTA
                                _ __
GAM706  LBR      3'  TTTTGCTTTTCTCCTGG     59355
                              CCGGGGAGAAAAGCAGGA
                              ||||||||||||||||||
                              GGTCCTCTTTTCGTTTT

GAM706  MEN1     5'  CCAGCTTCCTCCTGGTG     93368         AA    A
                              CACCGGGAG  AAGC GG
                              |||||||||  |||| ||
                              GTGGTCCTC  TTCG CC
                                   C_   A
GAM706  MNT      3'  CCTGCTTCTCCCGG       39709         AA
                              CCGGGAGA  AGCAGG
                              ||||||||  ||||||
                              GGCCCTCT  TCGTCC
                                   __
GAM706  MYBBP1A  3'  ATTCCTGCGGGGGTCCCAGG  27228    _   GAAAA
                              CC GGGA    GCAGGAAT
                              || ||||    ||||||||
                              GG CCCT    CGTCCTTA
                               A   GGGGG
GAM706  NPEPPS   3'  CTGGCTTCTCCCGGT      20875         AA   A
                              ACCGGGAGA  AGC GG
                              |||||||||  ||| ||
                              TGGCCCTCT  TCG TC
                                   __  G
GAM706  NTRK2    3'  ATTCCTGCCTTTGATGTGG   20520     GGAG   A
                              CCG    AAA GCAGGAAT
                              |||    ||| ||||||||
                              GGT    TTT CGTCCTTA
                                GTAG   C
GAM706  PIG8     3'  TTTGTTTTTCTCCCTGTG    16874     C
                              CAC GGGAGAAAAGCAGG
                              ||| ||||||||||||||
                              GTG CCCTCTTTTTGTTT
                                T
GAM706  PSG4     3'  ATTCCATTTTCTCCC       10937          GCA
                              GGGAGAAAA   GGAAT
                              |||||||||   |||||
```

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                                CCCTCTTTT  CCTTA
                                     A__
GAM706  RARG    3' ATTCCCATTGGCTCCCTGTG  6377    C    AA  GCA
                                CAC GGGAG  AA  GGAAT
                                ||| |||||  ||  |||||
                                GTG CCCTC  TT  CCTTA
                                  T    GG  AC_
GAM706  RFX5    3' ATTCCTGCTTCCCTCTC    4821      AA
                                GGGAG  AAGCAGGAAT
                                |||||  ||||||||||
                                CTCTC  TTCGTCCTTA
                                   CC
GAM706  RNH     3' TCCGCTTATTTCTGCCAGT   11369   C  G   __  A
                                AC GG AGAAA  AGC GGA
                                || || |||||  ||| |||
                                TG CC TCTTT  TCG CCT
                                 A  G    AT  _
GAM706  RNH     3' TCCGCTTATTTCTGCCAGT   59624   C  G   __  A
                                AC GG AGAAA  AGC GGA
                                || || |||||  ||| |||
                                TG CC TCTTT  TCG CCT
                                 A  G    AT  _
GAM706  SCN4A   3' ATTCCTGCCTGGTCCAGTG   4409    C  AGAAAA
                                CAC GGG    GCAGGAAT
                                ||| |||    ||||||||
                                GTG CCT    CGTCCTTA
                                  A  GGTC__
GAM706  SLC20A1  3' ATTCCTGCTCCCCTG     59390    A  AAA
                                CGGG GA  GCAGGAAT
                                |||| ||  ||||||||
                                GTCC CT  CGTCCTTA
                                  C  ___
GAM706  SLC7A6   3' TTCTGTTTTCTCCCTGTG   14316   C      G
                                CAC GGGAGAAAA CAGGA
                                ||| ||||||||| |||||
                                GTG CCCTCTTTT GTCTT
                                  T       _
GAM706  SLC9A1   3' TCCAGGCTTCTCCCGG     70411      AA  A_
                                CCGGGAGA  AGC  GGA
                                ||||||||  |||  |||
                                GGCCCTCT  TCG  CCT
                                     __  GA
GAM706  SMARCA3  3' TCCTTTTCTCCCTGTG     57398    C      AGC
                                CAC GGGAGAAA  AGGA
                                ||| ||||||||  ||||
                                GTG CCCTCTTT  TCCT
                                  T      ___
GAM706  SMARCA3  3' TCCTTTTCTCCCTGTG     11792    C      AGC
                                CAC GGGAGAAA  AGGA
                                ||| ||||||||  ||||
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                                GTG CCCTCTTT  TCCT
                                  T      ___
GAM706  SOX13    3'  TCCTGCTTCTCTGGG      19087    G    AA
                                CC GGAGA  AGCAGGA
                                || |||||  |||||||
                                GG TCTCT  TCGTCCT
                                 G    __
GAM706  SPOCK    3'  ATTCTTGTTTCTACC       62814    G   AA
                                GG AGAA  GCAGGAAT
                                || ||||  ||||||||
                                CC TCTT  TGTTCTTA
                                 A   __
GAM706  STK10    3'  TTCTGCTTCTCCCG        19991        AA
                                CGGGAGA  AGCAGGA
                                |||||||  |||||||
                                GCCCTCT  TCGTCTT
                                    __
GAM706  STK10    3'  ATTCCTCCTGTTCTCCC     19981        A  C
                                GGGAGAA AG AGGAAT
                                ||||||| || ||||||
                                CCCTCTT TC TCCTTA
                                    G  C
GAM706  SURF6    3'  ATTCCTTTCTGTTCCCCAGTG  22187     C   A   A  C_
                                CAC GGG GAA AG  AGGAAT
                                ||| ||| ||| ||  ||||||
                                GTG CCC CTT TC  TCCTTA
                                  A  _  G  TT
GAM706  TAT      3'  TTCCTGCTTTTCCCC       4479      A
                                GGG GAAAAGCAGGAA
                                ||| ||||||||||||
                                CCC CTTTTCGTCCTT
                                 _
GAM706  TGM3     3'  ATTCCTGCTTCTCTCTCAGG   12279    _     A
                                CC GGGAGA AAGCAGGAAT
                                || |||||| ||||||||||
                                GG CTCTCT TTCGTCCTTA
                                 A     C
GAM706  TMEM1    3'  ATTCCTGCTTTTCTCACC     12333    _
                                GG GAGAAAAGCAGGAAT
                                || ||||||||||||||
                                CC CTCTTTTCGTCCTTA
                                 A
GAM706  TMPRSS3  5'  ATTCCTGCCTTCCTCCC     50522      A  A
                                GGGAG AA GCAGGAAT
                                ||||| || ||||||||
                                CCCTC TT CGTCCTTA
                                   C  C
GAM706  USH3A    5'  ATTCCTGCCTCAGTTGTG    53782     CGG_  AAAA
                                CAC   GAG   GCAGGAAT
                                |||   |||   ||||||||
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                                GTG   CTC   CGTCCTTA
                                  TTGA  ____
GAM706  VIPR2    3'  CTGGTTTCTCCTGGT      12610          AG
                                ACCGGGAGAAA  CAG
                                ||||||||||  |||
                                TGGTCCTCTTT  GTC
                                      G_
GAM706  ZFP36L1  3'  ATTCCTCCTCCCCTCTTCCCGG 17005        _  AA__  C
            TG                    CACCGGGA GA   AG AGGAAT
                                ||||||||  ||   ||  ||||||
                                GTGGCCCT CT   TC TCCTTA
                                     T  CCCC  C
GAM706  ARHGAP9  3'  CCTGCTTCTCTTCTTGT    50678    C     A
                                AC GGGAGA AAGCAGG
                                ||  ||||||  |||||||
                                TG TCTTCT TTCGTCC
                                 T     C
GAM706  BAD      3'  ATTCCCTTCCGGTG       52189          AAAAGCA
                                CACCGGGAG      GGAAT
                                |||||||||      |||||
                                GTGGCCTTC      CCTTA
                                       ________
GAM706  BAD      3'  ATTCCCTTCCGGTG       15061          AAAAGCA
                                CACCGGGAG      GGAAT
                                |||||||||      |||||
                                GTGGCCTTC      CCTTA
                                       ________
GAM706  CABP5    3'  TCCCGTTTCTCTCTCCCGGT   39080         A__    A
                                ACCGGGAGA   AAGC GGA
                                |||||||||   |||| |||
                                TGGCCCTCT   TTTG CCT
                                      CTC   C
GAM706  CALN1    3'  TTCTTCTTGCTCCCAGTG    48880     C    AA   C
                                CAC GGGAG  AAG AGGAA
                                |||  |||||  |||  |||||
                                GTG CCCTC  TTC TTCTT
                                  A    G_  _
GAM706  CECR7    3'  TCTGCTGCCCTCTCCTGG    79626         AA__
                                CCGGGAGA   AGCAGG
                                ||||||||   ||||||
                                GGTCCTCT   TCGTCT
                                     CCCG
GAM706  CENTB5   3'  ATTCTTGCCCCTCTCCCTGTG  95483     C     AAA
                                CAC GGGAGA   GCAGGAAT
                                |||  ||||||   ||||||||
                                GTG CCCTCT   CGTTCTTA
                                  T     CCC
GAM706  cerk     3'  ATTCCTGCCGCGCTCCCCGG   42844       _  AAAA
                                CCGGG AG   GCAGGAAT
                                |||||  ||   ||||||||
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                                GGCCC TC    CGTCCTTA
                                   C  GCGC
GAM706  CLECSF9  3'  ATTCCTGCTCAGAATACCGGT  26837      GAGAAA_
                                ACCGG      AGCAGGAAT
                                |||||      |||||||||
                                TGGCC      TCGTCCTTA
                                   ATAAGAC
GAM706  CLSTN3   5'  ATTCCTGCCCCTCTCTGCCC   28204     _  AAA__
                                GGG AGA    GCAGGAAT
                                ||| |||    ||||||||
                                CCC TCT    CGTCCTTA
                                  G   CTCCC
GAM706  CNOT3    5'  ATTTCTGTCTTCTCCCAGG   27216    _     AA
                                CC GGGAGAA  GCAGGAAT
                                || |||||||  ||||||||
                                GG CCCTCTT  TGTCTTTA
                                 A      C_
GAM706  CSE-C    3'  TCTTTCTTTCTCCCG       91483          A C
                                CGGGAGAAA G AGGA
                                ||||||||| | ||||
                                GCCCTCTTT C TTCT
                                      _ T
GAM706  DCTD     3'  ATTCCTGCTCTCCC        8621        AAA
                                GGGAGA   GCAGGAAT
                                ||||||   ||||||||
                                CCCTCT   CGTCCTTA
                                   ___
GAM706  dJ309H15.1 3'  TCCTGCTTCCCCAGG       56798    _   A  AA
                                CC GGG GA  AGCAGGA
                                || ||| ||  |||||||
                                GG CCC CT  TCGTCCT
                                 A  _  __
GAM706  DKFZp434J1015 3'  ATTCCTGCCCCTCTCCC     92632       AAA
                                GGGAGA   GCAGGAAT
                                ||||||   ||||||||
                                CCCTCT   CGTCCTTA
                                    CCC
GAM706  DKFZp547I014 5'  TCATGTGCTTCTCCCGCTG   39548    C       AA   G
                                CA CGGGAGAA  GCA GA
                                || ||||||||  ||| ||
                                GT GCCCTCTT  TGT CT
                                 C       CG   A
GAM706  DKFZp566D133 5'  ATTCCTGCTCCACAACCTGTG  71761     C  GAGAAA
                                CAC GG     AGCAGGAAT
                                ||| ||     |||||||||
                                GTG CC     TCGTCCTTA
                                  T  AACACC
GAM706  DKFZp761A052 5'  TCCGGGTTCTCTCCCGG     73009         AA   A_
                                CCGGGAGA  AGC  GGA
                                ||||||||  |||  |||
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                              GGCCCTCT  TTG  CCT
                                  C_  GG
GAM706  FLJ10290 3' CCTGCTTCTGTTTGGT     35971       _  AA
                              ACCGGG AGA  AGCAGG
                              ||||||| |||  ||||||
                              TGGTTT TCT  TCGTCC
                                 G  __
GAM706  FLJ10898 3' TTTCTCCTTTCTTCC       59441        A C
                              GGGAGAAA G AGGAA
                              |||||||| | |||||
                              CCTTCTTT C TCTTT
                                   _ C
GAM706  FLJ11000 3' ATTCCTGCTTTAATTAATGG  36960     G_  GA
                              CCG  GA  AAAGCAGGAAT
                              |||  ||  ||||||||||
                              GGT  TT  TTTCGTCCTTA
                                AA  AA
GAM706  FLJ12700 3' ATTCCTGCTCTCCT        46115       AAA
                              GGGAGA  GCAGGAAT
                              ||||||  ||||||||
                              TCCTCT  CGTCCTTA
                                 ___
GAM706  FLJ13195 3' ATTCCTGCCTCTCCC       43258       AAA
                              GGGAGA  GCAGGAAT
                              ||||||  ||||||||
                              CCCTCT  CGTCCTTA
                                 C__
GAM706  FLJ14298 5' TTCTCTTCTCCCGTTG      45432    C      AA  C
                              CA CGGGAGA  AG AGGA
                              || |||||||  || ||||
                              GT GCCCTCT  TC TCTT
                               T     __ _
GAM706  FLJ14665 3' ATTCCTGCTTCCCTCCC     51511       AA
                              GGGAG  AAGCAGGAAT
                              |||||  ||||||||||
                              CCCTC  TTCGTCCTTA
                                 CC
GAM706  FLJ14827 3' ATTCTTGCCTTTTTCTCCCG  51648          __
                              CGGGAGAAAA  GCAGGAAT
                              |||||||||  ||||||||
                              GCCCTCTTTT  CGTTCTTA
                                    TC
GAM706  FLJ20036 5' TCCTGCCTGTCTCCCGGTG   34398          AAA
                              CACCGGGAGA  GCAGGA
                              ||||||||||  ||||||
                              GTGGCCCTCT  CGTCCT
                                    GTC
GAM706  FLJ20254 3' ATTCCTGCTTCTCC        34785       AA
                              GGAGA  AGCAGGAAT
                              |||||  |||||||||
```

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                                CCTCT  TCGTCCTTA
                                   __
GAM706  FLJ20772  3'  TCCCTTTTGTCCCCTGGTG   35659     __   G    CA
                                CACC  GGGA AAAAG  GGA
                                ||||  |||| |||||  |||
                                GTGG  CCCT TTTTC  CCT
                                  TC   G   __
GAM706  FLJ21952  3'  ATTCCTGCCCTTCTTTACC   42555   __    AA
                                GG  GAGAA  GCAGGAAT
                                ||  |||||  ||||||||
                                CC  TTCTT  CGTCCTTA
                                 AT    CC
GAM706  FLJ22035  3'  ATTCCTTCTTTTCTCCC     44534         C
                                GGGAGAAAAG AGGAAT
                                |||||||||| ||||||
                                CCCTCTTTTC TCCTTA
                                      T
GAM706  FLJ22055  3'  TGCTTCCCTCCTGGTG      45501         AA
                                CACCGGGAG  AAGCA
                                |||||||||  |||||
                                GTGGTCCTC  TTCGT
                                     CC
GAM706  FLJ22624  5'  TTCGGCTTCTCCCGG       45653        AA   A
                                CCGGGAGA  AGC GGA
                                ||||||||  ||| |||
                                GGCCCTCT  TCG CTT
                                    __  G
GAM706  FLJ23519  3'  TCCGCTTATTTCTGCCAGT   69207    C  G    __   A
                                AC GG AGAAA  AGC GGA
                                || || |||||  ||| |||
                                TG CC TCTTT  TCG CCT
                                 A  G    AT  _
GAM706  GGA2      3'  ATTCCTGCTTCGTCTG      56871     GA  AA
                                CGG  GA  AGCAGGAAT
                                |||  ||  |||||||||
                                GTC  CT  TCGTCCTTA
                                  TG  __
GAM706  GGA2      3'  ATTCCTGCTTCGTCTG      30458     GA  AA
                                CGG  GA  AGCAGGAAT
                                |||  ||  |||||||||
                                GTC  CT  TCGTCCTTA
                                  TG  __
GAM706  GTF2F2    3'  TTTGATTTCTCTCGGT      14681          AG
                                ACCGGGAGAAA  CAGG
                                ||||||||||  ||||
                                TGGCTCTCTTT  GTTT
                                      A_
GAM706  HELO1     3'  TTTTGCTTTCCACCAGTG    41500     C  GA   A
                                CAC GG  GAAA GCAGGA
                                ||| ||  |||| ||||||
```

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                              GTG CC  CTTT CGTTTT
                                A  AC   _
GAM706  KIAA0062 3' CCTCCTTTTCTCTCAGTG    70237     C        C
                              CAC GGGAGAAAAG AGG
                              ||| |||||||||| |||
                              GTG CTCTCTTTTC TCC
                                A         C
GAM706  KIAA0319 3' CTGACTCCTCTCGGTG      29034         AAA  _
                              CACCGGGAG   AG CAG
                              |||||||||   || |||
                              GTGGCTCTC   TC GTC
                                    C__  A
GAM706  KIAA0319 3' TCCTGCCTTGATGGATG     29040    _  G_   AAAA
                              CA CCG  GAG    GCAGGA
                              || |||  |||    ||||||
                              GT GGT  TTC    CGTCCT
                               A   AG  _____
GAM706  KIAA0323 3' ATTCCTGCCAGGTCCCCG    63257      A  AAA_
                              CGGG GA    GCAGGAAT
                              |||| ||    ||||||||
                              GCCC CT    CGTCCTTA
                                _  GGAC
GAM706  KIAA0607 3' ATTCCTGTCCCCCTGGTG    72567        AGAAAA
                              CACCGGG     GCAGGAAT
                              |||||||     ||||||||
                              GTGGTCC     TGTCCTTA
                                  CCC___
GAM706  KIAA0676 3' ATTCCTGCCTCTTGG       30449        AAAA
                              CCGGGAG    GCAGGAAT
                              |||||||    ||||||||
                              GGTTCTC    CGTCCTTA

                                 _____
GAM706  KIAA0939 3' ATTCCTGCTTCTCAAGG     62005    GG    AA
                              CC  GAGA  AGCAGGAAT
                              ||  ||||  |||||||||
                              GG  CTCT  TCGTCCTTA
                               AA   __
GAM706  KIAA0939 3' ATTCCTGCTTCTCTGGG     62006    G     AA
                              CC GGAGA  AGCAGGAAT
                              || |||||  |||||||||
                              GG TCTCT  TCGTCCTTA
                               G    __
GAM706  KIAA1190 3' ATTCCTGCCTTTAATATGG   71096    GGAG   A
                              CCG    AAA GCAGGAAT
                              |||    ||| ||||||||
                              GGT    TTT CGTCCTTA
                                ATAA   C
GAM706  KIAA1854 3' ATTCAGTCTTCTCCTG      71737        AA  AG
                              CGGGAGAA  GC  GAAT
                              ||||||||  ||  ||||
```

```
                              GTCCTCTT  TG  CTTA
                                  C_  A_
GAM706  KIAA1887 5' CCTTTTCTCTCCCGG      76775        A   C
                              CCGGGAGA AAG AGG
                              |||||||| ||| |||
                              GGCCCTCT TTT TCC
                                  C   _
GAM706  KIAA1944 3' ATTCCTGCCTCATCTCACG   75556    G   AAA_
                              CG GAGA    GCAGGAAT
                              || ||||    ||||||||
                              GC CTCT    CGTCCTTA
                               A    ACTC
GAM706  KIAA1949 3' TTCTGTTTCTCCTAGTG     92090     CG     AA
                              CAC  GGAGAA  GCAGGA
                              |||  ||||||  ||||||
                              GTG  CCTCTT  TGTCTT
                                AT     __
GAM706  KIAA1949 3' TTCTGTTTCTCCTAGTG     97758     CG     AA
                              CAC  GGAGAA  GCAGGA
                              |||  ||||||  ||||||
                              GTG  CCTCTT  TGTCTT
                                AT     __
GAM706  KIAA1949 3' TTCTGTTTCTCCTAGTG     97880     CG     AA
                              CAC  GGAGAA  GCAGGA
                              |||  ||||||  ||||||
                              GTG  CCTCTT  TGTCTT
                                AT     __
GAM706  KSP37    5' TTGTGTTCTCTCTCCTGGTG  49210         AA_   G
                              CACCGGGAGA   AGCA GA
                              ||||||||||   |||| ||
                              GTGGTCCTCT   TTGT TT
                                    CTC    G
GAM706  LBP-9    3' TCCTGCTTTCCTAACTCCT   27282       A____
                              GGGAG    AAAGCAGGA
                              |||||    |||||||||
                              TCCTC    TTTCGTCCT
                                 AATCC
GAM706  MAWBP    3' TCTTGTGTTTCTCCTG      42110         A
                              CGGGAGAAA GCAGGA
                              ||||||||| ||||||
                              GTCCTCTTT TGTTCT
                                    G
GAM706  MGC14436 5' ATTCCTGCCCGTCCCTGTG   51852     C   GAAAA
                              CAC GGGA    GCAGGAAT
                              ||| ||||    ||||||||
                              GTG CCCT    CGTCCTTA
                                T   GCC__
GAM706  MGC21738 5' ATTCCTGCCTTTCCTC      58914     A   A
                              GGG GAAA GCAGGAAT
                              ||| |||| ||||||||
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                                CTC CTTT CGTCCTTA
                                  _   C
GAM706  MGC4266  3'  TCCAGTTTATTCCTCCTGGTG  51060        _ _   A
                                CACCGGGAG AA AAGC GGA
                                ||||||||| || |||| |||
                                GTGGTCCTC TT TTTG CCT
                                     C  A   A
GAM706  MGC4309  5'  TCCTGCTTCCCCTTAGG    44133   ___  A  AA
                                CC   GGG GA  AGCAGGA
                                ||   ||| ||  |||||||
                                GG   CCC CT  TCGTCCT
                                 ATT  _ __
GAM706  MMD      3'  ATTTTTACTTTTCTCTCAGTG  59806    C       C
                                CAC GGGAGAAAAG AGGAAT
                                ||| |||||||||| ||||||
                                GTG CTCTCTTTTC TTTTTA
                                  A        A
GAM706  NET-7    3'  ATTCTTGCCCTTCCCCC    24708    A   AA
                                GGG GAA  GCAGGAAT
                                ||| |||  ||||||||
                                CCC CTT  CGTTCTTA
                                  C   CC
GAM706  NUP160   5'  CCTCATTCTCCCGGTG     87595          AAGC
                                CACCGGGAGAA   AGG
                                ||||||||||    |||
                                GTGGCCCTCTT   TCC
                                      AC__
GAM706  PDZ-GEF1 3'  TCTGCTCCTTCCCCAGTG   26495    C   A   A_
                                CAC GGG GAA  AGCAGG
                                ||| ||| |||  ||||||
                                GTG CCC CTT  TCGTCT
                                  A   _  CC
GAM706  PIP3-E   3'  ATTCGTGTTTTTCCCCCTGT  66797   C   A      G
                                AC GGG GAAAAGCA GAAT
                                || ||| |||||||| ||||
                                TG CCC CTTTTTGT CTTA
                                 T   C       G
GAM706  PLAGL2   3'  TTCTGTTTTTCTCCAAGT   70460   CG
                                AC  GGAGAAAAGCAGGA
                                ||  ||||||||||||||
                                TG  CCTCTTTTTGTCTT
                                 AA
GAM706  PSK      3'  TCTGTGTTCTCCTGG      32364         AA
                                CCGGGAGAA  GCAGG
                                |||||||||  |||||
                                GGTCCTCTT  TGTCT
                                     G_
GAM706  RAI      3'  ATTCCTGCCTTCCCTCC     21872      AA  _
                                GGAG  AAG CAGGAAT
                                ||||  ||| |||||||
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                                CCTC  TTC GTCCTTA
                                  CC   C
GAM706  RAI17    3'  ATTCCTGCTTGGGGACTGGTG  91275       GAGAA
                                CACCGG    AAGCAGGAAT
                                ||||||    ||||||||||
                                GTGGTC    TTCGTCCTTA
                                   AGGGG
GAM706  RNF9     3'  CCTCCTTCCTCCTGGTG     53410         AA   C
                                CACCGGGAG  AAG AGG
                                |||||||||  ||| |||
                                GTGGTCCTC  TTC TCC
                                     C_   C
GAM706  SEMA4G   5'  TTTCTCTTTCTCCCAGG     35438    _       A C
                                CC GGGAGAAA G AGGAA
                                || |||||||| | |||||
                                GG CCCTCTTT C TCTTT
                                 A      _ _
GAM706  SEMA4G   5'  TTTCTCTTTCTCCCAGG     94688    _       A C
                                CC GGGAGAAA G AGGAA
                                || |||||||| | |||||
                                GG CCCTCTTT C TCTTT
                                 A      _ _
GAM706  SLC21A14 3'  TCCTATAGTATTTTCTCCC    33832          _ ___
                                GGGAGAAAA GC   AGGA
                                |||||||| ||   ||||
                                CCCTCTTTT TG   TCCT
                                     A  ATA
GAM706  SLC39A3  3'  ATTCCTGCTGTTCCGCGTG    57972     _    GAAA
                                CAC CGGGA    AGCAGGAAT
                                ||| |||||    |||||||||
                                GTG GCCTT    TCGTCCTTA
                                  C    G___
GAM706  SMOC1    3'  ATTCCTGCTCTCCGG       42149      G   AAA
                                CCGG AGA   GCAGGAAT
                                |||| |||   ||||||||
                                GGCC TCT   CGTCCTTA
                                  _  ___
GAM706  SPRY2    5'  ATTCTCTTTTTTTCTCCCG    19556          C _
                                CGGGAGAAAAG AG GAAT
                                |||||||||| || ||||
                                GCCCTCTTTTT TC CTTA
                                     T  T
GAM706  SYNPO2   3'  ATTCCTGCTCTTTTTCTGCTG  71893    C       A
                                CA CGGGAGAA AGCAGGAAT
                                || |||||||| |||||||||
                                GT GTCTTTTT TCGTCCTTA
                                 C       C
GAM706  SYT12    3'  CCTGCTCCTCCCGGT       94729         AAA
                                ACCGGGAG   AGCAGG
                                ||||||||   ||||||
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                                TGGCCCTC   TCGTCC
                                    C__
GAM706  TBLR1    3' ATTCCTGCTTTTATTGCTG   45098    G _
                                CGG AG AAAAGCAGGAAT
                                ||| || ||||||||||||
                                GTC TT TTTTCGTCCTTA
                                  G  A
GAM706  TUBAL2   3' ATTCCTGCCTTACCCAGG    38446   _  A  AAA
                                CC GGG GA   GCAGGAAT
                                || ||| ||   ||||||||
                                GG CCC TT   CGTCCTTA
                                 A   A  C__
GAM706  VANGL1   3' ATTCCTGCCTTTCGTCCAGT  57249    C  GA   A
                                AC GG  GAAA GCAGGAAT
                                || ||  |||| ||||||||
                                TG CC  CTTT CGTCCTTA
                                 A  TG   C
GAM706  VPS45A   3' CCCACTTTTCTCCGGT     23426      G     CA
                                ACCGG AGAAAAG  GG
                                ||||| |||||||  ||
                                TGGCC TCTTTTC  CC
                                   _      AC
GAM706  ZFPL1    3' CTTGCTTTCCTCCCGG      59655       A
                                CCGGGAG AAAGCAGG
                                |||||||  ||||||||
                                GGCCCTC TTTCGTTC
                                    C
GAM706  LOC116173 5' CCTGCCTTCTCTCCCGG    56641       A  _
                                CCGGGAGA AAG CAGG
                                |||||||| ||| ||||
                                GGCCCTCT TTC GTCC
                                     C   C
GAM706  LOC118738 3' ATTCCTGCCTCTCACC     75486   _   AAA
                                GG GAGA   GCAGGAAT
                                || ||||   ||||||||
                                CC CTCT   CGTCCTTA
                                 A   C__
GAM706  LOC123036 3' TGTATTTTCTCCCGGT     74195          _
                                ACCGGGAGAAAA GCA
                                |||||||||||| |||
                                TGGCCCTCTTTT TGT
                                       A
GAM706  LOC124753 5' CCGGCTCTTCTCCCGG     74321        A  A
                                CCGGGAGAA AGC GG
                                ||||||||| ||| ||
                                GGCCCTCTT TCG CC
                                     C   G
GAM706  LOC128077 3' ATTCCTGCTTCCTCTTGG   74705       AA
                                CCGGGAG  AAGCAGGAAT
                                |||||||  ||||||||||
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                                GGTTCTC  TTCGTCCTTA
                                   C_
GAM706  LOC129831 5'  TCCTCTTTCTCCCGG       74895          A C
                                CCGGGAGAAA G AGGA
                                |||||||||| | ||||
                                GGCCCTCTTT C TCCT
                                      _ _
GAM706  LOC130074 3'  ATTGCTGTTTTTCCCC      76125     A       G
                                GGG GAAAAGCAG AAT
                                ||| ||||||||| |||
                                CCC CTTTTTGTC TTA
                                  _       G
GAM706  LOC131368 3'  ATTCCTGCTCTCTGG       75857      G   AAA
                                CCGG AGA   GCAGGAAT
                                |||| |||   ||||||||
                                GGTC TCT   CGTCCTTA
                                  _   ___
GAM706  LOC132332 5'  TCCCTTCCTCCCGGTG      76163         AA   CA
                                CACCGGGAG  AAG  GGA
                                |||||||||  |||  |||
                                GTGGCCCTC  TTC  CCT
                                     C_   __
GAM706  LOC134265 3'  ATTGTTACTTTTCTCCC     75172          C  G
                                GGGAGAAAAG AG AAT
                                |||||||||| || |||
                                CCCTCTTTTC TT TTA
                                      A  G
GAM706  LOC143879 3'  ATTCCTGCTTTTAGTT      76653     AG
                                GG  AAAAGCAGGAAT
                                ||  ||||||||||||
                                TT  TTTTCGTCCTTA
                                 GA
GAM706  LOC145601 3'  ATTCCTGCTCTTCGTTTTC   83361    GG __   A
                                G  A  GAA AGCAGGAAT
                                |  |  ||| |||||||||
                                C  T  CTT TCGTCCTTA
                                 TT TG   C
GAM706  LOC147054 3'  CCTCATTCTCCTGGTG      83918           AAGC
                                CACCGGGAGAA    AGG
                                ||||||||||    |||
                                GTGGTCCTCTT    TCC
                                      AC__
GAM706  LOC147917 3'  CCTCCTTTCTCCCAGTG     78567     C       A C
                                CAC GGGAGAAA G AGG
                                ||| |||||||| | |||
                                GTG CCCTCTTT C TCC
                                  A       _ C
GAM706  LOC148223 3'  CCTCCTTCCTCTCCCGG     78736         A_   C
                                CCGGGAGA  AAG AGG
                                ||||||||  ||| |||
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                                GGCCCTCT  TTC TCC
                                    CC   C
GAM706  LOC148250 5' ATTCCTGCTCTTCCTG     78755       AAA
                                CGGGAG   AGCAGGAAT
                                ||||||   |||||||||
                                GTCCTT   TCGTCCTTA
                                   C__
GAM706  LOC153733 3' ATTCCTGCTTCTACC      80920    G   AA
                                GG AGA  AGCAGGAAT
                                || |||  |||||||||
                                CC TCT  TCGTCCTTA
                                 A  __
GAM706  LOC196549 5' ATTCCTGCTCCCTGGT     59230       A  AAA
                                ACCGGG GA   GCAGGAAT
                                |||||| ||   ||||||||
                                TGGTCC CT   CGTCCTTA
                                  _ ____
GAM706  LOC199886 3' TCCTGCCCTTCCTTCTG    88455       _  AA
                                CGGGAG AA  GCAGGA
                                |||||| ||  ||||||
                                GTCTTC TT  CGTCCT
                                   C  CC
GAM706  LOC200150 3' ATTCCTGCTCCTTTCT     88588      AA
                                GGAGA  AGCAGGAAT
                                |||||  |||||||||
                                TCTTT  TCGTCCTTA
                                  CC
GAM706  LOC201242 3' ATTTTTGTTTTCCCCCGG   87360      A    G
                                CCGGG GAAAA CAGGAAT
                                ||||| ||||| |||||||
                                GGCCC CTTTT GTTTTTA
                                  C   _
GAM706  LOC219654 3' TTCCTTTCTCCCGG       91311        AAGC
                                CCGGGAGAA   AGGAA
                                |||||||||   |||||
                                GGCCCTCTT   TCCTT
                                     ____
GAM706  LOC219793 5' TCCTTCTTCTCCCGG      91376        AA  C
                                CCGGGAGA  AG AGGA
                                ||||||||  || ||||
                                GGCCCTCT  TC TCCT
                                    __  T
GAM706  LOC221303 3' ATTCCTGCCTTTTCTCAGCC  91899   __      _
                                GG  GAGAAAAG CAGGAAT
                                ||  |||||||| |||||||
                                CC  CTCTTTTC GTCCTTA
                                 GA       C
GAM706  LOC221641 5' CCTGTTTTTCTTCCAGTG   93727    C
                                CAC GGGAGAAAAGCAGG
                                ||| ||||||||||||||
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                                GTG CCTTCTTTTTGTCC
                                  A
GAM706  LOC223009 5'  ATTCCTGCCTGTCTCCC     94370       AAA
                                GGGAGA   GCAGGAAT
                                ||||||   ||||||||
                                CCCTCT   CGTCCTTA
                                   GTC
GAM706  LOC253959 5'  ATTCCTGCTCCACAACCTGTG  94933     C  GAGAAA
                                CAC GG     AGCAGGAAT
                                ||| ||     |||||||||
                                GTG CC     TCGTCCTTA
                                  T  AACACC
GAM706  LOC255452 3'  ATTCCTGCTTTTCAGAGTGG   97525     GGA_
                                CCG    GAAAAGCAGGAAT
                                |||    ||||||||||||
                                GGT    CTTTTCGTCCTTA
                                  GAGA
GAM706  LOC255975 5'  ATTCCTGCGTGTCTCCC     95879       AAA
                                GGGAGA   GCAGGAAT
                                ||||||   ||||||||
                                CCCTCT   CGTCCTTA
                                   GTG
GAM706  LOC256950 3'  TCCTGCTTCACGGTG       95427       G  GAAA
                                CACCG GA    AGCAGGA
                                ||||| ||    |||||||
                                GTGGC CT    TCGTCCT
                                  A  ____
GAM706  LOC257422 3'  ATTCCTGCTTTTCCTT      96574     A
                                GGG GAAAAGCAGGAAT
                                ||| ||||||||||||
                                TTC CTTTTCGTCCTTA
                                  _
GAM706  LOC257422 5'  ATTCCTGTCATATTCCCAGT   96575    C    AAAA
                                AC GGGAG    GCAGGAAT
                                || |||||    ||||||||
                                TG CCCTT    TGTCCTTA
                                 A    ATAC
GAM706  LOC51087  3'  ATTTTTGTTTTCCCCCGG    32011       A    G
                                CCGGG GAAAA CAGGAAT
                                ||||| ||||| |||||||
                                GGCCC CTTTT GTTTTTA
                                   C    _
GAM706  LOC51279  3'  ATTCCTGCTTCTGCG       33307    GG   AA
                                CG  AGA  AGCAGGAAT
                                ||  |||  |||||||||
                                GC  TCT  TCGTCCTTA
                                 G_  __
GAM706  LOC51705  3'  ATTCCTGCTTTCGTG       32692    G  GAA
                                CG GA   AAGCAGGAAT
                                || ||   ||||||||||
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                              GT CT   TTCGTCCTTA
                               G ___
GAM706  LOC56267  3' TCTGGTTTTTCCCAGT     39015    C      AG
                              AC GGGAGAAA  CAGG
                              || ||||||||  ||||
                              TG CCCTTTTT  GTCT
                               A       G_
GAM706  LOC89894  5' CTTGTTTTCTCTCCCAGG    60603    _    _
                              CC GGGAGA AAAGCAGG
                              || |||||| ||||||||
                              GG CCCTCT TTTTGTTC
                               A     C
GAM706  LOC89932  5' TTCTGTTTCTCCCG        60824        AA
                              CGGGAGAA  GCAGGA
                              ||||||||  ||||||
                              GCCCTCTT  TGTCTT

                                  __
GAM706  LOC90835  5' TCCTCTTTCTCTCGGTG     64133          A C
                              CACCGGGAGAAA G AGGA
                              |||||||||||| | ||||
                              GTGGCTCTCTTT C TCCT

                                    _ _
GAM706  LOC90841  3' CTTGGAGCCTCTCTCGGTG   64197         AAAG_
                              CACCGGGAGA    CAGG
                              ||||||||||    ||||
                              GTGGCTCTCT    GTTC
                                    CCGAG
GAM706  LOC91064  5' ATTCCTGCTCTTGGGGGTG   64761     GG_   AAA
                              CACC   GAGA   GCAGGAAT
                              ||||   ||||   ||||||||
                              GTGG   TTCT   CGTCCTTA
                                GGG   ___
GAM706  LOC91133  3' ATTCCTGCTTCTGCC       65009    G   AA
                              GG AGA  AGCAGGAAT
                              || |||  |||||||||
                              CC TCT  TCGTCCTTA
                               G  __
GAM706  LOC91408  3' TTTTGCACTTCCTCCCAGG   65929    _    _ AA
                              CC GGGAG AA  GCAGGA
                              || ||||| ||  ||||||
                              GG CCCTC TT  CGTTTT
                               A    C  CA
GAM706  LOC91748  5' GTTCTTTCTCCCAGTG      67057     C      _
                              CAC GGGAGAAA AGC
                              ||| |||||||| |||
                              GTG CCCTCTTT TTG
                                A       C
GAM706  LOC91750  3' CCAAGCTCCCTTCCCGGTG   67059         AAA  A_
                              CACCGGGAG   AGC  GG
                              |||||||||   |||  ||
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                              GTGGCCCTT  TCG  CC
                                   CCC  AA
GAM706  LOC91759  3' ATTCCTGCCTTTCCCC     67085    A   A
                              GGG GAAA GCAGGAAT
                              ||| |||| ||||||||
                              CCC CTTT CGTCCTTA
                                _   C
GAM706  LOC92370  3' ATTCAGGCACTTTCTTCC    69133       A_  AG
                              GGGAGAAA  GC  GAAT
                              ||||||||  ||  ||||
                              CCTTCTTT  CG  CTTA
                                   CA  GA
GAM706  LOC92391  3' ATTCCTGCTTTTGAGG     69155    GGGAG
                              CC    AAAAGCAGGAAT
                              ||    ||||||||||||
                              GG    TTTTCGTCCTTA
                               AG___
GAM706  LOC92973  5' ATTCCTGCTTCCTGGCTG    71035    _    GAAA
                              CA CCGGGA   AGCAGGAAT
                              || ||||||   |||||||||
                              GT GGTCCT   TCGTCCTTA
                               C    _____
GAM706  LOC92973  5' CTGTGGCTTTCCCGGTG     71038         AAA
                              CACCGGGAGA  GCAG
                              ||||||||||  ||||
                              GTGGCCCTTT  TGTC
                                   CGG
GAM706  LOC93380  3' CCTCTCATTTTCTCCCAGTG  72199    C       GC__
                              CAC GGGAGAAAA   AGG
                              ||| |||||||||   |||
                              GTG CCCTCTTTT   TCC
                                A       ACTC
GAM707  FLJ22672  3' AACCAGGCCGAGAGGCCAC   46066      ___
                              GTGGTC  CGGCCTGGTT
                              ||||||  ||||||||||
                              CACCGG  GCCGGACCAA
                                 AGA
GAM707  RBT1    3'  AACCAGGCCGGACCACGTGCAA 25348
          TA                   TATTGCACGTGGTCCGGCCTGGTT
                              ||||||||||||||||||||||||
                              ATAACGTGCACCAGGCCGGACCAA

GAM708  CALM1   3'  CACACCCTGGTGGCATGCCCGT 22553    A  CA  TG AA_
                              ATG GCA  GT  T   GGTGTG
                              ||| |||  ||  |   ||||||
                              TGC CGT  CG  G   CCACAC
                                C  A_  GT GTC
GAM708  GJB3    3'  CCCCACAACTGTGCTCA    43765          AA
                              TGAGCACAGTTGT  GG
                              ||||||||||||  ||
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                                ACTCGTGTCAACA  CC
                                       CC
GAM708  L1CAM    3'  GGCACACCTCCTCCCACTGCCC 43755    A   CAGTTGTA
              A                  TG GCA       AGGTGTGCC
                                 || |||       |||||||||
                                 AC CGT       TCCACACGG
                                  C   CACCCTCC
GAM708  L1CAM    3'  GGCACACCTCCTCCCACTGCCC 4717     A   CAGTTGTA
              A                  TG GCA       AGGTGTGCC
                                 || |||       |||||||||
                                 AC CGT       TCCACACGG
                                  C   CACCCTCC
GAM708  TCF2     3'  GCACACCTCATGCTGAGCGCTC 21379     A__    TGTA
                                 GAGC   CAGT    AGGTGTGC
                                 ||||   ||||    ||||||||
                                 CTCG   GTCG    TCCACACG
                                   CGA    TAC_
GAM708  DDX34    3'  ACCTACAACTGCCTCA     27975      CA       A
                                 TGAG  CAGTTGTA GGT
                                 ||||  |||||||| |||
                                 ACTC  GTCAACAT CCA
                                   C_       _
GAM708  GMPPB    3'  GGCACACCCCACAAACCCCACT 41747     CACAG_    AA
              C                  GAG     TTGT  GGTGTGCC
                                 |||     ||||  ||||||||
                                 CTC     AACA  CCACACGG
                                   ACCCCA    CC
GAM708  GMPPB    3'  GGCACACCCCACAAACCCCACT 25303     CACAG_    AA
              C                  GAG     TTGT  GGTGTGCC
                                 |||     ||||  ||||||||
                                 CTC     AACA  CCACACGG
                                   ACCCCA    CC
GAM708  GMPPB    5'  GGCACACCCCACAAACCCCACT 95747     CACAG_    AA
              C                  GAG     TTGT  GGTGTGCC
                                 |||     ||||  ||||||||
                                 CTC     AACA  CCACACGG
                                   ACCCCA    CC
GAM708  KIAA1211 3'  GCACCCAACTGTGCCCAT    68894     A       TAA
                                 ATG GCACAGTTG   GGTGT
                                 ||| |||||||||   |||||
                                 TAC CGTGTCAAC   CCACG
                                   C       ___
GAM708  KIAA1266 3'  GCACGCACCTGTGCTCAT    66120          TTGTAAG
                                 ATGAGCACAG      GTGTGC
                                 ||||||||||      ||||||
                                 TACTCGTGTC      CGCACG
                                       CA_____
GAM708  MGC11349 3'  CACACCTTCCCTGAGACTCAT  47075      CA_   TTGT
                                 ATGAG   CAG    AAGGTGTG
                                 |||||   |||    ||||||||
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                                TACTC  GTC   TTCCACAC
                                  AGA  CC__
GAM708  MGC4840   3'  GGCACACCTCACAGAAGC   71568   ACAG   A
                                GC   TTGT AGGTGTGCC
                                ||   |||| |||||||||
                                CG   GACA TCCACACGG
                                 AA__   C
GAM708  NDRG4     3'  GCACACCTGTTTCTGTCTCAT  43289     C   TTGTA
                                ATGAG ACAG    AGGTGTGC
                                ||||| ||||    ||||||||
                                TACTC TGTC    TCCACACG
                                  _   TTTG_
GAM708  NDRG4     3'  GCACACCTGTTTCTGTCTCAT  39986     C   TTGTA
                                ATGAG ACAG    AGGTGTGC
                                ||||| ||||    ||||||||
                                TACTC TGTC    TCCACACG
                                  _   TTTG_
GAM708  PRO0611   3'  GCACACCTGGGGGTGCTC    26011      AGTTGTA
                                GAGCAC      AGGTGTGC
                                ||||||      ||||||||
                                CTCGTG      TCCACACG
                                   GGGG___
GAM708  RCD-8     3'  GGCACACCTGTACCCTCTGCCC 26750    A  C  TT  _
          A                      TG GCA AG  GTA AGGTGTGCC
                                || ||| ||  ||| |||||||||
                                AC CGT TC  CAT TCCACACGG
                                 C  C  C_  G
GAM708  LOC151568 3'  GGCACACCCCAGACCCCATGTC 56701     G  CA__  GTAA
          AT                     ATGA CA   GTT   GGTGTGCC
                                |||| ||   |||   ||||||||
                                TACT GT   CAG   CCACACGG
                                  _ ACCC  ACC_
GAM708  LOC153196 5'  GCACAGAGCTGTGCCCAT    85962    A      GTAAGG
                                ATG GCACAGTT     TGTGC
                                ||| ||||||||     |||||
                                TAC CGTGTCGA     ACACG
                                  C       G_____
GAM708  LOC221486 3'  GCACACCTCAGCCCCACTG   91010     T__  A_
                                CAGT   GT  AGGTGTGC
                                ||||   ||  ||||||||
                                GTCA   CG  TCCACACG
                                   CCC  AC
GAM708  LOC91138  5'  ACACAGAATAACTGTGCT    65027         AAG
                                AGCACAGTTGT   GTGT
                                ||||||||||   ||||
                                TCGTGTCAATA   CACA
                                       AGA
GAM709  HUS1      3'  AGAAAGAACAGCCTCTGTCAC  91098   C
                                GT ACAGAGGCTGTTCTTTTT
                                || |||||||||||||||||
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                                CA TGTCTCCGACAAGAAAGA
                                 C
GAM709  NDUFS1   5' AGAACAGCCTCCGCGGC    59463    ACA
                                GTC  GAGGCTGTTCT
                                |||  ||||||||||
                                CGG  CTCCGACAAGA
                                  CGC
GAM709  WHSC1    3' TGAAAAAATACCCTCTG    29919     CT  TC
                                CAGAGG  GT  TTTTTCA
                                ||||||  ||  |||||||
                                GTCTCC  CA  AAAAAGT
                                    __  TA
GAM709  WHSC1    3' TGAAAAAATACCCTCTG    55837     CT  TC
                                CAGAGG  GT  TTTTTCA
                                ||||||  ||  |||||||
                                GTCTCC  CA  AAAAAGT
                                    __  TA
GAM709  WHSC1    3' TGAAAAAATACCCTCTG    55854     CT  TC
                                CAGAGG  GT  TTTTTCA
                                ||||||  ||  |||||||
                                GTCTCC  CA  AAAAAGT
                                    __  TA
GAM709  WHSC1    5' TGAAAAAATACCCTCTG    55861     CT  TC
                                CAGAGG  GT  TTTTTCA
                                ||||||  ||  |||||||
                                GTCTCC  CA  AAAAAGT
                                    __  TA
GAM709  C1orf22  3' TGAAAAAGATGTCTGT    47258     GGCTGT
                                ACAGA    TCTTTTTCA
                                |||||    |||||||||
                                TGTCT    AGAAAAAGT
                                   GT____
GAM709  CSAD     3' AAAAAGAACAGCCTTT    32027
                                AGAGGCTGTTCTTTTT
                                ||||||||||||||||
                                TTTCCGACAAGAAAAA

GAM709  DKFZP434F0318 3' AACGGTGCCTCTGTTAC    48002    C     __
                                GT ACAGAGGC  TGTT
                                || ||||||||  ||||
                                CA TGTCTCCG  GCAA
                                 T      TG
GAM709  GMNN     5' AAGGCGCACAGCCTCTAGAC  31904    AC     ___
                                GTC  AGAGGCTGT   TCTT
                                |||  |||||||||  ||||
                                CAG  TCTCCGACA   GGAA
                                  A_       CGC
GAM709  KIAA0912 5' GGTAACAGCCTCCGTGGC    64413     A      _
                                GTCAC GAGGCTGTT CT
                                ||||| ||||||||| ||
```

```
                                CGGTG CTCCGACAA GG
                                   C       T
GAM709  KIAA1493  3'  AAAAAGTGGAGGCCTCTG    64151        GTT_
                                CAGAGGCT   CTTTTT
                                ||||||||   ||||||
                                GTCTCCGG   GAAAAA
                                     AGGT
GAM709  KIAA1719  3'  GGGAACAGCCCCTGTGAC    68170        A
                                GTCACAG GGCTGTTCTT
                                ||||||| ||||||||||
                                CAGTGTC CCGACAAGGG
                                     C
GAM709  LRP1B     3'  TGAAAAAGAACTGCACT     37674    _ T
                                AG GC GTTCTTTTTCA
                                || || ||||||||||
                                TC CG CAAGAAAAAGT
                                 A  T
GAM709  MGC29898  3'  AAAAAGAACAGTTACT      58924    AG
                                AG  GCTGTTCTTTTT
                                ||  ||||||||||||
                                TC  TGACAAGAAAAA
                                 AT
GAM709  MGC32104  3'  AAAAAGAACAAGACTGTG     58399      AGGC
                                CACAG    TGTTCTTTTT
                                |||||    ||||||||||
                                GTGTC    ACAAGAAAAA
                                   AGA_
GAM709  PCDH19    3'  GTGAAAAAAAAAAAGCTCTGGAC 63705     A    G  G  C
                                GTC CAGAG CT TT TTTTTCAC
                                ||| ||||| || || ||||||||
                                CAG GTCTC GA AA AAAAAGTG
                                  _    _ A  A
GAM709  PCL1      3'  AAAAAGAACAAAATCTG     32825      GGC
                                CAGA   TGTTCTTTTT
                                ||||   ||||||||||
                                GTCT   ACAAGAAAAA
                                   AAA
GAM709  TSP-NY    3'  TGAAAAAGACTTCTCTGT    50812        CT  T
                                ACAGAGG  GT CTTTTTCA
                                |||||||  || ||||||||
                                TGTCTCT  CA GAAAAAGT
                                     T_  _
GAM709  LOC196047 5'  AAAAAGAACCCTACTG      89583     _  CT
                                CAG AGG  GTTCTTTTT
                                ||| |||  |||||||||
                                GTC TCC  CAAGAAAAA
                                  A  __
GAM709  LOC203232 3'  AACAGCCATCTGTGAC      71409         _
                                GTCACAGA GGCTGTT
                                |||||||| |||||||
```

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                                CAGTGTCT CCGACAA
                                     A
GAM709  LOC221833 3'  AAAAAGAACCTTTGT      92537       CTG
                                ACAGAGG   TTCTTTTT
                                |||||||   ||||||||
                                TGTTTCC   AAGAAAAA
                                    ___
GAM709  LOC253936 3'  AACAGCCGTCTGTGAC      94666        _
                                GTCACAGA GGCTGTT
                                |||||||| |||||||
                                CAGTGTCT CCGACAA
                                     G
GAM710  CDH12    5'  ACAGAAGAGAAGGGTCTC    14488       __
                                GAGGCC  TCTCTTCTGT
                                ||||||  ||||||||||
                                CTCTGG  AGAGAAGACA
                                   GA
GAM710  EFEMP2   3'  AGGCCCAGGGGCCCCCATTGAC 33741        A     CT_
                                GTCAATGG GGCCTCT   TCT
                                |||||||| |||||||   |||
                                CAGTTACC CCGGGGA   GGA
                                     C      CCC
GAM710  F2R      3'  ACAGAAGAAAATAGAATTGAC  8832       GGAGGCCTC
                                GTCAAT       TCTTCTGT
                                ||||||       ||||||||
                                CAGTTA       AGAAGACA
                                   AGATAAA__
GAM710  FOXE3    3'  GACAGAAGCGTCCCCTTTGAC  24105      T  A   CTCT
                                GTCAA GG GGC    CTTCTGTC
                                ||||| || |||    ||||||||
                                CAGTT CC CTG    GAAGACAG
                                   T  C   C___
GAM710  KLRC1    5'  GACAGAAGAGTACAGTCCCTGA 9615      AT  A   CT__
            C                    GTCA  GG GGC    CTCTTCTGTC
                                ||||  || |||    ||||||||||
                                CAGT  CC CTG    GAGAAGACAG
                                  __  _   ACAT
GAM710  KLRC1    5'  GACAGAAGAGTACAGTCCCTGA 23648     AT  A   CT__
            C                    GTCA  GG GGC    CTCTTCTGTC
                                ||||  || |||    ||||||||||
                                CAGT  CC CTG    GAGAAGACAG
                                  __  _   ACAT
GAM710  MC1R     5'  GGAGGCCTCCAACGAC      9955      AA
                                GTC  TGGAGGCCTCT
                                |||  ||||||||||
                                CAG  ACCTCCGGAGG
                                  CA
GAM710  PIK3C2B  3'  AGAAGCTCCATTGAC       10558          GCCTCT
                                GTCAATGGAG     CTTCT
                                ||||||||||     |||||
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                                CAGTTACCTC     GAAGA
                                           ______
GAM710  SCN8A    3'  CAGAAGAGAGGCTGCC      26382    A
                                GG GGCCTCTCTTCTG
                                || ||||||||||||
                                CC TCGGAGAGAAGAC
                                  G
GAM710  DGS-A    3'  GAGAGAGGCCTCCATTG     84898
                                CAATGGAGGCCTCTCTT
                                ||||||||||||||||
                                GTTACCTCCGGAGAGAG

GAM710  DKFZP434P0111 3'  GACCTGAGGCCTCCACTGGC  67370     A        TCT
                                GTCA TGGAGGCCTC   TC
                                |||| ||||||||||   ||
                                CGGT ACCTCCGGAG   AG
                                   C         TCC
GAM710  DKFZP761F241 3'  GACAGAAGAGAGACTTTTA   48795       C
                                TGGAGG CTCTCTTCTGTC
                                |||||| ||||||||||||
                                ATTTTC GAGAGAAGACAG
                                    A
GAM710  EBF2     3'  ACAAAAGATGTCATTGAC    42641         AGGCCTC    C
                                GTCAATGG      TCTT TGT
                                ||||||||      |||| |||
                                CAGTTACT      AGAA ACA
                                     GT_____    A
GAM710  FLJ13881  3'  GACAGAAGCCCCAGGCCTCCA  45310         CT__
                                TGGAGGCCT    CTTCTGTC
                                |||||||||    ||||||||
                                ACCTCCGGA    GAAGACAG
                                     CCCC
GAM710  FLJ20477  3'  GACAGTCTTAAACCTACCATTG 35241         _   CCTCTCTT
            AC                    GTCAATGG AGG       CTGTC
                                ||||||||| |||       |||||
                                CAGTTACC TCC       GACAG
                                     A   AAATTCT_
GAM710  FLJ20568  3'  ACAGAAGAGACCAGCGAC    35415     AA   AGGCC
                                GTC  TGG    TCTCTTCTGT
                                |||  |||    ||||||||||
                                CAG  ACC    AGAGAAGACA
                                  CG  ______
GAM710  KIAA1240  3'  GACAGAAAAGAGAGGAATTCAT 66732       GG      __
                                ATGGA  CCTCTCT  TCTGTC
                                |||||  |||||||  ||||||
                                TACTT  GGAGAGA  AGACAG
                                   AA      AA
GAM710  TUBB4    5'  GGAGGCCTCCAACGAC      70627     AA
                                GTC  TGGAGGCCTCT
                                |||  ||||||||||
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                                CAG  ACCTCCGGAGG
                                  CA
GAM710  LOC152002 3'  ACACAGGGAGGCCCCCAT    80430      A        TC
                                ATGG GGCCTCTCT  TGT
                                |||| |||||||||  |||
                                TACC CCGGAGGGA  ACA
                                  C        C_
GAM710  LOC253187 3'  CAGAAGAGAGGCTGCC      97113    A
                                GG GGCCTCTCTTCTG
                                || ||||||||||||
                                CC TCGGAGAGAAGAC
                                 G
GAM711  ADA      3'  ACCCTATGTGTCCATTTCTGCA 61795    G       _  AGTC   A
                                TG AGAAATGG CA    TAG GT
                                || |||||||| ||    ||| ||
                                AC TCTTTACC GT    ATC CA
                                 G       T  GT__   C
GAM711  CYFIP2   3'  ACTCCTAGTTTCACCCTTTCTC 73586        T  CAAGT   _
           CA                     TGGAGAAA GG     CTAG AGT
                                |||||||| ||     |||| |||
                                ACCTCTTT CC     GATC TCA
                                     C  ACTTT    C
GAM711  GDF5     3'  GACTCAGCCCACCATTTCTCC  5104          CAA T  A
                                GGAGAAATGG   G CT GAGTC
                                ||||||||||   | || |||||
                                CCTCTTTACC   C GA CTCAG
                                      ACC _  _
GAM711  GM2A     3'  ACTCCTGTGGCACCATTTCTCC 67765         CAA   TA__
                                GGAGAAATGG   GTC    GAGT
                                ||||||||||   |||    ||||
                                CCTCTTTACC   CGG    CTCA
                                      A__   TGTC
GAM711  GNAO1    3'  ACTCACCATTTCATCCA     90966     _     CA
                                TGGA GAAATGG  AGT
                                |||| |||||||  |||
                                ACCT CTTTACC  TCA
                                  A      AC
GAM711  HMGA2    3'  ACTTTTCTACCATTTCTGCA   12993    G      CAAGTCT
                                TG AGAAATGG      AGAGT
                                || ||||||||      |||||
                                AC TCTTTACC      TTTCA
                                 G       ATCT___
GAM711  PRKACB   5'  GACCCCTTCTTGCCATCGCCCC 10795    AGAA       TCTAGA
           A                     TGG   ATGGCAAG     GTC
                                |||   ||||||||     |||
                                ACC   TACCGTTC     CAG
                                  CCGC       TTCCC_
GAM711  WHSC1L1  3'  ACTCCAGACTTGTAGTCTCCA  35027       AATG       A
                                TGGAGA   GCAAGTCT GAGT
                                ||||||   |||||||| ||||
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                                ACCTCT    TGTTCAGA CTCA
                                   GA__       C
GAM711  C6orf33   3'  GACTCTAGGGGTTCATTTCCCA 55881     A      CAAG
                                TGG GAAATGG    TCTAGAGTC
                                ||| |||||||    |||||||||
                                ACC CTTTACT    GGATCTCAG
                                  _      TGG_
GAM711  FBH1      3'  GGACCTGCCATTTCTCCA     51451           A
                                TGGAGAAATGGCA GTCT
                                |||||||||||| ||||
                                ACCTCTTTACCGT CAGG
                                         C
GAM711  FLJ14936  5'  ACTTCTTCCACCTTTCTCCA   50132        __  C   TCTA
                                TGGAGAAA  TGG AAG    GAGT
                                ||||||||  ||| |||    ||||
                                ACCTCTTT  ACC TTC    TTCA
                                     CC  _  _____
GAM711  FXC1      3'  ACTTCAGCCATTTCCCCA     69032     A      __
                                TGG GAAATGGC  AAGT
                                ||| ||||||||  ||||
                                ACC CTTTACCG  TTCA
                                  C       AC
GAM711  KIAA0828  3'  ACTCCAAGCCTTTTCTCCA    81190        T   AAGTCTA
                                TGGAGAAA GGC      GAGT
                                |||||||| |||      ||||
                                ACCTCTTT CCG      CTCA
                                     T   AAC_____
GAM711  KIAA0861  3'  GACACGCCCGCATTTCTCCA   88924         ___   AA
                                TGGAGAAAT   GGC  GTC
                                |||||||||   |||  |||
                                ACCTCTTTA   CCG  CAG
                                      CGC   CA
GAM711  KIAA1467  3'  GACCCCGTTTTTGCCATCCCCC 71607     AGAA       TCTAGA
           A                     TGG    ATGGCAAG     GTC
                                |||    ||||||||     |||
                                ACC    TACCGTTT     CAG
                                  CCC_       TTGCCC
GAM711  KIAA1904  3'  GCTTGCCATTTCCCCA      73491     A
                                TGG GAAATGGCAAGT
                                ||| ||||||||||||
                                ACC CTTTACCGTTCG
                                  C
GAM711  RAE1      3'  GACTTGCCGTCTCTCCA     13215       A
                                TGGAGA ATGGCAAGTC
                                |||||| ||||||||||
                                ACCTCT TGCCGTTCAG
                                   C
GAM711  SNAP29    3'  GACCTTTGCCATTTCCCA    16543     A        __
                                TGG GAAATGGCAA  GTC
                                ||| ||||||||||  |||
```

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                                ACC CTTTACCGTT  CAG
                                  _        TC
GAM711  ST6GalNAcI 3'  ACTCTTTGGCCATTTCCCA   37286     A       AAGTCT
                                TGG GAAATGGC     AGAGT
                                ||| ||||||||     |||||
                                ACC CTTTACCG     TCTCA
                                  _      GTT___
GAM711  TCEA3    3'  GACTCCAGATCATATCCCTCTA 88507      AA   GCAA    A
                                TGGAG  ATG    GTCT GAGTC
                                |||||  |||    |||| |||||
                                ATCTC  TAT    TAGA CTCAG
                                   CC   AC__    C
GAM711  TGIF2    3'  CTGATGCTGCCATTTGCCCA   41450     AG       A_   T
                                TGG  AAATGGCA  GTC AG
                                |||  ||||||||  ||| ||
                                ACC  TTTACCGT  TAG TC
                                  CG       CG   _
GAM711  TGIF2    3'  GACTCTGCCGTTTCTCCA    41453           _
                                TGGAGAAATGGCA AGTC
                                |||||||||||| ||||
                                ACCTCTTTGCCGT TCAG
                                        C
GAM711  UBE3B    3'  GGACTTGCCACTTTCTCCA    76921        _
                                TGGAGAAA TGGCAAGTCT
                                |||||||| ||||||||||
                                ACCTCTTT ACCGTTCAGG
                                     C
GAM711  ZFP91    3'  AGATTTGCCATTTCTCCA    53817
                                TGGAGAAATGGCAAGTCT
                                ||||||||||||||||||
                                ACCTCTTTACCGTTTAGA

GAM711  LOC145719 3'  ACTTTTTTTTGCCACTTTTCCA 83445        A      TCT
                                TGGAGAA TGGCAAG   AGAGT
                                ||||||| |||||||   |||||
                                ACCTTTT ACCGTTT   TTTCA
                                     C      TT_
GAM711  LOC145720 3'  ACTTTTTTTTGCCACTTTTCCA 83426        A      TCT
                                TGGAGAA TGGCAAG   AGAGT
                                ||||||| |||||||   |||||
                                ACCTTTT ACCGTTT   TTTCA
                                     C      TT_
GAM711  LOC158856 5'  GACTCTAGACCTACGCCGCCA  86916     AGAAA    AA__
                                TGG    TGGC    GTCTAGAGTC
                                |||    ||||    ||||||||||
                                ACC    GCCG    CAGATCTCAG
                                  ______   CATC
GAM711  LOC197117 3'  ACTTTTTTTTGCCACTTTTCCA 89713        A      TCT
                                TGGAGAA TGGCAAG   AGAGT
                                ||||||| |||||||   |||||
```

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                                ACCTTTT ACCGTTT   TTTCA
                                   C      TT_
GAM711  LOC255919 3'  ACATCTGCTTGCCATCCCCA  95031    A  AA      CT  _
                                TGG GA  TGGCAAGT  AGA GT
                                ||| ||  ||||||||  ||| ||
                                ACC CT  ACCGTTCG  TCT CA
                                  C __      __  A
GAM711  LOC256529 3'  GACGCAGTTACCTGGCCATTTC 97568         AA_  CTAGA_
           TCC                    GGAGAAATGGC  GT    GTC
                                ||||||||||  ||    |||
                                CCTCTTTACCG  CA    CAG
                                      GTC  TTGACG
GAM711  LOC256529 5'  GACGCAGTTACCTGGCCATTTC 97569         AA_  CTAGA_
           TCC                    GGAGAAATGGC  GT    GTC
                                ||||||||||  ||    |||
                                CCTCTTTACCG  CA    CAG
                                      GTC  TTGACG
GAM712  FACL2    3'  CAAGCACAACAGGGCTTGCACT 40883     ___  GGT
                                AGTGC  CCT  TGTTGTGCTTG
                                |||||  |||  ||||||||||
                                TCACG  GGG  ACAACACGAAC
                                  TTC  ___
GAM712  TRPM1    5'  CAAGCACACCCAGAGCTACCCA 10055    A  _  C   TTGT
                                TG GT GC CTGG   TGTGCTTG
                                || || || ||||   ||||||||
                                AC CA CG GACC   ACACGAAC
                                 C  T  A   C___
GAM712  ALOXE3   5'  AAGCACTCCAGGGCATCA   41260    G      TTGTT
                                TGA TGCCCTGG   GTGCTT
                                ||| ||||||||   ||||||
                                ACT ACGGGACC   CACGAA
                                  _      T____
GAM712  DCTN2    5'  CAAGCACAAGTGTGGAACACAT 71064    _  C_  TGGTTG
           CA                     TGA GTG  CC    TTGTGCTTG
                                ||| |||  ||    |||||||||
                                ACT CAC  GG    AACACGAAC
                                  A   AA  TGTG__
GAM712  KIAA1915  3'  CAAGCACAAAGAAAAGCACAC  73277    CC  GG  G
                                GTG  CT  TT TTGTGCTTG
                                |||  ||  || |||||||||
                                CAC  GA  AG AACACGAAC
                                  AC  AA  A
GAM712  LOC145371 3'  CAAAATCCAGGGCACTCA    77150         TTG
                                TGAGTGCCCTGG   TTG
                                ||||||||||||  |||
                                ACTCACGGGACC   AAC
                                      TAA
GAM712  LOC90573  3'  TACACAACCAGGACACTC    63276      C       T
                                GAGTG CCTGGTTGT GTG
                                ||||| ||||||||| |||
```

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                                CTCAC GGACCAACA CAT
                                   A       _
GAM713  HUS1     3'  AGAAAGAACAGCCTCTGTCAC  91098    C
                                GT ACAGAGGCTGTTCTTTTT
                                || ||||||||||||||||||
                                CA TGTCTCCGACAAGAAAGA
                                 C
GAM713  NDUFS1   5'  AGAACAGCCTCCGCGGC     59463     ACA
                                GTC   GAGGCTGTTCT
                                |||   ||||||||||
                                CGG   CTCCGACAAGA
                                  CGC
GAM713  WHSC1    3'  TGAAAAAATACCCTCTG     29919      CT  TC
                                CAGAGG  GT  TTTTTCA
                                ||||||  ||  |||||||
                                GTCTCC  CA  AAAAAGT
                                   __  TA
GAM713  WHSC1    3'  TGAAAAAATACCCTCTG     55837      CT  TC
                                CAGAGG  GT  TTTTTCA
                                ||||||  ||  |||||||
                                GTCTCC  CA  AAAAAGT
                                   __  TA
GAM713  WHSC1    3'  TGAAAAAATACCCTCTG     55854      CT  TC
                                CAGAGG  GT  TTTTTCA
                                ||||||  ||  |||||||
                                GTCTCC  CA  AAAAAGT
                                   __  TA
GAM713  WHSC1    5'  TGAAAAAATACCCTCTG     55861      CT  TC
                                CAGAGG  GT  TTTTTCA
                                ||||||  ||  |||||||
                                GTCTCC  CA  AAAAAGT
                                   __  TA
GAM713  C1orf22  3'  TGAAAAAGATGTCTGT      47258      GGCTGT
                                ACAGA     TCTTTTTCA
                                |||||     |||||||||
                                TGTCT     AGAAAAAGT
                                   GT____
GAM713  CSAD     3'  AAAAAGAACAGCCTTT      32027
                                AGAGGCTGTTCTTTTT
                                ||||||||||||||||
                                TTTCCGACAAGAAAAA

GAM713  DKFZP434F0318 3'  AACGGTGCCTCTGTTAC     48002    C      __
                                GT ACAGAGGC  TGTT
                                || ||||||||  ||||
                                CA TGTCTCCG  GCAA
                                 T       TG
GAM713  GMNN     5'  AAGGCGCACAGCCTCTAGAC   31904     AC       ___
                                GTC  AGAGGCTGT   TCTT
                                |||  |||||||||   ||||
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                                CAG  TCTCCGACA   GGAA
                                  A_       CGC
GAM713  KIAA0912  5'  GGTAACAGCCTCCGTGGC    64413      A       _
                                GTCAC GAGGCTGTT CT
                                ||||| ||||||||| ||
                                CGGTG CTCCGACAA GG
                                   C       T
GAM713  KIAA1493  3'  AAAAAGTGGAGGCCTCTG    64151        GTT_
                                CAGAGGCT    CTTTTT
                                ||||||||    ||||||
                                GTCTCCGG    GAAAAA
                                     AGGT
GAM713  KIAA1719  3'  GGGAACAGCCCCTGTGAC    68170        A
                                GTCACAG GGCTGTTCTT
                                ||||||| ||||||||||
                                CAGTGTC CCGACAAGGG
                                     C
GAM713  LRP1B     3'  TGAAAAAGAACTGCACT     37674    _ T
                                AG GC GTTCTTTTTCA
                                || || ||||||||||
                                TC CG CAAGAAAAAGT
                                 A  T
GAM713  MGC29898  3'  AAAAAGAACAGTTACT      58924    AG
                                AG  GCTGTTCTTTTT
                                ||  ||||||||||||
                                TC  TGACAAGAAAAA
                                 AT
GAM713  MGC32104  3'  AAAAAGAACAAGACTGTG    58399      AGGC
                                CACAG    TGTTCTTTTT
                                |||||    ||||||||||
                                GTGTC    ACAAGAAAAA
                                   AGA_
GAM713  PCDH19    3'  GTGAAAAAAAAAAAGCTCTGGAC 63705     A    G  G  C
                                GTC CAGAG CT TT TTTTTCAC
                                ||| ||||| || || ||||||||
                                CAG GTCTC GA AA AAAAAGTG
                                  _    _ A  A
GAM713  PCL1      3'  AAAAAGAACAAAATCTG     32825      GGC
                                CAGA   TGTTCTTTTT
                                ||||   ||||||||||
                                GTCT   ACAAGAAAAA
                                   AAA
GAM713  TSP-NY    3'  TGAAAAAGACTTCTCTGT    50812        CT  T
                                ACAGAGG  GT CTTTTTCA
                                |||||||  || ||||||||
                                TGTCTCT  CA GAAAAAGT
                                     T_ _
GAM713  LOC196047 5'  AAAAAGAACCCTACTG      89583     _  CT
                                CAG AGG  GTTCTTTTT
                                ||| |||  |||||||||
```

```
                                GTC TCC  CAAGAAAAA
                                  A  __
GAM713  LOC203232 3'  AACAGCCATCTGTGAC      71409         _
                                GTCACAGA GGCTGTT
                                |||||||| |||||||
                                CAGTGTCT CCGACAA
                                    A
GAM713  LOC221833 3'  AAAAAGAACCTTTGT       92537        CTG
                                ACAGAGG   TTCTTTTT
                                |||||||   ||||||||
                                TGTTTCC   AAGAAAAA
                                   ___
GAM713  LOC253936 3'  AACAGCCGTCTGTGAC      94666         _
                                GTCACAGA GGCTGTT
                                |||||||| |||||||
                                CAGTGTCT CCGACAA
                                    G
GAM714  NFIA     3'  ACTACTACTACTACTGTTC    70366     G       C
                                GAA TAGTAGTAG AGTAGT
                                ||| ||||||||| ||||||
                                CTT GTCATCATC TCATCA
                                  _       A
GAM714  RDX      3'  ACTACCTCACTACTACATCT   11276     A      _ CA
                                AGA GTAGTAGT AG  GTAGT
                                ||| |||||||| ||  |||||
                                TCT CATCATCA TC  CATCA
                                  A       C  __
GAM714  RRM2B    3'  ACTACTACTGTTAGCACCACTA 67823       A  ___
           CT                     AGTAGT GT   AGCAGTAGTAGT
                                |||||| ||   ||||||||||||
                                TCATCA CA   TTGTCATCATCA
                                   C  CGA
GAM714  STATH    3'  TATCACACTACTACCACTTTT  12028       A      CA  A
                                AGAAGT GTAGTAG  GT GTA
                                |||||| |||||||  || |||
                                TTTTCA CATCATC  CA TAT
                                   C      A_  C
GAM714  TM4SF4   3'  ACTGCCATACTACTTCT     16068          GTA
                                AGAAGTAGTA   GCAGT
                                ||||||||||   |||||
                                TCTTCATCAT   CGTCA
                                     AC_
GAM714  BIKE     3'  ACTCTGCTACTACTGC      34182            T
                                GTAGTAGTAGCAG AGT
                                |||||||||||| |||
                                CGTCATCATCGTC TCA
                                                _
GAM714  C3IP1    3'  ACTACTACACTATTACACTTC  41279       A      CA
                                GAAGT GTAGTAG  GTAGTAGT
                                ||||| |||||||  ||||||||
```

```
                                CTTCA CATTATC  CATCATCA
                                   _      A_
GAM714  FLJ10482  3'  GCTGCTACTCTACCACTTC    36163      A  __
                                GAAGT GT  AGTAGCAGT
                                ||||| ||  |||||||||
                                CTTCA CA  TCATCGTCG
                                   C  TC
GAM714  FLJ14399  3'  ACTACTACTGGACTACTAGCCT 51330    A  _     AG
          C                      GA GT AGTAGT  CAGTAGTAGT
                                || || ||||||  ||||||||||
                                CT CG TCATCA  GTCATCATCA
                                 C  A     G_
GAM714  HSNOV1    3'  TGCTATTACTACTTCT      34016
                                AGAAGTAGTAGTAGCA
                                ||||||||||||||||
                                TCTTCATCATTATCGT

GAM714  KIAA1244  3'  ACTTAAACTACTACTACTGTCT 71985     _         CAGT
                                AGA AGTAGTAGTAG    AGT
                                ||| ||||||||||    |||
                                TCT TCATCATCATC    TCA
                                  G          AAAT
GAM714  KIAA1866  3'  ACTACCATGCAGCCCACCACTA 60931       A  A_  A   __
          CT                     AGTAGT GT  GC GTA  GTAGT
                                |||||| ||  || |||  |||||
                                TCATCA CA  CG CGT  CATCA
                                   C  CC  A   AC
GAM714  PROL3     3'  ACTACCCTTGTAACTACTGCTT 21934           A    TA
          CT                     AGAAGTAGTAGT GCAG  GTAGT
                                |||||||||||| ||||  |||||
                                TCTTCGTCATCA TGTT  CATCA
                                      A    CC
GAM714  LOC153937 5'  CTGCTACTACTCCTCT      81006     A T
                                AGA G AGTAGTAGCAG
                                ||| | ||||||||||
                                TCT C TCATCATCGTC
                                  _ C
GAM714  LOC203378 5'  ACTGCTACCACCACTTT     90591       A  A
                                GAAGT GT GTAGCAGT
                                ||||| || ||||||||
                                TTTCA CA CATCGTCA
                                   C  C
GAM714  LOC206012 5'  ACTACTCAAACTACTACTACT  89523           CAGT
                                AGTAGTAGTAG    AGTAGT
                                ||||||||||    ||||||
                                TCATCATCATC    TCATCA
                                      AAAC
GAM714  LOC90342  5'  TACTACCAGCTCTTCT      62362       TAGTAGT   A_
                                AGAAG      AGC  GTAGTA
                                |||||      |||  ||||||
```

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                                TCTTC      TCG  CATCAT
                                  _______  AC
GAM715  DDEF1    3'  GAGCTTTAGCAGCCTC      59564    A   AGATAC       A
                                GA GCT     CTAAAGCT C
                                || |||     |||||||| |
                                CT CGA     GATTTCGA G
                                 C  C_____       C
GAM715  DDX3     3'  GAGCCTTAGGTATTTG      43759          A   A
                                TAGATACCTAA GCT C
                                |||||||||||| ||| |
                                GTTTATGGATT CGA G
                                      C  C
GAM715  GRAF     3'  GGTAACTCCCTCCCTAGCTTC  30573        ATACCTAA  C
                                GAAGCTAG       AG TACC
                                ||||||||       || ||||
                                CTTCGATC       TC ATGG
                                     CCTCCC__  A
GAM715  MAT1A    3'  AGCTTTAGAATCCCAGC     90825     A_   AC
                                GCT  GAT  CTAAAGCT
                                |||  |||  ||||||||
                                CGA  CTA  GATTTCGA
                                  CC   A_
GAM715  MYLK     3'  AGCTTCAGACATTTGGTT    97018        AC  A
                                AGCTAGAT  CT AAGCT
                                ||||||||  || |||||
                                TTGGTTTA  GA TTCGA
                                     CA  C
GAM715  RGL      3'  GTAGCTAAAACTTAGCTTCA  30736         ATACCTAA
                                TGAAGCTAG       AGCTAC
                                |||||||||       ||||||
                                ACTTCGATT       TCGATG
                                     CAAAA___
GAM715  ZFP93    3'  GTAGCCTTAATAACGTTAGTTT 14887         ATACC_   A
            CA                    TGAAGCTAG     TAA GCTAC
                                |||||||||     ||| |||||
                                ACTTTGATT     ATT CGATG
                                     GCAATA   C
GAM715  C3orf4   3'  AGCATTGACACATAGCTTCA  39118        GATACC   A
                                TGAAGCTA     TAA GCT
                                ||||||||     ||| |||
                                ACTTCGAT     GTT CGA
                                     ACACA_   A
GAM715  D2S448   3'  GGCAGGAGTCCTAGCTTCA   73527         _  A   AAA
                                TGAAGCTAG AT CCT   GCT
                                ||||||||| || |||   |||
                                ACTTCGATC TG GGA   CGG
                                     C  A  ___
GAM715  FLJ12604 3'  AGCTTTAGTATTGACTTCA   64436      CTA    C
                                TGAAG   GATAC TAAAGCT
                                |||||   ||||| |||||||
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                                ACTTC   TTATG ATTTCGA
                                  AG_    _
GAM715  FLJ14280  5'  GGTAGCTCCTGGCCAGCTCA   45999    A   AGATA  TAA
                                TGA GCT    CC   AGCTACC
                                ||| |||    ||   |||||||
                                ACT CGA    GG   TCGATGG
                                  _  CC___  TCC
GAM715  H2AFJ    3'  GTTGTCAAGTTTCTAGCTTCA  36842         T  CTAA_
                                TGAAGCTAGA AC    AGC
                                ||||||||||  ||    |||
                                ACTTCGATCT TG    TTG
                                      T  AACTG
GAM715  KIAA0441  3'  TAGCTTTGTTAATCTAGCCTC  28960    A      ACC
                                GA GCTAGAT   TAAAGCTA
                                || |||||||   ||||||||
                                CT CGATCTA   GTTTCGAT
                                 C      ATT
GAM715  KIAA1128  3'  TAGCTTTATGTGCAGCTTGCA  68483    _    AGA   C
                                TG AAGCT   TAC TAAAGCTA
                                || |||||   ||| ||||||||
                                AC TTCGA   GTG ATTTCGAT
                                 G    C__   T
GAM715  KIAA1750  3'  TAGCCCCAGGAGTGGGCTTTA  68254       AG  A   AAA
                                TGAAGCT  AT CCT   GCTA
                                |||||||  || |||   ||||
                                ATTTCGG  TG GGA   CGAT
                                    G_  A   CCC
GAM715  KPNA5    3'  GGTAGCTTCAGGTAACT     9629     A    A
                                AG TACCT AAGCTACC
                                || ||||| ||||||||
                                TC ATGGA TTCGATGG
                                 A    C
GAM715  MAGEH1    5'  GGTAGCTTCAGCGGCAGCAGCT 25924       AGATAC_  A
            TC                    GAAGCT      CT AAGCTACC
                                ||||||      || ||||||||
                                CTTCGA      GA TTCGATGG
                                   CGACGGC  C
GAM715  MGC12921  3'  AGCCCTATTTAGCTTC      63774          CCTAAA
                                GAAGCTAGATA     GCT
                                ||||||||||     |||
                                CTTCGATTTAT     CGA
                                      CC_____
GAM715  MGC30052  3'  AGCTTTAGAATAGCTTC     58532       GATAC
                                GAAGCTA    CTAAAGCT
                                |||||||    ||||||||
                                CTTCGAT    GATTTCGA
                                    AA___
GAM715  RNF34    3'  AGCAAGGGCTGCATCTAGCTTC 47094         A___   AAA
                                GAAGCTAGAT   CCT   GCT
                                |||||||||   |||  |||
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                                CTTCGATCTA   GGG  CGA
                                     CGTC  AA_
GAM715  TNFRSF19L 3'  GTAGCTTTTATCCCAGC    51779    A_   CCT
                                GCT  GATA  AAAGCTAC
                                |||  ||||  ||||||||
                                CGA  CTAT  TTTCGATG
                                  CC   ____
GAM715  LOC121536 3'  AGCAAATCACATTTAGCTTCA  74082          ACCTAAA
                                TGAAGCTAGAT     GCT
                                ||||||||||      |||
                                ACTTCGATTTA     CGA
                                      CACTAAA
GAM715  LOC255452 3'  TAGGTACCTACCTTCA     97544      C  A
                                TGAAG TAG TACCTA
                                ||||| ||| ||||||
                                ACTTC ATC ATGGAT
                                   C  C
GAM715  LOC257396 3'  GGCAGCTTTAGGCTTAACTT  97139    C  ATA       A
                                AAG TAG  CCTAAAGCT CC
                                ||| |||  ||||||||| ||
                                TTC ATT  GGATTTCGA GG
                                  A  C__       C
GAM715  LOC92710  3'  GTACAAGGCATCTAGCTT    70359         A  AAAGC
                                AAGCTAGAT CCT    TAC
                                ||||||||| |||    |||
                                TTCGATCTA GGA    ATG
                                     C  AC___
GAM716  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT  TGTCTGAG
                                |||| |||||  ||||||||
                                TAAA TGAAA  ACAGATTC
                                  A    T__
GAM716  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC  C  T
                                CATTT  TTT AC GTCTGAGAT
                                |||||  ||| || |||||||||
                                GTAAA  AAA TG TAGACTCTA
                                   TA_  T  _
GAM716  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM716  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                   CATTTCACTTTCACTGTCTGAGAT
                                ||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM716  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
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                                GT  AGGTGACAGAC CT
                                 AT         C
GAM716  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM716  PKD2     3'  TCCAGGTTGAAAGTGAAA     60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM716  WRN      3'  GGGCAGTGAAAATGAAA      5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM716  ZNF216   3'  ATCTGCACAGCAAAGTGAAA   20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_    CG_
GAM716  CG012    5'  CTCACTCTGAAAGTGAA      83218          CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM716  EIF2C2   3'  ATCTTCTGAGAGTGAAAG     71946         G  T_
                                CTTTCACT TC  GAGAT
                                |||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM716  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                |||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM716  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281         CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM716  KIAA0984 3'  TTTGTCCAGTGAAAATGAA    65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM716  KLHL6    3'  ATCTCAGAGCAGGAAA       55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
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                                AAAG GAC AGACTCTA
                                  _  G
GAM716  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM716  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM716  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM716  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148         TCAC   C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM716  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM716  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM716  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM716  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM716  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||   |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM716  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
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                                GTAAAGTGAA GTGACA
                                        _
GAM717  CABC1    5'  GCACAAACAGACGCTC      39654      CTGGC
                                GAGC    TCTGTTTGTGC
                                ||||    ||||||||||
                                CTCG    AGACAAACACG
                                  C____
GAM717  CEACAM5  3'  AACAGAGCAAGACTCCA      15153       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM717  F2R      3'  AACAGAGCAAGACTCCA      8831        C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM717  FGFR2    3'  GACAGAGCGAGACTCCA      43377       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM717  FGFR2    3'  GACAGAGCGAGACTCCA      43383       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM717  FUT6     3'  GACAGAGCAAGACTCCA      3812        C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  GCLM     5'  GGCGCAGACCAGGCTCCA     9026          C    TTGT _
                                TGGAGCCTGG TCTGT    GC C
                                |||||||||| |||||    || |
                                ACCTCGGACC AGACG    CG G
                                      _    _____  A
GAM717  GPC1     3'  GGCTGCAGAGCCCGGCCCCA   9103      A  T      TTGT
                                TGG GCC GGCTCTGT    GCC
                                ||| ||| ||||||||    |||
                                ACC CGG CCGAGACG    CGG
                                  C  C       T___
GAM717  HPSE     3'  CAAACAGGCCAGGCTCCA     21890          T
                                TGGAGCCTGGC CTGTTTG
                                |||||||||| |||||||
                                ACCTCGGACCG GACAAAC
                                        _
GAM717  IFIT4    3'  AACAGAGCAAGACTCCA      70918       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  A
GAM717  KCNJ5    3'  GACAGAGCGAGACTCCA     6091       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM717  LY94     3'  GACAGAGCGAGACTCCA     16705      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM717  LZTS1    3'  ACAGAGCCTGGCCCCA      40676     A  T
                                TGG GCC GGCTCTGT
                                ||| ||| ||||||||
                                ACC CGG CCGAGACA
                                  C  T
GAM717  MSH3     3'  AACAGAGCAAGACTCCA     10116      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM717  POLH     3'  AACAGAGCGAGACTCCA     21461      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM717  PRKAB1   3'  GCACACCACCAGGCTCCA    20736         CTC  TT
                                TGGAGCCTGG  TG TGTGC
                                ||||||||||  ||  |||||
                                ACCTCGGACC  AC ACACG
                                      ___ C_
GAM717  SIGLEC6  3'  AACAGAGCGAGACTCCA     59925      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM717  SLC10A2  5'  AGCAGAGCCAGGGCCCA     4840      AG
                                TGG  CCTGGCTCTGTT
                                |||  ||||||||||||
                                ACC  GGACCGAGACGA
                                  CG
GAM717  SNRPN    5'  CAAGCAAAAACCAGGCTCCA  42991         CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM717  SNRPN    5'  CAAGCAAAAACCAGGCTCCA  42998         CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
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                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM717  SNRPN    5'  CAAGCAAAAACCAGGCTCCA  43005        CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM717  SNRPN    5'  CAAGCAAAAACCAGGCTCCA  43013        CTC_
                                TGGAGCCTGG   TGTTTG
                                ||||||||||   ||||||
                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM717  TNFSF11  5'  CAGGAGCCAAAGCCGGGCTCCA 13512          CT_   G
                                TGGAGCCTGGCT  GTTT TG
                                ||||||||||||  |||| ||
                                ACCTCGGGCCGA  CGAG AC
                                      AAC   G
GAM717  TSNAX    3'  GGTAACAGAGCAAGACTCCA  20002     C  G     TTG
                                TGGAG CT GCTCTGT  TGCC
                                ||||| || |||||||  ||||
                                ACCTC GA CGAGACA  ATGG
                                   A  A     ___
GAM717  UBE2L3   3'  GCCTTTGCAGAGTCAAGCTCCA 12503      C       TTGT
                                TGGAGC TGGCTCTGT   GC
                                |||||| |||||||||   ||
                                ACCTCG ACTGAGACG   CG
                                    A       TTTC
GAM717  ZNF264   3'  AACAGAGCGAGACTCCA    12738     C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM717  ARNTL2   3'  GACAGAGCGAGACTCCA    39466     C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM717  C22orf5  3'  GGATCAGAGCCAGACACCA   24344    AGC      TTTGTG
                                TGG  CTGGCTCTG    CC
                                |||  |||||||||    ||
                                ACC  GACCGAGAC    GG
                                  ACA       TA____
GAM717  DKFZp547C176 3'  GACAGAGCAAGACTCCA    67223     C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  DKFZp564K142 3'  AACAGAGCGAGACTCCA    49522     C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  G
GAM717  FADS1    3' GACAGAGCAAGACTCCA     25477      C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  FLJ12298 3' AACAGAGCGAGACTCCA     49664      C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM717  FLJ14117 3' AACAGAGCAAGACTCCA     42896      C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM717  FLJ14251 3' GGTAACAGAGCGAGACTCCA  45977      C  G     TTG
                                TGGAG CT GCTCTGT  TGCC
                                |||||| || |||||||  ||||
                                ACCTC GA CGAGACA  ATGG
                                   A  G     ___
GAM717  FLJ14327 3' AACAGAGCTAGACTCCA     46127      C
                                TGGAG CTGGCTCTGTT
                                ||||| ||||||||||
                                ACCTC GATCGAGACAA
                                   A
GAM717  FLJ14566 5' GGCCACAGAGCCAGCCCCA   51446     A  C       TT T
                                TGG GC TGGCTCTGT  G GCC
                                ||| || |||||||||  | |||
                                ACC CG ACCGAGACA  C CGG
                                  C  _       __ _
GAM717  FLJ20084 3' AACAGAGCGAGACTCCA     34511      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM717  FLJ20306 3' GACAGAGCAAGACTCCA     34917      C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  FLJ20456 3' GGTAACAGAGCTAGACTCCA  35215      C       TTG
                                TGGAG CTGGCTCTGT  TGCC
                                ||||| ||||||||||  ||||
                                ACCTC GATCGAGACA  ATGG
                                   A       ___
GAM717  FLJ22054 3' AACAGAGCAAGACTCCA     94391      C  G
                                TGGAG CT GCTCTGTT
                                |||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  A
GAM717  FLJ22393  5'  AGCAGGAACCAGGCTCCA    47058          C_
                                TGGAGCCTGG  TCTGTT
                                ||||||||||  ||||||
                                ACCTCGGACC  GGACGA
                                      AA
GAM717  FLJ23598  3'  GCCAAGAGCCAGCTCCA     45522       C      GTT  T
                                TGGAGC TGGCTCT   TG GC
                                |||||| |||||||   || ||
                                ACCTCG ACCGAGA   AC CG
                                   _      ___  _
GAM717  FLJ31168  3'  GACAGAGCGAGACTCCA     58502       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM717  GP5       3'  GACAGAGCGAGACTCCA     15646       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM717  GTPBP5    3'  GACAGAGCAAGACTCCA     65357       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  HIC       3'  AACAGAGCGAGACTCCA     67444       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM717  ING1-like 3'  GACAGAGCGAGACTCCA     54156       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM717  KBRAS2    3'  AACAGAGCAAGACTCCA     34191       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM717  KIAA0189  3'  CAGGAGCAGAGCCAGGCCCA  28273      A           G
                                TGG GCCTGGCTCTGTTT TG
                                ||| |||||||||||||| ||
                                ACC CGGACCGAGACGAG AC
                                  _           G
GAM717  KIAA0472  3'  AGCAGAGCAAGACTCCA     71853       C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
```

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                                ACCTC GA CGAGACGA
                                   A  A
GAM717  KIAA0563  3'  GACAGAGCAAGACTCCA     29188      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  KIAA0565  3'  GACAGAGCAAGACTCCA     66890      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  KIAA0648  3'  CAAACAGAAGCAGGCTCCA   82651         GC
                                TGGAGCCTG  TCTGTTTG
                                |||||||||  ||||||||
                                ACCTCGGAC  AGACAAAC
                                      GA
GAM717  KIAA0924  3'  AACAGAGCGAGACTCCA     29712      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM717  KIAA1028  3'  CAGAGCACAGGCTCCA      91934         _
                                TGGAGCCTG GCTCTG
                                |||||||||  ||||||
                                ACCTCGGAC CGAGAC
                                      A
GAM717  KIAA1719  3'  GGCCAGGGCCAGGCCCCA    68169     A         TTTGT
                                TGG GCCTGGCTCTG    GCC
                                |||  ||||||||||     |||
                                ACC CGGACCGGGAC    CGG
                                  C         ______
GAM717  KIAA1940  3'  GGTCTCAGAACCAAGGCTCCA  79988         _  C    TTTGT
                                TGGAGCCT GG TCTG    GCC
                                ||||||||  ||  ||||     |||
                                ACCTCGGA CC AGAC    TGG
                                     A  A   TC___
GAM717  LGI2      3'  CAAATCAAAGCCAGGCTC     36397          C  _
                                GAGCCTGGCT TG TTTG
                                ||||||||||  ||  ||||
                                CTCGGACCGA AC AAAC
                                      A  T
GAM717  MGC10200  3'  AACAGAGCGAGACTCCA     58980      C  G
                                TGGAG CT GCTCTGTT
                                |||||  || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM717  MGC2705   5'  GCACCAAGCCAGGCTCC     51113          C  TTT
                                GGAGCCTGGCT TG   GTGC
                                ||||||||||  ||   ||||
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                                CCTCGGACCGA AC   CACG
                                          _  ___
GAM717  MGC4562  3' AACAGAGCGAGACTCCA     55908      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM717  MGC4663  3' AACAGAGCCAGACTCC      44501     C
                                GGAG CTGGCTCTGTT
                                |||| ||||||||||
                                CCTC GACCGAGACAA
                                  A
GAM717  NPTXR    3' AACAGAGCAAGACTCCA     26635      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM717  NPTXR    3' AACAGAGCAAGACTCCA     54171      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM717  OR7C1    5' AACAGAGCCAAGTCCA      82428      G C
                                TGGA C TGGCTCTGTT
                                |||| | ||||||||||
                                ACCT G ACCGAGACAA
                                  _ A
GAM717  POFUT1   3' AACAGAGCGAGACTCCA     70462      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM717  PTK6     3' GACAGAGCGAGACTCCA     19936      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM717  RASGRF2  3' GCACGAAGCCAGGCTCC     61042          CTGT
                                GGAGCCTGGCT   TTGTGC
                                ||||||||||    ||||||
                                CCTCGGACCGA   AGCACG
                                          ____
GAM717  SC65     3' GACAGAGCGAGACTCCA     21289      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM717  SNURF    3' CAAGCAAAAACCAGGCTCCA  19052          CTC_
                                TGGAGCCTGG    TGTTTG
                                ||||||||||    ||||||
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                                ACCTCGGACC   ACGAAC
                                     AAAA
GAM717  TMG4     3'  GACAGAGCAAGACTCCA     43989      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  WBSCR23  3'  GACAGAGCAAGACTCCA     46762      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  WIRE     3'  GACAGAGCCAGACTCC      78305      C
                                GGAG CTGGCTCTGTT
                                |||| ||||||||||
                                CCTC GACCGAGACAG
                                   A
GAM717  WSB1     3'  AACAGAGCGAGACTCCA     56138      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM717  WSB1     3'  AACAGAGCGAGACTCCA     56144      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM717  LOC115704 3' CAGCCAGAGCCAGGCCCC    73541    A        T
                                GG GCCTGGCTCTG TTG
                                || |||||||||| |||
                                CC CGGACCGAGAC GAC
                                 C         C
GAM717  LOC124220 5' GGCACAACCAGACGCC      59146    _   T
                                GGC TCTG TTGTGCC
                                ||| |||| |||||||
                                CCG AGAC AACACGG
                                  C   C
GAM717  LOC127262 3' GACAGAGCGAGACTCCA     76110      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM717  LOC129563 3' AGCAGAGCAGGCCCCA      74878    A   G
                                TGG GCCTG CTCTGTT
                                ||| ||||| |||||||
                                ACC CGGAC GAGACGA
                                  C   _
GAM717  LOC129880 3' AACAGAGCAAGACTCCA     74900      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  A
GAM717  LOC143196 3'  AACAGAGCGAGACTCCA     82903      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM717  LOC144319 3'  GGCACAAACAGGCGCCCC    83057    A  CTG  T
                                GG GC   GC CTGTTTGTGCC
                                || ||   || ||||||||||
                                CC CG   CG GACAAACACGG
                                 C  ___  _
GAM717  LOC145216 3'  GACAGAGCAAGACTCCA     83267      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  LOC145820 3'  GACAGAGCAAGACTCCA     77514      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  LOC146227 3'  GGTCAGAGCCAGACCCC     77711    AGC       TTTGT
                                GG   CTGGCTCTG    GCC
                                ||   |||||||||    |||
                                CC   GACCGAGAC    TGG
                                 CCA       _____
GAM717  LOC146713 3'  AACAGAGCAAGACTCCA     83720      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM717  LOC147071 3'  GACAGAGCAAGACTCCA     72999      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  LOC147649 3'  GACAGAGCGAGACTCCA     78414      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM717  LOC148936 3'  AACAGAGCAAGACTCCA     84286      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM717  LOC149803 5'  CAGGCAGAGCAAGCTCCA    79538       CTG
                                TGGAGC   GCTCTGTTTG
                                ||||||   ||||||||||
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                                ACCTCG   CGAGACGGAC
                                   AA_
GAM717  LOC150299 3'  GACAGAGCAAGACTCCA     84970      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  LOC151429 3'  GACAGAGCAAGACTCCA     85353      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  LOC151904 3'  AACAGAGCGAGACTCCA     80382      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  G
GAM717  LOC158292 5'  GACAGAGCGAGACTCCA     86730      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM717  LOC162137 5'  CAAGCAGGCCAAGCCCCA    87111     A  C   T
                                TGG GC TGGC CTGTTTG
                                ||| || |||| |||||||
                                ACC CG ACCG GACGAAC
                                  C  A   _
GAM717  LOC163033 5'  CGACCAGGACCAAGCCCCA   82396     A  C   CT   T
                                TGG GC TGG  CTG TTG
                                ||| || |||  ||| |||
                                ACC CG ACC  GAC AGC
                                  C  A   AG   C
GAM717  LOC163682 3'  ACACTCAAAGCCGGGCTCCA  87020           C  TT
                                TGGAGCCTGGCT TG  TGT
                                |||||||||||| ||  |||
                                ACCTCGGGCCGA AC  ACA
                                       A  TC
GAM717  LOC200261 3'  GCACAAACCTCTGGAGGCCCA 88655     A   GGCTCT
                                TGG GCCT     GTTTGTGC
                                ||| ||||     ||||||||
                                ACC CGGA     CAAACACG
                                  _   GGTCTC
GAM717  LOC201173 3'  GACAGAGCAAGACTCCA     87329      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  LOC201182 5'  AACAGAGCAAGACTCCA     89760      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
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                                ACCTC GA CGAGACAA
                                   A  A
GAM717  LOC219627 3'  GACAGAGCGAGACTCCA     92178      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  G
GAM717  LOC221543 5'  GACAGAGCAAGACTCCA     93742      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  LOC221943 5'  GACAGAGCAAGACTCCA     93989      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  LOC222160 5'  GACAGAGCAAGACTCCA     94127      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  LOC253039 5'  GGCTCCAAAACCAGGCTCTA   96159          CTCTG   T_
                                TGGAGCCTGG    TTTG  GCC
                                ||||||||||    ||||  |||
                                ATCTCGGACC    AAAC  CGG
                                      A____    CT
GAM717  LOC254659 3'  AAACAGAGCAAGACTCCA     95109      C  G
                                TGGAG CT GCTCTGTTT
                                ||||| || |||||||||
                                ACCTC GA CGAGACAAA
                                   A  A
GAM717  LOC256158 5'  AACATCGAGCCAGGCCCA     97639      A       __
                                TGG GCCTGGCTC  TGTT
                                ||| |||||||||  ||||
                                ACC CGGACCGAG  ACAA
                                  _       CT
GAM717  LOC256207 3'  GACAGAGCAAGACTCCA     95169      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  LOC257596 5'  GACAGAGCAAGACTCCA     97935      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAG
                                   A  A
GAM717  LOC56963  3'  GCACAAAGCCAGGCTTCA    71455          CTGT
                                TGGAGCCTGGCT   TTGTGC
                                ||||||||||||   ||||||
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                                ACTTCGGACCGA   AACACG
                                      _____
GAM717  LOC91149  3'  GCTGAACCAGAGCCAGACTCCA 65079      C       _   T
                                TGGAG CTGGCTCTG TTTG GC
                                ||||| ||||||||| |||| ||
                                ACCTC GACCGAGAC AAGT CG
                                   A       C   _
GAM717  LOC91409  3'  AGGCAAGGCCAGGCCCCA   65951    A      TC
                                TGG GCCTGGC  TGTTT
                                ||| |||||||  |||||
                                ACC CGGACCG  ACGGA
                                  C      GA
GAM717  LOC91862  3'  GGTGACAGAGCGAGACTCCA   53470      C  G      TGT
                                TGGAG CT GCTCTGTT   GCC
                                ||||| || ||||||||   |||
                                ACCTC GA CGAGACAG   TGG
                                   A  G      ___
GAM717  LOC92482  3'  AACAGAGCAAGACTCCA     69485      C  G
                                TGGAG CT GCTCTGTT
                                ||||| || ||||||||
                                ACCTC GA CGAGACAA
                                   A  A
GAM718  AP2B1     3'  AGATGAAGTGAGCTTAGAGATG 7054       G      G  GA_
          TTG                     TAACG CTCTGAGT CA   TATCT
                                ||||| |||||||| ||   |||||
                                GTTGT GAGATTCG GT   GTAGA
                                   A       A  GAA
GAM718  BACH2     3'  AGATAGAGAGTTCAGAGTTG   41484          GCAGA
                                CGGCTCTGAGT    TATCT
                                ||||||||||     |||||
                                GTTGAGACTTG    ATAGA
                                      AGAG_
GAM718  BRCA1     3'  CTGTTTATAGCTGTTG     23529        C   GT
                                TAACGGCT TGA  GCAG
                                |||||||| |||  ||||
                                GTTGTCGA ATT  TGTC
                                     T   __
GAM718  BRCA1     3'  CTGTTTATAGCTGTTG     23537        C   GT
                                TAACGGCT TGA  GCAG
                                |||||||| |||  ||||
                                GTTGTCGA ATT  TGTC
                                     T   __
GAM718  BRCA1     3'  CTGTTTATAGCTGTTG     23545        C   GT
                                TAACGGCT TGA  GCAG
                                |||||||| |||  ||||
                                GTTGTCGA ATT  TGTC
                                     T   __
GAM718  BRCA1     3'  CTGTTTATAGCTGTTG     23553        C   GT
                                TAACGGCT TGA  GCAG
                                |||||||| |||  ||||
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                              GTTGTCGA ATT  TGTC
                                  T  __
GAM718  BRCA1   3' CTGTTTATAGCTGTTG     23561       C  GT
                              TAACGGCT TGA  GCAG
                              |||||||| |||  ||||
                              GTTGTCGA ATT  TGTC
                                  T  __
GAM718  BRCA1   3' CTGTTTATAGCTGTTG     23570       C  GT
                              TAACGGCT TGA  GCAG
                              |||||||| |||  ||||
                              GTTGTCGA ATT  TGTC
                                  T  __
GAM718  BRCA1   3' CTGTTTATAGCTGTTG     23578       C  GT
                              TAACGGCT TGA  GCAG
                              |||||||| |||  ||||
                              GTTGTCGA ATT  TGTC
                                  T  __
GAM718  BRCA1   3' CTGTTTATAGCTGTTG     23586       C  GT
                              TAACGGCT TGA  GCAG
                              |||||||| |||  ||||
                              GTTGTCGA ATT  TGTC
                                  T  __
GAM718  BRCA1   3' CTGTTTATAGCTGTTG     23594       C  GT
                              TAACGGCT TGA  GCAG
                              |||||||| |||  ||||
                              GTTGTCGA ATT  TGTC
                                  T  __
GAM718  BRCA1   3' CTGTTTATAGCTGTTG     23520       C  GT
                              TAACGGCT TGA  GCAG
                              |||||||| |||  ||||
                              GTTGTCGA ATT  TGTC
                                  T  __
GAM718  CAPZA1  3' AGGTGTTTGTGCTTCCGTT   72624     CTCT  TG
                              AACGG   GAG CAGATATCT
                              |||||   ||| |||||||||
                              TTGCC   TTC GTTTGTGGA
                                 ____  GT
GAM718  CD53    5' GGATATCTGTGTTACCAGCC  5112     CTG  TG
                              GGCT  AG CAGATATCT
                              ||||  ||  |||||||||
                              CCGA  TT GTCTATAGG
                                CCA  GT
GAM718  CNR1    3' GATGTTTGTTGAGCTG     32214      TGAGT
                              CGGCTC    GCAGATATC
                              ||||||    |||||||||
                              GTCGAG    TGTTTGTAG
                                 T____
GAM718  CPE     3' AGATACAGCTCGGAGTTGT   8525         GCAGA
                              ACGGCTCTGAGT    TATCT
                              ||||||||||||    |||||
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                                TGTTGAGGCTCG    ATAGA
                                      AC___
GAM718  DGKG    5'  AGATAGACAGCTTTGGAGCTG  7202      TG  T  AGA_
                                CGGCTC  AG GC   TATCT
                                ||||||  || ||   |||||
                                GTCGAG  TT CG   ATAGA
                                   GT  _  ACAG
GAM718  DGKI    3'  AGATGTCTGTGCTTGGAGGTAC 16342   ___  TG  TG
          C                      GG   CTC  AG  CAGATATCT
                                 ||   |||  ||  |||||||||
                                 CC   GAG  TC  GTCTGTAGA
                                  ATG   GT  GT
GAM718  EGLN3   3'  AGATGTTCTTAATCCAGGGCTG 41969         AG GCA_
          TTG                     TAACGGCTCTG  T   GATATCT
                                  ||||||||||  |   |||||||
                                  GTTGTCGGGAC  A   TTGTAGA
                                        CT ATTC
GAM718  EGLN3   3'  AGATGTTCTTAATCCAGGGCTG 52911         AG GCA_
          TTG                     TAACGGCTCTG  T   GATATCT
                                  ||||||||||  |   |||||||
                                  GTTGTCGGGAC  A   TTGTAGA
                                        CT ATTC
GAM718  ESR1    3'  GTGTGTGTGTTTAGAGCTGT  3705          TG  G
                                ACGGCTCTGAG  CA ATAT
                                ||||||||||  || ||||
                                TGTCGAGATTT  GT TGTG
                                      GT  G
GAM718  GABRP   3'  AGATTACAAATGTACTCAGGGC 26396           GAT___
          TGTT                    CGGCTCTGAGTGCA    ATCT
                                  ||||||||||||||    ||||
                                  GTCGGGACTCATGT    TAGA
                                        AAACAT
GAM718  GARS    5'  GTCTCGCTCAGAGCTGT    8989           C
                                ACGGCTCTGAGTG AGAT
                                ||||||||||||| ||||
                                TGTCGAGACTCGC TCTG
                                      _
GAM718  HIVEP1  5'  GTTATGTTTGTGTTTGGGGTTG 9202       TG  TG     CT
          T                      ACGGCTC  AG  CAGATAT
                                 |||||||  ||  |||||||
                                 TGTTGGG  TT  GTTTGTA
                                    GT  GT     TTGG
GAM718  IPF1    3'  GGATTGGCGTTGTTTGTGGCTG 3981       CT  ___  AGAT
          TTG                     ACGGCT  GAG  TGC   ATCT
                                  ||||||  |||  |||   ||||
                                  TGTCGG  TTT  GCG   TAGG
                                     TG   GTT  GT__
GAM718  IRTA2   5'  AGATGTGCTCCTTGGAGCTG  48401      TG  T_  GA
                                CGGCTC  AG  GCA  TATCT
                                ||||||  ||  |||  |||||
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                              GTCGAG  TC  CGT  GTAGA
                                 GT  CT  __
GAM718  JAK2    5'  GTCGTTCAGAGCCGT      17128         GT  A
                              ACGGCTCTGA  GC GAT
                              ||||||||||  || |||
                              TGCCGAGACT  TG CTG
                                    __  _
GAM718  KLK3    3'  GGGTGTCTGTGTTATTTGTGG  7922    G  TCTG  TG
                              C GC   AG  CAGATATCT
                              | ||   ||  |||||||||
                              G TG   TT  GTCTGTGGG
                               G  TTTA  GT
GAM718  LCT     3'  TTGTTAAGGGTTGTTA     9699          GAGT
                              TAACGGCTCT   GCAG
                              ||||||||||   ||||
                              ATTGTTGGGA   TGTT
                                    AT__
GAM718  LHX3    3'  GGGTGGGCGGCTCGGGGCTG   27378          _  AGA
                              CGGCTCTGAGT GC   TATCT
                              |||||||||||  ||   |||||
                              GTCGGGGCTCG CG   GTGGG
                                    G  G__
GAM718  MAD2L1   3'  GGATATTTGTACTGTTTAATGT 9877      GCTCTG
           T                   AACG     AGTGCAGATATCT
                              ||||     ||||||||||||
                              TTGT     TCATGTTTATAGG
                                AATTTG
GAM718  MLLT2    3'  GGATGTAGAGATTTGGGGTGGT 19847     G   TG   GCAG
           TG                   TAAC GCTC  AGT   ATATCT
                              |||| ||||  |||   ||||||
                              GTTG TGGG  TTA   TGTAGG
                                G   GT   GAGA
GAM718  MORF    5'  GGATGTTTGTAAGATGTTG   24681     _  GAG
                              CGGC TCT   TGCAGATATCT
                              |||| |||   ||||||||||
                              GTTG AGA   ATGTTTGTAGG
                                T  ___
GAM718  MYCL2    5'  GGGTCGCGCGCTCGGTGGCCGT 18185        _      A_  ATCT
           TG                   TAACGGCT CTGAGTGC  GAT
                              |||||||| ||||||||  |||
                              GTTGCCGG GGCTCGCG  CTG
                                   T       CG   GG
GAM718  NKTR    3'  GGATTCTCTGCTCAGGGTC   18201          C   T
                              GGCTCTGAGTG AGA ATCT
                              |||||||||||| ||| ||||
                              CTGGGACTCGT TCT TAGG
                                    C  _
GAM718  NR5A2    3'  GGGTATTTGTATTGCAAACTGT 13790     CTC  _
                              ACGG   TG AGTGCAGATATCT
                              ||||   || ||||||||||||
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                                TGTC   AC TTATGTTTATGGG
                                  AA_  G
GAM718  PIK3R3   3'  AGATGGCTTAGTGTTTAGACTG 61048      C     TG __  A
            TTA                   AACGG TCTGAG  C  AG TATCT
                                  ||||| ||||||  |  || |||||
                                  TTGTC AGATTT  G  TC GTAGA
                                    _     GT AT  G
GAM718  PPP2R5E  3'  CTGTTTGGAGTTGTTG     20725         TG GT
                                  TAACGGCTC  A  GCAG
                                  |||||||||  |  ||||
                                  GTTGTTGAG  T  TGTC
                                       GT __
GAM718  RTN1     3'  GGATATTTGCACTTATGT    40910    TC
                                  GC  TGAGTGCAGATATCT
                                  ||  ||||||||||||||
                                  TG  ATTCACGTTTATAGG
                                   T_
GAM718  SEDL     3'  TGCATTTAGAGATGTTA     27365      G
                                  TAACG CTCTGAGTGCA
                                  ||||| ||||||||||
                                  ATTGT GAGATTTACGT
                                     A
GAM718  STAU2    3'  TTTTTGCTTGGAGCTGTTG    26912         TG    C
                                  TAACGGCTC  AGTG AGA
                                  |||||||||  |||| |||
                                  GTTGTCGAG  TCGT TTT
                                       GT    T
GAM718  STK6     3'  GCCATGTGTCTCAGAGCTGTTA 13186           T   G  ATCT
                                  TAACGGCTCTGAG GCA AT
                                  |||||||||||| ||| ||
                                  ATTGTCGAGACTC TGT TA
                                          _  G  CCGG
GAM718  STMN1    3'  AGATGGGGCCTTTGGGGCTG   18717       TG  T  AGA
                                  CGGCTC  AG GC   TATCT
                                  ||||||  || ||   |||||
                                  GTCGGG  TT CG   GTAGA
                                     GT  C  GG_
GAM718  SYNGR1   3'  GGGTATTTGCATTCATACATTG 16321     CTC_
            T                      ACGG    TGAGTGCAGATATCT
                                  ||||    ||||||||||||||
                                  TGTT    ACTTACGTTTATGGG
                                    ACAT
GAM718  TEM7     3'  ATGTCTGCGGTTGTC      39881     TCT  G
                                  GGC   GA TGCAGATAT
                                  |||   || |||||||||
                                  CTG   TT GCGTCTGTA
                                    ___  G
GAM718  TJP1     3'  TGCACAGAGTTGTTA      12301          GA
                                  TAACGGCTCT  GTGCA
                                  ||||||||||  |||||
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                                ATTGTTGAGA  CACGT
                                    __
GAM718  TNFRSF10B 3'  ATCACACATTCAGACTGTTG   13865      C      CA_
                                TAACGG TCTGAGTG   GAT
                                |||||| ||||||||   |||
                                GTTGTC AGACTTAC   CTA
                                   _      ACA
GAM718  TOX     3'  AGGTGTTTGTAAGTAAATTTGT 28289      CTC  AG
           TA                    TAACGG   TG  TGCAGATATCT
                                |||||||  ||  ||||||||||||
                                ATTGTT   AT  ATGTTTGTGGA
                                   TAA  GA
GAM718  TTC3    3'  AGGTATCTGTGTTACAATCGTT 12415     CTCTG  TG
                                AACGG    AG  CAGATATCT
                                |||||    ||  |||||||||
                                TTGCT    TT  GTCTATGGA
                                   AACA_  GT
GAM718  UTX     5'  GGGTGTCGGCGTTGGAGTTGT  62034       TG G   A
                                ACGGCTC  A TGC GATATCT
                                |||||||  | ||| |||||||
                                TGTTGAG  T GCG CTGTGGG
                                    GT _   G
GAM718  VAPA    3'  GAATTGTTCAGAGTC      13115        GT   ATA
                                GGCTCTGA  GCAG   TC
                                ||||||||  ||||   ||
                                CTGAGACT  TGTT   AG
                                   __    A__
GAM718  WNT5A   3'  AGATGTTGATTTGAAGCTGTTA 12661        CT   G  G
                                TAACGGCT  GAGT CA ATATCT
                                ||||||||  |||| || ||||||
                                ATTGTCGA  TTTA GT TGTAGA
                                    AG   _ _
GAM718  ZNF216  3'  AGATGTCTGCATTACTCATTGC 20016    TC    ___
           T                     GGC  TGAGT   GCAGATATCT
                                |||  |||||   ||||||||||
                                TCG  ACTCA   CGTCTGTAGA
                                  TT    TTA
GAM718  ZNF256  3'  AGGTAACACACATAGGGCTGTT 19317          A   CAGA
           A                     TAACGGCTCTG GTG    TATCT
                                ||||||||||| |||    |||||
                                ATTGTCGGGAT CAC    ATGGA
                                      A   ACA_
GAM718  ACAS2L  3'  AGATGTTTGTACCTCTGTC   68074    TCT  _
                                GGC   GAG TGCAGATATCT
                                |||   ||| ||||||||||
                                CTG   CTC ATGTTTGTAGA
                                  T__   C
GAM718  AHCYL1  5'  GTCGGAGCTCGGAGCTG    21766          GCA
                                CGGCTCTGAGT   GAT
                                ||||||||||   |||
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                                GTCGAGGCTCG   CTG
                                      AGG
GAM718  C1orf22   3'  TGTAAGTGGAGCTGTTA     47261          AG
                                TAACGGCTCTG  TGCA
                                ||||||||||  ||||
                                ATTGTCGAGGT  ATGT
                                      GA
GAM718  CACNG4    3'  AGGTAAAGGCTGGGGGCTGTTG 26951          G   GCAGA
                                TAACGGCTCT AGT     TATCT
                                |||||||||| |||    |||||
                                GTTGTCGGGG TCG     ATGGA
                                      G   GAA__
GAM718  CARD6     3'  ATATCTGTAAGTGTT      50854     T  GAG
                                GGC CT   TGCAGATAT
                                ||| ||   |||||||||
                                TTG GA   ATGTCTATA
                                  T  ___
GAM718  CDC14B    3'  GGAATTCTGACTTAGAGTCGTT 52835            G    TA
              G                   TAACGGCTCTGAGT CAGA  TCT
                                ||||||||||||| ||||  |||
                                GTTGCTGAGATTCA GTCT  AGG
                                        _   TA
GAM718  CDK5RAP3  3'  AGATGATAGCCAGGGCTGTTG  47278          A  GCAGA
                                TAACGGCTCTG GT     TATCT
                                |||||||||| ||     |||||
                                GTTGTCGGGAC CG     GTAGA
                                      _  ATA__
GAM718  CECR5     3'  GGATGTCTGTGCAGAGCC    52353       GA TG
                                GGCTCT  G  CAGATATCT
                                ||||||  |  |||||||||
                                CCGAGA  C  GTCTGTAGG
                                   __ GT
GAM718  CECR5     3'  GGATGTCTGTGCAGAGCC    35208       GA TG
                                GGCTCT  G  CAGATATCT
                                ||||||  |  |||||||||
                                CCGAGA  C  GTCTGTAGG
                                   __ GT
GAM718  CSRP2BP   5'  GTCCAGTGCTTAGGGTTGTTA  70115           TG A_
                                TAACGGCTCTGAG  C  GAT
                                ||||||||||||  |  |||
                                ATTGTTGGGATTC  G  CTG
                                      GT AC
GAM718  DKFZP434O047 5'  GGGTGTCTGGTGGGAGTGTCGT 31516        T  GAGTG
              TG                  TAACGGC CT     CAGATATCT
                                ||||||| ||     |||||||||
                                GTTGCTG GA     GTCTGTGGG
                                   T  GGGTG
GAM718  DKFZP564I052 3'  TCTGTATTTGGAGTTGT     66720        TG
                                ACGGCTC  AGTGCAGA
                                |||||||  ||||||||
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                                TGTTGAG  TTATGTCT
                                    GT
GAM718  DKFZP586F1318 3'  AGGTATTAAGTAATGTTTAGAG 31617        ___  A_
          TTGT                  GGCTCTGAG   TGC  GATATCT
                                |||||||||   |||  |||||||
                                TTGAGATTT   ATG  TTATGGA
                                   GTA   AA
GAM718  DKFZP586M1120 3'  GCCTGCTGAGGGCTGTTG    48460         G  __
                                TAACGGCTCT AGT  GC
                                |||||||||| |||  ||
                                GTTGTCGGGA TCG  CG
                                     G   TC
GAM718  ELL2     3'  GGTGTTTGCTAGTTGT      23872       CTGAGT
                                ACGGCT     GCAGATATC
                                ||||||     |||||||||
                                TGTTGA     CGTTTGTGG
                                   T_____
GAM718  ENPP4    3'  TTGTATTTGTGGTTGTTG    30052        CT
                                TAACGGCT  GAGTGCAG
                                ||||||||  ||||||||
                                GTTGTTGG  TTTATGTT
                                     TG
GAM718  FJX1     3'  AAAACTTGCGTTTGAGCCGTTG 26785         T      ATATCT
                                TAACGGCTC GAGTGCAG
                                ||||||||| ||||||||
                                GTTGCCGAG TTTGCGTT
                                     _       CAAAAG
GAM718  FLJ10199  3'  AGATGCTGCCTTGGAGCTG   71229       TG  T   A
                                CGGCTC  AG GCAG TATCT
                                ||||||  || |||| |||||
                                GTCGAG  TC CGTC GTAGA
                                   GT  _   _
GAM718  FLJ10241  3'  AGGTAAAGGCTCAGGCTGTTA  35932        T     GCAGA
                                TAACGGC CTGAGT    TATCT
                                ||||||| ||||||    |||||
                                ATTGTCG GACTCG    ATGGA
                                     _     GAA__
GAM718  FLJ10743  3'  AGATGTCTGTAGTCGGTCG   36547      CT  G
                                CGGCT  GA TGCAGATATCT
                                |||||  || ||||||||||
                                GCTGG  CT ATGTCTGTAGA
                                   __  G
GAM718  FLJ11045  5'  AGATTTATGTTCAGTGGTTGTT 38754        _   GT   GAT
          A                     TAACGGCT CTGA  GCA   ATCT
                                |||||||| ||||  |||   ||||
                                ATTGTTGG GACT  TGT   TAGA
                                     T    __   ATT
GAM718  FLJ11222  5'  AGGTGCGCTCCTTGGGGCTG   37171        ___      GATATCT
                                CGGCTCT   GAGTGCA
                                |||||||   |||||||
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                              GTCGGGG  CTCGCGT
                                 TTC     GGA  T
GAM718  FLJ12903 3' GGATGTCTTAGGAGTTG    42776      GAGTGC
                              CGGCTCT    AGATATCT
                              |||||||    ||||||||
                              GTTGAGG    TCTGTAGG
                                 AT____
GAM718  FLJ12903 3' GGGTATCTCGGGGGAGCT   42777     GAG C
                              GGCTCT  TG AGATATCT
                              ||||||  || ||||||||
                              TCGAGG  GC TCTATGGG
                                 GG_ _
GAM718  FLJ13197 3' GGAAATGTGCTCAGAGCTG  44860       TG GATA
                              CGGCTCTGAG CA   TCT
                              ||||||||||  ||   |||
                              GTCGAGACTC GT   AGG
                                    GT AA__
GAM718  FLJ13868 3' TTGTGTTTAAAGCCGTTG   42734      C   TG
                              TAACGGCT TGAG CAG
                              |||||||| ||||  |||
                              GTTGCCGA ATTT GTT
                                  A   GT
GAM718  FLJ14564 3' GGTGTCTGCACTTGGTTCG  76504    CT TG
                              CGG C AGTGCAGATATC
                              |||  |  ||||||||||||
                              GCT G TCACGTCTGTGG
                                T_ GT
GAM718  FLJ14735 3' AGATGTCTGTACTCTATATGT 51594   GCTCT
                              ACG   GAGTGCAGATATCT
                              |||   ||||||||||||||
                              TGT   CTCATGTCTGTAGA
                                ATAT_
GAM718  FLJ14753 3' AGATATTTGTAAAGGGTT   50775     GAG
                              GGCTCT  TGCAGATATCT
                              ||||||  ||||||||||
                              TTGGGA  ATGTTTATAGA
                                 A__
GAM718  FLJ20039 3' AGATGTTTCCCCCTTGGAGTT 34403     TG TGC_
                              GGCTC AG   AGATATCT
                              |||||  ||   ||||||||
                              TTGAG TC   TTTGTAGA
                                 GT CCCC
GAM718  FLJ20294 3' GGATGTCTGCACCTTCGCTTG 34881  C  TCTGA
                              A GGC    GTGCAGATATCT
                              | |||    ||||||||||||
                              G TCG    CACGTCTGTAGG
                               T  CTTC_
GAM718  FLJ20294 5' TGTGTTGGAGCTGTTA     34885       G TG
                              TAACGGCTCT AG  CA
                              |||||||||| ||  ||
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                                ATTGTCGAGG TT  GT
                                      _ GT
GAM718  FLJ21313  3'  GGATGTCTGTATTCAGCATTC  43686    CT_
                                GG   CTGAGTGCAGATATCT
                                ||   ||||||||||||||||
                                CT   GACTTATGTCTGTAGG
                                 TAC
GAM718  FLJ22624  5'  AGGTGACTATTTTAGAGCTG   45651          TGC  A
                                CGGCTCTGAG   AG TATCT
                                ||||||||||   || |||||
                                GTCGAGATTT   TC GTGGA
                                      TA_  A
GAM718  FLJ22644  3'  GTACATTTCAGAGCTGTT    47003           ___
                                AACGGCTCTGA   GTGC
                                ||||||||||   ||||
                                TTGTCGAGACT   CATG
                                      TTA
GAM718  FLJ22969  3'  GGTGTCAGCAGAGCTGT     68658         AGTGCA
                                ACGGCTCTG     GATATC
                                |||||||||     ||||||
                                TGTCGAGAC     CTGTGG
                                     GA____
GAM718  FLJ23017  3'  AGATGGGGAATATTTGGAGTTG 43120         TG    CAGA_
          TT                     AACGGCTC  AGTG    TATCT
                                ||||||||  ||||    |||||
                                TTGTTGAG  TTAT    GTAGA
                                     GT    AAGGG
GAM718  FLJ23471  3'  TTGTACTCGGGGCCGT      45302
                                ACGGCTCTGAGTGCAG
                                ||||||||||||||||
                                TGCCGGGGCTCATGTT

GAM718  FLJ23556  3'  TGACTCGGGCTGTTG       45960         T     G
                                TAACGGC CTGAGT CA
                                ||||||| |||||| ||
                                GTTGTCG GGCTCA GT
                                     _     _
GAM718  FLJ23878  3'  AGGTGGCTGCGCTCAGAGCTGT 58708               A
                                ACGGCTCTGAGTGCAG TATCT
                                |||||||||||||||| |||||
                                TGTCGAGACTCGCGTC GTGGA
                                        G
GAM718  H2BFB     3'  AGGTGTTTGCACTTCATGTTA  56970       GCTCT
                                TAACG    GAGTGCAGATATCT
                                |||||    ||||||||||||||
                                ATTGT    TTCACGTTTGTGGA
                                   AC___
GAM718  HEY1      3'  GTCTCATTTGGAGTGTTG    91252       G  TG   C
                                TAACG CTC  AGTG AGAT
                                ||||| |||  |||| ||||
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                                GTTGT GAG  TTAC TCTG
                                  _  GT   _
GAM718  HSPC016  3' GTGTTGTCTTGGAGCTGTTG  31940        TG  T   G
                                TAACGGCTC  AG GCA ATAT
                                |||||||||  || ||| ||||
                                GTTGTCGAG  TC TGT TGTG
                                     GT  _  _
GAM718  HSPCAL3  3' GCTTTCAGAGCTGTTA     76558           T
                                TAACGGCTCTGAG GC
                                |||||||||||||| ||
                                ATTGTCGAGACTT CG
                                       T
GAM718  ING3     3' CTGTACTCCAGAGCTGTTA   38833          _
                                TAACGGCTCTG AGTGCAG
                                |||||||||||| |||||||
                                ATTGTCGAGAC TCATGTC
                                       C
GAM718  ITGB5    3' AGGTGTTGGTGATGGGGCTGTT 59498         GAG   A
          G                      TAACGGCTCT   TGC GATATCT
                                |||||||||||   ||| |||||||
                                GTTGTCGGGG   GTG TTGTGGA
                                     TA_   G
GAM718  KIAA0057 3' GGATGTTTGGGGGGGGGTGGTTA 24436     G    GAGTG
                                TAAC GCTCT    CAGATATCT
                                |||| |||||    |||||||||
                                ATTG TGGGG    GTTTGTAGG
                                  G    GGG__
GAM718  KIAA0143 3' GGATGTTTGTGTTTATGGCT  64788     C   TG
                                GGCT TGAG  CAGATATCT
                                |||| ||||  |||||||||
                                TCGG ATTT  GTTTGTAGG
                                  T   GT
GAM718  KIAA0215 3' GGGTATTTGTACCAGGTCAGGG 28420  G     ____
          TTTTTG                 GCTCTGA   GTGCAGATATCT
                                 |||||||   ||||||||||||
                                 TGGGACT   CATGTTTATGGG
                                T      GGAC
GAM718  KIAA0319 3' AGGTGTCTGTATTTTCTGT   29028     CTCT
                                ACGG   GAGTGCAGATATCT
                                ||||   ||||||||||||||
                                TGTC   TTTATGTCTGTGGA
                                  T___
GAM718  KIAA0368 3' GATGTTTGAGGGGTGGTTG   65165     G    GAGTG
                                TAAC GCTCT    CAGATATC
                                |||| |||||    ||||||||
                                GTTG TGGGG    GTTTGTAG
                                  G    A____
GAM718  KIAA0475 3' GGATTTCCTCTCAGAGCTGTTG 29501          TGCA  T
                                TAACGGCTCTGAG   GA ATCT
                                ||||||||||||   || ||||
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                                GTTGTCGAGACTC   CT TAGG
                                      TC__  T
GAM718  KIAA0599 3' GTACTTTTGAGGGTTGTTG   77185        ___
                                TAACGGCTCT  GAGTGC
                                ||||||||||  ||||||
                                GTTGTTGGGA  TTCATG
                                     GTT
GAM718  KIAA0752 5' TGTGCTTATAGTTGTTG    67052       C   TG
                                TAACGGCT TGAG  CA
                                |||||||| ||||  ||
                                GTTGTTGA ATTC  GT
                                     T   GT
GAM718  KIAA0884 3' AGATATTTGTTGTCTGAGTT  70198     T  GT
                                GGCTC GA  GCAGATATCT
                                ||||| ||  ||||||||||
                                TTGAG CT  TGTTTATAGA
                                   T  GT
GAM718  KIAA0916 3' AGGTGTTTGCATGTGGCC    30491     CTGA
                                GGCT   GTGCAGATATCT
                                ||||   ||||||||||||
                                CCGG   TACGTTTGTGGA
                                  TG__
GAM718  KIAA1028 3' GTTTGTGCTCAGAGCCG     91947        TG
                                CGGCTCTGAG  CAGAT
                                ||||||||||  |||||
                                GCCGAGACTC  GTTTG
                                     GT
GAM718  KIAA1040 3' AGATAATTCTTGGCAGCTGTTG 72218       _ TG  TGCAGA
                                TAACGGCT C  AG     TATCT
                                |||||||| |  ||     |||||
                                GTTGTCGA G  TC     ATAGA
                                     C GT  TTA___
GAM718  KIAA1157 3' GGTGTTTGTGCAAGTGTTG   72251     T  GA TG
                                CGGC CT  G  CAGATATC
                                |||| ||  |  ||||||||
                                GTTG GA  C  GTTTGTGG
                                  T  A_ GT
GAM718  KIAA1161 5' TGACTTGGGTGCTGTTA     81763       _  TG   G
                                TAACGGC TC  AGT CA
                                |||||||  ||  ||| ||
                                ATTGTCG GG  TCA GT
                                     T  GT  _
GAM718  KIAA1336 3' GAAATGTTCAGGGTTGT     72324        GT   GATA
                                ACGGCTCTGA  GCA   TC
                                ||||||||||  |||   ||
                                TGTTGGGACT  TGT   AG
                                      __  AA__
GAM718  KIAA1449 3' GGATCATAGCACTTGGACTGTT 40452       C  TG    AGAT
           G                     TAACGG TC  AGTGC   ATCT
                                ||||||  ||  |||||   ||||
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                              GTTGTC AG  TCACG    TAGG
                                 _ GT    ATAC
GAM718  KIAA1456 3' GGGTATTTGTGCTTAAATGTTA 67003      GCTC    TG
                              TAACG   TGAG  CAGATATCT
                              |||||   ||||  |||||||||
                              ATTGT   ATTC  GTTTATGGG
                                 AA__   GT
GAM718  KIAA1468 3' GATATTTGCACTGCTTTTA   91774    C   TCTG
                              TAA GGC   AGTGCAGATATC
                              ||| |||   ||||||||||||
                              ATT TCG   TCACGTTTATAG
                                T  ____
GAM718  KIAA1494 3' GATGTTTGTGTGGGTT     68458      TGA TG
                              GGCTC   G  CAGATATC
                              |||||   |  ||||||||
                              TTGGG   T  GTTTGTAG
                                 ___ GT
GAM718  KIAA1674 3' TGTATTTTGAGTTGTTG    68797         T
                              TAACGGCTC GAGTGCA
                              ||||||||| |||||||
                              GTTGTTGAG TTTATGT
                                    T
GAM718  KIAA1764 5' AGATACCCACTGCTTAGAGTTA 69286   CG     GT   A___
          TTG                   A  GCTCTGA  GCAG   TATCT
                              |  |||||||  ||||   |||||
                              T  TGAGATT  CGTC   ATAGA
                               AT     __   ACCC
GAM718  KIAA1775 3' GTCTGTGTTTGGAGGTGTTA  52384     G   TG  TG
                              TAACG CTC  AG  CAGAT
                              ||||| |||  ||  |||||
                              ATTGT GAG  TT  GTCTG
                                 G   GT  GT
GAM718  KIAA1786 3' ATCGCAAGCTCAGAGCTGT   66023          GCA_
                              ACGGCTCTGAGT   GAT
                              ||||||||||||   |||
                              TGTCGAGACTCG   CTA
                                     AACG
GAM718  KIAA1944 3' AGATGTGGCCTCGAGGCTGTTG 75555       TC   T  AG
                              TAACGGC  TGAG GC  ATATCT
                              |||||||  |||| ||  ||||||
                              GTTGTCG  GCTC CG  TGTAGA
                                  GA   _ G_
GAM718  KIAA1944 5' GGATACCTTTCGGAGCTATTA  75563    CG      TGC  A
                              TAA  GCTCTGAG   AG TATCT
                              |||  ||||||||   || |||||
                              ATT  CGAGGCTT   TC ATAGG
                                AT       ___  C
GAM718  KIS      3' GGATATCTGTATCAAACC    58229    CTC   G
                              GG   TGA TGCAGATATCT
                              ||   ||| ||||||||||
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                                CC   ACT ATGTCTATAGG
                                 AA_  _
GAM718  KR18     3'  GGATATTTGTAGGCAGTCAGTT 52749     GGCT   AG
              A                   TAAC   CTG  TGCAGATATCT
                                  ||||   |||  ||||||||||
                                  ATTG   GAC  ATGTTTATAGG
                                    ACT_   GG
GAM718  L3MBTL2  5'  AGATGACGACTTGGAGCTGTT  88758       TG   GCAGA
                                  AACGGCTC  AGT    TATCT
                                  ||||||||  |||    |||||
                                  TTGTCGAG  TCA    GTAGA
                                      GT   GCA__
GAM718  LIN-7-C   3'  AGGTATTTGTTGTAGAGCT   37163       AGT
                                  GGCTCTG   GCAGATATCT
                                  |||||||   ||||||||||
                                  TCGAGAT   TGTTTATGGA
                                      GT_
GAM718  MAPK13   3'  GGTGTTGGCAGGGCTGT     10857        AGTGCA
                                  ACGGCTCTG     GATATC
                                  |||||||||     ||||||
                                  TGTCGGGAC     TTGTGG
                                       GG____
GAM718  MGC14386  5'  AGGTGGAGGCCGCTTGGAGCTG 53206       TG   _ AGA
              T                   ACGGCTC  AGTG C   TATCT
                                  |||||||  |||| |   |||||
                                  TGTCGAG  TCGC G   GTGGA
                                      GT    C GAG
GAM718  MGC21738  3'  AGGTATCTGTTAGAG      58913      AGT
                                  CTCTG   GCAGATATCT
                                  |||||   ||||||||||
                                  GAGAT   TGTCTATGGA
                                     ___
GAM718  MGC5139   5'  TGCCAGGGCTGTTA       74111          AGT
                                  TAACGGCTCTG   GCA
                                  ||||||||||   |||
                                  ATTGTCGGGAC   CGT
                                      ___
GAM718  MIL1     3'  GGATGTAAGGTTGGAGTTGT   31093       TG GTGCAG
                                  ACGGCTC  A     ATATCT
                                  |||||||  |     ||||||
                                  TGTTGAG  T     TGTAGG
                                      GT GGAA__
GAM718  NCOA5    3'  GTTTATACTGCATTTGGGGCTG 40585       TG      _   TCT
              T                   ACGGCTC  AGTGCAG ATA
                                  |||||||  ||||||| |||
                                  TGTCGGG  TTACGTC TAT
                                      GT      A   TTGA
GAM718  NS1-BP   5'  AGGTCGGTCGCTCAGAGCTG   72541          _ A   ATCT
                                  CGGCTCTGAGTG C GAT
                                  |||||||||||| | |||
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                                GTCGAGACTCGC G CTG
                                      T G   GA
GAM718  PAFAH2   3'  GATGTCTTTGGGGGTT      4763        G  TGC
                                GGCTCT AG   AGATATC
                                |||||| ||   |||||||
                                TTGGGG TT   TCTGTAG
                                   G ___
GAM718  PCDH10   3'  GGGTGTCTGTACATTTTGTGG  51993    G  TCTGA
                                C GC     GTGCAGATATCT
                                | ||     ||||||||||||
                                G TG     CATGTCTGTGGG
                                 G  TTTTA
GAM718  PCQAP    3'  TGCACTCAGGGTGTTG      31897       G
                                TAACG CTCTGAGTGCA
                                ||||| ||||||||||
                                GTTGT GGGACTCACGT
                                  _
GAM718  PLCL1    3'  AGATATGGCAGCTTAGAGGTGT 20631       G      _   AG
              TG                  TAACG CTCTGAG TGC  ATATCT
                                ||||| ||||||| |||  ||||||
                                GTTGT GAGATTC ACG  TATAGA
                                   G      G  G_
GAM718  PPFIA1   3'  AGATATTTTATTACAGAGTTTT 13263     CG     _   C
              TA                  TAA  GCTCTG AGTG AGATATCT
                                |||  |||||| |||| ||||||||
                                ATT  TGAGAC TTAT TTTATAGA
                                  TT     A   _
GAM718  PRO1331  3'  CCATATTTGTATTAAGAGTTGT 47834          G         CT
              TG                  TAACGGCTCT AGTGCAGATAT
                                |||||||||| ||||||||||
                                GTTGTTGAGA TTATGTTTATA
                                      A          CCA
GAM718  PRO2198  3'  GTCATCAGAGTTGTTG      37794           GT
                                TAACGGCTCTGA  GC
                                ||||||||||||  ||
                                GTTGTTGAGACT  TG
                                      AC
GAM718  PSMD13   3'  GGGTGGAGGTCTCAGGGTC    68354         T  AGA
                                GGCTCTGAG GC   TATCT
                                |||||||| ||   |||||
                                CTGGGACTC TG   GTGGG
                                     _ GAG
GAM718  R32184_3 5'  CACTTGCGGGTCGTTA      53062         _
                                TAACGGCTC TGAGTG
                                ||||||||| ||||||
                                ATTGCTGGG GTTCAC
                                      C
GAM718  RAB3GAP  3'  TGGGCTTGAGCTGTTG      66950         T   G
                                TAACGGCTC GAGT CA
                                ||||||||| |||| ||
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                                GTTGTCGAG TTCG GT
                                    _   G
GAM718  ROBO2    3'  AGGTGTTTTGCAAGAGCTGT  62486       GAG    _
                                ACGGCTCT  TGCAGA TATCT
                                ||||||||  |||||| |||||
                                TGTCGAGA  ACGTTT GTGGA
                                    ___     T
GAM718  RYK      3'  AGAGCGGGTGCTTGAGTTGTTG 82612        T  TG AGATA
                                TAACGGCTC GAG  C    TCT
                                ||||||||| |||  |    |||
                                GTTGTTGAG TTC  G    AGA
                                    _  GT GGCG_
GAM718  SCYA3    3'  GGATGCTTTTGTTCAGGGCTGT 59846        GT   __
                                ACGGCTCTGA  GCAGA  TATCT
                                ||||||||||  |||||  |||||
                                TGTCGGGACT  TGTTT  GTAGG
                                    __    TC
GAM718  SDCCAG10 5'  AGATATTGACATAGAGTTGT  19642       GA  CA
                                ACGGCTCT  GTG  GATATCT
                                ||||||||  |||  |||||||
                                TGTTGAGA  TAC  TTATAGA
                                    __  AG
GAM718  SERP1    3'  AGATATTTGGCTTTAAGTTGTT 27057       CT   G
          G                      TAACGGCT  GAGT CAGATATCT
                                ||||||||  |||| |||||||||
                                GTTGTTGA  TTCG GTTTATAGA
                                    AT   _
GAM718  SNAPC4   3'  GGTATCTGCTGGCCG      11850      CTGAGT
                                CGGCT     GCAGATATC
                                |||||     |||||||||
                                GCCGG     CGTCTATGG
                                   T_____
GAM718  SNPH     5'  GGCCAGTGGACTCAGGGTTGTT 28244           G  GATATCT
          G                      TAACGGCTCTGAGT CA
                                |||||||||||||| ||
                                GTTGTTGGGACTCA GT
                                      G  GACCGGG
GAM718  SNX11    3'  CTGTCCGGGGCTGTTA     25269          AGT
                                TAACGGCTCTG   GCAG
                                ||||||||||   ||||
                                ATTGTCGGGGC   TGTC
                                    C__
GAM718  SSH2     3'  GATATTTGTGTGTTGT     62208      TCTGA TG
                                ACGGC    G  CAGATATC
                                |||||    |  ||||||||
                                TGTTG    T  GTTTATAG
                                   _____ GT
GAM718  STX6     3'  AGATGTCTGCACTCCTGGCTG  19484      CT
                                CGGCT  GAGTGCAGATATCT
                                |||||  ||||||||||||||
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                                GTCGG  CTCACGTCTGTAGA
                                   TC
GAM718  SYNJ2    3'  AGATTGGATTTGGAGTTG    61762       TG   G  GAT
                                CGGCTC  AGT CA   ATCT
                                ||||||  ||| ||   ||||
                                GTTGAG  TTA GT   TAGA
                                   GT   G  ___
GAM718  TA-PP2C  3'  AGATGTTTGTGTTCCTGTGGTT 57755     G  TCT   TG
           A                     TAAC GC   GAG  CAGATATCT
                                ||||  ||   |||  |||||||||
                                ATTG TG   CTT  GTTTGTAGA
                                  G  TC_   GT
GAM718  TOMM34   3'  TGTGTTTAAGCTGTTG      22338        C    TG
                                TAACGGCT TGAG  CA
                                ||||||||  ||||  ||
                                GTTGTCGA ATTT  GT
                                     _    GT
GAM718  TOMM70A  3'  AGGTGTTGTGGGTGTGGCTGTT 29078         CT AG    G
           G                     TAACGGCT  G  TGCA ATATCT
                                ||||||||  |  ||||  ||||||
                                GTTGTCGG  T  GTGT TGTGGA
                                     TG GG   _
GAM718  U5-116KD 3'  GATGGCTTGGGAGTTGTTG    14909         G  T  AGA
                                TAACGGCTCT AG GC   TATC
                                ||||||||||  ||  ||   ||||
                                GTTGTTGAGG TT CG   GTAG
                                      G  _  ___
GAM718  ZNF31    5'  GGGTGTCTCGGTGGAGCC     64986        AG  C
                                GGCTCTG  TG AGATATCT
                                |||||||  ||  ||||||||
                                CCGAGGT  GC TCTGTGGG
                                    G_  _
GAM718  ZNF33A   3'  CTGCCCAGGGCTGTTG      91348          AGT
                                TAACGGCTCTG   GCAG
                                ||||||||||   ||||
                                GTTGTCGGGAC   CGTC
                                      C__
GAM718  LOC112970 3'  GTACTGTACTAGAGCTGTTG   56536         G      A
                                TAACGGCTCT AGTGCAG TAT
                                |||||||||  |||||||  |||
                                GTTGTCGAGA TCATGTC ATG
                                      _      _
GAM718  LOC122830 3'  GGGTGTTTGTAAAGATGACGTT 74168       GC_   GAG
           A                     TAACG   TCT   TGCAGATATCT
                                |||||   |||   ||||||||||
                                ATTGC   AGA   ATGTTTGTGGG
                                   AGT   A__
GAM718  LOC126353 3'  GCACATTTGGGACTGTTG    74500        _   T  _
                                TAACGG CTC GA GTGC
                                ||||||  |||  ||  ||||
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                                GTTGTC GGG TT CACG
                                   A  T  A
GAM718  LOC127294 3'  GGATACCAGGCTTGGAGCTG  74657      TG  GCAGA
                                CGGCTC  AGT    TATCT
                                ||||||  |||    |||||
                                GTCGAG  TCG    ATAGG
                                   GT   GACC_
GAM718  LOC133688 3'  AGGTAGCCCATTCAGGGCTGTT 75112           CAGA
           G                     TAACGGCTCTGAGTG   TATCT
                                ||||||||||||||||   |||||
                                GTTGTCGGGACTTAC   ATGGA
                                       CCG_
GAM718  LOC144161 3'  AGATATTTGCGTTAATGTTTTT 83005    CG  TC  G
           G                     TAA  GC  TGA TGCAGATATCT
                                |||  ||  ||| ||||||||||
                                GTT  TG  ATT GCGTTTATAGA
                                  TT  TA  _
GAM718  LOC145231 3'  GATAAGGCTGGGGCCGTTG   83286        AGT  AGA
                                TAACGGCTCTG   GC   TATC
                                ||||||||||   ||   ||||
                                GTTGCCGGGGT   CG   ATAG
                                      ___  GA_
GAM718  LOC145447 3'  GGATATTTGTGAATAAGGTAGT 77204     G  TC  AG
           TG                    TAAC GC  TG  TGCAGATATCT
                                |||| ||  ||  ||||||||||
                                GTTG TG  AT  GTGTTTATAGG
                                  A  GA  AA
GAM718  LOC145786 5'  AGATTGGAATTTAGAGTTGTTA 83488          GCAGAT
                                TAACGGCTCTGAGT     ATCT
                                ||||||||||||||     ||||
                                ATTGTTGAGATTTA     TAGA
                                       AGGT__
GAM718  LOC148137 3'  GGGTATCCCTTGGGGCTGTT   58438       TG  TGCA
                                AACGGCTC  AG   GATATCT
                                ||||||||  ||   |||||||
                                TTGTCGGG  TC   CTATGGG
                                     GT  C___
GAM718  LOC149372 5'  GGATATTTGCATTTAAGCC   79326     C
                                GGCT TGAGTGCAGATATCT
                                |||| ||||||||||||||
                                CCGA ATTTACGTTTATAGG
                                  _
GAM718  LOC151188 5'  AGATGAGGCTTTGGGGCTGT   80155       TG  T  AGA
                                ACGGCTC  AG GC   TATCT
                                |||||||  || ||   |||||
                                TGTCGGG  TT CG   GTAGA
                                   GT  _  GA_
GAM718  LOC152890 5'  GCGCTCGGGCCGTTG      80719       T
                                TAACGGC CTGAGTGC
                                |||||||  ||||||||
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                                GTTGCCG GGCTCGCG
                                      _
GAM718  LOC154739 5'  AGGTGTTTGTAAGGAAGGCTTT 86224     C   T  GAG_
                TA                     TAA GGC CT    TGCAGATATCT
                                       ||| ||| ||    ||||||||||
                                       ATT TCG GA    ATGTTTGTGGA
                                         T   _  AGGA
GAM718  LOC157653 5'  GATGTGTGTCAGAGCT      81525        AGT   G
                                       GGCTCTG   GCA ATATC
                                       |||||||   ||| |||||
                                       TCGAGAC   TGT TGTAG
                                           ___   G
GAM718  LOC157693 3'  CTGTTTCAGAGCCGTTA     81555             T
                                       TAACGGCTCTGAG GCAG
                                       |||||||||||| ||||
                                       ATTGCCGAGACTT TGTC
                                              _
GAM718  LOC158357 3'  AGATGTCTGTTAAATCTGTTG  81883       CTCTGAGT
                                       TAACGG       GCAGATATCT
                                       ||||||       ||||||||||
                                       GTTGTC       TGTCTGTAGA
                                          TAAAT___
GAM718  LOC159723 5'  GCGCCCGGGGCCGTTA      82192           A
                                       TAACGGCTCTG GTGC
                                       |||||||||| ||||
                                       ATTGCCGGGGC CGCG
                                              C
GAM718  LOC162333 5'  AGATATCTGCATTTAAGTGT   87119     G  C
                                       ACG CT TGAGTGCAGATATCT
                                       ||| || ||||||||||||||
                                       TGT GA ATTTACGTCTATAGA
                                         _ _
GAM718  LOC165476 3'  AGAAACAGGTGCCGGAGCTGTT 87196           A TG AGATA
                G                       TAACGGCTCTG G  C     TCT
                                        |||||||||| |  |     |||
                                        GTTGTCGAGGC C  G     AGA
                                              _ GT GACAA
GAM718  LOC196955 3'  AGGTGCAGGCCTTGGAGCC    77364       TG  T  AGA
                                        GGCTC  AG GC   TATCT
                                        |||||  || ||   |||||
                                        CCGAG  TC CG   GTGGA
                                           GT  _  GAC
GAM718  LOC199907 3'  AGGTGTTTGTAACTTGGCC    88460      CT   _
                                        GGCT  GAGT GCAGATATCT
                                        ||||  |||| ||||||||||
                                        CCGG  TTCA TGTTTGTGGA
                                          __    A
GAM718  LOC201910 5'  GCGCTCGGGCCGTTG       89102        T
                                        TAACGGC CTGAGTGC
                                        |||||||  ||||||||
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                                GTTGCCG GGCTCGCG
                                      _
GAM718  LOC203276 3'  AGGTGTTTGTAAGGAAGGCTTT 90471    C  T  GAG_
            TA                  TAA GGC CT   TGCAGATATCT
                                ||| ||| ||   ||||||||||
                                ATT TCG GA   ATGTTTGTGGA
                                  T  _  AGGA
GAM718  LOC203305 3'  AGGTGTTTGTAAGGAAGGCTTT 90515    C  T  GAG_
            TA                  TAA GGC CT   TGCAGATATCT
                                ||| ||| ||   ||||||||||
                                ATT TCG GA   ATGTTTGTGGA
                                  T  _  AGGA
GAM718  LOC204285 3'  AGGTATCTGCACGGTCTGT   89457    _  CTGA
                                ACGG CT   GTGCAGATATCT
                                |||| ||   ||||||||||
                                TGTC GG   CACGTCTATGGA
                                  T ____
GAM718  LOC219540 3'  AGGTGTAAGTGTTGCTTAGAGT 93594       ___  AG
            C                    GGCTCTGAGT  GC  ATATCT
                                |||||||||  ||  ||||||
                                CTGAGATTCG  TG  TGTGGA
                                     TTG  AA
GAM718  LOC219790 3'  TGATCTCAGGGCTGTT    91360         TG
                                AACGGCTCTGAG  CA
                                ||||||||||| ||
                                TTGTCGGGACTC  GT
                                      TA
GAM718  LOC222865 3'  GGGTTCATTTGCGTGGGGCTGT 92867        AG    __
            TG                  TAACGGCTCTG  TGCAGAT  ATCT
                                |||||||||| |||||||  ||||
                                GTTGTCGGGGT  GCGTTTA  TGGG
                                     __     CT
GAM718  LOC253964 5'  GTTGTCAGAGCTGTTG    97441         GT
                                TAACGGCTCTGA  GC
                                |||||||||| ||
                                GTTGTCGAGACT  TG
                                      GT
GAM718  LOC254243 3'  AGGTGTTTGTAAGGAAGGCTTT 97400    C  T  GAG_
            TA                  TAA GGC CT   TGCAGATATCT
                                ||| ||| ||   ||||||||||
                                ATT TCG GA   ATGTTTGTGGA
                                  T  _  AGGA
GAM718  LOC254552 3'  GGTGTTTGCACTGCCG    94777    TCTG
                                CGGC   AGTGCAGATATC
                                ||||   ||||||||||||
                                GCCG   TCACGTTTGTGG
                                    ____
GAM718  LOC255783 3'  GGGTGTCAGCTCGGGGCC   95264        GCA
                                GGCTCTGAGT  GATATCT
                                |||||||||  |||||||
```

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                                CCGGGGCTCG  CTGTGGG
                                    A__
GAM718  LOC51580  3'  AGATTTGGTGCATTCAGGGTTG 31859          GAT_
            T                    ACGGCTCTGAGTGCA   ATCT
                                 ||||||||||||||   ||||
                                 TGTTGGGACTTACGT   TAGA
                                       GGTT
GAM718  LOC54516  3'  AGATGTTTGTGTTTGTC    38759    TCT  TG
                                 GGC  GAG  CAGATATCT
                                 |||  |||  |||||||||
                                 CTG  TTT  GTTTGTAGA
                                   ___  GT
GAM718  LOC90038  3'  AGGTGTTTGTAAGGAAGGCTTT 61144    C  T  GAG_
            TA                    TAA GGC CT   TGCAGATATCT
                                 ||| ||| ||   ||||||||||
                                 ATT TCG GA   ATGTTTGTGGA
                                   T  _ AGGA
GAM718  LOC90288  3'  GGGTATTATGGCAGGGTTG   62103       AGTGCA
                                 CGGCTCTG    GATATCT
                                 ||||||||    |||||||
                                 GTTGGGAC    TTATGGG
                                     GGTA__
GAM718  LOC90670  3'  AGATATTTAATGGAGCTG    63739       GA  GC
                                 CGGCTCT  GT  AGATATCT
                                 |||||||  ||  ||||||||
                                 GTCGAGG  TA  TTTATAGA
                                    __ A_
GAM718  LOC91768  3'  GACAAACTGCGTTTGGAGCTGT 67115       TG     ATATCT
                                 ACGGCTC  AGTGCAG
                                 |||||||  |||||||
                                 TGTCGAG  TTGCGTC
                                    GT     AAACAGG
GAM718  LOC92340  3'  AGGTGTTTGTATTCGGGCT   68987    T
                                 GGC CTGAGTGCAGATATCT
                                 ||| ||||||||||||||||
                                 TCG GGCTTATGTTTGTGGA
                                   _
GAM718  LOC96573  3'  ATATATCAACACTTGGAATTGT 63170      C  TG   CA    CT
            TA                    TAACGG TC  AGTG  GATAT
                                 ||||||  ||  ||||  |||||
                                 ATTGTT AG  TCAC  CTATA
                                    A  GT   AA    TAG
GAM718  LOC96626  3'  GCTATTCATGGGCTGTTG    53181        _   _
                                 TAACGGCTC TGAGT GC
                                 |||||||||  |||||  ||
                                 GTTGTCGGG ACTTA CG
                                      T    T
GAM719  BAZ2A    3'  CTCTGTGTTCCTGTCATAGC   25599    _       T
                                 GC ATGACAGGAAC TGGAG
                                 ||  ||||||||||  |||||
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                                CG TACTGTCCTTG GTCTC
                                 A         T
GAM719  CALCRL   3'  CCTCTTCCTGTCTTACCAAA  19387      CAT      CTT
                                TTTGG  GACAGGAA  GG
                                |||||  ||||||||  ||
                                AAACC  CTGTCCTT  CC
                                   ATT      CT_
GAM719  GLB1     3'  TCCTCCCTGTCATGCCA    4638          AACTT
                                TGGCATGACAGG   GGA
                                ||||||||||||   |||
                                ACCGTACTGTCC   CCT
                                       CT___
GAM719  OGG1     5'  ACCCCAAATCCCTATGCTAAA  10328        ACA  AC   A
                                TTTGGCATG  GGA  TTGG GT
                                |||||||||  |||  |||| ||
                                AAATCGTAT  CCT  AACC CA
                                     C__  A_   C
GAM719  OGG1     5'  ACCCCAAATCCCTATGCTAAA  33656        ACA  AC   A
                                TTTGGCATG  GGA  TTGG GT
                                |||||||||  |||  |||| ||
                                AAATCGTAT  CCT  AACC CA
                                     C__  A_   C
GAM719  OGG1     5'  ACCCCAAATCCCTATGCTAAA  33664        ACA  AC   A
                                TTTGGCATG  GGA  TTGG GT
                                |||||||||  |||  |||| ||
                                AAATCGTAT  CCT  AACC CA
                                     C__  A_   C
GAM719  VAMP5    3'  CTGCATTTCCTGTCATGCCA  59443           CT  G
                                TGGCATGACAGGAA  TG AG
                                ||||||||||||||  || ||
                                ACCGTACTGTCCTT  AC TC
                                       T_  G
GAM719  FLJ12595 5'  CTCCAATGATCATGCCAA   46505         _  GGAAC
                                TTGGCATGA CA   TTGGAG
                                |||||||||  ||   ||||||
                                AACCGTACT GT   AACCTC
                                     A  _____
GAM719  KIAA0514 3'  TCCATGTCATGCCAAA     28095          _
                                TTTGGCATGACA GGA
                                |||||||||||| |||
                                AAACCGTACTGT CCT
                                       A
GAM719  YAF2     3'  ACTTCTGTCCTACCATGC    19235      AC   ACTT
                                GCATG  AGGA   GGAGT
                                |||||  ||||   |||||
                                CGTAC  TCCT   CTTCA
                                   CA   GT__
GAM720  ADAMTS8  5'  TCGGGCCGCCAGCACCTG   22886    _     ATAAG
                                CAG TGCTGGC    CTGA
                                ||| |||||||    ||||
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                                GTC ACGACCG    GGCT
                                  C      CCG__
GAM720  BAP1    3'  TCAGGGACCCAGCACTGG    16219          CATAAG
                                CCAGTGCTGG     CTGA
                                ||||||||||     ||||
                                GGTCACGACC     GACT
                                     CAGG__
GAM720  BF      5'  TTCAGCTTGGACACTG      8140       CTGGCA
                                CAGTG     TAAGCTGAA
                                |||||     |||||||||
                                GTCAC     GTTCGACTT
                                   AG_____
GAM720  C1QB    3'  TTCAACTCTGTGTCCCAGCACT 4923     A        __    _ C
            GGC                    G CCAGTGCTGG  CATA AG TGAA
                                | ||||||||||  |||| || ||||
                                C GGTCACGACC  GTGT TC ACTT
                                _        CT    C  A
GAM720  CHC1    3'  CAGCCCTGAGCACTGTGTC    7020      _      __ CATAA
                                GAC CAGTGCT  GG    GCTG
                                ||| |||||||  ||    ||||
                                CTG GTCACGA  CC    CGAC
                                  T      GT  _____
GAM720  CMRF35  5'  CAGAGCTGTCAGCACCGG    21929    A       TAAG
                                CC GTGCTGGCA    CTG
                                || |||||||||    |||
                                GG CACGACTGT    GAC
                                 C        CGA_
GAM720  EPHB6   3'  TCAGCCCTGGACACTGGTC    15466        _ TG CATAA
                                GACCAGTG C  G    GCTGA
                                ||||||||  |  |    |||||
                                CTGGTCAC G  C    CGACT
                                     A GT C____
GAM720  EVPL    5'  CAGCCTGAGCCAGCACT     8803          A  A
                                AGTGCTGGC TA GCTG
                                ||||||||| || ||||
                                TCACGACCG GT CGAC
                                     A  C
GAM720  GARP    3'  CAGCCCAGCACTGG        18594          CATAA
                                CCAGTGCTGG    GCTG
                                ||||||||||    ||||
                                GGTCACGACC    CGAC
                                      _____
GAM720  GJB5    3'  CAGCTCGACGGCACTGG     17945         GCATA
                                CCAGTGCTG    AGCTG
                                |||||||||    |||||
                                GGTCACGGC    TCGAC
                                     AGC__
GAM720  GPR81   3'  CTTACCAGCATTAGTC      50757     C       CA
                                GAC AGTGCTGG  TAAG
                                ||| ||||||||  ||||
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                                CTG TTACGACC  ATTC
                                  A      __
GAM720  IFI16    5'  AGCAAGCCAGCACTAGTC    71221     C       ATAA
                                GAC AGTGCTGGC    GCT
                                ||| |||||||||    |||
                                CTG TCACGACCG    CGA
                                  A       AA__
GAM720  KRT4     3'  CAGCTGGGCCCAGCACTGGT   9635          _ ATA
                                ACCAGTGCTGG C   AGCTG
                                |||||||||||  |   |||||
                                TGGTCACGACC G   TCGAC
                                      C GG_
GAM720  MAP3K9   3'  TTCAGCTTCCCAAACACCAGT  60709    CA   C_   CAT
                                AC  GTG  TGG   AAGCTGAA
                                ||  |||  |||   ||||||||
                                TG  CAC  ACC   TTCGACTT
                                 AC   AA   C__
GAM720  MGAT5    5'  TCAGCTTACAGTTCCTG     10028     T_   GCA
                                CAG  GCTG   TAAGCTGA
                                |||  ||||   ||||||||
                                GTC  TGAC   ATTCGACT
                                  CT    ____
GAM720  MOCS1    3'  TTCAGCTTAACAGTTGCCCGGT 92037      A_   _   GCA
           C                     GACC  GTG CTG   TAAGCTGAA
                                ||||  ||| |||   |||||||||
                                CTGG  CGT GAC   ATTCGACTT
                                  CC   T   A__
GAM720  P23      3'  TCAGCTTATACCCGGGCT    21719     G    C_
                                AGT CTGG  ATAAGCTGA
                                ||| ||||  |||||||||
                                TCG GGCC  TATTCGACT
                                  _    CA
GAM720  PFKFB4   3'  TCAGCCACATGCAACACTGTGT 15874     _     CTG    AA_
           C                     GAC CAGTG   GCAT   GCTGA
                                ||| |||||   ||||   |||||
                                CTG GTCAC   CGTA   CGACT
                                  T     AA_    CAC
GAM720  PTPRK    3'  TTCAGCCTGTGGCCCAGCACTG 11125           __    A
           GTC                     GACCAGTGCTGG  CATA GCTGAA
                                ||||||||||||  |||| ||||||
                                CTGGTCACGACC  GTGT CGACTT
                                      CG    C
GAM720  RNPEPL1  3'  CGGATGCCAGCACCTG      36676     _       AAG
                                CAG TGCTGGCAT   CTG
                                ||| |||||||||   |||
                                GTC ACGACCGTA   GGC
                                  C       ____
GAM720  UBE2L3   3'  TCAGCCCTGGCACTGGC     12507    A      TG CATAA
                                G CCAGTGC  G    GCTGA
                                | |||||||  |    |||||
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                                C GGTCACG  C    CGACT
                                 _     GT C____
GAM720  APXL2    5'  CAGCCTCAGCACTCATC    75185   CC      CATAA
                                GA  AGTGCTGG    GCTG
                                ||  ||||||||    ||||
                                CT  TCACGACT    CGAC
                                  AC      C____
GAM720  ARHGEF9  3'  TTCAGCTTACCAAGCA     30824     _  CA
                                TGCT GG  TAAGCTGAA
                                |||| ||  |||||||||
                                ACGA CC  ATTCGACTT
                                  A  __
GAM720  CEGP1    3'  TTCAGCTTCCTCTAGCCCGG  40589   AGT   CAT
                                CC   GCTGG   AAGCTGAA
                                ||   |||||   ||||||||
                                GG   CGATC   TTCGACTT
                                 CC_    TCC
GAM720  DKFZp547D155 3'  CAGCCCTGAGACCACTGGTC  70435       CTGG  TAA
                                GACCAGTG   CA   GCTG
                                ||||||||   ||   ||||
                                CTGGTCAC   GT   CGAC
                                     CAGA  CC_
GAM720  DKFZP727G051 3'  TTCAGCCCATCAACCAGCATTG 69483          CATAA__
           GTC                   GACCAGTGCTGG     GCTGAA
                                ||||||||||||     ||||||
                                CTGGTTACGACC     CGACTT
                                       AACTACC
GAM720  DUSP14   5'  CACTGTCACCAGCACTGCTC  22834   C       CATA  C
                                GA CAGTGCTGG   AG TG
                                || |||||||||   || ||
                                CT GTCACGACC   TC AC
                                 C       ACTG  _
GAM720  FLJ10206 5'  CAGCTTATGCCAGGAGTC   35898    CAGTG
                                GAC    CTGGCATAAGCTG
                                |||    ||||||||||||
                                CTG    GACCGTATTCGAC
                                  AG___
GAM720  FLJ20967 5'  GGCGCCCAGCACTGGTT    41962          CATAA
                                GACCAGTGCTGG    GCT
                                ||||||||||||    |||
                                TTGGTCACGACC    CGG
                                       CG___
GAM720  FLJ22569 3'  TTCAGCTTACTAAACTG    43679     GC   CA
                                CAGT  TGG  TAAGCTGAA
                                ||||  |||  |||||||||
                                GTCA  ATC  ATTCGACTT
                                  A_   __
GAM720  FOXN4    3'  TTCAGCTTGGACACACTGG   75574       C  GCA
                                CCAGTG TG   TAAGCTGAA
                                ||||||  ||   |||||||||
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                                GGTCAC AC   GTTCGACTT
                                   _ AG_
GAM720  GW112    3'  TTCAACTGAAGCCAGCACTGGT 21194          ATA  C
           T                    GACCAGTGCTGGC   AG TGAA
                                ||||||||||||   || ||||
                                TTGGTCACGACCG   TC ACTT
                                      AAG  A
GAM720  HOOK2    3'  CAGCTCACATGGCGCCCAGCAC 25256        _____  A__
           TGG                    CCAGTGCTGG   CAT   AGCTG
                                ||||||||||   |||  |||||
                                GGTCACGACC   GTA   TCGAC
                                      CGCG   CAC
GAM720  jdp2     3'  TTCAGCACAGCCAGCAT     55327        ATAA
                                GTGCTGGC    GCTGAA
                                ||||||||    ||||||
                                TACGACCG    CGACTT
                                    ACA_
GAM720  KIAA0767 3'  TCTGCTGCCAGCACAGG     60632    A       TAA  T
                                CC GTGCTGGCA   GC GA
                                || |||||||||   || ||
                                GG CACGACCGT   CG CT
                                 A        ___  T
GAM720  KIAA0923 3'  TCAGCTTGATGCATGGTC    25838      G   TGGCA
                                GACCA TGC    TAAGCTGA
                                ||||| |||    ||||||||
                                CTGGT ACG    GTTCGACT
                                   _   TA___
GAM720  KIAA0982 3'  TTCACTGTTTGCCAGCAC    25852        TA_  C
                                GTGCTGGCA   AG TGAA
                                |||||||||   || ||||
                                CACGACCGT   TC ACTT
                                      TTG  _
GAM720  KIAA1000 3'  TTCAGCTTTGCAAAGTACTGG  65281        G_   T
                                CCAGTGCT  GCA AAGCTGAA
                                ||||||||  ||| ||||||||
                                GGTCATGA  CGT TTCGACTT
                                     AA  _
GAM720  MAP3K3   3'  TCAGCCTGGGCGCTGGTC    9999          GG  TAA
                                GACCAGTGCT  CA   GCTGA
                                ||||||||||  ||   |||||
                                CTGGTCGCGG  GT   CGACT
                                      __  C__
GAM720  MGC16037 5'  CTTGTCCAGCACTAGTC     51821     C       C
                                GAC AGTGCTGG ATAAG
                                ||| |||||||| |||||
                                CTG TCACGACC TGTTC
                                  A       _
GAM720  MIDORI   3'  TCAGCTTATCCTGCAACT    73792     _  T  C
                                AGT GC GG ATAAGCTGA
                                ||| || || |||||||||
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                                TCA CG CC TATTCGACT
                                  A  T  _
GAM720  MtFMT     5'  CAGTGGCGAGCACTGG      57651         G  ATAA
                                CCAGTGCT GC    GCTG
                                |||||||| ||    ||||
                                GGTCACGA CG    TGAC
                                     G  G___
GAM720  PCDH16    5'  TCAGTTCCAACCACTGG     72826       C_  CATA
                                CCAGTG  TGG    AGCTGA
                                ||||||  |||    ||||||
                                GGTCAC  ACC    TTGACT
                                   CA  _____
GAM720  QKI       3'  CAGCTTATCAACTCGTC     65439     C   GCTGGC
                                GAC AGT      ATAAGCTG
                                ||| |||      ||||||||
                                CTG TCA      TATTCGAC
                                  C   AC_____
GAM720  TNRC6     3'  CAACTTTTAGCACTG       70506         CAT   C
                                CAGTGCTGG   AAG TG
                                |||||||||   ||| ||
                                GTCACGATT   TTC AC
                                     ___   A
GAM720  TOB2      3'  CAGCCCAGGCCAGCACTG    95618          ATAA
                                CAGTGCTGGC    GCTG
                                ||||||||||    ||||
                                GTCACGACCG    CGAC
                                      GACC
GAM720  TU12B1-TY 3'  TCAGCCCACAGCACTGTC    33406     C      GCATAA
                                GAC AGTGCTG      GCTGA
                                ||| |||||||      |||||
                                CTG TCACGAC      CGACT
                                  _      ACC___
GAM720  TUSP      3'  TCAGCCTAAGAGCGCAGCACTG 39641         _  A__  A
                                CAGTGCTG GC   TA GCTGA
                                |||||||| ||   || |||||
                                GTCACGAC CG   AT CGACT
                                     G  AGA  C
GAM720  USP19     3'  TCAGCTTATGCATCTGGT    88959       TGCTG
                                ACCAG     GCATAAGCTGA
                                |||||     ||||||||||
                                TGGTC     CGTATTCGACT
                                   TA___
GAM720  ZD52F10   3'  CAGCCTGTGCCAGCCCTGG   52819      T       A
                                CCAG GCTGGCATA GCTG
                                |||| ||||||||| ||||
                                GGTC CGACCGTGT CGAC
                                  C        C
GAM720  LOC145268 3'  TCAGCTTACAAGAGCCACTG  77062       _  GGCA
                                CAGTG CT    TAAGCTGA
                                ||||| ||    ||||||||
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                                GTCAC GA   ATTCGACT
                                   C  GAAC
GAM720  LOC149296 5'  CAGCTTATGGGCAGCA     79256      G_
                                TGCTG  CATAAGCTG
                                |||||  |||||||||
                                ACGAC  GTATTCGAC
                                   GG
GAM720  LOC161877 5'  TCAGGGCAGGCCAGCGCTGG  82326         ATAAG
                                CCAGTGCTGGC    CTGA
                                ||||||||||    ||||
                                GGTCGCGACCG    GACT
                                      GACGG
GAM720  LOC163115 5'  TCAGCCCCTGACAGCACTGG  82413        G  TAA
                                CCAGTGCTG CA   GCTGA
                                ||||||||| ||   |||||
                                GGTCACGAC GT   CGACT
                                     A  CCC
GAM720  LOC196500 3'  TCAGCTCACTCAGTGGTC    87744     AGT    CATA
                                GACC   GCTGG   AGCTGA
                                ||||   |||||   ||||||
                                CTGG   TGACT   TCGACT
                                  ___    CAC_
GAM720  LOC197287 3'  TCAGCTCATGTGTTTTGCACTG 60865       T_    __
                                CAGTGC  GGCATA  AGCTGA
                                ||||||  ||||||  ||||||
                                GTCACG  TTGTGT  TCGACT
                                   TT     AC
GAM720  LOC200470 5'  TCAGCCTGCGGCGCTGG     90069        G  TAA
                                CCAGTGCTG CA   GCTGA
                                ||||||||| ||   |||||
                                GGTCGCGGC GT   CGACT
                                      _ C__
GAM720  LOC221584 3'  CAGCTTATGTGGCAC       93828       G
                                GTGCTG CATAAGCTG
                                ||||||  |||||||||
                                CACGGT GTATTCGAC
                                  _
GAM720  LOC51716  3'  CAGCTCATGGCCCTAGCA    32787       ___  A
                                TGCTGG   CAT AGCTG
                                ||||||   ||| |||||
                                ACGATC   GTA TCGAC
                                   CCG   C
GAM720  LOC92196  5'  CAGAGCACCAGCACTGGC    68456   A       CATAAG
                                G CCAGTGCTGG     CTG
                                | ||||||||||     |||
                                C GGTCACGACC     GAC
                                _        ACGA__
GAM721  RFXAP     3'  TCGACTTAATCATGGCTGTT   5016        CCT   C__
                                AACAGCCA   TGA   AGTCGA
                                ||||||||   |||   ||||||
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                                TTGTCGGT  ACT  TCAGCT
                                   ___  AAT
GAM721  NYD-SP25  5'  TCAACTGTCAAGGTGTCCATTG 53189      CAGC        C
          TA                    TATAA   CACCTTGACAGT GA
                                |||||   |||||||||||| ||
                                ATGTT   GTGGAACTGTCA CT
                                  ACCT         A
GAM721  TCF-3    3'  CGACCCCTGCAGGCTGT    48425      ACCT  A ___
                                ACAGCC   TG CA  GTCG
                                ||||||   || ||  ||||
                                TGTCGG   AC GT  CAGC
                                   ____ _ CCC
GAM721  TOB2     3'  CAAGTAGGCAACTGTTATG   95617       ___  AC
                                TATAACA  GCC  CTTG
                                |||||||  |||  ||||
                                GTATTGT  CGG  GAAC
                                    CAA  AT
GAM721  LOC158236 5'  CGGGTGGAAGGTGGTT     86706        GA  G
                                AGCCACCTT  CA TCG
                                |||||||||  || |||
                                TTGGTGGAA  GT GGC
                                     G_  G
GAM721  LOC170281 5'  TCAACCACTGGCTGTTATA   87251         CC__
                                TATAACAGCCA   TTGA
                                ||||||||||   ||||
                                ATATTGTCGGT   AACT
                                      CACC
GAM721  LOC219793 5'  TCAACTGTCTTTTCCGGCTGT  91375      ACCTT_    C
                                ACAGCC    GACAGT GA
                                ||||||    |||||| ||
                                TGTCGG    CTGTCA CT
                                   CCTTTT    A
GAM721  LOC221362 3'  CTGCAAGATGGCTGT      93760       C   A
                                ACAGCCA CTTG CAG
                                ||||||| |||| |||
                                TGTCGGT GAAC GTC
                                    A   _
GAM721  LOC90906  3'  CAAGGTGGCTGTTATA     64294
                                TATAACAGCCACCTTG
                                ||||||||||||||||
                                ATATTGTCGGTGGAAC

GAM722  CA12     3'  AGACACTGCACAGACCTTAGG  6874      CA  GACGA
                                CCTA  GT    CAGTGTCT
                                ||||  ||    ||||||||
                                GGAT  CA    GTCACAGA
                                  TC  GACAC
GAM722  CACNB1   3'  CATAGTCGTCAGCGTAGG    5569       AG      A
                                CCTAC  TGACGAC GTG
                                |||||  ||||||| |||
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                                GGATG  ACTGCTG TAC
                                  CG      A
GAM722  DEFB103  5' ATAATGTCATCACTGTA    37864        C   G
                                TACAGTGA GACA TGT
                                |||||||| |||| |||
                                ATGTCACT CTGT ATA
                                    A   A
GAM722  MUTYH    5' CGCCATCGTCACTGTCGG    24231    T       CA
                                CC ACAGTGACGA  GTG
                                || ||||||||||  |||
                                GG TGTCACTGCT  CGC
                                 C         AC
GAM722  PPP2R2C  5' ACGGTGACGTCACTGCAGG   61760    A      A  G
                                CCT CAGTGACG CA TGT
                                ||| |||||||| || |||
                                GGA GTCACTGC GT GCA
                                  C       A  G
GAM722  SYN3     3' GAGACACTGTAGTCA      56093     G       A
                                TGAC ACAGTGTCT C
                                |||| ||||||||| |
                                ACTG TGTCACAGA G
                                  A        C
GAM722  SYN3     3' GAGACACTGTAGTCA      56097     G       A
                                TGAC ACAGTGTCT C
                                |||| ||||||||| |
                                ACTG TGTCACAGA G
                                  A        C
GAM722  SYN3     3' GAGACACTGTAGTCA      13018     G       A
                                TGAC ACAGTGTCT C
                                |||| ||||||||| |
                                ACTG TGTCACAGA G
                                  A        C
GAM722  C20orf81 5' GGCCATCACCACTGTGGG    42814        AC  CAGT
                                CCTACAGTG  GA   GTC
                                |||||||||  ||   |||
                                GGGTGTCAC  CT   CGG
                                     CA  AC__
GAM722  CNNM2    3' CTGTCATCACTGTGGG      34460         C
                                CCTACAGTGA GACAG
                                |||||||||| |||||
                                GGGTGTCACT CTGTC
                                     A
GAM722  CPR2     3' ACAGCCCTCAGCACTGTAGG  48085        AC  CA _
                                CCTACAGTG  GA  G TGT
                                |||||||||  ||  | |||
                                GGATGTCAC  CT  C ACA
                                     GA  CC G
GAM722  FLJ22283 5' CACTGTGTCGTCACTG     49914         __
                                CAGTGACGACA  GTG
                                ||||||||||  |||
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                                GTCACTGCTGT  CAC
                                      GT
GAM722  FLJ22644 3' GGCCCATCACCACTGTGGG   47002        AC  CAGT
                                CCTACAGTG  GA   GTC
                                |||||||||  ||   |||
                                GGGTGTCAC  CT   CGG
                                     CA  ACC_
GAM722  H2AV    3' TAGACAATTACTGTAG     24835        CGACAG
                                CTACAGTGA    TGTCTA
                                |||||||||    ||||||
                                GATGTCATT    ACAGAT
                                     A_____
GAM722  KIAA0711 3' AGACACTGTGCTGGCAGG   29513    A_   GACG
                                CCT  CAGT   ACAGTGTCT
                                |||  ||||   |||||||||
                                GGA  GTCG   TGTCACAGA
                                  CG   ____
GAM722  KIAA1817 3' ACTGTCCCACTGTAGG     68222        AC
                                CCTACAGTG  GACAGT
                                |||||||||  ||||||
                                GGATGTCAC  CTGTCA
                                     C_
GAM722  MGC21636 5' AGATCTGTCAGCCACTGTAGG  58856        AC_    T
                                CCTACAGTG   GACAG GTCT
                                |||||||||   ||||| ||||
                                GGATGTCAC   CTGTC TAGA
                                     CGA    _
GAM722  NCE2    3' TAGAGTCATTCACTGTAG    54763        C_  AGTG
                                CTACAGTGA  GAC   TCTA
                                |||||||||  |||   ||||
                                GATGTCACT  CTG   AGAT
                                     TA   ____
GAM722  OBSCN   3' AGAGACCATCACCACTGTGG  70650        AC  CA  G
                                CTACAGTG  GA  GT TCT
                                ||||||||  ||  || |||
                                GGTGTCAC  CT  CA AGA
                                     CA  AC  G
GAM722  PTR4    3' TAGCCATATCTCACTGTA    74056        C  CA   T
                                TACAGTGA GA  GTG CTA
                                ||||||||  ||  ||| |||
                                ATGTCACT CT  TAC GAT
                                     _  A_   C
GAM722  PTRF    5' CGCAGACACTGCGGCGCGTGG  63500     A   A  A      A
                                CTAC GTG CG CAGTGTCT CG
                                |||| ||| || |||||||| ||
                                GGTG CGC GC GTCACAGA GC
                                  _   G  _       C
GAM722  RAB10   5' TGGACGCCGCCACTGTCGG   85179    T     A  ACA
                                CC ACAGTG CG   GTGTCTA
                                || |||||| ||   |||||||
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                                GG TGTCAC GC   CGCAGGT
                                 C     C ___
GAM722  SEPT3    3'  CACAGGTGGTCACTGTAGG   38884          G  A_
                                CCTACAGTGAC AC  GTG
                                |||||||||| ||  |||
                                GGATGTCACTG TG  CAC
                                      G  GA
GAM722  SSAT2    3'  AGACACTGATGCTGAGG     56040     A    ACGA
                                CCT CAGTG    CAGTGTCT
                                ||| |||||    ||||||||
                                GGA GTCGT    GTCACAGA
                                  _    A___
GAM722  USP24    3'  TGCCGTCCTCACTGTA      91154         C   A
                                TACAGTGA GAC GTG
                                |||||||| ||| |||
                                ATGTCACT CTG CGT
                                     C   C
GAM722  LOC148932 3'  AGACCATGACCACTGTAGG   79102          ACGA  GT
                                CCTACAGTG    CA  GTCT
                                |||||||||    ||  ||||
                                GGATGTCAC    GT  CAGA
                                     CA__  AC
GAM722  LOC152065 5'  ACCTGATCATCGTCACTG    85551          ____   T
                                CAGTGACGA    CAG GT
                                |||||||||    ||| ||
                                GTCACTGCT    GTC CA
                                     ACTA  _
GAM722  LOC152742 3'  GTAGACCATCACTGTG      85860         CGACAGT
                                TACAGTGA      GTCTAC
                                ||||||||      ||||||
                                GTGTCACT      CAGATG
                                     AC_____
GAM722  LOC169693 3'  GATGCCACCACTGTGGG     87293          ACGACA
                                CCTACAGTG     GTGTC
                                |||||||||     |||||
                                GGGTGTCAC     CGTAG
                                     CAC___
GAM722  LOC220980 5'  TGTGTTCACCATCACTGAGG  93153     A     CGACA   TC
                                CCT CAGTGA    GTG  TACG
                                ||| ||||||    |||  ||||
                                GGA GTCACT    CAC  GTGT
                                  _     AC___   TT
GAM722  LOC254573 3'  TAGACAATTACTGTAG      94953         CGACAG
                                CTACAGTGA     TGTCTA
                                |||||||||     ||||||
                                GATGTCATT     ACAGAT
                                     A_____
GAM722  LOC255650 3'  GGGCGGTCGTCACTGCAG    96715    A        AG
                                CT CAGTGACGAC  TGTCT
                                || ||||||||||  |||||
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                                GA GTCACTGCTG  GCGGG
                                 C        __
GAM722  LOC255650 3'  GGGCGTTCGTCACTGCAG    96716    A       CAG
                                CT CAGTGACGA   TGTCT
                                || |||||||||  |||||
                                GA GTCACTGCT   GCGGG
                                 C        T__
GAM722  LOC255650 3'  GGGCGTTCGTCACTGCAG    96717    A       CAG
                                CT CAGTGACGA   TGTCT
                                || |||||||||  |||||
                                GA GTCACTGCT   GCGGG
                                 C        T__
GAM722  LOC257060 3'  CATTGTGATCACTGTA      94460        CG
                                TACAGTGA  ACAGTG
                                ||||||||  ||||||
                                ATGTCACT  TGTTAC
                                     AG
GAM723  ASH1    3'  AAGCACTTGTAACTGCTGC    37497      TTG
                                GCAGCA   TACAGGTGCTT
                                ||||||   ||||||||||
                                CGTCGT   ATGTTCACGAA
                                   CA_
GAM723  CASP3   3'  AGGTGCTACAATGCCCCT    52192    CA     ACA  TG
                                AG  GCATTGT   GG  CTT
                                ||  |||||||   ||  |||
                                TC  CGTAACA   TC  GGA
                                 CC      ___  GT
GAM723  CASP3   3'  AGGTGCTACAATGCCCCT    15096    CA     ACA  TG
                                AG  GCATTGT   GG  CTT
                                ||  |||||||   ||  |||
                                TC  CGTAACA   TC  GGA
                                 CC      ___  GT
GAM723  CDC25A  5'  AGCACCCGTGCCTGT       8363      CATT   A
                                GCAG   GTAC GGTGCT
                                ||||   |||| ||||||
                                TGTC   CGTG CCACGA
                                  ____   C
GAM723  CFTR    3'  CATATATTACAATGCTGT    4928          CAG_
                                GCAGCATTGTA   GTG
                                ||||||||||   |||
                                TGTCGTAACAT   TAC
                                      TATA
GAM723  COL14A1 5'  ATGTGTACAATGTTGC      69077          G
                                GCAGCATTGTACA GT
                                |||||||||||| ||
                                CGTTGTAACATGT TA
                                        G
GAM723  COLQ    3'  ACCGGCTACAATGCTCT     54476    C       CA_
                                AG AGCATTGTA   GGT
                                || |||||||||  |||
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                                TC TCGTAACAT   CCA
                                 _       CGG
GAM723  COLQ    3'  ACCGGCTACAATGCTCT    54488    C       CA_
                                AG AGCATTGTA   GGT
                                || |||||||||   |||
                                TC TCGTAACAT   CCA
                                 _       CGG
GAM723  COLQ    3'  ACCGGCTACAATGCTCT    19047    C       CA_
                                AG AGCATTGTA   GGT
                                || |||||||||   |||
                                TC TCGTAACAT   CCA
                                 _       CGG
GAM723  COLQ    3'  ACCGGCTACAATGCTCT    54470    C       CA_
                                AG AGCATTGTA   GGT
                                || |||||||||   |||
                                TC TCGTAACAT   CCA
                                 _       CGG
GAM723  COLQ    3'  ACCGGCTACAATGCTCT    54494    C       CA_
                                AG AGCATTGTA   GGT
                                || |||||||||   |||
                                TC TCGTAACAT   CCA
                                 _       CGG
GAM723  COLQ    3'  ACCGGCTACAATGCTCT    54482    C       CA_
                                AG AGCATTGTA   GGT
                                || |||||||||   |||
                                TC TCGTAACAT   CCA
                                 _       CGG
GAM723  CYP7A1  3'  TGCCTGTGTACAACAATGCT  5764          _____
                                AGCATTGT    ACAGGTG
                                ||||||||    |||||||
                                TCGTAACA    TGTCCGT
                                     ACATG
GAM723  DDX11   5'  AGCGTAGCAATGCTGC     15298          ACAGG
                                GCAGCATTGT    TGCT
                                ||||||||||    ||||
                                CGTCGTAACG    GCGA
                                      AT___
GAM723  DGKA    3'  AGGCTCTGTACATTGCTGC   7200       T       T
                                GCAGCA TGTACAGG GCTT
                                |||||| |||||||| ||||
                                CGTCGT ACATGTCT CGGA
                                   T      _
GAM723  HAT1    3'  TCTGTACAATGTGCT      13318      G
                                AGCA CATTGTACAGG
                                |||| ||||||||||
                                TCGT GTAACATGTCT
                                  _
GAM723  HNF3B   3'  AAGCACCTGCAGATTCTG   41413     C   GTA
                                CAG ATT   CAGGTGCTT
                                ||| |||   |||||||||
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                                GTC TAG   GTCCACGAA
                                  T   AC_
GAM723   IFNAR2   3'  AAGCACCTACAGGGTTCT    6035     C   A    AC
                                AG AGC TTGT  AGGTGCTT
                                || ||| ||||  ||||||||
                                TC TTG GACA  TCCACGAA
                                 _   G    __
GAM723   IL1RN    3'  AAGCACCTAGCCTCGCTCT   5140     C   ATT  AC
                                AG AGC   GT  AGGTGCTT
                                || |||   ||  ||||||||
                                TC TCG   CG  TCCACGAA
                                 _   CTC  A_
GAM723   ITPR1    3'  AAGCACCTGATTTGC       9441      TT  A
                                GCA  GT CAGGTGCTT
                                |||  || |||||||||
                                CGT  TA GTCCACGAA
                                  T_  _
GAM723   JJAZ1    3'  AGGATCAATGCTGCT       31074          TACAG  G
                                AGCAGCATTG    GT CT
                                ||||||||||    || ||
                                TCGTCGTAAC    TA GA
                                      _____  G
GAM723   KCNN4    3'  CACTCTCACTATGCTGCT    9566         T  ACA
                                AGCAGCAT GT   GGTG
                                |||||||| ||   ||||
                                TCGTCGTA CA   TCAC
                                     T  CTC
GAM723   MADD     3'  AGTGCACGATGCTGCT     55352          ACAG TG
                                AGCAGCATTGT   G  CT
                                ||||||||||   |  ||
                                TCGTCGTAGCA   C  GA
                                      ____ GT
GAM723   MADD     3'  AGTGCACGATGCTGCT     55341          ACAG TG
                                AGCAGCATTGT   G  CT
                                ||||||||||   |  ||
                                TCGTCGTAGCA   C  GA
                                      ____ GT
GAM723   MADD     3'  AGTGCACGATGCTGCT     55329          ACAG TG
                                AGCAGCATTGT   G  CT
                                ||||||||||   |  ||
                                TCGTCGTAGCA   C  GA
                                      ____ GT
GAM723   MADD     3'  AGTGCACGATGCTGCT     55346          ACAG TG
                                AGCAGCATTGT   G  CT
                                ||||||||||   |  ||
                                TCGTCGTAGCA   C  GA
                                      ____ GT
GAM723   MADD     3'  AGTGCACGATGCTGCT     13461          ACAG TG
                                AGCAGCATTGT   G  CT
                                ||||||||||   |  ||
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                                TCGTCGTAGCA   C  GA
                                      ____ GT
GAM723  MADD    3'  AGTGCACGATGCTGCT     55336          ACAG TG
                                AGCAGCATTGT   G  CT
                                ||||||||||   |  ||
                                TCGTCGTAGCA   C  GA
                                      ____ GT
GAM723  MAT1A   3'  AAGCACCTGTAATGTGC     90824      TG
                                GCAT  TACAGGTGCTT
                                ||||  ||||||||||
                                CGTG  ATGTCCACGAA
                                  TA
GAM723  MGAT5   3'  AGCCCTGCACCATGCTGCT   10021        T  A   T
                                AGCAGCAT GT CAGG GCT
                                |||||||| || |||| |||
                                TCGTCGTA CA GTCC CGA
                                     C  C   _
GAM723  MME     3'  ATGTGTCCAATGCTGC      23485         T   G
                                GCAGCATTG ACA GT
                                ||||||||| ||| ||
                                CGTCGTAAC TGT TA
                                     C   G
GAM723  MME     3'  ATGTGTCCAATGCTGC      6138          T   G
                                GCAGCATTG ACA GT
                                ||||||||| ||| ||
                                CGTCGTAAC TGT TA
                                     C   G
GAM723  MME     3'  ATGTGTCCAATGCTGC      23505         T   G
                                GCAGCATTG ACA GT
                                ||||||||| ||| ||
                                CGTCGTAAC TGT TA
                                     C   G
GAM723  MME     3'  ATGTGTCCAATGCTGC      23495         T   G
                                GCAGCATTG ACA GT
                                ||||||||| ||| ||
                                CGTCGTAAC TGT TA
                                     C   G
GAM723  NOTCH2  3'  TTTGTAAATGCTGCT       44318         G
                                AGCAGCATT TACAGG
                                ||||||||| ||||||
                                TCGTCGTAA ATGTTT
                                          _
GAM723  OLR1    3'  AAGTGTCACAATGCTCCT     10334    C       ACA  TG
                                AG AGCATTGT   GG  CTT
                                || ||||||||   ||  |||
                                TC TCGTAACA   CT  GAA
                                 C       ___  GT
GAM723  PKHD1   5'  AAGCACAAAAGCTATGCTGCT  56911         T  ACAG
                                AGCAGCAT GT    GTGCTT
                                |||||||| ||    ||||||
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                                TCGTCGTA CG    CACGAA
                                     T  AAAA
GAM723  POP2     3'  AAGCACCTAGCACATGCCGT  42143    A   _   AC
                                GC GCAT TGT  AGGTGCTT
                                || |||| |||  ||||||||
                                TG CGTA ACG  TCCACGAA
                                 C    C   A_
GAM723  RUNX3    3'  AAGCACCTACAGACCGGCT   15107     AGCA    AC
                                AGC    TTGT  AGGTGCTT
                                |||    ||||  ||||||||
                                TCG    GACA  TCCACGAA
                                  GCCA   __
GAM723  SH3BP2   3'  CACACAATGCTGCT        11594          ACAG
                                AGCAGCATTGT    GTG
                                ||||||||||    |||
                                TCGTCGTAACA    CAC
                                      _____
GAM723  SLC1A3   3'  AAGCACCTGCCCTCTGTT    14796      CATTGTA
                                AGCAG      CAGGTGCTT
                                |||||      |||||||||
                                TTGTC      GTCCACGAA
                                   TCCC___
GAM723  SLC20A2  3'  ACTATGGAAATGCTGCT     22174         GTA  _
                                AGCAGCATT   CA GGT
                                |||||||||   || |||
                                TCGTCGTAA   GT TCA
                                      AG_  A
GAM723  SRM      3'  AAGCCCCAGAATGCTGC      11955        GTACA  T
                                GCAGCATT    GG GCTT
                                ||||||||    || ||||
                                CGTCGTAA    CC CGAA
                                     GAC__  _
GAM723  SUOX     5'  AGGTCTGCTACAATGCTGCT   4851           _   GT
                                AGCAGCATTGTA CAG  GCTT
                                |||||||||||| |||  ||||
                                TCGTCGTAACAT GTC  TGGA
                                       C   __
GAM723  TJP1     3'  ATTTGTGATACAATGCTGT    12295          ___
                                GCAGCATTGT   ACAGGT
                                |||||||||   ||||||
                                TGTCGTAACA   TGTTTA
                                      TAG
GAM723  UTY      3'  AAGCAACTGGACACAGTGCTGC 23066          A__   G
                                GCAGCATTGT   CAG TGCTT
                                |||||||||   ||| |||||
                                CGTCGTGACA   GTC ACGAA
                                      CAG   A
GAM723  WNT7A    3'  CACCCAATGCTGCT        16119          TACA
                                AGCAGCATTG    GGTG
                                |||||||||    ||||
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                                TCGTCGTAAC   CCAC
                                      ____
GAM723  AKAP11   3'  ATTTGCCAATGCTGC      32701        TA
                                GCAGCATTG  CAGGT
                                |||||||||  |||||
                                CGTCGTAAC  GTTTA
                                     C_
GAM723  ANKRD6   3'  TTGTAATAAAATGCTGCT    30093        G___
                                AGCAGCATT   TACAG
                                |||||||||   |||||
                                TCGTCGTAA   ATGTT
                                     AATA
GAM723  C1orf19  3'  ACTTGTCAACACTGCT     68187      CA  T
                                AGCAG  TTG ACAGGT
                                |||||  ||| ||||||
                                TCGTC  AAC TGTTCA
                                   AC  _
GAM723  CDC14B   3'  AAGCACCTGCCAGCACCGC   52841    AT  A__
                                GC  TGT   CAGGTGCTT
                                ||  |||   |||||||||
                                CG  ACG   GTCCACGAA
                                 CC   ACC
GAM723  D15Wsu75e 3'  TGTAGACAATGCTGCT     66650          __
                                AGCAGCATTGT  ACA
                                ||||||||||  |||
                                TCGTCGTAACA  TGT
                                      GA
GAM723  EDG2     3'  AGCAAACAATGCTCT      54061    C      ACAGG
                                AG AGCATTGT    TGCT
                                || ||||||||    ||||
                                TC TCGTAACA    ACGA
                                 _      A____
GAM723  EDG2     3'  AGCAAACAATGCTCT      7378     C      ACAGG
                                AG AGCATTGT    TGCT
                                || ||||||||    ||||
                                TC TCGTAACA    ACGA
                                 _      A____
GAM723  EPHA7    3'  GCATAGAATGCTGCT      15434        G ACAG
                                AGCAGCATT T   GTGC
                                ||||||||| |   ||||
                                TCGTCGTAA A   TACG
                                     G ____
GAM723  FADS1    3'  AAGCACCTGAACCACTGT   25468     CATT  A
                                GCAG   GT CAGGTGCTT
                                ||||   || |||||||||
                                TGTC   CA GTCCACGAA
                                  AC__  A
GAM723  FLJ10246 3'  TGCCACAATGCTGCT      35944          ACA
                                AGCAGCATTGT   GGTG
                                ||||||||||   ||||
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                              TCGTCGTAACA  CCGT
                                    ___
GAM723  FLJ10307 3' AGCTAACGATGCTGCT     36004         ACAGGT
                              AGCAGCATTGT    GCT
                              ||||||||||     |||
                              TCGTCGTAGCA    CGA
                                    AT____
GAM723  FLJ11155 5' AAGCACCTGCCTCAGCTG   37116     AT  TA_
                              CAGC  TG  CAGGTGCTT
                              ||||  ||  |||||||||
                              GTCG  AC  GTCCACGAA
                                __ TCC
GAM723  FLJ13848 3' AAGCACCTAACAGCT      45457     AT  AC
                              AGC  TGT  AGGTGCTT
                              |||  |||  ||||||||
                              TCG  ACA  TCCACGAA
                                __  A_
GAM723  FLJ20128 3' AAGCACCTCAGCGCACTTGC  34595     CAT  AC
                              GCAG  TGT  AGGTGCTT
                              ||||  |||  ||||||||
                              CGTT  GCG  TCCACGAA
                                CAC  AC
GAM723  FLJ20281 5' AAGCACCTTGAGTTACTGGCT 90976     ATT  _ ___
                              AGC  GTA C  AGGTGCTT
                              |||  ||| |  ||||||||
                              TCG  CAT G  TCCACGAA
                                GT_  T AGT
GAM723  FLJ20716 3' AAGTGTTACAATGCCGCT    35598     A      CAG TG
                              AGC GCATTGTA  G  CTT
                              ||| ||||||||  |  |||
                              TCG CGTAACAT  T  GAA
                                C       ___ GT
GAM723  FLJ21709 3' AAGCACCTAGAGCAGCTCT   77917    C  AT  AC_
                              AG AGC  TGT  AGGTGCTT
                              || |||  |||  ||||||||
                              TC TCG  ACG  TCCACGAA
                               _  __  AGA
GAM723  FLJ22626 3' GCTTTACAGTGCTACT      44553    C       C
                              AG AGCATTGTA AGGT
                              || |||||||| ||||
                              TC TCGTGACAT TTCG
                               A       _
GAM723  FLJ23056 3' ACCACAATGCTGCT        44720         ACA
                              AGCAGCATTGT  GGT
                              ||||||||||   |||
                              TCGTCGTAACA  CCA
                                    ___
GAM723  HEF1     3' AAGCACCTTCTAATGCTGC   21134        TAC
                              GCAGCATTG  AGGTGCTT
                              |||||||||  ||||||||
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                                CGTCGTAAT   TCCACGAA
                                     CT_
GAM723  HEMK     3'  AAGCTCCAACACAAATGCTGC  32423        _  ACA  T
                                GCAGCATT GT   GG GCTT
                                |||||||| ||   || ||||
                                CGTCGTAA CA   CC CGAA
                                     A  CAA  T
GAM723  HRH3     3'  AAGCACCTGGGTGTGCT     23363      TGTA
                                AGCAT    CAGGTGCTT
                                |||||    |||||||||
                                TCGTG    GTCCACGAA
                                   TGG_
GAM723  HSA243666 3'  AGTCCCACTCAATGCTGCT   34145         TACA  TG
                                AGCAGCATTG    GG  CT
                                ||||||||||    ||  ||
                                TCGTCGTAAC    CC  GA
                                      TCA_  CT
GAM723  IMAGE:4907098 5'  AAGCACCTGCACTTGCT     91655      TT  A
                                AGCA  GT CAGGTGCTT
                                ||||  || |||||||||
                                TCGT  CA GTCCACGAA
                                  T_  C
GAM723  KCNMB2   5'  ACCTTGGTATAAATGCTGCT   19538         _    __
                                AGCAGCATT GTAC  AGGT
                                ||||||||| ||||  ||||
                                TCGTCGTAA TATG  TCCA
                                      A    GT
GAM723  KIAA0276  3'  AAGCACACAGACAGTGCTACT  70960    C       ACAG
                                AG AGCATTGT    GTGCTT
                                || ||||||||    ||||||
                                TC TCGTGACA    CACGAA
                                 A       GACA
GAM723  KIAA0472  5'  AGATCTTAAATGCTGC      71852        GTAC    G
                                GCAGCATT    AGGT CT
                                ||||||||    |||| ||
                                CGTCGTAA    TCTA GA
                                     AT__    _
GAM723  KIAA0513  3'  AGCAAACAGTGCTGCT      28337          ACAGG
                                AGCAGCATTGT     TGCT
                                ||||||||||     ||||
                                TCGTCGTGACA     ACGA
                                      A____
GAM723  KIAA0555  3'  AAGCTACTTTGTACAATGCTCT 60110    C         _ _
                                AG AGCATTGTACAG GT GCTT
                                || |||||||||||| || ||||
                                TC TCGTAACATGTT CA CGAA
                                 _         T  T
GAM723  KIAA0779  3'  AAGTCTTGCTGTAAATGCTGC  85722        G    GT__
                                GCAGCATT TACAG    GCTT
                                |||||||| |||||    ||||
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                                CGTCGTAA ATGTC   TGAA
                                     _   GTTC
GAM723  KIAA1265  3'  ACTTGTACAATGCTGT     70786
                                GCAGCATTGTACAGGT
                                ||||||||||||||||
                                TGTCGTAACATGTTCA

GAM723  KIAA1878  3'  CACCTGTCCAATGCTGCT    91709         T
                                AGCAGCATTG ACAGGTG
                                |||||||||| |||||||
                                TCGTCGTAAC TGTCCAC
                                      C
GAM723  KIAA1879  5'  AAGCAGGAGCTGGACAATGCTG 73558          A  G___
            CT                    AGCAGCATTGT CAG   TGCTT
                                ||||||||||| |||   |||||
                                TCGTCGTAACA GTC   ACGAA
                                      G  GAGG
GAM723  KIAA1958  3'  AAGACTCAACCAATGCTGC   81897        TACA  G
                                GCAGCATTG   GGT CTT
                                |||||||||   ||| |||
                                CGTCGTAAC   TCA GAA
                                     CAAC  _
GAM723  KRTHB5    3'  AAGCACCTGCCTGCCTGC    9651      _ TTGTA
                                GCAG CA    CAGGTGCTT
                                |||| ||    |||||||||
                                CGTC GT    GTCCACGAA
                                  C  CC___
GAM723  LRRN3     3'  AAGCTTCACCAATGCTGCT   69437        TACA  T
                                AGCAGCATTG   GG GCTT
                                ||||||||||   || ||||
                                TCGTCGTAAC   CT CGAA
                                     CA__  T
GAM723  MGC12945  5'  AAGTGTGTACCATGCTGCT   50297        T   GG
                                AGCAGCAT GTACA  TGCTT
                                |||||||| |||||  |||||
                                TCGTCGTA CATGT  GTGAA
                                     C    __
GAM723  MGC1842   3'  AAGCACCTGCTGGCTGCT    65633      ATTGTA
                                AGCAGC     CAGGTGCTT
                                ||||||     |||||||||
                                TCGTCG     GTCCACGAA
                                   GTC___
GAM723  MGC20470  3'  GGGACACCAATGCTGCT     58964        GTACA  _
                                AGCAGCATT    GGTG CTT
                                |||||||||    |||| |||
                                TCGTCGTAA    CCAC GGG
                                     _____   A
GAM723  MGC23980  3'  AAGCACTTAGAACAGTGC    58757       AC_
                                GCATTGT   AGGTGCTT
                                |||||||   ||||||||
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                                CGTGACA   TTCACGAA
                                    AGA
GAM723  MGC26914  3'  AGCACGTAACAATGCT      58664        _  AG
                                AGCATTGT AC  GTGCT
                                |||||||| ||  |||||
                                TCGTAACA TG  CACGA
                                    A  __
GAM723  MGC33887  5'  AGCTTCACAATGCTGT      58872         ACA  T
                                GCAGCATTGT   GG GCT
                                ||||||||||   || |||
                                TGTCGTAACA   CT CGA
                                      ___  T
GAM723  PAK2      5'  AAGCACCTGCAGTAGTG     66534       TA_
                                CATTG   CAGGTGCTT
                                |||||   |||||||||
                                GTGAT   GTCCACGAA
                                   GAC
GAM723  PARVA     3'  AAGCAAATGTACAATATGCT  36648      GC      GG
                                AGCA  ATTGTACA  TGCTT
                                ||||  ||||||||  |||||
                                TCGT  TAACATGT  ACGAA
                                  A_       AA
GAM723  PLAC3     3'  GTTCCACACATGCTGCT     69346        _  ACA  T
                                AGCAGCAT TGT   GG GC
                                |||||||| |||   || ||
                                TCGTCGTA ACA   CC TG
                                    C   ___  T
GAM723  PP1665    5'  AAGCACTTGGAACAATGC    47909        A_
                                GCATTGT  CAGGTGCTT
                                |||||||  |||||||||
                                CGTAACA  GTTCACGAA
                                    AG
GAM723  Rab11-FIP2 3'  AAGGATCACAGTGCTGCT   29778          ACA   G
                                AGCAGCATTGT   GGT CTT
                                ||||||||||   ||| |||
                                TCGTCGTGACA   CTA GAA
                                      ___  G
GAM723  SLC6A14   3'  CACATACAGTGCTGCT      23347          CAG
                                AGCAGCATTGTA   GTG
                                ||||||||||||   |||
                                TCGTCGTGACAT   CAC
                                      A__
GAM723  SMCR5     3'  AAGTCATCTGCACAAGGCT   58588     A   A    _
                                AGC TTGT CAGGTG CTT
                                ||| |||| |||||| |||
                                TCG AACA GTCTAC GAA
                                  G   C     T
GAM723  WAP1      3'  ATCCGTACATGCTGCT      79512         T   A
                                AGCAGCAT GTAC GGT
                                |||||||| |||| |||
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                                TCGTCGTA CATG CTA
                                    _   C
GAM723  ZNF323   3' AAGTTATCTAAATGCTGCT   48075       GTAC   _
                                AGCAGCATT   AGGTG CTT
                                |||||||||   ||||| |||
                                TCGTCGTAA   TCTAT GAA
                                    A___    T
GAM723  LOC115442 5' ACTTGTATAAATGCTGCT   72675       _
                                AGCAGCATT GTACAGGT
                                ||||||||| ||||||||
                                TCGTCGTAA TATGTTCA
                                    A
GAM723  LOC122553 3' AAGCACCTGAATTGTGCTTCT 74128   C   T A
                                AG AGCAT GT CAGGTGCTT
                                || ||||| || |||||||||
                                TC TCGTG TA GTCCACGAA
                                 T   T A
GAM723  LOC124045 3' AAGCACCTTTGCATGGC    76030   AT   C
                                GC  TGTA AGGTGCTT
                                ||  |||| ||||||||
                                CG  ACGT TCCACGAA
                                 GT   T
GAM723  LOC144481 3' AAGCACCTGTACACAAGC   83091   AT_
                                GC   TGTACAGGTGCTT
                                ||   ||||||||||||
                                CG   ACATGTCCACGAA
                                 AAC
GAM723  LOC144559 5' TGTTTGTATAATGCCACT   76884   CA       GT
                                AG  GCATTGTACAG  G
                                ||  |||||||||||  |
                                TC  CGTAATATGTT  T
                                 AC         TG
GAM723  LOC145601 3' CACCCAGTGCTGCT       83363         TACA
                                AGCAGCATTG   GGTG
                                ||||||||||   ||||
                                TCGTCGTGAC   CCAC
                                     ____
GAM723  LOC149050 3' AGCTCCTTGTACAACACGC   60428   AGCA     _ T
                                GC   TTGTACA GG GCT
                                ||   ||||||| || |||
                                CG   AACATGT CC CGA
                                 CAC_     T  T
GAM723  LOC149175 3' AAGCACCTTCCTATGTGCT   79205     G  TGTAC
                                AGCA CAT    AGGTGCTT
                                |||| |||    ||||||||
                                TCGT GTA    TCCACGAA
                                  _  TCCT_
GAM723  LOC149351 5' GAGTAGCACAGTGCTGCT   79307         ACAGG
                                AGCAGCATTGT    TGCTT
                                ||||||||||    |||||
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                                TCGTCGTGACA    ATGAG
                                      CG___
GAM723  LOC196411 3'  TCTGTACAAGGCTGCT     87688       A
                                AGCAGC TTGTACAGG
                                |||||| |||||||||
                                TCGTCG AACATGTCT
                                   G
GAM723  LOC200583 3'  AAGCAATTAACAGTGCTACT  88831    C      ACAGG
                                AG AGCATTGT    TGCTT
                                || ||||||||    |||||
                                TC TCGTGACA    ACGAA
                                 A       ATTA_
GAM723  LOC201304 3'  CACTTCATGCTGCT       88228        T TAC
                                AGCAGCAT G   AGGTG
                                |||||||| |   |||||
                                TCGTCGTA C   TTCAC

                                   _ ___
GAM723  LOC219918 5'  TGTTTGTATAATGCCACT    91543    CA       GT
                                AG  GCATTGTACAG  G
                                ||  ||||||||||  |
                                TC  CGTAATATGTT  T
                                 AC          TG
GAM723  LOC220071 5'  TGTTTGTATAATGCCACT    93438    CA       GT
                                AG  GCATTGTACAG  G
                                ||  ||||||||||  |
                                TC  CGTAATATGTT  T
                                 AC          TG
GAM723  LOC220766 5'  AAGCACCTAAACAGGT      90789    A   AC
                                GC TTGT  AGGTGCTT
                                || ||||  ||||||||
                                TG GACA  TCCACGAA
                                 _   AA
GAM723  LOC221773 3'  AAGCACCTAGTAAGTGCCTGCT 91033      _   G  _
                                AGCAG CATT TAC AGGTGCTT
                                ||||| |||| ||| ||||||||
                                TCGTC GTGA ATG TCCACGAA
                                   C   _  A
GAM723  LOC253517 3'  AAGCACCTTTGCATGGC     95103    AT   C
                                GC  TGTA AGGTGCTT
                                ||  |||| ||||||||
                                CG  ACGT TCCACGAA
                                 GT   T
GAM723  LOC254045 3'  AAGCACCTGTACACAAGC    96500    AT_
                                GC   TGTACAGGTGCTT
                                ||   ||||||||||||
                                CG   ACATGTCCACGAA
                                 AAC
GAM723  LOC254173 3'  TCTGTACATGCTGCT       96845        T
                                AGCAGCAT GTACAGG
                                |||||||| |||||||
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                                TCGTCGTA CATGTCT
                                        _
GAM723  LOC254611 5'  AAGCACCTATCCAAACTGT   97604     CA   TAC
                                GCAG  TTG   AGGTGCTT
                                ||||  |||   ||||||||
                                TGTC  AAC   TCCACGAA
                                  A_   CTA
GAM723  LOC255736 5'  ACTTAGTGTACAATGCTGT   95332           ___
                                GCAGCATTGTACA   GGT
                                ||||||||||||   |||
                                TGTCGTAACATGT   TCA
                                       GAT
GAM723  LOC255855 3'  AGCAACTATGCTGCT      96224        T  ACAGG
                                AGCAGCAT GT    TGCT
                                ||||||||  ||    ||||
                                TCGTCGTA CA    ACGA
                                     T  _____
GAM723  LOC257438 3'  AGCTAACGATGCTGCT     93969          ACAGGT
                                AGCAGCATTGT     GCT
                                ||||||||||      |||
                                TCGTCGTAGCA     CGA
                                      AT____
GAM723  LOC57826  3'  ATTTGCACAGATGCTGCT    41015        _  A
                                AGCAGCAT TGT CAGGT
                                ||||||||  |||  |||||
                                TCGTCGTA ACA GTTTA
                                     G   C
GAM723  LOC64744  3'  CACCTGTATGGCTGC      61796      ATT
                                GCAGC   GTACAGGTG
                                |||||   |||||||||
                                CGTCG   TATGTCCAC
                                   G__
GAM723  LOC90906  3'  TGTTTGTATAATGCTACT    64316    C         GT
                                AG AGCATTGTACAG  G
                                ||  ||||||||||||  |
                                TC TCGTAATATGTT  T
                                 A          TG
GAM723  LOC90906  3'  AAGCACCTGATCTTGT      64290     TT  A
                                GCA  GT CAGGTGCTT
                                |||  ||  |||||||||
                                TGT  TA GTCCACGAA
                                  TC  _
GAM723  LOC93268  5'  AAGCACCTAGGTAGCAGC    71874    A  ATTG  __
                                GC GC    TAC  AGGTGCTT
                                ||  ||    |||  ||||||||
                                CG CG    ATG  TCCACGAA
                                 A  _____   GA
GAM724  CNGA1     3'  CAACTGATAATGTGCAAA    59507          GC   A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
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                                AAACGTGTAAT  GTC AAC
                                      A_  _
GAM724  ESRRG    3'  TGGCAGTCTTATGTGCAAA   66396        TAGCT
                                TTTGCACAT    AGATTGCCA
                                |||||||||    |||||||||
                                AAACGTGTA    TCTGACGGT
                                     T____
GAM724  KCNJ3    3'  GCAATAATGTGCAAA      9525          GCTAGA
                                TTTGCACATTA     TTGC
                                ||||||||||     ||||
                                AAACGTGTAAT     AACG
                                       ______
GAM724  SDC2     3'  GCAAATTAATGTGTAAA    67132          CTAGA
                                TTTGCACATTAG    TTGC
                                ||||||||||||    ||||
                                AAATGTGTAATT    AACG
                                      A____
GAM724  USP9X    3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
              A                  TTTGCACATTAGC     GCCAT
                                 ||||||||||||      |||||
                                 AAATGTGTAATCG     CGGTA
                                       TAGTC_
GAM724  AMOTL1   3'  GGCAAGTAATGTGCAAA    73650         G  AGAT
                                TTTGCACATTA CT    TGCC
                                |||||||||| ||    ||||
                                AAACGTGTAAT GA    ACGG
                                      _ ____
GAM724  BCAR3    3'  AGTAATAATGTGCAAA     13098         __
                                TTTGCACATTA  GCT
                                ||||||||||  |||
                                AAACGTGTAAT  TGA
                                      AA
GAM724  DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930         AGCTA    C
                                TTTGCACATT     GATTG CA
                                ||||||||||     ||||| ||
                                AGACGTGTAA     TTAAC GT
                                     A____     A
GAM724  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                TTTGCACATTAG  AGA TG CAT
                                ||||||||||||  ||| || |||
                                AGACGTGTAATC  TTT AC GTA
                                      __  T  A
GAM724  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
              AA                  TTTGCACATTAGCTAGATTGCCAT
                                  ||||||||||||||||||||||||
                                  AAACGTGTAATCGATCTAACGGTA

GAM725  ADAM19   3'  CAGGAAGAAGACTGGCCATTAT 52703       C    CTGAG
              G                   CATGA GGCT     TTCTTCCTG
                                  ||||| ||||     |||||||||
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                                GTATT CCGG    AAGAAGGAC
                                   A   TCAG_
GAM725  FACL5    5' CAGGAAGAACTCAGAGCCG   64186
                                CGGCTCTGAGTTCTTCCTG
                                ||||||||||||||||||
                                GCCGAGACTCAAGAAGGAC

GAM725  GNAL     5' CAGGAAAGAGAGGAGCCGTCG 9058          GAG TC
                                TGACGGCTCT  T  TTCCTG
                                ||||||||||  |  ||||||
                                GCTGCCGAGG  A  AAGGAC
                                      AG_ GA
GAM725  KAL1     3' CAGGAAGAACTTCTGTCA    4013       CTCT
                                TGACGG   GAGTTCTTCCTG
                                ||||||   ||||||||||||
                                ACTGTC   TTCAAGAAGGAC
                                  ____
GAM725  MYO1E    3' CAGGAGGACAAAACCACCATG 17187     AC  CTC  AGT
                                CATG  GG  TG  TCTTCCTG
                                ||||  ||  ||  ||||||||
                                GTAC  CC  AC  AGGAGGAC
                                  CA  AAA  ___
GAM725  PRKAR2B  3' CAGAAAGAACTCAGATGT    10804   _        C
                                GC TCTGAGTTCTT CTG
                                || ||||||||||| |||
                                TG AGACTCAAGAA GAC
                                 T         A
GAM725  PUM2     3' AGGATCAAAGCTGTCATG    31014         C   GTTCT
                                CATGACGGCT TGA    TCCT
                                |||||||||| |||    ||||
                                GTACTGTCGA ACT    AGGA
                                      A  _____
GAM725  SKI      3' CAGGAAGTGCAGAGCCGCA   11701    A      AGTT
                                TG CGGCTCTG   CTTCCTG
                                || ||||||||   |||||||
                                AC GCCGAGAC   GAAGGAC
                                 _      GT__
GAM725  TEM8     3' AGGAAGATGCAACCCCATG   36326     AC  CTC  AGT
                                CATG  GG  TG  TCTTCCT
                                ||||  ||  ||  |||||||
                                GTAC  CC  AC  AGAAGGA
                                  C_  A__  GT_
GAM725  ARHGEF4  5' AGAAAAAACTCAGGGC      52207         C  C
                                GCTCTGAGTT TT CT
                                |||||||||| || ||
                                CGGGACTCAA AA GA
                                      A  A
GAM725  FLJ31978 3' CAGGAAGGAACAAGCGCC    58348     T  GAG
                                GGC CT   TTCTTCCTG
                                ||| ||   |||||||||
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                                CCG GA   AGGAAGGAC
                                  C  ACA
GAM725  HSU24186  5'  AGAACTCAAAGCCGTC      25324        C
                                GACGGCT TGAGTTCT
                                ||||||| ||||||||
                                CTGCCGA ACTCAAGA
                                    A
GAM725  KCNT1     3'  AGCTCCCAGGGCCGCCA     61825    A     __
                                TG CGGCTCT  GAGTT
                                || |||||||  |||||
                                AC GCCGGGA  CTCGA
                                 C      CC
GAM725  KIAA1867  3'  CAGGAAGAACCCAAGAGCTCAT 94822      CG    GA_
                                ATGA  GCTCT   GTTCTTCCTG
                                ||||  |||||   ||||||||||
                                TACT  CGAGA   CAAGAAGGAC
                                  __    ACC
GAM725  KIAA1878  3'  AATTCAGAGAATCGTCATG    91707         __
                                CATGACGG  CTCTGAGTT
                                ||||||||  |||||||||
                                GTACTGCT  GAGACTTAA
                                    AA
GAM725  MFN1      3'  CAGGAAGAACTCATGA      35541    _
                                TC TGAGTTCTTCCTG
                                || ||||||||||||
                                AG ACTCAAGAAGGAC
                                 T
GAM725  MIDORI    3'  CAGGGCCCTTCCAGAGCCTGTC 73784       _      AGTTCT
            ATG                   CATGAC GGCTCTG     TCCTG
                                ||||||| |||||||      |||||
                                GTACTG CCGAGAC     GGGAC
                                   T      CTTCCC
GAM725  MYH7B     3'  CAGGAAGAACCTGGCTCGCATG 70530      A  _   CTGA
                                CATG CG GCT    GTTCTTCCTG
                                |||| || |||    ||||||||||
                                GTAC GC CGG    CAAGAAGGAC
                                  _  T   TC__
GAM725  RNAHP     3'  AGAAAGCAGCAGCCGTCAT    23761         _   AG
                                ATGACGGCT CTG  TTCT
                                ||||||||| |||  ||||
                                TACTGCCGA GAC  AAGA
                                    C   GA
GAM725  SLC37A1   3'  AGACGGAGCTCAGACCC      38561    C        TC
                                GG TCTGAGTTCT  CT
                                || ||||||||||  ||
                                CC AGACTCGAGG  GA
                                 C         CA
GAM725  LOC116236 3'  CAGGAAAAGCACAAACCTCAT  73809      C  CTC  A   C
                                ATGA GG   TG GTT TTCCTG
                                |||| ||   || ||| ||||||
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                                TACT CC   AC CGA AAGGAC
                                  _ AA_ A   A
GAM725  LOC124801 3'  CAGGAAGAACTCTCTTGCATG  74336     A   CTCT
                                CATG CGG    GAGTTCTTCCTG
                                |||| |||    ||||||||||||
                                GTAC GTT    CTCAAGAAGGAC
                                  _   CT__
GAM725  LOC222160 5'  AGGAAGAACTCACCCC      94117    CTC
                                GG   TGAGTTCTTCCT
                                ||   ||||||||||||
                                CC   ACTCAAGAAGGA
                                 CC_
GAM725  LOC51094  3'  CAGGAAGAATAAAGCC      32045      CTGA
                                GGCT    GTTCTTCCTG
                                ||||    ||||||||||
                                CCGA    TAAGAAGGAC
                                  AA__
GAM725  LOC92078  3'  CAGGAAGAAGAATCGACCGTC  67977      C  T  G__
                                GACGG TC GA   TTCTTCCTG
                                ||||| || ||   |||||||||
                                CTGCC AG CT   AAGAAGGAC
                                  _ _ AAG
GAM726  DRD2     3'  CCAGACTGCAGGTTGGACCCC  5842     AACG  TT   A_
                                GG    CT  GCC  CAGTCTGG
                                ||    ||  |||  ||||||||
                                CC    GG  TGG  GTCAGACC
                                 CCA_  T_   AC
GAM726  DKFZP434B103 3'  CAGACTGTGACAAACCC     31589    AACGC    C
                                GG     TTTG CACAGTCTG
                                ||     |||| |||||||||
                                CC     AAAC GTGTCAGAC
                                 C_____    A
GAM726  FLJ10737  3'  CCAGACTGCAGCCTGGCCC   36520    AAC   TT  CA
                                GG   GCT  GC  CAGTCTGG
                                ||   |||  ||  ||||||||
                                CC   CGG  CG  GTCAGACC
                                  ___   TC  AC
GAM726  ISL2     3'  CCAGACTGCAGACCCCTGCTCC 70839      A  C___     CAC
          G                      CGGA CG    TTTGC   AGTCTGG
                                |||| ||    |||||   |||||||
                                GCCT GT    AGACG   TCAGACC
                                  C  CCCC    ___
GAM726  K6HF     3'  CCAGACTGCCAGCAGCACCCGT 16270      AAC   TT  CA_
                                ACGG   GCT  GC   CAGTCTGG
                                ||||   |||  ||   ||||||||
                                TGCC   CGA  CG   GTCAGACC
                                  CA_   __  ACC
GAM726  LOC145053 5'  CCAGACTGCGCGCCGCGCCG  83232     AA   TT   CA
                                CGG  CGC  TGC  CAGTCTGG
                                |||  |||  |||  ||||||||
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                                GCC  GCG  GCG  GTCAGACC
                                  __   CC   C_
GAM726  LOC150372 5'  CCAACCAGCAAAGCGCCCC   79792    AA       CACA  C
                                GG  CGCTTTGC    GT TGG
                                ||  ||||||||    || |||
                                CC  GCGAAACG    CA ACC
                                 CC       AC__  _
GAM726  LOC162333 5'  CCAGACTGCAGGTCTCTGTTCC 87127       CTTT   A_
                                GGAACG    GCC  CAGTCTGG
                                ||||||    |||  ||||||||
                                CCTTGT    TGG  GTCAGACC
                                   CTC_   AC
GAM726  LOC221042 3'  CTATGGCAAAGCGTGCC     93184    A         C
                                GG ACGCTTTGCCA AG
                                || ||||||||||| ||
                                CC TGCGAAACGGT TC
                                 G          A
GAM726  LOC90594  3'  TGTGGAAAAGCGTTCC      63472          G
                                GGAACGCTTT CCACA
                                |||||||||| |||||
                                CCTTGCGAAA GGTGT
                                      A
GAM727  ARNT2     3'  AAACAACCCGTGCATCCCTGC  29450     A    TTTTA
                                GTA GGAT     GGGTTGTTT
                                ||| ||||     |||||||||
                                CGT CCTA     CCCAACAAA
                                  C    CGTG_
GAM727  LCT       3'  AACCGTAAAAATCCTT      9697           G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
                                TTCCTAAAAAT CCAA
                                      G
GAM727  RPL15     3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM727  FBXO30    3'  AACTAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                 G        AA
GAM727  KIAA0494  3'  AACAACCCTTACTTAC      28736      GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM727  PRO0641   5'  AAACAACCCCAAAACTTG    26210      GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
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                                GTTC   AAAA CCCAACAAA
                                  ___    C
GAM727   SMT3H2    3'  AACAACATAAAAATCCTTGC   22670          GG
                                GTAAGGATTTTTA  GTTGTT
                                |||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM727   LOC120103 3'  AACCTATGAAAAATCCTTGC   74002          A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
                                CGTTCCTAAAAA   TCCAA
                                       GTA
GAM727   LOC129831 3'  AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  ||  |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM727   LOC133088 5'  AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
           C                     GTA GGATTTTT     TTGTTT
                                |||  ||||||||     ||||||
                                CGT CCTAAAAA     AACAAA
                                  C       GATAA
GAM727   LOC148089 3'  GGCCCTAAAAATTCCTAC     78637     A
                                GTA GGATTTTTAGGGTT
                                |||  ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM727   LOC154547 3'  AACAACATAAAAATCCTTGC   76050          GG
                                GTAAGGATTTTTA  GTTGTT
                                |||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM727   LOC158104 3'  ACAGCCAAAAATCCTTA      60313          AG
                                TAAGGATTTTT  GGTTGT
                                ||||||||||  ||||||
                                ATTCCTAAAAA  CCGACA
                                       __
GAM727   LOC205880 5'  AAACAACCATCATCCTGAC    90709     A    TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM727   LOC221561 3'  AACAACATAAAAATCCTTGC   92130          GG
                                GTAAGGATTTTTA  GTTGTT
                                |||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM727   LOC257591 3'  AACAACATAAAAATCCTTGC   97840          GG
                                GTAAGGATTTTTA  GTTGTT
                                |||||||||||||  ||||||
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                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM727  LOC51145 3' AGCTAAAATCCTTAC      32393          TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
                                CATTCCTAAAA   TCGA
                                      ___
GAM728  FBXW1B   3' TACTTCAGCTACTGATTC    24525    C  T  A  A
                                GA GTC GG TA CTGAAGTA
                                || ||| || || ||||||||
                                CT TAG TC AT GACTTCAT
                                 _  _ _ C
GAM728  FBXW1B   3' TACTTCAGCTACTGATTC    53329    C  T  A  A
                                GA GTC GG TA CTGAAGTA
                                || ||| || || ||||||||
                                CT TAG TC AT GACTTCAT
                                 _  _ _ C
GAM728  FBXW1B   3' TACTTCAGCTACTGATTC    53340    C  T  A  A
                                GA GTC GG TA CTGAAGTA
                                || ||| || || ||||||||
                                CT TAG TC AT GACTTCAT
                                 _  _ _ C
GAM728  NR4A2    3' ACTTCAGTAATGTCTA      20529        CTGGATA
                                TAGACGT      ACTGAAGT
                                |||||||      ||||||||
                                ATCTGTA      TGACTTCA
                                    A_______
GAM728  TAF5     3' TACTTCAGCTAAAACAGC    22712   T  GA_  A
                                G CTG   TA CTGAAGTA
                                | |||   || ||||||||
                                C GAC   AT GACTTCAT
                                 _  AAA  C
GAM728  TAF5     3' TACTTCAGCTAAAACAGC    57401   T  GA_  A
                                G CTG   TA CTGAAGTA
                                | |||   || ||||||||
                                C GAC   AT GACTTCAT
                                 _  AAA  C
GAM728  TPM1     5' TTATTTTCATCCAGACATCTG  4527      C       AACT
                                TAGA GTCTGGAT    GAAGTAA
                                |||| ||||||||    |||||||
                                GTCT CAGACCTA    TTTTATT
                                  A       C___
GAM728  USP21    3' ACCTCAGAGACGTCTA      25012         GGATAA   A
                                TAGACGTCT     CTGA GT
                                |||||||||     |||| ||
                                ATCTGCAGA     GACT CA
                                      _______  C
GAM728  USP21    3' ACCTCAGAGACGTCTA      33361         GGATAA   A
                                TAGACGTCT     CTGA GT
                                |||||||||     |||| ||
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                                ATCTGCAGA     GACT CA
                                       _____   C
GAM728  ZYX      3'  ACCTCAGTTATTGTTTTGATGT 12933        TG___       A
            CTA                    TAGACGTC    GATAACTGA GT
                                   ||||||||    ||||||||| ||
                                   ATCTGTAG    TTATTGACT CA
                                       TTTTG       C
GAM728  DC-TM4F2  3'  ACTGGCATCCAGACATCTG   48170     C      AACTGA
                                   TAGA GTCTGGAT     AGT
                                   |||| ||||||||     |||
                                   GTCT CAGACCTA     TCA
                                     A       CGG___
GAM728  FLJ10287  3'  TTACTTCAGAAATCCAAAC   38846    C    AA
                                   GT TGGAT  CTGAAGTAA
                                   || |||||  |||||||||
                                   CA ACCTA  GACTTCATT
                                    A    AA
GAM728  KIAA1754  3'  TACTTCAGTTACCCTTGC    63242    CT  A
                                   GT  GG TAACTGAAGTA
                                   ||  || ||||||||||
                                   CG  CC ATTGACTTCAT
                                    TT  C
GAM728  SCGF     5'  ACCCCAGACATCCAGACATCTG 11437      C       AA   AA
                                   TAGA GTCTGGAT  CTG  GT
                                   |||| ||||||||  |||  ||
                                   GTCT CAGACCTA  GAC  CA
                                     A       CA   CC
GAM728  LOC153592 5'  TTACTTCATTCCAGACATC    86069    C      TAAC
                                   GA GTCTGGA    TGAAGTAA
                                   || |||||||    ||||||||
                                   CT CAGACCT    ACTTCATT
                                    A      T___
GAM728  LOC158865 5'  TGCTTCCCAGGCGTC       86943         ATAACT
                                   GACGTCTGG     GAAGTA
                                   |||||||||     ||||||
                                   CTGCGGACC     CTTCGT
                                                 _____
GAM728  LOC206185 5'  AGATTATCCAGACATC      90712    C        _
                                   GA GTCTGGATAA CT
                                   || |||||||||| ||
                                   CT CAGACCTATT GA
                                    A         A
GAM728  LOC219404 3'  ACTTCAGTTACCAGAGGTT    93491     G    A
                                   GAC TCTGG TAACTGAAGT
                                   ||| ||||| ||||||||||
                                   TTG AGACC ATTGACTTCA
                                     G    _
GAM728  LOC253782 3'  ACTTCACACAGTCGTCTA    95694       T   GATAAC
                                   TAGACG CTG     TGAAGT
                                   |||||| |||     ||||||
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                                ATCTGC GAC     ACTTCA
                                   T   AC____
GAM728  LOC256277 5'  ACCTCAGTTATCACCTC     94697    C  CTG       A
                                GA GT   GATAACTGA GT
                                || ||   ||||||||| ||
                                CT CA   CTATTGACT CA
                                 C ___       C
GAM728  LOC91266  5'  ACTTCAGTTTTGCCAGAT    65406       AT_
                                GTCTGG   AACTGAAGT
                                ||||||   |||||||||
                                TAGACC   TTGACTTCA
                                   GTT
GAM729  ADAM20    5'  CAGCACTGCAGCTCTGA     13764     A       AT   C
                                TCA AGCTGCAG  TGC TG
                                ||| ||||||||  ||| ||
                                AGT TCGACGTC  ACG AC
                                  C       __  _
GAM729  E2F1      3'  CAATCTGCACTTTGA       84794       C
                                TCAAAG TGCAGATTG
                                |||||| |||||||||
                                AGTTTC ACGTCTAAC
                                   _
GAM729  E2F1      3'  TCACCTTGTCTCTGCAGCCCTG 84803     AA       TTGCCT
           G                     TCA  GCTGCAGA     GTGA
                                |||  ||||||||     ||||
                                GGT  CGACGTCT     CACT
                                  CC       CTGTTC
GAM729  FPRL1     5'  CACTGCATTTGCAGCCTTGA   7589      A       T  CT
                                TCAA GCTGCAGAT GC  GTG
                                |||| ||||||||| ||  |||
                                AGTT CGACGTTTA CG  CAC
                                  C       _  T_
GAM729  FSHPRH1   5'  TCACGGCTCTCTGCAGC     22116        TT   T
                                GCTGCAGA  GCC GTGA
                                ||||||||  ||| ||||
                                CGACGTCT  CGG CACT
                                     CT  _
GAM729  GPR44     3'  CACAGGGTCTGCACT       16522    C     TG
                                AG TGCAGAT  CCTGTG
                                || |||||||  ||||||
                                TC ACGTCTG  GGACAC
                                  _     __
GAM729  IL10RA    3'  CACAGGCATGGAAGCTGTGA   59640     A   GCAGAT
                                TCA AGCT     TGCCTGTG
                                ||| ||||     ||||||||
                                AGT TCGA     ACGGACAC
                                  G   AGGT__
GAM729  ITGA2     3'  ATCACAGACACTACATATCTAA 9371     GC   _______  C     III
           AGCTTTGA                CT  AGAT     TG CTGTGA   T
                                ||  ||||     || ||||||  |
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                                GA  TCTA     AC GACACT   A
                                 AA    TACATC  A     III
GAM729  LZTFL1   3'  ACAATGCAGCTTTGG       39750          GATTGCC
                                TCAAAGCTGCA      TGT
                                ||||||||||       |||
                                GGTTTCGACGT      ACA
                                      A_______
GAM729  MLC1     3'  CACCTCCCTGCAGCTTTGA   30776          ATTGCCT
                                TCAAAGCTGCAG      GTG
                                ||||||||||||      |||
                                AGTTTCGACGTC      CAC
                                      CCTC___
GAM729  MLC1     3'  CACCTCCCTGCAGCTTTGA   57588          ATTGCCT
                                TCAAAGCTGCAG      GTG
                                ||||||||||||      |||
                                AGTTTCGACGTC      CAC
                                      CCTC___
GAM729  MPP3     3'  TCACAGGCAAGCTGACCCT   8638     CTG   A
                                AG   CAG TTGCCTGTGA
                                ||   ||| ||||||||||
                                TC   GTC AACGGACACT
                                 CCA   G
GAM729  OCM      3'  CACAGGCAATGCCTCT     20545    CT   GA
                                AG  GCA  TTGCCTGTG
                                ||  |||  |||||||||
                                TC  CGT  AACGGACAC
                                 TC   __
GAM729  PACE4    3'  GGGAATCCACAGCTCTGG    56347     A    CA    G
                                TCA AGCTG  GATT CC
                                ||| |||||  |||| ||
                                GGT TCGAC  CTAA GG
                                  C    AC    G
GAM729  PACE4    3'  GGGAATCCACAGCTCTGG    10402     A    CA    G
                                TCA AGCTG  GATT CC
                                ||| |||||  |||| ||
                                GGT TCGAC  CTAA GG
                                  C    AC    G
GAM729  PIGK     3'  TCATGGAATCCTGCAGCTTT   66702          _   G  T
                                AAAGCTGCAG ATT CC GTGA
                                |||||||||| ||| || ||||
                                TTTCGACGTC TAA GG TACT
                                      C   _  _
GAM729  RNMT     3'  CACCACCTGCAGCTTGA     13711      A      AT  CCT
                                TCAA GCTGCAG  TG   GTG
                                ||||  |||||||  ||   |||
                                AGTT CGACGTC  AC   CAC
                                  _      C_  ____
GAM729  STARD4   3'  TCACAGCTCACTGCAGCTTTGA 57517            ATT  C
                                TCAAAGCTGCAG   GC TGTGA
                                ||||||||||||   || |||||
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                                AGTTTCGACGTC   CG ACACT
                                      ACT  _
GAM729  TUFT1    3'  CAGTGAACCTAAGCTTTGA   39255       GC  A  GC
                                TCAAAGCT  AG TT  CTG
                                ||||||||  || ||  |||
                                AGTTTCGA  TC AA  GAC
                                    A_  C  GT
GAM729  C11orf9  3'  CACTCATTCTCAGCTTTGA   25206       C   T  CCT
                                TCAAAGCTG AGA TG   GTG
                                ||||||||| ||| ||   |||
                                AGTTTCGAC TCT AC   CAC
                                      _  T  T__
GAM729  C20orf98 3'  CACAGGCAATTACTAGC    71511     CA
                                GCTG  GATTGCCTGTG
                                ||||  ||||||||||
                                CGAT  TTAACGGACAC
                                  CA
GAM729  C5orf5   5'  CACAGCCGTAGCTTT      33465       AGATT C
                                AAAGCTGC    G CTGTG
                                ||||||||    | |||||
                                TTTCGATG    C GACAC
                                     _____ C
GAM729  C6orf5   3'  CAGCTCACTGCAGCTTTGA   31342         ATT  C
                                TCAAAGCTGCAG   GC TG
                                ||||||||||||   || ||
                                AGTTTCGACGTC   CG AC
                                      ACT  _
GAM729  CHST3    3'  CACAGACAATCTGCCGT     14969    T      C
                                GC GCAGATTG CTGTG
                                || ||||||| |||||
                                TG CGTCTAAC GACAC
                                 C       A
GAM729  FLJ12331 3'  CACAATCAGTGCAGTTTGA   46476      G    GA   CC
                                TCAAA CTGCA  TTG  TGTG
                                ||||| |||||  |||  ||||
                                AGTTT GACGT  GAC  ACAC
                                  _    __   TA
GAM729  FLJ12650 3'  CACAGGCATGGAGCT       44523     G  GAT
                                AGCT CA   TGCCTGTG
                                |||| ||   ||||||||
                                TCGA GT   ACGGACAC
                                  G  ___
GAM729  FLJ14082 5'  CACATGGAGAGCTGCAGCT   46669       ATTG  _
                                AGCTGCAG    CC TGTG
                                ||||||||    || ||||
                                TCGACGTC    GG ACAC
                                    GAGA  T
GAM729  FLJ14326 5'  CACATCCTGCCCCAGCTTTGA  49802        ___    ATTGCC
                                TCAAAGCT   GCAG     TGTG
                                ||||||||   ||||     ||||
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                                AGTTTCGA  CGTC     ACAC
                                     CCC   CT____
GAM729  FLJ23185  3'  CACAGGCCACCGGCTCCAGCTT 46827         C  ATT___
            TGA                   TCAAAGCTG AG     GCCTGTG
                                |||||||||  ||     |||||||
                                AGTTTCGAC TC     CGGACAC
                                     C  GGCCAC
GAM729  FLJ23563  5'  TCACGGTCACCCACAGCTTTGA 67598         CAGAT  C
                                TCAAAGCTG    TG CTGTGA
                                |||||||||    || ||||||
                                AGTTTCGAC    AC GGCACT
                                     ACCC_  T
GAM729  HRH4      3'  ACAGATCTGCACTTTGA     41242       C      TGC
                                TCAAAG TGCAGAT   CTGT
                                ||||||  |||||||   ||||
                                AGTTTC ACGTCTA   GACA
                                  _      ____
GAM729  KIAA1348  3'  CACAAAAATCTGCAAATTTGA  68573      GC       GCC
                                TCAAA  TGCAGATT   TGTG
                                |||||  ||||||||   ||||
                                AGTTT  ACGTCTAA   ACAC
                                   AA       AA_
GAM729  KIAA1579  3'  TCACAAATTGCTGCAGTCTGA  36611     AA      ATTGCC
                                TCA  GCTGCAG     TGTGA
                                |||  |||||||     |||||
                                AGT  TGACGTC     ACACT
                                  C_      GTTAA_
GAM729  MGC11034  3'  TCATTAGAATCCAAGCTTTGA  48789        GCA    GCCT
                                TCAAAGCT   GATT    GTGA
                                ||||||||   ||||    ||||
                                AGTTTCGA   CTAA    TACT
                                     AC_    GAT_
GAM729  MGC20258  5'  CAGGAATCTGCAGCCTGGA    58149    AAA        G
                                TC   GCTGCAGATT CCTG
                                ||   |||||||||| ||||
                                AG   CGACGTCTAA GGAC
                                  GTC         _
GAM729  MGC4832   3'  CACTCTGCAGCTTGGA      59000    A         T
                                TC AAGCTGCAGA TG
                                || |||||||||| ||
                                AG TTCGACGTCT AC
                                  G         C
GAM729  MIC2L1    3'  CACTGGAATCTGCAGC      48819          G  T
                                GCTGCAGATT CC GTG
                                |||||||||| || |||
                                CGACGTCTAA GG CAC
                                       _  T
GAM729  MYO5C     3'  CACAGGTGACAGCTGTGA    38105     A    CAGA TG
                                TCA AGCTG    T  CCTGTG
                                ||| |||||    |  ||||||
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                                AGT TCGAC    A  GGACAC
                                  G     _____ GT
GAM729  NSE1     3'  CACCGTCCACAGCTTTGG    59023         CA   TGCCT
                                TCAAAGCTG  GAT     GTG
                                |||||||||  |||     |||
                                GGTTTCGAC  CTG     CAC
                                     AC   C_____
GAM729  TOLLIP   3'  TCACAAGTGATGCACTTT    38688      C    GA TG C
                                AAAG TGCA  T  C TGTGA
                                |||| ||||  |  | |||||
                                TTTC ACGT  A  G ACACT
                                  _    __ GT A
GAM729  LOC124976 3'  CGATCTGCAGCTTTGA     74378
                                TCAAAGCTGCAGATTG
                                ||||||||||||||||
                                AGTTTCGACGTCTAGC

GAM729  LOC130471 3'  CAGCACTGCAGCTCTGA     74939     A       AT   C
                                TCA AGCTGCAG  TGC TG
                                ||| ||||||||  ||| ||
                                AGT TCGACGTC  ACG AC
                                  C       __   _
GAM729  LOC146819 3'  TCACATTATTTTGCAGCTCTGA 78152     A        TTGCC
                                TCA AGCTGCAGA     TGTGA
                                ||| |||||||||     |||||
                                AGT TCGACGTTT     ACACT
                                  C        TATT_
GAM729  LOC146821 3'  TCACATTATTTTGCAGCTCTGA 78144     A        TTGCC
                                TCA AGCTGCAGA     TGTGA
                                ||| |||||||||     |||||
                                AGT TCGACGTTT     ACACT
                                  C        TATT_
GAM729  LOC149372 3'  TCAAAGGATCCTGCAGCTTT   79329          ATTG   G
                                AAAGCTGCAG    CCT TGA
                                ||||||||||    ||| |||
                                TTTCGACGTC    GGA ACT
                                      CTA_   A
GAM729  LOC149910 3'  CACGCCTCTCTGCAGCT     79530         TT_  CT
                                AGCTGCAGA   GC  GTG
                                |||||||||   ||  |||
                                TCGACGTCT   CG  CAC
                                     CTC  __
GAM729  LOC165283 5'  TCAACCCTAATCTGCAGC    87194           CCTG
                                GCTGCAGATTG    TGA
                                ||||||||||||   |||
                                CGACGTCTAAT    ACT
                                       CCCA
GAM729  LOC168667 3'  TCACCCTCGTATCTGCAGCCTG 92759     AA        _  CCT
             A                   TCA  GCTGCAGAT TG   GTGA
                                |||  |||||||| ||   ||||
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                                AGT  CGACGTCTA GC   CACT
                                  C_        T  TCC
GAM729   LOC201324 3'  CACATCAGCTGCAGCT      68560         A   CC
                                AGCTGCAG TTG  TGTG
                                |||||||| |||  ||||
                                TCGACGTC GAC  ACAC
                                     _   T_
GAM729   LOC219818 3'  CAGTCTTATTACAGCTTTGA   90886         C____
                                TCAAAGCTG     AGATTG
                                |||||||||     ||||||
                                AGTTTCGAC     TCTGAC
                                      ATTAT
GAM729   LOC220980 3'  CACATACTGCAGTTTGA     93147       G     ATTGCC
                                TCAAA CTGCAG     TGTG
                                ||||| ||||||     ||||
                                AGTTT GACGTC     ACAC
                                   _     AT____
GAM729   LOC221583 3'  CACAGATTTGCAGGCTT     92142       _      TGC
                                AAGC TGCAGAT   CTGTG
                                |||| |||||||   |||||
                                TTCG ACGTTTA   GACAC
                                  G      ___
GAM729   LOC254962 3'  TCACAGGCAATCTTGCTTCT   96616     CT   _
                                AG  GCA GATTGCCTGTGA
                                ||  ||| ||||||||||||
                                TC  CGT CTAACGGACACT
                                 TT   T
GAM729   LOC255299 5'  CAGCAACCTGGAGCTTTGA    97466         G   A    C
                                TCAAAGCT CAG TTGC TG
                                |||||||| ||| |||| ||
                                AGTTTCGA GTC AACG AC
                                     G   C    _
GAM729   LOC256940 3'  CACAGGTTTTCTGCAGT      96491         TT
                                GCTGCAGA  GCCTGTG
                                ||||||||  |||||||
                                TGACGTCT  TGGACAC
                                     TT
GAM729   LOC51075  3'  CACAAGCCTGAGGTGCAGCTTT 31988          GA  __  C
                                AAAGCTGCA  TT  GC TGTG
                                |||||||||  ||  || ||||
                                TTTCGACGT  AG  CG ACAC
                                      GG  TC  A
GAM730   ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM730   AHR      3'  ATCTCAGATGTTAAAATAAATG 7875        CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
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                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM730  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                                _
GAM730  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                   CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM730  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||  ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM730  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM730  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM730  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM730  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_    CG_
GAM730  CG012    5'  CTCACTCTGAAAGTGAA     83218          CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM730  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM730  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
              G                   CATTTC        GTCTGAGAT
                                ||||||        |||||||||
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                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM730  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA  TCACTGTCTGAGAT
                                |||||||  ||||||||||||||
                                GTAAAGT  AGTGACAGACTCTA
                                   C__
GAM730  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM730  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM730  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM730  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM730  PP35      3'  ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM730  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148        TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM730  SEP15     3'  TCCTACAGTAAGAGTGAAA   14934       C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM730  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA  73941       CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM730  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
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                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM730  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM730  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM730  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA

                                        _
GAM731  ADRA2B   3'  AGGAGAAGAGAGAGC       5457       CT
                                GCTC  TTTCTTCTCCT
                                ||||  ||||||||||
                                CGAG  AGAGAAGAGGA

                                  __
GAM731  AP1G1    3'  GGAAGAAAAGGACTGC      6674       C
                                GCAG TCCTTTTCTTCT
                                |||| ||||||||||||
                                CGTC AGGAAAAGAAGG

                                  _
GAM731  CALCR    3'  GAAGAAAAAGACCTGC      8219       C  C
                                GCAG TC TTTTCTTC
                                |||| || ||||||||
                                CGTC AG AAAAGAAG
                                  C  A
GAM731  CKAP1    5'  AAGAGGGCGGAGCTGC      73535          _
                                GCAGCTCC TTTTCTT
                                |||||||| |||||||
                                CGTCGAGG GGGAGAA
                                     C
GAM731  CORT     5'  CAGGAAGGAAGAGCAGC     7118       C       C    A
                                GCT CTTTTCTT TCCT G
                                ||| |||||||| |||| |
                                CGA GAGAAGGA AGGA C
                                  C       _    C
GAM731  CRHR1    3'  GCCAGGAGAAGACCCCTGC    15211      CTCCTTT        A
                                GCAG      TCTTCTCCT GC
                                ||||      ||||||||| ||
                                CGTC      AGAAGAGGA CG
                                  CCC_____        C
GAM731  DYRK3    5'  CTAGGAGATGGGAGGC       13124     AG     TTTCT
                                GC  CTCCT     TCTCCTAG
                                ||  |||||     ||||||||
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                                CG  GAGGG    AGAGGATC
                                 __    T____
GAM731  EPHB4    3'  AGAGGAAAAGGAAGTGC     15459     GC
                                GCA  TCCTTTTCTTCT
                                |||  ||||||||||||
                                CGT  AGGAAAAGGAGA
                                  GA
GAM731  FSTL1    3'  GCTAGGAAGGGAAGGGC     23012    T   TT  TC
                                GC CCTT  CT  TCCTAGC
                                || ||||  ||  |||||||
                                CG GGAA  GA  AGGATCG
                                 _   GG  __
GAM731  GCK      5'  AGGAGAGAAAGCGC       3864     A   CCTT   T
                                GC GCT    TTCT CTCCT
                                || |||    |||| |||||
                                CG CGA    AAGA GAGGA
                                 _  ____   _
GAM731  HAS3     3'  CTAGGAGATGAAACTGG     18038    T_   T
                                CC  TTTC TCTCCTAG
                                ||  |||| ||||||||
                                GG  AAAG AGAGGATC
                                 TC    T
GAM731  HIVEP3   5'  CTAAAGGGGAGAAGAGC     44435     C       CC
                                GCTC TTTTCTTCT  TAG
                                |||| |||||||||  |||
                                CGAG AAGAGGGGA  ATC
                                  _       A_
GAM731  IL1RL1LG 5'  GCTAGCGCTTAAAGGAGCCGC  22471    A      TCTTCTC
                                GC GCTCCTTT      CTAGC
                                || ||||||||      |||||
                                CG CGAGGAAA      GATCG
                                 C       TTCGC__
GAM731  INPP5D   3'  GAAGAAAGGAACTGC      82809     C     T
                                GCAG TCCTTT CTTC
                                |||| |||||| ||||
                                CGTC AGGAAA GAAG
                                  A     _
GAM731  LAD1     3'  AGGGGAGAAGGAGCTGC     18698
                                GCAGCTCCTTTTCTTCT
                                |||||||||||||||||
                                CGTCGAGGAAGAGGGGA

GAM731  MAP3K7IP1 3'  GCCAGGTGGAAAGGAGC     20379         TTCT   A
                                GCTCCTTTTC    CCT GC
                                ||||||||||    ||| ||
                                CGAGGAAAGG    GGA CG
                                       T___   C
GAM731  MEIS2    3'  AGAAGAAAATGCTGT       39318       TCC
                                GCAGC   TTTTCTTCT
                                |||||   |||||||||
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                                TGTCG   AAAAGAAGA
                                  T__
GAM731  MFAP3    3'  GCTAAGATTTAAAGGAGC    19808        TCT   CC
                                GCTCCTTT   TCT  TAGC
                                ||||||||   |||  ||||
                                CGAGGAAA   AGA  ATCG
                                    TTT   __
GAM731  NVL      5'  CTATGGTCGAAGAAAAAGAAAT 10301     GC  C      T_ _
           GC                     GCA  TC TTTTCTTC  CC TAG
                                |||  || ||||||||  || |||
                                CGT  AG AAAAGAAG  GG ATC
                                  AA  A       CT  T
GAM731  TMEM2    3'  GGAAAAAAAGGAGCGC      25422    A       C
                                GC GCTCCTTTT TTCT
                                || |||||||| ||||
                                CG CGAGGAAAA AAGG
                                 _       A
GAM731  TRIM34   5'  AGAAGAAAAGAAGACGC     55222    AG  C
                                GC  CT CTTTTCTTCT
                                ||  || ||||||||||
                                CG  GA GAAAAGAAGA
                                 CA  A
GAM731  TXNIP    3'  GGAAGAAAAGAAGCAGC     21351    A   C
                                GC GCT CTTTTCTTCT
                                || ||| ||||||||||
                                CG CGA GAAAAGAAGG
                                 A   A
GAM731  TYRO3    3'  GCCAGGAGAAGTTGAGGGGAGC 20844    _       __      A
           ATGC                   GCA GCTCCTTTT  CTTCTCCT GC
                                ||| |||||||||  |||||||| ||
                                CGT CGAGGGGAG  GAAGAGGA CG
                                  A       TT       C
GAM731  ABLIM    3'  CTTGAGAAGAAAAAAAGCT   22028     CC       CT
                                AGCT  TTTTCTTCTC  AG
                                ||||  ||||||||||  ||
                                TCGA  AAAAGAAGAG  TC
                                  AA        T_
GAM731  ABLIM    3'  CTTGAGAAGAAAAAAAGCT   9767      CC       CT
                                AGCT  TTTTCTTCTC  AG
                                ||||  ||||||||||  ||
                                TCGA  AAAAGAAGAG  TC
                                  AA        T_
GAM731  ARNTL2   3'  GCTAGAAGCCATAAAGAAAAGC 39468      CCT     _____  C
           TGC                    CAGCT   TTTCTT    CT CTAGC
                                |||||   ||||||    || |||||
                                GTCGA   AAAGAA    GA GATCG
                                   ___     ATACC  A
GAM731  BAGE     5'  AGGAGAAGGGGGAGCTG     6805         TT
                                CAGCTCCT  TCTTCTCCT
                                ||||||||  |||||||||
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                                GTCGAGGG  GGAAGAGGA
                                    __
GAM731  C20orf130 3'  GCCAGGCCCTGAGAAGGAGC  61755         TTCT   A
                                GCTCCTTTTC    CCT GC
                                ||||||||||    ||| ||
                                CGAGGAAGAG    GGA CG
                                     TCCC   C
GAM731  CLONE24945 3'  AGAAGAAGAGACCTGC      31624      CTC
                                GCAG   CTTTTCTTCT
                                ||||   ||||||||||
                                CGTC   GAGAAGAAGA
                                  CA_
GAM731  COLEC12   3'  GCCAGGAGAAGACTGTGCTG   47868      TCCTTT       A
                                CAGC     TCTTCTCCT GC
                                ||||     ||||||||| ||
                                GTCG     AGAAGAGGA CG
                                  TGTC__       C
GAM731  DAPK2     3'  GCCAGGAGACCCTGGGAGCTGT 26738         TTTCT     A
                                GCAGCTCCT    TCTCCT GC
                                |||||||||    |||||| ||
                                TGTCGAGGG    AGAGGA CG
                                     TCCC_    C
GAM731  DDX28     3'  GCATTGGAGAAGAAGCTGC   37213       CCTTT       TA_
                                GCAGCT    TCTTCTCC   GC
                                ||||||    ||||||||   ||
                                CGTCGA    AGAAGAGG   CG
                                   _____       TTA
GAM731  DDX31     3'  GCTAGGAGACAAAGGAG     56830       TCT
                                CTCCTTT   TCTCCTAGC
                                |||||||   |||||||||
                                GAGGAAA   AGAGGATCG
                                    C__
GAM731  DKFZP586M1120 3'  CAGGAGAAGGAAGTGC      48453     GCTCC          A
                                GCA    TTTTCTTCTCCT G
                                |||    |||||||||||| |
                                CGT    GAAGGAAGAGGA C
                                  _____          C
GAM731  DKK2      5'  GCTAACTTTGAAAAGGAGC    27016         TTCTCC
                                GCTCCTTTTC     TAGC
                                ||||||||||     ||||
                                CGAGGAAAAG     ATCG
                                     TTTCA_
GAM731  DOK4      3'  CAGGAGGGAAGGCCGC      36179    A   CCTT    T    A
                                GC GCT    TTCT CTCCT G
                                || |||    |||| ||||| |
                                CG CGG    AAGG GAGGA C
                                 C  ____   _    C
GAM731  ERp44     3'  GCTAGAAAAAGAAATGGGAGCT 81693        _     CTC
              G                  CAGCTCCT TTTCTT   CTAGC
                                 |||||||| ||||||   |||||
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                                GTCGAGGG AAAGAA   GATCG
                                    T     AAA
GAM731  FLJ10404  5' AGGCGGAAAGAGGAGCTGC   38797          C   T
                                GCAGCTCCTTTT TTC CCT
                                |||||||||||| ||| |||
                                CGTCGAGGAGAA AGG GGA
                                       _  C
GAM731  FLJ12154  5' GCTAGGAGAGCACAGGATCTGC 41671     C    TTTC
                                GCAG TCCT    TTCTCCTAGC
                                |||| ||||    ||||||||||
                                CGTC AGGA    GAGAGGATCG
                                  T    CAC_
GAM731  FLJ12586  3' GCTAAGATGGAAAGGGCTGC   44879      T      T   CC
                                GCAGC CCTTTTC TCT  TAGC
                                ||||| ||||||| |||  ||||
                                CGTCG GGAAAGG AGA  ATCG
                                  _      T   __
GAM731  FLJ14054  3' GCTAGGAGAACAAAGCTGT    44659       CCTT  C
                                GCAGCT    TT TTCTCCTAGC
                                ||||||    || ||||||||||
                                TGTCGA    AA AAGAGGATCG
                                   _____  C
GAM731  FLJ14454  5' GCTCAAGAAGAAAAGAAGCT   51381      C         CCT
                                AGCT CTTTTCTTCT   AGC
                                |||| ||||||||||   |||
                                TCGA GAAAAGAAGA   TCG
                                  A         AC_
GAM731  FLJ14810  5' AGGAGCAGGAGCTGC       51621          TTTCTT
                                GCAGCTCCT     CTCCT
                                |||||||||     |||||
                                CGTCGAGGA     GAGGA
                                     C_____
GAM731  FLJ20574  3' AGGAAAAAAAAAGGAGATGC   35418     G       C  C
                                GCA CTCCTTTT TT TCCT
                                ||| |||||||| || ||||
                                CGT GAGGAAAA AA AGGA
                                  A       A  A
GAM731  FLJ20856  5' CTAGAAAGGAAGAGC       47119      CT     CTC
                                GCTC  TTTCTT   CTAG
                                ||||  ||||||   ||||
                                CGAG  AAGGAA   GATC
                                  __      A__
GAM731  FLJ21034  5' AGGAGAAGGTTGAGCTGC    46292        CTTT
                                GCAGCTC    TCTTCTCCT
                                |||||||    |||||||||
                                CGTCGAG    GGAAGAGGA
                                    TT__
GAM731  FLJ21324  5' AGGAGAGGCCTGGGCTGC    91187       T  TTTT
                                GCAGC CC    CTTCTCCT
                                ||||| ||    ||||||||
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                                CGTCG GG    GGAGAGGA
                                   _ TCC_
GAM731  FLJ22601  3'  GCTATGGGAAGAAAAAGA    45695    C        C
                                TC TTTTCTTCTC TAGC
                                || |||||||||| ||||
                                AG AAAAGAAGGG ATCG
                                  A         T
GAM731  HEY2      3'  CTAGGAAGAGAAAAGCT     24317     CCT     TC
                                AGCT   TTTCT  TCCTAG
                                ||||   |||||  ||||||
                                TCGA   AAAGA  AGGATC
                                   ___    GA
GAM731  HGC6.1.1  3'  AGGAGAACAAGGAGCT      26825         TTC
                                AGCTCCTT   TTCTCCT
                                ||||||||   |||||||
                                TCGAGGAA   AAGAGGA
                                     C__
GAM731  KIAA0420  3'  AGAAGAAAGAAGCTGC      63351       CC
                                GCAGCT  TTTTCTTCT
                                ||||||  |||||||||
                                CGTCGA  GAAAGAAGA
                                   A_
GAM731  KIAA0472  3'  AGAAGAAAAAAAGCAGC     71851    A   CC
                                GC GCT  TTTTCTTCT
                                || |||  |||||||||
                                CG CGA  AAAAGAAGA
                                 A   AA
GAM731  KIAA0638  3'  GCCAGAAGAAGAAAAGTAGAGG 72400    AG  C        C  A
          T                      GC  CT CTTTTCTTCT CT GC
                                ||  || |||||||||| || ||
                                TG  GA GAAAAGAAGA GA CG
                                 GA  T         A  C
GAM731  KIAA1032  3'  CAGGAGAGAAGAACTGT     66153      CTCC     T    A
                                GCAG    TTTTCT CTCCT G
                                ||||    |||||| ||||| |
                                TGTC    AGAAGA GAGGA C
                                  A___     _    C
GAM731  KIAA1237  3'  GAGAAAAAAAGGAGGC      80469    AG       C
                                GC  CTCCTTTT TTCTC
                                ||  |||||||| |||||
                                CG  GAGGAAAA AAGAG
                                  __       A
GAM731  KIAA1715  3'  AGAAGAGAAAGCTG        68115       CC
                                CAGCT  TTTTCTTCT
                                |||||  |||||||||
                                GTCGA  AAGAGAAGA
                                   __
GAM731  KIAA1775  3'  CTAGAAGAGCATCAGGGCTGC  52379       T   TTTC    C
                                GCAGC CCT    TTCT CTAG
                                ||||| |||    |||| ||||
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                                CGTCG GGA    GAGA GATC
                                  _  CTAC    A
GAM731  KIAA1884  3'  GCTAAGAAGGGAGGAGC     73337       T TT     CC
                                GCTCC T  CTTCT  TAGC
                                |||||| |  |||||  ||||
                                CGAGG A  GAAGA  ATCG
                                  _ GG     __
GAM731  KIAA1912  5'  GCTAGGAGAGGGGAGAAGC    73366    AG    TTTT
                                GC  CTCC    CTTCTCCTAGC
                                ||  ||||    ||||||||||
                                CG  GAGG    GGAGAGGATCG
                                 AA   _____
GAM731  KIAA1915  5'  AGAAGAAAAAGAGCTGT     73272        C
                                GCAGCTC TTTTCTTCT
                                ||||||| |||||||||
                                TGTCGAG AAAAGAAGA
                                    A
GAM731  KIAA1918  5'  GCCAGGAGAAATGGGAAAAGCT 73162       ___    TTTC      A
          GT                    GCAGC   TCCT    TTCTCCT GC
                                ||||||   ||||   ||||||| ||
                                TGTCG   AGGG    AAGAGGA CG
                                  AAA    TA__      C
GAM731  KIAA1925  5'  AGAACAAAAAAGGAGCT     92077          C__
                                AGCTCCTTTT   TTCT
                                ||||||||||   ||||
                                TCGAGGAAAA   AAGA
                                     AAC
GAM731  KIAA1946  3'  AGAAGAAAAAGAGATGC     82468     G   C
                                GCA CTC TTTTCTTCT
                                ||| ||| |||||||||
                                CGT GAG AAAAGAAGA
                                  A   A
GAM731  KIF1C     3'  GCTAGGAGAAGGGAAGACGC   61225    TC   TT
                                GC  CTT  CTTCTCCTAGC
                                ||  |||  ||||||||||
                                CG  GAA  GAAGAGGATCG
                                 CA   GG
GAM731  KRT20     3'  AGAAGGAGATGCTGC       71755       TCC
                                GCAGC   TTTTCTTCT
                                |||||   |||||||||
                                CGTCG   AGAGGAAGA
                                  T__
GAM731  MANBAL    5'  GCTGGGAAGAAAAAGAGC    41979     C     TC
                                GCTC TTTTCT  TCCTAGC
                                |||| ||||||  |||||||
                                CGAG AAAAGA  AGGGTCG
                                  A     __
GAM731  MCPR      3'  CTAGGGGGAAATGAGCTGC   42646       CT    TT
                                GCAGCTC  TTTC  CTCCTAG
                                |||||||  ||||  |||||||
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                                CGTCGAG  AAAG  GGGGATC
                                   T_   __
GAM731  MGC15631  3'  GCCAGGAGTGGATGGAGCTGC  51266        TTT   T    A
                                GCAGCTCC   TCT CTCCT GC
                                ||||||||   ||| ||||| ||
                                CGTCGAGG   AGG GAGGA CG
                                     T__   T    C
GAM731  MGC2663   3'  CTGGAGAGAAGAAGCTGC    44094       CCTTT     _
                                GCAGCT    TCTTCTC CTAG
                                ||||||    ||||||| ||||
                                CGTCGA    AGAAGAG GGTC
                                   ______     A
GAM731  MGC2835   3'  CTAGGAGGCAGGGGCTGC    43961        TTTCT
                                GCAGCTCCT    TCTCCTAG
                                |||||||||    ||||||||
                                CGTCGGGGA    GGAGGATC
                                     C_____
GAM731  MSE55     5'  CAGGGCAAAGGAGCTG      22940         TCTTC   A
                                CAGCTCCTTT    TCCT G
                                ||||||||||    |||| |
                                GTCGAGGAAA    GGGA C
                                      C_____   C
GAM731  MYH7B     3'  AGAAGAAGAAGCTG       70529      CC
                                CAGCT  TTTTCTTCT
                                |||||  |||||||||
                                GTCGA  AGAAGAAGA
                                   __
GAM731  PB1       3'  AGGAGGGGAAAAAGC      36367     CC
                                GCT  TTTTCTTCTCCT
                                |||  ||||||||||||
                                CGA  AAAAGGGGAGGA
                                   __
GAM731  SPINT1    3'  GCCAGGAGAAGCTCAGCTGC   62651       CCTTTT      A
                                GCAGCT     CTTCTCCT GC
                                ||||||     |||||||| ||
                                CGTCGA     GAAGAGGA CG
                                   CTC___       C
GAM731  SYT12     3'  GCCAGGAGAAGACTGAATGC   94732     GC  CTTT      A
                                GCA  TC    TCTTCTCCT GC
                                |||  ||    ||||||||| ||
                                CGT  AG    AGAAGAGGA CG
                                  A_  TC__       C
GAM731  THEA      3'  GAGTGCTTAAAGGAGCTGC    66284         TCTT_
                                GCAGCTCCTTT    CTC
                                ||||||||||    |||
                                CGTCGAGGAAA    GAG
                                      TTCGT
GAM731  TLN1      5'  GCCAGGCTGGAGAAAAGAAGCT 20819       C       T_   A
              GC                    GCAGCT CTTTTCTTC  CCT GC
                                ||||||  |||||||||  ||| ||
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                                CGTCGA GAAAAGAGG  GGA CG
                                   A        TC   C
GAM731  TSPEAR   3'  AGAAGAAAAAAGCTG       58713       CC
                                CAGCT  TTTTCTTCT
                                |||||  |||||||||
                                GTCGA  AAAAGAAGA
                                   A_
GAM731  USP10    3'  GCTAGAATGAAAAGGAGATGC  63946     G       TTCTC
                                GCA CTCCTTTTC     CTAGC
                                |||  |||||||||     |||||
                                CGT GAGGAAAAG     GATCG
                                  A        TAA__
GAM731  VIT1     3'  GAAGAAAATAAGCTGC      37974       CC
                                GCAGCT  TTTTCTTC
                                ||||||  ||||||||
                                CGTCGA  AAAAGAAG
                                   AT
GAM731  LOC115286 3'  GCTAAGAGAAGAAAACGGGGT  73374       _        C
                                GCTCC TTTTCTTCTC TAGC
                                |||||  |||||||||| ||||
                                TGGGG AAAAGAAGAG ATCG
                                   C         A
GAM731  LOC131377 3'  GCTAGGAGAGGCCAGAGT    76271      CTTTT
                                GCTC    CTTCTCCTAGC
                                ||||    ||||||||||
                                TGAG    GGAGAGGATCG
                                  ACC__
GAM731  LOC140275 3'  AGAAGAAATTGAATTGC     74794      C  CT
                                GCAG TC  TTTCTTCT
                                ||||  ||  ||||||||
                                CGTT AG  AAAGAAGA
                                  A  TT
GAM731  LOC143279 5'  GAAGAAAGAAGCTGC       76508       CC
                                GCAGCT  TTTTCTTC
                                ||||||  ||||||||
                                CGTCGA  GAAAGAAG
                                   A_
GAM731  LOC145824 3'  AAGAGAGAGGAGCAGC      77521     A       _
                                GC GCTCCTTT TCTT
                                ||  |||||||| ||||
                                CG CGAGGAGA AGAA
                                  A       G
GAM731  LOC146179 5'  GCTTTTTAGAAAAGGAGCTG   77701             TCTCCT
                                CAGCTCCTTTTCT     AGC
                                ||||||||||||     |||
                                GTCGAGGAAAAGA     TCG
                                         TTTT__
GAM731  LOC146336 5'  GCCAGGAGAGGAAGGAGCGGC  77833     A      TT        A
                                GC GCTCCT  TCTTCTCCT GC
                                ||  ||||||  |||||||||  ||
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                                CG CGAGGA  AGGAGAGGA CG
                                 G     __       C
GAM731   LOC148932 3'  CGCCAGGAGAAGAAGAGGGAGA 79106  ___   _         A  III
                AACTGT                    CTCC TTTTCTTCTCCT GC   G
                                  |||| |||||||||||| ||   |
                                  GAGG AGAAGAAGAGGA CG   C
                                AAA   G          C  III
GAM731   LOC150311 5'  CTAGGAGTGAGGAGC       79753        TTCTT
                                GCTCCTT    CTCCTAG
                                |||||||    |||||||
                                CGAGGAG    GAGGATC
                                    T_____
GAM731   LOC150423 3'  GCTAGAATGAAAAGGAGATGC  79866     G       TTCTC
                                GCA CTCCTTTTC    CTAGC
                                ||| |||||||||    |||||
                                CGT GAGGAAAAG    GATCG
                                  A        TAA__
GAM731   LOC150568 3'  CTAGAAAAAAGGAGCCGT    85043    A       CTTCTC
                                GC GCTCCTTTT     CTAG
                                || |||||||||     ||||
                                TG CGAGGAAAA     GATC
                                 C        AA_____
GAM731   LOC153243 5'  GCTAGGAGAAACTGAAGCTG   80798      CCTTTTC
                                CAGCT      TTCTCCTAGC
                                |||||      ||||||||||
                                GTCGA      AAGAGGATCG
                                   AGTCA__
GAM731   LOC154992 3'  GCTAGAAAAGGCAAAGGAGC   81217        _   CTC
                                GCTCCTTT TCTT   CTAGC
                                |||||||| ||||   |||||
                                CGAGGAAA GGAA   GATCG
                                    C    AA_
GAM731   LOC157931 3'  AGAAAAAATGGAGCTGC     86655        T   C
                                GCAGCTCC TTT TTCT
                                |||||||| ||| ||||
                                CGTCGAGG AAA AAGA
                                     T   A
GAM731   LOC158801 3'  GCTAAGAAAAAGGAAAAGAAAT 86893     GC  C      C_  C
                  GC                GCA  TC TTTTCTT  TC TAGC
                                |||  || |||||||  || ||||
                                CGT  AG AAAGGAA  AG ATCG
                                  AA  A      AA  A
GAM731   LOC163132 5'  GAAAAATAGGAGCTGC      87179         T  C
                                GCAGCTCCT TT TTC
                                |||||||||| || |||
                                CGTCGAGGA AA AAG
                                     T  A
GAM731   LOC170370 3'  GCCAGGAGACTGGAAGGA    82839        CT     A
                                TCCTTTT  TCTCCT GC
                                |||||||  |||||| ||
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                                AGGAAGG  AGAGGA CG
                                   TC     C
GAM731   LOC196485 3'  CTAGGAGAAAAGCTGC      87731       CCTTTTC
                                GCAGCT      TTCTCCTAG
                                ||||||      |||||||||
                                CGTCGA      AAGAGGATC
                                  A_______
GAM731   LOC201245 3'  GGAGGAAAAGAGCTGC      87364        C
                                GCAGCTC TTTTCTTCT
                                ||||||| |||||||||
                                CGTCGAG AAAAGGAGG
                                     _
GAM731   LOC202025 3'  CTAGGAAAAGGAAACTG     90286     CTCC      C
                                CAG    TTTTCTT TCCTAG
                                |||    ||||||| ||||||
                                GTC    AAAGGAA AGGATC
                                 ____       A
GAM731   LOC202986 3'  CTAGGAGAAAAGCTGC      90442       CCTTTTC
                                GCAGCT      TTCTCCTAG
                                ||||||      |||||||||
                                CGTCGA      AAGAGGATC
                                  A_______
GAM731   LOC203245 3'  GCTAAAAAGAGAAGACGCTGC  89300       TC       CTCC
                                GCAGC  CTTTTCTT    TAGC
                                |||||  ||||||||    ||||
                                CGTCG  GAAGAGAA    ATCG
                                  CA       AA__
GAM731   LOC221410 3'  GCCAGGAGCCCTGAAGGAGC   92059        TCTT     A
                                GCTCCTTT    CTCCT GC
                                ||||||||    ||||| ||
                                CGAGGAAG    GAGGA CG
                                     TCCC     C
GAM731   LOC221755 3'  CTAAGAGAAGAAATCGTGT    92395     TCCT       C
                                GC    TTTCTTCTC TAG
                                ||    ||||||||| |||
                                TG    AAAGAAGAG ATC
                                 TGCT        A
GAM731   LOC254130 3'  GCCAGAAGATGGAGAGGAGGCT 95672       _       T   C  A
            GC                    GCAGC TCCTTTTC TCT CT GC
                                ||||| |||||||| ||| || ||
                                CGTCG AGGAGAGG AGA GA CG
                                  G       T   A  C
GAM731   LOC254848 5'  AGGAAAGAGGAGATGC      97087     G       CTTC
                                GCA CTCCTTTT    TCCT
                                ||| ||||||||    ||||
                                CGT GAGGAGAA    AGGA
                                 A       ____
GAM731   LOC257354 3'  AGAAGAAAGAAGCTGC      95084        CC
                                GCAGCT  TTTTCTTCT
                                ||||||  |||||||||
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                                CGTCGA  GAAAGAAGA
                                   A_
GAM731  LOC63928  3' CAAGAGAAGAAAGCTG     42030      CCTT      CTA
                                CAGCT   TTCTTCTC   G
                                |||||   ||||||||  |
                                GTCGA   AAGAAGAG   C
                                   _____      AAC
GAM731  LOC90313  3' AGGGGAGAAAAGGAGCCGC   62220    A         T
                                GC GCTCCTTTTCTTC CCT
                                || ||||||||||||| |||
                                CG CGAGGAAAAGAGG GGA
                                 C          _
GAM731  LOC91097  3' AGGAGAGGCCTGGGCTGC    64833      T  TTTT
                                GCAGC CC    CTTCTCCT
                                ||||| ||    ||||||||
                                CGTCG GG    GGAGAGGA
                                   _ TCC_
GAM731  LOC92606  3' GTTAAAAGAAGAAAAAAATCTG 69988     CTCC       CC
             C                   GCAG    TTTTCTTCT  TAGC
                                ||||   |||||||||  ||||
                                CGTC    AAAAGAAGA  ATTG
                                  TAAA       AA
GAM731  LOC93624  5' AGGAGGAGAAGGAGCTGC    72726        TT
                                GCAGCTCCT  TCTTCTCCT
                                |||||||||  |||||||||
                                CGTCGAGGA  AGAGGAGGA
                                           __
GAM732  ARF3      3' CTGCCCCAGTCTTTGA      8000         CAAAG  TAT
                                TCGAAGAC    TG   GCAG
                                ||||||||    ||  ||||
                                AGTTTCTG    AC   CGTC
                                     ______ CC_
GAM732  EMX2      3' ACCGCATACACGTTCACCGA   87560     AA  CCAAA      A
                                TCG  GA    GTGTATGC GT
                                |||  ||    |||||||| ||
                                AGC  CT    CACATACG CA
                                  CA  TG___       C
GAM732  JUN       3' ACTGCATGGACCTAACATTCGA 9474       GACCAAA  G
                                TCGAA      GT TATGCAGT
                                |||||      || ||||||||
                                AGCTT      CA GTACGTCA
                                   ACAATC_  G
GAM732  NCAM2     3' GACTGGCACCAACACTTTGGTA 15801     G        A__  _
             TTC                  GAA ACCAAAGTGT   TGC AGTC
                                ||| ||||||||||   ||| ||||
                                CTT TGGTTTCACA   ACG TCAG
                                  A        ACC   G
GAM732  QDPR      3' ACTGCATAGGAGGCTCTCGA   4355      A  _  AAAGTG
                                TCGA GA CC     TATGCAGT
                                |||| || ||     ||||||||
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                                AGCT CT GG     ATACGTCA
                                  _  C  AGG___
GAM732  SLC11A3  3'  ACTGCATACAGACTTC     27434     ACCAAAG
                                GAAG      TGTATGCAGT
                                ||||      ||||||||||
                                CTTC      ACATACGTCA
                                  AG_____
GAM732  ZNF239   5'  ACTACAGAAACTTGGTCTTGGA 19037    G      A  GTA  C
                                TC AAGACCAA GT   TG AGT
                                || |||||||| ||   || |||
                                AG TTCTGGTT CA   AC TCA
                                 G       _  AAG  A
GAM732  FLJ12455 3'  GACCGCTTGTCTTTGGTCTC   41983    A      TGTAT  A
                                GA GACCAAAG     GC GTC
                                || ||||||||     || |||
                                CT CTGGTTTC     CG CAG
                                 _       TGTT_  C
GAM732  FLJ23042 3'  ACTGCATGCAGCCTTC     47166     ACCAAAG
                                GAAG      TGTATGCAGT
                                ||||      ||||||||||
                                CTTC      ACGTACGTCA
                                  CG_____
GAM732  FREQ     3'  ACACTTTGGTCCTCGG     26568     A
                                TCGA GACCAAAGTGT
                                |||| ||||||||||
                                GGCT CTGGTTTCACA
                                  C
GAM732  MGC2848  3'  CTGCTGACACTTTGATCTTGGA 51893    G   C      AT
                                TC AAGA CAAAGTGT  GCAG
                                || |||| ||||||||  ||||
                                AG TTCT GTTTCACA  CGTC
                                 G   A       GT
GAM732  PAFAH2   3'  ACTGGGTACTTTGATCTTAGA  4758     G   C     GT  G
                                TC AAGA CAAAGT  AT CAGT
                                || |||| ||||||  || ||||
                                AG TTCT GTTTCA  TG GTCA
                                 A   A     __  G
GAM732  SCMH1    3'  GACTGCCCTGCTTTGGTCCCAG 24254    GAA       TAT
           A                     TC   GACCAAAGTG   GCAGTC
                                ||   ||||||||||   ||||||
                                AG   CTGGTTTCGT   CGTCAG
                                 ACC         CC_
GAM732  LOC146475 5'  GACTGAGAGCCTCAGTCTTTGA 83687        CAA  T  ATG
                                TCGAAGAC   AG GT   CAGTC
                                ||||||||   || ||   |||||
                                AGTTTCTG   TC CG   GTCAG
                                     AC_  _  AGA
GAM732  LOC149911 5'  GACTGCTGGACTTCAGTCTTCG 84708        CA   G  T
           G                     TCGAAGAC  AAGT TA GCAGTC
                                ||||||||  |||| || ||||||
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                                GGCTTCTG  TTCA GT CGTCAG
                                    AC   G  _
GAM732  LOC157273 3'  GACCATGCTGACACTTTGATCT 86430    G   C      AT  __
           TGGA                   TC AAGA CAAAGTGT  GCA  GTC
                                || |||| ||||||||  |||  |||
                                AG TTCT GTTTCACA  CGT  CAG
                                 G   A       GT   AC
GAM732  LOC221466 5'  ACTGCATACATGTGG      93682     AA
                                CCA  GTGTATGCAGT
                                |||  ||||||||||
                                GGT  TACATACGTCA
                                  G_
GAM732  LOC255458 3'  TATGACTTTGGTCTT      97149          G
                                AAGACCAAAGT TATG
                                |||||||||| ||||
                                TTCTGGTTTCA GTAT
                                      _
GAM732  LOC51133  3'  GACTGCATTCCTAATCTTC   32282      CCAA  TGT
                                GAAGA   AG   ATGCAGTC
                                |||||   ||   ||||||||
                                CTTCT   TC   TACGTCAG
                                   AA__  CT_
GAM733  DES     3'  TCCTCACTGCTCCCTGAAGC   72131    G_   C  AAA
                                GC  TAGG AG   CAGTGAGGA
                                ||  |||| ||   |||||||||
                                CG  GTCC TC   GTCACTCCT
                                 AA   C ___
GAM733  KCND3    3'  TCCCCACTATTTCTGCCTGC   17145          C   A
                                GTAGGCAGAAA AGTG GGA
                                |||||||||| |||| |||
                                CGTCCGTCTTT TCAC CCT
                                      A   C
GAM733  NFE2L1   3'  CCTCGGGCCTCTGCCTACCAA  12170     C       AACAG
                                TTG GTAGGCAGA    TGAGG
                                ||| |||||||||    |||||
                                AAC CATCCGTCT    GCTCC
                                  _       CCGG_
GAM733  PSEN1    3'  TCCTCATTCTTCTCTCCCACAC 3425     C  A  C   _  C
           AA                    TTG GT GG AGA AA AGTGAGGA
                                ||| || || ||| || ||||||||
                                AAC CA CC TCT TT TTACTCCT
                                  A  C  _   C  C
GAM733  PSEN1    3'  TCCTCATTCTTCTCTCCCACAC 23627     C  A  C   _  C
           AA                    TTG GT GG AGA AA AGTGAGGA
                                ||| || || ||| || ||||||||
                                AAC CA CC TCT TT TTACTCCT
                                  A  C  _   C  C
GAM733  RALBP1   3'  TCCTCACTGCGGGGACCAGCAA 22298      GTA  CAGAAA
                                TTGC   GG     CAGTGAGGA
                                ||||   ||     |||||||||
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                                AACG  CC    GTCACTCCT
                                  A__ AGGGGC
GAM733  WISP2    3' CCCACTCCCTGCCTACACA  13933   C     AAAC   A
                                TG GTAGGCAG   AGTG GG
                                || ||||||||   |||| ||
                                AC CATCCGTC   TCAC CC
                                 A      CC__   _
GAM733  XPC      3' CCTCACTGCCTCTTTGCAG  16131     T  C  AAA
                                TTGCG AGG AG  CAGTGAGG
                                ||||| ||| ||  ||||||||
                                GACGT TTC TC  GTCACTCC
                                   _  _ C__
GAM733  DKFZP586F1524 3' TCCTCATAAGCCCTGCCTAC  31493       AAACA
                                GTAGGCAG   GTGAGGA
                                ||||||||   |||||||
                                CATCCGTC   TACTCCT
                                     CCGAA
GAM733  DKFZP761G1913 3' CCTCACTGCCTTGCTCCAC  48910   A_   AAA
                                GT  GGCAG  CAGTGAGG
                                ||  |||||  ||||||||
                                CA  TCGTT  GTCACTCC
                                 CC   CC_
GAM733  KIAA0323  3' TTACTTCTGCCTAC      63271       AAC
                                GTAGGCAGA  AGTGA
                                |||||||||  |||||
                                CATCCGTCT  TCATT
                                       ___
GAM733  KIAA1655  3' TCCTCACTGCCTCTTTCTA  66632    C  AA
                                TAGG AGA  CAGTGAGGA
                                ||||| |||  |||||||||
                                ATCT TCT  GTCACTCCT
                                  T  CC
GAM733  PISD     3' TCCCGTTCCTTCTGCCTAC  26774       AC   A
                                GTAGGCAGAA  AGTG GGA
                                ||||||||||  |||| |||
                                CATCCGTCTT  TTGC CCT
                                      CC   _
GAM733  STARD7   3' CTCCCTGCCTGCACAA    57698    C     AAACAGT
                                TTG GTAGGCAG     GAG
                                ||| ||||||||     |||
                                AAC CGTCCGTC     CTC
                                  A      C_______
GAM733  STARD7   3' CTCCCTGCCTGCACAA    39331    C     AAACAGT
                                TTG GTAGGCAG     GAG
                                ||| ||||||||     |||
                                AAC CGTCCGTC     CTC
                                  A      C_______
GAM733  TED      3' CCCTGGGCCCTGCCTACACA  31633   C     AAA_  TGA
                                TG GTAGGCAG   CAG  GG
                                || ||||||||   |||  ||
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                                AC CATCCGTC   GTC  CC
                                 A      CCGG  ___
GAM733  LOC137964 5'  TCCTCACTGCTCACTTGCACAG 75287    C    CA  AA
                                TTG GTAGG  GA  CAGTGAGGA
                                ||| |||||  ||  |||||||||
                                GAC CGTTC  CT  GTCACTCCT
                                  A    A_  C_
GAM733  LOC158835 3'  CCTCACTCAGTTTCTGCCTCAC 82010   _       __
                                GT AGGCAGAAAC  AGTGAGG
                                || ||||||||||  |||||||
                                CA TCCGTCTTTG  TCACTCC
                                 C        AC
GAM733  LOC221504 3'  CCTCACTGCCATGGCACACCA  92420   C  AG  AGAAA
                                TG GT  GC    CAGTGAGG
                                || ||  ||    ||||||||
                                AC CA  CG    GTCACTCC
                                 _  CA  GTACC
GAM733  LOC255446 3'  TCCTCACTACCCACCCACGCA  97156     A  CAGAAAC
                                TGCGT GG      AGTGAGGA
                                ||||| ||      ||||||||
                                ACGCA CC      TCACTCCT
                                   C  ACCCA__
GAM733  LOC51667  3'  CCTCACTGCGCCACGCA     32272     A   AGAAA
                                TGCGT GGC     CAGTGAGG
                                ||||| |||     ||||||||
                                ACGCA CCG     GTCACTCC
                                   _   C____
GAM733  LOC63929  3'  CAAGGTCTCTGCCTATGCAA   42042          A  AG
                                TTGCGTAGGCAGA AC  TG
                                |||||||||||| ||  ||
                                AACGTATCCGTCT TG  AC
                                       C  GA
GAM734  CNGA1     3'  CAACTGATAATGTGCAAA    59507          GC   A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                      A_   _
GAM734  ESRRG     3'  TGGCAGTCTTATGTGCAAA   66396        TAGCT
                                TTTGCACAT     AGATTGCCA
                                |||||||||     |||||||||
                                AAACGTGTA     TCTGACGGT
                                     T____
GAM734  KCNJ3     3'  GCAATAATGTGCAAA       9525          GCTAGA
                                TTTGCACATTA      TTGC
                                ||||||||||      ||||
                                AAACGTGTAAT      AACG
                                                 _____
GAM734  SDC2      3'  GCAAATTAATGTGTAAA     67132          CTAGA
                                TTTGCACATTAG     TTGC
                                ||||||||||||     ||||
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                                AAATGTGTAATT    AACG
                                      A____
GAM734  USP9X    3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
              A                  TTTGCACATTAGC     GCCAT
                                 ||||||||||||     |||||
                                 AAATGTGTAATCG     CGGTA
                                       TAGTC_
GAM734  AMOTL1   3'  GGCAAGTAATGTGCAAA    73650         G  AGAT
                                 TTTGCACATTA CT    TGCC
                                 |||||||||| ||    ||||
                                 AAACGTGTAAT GA    ACGG
                                      _ ____
GAM734  BCAR3    3'  AGTAATAATGTGCAAA     13098          __
                                 TTTGCACATTA  GCT
                                 ||||||||||  |||
                                 AAACGTGTAAT  TGA
                                       AA
GAM734  DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930         AGCTA    C
                                 TTTGCACATT    GATTG CA
                                 |||||||||    ||||| ||
                                 AGACGTGTAA    TTAAC GT
                                      A____    A
GAM734  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                 TTTGCACATTAG  AGA TG CAT
                                 ||||||||||||  ||| || |||
                                 AGACGTGTAATC  TTT AC GTA
                                       __  T  A
GAM734  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
              AA                   TTTGCACATTAGCTAGATTGCCAT
                                   ||||||||||||||||||||||||
                                   AAACGTGTAATCGATCTAACGGTA

GAM735  C20orf98  3'  ACAGGCAATTACTAGCCCTA   71509
                                 TGGGGCTAGTAATTGTTTGT
                                 ||||||||||||||||||||
                                 ATCCCGATCATTAACGGACA

GAM735  KIAA1040  3'  CACAATTTGGTACCACTAGTCC 72222         AATTGTTT
              CA                   TGGGGCTAGT       GTTGTG
                                   ||||||||||       ||||||
                                   ACCCTGATCA       TAACAC
                                        CCATGGTT
GAM736  CACNA2D2  3'  AGCCACATCCCCAAGCCCACCA 20077       ATCCA    T__  A
                                 TGGTGG    TTTGG   TGT GCT
                                 ||||||    |||||   ||| |||
                                 ACCACC    GAACC   ACA CGA
                                    C____    CCT   C
GAM736  DIAPH2   3'  ACAGTCAAATAAATCCAC    22059       CC    GT
                                 GTGGAT  ATTTG  TGT
                                 ||||||  |||||  |||
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                                CACCTA  TAAAC  ACA
                                   AA    TG
GAM736  DPH2L1   5'  CTACAACTTTGAGATCCCCA  7278     T    _ TTT
                                TGG GGATC CA   GGTTGTAG
                                ||| ||||| ||   ||||||||
                                ACC CCTAG GT   TCAACATC
                                  _    A  T__
GAM736  FUT9     3'  AACCAAATAAACCTACCA    67842       ATCC
                                TGGTGG   ATTTGGTT
                                ||||||   ||||||||
                                ACCATC   TAAACCAA
                                   CAAA
GAM736  TTN      3'  ACTTCCAAACAGGTCCACCA  55923         CA    TT
                                TGGTGGATC  TTTGG  GT
                                |||||||||  |||||  ||
                                ACCACCTGG  AAACC  CA
                                     AC    TT
GAM736  CD109    3'  AGCTATTTAAAAATAAATCCAT 56044         CC    GGTT
           CA                     TGGTGGAT  ATTT   GTAGCT
                                |||||||  ||||   ||||||
                                ACTACCTA  TAAA   TATCGA
                                    AA    AATT
GAM736  FLJ23323 3'  AACTAAATGAATCCAC     45048       C
                                GTGGAT CATTTGGTT
                                |||||| |||||||||
                                CACCTA GTAAATCAA
                                   A
GAM736  KIAA1908 5'  AGCCACATCTCACTGGATCCAC 73393          TTT  T   A
           CA                     TGGTGGATCCA   GG TGT GCT
                                ||||||||||   || ||| |||
                                ACCACCTAGGT   TC ACA CGA
                                      CAC  T   C
GAM736  MCAM     3'  CTACAACCAAAAGGCACAC   21452     GAT  A
                                GTG   CC TTTGGTTGTAG
                                |||   || ||||||||||
                                CAC   GG AAACCAACATC
                                  AC_  A
GAM736  MGC34923 5'  AGCCACATCTGGATCCCCA   58518    T     TT__
                                TGG GGATCCA   TGGTT
                                ||| |||||||   |||||
                                ACC CCTAGGT   ACCGA
                                  _     CTAC
GAM736  PRDM7    3'  TAATTAAACAAATCCGCCA   53792       CCA
                                TGGTGGAT   TTTGGTTG
                                ||||||||   ||||||||
                                ACCGCCTA   AAATTAAT
                                    AAC
GAM736  PRDM9    3'  ACTGATTAAACAAATCCGCCA  39573        CCA     _
                                TGGTGGAT   TTTGGTT GT
                                ||||||||   ||||||| ||
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                                ACCGCCTA   AAATTAG CA
                                    AAC      T
GAM736  RALGPS1A  3'  ACGACCAAAAGACCCACCA   27594       A  CA
                                TGGTGG TC  TTTGGTTGT
                                |||||| ||  |||||||||
                                ACCACC AG  AAACCAGCA
                                   C  A_
GAM736  UREB1     3'  AACCAATAAATGAAATCCACCA 48578        C_   ___
                                TGGTGGAT  CATT   TGGTT
                                ||||||||  ||||   |||||
                                ACCACCTA  GTAA   ACCAA
                                    AA    ATA
GAM736  LOC162417 3'  AGCTACAACCAAATGGCCTTCG 82345     T  AT
                                TGG GG  CCATTTGGTTGTAGCT
                                ||| ||  ||||||||||||||||
                                GCT CC  GGTAAACCAACATCGA
                                  T  __
GAM736  LOC254122 3'  AGTTACAACAAACCCACCA   94751       ATCCATTTG
                                TGGTGG       GTTGTAGCT
                                ||||||       |||||||||
                                ACCACC       CAACATTGA
                                   CAAA_____
GAM737  ABCC1     3'  TGATGTGGGGTAAATATTAAGG 17183     CA       AAA  C
          A                      TCC  AATATTTAC   GC ATCA
                                 |||  |||||||||   || ||||
                                 AGG  TTATAAATG   TG TAGT
                                   AA       GGG  _
GAM737  ABCC1     3'  TGATGTGGGGTAAATATTAAGG 39128     CA       AAA  C
          A                      TCC  AATATTTAC   GC ATCA
                                 |||  |||||||||   || ||||
                                 AGG  TTATAAATG   TG TAGT
                                   AA       GGG  _
GAM737  ABCC1     3'  TGATGTGGGGTAAATATTAAGG 39136     CA       AAA  C
          A                      TCC  AATATTTAC   GC ATCA
                                 |||  |||||||||   || ||||
                                 AGG  TTATAAATG   TG TAGT
                                   AA       GGG  _
GAM737  ASIC4     3'  TTTGTAAATATTTAGGG     37924     _
                                 CCC AAATATTTACAAA
                                 ||| |||||||||||||
                                 GGG TTTATAAATGTTT
                                   A
GAM737  CREBBP    3'  GATAACTTTGTGATGTTTCGGG 15207     _      T     CC
          A                      TCCC AAATATT ACAAAG  ATC
                                 |||| ||||||| ||||||  |||
                                 AGGG TTTGTAG TGTTTC  TAG
                                   C       _      AA
GAM737  CTSS      3'  TGATGGCTTAAAAATA      14545       ACA
                                 TATTT   AAGCCATCA
                                 |||||   |||||||||
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                                ATAAA  TTCGGTAGT
                                  AA_
GAM737  EYA1    5'  GATGGCTCCGAGTTTGGGG  4954       ATTTACAA
                                TCCCAAAT      AGCCATC
                                ||||||||      |||||||
                                GGGGTTTG      TCGGTAG
                                    AGCC____
GAM737  FBXW1B  3'  TGACAGCTTTGTACTGTGG  24527    AATATT     CA
                                CCA    TACAAAGC  TCA
                                |||    ||||||||  |||
                                GGT    ATGTTTCG  AGT
                                  GTC___      AC
GAM737  FBXW1B  3'  TGACAGCTTTGTACTGTGG  53331    AATATT     CA
                                CCA    TACAAAGC  TCA
                                |||    ||||||||  |||
                                GGT    ATGTTTCG  AGT
                                  GTC___      AC
GAM737  FBXW1B  3'  TGACAGCTTTGTACTGTGG  53342    AATATT     CA
                                CCA    TACAAAGC  TCA
                                |||    ||||||||  |||
                                GGT    ATGTTTCG  AGT
                                  GTC___      AC
GAM737  GCN5L2  3'  TGATGGCTTCAGGGGTTGG  59841    ATA  ACA
                                CCAA  TTT  AAGCCATCA
                                ||||  |||  |||||||||
                                GGTT  GGA  TTCGGTAGT
                                  GG_  C__
GAM737  GSPT1   3'  GCTTTGTAAGTGATGTGG   9143    AA_
                                CCA  TATTTACAAAGC
                                |||  ||||||||||||
                                GGT  GTGAATGTTTCG
                                  GTA
GAM737  PTPN11  3'  TGATGAGAAGAAATGATTTGGG 11085       _   ACAAAGC
          A                      TCCCAAAT ATTT     CATCA
                                ||||||||| ||||     |||||
                                AGGGTTTA TAAA     GTAGT
                                    G   GAAGA__
GAM737  RNMT    3'  TGATAGCTTTGTAGGTACAGGA 13725    CAAA        C
                                TCC   TATTTACAAAGC ATCA
                                |||   |||||||||||| ||||
                                AGG   ATGGATGTTTCG TAGT
                                  AC__         A
GAM737  ROR2    3'  TGACAGCTTTGTATTTGGTGA  15855   _   TATT     CA
                                TC CCAAA   TACAAAGC  TCA
                                || |||||   ||||||||  |||
                                AG GGTTT   ATGTTTCG  AGT
                                 T    _____      AC
GAM737  STAM    3'  TTGTAATTATTTGGGA     12964        T
                                TCCCAAATA TTACAA
                                ||||||||| ||||||
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                                AGGGTTTAT AATGTT
                                     T
GAM737  TGFBR2   3' CTTTATAAATATTTGG      12267          C
                                CCAAATATTTA AAAG
                                |||||||||| ||||
                                GGTTTATAAAT TTTC
                                     A
GAM737  ZNF14    3' TGTAAGACATTTGGGA      40718        A_
                                TCCCAAAT  TTTACA
                                ||||||||  ||||||
                                AGGGTTTA  GAATGT
                                    CA
GAM737  DKFZP434L1123 5' TGGTTTGTAAATATTTG     49585            G
                                CAAATATTTACAAA CCA
                                ||||||||||||| |||
                                GTTTATAAATGTTT GGT
                                              _
GAM737  DKFZP434O047 5' TGATGGCTCCACATCTTGGGG  31517       ATATTTACAA
                                TCCCAA         AGCCATCA
                                ||||||         ||||||||
                                GGGGTT         TCGGTAGT
                                   CTACACC___
GAM737  DKFZP564G092 5' TGGACAGTAAATATTTG     31539          AAAG
                                CAAATATTTAC   CCA
                                ||||||||||    |||
                                GTTTATAAATG   GGT
                                      ACA_
GAM737  DKFZP564O0823 3' ATGGCTGTAAAATGTTT     59519        ACAA
                                AAATATTT   AGCCAT
                                ||||||||   ||||||
                                TTTGTAAA   TCGGTA
                                     ATG_
GAM737  FLJ10036  3' GCTTTGTAAATATTTCAGA   94950    CC
                                TC  AAATATTTACAAAGC
                                ||  ||||||||||||||
                                AG  TTTATAAATGTTTCG
                                 AC
GAM737  FLJ11267  5' TGATGGCTCTAGAATGTCTAGG 39007     CAA     ACAA
           A                     TCC   ATATTT   AGCCATCA
                                |||   ||||||   ||||||||
                                AGG   TGTAAG   TCGGTAGT
                                  ATC     ATC_
GAM737  FLJ11730  3' TGGAGGCTGTAAATATCTGG   42798     A       AA   AT
                                CCA ATATTTACA  GCC  CA
                                ||| |||||||||  |||  ||
                                GGT TATAAATGT  CGG  GT
                                  C        __   AG
GAM737  FLJ13194  3' TGATAACTTTGTAAGATGGGA  47131      AATA       CC
                                TCCCA   TTTACAAAG  ATCA
                                |||||   |||||||||  ||||
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                                AGGGT   GAATGTTTC  TAGT
                                  A___       AA
GAM737  FLJ14564  3'  ATGGGGAAAATATTTGGGA   76499          ACAAAG
                                TCCCAAATATTT     CCAT
                                ||||||||||||     ||||
                                AGGGTTTATAAA     GGTA
                                      AGG___
GAM737  FLJ22596  5'  TGATGGCTTGATGGTATCTGG  46964    A    TACA
                                CCA ATATT   AAGCCATCA
                                ||| |||||   |||||||||
                                GGT TATGG   TTCGGTAGT
                                  C    TAG_
GAM737  FLJ25200  5'  TGATGGCTTCATTAACTATCTG 58514    A  T  CA_
          G                      CCA ATA TTA   AAGCCATCA
                                ||| ||| |||   |||||||||
                                GGT TAT AAT   TTCGGTAGT
                                  C  C   TAC
GAM737  FRAT1    3'  TGAGGGCCAAAATATTTGG   18496         ACAAA  A
                                CCAAATATTT    GCC TCA
                                ||||||||||    ||| |||
                                GGTTTATAAA    CGG AGT
                                      AC___   G
GAM737  GLUC     3'  ATGGCCTTTATTTGTATTTGG  40586        TTAC   _
                                CCAAATAT    AAAG CCAT
                                ||||||||    |||| ||||
                                GGTTTATG    TTTC GGTA
                                     TTTA   C
GAM737  GPR      3'  GGATTGTAAATTCTTGG     23336     AT      AG
                                CCAA  ATTTACAA  CC
                                ||||  ||||||||  ||
                                GGTT  TAAATGTT  GG
                                  CT       A_
GAM737  GSPT2    3'  GCTTTGTAAGTGATGTGG    36120     AA_
                                CCA   TATTTACAAAGC
                                |||   ||||||||||||
                                GGT   GTGAATGTTTCG
                                  GTA
GAM737  KIAA0453 3'  GTGTGTTTGTAAATATATAGGA 69051    CAA        GC
                                TCC   ATATTTACAAA  CAT
                                |||   ||||||||||  |||
                                AGG   TATAAATGTTT  GTG
                                  ATA         GT
GAM737  KIAA0746 3'  GCTTTGTAAATTGG       69454     AAT
                                CCA   ATTTACAAAGC
                                |||   ||||||||||
                                GGT   TAAATGTTTCG
                                      ___
GAM737  KIAA0884 3'  TGATTATTGTAAATATTTTGGA 70207    C         AGCC
                                TCC AAATATTTACAA    ATCA
                                ||| ||||||||||||    ||||
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                                AGG TTTATAAATGTT   TAGT
                                  T         AT__
GAM737  KIAA0930  3'  TGATGGCTTTGCCCTGGGCTGG 70554      AATATTTA
                GA                 TCCCA       CAAAGCCATCA
                                   |||||       ||||||||||||
                                   AGGGT       GTTTCGGTAGT
                                     CGGGTCCC
GAM737  KIAA1052  3'  TGATGGCTTTTATCCTCCTGGG 30252      AATATT  C
                A                  TCCCA     TA AAAGCCATCA
                                   |||||     || ||||||||||
                                   AGGGT     AT TTTCGGTAGT
                                     CCTCCT  _
GAM737  KIAA1557  3'  TTGTAAATATTTGTGA     61140    C
                                   TC CAAATATTTACAA
                                   || ||||||||||||
                                   AG GTTTATAAATGTT
                                    T
GAM737  KIAA1587  3'  TGATAGCTCTATAAAATGTTTT 40512     C       ACAA_   C
                GGA                  TCC AAATATTT     AGC ATCA
                                   ||| ||||||||     ||| ||||
                                   AGG TTTGTAAA     TCG TAGT
                                     T       ATATC   A
GAM737  LIPI     3'  ATGACTTTGTAAATATTT    79564             C
                                   AAATATTTACAAAG CAT
                                   |||||||||||||| |||
                                   TTTATAAATGTTTC GTA
                                          A
GAM737  MARCKS   3'  GTTTTGTAAATACTGGAGA   9870     _   AA
                                   TC CCA  TATTTACAAAGC
                                   || |||  ||||||||||||
                                   AG GGT  ATAAATGTTTTG
                                    A   C_
GAM737  MED6     3'  TGATGGCTTTGTTGCAGCTGAG 18439    C  AATATTT
                A                  TC CA      ACAAAGCCATCA
                                   || ||      ||||||||||||
                                   AG GT      TGTTTCGGTAGT
                                    A  CGACGT_
GAM737  MGC17330  3'  GTTTTTAAAATATTTGGGA   53531           AC
                                   TCCCAAATATTT  AAAGC
                                   ||||||||||||  |||||
                                   AGGGTTTATAAA  TTTTG
                                          AT
GAM737  OR51E2   3'  ATGGCTTTGTACTTGTGATG  47790    A_   TT
                                   CA  ATA  TACAAAGCCAT
                                   ||  |||  ||||||||||||
                                   GT  TGT  ATGTTTCGGTA
                                    AG   TC
GAM737  PSTPIP2  3'  CTTTCACAAATATTTGGG    44389          AC_
                                   CCCAAATATTT   AAAG
                                   ||||||||||   ||||
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                                GGGTTTATAAA  TTTC
                                      CAC
GAM737  PURG    3'  ATGGCTTTGCTATGG      25336    AATATT  _
                                CCA     TA CAAAGCCAT
                                |||     || |||||||||
                                GGT     AT GTTTCGGTA
                                  _______  C
GAM737  VDU1    3'  TGATGGCTTTGTTTTGGTTTGG 30431        ATTT
          GG                      TCCCAAAT   ACAAAGCCATCA
                                |||||||||   ||||||||||||
                                GGGGTTTG   TGTTTCGGTAGT
                                    GTTT
GAM737  ZNF294  3'  GCTTTGTAAATGTTTGG    70828
                                CCAAATATTTACAAAGC
                                |||||||||||||||||
                                GGTTTGTAAATGTTTCG

GAM737  LOC127162 3'  TGATGGCTACATATACTAGGGA 74638     AAA   TTACAA
                                TCCC   TAT     AGCCATCA
                                ||||   |||     ||||||||
                                AGGG   ATA     TCGGTAGT
                                  ATC   TACA__
GAM737  LOC148936 5'  TGATGGCTCTATAAGGGGGA   84303     AAA   TTACAA
                                TCCC   TAT     AGCCATCA
                                ||||   |||     ||||||||
                                AGGG   ATA     TCGGTAGT
                                  GGA   TC____
GAM737  LOC148938 5'  TGATGGCTCTATAAGGGGGA   84284     AAA   TTACAA
                                TCCC   TAT     AGCCATCA
                                ||||   |||     ||||||||
                                AGGG   ATA     TCGGTAGT
                                  GGA   TC____
GAM737  LOC152084 5'  GATGGCTTTCCTCAGCCTGGGA 85553      AATATTTAC
                                TCCCA        AAAGCCATC
                                |||||        |||||||||
                                AGGGT        TTTCGGTAG
                                   CCGACTCC_
GAM737  LOC152573 3'  GATGACTATATATTTGGG    80618         TTACAA  C
                                CCCAAATAT     AG CATC
                                |||||||||     || ||||
                                GGGTTTATA     TC GTAG
                                     TA____  A
GAM737  LOC152627 5'  ATGGCTTCTAAGTATTCAGG   80627    CA       CA
                                CC  AATATTTA  AAGCCAT
                                ||  ||||||||  |||||||
                                GG  TTATGAAT  TTCGGTA
                                 AC       C_
GAM737  LOC200301 3'  GCTTGTTATTTGGGG       88748         TTT    A
                                TCCCAAATA   ACAA GC
                                |||||||||   |||| ||
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                              GGGGTTTAT   TGTT CG
                                  ___   _
GAM738  ADAM19   3'  CAGGAAGAAGACTGGCCATTAT 52703      C   CTGAG
            G                    CATGA GGCT    TTCTTCCTG
                                 ||||| ||||    |||||||||
                                 GTATT CCGG    AAGAAGGAC
                                   A   TCAG_
GAM738  FACL5    5'  CAGGAAGAACTCAGAGCCG   64186
                                 CGGCTCTGAGTTCTTCCTG
                                 ||||||||||||||||||
                                 GCCGAGACTCAAGAAGGAC

GAM738  GNAL     5'  CAGGAAAGAGAGGAGCCGTCG  9058         GAG TC
                                 TGACGGCTCT   T  TTCCTG
                                 ||||||||||   |  ||||||
                                 GCTGCCGAGG   A  AAGGAC
                                      AG_ GA
GAM738  KAL1     3'  CAGGAAGAACTTCTGTCA    4013       CTCT
                                 TGACGG   GAGTTCTTCCTG
                                 ||||||   ||||||||||||
                                 ACTGTC   TTCAAGAAGGAC
                                     ____
GAM738  MYO1E    3'  CAGGAGGACAAAACCACCATG  17187     AC  CTC  AGT
                                 CATG  GG   TG   TCTTCCTG
                                 ||||  ||   ||   ||||||||
                                 GTAC  CC   AC   AGGAGGAC
                                   CA  AAA  ___
GAM738  PRKAR2B  3'  CAGAAAGAACTCAGATGT    10804    _        C
                                 GC TCTGAGTTCTT CTG
                                 || ||||||||||| |||
                                 TG AGACTCAAGAA GAC
                                  T         A
GAM738  PUM2     3'  AGGATCAAAGCTGTCATG    31014         C   GTTCT
                                 CATGACGGCT TGA    TCCT
                                 |||||||||| |||    ||||
                                 GTACTGTCGA ACT    AGGA
                                      A  _____
GAM738  SKI      3'  CAGGAAGTGCAGAGCCGCA   11701    A      AGTT
                                 TG CGGCTCTG   CTTCCTG
                                 || ||||||||   |||||||
                                 AC GCCGAGAC   GAAGGAC
                                  _       GT__
GAM738  TEM8     3'  AGGAAGATGCAACCCCATG   36326     AC  CTC  AGT
                                 CATG  GG   TG   TCTTCCT
                                 ||||  ||   ||   |||||||
                                 GTAC  CC   AC   AGAAGGA
                                   C_  A__  GT_
GAM738  ARHGEF4  5'  AGAAAAAACTCAGGGC     52207         C  C
                                 GCTCTGAGTT TT CT
                                 |||||||||| || ||
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                                CGGGACTCAA AA GA
                                      A  A
GAM738  FLJ31978  3'  CAGGAAGGAACAAGCGCC    58348     T  GAG
                                GGC CT   TTCTTCCTG
                                ||| ||   |||||||||
                                CCG GA   AGGAAGGAC
                                  C  ACA
GAM738  HSU24186  5'  AGAACTCAAAGCCGTC      25324        C
                                GACGGCT TGAGTTCT
                                ||||||| ||||||||
                                CTGCCGA ACTCAAGA
                                    A
GAM738  KCNT1     3'  AGCTCCCAGGGCCGCCA     61825    A      __
                                TG CGGCTCT  GAGTT
                                || |||||||  |||||
                                AC GCCGGGA  CTCGA
                                 C      CC
GAM738  KIAA1867  3'  CAGGAAGAACCCAAGAGCTCAT 94822      CG     GA_
                                ATGA  GCTCT   GTTCTTCCTG
                                ||||  |||||   ||||||||||
                                TACT  CGAGA   CAAGAAGGAC
                                  __    ACC
GAM738  KIAA1878  3'  AATTCAGAGAATCGTCATG   91707         __
                                CATGACGG  CTCTGAGTT
                                ||||||||  |||||||||
                                GTACTGCT  GAGACTTAA
                                     AA
GAM738  MFN1      3'  CAGGAAGAACTCATGA      35541    _
                                TC TGAGTTCTTCCTG
                                || ||||||||||||
                                AG ACTCAAGAAGGAC
                                 T
GAM738  MIDORI    3'  CAGGGCCCTTCCAGAGCCTGTC 73784        _      AGTTCT
            ATG                   CATGAC GGCTCTG     TCCTG
                                |||||| |||||||     |||||
                                GTACTG CCGAGAC     GGGAC
                                   T      CTTCCC
GAM738  MYH7B     3'  CAGGAAGAACCTGGCTCGCATG 70530      A  _  CTGA
                                CATG CG GCT    GTTCTTCCTG
                                |||| || |||    ||||||||||
                                GTAC GC CGG    CAAGAAGGAC
                                  _ T   TC__
GAM738  RNAHP     3'  AGAAAGCAGCAGCCGTCAT    23761         _  AG
                                ATGACGGCT CTG  TTCT
                                ||||||||| |||  ||||
                                TACTGCCGA GAC  AAGA
                                      C   GA
GAM738  SLC37A1   3'  AGACGGAGCTCAGACCC     38561    C        TC
                                GG TCTGAGTTCT  CT
                                || ||||||||||  ||
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                                CC AGACTCGAGG  GA
                                 C         CA
GAM738  LOC116236 3'  CAGGAAAAGCACAAACCTCAT  73809     C  CTC  A   C
                                ATGA GG   TG GTT TTCCTG
                                |||| ||   || ||| ||||||
                                TACT CC   AC CGA AAGGAC
                                  _  AA_  A   A
GAM738  LOC124801 3'  CAGGAAGAACTCTCTTGCATG  74336     A   CTCT
                                CATG CGG    GAGTTCTTCCTG
                                |||| |||    ||||||||||||
                                GTAC GTT    CTCAAGAAGGAC
                                  _   CT__
GAM738  LOC222160 5'  AGGAAGAACTCACCCC      94117    CTC
                                GG   TGAGTTCTTCCT
                                ||   ||||||||||||
                                CC   ACTCAAGAAGGA
                                 CC_
GAM738  LOC51094  3'  CAGGAAGAATAAAGCC      32045     CTGA
                                GGCT    GTTCTTCCTG
                                ||||    ||||||||||
                                CCGA    TAAGAAGGAC
                                  AA__
GAM738  LOC92078  3'  CAGGAAGAAGAATCGACCGTC  67977      C  T  G__
                                GACGG TC GA   TTCTTCCTG
                                ||||| || ||   |||||||||
                                CTGCC AG CT   AAGAAGGAC
                                  _ _  AAG
GAM739  A1BG      3'  CAGGGTCTCACTGTGTTGC    55413        TAT_
                                GCAACACA    GGCTTTG
                                ||||||||    |||||||
                                CGTTGTGT    CTGGGAC
                                    CACT
GAM739  ACPT      3'  CACCCCGCCATATGCTGC     54986     ACA      TTT
                                GCA   CATATGGC   GTG
                                |||   ||||||||   |||
                                CGT   GTATACCG   CAC
                                  C__       CCC
GAM739  ACPT      3'  CACCCCGCCATATGCTGC     54980     ACA      TTT
                                GCA   CATATGGC   GTG
                                |||   ||||||||   |||
                                CGT   GTATACCG   CAC
                                  C__       CCC
GAM739  AHCY      3'  CACAAAGCCCATGTGTTTTGC  5473       C       _
                                GCAA ACATATGG CTTTGTG
                                |||| |||||||| |||||||
                                CGTT TGTGTACC GAAACAC
                                  T       C
GAM739  BCL7A     3'  CAGGATTCCATTTGTGTTGCT  40638         T   CT  G
                                AGCAACACA ATGG  TT TG
                                ||||||||| ||||  || ||
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                                TCGTTGTGT TACC  AG AC
                                     T    TT  G
GAM739  CDK5R2   3'  CACAAAGCCACCGCCGCTGTT  14132      ACACATA
                                AGCA      TGGCTTTGTG
                                ||||      ||||||||||
                                TTGT      ACCGAAACAC
                                  CGCCGCC
GAM739  CHC1     3'  CACAAAGCATACTCTTGC    7019       CACA    G
                                GCAA    TATG CTTTGTG
                                ||||    |||| |||||||
                                CGTT    ATAC GAAACAC
                                  CTC_    _
GAM739  CIT      3'  CACAAGGCATCTGTTGCT    69741        CATATG
                                AGCAACA     GCTTTGTG
                                |||||||     ||||||||
                                TCGTTGT     CGGAACAC
                                    CTA___
GAM739  COL6A2   5'  CAGGGCCACAGGTGCTGC    54168     A   ATA
                                GCA CAC   TGGCTTTG
                                ||| |||   ||||||||
                                CGT GTG   ACCGGGAC
                                  C   GAC
GAM739  COL6A2   5'  CAGGGCCACAGGTGCTGC    8480      A   ATA
                                GCA CAC   TGGCTTTG
                                ||| |||   ||||||||
                                CGT GTG   ACCGGGAC
                                  C   GAC
GAM739  EYA1     3'  CACAGCGTTATGTGTCTGC    4952      AC       T
                                GCA  ACATATGGC TTGTG
                                |||  ||||||||| |||||
                                CGT  TGTGTATTG GACAC
                                  C_       C
GAM739  FBN2     3'  CAAGGAACCATATGTG      8844          __
                                CACATATGG  CTTTG
                                |||||||||  |||||
                                GTGTATACC  GGAAC
                                     AA
GAM739  FMO1     3'  CACAAATGATTGTGTTGT    8924         TATGGC
                                GCAACACA     TTTGTG
                                ||||||||     ||||||
                                TGTTGTGT     AAACAC
                                    TAGT__
GAM739  GALNT2   3'  CACAAAGCCGTTCGCAGCT   15594     AACACAT
                                AGC      ATGGCTTTGTG
                                |||      ||||||||||
                                TCG      TGCCGAAACAC
                                  ACGCT__
GAM739  GALNT2   3'  CACAAAGCCGAGTCGTGT    15593      _  A
                                ACAC AT TGGCTTTGTG
                                |||| || ||||||||||
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```
                                TGTG TG GCCGAAACAC
                                  C  A
GAM739  GPR4    3'  CAGGGTCTCACTGTGTTGC   59902       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM739  HNMT    3'  CACAAAGCCTGTGTTACT   22567   C    TAT
                                AG AACACA  GGCTTTGTG
                                || ||||||  |||||||||
                                TC TTGTGT  CCGAAACAC
                                 A    ___
GAM739  IL1RN   3'  CACAAAGCCCTTCCATGTCGC 5141    A  CATAT_
                                GC ACA     GGCTTTGTG
                                || |||     |||||||||
                                CG TGT     CCGAAACAC
                                 C  ACCTTC
GAM739  IL2RB   3'  CACAAAGTGGATGCCTGCT   6069     ACA  ATG
                                AGCA  CAT  GCTTTGTG
                                ||||  |||  ||||||||
                                TCGT  GTA  TGAAACAC
                                  CC_  GG_
GAM739  ITSN2   3'  CACAAAGCCATGCACGCT   38971    AACACA
                                AGC    TATGGCTTTGTG
                                |||    ||||||||||||
                                TCG    GTACCGAAACAC
                                 CAC___
GAM739  JRK     3'  CAGGGTCTCACTGTGTTGC   86524       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM739  LANCL1  3'  CACAATTTTATATGTATGCT  20210    AC     CT
                                AGCA ACATATGG TTGTG
                                |||| |||||||| |||||
                                TCGT TGTATATT AACAC
                                  A_      TT
GAM739  LGR6    5'  GGCCATCGTGTTGCT     84200       AT
                                AGCAACAC ATGGCT
                                |||||||| ||||||
                                TCGTTGTG TACCGG
                                    C_
GAM739  LRRC2   3'  CAAGGCACCATGTGTTACT   44465   C    ATG
                                AG AACACAT  GCTTTG
                                || |||||||  ||||||
                                TC TTGTGTA  CGGAAC
                                 A     CCA
GAM739  MYBL2   3'  CAGGGCCATGTGCTGC     10154    ACA
                                GCA  CATATGGCTTTG
                                |||  ||||||||||||
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                              CGT   GTGTACCGGGAC
                                C__
GAM739  OCLN    3'  CACAAAGTTTTGGTTGCT    10314       A  TAT
                              AGCAAC CA   GGCTTTGTG
                              |||||| ||   |||||||||
                              TCGTTG GT   TTGAAACAC
                                 _  T__
GAM739  OSR1    3'  CACAAAGTAATATGTG      17566       G
                              CACATAT GCTTTGTG
                              ||||||| ||||||||
                              GTGTATA TGAAACAC
                                  A
GAM739  PCDH9   5'  CACAAAGTGACAGTGCTGGCT  82794     AA_   ATATG
                              AGC   CAC    GCTTTGTG
                              |||   |||    ||||||||
                              TCG   GTG    TGAAACAC
                                GTC   ACAG_
GAM739  PRDM2   5'  CACAAAGCCACATCCTGC    31847     ACAC  A
                              GCA    AT TGGCTTTGTG
                              |||    || ||||||||||
                              CGT    TA ACCGAAACAC
                                CC__  C
GAM739  PRDM2   5'  CACAAAGCCACATCCTGC    24246     ACAC  A
                              GCA    AT TGGCTTTGTG
                              |||    || ||||||||||
                              CGT    TA ACCGAAACAC
                                CC__  C
GAM739  PRG4    3'  CACAAAGCTTTATCGTGTTGT  19415       _   T
                              GCAACAC ATA GGCTTTGTG
                              ||||||| ||| |||||||||
                              TGTTGTG TAT TCGAAACAC
                                  C   T
GAM739  RXRB    3'  CACAAAGCACTGGCCTTGC    41757      CA_  TATG
                              GCAA   CA    GCTTTGTG
                              ||||   ||    ||||||||
                              CGTT   GT    CGAAACAC
                                CCG  CA__
GAM739  SMARCD1 3'  CACAAAGTTCCCATGTG      57429       ___
                              CATATGG   CTTTGTG
                              |||||||   |||||||
                              GTGTACC   GAAACAC
                                  CTT
GAM739  SMARCD1 3'  CACAAAGTTCCCATGTG      11811       ___
                              CATATGG   CTTTGTG
                              |||||||   |||||||
                              GTGTACC   GAAACAC
                                  CTT
GAM739  SMURF1  3'  CACGTGTGATCTGTGTTGC    92448        T  G  TT
                              GCAACACA AT GC  TGTG
                              |||||||| || ||  ||||
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                                CGTTGTGT TA TG  GCAC
                                    C  G  T_
GAM739  STX7    3'  CACCAAGATGTGTGTTACT   13108   C      GG   T
                                AG AACACATAT  CTT GTG
                                || |||||||||  ||| |||
                                TC TTGTGTGTA  GAA CAC
                                 A       __  C
GAM739  TAF4B   3'  CACAAAGCATTGTTGC     87167      CATATG
                                GCAACA    GCTTTGTG
                                ||||||    ||||||||
                                CGTTGT    CGAAACAC
                                   TA____
GAM739  TF      3'  CACAGCTCTGTGTTGC     6512       TAT   T
                                GCAACACA  GGCT TG
                                ||||||||  |||| ||
                                CGTTGTGT  TCGA AC
                                    C__   C
GAM739  TLR4    5'  CACAGGGCCACTGCTGCT   56727    A  CATA
                                AGCA CA   TGGCTTTGTG
                                |||| ||   ||||||||||
                                TCGT GT   ACCGGGACAC
                                  C  C___
GAM739  TLR4    5'  CACAGGGCCACTGCTGCT   56736    A  CATA
                                AGCA CA   TGGCTTTGTG
                                |||| ||   ||||||||||
                                TCGT GT   ACCGGGACAC
                                  C  C___
GAM739  TLR4    5'  CACAGGGCCACTGCTGCT   12317    A  CATA
                                AGCA CA   TGGCTTTGTG
                                |||| ||   ||||||||||
                                TCGT GT   ACCGGGACAC
                                  C  C___
GAM739  TLR4    5'  CACAGGGCCACTGCTGCT   56732    A  CATA
                                AGCA CA   TGGCTTTGTG
                                |||| ||   ||||||||||
                                TCGT GT   ACCGGGACAC
                                  C  C___
GAM739  VIPR2   3'  CACAGTCTCCATGTGTGTGC  12605    A      CT_
                                GCA CACATATGG  TTGTG
                                ||| |||||||||  |||||
                                CGT GTGTGTACC  GACAC
                                  _       TCT
GAM739  ANKT    3'  CAGGGTCTCACTGTGTTGC   33024       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM739  ATP9A   3'  CACAAAGCCAGTGGCTGTT   62039    A_  ATA
                                AGCA  CAC  TGGCTTTGTG
                                ||||  |||  ||||||||||
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                                TTGT  GTG   ACCGAAACAC
                                  CG  ___
GAM739  CETN2    3'  CACATGTTACACCTGTGTTGC  15093        TA  GCTT_
                                GCAACACA  TG    TGTG
                                ||||||||  ||    ||||
                                CGTTGTGT  AC    ACAC
                                    CC  ATTGT
GAM739  CYLD     3'  CACAAGGTTTTATACTGCT   30883     ACAC   TG
                                AGCA   ATA  GCTTTGTG
                                ||||   |||  ||||||||
                                TCGT   TAT  TGGAACAC
                                  CA__   TT
GAM739  DKFZP586A0522 3'  CAGGGTCTCACTGTGTTGC   25871        TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM739  DKFZp762K222 3'  ACAGATGCGTGTTGCT     71116        ATATG  _
                                AGCAACAC    GC TTTGT
                                ||||||||    || |||||
                                TCGTTGTG    CG AGACA
                                    _____  T
GAM739  FLJ10297  3'  CAGGGCTTCACTGTGTTGC   35979        TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   TCGGGAC
                                    CACT
GAM739  FLJ10511  3'  CACATGTGTATGTGCAGCT   36204     AA      G TT
                                AGC  CACATATG C  TGTG
                                |||  |||||||| |  ||||
                                TCG  GTGTATGT G  ACAC
                                  AC       _ T_
GAM739  FLJ11029  5'  CACTAGCACCTGTGTTGCT   60973        TATG   TT
                                AGCAACACA   GCT  GTG
                                |||||||||   |||  |||
                                TCGTTGTGT   CGA  CAC
                                    CCA_   T_
GAM739  FLJ11117  3'  CACAAAGCTTGTATGTG     37073        _
                                CACATATG GCTTTGTG
                                |||||||| ||||||||
                                GTGTATGT CGAAACAC
                                    T
GAM739  FLJ11715  3'  CAGGGTCTCCATATGTTGC   44668      C  AT_
                                GCAACA AT   GGCTTTG
                                ||||||  ||  |||||||
                                CGTTGT TA   CTGGGAC
                                   A  CCT
GAM739  FLJ20275  3'  CACAAAGGGCTTTATGTGTCAG 34819     A_     T   __
            CT                    AGC  ACACATA GGCT  TTGTG
                                |||  ||||||| ||||  |||||
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                                TCG  TGTGTAT TCGG  AACAC
                                  AC      T   GA
GAM739  FLJ20413  3'  CAGAGCCGCATGCACTGCT   35131     ACA   A
                                AGCA   CAT TGGCTTTG
                                ||||   ||| ||||||||
                                TCGT   GTA GCCGAGAC
                                  CAC   C
GAM739  FLJ20450  3'  CACCTGGGACCTGTGTTGCT   35192        TAT  _   T_
                                AGCAACACA   GG CTT  GTG
                                |||||||||   || |||  |||
                                TCGTTGTGT   CC GGG  CAC
                                     ___  A   TC
GAM739  FLJ20671  3'  CAATTCAAATGTGTTGC     35516         A   CT
                                GCAACACAT TGG  TTG
                                ||||||||| |||  |||
                                CGTTGTGTA ACT  AAC
                                      A   T_
GAM739  FLJ23598  3'  CACAAAGAGAGGCTGTGCTGC  45521     A    TATGG_
                                GCA CACA     CTTTGTG
                                ||| ||||     |||||||
                                CGT GTGT     GAAACAC
                                  C    CGGAGA
GAM739  FRSB      3'  CATAGGCCATACATGTTACT   19090    C    CA      T
                                AG AACA  TATGGCTT GTG
                                || ||||  |||||||| |||
                                TC TTGT  ATACCGGA TAC
                                 A    AC       _
GAM739  H2AV      3'  CACAGCCATATGTATTGTT    56845      C        T
                                AGCAA ACATATGGCT TG
                                ||||| |||||||||| ||
                                TTGTT TGTATACCGA AC
                                   A         C
GAM739  HIC2      3'  CACAAAGTCTGTACCGC     65256    AAC   TAT
                                GC   ACA   GGCTTTGTG
                                ||   |||   |||||||||
                                CG   TGT   CTGAAACAC
                                 CCA   ___
GAM739  KIAA0140  3'  CACATGGCCATGTCTTGC    27806     CAC       T
                                GCAA   ATATGGCT TGTG
                                ||||   |||||||| ||||
                                CGTT   TGTACCGG ACAC
                                  C__       T
GAM739  KIAA0215  3'  CAAATTCCATATGTAATGC   28416     AC       C_
                                GCA  ACATATGG  TTTG
                                |||  ||||||||  ||||
                                CGT  TGTATACC  AAAC
                                  AA       TT
GAM739  KIAA0254  3'  AGCCACCTGTGTTGCT      28595         TA
                                AGCAACACA  TGGCT
                                |||||||||  |||||
```

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                              TCGTTGTGT  ACCGA
                                   CC
GAM739  KIAA0618 3' CACAAAAACATGTGTTGT    29162       TA  GC
                              GCAACACA  TG  TTTGTG
                              ||||||||  ||  ||||||
                              TGTTGTGT  AC  AAACAC
                                   __  AA
GAM739  KIAA0953 3' AGCTTTCATAGTGTTGCT    66778       A   ___
                              AGCAACAC TATG   GCT
                              |||||||| ||||   |||
                              TCGTTGTG ATAC   CGA
                                   _   TTT
GAM739  KIAA1193 3' CACAGAGCCATATACCTCGCT 67630     AACAC
                              AGC    ATATGGCTTTGTG
                              |||    ||||||||||||||
                              TCG    TATACCGAGACAC
                                CTCCA
GAM739  KIAA1281 3' CACAGAGTAACAAATGTTGCT 89151       CATATG
                              AGCAACA     GCTTTGTG
                              |||||||     ||||||||
                              TCGTTGT     TGAGACAC
                                  AAACAA
GAM739  KIAA1466 5' AGCCATATGTGCGCT      71913     AA
                              AGC  CACATATGGCT
                              |||  ||||||||||
                              TCG  GTGTATACCGA
                                C_
GAM739  KIAA1821 3' CAGGGTCTCACTGTGTTGC   71780       TAT_
                              GCAACACA    GGCTTTG
                              ||||||||    |||||||
                              CGTTGTGT    CTGGGAC
                                   CACT
GAM739  KIF13B   3' CACAAAGTCCGTGGTGC     30904     A  ATAT
                              GCA CAC    GGCTTTGTG
                              ||| |||    |||||||||
                              CGT GTG    CTGAAACAC
                                G  C___
GAM739  KIF13B   3' CACAAAGTCCGTGGTGC     82820     A  ATAT
                              GCA CAC    GGCTTTGTG
                              ||| |||    |||||||||
                              CGT GTG    CTGAAACAC
                                G  C___
GAM739  MGC12921 3' CACAAAGGCCGTTATTGC    63775     CACAT   _
                              GCAA    ATGGC TTTGTG
                              ||||    ||||| ||||||
                              CGTT    TGCCG AAACAC
                                AT___    G
GAM739  MGC14836 5' CACAAAGCTATCATCCTGC   53035     ACACAT
                              GCA     ATGGCTTTGTG
                              |||     ||||||||||
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                              CGT     TATCGAAACAC
                                CCTAC_
GAM739  MGC15429 3' CACATTGTCATGTGCAGCT   51249    AACA      TT
                              AGC   CATATGGC  TGTG
                              |||   ||||||||  ||||
                              TCG   GTGTACTG  ACAC
                                AC__      TT
GAM739  MGC15875 3' CGAGGCCATAATGCT     51908     ACACA
                              AGCA    TATGGCTTTG
                              ||||    ||||||||||
                              TCGT    ATACCGGAGC
                                A____
GAM739  MGC16279 5' GAAGCCATCGTGTCGCT    51888    A   AT
                              AGC ACAC  ATGGCTTT
                              ||| ||||  ||||||||
                              TCG TGTG  TACCGAAG
                                C   C_
GAM739  MGC27434 3' CACAATAAGTATGTGTT    58947        GGCT
                              AACACATAT   TTGTG
                              |||||||||   |||||
                              TTGTGTATG   AACAC
                                   AAT_
GAM739  MGC3048  3' CACAAAGCATGAATGTT    43899     CA   G
                              AACA  TATG CTTTGTG
                              ||||  |||| |||||||
                              TTGT  GTAC GAAACAC
                                AA   _
GAM739  MIG-6    3' CACAAGCTGGCCTTGTGTTGCT 38486        TAT   ___
                              AGCAACACA   GGCT   TTGTG
                              |||||||||   ||||   |||||
                              TCGTTGTGT   CCGG   AACAC
                                   T__    TCG
GAM739  MUC17    3' CACTGCCCCATATGTGTCCCT  94271    CA       CTTT
                              AG  ACACATATGG   GTG
                              ||  ||||||||||   |||
                              TC  TGTGTATACC   CAC
                               CC        CCGT
GAM739  MYO3B    3' CACTCTCCCACATGTGTTGT   57301        A   CTTT
                              GCAACACAT TGG    GTG
                              |||||||| |||    |||
                              TGTTGTGTA ACC    CAC
                                   C   CTCT
GAM739  NS1-BP   3' CACAAAGCTTTTGCATATTGC  72542     CA__  TAT
                              GCAA   CA   GGCTTTGTG
                              ||||   ||   |||||||||
                              CGTT   GT   TCGAAACAC
                                ATAC  TT_
GAM739  OR51E2   3' CACAGGTTTTATGTGTTCT   47791    C      TG   T
                              AG AACACATA  GCTT GTG
                              || ||||||||  |||| |||
```

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                                TC TTGTGTAT  TGGA CAC
                                 _      TT   _
GAM739  PRDM11   3'  CAGGTGCTCCATGTGTTGC   39581        AT  _
                                GCAACACAT  GGC TTTG
                                |||||||||  ||| ||||
                                CGTTGTGTA  TCG GGAC
                                     CC   T
GAM739  PRO0943  5'  CACAAAAGTGTTATATGTG   37701        ___
                                CACATATGGC   TTTGTG
                                ||||||||||   ||||||
                                GTGTATATTG   AAACAC
                                      TGA
GAM739  SULT1C2  5'  CACAACGCAGCCATATGCTG  21674   _      ___
                                CA CATATGGCT   TTGTG
                                || |||||||||   |||||
                                GT GTATACCGA   AACAC
                                 C        CGC
GAM739  VEST1    3'  CACCTGCCATACATGTTGT   53685      CA     TTT
                                GCAACA  TATGGC   GTG
                                ||||||  ||||||   |||
                                TGTTGT  ATACCG   CAC
                                   AC     TC_
GAM739  ZFP100   3'  AGTCACCTGTGTTGCT     70049        TA
                                AGCAACACA  TGGCT
                                |||||||||  |||||
                                TCGTTGTGT  ACTGA
                                     CC
GAM739  ZNF363   5'  AGCCATATTGTCGCT      73452     A  C
                                AGC ACA ATATGGCT
                                ||| ||| ||||||||
                                TCG TGT TATACCGA
                                  C  _
GAM739  LOC118611 5'  CACAGAGCATTTGCGTTACT  75469    C   A  TATG
                                AG AAC CA    GCTTTGTG
                                || ||| ||    ||||||||
                                TC TTG GT    CGAGACAC
                                 A   C  TTA_
GAM739  LOC120526 3'  CAGGGCCATTGCACTGCT    74015     ACA  T
                                AGCA   CA ATGGCTTTG
                                ||||   || |||||||||
                                TCGT   GT TACCGGGAC
                                  CAC  _
GAM739  LOC126669 3'  CACAAAGTTCCATATGT     75399        __
                                ACATATGG  CTTTGTG
                                ||||||||  |||||||
                                TGTATACC  GAAACAC
                                     TT
GAM739  LOC139840 5'  CACAAGAGCCATGGGT      76266     A       _
                                AC TATGGCTTT GTG
                                || |||||||| |||
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                                TG GTACCGAGA CAC
                                 G       A
GAM739  LOC143465 5'  CACATGCACATATGTG     82962        _  TT
                                CACATATG GC  TGTG
                                |||||||| ||  ||||
                                GTGTATAC CG  ACAC
                                    A  T_
GAM739  LOC146774 3'  CACTGACATGTGTGTGC     78094     A      GCTTT
                                GCA CACATATG    GTG
                                ||| ||||||||    |||
                                CGT GTGTGTAC    CAC
                                  _      AGT__
GAM739  LOC147407 5'  CACAAAGCTATCATCCTGC   76322     ACACAT
                                GCA     ATGGCTTTGTG
                                |||     ||||||||||
                                CGT     TATCGAAACAC
                                  CCTAC_
GAM739  LOC151057 3'  ACAGAGCACATACTGT      85199     _   _
                                ACA TATG GCTTTGT
                                ||| |||| |||||||
                                TGT ATAC CGAGACA
                                  C   A
GAM739  LOC151473 3'  CACAACAACCTATGTGTT    80254        T  CT_
                                AACACATA GG   TTGTG
                                |||||||| ||   |||||
                                TTGTGTAT CC   AACAC
                                    _ AAC
GAM739  LOC154739 5'  CACAAAGTTCAAATGTATGC  86227     AC   A  _
                                GCA  ACAT TGG CTTTGTG
                                |||  |||| ||| |||||||
                                CGT  TGTA ACT GAAACAC
                                  A_   A  T
GAM739  LOC157507 5'  CACAGCTGTGTATGTGTGCT  81454      A     __   T
                                AGCA CACATAT  GGCT TG
                                |||| |||||||  |||| ||
                                TCGT GTGTATG  TCGA AC
                                  _      TG   C
GAM739  LOC161734 3'  CACAAACATTTAGTGTTGCT  87097        AT_  GC
                                AGCAACAC   ATG  TTTGTG
                                ||||||||   |||  ||||||
                                TCGTTGTG   TAC  AAACAC
                                    ATT  __
GAM739  LOC196410 3'  CACAAAAGTCATGGTG      87657     A       _
                                CAC TATGGCTTT GTG
                                ||| ||||||||| |||
                                GTG GTACTGAAA CAC
                                  _       A
GAM739  LOC196485 3'  CACAAAAACCTGTGTTGT    87730        TAT  C_
                                GCAACACA   GG  TTTGTG
                                ||||||||   ||  ||||||
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                                TGTTGTGT  CC  AAACAC
                                    ___  AA
GAM739  LOC196529 3'  CAGGGTCTCACTGTGTTGC   87771       TAT_
                                GCAACACA   GGCTTTG
                                ||||||||   |||||||
                                CGTTGTGT   CTGGGAC
                                    CACT
GAM739  LOC197003 5'  CACAAAGCTCCATGCTGT    87870    _  AT
                                ACA CAT  GGCTTTGTG
                                ||| |||  |||||||||
                                TGT GTA  TCGAAACAC
                                  C   CC
GAM739  LOC202025 5'  CACAGTTGTATGGTTGCT    90281      A   TG  T
                                AGCAAC CATA  GCT TG
                                |||||| ||||  ||| ||
                                TCGTTG GTAT  TGA AC
                                   _   GT  C
GAM739  LOC203276 3'  CACAAAGTTCAAGTGTATGC  90475    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM739  LOC203292 3'  CAGGGTTTCATATGTGTT    90509        __
                                AACACATATG  GCTTTG
                                ||||||||||  ||||||
                                TTGTGTATAC  TGGGAC
                                     TT
GAM739  LOC203305 3'  CACAAAGTTCAAGTGTATGC  90519    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM739  LOC221354 3'  CACAAAAACATGTGTTGT    92409       TA  GC
                                GCAACACA  TG  TTTGTG
                                ||||||||  ||  ||||||
                                TGTTGTGT  AC  AAACAC
                                    __  AA
GAM739  LOC254243 3'  CACAAAGTTCAAGTGTATGC  97404    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
                                CGT TGTG   TTGAAACAC
                                  A   AAC_
GAM739  LOC255870 3'  CACAACTGGCCATGTCCTGC  94657    ACAC     __
                                GCA   ATATGGCT  TTGTG
                                |||   ||||||||  |||||
                                CGT   TGTACCGG  AACAC
                                  CC__      TC
GAM739  LOC90038  3'  CACAAAGTTCAAGTGTATGC  61148    _   ATAT
                                GCA ACAC   GGCTTTGTG
                                ||| ||||   |||||||||
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                                CGT TGTG    TTGAAACAC
                                  A    AAC_
GAM739  LOC90321  3'  CACAAATGGATTGTGTGTGC   62262     A     TGGC_
                                GCA CACATA     TTTGTG
                                ||| ||||||     ||||||
                                CGT GTGTGT     AAACAC
                                  _     TAGGT
GAM739  LOC90750  3'  CACAAAGTTAAGATTGCT    63917      CACATA
                                AGCAA     TGGCTTTGTG
                                |||||     ||||||||||
                                TCGTT     ATTGAAACAC
                                   AGA___
GAM739  LOC91069  3'  GAAGCCATCGTGTCACT     64778    CA    AT
                                AG  ACAC  ATGGCTTT
                                ||  ||||  ||||||||
                                TC  TGTG  TACCGAAG
                                 AC    C_
GAM739  LOC92539  3'  CACAAAGCCACTGTAGC     69630    A   CATA
                                GC ACA    TGGCTTTGTG
                                || |||    ||||||||||
                                CG TGT    ACCGAAACAC
                                 A   C___
GAM740  PMX1      3'  TAATACTTACCTACCTCA    22595           C
                                TGAGGTAGGTAAGT ATTG
                                |||||||||||||| ||||
                                ACTCCATCCATTCA TAAT
                                              _
GAM740  PMX1      3'  TAATACTTACCTACCTCA    42662           C
                                TGAGGTAGGTAAGT ATTG
                                |||||||||||||| ||||
                                ACTCCATCCATTCA TAAT
                                              _
GAM740  WIG1      3'  GTGACCTACCTACCCCA     94469    A      A
                                TG GGTAGGTA GTCAT
                                || |||||||| |||||
                                AC CCATCCAT CAGTG
                                 C       C
GAM740  ABCF2     5'  TGAAACAACAGTAACCTACC   19099       AAGTCA
                                GGTAGGT     TTGTTTCA
                                |||||||     ||||||||
                                CCATCCA     AACAAAGT
                                    ATGAC_
GAM740  CTPS2     3'  AAACCCATACTACTACCTCA   39081       GTA   CATT
                                TGAGGTAG   AGT    GTTT
                                ||||||||   |||    ||||
                                ACTCCATC   TCA    CAAA
                                    A__    TACC
GAM740  CYP4F8    3'  CAGTGACCCACCCACCT     23409     A   AA
                                AGGT GGT  GTCATTG
                                |||| |||  |||||||
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                                TCCA CCA  CAGTGAC
                                  C   CC
GAM740  DKFZp761N1114 3' AGTACCTACCCTACCTCA    79013        TA  TC
                                TGAGGTAGG  AG  ATT
                                |||||||||  ||  |||
                                ACTCCATCC  TC  TGA
                                     CA  CA
GAM740  FLJ11082  3' TGAAACAATAACTCTGCACCA  37036    AG   GTA   C
                                TG  GTAG   AGT ATTGTTTCA
                                ||  ||||   ||| |||||||||
                                AC  CGTC   TCA TAACAAAGT
                                 CA   ___  A
GAM740  FLJ11560  3' AGACTCTGACCCACCTACCTCA 47215         AA   TT
                                TGAGGTAGGT  GTCA  GTTT
                                ||||||||||  ||||  ||||
                                ACTCCATCCA  CAGT  CAGA
                                      CC    CT
GAM740  FLJ20485  3' CAGTGACTCTCCCACCTCA   38765       A  TA
                                TGAGGT GG  AGTCATTG
                                ||||||  ||  ||||||||
                                ACTCCA CC  TCAGTGAC
                                   C  TC
GAM740  FLJ20511  3' AAACAATGAATGAGCCACCTTA 35316       A   AAG_
                                TGAGGT GGT    TCATTGTTT
                                ||||||  |||   |||||||||
                                ATTCCA CCG    AGTAACAAA
                                   _  AGTA
GAM740  KIAA0557  3' TGACTTCCTACCTCA       78011         T
                                TGAGGTAGG AAGTCA
                                ||||||||| ||||||
                                ACTCCATCC TTCAGT

                                      _
GAM740  KIAA1274  3' TAATACTTGCCTACCT      91369           C
                                AGGTAGGTAAGT ATTG
                                |||||||||||| ||||
                                TCCATCCGTTCA TAAT

                                     _
GAM740  KIAA1297  3' TGACTCTCCTACCTCA      72188         TA
                                TGAGGTAGG  AGTCA
                                |||||||||  |||||
                                ACTCCATCC  TCAGT
                                     TC
GAM740  KIAA1571  5' TAGTGACTGACCCACCTCA   60959       A   A
                                TGAGGT GGT AGTCATTG
                                ||||||  ||| ||||||||
                                ACTCCA CCA TCAGTGAT
                                   C   G
GAM740  ZNF396    3' GAAACAACAAGTGCCTCA    75668        GGTAAGTCA
                                TGAGGTA       TTGTTTC
                                |||||||       |||||||
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                                ACTCCGT       AACAAAG
                                   GAAC_____
GAM740  LOC130576 5'  AAACAATAACTGCCTA     74953       A  C
                                TAGGTA GT ATTGTTT
                                ||||||| || |||||||
                                ATCCGT CA TAACAAA
                                   _  A
GAM740  LOC153339 3'  TGATTACCTACCTCA      86015           G
                                TGAGGTAGGTAA TCA
                                |||||||||||| |||
                                ACTCCATCCATT AGT
                                      _
GAM740  LOC158563 3'  TAATTGCCCTACCTACCTCA  81952          A_  C
                                TGAGGTAGGTA  GT ATTG
                                ||||||||||  || ||||
                                ACTCCATCCAT  CG TAAT
                                      CC  T
GAM740  LOC200942 3'  TGAAACCTTCCTACCCTACCTA 88949          A_  CATT__
          CCTCA                    TGAGGTAGGTA  GT     GTTTCA
                                ||||||||||  ||     ||||||
                                ACTCCATCCAT  CA     CAAAGT
                                      CC  TCCTTC
GAM740  LOC255349 3'  GAAATCATACCTACCTCA    95612          AGTCAT  _
                                TGAGGTAGGTA     TG TTTC
                                ||||||||||     || ||||
                                ACTCCATCCAT     AC AAAG
                                      _______ T
GAM741  DAAM2    3'  CACCTGGAAACAAAAGGAC   92284    A_  C  C
                                GT  TT TG TTCCAGGTG
                                ||  || || |||||||||
                                CA  AA AC AAGGTCCAC
                                  GG  A  A
GAM741  HLCS     5'  CTTGAAGCAGAACACATAGCA  4665         A       C
                                TGCTATGT TTCTGCTTC AG
                                |||||||| ||||||||| ||
                                ACGATACA AAGACGAAG TC
                                     C       T
GAM741  PHKA2    3'  ACCTGGAAACATGATCACA   4304      AT  _  C
                                TGT  TC TG TTCCAGGT
                                |||  || || ||||||||
                                ACA  AG AC AAGGTCCA
                                  CT  T  A
GAM741  CLDN1    3'  CACCTGGAAACAGACCAATAGA 40848    _   GTAT   C
          CA                      TG CTAT   TCTG TTCCAGGTG
                                || ||||   |||| |||||||||
                                AC GATA   AGAC AAGGTCCAC
                                 A   ACC_   A
GAM741  FLJ00024  3'  CACCTGGACCGCCGACACACAG 63750     A   AT  T  T_
          C                       GCT TGT  TC GC  TCCAGGTG
                                ||| |||  || ||  ||||||||
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                                CGA ACA  AG CG  AGGTCCAC
                                  C   C_  C  CC
GAM741  KRT6IRS   3'  CACCCAGAAGCAGAGAAAAGCA 53085      ATGTA        CA
                                TGCT    TTCTGCTTC  GGTG
                                ||||    |||||||||  ||||
                                ACGA    GAGACGAAG  CCAC
                                  AAA__        AC
GAM741  MGC10924  3'  CACCTGGAAGCAAAATCATAGT 47551       T   C
                                GCTATG ATT TGCTTCCAGGTG
                                |||||| ||| ||||||||||||
                                TGATAC TAA ACGAAGGTCCAC
                                   _   A
GAM741  PNMA5    5'  CACCCGAAGCACACACAGCA   73591      A   ATTC     CA
                                TGCT TGT    TGCTTC  GGTG
                                |||| |||    ||||||  ||||
                                ACGA ACA    ACGAAG  CCAC
                                  C   C___      C_
GAM741  RI58     3'  ACCTGAAAGTACATA       24844       ATTCT    C
                                TATGT     GCTT CAGGT
                                |||||     |||| |||||
                                ATACA     TGAA GTCCA
                                  _____    A
GAM741  SLC37A1   3'  ACCTGGAAAAGACACA      38560      AT   GC
                                TGT  TCT  TTCCAGGT
                                |||  |||  ||||||||
                                ACA  AGA  AAGGTCCA
                                  C_   A_
GAM741  LOC148418 3'  TTTGTAAACAGAATACATACA  78853     C         C  C
                                TG TATGTATTCTG TT CAGG
                                || |||||||||| || ||||
                                AC ATACATAAGAC AA GTTT
                                  _         A  T
GAM741  LOC90673  5'  AAGGAGAATACACAGCA     63821      A       G
                                TGCT TGTATTCT CTT
                                |||| |||||||| |||
                                ACGA ACATAAGA GAA
                                  C       G
GAM741  LOC93259  5'  CACCTGGAAGGGCTTTTACA   71805      TTCTG_
                                TGTA     CTTCCAGGTG
                                ||||     ||||||||||
                                ACAT     GAAGGTCCAC
                                   TTTCGG
GAM742  ACCN1    3'  AGTCACCCAGCACTCCCTC    6581       A       CATT
                                GAGG AGTGCTGG    GCT
                                |||| ||||||||    |||
                                CTCC TCACGACC    TGA
                                  C       CAC_
GAM742  ALDH3B2   3'  CCAACTGCACCAGCACTGCCTC 5502       A       CAT   ___
                                GAGG AGTGCTGG   TGC   TGG
                                |||| ||||||||   |||   |||
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                                CTCC TCACGACC   ACG   ACC
                                  G       ___   TCA
GAM742  B4GALT4  5'  CACGCAACACTTCCTC      13671         CTGGCA   _
                                GAGGAAGTG     TTGC TG
                                |||||||||     |||| ||
                                CTCCTTCAC     AACG AC
                                      _______   C
GAM742  CDKN1A   3'  ATGCCAGCTACTTCCTC     54292         _
                                GAGGAAGT GCTGGCAT
                                |||||||| ||||||||
                                CTCCTTCA CGACCGTA
                                     T
GAM742  CELSR2   3'  CCATCTAGTGCCAACTCCC   7407     A   GC       C_
                                GG AGT  TGGCATTG  TGG
                                || |||  ||||||||  |||
                                CC TCA  ACCGTGAT  ACC
                                 C  __       CT
GAM742  CERD4    3'  CCAGACTGGCAGCACTTCC   23850          G  TTG
                                GGAAGTGCTG CA   CTGG
                                |||||||||| ||   ||||
                                CCTTCACGAC GT   GACC
                                      G  CA_
GAM742  CRP      3'  CCAGCAATACCACGCAGTCCCT 71626      AAG   _   C
           C                     GAGG   TGC TGG ATTGCTGG
                                ||||   ||| ||| ||||||||
                                CTCC   ACG ACC TAACGACC
                                  CTG   C   A
GAM742  CRYGS    3'  CCAGCAATACAGTGCTCGCC   34076    A_  TG   GC
                                GG  AG  CTG  ATTGCTGG
                                ||  ||  |||  ||||||||
                                CC  TC  GAC  TAACGACC
                                 GC  GT   A_
GAM742  CTSD     3'  TGGTGCCAGCCTTCCTC     8586         T
                                GAGGAAG GCTGGCATTG
                                ||||||| ||||||||||
                                CTCCTTC CGACCGTGGT
                                      _
GAM742  DPP4     3'  CCAGCAACGCAGGCCCCC    8656     AAGT   G  A
                                GG    GCT GC TTGCTGG
                                ||    ||| || |||||||
                                CC    CGG CG AACGACC
                                 CC__   A  C
GAM742  EGLN1    3'  CCAGCAATACCCCACTTC    41894       CT  C
                                GAAGTG  GG ATTGCTGG
                                ||||||  || ||||||||
                                CTTCAC  CC TAACGACC
                                   C_  A
GAM742  EPHA3    5'  CCAGCAATCAGAGCGCTCCC   17868    A     GGC
                                GG AGTGCT   ATTGCTGG
                                || ||||||   ||||||||
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                                CC TCGCGA   TAACGACC
                                 C     GAC
GAM742  GALNT2   3'  CCAGCAATACCGCTGCCCCCT  15597     AA  _  T  C
                                AGG  GT GC GG ATTGCTGG
                                |||  || || || ||||||||
                                TCC  CG CG CC TAACGACC
                                  CC  T  _  A
GAM742  GPRK6    3'  CCAGCAATAATCCGCCCCTTC  9108      T_  T  C__
                                GAAG  GC GG   ATTGCTGG
                                ||||  || ||   ||||||||
                                CTTC  CG CC   TAACGACC
                                  CC  _  TAA
GAM742  INPP4A   5'  CGGTGCCAGCACTTCCC     7802     A
                                G GGAAGTGCTGGCATTG
                                | ||||||||||||||||
                                C CCTTCACGACCGTGGC
                                _
GAM742  INPP4A   5'  CGGTGCCAGCACTTCCC     14437    A
                                G GGAAGTGCTGGCATTG
                                | ||||||||||||||||
                                C CCTTCACGACCGTGGC
                                _
GAM742  KCNJ1    5'  CCAACAACCAGCACCACTTCCT 4025          ___     CA   C
          T                      GAGGAAGT   GCTGG  TTG TGG
                                ||||||||   |||||  ||| |||
                                TTCCTTCA   CGACC  AAC ACC
                                     CCA    __   A
GAM742  MAP1A    3'  CCAGCAATGTGTGACTCCCCC  9897    A  A   _  TG
                                G GG AGT GC  GCATTGCTGG
                                | || ||| ||  ||||||||||
                                C CC TCA TG  TGTAACGACC
                                 C  C   G  __
GAM742  MAPT     3'  CCACATCCAACATTTCCTC    19777         C   CAT  C
                                GAGGAAGTG TGG   TG TGG
                                ||||||||| |||   || |||
                                CTCCTTTAC ACC   AC ACC
                                     A   T__  _
GAM742  MAPT     3'  CCACATCCAACATTTCCTC    33688         C   CAT  C
                                GAGGAAGTG TGG   TG TGG
                                ||||||||| |||   || |||
                                CTCCTTTAC ACC   AC ACC
                                     A   T__  _
GAM742  MAPT     3'  CCACATCCAACATTTCCTC    33697         C   CAT  C
                                GAGGAAGTG TGG   TG TGG
                                ||||||||| |||   || |||
                                CTCCTTTAC ACC   AC ACC
                                     A   T__  _
GAM742  MAPT     3'  CCACATCCAACATTTCCTC    33707         C   CAT  C
                                GAGGAAGTG TGG   TG TGG
                                ||||||||| |||   || |||
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                                CTCCTTTAC ACC   AC ACC
                                     A  T__ _
GAM742  MFAP4    3'  CAGCCCAGCACTCCTC      69253       A      CATT
                                GAGGA GTGCTGG    GCTG
                                ||||| |||||||    ||||
                                CTCCT CACGACC    CGAC
                                  _     _____
GAM742  MMP14    3'  TGGTGCCAGCACCCCTC     17176      AA
                                GAGG  GTGCTGGCATTG
                                ||||  ||||||||||||
                                CTCC  CACGACCGTGGT
                                  C_
GAM742  MUC4     3'  CAGTGCCAGCACCTGCC     56320    AA_
                                GG   GTGCTGGCATTG
                                ||   ||||||||||||
                                CC   CACGACCGTGAC
                                 GTC
GAM742  PSCD4    3'  CCAGCAATGAGGCCCCCT    25403     AAGT   GG
                                AGG    GCT  CATTGCTGG
                                |||    |||  |||||||||
                                TCC    CGG  GTAACGACC
                                  CC__   A_
GAM742  SYN3     3'  CCAAGAAGCCAGCACCACC   56091    AA       A  GC
                                GG  GTGCTGGC TT  TGG
                                ||  |||||||| ||  |||
                                CC  CACGACCG AG  ACC
                                 AC       A  A_
GAM742  TCF20    3'  ATGCCAGCACTTCCTT      66954
                                GAGGAAGTGCTGGCAT
                                ||||||||||||||||
                                TTCCTTCACGACCGTA

GAM742  WHN      3'  CCAGAGGAACCAGCACTCC    13172     A      CATTG
                                GGA GTGCTGG     CTGG
                                ||| |||||||     ||||
                                CCT CACGACC     GACC
                                  _      AAGGA
GAM742  ABIN-2   3'  CTGGTGTGCCAGCCCCTC    44207      AAGT       T  TG
                                GAGG    GCTGGCAT GC  G
                                ||||    |||||||| ||  |
                                CTCC    CGACCGTG TG  C
                                  C___       _  GT
GAM742  ARL8     3'  TGACCAGCACTCCCTC      93199      A       _
                                GAGG AGTGCTGG CA
                                |||| |||||||| ||
                                CTCC TCACGACC GT
                                  C       A
GAM742  C20orf162 5' CCACATCCAGCACTCCCTC   54600      A       CAT  C
                                GAGG AGTGCTGG   TG TGG
                                |||| ||||||||   || |||
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                                CTCC TCACGACC   AC ACC
                                  C       T__  _
GAM742  C20orf98  3'  CCAAGATACCAGCATTCCTC  71513       G     C   GC
                                GAGGAA TGCTGG ATT  TGG
                                |||||| |||||| |||  |||
                                CTCCTT ACGACC TAG  ACC
                                   _     A  A_
GAM742  DKFZP434A0131 3'  CAATTCCAGGACTTCCTC    38626        G    C
                                GAGGAAGT CTGG ATTG
                                |||||||| |||| ||||
                                CTCCTTCA GACC TAAC
                                     G    T
GAM742  DKFZp434F142 3'  CCAGGCCCAGAACTTCCTC    50019        G    CATTG
                                GAGGAAGT CTGG     CTGG
                                |||||||| ||||     ||||
                                CTCCTTCA GACC     GACC
                                     A    CG___
GAM742  DKFZp434F142 3'  CCAGGTGCAAAACTTCCTC    50020        GCTG    TG
                                GAGGAAGT    GCAT  CTGG
                                ||||||||    ||||  ||||
                                CTCCTTCA    CGTG  GACC
                                     AAA_   __
GAM742  FLJ12747  3'  CCAGCAATACCAACCATT    49713      C_   C
                                AGTG  TGG ATTGCTGG
                                ||||  ||| ||||||||
                                TTAC  ACC TAACGACC
                                  CA   A
GAM742  FLJ13224  3'  CAACAATGCCACCTC       45621      AAGTGC       C
                                GAGG     TGGCATTG TG
                                ||||     |||||||| ||
                                CTCC     ACCGTAAC AC
                                  _______       A
GAM742  FLJ21736  3'  CCAGCAGTGACAACCCCCCTC  46227      AA_  GCTGG
                                GAGG   GT    CATTGCTGG
                                ||||   ||    |||||||||
                                CTCC   CA    GTGACGACC
                                  CCC  ACA__
GAM742  FLJ22551  5'  CGAGCCAGGACTTCCTC     45237        G    A
                                GAGGAAGT CTGGC TTG
                                |||||||| ||||| |||
                                CTCCTTCA GACCG AGC
                                     G    _
GAM742  FLJ25416  3'  CCAGCAATGGAGACATCC    58803     A  G  GG
                                GGA GT CT  CATTGCTGG
                                ||| || ||  |||||||||
                                CCT CA GA  GTAACGACC
                                  A  _  G_
GAM742  KIAA0143  3'  CCAGCAATTAACTTCTCC    64783    AG    GCTGGC
                                G  GAAGT     ATTGCTGG
                                |  |||||     ||||||||
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                              C  CTTCA     TAACGACC
                               CT    AT____
GAM742  KIAA0265  3'  CAGCAATGGCCTTTCC      69876      T  TGG
                              GGAAG GC   CATTGCTG
                              ||||| ||   ||||||||
                              CCTTT CG   GTAACGAC
                                 C  ___
GAM742  KIAA0544  3'  CCAAGCTCCACACCTCCTC   70897      A   C   CATT  _
                              GAGGA GTG TGG    GCT GG
                              ||||| ||| |||    ||| ||
                              CTCCT CAC ACC    CGA CC
                                 C   _   T___   A
GAM742  KIAA0759  3'  CCATGTATCCAGCGCTCCC   67321    A       CAT   _
                              GG AGTGCTGG   TGC TGG
                              || ||||||||   ||| |||
                              CC TCGCGACC   ATG ACC
                               C       T__   T
GAM742  KIAA0889  3'  CCAGAGACTGCCAGCATCCCCT 31132      AA        TTG_
            C                  GAGG  GTGCTGGCA    CTGG
                              ||||  |||||||||    ||||
                              CTCC  TACGACCGT    GACC
                                CC        CAGA
GAM742  KIAA1210  3'  CCAGAAACCCAGCATTTCCTC  96326           CATTG
                              GAGGAAGTGCTGG    CTGG
                              ||||||||||||     ||||
                              CTCCTTTACGACC    GACC
                                     CAAA_
GAM742  MGC10520  3'  CAGCTGAGCACTTCCT      47570          GGCATT
                              AGGAAGTGCT     GCTG
                              ||||||||||     ||||
                              TCCTTCACGA     CGAC
                                   GT____
GAM742  MGC2668   3'  CCAGAGCCCAGCACTCCCTT   60575      A       CATTG
                              GAGG AGTGCTGG    CTGG
                              |||| ||||||||    ||||
                              TTCC TCACGACC    GACC
                                C       CGA__
GAM742  MGC4172   3'  CCAGGGCTCCAGACTTCCTC   44200        G    CATTG
                              GAGGAAGT CTGG    CTGG
                              |||||||| ||||    ||||
                              CTCCTTCA GACC    GACC
                                   _   TCGG_
GAM742  MGC4175   5'  CGGCGCCAGCGCTTCC      44232           ATT  TG
                              GGAAGTGCTGGC   GC  G
                              ||||||||||||   ||  |
                              CCTTCGCGACCG   CG  C
                                     ___  GT
GAM742  OS4       3'  CCAACAATGCCATTCCC     19177    A   GTGC       C
                              G GGAA    TGGCATTG TGG
                              | ||||    |||||||| |||
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                                C CCTT    ACCGTAAC ACC
                                 _   ____       A
GAM742  PDGFC    5'  CAGTGCAGCCTTCC       32496      T   G
                                GGAAG GCTG CATTG
                                ||||| |||| |||||
                                CCTTC CGAC GTGAC
                                  _   _
GAM742  PLAGL2   3'  CCAGCAATGAGCTGTCC     70444     AGT   GG
                                GGA   GCT  CATTGCTGG
                                |||   |||  |||||||||
                                CCT   CGA  GTAACGACC
                                  GT_  __
GAM742  PLSCR3   3'  CCACTGTCCCAGCAGTCCCTC  90760      AAG     C  TGC
                                GAGG   TGCTGG AT   TGG
                                ||||   |||||| ||   |||
                                CTCC   ACGACC TG   ACC
                                   CTG     C  TC_
GAM742  PLSCR3   3'  CCACTGTCCCAGCAGTCCCTC  39793      AAG     C  TGC
                                GAGG   TGCTGG AT   TGG
                                ||||   |||||| ||   |||
                                CTCC   ACGACC TG   ACC
                                   CTG     C  TC_
GAM742  PLU-1    5'  CCAGCAATGCCAACGGGCT   21756    AAG  C
                                GG   TG TGGCATTGCTGG
                                ||   || ||||||||||||
                                TC   GC ACCGTAACGACC
                                 GG_  A
GAM742  PRSC     3'  CCAGCAACCTGGACTGCCTC   21672      A   G TG CA
                                GAGG AGT C  G  TTGCTGG
                                |||| ||| |  |  |||||||
                                CTCC TCA G  C  AACGACC
                                   G   _ GT C_
GAM742  SCAND2   3'  CCAGCAATACCCCACTTC    41886       CT  C
                                GAAGTG  GG ATTGCTGG
                                ||||||  || ||||||||
                                CTTCAC  CC TAACGACC
                                    C_  A
GAM742  SYTL2    5'  CCACAGACCAGGACTTCCTC   51958        G    CA   C
                                GAGGAAGT CTGG  TTG TGG
                                |||||||| ||||  ||| |||
                                CTCCTTCA GACC  GAC ACC
                                     G    A_  _
GAM742  TLN1     3'  CAACCCCAGCACTCCCC     20814    A  A       CA
                                G GG AGTGCTGG  TTG
                                | || ||||||||  |||
                                C CC TCACGACC  AAC
                                 _ C       CC
GAM742  LOC143384 3'  CAAAATCAGCAGCTTCCTC    76552         _      CA
                                GAGGAAG TGCTGG  TTG
                                ||||||| ||||||  |||
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                                CTCCTTC ACGACT  AAC
                                    G     AA
GAM742  LOC144695 5'  CCAAGGTTCCCAGCACTCCCTC 83179      A       C_   GC
                                GAGG AGTGCTGG  ATT  TGG
                                |||| ||||||||  |||  |||
                                CTCC TCACGACC  TGG  ACC
                                  C       CT   A_
GAM742  LOC145990 3'  CCAGCAACGTGCTGCACTTCTT 77601          T    __
          C                      GAGGAAGTGC GGCAT  TGCTGG
                                |||||||||| |||||  ||||||
                                CTTCTTCACG TCGTG  ACGACC
                                      _    CA
GAM742  LOC146988 3'  CCAGCAATAGATACTCCC    83892    A   _  GGC
                                GG AGTG CT   ATTGCTGG
                                || |||| ||   ||||||||
                                CC TCAT GA   TAACGACC
                                 C    A  ___
GAM742  LOC148018 5'  CGGGGCCAGCATCCCTC     82419      AA       ATTG
                                GAGG  GTGCTGGC    CTG
                                ||||  ||||||||    |||
                                CTCC  TACGACCG    GGC
                                  C_       G___
GAM742  LOC148066 5'  CCTGCGCCAGCACCTCCT    78623      A       ATT  T
                                AGGA GTGCTGGC   GC GG
                                |||| ||||||||   || ||
                                TCCT CACGACCG   CG CC
                                  C        ___  T
GAM742  LOC150886 3'  CCAACATCATATACTTCCTC   85151          C  GCAT  C
                                GAGGAAGTG TG    TG TGG
                                |||||||||  ||    || |||
                                CTCCTTCAT AT    AC ACC
                                      _  ACT_  A
GAM742  LOC153205 5'  CCAGCGCCTGACCAGAACTTCC 85942          G    _  T_
          TC                      GAGGAAGT CTGG CA  TGCTGG
                                |||||||| |||| ||  ||||||
                                CTCCTTCA GACC GT  GCGACC
                                    A   A  CC
GAM742  LOC153320 3'  CAGCAATGCCAGAGCT      85991     G
                                AGT CTGGCATTGCTG
                                ||| ||||||||||||
                                TCG GACCGTAACGAC
                                  A
GAM742  LOC153546 5'  CCAGCAGGAGCACTTCCTC    80884           GGCA
                                GAGGAAGTGCT    TTGCTGG
                                ||||||||||    |||||||
                                CTCCTTCACGA    GACGACC
                                      G___
GAM742  LOC153579 3'  CCAAGGGTGCGCACTTCC     80893         TG    GC
                                GGAAGTGC  GCATT  TGG
                                ||||||||  |||||  |||
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                                CCTTCACG  CGTGG  ACC
                                   __     GA
GAM742   LOC157226 5'  CCAACAATGCCGGCCCT     63930     AAGT        C
                                AGG    GCTGGCATTG TGG
                                |||    |||||||||| |||
                                TCC    CGGCCGTAAC ACC
                                 _____         A
GAM742   LOC164714 5'  CCAGCAGTACTACTCCCTC    87225      A   GCT  C
                                GAGG AGT   GG ATTGCTGG
                                |||| |||   || ||||||||
                                CTCC TCA   TC TGACGACC
                                  C   ___  A
GAM742   LOC165257 5'  CCAGCGCAAGCACTCCCT     82479     A     G  ATT
                                AGG AGTGCT GC   GCTGG
                                ||| ||||||  ||   |||||
                                TCC TCACGA CG   CGACC
                                  C     A  ___
GAM742   LOC197414 3'  CCAGCTCCCAGCTCTCCC     88063    A  T    CATT
                                GG AG GCTGG    GCTGG
                                || || |||||    |||||
                                CC TC CGACC    CGACC
                                 C  T    CT__
GAM742   LOC199800 5'  CCAGAGCCAGCGCTTCC      89857          ATTG
                                GGAAGTGCTGGC    CTGG
                                ||||||||||||   ||||
                                CCTTCGCGACCG    GACC
                                      A___
GAM742   LOC200186 3'  CAGTGCCAGCCCCTCCTC     89963      AGT
                                GAGGA   GCTGGCATTG
                                |||||   ||||||||||
                                CTCCT   CGACCGTGAC
                                   CCC
GAM742   LOC202870 3'  CCAGCAATGTTCTCTTCCTC   63121       TGCT
                                GAGGAAG    GGCATTGCTGG
                                |||||||    ||||||||||
                                CTCCTTC    TTGTAACGACC
                                    TC__
GAM742   LOC205081 5'  CCAGCAATCCTGTCACACCC   90692    AA  _ T  C
                                GG  GTG C GG ATTGCTGG
                                ||  ||| | || ||||||||
                                CC  CAC G CC TAACGACC
                                 CA   T T  _
GAM742   LOC219920 5'  GGCAGGACCAGCCACTTCCTC  93316         _   CA
                                GAGGAAGTG CTGG  TTGCT
                                |||||||| ||||  |||||
                                CTCCTTCAC GACC  GACGG
                                      C    AG
GAM742   LOC221474 3'  CCAGAGCCAGCAGTTCC     92375      G      ATTG
                                GGAA TGCTGGC    CTGG
                                |||| |||||||    ||||
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                                CCTT ACGACCG   GACC
                                  G     A___
GAM742  LOC222057 3'  CCAGGTGCAAAACTTCCTC   92769      GCTG   TG
                                GAGGAAGT   GCAT  CTGG
                                ||||||||   ||||  ||||
                                CTCCTTCA   CGTG  GACC
                                    AAA_   __
GAM742  LOC222057 3'  CCAGTCCCAAAACTTCCTC   92770      GC   CATT
                                GAGGAAGT  TGG   GCTGG
                                ||||||||  |||   |||||
                                CTCCTTCA  ACC   TGACC
                                    AA   C___
GAM742  LOC223009 5'  CCAGGCCCAAAACTTCCTC   94375      GCT_  ATTG
                                GAGGAAGT   GGC   CTGG
                                ||||||||   |||   ||||
                                CTCCTTCA   CCG   GACC
                                    AAAC  _____
GAM742  LOC255975 5'  CCAGTCCCAAAACTTCCTC   95889      GC   CATT
                                GAGGAAGT  TGG   GCTGG
                                ||||||||  |||   |||||
                                CTCCTTCA  ACC   TGACC
                                    AA   C___
GAM742  LOC257486 3'  CCAGAAACCCAGCATTTCCTC  69243         CATTG
                                GAGGAAGTGCTGG    CTGG
                                ||||||||||||    ||||
                                CTCCTTTACGACC    GACC
                                      CAAA_
GAM742  LOC51720  3'  CCAGCACCACCAGCACCTACC  32821    AA_     CAT
                                GG   GTGCTGG   TGCTGG
                                ||   |||||||  ||||||
                                CC   CACGACC   ACGACC
                                 ATC      ACC
GAM742  LOC90462  3'  CCAGCAGAGGGCAGCACCCCC  62903    AA     GCA_
                                GG  GTGCTG   TTGCTGG
                                ||  ||||||   |||||||
                                CC  CACGAC   GACGACC
                                 CC     GGGA
GAM742  LOC93109  3'  CCGGGTACCAGGACTTCCTC   71415       G   C  TG
                                GAGGAAGT CTGG AT  CTGG
                                |||||||| |||| ||  ||||
                                CTCCTTCA GACC TG  GGCC
                                    G   A  __
GAM743  GAGED2    3'  GAAGCAGGTGAAGAGCAACCAC 55929       A  AGGTT_
          A                   TGTGGTT GT     TCTGCTTC
                              |||||||  ||     ||||||||
                              ACACCAA CG     GGACGAAG
                                  _  AGAAGT
GAM743  KIT       3'  GGAAACAATATAACCACA    4040         GTAG
                                TGTGGTTA   GTTTCT
                                ||||||||   ||||||
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                                ACACCAAT    CAAAGG
                                    ATAA
GAM743  TRIM39   3'  GGAAACAGAAACCCCTGCACA  41173      GT   TA       C
                                TGTG  TAG  GGTTTCTG TTCC
                                ||||  |||  |||||||| ||||
                                ACAC  GTC  CCAAAGAC AAGG
                                  __   C_       A
GAM743  TRPM7    3'  AAGCAGAAACCTAACTCAC    62124      TTAG
                                GTGG    TAGGTTTCTGCTT
                                ||||    ||||||||||||
                                CACT    ATCCAAAGACGAA
                                  CA__
GAM743  CEP3     3'  AAACAAACTAACCACA      21244          AG
                                TGTGGTTAGT  GTTT
                                ||||||||||  ||||
                                ACACCAATCA  CAAA
                                    AA
GAM743  EHM2     3'  AAGCAACCCCCTAACCACA    38908         TA   TTC
                                TGTGGTTAG  GGT   TGCTT
                                |||||||||  |||   |||||
                                ACACCAATC  CCA   ACGAA
                                    CC   ___
GAM743  LOC122330 5'  GGCCAAACCTACTAACAACA   76265     G          CT
                                TGT GTTAGTAGGTTT  GCT
                                ||| ||||||||||||  |||
                                ACA CAATCATCCAAA  CGG
                                  A          C_
GAM743  LOC148645 3'  GAAGCAGATCTAAGCACA    84180      G    TAGGTT
                                TGTG TTAG     TCTGCTTC
                                |||| ||||     ||||||||
                                ACAC AATC     AGACGAAG
                                  G    T_____
GAM743  LOC150596 3'  AGAAACAATGTTGATAACCACA 79948         GTAG____
                                TGTGGTTA       GTTTCT
                                ||||||||       ||||||
                                ACACCAAT       CAAAGA
                                    AGTTGTAA
GAM743  LOC221688 3'  CAGAAACCCTGAGCCGCA    93676        AGTA
                                TGTGGTT    GGTTTCTG
                                |||||||    ||||||||
                                ACGCCGA    CCAAAGAC
                                    GTC_
GAM744  CLC      3'  CACCTCCCAAAGGTCTACCGAG 25106    T  AGCCAG_
            CT                    AG CTC      CTTTGGGAGGTG
                                || |||      ||||||||||||
                                TC GAG      GAAACCCTCCAC
                                 _  CCATCTG
GAM744  EGFL5    5'  CACCTCTCAGGCGCCGACCAGA 86613      CAGCCA_   T
            C                     GTCT      GCTT GGGAGGTG
                                ||||      |||| ||||||||
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                                CAGA      CGGA CTCTCCAC
                                  CCAGCCG   _
GAM744  FLRT2    3'  CACATCAAAGCTGGC      25057          GAG
                                GCCAGCTTTGG   GTG
                                ||||||||||   |||
                                CGGTCGAAACT   CAC
                                     A__
GAM744  KIR2DL5  3'  CCTCTCCAACTGAACT     40078     C    CCAGCT   _
                                AGT TCAG     TTGG GAGG
                                ||| ||||     |||| ||||
                                TCA AGTC     AACC CTCC
                                  _   _______   T
GAM744  NCOA6    5'  CACCTCCCATGCCAGTTGAGAC 25958        CA  TT
                                GTCTCAGC  GC  TGGGAGGTG
                                ||||||||  ||  |||||||||
                                CAGAGTTG  CG  ACCCTCCAC
                                     AC  T_
GAM744  SF1      5'  CACCTCCCAGCCCACCGAACT  16145     C  AGCCA   TT
                                AGT TC    GCT  GGGAGGTG
                                ||| ||    |||  ||||||||
                                TCA AG    CGA  CCCTCCAC
                                  _ CCACC   __
GAM744  THRA     3'  CACCTCCCATCCCGTAAGAC   12285      CA  CAGCTT
                                GTCT  GC     TGGGAGGTG
                                ||||  ||     |||||||||
                                CAGA  TG     ACCCTCCAC
                                  A_  CCCT__
GAM744  ZNF76    3'  CACCTCCCTGGAGGCCAGCTGA 12806        CA    __
           GAT                    GTCTCAGC  GCTTT  GGGAGGTG
                                ||||||||  |||||  ||||||||
                                TAGAGTCG  CGGAG  CCCTCCAC
                                     AC    GT
GAM744  BICD2    3'  CACCCTGTGGGACCAGCTGGAC 70389     T   CAG_  TG  A
                                GTC CAGC    CTT  GG GGTG
                                ||| ||||    |||  || ||||
                                CAG GTCG    GGG  TC CCAC
                                  _    ACCA   TG  _
GAM744  FLJ10847 3'  CCAGAGTAGCTGAGACT     36746         CA
                                AGTCTCAGC  GCTTTGG
                                |||||||||  |||||||
                                TCAGAGTCG  TGAGACC
                                     A_
GAM744  HPCAL4   3'  ACCTCCCAACCTGATGAC    32728     _   CCAGCT
                                GTC TCAG     TTGGGAGGT
                                ||| ||||     |||||||||
                                CAG AGTC     AACCCTCCA
                                  T   C_____
GAM744  HPCAL4   3'  CACCTCCCACTTGGCCAGA   32731     CA    CTT
                                TCT  GCCAG   TGGGAGGTG
                                |||  |||||   |||||||||
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                                AGA  CGGTT   ACCCTCCAC
                                  C_    C__
GAM744  HSPC189   3'  CACCCCCCAACCAGGCCTGAGA 95275        _ AGCT    A
              CT                    AGTCTCAG CC    TTGGG GGTG
                                ||||||||  ||    ||||| ||||
                                TCAGAGTC GG    AACCC CCAC
                                     C  ACC_    C
GAM744  KIAA0561  3'  CAAAGCAGCTGAGAC       65874         CA
                                GTCTCAGC  GCTTTG
                                ||||||||  ||||||
                                CAGAGTCG  CGAAAC
                                     A_
GAM744  KIAA1449  3'  CAAAGCGAGCTGAGAC      40448         CA
                                GTCTCAGC  GCTTTG
                                ||||||||  ||||||
                                CAGAGTCG  CGAAAC
                                     AG
GAM744  MGC2628   3'  CACCTCCCTGCCAGGCCAAGC  43969    T  CA   A_  TTT
                                G CT  GCC  GC   GGGAGGTG
                                | ||  |||  ||   ||||||||
                                C GA  CGG  CG   CCCTCCAC
                                 _ AC   AC  T__
GAM744  moblak    3'  CACCTCCTCTCCCTGGCTGA   55487         CTTT
                                TCAGCCAG    GGGAGGTG
                                ||||||||    ||||||||
                                AGTCGGTC    TCCTCCAC
                                     CCTC
GAM744  RYK       3'  CACAGTTAAGCTGGCTCAGACT 82616       C        TGGGAG
                                AGTCT AGCCAGCTT     GTG
                                ||||| |||||||||     |||
                                TCAGA TCGGTCGAA     CAC
                                   C        TTGA__
GAM744  TBX19     3'  CACCTCCCAGAGCCTGGCTGAA 17651     C       _
              AC                    GT TCAGCCAG CTTTGGGAGGTG
                                || ||||||||  ||||||||||||
                                CA AGTCGGTC GAGACCCTCCAC
                                 A       C
GAM744  LOC115399 3'  CACCTCCCAAGCACCCAAGGC  73424      CAGCCA    T
                                GTCT      GCTT GGGAGGTG
                                ||||      |||| ||||||||
                                CGGA      CGAA CCCTCCAC
                                   ACCCA_    _
GAM744  LOC199796 5'  TCAAAGTTGGCCGAGACT     74458        A
                                AGTCTC GCCAGCTTTGG
                                ||||||  ||||||||||
                                TCAGAG CGGTTGAAACT
                                    C
GAM744  LOC220565 3'  CACCTCCCAAGTGACTAGA    90745     C  CCA    T
                                TCT AG   GCTT GGGAGGTG
                                |||  ||   |||| ||||||||
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                                AGA TC   TGAA CCCTCCAC
                                  _ AG_   _
GAM744  LOC256113 5'  CCACAGCTGGCTGAACT     96769     C        T
                                AGT TCAGCCAGCT TGG
                                ||| |||||||||| |||
                                TCA AGTCGGTCGA ACC
                                  _        C
GAM745  GPR44    3'  ACTGAAGGCCTGGCCCACAGCA 16520     CATA  __    TCT
                                TGT   GGC  GGCCT   TCAGT
                                |||   |||  |||||   |||||
                                ACG   CCG  CCGGA   AGTCA
                                  ACAC   GT    ___
GAM745  OTOF     5'  ACTGAAGAACCCCCATGA    16638      A  C  CC
                                TCAT GG GG  TTCTTCAGT
                                |||| || ||  |||||||||
                                AGTA CC CC  AAGAAGTCA
                                  C  _  __
GAM745  PCDH11X  3'  ACTGAAGAAAACCACTAATAAC 52014     C  A  C  CC
            A                    TGT AT GG GG  TTCTTCAGT
                                |||  || || ||  |||||||||
                                ACA TA TC CC  AAGAAGTCA
                                  A  A  A  AA
GAM745  PCDH11X  3'  ACTGAAGAAAACCACTAATAAC 52036     C  A  C  CC
            A                    TGT AT GG GG  TTCTTCAGT
                                |||  || || ||  |||||||||
                                ACA TA TC CC  AAGAAGTCA
                                  A  A  A  AA
GAM745  PCDH11Y  3'  ACTGAAGAAAACCACTAATAAC 52072     C  A  C  CC
            A                    TGT AT GG GG  TTCTTCAGT
                                |||  || || ||  |||||||||
                                ACA TA TC CC  AAGAAGTCA
                                  A  A  A  AA
GAM745  STXBP1   3'  ACTGAAGAAACTGAATAAAACA 12045     CA  GG   CC
                                TGT  TA  CGG  TTCTTCAGT
                                |||  ||  |||  |||||||||
                                ACA  AT  GTC  AAGAAGTCA
                                  AA  AA   A_
GAM745  TMEPAI   3'  CTGAAGAAGCAGTGACA     39446       AGGCG  C
                                TGTCAT    GC TTCTTCAG
                                ||||||    || ||||||||
                                ACAGTG    CG AAGAAGTC
                                   A_____  _
GAM745  VMD2     3'  ACTGAAGAACATGTCCTACAAC 14817     CA   _  GCC
            A                    TGT  TAGG CG   TTCTTCAGT
                                |||  ||||  ||   |||||||||
                                ACA  ATCC GT   AAGAAGTCA
                                  AC    T  AC_
GAM745  WW45     3'  CTGAAGAAATGTTGACA     41520       TAG   GCC
                                TGTCA   GCG   TTCTTCAG
                                |||||   |||   ||||||||
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                                ACAGT  TGT  AAGAAGTC
                                   ___  A__
GAM745  ZNF124   3'  ACTGAAGAAAATCCATATGA  12823      _ CGGCC
                                TCATA GG    TTCTTCAGT
                                ||||| ||    |||||||||
                                AGTAT CC    AAGAAGTCA
                                   A  TAA__
GAM745  DKFZP564O0423 3'  AGAAGGCCACCCATGGCA   91676      A  C
                                TGTCAT GG GGCCTTCT
                                |||||| || ||||||||
                                ACGGTA CC CCGGAAGA
                                   C  A
GAM745  FLJ20139  3'  CTGAAGAAACCATGA      34623     A  CGGCC
                                TCAT GG    TTCTTCAG
                                |||| ||    ||||||||
                                AGTA CC    AAGAAGTC
                                  _  A____
GAM745  KIAA1411  3'  ACTGAAGAAAGCTCTGTAGCA  40430    TC   GC   C
                                TG  ATAG  GGC TTCTTCAGT
                                ||  ||||  ||| |||||||||
                                AC  TGTC  TCG AAGAAGTCA
                                 GA   __  A
GAM745  MKNK1    5'  ACTGAAGATTGCCACCTACGCA 13478    CA   C  CT
                                TGT  TAGG GGC  TCTTCAGT
                                |||  |||| |||  ||||||||
                                ACG  ATCC CCG  AGAAGTCA
                                  C_   A  TT
GAM745  LOC133634 3'  ACTGAAGAAAAGACCTGTATAC 75102    C_    CGGCC
           A                     TGT  ATAGG    TTCTTCAGT
                                |||  |||||    |||||||||
                                ACA  TGTCC    AAGAAGTCA
                                  TA    AGAA_
GAM745  LOC150759 3'  ACTGAAGAAGGAGTGAGCAGAC 80001     ATAG  GG___
           A                     TGTC   GC    CCTTCTTCAGT
                                ||||   ||    ||||||||||
                                ACAG   CG    GGAAGAAGTCA
                                  A___  AGTGA
GAM745  LOC151323 3'  ACTGAAGAAGGAGTGAGCAGAC 80213     ATAG  GG___
           A                     TGTC   GC    CCTTCTTCAGT
                                ||||   ||    ||||||||||
                                ACAG   CG    GGAAGAAGTCA
                                  A___  AGTGA
GAM745  LOC164295 5'  ACCGAAGAAGGCCTCAGC    82507    ___       A
                                GC   GGCCTTCTTC GT
                                ||   |||||||||| ||
                                CG   CCGGAAGAAG CA
                                 ACT        C
GAM745  LOC200399 3'  ACTGAAGAAGGAGTGAGCAGAC 88804     ATAG  GG___
           A                     TGTC   GC    CCTTCTTCAGT
                                ||||   ||    ||||||||||
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                                ACAG   CG    GGAAGAAGTCA
                                  A___  AGTGA
GAM746  ARHGEF6  3'  CAAACTTGAAGCCAGGC    68197       ACCA
                                GCCTGG   CAAGTTTG
                                ||||||   ||||||||
                                CGGACC   GTTCAAAC
                                   GAA_
GAM746  CNTN2    3'  GTCACAACCCAGGTGA     17411        ACCACAA  _
                                TCGCCTGG     GTT TGAC
                                ||||||||     ||| ||||
                                AGTGGACC     CAA ACTG
                                    ________  C
GAM746  CORO2A   3'  AAACTGTGGTCCAGAGA    12642    GC        A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM746  CORO2A   3'  AAACTGTGGTCCAGAGA    53398    GC        A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM746  GRLF1    3'  AGGTCAGAAAGTGGCCCAGG   78551      A    AAG
                                CCTGG CCAC   TTTGACCT
                                ||||| ||||   ||||||||
                                GGACC GGTG   AGACTGGA
                                   C    AA_
GAM746  LAPTM5   3'  AGGCTTGTGGTCAAGC     22199    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCGGA
                                 AA_
GAM746  POU2AF1  3'  AGATTTACAGTCCAGGC     20647        CAC
                                GCCTGGAC   AAGTTT
                                ||||||||   ||||||
                                CGGACCTG   TTTAGA
                                     ACA
GAM746  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  54574        C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM746  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  6355         C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM746  TRIM34   5'  AGGTCAAGTTGAGCCCAG    55224     ACCA   G
                                CTGG    CAA TTTGACCT
                                ||||    ||| ||||||||
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                                GACC    GTT GAACTGGA
                                  CGA_  _
GAM746  TRIM9    5'  AGGCCAGGCAAGTCCAGGC   30749        CACAA    A
                                GCCTGGAC    GTTTG CCT
                                ||||||||    ||||| |||
                                CGGACCTG    CGGAC GGA
                                    AA___    C
GAM746  ABLIM    5'  GATATGTAACCCAGGCGG    22030        ACC   A
                                TCGCCTGG   ACA GTT
                                ||||||||   ||| |||
                                GGCGGACC   TGT TAG
                                    CAA   A
GAM746  AMOT     3'  AGGCATCTTCATGGTCCAGGGA 55716    G       C_   TT  A
                                TC CCTGGACCA  AAG  TG CCT
                                || |||||||||  |||  || |||
                                AG GGACCTGGT  TTC  AC GGA
                                 _       AC   T_ _
GAM746  DKFZp434D177 5'  TTAGACCCAGGCGA       50056        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                              _______
GAM746  DKFZp434D177 5'  TTAGACCCAGGCGA       79443        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                              _______
GAM746  FLJ23420  3'  CAAGTGGGTCCAGGC       46845         A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                              _ __
GAM746  HSA249128 5'  GGCGCGGTCCAGGCGG      34152          ACAA
                                TCGCCTGGACC    GTT
                                ||||||||||    |||
                                GGCGGACCTGG    CGG
                                       CG__
GAM746  MGC15668  5'  AGACCCGGTGGTCCAGACG    51277    C       AA_
                                CG CTGGACCAC   GTTT
                                || |||||||||   ||||
                                GC GACCTGGTG   CAGA
                                 A        GCC
GAM746  MGC22014  3'  AGGTCCCGAGTGTAACCCAGGT 64486        ACC   AGTTT
                   GA                  TCGCCTGG   ACA    GACCT
                                ||||||||   |||    |||||
                                AGTGGACC   TGT    CTGGA
                                    CAA   GAGCC
GAM746  SDCCAG10  5'  AGAGTTGTGGTCCAAAGA    19641    GCC        G
                                TC   TGGACCACAA TTT
                                ||   |||||||||| |||
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                                AG   ACCTGGTGTT AGA
                                 AA_         G
GAM746   LOC115442 3'  AGGTCAGGGATGGTCCAG    72676         CAAG
                                CTGGACCA    TTTGACCT
                                ||||||||    ||||||||
                                GACCTGGT    GGACTGGA
                                     AG__
GAM746   LOC129011 5'  AGACCTGCGGTCCAGGC     74862          A  A
                                GCCTGGACC CA GTTT
                                ||||||||| || ||||
                                CGGACCTGG GT CAGA
                                      C  C
GAM746   LOC130536 5'  GCAAAGTCCAGGCG        75746          CACAAG    A
                                CGCCTGGAC     TTTG C
                                |||||||||     |||| |
                                GCGGACCTG     AAAC G
                                     _______   C
GAM746   LOC149108 3'  AGACTTCACTGTGGTCCA    84357          _____
                                TGGACCACA    AGTTT
                                |||||||||    |||||
                                ACCTGGTGT    TCAGA
                                      CACT
GAM746   LOC221688 5'  AGACTCGGGCCCAGACGA    93674     C    A  ACA
                                TCG CTGG CC   AGTTT
                                ||| |||| ||   |||||
                                AGC GACC GG   TCAGA
                                  A   C  GC_
GAM746   LOC256228 5'  AGACTTGTGGTCAAAGC     96233     CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCAGA
                                 AAA
GAM746   LOC257441 5'  TTAGACCCAGGCGA        95566         ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                     _______
GAM746   LOC91960  3'  AGGTGCCTCTCGTGGTCCAAGC 67657     C       A  TTTG
                                GC TGGACCAC AG    ACCT
                                || |||||||| ||    ||||
                                CG ACCTGGTG TC    TGGA
                                 A       C  TCCG
GAM746   LOC92840  3'  GTCCCTCGGGTCCAGGC     56435         ACA  TTT
                                GCCTGGACC   AG   GAC
                                |||||||||   ||   |||
                                CGGACCTGG   TC   CTG
                                      GC_  C__
GAM747   ARNT2     3'  AAACAACCCGTGCATCCCTGC  29450     A    TTTTA
                                GTA GGAT     GGGTTGTTT
                                ||| ||||     |||||||||
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                                CGT CCTA    CCCAACAAA
                                  C   CGTG_
GAM747  LCT      3'  AACCGTAAAAATCCTT     9697          G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
                                TTCCTAAAAAT CCAA
                                      G
GAM747  RPL15    3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM747  FBXO30   3'  AACTAAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                  G        AA
GAM747  KIAA0494 3'  AACAACCCTTACTTAC      28736      GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM747  PRO0641  5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                   ___    C
GAM747  SMT3H2   3'  AACAACATAAAAATCCTTGC  22670          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM747  LOC120103 3' AACCTATGAAAAATCCTTGC  74002          A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
                                CGTTCCTAAAAA   TCCAA
                                       GTA
GAM747  LOC129831 3' AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                   T_  C
GAM747  LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                      GTA GGATTTTT     TTGTTT
                                ||| ||||||||    ||||||
                                CGT CCTAAAAA     AACAAA
                                  C       GATAA
GAM747  LOC148089 3' GGCCCTAAAAATTCCTAC    78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
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                                CAT CTTAAAAATCCCGG
                                  C
GAM747  LOC154547 3'  AACAACATAAAAATCCTTGC  76050          GG
                                GTAAGGATTTTTA GTTGTT
                                ||||||||||||| ||||||
                                CGTTCCTAAAAAT CAACAA
                                       A_
GAM747  LOC158104 3'  ACAGCCAAAAATCCTTA    60313          AG
                                TAAGGATTTTT GGTTGT
                                |||||||||||  ||||||
                                ATTCCTAAAAA CCGACA
                                       __
GAM747  LOC205880 5'  AAACAACCATCATCCTGAC   90709    A    TTTTAG
                                GT AGGAT    GGTTGTTT
                                || |||||    ||||||||
                                CA TCCTA    CCAACAAA
                                 G   CTA___
GAM747  LOC221561 3'  AACAACATAAAAATCCTTGC  92130          GG
                                GTAAGGATTTTTA GTTGTT
                                ||||||||||||| ||||||
                                CGTTCCTAAAAAT CAACAA
                                       A_
GAM747  LOC257591 3'  AACAACATAAAAATCCTTGC  97840          GG
                                GTAAGGATTTTTA GTTGTT
                                ||||||||||||| ||||||
                                CGTTCCTAAAAAT CAACAA
                                       A_
GAM747  LOC51145  3'  AGCTAAAATCCTTAC      32393          TAG
                                GTAAGGATTTT  GGTT
                                ||||||||||  ||||
                                CATTCCTAAAA  TCGA
                                       ___
GAM748  PMX1      3'  TAATACTTACCTACCTCA    22595           C
                                TGAGGTAGGTAAGT ATTG
                                |||||||||||||| ||||
                                ACTCCATCCATTCA TAAT
                                       _
GAM748  PMX1      3'  TAATACTTACCTACCTCA    42662           C
                                TGAGGTAGGTAAGT ATTG
                                |||||||||||||| ||||
                                ACTCCATCCATTCA TAAT
                                       _
GAM748  WIG1      3'  GTGACCTACCTACCCCA    94469    A      A
                                TG GGTAGGTA GTCAT
                                || |||||||| |||||
                                AC CCATCCAT CAGTG
                                 C       C
GAM748  ABCF2     5'  TGAAACAACAGTAACCTACC  19099       AAGTCA
                                GGTAGGT     TTGTTTCA
                                |||||||     ||||||||
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                                CCATCCA     AACAAAGT
                                    ATGAC_
GAM748  CTPS2    3' AAACCCATACTACTACCTCA  39081       GTA   CATT
                                TGAGGTAG  AGT   GTTT
                                ||||||||  |||   ||||
                                ACTCCATC  TCA   CAAA
                                    A__   TACC
GAM748  CYP4F8   3' CAGTGACCCACCCACCT    23409     A   AA
                                AGGT GGT  GTCATTG
                                |||| |||  |||||||
                                TCCA CCA  CAGTGAC
                                  C   CC
GAM748  DKFZp761N1114 3' AGTACCTACCCTACCTCA    79013        TA  TC
                                TGAGGTAGG  AG  ATT
                                |||||||||  ||  |||
                                ACTCCATCC  TC  TGA
                                     CA  CA
GAM748  FLJ11082 3' TGAAACAATAACTCTGCACCA  37036    AG   GTA   C
                                TG  GTAG   AGT ATTGTTTCA
                                ||  ||||   ||| |||||||||
                                AC  CGTC   TCA TAACAAAGT
                                 CA    ___   A
GAM748  FLJ11560 3' AGACTCTGACCCACCTACCTCA 47215         AA   TT
                                TGAGGTAGGT  GTCA  GTTT
                                ||||||||||  ||||  ||||
                                ACTCCATCCA  CAGT  CAGA
                                      CC    CT
GAM748  FLJ20485 3' CAGTGACTCTCCCACCTCA   38765      A  TA
                                TGAGGT GG  AGTCATTG
                                ||||||  ||  ||||||||
                                ACTCCA CC  TCAGTGAC
                                   C  TC
GAM748  FLJ20511 3' AAACAATGAATGAGCCACCTTA 35316      A   AAG_
                                TGAGGT GGT    TCATTGTTT
                                ||||||  |||   |||||||||
                                ATTCCA CCG    AGTAACAAA
                                   _   AGTA
GAM748  KIAA0557 3' TGACTTCCTACCTCA      78011         T
                                TGAGGTAGG AAGTCA
                                |||||||||  ||||||
                                ACTCCATCC TTCAGT
                                          _
GAM748  KIAA1274 3' TAATACTTGCCTACCT     91369          C
                                AGGTAGGTAAGT ATTG
                                ||||||||||||  ||||
                                TCCATCCGTTCA TAAT
                                          _
GAM748  KIAA1297 3' TGACTCTCCTACCTCA     72188         TA
                                TGAGGTAGG  AGTCA
                                |||||||||  |||||
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                                ACTCCATCC  TCAGT
                                     TC
GAM748  KIAA1571  5'  TAGTGACTGACCCACCTCA   60959      A   A
                                TGAGGT GGT AGTCATTG
                                ||||||| ||| ||||||||
                                ACTCCA CCA TCAGTGAT
                                   C   G
GAM748  ZNF396    3'  GAAACAACAAGTGCCTCA    75668      GGTAAGTCA
                                TGAGGTA       TTGTTTC
                                |||||||       |||||||
                                ACTCCGT       AACAAAG
                                   GAAC_____
GAM748  LOC130576 5'  AAACAATAACTGCCTA     74953      A  C
                                TAGGTA GT ATTGTTT
                                |||||| || |||||||
                                ATCCGT CA TAACAAA
                                   _ A
GAM748  LOC153339 3'  TGATTACCTACCTCA      86015          G
                                TGAGGTAGGTAA TCA
                                |||||||||||| |||
                                ACTCCATCCATT AGT
                                          _
GAM748  LOC158563 3'  TAATTGCCCTACCTACCTCA  81952          A_  C
                                TGAGGTAGGTA  GT ATTG
                                ||||||||||  || ||||
                                ACTCCATCCAT  CG TAAT
                                      CC  T
GAM748  LOC200942 3'  TGAAACCTTCCTACCCTACCTA 88949          A_  CATT__
          CCTCA                   TGAGGTAGGTA  GT     GTTTCA
                                ||||||||||  ||     ||||||
                                ACTCCATCCAT  CA     CAAAGT
                                      CC  TCCTTC
GAM748  LOC255349 3'  GAAATCATACCTACCTCA    95612          AGTCAT  _
                                TGAGGTAGGTA     TG TTTC
                                ||||||||||     || ||||
                                ACTCCATCCAT     AC AAAG
                                      _______  T
GAM749  ACP2      3'  AGAAAGTTCTAGACTG      7851       GC  TC
                                CAGT  CT  AGAACTTTCT
                                ||||  ||  ||||||||||
                                GTCA  GA  TCTTGAAAGA
                                   __  __
GAM749  APTX      5'  AAGAGAAAGAGATCAGGCA   34655      TCAGAA
                                TGCCT     CTTTCTCTT
                                |||||     |||||||||
                                ACGGA     GAAAGAGAA
                                   CTAGA_
GAM749  BCL7A     3'  AGGCTGTCTCCTTAAGGCACTG 40637         C  A__  TT
                                CAGTGCCTT AG   AC  TCT
                                ||||||||| ||   ||  |||
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                                GTCACGGAA TC   TG  GGA
                                     T  CTC  TC
GAM749  CLC     3'  AAGAGAAAATACTGAAAGCACA 25105    A   C    AAC
            GG                   CC GTGC TTCAG   TTTCTCTT
                                 || |||| |||||   ||||||||
                                 GG CACG AAGTC   AAAGAGAA
                                  A   A    ATA
GAM749  CNK     3'  AAGCCCTGAAGGCCTG     14517     T      AA
                                 CAG GCCTTCAG  CTT
                                 ||| ||||||||  |||
                                 GTC CGGAAGTC  GAA
                                   _      CC
GAM749  COL4A3   3'  AAGTGCAGGTTCTGAGGGCACC 48549    A           TCT
            GG                   CC GTGCCTTCAGAACTT   CTT
                                 || ||||||||||||||   |||
                                 GG CACGGGAGTCTTGGA   GAA
                                  C            CGT
GAM749  CSPG4    3'  AAGAGAGACCTGGAGACAC    8570     C     AAC
                                 GTG CTTCAG   TTTCTCTT
                                 ||| ||||||   ||||||||
                                 CAC GAGGTC   AGAGAGAA
                                   A     C__
GAM749  CYP1B1   3'  AAGAGAAAAGAGAGAAACACTG 3651       CC   AGAAC
                                 CAGTG  TTC    TTTCTCTT
                                 |||||  |||    ||||||||
                                 GTCAC  AAG    AAAGAGAA
                                    A_   AGAGA
GAM749  DLG3     3'  AAGAGAAAAGAGGAGGACTG   40880     G    AGAAC
                                 CAGT CCTTC    TTTCTCTT
                                 |||| |||||    ||||||||
                                 GTCA GGAGG    AAAGAGAA
                                   _    AGA__
GAM749  DLG5     5'  AGGCAGACTCTGAAGGC     82909         A_  T
                                 GCCTTCAGA  CT TCT
                                 |||||||||  || |||
                                 CGGAAGTCT  GA GGA
                                      CA  C
GAM749  FLT1     3'  AAGAGAAACCGGGAGAAGGCAT 8910         AGAAC_
                                 GTGCCTTC     TTTCTCTT
                                 ||||||||     ||||||||
                                 TACGGAAG     AAAGAGAA
                                     AGGGCC
GAM749  GRB10    3'  AGAGAAAATGGCACCTGG    17971     _   TTCAGAAC
                                 CCAG TGCC       TTTCTCT
                                 |||| ||||       |||||||
                                 GGTC ACGG       AAAGAGA
                                   C   TA_______
GAM749  LFG      3'  AAGAGAAAAGGAGCCAAGAACT 76711      GC   CAGAA   _
            GG                   CCAGT  CTT    CTTT CTCTT
                                 |||||  |||    |||| |||||
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                                GGTCA  GAA    GAAA GAGAA
                                  A_   CCGAG   A
GAM749  MAN2A2   3'  AAGAGAAAGTTCATTCAC    20391    CCTTCA
                                GTG     GAACTTTCTCTT
                                |||     ||||||||||||
                                CAC     CTTGAAAGAGAA
                                  TTA___
GAM749  NLGN3    3'  AAGAAAAGTTCTTAAAACACT  38596     CC  C      C
                                AGTG  TT AGAACTTT TCTT
                                ||||  || |||||||| ||||
                                TCAC  AA TCTTGAAA AGAA
                                  AA  T      _
GAM749  NPAS1    5'  AAGGTCTCCCGAGGGCACT   59879        A_  _
                                AGTGCCTTC  GA ACTTT
                                |||||||||  || |||||
                                TCACGGGAG  CT TGGAA
                                     CC  C
GAM749  PLAG1    3'  AGTGTGTTCCAAAGGCATT   10605       CA    TTT
                                AGTGCCTT  GAAC   CT
                                ||||||||  ||||   ||
                                TTACGGAA  CTTG   GA
                                    AC    TGT
GAM749  PLXNA1   3'  AGAAAATGAAGGCAGTGG    72309    G      GAAC
                                CCA TGCCTTCA    TTTCT
                                ||| ||||||||    |||||
                                GGT ACGGAAGT    AAAGA
                                  G       A___
GAM749  PPP4R1   3'  AAGAGAAAGTACAGTAAACACT 17620     CCTTCAGA
                                AGTG       ACTTTCTCTT
                                ||||       ||||||||||
                                TCAC       TGAAAGAGAA
                                  AAATGACA
GAM749  ACYP2    3'  AAGAGAAAAATTGTAACACACT 56612      CC  _   AAC
          G                      CAGTG  TT CAG   TTTCTCTT
                                |||||  || |||   ||||||||
                                GTCAC  AA GTT   AAAGAGAA
                                   AC  T   AA_
GAM749  B3GNT6   3'  AGAAATCAGATGAAGGCAT   22503        GAAC_
                                GTGCCTTCA     TTTCT
                                |||||||||     |||||
                                TACGGAAGT     AAAGA
                                     AGACT
GAM749  BAG5     3'  AAGAGAAGGGATAAAGGAC   16835    G   CAGAA
                                GT CCTT     CTTTCTCTT
                                || ||||     |||||||||
                                CA GGAA     GGAAGAGAA
                                 _    ATAG_
GAM749  BIVM     3'  AAGAGAAAAGACTCAAGAAACT 34665     GC   C  AAC
          G                      CAGT  CTT AG   TTTCTCTT
                                ||||  ||| ||   ||||||||
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                                GTCA  GAA TC   AAAGAGAA
                                  AA   C  AGA
GAM749  C15orf5   3'  AGAGAAAAGAAAGCAC      48195      C   AGAAC
                                GTGC TTC     TTTCTCT
                                |||| |||     |||||||
                                CACG AAG     AAAGAGA
                                  A   A_____
GAM749  C20orf80  5'  AAGAGAAGAAGATGAAGAAAC  65282    GC     GAAC
                                GT  CTTCA    TTTCTCTT
                                ||  |||||    ||||||||
                                CA  GAAGT    GAAGAGAA
                                 AA     AGAA
GAM749  CLSTN1    3'  AGTTCTGAGGACACTGG     30103       C
                                CCAGTG CTTCAGAACT
                                |||||| ||||||||||
                                GGTCAC GGAGTCTTGA
                                   A
GAM749  DKFZP434P0111 3'  AAGAGAAAGTTTCTGCAC     67368      CTTCA
                                GTGC     GAACTTTCTCTT
                                ||||     ||||||||||||
                                CACG     TTTGAAAGAGAA
                                  TC___
GAM749  DORFIN    5'  AGAATTCTCTGAAGGAAC     31257     G       ACT
                                GT CCTTCAGA   TTCT
                                || ||||||||   ||||
                                CA GGAAGTCT   AAGA
                                 A       CTT
GAM749  FLJ10300  5'  AAGAGAAAGATGAAGACTCTG  35997     TGC     GAA
                                CAG   CTTCA   CTTTCTCTT
                                |||   |||||   |||||||||
                                GTC   GAAGT   GAAAGAGAA
                                  TCA    A__
GAM749  FLJ20373  3'  AAGAGAAGAAGGAAAGGCACAG 35070     A      _ AGAAC
          G                      CC GTGCCTT C     TTTCTCTT
                                || ||||||| |     ||||||||
                                GG CACGGAA G     GAAGAGAA
                                 A      A GAA__
GAM749  FLJ23511  5'  AGAGAAAAACAAGGCAT     49956        CAGAAC
                                GTGCCTT      TTTCTCT
                                |||||||      |||||||
                                TACGGAA      AAAGAGA
                                   CAA___
GAM749  FLJ30681  3'  AGAGAAGAAAGACCACTGG   91782       CCT  AGAAC
                                CCAGTG   TC     TTTCTCT
                                ||||||   ||     |||||||
                                GGTCAC   AG     GAAGAGA
                                   C__  AAA__
GAM749  HDAC11    3'  GAGCTATAGGCACTGG      45717         TC  AACTTT
                                CCAGTGCCT  AG      CTC
                                |||||||||  ||     |||
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                                GGTCACGGA  TC     GAG
                                     TA _______
GAM749  IKKE     5'  AGTGAGCCCTGAAAGCTCTGG  25745      T  C    AA   T
                                CCAG GC TTCAG  CTT CT
                                |||| || |||||  ||| ||
                                GGTC CG AAGTC  GAG GA
                                  T A    CC   T
GAM749  KIAA0680 3'  AGAGAAAATTGAAGCAT     28232      C    AAC
                                GTGC TTCAG   TTTCTCT
                                |||| |||||   |||||||
                                TACG AAGTT   AAAGAGA
                                  _    A__
GAM749  KIAA1228 3'  AGGGGGTGATTCTGAGGCACTG 65035        T   ___   TT
                                CAGTGCCT CAGA   ACT  CT
                                |||||||| ||||   |||  ||
                                GTCACGGA GTCT   TGG  GA
                                     _   TAG   GG
GAM749  KIAA1300 5'  AGGAACCCTGAAGGCA      62860         AAC
                                TGCCTTCAG   TTTCT
                                |||||||||   |||||
                                ACGGAAGTC   AAGGA
                                     CC_
GAM749  KIAA1805 3'  AAGAGAAAGTAGAAGCAGCA   79966     __    AGA
                                TGC  CTTC   ACTTTCTCTT
                                |||  ||||   ||||||||||
                                ACG  GAAG   TGAAAGAGAA
                                  AC    A__
GAM749  LENG1    5'  AAGAGAAAGCTCTGGGCATCCT 84074     __    TT    A
           G                     CAG  TGCC  CAGA CTTTCTCTT
                                |||  ||||  |||| |||||||||
                                GTC  ACGG  GTCT GAAAGAGAA
                                  CT    __    C
GAM749  LHX6     3'  AAGAGAAAACTCTGGGGTCA   26854    C      AC
                                TG CTTCAGA  TTTCTCTT
                                || |||||||  ||||||||
                                AC GGGGTCT  AAAGAGAA
                                 T      CA
GAM749  N4BP3    3'  AGCTCCAGAAGGCACTGG     66250          A_  A
                                CCAGTGCCTTC  GA CT
                                ||||||||||  || ||
                                GGTCACGGAAG  CT GA
                                      AC  C
GAM749  NASP     3'  AGAGGGTGAAGAAACTG     67966      GC    AGA
                                CAGT  CTTC   ACTTTCT
                                ||||  ||||   |||||||
                                GTCA  GAAG   TGGGAGA
                                  AA   ___
GAM749  SMARCF1  3'  AAAATTCTGAAGGAC       57480    G       C
                                GT CCTTCAGAA TTT
                                || |||||||| |||
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                                CA GGAAGTCTT AAA
                                 _       A
GAM749  SMARCF1  3'  AAAATTCTGAAGGAC      37430    G       C
                                GT CCTTCAGAA TTT
                                || ||||||||| |||
                                CA GGAAGTCTT AAA
                                 _       A
GAM749  SMARCF1  3'  AAAATTCTGAAGGAC      20034    G       C
                                GT CCTTCAGAA TTT
                                || ||||||||| |||
                                CA GGAAGTCTT AAA
                                 _       A
GAM749  TED      3'  AAGAGAAAGTCCAGGGACTGG  31630      G   TCA  A
                                CCAGT CCT   GA CTTTCTCTT
                                ||||| |||   || |||||||||
                                GGTCA GGA   CT GAAAGAGAA
                                   G   C__  _
GAM749  TGIF2    3'  AGAAGGGTGCTGAAGGC     41447        AA_
                                GCCTTCAG   CTTTCT
                                ||||||||   ||||||
                                CGGAAGTC   GGAAGA
                                     GTG
GAM749  WBSCR20A 3'  AAGAGAAAGAAGAGACAGCA   35958     CT  AGAA
                                TGC  TC    CTTTCTCTT
                                |||  ||    |||||||||
                                ACG  AG    GAAAGAGAA
                                  AC  AGAA
GAM749  LOC115273 3'  AGAAAGTTCTGATGGCCAGG   73356    AGT   T
                                CC   GCC TCAGAACTTTCT
                                ||   ||| ||||||||||||
                                GG   CGG AGTCTTGAAAGA
                                 AC_   T
GAM749  LOC145761 5'  AAGAGAAAGTGGAAGGCATGG  83472     G      AGA
                                CCA TGCCTTC   ACTTTCTCTT
                                ||| |||||||   ||||||||||
                                GGT ACGGAAG   TGAAAGAGAA
                                  _      G__
GAM749  LOC146179 5'  AGAAAGTTTTGGGCCT      77700    T   TT
                                AG GCC  CAGAACTTTCT
                                || |||  ||||||||||
                                TC CGG  GTTTTGAAAGA
                                  _  __
GAM749  LOC147072 3'  AAGAGAAAGTGAGAAGAAACTG 60407      GC    AGA
                                CAGT  CTTC   ACTTTCTCTT
                                ||||  ||||   ||||||||||
                                GTCA  GAAG   TGAAAGAGAA
                                  AA   AG_
GAM749  LOC148758 5'  AGAAAGTTCTGAGAAAC     78962    GCC
                                GT   TTCAGAACTTTCT
                                ||   ||||||||||||
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                                CA  GAGTCTTGAAAGA
                                 AA_
GAM749  LOC148932 3'  AGGAATCTGAAGGCACTGG   79103           AC
                                CCAGTGCCTTCAGA  TTTCT
                                |||||||||||||  |||||
                                GGTCACGGAAGTCT  AAGGA
                                      __
GAM749  LOC149386 5'  AAGTTTTGAAAGCACT     84400      C
                                AGTGC TTCAGAACTT
                                ||||| ||||||||||
                                TCACG AAGTTTTGAA
                                   A
GAM749  LOC150139 3'  AGAAAATAGAAAAAGGCGCTGG 79583         CAGAAC_
                                CCAGTGCCTT      TTTCT
                                ||||||||||      |||||
                                GGTCGCGGAA      AAAGA
                                      AAAGATA
GAM749  LOC152756 3'  AAGATGCAGTTCTGAAAACCTG 85871    TGCC       TTC
                                CAG   TTCAGAACT  TCTT
                                |||   |||||||||  ||||
                                GTC   AAGTCTTGA  AGAA
                                  CAA_       CGT
GAM749  LOC162333 5'  AAGAGAAAGCGATGACACTG  87114     CCT  GAA
                                CAGTG  TCA  CTTTCTCTT
                                |||||  |||  |||||||||
                                GTCAC  AGT  GAAAGAGAA
                                   ___  AGC
GAM749  LOC199221 3'  AAGAGAAGCTCGAAAGCATGG  80347    G  C  A  A  T
                                CCA TGC TTC GA CTT CTCTT
                                ||| ||| ||| || ||| |||||
                                GGT ACG AAG CT GAA GAGAA
                                  _  A  _ C  _
GAM749  LOC203339 3'  AGAGAAAATTGGGCCTG    90542    T  TCAGAAC
                                CAG GCCT      TTTCTCT
                                ||| ||||      |||||||
                                GTC CGGG      AAAGAGA
                                  _   TTA____
GAM749  LOC255017 3'  AGAAAGAGGAACTGG      94624      G  TCAGAA
                                CCAGT CCT     CTTTCT
                                ||||| |||     ||||||
                                GGTCA GGA     GAAAGA
                                   A  _______
GAM749  LOC256021 3'  AAGAGAAACAAAGACAACACTG 96512      CCT  AGAAC
          G                      CCAGTG  TC    TTTCTCTT
                                ||||||  ||    ||||||||
                                GGTCAC  AG    AAAGAGAA
                                   AAC  AAAC_
GAM749  LOC90139  3'  AGAATCCCGAAGGCAT     55396        A_  ACT
                                GTGCCTTC  GA  TTCT
                                ||||||||  ||  ||||
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                                TACGGAAG  CT   AAGA
                                    CC  ___
GAM750  AQP3     3'  TTCACGATCCACCCTTTC    59593      T_   _
                                GAAA  GTGG TCGTGAA
                                ||||  |||| |||||||
                                CTTT  CACC AGCACTT
                                  CC    T
GAM750  ARSB     3'  TCACGACTCTTGTC       3502         AATGTG
                                GACAAGA     GTCGTGA
                                |||||||     |||||||
                                CTGTTCT     CAGCACT
                                    _______
GAM750  B4GALT5  3'  TTTTCACAAAAATAGTCCTTTG 16519        AAA_   GGTC
             TCA                  TGACAAG    TGT    GTGAAAA
                                |||||||    |||    |||||||
                                ACTGTTT    ATA    CACTTTT
                                    CCTG   AAAA
GAM750  CHRNA3   3'  TCGTTACCCATTTCTT     5610         T   CG
                                AAGAAATG GGT  TGA
                                |||||||| |||  |||
                                TTCTTTAC CCA  GCT
                                    _  TT
GAM750  DRD1     3'  TTACAACCACATTTCTGGCCA  5840     ACA         C
                                TG   AGAAATGTGGT GTGA
                                ||   |||||||||||| ||||
                                AC   TCTTTACACCA CATT
                                 CGG          A
GAM750  FUT1     3'  TCTGATCACATCCCCTGTC   3798      AGAA        T
                                GACA    ATGTGGTCG GA
                                ||||    ||||||||| ||
                                CTGT    TACACTAGT CT
                                  CCCC        _
GAM750  IRF1     3'  GCCACATTTCTGATCA      64345     CA
                                TGA  AGAAATGTGGT
                                |||  ||||||||||
                                ACT  TCTTTACACCG
                                  AG
GAM750  MAP3K8   5'  TCACGACCACCTCATG      17791     A  AAT
                                CA GA   GTGGTCGTGA
                                || ||   ||||||||||
                                GT CT   CACCAGCACT
                                 A  C__
GAM750  NGFR     3'  TTCTGACCACACTTCCTGTC   10231      A   A       T
                                GACA GAA TGTGGTCG GAA
                                |||| ||| |||||||| |||
                                CTGT CTT ACACCAGT CTT
                                  C   C       _
GAM750  OLR1     3'  TTCACAACAGTTCTTGTTA    10341          ATGTG  C
                                TGACAAGAA     GT GTGAA
                                |||||||||     || |||||
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                                ATTGTTCTT    CA CACTT
                                     GA___  A
GAM750  POU4F1   3'  CACTGAAAACATTTTTGTCA  20660        A  GG  _
                                TGACAAGAA TGT  TC GTG
                                ||||||||| |||  || |||
                                ACTGTTTTT ACA  AG CAC
                                     _  AA  T
GAM750  SMP1     3'  TTTCACATGAATAATTTTTGTC 26705        A  GGTC
          A                      TGACAAGAA TGT   GTGAAA
                                ||||||||| |||   ||||||
                                ACTGTTTTT ATA   CACTTT
                                     A  AGTA
GAM750  ZNF264   3'  TTCTATTAACATTTCTTTTCA  12769    C       GGTCGT
                                TGA AAGAAATGT     GAA
                                ||| |||||||||     |||
                                ACT TTCTTTACA     CTT
                                  T       ATTAT_
GAM750  C20orf175 3'  CGAGCTCCACGTTTCCTGCCA  55063    A  A       ___
                                TG CA GAAATGTGG   TCG
                                || || |||||||||   |||
                                AC GT CTTTGCACC   AGC
                                 C  C        TCG
GAM750  CAPNS2   3'  TTTCACAACCCTACATATTTCT 50323     CA      ____  C
          GATCA                    TGA  AGAAATGT    GGT GTGAAA
                                |||  ||||||||   ||| ||||||
                                ACT  TCTTTATA    CCA CACTTT
                                  AG       CATC   A
GAM750  CLDN6    3'  TTTACACTCACATTTTTATCA  41041     CA       _  C
                                TGA  AGAAATGTG GT GTGAA
                                |||  ||||||||| || |||||
                                ACT  TTTTTACAC CA CATTT
                                  A_       T  _
GAM750  DKFZP564L0864 3'  GCACCAATTTCTTGCCA     72555    A      G   C
                                TG CAAGAAAT TGGT GT
                                || |||||||| |||| ||
                                AC GTTCTTTA ACCA CG
                                 C       _   _
GAM750  DKFZP566B183 3'  TTTCCATAAACATTTCTTTTCA 31330     C       GGTCGT
                                TGA AAGAAATGT     GAAA
                                ||| |||||||||     ||||
                                ACT TTCTTTACA     CTTT
                                  T       AATAC_
GAM750  GTF2E1   3'  TACAGACCTCTTGTCA      18616        AATGT   _
                                TGACAAGA    GGTC GTG
                                ||||||||    |||| |||
                                ACTGTTCT    CCAG CAT
                                     _____   A
GAM750  KIAA0089  3'  TTTTAATTCACATTTCTT    69967          TCG
                                AAGAAATGTGG   TGAAA
                                ||||||||||   |||||
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                                TTCTTTACACT   ATTTT
                                      TA_
GAM750  KIAA0373  5'  TTTTCAAAGTAACATTTCTT   28015        GGTCG
                                AAGAAATGT    TGAAAA
                                |||||||||    ||||||
                                TTCTTTACA    ACTTTT
                                     ATGAA
GAM750  KIAA1813  3'  TTTTCACACTGTAAATTTCTTG 70314        __ TG  C
           T                     ACAAGAAAT  G  GT GTGAAAA
                                |||||||||  |  || |||||||
                                TGTTCTTTA  T  CA CACTTTT
                                     AA GT  _
GAM750  KIAA1951  3'  TTCCAGGCTTCTCTTGTCA   73766        AATGT   GT
                                TGACAAGA    GGTC  GAA
                                ||||||||    ||||  |||
                                ACTGTTCT    TCGG  CTT
                                     CT___    AC
GAM750  MGC4170   3'  TTCACCATTTCTTGTC      44227          TGGTC
                                GACAAGAAATG    GTGAA
                                ||||||||||    |||||
                                CTGTTCTTTAC    CACTT
                                      _____
GAM750  NRN1      3'  CACTGCACATTTCTCCTCA   33432     CA       GTC
                                TGA  AGAAATGTG   GTG
                                |||  |||||||||   |||
                                ACT  TCTTTACAC   CAC
                                  CC        GT_
GAM750  PLA2G12   3'  TTTTCACAACCACATTT     48028         C
                                AAATGTGGT GTGAAAA
                                ||||||||| |||||||
                                TTTACACCA CACTTTT
                                     A
GAM750  PPY2      3'  CACTCCACATTCCTGGCCA   40819    ACA  A      TC
                                TG   AG AATGTGG  GTG
                                ||   || |||||||  |||
                                AC   TC TTACACC  CAC
                                  CGG  C      T_
GAM750  ZNF31     3'  TTTGTAGACCACATTTCCTGTT 64992       A         _ TG
           A                     TGACA GAAATGTGGTC G  AA
                                |||||| |||||||||||  |  ||
                                ATTGT CTTTACACCAG T  TT
                                   C          A GT
GAM750  LOC115219 3'  CACGACAACGGGTCCTCA    73295     CAA  AA   G
                                TGA   GA  TGT GTCGTG
                                |||   ||  ||| ||||||
                                ACT   CT  GCA CAGCAC
                                  C__  GG   A
GAM750  LOC120376 5'  TTCAGAGCATTTCTTTCA    75986     C       GG  G
                                TGA AAGAAATGT  TC TGAA
                                ||| |||||||||  || ||||
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                                ACT TTCTTTACG  AG ACTT
                                  _       __ _
GAM750  LOC133418 3'  TTTCATATACATTTTTTGCCA  75094    A        GTC
                                TG CAAGAAATGTG   GTGAAA
                                || ||||||||||   ||||||
                                AC GTTTTTTACAT   TACTTT
                                 C         A__
GAM750  LOC151199 3'  TTAAAACCACAGCTCTTGCCA  80174    A    AA     CG
                                TG CAAGA  TGTGGT  TGA
                                || |||||  ||||||  |||
                                AC GTTCT  ACACCA  ATT
                                 C    CG     AA
GAM750  LOC152317 5'  TCACACTGACTTTTGTCA    85649        AATG   C
                                TGACAAGA    TGGT GTGA
                                ||||||||    |||| ||||
                                ACTGTTTT    GTCA CACT
                                     CA__    _
GAM750  LOC152674 3'  TTCAACCCACCCTCTTGTCA   85841        AAT    TCG
                                TGACAAGA   GTGG   TGAA
                                ||||||||   ||||   ||||
                                ACTGTTCT   CACC   ACTT
                                     CC_    CA_
GAM750  LOC152845 5'  CATGACCACATTTTTCA     60330     CAA
                                TGA   GAAATGTGGTCGTG
                                |||   ||||||||||||||
                                ACT   TTTTACACCAGTAC
                                  ____
GAM750  LOC154743 3'  TTTAGTCCACATTGTCTTGTCA 81118         _      TCG
                                TGACAAGA AATGTGG   TGAA
                                |||||||| |||||||   ||||
                                ACTGTTCT TTACACC   ATTT
                                     G      TG_
GAM750  LOC165476 5'  TTCACGGCACCTTCT       87201      AT   G
                                AGAA  GTG TCGTGAA
                                ||||  ||| |||||||
                                TCTT  CAC GGCACTT
                                  C_  _
GAM750  LOC254266 5'  TTTTCGGTCACACATCTTATCA 97356     C    AA    GT  T
                                TGA AAGA  TGTG  CG GAA
                                ||| ||||  ||||  || |||
                                ACT TTCT  ACAC  GC TTT
                                  A   AC    TG  T
GAM750  LOC255919 3'  TTTCATTCTTACATTTCTAATC 95043     CA        TC
           A                     TGA  AGAAATGTGG  GTGAAA
                                |||  ||||||||||  ||||||
                                ACT  TCTTTACATT  TACTTT
                                  AA         CT
GAM750  LOC51754  5'  CACGGCCACATCTCTGTCA    71027      A  A
                                TGACA GA ATGTGGTCGTG
                                ||||| || ||||||||||
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                                ACTGT CT TACACCGGCAC
                                  _ C
GAM750  LOC55862  3'  ACCTCATTTCTTGCCA     37485    A       T
                                TG CAAGAAATG GGT
                                || ||||||||| |||
                                AC GTTCTTTAC CCA
                                 C       T
GAM750  LOC55954  3'  CACGTGGTCACTTTTCTCATCA 38877    CA    T   GT __
                                TGA  AGAAA GTG  C  GTG
                                |||  ||||| |||  |  |||
                                ACT  TCTTT CAC  G  CAC
                                  AC    T   TG TG
GAM751  ADRA1A   3'  GGAAAAGAGCCTTCAGGGA   52785       A_  ___
                                TCCCTGAG  CTC   TCC
                                ||||||||  |||   |||
                                AGGGACTT  GAG   AGG
                                     CC   AAA
GAM751  ANGPT4   3'  ACACAGGAGAAGCTCGG    32024      AC
                                CTGAG  TCTCCTGTGT
                                |||||  ||||||||||
                                GGCTC  AGAGGACACA
                                   GA
GAM751  ARHGAP6  3'  GGCCACACTCCAAGTCTCAG  20409       CTCCT   A
                                CTGAGACT    GTGT GCC
                                ||||||||    |||| |||
                                GACTCTGA    CACA CGG
                                     ACCT_   C
GAM751  ARHGAP6  3'  GGCCACACTCCAAGTCTCAG  25518       CTCCT   A
                                CTGAGACT    GTGT GCC
                                ||||||||    |||| |||
                                GACTCTGA    CACA CGG
                                     ACCT_   C
GAM751  CTSD     3'  ACAGAGGAGAGTCCCAG     8583     A       G
                                CTG GACTCTCCT TGT
                                ||| |||||||| |||
                                GAC CTGAGAGGA ACA
                                  C       G
GAM751  DAAM2    3'  GCCACACAGGAGGCCGGG    92289     AGAC       A
                                CCTG   TCTCCTGTGT GC
                                ||||   |||||||||| ||
                                GGGC   GGAGGACACA CG
                                  C___        C
GAM751  DISC1    3'  GGCTACACAACCTTCTCAGG  37885       CTCTCC
                                CCTGAGA    TGTGTAGCC
                                |||||||    |||||||||
                                GGACTCT    ACACATCGG
                                    TCCA__
GAM751  DOK1     3'  GGCCTGTGTGGAGGCCTCAGGG 7274        A T   T TG  _
           A                     TCCCTGAG C CTCC G  TAG CC
                                ||||||||| | |||| |  ||| ||
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                                AGGGACTC G GAGG T  GTC GG
                                    C _   _ GT  C
GAM751  DPP4    3'  CTATTCAAACAGTCTCAGG   8657        CTCC  T
                                CCTGAGACT   TG GTAG
                                |||||||||   || ||||
                                GGACTCTGA   AC TATC
                                     CAA_  T
GAM751  DRIL1   3'  GCCACACAGGGGCCAGG    17828     AGACT       A
                                CCTG    CTCCTGTGT GC
                                ||||    ||||||||| ||
                                GGAC    GGGGACACA CG
                                  C____       C
GAM751  ENAM    3'  GCAGGAAAAAAGTCTCAG    49078       C___
                                CTGAGACT   TCCTGT
                                ||||||||   ||||||
                                GACTCTGA   AGGACG
                                     AAAA
GAM751  FCMD    3'  GCTACACAGGAGGCTGAGG   22092    G  A T
                                CCT AG C CTCCTGTGTAGC
                                ||| || | ||||||||||||
                                GGA TC G GAGGACACATCG
                                 G  _ _
GAM751  GNA11   3'  GCCCCAGGAGAGTCCCAGG   76101     A       TGTA
                                CCTG GACTCTCCTG   GC
                                |||| ||||||||||   ||
                                GGAC CTGAGAGGAC   CG
                                  C        CC__
GAM751  ICMT    3'  GCTACACAAAAATGGGCAG   24816    AGA  TCC__
                                CTG  CTC    TGTGTAGC
                                |||  |||    ||||||||
                                GAC  GGG    ACACATCG
                                  ___  TAAAA
GAM751  KCNA7   3'  ACAACAGAGTCTCAGGGA    49045          CC
                                TCCCTGAGACTCT  TGT
                                ||||||||||||  |||
                                AGGGACTCTGAGA  ACA
                                       CA
GAM751  KLHL3   3'  GCATGGAGAAGCCTCAGGGA  87457       A  _   T
                                TCCCTGAG CT CTCC GTGT
                                |||||||| || |||| ||||
                                AGGGACTC GA GAGG TACG
                                     C  A   _
GAM751  LFG     5'  GCCACCCGGGCCTCAGGGA   76721       ACTCT   T  A
                                TCCCTGAG    CCTG GT GC
                                ||||||||    |||| || ||
                                AGGGACTC    GGGC CA CG
                                     C_____   C  C
GAM751  MMP14   3'  ACCTTGGGAGGAAAACTCAGAG 17166   C    AC__     T_
            A                    TC CTGAG   TCTCCTG  GT
                                || |||||   |||||||  ||
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                                AG GACTC   GGAGGGT  CA
                                 A    AAAA     TC
GAM751  PDE4B   5' GCAGAGAGAGTCTGAG     10480   G      _
                                CT AGACTCTC CTGT
                                || |||||||| ||||
                                GA TCTGAGAG GACG
                                 G       A
GAM751  PRX     3' GCTGCCAAAAGTCTCAGAGA  40533   C      CTCC  T
                                TC CTGAGACT   TG GTAGC
                                || ||||||||   || |||||
                                AG GACTCTGA   AC CGTCG
                                 A       AA__ _
GAM751  SIM1    3' ACATGTGGAAAGCCTCAGGAGA 17377   _    A  C   _
                                TC CCTGAG CT TCC TGTGT
                                || |||||| || ||| |||||
                                AG GGACTC GA AGG GTACA
                                 A     C  A   T
GAM751  TIMM23  3' GCTACACAAAAGGCATCA    60141    GA T  CC
                                TGA  C CT  TGTGTAGC
                                |||  | ||  ||||||||
                                ACT  G GA  ACACATCG
                                  AC _  AA
GAM751  TNR     3' GGCCCAGAGAAAAGAGCCTCAG 12355     A   C__  G  TA
                                CTGAG CTCT   CT TG  GCC
                                ||||| ||||   || ||  |||
                                GACTC GAGA   GA AC  CGG
                                   C    AAA  G  C_
GAM751  WHSC1   3' CTACACAGAGGACCCAGGGG  55827     AGAC  TC
                                TCCCTG   TC  CTGTGTAG
                                ||||||   ||  ||||||||
                                GGGGAC   AG  GACACATC
                                   CC__  GA
GAM751  WHSC1   3' CTACACAGAGGACCCAGGGG  55844     AGAC  TC
                                TCCCTG   TC  CTGTGTAG
                                ||||||   ||  ||||||||
                                GGGGAC   AG  GACACATC
                                   CC__  GA
GAM751  WHSC1   3' CTACACAGAGGACCCAGGGG  29909     AGAC  TC
                                TCCCTG   TC  CTGTGTAG
                                ||||||   ||  ||||||||
                                GGGGAC   AG  GACACATC
                                   CC__  GA
GAM751  ZNF144  3' GCCACTGGAGTCTCA     23079       CCT   TA
                                TGAGACTCT   GTG  GC
                                |||||||||   |||  ||
                                ACTCTGAGG   CAC  CG
                                     T__   __
GAM751  ABCA5   5' ATACAGGAGAATTCAG     37913     AC
                                CTGAG  TCTCCTGTGT
                                |||||  ||||||||||
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                                GACTT  AGAGGACATA
                                  A_
GAM751  AMAC     5'  ACCTCAGGAGAGTTCCAGGGA  53995       AG       T_
                                TCCCTG  ACTCTCCTG  GT
                                ||||||  |||||||||  ||
                                AGGGAC  TGAGAGGAC  CA
                                   CT       TC
GAM751  CNNM1    3'  CACAGCCAGCCTTAGGGA    39769        A  CTC
                                TCCCTGAG CT   CTGTG
                                ||||||||  ||   |||||
                                AGGGATTC GA   GACAC
                                     C  CC_
GAM751  Cyt19    3'  GCAGAGGGTCTCAGG       72937           C
                                CCTGAGACTCTC TGT
                                |||||||||||| |||
                                GGACTCTGGGAG ACG

                                          _
GAM751  DKFZP434N178 3'  ACGGGAGTCTCAGAGA      71900    C       T  T
                                TC CTGAGACTC CC GT
                                || |||||||||  || ||
                                AG GACTCTGAG GG CA
                                 A       _ _
GAM751  DKFZP564D0462 3'  GGCTACACAGCAACCCAAGGGA 70499       GAGACTCTC
                                TCCCT        CTGTGTAGCC
                                |||||        ||||||||||
                                AGGGA        GACACATCGG
                                   ACCCAAC__
GAM751  DKFZp566H0824 5'  AGGAGAGTCTCGAGGA      34047     C
                                TCC TGAGACTCTCCT
                                ||| ||||||||||||
                                AGG GCTCTGAGAGGA
                                  A
GAM751  FLJ10057  5'  GGTCCAGGAGAGTCTCA     35781           TGTA
                                TGAGACTCTCCTG    GCC
                                ||||||||||||||   |||
                                ACTCTGAGAGGAC    TGG
                                       C___
GAM751  FLJ12800  5'  CTGCGGAAAAGTTCAGGGA   43230        ACTC   TGT
                                TCCCTGAG    TCC   GTAG
                                ||||||||    |||   ||||
                                AGGGACTT    AGG   CGTC
                                     GAAA   ___
GAM751  FLJ13189  3'  CACAAGAATTCAGGGA      45982        AC   CC
                                TCCCTGAG  TCT  TGTG
                                ||||||||  |||  ||||
                                AGGGACTT  AGA  ACAC
                                     A_   __
GAM751  FLJ14326  5'  GCATCTGAAAAGTCTCAG    49809        C_  CT
                                CTGAGACT  TC  GTGT
                                ||||||||  ||  ||||
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                                GACTCTGA  AG  TACG
                                    AA  TC
GAM751  FLJ14641  3'  GGCTACACTGAACCTCCAG   51488    A  CTC  CT
                                CTG GA   TC  GTGTAGCC
                                ||| ||   ||  ||||||||
                                GAC CT   AG  CACATCGG
                                  _  CCA  T_
GAM751  FLJ22938  5'  AGGAGAGTGTCAAGGA     45157    C   G
                                TCC TGA ACTCTCCT
                                ||| ||| ||||||||
                                AGG ACT TGAGAGGA
                                  A   G
GAM751  GAB3      3'  TTGCAAAGAGTCTCAGG     54636          CCTG
                                CCTGAGACTCT    TGTAG
                                ||||||||||    |||||
                                GGACTCTGAGA    ACGTT
                                      A___
GAM751  H963      5'  GCTACACAACCTTGGAGTCTTA 94634         CC___
          G                      CTGAGACTCT    TGTGTAGC
                                ||||||||||    ||||||||
                                GATTCTGAGG    ACACATCG
                                      TTCCA
GAM751  H963      5'  GCTACACAACCTTGGAGTCTTA 25253         CC___
          G                      CTGAGACTCT    TGTGTAGC
                                ||||||||||    ||||||||
                                GATTCTGAGG    ACACATCG
                                      TTCCA
GAM751  IBTK      3'  GCTGTGGAAAAGAGTCTTAGAG 67489    C        CCTGTG
          A                      TC CTGAGACTCT     TAGC
                                || ||||||||||      ||||
                                AG GATTCTGAGA     GTCG
                                 A         AAAGGT
GAM751  KIAA0453  3'  GCAGGGAGAGTTCCAG      69048     AG       G
                                CTG  ACTCTCCT TGT
                                |||  |||||||| |||
                                GAC  TGAGAGGG ACG
                                  CT       _
GAM751  KIAA1223  3'  GCATGAAAATTCTCAGGGA   71146         CTC_  C
                                TCCCTGAGA    TC TGT
                                |||||||||    || |||
                                AGGGACTCT    AG ACG
                                      TAAA  T
GAM751  KIAA1503  5'  GCCACACAGGAGCAGGGG    68348       AGACT       A
                                TCCCTG    CTCCTGTGT GC
                                ||||||    ||||||||| ||
                                GGGGAC    GAGGACACA CG
                                    _____         C
GAM751  KIAA1656  3'  GCTTGGAGAGTCTCAG      65799           TGT
                                CTGAGACTCTCC   GT
                                ||||||||||||   ||
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                                GACTCTGAGAGG  CG
                                      TT_
GAM751  KIAA1674  3'  GGCTTCCTGGTGAGCCTCAGGG 68786       A  T  TGTGT
            A                  TCCCTGAG CTC CC    AGCC
                               |||||||| ||| ||    ||||
                               AGGGACTC GAG GG    TCGG
                                   C  T  TCCT_
GAM751  KIAA1786  3'  GCAGAGACCTCAGGGA     66031       AC   C
                               TCCCTGAG  TCTC TGT
                               ||||||||  |||| |||
                               AGGGACTC  AGAG ACG
                                   C_   _
GAM751  KIAA1841  3'  GCCAGGCAGAAAGAGTGCTCAG 80046       _   _____   T
            GGA                  TCCCTGAG ACTCT    CCTG GT
                               |||||||| |||||    |||| ||
                               AGGGACTC TGAGA    GGAC CG
                                   G    AAGAC   _
GAM751  KIAA1893  3'  GCCAGAGGGTCTCAGG     73214          C  T
                               CCTGAGACTCTC TG GT
                               |||||||||||| || ||
                               GGACTCTGGGAG AC CG
                                      _ _
GAM751  KNTC1    5'  ACTCAGGAAGACAGTCTCAG   28177       C___    T
                               CTGAGACT   TCCTG GT
                               ||||||||   ||||| ||
                               GACTCTGA   AGGAC CA
                                   CAGA    T
GAM751  MAD4     3'  GCCACCCAGCGTCTCAGGGA   21279        TCTC   T  A
                               TCCCTGAGAC   CTG GT GC
                               ||||||||||   ||| || ||
                               AGGGACTCTG   GAC CA CG
                                    C___   C  C
GAM751  MGC13102  3'  GCAGAGCGCCTCAGGGA    50316       ACT   C
                               TCCCTGAG   CTC TGT
                               ||||||||   ||| |||
                               AGGGACTC   GAG ACG
                                   CGC  _
GAM751  moblak   3'  GCCTGAGCATCTCAGGGA    55501       CT   CT
                               TCCCTGAGA  CTC  GT
                               |||||||||  |||  ||
                               AGGGACTCT  GAG  CG
                                    AC   TC
GAM751  NSE1     3'  GCAGGAAGTCTCAGG      59073        C
                               CCTGAGACT TCCTGT
                               ||||||||| ||||||
                               GGACTCTGA AGGACG
                                      _
GAM751  NSG-X    3'  ATGTAGGAAGGCCTCAAGGA   26970    C   A TC    TG
                               TCC TGAG C  TCCTG  T
                               ||| |||| |  |||||  |
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                                AGG ACTC G  AGGAT  A
                                  A   C GA    GT
GAM751  OSBPL5   3'  GGCCACACAGGAGAAGTTT   72688      _       A
                                AGACT CTCCTGTGT GCC
                                ||||| ||||||||| |||
                                TTTGA GAGGACACA CGG
                                   A       C
GAM751  PPP1R12C 3'  GGCTCCGGGGGAAGTCTCAGAG 34281    C      _     TGT
           A                     TC CTGAGACT CTCCTG   AGCC
                                || |||||||| ||||||   ||||
                                AG GACTCTGA GGGGGC   TCGG
                                 A       A     C__
GAM751  RBT1     3'  CACTGGGGCCTCAGGGA     25349        ACT   T
                                TCCCTGAG   CTCC GTG
                                ||||||||   |||| |||
                                AGGGACTC   GGGG CAC
                                     C__    T
GAM751  SMOC1    3'  GGCAGGTGGAGAGTCCAGGGA  42152       A      TGTGTA
                                TCCCTG GACTCTCC     GCC
                                |||||| ||||||||     |||
                                AGGGAC CTGAGAGG     CGG
                                   _       TGGA__
GAM751  STRAIT11499 5'  GCAGGAGAGTCTCAAGG     41143    C
                                CC TGAGACTCTCCTGT
                                || ||||||||||||||
                                GG ACTCTGAGAGGACG
                                 A
GAM751  TED      3'  GCCAGAGGGCCTCAGGGA    31638        A    C  T
                                TCCCTGAG CTCTC TG GT
                                |||||||| ||||| || ||
                                AGGGACTC GGGAG AC CG
                                     C    _ _
GAM751  TMLHE    3'  CACGAAAAGGGTCTCAGGGA   36511          CC_
                                TCCCTGAGACTCT   TGTG
                                ||||||||||||   ||||
                                AGGGACTCTGGGA   GCAC
                                        AAA
GAM751  TNFAIP3  3'  CTGCAAGAAGCTCAAGGA    20824     C   AC   CCTG
                                TCC TGAG  TCT    TGTAG
                                ||| ||||  |||    |||||
                                AGG ACTC  AGA    ACGTC
                                  A   GA  _____
GAM751  VIT      5'  ATGCAGGAAAGCCTAAGGGA   53902      G  A  C
                                TCCCT AG CT TCCTGTGT
                                ||||| || || ||||||||
                                AGGGA TC GA AGGACGTA
                                   A  C  A
GAM751  LOC121512 5'  AGAAGAGGCTCAGGGA      57642        A   C
                                TCCCTGAG CTCT CT
                                |||||||| |||| ||
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                                AGGGACTC GAGA GA
                                     G    A
GAM751   LOC144144 5' CATTAAAAGAACTCAGGGA   60164        AC   CCT_
                                TCCCTGAG  TCT    GTG
                                ||||||||  |||    |||
                                AGGGACTC  AGA    TAC
                                     A_   AAAT
GAM751   LOC146159 5' CTGCAGGAGTCCCAGG      77681      A     CCTG
                                CCTG GACTCT    TGTAG
                                |||| ||||||    |||||
                                GGAC CTGAGG    ACGTC
                                  C     _____
GAM751   LOC146713 5' GCTGCAAAGGCCTCAGGGA   83730        ACTCT   G
                                TCCCTGAG    CCT TGTAGC
                                ||||||||    ||| ||||||
                                AGGGACTC    GGA ACGTCG
                                     C____   A
GAM751   LOC146741 5' ACCTCAGGAGAGTTCCAGGGA  76285       AG       T_
                                TCCCTG  ACTCTCCTG  GT
                                ||||||  |||||||||  ||
                                AGGGAC  TGAGAGGAC  CA
                                    CT       TC
GAM751   LOC146861 5' ACCTCAGGAGAGTTCCAGGGA  76295       AG       T_
                                TCCCTG  ACTCTCCTG  GT
                                ||||||  |||||||||  ||
                                AGGGAC  TGAGAGGAC  CA
                                    CT       TC
GAM751   LOC150606 3' GCCACCTGGTCTCAGAGA    85090    C      CTCCT   TA
                                TC CTGAGACT    GTG  GC
                                || ||||||||    |||  ||
                                AG GACTCTGG    CAC  CG
                                 A       TC___   __
GAM751   LOC150998 3' GCTACACAGGAGGCTAAGG   85185     G  A T
                                CCT AG C CTCCTGTGTAGC
                                ||| || | ||||||||||||
                                GGA TC G GAGGACACATCG
                                  A  _ _
GAM751   LOC151304 3' ACACCGGGGAGCCTCAGGGA  85307        A     T
                                TCCCTGAG CTCTCC GTGT
                                |||||||| |||||| ||||
                                AGGGACTC GAGGGG CACA
                                     C     C
GAM751   LOC157292 3' GCTACATGGCAGCCCCAGGG  86417      AGACT  C
                                CCCTG    CT CTGTGTAGC
                                |||||    || |||||||||
                                GGGAC    GA GGTACATCG
                                   CCC__  C
GAM751   LOC158629 5' GCTTCTGGGGAGGCCTCAGGGA 86878        A_     TGTGT
                                TCCCTGAG  CTCTCC    AGC
                                ||||||||  ||||||    |||
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                                AGGGACTC  GAGGGG    TCG
                                    CG     TCT__
GAM751  LOC158972 3'  GCCGGCAAGTCCCAGGGA    86952       A   CT  T
                                TCCCTG GACT  CC GT
                                |||||| ||||  || ||
                                AGGGAC CTGA  GG CG
                                   C    AC  C
GAM751  LOC199958 3'  ACGTAGGGAGCCCCAGG     89881     AGA   T
                                CCTG   CTC CCTGTGT
                                ||||   ||| |||||||
                                GGAC   GAG GGATGCA
                                  CCC   _
GAM751  LOC221477 3'  GCTACACAGGAAGCTGAGG   92156     G  A  C
                                CCT AG CT TCCTGTGTAGC
                                ||| || || ||||||||||
                                GGA TC GA AGGACACATCG
                                  G  _  _
GAM751  LOC221495 3'  GCCACTGAGTTCAGGGA     93857        A   TCC  T
                                TCCCTGAG CTC   TG GT
                                |||||||| |||   || ||
                                AGGGACTT GAG   AC CG
                                     _   TC_  _
GAM751  LOC58525  3'  GGCCCCCCAAAGAGCCTCAGGG 78649        A    CC  TGTA
           G                     TCCCTGAG CTCT  TG    GCC
                                |||||||| ||||  ||    |||
                                GGGGACTC GAGA  AC    CGG
                                     C    A_  CCCC
GAM751  LOC90190  3'  GCCACTTGATGTCTCAGGGA   61778         TC  CT   TA
                                TCCCTGAGAC  TC  GTG  GC
                                ||||||||||  ||  |||  ||
                                AGGGACTCTG  AG  CAC  CG
                                      T_  TT   __
GAM751  LOC92340  3'  ACTTGGAAAGAACTTCAGGGA  68985        A__  C   TGT
                                TCCCTGAG   CT TCC   GT
                                ||||||||   || |||   ||
                                AGGGACTT   GA AGG   CA
                                     CAA  A   TT_
GAM751  LOC93496  3'  GTCAGTAGAGTCCCAAGGA    72437     C  A     C   TGTA
                                TCC TG GACTCT CTG    GC
                                ||| || |||||| |||    ||
                                AGG AC CTGAGA GAC    TG
                                  A  C     T  _____
GAM751  LOC93626  3'  GCCCCAGGAGAGTCCCAGG    72771      A         TGTA
                                CCTG GACTCTCCTG    GC
                                |||| ||||||||||    ||
                                GGAC CTGAGAGGAC    CG
                                  C         CC__
GAM752  APPL      3'  TGCTTTGTATATTTGGTGA   23933       C    CAA
                                TCACC AATG   ACAAAGCA
                                ||||| ||||   ||||||||
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                                AGTGG TTAT   TGTTTCGT
                                  T   A__
GAM752  AQP1    3'  TGCTTTGTGCCTTTGGG    4607      T_ AA
                                CCCAA  GC  ACAAAGCA
                                |||||  ||  ||||||||
                                GGGTT  CG  TGTTTCGT
                                  TC  __
GAM752  C8A     5'  CTTTGTTTTATTGGG      5114        C
                                CCCAATG AAACAAAG
                                ||||||| ||||||||
                                GGGTTAT TTTGTTTC
                                  _
GAM752  CDO1    3'  TGCTTTGTTACCTGGAGGA   8401    AC   ATGCA
                                TC  CCA    AACAAAGCA
                                ||  |||    |||||||||
                                AG  GGT    TTGTTTCGT
                                 GA   CCA__
GAM752  CHD2    3'  TGCTTTGTTTTTGG      7037      TGC
                                CCAA   AAACAAAGCA
                                ||||   ||||||||||
                                GGTT   TTTGTTTCGT
                                  ___
GAM752  CUTL1   3'  TGCGAGGCTAATTGGGTGA   8591         __ AAACAAA
                                TCACCCAAT  GC     GCA
                                |||||||||  ||     |||
                                AGTGGGTTA  CG     CGT
                                     AT  GAG____
GAM752  DDOST   3'  TGCTTTGTTTAAAGCCGTGG   17820    AT ___
                                CCA  GC   AAACAAAGCA
                                |||  ||   ||||||||||
                                GGT  CG   TTTGTTTCGT
                                  GC  AAA
GAM752  DSCR1   3'  TGTTGTACACTTGGGTGA    15337       ___    A
                                TCACCCAA   TGCAA CA
                                ||||||||   ||||| ||
                                AGTGGGTT   ATGTT GT
                                     CAC    _
GAM752  E2F3    3'  TTTTGTTTGCATTAAGT    8705    CC
                                AC  AATGCAAACAAAG
                                ||  |||||||||||||
                                TG  TTACGTTTGTTTT
                                 AA
GAM752  ELMO1   3'  TGCTTTGTTTTTGG      55286     TGC
                                CCAA   AAACAAAGCA
                                ||||   ||||||||||
                                GGTT   TTTGTTTCGT
                                  ___
GAM752  ITK     3'  TGCTTGGAGCATTGGGT     18684        AAA   A
                                ACCCAATGC   CAA GCA
                                |||||||||   ||| |||
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                                TGGGTTACG   GTT CGT
                                     AG_  _
GAM752  MB      3'  TGCTTTGTTTAGTAGAGGTGG  18116      CAA  _
                                TCACC   TGC AAACAAAGCA
                                |||||   ||| ||||||||||
                                GGTGG   ATG TTTGTTTCGT
                                   AG_  A
GAM752  MEN1    5'  TGCTTTGTCTGCTGGTGA    93383      CAAT  A
                                TCACC    GCA ACAAAGCA
                                |||||    ||| ||||||||
                                AGTGG    CGT TGTTTCGT
                                   T___  C
GAM752  MYOM2   3'  TGCTTTTGATTTTTGCATTTGG 14269      C      ___   _
           TGA                     TCACC AATGCAAA   CAAA GCA
                                |||||| ||||||||   |||| |||
                                AGTGG TTACGTTT   GTTT CGT
                                   T       TTA   T
GAM752  OCLN    3'  TTTGTTTGCATAGGTGA     10319      CA
                                TCACC  ATGCAAACAAA
                                |||||  ||||||||||||
                                AGTGG  TACGTTTGTTT
                                   A_
GAM752  PCDHB3  3'  TGCTTTGTCCATTGG       38432       CAA
                                CCAATG   ACAAAGCA
                                ||||||   ||||||||
                                GGTTAC   TGTTTCGT
                                   C__
GAM752  PCMT1   3'  TGCTTTTGTGCATTGG      18226        AAC
                                CCAATGCA   AAAGCA
                                ||||||||   ||||||
                                GGTTACGT   TTTCGT
                                     GT_
GAM752  PIM1    3'  TGCTCTGTTTGTGGGGTGA   91032       AAT      A
                                TCACCC   GCAAACA AGCA
                                ||||||   ||||||| ||||
                                AGTGGG   TGTTTGT TCGT
                                   G__      C
GAM752  PPT1    3'  TGCTTTGTTTTGCTGGTGA   61805      CAAT    _
                                TCACC    GCAAA CAAAGCA
                                |||||    ||||| |||||||
                                AGTGG    CGTTT GTTTCGT
                                   T___     T
GAM752  PXN     3'  TGCTTTGTCTGTGGGGTGG   11165       AAT   A
                                TCACCC   GCA ACAAAGCA
                                ||||||   ||| ||||||||
                                GGTGGG   TGT TGTTTCGT
                                   G__   C
GAM752  RNF28   3'  TGCCTGGTCATTGGGTGA    50864          CAA  AAA
                                TCACCCAATG   AC   GCA
                                ||||||||||   ||   |||
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                                AGTGGGTTAC  TG  CGT
                                     ___ GTC
GAM752  SDC1    3' CTTTGTTTCGTGGGG      11473    A  C
                                CCC ATG AAACAAAG
                                ||| ||| ||||||||
                                GGG TGC TTTGTTTC
                                  G  _
GAM752  TEC     3' TGCTCTGGAGCATTGGGTGA  12224         AAA  A
                                TCACCCAATGC  CA AGCA
                                ||||||||||  || ||||
                                AGTGGGTTACG  GT TCGT
                                      AG_  C
GAM752  ANKRD6  3' TGCCTTGTTTGTGGAGT    30091   _ AAT      A
                                AC CC  GCAAACAA GCA
                                || ||  |||||||| |||
                                TG GG  TGTTTGTT CGT
                                 A ___      C
GAM752  C21orf18 3' TGCTCTGATACCATTGGGT  33846       CAAA  A
                                ACCCAATG   CA AGCA
                                ||||||||   || ||||
                                TGGGTTAC   GT TCGT
                                     CATA  C
GAM752  C21orf25 3' TGCTTTGTTTAAGGAGGTG  63559     CAATGC
                                CACC     AAACAAAGCA
                                ||||     ||||||||||
                                GTGG     TTTGTTTCGT
                                  AGGAA_
GAM752  C3F     5' TGCTTTGTTTTATCGG     19300    A  C
                                CC ATG AAACAAAGCA
                                || ||| ||||||||||
                                GG TAT TTTGTTTCGT
                                 C  _
GAM752  CPGL2   5' GCTTTGTTCTCCAGATGTGA  74415     CCAA  CA_
                                TCAC   TG  AACAAAGC
                                ||||   ||  ||||||||
                                AGTG   AC  TTGTTTCG
                                  TAG_  CTC
GAM752  DKFZp761D081 3' TGCTTTGTAAGTGGATTG   34283     G  A__
                                CAAT CA  ACAAAGCA
                                |||| ||  ||||||||
                                GTTA GT  TGTTTCGT
                                  G  GAA
GAM752  DKFZp761H2121 3' TGCTCTGTTTACAATGG    56373    A  C    A
                                CCA TG AAACA AGCA
                                ||| || ||||| ||||
                                GGT AC TTTGT TCGT
                                  A  A    C
GAM752  DOK4    3' TGCTTTGTAGGCTGGG     36184     AT  AA
                                CCCA  GC  ACAAAGCA
                                ||||  ||  ||||||||
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                              GGGT  CG  TGTTTCGT
                                __  GA
GAM752  FLJ13590  5'  TGCTTTGTTTTTTGGTG    45790     C  TGC
                              CACC AA   AAACAAAGCA
                              |||| ||   ||||||||||
                              GTGG TT   TTTGTTTCGT
                                T  ___
GAM752  FLJ14146  3'  TGCTTTGTCCTGGGTGG    45246       ATGCAA
                              TCACCCA     ACAAAGCA
                              |||||||     ||||||||
                              GGTGGGT     TGTTTCGT
                                 CC____
GAM752  FLJ14326  3'  TGCTCGCAGTTGGGTGA    49820       _  AAACAA
                              TCACCCAA TGC     AGCA
                              |||||||| |||     ||||
                              AGTGGGTT ACG     TCGT
                                   G  C_____
GAM752  FLJ20294  3'  TGCCCTGTCCACCTGTTGGGTG 34884        GCAA__  AA
          G                    TCACCCAAT     ACA  GCA
                              |||||||||     |||  |||
                              GGTGGGTTG     TGT  CGT
                                   TCCACC   CC
GAM752  FLJ20400  3'  TGCTTTGTTCGGCCTGGTG   66513     CAAT  A_
                              CACC    GC  AACAAAGCA
                              ||||    ||  |||||||||
                              GTGG    CG  TTGTTTCGT
                                TC__  GC
GAM752  FLJ21080  3'  TGCTTTGTTAGCTGTGTGA   42727     C  AT  A
                              TCAC CA  GC AACAAAGCA
                              |||| ||  || |||||||||
                              AGTG GT  CG TTGTTTCGT
                                T  __  A
GAM752  FLJ22479  3'  CTTTGTTTCTTGGGT       46074       TGC
                              ACCCAA   AAACAAAG
                              ||||||   ||||||||
                              TGGGTT   TTTGTTTC
                                 C__
GAM752  FLJ31153  3'  GCTTTGTTTGGGGT       58127     AATG
                              ACCC    CAAACAAAGC
                              ||||    ||||||||||
                              TGGG    GTTTGTTTCG
                                      ____
GAM752  HNRPAB    3'  TGCTTTGTTTGGATATGG    48375     _  G
                              CCA AT CAAACAAAGCA
                              ||| || ||||||||||
                              GGT TA GTTTGTTTCGT
                                A  G
GAM752  KIAA0042  3'  CTTTGTAACTATGCTTGGGTGA 29611         T   A____
                              TCACCCAA GCA    ACAAAG
                              |||||||| |||    ||||||
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                                AGTGGGTT CGT    TGTTTC
                                    _  ATCAA
GAM752  KIAA0446 5' TGCTTTGTCCCGGCTGGGTG  68882      AT  AA__
                                CACCCA  GC   ACAAAGCA
                                ||||||  ||   ||||||||
                                GTGGGT  CG   TGTTTCGT
                                   __ GCCC
GAM752  KIAA0446 5' GCTCTGCTTGGGTGA     68872       T   AACAA
                                TCACCCAA GCA    AGC
                                |||||||| |||    |||
                                AGTGGGTT CGT    TCG
                                    _  C____
GAM752  KIAA0446 5' TGCTTTGTCCTGTAGG    68883    AA   A_
                                CC  TGCA  ACAAAGCA
                                ||  ||||  ||||||||
                                GG  ATGT  TGTTTCGT
                                 __   CC
GAM752  KIAA0836 3' TGCTTTGTTTGCATACTGG   64565    __
                                CCA  ATGCAAACAAAGCA
                                |||  ||||||||||||||
                                GGT  TACGTTTGTTTCGT
                                  CA
GAM752  KIAA1203 3' CTTTACGTTAACATTGGGT   71638       CA  __
                                ACCCAATG  AAC  AAAG
                                ||||||||  |||  ||||
                                TGGGTTAC  TTG  TTTC
                                    AA   CA
GAM752  KIAA1210 3' TGCTTTCTCCTTGGGTGA    96336       TGCAAAC
                                TCACCCAA     AAAGCA
                                ||||||||     ||||||
                                AGTGGGTT     TTTCGT
                                    CCTC___
GAM752  KIAA1237 3' CTTTAGTAAATTGGGTGG    80468       GCAA  _
                                TCACCCAAT   AC AAAG
                                |||||||||   || ||||
                                GGTGGGTTA   TG TTTC
                                     AA__  A
GAM752  KIAA1391 3' TGCTTTGAGTTTGTAT     67266       __
                                ATGCAAAC  AAAGCA
                                ||||||||  ||||||
                                TATGTTTG  TTTCGT
                                    AG
GAM752  KIAA1944 3' TTGTTTGGTTGGGTGA     75568       G
                                TCACCCAAT CAAACAA
                                ||||||||| |||||||
                                AGTGGGTTG GTTTGTT
                                    _
GAM752  LAT1-3TM 3' TGCTGAGGAGCATTGGGGA  48315    A      AAACAA
                                TC CCCAATGC     AGCA
                                || ||||||||     ||||
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                              AG GGGTTACG     TCGT
                               _      AGGAG_
GAM752  MAPK8IP3 3' TGCCTGTGACACATTGGGT   52996        CAA_  AA
                              ACCCAATG   ACA  GCA
                              ||||||||   |||  |||
                              TGGGTTAC   TGT  CGT
                                  ACAG   C_
GAM752  MGC14839 3' TGCTTTGGGGAATTGGGTGG  54700         GCAAA
                              TCACCCAAT    CAAAGCA
                              |||||||||    |||||||
                              GGTGGGTTA    GTTTCGT
                                   AGGG_
GAM752  MGC16291 3' TGCTTTGTTTTTCGTAAGG   51307    CA   C_
                              CC  ATG  AAACAAAGCA
                              ||  |||  ||||||||||
                              GG  TGC  TTTGTTTCGT
                               AA   TT
GAM752  MGC1842  3' TGCTTTGTCTGCCAGTG     65662    CCAAT   A
                              CAC    GCA ACAAAGCA
                              |||    ||| ||||||||
                              GTG    CGT TGTTTCGT
                                AC___   C
GAM752  OPRL1    3' GCTCTGTTTGGGTGG       6198         TGCAA   A
                              TCACCCAA    ACA AGC
                              ||||||||    ||| |||
                              GGTGGGTT    TGT TCG
                                   _____   C
GAM752  PIP5K2B  3' TGTTCTGCATTGGGGGA     13082    A       _
                              TC CCCAATGCA AACA
                              || |||||||| ||||
                              AG GGGTTACGT TTGT
                               G        C
GAM752  PRO2266  5' TGCCTTGCCCGTATTGGGT   37584         AAA   A
                              ACCCAATGC   CAA GCA
                              |||||||||   ||| |||
                              TGGGTTATG   GTT CGT
                                   CCC   C
GAM752  RBM12    3' TGCTTTGTTTGTCTAATTG   20162     ___
                              CAAT   GCAAACAAAGCA
                              ||||   ||||||||||||
                              GTTA   TGTTTGTTTCGT
                                ATC
GAM752  RBM12    3' TGCTTTGTTATAGGGT      20161     A   CAA
                              ACCC ATG   ACAAAGCA
                              |||| |||   ||||||||
                              TGGG TAT   TGTTTCGT
                                A  ___
GAM752  RGS10    3' TGCTTTGTTATTTGTAAGG   11332    CAA    ___
                              CC   TGCAA   ACAAAGCA
                              ||   |||||   ||||||||
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                                GG  ATGTT  TGTTTCGT
                                 A__    TAT
GAM752  SCYA20   3'  TGCTTTGTTTAAGCATCA   15973   A   __
                                C ATGC  AAACAAAGCA
                                | ||||  ||||||||||
                                A TACG  TTTGTTTCGT
                                 C   AA
GAM752  SDS3     3'  TGATTCATTGGGTGA      69236         C  A
                                TCACCCAATG AA CA
                                |||||||||| || ||
                                AGTGGGTTAC TT GT
                                      _ A
GAM752  SLC17A6  3'  TGCTTTGTGCCTCAAAGTGA  39747     CCAAT_  AA
                                TCAC     GC  ACAAAGCA
                                ||||     ||  ||||||||
                                AGTG     CG  TGTTTCGT
                                  AAACTC  __
GAM752  SSH2     3'  GCTTTGTTTTGTAGG      62209    AA    _
                                CC  TGCAAA CAAAGC
                                ||  |||||| ||||||
                                GG  ATGTTT GTTTCG
                                 __     T
GAM752  STIM2    3'  TGCTTTGTTCTCAGTGA     40481     CCAA  CA
                                TCAC   TG  AACAAAGCA
                                ||||   ||  |||||||||
                                AGTG   AC  TTGTTTCGT
                                  _____ TC
GAM752  T2BP     3'  TGCTTTGTTTTTGTAAGG    69998    CA   C
                                CC  ATG AAACAAAGCA
                                ||  ||| ||||||||||
                                GG  TGT TTTGTTTCGT
                                 AA   T
GAM752  ZMPSTE24  3'  TGCTCCGCTGACATTTGGGTGA 19599        _ _  AACAA
                                TCACCCAA TG CA    AGCA
                                |||||||| || ||    ||||
                                AGTGGGTT AC GT    TCGT
                                     T  A  CGCC_
GAM752  ZNF213   3'  TGCTTTGTTCACCACTGGG   65106     A  CA_
                                CCCA TG   AACAAAGCA
                                |||| ||   |||||||||
                                GGGT AC   TTGTTTCGT
                                  C  CAC
GAM752  ZNF294   3'  TGCTTTGTAAATGTTTGG    70831     T   A__
                                CCAA GCA   ACAAAGCA
                                |||| |||   ||||||||
                                GGTT TGT   TGTTTCGT
                                  _   AAA
GAM752  LOC123624 3'  TGCTTTGTTGTTAAAGGG    75616     AAT_   A
                                CCC    GCAA CAAAGCA
                                |||    |||| |||||||
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                              GGG   TGTT GTTTCGT
                                AAAT   _
GAM752  LOC127703 3'  TGCTTTGTTCTTGGG      74681      TGCA
                              CCCAA   AACAAAGCA
                              |||||   |||||||||
                              GGGTT   TTGTTTCGT
                                C___
GAM752  LOC137991 5'  TGTTGATTGGGTGA       75291        G  A
                              TCACCCAAT CAA CA
                              ||||||||| ||| ||
                              AGTGGGTTA GTT GT
                                   _  _
GAM752  LOC143680 3'  TGCTTTGTACTTGTAT     82990       __
                              ATGCAA  ACAAAGCA
                              ||||||  ||||||||
                              TATGTT  TGTTTCGT
                                 CA
GAM752  LOC145693 5'  TGCCTTGTTTGCTGAGGG   77355    AAT      A
                              CCC   GCAAACAA GCA
                              |||   |||||||| |||
                              GGG   CGTTTGTT CGT
                                AGT      C
GAM752  LOC146108 3'  TGCTTTGTTTTCTGTTG    77671      C_
                              CAATG  AAACAAAGCA
                              |||||  ||||||||||
                              GTTGT  TTTGTTTCGT
                                 CT
GAM752  LOC146856 3'  TTTTGTTTGCATCAAGT    82806    CCA
                              AC   ATGCAAACAAAG
                              ||   ||||||||||||
                              TG   TACGTTTGTTTT
                               AAC
GAM752  LOC148604 3'  TGCTTTGTTAAGTATT     78918      A_
                              AATGC  AACAAAGCA
                              |||||  |||||||||
                              TTATG  TTGTTTCGT
                                 AA
GAM752  LOC150225 3'  TGCTTTGTGGCTGGGTG    85016      AT  AA
                              CACCCA  GC  ACAAAGCA
                              ||||||  ||  ||||||||
                              GTGGGT  CG  TGTTTCGT
                                 __  G_
GAM752  LOC154007 3'  TGTTTGCATTAGTGA      81025     CC
                              TCAC  AATGCAAACA
                              ||||  ||||||||||
                              AGTG  TTACGTTTGT
                                A_
GAM752  LOC154761 3'  TGCTTTGTGATGTGCGTGTGA 81128     CCA    A___
                              TCAC   ATGCA   ACAAAGCA
                              ||||   |||||   ||||||||
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                                AGTG   TGCGT    TGTTTCGT
                                  ___    GTAG
GAM752   LOC154834 3'  TGCTTTGTCCATCTGG      86268     _   CAA
                                CCA ATG   ACAAAGCA
                                ||| |||   ||||||||
                                GGT TAC   TGTTTCGT
                                  C   C__
GAM752   LOC203286 5'  TGCCCTGATGGTTGGGTG    90504        G  AA  AA
                                CACCCAAT CA  CA  GCA
                                |||||||| ||  ||  |||
                                GTGGGTTG GT  GT  CGT
                                     _ A_  CC
GAM752   LOC203429 3'  CTTTGTTTTGCTGTGGGT    89365      AT    _
                                ACCCA  GCAAA CAAAG
                                |||||  ||||| |||||
                                TGGGT  CGTTT GTTTC
                                   GT    T
GAM752   LOC220565 5'  TGCTGAGGAGCATTGGGGA   90757    A      AAACAA
                                TC CCCAATGC     AGCA
                                || ||||||||     ||||
                                AG GGGTTACG     TCGT
                                 _      AGGAG_
GAM752   LOC220739 5'  TGCTTTGTCCACAGGTG     92939     CAA  CAA
                                CACC   TG   ACAAAGCA
                                ||||   ||   ||||||||
                                GTGG   AC   TGTTTCGT
                                  ___  ACC
GAM752   LOC253221 3'  TGCTTTGTTAAGTATT      96824      A_
                                AATGC  AACAAAGCA
                                |||||  |||||||||
                                TTATG  TTGTTTCGT
                                   AA
GAM752   LOC253443 3'  TGCTTTGTGTTGGTGTG     95871     _    GCAA
                                CAC CCAAT    ACAAAGCA
                                ||| |||||    ||||||||
                                GTG GGTTG    TGTTTCGT
                                  T    _____
GAM752   LOC253613 3'  TGCCTTGAAGTATTGGG     96194        AAA   A
                                CCCAATGC   CAA GCA
                                ||||||||   ||| |||
                                GGGTTATG   GTT CGT
                                     AA_   C
GAM752   LOC255040 3'  TGCTTTGTTTATTTGGTGA   96385      C    CA
                                TCACC AATG  AACAAAGCA
                                ||||| ||||  |||||||||
                                AGTGG TTAT  TTGTTTCGT
                                   T    __
GAM752   LOC255041 3'  TGCTTTGTTTATTTGGTGA   96390      C    CA
                                TCACC AATG  AACAAAGCA
                                ||||| ||||  |||||||||
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                                AGTGG TTAT  TTGTTTCGT
                                  T   __
GAM752  LOC257336 3'  GCTTTGAAGAGGCATTGGG   96180        AAA__
                                CCCAATGC    CAAAGC
                                ||||||||    ||||||
                                GGGTTACG    GTTTCG
                                    GAGAA
GAM752  LOC257486 3'  TGCTTTCTCCTTGGGTGA    69251        TGCAAAC
                                TCACCCAA     AAAGCA
                                ||||||||     ||||||
                                AGTGGGTT     TTTCGT
                                    CCTC___
GAM752  LOC51030  3'  TGCTTTGTTACATTGGGGA   32186    A      CA
                                TC CCCAATG  AACAAAGCA
                                || |||||||  |||||||||
                                AG GGGTTAC  TTGTTTCGT
                                 _      A_
GAM752  LOC90719  3'  TGCTTTGTGGGTGGGTG     63890       ATGCAA
                                CACCCA     ACAAAGCA
                                ||||||     ||||||||
                                GTGGGT     TGTTTCGT
                                   GGG___
GAM752  LOC92270  5'  TGCTCTCCAGCTTGGGTGA   68636        T  AAACAA
                                TCACCCAA GC     AGCA
                                |||||||| ||     ||||
                                AGTGGGTT CG     TCGT
                                    _  ACCTC_
GAM752  LOC92973  3'  TGCTTTGTAAGGTGGGAGA   71040    A   ATGCAA
                                TC CCCA     ACAAAGCA
                                || ||||     ||||||||
                                AG GGGT     TGTTTCGT
                                 A   GGAA__
GAM753  ADH1B     3'  CTTAGACATAAAGTAAAAT   72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM753  AHR       3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM753  FDFT1     3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM753  JTB       3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
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                                GTAAAGTGAAAGTGACAGACTCTA

GAM753  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM753  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM753  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM753  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM753  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_   CG_
GAM753  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM753  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM753  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||         |||||||||
                                GTAAAG         CAGACTCTA
                                   AAACATTT_
GAM753  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM753  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
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                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM753  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM753  NIR3     3'  GCAGTGAAAGTGCAAT      66242      T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM753  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM753  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM753  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__   TT
GAM753  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM753  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM753  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM753  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM753  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
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                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM753  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM754  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM754  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM754  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM754  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
           TG                     CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM754  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM754  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM754  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM754  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM754  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
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                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM754  CG012    5' CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                     CT  __
GAM754  EIF2C2   3' ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM754  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC       GTCTGAGAT
                                ||||||       |||||||||
                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM754  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM754  KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM754  KLHL6    3' ATCTCAGAGCAGGAAA      55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM754  NIR3     3' GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM754  PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM754  PP35     3' ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM754  PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148         TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
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                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM754  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM754  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941        CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM754  LOC149703 3' ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM754  LOC154007 3' ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM754  LOC155004 3' TCATTTAAGTGAAAGGAAA    81226     A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM754  LOC222134 5' ACAGTGAAGTGAAATG       94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM755  ASPH     3'  CATCATTTTGAAAGG       50616     TA
                                CCTT  TCAGGATGATG
                                ||||  ||||||||||
                                GGAA  AGTTTTACTAC
                                    __
GAM755  ASPH     3'  CATCATTTTGAAAGG       50629     TA
                                CCTT  TCAGGATGATG
                                ||||  ||||||||||
                                GGAA  AGTTTTACTAC
                                    __
GAM755  DDX6     5'  CTGCATTGCAATAAAGG     15287       CAGGAT
                                CCTTTAT     GATGCAG
                                |||||||     |||||||
                                GGAAATA     TTACGTC
                                    ACG___
GAM755  TRIP15   3'  CTGCAGTGTAGTAAAGGTTT  14893         CAGGATGA
                                AAACCTTTAT       TGCAG
                                ||||||||||       |||||
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                                TTTGGAAATG       ACGTC
                                      ATGTG___
GAM755  FLJ13593  3'  CAGACCTGGCAAAGGTTT    45503        AT    A_
                                AAACCTTT  CAGG  TG
                                ||||||||  ||||  ||
                                TTTGGAAA  GTCC  AC
                                    CG    AG
GAM755  FLJ21988  3'  CTGCATCATCCCCCAGCCAGGT 42554    A    TTATCA_
          CC                      A ACCT      GGATGATGCAG
                                | ||||      ||||||||||
                                C TGGA      CCTACTACGTC
                                 C    CCGACCC
GAM755  HIRIP5    5'  CTGCATCAGTTTGTACAAAG   31653     AT_    A
                                CTTT   CAGG TGATGCAG
                                ||||   |||| ||||||||
                                GAAA   GTTT ACTACGTC
                                  CAT    G
GAM755  KIAA0547  3'  TGCATCATCCCAGGTTT     28917       TTATCA
                                AAACCT     GGATGATGCA
                                ||||||     ||||||||||
                                TTTGGA     CCTACTACGT
                                   C_____
GAM755  KIAA1223  3'  CTGCAGTTCCCTGATAAA    71145         ATGA
                                TTTATCAGG    TGCAG
                                |||||||||    |||||
                                AAATAGTCC    ACGTC
                                     CTTG
GAM755  KIAA1951  3'  CTGCATCACCCTGGTG      73759        A
                                TATCAGG TGATGCAG
                                ||||||| ||||||||
                                GTGGTCC ACTACGTC
                                    C
GAM755  PFDN1     3'  CTGCATCACCCTGAGCCCCATT 10511      CCTTTA    A
          TG                      CAAA     TCAGG TGATGCAG
                                ||||     ||||| ||||||||
                                GTTT     AGTCC ACTACGTC
                                  ACCCCG    C
GAM755  SLC22A6   3'  CATCATTAAAAGGTTTG     16570         ATCAG
                                CAAACCTTT    GATGATG
                                |||||||||    |||||||
                                GTTTGGAAA    TTACTAC
                                     A____
GAM755  LOC90835  3'  CATTTTCCCCAATAAAGGTCTG 64127    A      CA_   T
                                CA ACCTTTAT   GGA GATG
                                || ||||||||   ||| ||||
                                GT TGGAAATA   CCT TTAC
                                 C       ACC   T
GAM755  LOC92218  3'  CTGCACTTTCTTGATAAATATT 68505     CC        TGA
          TG                      CAAA  TTTATCAGGA   TGCAG
                                ||||  ||||||||||   |||||
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                                GTTT  AAATAGTTCT   ACGTC
                                  AT         TTC
GAM756  DNAJC8   3'  GTACCATGTCCTAGCC     26560     G   ATGCT    A
                                GGC TAG     GGCAT GTAC
                                ||| |||     ||||| ||||
                                CCG ATC     CTGTA CATG
                                  _  _____     C
GAM756  FLJ10933  3'  GCAGACAGCATCTACTCC     36901     C        ___
                                GG GTAGATGCTG   GC
                                || ||||||||||   ||
                                CC CATCTACGAC   CG
                                 T         AGA
GAM756  KIAA0211  5'  CAGCCCTTGCCAGCATCCAGCC 27547     GTA        T  TA
                                GGC   GATGCTGGCA AG  CTG
                                |||   |||||||||| ||  |||
                                CCG   CTACGACCGT TC  GAC
                                  AC_         _  CC
GAM756  LOC146540 5'  CAGGAAAGCGCCAGCATCTCC  77972    CGT        ATAGTA
                                GG   AGATGCTGGC     CTG
                                ||   ||||||||||      |||
                                CC   TCTACGACCG     GAC
                                 ___         CGAAAG
GAM756  LOC170409 3'  CAGTACTACGCTCAGC      82858      _  A
                                GCTG GC TAGTACTG
                                |||| || ||||||||
                                CGAC CG ATCATGAC
                                  T  C
GAM756  LOC51720  3'  CAGCACCACCAGCACCTACCC  32820    C    A     CATA  A
                                GG GTAG TGCTGG    GT CTG
                                || |||| ||||||    || |||
                                CC CATC ACGACC    CA GAC
                                 _    C      AC__  C
GAM756  LOC90190  3'  AGCACCTCGGCATCCACCC    61772    C  A      CATA  A
                                GG GT GATGCTGG    GT CT
                                || || ||||||||    || ||
                                CC CA CTACGGCT    CA GA
                                 _  C       C___  C
GAM757  PRO2900   3'  TGTGCGCATCTCAATCA     37808         CC
                                TGATTGAG  GCGCACG
                                ||||||||  |||||||
                                ACTAACTC  CGCGTGT
                                     TA
GAM758  FOXM1    3'  AGTATCTGATTCCTCTGCTGT  41703     C   TT   A
                                GCA CAG  GAA TCAGATACT
                                ||| |||  ||| |||||||||
                                TGT GTC  CTT AGTCTATGA
                                  C   TC  _
GAM758  LAMP2    3'  CTATTCCAACTGGGC       25711     A      A   C
                                GC CCAGTTG AAT AG
                                || ||||||| ||| ||
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                                CG GGTCAAC TTA TC
                                 _      C   _
GAM758  LHX4     3'  TTTGCTCCAACTGGTGTGT   52909           AAAT
                                ACGCACCAGTTG    CAGA
                                ||||||||||||    ||||
                                TGTGTGGTCAAC    GTTT
                                       CTC_
GAM758  MAPK4    3'  GACCTCAATGGTGCGT      10829         G    AA
                                ACGCACCA TTGA  TC
                                |||||||| ||||  ||
                                TGCGTGGT AACT  AG
                                     _   CC
GAM758  NAB1     3'  ATCTGGTTATCAATGC      19907     CCAG   _
                                GCA    TTGA AATCAGAT
                                |||    |||| ||||||||
                                CGT    AACT TTGGTCTA
                                 _____   A
GAM758  OPHN1    3'  AGCATCTAATTTCAATTATAGT 10352      ACC        C    A
           GT                     ACGC   AGTTGAAAT AGAT CT
                                ||||   ||||||||| |||| ||
                                TGTG   TTAACTTTA TCTA GA
                                  ATA        A    C
GAM758  ORC1L    3'  AGCATCTGATTTTGGAAGT    14735     CAG TG        A
                                AC   T  AAATCAGAT CT
                                ||   |  ||||||||| ||
                                TG   G  TTTAGTCTA GA
                                 AA_ GT        C
GAM758  RAB7L1   3'  ATCTGATTCTGGAATGC     14104     __    TTGA
                                GCA  CCAG    AATCAGAT
                                |||  ||||    ||||||||
                                CGT  GGTC    TTAGTCTA
                                  AA   _____
GAM758  ZNF137   3'  AGCATCTGATTTCAAACTCTTA 12858     ACC_   _        A
           GC                     GC    AGTT GAAATCAGAT CT
                                ||    |||| |||||||||| ||
                                CG    TCAA CTTTAGTCTA GA
                                 ATTC    A         C
GAM758  ABCA8    3'  AGTATCTGATATCAAT      23149       A
                                GTTGA ATCAGATACT
                                ||||| ||||||||||
                                TAACT TAGTCTATGA
                                  A
GAM758  DKFZP434L187 5'  AGTATCTGATAAAGTGG     68801     G  GAA
                                CCA TT   ATCAGATACT
                                ||| ||   ||||||||||
                                GGT AA   TAGTCTATGA
                                  G  A__
GAM758  FLJ12568 3'  AGTATCTGATTTTAGATG    46498    G
                                CA TTGAAATCAGATACT
                                || ||||||||||||||
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                                GT GATTTTAGTCTATGA
                                 A
GAM758  FLJ31153  3'  TATCTGATTACATTGATG    58129    C    T A
                                CA CAGT G AATCAGATA
                                || |||| | |||||||||
                                GT GTTA C TTAGTCTAT
                                 A   _ A
GAM758  GREAT     3'  ATCTGATTCCAGTGTG      55480      CAGT  A
                                CGCAC   TG AATCAGAT
                                ||||||   || ||||||||
                                GTGTG   AC TTAGTCTA
                                   _____ C
GAM758  KIAA1323  3'  GTATCTATTAACTGG       63044        AATC
                                CCAGTTGA   AGATAC
                                ||||||||   ||||||
                                GGTCAATT   TCTATG
                                     A___
GAM758  SLC19A3   3'  CTGATTTTTAAATGGTAGC   47487   _   GTT_
                                GC ACCA   GAAATCAG
                                || ||||   ||||||||
                                CG TGGT   TTTTAGTC
                                 A   AAAT
GAM758  VEST1     5'  TATCTGATTTTTTGAGC     53688    AC   TT
                                GC  CAG  GAAATCAGATA
                                ||  |||  ||||||||||
                                CG  GTT  TTTTAGTCTAT
                                 A_  __
GAM758  LOC221935 3'  GTATCTGACCAGTGC       92626     CAGT  AAA
                                GCAC   TG   TCAGATAC
                                ||||   ||   ||||||||
                                CGTG   AC   AGTCTATG
                                  _____ C__
GAM758  LOC256515 5'  TACCTGATTGGTCCGT      96465    C   GTTGAA    A
                                ACG ACCA     ATCAG TA
                                ||| ||||     ||||| ||
                                TGC TGGT     TAGTC AT
                                  C   _______    C
GAM759  ARHGEF6   3'  CAAACTTGAAGCCAGGC     68197       ACCA
                                GCCTGG   CAAGTTTG
                                ||||||   ||||||||
                                CGGACC   GTTCAAAC
                                   GAA_
GAM759  CNTN2     3'  GTCACAACCCAGGTGA      17411        ACCACAA  _
                                TCGCCTGG      GTT TGAC
                                ||||||||      ||| ||||
                                AGTGGACC      CAA ACTG
                                    ________  C
GAM759  CORO2A    3'  AAACTGTGGTCCAGAGA     53398    GC        A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
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                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM759  CORO2A   3'  AAACTGTGGTCCAGAGA     12642    GC        A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM759  GRLF1    3'  AGGTCAGAAAGTGGCCCAGG   78551      A    AAG
                                CCTGG CCAC   TTTGACCT
                                ||||| ||||   ||||||||
                                GGACC GGTG   AGACTGGA
                                   C    AA_
GAM759  LAPTM5   3'  AGGCTTGTGGTCAAGC      22199    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCGGA
                                 AA_
GAM759  POU2AF1  3'  AGATTTACAGTCCAGGC     20647        CAC
                                GCCTGGAC   AAGTTT
                                ||||||||   ||||||
                                CGGACCTG   TTTAGA
                                     ACA
GAM759  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  54574        C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM759  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  6355         C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM759  TRIM34   5'  AGGTCAAGTTGAGCCCAG    55224      ACCA   G
                                CTGG    CAA TTTGACCT
                                ||||    ||| ||||||||
                                GACC    GTT GAACTGGA
                                  CGA_   _
GAM759  TRIM9    5'  AGGCCAGGCAAGTCCAGGC   30749        CACAA    A
                                GCCTGGAC    GTTTG CCT
                                ||||||||    ||||| |||
                                CGGACCTG    CGGAC GGA
                                     AA___    C
GAM759  ABLIM    5'  GATATGTAACCCAGGCGG    22030        ACC   A
                                TCGCCTGG   ACA GTT
                                ||||||||   ||| |||
                                GGCGGACC   TGT TAG
                                     CAA   A
GAM759  AMOT     3'  AGGCATCTTCATGGTCCAGGGA 55716    G       C_   TT  A
                                TC CCTGGACCA  AAG  TG CCT
                                || |||||||||  |||  || |||
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                                AG GGACCTGGT  TTC  AC GGA
                                 _       AC   T_ _
GAM759  DKFZp434D177 5'  TTAGACCCAGGCGA       79443        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                          _______
GAM759  DKFZp434D177 5'  TTAGACCCAGGCGA       50056        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                          _______
GAM759  FLJ23420  3'  CAAGTGGGTCCAGGC       46845         A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                          _ __
GAM759  HSA249128 5'  GGCGCGGTCCAGGCGG      34152          ACAA
                                TCGCCTGGACC    GTT
                                ||||||||||    |||
                                GGCGGACCTGG    CGG
                                       CG__
GAM759  MGC15668  5'  AGACCCGGTGGTCCAGACG    51277    C       AA_
                                CG CTGGACCAC   GTTT
                                || |||||||||   ||||
                                GC GACCTGGTG   CAGA
                                 A        GCC
GAM759  MGC22014  3'  AGGTCCCGAGTGTAACCCAGGT 64486        ACC   AGTTT
           GA                     TCGCCTGG   ACA    GACCT
                                ||||||||   |||    |||||
                                AGTGGACC   TGT    CTGGA
                                     CAA   GAGCC
GAM759  SDCCAG10  5'  AGAGTTGTGGTCCAAAGA    19641    GCC        G
                                TC   TGGACCACAA TTT
                                ||   |||||||||| |||
                                AG   ACCTGGTGTT AGA
                                 AA_         G
GAM759  LOC115442 3'  AGGTCAGGGATGGTCCAG    72676        CAAG
                                CTGGACCA    TTTGACCT
                                ||||||||    ||||||||
                                GACCTGGT    GGACTGGA
                                     AG__
GAM759  LOC129011 5'  AGACCTGCGGTCCAGGC     74862         A  A
                                GCCTGGACC CA GTTT
                                ||||||||| || ||||
                                CGGACCTGG GT CAGA
                                      C  C
GAM759  LOC130536 5'  GCAAAGTCCAGGCG        75746         CACAAG    A
                                CGCCTGGAC     TTTG C
                                |||||||||     |||| |
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                                GCGGACCTG     AAAC G
                                      _____   C
GAM759  LOC149108 3'  AGACTTCACTGTGGTCCA    84357        ____
                                TGGACCACA   AGTTT
                                |||||||||   |||||
                                ACCTGGTGT   TCAGA
                                     CACT
GAM759  LOC221688 5'  AGACTCGGGCCCAGACGA    93674    C   A  ACA
                                TCG CTGG CC   AGTTT
                                ||| |||| ||   |||||
                                AGC GACC GG   TCAGA
                                  A   C  GC_
GAM759  LOC256228 5'  AGACTTGTGGTCAAAGC     96233    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCAGA
                                 AAA
GAM759  LOC257441 5'  TTAGACCCAGGCGA        95566        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                      _______
GAM759  LOC91960  3'  AGGTGCCTCTCGTGGTCCAAGC 67657    C       A  TTTG
                                GC TGGACCAC AG    ACCT
                                || |||||||| ||    ||||
                                CG ACCTGGTG TC    TGGA
                                 A       C  TCCG
GAM759  LOC92840  3'  GTCCCTCGGGTCCAGGC     56435        ACA  TTT
                                GCCTGGACC   AG   GAC
                                |||||||||   ||   |||
                                CGGACCTGG   TC   CTG
                                     GC_  C__
GAM760  C18orf2   3'  TCTGACATTCAACTAGATGTGG 48632          ACACAAG_
          AA                    TTCCACATCTAG       CAGA
                                ||||||||||||       ||||
                                AAGGTGTAGATC       GTCT
                                      AACTTACA
GAM760  CCNT2     3'  CTTGGTAATTTAGATGTG    54265         CA__
                                CACATCTAGA    CAAG
                                ||||||||||    ||||
                                GTGTAGATTT    GTTC
                                     AATG
GAM760  CPB2      3'  TCTGCTTGTGCCTTTAGA    33103       __
                                TCTAGA  CACAAGCAGA
                                ||||||  ||||||||||
                                AGATTT  GTGTTCGTCT
                                   CC
GAM760  CPB2      3'  TCTGCTTGTGCCTTTAGA    8524        __
                                TCTAGA  CACAAGCAGA
                                ||||||  ||||||||||
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                                AGATTT  GTGTTCGTCT
                                   CC
GAM760  CSRP1    3'  CTGCTTGATCCTCAGATGTGGA 14531          _ ACA
           G                    TTCCACATCT AG   CAAGCAG
                                |||||||||| ||   |||||||
                                GAGGTGTAGA TC   GTTCGTC
                                     C  CTA
GAM760  ENO2     3'  TCTGCTTGCCTGGAGACGTGGA 8780        A__    ACA
           A                    TTCCAC   TCTAG   CAAGCAGA
                                ||||||   |||||   ||||||||
                                AAGGTG   AGGTC   GTTCGTCT
                                   CAG    C__
GAM760  FLOT2    3'  CTGCTTGTGCTCAGGGAA    15575     ACATCT  A
                                TTCC     AG CACAAGCAG
                                ||||     || |||||||||
                                AAGG     TC GTGTTCGTC
                                  GAC___  _
GAM760  FZD4     3'  TGTGTCTAGATACTGAA     24157     CAC
                                TTC   ATCTAGACACA
                                |||   ||||||||||
                                AAG   TAGATCTGTGT
                                  TCA
GAM760  GPR34    3'  CTGCTTGTATTTGTGAT     17961     _   C
                                ATC TAGA ACAAGCAG
                                ||| |||| ||||||||
                                TAG GTTT TGTTCGTC
                                  T   A
GAM760  ITGAL    3'  TGATCTAAATGTGGAG      9396         C   _
                                TTCCACAT TAGA CA
                                |||||||| |||| ||
                                GAGGTGTA ATCT GT
                                     A   A
GAM760  LTB4R    5'  TGTGTCTAAAGTGGAA      5655         ATC
                                TTCCAC   TAGACACA
                                ||||||   ||||||||
                                AAGGTG   ATCTGTGT
                                   AA_
GAM760  MYL1     3'  TCTGCTGCTCTAGATGAGAA   54378     CA       CACA
                                TTC  CATCTAGA    AGCAGA
                                |||  ||||||||    ||||||
                                AAG  GTAGATCT    TCGTCT
                                  A_       CG__
GAM760  PLCB2    5'  CTGCCTGTGTCTGCTG      15892    TC       A
                                CA  TAGACACA GCAG
                                ||  |||||||| ||||
                                GT  GTCTGTGT CGTC
                                 C_       C
GAM760  PSAP     3'  TCTACTTGTGTGTCTGGGGGAA 69358      ACA         __  C
                                TTCC   TCTAGACACA  AG AGA
                                ||||   ||||||||||  || |||
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                                AAGG  GGGTCTGTGT  TC TCT
                                  ___       GT  A
GAM760  SLC29A1  3'  CTGCTTGTGCAGGCCAGTGGAG 17075      ATCTAGA
                                TTCCAC     CACAAGCAG
                                ||||||     |||||||||
                                GAGGTG     GTGTTCGTC
                                   ACCGGAC
GAM760  SLC7A7   3'  TCTGGAATCCTGATGTGGAA  14294       TA  CACAAG
                                TTCCACATC  GA    CAGA
                                |||||||||  ||    ||||
                                AAGGTGTAG  CT    GTCT
                                     TC  AAG___
GAM760  TMEM1    3'  CTGATTCTAATGTGGAA    12335       C   CACAAG
                                TTCCACAT TAGA    CAG
                                |||||||| ||||    |||
                                AAGGTGTA ATCT    GTC
                                   _   TA____
GAM760  XKRY     3'  CTGCTTGTCAGCAGTG     60018    AT  A   CA
                                CAC  CT GACA  AGCAG
                                |||  || ||||  |||||
                                GTG  GA CTGT  TCGTC
                                  AC  _   __
GAM760  YES1     3'  GTGTCTTAATGTGGAA     18356       CT
                                TTCCACAT  AGACAC
                                ||||||||  ||||||
                                AAGGTGTA  TCTGTG
                                     AT
GAM760  AKAP11   3'  CTGCTCTGAAGATGTGGA   32707       AGA  CA
                                TCCACATCT   CA  AGCAG
                                |||||||||   ||  |||||
                                AGGTGTAGA   GT  TCGTC
                                     A__  C_
GAM760  DDM36    3'  GCCCAGTGCGGGTGTGGAG   40573       AGA  AA_
                                TTCCACATCT   CAC   GC
                                ||||||||||   |||   ||
                                GAGGTGTGGG   GTG   CG
                                     C__   ACC
GAM760  DKFZP434L1123 3'  CTGCTTGCATTTATGGA    49583     CATC   CA
                                TCCA   TAGA  CAAGCAG
                                ||||   ||||  |||||||
                                AGGT   ATTT  GTTCGTC
                                  _____   AC
GAM760  DKFZP564B167 3'  CTGAACAATCTAGATGTGGA  31214         CACAAG
                                TCCACATCTAGA     CAG
                                ||||||||||||     |||
                                AGGTGTAGATCT     GTC
                                      AACAA_
GAM760  EAT2     3'  CTGCTTGTGTCAGGTG     79276      A
                                CATCT GACACAAGCAG
                                ||||| ||||||||||
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                                GTGGA CTGTGTTCGTC
                                    _
GAM760  FLJ12687  3' CTGCTTATGGTGTGGA     46192       TAGACAC
                                TCCACATC     AAGCAG
                                ||||||||     ||||||
                                AGGTGTGG     TTCGTC
                                   TA_____
GAM760  FLJ20195  5' TGTTCTAGATGTGGAG     34719          C
                                TTCCACATCTAGA ACA
                                |||||||||||| |||
                                GAGGTGTAGATCT TGT
                                      _
GAM760  FLJ21324  3' CTGCTTGTGCCATGTGGA    91202       CTAGA
                                TCCACAT    CACAAGCAG
                                |||||||    |||||||||
                                AGGTGTA    GTGTTCGTC
                                   CC___
GAM760  FLJ22055  3' CTGCTTGTAGTATTAGA     45495      _ _
                                TCTAG AC ACAAGCAG
                                ||||| || ||||||||
                                AGATT TG TGTTCGTC
                                  A  A
GAM760  GTF2H3    3' CTTGGCCTCCTAAAGTGTGGAA 7704        C_  ACA__
                                TTCCACAT  TAG    CAAG
                                ||||||||  |||    ||||
                                AAGGTGTG  ATC    GTTC
                                   AA   CTCCG
GAM760  IMPACT    3' CTACTTTTTAGATGGGAA    37388     A      CAC   C
                                TTCC CATCTAGA   AAG AG
                                |||| ||||||||   ||| ||
                                AAGG GTAGATTT   TTC TC
                                  _      ___   A
GAM760  KIAA0172  3' TGTACTAAATGTGGAA      64971       C  _
                                TTCCACAT TAG ACA
                                |||||||| ||| |||
                                AAGGTGTA ATC TGT
                                   A   A
GAM760  KIAA0256  3' CTTTTGACTAAATGTGGAA   64420       C  A  C
                                TTCCACAT TAG CA AAG
                                |||||||| ||| || |||
                                AAGGTGTA ATC GT TTC
                                   A   A  T
GAM760  KIAA0478  3' TCTGCTTGTATCCCAGTG    29560    ATCTA  C
                                CAC    GA ACAAGCAGA
                                |||    || |||||||||
                                GTG    CT TGTTCGTCT
                                  ACC__  A
GAM760  KIAA0515  3' TGTGTCTAGTGTAGAA      63817    C   T
                                TTC ACA CTAGACACA
                                ||| ||| |||||||||
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                                AAG TGT GATCTGTGT
                                  A  _
GAM760  KIAA0527  3'  CTGTTCTCTAGTGTGGAA    95799       T    CACA
                                TTCCACA CTAGA   AGCAG
                                ||||||| |||||   |||||
                                AAGGTGT GATCT   TTGTC
                                   _    C___
GAM760  KIAA1678  3'  TCTGCTTGTGTCTTGA     72308    T
                                TC AGACACAAGCAGA
                                || ||||||||||||
                                AG TCTGTGTTCGTCT
                                 T
GAM760  MGC2734   3'  ATCTGCCTGTGTACTTTGTAGA 52414     ____ _    A    III
           TGTG                   CATCT   AG ACACA GCAGA   T
                                |||||   || ||||| |||||  |
                                GTAGA   TC TGTGT CGTCT   A
                                   TGTT  A    C    III
GAM760  PP3111    3'  CTGCTACTTAATGTGGAA    42203       CT  ACACA
                                TTCCACAT  AG    AGCAG
                                ||||||||  ||    |||||
                                AAGGTGTA  TC    TCGTC
                                    AT  A____
GAM760  PSMF1     3'  CTGCTCATGTGTGTGGAG    22353       CTAG   CA
                                TTCCACAT   ACA  AGCAG
                                ||||||||   |||  |||||
                                GAGGTGTG   TGT  TCGTC
                                    ____  AC
GAM760  SHARP     3'  CTGCTCCCGCGATGTGGAA   30397       TAGACACA
                                TTCCACATC      AGCAG
                                |||||||||      |||||
                                AAGGTGTAG      TCGTC
                                    CGCCC___
GAM760  SLC26A9   3'  CTGCATGCAGATGTGGAA    53621        AGACA  A
                                TTCCACATCT    CA GCAG
                                ||||||||||    || ||||
                                AAGGTGTAGA    GT CGTC
                                    C____  A
GAM760  SLC26A9   3'  CTGCATGCAGATGTGGAA    56182        AGACA  A
                                TTCCACATCT    CA GCAG
                                ||||||||||    || ||||
                                AAGGTGTAGA    GT CGTC
                                    C____  A
GAM760  TOLLIP    3'  GCCTGTGTCAGGTGTGGA    38684        A     A
                                TCCACATCT GACACA GC
                                ||||||||| |||||| ||
                                AGGTGTGGA CTGTGT CG
                                   _     C
GAM760  TU12B1-TY 3'  CTTTGTCTAGATGGAA     33381       CA       C
                                TTCCA  TCTAGACA AAG
                                |||||  |||||||| |||
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                                AAGGT  AGATCTGT TTC
                                  __     _
GAM760  WBSCR17   3'  CTGCCTGTGTCTAGAGGAA   81300     ACA       A
                                TTCC   TCTAGACACA GCAG
                                ||||   |||||||||| ||||
                                AAGG   AGATCTGTGT CGTC
                                  ___        C
GAM760  LOC145955 3'  CGCTTTTAAATGTGGAG     83590       C   CACA   A
                                TTCCACAT TAGA    AGC G
                                |||||||| ||||    ||| |
                                GAGGTGTA ATTT    TCG C
                                    A   _____  C
GAM760  LOC145990 3'  TCTGCTTGTATGGCAATGTGGA 77604        CTAGAC
          G                      TTCCACAT     ACAAGCAGA
                                |||||||||     |||||||||
                                GAGGTGTA     TGTTCGTCT
                                    ACGGTA
GAM760  LOC147975 3'  CTGCTTATTCATGTGGAG    84084       CTA  CAC
                                TTCCACAT   GA   AAGCAG
                                ||||||||   ||   ||||||
                                GAGGTGTA   CT   TTCGTC
                                    ____ TA_
GAM760  LOC149995 5'  TCTGCTTGTGTTGGAGTG    84849     A    A
                                CAC TCTAG CACAAGCAGA
                                ||| ||||| ||||||||||
                                GTG AGGTT GTGTTCGTCT
                                  _    _
GAM760  LOC152286 3'  CTGCTGTGCACTAGATGT    85629       A_   A
                                ACATCTAG  CACA GCAG
                                ||||||||  |||| ||||
                                TGTAGATC  GTGT CGTC
                                    AC   _
GAM760  LOC153196 5'  TCTGCTTGTGTGCTCATG    85980     CT  _
                                CAT  AG ACACAAGCAGA
                                |||  || ||||||||||
                                GTA  TC TGTGTTCGTCT
                                  C_  G
GAM760  LOC153711 3'  TGGCTCCAGAGTGTGGAA    86139       _  A  CA
                                TTCCACA TCT GA  CA
                                ||||||| ||| ||  ||
                                AAGGTGT AGA CT  GT
                                    G   C  CG
GAM760  LOC155066 3'  TCTGACACGTCTAGATGTG   81285         ACAAG
                                CACATCTAGAC     CAGA
                                ||||||||||     ||||
                                GTGTAGATCTG     GTCT
                                      CACA_
GAM760  LOC158125 5'  TCCGCCTGTGGGATGTGG    81718       AGA   A  A
                                CCACATCT   CACA GC GA
                                ||||||||   |||| || ||
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                                GGTGTAGG  GTGT CG CT
                                   ___    C  C
GAM760  LOC160897 3'  TCTGCTTGCATTTATGA     82248    _    CA
                                TC TAGA  CAAGCAGA
                                || ||||  ||||||||
                                AG ATTT  GTTCGTCT
                                 T    AC
GAM760  LOC200933 3'  GCATGCAGATGTGGAA      90199          AGACA  A
                                TTCCACATCT     CA GC
                                ||||||||||     || ||
                                AAGGTGTAGA     GT CG
                                      C____  A
GAM760  LOC205251 5'  TCTGCTTGTGTCTCGGGTGGAA 90674       A  T
                                TTCCAC TC AGACACAAGCAGA
                                |||||| || ||||||||||||
                                AAGGTG GG TCTGTGTTCGTCT
                                   _  C
GAM760  LOC220692 5'  TCTGCTTGTACATTGGG     91221       AC_
                                TCTAG   ACAAGCAGA
                                |||||   |||||||||
                                GGGTT   TGTTCGTCT
                                  ACA
GAM760  LOC221975 3'  TCTGCTTGTTAAAATGGAA    92609      CATCTAGAC
                                TTCCA        ACAAGCAGA
                                |||||        |||||||||
                                AAGGT        TGTTCGTCT
                                  AAAAT____
GAM760  LOC253933 3'  CTGCTTCAAGGATGTGGAA    96040          AGACAC
                                TTCCACATCT     AAGCAG
                                ||||||||||     ||||||
                                AAGGTGTAGG     TTCGTC
                                      AAC___
GAM760  LOC254661 5'  TCTGCTTGTGTCTCAGGAA    96047      ACATCT
                                TTCC     AGACACAAGCAGA
                                ||||     ||||||||||||
                                AAGG     TCTGTGTTCGTCT
                                  AC____
GAM760  LOC255105 3'  CTGCTTCAAGGATGTGGAA    96066          AGACAC
                                TTCCACATCT     AAGCAG
                                ||||||||||     ||||||
                                AAGGTGTAGG     TTCGTC
                                      AAC___
GAM760  LOC255925 3'  CTGCTTCAAGGATGTGGAA    96479          AGACAC
                                TTCCACATCT     AAGCAG
                                ||||||||||     ||||||
                                AAGGTGTAGG     TTCGTC
                                      AAC___
GAM760  LOC256222 3'  CTGAAATTTCTAAATGTGGAA  97222          C    CACAAG
                                TTCCACAT TAGA     CAG
                                |||||||| ||||     |||
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                                AAGGTGTA ATCT     GTC
                                    A    TTAAA_
GAM760  LOC257355 3'  CTGCCTGTGTCTGCTGCTGAG  94407     CA  TC       A
                                TTC  CA  TAGACACA GCAG
                                ||| ||  |||||||| ||||
                                GAG  GT  GTCTGTGT CGTC
                                  TC  C_       C
GAM760  LOC51172  3'  CTGCCTGTGTCTGCTGCCGAG  63349     CA  TC       A
                                TTC  CA  TAGACACA GCAG
                                ||| ||  |||||||| ||||
                                GAG  GT  GTCTGTGT CGTC
                                  CC  C_       C
GAM760  LOC51275  5'  CTGAAGGATTAGATGTGGAA   33291           ACACAAG
                                TTCCACATCTAG      CAG
                                ||||||||||||      |||
                                AAGGTGTAGATT      GTC
                                      AGGAA__
GAM760  LOC51336  5'  TGTGTCTAAATGTGGAA     33584         C
                                TTCCACAT TAGACACA
                                |||||||| ||||||||
                                AAGGTGTA ATCTGTGT
                                    A
GAM760  LOC93349  3'  TCTGCTTGTGTCTAGATGGGGA 56469      A
          A                      TTCC CATCTAGACACAAGCAGA
                                |||| ||||||||||||||||||
                                AAGG GTAGATCTGTGTTCGTCT
                                  G
GAM761  BACE      3'  CAACAGCTTCTTGCT       57285           G
                                GGCAAGAAGCTG TTG
                                |||||||||||| |||
                                TCGTTCTTCGAC AAC
                                      _
GAM761  BACE      3'  CAACAGCTTCTTGCT       23975           G
                                GGCAAGAAGCTG TTG
                                |||||||||||| |||
                                TCGTTCTTCGAC AAC
                                      _
GAM761  BLMH      3'  CAGCTCAGGATCTCTTAGC    4609     _   AG_  GGT
                                GC AAGA   CT   TGAGCTG
                                || ||||   ||   |||||||
                                CG TTCT   GG   ACTCGAC
                                 A   CTA  ____
GAM761  CYP21A2   3'  GCAGCTCAGCCTCCCCCCGCT  4948      AAGAAGCT
                                GGC       GGTTGAGCTGC
                                |||       ||||||||||
                                TCG       CCGACTCGACG
                                  CCCCCCT_
GAM761  DHCR24    3'  TGACAGCCCAACACCACCTTCC 28636    CAA   C   __  A   C
          TCC                     GG   GAAG TGGT  TG GCTG CA
                                ||   |||| ||||  || |||| ||
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                                CC   CTTC ACCA  AC CGAC GT
                                 TC_   C   CA  C   A
GAM761   E2F1    3'  CAGCTCTGTTCCCTCCTGCT  84797     A  AGCT  TT__
                                GGCA GA   GG   GAGCTG
                                |||| ||   ||   ||||||
                                TCGT CT   CC   CTCGAC
                                  C  C___  TTGT
GAM761   EGR2    5'  GCAACTCCTGGCTTCCC    4629    CAA    TG TT   C
                                GG   GAAGC  G  GAG TGC
                                ||   |||||  |  ||| |||
                                CC   CTTCG  C  CTC ACG
                                 ___    GT __   A
GAM761   ENPP3   3'  CAGCTTAGGCACTCCTTGCC  17224       A  C  G
                                GGCAAG AG TG TTGAGCTG
                                |||||| || || ||||||||
                                CCGTTC TC AC GATTCGAC
                                   C  _  G
GAM761   FGF23   3'  CAACAACAGCTTCTTCC    40192    C       __
                                GG AAGAAGCTG  GTTG
                                || |||||||||  ||||
                                CC TTCTTCGAC  CAAC
                                 _       AA
GAM761   GPR30   3'  GCGGTGACCAGCCTGTC    7693      AGAA     GA
                                GGCA   GCTGGTT  GCTGC
                                ||||   |||||||  |||||
                                CTGT   CGACCAG  TGGCG
                                  C___      __
GAM761   IKBKB   3'  GGCAGCTCCTTCCTCTGCC   63209     A  AGCT  TT_
                                GGCA GA   GG   GAGCTGCC
                                |||| ||   ||   ||||||||
                                CCGT CT   CC   CTCGACGG
                                  _ _____  TTC
GAM761   LETM1   3'  TGGCACCTCCATCCTCCTGCC  24625     A  AGCT   T   C
                                GGCA GA   GGT GAG TGCCA
                                |||| ||   ||| ||| |||||
                                CCGT CT   CTA CTC ACGGT
                                  C  C___   C   C
GAM761   LMO2    5'  GGCAGCCGGCCAGCCCCGCGCC 18741    AAGAA      A
                                GGC    GCTGGTTG GCTGCC
                                |||    |||||||| ||||||
                                CCG    CGACCGGC CGACGG
                                 CGCCC       _
GAM761   LTB4R   5'  CAGCTTCCAACCAGTTCCTGCC 5643      A   G     __
                                GGCA GAA CTGGTTG  AGCTG
                                |||| ||| |||||||  |||||
                                CCGT CTT GACCAAC  TCGAC
                                  C   _      CT
GAM761   NRG1    3'  GCAGTTCAGCTCCTTC     25655     CT
                                GAAG  GGTTGAGCTGC
                                ||||  ||||||||||
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                                CTTC  TCGACTTGACG
                                  C_
GAM761  PCDH11X  3'  TGACAGCTCAATAGGCTGTTAC 52030    C  GA   G       C
           C                     GG AA  AGCT GTTGAGCTG CA
                                 || ||  |||| ||||||||| ||
                                 CC TT  TCGG TAACTCGAC GT
                                  A  G_   A       A
GAM761  PCDH11X  3'  TGACAGCTCAATAGGCTGTTAC 52052    C  GA   G       C
           C                     GG AA  AGCT GTTGAGCTG CA
                                 || ||  |||| ||||||||| ||
                                 CC TT  TCGG TAACTCGAC GT
                                  A  G_   A       A
GAM761  PCDH11Y  3'  TGACAGCTCAATAGGCTGTTAC 52086    C  GA   G       C
           C                     GG AA  AGCT GTTGAGCTG CA
                                 || ||  |||| ||||||||| ||
                                 CC TT  TCGG TAACTCGAC GT
                                  A  G_   A       A
GAM761  PLD1     3'  TGGCAGCTCAAAGACTTCCACC 10626    CAA   _  GG
                                 GG   GAAG CT  TTGAGCTGCCA
                                 ||   |||| ||  ||||||||||
                                 CC   CTTC GA  AACTCGACGGT
                                  AC_   A  __
GAM761  PMM2     3'  GGCAAAACAGTCCTTGCC    72091       AA   GTTGAGC
                                 GGCAAG  GCTG      TGCC
                                 ||||||  ||||      ||||
                                 CCGTTC  TGAC      ACGG
                                    C_   AAA____
GAM761  REQ      3'  TGGCAGCTCTGACCACCTCTGG 20771     A   A C    _
           CC                      GGC AGA G TGGTT GAGCTGCCA
                                 ||| ||| | ||||| |||||||||
                                 CCG TCT C ACCAG CTCGACGGT
                                   G   _ C    T
GAM761  SLC31A1  3'  TGGCAGCTGAGGGAAATTCTTG 8514         GCTGG  G
           CC                      GGCAAGAA     TT AGCTGCCA
                                 ||||||||     || ||||||||
                                 CCGTTCTT     GA TCGACGGT
                                      AAAGG  G
GAM761  SPAM1    5'  AGACCAGCCAACTTCTTGCC   11897         C     AG
                                 GGCAAGAAG TGGTTG  CT
                                 |||||||| ||||||  ||
                                 CCGTTCTTC ACCGAC  GA
                                      A     CA
GAM761  SURF4    3'  TGGCAGCTGGAAGCCTCCCC   52547    CAA  A   GG  G
                                 GG   GA GCT  TT AGCTGCCA
                                 ||   || |||  || ||||||||
                                 CC   CT CGA  AG TCGACGGT
                                  C__  C   __  G
GAM761  SYT5     5'  GCAACAACCCGTTGCC      12075      AGAA  T    AGC
                                 GGCA   GC GGTTG   TGC
                                 ||||   || |||||   |||
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                                CCGT   TG CCAAC   ACG
                                  ____ C    A__
GAM761  TEM8    3'  CAGCTCACAGTTTCTTGCC   49852          GT
                                GGCAAGAAGCTG  TGAGCTG
                                ||||||||||||  |||||||
                                CCGTTCTTTGAC  ACTCGAC
                                      __
GAM761  TNS     5'  TGGGGGAAACCAGCTTCTTGCC 42632            GAG  G
                                GGCAAGAAGCTGGTT   CT CCA
                                ||||||||||||||||  || |||
                                CCGTTCTTCGACCAA   GG GGT
                                         A__  G
GAM761  YWHAZ   3'  TGGCAGCTAATGGGCTCTTACC 12709    C    A   G   G
                                GG AAGA GCT GTT AGCTGCCA
                                || |||| ||| ||| ||||||||
                                CC TTCT CGG TAA TCGACGGT
                                 A   _  G  _
GAM761  C1orf17  3'  CAGCAACTATCCTTGCC    68210       AAGC    GA
                                GGCAAG   TGGTT  GCTG
                                ||||||   |||||  ||||
                                CCGTTC   ATCAA  CGAC
                                   CT__    __
GAM761  C20orf110 3'  TGACAGCTCAGTCTTCACCTTG 79550       AAGCT GT      C
           CC                    GGCAAG    G  TGAGCTG CA
                                ||||||    |  ||||||| ||
                                CCGTTC    C  ACTCGAC GT
                                   CACTT TG      A
GAM761  DAPK2   5'  GGCAGCTCAGCCTCCCGCC   26741    AA  AGCT
                                GGC  GA   GGTTGAGCTGCC
                                |||  ||   ||||||||||||
                                CCG  CT   CCGACTCGACGG
                                 CC  ____
GAM761  DDX34   3'  CAGCAAACACCAGCTCCTCAGC 27978    A_  A     TGA_
                                GC  AG AGCTGGT   GCTG
                                ||  || |||||||   ||||
                                CG  TC TCGACCA   CGAC
                                 AC  C      CAAA
GAM761  DKFZP434G156 5'  CAGCCCGCAGCCAGCCCCCC   69779    CAAGAA      A__
                                GG     GCTGGTTG   GCTG
                                ||     ||||||||   ||||
                                CC     CGACCGAC   CGAC
                                 CCC___       GCC
GAM761  DKFZp547H025 3'  CAGGGGAACTAGCTTCCC    39354    CAA       GAG
                                GG   GAAGCTGGTT   CTG
                                ||   ||||||||||   |||
                                CC   CTTCGATCAA   GAC
                                 ___        GGG
GAM761  DKFZP564L0864 3'  TAGCACCAATTTCTTGCC    72556         C    TGA
                                GGCAAGAAG TGGT   GCTG
                                |||||||| ||||   ||||
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                                CCGTTCTTT ACCA   CGAT
                                     A   ___
GAM761  DKFZp566O084 3'  CAACAAGCTTCTTCC      31331    C      G
                                GG AAGAAGCT GTTG
                                || |||||||| ||||
                                CC TTCTTCGA CAAC
                                 _      A
GAM761  DKFZP727M111 5'  GGCTACCAGCCTGCTGCC    31412     AGAA  T    AGCT
                                GGCA   GC GGTTG   GCC
                                ||||   || |||||   |||
                                CCGT   CG CCGAC   CGG
                                  _____ T    CAT_
GAM761  FLJ11099  3'  TGACAGATGTCAGCTTCTCC  37047    CA       TTGAG   C
                                GG  AGAAGCTGG    CTG CA
                                ||  |||||||||    ||| ||
                                CC  TCTTCGACT    GAC GT
                                 __       GTA__   A
GAM761  FLJ14437  5'  TGACAGGTTGTCCAGCTTCTT  50830         T   G   C
                                AAGAAGCTGG TGA CTG CA
                                |||||||||| ||| ||| ||
                                TTCTTCGACC GTT GAC GT
                                     T   G   A
GAM761  FLJ14810  3'  TGGCAGCTCACTGATCTCTTGC 51632        AGC    T
          C                      GGCAAGA   TGGT GAGCTGCCA
                                |||||||   |||| |||||||||
                                CCGTTCT   GTCA CTCGACGGT
                                    CTA   _
GAM761  FLJ20174  3'  GCAGCTTGGACTTCCTGCC   34689     A   CTGG TG
                                GGCA GAAG    T  AGCTGC
                                |||| ||||    |  ||||||
                                CCGT CTTC    G  TCGACG
                                  C    A___ GT
GAM761  FLJ20548  3'  GGCAGCTGTGCTTTTGCC    35379       A  TGGTTG
                                GGCAAGA GC     AGCTGCC
                                ||||||| ||     |||||||
                                CCGTTTT CG     TCGACGG
                                    _  TG_____
GAM761  FLJ23042  3'  TAGCGTCAACCCACCTCTTGCC 47175        AGCT     _
                                GGCAAGA    GGTTGA GCTG
                                |||||||    |||||| ||||
                                CCGTTCT    CCAACT CGAT
                                    CCAC     G
GAM761  GGA2     3'  CAGCCAGCCCTTGCC      56873       AA
                                GGCAAG  GCTGGTTG
                                ||||||  ||||||||
                                CCGTTC  CGACCGAC
                                   C_
GAM761  GGA2     3'  CAGCCAGCCCTTGCC      30459       AA
                                GGCAAG  GCTGGTTG
                                ||||||  ||||||||
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                                CCGTTC  CGACCGAC
                                   C_
GAM761  KCNJ9    5' GCAGCTCGGGCCCCCGCC    17155    AAGAA   GGT
                                GGC    GCT   TGAGCTGC
                                |||    |||  ||||||||
                                CCG    CGG   GCTCGACG
                                  CCCC_  ___
GAM761  KCNT1    3' CAGCTCAGCCCTGCTGCC    61827    AGAA  T_
                                GGCA   GC  GGTTGAGCTG
                                ||||   ||  ||||||||||
                                CCGT   CG  CCGACTCGAC
                                  ____ TC
GAM761  KIAA0087 3' GCAGCTTAGACTTCCGCC    28697    AA   CTGG
                                GGC  GAAG   TTGAGCTGC
                                |||  ||||   |||||||||
                                CCG  CTTC   GATTCGACG
                                  C_   A___
GAM761  KIAA0125 5' GGCAGCTCACGTTCTGCC    28898     A   G TGGT
                                GGCA GAA C    TGAGCTGCC
                                |||| ||| |    |||||||||
                                CCGT CTT G    ACTCGACGG
                                  _   _ C___
GAM761  KIAA0217 3' AGTAACCAGCTTCTCACT    67034    CA        GA
                                GG  AGAAGCTGGTT  GCT
                                ||  ||||||||||  |||
                                TC  TCTTCGACCAA  TGA
                                 AC         __
GAM761  KIAA0792 3' GGCATCCAGCTCCCTGCT    28105     AGA     TTGAGC
                                GGCA   AGCTGG     TGCC
                                ||||   ||||||     ||||
                                TCGT   TCGACC     ACGG
                                  CCC     T_____
GAM761  KIAA0889 3' TGACAACCTCAGCAGCTTCTCC 31148    CA      G    C_  C
                                GG  AGAAGCTG TTGAG  TG CA
                                ||  |||||||| |||||  || ||
                                CC  TCTTCGAC GACTC  AC GT
                                 __       _    CA  A
GAM761  KIAA1058 3' GGCAGCTGTGCTCCTCGGCC   82255    A_  A   TGGTTG
                                GGC  AG AGC     AGCTGCC
                                |||  || |||     |||||||
                                CCG  TC TCG     TCGACGG
                                  GC  C   TG____
GAM761  KIAA1320 5' TGGCAGCTGGGTGCTTCTTGCC 69313          TGG  G
                                GGCAAGAAGC   TT AGCTGCCA
                                ||||||||||   || ||||||||
                                CCGTTCTTCG   GG TCGACGGT
                                      T__  G
GAM761  KIAA1754 3' CAGCTCAGCAGCCCCCC     63234    CAAGAA   G
                                GG     GCTG TTGAGCTG
                                ||     |||| ||||||||
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                                CC     CGAC GACTCGAC
                                 CCC___   _
GAM761  KIAA1940  3'  TGGCAGCTTTGCAGCCCCTGCC 79994     A AA   GTT
                                GGCA G  GCTG   GAGCTGCCA
                                |||| |  ||||   |||||||||
                                CCGT C  CGAC   TTCGACGGT
                                  _ CC   GT_
GAM761  MGC16063  3'  TGGCAACTCAAAACCACCTTGC 53863       AAGC   __   C
           C                     GGCAAG   TGGT  TGAG TGCCA
                                ||||||   ||||  |||| |||||
                                CCGTTC   ACCA  ACTC ACGGT
                                   C___   AA   A
GAM761  MGC17330  3'  TGGCAAGAGCCCAGCTTCCTG  53533    A      TTGAGC
                                CA GAAGCTGG     TGCCA
                                || ||||||||     |||||
                                GT CTTCGACC     ACGGT
                                 C       CGAGA_
GAM761  MGC3020   3'  GGCCATCCAGCTTCCC     43895    CAA      T  A
                                GG   GAAGCTGG TG GCT
                                ||   |||||||| || |||
                                CC   CTTCGACC AC CGG
                                 ___       T  _
GAM761  MGC3101   3'  GGCAAACCCAGTTCCTGCC   43882     A   G   TTGAGC
                                GGCA GAA CTGG     TGCC
                                |||| ||| ||||     ||||
                                CCGT CTT GACC     ACGG
                                  C   _   CAA___
GAM761  MGC3178   3'  GCAGCATCTCGACCAGCCTCTG 47988     A  A       ___
           CC                     GGCA GA GCTGGTTGA   GCTGC
                                |||| || |||||||||   |||||
                                CCGT CT CGACCAGCT   CGACG
                                  _ C       CTA
GAM761  RAB11B    3'  GCAGCTCGCACAGGCCTCCC   73905    CAA  A   G  _
                                GG   GA GCT GT TGAGCTGC
                                ||   || ||| || ||||||||
                                CC   CT CGG CA GCTCGACG
                                 ___  C   A  C
GAM761  RASD2     3'  TGGCAGCTGGGAGAACTTCTCT 26690    CA    CTGG  G
           CC                     GG  AGAAG    TT AGCTGCCA
                                ||  |||||    || ||||||||
                                CC  TCTTC    GG TCGACGGT
                                 TC     AAGA  G
GAM761  SCYA23    3'  CAGCCACCAACTTTCTTGCC   17354         _ C    T A
                                GGCAAGAA G TGGT G GCTG
                                |||||||| | |||| | ||||
                                CCGTTCTT C ACCA C CGAC
                                     T A    _ _
GAM761  SDF1      3'  CAATCAGCTCCTTCC      90855    C   A
                                GG AAG AGCTGGTTG
                                || ||| |||||||||
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                                CC TTC TCGACTAAC
                                 _  C
GAM761  SLC12A5  3'  GGCAGCTCCTGTCTCGCC   40385    A  AGCT  TTG
                                GGC AGA   GG  AGCTGCC
                                ||| |||   ||  |||||||
                                CCG TCT   CC  TCGACGG
                                  C  GT__ ___
GAM761  STRN3    5'  GGCAGCCGGCAGCTCCCTGCT  27408     AGA    G  A
                                GGCA  AGCTG TTG GCTGCC
                                ||||  ||||| ||| ||||||
                                TCGT  TCGAC GGC CGACGG
                                  CCC   _  _
GAM761  TIEG     5'  GCAGCCAGTCAGCTTGCC   18958     AGA    GT  A
                                GGCA  AGCTG  TG GCTGC
                                ||||  |||||  || |||||
                                CCGT  TCGAC  AC CGACG
                                  ___    TG  _
GAM761  YAP      5'  CAAATCCACCTTCTTGCC   57462        C  __
                                GGCAAGAAG TGG  TTG
                                ||||||||| |||  |||
                                CCGTTCTTC ACC  AAC
                                     C  TA
GAM761  LOC112885 3'  TGGCAGCTTGTCACCCTTGCC  56531      AAGCT  __
                                GGCAAG    GGT  TGAGCTGCCA
                                ||||||    |||  ||||||||||
                                CCGTTC    CCA  GTTCGACGGT
                                   _____  CT
GAM761  LOC144058 5'  CAGAGGCACCAGCTTCCTCC  76665    CAA       T AG_
                                GG  GAAGCTGGT G  CTG
                                ||  ||||||||| |  |||
                                CC  CTTCGACCA C  GAC
                                 TC_       _ GGA
GAM761  LOC144699 3'  TGACAGCTCAGGTTTCCCTGCC 76916     A_     GGT     C
                                GGCA  GAAGCT  TGAGCTG CA
                                ||||  ||||||  ||||||| ||
                                CCGT  CTTTGG  ACTCGAC GT
                                  CC     ___      A
GAM761  LOC146433 3'  CAGCAGGGCTCAGCTTCCTGCC 77871     A     _  GA
                                GGCA GAAGCTG GTT  GCTG
                                |||| ||||||| |||  ||||
                                CCGT CTTCGAC CGG  CGAC
                                  C      T  GA
GAM761  LOC146733 3'  GCAGGTACCAGCTCCTCCCC  83766    CA A     TGAG
                                GG  AG AGCTGGT    CTGC
                                ||  || |||||||   ||||
                                CC  TC TCGACCA    GACG
                                 CC  C      TG__
GAM761  LOC150372 5'  GGCAGCTCACCCACCGCC    79804     AAGAAGC  T
                                GGC      TGG TGAGCTGCC
                                |||      ||| |||||||||
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                                CCG      ACC ACTCGACGG
                                  CC_____   C
GAM761   LOC151414 3'  GCACTCCCAGTTCCTGCC    80237     A  G   TT  C
                                GGCA GAA CTGG  GAG TGC
                                |||| ||| ||||  ||| |||
                                CCGT CTT GACC  CTC ACG
                                  C  _   __  _
GAM761   LOC153577 3'  TGGCAGGGAGACAGCCTCTTCC 86063    C   A   G  GAG
                                GG AAGA GCTG TT   CTGCCA
                                || |||| |||| ||   ||||||
                                CC TTCT CGAC AG   GACGGT
                                  _   C   _ AGG
GAM761   LOC158402 5'  TGGCAGCCTCCACCTCTTGACC 86816    _    AGCT  T  _
                                GG CAAGA    GGT GAG CTGCCA
                                || |||||    ||| ||| ||||||
                                CC GTTCT    CCA CTC GACGGT
                                 A    _____  C  C
GAM761   LOC200918 3'  TGGCAGCTGAGGGAAATTCTCG 88942     A   GCTGG  G
            CC                    GGC AGAA     TT AGCTGCCA
                                ||| ||||    || ||||||||
                                CCG TCTT    GA TCGACGGT
                                  C   AAAGG  G
GAM761   LOC201695 5'  TGGCATGTGATCAGCCCCTTAC 90706    C  AA      AGC
            C                     GG AAG  GCTGGTTG   TGCCA
                                || |||  ||||||||   |||||
                                CC TTC  CGACTAGT   ACGGT
                                 A  CC       GT_
GAM761   LOC255452 5'  AGATAACCAGCTCCCC     97523    CAA  A      AG
                                GG   GA GCTGGTTG  CT
                                ||   || ||||||||  ||
                                CC   CT CGACCAAT  GA
                                 C__  _       A_
GAM761   LOC256286 5'  TGGCAGCTGGGGGCTCCTGCC  95204     A  A   GG  G
                                GGCA GA GCT  TT AGCTGCCA
                                |||| || |||  || ||||||||
                                CCGT CT CGG  GG TCGACGGT
                                  C  _  __  G
GAM761   LOC257054 3'  GCAGCTCAAGGCCCTGCT    95661     AGAA   GG
                                GGCA    GCT  TTGAGCTGC
                                ||||    |||  |||||||||
                                TCGT    CGG  AACTCGACG
                                  CC__   __
GAM761   LOC257426 3'  CAGCAGCCGGCTCCATGCC    66644     AGA      GA
                                GGCA   AGCTGGTT  GCTG
                                ||||   ||||||||  ||||
                                CCGT   TCGGCCGA  CGAC
                                  ACC       __
GAM761   LOC257468 3'  TGGCAGCTAGGGCCTCGCC    95190     AA  A   GGTTG
                                GGC  GA GCT    AGCTGCCA
                                |||  || |||    ||||||||
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                                CCG  CT CGG    TCGACGGT
                                  __ C  GA___
GAM761  LOC90072  3'  TGACAACCTCAGCAGCTTCTCC 61305   CA     G   C_ C
                                GG  AGAAGCTG TTGAG  TG CA
                                ||  |||||||| |||||  || ||
                                CC  TCTTCGAC GACTC  AC GT
                                 __      _    CA  A
GAM761  LOC90342  5'  TGGCAGCTCCGCAGCCTCCTCC 62363   CAA  A   GTT
                                GG   GA GCTG   GAGCTGCCA
                                ||   || ||||   |||||||||
                                CC   CT CGAC   CTCGACGGT
                                 TC_  C   GC_
GAM761  LOC91145  3'  CAGCAATCTGCTTCTTGCC   65056        T   GA
                                GGCAAGAAGC GGTT  GCTG
                                |||||||||| ||||  ||||
                                CCGTTCTTCG CTAA  CGAC
                                      T   __
GAM761  LOC91191  5'  GCAGCCCCTTCTTTCTTGCC   65191       CT_  TTGA
                                GGCAAGAAG   GG   GCTGC
                                |||||||||   ||   |||||
                                CCGTTCTTT   CC   CGACG
                                     CTT  C___
GAM761  LOC91286  3'  GCAGCTCAAGACCAGCCCGGCC 65452    AAGAA    __
                                GGC    GCTGGT  TGAGCTGC
                                |||    ||||||  ||||||||
                                CCG    CGACCA  ACTCGACG
                                  GCC__     GA
GAM762  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM762  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM762  FDFT1    3'  TAGGAAAGTGAAATG      15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                        _
GAM762  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                   CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM762  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
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                                GT  AGGTGACAGAC CT
                                 AT         C
GAM762  PHYH    3'  ACAGTAAAAGTGAAAT     20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                     A
GAM762  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM762  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM762  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM762  CG012   5'  CTCACTCTGAAAGTGAA     83218          CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM762  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                |||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM762  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                |||||||       |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM762  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM762  KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM762  KLHL6   3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
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                                AAAG GAC AGACTCTA
                                  _  G
GAM762  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM762  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM762  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM762  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148         TCAC   C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM762  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM762  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM762  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM762  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM762  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||   |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM762  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
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                                GTAAAGTGAA GTGACA
                                       _
GAM763  FTSJ2    3'  CCAAAAAGAGATGACAAAACT  25434       T       ACAA
                                AGTTTT TCATCTCT    TGG
                                |||||| ||||||||    |||
                                TCAAAA AGTAGAGA    ACC
                                   C       AAA_
GAM763  LDHB     5'  CCATTTTGGAGATGAAGAAACT 9708               C
           GA                     TCAGTTTTTTCATCTCTA AATGG
                                  |||||||||||||||||| |||||
                                  AGTCAAAGAAGTAGAGGT TTACC
                                           T
GAM763  MYCL1    3'  CCATTAACAGATGGAAAAACTG 18161             CTAC
           A                      TCAGTTTTTTCATCT    AATGG
                                  ||||||||||||||    |||||
                                  AGTCAAAAAGGTAGA    TTACC
                                           CAA_
GAM763  NT5E     3'  CCACCTGTCAGATGAAAAAACT 10280             CT   A_
           GA                     TCAGTTTTTTCATCT  ACA  TGG
                                  ||||||||||||||  |||  |||
                                  AGTCAAAAAAGTAGA  TGT  ACC
                                           C_   CC
GAM763  PTGIS    3'  CCACTTCATAGATGAGAAAACT 6327              CTACAA
           GA                     TCAGTTTTTTCATCT     TGG
                                  ||||||||||||||     |||
                                  AGTCAAAAGAGTAGA     ACC
                                           TACTTC
GAM763  ZNF83    3'  TTGAGAGAAACAAAAACACTGA 36982       _    CA_    A
                                TCAGT TTTTT   TCTCT CAA
                                ||||| |||||   ||||| |||
                                AGTCA AAAAA   AGAGA GTT
                                   C    CAA    _
GAM763  KIAA0040 5'  CCATTTTGGAGATGAAGAAACT 27782               C
           GA                     TCAGTTTTTTCATCTCTA AATGG
                                  |||||||||||||||||| |||||
                                  AGTCAAAGAAGTAGAGGT TTACC
                                           T
GAM763  KIAA1922 5'  CCTTTTAGAGATGAGAAAACTG 73623               C  T
           A                      TCAGTTTTTTCATCTCTA AA GG
                                  |||||||||||||||||| || ||
                                  AGTCAAAAGAGTAGAGAT TT CC
                                           T  _
GAM763  KRTAP1-3 3'  AGAAATGAAAAAGCCGA     48237     A        C
                                TC GTTTTTTCAT TCT
                                || |||||||||| |||
                                AG CGAAAAAGTA AGA
                                 C         A
GAM763  SGP28    3'  AGTAATGAAAAAACTGA     20227            CT
                                TCAGTTTTTTCAT  CT
                                ||||||||||||  ||
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                                AGTCAAAAAAGTA  GA
                                       AT
GAM763  SIAT4A   5'  TGGAGATGAAGAAACTGA    11677
                                TCAGTTTTTTCATCTCTA
                                ||||||||||||||||||
                                AGTCAAAGAAGTAGAGGT

GAM763  LOC113146 3'  AGAGATGCAAAAAACT      72970        _
                                AGTTTTTT CATCTCT
                                |||||||| |||||||
                                TCAAAAAA GTAGAGA
                                     C
GAM763  LOC151720 5'  CCATTTACAGATGAAGAAACTG 80338            C  C
           A                     TCAGTTTTTTCATCT TA AATGG
                                ||||||||||||||| || |||||
                                AGTCAAAGAAGTAGA AT TTACC
                                       C  _
GAM763  LOC152580 3'  CCAGGTTTAGATGAAAAACT   85775       T    CT  AA
                                AGTTTTT CATCT  AC  TGG
                                ||||||| |||||  ||  |||
                                TCAAAAA GTAGA  TG  ACC
                                   _    TT  G_
GAM763  LOC158696 3'  CCATTGTATCTTGGAAATAACT 81972     T   ATCTC
                                AGTT TTTC    TACAATGG
                                |||| ||||    ||||||||
                                TCAA AAAG    ATGTTACC
                                  T   GTTCT
GAM763  LOC253805 3'  CCATTTTCCAGATGAAGAAACT 96427            CTAC
           GA                    TCAGTTTTTTCATCT   AATGG
                                ||||||||||||||   |||||
                                AGTCAAAGAAGTAGA   TTACC
                                       CCTT
GAM763  LOC92078  5'  CCATTTTACAGATGAGAAAACT 67979            C  C
           GA                    TCAGTTTTTTCATCT TA AATGG
                                ||||||||||||||| || |||||
                                AGTCAAAAGAGTAGA AT TTACC
                                       C  T
GAM764  ASB1     3'  GCTGTGCTGCTGCTGGTC    32268       _ T    A
                                GACCAGT GC GGCATA GC
                                ||||||| || |||||| ||
                                CTGGTCG CG TCGTGT CG
                                   T  _    _
GAM764  B3GAT1   3'  TTCAGAATATAGCATTGGTT  37834         GCATAAG
                                GACCAGTGCTG     CTGAA
                                ||||||||||      |||||
                                TTGGTTACGAT     GACTT
                                      ATAA___
GAM764  B3GAT1   3'  TTCAGAATATAGCATTGGTT  53982         GCATAAG
                                GACCAGTGCTG     CTGAA
                                ||||||||||      |||||
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                                TTGGTTACGAT      GACTT
                                      ATAA___
GAM764  BLTR2    5'  TTCAGCTTGTGCTGTTTCCTGG 39045     T__  T
                                CCAG   GC GGCATAAGCTGAA
                                ||||   || ||||||||||||
                                GGTC   TG TCGTGTTCGACTT
                                  CTT  _
GAM764  C4B      3'  TGGCAGCAAAGTGTCAGTGTTG 5173      TG      AA_   AA
            G                    CCAG  CTGGCAT   GCTG
                                ||||  |||||||   ||||
                                GGTT  GACTGTG   CGAC
                                  GT      AAA    GGTT
GAM764  CAPN1    3'  TTCAGGGACTTGTGTACTGGTT 17752        GCTG      ___
                                GACCAGT    GCATAAG   CTGAA
                                |||||||    |||||||   |||||
                                TTGGTCA    TGTGTTC   GACTT
                                    ____      AGG
GAM764  CASP8AP2 3'  TTCAGCTTGTGCTAGTCAT    24005     _
                                GTG CTGGCATAAGCTGAA
                                ||| ||||||||||||||
                                TAC GATCGTGTTCGACTT
                                  T
GAM764  COL1A2   3'  TCAGATTCAGCATTTGTT     3613      C       CATAAG
                                GAC AGTGCTGG      CTGA
                                ||| ||||||||      ||||
                                TTG TTACGACT      GACT
                                  T       TA____
GAM764  COX7A2   5'  TTCAGTTGTGGCGGTTGCTGGT 8518          _   G     G
            C                    GACCAGTG CTG CATAA CTGAA
                                |||||||| ||| ||||| |||||
                                CTGGTCGT GGC GTGTT GACTT
                                     T   G    _
GAM764  CRYGB    3'  TTAGCTTGTGTTTCTGG     94626      TGCT
                                CCAG    GGCATAAGCTGA
                                ||||    ||||||||||||
                                GGTC    TTGTGTTCGATT
                                  T___
GAM764  CRYGB    3'  TTAGCTTGTGTTTCTGG     17799      TGCT
                                CCAG    GGCATAAGCTGA
                                ||||    ||||||||||||
                                GGTC    TTGTGTTCGATT
                                  T___
GAM764  CSE1L    3'  TTCAGTGTATGGCGTTGGTT   61859         TGG    A
                                GACCAGTGC   CATA GCTGAA
                                |||||||||   |||| ||||||
                                TTGGTTGCG   GTAT TGACTT
                                     ___    G
GAM764  CUL4B    3'  GAGATTCTGTGTCATGCTGGTT 13141         C      AGCTGAA
                                GACCAGTG TGGCATA
                                |||||||| |||||||
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                                TTGGTCGT ACTGTGT
                                   _     CTTAGAGT
GAM764  CXCL6   3'  TTCCTGTGTGTCATGTTGGTT  11466     GT C     AGCT
                                GACCA  G TGGCATA   GAA
                                |||||  | |||||||   |||
                                TTGGT  T ACTGTGT   CTT
                                  TG _     GTC_
GAM764  DUSP11  5'  TTTGGCCGGCTTGGCATTGG  13134       _ ATAA  TG
                                CCAGTGCTG GC   GC  AA
                                |||||||||  ||   ||  ||
                                GGTTACGGT CG   CG  TT
                                     T  GC__  GT
GAM764  DUSP4   5'  TGAGCTTGTCGGCGCTGGT   54057         TA   GAA
                                ACCAGTGCTGGCA  AGCT
                                ||||||||||||  ||||
                                TGGTCGCGGCTGT  TCGA
                                       __   GTT
GAM764  DYRK1A  3'  TTCAGATGTTGGTCTTGGTC  55208     T  TG   AAG
                                GACCAG GC  GCAT   CTGAA
                                ||||||  ||  ||||   |||||
                                CTGGTT TG  TGTA   GACTT
                                   C  GT   ___
GAM764  DYRK1A  3'  TTCAGATGTTGGTCTTGGTC  55251     T  TG   AAG
                                GACCAG GC  GCAT   CTGAA
                                ||||||  ||  ||||   |||||
                                CTGGTT TG  TGTA   GACTT
                                   C  GT   ___
GAM764  DYRK1A  3'  TTCAGATGTTGGTCTTGGTC  7357      T  TG   AAG
                                GACCAG GC  GCAT   CTGAA
                                ||||||  ||  ||||   |||||
                                CTGGTT TG  TGTA   GACTT
                                   C  GT   ___
GAM764  EFNB2   3'  TTTGGTTTATGCGGTGCTG   14581    TG  G     TG
                                CAG  CTG CATAAGC  AA
                                |||  ||| |||||||  ||
                                GTC  GGC GTATTTG  TT
                                  GT  _     GT
GAM764  ESRRG   3'  TTTATGTTGTGTGCCAGTCTGG 66398      T      _  _
          TC                    GACCAG GCTGGCATA AGC TGAA
                                ||||||  |||||||| ||| ||||
                                CTGGTC TGACCGTGT TTG ATTT
                                   _      G  T
GAM764  ETV3    3'  TTTGGTTTATTTGGTTGGTT  17883     GT  TG C     TG
                                GACCA  GC  G ATAAGC  AA
                                |||||  ||  | ||||||  ||
                                TTGGT  TG  T TATTTG  TT
                                   __ GT _     GT
GAM764  FGF5    3'  TTCAGCTGAATTATATTGGTC  52496       C   CATA
                                GACCAGTG TGG   AGCTGAA
                                ||||||||  |||   |||||||
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                                CTGGTTAT ATT    TCGACTT
                                     _  AAG_
GAM764  FGF5    3'  TTCAGCTGAATTATATTGGTC  15551       C   CATA
                                GACCAGTG TGG    AGCTGAA
                                |||||||| |||    |||||||
                                CTGGTTAT ATT    TCGACTT
                                     _  AAG_
GAM764  FMOD    3'  TTTGGCTTGATGGTTTGGTT   8934       T   GCA    TG
                                GACCAG GCTG   TAAGC  AA
                                |||||| ||||   |||||  ||
                                TTGGTT TGGT   GTTCG  TT
                                   _   A__    GT
GAM764  FOXG1B  3'  TCAGTTTGTGTTGTGTAT    17902     _
                                GTGC TGGCATAAGCTGA
                                |||| ||||||||||||
                                TATG GTTGTGTTTGACT
                                  T
GAM764  GCH1    3'  TTCAGTGTGTGTGCGTTGGTT  3862        TG    A
                                GACCAGTGC  GCATA GCTGAA
                                |||||||||  ||||| ||||||
                                TTGGTTGCG  TGTGT TGACTT
                                     __    G
GAM764  GCK     3'  TTCAGCTCCCATAGCGCTGG   3872        GCATA
                                CCAGTGCTG    AGCTGAA
                                |||||||||    |||||||
                                GGTCGCGAT    TCGACTT
                                     ACCC_
GAM764  GCK     3'  TTCAGCTCCCATAGCGCTGG   53174       GCATA
                                CCAGTGCTG    AGCTGAA
                                |||||||||    |||||||
                                GGTCGCGAT    TCGACTT
                                     ACCC_
GAM764  GCK     3'  TTCAGCTCCCATAGCGCTGG   53180       GCATA
                                CCAGTGCTG    AGCTGAA
                                |||||||||    |||||||
                                GGTCGCGAT    TCGACTT
                                     ACCC_
GAM764  GLI3    3'  TTCAGTTTTGAATCAGTATTG  3912        CAT_
                                CAGTGCTGG    AAGCTGAA
                                |||||||||    ||||||||
                                GTTATGACT    TTTGACTT
                                     AAGT
GAM764  GPR85   3'  TTTACAAATGCTAGATATTGGT 38582       _     AAGCTGAA
          C                      GACCAGTG CTGGCAT
                                ||||||||| |||||||
                                CTGGTTAT GATCGTA
                                     A      AACATTT
GAM764  H3F3B   5'  TTCGTTGGGCGGTGCTGGTT   18026      TG   G ATA   T
                                GACCAG  CTG C   AGC GAA
                                ||||||  ||| |   ||| |||
```

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                                TTGGTC  GGC G   TTG CTT
                                   GT   _ GG_  _
GAM764  HRASLS   5'  TTCAGCGTGGCGGCGCTGGT  39855        G   AA
                                ACCAGTGCTG CAT  GCTGAA
                                |||||||||| |||  ||||||
                                TGGTCGCGGC GTG  CGACTT
                                     G  __
GAM764  HYOU1    3'  TTCAGTAGCTGTTGATGCTGGT 59653       CT   TAA
           T                     GACCAGTG  GGCA   GCTGAA
                                |||||||| ||||  ||||||
                                TTGGTCGT  TTGT   TGACTT
                                    AG   CGA
GAM764  JRK      3'  GCCCAGTGTCAGCATGGTC   86529      G       AA_
                                GACCA TGCTGGCAT   GC
                                ||||| |||||||||  ||
                                CTGGT ACGACTGTG   CG
                                  _       ACC
GAM764  KCNJ1    5'  TCAGCTTGGGGCTTGGTC    4027       T  GGCA
                                GACCAG GCT    TAAGCTGA
                                |||||| |||   ||||||||
                                CTGGTT CGG    GTTCGACT
                                   _  G___
GAM764  KLF8     3'  TTTGGTTTTCAGACAGTGCTGG 23407      TG  GCAT_   TG
           T                     ACCAG  CTG    AAGC  AA
                                ||||| |||    ||||  ||
                                TGGTC  GAC    TTTG  TT
                                   GT   AGACT   GT
GAM764  MEN1     5'  AGTTGTTAGTGTTGGTT     93367       TG     TAA
                                GACCAG  CTGGCA   GCT
                                ||||||  ||||||  |||
                                TTGGTT  GATTGT   TGA
                                   GT     ___
GAM764  MPZ      3'  TCAGTATAGCATTGGTT     4999          GCATAA
                                GACCAGTGCTG     GCTGA
                                ||||||||||     |||||
                                TTGGTTACGAT     TGACT
                                     A_____
GAM764  MTNR1A   3'  TTCAGCTGGCAGAGTTAGCATT 19893         ATA___
           GG                    CCAGTGCTGGC     AGCTGAA
                                ||||||||||     |||||||
                                GGTTACGATTG     TCGACTT
                                     AGACGG
GAM764  MYCBP    3'  TTAGGAATGATGGCACTGGTT  24697        GG  AAG
                                GACCAGTGCT  CAT   CTGA
                                ||||||||||  |||   ||||
                                TTGGTCACGG  GTA   GATT
                                     TA  AG_
GAM764  NAV2     3'  TTTGGTCCTGCTCAGTTTTGGT 60163       T   _   TAA  TG
           T                     GACCAG GCTG GCA   GC  AA
                                |||||| |||| |||   ||  ||
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                                TTGGTT TGAC CGT   TG  TT
                                   T   T   CC_  GT
GAM764  NCAM2    3'  TTTAGTTTATGTTTGTCTG   15807     T  TG
                                CAG GC  GCATAAGCTGAA
                                ||| ||  ||||||||||||
                                GTC TG  TGTATTTGATTT
                                  _  TT
GAM764  NEURL    3'  TTTGGTTTGTGGTTTTGG    14868     T  TGG     TG
                                CCAG GC   CATAAGC  AA
                                |||| ||   |||||||  ||
                                GGTT TG   GTGTTTG  TT
                                  T ___      GT
GAM764  NRG1     5'  TTCAGTTTGGGCTACTGGTT   25652       GCT   A
                                GACCAGT   GGC TAAGCTGAA
                                |||||||   ||| |||||||||
                                TTGGTCA   TCG GTTTGACTT
                                   ___  G
GAM764  NUP98    3'  TGGTTTGGTCCCTGGTT     32864       TGCT   A    TG
                                GACCAG    GGC TAAGC  A
                                ||||||    ||| |||||  |
                                TTGGTC    CTG GTTTG  T
                                   C___   _    GT
GAM764  OLFM1    3'  TTCAGTTTATGCGATGATTG   26557     GCTG
                                CAGT    GCATAAGCTGAA
                                ||||    ||||||||||||
                                GTTA    CGTATTTGACTT
                                  GTAG
GAM764  PCDHGA11 3'  TTCAACTATGCTGGTTTGGTT  49456       T  TG    A C
                                GACCAG GC  GCATA G TGAA
                                |||||| ||  ||||| | ||||
                                TTGGTT TG  CGTAT C ACTT
                                   _ GT    _ A
GAM764  PCSK1    3'  TGGCTTGAAGTATGGTT     4777       G   GGCA    TG
                                GACCA TGCT    TAAGC  A
                                ||||| ||||   |||||  |
                                TTGGT ATGA    GTTCG  T
                                  _   A___     GT
GAM764  PER2     3'  TGGCTTCTGGTGTGGTC     43049      G   TG CAT    TG
                                GACCA TGC  G   AAGC  A
                                ||||| |||  |  ||||  |
                                CTGGT GTG  C   TTCG  T
                                  _  GT ___    GT
GAM764  PER2     3'  TTCAGAAAATTTAATATTGGTC 43050        C   CATAAG
                                GACCAGTG TGG     CTGAA
                                |||||||| |||     |||||
                                CTGGTTAT ATT     GACTT
                                    A  TAAAA_
GAM764  PIGH     3'  TTCAGAAGGCCAGCATTG    15880          ATAAG
                                CAGTGCTGGC    CTGAA
                                ||||||||||    |||||
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                                GTTACGACCG    GACTT
                                      GAA__
GAM764  PIGN    3'  TCAGCTTTCAGCACTGGTT   24673          CAT     A
                                GACCAGTGCTGG   AAGCTGA
                                ||||||||||||  |||||||
                                TTGGTCACGACT   TTCGACT
                                      ___      A
GAM764  PPP2R5E  3'  TTCAGTACCTGACCAGTATTAG 20730     C      _  TAA
          TT                     GAC AGTGCTGG CA   GCTGAA
                                ||| |||||||| ||   ||||||
                                TTG TTATGACC GT   TGACTT
                                  A       A  CCA
GAM764  PRPS2   3'  GCAGTGCTTGTATTGGTT    10903         T    AA
                                GACCAGTGC GGCAT  GC
                                |||||||||  |||||  ||
                                TTGGTTATG TCGTG  CG
                                      T    A_
GAM764  PTPRK   3'  TTCAGCCTGTGGCCCAGCACTG 11125          __   A
          GTC                     GACCAGTGCTGG  CATA GCTGAA
                                ||||||||||||  ||||  ||||||
                                CTGGTCACGACC  GTGT CGACTT
                                      CG    C
GAM764  PTX3    3'  TCAGTTTAATGCTGTGT     11144    TG T    _
                                G  C GGCAT AAGCTGA
                                |  |  |||||  |||||||
                                T  G TCGTA TTTGACT
                                 GT _     A
GAM764  QPCT    3'  TTTAGTTTAGGATAATTGGTT  24837       GCTGGCA
                                GACCAGT      TAAGCTGAA
                                |||||||      |||||||||
                                TTGGTTA      ATTTGATTT
                                    ATAGG__
GAM764  RAB6A   3'  TCAGGCTGGTTTTGGTT     11199       T  TG  ATAAG
                                GACCAG GC  GC     CTGA
                                ||||||  ||  ||     ||||
                                TTGGTT TG  CG     GACT
                                   T  GT  _____
GAM764  RAD18   3'  TTTGGTTTGGTTTGGTTTGGTT 39399       T  TG CA    TG
                                GACCAG GC  G  TAAGC  AA
                                ||||||  ||  |  |||||  ||
                                TTGGTT TG  T  GTTTG  TT
                                   _  GT TG     GT
GAM764  RAD50   3'  TTCAGTCACATGGCATGGTT   56010      G    GCATAA
                                GACCA TGCTG     GCTGAA
                                |||||  |||||     ||||||
                                TTGGT ACGGT     TGACTT
                                   _    ACAC__
GAM764  RAD50   3'  TTCAGTCACATGGCATGGTT   19196      G    GCATAA
                                GACCA TGCTG     GCTGAA
                                |||||  |||||     ||||||
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                                TTGGT ACGGT     TGACTT
                                  _    ACAC__
GAM764  RALBP1   3'  TTACAAATGTCTCAGCATTGGT 22300          __   AAGCTGAA
           T                    GACCAGTGCTG  GCAT
                                ||||||||||  ||||
                                TTGGTTACGAC  TGTA
                                     TC    AACATT
GAM764  RANBP2L1 3'  TTTGGTTACACAGAACATTGGT 17317        __  GCATA  TG
           T                    GACCAGTG  CTG    AGC  AA
                                ||||||||  |||    |||  ||
                                TTGGTTAC  GAC    TTG  TT
                                   AA   ACA__   GT
GAM764  RB1      3'  TTTAAGTCAGTATGGTC     90917      G      A
                                GACCA TGCTGGC TAAG
                                ||||| ||||||| ||||
                                CTGGT ATGACTG ATTT
                                  _      A
GAM764  RDS      3'  TTTGGACACCCTGTCAGACGTT 4367       _     TAAG__ TG
           GGTC                   CCAGTG CTGGCA     C  AA
                                ||||||| ||||||     |  ||
                                GGTTGC GACTGT     G  TT
                                   A     CCCACA GT
GAM764  SERPINB9 3'  TTCAGTGCCACTTAGTATTG   14772        CATAA
                                CAGTGCTGG    GCTGAA
                                |||||||||    ||||||
                                GTTATGATT    TGACTT
                                     CACCG
GAM764  SIAT7D   3'  TGACCTTGTGCCAGTCCTGGTC 26950      TG       CTGAA
                                GACCAG  CTGGCATAAG
                                ||||||  ||||||||||
                                CTGGTC  GACCGTGTTC
                                   CT        CAGT
GAM764  SLC19A2  3'  TTTGGTTTTCATGTTGGCACTG 68983    C     TG   __   TG
           CTC                    GA CAGTGC  GCAT  AAGC  AA
                                || ||||||  ||||  ||||  ||
                                CT GTCACG  TGTA  TTTG  TT
                                 C     GT   CT   GT
GAM764  SLC5A1   3'  CGGGTGTCAGTGTGGTT    4428      G       AAG
                                GACCA TGCTGGCAT   CTG
                                ||||| |||||||||   |||
                                TTGGT GTGACTGTG   GGC
                                  _       ___
GAM764  SMURF1   3'  TTTAGCCTTTGGCTTTGGTC  92462      T  TG CATAA
                                GACCAG GC  G    GCTGAA
                                |||||| ||  |    ||||||
                                CTGGTT CG  T    CGATTT
                                   T  GT TC___
GAM764  SPAP1    3'  TTCAGCGCTTGATATTGGTC  47775       CT_   ATAA
                                GACCAGTG   GGC   GCTGAA
                                ||||||||   |||   ||||||
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                                CTGGTTAT  TCG   CGACTT
                                    AGT  ____
GAM764  SRGAP1   3'  TTGGAGTATAGCCAGTGTTGGT 72268      TG   _  AG TG A
            C                    GACCAG  CTGGC ATA  C  A
                                 ||||||  ||||| |||  |  |
                                 CTGGTT  GACCG TAT  G  T
                                    GT    A   GA GT
GAM764  STAU2    3'  TTCTGTTGCTAGTATTG    26911         TAA  T
                                 CAGTGCTGGCA   GC GAA
                                 ||||||||||   || |||
                                 GTTATGATCGT   TG CTT
                                       ___  T
GAM764  STK24    3'  TTTGGAATCGTGCCACTGCTGG 13119      GC    AAG_ TG
            TC                    GACCAGT  TGGCAT   C  AA
                                  |||||||  ||||||   |  ||
                                  CTGGTCG  ACCGTG   G  TT
                                     TC    CTAA GT
GAM764  TAF7     3'  TCAGTCTTCAGACTGGTC    18913       G   CATAA
                                 GACCAGT CTGG    GCTGA
                                 |||||||  ||||    |||||
                                 CTGGTCA GACT    TGACT
                                    _   TC___
GAM764  TCF7     3'  TTTAGTTCCTACTTTAGCCACT 12165      _   CA __
            GGTT                    CCAGTG CTGG  TA  AGCTGAA
                                    ||||||  ||||  ||  |||||||
                                    GGTCAC GATT  AT  TTGATTT
                                       C   TC  CC
GAM764  TEX15    3'  TGGTTTATGTTTGGTT     48391      TGCTG      TG
                                 GACCAG    GCATAAGC  A
                                 ||||||    ||||||||  |
                                 TTGGTT    TGTATTTG  T
                                    _____      GT
GAM764  TIA1     3'  TTCAGCTTGTGCACAATTCTG  41852     TGC  _
                                 CAG   TG GCATAAGCTGAA
                                 |||   || ||||||||||||
                                 GTC   AC CGTGTTCGACTT
                                   TTA  A
GAM764  TIA1     3'  TTCAGCTTGTGCACAATTCTG  42249     TGC  _
                                 CAG   TG GCATAAGCTGAA
                                 |||   || ||||||||||||
                                 GTC   AC CGTGTTCGACTT
                                   TTA  A
GAM764  TIMELESS 3'  TCAGCAGCAGTATTGG      14053        G ATAA
                                 CCAGTGCTG C    GCTGA
                                 |||||||||  |   |||||
                                 GGTTATGAC G    CGACT
                                      _ A___
GAM764  TRPM7    3'  TTCAGTGATGATATCACTGGTT 62132        C  G   AA
                                 GACCAGTG TG CAT  GCTGAA
                                 |||||||| || |||  ||||||
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                                TTGGTCAC AT GTA  TGACTT
                                     T  A   G_
GAM764  TRPS1    3'  TTTGGTTTTTCAGTACTG    26088         CAT    TG
                                CAGTGCTGG   AAGC  AA
                                |||||||||   ||||  ||
                                GTCATGACT   TTTG  TT
                                     T__    GT
GAM764  TXNRD1   3'  TTTAGTTTATTGTGTGCTGGTC 12463        TG TG  _
                                GACCAG  C  GCA TAAGCTGAA
                                ||||||  |  ||| |||||||||
                                CTGGTC  G  TGT ATTTGATTT
                                   GT __   T
GAM764  UBL3     3'  TTCAAATGGTCAGCGTTG    23035          ATAAGC
                                CAGTGCTGGC     TGAA
                                ||||||||||     ||||
                                GTTGCGACTG     ACTT
                                     GTAA__
GAM764  USP6     3'  TGTGATTTGTGTTATACTGGTT 91150         C        CTGAA
                                GACCAGTG TGGCATAAG
                                |||||||| |||||||||
                                TTGGTCAT ATTGTGTTT
                                     _        AGTGTG
GAM764  VDR      3'  TTTAGCTGCAGAACTGTATTGG 4576          TGGCATA_
           TC                     GACCAGTGC       AGCTGAA
                                |||||||||       |||||||
                                CTGGTTATG       TCGATTT
                                     TCAAGACG
GAM764  YES1     3'  TTCATGCAAGTTGGCAGTGGTT 18359       G   TG  ATAA  _
                                GACCA TGC  GC    GC TGAA
                                |||||  |||  ||    || ||||
                                TTGGT ACG  TG    CG ACTT
                                   G   GT  AA__  T
GAM764  ZNF265   3'  TTAGTTTGTTTTCTGGTT    18399       TGCT    TA
                                GACCAG   GGCA  AGCTGA
                                ||||||   ||||  ||||||
                                TTGGTC   TTGT  TTGATT
                                   TT__    __
GAM764  ACAS2    3'  TTGTGCCAGATGCCAGTACTG  37934           AA_  TGAA
                                CAGTGCTGGCAT   GC
                                ||||||||||||   ||
                                GTCATGACCGTA   CG
                                     GAC  TGTTT
GAM764  ACAS2    3'  TTGTGCCAGATGCCAGTACTG  57704           AA_  TGAA
                                CAGTGCTGGCAT   GC
                                ||||||||||||   ||
                                GTCATGACCGTA   CG
                                     GAC  TGTTT
GAM764  AMOT     3'  TTTGGTTTAAAATGTATGTGGT 55732       _   TGGCA    TG
           C                     GACCA GTGC    TAAGC  AA
                                |||||  ||||    |||||  ||
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                                CTGGT TATG    ATTTG  TT
                                  G   TAAA_    GT
GAM764  BIRC2    5'  TTTAGCTATCAAACAGTACTG  67205        GCATA_
                                CAGTGCTG     AGCTGAA
                                ||||||||     |||||||
                                GTCATGAC     TCGATTT
                                    AAACTA
GAM764  BM-002   3'  TTCAGTTTACATGCATTATTGG 33528        CTG   __
          TT                     GACCAGTG   GCA  TAAGCTGAA
                                ||||||||   |||  |||||||||
                                TTGGTTAT   CGT  ATTTGACTT
                                    TA_   AC
GAM764  BMF      3'  TCAGCTTGTGTTCTGC      53164    T_
                                GC  GGCATAAGCTGA
                                ||  ||||||||||||
                                CG  TTGTGTTCGACT
                                 TC
GAM764  BS69     3'  TTCAGCTTAATTTACTGTTC  21769    C    CTGGCA
                                GA CAGTG     TAAGCTGAA
                                || |||||     |||||||||
                                CT GTCAT     ATTCGACTT
                                 T    TTA___
GAM764  C19orf7  3'  TTCAGCCACCAGTGTTGG    61133     TG   CATAA
                                CCAG  CTGG    GCTGAA
                                ||||  ||||    ||||||
                                GGTT  GACC    CGACTT
                                  GT   AC___
GAM764  C20orf164 3'  TTAGCTGAAGCATTGG      79480        GGCATA
                                CCAGTGCT     AGCTGA
                                ||||||||     ||||||
                                GGTTACGA     TCGATT
                                    AG____
GAM764  CGGBP1   3'  TTTAGCTTCTGGTCAGCACTG  13366         AT_
                                CAGTGCTGGC   AAGCTGAA
                                ||||||||||   ||||||||
                                GTCACGACTG   TTCGATTT
                                     GTC
GAM764  COLEC12  3'  TTCGGCTTGTGCTCTGCAGTC  47877    CAG   T_
                                GAC   TGC  GGCATAAGCTGAA
                                |||   |||  ||||||||||||
                                CTG   ACG  TCGTGTTCGGCTT
                                  ___   TC
GAM764  DKFZp564A176 5'  TTCAGTAGCCCCTAGCATTGG  49974          CATAA
                                CCAGTGCTGG    GCTGAA
                                ||||||||||    ||||||
                                GGTTACGATC    TGACTT
                                     CCCGA
GAM764  DKFZP586D0623 3'  TTCAGTTTATGTTAGAC     71978    G
                                GT CTGGCATAAGCTGAA
                                || ||||||||||||||
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                                CA GATTGTATTTGACTT
                                  _
GAM764  DKFZp761D0614 3'  TTGTGTTGGCTTGGTC      87558       T  TG
                                GACCAG GC  GCATAA
                                |||||| ||  ||||||
                                CTGGTT CG  TGTGTT
                                   _ GT
GAM764  DMRTB1    3'  TTCAGCCATTATGGGCACTGGT 66247          GG    __
          T                      GACCAGTGCT  CATAA  GCTGAA
                                |||||||||| |||||  ||||||
                                TTGGTCACGG  GTATT  CGACTT
                                     __     AC
GAM764  FLJ10330  3'  TTTGGCATGGTTGCCATGTTGG 36033       GT C     TAA__  TG
          TT                     GACCA  G TGGCA     GC  AA
                                ||||| | |||||     ||  ||
                                TTGGT  T ACCGT     CG  TT
                                   TG _     TGGTA  GT
GAM764  FLJ10701  3'  GTTAGATGTACAGCATTGGTT  36431          _    AAG    A
                                GACCAGTGCTG GCAT   CTGA
                                |||||||||| ||||   ||||
                                TTGGTTACGAC TGTA   GATT
                                      A    ___    GT
GAM764  FLJ10803  3'  TTTGGTTTATTGCAGTGGTC   36673       G   TGGC     TG
                                GACCA TGC    ATAAGC  AA
                                ||||| |||    ||||||  ||
                                CTGGT ACG    TATTTG  TT
                                   G   T___     GT
GAM764  FLJ10971  3'  TTTAGCTTGTGTATATAATTGT 36932     _    GCTG_
          GTT                     GAC CAGT     GCATAAGCTGAA
                                ||| ||||     ||||||||||||
                                TTG GTTA     TGTGTTCGATTT
                                  T    ATATA
GAM764  FLJ12587  3'  TCAGCTTTGCAGTGGTT     42499       G   TGGCAT
                                GACCA TGC     AAGCTGA
                                ||||| |||     |||||||
                                TTGGT ACG     TTCGACT
                                   G   T_____
GAM764  FLJ13153  5'  TGGCTGTCAGTGCTGGTC    45559       TG     TAA  TG
                                GACCAG  CTGGCA   GC  A
                                ||||||  ||||||   ||  |
                                CTGGTC  GACTGT   CG  T
                                   GT     ___  GT
GAM764  FLJ14075  3'  TTCGGCTTGTTTATGTATTAGT 46051     C     TGGC
          T                      GAC AGTGC    ATAAGCTGAA
                                ||| |||||    ||||||||||
                                TTG TTATG    TGTTCGGCTT
                                  A    TATT
GAM764  FLJ20070  5'  TCGGCGACGCCGCTGGTC    34477        GCT   ATAA
                                GACCAGT   GGC    GCTGA
                                |||||||   |||    |||||
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                                CTGGTCG  CCG   CGGCT
                                   ___  CAG_
GAM764  FLJ20701  3'  TTCAGCAAAGGCAGCATTGGTC 35592         G ATAA
                                GACCAGTGCTG C   GCTGAA
                                |||||||||| |   ||||||
                                CTGGTTACGAC G   CGACTT
                                      _ GAAA
GAM764  FOXN4     3'  TTCAGCTTGGACACACTGG   75574      C  GCA
                                CCAGTG TG   TAAGCTGAA
                                |||||| ||   |||||||||
                                GGTCAC AC   GTTCGACTT
                                   _ AG_
GAM764  GL004     3'  TTAGTTTTGCACTTGGTT    65996      _   TGGCAT
                                GACCA GTGC     AAGCTGA
                                ||||| ||||     |||||||
                                TTGGT CACG     TTTGATT
                                   T   T_____
GAM764  GRWD      3'  TTTAGAGGCTGGTGCTGTGTC  48974     _  TG TG  ATAAG
                                GAC CAG  C  GC    CTGAA
                                ||| |||  |  ||    |||||
                                CTG GTC  G  CG    GATTT
                                  T  GT GT  GA___
GAM764  GW112     3'  TTCAACTGAAGCCAGCACTGGT 21194          ATA  C
           T                     GACCAGTGCTGGC   AG TGAA
                                 ||||||||||||   || ||||
                                 TTGGTCACGACCG   TC ACTT
                                       AAG  A
GAM764  IRAK3     3'  TTTAGCTTGCTTGCACGGGTT  23245     A   T   TA
                                GACC GTGC GGCA  AGCTGAA
                                |||| |||| ||||  |||||||
                                TTGG CACG TCGT  TCGATTT
                                  G   T   __
GAM764  KIAA0057  3'  TCAGCCCCATGCTGGTC     24441       C   CATAA
                                GACCAGTG TGG    GCTGA
                                |||||||| |||    |||||
                                CTGGTCGT ACC    CGACT
                                   _   C____
GAM764  KIAA0205  3'  TTTGGTTTGGGTACTGGTT   29594        GGCA    TG
                                GACCAGTGCT   TAAGC  AA
                                ||||||||||   |||||  ||
                                TTGGTCATGG   GTTTG  TT
                                     ____    GT
GAM764  KIAA0212  3'  TTTGGTTTGGGGCACTGG    27947       GGCA    TG
                                CCAGTGCT   TAAGC  AA
                                ||||||||   |||||  ||
                                GGTCACGG   GTTTG  TT
                                   G___    GT
GAM764  KIAA0336  3'  TTTGGTTACACAGAACATTGGT 27592       __  GCATA   TG
           T                     GACCAGTG  CTG    AGC  AA
                                 ||||||||  |||    |||  ||
```

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                                TTGGTTAC  GAC    TTG  TT
                                    AA   ACA__   GT
GAM764  KIAA0410 3' TTAGCTTAGTGTAGGTT    28781     A TG   GCATA
                                GACC G  CTG    AGCTGA
                                |||| |  |||    ||||||
                                TTGG T  GAT    TCGATT
                                  A GT  _____
GAM764  KIAA0459 3' TTTAGTAATTTTACTACTGGTT 61013        C   CATAA
                                GACCAGTG TGG    GCTGAA
                                |||||||| |||    ||||||
                                TTGGTCAT ATT    TGATTT
                                    C   TTAA_
GAM764  KIAA0534 5' TTCAGTTCTCTTAGCATTG   71438        CATA
                                CAGTGCTGG   AGCTGAA
                                |||||||||   |||||||
                                GTTACGATT   TTGACTT
                                     CTC_
GAM764  KIAA0630 3' TCAGCACTATATTGGTC     89397        C   CATAA
                                GACCAGTG TGG    GCTGA
                                |||||||| |||    |||||
                                CTGGTTAT ATC    CGACT
                                    _   A____
GAM764  KIAA0801 5' GTGTTTAGCGCTGGTC      29151          _
                                GACCAGTGCTGG CAT
                                |||||||||||| |||
                                CTGGTCGCGATT GTG
                                       T
GAM764  KIAA0923 3' TCAGCTTGATGCATGGTC    25838      G   TGGCA
                                GACCA TGC    TAAGCTGA
                                ||||| |||    ||||||||
                                CTGGT ACG    GTTCGACT
                                  _   TA___
GAM764  KIAA1000 3' TTCAGCTTTGCAAAGTACTGG  65281        G_   T
                                CCAGTGCT  GCA AAGCTGAA
                                ||||||||  ||| ||||||||
                                GGTCATGA  CGT TTCGACTT
                                    AA  _
GAM764  KIAA1068 3' TTCAGCTGCCACCGGCACTG   31044        CATA
                                CAGTGCTGG   AGCTGAA
                                |||||||||   |||||||
                                GTCACGGCC   TCGACTT
                                     ACCG
GAM764  KIAA1089 3' TGGCCTGTGCCAGCACGGTC   68848     A         A
                                GACC GTGCTGGCATA GCTG
                                |||| |||||||||| ||||
                                CTGG CACGACCGTGT CGGT
                                  _         C
GAM764  KIAA1189 3' TATGCTAACGCTGGTC      72047        C
                                GACCAGTG TGGCATA
                                |||||||| |||||||
```

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                                CTGGTCGC ATCGTAT
                                    A
GAM764  KIAA1383  3'  TCAGTTTGTTCAATGGTT    69785      GTGC   C
                                GACCA    TGG ATAAGCTGA
                                |||||    ||| |||||||||
                                TTGGT    ACT TGTTTGACT
                                  A___   _
GAM764  KIAA1467  3'  TTTAGCTTGTGTTAGTAAAAGG 71620    AG_
                                CC   TGCTGGCATAAGCTGAA
                                ||   ||||||||||||||||
                                GG   ATGATTGTGTTCGATTT
                                 AAA
GAM764  KIAA1508  5'  TTGCTCTGTGCCAGTGCTGG   61895     TG      _   TGAA
                                CCAG  CTGGCATA AGC
                                ||||  |||||||| |||
                                GGTC  GACCGTGT TCG
                                  GT       C   TT
GAM764  KIAA1608  3'  TTTAGTTTTGTTGGTTGGTT   45691      GT  TG   T
                                GACCA  GC  GCA AAGCTGAA
                                |||||  ||  ||| ||||||||
                                TTGGT  TG  TGT TTTGATTT
                                  __ GT  _
GAM764  KIAA1813  5'  TCAGACCAGCATTGG       70308          CATAAG
                                CCAGTGCTGG     CTGA
                                ||||||||||     ||||
                                GGTTACGACC     GACT
                                   A_____
GAM764  MGC12217  3'  TTTAGCAGCAGACATTGGTT   51314        _   G ATAA
                                GACCAGTG CTG C    GCTGAA
                                |||||||| ||| |    ||||||
                                TTGGTTAC GAC G    CGATTT
                                   A   _ A___
GAM764  MGC12972  3'  TTCAGCTCCGGAGCATTGG    51079        __  CATA
                                CCAGTGCT  GG    AGCTGAA
                                ||||||||  ||    |||||||
                                GGTTACGA  CC    TCGACTT
                                   GG  ____
GAM764  MGC3047   3'  TGGCTTCTGTACTGG       50365        T  CAT    TG
                                CCAGTGC GG   AAGC  A
                                ||||||| ||   ||||  |
                                GGTCATG TC   TTCG  T
                                  _ ___    GT
GAM764  MGC4161   3'  TTTGGTTTGTGTTGCTGTTC   44192    C    GCT       TG
                                GA CAGT   GGCATAAGC  AA
                                || ||||   |||||||||  ||
                                CT GTCG   TTGTGTTTG  TT
                                 T   ___        GT
GAM764  MGC5469   3'  TTCATGTGGTTAGTTTGGTC   50398       T     ATAAGC
                                GACCAG GCTGGC     TGAA
                                |||||| ||||||     ||||
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                                CTGGTT TGATTG     ACTT
                                   _     GTGT__
GAM764  NPEPL1   3'  TTTGGTTTGTCTTTCTGGTC  45093      TGCT  C     TG
                                GACCAG   GG ATAAGC  AA
                                ||||||   || ||||||  ||
                                CTGGTC   TC TGTTTG  TT
                                   TT__ _     GT
GAM764  ORCTL3   3'  AGCTGCTGCTGGTT      14917       GCT   TAA
                                GACCAGT   GGCA   GCT
                                |||||||   ||||   |||
                                TTGGTCG   TCGT   CGA
                                   ___   ___
GAM764  PANK     3'  TATGTAAGCGCTGGTC     56335         G
                                GACCAGTGCT GCATA
                                |||||||||| |||||
                                CTGGTCGCGA TGTAT
                                      A
GAM764  PDCD7    3'  TTTGGTTCTGTTTTGGTTTGGT 72145      T  TG C  _  TG
           T                     GACCAG GC  G ATA AGC  AA
                                |||||| ||  | ||| |||  ||
                                TTGGTT TG  T TGT TTG  TT
                                   _ GT T   C   GT
GAM764  PIGM     3'  TTTAAGCCAGTATTTGTT    59048     C       A
                                GAC AGTGCTGGC TAAG
                                ||| |||||||| ||||
                                TTG TTATGACCG ATTT
                                  T       A
GAM764  PPIL3    5'  TGTGTTGCTACTGGTT      55662       _  T
                                GACCAGT GC GGCATA
                                ||||||| || ||||||
                                TTGGTCA CG TTGTGT
                                   T _
GAM764  PRO0800  3'  TGGCTTTTGTCTGGTT      37743      TGCTG  T   TG
                                GACCAG    GCA AAGC  A
                                ||||||    ||| ||||  |
                                TTGGTC    TGT TTCG  T
                                   _____  T   GT
GAM764  PRO2831  5'  TCAGTATGGTTGCTGGTC    37602      GCT   ATAA
                                GACCAGT   GGC   GCTGA
                                |||||||   |||   |||||
                                CTGGTCG   TTG   TGACT
                                   ___  GTA_
GAM764  PSMA4    5'  TTCGGTGAGCGGTGGTGGTT  10942     G    G ATAA
                                GACCA TGCTG C   GCTGAA
                                ||||| ||||| |   ||||||
                                TTGGT GTGGC G   TGGCTT
                                  G    _ AG__
GAM764  RAB6C    3'  TCAGGCTGGTTTTGGTT     49571      T  TG  ATAAG
                                GACCAG GC  GC    CTGA
                                |||||| ||  ||    ||||
```

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                                TTGGTT TG  CG    GACT
                                   T  GT  _____
GAM764  RAI17    3'  TTTAGCTTCAGTGTACTAGTC  91288     C    TG  AT
                                GAC AGTGC  GC  AAGCTGAA
                                ||| |||||  ||  ||||||||
                                CTG TCATG  TG  TTCGATTT
                                  A    __  AC
GAM764  RGS18    3'  TTGGGCATCTGCCACATTGGTT 55395        C    TAA  G
                                GACCAGTG TGGCA   GCT AA
                                |||||||| |||||   ||| ||
                                TTGGTTAC ACCGT   CGG TT
                                     _    CTA   G
GAM764  SAE1     3'  TCAGGGCTATGTTGGTC     18534      GT C    ATAAG
                                GACCA  G TGGC    CTGA
                                |||||  | ||||    ||||
                                CTGGT  T ATCG    GACT
                                   TG _   G____
GAM764  TBCC     3'  TTCAGCTTCCCAAAGTGCTGG  12144     TG  GGCAT
                                CCAG  CT    AAGCTGAA
                                ||||  ||    ||||||||
                                GGTC  GA    TTCGACTT
                                  GT  AACCC
GAM764  TERA     3'  TGGCTGCAGTATTGGT     41137         G  TAA  TG
                                ACCAGTGCTG CA   GC  A
                                |||||||||| ||   ||  |
                                TGGTTATGAC GT   CG  T
                                     _ ___  GT
GAM764  TRIM4    3'  TTTGGTTTTCTGTTCATGTGTT 52258     TG _   _ T_   TG
           GGTT                   CCAG  C TGG CA  AAGC  AA
                                ||||  | ||| ||  ||||  ||
                                GGTT  G ACT GT  TTTG  TT
                                  GT T   T  CT    GT
GAM764  TSPAN-2  3'  TGGCTCATTACTGGTT     19167        C  GCATA   TG
                                GACCAGTG TG    AGC  A
                                |||||||| ||    |||  |
                                TTGGTCAT AC    TCG  T
                                     T _____   GT
GAM764  WBP4     3'  TTTAGTTTGAACCAGGCATTGT 23233     _     _  CA
           GTT                    GAC CAGTGC TGG  TAAGCTGAA
                                ||| |||||| |||  |||||||||
                                TTG GTTACG ACC  GTTTGATTT
                                  T     G   AA
GAM764  X123     5'  TTCAGCCCTGTAGTGCTGTTC  69926    C   TG   G  TAA
                                GA CAG  CTG CA   GCTGAA
                                || |||  ||| ||   ||||||
                                CT GTC  GAT GT   CGACTT
                                 T  GT   _  CC_
GAM764  ZNF340   5'  TTAGCTTGTGCTCAAGT     84565     __
                                GCT  GGCATAAGCTGA
                                |||  ||||||||||||
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                                TGA  TCGTGTTCGATT
                                  AC
GAM764   LOC144486 3'  TTTAGCAAGTACAGTGCTG   83089    TG   GC  AA
                                CAG  CTG  AT  GCTGAA
                                |||  |||  ||  |||||||
                                GTC  GAC  TG  CGATTT
                                  GT   A_  AA
GAM764   LOC147077 3'  TTTAGGGTGATCAGTGCTGG   78251     TG   _  AAG
                                CCAG  CTGG CAT   CTGAA
                                ||||  |||| |||   |||||
                                GGTC  GACT GTG   GATTT
                                  GT    A   G__
GAM764   LOC148734 5'  TTCAGCTTTTGTGCTCTGGTT  78959      T  TG   T
                                GACCAG GC  GCA AAGCTGAA
                                ||||||| ||  ||| ||||||||
                                TTGGTC CG  TGT TTCGACTT
                                    T  __   T
GAM764   LOC150311 5'  TTCAGCCATGGTAGTGCTGGTT 79760       TG   G   AA
                                GACCAG  CTG CAT  GCTGAA
                                ||||||  ||| |||  ||||||
                                TTGGTC  GAT GTA  CGACTT
                                    GT   G   C_
GAM764   LOC150406 3'  TTGTGTGGGCATTGGTT     79860          G
                                GACCAGTGCT GCATAA
                                |||||||||| ||||||
                                TTGGTTACGG TGTGTT
                                     G
GAM764   LOC150862 3'  TGTGCCATACTGGTC       80021         C
                                GACCAGTG TGGCATA
                                |||||||| |||||||
                                CTGGTCAT ACCGTGT
                                     _
GAM764   LOC151201 5'  TTTAGTTTATACCATTGG    85299      TGC   C
                                CCAG   TGG ATAAGCTGAA
                                ||||   ||| ||||||||||
                                GGTT   ACC TATTTGATTT
                                  ___   A
GAM764   LOC151518 3'  TCAGCTTACTATTGGTT     85435        CTGGCA
                                GACCAGTG     TAAGCTGA
                                ||||||||     ||||||||
                                TTGGTTAT     ATTCGACT
                                    C_____
GAM764   LOC155038 3'  GCGTGTTATGCTGGTT      81258         C     AA
                                GACCAGTG TGGCAT  GC
                                |||||||| ||||||  ||
                                TTGGTCGT ATTGTG  CG
                                     _     __
GAM764   LOC157660 3'  TTTAGTTTATGCCTTGTGTT   86514    TG T_
                                AG  C  GGCATAAGCTGAA
                                ||  |  ||||||||||||
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                                TT  G  CCGTATTTGATTT
                                 GT TT
GAM764   LOC158187 3'  TTTGGCTTGTGCTAGAAC    86698    G         TG
                                GT CTGGCATAAGC  AA
                                || ||||||||||  ||
                                CA GATCGTGTTCG  TT
                                 A          GT
GAM764   LOC158332 3'  GCTGTGCTAGTATCGGTT    81889     A         A
                                GACC GTGCTGGCATA GC
                                |||| |||||||||| ||
                                TTGG TATGATCGTGT CG
                                  C         _
GAM764   LOC158337 5'  TTAGCTGACAGCACTGG     86775          GCATA
                                CCAGTGCTG    AGCTGA
                                |||||||||    ||||||
                                GGTCACGAC    TCGATT
                                      AG___
GAM764   LOC163882 3'  TTTGGTTTACACTTGTTGGGTC 82170      AGT  T  CA    TG
                                GACC   GC GG  TAAGC  AA
                                ||||   || ||  |||||  ||
                                CTGG   TG TC  ATTTG  TT
                                  GT_  T  AC    GT
GAM764   LOC166754 5'  TTTGTAGCCAGCGCTGG     82662          _
                                CCAGTGCTGGC ATAAG
                                |||||||||| |||||
                                GGTCGCGACCG TGTTT
                                       A
GAM764   LOC168448 3'  TTCAGCTTGTGACCCTGTGTC  82701     _   TGCT  _
                                GAC CAG    GG CATAAGCTGAA
                                ||| |||    || ||||||||||
                                CTG GTC    CC GTGTTCGACTT
                                  T  _____  A
GAM764   LOC199692 3'  TTGTGTTATGTCAGTGTTGGT  59244       TG        GCTGAA
                                ACCAG  CTGGCATAA
                                |||||  |||||||||
                                TGGTT  GACTGTATT
                                   GT        GTGTT
GAM764   LOC200734 3'  TTTGGTTTGTGAAGGCATCGGT 88867      A    GG      TG
           T                     GACC GTGCT  CATAAGC  AA
                                ||||  |||||  |||||||  ||
                                TTGG TACGG  GTGTTTG  TT
                                  C     AA      GT
GAM764   LOC201965 3'  TTTGTGGTTGTATTGGTT    89116          TGG
                                GACCAGTGC   CATAAG
                                |||||||||   ||||||
                                TTGGTTATG   GTGTTT
                                      TTG
GAM764   LOC220692 3'  TTTGGTTACACAGAACATTGGT 91224         __   GCATA   TG
           T                     GACCAGTG  CTG    AGC  AA
                                ||||||||  |||    |||  ||
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                                TTGGTTAC  GAC    TTG  TT
                                    AA   ACA__   GT
GAM764   LOC221596 3'  TTCAGTGATTGGTTAGCACTTG 91985     C       ATAA_
           TT                    GAC AGTGCTGGC     GCTGAA
                                ||| |||||||||     ||||||
                                TTG TCACGATTG     TGACTT
                                  T       GTTAG
GAM764   LOC221830 3'  TTTAGTACCAGACATAGTGCTG 92515       TG   GCATAA__
           GTC                   GACCAG  CTG       GCTGAA
                                ||||||  |||       ||||||
                                CTGGTC  GAT       TGATTT
                                   GT   ACAGACCA
GAM764   LOC221882 3'  TTTGTGTTTGCTTGGTGCTGGT 92503       TG   _   TAA  TGAA
           T                     GACCAG  CTG GCA   GC
                                ||||||  ||| |||   ||
                                TTGGTC  GGT CGT   TG
                                   GT   T   TTG  TTT
GAM764   LOC221975 5'  TTCGTCCGGGTGCCAGCGCTGG 92611           AAGC_
                                CCAGTGCTGGCAT    TGAA
                                ||||||||||||    ||||
                                GGTCGCGACCGTG    GCTT
                                      GGCCT
GAM764   LOC253891 3'  TTCCACGTGTGTTGTGTTGGTT 94418       TG T     AGCT
                                GACCAG  C GGCATA    GAA
                                ||||||  | ||||||    |||
                                TTGGTT  G TTGTGT    CTT
                                   GT _     GCAC
GAM764   LOC254251 3'  TTTGGTTTAAATGTGCTGGTT  95915       TG TGGCA    TG
                                GACCAG  C    TAAGC  AA
                                ||||||  |    |||||  ||
                                TTGGTC  G    ATTTG  TT
                                   GT TAA__    GT
GAM764   LOC255242 3'  TTCATGTGGTTAGTTTGGTC   95930       T     ATAAGC
                                GACCAG GCTGGC     TGAA
                                |||||| ||||||     ||||
                                CTGGTT TGATTG     ACTT
                                   _     GTGT__
GAM764   LOC255870 5'  TTTGGCAAGGCATGTTGGTT   94660      __    GGCATAA  TG
                                GACCA  GTGCT      GC  AA
                                |||||  |||||      ||  ||
                                TTGGT  TACGG      CG  TT
                                   TG    AA_____  GT
GAM764   LOC63920  5'  TCAGTTAGCCACTGGTT     42025       GCT   ATA
                                GACCAGT   GGC   AGCTGA
                                |||||||   |||   ||||||
                                TTGGTCA   CCG   TTGACT
                                    ___   A__
GAM764   LOC84570  5'  TTCGGCTTCGCGAGTAGCATTG 50713         ___  AT
           GTT                    ACCAGTGCTG   GC  AAGCTGAA
                                ||||||||||   ||  ||||||||
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                                TGGTTACGAT  CG  TTCGGCTT
                                     GAG  C_
GAM764  LOC90826  5'  TTTGGTTTGTGCTCCAGC   64096     __      TG
                                GCTG  GCATAAGC  AA
                                ||||  ||||||||  ||
                                CGAC  CGTGTTTG  TT
                                  CT       GT
GAM764  LOC91694  3'  GCACATCTAGTGCTGGTT   66962      TG   C  AA
                                GACCAG  CTGG AT  GC
                                ||||||  |||| ||  ||
                                TTGGTC  GATC TA  CG
                                   GT   _  CA
GAM765  BN51T     3'  GCACAGTGACCTTCCTGCA   87495        A   _  A
                                TGCAGGAAG GTCG TG GC
                                ||||||||| |||| || ||
                                ACGTCCTTC CAGT AC CG
                                     _   G  A
GAM765  FZD5      3'  ATGGTGCTGTTGCCCCCTCCCG 60060    A   AGAGT  TG
          C                      GC GGA    CG  AGCACCAT
                                || |||    ||  ||||||||
                                CG CCT    GT  TCGTGGTA
                                 C  CCCCC  TG
GAM765  GJA1      3'  CACTTTTCTTCTTGCA      3900           TC
                                TGCAGGAAGAG  GTG
                                ||||||||||  |||
                                ACGTTCTTCTT  CAC
                                      TT
GAM765  MADD      3'  ATGATGCTCGTGTGTCCTCTGC 13462       AA  GT      C
          A                     TGCAGG  GA  CGTGAGCA CAT
                                ||||||  ||  |||||||| |||
                                ACGTCT  CT  GTGCTCGT GTA
                                   C_  GT       A
GAM765  MADD      3'  ATGATGCTCGTGTGTCCTCTGC 55330       AA  GT      C
          A                     TGCAGG  GA  CGTGAGCA CAT
                                ||||||  ||  |||||||| |||
                                ACGTCT  CT  GTGCTCGT GTA
                                   C_  GT       A
GAM765  MADD      3'  ATGATGCTCGTGTGTCCTCTGC 55337       AA  GT      C
          A                     TGCAGG  GA  CGTGAGCA CAT
                                ||||||  ||  |||||||| |||
                                ACGTCT  CT  GTGCTCGT GTA
                                   C_  GT       A
GAM765  MADD      3'  ATGATGCTCGTGTGTCCTCTGC 55342       AA  GT      C
          A                     TGCAGG  GA  CGTGAGCA CAT
                                ||||||  ||  |||||||| |||
                                ACGTCT  CT  GTGCTCGT GTA
                                   C_  GT       A
GAM765  MADD      3'  ATGATGCTCGTGTGTCCTCTGC 55347       AA  GT      C
          A                     TGCAGG  GA  CGTGAGCA CAT
                                ||||||  ||  |||||||| |||
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                                ACGTCT  CT  GTGCTCGT GTA
                                   C_  GT       A
GAM765  MADD     3'  ATGATGCTCGTGTGTCCTCTGC 55353       AA  GT      C
            A                    TGCAGG  GA  CGTGAGCA CAT
                                ||||||  ||  |||||||| |||
                                ACGTCT  CT  GTGCTCGT GTA
                                   C_  GT       A
GAM765  MYCBP    3'  GTGCTTTTCTCCCTCA     24696    C   A   TCGT
                                TG AGG AGAG    GAGCAC
                                || ||| ||||    ||||||
                                AC TCC TCTT    TTCGTG
                                 _   C   ____
GAM765  PTPN1    3'  ATGGTGCTCACGACTCTTCCTG 11046
            CA                    TGCAGGAAGAGTCGTGAGCACCAT
                                ||||||||||||||||||||||||||
                                ACGTCCTTCTCAGCACTCGTGGTA

GAM765  SOX13    3'  ATGGTGCTCCCCTTCCTGC    19079        AGTCGT
                                GCAGGAAG     GAGCACCAT
                                ||||||||     |||||||||
                                CGTCCTTC     CTCGTGGTA
                                    CC____
GAM765  DKFZp547C176 3'  GCCAAACTGTTCCTGCA     67225        G   CG  A
                                TGCAGGAA AGT  TG GC
                                |||||||| |||  || ||
                                ACGTCCTT TCA  AC CG
                                    G   A_  _
GAM765  DKFZp547M236 5'  GCACAGTCGCTCTTCCTGCA   38036          CG_  A
                                TGCAGGAAGAGT   TG GC
                                ||||||||||||   || ||
                                ACGTCCTTCTCG   AC CG
                                      CTG  A
GAM765  FLJ00024  3'  GGTGCTCAGGGGGCCCCTG    63764      AAGAG  G
                                CAGG     TC TGAGCACC
                                ||||     || ||||||||
                                GTCC     GG ACTCGTGG
                                  CCGG_  G
GAM765  FLJ12443  3'  GCTGACCTTCCTGCA       45729         A   GTG
                                TGCAGGAAG GTC   AGC
                                ||||||||| |||   |||
                                ACGTCCTTC CAG   TCG
                                          _   ____
GAM765  FLJ31300  3'  GCACACACCCTTCCTGCA     58285         A  C   A
                                TGCAGGAAG GT GTG GC
                                ||||||||| || ||| ||
                                ACGTCCTTC CA CAC CG
                                    C  _   A
GAM765  FLJ32468  3'  GCTCAGACTCTTCCCCCA     59044     CA       G
                                TG  GGAAGAGTC TGAGC
                                ||  ||||||||| |||||
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                                AC  CCTTCTCAG ACTCG
                                 CC       _
GAM765  KIAA1229  3'  GTGCCCTGCTTACCTGCA    62068      AA   CGTGA
                                TGCAGG  GAGT    GCAC
                                ||||||  ||||    ||||
                                ACGTCC  TTCG    CGTG
                                   A_   TCC__
GAM765  KIAA1486  5'  ATGGTGCTGGATTACTCCTACA 67377    C   AG   GTG
                                TG AGGA  AGTC   AGCACCAT
                                || ||||  ||||  ||||||||
                                AC TCCT  TTAG   TCGTGGTA
                                 A   CA   G__
GAM765  KIAA1649  3'  ATGGTAAATATCCTCCCTGCA  66974      AA  TC  AGC
                                TGCAGG  GAG  GTG   ACCAT
                                ||||||  |||  |||   |||||
                                ACGTCC  CTC  TAT   TGGTA
                                   __   C_   AAA
GAM765  KIAA1649  3'  ATGGTAAATATCCTCCCTGCA  50245      AA  TC  AGC
                                TGCAGG  GAG  GTG   ACCAT
                                ||||||  |||  |||   |||||
                                ACGTCC  CTC  TAT   TGGTA
                                   __   C_   AAA
GAM765  MGC15875  5'  GCTCATCAGCTCTTCCTGCA  51909          C_
                                TGCAGGAAGAGT  GTGAGC
                                ||||||||||||  ||||||
                                ACGTCCTTCTCG  TACTCG
                                      AC
GAM765  PNPASE    3'  ACAGATCTCTTCCTACA    70869    C      _ _
                                TG AGGAAGAG TC GT
                                || |||||||| || ||
                                AC TCCTTCTC AG CA
                                 A       T  A
GAM765  PRMT6     3'  GGTACTTCTTCCTCA      36271    C     GTCGTG  C
                                TG AGGAAGA     AG ACC
                                || |||||||     || |||
                                AC TCCTTCT     TC TGG
                                 _     _______  A
GAM765  RABEX5    3'  TGGTACCACTCTTCC      27190        C  GAGC
                                GGAAGAGT GT    ACCA
                                ||||||||  ||    ||||
                                CCTTCTCA CA    TGGT
                                    C  ____
GAM765  UBE2G1    3'  TGGCACTGTTTTTCCTGCA   12487          TC   AGCA
                                TGCAGGAAGAG  GTG   CCA
                                ||||||||||  |||   |||
                                ACGTCCTTTTT  CAC   GGT
                                      GT  ____
GAM765  LOC144347 3'  CACCTTACTCCTTCCTGC    76812        _  C__
                                GCAGGAAG AGT   GTG
                                ||||||||  |||   |||
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                                CGTCCTTC TCA   CAC
                                     C   TTC
GAM765  LOC149668 5'  GCTGAACACCTCTTCCTACA  84543    C       TC  G_
                                TG AGGAAGAG  GT  AGC
                                || ||||||||  ||  |||
                                AC TCCTTCTC  CA  TCG
                                 A       CA  AG
GAM765  LOC150538 3'  ATGGCACCCTGTCTTCCTGTA  79931          GTC_   AGCA
                                TGCAGGAAGA    GTG    CCAT
                                ||||||||||    |||    ||||
                                ATGTCCTTCT    CAC    GGTA
                                      GTCC  _____
GAM765  LOC158308 3'  TGGTGGCATCTTCCTGCA    86745          GTCG  AG
                                TGCAGGAAGA    TG  CACCA
                                ||||||||||    ||  |||||
                                ACGTCCTTCT    AC  GTGGT
                                      _____  G_
GAM765  LOC163412 5'  GGTGCTCACCGCCCCGC     82137    A  AAGA  C
                                GC GG    GT GTGAGCACC
                                || ||    || |||||||||
                                CG CC    CG CACTCGTGG
                                 C  _____  C
GAM765  LOC201249 3'  CACGACTGTTCCTGCA      88164         G
                                TGCAGGAA AGTCGTG
                                |||||||| |||||||
                                ACGTCCTT TCAGCAC
                                     G
GAM765  LOC221296 3'  ATGGTACTTCATTGCTCTTCCT 91957    C       C    _ C
           TCA                    TG AGGAAGAGT GTGA G ACCAT
                                || |||||||| |||| | |||||
                                AC TCCTTCTCG TACT C TGGTA
                                 T       T    T A
GAM765  LOC94431  5'  ATGATAATCTTCCTGCA     68593          __
                                TGCAGGAAGA  GTCGT
                                ||||||||||  |||||
                                ACGTCCTTCT  TAGTA
                                      AA
GAM766  AGR2      3'  CAAGGAAGGGACAAGACAA    21143      A       GG
                                TTGT CTTGTCCC  CCTTG
                                |||| ||||||||  |||||
                                AACA GAACAGGG  GGAAC
                                  _       AA
GAM766  ATP8B2    5'  CAAGACCTCCAAGTACAA     65212         TCCC  C
                                TTGTACTTG    GG CTTG
                                |||||||||    || ||||
                                AACATGAAC    CC GAAC
                                      CT__  A
GAM766  CPNE7     3'  CAAGGCCGAAGGGTGACAA    27037      _    GTCC
                                TTGT ACTT    CGGCCTTG
                                |||| ||||    ||||||||
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                                AACA TGGG    GCCGGAAC
                                  G    AA__
GAM766  TMOD2    3'  CAAAGCCTGTGAAAGTACAAG  27247         GTCCC   C
                                CTTGTACTT     GGC TTG
                                |||||||||     ||| |||
                                GAACATGAA     CCG AAC
                                     AGTGT   A
GAM766  API5     3'  CAAAGCCATTTCAAGTACAGA  21686     T      TCCC   C
                                TCT GTACTTG    GGC TTG
                                ||| |||||||    ||| |||
                                AGA CATGAAC    CCG AAC
                                  _      TTTA   A
GAM766  BRAG     3'  CAAAGCCAGAAAGTGCAAG   29471         G  CC   C
                                CTTGTACTT TC  GGC TTG
                                ||||||||| ||  ||| |||
                                GAACGTGAA AG  CCG AAC
                                     _ A_   A
GAM766  COLEC10  3'  CAAAGCCAGACATGTACAAGG  21228         T    CC   C
                                TCTTGTAC TGTC  GGC TTG
                                |||||||| ||||  ||| |||
                                GGAACATG ACAG  CCG AAC
                                     T    A_   A
GAM766  FENS-1   3'  CAAAGCAGTCACAAGTACAG   40438         CCCG  C
                                TTGTACTTGT    GC TTG
                                ||||||||||    || |||
                                GACATGAACA    CG AAC
                                     CTGA  A
GAM766  FLJ20972 3'  CAAGAGACAAAGTACAAGA    46724          _   CCGGC
                                TCTTGTACTT GTC     CTTG
                                |||||||||| |||     ||||
                                AGAACATGAA CAG     GAAC
                                     A   A_____
GAM766  FLJ32861 3'  CAAGGCCAGGAGTGCAAGA    58726         TTG   C
                                TCTTGTAC   TCC GGCCTTG
                                ||||||||   ||| |||||||
                                AGAACGTG   AGG CCGGAAC
                                     ___   A
GAM766  LOC120120 5' AAGGTGGAACAAGTACAAGA   75544           C   G
                                TCTTGTACTTGT CCG CCTT
                                |||||||||||| ||| ||||
                                AGAACATGAACA GGT GGAA
                                     A   _
GAM766  LOC253502 3' CAAGGCCGAAGGGTGACAA    94577      _    GTCC
                                TTGT ACTT    CGGCCTTG
                                |||| ||||    ||||||||
                                AACA TGGG    GCCGGAAC
                                  G    AA__
GAM767  ADAM19   3'  CAGGAAGAAGACTGGCCATTAT 52703      C    CTGAG
           G                     CATGA GGCT     TTCTTCCTG
                                |||||| ||||     |||||||||
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                                GTATT CCGG    AAGAAGGAC
                                   A   TCAG_
GAM767  FACL5    5'  CAGGAAGAACTCAGAGCCG   64186
                                CGGCTCTGAGTTCTTCCTG
                                ||||||||||||||||||
                                GCCGAGACTCAAGAAGGAC

GAM767  GNAL     5'  CAGGAAAGAGAGGAGCCGTCG  9058          GAG TC
                                TGACGGCTCT   T  TTCCTG
                                ||||||||||   |  ||||||
                                GCTGCCGAGG   A  AAGGAC
                                      AG_ GA
GAM767  KAL1     3'  CAGGAAGAACTTCTGTCA    4013        CTCT
                                TGACGG   GAGTTCTTCCTG
                                ||||||   ||||||||||||
                                ACTGTC   TTCAAGAAGGAC
                                     ____
GAM767  MYO1E    3'  CAGGAGGACAAAACCACCATG  17187     AC  CTC  AGT
                                CATG  GG   TG   TCTTCCTG
                                ||||  ||   ||   ||||||||
                                GTAC  CC   AC   AGGAGGAC
                                  CA  AAA  ___
GAM767  PRKAR2B  3'  CAGAAAGAACTCAGATGT    10804   _        C
                                GC TCTGAGTTCTT CTG
                                || ||||||||||| |||
                                TG AGACTCAAGAA GAC
                                 T          A
GAM767  PUM2     3'  AGGATCAAAGCTGTCATG    31014         C   GTTCT
                                CATGACGGCT TGA    TCCT
                                |||||||||| |||    ||||
                                GTACTGTCGA ACT    AGGA
                                      A  _____
GAM767  SKI      3'  CAGGAAGTGCAGAGCCGCA   11701    A      AGTT
                                TG CGGCTCTG   CTTCCTG
                                || ||||||||   |||||||
                                AC GCCGAGAC   GAAGGAC
                                 _      GT__
GAM767  TEM8     3'  AGGAAGATGCAACCCCATG   36326     AC  CTC  AGT
                                CATG  GG   TG   TCTTCCT
                                ||||  ||   ||   |||||||
                                GTAC  CC   AC   AGAAGGA
                                  C_  A__  GT_
GAM767  ARHGEF4  5'  AGAAAAAACTCAGGGC      52207         C  C
                                GCTCTGAGTT TT CT
                                |||||||||| || ||
                                CGGGACTCAA AA GA
                                      A  A
GAM767  FLJ31978 3'  CAGGAAGGAACAAGCGCC    58348     T  GAG
                                GGC CT   TTCTTCCTG
                                ||| ||   |||||||||
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                                CCG GA   AGGAAGGAC
                                  C  ACA
GAM767  HSU24186  5'  AGAACTCAAAGCCGTC      25324        C
                                GACGGCT TGAGTTCT
                                ||||||| ||||||||
                                CTGCCGA ACTCAAGA
                                    A
GAM767  KCNT1     3'  AGCTCCCAGGGCCGCCA     61825     A      __
                                TG CGGCTCT  GAGTT
                                || |||||||  |||||
                                AC GCCGGGA  CTCGA
                                 C      CC
GAM767  KIAA1867  3'  CAGGAAGAACCCAAGAGCTCAT 94822      CG     GA_
                                ATGA  GCTCT   GTTCTTCCTG
                                ||||  |||||   ||||||||||
                                TACT  CGAGA   CAAGAAGGAC
                                  __    ACC
GAM767  KIAA1878  3'  AATTCAGAGAATCGTCATG    91707         __
                                CATGACGG  CTCTGAGTT
                                ||||||||  |||||||||
                                GTACTGCT  GAGACTTAA
                                    AA
GAM767  MFN1      3'  CAGGAAGAACTCATGA      35541     _
                                TC TGAGTTCTTCCTG
                                || ||||||||||||
                                AG ACTCAAGAAGGAC
                                 T
GAM767  MIDORI    3'  CAGGGCCCTTCCAGAGCCTGTC 73784        _      AGTTCT
            ATG                   CATGAC GGCTCTG     TCCTG
                                ||||||| |||||||      |||||
                                GTACTG CCGAGAC      GGGAC
                                   T      CTTCCC
GAM767  MYH7B     3'  CAGGAAGAACCTGGCTCGCATG 70530      A  _   CTGA
                                CATG CG GCT    GTTCTTCCTG
                                |||| || |||    ||||||||||
                                GTAC GC CGG    CAAGAAGGAC
                                  _  T   TC__
GAM767  RNAHP     3'  AGAAAGCAGCAGCCGTCAT    23761         _   AG
                                ATGACGGCT CTG  TTCT
                                ||||||||| |||  ||||
                                TACTGCCGA GAC  AAGA
                                    C   GA
GAM767  SLC37A1   3'  AGACGGAGCTCAGACCC      38561     C        TC
                                GG TCTGAGTTCT  CT
                                || ||||||||||  ||
                                CC AGACTCGAGG  GA
                                 C         CA
GAM767  LOC116236 3'  CAGGAAAAGCACAAACCTCAT  73809      C  CTC  A   C
                                ATGA GG   TG GTT TTCCTG
                                |||| ||   || ||| ||||||
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                                TACT CC   AC CGA AAGGAC
                                  _ AA_ A   A
GAM767  LOC124801 3'  CAGGAAGAACTCTCTTGCATG  74336     A   CTCT
                                CATG CGG    GAGTTCTTCCTG
                                |||| |||    ||||||||||||
                                GTAC GTT    CTCAAGAAGGAC
                                  _   CT__
GAM767  LOC222160 5'  AGGAAGAACTCACCCC      94117    CTC
                                GG   TGAGTTCTTCCT
                                ||   ||||||||||||
                                CC   ACTCAAGAAGGA
                                 CC_
GAM767  LOC51094  3'  CAGGAAGAATAAAGCC      32045      CTGA
                                GGCT    GTTCTTCCTG
                                ||||    ||||||||||
                                CCGA    TAAGAAGGAC
                                  AA__
GAM767  LOC92078  3'  CAGGAAGAAGAATCGACCGTC  67977      C  T  G__
                                GACGG TC GA   TTCTTCCTG
                                ||||| || ||   |||||||||
                                CTGCC AG CT   AAGAAGGAC
                                  _ _  AAG
GAM768  ABCD1     3'  GCCCCTGGCACTGCAGGTG   3464     G       GAA
                                CA CTGCAGTGT   AGGGGC
                                || |||||||||   ||||||
                                GT GACGTCACG   TCCCCG
                                 G        G__
GAM768  ABR       3'  GCCCTAACGCTGCAGC      6574          GAAA
                                GCTGCAGTGT    GGGGC
                                ||||||||||    |||||
                                CGACGTCGCA    TCCCG
                                      A___
GAM768  ABR       3'  GCCCTAACGCTGCAGC      41726         GAAA
                                GCTGCAGTGT    GGGGC
                                ||||||||||    |||||
                                CGACGTCGCA    TCCCG
                                      A___
GAM768  ACTR1B    3'  GCCCCTTTCACACTCTG     70821     CTGC
                                CAG    AGTGTGAAAGGGGC
                                |||    ||||||||||||||
                                GTC    TCACACTTTCCCCG
                                  _____
GAM768  AR        5'  GCTTCAGCACTGCAGC      3494          GAAA
                                GCTGCAGTGT    GGGGC
                                ||||||||||    |||||
                                CGACGTCACG    CTTCG
                                      A___
GAM768  ARHA      3'  GCCCAAGTTCATGCAGCTG   70696        GTG   AG_
                                CAGCTGCA   TGAA   GGGC
                                ||||||||   ||||   ||||
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                                GTCGACGT  ACTT  CCCG
                                   ___   GAA
GAM768  ARHGAP6  5' CCCCACACTGCAGC      20404         AAA
                                GCTGCAGTGTG  GGG
                                ||||||||||  |||
                                CGACGTCACAC  CCC
                                   ___
GAM768  ARHGAP6  5' CCCCACACTGCAGC      6760          AAA
                                GCTGCAGTGTG  GGG
                                ||||||||||  |||
                                CGACGTCACAC  CCC
                                   ___
GAM768  CACNA2D2 3' GCCCCTTTCAGGCCTACAGC  20087     CA_  G
                                GCTG  GT TGAAAGGGGC
                                ||||  || ||||||||||
                                CGAC  CG ACTTTCCCCG
                                  ATC  G
GAM768  CASQ2    3' CCCCTTCTCTGTAGCTG    6935        TGTGA
                                CAGCTGCAG   AAGGGG
                                |||||||||   ||||||
                                GTCGATGTC   TTCCCC
                                     TC___
GAM768  CLASP1   3' CCCTGACAGCTGCAGCTG   65299        GTGAA
                                CAGCTGCAGT   AGGG
                                ||||||||||   ||||
                                GTCGACGTCG   TCCC
                                     ACAG_
GAM768  CLASP1   3' GCCCCCTAGACCCTGACAGCTG 65303      _  T  GAAA
                                CAGCTG CAG GT   GGGGC
                                ||||||| ||| ||   |||||
                                GTCGAC GTC CA   CCCCG
                                   A  C  GATC
GAM768  COL1A1   3' CCCTCCTCCACAGCTG     3604      GCA  T  AA
                                CAGCT  GTG GA  GGGG
                                |||||  ||| ||  ||||
                                GTCGA  CAC CT  TCCC
                                  ___  _ CC
GAM768  COX10    3' GCCCCTTTCCCTCCGCTGC   7121       T___
                                GCAGTG   GAAAGGGGC
                                ||||||   |||||||||
                                CGTCGC   CTTTCCCCG
                                   CTCC
GAM768  CPE      5' GCCCCCTGCCTCGCAGT    8526      _  T  AAA
                                GCTGC AG GTG  GGGGC
                                ||||| || |||  |||||
                                TGACG TC CGT  CCCCG
                                  C  _  C__
GAM768  DLK1     5' CCCCTTTCGCGTCCGCA    13841    AG_
                                TGC  TGTGAAAGGGG
                                |||  ||||||||||
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                                ACG   GCGCTTTCCCC
                                  CCT
GAM768  DMPK    3'  GCCCCCCTCCTCACTTGCGCTG 15324     T  _  T_  AA
                                CAGC GCA GTG  GA  GGGGC
                                |||| ||| |||  ||  |||||
                                GTCG CGT CAC  CT  CCCCG
                                  _  T  TC  CC
GAM768  ED1     5'  CCCCTCGGAGTAGAGCTG    7365       __  AG  TGAA
                                CAGCT  GC  TG   AGGGG
                                |||||  ||  ||   |||||
                                GTCGA  TG  GC   TCCCC
                                   GA  AG  ____
GAM768  ENSA    3'  GCCCCTTCCTGCTTTTGCAGC  15426       T_  A_
                                GCTGCAG  GTG  AAGGGGC
                                |||||||  |||  |||||||
                                CGACGTT  CGT  TTCCCCG
                                    TT   CC
GAM768  EPHB2   3'  CCCCCAGGTCTGCAGCT     15443        _ G  AAA
                                AGCTGCAG T TG   GGGG
                                |||||||| | ||   ||||
                                TCGACGTC G AC   CCCC
                                    T G  ___
GAM768  EPHB2   3'  CCCCCAGGTCTGCAGCT     33886        _ G  AAA
                                AGCTGCAG T TG   GGGG
                                |||||||| | ||   ||||
                                TCGACGTC G AC   CCCC
                                    T G  ___
GAM768  FGFR1   3'  CCCCACACTGCGCTG       43638     T      AAA
                                CAGC GCAGTGTG   GGG
                                |||| ||||||||   |||
                                GTCG CGTCACAC   CCC
                                  _      ___
GAM768  G6PT1   5'  CCCCTTTCTATCGCGC      7597     T  A  T
                                GC GC GTG GAAAGGGG
                                || || ||| ||||||||
                                CG CG TAT CTTTCCCC
                                 _  C  _
GAM768  GABRE   3'  CCCCTTTCTCTGCAG       17109       TGT
                                CTGCAG   GAAAGGGG
                                ||||||   ||||||||
                                GACGTC   CTTTCCCC
                                   T__
GAM768  GABRE   3'  CCCCTTTCTCTGCAG       41773       TGT
                                CTGCAG   GAAAGGGG
                                ||||||   ||||||||
                                GACGTC   CTTTCCCC
                                   T__
GAM768  GABRE   3'  CCCCTTTCTCTGCAG       41782       TGT
                                CTGCAG   GAAAGGGG
                                ||||||   ||||||||
```

```
                                GACGTC  CTTTCCCC
                                   T__
GAM768  GABRE   3'  CCCCTTTCTCTGCAG      41803      TGT
                                CTGCAG  GAAAGGGG
                                ||||||  ||||||||
                                GACGTC  CTTTCCCC
                                   T__
GAM768  GNA11   5'  GCCCCCACACCGCAGC      76102      A    AAA
                                GCTGC GTGTG  GGGGC
                                ||||| |||||  |||||
                                CGACG CACAC  CCCCG
                                   C   ___
GAM768  GNAI1   5'  GCCCCTTTGCGGACAGC     9054      CAG  G
                                GCTG  TGT AAAGGGGC
                                ||||  ||| ||||||||
                                CGAC  GCG TTTCCCCG
                                  AG_  _
GAM768  GRB10   3'  CCCCTGCTGCTGCAGT      17975        TGAA
                                GCTGCAGTG   AGGGG
                                |||||||||   |||||
                                TGACGTCGT   TCCCC
                                     CG__
GAM768  HDAC4   3'  TTTTTCCACTGCAGC       20125        T
                                GCTGCAGTG GAAAGG
                                ||||||||| ||||||
                                CGACGTCAC CTTTTT
                                          _
GAM768  HIRA    3'  GCCCCTGCTGCTGCAGGC    12437   _     TGAA
                                GC TGCAGTG   AGGGGC
                                || |||||||   ||||||
                                CG ACGTCGT   TCCCCG
                                 G     CG__
GAM768  HIS1    5'  CCCCTTGGACCCGCTAGCTG  21314     _ AGT  GA
                                CAGCT GC  GT  AAGGGG
                                ||||| ||  ||  ||||||
                                GTCGA CG  CA  TTCCCC
                                   T  CC_  GG
GAM768  HLA-E   3'  CCCCTTCCTCACACTG      91022        __
                                CAGTGTGA  AAGGGG
                                ||||||||  ||||||
                                GTCACACT  TTCCCC
                                     CC
GAM768  HMG20A  3'  GCCCCACACCACTGCAGGC   36542   _     _ AAA
                                GC TGCAGTG TG  GGGGC
                                || ||||||| ||  |||||
                                CG ACGTCAC AC  CCCCG
                                 G     C  A__
GAM768  HRC     3'  CCCCTTTCCACGAGCT      9280      GCA  T
                                AGCT  GTG GAAAGGGG
                                ||||  ||| ||||||||
```

```
                                TCGA   CAC CTTTCCCC
                                  G__   _
GAM768  IHPK1    3'  CCCCTTCCTCTCCACTGCAGGC 95757    _     T _____
                                GC TGCAGTG GA    AAGGGG
                                || ||||||| ||    ||||||
                                CG ACGTCAC CT    TTCCCC
                                 G      _ CTCC
GAM768  IVD      3'  CCCCTTTTCCTGCACCT     9461     C     TGT
                                AG TGCAG   GAAAGGGG
                                || |||||   ||||||||
                                TC ACGTC   TTTTCCCC
                                 C    C__
GAM768  JUND     3'  GCCCCTTTGTACACCGCGC    18085    T  A    _
                                GC GC GTGTG AAAGGGGC
                                || || ||||| ||||||||
                                CG CG CACAT TTTCCCCG
                                 _ C    G
GAM768  KCND2    5'  CTGTCACACTGCACCTG     24397     C        A
                                CAG TGCAGTGTGA AG
                                ||| |||||||||| ||
                                GTC ACGTCACACT TC
                                  C        G
GAM768  KLHL3    3'  GCCCCTCATGTTCAGCTG    87458       C  TG   AA
                                CAGCTG AG  TGA  GGGGC
                                |||||| ||  |||  |||||
                                GTCGAC TT  ACT  CCCCG
                                   _ GT  __
GAM768  LARS2    3'  CCCCACCCACACTGCAG     31054          AAA
                                CTGCAGTGTG   GGGG
                                ||||||||||   ||||
                                GACGTCACAC   CCCC
                                      CCA
GAM768  LIMK1    3'  GCCCCTTTCCACACGCCGCTG  33648      T  A    _
                                CAGC GC GTGTG AAAGGGGC
                                |||| || ||||| ||||||||
                                GTCG CG CACAC TTTCCCCG
                                  C _    C
GAM768  LIMK1    3'  GCCCCTTTCCACACGCCGCTG  9786       T  A    _
                                CAGC GC GTGTG AAAGGGGC
                                |||| || ||||| ||||||||
                                GTCG CG CACAC TTTCCCCG
                                  C _    C
GAM768  MAP3K8   5'  GCCCCTGACACTGCACTG    17790     C       GAA
                                CAG TGCAGTGT   AGGGGC
                                ||| ||||||||   ||||||
                                GTC ACGTCACA   TCCCCG
                                  _      G__
GAM768  MAT1A    3'  CCCCTTTCACAGGCA       90830     AG
                                TGC  TGTGAAAGGGG
                                |||  ||||||||||
```

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                                ACG  ACACTTTCCCC
                                  G_
GAM768  MSF     3'  CCCCTTCGACATGCTGC     88080        A__
                                GCAGTGTG   AAGGGG
                                ||||||||   ||||||
                                CGTCGTAC   TTCCCC
                                    AGC
GAM768  MVK     3'  GCCCACGACACTGCAGC     60651         GAAAG
                                GCTGCAGTGT    GGGC
                                ||||||||||    ||||
                                CGACGTCACA    CCCG
                                     GCA__
GAM768  NAP1L4   3'  CCCCTCCTGCAGTTG      19920         TGTGAA
                                CAGCTGCAG     AGGGG
                                |||||||||     |||||
                                GTTGACGTC     TCCCC
                                     C_____
GAM768  NGFR     3'  CCCCTTCTCCCACACTGC    10223         A___
                                GCAGTGTG   AAGGGG
                                ||||||||   ||||||
                                CGTCACAC   TTCCCC
                                    CCTC
GAM768  NKX3A    3'  CTCCACACTGCTGCT       20502     T       AAA
                                AGC GCAGTGTG   GGG
                                ||| ||||||||   |||
                                TCG CGTCACAC   CTC
                                  T      ___
GAM768  OSCAR    3'  GCCCCAGGAGCACTGCAGC   55373          GAAA
                                GCTGCAGTGT   GGGGC
                                ||||||||||   |||||
                                CGACGTCACG   CCCCG
                                     AGGA
GAM768  OSCAR    3'  GCCCCAGGAGCACTGCAGC   55666          GAAA
                                GCTGCAGTGT   GGGGC
                                ||||||||||   |||||
                                CGACGTCACG   CCCCG
                                     AGGA
GAM768  OSCAR    3'  GCCCCAGGAGCACTGCAGC   55670          GAAA
                                GCTGCAGTGT   GGGGC
                                ||||||||||   |||||
                                CGACGTCACG   CCCCG
                                     AGGA
GAM768  PGAM1    3'  GCCCCTCCCACCTGCA      76275      T   AA
                                TGCAG GTG  AGGGGC
                                ||||| |||  ||||||
                                ACGTC CAC  TCCCCG
                                   _  CC
GAM768  PLD1     5'  GCCCCTTCGCCCTGCAGC    10625        T    A
                                GCTGCAG GTGAA GGGGC
                                ||||||| ||||| |||||
```

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                                CGACGTC CGCTT CCCCG
                                    C    _
GAM768  POLL    5'  GCCCCATCTCCCCGCAGCTG  25178       AGTGT  AA
                                CAGCTGC    GA  GGGGC
                                |||||||    ||  |||||
                                GTCGACG    CT  CCCCG
                                    CCCCT  A_
GAM768  PPP1R2  3'  CTGTCACATGCAGCTG     20691        G    A
                                CAGCTGCA TGTGA AG
                                |||||||| ||||| ||
                                GTCGACGT ACACT TC
                                    _    G
GAM768  RAB36   3'  CCTGGCACACTGCAGCTG    16955           AA
                                CAGCTGCAGTGTG  AGG
                                ||||||||||||  |||
                                GTCGACGTCACAC  TCC
                                      GG
GAM768  RAD52   3'  GCCCTGGGACACCCACAGCTG 56197      CA_   GAAA
                                CAGCTG   GTGT   GGGGC
                                ||||||   ||||   |||||
                                GTCGAC   CACA   TCCCG
                                   ACC   GGG_
GAM768  RAD52   3'  GCCCTGGGACACCCACAGCTG 56204      CA_   GAAA
                                CAGCTG   GTGT   GGGGC
                                ||||||   ||||   |||||
                                GTCGAC   CACA   TCCCG
                                   ACC   GGG_
GAM768  RAD52   3'  GCCCTGGGACACCCACAGCTG 56213      CA_   GAAA
                                CAGCTG   GTGT   GGGGC
                                ||||||   ||||   |||||
                                GTCGAC   CACA   TCCCG
                                   ACC   GGG_
GAM768  RAI3    3'  CCCCTCTCTTCTTGCACTG   14283    C    TGT  A
                                CAG TGCAG   GA AGGGG
                                ||| |||||   || |||||
                                GTC ACGTT   CT TCCCC
                                  _    CTT  C
GAM768  RHBG    3'  GCCCCTTTCCACAGGCAGC   39901      A_   T
                                GCTGC  GTG GAAAGGGGC
                                |||||  ||| |||||||||
                                CGACG  CAC CTTTCCCCG
                                   GA  _
GAM768  SLC2A4  3'  TTCCTTTCCTCTGCAGC     6444        TGT
                                GCTGCAG   GAAAGGGG
                                |||||||   ||||||||
                                CGACGTC   CTTTCCTT
                                    TC_
GAM768  SMURF1  3'  GCCCCTTTCCCAGTGGCAGCT  92452       _ G  T
                                AGCTGC A TG GAAAGGGGC
                                |||||| | || |||||||||
```

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                                TCGACG T AC CTTTCCCCG
                                   G G  C
GAM768  SPOCK    3'  GCCCCTTGGCTGCAGC      62818        GTGA
                                GCTGCAGT    AAGGGGC
                                ||||||||    |||||||
                                CGACGTCG    TTCCCCG
                                     G___
GAM768  SRRM1    3'  CCCCTGCAGCCATTGCAGCTG  19551          _ GAA
                                CAGCTGCAGTG T   AGGGG
                                ||||||||||| |   |||||
                                GTCGACGTTAC G   TCCCC
                                      C ACG
GAM768  TARBP2   3'  GCCCCCCCCATGGAACTGCAGC  56166         ___  AAA
                                GCTGCAGT   GTG   GGGGC
                                ||||||||   |||   |||||
                                CGACGTCA   TAC   CCCCG
                                     AGG   CC_
GAM768  TKTL1    3'  GCCATCCCACCTGCAGCTG    24298         T   AAAGG
                                CAGCTGCAG GTG    GGC
                                |||||||||  |||    |||
                                GTCGACGTC CAC    CCG
                                     _  CCTA_
GAM768  TNFRSF1A 5'  GCCCCAGCACTGCCGCTG    6514      T     GAAA
                                CAGC GCAGTGT    GGGGC
                                ||||  |||||||   |||||
                                GTCG CGTCACG    CCCCG
                                  C      A___
GAM768  UNRIP    5'  GCCCGAGGCACTGCAGC     23201         GAAAG
                                GCTGCAGTGT    GGGC
                                ||||||||||    ||||
                                CGACGTCACG    CCCG
                                     GAG__
GAM768  WNT3A    3'  GCCCCCTTCTTTGCAGCTG   52433         TGT   A
                                CAGCTGCAG   GAA GGGGC
                                |||||||||   ||| |||||
                                GTCGACGTT   CTT CCCCG
                                     T__   C
GAM768  WNT3A    3'  GCCCCTTCCACGGGGGCTG   52434      GCA   T   A
                                CAGCT   GTG GAA GGGGC
                                |||||   ||| ||| |||||
                                GTCGG   CAC CTT CCCCG
                                   GGG  _  _
GAM768  ZNF9     3'  CCCCTTTCCGTGCCACTG    12772     CT   G  T
                                CAG  GCA TG GAAAGGGG
                                |||  ||| || ||||||||
                                GTC  CGT GC CTTTCCCC
                                  AC   _ _
GAM768  AF9Q34   3'  CCCCTCTGCCCCTGCAGCTG  50734         T_  GAA
                                CAGCTGCAG  GT   AGGGG
                                |||||||||  ||   |||||
```

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                                GTCGACGTC  CG   TCCCC
                                     CC  TC_
GAM768  APCL     3'  CCCCTTTCAGGACACAGCGG  19668     A   ___
                                CTGC GTGT   GAAAGGGG
                                |||| ||||   ||||||||
                                GGCG CACA   CTTTCCCC
                                  A   GGA
GAM768  APELIN   3'  GCCCCTTTACCTATGCTGCTG  33784     T   GTGTG
                                CAGC GCA    AAAGGGGC
                                |||| |||    ||||||||
                                GTCG CGT    TTTCCCCG
                                  T  ATCCA
GAM768  ARHGAP4  3'  GCCCCTTTTGGAGGCAGCTG  8020        AGTGT
                                CAGCTGC    GAAAGGGGC
                                |||||||    |||||||||
                                GTCGACG    TTTTCCCCG
                                    GAGG_
GAM768  ARHGEF4  3'  CCCCTCTTCAGGCTGC     52209     G   _
                                GCAGT TGAA AGGGG
                                ||||| |||| |||||
                                CGTCG ACTT TCCCC
                                  G   C
GAM768  ASAH     3'  CCGAACACTGCAGCTG      15049         GAAA
                                CAGCTGCAGTGT   GG
                                ||||||||||||   ||
                                GTCGACGTCACA   CC
                                       AG__
GAM768  BCL2L12  5'  CCCCTTTCCCGTCAGCTG   56864      CAG  T
                                CAGCTG   TG GAAAGGGG
                                ||||||   || ||||||||
                                GTCGAC   GC CTTTCCCC
                                   T__  C
GAM768  BICD2    3'  CCGCACGCTGCAGCT      70390         AAAGG
                                AGCTGCAGTGTG    GG
                                ||||||||||||    ||
                                TCGACGTCGCAC    CC
                                       G____
GAM768  BICD2    3'  GCCCTGTCACACTGCAGC    70396         AA
                                GCTGCAGTGTGA  GGGGC
                                ||||||||||||  |||||
                                CGACGTCACACT  TCCCG
                                       G_
GAM768  C11orf11 3'  CCCCCAAGGCTGCAGC     93253       G_  AAA
                                GCTGCAGT  TG   GGGG
                                ||||||||  ||   ||||
                                CGACGTCG  AC   CCCC
                                     GA  ___
GAM768  C16orf7  3'  CCCATCGCTGCAGCTG     16938         TGAAAG
                                CAGCTGCAGTG     GGG
                                ||||||||||      |||
```

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                                GTCGACGTCGC     CCC
                                      TA____
GAM768  C1QTNF6   3'  GCCTGCACCACTGCAGC    49147        _  AAAG
                                GCTGCAGTG TG   GGGC
                                ||||||||| ||   ||||
                                CGACGTCAC AC   TCCG
                                     C  G___
GAM768  C20orf151 3'  CCCCTGCTGTGCACTGCAGC  88699         AA__
                                GCTGCAGTGTG   AGGGG
                                ||||||||||   |||||
                                CGACGTCACGT   TCCCC
                                      GTCG
GAM768  C20orf162 5'  GCCCCCTGCCAGCTGCAGCTG  54602         GTGAAA
                                CAGCTGCAGT    GGGGC
                                |||||||||     |||||
                                GTCGACGTCG    CCCCG
                                      ACCGTC
GAM768  CHIT1     3'  GCCCCTTTCACTTGCA     12949      T
                                TGCAG GTGAAAGGGGC
                                ||||| ||||||||||
                                ACGTT CACTTTCCCCG
                                  _
GAM768  CHST3     3'  CCCCTTCACAGCATACACTG  14970    C___  AG     A
                                CAG   TGC  TGTGAA GGGG
                                |||   |||  |||||| ||||
                                GTC   ACG  ACACTT CCCC
                                  ACAT  __    _
GAM768  CHST8     5'  GCCCAGAAGCAGCTGCAGC   42438       _  GAAAG
                                GCTGCAG TGT    GGGC
                                ||||||| |||    ||||
                                CGACGTC ACG    CCCG
                                    G  AAGA_
GAM768  DKFZP434C128 3'  CCCCAGTCTCCCTGCAGCTG  64845        TGT  AA
                                CAGCTGCAG  GA  GGGG
                                |||||||||  ||  ||||
                                GTCGACGTC  CT  CCCC
                                      CCT  GA
GAM768  DKFZP434K1772 5'  CCCAGCACCGCCAGCTG    67710       _ A   GAAA
                                CAGCTG C GTGT   GGG
                                |||||| | ||||   |||
                                GTCGAC G CACG   CCC
                                   C C   A___
GAM768  DKFZP586J0619 3'  GCCCCAGCATTGCAGC     81392         GAAA
                                GCTGCAGTGT   GGGGC
                                ||||||||||   |||||
                                CGACGTTACG   CCCCG
                                      A___
GAM768  DKFZP586M1120 3'  CCCCTCCGCATTGCAGC    48454          AA
                                GCTGCAGTGTG  AGGGG
                                ||||||||||  |||||
```

```
                                CGACGTTACGC  TCCCC
                                      C_
GAM768  DKFZP586M1120 3'  GCCCCCTGTGTTGCAGGC    48459    _    TG  AAA
                                GC TGCAG  TG   GGGGC
                                || |||||  ||   |||||
                                CG ACGTT  GT   CCCCG
                                 G    GT  C__
GAM768  DKFZP727M111 5'  GCCCCAGCAGTGCAGCTG    31410        G   GAAA
                                CAGCTGCA TGT    GGGGC
                                |||||||| |||    |||||
                                GTCGACGT ACG    CCCCG
                                     G   A___
GAM768  DKFZp762E1312 5'  GCCCCCGGATACTGCAGT    37285          GAAA
                                GCTGCAGTGT    GGGGC
                                ||||||||||    |||||
                                TGACGTCATA    CCCCG
                                      GGC_
GAM768  DNAJC5   3'  CCCTTTCACGGCAGCTG     61450        AG
                                CAGCTGC  TGTGAAAGGG
                                |||||||  ||||||||||
                                GTCGACG  GCACTTTCCC
                                      __
GAM768  EFA6R    3'  CCCCTCTCTAGGGTTGCAGTTG 30982          TGT__  A
                                CAGCTGCAG    GA AGGGG
                                |||||||||    || |||||
                                GTTGACGTT    CT TCCCC
                                      GGGAT  C
GAM768  ELF4     5'  CCCCTATTTTACTGCAGCT    7430           T  A
                                AGCTGCAGTG GA AGGGG
                                |||||||||| || |||||
                                TCGACGTCAT TT TCCCC
                                      T  A
GAM768  EPSIN    5'  GCCCCTTGCTGCTGCAGC    25298         TGA
                                GCTGCAGTG   AAGGGGC
                                |||||||||   |||||||
                                CGACGTCGT   TTCCCCG
                                      CG_
GAM768  FAM10A7   3'  CCCCTCTCCCCCAAATGCAGCT 81244         GTGT___  A
           G                     CAGCTGCA      GA AGGGG
                                |||||||       || |||||
                                GTCGACGT      CT TCCCC
                                     AAACCCC  C
GAM768  FATE     3'  GCCCCTTTCATCTCCCAGC   52359     CAGT
                                GCTG   GTGAAAGGGGC
                                ||||   ||||||||||
                                CGAC   TACTTTCCCCG
                                  CCTC
GAM768  FLJ10737  3'  CCCCCTCCACGGCCTG     36521     CT  A  T  AA
                                CAG  GC GTG GA  GGGG
                                |||  || ||| ||  ||||
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```
                                GTC  CG CAC CT  CCCC
                                  __  G  _ C_
GAM768  FLJ10936  5' GCCCCTTTGCAGCCGCTG    36908     T  AG  G
                                CAGC GC  TGT AAAGGGGC
                                |||| ||  ||| ||||||||
                                GTCG CG  ACG TTTCCCCG
                                  C  __  _
GAM768  FLJ11783  3' GCCCCTCCTTTCAAGGAGCTG  46031      GCAGTG  ___
                                CAGCT     TGAA  AGGGGC
                                |||||     ||||  ||||||
                                GTCGA     ACTT  TCCCCG
                                   GGA___   TCC
GAM768  FLJ12650  3' GCCCCTTTCTACTCA      44527    C   T
                                TG AGTG GAAAGGGGC
                                || |||| |||||||||
                                AC TCAT CTTTCCCCG
                                 _   _
GAM768  FLJ12921  3' CCCCTGTTTGCACTAAGC    45908    GC   TG  _
                                GCT  AGTG  AA AGGGG
                                |||  ||||  || |||||
                                CGA  TCAC  TT TCCCC
                                  A_   GT  G
GAM768  FLJ13197  5' GCCCCCCCCCAACACCAGCGCTG 44854     T  A_   GAAA_
                                CAGC GC  GTGT    GGGGC
                                |||| ||  ||||    |||||
                                GTCG CG  CACA    CCCCG
                                  _ AC    ACCCC
GAM768  FLJ14154  3' GCCCCTAATCACTGCAGT    45819        TGAA
                                GCTGCAGTG   AGGGGC
                                |||||||||   ||||||
                                TGACGTCAC   TCCCCG
                                     TAA_
GAM768  FLJ14936  3' GCTCTCCCACACTGCGCT    50134     T      AAA
                                AGC GCAGTGTG  GGGGC
                                ||| ||||||||  |||||
                                TCG CGTCACAC  TCTCG
                                  _      CC_
GAM768  FLJ14957  3' GCCCCTGTTCCACAGC      51749    A  T  _
                                GC GTG GAA AGGGGC
                                || ||| ||| ||||||
                                CG CAC CTT TCCCCG
                                 A  _  G
GAM768  FLJ20040  3' GCCCCTCCCACTGCGGGCT   38631     _    T  AA
                                AGCT GCAGTG GA  GGGGC
                                |||| |||||| ||  |||||
                                TCGG CGTCAC CT  CCCCG
                                  G    C __
GAM768  FLJ20507  3' GCCCCCTTCACATTCA      60226    C      A
                                TG AGTGTGAA GGGGC
                                || |||||||| |||||
```

```
                                AC TTACACTT CCCCG
                                 _      C
GAM768  FLJ20507  3'  GCCCCTCCCTCAACTCTGCAGC 60227       TG_  A__
           T                    AGCTGCAG  TGA  AGGGGC
                                ||||||||  |||  ||||||
                                TCGACGTC  ACT  TCCCCG
                                    TCA  CCC
GAM768  FLJ20507  3'  GCCCCCTTCACATTCA     35291    C      A
                                TG AGTGTGAA GGGGC
                                || |||||||| |||||
                                AC TTACACTT CCCCG
                                 _      C
GAM768  FLJ20507  3'  GCCCCTCCCTCAACTCTGCAGC 35292       TG_  A__
           T                    AGCTGCAG  TGA  AGGGGC
                                ||||||||  |||  ||||||
                                TCGACGTC  ACT  TCCCCG
                                    TCA  CCC
GAM768  FLJ21865  3'  GCCCAGGCCGCTGCAGCTG   42808        TGAAAG
                                CAGCTGCAGTG    GGGC
                                ||||||||||     ||||
                                GTCGACGTCGC    CCCG
                                     CGGA__
GAM768  FLJ22169  3'  CCCCTCACCCAGCTG      44001      CA  TGAA
                                CAGCTG  GTG   AGGGG
                                ||||||  |||   |||||
                                GTCGAC  CAC   TCCCC
                                   C_  ____
GAM768  FLJ23058  3'  CCCCTTTTCCACCAGC     45201     CA  TG
                                GCTG  GTG  AAAGGGG
                                ||||  |||  |||||||
                                CGAC  CAC  TTTCCCC
                                  __  CT
GAM768  GOLGA3    3'  CCCCCGGCTGCAGTTG     19713        GTGAAA
                                CAGCTGCAGT    GGGG
                                ||||||||||    ||||
                                GTTGACGTCG    CCCC
                                     GC____
GAM768  H326      3'  GCCCCTTTCCCAGCAGCT   31706      AG  T
                                AGCTGC  TG GAAAGGGGC
                                ||||||  || |||||||||
                                TCGACG  AC CTTTCCCCG
                                   __  C
GAM768  HGC6.1.1  5'  GCCCCCGTGACACTGCAGC   26830        GAAA
                                GCTGCAGTGT   GGGGC
                                ||||||||||   |||||
                                CGACGTCACA   CCCCG
                                     GTGC
GAM768  HIF1AN    3'  CCCCTCTCAGGGCTGCAGCT  61971        G_  A
                                AGCTGCAGT  TGA AGGGG
                                |||||||||  ||| |||||
```

```
                                TCGACGTCG  ACT TCCCC
                                     GG   C
GAM768  HRD1     3'  GCCCCTTTCCTCTGCAGCT   69558        TGT
                                AGCTGCAG   GAAAGGGGC
                                ||||||||   |||||||||
                                TCGACGTC   CTTTCCCCG
                                    TC_
GAM768  HRD1     3'  GCGGAGTCACACTGCAGT    69559          AAGGG
                                GCTGCAGTGTGA    GC
                                ||||||||||||    ||
                                TGACGTCACACT    CG
                                      GAGG_
GAM768  HRI      3'  GCCCCTTTCACACTGCAGCTG  26986
                                CAGCTGCAGTGTGAAAGGGGC
                                |||||||||||||||||||||
                                GTCGACGTCACACTTTCCCCG

GAM768  HSPC166  3'  GCCCTTGCAGCTGCAGCTG   26368         GTGAA
                                CAGCTGCAGT    AGGGGC
                                ||||||||||    ||||||
                                GTCGACGTCG    TTCCCG
                                     ACG__
GAM768  HSPC171  3'  GCCCCTGGTTCACTGCAG    26371        TGAA
                                CTGCAGTG    AGGGGC
                                ||||||||    ||||||
                                GACGTCAC    TCCCCG
                                    TTGG
GAM768  KCNH8    5'  TTTCACACCACGCTG       58262      _  CA
                                CAGC TG  GTGTGAAA
                                ||||  ||  ||||||||
                                GTCG AC  CACACTTT
                                  C  __
GAM768  KCNT1    3'  GCCCCCTTCTGCTGCCTGCGGC 61833         T  ____   A
           TG                     CAGCTGCAG GT    GAA GGGGC
                                |||||||||  ||    ||| |||||
                                GTCGGCGTC CG    CTT CCCCG
                                     _  TCGT   C
GAM768  KIAA0064 3'  GCCCCTTCTCTTTTCAGAGCTG 28542       GCAGTGT  _
                                CAGCT      GA AAGGGGC
                                |||||      || |||||||
                                GTCGA      CT TTCCCCG
                                   GACTTTT  C
GAM768  KIAA0169 3'  CCCCTCTCCACCAGC       72817      CA   T  A
                                GCTG  GTG GA AGGGG
                                ||||  ||| || |||||
                                CGAC  CAC CT TCCCC
                                  __   _  C
GAM768  KIAA0296 3'  GCCCCTTTTCCCTCTGCTGC   28114    T    TGT_
                                GC GCAG    GAAAGGGGC
                                || ||||    |||||||||
```

```
                                CG CGTC    TTTTCCCCG
                                 T   TCCC
GAM768  KIAA0329  3' CCCCACACCGCACTG      29272     C   A    AAA
                                CAG TGC GTGTG   GGG
                                ||| ||| |||||   |||
                                GTC ACG CACAC   CCC
                                  _  C    ___
GAM768  KIAA0367  3' GCTACTTTCACACTACAGC   67300      C        GG
                                GCTG AGTGTGAAAG  GC
                                |||| ||||||||||  ||
                                CGAC TCACACTTTC  CG
                                  A        AT
GAM768  KIAA0542  3' GCCCAGCAGAGACTGCAGCTG  66086          GTGAAAG
                                CAGCTGCAGT      GGGC
                                ||||||||||      ||||
                                GTCGACGTCA      CCCG
                                     GAGACGA
GAM768  KIAA0562  3' GCCCCTTCCACATCCATGTTG  28156      TGCA    A
                                CAGC   GTGTG AAGGGGC
                                ||||   ||||| |||||||
                                GTTG   TACAC TTCCCCG
                                  TACC    C
GAM768  KIAA0657  5' GCCCCCCCCACCGTTCGCCGCTG 72198      T  AGT__   AAA
                                CAGC GC    GTG   GGGGC
                                |||| ||    |||   |||||
                                GTCG CG    CAC   CCCCG
                                  C  CTTGC   CC_
GAM768  KIAA0779  3' CCCCAACCTCAGCTG      85724       C  T  GAAA
                                CAGCTG AG GT    GGGG
                                |||||| || ||    ||||
                                GTCGAC TC CA    CCCC
                                   _ _  A___
GAM768  KIAA0789  3' GCCCCTTTCTATCCATGCTG   63684      TGCA   T
                                CAGC    GTG GAAAGGGGC
                                ||||    ||| |||||||||
                                GTCG    TAT CTTTCCCCG
                                  TACC   _
GAM768  KIAA0852  3' GCCCCTCAACCCTGTAGCTG   30079         T  GAA
                                CAGCTGCAG GT   AGGGGC
                                |||||||| ||   ||||||
                                GTCGATGTC CA   TCCCCG
                                     C  AC_
GAM768  KIAA0863  5' GCCCCTTTGTGACAACTG    95246      _ G__
                                CAGT GT   AAAGGGGC
                                |||| ||   ||||||||
                                GTCA CA   TTTCCCCG
                                  A  GTG
GAM768  KIAA0960  3' TTCCTCATCACTGCAGC     92658          _   AA
                                GCTGCAGTG TGA  GGGG
                                ||||||||| |||  ||||
```

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                              CGACGTCAC ACT  CCTT
                                   T  __
GAM768  KIAA1023  3' GCCCCTTTTTACACAGCTG   34262      GCA     _
                              CAGCT  GTGTGAAA GGGGC
                              |||||  |||||||| |||||
                              GTCGA  CACATTTT CCCCG
                                 ___      T
GAM768  KIAA1054  3' GCCCCTCTCACAGACAG    68439    CAG    A
                              CTG  TGTGA AGGGGC
                              |||  ||||| ||||||
                              GAC  ACACT TCCCCG
                                AG_    C
GAM768  KIAA1077  3' GCCCCGTCTCACTGCAG    72907       T  AA
                              CTGCAGTG GA  GGGGC
                              |||||||| ||  |||||
                              GACGTCAC CT  CCCCG
                                   T  G_
GAM768  KIAA1130  3' CCCTATCCCTGCAGCTG    62414       TGT  A
                              CAGCTGCAG  GA AGGG
                              |||||||||  || ||||
                              GTCGACGTC  CT TCCC
                                   C__  A
GAM768  KIAA1183  3' CCCCTCCCATAGGCTG     62528     GCAG   AA
                              CAGCT   TGTG  AGGGG
                              |||||   ||||  |||||
                              GTCGG   ATAC  TCCCC
                                 _____  CC
GAM768  KIAA1283  5' GCCCCTCTTTCACAACCAG  72059    CAG    __
                              CTG  TGTGAA  AGGGGC
                              |||  ||||||  ||||||
                              GAC  ACACTT  TCCCCG
                                CA_    TC
GAM768  KIAA1297  5' GCCCCGCCCACTGCAGC    72180       TGAAA
                              GCTGCAGTG   GGGGC
                              |||||||||   |||||
                              CGACGTCAC   CCCCG
                                   CCG__
GAM768  KIAA1441  3' GCCCCCTACCCCTGCAGT   88411      T_  AAA
                              GCTGCAG  GTG  GGGGC
                              |||||||  |||  |||||
                              TGACGTC  CAT  CCCCG
                                 CC  C__
GAM768  KIAA1484  3' GCCCCCTGACACTGCAGC   69976       GAAA
                              GCTGCAGTGT   GGGGC
                              ||||||||||   |||||
                              CGACGTCACA   CCCCG
                                   GTC_
GAM768  KIAA1614  3' GCCCTAGGCAACTGCAGCTG  70119       G  AAA
                              CAGCTGCAGT TG  GGGGC
                              |||||||||| ||  |||||
```

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                                GTCGACGTCA AC   TCCCG
                                      _ GGA
GAM768  KIAA1656 3' GCCCCTTTCACTAGGCA     65797     AGT
                                TGC   GTGAAAGGGGC
                                |||   ||||||||||
                                ACG   CACTTTCCCCG
                                  GAT
GAM768  KIAA1908 5' CCCCTTTTGCCAGCTG      73396       CAGT TG
                                CAGCTG    G  AAAGGGG
                                ||||||    |  |||||||
                                GTCGAC    C  TTTCCCC
                                   ____ GT
GAM768  KIAA1949 3' GCCCCTTTGTTTACAGCT    97751      C  TGTG
                                AGCTG AG    AAAGGGGC
                                ||||| ||    ||||||||
                                TCGAC TT    TTTCCCCG
                                   A  TG__
GAM768  KIAA1949 3' GCCCCTTTGTTTACAGCT    97873      C  TGTG
                                AGCTG AG    AAAGGGGC
                                ||||| ||    ||||||||
                                TCGAC TT    TTTCCCCG
                                   A  TG__
GAM768  KIAA1949 3' GCCCCTTTGTTTACAGCT    92083      C  TGTG
                                AGCTG AG    AAAGGGGC
                                ||||| ||    ||||||||
                                TCGAC TT    TTTCCCCG
                                   A  TG__
GAM768  LLGL2    3' GCTTCCACAATGCAGCTG    15752        G    AAA
                                CAGCTGCA TGTG   GGGGC
                                |||||||| ||||   |||||
                                GTCGACGT ACAC   CTTCG
                                     A   ___
GAM768  MAGE-E1  5' GCCCCCTCCCCCTGCAGCTG  47946         TGT  AA
                                CAGCTGCAG   GA  GGGGC
                                |||||||||   ||  |||||
                                GTCGACGTC   CT  CCCCG
                                      CCC  C_
GAM768  MCF2L    3' GCCCCTGCCTCACTGCACTG   60845     C      TGAA
                                CAG TGCAGTG    AGGGGC
                                ||| |||||||    ||||||
                                GTC ACGTCAC    TCCCCG
                                  _      TCCG
GAM768  MGC10981 3' CCCCACACTGCAGC        51015          AAA
                                GCTGCAGTGTG   GGG
                                ||||||||||   |||
                                CGACGTCACAC   CCC
                                        ___
GAM768  MGC12760 3' GCTCCCCACACTGCA       51175         AAA
                                TGCAGTGTG   GGGGC
                                |||||||||   |||||
```

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                                ACGTCACAC  CCTCG
                                    C__
GAM768  MGC12904 3' GCCCCTTCTTTCTCCACAGCT 48334     C__ TGT  A
                                AGCTG  AG  GAA GGGGC
                                |||||  ||  ||| |||||
                                TCGAC  TC  CTT CCCCG
                                  ACC  TTT  _
GAM768  MGC16025 5' GCCCCCTCTGGCTGCACTG  51922    C    GT  AA
                                CAG TGCAGT  GA  GGGGC
                                ||| ||||||  ||  |||||
                                GTC ACGTCG  CT  CCCCG
                                  _    GT  C_
GAM768  MGC16179 3' GCCCCTCCCAGTTCTGCGGCTG 51303       TG_  AA
                                CAGCTGCAG  TG  AGGGGC
                                |||||||||  ||  ||||||
                                GTCGGCGTC  AC  TCCCCG
                                     TTG  CC
GAM768  MGC16703 3' CCCCTTTTCACGTCAGCT   73099     CA  T
                                AGCTG  GTG GAAAGGGG
                                |||||  ||| ||||||||
                                TCGAC  CAC TTTTCCCC
                                  TG  _
GAM768  MGC3035  5' GCCCCTGCTCATGCAGCTG  44151      GTG  A_
                                CAGCTGCA  TGA  AGGGGC
                                ||||||||  |||  ||||||
                                GTCGACGT  ACT  TCCCCG
                                    ____  CG
GAM768  MGC3113  3' CCCCCTTCGCCAGCAGCT   43844     AGT   A
                                AGCTGC  GTGAA GGGG
                                ||||||  ||||| ||||
                                TCGACG  CGCTT CCCC
                                  AC_   C
GAM768  MGC3130  3' GCCCCCTCATCTCTGCGCTG  43821    T  T_  AA
                                CAGC GCAG  GTGA  GGGGC
                                |||| ||||  ||||  |||||
                                GTCG CGTC  TACT  CCCCG
                                  _  TC  C_
GAM768  MGC4604  3' GCCCCTTTCTCTACTGAGCT  48979    G   T_
                                AGCT CAGTG  GAAAGGGGC
                                |||| |||||  |||||||||
                                TCGA GTCAT  CTTTCCCCG
                                  _   CT
GAM768  MGC4701  5' CCCCCGTCTTCTGCAGCT   64557      TGT  AA
                                AGCTGCAG  GA  GGGG
                                ||||||||  ||  ||||
                                TCGACGTC  CT  CCCC
                                    TT_  GC
GAM768  MRPS2    3' GCCCCTTGGCTGCAGTT    32091       GTGA
                                AGCTGCAGT   AAGGGGC
                                |||||||||   |||||||
```

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                                TTGACGTCG   TTCCCCG
                                    G___
GAM768  NFAT5   5'  CCCCTCCGCGCCTGCGCTG   56942     T   T  AA_
                                CAGC GCAG GTG   AGGGG
                                |||| |||| |||   |||||
                                GTCG CGTC CGC   TCCCC
                                  _   _  GCC
GAM768  NICE-1  3'  CCCCCAGCGCTGCGCT     38803     T     GAAA
                                AGC GCAGTGT   GGGG
                                ||| |||||||   ||||
                                TCG CGTCGCG   CCCC
                                  _     AC__
GAM768  NMT1    3'  GCCCCTTTCCAAGATACAGC  40785     CAG__  T
                                GCTG    TG GAAAGGGGC
                                ||||    || |||||||||
                                CGAC    AC CTTTCCCCG
                                  ATAGA  _
GAM768  P17.3   5'  CCCCACTGCAGCTG       38795         GTGAAA  _
                                CAGCTGCAGT    GGG G
                                ||||||||||    ||| |
                                GTCGACGTCA    CCC C
                                      _______  A
GAM768  PIP5K2B 5'  CCTCTTTCGCCGCCGC     56893    T  AGT
                                GC GC   GTGAAAGGGG
                                || ||   ||||||||||
                                CG CG   CGCTTTCTCC
                                 C  C__
GAM768  PIP5K2B 5'  CCTCTTTCGCCGCCGC     13071    T  AGT
                                GC GC   GTGAAAGGGG
                                || ||   ||||||||||
                                CG CG   CGCTTTCTCC
                                 C  C__
GAM768  PLEKHA3 5'  GCCCCCAAGCTCCACGCTG   38862     _ C   G  AAA
                                CAGC TG AGT TG   GGGGC
                                |||| || ||| ||   |||||
                                GTCG AC TCG AC   CCCCG
                                  C  C   A  ___
GAM768  PP1057  5'  GCCCCCTCCAAACTGCAGCTG 48434         G  AAA
                                CAGCTGCAGT TG   GGGGC
                                |||||||||| ||   |||||
                                GTCGACGTCA AC   CCCCG
                                      A  CTC
GAM768  PPM1G   3'  CTCCACACTGCAGC       10710         AAA
                                GCTGCAGTGTG   GGG
                                ||||||||||   |||
                                CGACGTCACAC   CTC
                                        ___
GAM768  PPP1R10 3'  CCCCTGTGGACTGCAGC     10730        G GAA
                                GCTGCAGT T   AGGGG
                                |||||||| |   |||||
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                                CGACGTCA G   TCCCC
                                     G TG_
GAM768  PRO2405  3'  CCCCCCGTGCAGCTG      37799        G  TGAAA
                                CAGCTGCA TG    GGGG
                                |||||||| ||    ||||
                                GTCGACGT GC    CCCC
                                     _  C____
GAM768  PRO2605  3'  GCCCCTGTGCCTGCTACT    94857    CT   T  GAA
                                AG  GCAG GT   AGGGGC
                                ||  |||| ||   ||||||
                                TC  CGTC CG   TCCCCG
                                 AT    _  TG_
GAM768  RGS19    5'  CCCCTTTCGGCAGC       19650      AGTG
                                GCTGC    TGAAAGGGG
                                |||||    |||||||||
                                CGACG    GCTTTCCCC

                                 ____
GAM768  RNPC1    5'  GCCCCCCATGCTGCTGCAGC   33990        _   AAA
                                GCTGCAGT GTG   GGGGC
                                |||||||| |||   |||||
                                CGACGTCG CGT   CCCCG
                                     T   ACC
GAM768  SFXN5    3'  GCCCCTTTGGACCTGCAGTTG  58036         T  G_
                                CAGCTGCAG GT  AAAGGGGC
                                ||||||||| ||  ||||||||
                                GTTGACGTC CA  TTTCCCCG
                                     _  GG
GAM768  SH3BGRL3 5'  CCCGGCAGTGCAGCTG      48437        G   GAAAG
                                CAGCTGCA TGT    GGG
                                |||||||| |||    |||
                                GTCGACGT ACG    CCC
                                     G   G____
GAM768  SNX10    3'  GCCCCTTTTAAAGCATCT    25265    C   AGTG
                                AG TGC    TGAAAGGGGC
                                || |||    ||||||||||
                                TC ACG    ATTTTCCCCG
                                 T   AA__
GAM768  SR-BP1   3'  GCCCCCTTCACCTGCAGCT    19634        T    A
                                AGCTGCAG GTGAA GGGGC
                                |||||||| ||||| |||||
                                TCGACGTC CACTT CCCCG
                                     _    C
GAM768  SRCRB4D  3'  CCCCTCCCTGCAGCTG      54955        TGTGAA
                                CAGCTGCAG     AGGGG
                                |||||||||     |||||
                                GTCGACGTC     TCCCC
                                     CC_____
GAM768  ST13     3'  CCCCTCTCCCCCAAATGCAGCT 14115        GTGT___  A
             G                   CAGCTGCA      GA AGGGG
                                ||||||||      || |||||
```

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                                GTCGACGT      CT TCCCC
                                     AAACCCC  C
GAM768  STX4A    3'  CCCCTTCCTCACACTG      16016         __
                                CAGTGTGA  AAGGGG
                                ||||||||  ||||||
                                GTCACACT  TTCCCC
                                     CC
GAM768  TNFRSF19L 3'  GCCCCTGGCCCTGCTGC     51777    T    T  GAA
                                GC GCAG GT   AGGGGC
                                || |||| ||   ||||||
                                CG CGTC CG   TCCCCG
                                 T   C  G__
GAM768  TRAP25   5'  GCCCCTTCCGGCCTGAAGCTG  54676      G   TG  A
                                CAGCT CAG  TG AAGGGGC
                                ||||| |||  || |||||||
                                GTCGA GTC  GC TTCCCCG
                                   A   CG  C
GAM768  TUBB5    3'  CCCCTCCCTCCGAGCTG     20298      GCAG  T  A__
                                CAGCT    TG GA   AGGGG
                                |||||    || ||   |||||
                                GTCGA    GC CT   TCCCC
                                   _____ _  CCC
GAM768  ZF       3'  GCCCCTCACAATGCAGCTG    41088        G     AA
                                CAGCTGCA TGTGA  GGGGC
                                |||||||| |||||  |||||
                                GTCGACGT ACACT  CCCCG
                                     A    __
GAM768  LOC112885 3'  CCCCTTTCTGTCAGT       56521      _  GTGT
                                GCTG CA    GAAAGGGG
                                |||| ||    ||||||||
                                TGAC GT    CTTTCCCC
                                  T  _____
GAM768  LOC113220 3'  CTCCACCTGCAGCTG       56551          T   AAA
                                CAGCTGCAG GTG   GGG
                                |||||||||  |||   |||
                                GTCGACGTC CAC   CTC
                                     _   ____
GAM768  LOC121793 5'  GCCCCTTCATCTGTCAGCTG   74114        _  T    A
                                CAGCTG CAG GTGAA GGGGC
                                |||||| ||| ||||| |||||
                                GTCGAC GTC TACTT CCCCG
                                   T  _    _
GAM768  LOC124842 5'  GCCCCTTGGAGATCTTGCAGCT 75659          T  GA__
          G                      CAGCTGCAG GT    AAGGGGC
                                |||||||||  ||    |||||||
                                GTCGACGTT TA    TTCCCCG
                                     C  GAGG
GAM768  LOC124930 3'  CCCCTTCCCACCAGCTGCTGCT 74356     T    __   A_
                                AGC GCAGT  GTG  AAGGGG
                                ||| |||||  |||  ||||||
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                                TCG CGTCG  CAC  TTCCCC
                                  T    AC   CC
GAM768  LOC124977 5'  TCCCTTCCTCACTGCAGC    76065        TGA
                                GCTGCAGTG   AAGGGG
                                |||||||||   ||||||
                                CGACGTCAC   TTCCCT
                                     TCC
GAM768  LOC128402 3'  GCCCCTTTCCACCAGC      75782      CA   T
                                GCTG  GTG GAAAGGGGC
                                ||||  ||| |||||||||
                                CGAC  CAC CTTTCCCCG
                                  __   _
GAM768  LOC130639 3'  CCTGACACTGCACTG       74968     C      GAAAG
                                CAG TGCAGTGT    GGG
                                ||| ||||||||    |||
                                GTC ACGTCACA    TCC
                                  _      G____
GAM768  LOC130644 3'  CCCCCACACCCATTGCAGCTG  75753        ____    AAA
                                CAGCTGCA   GTGTG   GGGG
                                ||||||||   |||||  ||||
                                GTCGACGT   CACAC   CCCC
                                     TACC    ___
GAM768  LOC138399 5'  CCCCTTTCCCTGCAGGCT    75326     _    TGT
                                AGC TGCAG   GAAAGGGG
                                ||| |||||   ||||||||
                                TCG ACGTC   CTTTCCCC
                                  G    C__
GAM768  LOC143451 3'  CTCCTCCCCACTGCAGC     76563        TGAA
                                GCTGCAGTG   AGGGG
                                |||||||||   |||||
                                CGACGTCAC   TCCTC
                                     CCC_
GAM768  LOC144110 3'  GCCCCTTTCACAGGCCCCT   76673    CT  AG
                                AG  GC  TGTGAAAGGGGC
                                ||  ||  ||||||||||||
                                TC  CG  ACACTTTCCCCG
                                 CC  G_
GAM768  LOC144483 3'  GCCCCTCCCACCTGCA      60178      T   AA
                                TGCAG GTG  AGGGGC
                                ||||| |||  ||||||
                                ACGTC CAC  TCCCCG
                                  _   CC
GAM768  LOC145125 3'  CTCCTCCCCACTGCAGC     77005        TGAA
                                GCTGCAGTG   AGGGG
                                |||||||||   |||||
                                CGACGTCAC   TCCTC
                                     CCC_
GAM768  LOC145623 3'  GCCAGGCACCCTGCAGCTG   83396         T   AAAGG
                                CAGCTGCAG GTG    GGC
                                ||||||||| |||    |||
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                                GTCGACGTC CAC    CCG
                                     C  GGA__
GAM768  LOC146287 5'  CCCAGAGGCCATTGCAGCTG  83651         TGAAAG
                                CAGCTGCAGTG    GGG
                                ||||||||||    |||
                                GTCGACGTTAC    CCC
                                     CGGAGA
GAM768  LOC146823 3'  GCCCCTATTCCGCACGCTG   83799    TGCA   _ _
                                CAGC   GTGTG AA AGGGGC
                                ||||   ||||| || ||||||
                                GTCG   CACGC TT TCCCCG
                                  ____   C  A
GAM768  LOC146988 3'  CCCCTCAAAATCACCCCAGCTG 83893      CA  TGAA__
                                CAGCTG  GTG    AGGGG
                                ||||||  |||    |||||
                                GTCGAC  CAC    TCCCC
                                   CC   TAAAAC
GAM768  LOC147136 5'  CCCCCTCCACTCAGC      78262     C   T  AA
                                GCTG AGTG GA  GGGG
                                |||| |||| ||  ||||
                                CGAC TCAC CT  CCCC
                                  _   _ C_
GAM768  LOC148758 5'  GCCCTAGGCAACTGCAGCTG  78971        G  AAA
                                CAGCTGCAGT TG  GGGGC
                                |||||||||| ||  |||||
                                GTCGACGTCA AC  TCCCG
                                     _ GGA
GAM768  LOC150848 5'  GCCCCTTTCCTTGCAG     85129      TGT
                                CTGCAG  GAAAGGGGC
                                ||||||  |||||||||
                                GACGTT  CTTTCCCCG
                                   C__
GAM768  LOC151391 3'  CCCCTTTATTTGCAGTTG    85331        TGTG
                                CAGCTGCAG   AAAGGGG
                                |||||||||   |||||||
                                GTTGACGTT   TTTCCCC
                                     TA__
GAM768  LOC155179 3'  GCCCCTTTTTACACAGCTG   81316     GCA     _
                                CAGCT  GTGTGAAA GGGGC
                                |||||  |||||||| |||||
                                GTCGA  CACATTTT CCCCG
                                  ____      T
GAM768  LOC157869 3'  GCCCCTTTCATTTGTGAAGT  81626    __   T
                                GCT  GCAG GTGAAAGGGGC
                                |||  |||| ||||||||||
                                TGA  TGTT TACTTTCCCCG
                                  AG   _
GAM768  LOC158373 5'  CCCCAGCACTGCAGGC     71043    _      GAAA
                                GC TGCAGTGT   GGGG
                                || ||||||||   ||||
```

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                                CG ACGTCACG    CCCC
                                 G       A___
GAM768   LOC158886 3'  CCCCTCTCCCCCAAATGCAGCT 82833        GTGT___  A
              G                   CAGCTGCA      GA AGGGG
                                  ||||||||      || |||||
                                  GTCGACGT      CT TCCCC
                                       AAACCCC  C
GAM768   LOC158972 3'  CCCCTCCCATGAAGCGCTG   86947     T  AG    AA
                                  CAGC GC  TGTG  AGGGG
                                  |||| ||  ||||  |||||
                                  GTCG CG  GTAC  TCCCC
                                    _ AA    CC
GAM768   LOC159184 5'  CCCCTTCATGCAGCAGCT    60046       A      A
                                  AGCTGC GTGTGAA GGGG
                                  |||||| ||||||| ||||
                                  TCGACG CGTACTT CCCC
                                     A      _
GAM768   LOC161048 5'  GCCATGGACATGCAGCTG    82259        G   GAAAGG
                                  CAGCTGCA TGT     GGC
                                  |||||||| |||     |||
                                  GTCGACGT ACA     CCG
                                       _   GGTA__
GAM768   LOC164945 5'  GCCCCCCGAGCAGCTGCAGC   87186        _   GAAA
                                  GCTGCAG TGT    GGGGC
                                  ||||||| |||    |||||
                                  CGACGTC ACG    CCCCG
                                       G   AGCC
GAM768   LOC170395 3'  GCCCCTCAGTTTGCAG      76371       TG   AA
                                  CTGCAG  TGA  GGGGC
                                  ||||||  |||  |||||
                                  GACGTT  ACT  CCCCG
                                     TG   __
GAM768   LOC197285 3'  CCCAACATGCAGCTG       87790        G   GAAAG
                                  CAGCTGCA TGT    GGG
                                  |||||||| |||    |||
                                  GTCGACGT ACA    CCC
                                       _   A____
GAM768   LOC197285 3'  CCCCCATCCTGCAGCTG     87791         TG  AAA
                                  CAGCTGCAG  TG   GGGG
                                  |||||||||  ||   ||||
                                  GTCGACGTC  AC   CCCC
                                        CT  ____
GAM768   LOC197358 3'  GCCCCTTTCCACTCACCTG    88038     C  C    T
                                  CAG TG AGTG GAAAGGGGC
                                  ||| || |||| |||||||||
                                  GTC AC TCAC CTTTCCCCG
                                    C  _    _
GAM768   LOC199906 5'  CCCCTTTCTCTGGGACAGT    88478      ___   TGT
                                  GCTG   CAG   GAAAGGGG
                                  ||||   |||   ||||||||
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```
                                TGAC   GTC   CTTTCCCC
                                  AGG   T__
GAM768   LOC199989 3'  GCCCCTCCCGCTGCAGC     89894         T  AA
                                GCTGCAGTG GA  GGGGC
                                ||||||||| ||  |||||
                                CGACGTCGC CT  CCCCG
                                     C  __
GAM768   LOC200035 5'  GCCCATTCACTGCAGCT     73254          TGAAAG
                                AGCTGCAGTG     GGGC
                                ||||||||||     ||||
                                TCGACGTCAC     CCCG
                                     TTA___
GAM768   LOC200301 5'  CCCTCCATTGCAGC        88740          T  AA
                                GCTGCAGTG GA  GGG
                                ||||||||| ||  |||
                                CGACGTTAC CT  CCC
                                     _  __
GAM768   LOC200958 3'  GCCCCCACCGACAGACTGCAGC 65925          G  AAA___
           TG                     CAGCTGCAGT TG     GGGGC
                                ||||||||||| ||     |||||
                                GTCGACGTCA AC     CCCCG
                                     G  AGCCAC
GAM768   LOC202025 5'  GCCCCTTTGTGCTGTA      90292       TG G
                                TGCAG  T AAAGGGGC
                                |||||  | ||||||||
                                ATGTC  G TTTCCCCG
                                   GT _
GAM768   LOC202126 3'  GCCCCTTTGGGTTCCAGC    90314      C  TG G
                                GCTG AG  T AAAGGGGC
                                ||||  ||  | ||||||||
                                CGAC TT  G TTTCCCCG
                                  C  GG _
GAM768   LOC202284 5'  GCCCCTTTCACCCTGC      90329      T
                                GCAG GTGAAAGGGGC
                                |||| ||||||||||
                                CGTC CACTTTCCCCG
                                  C
GAM768   LOC204970 3'  GCCCCTTGGCTGCAGC      89410         GTGA
                                GCTGCAGT    AAGGGGC
                                ||||||||    |||||||
                                CGACGTCG    TTCCCCG
                                     G___
GAM768   LOC219920 5'  GCCCCGCTCCTGCAGCTG    93314         TGT  AA
                                CAGCTGCAG   GA  GGGGC
                                |||||||||   ||  |||||
                                GTCGACGTC   CT  CCCCG
                                     ___  CG
GAM768   LOC220827 3'  TTTTCACACTACACT       91247     C  C
                                AG TG AGTGTGAAAG
                                || || ||||||||||
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                                TC AC TCACACTTTT
                                 _  A
GAM768  LOC245718 3'  CCCCTCTCCCCCAAATGCAGCT 90719        GTGT___  A
                G                CAGCTGCA      GA AGGGG
                                 ||||||||      || |||||
                                 GTCGACGT      CT TCCCC
                                      AAACCCC  C
GAM768  LOC254105 3'  GCCCCTGGGCCTGCACTG    94770     C    T  GAA
                                 CAG TGCAG GT   AGGGGC
                                 ||| ||||| ||   ||||||
                                 GTC ACGTC CG   TCCCCG
                                   _    _  GG_
GAM768  LOC254263 3'  CCCCCAAACTGCTGCTG     94717      T    G  AAA
                                 CAGC GCAGT TG   GGGG
                                 |||| ||||| ||   ||||
                                 GTCG CGTCA AC   CCCC
                                   T    A  ___
GAM768  LOC254440 3'  CTCCTCCCCACTGCAGC     97065         TGAA
                                 GCTGCAGTG    AGGGG
                                 |||||||||    |||||
                                 CGACGTCAC    TCCTC
                                      CCC_
GAM768  LOC254873 3'  TTCCTTTCCTCTGCAGC     94574        TGT
                                 GCTGCAG   GAAAGGGG
                                 |||||||   ||||||||
                                 CGACGTC   CTTTCCTT
                                     TC_
GAM768  LOC256158 5'  CCCACACGCTGCAGCTG     97656           AAA
                                 CAGCTGCAGTGTG   GGG
                                 ||||||||||||   |||
                                 GTCGACGTCGCAC   CCC
                                        A__
GAM768  LOC256158 5'  CCCAGCCTGCAGCTG       97657         T  GAAAG
                                 CAGCTGCAG GT    GGG
                                 |||||||||  ||    |||
                                 GTCGACGTC CG    CCC
                                      _  A____
GAM768  LOC256598 5'  GCCCCTCGTGGCTGCAGC    96352        GTGAA
                                 GCTGCAGT    AGGGGC
                                 ||||||||    ||||||
                                 CGACGTCG    TCCCCG
                                      GTGC_
GAM768  LOC257203 5'  GCCCCCTGGCGCCCAGCTG   96931       CA   GAAA
                                 CAGCTG  GTGT    GGGGC
                                 ||||||  ||||    |||||
                                 GTCGAC  CGCG    CCCCG
                                    C_    GTC_
GAM768  LOC257319 3'  GCCCCTTATACACATGCTG   95774      TGCA    A
                                 CAGC    GTGTG AAGGGGC
                                 ||||    ||||| |||||||
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                                GTCG    CACAT TTCCCCG
                                  TA__     A
GAM768  LOC257476 3'  CCCCTTCCTCTCCACTGCAGGC 61252    _      T ____
                                GC TGCAGTG GA    AAGGGG
                                || ||||||| ||    ||||||
                                CG ACGTCAC CT    TTCCCC
                                 G      _ CTCC
GAM768  LOC257539 3'  CCCCTTCCTCACACTG      97700         __
                                CAGTGTGA  AAGGGG
                                ||||||||  ||||||
                                GTCACACT  TTCCCC
                                     CC
GAM768  LOC257578 3'  CCCCTTCCTCACACTG      97820         __
                                CAGTGTGA  AAGGGG
                                ||||||||  ||||||
                                GTCACACT  TTCCCC
                                     CC
GAM768  LOC51195  3'  GCCCCCTCCCTGCTACTG    32945     CT    TGT  AA
                                CAG  GCAG   GA  GGGGC
                                |||  ||||   ||  |||||
                                GTC  CGTC   CT  CCCCG
                                  AT    C__  C_
GAM768  LOC54103  5'  GCCCCTAGGGCCACTACACTG  94214     C  C    TGAA_
                                CAG TG AGTG     AGGGGC
                                ||| || ||||     ||||||
                                GTC AC TCAC     TCCCCG
                                  _ A    CGGGA
GAM768  LOC55971  3'  GCCCCTTTATTACAGC      38129      C    TGA
                                GCTG AGTG   AAGGGGC
                                |||| ||||   |||||||
                                CGAC TTAT   TTCCCCG
                                  A    ____
GAM768  LOC84570  5'  GCCCCTTTCGCGCTGCGCTG   50711      T
                                CAGC GCAGTGTGAAAGGGGC
                                |||| ||||||||||||||||
                                GTCG CGTCGCGCTTTCCCCG
                                  _
GAM768  LOC85414  3'  GCCCCTTAACCTGCAGCT    52398         T  GA
                                AGCTGCAG GT  AAGGGGC
                                |||||||| ||  |||||||
                                TCGACGTC CA  TTCCCCG
                                     _ A_
GAM768  LOC87769  5'  CCTGGGTTCTCACTGCAGCTG  71321           T   AG_
                                CAGCTGCAGTG GAA   GGG
                                |||||||||| |||   |||
                                GTCGACGTCAC CTT   TCC
                                       T   GGG
GAM768  LOC90024  3'  GCCCCTCTCCCCGACCAACTG  61112     C  CAG  T_  A
                                CAG TG   TG  GA AGGGGC
                                ||| ||   ||  || ||||||
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                                GTC AC   GC  CT TCCCCG
                                  A  CA_  CC  C
GAM768  LOC90719  3' GCAGAATCTCACTGCAGCTG   63884          T  AAGGG
                                CAGCTGCAGTG GA     GC
                                |||||||||||  ||     ||
                                GTCGACGTCAC CT     CG
                                      T  AAGA_
GAM768  LOC90768  5' GCCCCTGGTGGGCACTGCAGC  63956          GAA__
                                GCTGCAGTGT    AGGGGC
                                ||||||||||    ||||||
                                CGACGTCACG    TCCCCG
                                      GGTGG
GAM768  LOC91464  5' CCCCTCAAGCTGCAGT      66138        G   AA
                                GCTGCAGT TGA  GGGG
                                ||||||||  |||  ||||
                                TGACGTCG ACT  CCCC
                                    A   __
GAM768  LOC91526  5' CCCCTCTGCATGCTGCAGC    66336          AA_
                                GCTGCAGTGTG   AGGGG
                                ||||||||||   |||||
                                CGACGTCGTAC   TCCCC
                                      GTC
GAM768  LOC91917  3' CCCAACATGCAGCTG       67528        G   GAAAG
                                CAGCTGCA TGT    GGG
                                ||||||||  |||    |||
                                GTCGACGT ACA    CCC
                                    _   A____
GAM768  LOC92148  5' GCCCCTGACCACACTGCCACT  68333    CT      AA_
                                AG  GCAGTGTG   AGGGGC
                                ||  ||||||||   ||||||
                                TC  CGTCACAC   TCCCCG
                                  AC       CAG
GAM768  LOC92299  3' GCCATCACACTGCAGC      68811          AAGG
                                GCTGCAGTGTGA   GGC
                                ||||||||||||   |||
                                CGACGTCACACT   CCG
                                      A___
GAM768  LOC92573  5' CCCCTTTCTGTCAGCT      69804      _  GTGT
                                AGCTG CA   GAAAGGGG
                                |||||  ||   ||||||||
                                TCGAC GT   CTTTCCCC
                                   T  ____
GAM768  LOC92840  3' CCGAGATCACCTGCAGCTG    56431        T   AA__
                                CAGCTGCAG GTGA   GG
                                |||||||||  ||||   ||
                                GTCGACGTC CACT   CC
                                    _   AGAG
GAM768  LOC93070  5' GCCCCTTTGCAGCCGCTG    71293     T  AG   G
                                CAGC GC  TGT AAAGGGGC
                                ||||  ||  |||  ||||||||
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                                GTCG CG  ACG TTTCCCCG
                                  C __  _
GAM768  LOC93320  3'  GCCAAGCCCACTGCAGCTG   72051          TGAAAGG
                                CAGCTGCAGTG      GGC
                                ||||||||||      |||
                                GTCGACGTCAC      CCG
                                     CCGAA__
GAM769  ADAMTS8   5'  TCGGGCCGCCAGCACCTG    22886    _     ATAAG
                                CAG TGCTGGC    CTGA
                                ||| |||||||    ||||
                                GTC ACGACCG    GGCT
                                  C      CCG__
GAM769  BAP1      3'  TCAGGGACCCAGCACTGG    16219          CATAAG
                                CCAGTGCTGG     CTGA
                                ||||||||||     ||||
                                GGTCACGACC     GACT
                                     CAGG__
GAM769  BF        5'  TTCAGCTTGGACACTG      8140       CTGGCA
                                CAGTG     TAAGCTGAA
                                |||||     |||||||||
                                GTCAC     GTTCGACTT
                                  AG____
GAM769  C1QB      3'  TTCAACTCTGTGTCCCAGCACT 4923    A        __   _ C
           GGC                    G CCAGTGCTGG  CATA AG TGAA
                                | ||||||||||  |||| || ||||
                                C GGTCACGACC  GTGT TC ACTT
                                _        CT    C  A
GAM769  CHC1      3'  CAGCCCTGAGCACTGTGTC    7020     _     __ CATAA
                                GAC CAGTGCT  GG    GCTG
                                ||| |||||||  ||    ||||
                                CTG GTCACGA  CC    CGAC
                                  T      GT  _____
GAM769  CMRF35    5'  CAGAGCTGTCAGCACCGG    21929    A       TAAG
                                CC GTGCTGGCA    CTG
                                || |||||||||    |||
                                GG CACGACTGT    GAC
                                 C        CGA_
GAM769  EPHB6     3'  TCAGCCCTGGACACTGGTC    15466        _ TG CATAA
                                GACCAGTG C  G    GCTGA
                                |||||||| |  |    |||||
                                CTGGTCAC G  C    CGACT
                                     A GT C____
GAM769  EVPL      5'  CAGCCTGAGCCAGCACT     8803          A  A
                                AGTGCTGGC TA GCTG
                                ||||||||| || ||||
                                TCACGACCG GT CGAC
                                     A  C
GAM769  GARP      3'  CAGCCCAGCACTGG        18594          CATAA
                                CCAGTGCTGG    GCTG
                                ||||||||||    ||||
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                                GGTCACGACC    CGAC
                                      _____
GAM769  GJB5    3'  CAGCTCGACGGCACTGG     17945        GCATA
                                CCAGTGCTG    AGCTG
                                |||||||||    |||||
                                GGTCACGGC    TCGAC
                                     AGC__
GAM769  GPR81   3'  CTTACCAGCATTAGTC     50757    C      CA
                                GAC AGTGCTGG  TAAG
                                ||| ||||||||  ||||
                                CTG TTACGACC  ATTC
                                  A      __
GAM769  IFI16   5'  AGCAAGCCAGCACTAGTC    71221    C       ATAA
                                GAC AGTGCTGGC   GCT
                                ||| |||||||||   |||
                                CTG TCACGACCG   CGA
                                  A       AA__
GAM769  KRT4    3'  CAGCTGGGCCCAGCACTGGT  9635          _ ATA
                                ACCAGTGCTGG C   AGCTG
                                |||||||||||  |  |||||
                                TGGTCACGACC G   TCGAC
                                      C GG_
GAM769  MAP3K9  3'  TTCAGCTTCCCAAACACCAGT  60709   CA  C_  CAT
                                AC  GTG  TGG   AAGCTGAA
                                ||  |||  |||   ||||||||
                                TG  CAC  ACC   TTCGACTT
                                 AC   AA   C__
GAM769  MGAT5   5'  TCAGCTTACAGTTCCTG    10028    T_   GCA
                                CAG  GCTG   TAAGCTGA
                                |||  ||||   ||||||||
                                GTC  TGAC   ATTCGACT
                                  CT   ____
GAM769  MOCS1   3'  TTCAGCTTAACAGTTGCCCGGT 92037     A_  _   GCA
            C                    GACC  GTG CTG   TAAGCTGAA
                                ||||  |||  |||   |||||||||
                                CTGG  CGT GAC   ATTCGACTT
                                   CC   T   A__
GAM769  P23     3'  TCAGCTTATACCCGGGCT    21719    G   C_
                                AGT CTGG  ATAAGCTGA
                                |||  ||||  |||||||||
                                TCG GGCC  TATTCGACT
                                  _    CA
GAM769  PFKFB4  3'  TCAGCCACATGCAACACTGTGT 15874    _    CTG   AA_
            C                    GAC CAGTG   GCAT   GCTGA
                                |||  |||||   ||||   |||||
                                CTG GTCAC   CGTA   CGACT
                                  T    AA_    CAC
GAM769  PTPRK   3'  TTCAGCCTGTGGCCCAGCACTG 11125          __   A
            GTC                    GACCAGTGCTGG  CATA GCTGAA
                                ||||||||||||  ||||  ||||||
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                                CTGGTCACGACC  GTGT CGACTT
                                      CG    C
GAM769  RNPEPL1   3'  CGGATGCCAGCACCTG     36676     _       AAG
                                CAG TGCTGGCAT   CTG
                                ||| |||||||||   |||
                                GTC ACGACCGTA   GGC
                                  C       ___
GAM769  UBE2L3    3'  TCAGCCCTGGCACTGGC     12507    A      TG CATAA
                                G CCAGTGC  G    GCTGA
                                | |||||||  |    |||||
                                C GGTCACG  C    CGACT
                                 _      GT C____
GAM769  APXL2     5'  CAGCCTCAGCACTCATC     75185    CC       CATAA
                                GA  AGTGCTGG    GCTG
                                ||  ||||||||    ||||
                                CT  TCACGACT    CGAC
                                  AC       C____
GAM769  ARHGEF9   3'  TTCAGCTTACCAAGCA      30824     _  CA
                                TGCT GG  TAAGCTGAA
                                |||| ||  |||||||||
                                ACGA CC  ATTCGACTT
                                  A  __
GAM769  CEGP1     3'  TTCAGCTTCCTCTAGCCCGG   40589    AGT    CAT
                                CC   GCTGG   AAGCTGAA
                                ||   |||||   ||||||||
                                GG   CGATC   TTCGACTT
                                 CC_    TCC
GAM769  DKFZp547D155 3'  CAGCCCTGAGACCACTGGTC   70435        CTGG  TAA
                                GACCAGTG    CA   GCTG
                                ||||||||    ||   ||||
                                CTGGTCAC    GT   CGAC
                                     CAGA  CC_
GAM769  DKFZP727G051 3'  TTCAGCCCATCAACCAGCATTG 69483           CATAA__
           GTC                    GACCAGTGCTGG      GCTGAA
                                ||||||||||||      ||||||
                                CTGGTTACGACC      CGACTT
                                      AACTACC
GAM769  DUSP14    5'  CACTGTCACCAGCACTGCTC   22834    C       CATA  C
                                GA CAGTGCTGG    AG TG
                                || |||||||||    || ||
                                CT GTCACGACC    TC AC
                                 C       ACTG  _
GAM769  FLJ10206  5'  CAGCTTATGCCAGGAGTC    35898     CAGTG
                                GAC    CTGGCATAAGCTG
                                |||    |||||||||||||
                                CTG    GACCGTATTCGAC
                                  AG___
GAM769  FLJ20967  5'  GGCGCCCAGCACTGGTT     41962           CATAA
                                GACCAGTGCTGG    GCT
                                ||||||||||||    |||
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                                TTGGTCACGACC    CGG
                                      CG___
GAM769  FLJ22569 3' TTCAGCTTACTAAACTG    43679     GC  CA
                                CAGT  TGG  TAAGCTGAA
                                ||||  |||  |||||||||
                                GTCA  ATC  ATTCGACTT
                                  A_  __
GAM769  FOXN4    3' TTCAGCTTGGACACACTGG   75574       C  GCA
                                CCAGTG TG   TAAGCTGAA
                                |||||| ||   |||||||||
                                GGTCAC AC   GTTCGACTT
                                   _ AG_
GAM769  GW112    3' TTCAACTGAAGCCAGCACTGGT 21194           ATA  C
           T                     GACCAGTGCTGGC   AG TGAA
                                ||||||||||||   || ||||
                                TTGGTCACGACCG   TC ACTT
                                      AAG  A
GAM769  HOOK2    3' CAGCTCACATGGCGCCCAGCAC 25256         _____  A__
           TGG                    CCAGTGCTGG    CAT   AGCTG
                                ||||||||||    |||  |||||
                                GGTCACGACC    GTA   TCGAC
                                     CGCG   CAC
GAM769  jdp2     3' TTCAGCACAGCCAGCAT     55327        ATAA
                                GTGCTGGC    GCTGAA
                                ||||||||    ||||||
                                TACGACCG    CGACTT
                                    ACA_
GAM769  KIAA0767 3' TCTGCTGCCAGCACAGG     60632    A       TAA  T
                                CC GTGCTGGCA   GC GA
                                || |||||||||   || ||
                                GG CACGACCGT   CG CT
                                 A       ___  T
GAM769  KIAA0923 3' TCAGCTTGATGCATGGTC    25838      G   TGGCA
                                GACCA TGC    TAAGCTGA
                                ||||| |||    ||||||||
                                CTGGT ACG    GTTCGACT
                                   _  TA___
GAM769  KIAA0982 3' TTCACTGTTTGCCAGCAC    25852        TA_  C
                                GTGCTGGCA   AG TGAA
                                |||||||||   || ||||
                                CACGACCGT   TC ACTT
                                     TTG  _
GAM769  KIAA1000 3' TTCAGCTTTGCAAAGTACTGG  65281        G_   T
                                CCAGTGCT  GCA AAGCTGAA
                                ||||||||  ||| ||||||||
                                GGTCATGA  CGT TTCGACTT
                                    AA  _
GAM769  MAP3K3   3' TCAGCCTGGGCGCTGGTC    9999          GG  TAA
                                GACCAGTGCT  CA   GCTGA
                                ||||||||||  ||   |||||
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                                CTGGTCGCGG  GT   CGACT
                                      __  C__
GAM769  MGC16037  5'  CTTGTCCAGCACTAGTC     51821     C       C
                                GAC AGTGCTGG ATAAG
                                ||| |||||||| |||||
                                CTG TCACGACC TGTTC
                                  A       _
GAM769  MIDORI    3'  TCAGCTTATCCTGCAACT    73792     _  T  C
                                AGT GC GG ATAAGCTGA
                                ||| || || |||||||||
                                TCA CG CC TATTCGACT
                                  A  T  _
GAM769  MtFMT     5'  CAGTGGCGAGCACTGG      57651        G  ATAA
                                CCAGTGCT GC    GCTG
                                |||||||| ||    ||||
                                GGTCACGA CG    TGAC
                                     G  G___
GAM769  PCDH16    5'  TCAGTTCCAACCACTGG     72826       C_  CATA
                                CCAGTG  TGG    AGCTGA
                                ||||||  |||    ||||||
                                GGTCAC  ACC    TTGACT
                                   CA  _____
GAM769  QKI       3'  CAGCTTATCAACTCGTC     65439     C   GCTGGC
                                GAC AGT      ATAAGCTG
                                ||| |||      ||||||||
                                CTG TCA      TATTCGAC
                                  C   AC_____
GAM769  TNRC6     3'  CAACTTTTAGCACTG       70506         CAT   C
                                CAGTGCTGG   AAG TG
                                |||||||||   ||| ||
                                GTCACGATT   TTC AC
                                      ___   A
GAM769  TOB2      3'  CAGCCCAGGCCAGCACTG    95618          ATAA
                                CAGTGCTGGC    GCTG
                                ||||||||||    ||||
                                GTCACGACCG    CGAC
                                      GACC
GAM769  TU12B1-TY 3'  TCAGCCCACAGCACTGTC    33406     C      GCATAA
                                GAC AGTGCTG     GCTGA
                                ||| |||||||     |||||
                                CTG TCACGAC     CGACT
                                  _      ACC___
GAM769  TUSP      3'  TCAGCCTAAGAGCGCAGCACTG 39641         _  A__  A
                                CAGTGCTG GC   TA GCTGA
                                |||||||| ||   || |||||
                                GTCACGAC CG   AT CGACT
                                     G  AGA  C
GAM769  USP19     3'  TCAGCTTATGCATCTGGT    88959       TGCTG
                                ACCAG    GCATAAGCTGA
                                |||||    ||||||||||
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                                TGGTC    CGTATTCGACT
                                  TA___
GAM769  ZD52F10  3'  CAGCCTGTGCCAGCCCTGG   52819     T       A
                                CCAG GCTGGCATA GCTG
                                |||| ||||||||| ||||
                                GGTC CGACCGTGT CGAC
                                  C       C
GAM769  LOC145268 3'  TCAGCTTACAAGAGCCACTG  77062     _ GGCA
                                CAGTG CT   TAAGCTGA
                                ||||| ||   ||||||||
                                GTCAC GA   ATTCGACT
                                  C  GAAC
GAM769  LOC149296 5'  CAGCTTATGGGCAGCA     79256      G_
                                TGCTG  CATAAGCTG
                                |||||  |||||||||
                                ACGAC  GTATTCGAC
                                  GG
GAM769  LOC161877 5'  TCAGGGCAGGCCAGCGCTGG  82326          ATAAG
                                CCAGTGCTGGC    CTGA
                                ||||||||||    ||||
                                GGTCGCGACCG    GACT
                                     GACGG
GAM769  LOC163115 5'  TCAGCCCCTGACAGCACTGG  82413        G  TAA
                                CCAGTGCTG CA   GCTGA
                                |||||||| ||   |||||
                                GGTCACGAC GT   CGACT
                                     A  CCC
GAM769  LOC196500 3'  TCAGCTCACTCAGTGGTC    87744     AGT    CATA
                                GACC   GCTGG    AGCTGA
                                ||||   |||||    ||||||
                                CTGG   TGACT    TCGACT
                                  ___    CAC_
GAM769  LOC197287 3'  TCAGCTCATGTGTTTTGCACTG 60865       T_    __
                                CAGTGC  GGCATA  AGCTGA
                                ||||||  ||||||  ||||||
                                GTCACG  TTGTGT  TCGACT
                                   TT     AC
GAM769  LOC200470 5'  TCAGCCTGCGGCGCTGG     90069        G  TAA
                                CCAGTGCTG CA   GCTGA
                                |||||||| ||   |||||
                                GGTCGCGGC GT   CGACT
                                     _ C__
GAM769  LOC221584 3'  CAGCTTATGTGGCAC       93828       G
                                GTGCTG CATAAGCTG
                                |||||| |||||||||
                                CACGGT GTATTCGAC
                                  _
GAM769  LOC51716  3'  CAGCTCATGGCCCTAGCA    32787       ___  A
                                TGCTGG   CAT AGCTG
                                ||||||   ||| |||||
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                                ACGATC   GTA TCGAC
                                   CCG   C
GAM769  LOC92196  5'  CAGAGCACCAGCACTGGC    68456   A        CATAAG
                                G CCAGTGCTGG     CTG
                                | ||||||||||     |||
                                C GGTCACGACC     GAC
                                _        ACGA__
GAM770  ARHGEF7   3'  ATTGCAGCACCGTGG      14001    _ AGAA
                                CCA GG    TGCTGCAAT
                                ||| ||    |||||||||
                                GGT CC    ACGACGTTA
                                  G ____
GAM770  BFSP2     3'  AGCTTTCTCCTGAGCT      13111    C       T
                                AGC CAGGAGAA GCT
                                ||| |||||||| |||
                                TCG GTCCTCTT CGA
                                  A       T
GAM770  C21orf33  3'  ATTGCAGCTCCTCAGC      16196    CC    GAAT
                                GC  AGGA    GCTGCAAT
                                ||  ||||    ||||||||
                                CG  TCCT    CGACGTTA
                                 AC   ____
GAM770  CCND2     3'  GCACACTCTCCTGGGC      8290          A  C
                                GCCCAGGAGA TG TGC
                                |||||||||| || |||
                                CGGGTCCTCT AC ACG
                                       C  _
GAM770  CDH11     5'  GCTGCATTCTCCTGTGC     53363    C         T
                                GC CAGGAGAATGC GC
                                || ||||||||||| ||
                                CG GTCCTCTTACG CG
                                 T         T
GAM770  EPHA2     3'  TTGCTTTCCTGGGC        15410          ATGCT
                                GCCCAGGAGA     GCAA
                                ||||||||||     ||||
                                CGGGTCCTTT     CGTT
                                               _____
GAM770  F2RL3     3'  GATTGCGCCACTGGACT     14181    C   GAGAAT  T
                                AG CCAG      GC GCAATC
                                || ||||      || ||||||
                                TC GGTC      CG CGTTAG
                                 A    AC____  _
GAM770  GLP1R     3'  CACATTCTCCTGTGC       9029     C        C
                                GC CAGGAGAATG TG
                                || ||||||||| ||
                                CG GTCCTCTTAC AC
                                 T        _
GAM770  HAS3      3'  GTAGCCTCCTCCTGGGCT    18041          AAT
                                AGCCCAGGAG   GCTGC
                                |||||||||   |||||
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                                TCGGGTCCTC  CGATG
                                     CTC
GAM770  HOXA7   3'  AGATATTCTCCCAGCTT    22570     CCA      _
                                AAGC  GGAGAATG CT
                                ||||  |||||||| ||
                                TTCG  CCTCTTAT GA
                                  AC_      A
GAM770  IFI16   5'  AGATTACAACATCCTGCGGTT  71220     _   GAA  C  C
                                AGCC CAGGA  TG TG AATCT
                                |||| |||||  || || |||||
                                TTGG GTCCT  AC AC TTAGA
                                  C    ___  A  A
GAM770  IFIT4   3'  GATTGCGCCCCTGCACT    70921    CC   AGAAT  T
                                AG  CAGG    GC GCAATC
                                ||  ||||    || ||||||
                                TC  GTCC    CG CGTTAG
                                 AC   C____  _
GAM770  LILRB4  3'  AGACTCAGTTCTCCTAGG    22430    C    AT   CAA
                                CC AGGAGA  GCTG  TCT
                                || ||||||  ||||  |||
                                GG TCCTCT  TGAC  AGA
                                 A     __   TC_
GAM770  MHC2TA  3'  AGATTGCAACAGGCTGGGCTT  4162       GAGAA  C
                                AAGCCCAG    TG TGCAATCT
                                ||||||||    || ||||||||
                                TTCGGGTC    AC ACGTTAGA
                                     GG___  A
GAM770  PCDHA9  5'  GATTGCAACTCCTGG      25762      AATGC
                                CCAGGAG    TGCAATC
                                |||||||    |||||||
                                GGTCCTC    ACGTTAG
                                   A____
GAM770  PCDHA9  5'  GATTGCAACTCCTGG      49015      AATGC
                                CCAGGAG    TGCAATC
                                |||||||    |||||||
                                GGTCCTC    ACGTTAG
                                   A____
GAM770  PTK7    3'  AGATCCCTGTCCTCCTGGGC  11014       AAT  TGCA
                                GCCCAGGAG  GC   ATCT
                                |||||||||  ||   ||||
                                CGGGTCCTC  TG   TAGA
                                     C__  TCCC
GAM770  TNXB    5'  ATTCTCCCCTGGGCTT     50638      __
                                AAGCCCA  GGAGAAT
                                |||||||  |||||||
                                TTCGGGT  CCTCTTA
                                   CC
GAM770  WHSC1L1 3'  AGACTTGTTTCTCCATGGGCT  35028      _    TGCT   _
                                AGCCCA GGAGAA   GCAA TCT
                                |||||| ||||||   |||| |||
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                                TCGGGT CCTCTT   TGTT AGA
                                   A    ____   C
GAM770  C8orf14   5'  TGGTCTCTGCCTGGGCT    54006       _  AT
                                AGCCCAGG AGA  GCTG
                                |||||||| |||  ||||
                                TCGGGTCC TCT  TGGT
                                    G  C_
GAM770  CIDEB    5'  AGACCGACATCCTTCTGGGC  27041        A  C  CAA
                                GCCCAGGAG ATG TG  TCT
                                ||||||||| ||| ||  |||
                                CGGGTCTTC TAC GC  AGA
                                     C  A  C__
GAM770  DKFZP434C0826 3'  AGATCCTTCTTTCCCTGGGCTT 84032        A  TGCTGCA
                                AAGCCCAGG GAA     ATCT
                                ||||||||| |||     ||||
                                TTCGGGTCC CTT     TAGA
                                     _  TCTTCC_
GAM770  DKFZP434H132 5'  TGGAGCATCCCCTGGGCTT   73611        A  A   G
                                AAGCCCAGG GA TGCT CA
                                ||||||||| || |||| ||
                                TTCGGGTCC CT ACGA GT
                                     C  _   G
GAM770  DKFZp434O0515 5'  ATTGCAGCACTCTTGAATGCT  65926    C__    AA
                                AGC  CAGGAG  TGCTGCAAT
                                |||  ||||||  |||||||||
                                TCG  GTTCTC  ACGACGTTA
                                  TAA    __
GAM770  FLJ10759  3'  AGACCACAACCTCCTGGG   36574       AA  C  CAA
                                CCCAGGAG  TG TG  TCT
                                ||||||||  || ||  |||
                                GGGTCCTC  AC AC  AGA
                                    CA  _  C__
GAM770  FLJ11117  3'  AGATTGCCTCTCTCCCAGCT  37071    CCA    ATGCT
                                AGC  GGAGA    GCAATCT
                                |||  |||||    |||||||
                                TCG  CCTCT    CGTTAGA
                                  AC_    CTC__
GAM770  FLJ12572  3'  GATTGCAGCACAGGGC     43251     AGGAGAA
                                GCCC      TGCTGCAATC
                                ||||      ||||||||||
                                CGGG      ACGACGTTAG
                                  AC_____
GAM770  FLJ13782  3'  AGACTGGGGCTTCCTCCTGGGC 46159        AAT  G  A
                                GCCCAGGAG  GCT CA TCT
                                |||||||||  ||| || |||
                                CGGGTCCTC  CGG GT AGA
                                     CTT  G  C
GAM770  FLJ20034  5'  TGAACATCTCCTGGGTT    34388         A  CTG
                                AGCCCAGGAGA TG  CA
                                |||||||||| ||  ||
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                                TTGGGTCCTCT AC   GT
                                      _  AA_
GAM770  FLJ20195  3'  GGACTAAGCCTCCTGGGC    34712        AAT   GCAA
                                GCCCAGGAG   GCT    TCT
                                |||||||||   |||    |||
                                CGGGTCCTC   CGA    AGG
                                     ____  ATC_
GAM770  FLJ22169  3'  AGACTGAGGTCTTCCTGGGC  43997        AAT   G  A
                                GCCCAGGAG   GCT CA TCT
                                |||||||||   ||| || |||
                                CGGGTCCTT   TGG GT AGA
                                     C__   A  C
GAM770  GRIN3A    5'  AGACCGCTCCAGCTCCTGGG   55966        AA  CT  AA
                                CCCAGGAG  TG  GC  TCT
                                ||||||||  ||  ||  |||
                                GGGTCCTC  AC  CG  AGA
                                    G_  CT  CC
GAM770  HERPUD1   3'  GATTGCCTCTCCTGG      28018        ATGCT
                                CCAGGAGA    GCAATC
                                ||||||||    ||||||
                                GGTCCTCT    CGTTAG
                                    C_____
GAM770  KCND1     5'  AGACAGCCACATTCTCCT    17140        CT  AA
                                AGGAGAATG  GC  TCT
                                |||||||||  ||  |||
                                TCCTCTTAC  CG  AGA
                                     AC  AC
GAM770  KIAA0174  3'  GCACAACACTCCCTCTGGGCT  78594       ___   AA_  C
                                AGCCCA   GGAG   TG TGC
                                ||||||   ||||   || |||
                                TCGGGT   CCTC   AC ACG
                                   CTC    ACA  _
GAM770  KIAA0295  3'  TAGTATTCCCCCCAGCTT    68109     CCA  A
                                AAGC   GG GAATGCTG
                                ||||   || ||||||||
                                TTCG   CC CTTATGAT
                                  ACC  C
GAM770  KIAA0523  3'  AGATTGGCCTTACCTCTGGACT 67727     C    AG_  T  TG
           T                     AAG CCAGG   AA GC  CAATCT
                                |||  |||||   ||  ||  ||||||
                                TTC GGTCT   TT CG  GTTAGA
                                  A    CCA  C  __
GAM770  KIAA0676  3'  CAGATTCCCTGGGC       30450        A   G
                                GCCCAGG GAAT CTG
                                ||||||| |||| |||
                                CGGGTCC CTTA GAC
                                     _   _
GAM770  KIAA1318  5'  AGATTTTCTTGCCTCCTGGGCT 67305         AAT  TGC__
                                AGCCCAGGAG   GC    AATCT
                                ||||||||||   ||    |||||
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                                TCGGGTCCTC  CG    TTAGA
                                    ___  TTCTT
GAM770  KIAA1336 3'  AGACCGCAACACCTGAATCCTG 72321         GAA___  C   AA
           GGTTT                  AAGCCCAGGA    TG TGC  TCT
                                |||||||||     || |||  |||
                                TTTGGGTCCT    AC ACG  AGA
                                    AAGTCC  A   CC
GAM770  KIAA1548 3'  ATTGCACTTTTCCTGACTT   40500    CC      TGC
                                AAG  CAGGAGAA   TGCAAT
                                |||  ||||||||   ||||||
                                TTC  GTCCTTTT   ACGTTA
                                  A_       C__
GAM770  Kv6.3    3'  GCTAACATTCTCCTGGGC    56038           CT_
                                GCCCAGGAGAATG   GC
                                ||||||||||||   ||
                                CGGGTCCTCTTAC   CG
                                      AAT
GAM770  MAP3K3   3'  AGACTGTGTGTGCCCTCTGGGC 9997         AGA_   T   A
           T                    AGCCCAGG    ATGC GCA TCT
                                ||||||||    |||| ||| |||
                                TCGGGTCT    TGTG TGT AGA
                                    CCCG    _   C
GAM770  MGC13183 3'  AGAGGCTGCCTTTCTCCTGAGC 50388    C       T_  T  AA
           T                    AGC CAGGAGAA  GC GC  TCT
                                ||| ||||||||  || ||  |||
                                TCG GTCCTCTT  CG CG  AGA
                                  A       TC  T  G_
GAM770  MGC2560  5'  GGCCACCTCTCCTGGGCTT   48783          AT__
                                AAGCCCAGGAGA    GCT
                                ||||||||||||   |||
                                TTCGGGTCCTCT    CGG
                                      CCAC
GAM770  PHYHIP   3'  AGACCTGCCCACCTCCTGGGCT 28604         AA  CT   A_
                                AGCCCAGGAG  TG  GCA  TCT
                                ||||||||||  ||  |||  |||
                                TCGGGTCCTC  AC  CGT  AGA
                                    C_  C_   CC
GAM770  PP1201   3'  CAGCATCTCCCCTGGGCTT   42188         A  _
                                AAGCCCAGG GA ATGCTG
                                |||||||| || ||||||
                                TTCGGGTCC CT TACGAC
                                    C  C
GAM770  RALGPS1A 3'  TGTTGCACTCTCCTGGGCT   27611          A   T
                                AGCCCAGGAGA TGC GCA
                                |||||||||| ||| |||
                                TCGGGTCCTCT ACG TGT
                                      C   T
GAM770  SLC12A8  5'  CAGCATTCCCCTGGGCT    44896         A
                                AGCCCAGG GAATGCTG
                                |||||||| ||||||||
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                                TCGGGTCC CTTACGAC
                                     C
GAM770  STAG3    3'  TGAAGCATTCCCCCAGGCTT  24912      CA  A      G
                                AAGCC  GG GAATGCT CA
                                |||||  || ||||||| ||
                                TTCGG  CC CTTACGA GT
                                   AC  C      A
GAM770  SYT12    3'  AGATTGCAGCAGAGGAGTGGGC 94721      GGAGAA
                                GCCCA     TGCTGCAATCT
                                |||||     ||||||||||
                                CGGGT     ACGACGTTAGA
                                   GAGGAG
GAM770  LOC112724 3'  AGGTGAGCACTGCCCTGGGCT  56491        AGAA   G  A
                                AGCCCAGG    TGCT CA TCT
                                ||||||||    |||| || |||
                                TCGGGTCC    ACGA GT GGA
                                     CGTC   _  _
GAM770  LOC124930 5'  CACCACACTCCTGGGCTT    74354          AA  C
                                AAGCCCAGGAG  TG TG
                                ||||||||||  || ||
                                TTCGGGTCCTC  AC AC
                                      AC  C
GAM770  LOC149108 3'  AGATCACTCCAACTCCTGGG  84358        AA  CTGCA
                                CCCAGGAG  TG    ATCT
                                ||||||||  ||    ||||
                                GGGTCCTC  AC    TAGA
                                     A_  CTCAC
GAM770  LOC151414 3'  AGATCACAATGTTTTCTGAGCT 80233     CCA      GC  CA
           T                     AAGC   GGAGAAT  TG  ATCT
                                ||||   |||||||  ||  ||||
                                TTCG   TCTTTTG  AC  TAGA
                                  AG_      TA  AC
GAM770  LOC152941 3'  AGATTGCAATATGCTT     80749     A   C
                                GAG ATG TGCAATCT
                                ||| ||| ||||||||
                                TTC TAT ACGTTAGA
                                  G   A
GAM770  LOC153339 5'  TGCCTCTTGGGCTT       86017          AATGCT
                                AAGCCCAGGAG     GCA
                                ||||||||||      |||
                                TTCGGGTTCTC     CGT
                                                _______
GAM770  LOC154222 5'  AGCGTCACCTCCTCCCAGGCT  86187     C___    A__
                                AGCC   AGGAG   ATGCT
                                ||||   |||||  |||||
                                TCGG   TCCTC   TGCGA
                                  ACCC    CAC
GAM770  LOC169026 3'  TAGCATTCTGCTGAGCTT    82728     C   G
                                AAGC CAG AGAATGCTG
                                |||| ||| |||||||||
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                                TTCG GTC TCTTACGAT
                                  A  G
GAM770  LOC199780 5'  AGACCCACGCTTCTCTGGGCT  78731       G   T _  CAA
                                AGCCCAG AGAA GC TG   TCT
                                ||||||| |||| || ||   |||
                                TCGGGTC TCTT CG AC   AGA
                                   _   _  C  CC_
GAM770  LOC201109 3'  AGACTCGGTCCTCCCTGGGCT  89758        A  AT   CAA
                                AGCCCAGG GA  GCTG   TCT
                                |||||||| ||  ||||   |||
                                TCGGGTCC CT  TGGC   AGA
                                     _ CC    TC_
GAM770  LOC202266 3'  GGCCCTCTCCTGGGCTT     90331           AT
                                AAGCCCAGGAGA  GCT
                                ||||||||||||  |||
                                TTCGGGTCCTCT  CGG
                                       CC
GAM770  LOC221922 5'  AGAAGGCCATTCTCCTGAGCT  92686     C        CT  AA
                                AGC CAGGAGAATG  GC  TCT
                                ||| ||||||||||  ||  |||
                                TCG GTCCTCTTAC  CG  AGA
                                  A         __  GA
GAM770  LOC222189 3'  CACATCTCCCCTGGGTCC    94170   A      A _   C
                                A GCCCAGG GA ATG TG
                                | ||||||| || ||| ||
                                C TGGGTCC CT TAC AC
                                 C      C  C   _
GAM770  LOC245787 3'  CACATCTCCCCTGGGTCC    81345   A      A _   C
                                A GCCCAGG GA ATG TG
                                | ||||||| || ||| ||
                                C TGGGTCC CT TAC AC
                                 C      C  C   _
GAM770  LOC253609 5'  TGATGGCATTTTCCCGGGCT   96764       A         _
                                AGCCC GGAGAATGCTG CA
                                ||||| |||||||||| ||
                                TCGGG CCTTTTACGGT GT
                                   C          A
GAM770  LOC253815 3'  CAGAACCCTCCTGGGCTT    95597           AATG
                                AAGCCCAGGAG    CTG
                                ||||||||||    |||
                                TTCGGGTCCTC    GAC
                                       CCAA
GAM770  LOC64102  5'  GCAGCACAGGAGTCCCCTGGGC 42174         A  A_____
          T                     AGCCCAGG GA     TGCTGC
                                ||||||||  ||     ||||||
                                TCGGGTCC CT     ACGACG
                                     C  GAGGAC
GAM770  LOC89919  5'  AGATCAGTCCACCTCTCCTGGG 60714    A        AT___    CA
          TCC                     A GCCCAGGAGA     GCTG  ATCT
                                | ||||||||||     ||||  ||||
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                                C TGGGTCCTCT    TGAC  TAGA
                                 C        CCACC   __
GAM770  LOC92689  3'  AGTGGCTGCTTCTCCTGAGCT  70217    C      T  T  AAT
                                AGC CAGGAGAA GC GC   CT
                                ||| |||||||| || ||   ||
                                TCG GTCCTCTT CG CG   GA
                                  A       _  T  GT_
GAM771  CBFA2T2  3'  CGTGCCTGACTCATCCAG    17463     GC       TT
                                CTGG  GAGTCAGGC  GCG
                                ||||  |||||||||  |||
                                GACC  CTCAGTCCG  TGC
                                  TA       __
GAM771  COL4A3   5'  CTGAGGGTCCCCGGACTCGCCC 3620          A  CTTGCG
            AG                    CTGGGCGAGTC GG     TCAG
                                ||||||||||| ||     ||||
                                GACCCGCTCAG CC     AGTC
                                      G  CCTGGG
GAM771  COL4A3   5'  CTGAGGGTCCCCGGACTCGCCC 48554          A  CTTGCG
            AG                    CTGGGCGAGTC GG     TCAG
                                ||||||||||| ||     ||||
                                GACCCGCTCAG CC     AGTC
                                      G  CCTGGG
GAM771  COL4A3   5'  CTGAGGGTCCCCGGACTCGCCC 48566          A  CTTGCG
            AG                    CTGGGCGAGTC GG     TCAG
                                ||||||||||| ||     ||||
                                GACCCGCTCAG CC     AGTC
                                      G  CCTGGG
GAM771  RNH      5'  CAGGCTGACCCACCCAG     59619      CGA    G
                                CTGGG   GTCAG CTTG
                                |||||   ||||| ||||
                                GACCC   CAGTC GGAC
                                   ACC    _
GAM771  RNH      5'  CAGGCTGACCCACCCAG     11364      CGA    G
                                CTGGG   GTCAG CTTG
                                |||||   ||||| ||||
                                GACCC   CAGTC GGAC
                                   ACC    _
GAM771  S100A10  5'  GCTCGCCCAGCTCGCCCAG   59322         CA   TT
                                CTGGGCGAGT  GGC  GC
                                |||||||||  |||  ||
                                GACCCGCTCG  CCG  CG
                                      AC   CT
GAM771  TAL1     3'  GGTGTGCCTGACTGCCCAG   12111       G      TT  GT
                                CTGGGC AGTCAGGC  GC  C
                                ||||||  ||||||||  ||  |
                                GACCCG TCAGTCCG  TG  G
                                   _       __  TG
GAM771  TNFSF6   5'  GGCCTGACTCACCAG      5318      GC
                                CTGG  GAGTCAGGCT
                                ||||  ||||||||||
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                                GACC  CTCAGTCCGG
                                  A_
GAM771  FLJ21032  5'  TGCGGGCGCCCACCTCGCCCAG 46090         TCAG__
                                CTGGGCGAG     GCTTGCG
                                |||||||||     |||||||
                                GACCCGCTC     CGGGCGT
                                    CACCCG
GAM771  FLJ23519  5'  CAGGCTGACCCACCCAG     49964      CGA    G
                                CTGGG   GTCAG CTTG
                                |||||   ||||| ||||
                                GACCC   CAGTC GGAC
                                  ACC    _
GAM771  FLJ23519  5'  CAGGCTGACCCACCCAG     69202      CGA    G
                                CTGGG   GTCAG CTTG
                                |||||   ||||| ||||
                                GACCC   CAGTC GGAC
                                  ACC    _
GAM771  MGC12992  3'  ATGCAGTCTGACCCACCCAG   50344      CGA      T
                                CTGGG   GTCAGGCT GCGT
                                |||||   |||||||| ||||
                                GACCC   CAGTCTGA CGTA
                                  ACC      _
GAM771  PEG10     3'  CGCGTACCCGACCTACCCAG   30523      CGA   A  CT
                                CTGGG   GTC GG  TGCG
                                |||||   ||| ||  ||||
                                GACCC   CAG CC  GCGC
                                  ATC   C  AT
GAM771  TRIAD3    3'  CTGAAGCAGGGCCTGGCCCACC 94504      CGA      _  G
          CA                      TGGG   GTCAGGCT TGC TCAG
                                ||||   |||||||| ||| ||||
                                ACCC   CGGTCCGG ACG AGTC
                                  ACC      G   A
GAM771  LOC146957 3'  GTGGGACTCCAACTCGCCCAG  78207          CA_ _  TG
                                CTGGGCGAGT   GG CT  C
                                ||||||||||   || ||  |
                                GACCCGCTCA   TC GG  G
                                     ACC  A  GT
GAM771  LOC147791 5'  GACGCAAGCCTGCCCCGG    84070      CGA T
                                CTGGG   G CAGGCTTGCGTC
                                |||||   | ||||||||||||
                                GGCCC   C GTCCGAACGCAG
                                  ____ _
GAM771  LOC151278 5'  CGCAGGCCTGACCGCCCAG    80201        A
                                CTGGGCG GTCAGGCTTGCG
                                ||||||| ||||||||||||
                                GACCCGC CAGTCCGGACGC
                                  _
GAM771  LOC253649 5'  CTGACGCAGAGCACTCACCCA  96167      C   CAG  _
                                TGGG GAGT   GCT TGCGTCAG
                                |||| ||||   ||| ||||||||
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                                ACCC CTCA   CGA ACGCAGTC
                                  A   ___   G
GAM771  LOC253650 5'  CTGACGCAGAGCACTCACCCA  96165     C   CAG  _
                                TGGG GAGT   GCT TGCGTCAG
                                |||| ||||   ||| ||||||||
                                ACCC CTCA   CGA ACGCAGTC
                                  A   ___   G
GAM772  BMPR2    3'  TGCTACAACCATGGTGTCT   52915    C    CA  A
                                AG TGCCA  TG TTGTAGCA
                                || |||||  || ||||||||
                                TC GTGGT  AC AACATCGT
                                 T    __  C
GAM772  CALM1    3'  GTTTTTCATGCATGCAGCTTGA 22554        CA_    TTGT
                                TCAAGCTGC   CATGA   AGC
                                |||||||||   |||||   |||
                                AGTTCGACG   GTACT   TTG
                                      TAC    TT__
GAM772  HAP1     3'  GCCCCACAGACAGCTTGA    14169       CCACA  AT  TA
                                TCAAGCTG    TG  TG  GC
                                ||||||||    ||  ||  ||
                                AGTTCGAC    AC  AC  CG
                                     AG___  __  CC
GAM772  PSEN1    3'  GCCCCATCAGCAGCTTGA    3424        CACA   T TA
                                TCAAGCTGC   TGAT G  GC
                                |||||||||   |||| |  ||
                                AGTTCGACG   ACTA C  CG
                                     ____   _ CC
GAM772  PSEN1    3'  GCCCCATCAGCAGCTTGA    23624       CACA   T TA
                                TCAAGCTGC   TGAT G  GC
                                |||||||||   |||| |  ||
                                AGTTCGACG   ACTA C  CG
                                     ____   _ CC
GAM772  RAB38    3'  TACCACATGTGGCAAGC     60289    _     ATT
                                GCT GCCACATG   GTA
                                ||| ||||||||   |||
                                CGA CGGTGTAC   CAT
                                  A       AC_
GAM772  TACSTD1  3'  CTCAAAATATAAGCAGCTTGA  9859        CACATGA   T
                                TCAAGCTGC      TTG AG
                                |||||||||      ||| ||
                                AGTTCGACG      AAC TC
                                     AATATAA   _
GAM772  TNFRSF6  3'  TGCTACAAATGGCAGCTT    3487        CATGA
                                AAGCTGCCA    TTGTAGCA
                                |||||||||    ||||||||
                                TTCGACGGT    AACATCGT
                                     A____
GAM772  UBE4A    3'  CTACTCAATTGTGCAGCTT    16564       C   TGATT
                                AAGCTGC ACA    GTAG
                                ||||||| |||    ||||
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                                TTCGACG TGT    CATC
                                   _  TAACT
GAM772  DKFZp434F142 3'  TACTGTCAGCCTCGTGGCAGC  50030        A____   T
                                GCTGCCAC    TGAT GTA
                                |||||||     |||| |||
                                CGACGGTG    ACTG CAT
                                   CTCCG    T
GAM772  FLJ12331  3'  TGCCACAATCAGTGCAGTTTGA 46480         C  A     A
                                TCAAGCTGC AC TGATTGT GCA
                                ||||||||| || ||||||| |||
                                AGTTTGACG TG ACTAACA CGT
                                   _ _     C
GAM772  FLJ20375  3'  ACATCACTGACAGCTTGA    35083        C  CA   T
                                TCAAGCTG CA  TGAT GT
                                |||||||| ||  |||| ||
                                AGTTCGAC GT  ACTA CA
                                   A  C_   _
GAM772  FLJ30574  5'  GCTAAGTTGTAGCAGCTTG   58246        C   TGATTG
                                CAAGCTGC ACA     TAGC
                                |||||||| |||     ||||
                                GTTCGACG TGT     ATCG
                                   A   TGA___
GAM772  FLJ31528  3'  TGCTACAGTCTCCAGGCAGCTT 58378         ACAT
          GA                      TCAAGCTGCC   GATTGTAGCA
                                ||||||||||   ||||||||||
                                AGTTCGACGG   CTGACATCGT
                                   ACCT
GAM772  H2AFP    3'  TACTAGTTTGTGGCAGCT    40741         T   _
                                AGCTGCCACA GATT GTA
                                |||||||||| |||| |||
                                TCGACGGTGT TTGA CAT
                                   _   T
GAM772  KIAA0819  3'  GCACACACGGCAGCCTG     63578    A     ACA  AT   A
                                CA GCTGCC   TG  TGT GC
                                || ||||||   ||  ||| ||
                                GT CGACGG   AC  ACA CG
                                 C     C__  __  _
GAM772  KIAA1018  3'  GCCACAGTGGCGGCTTGA    30350          ATGAT   A
                                TCAAGCTGCCAC    TGT GC
                                ||||||||||||    ||| ||
                                AGTTCGGCGGTG    ACA CG
                                      _____  C
GAM772  KIAA1681  3'  TGCTACAATCAGCTCACCTGA  61076     A C  CCACA
                                TCA G TG    TGATTGTAGCA
                                ||| | ||    ||||||||||
                                AGT C AC    ACTAACATCGT
                                  _ C  TCG__
GAM772  MGC4832  3'  ATCACATGGCAGCTGA      58999     A      CA
                                TCA GCTGCCA  TGAT
                                ||| |||||||  ||||
```

```
                                AGT CGACGGT  ACTA
                                  _     AC
GAM772  SCYA28   3'  TGCTCTATAGATAACAGCTTGA 39060       CCACATGAT  T
                                TCAAGCTG       TG AGCA
                                ||||||||       || ||||
                                AGTTCGAC       AT TCGT
                                    AATAGAT__  C
GAM772  SR-BP1   3'  ACACATCACAGCTTGA     19631       CCACA   _
                                TCAAGCTG    TGAT TGT
                                ||||||||    |||| |||
                                AGTTCGAC    ACTA ACA
                                    _____   C
GAM772  UBCE7IP5 3'  TGCTTCCCACCAGCAGCTTGA 30164       CACA  ATTGT
                                TCAAGCTGC   TG    AGCA
                                |||||||||   ||    ||||
                                AGTTCGACG   AC    TCGT
                                    ACC_  CCT__
GAM772  LOC133634 3' GCCACTCAGCAGCTTGA    75105       CACA   TT  A
                                TCAAGCTGC   TGA  GT GC
                                |||||||||   |||  || ||
                                AGTTCGACG   ACT  CA CG
                                    ____   __  C
GAM772  LOC149117 3' TGCCAGTCGTCACAGCAGCT  84353      CAC_     TA
                                AGCTGC   ATGATTG  GCA
                                ||||||   |||||||  |||
                                TCGACG   TGCTGAC  CGT
                                   ACAC     __
GAM772  LOC152283 5' TACCTGAATGACAGCTTGA   85686       CCA   GATT
                                TCAAGCTG   CAT   GTA
                                ||||||||   |||   |||
                                AGTTCGAC   GTA   CAT
                                    A__   AGTC
GAM772  LOC161742 3' TTATATGACAGCTTGA     82293       C  C
                                TCAAGCTG CA ATGA
                                |||||||| || ||||
                                AGTTCGAC GT TATT
                                    A  A
GAM772  LOC255252 3' GCTCCACACCACAGCTTGA  95008       CCACA  AT  T
                                TCAAGCTG    TG  TG AGC
                                ||||||||    ||  || |||
                                AGTTCGAC    AC  AC TCG
                                    ACC__  __  C
GAM772  LOC257319 3' TACACATGCTGCAGCTTGA  95778       CA   AT
                                TCAAGCTGC  CATG  TGTA
                                |||||||||  ||||  ||||
                                AGTTCGACG  GTAC  ACAT
                                     TC   __
GAM772  LOC51634  3' TACTAGGTTTGGACAGCTTGA 32065       _  C  GATT
                                TCAAGCTG CCA AT   GTA
                                |||||||| ||| ||   |||
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                                AGTTCGAC GGT TG    CAT
                                    A   T  GAT_
GAM772  LOC89932  5'  GCTACAAGAACAGGTTGA    60803      G   CCACATGA
                                TCAA CTG       TTGTAGC
                                |||| |||       |||||||
                                AGTT GAC       AACATCG
                                  G   AAG_____
GAM773  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A     T__
GAM773  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM773  FDFT1    3'  TAGGAAAGTGAAATG       15518            A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM773  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM773  KLF4     3'  TCCCAGACAGTGGATATG     14891     CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||  ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM773  PHYH     3'  ACAGTAAAAGTGAAAT      20608           C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM773  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096           CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM773  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM773  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
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                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM773  CG012    5' CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                     CT  __
GAM773  EIF2C2   3' ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM773  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC       GTCTGAGAT
                                ||||||       |||||||||
                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM773  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM773  KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM773  KLHL6    3' ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM773  NIR3     3' GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM773  PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM773  PP35     3' ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM773  PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148         TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
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                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM773  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM773  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941        CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM773  LOC149703 3' ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM773  LOC154007 3' ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM773  LOC155004 3' TCATTTAAGTGAAAGGAAA   81226     A      GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _      ATTT
GAM773  LOC222134 5' ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM774  ASH1     3'  AAGCACTTGTAACTGCTGC   37497      TTG
                                GCAGCA   TACAGGTGCTT
                                ||||||   ||||||||||
                                CGTCGT   ATGTTCACGAA
                                   CA_
GAM774  CASP3    3'  AGGTGCTACAATGCCCCT    52192    CA     ACA  TG
                                AG  GCATTGT   GG  CTT
                                ||  |||||||   ||  |||
                                TC  CGTAACA   TC  GGA
                                 CC      ___  GT
GAM774  CASP3    3'  AGGTGCTACAATGCCCCT    15096    CA     ACA  TG
                                AG  GCATTGT   GG  CTT
                                ||  |||||||   ||  |||
                                TC  CGTAACA   TC  GGA
                                 CC      ___  GT
GAM774  CDC25A   5'  AGCACCCGTGCCTGT      8363      CATT   A
                                GCAG   GTAC GGTGCT
                                ||||   |||| ||||||
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                                TGTC   CGTG CCACGA
                                  ____   C
GAM774  CFTR     3'  CATATATTACAATGCTGT    4928          CAG_
                                GCAGCATTGTA   GTG
                                ||||||||||   |||
                                TGTCGTAACAT   TAC
                                    TATA
GAM774  COL14A1  5'  ATGTGTACAATGTTGC     69077           G
                                GCAGCATTGTACA GT
                                |||||||||||| ||
                                CGTTGTAACATGT TA
                                    G
GAM774  COLQ     3'  ACCGGCTACAATGCTCT     54476    C      CA_
                                AG AGCATTGTA   GGT
                                || |||||||||   |||
                                TC TCGTAACAT   CCA
                                 _       CGG
GAM774  COLQ     3'  ACCGGCTACAATGCTCT     54494    C      CA_
                                AG AGCATTGTA   GGT
                                || |||||||||   |||
                                TC TCGTAACAT   CCA
                                 _       CGG
GAM774  COLQ     3'  ACCGGCTACAATGCTCT     54482    C      CA_
                                AG AGCATTGTA   GGT
                                || |||||||||   |||
                                TC TCGTAACAT   CCA
                                 _       CGG
GAM774  COLQ     3'  ACCGGCTACAATGCTCT     54470    C      CA_
                                AG AGCATTGTA   GGT
                                || |||||||||   |||
                                TC TCGTAACAT   CCA
                                 _       CGG
GAM774  COLQ     3'  ACCGGCTACAATGCTCT     54488    C      CA_
                                AG AGCATTGTA   GGT
                                || |||||||||   |||
                                TC TCGTAACAT   CCA
                                 _       CGG
GAM774  COLQ     3'  ACCGGCTACAATGCTCT     19047    C      CA_
                                AG AGCATTGTA   GGT
                                || |||||||||   |||
                                TC TCGTAACAT   CCA
                                 _       CGG
GAM774  CYP7A1   3'  TGCCTGTGTACAACAATGCT  5764          _____
                                AGCATTGT    ACAGGTG
                                ||||||||    |||||||
                                TCGTAACA    TGTCCGT
                                    ACATG
GAM774  DDX11    5'  AGCGTAGCAATGCTGC      15298          ACAGG
                                GCAGCATTGT    TGCT
                                ||||||||||    ||||
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                                CGTCGTAACG    GCGA
                                      AT___
GAM774  DGKA    3'  AGGCTCTGTACATTGCTGC   7200       T      T
                                GCAGCA TGTACAGG GCTT
                                |||||| |||||||| ||||
                                CGTCGT ACATGTCT CGGA
                                   T      _
GAM774  HAT1    3'  TCTGTACAATGTGCT      13318      G
                                AGCA CATTGTACAGG
                                |||| ||||||||||
                                TCGT GTAACATGTCT
                                  _
GAM774  HNF3B   3'  AAGCACCTGCAGATTCTG   41413     C   GTA
                                CAG ATT   CAGGTGCTT
                                ||| |||   |||||||||
                                GTC TAG   GTCCACGAA
                                  T   AC_
GAM774  IFNAR2  3'  AAGCACCTACAGGGTTCT   6035     C   A    AC
                                AG AGC TTGT  AGGTGCTT
                                || ||| ||||  ||||||||
                                TC TTG GACA  TCCACGAA
                                 _  G   __
GAM774  IL1RN   3'  AAGCACCTAGCCTCGCTCT   5140     C   ATT  AC
                                AG AGC   GT  AGGTGCTT
                                || |||   ||  ||||||||
                                TC TCG   CG  TCCACGAA
                                 _  CTC  A_
GAM774  ITPR1   3'  AAGCACCTGATTTGC      9441      TT  A
                                GCA  GT CAGGTGCTT
                                |||  || |||||||||
                                CGT  TA GTCCACGAA
                                  T_ _
GAM774  JJAZ1   3'  AGGATCAATGCTGCT      31074          TACAG  G
                                AGCAGCATTG    GT CT
                                ||||||||||    || ||
                                TCGTCGTAAC    TA GA
                                      _____  G
GAM774  KCNN4   3'  CACTCTCACTATGCTGCT   9566         T  ACA
                                AGCAGCAT GT   GGTG
                                |||||||| ||   ||||
                                TCGTCGTA CA   TCAC
                                     T  CTC
GAM774  MADD    3'  AGTGCACGATGCTGCT     55329          ACAG TG
                                AGCAGCATTGT   G  CT
                                ||||||||||   |  ||
                                TCGTCGTAGCA   C  GA
                                      ____ GT
GAM774  MADD    3'  AGTGCACGATGCTGCT     55352          ACAG TG
                                AGCAGCATTGT   G  CT
                                ||||||||||   |  ||
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                              TCGTCGTAGCA   C  GA
                                    ____ GT
GAM774  MADD    3' AGTGCACGATGCTGCT    55336        ACAG TG
                              AGCAGCATTGT   G  CT
                              ||||||||||    |  ||
                              TCGTCGTAGCA   C  GA
                                    ____ GT
GAM774  MADD    3' AGTGCACGATGCTGCT    55341        ACAG TG
                              AGCAGCATTGT   G  CT
                              ||||||||||    |  ||
                              TCGTCGTAGCA   C  GA
                                    ____ GT
GAM774  MADD    3' AGTGCACGATGCTGCT    13461        ACAG TG
                              AGCAGCATTGT   G  CT
                              ||||||||||    |  ||
                              TCGTCGTAGCA   C  GA
                                    ____ GT
GAM774  MADD    3' AGTGCACGATGCTGCT    55346        ACAG TG
                              AGCAGCATTGT   G  CT
                              ||||||||||    |  ||
                              TCGTCGTAGCA   C  GA
                                    ____ GT
GAM774  MAT1A   3' AAGCACCTGTAATGTGC    90824     TG
                              GCAT  TACAGGTGCTT
                              ||||  ||||||||||
                              CGTG  ATGTCCACGAA
                                TA
GAM774  MGAT5   3' AGCCCTGCACCATGCTGCT  10021       T A   T
                              AGCAGCAT GT CAGG GCT
                              |||||||| || |||| |||
                              TCGTCGTA CA GTCC CGA
                                   C  C   _
GAM774  MME     3' ATGTGTCCAATGCTGC     6138        T   G
                              GCAGCATTG ACA GT
                              ||||||||| ||| ||
                              CGTCGTAAC TGT TA
                                    C   G
GAM774  MME     3' ATGTGTCCAATGCTGC     23505       T   G
                              GCAGCATTG ACA GT
                              ||||||||| ||| ||
                              CGTCGTAAC TGT TA
                                    C   G
GAM774  MME     3' ATGTGTCCAATGCTGC     23485       T   G
                              GCAGCATTG ACA GT
                              ||||||||| ||| ||
                              CGTCGTAAC TGT TA
                                    C   G
GAM774  MME     3' ATGTGTCCAATGCTGC     23495       T   G
                              GCAGCATTG ACA GT
                              ||||||||| ||| ||
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                                CGTCGTAAC TGT TA
                                     C   G
GAM774  NOTCH2   3'  TTTGTAAATGCTGCT      44318        G
                                AGCAGCATT TACAGG
                                ||||||||| ||||||
                                TCGTCGTAA ATGTTT
                                          _
GAM774  OLR1     3'  AAGTGTCACAATGCTCCT    10334    C      ACA  TG
                                AG AGCATTGT   GG  CTT
                                || ||||||||   ||  |||
                                TC TCGTAACA   CT  GAA
                                 C       ___  GT
GAM774  PKHD1    5'  AAGCACAAAAGCTATGCTGCT  56911        T  ACAG
                                AGCAGCAT GT    GTGCTT
                                |||||||| ||    ||||||
                                TCGTCGTA CG    CACGAA
                                     T  AAAA
GAM774  POP2     3'  AAGCACCTAGCACATGCCGT   42143    A   _   AC
                                GC GCAT TGT  AGGTGCTT
                                || |||| |||  ||||||||
                                TG CGTA ACG  TCCACGAA
                                 C   C  A_
GAM774  RUNX3    3'  AAGCACCTACAGACCGGCT    15107     AGCA    AC
                                AGC    TTGT  AGGTGCTT
                                |||    ||||  ||||||||
                                TCG    GACA  TCCACGAA
                                  GCCA   __
GAM774  SH3BP2   3'  CACACAATGCTGCT        11594          ACAG
                                AGCAGCATTGT    GTG
                                ||||||||||    |||
                                TCGTCGTAACA    CAC
                                          ____
GAM774  SLC1A3   3'  AAGCACCTGCCCTCTGTT    14796      CATTGTA
                                AGCAG      CAGGTGCTT
                                |||||      |||||||||
                                TTGTC      GTCCACGAA
                                   TCCC___
GAM774  SLC20A2  3'  ACTATGGAAATGCTGCT     22174         GTA  _
                                AGCAGCATT   CA GGT
                                |||||||||   || |||
                                TCGTCGTAA   GT TCA
                                     AG_  A
GAM774  SRM      3'  AAGCCCCAGAATGCTGC      11955        GTACA  T
                                GCAGCATT    GG GCTT
                                ||||||||    || ||||
                                CGTCGTAA    CC CGAA
                                     GAC__  _
GAM774  SUOX     5'  AGGTCTGCTACAATGCTGCT   4851           _   GT
                                AGCAGCATTGTA CAG  GCTT
                                |||||||||||| |||  ||||
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                                TCGTCGTAACAT GTC  TGGA
                                      C  __
GAM774  TJP1     3'  ATTTGTGATACAATGCTGT   12295        ___
                                GCAGCATTGT  ACAGGT
                                ||||||||||  ||||||
                                TGTCGTAACA  TGTTTA
                                      TAG
GAM774  UTY      3'  AAGCAACTGGACACAGTGCTGC 23066        A__  G
                                GCAGCATTGT  CAG TGCTT
                                ||||||||||  ||| |||||
                                CGTCGTGACA  GTC ACGAA
                                      CAG  A
GAM774  WNT7A    3'  CACCCAATGCTGCT       16119        TACA
                                AGCAGCATTG   GGTG
                                ||||||||||   ||||
                                TCGTCGTAAC   CCAC

                                     _____
GAM774  AKAP11   3'  ATTTGCCAATGCTGC      32701        TA
                                GCAGCATTG  CAGGT
                                |||||||||  |||||
                                CGTCGTAAC  GTTTA
                                     C_
GAM774  ANKRD6   3'  TTGTAATAAAATGCTGCT   30093        G___
                                AGCAGCATT   TACAG
                                |||||||||   |||||
                                TCGTCGTAA   ATGTT
                                      AATA
GAM774  C1orf19  3'  ACTTGTCAACACTGCT     68187      CA  T
                                AGCAG  TTG ACAGGT
                                |||||  ||| ||||||
                                TCGTC  AAC TGTTCA
                                   AC  _
GAM774  CDC14B   3'  AAGCACCTGCCAGCACCGC   52841    AT  A__
                                GC  TGT  CAGGTGCTT
                                ||  |||  |||||||||
                                CG  ACG  GTCCACGAA
                                 CC  ACC
GAM774  D15Wsu75e 3'  TGTAGACAATGCTGCT     66650         __
                                AGCAGCATTGT  ACA
                                ||||||||||  |||
                                TCGTCGTAACA  TGT
                                      GA
GAM774  EDG2     3'  AGCAAACAATGCTCT      54061    C      ACAGG
                                AG AGCATTGT    TGCT
                                || ||||||||    ||||
                                TC TCGTAACA    ACGA
                                 _      A_____
GAM774  EDG2     3'  AGCAAACAATGCTCT      7378     C      ACAGG
                                AG AGCATTGT    TGCT
                                || ||||||||    ||||
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```
                                TC TCGTAACA    ACGA
                                 _      A____
GAM774  EPHA7    3'  GCATAGAATGCTGCT      15434        G ACAG
                                AGCAGCATT T   GTGC
                                ||||||||| |   ||||
                                TCGTCGTAA A   TACG
                                    G ____
GAM774  FADS1    3'  AAGCACCTGAACCACTGT    25468     CATT  A
                                GCAG   GT CAGGTGCTT
                                ||||   || |||||||||
                                TGTC   CA GTCCACGAA
                                  AC__  A
GAM774  FLJ10246 3'  TGCCACAATGCTGCT      35944          ACA
                                AGCAGCATTGT   GGTG
                                ||||||||||   ||||
                                TCGTCGTAACA   CCGT
                                     ___
GAM774  FLJ10307 3'  AGCTAACGATGCTGCT     36004          ACAGGT
                                AGCAGCATTGT    GCT
                                ||||||||||     |||
                                TCGTCGTAGCA    CGA
                                      AT____
GAM774  FLJ11155 5'  AAGCACCTGCCTCAGCTG   37116     AT  TA_
                                CAGC  TG   CAGGTGCTT
                                ||||  ||   |||||||||
                                GTCG  AC   GTCCACGAA
                                  __ TCC
GAM774  FLJ13848 3'  AAGCACCTAACAGCT      45457     AT   AC
                                AGC  TGT  AGGTGCTT
                                |||  |||  ||||||||
                                TCG  ACA  TCCACGAA
                                  __   A_
GAM774  FLJ20128 3'  AAGCACCTCAGCGCACTTGC  34595     CAT   AC
                                GCAG   TGT  AGGTGCTT
                                ||||   |||  ||||||||
                                CGTT   GCG  TCCACGAA
                                  CAC   AC
GAM774  FLJ20281 5'  AAGCACCTTGAGTTACTGGCT 90976     ATT  _ ___
                                AGC   GTA C   AGGTGCTT
                                |||   ||| |   ||||||||
                                TCG   CAT G   TCCACGAA
                                  GT_   T AGT
GAM774  FLJ20716 3'  AAGTGTTACAATGCCGCT    35598     A      CAG TG
                                AGC GCATTGTA   G  CTT
                                ||| ||||||||   |  |||
                                TCG CGTAACAT   T  GAA
                                  C       ___ GT
GAM774  FLJ21709 3'  AAGCACCTAGAGCAGCTCT   77917    C   AT   AC_
                                AG AGC  TGT   AGGTGCTT
                                || |||  |||   ||||||||
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                                TC TCG  ACG   TCCACGAA
                                 _  __  AGA
GAM774  FLJ22626  3'  GCTTTACAGTGCTACT     44553    C       C
                                AG AGCATTGTA AGGT
                                || ||||||||| ||||
                                TC TCGTGACAT TTCG
                                 A       _
GAM774  FLJ23056  3'  ACCACAATGCTGCT       44720          ACA
                                AGCAGCATTGT   GGT
                                ||||||||||   |||
                                TCGTCGTAACA   CCA
                                      ___
GAM774  HEF1      3'  AAGCACCTTCTAATGCTGC   21134         TAC
                                GCAGCATTG   AGGTGCTT
                                |||||||||   ||||||||
                                CGTCGTAAT   TCCACGAA
                                     CT_
GAM774  HEMK      3'  AAGCTCCAACACAAATGCTGC 32423        _  ACA  T
                                GCAGCATT GT   GG GCTT
                                |||||||| ||   || ||||
                                CGTCGTAA CA   CC CGAA
                                    A  CAA  T
GAM774  HRH3      3'  AAGCACCTGGGTGTGCT     23363      TGTA
                                AGCAT    CAGGTGCTT
                                |||||    |||||||||
                                TCGTG    GTCCACGAA
                                   TGG_
GAM774  HSA243666 3'  AGTCCCACTCAATGCTGCT   34145         TACA  TG
                                AGCAGCATTG    GG  CT
                                ||||||||||    ||  ||
                                TCGTCGTAAC    CC  GA
                                      TCA_  CT
GAM774  IMAGE:4907098 5'  AAGCACCTGCACTTGCT     91655      TT  A
                                AGCA  GT CAGGTGCTT
                                ||||  || |||||||||
                                TCGT  CA GTCCACGAA
                                  T_  C
GAM774  KCNMB2    5'  ACCTTGGTATAAATGCTGCT   19538         _   __
                                AGCAGCATT GTAC  AGGT
                                ||||||||| ||||  ||||
                                TCGTCGTAA TATG  TCCA
                                     A    GT
GAM774  KIAA0276  3'  AAGCACACAGACAGTGCTACT  70960    C       ACAG
                                AG AGCATTGT    GTGCTT
                                || ||||||||    ||||||
                                TC TCGTGACA    CACGAA
                                 A       GACA
GAM774  KIAA0472  5'  AGATCTTAAATGCTGC      71852        GTAC   G
                                GCAGCATT    AGGT CT
                                ||||||||    |||| ||
```

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                                CGTCGTAA   TCTA GA
                                    AT__   _
GAM774  KIAA0513  3'  AGCAAACAGTGCTGCT     28337          ACAGG
                                AGCAGCATTGT    TGCT
                                ||||||||||    ||||
                                TCGTCGTGACA    ACGA
                                     A____
GAM774  KIAA0555  3'  AAGCTACTTTGTACAATGCTCT 60110    C         _ _
                                AG AGCATTGTACAG GT GCTT
                                || ||||||||||| || ||||
                                TC TCGTAACATGTT CA CGAA
                                 _         T  T
GAM774  KIAA0779  3'  AAGTCTTGCTGTAAATGCTGC  85722        G    GT__
                                GCAGCATT TACAG   GCTT
                                |||||||| |||||   ||||
                                CGTCGTAA ATGTC   TGAA
                                    _    GTTC
GAM774  KIAA1265  3'  ACTTGTACAATGCTGT     70786
                                GCAGCATTGTACAGGT
                                ||||||||||||||||
                                TGTCGTAACATGTTCA

GAM774  KIAA1878  3'  CACCTGTCCAATGCTGCT    91709          T
                                AGCAGCATTG ACAGGTG
                                |||||||||| |||||||
                                TCGTCGTAAC TGTCCAC
                                     C
GAM774  KIAA1879  5'  AAGCAGGAGCTGGACAATGCTG 73558          A   G___
          CT                    AGCAGCATTGT CAG   TGCTT
                                |||||||||| |||   |||||
                                TCGTCGTAACA GTC   ACGAA
                                     G   GAGG
GAM774  KIAA1958  3'  AAGACTCAACCAATGCTGC   81897         TACA   G
                                GCAGCATTG   GGT CTT
                                |||||||||   ||| |||
                                CGTCGTAAC   TCA GAA
                                     CAAC   _
GAM774  KRTHB5    3'  AAGCACCTGCCTGCCTGC    9651       _  TTGTA
                                GCAG CA    CAGGTGCTT
                                |||| ||    |||||||||
                                CGTC GT    GTCCACGAA
                                  C  CC___
GAM774  LRRN3     3'  AAGCTTCACCAATGCTGCT   69437          TACA  T
                                AGCAGCATTG   GG GCTT
                                ||||||||||   || ||||
                                TCGTCGTAAC   CT CGAA
                                     CA__  T
GAM774  MGC12945  5'  AAGTGTGTACCATGCTGCT   50297         T    GG
                                AGCAGCAT GTACA  TGCTT
                                |||||||| |||||  |||||
```

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                                TCGTCGTA CATGT  GTGAA
                                    C    __
GAM774  MGC1842  3' AAGCACCTGCTGGCTGCT   65633      ATTGTA
                                AGCAGC    CAGGTGCTT
                                ||||||    |||||||||
                                TCGTCG    GTCCACGAA
                                   GTC___
GAM774  MGC20470 3' GGGACACCAATGCTGCT    58964       GTACA  _
                                AGCAGCATT   GGTG CTT
                                |||||||||   |||| |||
                                TCGTCGTAA   CCAC GGG
                                     _____  A
GAM774  MGC23980 3' AAGCACTTAGAACAGTGC   58757       AC_
                                GCATTGT  AGGTGCTT
                                |||||||  ||||||||
                                CGTGACA  TTCACGAA
                                    AGA
GAM774  MGC26914 3' AGCACGTAACAATGCT     58664       _ AG
                                AGCATTGT AC  GTGCT
                                |||||||| ||  |||||
                                TCGTAACA TG  CACGA
                                    A  __
GAM774  MGC33887 5' AGCTTCACAATGCTGT     58872        ACA  T
                                GCAGCATTGT  GG GCT
                                ||||||||||  || |||
                                TGTCGTAACA  CT CGA
                                     ___  T
GAM774  PAK2     5' AAGCACCTGCAGTAGTG    66534      TA_
                                CATTG  CAGGTGCTT
                                |||||  |||||||||
                                GTGAT  GTCCACGAA
                                   GAC
GAM774  PARVA    3' AAGCAAATGTACAATATGCT  36648     GC      GG
                                AGCA  ATTGTACA  TGCTT
                                ||||  ||||||||  |||||
                                TCGT  TAACATGT  ACGAA
                                  A_       AA
GAM774  PLAC3    3' GTTCCACACATGCTGCT     69346       _  ACA  T
                                AGCAGCAT TGT  GG GC
                                |||||||| |||  || ||
                                TCGTCGTA ACA  CC TG
                                    C  ___  T
GAM774  PP1665   5' AAGCACTTGGAACAATGC    47909       A_
                                GCATTGT  CAGGTGCTT
                                |||||||  |||||||||
                                CGTAACA  GTTCACGAA
                                    AG
GAM774  Rab11-FIP2 3' AAGGATCACAGTGCTGCT   29778         ACA  G
                                AGCAGCATTGT  GGT CTT
                                ||||||||||  ||| |||
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                                TCGTCGTGACA  CTA GAA
                                     ___  G
GAM774  SLC6A14  3'  CACATACAGTGCTGCT     23347          CAG
                                AGCAGCATTGTA  GTG
                                ||||||||||||  |||
                                TCGTCGTGACAT  CAC
                                      A__
GAM774  SMCR5    3'  AAGTCATCTGCACAAGGCT   58588    A   A    _
                                AGC TTGT CAGGTG CTT
                                ||| |||| |||||| |||
                                TCG AACA GTCTAC GAA
                                  G   C     T
GAM774  WAP1     3'  ATCCGTACATGCTGCT      79512        T   A
                                AGCAGCAT GTAC GGT
                                |||||||| |||| |||
                                TCGTCGTA CATG CTA
                                    _   C
GAM774  ZNF323   3'  AAGTTATCTAAATGCTGCT   48075        GTAC   _
                                AGCAGCATT   AGGTG CTT
                                |||||||||   ||||| |||
                                TCGTCGTAA   TCTAT GAA
                                     A___    T
GAM774  LOC115442 5'  ACTTGTATAAATGCTGCT    72675         _
                                AGCAGCATT GTACAGGT
                                ||||||||| ||||||||
                                TCGTCGTAA TATGTTCA
                                     A
GAM774  LOC122553 3'  AAGCACCTGAATTGTGCTTCT  74128   C    T  A
                                AG AGCAT GT CAGGTGCTT
                                || ||||| || |||||||||
                                TC TCGTG TA GTCCACGAA
                                 T    T  A
GAM774  LOC124045 3'  AAGCACCTTTGCATGGC     76030   AT   C
                                GC  TGTA AGGTGCTT
                                ||  |||| ||||||||
                                CG  ACGT TCCACGAA
                                 GT   T
GAM774  LOC144481 3'  AAGCACCTGTACACAAGC    83091    AT_
                                GC   TGTACAGGTGCTT
                                ||   ||||||||||||
                                CG   ACATGTCCACGAA
                                 AAC
GAM774  LOC144559 5'  TGTTTGTATAATGCCACT    76884    CA        GT
                                AG  GCATTGTACAG  G
                                ||  ||||||||||  |
                                TC  CGTAATATGTT  T
                                 AC         TG
GAM774  LOC145601 3'  CACCCAGTGCTGCT        83363          TACA
                                AGCAGCATTG   GGTG
                                |||||||||   ||||
```

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                                TCGTCGTGAC    CCAC
                                      ____
GAM774   LOC149050 3'  AGCTCCTTGTACAACACGC    60428    AGCA      _  T
                                GC    TTGTACA GG GCT
                                ||    ||||||| || |||
                                CG    AACATGT CC CGA
                                 CAC_      T  T
GAM774   LOC149175 3'  AAGCACCTTCCTATGTGCT    79205     G   TGTAC
                                AGCA CAT     AGGTGCTT
                                |||| |||     ||||||||
                                TCGT GTA     TCCACGAA
                                  _   TCCT_
GAM774   LOC149351 5'  GAGTAGCACAGTGCTGCT    79307          ACAGG
                                AGCAGCATTGT     TGCTT
                                ||||||||||     |||||
                                TCGTCGTGACA     ATGAG
                                       CG___
GAM774   LOC196411 3'  TCTGTACAAGGCTGCT      87688       A
                                AGCAGC TTGTACAGG
                                |||||| |||||||||
                                TCGTCG AACATGTCT
                                   G
GAM774   LOC200583 3'  AAGCAATTAACAGTGCTACT   88831    C       ACAGG
                                AG AGCATTGT     TGCTT
                                || ||||||||     |||||
                                TC TCGTGACA     ACGAA
                                 A       ATTA_
GAM774   LOC201304 3'  CACTTCATGCTGCT        88228         T TAC
                                AGCAGCAT G   AGGTG
                                |||||||| |   |||||
                                TCGTCGTA C   TTCAC
                                      _ ___
GAM774   LOC219918 5'  TGTTTGTATAATGCCACT    91543    CA         GT
                                AG  GCATTGTACAG  G
                                ||  ||||||||||  |
                                TC  CGTAATATGTT  T
                                 AC          TG
GAM774   LOC220071 5'  TGTTTGTATAATGCCACT    93438    CA         GT
                                AG  GCATTGTACAG  G
                                ||  ||||||||||  |
                                TC  CGTAATATGTT  T
                                 AC          TG
GAM774   LOC220766 5'  AAGCACCTAAACAGGT      90789    A    AC
                                GC TTGT  AGGTGCTT
                                || ||||  ||||||||
                                TG GACA  TCCACGAA
                                 _    AA
GAM774   LOC221773 3'  AAGCACCTAGTAAGTGCCTGCT 91033       _    G   _
                                AGCAG CATT TAC AGGTGCTT
                                ||||| |||| ||| ||||||||
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                                TCGTC GTGA ATG TCCACGAA
                                  C   _  A
GAM774  LOC253517 3'  AAGCACCTTTGCATGGC    95103    AT   C
                                GC  TGTA AGGTGCTT
                                ||  |||| ||||||||
                                CG  ACGT TCCACGAA
                                 GT   T
GAM774  LOC254045 3'  AAGCACCTGTACACAAGC    96500    AT_
                                GC   TGTACAGGTGCTT
                                ||   ||||||||||||
                                CG   ACATGTCCACGAA
                                 AAC
GAM774  LOC254173 3'  TCTGTACATGCTGCT      96845       T
                                AGCAGCAT GTACAGG
                                |||||||| |||||||
                                TCGTCGTA CATGTCT
                                   _
GAM774  LOC254611 5'  AAGCACCTATCCAAACTGT   97604     CA   TAC
                                GCAG  TTG   AGGTGCTT
                                ||||  |||   ||||||||
                                TGTC  AAC   TCCACGAA
                                  A_  CTA
GAM774  LOC255736 5'  ACTTAGTGTACAATGCTGT   95332          ___
                                GCAGCATTGTACA   GGT
                                ||||||||||||   |||
                                TGTCGTAACATGT   TCA
                                      GAT
GAM774  LOC255855 3'  AGCAACTATGCTGCT      96224       T  ACAGG
                                AGCAGCAT GT    TGCT
                                |||||||| ||    ||||
                                TCGTCGTA CA    ACGA
                                    T _____
GAM774  LOC257438 3'  AGCTAACGATGCTGCT     93969          ACAGGT
                                AGCAGCATTGT     GCT
                                ||||||||||     |||
                                TCGTCGTAGCA     CGA
                                      AT____
GAM774  LOC57826  3'  ATTTGCACAGATGCTGCT   41015       _  A
                                AGCAGCAT TGT CAGGT
                                |||||||| ||| |||||
                                TCGTCGTA ACA GTTTA
                                    G   C
GAM774  LOC64744  3'  CACCTGTATGGCTGC      61796      ATT
                                GCAGC   GTACAGGTG
                                |||||   |||||||||
                                CGTCG   TATGTCCAC
                                  G__
GAM774  LOC90906  3'  AAGCACCTGATCTTGT     64290     TT  A
                                GCA  GT CAGGTGCTT
                                |||  || |||||||||
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                                TGT  TA GTCCACGAA
                                  TC  _
GAM774  LOC90906  3'  TGTTTGTATAATGCTACT    64316    C          GT
                                AG AGCATTGTACAG  G
                                || ||||||||||||  |
                                TC TCGTAATATGTT  T
                                 A           TG
GAM774  LOC93268  5'  AAGCACCTAGGTAGCAGC    71874    A  ATTG   __
                                GC GC    TAC  AGGTGCTT
                                || ||    |||  ||||||||
                                CG CG    ATG  TCCACGAA
                                 A  _____   GA
GAM775  ADAMTS5   3'  TAGGTGAGAAAAAAAAT     22895           T T
                                ATTTTTTTTCTC C CTA
                                |||||||||||| | |||
                                TAAAAAAAAGAG G GAT
                                       T _
GAM775  AKAP2     3'  AGGTAGAGAGAGAAAAAGGGAG 23257     A
              GG                    CTC TTTTTTTTCTCTCTCTACCT
                                ||| ||||||||||||||||||||
                                GGG GGGAAAAAGAGAGAGATGGA
                                  A
GAM775  CA12      3'  GTAGAGAGAAAAAAGAAA     6881          C
                                TTTTTTTT TCTCTCTAC
                                |||||||| |||||||||
                                AAAGAAAA AGAGAGATG
                                     A
GAM775  CA14      5'  AGAGAGAGGGCAAAGA      24002       T
                                TTTTT TTCTCTCTCT
                                ||||| ||||||||||
                                AGAAA GGGAGAGAGA
                                   C
GAM775  CCND1     3'  AGAGAGAGAAAAAAAA      53882
                                TTTTTTTTCTCTCTCT
                                ||||||||||||||||
                                AAAAAAAAGAGAGAGA

GAM775  DHFR      3'  GTAGAGAGAAAATAAAAGAA   5813         TC__
                                TTTTTTT    TCTCTCTAC
                                |||||||    |||||||||
                                AAGAAAA    AGAGAGATG
                                     TAAA
GAM775  DSPP      3'  GTAAAGAAAGGGGAGAAAT    26391        TT  C   C
                                ATTTTTT  CT TCT TAC
                                |||||||  || ||| |||
                                TAAAGAG  GA AGA ATG
                                     GG  A   A
GAM775  EPHB2     3'  TAGAAGAAAAAGAATGA      15447            CTC
                                TCATTTTTTTTCT   TCTA
                                ||||||||||||   ||||
```

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                                AGTAAGAAAAAGA  AGAT
                                      ___
GAM775  GPC6    3'  AGAGAAAAATAAATGA     19123       _
                                TCATTT TTTTTCTCT
                                |||||| |||||||||
                                AGTAAA AAAAAGAGA
                                   T
GAM775  HMGCS2  3'  AGAAAGAGAAAAAAAA     18624           C
                                TTTTTTTTCTCT TCT
                                |||||||||||| |||
                                AAAAAAAAGAGA AGA
                                      A
GAM775  HOXA3   3'  AGAGTGAGAAAAAAAAT    47685           T
                                ATTTTTTTTCTC CTCT
                                |||||||||||| ||||
                                TAAAAAAAAGAG GAGA
                                      T
GAM775  HOXC6   3'  AGAGAGAAAAAAAGTGA    15698
                                TCATTTTTTTTCTCTCT
                                |||||||||||||||||
                                AGTGAAAAAAAGAGAGA

GAM775  HOXD4   5'  AGAAAGAGAGAAAGAG     27519           C
                                TTTTTTTTCTCT TCT
                                |||||||||||| |||
                                GAGAAAGAGAGA AGA
                                      A
GAM775  HUNK    3'  AGCAGAGAGAAGAAAA     27437           _
                                TTTTTTTCTCTCT CT
                                |||||||||||| ||
                                AAAAGAAGAGAGA GA
                                      C
GAM775  IL1F5   3'  AGAAAGAGAAAAAAAA     24376           C
                                TTTTTTTTCTCT TCT
                                |||||||||||| |||
                                AAAAAAAAGAGA AGA
                                      A
GAM775  LEP     3'  AGGCAGAGAAAGAAGAGA   4045        C   A
                                TTTTTTCT TCTCT CCT
                                |||||||| ||||| |||
                                AGAGAAGA AGAGA GGA
                                     A   C
GAM775  MID1    3'  AGACAGAGAATGAAAAGAG   4599    A   T   C
                                CTC TTTTT TTCTCT TCT
                                ||| ||||| |||||| |||
                                GAG AAAAG AAGAGA AGA
                                  _   T   C
GAM775  MID1    3'  AGACAGAGAATGAAAAGAG   52754   A   T   C
                                CTC TTTTT TTCTCT TCT
                                ||| ||||| |||||| |||
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                                GAG AAAAG AAGAGA AGA
                                  _    T     C
GAM775  MPZ      3'  AGACAGAGAGAGAGAATGG   4997              C
                                TCATTTTTTTTCTCT TCT
                                ||||||||||||||| |||
                                GGTAAGAGAGAGAGA AGA
                                        C
GAM775  MYBPC1   3'  GTTGAAGAGAAAAAAAA    10152           C  T
                                TTTTTTTTCTCT TC AC
                                |||||||||||| || ||
                                AAAAAAAAGAGA AG TG
                                      _  T
GAM775  NAV2     3'  AGAGAGAAAAAAAAAAAAGAG  60154     A       C
                                CTC TTTTTTTT TCTCTCT
                                ||| |||||||| |||||||
                                GAG AAAAAAAA AGAGAGA
                                  A       A
GAM775  PRG4     3'  AGGTAGAGATACAACAAATGA  19414       TTTTTCTC
                                TCATTT       TCTCTACCT
                                ||||||       |||||||||
                                AGTAAA       AGAGATGGA
                                   CAACAT__
GAM775  PTPRC    3'  AGACAGAGAAAGAGAGAG    55163     AT        C
                                CTC  TTTTTTTCTCT TCT
                                |||  |||||||||| |||
                                GAG  AGAGAAAGAGA AGA
                                  __         C
GAM775  PTPRC    3'  AGACAGAGAAAGAGAGAG    11098     AT        C
                                CTC  TTTTTTTCTCT TCT
                                |||  |||||||||| |||
                                GAG  AGAGAAAGAGA AGA
                                  __         C
GAM775  RORB     5'  AGAGAAAGAAAAAGAA      22605          C
                                TTTTTTTTCT TCTCT
                                |||||||||| |||||
                                AAGAAAAAGA AGAGA
                                       A
GAM775  RORB     3'  AGGTAGAAAGAGAAGACCCAGA 22607     ATTTT       C
           G                     CTC     TTTTCTCT TCTACCT
                                |||     |||||||| |||||||
                                GAG     AGAAGAGA AGATGGA
                                  ACCC_       A
GAM775  RUNX1    3'  GGCTAGAAAAAAAGAATGAG   8264           C   CT
                                CTCATTTTTTTT TCT  CT
                                |||||||||||| |||  ||
                                GAGTAAGAAAAA AGA  GG
                                       A   TC
GAM775  SCNN1B   3'  GTAGAAAATACTGAGAAAAAAA 4419           TC_____
           A                     TTTTTTTTCTC      TCTAC
                                ||||||||||       |||||
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                                AAAAAAAAGAG      AGATG
                                      TCATAAA
GAM775  SEL1L    3'  TAGTATGGGAAAAAAACTGA  17364     T        TCT
                                TCA TTTTTTTCTC   CTA
                                ||| ||||||||||   |||
                                AGT AAAAAAAGGG   GAT
                                  C         TAT
GAM775  SHOX     3'  AGGGGTAGAAAAAAAA      4831          CT
                                TTTTTTTTCT  CTCT
                                |||||||||  ||||
                                AAAAAAAAGA  GGGA
                                      TG
GAM775  SLC21A2  3'  AGAGAGAGAAAAAGGGT     18855
                                ATTTTTTTTCTCTCTCT
                                |||||||||||||||||
                                TGGGAAAAAGAGAGAGA

GAM775  SLC9A3R2 3'  AGAGAGAGAGCGAGCGAG    61432     ATT   T
                                CTC   TTT TTCTCTCTCT
                                |||   ||| ||||||||||
                                GAG   GAG GAGAGAGAGA
                                  C__   C
GAM775  SNX15    3'  AGAATGAGAAAAATAATGA    73733       T       TC
                                TCATT TTTTTCTC  TCT
                                ||||| ||||||||  |||
                                AGTAA AAAAAGAG  AGA
                                   T       TA
GAM775  SOX4     3'  GGAGAAAAAAAAAAGTGA     11876           C
                                TCATTTTTTTT TCTCT
                                |||||||||| |||||
                                AGTGAAAAAAA AGAGG
                                      A
GAM775  TFAP4    3'  AGTGGGGAGAAAAAAAA     12235             _
                                TTTTTTTTCTCTCT CT
                                |||||||||||||| ||
                                AAAAAAAAGAGGGG GA
                                       T
GAM775  TLR4     3'  AGACAGAGAAAACAGAAAGAG  12316     A   _       C
                                CTC TTTT TTTTCTCT TCT
                                ||| |||| |||||||| |||
                                GAG AAGA AAAAGAGA AGA
                                  A   C       C
GAM775  TLR4     3'  AGACAGAGAAAACAGAAAGAG  56726     A   _       C
                                CTC TTTT TTTTCTCT TCT
                                ||| |||| |||||||| |||
                                GAG AAGA AAAAGAGA AGA
                                  A   C       C
GAM775  TLR4     3'  AGACAGAGAAAACAGAAAGAG  56731     A   _       C
                                CTC TTTT TTTTCTCT TCT
                                ||| |||| |||||||| |||
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                                GAG AAGA AAAAGAGA AGA
                                  A   C       C
GAM775  TM7SF2   3'  AGAGCAAGGAAAAAAATGA   12330           CT
                                TCATTTTTTTTCT  CTCT
                                ||||||||||||  ||||
                                AGTAAAAAAAGGA  GAGA
                                    AC
GAM775  TNFRSF5  3'  AGAGGCAGAAAAAAAA     6976          C
                                TTTTTTTTCT TCTCT
                                |||||||||| |||||
                                AAAAAAAAGA GGAGA
                                    C
GAM775  ZIC1     5'  AGAGAGGGAAAAACGGAG    12721     ATTT
                                CTC   TTTTTCTCTCTCT
                                |||   ||||||||||||
                                GAG   AAAAAGGGAGAGA
                                  GC__
GAM775  ZNF134   3'  AGGGAAAGAAAAAAAA     12844          C
                                TTTTTTTTCT TCTCT
                                |||||||||| |||||
                                AAAAAAAAGA AGGGA
                                    A
GAM775  AGPAT1   3'  AGAGAGAGAGAAAAAA     21146
                                TTTTTTTTCTCTCTCT
                                ||||||||||||||||
                                AAAAAAGAGAGAGAGA

GAM775  AGPAT1   3'  AGAGAGAGAAAAAAAA     51231
                                TTTTTTTTCTCTCTCT
                                ||||||||||||||||
                                AAAAAAAAGAGAGAGA

GAM775  AGPAT1   3'  AGAGAGAGAGAGAAAA     51232
                                TTTTTTTTCTCTCTCT
                                ||||||||||||||||
                                AAAAGAGAGAGAGAGA

GAM775  AGPAT1   3'  AGAGAGAGAAAAAAAA     51230
                                TTTTTTTTCTCTCTCT
                                ||||||||||||||||
                                AAAAAAAAGAGAGAGA

GAM775  APOBEC3G 3'  GGTAGAGGAATAAAATGA   41527       TTTTC  T
                                TCATTTT    TC CTCTACC
                                |||||||    || |||||||
                                AGTAAAA    AG GAGATGG
                                    TA___  _
GAM775  ASE-1    3'  AGGGAGAAAAAAATGAG     23944          T
                                CTCATTTTTTT CTCTCT
                                |||||||||| ||||||
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                                GAGTAAAAAAA GAGGGA
                                          _
GAM775  BC008967 5' AGAGAGAGGATGAG      60764      TTTTTT
                                CTCATT    CTCTCTCT
                                ||||||    ||||||||
                                GAGTAG    GAGAGAGA
                                        _______
GAM775  BC022889 3' AGCAGAGAAAAAAGGTGG   83644           _
                                TCATTTTTTTTCTCT CT
                                |||||||||||||| ||
                                GGTGGAAAAAAGAGA GA
                                          C
GAM775  BCoR     3' GGAGAAAAAAAAAATGAG    34864          C
                                CTCATTTTTTTT TCTCT
                                |||||||||||| |||||
                                GAGTAAAAAAAA AGAGG
                                          _
GAM775  CAMTA1   3' GGTAGAAATGAAAAGTGAG  67917        TTCTCTC
                                CTCATTTTTT     TCTACC
                                ||||||||||     ||||||
                                GAGTGAAAAG     AGATGG
                                      TAA____
GAM775  CASPR3   3' AGGTAAAGGAGAAAAAAAA  45932         T  C
                                TTTTTTTTCTC CT TACCT
                                |||||||||| || |||||
                                AAAAAAAAGAG GA ATGGA
                                         _ A
GAM775  CGI-85   3' AGAGAAAGGAAAGAG      32079     A
                                CTC TTTTTTTTCTCT
                                ||| ||||||||||||
                                GAG AAAGGAAAGAGA
                                 _
GAM775  CLIC5    3' AGACAGAGAGAGTGAATGG   33716       T       C
                                TCATTT TTTTCTCT TCT
                                |||||| |||||||| |||
                                GGTAAG GAGAGAGA AGA
                                   T       C
GAM775  DCAMKL1  3' AGCAGAGAAAAAAAAAATG   16407         C    _
                                CATTTTTTTT TCTCT CT
                                |||||||||| ||||| ||
                                GTAAAAAAAA AGAGA GA
                                         _    C
GAM775  DIO2     5' AGAGAGTGAGAAAAAAGAG   5824      A       T
                                CTC TTTTTTTTC CTCTCT
                                ||| ||||||||| ||||||
                                GAG AAAAAAGAG GAGAGA
                                  _       T
GAM775  DIO2     5' AGAGAGTGAGAAAAAAGAG   25676     A       T
                                CTC TTTTTTTTC CTCTCT
                                ||| ||||||||| ||||||
```

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                                GAG AAAAAAGAG GAGAGA
                                  _       T
GAM775  DKFZP434A0225 3'  AGAAAGAGAAACAAAAATGA  93905        _     C
                                TCATTTTT TTTCTCT TCT
                                |||||||| ||||||| |||
                                AGTAAAAA AAAGAGA AGA
                                    C      A
GAM775  DREV1    3'  TAGAAAGAGGAAATGAG     32070       TTTT     C
                                CTCATT    TTCTCT TCTA
                                ||||||    |||||| ||||
                                GAGTAA    AGGAGA AGAT
                                   ____     A
GAM775  FLB6421  3'  AGATAGAAAAAAGGGATGAG  39223          C  C
                                CTCATTTTTTTT TCT TCT
                                |||||||||||| ||| |||
                                GAGTAGGGAAAA AGA AGA
                                      A  T
GAM775  FLJ10300 5'  AGATAGAGAAAGAAGATACCGA 35998    ___          C
          G                      CTC   ATTTTTTTTCTCT TCT
                                |||   |||||||||||||| |||
                                GAG   TAGAAGAAAGAGA AGA
                                  CCA           T
GAM775  FLJ10378 5'  AGAGAAAAAAGAGATGA     36080          C
                                TCATTTTTTTT TCTCT
                                |||||||||| |||||
                                AGTAGAGAAAA AGAGA
                                      A
GAM775  FLJ10583 3'  AGAGAGATTAAAGAAA      36308        TC
                                TTTTTTT  TCTCTCT
                                |||||||  |||||||
                                AAAGAAA  AGAGAGA
                                    TT
GAM775  FLJ11267 3'  GTGGCAGAAAAAAAATGA    39006          CTCT
                                TCATTTTTTTTCT   CTAC
                                ||||||||||||   ||||
                                AGTAAAAAAAAGA   GGTG
                                      C___
GAM775  FLJ20686 5'  AGAGGAGAAAAAAGA       35533          T
                                TTTTTTTTCTC CTCT
                                |||||||||| ||||
                                AGAAAAAAGAG GAGA
                                   _
GAM775  FLJ22595 5'  AGAGAGAGAAAAAGGCTGA   46783     T
                                TCA TTTTTTTCTCTCTCT
                                ||| ||||||||||||||
                                AGT GGAAAAAGAGAGAGA
                                  C
GAM775  FLJ23556 3'  AGAGAGAGAGATAGAG      45941      T
                                TTTT TTTCTCTCTCT
                                |||| ||||||||||
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                                GAGA AGAGAGAGAGA
                                  T
GAM775  GDAP1L1   3'  AGAGAGAGAGAAAAAA      43827
                                TTTTTTTTCTCTCTCT
                                ||||||||||||||||
                                AAAAAAGAGAGAGAGA

GAM775  GDF11     3'  AGGCAAAGAGAGAGGCAGAAGA 19440        T        A__
                                TTTTTT TCTCTCTCT   CCT
                                |||||| |||||||||   |||
                                AGAAGA GGAGAGAGA   GGA
                                   C        AAC
GAM775  HSA243666 3'  AGAAAAAGAAAATGAG      34143            C
                                CTCATTTTTTTT TCT
                                |||||||||||| |||
                                GAGTAAAAGAAA AGA
                                      A
GAM775  HSA404617 3'  AGAGAAAATAAATGAG      72706         T
                                CTCATTT TTTTCTCT
                                ||||||| ||||||||
                                GAGTAAA AAAAGAGA
                                   T
GAM775  HSA9761   3'  GGTCAAGAAAAGAAATGA    27126             CTCTCT
                                TCATTTTTTTTCT     ACC
                                ||||||||||||      |||
                                AGTAAAGAAAAGA     TGG
                                      AC____
GAM775  HT009     3'  AGAGAAAGAAAAAAAA      37471          C
                                TTTTTTTTCT TCTCT
                                |||||||||| |||||
                                AAAAAAAAGA AGAGA
                                      A
GAM775  HT009     3'  AGAGAAAGAAAAAAAA      37472          C
                                TTTTTTTTCT TCTCT
                                |||||||||| |||||
                                AAAAAAAAGA AGAGA
                                      A
GAM775  HTCD37    3'  AGAGGAGAAAAAAAAGTGA    67670             T
                                TCATTTTTTTTCTC CTCT
                                |||||||||||||| ||||
                                AGTGAAAAAAAGAG GAGA
                                                _
GAM775  IMP-2     3'  GAGTTGGAAAAAAAAT      21570          CT
                                ATTTTTTTTCT  CTC
                                ||||||||||  |||
                                TAAAAAAAAGG  GAG
                                      TT
GAM775  KIAA0226  3'  AGGGAAAGAAAAAAAA      63511          C
                                TTTTTTTTCT TCTCT
                                |||||||||| |||||
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                                AAAAAAAAGA AGGGA
                                      A
GAM775  KIAA0265 3' GGTAGAAAAGGAAAAGGA    69882         CTC
                                TTTTTTTTCT   TCTACC
                                ||||||||||   ||||||
                                AGGAAAAGGA   AGATGG
                                      AA_
GAM775  KIAA0373 5' AGATAGAAAGAGAAAAGAA    28013          C   C
                                TTTTTTTCTCT TCTA CT
                                |||||||||| |||| ||
                                AAGAAAAGAGA AGAT GA
                                      A   A
GAM775  KIAA0408 3' AGAGCTGAGAAAAAAAA     28129          T_
                                TTTTTTTTCTC  CTCT
                                ||||||||||  ||||
                                AAAAAAAAGAG  GAGA
                                      TC
GAM775  KIAA0408 5' AGATGGTCTGAGAAAAGAAA   28130          TCT   C
                                TTTTTTTTCTC   CTA CT
                                ||||||||||   ||| ||
                                AAAGAAAAGAG   GGT GA
                                      TCT   A
GAM775  KIAA0595 3' AGAGAGAGAAAAAAAA      30497
                                TTTTTTTTCTCTCTCT
                                ||||||||||||||||
                                AAAAAAAAGAGAGAGA

GAM775  KIAA0652 3' GGCAGAAAGAGGAAGGA     28462          C   A
                                TTTTTTCTCT TCT CC
                                ||||||||| ||| ||
                                AGGAAGGAGA AGA GG
                                      A   C
GAM775  KIAA0748 5' AGAGAGAGAGAAGAAA      28933
                                TTTTTTTTCTCTCTCT
                                ||||||||||||||||
                                AAAGAAGAGAGAGAGA

GAM775  KIAA0912 3' AGAATGAGAAAAAGAA      64404          TC
                                TTTTTTTTCTC  TCT
                                ||||||||||  |||
                                AAGAAAAAGAG  AGA
                                      TA
GAM775  KIAA1247 3' GGTACTGAAAAGAAATGA    61854          TCTCTC
                                TCATTTTTTTTC     TACC
                                ||||||||||||     ||||
                                AGTAAAGAAAAG     ATGG
                                      TC____
GAM775  KIAA1634 3' AGGTCTCCAGAGAAAAAAA   63384          CTCT
                                TTTTTTTCTCT    ACCT
                                ||||||||||    ||||
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                                AAAAAAAGAGA   TGGA
                                      CCTC
GAM775  KIAA1765 3'  GTTTGAGAGAAAAACAATGA  70613      T       TCT
                                TCATT TTTTTCTCTC  AC
                                ||||| ||||||||||  ||
                                AGTAA AAAAAGAGAG  TG
                                   C        TT_
GAM775  KIAA1877 3'  AGACAGAGAAAGGGAGTGAG  66160            C
                                CTCATTTTTTTTCTCT TCT
                                |||||||||||||||| |||
                                GAGTGAGGGAAAGAGA AGA
                                          C
GAM775  MGC10963 3'  AGACGGAGAAAAAAAA     47554          C
                                TTTTTTTTCTCT TCT
                                |||||||||||| |||
                                AAAAAAAAGAGG AGA
                                      C
GAM775  MGC35558 3'  AGGCAGAGAGAGAAGGA    58773          A
                                TTTTTCTCTCTCT CCT
                                |||||||||||| |||
                                AGGAAGAGAGAGA GGA
                                       C
GAM775  MMD     3'  AGGGAAAGAAAAAAAAT     59804          C
                                ATTTTTTTTCT TCTCT
                                |||||||||| |||||
                                TAAAAAAAAGA AGGGA
                                      A
GAM775  NRF     3'  AGGTAGAAAAAGACGGAAGGAA 34080        _  C__
                                TTTTTTTC TCT   TCTACCT
                                |||||||| |||   |||||||
                                AAGGAAGG AGA   AGATGGA
                                     C   AAA
GAM775  PAK7    3'  GTAGAAAGAAAAGAAAAAGA  69649    A      C  C
                                TC TTTTTTTT TCT TCTAC
                                || |||||||| ||| |||||
                                AG AAAAAGAA AGA AGATG
                                 _       A  A
GAM775  PMPCB   3'  AGAGCTAGAGAAAAATAAAAAT 15000       ____     __
            GA                    TCATTTTT   TTTCTCT  CTCT
                                |||||||   |||||||  ||||
                                AGTAAAAA   AAAGAGA  GAGA
                                     TAA      TC
GAM775  PRO1598  5'  GGAAAAAAAAAATGAG     37537          C
                                CTCATTTTTTTT TCT
                                |||||||||||| |||
                                GAGTAAAAAAAA AGG
                                      A
GAM775  RHOBTB1  3'  AGGAAGAGAAAAAAAA     91439          CT
                                TTTTTTTTCTCT  CT
                                ||||||||||||  ||
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                                AAAAAAAAGAGA  GA
                                      AG
GAM775  RODH-4   5'  GGCAGAGAGAAACCAGGAG   13536    ATTTTT      CTA
                                CTC     TTTCTCTCT   CC
                                |||     |||||||||   ||
                                GAG     AAAGAGAGA   GG
                                  GACC__        C__
GAM775  STAT5A   3'  AGAGAGAGAGAAAGAG      12008
                                TTTTTTTTCTCTCTCT
                                ||||||||||||||||
                                GAGAAAGAGAGAGAGA

GAM775  TBDN100  3'  AGATAGAAGAAGAGAAAAAAAA 46950    _          _ _  C
            TGCAG                   CT CATTTTTTTTCTCT CT CTA CT
                                || ||||||||||||| || ||| ||
                                GA GTAAAAAAAAGAGA GA GAT GA
                                 C           A  A   A
GAM775  THTPA    5'  GGTAGAGAGAAAAGGG      44261      C
                                TTTTT TCTCTCTACC
                                ||||| ||||||||||
                                GGGAA AGAGAGATGG
                                   A
GAM775  TLK1     3'  AGATAGAGGAAAAAAA      24454           C
                                TTTTTTTTCTCT TCT
                                |||||||||||| |||
                                AAAAAAAGGAGA AGA
                                      T
GAM775  TRIAD3   5'  AGAAGAGAAAACAAATGA    94499       T      C
                                TCATTT TTTTCTCT TCT
                                |||||| |||||||| |||
                                AGTAAA AAAAGAGA AGA
                                   C      _
GAM775  LOC112840 3'  AGACAAAGAGAAAAGATGA   54726           CTC
                                TCATTTTTTTTCT   TCT
                                ||||||||||||   |||
                                AGTAGAAAAGAGA   AGA
                                      AAC
GAM775  LOC115294 3'  GGTAGAAATGAAAAATGA    73017         TTCTCTC
                                TCATTTTTT      TCTACC
                                |||||||||      ||||||
                                AGTAAAAAG      AGATGG
                                     TAA_____
GAM775  LOC123876 3'  AGAGAAGAAAGGAAAGA     74241    A        C
                                TC TTTTTTTTCT TCTCT
                                || ||||||||||  |||||
                                AG AAAGGAAAGA AGAGA
                                  _       _
GAM775  LOC123876 3'  AGAGAGAAAGAGAAAGA     74242    A
                                TC TTTTTTTTCTCTCT
                                || ||||||||||||||
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                                AG AAGAGAAAGAGAGA
                                 A
GAM775  LOC127255 3'  AGAAAGAGAAAAAAAA      59159           C
                                TTTTTTTTCTCT TCT
                                |||||||||||| |||
                                AAAAAAAAGAGA AGA
                                       A
GAM775  LOC127255 3'  AGGTAAGAGTAAAAAAAAA   59160        CT   C
                                TTTTTTTT  CTCT TACCT
                                ||||||||  |||| |||||
                                AAAAAAAA  GAGA ATGGA
                                     AT   _
GAM775  LOC127428 3'  GGCAGAGAGGAAAATGGG    74671         TTTCT     A
                                CTCATTTTT    CTCTCT CC
                                |||||||||    |||||| ||
                                GGGTAAAAG    GAGAGA GG
                                     _____     C
GAM775  LOC129401 3'  GTGGTGAGAAAAAAAAAA    56284        C   T
                                TTTTTTTT TCTC CTAC
                                |||||||| |||| ||||
                                AAAAAAAA AGAG GGTG
                                     A   T
GAM775  LOC144473 5'  AGGCAGAAAGGTTGGAAAAATG 83068         TC   C   A
                                CATTTTTTT  TCT TCT CCT
                                |||||||||  ||| ||| |||
                                GTAAAAAGG  GGA AGA GGA
                                      TT   A   C
GAM775  LOC145098 5'  AGAGAGAAAAAACAGAG     76988     ATT
                                CTC   TTTTTTCTCTCT
                                |||   ||||||||||||
                                GAG   AAAAAAGAGAGA
                                  AC_
GAM775  LOC146485 5'  AGATAGAGAAAAAAGAGAG    59786     A          C
                                CTC TTTTTTTTCTCT TCT
                                ||| |||||||||||| |||
                                GAG AGAAAAAAGAGA AGA
                                  _          T
GAM775  LOC146520 5'  AGGGAGAGACAAAAAAAT     77951          _
                                ATTTTTTT TCTCTCTCT
                                |||||||| |||||||||
                                TAAAAAAA AGAGAGGGA
                                     C
GAM775  LOC148809 3'  AGCAGAGAGGAAAATGGA     78998     ATTT         _
                                TC    TTTTTCTCTCT CT
                                ||    |||||||||||| ||
                                AG    AAAAGGAGAGA GA
                                  GT__          C
GAM775  LOC149863 3'  AGAAAGAAAGAAAAAATGAG   84715           C   C
                                CTCATTTTTTTT TCT TCT
                                |||||||||||| ||| |||
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                                GAGTAAAAAAGA AGA AGA
                                       A   A
GAM775   LOC150969 3'  AGGCAGAGTGGAAAAAAAGAG  80085     A       T    CTA
                                CTC TTTTTTTTC CTCT   CCT
                                ||| ||||||||| ||||   |||
                                GAG AAAAAAAGG GAGA   GGA
                                  _       T   C__
GAM775   LOC152215 3'  GTAGAGAAAAATGGGAAAATG  80489         TCTC_
                                CATTTTTTT    TCTCTAC
                                |||||||||    |||||||
                                GTAAAAGGG    AGAGATG
                                     TAAAA
GAM775   LOC152905 3'  GGTAAAAGAGAAAATGA     60479       TTTT    CTC
                                TCATTT   TCTCT   TACC
                                ||||||   |||||  ||||
                                AGTAAA   AGAGA   ATGG
                                   ____    AA_
GAM775   LOC153727 5'  AGGAAGAAAAAAAATG      86151          CT
                                CATTTTTTTTCT  CT
                                ||||||||||||  ||
                                GTAAAAAAAAGA  GA
                                       AG
GAM775   LOC157273 5'  AGAGAGAGAGAGATGAG     86428        TTT
                                CTCATTTT   TCTCTCTCT
                                ||||||||   |||||||||
                                GAGTAGAG   AGAGAGAGA
                                   ___
GAM775   LOC196403 3'  AGGCAGAGAAAGAGCTGAAGAA 89627       TT   __    A
                                TTTTTT  CTC  TCTCT CCT
                                ||||||  |||  ||||| |||
                                AAGAAG  GAG  AGAGA GGA
                                    TC   AA    C
GAM775   LOC199786 3'  AGGCAGAGAGAGAGAGGAGA   88365             A
                                TTTTTTTTCTCTCTCT CCT
                                |||||||||||||||| |||
                                AGAGGAGAGAGAGAGA GGA
                                          C
GAM775   LOC199906 3'  AGGTAGAGAGAGAAAGTGCATG 88473     TTT
                                CAT   TTTTCTCTCTCTACCT
                                |||   ||||||||||||||||
                                GTA   GAAAGAGAGAGATGGA
                                  CGT
GAM775   LOC201895 3'  AGGAAGAGAGAAAAAATGA    89085            CT
                                TCATTTTTTTTCTCT  CT
                                ||||||||||||||  ||
                                AGTAAAAAAGAGAGA  GA
                                          AG
GAM775   LOC222193 3'  GGTAAAGAAGAAAAAGAA    94182          C   C
                                TTTTTTTTCT TCT TACC
                                |||||||||| ||| ||||
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                                AAGAAAAAGA AGA ATGG
                                      _  A
GAM775  LOC253187 3'  AGTTGAGAAAAAAGATGA    97111          TCT
                                TCATTTTTTTTCTC  CT
                                |||||||||||||  ||
                                AGTAGAAAAAAGAG  GA
                                      TT_
GAM775  LOC253612 3'  AGGCAGAGAGAAAAAGA     96739          CTA
                                TTTTTTTCTCTCT  CCT
                                |||||||||||||  |||
                                AGAAAAAGAGAGA  GGA
                                      C__
GAM775  LOC255030 3'  GGAGAAAAAAAAAAGAG     97269     A_
                                CTC  TTTTTTTTCTCT
                                |||  ||||||||||||
                                GAG  AAAAAAAAGAGG
                                  AA
GAM775  LOC255481 3'  GGCAGAAGAGAAAAACGA    94441    T       C  A
                                TT TTTTTCTCT TCT CC
                                || |||||||| ||| ||
                                AG AAAAAGAGA AGA GG
                                 C       _  C
GAM775  LOC257600 3'  AGAAGAAAGAAAATGA      97849          C
                                TCATTTTTTTTCT TCT
                                |||||||||||| |||
                                AGTAAAAGAAAGA AGA
                                      _
GAM775  LOC56920  3'  GGTAGAGAAAAGGACGAA    39391    T   C_
                                TTT TTCT  TCTCTACC
                                ||| ||||  ||||||||
                                AAG AGGA  AGAGATGG
                                  C   AA
GAM775  LOC56920  3'  GGAGGGGAAAAAAAGAT     39388        CT
                                ATTTTTTTT  CTCTCT
                                |||||||||  ||||||
                                TAGAAAAAA  GGGAGG
                                     AG
GAM775  LOC90120  3'  GGTAGAGAAAGCAAAAAA    61540      T  C
                                TTTTTT CT TCTCTACC
                                |||||| || ||||||||
                                AAAAAA GA AGAGATGG
                                   C  A
GAM776  ARNT2     3'  AAACAACCCGTGCATCCCTGC  29450    A   TTTTA
                                GTA GGAT    GGGTTGTTT
                                ||| ||||    |||||||||
                                CGT CCTA    CCCAACAAA
                                  C   CGTG_
GAM776  LCT       3'  AACCGTAAAAATCCTT      9697          G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
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                                TTCCTAAAAAT CCAA
                                      G
GAM776  RPL15    3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM776  FBXO30   3'  AACTAAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                  G        AA
GAM776  KIAA0494 3'  AACAACCCTTACTTAC      28736      GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM776  PRO0641  5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                   ___    C
GAM776  SMT3H2   3'  AACAACATAAAAATCCTTGC   22670           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM776  LOC120103 3' AACCTATGAAAAATCCTTGC   74002           A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
                                CGTTCCTAAAAA   TCCAA
                                      GTA
GAM776  LOC129831 3' AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM776  LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                      GTA GGATTTTT     TTGTTT
                                ||| ||||||||     ||||||
                                CGT CCTAAAAA     AACAAA
                                  C       GATAA
GAM776  LOC148089 3' GGCCCTAAAAATTCCTAC    78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM776  LOC154547 3' AACAACATAAAAATCCTTGC   76050           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
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                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM776  LOC158104 3'  ACAGCCAAAAATCCTTA     60313          AG
                                TAAGGATTTTT  GGTTGT
                                |||||||||||  ||||||
                                ATTCCTAAAAA  CCGACA
                                       __
GAM776  LOC205880 5'  AAACAACCATCATCCTGAC   90709    A    TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM776  LOC221561 3'  AACAACATAAAAATCCTTGC   92130          GG
                                GTAAGGATTTTTA  GTTGTT
                                |||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM776  LOC257591 3'  AACAACATAAAAATCCTTGC   97840          GG
                                GTAAGGATTTTTA  GTTGTT
                                |||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM776  LOC51145  3'  AGCTAAAATCCTTAC       32393          TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
                                CATTCCTAAAA   TCGA
                                       ___
GAM777  AICDA    5'  GCCTGAGACTTGCAGGGAGGCA 40329     C       ATTTGC__
          AGAA                   TTC TGCCTCCCT       CAGGC
                                |||  |||||||||       |||||
                                AAG ACGGAGGGA       GTCCG
                                  A        CGTTCAGA
GAM777  ANK1     3'  GCCTCCGGCCCAGGGAGGCCAG 40027     CT      ATTT  __
          AA                     TTC  GCCTCCCT    GCC  AGGC
                                |||  ||||||||    |||  ||||
                                AAG  CGGAGGGA    CGG  TCCG
                                  AC       CC__   CC
GAM777  ANK1     3'  GCCTCCGGCCCAGGGAGGCCAG 3473      CT      ATTT  __
          AA                     TTC  GCCTCCCT    GCC  AGGC
                                |||  ||||||||    |||  ||||
                                AAG  CGGAGGGA    CGG  TCCG
                                  AC       CC__   CC
GAM777  EIF2C1   3'  CCCAAATCCAGAGGAAGCAAGG 24170     _  C   _  __    CCA
          A                       TCCT GC TCC CT  ATTTG   GG
                                ||||  ||  |||  ||  |||||   ||
                                AGGA CG AGG GA  TAAAC   CC
                                  A  A   A  CC    ____
GAM777  IKBKG    3'  CCCGGCACTGGGGAAGTCAAGA 94663     C  _ C     TT    A
          A                       TTC TG C TCCCTA  TGCC GG
                                |||  ||  |  ||||||  ||||  ||
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                                AAG AC G AGGGGT  ACGG CC
                                  A  T A     C_    C
GAM777  IKBKG    3'  CCCGGCACTGGGGAAGTCAAGA 13311     C  _ C     TT    A
              A                   TTC TG C TCCCTA  TGCC GG
                                ||| || | ||||||  |||| ||
                                AAG AC G AGGGGT  ACGG CC
                                  A  T A     C_    C
GAM777  LY9      3'  AAATAAAAGGCAGGAA      71680         CCC
                                TTCCTGCCT   TATTT
                                |||||||||   |||||
                                AAGGACGGA   ATAAA
                                     AA_
GAM777  MAFF     3'  TGGCAAATAGGGAGACAAGGA  24655      GC_
                                TCCT   CTCCCTATTTGCCA
                                ||||   ||||||||||||||
                                AGGA   GAGGGATAAACGGT
                                  ACA
GAM777  MC1R     5'  GCCCAGATGGAAGGAGGCAGG  9954          __      CCA
                                CCTGCCTCC  CTATTTG   GGC
                                |||||||||  |||||||   |||
                                GGACGGAGG  GGTAGAC   CCG
                                     AA      ___
GAM777  MYO15A   3'  GCCTGAGGGAGGAGGCAGGAG  32671           _ ATTTGC
                                TTCCTGCCTCC CT     CAGGC
                                ||||||||||| ||     |||||
                                GAGGACGGAGG GG     GTCCG
                                      A  GA____
GAM777  NRG1     3'  GCAAATAGAAAACAGGAA    25659       CCTCC
                                TTCCTG     CTATTTGC
                                ||||||     ||||||||
                                AAGGAC     GATAAACG
                                   AAAA_
GAM777  NRG1     3'  GCAAATAGAAAACAGGAA    25646       CCTCC
                                TTCCTG     CTATTTGC
                                ||||||     ||||||||
                                AAGGAC     GATAAACG
                                   AAAA_
GAM777  SEPN1    3'  GCCTGGCAGAGGAAGAAGGAA  66369      GC  C   AT
                                TTCCT  CT CCT  TTGCCAGGC
                                |||||  || |||  |||||||||
                                AAGGA  GA GGA  GACGGTCCG
                                   A_  A   __
GAM777  SMURF1   3'  GCCTAACCCGCGGGAGGCGGAA 92453      T      TATTTGCC
                                TTCC GCCTCCC       AGGC
                                |||| |||||||       ||||
                                AAGG CGGAGGG       TCCG
                                   _      CGCCCAA_
GAM777  STAT6    3'  GCCTAGGACGGATAGGCAGGAA 12021          CCCT    _ _
                                TTCCTGCCT    ATTTG CC AGGC
                                |||||||||    ||||| || ||||
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                                AAGGACGGA   TAGGC GG TCCG
                                    ____    A  A
GAM777  TFF3    3'  GCCCAGGCCTCAAGGGCAGGAA 63566       CCCTATTT  A_
                                TTCCTGCCT      GCC  GGC
                                |||||||||      |||  |||
                                AAGGACGGG      CGG  CCG
                                    AACTC___   AC
GAM777  TOP3B   5'  GCCCGGCGGCTCAGAAAGGCGG 14129       CC  AT_   A
          GAA                   TTCCTGCCT  CT   TTGCC GGC
                                |||||||||  ||   ||||| |||
                                AAGGGCGGA  GA   GGCGG CCG
                                    AA  CTC    C
GAM777  VAV1    3'  GCCTTGGCAGAGAGACGAG   18305    C_ A     _
                                CTC  CT TTTGCCA GGC
                                |||  || ||||||| |||
                                GAG  GA AGACGGT CCG
                                  CA  G      T
GAM777  YWHAB   5'  GCTGTGGATAGAGAAGCAGGAA 12692       C  C    TG CA
                                TTCCTGC TC CTATT  C  GGC
                                ||||||| || |||||  |  |||
                                AAGGACG AG GATAG  G  TCG
                                    A  A    GT __
GAM777  AF020591 3'  GCCTGGCAAACATGGCA    27141     TCCCTA
                                TGCC     TTTGCCAGGC
                                ||||     ||||||||||
                                ACGG     AAACGGTCCG
                                  TAC___
GAM777  BCL2L1  3'  CCTCAGGCAGGAAGGGCAGGAA 56804       CC  ATT   __
                                TTCCTGCCT  CT   TGCC  AGG
                                |||||||||  ||   ||||  |||
                                AAGGACGGG  GG   ACGG  TCC
                                    AA  ___    AC
GAM777  BNIP-S  5'  TAAAGAAGGAGGCAGGAA    56263         CTA
                                TTCCTGCCTCC   TTTG
                                ||||||||||   ||||
                                AAGGACGGAGG   AAAT
                                      AAG
GAM777  BTBD3   5'  GCAAATAAGAGAAACAGGAA   30311      C__  CC
                                TTCCTG   CTC  TATTTGC
                                ||||||   |||  |||||||
                                AAGGAC   GAG  ATAAACG
                                   AAA   A_
GAM777  C20orf28 3'  GCCTGAGACGGGAGGCAGGAA 31224         TAT  GC
                                TTCCTGCCTCCC   TT  CAGGC
                                ||||||||||||   ||  |||||
                                AAGGACGGAGGG   AG  GTCCG
                                      C__  A_
GAM777  CHODL   5'  CCCGGCAGGGAGGCAGGGA   46310          ATTT  A
                                TTCCTGCCTCCCT   GCC GG
                                ||||||||||||    ||| ||
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                                AGGGACGGAGGGA   CGG CC
                                      ____  C
GAM777  D2S448   3'  CCTGAAGGGAAGCAGG     73519      C    ATTTGC
                                CCTGC TCCCT     CAGG
                                ||||| |||||     ||||
                                GGACG AGGGA     GTCC
                                   A    A_____
GAM777  DKFZP434K1772 3'  GCCTTACTCAGGAAGGCAGGAG 67714         C   ATTTGCC
                                TTCCTGCCT CCT      AGGC
                                ||||||||| |||      ||||
                                GAGGACGGA GGA      TCCG
                                     A  CTCAT__
GAM777  DKFZp547I094 3'  CCTGGCAACCTGAGGGAGG   49637       AT__
                                CCTCCCT   TTGCCAGG
                                |||||||   ||||||||
                                GGAGGGA   AACGGTCC
                                    GTCC
GAM777  DKFZP547L112 3'  CCTGGATATAGCAAGGCAGGAA 66529        CC   TTG
                                TTCCTGCCT  CTAT   CCAGG
                                |||||||||  ||||   |||||
                                AAGGACGGA  GATA   GGTCC
                                     AC   TA_
GAM777  FABP7    5'  CAAATAAGAAGGCAGGAG    7542         CCC
                                TTCCTGCCT   TATTTG
                                |||||||||   ||||||
                                GAGGACGGA   ATAAAC
                                     AGA
GAM777  FLJ14957  3'  CCCAAAGTGGGAGGCAGGGA   51744          TA   CCA
                                TTCCTGCCTCCC  TTTG   GG
                                ||||||||||||  ||||   ||
                                AGGGACGGAGGG  AAAC   CC
                                       TG   ___
GAM777  FLJ20343  3'  CCTGGCAAACTGACCAG     34998     CC  CCTA
                                CTG  TC    TTTGCCAGG
                                |||  ||    |||||||||
                                GAC  AG    AAACGGTCC
                                  C_  TC__
GAM777  FLJ23185  3'  CCTGGCAGGATGAGGCAGAGA  46830    _      CCTA
                                TC CTGCCTC    TTTGCCAGG
                                || |||||||    |||||||||
                                AG GACGGAG    GGACGGTCC
                                 A      TA__
GAM777  GGA2     3'  GCCTGATGGGTGGGAGAAGGAA 56882       GC    T   GC
                                TTCCT  CTCCC ATTT  CAGGC
                                |||||  ||||| ||||  |||||
                                AAGGA  GAGGG TGGG  GTCCG
                                   A_     _    TA
GAM777  GGA2     3'  GCCTGATGGGTGGGAGAAGGAA 30468       GC    T   GC
                                TTCCT  CTCCC ATTT  CAGGC
                                |||||  ||||| ||||  |||||
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                                AAGGA  GAGGG TGGG  GTCCG
                                  A_    _   TA
GAM777  HDAC11   3'  GCCCATAGGTCCAGGGAGGCAG 45718         ATTT  A___
            G                    CCTGCCTCCCT   GCC   GGC
                                 ||||||||||    |||   |||
                                 GGACGGAGGGA   TGG   CCG
                                       CC__   ATAC
GAM777  IKKE     5'  CACAAGGAGGCAGGGA     25746         CTAT  CCA
                                 TTCCTGCCTCC   TTG  G
                                 ||||||||||    |||  |
                                 AGGGACGGAGG   AAC  C
                                       ____  A__
GAM777  IL1F10   3'  CAAGAAGGAGGCAGGAA     50771          CTA
                                 TTCCTGCCTCC   TTTG
                                 ||||||||||   ||||
                                 AAGGACGGAGG   GAAC
                                       AA_
GAM777  KIAA0370 5'  GCCCAGCAAATAGGAGCCTGGA 73209     T_ CTC       CA
            G                    TTCC  GC   CCTATTTGC  GGC
                                 ||||  ||   |||||||||  |||
                                 GAGG  CG   GGATAAACG  CCG
                                   TC  A__       AC
GAM777  KIAA0551 3'  GCCTGGTTGAGAAGGAGAG   66839    _  A_  T
                                 CTC CCT  TT GCCAGGC
                                 ||| |||  || |||||||
                                 GAG GGA  AG TGGTCCG
                                   A  AG  T
GAM777  KIAA1183 3'  CCCGGATGGGAGGAGGAA    62530      G     TATTTG  A
                                 TTCCT CCTCCC     CC GG
                                 ||||| ||||||     || ||
                                 AAGGA GGAGGG     GG CC
                                    _     TA_____  C
GAM777  KIAA1464 3'  CCTGACCCATGGAGGCAGGAG  68264          CTATTTGC
                                 TTCCTGCCTCC       CAGG
                                 ||||||||||       ||||
                                 GAGGACGGAGG       GTCC
                                       TACCCA__
GAM777  MAPK8IP3 3'  GCCTGGTAGATGAAGCAG    52987      C  CCT
                                 CTGC TC   ATTTGCCAGGC
                                 |||| ||   ||||||||||
                                 GACG AG   TAGATGGTCCG
                                   A  ___
GAM777  MGC2306  3'  GCCTGGCAGGGGGTGAAGGCAG 50963         ___   AT
            GAG                    TTCCTGCCT   CCCT  TTGCCAGGC
                                   |||||||||   ||||  |||||||||
                                   GAGGACGGA   GGGG  GACGGTCCG
                                       AGT   __
GAM777  MGC2865  5'  GCCTGGCAAACCGAAGCAAGAA 50451     C   C  CCTA
                                 TTC TGC TC    TTTGCCAGGC
                                 ||| ||| ||    ||||||||||
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                                AAG ACG AG    AAACGGTCCG
                                  A   A  CC__
GAM777  MGC9753   3'  GCCTGATTTTGGGGAGGAGGAA 53049      G       TTTGC
                                TTCCT CCTCCCTA     CAGGC
                                ||||| ||||||||     |||||
                                AAGGA GGAGGGGT     GTCCG
                                  _       TTTA_
GAM777  PALM      3'  GCCTGGTAGGAGAGAGACAGGA 10414      C   C  A
                                TCCTG CTC CT TTTGCCAGGC
                                ||||| ||| || ||||||||||
                                AGGAC GAG GA GGATGGTCCG
                                  A   A  _
GAM777  PDZD2     5'  CCTGGCACGGAAGGAGGAA   80866      G   C  TATT
                                TTCCT CCT CC    TGCCAGG
                                ||||| ||| ||    |||||||
                                AAGGA GGA GG    ACGGTCC
                                  _   A  C___
GAM777  PLPL      3'  CCTGGAGGGGGAGGCAGGAG   39431          ATTTG
                                TTCCTGCCTCCCT     CCAGG
                                ||||||||||||     |||||
                                GAGGACGGAGGGG     GGTCC
                                       GA___
GAM777  RABEX5    3'  GCCTGGAATGGAAGGCGGGAA  27186        C  TATTTG
                                TTCCTGCCT CC      CCAGGC
                                |||||||| ||      ||||||
                                AAGGGCGGA GG      GGTCCG
                                    A  TAA___
GAM777  SHANK3    5'  GCCTGCTCGCAGGGAGGCAGAG 65500    _       ATTT  C
              A                  TC CTGCCTCCCT    GC AGGC
                                || ||||||||||    || ||||
                                AG GACGGAGGGA    CG TCCG
                                 A        CGCT  _
GAM777  SRF       5'  CCGGGCCACAGGGGCAGGAA   11944         CCTATTT   A
                                TTCCTGCCTC      GCC GG
                                ||||||||||      ||| ||
                                AAGGACGGGG      CGG CC
                                      ACAC___   G
GAM777  TREX1     5'  CCCAGCAGAGGGAGGCAG    53280         AT   CA
                                CTGCCTCCCT  TTGC  GG
                                ||||||||||  ||||  ||
                                GACGGAGGGA  GACG  CC
                                      __    AC
GAM777  TREX1     5'  CCCAGCAGAGGGAGGCAG    53290         AT   CA
                                CTGCCTCCCT  TTGC  GG
                                ||||||||||  ||||  ||
                                GACGGAGGGA  GACG  CC
                                      __    AC
GAM777  URG4      3'  GCCCCCAGGGTAGGGAGACA  35506    C       GCCA
                                TG CTCCCTATTT    GGC
                                || ||||||||||    |||
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                                AC GAGGGATGGG   CCG
                                 A        ACCC
GAM777  LOC124222 3'  CCTGACAAACAGGCAGGGA   74271        CCCTA   C
                                TTCCTGCCT    TTTG CAGG
                                |||||||||    |||| ||||
                                AGGGACGGA    AAAC GTCC
                                     C____   A
GAM777  LOC131873 5'  CCCGGAGGAGAGGCAGGGA   75877        _  ATTTG  A
                                TTCCTGCCTC CCT    CC GG
                                |||||||||| |||    || ||
                                AGGGACGGAG GGA    GG CC
                                      A  _____  C
GAM777  LOC144348 5'  CCTTCCGTAGAAAGACAGGCA  76806     CC  A    C__
                                TGCCT  CT TTTGC   AGG
                                |||||  || |||||   |||
                                ACGGA  GA AGATG   TCC
                                   CA  A    CCT
GAM777  LOC146316 5'  CTTCGAGAGGCAGGAA     60872        CCTAT   CC
                                TTCCTGCCTC    TTG  AG
                                ||||||||||    |||  ||
                                AAGGACGGAG    AGC  TC
                                      _____   T_
GAM777  LOC148529 5'  CCTGGCAGACAGGAAGACA   84167    C  C   A
                                TG CT CCT TTTGCCAGG
                                || || ||| |||||||||
                                AC GA GGA AGACGGTCC
                                 A  A   C
GAM777  LOC149606 3'  GCCCGCGGAGCAGGGAG     79454       A_    CA
                                CTCCCT  TTTGC  GGC
                                ||||||  |||||  |||
                                GAGGGA  AGGCG  CCG
                                   CG    C_
GAM777  LOC151057 3'  CCAGGAAAGAAGGCAGGAA   85209        CCCTA   G  A
                                TTCCTGCCT    TTT CC GG
                                |||||||||    ||| || ||
                                AAGGACGGA    AAA GG CC
                                     AG___  _  A
GAM777  LOC153346 5'  CCCAGATGGAAGGCA       86022      CC      CCA
                                TGCCT  CTATTTG   GG
                                |||||  |||||||   ||
                                ACGGA  GGTAGAC   CC
                                   A_      ___
GAM777  LOC196418 5'  CCTTCCGTAGAAAGACAGGCA  87696     CC  A    C__
                                TGCCT  CT TTTGC   AGG
                                |||||  || |||||   |||
                                ACGGA  GA AGATG   TCC
                                   CA  A    CCT
GAM777  LOC199786 3'  GCCTGGCAGCTGAGGCAGAGA  88386    _     CCTAT
                                TC CTGCCTC    TTGCCAGGC
                                || |||||||    |||||||||
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                                AG GACGGAG    GACGGTCCG
                                 A      TC___
GAM777  LOC200058 3'  CCTGAAGGATGGGAAGCCAGGA 88556       C  C      GC
            A                     TTCCTG CT CCTATTT  CAGG
                                  ||||||  ||  |||||||  ||||
                                  AAGGAC GA GGGTAGG  GTCC
                                     C  A      AA
GAM777  LOC204579 5'  CCCGGCTATGAGGCAGGAA    89465         CCTATTT   A
                                  TTCCTGCCTC      GCC GG
                                  ||||||||||      ||| ||
                                  AAGGACGGAG      CGG CC
                                        TAT_____   C
GAM777  LOC219700 5'  GCCTGGCAGTCCAAAGACCAAG 93064     C  CCTCCCTAT
            AA                    TTC TG        TTGCCAGGC
                                  ||| ||        |||||||||
                                  AAG AC        GACGGTCCG
                                    A  CAGAAACCT
GAM777  LOC253181 5'  GCCTGGCAAACAGCACAGGA   97558      CCTCC  A
                                  TCCTG    CT TTTGCCAGGC
                                  |||||    || ||||||||||
                                  AGGAC    GA AAACGGTCCG
                                     AC___  C
GAM777  LOC253296 3'  GCCTGGGGCCACAGGAAAGGCA 94490         C_   ATTTG_
            GGAA                    TTCCTGCCT  CCT     CCAGGC
                                  |||||||||  |||     ||||||
                                  AAGGACGGA  GGA     GGTCCG
                                       AA   CACCGG
GAM777  LOC253298 5'  GCCTGGGGCCACAGGAAAGGCA 97215         C_   ATTTG_
            GGAA                    TTCCTGCCT  CCT     CCAGGC
                                  |||||||||  |||     ||||||
                                  AAGGACGGA  GGA     GGTCCG
                                       AA   CACCGG
GAM777  LOC254107 5'  CCCAGAGGGCAGGAA      94384         CCCTA    CCA
                                  TTCCTGCCT    TTTG   G
                                  |||||||||    ||||   |
                                  AAGGACGGG    AGAC   C
                                        _____   C__
GAM777  LOC255189 5'  CTGACCAAGGCAGGAA      96589         CCCTATT  C_
                                  TTCCTGCCT      TG  CAG
                                  |||||||||      ||  |||
                                  AAGGACGGA      AC  GTC
                                        ________  CA
GAM777  LOC257160 3'  CCTGACTGGGGAGGAAG     94846    G       TTTGC
                                  CT CCTCCCTA     CAGG
                                  ||  ||||||||    ||||
                                  GA GGAGGGGT     GTCC
                                    A       CA___
GAM777  LOC257570 3'  GCCTGGGGCCACAGGAAAGGCA 97833         C_   ATTTG_
            GGAA                    TTCCTGCCT  CCT     CCAGGC
                                  |||||||||  |||     ||||||
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                                AAGGACGGA  GGA     GGTCCG
                                    AA   CACCGG
GAM777  LOC257571 5'  GCCTGGGGCCACAGGAAAGGCA 97945         C_   ATTTG_
           GGAA                   TTCCTGCCT  CCT     CCAGGC
                                |||||||||  |||     ||||||
                                AAGGACGGA  GGA     GGTCCG
                                    AA   CACCGG
GAM778  B4GALT1   3'  CAAGAGTCAGAACTGTAGA   7666         GTCAA  TG
                                TCTACAGT    TG  TCTTG
                                ||||||||    ||  |||||
                                AGATGTCA    AC  AGAAC
                                    AG___  TG
GAM778  DGKA     3'  CAAAACACATACATTG      7201         CA     C
                                CAGTGT  ATGTGT TTG
                                ||||||  |||||| |||
                                GTTACA  TACACA AAC
                                   __     A
GAM778  MTMR6    3'  CTCAAAACACAATTTGCACTGT 93549         C   _   C
           A                     TACAGTGT AAT GTGT TTGAG
                                |||||||| ||| |||| |||||
                                ATGTCACG TTA CACA AACTC
                                    T   A    A
GAM778  SLC4A4   3'  CTCAAGACACAGACACCCACAG 13635     ACA_    AA
           A                     TCT    GTGTC  TGTGTCTTGAG
                                |||    |||||  ||||||||||
                                AGA    CACAG  ACACAGAACTC
                                  CACC    __
GAM778  CUL4A    3'  CTCAAGACTTCAACCTGCAGA  13153     A   T  CAA  T_
                                TCT CAG GT   TG  GTCTTGAG
                                ||| ||| ||   ||  ||||||||
                                AGA GTC CA   AC  CAGAACTC
                                  C   _ ___  TT
GAM778  FLJ11301  3'  CAAGACACTAGCACTGTAGA   37226          CAAT
                                TCTACAGTGT   GTGTCTTG
                                ||||||||||   ||||||||
                                AGATGTCACG   CACAGAAC
                                     AT__
GAM778  GPR105   3'  GACACACCCACACCGTAGA   29655       A   CAA
                                TCTAC GTGT   TGTGTC
                                ||||| ||||   ||||||
                                AGATG CACA   ACACAG
                                   C    CCC
GAM778  LAP1B    5'  CTCAAGACACACCATGGGC   64584     AA___
                                GTC    TGTGTCTTGAG
                                |||    ||||||||||
                                CGG    ACACAGAACTC
                                  GTACC
GAM778  PRDM10   3'  CTCAAGACACATTGACACTGTA 39578
           GA                     TCTACAGTGTCAATGTGTCTTGAG
                                |||||||||||||||||||||||
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                                AGATGTCACAGTTACACAGAACTC

GAM778  SEMA3C   3'  CTCTTCTACATTGACAC    21061          TCTT
                                GTGTCAATGTG   GAG
                                ||||||||||   |||
                                CACAGTTACAT   CTC
                                      CTT_
GAM778  LOC255654 3'  GACATCCACACTGTAGA    96887         CAAT
                                TCTACAGTGT   GTGTC
                                ||||||||||   |||||
                                AGATGTCACA   TACAG
                                      CC__
GAM778  LOC96652  3'  CTCAAGACAGGACACTGCGGA  65467   TA     AATG
                                TC  CAGTGTC   TGTCTTGAG
                                ||  |||||||   |||||||||
                                AG  GTCACAG   ACAGAACTC
                                 GC     G___
GAM779  BIN3     3'  CACCCTCCAGCAGGCAGCCCAG 37955        C    AT  CA
            CA                   TGCTGGGCT CCTGC  GA  GTG
                                |||||||| |||||  ||  |||
                                ACGACCCGA GGACG  CT  CAC
                                     C    AC  CC
GAM779  CRSP8    3'  CACGCAGGAAGCCCACA    80963    C    C    A
                                TG TGGGCT CCTGC TG
                                || |||||| ||||| ||
                                AC ACCCGA GGACG AC
                                 _     A    C
GAM779  ENG      5'  CACTGCCATCCATTGGAGCCCA 3687          C_  C   A
            GCA                   TGCTGGGCTCC  TG ATG CAGTG
                                ||||||||||  || ||| |||||
                                ACGACCCGAGG  AC TAC GTCAC
                                      TT  C   C
GAM779  HD       3'  CACTGTTAGTGACAGAGCCCAG 9181          CC  _  _
            CA                    TGCTGGGCTC  TG CA TGACAGTG
                                ||||||||||  || || ||||||||
                                ACGACCCGAG  AC GT ATTGTCAC
                                      __  A  G
GAM779  IGLL1    5'  CACTCTCTAGGGAGCCCACA   39174    C        CAT  C
                                TG TGGGCTCCCTG   GA AGTG
                                || ||||||||||   || ||||
                                AC ACCCGAGGGAT   CT TCAC
                                 _         ___  C
GAM779  THBD     3'  CACTGCCACACAGGGTCTGCA  4494      T   CT    CA  A
                                TGC GGG  CCCTG  TG CAGTG
                                ||| |||  |||||  || |||||
                                ACG TCT  GGGAC  AC GTCAC
                                  _  __     AC  C
GAM779  ARHGEF16 3'  CACCGTGTCCCAGGGAGCCCAG 27069           CAT   __
            C                     GCTGGGCTCCCTG   GACA  GTG
                                ||||||||||||   ||||  |||
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                                CGACCCGAGGGAC  CTGT  CAC
                                      C__   GC
GAM779  CABIN1   3' ACCACATGGGAGCCCAG    24479        TGC  ACA
                                CTGGGCTCCC  ATG  GT
                                ||||||||||  |||  ||
                                GACCCGAGGG  TAC  CA
                                     ___  AC_
GAM779  FLJ10232 3' ACTGTCAGGAACCCAG     35920     C  CTGCA
                                CTGGG TCC    TGACAGT
                                ||||| |||    |||||||
                                GACCC AGG    ACTGTCA
                                  A  _____
GAM779  FLJ20154 5' GCCTTCAGGCCCAGCA     72927        CCCTGCA  CA
                                TGCTGGGCT     TGA  GT
                                |||||||||     |||  ||
                                ACGACCCGG     ACT  CG
                                     ________  TC
GAM779  FLJ21865 3' CACCGCCATGCAGGGCTCGC  42805   T   TC      ACA
                                GC GGGC  CCTGCATG  GTG
                                || ||||  ||||||||  |||
                                CG CTCG  GGACGTAC  CAC
                                 _  __      CGC
GAM779  IRF7     3' CACCGCGGTGCAAGAGCCCAGC 14443       CC    GACA
                                GCTGGGCTC  TGCAT   GTG
                                |||||||||  |||||   |||
                                CGACCCGAG  ACGTG   CAC
                                     A_    GCGC
GAM779  KIAA0864 3' CACTGTCAGTATTAAGGCCCAG 63247       CCC_  A
           CA                    TGCTGGGCT   TGC TGACAGTG
                                |||||||||   ||| ||||||||
                                ACGACCCGG   ATG ACTGTCAC
                                     AATT  _
GAM779  MFN2     3' ACAAGGCAGGGGCCCAGCA   29595       T    ATGACA
                                TGCTGGGC CCCTGC     GT
                                |||||||| ||||||     ||
                                ACGACCCG GGGACG     CA
                                     _     GAA___
GAM779  MGC3101  3' GTCACACAGAGCCCAGCA    43883        CC  CA
                                TGCTGGGCTC  TG  TGAC
                                ||||||||||  ||  ||||
                                ACGACCCGAG  AC  ACTG
                                     __  AC
GAM779  SCYB11   3' CACTGCCCAAAGGAGTCCAACA 87442    C      CTGCATGA
                                TG TGGGCTCC       CAGTG
                                || ||||||||       |||||
                                AC ACCTGAGG       GTCAC
                                 A       AAACCC__
GAM779  TIX1     3' CATGTAAGGAGCCCAGCA    61739          C
                                TGCTGGGCTCC TGCATG
                                |||||||||| ||||||
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                                ACGACCCGAGG ATGTAC
                                      A
GAM779  UBP1     3'  CTGCCATAGCCAAGCA     27224     G   CCCTGC  A
                                TGCT GGCT     ATG CAG
                                |||| ||||     ||| |||
                                ACGA CCGA     TAC GTC
                                  A   _______  C
GAM779  LOC123242 3' ACCATTAAGCAGCCCAGCA   75589        CCCT  A   CA
                                TGCTGGGCT   GC TGA  GT
                                |||||||||   || |||  ||
                                ACGACCCGA   CG ATT  CA
                                     _____  A   AC
GAM779  LOC144058 5' CTGGATGCAGGGCACCCAACA  76666    C   CT      GA
                                TG TGGG  CCCTGCAT  CAG
                                || ||||  ||||||||  |||
                                AC ACCC  GGGACGTA  GTC
                                 A   AC      G_
GAM779  LOC147160 5' CACAGGGGAGCCCAGCA     83958          GCA
                                TGCTGGGCTCCCT   TG
                                ||||||||||||   ||
                                ACGACCCGAGGGG   AC
                                       AC_
GAM779  LOC148870 5' CACTGCTCCCAGGAGCCCACA  79041    C      C  CAT  _
                                TG TGGGCTCC TG   GA CAGTG
                                || ||||||| ||   || |||||
                                AC ACCCGAGG AC   CT GTCAC
                                 _      _ C__  C
GAM779  LOC149421 5' CACTGCCAACGTAGAGGGCCCA 79355         C   A_  A
           GCA                    TGCTGGGCTC CTGC  TG CAGTG
                                ||||||||| ||||  || |||||
                                ACGACCCGGG GATG  AC GTCAC
                                      A   CA  C
GAM779  LOC151360 3' CACTGTCACACCGTAGCCCACA 85311    C     CCCTGCA
                                TG TGGGCT      TGACAGTG
                                || ||||||      ||||||||
                                AC ACCCGA      ACTGTCAC
                                 _     TGCCAC_
GAM779  LOC151361 3' CACTGTCACACCGTAGCCCACA 85320    C     CCCTGCA
                                TG TGGGCT      TGACAGTG
                                || ||||||      ||||||||
                                AC ACCCGA      ACTGTCAC
                                 _     TGCCAC_
GAM779  LOC152286 3' CACTAGACAGCCAGGAGCCCAG 85626          CT  A  AC_
           CA                     TGCTGGGCTCC  GC TG   AGTG
                                ||||||||||  || ||   ||||
                                ACGACCCGAGG  CG AC   TCAC
                                      AC  _  AGA
GAM779  LOC152674 3' CACTGTCACCTGGAAGCCCAG  85834       C  TGCA
                                CTGGGCT CC    TGACAGTG
                                ||||||| ||    ||||||||
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                                GACCCGA GG    ACTGTCAC
                                    A  TCC_
GAM779  LOC253001 3'  ACCATTAAGCAGCCCAGCA   96249        CCCT  A   CA
                                TGCTGGGCT    GC TGA  GT
                                |||||||||    || |||  ||
                                ACGACCCGA    CG ATT  CA
                                     ____  A   AC
GAM779  LOC255030 3'  ACTGAGAAGAAGCCCAGC    97267        CC  GCATGA
                                GCTGGGCT  CT     CAGT
                                ||||||||  ||     ||||
                                CGACCCGA  GA     GTCA
                                    A_  AGA___
GAM779  LOC51131  3'  ACTGTCACACTCCCAGCA    32277       CTCCC  CA
                                TGCTGGG    TG  TGACAGT
                                |||||||    ||  |||||||
                                ACGACCC    AC  ACTGTCA
                                    TC___  __
GAM780  ABCB10    3'  TTTACGAAATTGCATTTCATTG 23889     _     TG __      AA
          TTA                     ACAA GAAATG  G  TCGTGAA
                                |||| ||||||  |  |||||||
                                TGTT CTTTAC  T  AGCATTT
                                  A     GT AA
GAM780  BMPR1A    3'  TTTTTGTGGTTATTATTTTTGT 15080        AT   GT  TG
          CA                      TGACAAGAA  GTG  CG  AAAA
                                |||||||||  |||  ||  ||||
                                ACTGTTTTT  TAT  GT  TTTT
                                     AT   TG  GT
GAM780  CACNA2D2  3'  ATGTCATGTTGCTTGTC     20078       A      T
                                GACAAG AATGTGG CGT
                                |||||| ||||||| |||
                                CTGTTC TTGTACT GTA
                                   G      _
GAM780  CALCR     3'  TGACCGCTTGTTTCTTGTTA  8224          __
                                TGACAAGAAAT  GTGGTCG
                                ||||||||||  |||||||
                                ATTGTTCTTTG  CGCCAGT
                                      TT
GAM780  CBFB      3'  TTTTCATGGTCACATTT     8279        GT
                                AAATGTG  CGTGAAAA
                                |||||||  ||||||||
                                TTTACAC  GTACTTTT
                                    TG
GAM780  CBFB      3'  TTTTCATGGTCACATTT     43146       GT
                                AAATGTG  CGTGAAAA
                                |||||||  ||||||||
                                TTTACAC  GTACTTTT
                                    TG
GAM780  CD164     3'  TTTACCTCACATTTTTTGTT  20052          TC
                                GACAAGAAATGTGG  GTGAA
                                ||||||||||||||  |||||
```

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                                TTGTTTTTTTACACT  CATTT
                                        C_
GAM780  CDK2     3'  TTTTTATGATTTGTCTCTGTCA 8393       _  AATGT
                                TGACA AGA    GGTCGTGAAAA
                                ||||| |||    ||||||||||
                                ACTGT TCT    TTAGTATTTTT
                                   C  GT___
GAM780  CHAC     3'  TTGTAATTGTATTTCTTG    52796        TG  CG
                                CAAGAAATG  GT  TGA
                                |||||||||  ||  |||
                                GTTCTTTAT  TA  GTT
                                     GT  AT
GAM780  CLOCK    3'  TGATTGCATATTTTGTTA    16913        A   TG
                                TGACAAGA ATG  GTCG
                                |||||||| |||  ||||
                                ATTGTTTT TAC  TAGT
                                     A   GT
GAM780  CPO      3'  TTTTTGTGGAACCATTGTTTGT 3640        AAAT    __ TG
             TA                   TGACAAG   GTGGT  CG  AAAA
                                |||||||   |||||  ||  ||||
                                ATTGTTT   TACCA  GT  TTTT
                                    GT__    AG  GT
GAM780  CTNNA1   3'  TTCTAGCTGTATTTTTTGT   65922         TG  CGT
                                ACAAGAAATG  GT   GAA
                                |||||||||  ||   |||
                                TGTTTTTTAT  CG   CTT
                                     GT  AT_
GAM780  DDX20    5'  TCCTCAGGCCACATTTTTTGT  23274            G   AAA
                                ACAAGAAATGTGGTC TGA
                                |||||||||||||| |||
                                TGTTTTTTACACCGG ACT
                                        _  CCTT
GAM780  DEK      3'  TTTTCACAGGTTTGTTTCTTG  12958         TGGTC
                                CAAGAAATG    GTGAAAA
                                |||||||||    |||||||
                                GTTCTTTGT    CACTTTT
                                     TTGGA
GAM780  EPS8     3'  TTTTTGGAAACACAATTTTTGT 15471         A   G_ G
             CA                   TGACAAGAA TGTG  TC TGAAAA
                                |||||||| ||||  || ||||||
                                ACTGTTTTT ACAC  AG GTTTTT
                                     A   AA  _
GAM780  ESRRBL1  3'  TATATCAAACTATATTTCATGT 35850      A        CG   AAA
             T                    GACA GAAATGTGGT  TGA
                                |||| ||||||||||  |||
                                TTGT CTTTATATCA  ACT
                                   A        A_   ATATT
GAM780  ESRRBL1  3'  TTTCATGGCTGTTGTCA     35851       AGAAAT TG
                                TGACA     G  GTCGTGAAA
                                |||||     |  |||||||||
```

```
                                ACTGT     T  CGGTACTTT
                                   _______ GT
GAM780  FOXE1    3'  TGTCCACTGTTTCTTGTCA    15561          _   T
                                TGACAAGAAAT GTGG CG
                                |||||||||||  |||| ||
                                ACTGTTCTTTG CACC GT
                                      T   T
GAM780  GHR      3'  TAGCACAGGCTAATTTTTTGTT 3886          G   _  AAAA
                                GACAAGAAAT TGGTC GTG
                                |||||||||| ||||| |||
                                TTGTTTTTTA ATCGG CAC
                                      _    A  GAT
GAM780  GNAO1    3'  TTTTCATGACCAATCCTATGTC 90969       AGAAATG
            A                    TGACA      TGGTCGTGAAAA
                                |||||      ||||||||||||
                                ACTGT      ACCAGTACTTTT
                                   ATCCTA_
GAM780  GNAZ     3'  TTTTCAAAACATATTTTTTTTC 9066      C        GTCG
            A                    TGA AAGAAATGTG    TGAAAA
                                ||| ||||||||||    ||||||
                                ACT TTTTTTATAC    ACTTTT
                                  T         AAA_
GAM780  GPM6B    3'  TTTTTATGATCACATGGTTC   67078     __
                                GAA  ATGTGGTCGTGAAAA
                                |||  ||||||||||||||
                                CTT  TACACTAGTATTTTT
                                  GG
GAM780  GRPR     5'  TTTTTGTGGCTAAGTTTTGTT  18003       AATG     TG
                                GACAAGA    TGGTCG  AAAA
                                |||||||    ||||||  ||||
                                TTGTTTT    ATCGGT  TTTT
                                    GA__      GT
GAM780  HEM1     5'  TTGCAGAGCTACTTTTCTTGTT 18054         T    CG  AAAA
                                GACAAGAAA GTGGT  TG
                                |||||||||  |||||  ||
                                TTGTTCTTT CATCG  AC
                                      T    AG  GTT
GAM780  HSF2BP   3'  TTTTAGTTCTATATTTTTTGT  22861           TCG
                                ACAAGAAATGTGG   TGAAA
                                ||||||||||||   |||||
                                TGTTTTTTATATC   ATTTT
                                       TTG
GAM780  IL1RAP   3'  TTTTTACTGGAATGTTTTTGTG 9315      _      GG  _
            TCA                   GACA AGAAATGT  TC GTGAAAA
                                |||| ||||||||  || |||||||
                                CTGT TTTTTGTA  GG CATTTTT
                                  G       A_  T
GAM780  IMMT     3'  TTTTCATAAAGTCATATTTCAT 22420      A       TC__
            GTCA                   GACA GAAATGTGG    GTGAAAA
                                |||| |||||||||    |||||||
```

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                                CTGT CTTTATACT    TACTTTT
                                  A        GAAA
GAM780  IPP      3'  TTTTTGCTTGCTCATATTTTTT 19730           _  C_ TG
             GTC                   GACAAGAAATGTG GT  G  AAAA
                                   |||||||||||||| ||  |  ||||
                                   CTGTTTTTTATAC CG  C  TTTT
                                         T  TT GT
GAM780  ITPR1    3'  TGGTTTTATTTCTTGTCA    9442           T GT
                                   TGACAAGAAATG G  CG
                                   |||||||||||| |  ||
                                   ACTGTTCTTTAT T  GT
                                         T TG
GAM780  KCNA7    3'  TTTTCGTGGCCACAGCGAGTTG 49066     GAAA_
                                   CAA     TGTGGTCGTGAAAA
                                   |||     ||||||||||||||
                                   GTT     ACACCGGTGCTTTT
                                     GAGCG
GAM780  KLRD1    3'  TTTTTAATTTTTAATTTTTTGT 23683          GTGGTCG
             CA                    TGACAAGAAAT      TGAAAA
                                   ||||||||||       ||||||
                                   ACTGTTTTTTA      ATTTTT
                                         ATTTTTA
GAM780  KLRD1    3'  TTTTTAATTTTTAATTTTTTGT 9624           GTGGTCG
             CA                    TGACAAGAAAT      TGAAAA
                                   ||||||||||       ||||||
                                   ACTGTTTTTTA      ATTTTT
                                         ATTTTTA
GAM780  LDB2     3'  TTTTTATAGTATATTTCTTGT  7095           GTC
                                   ACAAGAAATGTG   GTGAAAA
                                   ||||||||||||   |||||||
                                   TGTTCTTTATAT   TATTTTT
                                         GA_
GAM780  LFNG     3'  CCCGTGGGCTGTGTTTCTTGTT 92639          TG   GTGAAAA
                                   GACAAGAAATG  GTC
                                   ||||||||||  |||
                                   TTGTTCTTTGT  CGG
                                         GT   GTGCCCT
GAM780  MEN1     5'  TTTTTATGATTACAAAACTCTT 93388       AA__
             G                      CAAGA    TGTGGTCGTGAAAA
                                    |||||    ||||||||||||||
                                    GTTCT    ACATTAGTATTTTT
                                       CAAA
GAM780  NAP1L3   3'  TGGTCATGTTTCTGTTA     15797       A       GT
                                   TGACA GAAATGTG  CG
                                   ||||| ||||||||  ||
                                   ATTGT CTTTGTAC  GT
                                      _       TG
GAM780  NAPB     3'  TTTTATGTCCTTTTTGTT    70196         ATGT  T
                                   GACAAGAA    GG CGTGAAA
                                   ||||||||    || |||||||
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                                TTGTTTTT   CC GTATTTT
                                     ____  T
GAM780  NOS1    3'  TTTTTATGATGACATTTTGGTT 5256     AA     G
                                GAC  GAAATGT GTCGTGAAAA
                                |||  ||||||| ||||||||||
                                TTG  TTTTACA TAGTATTTTT
                                  G_     G
GAM780  NOVA1   3'  TTTTTGTTGTTCATTTGTTTCT 21414       __   TC_ TG
          TGTCA                   CAAGAAAT  GTGG   G  AAAA
                                |||||||||  ||||  |  ||||
                                GTTCTTTG  TACT   T  TTTT
                                     TT   TGT GT
GAM780  PCDHB16 3'  TCCTATGTTACATTTCTT   40557         T   AAAA
                                AAGAAATGTGG CGTG
                                |||||||||||| ||||
                                TTCTTTACATT GTAT
                                      _   CCTT
GAM780  PCDHB6  3'  TTTTTGTGACTATAGACTTTA  38440   C   AAA      TG
                                A AAG   TGTGGTCG  AAAA
                                | |||   |||||||||  ||||
                                A TTC   ATATCAGT  TTTT
                                 T   AG_      GT
GAM780  PDCL    3'  TGTCATATTTCTAGTCA    18220     A       T
                                TGAC AGAAATGTGG CG
                                |||| ||||||||||  ||
                                ACTG TCTTTATACT GT
                                  A        _
GAM780  PLXNA2  3'  TTTTTGCTACTGTTTTTTGTT  47212         GT   C TG
                                GACAAGAAAT  GGT G  AAAA
                                ||||||||||  ||| |  ||||
                                TTGTTTTTTG  TCA C  TTTT
                                      __   T GT
GAM780  PPP1R8  3'  TTTACCTGTTTTTCTTGTCA   56744         T TG TC
                                TGACAAGAAA G  G  GTGAA
                                ||||||||||  |  |  |||||
                                ACTGTTCTTT T  C  CATTT
                                      T GT __
GAM780  PPP1R8  3'  TTTACCTGTTTTTCTTGTCA   26069         T TG TC
                                TGACAAGAAA G  G  GTGAA
                                ||||||||||  |  |  |||||
                                ACTGTTCTTT T  C  CATTT
                                      T GT __
GAM780  PPP1R8  3'  TTTACCTGTTTTTCTTGTCA   10728         T TG TC
                                TGACAAGAAA G  G  GTGAA
                                ||||||||||  |  |  |||||
                                ACTGTTCTTT T  C  CATTT
                                      T GT __
GAM780  PRDM2   3'  TTTACATTTCACTTTTTTTGTT 31852         T   TC_    AA
                                GACAAGAAA GTGG   GTGAA
                                |||||||||  ||||   |||||
```

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                                TTGTTTTTT CACT   CATTT
                                     T    TTA
GAM780  PYCS     3'  TTTTCGCGTTTTATTTCTTTCA 11169     C       TG T
                                TGA AAGAAATG  G CGTGAAAA
                                ||| ||||||||  | ||||||||
                                ACT TTCTTTAT  T GCGCTTTT
                                  _       TT _
GAM780  RELN     3'  ACTGTATTTACTTGTTA     94301        _    TG
                                TGACAAG AAATG  GT
                                ||||||| |||||  ||
                                ATTGTTC TTTAT  CA
                                    A     GT
GAM780  RPL15    3'  TTTTCAAGTGGCTGCGTTTTTT 11388         TG   __
                                AAGAAATG  GTCG  TGAAAA
                                ||||||||  ||||  ||||||
                                TTTTTTGC  CGGT  ACTTTT
                                     GT    GA
GAM780  SEL1L    3'  TTTTACTTTGCATTTCTTTTT  17368    C       TG TC
                                GA AAGAAATG  G  GTGAAA
                                || ||||||||  |  ||||||
                                TT TTCTTTAC  T  CATTTT
                                 T       GT T_
GAM780  SPON1     3'  TTTTCTTCCTGCATTTATTGTT 62461       G     TG TCGT
                                GACAA AAATG  G    GAAAA
                                ||||| |||||  |    |||||
                                TTGTT TTTAC  C    CTTTT
                                   A     GT CTT_
GAM780  SYT4     3'  TTTTTATGACTATGCCTAATGT 62442     AGAAAT
                                ACA      GTGGTCGTGAAAA
                                |||      ||||||||||||||
                                TGT      TATCAGTATTTTT
                                  AATCCG
GAM780  TAF4B    3'  TTAAATTGGCCACATTTTTTTT 87169     C            TGAAAA
                T                GA AAGAAATGTGGTCG
                                || ||||||||||||||
                                TT TTTTTTACACCGGT
                                 T            TAAATTT
GAM780  TIRAP    3'  TTTTCTTCTGTATTTCTTTTCA 53573     C       TG TCGT
                                TGA AAGAAATG  G    GAAAA
                                ||| ||||||||  |    |||||
                                ACT TTCTTTAT  C    CTTTT
                                  T       GT TT__
GAM780  TMOD2     3'  GCAGATGATTGCATTTTTTG   27249         TG    GAAAA
                                CAAGAAATG  GTCGT
                                |||||||||  |||||
                                GTTTTTTAC  TAGTA
                                     GT     GACGT
GAM780  TNFRSF11A 3'  TTTTATGACTATCCTGTT    13858      A  AATG
                                GACA GA    TGGTCGTGAAA
                                |||| ||    ||||||||||
```

```
                                TTGT CT    ATCAGTATTTT
                                  C _____
GAM780  TRAF5    3'  TTGTGATGTTTCTTGTCA    16092          GTG    TG
                                TGACAAGAAAT   GTCG  A
                                ||||||||||   ||||  |
                                ACTGTTCTTTG   TAGT  T
                                      ___    GT
GAM780  TRHDE    3'  TTTTCATGGCTGTGTGTTGTGT 25392     AGAA   TG
                                ACA    ATG  GTCGTGAAAA
                                |||    |||  ||||||||||
                                TGT    TGT  CGGTACTTTT
                                  GTTG   GT
GAM780  UBL3     3'  TTTTTATTTCTTGTATTTTTTG 23036          TG TC_
             TT                   GACAAGAAATG  G   GTGAAAA
                                ||||||||||  |   |||||||
                                TTGTTTTTTAT  T   TATTTTT
                                      GT CTT
GAM780  WHSC1    3'  TTTTATGGCCTTTTCTT     29922       TGT
                                AAGAAA   GGTCGTGAAA
                                ||||||   ||||||||||
                                TTCTTT   CCGGTATTTT
                                   T__
GAM780  WHSC1    3'  TTTTATGGCCTTTTCTT     55840       TGT
                                AAGAAA   GGTCGTGAAA
                                ||||||   ||||||||||
                                TTCTTT   CCGGTATTTT
                                   T__
GAM780  WHSC1    3'  TTTTATGGCCTTTTCTT     55857       TGT
                                AAGAAA   GGTCGTGAAA
                                ||||||   ||||||||||
                                TTCTTT   CCGGTATTTT
                                   T__
GAM780  ZNF124   3'  TTTAATCACTACAGTTTTTGTC 12825         A     CG_   AA
             A                    TGACAAGAA TGTGGT   TGAA
                                |||||||| ||||||   ||||
                                ACTGTTTTT ACATCA   ATTT
                                     G     CTA
GAM780  ZNF216   3'  TTTTCATGTGCATCTTTTGTC  20023        A   GGT
                                GACAAGA ATGT   CGTGAAAA
                                ||||||| ||||   ||||||||
                                CTGTTTT TACG   GTACTTTT
                                   C    T__
GAM780  ZNF236   3'  TTTTCCTTCATGTTTCTGGTTA 23723      A        TCGT
                                TGAC AGAAATGTGG    GAAAA
                                |||| ||||||||||    |||||
                                ATTG TCTTTGTACT    CTTTT
                                  G         TC__
GAM780  ANKRD6   3'  TTTTCATGGTTATGCCTTGTT  30095       AAA    GT
                                GACAAG   TGTG  CGTGAAAA
                                ||||||   ||||  ||||||||
```

```
                                TTGTTC  GTAT  GTACTTTT
                                   C__   TG
GAM780  ARHGEF9  3' TTCATTGCTTTTCTTGTTA  30825        TGT  C
                                TGACAAGAAA  GGT GTGAA
                                ||||||||||  ||| |||||
                                ATTGTTCTTT  TCG TACTT
                                      ___  T
GAM780  BRD4     3' TTTTCTATATATATTTTTTGTT 54280          GTCGT
                                GACAAGAAATGTG   GAAAA
                                ||||||||||||    |||||
                                TTGTTTTTTATAT   CTTTT
                                       ATAT_
GAM780  BRDG1    3' ACCACATTTTTTGTTA     23991
                                TGACAAGAAATGTGGT
                                ||||||||||||||||
                                ATTGTTTTTTACACCA

GAM780  C1orf26  3' TTTTATGATCAAACTGTCA  34583      AGAAATG
                                TGACA     TGGTCGTGAAA
                                |||||     ||||||||||
                                ACTGT     ACTAGTATTTT
                                   CAA____
GAM780  C21orf91 3' TTTTTATGGTCATTAAATTTGC 33883   A   AAAT  GT
           CA                    TG CAAG   GTG  CGTGAAAA
                                || ||||   |||  ||||||||
                                AC GTTT   TAC  GTATTTTT
                                 C   AAAT  TG
GAM780  C4S-2    3' TTTTTATGACCTACGATTTTGC 37821   A   AA  _
           A                     TG CAAGA  TGT GGTCGTGAAAA
                                || |||||  ||| ||||||||||
                                AC GTTTT  GCA CCAGTATTTTT
                                 _    A_  T
GAM780  C9orf5   3' TTTTATTAGTTTCTTGTC    49286         GTGGTC
                                GACAAGAAAT    GTGAAA
                                ||||||||||    ||||||
                                CTGTTCTTTG    TATTTT
                                      AT____
GAM780  CDW92    3' TTTTTATGCTTATTTTTGTCA  54508        ATGT  T
                                TGACAAGAA   GG CGTGAAAA
                                |||||||||   || ||||||||
                                ACTGTTTTT   TC GTATTTTT
                                      AT__  _
GAM780  CYorf15B 3' TTTTACATATATTCTCTTGTCA 50822        _    GTC
                                TGACAAGA AATGTG  GTGAAA
                                |||||||| ||||||  ||||||
                                ACTGTTCT TTATAT  CATTTT
                                     C    A__
GAM780  DJ122O8.2 3' TTTTCAAAGTCTCCATGTGTTT 39995      A    TCG___
           TGTT                    CAAGA ATGTGG     TGAAAA
                                |||||  ||||||     ||||||
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                                GTTTT TGTACC     ACTTTT
                                   G     TCTGAA
GAM780  DKFZp434A171 3'  TTTTTATGACCATGTAATGTT  50013      AGAA
                                GACA   ATGTGGTCGTGAAAA
                                ||||   ||||||||||||||
                                TTGT   TGTACCAGTATTTTT
                                  AA__
GAM780  DKFZP434C171 3'  TTTCATGAAGCTTTTTGCA   31564    A     AT  GG
                                TG CAAGAA  GT  TCGTGAAA
                                || ||||||  ||  ||||||||
                                AC GTTTTT  CG  AGTACTTT
                                 _     __  A_
GAM780  DKFZp434K2435 3'  TTTTGCGTATGTGTTTTTTGTT 50037          TG  GT  TG   A
                                GACAAGAAA  TG  CG  AAA
                                |||||||||  ||  ||  |||
                                TTGTTTTTT  GT  GC  TTT
                                      GT  AT  GT
GAM780  DKFZP434L187 3'  TTTACATTTACATTTATTGTCA 68806       G       TC
                                TGACAA AAATGTGG  GTGAA
                                ||||||| ||||||||  |||||
                                ACTGTT TTTACATT  CATTT
                                   A       TA
GAM780  DKFZp547A023 3'  TTTTTATGGCTCACATCTTTTT 72618       _    _
                                AAGAA ATGTG GTCGTGAAAA
                                ||||| ||||| ||||||||||
                                TTTTT TACAC CGGTATTTTT
                                   C    T
GAM780  DKFZP727C091 3'  TTTTTGTTTCCATGTTTTCTTG 66213          _    TC TG
          TCA                    TGACAAGAAA TGTGG  G  AAAA
                                ||||||||||| |||||  |  ||||
                                ACTGTTCTTT GTACC  T  TTTT
                                      T    TT GT
GAM780  DKFZp761F2014 3'  TTTCATGATCAACTTGT     39544       AAATG
                                ACAAG    TGGTCGTGAAA
                                |||||    ||||||||||
                                TGTTC    ACTAGTACTTT
                                   A____
GAM780  FER1L4   3'  GGCTACATTTTTTTCA      47359     C
                                TGA AAGAAATGTGGTC
                                ||| ||||||||||||
                                ACT TTTTTTACATCGG
                                  _
GAM780  FKBP5    3'  TTTTTATGAAATATTTCTT    14655         GG
                                AAGAAATGT  TCGTGAAAA
                                |||||||||  |||||||||
                                TTCTTTATA  AGTATTTTT
                                      A_
GAM780  FLJ10055  3'  TGAATTGTATTTCTTGT     35777          TG  _
                                ACAAGAAATG  GT CG
                                ||||||||||  || ||
```

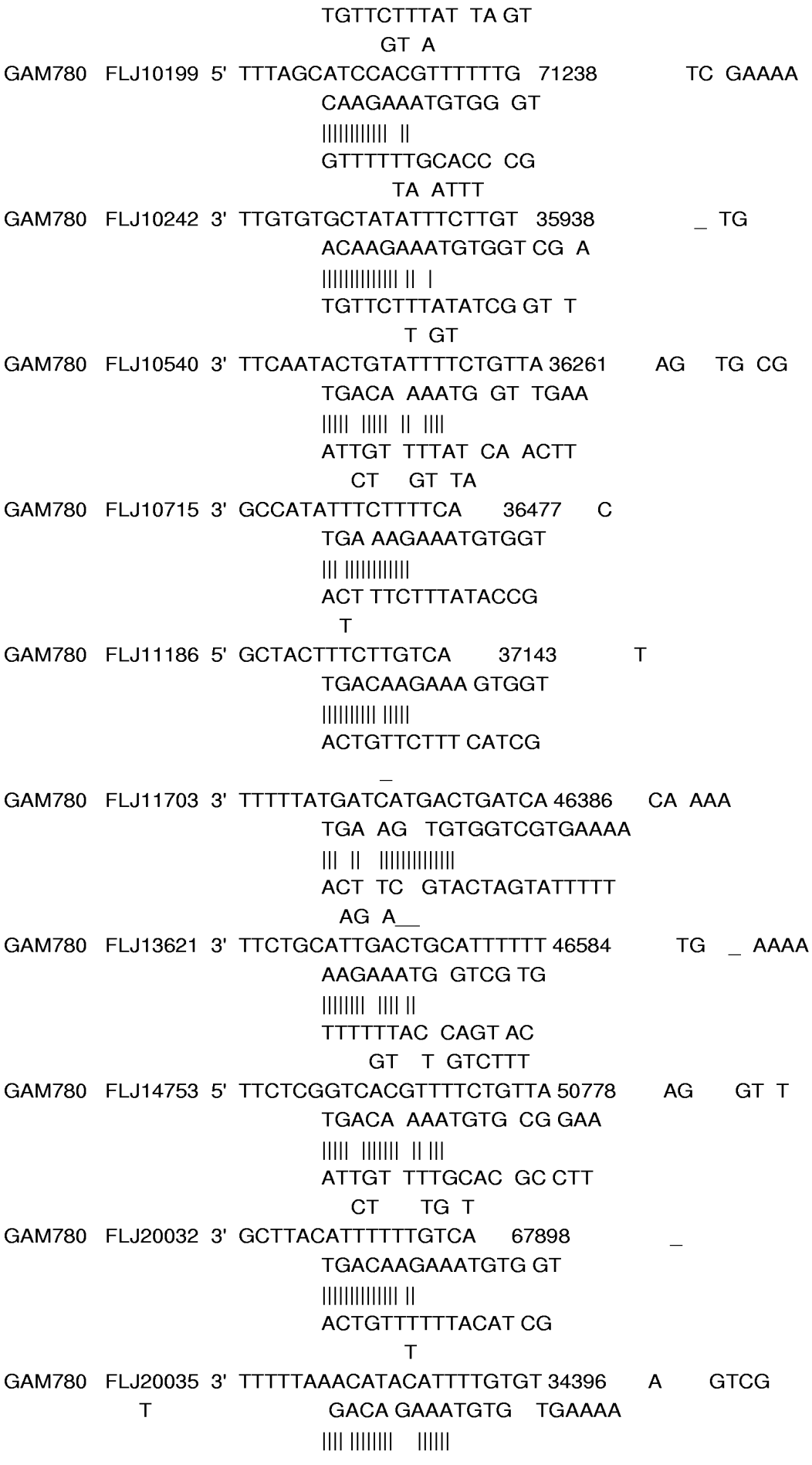
TGTTCTTTAT TA GT
GT A
GAM780 FLJ10199 5' TTTAGCATCCACGTTTTTTG 71238 TC GAAAA
CAAGAAATGTGG GT
GTTTTTTGCACC CG
TA ATTT
GAM780 FLJ10242 3' TTGTGTGCTATATTTCTTGT 35938 _ TG
ACAAGAAATGTGGT CG A
TGTTCTTTATATCG GT T
T GT
GAM780 FLJ10540 3' TTCAATACTGTATTTTCTGTTA 36261 AG TG CG
TGACA AAATG GT TGAA
ATTGT TTTAT CA ACTT
CT GT TA
GAM780 FLJ10715 3' GCCATATTTCTTTTCA 36477 C
TGA AAGAAATGTGGT
ACT TTCTTTATACCG
T
GAM780 FLJ11186 5' GCTACTTTCTTGTCA 37143 T
TGACAAGAAA GTGGT
ACTGTTCTTT CATCG
_
GAM780 FLJ11703 3' TTTTTATGATCATGACTGATCA 46386 CA AAA
TGA AG TGTGGTCGTGAAAA
ACT TC GTACTAGTATTTTT
AG A__
GAM780 FLJ13621 3' TTCTGCATTGACTGCATTTTTT 46584 TG _ AAAA
AAGAAATG GTCG TG
TTTTTTAC CAGT AC
GT T GTCTTT
GAM780 FLJ14753 5' TTCTCGGTCACGTTTTCTGTTA 50778 AG GT T
TGACA AAATGTG CG GAA
ATTGT TTTGCAC GC CTT
CT TG T
GAM780 FLJ20032 3' GCTTACATTTTTTGTCA 67898 _
TGACAAGAAATGTG GT
ACTGTTTTTTACAT CG
T
GAM780 FLJ20035 3' TTTTTAAACATACATTTTGTGT 34396 A GTCG
T GACA GAAATGTG TGAAAA

```
                                TTGT TTTTACAT    ATTTTT
                                  G       ACAA
GAM780  FLJ20152  3'  TTTTTGTGATTGCTTATGTCA  38649      AGAAAT TG    TG
                                TGACA     G  GTCG  AAAA
                                |||||     |  ||||  ||||
                                ACTGT     C  TAGT  TTTT
                                   ATT___ GT    GT
GAM780  FLJ20273  3'  ACCATGTTTCTTGCA      38725    A
                                TG CAAGAAATGTGGT
                                || ||||||||||||
                                AC GTTCTTTGTACCA
                                 _
GAM780  FLJ20456  3'  TGTCCATGTTTATTGTTA    35217       G       T
                                TGACAA AAATGTGG CG
                                |||||| |||||||| ||
                                ATTGTT TTTGTACC GT
                                   A       T
GAM780  FLJ21615  3'  TTTTTGCGGCCTTATATTTTG  49841      A   T    TG
                                CAAGA ATG GGTCG  AAAA
                                ||||| ||| |||||  ||||
                                GTTTT TAT CCGGC  TTTT
                                   A   T    GT
GAM780  FLJ21941  3'  TTTTACCTCATATTTTCTGTCA 46747      AG       TC
                                TGACA  AAATGTGG  GTGAAA
                                |||||  ||||||||  ||||||
                                ACTGT  TTTATACT  CATTTT
                                   CT       C_
GAM780  FLJ23556  3'  TTTTCATGATCACCAAAGTGTT 45964      AGAAAT
                                GACA     GTGGTCGTGAAAA
                                ||||     ||||||||||||||
                                TTGT     CACTAGTACTTTT
                                  GAAAC_
GAM780  FLJ23563  3'  TTACATTTTCTTGTCA      67605          _
                                TGACAAGAAA TGTGG
                                |||||||||| |||||
                                ACTGTTCTTT ACATT
                                      T
GAM780  FLJ25442  3'  TTTTCCAGTTGATGTTTTTTGT 58842           GGTCGT
          CA                    TGACAAGAAATGT     GAAAA
                                ||||||||||||      |||||
                                ACTGTTTTTTGTA     CTTTT
                                      GTTGAC
GAM780  FLJ30046  3'  TTTTTGTGCCTATTTCTTTTTA 58104     C       T  T  TG
                                TGA AAGAAATG GG CG  AAAA
                                ||| |||||||| || ||  ||||
                                ATT TTCTTTAT CC GT  TTTT
                                  T       _ _  GT
GAM780  FLJ31153  3'  TTTTTACGAAGTATTTTTTGTT 58134          TGG
                                GACAAGAAATG   TCGTGAAAA
                                ||||||||||   |||||||||
```

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                                TTGTTTTTTTAT  AGCATTTTT
                                      GA_
GAM780  FPGT    3'  TTTTCATCTTATTTTTTGTC  13850         TGGTC
                                GACAAGAAATG   GTGAAAA
                                ||||||||||   |||||||
                                CTGTTTTTTAT   TACTTTT
                                      TC___
GAM780  GTF2F2  3'  TAAACAGGTGATCACGTTTCTT 14680    C          GAAAA
          TTCA                    TGA AAGAAATGTGGTCGT
                                ||| ||||||||||||||
                                ACT TTCTTTGCACTAGTG
                                  T           GACAAATT
GAM780  GTF3C2  3'  TTTTGTGACCACTTGT     7725      GAAAT     TG
                                ACAA    GTGGTCG  AAA
                                ||||    |||||||  |||
                                TGTT    CACCAGT  TTT
                                  _____      GT
GAM780  HARC    3'  TTTTTGTGGCTACTAAATTTG  35486     AAAT     TG
                                CAAG   GTGGTCG  AAAA
                                ||||   |||||||  ||||
                                GTTT   CATCGGT  TTTT
                                  AAAT     GT
GAM780  HERC1   3'  TTTTCCCTCCATATTTTTGGTC 14068     A       TCGT
          A                     TGAC AGAAATGTGG   GAAAA
                                ||||  ||||||||||   |||||
                                ACTG TTTTTATACC   CTTTT
                                  G        TCC_
GAM780  HGRG8   3'  TTTTTATGAAGAATTTTTGTC  32744       ATGTGG
                                GACAAGAA    TCGTGAAAA
                                ||||||||    |||||||||
                                CTGTTTTT    AGTATTTTT
                                     AAGA__
GAM780  HSPC152  3'  TCTTGTTATGACTGTGTATTTT 33085       _  TG     AAA
          TGTT                    GACAAGAA ATG  GTCGTGA
                                ||||||||  |||  |||||||
                                TTGTTTTT TGT  CAGTATT
                                     A  GT     GTTCTT
GAM780  HSPC152  3'  TCTTGTTATGACTGTGTATTTT 94519       _  TG     AAA
          TGTT                    GACAAGAA ATG  GTCGTGA
                                ||||||||  |||  |||||||
                                TTGTTTTT TGT  CAGTATT
                                     A  GT     GTTCTT
GAM780  HSPC195  3'  TTTTTATATATATATTTTTTGT 80968          GTC
          T                     GACAAGAAATGTG  GTGAAAA
                                ||||||||||||  |||||||
                                TTGTTTTTTATAT  TATTTTT
                                       ATA
GAM780  IMPACT  3'  TTATAACTATATTTTATGTT  37395     A       CG
                                GACA GAAATGTGGT  TGA
                                ||||  ||||||||||  |||
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                                TTGT TTTTATATCA  ATT
                                  A        AT
GAM780  JWA      3'  TTTACCTTGCACATTTTTTGTT 21142           GTC_    AA
                                GACAAGAAATGTG   GTGAA
                                ||||||||||||   |||||
                                TTGTTTTTTACAC   CATTT
                                     GTTC
GAM780  KIAA0095 3'  TTTCTGTATTATGTATTTTTGT 90921        _     _ T   A
           CA                    TGACAAGAA ATGTGGT CG GAAA
                                ||||||||| ||||||| || ||||
                                ACTGTTTTT TGTATTA GT CTTT
                                     A      T _
GAM780  KIAA0164 3'  TTTCATGACCCTTTTATTG   28454     G   TGT
                                CAA AAA   GGTCGTGAAA
                                ||| |||   ||||||||||
                                GTT TTT   CCAGTACTTT
                                  A   TC_
GAM780  KIAA0212 3'  TTTATGTTGCATTTTTAGTCA  27946      A      TG T
                                TGAC AGAAATG  G CGTGAA
                                |||| |||||||  | ||||||
                                ACTG TTTTTAC  T GTATTT
                                  A      GT _
GAM780  KIAA0240 3'  TTTATTTTTATTTCTTGTCA   92444          TGGTC
                                TGACAAGAAATG    GTGAA
                                ||||||||||||    |||||
                                ACTGTTCTTTAT    TATTT
                                     TTT__
GAM780  KIAA0293 3'  TTATGCCGTTTACGTTTTTTGT 60609          _____ T    AAA
           T                     ACAAGAAATGT    GG CGTGA
                                ||||||||||||    || |||||
                                TGTTTTTTGCA    CC GTATT
                                     TTTG  _
GAM780  KIAA0447 3'  TGGCTATTTTTTTGTT      71679         T
                                GACAAGAAA GTGGTCG
                                ||||||||| |||||||
                                TTGTTTTTT TATCGGT
                                     _
GAM780  KIAA0453 3'  TGGCTTGTGGTTTTTGTCA    69057         ATGT_
                                TGACAAGAA     GGTCG
                                |||||||||     |||||
                                ACTGTTTTT     TCGGT
                                   GGTGT
GAM780  KIAA0680 3'  TTTCAAAATTGCATTTCTTGT  28235         TG  CG
                                ACAAGAAATG  GT  TGAAA
                                ||||||||||  ||  |||||
                                TGTTCTTTAC  TA  ACTTT
                                     GT  AA
GAM780  KIAA0831 3'  TTTTCAGCTCACGTGTCTTGTC 29986         A    _  CG
           A                     TGACAAGA ATGTG GT  TGAAAA
                                ||||||||| ||||| ||  ||||||
```

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                                ACTGTTCT TGCAC CG  ACTTTT
                                     G    T __
GAM780  KIAA0892 3' TTTTCATGACCACCCTGTTA  71017      A AAAT
                                TGACA G   GTGGTCGTGAAAA
                                ||||| |   ||||||||||||
                                ATTGT C   CACCAGTACTTTT
                                  _ C___
GAM780  KIAA0976 3' TTTGTGAATTGCATTTTTGTGT 29899     _     TG _ TG  AA
           T                     GACA AGAAATG  GT CG  AA
                                |||| |||||||  || ||  ||
                                TTGT TTTTTAC  TA GT  TT
                                  G      GT  A  GT
GAM780  KIAA1025 3' TTTTTGTGACTTTATTTTTTTA 63980   C      T    TG
                                A AAGAAATG GGTCG  AAAA
                                | ||||||||| |||||  ||||
                                A TTTTTTAT TCAGT  TTTT
                                 T       T    GT
GAM780  KIAA1058 3' TTTTTGTGACTAGTTTTTG   82258      ATG    TG
                                CAAGAA   TGGTCG  AAAA
                                ||||||   ||||||  ||||
                                GTTTTT   ATCAGT  TTTT
                                   G__     GT
GAM780  KIAA1185 3' TTTTCACCCCAGTTTTTTTGTT 62613        TG   TC
                                GACAAGAAA  TGG  GTGAAAA
                                |||||||||  |||  |||||||
                                TTGTTTTTT  ACC  CACTTTT
                                     TG   C_
GAM780  KIAA1254 3' TTTTTATGATTTGATGAGTTTC 70029       GT____
           TTGT                  AAGAAAT     GGTCGTGAAAA
                                |||||||     ||||||||||||
                                TTCTTTG     TTAGTATTTTT
                                   AGTAGT
GAM780  KIAA1320 3' ACCACGTTTCTTTTCA     69290     C
                                TGA AAGAAATGTGGT
                                ||| ||||||||||||
                                ACT TTCTTTGCACCA
                                  T
GAM780  KIAA1348 3' TTTTTGTGATTATGCTTGT   68578      AAA      TG
                                ACAAG   TGTGGTCG  AAAA
                                |||||   ||||||||  ||||
                                TGTTC   GTATTAGT  TTTT
                                  ___       GT
GAM780  KIAA1349 3' TTTTTATGATTTTATTTTTT   70762       TG
                                AAGAAATG  GTCGTGAAAA
                                ||||||||  ||||||||||
                                TTTTTTAT  TAGTATTTTT
                                     TT
GAM780  KIAA1456 5' ATTATATTTCTTGTTA     66990
                                TGACAAGAAATGTGGT
                                ||||||||||||||||
```

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                                ATTGTTCTTTATATTA

GAM780  KIAA1462 3' TAACAAAGTGACTATATTTCTT 91388     C          GTGAAAA
            TTTA                  TGA AAGAAATGTGGTC
                                  ||| ||||||||||||
                                  ATT TTCTTTATATCAG
                                    T          TGAAACAATT
GAM780  KIAA1786 3' TTGGTGTATTACATTTTTTGTT 66044              CGTGAAAA
            A                     TGACAAGAAATGTGGT
                                  ||||||||||||||||
                                  ATTGTTTTTTACATTA
                                            TGTGGTT
GAM780  KRTAP9-2 3' TTTTCATGATAAATTTGTGTT  49233     AG   GTG
                                  GACA  AAAT   GTCGTGAAAA
                                  ||||  ||||   ||||||||||
                                  TTGT  TTTA   TAGTACTTTT
                                    G_    AA_
GAM780  LNX      3' TTTCAAATACCATGTTATTTGT 50923        A      CG_    A
            TA                    TGACAAG AATGTGGT   TGAAA
                                  ||||||| ||||||||   |||||
                                  ATTGTTT TTGTACCA   ACTTT
                                      A       TAA
GAM780  MADP-1   3' TTTTGTCATCATATTTCTTGT  52411           C TG   A
                                  ACAAGAAATGTGGT G  AAA
                                  |||||||||||||| |  |||
                                  TGTTCTTTATACTA T  TTT
                                          C GT
GAM780  MGC12466 3' TTTTTATGGGAAAACTACTTTT 52633      T    _____
            TTGTT                   AGAAA GTGGT    CGTGAAAA
                                  ||||| |||||    ||||||||
                                  TTTTT CATCA    GTATTTTT
                                    _    AAAGG
GAM780  MGC12466 3' TTTTTATGGGAAAACTACTTTT 79039      T    _____
            TTGTT                   AGAAA GTGGT    CGTGAAAA
                                  ||||| |||||    ||||||||
                                  TTTTT CATCA    GTATTTTT
                                    _    AAAGG
GAM780  MGC14844 3' TTTTCCTGCTGCATTTCTTGT  50342         TG T  T
                                  ACAAGAAATG  G CG GAAAA
                                  ||||||||||  | || |||||
                                  TGTTCTTTAC  C GT CTTTT
                                        GT _  C
GAM780  MGC3329  3' TTTTTGTGGCTTCACTTGT   44021      AAA  T    TG
                                  ACAAG   TG GGTCG  AAAA
                                  |||||   || |||||  ||||
                                  TGTTC   AC TCGGT  TTTT
                                    ___  T    GT
GAM780  MGC5395  3' TTTTGTGACCGTTCTTTG    43935   C    ATG     TG
                                  A AAGAA   TGGTCG  AAA
                                  | |||||   ||||||  |||
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                                G TTCTT   GCCAGT  TTT
                                 T    ___     GT
GAM780  MKI67IP   3'  TTTTCAATGTATTATATTTCTT 50498          _  _
                                AAGAAATGTGGT CGT GAAAA
                                |||||||||||| ||| |||||
                                TTCTTTATATTA GTA CTTTT
                                      T   A
GAM780  MO25     3'  TTTTGCACCACTTTTTTGTTA  32818          T    C TG
                                TGACAAGAAA GTGGT G  AAA
                                |||||||||| ||||| |  |||
                                ATTGTTTTTT CACCA C  TTT
                                      _    _ GT
GAM780  OSBPL3    3'  CTATACTTTCTTGTTA      31436          _
                                TGACAAGAAA TGTGG
                                |||||||||| |||||
                                ATTGTTCTTT ATATC
                                      C
GAM780  PAPSS2    3'  TTTTTATGATTAGATGCTTTGT 59598       AA  G
                                ACAAG  AT TGGTCGTGAAAA
                                |||||  || ||||||||||||
                                TGTTT  TA ATTAGTATTTTT
                                   CG  G
GAM780  PCDH19    3'  TTTTTATGACTAATAGTTTTTT 63714         G__
           G                     CAAGAAAT   TGGTCGTGAAAA
                                ||||||||   ||||||||||||
                                GTTTTTTG   ATCAGTATTTTT
                                     ATA
GAM780  PEF      3'  TTTTTAATTTGCATTTTTTTTC 24755     C       TG TCG
           A                     TGA AAGAAATG  G   TGAAAA
                                ||| ||||||||  |   ||||||
                                ACT TTTTTTAC  T   ATTTTT
                                  T       GT TA_
GAM780  PIG7     3'  TTTTATGACCTCCTTTTG    16796       AATGT
                                CAAGA    GGTCGTGAAA
                                |||||    ||||||||||
                                GTTTT    CCAGTATTTT
                                   CCT__
GAM780  PLEKHA3   3'  TTTTTATGTATTTATTTTCTTG 38865         TGT   _
           TT                    GACAAGAAA   GGT CGTGAAAA
                                |||||||||   ||| ||||||||
                                TTGTTCTTT   TTA GTATTTTT
                                     TAT   T
GAM780  PRDM15    3'  TGGCTGTATTTCCTGTCA    61714       A     TG
                                TGACA GAAATG  GTCG
                                ||||| ||||||  ||||
                                ACTGT CTTTAT  CGGT
                                   C     GT
GAM780  PRRG1     3'  TTTTCTTTAGTTTTGTTTCTTG 6289           TGGTCGT_
           TTA                    TGACAAGAAATG       GAAAA
                                ||||||||||||       |||||
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                                ATTGTTCTTTGT       CTTTT
                                      TTTGATTT
GAM780  RGS18    3'  TGATTATATTCTTGTTA     55394          A
                                TGACAAGAA TGTGGTCG
                                ||||||||| ||||||||
                                ATTGTTCTT ATATTAGT
                                          _
GAM780  RNPC2    3'  TTTCAAAATTATATTTCTTG   16923            CG     A
                                CAAGAAATGTGGT  TGAAA
                                |||||||||||||  |||||
                                GTTCTTTATATTA  ACTTT
                                      AA
GAM780  SEC15B   3'  TTTTCATTGACCTTTGCATTTT 66692          ____    _
            TTTCA                    AAGAAATGT   GGTCG TGAAAA
                                |||||||||   ||||| ||||||
                                TTTTTTACG   CCAGT ACTTTT
                                      TTT    T
GAM780  SOX6     3'  TTTTCATGAACTTGAGTTTTTT 52829          GT_  _
            GTT                     GACAAGAAAT   GGT CGTGAAAA
                                |||||||||||   ||| ||||||||
                                TTGTTTTTTG   TCA GTACTTTT
                                      AGT   A
GAM780  Spir-1   3'  ACTATCATTTTTTGTT      64694          _
                                GACAAGAAATG TGGT
                                |||||||||||| ||||
                                TTGTTTTTTAC ATCA
                                      T
GAM780  TIX1     3'  CGGCTACGTTTCATGTCA    61741       A
                                TGACA GAAATGTGGTCG
                                ||||| ||||||||||||
                                ACTGT CTTTGCATCGGC
                                   A
GAM780  TOB2     3'  TTTTTATTTTTTACATTTTTTG 95628           TC_
                                CAAGAAATGTGG   GTGAAAA
                                ||||||||||||   |||||||
                                GTTTTTTACATT   TATTTTT
                                      TTT
GAM780  TOPK     3'  TTTGAGGACCATAGTTTCTTGT 37507          _      GTGAAAA
            TA                      TGACAAGAAA TGTGGTC
                                |||||||||| |||||||
                                ATTGTTCTTT ATACCAG
                                      G       GAGTTT
GAM780  ZNF238   3'  TTTTCAATATATTTTTTGTC   20977           GTCG
                                GACAAGAAATGTG    TGAAAA
                                ||||||||||||||    ||||||
                                CTGTTTTTTATAT    ACTTTT
                                      A___
GAM780  ZNF31    3'  TTTGTAGACCACATTTCCTGTT 64993       A         GTGAAAA
            A                       TGACA GAAATGTGGTC
                                ||||| ||||||||||
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                                ATTGT CTTTACACCAG
                                  C         ATGTTT
GAM780  LOC114932 3'  TTTTTGTGGTCACGTTTATTCT 72717       ___    GT  TG
          TGTTA                    CAAGAA   ATGTG  CG  AAAA
                                |||||||   |||||  ||  ||||
                                GTTCTT   TGCAC  GT  TTTT
                                   ATT     TG  GT
GAM780  LOC115294 3'  ATTTTCATGATCATTGCATATT 73012        _____
          TCTTGTCA                  GAAATGTG    GTCGTGAAAA   T
                                |||||||||    ||||||||||  |
                                CTTTATAC    TAGTACTTTT   A
                                     GTTAC
GAM780  LOC122525 3'  TTTATATGAGCATATTTTATGT 76009      A       G     AAAA
          T                         GACA GAAATGTG TCGTG
                                |||| |||||||| |||||
                                TTGT TTTTATAC AGTAT
                                  A       G     ATTTT
GAM780  LOC144203 3'  TTGCAGTGGGCTATGGTTTCTT 76709          _     GTGAAAA
          GTCA                      GACAAGAAAT GTGGTC
                                ||||||||||| ||||||
                                CTGTTCTTTG TATCGG
                                      G     GTGACGTTT
GAM780  LOC145645 3'  TTTTAATAATTCATATTTCATG 77327      A       TCG__    A
          TT                        GACA GAAATGTGG     TGAAA
                                |||| |||||||||     |||||
                                TTGT CTTTATACT     ATTTT
                                  A        TAATA
GAM780  LOC146381 5'  TTTTGCGGCCACCATTGT     77868      GAAAT      TG
                                ACAA     GTGGTCG  AAA
                                ||||     |||||||  |||
                                TGTT     CACCGGC  TTT
                                  AC___       GT
GAM780  LOC146839 5'  TTGTTATTATTATATTTTTGTC 83819         A     C    AAA
          A                         TGACAAGAA TGTGGT GTGA
                                ||||||||| |||||| ||||
                                ACTGTTTTT ATATTA TATT
                                      _     T   GTTT
GAM780  LOC147671 3'  TTTTTATTTTTTACATTTTTTG 78464           TC_
                                CAAGAAATGTGG   GTGAAAA
                                ||||||||||||   |||||||
                                GTTTTTTACATT   TATTTTT
                                       TTT
GAM780  LOC149628 3'  TTTTCACACACCATATTTCTTT 79466     C          C_
          CA                        TGA AAGAAATGTGGT  GTGAAAA
                                |||  ||||||||||||  |||||||
                                ACT TTCTTTATACCA  CACTTTT
                                  _          CA
GAM780  LOC150280 3'  TTTTTGCTCAATTTTTTTTGTC 79714          TG_   TC TG
          A                         TGACAAGAAA   TGG  G  AAAA
                                ||||||||||   |||  |  ||||
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                                ACTGTTTTTT  ACT  C  TTTT
                                      TTA  __ GT
GAM780  LOC150482 3'  TTTTTATGACCACGTAATGTT  63076     AGAA
                                GACA   ATGTGGTCGTGAAAA
                                ||||   ||||||||||||||
                                TTGT   TGCACCAGTATTTTT
                                  AA__
GAM780  LOC150886 3'  TTTTCATGATTGCATTTT    85155       TG
                                GAAATG  GTCGTGAAAA
                                ||||||  ||||||||||
                                TTTTAC  TAGTACTTTT
                                   GT
GAM780  LOC151188 3'  ATTTTCATGTATGTACTACATT 80157          _____
           TTTTG                  GAAATGTGGT    CGTGAAAA  T
                                ||||||||||    ||||||||  |
                                TTTTACATCA    GTACTTTT  A
                                      TGTAT
GAM780  LOC151201 3'  TTTTCATGATTGCTTTTTGTT  85301        AT TG
                                GACAAGAA  G  GTCGTGAAAA
                                ||||||||  |  ||||||||||
                                TTGTTTTT  C  TAGTACTTTT
                                     __ GT
GAM780  LOC151470 3'  TTTTGTTATTACCTTTTTTGTT 80262         T    C TG   A
                                GACAAGAAA GTGGT G  AAA
                                |||||||||| ||||| |  |||
                                TTGTTTTTT CATTA T  TTT
                                      C    T GT
GAM780  LOC152215 3'  TGTCACATTTTTTTGTTA    80492          _    T
                                TGACAAGAAA TGTGG CG
                                |||||||||| ||||| ||
                                ATTGTTTTTT ACACT GT
                                      T    _
GAM780  LOC152313 3'  GCCAATGGTCACAATTTTTGTT 85664         A   GT   GAAAA
                                GACAAGAA TGTG  CGT
                                |||||||| ||||  |||
                                TTGTTTTT ACAC  GTA
                                     A   TG   ACCGT
GAM780  LOC153279 3'  GATTTTATTTTTTGTTA     80807          TG
                                TGACAAGAAATG  GTC
                                ||||||||||||  |||
                                ATTGTTTTTTAT  TAG
                                       TT
GAM780  LOC153346 5'  GGCTGTATTTTTGGTCA     86024      A      TG
                                TGAC AGAAATG  GTC
                                |||| |||||||  |||
                                ACTG TTTTTAT  CGG
                                  G      GT
GAM780  LOC154743 3'  TTTAGTCCACATTGTCTTGTCA 81118         _      TCG
                                TGACAAGA AATGTGG   TGAA
                                |||||||| |||||||   ||||
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                                ACTGTTCT TTACACC   ATTT
                                    G      TG_
GAM780   LOC154743 3'  TTTCATAACTTTCTTGTT    81119        ATGT   CG
                                GACAAGAA    GGT  TGAAA
                                ||||||||    |||  |||||
                                TTGTTCTT    TCA  ACTTT
                                    _____   AT
GAM780   LOC155061 3'  TTTTCAGGGCGTGCATTTCTGT 81273       A      _  G
           CA                     TGACA GAAATGTG GTC TGAAAA
                                |||||  |||||||| ||| ||||||
                                ACTGT CTTTACGT CGG ACTTTT
                                  _      G  G
GAM780   LOC157708 3'  GGAAGATGCCACATTTTTTGTT 81560             T   GAAAA
           A                     TGACAAGAAATGTGG CGT
                                |||||||||||||| |||
                                ATTGTTTTTTACACC GTA
                                      _  GAAGGG
GAM780   LOC196812 3'  TTTTATGTTTTGTTTTTTGTCA 89580           TG T
                                TGACAAGAAATG  G CGTGAAA
                                ||||||||||||  | |||||||
                                ACTGTTTTTTGT  T GTATTTT
                                       TT _
GAM780   LOC197439 5'  TTTTGCGGCCACCATTGT    88076     GAAAT      TG
                                ACAA    GTGGTCG  AAA
                                ||||    |||||||  |||
                                TGTT    CACCGGC  TTT
                                  AC___      GT
GAM780   LOC200728 3'  ACATATGACCATGTTTCTTG   90113              AAAA
                                CAAGAAATGTGGTCGTG
                                |||||||||||||||||
                                GTTCTTTGTACCAGTAT
                                       ACAT
GAM780   LOC200853 3'  TAGTACACCGTGTTTCTGTT   88917     A   TG   C   AAAA
                                GACA GAAA  TGGT GTG
                                |||| ||||  |||| |||
                                TTGT CTTT  GCCA CAT
                                  _   GT   _  GATT
GAM780   LOC201484 3'  TTTTCATGGTCACAGATTGT   89787     GAAA   GT
                                ACAA    TGTG  CGTGAAAA
                                ||||    ||||  ||||||||
                                TGTT    ACAC  GTACTTTT
                                  AG__    TG
GAM780   LOC202025 3'  TTCAGATTGCATCTTTTGTC   90300       A  TG  G
                                GACAAGA ATG  GTC TGAA
                                |||||||  |||  ||| ||||
                                CTGTTTT TAC  TAG ACTT
                                    C  GT  _
GAM780   LOC202451 3'  TGTCCTACATTTCTTTCA    90356     C       _ T
                                TGA AAGAAATGT GG CG
                                |||  ||||||||| || ||
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```
                                ACT TTCTTTACA CC GT
                                  _       T  T
GAM780   LOC202986 3'  TTTTGCTCACATGTTTTTTGTT 90446           GTC TG   A
                                GACAAGAAATGTG   G  AAA
                                ||||||||||||   |  |||
                                TTGTTTTTTGTAC   C  TTT
                                       ACT GT
GAM780   LOC219914 3'  GCGGCCGTGTTTTCTGTT    93327     AG   TG
                                GACA  AAA  TGGTCGT
                                ||||  |||  |||||||
                                TTGT  TTT  GCCGGCG
                                  CT   GT
GAM780   LOC220930 5'  TTTATGCTTATAATTTTTGTCA 93134         A     T
                                TGACAAGAA TGTGG CGTGAA
                                ||||||||| ||||| ||||||
                                ACTGTTTTT ATATT GTATTT
                                      A    C
GAM780   LOC221354 3'  TTTTGCTCACATGTTTTTTG   92415          GTC TG   A
                                CAAGAAATGTG   G  AAA
                                ||||||||||   |  |||
                                GTTTTTTGTAC   C  TTT
                                       ACT GT
GAM780   LOC221763 3'  TTTTTAAACCATTTTTTCTTG  93799        T_    CG
                                CAAGAAA  GTGGT  TGAAAA
                                |||||||  |||||  ||||||
                                GTTCTTT  TACCA  ATTTTT
                                     TT    A_
GAM780   LOC253233 5'  TGGACAGACTGCATTGCTTGTT 95635       A    TG   _  GAAAA
                                GACAAG AATG  GTC GT
                                ||||||| ||||  ||| ||
                                TTGTTC TTAC  CAG CA
                                   G    GT   A  GGT
GAM780   LOC254778 3'  TTTCATGGCCATTTG       96132     GAAAT
                                CAA    GTGGTCGTGAAA
                                |||    ||||||||||||
                                GTT    TACCGGTACTTT
                                  _____
GAM780   LOC255308 3'  TTTGGCCCCATATTTTATGTT  94539      A        TC  G
                                GACA GAAATGTGG  GT AAA
                                |||| |||||||||  || |||
                                TTGT TTTTATACC  CG TTT
                                  A        C_  G
GAM780   LOC255324 3'  TTTCACTCTGGGTTTTTTGTT  95876          G   TC
                                GACAAGAAAT TGG  GTGAAA
                                |||||||||| |||  ||||||
                                TTGTTTTTTG GTC  CACTTT
                                      G   T_
GAM780   LOC256730 3'  CATTGCGACTGTGTTTCTGTTA 95229       A     TG    TG AAA
                                TGACA GAAATG  GTCG  A
                                ||||| ||||||  ||||  |
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                                ATTGT CTTTGT  CAGC  T
                                  _     GT    GT ACA
GAM780  LOC257277 5'  TTTCATGATCACTATTT     95263      _
                                AAAT GTGGTCGTGAAA
                                |||| ||||||||||||
                                TTTA CACTAGTACTTT
                                  T
GAM780  LOC257465 3'  TTTTTACCAGTTTTATTTTCTT 81604         T    TC___
          GTCA                    ACAAGAAA GTGG     GTGAAAA
                                |||||||| ||||     |||||||
                                TGTTCTTT TATT     CATTTTT
                                     _    TTGAC
GAM780  LOC51313  3'  TTTTCACGGTTACGTCTGTTA  33515       A  AA    GT
                                TGACA GA  TGTG  CGTGAAAA
                                ||||| ||  ||||  ||||||||
                                ATTGT CT  GCAT  GCACTTTT
                                  _ __    TG
GAM780  LOC90509  3'  TTTTCATGGTAACATTTTTCA  63108    A       GG
                                C AGAAATGT  TCGTGAAAA
                                | ||||||||  |||||||||
                                A TTTTTACA  GGTACTTTT
                                 C       AT
GAM780  LOC90670  3'  TAGGATTTATTTTTTGTCA    63742           T    G
                                TGACAAGAAATG GGTC TG
                                |||||||||||| |||| ||
                                ACTGTTTTTTAT TTAG AT
                                     _    G
GAM780  LOC92405  3'  TTCCTAGGCCAGTTTCTTGTT  69195          G     GT_
                                GACAAGAAAT TGGTC   GAA
                                |||||||||| |||||   |||
                                TTGTTCTTTG ACCGG   CTT
                                     _     ATC
GAM781  CNGA1     3'  CAACTGATAATGTGCAAA     59507          GC   A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                     A_   _
GAM781  ESRRG     3'  TGGCAGTCTTATGTGCAAA    66396         TAGCT
                                TTTGCACAT     AGATTGCCA
                                |||||||||     |||||||||
                                AAACGTGTA     TCTGACGGT
                                     T_____
GAM781  KCNJ3     3'  GCAATAATGTGCAAA       9525           GCTAGA
                                TTTGCACATTA      TTGC
                                ||||||||||      ||||
                                AAACGTGTAAT      AACG
                                                 _______
GAM781  SDC2      3'  GCAAATTAATGTGTAAA      67132           CTAGA
                                TTTGCACATTAG     TTGC
                                ||||||||||||     ||||
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                                AAATGTGTAATT    AACG
                                      A____
GAM781  USP9X    3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
              A                  TTTGCACATTAGC     GCCAT
                                 ||||||||||||     |||||
                                 AAATGTGTAATCG     CGGTA
                                       TAGTC_
GAM781  AMOTL1   3'  GGCAAGTAATGTGCAAA    73650         G  AGAT
                                 TTTGCACATTA CT    TGCC
                                 |||||||||| ||    ||||
                                 AAACGTGTAAT GA    ACGG
                                      _ ____
GAM781  BCAR3    3'  AGTAATAATGTGCAAA     13098         __
                                 TTTGCACATTA  GCT
                                 ||||||||||  |||
                                 AAACGTGTAAT  TGA
                                       AA
GAM781  DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930        AGCTA    C
                                 TTTGCACATT    GATTG CA
                                 |||||||||    ||||| ||
                                 AGACGTGTAA    TTAAC GT
                                      A____    A
GAM781  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                 TTTGCACATTAG  AGA TG CAT
                                 ||||||||||||  ||| || |||
                                 AGACGTGTAATC  TTT AC GTA
                                       __  T  A
GAM781  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
              AA                   TTTGCACATTAGCTAGATTGCCAT
                                   ||||||||||||||||||||||||
                                   AAACGTGTAATCGATCTAACGGTA

GAM782  ABCF1    3'  GCCCAAGATTTGGTGCCTGCAG 6567         AA  C
                                 CTGCAGGTA  GG ATCTTGGGC
                                 |||||||||  || |||||||||
                                 GACGTCCGT  TT TAGAACCCG
                                      GG  _
GAM782  AIM1     3'  TGCCTTCCCTGCAGT      91832        TA
                                 ACTGCAGG  AAGGCA
                                 ||||||||  ||||||
                                 TGACGTCC  TTCCGT
                                     C_
GAM782  ARCN1    3'  CCTCCTCTACCTTTACCTAAGT 7978     GC       CATCTT
                                 ACT  AGGTAAAGG     GGG
                                 |||  |||||||||     |||
                                 TGA  TCCATTTCC     TCC
                                   A_       ATCTCC
GAM782  BCL10    5'  GCCCAGGGCTCTACCTGTAG   14058        AA   AT
                                 CTGCAGGTA  GGC  CTTGGGC
                                 |||||||||  |||  |||||||
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                                GATGTCCAT  TCG  GGACCCG
                                    C_  __
GAM782  CD5     5'  GCCAGACACCCTCACCTGCGGT 26390        AAA  CA   TG
                                ACTGCAGGT   GG  TCT  GGC
                                |||||||||   ||  |||  |||
                                TGGCGTCCA   CC  AGA  CCG
                                    CTC  AC   __
GAM782  CHC1    3'  TCCATTCGGCTTCACCTGCAG  7024        AA   ATCT
                                CTGCAGGT  AGGC   TGGG
                                ||||||||  ||||   ||||
                                GACGTCCA  TTCG   ACCT
                                    C_   GCTT
GAM782  CLTCL1  3'  CCACCCTACCTGCAG      63670        AA  CATCT
                                CTGCAGGTA  GG    TGG
                                |||||||||  ||    |||
                                GACGTCCAT  CC    ACC
                                    C_  ______
GAM782  CRY2    3'  CCCAAGCAGCCACCGCAG    72206     A   AAA   AT
                                CTGC GGT   GGC  CTTGGG
                                ||||  |||   |||  ||||||
                                GACG CCA   CCG  GAACCC
                                  _   ___   AC
GAM782  DRD1    5'  GCCCAAGACAGTGACCTGCAG  5839        AAAGGCA
                                CTGCAGGT     TCTTGGGC
                                ||||||||     ||||||||
                                GACGTCCA     AGAACCCG
                                    GTGAC__
GAM782  EBI3    3'  CCTTTACCTTTACCACAGT    19244     CA      CATCTT
                                ACTG  GGTAAAGG     GGG
                                ||||  ||||||||     |||
                                TGAC  CCATTTCC     TCC
                                  A_       ATT___
GAM782  FMNL    5'  GCCCAGATCTCGCACCTGCAG  19705        AAA  C    T
                                CTGCAGGT   GG ATCT GGGC
                                ||||||||   || |||| ||||
                                GACGTCCA   CT TAGA CCCG
                                    CG_  C   _
GAM782  FPGS    3'  CCCACCCCACACCTGCAGT    17084        AAA  CATCT
                                ACTGCAGGT   GG    TGGG
                                |||||||||  ||    ||||
                                TGACGTCCA   CC    ACCC
                                    CA_  CC___
GAM782  GPRK6   3'  GCCCGAGGCCCCCACCAGCAGT 9112       A   AAA   AT
                                ACTGC GGT   GGC  CTTGGGC
                                |||||  |||   |||  |||||||
                                TGACG CCA   CCG  GAGCCCG
                                  A   CCC   __
GAM782  KIR2DS1 3'  GCCCAAGACACCCCCAACAG   27209     CA  TAAA  CA
                                CTG  GG    GG  TCTTGGGC
                                |||  ||    ||  ||||||||
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                              GAC CC   CC AGAACCCG
                                AA C___ AC
GAM782  KIR2DS2  3' GCCCAAGACACCCCCAACAG  24598    CA TAAA CA
                              CTG GG   GG TCTTGGGC
                              ||| ||   || ||||||||
                              GAC CC   CC AGAACCCG
                                AA C___ AC
GAM782  KIR2DS4  3' GCCCAAGACACCCCCAACAG  24601    CA TAAA CA
                              CTG GG   GG TCTTGGGC
                              ||| ||   || ||||||||
                              GAC CC   CC AGAACCCG
                                AA C___ AC
GAM782  NAP1L4   3' CCCACCCCTCCTGCAGT    19919       TAA  CATCT
                              ACTGCAGG  AGG   TGGG
                              ||||||||  |||   ||||
                              TGACGTCC  TCC   ACCC
                                  ___  CC___
GAM782  NFE2L1   5' CCCAAGACGAAAGGCCTGTAG 12169       AAAGGCA
                              CTGCAGGT     TCTTGGG
                              ||||||||     |||||||
                              GATGTCCG     AGAACCC
                                   GAAAGC_
GAM782  PDGFRB   3' CAGGACACCCCCAGCCTGCAG 65972       AAA_ CA
                              CTGCAGGT   GG TCTTG
                              ||||||||   || |||||
                              GACGTCCG   CC AGGAC
                                   ACCC AC
GAM782  POLL     5' GCCCGGGACTTCACCCGCAG  25179    A  A  GCA
                              CTGC GGT AAG  TCTTGGGC
                              |||| ||| |||  ||||||||
                              GACG CCA TTC  AGGGCCCG
                                C  C  ___
GAM782  PTBP1    3' CCACGCCTTCACCTGCAGT   49250       A   ATCT
                              ACTGCAGGT AAGGC   TGG
                              ||||||||| |||||   |||
                              TGACGTCCA TTCCG   ACC
                                   C    C___
GAM782  PTBP1    3' CCACGCCTTCACCTGCAGT   11005       A   ATCT
                              ACTGCAGGT AAGGC   TGG
                              ||||||||| |||||   |||
                              TGACGTCCA TTCCG   ACC
                                   C    C___
GAM782  RECQL5   3' CCACCCTTGCCTGCAG     14926       A CATCT
                              CTGCAGGTAA GG    TGG
                              |||||||||| ||    |||
                              GACGTCCGTT CC    ACC
                                    C _____
GAM782  RNMT     3' CCCATCCACCACCTGCAG    13716       AAA CATCT
                              CTGCAGGT  GG    TGGG
                              ||||||||  ||    ||||
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                                GACGTCCA  CC    ACCC
                                    ___  ACCT_
GAM782  STAT6    3'  ATGCCTGCACCTGCAG     12019        AA
                                CTGCAGGT  AGGCAT
                                ||||||||  ||||||
                                GACGTCCA  TCCGTA
                                    CG
GAM782  TIMM44   3'  GCCCAGGGACTCCCCCCACAG 71421     CA  TAAA  CA_
                                CTG  GG   GG   TCTTGGGC
                                |||  ||   ||   ||||||||
                                GAC  CC   CC   GGGACCCG
                                  AC  C___  TCA
GAM782  ARHGEF2  3'  TGCCTTCATCTGCAGT     16365        A
                                ACTGCAGGT AAGGCA
                                ||||||||| ||||||
                                TGACGTCTA TTCCGT
                                     C
GAM782  CNNM2    3'  CCCAAGATGCTGCTAC     34458     AA
                                GTA  GGCATCTTGGG
                                |||  ||||||||||
                                CAT  TCGTAGAACCC
                                  CG
GAM782  DJ37E16.5 3'  CCACTGCACCTGCAG      39729        AAAG   TCT
                                CTGCAGGT   GCA   TGG
                                ||||||||   |||   |||
                                GACGTCCA   CGT   ACC
                                    _____   C__
GAM782  DKFZP434P0111 3'  CCCATTCCTCCCCTGCAGT   67369        TAA   CATCT
                                ACTGCAGG   AGG    TGGG
                                ||||||||   |||    ||||
                                TGACGTCC   TCC    ACCC
                                    CC_   TT___
GAM782  DKFZP564D0478 3'  CCCATCTCCCCCTGCAGT    49532        TAAA  CATCT
                                ACTGCAGG   GG    TGGG
                                ||||||||   ||    ||||
                                TGACGTCC   CC    ACCC
                                    _____  CTCT_
GAM782  FLJ14050  5'  CCCAAGGACCCCTGCA     60327       TAAA  CA
                                TGCAGG   GG  TCTTGGG
                                ||||||   ||  |||||||
                                ACGTCC   CC  GGAACCC
                                    _____  A_
GAM782  FLJ14871  3'  CCCAGTGGCTACACCCACAG   51666     CA   AA  G   CT
                                CTG  GGT  AG CAT  TGGG
                                |||  |||  || |||  ||||
                                GAC  CCA  TC GTG  ACCC
                                  AC   CA  G   __
GAM782  FLJ20507  5'  GCCCAGTCCCGGCTTCACCTGC 35290        AA   ATC__
            AG                    CTGCAGGT  AGGC    TTGGGC
                                ||||||||  ||||    ||||||
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                                GACGTCCA TTCG   GACCCG
                                    C_   GCCCT
GAM782  FLJ20507  5' GCCCAGTCCCGGCTTCACCTGC 60225       AA   ATC__
          AG                  CTGCAGGT AGGC   TTGGGC
                              |||||||| ||||   ||||||
                              GACGTCCA TTCG   GACCCG
                                  C_   GCCCT
GAM782  FLJ32978  5' GCCCAAGAAAAACACCAGCAG 58232     A  AAAGGCA
                              CTGC GGT     TCTTGGGC
                              |||| |||     ||||||||
                              GACG CCA     AGAACCCG
                                A  CAAAA__
GAM782  GMPPB   5' CATGTGCCTCTTCCTGCAGT  95727       TAA    CT
                              ACTGCAGG  AGGCAT  TG
                              ||||||||  ||||||  ||
                              TGACGTCC  TCCGTG  AC
                                  TTC    T_
GAM782  KIAA0217  3' CCCTCCTTTACCCCCAG    67036    CA     CATCTT
                              CTG  GGTAAAGG    GGG
                              |||  ||||||||    |||
                              GAC  CCATTTCC    CCC
                                CC      T_____
GAM782  KIAA0229  3' CCATCGCCTCACCTGCAG   92424       AA   ATCTTG
                              CTGCAGGT  AGGC    GG
                              ||||||||  ||||    ||
                              GACGTCCA  TCCG    CC
                                  C_   CTA___
GAM782  KIAA0415  3' CAGGCAGCTCTACCTGCAG   92573       AA   AT
                              CTGCAGGTA  GGC  CTTG
                              |||||||||  |||  ||||
                              GACGTCCAT  TCG  GGAC
                                   C_   AC
GAM782  KIAA0596  3' GCCTTCACCTCTACCTGCA   62832       A   CATCTT
                              TGCAGGTA AGG    GGGC
                              |||||||| |||    ||||
                              ACGTCCAT TCC    TCCG
                                  C   ACT___
GAM782  KIAA0802  5' CTCCGCCGCCACCTGCAGT   62565       AAA  ATCTT
                              ACTGCAGGT  GGC   GGG
                              |||||||||  |||   |||
                              TGACGTCCA  CCG   CTC
                                   CCG  C____
GAM782  KIR3DS1   3' GCCCAAGACACCCCCAACAG  27212    CA  TAAA  CA
                              CTG  GG   GG  TCTTGGGC
                              |||  ||   ||  ||||||||
                              GAC  CC   CC  AGAACCCG
                                AA  C___  AC
GAM782  MGC19556  5' CCCAAGATATCCCTGCTGT   53228    T    TAAA GC
                              AC GCAGG   G  ATCTTGGG
                              || |||||   |  ||||||||
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                                TG CGTCC   C  TAGAACCC
                                 T    ____ TA
GAM782  MSC     3'  GCTCCTGCTCCTACCTGCAG  76349       AA   TCTT
                                CTGCAGGTA  GGCA   GGGC
                                |||||||||  ||||   ||||
                                GACGTCCAT  TCGT   CTCG
                                     CC   C___
GAM782  MUC16   5'  CCTCCTCTGCACCTACCTGCAG 60527       AAG   TCTT
                                CTGCAGGTA   GCA   GGG
                                |||||||||   |||   |||
                                GACGTCCAT   CGT   TCC
                                     CCA   CTCC
GAM782  OATL1   5'  GCCTCCAAACCTTACCTGCA  70492       A  CATCTT
                                TGCAGGTAA GG    GGGC
                                |||||||||  ||    ||||
                                ACGTCCATT CC    TCCG
                                     _  AAACC_
GAM782  ODC-p   3'  CCCCCGCGCTCCACCTGCAGT  53795       AA  _  ATCTT
                                ACTGCAGGT  AG GC   GGG
                                |||||||||  || ||   |||
                                TGACGTCCA  TC CG   CCC
                                     CC  G  CC___
GAM782  PRO0245  5'  CCCACCGTTACCCACAG    26126    CA    A  CATCT
                                CTG  GGTAA GG   TGGG
                                |||  ||||| ||   ||||
                                GAC  CCATT CC   ACCC
                                  AC    G  _____
GAM782  RNAHP   3'  GCCCAAGATGGAACCCAAAGT  23764    GCA   AAAGG
                                ACT   GGT   CATCTTGGGC
                                |||   |||   ||||||||||
                                TGA   CCA   GTAGAACCCG
                                  AAC   AG___
GAM782  SEC14L1  3'  CCCTCTCACCTGCAGT     11489       AA   CATCTT
                                ACTGCAGGT  AGG    GG
                                |||||||||  |||    ||
                                TGACGTCCA  TCT    CC
                                     C_   C_____
GAM782  LOC144519 5'  CCTACCTCTATCTACAGT   76867    C    A   CATCT
                                ACTG AGGTA AGG   TGGG
                                |||| ||||| |||   ||||
                                TGAC TCTAT TCC   ATCC
                                  A    C  _____
GAM782  LOC147160 5'  CCCAGGCCCACCTGCAG    83962       AAA   ATC
                                CTGCAGGT   GGC   TTGGG
                                ||||||||   |||   |||||
                                GACGTCCA   CCG   GACCC
                                     C__   ___
GAM782  LOC164397 5'  CAATACCCTCATCTGCAG   82520       AA   CATC
                                CTGCAGGT  AGG   TTG
                                ||||||||  |||   |||
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                                GACGTCTA  TCC    AAC
                                    C_   CAT_
GAM782   LOC200213 5'  CCGGTGCACCTTTGCCCGCAGT 88632      A      __    TT
                                ACTGC GGTAAAG  GCATC  GG
                                ||||| |||||||  |||||  ||
                                TGACG CCGTTTC  CGTGG  CC
                                   C      CA    __
GAM782   LOC219988 5'  GCCCAGGACCCCACCTGCA   91623       AAA  CA
                                TGCAGGT   GG  TCTTGGGC
                                |||||||   ||  ||||||||
                                ACGTCCA   CC  AGGACCCG
                                    ___  CC
GAM782   LOC256117 3'  GCCTTGGCCTTTAACCTGCAG  96358        _     ATCTT
                                CTGCAGGT AAAGGC    GGGC
                                |||||||| ||||||    ||||
                                GACGTCCA TTTCCG    TCCG
                                    A     GT___
GAM782   LOC257060 3'  GACGCCTCTCCCTGCAGT    94461       TAA    A
                                ACTGCAGG   AGGC TC
                                ||||||||   |||| ||
                                TGACGTCC   TCCG AG
                                    CTC    C
GAM782   LOC56965  3'  CCCATCCTCTCCTGCAGT    39527       TAA   CATCT
                                ACTGCAGG   AGG    TGGG
                                ||||||||   |||    ||||
                                TGACGTCC   TCC    ACCC
                                    TC_   T____
GAM782   LOC57106  3'  GCCTCTCCAACCCCTACCTCAG 64136    C    AA  CATCTT
                                CTG AGGTA  GG     GGGC
                                ||| |||||  ||     ||||
                                GAC TCCAT  CC     TCCG
                                  _    CC  AACCTC
GAM783   CNGA1    3'  CAACTGATAATGTGCAAA    59507       GC   A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                     A_  _
GAM783   CNGA1    3'  CAACTGATAATGTGCAAA    59507       GC   A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                     A_  _
GAM783   ESRRG    3'  TGGCAGTCTTATGTGCAAA   66396       TAGCT
                                TTTGCACAT    AGATTGCCA
                                |||||||||    |||||||||
                                AAACGTGTA    TCTGACGGT
                                    T____
GAM783   ESRRG    3'  TGGCAGTCTTATGTGCAAA   66396       TAGCT
                                TTTGCACAT    AGATTGCCA
                                |||||||||    |||||||||
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                                AAACGTGTA    TCTGACGGT
                                     T____
GAM783  KCNJ3   3' GCAATAATGTGCAAA      9525          GCTAGA
                                TTTGCACATTA     TTGC
                                ||||||||||     ||||
                                AAACGTGTAAT     AACG
                                      ______
GAM783  KCNJ3   3' GCAATAATGTGCAAA      9525          GCTAGA
                                TTTGCACATTA     TTGC
                                ||||||||||     ||||
                                AAACGTGTAAT     AACG
                                      ______
GAM783  SDC2    3' GCAAATTAATGTGTAAA     67132          CTAGA
                                TTTGCACATTAG    TTGC
                                ||||||||||||    ||||
                                AAATGTGTAATT    AACG
                                     A____
GAM783  SDC2    3' GCAAATTAATGTGTAAA     67132          CTAGA
                                TTTGCACATTAG    TTGC
                                ||||||||||||    ||||
                                AAATGTGTAATT    AACG
                                     A____
GAM783  USP9X   3' ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
          A                      TTTGCACATTAGC     GCCAT
                                ||||||||||||     |||||
                                AAATGTGTAATCG     CGGTA
                                      TAGTC_
GAM783  USP9X   3' ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
          A                      TTTGCACATTAGC     GCCAT
                                ||||||||||||     |||||
                                AAATGTGTAATCG     CGGTA
                                      TAGTC_
GAM783  AMOTL1  3' GGCAAGTAATGTGCAAA     73650          G  AGAT
                                TTTGCACATTA CT    TGCC
                                |||||||||| ||    ||||
                                AAACGTGTAAT GA    ACGG
                                     _ ____
GAM783  AMOTL1  3' GGCAAGTAATGTGCAAA     73650          G  AGAT
                                TTTGCACATTA CT    TGCC
                                |||||||||| ||    ||||
                                AAACGTGTAAT GA    ACGG
                                     _ ____
GAM783  BCAR3   3' AGTAATAATGTGCAAA      13098          __
                                TTTGCACATTA  GCT
                                ||||||||||  |||
                                AAACGTGTAAT  TGA
                                      AA
GAM783  BCAR3   3' AGTAATAATGTGCAAA      13098          __
                                TTTGCACATTA  GCT
                                ||||||||||  |||
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                                AAACGTGTAAT  TGA
                                      AA
GAM783  DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930        AGCTA    C
                                TTTGCACATT    GATTG CA
                                ||||||||||    ||||| ||
                                AGACGTGTAA    TTAAC GT
                                      A____    A
GAM783  DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930        AGCTA    C
                                TTTGCACATT    GATTG CA
                                ||||||||||    ||||| ||
                                AGACGTGTAA    TTAAC GT
                                      A____    A
GAM783  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                TTTGCACATTAG  AGA TG CAT
                                ||||||||||||  ||| || |||
                                AGACGTGTAATC  TTT AC GTA
                                      __  T  A
GAM783  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                TTTGCACATTAG  AGA TG CAT
                                ||||||||||||  ||| || |||
                                AGACGTGTAATC  TTT AC GTA
                                      __  T  A
GAM783  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
          AA                    TTTGCACATTAGCTAGATTGCCAT
                                ||||||||||||||||||||||||
                                AAACGTGTAATCGATCTAACGGTA

GAM783  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
          AA                    TTTGCACATTAGCTAGATTGCCAT
                                ||||||||||||||||||||||||
                                AAACGTGTAATCGATCTAACGGTA

GAM784  AICDA    5'  GCCTGAGACTTGCAGGGAGGCA 40329     C       ATTTGC__
          AGAA                    TTC TGCCTCCCT       CAGGC
                                ||| |||||||||       |||||
                                AAG ACGGAGGGA       GTCCG
                                  A       CGTTCAGA
GAM784  ANK1     3'  GCCTCCGGCCCAGGGAGGCCAG 40027     CT      ATTT  __
          AA                    TTC  GCCTCCCT    GCC  AGGC
                                |||  ||||||||    |||  ||||
                                AAG  CGGAGGGA    CGG  TCCG
                                  AC       CC__   CC
GAM784  ANK1     3'  GCCTCCGGCCCAGGGAGGCCAG 3473      CT      ATTT  __
          AA                    TTC  GCCTCCCT    GCC  AGGC
                                |||  ||||||||    |||  ||||
                                AAG  CGGAGGGA    CGG  TCCG
                                  AC       CC__   CC
GAM784  EIF2C1   3'  CCCAAATCCAGAGGAAGCAAGG 24170      _  C  _  __    CCA
          A                     TCCT GC TCC CT  ATTTG   GG
                                |||| || ||| ||  |||||   ||
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                                AGGA CG AGG GA  TAAAC   CC
                                  A  A   A  CC    ___
GAM784  IKBKG    3'  CCCGGCACTGGGGAAGTCAAGA 13311     C  _ C     TT    A
              A                   TTC TG C TCCCTA  TGCC GG
                                  ||| || | ||||||  |||| ||
                                  AAG AC G AGGGGT  ACGG CC
                                    A  T A     C_    C
GAM784  IKBKG    3'  CCCGGCACTGGGGAAGTCAAGA 94663     C  _ C     TT    A
              A                   TTC TG C TCCCTA  TGCC GG
                                  ||| || | ||||||  |||| ||
                                  AAG AC G AGGGGT  ACGG CC
                                    A  T A     C_    C
GAM784  LY9      3'  AAATAAAAGGCAGGAA      71680          CCC
                                  TTCCTGCCT   TATTT
                                  |||||||||   |||||
                                  AAGGACGGA   ATAAA
                                       AA_
GAM784  MAFF     3'  TGGCAAATAGGGAGACAAGGA  24655      GC_
                                  TCCT   CTCCCTATTTGCCA
                                  ||||   ||||||||||||||
                                  AGGA   GAGGGATAAACGGT
                                    ACA
GAM784  MC1R     5'  GCCCAGATGGAAGGAGGCAGG  9954           __      CCA
                                  CCTGCCTCC  CTATTTG   GGC
                                  |||||||||  |||||||   |||
                                  GGACGGAGG  GGTAGAC   CCG
                                       AA      ___
GAM784  MYO15A   3'  GCCTGAGGGAGGAGGCAGGAG  32671           _  ATTTGC
                                  TTCCTGCCTCC CT      CAGGC
                                  |||||||||||  ||     |||||
                                  GAGGACGGAGG GG      GTCCG
                                         A  GA____
GAM784  NRG1     3'  GCAAATAGAAAACAGGAA    25646        CCTCC
                                  TTCCTG    CTATTTGC
                                  ||||||    ||||||||
                                  AAGGAC    GATAAACG
                                     AAAA_
GAM784  NRG1     3'  GCAAATAGAAAACAGGAA    25659        CCTCC
                                  TTCCTG    CTATTTGC
                                  ||||||    ||||||||
                                  AAGGAC    GATAAACG
                                     AAAA_
GAM784  SEPN1    3'  GCCTGGCAGAGGAAGAAGGAA  66369       GC  C   AT
                                  TTCCT  CT CCT  TTGCCAGGC
                                  |||||  || |||  |||||||||
                                  AAGGA  GA GGA  GACGGTCCG
                                    A_  A  __
GAM784  SMURF1   3'  GCCTAACCCGCGGGAGGCGGAA 92453      T      TATTTGCC
                                  TTCC GCCTCCC       AGGC
                                  |||| |||||||       ||||
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                                AAGG CGGAGGG       TCCG
                                  _      CGCCCAA_
GAM784  STAT6    3'  GCCTAGGACGGATAGGCAGGAA 12021         CCCT    _ _
                                TTCCTGCCT    ATTTG CC AGGC
                                |||||||||    ||||| || ||||
                                AAGGACGGA    TAGGC GG TCCG
                                     ____     A  A
GAM784  TFF3     3'  GCCCAGGCCTCAAGGGCAGGAA 63566         CCCTATTT   A_
                                TTCCTGCCT       GCC  GGC
                                |||||||||       |||  |||
                                AAGGACGGG       CGG  CCG
                                     AACTC___   AC
GAM784  TOP3B    5'  GCCCGGCGGCTCAGAAAGGCGG 14129         CC  AT_    A
           GAA                    TTCCTGCCT  CT   TTGCC GGC
                                |||||||||  ||   ||||| |||
                                AAGGGCGGA  GA   GGCGG CCG
                                     AA  CTC    C
GAM784  VAV1     3'  GCCTTGGCAGAGAGACGAG    18305     C_  A      _
                                CTC  CT TTTGCCA GGC
                                |||  || ||||||| |||
                                GAG  GA AGACGGT CCG
                                  CA  G      T
GAM784  YWHAB    5'  GCTGTGGATAGAGAAGCAGGAA 12692        C  C     TG CA
                                TTCCTGC TC CTATT  C  GGC
                                ||||||| || |||||  |  |||
                                AAGGACG AG GATAG  G  TCG
                                    A  A    GT __
GAM784  AF020591 3'  GCCTGGCAAACATGGCA     27141      TCCCTA
                                TGCC     TTTGCCAGGC
                                ||||     ||||||||||
                                ACGG     AAACGGTCCG
                                  TAC___
GAM784  BCL2L1   3'  CCTCAGGCAGGAAGGGCAGGAA 56804         CC  ATT    __
                                TTCCTGCCT  CT   TGCC  AGG
                                |||||||||  ||   ||||  |||
                                AAGGACGGG  GG   ACGG  TCC
                                     AA  ___    AC
GAM784  BNIP-S   5'  TAAAGAAGGAGGCAGGAA    56263          CTA
                                TTCCTGCCTCC   TTTG
                                ||||||||||   ||||
                                AAGGACGGAGG   AAAT
                                      AAG
GAM784  BTBD3    5'  GCAAATAAGAGAAACAGGAA   30311       C__   CC
                                TTCCTG   CTC  TATTTGC
                                ||||||   |||  |||||||
                                AAGGAC   GAG  ATAAACG
                                   AAA   A_
GAM784  C20orf28 3'  GCCTGAGACGGGAGGCAGGAA 31224          TAT  GC
                                TTCCTGCCTCCC   TT  CAGGC
                                ||||||||||||   ||  |||||
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                                AAGGACGGAGGG  AG  GTCCG
                                      C__  A_
GAM784  CHODL    5'  CCCGGCAGGGAGGCAGGGA   46310          ATTT  A
                                TTCCTGCCTCCCT   GCC GG
                                |||||||||||||   ||| ||
                                AGGGACGGAGGGA   CGG CC
                                     _____  C
GAM784  D2S448   3'  CCTGAAGGGAAGCAGG     73519      C    ATTTGC
                                CCTGC TCCCT     CAGG
                                |||||| |||||     ||||
                                GGACG AGGGA     GTCC
                                   A    A_____
GAM784  DKFZP434K1772 3'  GCCTTACTCAGGAAGGCAGGAG 67714        C  ATTTGCC
                                TTCCTGCCT CCT      AGGC
                                ||||||||| |||      ||||
                                GAGGACGGA GGA      TCCG
                                      A  CTCAT__
GAM784  DKFZp547I094 3'  CCTGGCAACCTGAGGGAGG   49637       AT__
                                CCTCCCT   TTGCCAGG
                                |||||||   ||||||||
                                GGAGGGA   AACGGTCC
                                    GTCC
GAM784  DKFZP547L112 3'  CCTGGATATAGCAAGGCAGGAA 66529        CC   TTG
                                TTCCTGCCT  CTAT   CCAGG
                                |||||||||  ||||   |||||
                                AAGGACGGA  GATA   GGTCC
                                      AC   TA_
GAM784  FABP7    5'  CAAATAAGAAGGCAGGAG    7542         CCC
                                TTCCTGCCT   TATTTG
                                |||||||||   ||||||
                                GAGGACGGA   ATAAAC
                                      AGA
GAM784  FLJ14957  3'  CCCAAAGTGGGAGGCAGGGA   51744          TA   CCA
                                TTCCTGCCTCCC  TTTG   GG
                                ||||||||||||  ||||   ||
                                AGGGACGGAGGG  AAAC   CC
                                       TG   ___
GAM784  FLJ20343  3'  CCTGGCAAACTGACCAG    34998     CC  CCTA
                                CTG  TC    TTTGCCAGG
                                |||  ||    |||||||||
                                GAC  AG    AAACGGTCC
                                  C_  TC__
GAM784  FLJ23185  3'  CCTGGCAGGATGAGGCAGAGA  46830    _      CCTA
                                TC CTGCCTC    TTTGCCAGG
                                || |||||||    |||||||||
                                AG GACGGAG    GGACGGTCC
                                 A      TA__
GAM784  GGA2     3'  GCCTGATGGGTGGGAGAAGGAA 56882       GC    T   GC
                                TTCCT  CTCCC ATTT  CAGGC
                                |||||  ||||| ||||  |||||
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                                AAGGA  GAGGG TGGG  GTCCG
                                  A_    _   TA
GAM784  GGA2     3'  GCCTGATGGGTGGGAGAAGGAA 30468      GC    T   GC
                                TTCCT  CTCCC ATTT  CAGGC
                                |||||  ||||| ||||  |||||
                                AAGGA  GAGGG TGGG  GTCCG
                                  A_    _   TA
GAM784  HDAC11   3'  GCCCATAGGTCCAGGGAGGCAG 45718          ATTT  A___
           G                     CCTGCCTCCCT   GCC   GGC
                                ||||||||||    |||   |||
                                GGACGGAGGGA   TGG   CCG
                                      CC__  ATAC
GAM784  IKKE     5'  CACAAGGAGGCAGGGA     25746          CTAT  CCA
                                TTCCTGCCTCC   TTG  G
                                ||||||||||    |||  |
                                AGGGACGGAGG   AAC  C
                                      ____  A__
GAM784  IL1F10   3'  CAAGAAGGAGGCAGGAA    50771          CTA
                                TTCCTGCCTCC   TTTG
                                ||||||||||   ||||
                                AAGGACGGAGG   GAAC
                                      AA_
GAM784  KIAA0370 5'  GCCCAGCAAATAGGAGCCTGGA 73209     T_ CTC       CA
           G                     TTCC  GC   CCTATTTGC  GGC
                                ||||  ||   |||||||||  |||
                                GAGG  CG   GGATAAACG  CCG
                                  TC  A__       AC
GAM784  KIAA0551 3'  GCCTGGTTGAGAAGGAGAG   66839    _  A_  T
                                CTC CCT  TT GCCAGGC
                                ||| |||  || |||||||
                                GAG GGA  AG TGGTCCG
                                  A  AG  T
GAM784  KIAA1183 3'  CCCGGATGGGAGGAGGAA    62530      G     TATTTG  A
                                TTCCT CCTCCC     CC GG
                                ||||| ||||||     || ||
                                AAGGA GGAGGG     GG CC
                                  _     TA____  C
GAM784  KIAA1464 3'  CCTGACCCATGGAGGCAGGAG  68264          CTATTTGC
                                TTCCTGCCTCC       CAGG
                                ||||||||||       ||||
                                GAGGACGGAGG       GTCC
                                      TACCCA__
GAM784  MAPK8IP3 3'  GCCTGGTAGATGAAGCAG    52987      C  CCT
                                CTGC TC   ATTTGCCAGGC
                                ||||  ||   ||||||||||
                                GACG AG   TAGATGGTCCG
                                  A  ___
GAM784  MGC2306  3'  GCCTGGCAGGGGGTGAAGGCAG 50963         ___    AT
           GAG                    TTCCTGCCT   CCCT  TTGCCAGGC
                                |||||||||   ||||  |||||||||
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                                GAGGACGGA  GGGG  GACGGTCCG
                                     AGT   __
GAM784  MGC2865  5' GCCTGGCAAACCGAAGCAAGAA 50451    C  C  CCTA
                                TTC TGC TC   TTTGCCAGGC
                                ||| ||| ||   ||||||||||
                                AAG ACG AG   AAACGGTCCG
                                  A  A  CC__
GAM784  MGC9753  3' GCCTGATTTTGGGGAGGAGGAA 53049     G      TTTGC
                                TTCCT CCTCCCTA    CAGGC
                                ||||| ||||||||    |||||
                                AAGGA GGAGGGGT    GTCCG
                                   _      TTTA_
GAM784  PALM     3' GCCTGGTAGGAGAGAGACAGGA 10414     C  C  A
                                TCCTG CTC CT TTTGCCAGGC
                                ||||| ||| || ||||||||||
                                AGGAC GAG GA GGATGGTCCG
                                   A  A  _
GAM784  PDZD2    5' CCTGGCACGGAAGGAGGAA   80866     G  C  TATT
                                TTCCT CCT CC   TGCCAGG
                                ||||| ||| ||   |||||||
                                AAGGA GGA GG   ACGGTCC
                                   _  A  C___
GAM784  PLPL     3' CCTGGAGGGGGAGGCAGGAG  39431         ATTTG
                                TTCCTGCCTCCCT    CCAGG
                                ||||||||||||    |||||
                                GAGGACGGAGGGG    GGTCC
                                      GA___
GAM784  RABEX5   3' GCCTGGAATGGAAGGCGGGAA 27186       C  TATTTG
                                TTCCTGCCT CC     CCAGGC
                                |||||||| ||     ||||||
                                AAGGGCGGA GG     GGTCCG
                                     A  TAA___
GAM784  SHANK3   5' GCCTGCTCGCAGGGAGGCAGAG 65500    _       ATTT  C
           A                     TC CTGCCTCCCT   GC AGGC
                                || ||||||||||   || ||||
                                AG GACGGAGGGA   CG TCCG
                                 A        CGCT  _
GAM784  SRF      5' CCGGGCCACAGGGGCAGGAA  11944        CCTATTT  A
                                TTCCTGCCTC      GCC GG
                                ||||||||||      ||| ||
                                AAGGACGGGG      CGG CC
                                      ACAC___   G
GAM784  TREX1    5' CCCAGCAGAGGGAGGCAG   53280        AT   CA
                                CTGCCTCCCT  TTGC  GG
                                ||||||||||  ||||  ||
                                GACGGAGGGA  GACG  CC
                                      __    AC
GAM784  TREX1    5' CCCAGCAGAGGGAGGCAG   53290        AT   CA
                                CTGCCTCCCT  TTGC  GG
                                ||||||||||  ||||  ||
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                                GACGGAGGGA  GACG  CC
                                      __    AC
GAM784  URG4     3'  GCCCCCAGGGTAGGGAGACA   35506    C        GCCA
                                TG CTCCCTATTT    GGC
                                || ||||||||||    |||
                                AC GAGGGATGGG    CCG
                                 A         ACCC
GAM784  LOC124222 3' CCTGACAAACAGGCAGGGA    74271         CCCTA    C
                                TTCCTGCCT    TTTG CAGG
                                |||||||||    |||| ||||
                                AGGGACGGA    AAAC GTCC
                                      C____    A
GAM784  LOC131873 5' CCCGGAGGAGAGGCAGGGA    75877          _   ATTTG  A
                                TTCCTGCCTC CCT    CC GG
                                |||||||||| |||    || ||
                                AGGGACGGAG GGA    GG CC
                                       A   _____  C
GAM784  LOC144348 5' CCTTCCGTAGAAAGACAGGCA  76806      CC  A    C__
                                TGCCT  CT TTTGC   AGG
                                |||||  || |||||   |||
                                ACGGA  GA AGATG   TCC
                                   CA  A    CCT
GAM784  LOC146316 5' CTTCGAGAGGCAGGAA      60872          CCTAT   CC
                                TTCCTGCCTC    TTG  AG
                                ||||||||||    |||  ||
                                AAGGACGGAG    AGC  TC
                                      _____   T_
GAM784  LOC148529 5' CCTGGCAGACAGGAAGACA    84167    C  C   A
                                TG CT CCT TTTGCCAGG
                                || || ||| |||||||||
                                AC GA GGA AGACGGTCC
                                 A  A   C
GAM784  LOC149606 3' GCCCGCGGAGCAGGGAG     79454       A_    CA
                                CTCCCT  TTTGC  GGC
                                ||||||  |||||  |||
                                GAGGGA  AGGCG  CCG
                                   CG    C_
GAM784  LOC151057 3' CCAGGAAAGAAGGCAGGAA    85209         CCCTA   G  A
                                TTCCTGCCT    TTT CC GG
                                |||||||||    ||| || ||
                                AAGGACGGA    AAA GG CC
                                      AG___   _  A
GAM784  LOC153346 5' CCCAGATGGAAGGCA       86022       CC      CCA
                                TGCCT  CTATTTG   GG
                                |||||  |||||||   ||
                                ACGGA  GGTAGAC   CC
                                   A_      ___
GAM784  LOC196418 5' CCTTCCGTAGAAAGACAGGCA  87696      CC  A    C__
                                TGCCT  CT TTTGC   AGG
                                |||||  || |||||   |||
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                                ACGGA  GA AGATG   TCC
                                   CA  A    CCT
GAM784  LOC199786 3'  GCCTGGCAGCTGAGGCAGAGA  88386   _     CCTAT
                                TC CTGCCTC    TTGCCAGGC
                                || |||||||    |||||||||
                                AG GACGGAG    GACGGTCCG
                                 A      TC___
GAM784  LOC200058 3'  CCTGAAGGATGGGAAGCCAGGA 88556      C  C     GC
          A                      TTCCTG CT CCTATTT  CAGG
                                |||||| || |||||||  ||||
                                AAGGAC GA GGGTAGG  GTCC
                                   C  A      AA
GAM784  LOC204579 5'  CCCGGCTATGAGGCAGGAA   89465        CCTATTT   A
                                TTCCTGCCTC      GCC GG
                                ||||||||||      ||| ||
                                AAGGACGGAG      CGG CC
                                      TAT_____   C
GAM784  LOC219700 5'  GCCTGGCAGTCCAAAGACCAAG 93064    C  CCTCCCTAT
          AA                     TTC TG       TTGCCAGGC
                                ||| ||        |||||||||
                                AAG AC        GACGGTCCG
                                 A  CAGAAACCT
GAM784  LOC253181 5'  GCCTGGCAAACAGCACAGGA   97558      CCTCC  A
                                TCCTG    CT TTTGCCAGGC
                                |||||    || ||||||||||
                                AGGAC    GA AAACGGTCCG
                                   AC___  C
GAM784  LOC253296 3'  GCCTGGGGCCACAGGAAAGGCA 94490        C_   ATTTG_
          GGAA                    TTCCTGCCT  CCT     CCAGGC
                                |||||||||  |||     ||||||
                                AAGGACGGA  GGA     GGTCCG
                                     AA   CACCGG
GAM784  LOC253298 5'  GCCTGGGGCCACAGGAAAGGCA 97215        C_   ATTTG_
          GGAA                    TTCCTGCCT  CCT     CCAGGC
                                |||||||||  |||     ||||||
                                AAGGACGGA  GGA     GGTCCG
                                     AA   CACCGG
GAM784  LOC254107 5'  CCCAGAGGGCAGGAA      94384        CCCTA    CCA
                                TTCCTGCCT    TTTG   G
                                |||||||||    ||||   |
                                AAGGACGGG    AGAC   C
                                     _____    C__
GAM784  LOC255189 5'  CTGACCAAGGCAGGAA     96589        CCCTATT  C_
                                TTCCTGCCT      TG  CAG
                                |||||||||      ||  |||
                                AAGGACGGA      AC  GTC
                                     ________  CA
GAM784  LOC257160 3'  CCTGACTGGGGAGGAAG     94846    G      TTTGC
                                CT CCTCCCTA    CAGG
                                || ||||||||    ||||
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                                GA GGAGGGGT    GTCC
                                 A       CA___
GAM784  LOC257570 3'  GCCTGGGGCCACAGGAAAGGCA 97833         C_  ATTTG_
          GGAA                    TTCCTGCCT  CCT     CCAGGC
                                |||||||||  |||     ||||||
                                AAGGACGGA  GGA     GGTCCG
                                     AA   CACCGG
GAM784  LOC257571 5'  GCCTGGGGCCACAGGAAAGGCA 97945         C_  ATTTG_
          GGAA                    TTCCTGCCT  CCT     CCAGGC
                                |||||||||  |||     ||||||
                                AAGGACGGA  GGA     GGTCCG
                                     AA   CACCGG
GAM785  C5orf5    3'  ACCAAAATCAAACTGAGATTTC 33463       AG        C
                                GAAGT  TAGTTTGATT TGGT
                                |||||  |||||||||| ||||
                                CTTTA  GTCAAACTAA ACCA
                                   GA        A
GAM785  KIAA1210  5'  ACCAGAAACCACTACCCCTC   96323    A TA    TTGA
                                GA G  GTAGT    TTCTGGT
                                || |  |||||    |||||||
                                CT C  CATCA    AAGACCA
                                 _ CC     CCA_
GAM785  PRO0611   3'  CAGACTGACTACTTCTA     26010          _
                                TAGAAGTAGT AGTTTG
                                |||||||||| ||||||
                                ATCTTCATCA TCAGAC
                                      G
GAM785  RAB24     3'  CAAACCCCTACTTCTA      55388          TA
                                TAGAAGTAG  GTTTG
                                |||||||||  |||||
                                ATCTTCATC  CAAAC
                                      CC
GAM785  LOC206012 5'  TCAAACTACTACTACTA     89524     A
                                TAG AGTAGTAGTTTGA
                                ||| ||||||||||||
                                ATC TCATCATCAAACT
                                  A
GAM785  LOC220469 3'  AGTCAAATCACTACTTC     76383         A
                                GAAGTAGT GTTTGATT
                                |||||||| ||||||||
                                CTTCATCA TAAACTGA
                                     C
GAM785  LOC257042 3'  ACCAGAATCAGAGTGC      96896     G
                                GTA TTTGATTCTGGT
                                ||| ||||||||||||
                                CGT AGACTAAGACCA
                                  G
GAM785  LOC257486 5'  ACCAGAAACCACTACCCCTC   69240    A TA    TTGA
                                GA G  GTAGT    TTCTGGT
                                || |  |||||    |||||||
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                                CT C  CATCA    AAGACCA
                                 _ CC     CCA_
GAM786  DOK1     3'  CAATCCCAGGAAGTCCTAAGAA 7272      C        AAA  T
                                TTC TGGGACTTC   TG GATTG
                                ||| |||||||||   || |||||
                                AAG ATCCTGAAG   AC CTAAC
                                  A        G__  C
GAM786  ITPR2    3'  ACAGTAAGCCCCAGGAA     9445         A   CAAA
                                TTCCTGGG CTT    TGT
                                |||||||| |||    |||
                                AAGGACCC GAA    ACA
                                     C   TG__
GAM786  PARG     3'  CAAGTTGAAATCCCAGGAA    13268         C     ATG
                                TTCCTGGGA TTCAA   TG
                                ||||||||| |||||   ||
                                AAGGACCCT AAGTT   AC
                                      A    GA_
GAM786  STK4     3'  CAGAGTTTTAAACCCCAGGAA  20789        AC  C    G_
                                TTCCTGGG  TT AAAT  TG
                                ||||||||  || ||||  ||
                                AAGGACCC  AA TTTG  AC
                                     CA  T    AG
GAM786  FLJ11026 3'  CATTTGAAATGCCCAGGAA    36991        AC_
                                TTCCTGGG   TTCAAATG
                                ||||||||   ||||||||
                                AAGGACCC   AAGTTTAC
                                     GTA
GAM786  FLJ11294 3'  CACCTGAATCCCAGGAA     37220         C    AAT
                                TTCCTGGGA TTCA   GTG
                                ||||||||| ||||   |||
                                AAGGACCCT AAGT   CAC
                                      _    C__
GAM786  H2AFA    3'  CAGTGATCCCGAGTCCCAG    40738         CAAAT  G
                                CTGGGACTT     GT ATTG
                                |||||||||     || ||||
                                GACCCTGAG     TA TGAC
                                      CCC__  G
GAM786  LIG-1    3'  CAACCACATTTGTTCACAGGAG 63892       _   TTC      A
                                TTCCTG GGAC   AAATGTG TTG
                                |||||| ||||   ||||||| |||
                                GAGGAC CTTG   TTTACAC AAC
                                   A    ___      C
GAM786  PRO0899  3'  CAACCACTCAAGTCCCAG    37692         CAAAT   A
                                CTGGGACTT     GTG TTG
                                |||||||||     ||| |||
                                GACCCTGAA     CAC AAC
                                      CT___   C
GAM786  LOC196047 5'  CACTTTTAAAGTCCCA      89595         C   T
                                TGGGACTT AAA GTG
                                |||||||| ||| |||
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                                ACCCTGAA TTT CAC
                                    A   T
GAM786  LOC196510 3'  CATTTGATTCAAGTCCCAAGAA 87747     C      ____
                                TTC TGGGACT    TCAAATG
                                ||| |||||||    |||||||
                                AAG ACCCTGA    AGTTTAC
                                  A       ACTT
GAM786  LOC200220 3'  CATTTGATTCAAGTCCCAAGAA 88637     C      ____
                                TTC TGGGACT    TCAAATG
                                ||| |||||||    |||||||
                                AAG ACCCTGA    AGTTTAC
                                  A       ACTT
GAM786  LOC222166 3'  CACCTGAGCCCCAGGAA     94091        A  T  AAT
                                TTCCTGGG CT CA   GTG
                                |||||||| || ||   |||
                                AAGGACCC GA GT   CAC
                                    C  _  C__
GAM786  LOC255294 5'  CAATCACAAGAAGTTCCAG    94472          AAA
                                CTGGGACTTC   TGTGATTG
                                ||||||||||   ||||||||
                                GACCTTGAAG   ACACTAAC
                                     A__
GAM786  LOC51285  3'  ACAGAAGCCCCAGGAA      33342        A    AAA
                                TTCCTGGG CTTC   TGT
                                |||||||| ||||   |||
                                AAGGACCC GAAG   ACA
                                    C    ___
GAM786  LOC93259  5'  CAATCGGCAGAAAACCCAGGAA 71804         AC   AAA  _
                                TTCCTGGG  TTC   TGT GATTG
                                ||||||||  |||   ||| |||||
                                AAGGACCC  AAG   ACG CTAAC
                                    AA   ___   G
GAM787  ARNT2     3'  AAACAACCCGTGCATCCCTGC  29450     A    TTTTA
                                GTA GGAT     GGGTTGTTT
                                ||| ||||     |||||||||
                                CGT CCTA     CCCAACAAA
                                  C    CGTG_
GAM787  LCT       3'  AACCGTAAAAATCCTT      9697            G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
                                TTCCTAAAAAT CCAA
                                     G
GAM787  RPL15     3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM787  FBXO30    3'  AACTAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
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                                CA TCCTAAAAA  TCAA
                                 G        AA
GAM787  KIAA0494  3'  AACAACCCTTACTTAC      28736       GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                  AT_____
GAM787  PRO0641   5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                  ___    C
GAM787  SMT3H2    3'  AACAACATAAAAATCCTTGC   22670           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM787  LOC120103 3'  AACCTATGAAAAATCCTTGC   74002           A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
                                CGTTCCTAAAAA   TCCAA
                                       GTA
GAM787  LOC129831 3'  AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM787  LOC133088 5'  AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                      GTA GGATTTTT     TTGTTT
                                ||| ||||||||     ||||||
                                CGT CCTAAAAA     AACAAA
                                  C       GATAA
GAM787  LOC148089 3'  GGCCCTAAAAATTCCTAC     78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM787  LOC154547 3'  AACAACATAAAAATCCTTGC   76050           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM787  LOC158104 3'  ACAGCCAAAAATCCTTA     60313           AG
                                TAAGGATTTTT  GGTTGT
                                ||||||||||  ||||||
                                ATTCCTAAAAA  CCGACA
                                       __
GAM787  LOC205880 5'  AAACAACCATCATCCTGAC    90709     A     TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
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                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM787  LOC221561 3'  AACAACATAAAAATCCTTGC   92130          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM787  LOC257591 3'  AACAACATAAAAATCCTTGC   97840          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM787  LOC51145  3'  AGCTAAAATCCTTAC      32393          TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
                                CATTCCTAAAA   TCGA
                                       ___
GAM788  ADRBK2    3'  TGGGAGACATATCAGT      17687      CAAA
                                ATTGG   GTGTCTCCCA
                                |||||   ||||||||||
                                TGACT   TACAGAGGGT
                                  A___
GAM788  APXL      3'  AGACACTTCACCAAAGA     7925     A   CA
                                TC TTGG  AAGTGTCT
                                || ||||  ||||||||
                                AG AACC  TTCACAGA
                                 A   AC
GAM788  CIT       3'  CTTGGGTTGCTCTGCCAATG   69746        A   GTCT
                                CATTGGCA AGT   CCCAAG
                                |||||||| |||   ||||||
                                GTAACCGT TCG   GGGTTC
                                     C   TT__
GAM788  CRAT      3'  CTAGGACTCAGGCCTGCCAATG 14352        AA T   C___  A
                                CATTGGCA  G GTCT   CC AG
                                ||||||||  | ||||   || ||
                                GTAACCGT  C CGGA   GG TC
                                     __ _   CTCA  A
GAM788  CRAT      3'  CTAGGACTCAGGCCTGCCAATG 5660         AA T   C___  A
                                CATTGGCA  G GTCT   CC AG
                                ||||||||  | ||||   || ||
                                GTAACCGT  C CGGA   GG TC
                                     __ _   CTCA  A
GAM788  FOSB      3'  CTTGGTTCTGCACTGTTGCCAA 22106        _    CTC_
              T                  ATTGGCAA AGTGT   CCAAG
                                ||||||||| |||||   |||||
                                TAACCGTT TCACG   GGTTC
                                     G    TCTT
GAM788  KCNN3     3'  TCCTGGTCGCTTTGCCA     9564         TCTC   A
                                TGGCAAAGTG   CCA GA
                                ||||||||||   ||| ||
```

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                                ACCGTTTCGC   GGT CT
                                     T___  C
GAM788  MYCL1   3' CTTAAGAGACACTCCAA    18164     CAA      CC
                                TTGG  AGTGTCTC  AAG
                                ||||  ||||||||  |||
                                AACC  TCACAGAG  TTC
                                  ___      AA
GAM788  MYO1D   3' TGGGAGACTCCCTTTGCCA   71772        T__
                                TGGCAAAG  GTCTCCCA
                                ||||||||  ||||||||
                                ACCGTTTC  CAGAGGGT
                                    CCT
GAM788  PKP2    3' TCTCAGGAGATACTTTACC   15888   C        CA
                                GG AAAGTGTCTCC  AGA
                                || ||||||||||  |||
                                CC TTTCATAGAGG  TCT
                                 A         AC
GAM788  PSMD9   3' TCTCAGGGATTCCTGCCAAT  10990       AAGT  T  CA
                                ATTGGCA   GTC CC  AGA
                                |||||||   ||| ||  |||
                                TAACCGT   TAG GG  TCT
                                    CCT_  _ AC
GAM788  XBP1    3' TCTTGGGAGGACACTTTTGCCA 17430          _   _
            ATGA                   TCATTGGCAAA GTGTC TCCCAAGA
                                ||||||||||| ||||| ||||||||
                                AGTAACCGTTT CACAG AGGGTTCT
                                      T   G
GAM788  AD-020  3' TCTTGAGAGTTTTGCCAAGA  39311   A      TGT  C
                                TC TTGGCAAAG  CTC CAAGA
                                || |||||||||  ||| |||||
                                AG AACCGTTTT  GAG GTTCT
                                 _       ___  A
GAM788  AD-020  3' TCTTGAGAGTTTTGCCAAGA  59387   A      TGT  C
                                TC TTGGCAAAG  CTC CAAGA
                                || |||||||||  ||| |||||
                                AG AACCGTTTT  GAG GTTCT
                                 _       ___  A
GAM788  APOA1BP 3' TCCTGGGAGCTCCTCTGGCAAT 58586     G  A  TGT    A
                                ATTG CA AG   CTCCCA GA
                                |||| || ||   |||||| ||
                                TAAC GT TC   GAGGGT CT
                                  G  C  CTC     C
GAM788  ARHGEF2 3' CTTGGGGACTCCAATTTGCCAA 16362          GT___  T
            TGA                   TCATTGGCAAA    GTC CCCAAG
                                ||||||||||    ||| ||||||
                                AGTAACCGTTT    CAG GGGTTC
                                      AACCT  _
GAM788  DDX37   3' TCTTGGGAGGGTGGCCGCCAA  51026      AAAGTG
                                TTGGC     TCTCCCAAGA
                                |||||     ||||||||||
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                                AACCG     GGAGGGTTCT
                                   CCGGTG
GAM788  DKFZp761O0113 5'  CTTGGAAAACACTTTAACAGT  37277     GC      CTC
                                ATTG  AAAGTGT   CCAAG
                                ||||  |||||||   |||||
                                TGAC  TTTCACA   GGTTC
                                  AA      AAA
GAM788  FLJ10751  3'  TGGGAGACACTTGGCC      36733     A
                                GGC AAGTGTCTCCCA
                                ||| ||||||||||||
                                CCG TTCACAGAGGGT
                                  G
GAM788  FLJ10751  3'  TGGGAGACACTTGGCC      36572     A
                                GGC AAGTGTCTCCCA
                                ||| ||||||||||||
                                CCG TTCACAGAGGGT
                                  G
GAM788  FLJ20337  3'  AGTCTCTTTGCCAGTGA     34961          TGT
                                TCATTGGCAAAG   CT
                                ||||||||||||   ||
                                AGTGACCGTTTC   GA
                                       TCT
GAM788  FLJ22635  3'  TCTCAGGTGCAGCTTTGCCAA  46982         GTCT  CA
                                TTGGCAAAGT    CC  AGA
                                |||||||||    ||  |||
                                AACCGTTTCG    GG  TCT
                                      ACGT  AC
GAM788  HH114     5'  GGACCTGGCCAATGA       50689        AA  T
                                TCATTGGC  AG GTCT
                                ||||||||  || ||||
                                AGTAACCG  TC CAGG
                                     G_  _
GAM788  KIAA1579  3'  CTTGGGAGAACCACCAA     36610      CAAA  G
                                TTGG    GT TCTCCCAAG
                                ||||    || |||||||||
                                AACC    CA AGAGGGTTC
                                  AC__  _
GAM788  KIAA1821  3'  CTTGAGAATTTGCCAAT     71784         GTG   CC
                                ATTGGCAAA   TCTC  AAG
                                |||||||||   ||||  |||
                                TAACCGTTT   AGAG  TTC
                                     A__    __
GAM788  KIAA1855  3'  TGGAAGCCACTGTCAATGA   92349         AA   T  C
                                TCATTGGCA  GTG CT CCA
                                |||||||||  ||| || |||
                                AGTAACTGT  CAC GA GGT
                                      __   C  A
GAM788  MGC2776   3'  TCCTGAGAGGACACTTCCAA  47522      CA      _  C  A
                                TTGG  AAGTGTC TC CA GA
                                ||||  ||||||| || || ||
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                                AACC  TTCACAG AG GT CT
                                  __      G  A  C
GAM788  PRO2015   3'  GACATTTGCCAATGA       37559          G
                                TCATTGGCAAA TGTC
                                |||||||||||  ||||
                                AGTAACCGTTT ACAG
                                          _
GAM788  PYY       3'  TCCTGGGAGATCTGCCAA    14779       AAGT       A
                                TTGGCA    GTCTCCCA GA
                                ||||||    |||||||| ||
                                AACCGT    TAGAGGGT CT
                                   C___       C
GAM788  SCYD1     3'  AGACAGTCCCTGCCAATGG   90922         AAG__
                                TCATTGGCA     TGTCT
                                |||||||||     |||||
                                GGTAACCGT     ACAGA
                                      CCCTG
GAM788  TPD52     3'  TCTTGGGAAACACCCTTTAGTG 17427       CAAA    C
                                CATTGG    GTGT TCCCAAGA
                                ||||||    |||| ||||||||
                                GTGATT    CACA AGGGTTCT
                                   TCC_   A
GAM788  LOC139709 5'  GGCCTTTGGCCAATGA      75383         _   T
                                TCATTGGC AAAG GTC
                                ||||||||  |||| |||
                                AGTAACCG TTTC CGG
                                      G   _
GAM788  LOC145317 3'  CTTGAGAGACACAACCGA    83322      CAAA      C
                                TTGG    GTGTCTC CAAG
                                ||||    ||||||| ||||
                                AGCC    CACAGAG GTTC
                                  AA__      A
GAM788  LOC148089 3'  TGGTTCTGTGCCAATGA     78640         A  TGTCTC
                                TCATTGGCA AG     CCA
                                |||||||||  ||     |||
                                AGTAACCGT TC     GGT
                                      G  TT_____
GAM788  LOC157623 5'  CTTGGGAAACAAGCCAA     81497      AAAG   C
                                TTGGC    TGT TCCCAAG
                                |||||    ||| |||||||
                                AACCG    ACA AGGGTTC
                                   A___   A
GAM788  LOC200149 5'  TCTTGGGAGTACATTACAAT   89421      GCAAA   _
                                ATTG     GTGT CTCCCAAGA
                                ||||     |||| |||||||||
                                TAAC     TACA GAGGGTTCT
                                  AT___    T
GAM788  LOC200470 5'  TCTCGGGGAGGCACCTTGC    90070      A        A_
                                GCAA GTGTCTCCC  AGA
                                |||| |||||||||  |||
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                                CGTT CACGGAGGG  TCT
                                  C       GC
GAM788  LOC219654 3'  GACCTTGCCAGTGA       91305          A T
                                TCATTGGCAA G GTC
                                |||||||||| | |||
                                AGTGACCGTT C CAG
                                     _ _
GAM788  LOC90643  3'  CTGACTGGACACTTGCCAATGA 63689          A     CCCA
                                TCATTGGCAA GTGTCT   AG
                                |||||||||| ||||||   ||
                                AGTAACCGTT CACAGG   TC
                                      _     TCAG
GAM788  LOC93276  5'  CTCAGGAACAGCCAATGA    71890        AAAG  C   CA
                                TCATTGGC   TGT TCC  AG
                                ||||||||   ||| |||  ||
                                AGTAACCG   ACA AGG  TC
                                     _____  _  AC
GAM789  CD244     3'  GCAGCTGAGGGCTGAG      33061          AG
                                CTCAGCCCTCA  TGT
                                ||||||||||  |||
                                GAGTCGGGAGT  ACG
                                      CG
GAM789  CDH18     3'  CAGTACTTGGAACTGAGGA    17032        CC T     _
                                TCCTCAG  C CAAGTG TG
                                |||||||  | |||||| ||
                                AGGAGTC  G GTTCAT AC
                                    AA _     G
GAM789  DEFA4     3'  TAATTTGCTTTGAGAGCTACAG 8629       C_  C     T TG
          GA                      TCCT  AGC CTCAAG G  GATTA
                                ||||  ||| ||||||  |  |||||
                                AGGA  TCG GAGTTT C  TTAAT
                                  CA  A     _ GT
GAM789  DSPG3     3'  TAATCCATTAAAGAGCATGA   60183     GCC   AAGT
                                TCA   CTC    GTGGATTA
                                |||   |||    ||||||||
                                AGT   GAG    TACCTAAT
                                  AC_   AAAT
GAM789  FLRT2     5'  TAATAAAGCTTGAGGACCAGGA 25065      CAGC       GTGG
                                TCCT    CCTCAAGT    ATTA
                                ||||    ||||||||    ||||
                                AGGA    GGAGTTCG    TAAT
                                  CCA_       AAA_
GAM789  MARS      3'  ACCCTAGGAGCTGAGGA     94893         _   CA  T
                                TCCTCAGC CCT  AG GT
                                |||||||| |||  || ||
                                AGGAGTCG GGA  TC CA
                                    A   __  C
GAM789  POLG      5'  GCACCGTGAGGACCGAGGA   10679       AGC    A_
                                TCCTC   CCTCA  GTGT
                                |||||   |||||  ||||
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                                AGGAG  GGAGT  CACG
                                  CCA    GC
GAM789  SLC2A5   3' ATCCAGAAAGCTGAGGA    11723       CC  AAGTG
                                TCCTCAGC  TC    TGGAT
                                ||||||||  ||    |||||
                                AGGAGTCG  AG    ACCTA
                                    AA  _____
GAM789  SPK      5' TGCTCTTGAGGGACGAG    16686    AG      T
                                CTC  CCCTCAAG GTG
                                |||  |||||||| |||
                                GAG  GGGAGTTC CGT
                                  CA       T
GAM789  TMEPAI   3' AATCCACAGGCCTGAAGA   39438    C   C  CAAGT
                                TC TCAG CCT    GTGGATT
                                || |||| |||    |||||||
                                AG AGTC GGA    CACCTAA
                                 A   C  _____
GAM789  YWHAG    3' CACACCTGAGGGCTGA     25016        A
                                TCAGCCCTCA GTGTG
                                |||||||||| |||||
                                AGTCGGGAGT CACAC
                                      C
GAM789  DKFZp547A023 5' TATACTTGAGGACTGA     72617     C
                                TCAG CCTCAAGTGTG
                                |||| ||||||||||
                                AGTC GGAGTTCATAT
                                  A
GAM789  EPN2     3' TAATCCACGCTCAGGCT    30328     CTCA
                                AGCC   AGTGTGGATTA
                                ||||   ||||||||||
                                TCGG   TCGCACCTAAT
                                  AC__
GAM789  FLJ21736 3' CCACCCAAGGGCTGAGGA   46226         CAAGT
                                TCCTCAGCCCT    GTGG
                                ||||||||||    ||||
                                AGGAGTCGGGA    CACC
                                      ACC__
GAM789  FLJ21777 5' ACTTGAGGGCGAGGA     49861      A
                                TCCTC GCCCTCAAGT
                                ||||| |||||||||
                                AGGAG CGGGAGTTCA
                                  _
GAM789  GPS2     5' GCTGAGGGCTGAGGA      15666          A
                                TCCTCAGCCCTCA GT
                                |||||||||||| ||
                                AGGAGTCGGGAGT CG
                                     _
GAM789  KCNH4    3' CCACCTGAGGGCTGTGGA    24405    T      A T
                                TCC CAGCCCTCA G GTGG
                                ||| ||||||||| | ||||
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                                AGG GTCGGGAGT C CACC
                                  T       _ _
GAM789  KIAA0415 3' CCACCCAAGGGCTGAGGA    92575          CAAGT
                                TCCTCAGCCCT    GTGG
                                ||||||||||    ||||
                                AGGAGTCGGGA    CACC
                                      ACC__
GAM789  KIAA0438 3' TATACTTGAAGGCCCAG     29071    CA   C
                                CT  GCC TCAAGTGTG
                                ||  ||| |||||||||
                                GA  CGG AGTTCATAT
                                 CC   A
GAM789  KIAA0444 3' ACACTTGAGGCCCAAGGA    62334     CAGC
                                TCCT    CCTCAAGTGT
                                ||||    ||||||||||
                                AGGA    GGAGTTCACA
                                  ACCC
GAM789  KIAA0560 5' ACTCTGAAGGCTGAGGA     61501        C  _
                                TCCTCAGCC TCA AGT
                                ||||||||| ||| |||
                                AGGAGTCGG AGT TCA
                                     A   C
GAM789  KIAA0930 3' TAATCCCAGCTACTCGGAAGGC 70553       C  A_  _ __
           TGAGGA                CCTCAGCC TC  AGT GT  GGATTA
                                ||||||||  ||  ||| ||  ||||||
                                GGAGTCGG AG  TCA CG  CCTAAT
                                     A  GC   T  AC
GAM789  KIAA1915 3' AATTAGTTTGAGGGCTGAG   73270          TGTG
                                CTCAGCCCTCAAG    GATT
                                ||||||||||||    ||||
                                GAGTCGGGAGTTT    TTAA
                                      GA__
GAM789  KIAA1936 3' ATACAGAAAGCTGAGGA     73458        CC  AA
                                TCCTCAGC  TC  GTGT
                                ||||||||  ||  ||||
                                AGGAGTCG  AG  CATA
                                     AA  A_
GAM789  LRRFIP2  5' CATCACTAAGGGCTGA      34782        CA   _
                                TCAGCCCT  AGTG TG
                                ||||||||  ||||  ||
                                AGTCGGGA  TCAC AC
                                     A_    T
GAM789  LRRFIP2  5' CATCACTAAGGGCTGA      20872        CA   _
                                TCAGCCCT  AGTG TG
                                ||||||||  ||||  ||
                                AGTCGGGA  TCAC AC
                                     A_    T
GAM789  MGC1842  3' AATCCCCCAGGGCTGAGGA   65634          CAAGTGT
                                TCCTCAGCCCT      GGATT
                                ||||||||||       |||||
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                                AGGAGTCGGGA      CCTAA
                                      CCC____
GAM789  MGC32043  3'  GCTCCTTGAGGGCAAGGA    58051     CA       T_
                                TCCT  GCCCTCAAG  GT
                                ||||  |||||||||  ||
                                AGGA  CGGGAGTTC  CG
                                  A_        CT
GAM789  NUDT5     5'  TCACCTGAGGGCTG       26236         A T
                                CAGCCCTCA G GTGG
                                ||||||||| | ||||
                                GTCGGGAGT C CACT
                                     _ _
GAM789  LOC128272 3'  GTCCACACTTCAAGGCCAAGGA 74729      CA   CTC
                                TCCT  GCC   AAGTGTGGAT
                                ||||  |||   ||||||||||
                                AGGA  CGG   TTCACACCTG
                                  AC   AAC
GAM789  LOC148946 3'  ATTCTTGAGGGCAAGGA     84307      CA       T
                                TCCT  GCCCTCAAG GT
                                ||||  ||||||||| ||
                                AGGA  CGGGAGTTC TA
                                  A_        T
GAM789  LOC154789 3'  ACTCTTGAGGGGCGAGGA    81130       AG       T
                                TCCTC  CCCTCAAG GT
                                |||||  |||||||| ||
                                AGGAG  GGGAGTTC CA
                                   CG        T
GAM789  LOC157773 3'  CAGATTTGAGGACTAAG     81606    C  C       G
                                CT AG CCTCAAGT TG
                                || || |||||||| ||
                                GA TC GGAGTTTA AC
                                 A  A       G
GAM789  LOC158230 3'  TCTGTCCTTGAGCGCTGAGGA  81801         C     TG
                                TCCTCAGC CTCAAG  TGGA
                                |||||||| ||||||  ||||
                                AGGAGTCG GAGTTC  GTCT
                                     C      CT
GAM789  LOC161424 3'  CATACTTGAAGACTGAGG    87088       CCC
                                CCTCAG   TCAAGTGTG
                                ||||||   |||||||||
                                GGAGTC   AGTTCATAC
                                   AGA
GAM789  LOC221584 5'  TACACTTGGGGCCAAG      93830    CA    T
                                CT  GCCC CAAGTGTG
                                ||  |||| ||||||||
                                GA  CGGG GTTCACAT
                                 AC    _
GAM789  LOC51233  5'  AATTTCGCTGAAGGCTGAGG   33192         C   A   T
                                CCTCAGCC TCA GTG GGATT
                                |||||||| ||| ||| |||||
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                                GGAGTCGG AGT CGC TTTAA
                                    A  _  _
GAM790  CLCA2   3'  ACAGATGAAATCTCACT     21535       CAAAGC
                                AGTGAG     TTCATCTGT
                                ||||||     |||||||||
                                TCACTC     AAGTAGACA
                                   TA_____
GAM790  DMRT2   3'  ACAGATGGAAATTGCCCA    21613    A   AGC
                                TG GCAA   TTCATCTGT
                                || ||||   |||||||||
                                AC CGTT   AGGTAGACA
                                 C   AA_
GAM790  EIF1A   3'  ACAGATGAAGTCTCTCATT    88600       CAAA
                                AGTGAG   GCTTCATCTGT
                                ||||||   ||||||||||
                                TTACTC   TGAAGTAGACA
                                   TC__
GAM790  HEPH    5'  ACAGATGAAGTGGCCCA     28963    A  AAA
                                TG GC   GCTTCATCTGT
                                || ||   ||||||||||
                                AC CG   TGAAGTAGACA
                                 C  G__
GAM790  MYO1E   3'  ACAGCACCCTGCTTGCTCAC   17185        A  TTCAT_
                                GTGAGCAA GC     CTGT
                                |||||||| ||     ||||
                                CACTCGTT CG     GACA
                                    _  TCCCAC
GAM790  MYO1F   3'  AGCGTGACTTTGCTCATT    82422          CT   _
                                AGTGAGCAAAG  TCAT CT
                                ||||||||||  |||| ||
                                TTACTCGTTTC  AGTG GA
                                      __    C
GAM790  PCSK2   3'  TGAAGCTTCACTCACT      10469       CA
                                AGTGAG  AAGCTTCA
                                ||||||  ||||||||
                                TCACTC  TTCGAAGT
                                   AC
GAM790  PROX1   3'  ACAGATGAGCAGCTCACT    10892       AAA   T
                                AGTGAGC   GCT CATCTGT
                                |||||||   ||| |||||||
                                TCACTCG   CGA GTAGACA
                                   A__   _
GAM790  RGS5    3'  ACAGCAGCTTTGCTCA      13235          TCAT
                                TGAGCAAAGCT    CTGT
                                ||||||||||    ||||
                                ACTCGTTTCGA    GACA
                                      C___
GAM790  TEM1    3'  ACAGATGGCTTCCTGCTC    39876       __    TT
                                GAGCA  AAGC  CATCTGT
                                |||||  ||||  |||||||
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                                CTCGT  TTCG  GTAGACA
                                  CC   __
GAM790  TRAP1    3'  ACAGATGACAGCCCCAC     32822     AGCAAA  _
                                GTG     GCT TCATCTGT
                                |||     ||| ||||||||
                                CAC     CGA AGTAGACA
                                  CC_____  C
GAM790  XT3      3'  ACAGATGAAGCACCACT     39515     AGCAAA
                                AGTG     GCTTCATCTGT
                                ||||     ||||||||||
                                TCAC     CGAAGTAGACA
                                  CA____
GAM790  XT3      3'  ACAGATTCCTTTGCTCAC    39516         CTTC
                                GTGAGCAAAG    ATCTGT
                                ||||||||||    ||||||
                                CACTCGTTTC    TAGACA
                                      CT__
GAM790  BOP      3'  ACAAATGAATGAATTTGCTTAC 85049         GC__    C
           T                     AGTGAGCAAA    TTCAT TGT
                                ||||||||||    ||||| |||
                                TCATTCGTTT    AAGTA ACA
                                      AAGT    A
GAM790  DKFZP434L187 5'  ATGGATTTGCTCACT       68802         GC
                                AGTGAGCAAA  TTCAT
                                ||||||||||  |||||
                                TCACTCGTTT  AGGTA
                                          __
GAM790  FLJ10829  3'  ACAGATGAGGCTGC       36707     AA
                                GCA  GCTTCATCTGT
                                |||  ||||||||||
                                CGT  CGGAGTAGACA
                                  __
GAM790  FLJ11539  5'  ACAAATGAAGTTTTCTC     45372     C        C
                                GAG AAAGCTTCAT TGT
                                ||| ||||||||| |||
                                CTC TTTTGAAGTA ACA
                                  _        A
GAM790  FLJ13089  5'  ACAGATGACAACTCACT     70860       CAAAGCT
                                AGTGAG      TCATCTGT
                                ||||||      ||||||||
                                TCACTC      AGTAGACA
                                   AAC_____
GAM790  FLJ13110  3'  GAAGCTGTTTGCTCAT      43302        __
                                GTGAGCAA  AGCTTC
                                ||||||||  ||||||
                                TACTCGTT  TCGAAG
                                     TG
GAM790  FLJ21276  5'  ACAGGTGGCCCTCATCAC    44912      GCAA  CT
                                GTGA   AG  TCATCTGT
                                ||||   ||  ||||||||
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                                CACT    TC  GGTGGACA
                                  AC__  CC
GAM790  FLJ22555  5'  ACAGGTCCACTTTGCTC     44511        CTTC
                                GAGCAAAG    ATCTGT
                                ||||||||    ||||||
                                CTCGTTTC    TGGACA
                                    ACC_
GAM790  GRIN3A    3'  ACAGATGAAACAGTTCA     55965      AAAGC
                                TGAGC     TTCATCTGT
                                |||||     |||||||||
                                ACTTG     AAGTAGACA
                                  ACA__
GAM790  HSA243666 3'  GGTAAGCTTTGCTCAC      34147           C
                                GTGAGCAAAGCTT ATC
                                |||||||||||| |||
                                CACTCGTTTCGAA TGG
                                          _
GAM790  HSJ1      3'  ACAGATGAACTGCCTC      22122     CAA  C
                                GAG   AG TTCATCTGT
                                |||   || |||||||||
                                CTC   TC AAGTAGACA
                                  CG_  _
GAM790  KIAA0628  3'  ACAGATGAGCAACCCACT    28859     AGCAAA   T
                                AGTG     GCT CATCTGT
                                ||||     ||| |||||||
                                TCAC     CGA GTAGACA
                                  CCAA__   _
GAM790  KIAA0672  3'  TGCAGCTTTGCTCACT      29418           T
                                AGTGAGCAAAGCT CA
                                |||||||||||| ||
                                TCACTCGTTTCGA GT
                                        C
GAM790  KIAA1237  3'  ATGAGTTTGCTCAC        80464         GC
                                GTGAGCAAA  TTCAT
                                |||||||||  |||||
                                CACTCGTTT  GAGTA
                                          __
GAM790  KIAA1643  3'  AGGTCAGCTTTGCCCA      64545    A       TC
                                TG GCAAAGCT  ATCT
                                || ||||||||  ||||
                                AC CGTTTCGA  TGGA
                                  C       C_
GAM790  KIAA1981  3'  ACAGGTGGCTGTGCTCAC    88339       A   TT
                                GTGAGCA AGC  CATCTGT
                                ||||||| |||  |||||||
                                CACTCGT TCG  GTGGACA
                                    G   __
GAM790  KRTAP4-12 3'  ACAGATGAAGGCTCTCATT   49009       CAA  _
                                AGTGAG   AGC TTCATCTGT
                                ||||||   ||| |||||||||
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                                TTACTC   TCG AAGTAGACA
                                   ___   G
GAM790  KRTHB2   3'  ACAGATACCATTTGCTCA    52283        GCTTC
                                TGAGCAAA    ATCTGT
                                ||||||||    ||||||
                                ACTCGTTT    TAGACA
                                    ACCA_
GAM790  MGC10924 3'  ACAAATGAAGCTTAATTACT   47550      GCA       C
                                AGTGA   AAGCTTCAT TGT
                                |||||   ||||||||| |||
                                TCATT   TTCGAAGTA ACA
                                   AA_       A
GAM790  MGC2487  5'  ACAGATGAAGCAGGTGTCCAC  43735     AG  AA_
                                GTG  CA   GCTTCATCTGT
                                |||  ||   ||||||||||
                                CAC  GT   CGAAGTAGACA
                                  CT  GGA
GAM790  MGC33317 3'  ACAGATGAAGGCAGCGC     58843     A_  AAAG
                                GTG  GC    CTTCATCTGT
                                |||  ||    ||||||||||
                                CGC  CG    GAAGTAGACA
                                  GA  ____
GAM790  PAIP1    3'  ACAGTTAGCTTTCTCACT    66923       C     TCAT
                                AGTGAG AAAGCT    CTGT
                                |||||| ||||||    ||||
                                TCACTC TTTCGA    GACA
                                   _     TT__
GAM790  PCDH16   3'  GAAGCCCTGTTGCTCACT    13606        A___
                                AGTGAGCAA    GCTTC
                                |||||||||    |||||
                                TCACTCGTT    CGAAG
                                     GTCC
GAM790  POPX1    3'  ACAGGTTTCCTTTGTTCACT   29792          CTTC
                                AGTGAGCAAAG    ATCTGT
                                ||||||||||    ||||||
                                TCACTTGTTTC    TGGACA
                                     CTT_
GAM790  PPP1R3B  3'  ACAGACAAGCCTAGCTCTGCTC 44814        A    TCA____
           ACT                    AGTGAGCA AGCT      TCTGT
                                ||||||| ||||      |||||
                                TCACTCGT TCGA      AGACA
                                    C    TCCGAAC
GAM790  PSR      3'  CAGGTCTCTGCTCACT      65177        A  CTTC
                                AGTGAGCA AG    ATCTG
                                |||||||| ||    |||||
                                TCACTCGT TC    TGGAC
                                    C  ____
GAM790  RAI16    3'  ACAGTTGCTGGCTTTGCTCCT  42751     T        T_  T
                                AG GAGCAAAGCT  CA CTGT
                                || ||||||||||  || ||||
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                                TC CTCGTTTCGG  GT GACA
                                 _       TC  T
GAM790  TIX1     3'  ACAGCCTGAAGCTTTGACCACT 61735     AG       T_
                                AGTG  CAAAGCTTCA  CTGT
                                ||||  ||||||||||  ||||
                                TCAC  GTTTCGAAGT  GACA
                                  CA        CC
GAM790  UNC5D    3'  ACAGATTTGCTCTTGCTCAT   55130       _  TTC
                                GTGAGCAA AGC   ATCTGT
                                |||||||| |||   ||||||
                                TACTCGTT TCG   TAGACA
                                    C   TT_
GAM790  ZNF297B  3'  ACAGATGATGCGTGCTACT   81806    G   AA  T
                                AGT AGCA  GC TCATCTGT
                                ||| ||||  || ||||||||
                                TCA TCGT  CG AGTAGACA
                                  _   G_  T
GAM790  ZNF297B  3'  ACAGATGATGCGTGCTACT   25773    G   AA  T
                                AGT AGCA  GC TCATCTGT
                                ||| ||||  || ||||||||
                                TCA TCGT  CG AGTAGACA
                                  _   G_  T
GAM790  LOC127281 3'  ACAGCCCCCGCCTTGCTCACT  74642        A  TTCAT
                                AGTGAGCAA GC    CTGT
                                |||||||| ||    ||||
                                TCACTCGTT CG    GACA
                                    C  CCCCC
GAM790  LOC128439 3'  CAGATGACAGCTCTC      57349     CAA   _
                                GAG   AGCT TCATCTG
                                |||   |||| |||||||
                                CTC   TCGA AGTAGAC
                                  ____   C
GAM790  LOC146880 3'  ACAGATTGTGTACCTTGTTCAC 78155        A__  TTC
           T                     AGTGAGCAA   GC   ATCTGT
                                |||||||||   ||   ||||||
                                TCACTTGTT   TG   TAGACA
                                    CCA  TGT
GAM790  LOC148764 5'  ACAGATGGAGCCCCACCCAC   78980    AGCAAA
                                GTG     GCTTCATCTGT
                                |||     ||||||||||
                                CAC     CGAGGTAGACA
                                  CCACCC
GAM790  LOC148918 5'  CAGATGAGTGATCACT     79065      GCAAA   T
                                AGTGA    GCT CATCTG
                                |||||    ||| ||||||
                                TCACT    TGA GTAGAC
                                  AG___  _
GAM790  LOC151056 3'  ATGAAGCTCTGCTCCT     80107    T    A
                                AG GAGCA AGCTTCAT
                                || ||||| ||||||||
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                                TC CTCGT TCGAAGTA
                                 _    C
GAM790  LOC151195 3'  CAGATATTTGCTTACT      80166          GCTTC
                                AGTGAGCAAA    ATCTG
                                ||||||||||    |||||
                                TCATTCGTTT    TAGAC
                                      A____
GAM790  LOC151200 3'  ACAGATGAAGCTTCTCATT   85303       CA
                                AGTGAG  AAGCTTCATCTGT
                                ||||||  ||||||||||||
                                TTACTC  TTCGAAGTAGACA
                                  __
GAM790  LOC151647 3'  ACAGATGAAGAATGACTGAC  80328    G  _  AAG
                                GT AG CA   CTTCATCTGT
                                || || ||   ||||||||||
                                CA TC GT   GAAGTAGACA
                                 G  A  AA_
GAM790  LOC151720 5'  ACAGATGAAGAAACTGACT   80336     G  CAAAG
                                AGT AG     CTTCATCTGT
                                ||| ||     ||||||||||
                                TCA TC     GAAGTAGACA
                                  G  AAA__
GAM790  LOC152453 5'  ACAGGCAGAGGCTCTGCTCACT 80590         A      A_
                                AGTGAGCA AGCTTC  TCTGT
                                |||||||| ||||||  |||||
                                TCACTCGT TCGGAG  GGACA
                                     C      AC
GAM790  LOC152573 3'  ACAGGTGGAGCCCTGCTC    80617       AA
                                GAGCA  GCTTCATCTGT
                                |||||  ||||||||||
                                CTCGT  CGAGGTGGACA
                                   CC
GAM790  LOC153222 3'  ACAAATGAACAATGTTGCTTAC 80779         AGC__     C
                                GTGAGCAA     TTCAT TGT
                                ||||||||     ||||| |||
                                CATTCGTT     AAGTA ACA
                                     GTAAC     A
GAM790  LOC153525 5'  ACAAATGAAGCTTAATTACT   86043       GCA        C
                                AGTGA   AAGCTTCAT TGT
                                |||||   ||||||||| |||
                                TCATT   TTCGAAGTA ACA
                                   AA_        A
GAM790  LOC158308 3'  ACAGATGAAAGCTGCCCA    86739    A   AA    _
                                TG GCA  GCTT CATCTGT
                                || |||  |||| |||||||
                                AC CGT  CGAA GTAGACA
                                 C   __    A
GAM790  LOC162333 5'  GTGAACCTTTGCTCACT     87137           C
                                AGTGAGCAAAG TTCAT
                                ||||||||||| |||||
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                                TCACTCGTTTC AAGTG
                                      C
GAM790  LOC163231 5'  ACAGTGGGAACCTGCTCACT   82431        AAGC   T
                                AGTGAGCA   TTCA CTGT
                                ||||||||   |||| ||||
                                TCACTCGT   GGGT GACA
                                    CCAA   _
GAM790  LOC163426 5'  ACAGATGAAGATGAAGCCCAC  82138     A  AAAG_
                                GTG GC    CTTCATCTGT
                                ||| ||    ||||||||||
                                CAC CG    GAAGTAGACA
                                  C  AAGTA
GAM790  LOC200558 3'  ACAGATGAAGATTCTGACT    88825     G  CAAAG
                                AGT AG    CTTCATCTGT
                                ||| ||    ||||||||||
                                TCA TC    GAAGTAGACA
                                  G  TTA__
GAM790  LOC201294 3'  ACAGGTGGTCCCTGCCCAC    88195     A   AAGCT
                                GTG GCA    TCATCTGT
                                ||| |||    ||||||||
                                CAC CGT    GGTGGACA
                                  C   CCCT_
GAM790  LOC202908 5'  ACAGTGGCATAACCTCTGCTCA 89224         A  CT____   T
          CT                    AGTGAGCA AG     TCA CTGT
                                |||||||| ||     ||| ||||
                                TCACTCGT TC     GGT GACA
                                    C  CAATAC  _
GAM790  LOC202986 5'  ACAGATGAAGAAAGCCA     90439    A  AAAG
                                TG GC    CTTCATCTGT
                                || ||    ||||||||||
                                AC CG    GAAGTAGACA
                                 _  AAA_
GAM790  LOC219513 5'  ACATTGAGAGCTTTGCCCA    94323    A      _   TC
                                TG GCAAAGCT TCA  TGT
                                || |||||||| |||  |||
                                AC CGTTTCGA AGT  ACA
                                 C       G   T_
GAM790  LOC220776 3'  ACAGTCCTCTCTGTTCACT    68380        A  CTTCAT
                                AGTGAGCA AG     CTGT
                                |||||||| ||     ||||
                                TCACTTGT TC     GACA
                                    C  TCCT__
GAM790  LOC221061 3'  ACAGATGAAACTTTTTGC     93220       C__
                                GCAAAG   TTCATCTGT
                                ||||||   |||||||||
                                CGTTTT   AAGTAGACA
                                   TCA
GAM790  LOC253832 3'  ACAAATAAGTTTTGCTTAC    94918           C  C
                                GTGAGCAAAGCTT AT TGT
                                |||||||||||| || |||
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                                CATTCGTTTTGAA TA ACA
                                        _ A
GAM790  LOC254543 5'  ACAGATGAAACTGGAAAACT  97578    GAGCAA  C
                                AGT     AG TTCATCTGT
                                |||     || |||||||||
                                TCA     TC AAGTAGACA
                                  AAAGG_ A
GAM790  LOC255452 5'  ACAGATGAAGCGATGC     97521     AA
                                GCA  GCTTCATCTGT
                                |||  ||||||||||
                                CGT  CGAAGTAGACA
                                  AG
GAM790  LOC51219  3'  GGGTGGGGCCTCAC       33125      CAAA
                                GTGAG   GCTTCATCT
                                |||||   |||||||||
                                CACTC   CGGGGTGGG
                                  _____
GAM790  LOC89919  5'  ACAGATGATTGCCTTCTCACT  60711      C  A  T_
                                AGTGAG AA GC  TCATCTGT
                                ||||||| || ||  ||||||||
                                TCACTC TT CG  AGTAGACA
                                   _ C  TT
GAM790  LOC91397  5'  TGAACGCTGCTCACT      65915       AA  _
                                AGTGAGCA  GC TTCA
                                ||||||||  || ||||
                                TCACTCGT  CG AAGT
                                   __ C
GAM790  LOC92539  5'  ACATTGAATTTGCTCAC     69625       GC    TC
                                GTGAGCAAA  TTCA  TGT
                                |||||||||  ||||  |||
                                CACTCGTTT  AAGT  ACA
                                     __   T_
GAM791  GCLC      3'  ATAAATACCCATTGAA      7677       CA
                                TTCAA  GGTATTTAT
                                |||||  |||||||||
                                AAGTT  CCATAAATA
                                   AC
GAM791  GNPI      3'  TACTCCAGATAAGTGGGTG   18449    GG        A
                                CA  TATTTATCTG AGTA
                                ||  |||||||||| ||||
                                GT  GTGAATAGAC TCAT
                                  GG        C
GAM791  MKI67     3'  ATAAATACTTGCTGAA      10040      A
                                TTCA CAGGTATTTAT
                                |||| ||||||||||
                                AAGT GTTCATAAATA
                                  C
GAM791  MPV17     3'  ACTCCATAAATATCTGTTGAA  70508            TC  A
                                TTCAACAGGTATTTA  TG AGT
                                ||||||||||||||  || |||
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                                AAGTTGTCTATAAAT  AC TCA
                                        __  C
GAM791  PML      3'  ATAAACACTTGTTGAA      52660          A
                                TTCAACAGGT TTTAT
                                |||||||||| |||||
                                AAGTTGTTCA AAATA
                                      C
GAM791  PML      3'  ATAAACACTTGTTGAA      52665          A
                                TTCAACAGGT TTTAT
                                |||||||||| |||||
                                AAGTTGTTCA AAATA
                                      C
GAM791  PML      3'  ATAAACACTTGTTGAA      52671          A
                                TTCAACAGGT TTTAT
                                |||||||||| |||||
                                AAGTTGTTCA AAATA
                                      C
GAM791  PML      3'  ATAAACACTTGTTGAA      52676          A
                                TTCAACAGGT TTTAT
                                |||||||||| |||||
                                AAGTTGTTCA AAATA
                                      C
GAM791  POU3F2   3'  ACTGAGATAAATACCTG     18812            GA
                                CAGGTATTTATCT  AGT
                                ||||||||||||  |||
                                GTCCATAAATAGA  TCA
                                   G_
GAM791  PX19     3'  ACTCAATAAATACTTGTTGAA  25085             C   A
                                TTCAACAGGTATTTAT TGA GT
                                |||||||||||||||| ||| ||
                                AAGTTGTTCATAAATA ACT CA
                                        _  _
GAM791  SP3      3'  CTTTTAAATCCTGTTGAA    82498          T    TCT
                                TTCAACAGG ATTTA   GAAG
                                ||||||||| |||||   ||||
                                AAGTTGTCC TAAAT   TTTC
                                      _   ____
GAM791  FLJ14564 3'  ACCCCAGATGAGCCCTG     76498      TA       AA
                                CAGG  TTTATCTG  GT
                                ||||  ||||||||  ||
                                GTCC  GAGTAGAC  CA
                                  C_       CC
GAM791  FLJ30567 3'  ACTCAGTAAATAGCTGTTGAA  58823         G     T   A
                                TTCAACAG TATTTA CTGA GT
                                |||||||| |||||| |||| ||
                                AAGTTGTC ATAAAT GACT CA
                                     G     _   _
GAM791  GOA      3'  ATAAACACTTGTTGAA      78074          A
                                TTCAACAGGT TTTAT
                                |||||||||| |||||
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                                AAGTTGTTCA AAATA
                                      C
GAM791  HSPC054   3'  TACTTCAGATTTAACTTTGAA 26263      CA   ATTT
                                TTCAA  GGT   ATCTGAAGTA
                                |||||  |||   ||||||||||
                                AAGTT  TCA   TAGACTTCAT
                                   __  ATT_
GAM791  KIAA0240  3'  TGGATAAATACTGTT      92441      G
                                AACAG TATTTATCTG
                                ||||| ||||||||||
                                TTGTC ATAAATAGGT
                                   _
GAM791  KIAA0298  3'  CAGAAATACCTGTT       76576          TA
                                AACAGGTATT  TCTG
                                ||||||||||  ||||
                                TTGTCCATAA  AGAC
                                      __
GAM791  KIAA0682  3'  TACCTCAGATAGACAGTGCC   32477       ___      A
                                GGTATT   TATCTGA GTA
                                ||||||   ||||||| |||
                                CCGTGA   ATAGACT CAT
                                    CAG      C
GAM791  KIAA1473  3'  ACTTCAGACTTTACACTG    70662    _   TTTA
                                CAG GTA    TCTGAAGT
                                ||| |||    ||||||||
                                GTC CAT    AGACTTCA
                                  A   TTC_
GAM791  MOST2     5'  TACTTCAGCAGGTCACCTGTGA 39691      A    _    AT
           A                     TTCA CAGGT ATTT  CTGAAGTA
                                ||||| ||||| ||||  ||||||||
                                AAGT GTCCA TGGA  GACTTCAT
                                   _    C    C_
GAM791  NR1H4     3'  TACTTCAATTCTATCTGTTGAA 17607          TTT  C
                                TTCAACAGGTA   AT TGAAGTA
                                ||||||||||   || |||||||
                                AAGTTGTCTAT   TA ACTTCAT
                                      CT_ _
GAM791  LOC148198 3'  ACTTCAGACTTTACACTG    70674    _   TTTA
                                CAG GTA    TCTGAAGT
                                ||| |||    ||||||||
                                GTC CAT    AGACTTCA
                                  A   TTC_
GAM791  LOC197125 3'  ACTCAGTAAATACTTGTTGAA  87896            T    A
                                TTCAACAGGTATTTA CTGA GT
                                |||||||||||||| |||| ||
                                AAGTTGTTCATAAAT GACT CA
                                      _   _
GAM791  LOC257273 5'  ACTTCAGACAAACTGT      95574      GTA   A
                                ACAG   TTT TCTGAAGT
                                ||||   ||| ||||||||
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                                TGTC   AAA AGACTTCA
                                  ___  C
GAM791  LOC257471 3'  CTTTTAAATCCTGTTGAA    95689        T    TCT
                                TTCAACAGG ATTTA   GAAG
                                ||||||||| |||||   ||||
                                AAGTTGTCC TAAAT   TTTC
                                    _    ____
GAM792  ABCA3    3'  TCCTGGAGGCTCTGCTCCCTT  6565     A_      AAGT_
                                AAG  AGCAGAGC    GGA
                                |||  ||||||||    |||
                                TTC  TCGTCTCG    CCT
                                  CC       GAGGT
GAM792  AKAP2    3'  TTTACTTGCCTCTTC      23273     C  A
                                GAAG AG GCAAGTGGA
                                |||| || |||||||||
                                CTTC TC CGTTCATTT
                                  _ _
GAM792  ARF3     3'  ATTTGCTCTGTTTCCTCA    7997     A
                                TGA GAAGCAGAGCAAGT
                                ||| ||||||||||||||
                                ACT CTTTGTCTCGTTTA
                                  C
GAM792  ARRB2    3'  CTGCAGCTCTGCTTCTCCA   60978    A        AA TG
                                TG AGAAGCAGAGC  G  G
                                || ||||||||||  |  |
                                AC TCTTCGTCTCG  C  C
                                 C         A_ GT
GAM792  ATF5     5'  CCACCTTCTTTCTTCA     23806       GC    CAA
                                TGAAGAA  AGAG   GTGG
                                |||||||  ||||   ||||
                                ACTTCTT  TCTT   CACC
                                    __    C__
GAM792  ATP8B2   3'  CCTCTCTGCTCCCTTCTTCA  65222        CA    _  T
                                TGAAGAAG  GAGCA AG GG
                                ||||||||  ||||| || ||
                                ACTTCTTC  CTCGT TC CC
                                     C_    C  T
GAM792  ATP8B2   3'  TCCTGTCTGCTTCCTCA    65240    A      G  AGT
                                TGA GAAGCAGA CA   GGA
                                ||| ||||||| ||   |||
                                ACT CTTCGTCT GT   CCT
                                  C       _ ____
GAM792  BACH1    3'  TCCTTGCTCTCTTCTCCA    6803    A    C      T
                                TG AGAAG AGAGCAAG GG
                                || ||||| |||||||| ||
                                AC TCTTC TCTCGTTC CT
                                 C    _       _
GAM792  BCL9     3'  TTTGCTCTGTCTCCTCA     15072    A  AG
                                TGA GA  CAGAGCAAG
                                ||| ||  |||||||||
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                                ACT CT  GTCTCGTTT
                                  C  CT
GAM792  CARPX    5'  GCTCCCTCCTCTTCTTCA    39423        CA   CA
                                TGAAGAAG  GAG  AGT
                                ||||||||  |||  |||
                                ACTTCTTC  CTC  TCG
                                     TC   CC
GAM792  CD81     3'  CCAGGGTGCTCTGCCTGCTCA  15134     A AA_      AG_
                                TGA G   GCAGAGCA   TGG
                                ||| |   ||||||||   |||
                                ACT C   CGTCTCGT   ACC
                                  _ GTC       GGG
GAM792  CD83     3'  CCACTGCTGCTTCTCCA     14883    A      GA   A
                                TG AGAAGCA  GCA GTGG
                                || |||||||  ||| ||||
                                AC TCTTCGT  CGT CACC
                                 C      __   _
GAM792  CLDN14   3'  CCACAGCCTGCTTCT      24032        A  AA
                                AGAAGCAG GC  GTGG
                                |||||||| ||  ||||
                                TCTTCGTC CG  CACC
                                     _  A_
GAM792  CLDN14   3'  CCACAGCCTGCTTCT      57838        A  AA
                                AGAAGCAG GC  GTGG
                                |||||||| ||  ||||
                                TCTTCGTC CG  CACC
                                     _  A_
GAM792  COL16A1  5'  CCTGGGCTCTGCTTCCTC    8498     A        AAGT
                                GA GAAGCAGAGC    GG
                                || ||||||||||    ||
                                CT CTTCGTCTCG    CC
                                 C         GGT_
GAM792  CPSF6    3'  TTTCCACTGCTGTTCTTCA    22805       GCAG    A
                                TGAAGAA    AGCA GTGGAAA
                                |||||||    |||| |||||||
                                ACTTCTT    TCGT CACCTTT
                                     G___    _
GAM792  CSHL1    3'  TCCTTCTGCTTCTCA      7166      A       CAAGT
                                TGA GAAGCAGAG     GGA
                                ||| |||||||||     |||
                                ACT CTTCGTCTT     CCT
                                  _       _____
GAM792  CSRP1    3'  TCCTAGGAGCCCCTGCTTCTCC 14537    A       A_  AAGT_
           A                     TG AGAAGCAG  GC     GGA
                                || ||||||||  ||     |||
                                AC TCTTCGTC  CG     CCT
                                 C       CC  AGGAT
GAM792  CYLN2    3'  CCACCTTCTGAACCTTCTTCA  12630         ___     CAA
                                TGAAGAAG   CAGAG   GTGG
                                ||||||||   |||||   ||||
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                                ACTTCTTC  GTCTT  CACC
                                     CAA    C__
GAM792  DAZ     3'  GCTTACTCTGCTTATCCA   82115   AAG      C
                                TG  AAGCAGAG AAGT
                                ||  |||||||| ||||
                                AC  TTCGTCTC TTCG
                                 CTA       A
GAM792  DLST    3'  TGCTGCTTTGCTTCTTCA   8648            A
                                TGAAGAAGCAGAGCA GTG
                                |||||||||||||| |||
                                ACTTCTTCGTTTCGT CGT
                                                _
GAM792  DPP6    5'  CTGCTGCTGCTGCCTCCCCA  55448   AA  A   _   A TG
                                TG  GA GCAG AGCA G  G
                                ||  || |||| |||| |  |
                                AC  CT CGTC TCGT C  C
                                 CC  C    G   _ GT
GAM792  EHD3    3'  TCCCTGCTCTGCCTC      27482   A      A T
                                GA GCAGAGCA G GGA
                                || |||||||| | |||
                                CT CGTCTCGT C CCT
                                 C      _ _
GAM792  ELK1    3'  TCCACTGTTTGTTTTACTTCCC 17845   AA   C    ___
          CA                     TG  GAAG AGAGCA  AGTGGA
                                ||  |||| ||||||  ||||||
                                AC  CTTC TTTTGT  TCACCT
                                 CC   A    TTG
GAM792  ERBB3   3'  CCATTCCTCAGCTTCTTCA   8796         A  CA
                                TGAAGAAGC GAG  AGTGG
                                |||||||| |||  |||||
                                ACTTCTTCG CTC  TTACC
                                     A  C_
GAM792  FBN1    3'  TTTGTAAACTTTGCTTCTCCA  64403   A       CAA TG
                                TG AGAAGCAGAG  G  GA
                                || ||||||||||  |  ||
                                AC TCTTCGTTTC  T  TT
                                 C        AAA GT
GAM792  FCN2    3'  CCTATGGCCCTGCTTCTTC   31737         A  AAGT
                                GAAGAAGCAG GC   GG
                                |||||||||| ||   ||
                                CTTCTTCGTC CG   CC
                                      C  GTAT
GAM792  FOXE3   3'  TCCACTTACCTGTCTGCCCTC  24106   A_   G ____
                                GA  GCAGA CA   AGTGGA
                                ||  ||||| ||   ||||||
                                CT  CGTCT GT   TCACCT
                                 CC    _ CCAT
GAM792  GFPT2   3'  CCACATCCCTCCACTTCTCCA  17575   A   CA  CAA_
                                TG AGAAG  GAG   GTGG
                                || |||||  |||   ||||
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                                AC TCTTC  CTC    CACC
                                 C    AC   CCTA
GAM792  GYG2     3'  TTTCCACTCAGCTCTTTC    14052     GC    A_
                                GAA  AGAGC  AGTGGAAA
                                |||  |||||  ||||||||
                                CTT  TCTCG  TCACCTTT
                                  __     AC
GAM792  IHH      3'  GTTTTCATACTCTGCCTC    72115    A     CAA
                                GA GCAGAG   GTGGAAAC
                                || ||||||   ||||||||
                                CT CGTCTC   TACTTTTG
                                 C     A__
GAM792  IKBKB    3'  CCATAACCCTGCTTCTTCA   63204          AGCAA
                                TGAAGAAGCAG    GTGG
                                ||||||||||     ||||
                                ACTTCTTCGTC    TACC
                                       CCAA_
GAM792  IL1RAP   3'  ACTATTCTGCTTCCTCA     9307      A       CA
                                TGA GAAGCAGAG  AGT
                                ||| |||||||||  |||
                                ACT CTTCGTCTT  TCA
                                  C        A_
GAM792  LDHB     5'  GTTTCTGTGCCTCTGACCCCTC 9717      AGAAG    CAA TG
            A                    TGA    CAGAG   G  GAAAC
                                |||    |||||   |  |||||
                                ACT    GTCTC   T  CTTTG
                                  CCCCA    CG_ GT
GAM792  MADH7    5'  TCGGCGCCCGACTTCTTCA   19746        CAGA  AA  G
                                TGAAGAAG    GC  GT GA
                                ||||||||    ||  || ||
                                ACTTCTTC    CG  CG CT
                                     AGCC  __  G
GAM792  MAP2K2   3'  TCTCAGAGGCTCTGCTTCCTTA 47694     A        AAG  _
                                TGA GAAGCAGAGC   TG GA
                                ||| ||||||||||   || ||
                                ATT CTTCGTCTCG   AC CT
                                  C         GAG  T
GAM792  MCM2     3'  TCCCTGTCTGTTTCCCCA    67930    AA       G  A T
                                TG  GAAGCAGA CA G GGA
                                ||  |||||||| || | |||
                                AC  CTTTGTCT GT C CCT
                                 CC       _  _ _
GAM792  MGAT4B   5'  TTTCCACTTCAGATGCCTTCTC 53952     A   _  GAGC
            A                    TGA GAAG CA    AAGTGGAAA
                                ||| |||| ||    |||||||||
                                ACT CTTC GT    TTCACCTTT
                                  _    C  AGAC
GAM792  MKI67    3'  TCCACGTTTGTTTCCCCA    10051    AA       GCAA
                                TG  GAAGCAGA    GTGGA
                                ||  ||||||||    |||||
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                                AC  CTTTGTTT   CACCT
                                 CC      G___
GAM792  MPP3    5'  TTCCACGCCGCTGTTTCTTCA  8639          AGCAA
                                TGAAGAAGCAG    GTGGAA
                                ||||||||||    ||||||
                                ACTTCTTTGTC    CACCTT
                                      GCCG_
GAM792  MSF     3'  TTTCATCAGGCTCTGTTCCTCA 88088    A  G    AA_
                                TGA GAA CAGAGC  GTGGAA
                                ||| ||| ||||||  ||||||
                                ACT CTT GTCTCG  TACTTT
                                  C  _    GAC
GAM792  NHLH1   3'  TCTCACTTCTGCTTCCTCA   18805    A     GCA   _
                                TGA GAAGCAGA  AGTG GA
                                ||| ||||||||  |||| ||
                                ACT CTTCGTCT  TCAC CT
                                  C       ___   T
GAM792  NPC2    3'  TCCAGCTCTGCTGCTTCA    21224      A      AAG
                                TGAAG AGCAGAGC  TGGA
                                |||||| ||||||||  ||||
                                ACTTC TCGTCTCG  ACCT
                                   G      ___
GAM792  NPY1R   5'  CCACCCTTCCTTCTTTA     6178         CA  CAA
                                TGAAGAAG  GAG  GTGG
                                ||||||||  |||  ||||
                                ATTTCTTC  TTC  CACC
                                     C_  C__
GAM792  OGG1    5'  TCTCCTAGCTCCCTGCTTTTTC 10333         __   A  TG
          A                      TGAAGAAGCA  GAGC AG  GA
                                ||||||||||  |||| ||  ||
                                ACTTTTTCGT  CTCG TC  CT
                                      CC    A  CT
GAM792  OGG1    5'  TCTCCTAGCTCCCTGCTTTTTC 33663         __   A  TG
          A                      TGAAGAAGCA  GAGC AG  GA
                                ||||||||||  |||| ||  ||
                                ACTTTTTCGT  CTCG TC  CT
                                      CC    A  CT
GAM792  OGG1    5'  TCTCCTAGCTCCCTGCTTTTTC 33669         __   A  TG
          A                      TGAAGAAGCA  GAGC AG  GA
                                ||||||||||  |||| ||  ||
                                ACTTTTTCGT  CTCG TC  CT
                                      CC    A  CT
GAM792  PLAT    3'  CCGCCTCTTCTTCTTCA    52235        C   CAA
                                TGAAGAAG AGAG  GTGG
                                |||||||| ||||  ||||
                                ACTTCTTC TCTC  CGCC
                                     T   ___
GAM792  PLAT    3'  CCGCCTCTTCTTCTTCA    6252         C   CAA
                                TGAAGAAG AGAG  GTGG
                                |||||||| ||||  ||||
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                                ACTTCTTC TCTC   CGCC
                                     T   ____
GAM792  PRX      3'  CCAAGTTCCGCTTCCCCA    40523    AA    A   AAG
                                TG  GAAGC GAGC   TGG
                                ||  ||||| ||||   |||
                                AC  CTTCG CTTG   ACC
                                 CC    C   A__
GAM792  PTPRCAP  3'  TCCCCGTGCCTCTGCTTC    18818        _  AGT
                                GAAGCAGAG CA   GGA
                                ||||||||| ||   |||
                                CTTCGTCTC GT   CCT
                                     C  GCC
GAM792  SDC1     3'  CCACTTGCCTCTTC       11470     C  A
                                GAAG AG GCAAGTGG
                                |||| || ||||||||
                                CTTC TC CGTTCACC
                                  _ _
GAM792  SFRP5    3'  TTCCTCAGCCTCTGCTTCT   11583         CAAGT
                                AGAAGCAGAG    GGAA
                                ||||||||||    ||||
                                TCTTCGTCTC    CCTT
                                     CGACT
GAM792  SMURF1   3'  TCCGTCTCTGCTTTTCCA    92460    A       CAAG
                                TG AGAAGCAGAG   TGGA
                                || ||||||||||   ||||
                                AC TTTTCGTCTC   GCCT
                                 C        T___
GAM792  SORCS2   3'  TCCCTGACTTTGCTTCTTCA   40421          CA  T
                                TGAAGAAGCAGAG  AG GGA
                                ||||||||||||  || |||
                                ACTTCTTCGTTTC  TC CCT
                                       AG  _
GAM792  STK13    3'  TCTCCTGCTCTGCCACCTCA   12036     AGAA      A TG
                                TGA   GCAGAGCA G  GA
                                |||   |||||||| |  ||
                                ACT   CGTCTCGT C  CT
                                  CCAC       _ CT
GAM792  TBL1X    3'  TCTGGTGAGCTCTGCTTTTTCA 18937           AAGT_
                                TGAAGAAGCAGAGC    GGA
                                ||||||||||||||    |||
                                ACTTTTTCGTCTCG    TCT
                                       AGTGG
GAM792  TIMP3    3'  CCACCCCTCTTGCTTCTTC   4504         _  CAA
                                GAAGAAGCA GAG   GTGG
                                ||||||||| |||   ||||
                                CTTCTTCGT CTC   CACC
                                     T  CC_
GAM792  TLL2     3'  TTCCGGCTATGCTTCTTCA   24968         G  AAG
                                TGAAGAAGCA AGC   TGGAA
                                |||||||||| |||   |||||
```

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                                ACTTCTTCGT TCG   GCCTT
                                      A  ___
GAM792  TLR6    3'  TCCTCTCCACTCTGCTTTCCCA 20270    AA       CA_  T
                                TG  GAAGCAGAG   AG GGA
                                ||  |||||||||   || |||
                                AC  TTTCGTCTC   TC CCT
                                 CC        ACC  T
GAM792  UBE2A   5'  TCCCCTTCTCCTGCTTCTCCA  12469    A      _  C   T
                                TG AGAAGCAG AG AAG GGA
                                || |||||||| || ||| |||
                                AC TCTTCGTC TC TTC CCT
                                 C       C  _   C
GAM792  WBP2    3'  CCAGCCTGCTTCTTC       73027          A  AAG
                                GAAGAAGCAG GC   TGG
                                |||||||||| ||   |||
                                CTTCTTCGTC CG   ACC

                                      _  ___
GAM792  Z39IG   3'  TTCAGTTCTGCTCCTCCA    23437    A  A      AAG
                                TG AG AGCAGAGC   TGGA
                                || || ||||||||   ||||
                                AC TC TCGTCTTG   ACTT
                                 C  C      ___
GAM792  AMOTL2  3'  CCAGAAGACTCTGCTTCTT   32481          CAAG_
                                AAGAAGCAGAG    TGG
                                ||||||||||     |||
                                TTCTTCGTCTC    ACC
                                      AGAAG
GAM792  APCL    3'  TCCCTGCCTCTGTTTCCCCA  19686    AA       CA  T
                                TG  GAAGCAGAG  AG GGA
                                ||  |||||||||  || |||
                                AC  CTTTGTCTC  TC CCT
                                 CC        CG  _
GAM792  B3GNT7  3'  CCACCGCACCCTGCTTCTCCA  71125    A       A__  AA
                                TG AGAAGCAG   GC  GTGG
                                || ||||||||   ||  ||||
                                AC TCTTCGTC   CG  CACC
                                 C       CCA  C_
GAM792  C6orf5  5'  TTCCACTTCCTGCTTC      31367        AGC
                                GAAGCAG   AAGTGGAA
                                |||||||   ||||||||
                                CTTCGTC   TTCACCTT
                                    C__
GAM792  CAMKK2  3'  TTCCCAGCTCTGCTTT      21590          AAGT
                                GAAGCAGAGC    GGAA
                                ||||||||||    ||||
                                TTTCGTCTCG    CCTT
                                      AC__
GAM792  CUL2    5'  CCCTTGCCCTGCTTCTGCA   13168    A       A    T
                                TG AGAAGCAG GCAAG GG
                                || |||||||| ||||| ||
```

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                                AC TCTTCGTC CGTTC CC
                                 G       C    _
GAM792  DKFZP434N178 5'  CCTCTCTGCCCTGCTTCTCG  71903     A      A  _  T
                                TGA GAAGCAG GCA AG GG
                                ||| ||||||| ||| || ||
                                GCT CTTCGTC CGT TC CC
                                  _      C  C  T
GAM792  DKFZp547I094 5'  CCTGTTGCCCTGCCTTCTTCA  49638         _  A   GT
                                TGAAGAAG CAG GCAA  GG
                                |||||||| ||| ||||  ||
                                ACTTCTTC GTC CGTT  CC
                                     C  C   GT
GAM792  DKFZP761G1913 3'  TTCCTCTCTGCTTCTCA     48919     A        CAAGT
                                TGA GAAGCAGAG     GGAA
                                ||| |||||||||     ||||
                                ACT CTTCGTCTC     CCTT
                                  _       T_____
GAM792  DKFZP761I2123 3'  TCCCTGCGCGCTCTGCTCCTTC 48769      A       AA __
                                GAAG AGCAGAGC  GT  GGA
                                |||| ||||||||  ||  |||
                                CTTC TCGTCTCG  CG  CCT
                                  C       CG  TC
GAM792  DKFZp762P2111 3'  TCCAGGCCTGCTTTTCA     86364       A    A  AAG
                                TGAAGA GCAG GC   TGGA
                                |||||| |||| ||   ||||
                                ACTTTT CGTC CG   ACCT
                                   _   _  G__
GAM792  ESPL1    5'  TTCCTCACTTTGCTTCTCCA   24463     A        CAAGT
                                TG AGAAGCAGAG     GGAA
                                || ||||||||||     ||||
                                AC TCTTCGTTTC     CCTT
                                 C         ACT__
GAM792  EZFIT    3'  TCCACATCTCTGTTTCTTCA   41113            CAA
                                TGAAGAAGCAGAG   GTGGA
                                ||||||||||||   |||||
                                ACTTCTTTGTCTC   CACCT
                                        TA_
GAM792  FBH1     3'  TCCACTTGCCTCCCCTCT    51452     A CA  _
                                AGA G  GAG CAAGTGGA
                                ||| |  ||| ||||||||
                                TCT C  CTC GTTCACCT
                                  _ CC   C
GAM792  FHR-3    3'  TTCCACTTTTCCACTTCTCA   40706     A   CA   C
                                TGA GAAG  GAG AAGTGGAA
                                ||| ||||  ||| ||||||||
                                ACT CTTC  CTT TTCACCTT
                                  _    AC   _
GAM792  FLJ10583  3'  TCCTCTCGCCTCTGCTTCCCCA 36310     AA        _ A  T
                                TG  GAAGCAGAG C AG GGA
                                ||  ||||||||| | || |||
```

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                                AC  CTTCGTCTC G TC CCT
                                 CC       C C  T
GAM792  FLJ11151  3'  GCTCTAAAACGCCGCTTCTTCA 67878        _________
                                TGAAGAAGC       AGAGC
                                |||||||||       |||||
                                ACTTCTTCG       TCTCG
                                     CCGCAAAA
GAM792  FLJ12221  3'  TCTTTCTGCTTCGCCCCTTCA  62555      AA  AG   AGT
                                TGAAG  GC  AGCA   GGA
                                |||||  ||  ||||   |||
                                ACTTC  CG  TCGT   TCT
                                   CC  CT    CTT
GAM792  FLJ12644  3'  TTCCACTTGGTGTTCCTCA   43558     A   G  GAG
                                TGA GAA CA   CAAGTGGAA
                                ||| ||| ||   |||||||||
                                ACT CTT GT   GTTCACCTT
                                  C   _ G__
GAM792  FLJ12704  3'  TCCTATGAAACTTGCTTCTCCA 46535    A       AG__  AGT
                                TG AGAAGCAG    CA   GGA
                                || ||||||||    ||   |||
                                AC TCTTCGTT    GT   CCT
                                 C       CAAA  AT_
GAM792  FLJ12783  3'  ACCTGACTCTGCTTCTCTCA   48673     _        _ A
                                TGA AGAAGCAGAG CA GT
                                ||| |||||||||| || ||
                                ACT TCTTCGTCTC GT CA
                                  C         A  C
GAM792  FLJ12788  3'  TTGGCCACTCTGTTTCTCCA   42551    A        CAA  G
                                TG AGAAGCAGAG   GT GA
                                || ||||||||||   || ||
                                AC TCTTTGTCTC   CG TT
                                 C         AC_  G
GAM792  FLJ12921  3'  CCACCCCCCACTCTGCTTTCCC 45907    AA       CAA___
          A                      TG  GAAGCAGAG     GTGG
                                ||  |||||||||     ||||
                                AC  TTTCGTCTC     CACC
                                 CC        ACCCCC
GAM792  FLJ13491  3'  GTTCCCATTCTGCTTCTGCCA  44888    A_       GCAA   A
                                TG  AGAAGCAGA    GTGG AAC
                                ||  |||||||||    |||| |||
                                AC  TCTTCGTCT    TACC TTG
                                 CG        _____    C
GAM792  FLJ13840  5'  TTACTGCTCTGCCTTC      45367      AA       A
                                GAAG  GCAGAGCA GTGG
                                ||||  |||||||| ||||
                                CTTC  CGTCTCGT CATT
                                   __       _
GAM792  FLJ14566  5'  TTCAAGTGGCTCTGCTACTCCA 51450    A  A       AAG_
                                TG AG AGCAGAGC    TGGA
                                || || ||||||||    ||||
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```
                                AC TC TCGTCTCG    ACTT
                                 C  A       GTGA
GAM792  FLJ20208  3'  GTTTCATCTTGCTCTATTCCTC 34747     A   GC       TG
             A                   TGA GAA  AGAGCAAG  GAAAC
                                 ||| |||  ||||||||  |||||
                                 ACT CTT  TCTCGTTC  CTTTG
                                   C   A_       TA
GAM792  FLJ20294  5'  TTACTTGCTCCTTC       34886      CA
                                 GAAG  GAGCAAGTGG
                                 ||||  ||||||||||
                                 CTTC  CTCGTTCATT
                                    __
GAM792  FLJ20950  3'  TCCTTCACTCTGGCTTCTTCA  46351          _    CAAGT
                                 TGAAGAAGC AGAG     GGA
                                 |||||||||| ||||     |||
                                 ACTTCTTCG TCTC     CCT
                                       G    ACTT_
GAM792  FLJ22471  3'  TTCTCTTGCCCTCTTCTTCA  47113         C  A     T
                                 TGAAGAAG AG GCAAG GGAA
                                 |||||||| || ||||| ||||
                                 ACTTCTTC TC CGTTC TCTT
                                      _  C     _
GAM792  FLJ22671  3'  TCCCATCTGCTTCTTC      45868           GCAAGT
                                 GAAGAAGCAGA      GGA
                                 ||||||||||      |||
                                 CTTCTTCGTCT      CCT
                                       AC_____
GAM792  FLJ23112  3'  CCTCTGCTCTGCCTTC      46247      AA       A T
                                 GAAG  GCAGAGCA G GG
                                 ||||  |||||||| | ||
                                 CTTC  CGTCTCGT C CC
                                    __       _ T
GAM792  GMPPB     3'  CCTTCTGCTCTGCCCCTGCA  95729    A  AA       AGT
                                 TG AG  GCAGAGCA   GG
                                 || ||  ||||||||   ||
                                 AC TC  CGTCTCGT   CC
                                  G  CC       CTT
GAM792  HSA9761   3'  CCTTTAGCTCTGTTCCTCCA   27125    A  A      A  T
                                 TG AG AGCAGAGC AG GG
                                 || || |||||||| || ||
                                 AC TC TTGTCTCG TT CC
                                  C  C       A  T
GAM792  HSPC063   3'  TCTGAATCCTGCTTCTCCA    26274    A       AGCAAG
                                 TG AGAAGCAG      TGGA
                                 || ||||||||      ||||
                                 AC TCTTCGTC      GTCT
                                  C       CTAA__
GAM792  ITPK1     3'  TCCCTGACCTGCCCCTTC     26414      AA    AG  A T
                                 GAAG  GCAG  CA G GGA
                                 ||||  ||||  || | |||
```

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                                CTTC  CGTC  GT C CCT
                                  CC    CA  _ _
GAM792  JM11     3'  TCTGACACCCTGCTTCTTC   53272          AGCAAG
                                GAAGAAGCAG     TGGA
                                ||||||||||     ||||
                                CTTCTTCGTC     GTCT
                                      CCACA_
GAM792  KIAA0040 3'  GTTTCTGTGCCTCTGACCCCTC 27789     AGAAG    CAA TG
            A                    TGA    CAGAG   G  GAAAC
                                |||    |||||  |  |||||
                                ACT    GTCTC   T  CTTTG
                                  CCCCA    CG_ GT
GAM792  KIAA0057 3'  GCTTAGGCTCTGCTTC      24435          __
                                GAAGCAGAGC  AAGT
                                ||||||||||  ||||
                                CTTCGTCTCG  TTCG
                                      GA
GAM792  KIAA0247 3'  CCCTGCCCTGGCTTCTTCA   28394          _  A   A T
                                TGAAGAAGC AG GCA G GG
                                |||||||||  ||  |||  |  ||
                                ACTTCTTCG TC CGT C CC
                                      G  C   _ _
GAM792  KIAA0337 3'  CCCCCTCGCTTCTTCA      28831          A   CAAGT
                                TGAAGAAGC GAG     GG
                                |||||||||  |||     ||
                                ACTTCTTCG CTC     CC
                                      _   CC___
GAM792  KIAA0774 5'  CCAAACAGGGCTCTGCTTCCTT 91751     A         AAG___
            A                    TGA GAAGCAGAGC     TGG
                                |||  ||||||||||      |||
                                ATT CTTCGTCTCG      ACC
                                  C         GGACAA
GAM792  KIAA0802 3'  TCCCTAGAGCCCTGCTTCTCCA 62567    A       A  A__  T
                                TG AGAAGCAG GC   AG GGA
                                ||  ||||||||  ||   ||  |||
                                AC TCTTCGTC CG   TC CCT
                                 C       C  AGA  _
GAM792  KIAA0825 3'  GTTTCCACTTTGGTTTTCTACT 61030    A  C     __
                                AG AG AGAGC  AAGTGGAAAC
                                ||  ||  |||||  ||||||||||
                                TC TC TTTTG  TTCACCTTTG
                                 A  _     GT
GAM792  KIAA1024 3'  CCAGATGCTCTGCCTCTCA    69060     A  A       AG
                                TGA GA GCAGAGCA  TGG
                                |||  ||  ||||||||  |||
                                ACT CT CGTCTCGT  ACC
                                  _  C       AG
GAM792  KIAA1061 3'  CCACCCTGCTTCTCCA      71176     A       AGCAA
                                TG AGAAGCAG     GTGG
                                ||  ||||||||     ||||
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                                AC TCTTCGTC    CACC
                                 C       C____
GAM792  KIAA1170 3' CCATGCCCAGCCTCTTCA    69848       A  AGA   AG
                                TGAAGA GC   GCA  TGG
                                |||||| ||   |||  |||
                                ACTTCT CG   CGT  ACC
                                   C  ACC   __
GAM792  KIAA1203 3' CCCTGTACTCACTTCTTCA    71636        CA   CA_  T
                                TGAAGAAG  GAG   AG GG
                                ||||||||  |||   || ||
                                ACTTCTTC  CTC   TC CC
                                    A_   ATG  _
GAM792  KIAA1271 3' CTTCTGGTCTTGCTTCTCCA   69544    A       AG A  T
                                TG AGAAGCAG  C AG GG
                                || ||||||||  | || ||
                                AC TCTTCGTT  G TC TC
                                 C       CT G  T
GAM792  KIAA1317 5' TTTTCTCTGCTTTACTTCTTCA 86035        C     A T
                                TGAAGAAG AGAGCA G GGAAA
                                |||||||| |||||| | |||||
                                ACTTCTTC TTTCGT C CTTTT
                                    A     _ T
GAM792  KIAA1328 3' TCCACCCAGCCTTCTTT     61654        CAGA  AA_
                                GAAGAAG   GC   GTGGA
                                |||||||   ||   |||||
                                TTTCTTC   CG   CACCT
                                   ____  ACC
GAM792  KIAA1538 5' CCTCTCCCCCTGCTTCTTC    71537         AGCA  T
                                GAAGAAGCAG    AG GG
                                ||||||||||    || ||
                                CTTCTTCGTC    TC CC
                                     CCCC  T
GAM792  KIAA1656 3' CCACCCTGCTTCTCA       65786     A      AGCAA
                                TGA GAAGCAG    GTGG
                                ||| |||||||    ||||
                                ACT CTTCGTC    CACC
                                  _      C____
GAM792  KIAA1668 3' TCCAGGGTTCTGCTCTTC     66481      A      AAG
                                GAAGA GCAGAGC   TGGA
                                ||||| |||||||   ||||
                                CTTCT CGTCTTG   ACCT
                                   _      GG_
GAM792  KIAA1750 3' TCCTCAAGCTCTGCTCCTTCA  68258      A       AAGT
                                TGAAG AGCAGAGC    GGA
                                ||||| ||||||||    |||
                                ACTTC TCGTCTCG    CCT
                                   C       AACT
GAM792  KIAA1813 5' TCCACTTGCCCCTCCTTCT    70310      C  A_
                                AGAAG AG  GCAAGTGGA
                                ||||| ||  |||||||||
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                                TCTTC TC  CGTTCACCT
                                  C  CC
GAM792  KIAA1922  3'  CCTCTCCTGCTTCTTCA     73622          AGCA  T
                                TGAAGAAGCAG    AG GG
                                ||||||||||    || ||
                                ACTTCTTCGTC    TC CC
                                      C___  T
GAM792  LDHL     5'  TTCTCTCTCTCCACTTCTTCA  52601        CA   CA  T
                                TGAAGAAG  GAG  AG GGAA
                                ||||||||  |||  || ||||
                                ACTTCTTC  CTC  TC TCTT
                                     AC   TC  _
GAM792  LYPLA2    3'  TCCACTCAGCTGCTTCTCA    23431     A      AGCA
                                TGA GAAGCAG    AGTGGA
                                ||| |||||||    ||||||
                                ACT CTTCGTC    TCACCT
                                  _      GAC_
GAM792  MESDC2    3'  GTTTCCACTTAGGAGCCTTC   72498     AA  AGAGC
                                GAAG  GC     AAGTGGAAAC
                                ||||  ||     ||||||||||
                                CTTC  CG     TTCACCTTTG
                                  __ AGGA_
GAM792  MGC3130   3'  CCTGTGGTTGCTCTGCTCATC  43819    A  A       G ___
                                GA GA GCAGAGCAA T   GG
                                || || ||||||||| |   ||
                                CT CT CGTCTCGTT G   CC
                                 A  _        G TGT
GAM792  MIG       3'  ACGTTTGCTCAGCTTCTCCA   10036    A     A    A_____
                                TG AGAAGC GAGCA      GT
                                || |||||| |||||      ||
                                AC TCTTCG CTCGT      CA
                                 C      A     TTGIII
GAM792  NX-17     3'  TGAAACGCTGTTGTTCTGCTTC 40337   A         A________  GGAA
            CTCA                    GAAGCAGAGCA       GT    A
                                 ||||||||||        ||    |
                                 CTTCGTCTTGT       CA    T
                                C          TGTCGIII  AAGG
GAM792  NY-REN-25 3'  TTCCACTGCTCTGCTCCCT    60637    A_       A
                                AG  AGCAGAGCA GTGGAA
                                ||  ||||||||| ||||||
                                TC  TCGTCTCGT CACCTT
                                 CC        _
GAM792  OPRL1     3'  CCAGCCCTGCTTCTCA      6195      A      A  AAG
                                TGA GAAGCAG GC   TGG
                                ||| ||||||| ||   |||
                                ACT CTTCGTC CG   ACC
                                  _      C  ___
GAM792  OS4       3'  TTTCCATAAGTCTGCTTTTCA  19187       A    G AA
                                TGAAGA GCAGA C  GTGGAAA
                                |||||| ||||| |  |||||||
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                                ACTTTT CGTCT G  TACCTTT
                                   _    _ AA
GAM792  P114-RHO-GEF 3'  GTTTCCCAAACTCTGCTTC   31023        CAAGT
                                GAAGCAGAG    GGAAAC
                                |||||||||    ||||||
                                CTTCGTCTC    CCTTTG
                                     AAAC_
GAM792  PMFBP1   3'  TTTCCACGGGTGTTTCTTCA  48449        AGA  AA
                                TGAAGAAGC  GC  GTGGAAA
                                |||||||||  ||  |||||||
                                ACTTCTTTG  TG  CACCTTT
                                     ___  GG
GAM792  POU4F2   3'  CCACCTCGGCTTCTTCA    15899        A  CAA
                                TGAAGAAGC GAG  GTGG
                                ||||||||| |||  ||||
                                ACTTCTTCG CTC  CACC
                                     G  ___
GAM792  PPFIBP1  3'  TCCACTTGCCTCTT      13255    C  A
                                AAG AG GCAAGTGGA
                                ||| || |||||||||
                                TTC TC CGTTCACCT
                                  _ _
GAM792  PRO1580  5'  TTCACTTCTGCTTCTTCA   37534          GCA
                                TGAAGAAGCAGA  AGTGGA
                                ||||||||||||  ||||||
                                ACTTCTTCGTCT  TCACTT
                                          ___
GAM792  Rab11-FIP3 3'  TCCCAGGTGCTGCTTCTCCA  28127   A      A  AAGT
                                TG AGAAGCAG GC   GGA
                                || |||||||| ||   |||
                                AC TCTTCGTC TG   CCT
                                 C       G  GAC_
GAM792  RIL      3'  CCACGCCTGCTTCTT      13487        A  AA
                                AAGAAGCAG GC  GTGG
                                ||||||||| ||  ||||
                                TTCTTCGTC CG  CACC
                                     _  __
GAM792  RNAC     3'  TTTCCAGCTGTTTCTCCA    19316   A      AGCAAG
                                TG AGAAGCAG     TGGAAA
                                || ||||||||     ||||||
                                AC TCTTTGTC     ACCTTT
                                 C       G_____
GAM792  SEC24C   3'  CCACGAGAAACACTGCTTCTCC 16995   A      AGCAA___
           A                     TG AGAAGCAG       GTGG
                                || ||||||||       ||||
                                AC TCTTCGTC       CACC
                                 C       ACAAAGAG
GAM792  SLC21A11 3'  GTTTCCACAGTCCCTGC    64468     A_  AA
                                GCAG  GC  GTGGAAAC
                                ||||  ||  ||||||||
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                                CGTC  TG  CACCTTTG
                                  CC  A_
GAM792  SYT13    3'  TGAAACATAATTGCTCTGCTTT 93461          A_______  GGAA
            TCCA                  AGAAGCAGAGCA       GT    A
                                ||||||||||||       ||    |
                                TTTTCGTCTCGT       CA    T
                                      TAATAIII  AAGG
GAM792  TCL6     3'  GTTTCCATAGCACCATTCCTCA 40113     A   GCAGA  AA
                                TGA GAA    GC  GTGGAAAC
                                ||| |||    ||  ||||||||
                                ACT CTT    CG  TACCTTTG
                                  C   ACCA_  A_
GAM792  TCL6     3'  GTTTCCATAGCACCATTCCTCA 40144     A   GCAGA  AA
                                TGA GAA    GC  GTGGAAAC
                                ||| |||    ||  ||||||||
                                ACT CTT    CG  TACCTTTG
                                  C   ACCA_  A_
GAM792  TRAF4    3'  CCTGGTGCTCTGCCCATTCA   62629      GAA       AGT
                                TGAA   GCAGAGCA   GG
                                ||||   ||||||||   ||
                                ACTT   CGTCTCGT   CC
                                   ACC       GGT
GAM792  UBCE7IP5  3'  TTTGCTCTGCTTCCTC      30167    A
                                GA GAAGCAGAGCAAG
                                || ||||||||||||
                                CT CTTCGTCTCGTTT
                                 C
GAM792  VPS39    3'  GCTTGGACTCTGCTTCCTC    62847    A        __
                                GA GAAGCAGAG  CAAGT
                                || |||||||||  |||||
                                CT CTTCGTCTC  GTTCG
                                 C        AG
GAM792  WFDC3    3'  CCTCTCTGCTCTGCTTCT    96925           _  T
                                AGAAGCAGAGCA AG GG
                                |||||||||||| || ||
                                TCTTCGTCTCGT TC CC
                                       C  T
GAM792  YEA      5'  TCTGTGCGCTTGCTTCCCCA   51536    AA     G   AA TG
                                TG  GAAGCA AGC  G  GA
                                ||  |||||| |||  |  ||
                                AC  CTTCGT TCG  T  CT
                                 CC      _   CG GT
GAM792  ZNF37A   5'  ACGTTTGCTCTGCTCTTC    64792      A      A_____
                                GAAGA GCAGAGCA     GT
                                |||||  ||||||||     ||
                                CTTCT CGTCTCGT     CA
                                   _       TTGIII
GAM792  LOC126536 5'  TCCGAGAAGCCCTCTTCTTCA  74540         C  A  AAG_
                                TGAAGAAG AG GC    TGGA
                                |||||||| || ||    ||||
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                                ACTTCTTC TC CG    GCCT
                                     _  C  AAGA
GAM792   LOC126917 3'  GCCTGCCTGCCTCTCCA     74586    A   A    A   A
                                TG AGA GCAG GCA GT
                                || ||| |||| ||| ||
                                AC TCT CGTC CGT CG
                                 C   C    _   C
GAM792   LOC127702 3'  ACGTTTGCTCACTTCTTCA    75456         CA    A_____
                                TGAAGAAG  GAGCA     GT
                                ||||||||  |||||     ||
                                ACTTCTTC  CTCGT     CA
                                     A_     TTGIII
GAM792   LOC130985 5'  TCCTGCTCTGTCCCCTCA    75000     AGAA       AGT
                                TGA    GCAGAGCA   GGA
                                |||    ||||||||   |||
                                ACT    TGTCTCGT   CCT
                                  CCCC       ____
GAM792   LOC143677 5'  TCCACTTGCTTCCTCCTC    82982    A  AGCA
                                GA GA    GAGCAAGTGGA
                                || ||    ||||||||||
                                CT CT    TTCGTTCACCT
                                 C  CC__
GAM792   LOC144079 5'  TTCACTTGCTCCTTC       76663      CA
                                GAAG  GAGCAAGTGGA
                                ||||  ||||||||||
                                CTTC  CTCGTTCACTT
                                   __
GAM792   LOC144698 3'  CTGCCTCTCTGCTTCCTCA    76909     A        CAA TG
                                TGA GAAGCAGAG   G  G
                                ||| |||||||||   |  |
                                ACT CTTCGTCTC   C  C
                                  C        TC_ GT
GAM792   LOC145474 3'  CTATATGTCTGCTTCTTCA    77211           G  A
                                TGAAGAAGCAGA CA GTGG
                                |||||||||||| || ||||
                                ACTTCTTCGTCT GT TATC
                                        _  A
GAM792   LOC145828 5'  CCCTGAGCTCTGTTCTCCA    83535    A   G     A_  T
                                TG AGAA CAGAGC  AG GG
                                || |||| ||||||  || ||
                                AC TCTT GTCTCG  TC CC
                                 C    _      AG  _
GAM792   LOC145921 3'  TTCCACTTCCTTCACTTC     76016      CA   C
                                GAAG  GAG AAGTGGAA
                                ||||  ||| ||||||||
                                CTTC  TTC TTCACCTT
                                  AC   C
GAM792   LOC147042 3'  TTTCCACTGGCTATGCCACTTC 83916       AA   G   A
           A                     TGAAG  GCA AGC AGTGGAAA
                                |||||  ||| ||| ||||||||
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                                ACTTC  CGT TCG TCACCTTT
                                  AC   A   G
GAM792   LOC148343 5'  GCTTGGGCTCTGCTTCTT    78795          __
                                AAGAAGCAGAGC  AAGT
                                ||||||||||||  ||||
                                TTCTTCGTCTCG  TTCG
                                     GG
GAM792   LOC148394 5'  TCCTGCTGTGCTCTGCT     84145        _  _
                                AGCAGAGCA AGT GGA
                                ||||||||| ||| |||
                                TCGTCTCGT TCG CCT
                                     G   T
GAM792   LOC148530 5'  TCCACCGACACCTGCTTCTTC  84163         AGCAA_
                                GAAGAAGCAG     GTGGA
                                ||||||||||     |||||
                                CTTCTTCGTC     CACCT
                                     CACAGC
GAM792   LOC150094 3'  TTCCGCATCCCCTTCTTCA    84864        CA  GCAA
                                TGAAGAAG  GA    GTGGAA
                                ||||||||  ||    ||||||
                                ACTTCTTC  CT    CGCCTT
                                     CC  A___
GAM792   LOC150291 3'  TCCCTCACCTCTGCTTC      84947        CA_  T
                                GAAGCAGAG   AG GGA
                                |||||||||   || |||
                                CTTCGTCTC   TC CCT
                                     CAC  _
GAM792   LOC151300 3'  TCCCCTCTCTGCTTCTCA     85306     A       CA  T
                                TGA GAAGCAGAG  AG GGA
                                ||| |||||||||  || |||
                                ACT CTTCGTCTC  TC CCT
                                  _       __  C
GAM792   LOC153894 5'  GCTGCGCCTGCTTCTTCA     80974          A  A_
                                TGAAGAAGCAG GC  AGT
                                ||||||||||| ||  |||
                                ACTTCTTCGTC CG  TCG
                                     _  CG
GAM792   LOC154467 3'  TTCCACTTGGCCCCTT       92015     AA  AGAG
                                AAG  GC    CAAGTGGAA
                                |||  ||    |||||||||
                                TTC  CG    GTTCACCTT
                                  CC  _____
GAM792   LOC157376 3'  TCCACTCGGTATTTGCTC     81431     A    _  A_
                                GA GCAGA GC  AGTGGA
                                || ||||| ||  ||||||
                                CT CGTTT TG  TCACCT
                                  _    A  GC
GAM792   LOC158055 3'  CCATCTGCTTCTTC         81666           GCAAG
                                GAAGAAGCAGA    TGG
                                ||||||||||     |||
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                                CTTCTTCGTCT    ACC
                                      _____
GAM792  LOC158287 3'  CCCTTGCTCTGCTCCTCA    86721    A  A       T
                                TGA GA GCAGAGCAAG GG
                                ||| || |||||||||| ||
                                ACT CT CGTCTCGTTC CC
                                  C  _       _
GAM792  LOC158629 5'  GTTTCCACTCTTTCTGCCCTC  86882    A_    CA
                                GA  GCAGAG  AGTGGAAAC
                                ||  ||||||  |||||||||
                                CT  CGTCTT  TCACCTTTG
                                 CC     TC
GAM792  LOC158972 3'  TCCAGCATTTCTGCTTCCTCA  86957    A       CAAG
                                TGA GAAGCAGAG    TGGA
                                ||| |||||||||    ||||
                                ACT CTTCGTCTT    ACCT
                                  C        TACG
GAM792  LOC196878 5'  GCTTGCTGCTGCTTCTCCA    87803    A      _
                                TG AGAAGCAG AGCAAGT
                                || |||||||| |||||||
                                AC TCTTCGTC TCGTTCG
                                 C       G
GAM792  LOC199699 3'  TTCCACTTGCCAGGCTC     88317    A  AGA
                                GA GC   GCAAGTGGAA
                                || ||   ||||||||||
                                CT CG   CGTTCACCTT
                                 _ GAC
GAM792  LOC199958 3'  TCCACTTGGCAACTTC      89889      AA  AGAG
                                GAAG  GC    CAAGTGGA
                                ||||  ||    ||||||||
                                CTTC  CG    GTTCACCT
                                  AA  ____
GAM792  LOC200010 3'  TTTCCACCCTCTTCTT      89925     C    CAA
                                AAG AGAG   GTGGAAA
                                ||| ||||   |||||||
                                TTC TCTC   CACCTTT
                                  T   C__
GAM792  LOC200781 5'  TCCTGCTCTGTCCCCTCA    90141     AGAA       AGT
                                TGA    GCAGAGCA   GGA
                                |||    ||||||||   |||
                                ACT    TGTCTCGT   CCT
                                  CCCC       ___
GAM792  LOC201102 3'  TCCACCCTGCACTTGCTCCTCA 88099     A  A   _ A   A_
                                TGA GA GCA G GCA  GTGGA
                                ||| || ||| | |||  |||||
                                ACT CT CGT C CGT  CACCT
                                  C  _   T A   CC
GAM792  LOC201245 5'  CCCTGCTCTGCCTCTTC     87362       A       A T
                                GAAGA GCAGAGCA G GG
                                ||||| |||||||| | ||
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                                CTTCT CGTCTCGT C CC
                                  C       _ _
GAM792  LOC202460 5'  TCTCATCTCTGCTTCT      89190          CAA  _
                                AGAAGCAGAG   GTG GA
                                ||||||||||   ||| ||
                                TCTTCGTCTC   TAC CT
                                     ____   T
GAM792  LOC202741 3'  TTCTCACTCTGCTTCTCA     89200     A        CAAGT
                                TGA GAAGCAGAG     GGAA
                                ||| |||||||||     ||||
                                ACT CTTCGTCTC     TCTT
                                  _       AC___
GAM792  LOC203197 3'  GTTTCCATCTCCAACCCCTTCA 89295       AAGCA_   CAA
                                TGAAG     GAG   GTGGAAAC
                                |||||     |||   ||||||||
                                ACTTC     CTC   TACCTTTG
                                   CCCAAC  ___
GAM792  LOC203248 3'  CCCTTCTCTGCTTC        89310          C   T
                                GAAGCAGAG AAG GG
                                ||||||||| ||| ||
                                CTTCGTCTC TTC CC
                                     _   _
GAM792  LOC203286 3'  TCCTGCCTCTCTTCTTCA     90503         C   _ AGT
                                TGAAGAAG AGAG CA   GGA
                                |||||||| |||| ||   |||
                                ACTTCTTC TCTC GT   CCT
                                     _    C  ___
GAM792  LOC203378 3'  CCACTTGGCTTCTTC       90597         AGAG
                                GAAGAAGC    CAAGTGG
                                ||||||||    |||||||
                                CTTCTTCG    GTTCACC
                                     _____
GAM792  LOC203378 3'  TCCTGGGGCACTCTGCTTACCC 90618     AAG      __ AAGT
           A                     TG   AAGCAGA  GC    GGA
                                ||   |||||||  ||    |||
                                AC   TTCGTCT  CG    CCT
                                 CCA      CA  GGGT
GAM792  LOC219654 3'  CCAGCCCTGCTTTTCA      91300       A   A  AAG
                                TGAAGA GCAG GC   TGG
                                |||||| |||| ||   |||
                                ACTTTT CGTC CG   ACC
                                   _    C  ___
GAM792  LOC219848 3'  TTTCCACTTCTGCCTCT     91497     A    GCA
                                AGA GCAGA   AGTGGAAA
                                ||| |||||   ||||||||
                                TCT CGTCT   TCACCTTT
                                  C    ___
GAM792  LOC220766 5'  ACTTCCTCTACTCCTTC     90791      A  C   C
                                GAAG AG AGAG AAGT
                                |||| || |||| ||||
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                                CTTC TC TCTC TTCA
                                  C A   C
GAM792  LOC220776 3'  TTTGCTCCAACTTCTTCA    68398        CA_
                                TGAAGAAG  GAGCAAG
                                ||||||||  |||||||
                                ACTTCTTC  CTCGTTT
                                     AAC
GAM792  LOC221042 3'  TCTACGGCTCTGCTTC      93192         AA
                                GAAGCAGAGC  GTGGA
                                ||||||||||  |||||
                                CTTCGTCTCG  CATCT
                                      G_
GAM792  LOC221399 5'  ACATTGTCTCCACTTCTTCA  93843        CA  _  A____
                                TGAAGAAG  GAG CA    GT
                                ||||||||  ||| ||    ||
                                ACTTCTTC  CTC GT    CA
                                     AC   T  TAIII
GAM792  LOC222899 5'  TTCCCTTAAAACATCCTGCTTC 94365    A      AGC_____  T
          TCCA                    TG AGAAGCAG       AAG GGAA
                                || ||||||||       ||| ||||
                                AC TCTTCGTC       TTC CCTT
                                 C       CTACAAAA  _
GAM792  LOC253011 3'  TTTACTTGCTCTGCTTC     95937
                                GAAGCAGAGCAAGTGGA
                                |||||||||||||||||
                                CTTCGTCTCGTTCATTT

GAM792  LOC253250 3'  TTTCCACTTGCCCTCAGTC   94706    AGC  A
                                GA   AG GCAAGTGGAAA
                                ||   || ||||||||||
                                CT   TC CGTTCACCTTT
                                 GAC  C
GAM792  LOC254196 5'  TCCTGCTGTGCTCTGCT     97348        _  _
                                AGCAGAGCA AGT GGA
                                ||||||||| ||| |||
                                TCGTCTCGT TCG CCT
                                     G   T
GAM792  LOC254228 3'  TTCTCAAGGCTCTGCTTCTT  95960          AAG  _
                                AAGAAGCAGAGC   TG GAA
                                ||||||||||||   || |||
                                TTCTTCGTCTCG   AC CTT
                                       GA_  T
GAM792  LOC254251 5'  TCAAAAAACTTTACTTCTTCA  95911        C   CAAG_
                                TGAAGAAG AGAG    TGG
                                |||||||| ||||    |||
                                ACTTCTTC TTTC    ACT
                                     A   AAAAA
GAM792  LOC254722 5'  CCTTCAACTCCGGCTTCTTCA  97566        A_   CAAGT
                                TGAAGAAGC  GAG    GG
                                |||||||||  |||    ||
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                                ACTTCTTCG  CTC    CC
                                     GC   AACTT
GAM792  LOC257181 3'  TCCACTTGGAAAGTTCTCA   94594    A   GCAGAG
                                TGA GAA     CAAGTGGA
                                ||| |||     ||||||||
                                ACT CTT     GTTCACCT
                                  _   GAAAG_
GAM792  LOC257426 3'  TTCCTTCCTGCTCTGCTCTCTC 66647    _   A      AGT_
           A                     TGA AGA GCAGAGCA    GGAA
                                ||| ||| ||||||||    ||||
                                ACT TCT CGTCTCGT    CCTT
                                  C   _       CCTT
GAM792  LOC51313  3'  TCCCTCTGCTTCTACA     33511    A        CAAGT
                                TG AGAAGCAGAG     GGA
                                || ||||||||||     |||
                                AC TCTTCGTCTC     CCT
                                 A         _____
GAM792  LOC55833  3'  CCACCCCATCTGCCTTCA    64913      AA    GCAA
                                TGAAG  GCAGA    GTGG
                                |||||  |||||    ||||
                                ACTTC  CGTCT    CACC
                                   __     ACCC
GAM792  LOC64744  3'  TCCAGGGTGCTCTGTTTCCCCA 61800    AA         AG_
                                TG  GAAGCAGAGCA   TGGA
                                ||  ||||||||||   ||||
                                AC  CTTTGTCTCGT   ACCT
                                 CC          GGG
GAM792  LOC90927  3'  TCTGTGGTTCTGCTTCCTCA   64430    A        AA TG
                                TGA GAAGCAGAGC  G  GA
                                ||| ||||||||||  |  ||
                                ACT CTTCGTCTTG  T  CT
                                  C         G_ GT
GAM792  LOC92391  3'  TCCCTGAGCCTCTGCTTTCCCA 69161    AA       _ A_  T
                                TG  GAAGCAGAG C  AG GGA
                                ||  |||||||||  |  || |||
                                AC  TTTCGTCTC G  TC CCT
                                 CC        C AG  _
GAM792  LOC93048  3'  CTCTGGCCTGCTTCTCCA    71249    A      A  A  T
                                TG AGAAGCAG GC AG GG
                                || ||||||||  || ||  ||
                                AC TCTTCGTC CG TC TC
                                 C       _  G  _
GAM793  BCLG     3'  CCATCTCTGGACTCACAGCTTC 56986    A   ACA     GTGT
           CA                    TG AAG   TGAGTT    GATGG
                                || |||   ||||||    |||||
                                AC TTC   ACTCAG    CTACC
                                 C  GAC     GTCT
GAM793  CLN6     3'  CCACCACCTGGCTCATCCCTCA 35403    A  AC       T   A
                                A AG  ATGAGTTG GTG TGG
                                | ||  |||||||| ||| |||
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                                A TC  TACTCGGT CAC ACC
                                 C  CC       C   C
GAM793  ELOVL4   3'  CATGAAACAACTCATGTCTTT  42686            GTG
                                AAAGACATGAGTTGT   ATG
                                |||||||||||||||   |||
                                TTTCTGTACTCAACA   TAC
                                       AAG
GAM793  HUNK     3'  CACCAAACTCATGTTTTCA   27444      A        GT
                                TGAA GACATGAGTT  GTG
                                ||||  ||||||||||  |||
                                ACTT TTGTACTCAA  CAC
                                   _        AC
GAM793  PPP1R3C  3'  CACAACTCACATCCTTCA    18249      A  CA
                                TGAA GA  TGAGTTGTG
                                ||||  ||  |||||||||
                                ACTT CT  ACTCAACAC
                                   C  AC
GAM793  SYBL1    3'  CATGTGACTCAAGCCTTTCA   18894       ACA    TG
                                TGAAAG   TGAGT  TGTG
                                ||||||   |||||  ||||
                                ACTTTC   ACTCA  GTAC
                                    CGA    GT
GAM793  UBE2G2   3'  CCATCACACTTAGAAATACTTC 64852    A   ACATGAGTT
           CA                     TG AAG        GTGTGATGG
                                || |||        |||||||||
                                AC TTC        CACACTACC
                                 C   ATAAAGATT
GAM793  C1orf22  3'  CATCACACAACCTTTTTTA   47255        CATGA
                                TGAAAGA    GTTGTGTGATG
                                |||||||    ||||||||||
                                ATTTTTT    CAACACACTAC
                                    C____
GAM793  DKFZp434J0226 3'  CCTTCATCCACTCATGTC    72333         T TG   T
                                GACATGAGT G  TGA GG
                                |||||||||  |  ||| ||
                                CTGTACTCA C  ACT CC
                                      _ CT   T
GAM793  GAL3ST-4  3'  CACATGACTCTGCCTCCCA   44932    AA  A  T   TG
                                TG  AG CA GAGT  TGTG
                                ||  || || ||||  ||||
                                AC  TC GT CTCA  ACAC
                                 CC  C  _   GT
GAM793  KIAA0987  3'  CATAAACAATTCATGCCTTTCA 24561       A        GTG
                                TGAAAG CATGAGTTGT   ATG
                                ||||||  ||||||||||  |||
                                ACTTTC GTACTTAACA   TAC
                                   C         AA_
GAM793  MGC27044  3'  CCAGTCAACTCATATCTT    58670      C       TGTGA
                                AAGA ATGAGTTG    TGG
                                ||||  ||||||||    |||
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                                TTCT TACTCAAC    ACC
                                  A      TG___
GAM793  RRN3     3'  CCATCACTTGTCATGCCCTCA  37354    AAGA    GTTGT
                                TGA   CATGA    GTGATGG
                                |||   |||||    |||||||
                                ACT   GTACT    CACTACC
                                  CCC_    GTT__
GAM793  TNKS1BP1 5'  CACCCCAGCTCATACCTCTC  53002    A  AC      T_
                                GA AG  ATGAGTTG  GTG
                                || ||  ||||||||  |||
                                CT TC  TACTCGAC  CAC
                                 C  CA       CC
GAM793  LOC122830 3'  CACACAGTACTCAGCCTTTCA  74162       ACA    __
                                TGAAAG   TGAGT  TGTGTG
                                ||||||   |||||  ||||||
                                ACTTTC   ACTCA  ACACAC
                                    CG_    TG
GAM793  LOC170217 5'  ATCACACAACCCAGT      82574    A  A
                                AC TG GTTGTGTGAT
                                || || ||||||||||
                                TG AC CAACACACTA
                                 _  C
GAM793  LOC170218 5'  ATCACACAACCCAGT      82575    A  A
                                AC TG GTTGTGTGAT
                                || || ||||||||||
                                TG AC CAACACACTA
                                 _  C
GAM793  LOC253272 5'  CATCACAGAATATCTTT     95358      CATGA   G
                                AAAGA     GTT TGTGATG
                                |||||     ||| |||||||
                                TTTCT     TAA ACACTAC
                                   A_____   G
GAM793  LOC57019  3'  CACCCTCTTGTCTTTCA     39722        T   TT
                                TGAAAGACA GAG  GTG
                                ||||||||| |||  |||
                                ACTTTCTGT CTC  CAC
                                      T   C_
GAM794  EIF2C1    3'  TTGTTGAATGCACTGA      24185        C_
                                TCAGTGCA  TAACAA
                                ||||||||  ||||||
                                AGTCACGT  GTTGTT
                                     AA
GAM794  LAMB2     3'  TGCATGTCTGCCTATGCACTGA 9673         CTAA  AT
                                TCAGTGCA    CA  TATGTA
                                ||||||||    ||  ||||||
                                AGTCACGT    GT  GTACGT
                                     ATCC  CT
GAM794  MAP3K4    3'  TTGTTGAGTGCACTGA      19801          _
                                TCAGTGCACT AACAA
                                |||||||||| |||||
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                                AGTCACGTGA TTGTT
                                      G
GAM794  MAP3K4   3'  TTGTTGAGTGCACTGA     22049          _
                                TCAGTGCACT AACAA
                                |||||||||| |||||
                                AGTCACGTGA TTGTT
                                      G
GAM794  PIK3R1   3'  TGTACATAATATTGGATGACT  68581    G _   CA
                                AGT CA CTAA  ATTATGTACA
                                ||| || ||||  ||||||||||
                                TCA GT GGTT  TAATACATGT
                                  _ A   A_
GAM794  RAD52    3'  ACATAATTTTGTGCAT     56210      TAAC
                                GTGCAC   AATTATGT
                                ||||||   ||||||||
                                TACGTG   TTAATACA
                                   TT__
GAM794  RAD52    3'  ACATAATTTTGTGCAT     56193      TAAC
                                GTGCAC   AATTATGT
                                ||||||   ||||||||
                                TACGTG   TTAATACA
                                   TT__
GAM794  RAD52    3'  ACATAATTTTGTGCAT     56201      TAAC
                                GTGCAC   AATTATGT
                                ||||||   ||||||||
                                TACGTG   TTAATACA
                                   TT__
GAM794  RAD52    3'  ACATAATTTTGTGCAT     11239      TAAC
                                GTGCAC   AATTATGT
                                ||||||   ||||||||
                                TACGTG   TTAATACA
                                   TT__
GAM794  STAU     3'  TGTACACAGAAGTGTGTGCACT 33898        TA  ATTA__
           GA                    TCAGTGCAC  ACA    TGTACA
                                 |||||||||  |||    ||||||
                                 AGTCACGTG  TGT    ACATGT
                                      __  GAAGAC
GAM794  STAU     3'  TGTACACAGAAGTGTGTGCACT 33904        TA  ATTA__
           GA                    TCAGTGCAC  ACA    TGTACA
                                 |||||||||  |||    ||||||
                                 AGTCACGTG  TGT    ACATGT
                                      __  GAAGAC
GAM794  STAU     3'  TGTACACAGAAGTGTGTGCACT 33911        TA  ATTA__
           GA                    TCAGTGCAC  ACA    TGTACA
                                 |||||||||  |||    ||||||
                                 AGTCACGTG  TGT    ACATGT
                                      __  GAAGAC
GAM794  STAU     3'  TGTACACAGAAGTGTGTGCACT 16012        TA  ATTA__
           GA                    TCAGTGCAC  ACA    TGTACA
                                 |||||||||  |||    ||||||
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                                AGTCACGTG  TGT     ACATGT
                                     __  GAAGAC
GAM794  TAF4     3'  TGTACATAACTTTTGGCACATG 12095    _   ACTAACAA
              A                   TCA GTGC       TTATGTACA
                                  ||| ||||       |||||||||
                                  AGT CACG       AATACATGT
                                    A   GTTTTC__
GAM794  TCF7L2   3'  TACATAACTGTTATGTA    47738     C    A
                                  TGCA TAACA TTATGTA
                                  |||| ||||| |||||||
                                  ATGT ATTGT AATACAT
                                    _   C
GAM794  TES      3'  ACTTAAAAGTTAGTGTACTGA  71999          AA   T
                                  TCAGTGCACTAACC  TTA GT
                                  ||||||||||||  ||| ||
                                  AGTCATGTGATTG  AAT CA
                                         AA   T
GAM794  VSNL1    3'  CATAATGTTAGTAGCACTGA   12623       _     A
                                  TCAGTGC ACTAACA TTATG
                                  ||||||| ||||||| |||||
                                  AGTCACG TGATTGT AATAC
                                     A     _
GAM794  FBXO30   3'  TATACAATTGTTAATGCAC   49580      C      A
                                  GTGCA TAACAATT TGTA
                                  ||||| |||||||| ||||
                                  CACGT ATTGTTAA ATAT
                                    A       C
GAM794  FLJ10545 3'  TACACTGTCTAGTGCAT     36263        _  ATTA
                                  GTGCACTA ACA    TGTA
                                  |||||||| |||    ||||
                                  TACGTGAT TGT    ACAT
                                     C   C___
GAM794  FLJ20533 3'  TGCATTCCGTTAGTGACTGA  35359      G      AATT
                                  TCAGT CACTAAC    ATGTA
                                  ||||| |||||||    |||||
                                  AGTCA GTGATTG    TACGT
                                    _      CCT_
GAM794  KIAA0217 3'  TGTAGTTGTCAGTTCACTGA  67042       C   A
                                  TCAGTG ACT ACAATTATG
                                  |||||| ||| |||||||||
                                  AGTCAC TGA TGTTGATGT
                                     T   C
GAM794  KIAA0546 3'  TGCATGCTAATGCACTGG    71314        C  ACAAT
                                  TCAGTGCA TA     TATGTA
                                  |||||||| ||     ||||||
                                  GGTCACGT AT     GTACGT
                                     A  C____
GAM794  KIAA1821 3'  TGCACATAATGGGGTTGCACTG 71798        _ AACA      A
              G                   TCAGTGCA CT    ATTATGT CA
                                  |||||||| ||    ||||||| ||
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                                GGTCACGT GG   TAATACA GT
                                    T  GG__     C
GAM794  NTKL     3'  TGTACATAATCAGAGCCAC   40348    CA  AACA
                                GTG  CT   ATTATGTACA
                                |||  ||   ||||||||||
                                CAC  GA   TAATACATGT
                                  C_  GAC_
GAM794  SEMA5A   3'  TGATTTTACAGTGCACTGA   14262        AAC_
                                TCAGTGCACT   AATTA
                                ||||||||||   |||||
                                AGTCACGTGA   TTAGT
                                     CATT
GAM794  TIP120A  3'  ATATGACCATACAATGCACTGA 37425       CTAACAA_
                                TCAGTGCA      TTATGT
                                ||||||||      ||||||
                                AGTCACGT      AGTATA
                                    AACATACC
GAM794  LOC115123 3'  TGCACTGGGGTCATGCACTGA  73222       CTA  AATTA
                                TCAGTGCA  AC    TGTA
                                ||||||||  ||    ||||
                                AGTCACGT  TG    ACGT
                                    AC_  GGGTC
GAM794  LOC144524 5'  TACAGCATGTTATTGCACTGA  83135       C    ATTA
                                TCAGTGCA TAACA   TGTA
                                ||||||||  |||||   ||||
                                AGTCACGT ATTGT   ACAT
                                    T    ACG_
GAM794  LOC196540 3'  ACAGCCTGCAAGTGCACTGA   89631        AA  ATTA
                                TCAGTGCACT  CA   TGT
                                ||||||||||  ||   |||
                                AGTCACGTGA  GT   ACA
                                     AC  CCG_
GAM794  LOC221596 3'  CATACCAGTAAATGCACTGA   91976       CTA  AAT
                                TCAGTGCA  AC   TATG
                                ||||||||  ||   ||||
                                AGTCACGT  TG   ATAC
                                    AAA  ACC
GAM794  LOC255121 5'  TACAAGGGACACTGGTGCACTG 97561         ACAA_ TA
          A                      TCAGTGCACTA    T  TGTA
                                 ||||||||||    |  ||||
                                 AGTCACGTGGT    G  ACAT
                                      CACAG GA
GAM794  LOC51110  3'  TGTACATAATTGCTTTGTCTTG 32078     T   CTAA
          A                      TCAG GCA    CAATTATGTACA
                                 ||||  |||    ||||||||||||
                                 AGTT TGT    GTTAATACATGT
                                   C   TTC_
GAM794  LOC92715  3'  TGCAGGTGCCTGTGCACTGA   70377        TAA  ATTA
                                TCAGTGCAC   CA    TGTA
                                |||||||||   ||    ||||
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                                AGTCACGTG  GT   ACGT
                                     TCC  GG__
GAM795  NCALD    3'  TGCTTTTCTGAGCAGATCAATA 49380         CC   CCTGT
                                TATTGATCTGT  CAG    GCA
                                ||||||||||  |||    |||
                                ATAACTAGACG  GTC    CGT
                                      A_   TTTT_
GAM795  FLJ10242 5'  TACTTCCTGAAGCAGATCAA   35934        CC   CCT
                                TTGATCTGT  CAG   GTG
                                |||||||||  |||   |||
                                AACTAGACG  GTC   CAT
                                     AA   CTT
GAM795  FLJ13842 3'  TGCACAGAACTGGAACAGATCA 44990        C    C_
                                TGATCTGT CCAG  CTGTGCA
                                ||||||||| ||||  |||||||
                                ACTAGACA GGTC  GACACGT
                                     A    AA
GAM795  GPR88    3'  CACAGTCAAGACGGATCAATA  41878          CCAGC
                                TATTGATCTGTC    CTGTG
                                ||||||||||||    |||||
                                ATAACTAGGCAG    GACAC
                                      AACT_
GAM795  KIAA0415 3'  TGCACCGTGGAGCAGATCAA   92582        TC   GCCT
                                TTGATCTG  CCA   GTGCA
                                ||||||||  |||   |||||
                                AACTAGAC  GGT   CACGT
                                     GA   GC__
GAM795  KIAA0513 3'  GCACAGGCTAAGACCACAGA   28359      CCC___
                                TCTGT     AGCCTGTGC
                                |||||     |||||||||
                                AGACA     TCGGACACG
                                   CCAGAA
GAM795  TCL6     3'  GCACAGGCTGGTCTCAA     40103     TCTGTC
                                TTGA     CCAGCCTGTGC
                                ||||     ||||||||||
                                AACT     GGTCGGACACG
                                  CT_____
GAM795  TCL6     3'  GCACAGGCTGGTCTCAA     40135     TCTGTC
                                TTGA     CCAGCCTGTGC
                                ||||     ||||||||||
                                AACT     GGTCGGACACG
                                  CT_____
GAM795  LOC219529 5'  TGCAACAGAAGACAGATTAA   92975         CCAGC   _
                                TTGATCTGTC    CTGT GCA
                                ||||||||||    |||| |||
                                AATTAGACAG    GACA CGT
                                      AA___    A
GAM795  LOC253281 5'  CACAGGCTGGAGGTGCTCA   97343     TC GT _
                                TGA  T  C CCAGCCTGTG
                                |||  |  | ||||||||||
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                                ACT  G  G GGTCGGACAC
                                  C_ TG A
GAM796  CAPN5    3'  TTGCTGTGTGACCTTAGG    90913    A  C  AG
                                CC AA GT  TACACAGCAA
                                || || ||  ||||||||||
                                GG TT CA  GTGTGTCGTT
                                 A  C  __
GAM796  DYRK1A   3'  TTGCTGTGTATATTGT     7358     TA
                                ACG  GTACACAGCAA
                                |||  ||||||||||
                                TGT  TATGTGTCGTT
                                  TA
GAM796  DYRK1A   3'  TTGCTGTGTATATTGT     55209    TA
                                ACG  GTACACAGCAA
                                |||  ||||||||||
                                TGT  TATGTGTCGTT
                                  TA
GAM796  DYRK1A   3'  TTGCTGTGTATATTGT     55252    TA
                                ACG  GTACACAGCAA
                                |||  ||||||||||
                                TGT  TATGTGTCGTT
                                  TA
GAM796  GPD2     3'  ATTTGCTGTACTTTATTTG   4645     CGT   AC
                                CAAA   AGT  ACAGCAAAT
                                ||||   |||  |||||||||
                                GTTT   TCA  TGTCGTTTA
                                  ATT   __
GAM796  PCTK3    3'  TGCCTAGTGCCAGTTTGGTA  72969       GTA   ACA
                                TACCAAAC   GTAC   GCA
                                ||||||||   ||||   |||
                                ATGGTTTG   CGTG   CGT
                                     AC_   ATC
GAM796  PSMC6    3'  ATTTGCTGCGTGAGCATTTTGT 10969    C   C  AG   A
          A                      TAC AAA GT  TAC CAGCAAAT
                                 ||| ||| ||  ||| ||||||||
                                 ATG TTT CG  GTG GTCGTTTA
                                   T   A  A_   C
GAM796  RBM8A    3'  TTGCTGTGTTTATATTT     17550    CG   T
                                AAA  TAG ACACAGCAA
                                |||  ||| |||||||||
                                TTT  ATT TGTGTCGTT
                                  AT   _
GAM796  FLJ20273 3'  ATTTGTATGCTGTACTACATTT 38726     C      _ _
          G                      CAAA GTAGTACA CA GCAAAT
                                 |||| |||||||| || ||||||
                                 GTTT CATCATGT GT TGTTTA
                                   A      C  A
GAM796  FLJ21272 3'  CTGTTACTAAGTTTGGTA   46737       G    C
                                TACCAAAC TAGTA ACAG
                                |||||||| ||||| ||||
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                                ATGGTTTG ATCAT TGTC
                                    A    _
GAM796  FLJ31812  3'  TTGCTGTGTAAATGTTTCTGG  58650     __    AG
                                CCA  AACGT  TACACAGCAA
                                |||  |||||  ||||||||||
                                GGT  TTGTA  ATGTGTCGTT
                                  CT    A_
GAM796  KIAA0111  3'  TGCTGTGTACTCCTGTTTGG  28455       T_
                                CCAAACG  AGTACACAGCA
                                |||||||  ||||||||||
                                GGTTTGT  TCATGTGTCGT
                                    CC
GAM796  KIAA1348  3'  ATTTGCCTCTACTACGTCAGG  68572    AA      CACA
                                CC  ACGTAGTA   GCAAAT
                                ||  ||||||||   ||||||
                                GG  TGCATCAT   CGTTTA
                                 AC      CTC_
GAM796  KIAA1374  3'  TTGCTGTGTATTTAGT     61245    GT
                                AC  AGTACACAGCAA
                                ||  ||||||||||||
                                TG  TTATGTGTCGTT
                                 AT
GAM796  MO25      3'  ATTTGCTGTTAGCTAT     32807      AC
                                GTAGT  ACAGCAAAT
                                |||||  |||||||||
                                TATCG  TGTCGTTTA
                                   AT
GAM796  QKI       3'  ATTTGCTGTATACATGT     65438     A   C
                                ACGT GTA ACAGCAAAT
                                |||| ||| |||||||||
                                TGTA CAT TGTCGTTTA
                                  _  A
GAM796  STIP-1    3'  CTGTATATTTTTGTTTGGTA  69663         T_   C
                                TACCAAACG  AGTA ACAG
                                |||||||||  |||| ||||
                                ATGGTTTGT  TTAT TGTC
                                     TT    A
GAM796  LOC146880 3'  ATTTGTTGTGTACTATGTTTGG 78156
          TA                    TACCAAACGTAGTACACAGCAAAT
                                |||||||||||||||||||||||||
                                ATGGTTTGTATCATGTGTTGTTTA

GAM796  LOC147299 3'  ATTTGCTGTGCCTCGT     78344     T  TA
                                ACG AG  CACAGCAAAT
                                |||  ||  ||||||||||
                                TGC TC  GTGTCGTTTA
                                  _  C_
GAM796  LOC147353 3'  GCTTTGTACTATATTTG     84009      CG      C
                                CAAA  TAGTACA AGC
                                ||||  ||||||| |||
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                                GTTT  ATCATGT TCG
                                  AT      T
GAM796  LOC147599 5'  TTGCTGTGTGGACCTGG     84044     AAC  AG
                                CCA   GT  TACACAGCAA
                                |||   ||  ||||||||||
                                GGT   CA  GTGTGTCGTT
                                  C__  G_
GAM796  LOC221510 3'  ATTTGCTGTGTTTCGTT     91055      TAGT
                                AACG    ACACAGCAAAT
                                ||||    ||||||||||
                                TTGC    TGTGTCGTTTA
                                  TT__
GAM796  LOC257469 3'  ATTTGCTGTTGGATCGTTT    95713       TAGTAC
                                AAACG     ACAGCAAAT
                                |||||     |||||||||
                                TTTGC     TGTCGTTTA
                                   TAGGT_
GAM796  LOC90155  3'  ATTTGCTGCATACTGTTAGG   61692    A   GT    CA
                                CC AAC  AGTA  CAGCAAAT
                                || |||  ||||  ||||||||
                                GG TTG  TCAT  GTCGTTTA
                                 A   __    AC
GAM796  LOC92370  3'  ATTTGCTGTACCTGCTTGGTG  69134       AC    TAC
                                TACCAA  GTAG   ACAGCAAAT
                                ||||||  ||||   |||||||||
                                GTGGTT  CGTC   TGTCGTTTA
                                    __    CA_
GAM797  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM797  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875        CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM797  FDFT1    3'  TAGGAAAGTGAAATG       15518            A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM797  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                   CATTTCACTTTCACTGTCTGAGAT
                                ||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM797  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
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                                GT  AGGTGACAGAC CT
                                 AT         C
GAM797  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                     A
GAM797  PKD2     3'  TCCAGGTTGAAAGTGAAA     60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM797  WRN      3'  GGGCAGTGAAAATGAAA      5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM797  ZNF216   3'  ATCTGCACAGCAAAGTGAAA   20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_    CG_
GAM797  CG012    5'  CTCACTCTGAAAGTGAA      83218          CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM797  EIF2C2   3'  ATCTTCTGAGAGTGAAAG     71946         G  T_
                                CTTTCACT TC  GAGAT
                                |||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM797  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                |||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM797  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281         CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM797  KIAA0984 3'  TTTGTCCAGTGAAAATGAA    65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM797  KLHL6    3'  ATCTCAGAGCAGGAAA       55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
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                                AAAG GAC AGACTCTA
                                  _  G
GAM797  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM797  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM797  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM797  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148         TCAC   C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM797  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM797  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM797  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM797  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM797  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||   |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM797  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
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                                GTAAAGTGAA GTGACA
                                      _
GAM798  CALU     3'  CTGTAAATGCCCCCATCCGGT  6885      A  T  A_  C
                                ACCG AT GG  CAT TACAG
                                |||| || ||  ||| |||||
                                TGGC TA CC  GTA ATGTC
                                  C  C  CC   A
GAM798  CML66    3'  AGATGTACAATTCAGTG     68232     C     G
                                CAC GAATTG ACATCT
                                ||| |||||| ||||||
                                GTG CTTAAC TGTAGA
                                  A     A
GAM798  HTRA3    3'  TTGCTGTAAATGGATTCCCAGT 89121      AC   ____
                                ATTGG  ATCT   ACAGCAA
                                |||||  ||||   |||||||
                                TGACC  TAGG   TGTCGTT
                                   CT   TAAA
GAM798  MERTK    3'  TGCTGTAGGAGAATCCAATT   20950       CA__
                                AATTGGA   TCTACAGCA
                                |||||||   |||||||||
                                TTAACCT   GGATGTCGT
                                    AAGA
GAM798  STC1     3'  TTGCTGCAGAGTGATTCGG    12033       GG  A   A
                                CCGAATT  AC TCT CAGCAA
                                |||||||  || ||| ||||||
                                GGCTTAG  TG AGA GTCGTT
                                   __  _  C
GAM798  STX7     3'  TGCTGTAGATTGCCTAGT     13109      A  _
                                ATTGG CA TCTACAGCA
                                ||||| || |||||||||
                                TGATC GT AGATGTCGT
                                   C  T
GAM798  UC28     5'  TTGCTACAGAGCTACAATTC   41294       GACA   AC
                                GAATTG   TCT  AGCAA
                                ||||||   |||  |||||
                                CTTAAC   AGA  TCGTT
                                    ATCG   CA
GAM798  ALTE     3'  TTGCTGTAAATACTTACCCGGT 16392      AATT  AC  C
                                ACCG   GG  AT TACAGCAA
                                ||||   ||  || ||||||||
                                TGGC   TC  TA ATGTCGTT
                                  CCAT  A_  A
GAM798  ALTE     3'  TTGCTGTAAATACTTACCCGGT 60361      AATT  AC  C
                                ACCG   GG  AT TACAGCAA
                                ||||   ||  || ||||||||
                                TGGC   TC  TA ATGTCGTT
                                  CCAT  A_  A
GAM798  DKFZp434G179 3'  TTGCTATAGATGTCTTCTGG  80092     AATT       C
                                CCG   GGACATCTA AGCAA
                                |||   ||||||||| |||||
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                                GGT    TCTGTAGAT TCGTT
                                  CT__       A
GAM798  FLJ14154  3'  CTGCAGTGTCCAGCCCAGTG   45817     CGAA      T  A
                                CAC    TTGGACA CT CAG
                                |||    ||||||| || |||
                                GTG    GACCTGT GA GTC
                                  ACCC      _  C
GAM798  HCA4      3'  TTGCTGTAAACGCTTCAAT    56940       CATC_
                                ATTGGA     TACAGCAA
                                ||||||     ||||||||
                                TAACTT     ATGTCGTT
                                   CGCAA
GAM798  HCA4      3'  TTGCTGTAAACGCTTCAAT    77596       CATC_
                                ATTGGA     TACAGCAA
                                ||||||     ||||||||
                                TAACTT     ATGTCGTT
                                   CGCAA
GAM798  KIAA0258  3'  TGCTGTAGACTCCTGGGTG    28823      GAATT   CA
                                CACC     GGA  TCTACAGCA
                                ||||     |||  |||||||||
                                GTGG     CCT  AGATGTCGT
                                  GT___   C_
GAM798  KIAA1486  3'  TTGCTGTAGACAACTTTCG    67387      TT  ACA
                                CGAA  GG   TCTACAGCAA
                                ||||  ||   ||||||||||
                                GCTT  TC   AGATGTCGTT
                                  __  AAC
GAM798  MAT2B     3'  TGCTGTAGACTTTTCAG     25227       CA_
                                TTGGA   TCTACAGCA
                                |||||   |||||||||
                                GACTT   AGATGTCGT
                                   TTC
GAM798  MGC12837  3'  TTGCTGTAGGCTCAAT      51184       ACA
                                ATTGG   TCTACAGCAA
                                |||||   ||||||||||
                                TAACT   GGATGTCGTT
                                  C__
GAM798  WBSCR21   5'  TTGCTGTAGATATCAGCCCAGT 48479     CGAATTG  C
           G                     CAC      GA ATCTACAGCAA
                                |||      || ||||||||||||
                                GTG      CT TAGATGTCGTT
                                  ACCCGA_  A
GAM798  LOC132422 5'  GCTGTAAACAATAGGTCGGTG  75887       A   GACATC
                                CACCGA TTG     TACAGC
                                |||||| |||     ||||||
                                GTGGCT GAT     ATGTCG
                                   G   AACAA_
GAM798  LOC145482 3'  TTGCTGTAAATGTCATCAAGG  77235    GAATTG    C
                                CC     GACAT TACAGCAA
                                ||     ||||| ||||||||
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                                GG     CTGTA ATGTCGTT
                                 AACTA_    A
GAM798  LOC149127 3'  TGCTGTCTTCCAATTTGGTG  84351          CATCT
                                CACCGAATTGGA    ACAGCA
                                ||||||||||||    ||||||
                                GTGGTTTAACCT    TGTCGT
                                      TC___
GAM798  LOC154084 5'  TGCTGTAGATTGCCTAGT    86165      A _
                                ATTGG CA TCTACAGCA
                                ||||| || |||||||||
                                TGATC GT AGATGTCGT
                                   C  T
GAM798  LOC158056 5'  CTGCAGACCAGTCTCGG    81685     _    ACA   A
                                CCGA ATTGG   TCT CAG
                                |||| |||||   ||| |||
                                GGCT TGACC   AGA GTC
                                  C    ___   C
GAM798  LOC164390 5'  GCTTGAATCCAATTCG     82515        CA  TAC
                                CGAATTGGA  TC   AGC
                                |||||||||  ||   |||
                                GCTTAACCT  AG   TCG
                                     A_  T__
GAM798  LOC199992 3'  TTGCTGTGGCCCCAACCTCGGT 88512      A_   ACAT
          G                      CACCGA  TTGG   CTACAGCAA
                                ||||||  ||||   |||||||||
                                GTGGCT  AACC   GGTGTCGTT
                                   CC   CC__
GAM798  LOC201595 3'  TGCTGTAAATGTCTAG     88981        C
                                TTGGACAT TACAGCA
                                |||||||| |||||||
                                GATCTGTA ATGTCGT
                                     A
GAM798  LOC202018 5'  CTGCAGATGTCTACAGTG    89142     CGAAT       A
                                CAC    TGGACATCT CAG
                                |||    ||||||||| |||
                                GTG    ATCTGTAGA GTC
                                  AC___        C
GAM798  LOC222060 5'  TGCTGTAGAGCCATTTAAT   94111       CA__
                                ATTGGA   TCTACAGCA
                                ||||||   |||||||||
                                TAATTT   AGATGTCGT
                                   ACCG
GAM798  LOC253974 5'  TTGCTGTAGCCAAATTC     97425      _ ACAT
                                GAATT GG   CTACAGCAA
                                ||||| ||   |||||||||
                                CTTAA CC   GATGTCGTT
                                  A ____
GAM798  LOC90231  3'  GCGGTGATGTCCATCTCGG   61867     AT      T  A
                                CCGA  TGGACATC AC GC
                                ||||  |||||||| || ||
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                                GGCT  ACCTGTAG TG CG
                                  CT       _ G
GAM799  ADAMTS5  3'  CTCTGCTTCTCTTACT     22892        C   G
                                AGTAAGAG AGT AGAG
                                |||||||| ||| ||||
                                TCATTCTC TCG TCTC
                                     T  _
GAM799  BDKRB1   5'  CTCCAAAAGCAGCTCTCACTAT 5543     C   A    A  GA___
           CA                     TGA AGT AGAGC GT    GAG
                                ||| ||| ||||| ||    |||
                                ACT TCA TCTCG CG    CTC
                                  A   C    A  AAAAC
GAM799  BRPF1    3'  CTCCCCTTTGCTCACTGTC   73086       AA     TGA_
                                GACAGT  GAGCAG   GAG
                                ||||||  ||||||   |||
                                CTGTCA  CTCGTT   CTC
                                   __     TCCC
GAM799  C14orf1  3'  CTCCGGCTCCTTACTGTCA   23178         _  AGT
                                TGACAGTAAG AGC   GAG
                                |||||||||| |||   |||
                                ACTGTCATTC TCG   CTC
                                     C   GC_
GAM799  CALM2    3'  CTTATCTTACTGTCA      8227          GCAG
                                TGACAGTAAGA   TGAG
                                ||||||||||    ||||
                                ACTGTCATTCT   ATTC
                                          ____
GAM799  CCR2     3'  CTCTCAGGCTTGCTGCCA    5382     A   AA   AG
                                TG CAGT  GAGC  TGAGAG
                                || ||||  ||||  ||||||
                                AC GTCG  TTCG  ACTCTC
                                  C   __   G_
GAM799  DAAM2    3'  CTCCCCACTGCTCCTGC     92287     A      A_
                                GTA GAGCAGTG  GAG
                                ||| ||||||||  |||
                                CGT CTCGTCAC  CTC
                                  C       CC
GAM799  EPHA3    5'  CTCTCACTGCCCTCTGCA    17870    A   TA  A
                                TG CAG  AG GCAGTGAGAG
                                || |||  || ||||||||||
                                AC GTC  TC CGTCACTCTC
                                  _  __  C
GAM799  EPHA8    3'  CTCTCACCGCTGCTTCA     40058     C   AAG   A
                                TGA AGT   AGC GTGAGAG
                                ||| |||   ||| |||||||
                                ACT TCG   TCG CACTCTC
                                  _  ___   C
GAM799  EZH1     3'  CTCACATGCTCTCACT      8819      A     _
                                AGT AGAGCA GTGAG
                                ||| |||||| |||||
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                                TCA TCTCGT CACTC
                                  C     A
GAM799  FECH    3'  CTCCCACTGCTTCTGGTC    3754     AGTAA      A
                                GAC    GAGCAGTG GAG
                                |||    |||||||| |||
                                CTG    TTCGTCAC CTC
                                  GTC__       C
GAM799  FGF2    3'  CTTTCAGACCTCTACTGTCA   8871         A   CAG
                                TGACAGTA GAG   TGAGAG
                                |||||||| |||   ||||||
                                ACTGTCAT CTC   ACTTTC
                                     _  CAG
GAM799  FGR     3'  CTCACTTCTCTCCTATCA    17895    C  TA   C
                                TGA AG  AGAG AGTGAG
                                ||| ||  |||| ||||||
                                ACT TC  TCTC TCACTC
                                  A  C_   T
GAM799  GTF2F1  3'  CTCTCACTGCCCCTTCGC    9150    _  A_
                                GT AAG  GCAGTGAGAG
                                || |||  ||||||||||
                                CG TTC  CGTCACTCTC
                                 C   CC
GAM799  IL7     3'  CATTGCTTTACTGTCA      6080         A
                                TGACAGTA GAGCAGTG
                                |||||||| ||||||||
                                ACTGTCAT TTCGTTAC
                                     _
GAM799  JAM3    3'  CTCTCACTACTCACCTTGTC   51422      TAA   C
                                GACAG   GAG AGTGAGAG
                                |||||   ||| ||||||||
                                CTGTT   CTC TCACTCTC
                                   CCA   A
GAM799  JUN     3'  CTCTCAGTGCTTCTTACTATTA 9478     C     _  G
                                TGA AGTAAGA GCA TGAGAG
                                ||| ||||||| ||| ||||||
                                ATT TCATTCT CGT ACTCTC
                                  A      T   G
GAM799  KRT6B   3'  CTCCTGTTGCTTACCATCA   18695    CA    _    T
                                TGA  GTAAG AGCAG GAG
                                |||  ||||| ||||| |||
                                ACT  CATTC TTGTC CTC
                                  AC    G    _
GAM799  LIFR    3'  CTCAATAAGCTCTTACTG    9744          AG__
                                CAGTAAGAGC    TGAG
                                ||||||||||    ||||
                                GTCATTCTCG    ACTC
                                      AATA
GAM799  LRRC2   3'  CTTTGGGCTCTTATGTCA    44470      G      AGT
                                TGACA TAAGAGC   GAG
                                ||||| |||||||   |||
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                                ACTGT ATTCTCG   TTC
                                  _     GGT
GAM799  MMP14    3'  CTCTCACTACTCTTTCTG    17169    T    C
                                CAG AAGAG AGTGAGAG
                                ||| ||||| ||||||||
                                GTC TTCTC TCACTCTC
                                  T    A
GAM799  MS4A8B   3'  CTCCCACTGTTTGTACTCTCA  48802    C   A      A
                                TGA AGTA GAGCAGTG GAG
                                ||| |||| |||||||| |||
                                ACT TCAT TTTGTCAC CTC
                                  C   G      C
GAM799  MSL3L1   3'  CTCTCATTGGGCCACTGCA   54366    A   AAGAG
                                TG CAGT    CAGTGAGAG
                                || ||||    |||||||||
                                AC GTCA    GTTACTCTC
                                 _   CCGG_
GAM799  NHLH1    3'  CTCTCACTGAATGCTG     18800      AGAG
                                CAGTA   CAGTGAGAG
                                |||||   |||||||||
                                GTCGT   GTCACTCTC
                                  AA__
GAM799  OGN      5'  CTCTGGCCCTTACTGCG    52244    A     A  AGT
                                TG CAGTAAG GC   GAG
                                || ||||||| ||   |||
                                GC GTCATTC CG   CTC
                                 _     C  GT_
GAM799  OGN      5'  CTCTGGCCCTTACTGCG    44326    A     A  AGT
                                TG CAGTAAG GC   GAG
                                || ||||||| ||   |||
                                GC GTCATTC CG   CTC
                                 _     C  GT_
GAM799  PIN1L    3'  CTCCCTGCCACTGTCA     20621       AAGA   T
                                TGACAGT   GCAG GAG
                                |||||||   |||| |||
                                ACTGTCA   CGTC CTC
                                    C___   C
GAM799  PRG2     5'  CTCTCAACTCCTTGCTGCCA  10781    A     AGCAG
                                TG CAGTAAG    TGAGAG
                                || |||||||    ||||||
                                AC GTCGTTC    ACTCTC
                                 C      CTCA_
GAM799  PYGO2    3'  CTCTCGCTCTCTCACT     63985    A   C
                                AGT AGAG AGTGAGAG
                                ||| |||| ||||||||
                                TCA TCTC TCGCTCTC
                                  C   _
GAM799  RHCE     3'  CTCTCACTGTTGCCTGCA    40044    A  TAAG
                                TG CAG   AGCAGTGAGAG
                                || |||   ||||||||||
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                                AC GTC   TTGTCACTCTC
                                 _  CG__
GAM799  RHCE    3' CTCTCACTGTTGCCTGCA   56823   A  TAAG
                                TG CAG   AGCAGTGAGAG
                                || |||   ||||||||||
                                AC GTC   TTGTCACTCTC
                                 _  CG__
GAM799  RHCE    3' CTCTCACTGTTGCCTGCA   56822   A  TAAG
                                TG CAG   AGCAGTGAGAG
                                || |||   ||||||||||
                                AC GTC   TTGTCACTCTC
                                 _  CG__
GAM799  RHCE    3' CTCTCACTGTTGCCTGCA   56824   A  TAAG
                                TG CAG   AGCAGTGAGAG
                                || |||   ||||||||||
                                AC GTC   TTGTCACTCTC
                                 _  CG__
GAM799  RHD     3' CTCTCACTGTTGCCTGCA   32615   A  TAAG
                                TG CAG   AGCAGTGAGAG
                                || |||   ||||||||||
                                AC GTC   TTGTCACTCTC
                                 _  CG__
GAM799  RHD     3' CTCTCACTGTTGCCTGCA   32306   A  TAAG
                                TG CAG   AGCAGTGAGAG
                                || |||   ||||||||||
                                AC GTC   TTGTCACTCTC
                                 _  CG__
GAM799  SH3BP4  3' CTGCGTGCCCTGCTGTCA   27234      A A  _  G
                                TGACAGTA G GCA GT AG
                                |||||||| | ||| || ||
                                ACTGTCGT C CGT CG TC
                                     _ C  G  _
GAM799  SH3GL1  3' CTCCCGGGCCTGCTGTCA   11621      A A  AG  A
                                TGACAGTA G GC  TG GAG
                                |||||||| | ||  || |||
                                ACTGTCGT C CG  GC CTC
                                     _ _  G_  C
GAM799  SIM1    5' CGCTGGTCTTTTACTGCCA   17378   A      __
                                TG CAGTAAGAG  CAGTG
                                || |||||||||  |||||
                                AC GTCATTTTC  GTCGC
                                 C       TG
GAM799  SLC21A2 3' CTCAGCTCTTACCTCA     18857    CA     AG
                                TGA  GTAAGAGC  TGAG
                                |||  ||||||||  ||||
                                ACT  CATTCTCG  ACTC
                                  C_      __
GAM799  SLC7A6  3' CTCCCACTGCTCAGACT    14304    AA     A
                                AGT  GAGCAGTG GAG
                                |||  |||||||| |||
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                                TCA  CTCGTCAC CTC
                                  GA       C
GAM799  SNX15    3'  CTCTCGCTCCTGCACTGCCA  73740    A    AAG  C
                                TG CAGT   AG AGTGAGAG
                                || ||||   || ||||||||
                                AC GTCA   TC TCGCTCTC
                                 C    CG_  C
GAM799  SPTAN1   3'  CTCTCACTTTCCACTGT     11937      AA   C
                                ACAGT  GAG AGTGAGAG
                                |||||  ||| ||||||||
                                TGTCA  CTT TCACTCTC
                                   C_   _
GAM799  TAT      3'  CTCTTATTGCCTCACTTCA   4467     C   A  A
                                TGA AGT AG GCAGTGAGAG
                                ||| ||| || ||||||||||
                                ACT TCA TC CGTTATTCTC
                                  _   C  _
GAM799  TEC      3'  CTCTCAGGAGACCCTGCTGTCA 12218         AGAGCAG_
                                TGACAGTA       TGAGAG
                                ||||||||       ||||||
                                ACTGTCGT       ACTCTC
                                     CCCAGAGG
GAM799  TGFBR3   3'  CTCTTCTGACCTTGCTGCCA   12273    A      AG   T
                                TG CAGTAAG  CAG GAGAG
                                || |||||||  ||| |||||
                                AC GTCGTTC  GTC TTCTC
                                 C      CA  _
GAM799  TXNIP    3'  CTCACTGCAGCTGCCA      21349    A    AAGA
                                TG CAGT    GCAGTGAG
                                || ||||    ||||||||
                                AC GTCG    CGTCACTC
                                 C    A___
GAM799  UBE2L3   3'  CTCACTGCACTCTGCTCA    12500     _   TA  A
                                TGA CAG  AG GCAGTGAG
                                ||| |||  || ||||||||
                                ACT GTC  TC CGTCACTC
                                  C   __  A
GAM799  VCL      3'  CTGTACTTCACTGTCA      12575        _  A
                                TGACAGT AAG GCAG
                                ||||||| ||| ||||
                                ACTGTCA TTC TGTC
                                     C   A
GAM799  VCL      3'  CTGTACTTCACTGTCA      25734        _  A
                                TGACAGT AAG GCAG
                                ||||||| ||| ||||
                                ACTGTCA TTC TGTC
                                     C   A
GAM799  XPC      3'  CTCACTGCCTCTTTGC      16133      _  _
                                GTAA GAG CAGTGAG
                                |||| ||| |||||||
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                                CGTT CTC GTCACTC
                                  T   C
GAM799  ZNF10    3'  CTCACTTCCCTTACAGTCA   31178      A    AGC
                                TGAC GTAAG   AGTGAG
                                |||| |||||   ||||||
                                ACTG CATTC   TCACTC
                                  A    CCT
GAM799  ZNF138   3'  CTCAACTCTTACTGCA      81186    A       CAG
                                TG CAGTAAGAG   TGAG
                                || |||||||||   ||||
                                AC GTCATTCTC   ACTC
                                 _       A__
GAM799  ZNF141   3'  CTCAACCCTTACTGTGCA     12872    _      AGCAG
                                TG ACAGTAAG    TGAG
                                || ||||||||    ||||
                                AC TGTCATTC    ACTC
                                 G       CCA__
GAM799  ZNF42    5'  CTCACTGCTCTCTCAGTC     12784     AGTA
                                GAC    AGAGCAGTGAG
                                |||    ||||||||||
                                CTG    TCTCGTCACTC
                                  ACTC
GAM799  AKR1D1   3'  CTTACACATCTTACTGTCA    19976          GCA
                                TGACAGTAAGA   GTGAG
                                ||||||||||   |||||
                                ACTGTCATTCT   CATTC
                                      ACA
GAM799  AMOTL2   3'  CTCTTCCTACTGTCA       32483        A   CAGT
                                TGACAGTA GAG    GAG
                                |||||||| |||    |||
                                ACTGTCAT CTT    CTC
                                     C  _____
GAM799  BTBD3    3'  CTAACGCTCACTGTCA      30307        AA    A  G
                                TGACAGT  GAGC GT AG
                                |||||||  |||| || ||
                                ACTGTCA  CTCG CA TC
                                   __   _ A
GAM799  C1orf19  3'  CTCTTTGTTTCTTGCTGCCA  68190    A       _   T
                                TG CAGTAAGAG CAG GAG
                                || |||||||| ||| |||
                                AC GTCGTTCTT GTT CTC
                                 C       T   T
GAM799  C20orf21 3'  CTCGTCCCTCACTGTC      35112       AA   CA
                                GACAGT  GAG  GTGAG
                                ||||||  |||  |||||
                                CTGTCA  CTC  TGCTC
                                   __  CC
GAM799  C21orf93 3'  CTTTCGCTCTCAGCT       59086     AA   C
                                AGT  GAG AGTGAGAG
                                |||  ||| ||||||||
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                                TCG  CTC TCGCTTTC
                                  A_  _
GAM799  CALN1    3'  CTCACCGCTTCCGTTCTTACTG 48867        _______  A
                                CAGTAAGA     GC GTGAG
                                ||||||||     || |||||
                                GTCATTCT     CG CACTC
                                     TGCCTT  C
GAM799  CECR7    5'  CTCCCACTGCTCCTGC      79619     A       A
                                GTA GAGCAGTG GAG
                                ||| |||||||| |||
                                CGT CTCGTCAC CTC
                                  C       C
GAM799  CENTG2   3'  CTCTCTAAATTCACTGTCA   29880       AA   CAGT
                                TGACAGT  GAG    GAGAG
                                |||||||  |||    |||||
                                ACTGTCA  CTT    CTCTC
                                    __   AAAT
GAM799  CHL1     3'  CTCTAGTCTACTGTCA      21747        A  G AGT
                                TGACAGTA GA C   GAG
                                |||||||| || |   |||
                                ACTGTCAT CT G   CTC
                                    _ _ AT_
GAM799  CHODL    5'  CTCAGCCTCTCACTTGTCA   46311      _ A    CAG
                                TGACA GT AGAG   TGAG
                                ||||| || ||||   ||||
                                ACTGT CA TCTC   ACTC
                                   T  C    CG_
GAM799  CNOT3    5'  CTCCCCTGGTCTCGCTGTCA  27219       TA   G   T_
                                TGACAG  AGA CAG  GAG
                                ||||||  ||| |||  |||
                                ACTGTC  TCT GTC  CTC
                                    GC   G   CC
GAM799  DDX33    3'  CTCTCTAACCCTCATTGTCA  39372       AA   CAGT_
                                TGACAGT  GAG    GAGAG
                                |||||||  |||    |||||
                                ACTGTTA  CTC    CTCTC
                                    __   CCAAT
GAM799  DKFZp434F142 3'  CTCTCCAGGCCTACTGTCA   50022        A A  AGT
                                TGACAGTA G GC   GAGAG
                                |||||||| | ||   |||||
                                ACTGTCAT C CG   CTCTC
                                    _ _  GAC
GAM799  DKFZp434F142 3'  CTCTTGCCTCACTGT       50024      A  A    T
                                ACAGT AG GCAG GAG
                                ||||| || |||| |||
                                TGTCA TC CGTT CTC
                                   C  _   _
GAM799  DKFZp547E052 3'  CTGATGTCTTACTGTCA     50098          G  G G
                                TGACAGTAAGA CA T AG
                                |||||||||| || | ||
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                                ACTGTCATTCT GT A TC
                                      _ _ G
GAM799  DKFZP564B1162 3'  CATAATGCTACTGTCA     48531       AAG   __
                                TGACAGT   AGCA  GTG
                                |||||||   ||||  |||
                                ACTGTCA   TCGT  TAC
                                    ___    AA
GAM799  DKFZP566J091 3'  CTCCCACTGCTTCCTGCA    48122    A   TAA      A
                                TG CAG   GAGCAGTG GAG
                                || |||   |||||||| |||
                                AC GTC   TTCGTCAC CTC
                                 _  C__       C
GAM799  DKFZP586F1318 5'  CTCCATCCTTTTACTGTCA   31619          CA   A
                                TGACAGTAAGAG  GTG GAG
                                ||||||||||||  ||| |||
                                ACTGTCATTTTC  TAC CTC
                                      C_  _
GAM799  DVS27    3'  TCTCCCTTACTGTCA      53083          AGCAGT
                                TGACAGTAAG     GAGA
                                ||||||||||     ||||
                                ACTGTCATTC     CTCT
                                     C_____
GAM799  EPB41L1  3'  CTCTCAATGTCTTGCTGTCA  70590          G  G
                                TGACAGTAAGA CA TGAGAG
                                |||||||||||  || ||||||
                                ACTGTCGTTCT GT ACTCTC
                                      _ A
GAM799  FLJ10074  5'  CTCGACTTCTTACTGTC     35796          CAG
                                GACAGTAAGAG   TGAG
                                ||||||||||   ||||
                                CTGTCATTCTT   GCTC
                                      CA_
GAM799  FLJ10898  5'  CTCTCACTAAAGACTGTCA    59430       AAGAGC
                                TGACAGT     AGTGAGAG
                                |||||||     ||||||||
                                ACTGTCA     TCACTCTC
                                    GAAA__
GAM799  FLJ10901  3'  CTCTCACTGTGCTCTTACCGCA 36823    ACA       __
                                TG   GTAAGAGCA  GTGAGAG
                                ||   |||||||||  |||||||
                                AC   CATTCTCGT  CACTCTC
                                 GC_       GT
GAM799  FLJ11026  3'  CTTTGGAGCTCTTACTGTC    36992          AGT_
                                GACAGTAAGAGC    GAG
                                ||||||||||||    |||
                                CTGTCATTCTCG    TTC
                                      AGGT
GAM799  FLJ11800  3'  CTCTCTTGCTTCCCACTGGTCA 46424      _  AA_     T
                                TGAC AGT   GAGCAG GAGAG
                                ||||  |||   ||||||  |||||
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                                ACTG TCA   TTCGTT CTCTC
                                  G   CCC     _
GAM799  FLJ11939  5' CTCTCACTGCCTGC       45174     A A
                                GTA G GCAGTGAGAG
                                ||| | ||||||||||
                                CGT C CGTCACTCTC
                                  _ _
GAM799  FLJ12056  3' CTCACAGGGCTTCACTGCCA  46253    A   AA   A__
                                TG CAGT  GAGC   GTGAG
                                || ||||  ||||   |||||
                                AC GTCA  TTCG   CACTC
                                 C   C_   GGA
GAM799  FLJ12768  3' CTTACCCTTGCTGTCA      47181          AGCA
                                TGACAGTAAG    GTGAG
                                ||||||||||    |||||
                                ACTGTCGTTC    CATTC
                                      C___
GAM799  FLJ12788  3' CTCTCACTGCTAGAATATTCA  42546     CAGTAAG
                                TGA      AGCAGTGAGAG
                                |||      ||||||||||||
                                ACT      TCGTCACTCTC
                                  TATAAGA
GAM799  FLJ12888  3' CTCTCACTCCTGCCGTCA    46318     A  AAG  C
                                TGAC GT   AG AGTGAGAG
                                |||| ||   || ||||||||
                                ACTG CG   TC TCACTCTC
                                  C  ___  C
GAM799  FLJ14107  5' CTCACTGCTCTCCTGT      46692      TA
                                ACAG  AGAGCAGTGAG
                                ||||  ||||||||||||
                                TGTC  TCTCGTCACTC
                                  C_
GAM799  FLJ20337  3' CTCCATATCCCTTACTGTCA  34966          AGCA   A
                                TGACAGTAAG    GTG GAG
                                ||||||||||    ||| |||
                                ACTGTCATTC    TAC CTC
                                      CCTA  _
GAM799  FLJ20489  3' CTCTCACTGCCCTTCAACT   35251     __   A
                                AGT  AAG GCAGTGAGAG
                                |||  ||| ||||||||||
                                TCA  TTC CGTCACTCTC
                                  AC   C
GAM799  FLJ21195  3' CTCTTCTTCCTCACTGTC    42450       AA   C  T
                                GACAGT  GAG AG GAGAG
                                ||||||  ||| || |||||
                                CTGTCA  CTC TT TTCTC
                                   __   C  C
GAM799  FLJ22002  3' CTCCCACACCCTCACTGTTA  45771        AA   CA_   A
                                TGACAGT  GAG   GTG GAG
                                |||||||  |||   ||| |||
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                                ATTGTCA  CTC   CAC CTC
                                   __  CCA   C
GAM799  GDAP1L1  3' CTCTCAGTAACTCACTGTC   43830      AA  CAG_
                                GACAGT  GAG   TGAGAG
                                ||||||  |||   ||||||
                                CTGTCA  CTC   ACTCTC
                                   __  AATG
GAM799  GMPPB    3' CTCACTGCTCCCACTGCA    95733    A   AA
                                TG CAGT  GAGCAGTGAG
                                || ||||  ||||||||||
                                AC GTCA  CTCGTCACTC
                                 _   CC
GAM799  HEYL     3' CTCTCCTTCTCACTGTTA    27395      AA  C  T
                                TGACAGT  GAG AG GAGAG
                                |||||||  ||| || |||||
                                ATTGTCA  CTC TC CTCTC
                                   __  T  _
GAM799  HSA9947  3' CTCAGTGCTGCTGTCA     42023      AAG   G
                                TGACAGT   AGCA TGAG
                                |||||||   |||| ||||
                                ACTGTCG   TCGT ACTC
                                   ___   G
GAM799  HSPBP1   3' CTCCCATGCTCTCACTCTCA  24361    C  A    GT_
                                TGA AGT AGAGCA   GAG
                                ||| ||| ||||||   |||
                                ACT TCA TCTCGT   CTC
                                  C  C     ACC
GAM799  humNRDR  3' CTGCTCACCTTACTGTT     40663       ___
                                GACAGTAA   GAGCAG
                                ||||||||   ||||||
                                TTGTCATT   CTCGTC
                                    CCA
GAM799  HXCP2    3' CTCTCTGTGCTTATGTCA    50836     G   A   T
                                TGACA TAAG GCAG GAG
                                ||||| |||| |||| |||
                                ACTGT ATTC TGTC CTC
                                   _   G   T
GAM799  ITGB5    3' CTCTCAGCTTTCCCTGCCA   59499    A  TA   AG
                                TG CAG  AGAGC  TGAGAG
                                || |||  |||||  ||||||
                                AC GTC  TTTCG  ACTCTC
                                 C  CC   __
GAM799  JIK      3' CTCTCTTACTCTTACTG     32798        CAGT
                                CAGTAAGAG   GAGAG
                                |||||||||   |||||
                                GTCATTCTC   CTCTC
                                    ATT_
GAM799  KIAA0022 3' CTCTTATTCCTCTACCGTCA  29665     A  A  C
                                TGAC GTA GAG AGTGAGAG
                                |||| ||| ||| ||||||||
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                                ACTG CAT CTC TTATTCTC
                                  C  _  C
GAM799  KIAA0247 3' CTGGCCTCTTGCTGCCA    28398   A      CA  G
                                TG CAGTAAGAG  GT AG
                                || |||||||||  || ||
                                AC GTCGTTCTC  CG TC
                                 C       __  G
GAM799  KIAA0321 5' CTCTCACTGCCTGGATG    62394   GTA  A
                                CA  AG GCAGTGAGAG
                                ||  || ||||||||||
                                GT  TC CGTCACTCTC
                                 AGG  _
GAM799  KIAA0408 3' TTGCTCTCTACTGTCA     28141        _
                                TGACAGTA AGAGCAG
                                |||||||| |||||||
                                ACTGTCAT TCTCGTT
                                     C
GAM799  KIAA0459 3' TGCTGCTCACTGCCA      61010   A   AA
                                TG CAGT  GAGCAGTG
                                || ||||  ||||||||
                                AC GTCA  CTCGTCGT
                                 C   __
GAM799  KIAA0865 3' CTCACTGTATATCCTCA    61248    CA  AGA
                                TGA  GTA  GCAGTGAG
                                |||  |||  ||||||||
                                ACT  TAT  TGTCACTC
                                  CC  A__
GAM799  KIAA1029 3' CTCTCATTGTCACTG      23473     AAGA
                                CAGT   GCAGTGAGAG
                                ||||   ||||||||||
                                GTCA   TGTTACTCTC
                                  C___
GAM799  KIAA1036 5' CTCACTGCTGCCCGTCA    29818     A_  AAG
                                TGAC  GT  AGCAGTGAG
                                ||||  ||  |||||||||
                                ACTG  CG  TCGTCACTC
                                  CC  ___
GAM799  KIAA1054 3' CTCTCACTTCTGCCTCCTATCA 68435    C  TA  A  ___
                                TGA AG  AG GCA  GTGAGAG
                                ||| ||  || |||  |||||||
                                ACT TC  TC CGT  CACTCTC
                                  A  C_  _  CTT
GAM799  KIAA1061 3' CATTGTCCCTTACTGCCA   71175   A    A_
                                TG CAGTAAG  GCAGTG
                                || |||||||  ||||||
                                AC GTCATTC  TGTTAC
                                 C      CC
GAM799  KIAA1332 3' CTCTCACCGTGTTCATTGTCA  71166       AA   __
                                TGACAGT  GAGCA  GTGAGAG
                                |||||||  |||||  |||||||
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                                ACTGTTA  CTTGT  CACTCTC
                                   __    GC
GAM799  KIAA1434  3'  CTCTCACTACCTATTAC    69610     G  C_
                                GTAA AG  AGTGAGAG
                                |||| ||  ||||||||
                                CATT TC  TCACTCTC
                                  A  CA
GAM799  KIAA1456  3'  CTCTCTGAAGCCTATTGTCA  66994       A A  AGT_
                                TGACAGTA G GC   GAGAG
                                |||||||| | ||   |||||
                                ACTGTTAT C CG   CTCTC
                                   _ _  AAGT
GAM799  KIAA1554  3'  CTCCGTTCTCCTCACTGTCA  95151       A___    AGT
                                TGACAGT   AGAGC  GAG
                                |||||||   |||||  |||
                                ACTGTCA   TCTTG  CTC
                                   CTCC    C__
GAM799  KIAA1560  3'  CTCTCACCACTTAACTCACTGT 64176      A ___  CA
                                ACAGT AG  AG  GTGAGAG
                                ||||| ||  ||  |||||||
                                TGTCA TC  TC  CACTCTC
                                  C  AAT  AC
GAM799  KIAA1799  5'  CTCTCACTACTCTGGC     74635    A   C
                                GT AGAG AGTGAGAG
                                || |||| ||||||||
                                CG TCTC TCACTCTC
                                 G   A
GAM799  KIF13B    3'  CTTATGTTGCTCTTTCTATCA  30907    C  T     __
                                TGA AG AAGAGCA  GTGAG
                                ||| || |||||||  |||||
                                ACT TC TTCTCGT  TATTC
                                  A  T      TG
GAM799  LMOD1     3'  CTGTCAGCCCTCACTGTCA   24043       A  A  AG   G
                                TGACAGT AG GC  TGA AG
                                ||||||| || ||  ||| ||
                                ACTGTCA TC CG  ACT TC
                                   C  C  __   G
GAM799  LRP1B     5'  CTCTCACTGCCCCTCTTGC   37668      ___
                                GTAAGA   GCAGTGAGAG
                                ||||||   ||||||||||
                                CGTTCT   CGTCACTCTC
                                   CCC
GAM799  MAD4      3'  CTCCCACTGCTCCCTGTCA   21273      TAA      A
                                TGACAG   GAGCAGTG GAG
                                ||||||   |||||||| |||
                                ACTGTC   CTCGTCAC CTC
                                   C__       C
GAM799  MAIL      3'  CTAGCAACACTCACTGTCA   48650       AA   CAG  AG
                                TGACAGT  GAG   TG  AG
                                |||||||  |||   ||  ||
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                                ACTGTCA  CTC   AC  TC
                                   __   ACA  GA
GAM799  MFN1     3'  CTCCCACTGCTCCTAC      35543     A       A
                                GTA GAGCAGTG GAG
                                ||| |||||||| |||
                                CAT CTCGTCAC CTC
                                  C       C
GAM799  MGC1127  3'  CTCCCAGATCTGCTCACTGCCA 53215    A    AA     ___ A
                                TG CAGT  GAGCAG   TG GAG
                                || ||||  ||||||   || |||
                                AC GTCA  CTCGTC   AC CTC
                                 C   __     TAG  C
GAM799  MGC16384 5'  TCTCACTGCTAGTGT       53870     G AAG
                                ACA T   AGCAGTGAGA
                                ||| |   ||||||||||
                                TGT A   TCGTCACTCT
                                  G ___
GAM799  MGC26744 5'  CGCGCTCTTACCTCA       58311     CA       A
                                TGA  GTAAGAGC GTG
                                |||  |||||||| |||
                                ACT  CATTCTCG CGC
                                  C_       _
GAM799  MGC3079  3'  CATACTCTTACTATCA      50950     C       CA
                                TGA AGTAAGAG  GTG
                                ||| ||||||||  |||
                                ACT TCATTCTC  TAC
                                  A       A_
GAM799  OLFM3    3'  CTCAAATATCTCACTGTCA    82143       A   GCAG
                                TGACAGT AGA    TGAG
                                ||||||| |||    ||||
                                ACTGTCA TCT    ACTC
                                    C   ATAA
GAM799  PEAS     3'  CTCCTGAGCCTGCTGTCA     54069        AGAG   T
                                TGACAGTA    CAG GAG
                                ||||||||    ||| |||
                                ACTGTCGT    GTC CTC
                                     CCGA   _
GAM799  PELI2    3'  CTCCATCCCTTTACTGTCA    41181        A   CA   A
                                TGACAGTA GAG  GTG GAG
                                |||||||| |||  ||| |||
                                ACTGTCAT TTC  TAC CTC
                                     _   CC   _
GAM799  PGLYRP   3'  CTCTCACTTTGGGCCACTGTC  53576       AAGA _____
                                GACAGT    GC    AGTGAGAG
                                ||||||    ||    ||||||||
                                CTGTCA    CG    TCACTCTC
                                   C___   GGTT
GAM799  PNMA5    5'  CTCTACCTCTCTTGCTGCCA   73596    A       C  TG
                                TG CAGTAAGAG AG  AGAG
                                || |||||||| ||  ||||
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                                AC GTCGTTCTC TC  TCTC
                                 C        _ CA
GAM799  PRO0038  5' CTCCCCGTTGCTTACTGT    26092        _  AGT
                                ACAGTAAG AGC   GAG
                                |||||||| |||   |||
                                TGTCATTC TTG   CTC
                                    G   CCC
GAM799  RGS17    3' CTCTGGTTGTTCACTGCCA   24841    A   AA     TG
                                TG CAGT  GAGCAG  AGAG
                                || ||||  ||||||  ||||
                                AC GTCA  CTTGTT  TCTC
                                 C   __     GG
GAM799  SBBI26   3' CTCTTTAGTCCTCACTGTTA  38134       A  AG AGT
                                TGACAGT AG  C   GAGAG
                                ||||||| ||  |   |||||
                                ATTGTCA TC  G   TTCTC
                                    C  CT AT_
GAM799  SEC6     3' CTCACTGTGCTGTCA      71594       AAGA
                                TGACAGT   GCAGTGAG
                                |||||||   ||||||||
                                ACTGTCG   TGTCACTC
                                    ____
GAM799  SHANK3   3' CTCACTGCCACTGCCA     65494    A   AAGA
                                TG CAGT   GCAGTGAG
                                || ||||   ||||||||
                                AC GTCA   CGTCACTC
                                 C   C___
GAM799  SLC26A10 5' CTCCCACTTCATCTCACTGT  56028     A  GC_   A
                                ACAGT AGA   AGTG GAG
                                ||||| |||   |||| |||
                                TGTCA TCT   TCAC CTC
                                   C  ACT   C
GAM799  SLC5A7   3' CTCACTCATACTGTCA     41510       A  GCA
                                TGACAGTA GA   GTGAG
                                |||||||| ||   |||||
                                ACTGTCAT CT   CACTC
                                    A  ___
GAM799  STAM2    3' CTTTTGCTCTCACTGTTA    19562       A     T
                                TGACAGT AGAGCAG GAG
                                ||||||| ||||||| |||
                                ATTGTCA TCTCGTT TTC
                                    C     _
GAM799  UBE2N    3' CTCACTAATAACATTGCTGTCA 94541        GAGC___
                                TGACAGTAA      AGTGAG
                                |||||||||      ||||||
                                ACTGTCGTT      TCACTC
                                     ACAATAA
GAM799  UBE2N    3' CTCACTAATAACATTGCTGTCA 12511        GAGC___
                                TGACAGTAA      AGTGAG
                                |||||||||      ||||||
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                                ACTGTCGTT      TCACTC
                                     ACAATAA
GAM799  UBP1     3'  CTCACTGTCACTGCCA     27223    A   AAGA
                                TG CAGT    GCAGTGAG
                                || ||||    ||||||||
                                AC GTCA    TGTCACTC
                                 C    C___
GAM799  ZNF297   3'  CTCCCACCACACTTACTGTC  18390         AGCA  A
                                GACAGTAAG    GTG GAG
                                |||||||||    ||| |||
                                CTGTCATTC    CAC CTC
                                     ACAC   C
GAM799  LOC132671 3' CTTGACTTCTTCACTGTCA   59169        _    CAG
                                TGACAGT AAGAG   TGAG
                                ||||||| |||||   ||||
                                ACTGTCA TTCTT   GTTC
                                    C    CA_
GAM799  LOC142779 5' CTCCTGCTCTCACTGCA     76395    A   A     T
                                TG CAGT AGAGCAG GAG
                                || |||| ||||||| |||
                                AC GTCA TCTCGTC CTC
                                 _   C     _
GAM799  LOC145566 5' CACCAGCTACCCTTACTGCCA 77271    A     ___   A_
                                TG CAGTAAG   AGC  GTG
                                || |||||||   |||  |||
                                AC GTCATTC   TCG  CAC
                                 C      CCA   AC
GAM799  LOC146159 5' CTCCCACGCTCTTACTGTCA  77680           A   A
                                TGACAGTAAGAGC GTG GAG
                                |||||||||||| ||| |||
                                ACTGTCATTCTCG CAC CTC
                                       _  C
GAM799  LOC146823 3' CTCCCACTGCTCCTTG      83796     TAA      A
                                CAG   GAGCAGTG GAG
                                |||   |||||||| |||
                                GTT   CTCGTCAC CTC
                                  C__       C
GAM799  LOC147229 5' CTCTCACCTGAGCCCTCACTG  78320     A  A  A___
                                CAGT AG GC    GTGAGAG
                                |||| || ||    |||||||
                                GTCA TC CG    CACTCTC
                                   C  C  AGTC
GAM799  LOC147639 3' CTCCATGAGTCTTGCTGCCA   78379    A      GCA   A
                                TG CAGTAAGA   GTG GAG
                                || ||||||||   ||| |||
                                AC GTCGTTCT   TAC CTC
                                 C       GAG  _
GAM799  LOC147976 3' CTCACTATGCCTTCACTG     78588     _   A   __
                                CAGT AAG GCA  GTGAG
                                |||| ||| |||  |||||
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                                GTCA TTC CGT  CACTC
                                  C   _   AT
GAM799   LOC148029 3'  CTCCCTTGGCTCACTGTC    78619       AA   __  T
                                GACAGT  GAGC  AG GAG
                                ||||||  ||||  || |||
                                CTGTCA  CTCG  TC CTC
                                   __   GT  C
GAM799   LOC148697 3'  CTCTTGTTTCTACTGCCA    78923    A    AG    T
                                TG CAGTA  AGCAG GAG
                                || |||||  ||||| |||
                                AC GTCAT  TTGTT CTC
                                 C    CT    _
GAM799   LOC148946 3'  CTCACTAGCCTTACTGTCA    84309          A  _
                                TGACAGTAAG GC AGTGAG
                                |||||||||| || ||||||
                                ACTGTCATTC CG TCACTC
                                      _  A
GAM799   LOC149267 3'  TACTGCTACTGTCA        56678        AAG
                                TGACAGT   AGCAGTG
                                |||||||   |||||||
                                ACTGTCA   TCGTCAT
                                    ___
GAM799   LOC149734 3'  CACTGCTCAGCTTCTCA     84632     C_   AA
                                TGA  AGT  GAGCAGTG
                                |||  |||  ||||||||
                                ACT  TCG  CTCGTCAC
                                  CT   A_
GAM799   LOC150113 3'  CTCCACGGCACTCCTGCTGTCA 87211         A   CA__   A
                                TGACAGTA GAG    GTG GAG
                                |||||||| |||    ||| |||
                                ACTGTCGT CTC    CAC CTC
                                     C   ACGG   _
GAM799   LOC150244 3'  CTCTCACTGCCCGTGAGTC    79735     AG  AGA
                                GAC  TA   GCAGTGAGAG
                                |||  ||   ||||||||||
                                CTG  GT   CGTCACTCTC
                                  A_  GCC
GAM799   LOC150538 3'  CTCTCCTCTTCTTACTCTCA   79932     C       C  T
                                TGA AGTAAGAG AG GAGAG
                                ||| |||||||| || |||||
                                ACT TCATTCTT TC CTCTC
                                  C       C  _
GAM799   LOC152273 3'  CTTGTTACTCTTACTGCA     80537    A       C  TG
                                TG CAGTAAGAG AG  AG
                                || |||||||| ||  ||
                                AC GTCATTCTC TT  TC
                                 _       A  GT
GAM799   LOC153364 5'  CTCACTGCGGGCCTCTGCTGTC 80811         A  _____
            A                    TGACAGTA GA     GCAGTGAG
                                ||||||||  ||     ||||||||
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                                ACTGTCGT CT    CGTCACTC
                                     _ CCGGG
GAM799  LOC158187 3' CTCTCTTGCCTCACTCTCA   86690    C  A A   T
                                TGA AGT AG GCAG GAGAG
                                ||| ||| || |||| |||||
                                ACT TCA TC CGTT CTCTC
                                  C  C _   _
GAM799  LOC158187 3' CTCTCAATATTGCTGTCA    86689        GAGCAG
                                TGACAGTAA     TGAGAG
                                |||||||||     ||||||
                                ACTGTCGTT     ACTCTC
                                      ATA___
GAM799  LOC163682 5' CTCTCACTGCCCTGCATGGTC  87033    AGTA_  A
                                GAC    AG GCAGTGAGAG
                                |||    || ||||||||||
                                CTG    TC CGTCACTCTC
                                  GTACG  C
GAM799  LOC199848 3' CTCTCTTCTTGTTACTGCCA   89863    A    G  CAGT
                                TG CAGTAA AG    GAGAG
                                || |||||| ||    |||||
                                AC GTCATT TT    CTCTC
                                 C     G  CTT_
GAM799  LOC203286 3' CTCTGGGTCTTGCTGTCA    90498         G AGT
                                TGACAGTAAGA C   GAG
                                |||||||||||  |   |||
                                ACTGTCGTTCT G   CTC
                                      _ GGT
GAM799  LOC203378 3' CTCCTTCTTACTGTC       90600         GC  T
                                GACAGTAAGA  AG GAG
                                ||||||||||  || |||
                                CTGTCATTCT  TC CTC
                                     __  _
GAM799  LOC203636 3' TCACTGCTACTGCCA       89432    A   AAG
                                TG CAGT   AGCAGTGA
                                || ||||   ||||||||
                                AC GTCA   TCGTCACT
                                 C   ____
GAM799  LOC219673 3' CTCGCTTTCACCGTCA      93029     A  AA   C
                                TGAC GT  GAG AGTGAG
                                |||| ||  ||| ||||||
                                ACTG CA  CTT TCGCTC
                                  C  __  _
GAM799  LOC220032 3' CATTGTGCTCTCGCTATCA   91668    C  TA    __
                                TGA AG  AGAGCA  GTG
                                ||| ||  ||||||  |||
                                ACT TC  TCTCGT  TAC
                                  A  GC     GT
GAM799  LOC220575 3' CTCTCTTGCTTCCCACTGGTCA 76308     _  AA_    T
                                TGAC AGT   GAGCAG GAGAG
                                |||| |||   |||||| |||||
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                                ACTG TCA   TTCGTT CTCTC
                                  G   CCC     _
GAM799   LOC221405 3'  CTCACTGCCTCTCACTTGCCA  93883    A _  A    _
                                TG CA GT AGAG CAGTGAG
                                || || || |||| |||||||
                                AC GT CA TCTC GTCACTC
                                 C  T  C    C
GAM799   LOC245771 3'  CTCTCACTGTGCTCTTACCGCA 92889    ACA       __
                                TG   GTAAGAGCA  GTGAGAG
                                ||   |||||||||  |||||||
                                AC   CATTCTCGT  CACTCTC
                                 GC_        GT
GAM799   LOC256146 5'  CTCCACTCCTTACTGCCA    97520    A      AGC    A
                                TG CAGTAAG   AGTG GAG
                                || |||||||   |||| |||
                                AC GTCATTC   TCAC CTC
                                 C      C__    _
GAM799   LOC257109 3'  CGGTGCCATTACTGTCA     95570         GA   G
                                TGACAGTAA  GCA TG
                                |||||||||  ||| ||
                                ACTGTCATT  CGT GC
                                      AC   G
GAM799   LOC257451 3'  CTCTCGCTCTCTCACT      95555     A    C
                                AGT AGAG AGTGAGAG
                                ||| |||| ||||||||
                                TCA TCTC TCGCTCTC
                                  C   _
GAM799   LOC51003  3'  CTCCTGGAACCTTACTGTC   32145         AG__   T
                                GACAGTAAG    CAG GAG
                                |||||||||    ||| |||
                                CTGTCATTC    GTC CTC
                                      CAAG   _
GAM799   LOC56270  3'  TTTACTGTCACTGTCA      39024        AAGA
                                TGACAGT    GCAGTGAG
                                |||||||    ||||||||
                                ACTGTCA    TGTCATTT
                                    C___
GAM799   LOC58525  5'  CTTGGATGCCCCTGCTGTCA  78646         AGA   G_
                                TGACAGTA   GCA  TGAG
                                ||||||||   |||  ||||
                                ACTGTCGT   CGT  GTTC
                                     CCC   AG
GAM799   LOC90768  3'  CTCCCTCTTACTGTC       63954          CAGT
                                GACAGTAAGAG    GAG
                                ||||||||||    |||
                                CTGTCATTCTC    CTC
                                       C___
GAM799   LOC91010  3'  CTCCCTTTCCTCTTACTGTACA 64616    _        C__  T
                                TG ACAGTAAGAG   AG GAG
                                || ||||||||||   || |||
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                                AC TGTCATTCTC   TC CTC
                                 A        CTT  C
GAM799  LOC92078  5'  TCTCAGGCTCACTGT      67989      AA   AG
                                ACAGT  GAGC  TGAGA
                                |||||  ||||  |||||
                                TGTCA  CTCG  ACTCT
                                  __   G_
GAM800  CD28      3'  AAAACACTGTCTCCCA      20432     A
                                TGG AGGCAGTGTTTT
                                ||| ||||||||||||
                                ACC TCTGTCACAAAA
                                  C
GAM800  GYPC      3'  TACAAGAGGCCACTCCC     33655     C    TT
                                GG AGTG  TTCTTGTA
                                || ||||  ||||||||
                                CC TCAC  GAGAACAT
                                 C   CG
GAM800  GYPC      3'  TACAAGAGGCCACTCCC     9165      C    TT
                                GG AGTG  TTCTTGTA
                                || ||||  ||||||||
                                CC TCAC  GAGAACAT
                                 C   CG
GAM800  ITPR2     3'  AAAACACTGCCTCCA       9444       A
                                TGGA GGCAGTGTTTT
                                |||| ||||||||||
                                ACCT CCGTCACAAAA
                                  _
GAM800  MUCDHL    3'  GCAGAAAACAGCACCTCCCA  48370     A   CAG       T
                                TGG AGG   TGTTTTCT GT
                                ||| |||   |||||||| ||
                                ACC TCC   ACAAAAGA CG
                                  C   ACG       _
GAM800  MUCDHL    3'  GCAGAAAACAGCACCTCCCA  87301     A   CAG       T
                                TGG AGG   TGTTTTCT GT
                                ||| |||   |||||||| ||
                                ACC TCC   ACAAAAGA CG
                                  C   ACG       _
GAM800  RGS3      5'  ATGGCTGAACACTGACTCCCA  40860     A  G       TC TG
                                TGG AG CAGTGTTT  T  T
                                ||| || ||||||||  |  |
                                ACC TC GTCACAAG  G  A
                                  C  A       TC GT
GAM800  SPON1     3'  ACAGGTTTACACTGCCTTCC   62446           TTT
                                GGAAGGCAGTGT   CTTGT
                                ||||||||||||   |||||
                                CCTTCCGTCACA   GGACA
                                       TTT
GAM800  FLJ10352  3'  CAATGACAAAACCGCCTTCCA  49557         A  G  T  _
                                TGGAAGGC GT TT TC TTG
                                |||||||| || || || |||
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                                ACCTTCCG CA AA AG AAC
                                    C  A  C  T
GAM800  FLJ21736 3'  ACAAGGCCGCCTCCCA     46224     A    A  GTTTT
                                TGG AGGC GT    CTTGT
                                ||| |||| ||    |||||
                                ACC TCCG CG    GAACA
                                  C   C _____
GAM800  KIAA0662 3'  GAAAACATCTGCCTCCCA    81854     A     _
                                TGG AGGCAG TGTTTTC
                                ||| |||||| |||||||
                                ACC TCCGTC ACAAAAG
                                  C     T
GAM800  KRT6     3'  TACAAGCCCCTCTGCCCCCA  82222     AA    TGTTTT
                                TGG  GGCAG     CTTGTA
                                |||  |||||     ||||||
                                ACC  CCGTC     GAACAT
                                  C_    TCCCC_
GAM800  MDS006   3'  TTACAAGAAAGGAAGAGCCTTC 39587        AGTG_
           CA                     TGGAAGGC    TTTTCTTGTAA
                                |||||||||    ||||||||||
                                ACCTTCCG    GAAAGAACATT
                                    AGAAG
GAM800  MGC14859 3'  TACCTGGGACACTGCCTCCC  61921    A         CTT
                                GG AGGCAGTGTTTT   GTA
                                || ||||||||||||   |||
                                CC TCCGTCACAGGG   CAT
                                 C          TC_
GAM800  MGC2452  3'  GAAAACACCAGCCTCCA     50983     A   A_
                                TGGA GGC  GTGTTTTC
                                |||| |||  ||||||||
                                ACCT CCG  CACAAAAG
                                  _  AC
GAM800  NUDEL    3'  GTTACAAAAAATACTTCCCTC  47970    A  C      C
                                GA GG AGTGTTTT TTGTAAC
                                || || |||||||| |||||||
                                CT CC TCATAAAA AACATTG
                                 C  T      _
GAM800  PRO0255  3'  TTACAAAAAAACATTCT     26143    C      C
                                GG AGTGTTTT TTGTAA
                                || |||||||| ||||||
                                TC TTACAAAA AACATT
                                  _      A
GAM800  SQV7L    5'  TGCAACCACTGCCTCCCA     70582     A      TTTTC
                                TGG AGGCAGTG    TTGTA
                                ||| ||||||||    |||||
                                ACC TCCGTCAC    AACGT
                                  C       C____
GAM800  VEST1    5'  AGAACACTGCCTCTCA      53682    GA
                                TG  AGGCAGTGTTTT
                                ||  ||||||||||||
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                                AC  TCCGTCACAAGA
                                 TC
GAM800   LOC128553 3'  ACAAGAAAACAAAGTGCC    74758      G__
                                GGCA   TGTTTTCTTGT
                                ||||   ||||||||||
                                CCGT   ACAAAAGAACA
                                  GAA
GAM800   LOC145497 5'  TACAAGAGAACTACTACCTCCA 77217      A  C  _
                                TGGA GG AGT GTTTTCTTGTA
                                |||| || ||| ||||||||||
                                ACCT CC TCA CAAGAGAACAT
                                  _ A   T
GAM800   LOC145837 5'  TACGGAAAACACTGCCCTCC   83546     A          T
                                GGA GGCAGTGTTTTCT GTA
                                ||| ||||||||||||| |||
                                CCT CCGTCACAAAAGG CAT
                                  C          _
GAM800   LOC146756 3'  GAAACACTGCCCCCA       83778     AA
                                TGG  GGCAGTGTTTT
                                |||  ||||||||||
                                ACC  CCGTCACAAAG
                                  C_
GAM800   LOC153339 3'  GTTATTTATACACTGCCTTCCA 86010           TTTCTT
                                TGGAAGGCAGTGT     GTAAC
                                ||||||||||||     |||||
                                ACCTTCCGTCACA     TATTG
                                        TATT__
GAM800   LOC153711 3'  ACAAGAAAATCTTC       86132      GCAGT
                                GAAG    GTTTTCTTGT
                                ||||    ||||||||||
                                CTTC    TAAAAGAACA
                                  _____
GAM800   LOC170082 5'  TGCAAACTCCGCCTTCCA    82567        AGT   TTCT
                                TGGAAGGC   GTT    TGTA
                                ||||||||   |||    ||||
                                ACCTTCCG   CAA    ACGT
                                     CCT   ____
GAM800   LOC202024 5'  ACATGGGACACTGCCCTCTA   89145      A         CT
                                TGGA GGCAGTGTTTT  TGT
                                |||| ||||||||||  |||
                                ATCT CCGTCACAGGG  ACA
                                  C         T_
GAM800   LOC203339 3'  TGCAACCACTGCCTCCCA    90552     A       TTTTC
                                TGG AGGCAGTG    TTGTA
                                ||| ||||||||    |||||
                                ACC TCCGTCAC    AACGT
                                  C       C____
GAM800   LOC219673 3'  TACAAGAAACCGCCC       93039     CA   T
                                GG  GTG TTTCTTGTA
                                ||  ||| |||||||||
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                                CC  CGC AAAGAACAT
                                 __   C
GAM800  LOC220074 3'  TGCAAACTCCGCCTTCCA    59288        AGT   TTCT
                                TGGAAGGC   GTT    TGTA
                                ||||||||   |||    ||||
                                ACCTTCCG   CAA    ACGT
                                    CCT   ____
GAM800  LOC221895 3'  AAAACACTGCCCTCTA      92518      A
                                TGGA GGCAGTGTTTT
                                |||| ||||||||||
                                ATCT CCGTCACAAAA
                                  C
GAM800  LOC254015 3'  GAAACACTGCCCCCA       96703      AA
                                TGG  GGCAGTGTTTT
                                |||  ||||||||||
                                ACC  CCGTCACAAAG
                                  C_
GAM800  LOC91661  3'  GGAAAAACTGCCTTCCA     56402          G
                                TGGAAGGCAGT TTTTCT
                                |||||||||| ||||||
                                ACCTTCCGTCA AAAAGG
                                          _
GAM801  ACCN1     3'  TCTTCTCTCCCTGTGA      6585           A
                                TCACAGGGAGA AAGA
                                |||||||||| ||||
                                AGTGTCCCTCT TTCT
                                     C
GAM801  ADORA1    5'  AGCCTCCTCTCCCTCTGTGA  5421       __     AA  A
                                TCACA  GGGAGA  AG CT
                                |||||  ||||||  || ||
                                AGTGT  CCCTCT  TC GA
                                   CT     CC  C
GAM801  AK2       3'  TCTTTCCATCCCTGTGA     7887          GA_
                                TCACAGGGA   AAAGA
                                |||||||||   |||||
                                AGTGTCCCT   TTTCT
                                     ACC
GAM801  ATF6      3'  TCTCTTCCCTCTGTGA      63949        A   A
                                TCACAGGG GAA AGA
                                |||||||| ||| |||
                                AGTGTCTC CTT TCT
                                     C   C
GAM801  BSND      5'  GTCTTCTCTCCCTGTG      54111          A
                                CACAGGGAGA AAGAC
                                |||||||||| |||||
                                GTGTCCCTCT TTCTG
                                     C
GAM801  CASP10    3'  ACTAGTATTCCCTGTG      52095        GAAAAG
                                CACAGGGA     ACTAGT
                                ||||||||     ||||||
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                                GTGTCCCT     TGATCA
                                     TA____
GAM801  DDB1    3'  GAAACATTTTCTCCCTGGA   8626    A       GACTAG
                                TC CAGGGAGAAAA     TC
                                || ||||||||||     ||
                                AG GTCCCTCTTTT     AG
                                 _         ACAA__
GAM801  EDN1    5'  GCTGCCTTTTCTCCCCGT    8728    A       AC
                                AC GGGAGAAAAG  TAGT
                                || ||||||||||  ||||
                                TG CCCTCTTTTC  GTCG
                                 C        C_
GAM801  ELMO2    3'  GACTAGTCTCGAAATTTCTCCC 55674        A_________  CTAG
           TG                     CAGGGAGAA       AGA   TC
                                |||||||||       |||   ||
                                GTCCCTCTT       TCT   AG
                                     TAAAGIIIC   GATC
GAM801  FEN1    5'  AGACTCTGTTCTCCCTGGA   14641   A       A  CTA
                                TC CAGGGAGAA AGA   GTCT
                                || |||||||||  |||   ||||
                                AG GTCCCTCTT TCT   CAGA
                                 _       G   ___
GAM801  GCGR    3'  GAGATTGGGCCTCCTCTCCCTG 3855        AA  A_
                                CAGGGAGA  AG  CTAGTCTC
                                ||||||||  ||  ||||||||
                                GTCCCTCT  TC  GGTTAGAG
                                     CC  CG
GAM801  GJA1    3'  GGGCTTTTTCTCCC       3902         GACT
                                GGGAGAAAA    AGTCT
                                |||||||||    |||||
                                CCCTCTTTT    TCGGG
                                     ____
GAM801  HNRPDL   3'  AGGCTTCATCTTCTCCCTGT   18424        AA   CT_
                                ACAGGGAGA  AGA   AGTCT
                                |||||||||  |||   |||||
                                TGTCCCTCT  TCT   TCGGA
                                     __   ACT
GAM801  HYAL2    3'  GAGGCCCCTTCTCTCCCTG    52531        A   ACTA
                                CAGGGAGA AAG    GTCTC
                                ||||||||  |||    |||||
                                GTCCCTCT TTC    CGGAG
                                     C   CC__
GAM801  HYAL2    3'  GAGGCCCCTTCTCTCCCTG    13665        A   ACTA
                                CAGGGAGA AAG    GTCTC
                                ||||||||  |||    |||||
                                GTCCCTCT TTC    CGGAG
                                     C   CC__
GAM801  IFNA21   3'  AGACTCATTTCTCCT       9298         A  CTA
                                GGGAGAAA GA   GTCT
                                ||||||||  ||   ||||
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                                TCCTCTTT CT   CAGA
                                    A ___
GAM801  JPH3     3'  GATCGGCCACCTCCTCCCTGTG 40306          AAAAGA_ TA
              A                  TCACAGGGAG      C  GTC
                                 ||||||||||      |  |||
                                 AGTGTCCCTC      G  TAG
                                     CTCCACC GC
GAM801  LFG      3'  AGTTCTCCTCTCCCTGGGA   76713    A      AA  _
                                 TC CAGGGAGA  AGA CT
                                 || ||||||||  ||| ||
                                 AG GTCCCTCT  TCT GA
                                  G       CC   T
GAM801  MNT      5'  GAGACATTGATTTTTCTCCCCG 39713     A        ACTA_
              TG                   CAC GGGAGAAAAG     GTCTC
                                 ||| ||||||||||     |||||
                                 GTG CCCTCTTTTT     CAGAG
                                   C         AGTTA
GAM801  MX1      3'  GAGCCCTGTCTCCTCTCTCTGT 10145         AA    TAGT
                                 ACAGGGAGA  AGAC    CTC
                                 |||||||||  ||||    |||
                                 TGTCTCTCT  TCTG    GAG
                                      CC    TCCC
GAM801  NOTCH2   3'  ACTAGTCTTAACTGTTGA    44311     _   GGAGAA
                                 TCA CAG     AAGACTAGT
                                 ||| |||     |||||||||
                                 AGT GTC     TTCTGATCA
                                   T   AA____
GAM801  NOTCH3   3'  GAGATGCTCCCTCCCCCTGTGA 4746         A  AAA  CTA
                                 TCACAGGG GA   GA   GTCTC
                                 |||||||| ||   ||   |||||
                                 AGTGTCCC CT   CT   TAGAG
                                      C  CC_  CG_
GAM801  NR4A1    5'  GACTGCTCCCCCCTCCTGTGA  9237         G  AAAA  C
                                 TCACAGG AG    GA TAGTC
                                 ||||||| ||    || |||||
                                 AGTGTCC TC    CT GTCAG
                                      _  CCCC  C
GAM801  PBX2     3'  AGATGCCATCTTCCCCTGTGA  10442         A  AA   CTA_
                                 TCACAGGG GA  AGA    GTCT
                                 |||||||| ||  |||    ||||
                                 AGTGTCCC CT  TCT    TAGA
                                      _ ___   ACCG
GAM801  PIK3R3   5'  AGCTTTTCTCCCCGGA      61049     ACA        A
                                 TC   GGGAGAAAAG CT
                                 ||   |||||||||| ||
                                 AG   CCCTCTTTTC GA
                                   GC_         _
GAM801  PKHD1    3'  AGACCAGTCTTTCTGGGA    56913    A   GAGAA     A
                                 TC CAGG    AAGACT GTCT
                                 || ||||    |||||| ||||
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                                AG GTCT    TTCTGA CAGA
                                 G  _____    C
GAM801  PPP1R2   3' ACTAGCTTTTTTCCC      20684         A
                                GGGAGAAAAG CTAGT
                                |||||||||| |||||
                                CCCTTTTTTC GATCA
                                      _
GAM801  PSMD9    3' ACTTGTCTTCTCTCCCTG    10980       A    T
                                CAGGGAGA AAGAC AGT
                                |||||||| ||||| |||
                                GTCCCTCT TTCTG TCA
                                    C    T
GAM801  PVR      3' GAGACCAGCCTCCCTCCCTGTG 21478        AAA  A  A
                                CACAGGGAG   AG CT GTCTC
                                |||||||||   || || |||||
                                GTGTCCCTC   TC GA CAGAG
                                     CC_  C  C
GAM801  RET      3' ACTATCCTTCCTCTCTGTGA   40173        A  A  C
                                TCACAGGGAG AA GA TAGT
                                |||||||||| || || ||||
                                AGTGTCTCTC TT CT ATCA
                                     C  C  _
GAM801  RGS19IP1 3' GAGAGGAGCCCCCTCCCTGTGG 62508         AAAAGA  AG
                                TCACAGGGAG     CT  TCTC
                                |||||||||     ||  ||||
                                GGTGTCCCTC     GA  AGAG
                                     CCCC__  GG
GAM801  SMARCA3  3' AGTCCTTTTCTCCCTGTG    57395          _
                                CACAGGGAGAAAAG ACT
                                |||||||||||||| |||
                                GTGTCCCTCTTTTC TGA
                                       C
GAM801  SMARCA3  3' AGTCCTTTTCTCCCTGTG    11786          _
                                CACAGGGAGAAAAG ACT
                                |||||||||||||| |||
                                GTGTCCCTCTTTTC TGA
                                       C
GAM801  TNFSF12  3' AGACAAGCTCCTCCCTTGA   13743    C     AAA  A  A
                                TCA AGGGAG   AG CT GTCT
                                ||| ||||||   || || ||||
                                AGT TCCCTC   TC GA CAGA
                                  _     C__  _  A
GAM801  UGT2B11  3' AGATTTCTTTCTTCCTGTGA  6535          A  CT
                                TCACAGGGAGAAA GA  AGTCT
                                |||||||||||| ||  |||||
                                AGTGTCCTTCTTT CT  TTAGA
                                      _  __
GAM801  UGT2B28  3' AGATTTCTTTCTTCCTGTGA  53839         A  CT
                                TCACAGGGAGAAA GA  AGTCT
                                |||||||||||| ||  |||||
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                                AGTGTCCTTCTTT CT  TTAGA
                                      _ __
GAM801  ALK7     3'  GAATAGTGCTTTTCTCCCTATG 75743    C        _   G
                                CA AGGGAGAAAAG ACTA TC
                                || |||||||||| ||||| ||
                                GT TCCCTCTTTTC TGAT AG
                                  A         G   A
GAM801  CCNE2    3'  TCTCTTCTCCCTTTGA     54120    C      A
                                TCA AGGGAGAA AGA
                                ||| |||||||| |||
                                AGT TCCCTCTT TCT
                                  T       C
GAM801  CCNE2    3'  TCTCTTCTCCCTTTGA     16292    C      A
                                TCA AGGGAGAA AGA
                                ||| |||||||| |||
                                AGT TCCCTCTT TCT
                                  T       C
GAM801  COPS7B   3'  AGGCCCCTCCCCTTGTGA   42691        A  AAAGACTA
                                TCACAGGG GA       GTCT
                                |||||||| ||       ||||
                                AGTGTTCC CT       CGGA
                                     C  CCC_____
GAM801  DC11     3'  GAATGTCTCTTCTCCCTG   39488        A   TAG
                                CAGGGAGAA AGAC   TC
                                ||||||||| ||||   ||
                                GTCCCTCTT TCTG   AG
                                     C    TA_
GAM801  DDM36    3'  GAGGCCCTTCCCACCCTGTGA 40571       AGAA   ACTA
                                TCACAGGG   AAG   GTCTC
                                ||||||||   |||   |||||
                                AGTGTCCC   TTC   CGGAG
                                     ACCC   C___
GAM801  EDG1     3'  AGACTAATGTCCCCATGTGA  59325     _  A  AAAGAC
                                TCACA GGG GA     TAGTCT
                                ||||| ||| ||     ||||||
                                AGTGT CCC CT     ATCAGA
                                   A  _  GTA___
GAM801  ENDO180  3'  GAGAGCCTCTTTCTCCC    20145       A  CTAG
                                GGGAGAAA GA    TCTC
                                |||||||| ||    ||||
                                CCCTCTTT CT    AGAG
                                     _  CCG_
GAM801  FADS1    3'  AGTTAGTCTTTTCTCCCT    25471            T
                                AGGGAGAAAAGACTAG CT
                                |||||||||||||||| ||
                                TCCCTCTTTTCTGATT GA
                                                 _
GAM801  FLJ10283 3'  ACTTATTTTTTCTCCC     35968          CT
                                GGGAGAAAAGA  AGT
                                ||||||||||  |||
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                                CCCTCTTTTTT  TCA
                                      AT
GAM801  FLJ12287  3'  AGACCACCTTTCTCCCCTG   42310      _    AGACTA
                                CAGGG AGAAA     GTCT
                                ||||| |||||     ||||
                                GTCCC TCTTT     CAGA
                                   C    CCAC__
GAM801  FLJ12768  3'  GAGCTGGCACTCTTCTCCCTGA 47183    A       A  A_   T
          GA                     TC CAGGGAGAA AG  CTAG CTC
                                || |||||||| ||  |||| |||
                                AG GTCCCTCTT TC  GGTC GAG
                                 A       C  AC   _
GAM801  FLJ14824  3'  AGACTTTAGAGTCCTCTCTCTG 51638         AAA   _____
          T                     ACAGGGAGA   GACT   AGTCT
                                |||||||||   ||||   |||||
                                TGTCTCTCT   CTGA   TCAGA
                                      C__   GATT
GAM801  FLJ20094  3'  ACTATCTTTTCTCTCTGTGA   34556             C
                                TCACAGGGAGAAAAGA TAGT
                                |||||||||||||||| ||||
                                AGTGTCTCTCTTTTCT ATCA
                                                _
GAM801  FLJ20195  3'  GAGATTGGCCCCCTCCCT    34709       AAAAGA
                                AGGGAG     CTAGTCTC
                                ||||||     ||||||||
                                TCCCTC     GGTTAGAG
                                   CCCC__
GAM801  FLJ20375  3'  AGATATTATCTTCTCCCTG   35084        AA   CTA_
                                CAGGGAGA  AGA   GTCT
                                ||||||||  |||   ||||
                                GTCCCTCT  TCT   TAGA
                                     __  ATTA
GAM801  FLJ20421  3'  AGACTTATTTTCCCTGT     35145          AAGACT
                                ACAGGGAGAA     AGTCT
                                ||||||||||     |||||
                                TGTCCCTTTT     TCAGA
                                      AT____
GAM801  FLJ22313  5'  GACGCTTCCTTTCTCCTCACGA 42340    ACA      A  CTA
                                TC   GGGAGAAA GA   GTC
                                ||   |||||||| ||   |||
                                AG   TCCTCTTT CT   CAG
                                 CAC       C  TCG
GAM801  FLJ23468  3'  AGACTAGTCTCATGCTGT    44906     GGAGAAA
                                ACAG      AGACTAGTCT
                                ||||      ||||||||||
                                TGTC      TCTGATCAGA
                                  GTAC___
GAM801  HYPH      3'  ACTAGTCTTCCCTGT       94897        GAAA
                                ACAGGGA   AGACTAGT
                                |||||||   ||||||||
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                                TGTCCCT    TCTGATCA
                                      ____
GAM801  KIAA0063  3'  GCTGGGCTTTCTCCCCCCTGTG 29634        A_ _   A
            A                    TCACAGGG  GA AAAG CTAGT
                                 ||||||||  || |||| |||||
                                 AGTGTCCC  CT TTTC GGTCG
                                     CC  C    G
GAM801  KIAA0063  5'  TCTTTTCTCCCAGTGA      29647      A
                                 TCAC GGGAGAAAAGA
                                 |||| ||||||||||
                                 AGTG CCCTCTTTTCT
                                   A
GAM801  KIAA0429  3'  GACTTCCTTTCTCCCATG    28557    _       A  CT
                                 CA GGGAGAAA GA  AGTC
                                 || |||||||| ||  ||||
                                 GT CCCTCTTT CT  TCAG
                                  A       C  __
GAM801  KIAA0563  5'  GACTAGTCTCGAAATTTTTCCC 29189         A_________   CTAG
            TGT                    CAGGGAGAA        AGA    TC
                                 |||||||||        |||    ||
                                 GTCCCTTTT        TCT    AG
                                      TAAAGIIIC   GATC
GAM801  KIAA0820  3'  GACTAGTCTCGAAACCAGTTCC 69025       GAAA_________   CTAG
            TGTGA                  CAGGGA          AGA    TC
                                 ||||||          |||    ||
                                 GTCCTT          TCT    AG
                                     GACCAAAGIIIC   GATC
GAM801  KIAA1046  3'  AGAGGTCTTTCTCCC       29989         A    AG
                                 GGGAGAAA GACT  TCT
                                 |||||||| ||||  |||
                                 CCCTCTTT CTGG  AGA
                                       _    __
GAM801  KIAA1136  3'  GAGACTTCCCTTTTTCTCCCTG 91318            ACT_
            T                     ACAGGGAGAAAAG    AGTCTC
                                 ||||||||||||||    ||||||
                                 TGTCCCTCTTTTT    TCAGAG
                                        CCCT
GAM801  KIAA1775  3'  AGACCAGTCTTTCTG       52372      GAGAA     A
                                 CAGG     AAGACT GTCT
                                 ||||     |||||| ||||
                                 GTCT     TTCTGA CAGA
                                   ______     C
GAM801  MADCAM1   3'  GACTAGTCTCAGCCTTTCCCCC 55358      A  A_________   CTAG
            TGTGA                  CAGGG GAA        AGA    TC
                                 ||||| |||        |||    ||
                                 GTCCC CTT        TCT    AG
                                   C   TCCGAIIIC   GATC
GAM801  MADCAM1   3'  GACTAGTCTCAGCCTTTCCCCC 55361      A  A_________   CTAG
            TGTGA                  CAGGG GAA        AGA    TC
                                 ||||| |||        |||    ||
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                                GTCCC CTT       TCT   AG
                                  C   TCCGAIIIC   GATC
GAM801  MADCAM1   3'  GACTAGTCTCAGCCTTTCCCCC 55364      A   A_________   CTAG
           TGTGA                  CAGGG GAA       AGA   TC
                                |||||| |||       |||   ||
                                GTCCC CTT       TCT   AG
                                  C   TCCGAIIIC   GATC
GAM801  MGC12904  3'  GACCTTTCCCCCTCTCCCTGCG 48333    A      AAA_  CTA
           G                    TC CAGGGAGA   GA   GTC
                                || ||||||||   ||   |||
                                GG GTCCCTCT   CT   CAG
                                 C       CCCC  TTC
GAM801  MGC16063  5'  GACTCCCTTTCTCCCTGGA   53859    A        A ACT
                                TC CAGGGAGAAA G   AGTC
                                || ||||||||||  |   ||||
                                AG GTCCCTCTTT C   TCAG
                                 _        _ CC_
GAM801  moblak    3'  GACTCTTCTCTCCCTGGA    55500    A      A   CTA
                                TC CAGGGAGA AAGA   GTC
                                || ||||||||  ||||   |||
                                AG GTCCCTCT TTCT   CAG
                                 _       C   ___
GAM801  MRP64     3'  ACTGTACTTTTCCCTGTGA   33239          AAG  T
                                TCACAGGGAGAA   AC AGT
                                ||||||||||||   || |||
                                AGTGTCCCTTTT   TG TCA
                                       CA_  _
GAM801  PDE4DIP   3'  GACCTTCCCTTCTCCCTTGA   27689     C      AA  CTA
                                TCA AGGGAGAA  GA   GTC
                                ||| ||||||||  ||   |||
                                AGT TCCCTCTT  CT   CAG
                                  _      CC  TC_
GAM801  PRO0386   5'  AGGGGGTCCCTTCTCCCTGCGG 37687    A       AA    AG
                                TC CAGGGAGAA  GACT  TCT
                                || |||||||||  ||||  |||
                                GG GTCCCTCTT  CTGG  GGA
                                 C       CC    G_
GAM801  SBB103    3'  GAGCTTCCTCTCTTCCTGTGA  19358          AA  ACT  T
                                TCACAGGGAGA  AG   AG CTC
                                ||||||||||  ||   || |||
                                AGTGTCCTTCT  TC   TC GAG
                                       C_  CT_  _
GAM801  SCYA22    3'  ACTAATGTCCCTCCCCTCTCCC 90937        AAA____   __
           TG                    CAGGGAGA      GAC  TAGT
                                |||||||       |||  ||||
                                GTCCCTCT      CTG  ATCA
                                    CCCCTCC   TA
GAM801  SDC3      3'  AGACAGTGTCCCTCCCTCCTGT 27738       ___     AAAA   TA_
           GA                    TCACA   GGGAG   GAC   GTCT
                                |||||   |||||   |||   ||||
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                                AGTGT  CCCTC   CTG  CAGA
                                  CCT   C___  TGA
GAM801  SIRPB1   3' GCTCTCCCTTCTCTCTCTGTGA 20256        A  ACT_
                                TCACAGGGAGA AAG   AGT
                                |||||||||| |||   |||
                                AGTGTCTCTCT TTC   TCG
                                    C  CCTC
GAM801  LOC123036 3' GAGATTTCCTTTCTCCCCTG  74190     _   A  CT
                                CAGGG AGAAA GA  AGTCTC
                                ||||| ||||| ||  ||||||
                                GTCCC TCTTT CT  TTAGAG
                                  C   C __
GAM801  LOC127702 3' GAGACTAACTTGCTTTCTCCCT 75459        A_  C_
          G                      CAGGGAGAAA  GA  TAGTCTC
                                |||||||||  ||  |||||||
                                GTCCCTCTTT  TT  ATCAGAG
                                     CG  CA
GAM801  LOC130074 3' ACTTTTCTTCCTCCCTGT   76124       AA   CT
                                ACAGGGAG  AAGA  AGT
                                ||||||||  ||||  |||
                                TGTCCCTC  TTCT  TCA
                                    C_   TT
GAM801  LOC144667 3' GAGGTGGGCCCTCTTCCCCCT  83168    A  A  A_  AG
                                AGGG GAA AG  CT  TCTC
                                |||| ||| ||  ||  ||||
                                TCCC CTT TC  GG  GGAG
                                  C  C  CC  GT
GAM801  LOC145231 3' GAGACTAGTCCCAATTCC   83285    GAAAA
                                GGGA   GACTAGTCTC
                                ||||   ||||||||||
                                CCTT   CTGATCAGAG
                                  AACC_
GAM801  LOC145951 5' GACATCTCATCTCCCTGTGA  77577        AA  CTA
                                TCACAGGGAGA  AGA  GTC
                                ||||||||||  |||  |||
                                AGTGTCCCTCT  TCT  CAG
                                     AC  A__
GAM801  LOC146733 5' AGAAGTTTTTTCCCT      83754    A      AG
                                GGG GAAAAGACT  TCT
                                ||| |||||||||  |||
                                TCC CTTTTTTGA  AGA
                                  _      __
GAM801  LOC147071 5' GACTAGTCTCGAAATTTTTCCC 73000        A_________  CTAG
          TGT                    CAGGGAGAA       AGA   TC
                                |||||||||       |||   ||
                                GTCCCTTTT       TCT   AG
                                    TAAAGIIIC   GATC
GAM801  LOC148809 5' ACAGTCTCTCCCTG       78994        AAA   A
                                CAGGGAGA   GACT GT
                                ||||||||   |||| ||
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                                GTCCCTCT   CTGA CA
                                   ___   _
GAM801   LOC149386 5'  ACTAGTCTTCCTACACTG    84401     GG_  AA
                                CAG   AG  AAGACTAGT
                                |||   ||  |||||||||
                                GTC   TC  TTCTGATCA
                                  ACA  C_
GAM801   LOC150290 3'  AGATAAATTTTCTGCCCTGTGA 79767         _     GACTA
                                TCACAGGG AGAAAA     GTCT
                                |||||||| ||||||     ||||
                                AGTGTCCC TCTTTT     TAGA
                                     G     AAA__
GAM801   LOC150622 5'  GAGACTGTCTCTTCTCCTGTGA 79959        G    A    T
                                TCACAGG AGAA AGAC AGTCTC
                                ||||||| |||| |||| ||||||
                                AGTGTCC TCTT TCTG TCAGAG
                                   _   C   _
GAM801   LOC150967 5'  GACTATCTCTTTTCTCCT    80081          C_
                                GGGAGAAAAGA  TAGTC
                                ||||||||||  |||||
                                TCCTCTTTTCT  ATCAG
                                      CT
GAM801   LOC152345 3'  GAGAGCGCTTCTCTCCCTG   80575        A   ACTAG
                                CAGGGAGA AAG     TCTC
                                |||||||| |||     ||||
                                GTCCCTCT TTC     AGAG
                                     C   GCG__
GAM801   LOC153743 3'  ACTAGCTTTTTTCCC       60511          A
                                GGGAGAAAAG CTAGT
                                |||||||||| |||||
                                CCCTTTTTTC GATCA
                                   _
GAM801   LOC158116 3'  AGTTTCCCTCCCCTCTGTGA   60320       ___    AAA
                                TCACA   GGGAG   AGACT
                                |||||   |||||   |||||
                                AGTGT   CCCTC   TTTGA
                                   CTC    CC_
GAM801   LOC170082 3'  GTTTTTTCCCCCTGTGA     82564         A
                                TCACAGGG GAAAAGAC
                                |||||||| ||||||||
                                AGTGTCCC CTTTTTTG
                                     C
GAM801   LOC196955 5'  GAGACTGCCTGTTCCTCCCTCT 77377         AAAA_  ___
           CTGTGA                 CACAGGGAG    GAC   TAGTCTC
                                |||||||||    |||  |||||||
                                GTGTCTCTC    TTG   GTCAGAG
                                     CCTCC   TCC
GAM801   LOC200014 3'  AGTGACTTTTTTCCCCATGA   88517     CA        __
                                TCA  GGGAGAAAAG  ACT
                                |||  ||||||||||  |||
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                                AGT  CCCTTTTTTC  TGA
                                  AC        AG
GAM801  LOC201173 5'  GACTAGTCTCGAAATTTTTCCC 87330        A_________  CTAG
           TGT                   CAGGGAGAA       AGA   TC
                                 |||||||||       |||   ||
                                 GTCCCTTTT       TCT   AG
                                     TAAAGIIIC   GATC
GAM801  LOC201220 5'  GACTAGTCTCGAAATTTTTCCC 87350        A_________  CTAG
           TGT                   CAGGGAGAA       AGA   TC
                                 |||||||||       |||   ||
                                 GTCCCTTTT       TCT   AG
                                     TAAAGIIIC   GATC
GAM801  LOC202934 3'  AGACTAGTCTTCAGGTTC    90399     AA__
                                 GAG   AAGACTAGTCT
                                 |||   ||||||||||
                                 CTT   TTCTGATCAGA
                                   GGAC
GAM801  LOC219736 3'  ACCAGTAAAATTTTCTCCTATG 93118     CA       G___  A
           A                     TCA  GGGAGAAAA   ACT GT
                                 |||  |||||||||   ||| ||
                                 AGT  TCCTCTTTT   TGA CA
                                   A_       AAAA  C
GAM801  LOC255465 3'  AGACTAGTCTTCAGGTTC    97277     AA__
                                 GAG   AAGACTAGTCT
                                 |||   ||||||||||
                                 CTT   TTCTGATCAGA
                                   GGAC
GAM801  LOC51068  3'  GAGAAGGAATTTTCTCTCT   31946        GA  AG
                                 AGGGAGAAAA  CT  TCTC
                                 ||||||||||  ||  ||||
                                 TCTCTCTTTT  GG  AGAG
                                      AA  A_
GAM801  LOC90917  5'  AGTCTTCCCTGCCCTGT     64334       _  AA
                                 ACAGGG AG  AAGACT
                                 ||||||  ||  ||||||
                                 TGTCCC TC  TTCTGA
                                    G  CC
GAM801  LOC91548  5'  GAGACCCAGTACCTCCCTGT   66415       AAAAG  A_
                                 ACAGGGAG    ACT  GTCTC
                                 ||||||||    |||  |||||
                                 TGTCCCTC    TGA  CAGAG
                                     CA___   CC
GAM801  LOC91628  3'  GAGAACTGTTTTCTCCCTG   66759        GAC   _
                                 CAGGGAGAAAA   TAGT CTC
                                 ||||||||||||  |||| |||
                                 GTCCCTCTTTT   GTCA GAG
                                       ___   A
GAM802  ATP6IP1   3'  AAGGGACCTCCACGACA     6787     C      CC
                                 TG CGTGGAGG  TCCCTT
                                 ||  ||||||||  ||||||
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                                AC GCACCTCC  AGGGAA
                                 A      __
GAM802  DKFZP564C103 3'  ACTTGCCTAAGGCCTCCCAGCA 31610     CGT       CCCTT
                                TGC   GGAGGCCT    CAAGT
                                |||   ||||||||    |||||
                                ACG   CCTCCGGA    GTTCA
                                  AC_       ATCC_
GAM802  FLJ13162  5'  ACCTGCAGCAAGCTCCACAGCA 46548     C     GC  CC  T  A
                                TGC GTGGAG  CT  CT CA GT
                                ||| ||||||  ||  || || ||
                                ACG CACCTC  GA  GA GT CA
                                  A     __ AC  C  C
GAM802  KIAA0189  3'  ACTTGGCATGAAGCCTCCACAG 28268    C       C  CCT
            C                    GC GTGGAGGC TC   TCAAGT
                                || |||||||| ||   ||||||
                                CG CACCTCCG AG   GGTTCA
                                 A       A  TAC
GAM802  KIAA1423  3'  ACTCAAAGGGAAGCCTT     61721       C     CA
                                GAGGC TCCCTT  AGT
                                ||||| ||||||  |||
                                TTCCG AGGGAA  TCA
                                   A     AC
GAM802  SLC5A7    3'  ACTTTATGGGAAGCCTCCAC   41503         C    TTC
                                GTGGAGGC TCCC   AAGT
                                |||||||| ||||   ||||
                                CACCTCCG AGGG   TTCA
                                     A    TAT
GAM802  LOC151610 3'  GGTGGGAAGCCTCCATAGCA   80289     CG      C    T
                                TGC  TGGAGGC TCCC TC
                                |||  ||||||| |||| ||
                                ACG  ACCTCCG AGGG GG
                                  AT      A    T
GAM802  LOC199757 5'  GAAGGGAGACCCCGC       89854      A  C
                                GTGG GG CTCCCTTC
                                |||| || ||||||||
                                CGCC CC GAGGGAAG
                                  _ A
GAM802  LOC221683 5'  ACTTGAAGAGAAGGTGACAGG  93710    G  GAG   _ C
                                CC TG   GCCT C CTTCAAGT
                                || ||   |||| | ||||||||
                                GG AC   TGGA G GAAGTTCA
                                 _ AG_    A A
GAM802  LOC92170  3'  CTGAAGGGGTCCACAGC     68369    C    GGCC       A
                                GC GTGGA    TCCCTTCA G
                                || |||||    |||||||| |
                                CG CACCT    GGGGAAGT C
                                 A     ____       C
GAM803  C1orf19   3'  ACTTTGTTTACAAATGTGGTGC 68188          C  GTTTAT
                                GCGCCACAT TG     AAGT
                                ||||||||| ||     ||||
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                                CGTGGTGTA AC     TTCA
                                     A  ATTTGT
GAM803  FLJ21596  3'  ACTTATAAATATCAGTGG    45696      ATCTG
                                CCAC    GTTTATAAGT
                                ||||    ||||||||||
                                GGTG    TAAATATTCA
                                  ACTA_
GAM804  AKAP1     3'  ACACTGGACAGGTGACTGTATG 13017       ACT   GCA_
                                CATACA  TCA   TCCAGTGT
                                ||||||  |||   ||||||||
                                GTATGT  AGT   AGGTCACA
                                   C__  GGAC
GAM804  AKAP1     3'  ACACTGGACAGGTGACTGTATG 57706       ACT   GCA_
                                CATACA  TCA   TCCAGTGT
                                ||||||  |||   ||||||||
                                GTATGT  AGT   AGGTCACA
                                   C__  GGAC
GAM804  GOCAP1    3'  TGGATGCTGAAGTTACATGA   42703     AC
                                TCAT  AACTTCAGCATCCA
                                ||||  ||||||||||||||
                                AGTA  TTGAAGTCGTAGGT
                                  CA
GAM804  AF020591  3'  ACACTGGAGGCAAACCCTATGA 27133       CAACTTCA  A
                                TCATA      GC TCCAGTGT
                                |||||      || ||||||||
                                AGTAT      CG AGGTCACA
                                   CCCAAA__  G
GAM804  DKFZP434C1715 3'  CACTGTAGAAGTTGTATG    86146          AGCATC
                                CATACAACTTC     CAGTG
                                ||||||||||     |||||
                                GTATGTTGAAG     GTCAC
                                      AT____
GAM804  DKFZp434I1610 3'  ACACTGGAGTGAAACCCTATGA 63449       CAAC   G A
                                TCATA   TTCA C TCCAGTGT
                                |||||   |||| | ||||||||
                                AGTAT   AAGT G AGGTCACA
                                   CCCA  _ _
GAM804  FLJ10891  3'  ACACTGGAAAGGAACTGTA   36804     AC   AGCA
                                TACA  TTC   TCCAGTGT
                                ||||  |||   ||||||||
                                ATGT  AAG   AGGTCACA
                                  C_  GAA_
GAM804  FLJ11722  3'  ACACTGGACTTCTGACCCCATG 46387     ACAACT   CA_
          A                      TCAT     TCAG   TCCAGTGT
                                ||||     ||||   ||||||||
                                AGTA     AGTC   AGGTCACA
                                  CCCC__    TTC
GAM804  FLJ20070  3'  ACACTGGAGGAAGGCCATATGA 34472      CAA_   AGCA
                                TCATA   CTTC   TCCAGTGT
                                |||||   ||||   ||||||||
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                                AGTAT   GAAG   AGGTCACA
                                  ACCG   G___
GAM804  HSZFP36  3'  ACACTGGAGAGAAACCCTATGA 63475     CAAC   AGCA
                                TCATA   TTC   TCCAGTGT
                                |||||   |||   ||||||||
                                AGTAT   AAG   AGGTCACA
                                  CCCA   AG__
GAM804  HSZFP36  3'  ACACTGGAGAGAAGCCATATGA 63476     CAA   AGCA
                                TCATA   CTTC   TCCAGTGT
                                |||||   ||||   ||||||||
                                AGTAT   GAAG   AGGTCACA
                                  ACC   AG__
GAM804  JIK      5'  ACAAAGGACTGAAGTT     32796       CA   AG
                                AACTTCAG  TCC  TGT
                                ||||||||  |||  |||
                                TTGAAGTC  AGG  ACA
                                    __   AA
GAM804  KIAA1553 3'  ACACTGGATGATGATGATATGA 91912      _  ACT   G
                                TCATA CA   TCA CATCCAGTGT
                                ||||| ||   ||| ||||||||||
                                AGTAT GT   AGT GTAGGTCACA
                                  A ___   A
GAM804  KIAA1900 3'  ACACTGGAACAGCAGTTGTTGA 73246     T     TCA  A__
                                TCA ACAACT   GC   TCCAGTGT
                                ||| ||||||   ||   ||||||||
                                AGT TGTTGA   CG   AGGTCACA
                                  _    ___  ACA
GAM804  LY75     3'  ACACTATGATAAAGTTGTA    9833        CAG   CC
                                TACAACTT   CAT  AGTGT
                                ||||||||   |||  |||||
                                ATGTTGAA   GTA  TCACA
                                    ATA   __
GAM804  SMBP     3'  TTGGATGCTAAAATTACATGA  72161      AC  C  C
                                TCAT  AA TT AGCATCCAG
                                ||||  || || |||||||||
                                AGTA  TT AA TCGTAGGTT
                                  CA  A  A
GAM804  UMP-CMPK 3'  TGTACAAAGTTGTATGA     32845          CA_
                                TCATACAACTT   GCA
                                ||||||||||   |||
                                AGTATGTTGAA   TGT
                                      ACA
GAM804  ZNF272   5'  ACACTGGAGAGAAGCCCTATGA 61899      CAA   AGCA
                                TCATA   CTTC   TCCAGTGT
                                |||||   ||||   ||||||||
                                AGTAT   GAAG   AGGTCACA
                                  CCC   AG__
GAM804  LOC115123 3'  TGGATGCTGCAATCATATGA   73223      CAACTT
                                TCATA     CAGCATCCA
                                |||||     |||||||||
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                                AGTAT     GTCGTAGGT
                                   ACTAAC
GAM804  LOC147837 3'  ACACTGGAGAGATGCTGTATGA 78511       ACT  AGCA
                                TCATACA   TC    TCCAGTGT
                                |||||||   ||    ||||||||
                                AGTATGT   AG    AGGTCACA
                                    CGT  AG__
GAM804  LOC151318 3'  ACAACTTGCTGAAGTCAATGA  80223     ACA       TCCAG
                                TCAT   ACTTCAGCA    TGT
                                ||||   |||||||||    |||
                                AGTA   TGAAGTCGT    ACA
                                  AC_       TCA__
GAM804  LOC206804 5'  ACACTGGACAGAAACCCTATGA 89541      CAAC   AGCA
                                TCATA    TTC    TCCAGTGT
                                |||||    |||    ||||||||
                                AGTAT    AAG    AGGTCACA
                                   CCCA   AC__
GAM804  LOC257017 5'  ACACTCTTCTAAAGTTGTAT   97370        C  CATCC
                                ATACAACTT AG     AGTGT
                                |||||||||  ||    |||||
                                TATGTTGAA TC     TCACA
                                     A  TTC__
GAM804  LOC90591  3'  ACACTGGAGAGAAACAGTATGA 63405       AAC   AGCA
                                TCATAC   TTC    TCCAGTGT
                                ||||||   |||    ||||||||
                                AGTATG   AAG    AGGTCACA
                                   ACA   AG__
GAM804  LOC90591  3'  ACACTGGAGAGAAACCCTATGA 63406      CAAC   AGCA
                                TCATA    TTC    TCCAGTGT
                                |||||    |||    ||||||||
                                AGTAT    AAG    AGGTCACA
                                   CCCA   AG__
GAM804  LOC90591  3'  ACACTGGAGAGAAACCCTATGA 63407      CAAC   AGCA
                                TCATA    TTC    TCCAGTGT
                                |||||    |||    ||||||||
                                AGTAT    AAG    AGGTCACA
                                   CCCA   AG__
GAM804  LOC90591  3'  ACACTGGAGAGAAACCCTATGA 63408      CAAC   AGCA
                                TCATA    TTC    TCCAGTGT
                                |||||    |||    ||||||||
                                AGTAT    AAG    AGGTCACA
                                   CCCA   AG__
GAM804  LOC90594  3'  ACACTGGAGAGAAACCCTATGA 63468      CAAC   AGCA
                                TCATA    TTC    TCCAGTGT
                                |||||    |||    ||||||||
                                AGTAT    AAG    AGGTCACA
                                   CCCA   AG__
GAM804  LOC90594  3'  ACACTGGAGAGAAACCTATGA  63469      CAAC   AGCA
                                TCATA    TTC    TCCAGTGT
                                |||||    |||    ||||||||
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                                AGTAT   AAG   AGGTCACA
                                  CCA_  AG__
GAM804  LOC90594  3'  ACACTGGGGAGAAACCGTAT  63470     AAC  AGCA
                                ATAC  TTC   TCCAGTGT
                                ||||  |||   ||||||||
                                TATG  AAG   GGGTCACA
                                  CCA  AG__
GAM804  LOC92285  5'  ACACTGGAGAGAAACCTTATGA 68750     CAAC  AGCA
                                TCATA   TTC   TCCAGTGT
                                |||||   |||   ||||||||
                                AGTAT   AAG   AGGTCACA
                                  TCCA  AG__
GAM805  ASPA    3'  TCTGCTAGTCTGTAAGCTCCTT 3505      A  C   T   TG
                                AAGGA CT ACAG CTAG  GG
                                ||||| || |||| ||||  ||
                                TTCCT GA TGTC GATC  CT
                                  C  A   T   GT
GAM805  ATP2B2   5'  AGCGTGGACTGTGAACCCCC  8064    AAC_      GTGG
                                GG   TCACAGTCTA   GCT
                                ||   ||||||||||   |||
                                CC   AGTGTCAGGT   CGA
                                 CCCA       G___
GAM805  CTSB    3'  GCTGACTGTGGCCCCCT    64728    AAC      T
                                AGG  TCACAGTC AGT
                                |||  |||||||| |||
                                TCC  GGTGTCAG TCG
                                  CCC      _
GAM805  FGA     3'  GCTAGACTGTAAGTTCCTT   41561       C
                                AAGGAACT ACAGTCTAGT
                                |||||||| ||||||||||
                                TTCCTTGA TGTCAGATCG
                                    A
GAM805  LHCGR   3'  AGCTGTAGACTGTAAACTCCT  4069     ACTC      GTG
                                AGGA   ACAGTCTA   GGCT
                                ||||   ||||||||   ||||
                                TCCT   TGTCAGAT   TCGA
                                  CAAA      G__
GAM805  LPO     3'  CTAGATTGTAAGCTCC     67866    A  C
                                GGA CT ACAGTCTAG
                                ||| || |||||||||
                                CCT GA TGTTAGATC
                                  C  A
GAM805  MPL     3'  ACTAGATTGTGAGCTCCTT   18125      A
                                AAGGA CTCACAGTCTAGT
                                ||||| ||||||||||||
                                TTCCT GAGTGTTAGATCA
                                   C
GAM805  OTX1    3'  CCACTAAGAGTTCCT      27304        ACAGTC
                                AGGAACTC    TAGTGG
                                ||||||||    ||||||
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                                TCCTTGAG     ATCACC
                                   A_____
GAM805  PAX4    3'  AGACTGTGGCTCCTT      20552      A T
                                AAGGA C CACAGTCT
                                ||||| | ||||||||
                                TTCCT G GTGTCAGA
                                  C _
GAM805  RFX2    3'  CCCACCAGACCATGGGTTCCTT 5308          CA   A
                                AAGGAACTCA  GTCT GTGGG
                                ||||||||||  |||| |||||
                                TTCCTTGGGT  CAGA CACCC
                                     AC   C
GAM805  RPIP8   3'  CCCACCAGACTGTGAGCTCC  21965    A        A
                                GGA CTCACAGTCT GTGGG
                                ||| |||||||||| |||||
                                CCT GAGTGTCAGA CACCC
                                  C         C
GAM805  SCNN1A  3'  ACTAGACTGTAAGTGCCTT   6420      A   C
                                AAGG ACT ACAGTCTAGT
                                |||| ||| ||||||||||
                                TTCC TGA TGTCAGATCA
                                  G   A
GAM805  SPON1   3'  GCCCATGATAAAGTTCCTT   62453        CACA   TA
                                AAGGAACT   GTC  GTGGGC
                                ||||||||   |||  ||||||
                                TTCCTTGA   TAG  TACCCG
                                   AA__   __
GAM805  SUFU    3'  AGCCCATGGTTTTGGAGTTCCT 32405        A   TCTA
                                AGGAACTC CAG   GTGGGCT
                                |||||||| |||   |||||||
                                TCCTTGAG GTT   TACCCGA
                                   _   TTGG
GAM805  TBP     3'  GCGTGACTGTGAGTTGCT    64739    G        TAGT G
                                AG AACTCACAGTC   G GC
                                || ||||||||||   | ||
                                TC TTGAGTGTCAG   T CG
                                 G         _____ G
GAM805  TRAF1   3'  CCCAGTCACTGTGAGCTCC   18972    A      CTAG
                                GGA CTCACAGT   TGGG
                                ||| ||||||||   ||||
                                CCT GAGTGTCA   ACCC
                                  C       CTG_
GAM805  ATP6V0A1 3'  CTAGACTTTGAGTTCC      17729        C
                                GGAACTCA AGTCTAG
                                |||||||| |||||||
                                CCTTGAGT TCAGATC
                                   T
GAM805  C12orf8 3'  CCTGCTGGCTGTGAGTCCCTT  22362     A      T   TG
                                AAGG ACTCACAG CTAG  GG
                                |||| |||||||| ||||  ||
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                                TTCC TGAGTGTC GGTC  CC
                                  C       _   GT
GAM805  C4.4A    3'  ACTAGACTGTGAGCTCCT    26940      A
                                AGGA CTCACAGTCTAGT
                                |||| ||||||||||||
                                TCCT GAGTGTCAGATCA
                                  C
GAM805  C6orf9   5'  ACTTGACTGTGGTCCC      42074    A  T      T
                                GG AC CACAGTC AGT
                                || || ||||||| |||
                                CC TG GTGTCAG TCA
                                 C  _      T
GAM805  DQX1     5'  ACTGGCTGTGAACCCCTT    56101      AAC     T
                                AAGG   TCACAG CTAGT
                                ||||   |||||| |||||
                                TTCC   AGTGTC GGTCA
                                  CCA     _
GAM805  E2F6     3'  ATTAGACTGTGAGCTCCTT    8711       A
                                AAGGA CTCACAGTCTAGT
                                ||||| ||||||||||||
                                TTCCT GAGTGTCAGATTA
                                  C
GAM805  FLJ20113 3'  AGCCCCCAGGCTGTGAGCTCCT 34571      A        AGT
          T                      AAGGA CTCACAGTCT   GGGCT
                                ||||| ||||||||||   |||||
                                TTCCT GAGTGTCGGA   CCCGA
                                  C         CC_
GAM805  FLJ22242 3'  CGCTAGACTGTGAGCTTCCT   46867      _
                                AGGAA CTCACAGTCTAGTG
                                ||||| ||||||||||||||
                                TCCTT GAGTGTCAGATCGC
                                  C
GAM805  HSD17B12 3'  AGCCCACTAAACTATGCTTTCC 32341      CT  C   C
          T                      AGGAA  CA AGT TAGTGGGCT
                                |||||  || ||| |||||||||
                                TCCTT  GT TCA ATCACCCGA
                                  TC  A   A
GAM805  JDD1     3'  CCATTACCATGAGTTC      63216       CA  CT
                                GAACTCA  GT  AGTGG
                                |||||||  ||  |||||
                                CTTGAGT  CA  TTACC
                                   AC  __
GAM805  KIAA0186 3'  AGCCTTGCTAAACTGTGAGTTC 40742          C    _
          T                      GGAACTCACAGT TAGTG GGCT
                                |||||||||||| ||||| ||||
                                TCTTGAGTGTCA ATCGT CCGA
                                       A    T
GAM805  KIAA0321 5'  AGCTGCTGCTGTGAGCCCCTT  62386      AA      CT  TG G
                                AAGG  CTCACAGT  AG  G CT
                                ||||  ||||||||  ||  | ||
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                                TTCC  GAGTGTCG  TC  C GA
                                  CC       __  GT _
GAM805  KIAA1029  3'  CCCACTAGAGATTGCCT    23472     AAC  ACAG
                                AGG   TC    TCTAGTGGG
                                |||   ||    |||||||||
                                TCC   AG    AGATCACCC
                                  GTT  ____
GAM805  KIAA1115  5'  GCAGACTGTGGCCCCT     30020     AA T       A
                                AGG  C CACAGTCT GT
                                |||  | ||||||| ||
                                TCC  G GTGTCAGA CG
                                  CC _       _
GAM805  KIAA1161  3'  AGCCACATGGAACTGTGAGTTC 81732           _   GTG
                                GAACTCACAGT CTA   GGCT
                                ||||||||||| |||   ||||
                                CTTGAGTGTCA GGT   CCGA
                                      A   ACA
GAM805  KIAA1184  3'  CTAGACTGTGAATCCTT     42613       AC
                                AAGGA  TCACAGTCTAG
                                |||||  ||||||||||
                                TTCCT  AGTGTCAGATC
                                  A_
GAM805  MGC32043  3'  TAGACTGTAAGCTCCTT     58057       A  C
                                AAGGA CT ACAGTCTA
                                ||||| || ||||||||
                                TTCCT GA TGTCAGAT
                                  C  A
GAM805  POLE3     3'  TCCAAAGTGTGAGTTCCT    33860           GTCTAG
                                AGGAACTCACA     TGGG
                                ||||||||||      ||||
                                TCCTTGAGTGT     ACCT
                                      GAA___
GAM805  PTPNS1    3'  GCGAAGACTTGAGTTCCT    55001         C    A_
                                AGGAACTCA AGTCT  GT
                                ||||||||| |||||  ||
                                TCCTTGAGT TCAGA  CG
                                     _    AG
GAM805  RASGRP4   3'  AGCCCTCAACTGTGAGCC    53646    AA       CTAGT
                                GG  CTCACAGT    GGGCT
                                ||  ||||||||    |||||
                                CC  GAGTGTCA    CCCGA
                                  __       ACT__
GAM805  SMC1L1    3'  AGCCCACTAGGTGCCGACCCCT 71957     AAC  A_  G
                                AGG   TC  CA TCTAGTGGGCT
                                |||   ||  || ||||||||||
                                TCC   AG  GT GGATCACCCGA
                                  CC_  CC  _
GAM805  TBX19     3'  ATTAGACTGTAAGCCT      17649     AA  C
                                AGG  CT ACAGTCTAGT
                                |||  || ||||||||||
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                                TCC  GA TGTCAGATTA
                                  __ A
GAM805  URG4     3'  CCCAGACTGTGAGCTCCTT   35504      A        AGT
                                AAGGA CTCACAGTCT   GGG
                                ||||| ||||||||||   |||
                                TTCCT GAGTGTCAGA   CCC
                                   C        ____
GAM805  XPO5     3'  CCTGTACTGTGAGTCC      91236     A       CTA TG
                                GGA CTCACAGT   G  GG
                                ||| ||||||||   |  ||
                                CCT GAGTGTCA   T  CC
                                  _       ___ GT
GAM805  LOC118611 5' AGCCCACTAGACATTTCCTT   75467       CTCACA
                                AAGGAA     GTCTAGTGGGCT
                                ||||||     ||||||||||||
                                TTCCTT     CAGATCACCCGA
                                    TA_____
GAM805  LOC118611 3' CCCACTGGATACAGTCCC    75472    A   CACA
                                GG ACT    GTCTAGTGGG
                                || |||    ||||||||||
                                CC TGA    TAGGTCACCC
                                 C   CA__
GAM805  LOC124460 3' GCAGACTGTGGCCCCT      76045     AA T       A
                                AGG  C CACAGTCT GT
                                |||  | ||||||||  ||
                                TCC  G GTGTCAGA CG
                                  CC _       _
GAM805  LOC144231 3' GCTAGACTGTAAGCCCTT    83017      AA  C
                                AAGG  CT ACAGTCTAGT
                                ||||  || ||||||||||
                                TTCC  GA TGTCAGATCG
                                  C_  A
GAM805  LOC146268 3' CTAGACTGTGAGCTCCT     77807      A
                                AGGA CTCACAGTCTAG
                                |||| ||||||||||||
                                TCCT GAGTGTCAGATC
                                  C
GAM805  LOC146446 3' AGCCCACTATCAAGTTCC    83685       CACAGTC
                                GGAACT      TAGTGGGCT
                                ||||||      |||||||||
                                CCTTGA      ATCACCCGA
                                   ACT_____
GAM805  LOC147136 3' CTCAAGACTGTGAGCTGCCT  78263     AA_        AG
                                AGG   CTCACAGTCT  TGGG
                                |||   ||||||||||  ||||
                                TCC   GAGTGTCAGA  ACTC
                                  GTC        __
GAM805  LOC151361 3' CCCAAACCTGTGAGTCTCTT  85322     GA       TCTAG
                                AAG  ACTCACAG    TGGG
                                |||  ||||||||    ||||
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                                TTC  TGAGTGTC    ACCC
                                  TC      CAA__
GAM805  LOC163231 3'  CCTGCTACTGTGAGCCACCT   82439    AA_      CT  TG
                                AGG   CTCACAGT  AG  GG
                                |||   ||||||||  ||  ||
                                TCC   GAGTGTCA  TC  CC
                                  ACC       __  GT
GAM805  LOC163231 3'  CCTGTTCACTGTGAGCC    82440    AA      CT  TG
                                GG  CTCACAGT  AG  GG
                                ||  ||||||||  ||  ||
                                CC  GAGTGTCA  TT  CC
                                  __      C_  GT
GAM805  LOC163404 3'  CCCACTAGACTGTGAGCTCCT  82124     A
                                AGGA CTCACAGTCTAGTGGG
                                |||| ||||||||||||||||
                                TCCT GAGTGTCAGATCACCC
                                  C
GAM805  LOC163682 3'  GCCCACTGCCCAGCTCCT    87036     A  CACAGTC
                                AGGA CT      TAGTGGGC
                                |||| ||      ||||||||
                                TCCT GA      GTCACCCG
                                  C  CCC____
GAM805  LOC196202 5'  CCCATTGGCCAAAAGCTCCTT  89439      A  CACA T
                                AAGGA CT    G CTAGTGGG
                                ||||| ||    | ||||||||
                                TTCCT GA    C GGTTACCC
                                   C  AAAC _
GAM805  LOC201546 5'  AGCCCGTGGCTGTGAATTCTTT 89517       C       TAG
                                AAGGAA TCACAGTC   TGGGCT
                                |||||| ||||||||   ||||||
                                TTTCTT AGTGTCGG   GCCCGA
                                   A       T__
GAM805  LOC203197 3'  GCTAGACTGTAAACTCCTT    89290      ACTC
                                AAGGA    ACAGTCTAGT
                                |||||    ||||||||||
                                TTCCT    TGTCAGATCG
                                   CAAA
GAM805  LOC221431 3'  AGCATGGGCTATGAGCTCC    92098     A   C     GTGG
                                GGA CTCA AGTCTA    GCT
                                ||| |||| ||||||    |||
                                CCT GAGT TCGGGT    CGA
                                  C   A     A___
GAM805  LOC51246  3'  CTGGCAACTGTGAGTCCCT    33216     A       __
                                AGG ACTCACAGT  CTAG
                                ||| |||||||||  ||||
                                TCC TGAGTGTCA  GGTC
                                  C        AC
GAM805  LOC55924  3'  GCCCAACTCCAAGTTCCTT    38875        CAC   CTAG
                                AAGGAACT   AGT    TGGGC
                                ||||||||   |||    |||||
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                                TTCCTTGA  TCA   ACCCG
                                    ACC  ____
GAM805  LOC93496 3' ACTAGAATGTGAGCTCCTT   72428      A     G
                                AAGGA CTCACA TCTAGT
                                ||||| |||||| ||||||
                                TTCCT GAGTGT AGATCA
                                   C     A
GAM806  ADH1B    3' CTTAGACATAAAGTAAAAT   72644      C    CAC
                                ATTT ACTTT  TGTCTGAG
                                |||| |||||  ||||||||
                                TAAA TGAAA  ACAGATTC
                                  A    T__
GAM806  AHR      3' ATCTCAGATGTTAAAATAAATG 7875       CAC  C  T
                                CATTT  TTT AC GTCTGAGAT
                                |||||  ||| || |||||||||
                                GTAAA  AAA TG TAGACTCTA
                                   TA_  T  _
GAM806  FDFT1    3' TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                        _
GAM806  JTB      3' ATCTCAGACAGTGAAAGTGAAA 21959
           TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM806  KLF4     3' TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM806  PHYH     3' ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM806  PKD2     3' TCCAGGTTGAAAGTGAAA    60096          CTG   A
                                TTTCACTTTCA  TCTG GA
                                ||||||||||  |||| ||
                                AAAGTGAAAGT  GGAC CT
                                       T__   _
GAM806  WRN      3' GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM806  ZNF216   3' ATCTGCACAGCAAAGTGAAA  20017        CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||  ||||
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                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM806  CG012    5' CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                     CT  __
GAM806  EIF2C2   3' ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM806  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC       GTCTGAGAT
                                ||||||       |||||||||
                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM806  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM806  KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM806  KLHL6    3' ATCTCAGAGCAGGAAA      55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM806  NIR3     3' GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM806  PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM806  PP35     3' ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM806  PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148         TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
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                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM806  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                      A    TC
GAM806  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941        CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                      AAAGG
GAM806  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM806  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM806  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226     A      GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM806  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM807  ANK2     3'  CCCAGTTCTCACACCA      40603     A   CA
                                TGGT TGA  GAACTGGG
                                |||| |||  ||||||||
                                ACCA ACT  CTTGACCC
                                  C   __
GAM807  ANK2     3'  CCCAGTTCTCACACCA      6709      A   CA
                                TGGT TGA  GAACTGGG
                                |||| |||  ||||||||
                                ACCA ACT  CTTGACCC
                                  C   __
GAM807  ATP11A   3'  CCAGTCCCTGCCACAGA     77022        TGACA  A
                                TCTGTGGTA    GA CTGG
                                |||||||||    || ||||
                                AGACACCGT    CT GACC
                                      CC___  _
GAM807  ATP11A   3'  CCAGTCCCTGCCACAGA     77023        TGACA  A
                                TCTGTGGTA    GA CTGG
                                |||||||||    || ||||
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                                AGACACCGT    CT GACC
                                     CC___  _
GAM807  ATP11A   3'  CCAGTCCCTGCCACAGA     77024         TGACA  A
                                TCTGTGGTA    GA CTGG
                                |||||||||    || ||||
                                AGACACCGT    CT GACC
                                     CC___  _
GAM807  DNCI1    5'  CCCAGTTCCGCCGCTGCCG   91062      _  ACA
                                TGGTA TG   GAACTGGG
                                ||||| ||   ||||||||
                                GCCGT GC   CTTGACCC
                                   C  CGC
GAM807  GSTA4    3'  CCCAGCTCTGTCATGGTGC   7698     G       A
                                GTG TATGACAGA CTGGG
                                ||| ||||||||| |||||
                                CGT GTACTGTCT GACCC
                                  G       C
GAM807  ITPKB    3'  CCCAGCCCTCGTCACCACAGG  9424        AT  _  AA
                                TCTGTGGT  GAC AG  CTGGG
                                ||||||||  ||| ||  |||||
                                GGACACCA  CTG TC  GACCC
                                     __  C  CC
GAM807  LARS2    3'  CCCAGCTCTGTCATGC      31053         A
                                GTATGACAGA CTGGG
                                |||||||||| |||||
                                CGTACTGTCT GACCC
                                      C
GAM807  LFNG     3'  CCCAGTTCCAGTGGCCCCACG  92638      TATG  A_
                                TGTGG    AC  GAACTGGG
                                |||||    ||  ||||||||
                                GCACC    TG  CTTGACCC
                                   CCGG  AC
GAM807  LZTS1    3'  CCCAGCCCCGGCAAGCCACAGG 40686        A  ACAGAA
                                TCTGTGGT TG     CTGGG
                                |||||||| ||     |||||
                                GGACACCG AC     GACCC
                                     A  GGCCCC
GAM807  MAT1A    3'  CCCAGCTCCCAGGACCACAGG  90828        A_  ACA  A
                                TCTGTGGT  TG   GA CTGGG
                                ||||||||  ||   || |||||
                                GGACACCA  AC   CT GACCC
                                     GG  C__  C
GAM807  NORE1    3'  CCCAGGCTGTGCCCCACCACAG 48716        ATG__    AA
              A                  TCTGTGGT    ACAG  CTGGG
                                 ||||||||    ||||  |||||
                                 AGACACCA    TGTC  GACCC
                                     CCCCG    G_
GAM807  SCA7     5'  CCAATTCCACCACAGA      4403          ATGACA   C
                                TCTGTGGT     GAA TGG
                                ||||||||     ||| |||
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                                AGACACCA     CTT ACC
                                    C_____   A
GAM807  SP3      5'  CCAGAATCTCATACCACAGA  82496          CAGAA
                                TCTGTGGTATGA    CTGG
                                ||||||||||||    ||||
                                AGACACCATACT    GACC
                                      CTAA_
GAM807  SRR      3'  CCCAACCTTTATACCACA    41687          C  AAC
                                TGTGGTATGA AG   TGGG
                                |||||||||| ||   ||||
                                ACACCATATT TC   ACCC
                                      _  CA_
GAM807  VSNL1    3'  CTGGTCCACACACCACAGA   12624         A  ACA  A TG
                                TCTGTGGT TG   GA C  G
                                |||||||| ||   || |  |
                                AGACACCA AC   CT G  C
                                    C  AC_  _ GT
GAM807  ABLIM    3'  CCCAATTCTGTCATCTCCA   9761      T_       C
                                TGG  ATGACAGAA TGGG
                                |||  ||||||||| ||||
                                ACC  TACTGTCTT ACCC
                                  TC       A
GAM807  ABLIM    3'  CCCAATTCTGTCATCTCCA   22022     T_       C
                                TGG  ATGACAGAA TGGG
                                |||  ||||||||| ||||
                                ACC  TACTGTCTT ACCC
                                  TC       A
GAM807  C14orf4  5'  CCCAACCTGCTACCGCAGA   67334         TGA   AAC
                                TCTGTGGTA   CAG   TGGG
                                |||||||||   |||   ||||
                                AGACGCCAT   GTC   ACCC
                                    C__   CA_
GAM807  CALN1    3'  CCCAGCCCTGTTCACACA    48861      GTAT    AA
                                TGTG   GACAG  CTGGG
                                ||||   |||||  |||||
                                ACAC   TTGTC  GACCC
                                  AC__    CC
GAM807  DKFZp547I094 3'  CCAGGGCACATCACAGA     49634         A  ACAGAA
                                TCTGTGGT TG     CTGG
                                |||||||| ||     ||||
                                AGACACTA AC     GACC
                                    C  GG____
GAM807  DKFZp761F2014 3'  CCCAGTTCTGTCAGCTCTAGA  39536      T   A
                                TCTG GGT TGACAGAACTGGG
                                |||| ||| ||||||||||||
                                AGAT TCG ACTGTCTTGACCC
                                  C  _
GAM807  FLJ11320  3'  CCCAGTTCTACCTCCCCAGA   37243      T  TATGAC
                                TCTG GG     AGAACTGGG
                                |||| ||     |||||||||
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                              AGAC CC     TCTTGACCC
                                C  TCCA__
GAM807  FLJ14871  3'  CCCAGTTCTGCAGACACA    51667     GTA  A
                              TGTG   TG CAGAACTGGG
                              ||||   || ||||||||||
                              ACAC   AC GTCTTGACCC
                                AG_  _
GAM807  FLJ20452  3'  CCCAGTCAGGTTACACA     35197     GTA   AGA
                              TGTG   TGAC   ACTGGG
                              ||||   ||||   ||||||
                              ACAC   ATTG   TGACCC
                                ___    GAC
GAM807  FLJ23168  3'  CCCGCTTTGCACACCACAGA   46822        A  A   AC
                              TCTGTGGT TG CAGA  TGGG
                              |||||||| || ||||  ||||
                              AGACACCA AC GTTT  GCCC
                                   C  _   C_
GAM807  KIAA0527  3'  CCCAGTTCTGTTTTTAACA   95796     GGTAT
                              TGT    GACAGAACTGGG
                              |||    ||||||||||||
                              ACA    TTGTCTTGACCC
                               ATTT_
GAM807  KIAA0781  3'  CCTGGTTCTGCCCCACCACA  67456       ATGA    TG
                              TGTGGT   CAGAAC  GG
                              ||||||   ||||||  ||
                              ACACCA   GTCTTG  CC
                                 CCCC     GT
GAM807  KIAA1751  3'  CCCAGCTCTGCCTGGTCACAGA 71691        ATGA   A
                              TCTGTGGT   CAGA CTGGG
                              ||||||||   |||| |||||
                              AGACACTG   GTCT GACCC
                                   GTCC   C
GAM807  KRTHB4    3'  CCCAGCCCTGTCCACTGCAGG  52323     TG  AT    AA
                              TCTG  GT  GACAG  CTGGG
                              ||||  ||  |||||  |||||
                              GGAC  CA  CTGTC  GACCC
                                GT  C_    CC
GAM807  MGC10812  3'  CCCAAATTTGACACCACAGA   48665       ATGA   AC
                              TCTGTGGT   CAGA  TGGG
                              ||||||||   ||||  ||||
                              AGACACCA   GTTT  ACCC
                                   CA__    AA
GAM807  NTSR2     5'  CCCAGTTCTAGAGGTTCCCAGA 24716     T  TATGAC_
                              TCTG GG      AGAACTGGG
                              |||| ||      |||||||||
                              AGAC CC      TCTTGACCC
                                _  TTGGAGA
GAM807  PDZD2     5'  CCCAGTTCCCCCCAGCAGA   80865     _  TATGACA
                              TCTG TGG      GAACTGGG
                              |||| |||      ||||||||
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                                AGAC ACC      CTTGACCC
                                  G  CCC_____
GAM807  PGLYRP   3'  CCCAGCCACATACCACA    53575         ACAGAA
                                TGTGGTATG     CTGGG
                                |||||||||     |||||
                                ACACCATAC     GACCC
                                    ACC___
GAM807  PLCE1    3'  CCCAATTCTGCCATTGTAG   32963     TG TA  A    C
                                CTG  G  TG CAGAA TGGG
                                |||  |  || ||||| ||||
                                GAT  T  AC GTCTT ACCC
                                  GT __  C    A
GAM807  SV2B     5'  CCCAAACCTCTACCACAGA   29296         T  CAGAAC
                                TCTGTGGTA GA     TGGG
                                ||||||||| ||     ||||
                                AGACACCAT CT     ACCC
                                    _  CCAA__
GAM807  ZAP3     5'  CCCAGTTCCACCAGCCTCCAG  77222     T_   A  ACA
                                CTG  GGT TG   GAACTGGG
                                |||  ||| ||   ||||||||
                                GAC  CCG AC   CTTGACCC
                                  CT   _  CAC
GAM807  LOC112970 3'  CCCTTTTTTCATACCACA    56535         C    CT
                                TGTGGTATGA AGAA  GGG
                                |||||||||| ||||  |||
                                ACACCATACT TTTT  CCC
                                    _    T_
GAM807  LOC130574 3'  CCCAAGTTCCATACCATA    74955         ACA    _
                                TGTGGTATG   GAACT GGG
                                |||||||||   ||||| |||
                                ATACCATAC   CTTGA CCC
                                    ___     A
GAM807  LOC131583 5'  CCCAACTCCCTACCACAGG   75864         TGACA  AC
                                TCTGTGGTA    GA  TGGG
                                |||||||||    ||  ||||
                                GGACACCAT    CT  ACCC
                                    CC___  CA
GAM807  LOC138428 3'  CCAGCCACTGCCACAGA     75333         _  ACAGAA
                                TCTGTGGTA TG     CTGG
                                ||||||||| ||     ||||
                                AGACACCGT AC     GACC
                                    C  C_____
GAM807  LOC142955 3'  CCCAACTCTGTCATCTGTA   76445    TG T       AC
                                TG  G ATGACAGA  TGGG
                                ||  | ||||||||  ||||
                                AT  C TACTGTCT  ACCC
                                  GT _       CA
GAM807  LOC143308 5'  CCCAGTTCCATCCTGGCCA   82937     AT_  CA
                                TGGT   GA  GAACTGGG
                                ||||   ||  ||||||||
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                                ACCG   CT  CTTGACCC
                                  GTC  AC
GAM807   LOC145241 3'  CCCTTACGTCAGTACCACA   62867       _   AGAACT
                                TGTGGTA TGAC     GGG
                                ||||||| ||||     |||
                                ACACCAT ACTG     CCC
                                    G    CATT__
GAM807   LOC148760 3'  CCCAACCCCTGCACCACAGG   84203       AT A   AAC_
                                TCTGTGGT  G CAG    TGGG
                                ||||||||  | |||    ||||
                                GGACACCA  C GTC    ACCC
                                    __ _  CCCA
GAM807   LOC149271 3'  CCCACCTCCCACCCACCACAGA 79239       ATGACA  AC
                                TCTGTGGT     GA  TGGG
                                ||||||||     ||  ||||
                                AGACACCA     CT  ACCC
                                     CCCACC  CC
GAM807   LOC196707 3'  CCCAGTTCCGCAGCAGA     87526      GGTA  ACA
                                TCTGT    TG   GAACTGGG
                                |||||    ||   ||||||||
                                AGACG    AC   CTTGACCC
                                   _____  GC_
GAM807   LOC197287 5'  CCAGTCCCTGCCACAGA     60863        TGACA  A
                                TCTGTGGTA    GA CTGG
                                |||||||||    || ||||
                                AGACACCGT    CT GACC
                                     CC___  _
GAM807   LOC197287 5'  CCAGTCCCTGCCACAGA     60861        TGACA  A
                                TCTGTGGTA    GA CTGG
                                |||||||||    || ||||
                                AGACACCGT    CT GACC
                                     CC___  _
GAM807   LOC197287 5'  CCAGTCCCTGCCACAGA     60862        TGACA  A
                                TCTGTGGTA    GA CTGG
                                |||||||||    || ||||
                                AGACACCGT    CT GACC
                                     CC___  _
GAM807   LOC197358 3'  CCCAGTCTGATGCACCACGGA  88027       AT A    A
                                TCTGTGGT  G CAGA CTGGG
                                ||||||||  | |||| |||||
                                AGGCACCA  T GTCT GACCC
                                     CG A   _
GAM807   LOC219857 5'  CTCGGCATCAGCACCACAGA   91510       A_   CAGAA
                                TCTGTGGT  TGA    CTGGG
                                ||||||||  |||    |||||
                                AGACACCA  ACT    GGCTC
                                     CG   AC___
GAM807   LOC221472 3'  CCAGCTCCTGCCACAGA     92298        T  CAGAA
                                TCTGTGGTA GA    CTGG
                                ||||||||| ||    ||||
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                                AGACACCGT CT    GACC
                                    C  C____
GAM807  LOC253573 3'  CCCAGTTCTGACATTCACAG  97047      T  A
                                CTGTGG ATG CAGAACTGGG
                                |||||| ||| ||||||||||
                                GACACT TAC GTCTTGACCC
                                   _  A
GAM807  LOC254263 3'  CCCAGCCCTGCCCCTTGGCCGC 94715       ATGA___  AA
          AGA                     TCTGTGGT     CAG  CTGGG
                                |||||||||     |||  |||||
                                AGACGCCG     GTC  GACCC
                                    GTTCCCC  CC
GAM807  LOC257065 5'  CCCAGTTCCACCCCCACCCAGA 97637     T  ATGACA_
                                TCTG GGT     GAACTGGG
                                |||| |||     ||||||||
                                AGAC CCA     CTTGACCC
                                  _  CCCCCAC
GAM807  LOC257471 5'  CCAGAATCTCATACCACAGA  95687         CAGAA
                                TCTGTGGTATGA    CTGG
                                ||||||||||||    ||||
                                AGACACCATACT    GACC
                                      CTAA_
GAM807  LOC92340  3'  CCAACTCCATCCACGGA    68988       T  ACA  AC
                                TCTGTGG ATG  GA  TGG
                                ||||||| |||  ||  |||
                                AGGCACC TAC  CT  ACC
                                   _  ____ CA
GAM808  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT  TGTCTGAG
                                |||| |||||  ||||||||
                                TAAA TGAAA  ACAGATTC
                                  A    T__
GAM808  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC  C  T
                                CATTT  TTT AC GTCTGAGAT
                                |||||  ||| || |||||||||
                                GTAAA  AAA TG TAGACTCTA
                                   TA_  T  _
GAM808  FDFT1    3'  TAGGAAAGTGAAATG      15518          A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM808  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
          TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM808  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
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                                GT  AGGTGACAGAC CT
                                 AT         C
GAM808  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                     A
GAM808  PKD2     3'  TCCAGGTTGAAAGTGAAA     60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM808  WRN      3'  GGGCAGTGAAAATGAAA      5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM808  ZNF216   3'  ATCTGCACAGCAAAGTGAAA   20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_    CG_
GAM808  CG012    5'  CTCACTCTGAAAGTGAA      83218          CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM808  EIF2C2   3'  ATCTTCTGAGAGTGAAAG     71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM808  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM808  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281         CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM808  KIAA0984 3'  TTTGTCCAGTGAAAATGAA    65534      C       TC
                                TTCA TTTCACTG  TGAG
                                ||||  ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM808  KLHL6    3'  ATCTCAGAGCAGGAAA       55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
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                                AAAG GAC AGACTCTA
                                  _  G
GAM808  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM808  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM808  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM808  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148         TCAC   C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM808  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM808  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM808  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM808  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM808  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||   |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM808  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
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                                GTAAAGTGAA GTGACA
                                      _
GAM809  CLCN5    5'  TGAAATACCTAAGCTGCTCCAA 3595          _______
                                TTGGAGCAG     GTTTCA
                                |||||||||     ||||||
                                AACCTCGTC     TAAAGT
                                     GAATCCA
GAM809  FLRT2    5'  ATTGAAAAATGAGGTCTGC   25056     GT    CTC
                                GCAG  TTCATT   CAAT
                                ||||  ||||||   ||||
                                CGTC  GAGTAA   GTTA
                                  TG     AAA
GAM809  IL17     3'  TGGGGAAAATGAAACCCTCC  9333      CA     __
                                GGAG  GGTTTCAT  TCTCCA
                                ||||  ||||||||  ||||||
                                CCTC  CCAAAGTA  AGGGGT
                                  __      AA
GAM809  NLGN1    5'  TGAAGATGCTGCTCCAA     30026        G__
                                TTGGAGCAG   TTTCA
                                |||||||||   |||||
                                AACCTCGTC   GAAGT
                                     GTA
GAM809  POLG     3'  GTGATAAACCTGCTCCAA    10682          __
                                TTGGAGCAGGTT  TCAT
                                ||||||||||||  ||||
                                AACCTCGTCCAA  AGTG
                                      AT
GAM809  TPK1     3'  GGAGAACCTGTCCAA       42384      G    TTCAT
                                TTGGA CAGGT    TCTCC
                                ||||| |||||    |||||
                                AACCT GTCCA    AGAGG
                                  _   ______
GAM809  C1orf8   5'  GAGAATGAAACCCTC       16832     CA
                                GAG  GGTTTCATTCTC
                                |||  ||||||||||||
                                CTC  CCAAAGTAAGAG
                                  __
GAM809  CLIC6    3'  TGGAGAACATGTTCCAA     82536        G  TTCAT
                                TTGGAGCA GT    TCTCCA
                                |||||||| ||    ||||||
                                AACCTTGT CA    AGAGGT
                                     A _____
GAM809  CLIPR-59 3'  TGGAGAATTTCAATGCCCCGA 31374      A   GGTTTC
                                TTGG GCA     ATTCTCCA
                                |||| |||     ||||||||
                                AGCC CGT     TAAGAGGT
                                  C   AACTT_
GAM809  DKFZP547L112 3'  TGGAGAACTCTTGCTCCA   66532         TTTCA
                                TGGAGCAGG    TTCTCCA
                                |||||||||    |||||||
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                                ACCTCGTTC    AAGAGGT
                                     TC___
GAM809  EPS8R3   5' GGACCACCTGCTCCAA     57404         TTCATTC
                                TTGGAGCAGGT     TCC
                                ||||||||||      |||
                                AACCTCGTCCA     AGG
                                     CC_____
GAM809  EPS8R3   5' GGACCACCTGCTCCAA     55701         TTCATTC
                                TTGGAGCAGGT     TCC
                                ||||||||||      |||
                                AACCTCGTCCA     AGG
                                     CC_____
GAM809  FLJ20552 3' AGAACAAAACTGCTCCAA    35389        G   CA
                                TTGGAGCAG TTT  TTCT
                                ||||||||| |||  ||||
                                AACCTCGTC AAA  AAGA
                                     _  AC
GAM809  FLJ22865 5' TGGAGAAAACTGCTCTAA    47071        GTTTCA
                                TTGGAGCAG     TTCTCCA
                                |||||||||     |||||||
                                AATCTCGTC     AAGAGGT
                                     AA____
GAM809  KIAA0372 5' ATTGAAATTTGTTACCTACTCC 27663       C    TT  TTCTC
           AA                    TTGGAG AGGT  CA    CAAT
                                ||||||| ||||  ||    ||||
                                AACCTC TCCA  GT    GTTA
                                   A    TT  TTAAA
GAM809  PRO0132  5' ATGAAACCACTCCAA      26101       CA
                                TTGGAG  GGTTTCAT
                                ||||||  ||||||||
                                AACCTC  CCAAAGTA
                                   A_
GAM809  TEX27    3' AGAGTGGAACCCGCTGCAA   41658     G   A
                                TTG AGC GGTTTCATTCT
                                ||| ||| ||||||||||
                                AAC TCG CCAAGGTGAGA
                                  G   C
GAM809  LOC149373 3' ATTGGGGTGATGATACCCACCC 79312      AGCA   T    _
           CAA                    TTGG    GGT TCATT CTCCAAT
                                ||||    ||| ||||| |||||||
                                AACC    CCA AGTAG GGGGTTA
                                  CCAC   T    T
GAM809  LOC152687 3' TTGGAGAATATTGCTCC     80643        GTTTC
                                GGAGCAG    ATTCTCCAA
                                |||||||    |||||||||
                                CCTCGTT    TAAGAGGTT
                                   A____
GAM809  LOC51202  3' ATTGGAGAATGAAACCTGCTCC 33017
           AA                    TTGGAGCAGGTTTCATTCTCCAAT
                                ||||||||||||||||||||||||
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                                AACCTCGTCCAAAGTAAGAGGTTA

GAM810  ACT     3'  CATGAGGCTAGTGTTTGCA   40041         ___  AC
                                TGTAAACAT   CCT  CATG
                                |||||||||   |||  ||||
                                ACGTTTGTG   GGA  GTAC
                                     ATC  __
GAM810  ACVR1   3'  CATGTGCTGATGTTTACA    6606          CTAC
                                TGTAAACATC    CATG
                                ||||||||||    ||||
                                ACATTTGTAG    GTAC
                                      TCGT
GAM810  ANKRA2  3'  GTGCACAGTGTGATTGTTTACA 43527        _  C   CA
                                TGTAAACA TC TAC  TGCAC
                                |||||||| || |||  |||||
                                ACATTTGT AG GTG  ACGTG
                                     T  T   AC
GAM810  BTEB1   3'  ATGGGGGAAATGTTTACA    6838         __   A
                                TGTAAACA  TCCT CCAT
                                ||||||||  |||| ||||
                                ACATTTGT  AGGG GGTA
                                     AA   _
GAM810  CCND1   3'  GCAGAGGATGTTCATA      53889     A      ACCA
                                TGT AACATCCT    TGC
                                ||| ||||||||    |||
                                ATA TTGTAGGA    ACG
                                  C       G___
GAM810  COX10   3'  GCTTGACAGGATGTTTTCA   7122     T       AC  T
                                TG AAACATCCT  CA GC
                                || |||||||||  || ||
                                AC TTTGTAGGA  GT CG
                                  T       CA  T
GAM810  CSPG3   3'  GTGCATGAGTGTATGTTTGCA  15234         CC  _
                                TGTAAACAT  TAC CATGCAC
                                |||||||||  ||| |||||||
                                ACGTTTGTA  GTG GTACGTG
                                     T_   A
GAM810  CUL3    3'  ATGGTAAGATGTTTATA     13160          C
                                TGTAAACATC TACCAT
                                |||||||||| ||||||
                                ATATTTGTAG ATGGTA
                                      A
GAM810  EVPL    3'  GCCAGGTAGGATACGTACA   8806      AAC      AT
                                TGTA   ATCCTACC  GC
                                ||||   ||||||||  ||
                                ACAT   TAGGATGG  CG
                                  GCA       AC
GAM810  FLT1    3'  GTATTTAGGATGTCTGCA    8921      A       CC
                                TGTA ACATCCTA  ATGC
                                |||| ||||||||  ||||
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                                ACGT TGTAGGAT  TATG
                                  C       T_
GAM810  FOXD1    3'  ATGGTTAACATGTTTACA    15560         CCT_
                                TGTAAACAT    ACCAT
                                |||||||||    |||||
                                ACATTTGTA    TGGTA
                                     CAAT
GAM810  GPX3     3'  GTGCAATGTGGGTGTTTACA  9124          T    CA
                                TGTAAACA CCTAC  TGCAC
                                |||||||| |||||  |||||
                                ACATTTGT GGGTG  ACGTG
                                     _    TA
GAM810  LEP      3'  TGCATGGTGCAGTTGACA    4060      A   ATCC
                                TGT AAC    TACCATGCA
                                ||| |||    |||||||||
                                ACA TTG    GTGGTACGT
                                  G   AC__
GAM810  P2RY1    3'  TATGGTAGGATGCTTA      10378     A
                                TAA CATCCTACCATG
                                ||| ||||||||||||
                                ATT GTAGGATGGTAT
                                  C
GAM810  PLCG2    3'  GCATGTGTGTTTGCA       72464         CCTAC
                                TGTAAACAT    CATGC
                                |||||||||    |||||
                                ACGTTTGTG    GTACG
                                     T_____
GAM810  SLC21A9  3'  GCTTTTAGGATGTTTATA    23422           CCAT
                                TGTAAACATCCTA    GC
                                ||||||||||||    ||
                                ATATTTGTAGGAT    CG
                                       TTT_
GAM810  TAF9     3'  TGCATGCTGGATGTTTTCA    12097    T      TAC
                                TG AAACATCC   CATGCA
                                || ||||||||   ||||||
                                AC TTTGTAGG   GTACGT
                                 T       TC_
GAM810  TIMM17A  3'  TATGGTAAAATGTTTATA    20937         CC
                                TGTAAACAT  TACCATG
                                |||||||||  |||||||
                                ATATTTGTA  ATGGTAT
                                     AA
GAM810  TNFSF9   3'  TGTTGCCAAGGTTGTTTACA  13759         T   ACCAT
                                TGTAAACA CCT    GCA
                                |||||||| |||    |||
                                ACATTTGT GGA    TGT
                                     T   ACCGT
GAM810  ABHD2    5'  GTGCATGGAGTTACTACA    22808     AACATC  A
                                TGTA     CT CCATGCAC
                                ||||     || ||||||||
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                                ACAT     GA GGTACGTG
                                  CATT__  _
GAM810  C11orf11  3'  GTGCTGTACATGTTTACA    93259         CC   CAT
                                TGTAAACAT  TAC   GCAC
                                |||||||||  |||   ||||
                                ACATTTGTA  ATG   CGTG
                                     C_   T__
GAM810  C20orf59  3'  GCACACTGTAGGATGCTTA    41994     A       CA__
                                TAA CATCCTAC    TGC
                                ||| ||||||||    |||
                                ATT GTAGGATG    ACG
                                  C       TCAC
GAM810  CAMTA2    3'  GTGCATGGGCTTGGTTTATA   61222        ATCCTA
                                TGTAAAC     CCATGCAC
                                |||||||     ||||||||
                                ATATTTG     GGTACGTG
                                    GTTCG_
GAM810  CECR6     3'  GCGGGGGGAAAATGTTTACA   49090         ___    A  A
                                TGTAAACA   TCCT CC TGC
                                ||||||||   |||| || |||
                                ACATTTGT   AGGG GG GCG
                                     AAA   _ _
GAM810  DDX36     3'  GTAAAAATAGGATGTTTAC    40483          CCA_
                                GTAAACATCCTA    TGC
                                ||||||||||||    |||
                                CATTTGTAGGAT    ATG
                                      AAAA
GAM810  FLJ13096  3'  GTATCTAAGGATGTTCTCA    46541    TA       ACC
                                TG  AACATCCT   ATGC
                                ||  ||||||||   ||||
                                AC  TTGTAGGA   TATG
                                  TC       ATC
GAM810  FLJ20725  3'  TGCCCTATGGTGTTTACA     35613         C  CCAT
                                TGTAAACATC TA    GCA
                                ||||||||||  ||    |||
                                ACATTTGTGG AT    CGT
                                      T  CC__
GAM810  GDBR1     3'  GCATCTGACAGGTGTTTACA   32421         T   AC  __
                                TGTAAACA CCT  CA  TGC
                                |||||||| |||  ||  |||
                                ACATTTGT GGA  GT  ACG
                                     _   CA  CT
GAM810  KIAA0435  5'  GTGCACTGAGGGGTGTTTACA  28980           AC  _
                                TGTAAACATCCT  CA TGCAC
                                ||||||||||||  || |||||
                                ACATTTGTGGGG  GT ACGTG
                                      A_  C
GAM810  KIAA0562  3'  GTTGATAGGATGTTTA      28158          C  T
                                TAAACATCCTA CA GC
                                ||||||||||| || ||
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                                ATTTGTAGGAT GT TG
                                      A  _
GAM810  KIAA0794  3'  TGCAGCTGGGATGTCTACA   80417     A      CCA
                                TGTA ACATCCTA  TGCA
                                |||| ||||||||  ||||
                                ACAT TGTAGGGT  ACGT
                                  C       CG_
GAM810  KIAA0820  3'  ATGGAGAATGTTTAC      69019       C  A
                                GTAAACAT CT CCAT
                                |||||||| || ||||
                                CATTTGTA GA GGTA
                                     A  _
GAM810  KIAA1494  3'  GTGCATGGTGTGTATAT    68463    A   CCT
                                GTA ACAT  ACCATGCAC
                                ||| ||||  |||||||||
                                TAT TGTG  TGGTACGTG
                                  A   ___
GAM810  KIAA1495  3'  GTACTGTAGATTGTTTACA  73188       TC   CA
                                TGTAAACA  CTAC  TGC
                                ||||||||  ||||  |||
                                ACATTTGT  GATG  ATG
                                     TA   TC
GAM810  MYLE    3'  GCGATGGATGTTTACA     25815         TACCA
                                TGTAAACATCC    TGC
                                ||||||||||    |||
                                ACATTTGTAGG    GCG
                                      TA___
GAM810  PTPRR   5'  GCTGAGGGATGTTTA      55615        AC  T
                                TAAACATCCT  CA GC
                                |||||||||  || ||
                                ATTTGTAGGG  GT CG
                                      A_  _
GAM810  RAB3-GAP150 3'  GTGCATGGTTATTTTACA   24838      CATCCT
                                TGTAAA     ACCATGCAC
                                ||||||     |||||||||
                                ACATTT     TGGTACGTG
                                   TAT___
GAM810  RABEX5  3'  GTGCATGGTAGAATGTT    27188     C
                                AACAT CTACCATGCAC
                                ||||| ||||||||||
                                TTGTA GATGGTACGTG
                                   A
GAM810  SEC14L1  3'  GTGCCCAGAGATGTTTATA   11505        _  ACCAT
                                TGTAAACATC CT    GCAC
                                |||||||||| ||    ||||
                                ATATTTGTAG GA    CGTG
                                      A  CC___
GAM810  SMC1L1   3'  GTGCATGTGAGTATGTTTGCA  71961        C  AC
                                TGTAAACAT CT  CATGCAC
                                |||||||| ||  |||||||
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                                ACGTTTGTA GA  GTACGTG
                                     T  GT
GAM810  TOR1B    3'  GTGCATGGCAGGCCCGGCA   27202     AAACAT   A
                                TGT      CCT CCATGCAC
                                |||      ||| ||||||||
                                ACG      GGA GGTACGTG
                                  GCCC__   C
GAM810  TPARL    3'  GTGTTTTAAGATGTTTAC    37478         C  CCAT
                                GTAAACATC TA    GCAC
                                ||||||||| ||    ||||
                                CATTTGTAG AT    TGTG
                                     A  TT__
GAM810  LOC127262 3'  TGCAAGTATGTTTACA      76114          C  ACCA
                                TGTAAACAT CT    TGCA
                                ||||||||| ||    ||||
                                ACATTTGTA GA    ACGT
                                     T  _____
GAM810  LOC131308 3'  GTGGGAAAATGTTTATA     75006         ___
                                TGTAAACA   TCCTAC
                                ||||||||   ||||||
                                ATATTTGT   AGGGTG
                                     AAA
GAM810  LOC145566 5'  GTGTTCTGAGGATGTTTCA    77278    T       ACCAT
                                TG AAACATCCT     GCAC
                                || |||||||||     ||||
                                AC TTTGTAGGA     TGTG
                                  _        GTCT_
GAM810  LOC148089 3'  GTGCATGGTAGGATTGTT    78639      _
                                AACA TCCTACCATGCAC
                                |||| ||||||||||||
                                TTGT AGGATGGTACGTG
                                   T
GAM810  LOC152674 3'  GCTTAGGATGTTCATA      85837     A       CCAT
                                TGT AACATCCTA    GC
                                ||| |||||||||    ||
                                ATA TTGTAGGAT    CG
                                  C        T___
GAM810  LOC157697 5'  GCACATGGATGTTTATA     81551           TACCA
                                TGTAAACATCC     TGC
                                ||||||||||     |||
                                ATATTTGTAGG     ACG
                                      TAC__
GAM810  LOC157867 5'  GCACATGGATGTTTATA     86558           TACCA
                                TGTAAACATCC     TGC
                                ||||||||||     |||
                                ATATTTGTAGG     ACG
                                      TAC__
GAM810  LOC157922 3'  GCGGAGGGTGTTCACA      86635     A       A  AT
                                TGT AACATCCT CC  GC
                                ||| |||||||| ||  ||
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                                ACA TTGTGGGA GG  CG
                                  C       _ __
GAM810  LOC220469 3'  GTGCAGTGAGGATGTTTCCA   76386    T       ACCA
                                TG AAACATCCT    TGCAC
                                || |||||||||    |||||
                                AC TTTGTAGGA    ACGTG
                                 C        GTG_
GAM810  LOC222008 5'  GCAGCAGGATGTTTGCA     94009           ACCA
                                TGTAAACATCCT    TGC
                                ||||||||||||    |||
                                ACGTTTGTAGGA    ACG
                                       CG__
GAM810  LOC91974  5'  TGCTCGGTTGTTTACA     67762        TCCT   AT
                                TGTAAACA    ACC  GCA
                                ||||||||    |||  |||
                                ACATTTGT    TGG  CGT
                                    _____   CT
GAM810  LOC92140  3'  CATGGCAGTATGTTTACA    68282         C  A
                                TGTAAACAT CT CCATG
                                ||||||||| || |||||
                                ACATTTGTA GA GGTAC
                                      T  C
GAM810  LOC92689  3'  CATGGTGGCATAATTACA    70221       AC  C
                                TGTAA  AT CTACCATG
                                |||||  || ||||||||
                                ACATT  TA GGTGGTAC
                                   AA  C
GAM810  LOC93259  5'  GTGCATGGCCAGAGGTGTTTAC 71825          _  A_
            A                    TGTAAACATC CT  CCATGCAC
                                ||||||||||  ||  ||||||||
                                ACATTTGTGG GA  GGTACGTG
                                      A  CC
GAM811  C1orf1    3'  CTCAGCACTTTACA       6858          TTCT
                                TGTAAAGT    GCTGAG
                                ||||||||    ||||||
                                ACATTTCA    CGACTC
                                            _____
GAM811  CASP10    3'  TCTGCAAGCAGAAACTTTACA  52108             _ _
                                TGTAAAGTTTCTGCT G AGA
                                |||||||||||||| | |||
                                ACATTTCAAAGACGA C TCT
                                          A G
GAM811  CASP10    3'  TCTGCAAGCAGAAACTTTACA  52124             _ _
                                TGTAAAGTTTCTGCT G AGA
                                |||||||||||||| | |||
                                ACATTTCAAAGACGA C TCT
                                          A G
GAM811  CEP2      5'  TTCTCAGCCGCCTTCTCCAGGC 23229       TA_   TTTCT
                                GCCTG   AAG    GCTGAGAA
                                |||||   |||    ||||||||
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                                CGGAC  TTC    CGACTCTT
                                   CTC  CGC__
GAM811  DGUOK    3'  AGAAACTCTTACAGGC      55156        _
                                GCCTGTAA AGTTTCT
                                |||||||| |||||||
                                CGGACATT TCAAAGA
                                     C
GAM811  EDN1     3'  TCTCAGCAGAAACACACAG   8730       AAA
                                CTGT  GTTTCTGCTGAGA
                                ||||  ||||||||||||
                                GACA  CAAAGACGACTCT
                                  CA_
GAM811  EPHB2    3'  TCTCTGCAGAAACCCTACA   15449      AA       T
                                TGTA  GTTTCTGC GAGA
                                ||||  |||||||| ||||
                                ACAT  CAAAGACG CTCT
                                  CC       T
GAM811  EVC      3'  AGAGAAACTTTCAG        27284     T       G
                                CTG AAAGTTTCT CT
                                ||| ||||||||| ||
                                GAC TTTCAAAGA GA
                                  _        _
GAM811  EVC      3'  CTGGACAGAAACTTCCAG    27296     TA       _ G
                                CTG  AAGTTTCTG CT AG
                                |||  ||||||||| || ||
                                GAC  TTCAAAGAC GG TC
                                  C_        A _
GAM811  GA       3'  CTCAGCAGACAGAGTACAG   25175      AAGTT
                                CTGTA    TCTGCTGAG
                                |||||    |||||||||
                                GACAT    AGACGACTC
                                   GAGAC
GAM811  GATA4    3'  TTTCTCAGATGCCTTTACACGC 9008     C      TTTCTG
                                GC TGTAAAG     CTGAGAAA
                                || |||||||     ||||||||
                                CG ACATTTC     GACTCTTT
                                 C      CGTA__
GAM811  GLRA2    5'  TTTCTCAGCAAACTGTACA   9034      A   TC
                                TGTA AGTT  TGCTGAGAAA
                                |||| ||||  ||||||||||
                                ACAT TCAA  ACGACTCTTT
                                  G   __
GAM811  GNB3     3'  CTCCCCAGCCCTTTGCAGGC  9076         TTT  CT
                                GCCTGTAAAG  CTG  GAG
                                ||||||||||  |||  |||
                                CGGACGTTTC  GAC  CTC
                                      CC_  CC
GAM811  MAP3K7IP1 3'  TCCCCAGCAGCCTCCTACAGAG 20381    _    A_  TTT     A_
            C                    GC CTGTA  AG   CTGCTG  GA
                                || |||||  ||  ||||||  ||
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                                CG GACAT  TC   GACGAC  CT
                                 A    CC  C__     CC
GAM811  MLLT2   3'  TTTCTCAGCCAGCTCTA     19857    A    TCT
                                TA AGTT   GCTGAGAAA
                                || ||||   |||||||||
                                AT TCGA   CGACTCTTT
                                 C    C__
GAM811  MNDA    5'  TTCTCAGCCCTTTACA      10101        TTTCT
                                TGTAAAG    GCTGAGAA
                                |||||||    ||||||||
                                ACATTTC    CGACTCTT
                                    C____
GAM811  MTRR    3'  TTCCCAGAGAACTTCACAG   10137     A    T  G   A
                                CTGT AAGTT CT CTG GAA
                                |||| ||||| || ||| |||
                                GACA TTCAA GA GAC CTT
                                  C    _ _  C
GAM811  MTRR    3'  TTCCCAGAGAACTTCACAG   43774     A    T  G   A
                                CTGT AAGTT CT CTG GAA
                                |||| ||||| || ||| |||
                                GACA TTCAA GA GAC CTT
                                  C    _ _  C
GAM811  NPY2R   3'  TTCTCAGCCCCTACGAGGC   6190      _  AAGTTTCT
                                GCCT GTA      GCTGAGAA
                                |||| |||      ||||||||
                                CGGA CAT      CGACTCTT
                                  G  CCC_____
GAM811  NPY2R   5'  TTCTCAGCCCCTACGAGGC   6189      _  AAGTTTCT
                                GCCT GTA      GCTGAGAA
                                |||| |||      ||||||||
                                CGGA CAT      CGACTCTT
                                  G  CCC_____
GAM811  TTC1    3'  CAAAAGCTTTACAAGC      12408    C       C
                                GC TGTAAAGTTT TG
                                || |||||||||| ||
                                CG ACATTTCGAA AC
                                 A        A
GAM811  ZNF192  3'  TTTCTAGGAAAATTTTACAG  20857         _ GCT
                                CTGTAAAGTTT CT   GAGA
                                |||||||||| ||   ||||
                                GACATTTTAAA GG   CTTT
                                       A  AT_
GAM811  BANP    5'  CAGCAGAAACCTCCAGGC    66216      TAAA
                                GCCTG   GTTTCTGCTG
                                |||||   ||||||||||
                                CGGAC   CAAAGACGAC
                                  CTC_
GAM811  BIKE    3'  CTCAGCAGCCGCCACAG     34184     AAA  TT
                                CTGT  GT  CTGCTGAG
                                ||||  ||  ||||||||
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                                GACA  CG  GACGACTC
                                  C__  CC
GAM811  C20orf38  3'  TTTCTCAGCAGAAACCCTACAA 37067    C   AA
            GC                    GC TGTA  GTTTCTGCTGAGAAA
                                  || ||||  ||||||||||||||
                                  CG ACAT  CAAAGACGACTCTTT
                                   A   CC
GAM811  C22orf2   3'  TTCTCAGCAGCAAGCACCAG   94459     TAAA   _
                                  CTG   GTTT CTGCTGAGAA
                                  |||   |||| ||||||||||
                                  GAC   CGAA GACGACTCTT
                                    CA__   C
GAM811  DKFZP434D193 5'  CATCAGAAACTTCTCAAGC   88876    C  TA       C
                                  GC TG  AAGTTTCTG TG
                                  || ||  ||||||||| ||
                                  CG AC  TTCAAAGAC AC
                                   A  TC        T
GAM811  DKFZp434O0320 5'  TCTCAGCAGCTACAGTGC    83698    _    AAGTTT
                                  GC CTGTA     CTGCTGAGA
                                  || |||||     |||||||||
                                  CG GACAT     GACGACTCT
                                   T    C_____
GAM811  DKFZP434P211 3'  TTTCTCAGGAACCTTTCAAGC  27272    C  T    T   TG
                                  GC TG AAAG TTC  CTGAGAAA
                                  || || |||| |||  ||||||||
                                  CG AC TTTC AAG  GACTCTTT
                                   A  _   C  __
GAM811  DKFZP564O043 3'  CTCAGCAGGAACAAAGGC    92491     GTAAA
                                  GCCT    GTTTCTGCTGAG
                                  ||||    ||||||||||||
                                  CGGA    CAAGGACGACTC
                                    AA___
GAM811  DKFZP727M111 5'  TTTCCCAGCAGAGAGCACTGGC 31416     T  AAAG       A
                                  GCC GT    TTTCTGCTG GAAA
                                  ||| ||    ||||||||| ||||
                                  CGG CA    AGAGACGAC CTTT
                                    T  CG__       C
GAM811  DOC-1R   3'  CAGCAGGGGCACAGGC     19577       AAA  TT
                                  GCCTGT   GT  CTGCTG
                                  ||||||   ||  ||||||
                                  CGGACA   CG  GACGAC
                                     ___  GG
GAM811  DQX1     5'  TCTCAGCCTCTCAGGC     56102      TAA  TTTCT
                                  GCCTG   AG    GCTGAGA
                                  |||||   ||    |||||||
                                  CGGAC   TC    CGACTCT
                                    TC_  ______
GAM811  FLJ20618  5'  CTCAGCAGAAAGGAGGG     35457     GTAAAG
                                  CCT     TTTCTGCTGAG
                                  |||     ||||||||||
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                                GGG     AAAGACGACTC
                                  AGG___
GAM811  FLJ21977  5'  TCTCAGCACTCACAG      49887     AA   TTCT
                                CTGT  AGT    GCTGAGA
                                ||||  |||    |||||||
                                GACA  TCA    CGACTCT
                                  C_  ____
GAM811  HSPC065  3'  TCTCAGCAGGCCAAGGC     26329     GTAAAGTT
                                GCCT       TCTGCTGAGA
                                ||||       ||||||||||
                                CGGA       GGACGACTCT
                                  ACC_____
GAM811  KIAA0430  3'  TTGTCAATAAACTTTACAAGC  38844    C        CTGC   G
                                GC TGTAAAGTTT    TGA AA
                                || ||||||||||    ||| ||
                                CG ACATTTCAAA    ACT TT
                                 A         TA__   G
GAM811  KIAA1602  3'  TCTCAGTGACTCACTCTACG   64634     A   T__  T
                                TGTA AGT   TC GCTGAGA
                                |||| |||   || |||||||
                                GCAT TCA   AG TGACTCT
                                  C   CTC  _
GAM811  KIAA1872  3'  TCTCAGCAAGTGCTATCCAGGC 62947      TAA   TTC
                                GCCTG   AGT   TGCTGAGA
                                |||||   |||   ||||||||
                                CGGAC   TCG   ACGACTCT
                                   CTA   TGA
GAM811  KIAA1887  5'  TCCCAGCACTTTACAGG     76778         TTCT    A
                                CCTGTAAAGT    GCTG GA
                                ||||||||||    |||| ||
                                GGACATTTCA    CGAC CT
                                      ____    C
GAM811  KIAA1894  3'  TTTCTCAACATGGTACTCTACT 73848     T   A   T  _  C
            GGC                   GCC GTA AGT TC TG TGAGAAA
                                ||| ||| ||| || || |||||||
                                CGG CAT TCA GG AC ACTCTTT
                                  T   C   T  T  A
GAM811  KIF13B   3'  TTCTCGGCAACTCCCAG     30916     TAA   TTC
                                CTG   AGT   TGCTGAGAA
                                |||   |||   |||||||||
                                GAC   TCA   ACGGCTCTT
                                  CC_   ___
GAM811  KIF13B   3'  TTCTCGGCAACTCCCAG     82829     TAA   TTC
                                CTG   AGT   TGCTGAGAA
                                |||   |||   |||||||||
                                GAC   TCA   ACGGCTCTT
                                  CC_   ___
GAM811  NCBP2    3'  CTTAGGAAGAAACTTTGCA   23747          G_
                                TGTAAAGTTTCT  CTGAG
                                ||||||||||||  |||||
```

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                                ACGTTTCAAAGA  GATTC
                                      AG
GAM811  NDRG4    3'  TCAGGGCAGGAACCCCACAG  39989     AAA       GA
                                CTGT   GTTTCTGCT  GA
                                ||||   |||||||||  ||
                                GACA   CAAGGACGG  CT
                                  CCC        GA
GAM811  NDRG4    3'  TCAGGGCAGGAACCCCACAG  43292     AAA       GA
                                CTGT   GTTTCTGCT  GA
                                ||||   |||||||||  ||
                                GACA   CAAGGACGG  CT
                                  CCC        GA
GAM811  PDZD2    5'  CAGCAGAAAAGTGAAGGC    80863     G  AAG
                                GCCT TA   TTTCTGCTG
                                |||| ||   |||||||||
                                CGGA GT   AAAGACGAC
                                  A  GA_
GAM811  PKNOX2   3'  TTTCTCAGCTCCTTTGACAG  90881     _    TTTCT
                                CTGT AAAG    GCTGAGAAA
                                |||| ||||    |||||||||
                                GACA TTTC    CGACTCTTT
                                  G    CT___
GAM811  RAB27B   5'  TCCCGGCAAGGAAACTTCGCAG 14784       TA       __    A
           GC                     GCCTG  AAGTTTCT  GCTG GA
                                |||||  ||||||||  |||| ||
                                CGGAC  TTCAAAGG  CGGC CT
                                   GC       AA    C
GAM811  SEC8     3'  TTCTCAGCTGCTGTTTACA   41444       GTTTCT
                                TGTAAA     GCTGAGAA
                                ||||||     ||||||||
                                ACATTT     CGACTCTT
                                   GTCGT_
GAM811  SHAPY    3'  TCTCTGTGGAAACTTCACGAGC 57112    C   A      TG T
                                GC TGT AAGTTTC  C GAGA
                                || ||| |||||||  | ||||
                                CG GCA TTCAAAG  G CTCT
                                 A   C      GT T
GAM811  LOC123872 5'  TCCCTGCAAAAACTCTGCAAGC 74238    C    A    C   TGA
                                GC TGTA AGTTT TGC   GA
                                || |||| ||||| |||   ||
                                CG ACGT TCAAA ACG   CT
                                 A    C     A   TCC
GAM811  LOC124801 3'  CTCCCCTTAAATTTTACAGGC  74337           CTGCT
                                GCCTGTAAAGTTT    GAG
                                ||||||||||||    |||
                                CGGACATTTTAAA    CTC
                                        TTCCC
GAM811  LOC127534 3'  TTCCCAGTACTTTGCAG     75443         TTCT    A
                                CTGTAAAGT    GCTG GAA
                                |||||||||    |||| |||
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                                GACGTTTCA   TGAC CTT
                                     ____   C
GAM811  LOC139522 5' TTTCTCAGAAATTCCACAGGC  75851      AA      CT
                                GCCTGT  AGTTTCTG  GAGA
                                ||||||  ||||||||  ||||
                                CGGACA  TTAAAGAC  CTTT
                                   CC       T_
GAM811  LOC143146 5' TTCCCAGCAGGCAGAGGC    60135     GTAAAGTT     A
                                GCCT       TCTGCTG GAA
                                ||||       ||||||| |||
                                CGGA       GGACGAC CTT
                                  GAC_____      C
GAM811  LOC146990 3' TCCCAGCATTTTTCTTTACAG  83889       TTTC_    A
                                CTGTAAAG    TGCTG GA
                                ||||||||    ||||| ||
                                GACATTTC    ACGAC CT
                                     TTTTT    C
GAM811  LOC147991 3' CAGAAACTTCCCAGGC     78602      TA
                                GCCTG  AAGTTTCTG
                                |||||  |||||||||
                                CGGAC  TTCAAAGAC
                                   CC
GAM811  LOC150174 3' TTTCTCAGGAACCTTTCAAGC  79614    C  T    T   TG
                                GC TG AAAG TTC  CTGAGAAA
                                || || |||| |||  ||||||||
                                CG AC TTTC AAG  GACTCTTT
                                 A  _    C   __
GAM811  LOC150213 3' TTTCTCAGGAACCTTTCAAGC  74861    C  T    T   TG
                                GC TG AAAG TTC  CTGAGAAA
                                || || |||| |||  ||||||||
                                CG AC TTTC AAG  GACTCTTT
                                 A  _    C   __
GAM811  LOC150236 3' TTTCTCAGGAACCTTTCAAGC  79693    C  T    T   TG
                                GC TG AAAG TTC  CTGAGAAA
                                || || |||| |||  ||||||||
                                CG AC TTTC AAG  GACTCTTT
                                 A  _    C   __
GAM811  LOC151904 5' CTCAGCAGAAGACAG       80388      AAAG
                                CTGT    TTTCTGCTGAG
                                ||||    ||||||||||
                                GACA    GAAGACGACTC
                                     ____
GAM811  LOC153338 3' TCTCAGCACCACATGGC     86002     _   AAAGTTTC
                                GCC TGT       TGCTGAGA
                                ||| |||       ||||||||
                                CGG ACA       ACGACTCT
                                  T   CC_______
GAM811  LOC153688 3' TCCCAGCAGAGACTACA     86123     AA         A
                                TGT  AGTTTCTGCTG GA
                                |||  |||||||||| ||
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                                ACA  TCAGAGACGAC CT
                                  __         C
GAM811  LOC153761 5'  CTCACAGAAACTCCAAG     80924    GTAA       C
                                CT    AGTTTCTG TGAG
                                ||    |||||||| ||||
                                GA    TCAAAGAC ACTC
                                 ACC_       _
GAM811  LOC155006 3'  TCTCAGCAAATTACAG      81243       AGTTTC
                                CTGTAA     TGCTGAGA
                                ||||||     ||||||||
                                GACATT     ACGACTCT
                                   AA____
GAM811  LOC196264 3'  TCTCAGTGCCTTACAG      87616       A  TTCT
                                CTGTAA GT    GCTGAGA
                                |||||| ||    |||||||
                                GACATT CG    TGACTCT
                                   C  _____
GAM811  LOC196758 3'  TTTCTCAGCACTCTTCCTACAA 87514     _  __   TTTC
           GG                     CCT GTA  AAG    TGCTGAGAAA
                                ||| |||  |||   ||||||||||
                                GGA CAT  TTC    ACGACTCTTT
                                 A   CC   TC__
GAM811  LOC199704 3'  TCTCAGCCTCACGGGC      88331       AA  TTTCT
                                GCCTGT  AG    GCTGAGA
                                ||||||  ||    |||||||
                                CGGGCA  TC    CGACTCT
                                   C_ ______
GAM811  LOC201175 5'  TTCCCCAACAGAAGACCCCCAA 88137      GTAAAG_     C  A_
           GGC                     GCCT      TTTCTG TG  GAA
                                ||||      |||||| ||  |||
                                CGGA      GAAGAC AC  CTT
                                  ACCCCCA     A  CC
GAM811  LOC219385 5'  CAGCAGAAACCCTAAAGC    94315    CTG  AA
                                GC   TA  GTTTCTGCTG
                                ||   ||  ||||||||||
                                CG   AT  CAAAGACGAC
                                 AA_  CC
GAM811  LOC222057 3'  TCTCAGCGCCTCTGCAGGC    92783       A  TTTC
                                GCCTGTA AG    TGCTGAGA
                                ||||||| ||    ||||||||
                                CGGACGT TC    GCGACTCT
                                   C  C___
GAM811  LOC254251 3'  CTGACCAAAAACTTTACAGG   95907          C  CTG
                                CCTGTAAAGTTT TG   AG
                                ||||||||||| ||   ||
                                GGACATTTCAAA AC   TC
                                       A  CAG
GAM811  LOC90408  3'  TTTCTCAGAGTGCTCCCAGGC  62674      TAA   TT  G
                                GCCTG   AGT  CT CTGAGAAA
                                |||||   |||  || ||||||||
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                                CGGAC   TCG  GA GACTCTTT
                                   CC_   T_  _
GAM811  LOC90844  3'  TTTCTCAGAGTCTCTACAG   64210      A  TTT  G
                                CTGTA AG   CT CTGAGAAA
                                |||||  ||   ||  ||||||||
                                GACAT TC   GA GACTCTTT
                                   C  T__  _
GAM812  ARNT2     3'  AAACAACCCGTGCATCCCTGC  29450     A    TTTTA
                                GTA GGAT     GGGTTGTTT
                                |||  ||||     |||||||||
                                CGT CCTA     CCCAACAAA
                                  C    CGTG_
GAM812  LCT       3'  AACCGTAAAAATCCTT      9697           G
                                AAGGATTTTTA GGTT
                                ||||||||||| ||||
                                TTCCTAAAAAT CCAA
                                       G
GAM812  RPL15     3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM812  FBXO30    3'  AACTAAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                ||  |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                  G        AA
GAM812  KIAA0494  3'  AACAACCCTTACTTAC      28736      GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM812  PRO0641   5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                   ___    C
GAM812  SMT3H2    3'  AACAACATAAAAATCCTTGC   22670           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM812  LOC120103 3'  AACCTATGAAAAATCCTTGC   74002           A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
                                CGTTCCTAAAAA   TCCAA
                                       GTA
GAM812  LOC129831 3'  AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  ||  |||||||||
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                                CCTG  AA CCCAACAAA
                                  T_  C
GAM812  LOC133088 5'  AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                        GTA GGATTTTT     TTGTTT
                                   ||| ||||||||     ||||||
                                   CGT CCTAAAAA     AACAAA
                                     C       GATAA
GAM812  LOC148089 3'  GGCCCTAAAAATTCCTAC    78637     A
                                   GTA GGATTTTTAGGGTT
                                   ||| ||||||||||||||
                                   CAT CTTAAAAATCCCGG
                                     C
GAM812  LOC154547 3'  AACAACATAAAAATCCTTGC   76050           GG
                                   GTAAGGATTTTTA  GTTGTT
                                   ||||||||||||  ||||||
                                   CGTTCCTAAAAAT  CAACAA
                                          A_
GAM812  LOC158104 3'  ACAGCCAAAAATCCTTA     60313           AG
                                   TAAGGATTTTT  GGTTGT
                                   ||||||||||  ||||||
                                   ATTCCTAAAAA  CCGACA
                                          __
GAM812  LOC205880 5'  AAACAACCATCATCCTGAC    90709    A    TTTTAG
                                   GT AGGAT     GGTTGTTT
                                   || |||||     ||||||||
                                   CA TCCTA     CCAACAAA
                                    G    CTA___
GAM812  LOC221561 3'  AACAACATAAAAATCCTTGC   92130           GG
                                   GTAAGGATTTTTA  GTTGTT
                                   ||||||||||||  ||||||
                                   CGTTCCTAAAAAT  CAACAA
                                          A_
GAM812  LOC257591 3'  AACAACATAAAAATCCTTGC   97840           GG
                                   GTAAGGATTTTTA  GTTGTT
                                   ||||||||||||  ||||||
                                   CGTTCCTAAAAAT  CAACAA
                                          A_
GAM812  LOC51145  3'  AGCTAAAATCCTTAC       32393           TAG
                                   GTAAGGATTTT   GGTT
                                   ||||||||||   ||||
                                   CATTCCTAAAA   TCGA
                                          ___
GAM813  AIM1      3'  ATATCAAGATTTCAAGACTGTG 91815         _  TT
                                   CACAGTCT GG  TCTTGATAT
                                   |||||||| ||  |||||||||
                                   GTGTCAGA CT  AGAACTATA
                                        A  TT
GAM813  BAAT      3'  CAAGCTAACCAAACTGGA    8113     A   C    T_
                                   TC CAGT TGGTT  CTTG
                                   || |||| |||||  ||||
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                              AG GTCA ACCAA  GAAC
                               _   A    TC
GAM813  LIPA    3' ATCAAACCTAACTGTGA    4078       CT   TCT
                              TCACAGT  GGTT   TGAT
                              |||||||  ||||   ||||
                              AGTGTCA  CCAA   ACTA
                                  AT   ___
GAM813  NCALD   3' AAACCAGCCTGTGATG     49367       T
                              CATCACAG CTGGTTT
                              |||||||| |||||||
                              GTAGTGTC GACCAAA
                                   C
GAM813  SOS2    5' TATCAGCAAACCAGGAC    68537    _    C
                              GTC TGGTTT TTGATA
                              ||| |||||| ||||||
                              CAG ACCAAA GACTAT
                                G     C
GAM813  EVI5    3' ATCAAGAAATCTGAATG    18990    G  T
                              CA TC GGTTTCTTGAT
                              || || ||||||||||
                              GT AG CTAAAGAACTA
                               A  T
GAM813  FLJ23375 5' ATATCAAAGGAAATCATGATG 46355     CAGTC      __
                              CATCA    TGGTTTCT  TGATAT
                              |||||    ||||||||  ||||||
                              GTAGT    ACTAAAGG  ACTATA
                                 _____      AA
GAM813  KIAA1958 3' AGAAACCAAACATGAT     81899     CA  C
                              ATCA  GT TGGTTTCT
                              ||||  || ||||||||
                              TAGT  CA ACCAAAGA
                                A_  A
GAM813  MAPK6   5' ATCAAGAAACCATCTTGCTGTG 10833      C___
                              CACAGT   TGGTTTCTTGAT
                              ||||||   ||||||||||||
                              GTGTCG   ACCAAAGAACTA
                                  TTCT
GAM813  MGC13102 3' CATCAAATGGGACTGTGGTG  50314         G   CT
                              CATCACAGTCT GTTT  TG
                              |||||||||| ||||  ||
                              GTGGTGTCAGG TAAA  AC
                                     G   CT
GAM813  SCMH1   5' TATCAAGAAGCTGCTG     24257     CT
                              CAGT  GGTTTCTTGATA
                              ||||  ||||||||||||
                              GTCG  TCGAAGAACTAT
                                 __
GAM813  SLC6A14  3' ATATCAAGGAAAACTGTGA   23346       CTGG
                              TCACAGT   TTTCTTGATAT
                              |||||||   ||||||||||
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                                AGTGTCA    AAGGAACTATA
                                   A___
GAM813  LOC151126 3'  TATCAACAAGACTGGAATG    80130     CA     G  TTCT
                                CAT  CAGTCT GT    TGATA
                                |||  |||||| ||    |||||
                                GTA  GTCAGA CA    ACTAT
                                  AG     A  ____
GAM813  LOC155081 3'  ATATCAGTGCCACAGATTGT   81289        GTTTC
                                ACAGTCTG    TTGATAT
                                ||||||||    |||||||
                                TGTTAGAC    GACTATA
                                   ACCGT
GAM813  LOC202802 3'  ATATCAGTGCCACAGATTGT   89203        GTTTC
                                ACAGTCTG    TTGATAT
                                ||||||||    |||||||
                                TGTTAGAC    GACTATA
                                   ACCGT
GAM813  LOC219401 5'  ATCAAGAAACACATAT      92812     C  _
                                GT TG GTTTCTTGAT
                                || || ||||||||||
                                TA AC CAAAGAACTA
                                 T  A
GAM813  LOC221399 5'  ATCAAGAAGGTTAACTGTG    93845       CTGG
                                CACAGT    TTTCTTGAT
                                ||||||    |||||||||
                                GTGTCA    GAAGAACTA
                                   ATTG
GAM813  LOC222228 3'  ATATCAGTGCCACAGATTGT   94293        GTTTC
                                ACAGTCTG    TTGATAT
                                ||||||||    |||||||
                                TGTTAGAC    GACTATA
                                   ACCGT
GAM813  LOC222233 3'  ATATCAGTGCCACAGATTGT   94250        GTTTC
                                ACAGTCTG    TTGATAT
                                ||||||||    |||||||
                                TGTTAGAC    GACTATA
                                   ACCGT
GAM813  LOC90643  3'  ATCAAGACCCTGACTGGA    63688    A    T  TT
                                TC CAGTC GG  TCTTGAT
                                || ||||| ||  |||||||
                                AG GTCAG CC  AGAACTA
                                 _    T  C_
GAM813  LOC91138  5'  CAAGTAACTAGACTATGAT    65029      C        T
                                ATCA AGTCTGGTT CTTG
                                |||| ||||||||| ||||
                                TAGT TCAGATCAA GAAC
                                  A        T
GAM813  LOC91818  5'  ATCAAGACCCTGACTGGA    67269    A    T  TT
                                TC CAGTC GG  TCTTGAT
                                || ||||| ||  |||||||
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                                AG GTCAG CC  AGAACTA
                                 _    T  C_
GAM813  LOC93052  5'  GAACCAAACTGTGATG     71261         C
                                CATCACAGT TGGTTT
                                ||||||||| ||||||
                                GTAGTGTCA ACCAAG
                                     A
GAM814  CD69      3'  TATGGAAAAAAAGGAAGA    8355        C__
                                TTTTTCT   TTTCCATA
                                |||||||   ||||||||
                                AGAAGGA   AAAGGTAT
                                    AAA
GAM814  CDC42     3'  ATGGAAAGACTCTTAATGCAGA 8370      T   TTTC_
                                TCTG CATT    TCTTTCCAT
                                |||| ||||    |||||||||
                                AGAC GTAA    AGAAAGGTA
                                  _   TTCTC
GAM814  COG6      3'  AGAGAGAAAAATAACAG     72878     C
                                CTGT ATTTTTCTCTTT
                                |||| ||||||||||||
                                GACA TAAAAAGAGAGA
                                  A
GAM814  COX7A2L   3'  ATGGAAAGAACACAGA      16348      CATTTTTC
                                TCTGT       TCTTTCCAT
                                |||||       |||||||||
                                AGACA       AGAAAGGTA
                                   CA_______
GAM814  GBP1      5'  AAGGAGAAAAAGAACAGA    9009       CA
                                TCTGT  TTTTTCTCTTT
                                |||||  ||||||||||
                                AGACA  AAAAAGAGGAA
                                   AG
GAM814  HSPD1     3'  GGAGAAAAATGAAGA       60172     G
                                TCT TCATTTTTCTCT
                                ||| ||||||||||||
                                AGA AGTAAAAAGAGG
                                  _
GAM814  OCRL      3'  AAAGAGGCAGATGATAGA    4254          T
                                TCTGTCATTT TCTCTTT
                                |||||||||| |||||||
                                AGATAGTAGA GGAGAAA
                                     C
GAM814  OCRL      3'  AAAGAGGCAGATGATAGA    7820          T
                                TCTGTCATTT TCTCTTT
                                |||||||||| |||||||
                                AGATAGTAGA GGAGAAA
                                     C
GAM814  TFRC      3'  TTATGAAAAGAGGGGACCAGA  12247      TCAT  TT     C
                                TCTG    TT  CTCTTT CATAA
                                ||||    ||  |||||| |||||
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                                AGAC    AG  GAGAAA GTATT
                                  C___  GG     A
GAM814  THBS1    3'  AAAGAGAAAAAAATGACA    12280          __
                                TGTCATTTT  TCTCTTT
                                |||||||||  |||||||
                                ACAGTAAAA  AGAGAAA
                                     AA
GAM814  XYLB     3'  AGAAATAAAATGACAGA     17556          TC_
                                TCTGTCATTTT   TCT
                                ||||||||||   |||
                                AGACAGTAAAA   AGA
                                      TAA
GAM814  BC022889 5'  GAATTTTCAAGATGACAGA   83647          TCTCT
                                TCTGTCATTTT    TTC
                                ||||||||||    |||
                                AGACAGTAGAA    AAG
                                      CTTTT
GAM814  CDT6     5'  GAAAGAGAGAAAACAACA    40944     CA_
                                TGT   TTTTTCTCTTTC
                                |||   ||||||||||||
                                ACA   AAAGAGAGAAAG
                                  ACA
GAM814  EDG2     3'  GAAAACTTGAAAAATGCAGA   54065      T       TC__
                                TCTG CATTTTTC    TTTC
                                |||| ||||||||    ||||
                                AGAC GTAAAAAG    AAAG
                                  _       TTCA
GAM814  EDG2     3'  GAAAACTTGAAAAATGCAGA   7381       T       TC__
                                TCTG CATTTTTC    TTTC
                                |||| ||||||||    ||||
                                AGAC GTAAAAAG    AAAG
                                  _       TTCA
GAM814  FLJ10407 3'  ATGGAAAGAAATTCTCAACAGA 36089       CATTTTTC
                                TCTGT       TCTTTCCAT
                                |||||       |||||||||
                                AGACA       AGAAAGGTA
                                   ACTCTTAA
GAM814  FLJ21615 3'  TGGAAAGAAAAATGAAGA    49839     G        CT
                                TCT TCATTTTTCT  TTCCA
                                ||| ||||||||||  |||||
                                AGA AGTAAAAAGA  AAGGT
                                  _       __
GAM814  GREB1    3'  AAAGAGAAAATACCAGA     72403      TCAT
                                TCTG    TTTTCTCTTT
                                ||||    ||||||||||
                                AGAC    AAAAGAGAAA
                                  CAT_
GAM814  KIAA0493 5'  ATGGTAAGAAAAATGAAGA   64271     G        CTTT
                                TCT TCATTTTTCT    CCAT
                                ||| ||||||||||    ||||
```

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                                AGA AGTAAAAAGA   GGTA
                                  _       AT__
GAM814  KIAA0997 3' GGAAAAAGAAAAATAAAAGA  30191    GTC      C
                                TCT  ATTTTTCT TTTCC
                                |||  |||||||| |||||
                                AGA  TAAAAAGA AAAGG
                                  AAA      A
GAM814  KIAA1033 3' GAGAAGAAAATGACAGA    64515         TC
                                TCTGTCATTTT  TCTT
                                ||||||||||  ||||
                                AGACAGTAAAA  AGAG
                                       GA
GAM814  KIAA1271 3' GAAAAAGAAAAATGCAGA    69545    T       C
                                TCTG CATTTTTCT TTTC
                                |||| |||||||| ||||
                                AGAC GTAAAAAGA AAAG
                                  _       A
GAM814  KIAA1872 3' AAAGAAAAAAAATGACAGA   62917          C_
                                TCTGTCATTTTT  TCTTT
                                ||||||||||  |||||
                                AGACAGTAAAAA  AGAAA
                                       AA
GAM814  MGC15438 5' GAGAAGAAAATGACAGA    51789         TC
                                TCTGTCATTTT  TCTT
                                ||||||||||  ||||
                                AGACAGTAAAA  AGAG
                                       GA
GAM814  Nup43    3' GAGTAGAGCAAAAATGACA   45002         _  _
                                TGTCATTTTT CTCT TTC
                                |||||||||| |||| |||
                                ACAGTAAAAA GAGA GAG
                                       C   T
GAM814  RASGRF2  3' ATGGAAAGCAGGACAGA    61041      ATTTTT _
                                TCTGTC     CT CTTTCCAT
                                ||||||     || ||||||||
                                AGACAG     GA GAAAGGTA
                                  _______ C
GAM814  S164     5' GAAAGAGAAAAAGACA     60779     A
                                TGTC TTTTTCTCTTTC
                                |||| ||||||||||||
                                ACAG AAAAAGAGAAAG
                                  _
GAM814  SGP28    3' GGGGAGAAAAATGACA     20230
                                TGTCATTTTTCTCTTT
                                ||||||||||||||||
                                ACAGTAAAAAGAGGGG

GAM814  ZAK      3' AAAGAGAAAAATAACAGG   56114      C
                                TCTGT ATTTTTCTCTTT
                                ||||| ||||||||||||
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                                GGACA TAAAAAGAGAAA
                                   A
GAM814   LOC134111 3'  TTATGAAAAGATGTGTGTACAG 75139      _  TTTTC    C
            A                    TCTGT CAT    TCTTT CATAA
                                 ||||| |||    ||||| |||||
                                 AGACA GTG    AGAAA GTATT
                                    T  TGT__    A
GAM814   LOC145384 5'  TGGAGATAAAAATGACA     77199         CTC
                                 TGTCATTTTT  TTTCCA
                                 ||||||||||  ||||||
                                 ACAGTAAAAA  AGAGGT
                                       T__
GAM814   LOC145945 5'  TTATGGTGAGAAAAATACCA  83581    TC       TTT
                                 TG ATTTTTCTC  CCATAA
                                 || |||||||||  ||||||
                                 AC TAAAAAGAG  GGTATT
                                  CA       T__
GAM814   LOC147381 5'  ATGGAAAGGGAAGACA     84011     ATTT
                                 TGTC   TTCTCTTTCCAT
                                 ||||   ||||||||||||
                                 ACAG   AAGGGAAAGGTA
                                   ____
GAM814   LOC151556 5'  ATGGTGGGAAAAATAAAGA   80273     GTC       TTT
                                 TCT  ATTTTTCTC  CCAT
                                 |||  |||||||||  ||||
                                 AGA  TAAAAAGGG  GGTA
                                   AA_       T__
GAM814   LOC151632 5'  AAGAAGAAAAATGACA     85462          _
                                 TGTCATTTTTCT CTT
                                 |||||||||||| |||
                                 ACAGTAAAAAGA GAA
                                       A
GAM814   LOC196527 3'  AAGGGAATAAAATGACA     87753         __
                                 TGTCATTTT  TCTCTT
                                 |||||||||  ||||||
                                 ACAGTAAAA  AGGGAA
                                      TA
GAM814   LOC219578 5'  ATGGAAAGATGAGAAA      94359       _
                                 TTTTTC TCTTTCCAT
                                 |||||| |||||||||
                                 AAAGAG AGAAAGGTA
                                    T
GAM814   LOC221795 5'  AAGAAGAAAAATGACA      92472          _
                                 TGTCATTTTTCT CTT
                                 |||||||||||| |||
                                 ACAGTAAAAAGA GAA
                                       A
GAM814   LOC222681 3'  GAAAATAGAGAAATGACAG   92852           C_
                                 CTGTCATTTTTCT  TTTC
                                 ||||||||||||  ||||
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                                GACAGTAAAGAGA  AAAG
                                      TA
GAM814  LOC222681 5'  GAAAATAGAGAAATGACAG   92853          C_
                                CTGTCATTTTTCT  TTTC
                                ||||||||||||  ||||
                                GACAGTAAAGAGA  AAAG
                                      TA
GAM814  LOC256515 5'  AAGAAGAAAAATGACA     96458          _
                                TGTCATTTTTCT CTT
                                |||||||||||| |||
                                ACAGTAAAAAGA GAA
                                       A
GAM814  LOC257507 3'  GAAAATAGAGAAATGACAG   97774          C_
                                CTGTCATTTTTCT  TTTC
                                ||||||||||||  ||||
                                GACAGTAAAGAGA  AAAG
                                      TA
GAM814  LOC257507 5'  GAAAATAGAGAAATGACAG   97775          C_
                                CTGTCATTTTTCT  TTTC
                                ||||||||||||  ||||
                                GACAGTAAAGAGA  AAAG
                                      TA
GAM814  LOC257625 3'  GAAAATAGAGAAATGACAG   97905          C_
                                CTGTCATTTTTCT  TTTC
                                ||||||||||||  ||||
                                GACAGTAAAGAGA  AAAG
                                      TA
GAM814  LOC257625 5'  GAAAATAGAGAAATGACAG   97906          C_
                                CTGTCATTTTTCT  TTTC
                                ||||||||||||  ||||
                                GACAGTAAAGAGA  AAAG
                                      TA
GAM814  LOC89919  3'  GTGGGAAAAAAATGAC     60727        CTC
                                GTCATTTTT   TTTCCAT
                                |||||||||   |||||||
                                CAGTAAAAA   AAGGGTG
                                      ___
GAM814  LOC90246  5'  TTATGGAAAAAGAAAA     61912       C
                                TTTTCT TTTCCATAA
                                |||||| |||||||||
                                AAAAGA AAAGGTATT
                                   A
GAM814  LOC91431  5'  GGAAAGAGTCTATGTGAGA   56924     GT   TTTT
                                TCT  CAT    CTCTTTCC
                                |||  |||    ||||||||
                                AGA  GTA    GAGAAAGG
                                  GT   TCT_
GAM815  ARNT2     3'  AAACAACCCGTGCATCCCTGC  29450     A    TTTTA
                                GTA GGAT    GGGTTGTTT
                                ||| ||||    |||||||||
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                                CGT CCTA    CCCAACAAA
                                  C   CGTG_
GAM815  LCT      3'  AACCGTAAAAATCCTT     9697          G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
                                TTCCTAAAAAT CCAA
                                      G
GAM815  RPL15    3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM815  FBXO30   3'  AACTAAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                  G        AA
GAM815  KIAA0494 3'  AACAACCCTTACTTAC      28736      GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM815  PRO0641  5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                   ___    C
GAM815  SMT3H2   3'  AACAACATAAAAATCCTTGC  22670          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM815  LOC120103 3' AACCTATGAAAAATCCTTGC  74002          A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
                                CGTTCCTAAAAA   TCCAA
                                      GTA
GAM815  LOC129831 3' AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                   T_  C
GAM815  LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                      GTA GGATTTTT     TTGTTT
                                ||| ||||||||    ||||||
                                CGT CCTAAAAA     AACAAA
                                  C       GATAA
GAM815  LOC148089 3' GGCCCTAAAAATTCCTAC    78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
```

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                                CAT CTTAAAAATCCCGG
                                  C
GAM815  LOC154547 3'  AACAACATAAAAATCCTTGC  76050          GG
                                GTAAGGATTTTTA GTTGTT
                                ||||||||||||| ||||||
                                CGTTCCTAAAAAT CAACAA
                                       A_
GAM815  LOC158104 3'  ACAGCCAAAAATCCTTA    60313         AG
                                TAAGGATTTTT GGTTGT
                                |||||||||||  ||||||
                                ATTCCTAAAAA CCGACA
                                       __
GAM815  LOC205880 5'  AAACAACCATCATCCTGAC   90709   A   TTTTAG
                                GT AGGAT    GGTTGTTT
                                || |||||    ||||||||
                                CA TCCTA    CCAACAAA
                                 G   CTA___
GAM815  LOC221561 3'  AACAACATAAAAATCCTTGC  92130          GG
                                GTAAGGATTTTTA GTTGTT
                                ||||||||||||| ||||||
                                CGTTCCTAAAAAT CAACAA
                                       A_
GAM815  LOC257591 3'  AACAACATAAAAATCCTTGC  97840          GG
                                GTAAGGATTTTTA GTTGTT
                                ||||||||||||| ||||||
                                CGTTCCTAAAAAT CAACAA
                                       A_
GAM815  LOC51145  3'  AGCTAAAATCCTTAC      32393         TAG
                                GTAAGGATTTT  GGTT
                                ||||||||||  ||||
                                CATTCCTAAAA  TCGA
                                       ___
GAM816  CALD1     3'  CCAACCACATCTGAAGTCA   52462     _  TAGGTT
                                TGATT CAG    TGTGGTTGG
                                ||||| |||    |||||||||
                                ACTGA GTC    ACACCAACC
                                   A  T_____
GAM816  CALD1     3'  CCAACCACATCTGAAGTCA   52467     _  TAGGTT
                                TGATT CAG    TGTGGTTGG
                                ||||| |||    |||||||||
                                ACTGA GTC    ACACCAACC
                                   A  T_____
GAM816  CALD1     3'  CCAACCACATCTGAAGTCA   52526     _  TAGGTT
                                TGATT CAG    TGTGGTTGG
                                ||||| |||    |||||||||
                                ACTGA GTC    ACACCAACC
                                   A  T_____
GAM816  TTN       3'  ACCAATACCTACTGAATCA   55915         TTG
                                TGATTCAGTAGGT  TGGT
                                ||||||||||||  ||||
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                                ACTAAGTCATCCA   ACCA
                                      TA_
GAM816  TTN     3'  ACCAATACCTACTGAATCA   55933          TTG
                                TGATTCAGTAGGT   TGGT
                                ||||||||||||   ||||
                                ACTAAGTCATCCA   ACCA
                                      TA_
GAM816  TTN     3'  ACCAATACCTACTGAATCA   55945          TTG
                                TGATTCAGTAGGT   TGGT
                                ||||||||||||   ||||
                                ACTAAGTCATCCA   ACCA
                                      TA_
GAM816  FLJ11053  3'  ACCAACCAGCTGTACATCTAAA 88729      C  TAG  TT_ _
            TCA                   TGATT AG   GT   G TGGTTGGT
                                ||||| ||   ||   | ||||||||
                                ACTAA TC   CA   C ACCAACCA
                                   A  TA_  TGT G
GAM816  KIAA0318  3'  ACCAACCACTTTAAACCAAC   68944    A    ___
                                GT GGTTT   GTGGTTGGT
                                || |||||   |||||||||
                                CA CCAAA   CACCAACCA
                                 A    TTT
GAM816  MGC2376   3'  ACCTCAGACCTACTGAATCA   43700             T
                                TGATTCAGTAGGTTTG GGT
                                |||||||||||||||| |||
                                ACTAAGTCATCCAGAC CCA
                                         T
GAM816  LOC221405 5'  ACCAACCAGCCTTAC      93879     _   TTG
                                GTA GGT   TGGTTGGT
                                ||| |||   ||||||||
                                CAT CCG   ACCAACCA
                                  T   ___
GAM817  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM817  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM817  FDFT1    3'  TAGGAAAGTGAAATG      15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                         _
GAM817  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                ||||||||||||||||||||||||
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                                GTAAAGTGAAAGTGACAGACTCTA

GAM817  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM817  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM817  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM817  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM817  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM817  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM817  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM817  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||         |||||||||
                                GTAAAG         CAGACTCTA
                                   AAACATTT_
GAM817  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM817  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
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                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM817  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM817  NIR3     3'  GCAGTGAAAGTGCAAT      66242      T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM817  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM817  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM817  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__   TT
GAM817  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM817  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM817  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM817  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM817  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
```

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                                AAAG GAAAGTGA   ACT
                                  _      ATTT
GAM817  LOC222134 5'  ACAGTGAAGTGAAATG     94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM818  ADRA2B   3'  ATCACTGGCATTCACCCCCTGC 5459      AA   CA  T
                                GCAGG  GTGG  GT CAGTGAT
                                |||||  ||||  || |||||||
                                CGTCC  CACT  CG GTCACTA
                                   CC   TA  _
GAM818  ALDH3A2  3'  TGGCACTGCTCACTTCCTGCC  69275         _   _
                                GGCAGGAAGTG GCAGT TCA
                                |||||||||| ||||| |||
                                CCGTCCTTCAC CGTCA GGT
                                       T   C
GAM818  ATF7     3'  AGCATGCCACTTCCTGCC    22462          _
                                GGCAGGAAGTGGCA GTT
                                |||||||||||||| |||
                                CCGTCCTTCACCGT CGA
                                         A
GAM818  AXUD1    3'  CTGCCCCCTCCACTTCCTGCC  52277         C  TT__
                                GGCAGGAAGTGG AG   CAG
                                |||||||||||| ||   |||
                                CCGTCCTTCACC TC   GTC
                                      _ CCCC
GAM818  BAZ2A    3'  ATCACCAGCTTACCACTTCCCA 25593    CA     C_   CA
           CT                     GG  GGAAGTGG  AGTT  GTGAT
                                ||  ||||||||  ||||  |||||
                                TC  CCTTCACC  TCGA  CACTA
                                 AC       AT   C_
GAM818  DDX3     3'  CACTAAAATGCCTCTGCC    7220       AAGT   G  C
                                GGCAGG   GGCA TT AGTG
                                ||||||   |||| || ||||
                                CCGTCT   CCGT AA TCAC
                                   ____   A  A
GAM818  LBX1     3'  TCCTCTGCCACTCCCGCC    21633    A   A     TTC  T
                                GGC GGA GTGGCAG   AG GA
                                ||| ||| |||||||   || ||
                                CCG CCT CACCGTC   TC CT
                                  C  _     ___  _
GAM818  ACAA2    3'  AACCACCACTTCTGCC     91765      G     CA
                                GGCAG AAGTGG  GTT
                                |||||  ||||||  |||
                                CCGTC TTCACC  CAA
                                   _     AC
GAM818  AD-020   5'  CACTGAACCCGGACCCCCTACC 39308    C   AA  __  CA
                                GG AGG  GT  GG  GTTCAGTG
                                || |||  ||  ||  ||||||||
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                                CC TCC  CA  CC  CAAGTCAC
                                 A  CC  GG  __
GAM818  AD-020   5'  CACTGAACCCGGACCCCCTACC 59384    C   AA  __  CA
                                GG AGG  GT  GG  GTTCAGTG
                                || |||  ||  ||  ||||||||
                                CC TCC  CA  CC  CAAGTCAC
                                 A  CC  GG  __
GAM818  C5orf4   3'  ATCACTTTGCCCCTTCCTGCC  50487         T    TTC
                                GGCAGGAAG GGCAG   AGTGAT
                                ||||||||| |||||   ||||||
                                CCGTCCTTC CCGTT   TCACTA
                                      C   ___
GAM818  C5orf4   3'  CACCTTCCCTTCCTGCC     50489         T  C  TTCA
                                GGCAGGAAG GG AG    GTG
                                ||||||||| || ||    |||
                                CCGTCCTTC CC TC    CAC
                                      _ T  ____
GAM818  C5orf4   3'  ATCACTTTGCCCCTTCCTGCC  32977         T    TTC
                                GGCAGGAAG GGCAG   AGTGAT
                                ||||||||| |||||   ||||||
                                CCGTCCTTC CCGTT   TCACTA
                                      C   ___
GAM818  C5orf4   5'  CACCTTCCCTTCCTGCC     32979         T  C  TTCA
                                GGCAGGAAG GG AG    GTG
                                ||||||||| || ||    |||
                                CCGTCCTTC CC TC    CAC
                                      _ T  ____
GAM818  D123     3'  AGCCGCAACTTCCTGCC     20068          G  A
                                GGCAGGAAGT GC GTT
                                |||||||||| || |||
                                CCGTCCTTCA CG CGA
                                      A  C
GAM818  FLJ20506 5'  ATCACCCCGCTCACCACTTCC  35266         C_   TCA
                                GGAAGTGG  AGT   GTGAT
                                ||||||||  |||   |||||
                                CCTTCACC  TCG   CACTA
                                     AC   CCC
GAM818  HRIHFB2122 3'  TCCTACTAACACTTCCTGCC  22862          GC   TC  T
                                GGCAGGAAGTG  AGT  AG GA
                                ||||||||||  |||  || ||
                                CCGTCCTTCAC  TCA  TC CT
                                      AA  __ _
GAM818  KIAA0356 3'  TCACTGAACTTGCCCAGCC   66197    AAGT   _
                                GG   GGCA GTTCAGTGA
                                ||   |||| |||||||||
                                CC   CCGT CAAGTCACT
                                 GAC_   T
GAM818  LMOD1    3'  AATTCCACTTCCTGCC      24037           C
                                GGCAGGAAGTGG AGTT
                                |||||||||||| ||||
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                                CCGTCCTTCACC TTAA
                                          _
GAM818  MARKL1   3'  AACCCCCACTTCCTGCC     48633          CA
                                GGCAGGAAGTGG  GTT
                                ||||||||||||  |||
                                CCGTCCTTCACC  CAA
                                      CC
GAM818  MGC4172  3'  ATCACGGGATACCACTTCCTGT 44199          CA   A
          C                      GGCAGGAAGTGG  GTTC GTGAT
                                ||||||||||||  |||| |||||
                                CTGTCCTTCACC  TAGG CACTA
                                      A_   G
GAM818  PIGQ     3'  ACTGGCACTGCCTGCC      14847       A   G
                                GGCAGG AGTG CAGT
                                ||||||| |||| ||||
                                CCGTCC TCAC GTCA
                                   G   G
GAM818  PRO1048  3'  CACTGTGTCCACCCCTGCC   37512       AA   _ GTT
                                GGCAGG  GTGG CA   CAGTG
                                ||||||  |||| ||   |||||
                                CCGTCC  CACC GT   GTCAC
                                   C_   T ___
GAM818  USP10    3'  TCACACTCACTTCCCGCC    63947     A     GC   TCA
                                GGC GGAAGTG  AGT   GTGA
                                ||| |||||||  |||   ||||
                                CCG CCTTCAC  TCA   CACT
                                  C     __  ___
GAM818  LOC122728 3'  TCACACTCACTTCCCGCC    74152     A     GC   TCA
                                GGC GGAAGTG  AGT   GTGA
                                ||| |||||||  |||   ||||
                                CCG CCTTCAC  TCA   CACT
                                  C     __  ___
GAM818  LOC145368 3'  TCACACTCACTTCCCGCC    77095     A     GC   TCA
                                GGC GGAAGTG  AGT   GTGA
                                ||| |||||||  |||   ||||
                                CCG CCTTCAC  TCA   CACT
                                  C     __  ___
GAM818  LOC149018 3'  CACCACTGCCACCTCC      79133     A      TCA
                                GGA GTGGCAGT   GTG
                                ||| ||||||||   |||
                                CCT CACCGTCA   CAC
                                  C      C__
GAM818  LOC200982 3'  CACTGAACTAGCTTACC     90216     AAGT  _
                                GG    GGC AGTTCAGTG
                                ||    ||| |||||||||
                                CC    TCG TCAAGTCAC
                                 AT__   A
GAM818  LOC221416 3'  CACTGGCTGCCAACTCCTGCC  93763       AG      T
                                GGCAGGA  TGGCAGT CAGTG
                                |||||||  ||||||| |||||
```

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                                CCGTCCT  ACCGTCG GTCAC
                                   CA      _
GAM818  LOC255870 3'  AACCACCACTTCTGCC      94656       G     CA
                                GGCAG AAGTGG  GTT
                                ||||| ||||||  |||
                                CCGTC TTCACC  CAA
                                   _      AC
GAM818  LOC256158 5'  CACCGAAGGCTCCCACGCC   97648     AGGAA   C  __  A
                                GGC    GTGG AGT  TC GTG
                                |||    |||| |||  || |||
                                CCG    CACC TCG  AG CAC
                                  ______   C   GA  C
GAM819  ASB1      3'  GCTGTGCTGCTGCTGGTC    32268        _  T     A
                                GACCAGT GC GGCATA GC
                                ||||||| || |||||| ||
                                CTGGTCG CG TCGTGT CG
                                   T  _     _
GAM819  B3GAT1    3'  TTCAGAATATAGCATTGGTT   37834          GCATAAG
                                GACCAGTGCTG      CTGAA
                                ||||||||||       |||||
                                TTGGTTACGAT      GACTT
                                      ATAA___
GAM819  B3GAT1    3'  TTCAGAATATAGCATTGGTT   53982          GCATAAG
                                GACCAGTGCTG      CTGAA
                                ||||||||||       |||||
                                TTGGTTACGAT      GACTT
                                      ATAA___
GAM819  BLTR2     5'  TTCAGCTTGTGCTGTTTCCTGG 39045      T__  T
                                CCAG   GC GGCATAAGCTGAA
                                ||||   || ||||||||||||
                                GGTC   TG TCGTGTTCGACTT
                                  CTT  _
GAM819  C4B       3'  TGGCAGCAAAGTGTCAGTGTTG 5173       TG      AA_   AA
            G                    CCAG  CTGGCAT   GCTG
                                ||||  |||||||   ||||
                                GGTT  GACTGTG   CGAC
                                  GT      AAA    GGTT
GAM819  CAPN1     3'  TTCAGGGACTTGTGTACTGGTT 17752        GCTG      ___
                                GACCAGT    GCATAAG   CTGAA
                                |||||||    |||||||   |||||
                                TTGGTCA    TGTGTTC   GACTT
                                   _____      AGG
GAM819  CASP8AP2  3'  TTCAGCTTGTGCTAGTCAT    24005     _
                                GTG CTGGCATAAGCTGAA
                                ||| ||||||||||||||
                                TAC GATCGTGTTCGACTT
                                  T
GAM819  COL1A2    3'  TCAGATTCAGCATTTGTT     3613      C       CATAAG
                                GAC AGTGCTGG      CTGA
                                ||| ||||||||      ||||
```

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                                TTG TTACGACT     GACT
                                  T      TA____
GAM819  COX7A2   5'  TTCAGTTGTGGCGGTTGCTGGT 8518        _  G    G
            C                    GACCAGTG CTG CATAA CTGAA
                                 |||||||| ||| ||||| |||||
                                 CTGGTCGT GGC GTGTT GACTT
                                     T  G    _
GAM819  CRYGB    3'  TTAGCTTGTGTTTCTGG     17799     TGCT
                                 CCAG   GGCATAAGCTGA
                                 ||||   ||||||||||||
                                 GGTC   TTGTGTTCGATT
                                   T___
GAM819  CRYGB    3'  TTAGCTTGTGTTTCTGG     94626     TGCT
                                 CCAG   GGCATAAGCTGA
                                 ||||   ||||||||||||
                                 GGTC   TTGTGTTCGATT
                                   T___
GAM819  CSE1L    3'  TTCAGTGTATGGCGTTGGTT  61859        TGG   A
                                 GACCAGTGC  CATA GCTGAA
                                 |||||||||  |||| ||||||
                                 TTGGTTGCG  GTAT TGACTT
                                     ___   G
GAM819  CUL4B    3'  GAGATTCTGTGTCATGCTGGTT 13141       C     AGCTGAA
                                 GACCAGTG TGGCATA
                                 |||||||| |||||||
                                 TTGGTCGT ACTGTGT
                                     _     CTTAGAGT
GAM819  CXCL6    3'  TTCCTGTGTGTCATGTTGGTT  11466     GT C     AGCT
                                 GACCA  G TGGCATA   GAA
                                 |||||  | |||||||   |||
                                 TTGGT  T ACTGTGT   CTT
                                    TG _     GTC_
GAM819  DUSP11   5'  TTTGGCCGGCTTGGCATTGG  13134       _ ATAA  TG
                                 CCAGTGCTG GC   GC  AA
                                 ||||||||| ||   ||  ||
                                 GGTTACGGT CG   CG  TT
                                     T  GC__  GT
GAM819  DUSP4    5'  TGAGCTTGTCGGCGCTGGT   54057         TA   GAA
                                 ACCAGTGCTGGCA  AGCT
                                 ||||||||||||  ||||
                                 TGGTCGCGGCTGT  TCGA
                                      __   GTT
GAM819  DYRK1A   3'  TTCAGATGTTGGTCTTGGTC  55208      T  TG   AAG
                                 GACCAG GC  GCAT   CTGAA
                                 ||||||  ||  ||||   |||||
                                 CTGGTT TG  TGTA   GACTT
                                    C  GT   ___
GAM819  DYRK1A   3'  TTCAGATGTTGGTCTTGGTC  55251      T  TG   AAG
                                 GACCAG GC  GCAT   CTGAA
                                 ||||||  ||  ||||   |||||
```

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                                CTGGTT TG  TGTA   GACTT
                                   C  GT   ___
GAM819  DYRK1A   3'  TTCAGATGTTGGTCTTGGTC   7357       T  TG    AAG
                                GACCAG GC  GCAT   CTGAA
                                |||||| ||  ||||   |||||
                                CTGGTT TG  TGTA   GACTT
                                   C  GT   ___
GAM819  EFNB2    3'  TTTGGTTTATGCGGTGCTG   14581     TG   G      TG
                                CAG  CTG CATAAGC  AA
                                |||  ||| |||||||  ||
                                GTC  GGC GTATTTG  TT
                                  GT   _      GT
GAM819  ESRRG    3'  TTTATGTTGTGTGCCAGTCTGG 66398       T       _  _
           TC                     GACCAG GCTGGCATA AGC TGAA
                                |||||| ||||||||| ||| ||||
                                CTGGTC TGACCGTGT TTG ATTT
                                   _       G   T
GAM819  ETV3     3'  TTTGGTTTATTTGGTTGGTT   17883      GT  TG C     TG
                                GACCA  GC  G ATAAGC  AA
                                |||||  ||  | ||||||  ||
                                TTGGT  TG  T TATTTG  TT
                                   __  GT _     GT
GAM819  FGF5     3'  TTCAGCTGAATTATATTGGTC  15551        C   CATA
                                GACCAGTG TGG    AGCTGAA
                                |||||||| |||    |||||||
                                CTGGTTAT ATT    TCGACTT
                                     _  AAG_
GAM819  FGF5     3'  TTCAGCTGAATTATATTGGTC  52496        C   CATA
                                GACCAGTG TGG    AGCTGAA
                                |||||||| |||    |||||||
                                CTGGTTAT ATT    TCGACTT
                                     _  AAG_
GAM819  FMOD     3'  TTTGGCTTGATGGTTTGGTT   8934       T   GCA    TG
                                GACCAG GCTG   TAAGC  AA
                                |||||| ||||   |||||  ||
                                TTGGTT TGGT   GTTCG  TT
                                   _   A__     GT
GAM819  FOXG1B   3'  TCAGTTTGTGTTGTGTAT    17902      _
                                GTGC TGGCATAAGCTGA
                                |||| ||||||||||||
                                TATG GTTGTGTTTGACT
                                  T
GAM819  GCH1     3'  TTCAGTGTGTGTGCGTTGGTT  3862         TG    A
                                GACCAGTGC  GCATA GCTGAA
                                |||||||||  ||||| ||||||
                                TTGGTTGCG  TGTGT TGACTT
                                     __    G
GAM819  GCK      3'  TTCAGCTCCCATAGCGCTGG   3872         GCATA
                                CCAGTGCTG    AGCTGAA
                                |||||||||    |||||||
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                                GGTCGCGAT    TCGACTT
                                     ACCC_
GAM819  GCK     3'  TTCAGCTCCCATAGCGCTGG  53174        GCATA
                                CCAGTGCTG    AGCTGAA
                                |||||||||    |||||||
                                GGTCGCGAT    TCGACTT
                                     ACCC_
GAM819  GCK     3'  TTCAGCTCCCATAGCGCTGG  53180        GCATA
                                CCAGTGCTG    AGCTGAA
                                |||||||||    |||||||
                                GGTCGCGAT    TCGACTT
                                     ACCC_
GAM819  GLI3    3'  TTCAGTTTTGAATCAGTATTG  3912         CAT_
                                CAGTGCTGG    AAGCTGAA
                                |||||||||    ||||||||
                                GTTATGACT    TTTGACTT
                                     AAGT
GAM819  GPR85   3'  TTTACAAATGCTAGATATTGGT 38582        _      AAGCTGAA
            C                    GACCAGTG CTGGCAT
                                ||||||||| |||||||
                                CTGGTTAT GATCGTA
                                     A      AACATTT
GAM819  H3F3B   5'  TTCGTTGGGCGGTGCTGGTT   18026       TG   G ATA   T
                                GACCAG  CTG C   AGC GAA
                                ||||||  ||| |   ||| |||
                                TTGGTC  GGC G   TTG CTT
                                   GT   _ GG_  _
GAM819  HRASLS  5'  TTCAGCGTGGCGGCGCTGGT  39855         G   AA
                                ACCAGTGCTG CAT  GCTGAA
                                |||||||||| |||  ||||||
                                TGGTCGCGGC GTG  CGACTT
                                     G   __
GAM819  HYOU1   3'  TTCAGTAGCTGTTGATGCTGGT 59653        CT    TAA
            T                    GACCAGTG  GGCA   GCTGAA
                                ||||||||  ||||   ||||||
                                TTGGTCGT  TTGT   TGACTT
                                     AG    CGA
GAM819  JRK     3'  GCCCAGTGTCAGCATGGTC   86529       G       AA_
                                GACCA TGCTGGCAT   GC
                                ||||| |||||||||   ||
                                CTGGT ACGACTGTG   CG
                                   _       ACC
GAM819  KCNJ1   5'  TCAGCTTGGGGCTTGGTC    4027        T   GGCA
                                GACCAG GCT    TAAGCTGA
                                |||||| |||    ||||||||
                                CTGGTT CGG    GTTCGACT
                                   _  G____
GAM819  KLF8    3'  TTTGGTTTTCAGACAGTGCTGG 23407      TG   GCAT_   TG
            T                    ACCAG  CTG    AAGC  AA
                                |||||  |||    ||||  ||
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                                TGGTC  GAC    TTTG  TT
                                  GT   AGACT    GT
GAM819  MEN1    5'  AGTTGTTAGTGTTGGTT    93367       TG     TAA
                                GACCAG  CTGGCA   GCT
                                ||||||  ||||||   |||
                                TTGGTT  GATTGT   TGA
                                   GT     ___
GAM819  MPZ     3'  TCAGTATAGCATTGGTT     4999           GCATAA
                                GACCAGTGCTG     GCTGA
                                ||||||||||     |||||
                                TTGGTTACGAT     TGACT
                                      A_____
GAM819  MTNR1A   3'  TTCAGCTGGCAGAGTTAGCATT 19893           ATA___
           GG                     CCAGTGCTGGC     AGCTGAA
                                ||||||||||     |||||||
                                GGTTACGATTG     TCGACTT
                                      AGACGG
GAM819  MYCBP    3'  TTAGGAATGATGGCACTGGTT  24697         GG   AAG
                                GACCAGTGCT  CAT   CTGA
                                ||||||||||  |||   ||||
                                TTGGTCACGG  GTA   GATT
                                     TA   AG_
GAM819  NAV2     3'  TTTGGTCCTGCTCAGTTTTGGT 60163       T   _   TAA  TG
           T                     GACCAG GCTG GCA   GC  AA
                                ||||||  |||| |||   ||  ||
                                TTGGTT TGAC CGT   TG  TT
                                   T   T   CC_  GT
GAM819  NCAM2    3'  TTTAGTTTATGTTTGTCTG    15807     T  TG
                                CAG GC  GCATAAGCTGAA
                                |||  ||  ||||||||||||
                                GTC TG  TGTATTTGATTT
                                  _  TT
GAM819  NEURL    3'  TTTGGTTTGTGGTTTTGG    14868      T  TGG      TG
                                CCAG GC   CATAAGC  AA
                                ||||  ||   |||||||  ||
                                GGTT TG   GTGTTTG  TT
                                  T  ___       GT
GAM819  NRG1     5'  TTCAGTTTGGGCTACTGGTT   25652        GCT   A
                                GACCAGT   GGC TAAGCTGAA
                                |||||||   |||  |||||||||
                                TTGGTCA   TCG GTTTGACTT
                                     ___   G
GAM819  NUP98    3'  TGGTTTGGTCCCTGGTT     32864       TGCT   A    TG
                                GACCAG    GGC TAAGC  A
                                ||||||    |||  |||||  |
                                TTGGTC    CTG GTTTG  T
                                   C___   _     GT
GAM819  OLFM1    3'  TTCAGTTTATGCGATGATTG   26557      GCTG
                                CAGT    GCATAAGCTGAA
                                ||||    ||||||||||||
```

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                                GTTA   CGTATTTGACTT
                                  GTAG
GAM819  PCDHGA11  3'  TTCAACTATGCTGGTTTGGTT  49456      T  TG    A C
                                GACCAG GC  GCATA G TGAA
                                |||||| ||  ||||| | ||||
                                TTGGTT TG  CGTAT C ACTT
                                   _ GT    _ A
GAM819  PCSK1    3'  TGGCTTGAAGTATGGTT    4777      G   GGCA    TG
                                GACCA TGCT   TAAGC  A
                                ||||| ||||   |||||  |
                                TTGGT ATGA   GTTCG  T
                                   _   A___    GT
GAM819  PER2     3'  TGGCTTCTGGTGTGGTC    43049     G   TG CAT   TG
                                GACCA TGC  G   AAGC  A
                                ||||| |||  |  ||||  |
                                CTGGT GTG  C   TTCG  T
                                   _  GT ___   GT
GAM819  PER2     3'  TTCAGAAAATTTAATATTGGTC 43050       C   CATAAG
                                GACCAGTG TGG     CTGAA
                                |||||||| |||     |||||
                                CTGGTTAT ATT     GACTT
                                     A  TAAAA_
GAM819  PIGH     3'  TTCAGAAGGCCAGCATTG    15880         ATAAG
                                CAGTGCTGGC    CTGAA
                                ||||||||||    |||||
                                GTTACGACCG    GACTT
                                     GAA__
GAM819  PIGN     3'  TCAGCTTTCAGCACTGGTT   24673          CAT     A
                                GACCAGTGCTGG   AAGCTGA
                                ||||||||||||  |||||||
                                TTGGTCACGACT   TTCGACT
                                      ___      A
GAM819  PPP2R5E  3'  TTCAGTACCTGACCAGTATTAG 20730    C      _  TAA
           TT                    GAC AGTGCTGG CA   GCTGAA
                                ||| |||||||| ||   ||||||
                                TTG TTATGACC GT   TGACTT
                                  A       A  CCA
GAM819  PRPS2    3'  GCAGTGCTTGTATTGGTT    10903        T    AA
                                GACCAGTGC GGCAT  GC
                                |||||||| |||||  ||
                                TTGGTTATG TCGTG  CG
                                     T    A_
GAM819  PTPRK    3'  TTCAGCCTGTGGCCCAGCACTG 11125          __   A
           GTC                    GACCAGTGCTGG  CATA GCTGAA
                                ||||||||||||  |||| ||||||
                                CTGGTCACGACC  GTGT CGACTT
                                      CG   C
GAM819  PTX3     3'  TCAGTTTAATGCTGTGT     11144   TG T    _
                                G  C GGCAT AAGCTGA
                                |  | ||||| |||||||
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                                T  G TCGTA TTTGACT
                                 GT _    A
GAM819  QPCT    3'  TTTAGTTTAGGATAATTGGTT  24837       GCTGGCA
                                GACCAGT      TAAGCTGAA
                                |||||||      |||||||||
                                TTGGTTA      ATTTGATTT
                                   ATAGG__
GAM819  RAB6A   3'  TCAGGCTGGTTTTGGTT     11199       T  TG  ATAAG
                                GACCAG GC  GC    CTGA
                                |||||| ||  ||    ||||
                                TTGGTT TG  CG    GACT
                                   T  GT  _____
GAM819  RAD18   3'  TTTGGTTTGGTTTGGTTTGGTT 39399       T  TG CA    TG
                                GACCAG GC  G  TAAGC  AA
                                |||||| ||  |  |||||  ||
                                TTGGTT TG  T  GTTTG  TT
                                   _  GT TG    GT
GAM819  RAD50   3'  TTCAGTCACATGGCATGGTT   56010      G    GCATAA
                                GACCA TGCTG     GCTGAA
                                |||||| |||||     ||||||
                                TTGGT ACGGT     TGACTT
                                   _    ACAC__
GAM819  RAD50   3'  TTCAGTCACATGGCATGGTT   19196      G    GCATAA
                                GACCA TGCTG     GCTGAA
                                |||||| |||||     ||||||
                                TTGGT ACGGT     TGACTT
                                   _    ACAC__
GAM819  RALBP1  3'  TTACAAATGTCTCAGCATTGGT 22300          __   AAGCTGAA
           T                     GACCAGTGCTG  GCAT
                                ||||||||||  ||||
                                TTGGTTACGAC  TGTA
                                      TC    AACATT
GAM819  RANBP2L1 3'  TTTGGTTACACAGAACATTGGT 17317        __  GCATA   TG
           T                     GACCAGTG  CTG    AGC  AA
                                |||||||  |||    |||  ||
                                TTGGTTAC  GAC    TTG  TT
                                   AA   ACA__   GT
GAM819  RB1     3'  TTTAAGTCAGTATGGTC     90917      G      A
                                GACCA TGCTGGC TAAG
                                ||||| ||||||| ||||
                                CTGGT ATGACTG ATTT
                                   _      A
GAM819  RDS     3'  TTTGGACACCCTGTCAGACGTT 4367       _     TAAG__ TG
           GGTC                    CCAGTG CTGGCA     C  AA
                                |||||| ||||||     |  ||
                                GGTTGC GACTGT     G  TT
                                   A     CCCACA GT
GAM819  SERPINB9 3'  TTCAGTGCCACTTAGTATTG  14772        CATAA
                                CAGTGCTGG    GCTGAA
                                |||||||||    ||||||
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                                GTTATGATT    TGACTT
                                     CACCG
GAM819  SIAT7D   3'  TGACCTTGTGCCAGTCCTGGTC 26950      TG       CTGAA
                                GACCAG  CTGGCATAAG
                                ||||||  ||||||||||
                                CTGGTC  GACCGTGTTC
                                    CT       CAGT
GAM819  SLC19A2  3'  TTTGGTTTTCATGTTGGCACTG 68983   C    TG   __   TG
            CTC                   GA CAGTGC  GCAT  AAGC  AA
                                || ||||||  ||||  ||||  ||
                                CT GTCACG  TGTA  TTTG  TT
                                 C     GT   CT   GT
GAM819  SLC5A1   3'  CGGGTGTCAGTGTGGTT    4428      G       AAG
                                GACCA TGCTGGCAT   CTG
                                ||||| |||||||||   |||
                                TTGGT GTGACTGTG   GGC
                                  _      ___
GAM819  SMURF1   3'  TTTAGCCTTTGGCTTTGGTC   92462      T  TG CATAA
                                GACCAG GC  G    GCTGAA
                                |||||| ||  |    ||||||
                                CTGGTT CG  T    CGATTT
                                    T  GT TC___
GAM819  SPAP1    3'  TTCAGCGCTTGATATTGGTC   47775       CT_   ATAA
                                GACCAGTG   GGC   GCTGAA
                                ||||||||   |||   ||||||
                                CTGGTTAT   TCG   CGACTT
                                     AGT   _____
GAM819  SRGAP1   3'  TTGGAGTATAGCCAGTGTTGGT 72268       TG    _   AG TG A
            C                   GACCAG  CTGGC ATA  C  A
                                ||||||  ||||| |||  |  |
                                CTGGTT  GACCG TAT  G  T
                                   GT     A   GA GT
GAM819  STAU2    3'  TTCTGTTGCTAGTATTG     26911          TAA  T
                                CAGTGCTGGCA   GC GAA
                                ||||||||||   || |||
                                GTTATGATCGT   TG CTT
                                      ___  T
GAM819  STK24    3'  TTTGGAATCGTGCCACTGCTGG 13119       GC     AAG_ TG
            TC                    GACCAGT  TGGCAT    C  AA
                                |||||||  ||||||   |  ||
                                CTGGTCG  ACCGTG    G  TT
                                    TC     CTAA GT
GAM819  TAF7     3'  TCAGTCTTCAGACTGGTC     18913       G    CATAA
                                GACCAGT CTGG    GCTGA
                                ||||||| ||||    |||||
                                CTGGTCA GACT    TGACT
                                   _    TC___
GAM819  TCF7     3'  TTTAGTTCCTACTTTAGCCACT 12165       _    CA  __
            GGTT                    CCAGTG CTGG  TA  AGCTGAA
                                |||||| ||||  ||  |||||||
```

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                                GGTCAC GATT  AT  TTGATTT
                                   C   TC  CC
GAM819  TEX15   3'  TGGTTTATGTTTGGTT     48391       TGCTG      TG
                                GACCAG    GCATAAGC  A
                                ||||||    ||||||||  |
                                TTGGTT    TGTATTTG  T
                                   _____      GT
GAM819  TIA1    3'  TTCAGCTTGTGCACAATTCTG  41852     TGC  _
                                CAG   TG GCATAAGCTGAA
                                |||   || ||||||||||||
                                GTC   AC CGTGTTCGACTT
                                  TTA  A
GAM819  TIA1    3'  TTCAGCTTGTGCACAATTCTG  42249     TGC  _
                                CAG   TG GCATAAGCTGAA
                                |||   || ||||||||||||
                                GTC   AC CGTGTTCGACTT
                                  TTA  A
GAM819  TIMELESS  3'  TCAGCAGCAGTATTGG      14053         G ATAA
                                CCAGTGCTG C    GCTGA
                                |||||||||  |    |||||
                                GGTTATGAC G    CGACT
                                     _ A___
GAM819  TRPM7   3'  TTCAGTGATGATATCACTGGTT 62132         C  G   AA
                                GACCAGTG TG CAT  GCTGAA
                                ||||||||  ||  |||  ||||||
                                TTGGTCAC AT GTA  TGACTT
                                     T  A   G_
GAM819  TRPS1   3'  TTTGGTTTTTCAGTACTG    26088         CAT    TG
                                CAGTGCTGG   AAGC  AA
                                |||||||||   ||||  ||
                                GTCATGACT   TTTG  TT
                                     T__    GT
GAM819  TXNRD1   3'  TTTAGTTTATTGTGTGCTGGTC 12463       TG TG  _
                                GACCAG  C  GCA TAAGCTGAA
                                ||||||  |  |||  |||||||||
                                CTGGTC  G  TGT ATTTGATTT
                                   GT __   T
GAM819  UBL3    3'  TTCAAATGGTCAGCGTTG    23035          ATAAGC
                                CAGTGCTGGC     TGAA
                                ||||||||||     ||||
                                GTTGCGACTG     ACTT
                                     GTAA__
GAM819  USP6    3'  TGTGATTTGTGTTATACTGGTT 91150         C        CTGAA
                                GACCAGTG TGGCATAAG
                                ||||||||  |||||||||
                                TTGGTCAT ATTGTGTTT
                                     _       AGTGTG
GAM819  VDR     3'  TTTAGCTGCAGAACTGTATTGG 4576          TGGCATA_
            TC                    GACCAGTGC       AGCTGAA
                                ||||||||        |||||||
```

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                                CTGGTTATG      TCGATTT
                                     TCAAGACG
GAM819  YES1    3'  TTCATGCAAGTTGGCAGTGGTT 18359      G   TG  ATAA  _
                                GACCA TGC  GC    GC TGAA
                                ||||| |||  ||    || ||||
                                TTGGT ACG  TG    CG ACTT
                                   G   GT  AA__  T
GAM819  ZNF265  3'  TTAGTTTGTTTTCTGGTT    18399      TGCT    TA
                                GACCAG   GGCA  AGCTGA
                                ||||||   ||||  ||||||
                                TTGGTC   TTGT  TTGATT
                                   TT__   __
GAM819  ACAS2   3'  TTGTGCCAGATGCCAGTACTG  37934          AA_  TGAA
                                CAGTGCTGGCAT   GC
                                ||||||||||||   ||
                                GTCATGACCGTA   CG
                                       GAC  TGTTT
GAM819  ACAS2   3'  TTGTGCCAGATGCCAGTACTG  57704          AA_  TGAA
                                CAGTGCTGGCAT   GC
                                ||||||||||||   ||
                                GTCATGACCGTA   CG
                                       GAC  TGTTT
GAM819  AMOT    3'  TTTGGTTTAAAATGTATGTGGT 55732      _   TGGCA    TG
          C                      GACCA GTGC    TAAGC  AA
                                ||||| ||||    |||||  ||
                                CTGGT TATG    ATTTG  TT
                                   G    TAAA_    GT
GAM819  BIRC2   5'  TTTAGCTATCAAACAGTACTG  67205        GCATA_
                                CAGTGCTG     AGCTGAA
                                ||||||||     |||||||
                                GTCATGAC     TCGATTT
                                     AAACTA
GAM819  BM-002  3'  TTCAGTTTACATGCATTATTGG 33528        CTG   __
          TT                     GACCAGTG   GCA  TAAGCTGAA
                                ||||||||   |||  |||||||||
                                TTGGTTAT   CGT  ATTTGACTT
                                     TA_   AC
GAM819  BMF     3'  TCAGCTTGTGTTCTGC     53164    T_
                                GC  GGCATAAGCTGA
                                ||  ||||||||||||
                                CG  TTGTGTTCGACT
                                 TC
GAM819  BS69    3'  TTCAGCTTAATTTACTGTTC  21769    C    CTGGCA
                                GA CAGTG     TAAGCTGAA
                                || |||||     |||||||||
                                CT GTCAT     ATTCGACTT
                                 T    TTA___
GAM819  C19orf7 3'  TTCAGCCACCAGTGTTGG    61133     TG   CATAA
                                CCAG  CTGG    GCTGAA
                                ||||  ||||    ||||||
```

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                                GGTT  GACC    CGACTT
                                  GT   AC___
GAM819  C20orf164 3'  TTAGCTGAAGCATTGG      79480        GGCATA
                                CCAGTGCT     AGCTGA
                                ||||||||     ||||||
                                GGTTACGA     TCGATT
                                    AG____
GAM819  CGGBP1    3'  TTTAGCTTCTGGTCAGCACTG  13366         AT_
                                CAGTGCTGGC   AAGCTGAA
                                ||||||||||   ||||||||
                                GTCACGACTG   TTCGATTT
                                     GTC
GAM819  COLEC12   3'  TTCGGCTTGTGCTCTGCAGTC  47877     CAG   T_
                                GAC   TGC  GGCATAAGCTGAA
                                |||   |||  ||||||||||||
                                CTG   ACG  TCGTGTTCGGCTT
                                  ___   TC
GAM819  DKFZp564A176 5'  TTCAGTAGCCCCTAGCATTGG  49974          CATAA
                                CCAGTGCTGG    GCTGAA
                                ||||||||||    ||||||
                                GGTTACGATC    TGACTT
                                     CCCGA
GAM819  DKFZP586D0623 3'  TTCAGTTTATGTTAGAC     71978    G
                                GT CTGGCATAAGCTGAA
                                || ||||||||||||||
                                CA GATTGTATTTGACTT
                                 _
GAM819  DKFZp761D0614 3'  TTGTGTTGGCTTGGTC      87558       T  TG
                                GACCAG GC  GCATAA
                                |||||| ||  ||||||
                                CTGGTT CG  TGTGTT
                                   _ GT
GAM819  DMRTB1    3'  TTCAGCCATTATGGGCACTGGT 66247          GG    __
           T                     GACCAGTGCT  CATAA  GCTGAA
                                ||||||||||  |||||  ||||||
                                TTGGTCACGG  GTATT  CGACTT
                                     __     AC
GAM819  FLJ10330  3'  TTTGGCATGGTTGCCATGTTGG 36033      GT C    TAA__  TG
           TT                     GACCA  G TGGCA    GC  AA
                                |||||  | |||||    ||  ||
                                TTGGT  T ACCGT    CG  TT
                                   TG _    TGGTA  GT
GAM819  FLJ10701  3'  GTTAGATGTACAGCATTGGTT  36431          _   AAG   A
                                GACCAGTGCTG GCAT   CTGA
                                |||||||||| ||||   ||||
                                TTGGTTACGAC TGTA   GATT
                                      A   ___    GT
GAM819  FLJ10803  3'  TTTGGTTTATTGCAGTGGTC   36673      G   TGGC     TG
                                GACCA TGC    ATAAGC  AA
                                ||||| |||    ||||||  ||
```

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                                CTGGT ACG    TATTTG  TT
                                  G   T___     GT
GAM819   FLJ10971  3'  TTTAGCTTGTGTATATAATTGT 36932     _    GCTG_
           GTT                    GAC CAGT    GCATAAGCTGAA
                                ||| ||||    ||||||||||||
                                TTG GTTA    TGTGTTCGATTT
                                  T   ATATA
GAM819   FLJ12587  3'  TCAGCTTTGCAGTGGTT     42499      G   TGGCAT
                                GACCA TGC     AAGCTGA
                                ||||| |||     |||||||
                                TTGGT ACG     TTCGACT
                                  G   T_____
GAM819   FLJ13153  5'  TGGCTGTCAGTGCTGGTC    45559       TG     TAA  TG
                                GACCAG  CTGGCA   GC  A
                                ||||||  ||||||   ||  |
                                CTGGTC  GACTGT   CG  T
                                   GT     ___  GT
GAM819   FLJ14075  3'  TTCGGCTTGTTTATGTATTAGT 46051     C     TGGC
           T                     GAC AGTGC    ATAAGCTGAA
                                ||| |||||    ||||||||||
                                TTG TTATG    TGTTCGGCTT
                                  A    TATT
GAM819   FLJ20070  5'  TCGGCGACGCCGCTGGTC    34477       GCT   ATAA
                                GACCAGT   GGC    GCTGA
                                |||||||   |||    |||||
                                CTGGTCG   CCG    CGGCT
                                    ___   CAG_
GAM819   FLJ20701  3'  TTCAGCAAAGGCAGCATTGGTC 35592          G ATAA
                                GACCAGTGCTG C    GCTGAA
                                ||||||||||| |    ||||||
                                CTGGTTACGAC G    CGACTT
                                     _ GAAA
GAM819   FOXN4     3'  TTCAGCTTGGACACACTGG    75574       C  GCA
                                CCAGTG TG   TAAGCTGAA
                                |||||| ||   |||||||||
                                GGTCAC AC   GTTCGACTT
                                   _  AG_
GAM819   GL004     3'  TTAGTTTTGCACTTGGTT     65996      _   TGGCAT
                                GACCA GTGC     AAGCTGA
                                ||||| ||||     |||||||
                                TTGGT CACG     TTTGATT
                                  T    T_____
GAM819   GRWD      3'  TTTAGAGGCTGGTGCTGTGTC  48974     _   TG TG  ATAAG
                                GAC CAG  C  GC    CTGAA
                                ||| |||  |  ||    |||||
                                CTG GTC  G  CG    GATTT
                                  T   GT GT  GA___
GAM819   GW112     3'  TTCAACTGAAGCCAGCACTGGT 21194           ATA  C
           T                     GACCAGTGCTGGC   AG TGAA
                                ||||||||||||   || ||||
```

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                                TTGGTCACGACCG   TC ACTT
                                      AAG  A
GAM819  IRAK3    3' TTTAGCTTGCTTGCACGGGTT 23245     A    T    TA
                                GACC GTGC GGCA  AGCTGAA
                                |||| |||| ||||  |||||||
                                TTGG CACG TCGT  TCGATTT
                                  G    T   __
GAM819  KIAA0057 3' TCAGCCCCATGCTGGTC     24441        C   CATAA
                                GACCAGTG TGG    GCTGA
                                |||||||| |||    |||||
                                CTGGTCGT ACC    CGACT
                                     _  C____
GAM819  KIAA0205 3' TTTGGTTTGGGTACTGGTT   29594         GGCA    TG
                                GACCAGTGCT    TAAGC  AA
                                ||||||||||    |||||  ||
                                TTGGTCATGG    GTTTG  TT
                                      ____    GT
GAM819  KIAA0212 3' TTTGGTTTGGGGCACTGG    27947        GGCA    TG
                                CCAGTGCT    TAAGC  AA
                                ||||||||    |||||  ||
                                GGTCACGG    GTTTG  TT
                                     G___    GT
GAM819  KIAA0336 3' TTTGGTTACACAGAACATTGGT 27592        __  GCATA   TG
          T                      GACCAGTG  CTG    AGC  AA
                                ||||||||  |||    |||  ||
                                TTGGTTAC  GAC    TTG  TT
                                     AA   ACA__   GT
GAM819  KIAA0410 3' TTAGCTTAGTGTAGGTT     28781     A TG   GCATA
                                GACC G  CTG    AGCTGA
                                |||| |  |||    ||||||
                                TTGG T  GAT    TCGATT
                                  A GT  _____
GAM819  KIAA0459 3' TTTAGTAATTTTACTACTGGTT 61013        C   CATAA
                                GACCAGTG TGG    GCTGAA
                                |||||||| |||    ||||||
                                TTGGTCAT ATT    TGATTT
                                     C   TTAA_
GAM819  KIAA0534 5' TTCAGTTCTCTTAGCATTG    71438        CATA
                                CAGTGCTGG    AGCTGAA
                                |||||||||    |||||||
                                GTTACGATT    TTGACTT
                                      CTC_
GAM819  KIAA0630 3' TCAGCACTATATTGGTC     89397        C   CATAA
                                GACCAGTG TGG    GCTGA
                                |||||||| |||    |||||
                                CTGGTTAT ATC    CGACT
                                     _   A____
GAM819  KIAA0801 5' GTGTTTAGCGCTGGTC      29151          _
                                GACCAGTGCTGG CAT
                                |||||||||||| |||
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                                CTGGTCGCGATT GTG
                                       T
GAM819  KIAA0923 3' TCAGCTTGATGCATGGTC    25838      G   TGGCA
                                GACCA TGC     TAAGCTGA
                                ||||| |||     ||||||||
                                CTGGT ACG     GTTCGACT
                                   _   TA___
GAM819  KIAA1000 3' TTCAGCTTTGCAAAGTACTGG  65281        G_   T
                                CCAGTGCT  GCA AAGCTGAA
                                ||||||||  ||| ||||||||
                                GGTCATGA  CGT TTCGACTT
                                     AA  _
GAM819  KIAA1068 3' TTCAGCTGCCACCGGCACTG   31044         CATA
                                CAGTGCTGG    AGCTGAA
                                |||||||||    |||||||
                                GTCACGGCC    TCGACTT
                                      ACCG
GAM819  KIAA1089 3' TGGCCTGTGCCAGCACGGTC   68848      A         A
                                GACC GTGCTGGCATA GCTG
                                |||| |||||||||||| ||||
                                CTGG CACGACCGTGT CGGT
                                   _         C
GAM819  KIAA1189 3' TATGCTAACGCTGGTC       72047         C
                                GACCAGTG TGGCATA
                                |||||||| |||||||
                                CTGGTCGC ATCGTAT
                                     A
GAM819  KIAA1383 3' TCAGTTTGTTCAATGGTT     69785       GTGC   C
                                GACCA    TGG ATAAGCTGA
                                |||||    ||| |||||||||
                                TTGGT    ACT TGTTTGACT
                                   A___   _
GAM819  KIAA1467 3' TTTAGCTTGTGTTAGTAAAAGG 71620     AG_
                                CC   TGCTGGCATAAGCTGAA
                                ||   |||||||||||||||||
                                GG   ATGATTGTGTTCGATTT
                                 AAA
GAM819  KIAA1508 5' TTGCTCTGTGCCAGTGCTGG   61895      TG       _   TGAA
                                CCAG  CTGGCATA AGC
                                ||||  |||||||| |||
                                GGTC  GACCGTGT TCG
                                   GT       C   TT
GAM819  KIAA1608 3' TTTAGTTTTGTTGGTTGGTT   45691       GT  TG   T
                                GACCA  GC  GCA AAGCTGAA
                                |||||  ||  ||| ||||||||
                                TTGGT  TG  TGT TTTGATTT
                                   __  GT   _
GAM819  KIAA1813 5' TCAGACCAGCATTGG        70308          CATAAG
                                CCAGTGCTGG     CTGA
                                ||||||||||     ||||
```

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                                GGTTACGACC     GACT
                                     A_____
GAM819  MGC12217  3'  TTTAGCAGCAGACATTGGTT  51314       _  G ATAA
                                GACCAGTG CTG C   GCTGAA
                                |||||||| ||| |   ||||||
                                TTGGTTAC GAC G   CGATTT
                                     A  _ A___
GAM819  MGC12972  3'  TTCAGCTCCGGAGCATTGG   51079       __ CATA
                                CCAGTGCT  GG   AGCTGAA
                                |||||||| ||   |||||||
                                GGTTACGA  CC   TCGACTT
                                     GG ____
GAM819  MGC3047   3'  TGGCTTCTGTACTGG      50365       T  CAT   TG
                                CCAGTGC GG   AAGC  A
                                ||||||| ||   ||||  |
                                GGTCATG TC   TTCG  T
                                     _ ___   GT
GAM819  MGC4161   3'  TTTGGTTTGTGTTGCTGTTC  44192    C   GCT      TG
                                GA CAGT   GGCATAAGC  AA
                                || ||||   |||||||||  ||
                                CT GTCG   TTGTGTTTG  TT
                                 T   ___       GT
GAM819  MGC5469   3'  TTCATGTGGTTAGTTTGGTC  50398      T    ATAAGC
                                GACCAG GCTGGC     TGAA
                                |||||| ||||||     ||||
                                CTGGTT TGATTG     ACTT
                                    _     GTGT__
GAM819  NPEPL1    3'  TTTGGTTTGTCTTTCTGGTC  45093      TGCT  C     TG
                                GACCAG    GG ATAAGC  AA
                                ||||||    || ||||||  ||
                                CTGGTC    TC TGTTTG  TT
                                   TT__ _     GT
GAM819  ORCTL3    3'  AGCTGCTGCTGGTT       14917       GCT   TAA
                                GACCAGT   GGCA   GCT
                                |||||||   ||||   |||
                                TTGGTCG   TCGT   CGA
                                     ___   ___
GAM819  PANK      3'  TATGTAAGCGCTGGTC     56335         G
                                GACCAGTGCT GCATA
                                |||||||||| |||||
                                CTGGTCGCGA TGTAT
                                     A
GAM819  PDCD7     3'  TTTGGTTCTGTTTTGGTTTGGT 72145      T  TG C  _  TG
           T                     GACCAG GC  G ATA AGC  AA
                                ||||||  ||  | ||| |||  ||
                                TTGGTT TG  T TGT TTG  TT
                                    _ GT T   C   GT
GAM819  PIGM      3'  TTTAAGCCAGTATTTGTT    59048     C       A
                                GAC AGTGCTGGC TAAG
                                ||| |||||||| ||||
```

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                                TTG TTATGACCG ATTT
                                  T       A
GAM819  PPIL3    5'  TGTGTTGCTACTGGTT     55662       _  T
                                GACCAGT GC GGCATA
                                ||||||| || ||||||
                                TTGGTCA CG TTGTGT
                                   T  _
GAM819  PRO0800  3'  TGGCTTTTGTCTGGTT     37743      TGCTG  T   TG
                                GACCAG    GCA AAGC  A
                                ||||||    ||| ||||  |
                                TTGGTC    TGT TTCG  T
                                   _____  T   GT
GAM819  PRO2831  5'  TCAGTATGGTTGCTGGTC    37602       GCT   ATAA
                                GACCAGT   GGC   GCTGA
                                |||||||   |||   |||||
                                CTGGTCG   TTG   TGACT
                                   ___  GTA_
GAM819  PSMA4    5'  TTCGGTGAGCGGTGGTGGTT   10942      G    G ATAA
                                GACCA TGCTG C   GCTGAA
                                ||||| ||||| |   ||||||
                                TTGGT GTGGC G   TGGCTT
                                   G    _ AG__
GAM819  RAB6C    3'  TCAGGCTGGTTTTGGTT     49571       T  TG  ATAAG
                                GACCAG GC  GC    CTGA
                                |||||| ||  ||    ||||
                                TTGGTT TG  CG    GACT
                                   T  GT  _____
GAM819  RAI17    3'  TTTAGCTTCAGTGTACTAGTC  91288     C    TG  AT
                                GAC AGTGC  GC  AAGCTGAA
                                |||  |||||  ||  ||||||||
                                CTG TCATG  TG  TTCGATTT
                                  A    __  AC
GAM819  RGS18    3'  TTGGGCATCTGCCACATTGGTT 55395        C    TAA  G
                                GACCAGTG TGGCA   GCT AA
                                |||||||| |||||   ||| ||
                                TTGGTTAC ACCGT   CGG TT
                                   _    CTA   G
GAM819  SAE1     3'  TCAGGGCTATGTTGGTC     18534      GT C   ATAAG
                                GACCA  G TGGC    CTGA
                                |||||  | ||||    ||||
                                CTGGT  T ATCG    GACT
                                   TG _   G____
GAM819  TBCC     3'  TTCAGCTTCCCAAAGTGCTGG  12144     TG  GGCAT
                                CCAG  CT    AAGCTGAA
                                ||||  ||    ||||||||
                                GGTC  GA    TTCGACTT
                                  GT  AACCC
GAM819  TERA     3'  TGGCTGCAGTATTGGT      41137         G  TAA  TG
                                ACCAGTGCTG CA   GC  A
                                |||||||||| ||   ||  |
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                                TGGTTATGAC GT   CG  T
                                      _ ___  GT
GAM819  TRIM4    3'  TTTGGTTTTCTGTTCATGTGTT 52258     TG _  _ T_   TG
            GGTT                  CCAG  C TGG CA  AAGC  AA
                                  ||||  | ||| ||  ||||  ||
                                  GGTT  G ACT GT  TTTG  TT
                                    GT T   T  CT    GT
GAM819  TSPAN-2  3'  TGGCTCATTACTGGTT     19167        C  GCATA   TG
                                  GACCAGTG TG    AGC  A
                                  ||||||||  ||    |||  |
                                  TTGGTCAT AC    TCG  T
                                       T _____  GT
GAM819  WBP4     3'  TTTAGTTTGAACCAGGCATTGT 23233     _     _  CA
            GTT                   GAC CAGTGC TGG  TAAGCTGAA
                                  |||  ||||||  |||  |||||||||
                                  TTG GTTACG ACC  GTTTGATTT
                                    T     G   AA
GAM819  X123     5'  TTCAGCCCTGTAGTGCTGTTC  69926    C   TG   G  TAA
                                  GA CAG  CTG CA   GCTGAA
                                  ||  |||  |||  ||   ||||||
                                  CT GTC  GAT GT   CGACTT
                                   T   GT   _  CC_
GAM819  ZNF340   5'  TTAGCTTGTGCTCAAGT     84565     __
                                  GCT  GGCATAAGCTGA
                                  |||  ||||||||||||
                                  TGA  TCGTGTTCGATT
                                    AC
GAM819  LOC144486 3'  TTTAGCAAGTACAGTGCTG    83089     TG   GC  AA
                                  CAG  CTG  AT  GCTGAA
                                  |||  |||  ||  ||||||
                                  GTC  GAC  TG  CGATTT
                                    GT   A_  AA
GAM819  LOC147077 3'  TTTAGGGTGATCAGTGCTGG   78251      TG   _  AAG
                                  CCAG  CTGG CAT   CTGAA
                                  ||||  |||| |||   |||||
                                  GGTC  GACT GTG   GATTT
                                    GT   A   G__
GAM819  LOC148734 5'  TTCAGCTTTTGTGCTCTGGTT  78959       T  TG   T
                                  GACCAG GC  GCA AAGCTGAA
                                  ||||||  ||  ||| ||||||||
                                  TTGGTC CG  TGT TTCGACTT
                                     T  __   T
GAM819  LOC150311 5'  TTCAGCCATGGTAGTGCTGGTT 79760       TG   G   AA
                                  GACCAG  CTG CAT  GCTGAA
                                  ||||||  ||| |||  ||||||
                                  TTGGTC  GAT GTA  CGACTT
                                     GT   G   C_
GAM819  LOC150406 3'  TTGTGTGGGCATTGGTT     79860          G
                                  GACCAGTGCT GCATAA
                                  ||||||||||  ||||||
```

```
                                TTGGTTACGG TGTGTT
                                      G
GAM819  LOC150862 3'  TGTGCCATACTGGTC       80021         C
                                GACCAGTG TGGCATA
                                |||||||| |||||||
                                CTGGTCAT ACCGTGT
                                       _
GAM819  LOC151201 5'  TTTAGTTTATACCATTGG     85299      TGC   C
                                CCAG   TGG ATAAGCTGAA
                                ||||   ||| ||||||||||
                                GGTT   ACC TATTTGATTT
                                  ___   A
GAM819  LOC151518 3'  TCAGCTTACTATTGGTT      85435         CTGGCA
                                GACCAGTG     TAAGCTGA
                                ||||||||     ||||||||
                                TTGGTTAT     ATTCGACT
                                     C_____
GAM819  LOC155038 3'  GCGTGTTATGCTGGTT       81258         C     AA
                                GACCAGTG TGGCAT  GC
                                |||||||| ||||||  ||
                                TTGGTCGT ATTGTG  CG
                                       _     __
GAM819  LOC157660 3'  TTTAGTTTATGCCTTGTGTT   86514     TG T_
                                AG  C  GGCATAAGCTGAA
                                ||  |  ||||||||||||||
                                TT  G  CCGTATTTGATTT
                                 GT TT
GAM819  LOC158187 3'  TTTGGCTTGTGCTAGAAC     86698    G         TG
                                GT CTGGCATAAGC  AA
                                ||  ||||||||||  ||
                                CA GATCGTGTTCG  TT
                                 A          GT
GAM819  LOC158332 3'  GCTGTGCTAGTATCGGTT     81889      A         A
                                GACC GTGCTGGCATA GC
                                |||| |||||||||| ||
                                TTGG TATGATCGTGT CG
                                  C         _
GAM819  LOC158337 5'  TTAGCTGACAGCACTGG      86775         GCATA
                                CCAGTGCTG     AGCTGA
                                |||||||||     ||||||
                                GGTCACGAC     TCGATT
                                     AG___
GAM819  LOC163882 3'  TTTGGTTTACACTTGTTGGGTC 82170      AGT  T  CA    TG
                                GACC   GC GG  TAAGC  AA
                                ||||   || ||  |||||  ||
                                CTGG   TG TC  ATTTG  TT
                                  GT_  T  AC    GT
GAM819  LOC166754 5'  TTTGTAGCCAGCGCTGG      82662           _
                                CCAGTGCTGGC ATAAG
                                |||||||||| |||||
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                                GGTCGCGACCG TGTTT
                                      A
GAM819  LOC168448 3'  TTCAGCTTGTGACCCTGTGTC  82701    _  TGCT  _
                                GAC CAG   GG CATAAGCTGAA
                                ||| |||   || ||||||||||
                                CTG GTC   CC GTGTTCGACTT
                                  T  ____  A
GAM819  LOC199692 3'  TTGTGTTATGTCAGTGTTGGT  59244     TG      GCTGAA
                                ACCAG  CTGGCATAA
                                |||||  |||||||||
                                TGGTT  GACTGTATT
                                   GT       GTGTT
GAM819  LOC200734 3'  TTTGGTTTGTGAAGGCATCGGT 88867     A    GG     TG
          T                      GACC GTGCT  CATAAGC  AA
                                |||| |||||  |||||||  ||
                                TTGG TACGG  GTGTTTG  TT
                                  C    AA     GT
GAM819  LOC201965 3'  TTTGTGGTTGTATTGGTT    89116        TGG
                                GACCAGTGC   CATAAG
                                |||||||||   ||||||
                                TTGGTTATG   GTGTTT
                                     TTG
GAM819  LOC220692 3'  TTTGGTTACACAGAACATTGGT 91224       __  GCATA  TG
          T                      GACCAGTG  CTG    AGC  AA
                                ||||||||  |||    |||  ||
                                TTGGTTAC  GAC    TTG  TT
                                    AA   ACA__   GT
GAM819  LOC221596 3'  TTCAGTGATTGGTTAGCACTTG 91985    C       ATAA_
          TT                      GAC AGTGCTGGC    GCTGAA
                                ||| |||||||||    ||||||
                                TTG TCACGATTG    TGACTT
                                  T       GTTAG
GAM819  LOC221830 3'  TTTAGTACCAGACATAGTGCTG 92515      TG   GCATAA__
          GTC                     GACCAG  CTG      GCTGAA
                                ||||||  |||      ||||||
                                CTGGTC  GAT      TGATTT
                                   GT   ACAGACCA
GAM819  LOC221882 3'  TTTGTGTTTGCTTGGTGCTGGT 92503      TG  _  TAA  TGAA
          T                      GACCAG  CTG GCA   GC
                                ||||||  ||| |||   ||
                                TTGGTC  GGT CGT   TG
                                   GT   T   TTG  TTT
GAM819  LOC221975 5'  TTCGTCCGGGTGCCAGCGCTGG 92611          AAGC_
                                CCAGTGCTGGCAT    TGAA
                                ||||||||||||    ||||
                                GGTCGCGACCGTG    GCTT
                                       GGCCT
GAM819  LOC253891 3'  TTCCACGTGTGTTGTGTTGGTT 94418      TG T     AGCT
                                GACCAG  C GGCATA    GAA
                                ||||||  | ||||||    |||
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                                TTGGTT  G TTGTGT   CTT
                                   GT _     GCAC
GAM819  LOC254251 3'  TTTGGTTTAAATGTGCTGGTT  95915      TG TGGCA    TG
                                GACCAG  C    TAAGC  AA
                                ||||||  |    |||||  ||
                                TTGGTC  G    ATTTG  TT
                                   GT TAA__    GT
GAM819  LOC255242 3'  TTCATGTGGTTAGTTTGGTC  95930      T    ATAAGC
                                GACCAG GCTGGC     TGAA
                                |||||| ||||||     ||||
                                CTGGTT TGATTG     ACTT
                                   _     GTGT__
GAM819  LOC255870 5'  TTTGGCAAGGCATGTTGGTT  94660      __    GGCATAA  TG
                                GACCA  GTGCT     GC  AA
                                |||||  |||||     ||  ||
                                TTGGT  TACGG     CG  TT
                                   TG    AA_____  GT
GAM819  LOC63920  5'  TCAGTTAGCCACTGGTT    42025      GCT   ATA
                                GACCAGT   GGC   AGCTGA
                                |||||||   |||   ||||||
                                TTGGTCA   CCG   TTGACT
                                   ___   A__
GAM819  LOC84570  5'  TTCGGCTTCGCGAGTAGCATTG 50713        ___  AT
          GTT                    ACCAGTGCTG   GC  AAGCTGAA
                                ||||||||||   ||  ||||||||
                                TGGTTACGAT   CG  TTCGGCTT
                                     GAG  C_
GAM819  LOC90826  5'  TTTGGTTTGTGCTCCAGC    64096     __      TG
                                GCTG  GCATAAGC  AA
                                ||||  ||||||||  ||
                                CGAC  CGTGTTTG  TT
                                  CT       GT
GAM819  LOC91694  3'  GCACATCTAGTGCTGGTT    66962      TG    C  AA
                                GACCAG  CTGG AT  GC
                                ||||||  |||| ||  ||
                                TTGGTC  GATC TA  CG
                                   GT    _  CA
GAM820  RFXAP     3'  TCGACTTAATCATGGCTGTT   5016       CCT   C__
                                AACAGCCA   TGA   AGTCGA
                                |||||||   |||   ||||||
                                TTGTCGGT   ACT   TCAGCT
                                   ___   AAT
GAM820  NYD-SP25  5'  TCAACTGTCAAGGTGTCCATTG 53189      CAGC         C
          TA                     TATAA    CACCTTGACAGT GA
                                |||||    |||||||||||| ||
                                ATGTT    GTGGAACTGTCA CT
                                   ACCT          A
GAM820  TCF-3     3'  CGACCCCTGCAGGCTGT     48425       ACCT  A  ___
                                ACAGCC    TG CA   GTCG
                                ||||||    || ||   ||||
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                                TGTCGG   AC GT   CAGC
                                   _____ _ CCC
GAM820  TOB2    3' CAAGTAGGCAACTGTTATG   95617       ___  AC
                                TATAACA  GCC  CTTG
                                |||||||  |||  ||||
                                GTATTGT  CGG  GAAC
                                    CAA  AT
GAM820  LOC158236 5' CGGGTGGAAGGTGGTT     86706        GA  G
                                AGCCACCTT  CA TCG
                                |||||||||  || |||
                                TTGGTGGAA  GT GGC
                                     G_  G
GAM820  LOC170281 5' TCAACCACTGGCTGTTATA   87251         CC__
                                TATAACAGCCA   TTGA
                                ||||||||||   ||||
                                ATATTGTCGGT   AACT
                                      CACC
GAM820  LOC219793 5' TCAACTGTCTTTTCCGGCTGT 91375      ACCTT_    C
                                ACAGCC    GACAGT GA
                                ||||||    |||||| ||
                                TGTCGG    CTGTCA CT
                                   CCTTTT    A
GAM820  LOC221362 3' CTGCAAGATGGCTGT      93760       C   A
                                ACAGCCA CTTG CAG
                                ||||||| |||| |||
                                TGTCGGT GAAC GTC
                                    A   _
GAM820  LOC90906  3' CAAGGTGGCTGTTATA     64294
                                TATAACAGCCACCTTG
                                ||||||||||||||||
                                ATATTGTCGGTGGAAC

GAM821  TFAP2C   3' AATCCTTCTCCACCGCA     12229       T   TTGTA
                                TGCGGTGG AGG    GATT
                                |||||||| |||    ||||
                                ACGCCACC TCT    CTAA
                                    _  TC___
GAM821  KIAA1918  3' AAGAATCTACAACCTGGAGC   73158    GG
                                GT  TAGGTTGTAGATTCTT
                                ||  ||||||||||||||||
                                CG  GTCCAACATCTAAGAA
                                 AG
GAM821  LOC133308 5' AAGAATCCTATCTTCCCACCGC 75084       T_   TGTA
          A                      TGCGGTGG  AGGT   GATTCTT
                                 ||||||||  ||||   |||||||
                                 ACGCCACC  TCTA   CTAAGAA
                                     CT   TC__
GAM822  ADH1B    3' CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
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                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM822  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM822  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                      _
GAM822  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM822  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM822  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM822  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                       T__    _
GAM822  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM822  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_    CG_
GAM822  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM822  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
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                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM822  FLJ23462  3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
              G                   CATTTC        GTCTGAGAT
                                  ||||||        |||||||||
                                  GTAAAG        CAGACTCTA
                                     AAACATTT_
GAM822  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                  CATTTCA   TCACTGTCTGAGAT
                                  |||||||   ||||||||||||||
                                  GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM822  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                  TTCA TTTCACTG  TGAG
                                  |||| ||||||||  ||||
                                  AAGT AAAGTGAC  GTTT
                                    A       CT
GAM822  KLHL6     3'  ATCTCAGAGCAGGAAA      55299     A  _
                                  TTTC CTG TCTGAGAT
                                  |||| ||| ||||||||
                                  AAAG GAC AGACTCTA
                                    _  G
GAM822  NIR3      3'  GCAGTGAAAGTGCAAT      66242     T
                                  ATT CACTTTCACTGT
                                  ||| ||||||||||||
                                  TAA GTGAAAGTGACG
                                   C
GAM822  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                  TTCACTTT  CT TCTGAGAT
                                  ||||||||  || ||||||||
                                  AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM822  PP35      3'  ATCTCAGACTGAAA       22814       CT
                                  TTTCA  GTCTGAGAT
                                  |||||  |||||||||
                                  AAAGT  CAGACTCTA
                                     __
GAM822  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148         TCAC   C_
                                  CATTTCACTT    TGT  TGAG
                                  ||||||||||    |||  ||||
                                  GTAAAGTGAA    ACG  ACTC
                                     TA__   TT
GAM822  SEP15     3'  TCCTACAGTAAGAGTGAAA    14934        C     CT
                                  TTTCACTTT ACTGT  GA
                                  ||||||||| |||||  ||
                                  AAAGTGAGA TGACA  CT
                                     A    TC
GAM822  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                  TTTCACTTT    TCTGAG
                                  |||||||||    ||||||
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                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM822  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM822  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM822  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226     A      GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM822  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM823  ABCB9    3'  TCCCCACACCCGCCCCTGTG   39038     TGAT   AAA  A
                                CAC    GGG   GT TGGGGA
                                |||    |||   || ||||||
                                GTG    CCC   CA ACCCCT
                                  TC__   GCC  C
GAM823  ACK1     3'  TCCATGTTTTCCCACCAG    19346     A
                                CTG TGGGAAAGTATGGG
                                ||| ||||||||||||||
                                GAC ACCCTTTTGTACCT
                                  C
GAM823  ADCY9    3'  CCCCATTGCCCACCCGCA    6656     A    AAA  _
                                TG TGGG   GTA TGGGG
                                || ||||   ||| |||||
                                AC GCCC   CGT ACCCC
                                 _    ACC   T
GAM823  ADRBK1   3'  CCCCATCCTGGCCCATCAGTGT 7867           AA  T
                                ACACTGATGGG  AG ATGGGG
                                ||||||||||  || ||||||
                                TGTGACTACCC  TC TACCCC
                                      GG  C
GAM823  AKAP13   3'  TCCCCATACTGTTTCCA     89687       _
                                TGGGAA AGTATGGGGA
                                |||||| ||||||||||
                                ACCTTT TCATACCCCT
                                   G
GAM823  AP2M1    3'  CCCCACCACACATCAGTGT    14514         GGAAAGTA
                                ACACTGATG       TGGGG
                                |||||||||       |||||
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                                TGTGACTAC       ACCCC
                                     ACACC___
GAM823  AQP6    5'  CCCCACATCCCACCCCATCAG  7943         AAA__  A
                                CTGATGGG    GT TGGGG
                                ||||||||    || |||||
                                GACTACCC    TA ACCCC
                                     CACCC  C
GAM823  AQP6    5'  CCCCACATCCCACCCCATCAG  53916        AAA__  A
                                CTGATGGG    GT TGGGG
                                ||||||||    || |||||
                                GACTACCC    TA ACCCC
                                     CACCC  C
GAM823  ARHG    3'  TCCTACCCCCATCAG       8018         AAA   T
                                CTGATGGG   GTA GGG
                                ||||||||   ||| |||
                                GACTACCC   CAT CCT
                                     C__   _
GAM823  BCL11B  5'  CCCCGGCTCCCCCCCATCAGTG  56800         AA_   A
                                CACTGATGGG   AGT TGGGG
                                ||||||||||   ||| |||||
                                GTGACTACCC   TCG GCCCC
                                      CCC   _
GAM823  BCL11B  5'  CCCCGGCTCCCCCCCATCAGTG  43186         AA_   A
                                CACTGATGGG   AGT TGGGG
                                ||||||||||   ||| |||||
                                GTGACTACCC   TCG GCCCC
                                      CCC   _
GAM823  ESRRA   3'  CCAGGGCTTCCCCATCAG    15481        A    A_
                                CTGATGGG AAGT  TGG
                                |||||||| ||||  |||
                                GACTACCC TTCG  ACC
                                     C    GG
GAM823  HLA-C   3'  CCCCACACTGACCTGTGTT   92103      TGAT   AA   A
                                AACAC    GGG  AGT TGGGG
                                |||||    |||  ||| |||||
                                TTGTG    TCC  TCA ACCCC
                                   _____  AG   C
GAM823  HMG20A  3'  CCCAGTCTTCTCCCATCATTG  36537    C       _   TA
                                CA TGATGGGA AAG  TGGG
                                || |||||||| |||  ||||
                                GT ACTACCCT TTC  ACCC
                                  T       C   TG
GAM823  HOXB5   3'  CCCCTCCCCATCTGTGTT    9265       T     AAAGTAT
                                AACAC GATGGG      GGGG
                                ||||| ||||||      ||||
                                TTGTG CTACCC      CCCC
                                   T     CT_____
GAM823  IDH3B   3'  TCCCCATACCCTTCAGTGCAGT 22579       ATGG   A_
              GT                  ACACTG   GAA  GTATGGGGA
                                ||||||   |||  |||||||||
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                                TGTGAC   CTT  CATACCCCT
                                   GTGA   CC
GAM823  IL1R1   3'  CCCATGCTTTCCCACCAG    6056     A
                                CTG TGGGAAAGTATGGG
                                ||| ||||||||||||||
                                GAC ACCCTTTCGTACCC
                                  C
GAM823  ITGA3   3'  CCCCTCCTCCCCCAGTGT    9376       AT   AAGTAT
                                ACACTG  GGGA    GGGG
                                ||||||  ||||    ||||
                                TGTGAC  CCCT    CCCC
                                   C_   CCT___
GAM823  ITGA3   3'  CCCCTCCTCCCCCAGTGT    18538      AT   AAGTAT
                                ACACTG  GGGA    GGGG
                                ||||||  ||||    ||||
                                TGTGAC  CCCT    CCCC
                                   C_   CCT___
GAM823  LIMD1   3'  CCCTCTCTTCCCATCA      26456        A TAT
                                TGATGGGAA G   GGGG
                                |||||||||  |   ||||
                                ACTACCCTT C   TCCC
                                      _ TC_
GAM823  MAZ     3'  CCCCTCTTTTCCCACCA     73387    A      TAT
                                TG TGGGAAAG   GGGG
                                || ||||||||   ||||
                                AC ACCCTTTT   CCCC
                                 C       CT_
GAM823  MFAP4   3'  TCCCCATACCCTCTGGGTGTT  69257      GAT   AAA
                                AACACT   GGG   GTATGGGGA
                                ||||||   |||   |||||||||
                                TTGTGG   TCC   CATACCCCT
                                   GTC   ___
GAM823  MKI67   3'  CCTGGAACTTTCCCACCAG    10042    A       A_
                                CTG TGGGAAAGT  TGGG
                                ||| |||||||||  ||||
                                GAC ACCCTTTCA  GTCC
                                  C        AG
GAM823  MPL     3'  TCCCCACACTTCCCATT     18157        A  A
                                GATGGGAA GT TGGGGA
                                |||||||| || ||||||
                                TTACCCTT CA ACCCCT
                                      _  C
GAM823  PIG3    5'  TCCCGCCGTTCCCATCTGTGTT 16878      T      AGTA
                                AACAC GATGGGAA    TGGGG
                                ||||| ||||||||    |||||
                                TTGTG CTACCCTT    GCCCT
                                   T       GCC_
GAM823  PODXL   3'  TCCCGGGGCCCCCCCATCAG   18239       AAA  A_
                                CTGATGGG   GT  TGGGG
                                ||||||||   ||  |||||
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                                GACTACCC  CG  GCCCT
                                    CC_  GG
GAM823  RORA    5'  CCCCATACTCCTCCCCATCA  11376       AA__
                                TGATGGG   AGTATGGGG
                                |||||||   |||||||||
                                ACTACCC   TCATACCCC
                                    CTCC
GAM823  RORA    5'  CCCCATACTCCTCCCCATCA  56135       AA__
                                TGATGGG   AGTATGGGG
                                |||||||   |||||||||
                                ACTACCC   TCATACCCC
                                    CTCC
GAM823  RTN4R   3'  CCCCATCTCCACCCCATCATGT 43431     C     AA__  T
          T                      AACA TGATGGG   AG ATGGGG
                                |||| |||||||   || ||||||
                                TTGT ACTACCC   TC TACCCC
                                  _     CACC  _
GAM823  SIAT1   3'  TCTATCTCTCCCATCAG    11664         A  T
                                CTGATGGGA AG ATGGG
                                ||||||||| || |||||
                                GACTACCCT TC TATCT
                                    C  _
GAM823  SPARC   3'  TCCCCTTCGTGTTTCCCCCAAT 11899     C  AT    GTAT__
          GTT                     AACA TG  GGGAAA    GGGGA
                                |||| ||  ||||||     |||||
                                TTGT AC  CCCTTT    CCCCT
                                  A  C_    GTGCTT
GAM823  TCF2    3'  TCCATACTTTCCCACAG    21385    A
                                CTG TGGGAAAGTATGGG
                                ||| ||||||||||||||
                                GAC ACCCTTTCATACCT
                                  _
GAM823  TEGT    3'  TCCGCTTTCCCACCAG     64626    A       AT
                                CTG TGGGAAAGT  GGG
                                ||| |||||||||  |||
                                GAC ACCCTTTCG  CCT
                                  C       __
GAM823  THY1    3'  CCCCTCGCCCATCAGTG    20810         AAAGTAT
                                CACTGATGGG     GGGG
                                ||||||||||     ||||
                                GTGACTACCC     CCCC
                                    GCT_____
GAM823  TMOD2   3'  CTTCTTCCCCATCAG     27248        A   TATG
                                CTGATGGG AAG   GGG
                                |||||||| |||   |||
                                GACTACCC TTC   TTC
                                    C  _____
GAM823  VDR     3'  CCCCACCCCCTTCAGTG    4568        T   AAAGTA
                                CACTGA GGG    TGGGG
                                |||||| |||    |||||
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                                GTGACT CCC     ACCCC
                                   T  CC____
GAM823  ZNF137   3'  TCCTCTATTTCCCATCA     12867         GTAT
                                TGATGGGAAA   GGGGA
                                ||||||||||   |||||
                                ACTACCCTTT   CTCCT
                                     AT__
GAM823  ACAA2    5'  TCCCTGTGTACCTCCCTCAG  91769     T   AA   __
                                CTGA GGGA  GTAT  GGGGA
                                |||| ||||  ||||  |||||
                                GACT CCCT  CATG  TCCCT
                                  _   C_   TG
GAM823  BRD4     3'  TTCCTTCCCACCTGTGTT    54279      TGA     AGTAT
                                AACAC   TGGGAA    GGGG
                                |||||   ||||||    ||||
                                TTGTG   ACCCTT    CCTT
                                   TCC     _____
GAM823  C20orf112 3'  TCCCCATACCTAACATTCCAT  54646       AA____
                                ATGGGA     GTATGGGGA
                                ||||||     |||||||||
                                TACCTT     CATACCCCT
                                   ACAATC
GAM823  CDC37    3'  CTGCAGCCCCCCATCAG     22957        AAA  A  G
                                CTGATGGG   GT TG GG
                                ||||||||   || || ||
                                GACTACCC   CG AC TC
                                     CC_  _  G
GAM823  CDH22    3'  CCCCAGGTTTCCCCCATCAGAG 41155     A      A_   TA
          TT                     AAC CTGATGGG  AAG  TGGGG
                                |||  ||||||||  |||  |||||
                                TTG GACTACCC  TTT  ACCCC
                                  A       CC   GG
GAM823  CRR9     3'  TCCCAAGTTCCCATCACGT    47881    _       AGTA
                                AC TGATGGGAA    TGGGG
                                || |||||||||    |||||
                                TG ACTACCCTT    ACCCT
                                 C        GA__
GAM823  CXYorf1  3'  CCGCTTTCTCATCAGTG     82044             AT
                                CACTGATGGGAAAGT  GG
                                ||||||||||||||  ||
                                GTGACTACTCTTTCG  CC
                                                __
GAM823  DCTN3    3'  CCCTCCCCCCCAATCAGTGTT  23373         _  AAAGTAT
                                AACACTGAT GGG      GGGG
                                ||||||||| |||      ||||
                                TTGTGACTA CCC      TCCC
                                     A  CCC_____
GAM823  DCTN3    3'  CCCTCCCCCCCAATCAGTGTT  44309         _  AAAGTAT
                                AACACTGAT GGG      GGGG
                                ||||||||| |||      ||||
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                                TTGTGACTA CCC      TCCC
                                     A   CCC____
GAM823   DKFZP434H132 5'  TCCCTGTACCCCCCCAGCA   73610    A   AAA
                                TG TGGG   GTATGGGGA
                                || ||||   |||||||||
                                AC ACCC   CATGTCCCT
                                 G    CCC
GAM823   DKFZP434J1813 5'  TCCACGCCTTTCCCACAATG   61791    C  A     _ TA
                                CA TG TGGGAAA G  TGGG
                                || || ||||||| |  ||||
                                GT AC ACCCTTT C  ACCT
                                 A  _      C GC
GAM823   DKFZP566G1424 5'  TCCCCATACCTAACATTCCAT  84790       AA____
                                ATGGGA     GTATGGGGA
                                ||||||     |||||||||
                                TACCTT     CATACCCCT
                                    ACAATC
GAM823   EIF4B    3'  CCCTTCTCCCATCAGT      75967          AAGTAT
                                ACTGATGGGA     GGGG
                                ||||||||||     ||||
                                TGACTACCCT     TCCC
                                     CT____
GAM823   FLJ13993  3'  TCCAAGACCTTTCCCATCCATG 60465    CT        TATGG
                                CA  GATGGGAAAG    GGA
                                ||  ||||||||||    |||
                                GT  CTACCCTTTC    CCT
                                 AC         CAGAA
GAM823   FLJ14665  3'  TCCTGCTTCCCTCCCATCA   51512        ___    T
                                TGATGGGA   AAGTA GGG
                                ||||||||   ||||| |||
                                ACTACCCT   TTCGT CCT
                                     CCC    _
GAM823   FLJ30473  5'  TCCGACAGCTCCCCATCTGTG  58465     T     AA   A  G_
                                CAC GATGGG  AGT TG  GGA
                                ||| ||||||  ||| ||  |||
                                GTG CTACCC  TCG AC  CCT
                                  T     C_  _  AG
GAM823   HEMK     3'  TCCCAAGGCCCCATCAGTG   32440         AAA  ATG
                                CACTGATGGG   GT   GGGA
                                ||||||||||   ||   ||||
                                GTGACTACCC   CG   CCCT
                                     ____  GAA
GAM823   HSA9947   3'  CCCCAGCTCCCCTCAGTG    42021       T   AA  A
                                CACTGA GGGA  GT TGGGG
                                |||||| ||||  || |||||
                                GTGACT CCCT  CG ACCCC
                                    C    __  _
GAM823   HUMAGCGB  5'  CCCCACACCTTCTGTACTCAG  25229      TG__    A  A
                                CTGA    GGAA GT TGGGG
                                ||||    |||| || |||||
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                                GACT    TCTT CA ACCCC
                                  CATG    C  C
GAM823  JDD1     3'  CCCCATACCTTGGGAG     63217    GA    AAA
                                CT  TGGG   GTATGGGG
                                ||  ||||   ||||||||
                                GA  GTTC   CATACCCC
                                 GG    ___
GAM823  KIAA0254 3'  TCCCCATACCTTCCCCTCATGT 28601      _   T     A
          GT                     ACAC TGA GGGAA GTATGGGGA
                                |||| ||| ||||| |||||||||
                                TGTG ACT CCCTT CATACCCCT
                                  T  C    C
GAM823  KIAA0450 5'  CCCCATGTGTCCCCAGTG    27628      AT    AAG
                                CACTG  GGGA   TATGGGG
                                |||||  ||||   |||||||
                                GTGAC  CCCT   GTACCCC
                                  __    GT_
GAM823  KIAA0470 3'  CCCCTTGACCCCATCAGT    29055        AAA  AT_
                                ACTGATGGG   GT   GGGG
                                |||||||||   ||   ||||
                                TGACTACCC   CA   CCCC
                                     ___  GTT
GAM823  KIAA1055 3'  CCCTTCCATCAGTGT       66060          AAGTAT
                                ACACTGATGGGA     GGG
                                ||||||||||||     |||
                                TGTGACTACCTT     CCC
                                          _______
GAM823  KIAA1297 3'  CCCCACACCCCCGTCAGT    72174         AAA  A
                                ACTGATGGG   GT TGGGG
                                |||||||||   || |||||
                                TGACTGCCC   CA ACCCC
                                     C__  C
GAM823  KIAA1319 3'  TCCCCATACCCCTCCAGT    40409      AT   AAA
                                ACTG  GGG   GTATGGGGA
                                ||||  |||   |||||||||
                                TGAC  CCC   CATACCCCT
                                  CT   ___
GAM823  KIAA1467 3'  TCCTTATTCTTTCCCACCTGT  71616    TGA       T
                                AC   TGGGAAAG ATGGGGA
                                ||   |||||||| |||||||
                                TG   ACCCTTTC TATTCCT
                                 TCC       T
GAM823  KIAA1821 3'  TCGTGCACTCCCCCATCCATG  71797    CT     AAA__
                                CA  GATGGG    GTATGG
                                ||  ||||||    ||||||
                                GT  CTACCC    CGTGCT
                                 AC     CCTCA
GAM823  KIAA1879 5'  CCTGCCCTCCCATCAGTGT    73567           AA   T
                                ACACTGATGGGA  GTA GG
                                ||||||||||||  ||| ||
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                                TGTGACTACCCT  CGT CC
                                      CC  _
GAM823  LAT1-3TM  5'  CCCTCCTCCATCAGTGT     68599          AAAGTAT
                                ACACTGATGGG     GGGG
                                ||||||||||      ||||
                                TGTGACTACCT     TCCC
                                      CC_____
GAM823  LAT1-3TM  3'  CCCTCCTCCATCAGTGT     48314          AAAGTAT
                                ACACTGATGGG     GGGG
                                ||||||||||      ||||
                                TGTGACTACCT     TCCC
                                      CC_____
GAM823  MAP2K5    3'  CCCCATACCTTCTGGTT     10863     G    A
                                GAT GGAA GTATGGGG
                                ||| |||| ||||||||
                                TTG TCTT CATACCCC
                                  G    C
GAM823  MGC15437  3'  CCCCATACACCAGTGTT     51780       ATGGGAAA
                                AACACTG       GTATGGGG
                                |||||||       ||||||||
                                TTGTGAC       CATACCCC
                                    CA_______
GAM823  MRPS34    3'  TCCCTTTCCCCCATTAGTG   43740         AAAGTAT
                                CACTGATGGG      GGGGA
                                ||||||||||      |||||
                                GTGATTACCC      TCCCT
                                      CCTT___
GAM823  NCOA2     3'  CCCCATACTCCCTATT      21545       AA
                                GATGGG  AGTATGGGG
                                ||||||  |||||||||
                                TTATCC  TCATACCCC
                                   C_
GAM823  PI4KII    3'  TCCATCTCCCATCAGTG     37347          AA T
                                CACTGATGGGA  G ATGGG
                                ||||||||||  | |||||
                                GTGACTACCCT  C TACCT
                                      __ _
GAM823  PIG11     3'  CCCCAAGCTGCCATCAATGT   61612     C     GAA   A
                                ACA TGATGG   AGT TGGGG
                                |||  ||||||   ||| |||||
                                TGT ACTACC   TCG ACCCC
                                  A     G__   A
GAM823  RAI15     3'  CCCCAACCCCCACCAG      66666     A   AAA  A
                                CTG TGGG   GT TGGGG
                                |||  ||||   ||  |||||
                                GAC ACCC   CA ACCCC
                                  C    C__  _
GAM823  TP53TG3   3'  ACTTTCCCACCAGTGT      31101       A
                                ACACTG TGGGAAAGT
                                ||||||  |||||||||
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                                TGTGAC ACCCTTTCA
                                   C
GAM823  LOC116113 3'  TCCCCATGTATTCCCCACCTGT 92221      TGAT_    AG
           GTT                   AACAC    GGGAA  TATGGGGA
                                 |||||    |||||  ||||||||
                                 TTGTG    CCCTT  GTACCCCT
                                    TCCAC    AT
GAM823  LOC128954 5'  CCCAGCTGCTCCCATCAG    75796        A_  A
                                 CTGATGGGA  AGT TGGG
                                 |||||||||  ||| ||||
                                 GACTACCCT  TCG ACCC
                                       CG  _
GAM823  LOC129138 3'  TCCTGTGCCTCTCACCAG    57125    A    AA
                                 CTG TGGGA  GTATGGGG
                                 ||| |||||  ||||||||
                                 GAC ACTCT  CGTGTCCT
                                   C    C_
GAM823  LOC144114 5'  TCCAGCTTTCCCCTCAATG    82211    C  T      A
                                 CA TGA GGGAAAGT TGGG
                                 || ||| |||||||| ||||
                                 GT ACT CCCTTTCG ACCT
                                  A  C      _
GAM823  LOC145622 3'  TCCACTTTACCATCAGTGTT   77315         G    AT
                                 AACACTGATGG AAAGT  GGG
                                 ||||||||||| |||||  |||
                                 TTGTGACTACC TTTCA  CCT
                                       A    __
GAM823  LOC145719 3'  TCCCCATGAAATCCACCAGGTG 83456      GATG   AAG
           T                      ACACT    GGA   TATGGGGA
                                  |||||    |||   ||||||||
                                  TGTGG    CCT   GTACCCCT
                                     ACCA   AAA
GAM823  LOC145720 3'  TCCCCATGAAATCCACCAGGTG 83438      GATG   AAG
           T                      ACACT    GGA   TATGGGGA
                                  |||||    |||   ||||||||
                                  TGTGG    CCT   GTACCCCT
                                     ACCA   AAA
GAM823  LOC146176 5'  TCCATGCCTTCGCATCAATG   77698    C    G   A
                                 CA TGATG GAA GTATGGG
                                 || ||||| ||| |||||||
                                 GT ACTAC CTT CGTACCT
                                  A    G   C
GAM823  LOC149301 5'  TCTGCACCTTCCCCATCAG    79252        A   TA  G
                                 CTGATGGG AAG  TG GGA
                                 |||||||| |||  || |||
                                 GACTACCC TTC  AC TCT
                                       C   C_  G
GAM823  LOC149478 3'  TCCCCAGCTCTGCCCCCATCGT 79383      T     AA_  TA_
           GTT                    AACAC GATGGG   AG   TGGGGA
                                  ||||| ||||||   ||   ||||||
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                                TTGTG CTACCC  TC  ACCCCT
                                  _    CCG  TCG
GAM823  LOC149506 3'  CCCCTCCCCATCAGTGT    84457         AAAGTAT
                                ACACTGATGGG     GGGG
                                ||||||||||     ||||
                                TGTGACTACCC     CCCC
                                     CT_____
GAM823  LOC157737 5'  CCCCACACCAGTGTTCATCAGT 86540        AAA__  A
                                ACTGATGGG    GT TGGGG
                                |||||||||    || |||||
                                TGACTACTT    CA ACCCC
                                     GTGAC  C
GAM823  LOC161244 3'  CCCCAGATCTCCCCGTCAG   87079        AA  TA_
                                CTGATGGG  AG   TGGGG
                                ||||||||  ||   |||||
                                GACTGCCC  TC   ACCCC
                                    C_  TAG
GAM823  LOC161244 3'  CCCCAGATCTCCCCGTCAG   87080        AA  TA_
                                CTGATGGG  AG   TGGGG
                                ||||||||  ||   |||||
                                GACTGCCC  TC   ACCCC
                                    C_  TAG
GAM823  LOC163944 5'  TCCCCGGGCTCCCATCAGTG   87048         AA  A
                                CACTGATGGGA  GT TGGGGA
                                ||||||||||  || ||||||
                                GTGACTACCCT  CG GCCCCT
                                     __  G
GAM823  LOC197114 3'  TCCCCATGAAATCCACCAGGTG 89709      GATG   AAG
          T                    ACACT   GGA   TATGGGGA
                               |||||   |||   ||||||||
                               TGTGG   CCT   GTACCCCT
                                  ACCA   AAA
GAM823  LOC197117 3'  TCCCCATAAAATCCACCAGGTG 89724      GATG   AAG
          T                    ACACT   GGA   TATGGGGA
                               |||||   |||   ||||||||
                               TGTGG   CCT   ATACCCCT
                                  ACCA   AAA
GAM823  LOC197363 5'  CCCCACAGTCACCTGTGTT   88056      TGAT  _  AAGTA
                                AACAC   GG GA    TGGGG
                                |||||   || ||    |||||
                                TTGTG   CC CT    ACCCC
                                  T___  A  GAC__
GAM823  LOC197423 5'  CCCTCCTCCATCAGTGT    77858         AAAGTAT
                                ACACTGATGGG     GGGG
                                ||||||||||     ||||
                                TGTGACTACCT     TCCC
                                     CC_____
GAM823  LOC201633 3'  TACTCTCCATCAGTG      90238         AA
                                CACTGATGGG  AGTA
                                |||||||||  ||||
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                                GTGACTACCT  TCAT
                                      C_
GAM823  LOC219754 3'  TCCTGCTTCCCCCCATCAG   91354       A__    T
                                CTGATGGG   AAGTA GGG
                                ||||||||   ||||| |||
                                GACTACCC   TTCGT CCT
                                     CCC    _
GAM823  LOC220469 3'  TCCTGTCCCTCCCATCAG    76387       AAGT
                                CTGATGGGA   ATGGGG
                                |||||||||   ||||||
                                GACTACCCT   TGTCCT
                                      CCC_
GAM823  LOC220565 5'  CCCTCCTCCATCAGTGT     90749        AAAGTAT
                                ACACTGATGGG     GGGG
                                ||||||||||      ||||
                                TGTGACTACCT     TCCC
                                      CC_____
GAM823  LOC220766 3'  CCCCTTGACCCCATCAGT    90795       AAA  AT_
                                ACTGATGGG   GT   GGGG
                                |||||||||   ||   ||||
                                TGACTACCC   CA   CCCC
                                     ___  GTT
GAM823  LOC221399 5'  TCCCCATACTGAATCAGCTGT  93851    _    GGGAA
                                ACA CTGAT    AGTATGGGGA
                                ||| |||||    ||||||||||
                                TGT GACTA    TCATACCCCT
                                  C    AG___
GAM823  LOC221463 3'  CCACCTGCCCATCAGCGT    92068    A      AAAGTAT _
                                AC CTGATGGG      GG GG
                                || ||||||||      || ||
                                TG GACTACCC      CC CC
                                 C       GT_____  A
GAM823  LOC253148 5'  CCCCACACCTCCCATCA     96875       AA  A
                                TGATGGGA  GT TGGGG
                                ||||||||  || |||||
                                ACTACCCT  CA ACCCC
                                     C_  C
GAM823  LOC256273 3'  TCAGGGCCTTTCCCACCTGTG  96408    TGA      TA__
                                CAC   TGGGAAAG    TGG
                                |||   ||||||||    |||
                                GTG   ACCCTTTC    ACT
                                  TCC       CGGG
GAM823  LOC51008  3'  TCCCCATAGATTCACCATT   31972      _  AG
                                GATGG GAA  TATGGGGA
                                ||||| |||  ||||||||
                                TTACC CTT  ATACCCCT
                                   A   AG
GAM823  LOC56834  5'  CCGGCTCTCCCATCAG      39341        A   A
                                CTGATGGGA AGT TGG
                                ||||||||| ||| |||
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                                GACTACCCT TCG GCC
                                     C  _
GAM823  LOC85414  3' CCCCAACTTTCCCCACCAG   52396    AT_     A
                                CTG  GGGAAAGT TGGGG
                                |||  |||||||| |||||
                                GAC  CCCTTTCA ACCCC
                                  CAC      _
GAM823  LOC90462  3' CCACCTTTCCCATCAGT    62901          TA
                                ACTGATGGGAAAG  TGG
                                ||||||||||||  |||
                                TGACTACCCTTTC  ACC
                                       C_
GAM823  LOC90841  3' TCCATTTTCCCCCAG      64203    AT    GT
                                CTG  GGGAAA  ATGGG
                                |||  ||||||  |||||
                                GAC  CCCTTT  TACCT
                                  C_    __
GAM823  LOC91040  3' CCGCTTTCTCATCAGTG    64714          AT
                                CACTGATGGGAAAGT  GG
                                ||||||||||||||  ||
                                GTGACTACTCTTTCG  CC
                                          __
GAM823  LOC91301  3' CCCCACCGCCCCCCATCAG   65540       AAA  A_
                                CTGATGGG   GT  TGGGG
                                ||||||||   ||  |||||
                                GACTACCC   CG  ACCCC
                                     CC_  CC
GAM823  LOC93380  3' TCCCTGCCCCCCATTAGT    72202       AAA   T
                                ACTGATGGG   GTA GGGG
                                |||||||||   ||| ||||
                                TGATTACCC   CGT CCCT
                                     C__  _
GAM824  CALCRL    3' CTAACCTGACATCACCA     19388    CAA     GC   C
                                TGG   GATGTCG  GGT AG
                                |||   |||||||  ||| ||
                                ACC   CTACAGT  CCA TC
                                  A__      __  A
GAM824  CSHL1     3' ACTCTATTCCGACATCCTCCA  7164    CAA     CGGTC
                                TGG   GATGTCGG    AGT
                                |||   ||||||||    |||
                                ACC   CTACAGCC    TCA
                                  TC_      TTATC
GAM824  MAP1A     3' ACTGCCTGACATCCCA      9895    CAA    _
                                TGG   GATGTC GGCGGT
                                |||   |||||| ||||||
                                ACC   CTACAG CCGTCA
                                  ____     T
GAM824  RAG1      3' ACTGAAACATTTTGCCA     4809          CGG
                                TGGCAAGATGT   CGGT
                                ||||||||||   ||||
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                                ACCGTTTTACA  GTCA
                                      AA_
GAM824  C1QR1    3'  ACTGTTGACATCCTCCA    23834    CAA
                                TGG  GATGTCGGCGGT
                                |||  ||||||||||||
                                ACC  CTACAGTTGTCA
                                  TC_
GAM824  DKFZP564O0423 3'  ACCAAGGACTTCTTGCCA    91675       T  GGC
                                TGGCAAGA GTC  GGT
                                |||||||| |||  |||
                                ACCGTTCT CAG  CCA
                                     T  GAA
GAM824  DKFZP586F1524 3'  CTGACCGACCATTGCCA    31490      GATGTC  _
                                TGGCAA    GG CGGTCAG
                                ||||||    || |||||||
                                ACCGTT    CC GCCAGTC
                                   A_____  A
GAM824  FBXO26   5'  ACCGACCGCCCAGACCGCC   46092    AAGAT  __     A
                                GGC   GTC  GGCGGTC GT
                                |||   |||  ||||||| ||
                                CCG   CAG  CCGCCAG CA
                                  C____  AC     C
GAM824  FLJ10120  3'  ACTGACAAACTCATCTTGGCA  35829   G     TCGGCG
                                TG CAAGATG    GTCAGT
                                || |||||||    ||||||
                                AC GTTCTAC    CAGTCA
                                 G     TCAAA_
GAM824  HIF1AN   3'  ACTGGACTCTTGCCA     61967       T  GG
                                TGGCAAGA GTC  CGGT
                                |||||||| |||  ||||
                                ACCGTTCT CAG  GTCA
                                      _  __
GAM824  PDZD2    3'  ACTGCTACTACATCTTGCCA  80856         C  CG T
                                TGGCAAGATGT GG  G CAGT
                                |||||||||| ||  | ||||
                                ACCGTTCTACA TC  C GTCA
                                      _  AT _
GAM824  RNF8     3'  ACTGACCATTCCATCCCA   14213    CAA   TCGGC
                                TGG  GATG   GGTCAGT
                                |||  ||||   |||||||
                                ACC  CTAC   CCAGTCA
                                  ___   CTTA_
GAM824  TNKS1BP1  3'  ACCAATGACATTTTGCCA   53001          GC
                                TGGCAAGATGTCG  GGT
                                ||||||||||||  |||
                                ACCGTTTTACAGT  CCA
                                       AA
GAM824  UPLC1    3'  ACTAACATCTCAACTTGCCA  34720       A  TCGGCG  C
                                TGGCAAG TG    GT AGT
                                ||||||| ||    || |||
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                                ACCGTTC AC     CA TCA
                                    A  TCTA__  A
GAM824   LOC146059 3'  ACTGCCTGGCATCCCACCA   77618     CAA     _
                                TGG   GATGTC GGCGGT
                                |||   |||||| ||||||
                                ACC   CTACGG CCGTCA
                                  ACC     T
GAM824   LOC146433 3'  TGCCACATCTTGCCA      77878           C
                                TGGCAAGATGT GGCG
                                |||||||||||| ||||
                                ACCGTTCTACA CCGT
                                          _
GAM824   LOC147172 3'  ACTAAGTTACATCTTGCC    78294          C   GGTC
                                GGCAAGATGT GGC    AGT
                                |||||||||| |||    |||
                                CCGTTCTACA TTG    TCA
                                      _   AA__
GAM824   LOC149302 5'  ACCATGACATTTGCCA      79268       A      GC
                                TGGCA GATGTCG  GGT
                                ||||| |||||||  |||
                                ACCGT TTACAGT  CCA
                                   _      A_
GAM824   LOC154761 3'  ACTGACCGCTCAGTCCTGTCCA 81121     _  A   GTC
                                TGG CA GAT   GGCGGTCAGT
                                ||| || |||   ||||||||||
                                ACC GT CTG   TCGCCAGTCA
                                  T  C   AC_
GAM824   LOC200473 5'  ACTAACCTGTTCCACACCTTGG 90071    G    A   C  C___   C
            CA                    TG CAAG TGT GG    GGT AGT
                                || |||| ||| ||    ||| |||
                                AC GTTC ACA CC    CCA TCA
                                 G    C   _  TTGT   A
GAM824   LOC220558 5'  ACTAACCGCCGACCAACCGCCA 91136      AAGAT        C
                                TGGC     GTCGGCGGT AGT
                                ||||     ||||||||| |||
                                ACCG     CAGCCGCCA TCA
                                  CCAAC        A
GAM824   LOC253187 5'  ACCAGGAGGCATCTTGCCA    97109           GGC_
                                TGGCAAGATGTC    GGT
                                ||||||||||||    |||
                                ACCGTTCTACGG    CCA
                                      AGGA
GAM824   LOC253573 3'  ACCGTGGACATCTTCCCA     97045     C       G
                                TGG AAGATGTC GCGGT
                                ||| |||||||| |||||
                                ACC TTCTACAG TGCCA
                                  C       G
GAM824   LOC253962 5'  ACTGCTGACATCCCCCA      96655     CAA
                                TGG   GATGTCGGCGGT
                                |||   ||||||||||||
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                                ACC   CTACAGTCGTCA
                                  CC_
GAM825  ACADS    3'  CACTGTGCCTCAAGTTCCT   3407        AA  A   GG
                                AGGAACTT  GA GTAT  AGTG
                                ||||||||  || ||||  ||||
                                TCCTTGAA  CT CGTG  TCAC
                                    __  C   __
GAM825  ATP2A3   3'  CACCGACATCCTCAGGTTCCT  17720        A  AAGT   GA_
                                AGGAACTT AG   ATG   GTG
                                |||||||| ||   |||   |||
                                TCCTTGGA TC   TAC   CAC
                                    C  C___   AGC
GAM825  CASP10   3'  CATACTTCTAAAATTCC     52091     C  A
                                GGAA TT AGAAGTATG
                                |||| || |||||||||
                                CCTT AA TCTTCATAC
                                  A  A
GAM825  CTSK     3'  CTCACTTCCTAAGTTCC     4622         A    ATG
                                GGAACTTA GAAGT   GAG
                                |||||||| |||||   |||
                                CCTTGAAT CTTCA   CTC
                                    C    ___
GAM825  DUOX2    3'  CACTTCGTCTCCCCTAGCTCCT 26020     A  TAAGA  T
                                AGGA CT    AG ATGGAGTG
                                |||| ||    || ||||||||
                                TCCT GA    TC TGCTTCAC
                                  C  TCCCC  _
GAM825  GRIK5    3'  CACTCCTTCCCAGGCTCC    9133     A   AA   GTAT
                                GGA CTT  GAA   GGAGTG
                                ||| |||  |||   ||||||
                                CCT GGA  CTT   CCTCAC
                                  C   CC  ____
GAM825  MLF2     3'  CACTCCATCTTCAAACCCCCT  18373    AACTTAA   T
                                AGG      GAAG ATGGAGTG
                                |||      |||| ||||||||
                                TCC      CTTC TACCTCAC
                                  CCCAAA_   _
GAM825  RAD1     5'  TCACTGCAGTTTCAAGTTCCT  55913       AA   GTA  G
                                AGGAACTT  GAA   TG AGTGA
                                ||||||||  |||   || |||||
                                TCCTTGAA  CTT   AC TCACT
                                    __   TG_  G
GAM825  UBE2V1   3'  CTCCTCCTCAAGTTCCT     41793        A  AAGTAT
                                AGGAACTT AG     GGAG
                                |||||||| ||     ||||
                                TCCTTGAA TC     CCTC
                                    C  CT____
GAM825  UBE2V1   3'  CTCCTCCTCAAGTTCCT     42370        A  AAGTAT
                                AGGAACTT AG     GGAG
                                |||||||| ||     ||||
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                                TCCTTGAA TC     CCTC
                                    C  CT____
GAM825  UBE2V1   3'  CTCCTCCTCAAGTTCCT     12518        A  AAGTAT
                                AGGAACTT AG     GGAG
                                |||||||| ||     ||||
                                TCCTTGAA TC     CCTC
                                    C  CT____
GAM825  VIPR1    3'  TCACCATTGCTGTCAAGTTCCT 16116        AAGA   TGGA
                                AGGAACTT   AGTA   GTGA
                                ||||||||   ||||   ||||
                                TCCTTGAA   TCGT   CACT
                                    CTG_   TAC_
GAM825  ZNF142   3'  CACTCCATCAAAGTCCCT    17432    A   AAGAAGT
                                AGG ACTT      ATGGAGTG
                                ||| ||||      ||||||||
                                TCC TGAA      TACCTCAC
                                  C   AC_____
GAM825  ZNF266   3'  CACTCCATATTTGTAAGCCCT  88322    AA   AG
                                AGG  CTTA  AAGTATGGAGTG
                                |||  ||||  ||||||||||||
                                TCC  GAAT  TTTATACCTCAC
                                  C_   G_
GAM825  AMOTL2   3'  CTCCTCCTCAAGTTCCT     32482        A  AAGTAT
                                AGGAACTT AG     GGAG
                                |||||||| ||     ||||
                                TCCTTGAA TC     CCTC
                                    C  CT____
GAM825  BCL2L1   3'  CACCCCACACTTGTTCC     56803      TTAAG   A  A
                                GGAAC    AAGT TGG GTG
                                |||||    |||| ||| |||
                                CCTTG    TTCA ACC CAC
                                   _____   C  C
GAM825  C(27)-3BETA-HSD 3'  CACCTCTCTACCTAAGTTCCT  47270         AGAA  T  _
                                AGGAACTTA   GTA GGAG TG
                                |||||||||   ||| |||| ||
                                TCCTTGAAT   CAT TCTC AC
                                     C___   C   C
GAM825  C21orf69  3'  TCACCCCATACTCTGTCACTGC 54215    AACTTA_  A    A
          C                   GG      AGA GTATGG GTGA
                              ||      ||| |||||| ||||
                              CC      TCT CATACC CACT
                               GTCACTG  _     C
GAM825  CLSTN2   3'  CACTTCTGCCCTAAGTTCC    42129        AGAA  T
                                GGAACTTA   GTA GGAGTG
                                ||||||||   ||| ||||||
                                CCTTGAAT   CGT CTTCAC
                                    CC__   _
GAM825  DKFZP434J037 3'  CACTCCACACTCTTGAGTCTCT 48206    GA      A  A
                                AG  ACTTAAGA GT TGGAGTG
                                ||  |||||||| || |||||||
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                                TC  TGAGTTCT CA ACCTCAC
                                 TC       _  C
GAM825  DKFZP566I1024 3'  TCACTCTAGCCTTGAATTCCT  70107      C    AAGTA
                                AGGAA TTAAG    TGGAGTGA
                                ||||| |||||    ||||||||
                                TCCTT AGTTC    ATCTCACT
                                   A    CG___
GAM825  ERN1     3'  TCAGACTTTTTAAATTCCT   7519       C       A
                                AGGAA TTAAGAAGT TGG
                                ||||| ||||||||| |||
                                TCCTT AATTTTTCA ACT
                                   A       G
GAM825  FLJ10292  3'  TCACTTCAGTTTCCCAGTTCCT 35976       TAA   GTA
                                AGGAACT   GAA   TGGAGTGA
                                |||||||   |||   ||||||||
                                TCCTTGA   CTT   ACTTCACT
                                    CC_   TG_
GAM825  FLJ10925  3'  CCAGTATTCCCCGAGTTCCT   36882       AA_   GTA
                                AGGAACTT   GAA   TGG
                                ||||||||   |||   |||
                                TCCTTGAG   CTT   ACC
                                    CCC   ATG
GAM825  FLJ14082  3'  CACTCCTGAGACCCAAGGTTCC 46671        AAGAAGTAT
          T                      AGGAACTT        GGAGTG
                                |||||||         ||||||
                                TCCTTGGA        CCTCAC
                                    ACCCAGAGT
GAM825  FLJ20275  3'  CCAACCCTTAAGTTCCT     34820          AA  A
                                AGGAACTTAAG  GT TGG
                                ||||||||||  || |||
                                TCCTTGAATTC  CA ACC
                                     C_  _
GAM825  FLJ21742  3'  CACCCTGGCCCTCAGGTTCCT  49844        A  AA  AT  A
                                AGGAACTT AG  GT  GG GTG
                                |||||||| ||  ||  || |||
                                TCCTTGGA TC  CG  CC CAC
                                    C  C_  GT  _
GAM825  FLJ23071  3'  CACTCCCTTCCCAAGTTCCT   47263        AA    TAT
                                AGGAACTT  GAAG   GGAGTG
                                ||||||||  ||||   ||||||
                                TCCTTGAA  CTTC   CCTCAC
                                    CC    ___
GAM825  KIAA0255  3'  CACCCCACACCTGAGTTCTT   28465        AGAA  A   A
                                AGGAACTTA    GT TGG GTG
                                |||||||||    || ||| |||
                                TTCTTGAGT    CA ACC CAC
                                     C___  C   C
GAM825  KIAA0444  3'  CCACCTTCCGAAGCTCCT    62338      A   AA    TA
                                AGGA CTT  GAAG  TGG
                                ||||  |||  ||||  |||
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                                TCCT GAA  CTTC  ACC
                                  C   GC    C_
GAM825  KIAA1319 3' CCATACCCCTCCAGTTCCT   40405       TA  AA
                                AGGAACT  AG  GTATGG
                                |||||||  ||  ||||||
                                TCCTTGA  TC  CATACC
                                   CC  CC
GAM825  KIAA1535 3' CATACTTCTAAGTTCC      79410        A
                                GGAACTTA GAAGTATG
                                |||||||| ||||||||
                                CCTTGAAT CTTCATAC
                                         _
GAM825  KIAA1671 3' TCACTCCAGCCTCCAACTCCT 65692      ACTTAA  A  A
                                AGGA     GA GT TGGAGTGA
                                ||||     || || ||||||||
                                TCCT     CT CG ACCTCACT
                                  CAAC__  C  _
GAM825  KIAA1856 3' TCACTCTGGGCTTCCCAAGCAC 92671    AA   AA    A
           C                     GG  CTT  GAAGT TGGAGTGA
                                ||  |||  ||||| ||||||||
                                CC  GAA  CTTCG GTCTCACT
                                 AC   CC    G
GAM825  MGC1127  3' TCACTCCATTTGGCAAGCTCT  53218     A   AAGAAGT
                                GGA CTT      ATGGAGTGA
                                ||| |||      |||||||||
                                TCT GAA      TACCTCACT
                                  C   CGGTT__
GAM825  MMPL1    3' TCACCCCACCGCCCTCTTAAGT 14723           A_  A_   A
           TTCT                   AGGAACTTAAGA  GT  TGG GTGA
                                ||||||||||||  ||  ||| ||||
                                TCTTTGAATTCT  CG  ACC CACT
                                      CC  CC   C
GAM825  NESCA    3' CACTCCATCCCTCCCAAGTTGC 26743    _    AA  AGT
           C                     GG AACTT  GA   ATGGAGTG
                                || |||||  ||   ||||||||
                                CC TTGAA  CT   TACCTCAC
                                 G    CC  CCC
GAM825  RNF32    3' CACTCCTTAAGTTCC       48187          GAAGTAT
                                GGAACTTAA      GGAGTG
                                |||||||||      ||||||
                                CCTTGAATT      CCTCAC
                                       _______
GAM825  SCMH1    5' CCAAACTTCTTAACCCCT    24253     AAC       A
                                AGG   TTAAGAAGT TGG
                                |||   ||||||||| |||
                                TCC   AATTCTTCA ACC
                                  CC_       A
GAM825  SEMA4G   5' CACTCCATACCCTTCTCC    94672     ACTT   AA
                                GGA    AAG  GTATGGAGTG
                                |||    |||  ||||||||||
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                                CCT    TTC  CATACCTCAC
                                  C___   C_
GAM825  TRAP95    3'  CACCCACCTCAAGTTCCT    65536        A  AAGTA   A
                                AGGAACTT AG     TGG GTG
                                |||||||| ||     ||| |||
                                TCCTTGAA TC     ACC CAC
                                    C  C____   _
GAM825  ZAK       3'  TCTCTTCCTAAGTTCC      33604         A    TAT
                                GGAACTTA GAAG   GGA
                                |||||||| ||||   |||
                                CCTTGAAT CTTC   TCT
                                    C   ___
GAM825  LOC149506 3'  CACTCCTACAAATTCC      84452      C  AAGAA   T
                                GGAA TT     GTA GGAGTG
                                |||| ||     ||| ||||||
                                CCTT AA     CAT CCTCAC
                                  A _____   _
GAM825  LOC152674 3'  CACTCCACACTTTATTAGCAAA 85833       ____  TAA    A
           TTCCT                  AGGAA    CT   GAAGT TGGAGTG
                                |||||    ||   ||||| |||||||
                                TCCTT    GA   TTTCA ACCTCAC
                                   AAAC  TTA     C
GAM825  LOC255096 5'  CACTCCATCCTCAACTCC    97622     ACTTAA  A T
                                GGA      GA G ATGGAGTG
                                |||      || | ||||||||
                                CCT      CT C TACCTCAC
                                  CAA___  _ C
GAM825  LOC257415 3'  TCACTCTTGCTGTCTTAAGTTC 96078          _    T
                                GAACTTAAGA AGTA GGAGTGA
                                |||||||||| |||| |||||||
                                CTTGAATTCT TCGT TCTCACT
                                     G   _
GAM826  ADAM17    3'  TTTCAGGTTTTAGTTTTTA    12085      T   TGAC
                                TGAG GCTA    AAACCTGGAA
                                |||| ||||    ||||||||||
                                ATTT TGAT    TTTGGACTTT
                                  T   _____
GAM826  ADAM17    3'  TTTCAGGTTTTAGTTTTTA    41559      T   TGAC
                                TGAG GCTA    AAACCTGGAA
                                |||| ||||    ||||||||||
                                ATTT TGAT    TTTGGACTTT
                                  T   _____
GAM826  ADARB1    3'  CTTCCGTGTGAGTTCTAGTGTT 31724      TG   T   AA  C
           CA                    TGAG  CTA GAC  AC TGGAAG
                                ||||  ||| |||  || ||||||
                                ACTT  GAT TTG  TG GCCTTC
                                  GT   C   AG  T
GAM826  AIRE      3'  TTTTCAGTTCAGTGGCATTCA  4603           GACAAAC
                                TGAGTGCTAT      CTGGAAG
                                ||||||||||      |||||||
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                                ACTTACGGTG      GACTTTT
                                     ACTT___
GAM826  AMPH     3'  CTTTCAGGTTTACTATG     7906       AC
                                TATG  AAACCTGGAAG
                                ||||  ||||||||||
                                GTAT  TTTGGACTTTC
                                  CA
GAM826  ANXA4    3'  TTTTTAGGTTTTGTCCATAGCA 62766    G      _    _
           TCA                    GA TGCTATG ACAAA CCTGGAAG
                                || ||||||| ||||| ||||||||
                                CT ACGATAC TGTTT GGATTTTT
                                  _     C    T
GAM826  ARHGEF5  3'  CTTCTACTGCCTTATAGTGCTT 18363     TG     CAAACC
           A                     TGAG  CTATGA     TGGAAG
                                ||||  ||||||     ||||||
                                ATTC  GATATT     ATCTTC
                                  GT     CCGTC_
GAM826  ATF7     3'  CTTCTAGGTTTGGGGTTTCTCA 22466     TGCT  GA
                                TGAG   AT  CAAACCTGGAAG
                                ||||   ||  ||||||||||||
                                ACTC   TG  GTTTGGATCTTC
                                  TT__  GG
GAM826  ATP1B3   3'  TTCCAGATCATAGTGTTCA   8060      TG     CAAAC
                                TGAG  CTATGA    CTGGAA
                                ||||  ||||||    ||||||
                                ACTT  GATACT    GACCTT
                                  GT     A_____
GAM826  ATP6V0B  3'  CTTTCAGAGGCTTGGTGTTCA  14460     TG   TGACAAAC
                                TGAG  CTA      CTGGAAG
                                ||||  |||      |||||||
                                ACTT  GGT      GACTTTC
                                  GT   TCGGA___
GAM826  B3GALT5  5'  TTTCTGGGTTCTCAGGCCTT   20223    T   A   CA   TG
                                GAG GCT TGA  AACC  GAAG
                                ||| ||| |||  ||||  ||||
                                TTC CGG ACT  TTGG  CTTT
                                  _  _  C_   GT
GAM826  B3GALT5  5'  TTTCTGGGTTCTCAGGCCTT   52566    T   A   CA   TG
                                GAG GCT TGA  AACC  GAAG
                                ||| ||| |||  ||||  ||||
                                TTC CGG ACT  TTGG  CTTT
                                  _  _  C_   GT
GAM826  B3GALT5  5'  TTTCTGGGTTCTCAGGCCTT   52574    T   A   CA   TG
                                GAG GCT TGA  AACC  GAAG
                                ||| ||| |||  ||||  ||||
                                TTC CGG ACT  TTGG  CTTT
                                  _  _  C_   GT
GAM826  B3GALT5  5'  TTTCTGGGTTCTCAGGCCTT   52582    T   A   CA   TG
                                GAG GCT TGA  AACC  GAAG
                                ||| ||| |||  ||||  ||||
```

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                                TTC CGG ACT  TTGG  CTTT
                                  _  _  C_   GT
GAM826  B4GALT6  3'  TTTCAGTTTTTTTATGGTACTC 59868          C  C    G
                                GAGTGCTATGA AAA CTGGAA
                                |||||||||||| ||| ||||||
                                CTCATGGTATT TTT GACTTT
                                      T  T
GAM826  BCL11B   3'  TTTCAAGTCGTAGCACTT    43198           AAACC
                                GAGTGCTATGAC    TGGAA
                                ||||||||||||    |||||
                                TTCACGATGCTG    ACTTT
                                      A____
GAM826  BIG1     3'  TTTTGGGTGGTGGGGCTT    21208     G   GACAA  TG
                                GAGT CTAT    ACC  GAA
                                |||| ||||    |||  |||
                                TTCG GGTG    TGG  TTT
                                  G   G____  GT
GAM826  BTEB1    3'  CTTTTGGGTTTTTTGGTTTTT  6845     T   TGAC   TG
                                GAG GCTA   AAACC  GAAG
                                ||| ||||   |||||  ||||
                                TTT TGGT   TTTGG  TTTC
                                  T   TT__   GT
GAM826  BTEB1    3'  TTTGTCAAGCACTTA       6854          A
                                TGAGTGCT TGACAAA
                                |||||||| |||||||
                                ATTCACGA ACTGTTT
                                         _
GAM826  C20orf1  5'  CTTCTGAGGCGGTTGCGGTGCT 24000    TG  AT   AAA  _
           C                     GAG  CT  GAC   CCT GGAAG
                                |||  ||  |||   ||| |||||
                                CTC  GG  TTG   GGA TCTTC
                                  GT  CG   GC_  G
GAM826  CARPX    3'  TACTGAGTTTGTGGCAATCA  39425    G   ATG    CT  AAG
                                TGA TGCT   ACAAAC  GG
                                ||| ||||   ||||||  ||
                                ACT ACGG   TGTTTG  TC
                                  A   ___     AG  ATT
GAM826  CCND3    3'  CTTCTAGGGTTATTGCATTT  8306       T    AAA
                                GAGTGC ATGAC   CCTGGAAG
                                |||||| |||||   ||||||||
                                TTTACG TATTG   GGATCTTC
                                   T    ___
GAM826  CDH12    5'  CTTCCAGGAAGAAAGTGGTGTC 14491    _    GACAAA
           T                     AG TGCTAT     CCTGGAAG
                                || ||||||     ||||||||
                                TC GTGGTG     GGACCTTC
                                  T     AAAGAA
GAM826  CDKN2A   3'  TTCTGGAGTGAGCACTCA    3579         ATGA  AAC TG
                                TGAGTGCT   CA   C  GAA
                                ||||||||   ||   |  |||
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                              ACTCACGA   GT   G  CTT
                                  _____  GA_  GT
GAM826  CDKN2A   3'  TTCTGGAGTGAGCACTCA    54231        ATGA  AAC TG
                              TGAGTGCT   CA   C  GAA
                              ||||||||   ||   |  |||
                              ACTCACGA   GT   G  CTT
                                  _____  GA_  GT
GAM826  CDKN2A   3'  TTCTGGAGTGAGCACTCA    54234        ATGA  AAC TG
                              TGAGTGCT   CA   C  GAA
                              ||||||||   ||   |  |||
                              ACTCACGA   GT   G  CTT
                                  _____  GA_  GT
GAM826  CDKN2A   3'  TTCTGGAGTGAGCACTCA    54239        ATGA  AAC TG
                              TGAGTGCT   CA   C  GAA
                              ||||||||   ||   |  |||
                              ACTCACGA   GT   G  CTT
                                  _____  GA_  GT
GAM826  CHST6    3'  CTTCCAGGTTTAGAAGCTTCA  41225     T   ATGAC
                              TGAG GCT    AAACCTGGAAG
                              |||| |||    ||||||||||
                              ACTT CGA    TTTGGACCTTC
                                _  AGA__
GAM826  CNR1     3'  TTTCCATAGTTTAGGTACTCA  32217        AT   AAACC
                              TGAGTGCT  GAC    TGGAAG
                              ||||||||  |||    ||||||
                              ACTCATGG  TTG    ACCTTT
                                   AT   AT___
GAM826  COPG2    3'  TTTTAGGCTAGTGGCATCA   81188     G     GACAAA
                              TGA TGCTAT     CCTGGAA
                              ||| ||||||     |||||||
                              ACT ACGGTG     GGATTTT
                                _     ATC___
GAM826  COX7A2L  3'  CTTTTAAAAATGTTATAGC   16350         AACC
                              GCTATGACA   TGGAAG
                              |||||||||   ||||||
                              CGATATTGT   ATTTTC
                                   AAAA
GAM826  CYP27B1  3'  TTTTTGGGCTTTCATAGTGTTC 5778      TG     C  A  TG
          A                   TGAG  CTATGA AA CC  GAAG
                              ||||  |||||| || ||  ||||
                              ACTT  GATACT TT GG  TTTT
                                GT     _  C  GT
GAM826  DDEF1    3'  CTTCCATCGTTACAGTGCTCA  59563     TG  A   AAACC
                              TGAG  CT TGAC    TGGAAG
                              ||||  || ||||    ||||||
                              ACTC  GA ATTG    ACCTTC
                                GT  C    CT___
GAM826  DGKI     3'  CTTTTAGGTTTTTGGTTTTCA  16344      T   TGAC
                              TGAG GCTA   AAACCTGGAAG
                              |||| ||||   ||||||||||
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                                ACTT TGGT    TTTGGATTTTC
                                  T    T___
GAM826  DTNA    5'  TTTTCAGCATATGTAGTACTT  52131          GACAAAC
                                GAGTGCTAT      CTGGAAG
                                |||||||||      |||||||
                                TTCATGATG      GACTTTT
                                    TATAC__
GAM826  DTNA    5'  CTTCCATCCCAGGTCTAGTATT 52134          T   AAACC_
          CA                      TGAGTGCTA GAC     TGGAAG
                                |||||||||| |||     ||||||
                                ACTTATGAT CTG     ACCTTC
                                    _   GACCCT
GAM826  DTNA    5'  CTTCCATCCCAGGTCTAGTATT 52136          T   AAACC_
          CA                      TGAGTGCTA GAC     TGGAAG
                                |||||||||| |||     ||||||
                                ACTTATGAT CTG     ACCTTC
                                    _   GACCCT
GAM826  DTNA    5'  TTTTCAGCATATGTAGTACTT  7326          GACAAAC
                                GAGTGCTAT      CTGGAAG
                                |||||||||      |||||||
                                TTCATGATG      GACTTTT
                                    TATAC__
GAM826  DTNA    5'  TTTTCAGCATATGTAGTACTT  7329          GACAAAC
                                GAGTGCTAT      CTGGAAG
                                |||||||||      |||||||
                                TTCATGATG      GACTTTT
                                    TATAC__
GAM826  E2F3    3'  TTTCTGTTCTTTGTTGTGGCTC 8704      T    TG    CC_
          TT                      GAG GCTA  ACAAA   TGGAAG
                                ||| ||||  |||||   ||||||
                                TTC CGGT  TGTTT   GTCTTT
                                  T   GT    CTT
GAM826  ENC1    3'  TAAGAAGTTTGTTATAGATTTA 13284       G         CTGGAAG
                                TGAGT CTATGACAAAC
                                ||||| ||||||||||
                                ATTTA GATATTGTTTG
                                   _         AAGAATT
GAM826  ETF1    3'  GGTTTGTCATGGTGTCA     16398     G
                                TGA TGCTATGACAAACC
                                ||| ||||||||||||||
                                ACT GTGGTACTGTTTGG
                                  _
GAM826  FBN1    3'  GGGTTTGTAATGGTGCTTA   64402      TG   G
                                TGAG  CTAT ACAAACCT
                                ||||  |||| ||||||||
                                ATTC  GGTA TGTTTGGG
                                  GT    A
GAM826  FBXL11  3'  TTTTGGGTTTTGGTTTTTA   24580      T    TGAC    TG
                                TGAG GCTA    AAACC  GAA
                                |||| ||||    |||||  |||
```

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                                ATTT TGGT   TTTGG  TTT
                                  T  ____    GT
GAM826  FGF13   3' TTTTTAGATTTGTGGTATTC  53323       ATG   C
                                GAGTGCT  ACAAA CTGGAAG
                                |||||||  ||||| |||||||
                                CTTATGG  TGTTT GATTTTT
                                   ___   A
GAM826  FZD4    3' CTTCTGGGTTTGTATTATGTCT 24138   T  TATG_     TG
                                AG GC    ACAAACC  GAAG
                                || ||    |||||||  ||||
                                TC TG    TGTTTGG  CTTC
                                 _ TATTA     GT
GAM826  GABRE   3' TTTCTGGGCCTGAGGTGCTCA  41778    TG  ATGA  AA  TG
                                TGAG  CT   CA  CC  GAAG
                                ||||  ||   ||  ||  ||||
                                ACTC  GG   GT  GG  CTTT
                                  GT  A___ CC  GT
GAM826  GABRE   3' TTTCTGGGCCTGAGGTGCTCA  41787    TG  ATGA  AA  TG
                                TGAG  CT   CA  CC  GAAG
                                ||||  ||   ||  ||  ||||
                                ACTC  GG   GT  GG  CTTT
                                  GT  A___ CC  GT
GAM826  GABRE   3' TTTCTGGGCCTGAGGTGCTCA  41810    TG  ATGA  AA  TG
                                TGAG  CT   CA  CC  GAAG
                                ||||  ||   ||  ||  ||||
                                ACTC  GG   GT  GG  CTTT
                                  GT  A___ CC  GT
GAM826  GABRE   3' TTTCTGGGCCTGAGGTGCTCA  17112    TG  ATGA  AA  TG
                                TGAG  CT   CA  CC  GAAG
                                ||||  ||   ||  ||  ||||
                                ACTC  GG   GT  GG  CTTT
                                  GT  A___ CC  GT
GAM826  GCMB    3' TTTGTTTAGCATTTA      16460        T
                                TGAGTGCTA GACAAA
                                ||||||||| ||||||
                                ATTTACGAT TTGTTT
                                   _
GAM826  GPM6A   3' CTTTGTTGTTTAGCACTTA   17951        T   ACCT
                                TGAGTGCTA GACAA   GG
                                ||||||||| |||||   ||
                                ATTCACGAT TTGTT   TC
                                   _   GTT_
GAM826  GRM7    3' CTTCTAGGTTGCAAGGT    5944     A  A   A
                                GCT TG CAA CCTGGAAG
                                ||| || ||| ||||||||
                                TGG AC GTT GGATCTTC
                                  A  _  _
GAM826  HCS     3' CTTGGCTAGTTGTGGCGTTTA  38469        TG  AAA  T
                                TGAGTGCTA  AC   CC GG
                                |||||||||  ||   || ||
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                                ATTTGCGGT  TG   GG TC
                                     GT  ATC  T
GAM826  HLCS     3'  TTTTTAGGTTTGTTTTGTTGTC 4680     GT  TAT
                                GA  GC   GACAAACCTGGAAG
                                ||  ||   ||||||||||||||
                                CT  TG   TTGTTTGGATTTTT
                                 GT  TT_
GAM826  HOXC10   3'  TTCGTGTGTTTGTCGTAGCACC 61273    A          C__   AG
           CA                     TG GTGCTATGACAAAC   TGGA
                                || ||||||||||||||   ||||
                                AC CACGATGCTGTTTG   GCTT
                                 C           TGT
GAM826  IMPA2    5'  CTTCTGGGGCCAAGTGTGTGCT 95240     TG _   GACAAA  TG
           CA                     TGAG  C TAT     CC  GAAG
                                ||||  | |||     ||  ||||
                                ACTC  G GTG     GG  CTTC
                                  GT T   AACCG_  GT
GAM826  ITGA6    3'  TTTGTATATGGTATTTA     3989          _
                                TGAGTGCTATG ACAAA
                                |||||||||| |||||
                                ATTTATGGTAT TGTTT
                                      A
GAM826  ITGB3BP  3'  CTTCTGTGGACTTTTAGCATTT 26599        TGACAAA  _
                                GAGTGCTA      CC TGGAAG
                                ||||||||      || ||||||
                                TTTACGAT      GG GTCTTC
                                     TTTCA__  T
GAM826  JMJ      3'  TTTCAGGTTTGTACTAC     17136     CTATG
                                GTG     ACAAACCTGGAA
                                |||     ||||||||||||
                                CAT     TGTTTGGACTTT
                                 CA___
GAM826  KCNS2    3'  CTTCTAGGATATAGTAT     68304         ACAAA
                                GTGCTATG     CCTGGAAG
                                ||||||||     ||||||||
                                TATGATAT     GGATCTTC
                                     A____
GAM826  KLRC4    3'  TTTTTAAGTCTGTGTAGTATTC 25524          G   A  C
           A                     TGAGTGCTAT ACA AC TGGAAG
                                |||||||||| ||| || ||||||
                                ACTTATGATG TGT TG ATTTTT
                                      _  C  A
GAM826  LAMP2    3'  TTTCATGTTTTAGCATTT     25723         T    AACC
                                GAGTGCTA GACA    TGGAA
                                |||||||| ||||    |||||
                                TTTACGAT TTGT    ACTTT
                                     T   _____
GAM826  LDB1     3'  CTTTTAGGGGGAGGGGGTACTC 13984         ATGACAAA
           A                     TGAGTGCT       CCTGGAAG
                                ||||||||       ||||||||
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```
                                ACTCATGG      GGATTTTC
                                    GGGAGGG_
GAM826  LRP8    3'  TTTTTAGGTTTTGGGCATTT  34028       ATGAC
                                GAGTGCT    AAACCTGGAAG
                                |||||||    ||||||||||
                                TTTACGG    TTTGGATTTTT
                                    GT___
GAM826  LRP8    3'  TTTTTGGGTTTTGGGGCATTT  16150       ATGAC    TG
                                GAGTGCT    AAACC  GAAG
                                |||||||    |||||  ||||
                                TTTACGG    TTTGG  TTTT
                                    GGT__    GT
GAM826  LRP8    3'  TTTTTGGGTTTTGGGGCATTT  52782       ATGAC    TG
                                GAGTGCT    AAACC  GAAG
                                |||||||    |||||  ||||
                                TTTACGG    TTTGG  TTTT
                                    GGT__    GT
GAM826  MAPK1   3'  TTTCTGGTAGTTGTGGCTTTTA 10821     T   TG  AA   T
                                TGAG GCTA  AC  ACC GGAAG
                                |||| ||||  ||  ||| |||||
                                ATTT CGGT  TG  TGG TCTTT
                                  T   GT  A_  _
GAM826  MASP1   3'  TTCTAGCTGGAGCACTCA    57477       ATGACAAAC
                                TGAGTGCT       CTGGAA
                                ||||||||       ||||||
                                ACTCACGA       GATCTT
                                    GGTC_____
GAM826  MEN1    5'  CTGGCTTTGTGTGGTACTCA  93369         G    C TG
                                TGAGTGCTAT ACAAA C  G
                                |||||||||| ||||| |  |
                                ACTCATGGTG TGTTT G  C
                                      _    C GT
GAM826  MGAT2   5'  TTTCCGGGACCCGTGGTGCT  10015   TG    ACAAA
                                AG  CTATG    CCTGGAAG
                                ||  |||||    ||||||||
                                TC  GGTGC    GGGCCTTT
                                 GT    CCA__
GAM826  MME     3'  TTTTCAGGTTTGTCATCAG   6145    _
                                CT ATGACAAACCTGGAAG
                                || ||||||||||||||||
                                GA TACTGTTTGGACTTTT
                                 C
GAM826  MME     3'  TTTTCAGGTTTGTCATCAG   23492   _
                                CT ATGACAAACCTGGAAG
                                || ||||||||||||||||
                                GA TACTGTTTGGACTTTT
                                 C
GAM826  MME     3'  TTTTCAGGTTTGTCATCAG   23502   _
                                CT ATGACAAACCTGGAAG
                                || ||||||||||||||||
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                                GA TACTGTTTGGACTTTT
                                 C
GAM826  MME     3'  TTTTCAGGTTTGTCATCAG   23514    _
                                CT ATGACAAACCTGGAAG
                                || ||||||||||||||||
                                GA TACTGTTTGGACTTTT
                                 C
GAM826  MMP8    3'  CTTCTAGGATTTATTGTTATAT 10064    C      A____
           TACTT                  TG TATGACAA    CCTGGAAG
                                || ||||||||    ||||||||
                                AT ATATTGTT    GGATCTTC
                                 T       ATTTA
GAM826  MSI1    3'  TTCTAGGTTTGTGAATGT    10126    TATG
                                GC    ACAAACCTGGAA
                                ||    ||||||||||||
                                TG    TGTTTGGATCTT
                                 TAAG
GAM826  MST1R   3'  CTTCTGGGCACAGTGGACTCA  10127      G    GACAAA  TG
                                TGAGT CTAT     CC  GAAG
                                ||||| ||||     ||  ||||
                                ACTCA GGTG     GG  CTTC
                                   _    ACAC__  GT
GAM826  MTMR6   5'  TTCTAGGAGACGGCGCTCA   93554        ATGACAAA
                                TGAGTGCT       CCTGGAA
                                ||||||||       |||||||
                                ACTCGCGG       GGATCTT
                                     CAGA_____
GAM826  MTMR8   3'  TTTTCAGGTTTTGAGCATACA  31303    A    ATGAC
                                TG GTGCT    AAACCTGGAAG
                                || |||||    ||||||||||
                                AC TACGA    TTTGGACTTTT
                                 A    GT___
GAM826  MYL4    3'  CTTCCAGGTGCCTGGCCCTT   10175     T    TGACAA
                                GAG GCTA     ACCTGGAAG
                                ||| ||||     |||||||||
                                TTC CGGT     TGGACCTTC
                                  C    CCG___
GAM826  NAPB    3'  AGTTTTTGTTGGACTTGAGTAC 70179      AT_____     CCTGGAAG
           TCA                    GTGCT      GACAAA
                                |||||      ||||||
                                CATGA      TTGTTT
                                   GTTCAGG     TT   GAA
GAM826  NAPB    3'  TTTGTCTTTGTGGCATGCA   70195    A     ___
                                TG GTGCTAT   GACAAA
                                || |||||||   ||||||
                                AC TACGGTG   CTGTTT
                                 G      TTT
GAM826  NCOA3   3'  CTTCTGCTGTGTATCATGGTGT 21528      TG     CAA  CT_
           TCA                    TGAG  CTATGA   AC   GGAAG
                                ||||  ||||||   ||   |||||
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                                ACTT  GGTACT   TG   TCTTC
                                  GT     ATG  TCG
GAM826  NFIA     3'  TTCCCTAGTCAAGCATTT    70368        A    AAACCT
                                GAGTGCT TGAC     GGAA
                                ||||||| ||||     ||||
                                TTTACGA ACTG     CCTT
                                   _   ATC___
GAM826  NORE1    3'  CTTCTTTGGTTGTGTTGCTCA  48717      GCTAT   _    T_
                                TGAGT    GACA AACC  GGAAG
                                |||||    |||| ||||  |||||
                                ACTCG    TTGT TTGG  TCTTC
                                  _____   G   TT
GAM826  NR3C1    3'  CTTCTAACCTGATGGCACTTA  3923          GA  AACC
                                TGAGTGCTAT  CA    TGGAAG
                                ||||||||||  ||    ||||||
                                ATTCACGGTA  GT    ATCTTC
                                     __  CCA_
GAM826  OFD1     3'  TCCAGTCATAGTATTT      13218           AAACC
                                GAGTGCTATGAC     TGGA
                                ||||||||||||     ||||
                                TTTATGATACTG     ACCT
                                     _____
GAM826  PAWR     3'  TTTTTGGTTTTGTGTGGTATTC 10433          G     C TG
          A                      TGAGTGCTAT ACAAA C  GAAG
                                 |||||||||| ||||| |  ||||
                                 ACTTATGGTG TGTTT G  TTTT
                                     _    T GT
GAM826  PCDHB3   3'  TTTTTAGGGATATAGTACTCA  38433          ACAAA
                                TGAGTGCTATG     CCTGGAAG
                                ||||||||||     ||||||||
                                ACTCATGATAT     GGATTTTT
                                     AG___
GAM826  PDYN     3'  TTTTCAGGTTGGAGTGCATTCA 44322        T  GA   A
                                TGAGTGC AT  CAA CCTGGAAG
                                ||||||| ||  ||| ||||||||
                                ACTTACG TG  GTT GGACTTTT
                                   _ AG  _
GAM826  PER2     3'  CTTTTAGGTCATTTGGACACTT 43033       _  TGACAA
                                GAGTG CTA      ACCTGGAAG
                                ||||| |||      |||||||||
                                TTCAC GGT      TGGATTTTC
                                   A   TTAC__
GAM826  PIN4     3'  CTTCCAGGACAGGTGGTATT   20626         GACAAA
                                AGTGCTAT     CCTGGAAG
                                ||||||||     ||||||||
                                TTATGGTG     GGACCTTC
                                     GACA__
GAM826  PKHD1    3'  TTTCTTTATCCTGTAGTAGCAT 56919         G   AACCT_
          TT                     GAGTGCTAT ACA     GGAAG
                                 ||||||||| |||     |||||
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                                TTTACGATG TGT     TCTTT
                                     A   CCTATT
GAM826  PPP6C    3'  TTTATTGTTTGTTGTGGTGTCT 10768    _    TG     CTG   G
                                AG TGCTA  ACAAAC   GAA
                                || |||||  ||||||   |||
                                TC GTGGT  TGTTTG   TTT
                                 T    GT     TTA
GAM826  PRKWNK3  3'  TTCCAGTGTGGTATTT     61562         ACAAAC     G
                                GAGTGCTATG     CTGGAA
                                ||||||||||     ||||||
                                TTTATGGTGT     GACCTT
                                      _______     G
GAM826  PTPN1    3'  TTCCAGGAATAGGCATTT    11052       ATGACAAA
                                GAGTGCT       CCTGGAA
                                |||||||       |||||||
                                TTTACGG       GGACCTT
                                    ATAA____
GAM826  PUM1     3'  CTTTTATGGTCGTAGCAT    27959         AAACC
                                GTGCTATGAC    TGGAAG
                                ||||||||||    ||||||
                                TACGATGCTG    ATTTTC
                                     GT___
GAM826  RAD17    5'  TTTCTAGTGTGTCGAGGTGTTT 11213     TG  A    AAC
          A                      TGAG  CT TGACA   CTGGAAG
                                ||||  || |||||   |||||||
                                ATTT  GG GCTGT   GATCTTT
                                  GT  A    GT_
GAM826  RAD52    3'  GGCTTTTCATAGTGCTCA    11242     TG     C  A
                                TGAG  CTATGA AA CC
                                ||||  |||||| || ||
                                ACTC  GATACT TT GG
                                  GT     T  C
GAM826  RAD52    3'  GGCTTTTCATAGTGCTCA    56198     TG     C  A
                                TGAG  CTATGA AA CC
                                ||||  |||||| || ||
                                ACTC  GATACT TT GG
                                  GT     T  C
GAM826  RAD52    3'  GGCTTTTCATAGTGCTCA    56206     TG     C  A
                                TGAG  CTATGA AA CC
                                ||||  |||||| || ||
                                ACTC  GATACT TT GG
                                  GT     T  C
GAM826  RAD52    3'  GGCTTTTCATAGTGCTCA    56215     TG     C  A
                                TGAG  CTATGA AA CC
                                ||||  |||||| || ||
                                ACTC  GATACT TT GG
                                  GT     T  C
GAM826  RAF1     3'  TTCCAGGCAAGGCACTC     80530        A  ACAAA
                                GAGTGCT TG    CCTGGAA
                                ||||||| ||    |||||||
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                                CTCACGG AC    GGACCTT
                                   A _____
GAM826  RAG1    3'  CTTCCAGGTGAACTGGAATTTA 4813      G  TGACAA
                                TGAGT CTA    ACCTGGAAG
                                ||||| |||    |||||||||
                                ATTTA GGT    TGGACCTTC
                                   A  CAAG__
GAM826  RGL     3'  TTCCAGGTTCCCGTGCTT   30740    TG TAT  CAA
                                GAG  C  GA  ACCTGGAA
                                |||  |  ||  ||||||||
                                TTC  G  CT  TGGACCTT
                                  GT CC_ ___
GAM826  RPL15   3'  TCCAGGAAGTACTCA      11384        ATGACAAA
                                TGAGTGCT      CCTGGA
                                ||||||||      ||||||
                                ACTCATGA      GGACCT
                                   A_______
GAM826  SACM1L  3'  CTTCCAGGTAGTTATAGTACTC 25822          AA
                                GAGTGCTATGAC  ACCTGGAAG
                                ||||||||||||  |||||||||
                                CTCATGATATTG  TGGACCTTC
                                      A_
GAM826  SCD     3'  AGTTTTTGGGTTAAAAGATGGT 17345  TG  A_______   TG
           TGTAGCATTTA              AC      AACC  GAAG   TT
                                ||      ||||  ||||   ||
                                TG      TTGG  TTTT   GA
                                GT  GTAGAAAA   GT
GAM826  SDC4    3'  TTTTCAGGAAATAGTGTGGTGT 11486    TG    ACAAA_
           TT                   GAG  CTATG    CCTGGAAG
                                |||  |||||    ||||||||
                                TTT  GGTGT    GGACTTTT
                                  GT    GATAAA
GAM826  SEL1L   3'  TTTCCTAAAGTTGAAGCATTT  17367       A   AAACCT
                                GAGTGCT TGAC    GGAAG
                                ||||||| ||||    |||||
                                TTTACGA GTTG    CCTTT
                                   A   AAAT__
GAM826  SFRS1   3'  CTAATTTGTCACAGTGCTTA  22637     TG  A     CC
                                TGAG  CT TGACAAA  TGG
                                ||||  || |||||||  |||
                                ATTC  GA ACTGTTT  ATC
                                  GT  C      A_
GAM826  SGCG    3'  TCCTTTATAGCATTCA     4063          CAAACCT
                                TGAGTGCTATGA      GGA
                                ||||||||||||      |||
                                ACTTACGATATT      CCT
                                      T_______
GAM826  SLC2A5  3'  CTTCCGGGGCCATGGGCATTT  11724        _  ACAAA
                                GAGTGCT ATG    CCTGGAAG
                                ||||||| |||    ||||||||
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                                TTTACGG TAC    GGGCCTTC
                                   G  CG___
GAM826  SLC4A4   3'  TTTTTAACTGTGTTAAAGTACT 13646       A    AACC
           T                    GAGTGCT TGACA   TGGAAG
                                ||||||| |||||   ||||||
                                TTCATGA ATTGT   ATTTTT
                                   A    GTCA
GAM826  SLC4A8   3'  TTTTTGGGTTTGACAACCACTT 16778      CTA  A    TG
           A                    TGAGTG  TG CAAACC  GAAG
                                ||||||  || ||||||  ||||
                                ATTCAC  AC GTTTGG  TTTT
                                   CA_  A    GT
GAM826  SNX6     3'  TTTCTTAATGATGTTAAGCATT 41164       A    AACCT_
           TA                    TGAGTGCT TGACA     GGAAG
                                ||||||||| |||||     |||||
                                ATTTACGA ATTGT     TCTTT
                                   _    AGTAAT
GAM826  SRP46    3'  TTATAAGTTTGTTAAGTACTTA 49465       A      CTGGAAG
                                TGAGTGCT TGACAAAC
                                |||||||| ||||||||
                                ATTCATGA ATTGTTTG
                                   _      AATATTT
GAM826  TARDBP   3'  CTTTTAGGAGATCATGGTGTCA 23772     G      CAAA
                                TGA TGCTATGA   CCTGGAAG
                                ||| ||||||||   ||||||||
                                ACT GTGGTACT   GGATTTTC
                                  _      AGA_
GAM826  TCF19    3'  TTTCCAGGGAGAATGTGCTT  97739     TG T  GACAAA
                                GAG  C AT     CCTGGAAG
                                |||  | ||     ||||||||
                                TTC  G TA     GGACCTTT
                                  GT _  AGAG__
GAM826  TCF19    3'  TTTCCAGGGAGAATGTGCTT  97869     TG T  GACAAA
                                GAG  C AT     CCTGGAAG
                                |||  | ||     ||||||||
                                TTC  G TA     GGACCTTT
                                  GT _  AGAG__
GAM826  TGM4     3'  TTCCTGAGTCATGGCCTCA   12264      T      AAACCT
                                TGAG GCTATGAC     GGAA
                                |||| ||||||||     ||||
                                ACTC CGGTACTG     CCTT
                                  _      AGT___
GAM826  UGCG     3'  TTTATTTTTGCATGGCACTT  12541         A    CC
                                GAGTGCTATG CAAA  TGGA
                                |||||||||| ||||  ||||
                                TTCACGGTAC GTTT  ATTT
                                   _   TT
GAM826  WDR8     5'  TTTTCGGGCGCAGGGTGGCGCC 35159    A      GACAAA
           CG                    TG GTGCTAT     CCTGGAAG
                                || |||||||     ||||||||
```

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                                GC CGCGGTG     GGGCTTTT
                                 C      GGACGC
GAM826  WNT2     5'  CTTTCGGGCTGCAGGCGCTC   12656        A  A  AA
                                GAGTGCT TG CA  CCTGGAAG
                                ||||||| || ||  ||||||||
                                CTCGCGG AC GT  GGGCTTTC
                                   _ _ C_
GAM826  XK       3'  TTTCTGGGTTTGATACTC    40803      CTATGA     TG
                                GAGTG     CAAACC  GAAG
                                |||||     ||||||  ||||
                                CTCAT     GTTTGG  CTTT
                                   A_____     GT
GAM826  YWHAG    3'  TTTTTGGTTCATAGGTGCTC   25024     TG _    CAA   TG
                                GAG  C TATGA   ACC  GAA
                                |||  | |||||   |||  |||
                                CTC  G ATACT   TGG  TTT
                                  GT G    ___   TT
GAM826  ZNF174   5'  TTTCTAGAATCTTTCTAGTATT 12897         T  CAAAC_
              CA                  TGAGTGCTA GA     CTGGAAG
                                |||||||||| ||     |||||||
                                ACTTATGAT CT     GATCTTT
                                     _ TTCTAA
GAM826  ZNF200   3'  TTTCTGGGTCTGATGGTGCT   12910    TG    GA  A   TG
                                AG  CTAT  CA ACC  GAAG
                                ||  ||||  || |||  ||||
                                TC  GGTA  GT TGG  CTTT
                                 GT   __ C   GT
GAM826  20D7-FC4 3'  TTCTAGCGTGTGGCAT      60910        GACAA  _
                                GTGCTAT    AC CTGGAA
                                |||||||    || ||||||
                                TACGGTG    TG GATCTT
                                   _____  C
GAM826  ACRBP    3'  TTCTGGGTCTGTTACTC     50658      GCTAT    A   TG
                                GAGT    GACA ACC  GAA
                                ||||    |||| |||  |||
                                CTCA    TTGT TGG  CTT
                                  _____   C   GT
GAM826  AFAP     3'  CTTCGCAATGTCACTGGTACTT 41304         _    AACC  _
              A                  GAGTGCTA TGACA    TG GAAG
                                |||||||| |||||    || ||||
                                TTCATGGT ACTGT    AC CTTC
                                    C    A___  G    T
GAM826  AKAP6    3'  CTTCATATGTCATGGTTTTCA  14991      T       AACCTG
                                TGAG GCTATGACA     GAAG
                                |||| |||||||||     ||||
                                ACTT TGGTACTGT     CTTC
                                  T       ATA___
GAM826  AMOTL2   3'  TTTTTAGGTTTGGTATGTGTT  32485    TG T   A
                                AG  C ATG CAAACCTGGAAG
                                ||  | ||| ||||||||||||
```

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                                TT  G TAT GTTTGGATTTTT
                                 GT _   G
GAM826  AP3M2    3'  TTCTAGGTTTGTAAGTGC    22318   TG  ATG
                                G  CT   ACAAACCTGGAA
                                |  ||   ||||||||||||
                                C  GA   TGTTTGGATCTT
                                 GT  A__
GAM826  Apg4B    3'  TTTCCAGTGCTGTGGCATTC  25291        GA  AAC
                                GAGTGCTAT  CA   CTGGAAG
                                |||||||||  ||   |||||||
                                CTTACGGTG  GT   GACCTTT
                                      TC  ____
GAM826  ARNTL2   3'  CTTTGTTGTCATAGTCTT    39464     T       ACCT
                                GAG GCTATGACAA    GG
                                ||| ||||||||||    ||
                                TTC TGATACTGTT    TC
                                  _        GTT_
GAM826  ARPP-19  3'  CTTCTGTAAGTCACAGTGCTTA 21794     TG  A    AA  CT
                                TGAG  CT TGAC  AC  GGAAG
                                ||||  || ||||  ||  |||||
                                ATTC  GA ACTG  TG  TCTTC
                                  GT  C    AA  __
GAM826  ATP6M8-9 3'  TTTCTAGAGTGAATTATAGTAT 19278         CAA  _
           T                     AGTGCTATGA   AC CTGGAAG
                                ||||||||||   || |||||||
                                TTATGATATT   TG GATCTTT
                                      AAG  A
GAM826  BCAR3    3'  TTTCTATTATCATGGTATTT   13100          C  ACC
                                GAGTGCTATGA AA   TGGAAG
                                ||||||||||| ||   ||||||
                                TTTATGGTACT TT   ATCTTT
                                      A  ____
GAM826  BHLHB2   3'  TTTCTAGGCCTAACCATTAGTA 13383        _  ACAAA_
           CTTA                   GAGTGCTA TG     CCTGGAAG
                                |||||||| ||     ||||||||
                                TTCATGAT AC     GGATCTTT
                                     T  CAATCC
GAM826  BIRC1    3'  TTTCCATATCATAGTATTT    15793          CAAACC
                                GAGTGCTATGA     TGGAAG
                                ||||||||||     ||||||
                                TTTATGATACT     ACCTTT
                                      AT_____
GAM826  BIRC2    5'  TTTTTGGGTTGTCATGTTAAAG 67206   G  _____      A  TG
           TGCTTA                   CT    ATGACAA CC  GAAG
                                 ||    ||||||| ||  ||||
                                 GA    TACTGTT GG  TTTT
                                T  AATTG      _  GT
GAM826  BTN1A1   3'  TTTCCAGGATAGATGTTGCTCA 8195       GCTAT    AA___
                                TGAGT    GACA    CCTGGAAG
                                |||||    ||||    ||||||||
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                                ACTCG    TTGT    GGACCTTT
                                  _____   AGATA
GAM826  C1orf16  3' CTTTTAGTTTGACATGGTGTTT 29232    TG    A    C
                                GAG  CTATG CAAAC TGGAAG
                                |||  ||||| ||||| ||||||
                                TTT  GGTAC GTTTG ATTTTC
                                  GT    A    _
GAM826  C5orf4   3' CTTCTAGGTTCAACCAGTGCT  50494    TG  ATGACA
                                AG  CT    AACCTGGAAG
                                ||  ||    ||||||||||
                                TC  GA    TTGGATCTTC
                                 GT  CCAAC_
GAM826  C5orf5   3' TTCGTTTTGTCAGGCACTCA   33473       A     CC
                                TGAGTGCT TGACAAA  TGGA
                                |||||||| |||||||  ||||
                                ACTCACGG ACTGTTT  GCTT
                                     _     T_
GAM826  CBX3     3' TTTGTTTTTAAGCATTCA    33430       AT__
                                TGAGTGCT   GACAAA
                                ||||||||   ||||||
                                ACTTACGA   TTGTTT
                                     ATTT
GAM826  CBX3     3' TTTGTTTTTAAGCATTCA    23457       AT__
                                TGAGTGCT   GACAAA
                                ||||||||   ||||||
                                ACTTACGA   TTGTTT
                                     ATTT
GAM826  CBX6     3' CTTCCGGGCTCCCATGCACTT  26614      T   ACAAA
                                GAGTGC ATG    CCTGGAAG
                                |||||| |||    ||||||||
                                TTCACG TAC    GGGCCTTC
                                   _  CCTC_
GAM826  CCT8     3' CTGTATTTGTAGTAGTACTCA  21671        G    CC
                                TGAGTGCTAT ACAAA  TGG
                                |||||||||| |||||  |||
                                ACTCATGATG TGTTT  GTC
                                     A    AT
GAM826  CD84-H1  3' TTTCCAGGGGAAGGAGGTGCTC 53081     TG  ATGACAAA
           A                     TGAG  CT      CCTGGAAG
                                ||||  ||      ||||||||
                                ACTC  GG      GGACCTTT
                                  GT  AGGAAGG_
GAM826  CDON     3' TTTGCATAGTATTCA      33772         A
                                TGAGTGCTATG CAAA
                                |||||||||| ||||
                                ACTTATGATAC GTTT
                                          _
GAM826  CGI-127  3' CTTCTAGATATTCTAGTATTT  32156       T  CAAAC
                                GAGTGCTA GA    CTGGAAG
                                |||||||| ||    |||||||
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                                TTTATGAT CT    GATCTTC
                                    _ TATA_
GAM826  CGR19    3'  TTCATATTTGTATGGTACTT  21643        A   CC
                                GAGTGCTATG CAAA  TGGA
                                |||||||||| ||||  ||||
                                TTCATGGTAT GTTT  ACTT
                                    _   AT
GAM826  CLDN1    3'  TTACCATAATCTTATAGCACTT 40853         CAAACC  AAG
                                GAGTGCTATGA    TGG
                                ||||||||||     |||
                                TTCACGATATT    ACC
                                    CTAAT_  ATTT
GAM826  COE2     3'  CTTTCGGGCAGGGTATGGTCTC 64253    T    ACAAA
          A                      TGAG GCTATG    CCTGGAAG
                                |||| ||||||    ||||||||
                                ACTC TGGTAT    GGGCTTTC
                                  _    GGGAC
GAM826  CTAGE-1  3'  TTCCAAAGTTATAGCACT    42651        AAACC
                                AGTGCTATGAC    TGGAA
                                ||||||||||    |||||
                                TCACGATATTG    ACCTT
                                    AA___
GAM826  CTPS2    3'  CTTCCATTTAGCATGGCGTTT  39085        AC  CC
                                GAGTGCTATG  AAA  TGGAAG
                                |||||||||  |||  ||||||
                                TTTGCGGTAC  TTT  ACCTTC
                                    GA  __
GAM826  DC2      5'  TTTCCGGGAGGCGCGTGGGGCT 64266    G    ACAAA
          T                      GAGT CTATG    CCTGGAAG
                                |||| |||||    ||||||||
                                TTCG GGTGC    GGGCCTTT
                                  G    GCGGA
GAM826  DCLRE1A  3'  TTGTCTGTGGCACTTA     69169        _
                                TGAGTGCTAT GACAA
                                |||||||||| |||||
                                ATTCACGGTG CTGTT
                                    T
GAM826  DIO2     3'  CTTCTAGCCATGTAGTGCTC  25683    TG   GACAAAC
                                GAG  CTAT     CTGGAAG
                                |||  ||||     |||||||
                                CTC  GATG     GATCTTC
                                  GT   TACC___
GAM826  DIO2     3'  CTTCTAGCCATGTAGTGCTC  5831     TG   GACAAAC
                                GAG  CTAT     CTGGAAG
                                |||  ||||     |||||||
                                CTC  GATG     GATCTTC
                                  GT   TACC___
GAM826  DJ37E16.5 3'  TTCCTGGTCATGGTACCCG  39735    A       AAACCT
                                TG GTGCTATGAC     GGAA
                                || ||||||||||     ||||
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                                GC CATGGTACTG     CCTT
                                 C        GT____
GAM826  DKFZP434A043 5'  TTTCCAGGATCATGC      31198    T   CAAA
                                GC ATGA   CCTGGAAG
                                || ||||   ||||||||
                                CG TACT   GGACCTTT
                                 _   A___
GAM826  DKFZp761D112 5'  TTTTTAGGTCTTTTTGGCATTT 50195         TGACAA
           A                     TGAGTGCTA     ACCTGGAAG
                                |||||||||     |||||||||
                                ATTTACGGT     TGGATTTTT
                                      TTTTC_
GAM826  DRF1     3'  GTTTGTTGTGTACTTA      47036        T TG
                                TGAGTGC A  ACAAAC
                                |||||||  |  ||||||
                                ATTCATG T  TGTTTG
                                    _ GT
GAM826  DRIL2    3'  TTTATCGTAGCACCA       21332    A       C
                                TG GTGCTATGA AAA
                                || |||||||| |||
                                AC CACGATGCT TTT
                                 _       A
GAM826  ENDOFIN  3'  CTTTTAAGAAATTTATAGCATT 28386          CAAACC
           TA                    TGAGTGCTATGA     TGGAAG
                                ||||||||||||     ||||||
                                ATTTACGATATT     ATTTTC
                                      TAAAGA
GAM826  ENPP4    3'  TTTCTGGGTGTAGAAAGTATTT 30053        ATGACAA   TG
                                GAGTGCT      ACC  GAAG
                                |||||||      |||  ||||
                                TTTATGA      TGG  CTTT
                                   AAGATG_   GT
GAM826  FLJ10315  5'  CTTCTGCTAGCTCATAGCACTC 36019          CAAACCT
                                GAGTGCTATGA      GGAAG
                                ||||||||||       |||||
                                CTCACGATACT      TCTTC
                                      CGATCG_
GAM826  FLJ10702  3'  TTTCCAAATGTGTTGAGCACTC 36444        A    AACC
                                GAGTGCT TGACA    TGGAAG
                                ||||||| |||||    ||||||
                                CTCACGA GTTGT    ACCTTT
                                   _     GTAA
GAM826  FLJ11259  3'  CTTCTGGGTTCAGGGTACT    37188       A   CAA   TG
                                AGTGCT TGA   ACC  GAAG
                                |||||| |||   |||  ||||
                                TCATGG ACT   TGG  CTTC
                                   G   ___   GT
GAM826  FLJ11767  3'  CTTTGTCTGCCATAGCATTTA  44758          A  A  CT
                                TGAGTGCTATG CA AC  GG
                                |||||||||| || ||  ||
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                                ATTTACGATAC GT TG  TC
                                      C  C  TT
GAM826  FLJ12190  3' CTTCTGGGTTCCATGGGCGC  46873     _  ACA   TG
                                GTGCT ATG   AACC  GAAG
                                ||||| |||   ||||  ||||
                                CGCGG TAC   TTGG  CTTC
                                   G   C__    GT
GAM826  FLJ12687  3' CTTTTGGGTTTTCTTGGT    46193     T  C    TG
                                GCTA GA AAACC  GAAG
                                |||| || |||||  ||||
                                TGGT CT TTTGG  TTTC
                                  T  _    GT
GAM826  FLJ12687  3' TTTCAGGTTTGGCATA     46206     A
                                TATG CAAACCTGGAA
                                |||| ||||||||||
                                ATAC GTTTGGACTTT
                                  G
GAM826  FLJ12700  3' TTCTTGGTTGTAGTTCTCA   46123     T    GACA   T
                                TGAG GCTAT    AACC GGAA
                                |||| |||||    |||| ||||
                                ACTC TGATG    TTGG TCTT
                                  T    _____    T
GAM826  FLJ12768  3' CTTCTGGGTGAGCTGGCACTC  47182        TGACAA   TG
                                GAGTGCTA     ACC  GAAG
                                ||||||||     |||  ||||
                                CTCACGGT     TGG  CTTC
                                     CGAG__   GT
GAM826  FLJ12891  5' TTTCAGGTTTTGTTGCTTA   46350      GCTAT    _
                                TGAGT    GACAAA CCTGGAA
                                |||||    ||||||| |||||||
                                ATTCG    TTGTTT GGACTTT
                                   _____     T
GAM826  FLJ12899  3' TTTTCAACGACAGTGATAGTGT 44765     TG   G  AAACC_
           TCA                    TGAG  CTAT AC     TGGAAG
                                ||||  |||| ||     ||||||
                                ACTT  GATA TG     ACTTTT
                                  GT   G  ACAGCA
GAM826  FLJ12975  3' CTTCAGTGATTTGTTGTAGTCT 69584    T   TG    C__    AG
           T                     GAG GCTA  ACAAA   CTGGA
                                ||| ||||  |||||   |||||
                                TTC TGAT  TGTTT   GACTT
                                  _   GT    AGT    C
GAM826  FLJ14213  3' TTTCTAGCATGTGAAGCACTT  45798       ATG   AAC
                                GAGTGCT   ACA   CTGGAAG
                                |||||||   |||   |||||||
                                TTCACGA   TGT   GATCTTT
                                    AG_   AC_
GAM826  FLJ20054  3' CCAGTGTTTGGTGCTTA    38784     TG   T    AAC
                                TGAG  CTA GACA   CTGG
                                ||||  ||| ||||   ||||
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                                ATTC  GGT TTGT   GACC
                                  GT  _   ___
GAM826  FLJ20202 3' TTCTAGATGTAGGCATTT    34731       ATG   AAC
                                GAGTGCT   ACA   CTGGAA
                                |||||||   |||   ||||||
                                TTTACGG   TGT   GATCTT
                                   A__   A__
GAM826  FLJ20232 3' TTCTAGGATGTGGCCTTA    38677     T     ACAAA
                                TGAG GCTATG    CCTGGAA
                                |||| ||||||    |||||||
                                ATTC CGGTGT    GGATCTT
                                  _     A____
GAM826  FLJ20254 3' CTTCCAGAAGAATATAGCAC  34790       ACAAAC
                                GTGCTATG     CTGGAAG
                                ||||||||     |||||||
                                CACGATAT     GACCTTC
                                     AAGAA_
GAM826  FLJ20274 3' CTTTCAGCCTTTATGGTATT  62643        CAAAC
                                AGTGCTATGA    CTGGAAG
                                ||||||||||    |||||||
                                TTATGGTATT    GACTTTC
                                      TCC__
GAM826  FLJ20308 3' TTCCAAGTCTAGCATTT     66859       T  AAACC
                                GAGTGCTA GAC    TGGAA
                                |||||||| |||    |||||
                                TTTACGAT CTG    ACCTT
                                   _  A____
GAM826  FLJ20320 3' CTTTTGGGGTGATAGCACTT  34942       G  AAA  TG
                                GAGTGCTAT AC   CC  GAAG
                                ||||||||| ||   ||  ||||
                                TTCACGATA TG   GG  TTTC
                                     G  ___  GT
GAM826  FLJ20400 3' TTTCTAGGCACTGTGGTTCTT 66515    T    GACAAA
                                GAG GCTAT     CCTGGAAG
                                ||| |||||     ||||||||
                                TTC TGGTG     GGATCTTT
                                  T    TCAC__
GAM826  FLJ20401 3' TTTCTGGGAGTTGTAGTTCTTA 35127     T   TG  AAA  TG
                                TGAG GCTA  AC   CC  GAAG
                                |||| ||||  ||   ||  ||||
                                ATTC TGAT  TG   GG  CTTT
                                  T   GT  A__  GT
GAM826  FLJ20417 3' TTTCTGGGCTAACATAGTCCTC 35137     TG    ACAAA  TG
           A                     TGAG  CTATG    CC  GAAG
                                 ||||  |||||    ||  ||||
                                 ACTC  GATAC    GG  CTTT
                                   CT    AATC_  GT
GAM826  FLJ20420 5' TTTCTGGGGGTCGTGGCCTT  35144    T      AAA  TG
                                GAG GCTATGAC   CC  GAAG
                                ||| ||||||||   ||  ||||
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                                TTC CGGTGCTG   GG  CTTT
                                  _       G__  GT
GAM826  FLJ20464  3'  CTTCTGGTTTCGTGTCCTGGTG 35232    TG   T   ___    T
              CTTA                   AG  CTA GACA   AACC GGAAG
                                ||  ||| ||||   |||| |||||
                                TC  GGT CTGT   TTGG TCTTC
                                 GT   C    GCT   _
GAM826  FLJ20548  3'  TTCCAGGTTCTGTTACTCA    35381      GCTAT   _
                                TGAGT    GACA AACCTGGAA
                                ||||||    |||| |||||||||
                                ACTCA    TTGT TTGGACCTT
                                   ______   C
GAM826  FLJ20694  3'  TTTCAGGAAGTGGAACTCA    35552      G    GACAAA
                                TGAGT CTAT     CCTGGAA
                                ||||| ||||     |||||||
                                ACTCA GGTG     GGACTTT
                                   A    AA____
GAM826  FLJ20783  3'  TTTTTAGAGTTAGGTGTAGTGC 35667      TG     ACA   _
              TTA                   TGAG  CTATG   AAC CTGGAAG
                                ||||  |||||   ||| |||||||
                                ATTC  GATGT   TTG GATTTTT
                                   GT    GGA   A
GAM826  FLJ21816  5'  TTTCTTGGAGTAATAGTGCTTA 45153      TG    G  AAA  T
                                TGAG  CTAT AC   CC GGAAG
                                ||||  |||| ||   || |||||
                                ATTC  GATA TG   GG TCTTT
                                   GT    A  A__  T
GAM826  FLJ21986  3'  TTTTTGGGCTATCTGTTACAGT 46153    TG  A     AA___  TG
              GCTTA                   G  CT TGACA     CC  GAAG
                                |  || |||||     ||  ||||
                                C  GA ATTGT     GG  TTTT
                                 GT  C     CTATC  GT
GAM826  FLJ22160  3'  CTTTCAGCAGGACAGGCATTTA 44734         A  ACAAAC
                                TGAGTGCT TG      CTGGAAG
                                |||||||| ||      |||||||
                                ATTTACGG AC      GACTTTC
                                     _  AGGAC_
GAM826  FLJ22476  3'  TTCACTCTAGCACTT       46776          T  CAAACC
                                GAGTGCTA GA      TGGA
                                |||||||| ||      ||||
                                TTCACGAT CT      ACTT
                                     _  C_____
GAM826  FLJ22833  3'  TTTCTGAAAACTCCATAGCATT 43110          ACAAACCT
              T                   GAGTGCTATG       GGAAG
                                ||||||||||       |||||
                                TTTACGATAC       TCTTT
                                      CTCAAAAG
GAM826  FLJ23074  5'  CTTCTAGGTATACTGTGGTCTC 46817      T     GACAA
              A                   TGAG GCTAT     ACCTGGAAG
                                |||| |||||     |||||||||
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                                ACTC TGGTG    TGGATCTTC
                                  _    TCATA
GAM826  FLJ23462  3'  TTTTTAGGTAACTGGTACTTA  45809        TGACAA
                                TGAGTGCTA    ACCTGGAAG
                                |||||||||    |||||||||
                                ATTCATGGT    TGGATTTTT
                                     CAA___
GAM826  FUSIP1   3'  TTTTTAGGCATGTATCATTCA  53961      CTATG  AA
                                TGAGTG   ACA  CCTGGAAG
                                ||||||   |||  ||||||||
                                ACTTAC   TGT  GGATTTTT
                                   TA___  AC
GAM826  GMFB     3'  CTTTTGTTAAGCATGGTGCTT  14667    TG    ACA  CT
                                GAG  CTATG   AAC  GGAAG
                                |||  |||||   |||  |||||
                                TTC  GGTAC   TTG  TTTTC
                                  GT    GAA  __
GAM826  GW112    3'  CTTCTAACGCCTTCATGGTAT  21189        CAAACC
                                GTGCTATGA    TGGAAG
                                |||||||||    ||||||
                                TATGGTACT    ATCTTC
                                     TCCGCA
GAM826  HCDI     3'  TTCCAGGTTAGGCACT     39493       ATGACA
                                AGTGCT    AACCTGGAA
                                ||||||    |||||||||
                                TCACGG    TTGGACCTT
                                   A_____
GAM826  HNT      3'  CTTCCGGCCCAAGCGTGGCGCT 33261         ACAAAC
                                AGTGCTATG    CTGGAAG
                                |||||||||    |||||||
                                TCGCGGTGC    GGCCTTC
                                     GAACCC
GAM826  HNT      3'  CTTCCGGCCCAAGCGTGGCGCT 33262         ACAAAC
          T                     GAGTGCTATG    CTGGAAG
                                ||||||||||    |||||||
                                TTCGCGGTGC    GGCCTTC
                                     GAACCC
GAM826  HRI      3'  CTTCCTCCTTTATTGTAGCACT 26984         TG C   CCT
          CA                      TGAGTGCTA  A AAA   GGAAG
                                |||||||||  | |||   |||||
                                ACTCACGAT  T TTT   CCTTC
                                     GT A   CCT
GAM826  HYPH     3'  TTTTGGGTTTTGTTCTCA    94903     TGCTAT    _  TG
                                TGAG     GACAAA CC  GAA
                                ||||     |||||| ||  |||
                                ACTC     TTGTTT GG  TTT
                                  _______     T  GT
GAM826  ICAP-1A  3'  TTCCCAGTCATGGTATCA    16480    G       AAACCT
                                TGA TGCTATGAC     GGAA
                                ||| |||||||||     ||||
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                                ACT ATGGTACTG     CCTT
                                  _       AC____
GAM826  IDI2     3'  TTTCCATTTTATAAGCACTT  52699       _   CAAACC
                                GAGTGCT ATGA     TGGAAG
                                ||||||| ||||     ||||||
                                TTCACGA TATT     ACCTTT
                                   A    TT____
GAM826  IMPACT   3'  TTTCATTTTATAGTGTTCA   37396     TG    CAAACC
                                TGAG  CTATGA     TGGAA
                                ||||  ||||||     |||||
                                ACTT  GATATT     ACTTT
                                  GT     TT____
GAM826  KIAA0090 3'  CTAGTTTGTTTTAGTATTCA  88442        T     C
                                TGAGTGCTA GACAAAC TGG
                                ||||||||| ||||||| |||
                                ACTTATGAT TTGTTTG ATC
                                     T     _
GAM826  KIAA0121 3'  TTCCAAGCTTTGGCATTCA   72666        TGACAAACC
                                TGAGTGCTA       TGGAA
                                |||||||||       |||||
                                ACTTACGGT       ACCTT
                                     TTCGA____
GAM826  KIAA0193 3'  CTTTCAGGTTAACAAGAGGCAT 28653       ATGACA_
           TT                    GAGTGCT      AACCTGGAAG
                                 |||||||      ||||||||||
                                 TTTACGG      TTGGACTTTC
                                    AGAACAA
GAM826  KIAA0226 3'  TTTCCACCTGCTGTGGTGCTT  63527    TG   GA  AACC
                                GAG  CTAT  CA   TGGAAG
                                |||  ||||  ||   ||||||
                                TTC  GGTG  GT   ACCTTT
                                  GT   TC  CC__
GAM826  KIAA0252 3'  CTTCTGGGTTTAGTAGAGCCTC 62792     T  ATG  _    TG
           A                     TGAG GCT   AC AAACC  GAAG
                                 |||| |||   || |||||  ||||
                                 ACTC CGA   TG TTTGG  CTTC
                                   _  GA_  A    GT
GAM826  KIAA0258 3'  TTTCAGCTATAGCATT      28825         ACAAAC
                                AGTGCTATG     CTGGAA
                                |||||||||     ||||||
                                TTACGATAT     GACTTT
                                     C_____
GAM826  KIAA0261 3'  TTCTTCGTCATGCATTC     68184       T    AAACCT
                                GAGTGC ATGAC     GGAA
                                |||||| |||||     ||||
                                CTTACG TACTG     TCTT
                                   _    CT____
GAM826  KIAA0268 3'  TTTCCCACTTGTATAGCATTCA 70007          A   ACCT
                                TGAGTGCTATG CAA    GGAAG
                                |||||||||| |||    |||||
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                                ACTTACGATAT GTT   CCTTT
                                      _  CAC_
GAM826  KIAA0316 3' TTTGCTCATAGTATTT     69677          _
                                GAGTGCTATGA CAAA
                                |||||||||| ||||
                                TTTATGATACT GTTT
                                  C
GAM826  KIAA0356 3' CTTCTCCCGGTCATGGCAC   66192         AAACCT
                                GTGCTATGAC    GGAAG
                                |||||||||     |||||
                                CACGGTACTG    TCTTC
                                     GCCC__
GAM826  KIAA0410 3' TTTCTGGGTTAGAAGCTATTC 28784     _  ATGACA   TG
                                GAGT GCT     AACC  GAAG
                                |||| |||     ||||  ||||
                                CTTA CGA     TTGG  CTTT
                                  T  AGA___   GT
GAM826  KIAA0444 3' CTTCCCTGTGTTGCAGCGCTCA 62343       AT   AACCT
                                TGAGTGCT  GACA    GGAAG
                                ||||||||  ||||    |||||
                                ACTCGCGA  TTGT    CCTTC
                                     CG   GTC__
GAM826  KIAA0459 3' CTTCCCTTCTGTTGTAGACTTA 60994     G  TG  AACCT
                                TGAGT CTA  ACA    GGAAG
                                |||||  |||  |||    |||||
                                ATTCA GAT  TGT    CCTTC
                                   _  GT   CTTC_
GAM826  KIAA0470 3' TTTGTTATGCATTTA      29058       T
                                TGAGTGC ATGACAAA
                                ||||||| ||||||||
                                ATTTACG TATTGTTT
                                     _
GAM826  KIAA0660 3' TTTCTGATATAGTACTT     24518         A  AACCT
                                GAGTGCTATG CA    GGAA
                                |||||||||| ||    ||||
                                TTCATGATAT GT    CTTT
                                     A  _____
GAM826  KIAA0828 3' TTTCCTCCACAGTTTTGGTATT 81205       T  AAACCT
           T                     GAGTGCTA GAC     GGAAG
                                |||||||| |||     |||||
                                TTTATGGT TTG     CCTTT
                                     T  ACACCT
GAM826  KIAA0976 3' CTTCTAGGCTGCTTTAATGGCA 29892       GACAAA__
           TTC                   GAGTGCTAT      CCTGGAAG
                                |||||||||       ||||||||
                                CTTACGGTA      GGATCTTC
                                     ATTTCGTC
GAM826  KIAA1034 3' TTTTTGGGTTTTTTTGGC    62477     T  C    TG
                                GCTA GA AAACC  GAAG
                                |||| || |||||  ||||
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                                CGGT TT TTTGG  TTTT
                                  T _    GT
GAM826  KIAA1040 3' TTTTTGGAGATAGTCAAGCATT 72235       A   AAAC_ TG
             TA                   TGAGTGCT TGAC    C  GAAG
                                |||||||| ||||    |  ||||
                                ATTTACGA ACTG    G  TTTT
                                     _   ATAGA GT
GAM826  KIAA1046 3' CTTCCAGTCTTTGCAGTATTCA 29996       AT A   C_
                                TGAGTGCT  G CAAA  CTGGAAG
                                |||||||| | ||||  |||||||
                                ACTTATGA  C GTTT  GACCTTC
                                     __ _   CT
GAM826  KIAA1078 3' TTTTAATGGTGTTACAGCATTT 65127       A   AA   TG_
                                GAGTGCT TGAC  ACC   GAAG
                                ||||||| ||||  |||   ||||
                                TTTACGA ATTG  TGG   TTTT
                                    C   __   TAA
GAM826  KIAA1096 3' CTTCGGATATGGTTATGGCATT 68529         AAAC_   AG
             T                   GAGTGCTATGAC    CTGGA
                                ||||||||||||    |||||
                                TTTACGGTATTG    GGCTT
                                      GTATA    C
GAM826  KIAA1211 3' TTCTAATTTTGAGCATTCA   68898       ATGA   CC
                                TGAGTGCT   CAAA  TGGAA
                                ||||||||   ||||  |||||
                                ACTTACGA   GTTT  ATCTT
                                     _____   TA
GAM826  KIAA1219 3' TTTCCATTCAGGTTATAGTATT 61374        AAACC
                                AGTGCTATGAC    TGGAAG
                                ||||||||||    ||||||
                                TTATGATATTG    ACCTTT
                                      GACTT
GAM826  KIAA1219 3' TTTTAGGAGGTTGTATTCA   61375       TAT   AAA
                                TGAGTGC   GAC   CCTGGAA
                                |||||||   |||   |||||||
                                ACTTATG   TTG   GGATTTT
                                     ___   GA_
GAM826  KIAA1247 3' TTTCCAGCAGACCTGTGGTATT 61856       GACAAAC
                                AGTGCTAT      CTGGAAG
                                ||||||||      |||||||
                                TTATGGTG      GACCTTT
                                     TCCAGAC
GAM826  KIAA1247 3' TTTTCAGGAGTGGTGGTGTCA  61857    G     G  AAA
                                TGA TGCTAT AC   CCTGGAAG
                                ||| |||||| ||   ||||||||
                                ACT GTGGTG TG   GGACTTTT
                                  _     G  A__
GAM826  KIAA1271 3' CTTCCGGGGCTGTGTGGC    69543      G   AA
                                GCTAT ACA  CCTGGAAG
                                ||||| |||  ||||||||
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                                CGGTG TGT  GGGCCTTC
                                  _  CG
GAM826  KIAA1321 3' TTTCTGGGTTTGTGACATACA 62229    C   __      TG
                                TG TATG  ACAAACC  GAAG
                                || ||||  |||||||  ||||
                                AC ATAC  TGTTTGG  CTTT
                                 _   AG      GT
GAM826  KIAA1332 3' TTTCCAGTGTGTAAGCATTT  71171       ATG   AAC
                                GAGTGCT   ACA   CTGGAAG
                                |||||||   |||   |||||||
                                TTTACGA   TGT   GACCTTT
                                    A__   GT_
GAM826  KIAA1364 3' TTTTAGGTTCTTAGCCTCA   63601     T   T  CAA
                                TGAG GCTA GA   ACCTGGAA
                                |||| |||| ||   ||||||||
                                ACTC CGAT CT   TGGATTTT
                                  _   T  ___
GAM826  KIAA1388 3' TGAAAGCAGTTTGTTATACTAT 93583       C        C  GAAG
           TCA                    TGAGTG TATGACAAAC TG
                                |||||| |||||||||| ||
                                ACTTAT ATATTGTTTG AC
                                   C        _ GAAAGTC
GAM826  KIAA1396 3' TCCAGCACAGCGCTT       62994        A  ACAAAC
                                GAGTGCT TG     CTGGA
                                |||||||  ||     |||||
                                TTCGCGA AC     GACCT
                                   C  _______
GAM826  KIAA1434 3' TTCCGAAGTCTGGCATTT    69622        T   AAACC
                                GAGTGCTA GAC    TGGAA
                                |||||||| |||    |||||
                                TTTACGGT CTG    GCCTT
                                    _   AA___
GAM826  KIAA1437 3' TTTTTGGGTTTTTTTGGTGTCT 60597    _    T  C    TG
           T                     GAG TGCTA GA AAACC  GAAG
                                ||| ||||| || |||||  ||||
                                TTC GTGGT TT TTTGG  TTTT
                                  T    T  _    GT
GAM826  KIAA1505 5' TTTCTATCATTCATAGTATTTA 94188          CAAACC
                                TGAGTGCTATGA     TGGAAG
                                ||||||||||||     ||||||
                                ATTTATGATACT     ATCTTT
                                      TACT__
GAM826  KIAA1554 3' TTCTATTTATGGCAC      95157         CAAACC
                                GTGCTATGA     TGGAA
                                |||||||||     |||||
                                CACGGTATT     ATCTT
                                     T_____
GAM826  KIAA1582 3' CTTCCAGGTTGACATCAGTAC  65372      _  ACA
                                GTGCT ATG   AACCTGGAAG
                                ||||| |||   ||||||||||
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                                CATGA TAC   TTGGACCTTC
                                  C  AG_
GAM826  KIAA1600 3' TTTCTTAATGTTTTCATAGTGC 71449     TG     C   CT__
            TCA                   GAG  CTATGA AAAC    GGAAG
                                ||| |||||| ||||   |||||
                                CTC  GATACT TTTG    TCTTT
                                  GT     _    TAAT
GAM826  KIAA1641 3' TTTCAGATTATAGCATACA   80212    A       CAAAC
                                TG GTGCTATGA    CTGGAA
                                || |||||||||    ||||||
                                AC TACGATATT    GACTTT
                                 A       A____
GAM826  KIAA1728 3' TTTCTGTGTTATGGTTCTTA  68421     T       AACCT
                                TGAG GCTATGACA    GGAA
                                |||| |||||||||    ||||
                                ATTC TGGTATTGT    CTTT
                                  T       GT___
GAM826  KIAA1765 3' TTTCTATGTGAAGTCAGGCGCT 70615        A   AA_  C
            CA                    TGAGTGCT TGAC   AC TGGAAG
                                |||||||| ||||   || ||||||
                                ACTCGCGG ACTG   TG ATCTTT
                                     _   AAG  T
GAM826  KIAA1843 3' CTTCCCAAGAATTTATAGCACT 62190          CAAACCT
            TA                    TGAGTGCTATGA      GGAAG
                                ||||||||||||      |||||
                                ATTCACGATATT      CCTTC
                                       TAAGAAC
GAM826  KIAA1866 3' TTCCAGGAATAGCAT      60936       GACAAA
                                GTGCTAT     CCTGGAA
                                |||||||     |||||||
                                TACGATA     GGACCTT
                                   A_____
GAM826  KIAA1906 3' TTTCTGGGGACCATGCATTT  73200       T  ACAAA  TG
                                GAGTGC ATG    CC  GAAG
                                |||||| |||    ||  ||||
                                TTTACG TAC    GG  CTTT
                                   _  CAG__  GT
GAM826  KIAA1910 3' TTTGTTAAAGCACTCA      73332        A
                                TGAGTGCT TGACAAA
                                |||||||| |||||||
                                ACTCACGA ATTGTTT
                                     A
GAM826  KIAA1918 3' TTTTTGGTTGTCATGGT     73167         A  TG
                                GCTATGACAA CC  GAA
                                |||||||||| ||  |||
                                TGGTACTGTT GG  TTT
                                      _ TT
GAM826  KIAA1922 3' CTTTCTTTCTTATAGCACTTA 73628          C   CCT
                                TGAGTGCTATGA AAA   GGAAG
                                |||||||||||| |||   |||||
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                                ATTCACGATATT TTT   CTTTC
                                      C  ___
GAM826  KIAA1958  3'  TTTCCAGGAGACAGATTGCGCT 81914       TATGACAAA
            T                  GAGTGC       CCTGGAAG
                               ||||||       ||||||||
                               TTCGCG       GGACCTTT
                                  TTAGACAGA
GAM826  KOC1      3'  CTTCCCTTTGTTGTAGTCTCA  91073     T   TG    CCT
                               TGAG GCTA  ACAAA   GGAAG
                               |||| ||||  |||||   |||||
                               ACTC TGAT  TGTTT   CCTTC
                                 _   GT    C__
GAM826  MDS029    3'  CTTTCACATTTATGGCATTT   37466         CAAACC
                               GAGTGCTATGA     TGGAAG
                               ||||||||||      ||||||
                               TTTACGGTATT     ACTTTC
                                      TAC___
GAM826  MEP50     3'  CTTTATTTTTTTATAGTGCTTA 44082      TG     C   CCTG
                               TGAG  CTATGA AAA    GAAG
                               ||||  |||||| |||    ||||
                               ATTC  GATATT TTT    TTTC
                                 GT     T   TA__
GAM826  MGC11242  3'  TTTTTAGGTTTGTATTTATGT  44238    _  TG_
                               GC TA   ACAAACCTGGAAG
                               || ||   ||||||||||||
                               TG AT   TGTTTGGATTTTT
                                T  TTA
GAM826  MGC13183  3'  TTTTTGGGCAATTTCATGGTGT 50391     TG     CAAA_  TG
            TT                  GAG  CTATGA    CC  GAAG
                               |||  ||||||    ||  ||||
                               TTT  GGTACT    GG  TTTT
                                 GT     TTAAC  GT
GAM826  MGC14161  5'  CTTTTGGGTTTGTTGTTCTTCA 51843      TGCT TG      TG
                               TGAG    A  ACAAACC  GAAG
                               ||||    |  |||||||  ||||
                               ACTT    T  TGTTTGG  TTTC
                                 CT__ GT      GT
GAM826  MGC14595  5'  TTTCCGGGTGAAACTGGCATT  50333       TGACAA
                               AGTGCTA     ACCTGGAAG
                               |||||||     |||||||||
                               TTACGGT     TGGGCCTTT
                                  CAAAG_
GAM826  MGC2306   3'  TTTCTGGGGGCTGGTTGGCATT 50967       TGA  AA_  TG
            T                   GAGTGCTA   CA   CC  GAAG
                               ||||||||   ||   ||  ||||
                               TTTACGGT   GT   GG  CTTT
                                    TG_  CGG  GT
GAM826  MGC2560   3'  CTTCTGTTGGTCATAGT     48782        A   CT
                               GCTATGAC AAC  GGAAG
                               |||||||| |||  |||||
```

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                                TGATACTG TTG  TCTTC
                                    G  __
GAM826  MGC2747  3' CTTTTAGGACTGAGTAGCCTT 44085    T    GA  AA
                                GAG GCTAT  CA  CCTGGAAG
                                ||| |||||  ||  ||||||||
                                TTC CGATG  GT  GGATTTTC
                                  _    A_  CA
GAM826  MGC29956 3'  TTTGTGTATGGTACTT     58282         _
                                GAGTGCTATG ACAAA
                                |||||||||| |||||
                                TTCATGGTAT TGTTT
                                      G
GAM826  MGC32043 3'  TTCTGGGTTTGGGTCTT    58059    T  ATGA    TG
                                GAG GCT   CAAACC  GAA
                                ||| |||   ||||||  |||
                                TTC TGG   GTTTGG  CTT
                                  _  _____    GT
GAM826  MRPS16   5'  TTTTCGGGCTTGTACCGCTT  32161     CTATG   A
                                GAGTG    ACAA CCTGGAAG
                                |||||    |||| ||||||||
                                TTCGC    TGTT GGGCTTTT
                                   CA___   C
GAM826  MSH5     5'  TTTGCAGGCTCGTGGCGGTC  10124   G      CAAA   G
                                GA TGCTATGA   CCTG AAG
                                || ||||||||   |||| |||
                                CT GCGGTGCT   GGAC TTT
                                 G      C___   G
GAM826  MST4     3'  TTTGTGATGGCGTTTA     33302         G
                                TGAGTGCTAT ACAAA
                                |||||||||| |||||
                                ATTTGCGGTA TGTTT
                                      G
GAM826  NDRG4    3'  TTCTGTCTCATAGCAC     43293        CAA  CT
                                GTGCTATGA  AC  GGAA
                                |||||||||  ||  ||||
                                CACGATACT  TG  TCTT
                                     C__  __
GAM826  NDRG4    3'  TTCTGTCTCATAGCAC     39990        CAA  CT
                                GTGCTATGA  AC  GGAA
                                |||||||||  ||  ||||
                                CACGATACT  TG  TCTT
                                     C__  __
GAM826  NIFU     5'  AATCAGGACATGGTATTC    67311         ACAAA    AAG
                                GAGTGCTATG    CCTGG
                                ||||||||||    |||||
                                CTTATGGTAC    GGACT
                                      A_____    AAC
GAM826  NY-REN-41 3'  CTTCTGGGAGACAATATATTCA 54687       C   GACAAA  TG
                                TGAGTG TAT     CC  GAAG
                                |||||| |||     ||  ||||
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                                ACTTAT ATA     GG  CTTC
                                   _  ACAGA_  GT
GAM826  PC326    3'  TTTGGCAAGCACTTA      37415         A  A
                                TGAGTGCT TG CAAA
                                |||||||| || ||||
                                ATTCACGA AC GTTT
                                     _ G
GAM826  PDZ-GEF1 3'  TTCTGTATCATGGCATTT    26498          CAA  CT
                                GAGTGCTATGA   AC  GGAA
                                ||||||||||   ||  ||||
                                TTTACGGTACT   TG  TCTT
                                      A__ __
GAM826  PHRET1   3'  CTTCCGGGTTTGGACCATTC   41059      CTATGA
                                GAGTG     CAAACCTGGAAG
                                |||||     ||||||||||||
                                CTTAC     GTTTGGGCCTTC
                                   CAG___
GAM826  PIF1     3'  TTTTCAGGGGATAAATAGTGTT 61024     TG    GACAAA
           T                     GAG  CTAT     CCTGGAAG
                                |||  ||||     ||||||||
                                TTT  GATA     GGACTTTT
                                  GT    AATAGG
GAM826  PIGPC1   3'  TTTTTAAGTAGTGTTATAGTTT 42094      T       A_  C
           CA                     TGAG GCTATGACA  AC TGGAAG
                                |||| |||||||||  || ||||||
                                ACTT TGATATTGT  TG ATTTTT
                                  _       GA  A
GAM826  PIP3-E   3'  CTTTTAGCACTGCATGGTGTTT 66804     TG    A  AAC
                                GAG  CTATG CA   CTGGAAG
                                |||  ||||| ||   |||||||
                                TTT  GGTAC GT   GATTTTC
                                  GT    _  CAC
GAM826  POLR3F   3'  TTTCCAATGTGATGGTATTT   59942         G   AACC
                                GAGTGCTAT ACA    TGGAAG
                                ||||||||| |||    ||||||
                                TTTATGGTA TGT    ACCTTT
                                     G   A___
GAM826  POPX1    3'  TTTCATAACCTGTTATGGTGCT 29804     TG       AACC_    G
           T                     GAG  CTATGACA     TGGAA
                                |||  ||||||||     |||||
                                TTC  GGTATTGT     ACTTT
                                  GT       CCAAT
GAM826  PORIMIN  3'  TAAGAAGTTTGTCACAGCACTC 53607         A       CTGGAAG
           A                      TGAGTGCT TGACAAAC
                                |||||||| ||||||||
                                ACTCACGA ACTGTTTG
                                     C       AAGAAT
GAM826  PRKCDBP  3'  TTTCAGAATGTAGCACTCA   58889          GACAAAC
                                TGAGTGCTAT      CTGGAA
                                ||||||||||      ||||||
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                                ACTCACGATG      GACTTT
                                      TAA____
GAM826  PROL2    3'  TTTGAGCATAGTACTT     22348          A_
                                GAGTGCTATG  CAAA
                                ||||||||||  ||||
                                TTCATGATAC  GTTT
                                      GA
GAM826  PTPRN2   3'  TTTCCAGGAAGAGTGTGCTT   55604     TG T  GACAAA
                                GAG  C AT     CCTGGAAG
                                |||  | ||     ||||||||
                                TTC  G TG     GGACCTTT
                                  GT _  AGAA__
GAM826  PTPRN2   3'  TTTCCAGGAAGAGTGTGCTT   55608     TG T  GACAAA
                                GAG  C AT     CCTGGAAG
                                |||  | ||     ||||||||
                                TTC  G TG     GGACCTTT
                                  GT _  AGAA__
GAM826  R32184_3 3'  CTTTCAGGGTTTCGTGGGGTTT 53066      G     CAAA
                                GAGT CTATGA    CCTGGAAG
                                |||| ||||||    ||||||||
                                TTTG GGTGCT    GGACTTTC
                                  G     TTG_
GAM826  RAB32    3'  TTCCAAGTTGTAGCTTTTA    22418      T    TG  AAACC
                                TGAG GCTA  AC    TGGAA
                                |||| ||||  ||    |||||
                                ATTT CGAT  TG    ACCTT
                                  T    GT  A____
GAM826  RAI17    3'  GTTGGTTATAGCATTT      91286           A
                                GAGTGCTATGAC AAC
                                |||||||||||| |||
                                TTTACGATATTG TTG
                                       G
GAM826  RRN3     3'  TTTCCAGGGCTTTGTATGCACT 37361       TATG    __
          T                      GAGTGC    ACAAA  CCTGGAAG
                                ||||||    |||||  ||||||||
                                TTCACG    TGTTT  GGACCTTT
                                   TA__     CG
GAM826  SDC3     3'  TTTTTGGGGCAGAGAGGCACTC 27771        ATGACAAA  TG
          A                      TGAGTGCT       CC  GAAG
                                ||||||||       ||  ||||
                                ACTCACGG       GG  TTTT
                                     AGAGACG_  GT
GAM826  SEC14L2  3'  TTTCTACCCCTTGTAGCAGTCA 24875     G     TG CAAACC
                                TGA TGCTA  A     TGGAAG
                                ||| |||||  |     ||||||
                                ACT ACGAT  T     ATCTTT
                                  G    GT CCCC__
GAM826  SEC24D   3'  TTTCCAGGAAGAGATGGCATTT 29095          GACAAA
          A                      TGAGTGCTAT     CCTGGAAG
                                ||||||||||     ||||||||
```

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                                ATTTACGGTA     GGACCTTT
                                      GAGAA_
GAM826  SEMA4G   3' CTTTTGGGGGAATCAAGCATTT 35436       A   CAAA  TG
                                GAGTGCT TGA    CC  GAAG
                                ||||||| |||    ||  ||||
                                TTTACGA ACT    GG  TTTC
                                    _   AAGG  GT
GAM826  SEMA4G   3' CTTTTGGGGGAATCAAGCATTT 94679       A   CAAA  TG
                                GAGTGCT TGA    CC  GAAG
                                ||||||| |||    ||  ||||
                                TTTACGA ACT    GG  TTTC
                                    _   AAGG  GT
GAM826  SEMA5A   3' CTTTTGGATTTCATGGCATTC  14256         CA  C TG
                                GAGTGCTATGA  AA C  GAAG
                                ||||||||||  || |  ||||
                                CTTACGGTACT  TT G  TTTC
                                      __  A GT
GAM826  SLC38A4  3' TTTCTTCACAGTCAAAGCATTT 35879       A    AAACCT
            A                    TGAGTGCT TGAC     GGAAG
                                ||||||| ||||      |||||
                                ATTTACGA ACTG     TCTTT
                                     A    ACACT_
GAM826  SPINLW1  3' TCCAGTAAAGTACTT       39872        A  ACAAAC
                                GAGTGCT TG     CTGGA
                                ||||||| ||     |||||
                                TTCATGA AT     GACCT
                                    A _______
GAM826  STAT5A   3' TTTCAGATCATGGCATCCA   12017    AG      CAAAC
                                TG  TGCTATGA    CTGGAA
                                ||  ||||||||    ||||||
                                AC  ACGGTACT    GACTTT
                                 CT       A____
GAM826  STK38L   3' TTTAAATATTTGTTGAGTACTT 69176        A      CCTGGAAG
            A                    TGAGTGCT TGACAAA
                                ||||||||| |||||||
                                ATTCATGA GTTGTTT
                                    _      ATAAATTTT
GAM826  SYT13    3' TTTGTTGAGCACTTA       93462        A
                                TGAGTGCT TGACAAA
                                ||||||| |||||||
                                ATTCACGA GTTGTTT
                                    _
GAM826  TIP120A  3' CTTCCATTGTTGTTTTTGTAGC 37426       ___    ACC
            ATTTA                GTGCTAT   GACAA   TGGAAG
                                |||||||   |||||   ||||||
                                TACGATG   TTGTT   ACCTTC
                                    TTT    GTT
GAM826  TP53TG3  3' TTTCAGGTTAAGTACTGCA   31109    _     ATGACA
                                TG AGTGCT     AACCTGGAA
                                || ||||||     |||||||||
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                                AC TCATGA     TTGGACTTT
                                 G     A_____
GAM826  TReP-132  5'  CTTTTGGGTTTGGTTTATTTA  37292       CTATGA     TG
                                TGAGTG     CAAACC  GAAG
                                ||||||     ||||||  ||||
                                ATTTAT     GTTTGG  TTTC
                                   TTG___     GT
GAM826  TReP-132  5'  CTTTTGGGTTTGGTTTATTTA  53139       CTATGA     TG
                                TGAGTG     CAAACC  GAAG
                                ||||||     ||||||  ||||
                                ATTTAT     GTTTGG  TTTC
                                   TTG___     GT
GAM826  TReP-132  5'  CTTTTGGGTTTGTTTTATTTA  53148       CTAT       TG
                                TGAGTG   GACAAACC  GAAG
                                ||||||   ||||||||  ||||
                                ATTTAT   TTGTTTGG  TTTC
                                   T___       GT
GAM826  TUSP      5'  TTTCTAGCCTCTATGGCACT   39646         ACAAAC
                                AGTGCTATG     CTGGAAG
                                |||||||||     |||||||
                                TCACGGTAT     GATCTTT
                                     CTCC__
GAM826  UBCE7IP5  3'  CTTCACCCTGTCATGGTCTCA  30152      T       AACCTG
                                TGAG GCTATGACA     GAAG
                                |||| |||||||||     ||||
                                ACTC TGGTACTGT     CTTC
                                  _       CCCA__
GAM826  UBE2G1    3'  TTCTGGGTTTGCTATTAC    12488     CT   A     TG
                                GTG  ATG CAAACC  GAA
                                |||  ||| ||||||  |||
                                CAT  TAT GTTTGG  CTT
                                  __  C     GT
GAM826  UMP-CMPK  3'  CTTCACCTTAGTTATGGTGCTC 32843      TG      A  CC    AG
           A                     TGAG  CTATGAC AA  TGGA
                                ||||  ||||||| ||  ||||
                                ACTC  GGTATTG TT  ACTT
                                  GT      A  CC    C
GAM826  WHIP      3'  TTTGTCATAGTATTTA      39300
                                TGAGTGCTATGACAAA
                                ||||||||||||||||
                                ATTTATGATACTGTTT

GAM826  YAP1      3'  TTCATGTCACAGCATTTA     20360         A     AACC
                                TGAGTGCT TGACA    TGGA
                                |||||||| |||||    ||||
                                ATTTACGA ACTGT    ACTT
                                     C     _____
GAM826  ZDHHC5    3'  TTTCTAGGCTCATTGGCATTTA 91566          _   CAAA
                                TGAGTGCTA TGA    CCTGGAAG
                                ||||||||| |||    ||||||||
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                                ATTTACGGT ACT   GGATCTTT
                                     T  C___
GAM826  ZF5128   5'  TTTCCAGGGGGTTCCTGGTGCT 26810    TG  T_  AAA
          C                   GAG  CTA  GAC   CCTGGAAG
                              |||  |||  |||   ||||||||
                              CTC  GGT  TTG   GGACCTTT
                                GT   CC   GG_
GAM826  ZNF297B  3'  CTTTTAGTGTTTTGTGGTATTT 25784       TG CA  _
                              GAGTGCTA  A  AAC CTGGAAG
                              ||||||||  |  ||| |||||||
                              TTTATGGT  T  TTG GATTTTC
                                   GT __  T
GAM826  ZNF361   5'  CTTCCAGCCATGTGGTAC    37660       GACAAAC
                              GTGCTAT      CTGGAAG
                              |||||||      |||||||
                              CATGGTG      GACCTTC
                                   TACC___
GAM826  LOC121441 3'  TTTGTCATGGAATTTA      74069      G
                              TGAGT CTATGACAAA
                              ||||| ||||||||||
                              ATTTA GGTACTGTTT
                                 A
GAM826  LOC123803 3'  TTTCCAGTAATATATGGCATT  74234        ACAAAC
                              AGTGCTATG     CTGGAAG
                              |||||||||     |||||||
                              TTACGGTAT     GACCTTT
                                   ATAAT_
GAM826  LOC124446 5'  TTTCCGGGGAGGGGGTGCTCA  74292     TG  ATGACAAA
                              TGAG  CT      CCTGGAAG
                              ||||  ||      ||||||||
                              ACTC  GG      GGGCCTTT
                                GT  GGGAG___
GAM826  LOC124987 5'  TTTGCTCATCAGTGCTCA    75663     TG  _   _
                              TGAG  CT ATGA CAAA
                              ||||  || |||| ||||
                              ACTC  GA TACT GTTT
                                GT  C   C
GAM826  LOC127294 3'  CTTTTAGGATCCCATAGTTTCA 74654     T     ACAAA
                              TGAG GCTATG    CCTGGAAG
                              |||| ||||||    ||||||||
                              ACTT TGATAC    GGATTTTC
                                _     CCTA_
GAM826  LOC133619 3'  TTTCACCTATCATAGTACTCA  55523          CAAACC
                              TGAGTGCTATGA     TGGAA
                              ||||||||||||     |||||
                              ACTCATGATACT     ACTTT
                                     ATCC__
GAM826  LOC134145 3'  TTTCTAAAACTCATGGCAC    75146        CAAACC
                              GTGCTATGA     TGGAAG
                              |||||||||     ||||||
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                                CACGGTACT     ATCTTT
                                     CAAA__
GAM826  LOC134266 3'  CTTGGTGTTGTAGTACTT    75166        TG  AA   T
                                GAGTGCTA  AC  ACC GG
                                ||||||||  ||  ||| ||
                                TTCATGAT  TG  TGG TC
                                    GT  __   T
GAM826  LOC135763 3'  CTTTCATTTACATAGTGCTTA  56790     TG    ACAAACC
                                TGAG  CTATG      TGGAAG
                                ||||  |||||      |||||||
                                ATTC  GATAC      ACTTTC
                                  GT    ATTT___
GAM826  LOC137991 3'  TTTCTGGGTTATATATACTT   75292      C    ACA    TG
                                GAGTG TATG   AACC  GAAG
                                ||||| ||||   ||||  ||||
                                TTCAT ATAT   TTGG  CTTT
                                  _   A__    GT
GAM826  LOC142927 3'  TTTTCAGGTGATGTGGACTCA  76436      G    ACAA
                                TGAGT CTATG    ACCTGGAAG
                                ||||| |||||    |||||||||
                                ACTCA GGTGT    TGGACTTTT
                                  _    AG__
GAM826  LOC143916 3'  CCATGTCATAGCCTT      76638     T       AACC
                                GAG GCTATGACA    TGG
                                ||| |||||||||    |||
                                TTC CGATACTGT    ACC
                                  _       _____
GAM826  LOC145135 5'  TTCCAGATGCAGTACTCA    83254        AT A  AAC
                                TGAGTGCT  G CA   CTGGAA
                                ||||||||  | ||   ||||||
                                ACTCATGA  C GT   GACCTT
                                    __ _  A__
GAM826  LOC145601 3'  TTTCCGGGTGTGGTGGTAT   83374       G  AA
                                GTGCTAT AC  ACCTGGAAG
                                |||||||  ||  |||||||||
                                TATGGTG TG  TGGGCCTTT
                                    G  __
GAM826  LOC145761 5'  CTTTCGGGCTGGGTGGTTTCA  83476     T    GA  AA
                                TGAG GCTAT  CA  CCTGGAAG
                                ||||  |||||  ||  ||||||||
                                ACTT TGGTG  GT  GGGCTTTC
                                  _    G_  C_
GAM826  LOC145814 3'  TTTCAATCCTGTATGTAGCACT 77509          _  AACC    G
          CA                    TGAGTGCTATG ACA    TGGAA
                                ||||||||||| |||    |||||
                                ACTCACGATGT TGT    ACTTT
                                      A   CCTA
GAM826  LOC145820 3'  TTTCCAGGTTTGGGCTGTTAC  77520     C  TGA
                                GTG TA   CAAACCTGGAAG
                                ||| ||   ||||||||||||
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                                CAT GT   GTTTGGACCTTT
                                  T  CGG
GAM826   LOC145826 5'  TTTCCCTTTTCATAGTGCTCA  83533     TG     C   CCT
                                TGAG  CTATGA AAA   GGAAG
                                ||||  |||||| |||   |||||
                                ACTC  GATACT TTT   CCTTT
                                  GT     _   C__
GAM826   LOC145844 3'  TTTCCAGAGAGTGTGGCACTCA 77540         G  AAAC
                                TGAGTGCTAT AC    CTGGAAG
                                |||||||||| ||    |||||||
                                ACTCACGGTG TG    GACCTTT
                                      _  AGA_
GAM826   LOC146287 5'  TTTTTGGGTTTGTTTTGCTTCA 83655     T  TAT       TG
                                TGAG GC   GACAAACC  GAAG
                                |||| ||   ||||||||  ||||
                                ACTT CG   TTGTTTGG  TTTT
                                  _  TT_       GT
GAM826   LOC146433 3'  CTTCCATAGCTGTCATGGCCTC 77874      T        AACC
           A                     TGAG GCTATGACA    TGGAAG
                                ||||| |||||||||    ||||||
                                ACTC CGGTACTGT    ACCTTC
                                  _        CGAT
GAM826   LOC146433 5'  CTTCTGGGCTGCCATGGGACTT 77875      G     A  AA  TG
                                GAGT CTATG CA  CC  GAAG
                                |||| ||||| ||  ||  ||||
                                TTCA GGTAC GT  GG  CTTC
                                  G    C  C_  GT
GAM826   LOC146481 5'  TTTGAGATCCTGGCACTCA   77928         T ____
                                TGAGTGCTA GA   CAAA
                                |||||||||  ||   ||||
                                ACTCACGGT CT   GTTT
                                     C  AGA
GAM826   LOC146956 5'  CTTCCGGGCCCTGCGTGGCAGT 78209    G      A  AA_
           T                     GA TGCTATG CA   CCTGGAAG
                                || |||||||  ||   ||||||||
                                TT ACGGTGC GT   GGGCCTTC
                                 G      _  CCC
GAM826   LOC147219 3'  CTTCTAGGCTGTATGTAGTGCT 83989    TG    _   AA
                                AG  CTATG ACA  CCTGGAAG
                                ||  ||||| |||  ||||||||
                                TC  GATGT TGT  GGATCTTC
                                 GT    A   C_
GAM826   LOC147429 3'  CTTTCACATCCTGCATAGCACT 78357          ACAAACC
           TA                     TGAGTGCTATG      TGGAAG
                                ||||||||||       ||||||
                                ATTCACGATAC      ACTTTC
                                      GTCCTAC
GAM826   LOC147694 3'  TTTCTATACTCTATGGTACTTA 78460          ACAAACC
                                TGAGTGCTATG      TGGAAG
                                ||||||||||       ||||||
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                                ATTCATGGTAT      ATCTTT
                                     CTCAT__
GAM826  LOC147694 3'  TTTTCATGTGCTTGTTAGGCAT 78461        A     __  C
            TT                    GAGTGCT TGACAA  AC TGGAAG
                                  ||||||| ||||||  || ||||||
                                  TTTACGG ATTGTT  TG ACTTTT
                                     _     CG  T
GAM826  LOC148764 5'  CTTCTGGGGCATGGCACTCA   78985          ACAAA  TG
                                  TGAGTGCTATG    CC  GAAG
                                  ||||||||||     ||  ||||
                                  ACTCACGGTAC    GG  CTTC
                                        G____  GT
GAM826  LOC148918 3'  TCTAGTTGTGGCATCA      79086     G    TG  AAACC
                                  TGA TGCTA  AC     TGGA
                                  ||| |||||  ||     ||||
                                  ACT ACGGT  TG     ATCT
                                    _    GT  _____
GAM826  LOC149832 5'  CTTCTGGGTTTGTGTTTGCCTT 84698     T  TATG      TG
                                  GAG GC    ACAAACC  GAAG
                                  ||| ||    |||||||  ||||
                                  TTC CG    TGTTTGG  CTTC
                                    _ TTTG      GT
GAM826  LOC150311 3'  CTTTCAGACCATACAGTATTCA 79754         ATGACAAAC
                                  TGAGTGCT       CTGGAAG
                                  ||||||||       |||||||
                                  ACTTATGA       GACTTTC
                                       CATACCA__
GAM826  LOC150311 5'  TTCCAGGGATGGTGTTTA    79761      TG   GACAAA
                                  TGAG  CTAT     CCTGGAA
                                  ||||  ||||     |||||||
                                  ATTT  GGTA     GGACCTT
                                    GT    G_____
GAM826  LOC150481 5'  TTTCTGGGACCCCAGTGGGGCT 79902       G   GACAAA  TG
            TA                    TGAGT CTAT     CC  GAAG
                                  ||||| ||||     ||  ||||
                                  ATTCG GGTG     GG  CTTT
                                     G    ACCCCA  GT
GAM826  LOC150606 3'  TTTGTCGTTGTAGTATTT    85095          ___
                                  GAGTGCTAT   GACAAA
                                  |||||||||   ||||||
                                  TTTATGATG   CTGTTT
                                       TTG
GAM826  LOC150889 3'  TTTCTGTTGTTTAAGGCACTCA 80030         AT_    ACCT
                                  TGAGTGCT   GACAA    GGAA
                                  ||||||||   |||||    ||||
                                  ACTCACGG   TTGTT    CTTT
                                       AAT    GT__
GAM826  LOC151465 3'  TTCCAGATCATAGTGTTCA    62781      TG     CAAAC
                                  TGAG  CTATGA    CTGGAA
                                  ||||  ||||||    ||||||
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                                ACTT  GATACT    GACCTT
                                  GT     A____
GAM826  LOC151470 3'  TTTCTGGGTTTGAAGCTGCT   80261    _  ATGA     TG
                                AGT GCT    CAAACC  GAAG
                                ||| |||    ||||||  ||||
                                TCG CGA    GTTTGG  CTTT
                                  T   A___     GT
GAM826  LOC151657 3'  TTTATGTTTGTTTGGTGTTTA  85479     TG   T      C
                                TGAG  CTA GACAAAC TGGA
                                ||||  ||| ||||||| ||||
                                ATTT  GGT TTGTTTG ATTT
                                  GT   _      T
GAM826  LOC152890 5'  CTTCTAGGAGTAGTGGTATC   80718    G     G  AAA
                                GA TGCTAT AC   CCTGGAAG
                                || |||||| ||   ||||||||
                                CT ATGGTG TG   GGATCTTC
                                 _     A  A__
GAM826  LOC152991 3'  TTTTCATGGTTGTGGTTCTCA  85898     T    GACA   _
                                TGAG GCTAT    AACC TGGAAG
                                |||| |||||    |||| ||||||
                                ACTC TGGTG    TTGG ACTTTT
                                  T    _____    T
GAM826  LOC153339 5'  CTTTTAGGTTCAGGGGTAC    86008      A_  CAA
                                GTGCT  TGA   ACCTGGAAG
                                |||||  |||   |||||||||
                                CATGG  ACT   TGGATTTTC
                                   GG   ___
GAM826  LOC153592 3'  TTTTGGGACGCAGCACTT    86070       A  ACAAA  TG
                                GAGTGCT TG    CC  GAA
                                ||||||| ||    ||  |||
                                TTCACGA GC    GG  TTT
                                    C  A____  GT
GAM826  LOC155072 5'  TTTCCTCTGTTGTGGTTTTCA  86388     T   TG   AACCT
                                TGAG GCTA  ACA    GGAAG
                                |||| ||||  |||    |||||
                                ACTT TGGT  TGT    CCTTT
                                  T   GT   CT___
GAM826  LOC158191 5'  TTTCTGGGACCCCGGTGGGGCT 81787      G   GACAAA  TG
           TA                    TGAGT CTAT     CC  GAAG
                                |||||  ||||     ||  ||||
                                ATTCG GGTG     GG  CTTT
                                   G   GCCCCA  GT
GAM826  LOC158777 3'  TTTCCAAATAGTTGTAGCCTTA 82003     T   TG  AAACC
                                TGAG GCTA  AC    TGGAAG
                                |||| ||||  ||    ||||||
                                ATTC CGAT  TG    ACCTTT
                                  _   GT  ATAA_
GAM826  LOC158969 5'  TTTTGGGTGTGGCAGTTA    82065    G    GACAA   TG
                                TGA TGCTAT    ACC  GAA
                                ||| ||||||    |||  |||
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                                ATT ACGGTG    TGG  TTT
                                  G     _____  GT
GAM826  LOC161742 3'  TTTTTAGTTGTTTTTTGTGGTA 82295        TG C   __
                TTCA                  GAGTGCTA  A AAAC  CTGGAAG
                                |||||||| | ||||  |||||||
                                CTTATGGT  T TTTG  GATTTTT
                                    GT T    TT
GAM826  LOC162427 3'  TTTTAGGTATGAGTGCTCA   82355     TG  ATGA  A
                                TGAG  CT    CA ACCTGGAA
                                ||||  ||    || ||||||||
                                ACTC  GA    GT TGGATTTT
                                  GT  ____  A
GAM826  LOC163882 3'  CTTTCAGGAATTCTGTAGCATT 82166         _  CAAA
                C                   GAGTGCTAT GA    CCTGGAAG
                                |||||||||  ||    ||||||||
                                CTTACGATG CT    GGACTTTC
                                     T  TAA_
GAM826  LOC164714 5'  CTTCCGGCGCACCATGGCATCC 87229    AG      ACAAAC
                A                   TG  TGCTATG     CTGGAAG
                                ||  |||||||     |||||||
                                AC  ACGGTAC     GGCCTTC
                                 CT      CACGC_
GAM826  LOC168359 5'  CTTTTACCTTTGCATAGCGTTT 87276           A    CC
                A                   TGAGTGCTATG CAAA  TGGAAG
                                ||||||||||| ||||  ||||||
                                ATTTGCGATAC GTTT  ATTTTC
                                      _   CC
GAM826  LOC197201 3'  TTCCAGGCAGTGCACTTA    87949        TA  ACAAA
                                TGAGTGC  TG    CCTGGAA
                                |||||||  ||    |||||||
                                ATTCACG  AC    GGACCTT
                                    TG  _____
GAM826  LOC197414 3'  CTTCCAGGACAGGAGGCATTTA 88065         ATGACAAA
                                TGAGTGCT       CCTGGAAG
                                ||||||||       ||||||||
                                ATTTACGG       GGACCTTC
                                     AGGACA__
GAM826  LOC199786 3'  CTTTTGGGTTTGTTTCCTAGCT 88382      GCTAT       TG
                C                   GAGT    GACAAACC  GAAG
                                ||||    ||||||||  ||||
                                CTCG    TTGTTTGG  TTTC
                                  ATCCT       GT
GAM826  LOC200169 5'  CTTCCAGACCTATGGCATTT   89949          ACAAAC
                                GAGTGCTATG     CTGGAAG
                                ||||||||||     |||||||
                                TTTACGGTAT     GACCTTC
                                     CCA___
GAM826  LOC200982 3'  CTTCCAGGCTGTGTGGCCTT   90220     T    G   AA
                                GAG GCTAT ACA  CCTGGAAG
                                ||| ||||| |||  ||||||||
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                                TTC CGGTG TGT  GGACCTTC
                                  _    _   C_
GAM826   LOC201910 5'  CTTCTAGGAGTAGTGGTATC   89100    G     G  AAA
                                GA TGCTAT AC   CCTGGAAG
                                || |||||| ||   ||||||||
                                CT ATGGTG TG   GGATCTTC
                                  _     A  A__
GAM826   LOC219333 3'  TTCCGATCATGGTAGTT     93544    G       CAAACC
                                GA TGCTATGA     TGGAA
                                || |||||||      |||||
                                TT ATGGTACT     GCCTT
                                 G       A_____
GAM826   LOC219667 3'  TTAGCTTTGTCATGCTGTTCA  91314     GT C        C
                                TGA  G TATGACAAA CTGG
                                |||  | |||||||||| ||||
                                ACT  T GTACTGTTT GATT
                                  TG C        C
GAM826   LOC220534 3'  TTCTAGCGTAGAGCATTTA    90724        ATG  AAAC
                                TGAGTGCT   AC    CTGGAA
                                ||||||||   ||    ||||||
                                ATTTACGA   TG    GATCTT
                                     GA_  C___
GAM826   LOC220766 3'  TTTGTTATGCATTTA       90803        T
                                TGAGTGC ATGACAAA
                                ||||||| ||||||||
                                ATTTACG TATTGTTT
                                        _
GAM826   LOC221456 3'  CTTCCAGAAGCCCTATAGCATT 93644          ACAAAC
                                AGTGCTATG     CTGGAAG
                                |||||||||     |||||||
                                TTACGATAT     GACCTTC
                                     CCCGAA
GAM826   LOC221751 5'  CTTCCAGGGAAATTGTGGTCTC 92048     T    TG CAAA
                                GAG GCTA  A    CCTGGAAG
                                ||| ||||  |    ||||||||
                                CTC TGGT  T    GGACCTTC
                                  _    GT AAAG
GAM826   LOC221830 3'  TTCCAGGTTTTGCACTC     92514       TATGAC
                                GAGTGC     AAACCTGGAA
                                ||||||     ||||||||||
                                CTCACG     TTTGGACCTT
                                   T_____
GAM826   LOC221895 3'  TTTCAGGGGAAGCATTCA    92528        ATGACAAA
                                TGAGTGCT       CCTGGAA
                                ||||||||       |||||||
                                ACTTACGA       GGACTTT
                                     AGG_____
GAM826   LOC222057 3'  TTCCAGGCCTAGCGTTT     92784         TGACAAA
                                GAGTGCTA      CCTGGAA
                                ||||||||      |||||||
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                                TTTGCGAT      GGACCTT
                                    CC_____
GAM826  LOC222104 3'  TTTCTGGGTTTGGGCCATTTCA 92719     T__  ATGA     TG
                                TGAG  GCT   CAAACC  GAAG
                                ||||  |||   ||||||  ||||
                                ACTT  CGG   GTTTGG  CTTT
                                  TAC  ____     GT
GAM826  LOC253573 3'  CTTCCAGGGAATAGTAGTT   97051    G     GACAAA
                                GA TGCTAT     CCTGGAAG
                                || ||||||     ||||||||
                                TT ATGATA     GGACCTTC
                                 G     AG____
GAM826  LOC253955 3'  TTTCCGGGTAGGAAGGTAGCAT 94435         GACAA_
           TT                    GAGTGCTAT     ACCTGGAAG
                                |||||||||     |||||||||
                                TTTACGATG     TGGGCCTTT
                                     GAAGGA
GAM826  LOC254655 3'  TTCTGGGTTCAAGCGCTT    95477       A   CAA   TG
                                GAGTGCT TGA   ACC  GAA
                                ||||||| |||   |||  |||
                                TTCGCGA ACT   TGG  CTT
                                  _   ___   GT
GAM826  LOC255919 3'  CTTCACTCATTGTTATGGGACT 95033      G       ACCTG
           TA                    TGAGT CTATGACAA     GAAG
                                ||||| |||||||||     ||||
                                ATTCA GGTATTGTT     CTTC
                                   G        ACTCA
GAM826  LOC255975 3'  TTCCAGGCCTAGCGTTT     95901        TGACAAA
                                GAGTGCTA      CCTGGAA
                                ||||||||      |||||||
                                TTTGCGAT      GGACCTT
                                    CC_____
GAM826  LOC51308  3'  TTCTGGGTCTAGGGCTC     33498     G   T  CAAA  TG
                                GAGT CTA GA    CC  GAA
                                |||| ||| ||    ||  |||
                                CTCG GAT CT    GG  CTT
                                  G   _  _____  GT
GAM826  LOC51313  3'  CTTCTACAGATTTATAGTACTC 33509          CAAACC
                                GAGTGCTATGA     TGGAAG
                                ||||||||||      ||||||
                                CTCATGATATT     ATCTTC
                                      TAGAC_
GAM826  LOC51315  3'  TTGATTGGGTTTGTTATAGT   33533           TG AAG
                                GCTATGACAAACC  G
                                ||||||||||||  |
                                TGATATTGTTTGG  T
                                       GT AGTTC
GAM826  LOC51580  3'  TTCTCAGGTTTGGTATTTA    31869       TATGA      _
                                TGAGTGC    CAAACCTG GAA
                                |||||||    |||||||| |||
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                                ATTTATG    GTTTGGAC CTT
                                   _____       T
GAM826  LOC90190  3' TTCTGGGTTGCAGCCTTA   61782     T  ATGACA   TG
                                TGAG GCT     AACC  GAA
                                |||| |||     ||||  |||
                                ATTC CGA     TTGG  CTT
                                  _  CG____    GT
GAM826  LOC91147  3' TTTCCCATTGTGTGTAGTATTT 65064         G  AACCT
          A                      TGAGTGCTAT ACA     GGAAG
                                |||||||||| |||    |||||
                                ATTTATGATG TGT    CCTTT
                                      _  GTTAC
GAM826  LOC91266  3' TTCTGGGTTAGCGCTT     65418        TGACAA   TG
                                GAGTGCTA     ACC  GAA
                                ||||||||     |||  |||
                                TTCGCGAT     TGG  CTT
                                   _______  GT
GAM826  LOC91373  3' CTTCTGACGGATCTTGGTGCTC 65839     TG   T  CAAA  T__
          A                      TGAG  CTA GA    CC   GGAAG
                                |||| ||| ||    ||   |||||
                                ACTC  GGT CT    GG   TCTTC
                                  GT   T  A___  CAG
GAM826  LOC91695  5' TTTCCAGGTAGCCTACGTGGTG 66972     TG    ACAA__
          TTC                    GAG  CTATG     ACCTGGAAG
                                |||  |||||     |||||||||
                                CTT  GGTGC     TGGACCTTT
                                  GT     ATCCGA
GAM826  LOC92148  5' TTTCTAGGGCCATGGGGTTT   68339     G    ACAAA
                                GAGT CTATG     CCTGGAAG
                                |||| |||||     ||||||||
                                TTTG GGTAC     GGATCTTT
                                  G     CG___
GAM826  LOC92876  5' CTTCTAGGGTTTTTATGGT    70804       C  A
                                GCTATGA AA CCTGGAAG
                                ||||||| || ||||||||
                                TGGTATT TT GGATCTTC
                                    T  G
GAM826  LOC93622  3' TTTTTGTTTTTATAGCATTT   56935         C    CT
                                GAGTGCTATGA AAAC  GGAA
                                |||||||||| ||||  ||||
                                TTTACGATATT TTTG  TTTT
                                      _    T_
GAM827  FLJ11280  5' AGTGGCCACAACCCAGCC    37208       ATCCC  A
                                GGCTGG     TG TGGCCACT
                                ||||||     || ||||||||
                                CCGACC     AC ACCGGTGA
                                   CA___  _
GAM827  KIAA0182  3' GCCAGGGATCCACCA       72032     C       GAT
                                TGG TGGATCCCT   GGC
                                ||| |||||||||   |||
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                                ACC ACCTAGGGA  CCG
                                  _     ___
GAM827  MGC2488  3' AAGTGGGAAGGGATCCAACA  43865   GC      GATGG
                                TG  TGGATCCCT   CCACTT
                                ||  |||||||||   ||||||
                                AC  ACCTAGGGA   GGTGAA
                                 A_      AG___
GAM827  NYD-SP11 3' AAGTGGCCATCAAGCCCAGC  49211     ATCCC
                                GCTGG   TGATGGCCACTT
                                |||||   ||||||||||||
                                CGACC   ACTACCGGTGAA
                                   CGA__
GAM827  SARM     3' GGTCAAAAGTCCAGCCA    30613       TCC  GA
                                TGGCTGGA  CT  TGGCC
                                ||||||||  ||  |||||
                                ACCGACCT  GA  ACTGG
                                    ___  AA
GAM827  TRPM3    3' GGCTCAAGAATCCAGCC    64910       CC  GAT
                                GGCTGGAT  CT  GGCC
                                ||||||||  ||  ||||
                                CCGACCTA  GA  TCGG
                                    A_  AC_
GAM827  LOC149606 3' AAGTGGCTCTAGACCCAGGCA  79446   G   A  CCT  TG
                                TG CTGG TC  GA  GCCACTT
                                || |||| ||  ||  |||||||
                                AC GACC AG  CT  CGGTGAA
                                 G   C  AT_  __
GAM827  LOC150468 5' ATCAGAAGTCCAGCCA     79875       CC
                                TGGCTGGAT  CTGAT
                                |||||||||  |||||
                                ACCGACCTG  GACTA
                                     AA
GAM827  LOC152048 3' GTCACGAGGGATCCAGCCA  85548         GA
                                TGGCTGGATCCCT  TGGC
                                ||||||||||||  ||||
                                ACCGACCTAGGGA  ACTG
                                       GC
GAM827  LOC222256 3' TGGAAAGAGTCCAGCCA    94263       CC  GATGG
                                TGGCTGGAT  CT   CCA
                                |||||||||  ||   |||
                                ACCGACCTG  GA   GGT
                                     A_  AA___
GAM827  LOC255743 5' CCAATCAGGGACCCAGC    95917     A     _
                                GCTGG TCCCTGAT GG
                                ||||| |||||||| ||
                                CGACC AGGGACTA CC
                                   C      A
GAM827  LOC256581 5' AAGTGGCTCTGGGGACCAGCCA 97572       A   GAT
                                TGGCTGG TCCCT  GGCCACTT
                                ||||||| |||||  ||||||||
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                                ACCGACC AGGGG   TCGGTGAA
                                    _    TC_
GAM827  LOC90784  5' ATCAGGAGTCCAGCCA     63998        TC
                                TGGCTGGA  CCTGAT
                                ||||||||  ||||||
                                ACCGACCT  GGACTA
                                     GA
GAM827  LOC91149  3' TGGCCATTTGATCCAGC     65085        CCT
                                GCTGGATC   GATGGCCA
                                ||||||||   ||||||||
                                CGACCTAG   TTACCGGT
                                     T__
GAM827  LOC91380  5' TGACACTCTGAAATCCAGTCA  65863         CCCT  _  GC
                                TGGCTGGAT    GA TG  CA
                                |||||||||    || ||  ||
                                ACTGACCTA    CT AC  GT
                                      AAGT  C  A_
GAM827  LOC92078  5' AAGTGGCTTGCCAAAACCCACC 67972     C   ATCCCTGAT
           CA                     TGG TGG        GGCCACTT
                                ||| |||        ||||||||
                                ACC ACC        TCGGTGAA
                                  C   CAAAACCGT
GAM828  ADAMTS8   5' GCGGGCTTCTTCCCTCTCCT   22884       T       A
                                AGGAGA GGAAGAAGT TGT
                                |||||| ||||||||| |||
                                TCCTCT CCTTCTTCG GCG
                                   C        G
GAM828  ALG6     5' TGTGTTTTCTTCCCCTCC    25315      AT       TATG
                                GGAG  GGAAGAAG    TACA
                                ||||  ||||||||    ||||
                                CCTC  CCTTCTTT    GTGT
                                  C_       T____
GAM828  APTX     3' TTGTCCAGTCCTTCCATGCCCT 34664     AG      AAGTA  T
                                AGG  ATGGAAG     TG ACAA
                                |||  |||||||     || ||||
                                TCC  TACCTTC     AC TGTT
                                  CG      CTG__  C
GAM828  ATP11A   3' ACACACCTCTTCTTTTCTT   77014       T     A  A
                                AGGAGA GGAAGA GT TGT
                                |||||| |||||| || |||
                                TTCTTT TCTTCT CA ACA
                                   _     C  C
GAM828  ATP8A2   3' TATGTTCACCCATCTCC     93518        AA   G
                                GGAGATGG  GAA TATG
                                ||||||||  ||| ||||
                                CCTCTACC  CTT GTAT
                                     CA  _
GAM828  B4GALT5  3' TGCAGCCTCCATCTCCT     16514          AGAA  A
                                AGGAGATGGA    GT TGTA
                                ||||||||||    || ||||
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                                TCCTCTACCT   CG ACGT
                                     C___  _
GAM828  B4GALT5  3'  TGCTCTCTCCCCATCTCCT   16515       A_  _
                                AGGAGATGG  AGA AGTA
                                |||||||||  ||| ||||
                                TCCTCTACC  TCT TCGT
                                     CC   C
GAM828  B4GALT6  5'  GCTCCCTCCCATTTCCT    59865       A  A_
                                AGGAGATGG AG  AGT
                                |||||||||  ||  |||
                                TCCTTTACC TC  TCG
                                     C  CC
GAM828  CACNA2D2 3'  TGCACACTCCATCTCCT    20089        AGAA  A
                                AGGAGATGGA   GT TGTA
                                ||||||||||   ||  ||||
                                TCCTCTACCT   CA ACGT
                                     ____  C
GAM828  CBFA2T2  3'  GCTCCCCTCCCCATCTCCT   17471       A_  A__
                                AGGAGATGG  AG   AGT
                                |||||||||  ||   |||
                                TCCTCTACC  TC   TCG
                                     CC  CCC
GAM828  CMRF35   3'  TGCTCTCTCCACATCTCCT   21930       GA_  _
                                AGGAGATG   AGA AGTA
                                ||||||||   ||| ||||
                                TCCTCTAC   TCT TCGT
                                     ACC   C
GAM828  CXCL16   3'  TGCAACCCCCATCTCC      41928       AAGAA  A
                                GGAGATGG    GT TGTA
                                ||||||||    ||  ||||
                                CCTCTACC    CA ACGT
                                     CC___  _
GAM828  CYP8B1   3'  TACCATTCACCCCATCTCC   15269       AA_  GTAT
                                GGAGATGG   GAA   GTA
                                ||||||||   |||   |||
                                CCTCTACC   CTT   CAT
                                     CCA   AC__
GAM828  DDX11    3'  TGTTTCTTCCCCTCCT     47665     AT
                                AGGAG  GGAAGAAGTA
                                |||||  ||||||||||
                                TCCTC  CCTTCTTTGT
                                   C_
GAM828  DDX26    5'  ACCTCTACCATCTCCT     24051       A  A
                                AGGAGATGG AGA GT
                                |||||||||  ||| ||
                                TCCTCTACC TCT CA
                                     A   C
GAM828  DIAPH2   3'  TGCATCTCCCTCTCCT     22071      T  A  A
                                AGGAGA GGA GA GTA
                                ||||||  ||| ||  |||
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                                TCCTCT CCT CT CGT
                                   C  _ A
GAM828  DPYSL3   3'  ATTTCTTCCACCTGCT     7312     G  A
                                AG AG TGGAAGAAGT
                                || || ||||||||||
                                TC TC ACCTTCTTTA
                                 G  C
GAM828  EGR4     3'  CGCTCTTCTTCCAACTCCT   8745       A       TA
                                AGGAG TGGAAGAAG  TG
                                ||||| |||||||||  ||
                                TCCTC ACCTTCTTC  GC
                                   A        TC
GAM828  ELK1     3'  ACATCTCCCCCACCTCC     17837     A   AA  A T
                                GGAG TGG  GA G ATGT
                                |||| |||  || | ||||
                                CCTC ACC  CT C TACA
                                  C   CC  _ _
GAM828  EN2      3'  ACTCCCTCCTCCTTCTCCT   7456       T   A ___
                                AGGAGA GGA GA   AGT
                                ||||||| ||| ||   |||
                                TCCTCT CCT CT   TCA
                                   T   C  CCC
GAM828  F8       3'  TGCTCCTTCCATCTGCC     3736    _       A
                                GG AGATGGAAG AGTA
                                || |||||||| ||||
                                CC TCTACCTTC TCGT
                                 G        C
GAM828  FCRH3    3'  CACACATCATCCATCTCT    53629        A  A  A
                                GGAGATGGA GA GT TG
                                ||||||||| || || ||
                                TCTCTACCT CT CA AC
                                      A  A  C
GAM828  GCN1L1   3'  TGCCTCCTCCATCTCT      69759        A  A
                                GGAGATGGA GA GTA
                                ||||||||| || |||
                                TCTCTACCT CT CGT
                                      C  C
GAM828  GMPR     3'  TGCTTTTCCCATCTCC      91004        A
                                GGAGATGG AGAAGTA
                                |||||||| |||||||
                                CCTCTACC TTTTCGT
                                      C
GAM828  GORASP1  3'  TGTACTTGCCCCCATCTCCT  49114        AAGAA  T
                                AGGAGATGG    GTA GTACA
                                |||||||||    ||| |||||
                                TCCTCTACC    CGT CATGT
                                      CC___  T
GAM828  GPR4     5'  ACATACTTCCTAATTGCCCT  59896    A_  GGAA
                                AGG  GAT   GAAGTATGT
                                |||  |||   |||||||||
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                                TCC  TTA   CTTCATACA
                                  CG   ATC_
GAM828  GYPC    3'  ATGCCTCCCCCATCTCC    33651       AA  A
                                GGAGATGG  GA GTAT
                                ||||||||  || ||||
                                CCTCTACC  CT CGTA
                                    CC  C
GAM828  GYPC    3'  ATGCCTCCCCCATCTCC    9161        AA  A
                                GGAGATGG  GA GTAT
                                ||||||||  || ||||
                                CCTCTACC  CT CGTA
                                    CC  C
GAM828  HEXA    3'  TGCATACTCATCCACCTCC   4977      A   A  A
                                GGAG TGGA GA GTATGTA
                                |||| |||| || |||||||
                                CCTC ACCT CT CATACGT
                                  C   A  _
GAM828  HHIP    5'  TGTACATATTTTTGTCCCCGCC 42490    A  AA_______
            ACCTCC                  GAG TGG      GAAGTATGTACA
                                ||| |||      ||||||||||||
                                CTC ACC      TTTTATACATGT
                                  C  GCCCCTGT
GAM828  HOXC5   3'  TGTCGGCGCTGCCCCATCTCC  38494       AAGA  A_  T
                                GGAGATGG   AGT  TG ACA
                                ||||||||   |||  || |||
                                CCTCTACC   TCG  GC TGT
                                    CCG_  CG  _
GAM828  IER3    3'  CGTGAGATCCTTCCATCTTCT  53384         AAG__
                                AGGAGATGGAAG   TATG
                                ||||||||||||   ||||
                                TCTTCTACCTTC   GTGC
                                      CTAGA
GAM828  IER3    3'  CGTGAGATCCTTCCATCTTCT  13994         AAG__
                                AGGAGATGGAAG   TATG
                                ||||||||||||   ||||
                                TCTTCTACCTTC   GTGC
                                      CTAGA
GAM828  IHH     3'  GCTCCTGCCATCTCCT     72114       A  A
                                AGGAGATGG AG AGT
                                |||||||| || |||
                                TCCTCTACC TC TCG
                                    G  C
GAM828  ITGA11  3'  TGCACTTGACCTCATCTCC   24207      AAG_  AT
                                GGAGATGG   AAGT  GTA
                                ||||||||   ||||  |||
                                CCTCTACT   TTCA  CGT
                                    CCAG   __
GAM828  JUP     3'  TGTTGGAGGCCCTCCCATCTCC 9492       A  AA  ATGT_
                                GGAGATGG AG  GT   ACA
                                ||||||| ||  ||   |||
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                                CCTCTACC TC  CG    TGT
                                    C  C_  GAGGT
GAM828  JUP     3'  TGTTTCAGACCCCCCCATTTCC 9493        AAGAA  A  T_
                                GGAGATGG    GT TG  ACA
                                ||||||||    || ||  |||
                                CCTTTACC    CA AC  TGT
                                    CCCC_  G  TT
GAM828  KCND2   5'  TGCACATCACCTCCATCTCT  24401        AGAA  _   A
                                GGAGATGGA   GT ATGT CA
                                |||||||||   || |||| ||
                                TCTCTACCT   CA TACA GT
                                    C___  C   C
GAM828  KIF2    3'  TTGTACATACCTTGCCCACTCC 15728      A   AA  A
            T                    AGGAG TGG  GA GTATGTACAA
                                |||||| |||  || ||||||||||
                                TCCTC ACC  TT CATACATGTT
                                  _  CG  C
GAM828  KIR3DL2 3'  CATGCTGTTCCACCTCC    22141     A    GA
                                GGAG TGGAA  AGTATG
                                |||| |||||  ||||||
                                CCTC ACCTT  TCGTAC
                                  C    G_
GAM828  KLHL3   3'  TATTCGCTCCCCCATCCTCC  87464     _   AA  A  AT
                                GGAG ATGG  GA GT  GTA
                                |||| ||||  || ||  |||
                                CCTC TACC  CT CG  TAT
                                  C   CC  _  CT
GAM828  KLHL3   3'  TATTCTCTTCTATCTCCT    87465          _
                                AGGAGATGGAAGA AGTA
                                |||||||||||| ||||
                                TCCTCTATCTTCT TTAT
                                      C
GAM828  LMO1    5'  ACGAGATTCCCCCATCTCTT  9789        AA   GTA
                                AGGAGATGG  GAA   TGT
                                |||||||||  |||   |||
                                TTCTCTACC  CTT   GCA
                                    CC   AGA
GAM828  MAP1A   3'  TGCACCCTTTCCTCCATTTCC  9904        A_   TA
                                GGAGATGGA  GAAG  TGTA
                                |||||||||  ||||  ||||
                                CCTTTACCT  TTTC  ACGT
                                    CC   CC
GAM828  MAP3K7IP1 3'  ACGCCCTCCCCATCTCC    20374       AA  A TA
                                GGAGATGG  GA G  TGT
                                ||||||||  || |  |||
                                CCTCTACC  CT C  GCA
                                    C_  _ CC
GAM828  MAPK10  5'  TACTCCTTCCCCCCTTCTCCT  57293      T____    A
                                AGGAGA    GGAAG AGTA
                                ||||||    ||||| ||||
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                                TCCTCT    CCTTC TCAT
                                   TCCCC    C
GAM828  MARK3   5' ACATCCTCCTCCGCCTCCT  9912      A   A  A T
                                AGGAG TGGA GA G ATGT
                                ||||| |||| || | ||||
                                TCCTC GCCT CT C TACA
                                  C   C  _ C
GAM828  MICB    3' TGACTCCTTCTTCCACCCCTCT 19836    A__      TAT  A
                                GGAG  TGGAAGAAG  GT CA
                                ||||  |||||||||  || ||
                                TCTC  ACCTTCTTC  CA GT
                                  CCC       CT_ _
GAM828  MKI67   3' GTACCTACCATCTCCT     10047       A  AAGTAT
                                AGGAGATGG AG     GTAC
                                ||||||||| ||     ||||
                                TCCTCTACC TC     CATG
                                     A _______
GAM828  MMP14   3' TGCTCCTTTTCCATCCCCT  17175    A       __
                                AGG GATGGAAGA  AGTA
                                ||| |||||||||  ||||
                                TCC CTACCTTTT  TCGT
                                  C       CC
GAM828  MN1     3' TACCAGGCCCTTCCTCTCC  10095     T    AA  AT_
                                GGAGA GGAAG  GT   GTA
                                ||||| |||||  ||   |||
                                CCTCT CCTTC  CG   CAT
                                   _    C_  GAC
GAM828  NDP     3' TGCAGTTCCCATCTCCT    4245       A  AA
                                AGGAGATGG AG  GTA
                                |||||||||  ||  |||
                                TCCTCTACC TT  CGT
                                     C  GA
GAM828  NFE2L1  3' TGCCTTGCCACTCCATCTCC  12176       A AA   T_
                                GGAGATGGA G  GTA  GTA
                                ||||||||| |  |||  |||
                                CCTCTACCT C  CGT  CGT
                                     _ AC   TC
GAM828  OPHN1   3' TTGTATTCTGTCTTCATCCCCT 10363    A   G    AGTAT
                                AGG GATG AAGA    GTACAA
                                ||| |||| ||||    ||||||
                                TCC CTAC TTCT    TATGTT
                                  C    _   GTCT_
GAM828  PACSIN1 3' ACCTCTTCTTCCTCCCCT   92252    A  T      TAT
                                AGG GA GGAAGAAG   GT
                                ||| || ||||||||   ||
                                TCC CT CCTTCTTC   CA
                                  C  _       TC_
GAM828  PAK1    3' TGCTTCTCCCATTTCCT     10409       A
                                AGGAGATGG AGAAGTA
                                ||||||||| |||||||
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                                TCCTTTACC TCTTCGT
                                      C
GAM828  PCDH1    5'  TGCTGACTTCTTTCATCCCC  50566    A         AT
                                GG GATGGAAGAAGT  GTA
                                || |||||||||||  |||
                                CC CTACTTTCTTCA  CGT
                                 C          GT
GAM828  PLCB2    3'  TACCTCCCCCTCCATCTCT   15895        A___  A
                                GGAGATGGA   GA GTA
                                |||||||||   || |||
                                TCTCTACCT   CT CAT
                                      CCCC  C
GAM828  PPP2R5A  5'  CGCGCCTCTCCCCCGCCTCCT  20708      A  A__   A TA
                                AGGAG TGG   AGA G  TG
                                ||||| |||   ||| |  ||
                                TCCTC GCC   TCT C  GC
                                   C   CCC   C GC
GAM828  RAB6A    3'  CATACTTCCTCATCCCCT    11193     A    AA
                                AGG GATGG  GAAGTATG
                                ||| |||||  ||||||||
                                TCC CTACT  CTTCATAC
                                  C    C_
GAM828  RGS19IP1 3'  GCAACCTCCTCCCCACCTCC   62510      A  A_  A  TA
                                GGAG TGG  AG AG  TGT
                                |||| |||  || ||  |||
                                CCTC ACC  TC TC  ACG
                                  C   CC  C  CA
GAM828  SALL2    3'  TGTACATTCCTTCTTCCTCCCC 63864    A  T      T_
                                GG GA GGAAGAAG  ATGTACA
                                || || ||||||||  |||||||
                                CC CT CCTTCTTC  TACATGT
                                 C  _       CT
GAM828  SCN4A    3'  ACTCCTTCCATCTCTT      4407           A
                                AGGAGATGGAAG AGT
                                |||||||||||| |||
                                TTCTCTACCTTC TCA
                                       C
GAM828  SHANK2   3'  ACAGATTCTTTTCCCCATCTCC 24581         ____    GTA
           T                    AGGAGATGG    AAGAA   TGT
                                |||||||||    |||||   |||
                                TCCTCTACC    TTCTT   ACA
                                     CCTT    AG_
GAM828  SLA2     3'  TGCAACCTCCATCTCCT     49911          AGAA  A
                                AGGAGATGGA    GT TGTA
                                ||||||||||    || ||||
                                TCCTCTACCT    CA ACGT
                                      C___  _
GAM828  SLC21A3  3'  TGTACTTCCTACATCTCCT   40829        GAA
                                AGGAGATG   GAAGTATG
                                ||||||||   ||||||||
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                                TCCTCTAC  CTTCATGT
                                    ATC
GAM828  SLC21A3  3'  TGTACTTCCTACATCTCCT   56229       GAA
                                AGGAGATG  GAAGTATG
                                ||||||||  ||||||||
                                TCCTCTAC  CTTCATGT
                                    ATC
GAM828  SLC39A1  3'  CATACCTATCTCCCTCCTCC  27051     AT  A  A__
                                GGAG  GG AGA  GTATG
                                ||||  || |||  |||||
                                CCTC  CC TCT  CATAC
                                  CT  C  ATC
GAM828  SLC7A8   3'  TACTCTCTCCTTCCTCCCC   24283    A  T    A  TAT
                                GG GA GGAAG AG  GTA
                                || || ||||| ||  |||
                                CC CT CCTTC TC  CAT
                                 C  _    C  TCT
GAM828  SMARCB1  3'  GCCTCTCCTCCATCTTCT    65583         __  A
                                AGGAGATGGA  AGA GT
                                ||||||||||  ||| ||
                                TCTTCTACCT  TCT CG
                                     CC  C
GAM828  SMOH     3'  TATATCCTCCTTCTCCT     18870       T  A  A
                                AGGAGA GGA GA GTA
                                |||||| ||| || |||
                                TCCTCT CCT CT TAT
                                   T  C  A
GAM828  SORCS3   3'  ACTTAACTCTTGCATCTCCT  30370        G   AG  T
                                AGGAGATG AAGA  TA GT
                                |||||||| ||||  || ||
                                TCCTCTAC TTCT  AT CA
                                     G   CA  T
GAM828  SPON1    3'  TATATTGTCCTCCACCTCC   62456     A   A  AGT
                                GGAG TGGA GA  ATGTA
                                |||| |||| ||  |||||
                                CCTC ACCT CT  TATAT
                                  C   C  GT_
GAM828  STIM1    3'  TGTACATACCTGCCCCCTC   60152     AT  A  AA
                                GAG  GG AG  GTATGTACA
                                |||  || ||  |||||||||
                                CTC  CC TC  CATACATGT
                                  CC  G  __
GAM828  TPD52L2  3'  ACTTCTTCCTCCTCCT      12365      AT
                                AGGAG  GGAAGAAGT
                                |||||  |||||||||
                                TCCTC  CCTTCTTCA
                                  CT
GAM828  TSG      3'  TATTCTCTTCCATTTCC     40239          _
                                GGAGATGGAAGA AGTA
                                |||||||||||| ||||
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                                CCTTTACCTTCT TTAT
                                      C
GAM828  VTN     3'  TGTAGCTCCCTCCTCCCATCTC 5316         A  A  TAT  _
          CT                    AGGAGATGG AG AG   GT ACA
                                ||||||||| || ||   || |||
                                TCCTCTACC TC TC   CG TGT
                                    C  C  CCT  A
GAM828  WBSCR1   3'  TGTGCTTCCCACCTCC     42233     A   AA
                                GGAG TGG  GAAGTATG
                                |||| |||  ||||||||
                                CCTC ACC  CTTCGTGT
                                  C  __
GAM828  WBSCR1   3'  TGTGCTTCCCACCTCC     49265     A   AA
                                GGAG TGG  GAAGTATG
                                |||| |||  ||||||||
                                CCTC ACC  CTTCGTGT
                                  C  __
GAM828  WNT2     3'  TACCCTATTCTATCCATCTCCT 12657          _   GTAT
                                AGGAGATGGA AGAA   GTA
                                |||||||||| ||||   |||
                                TCCTCTACCT TCTT   CAT
                                     A   ATCC
GAM828  ZIC3     5'  TGCTCTTTCTTCCCCTCCT   12730      AT      TAT
                                AGGAG  GGAAGAAG   GTA
                                |||||  ||||||||   |||
                                TCCTC  CCTTCTTT   CGT
                                  C_      CT_
GAM828  ZNF192   3'  TGTGCTTCTTCCCATCTCCT   20856        _
                                AGGAGATGG AAGAAGTATG
                                ||||||||| ||||||||||
                                TCCTCTACC TTCTTCGTGT
                                     C
GAM828  ZNF214   3'  TATAGTTTCCCCTATCTCC   25117        AA   _
                                GGAGATGG  GAAG TATG
                                ||||||||  |||| ||||
                                CCTCTATC  CTTT ATAT
                                    CC   G
GAM828  AAK1     3'  TGCAGCCTCCATCTCC      29858         AGAA  A
                                GGAGATGGA   GT TGTA
                                |||||||||   || ||||
                                CCTCTACCT   CG ACGT
                                     C___  _
GAM828  ABHD2    3'  TGTTTCAGGTCTCCCATCTCC  22809        A   AGTA  T_
                                GGAGATGG AGA   TG  ACA
                                |||||||| |||   ||  |||
                                CCTCTACC TCT   AC  TGT
                                    C  GG__  TT
GAM828  AIF1     5'  TGCCTGCCCCTCCTCCTCCT   16755      AT   A AA   T
                                AGGAG  GGA G  GTA GTA
                                |||||  ||| |  ||| |||
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                                TCCTC  CCT C  CGT CGT
                                   CT   _ CC   C
GAM828  ATF3     3'  TGCTCTCCCATCTCC       14436         A   A
                                GGAGATGG AGA GTA
                                |||||||| ||| |||
                                CCTCTACC TCT CGT
                                     C   _
GAM828  ATP9A    3'  TATTTGGTTTCTTCCCCTCC   62052      AT       AT_
                                GGAG  GGAAGAAGT   GTA
                                ||||  |||||||||   |||
                                CCTC  CCTTCTTTG   TAT
                                  C_        GTT
GAM828  C20orf98 3'  TGCACCCCTTCCATCCC     71516    A       AAGTA
                                GG GATGGAAG     TGTA
                                || ||||||||     ||||
                                CC CTACCTTC     ACGT
                                 _       CCC__
GAM828  C5orf6   3'  GCTCCTCCCTATCTCCT     33485          A_  A
                                AGGAGATGG  AG AGT
                                |||||||||  || |||
                                TCCTCTATC  TC TCG
                                     CC  C
GAM828  CAMKK2   3'  TGCCCTTTTCCACCTCC     21588      A      A_
                                GGAG TGGAAGA  GTA
                                |||| |||||||  |||
                                CCTC ACCTTTT  CGT
                                  C       CC
GAM828  CBX5     3'  TTGTACATAATACATTCACCTC 24006      A    AGAAG
           C                     GGAG TGGA     TATGTACAA
                                |||| ||||     |||||||||
                                CCTC ACTT     ATACATGTT
                                  C    ACATA
GAM828  CORO1B   3'  ACACGCCACCTTCATCTCCT   39948          AGAA TA
                                AGGAGATGGA    G  TGT
                                ||||||||||    |  |||
                                TCCTCTACTT    C  ACA
                                      CCAC GC
GAM828  CTPS2    3'  TGTACACACTAGCAGTCACTCC 39091      A   AAGA_   A
                                GGAG TGG     AGT TGTACA
                                |||| |||     ||| ||||||
                                CCTC ACT     TCA ACATGT
                                  _   GACGA   C
GAM828  DDX31    3'  TGCTTTCCTCCACCTTCT     56831       A    A_
                                AGGAG TGGA  GAAGTA
                                ||||| ||||  ||||||
                                TCTTC ACCT  TTTCGT
                                  C    CC
GAM828  DKFZP434L1435 5'  CATGGATCTCCCATCTCC    92169         A   AG
                                GGAGATGG AGA  TATG
                                |||||||| |||  ||||
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                                CCTCTACC TCT  GTAC
                                     C   AG
GAM828  DKFZP564B1162 3'  CAAACCTCTCCCATCTCC    48530        A   A  A
                                GGAGATGG AGA GT TG
                                |||||||| ||| || ||
                                CCTCTACC TCT CA AC
                                     C   C  A
GAM828  DKFZP586N0721 5'  TATTTTTCTCCATCTCC     31205        _
                                GGAGATGGA AGAAGTA
                                ||||||||| |||||||
                                CCTCTACCT TTTTTAT
                                      C
GAM828  DNAJB5   3'  TGTACATAGCATGTCCTCCTCC 24355     AT   AGAAG
                                GGAG  GGA    TATGTACA
                                ||||  |||    ||||||||
                                CCTC  CCT    ATACATGT
                                  CT   GTACG
GAM828  DOC2B    3'  TGCATCCCTCATCTCCT     13136        AA  A
                                AGGAGATGG  GA GTA
                                |||||||||  || |||
                                TCCTCTACT  CT CGT
                                     CC  A
GAM828  FATE     3'  TGCCCCTTTCATCTCC      52360         AA
                                GGAGATGGAAG  GTA
                                ||||||||||  |||
                                CCTCTACTTTC  CGT
                                      CC
GAM828  FIGN     3'  ACCTCTCCATCTCCT       95638         A  A
                                AGGAGATGGA GA GT
                                |||||||||| || ||
                                TCCTCTACCT CT CA
                                     _  C
GAM828  FLJ00058  5'  TGTCCAGACCCCACCATCTCC  78767        AAGAA  A  T
                                GGAGATGG    GT TG ACA
                                ||||||||    || || |||
                                CCTCTACC    CA AC TGT
                                     ACCC_  G  C
GAM828  FLJ10139  3'  TATCTCTCCCATCTCTT     35843        A   AG
                                AGGAGATGG AGA  TA
                                ||||||||| |||  ||
                                TTCTCTACC TCT  AT
                                     C   CT
GAM828  FLJ10276  3'  TGCGTTTCTTCCCCTCC     35967     AT     GT
                                GGAG  GGAAGAA  ATGTA
                                ||||  |||||||  |||||
                                CCTC  CCTTCTT  TGCGT
                                  C_      __
GAM828  FLJ10922  3'  ATTTCTCCCGTCTCCT      36869        A
                                AGGAGATGG AGAAGT
                                ||||||||| ||||||
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                                TCCTCTGCC TCTTTA
                                     C
GAM828  FLJ11125  5'  TGCAGCCTCCATCTCCT     59585          AGAA  A
                                AGGAGATGGA    GT TGTA
                                ||||||||||    || ||||
                                TCCTCTACCT    CG ACGT
                                     C___  _
GAM828  FLJ11362  3'  CGCCCTTCCCCCACCTCCT   41681      A   AA    TA
                                AGGAG TGG  GAAG  TG
                                ||||| |||  ||||  ||
                                TCCTC ACC  CTTC  GC
                                   C   CC    CC
GAM828  FLJ12668  3'  TGCAACCTCCATCTCC      46528         AGAA  A
                                GGAGATGGA    GT TGTA
                                |||||||||    || ||||
                                CCTCTACCT    CA ACGT
                                     C___  _
GAM828  FLJ12704  3'  TGCATCATTTTCCATCCCC    46536    A       AGT
                                GG GATGGAAGA   ATGTA
                                || |||||||||   |||||
                                CC CTACCTTTT   TACGT
                                 C        AC_
GAM828  FLJ13193  3'  TGCAGCTTCCATCTCC      49775          AA
                                GGAGATGGAAG  GTA
                                ||||||||||  |||
                                CCTCTACCTTC  CGT
                                      GA
GAM828  FLJ13590  5'  TGCAGCCTCCATCTCC      45789         AGAA  A
                                GGAGATGGA    GT TGTA
                                |||||||||    || ||||
                                CCTCTACCT    CG ACGT
                                     C___  _
GAM828  FLJ14326  3'  TTGCACAGGGGCCTTCCTCATC 49821        __    AAGTA   A
           TCCT                    AGGAGAT  GGAAG     TGT CAA
                                |||||||  |||||    ||| |||
                                TCCTCTA  CCTTC     ACA GTT
                                    CT    CGGGG   C
GAM828  FLJ14594  3'  TTGTTTTTCTCTTCCTCCTCCT 51454      AT     A TATGT
                                AGGAG  GGAAGA G    ACAA
                                |||||  |||||| |    ||||
                                TCCTC  CCTTCT C    TGTT
                                   CT     _ TTTT_
GAM828  FLJ20010  3'  TACCATCTTCCATCTCC     38717          A_
                                GGAGATGGAAGA  GTA
                                ||||||||||||  |||
                                CCTCTACCTTCT  CAT
                                      AC
GAM828  FLJ20154  3'  CATACCCTAACTCCATCTCCT  72924          AGAA__
                                AGGAGATGGA     GTATG
                                ||||||||||     |||||
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                                TCCTCTACCT     CATAC
                                      CAATCC
GAM828  FLJ20154  3'  TGCATTTTCCTCCATCTCC    72935         A    T
                                GGAGATGGA GAAG ATGTA
                                ||||||||| |||| |||||
                                CCTCTACCT CTTT TACGT
                                      C    _
GAM828  FLJ20294  3'  TGCCCTCTTCCTCCCCT     34883     A  T     A_
                                AGG GA GGAAGA  GTA
                                ||| || ||||||  |||
                                TCC CT CCTTCT  CGT
                                  C  _     CC
GAM828  FLJ22596  5'  TGTACATACCCCCACTCCT    46965      A   AAGAA
                                AGGAG TGG    GTATGTACA
                                ||||| |||    |||||||||
                                TCCTC ACC    CATACATGT
                                   _  CC___
GAM828  FLJ30681  3'  TATATCTCCACCTCCT      91789      A    A  A
                                AGGAG TGGA GA GTA
                                ||||| |||| || |||
                                TCCTC ACCT CT TAT
                                   C    _ A
GAM828  FLJ31528  3'  TACCTCAGTTTCCCCCATCTCC 58377         AA    TAT__
          T                      AGGAGATGG  GAAG    GTA
                                ||||||||| ||||    |||
                                TCCTCTACC  CTTT    CAT
                                      CC    GACTC
GAM828  FLJ32926  3'  TGTGGATCCCCCACCTCCT    58025      A   AA  AGTA G
                                AGGAG TGG  GA    T TACA
                                ||||| |||  ||    | ||||
                                TCCTC ACC  CT    A GTGT
                                   C   CC  _____ G
GAM828  G2        5'  CATGCCTCCCCATCTCCT    66658         AA  A
                                AGGAGATGG  GA GTATG
                                |||||||||  || |||||
                                TCCTCTACC  CT CGTAC
                                      C_  C
GAM828  GABARAPL3 3'  ACTTCTACCATCTCCT      50798         A
                                AGGAGATGG AGAAGT
                                ||||||||| ||||||
                                TCCTCTACC TCTTCA
                                      A
GAM828  GIT1      3'  ACTTCCCTCCCATCTCCT    25863         AA__
                                AGGAGATGG    GAAGT
                                |||||||||    |||||
                                TCCTCTACC    CTTCA
                                      CTCC
GAM828  GPA33     3'  ACACACTTTCCATCTCT     19452          GA  A
                                GGAGATGGAA  AGT TGT
                                ||||||||||  ||| |||
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                                TCTCTACCTT  TCA ACA
                                      __  C
GAM828  HBOA     3'  ACGAACTCCTCCTCCATTTCCT 22964         A  __  A
                                AGGAGATGGA GA  AGT TGT
                                |||||||||| ||  ||| |||
                                TCCTTTACCT CT  TCA GCA
                                     C  CC   A
GAM828  HSPC063  3'  TACCACTCTTCATCTCC     26273        G   A  AT
                                GGAGATG AAGA GT  GTA
                                ||||||| |||| ||  |||
                                CCTCTAC TTCT CA  CAT
                                   _   _ C_
GAM828  IL-17RC  3'  TGGATAGCTACTTCCATCCCC  51201    A      A  A  A
                                GG GATGGAAG AGT TGT CA
                                || |||||||| ||| ||| ||
                                CC CTACCTTC TCG ATA GT
                                 C       A  _  G
GAM828  KDELR2   3'  TATGTATTCTTCCATCCCT   22454    A       G
                                AGG GATGGAAGAA TATGTA
                                ||| |||||||||| ||||||
                                TCC CTACCTTCTT ATGTAT
                                  _        _
GAM828  KIAA0342 3'  TATGGATTCCCTCATCTCCT   70621        AA  G_
                                AGGAGATGG  GAA  TATG
                                |||||||||  |||  ||||
                                TCCTCTACT  CTT  GTAT
                                     CC   AG
GAM828  KIAA0453 3'  ATCTTCTTCCCCTCC      69043     AT      T
                                GGAG  GGAAGAAG AT
                                ||||  |||||||| ||
                                CCTC  CCTTCTTC TA
                                  C_       _
GAM828  KIAA0515 3'  GCTCCCTTCCATCTCT      63810          A_
                                GGAGATGGAAG  AGT
                                ||||||||||  |||
                                TCTCTACCTTC  TCG
                                      CC
GAM828  KIAA0523 3'  ACATTCATTCCTCCATTTCCT  67726         A  GT_
                                AGGAGATGGA GAA   ATGT
                                |||||||||| |||   ||||
                                TCCTTTACCT CTT   TACA
                                     C   ACT
GAM828  KIAA0537 3'  TACTCCCTTCTTCCTCCCC   29259    A  T      TAT
                                GG GA GGAAGAAG   GTA
                                || || ||||||||   |||
                                CC CT CCTTCTTC   CAT
                                 C  _       CCT
GAM828  KIAA0561 5'  GCGTCTCTCCCATCTTC     65889        A  A T
                                GGAGATGG AGA G ATGT
                                |||||||| ||| | ||||
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                                CTTCTACC TCT C TGCG
                                     C  _ _
GAM828  KIAA0759 3' GCTTCCCTTCCATTTCCT    67326          __
                                AGGAGATGGAA  GAAGT
                                ||||||||||  |||||
                                TCCTTTACCTT  CTTCG
                                      CC
GAM828  KIAA0759 3' TGCTATCTCCCATCTCC     67330        A  _
                                GGAGATGG AGA AGTA
                                |||||||| ||| ||||
                                CCTCTACC TCT TCGT
                                     C   A
GAM828  KIAA0789 5' CAAGCCCCTTCCATCCTCT   63682    GA      AA  A
                                AG  GATGGAAG  GT TG
                                ||  ||||||||  || ||
                                TC  CTACCTTC  CG AC
                                 TC       CC  A
GAM828  KIAA0795 3' CATCTTTCCTTCCTATCTCC  46589       _    _  T
                                GGAGAT GGAAG AAG ATG
                                |||||| ||||| ||| |||
                                CCTCTA CCTTC TTT TAC
                                    T    C  C
GAM828  KIAA0939 3' CATCCTCTCCTCATCTCC    62010       _ A   A T
                                GGAGATG G AGA G ATG
                                ||||||| | ||| | |||
                                CCTCTAC C TCT C TAC
                                     T C  _ C
GAM828  KIAA0972 5' GCGGCACTTCTTCATCCCCT  30011    A   G     A_
                                AGG GATG AAGAAGT  TGT
                                ||| |||| |||||||  |||
                                TCC CTAC TTCTTCA  GCG
                                  C   _      CG
GAM828  KIAA1034 3' CGTACACATTCCATCTACC   62469   _      GAA
                                GG AGATGGAA   GTATG
                                || ||||||||   |||||
                                CC TCTACCTT   CATGC
                                 A       ACA
GAM828  KIAA1037 3' ATATGCCCCCCCCCATCTCCT 30433         AAGAA_
                                AGGAGATGG     GTATGT
                                |||||||||     ||||||
                                TCCTCTACC     CGTATA
                                     CCCCCC
GAM828  KIAA1170 3' TACATGTTGCCCCTCTCC    69859      T  AA  AG
                                GGAGA GG  GA  TATGTA
                                ||||| ||  ||  ||||||
                                CCTCT CC  TT  GTACAT
                                   C  CG  __
GAM828  KIAA1271 3' TGCTTCTCCCATCTCT      69554        A
                                GGAGATGG AGAAGTA
                                |||||||| |||||||
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                                TCTCTACC TCTTCGT
                                     C
GAM828  KIAA1280  5'  TGCACACACCATCTCCATCTCC 69733        A  A_  A   A
                                GGAGATGGA GA  GT TGT CA
                                |||||||||  ||  ||  |||  ||
                                CCTCTACCT CT  CA ACA GT
                                     _  AC  C   C
GAM828  KIAA1297  3'  TGTCAGCCCCTCATCTCC    72192       GA  AA  A  T
                                GGAGATG  AG  GT TG ACA
                                |||||||  ||  ||  ||  |||
                                CCTCTAC  TC  CG AC TGT
                                     __  CC  _  _
GAM828  KIAA1363  3'  TGCCTAGATCCCCCATCTCCT  69265        AA  AG  T
                                AGGAGATGG  GA  TA GTA
                                |||||||||  ||  ||  |||
                                TCCTCTACC  CT  AT CGT
                                     CC  AG  C
GAM828  KIAA1437  3'  TATTTTTCTCCATCTCC     60593        _
                                GGAGATGGA AGAAGTA
                                |||||||||  |||||||
                                CCTCTACCT TTTTTAT
                                     C
GAM828  KIAA1536  3'  TGTATCCTCTCCTCGCATCTCC 40493       GA  A  TAT
     T                           AGGAGATG  AG AG   GTACA
                                |||||||  ||  ||   |||||
                                TCCTCTAC  TC TC   TATGT
                                     GC  C  TCC
GAM828  KIAA1538  5'  TGCCTCTTCCTCCTCCT     71560      AT     A
                                AGGAG  GGAAGA GTA
                                |||||  ||||||  |||
                                TCCTC  CCTTCT CGT
                                   CT     C
GAM828  KIAA1843  3'  GTATCTTCTTCCCCTCC     62191      AT      TAT
                                GGAG  GGAAGAAG   GTAC
                                ||||  ||||||||   ||||
                                CCTC  CCTTCTTC   TATG
                                   C_       ___
GAM828  KIAA1867  3'  TGTGTACTCCTCCCCTCC    94825      AT   A  A   TG
                                GGAG  GGA GA GTA  TA
                                ||||  |||  ||  |||  ||
                                CCTC  CCT CT CAT  GT
                                   C_   C  _   GT
GAM828  MANBAL    3'  TGTACATCCCCCATCCCT    41982     A    AA  AGTA
                                AGG GATGG  GA    TGTACA
                                |||  |||||  ||    ||||||
                                TCC CTACC  CT    ACATGT
                                   _     CC  ____
GAM828  MESDC1    3'  CATACCCCTTCTTCCACCCCC  42593    AGA       ___
                                GG   TGGAAGAA   GTATG
                                ||   ||||||||   |||||
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                                CC  ACCTTCTT  CATAC
                                 CCC      CCC
GAM828  MGC10960 3' GTGCTTCCCTCCATCTCC   51010       A_
                                GGAGATGGA GAAGTAT
                                ||||||||| |||||||
                                CCTCTACCT CTTCGTG
                                     CC
GAM828  MGC11324 3' GTACCCCTCCCATCTACT   51170   G    A AA
                                AG AGATGG AG GTAT
                                || |||||| ||  ||||
                                TC TCTACC TC CATG
                                 A    C CC
GAM828  MGC16386 3' TGTACATAGCCACCTCC    54738    A  AAGAAG
                                GGAG TGG    TATGTACA
                                |||| |||    ||||||||
                                CCTC ACC    ATACATGT
                                  C  G_____
GAM828  MGC3248  3' CATTTTCCTCCGTCTCC    50654       A   T
                                GGAGATGGA GAAG ATG
                                ||||||||| |||| |||
                                CCTCTGCCT CTTT TAC
                                     C  _
GAM828  MGC4643  3' TGCCTTTTCTTCCTCCTCCT  51157     AT     TAT
                                AGGAG GGAAGAAG  GTA
                                ||||| |||||||  |||
                                TCCTC CCTTCTTT  CGT
                                   CT      TC_
GAM828  MGC4796  3' TACCAACTTCTCTCCCATCTCT 61495       A__    AT
                                GGAGATGG  AGAAGT GTA
                                ||||||||  ||||||  |||
                                TCTCTACC  TCTTCA CAT
                                    CTC    AC
GAM828  MGC4827  3' TGCTCCTTCTCACCTCCT   44125     A _  A
                                AGGAG TG GAAG AGTA
                                ||||| || |||| ||||
                                TCCTC AC CTTC TCGT
                                   C T  C
GAM828  MGC5601  5' ACTCCTTCCATCTGCC    47504   _      A
                                GG AGATGGAAG AGT
                                || |||||||| |||
                                CC TCTACCTTC TCA
                                 G       C
GAM828  MRPS21   3' TGTACAATCCCATTTCCT   49117       AA AGTA
                                AGGAGATGG GA   TGTACA
                                |||||||||  ||   ||||||
                                TCCTTTACC  CT   ACATGT
                                     __ A___
GAM828  MRPS21   3' TGTACAATCCCATTTCCT   38643       AA AGTA
                                AGGAGATGG GA   TGTACA
                                |||||||||  ||   ||||||
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                                TCCTTTACC  CT   ACATGT
                                    __ A___
GAM828  MY014    3'  TACAGGCTCTTCCATCTCT   48143         A  A
                                GGAGATGGAAGA GT TGTA
                                |||||||||||| || ||||
                                TCTCTACCTTCT CG ACAT
                                     _ G
GAM828  NFASC    3'  TGCTCCCCTTCCATCTCT    70350         A__
                                GGAGATGGAAG  AGTA
                                ||||||||||  ||||
                                TCTCTACCTTC  TCGT
                                     CCC
GAM828  NYD-SP18 3'  TGTACATAACCACGTCCT    50877     GA  AAGAAG
                                AGGA  TGG    TATGTACA
                                ||||  |||    ||||||||
                                TCCT  ACC    ATACATGT
                                  GC  A_____
GAM828  OR51E2   3'  TGTCTCTTACATCTCCT     47802       G   AG
                                AGGAGATG AAGA  TA
                                |||||||| ||||  ||
                                TCCTCTAC TTCT  GT
                                    A   CT
GAM828  OSBPL1A  3'  TACCCCTTCCATCTTC      54584         AA
                                GGAGATGGAAG  GTA
                                ||||||||||  |||
                                CTTCTACCTTC  CAT
                                     CC
GAM828  OSBPL1A  3'  TACCCCTTCCATCTTC      35910         AA
                                GGAGATGGAAG  GTA
                                ||||||||||  |||
                                CTTCTACCTTC  CAT
                                     CC
GAM828  OSBPL1A  3'  TACCCCTTCCATCTTC      55743         AA
                                GGAGATGGAAG  GTA
                                ||||||||||  |||
                                CTTCTACCTTC  CAT
                                     CC
GAM828  PDGFC    3'  CATATCTTCCATTCCT      32497      A     AG
                                AGGAG TGGAAGA  TATG
                                ||||| |||||||  ||||
                                TCCTT ACCTTCT  ATAC
                                    _     __
GAM828  PI4KII   3'  CAAGCCTCCTCCATCTCC    37342        A  A  A
                                GGAGATGGA GA GT TG
                                ||||||||| || || ||
                                CCTCTACCT CT CG AC
                                     C  C  A
GAM828  PISD     3'  TGCTCCTCCCCCCCATCACCT  26775     A    A___  A
                                AGG GATGG    AG AGTA
                                ||| |||||    || ||||
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                                TCC CTACC    TC TCGT
                                  A     CCCC  C
GAM828  PRO2955  3'  TACATGCTGTTCCTCTCCT   37644       T    GA
                                AGGAGA GGAA  AGTATGTA
                                |||||| ||||  ||||||||
                                TCCTCT CCTT  TCGTACAT
                                   _    G_
GAM828  PSMD12   3'  TGCTCTTCTTCCTCTCC     11002      T       TAT
                                GGAGA GGAAGAAG   GTA
                                ||||| ||||||||   |||
                                CCTCT CCTTCTTC   CGT
                                   _       T__
GAM828  RAB6C    3'  CATACTTCCTCATCCCCT    49567     A     AA
                                AGG GATGG  GAAGTATG
                                ||| |||||  ||||||||
                                TCC CTACT  CTTCATAC
                                  C    C_
GAM828  SAD1     3'  TATGGTTCCCCCCATTTCCT   64024         AA_   G
                                AGGAGATGG   GAA TATG
                                |||||||||   ||| ||||
                                TCCTTTACC   CTT GTAT
                                     CCC   G
GAM828  SBB103   3'  TACATTTCTTCCACTCC     19362      A       GT
                                GGAG TGGAAGAA  ATGTA
                                |||| ||||||||  |||||
                                CCTC ACCTTCTT  TACAT
                                   _      ___
GAM828  SEPT3    3'  TACAACCTTCTGTCCCATCTCC 38893         A__     TA
           T                     AGGAGATGG   AGAAG  TGTA
                                |||||||||   |||||  ||||
                                TCCTCTACC   TCTTC  ACAT
                                     CTG    CA
GAM828  SEPT3    3'  TACATACTTGACCTCTCT    38894       T  AAG
                                GGAGA GG   AAGTATGTA
                                ||||| ||   |||||||||
                                TCTCT CC   TTCATACAT
                                   _  AG_
GAM828  SEPT3    3'  TTGTACATCCTCCCCACCTC   38897     A   AA  A T
                                GAG TGG  GA G ATGTACAA
                                ||| |||  || | ||||||||
                                CTC ACC  CT C TACATGTT
                                  C   C_  _ C
GAM828  SIAT8C   5'  GCAGCCCCTCCATCTTC     31880         A AA  A
                                GGAGATGGA G  GT TGT
                                |||||||||  |  || |||
                                CTTCTACCT C  CG ACG
                                     _ CC  _
GAM828  SLI      3'  ACATGCCGTCCATCTCCT    78584          AGAA
                                AGGAGATGGA    GTATGT
                                ||||||||||    ||||||
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                                TCCTCTACCT   CGTACA
                                     GC__
GAM828  SNX11    3'  TACTTTCCCACCTCCT     25273      A  AA
                                AGGAG TGG  GAAGTA
                                ||||| |||  ||||||
                                TCCTC ACC  TTTCAT
                                   C  C_
GAM828  SV2      3'  GTGCCCTCTCACATCTCCT   29313       GA  A_
                                AGGAGATG  AGA  GTAT
                                ||||||||  |||  ||||
                                TCCTCTAC  TCT  CGTG
                                    AC  CC
GAM828  THTPA    3'  TGTTTCTTCCCCCTCCT     44264      AT
                                AGGAG  GGAAGAAGTA
                                |||||  ||||||||||
                                TCCTC  CCTTCTTTGT
                                   CC
GAM828  TOMM40   3'  ACTTTCCCATCTCCT      20369       AA
                                AGGAGATGG  GAAGT
                                |||||||||  |||||
                                TCCTCTACC  TTTCA
                                     C_
GAM828  WBP11    3'  TGTTTCTTCCCCTCCT     32850      AT
                                AGGAG  GGAAGAAGTA
                                |||||  ||||||||||
                                TCCTC  CCTTCTTTGT
                                   C_
GAM828  WBSCR17  3'  CATCTCCTCACCCCATCTCC  81298       A___  A  T
                                GGAGATGG    AG AG ATG
                                ||||||||    || || |||
                                CCTCTACC    TC TC TAC
                                     CCAC  C  _
GAM828  LOC112476 3'  TGCACTTCTTCCAGCCCC    59117    AGA       AT
                                GG   TGGAAGAAGT  GTA
                                ||   ||||||||||  |||
                                CC   ACCTTCTTCA  CGT
                                 CCG        __
GAM828  LOC115110 5'  TGCTTTCCCCACCTCCT     71723      A  AA
                                AGGAG TGG  GAAGTA
                                ||||| |||  ||||||
                                TCCTC ACC  TTTCGT
                                   C  CC
GAM828  LOC120792 5'  GCTGTCTTCCATCTCC      75552          _
                                GGAGATGGAAGA AGT
                                |||||||||||| |||
                                CCTCTACCTTCT TCG
                                       G
GAM828  LOC122416 5'  TTGTTTTCACCCTCCTATCTCC 74123        A  AA  ATGT
           T                     AGGAGATGG AG  GT    ACAA
                                 |||||||| ||  ||    ||||
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                                TCCTCTATC TC  CA    TGTT
                                     C  C_  CTTT
GAM828  LOC126526 3'  GCTTCTTCCTCTCCT       74536        T
                                AGGAGA GGAAGAAGT
                                |||||| |||||||||
                                TCCTCT CCTTCTTCG
                                   _
GAM828  LOC133121 3'  TGTACTGTTCCTTCCATCCCT  75083     A       AAGTAT
                                AGG GATGGAAG      GTACA
                                ||| ||||||||      |||||
                                TCC CTACCTTC      CATGT
                                  _       CTTGT_
GAM828  LOC133686 3'  TGCAACCTCCATCTCC       75127          AGAA  A
                                GGAGATGGA    GT TGTA
                                |||||||||    || ||||
                                CCTCTACCT    CA ACGT
                                     C___  _
GAM828  LOC142913 5'  GCGGCTCTCCTTGCCATCTCCT 76417          _   A  TA_
                                AGGAGATGG AAG AG   TGT
                                ||||||||| ||| ||   |||
                                TCCTCTACC TTC TC   GCG
                                     G   C  TCG
GAM828  LOC142972 5'  TGTGTCTCTTCATCTCC      65131        G    AG
                                GGAGATG AAGA  TATG
                                ||||||| ||||  ||||
                                CCTCTAC TTCT  GTGT
                                   _    CT
GAM828  LOC143720 3'  TGCTCCTTCTCACCTCCT     60438       A  _    A
                                AGGAG TG GAAG AGTA
                                ||||| || |||| ||||
                                TCCTC AC CTTC TCGT
                                  C  T    C
GAM828  LOC144058 5'  GTACATACCTCCCTCCT      76669       AT   AGAA
                                AGGAG  GGA    GTATGTAC
                                |||||  |||    ||||||||
                                TCCTC  CCT    CATACATG
                                   __   C___
GAM828  LOC144100 3'  TGTGCCTCCATCTCC        76671          A AAGTAT
                                GGAGATGGA G      GTACA
                                ||||||||| |      |||||
                                CCTCTACCT C      CGTGT
                                     _ _______
GAM828  LOC144147 3'  TGCTCCTTCTCACCTCCT     71731       A  _    A
                                AGGAG TG GAAG AGTA
                                ||||| || |||| ||||
                                TCCTC AC CTTC TCGT
                                  C  T    C
GAM828  LOC144481 3'  TGTACACAAGCCCCATCTCC   83101         AAGAAGTA
                                GGAGATGG       TGTACA
                                ||||||||       ||||||
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                                CCTCTACC       ACATGT
                                     CCGAAC__
GAM828   LOC145134 5'  CACACTGAATCCCCACATCTCC 83255        ____   AGA   A
           T                    AGGAGAT    GGA   AGT TG
                                |||||||    |||   ||| ||
                                TCCTCTA    CCT   TCA AC
                                    CACC   AAG   C
GAM828   LOC145601 3'  TTGACATTCTCTCTCCATCTCC 83372         _   A T    A
                                GGAGATGGA AGA G ATGT CAA
                                ||||||||| ||| | |||| |||
                                CCTCTACCT TCT C TACA GTT
                                     C   _ T   _
GAM828   LOC145719 5'  GCTTCTCCCTCCATCTCC    83453         ___
                                GGAGATGGA   AGAAGT
                                |||||||||   ||||||
                                CCTCTACCT   TCTTCG
                                     CCC
GAM828   LOC145720 5'  GCTTCTCCCTCCATCTCC    83435         ___
                                GGAGATGGA   AGAAGT
                                |||||||||   ||||||
                                CCTCTACCT   TCTTCG
                                     CCC
GAM828   LOC145837 5'  ACTTCTTCCATCTGCC      83541    _
                                GG AGATGGAAGAAGT
                                || ||||||||||||
                                CC TCTACCTTCTTCA
                                 G
GAM828   LOC146488 5'  CAACCTCCTCCCAGCCTCCT   70809      A_   A  A  TA
                                AGGAG  TGG AG AG  TG
                                |||||  ||| || ||  ||
                                TCCTC  ACC TC TC  AC
                                   CG   C  C  CA
GAM828   LOC146988 5'  GTAGTGTTCCCCCATCTCCT   83896        AA   G   G
                                AGGAGATGG  GAA TAT TAC
                                |||||||||  ||| ||| |||
                                TCCTCTACC  CTT GTG ATG
                                     CC   _   _
GAM828   LOC147429 5'  TGCAATCTCCATCTCC      78366         A  AGTA
                                GGAGATGGA GA    TGTA
                                |||||||||  ||    ||||
                                CCTCTACCT CT    ACGT
                                     _  A___
GAM828   LOC148397 3'  CATGCCCCCTTCTATCTCC    78813          AA_
                                GGAGATGGAAG   GTATG
                                ||||||||||||  |||||
                                CCTCTATCTTC   CGTAC
                                      CCC
GAM828   LOC148918 5'  GCTTCTTCTACCTCCT      79076       A
                                AGGAG TGGAAGAAGT
                                ||||| ||||||||||
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                                TCCTC ATCTTCTTCG
                                   C
GAM828  LOC150406 3'  TGTACATACTTATTTCC     79859       _
                                GGAAG AAGTATGTACA
                                ||||| ||||||||||
                                CCTTT TTCATACATGT
                                   A
GAM828  LOC150519 3'  TGCAACCTGCCACCTCCT    79926       A  A  AA  A
                                AGGAG TGG AG  GT TGTA
                                ||||| ||| ||  || ||||
                                TCCTC ACC TC  CA ACGT
                                   C  G  __  _
GAM828  LOC150967 5'  ACTCCTTTTCCATCTCC     80077            __
                                GGAGATGGAAGA  AGT
                                ||||||||||||  |||
                                CCTCTACCTTTT  TCA
                                      CC
GAM828  LOC151391 5'  TATTCTCATCCATCCCCT    85332     A     A  _
                                AGG GATGGA GA AGTA
                                ||| |||||| || ||||
                                TCC CTACCT CT TTAT
                                  C     A  C
GAM828  LOC153020 3'  TGCACATTATTCATCTCCT   80764          AGA   A
                                AGGAGATGGA   AGT TGTA
                                ||||||||||   ||| ||||
                                TCCTCTACTT   TTA ACGT
                                      A__   C
GAM828  LOC153196 5'  ACTTCTTCTATCCCCT      85952     A
                                AGG GATGGAAGAAGT
                                ||| ||||||||||||
                                TCC CTATCTTCTTCA
                                  C
GAM828  LOC157681 5'  TATTTCCTCATCTCC       81544         AA
                                GGAGATGG  GAAGTA
                                ||||||||  ||||||
                                CCTCTACT  CTTTAT
                                     C_
GAM828  LOC157918 3'  TGTGTGCTCCCTCCACGTCCT 86652     GA   AGA   TG
                                AGGA  TGGA   AGTA  TA
                                ||||  ||||   ||||  ||
                                TCCT  ACCT   TCGT  GT
                                   GC    CCC    GT
GAM828  LOC162333 5'  TACTTCCCCATCTCCT      87138         AA
                                AGGAGATGG  GAAGTA
                                |||||||||  ||||||
                                TCCTCTACC  CTTCAT
                                     C_
GAM828  LOC196528 3'  ACCTACCCTTCCATTTCCT   87761           AA   T
                                AGGAGATGGAAG  GTA GT
                                ||||||||||||  ||| ||
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                                TCCTTTACCTTC  CAT CA
                                      C_   C
GAM828   LOC197114 5'  GCTTCTCCCTCCATCTTC    89707        ___
                                GGAGATGGA   AGAAGT
                                |||||||||   ||||||
                                CTTCTACCT   TCTTCG
                                     CCC
GAM828   LOC199704 3'  TGTTAACTTTCTTCCTTCCCCT 88332    A  T      TATGT
                                AGG GA GGAAGAAG    ACA
                                ||| || ||||||||    |||
                                TCC CT CCTTCTTT    TGT
                                  C  T       CAAT_
GAM828   LOC200819 3'  ACCTGCCCCCCATCTCCT    90142        AAGAA   T
                                AGGAGATGG    GTA GT
                                |||||||||    ||| ||
                                TCCTCTACC    CGT CA
                                     CCC__   C
GAM828   LOC200860 3'  ACAGCCCCTTCCTCCATCTC   90153        A   TA__
                                GAGATGGA GAAG    TGT
                                |||||||| ||||    |||
                                CTCTACCT CTTC    ACA
                                     C    CCCG
GAM828   LOC206372 3'  ACTTCTTCCTCCCCT      89530    A  T
                                AGG GA GGAAGAAGT
                                ||| || |||||||||
                                TCC CT CCTTCTTCA
                                  C  _
GAM828   LOC219894 3'  CATGTTTTCCTCCCATCTTCT  93279        A  __
                                AGGAGATGG AG  AAGTATG
                                ||||||||| ||  |||||||
                                TCTTCTACC TC  TTTGTAC
                                     C  CT
GAM828   LOC220018 5'  TGCTCCCTTCCATCTCT     93405         A_
                                GGAGATGGAAG  AGTA
                                ||||||||||  ||||
                                TCTCTACCTTC  TCGT
                                      CC
GAM828   LOC220883 3'  ACTCCTCCTCCATTTCCT    91257         A  __
                                AGGAGATGGA GA  AGT
                                |||||||||| ||  |||
                                TCCTTTACCT CT  TCA
                                     C  CC
GAM828   LOC221683 5'  TGCTTCTCCCATCCCT     93719     A    A
                                AGG GATGG AGAAGTA
                                ||| ||||| |||||||
                                TCC CTACC TCTTCGT
                                  _    C
GAM828   LOC253891 3'  TGCAGTCTCCCATCTCCT    94417        A   A_
                                AGGAGATGG AGA  GTA
                                ||||||||| |||  |||
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                                TCCTCTACC TCT  CGT
                                     C   GA
GAM828  LOC254045 3'  TGTACACAAGCCCCATCTCC   96510        AAGAAGTA
                                GGAGATGG       TGTACA
                                ||||||||       ||||||
                                CCTCTACC       ACATGT
                                     CCGAAC__
GAM828  LOC254122 3'  TGCGCTTCTTCACCTCCT    94754      ATG       AT
                                AGGAG   GAAGAAGT  GTA
                                |||||   ||||||||  |||
                                TCCTC   CTTCTTCG  CGT
                                  CA_       __
GAM828  LOC255481 3'  TACACACACCCTTGCATCTTCT 94442        G   AA_  A
                                AGGAGATG AAG   GT TGTA
                                |||||||| |||   || ||||
                                TCTTCTAC TTC   CA ACAT
                                     G   CCA  C
GAM828  LOC256073 5'  CATACAACCTTCCATCCCC    96662    A       AA_
                                GG GATGGAAG   GTATG
                                || ||||||||   |||||
                                CC CTACCTTC   CATAC
                                 C       CAA
GAM828  LOC256087 3'  CAACTCTTCTTCCTTCCCCT   95115     A  T       TA_
                                AGG GA GGAAGAAG   TG
                                ||| || ||||||||   ||
                                TCC CT CCTTCTTC   AC
                                  C  T       TCA
GAM828  LOC256855 3'  GCTTTCTTCCTCTCCT      95274       T      _
                                AGGAGA GGAAGAA GT
                                |||||| ||||||| ||
                                TCCTCT CCTTCTT CG
                                   _      T
GAM828  LOC257122 5'  TGCTTCCCTTCCTTCCATCCCC 96214     A       _   TAT_
           T                     AGG GATGGAAG AAG    GTA
                                ||| |||||||| |||    |||
                                TCC CTACCTTC TTC    CGT
                                  C       C   CCTT
GAM828  LOC90161  3'  TGTACATACTTCTCCCA     61701     A
                                TGG AGAAGTATGTACA
                                ||| ||||||||||||
                                ACC TCTTCATACATGT
                                  C
GAM828  LOC90346  3'  TGACCCCTTCTTCCACCCGCCT 56391     AGA_       TAT  A
                                AGG    TGGAAGAAG   GT CA
                                |||    |||||||||   || ||
                                TCC    ACCTTCTTC   CA GT
                                  GCCC        CC_  _
GAM828  LOC90637  5'  TACGTCTCTTCCATCTGCT    63649    G        A T
                                AG AGATGGAAGA G ATGTA
                                || ||||||||| | |||||
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                                TC TCTACCTTCT C TGCAT
                                 G       _ _
GAM828  LOC91010  3'  TGTACATGTACCACCTCC    64619     A  AAGAAG
                                GGAG TGG     TATGTACA
                                |||| |||     ||||||||
                                CCTC ACC     GTACATGT
                                  C  AT____
GAM828  LOC91191  3'  TGTATTTTCTTCCACCCCC   65192    AGA       TAT
                                GG  TGGAAGAAG  GTACA
                                ||  |||||||||  |||||
                                CC  ACCTTCTTT  TATGT
                                 CCC       ___
GAM829  ADCY2     3'  ACACTTTCTGACTGCAACTT  65013    C      CT  C
                                AAG TGCAGTCG  GAA TGT
                                ||| ||||||||  ||| |||
                                TTC ACGTCAGT  TTT ACA
                                  A       C_  C
GAM829  AIM1      3'  ACAATCACGGCTCACTGCAGC 91810       C_   AAC_
                                GCTGCAGT  GCTG   TGT
                                ||||||||  ||||   |||
                                CGACGTCA  CGGC   ACA
                                    CT    ACTA
GAM829  BAP1      3'  ACAGCGAGGTACTGCAGCTT  16211        C  GAA
                                AAGCTGCAGT GCT  CTGT
                                |||||||||| |||  ||||
                                TTCGACGTCA TGG  GACA
                                    _  AGC
GAM829  BDKRB1    5'  ACAATCATAGCTCGCTGCAGC 5541        C_   AAC_
                                GCTGCAGT  GCTG   TGT
                                ||||||||  ||||   |||
                                CGACGTCG  CGAT   ACA
                                    CT    ACTA
GAM829  BRCA1     3'  ACAGCCACTACTGACTGCAGC 23566        C  AA__
                                GCTGCAGTCG TG   CTGT
                                |||||||||| ||   ||||
                                CGACGTCAGT AT   GACA
                                    C  CACC
GAM829  CACNG6    3'  TACAACTCATCTGCAGCT    49103      TCGC  AC
                                AGCTGCAG   TGA  TGTA
                                ||||||||   |||  ||||
                                TCGACGTC   ACT  ACAT
                                    T___   CA
GAM829  CANX      3'  TACAGAATTGACTGCAGTT   87484        CTGAA
                                AGCTGCAGTCG    CTGTA
                                ||||||||||    |||||
                                TTGACGTCAGT    GACAT
                                     TAA__
GAM829  COL9A2    3'  TACAGTTCCACCCCTCAGCTT 8490      C  TCGCT
                                AAGCTG AG    GAACTGTA
                                ||||||  ||    ||||||||
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                                TTCGAC TC    CTTGACAT
                                   _ CCCAC
GAM829  EDG8    3' ACAATTATAGCTCACTGCAGC 78475       C_   _ C
                                GCTGCAGT  GCTG AA TGT
                                ||||||||  |||| || |||
                                CGACGTCA  CGAT TT ACA
                                    CT   A  A
GAM829  HUNK    3' ACAGTTCACTGCAGC      27436       CGCT
                                GCTGCAGT   GAACTGT
                                ||||||||   |||||||
                                CGACGTCA   CTTGACA
                                    ____
GAM829  IL6R    3' TACAGTTCAAAAACAGCT    5124      CAGTCGC
                                AGCTG     TGAACTGTA
                                |||||     |||||||||
                                TCGAC     ACTTGACAT
                                  AAAA___
GAM829  MBL2    3' ACAGTTTAATACCACAGCTT  4113      CA  CGC
                                AAGCTG  GT   TGAACTGT
                                ||||||  ||   ||||||||
                                TTCGAC  CA   ATTTGACA
                                   AC  TA_
GAM829  MPP2    3' ACAGCTGCAGAGCACTGCAGCT 59814       CG_  AA_
                                AGCTGCAGT   CTG   CTGT
                                |||||||||   |||   ||||
                                TCGACGTCA   GAC   GACA
                                     CGA   GTC
GAM829  OSCAR   3' CAGGAGCACTGCAGC      55669       C   GAA
                                GCTGCAGT GCT   CTG
                                |||||||| |||   |||
                                CGACGTCA CGA   GAC
                                    _   G__
GAM829  OSCAR   3' CAGGAGCACTGCAGC      55372       C   GAA
                                GCTGCAGT GCT   CTG
                                |||||||| |||   |||
                                CGACGTCA CGA   GAC
                                    _   G__
GAM829  OSCAR   3' CAGGAGCACTGCAGC      55665       C   GAA
                                GCTGCAGT GCT   CTG
                                |||||||| |||   |||
                                CGACGTCA CGA   GAC
                                    _   G__
GAM829  PIN1L   3' ACAATTCAGCGACTGCAGCT  20617           C
                                AGCTGCAGTCGCTGAA TGT
                                |||||||||||||||| |||
                                TCGACGTCAGCGACTT ACA
                                          A
GAM829  PLN     3' TACAACCTCTAGATCTGCAGCT 10648       _  GCT  AC_
          T                      AAGCTGCAG TC   GA   TGTA
                                 |||||||||  ||   ||   ||||
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                                TTCGACGTC AG   CT   ACAT
                                     T  AT_  CCA
GAM829  PTGES    3'  TACAATCTGGCTCACTGCAGC  16863        C_   AAC
                                GCTGCAGT  GCTG   TGTA
                                |||||||| ||||  ||||
                                CGACGTCA  CGGT   ACAT
                                     CT    CTA
GAM829  PVR      3'  ACAGTTCATTGCAGC       21470        TCGC
                                GCTGCAG   TGAACTGT
                                |||||||   ||||||||
                                CGACGTT   ACTTGACA
                                     ____
GAM829  RANBP2   3'  TCAGAAACTGCAGCTT      20767         CG
                                AAGCTGCAGT  CTGA
                                ||||||||||  ||||
                                TTCGACGTCA  GACT
                                      AA
GAM829  ROCK2    3'  TACAGTGATATTGACTGCATCT 66017     C      C  A_
           T                     AAG TGCAGTCG TG  ACTGTA
                                ||| |||||||| ||  ||||||
                                TTC ACGTCAGT AT  TGACAT
                                  T       T  AG
GAM829  SOX15    3'  TACAGTTCAGAGGCAGC     22691      AGTCG
                                GCTGC    CTGAACTGTA
                                |||||    ||||||||||
                                CGACG    GACTTGACAT
                                   GA___
GAM829  STARD4   3'  CAGCTCACTGCAGCTT      57511         C_
                                AAGCTGCAGT  GCTG
                                ||||||||||  ||||
                                TTCGACGTCA  CGAC
                                      CT
GAM829  TLR5     5'  ACAATCTCGGCTGACTGCA   12320       _    AC_
                                TGCAGTC GCTGA   TGT
                                ||||||| |||||   |||
                                ACGTCAG CGGCT   ACA
                                     T    CTA
GAM829  UCP3     3'  ACAGAGCTGGCGACTGCAGCT  12533           AA_
                                AGCTGCAGTCGCTG   CTGT
                                ||||||||||||||   ||||
                                TCGACGTCAGCGGT   GACA
                                       CGA
GAM829  XRCC2    3'  ACAATCTCGGCCCGCTGCAGC  18317        C_    AC_
                                GCTGCAGT  GCTGA   TGT
                                ||||||||  |||||   |||
                                CGACGTCG  CGGCT   ACA
                                     CC    CTA
GAM829  XRCC2    3'  ACAATCATGGCTCACTGCAGC  18316        C_   GAAC_
                                GCTGCAGT  GCT    TGT
                                ||||||||  |||    |||
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                                CGACGTCA CGG    ACA
                                    CT  TACTA
GAM829  ZNF74    3' ACAGCACTGCACTGCAGC    12788       C TGAA
                                GCTGCAGT GC   CTGT
                                |||||||| ||   ||||
                                CGACGTCA CG   GACA
                                    _ TCAC
GAM829  APOARGC  3' ACAGAAGGGACTGCAGT    44414       G GAA
                                GCTGCAGTC CT  CTGT
                                ||||||||| ||  ||||
                                TGACGTCAG GA  GACA
                                    G A__
GAM829  APPD     3' CAGGCCCAGGGACTGCAGC   44211       G  AA_
                                GCTGCAGTC CTG  CTG
                                ||||||||| |||  |||
                                CGACGTCAG GAC  GAC
                                    G  CCG
GAM829  ATPAF2   5' TACAGCCCGACCGTGCGGCTT 74395       __   CTGAA
                                AAGCTGCA GTCG   CTGTA
                                |||||||| ||||   |||||
                                TTCGGCGT CAGC   GACAT
                                    GC   CC___
GAM829  C21orf58 5' TACAGTCGTCTCCTGCAGCT  54196       TCGC  A
                                AGCTGCAG   TGA CTGTA
                                |||||||   ||| |||||
                                TCGACGTC   GCT GACAT
                                    CTCT  _
GAM829  C6orf5   3' ACAGTCTCAGCTCACTGCAGCT 31336       C_   _
          T                      AAGCTGCAGT  GCTGA ACTGT
                                |||||||||  ||||| |||||
                                TTCGACGTCA  CGACT TGACA
                                    CT   C
GAM829  DKFZP434G1415 3' ACGTATAGCACTGCAGC    48445       C   A  T
                                GCTGCAGT GCTG AC GT
                                |||||||| |||| || ||
                                CGACGTCA CGAT TG CA
                                    _   A  _
GAM829  DKFZP434H132 5' ATACAGCCCAGCACTCCCACTG 73603      C_____   AA   III
          CAGC                   TGCAGT    GCTG  CTGTA  T
                                ||||||    ||||  |||||  |
                                ACGTCA    CGAC  GACAT  A
                                   CCCTCA   CC   III
GAM829  DKFZp566H0824 5' TACAGTTCTGCTGTA      34058       CGCT
                                TGCAGT   GAACTGTA
                                ||||||   ||||||||
                                ATGTCG   CTTGACAT
                                   T___
GAM829  DKFZP566K0524 3' TACATAAAACGATTGCAGCTT 69353          CTGAAC
                                AAGCTGCAGTCG    TGTA
                                ||||||||||||    ||||
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                                TTCGACGTTAGC     ACAT
                                      AAAAT_
GAM829  FLJ10052  3' ACAGTTCACATTATGCATCT  35769    C   GTCGC
                                AG TGCA    TGAACTGT
                                || ||||    ||||||||
                                TC ACGT    ACTTGACA
                                 T   ATTAC
GAM829  FLJ10420  3' ACAGTTCAGCGGGAGGCTT   36105     GCAG
                                AAGCT   TCGCTGAACTGT
                                |||||   ||||||||||||
                                TTCGG   GGCGACTTGACA
                                  AG__
GAM829  FLJ10737  3' ACACGTGCTGACCGCAGC    36518     A  _ TGA  _
                                GCTGC GTC GC   AC TGT
                                ||||| ||| ||   || |||
                                CGACG CAG CG   TG ACA
                                  C   T  ___  C
GAM829  FLJ11467  3' TACAGTGGCGTGATCACAGCT 46378     CA    TGA
                                AGCTG  GTCGC   ACTGTA
                                |||||  |||||   ||||||
                                TCGAC  TAGTG   TGACAT
                                  AC    CGG
GAM829  FLJ11710  3' ACAATCAAAGCTCACTGCAGC  45823       C_  GAAC_
                                GCTGCAGT  GCT    TGT
                                ||||||||  |||    |||
                                CGACGTCA  CGA    ACA
                                     CT   AACTA
GAM829  FLJ11726  3' ACAATTAGTGACTCCAGCTT   46404     C       AC
                                AAGCTG AGTCGCTGA  TGT
                                ||||||| |||||||||  |||
                                TTCGAC TCAGTGATT  ACA
                                  C       A_
GAM829  FLJ11800  3' ACAATCAAGGCTCACTGCAGC  46421       C_  GAAC_
                                GCTGCAGT  GCT    TGT
                                ||||||||  |||    |||
                                CGACGTCA  CGG    ACA
                                     CT   AACTA
GAM829  FLJ12998  3' ACAGCGCGCAGAGACTGCAGC  42833       G  AA__
                                GCTGCAGTC CTG    CTGT
                                ||||||||| |||    ||||
                                CGACGTCAG GAC    GACA
                                     A   GCGC
GAM829  FLJ14642  3' CAGCCTGGCTGCACCTT     51496     C     __
                                AAG TGCAGTC  GCTG
                                ||| |||||||  ||||
                                TTC ACGTCGG  CGAC
                                  C      TC
GAM829  FLJ20249  3' ACAGTCCTTTCTGCAGCTT    79423       TCGCT  A
                                AAGCTGCAG    GA CTGT
                                |||||||||    || ||||
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                                TTCGACGTC    CT GACA
                                    TTTC_ _
GAM829  FLJ20793  5' ACAGTCAGCTTCTGCAGCT   91801       TC    A
                                AGCTGCAG  GCTGA CTGT
                                ||||||||  ||||| ||||
                                TCGACGTC  CGACT GACA
                                    TT    _
GAM829  GPR9      3' ACAGCCCAGGCCTCCAGCT   7683      C  TCG   AA
                                AGCTG AG   CTG  CTGT
                                ||||| ||   |||  ||||
                                TCGAC TC   GAC  GACA
                                   C  CG_   CC
GAM829  HUMZD58C02 5' ACACTCAACTGCAGCTT    79763        CGC   AC
                                AAGCTGCAGT   TGA  TGT
                                ||||||||||   |||  |||
                                TTCGACGTCA   ACT  ACA
                                    ___  C_
GAM829  KIAA0056  3' ACAACTTTAAAACTGCAGCTT 91553        CGC   C_
                                AAGCTGCAGT   TGAA  TGT
                                ||||||||||   ||||  |||
                                TTCGACGTCA   ATTT  ACA
                                    AA_   CA
GAM829  KIAA0090  3' ACAGTCATAGCTCACTGCAGC  88436       C_   A_
                                GCTGCAGT  GCTG  ACTGT
                                ||||||||  ||||  |||||
                                CGACGTCA  CGAT  TGACA
                                    CT    AC
GAM829  KIAA0406  5' TACAGTGGCACAATCACAGCT  61331     CA___  C   GA
                                AGCTG    GT GCT  ACTGTA
                                |||||    || |||  ||||||
                                TCGAC    CA CGG  TGACAT
                                   ACTAA  _  __
GAM829  KIAA0469  3' ACAGTTCATGGCGGCT     29316       __
                                AGTCGCT  GAACTGT
                                |||||||  |||||||
                                TCGGCGG  CTTGACA
                                    TA
GAM829  KIAA0469  3' TACAATCATGGCTCACTGCAGC 29347       C_   GAAC_
                                GCTGCAGT  GCT    TGTA
                                ||||||||  |||    ||||
                                CGACGTCA  CGG    ACAT
                                    CT   TACTA
GAM829  KIAA0534  3' ACAGTTCACTAAAGCT     71425     GC   CGCT
                                AGCT  AGT   GAACTGT
                                ||||  |||   |||||||
                                TCGA  TCA   CTTGACA
                                  AA  _____
GAM829  KIAA0711  5' GCAGTCAACTGCAGCT     29520        CGC   A
                                AGCTGCAGT   TGA CTGT
                                |||||||||   ||| ||||
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                                TCGACGTCA   ACT GACG
                                    ___  _
GAM829  KIAA1255 5' TACAGTTCAAAGAAACACT   67165    C  CAG  GC
                                AG TG   TC  TGAACTGTA
                                || ||   ||  |||||||||
                                TC AC   AG  ACTTGACAT
                                 _ AA_  AA
GAM829  KIAA1464 3' ACAGGCCGAGCTGCAGC     68259        CGC  AA
                                GCTGCAGT   TG  CTGT
                                ||||||||   ||  ||||
                                CGACGTCG   GC  GACA
                                     A__  CG
GAM829  KIAA1560 3' TACAGTTCTCTGGCCACAGCT  64180      CA   CT
                                AGCTG  GTCG  GAACTGTA
                                |||||  ||||  ||||||||
                                TCGAC  CGGT  CTTGACAT
                                   AC    CT
GAM829  KIAA1727 3' ACAATCATAGCTCACTGCAGCT 64052         C_   AAC_
           T                     AAGCTGCAGT  GCTG   TGT
                                ||||||||||  ||||   |||
                                TTCGACGTCA  CGAT   ACA
                                     CT    ACTA
GAM829  KIAA1784 3' ACAGCCCAGATGCAGTT     65138       GTCG   AA
                                AGCTGCA    CTG  CTGT
                                |||||||    |||  ||||
                                TTGACGT    GAC  GACA
                                    A___   CC
GAM829  KIAA1829 3' ACAATCATGGCTCACTGCAGC  61942        C_   GAAC_
                                GCTGCAGT  GCT    TGT
                                ||||||||  |||    |||
                                CGACGTCA  CGG    ACA
                                     CT   TACTA
GAM829  LHPP     3' ACAGTGAGAACTGTAGC     42098        CG  GA
                                GCTGCAGT  CT  ACTGT
                                ||||||||  ||  |||||
                                CGATGTCA  GA  TGACA
                                    A_  G_
GAM829  LHX6     3' TACAGCTCAGCTCAGC      26861      CAGTC    A
                                GCTG    GCTGA CTGTA
                                ||||    ||||| |||||
                                CGAC    CGACT GACAT
                                  T____    C
GAM829  LIMK2    3' ACAGTTCAGCATTGTGTGGCT  33619      __    C
                                AGCT  GCAGT GCTGAACTGT
                                ||||  ||||| ||||||||||
                                TCGG  TGTTA CGACTTGACA
                                  TG    _
GAM829  LIMK2    3' ACAGTTCAGCATTGTGTGGCT  18721      __    C
                                AGCT  GCAGT GCTGAACTGT
                                ||||  ||||| ||||||||||
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                                TCGG  TGTTA CGACTTGACA
                                  TG    _
GAM829  MGC11386 3'  ACAGTGGTGCGATCACAGCT  51947      CA    TGA
                                AGCTG  GTCGC   ACTGT
                                |||||  |||||   |||||
                                TCGAC  TAGCG   TGACA
                                   AC    TGG
GAM829  MRPL13   3'  TACAGTTCAGCACCTGT    26017     TC
                                GCAG  GCTGAACTGTA
                                ||||  ||||||||||
                                TGTC  CGACTTGACAT
                                  CA
GAM829  NDUFC2   3'  ACAGTTCACTGCAGC      15822       CGCT
                                GCTGCAGT   GAACTGT
                                ||||||||   |||||||
                                CGACGTCA   CTTGACA
                                           _____
GAM829  OSBPL1A  3'  ACAGTTTTCTGCAGT      54582       TCGCT
                                GCTGCAG    GAACTGT
                                |||||||    |||||||
                                TGACGTC    TTTGACA
                                   T_____
GAM829  OSBPL1A  3'  ACAGTTTTCTGCAGT      55741       TCGCT
                                GCTGCAG    GAACTGT
                                |||||||    |||||||
                                TGACGTC    TTTGACA
                                   T_____
GAM829  OSBPL1A  3'  ACAGTTTTCTGCAGT      35906       TCGCT
                                GCTGCAG    GAACTGT
                                |||||||    |||||||
                                TGACGTC    TTTGACA
                                   T_____
GAM829  SNRPD1   3'  TACAGTTCAGCGTTTGC    22679     T
                                GCAG CGCTGAACTGTA
                                |||| ||||||||||||
                                CGTT GCGACTTGACAT
                                  T
GAM829  TLK2     3'  TAGAAGACTGCAGCTT     22451         G_
                                AAGCTGCAGTC  CTG
                                ||||||||||  |||
                                TTCGACGTCAG  GAT
                                      AA
GAM829  TLK2     3'  TAGAAGACTGCAGCTT     78200         G_
                                AAGCTGCAGTC  CTG
                                ||||||||||  |||
                                TTCGACGTCAG  GAT
                                      AA
GAM829  VPS28    3'  ACAACTCACTGTCTGCAGCT  32503       T  C   AC
                                AGCTGCAG CG TGA  TGT
                                |||||||| || |||  |||
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                                TCGACGTC GT ACT  ACA
                                    T  C   CA
GAM829  YKT6     3'  ACATCAGAACTGCAGC      21595        CG    AC
                                GCTGCAGT  CTGA  TGT
                                ||||||||  ||||  |||
                                CGACGTCA  GACT  ACA
                                    A_   __
GAM829  ZNF364   5'  CGGCGACGACTGCAGCT     66770          ___
                                AGCTGCAGTC   GCTG
                                ||||||||||   ||||
                                TCGACGTCAG   CGGC
                                     CAG
GAM829  LOC112970 3'  TACAGTTCTACATCTGCACCT  56537    C     TCGCT
                                AG TGCAG    GAACTGTA
                                || |||||    ||||||||
                                TC ACGTC    CTTGACAT
                                 C    TACAT
GAM829  LOC126133 3'  ACAATCTCGGCCCACTGCAGC  74439        C_    AC_
                                GCTGCAGT  GCTGA   TGT
                                ||||||||  |||||   |||
                                CGACGTCA  CGGCT   ACA
                                    CC    CTA
GAM829  LOC130479 5'  ACAGTTTATCTGAGC      75745     G   TCGC
                                GCT CAG    TGAACTGT
                                ||| |||    ||||||||
                                CGA GTC    ATTTGACA
                                  _  T___
GAM829  LOC133088 5'  TACAGTTCACCATTTCAGC    75079      C   CGC
                                GCTG AGT   TGAACTGTA
                                |||| |||   |||||||||
                                CGAC TTA   ACTTGACAT
                                  T  CC_
GAM829  LOC145622 3'  TACAATAAAGTCAATGCAGCTT 77311         GTC   GAAC
                                AAGCTGCA   GCT    TGTA
                                ||||||||   |||    ||||
                                TTCGACGT   TGA    ACAT
                                    AAC   AATA
GAM829  LOC146420 3'  CAGGGCGACTACAGTT      83666       C      GAA
                                AGCTG AGTCGCT   CTG
                                ||||| |||||||   |||
                                TTGAC TCAGCGG   GAC
                                  A      ___
GAM829  LOC146545 5'  ACAGTTCCTGGCTGCAGGCT   77981     _       CT
                                AGC TGCAGTCG  GAACTGT
                                ||| ||||||||  |||||||
                                TCG ACGTCGGT  CTTGACA
                                 G       C_
GAM829  LOC148809 5'  ACAGTCTCTCCCTGCAGCTT   78995         TCGCT  _
                                AAGCTGCAG    GA ACTGT
                                |||||||||    || |||||
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                                TTCGACGTC    CT TGACA
                                     CCT__  C
GAM829  LOC149464 5'  TACAGTCTGTGCTGCAGT    84434       T  T  A
                                GCTGCAG CGC GA CTGTA
                                ||||||| ||| || |||||
                                TGACGTC GTG CT GACAT
                                   _  T  _
GAM829  LOC149837 3'  TACAGTTCTGTGCAGTCC    84746   A    AGTC  T
                                A GCTGC    GC GAACTGTA
                                | |||||    || ||||||||
                                C TGACG    TG CTTGACAT
                                 C    _____ T
GAM829  LOC152345 3'  CAGTATACTGCAGTTT      80574         C_
                                AAGCTGCAGT  GCTG
                                ||||||||||  ||||
                                TTTGACGTCA  TGAC
                                     TA
GAM829  LOC153811 5'  ACAGTCATGGCTCGCTGCAGC  80938       C_  GA_
                                GCTGCAGT  GCT   ACTGT
                                ||||||||  |||   |||||
                                CGACGTCG  CGG   TGACA
                                     CT   TAC
GAM829  LOC154834 3'  GCAGGCAACTGCAGCT      86267        C  TGAA
                                AGCTGCAGT GC    CTGT
                                |||||||| ||    ||||
                                TCGACGTCA CG    GACG
                                     A  _____
GAM829  LOC163724 5'  ACACCAGCTGCAGCTT      82151       GTC   AAC
                                AAGCTGCA   GCTG   TGT
                                ||||||||   ||||   |||
                                TTCGACGT   CGAC   ACA
                                     ___    C__
GAM829  LOC169611 3'  TACAGCTAAGAACATGCAGCTT 82776       GTCG  GAA
                                AAGCTGCA    CT   CTGTA
                                ||||||||    ||   |||||
                                TTCGACGT    GA   GACAT
                                     ACAA  ATC
GAM829  LOC196337 5'  ACAGCCCCGTGCTGCAGC    87642       T   TGAA
                                GCTGCAG CGC    CTGT
                                ||||||| |||    ||||
                                CGACGTC GTG    GACA
                                   _  CCCC
GAM829  LOC200470 5'  TACGGGGTAGACTGCAGC    90068        GC  AA
                                GCTGCAGTC  TG  CTGTA
                                |||||||||  ||  |||||
                                CGACGTCAG  AT  GGCAT
                                     __ GG
GAM829  LOC201292 3'  ACAATCATGGCTCACTGCAGC  88184       C_  GAAC_
                                GCTGCAGT  GCT    TGT
                                ||||||||  |||    |||
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                                CGACGTCA  CGG    ACA
                                     CT   TACTA
GAM829   LOC201627 3'  ACAGTTCAGCTGCTAGTCTT   89001    _ _  GTC
                                AAG CT GCA   GCTGAACTGT
                                ||| || |||   ||||||||||
                                TTC GA CGT   CGACTTGACA
                                  T  T  ___
GAM829   LOC201931 3'  CGGGGAACTGCAGCTT      89110         _ G
                                AAGCTGCAGT C CTG
                                |||||||||| | |||
                                TTCGACGTCA G GGC
                                      A G
GAM829   LOC203427 3'  ACAATCATAGCTCACTGCAGC  89356       C_   AAC_
                                GCTGCAGT  GCTG   TGT
                                ||||||||  ||||   |||
                                CGACGTCA  CGAT   ACA
                                     CT   ACTA
GAM829   LOC220522 3'  CAGGCAGTGACTGCAGC     60521           AA
                                GCTGCAGTCGCTG  CTG
                                ||||||||||||  |||
                                CGACGTCAGTGAC  GAC
                                       G_
GAM829   LOC221584 5'  TACAGCCCATAACAGCTGCAGC 93831        CGC__  AA
                                GCTGCAGT    TG  CTGTA
                                ||||||||    ||  |||||
                                CGACGTCG    AC  GACAT
                                     ACAAT  CC
GAM829   LOC222160 5'  TACAGTCTTGATGACTGCATCT 94132    C      CT  _
           T                     AAG TGCAGTCG  GA ACTGTA
                                ||| ||||||||  || ||||||
                                TTC ACGTCAGT  TT TGACAT
                                  T       AG  C
GAM829   LOC253783 5'  ACAGTTCATTGCAGC       95265       TCGC
                                GCTGCAG   TGAACTGT
                                |||||||   ||||||||
                                CGACGTT   ACTTGACA
                                     ____
GAM829   LOC255004 5'  AGTTCAGCAACTGCAGC     95548        C
                                GCTGCAGT GCTGAACT
                                |||||||| ||||||||
                                CGACGTCA CGACTTGA
                                     A
GAM829   LOC256849 5'  ACAGTCTGGCCACTGCAGCT   96946        C   GA
                                AGCTGCAGT GCT  ACTGT
                                ||||||||| |||  |||||
                                TCGACGTCA CGG  TGACA
                                     C   TC
GAM829   LOC257054 5'  ACAGTTGCAGCTCACTGCAGC  95654        C_   _
                                GCTGCAGT  GCTG AACTGT
                                ||||||||  |||| ||||||
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                                CGACGTCA  CGAC TTGACA
                                     CT    G
GAM829  LOC51008  5'  TACAGGCGTGACGACTGCACCT 31969    C       CT AA_
                                AG TGCAGTCG  G   CTGTA
                                || ||||||||  |   |||||
                                TC ACGTCAGC  T   GACAT
                                 C       AG GCG
GAM829  LOC90829  3'  TACAGTTTTTGTGCTGAGCT   64100     G   T   T_
                                AGCT CAG CGC  GAACTGTA
                                |||| ||| |||  ||||||||
                                TCGA GTC GTG  TTTGACAT
                                  _  _  TT
GAM829  LOC93109  3'  ACAGTTCACAGAAGCTT     71414      GCAG  GC
                                AAGCT    TC  TGAACTGT
                                |||||    ||  ||||||||
                                TTCGA    AG  ACTTGACA
                                   ____  AC
GAM829  LOC93589  3'  TACAGCAGAAGACACTGCAGCT 72671         CG  GAA_
                                AGCTGCAGT  CT    CTGTA
                                |||||||||  ||    |||||
                                TCGACGTCA  GA    GACAT
                                     CA  AGAC
GAM830  ABL1      5'  GGTGGCTTTGGGCCGGGCTC   17678    A   AGATA
                                GA GCT     CCTAAAGCTACC
                                || |||     ||||||||||||
                                CT CGG     GGGTTTCGGTGG
                                 _   GCC__
GAM830  CASP3     3'  GGTGGTTTTTTTTAGTTT     15103         TACCT
                                AAGCTAGA     AAAGCTACC
                                ||||||||     |||||||||
                                TTTGATTT     TTTTGGTGG
                                     T____
GAM830  CASP3     3'  GGTGGTTTTTTTTAGTTT     52197         TACCT
                                AAGCTAGA     AAAGCTACC
                                ||||||||     |||||||||
                                TTTGATTT     TTTTGGTGG
                                     T____
GAM830  CDKN2D    3'  GGCTTATAGGTGTTGGTTTT   54380        G     _
                                GAAGCTA ATACCTA AAGCT
                                ||||||| ||||||| |||||
                                TTTTGGT TGTGGAT TTCGG
                                   _      A
GAM830  CDKN2D    3'  GGCTTATAGGTGTTGGTTTT   8397         G     _
                                GAAGCTA ATACCTA AAGCT
                                ||||||| ||||||| |||||
                                TTTTGGT TGTGGAT TTCGG
                                   _      A
GAM830  EHD3      3'  GGTGGTTTTAGTTCATAGATTT 27480      _   GATAC
           T                     GAAG CTA     CTAAAGCTACC
                                 |||| |||     ||||||||||
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                                TTTT GAT    GATTTTGGTGG
                                  A  ACTT_
GAM830  EMS1    3' GGTGGTTTTGGGTTTTTTCT  17853    CT  T
                                AG  AGA ACCTAAAGCTACC
                                ||  ||| ||||||||||||||
                                TC  TTT TGGGTTTTGGTGG
                                 T_  T
GAM830  EMS1    3' GGTGGTTTTGGGTTTTTTCT  56753    CT  T
                                AG  AGA ACCTAAAGCTACC
                                ||  ||| ||||||||||||||
                                TC  TTT TGGGTTTTGGTGG
                                 T_  T
GAM830  FMR1    3' TTGGGGTTTGGTTTT      8942          A
                                GAAGCTAGAT CCTAA
                                |||||||||| |||||
                                TTTTGGTTTG GGGTT
                                      _
GAM830  GRF2    3' GGTGGTTTTCTGGTTTGGTTTT 17996         ACCT
                                GAAGCTAGAT   AAAGCTACC
                                ||||||||||   |||||||||
                                TTTTGGTTTG   TTTTGGTGG
                                     GTC_
GAM830  GYPA    5' GGTAGTTTTTTTGCACTAACTT 87451      C  ATACCT
          CA                    TGAAG TAG    AAAGCTACC
                                ||||| |||    |||||||||
                                ACTTC ATC    TTTTGATGG
                                  A  ACGTTT
GAM830  GYPB    5' GGTAGTTTTTTTGCACTAACTT 9160       C  ATACCT
          CA                    TGAAG TAG    AAAGCTACC
                                ||||| |||    |||||||||
                                ACTTC ATC    TTTTGATGG
                                  A  ACGTTT
GAM830  GYPE    5' GGTAGTTTTTTTGCACTAACTT 9167       C  ATACCT
          CA                    TGAAG TAG    AAAGCTACC
                                ||||| |||    |||||||||
                                ACTTC ATC    TTTTGATGG
                                  A  ACGTTT
GAM830  HCFC1   3' GGCCTGGGTGTCTGGTT    70998          AA
                                AGCTAGATACCTA  GCT
                                ||||||||||||  |||
                                TTGGTCTGTGGGT  CGG
                                      C_
GAM830  KCNN3   5' GGTGGCTTTGGGGTGGGGGCTT 9563      AGATA
                                AAGCT    CCTAAAGCTACC
                                |||||    ||||||||||||
                                TTCGG    GGGTTTCGGTGG
                                  GGGTG
GAM830  KLF4    5' GGTTTTGGGTTTTGGCTTC   14890        T
                                GAAGCTAGA ACCTAAAGCT
                                ||||||||| ||||||||||
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                                CTTCGGTTT TGGGTTTTGG
                                        _
GAM830  KRT16   5'  GGTGGCCTTGGTGCTGGCTTC  95200        A   T  A
                                GAAGCTAG TACC AA GCTACC
                                |||||||| |||| || ||||||
                                CTTCGGTC GTGG TT CGGTGG
                                    _   _ C
GAM830  MBL2    3'  GTGGTTTTAGTGATTTTA    4116    T    AC
                                C AGAT  CTAAAGCTAC
                                | ||||  ||||||||||
                                A TTTA  GATTTTGGTG
                                 T   GT
GAM830  OXCT    3'  GGTGGTTTTTTATTAGTTTT  4754         ATACCT
                                GAAGCTAG     AAAGCTACC
                                ||||||||     |||||||||
                                TTTTGATT     TTTTGGTGG
                                    ATT___
GAM830  RAB27A  3'  GGTGGTTTTAATATATGTTTCA 15927       TAG   CC
                                TGAAGC   ATA  TAAAGCTACC
                                ||||||   |||  ||||||||||
                                ACTTTG   TAT  ATTTTGGTGG
                                   TA_   A_
GAM830  RAG1    3'  GGTGAACTGGAATTTAGTTTT  4816         A  TAAA_
                                GAAGCTAGAT CC     GCT
                                |||||||||| ||     |||
                                TTTTGATTTA GG     TGG
                                     A  TCAAG
GAM830  RBM3    5'  GGTCCAGGGGTTTTGGTTTCA  70490         T    AAA_
                                TGAAGCTAGA ACCT    GCT
                                |||||||||| ||||    |||
                                ACTTTGGTTT TGGG    TGG
                                     _    GACC
GAM830  ROBO1   3'  GGTGGTATTTTATTTTGGCTTC 56088         TACCT  A
          A                      TGAAGCTAGA     AA GCTACC
                                 ||||||||||     || ||||||
                                 ACTTCGGTTT     TT TGGTGG
                                      TATT_  A
GAM830  ROBO1   3'  GGTGGTATTTTATTTTGGCTTC 11374         TACCT  A
          A                      TGAAGCTAGA     AA GCTACC
                                 ||||||||||     || ||||||
                                 ACTTCGGTTT     TT TGGTGG
                                      TATT_  A
GAM830  SSPN    3'  GTAGTTTTAGTTGTTT      17443       C
                                AGATA CTAAAGCTAC
                                ||||| ||||||||||
                                TTTGT GATTTTGATG
                                   T
GAM830  STARD4  3'  GGTAGTTTGATCTGTGTTTTA  57513       _    ACCTA
                                TGAAGC TAGAT     AAGCTACC
                                |||||| |||||     ||||||||
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                                ATTTTG GTCTA    TTTGATGG
                                   T   G____
GAM830  USP6    3'  CGGTGGTTTTAGGAAGTCAACT 91145   _____  A_
            TTAGTTTT              A   GAT  CCTAAAGCTACC  G
                                |   |||  ||||||||||||  |
                                T   CTG  GGATTTTGGTGG  C
                                 TTCAA  AA
GAM830  ADNP    3'  GCATTTTGGATATTTAGTTTTA 31047          _ T  _
                                TGAAGCTAGATA CC AAA GC
                                |||||||||||| || ||| ||
                                ATTTTGATTTAT GG TTT CG
                                      A T  A
GAM830  ARHGAP11A 3'  GGTAGTTTTTCAGATTGGTT  28798      ATACCT
                                AGCTAG    AAAGCTACC
                                ||||||    |||||||||
                                TTGGTT    TTTTGATGG
                                   AGACT_
GAM830  C12orf22  3'  GCTTAATTGGGAATTTGGCTTT 47979        A   ___  TACC
            A                    GAAGCTAGAT CCTAA  AGC
                                ||||||||||  |||||  |||
                                TTTCGGTTTA GGGTT  TCG
                                      A    AAT    C
GAM830  DCNP1   3'  GTGGCTTTAACAGTTTCA   55626       AGATACC
                                TGAAGCT     TAAAGCTAC
                                |||||||     |||||||||
                                ACTTTGA     ATTTCGGTG
                                    CA_____
GAM830  DKFZp434E0519 3'  GGTGGTTTTGGCTAATTAGTTT 49991        A  C
            T                    GAAGCTAG TA CTAAAGCTACC
                                ||||||||  ||  ||||||||||
                                TTTTGATT AT GGTTTTGGTGG
                                    A  C
GAM830  DKFZp434F142 3'  GTAGCCTCTTCTGGTTTT    50029        TACCTAAA
                                GAAGCTAGA      GCTAC
                                |||||||||      |||||
                                TTTTGGTCT      CGATG
                                     TCTC____
GAM830  DKFZp761D112 3'  ATTTTTTTAGGTATCTAATTTT 50188      C          CTACC
            A                    TGAAG TAGATACCTAAAG
                                |||||  ||||||||||||
                                ATTTT ATCTATGGATTTT
                                   A          TTTAG
GAM830  DRCTNNB1A 3'  GGTGGTTTTTCTTGTTTTGGTT 50843        TACCT_
            T                    AAGCTAGA    AAAGCTACC
                                ||||||||    |||||||||
                                TTTGGTTT    TTTTGGTGG
                                     TGTTCT
GAM830  ELAC1   3'  TTGGCTAGGTGTTTATTTTA  90973      C       AA    CC
                                TGAAG TAGATACCT  AGCTA
                                |||||  |||||||||  |||||
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                                ATTTT ATTTGTGGA  TCGGT
                                  _       __    TT
GAM830  FBX30    3'  GGTGGCTTTGGCCCAGAGGCTC 52587     A   AGATAC
            A                    TGA GCT     CTAAAGCTACC
                                 ||| |||     ||||||||||
                                 ACT CGG     GGTTTCGGTGG
                                   _  AGACCC
GAM830  FLJ10647  5'  GGTGGTTTCTAGCTCAGGCTTT 36374       A  TAC  _
            A                    TGAAGCT GA   CTA AAGCTACC
                                 ||||||| ||   ||| ||||||||
                                 ATTTCGG CT   GAT TTTGGTGG
                                     A  C__   C
GAM830  FLJ10916  3'  GGTGGCTTTCTTTAGGCTTCA  36859       A  TACCT
                                 TGAAGCT GA    AAAGCTACC
                                 ||||||| ||    |||||||||
                                 ACTTCGG TT    TTTCGGTGG
                                     A  TC___
GAM830  FLJ20337  3'  GGTGGTTTTATTTTTTTAGTTT 34968        TACC
            T                    GAAGCTAGA   TAAAGCTACC
                                 |||||||||   ||||||||||
                                 TTTTGATTT   ATTTTGGTGG
                                      TTTT
GAM830  FLJ21918  3'  GTAGCTTCTTTCTGGCTT    46290        TACCTA
                                 AAGCTAGA    AAGCTAC
                                 ||||||||    |||||||
                                 TTCGGTCT    TTCGATG
                                     TTC___
GAM830  FUBP3    3'  GTATCTTGGCTGTCTGGTTTTA 63732          _  TA   C
                                 TGAAGCTAGATA CC  AAG TAC
                                 |||||||||||| ||  ||| |||
                                 ATTTTGGTCTGT GG  TTC ATG
                                       C  __   T
GAM830  KIAA0179  3'  GTACAATTAGGTATCTGACTTT 64829      C        AGC   C
            A                    TGAAG TAGATACCTAA   TAC
                                 ||||| ||||||||||   |||
                                 ATTTC GTCTATGGATT   ATG
                                    A         AAC
GAM830  KIAA0469  3'  GGTGGCTTTGGTGGTTGGTTCC 29344    A     A    T
            A                    TG AGCTAG TACC AAAGCTACC
                                 || |||||| |||| |||||||||
                                 AC TTGGTT GTGG TTTCGGTGG
                                  C     G   _
GAM830  KIAA0853  3'  GGTGGTAGGGGTTGTTTGGTTT 30542          _  AAA
            T                    GAAGCTAGATA CCT   GCTACC
                                 |||||||||| |||   ||||||
                                 TTTTGGTTTGT GGG   TGGTGG
                                       T  GA_
GAM830  KIAA1126  3'  GGTGGCTGAAGAGCTAGCTTT  71935       ATAC  AA
                                 GAAGCTAG    CT  AGCTACC
                                 ||||||||    ||  |||||||
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                                TTTCGATC   GA  TCGGTGG
                                    GA__  AG
GAM830  KIAA1486  3'  GGTGGTTTTATTTTTATTTAGC 67384          CC__
            TT                   AAGCTAGATA   TAAAGCTACC
                                 ||||||||||   ||||||||||
                                 TTCGATTTAT   ATTTTGGTGG
                                      TTTT
GAM830  MGC14844  3'  TAGCTTCTCTGTTTT      50341      T   TACCTA
                                 GAAGC AGA     AAGCTA
                                 ||||| |||     ||||||
                                 TTTTG TCT     TTCGAT
                                   _  C_____
GAM830  MGC16063  3'  GGTAGCATGTATCTGGTCTTA  53862     AG      CTAAA
                                 TGA  CTAGATAC    GCTACC
                                 |||  ||||||||    ||||||
                                 ATT  GGTCTATG    CGATGG
                                   CT       TA___
GAM830  MGC21688  3'  GGCTCATTAGGTGTTTATTTT  58269     C        __
                                 GAAG TAGATACCTAA  AGCT
                                 |||| ||||||||||  ||||
                                 TTTT ATTTGTGGATT  TCGG
                                   _         AC
GAM830  PHCA     3'  GGCCTGCTGGGTGTTTAGCTCA 37179     A        AA   TA_
                                 TGA GCTAGATACCT  AGC   CC
                                 ||| ||||||||||  |||   ||
                                 ACT CGATTTGTGGG  TCG   GG
                                   _         __  TCC
GAM830  QSCN6    3'  TGGGGTTTGGCTTCA       11043          A
                                 TGAAGCTAGAT CCTA
                                 |||||||||| ||||
                                 ACTTCGGTTTG GGGT
                                          _
GAM830  SERP1    3'  GGTTTACTATAGATATTTGGCT 27062          C   A  CT_
            TTA                    TGAAGCTAGATA CTA AG   ACC
                                 |||||||||| ||| ||   |||
                                 ATTTCGGTTTAT GAT TC   TGG
                                        A   A  ATT
GAM830  SRPK2    3'  GGTAGCTTTACGTGTGGCTACA 11970    A   AG   C
                                 TG AGCT  ATAC TAAAGCTACC
                                 || ||||  |||| ||||||||||
                                 AC TCGG  TGTG ATTTCGATGG
                                   A   __   C
GAM830  TAF9L    3'  GGTAGTTTTGGGTCAGTT    32006     AGAT
                                 AGCT   ACCTAAAGCTACC
                                 ||||   ||||||||||||
                                 TTGA   TGGGTTTTGATGG
                                   C___
GAM830  TCL6     3'  GGCTGCTGGCTGTCTGGCTTC  24986          _  TAA
                                 GAAGCTAGATA CC   AGCT
                                 |||||||||| ||   ||||
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                                CTTCGGTCTGT GG   TCGG
                                      C  TCG
GAM830  TCL6     3'  GGCTGCTGGCTGTCTGGCTTC  27002          _  TAA
                                GAAGCTAGATA CC   AGCT
                                |||||||||||  ||   ||||
                                CTTCGGTCTGT GG   TCGG
                                      C  TCG
GAM830  VDAC3    5'  GTGGAGGTCTTTGGTTTCA   18983          T   AAAG
                                TGAAGCTAGA ACCT   CTAC
                                |||||||||| ||||   ||||
                                ACTTTGGTTT TGGA   GGTG
                                      C  ____
GAM830  VPS16    3'  GGTAGCAGGGCTGTCTGGTTTT 42621          _  AAA
           A                     TGAAGCTAGATA CCT   GCTACC
                                |||||||||||| |||   ||||||
                                ATTTTGGTCTGT GGG   CGATGG
                                      C  A__
GAM830  VPS16    3'  GGTAGCAGGGCTGTCTGGTTTT 54417          _  AAA
           A                     TGAAGCTAGATA CCT   GCTACC
                                |||||||||||| |||   ||||||
                                ATTTTGGTCTGT GGG   CGATGG
                                      C  A__
GAM830  ZNF262   3'  GGTAGCTTTGGAGTGAAACTTT 17489     CTAGA  _
                                GAAG    TAC CTAAAGCTACC
                                ||||    ||| ||||||||||
                                TTTC    GTG GGTTTCGATGG
                                  AAA__  A
GAM830  LOC115294 3'  TTTGGGTGTTTATTTT     73021     C
                                GAAG TAGATACCTAAA
                                |||| ||||||||||||
                                TTTT ATTTGTGGGTTT
                                  _
GAM830  LOC116236 3'  TGGGTATTTGGTTTTA     73818
                                TGAAGCTAGATACCTA
                                ||||||||||||||||
                                ATTTTGGTTTATGGGT

GAM830  LOC144319 5'  GGTGGTTTTTAATTTTGCTTT  83059     T   ACCT
                                GAAGC AGAT   AAAGCTACC
                                ||||| ||||   |||||||||
                                TTTCG TTTA   TTTTGGTGG
                                   T   AT__
GAM830  LOC145601 3'  GGTGGTATCTGTGGCTGGTTTT 83369        A  CTAAA
           A                     TGAAGCTAG TAC    GCTACC
                                |||||||||  |||    ||||||
                                ATTTTGGTC GTG    TGGTGG
                                      G  TCTA_
GAM830  LOC146489 5'  GGTAGCTTTGGAAGCTGCTTT  70801     T  ATAC
                                GAAGC AG   CTAAAGCTACC
                                ||||| ||   ||||||||||
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                                TTTCG TC    GGTTTCGATGG
                                  _ GAA_
GAM830   LOC146714 5'  GGTCACAGGTGTTTGGCTT   83741           AAA
                                AAGCTAGATACCT   GCT
                                ||||||||||||   |||
                                TTCGGTTTGTGGA   TGG
                                     CAC
GAM830   LOC146956 3'  GTATTATGTATTTAGTTTCA   78210          C   A
                                TGAAGCTAGATAC TAA GC
                                |||||||||||| ||| ||
                                ACTTTGATTTATG ATT TG
                                     T   A
GAM830   LOC149650 3'  GCTTTTGGGTATCTGCTTT   79469      T        _
                                GAAGC AGATACCTAAA GC
                                ||||| |||||||||| ||
                                TTTCG TCTATGGGTTT CG
                                  _         T
GAM830   LOC153196 5'  GGTAACTTATGTGTCTGGTTTT 85970          CTA   C
                                GAAGCTAGATAC   AAG TACC
                                ||||||||||   ||| ||||
                                TTTTGGTCTGTG   TTC ATGG
                                     TA_   A
GAM830   LOC158187 3'  GGTGGCTTTCAACCTTGGCT   86695      ATACCT
                                AGCTAG     AAAGCTACC
                                ||||||     |||||||||
                                TCGGTT     TTTCGGTGG
                                   CCAAC_
GAM830   LOC158219 3'  GTATTAGGTATTTATTTTCA   81792      C        A
                                TGAAG TAGATACCTAA GC
                                ||||| |||||||||| ||
                                ACTTT ATTTATGGATT TG
                                   T         A
GAM830   LOC196707 5'  GTAGTTTTGAGTTGCTTT    87530      TAGAT  C
                                GAAGC    AC TAAAGCTAC
                                |||||    || |||||||||
                                TTTCG    TG GTTTTGATG
                                   T____  A
GAM830   LOC200268 3'  GGTAGCTTCCTTTTAGTCTTCA 88685      _    TACCTA
                                TGAAG CTAGA     AAGCTACC
                                ||||| |||||     ||||||||
                                ACTTC GATTT     TTCGATGG
                                   T    TCC___
GAM830   LOC200301 3'  CCAGCTTTGGGGTCTGGCTTTA 88739          A       ACC
                                TGAAGCTAGAT CCTAAAGCT
                                |||||||||| |||||||||
                                ATTTCGGTCTG GGGTTTCGA
                                     _       CCC
GAM830   LOC202108 3'  GGTAGTTTTAAGTTATTAGTTT 89155        AT  C
            T                    GAAGCTAG  AC TAAAGCTACC
                                |||||||  || ||||||||||
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                                TTTTGATT  TG ATTTTGATGG
                                     AT  A
GAM830  LOC220573 3'  CGGTGGTTTTAGGAAGTCAACT 69601   _____  A_
           TTAGTTTT               A    GAT  CCTAAAGCTACC  G
                                |   |||  ||||||||||||  |
                                T    CTG  GGATTTTGGTGG  C
                                 TTCAA   AA
GAM830  LOC245728 5'  GGTAGCTTTGGAAGCTGCTTT  91133      T  ATAC
                                GAAGC AG    CTAAAGCTACC
                                ||||| ||    ||||||||||
                                TTTCG TC    GGTTTCGATGG
                                   _  GAA_
GAM830  LOC254428 3'  TGGGGTTTGGCTTTA      95465          A
                                TGAAGCTAGAT CCTA
                                |||||||||| ||||
                                ATTTCGGTTTG GGGT
                                          _
GAM830  LOC255231 3'  TTGGGTATTTACCTTT     95380      C
                                GAAG TAGATACCTAA
                                |||| ||||||||||
                                TTTC ATTTATGGGTT
                                  C
GAM830  LOC256158 5'  TTGGAGTGTCTGGCTTC    97684          _
                                GAAGCTAGATAC CTAA
                                |||||||||||| ||||
                                CTTCGGTCTGTG GGTT
                                       A
GAM830  LOC257048 3'  TTGGGTATTTGGTATCA    96217     A
                                TGA GCTAGATACCTAA
                                ||| ||||||||||||
                                ACT TGGTTTATGGGTT
                                  A
GAM830  LOC90019  5'  GGTGAGGGTATCTGGCCTCA  56769     A         AAA
                                TGA GCTAGATACCT   GCT
                                ||| ||||||||||   |||
                                ACT CGGTCTATGGG   TGG
                                  C          AG_
GAM830  LOC90639  5'  TTGGGTATTTAATTTCA     63665      C
                                TGAAG TAGATACCTAA
                                ||||| ||||||||||
                                ACTTT ATTTATGGGTT
                                   A
GAM830  LOC93132  5'  GGTGGTTTTAAAATATAGCTAC 71499    A    GATACC
           A                     TG AGCTA     TAAAGCTACC
                                || |||||     ||||||||||
                                AC TCGAT     ATTTTGGTGG
                                 A    ATAAA_
GAM831  ADH4      3'  TAAAAAGATTTTTACTGGA    5408          CGT
                                TCCAGTGG   TCTTTTTA
                                ||||||||   ||||||||
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                                AGGTCATT  AGAAAAAT
                                    TTT
GAM831  B4GALT2  3'  AGTAAAAAACGTGAATGGA  47580    GTG   CT
                                TCCA  GCGTT  TTTTACT
                                ||||  |||||  |||||||
                                AGGT  TGCAA  AAAATGA
                                  AAG   __
GAM831  CTBP1    3'  AAAAAGAAAACCTGAAGGAG  67941    AGT_  CG
                                CTCC   GG  TTCTTTTT
                                ||||   ||  ||||||||
                                GAGG   CC  AAGAAAAA
                                  AAGT  AA
GAM831  ENPP3    3'  TAAAAAGAACAGCAGAGAG   17226    CAGTG  _
                                CTC    GC GTTCTTTTTA
                                |||    || ||||||||||
                                GAG    CG CAAGAAAAAT
                                  AGA__  A
GAM831  F8       3'  TAAAAAAATAAGTCAGGAGGA  3732       AG   GTTC_
                                TCCTCC  TGGC    TTTTTA
                                ||||||  ||||    ||||||
                                AGGAGG  ACTG    AAAAAT
                                   __   AATAA
GAM831  GK       3'  AGCAAAAAGAATGCTAT    3911           A
                                GTGGCGTTCTTTTT CT
                                |||||||||||||| ||
                                TATCGTAAGAAAAA GA
                                      C
GAM831  ID4      3'  GAAAAAAAGCCACCGGAGGA  7755       A    GTTC
                                TCCTCC GTGGC   TTTTT
                                |||||| |||||   |||||
                                AGGAGG CACCG   AAAAG
                                   C    AAA_
GAM831  PITX1    3'  GAAAAAGACGTCGGAG     10599     AGT    T    A
                                CTCC   GGCGT CTTTTT C
                                ||||   ||||| |||||| |
                                GAGG   CTGCA GAAAAA G
                                  ___    _     C
GAM831  TDG      3'  GAAAAAGATGCTGGAG     12191       GCGT     A
                                CTCCAGTG   TCTTTTT C
                                ||||||||   ||||||| |
                                GAGGTCGT   AGAAAAA G
                                     ____      C
GAM831  XRCC2    3'  AGCAAAAAGAACAAAGCTGGAG 18318        GGC       A
          G                    CCTCCAGT   GTTCTTTTT CT
                               ||||||||   ||||||||| ||
                               GGAGGTCG   CAAGAAAAA GA
                                    AAA       C
GAM831  DKFZP727M111 5'  AAAAGGAAAAGCCCTGAAG   31401    C   T   G_
                                CT CAG GGC  TTCTTTTT
                                || ||| |||  ||||||||
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                                GA GTC CCG  AAGGAAAA
                                 A  _  AA
GAM831  ELKS     3'  AGTGGTCAACGCCCTGGAAGA  30501    C    T     CTTT
                                TC TCCAG GGCGTT   TTACT
                                || ||||| ||||||   |||||
                                AG AGGTC CCGCAA   GGTGA
                                 A    _     CT__
GAM831  FLJ10648  3'  AGCAAAAAGAACAAAGTCCTGG 36378         T  ___       A
           AGGA                    TCCTCCAG GGC   GTTCTTTTT CT
                                ||||||||| |||   ||||||||| ||
                                AGGAGGTC CTG   CAAGAAAAA GA
                                     _  AAA        C
GAM831  FLJ20151  3'  AAAGACCCTGGAGGA       34648         T  CGT
                                TCCTCCAG GG   TCTTT
                                |||||||| ||   |||||
                                AGGAGGTC CC   AGAAA
                                     _ ___
GAM831  FLJ20435  3'  TAAAAAGAGCCATCTGGAGGA  35162         _   GT
                                TCCTCCAG TGGC  TCTTTTTA
                                |||||||| ||||  ||||||||
                                AGGAGGTC ACCG  AGAAAAAT
                                     T   __
GAM831  MDS024    3'  AAAAAGAATTGCCAAGGA    41522     AG    _
                                TCC  TGGCG TTCTTTTT
                                |||  ||||| ||||||||
                                AGG  ACCGT AAGAAAAA
                                  A_    T
GAM831  ShrmL     5'  AGAGCGCCACTGAAGGA     40463      C
                                TCCT CAGTGGCGTTCT
                                |||| ||||||||||||
                                AGGA GTCACCGCGAGA
                                   A
GAM831  SIAT8C    5'  TAAAAAAGCCCCACAGAGGA   31883       CA    C   C
                                TCCTC  GTGG GTT TTTTTA
                                |||||  |||| ||| ||||||
                                AGGAG  CACC CGA AAAAAT
                                   A_    C   _
GAM831  VEST1     5'  AAAAAGATGCACTGGGGA    53678     T     G   T
                                TCC CCAGTG CGT CTTTTT
                                ||| |||||| ||| ||||||
                                AGG GGTCAC GTA GAAAAA
                                     _     _  _
GAM831  ZFD25     5'  AAAAAGAGCCCTGGA       32573       T   GT
                                TCCAG GGC  TCTTTTT
                                ||||| |||  |||||||
                                AGGTC CCG  AGAAAAA
                                     _  __
GAM831  LOC124626 3'  AGTAAGACCAAACCACTGGA   74313         CGTTCT
                                TCCAGTGG     TTTTACT
                                ||||||||     |||||||
```

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                                AGGTCACC     AGAATGA
                                     AAACC_
GAM831  LOC144577 3'  TAAAAAGAAGCCACAAAGAG  76902     CA_    G
                                CTC   GTGGC TTCTTTTTA
                                |||   ||||| |||||||||
                                GAG   CACCG AAGAAAAAT
                                  AAA    _
GAM831  LOC145837 5'  AGCAAAAAGAACCAAAGAGGA  83542      CAG   CG      A
                                TCCTC   TGG  TTCTTTTT CT
                                |||||   |||  |||||||| ||
                                AGGAG   ACC  AAGAAAAA GA
                                   AA_  __       C
GAM831  LOC151194 3'  TAAAAAAACTGGGGA      59215     T    GGCGTTC
                                TCC CCAGT      TTTTTA
                                ||| |||||      ||||||
                                AGG GGTCA      AAAAAT
                                  _    A_______
GAM831  LOC154789 5'  AGTAAAATCTCAGGCCACTAGA 81131     C     GTTCT_
          G                      CTC AGTGGC     TTTTACT
                                ||| ||||||     |||||||
                                GAG TCACCG     AAAATGA
                                  A     GACTCT
GAM831  LOC197322 3'  AAAGACTCCACTGGAGGA    89736          C  T
                                TCCTCCAGTGG GT CTTT
                                |||||||||| || ||||
                                AGGAGGTCACC CA GAAA
                                       T  _
GAM831  LOC221596 3'  TAAAAACCTCACACTGGAGAGA 91980    _      GCGTTC
                                TC CTCCAGTG     TTTTTA
                                || ||||||||     ||||||
                                AG GAGGTCAC     AAAAAT
                                 A       ACTCC_
GAM831  LOC91796  3'  AGCAAAAAGAACAAGGCTGGA  67208       GGC       A
                                TCCAGT   GTTCTTTTT CT
                                ||||||   |||||||| ||
                                AGGTCG   CAAGAAAAA GA
                                   GAA       C
GAM831  LOC92539  5'  TAAAAAGTGTCACTG       69638        TT
                                CAGTGGCG  CTTTTTA
                                ||||||||  |||||||
                                GTCACTGT  GAAAAAT
                                          __
GAM832  ACADS    3'  CACTGTGCCTCAAGTTCCT   3407        AA  A   GG
                                AGGAACTT  GA GTAT  AGTG
                                ||||||||  || ||||  ||||
                                TCCTTGAA  CT CGTG  TCAC
                                     __  C   __
GAM832  ATP2A3   3'  CACCGACATCCTCAGGTTCCT  17720        A  AAGT   GA_
                                AGGAACTT AG    ATG   GTG
                                |||||||| ||    |||   |||
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                                TCCTTGGA TC   TAC  CAC
                                    C  C___  AGC
GAM832  CASP10   3'  CATACTTCTAAAATTCC    52091     C  A
                                GGAA TT AGAAGTATG
                                |||| || |||||||||
                                CCTT AA TCTTCATAC
                                  A  A
GAM832  CTSK     3'  CTCACTTCCTAAGTTCC     4622        A    ATG
                                GGAACTTA GAAGT  GAG
                                |||||||| |||||  |||
                                CCTTGAAT CTTCA  CTC
                                    C    ___
GAM832  DUOX2    3'  CACTTCGTCTCCCCTAGCTCCT 26020     A  TAAGA  T
                                AGGA CT    AG ATGGAGTG
                                |||| ||    || ||||||||
                                TCCT GA    TC TGCTTCAC
                                  C  TCCCC  _
GAM832  GRIK5    3'  CACTCCTTCCCAGGCTCC    9133     A  AA  GTAT
                                GGA CTT  GAA   GGAGTG
                                ||| |||  |||   ||||||
                                CCT GGA  CTT   CCTCAC
                                  C  CC  ____
GAM832  MLF2     3'  CACTCCATCTTCAAACCCCCT  18373    AACTTAA   T
                                AGG      GAAG ATGGAGTG
                                |||      |||| ||||||||
                                TCC      CTTC TACCTCAC
                                  CCCAAA_  _
GAM832  RAD1     5'  TCACTGCAGTTTCAAGTTCCT  55913       AA  GTA  G
                                AGGAACTT  GAA  TG AGTGA
                                ||||||||  |||  || |||||
                                TCCTTGAA  CTT  AC TCACT
                                    __  TG_  G
GAM832  UBE2V1   3'  CTCCTCCTCAAGTTCCT    41793       A  AAGTAT
                                AGGAACTT AG    GGAG
                                |||||||| ||    ||||
                                TCCTTGAA TC    CCTC
                                    C  CT____
GAM832  UBE2V1   3'  CTCCTCCTCAAGTTCCT    12518       A  AAGTAT
                                AGGAACTT AG    GGAG
                                |||||||| ||    ||||
                                TCCTTGAA TC    CCTC
                                    C  CT____
GAM832  UBE2V1   3'  CTCCTCCTCAAGTTCCT    42370       A  AAGTAT
                                AGGAACTT AG    GGAG
                                |||||||| ||    ||||
                                TCCTTGAA TC    CCTC
                                    C  CT____
GAM832  VIPR1    3'  TCACCATTGCTGTCAAGTTCCT 16116       AAGA   TGGA
                                AGGAACTT   AGTA   GTGA
                                ||||||||   ||||   ||||
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                                TCCTTGAA   TCGT   CACT
                                    CTG_   TAC_
GAM832  ZNF142   3' CACTCCATCAAAGTCCCT   17432    A   AAGAAGT
                                AGG ACTT     ATGGAGTG
                                ||| ||||     ||||||||
                                TCC TGAA     TACCTCAC
                                  C   AC_____
GAM832  ZNF266   3' CACTCCATATTTGTAAGCCCT  88322    AA   AG
                                AGG  CTTA  AAGTATGGAGTG
                                |||  ||||  ||||||||||||
                                TCC  GAAT  TTTATACCTCAC
                                  C_   G_
GAM832  AMOTL2   3' CTCCTCCTCAAGTTCCT    32482       A  AAGTAT
                                AGGAACTT AG    GGAG
                                |||||||| ||    ||||
                                TCCTTGAA TC    CCTC
                                    C  CT____
GAM832  BCL2L1   3' CACCCCACACTTGTTCC    56803      TTAAG   A   A
                                GGAAC    AAGT TGG GTG
                                |||||    |||| ||| |||
                                CCTTG    TTCA ACC CAC
                                   _____   C   C
GAM832  C(27)-3BETA-HSD 3' CACCTCTCTACCTAAGTTCCT  47270         AGAA   T   _
                                AGGAACTTA   GTA GGAG TG
                                |||||||||   ||| |||| ||
                                TCCTTGAAT   CAT TCTC AC
                                    C___   C   C
GAM832  C21orf69  3' TCACCCCATACTCTGTCACTGC 54215   AACTTA_  A    A
           C                     GG      AGA GTATGG GTGA
                                ||      ||| |||||| ||||
                                CC      TCT CATACC CACT
                                 GTCACTG  _     C
GAM832  CLSTN2   3' CACTTCTGCCCTAAGTTCC   42129       AGAA   T
                                GGAACTTA   GTA GGAGTG
                                ||||||||   ||| ||||||
                                CCTTGAAT   CGT CTTCAC
                                    CC__   _
GAM832  DKFZP434J037 3' CACTCCACACTCTTGAGTCTCT 48206    GA      A  A
                                AG  ACTTAAGA GT TGGAGTG
                                ||  |||||||| || |||||||
                                TC  TGAGTTCT CA ACCTCAC
                                 TC       _  C
GAM832  DKFZP566I1024 3' TCACTCTAGCCTTGAATTCCT  70107      C    AAGTA
                                AGGAA TTAAG    TGGAGTGA
                                ||||| |||||    ||||||||
                                TCCTT AGTTC    ATCTCACT
                                   A    CG___
GAM832  ERN1     3' TCAGACTTTTTAAATTCCT   7519       C       A
                                AGGAA TTAAGAAGT TGG
                                ||||| ||||||||| |||
```

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                                TCCTT AATTTTTCA ACT
                                   A       G
GAM832  FLJ10292  3' TCACTTCAGTTTCCCAGTTCCT 35976       TAA  GTA
                                AGGAACT  GAA  TGGAGTGA
                                |||||||  |||  ||||||||
                                TCCTTGA  CTT  ACTTCACT
                                   CC_  TG_
GAM832  FLJ10925  3' CCAGTATTCCCCGAGTTCCT  36882       AA_  GTA
                                AGGAACTT  GAA  TGG
                                ||||||||  |||  |||
                                TCCTTGAG  CTT  ACC
                                    CCC  ATG
GAM832  FLJ14082  3' CACTCCTGAGACCCAAGGTTCC 46671       AAGAAGTAT
          T                      AGGAACTT       GGAGTG
                                ||||||||       ||||||
                                TCCTTGGA       CCTCAC
                                    ACCCAGAGT
GAM832  FLJ20275  3' CCAACCCTTAAGTTCCT    34820         AA  A
                                AGGAACTTAAG  GT TGG
                                ||||||||||  || |||
                                TCCTTGAATTC  CA ACC
                                     C_ _
GAM832  FLJ21742  3' CACCCTGGCCCTCAGGTTCCT  49844       A  AA  AT  A
                                AGGAACTT AG  GT  GG GTG
                                |||||||| ||  ||  || |||
                                TCCTTGGA TC  CG  CC CAC
                                    C  C_  GT  _
GAM832  FLJ23071  3' CACTCCCTTCCCAAGTTCCT  47263       AA   TAT
                                AGGAACTT  GAAG  GGAGTG
                                ||||||||  ||||  ||||||
                                TCCTTGAA  CTTC  CCTCAC
                                    CC   ___
GAM832  KIAA0255  3' CACCCCACACCTGAGTTCTT  28465       AGAA  A  A
                                AGGAACTTA   GT TGG GTG
                                |||||||||   || ||| |||
                                TTCTTGAGT   CA ACC CAC
                                     C___  C  C
GAM832  KIAA0444  3' CCACCTTCCGAAGCTCCT   62338     A  AA   TA
                                AGGA CTT  GAAG  TGG
                                |||| |||  ||||  |||
                                TCCT GAA  CTTC  ACC
                                  C  GC   C_
GAM832  KIAA1319  3' CCATACCCCTCCAGTTCCT  40405       TA  AA
                                AGGAACT  AG  GTATGG
                                |||||||  ||  ||||||
                                TCCTTGA  TC  CATACC
                                    CC  CC
GAM832  KIAA1535  3' CATACTTCTAAGTTCC     79410        A
                                GGAACTTA GAAGTATG
                                |||||||| ||||||||
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                                CCTTGAAT CTTCATAC
                                        _
GAM832  KIAA1671  3'  TCACTCCAGCCTCCAACTCCT  65692      ACTTAA  A  A
                                AGGA     GA GT TGGAGTGA
                                ||||     || || ||||||||
                                TCCT     CT CG ACCTCACT
                                  CAAC__  C  _
GAM832  KIAA1856  3'  TCACTCTGGGCTTCCCAAGCAC 92671    AA   AA    A
          C                      GG  CTT  GAAGT TGGAGTGA
                                ||  |||  ||||| ||||||||
                                CC  GAA  CTTCG GTCTCACT
                                 AC   CC    G
GAM832  MGC1127   3'  TCACTCCATTTGGCAAGCTCT  53218     A   AAGAAGT
                                GGA CTT      ATGGAGTGA
                                ||| |||      |||||||||
                                TCT GAA      TACCTCACT
                                  C   CGGTT__
GAM832  MMPL1     3'  TCACCCCACCGCCCTCTTAAGT 14723           A_  A_   A
          TTCT                    AGGAACTTAAGA  GT  TGG GTGA
                                ||||||||||||  ||  ||| ||||
                                TCTTTGAATTCT  CG  ACC CACT
                                      CC  CC   C
GAM832  NESCA     3'  CACTCCATCCCTCCCAAGTTGC 26743    _     AA  AGT
          C                      GG AACTT  GA   ATGGAGTG
                                || |||||  ||   ||||||||
                                CC TTGAA  CT   TACCTCAC
                                 G    CC  CCC
GAM832  RNF32     3'  CACTCCTTAAGTTCC       48187          GAAGTAT
                                GGAACTTAA      GGAGTG
                                |||||||||      ||||||
                                CCTTGAATT      CCTCAC
                                       ________
GAM832  SCMH1     5'  CCAAACTTCTTAACCCCT    24253     AAC        A
                                AGG   TTAAGAAGT TGG
                                |||   ||||||||| |||
                                TCC   AATTCTTCA ACC
                                  CC_        A
GAM832  SEMA4G    5'  CACTCCATACCCTTCTCC    94672     ACTT   AA
                                GGA    AAG  GTATGGAGTG
                                |||    |||  ||||||||||
                                CCT    TTC  CATACCTCAC
                                  C___   C_
GAM832  TRAP95    3'  CACCCACCTCAAGTTCCT    65536         A  AAGTA   A
                                AGGAACTT AG     TGG GTG
                                |||||||| ||     ||| |||
                                TCCTTGAA TC     ACC CAC
                                     C  C____   _
GAM832  ZAK       3'  TCTCTTCCTAAGTTCC      33604          A    TAT
                                GGAACTTA GAAG   GGA
                                |||||||| ||||   |||
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                                CCTTGAAT CTTC   TCT
                                     C   ___
GAM832  LOC149506 3'  CACTCCTACAAATTCC      84452      C  AAGAA   T
                                GGAA TT    GTA GGAGTG
                                |||| ||    ||| ||||||
                                CCTT AA    CAT CCTCAC
                                  A _____  _
GAM832  LOC152674 3'  CACTCCACACTTTATTAGCAAA 85833       ____  TAA    A
          TTCCT                    AGGAA   CT   GAAGT TGGAGTG
                                |||||   ||  ||||| |||||||
                                TCCTT   GA   TTTCA ACCTCAC
                                   AAAC  TTA    C
GAM832  LOC255096 5'  CACTCCATCCTCAACTCC    97622     ACTTAA  A T
                                GGA     GA G ATGGAGTG
                                |||     || | ||||||||
                                CCT     CT C TACCTCAC
                                  CAA___  _ C
GAM832  LOC257415 3'  TCACTCTTGCTGTCTTAAGTTC 96078          _    T
                                GAACTTAAGA AGTA GGAGTGA
                                |||||||||| |||| |||||||
                                CTTGAATTCT TCGT TCTCACT
                                     G   _
GAM833  ANXA2    3'  CCTGTCTAGTCTCTCCTGT   14458     AAGC   TG
                                ACAG   AGAG  TAGACAGG
                                ||||   ||||  ||||||||
                                TGTC   TCTC  ATCTGTCC
                                  C___   TG
GAM833  BAK1     5'  CTGCCCTCTGCTTCTG     91990          T
                                CAGAAGCAGAG GTAG
                                |||||||||| ||||
                                GTCTTCGTCTC CGTC
                                      C
GAM833  CHST6    3'  CTGCACTTTCTGCTTCT     41224         __
                                AGAAGCAGA  GTGTAG
                                |||||||||  ||||||
                                TCTTCGTCT  CACGTC
                                     TT
GAM833  DIO3     3'  CCTGGGACTCTGCTTCTGT   7243            GTAGA
                                ACAGAAGCAGAGT    CAGG
                                ||||||||||||    ||||
                                TGTCTTCGTCTCA    GTCC
                                       GG___
GAM833  DNM1     3'  CCTGCCTGGACGGCTGTTCTGT 15320        G   A_  G   A
          GA                     TCACAGAA CAG  GT TAG CAGG
                                |||||||| |||  || ||| ||||
                                AGTGTCTT GTC  CA GTC GTCC
                                     _  GG  G   C
GAM833  DPP6     3'  CCGCCCACACTAGCCTCTGTG  55446       A  AG    AGACA
                                CACAGA GC  AGTGT    GG
                                |||||| ||  |||||    ||
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                                GTGTCT CG  TCACA    CC
                                   C  A_    CCCG_
GAM833  DPYSL3   3'  CTATCATGCTGCTTCTG     7316          A  _
                                CAGAAGCAG GTG TAG
                                ||||||||| ||| |||
                                GTCTTCGTC TAC ATC
                                     G   T
GAM833  EIF2C1   3'  CCTGCCTGTCTGCCTATGTGA 24171      GAA    GTG   A
                                TCACA   GCAGA   TAG CAGG
                                |||||   |||||   ||| ||||
                                AGTGT   CGTCT   GTC GTCC
                                   ATC    ___   C
GAM833  FOXM1    3'  CTGCCCTTGCCCCTGTG     41704      AA   G  T
                                CACAG  GCA AG GTAG
                                |||||  ||| || ||||
                                GTGTC  CGT TC CGTC
                                   CC   _  C
GAM833  GCNT3    5'  CTGTCTCCCATTCTGT      16456        T_
                                GCAGAGTG  AGACAG
                                ||||||||  ||||||
                                TGTCTTAC  TCTGTC
                                     CC
GAM833  HPN      3'  CCTGTCTAGGTGCCCCTGATGA 9275      _  AA   GAG G
                                TCA CAG  GCA   T TAGACAGG
                                ||| |||  |||   | ||||||||
                                AGT GTC  CGT   G ATCTGTCC
                                  A   CC   ___ G
GAM833  LENG4    3'  CCGCCTACACTCCTACGTG    44163     AGA  CA       ACA
                                CAC   AG  GAGTGTAG   GG
                                |||   ||  ||||||||   ||
                                GTG   TC  CTCACATC   CC
                                  CA_  __       CG_
GAM833  MAGEA12  3'  CTCACTCTATTCTGT       18111        GC     T
                                ACAGAA  AGAGTG AG
                                ||||||  |||||| ||
                                TGTCTT  TCTCAC TC
                                   A_     _
GAM833  PRX      3'  CCCGTCCCTACACTCCTGTT   40526       _     __   A
                                AGCAG AGTGTA  GAC GG
                                ||||| ||||||  ||| ||
                                TTGTC TCACAT  CTG CC
                                   C     CC   C
GAM833  PTPN7    3'  CCTATCAGTGACTCTGCTCCCT 11066     A_       _ TA  C
           G                     CAG  AGCAGAGT G  GA AGG
                                |||  |||||||| |  || |||
                                GTC  TCGTCTCA T  CT TCC
                                  CC       G GA  A
GAM833  PTPN7    3'  CCTATCAGTGACTCTGCTCCCT 54548     A_       _ TA  C
           G                     CAG  AGCAGAGT G  GA AGG
                                |||  |||||||| |  || |||
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                                GTC  TCGTCTCA T  CT TCC
                                  CC       G GA  A
GAM833  PTPN7    3'  CCTATCAGTGACTCTGCTCCCT 54559     A_       _ TA  C
              G                    CAG  AGCAGAGT G  GA AGG
                                |||  |||||||| |  || |||
                                GTC  TCGTCTCA T  CT TCC
                                  CC       G GA  A
GAM833  RAP1GA1  3'  CTACCCTGCTTCTTGA      11252     C       AGT
                                TCA AGAAGCAG   GTAG
                                |||  |||||||   ||||
                                AGT TCTTCGTC   CATC
                                  _       C__
GAM833  SHB      3'  CTGCCCTGCTCTGTGA      11640        A    AGT
                                TCACAGA GCAG   GTAG
                                |||||||  ||||   ||||
                                AGTGTCT CGTC   CGTC
                                    _    C__
GAM833  SOX12    3'  CTGTCTAGGCCTCTATGT    22697     GA  C  A  G
                                ACA  AG AG GT TAGACAG
                                |||  || || || |||||||
                                TGT  TC TC CG ATCTGTC
                                  A_  _  _  G
GAM833  SYT1     3'  CATTCACTTCTGTGA       18898         CA
                                TCACAGAAG  GAGTG
                                |||||||||  |||||
                                AGTGTCTTC  CTTAC
                                     A_
GAM833  WBSCR1   3'  CCTGTCAGCTTCTCTGCTTCTG 49258    A         T_  A
              AGA                    TC CAGAAGCAGAG  GT GACAGG
                                ||  ||||||||||  ||  ||||||
                                AG GTCTTCGTCTC  CG CTGTCC
                                 A          TT  A
GAM833  WBSCR1   3'  CCTGTCAGCTTCTCTGCTTCTG 42226    A         T_  A
              AGA                    TC CAGAAGCAGAG  GT GACAGG
                                ||  ||||||||||  ||  ||||||
                                AG GTCTTCGTCTC  CG CTGTCC
                                 A          TT  A
GAM833  C6orf31  3'  CCTGTAAACGCTCTGT      47641          AG
                                GCAGAGTGT  ACAGG
                                |||||||||  |||||
                                TGTCTCGCA  TGTCC
                                     AA
GAM833  CAC-1    3'  CCTGCAAGCAACTCTGCTCTGT 53167        A      _  AGA
              GA                     TCACAGA GCAGAGT GT   CAGG
                                |||||||  |||||||  ||   ||||
                                AGTGTCT CGTCTCA CG   GTCC
                                    _      A  AAC
GAM833  CLSTN2   3'  CCTGTCTGGGCACCTGCT    42130       A   __
                                AGCAG GTGT  AGACAGG
                                |||||  ||||  |||||||
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                                TCGTC CACG  TCTGTCC
                                  _   GG
GAM833  CUL2     5'  CCTGCCCCTTGCCCTGCTTCTG 13169        A   TAGA_
                                CAGAAGCAG GTG    CAGG
                                ||||||||| |||    ||||
                                GTCTTCGTC CGT    GTCC
                                     C   TCCCC
GAM833  DKFZp434I099 3'  CCTGTTTGTTCCTGCTTCTCAT 50082    C_      AGTG
           GA                    TCA  AGAAGCAG   TAGACAGG
                                ||| ||||||||  ||||||||
                                AGT  TCTTCGTC   GTTTGTCC
                                  AC       CTT_
GAM833  FHX      3'  CCTTTTTCCCATTCTGC     37303        T_  C
                                GCAGAGTG  AGA AGG
                                ||||||||  ||| |||
                                CGTCTTAC  TTT TCC
                                     CC   T
GAM833  FLJ12704  5'  TGTTTCCCTTCTGTGA     46537        CA  GTGTA
                                TCACAGAAG  GA    GACA
                                |||||||||  ||    ||||
                                AGTGTCTTC  CT    TTGT
                                     C_  _____
GAM833  FLJ20793  3'  CCTGTCCGTGTCTGCTTC    91805        G  TA
                                GAAGCAGA TG  GACAGG
                                |||||||| ||  ||||||
                                CTTCGTCT GT  CTGTCC
                                     _  GC
GAM833  FLJ21777  3'  CCTGTCTGGTTCTGCTTCTGTG 49863          GTG
           G                     TCACAGAAGCAGA   TAGACAGG
                                ||||||||||||||  ||||||||
                                GGTGTCTTCGTCT   GTCTGTCC
                                       TG_
GAM833  FLJ23584  3'  CCTGATTCTACTCTGCCTC    44736    A      T  A
                                GA GCAGAGTG AG CAGG
                                || |||||||| || ||||
                                CT CGTCTCAT TT GTCC
                                 C       C  A
GAM833  FLJ32332  3'  CCTGTAGTAGCCTGCCTCT    58302    A    A  GTAG
                                AGA GCAG GT    ACAGG
                                ||| |||| ||    |||||
                                TCT CGTC CG    TGTCC
                                  C    _  ATGA
GAM833  GMPPB     3'  CCTGCCTTCTGCTCTGCCCCTG 95728     AA      GT_  A
                                CAG  GCAGAGT   AG CAGG
                                |||  |||||||   || ||||
                                GTC  CGTCTCG   TC GTCC
                                  CC      TCT  C
GAM833  KIAA0229  3'  CCGGTGCGCCTCTGCTTCT    92425          T  AG  A
                                AGAAGCAGAG GT  AC GG
                                ||||||||| ||  || ||
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                                TCTTCGTCTC CG  TG CC
                                     _ CG  G
GAM833  KIAA0775  3'  CTACATTTCCTCTGTGA     28279        AGCA
                                TCACAGA   GAGTGTAG
                                |||||||   ||||||||
                                AGTGTCT   TTTACATC
                                    CC__
GAM833  MGC15437  3'  CCTATCCCCCCTCCTTGCTTCT 51781          __  TGTA  C
           GTGA                   TCACAGAAGCA  GAG   GA AGG
                                |||||||||||  |||   || |||
                                AGTGTCTTCGT  CTC   CT TCC
                                      TC   CCCC  A
GAM833  MGC2641   3'  CTGCCTAATTTCTGTGA     50942        CAG  T
                                TCACAGAAG   AG GTAG
                                |||||||||   || ||||
                                AGTGTCTTT   TC CGTC
                                     AA_  _
GAM833  MGC4737   3'  CTGCACCCATTTCTGTGA    48848         CAGA
                                TCACAGAAG   GTGTAG
                                |||||||||   ||||||
                                AGTGTCTTT   CACGTC
                                     ACC_
GAM833  NFKBIE    3'  CTAGGCTCTGTTCCATGA    92022     CA  G     G
                                TCA  GAA CAGAGT TAG
                                |||  ||| |||||| |||
                                AGT  CTT GTCTCG ATC
                                  AC  _     G
GAM833  OPN4      3'  ACACTCTGCGTCTGTGA     52716        A
                                TCACAGA GCAGAGTGT
                                ||||||| |||||||||
                                AGTGTCT CGTCTCACA
                                    G
GAM833  OXCT2     5'  CGCCCTGCTCTGTGA       42092        A   A
                                TCACAGA GCAG GTG
                                ||||||| |||| |||
                                AGTGTCT CGTC CGC
                                    _   C
GAM833  PDE10A    3'  CTGCCAATCTCTTCTGTGA    21863        C   GT_
                                TCACAGAAG AGA   GTAG
                                ||||||||| |||   ||||
                                AGTGTCTTC TCT   CGTC
                                     _  AAC
GAM833  PPP4R1L   5'  CCTGCTACTCCCCCGATTCTGT 79500        GCAGAGT_   A
           GA                    TCACAGAA       GTAG CAGG
                                ||||||||       |||| ||||
                                AGTGTCTT       CATC GTCC
                                    AGCCCCCT   _
GAM833  REM       3'  CCCATCTACACTTGACTGTAGA 25806    _   AAGCA       CA
                                TC ACAG    GAGTGTAGA  GG
                                || ||||    |||||||||  ||
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                                AG TGTC    TTCACATCT  CC
                                 A   AG___       AC
GAM833  RODH-4   5' CCTGTCTGTGTCTGTCCTCTG 13531     A_   A TG
                                CAGA  GCAG G  TAGACAGG
                                ||||  |||| |  ||||||||
                                GTCT  TGTC T  GTCTGTCC
                                  CC   _ GT
GAM833  Rpo1-2   3' CCTTCTACCCTGTTTCTATGA 38700     C      AGT    C
                                TCA AGAAGCAG   GTAGA AGG
                                ||| ||||||||   ||||| |||
                                AGT TCTTTGTC   CATCT TCC
                                  A       C__    _
GAM833  Rpo1-2   3' CCTTCTACCCTGTTTCTATGA 49876     C      AGT    C
                                TCA AGAAGCAG   GTAGA AGG
                                ||| ||||||||   ||||| |||
                                AGT TCTTTGTC   CATCT TCC
                                  A       C__    _
GAM833  TED      3' TCTTACCCTGCCTCTGTG    31645       A   A   T
                                CACAGA GCAG GTG AGA
                                |||||| |||| ||| |||
                                GTGTCT CGTC CAT TCT
                                   C   C   _
GAM833  TEX27    3' CTGCAGTATCTGTTCTGTGA   41661        G   G__
                                TCACAGAA CAGA   TGTAG
                                |||||||| ||||   |||||
                                AGTGTCTT GTCT   ACGTC
                                     _   ATG
GAM833  TNKS1BP1  5' CCTGTCCCACACTCTGCCTCTG 53005      A       A_
          T                      ACAGA GCAGAGTGT  GACAGG
                                |||||| |||||||||  ||||||
                                TGTCT CGTCTCACA  CTGTCC
                                  C        CC
GAM833  LOC123855 5' CCTGTGTGCTCTGCTACCATGA 75627     CAGA      TG AG
                                TCA   AGCAGAG  T  ACAGG
                                |||   |||||||  |  |||||
                                AGT   TCGTCTC  G  TGTCC
                                  ACCA      GT __
GAM833  LOC124935 5' CTGCCTGTGCTTCAGTGA    74370     A     G  T
                                TCAC GAAGCA AG GTAG
                                |||| |||||| || ||||
                                AGTG CTTCGT TC CGTC
                                  A     G  _
GAM833  LOC126133 3' CTAGCTGTGCTTCTGCGA    74441    A      G   G
                                TC CAGAAGCA AGT TAG
                                || |||||||| ||| |||
                                AG GTCTTCGT TCG ATC
                                 C       G   _
GAM833  LOC126767 3' ACCTACTCTTCTGTGA      75431         C  _  T
                                TCACAGAAG AG AG GT
                                |||||||| || || ||
```

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                                AGTGTCTTC TC TC CA
                                    _ A _
GAM833  LOC144438 3'  CCTGGAGCCTCAGCTTCTGT  76834       A  T  AGA
                                ACAGAAGC GAG GT  CAGG
                                |||||||| ||| ||  ||||
                                TGTCTTCG CTC CG  GTCC
                                   A  _ AG_
GAM833  LOC145225 3'  CCTGCCCCACTTTGTCCTGTGA 83302      AA      TAGA
                                TCACAG  GCAGAGTG  CAGG
                                ||||||  ||||||||  ||||
                                AGTGTC  TGTTTCAC  GTCC
                                  C_      CCC_
GAM833  LOC146733 3'  CTGTGACCACTTCTGTGA   83762      AGCAG   TAG
                                TCACAGA   AGTG  ACAG
                                |||||||   ||||  ||||
                                AGTGTCT   TCAC  TGTC
                                   _____  CAG
GAM833  LOC148046 3'  CCCATCGTTCCCTGGTTCTGTG 84105       G  AGTGTA  CA
          A                     TCACAGAA CAG    GA  GG
                                |||||||| |||    ||  ||
                                AGTGTCTT GTC    CT  CC
                                   G  CCTTG_  AC
GAM833  LOC148223 3'  CACCCTGCACTTCTGTG    78733       __  A
                                CACAGAA  GCAG GTG
                                |||||||  |||| |||
                                GTGTCTT  CGTC CAC
                                   CA  C
GAM833  LOC149657 3'  CTGCCCGTTGCTTCTGTG   84572        AGT
                                CACAGAAGCAG  GTAG
                                ||||||||||  ||||
                                GTGTCTTCGTT  CGTC
                                     GCC
GAM833  LOC150005 3'  CTGTGTCTGTTTCTG      84819        GTGTAG
                                CAGAAGCAGA    ACAG
                                ||||||||||    ||||
                                GTCTTTGTCT    TGTC
                                     G_____
GAM833  LOC152343 5'  CCTTTCTACTCTGCCTCCATGA 80561    CA  A     GT  C
                                TCA  GA GCAGAGT  AGA AGG
                                |||  || |||||||  ||| |||
                                AGT  CT CGTCTCA  TCT TCC
                                  AC  C      __  T
GAM833  LOC158972 3'  CCTTCTTGCTGCTTCTGTG   86948        AGTGT  C
                                CACAGAAGCAG    AGA AGG
                                ||||||||||    ||| |||
                                GTGTCTTCGTC    TCT TCC
                                     GT___  _
GAM833  LOC160777 3'  CCTGCCTGTGTTCCTGCCTCCT 82239    AA_  _ TG  A
          G                     CAG  GCAG AG  TAG CAGG
                                |||  |||| ||  ||| ||||
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                                GTC   CGTC TT  GTC GTCC
                                  CTC    C  GT   C
GAM833   LOC164945 5'  CTGCCTCCTGCCTCTGTG    87185       A    _  T
                                CACAGA GCAG AG GTAG
                                ||||||| |||| || ||||
                                GTGTCT CGTC TC CGTC
                                   C    C  _
GAM833   LOC197319 3'  CTGTTTCCACTTTTGTGA    87971       AGCAG    T
                                TCACAGA    AGTG AGACAG
                                |||||||    |||| ||||||
                                AGTGTTT    TCAC TTTGTC
                                    _____   C
GAM833   LOC200895 5'  CCTGTGCGGCCCCTGCTTCTGC 88918    A       AGT  AG_
           GG                     TC CAGAAGCAG   GT   ACAGG
                                || |||||||||   ||   |||||
                                GG GTCTTCGTC   CG   TGTCC
                                 C        CC_  GCG
GAM833   LOC219700 3'  ACCTCTGTTTATTCTGT     93058       ___     T
                                ACAGAA   GCAGAG GT
                                ||||||   |||||| ||
                                TGTCTT   TGTCTC CA
                                   ATT     _
GAM833   LOC219701 3'  ACCTCTGTTTATTCTGT     93057       ___     T
                                ACAGAA   GCAGAG GT
                                ||||||   |||||| ||
                                TGTCTT   TGTCTC CA
                                   ATT     _
GAM833   LOC221025 3'  CCTGTCTAGTCTCTCCTGT   93176     AAGC    TG
                                ACAG    AGAG  TAGACAGG
                                ||||    ||||  ||||||||
                                TGTC    TCTC  ATCTGTCC
                                  C___    TG
GAM833   LOC221692 3'  CCTAGTATTCTGTGCTTCTGT  92238         G  TGTAG  _
                                ACAGAAGCA AG     AC AGG
                                ||||||||| ||     || |||
                                TGTCTTCGT TC     TG TCC
                                     G  TTA__  A
GAM833   LOC254359 3'  CCGCCTACACTCCTACGTG   94781     AGA  CA      ACA
                                CAC   AG  GAGTGTAG   GG
                                |||   ||  ||||||||   ||
                                GTG   TC  CTCACATC   CC
                                  CA_  __       CG_
GAM833   LOC255126 5'  CCTGTCTACAGCATCAGCTTCT 97472          A  _ _
           GTGA                   TCACAGAAGC GA G TGTAGACAGG
                                ||||||||||| || | ||||||||||
                                AGTGTCTTCG CT C ACATCTGTCC
                                     A  A G
GAM833   LOC255515 3'  TGTCTATGCCTCCTG       96100     AAGC  A
                                CAG    AG GTGTAGACA
                                |||    || |||||||||
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                                GTC    TC CGTATCTGT
                                  C___  _
GAM833  LOC257020 5'  CTGCGGCTGCCCCGGTTCTGTG 97490        _____   AG
              A                    TCACAGAA    GCAG  TGTAG
                                   ||||||||    ||||  |||||
                                   AGTGTCTT    CGTC  GCGTC
                                       GGCCC    G_
GAM833  LOC56834  3'  CCTGCCACCTCTGCTTC     39342         T  AGA
                                   GAAGCAGAG GT   CAGG
                                   |||||||||  ||   ||||
                                   CTTCGTCTC CA   GTCC
                                         _ CC_
GAM833  LOC91496  5'  CTACCAGATCTGCTTTATGA   66221     CA       GT__
                                   TCA  GAAGCAGA    GTAG
                                   |||  ||||||||    ||||
                                   AGT  TTTCGTCT    CATC
                                     A_       AGAC
GAM833  LOC91661  3'  CTGAGCTCTGCCTTCTGTGA   56400         _     G
                                   TCACAGAAG CAGAGT TAG
                                   |||||||||  |||||| |||
                                   AGTGTCTTC GTCTCG GTC
                                         C     A
GAM833  LOC92691  5'  CCCATCTAGGAAGAAGTTCTGT 56422         GCAGAGTG    CA
              GA                     TCACAGAA       TAGA  GG
                                   ||||||||       ||||  ||
                                   AGTGTCTT       ATCT  CC
                                       GAAGAAGG    AC
GAM834  ACADSB    3'  GGGATGAGCCACCATGCCTGGC 7848          A   T  A
              T                     AGTCAGGTGT GGT GC TGTCTC
                                   ||||||||||  ||| ||  ||||||
                                   TCGGTCCGTA CCA CG GTAGGG
                                         _   C  A
GAM834  ADAM12    3'  GTCCAGGCTGTGTTTGGCT    12971        TG   G   C
                                   AGTCAGG  TAG TTG AT
                                   |||||||  |||  |||  ||
                                   TCGGTTT  GTC GAC TG
                                       GT   G   C
GAM834  ADAM20    3'  GAGACTAAACTTTATACTTCAT 13766     C       _   GCAT
              T                     AGT AGGTGTAG GTT    GTCTC
                                   |||  ||||||||  |||    |||||
                                   TTA TTCATATT CAA    CAGAG
                                     C       T   AT__
GAM834  ADAT1     3'  GCAAGCTATACTTGATT     23899           G
                                   AGTCAGGTGTAG TTGC
                                   ||||||||||||  ||||
                                   TTAGTTCATATC AACG
                                           G
GAM834  ADH4      3'  TAATTTATTACCTGATT     5410          _
                                   AGTCAGGTG TAGGTTG
                                   |||||||||  |||||||
```

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                                TTAGTCCAT ATTTAAT
                                      T
GAM834  ADRA2A   3'  GAGACTTTGTGTTTACATCTGC 5452    T      GG T   T_
                                G CAGGTGTA  T GCA  GTCTC
                                | ||||||||  | |||  |||||
                                C GTCTACAT  G TGT  CAGAG
                                 _       TT _   TT
GAM834  ALDH1A3  3'  GAGATATAAATTACCACATTTG 5500          A   TGC__
           GCT                    GTCAGGTGT GGT    ATGTCTC
                                |||||||||| |||    |||||||
                                CGGTTTACA CCA    TATAGAG
                                      _  TTAAA
GAM834  ALPPL2   3'  GGGACTGGGGATTTGTGCCTGG 68841       TG     GCAT
           C                     GTCAGG  TAGGTT   GTCTC
                                ||||||  ||||||   |||||
                                CGGTCC  GTTTAG   CAGGG
                                   GT     GGGT
GAM834  AMPH     3'  AGACTCTTGTACTTGAT     7905           TTGCAT
                                GTCAGGTGTAGG     GTCT
                                ||||||||||||     ||||
                                TAGTTCATGTTC     CAGA
                                       T_____
GAM834  APBA2    3'  GGGACATGTGATTGATTGATT  18562       GTGTA   TG
                                AGTCAG    GGT  CATGTCTC
                                ||||||    |||  ||||||||
                                TTAGTT    TTA  GTACAGGG
                                   AG___   GT
GAM834  APLP2    3'  GAGATTAGCCTGTAGCTTATAT 90896           T____
           TTGAC                   AGGTGTAGGTTGCA    GTCTC
                                ||||||||||||||    |||||
                                TTTATATTCGATGT    TAGAG
                                       CCGAT
GAM834  APPL     3'  GAGATTAAGCTTTATATTTGCT 23925    T       _  GCAT
                                AG CAGGTGTAG GTT    GTCTC
                                || |||||||| |||    |||||
                                TC GTTTATATT CGA    TAGAG
                                 _       T   AT__
GAM834  ARF1     5'  GGGAGCAAAACCAACGCCTGGC 70659          A  __  ATG
           T                     AGTCAGGTGT GGT  TGC   TCTC
                                |||||||||| |||  |||   ||||
                                TCGGTCCGCA CCA  ACG   AGGG
                                      A   AA  ___
GAM834  ARIH1    5'  GCGGAGCCGCGTCTGACT    19230       GT  A  __
                                AGTCAG  GT GGT  TGC
                                ||||||  || |||  |||
                                TCAGTC  CG CCG  GCG
                                   TG  _   AG
GAM834  ARNT2    3'  GAGGCACTTGTGACTTTGTTTG 29459      GT T    TG  __
           ACT                     GTCAG  G AGGT  CA  TGTCTC
                                |||||  | ||||  ||  ||||||
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                                CAGTT  T TTCA  GT  ACGGAG
                                   TG _   GT  TC
GAM834  ARSA    3'  AGGGGGTTTGTGCCTGAT   4912       TG  GTT  ATG
                                GTCAGG  TAG   GC   TCT
                                ||||||  |||   ||   |||
                                TAGTCC  GTT   TG   GGA
                                   GT   ____  GG_
GAM834  ASTN    3'  GGCTTGGCCGATGTCTGATT   69334       TG A   TG  T
                                AGTCAGG  T GGT  CA GTC
                                |||||||  | |||  || |||
                                TTAGTCT  A CCG  GT CGG
                                   GT G   __  T
GAM834  ATP2B4   3'  GATTTCAACTTAAGCTTGACT  70342        G      CAT
                                AGTCAGGT TAGGTTG   GTC
                                ||||||||  |||||||   |||
                                TCAGTTCG ATTCAAC   TAG
                                    A      TT_
GAM834  ATP7A    3'  GGGAAATGGATTTATATTTGA  3528           G   G
                                TCAGGTGTAGGTT CAT TCTC
                                |||||||||||||  ||| ||||
                                AGTTTATATTTAG GTA AGGG
                                       _  A
GAM834  AXUD1    3'  GAGCTCTGTGATCTATGTCTGC 52278    T   TG    TG  TGT
           T                     AG CAGG  TAGGT  CA   CTC
                                || ||||  |||||  ||   |||
                                TC GTCT  ATCTA  GT   GAG
                                 _   GT    GT  CTC
GAM834  B4GALT1  3'  GAGACAGAAGCCTCTGCACCTA 7671     C     __     GCA
           CT                     AGT AGGTGT  AGGTT   TGTCTC
                                ||| ||||||  |||||   ||||||
                                TCA TCCACG  TCCGA   ACAGAG
                                  _     TC    AG_
GAM834  B4GALT6  3'  GCTTGCAATCTCATCTGATT   59866        T      T
                                AGTCAGGTG AGGTTGCA GT
                                |||||||||  ||||||||  ||
                                TTAGTCTAC TCTAACGT CG
                                       _       T
GAM834  BCL2     3'  AGACTCTTTGCATATGACT   5296       G     TTGCAT
                                AGTCA GTGTAGG     GTCT
                                |||||  |||||||     ||||
                                TCAGT TACGTTT     CAGA
                                   A      CT____
GAM834  BCRP2    3'  AGTTTGTGACTATGCTTGATT  62403          G TG  TGT  C
                                AGTCAGGTGTAG T  CA   CT
                                ||||||||||||  |  ||   ||
                                TTAGTTCGTATC A  GT   GA
                                       _ GT  TT_  A
GAM834  BIN1     3'  GACACCAGCCTAGCCTGGCT   57811        G      CA
                                AGTCAGGT TAGGTTG  TGTC
                                ||||||||  |||||||  ||||
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                                TCGGTCCG ATCCGAC  ACAG
                                   _      C_
GAM834  BIN1     3'  GACACCAGCCTAGCCTGGCT   15038        G      CA
                                AGTCAGGT TAGGTTG  TGTC
                                |||||||| |||||||  ||||
                                TCGGTCCG ATCCGAC  ACAG
                                   _      C_
GAM834  BSCL2    5'  GATGTCTAGCCTGCATTGATT  51029       G       C
                                AGTCAG TGTAGGTTG ATGTC
                                |||||| ||||||||| |||||
                                TTAGTT ACGTCCGAT TGTAG
                                   _       C
GAM834  C14orf1  3'  GAGAATCACAGCTTTATGCCTG 23180           _   CATG
          ATT                     AGTCAGGTGTAG GTTG    TCTC
                                |||||||||||| ||||    ||||
                                TTAGTCCGTATT CGAC    AGAG
                                      T    ACTA
GAM834  CASP8    3'  GGGGCCCGCCACCACACCTGGC 52925         A   T  AT
          T                      AGTCAGGTGT GGT GC  GTCTC
                                |||||||||| ||| ||  |||||
                                TCGGTCCACA CCA CG  CGGGG
                                   _  C  CC
GAM834  CASP8    3'  GGGGCCCGCCACCACACCTGGC 52936         A   T  AT
          T                      AGTCAGGTGT GGT GC  GTCTC
                                |||||||||| ||| ||  |||||
                                TCGGTCCACA CCA CG  CGGGG
                                   _  C  CC
GAM834  CASP8    3'  GGGGCCCGCCACCACACCTGGC 6919          A   T  AT
          T                      AGTCAGGTGT GGT GC  GTCTC
                                |||||||||| ||| ||  |||||
                                TCGGTCCACA CCA CG  CGGGG
                                   _  C  CC
GAM834  CASP8    3'  GGGGCCCGCCACCACACCTGGC 52951         A   T  AT
          T                      AGTCAGGTGT GGT GC  GTCTC
                                |||||||||| ||| ||  |||||
                                TCGGTCCACA CCA CG  CGGGG
                                   _  C  CC
GAM834  CCR9     5'  GCAGGCTTGCATCTGACT    48300           _
                                AGTCAGGTGTAGGT TGC
                                |||||||||||||| |||
                                TCAGTCTACGTTCG ACG
                                      G
GAM834  CD22     3'  GGGGCCCAGTCCTGGCCTGGCT 8338        G   _   CAT
                                AGTCAGGT TAGG TTG   GTCTC
                                |||||||| |||| |||   |||||
                                TCGGTCCG GTCC GAC   CGGGG
                                   _   T  C__
GAM834  CD244    3'  AGATTCCCTCCACCTGATT   33060         T   TTGCAT
                                AGTCAGGTG AGG     GTCT
                                |||||||| |||     ||||
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                                TTAGTCCAC TCC     TAGA
                                    C  CT____
GAM834  CDH13   3'  TTTCTTATGCAATCTATGTTTG 6998    _   TG        TCTC
          CACT                  GT CAGG  TAGGTTGCATG
                                || ||||  ||||||||||
                                CA GTTT  ATCTAACGTAT
                                 C   GT         TCTTTC
GAM834  CDKN1B  3'  GGGGTATGAAGAGCTTGCTTTG 14512      T    TG__  GT
          ATT                   GTCAGG GTAGGT   CAT  CTC
                                |||||| ||||||   |||  |||
                                TAGTTT CGTTCG   GTA  GGG
                                   _    AGAA   TG
GAM834  CENTD1  3'  GAGGTATGTGGAAATTAATATT 30852      AGG___ TG   GT
          TGG                   CAGGTGT    T  CAT  CTC
                                |||||||    |  |||  |||
                                GTTTATA    G  GTA  GAG
                                    ATTAAA GT   TG
GAM834  CENTD1  3'  GAGGTATGTGGAAATTAATATT 57562      AGG___ TG   GT
          TGG                   CAGGTGT    T  CAT  CTC
                                |||||||    |  |||  |||
                                GTTTATA    G  GTA  GAG
                                    ATTAAA GT   TG
GAM834  CEP2    3'  GCAAATTGCATTTGCT    23228   T      G
                                AG CAGGTGTAG TTGC
                                || |||||||| ||||
                                TC GTTTACGTT AACG
                                 _       A
GAM834  CHC1L   3'  GATGAGCTATGTTTGGCT   7015       TG   G  GCAT
                                AGTCAGG  TAG TT   GTC
                                |||||||  ||| ||   |||
                                TCGGTTT  ATC AG   TAG
                                    GT   G  ____
GAM834  CHRM1   5'  GGGACATGCCAATCACTGGCT  94792      GTGTA   _
                                AGTCAG    GGTTG CATGTCTC
                                ||||||    ||||| ||||||||
                                TCGGTC    CTAAC GTACAGGG
                                   A____    C
GAM834  CHRNA7  5'  GAGACGTGGAGCGCGCCGGCT  5620     A    AG   G
                                AGTC GGTGT  GTT CATGTCTC
                                |||| |||||  ||| ||||||||
                                TCGG CCGCG  CGA GTGCAGAG
                                  _    __  G
GAM834  CLCN7   3'  AGGCTCCTCTGGCCTGGCT   7087       G   TTGCAT
                                AGTCAGGT TAGG     GTCT
                                |||||||| ||||     ||||
                                TCGGTCCG GTCT     CGGA
                                    _   CCT___
GAM834  CLN5    3'  GGGGTATGCAGGAACATGGCT  21430     G  GTAGG    GT
                                AGTCA GT    TTGCAT  CTC
                                ||||| ||    ||||||  |||
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                                TCGGT CA    GACGTA  GGG
                                  A  AG___     TG
GAM834  COL4A3   3'  GAGGCTAAATCAGTGTTTGATT 48555       TG A    GCAT
                                AGTCAGG  T GGTT    GTCTC
                                |||||||  | ||||    |||||
                                TTAGTTT  G CTAA    CGGAG
                                   GT A    AT__
GAM834  COL4A3   3'  GAGGCTAAATCAGTGTTTGATT 48567       TG A    GCAT
                                AGTCAGG  T GGTT    GTCTC
                                |||||||  | ||||    |||||
                                TTAGTTT  G CTAA    CGGAG
                                   GT A    AT__
GAM834  COL4A3   3'  GAGGCTAAATCAGTGTTTGATT 3621        TG A    GCAT
                                AGTCAGG  T GGTT    GTCTC
                                |||||||  | ||||    |||||
                                TTAGTTT  G CTAA    CGGAG
                                   GT A    AT__
GAM834  COX15    3'  GGGGCGGATCCCTTATGTATGA 15195      G TG    TTGCA
           CT                    AGTCA G  TAGG    TGTCTC
                                |||||  |  ||||    ||||||
                                TCAGT T  ATTC    GCGGGG
                                  A GT    CCTAG
GAM834  COX4I1   3'  GCCTGCACCTGCGCCTGGCT   8516            T   T
                                AGTCAGGTGTAGGT GCA GT
                                |||||||||||||| ||| ||
                                TCGGTCCGCGTCCA CGT CG
                                      _   C
GAM834  CRIM1    3'  GAGAATTATCTGCAACTTGATT 33175        _     TGCATG
                                AGTCAGGT GTAGGT     TCTC
                                ||||||||  ||||||     ||||
                                TTAGTTCA CGTCTA     AGAG
                                   A     TTA___
GAM834  CSNK2A1  3'  ATGCAGCTTGCGCCTGGC    8555
                                GTCAGGTGTAGGTTGCAT
                                ||||||||||||||||||
                                CGGTCCGCGTTCGACGTA

GAM834  CTSK     3'  GAGATGTGACTACAGCCTGCCC 4623      T      _____
           CTGACT                 AGG GTAGGTTG    CATGTCTC
                                ||| ||||||||    ||||||||
                                TCC CGTCCGAC    GTGTAGAG
                                  C       ATCA
GAM834  CYP27B1  3'  GTGCATCTGGTCTGTACCTGGT 5777    GT        TT C    CTC
           T                    A  CAGGTGTAGG  G ATGT
                                |  ||||||||||  | ||||
                                T  GTCCATGTCT  T TACG
                                 TG        GG C    TG
GAM834  DDX11    3'  GGGGTACCATGCAGCCGGTGTC 47661      TG A       ___
           TGACT                  CAGG  T GGTTGCATG   TCTC
                                ||||  | |||||||||   ||||
```

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                                GTCT  G CCGACGTAC   GGGG
                                  GT G        CAT
GAM834  DNASE2   3'  GAACCAGTTTGGACTTGATT   7265         G  GG   CATG
                                AGTCAGGT TA  TTG    TC
                                |||||||| ||  |||    ||
                                TTAGTTCA GT  GAC    AG
                                    G  TT   CA__
GAM834  DOK1     3'  GAGATGTTGGACTGTGCCTGG  7273       TG   GTT_   G  TC
                                TCAGG  TAG    GCAT TC
                                |||||  |||    |||| ||
                                GGTCC  GTC    TGTA AG
                                  GT   AGGT    G
GAM834  DPYSL3   3'  ACAGGCAGTTTGTGTTTGATT  7308         TG  GG    A
                                AGTCAGG  TA  TTGC TGT
                                |||||||  ||  |||| |||
                                TTAGTTT  GT  GACG ACA
                                    GT  TT    G
GAM834  DTNA     5'  GGGGCATGTTGGTGCATTTAAC 7325      C      GGTT
           T                     AGT AGGTGTA    GCATGTCTC
                                 ||| |||||||    |||||||||
                                 TCA TTTACGT    TGTACGGGG
                                   A      GGT_
GAM834  DTNA     5'  GGGGCATGTTGGTGCATTTAAC 7328      C      GGTT
           T                     AGT AGGTGTA    GCATGTCTC
                                 ||| |||||||    |||||||||
                                 TCA TTTACGT    TGTACGGGG
                                   A      GGT_
GAM834  DTNA     5'  GGGGCATGTTGGTGCATTTAAC 52130     C      GGTT
           T                     AGT AGGTGTA    GCATGTCTC
                                 ||| |||||||    |||||||||
                                 TCA TTTACGT    TGTACGGGG
                                   A      GGT_
GAM834  DUSP5    3'  GGGACATGATCAGCATCCTGAT 15354        _   A   TG
           T                     AGTCAGG TGT GGT  CATGTCTC
                                 ||||||| ||| |||  ||||||||
                                 TTAGTCC ACG CTA  GTACAGGG
                                     T   A  __
GAM834  DUT      3'  GGGACTGATTCTGTGGCTTACC 8696     T     TG  T_____
           TTGATT                  GG GTAGGT  CA      GTCTC
                                 || ||||||  ||     |||||
                                 TC CATTCG  GT     CAGGG
                                  _     GT  CTTAGT
GAM834  DXF68S1E 3'  GAGATGGTAGTTCTGCCTGGTT 60006   GT    GTA GT   A
                                A  CAGGT   G  TGC TGTCTC
                                |  |||||   |  ||| ||||||
                                T  GTCCG   T  ATG GTAGAG
                                 TG    TC_ TG  _
GAM834  DYRK1A   5'  GATTTTAGCTTGTACTTGTCT  55245    T          CAT
                                AG CAGGTGTAGGTTG   GTC
                                || ||||||||||||   |||
```

```
                                TC GTTCATGTTCGAT   TAG
                                 T          TT_
GAM834  DYRK1B   3'  GGGTGGGTGAGGCCTGCACTGA 16331       G      TG  GT_
            TT                   AGTCAG TGTAGGT  CAT   CTC
                                 |||||| |||||||  |||   |||
                                 TTAGTC ACGTCCG  GTG   GGG
                                    _      GA   GGT   G
GAM834  E2F4     3'  GGACATGCCCTGTGTGGCT    8706      AG TG    TT
                                 AGTC  G  TAGG  GCATGTCT
                                 ||||  |  ||||  ||||||||
                                 TCGG  T  GTCC  CGTACAGG
                                   __ GT   __
GAM834  EGFL3    3'  GAGGCGCCTCCTGGCCTGGCT  62616        G    TT  AT
                                 AGTCAGGT TAGG  GC  GTCTC
                                 |||||||| ||||  ||  |||||
                                 TCGGTCCG GTCC  CG  CGGAG
                                     _    TC  __
GAM834  EIF2B1   3'  GCTGAATCTGCATCTGGCT    59659             __
                                 AGTCAGGTGTAGGTT  GC
                                 ||||||||||||||  ||
                                 TCGGTCTACGTCTAA  CG
                                          GT
GAM834  EIF2C1   3'  GACATGGGGTTTGGCT      24176        TGTAGG  G
                                 AGTCAGG     TT CATGTC
                                 |||||||     || ||||||
                                 TCGGTTT     GG GTACAG
                                    _______  G
GAM834  ENO2     3'  GTTGGGCATGTGATCACGCCTG 8779           A   TG      C
            GCT                    AGTCAGGTGT GGT  CATGTCT
                                 ||||||||||| |||  |||||||
                                 TCGGTCCGCA CTA  GTACGGG
                                      _  GT      TTGT
GAM834  EZH1     3'  GGGGTGGATGACTTATGCGTGA 8823       G         CA GT
            TT                     AGTCA GTGTAGGTTG  T  CTC
                                 ||||| ||||||||||  |  |||
                                 TTAGT CGTATTCAGT  G  GGG
                                    G         AG TG
GAM834  FBLN1    3'  GACTGTGGTCTGTACTTG    21398          TT   T
                                 CAGGTGTAGG  GCA GTC
                                 |||||||||  ||| |||
                                 GTTCATGTCT  TGT CAG
                                       GG  _
GAM834  FEN1     3'  CTTGCTATGTAATTTGTGTCT  14643     TG         TCTC
                                 AGG  TAGGTTGCATG
                                 |||  ||||||||||
                                 TCT  GTTTAATGTAT
                                   GT         CGTTCA
GAM834  FGF12    3'  CGATGTGTGGTTTTGCTTGATT 40720          T GG TG     TC
                                 AGTCAGGTG A  T  CATGTC
                                 |||||||| |  |  ||||||
```

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                                TTAGTTCGT T  G  GTGTAG
                                     _ TT GT     CG
GAM834  FGF23    3'  GGGGCATGTATGGAATTTGCT  40194    T    GTAGGT
                                AG CAGGT     TGCATGTCTC
                                || |||||     ||||||||||
                                TC GTTTA     ATGTACGGGG
                                 _    AGGT__
GAM834  FGFR2    3'  GGACTGAGCCTGTGGCTGGCT  43365      G GT    G  T   C
                                AGTCAG T  AGGTT CA GTCT
                                |||||| |  ||||| || ||||
                                TCGGTC G  TCCGA GT CAGG
                                   G TG    _ _   A
GAM834  FOXO1A   3'  TATGCAGCCTTGTTTGATT   8906       GT T
                                AGTCAG  G AGGTTGCATG
                                ||||||  | ||||||||||
                                TTAGTT  T TCCGACGTAT
                                   TG _
GAM834  FZD1     3'  CAGCCTGCGCTTAGATT     13031     _
                                AGTC AGGTGTAGGTTG
                                |||| ||||||||||||
                                TTAG TTCGCGTCCGAC
                                  A
GAM834  GALNS    3'  GAGGCGTGTAGCTTCTTATC   4964      T_
                                GGTG  AGGTTGCATGTCTC
                                ||||  ||||||||||||||
                                CTAT  TTCGATGTGCGGAG
                                  TC
GAM834  GCLM     3'  AGATGTGTAAAATCTA      9024      ___
                                TAGGT  TGCATGTCT
                                |||||  |||||||||
                                ATCTA  ATGTGTAGA
                                  AA
GAM834  GCNT3    3'  GGGATATGTGGTAGAGCACTTG 16459         AG_ TT
           ATT                    AGTCAGGTGT   G  GCATGTCTC
                                |||||||||||   |  |||||||||
                                TTAGTTCACG   T  TGTATAGGG
                                     AGA GG
GAM834  GEM      3'  GGGACCAATAATCTATATTAGA 17929      AG        CAT
           TT                     AGTC  GTGTAGGTTG   GTCTC
                                ||||  ||||||||||   |||||
                                TTAG  TATATCTAAT   CAGGG
                                  AT         AAC
GAM834  GHR      3'  GCAGTTTATATTTAACT     3884      C      GG
                                AGT AGGTGTA  TTGC
                                ||| |||||||  ||||
                                TCA TTTATAT  GACG
                                  A      TT
GAM834  GMPR     3'  GGGACAAAGCAGCGTCTGGCT  91003       GT  AGGT   A_
                                AGTCAG  GT    TGC  TGTCTC
                                ||||||  ||    |||  ||||||
```

```
                                TCGGTC  CG    ACG  ACAGGG
                                   TG  _____  AA
GAM834  GNB1     3'  GAGATGCCTGTCCTGTGCTTGG 9070       TG   TT__   G  TC
                                TCAGG  TAGG   GCAT TC
                                |||||  ||||   |||| ||
                                GGTTC  GTCC   CGTA AG
                                   GT   TGTC   G
GAM834  GORASP1  3'  GGCTACAATGCTACACTTGGCT 49111          _   CAT
                                AGTCAGGTGTAG GTTG  GTC
                                ||||||||||| ||||  |||
                                TCGGTTCACATC TAAC  CGG
                                      G   AT_
GAM834  GRINL1A  3'  GAGATGTCATCATCTTACATCA 69514     A      T  C__
           GACT                  GTC GGTGTAGG TG  ATGTCTC
                                ||| |||||||| ||  |||||||
                                CAG CTACATTC AC  TGTAGAG
                                  A       T  TAC
GAM834  GRLF1    3'  GGGGCATCCCTGTGCCTCACT  78560     C   TG   TTGC
                                AGT AGG  TAGG   ATGTCTC
                                ||| |||  ||||   |||||||
                                TCA TCC  GTCC   TACGGGG
                                  C  GT   C___
GAM834  GRM6     3'  AGGCATTTCTACACTGATT   5925       G     TTGC
                                AGTCAG TGTAGG   ATGTCT
                                ||||||| ||||||   ||||||
                                TTAGTC ACATCT   TACGGA
                                   _     T___
GAM834  HDLBP    3'  AGCCTAGCGCCTGGCT      67921          _
                                AGTCAGGTGT AGGTT
                                |||||||||| |||||
                                TCGGTCCGCG TCCGA
                                      A
GAM834  HEBP1    3'  GGGAAAATGTGATTTGTGCCTG 32025       TG    TG   G_
           AT                    GTCAGG  TAGGT  CAT  TCTC
                                ||||||  |||||  |||  ||||
                                TAGTCC  GTTTA  GTA  AGGG
                                   GT    GT   AA
GAM834  HFE      3'  GGATTCTTCCATCTGATT    57322         T   TTGCAT
                                AGTCAGGTG AGG     GTCT
                                |||||||| |||     ||||
                                TTAGTCTAC TTC     TAGG
                                     C   T_____
GAM834  HFE      3'  GGATTCTTCCATCTGATT    4655          T   TTGCAT
                                AGTCAGGTG AGG     GTCT
                                |||||||| |||     ||||
                                TTAGTCTAC TTC     TAGG
                                     C   T_____
GAM834  HIP1     3'  GGGAAGAACCCTATACTTGGTT 18063   GT        TTGCATG
                                A  CAGGTGTAGG      TCTC
                                |  ||||||||||      ||||
```

```
                                T  GTTCATATCC      AGGG
                                 TG        CAAGA__
GAM834  HIP2     3'  TGCATGCTTGTACTTGACT    18069           _
                                AGTCAGGTGTAGGT TGCA
                                |||||||||||||| ||||
                                TCAGTTCATGTTCG ACGT
                                       T
GAM834  HNRPH1   3'  GCTTGTGATTTATGCTTACT   18629     C       TG  T
                                AGT AGGTGTAGGT  CA GT
                                ||| ||||||||||  || ||
                                TCA TTCGTATTTA  GT CG
                                  _       GT  T
GAM834  HRH2     5'  AGATCCCCAGTACTTGACT    42251         TA  TTGCAT
                                AGTCAGGTG  GG     GTCT
                                |||||||||  ||     ||||
                                TCAGTTCAT  CC     TAGA
                                     GA  CC_____
GAM834  HSPB2    3'  GGGACATGTCATAGCCTTGGTT 7742    GT    T  AG  T
                                A  CAGG GT  GT GCATGTCTC
                                |  |||| ||  || |||||||||
                                T  GTTC CG  TA TGTACAGGG
                                 TG   _  A_  C
GAM834  IDH3G    5'  GGGACGTGCGGAGGCTCTCACT 14706     C   T  AGG
                                AGT AGG GT   TTGCATGTCTC
                                ||| ||| ||   ||||||||||
                                TCA TCT CG   GGCGTGCAGGG
                                  C   _  GA_
GAM834  IER3     3'  GAGATGTGTACGTAATATTT   13995       _ G  T
                                AGGTGT A GT GCATGTCTC
                                ||||||  | || |||||||||
                                TTTATA T CA TGTGTAGAG
                                    A G  _
GAM834  IER3     3'  GAGATGTGTACGTAATATTT   53385       _ G  T
                                AGGTGT A GT GCATGTCTC
                                ||||||  | || |||||||||
                                TTTATA T CA TGTGTAGAG
                                    A G  _
GAM834  IFNAR2   3'  GGGGTGAGCCGCTGTGCCTGGC 6045         TG  __   G   G  TC
           T                     AGTCAGG  TA  GGTT CAT TC
                                 |||||||  ||  |||| ||| ||
                                 TCGGTCC  GT  CCGA GTG GG
                                     GT  CG   _   G
GAM834  IFNW1    5'  GTTAGTGTAGTGTGTGTCTGAT 9301         TG  GG     GTCTC
           T                     AGTCAGG  TA  TTGCAT
                                 |||||||  ||  ||||||
                                 TTAGTCT  GT  GATGTG
                                     GT  GT     ATTG
GAM834  IL10RA   3'  GAGGCCTGTGCTTGTGTTTGCT 59642    T   TG    T  T
                                AG CAGG  TAGGT GCA GTCTC
                                || ||||  ||||| ||| |||||
```

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                                TC GTTT  GTTCG TGT CGGAG
                                 _   GT    _  C
GAM834  IL11    3'  GGACATCTGTGCCTTATT    5330     C   TG  GTTGC
                                AGT AGG  TAG    ATGTCT
                                ||| |||  |||    ||||||
                                TTA TCC  GTC    TACAGG
                                  T  GT  _____
GAM834  IL18RAP  5'  AGACCCTCTACACCTGG     13900          TTGCAT
                                TCAGGTGTAGG     GTCT
                                ||||||||||     ||||
                                GGTCCACATCT     CAGA
                                      CC____
GAM834  IL2RA    3'  GAGACATCCGTTGTGCTTGCCT 4697     T   TG  GT  C
                                AG CAGG  TAG  TG ATGTCTC
                                || ||||  |||  || |||||||
                                TC GTTC  GTT  GC TACAGAG
                                 C   GT  __ C
GAM834  IL6R     3'  GGGGTGTGCGGCCTTTGGCT   5123       GTGT       GT
                                AGTCAG   AGGTTGCAT  CTC
                                ||||||   |||||||||  |||
                                TCGGTT   TCCGGCGTG  GGG
                                   ____       TG
GAM834  INPP5D   3'  GAGATGCCAAGGCCTGTGCC   82810    TG    ___   G  TC
                                GG  TAGGTT   GCAT TC
                                ||  ||||||   |||| ||
                                CC  GTCCGG   CGTA AG
                                 GT     AAC    G
GAM834  ITK      3'  GAGACTATGTATTTATATTTGG 18683          T   _
                                TCAGGTGTAGGT GCAT GTCTC
                                |||||||||||| |||| |||||
                                GGTTTATATTTA TGTA CAGAG
                                      _   T
GAM834  JMJ      3'  GAGGGAGACCTGTGCCTGATT  17131       TG     GCATG
                                AGTCAGG  TAGGTT    TCTC
                                |||||||  ||||||    ||||
                                TTAGTCC  GTCCAG    GGAG
                                   GT     AG___
GAM834  KCNJ8    3'  GAGGATTCATGGCTTATGCTTG 17148         TG   ___
                                CAGGTGTAGGT  CATG   TCTC
                                ||||||||||  ||||  ||||
                                GTTCGTATTCG  GTAC   GGAG
                                      __    TTA
GAM834  KCNK5    3'  GGGGCATCTGTCCTGAGCTTGG 13612        G   TTGC
          CT                    AGTCAGGT TAGG    ATGTCTC
                                ||||||||  ||||    |||||||
                                TCGGTTCG GTCC    TACGGGG
                                   A    TGTC
GAM834  KDR      3'  GTAGCCGCATTTGATT      9595          A
                                AGTCAGGTGT GGTTGC
                                ||||||||| ||||||
```

```
                                TTAGTTTACG CCGATG
                                          _
GAM834  KIAA0857  3'  GGGCTTGCCTGGCTTGGCT   66676       G    TGCAT
                                AGTCAGGT TAGGT    GTCT
                                |||||||| |||||    ||||
                                TCGGTTCG GTCCG    CGGG
                                     _    TT___
GAM834  KIF2      3'  GAGACATTTTTTGTGTGTGACT 15726      G TG   TTGC
                                AGTCA G  TAGG   ATGTCTC
                                ||||| |  ||||   |||||||
                                TCAGT T  GTTT   TACAGAG
                                   G GT   TT__
GAM834  KIF3C     3'  GAGGATCAAGCTTGGGTCTGAT 9603       TG    GCATG
            T                    AGTCAGG  TAGGTT    TCTC
                                |||||||  ||||||    ||||
                                TTAGTCT  GTTCGA    GGAG
                                    GG     ACTA_
GAM834  KMO       3'  TGATCTGCATTTCACT      13460     C
                                AGT AGGTGTAGGTTG
                                ||| ||||||||||||
                                TCA TTTACGTCTAGT
                                  C
GAM834  KRT16     5'  GAGATGCTGGGCCTGGTT    95198   GT    G  GGTT   G
                                A  CAGGT TA    GCAT TC
                                |  ||||| ||    |||| ||
                                T  GTCCG GT    CGTA AG
                                 TG    G _____   G
GAM834  LHX5      5'  GGGGCGTGCGGCCCGTGGC   42306     GGTGTA
                                GTCA     GGTTGCATGTCTC
                                ||||     ||||||||||||
                                CGGT     CCGGCGTGCGGGG
                                  GC_____
GAM834  LMO7      3'  GAGGCAGATAATGATCTAGTTT 31765     GG G     GCA___
              GACT                  TCA  T TAGGTT     TGTCTC
                                |||  | ||||||     ||||||
                                AGT  G ATCTAG     ACGGAG
                                  TT _     TAATAG
GAM834  LMO7      3'  GAGGCAGATAATGATCTAGTTT 18089     GG G     GCA___
              GACT                  TCA  T TAGGTT     TGTCTC
                                |||  | ||||||     ||||||
                                AGT  G ATCTAG     ACGGAG
                                  TT _     TAATAG
GAM834  LNK       3'  GACATCCTGTGTTTGGTT    18464   GT    TG    TTGC
                                A  CAGG  TAGG   ATGTC
                                |  ||||  ||||   |||||
                                T  GTTT  GTCC   TACAG
                                 TG   GT   _____
GAM834  LOH11CR2A 5'  GGACGTGGAACTCCTGATT   27541       TGTA   G
                                AGTCAGG   GGTT CATGTCT
                                |||||||   |||| |||||||
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                                TTAGTCC    TCAA GTGCAGG
                                    ____    G
GAM834  LPL     3'  GGGCCATAGCCTATAATTGGTT 4088    GT   G       CAT
                                A  CAG TGTAGGTTG   GTCT
                                |  ||| |||||||||   ||||
                                T  GTT ATATCCGAT   CGGG
                                 TG   A       AC_
GAM834  MAK     3'  GAGGCGTGTGCCACCATGCCTG 19761         A  __
           GCT                    GTCAGGTGT GGT  TGCATGTCTC
                                |||||||||| |||  ||||||||||
                                CGGTCCGTA CCA  GTGTGCGGAG
                                     _  CC
GAM834  MAN2A2  3'  GGGCACTTGGCCTATGTACTGA 20398       _ TG      CA    C
           TT                    AGTCAG G  TAGGTTG  TGTCT
                                |||||| |  |||||||  |||||
                                TTAGTC T  ATCCGGT  ACGGG
                                   A GT      TC
GAM834  MAPK7   3'  GGCCCCCAGCCTGTGCCTTGCT 57381     C   TG      CAT
                                AGT AGG  TAGGTTG   GTC
                                ||| |||  |||||||   |||
                                TCG TCC  GTCCGAC   CGG
                                  T   GT      CCC
GAM834  MAPK7   3'  GGCCCCCAGCCTGTGCCTTGCT 57384     C   TG      CAT
                                AGT AGG  TAGGTTG   GTC
                                ||| |||  |||||||   |||
                                TCG TCC  GTCCGAC   CGG
                                  T   GT      CCC
GAM834  MAPK7   3'  GGCCCCCAGCCTGTGCCTTGCT 57387     C   TG      CAT
                                AGT AGG  TAGGTTG   GTC
                                ||| |||  |||||||   |||
                                TCG TCC  GTCCGAC   CGG
                                  T   GT      CCC
GAM834  MAPK7   3'  GGCCCCCAGCCTGTGCCTTGCT 10841     C   TG      CAT
                                AGT AGG  TAGGTTG   GTC
                                ||| |||  |||||||   |||
                                TCG TCC  GTCCGAC   CGG
                                  T   GT      CCC
GAM834  MARS    3'  GACAAGGTATTCTATGTCTGGT 94894   GT   TG   GT   A_   TC
           T                     A  CAGG  TAG  TGC  TGTC
                                |  ||||  |||  |||  ||||
                                T  GTCT  ATC  ATG  ACAG
                                 TG   GT   TT   GA
GAM834  MAT1A   3'  GAGACATGCAGAGATTGG    90833     GTGTAGG
                                TCAG      TTGCATGTCTC
                                ||||      ||||||||||||
                                GGTT      GACGTACAGAG
                                  AGA____
GAM834  MATN2   3'  TTAGTGTGCAATCTCATTTGAC 9932          T       TG CTC
           T                     AGTCAGGTG AGGTTGCA  T
                                |||||||| ||||||||  |
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                                TCAGTTTAC TCTAACGT  G
                                      _       GT ATTC
GAM834  MAX      3'  GAGCCATGGGTCTGTGCTGACT 59038       G TG   GT G    T
                                AGTCA G  TAG  T CATG CTC
                                ||||| |  |||  | |||| |||
                                TCAGT C  GTC  G GTAC GAG
                                   _ GT   TG _    C
GAM834  MEL      3'  ACAGCAGTCTGGCTTGATT    18118         G   GT   A
                                AGTCAGGT TAG  TGC TGT
                                |||||||| |||  ||| |||
                                TTAGTTCG GTC  ACG ACA
                                      _  TG  _
GAM834  MFAP4    3'  TAGCCTGGACCTGGCT      69256         G
                                AGTCAGGT TAGGTTG
                                |||||||| |||||||
                                TCGGTCCA GTCCGAT
                                     G
GAM834  MGAM     3'  GGAAAGGTCTGGCCTGATT    72363         G   GT GCATG
                                AGTCAGGT TAG  T    TCT
                                |||||||| |||  |    |||
                                TTAGTCCG GTC  G    AGG
                                      _  TG AA___
GAM834  MLLT2    3'  GGGAACCAACATTTATACCTGA 19848          __    CATG
           C                     GTCAGGTGTAG  GTTG    TCTC
                                ||||||||||  ||||   ||||
                                CAGTCCATATT  CAAC    AGGG
                                       TA   CA__
GAM834  MPHOSPH1 3'  GGGGTATGTGAGATGTTTTGAC 32471        TGT GG TG   GT
                                GTCAGG   A  T  CAT  CTC
                                ||||||  | |  |||  |||
                                CAGTTT   T  A  GTA  GGG
                                   TG_ AG GT   TG
GAM834  MSI1     3'  GAGCGCCCCAGCCTGCAGCTGA 10125        G        CA_  T
           CT                     AGTCAG TGTAGGTTG   TG CTC
                                |||||| |||||||||   || |||
                                TCAGTC ACGTCCGAC   GC GAG
                                   G        CCC  _
GAM834  MYB      3'  GAGATATGACGGTGTACTTACT 59538    GT_   G TT _
                                AG   GTA G  G CATGTCTC
                                ||   ||| |  | ||||||||
                                TC   CAT T  C GTATAGAG
                                 ATT   G GG A
GAM834  MYEOV    3'  GGGGCTACGAGGCTGCATCTGG 57052           G  GCAT
           CT                     AGTCAGGTGTAG TT    GTCTC
                                ||||||||||| ||    |||||
                                TCGGTCTACGTC GA    CGGGG
                                       G  GCAT
GAM834  NBS1     3'  CGAGATATTACACCTAGTCTGT 69497    G_______    TGC
           GGCTTGACT                T      TAGGT   ATGTCTC   G
                                |      |||||   |||||||   |
```

```
                                G      ATCCA   TATAGAG   C
                                 GTGTCTG    CAT
GAM834  NDUFA8   3'  CATGCGGTTTGCATCGACT   26437      A     GG
                                AGTC GGTGTA  TTGCATG
                                |||| ||||||  |||||||
                                TCAG CTACGT  GGCGTAC
                                  _     TT
GAM834  NDUFB3   5'  CCCTCATGTAGTCTCTACCTGA 10193         T  GT     TCTC
           TT                    AGTCAGGTG AG  TGCATG
                                |||||||||  ||  ||||||
                                TTAGTCCAT TC  ATGTAC
                                     C  TG     TCCCT
GAM834  NEO1     3'  GCGAGAAGTGCAACCTGCATTT 10203     C            G
           CACT                     AGT AGGTGTAGGTTGCAT TCTC
                                ||| ||||||||||||||| ||||
                                TCA TTTACGTCCAACGTG AGAG
                                  C            A    CGG
GAM834  NET1     5'  AGGCATGGGCACGTGGCT    19614       G    AGGTTG
                                AGTCA GTGT     CATGTCT
                                ||||| ||||     |||||||
                                TCGGT CACG     GTACGGA
                                   G    G_____
GAM834  NKTR     3'  TGTGACCTGCAGCTGACT    18205       G      TG
                                AGTCAG TGTAGGT  CA
                                |||||| |||||||  ||
                                TCAGTC ACGTCCA  GT
                                    G      GT
GAM834  NPAT     3'  GAGGTGCCTTCTCTGTATTAGA 67236      AG     _ TT_    G  TC
           CT                     AGTC  GTGTAG G   GCAT TC
                                ||||  |||||| |   |||| ||
                                TCAG  TATGTC C   CGTG AG
                                  AT     T TTC    G
GAM834  NPY2R    3'  AGGTGTGCAGTTCGCTGCT    6182      CA    TAGG     GT
                                AGT  GGTG    TTGCAT  CT
                                |||  ||||    ||||||  ||
                                TCG  TCGC    GACGTG  GA
                                  __    TT__      TG
GAM834  NR3C2    3'  GTAACTTTGCTTGATT      6135          T
                                AGTCAGGTG AGGTTGC
                                |||||||||  |||||||
                                TTAGTTCGT TTCAATG
                                      _
GAM834  NR4A2    3'  GGGAAATGTTTGGCCATGCTTG 20533   GT      A    __    G
           GTT                      CAGGTGT GGTT  GCAT TCTC
                                 |||||||  ||||  ||||  ||||
                                 GTTCGTA CCGG  TGTA AGGG
                                TG      _    TT    A
GAM834  NUMA1    5'  GGGTGAACAGTCTACACGTGGC 93440       G     GT  CA GT  C
           T                      AGTCA GTGTAG  TG  T  CT
                                |||||  ||||||  ||  |  ||
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                                TCGGT CACATC  AC  G  GG
                                   G     TG  AA TG
GAM834  OGT     5'  GAACATGGTGGTTTGCACTTGG 13203         GG TG _   CTC
                                TCAGGTGTA  T  C ATGT
                                |||||||||  |  | ||||
                                GGTTCACGT  G  G TACA
                                     TT GT G    AG
GAM834  OGT     5'  GACATTGCGCCTGCCT     13204    T     T  _
                                GG GTAGGT GCA TGTC
                                || |||||| ||| ||||
                                TC CGTCCG CGT ACAG
                                 _     _  T
GAM834  OLIG2   3'  GGACTGGCCTGCGCTGGGCT   19412     A       TG  T
                                AGTC GGTGTAGGT  CA GTCT
                                |||| |||||||||  || ||||
                                TCGG TCGCGTCCG  GT CAGG
                                   G       __ _
GAM834  OPA3    3'  ATCTTGATGCAACTTGGCATTT 47107   GT     _       GTCTC
            GGTT                    CAGGTGT AGGTTGCAT
                                 |||||||| |||||||||
                                 GTTTACG TTCAACGTA
                                TG      G       GTTCTAG
GAM834  OTOF    3'  GACACGGCCTTCGTCTGGTT   16644   GT   GT T    CA
                                A  CAG  G AGGTTG  TGTC
                                |  |||  | ||||||  ||||
                                T  GTC  C TCCGGC  ACAG
                                 TG   TG T    __
GAM834  OTP     3'  GAGGCCTCCCCTCCGCCTGATT 49499         T   TTGCAT
                                AGTCAGGTG AGG     GTCTC
                                |||||||||| |||     |||||
                                TTAGTCCGC TCC     CGGAG
                                     C   CCTC__
GAM834  P2RY6   3'  GAGATGGACAGACCTGGGCCTG 14741         G     GCA_
            GCT                    AGTCAGGT TAGGTT    TGTCTC
                                |||||||| ||||||    ||||||
                                TCGGTCCG GTCCAG    GTAGAG
                                     G     ACAG
GAM834  PABPN1  5'  GAGGTGCGCTTATTTGATT    16182       GT     T   G
                                AGTCAG  GTAGGT GCAT TC
                                ||||||  |||||| |||| ||
                                TTAGTT  TATTCG CGTG AG
                                   __     _   G
GAM834  PAP     3'  AAGTCAGCAGCCTGTGTTTGG  10419       TG       A  T  C
                                TCAGG  TAGGTTGC TG CT
                                |||||  |||||||| || ||
                                GGTTT  GTCCGACG AC GA
                                   GT       _  T  AG
GAM834  PAP     3'  AAGTCAGCAGCCTGTGTTTGG  57235       TG       A  T  C
                                TCAGG  TAGGTTGC TG CT
                                |||||  |||||||| || ||
```

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                                GGTTT  GTCCGACG AC GA
                                  GT       _ T  AG
GAM834  PAP      3'  AAGTCAGCAGCCTGTGTTTGG  57237      TG       A  T  C
                                TCAGG  TAGGTTGC TG CT
                                |||||  |||||||| || ||
                                GGTTT  GTCCGACG AC GA
                                  GT       _ T  AG
GAM834  PIK3C2B  3'  GAGGGCTGCCTGTGCTGGACT  10568      A  TG    T  ATG
                                AGTC GG  TAGGT GC   TCTC
                                ||||  ||  |||||  ||   ||||
                                TCAG TC  GTCCG CG   GGAG
                                  G  GT    T  ___
GAM834  PLA2G10  5'  GAGACTTCCCTGGGCCTGACT  13086        G    TTGCAT
                                AGTCAGGT TAGG     GTCTC
                                ||||||||  ||||     |||||
                                TCAGTCCG GTCC     CAGAG
                                    G    CTT___
GAM834  PLA2G10  5'  GGGGTGTGTGTCCGCCGGGCT  13090      A   GTA  T    GT
                                AGTC GGT   GG TGCAT  CTC
                                ||||  |||   ||  |||||  |||
                                TCGG CCG   CC GTGTG  GGG
                                  G   ___  T    TG
GAM834  PLIN     3'  GAGCCGCAGCCTGCTCTGATT  10642        T        AT T
                                AGTCAGG GTAGGTTGC  G CTC
                                |||||||  |||||||||  | |||
                                TTAGTCT CGTCCGACG  C GAG
                                    _        C_ _
GAM834  PPP4R1   3'  GTGTCTGTGTCTGATT      17621        TG   GTT
                                AGTCAGG  TAG   GCAT
                                |||||||  |||   ||||
                                TTAGTCT  GTC   TGTG
                                    GT   ___
GAM834  PRDM2    3'  ATTATATGTGATTTACATTTCA 31845     C        TG    CTC
          CT                      AGT AGGTGTAGGT  CATGT
                                |||  ||||||||||  |||||
                                TCA TTTACATTTA  GTATA
                                  C        GT    TTAT
GAM834  PRex1    3'  GGGCACGAGATTTGCTCTGACT 40433        T     GCA
                                AGTCAGG GTAGGTT   TGTCT
                                |||||||  |||||||   |||||
                                TCAGTCT CGTTTAG   ACGGG
                                    _      AGC
GAM834  PRKCA    3'  GGCCACGGCTTGTGTCTGATT  10808        TG     CAT
                                AGTCAGG  TAGGTTG   GTC
                                |||||||  |||||||   |||
                                TTAGTCT  GTTCGGC   CGG
                                    GT      AC_
GAM834  PTGES    3'  GAGATGTGTGATTTTTAGTC   16860    _  T   TG
                                GG TG AGGT  CATGTCTC
                                || || ||||  ||||||||
```

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                                CT AT TTTA  GTGTAGAG
                                 G  T    GT
GAM834  PTGS1    3'  GTGAGCTGCACCTGATT     6356          G TG
                                AGTCAGGTGTAG T  C
                                |||||||||||| |  |
                                TTAGTCCACGTC A  G
                                       G GT
GAM834  PTGS1    3'  GTGAGCTGCACCTGATT     54575          G TG
                                AGTCAGGTGTAG T  C
                                |||||||||||| |  |
                                TTAGTCCACGTC A  G
                                       G GT
GAM834  PTPN2    3'  GATTTTAACCTGCACTTGAT   11055            CAT
                                GTCAGGTGTAGGTTG   GTC
                                ||||||||||||||   |||
                                TAGTTCACGTCCAAT   TAG
                                          TT_
GAM834  PTPRK    3'  GCTTGCAGTTTGTAATTGACT  11121       G    GG     T
                                AGTCAG TGTA  TTGCA GT
                                |||||| ||||  ||||| ||
                                TCAGTT ATGT  GACGT CG
                                   A    TT     T
GAM834  RAB23    3'  GGGGTGTGCATGCAGATGTCTG 32785       TG AG  _     GT
          G                      TCAGG  T  GT TGCAT  CTC
                                |||||  |  || |||||  |||
                                GGTCT  A  CG ACGTG  GGG
                                   GT GA  T    TG
GAM834  RAI2     5'  TAACCTCACTTGGCT       41416          T
                                AGTCAGGTG AGGTTG
                                ||||||||| ||||||
                                TCGGTTCAC TCCAAT
                                          _
GAM834  RBBP2    3'  GACCTCAGCGATTTGTGCTTG  17321      TG       AT__   TC
                                CAGG  TAGGTTGC    GTC
                                ||||  ||||||||    |||
                                GTTC  GTTTAGCG    CAG
                                  GT       ACTC
GAM834  RFPL1    5'  GGGATGTGCTTGAGTGTTTGTA 40708     _    TG AGGTT
          CT                     AGT CAGG  T    GCATGTCTC
                                ||| ||||  |    |||||||||
                                TCA GTTT  G    CGTGTAGGG
                                  T   GT AGTT_
GAM834  RFPL2    5'  GGGATGTGCTTGAGTGTTTGTA 21725     _    TG AGGTT
          CT                     AGT CAGG  T    GCATGTCTC
                                ||| ||||  |    |||||||||
                                TCA GTTT  G    CGTGTAGGG
                                  T   GT AGTT_
GAM834  RFPL3    5'  GGGATGTGCTTGAGTGTTTGTA 21721     _    TG AGGTT
          CT                     AGT CAGG  T    GCATGTCTC
                                ||| ||||  |    |||||||||
```

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                                TCA GTTT  G     CGTGTAGGG
                                  T    GT AGTT_
GAM834  RFX5     3'  GAGGCCCTTCTTTGCACTTGCT 4824      T         TTGCAT
                                AG CAGGTGTAGG      GTCTC
                                || ||||||||||      |||||
                                TC GTTCACGTTT      CGGAG
                                 _         CTTCC_
GAM834  RFXAP    3'  GGGATGTGTCTCCTACAGTTGG 5015        G      TT
             CT                   AGTCAG TGTAGG  GCATGTCTC
                                |||||| ||||||  |||||||||
                                TCGGTT ACATCC  TGTGTAGGG
                                   G     TC
GAM834  RHO      3'  GCAGCAACTCATACTTGGCT   5019           AG     A
                                AGTCAGGTGT  GTTGC TGT
                                ||||||||||  ||||| |||
                                TCGGTTCATA  CAACG ACG
                                      CT    _
GAM834  RIG      3'  CAGTTGAAGTGATTTATGCTTG 21128             TG ATGTCTC
             ATT                   AGTCAGGTGTAGGT  C
                                |||||||||||||| |
                                TTAGTTCGTATTTA  G
                                        GT AAGTTGACG
GAM834  RLF      3'  GGGATATGGAGTTCTTACTTGA 24851          TA GT G
             CT                   AGTCAGGTG  G  T CATGTCTC
                                |||||||||  |  | ||||||||
                                TCAGTTCAT  T  A GTATAGGG
                                     TC TG G
GAM834  RNF26    3'  TGGGGGATGCATCTGCACCTGA 49312             T    G
             CT                   AGTCAGGTGTAGGT GCAT TCTC
                                |||||||||||||| |||| ||||
                                TCAGTCCACGTCTA CGTA GGGG
                                        _   G    TA
GAM834  RNMT     3'  GAAATAAGTAATACTGCATCTG 13721           _    A   CTC
             ACT                   AGTCAGGTGTAG GTTGC TGT
                                |||||||||||| ||||| |||
                                TCAGTCTACGTC TAATG ATA
                                      A    A   AAG
GAM834  RNPEPL1  3'  GGGACCTCCTTGTGTCTGGC   36679       TG    TTGCAT
                                GTCAGG  TAGG     GTCTC
                                ||||||  ||||     |||||
                                CGGTCT  GTTC     CAGGG
                                   GT    CTC___
GAM834  RTN4R    3'  GAGATATGCATTTTATTTTACT 43433     C     TAGGT
                                AGT AGGTG    TGCATGTCTC
                                ||| |||||    ||||||||||
                                TCA TTTAT    ACGTATAGAG
                                  T    TTT__
GAM834  SEL1L    3'  GGAACACTTGCATTTGATT    17361            TGCATG
                                AGTCAGGTGTAGGT     TCT
                                ||||||||||||||     |||
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                                TTAGTTTACGTTCA     AGG
                                      CA____
GAM834  SERPINB6  5'  AGGAAACTGCACTTGATT    15877          GTTGCATG
                                AGTCAGGTGTAG       TCT
                                ||||||||||||       |||
                                TTAGTTCACGTC       GGA
                                      AAA_____
GAM834  SERPINB9  3'  AGACCTTTTGTGTCTGGCT   14748       TG    TTGCAT
                                AGTCAGG  TAGG     GTCT
                                |||||||  ||||     ||||
                                TCGGTCT  GTTT     CAGA
                                   GT    TC____
GAM834  SFRP1     3'  GAGCTCCAGTTTGCATTTGG  11569        GG   CAT T
                                TCAGGTGTA  TTG   G CTC
                                |||||||||  |||   | |||
                                GGTTTACGT  GAC   C GAG
                                     TT   CT_ _
GAM834  SFRP1     3'  GAGGGGCAGCCTGTGCCTGCCT 11570    T    TG       ATG
                                AG CAGG  TAGGTTGC   TCTC
                                || ||||  ||||||||   ||||
                                TC GTCC  GTCCGACG   GGAG
                                 C    GT       G__
GAM834  SFRP4     3'  GAGGTATGTCACTCATCTTACT 11578    C     TA   T    GT
                                AGT AGGTG  GGT GCAT  CTC
                                ||| |||||  ||| ||||  |||
                                TCA TCTAC  TCA TGTA  GAG
                                  T    __   C    TG
GAM834  SH2D1A    5'  GGTGGTTGACTTGTGCCTGGCT 9850         TG     GCA GT
                                AGTCAGG  TAGGTT   T  C
                                |||||||  ||||||   |  |
                                TCGGTCC  GTTCAG   G  G
                                   GT     TTG TG
GAM834  SH3BP2    3'  GGCCTTAATTTGCATTTAGCT  11609    TC          CAT
                                AG  AGGTGTAGGTTG   GTC
                                ||  ||||||||||||   |||
                                TC  TTTACGTTTAAT   CGG
                                 GA          TC_
GAM834  SH3GL3    5'  GAGGCTGGTTCTTGGGTTTGAC 11633      GG G    TT  AT
           T                     AGTCA  T TAGG  GC  GTCTC
                                |||||  | ||||  ||  |||||
                                TCAGT  G GTTC  TG  CGGAG
                                   TT G    T_  GT
GAM834  SHANK2    3'  GCTAATCTGCCTTGGTT     24586   GT    T      _
                                A  CAGG GTAGGTT GC
                                |  |||| ||||||| ||
                                T  GTTC CGTCTAA CG
                                 TG    _      T
GAM834  SLC12A7   3'  GGCCTTGGGCTACGTCTGGCT  21704       GT    G   CAT
                                AGTCAG  GTAG TTG   GTC
                                ||||||  |||| |||   |||
```

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                              TCGGTC  CATC GGT   CGG
                                 TG   G  TC_
GAM834  SLC16A1  3' GAGATATGTGTGTGTTTGG   11742      TG  GGT
                              TCAGG  TA   TGCATGTCTC
                              |||||  ||   ||||||||||
                              GGTTT  GT   GTGTATAGAG
                                 GT  ___
GAM834  SLC22A5  3' GTCCTCTTGACCTGTGTCTGAC 11764       TG     CATGTCTC
           T                   AGTCAGG  TAGGTTG
                              |||||||  |||||||
                              TCAGTCT  GTCCAGT
                                 GT     TCTCCTG
GAM834  SLC5A2   3' GGGCCCACTGCATCTGATT   11726          GTTGCAT
                              AGTCAGGTGTAG     GTCT
                              ||||||||||||     ||||
                              TTAGTCTACGTC     CGGG
                                    ACC_____
GAM834  SLC6A6   3' TGCCGTTTGTGTCTGATT    11730       TG   TT
                              AGTCAGG  TAGG  GCA
                              |||||||  ||||  |||
                              TTAGTCT  GTTT  CGT
                                 GT   GC
GAM834  SMARCA3  5' GAGACGGCGTCGACGTCTGACT 11791       GT  AGGT   A
                              AGTCAG  GT    TGC TGTCTC
                              ||||||  ||    ||| ||||||
                              TCAGTC  CA    GCG GCAGAG
                                 TG  GCT_  _
GAM834  SMARCA3  5' GAGACGGCGTCGACGTCTGACT 57397       GT  AGGT   A
                              AGTCAG  GT    TGC TGTCTC
                              ||||||  ||    ||| ||||||
                              TCAGTC  CA    GCG GCAGAG
                                 TG  GCT_  _
GAM834  SMARCC2  3' GAGGCATGCATTTTTATATCAG 57408     A      T_
           ATT                  AGTC GGTGTAGG  TGCATGTCTC
                              ||||  ||||||||  ||||||||||
                              TTAG CTATATTT  ACGTACGGAG
                                 A      TT
GAM834  SMARCC2  3' GAGGCATGCATTTTTATATCAG 11805     A      T_
           ATT                  AGTC GGTGTAGG  TGCATGTCTC
                              ||||  ||||||||  ||||||||||
                              TTAG CTATATTT  ACGTACGGAG
                                 A      TT
GAM834  SMOH     3' GAGGCAGCCTAGCCTATGTCTG 18866       TG     CA_
           GC                   GTCAGG  TAGGTTG   TGTCTC
                              ||||||  |||||||   ||||||
                              CGGTCT  ATCCGAT   ACGGAG
                                 GT     CCG
GAM834  SMP1     3' TGTGGTATGCACTTGATT    26704          GG TG
                              AGTCAGGTGTA  T  CA
                              ||||||||||  |  ||
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                                TTAGTTCACGT  G  GT
                                      AT GT
GAM834  SPTBN1   5'  GAGATTCTCTCCTGTGCCTGAT 11940       TG   TTGCAT
           T                   AGTCAGG  TAGG     GTCTC
                               |||||||  ||||     |||||
                               TTAGTCC  GTCC     TAGAG
                                  GT    TCTCT_
GAM834  STEAP    5'  GAGGCGGGGCCTGCAGCTGGCT 24916       G      TGCA
                               AGTCAG TGTAGGT    TGTCTC
                               ||||||| |||||||    ||||||
                               TCGGTC ACGTCCG    GCGGAG
                                  G      GG__
GAM834  STK10    3'  GAGGAGCCAGGCCTGCAGCTGG 19985       G       GCATG
           CT                    AGTCAG TGTAGGTT     TCTC
                               |||||| ||||||||     ||||
                               TCGGTC ACGTCCGG     GGAG
                                  G       ACCGA
GAM834  TAF7     5'  GGGACTTGGCATTGCATCTGAT 18910          GT   AT_
           T                   AGTCAGGTGTAG  TGC   GTCTC
                               ||||||||||||  |||   |||||
                               TTAGTCTACGTT  ACG   CAGGG
                                     __   GTT
GAM834  TBX22    3'  GAGATATGCAATAAATATTATT 33781       TAG___
           TGAT                   CAGGTG     GTTGCATGTCTC
                               ||||||     ||||||||||||
                               GTTTAT     TAACGTATAGAG
                                  TATAAA
GAM834  TBX5     5'  GAGATAGTCGCTATCGCCTGGT 54889    GT     TA   T  A
           T                    A  CAGGTG  GGT GC TGTCTC
                               |  ||||||  ||| || ||||||
                               T  GTCCGC  TCG TG ATAGAG
                                TG     TA   C  _
GAM834  TBX5     5'  GAGATAGTCGCTATCGCCTGGT 3957    GT     TA   T  A
           T                    A  CAGGTG  GGT GC TGTCTC
                               |  ||||||  ||| || ||||||
                               T  GTCCGC  TCG TG ATAGAG
                                TG     TA   C  _
GAM834  TEM6     3'  TATGTAATTTATATTTTACT   42749     C
                               AGT AGGTGTAGGTTGCATG
                               ||| ||||||||||||||||
                               TCA TTTATATTTAATGTAT
                                 T
GAM834  TES      3'  GAGACTATGATTTATATTGATT 72006       G       CAT
                               AGTCAG TGTAGGTTG   GTCTC
                               |||||| |||||||||   |||||
                               TTAGTT ATATTTAGT   CAGAG
                                  _       AT_
GAM834  TGFBR1   3'  GAAAGTGATTTACTCCTGGTT  16048   GT   T     TG ATG
                               A  CAGG GTAGGT  C   TC
                               |  |||| ||||||  |   ||
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```
                                T  GTCC CATTTA  G   AG
                                 TG   T     GT AA_
GAM834  TGM2     3'  GGGAGCCCTGACCTGTGCTGAC 16054      G TG     GCATG
             T                    AGTCA G  TAGGTT     TCTC
                                  ||||| |  ||||||     ||||
                                  TCAGT C  GTCCAG     AGGG
                                    _ GT     TCCCG
GAM834  TMPRSS3  3'  GAGGCACCCTTCCATCTGATT  43796        T_   TTGCA
                                  AGTCAGGTG  AGG    TGTCTC
                                  |||||||||  |||    ||||||
                                  TTAGTCTAC  TCC    ACGGAG
                                       CT   C____
GAM834  TMPRSS3  3'  GAGGCACCCTTCCATCTGATT  50528        T_   TTGCA
                                  AGTCAGGTG  AGG    TGTCTC
                                  |||||||||  |||    ||||||
                                  TTAGTCTAC  TCC    ACGGAG
                                       CT   C____
GAM834  TMPRSS3  3'  GAGGCACCCTTCCATCTGATT  50507        T_   TTGCA
                                  AGTCAGGTG  AGG    TGTCTC
                                  |||||||||  |||    ||||||
                                  TTAGTCTAC  TCC    ACGGAG
                                       CT   C____
GAM834  TRIM34   3'  GAGATGTATGGTGTATTTGGCT 41236          GGT    G
                                  AGTCAGGTGTA   TGCAT TC
                                  ||||||||||   ||||| ||
                                  TCGGTTTATGT   ATGTA AG
                                        GGT    G
GAM834  TRIM34   3'  GAGATGTATGGTGTATTTGGCT 55225          GGT    G
                                  AGTCAGGTGTA   TGCAT TC
                                  ||||||||||   ||||| ||
                                  TCGGTTTATGT   ATGTA AG
                                        GGT    G
GAM834  TRIM9    3'  TCGGGCAACACTAGTTTGATAT 30769      _______ _    ATGTCTC
            TTGATT                 GTGT     AG GTTGC
                                  ||||     || |||||
                                  TATA     TC CAACG
                                    GTTTGA  A    GG   CTC
GAM834  TRPV1    5'  GGGGTGTGCCTGCGTCTAGCT  38093    TC  GT     T    G
                                  AG  AG  GTAGGT GCAT TC
                                  ||  ||  |||||| |||| ||
                                  TC  TC  CGTCCG TGTG GG
                                   GA  TG     _    G
GAM834  UBE2A    3'  GAGGTGCTTATGCTTAGCT   12465    TC      GTT    G
                                  AG  AGGTGTAG   GCAT TC
                                  ||  ||||||||   |||| ||
                                  TC  TTCGTATT   CGTG AG
                                   GA       ___    G
GAM834  UFD1L    3'  GACTTTGTAGTTGTATGCTTGA 73287          _ GT    T_   TC
             TT                    AGTCAGGTGTA G  TGCA  GTC
                                  |||||||||| |  ||||  |||
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                                TTAGTTCGTAT T  ATGT  CAG
                                      G TG    TT
GAM834  UNC13    3'  AAGGTGTGGAACTTGTGCCTGG 21054       TG     G   GT  C
          CT                     AGTCAGG  TAGGTT CAT  CT
                                |||||||  |||||| |||  ||
                                TCGGTCC  GTTCAA GTG  GA
                                   GT     G   TG  AG
GAM834  USH2A    3'  TAGCTTTTGCCTGATT      23064         T
                                AGTCAGGTG AGGTTG
                                |||||||||| ||||||
                                TTAGTCCGT TTCGAT
                                      T
GAM834  USP18    5'  GAGATTCCATCGTGCCTGGCT  63616       TG A   T CAT
                                AGTCAGG  T GGT G   GTCTC
                                |||||||  | ||| |   |||||
                                TCGGTCC  G CTA C   TAGAG
                                   GT _   _ CT_
GAM834  VAPB     3'  AGGCGTGTGTTGACTGATT    16439       GTGTAGGT
                                AGTCAG       TGCATGTCT
                                ||||||       |||||||||
                                TTAGTC       GTGTGCGGA
                                   AGTT____
GAM834  VARS2    5'  GCGGCCGGCGCCTGGCT     20849          A
                                AGTCAGGTGT GGTTGC
                                |||||||||| ||||||
                                TCGGTCCGCG CCGGCG
                                      G
GAM834  VCP      3'  GCATCTGCACTTGACT      75370            T
                                AGTCAGGTGTAGGT GC
                                |||||||||||||| ||
                                TCAGTTCACGTCTA CG
                                         _
GAM834  VSX1     3'  GAGATGTGTGGTTCAATGTACT 27467     _ GG  TA  TT
                                AGT CA  TG  GG  GCATGTCTC
                                |||  ||  ||  ||  |||||||||
                                TCA GT  AC  TT  TGTGTAGAG
                                  T  A_  __  GG
GAM834  YWHAH    3'  GAGGCATTTTACTATGCCTG   12697         GTTGC
                                CAGGTGTAG    ATGTCTC
                                |||||||||    |||||||
                                GTCCGTATC    TACGGAG
                                      ATTT_
GAM834  ZK1      5'  GCAGCCTTTGTCTGGCT     19463       GT T
                                AGTCAG  G AGGTTGC
                                ||||||  | |||||||
                                TCGGTC  T TCCGACG
                                   TG T
GAM834  ZNF140   5'  GAGCGTCTGGCCTGTGTTGGCT 12869      G TG      C   T
                                AGTCA G  TAGGTTG ATG CTC
                                |||||  |  ||||||| ||| |||
```

```
                                TCGGT T  GTCCGGT TGC GAG
                                  _ GT      C  _
GAM834  ZNF179   3'  GAACACCCGGCCTGTTTCTGGT 23102   GT   TG     CA  CTC
           T                     A  CAGG  TAGGTTG  TGT
                                 |  ||||  |||||||  |||
                                 T  GTCT  GTCCGGC  ACA
                                  TG   TT     CC   AG
GAM834  ZNF256   5'  GAGACAGATTTTGCACTTGGTT 19319   GT       TTGCA
                                 A  CAGGTGTAGG    TGTCTC
                                 |  ||||||||||    ||||||
                                 T  GTTCACGTTT    ACAGAG
                                  TG       TAG__
GAM834  ABCC13   3'  GAAACCTTGACTTATACCTAGC 56992    TC        CATGTCTC
           T                     AG  AGGTGTAGGTTG
                                 ||  ||||||||||||
                                 TC  TCCATATTCAGT
                                  GA         TCCAAAG
GAM834  ABCC13   3'  GGGGTGGCAGTCCTTGTGTTTG 56994     TG  _  _   A GT
                                 CAGG  TA GG TTGC T  CTC
                                 ||||  || || |||| |  |||
                                 GTTT  GT CC GACG G  GGG
                                   GT  T  T   _ TG
GAM834  ABLIM    3'  GAGACCAGCTCTTGCTTGGTT  9769    GT    TA    CAT
                                 A  CAGGTG  GGTTG   GTCTC
                                 |  ||||||  |||||   |||||
                                 T  GTTCGT  TCGAC   CAGAG
                                  TG     TC    ___
GAM834  ABLIM    3'  GAGACCAGCTCTTGCTTGGTT  22029   GT    TA    CAT
                                 A  CAGGTG  GGTTG   GTCTC
                                 |  ||||||  |||||   |||||
                                 T  GTTCGT  TCGAC   CAGAG
                                  TG     TC    ___
GAM834  ADPRTL3  3'  GTAACCAGCATTTGACT     18502         A
                                 AGTCAGGTGT GGTTGC
                                 ||||||||||| ||||||
                                 TCAGTTTACG CCAATG
                                       A
GAM834  AIBZIP   3'  GAGGCCTAGTCTGCATTTG   55653        GT  CAT
                                 CAGGTGTAG  TG   GTCTC
                                 |||||||||  ||   |||||
                                 GTTTACGTC  AT   CGGAG
                                      TG  C__
GAM834  AKAP11   3'  GAGATGTGGCAGCACTGGACT  32710     A    AG  TG   G
                                 AGTC GGTGT  GT  CAT TC
                                 |||| |||||  ||  ||| ||
                                 TCAG TCACG  CG  GTA AG
                                   G    A_  GT   G
GAM834  ALDRL6   3'  GCAACTTGTGCCTGGC      34155       TG
                                 GTCAGG  TAGGTTGC
                                 ||||||  ||||||||
```

```
                                CGGTCC  GTTCAACG
                                   GT
GAM834  ALS2CR3  3'  AAACATGTGGTCTGGTCTGACT 30481      GTG   TT    CTC
                                AGTCAG  TAGG  GCATGT
                                ||||||  ||||  ||||||
                                TCAGTC  GTCT  TGTACA
                                   TG_   GG    AAG
GAM834  ANXA10   5'  ACATATTTACATTTGATT   23236          TGC
                                AGTCAGGTGTAGGT  ATGT
                                ||||||||||||||  ||||
                                TTAGTTTACATTTA  TACA
                                      ___
GAM834  APCL     5'  GAGGTGCCAGCCTCTGCCACCT 19675      T___    _  G  TC
           GACT                 CAGGTG   AGGTTG CAT TC
                                ||||||   |||||| ||| ||
                                GTCCAC   TCCGAC GTG AG
                                   CGTC    C  G
GAM834  APOARGC  5'  GAGAATCATTAACTTAATTTGA 44420       G     C  __
           CT                   AGTCAGGT TAGGTTG ATG  TCTC
                                ||||||||| ||||||| |||  ||||
                                TCAGTTTA ATTCAAT TAC  AGAG
                                   _     _  TA
GAM834  APOL6    3'  GAGATAGATACATATCTGATT  47619        AG  GCA
                                AGTCAGGTGT  GTT  TGTCTC
                                ||||||||||  |||  ||||||
                                TTAGTCTATA  TAG  ATAGAG
                                     CA  ___
GAM834  ARH2     3'  GAGGCTCCACTGCGGTCTGTGC 56563    TG  GT   T____
           CTGACT                AGG  TAG  TGCA    GTCTC
                                |||  |||  ||||    |||||
                                TCC  GTC  GCGT    CGGAG
                                  GT   TG   CACCT
GAM834  ARHGEF16 3'  GCAAGTGGTCGTGCCTGGCT   27070       TG A  TT  A
                                AGTCAGG  T GG  GC TGT
                                |||||||  | ||  || |||
                                TCGGTCC  G CT  TG ACG
                                   GT _  GG  A
GAM834  B1       5'  GATCAAGGCTGTTTGTGTCTGG 27081       TG   TT  AT__  TC
           CT                   AGTCAGG  TAGG  GC   GTC
                                |||||||  ||||  ||   |||
                                TCGGTCT  GTTT  CG   TAG
                                   GT   GT  GAAC
GAM834  B3GNT5   5'  GACAGGCAGGTTACATTTGGTT 49426   GT      G   A
                                A  CAGGTGTAG TTGC TGTC
                                |  |||||||||  |||| ||||
                                T  GTTTACATT GACG ACAG
                                 TG       G   G
GAM834  BNIP-S   3'  GGGATATGCAGAGCTCTGG   56262      T  AGG
                                TCAGG GT   TTGCATGTCTC
                                |||||  ||   ||||||||||
```

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                                GGTCT CG   GACGTATAGGG
                                  _ A__
GAM834  BPES     3'  GGCTCCACGGCCTGTACTCGGT 43534   GT AG       CAT_   TC
           T                     A  C  GTGTAGGTTG    GTC
                                 | |  ||||||||||    |||
                                 T  G  CATGTCCGGC    CGG
                                  TG CT         ACCT
GAM834  BTBD3    3'  GACAGTGGTTGTGTTTGGCT   30309       TG  G TT  A
                                 AGTCAGG  TA G  GC TGTC
                                 |||||||  || |  || ||||
                                 TCGGTTT  GT T  TG ACAG
                                     GT  _ GG  _
GAM834  C11orf11  5'  GGGGCACCACGGCACCTGGCT  93256         AG  TGCA
                                 AGTCAGGTGT  GT    TGTCTC
                                 ||||||||||  ||    ||||||
                                 TCGGTCCACG  CA    ACGGGG
                                       G_  CC__
GAM834  C11orf11  3'  GGGGTATGGTGGGCCTTGGCT  93257       T  AGGTTG   GT
                                 AGTCAGG GT     CAT  CTC
                                 |||||||  ||     |||  |||
                                 TCGGTTC CG     GTA  GGG
                                     _  GGTG__   TG
GAM834  C17orf31  3'  GGGGCACCGTCGCCTAACCTGG 34125   GT    G     T  A_
           TT                     A  CAGGT TAGGT GC  TGTCTC
                                  |  ||||| ||||| ||  ||||||
                                  T  GTCCA ATCCG TG  ACGGGG
                                   TG    _    C  CC
GAM834  C1orf34   3'  GAGACCTGTCATCTGCATCTGG 60671           T   T
                                 TCAGGTGTAGGT GCA GTCTC
                                 ||||||||||||  ||| |||||
                                 GGTCTACGTCTA TGT CAGAG
                                       C   C
GAM834  C20orf112 3'  GAGGCTGTCCCAGCCTGGACCT 54642        G      CAT__
           GGCT                     GTCAGGT TAGGTTG    GTCTC
                                 |||||||  |||||||     |||||
                                 CGGTCCA GTCCGAC     CGGAG
                                     G      CCTGT
GAM834  C20orf112 3'  GATTGCTAGTCTGTGTCTGTCT 54643    T    TG   GT _   T
                                 AG CAGG  TAG  T GCA GTC
                                 || ||||  |||  | ||| |||
                                 TC GTCT  GTC  A CGT TAG
                                  T   GT   TG T   _
GAM834  C20orf142 3'  AGAAGCACTACACCTGACT    74765           GT   ATG
                                 AGTCAGGTGTAG  TGC   TCT
                                 ||||||||||||  |||   |||
                                 TCAGTCCACATC  ACG   AGA
                                       __   A__
GAM834  C20orf163 3'  GGGGCCCCAGACCTGTGGCTGG 54959       G GT    GCAT
           CT                     AGTCAG T  AGGTT    GTCTC
                                 ||||||  |  |||||    |||||
```

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                                TCGGTC G  TCCAG    CGGGG
                                   G TG     ACCC
GAM834  C20orf29  5'  GGGGTGCCCCATTTAGGCCTGG 37128        G     T__    G  TC
           CT                     AGTCAGGT TAGGT   GCAT TC
                                ||||||||| |||||   |||| ||
                                TCGGTCCG ATTTA   CGTG GG
                                    G    CCC    G
GAM834  C20orf81  5'  GCAGCCTCACTTGGCT      42813          T
                                AGTCAGGTG AGGTTGC
                                ||||||||| |||||||
                                TCGGTTCAC TCCGACG
                                    _
GAM834  C21orf108 3'  ACATGGTCTTCACCTGACT    88714         T   TTG
                                AGTCAGGTG AGG   CATGT
                                ||||||||| |||   |||||
                                TCAGTCCAC TTC   GTACA
                                    _  TG_
GAM834  C22orf20  3'  GAGCACACAACTTGAACCTGGC 47430         G      CA  T
           T                     AGTCAGGT TAGGTTG  TG CTC
                                ||||||||| |||||||  || |||
                                TCGGTCCA GTTCAAC  AC GAG
                                    A      AC  _
GAM834  C3orf4    3'  CGAGATATGGCAGCTGTTTGTA 39120      TA___     _
           TCTGCACT                GGTG    GGTTGC ATGTCTC   G
                                ||||    |||||| |||||||   |
                                CTAT    TCGACG TATAGAG   C
                                  GTTTG     G
GAM834  C6.1A     3'  GGGGTGTGGGGTATGTATGACT 44285      G TG  GG TG   G
                                AGTCA G  TA  T  CAT TC
                                ||||| |  ||  |  ||| ||
                                TCAGT T  AT  G  GTG GG
                                   A GT  GG GT   G
GAM834  C6.1A     3'  GGACTCATTTTACCTGACT    44284         T    TGCAT
                                AGTCAGGTG AGGT    GTCT
                                ||||||||| ||||    ||||
                                TCAGTCCAT TTTA    CAGG
                                    _   CT___
GAM834  CASPR3    3'  GGGATTTTAAATGGTCTGTATC 45937          TT CAT___
           TGG                    CAGGTGTAGG  G     GTCTC
                                |||||||||  |     |||||
                                GTCTATGTCT  T     TAGGG
                                     GG AAATTT
GAM834  CBX6      3'  GGGGTGGGTCTGTGCCGATT   26622      A  TG   GT G   G
                                AGTC GG  TAG  T CAT TC
                                ||||  ||  |||  | ||| ||
                                TTAG CC  GTC  G GTG GG
                                  _  GT   TG _   G
GAM834  CD109     3'  GGGGTGTGAGCATTAGACT    56049      AG    AGG TG   G
                                AGTC  GTGT   T  CAT TC
                                ||||  ||||   |  ||| ||
```

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                                TCAG  TACG   A  GTG GG
                                  AT   ___ GT   G
GAM834  CDV-1    3'  ACAGGCGTGAGCCTGCGCCTGG 48903            G      C
           CT                    AGTCAGGTGTAGGTT CATGTCT
                                 ||||||||||||||| |||||||
                                 TCGGTCCGCGTCCGA GTGCGGA
                                         _      CAT
GAM834  CG012    5'  GTCAGGTGTAGCTTATGTTTGG 83226       TG        GTCTC
           C                     GTCAGG  TAGGTTGCAT
                                 ||||||  ||||||||||
                                 CGGTTT  ATTCGATGTG
                                    GT         GACTGG
GAM834  CG018    3'  GAGATGTGCGACTCTTATGAT  53393     GGTGT  _
                                 GTCA     AG GTTGCATGTCTC
                                 ||||     || ||||||||||||
                                 TAGT     TC CAGCGTGTAGAG
                                   AT___  T
GAM834  CLIC5    3'  GGTGATTACAGGCCTGGGTTTG 33720      GG G     GCAT   TC
           ACT                     AGTCA  T TAGGTT    GTC
                                 |||||  | ||||||    |||
                                 TCAGT  G GTCCGG    TAG
                                    TT G     ACAT   TGGA
GAM834  CMRF-35H  3'  GGGACAGCTCCCTTATACCTGG 70419          _  TT  A
           C                      GTCAGGTGTA GG  GC TGTCTC
                                 |||||||||| ||  || ||||||
                                 CGGTCCATAT CC  CG ACAGGG
                                       T  CT  _
GAM834  COLEC12  3'  GGAGCCACTGCACCTGGCT   47870          GTT  ATG
                                 AGTCAGGTGTAG   GC   TCT
                                 ||||||||||||   ||   |||
                                 TCGGTCCACGTC   CG   AGG
                                       AC_  ___
GAM834  COLEC12  3'  GGGGTATGCCACCACACCTGGC 47871          A   T    GT
           T                      AGTCAGGTGT GGT GCAT  CTC
                                 |||||||||| ||| ||||  |||
                                 TCGGTCCACA CCA CGTA  GGG
                                       _  C    TG
GAM834  CRK7     3'  GAGGTAATCATCTGCATTTGGC 33253            TGCA GT
           T                      AGTCAGGTGTAGGT    T  CTC
                                 ||||||||||||||    |  |||
                                 TCGGTTTACGTCTA    A  GAG
                                       CTA_ TG
GAM834  CSE-C    3'  GAGGCGTGGGAAACTCTGGCT  91481        T  AGG  G
                                 AGTCAGG GT   TT CATGTCTC
                                 ||||||| ||   || ||||||||
                                 TCGGTCT CA   AG GTGCGGAG
                                    _ A__  G
GAM834  CTNNBIP1  3'  GGGACATTAGTCGTTATATTTG 39667          __ GT  C
           ACT                      GTCAGGTGTA  G  TG ATGTCTC
                                 |||||||||  |  || |||||||
```

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                                CAGTTTATAT  C  AT TACAGGG
                                      TG TG  _
GAM834  CTNNBIP1  3'  GGGATGGACTTGTGATTGGCT  39668       GTG     G  G
                                AGTCAG   TAGGTT CAT TC
                                ||||||   |||||| ||| ||
                                TCGGTT   GTTCAG GTA GG
                                   AGT     _  G
GAM834  CYLD      3'  GAGATGTACTGAGTTTGATT   30884      GG GTA   T    G
                                AGTCA  T   GGT GCAT TC
                                |||||  |   ||| |||| ||
                                TTAGT  G   TCA TGTA AG
                                   TT AG_  _    G
GAM834  DDX33     3'  GAGACATGTAAGCTTCCTGG   39375      TGT  G
                                TCAGG   AG TTGCATGTCTC
                                |||||   || ||||||||||
                                GGTCC   TC AATGTACAGAG
                                   T__  G
GAM834  DKFZP434A043 3'  GAACCAGCCTCATTTGATT    31191         T     CATG
                                AGTCAGGTG AGGTTG    TC
                                |||||||| ||||||    ||
                                TTAGTTTAC TCCGAC    AG
                                      _     CA__
GAM834  DKFZp434A2417 3'  GAGGCGTGAGCCACTGCACCTG 66102          __    G
           GC                     GTCAGGTGTA  GGTT CATGTCTC
                                |||||||||  |||| ||||||||
                                CGGTCCACGT  CCGA GTGCGGAG
                                      CA   _
GAM834  DKFZp434C0328 3'  ATGTGTGTGACTTGTTTTGATT 34130        TGT    TG  TG CTC
                                AGTCAGG   AGGT  CA  T
                                |||||||   ||||  ||  |
                                TTAGTTT   TTCA  GT  G
                                    TG_    GT  GT TAT
GAM834  DKFZp434E2220 3'  GAGATGTGAATATGACCTGGTT 34296    GT     GTAG   G
                                A  CAGGT    GTT CATGTCTC
                                |  |||||    ||| ||||||||
                                T  GTCCA    TAA GTGTAGAG
                                 TG     GTA_  _
GAM834  DKFZP434K2235 3'  CGGGACATGGCCACCTGACCTG 83497   TG     _____  _
           TGTGTGGCT                  TAGGTT    GC ATGTCTC   G
                                 ||||||    || |||||||  |
                                 GTCCAG    CG TACAGGG   C
                                GT     TCCAC  G
GAM834  DKFZP434N1511 5'  GGGGCAGGTCACGCTTGGGCCT 91420        G    _ _ A
           GGCT                    GTCAGGT TAGGT TG C TGTCTC
                                ||||||| ||||| || | ||||||
                                CGGTCCG GTTCG AC G ACGGGG
                                    G    C  T G
GAM834  DKFZp434O0320 3'  AGACCTGTGCACCTGGTT    83689    GT      AGGTT   T
                                A  CAGGTGT    GCA GTCT
                                |  |||||||    ||| ||||
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                                T  GTCCACG    TGT CAGA
                                TG      _____  C
GAM834  DKFZP547E2110 3'  GAGATGTTGGACAGCATTTGGT 90988   GT     AG  GC
           T                     A  CAGGTGT  GTT  ATGTCTC
                                 |  |||||||  |||  |||||||
                                 T  GTTTACG  CAG  TGTAGAG
                                 TG      A_  GT
GAM834  DKFZp547I224 5'  GACGAAATCTACGTCTGATT   39558      GT     GCAT
                                 AGTCAG  GTAGGTT   GTC
                                 ||||||  |||||||   |||
                                 TTAGTC  CATCTAA   CAG
                                    TG      AG__
GAM834  DKFZp547I224 5'  GAGATTATATCCCGCACCTGGC 39559        TA  TTGCAT
           T                     AGTCAGGTG  GG     GTCTC
                                 |||||||||  ||     |||||
                                 TCGGTCCAC  CC     TAGAG
                                       GC  TATAT_
GAM834  DKFZp547J036 3'  GAGACATGGTTATGCCT     50127        GTTG
                                 AGGTGTAG    CATGTCTC
                                 ||||||||    ||||||||
                                 TCCGTATT    GTACAGAG
                                      G___
GAM834  DKFZP564D0478 3'  GGGACATGTGTGCCCATCTGGC 49533        TA  _
                                 GTCAGGTG  GGT TGCATGTCTC
                                 ||||||||  ||| ||||||||||
                                 CGGTCTAC  CCG GTGTACAGGG
                                      __   T
GAM834  DKFZP564I1171 3'  GACCCTTGGGCCTGCATCTGAC 71588            G  T__   TC
           T                     AGTCAGGTGTAGGTT CA   GTC
                                 ||||||||||||||| ||   |||
                                 TCAGTCTACGTCCGG GT   CAG
                                           _  TCC
GAM834  DKFZP566G1424 5'  GATTGCTAGTCTGTGTCTGTCT 84785    T   TG   GT _   T
                                 AG CAGG  TAG  T GCA GTC
                                 || ||||  |||  | ||| |||
                                 TC GTCT  GTC  A CGT TAG
                                  T   GT   TG T  _
GAM834  DKFZP761F241 3'  GATAAATTATACCTGATT    48796          GTTGCA
                                 AGTCAGGTGTAG     TGTC
                                 ||||||||||||     ||||
                                 TTAGTCCATATT     ATAG
                                       AA_____
GAM834  DKFZp761G2113 3'  GATTGTGGCTCATGCCTGGTT  69904   GT     AG  TG  T
                                 A  CAGGTGT  GT  CA GTC
                                 |  |||||||  ||  || |||
                                 T  GTCCGTA  CG  GT TAG
                                  TG      CT  GT  _
GAM834  DKFZp761N0624 3'  GGGATACCTAATTTGCATTCGG 50181   GT AG        CA
           TT                    A  C  GTGTAGGTTG  TGTCTC
                                 |  |  ||||||||||  ||||||
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                                T  G  TACGTTTAAT  ATAGGG
                                 TG CT         CC
GAM834  DKK2     5'  GAGAAAGCGCCTCGCATTTGAT 27015          _    T  ATG
              T                   AGTCAGGTGT AGGT GC   TCTC
                                  |||||||||| |||| ||   ||||
                                  TTAGTTTACG TCCG CG   AGAG
                                        C    _  AA_
GAM834  DKK3     3'  GAGGTGTTGTGCATTTG     25131         GGTT    G
                                  CAGGTGTA    GCAT TC
                                  ||||||||    |||| ||
                                  GTTTACGT    TGTG AG
                                       GT__    G
GAM834  DNAJA2   3'  GTATCTGTGCTTGATT      59781         TG     T
                                  AGTCAGG  TAGGT GC
                                  |||||||  ||||| ||
                                  TTAGTTC  GTCTA TG
                                      GT    _
GAM834  DUSP9    3'  AGAGGATCTATGCTTG      7340             GCATG
                                  CAGGTGTAGGTT     TCT
                                  ||||||||||||     |||
                                  GTTCGTATCTAG     AGA
                                         G____
GAM834  EPN2     3'  GGACATGCAGGCTCTGA     30326      GTGT  G
                                  TCAG    AG TTGCATGTCT
                                  ||||    || ||||||||||
                                  AGTC    TC GACGTACAGG
                                     ____  G
GAM834  ERAL1    3'  GACATGAACACTGACT      62624        G   AGGTTG
                                  AGTCAG TGT     CATGTC
                                  |||||| |||     ||||||
                                  TCAGTC ACA     GTACAG
                                     _   A_____
GAM834  EREG     3'  GGGATAACAGTGTGCCTGGTT  7508    GT    TG  GG   CA
                                  A  CAGG  TA  TTG  TGTCTC
                                  |  ||||  ||  |||  ||||||
                                  T  GTCC  GT  GAC  ATAGGG
                                   TG    GT  __   A_
GAM834  EZF-2    5'  GACCCAGCCTGGACTTGACT   37101         G      CAT
                                  AGTCAGGT TAGGTTG   GTC
                                  |||||||| |||||||   |||
                                  TCAGTTCA GTCCGAC   CAG
                                       G      C__
GAM834  FADS1    3'  GGGATAGGTATGACCTATGTCT 25482    T    TG     __  A
              GCCT                    G CAGG  TAGGTT  GC TGTCTC
                                  |  ||||  ||||||  ||  ||||||
                                  C GTCT  ATCCAG  TG ATAGGG
                                   C    GT     TA  G
GAM834  FASTK    3'  GGGGTGGATGATTTGCACTTTG 46994    GT   _         CA GT
              GTT                     A  CAG GTGTAGGTTG  T  CTC
                                  |  ||| ||||||||||  |  |||
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                              T  GTT CACGTTTAGT  G  GGG
                               TG   T        AG TG
GAM834  FASTK    3'  GGGGTGGATGATTTGCACTTTG 52248    GT  _       CA GT
            GTT                  A  CAG GTGTAGGTTG  T  CTC
                              |  ||| ||||||||||  |  |||
                              T  GTT CACGTTTAGT  G  GGG
                               TG   T        AG TG
GAM834  FASTK    3'  GGGGTGGATGATTTGCACTTTG 22010    GT  _       CA GT
            GTT                  A  CAG GTGTAGGTTG  T  CTC
                              |  ||| ||||||||||  |  |||
                              T  GTT CACGTTTAGT  G  GGG
                               TG   T        AG TG
GAM834  FBXO21   3'  GGGGCCTGTCTCTGCACCTGTC 53239    T       TT   T
            T                   AG CAGGTGTAGG  GCA GTCTC
                              ||  ||||||||||  |||  |||||
                              TC GTCCACGTCT  TGT CGGGG
                               T        C_   C
GAM834  FLJ00001 3'  AGGCATGAAACTCTGGCT    81811       GTGTA    G
                              AGTCAG    GGTT CATGTCT
                              ||||||    ||||  |||||||
                              TCGGTC    TCAA GTACGGA
                                 _____   A
GAM834  FLJ10036 3'  GGGATAAATGCCTGAATTTGGT 94951    GT    G    TGCA
            T                   A  CAGGT TAGGT    TGTCTC
                              |  |||||  |||||   ||||||
                              T  GTTTA GTCCG    ATAGGG
                               TG    A    TAA_
GAM834  FLJ10422 3'  GAGGCCTGCAGGTGGCCTATTT 36114     T    ____    T
            TGACT                  AGG GTAGGT    TGCA GTCTC
                              |||  ||||||   ||||  |||||
                              TTT TATCCG    ACGT CGGAG
                                _     GTGG    C
GAM834  FLJ10477 3'  GATAATCTTGCACTTGACT    36153           TTGCA
                              AGTCAGGTGTAGG     TGTC
                              ||||||||||||     ||||
                              TCAGTTCACGTTC     ATAG
                                       TA___
GAM834  FLJ10483 3'  GAGGTGTGGTTCACATTTGGC  36171         AG TT    G
                              GTCAGGTGT  G  GCAT TC
                              |||||||||  |  ||||  ||
                              CGGTTTACA  T  TGTG AG
                                   CT GG    G
GAM834  FLJ10709 3'  GAGATGCATTTTCCGTCTGGCT 36464       GT T   T    G
                              AGTCAG  G AGG TGCAT TC
                              ||||||  | |||  |||||  ||
                              TCGGTC  C TTT ACGTA AG
                                 TG C   T    G
GAM834  FLJ10811 3'  GATCAGCAGCTTGTGCCTGGC  36683       TG       AT
                              GTCAGG  TAGGTTGC  GTC
                              ||||||  ||||||||  |||
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                                CGGTCC  GTTCGACG  TAG
                                   GT       AC
GAM834  FLJ10853  3' GAGATGTAGGTTACCTGATT   36768        TA G     G
                                AGTCAGGTG  G TTGCAT TC
                                |||||||||  | ||||||  ||
                                TTAGTCCAT  T GATGTA AG
                                     __ G     G
GAM834  FLJ10856  3' CATGTGACTTGTGTCTACT    36774     C   TG     TG
                                AGT AGG  TAGGT  CATG
                                |||  |||  |||||  ||||
                                TCA TCT  GTTCA  GTAC
                                  _  GT    GT
GAM834  FLJ11088  3' GGGTGTGTGTGGTGTATGCTTG 37040        G TT   TG _
                                CAGGTGTA G  GCA  T CTC
                                ||||||||  |  |||  | |||
                                GTTCGTAT T  TGT  G GGG
                                     G GG   GT T   G
GAM834  FLJ11181  3' TGGCCACATTTGACT       37139          A
                                AGTCAGGTGT GGTTG
                                ||||||||||  |||||
                                TCAGTTTACA CCGGT
                                     _
GAM834  FLJ11800  3' GAACTGCTGGTTTGTACCTGGC 46425          GG  _   TG  TC
           T                     AGTCAGGTGTA  TT GCA  TC
                                ||||||||||  ||  |||  ||
                                TCGGTCCATGT  GG CGT  AG
                                     TT  T   CA
GAM834  FLJ11800  3' GAGGTGTGTGCATTTCTGACT  46427       TGTAG  T    GT
                                AGTCAGG    GT GCAT  CTC
                                |||||||    ||  ||||  |||
                                TCAGTCT    CG TGTG  GAG
                                   TTA__  _    TG
GAM834  FLJ12122  3' GGGCAGCGCCCACGTCTGGCT  46463       GT  A   T  A    C
                                AGTCAG  GT GGT GC TGTCT
                                ||||||  ||  |||  ||  |||||
                                TCGGTC  CA CCG CG ACGGG
                                   TG  C   _  _    A
GAM834  FLJ12190  3' AGTAGGCCTGTGTCTGGC    46871       TG     GCATGT
                                GTCAGG  TAGGTT     CT
                                ||||||  ||||||     ||
                                CGGTCT  GTCCGG     GA
                                   GT     AT____
GAM834  FLJ12229  3' GGGCTTCCCAGTCTTGCCTGGC 45918         T  GT  CAT_   C
           T                     AGTCAGGTG AG  TG    GTCT
                                |||||||||  ||  ||    ||||
                                TCGGTCCGT TC  AC    CGGG
                                     _  TG  CCTT
GAM834  FLJ12242  3' GGGGCCCTCCTGTGTTTGACT  45182       TG    TTGCAT
                                AGTCAGG  TAGG     GTCTC
                                |||||||  ||||     |||||
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                                TCAGTTT  GTCC     CGGGG
                                    GT    TCC___
GAM834   FLJ12377  3'  TTTTACATGTAACATTATATTT 46488   GT       _       CTC
          GGTT                    CAGGTGTAG GTTGCATGT
                                  ||||||||| |||||||||
                                  GTTTATATT CAATGTACA
                                TG        A        TTTTG
GAM834   FLJ12586  3'  GAGGCGTGTCTTAGATCTGACT 44877        G    TT
                                AGTCAGGT TAGG  GCATGTCTC
                                |||||||| ||||  |||||||||
                                TCAGTCTA ATTC  TGTGCGGAG
                                    G   __
GAM834   FLJ12592  3'  GGGAGCAAGAATTTGACCTGGC 49699        G     GCA  _
          T                      AGTCAGGT TAGGTT   TG TCTC
                                |||||||| ||||||   || ||||
                                TCGGTCCA GTTTAA   AC AGGG
                                    _     GA_  G
GAM834   FLJ12604  3'  GGGACATGTAACCTGCTTCT   64439     T
                                AGG GTAGGTTGCATGTCTC
                                ||| ||||||||||||||||
                                TCT CGTCCAATGTACAGGG
                                  T
GAM834   FLJ12671  3'  GGTGTTGTGTCCTGTGTCTGGT 48282   GT   TG   T   _ GT TC
          T                      A  CAGG  TAGG TGCA T  C
                                |  ||||  |||| |||| |  |
                                T  GTCT  GTCC GTGT G  G
                                 TG   GT   T   T TG
GAM834   FLJ12783  3'  GGGACCCTGCCTACACCTCATT 48682     C        TGCAT
                                AGT AGGTGTAGGT    GTCTC
                                ||| ||||||||||    |||||
                                TTA TCCACATCCG    CAGGG
                                  C        TCC__
GAM834   FLJ13114  3'  GGGCCTGGGGCTGTGCTTGGCT 44602       TG   G  G  T
                                AGTCAGG  TAG TT CA GTCT
                                |||||||  ||| || || ||||
                                TCGGTTC  GTC GG GT CGGG
                                    GT   _  G  C
GAM834   FLJ13265  3'  GAGGTGGCACCTAGACTTGATT 45925        G    T  A GT
                                AGTCAGGT TAGGT GC T  CTC
                                |||||||| ||||| || |  |||
                                TTAGTTCA ATCCA CG G  GAG
                                    G    _ _ TG
GAM834   FLJ13340  3'  GGCTTTAGCATCTGACT     54107          __
                                AGTCAGGTGT  AGGTT
                                ||||||||||  |||||
                                TCAGTCTACG  TTCGG
                                      AT
GAM834   FLJ13391  5'  AGATATGTAGCGGCTGAC    49788      G   AGGT
                                GTCAG TGT    TGCATGTCT
                                ||||| |||    |||||||||
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                                CAGTC GCG    ATGTATAGA
                                   G  ____
GAM834  FLJ13855  3'  GAGATGTCTTTATATCTGACT  43588           TT    G
                                AGTCAGGTGTAGG  GCAT TC
                                ||||||||||||  |||| ||
                                TCAGTCTATATTT  TGTA AG
                                      C_    G
GAM834  FLJ14129  3'  GGGGCCCACCGTCTGCACTTGG 48069           TTGCAT
              C                  GTCAGGTGTAGG     GTCTC
                                ||||||||||||     |||||
                                CGGTTCACGTCT     CGGGG
                                      GCCACC
GAM834  FLJ14547  3'  GTAGCCACATCTGGTT      51437    GT      A
                                A  CAGGTGT GGTTGC
                                |  ||||||| ||||||
                                T  GTCTACA CCGATG
                                 TG      _
GAM834  FLJ14564  3'  GTGTCTGCACTTGGTT      76506    GT       GTT
                                A  CAGGTGTAG   GCAT
                                |  |||||||||   ||||
                                T  GTTCACGTC   TGTG
                                 TG       ___
GAM834  FLJ20060  5'  GCAGTTTTATCTGATT      34449          T GG
                                AGTCAGGTG A  TTGC
                                |||||||||  |  ||||
                                TTAGTCTAT T  GACG
                                      _ TT
GAM834  FLJ20060  3'  GGGATGTGTAGTCAAGATGAC  34450      GGTGTA GT
                                GTCA     G  TGCATGTCTC
                                ||||     |  ||||||||||
                                CAGT     C  ATGTGTAGGG
                                   AGAA__ TG
GAM834  FLJ20079  3'  GAGATATGCACTCTATTTTG   34493      T    GT
                                CAGG GTAG  TGCATGTCTC
                                |||| ||||  ||||||||||
                                GTTT TATC  ACGTATAGAG
                                   _    TC
GAM834  FLJ20128  3'  GTACCAGCAACCTGCTTCTGAC 34598         T       ATGTCTC
              T                  AGTCAGG GTAGGTTGC
                                |||||||  |||||||||
                                TCAGTCT CGTCCAACG
                                     T        ACCATG
GAM834  FLJ20130  3'  TCTATATGTGTAATTTATGTCT 34606     C   TG          CTC
              TACT                 AGT AGG  TAGGTTGCATGT
                                ||| |||  ||||||||||||
                                TCA TCT  ATTTAATGTGTA
                                  T   GT          TATCTC
GAM834  FLJ20294  3'  CAGCCTGGCTTGGCT       34872         G
                                AGTCAGGT TAGGTTG
                                ||||||||  |||||||
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                                TCGGTTCG GTCCGAC
                                   _
GAM834  FLJ20296 3' GGGACAGGAAATGCCTGTGTCT 34892      TG    TGCA__
           GGC                  GTCAGG  TAGGT     TGTCTC
                                |||||| |||||     ||||||
                                CGGTCT  GTCCG     ACAGGG
                                   GT    TAAAGG
GAM834  FLJ20300 3' GAAGTGATGTAGCTTGCCCTGA 34908       T        GT  C
           TT                   AGTCAGG GTAGGTTGCAT  CT
                                ||||||| |||||||||||  ||
                                TTAGTCC CGTTCGATGTA  GA
                                   _        GT  AGG
GAM834  FLJ20308 3' ATGTCTGCACTTGGTT     66853   GT       GTT
                                A  CAGGTGTAG   GCAT
                                |  |||||||||   ||||
                                T  GTTCACGTC   TGTA
                                 TG       ___
GAM834  FLJ20371 3' GCAGCCTGTGCTGGCT     35060      G TG
                                AGTCA G  TAGGTTGC
                                ||||| |  ||||||||
                                TCGGT C  GTCCGACG
                                   _ GT
GAM834  FLJ20373 3' GGGGCTTCCTGGTCTGTGCTTT 35073     C   TG    TT CAT_
           ACT                    AGT AGG  TAGG  G    GTCTC
                                ||| |||  ||||  |    |||||
                                TCA TTC  GTCT  T    CGGGG
                                  T   GT    GG CCTT
GAM834  FLJ20400 3' ATGCAGTTTCTGCTTGACT    66511        GT GG
                                AGTCAGGT  A  TTGCAT
                                ||||||||  |  ||||||
                                TCAGTTCG  T  GACGTA
                                     TC TT
GAM834  FLJ20651 3' GAGATGTGTAGAAACGTTGG   35497     _  GTAGG
                                TCAG GT    TTGCATGTCTC
                                |||| ||    ||||||||||
                                GGTT CA    GATGTGTAGAG
                                   G  AA___
GAM834  FLJ20700 3' AAACATGGCAGCTTGGCCTGGT 35567   GT    G      _    CTC
           T                    A  CAGGT TAGGTTGC ATGT
                                |  ||||| |||||||| ||||
                                T  GTCCG GTTCGACG TACA
                                 TG    _       G    AAG
GAM834  FLJ21016 3' GGGGCCAAACATTTACACCTTG 47180     C        TGCAT
           CT                    AGT AGGTGTAGGT    GTCTC
                                ||| ||||||||||    |||||
                                TCG TCCACATTTA    CGGGG
                                  T        CAAAC
GAM834  FLJ21032 3' GAGATGTGCAATAAATATTTG  46089        AG
                                CAGGTGT  GTTGCATGTCTC
                                |||||||  ||||||||||||
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                                GTTTATA  TAACGTGTAGAG
                                    AA
GAM834  FLJ21103  3'  TGTACTCTATACTTGGTT    44648   GT       GT
                                A  CAGGTGTAG  TGCA
                                |  |||||||||  ||||
                                T  GTTCATATC  ATGT
                                 TG        TC
GAM834  FLJ21313  3'  GAGGCATGTGACTGAAGTACT  43684     TA__   TG
                                GGTG   GGT  CATGTCTC
                                ||||   |||  ||||||||
                                TCAT   TCA  GTACGGAG
                                  GAAG   GT
GAM834  FLJ21369  3'  GAGTTCAGGTGTTATGCCTGAT 45636          GT   A  T_
          T                      AGTCAGGTGTAG  TGC TG  CTC
                                ||||||||||||  ||| ||  |||
                                TTAGTCCGTATT  GTG AC  GAG
                                      __   G  TT
GAM834  FLJ21478  3'  AGGCAGATGCACCTGACT    44869          GGTTGCA
                                AGTCAGGTGTA      TGTCT
                                ||||||||||       |||||
                                TCAGTCCACGT      ACGGA
                                      AG_____
GAM834  FLJ22009  3'  TGTATTTTATATTTGATT    60286           T
                                AGTCAGGTGTAGG TGCA
                                |||||||||||| ||||
                                TTAGTTTATATTT ATGT
                                       T
GAM834  FLJ22167  5'  GCAACCGCGCCTGGCT      44575          A
                                AGTCAGGTGT GGTTGC
                                |||||||||| ||||||
                                TCGGTCCGCG CCAACG
                                      _
GAM834  FLJ22601  3'  CATGTAGTGTACATTTGATT   45694          GG
                                AGTCAGGTGTA  TTGCATG
                                ||||||||||  |||||||
                                TTAGTTTACAT  GATGTAC
                                      GT
GAM834  FLJ22794  5'  GAGAATAGTAGCTTATATATGG 91607      G         ATG
          CT                     AGTCA GTGTAGGTTGC   TCTC
                                ||||| ||||||||||   ||||
                                TCGGT TATATTCGATG   AGAG
                                   A          ATA
GAM834  FLJ22843  3'  GAGATGTGAAGATGTTTGGCT  47227       TG AGG TG   G
                                AGTCAGG  T   T  CAT TC
                                |||||||  |   |  ||| ||
                                TCGGTTT  A   A  GTA AG
                                    GT GA_ GT   G
GAM834  FLJ22938  3'  GGGACCGCGGCCTGACCTGGCT 45163        G       AT
                                AGTCAGGT TAGGTTGC  GTCTC
                                |||||||| ||||||||  |||||
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                                TCGGTCCA GTCCGGCG  CAGGG
                                   _       C_
GAM834  FLJ23191  3'  GAGAAGTTGTGACCTGTACTTG 44709    _        TG  TG_
            TACT                  GT CAGGTGTAGGT  CA   TCTC
                                || ||||||||||  ||   ||||
                                CA GTTCATGTCCA  GT   AGAG
                                 T         GT  TGA
GAM834  FLJ23309  3'  GAGGTGGTTTTCTATGCCTG   46063          TT  A GT
                                CAGGTGTAGG  GC T  CTC
                                |||||||||  || |  |||
                                GTCCGTATCT  TG G  GAG
                                      TT  _ TG
GAM834  FLJ23360  3'  GGGAGCCCCGCCTGCGCTTGGC 43571            T__  ATG
                                GTCAGGTGTAGGT   GC   TCTC
                                ||||||||||||   ||   ||||
                                CGGTTCGCGTCCG   CG   AGGG
                                       CCC  ___
GAM834  FLJ23451  3'  TGTGACTTGAATTTGACT    45433         G     TG
                                AGTCAGGT TAGGT  CA
                                |||||||| |||||  ||
                                TCAGTTTA GTTCA  GT
                                    A     GT
GAM834  FLJ23506  3'  AGACTTACCTGTGTTGATT    45744       G TG     TGCAT
                                AGTCA G  TAGGT    GTCT
                                ||||| |  |||||    ||||
                                TTAGT T  GTCCA    CAGA
                                   _ GT    TT___
GAM834  FLJ23548  3'  CAGCTTGCACCTCATT      44747     C
                                AGT AGGTGTAGGTTG
                                ||| ||||||||||||
                                TTA TCCACGTTCGAC
                                  C
GAM834  FLJ23563  3'  TCTTTTGTGATTTTACTTGATT 67603          T    TG  TGTCTC
                                AGTCAGGTG AGGT  CA
                                |||||||| ||||  ||
                                TTAGTTCAT TTTA  GT
                                     _   GT  TTTCTA
GAM834  FLJ32356  3'  GGGACCAGGTCTTGCTTGGCT  58365          T  GT GCAT
                                AGTCAGGTG AG  T    GTCTC
                                |||||||| ||  |    |||||
                                TCGGTTCGT TC  G    CAGGG
                                     _  TG AC__
GAM834  FLJ32783  3'  GATTGTGGTCTATGTTTGAT   58644       TG    TT   T
                                GTCAGG  TAGG  GCA GTC
                                ||||||  ||||  ||| |||
                                TAGTTT  ATCT  TGT TAG
                                   GT    GG  _
GAM834  FOXJ1     3'  GGGGCGTGGGGCGTGCCTTGCT 7575     T    T   G   G
                                AG CAGG GTA GTT CATGTCTC
                                || |||| ||| ||| ||||||||
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                                TC GTTC CGT CGG GTGCGGGG
                                 _   _   G   G
GAM834  FUSIP1   3'  CACCACATGCAGTTTACATCTG 21772    T       GG       CTC
           TCT                    AG CAGGTGTA  TTGCATGT
                                || ||||||||  ||||||||
                                TC GTCTACAT  GACGTACA
                                 T       TT       CCACA
GAM834  GGA2     3'  GAGAAGGAACCTGAGCCTGGCT 56880        G     GCATG
                                AGTCAGGT TAGGTT    TCTC
                                |||||||| ||||||    ||||
                                TCGGTCCG GTCCAA    AGAG
                                     A     GGA__
GAM834  GGA2     3'  GAGAAGGAACCTGAGCCTGGCT 30466        G     GCATG
                                AGTCAGGT TAGGTT    TCTC
                                |||||||| ||||||    ||||
                                TCGGTCCG GTCCAA    AGAG
                                     A     GGA__
GAM834  GHITM    3'  ATGTGGTCATGTTTGACT    26915        TG A  TT
                                AGTCAGG  T GG  GCAT
                                |||||||  | ||  ||||
                                TCAGTTT  A CT  TGTA
                                     GT _  GG
GAM834  GOLPH3   3'  GAGAAAAGATGTGTGTCTGATT 42112        TG  G   GCATG
                                AGTCAGG  TA GTT    TCTC
                                |||||||  || |||    ||||
                                TTAGTCT  GT TAG    AGAG
                                     GT  G   AAA__
GAM834  GREB1    3'  GGAAGAATCTCACTTGACT    27882         T    GCATG
                                AGTCAGGTG AGGTT    TCT
                                |||||||||| |||||    |||
                                TCAGTTCAC TCTAA    AGG
                                     _    GA___
GAM834  GTPBP1   3'  GAGACAATCCTGCGTTTGCCT  15014    T  GG     TTGCA
                                AG CA  TGTAGG    TGTCTC
                                || ||  ||||||    ||||||
                                TC GT  GCGTCC    ACAGAG
                                 C  TT     TA___
GAM834  HARS2    3'  GAGGTATGTGGTATTGATTTGT 55034    T    GTAG TT   GT
           CT                     AG CAGGT   G  GCAT  CTC
                                || |||||   |  ||||  |||
                                TC GTTTA   T  TGTA  GAG
                                 T    GTTA GG   TG
GAM834  HBP1     3'  GGGGCAGACTTTGCACTTACT  24313     C      _  GCA
                                AGT AGGTGTAG GTT   TGTCTC
                                ||| |||||||| |||   ||||||
                                TCA TTCACGTT CAG   ACGGGG
                                  _       T   ____
GAM834  HCA4     3'  GGTATTAACTTATACCTG    77588           C  GT
                                CAGGTGTAGGTTG AT  C
                                ||||||||||||| ||  |
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                                GTCCATATTCAAT TA  G
                                       _ TG
GAM834  HN1      3'  GAGAACTGCACAACTTGAGCCT 32462        G    __   TG
            GACT                   GTCAGGT TAGGT  TGCA  TCTC
                                   ||||||| |||||  ||||  ||||
                                   CAGTCCG GTTCA  ACGT  AGAG
                                       A    AC    CA
GAM834  HSA9761  3'  AGACATTATTTACTTGACT   27124         TAGGT  C
                                   AGTCAGGTG    TG ATGTCT
                                   |||||||||    || ||||||
                                   TCAGTTCAT    AT TACAGA
                                        TT___  _
GAM834  HSPC009  3'  GAGGTGTGCATGCGACCGTGGC 25829      _  _  GGT    GT
            T                       AGTCA GGT GTA   TGCAT  CTC
                                   ||||| ||| |||   |||||  |||
                                   TCGGT CCA CGT   ACGTG  GAG
                                      G  G  ___     TG
GAM834  HSPC216  3'  GAGTGTCAACTATCTGCATCTG 33211         ___   _  GTCTC
            GCT                      CAGGTGTAG   GTTG CAT
                                   |||||||||   |||| |||
                                   GTCTACGTC   CAAC GTG
                                        TAT    T   AG   C
GAM834  HTCD37   3'  GGGGTATGTGATGGTTTTGGC  67677       TGTAG  TG   GT
                                   GTCAGG    GT  CAT  CTC
                                   ||||||    ||  |||  |||
                                   CGGTTT    TA  GTA  GGG
                                       TGG__  GT   TG
GAM834  HTGN29   3'  GGGATTCATTTATGTCTGTCT  39507    T   TG    TGCAT
                                   AG CAGG  TAGGT    GTCTC
                                   || ||||  |||||    |||||
                                   TC GTCT  ATTTA    TAGGG
                                    T   GT    CT___
GAM834  HUMGT198A 3'  GAGATGTCTTGCACTGGCT   33331       G     TT   G
                                   AGTCAG TGTAGG  GCAT TC
                                   |||||| ||||||  |||| ||
                                   TCGGTC ACGTTC  TGTA AG
                                      _     __    G
GAM834  HUMGT198A 3'  GAGATGTCTTGCACTGGCT   25234       G     TT   G
                                   AGTCAG TGTAGG  GCAT TC
                                   |||||| ||||||  |||| ||
                                   TCGGTC ACGTTC  TGTA AG
                                      _     __    G
GAM834  HYA22    3'  GGGACATGCATTTTAC      19427       T
                                   GTAGG TGCATGTCTC
                                   ||||| ||||||||||
                                   CATTT ACGTACAGGG
                                      T
GAM834  ICAM4    3'  GGGATGTTCTATGCCGGCT    7750       A       TT   G
                                   AGTC GGTGTAGG  GCAT TC
                                   |||| ||||||||  |||| ||
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                                TCGG CCGTATCT  TGTA GG
                                  _      __   G
GAM834  ICAM4    3'  GGGATGTTCTATGCCGGCT   42354     A      TT   G
                                AGTC GGTGTAGG  GCAT TC
                                |||| ||||||||  |||| ||
                                TCGG CCGTATCT  TGTA GG
                                  _      __   G
GAM834  ICK      3'  GAGATGGAATTTTGTGCCTAGC 29929    TC   TG   _ G   G  TC
           T                     AG  AGG  TAGG TT CAT TC
                                ||  |||  |||| || ||| ||
                                TC  TCC  GTTT AA GTA AG
                                 GA   GT    T G   G
GAM834  IFI44    5'  GGGCATTTTGTGCCTGCCT   21180    T    TG    TTGC
                                AG CAGG  TAGG    ATGTCT
                                || ||||  ||||    ||||||
                                TC GTCC  GTTT    TACGGG
                                 C   GT   _____
GAM834  IL10RB   3'  GAGATGTTACATCTGG     5278          GGTT    G
                                TCAGGTGTA    GCAT TC
                                |||||||||    |||| ||
                                GGTCTACAT    TGTA AG
                                     _____   G
GAM834  IMP-2    3'  CAACTTACACTTGGTT     21568    GT
                                A  CAGGTGTAGGTTG
                                |  ||||||||||||
                                T  GTTCACATTCAAC
                                 TG
GAM834  INA      3'  GGGAATGATATGCATTTGACT  51188          GGTTG   G
                                AGTCAGGTGTA     CAT TCTC
                                ||||||||||     ||| ||||
                                TCAGTTTACGT    GTA AGGG
                                      ATA__   _
GAM834  INA      3'  GGGTGTGCATGCGCCTACT    51189     C      GGT    GT
                                AGT AGGTGTA   TGCAT  CT
                                ||| |||||||   |||||  ||
                                TCA TCCGCGT   ACGTG  GG
                                  _      ___     TG
GAM834  INSM2    3'  GCAACTTGTTTTTGATT     50866        TG
                                AGTCAGG  TAGGTTGC
                                |||||||  ||||||||
                                TTAGTTT  GTTCAACG
                                    TT
GAM834  ITGA10   3'  GACCAGCAGCCTGACTTGACT  59378         G       AT
                                AGTCAGGT TAGGTTGC  GTC
                                |||||||| ||||||||  |||
                                TCAGTTCA GTCCGACG  CAG
                                     _       AC
GAM834  JM11     3'  GGGAAACTGTGATCTCATCTGG 53266    GT     T    TG  TG_
           TT                     A  CAGGTG AGGT  CA   TCTC
                                |  |||||| ||||  ||   ||||
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                                T  GTCTAC TCTA  GT   AGGG
                                 TG     _    GT  CAA
GAM834  KIAA0014  3'  GAGGCCTGCACCTGCGTCTAAC 27844     C  GT     T   T
            T                    AGT AG  GTAGGT GCA GTCTC
                                 ||| ||  |||||| ||| |||||
                                 TCA TC  CGTCCA CGT CGGAG
                                   A  TG     _   C
GAM834  KIAA0016  3'  GAGGTGTGCTGCTGTGCTGGGT 28646   GT A  TG   GTT    GT
            T                    A  C GG  TAG   GCAT  CTC
                                 |  | ||  |||   ||||  |||
                                 T  G TC  GTC   CGTG  GAG
                                  TG G  GT   GT_    TG
GAM834  KIAA0057  3'  GACGCAGTAGCTTACGCCTG   24426            A_
                                 CAGGTGTAGGTTGC  TGTC
                                 ||||||||||||||  ||||
                                 GTCCGCATTCGATG  GCAG
                                          AC
GAM834  KIAA0057  3'  GGGATGTGCCAGGTGCCTGC   24438    T    TG AGGTT
                                 G CAGG  T     GCATGTCTC
                                 | ||||  |     |||||||||
                                 C GTCC  G     CGTGTAGGG
                                  _    GT GAC__
GAM834  KIAA0064  3'  GGGATGGGCAGAGGTCTGTGTT 28544      TG    ___    AT
            TGG                     CAGG  TAGG   TTGC  GTCTC
                                 ||||  ||||   ||||  |||||
                                 GTTT  GTCT   GACG  TAGGG
                                   GT    GGA    GG
GAM834  KIAA0125  5'  GGGAATGGCGCTGGCATCTGGC 28900          A   T  ATG
            T                    AGTCAGGTGT GGT GC   TCTC
                                 ||||||||||  ||| ||   ||||
                                 TCGGTCTACG TCG CG   AGGG
                                       G   _  GTA
GAM834  KIAA0125  5'  GGGGTATGTGACTGCCTCTGTG 28901     _    T    G TG   GT
            CT                    AGT CAGG GTAG T  CAT  CTC
                                 ||| |||| |||| |  |||  |||
                                 TCG GTCT CGTC A  GTA  GGG
                                   T    C    _ GT   TG
GAM834  KIAA0179  3'  GGGGTTGCAGAGCTTGCATTGG 64828   GT AG       __    TGT
            GTT                     C  GTGTAGGT  TGCA   CTC
                                  |  ||||||||  ||||   |||
                                  G  TACGTTCG  ACGT   GGG
                                 TG GT       AG    TG_
GAM834  KIAA0186  3'  GACATACTAATTTATCATCTGG 40750          _      C_    TC
            CT                    AGTCAGGTG TAGGTTG  ATGTC
                                 |||||||||  |||||||  |||||
                                 TCGGTCTAC ATTTAAT  TACAG
                                       T      CA
GAM834  KIAA0237  3'  GGGCATGCGGCCACTGG     28532      GTGTA
                                 TCAG    GGTTGCATGTCT
                                 ||||    ||||||||||||
```

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                                GGTC    CCGGCGTACGGG
                                  A____
GAM834  KIAA0237 3' GGGGCTGGACTGGCCTGGTCTG 28534     GTG    GCAT__
            GCT                   GTCAG   TAGGTT    GTCTC
                                |||||  ||||||    |||||
                                CGGTC  GTCCGG    CGGGG
                                  TG_    TCAGGT
GAM834  KIAA0256 5' GAGGCGCTGTTTACACCGACT  64421     A      TT  AT
                                AGTC GGTGTAGG  GC  GTCTC
                                |||| ||||||||  ||  |||||
                                TCAG CCACATTT  CG  CGGAG
                                  _      GT  __
GAM834  KIAA0276 3' GGACATGTTGGTGTTTGCT   70965    T   TG AGGTT
                                AG CAGG  T    GCATGTCT
                                || ||||  |    ||||||||
                                TC GTTT  G    TGTACAGG
                                 _   GT GT___
GAM834  KIAA0316 3' GAACCAAGCAGCCCATGCCTGG 69672         A     A  TC
            CT                  AGTCAGGTGT GGTTGC TG  TC
                                ||||||||||  ||||||  ||  ||
                                TCGGTCCGTA CCGACG AC  AG
                                     C     A  CA
GAM834  KIAA0317 3' GGGGCATGCCTAGGCATATGGC 29088      G    AGGTT
            T                   AGTCA GTGT    GCATGTCTC
                                |||||  ||||    |||||||||
                                TCGGT TACG    CGTACGGGG
                                  A    GATC_
GAM834  KIAA0356 3' GGGTCACACTCTCTGCCTGACT 66194       GT  GT  CA  T
                                AGTCAGGT  AG  TG  TG CTC
                                ||||||||  ||  ||  || |||
                                TCAGTCCG  TC  AC  AC GGG
                                    TC  TC  __  T
GAM834  KIAA0390 3' GGGTATTACTGCTTGTGTCTGA 28202       TG    TGC_  GT  C
            TT                  AGTCAGG  TAGGT    AT  CT
                                |||||||  |||||   ||  ||
                                TTAGTCT  GTTCG    TA  GG
                                   GT    TCAT  TG
GAM834  KIAA0435 3' GGGGCAGCTTCATGACCGATGT 28979    TG A   _____  A
            CTGGCT                GG  T GGTT    GC TGTCTC
                                ||  | ||||    || ||||||
                                CT  A CCAG    CG ACGGGG
                                 GT G    TACTT  _
GAM834  KIAA0446 3' GAGACGTGTGACCTGGATGAT  68868     GGTG    TG
                                GTCA    TAGGT  CATGTCTC
                                ||||    |||||  ||||||||
                                TAGT    GTCCA  GTGCAGAG
                                  AG__    GT
GAM834  KIAA0447 3' GGCTAGTTCTGTGTCTGGCT   71673       TG   TT  AT
                                AGTCAGG  TAGG  GC  GTC
                                |||||||  ||||  ||  |||
```

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                                TCGGTCT  GTCT  TG  CGG
                                    GT   __  AT
GAM834  KIAA0449  3'  GGATGTGTGGCCTGGGC    34202   G   TG
                                GT TAGGT  CATGTCT
                                || |||||  |||||||
                                CG GTCCG  GTGTAGG
                                 G    GT
GAM834  KIAA0483  3'  GATCAATTCTATGTCTGACT  30791      TG  _  CAT
                                AGTCAGG  TAGG TTG  GTC
                                |||||||  |||| |||  |||
                                TCAGTCT  ATCT AAC  TAG
                                    GT   T  ___
GAM834  KIAA0493  3'  AGGAAAACCTGATTTGGCT   64268       G    GCATG
                                AGTCAGGT TAGGTT    TCT
                                |||||||| ||||||    |||
                                TCGGTTTA GTCCAA    GGA
                                   _     AA___
GAM834  KIAA0494  3'  GAGCCTGTGACTTGTATTTAGC 28743   TC       TG  T T
          T                      AG  AGGTGTAGGT  CA G CTC
                                ||  ||||||||||  || | |||
                                TC  TTTATGTTCA  GT C GAG
                                 GA        GT  C _
GAM834  KIAA0523  3'  GCCTCCTTGCCTGGCT     67738        T   TT
                                AGTCAGGTG AGG  GC
                                |||||||| |||  ||
                                TCGGTCCGT TCC  CG
                                    _  TC
GAM834  KIAA0543  3'  GACAGCTGGCCTGGCT     68934       GTAGGTT  A
                                AGTCAGGT      GC TGTC
                                ||||||||      || ||||
                                TCGGTCCG      CG ACAG
                                    GT_____  _
GAM834  KIAA0552  3'  GGGAGCAGATGGCCTGCCTTTG 28318       T      CA  _
          GCT                     AGTCAGG GTAGGTTG  TG TCTC
                                ||||||| ||||||||  || ||||
                                TCGGTTT CGTCCGGT  AC AGGG
                                    C       AG  G
GAM834  KIAA0626  5'  GTGATTGCATTTGATT     67441          G TG
                                AGTCAGGTGTAG T  C
                                ||||||||||| |  |
                                TTAGTTTACGTT A  G
                                    _ GT
GAM834  KIAA0628  3'  AGGGCATTGACACCTGGCT   28862        AGGT   ATG
                                AGTCAGGTGT   TGC   TCT
                                ||||||||||   |||  |||
                                TCGGTCCACA   ACG   GGA
                                    GTT_  ___
GAM834  KIAA0628  3'  GGACAGTGATCATATCTGATT  28874         A   TG A    C
                                AGTCAGGTGT GGT  C TGTCT
                                |||||||||| |||  | |||||
```

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                                TTAGTCTATA CTA  G ACAGG
                                      _  GT _    A
GAM834  KIAA0633  5' GGCGGTAGCCAGCGCCTGACT  94054         A     A
                                AGTCAGGTGT GGTTGC TGTC
                                |||||||||| |||||| ||||
                                TCAGTCCGCG CCGATG GCGG
                                     A    _
GAM834  KIAA0672  3' AGGCTCACTTTGCCTGGTT   29405   GT    T   TGCAT
                                A  CAGGTG AGGT    GTCT
                                |  |||||| ||||    ||||
                                T  GTCCGT TTCA    CGGA
                                 TG    _   CT___
GAM834  KIAA0672  3' GGGATGTGCAGAGTTTTGAT   29414       TGTAGG
                                GTCAGG     TTGCATGTCTC
                                ||||||     ||||||||||
                                TAGTTT     GACGTGTAGGG
                                    TGA___
GAM834  KIAA0674  5' GTGGCCTATACCGGCT     60616     A       TG
                                AGTC GGTGTAGGT  C
                                |||| |||||||||  |
                                TCGG CCATATCCG  G
                                  _       GT
GAM834  KIAA0720  3' GGGGCGTGCCGGCACCTGCT   62326    T     AGGTT
                                AG CAGGTGT    GCATGTCTC
                                || |||||||    |||||||||
                                TC GTCCACG    CGTGCGGGG
                                 _     GC___
GAM834  KIAA0757  3' ATGTTTTACATTTGATT     20126           TT
                                AGTCAGGTGTAGG  GCAT
                                ||||||||||||  ||||
                                TTAGTTTACATTT  TGTA
                                      __
GAM834  KIAA0757  3' GAGGCGGAGGCCTGCACTTGAC 20132           GCA
                                GTCAGGTGTAGGTT   TGTCTC
                                ||||||||||||||   ||||||
                                CAGTTCACGTCCGG   GCGGAG
                                      AG_
GAM834  KIAA0757  3' GCAAGTTTAAGTCTGGCT    20133       TG   _
                                AGTCAGG  TAGG TTGC
                                |||||||  |||| ||||
                                TCGGTCT  ATTT AACG
                                    GA   G
GAM834  KIAA0763  3' GGGCGAAGCTCACGCCTGACT  29535         AG   GCAT
                                AGTCAGGTGT  GTT   GTCT
                                ||||||||||  |||   ||||
                                TCAGTCCGCA  CGA   CGGG
                                      CT   AG__
GAM834  KIAA0767  3' GCCGCCTGCGCTGGGCT     60627     A       T
                                AGTC GGTGTAGGT GC
                                |||| ||||||||| ||
```

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                                TCGG TCGCGTCCG CG
                                  G       C
GAM834  KIAA0841 3' GGATGTGTGATTTGAATTG   71392    GTG    TG
                                CAG   TAGGT  CATGTCT
                                |||   |||||  |||||||
                                GTT   GTTTA  GTGTAGG
                                  AA_    GT
GAM834  KIAA0884 3' GCATCTTACATTTGATT     70204           T
                                AGTCAGGTGTAGG TGC
                                |||||||||||| |||
                                TTAGTTTACATTC ACG
                                        T
GAM834  KIAA0892 3' GAGGCGTGCTTCCTTCCTGATT 71011       TGT   TT
                                AGTCAGG   AGG  GCATGTCTC
                                |||||||   |||  |||||||||
                                TTAGTCC   TCC  CGTGCGGAG
                                    T__   TT
GAM834  KIAA0892 3' GCACCACGCCTGACT      71012         A   T
                                AGTCAGGTGT GGT GC
                                |||||||||| ||| ||
                                TCAGTCCGCA CCA CG
                                        _  _
GAM834  KIAA0940 3' GAGGTGTTCTGACCTGCAACTT 29870      _     ___    G  TC
          GACT                    CAGGT GTAGGTT   GCAT TC
                                |||||| |||||||   |||| ||
                                GTTCA CGTCCAG   TGTG AG
                                   A      TCT    G
GAM834  KIAA0982 3' AGGCTGCCTGTGTTGGCT    25843      G TG    TGCAT
                                AGTCA G  TAGGT    GTCT
                                ||||| |  |||||    ||||
                                TCGGT T  GTCCG    CGGA
                                   _ GT    T____
GAM834  KIAA0993 3' GCGTCTTGTACCTGGCT     64142           T
                                AGTCAGGTGTAGG TGC
                                |||||||||||| |||
                                TCGGTCCATGTTC GCG
                                        T
GAM834  KIAA1001 3' GAGGTGTGCTTCTCATCATGAC 30291      _   T   TT    GT
          T                      AGTCA GGTG AGG  GCAT  CTC
                                ||||| |||| |||  ||||  |||
                                TCAGT CTAC TCT  CGTG  GAG
                                   A    _   T_    TG
GAM834  KIAA1010 3' GAGGCAGTGCTTGCACATGGCT 72072      G       TGCA
                                AGTCA GTGTAGGT    TGTCTC
                                ||||| ||||||||    ||||||
                                TCGGT CACGTTCG    ACGGAG
                                   A       TG__
GAM834  KIAA1023 3' GAGGCGTGCAGCCTCTGGGC   34261     A  TGT
                                GTC GG   AGGTTGCATGTCTC
                                ||| ||   ||||||||||||||
```

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                                CGG TC   TCCGACGTGCGGAG
                                  G ___
GAM834  KIAA1029 3' GAGCTACCATGTGACTTTACCT 23474       T   TG   T___
            GATT                  TCAGGTG AGGT  CATG   CTC
                                |||||||| ||||  ||||   |||
                                AGTCCAT TTCA  GTAC   GAG
                                   _   GT   CATC
GAM834  KIAA1036 3' GGGGCATGGTGACCCTTGACT  29825       TGTA  TG _
                                AGTCAGG   GGT  C ATGTCTC
                                |||||||   |||  | |||||||
                                TCAGTTC   CCA  G TACGGGG
                                   _____  GT G
GAM834  KIAA1068 3' GAGATGCCCTGCACCT     31032         TT   G
                                AGGTGTAGG  GCAT TC
                                |||||||||  |||| ||
                                TCCACGTCC  CGTA AG
                                    __   G
GAM834  KIAA1086 3' CAGCCTGCATGTGGCT     70742      G
                                AGTCA GTGTAGGTTG
                                ||||| ||||||||||
                                TCGGT TACGTCCGAC
                                  G
GAM834  KIAA1096 3' GAGGCTTTGCAAGCTTGTACCT 68530    C        _  T_
            ACT                   GT AGGTGTAGGTT GCA  GTCTC
                                || ||||||||||| |||  |||||
                                CA TCCATGTTCGA CGT  CGGAG
                                 _         A   TT
GAM834  KIAA1145 3' GCAACCAACACCTGATT     65624          A
                                AGTCAGGTGT GGTTGC
                                |||||||||| ||||||
                                TTAGTCCACA CCAACG
                                     A
GAM834  KIAA1171 3' GAGGGTGGGATTTGTGCTGGGC 87982      A  TG     G   G
            T                   AGTC GG  TAGGTT CAT TCTC
                                |||| ||  |||||| ||| ||||
                                TCGG TC  GTTTAG GTG GGAG
                                  G  GT     G  _
GAM834  KIAA1191 3' GTGTTAACTTACTTTGATT    39960        T      _
                                AGTCAGG GTAGGTTG CAT
                                ||||||| |||||||| |||
                                TTAGTTT CATTCAAT GTG
                                   _       T
GAM834  KIAA1209 3' GAGGTGTGTGTAAGTGCATTTG 60756        GGT_    GT
                                CAGGTGTA    TGCAT  CTC
                                ||||||||    |||||  |||
                                GTTTACGT    GTGTG  GAG
                                     GAAT    TG
GAM834  KIAA1237 3' GGGCAAAACAACTTATATTTGG 80473   GT          CA_    C
            TT                   A  CAGGTGTAGGTTG   TGTCT
                                |  ||||||||||||   |||||
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                                T  GTTTATATTCAAC   ACGGG
                                 TG          AAA
GAM834  KIAA1240  3'  ATGTTTTGCATTTGACT     66730           TT
                                AGTCAGGTGTAGG  GCAT
                                ||||||||||||  ||||
                                TCAGTTTACGTTT  TGTA
                                      __
GAM834  KIAA1272  3'  GAGGAATCTGATCTGCATTGAT 70175       G       C  GT
          T                      AGTCAG TGTAGGTTG AT  CTC
                                ||||||| |||||||| ||  |||
                                TTAGTT ACGTCTAGT TA  GAG
                                   _       C  AG
GAM834  KIAA1274  3'  GAGGCTGTCCACCTTGCTTGGC 91364         T   T_  T
          T                      AGTCAGGTG AGGT  GCA GTCTC
                                ||||||||| ||||  ||| |||||
                                TCGGTTCGT TCCA  TGT CGGAG
                                     _   CC  _
GAM834  KIAA1322  3'  GAGGCTGCCTCTGTGTGTGGTT 72737   GT  G TG   TT  T
                                A  CA G  TAGG  GCA GTCTC
                                |  || |  ||||  ||| |||||
                                T  GT T  GTCT  CGT CGGAG
                                 TG  G GT   C_  _
GAM834  KIAA1361  3'  GGGATGTCATAGTACTTGGCT  62197         TAG  T   G
                                AGTCAGGTG   GT GCAT TC
                                |||||||||   || |||| ||
                                TCGGTTCAT   TA TGTA GG
                                     GA_  C   G
GAM834  KIAA1371  3'  GAGAAAAATAACTTACCCTGGT 89044   GT   T      CATG
          T                      A  CAGG GTAGGTTG   TCTC
                                |  |||| |||||||||   ||||
                                T  GTCC CATTCAAT   AGAG
                                 TG   _       AAAA
GAM834  KIAA1373  3'  GTGGAATTTCATTTGGCT    70949         T    G
                                AGTCAGGTG AGGTT CAT
                                ||||||||| ||||| |||
                                TCGGTTTAC TTTAA GTG
                                     _    G
GAM834  KIAA1388  5'  GTGGGTTGCATCTGACT     93580           G TG
                                AGTCAGGTGTAG T  C
                                ||||||||||||| |  |
                                TCAGTCTACGTT G  G
                                      G GT
GAM834  KIAA1431  3'  GAGACGTCATTTCTGTTTGACT 62998        TG   T_  C
                                AGTCAGG  TAGG  TG ATGTCTC
                                |||||||  ||||  || |||||||
                                TCAGTTT  GTCT  AC TGCAGAG
                                   __   TT  _
GAM834  KIAA1458  3'  GATTTTAACTTATGTTTGAT   69004       TG     CAT
                                GTCAGG  TAGGTTG   GTC
                                ||||||  |||||||   |||
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                                TAGTTT  ATTCAAT   TAG
                                   GT      TT_
GAM834  KIAA1484  3'  GGGGCCCATTTCTTGTATCTGG 69978           TTGCAT
              CT                  AGTCAGGTGTAGG     GTCTC
                                  ||||||||||||     |||||
                                  TCGGTCTATGTTC     CGGGG
                                        TTTACC
GAM834  KIAA1577  5'  GAGGCATGCGATCTCCACTGGC 64478       G  T
                                  GTCAG TG AGGTTGCATGTCTC
                                  ||||| || ||||||||||||||
                                  CGGTC AC TCTAGCGTACGGAG
                                     _  C
GAM834  KIAA1579  3'  CAATTGACGCCTGATT      36603          AG
                                  AGTCAGGTGT  GTTG
                                  ||||||||||  ||||
                                  TTAGTCCGCA  TAAC
                                        GT
GAM834  KIAA1594  3'  GGGGCATTACTGTCACCTGACT 72086         _  GTTGC
                                  AGTCAGGTG TAG    ATGTCTC
                                  ||||||||| |||    |||||||
                                  TCAGTCCAC GTC    TACGGGG
                                       T  AT___
GAM834  KIAA1600  3'  GGGCACAGCATGCTTGTACTTG 71445           _  A_    C
              ATT                   GTCAGGTGTAGGT TGC  TGTCT
                                  ||||||||||||| |||  |||||
                                  TAGTTCATGTTCG ACG  ACGGG
                                        T  AC
GAM834  KIAA1622  3'  AGACAAGTCTGCATTT      54259        GT GCA
                                  AGGTGTAG  T   TGTCT
                                  ||||||||  |   |||||
                                  TTTACGTC  A   ACAGA
                                       TG ___
GAM834  KIAA1649  3'  GAGGTCAGTTTGTTCCTGGCT  66978       TG  GG   C  G
                                  AGTCAGG  TA  TTG AT TC
                                  |||||||  ||  ||| || ||
                                  TCGGTCC  GT  GAC TG AG
                                       TT  TT   _  G
GAM834  KIAA1655  5'  GAGCACAGGTGACCTGCATTGA 66609       G      TG A  _
              TT                   AGTCAG TGTAGGT  C TGT CTC
                                  |||||| |||||||  | ||| |||
                                  TTAGTT ACGTCCA  G ACA GAG
                                     _      GT G   C
GAM834  KIAA1655  5'  GAGGCATGTGTCACACCGGCT  66610     A    AGGT
                                  AGTC GGTGT    TGCATGTCTC
                                  |||| |||||    ||||||||||
                                  TCGG CCACA    GTGTACGGAG
                                     _    CT__
GAM834  KIAA1656  3'  GACCTGTGTCTGCGTTTGGCT  65795      GG    GTT   T
                                  AGTCA  TGTAG   GCA GTC
                                  |||||  |||||   ||| |||
```

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                                TCGGT  GCGTC   TGT CAG
                                   TT    TG_  C
GAM834  KIAA1656 3' GGGACAACCAGACCTGTGTCTG 65802   T   TG    GCA_
            C                   G CAGG  TAGGTT   TGTCTC
                                | ||||  ||||||   ||||||
                                C GTCT  GTCCAG   ACAGGG
                                _   GT    ACCA
GAM834  KIAA1666 3' GGGATGTGAGGGTGATCTGGCT 65251       GTAGGTTG
                                AGTCAGGT      CATGTCTC
                                ||||||||      ||||||||
                                TCGGTCTA      GTGTAGGG
                                    GTGGGA__
GAM834  KIAA1677 3' GTAGTCTATATCTGAT     67071          GT
                                GTCAGGTGTAG  TGC
                                ||||||||||  |||
                                TAGTCTATATC  ATG
                                      TG
GAM834  KIAA1678 3' GAGTATTCCGTAACCTATATTT 72305    C         AT_ _
            TACT                GT AGGTGTAGGTTGC   GT CTC
                                || ||||||||||||   || |||
                                CA TTTATATCCAATG   TA GAG
                                 T          CCT  T
GAM834  KIAA1691 3' GAGACTGGGCAGCTGTGTCTGG 92555   GT   TG   G   AT_
            TT                   A  CAGG  TAG TTGC   GTCTC
                                |  ||||  ||| ||||   |||||
                                T  GTCT  GTC GACG   CAGAG
                                 TG   GT   _   GGT
GAM834  KIAA1701 3' GACATTTGGCTACATCTGGCT  67818          G   C
                                AGTCAGGTGTAG TTG ATGTC
                                |||||||||||| ||| |||||
                                TCGGTCTACATC GGT TACAG
                                      _  T
GAM834  KIAA1719 3' GGATGTGCTTTGCCTGGC    68168        TAGGTT
                                GTCAGGTG     GCATGTCT
                                ||||||||     ||||||||
                                CGGTCCGT     CGTGTAGG
                                    TT____
GAM834  KIAA1754 3' GATCCAGTCTGTACTTGA    63237         GT  CAT
                                TCAGGTGTAG  TG   GTC
                                ||||||||||  ||   |||
                                AGTTCATGTC  AC   TAG
                                     TG  C__
GAM834  KIAA1755 3' GAGAACTGTCGACCTGCCCCTG 61346       T      _ TG
            GCT                   AGTCAGG GTAGGTTG CA  TCTC
                                ||||||| |||||||| ||  ||||
                                TCGGTCC CGTCCAGC GT  AGAG
                                   C       T  CA
GAM834  KIAA1789 5' ATGATTTTATATTTGGCT    67100           TTG
                                AGTCAGGTGTAGG   CAT
                                ||||||||||||   |||
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                                TCGGTTTATATTT  GTA
                                       TA_
GAM834  KIAA1795 3' GAGAAAATTAATTTGTGCTTGC 72151   T   TG     CATG
            T                   AG CAGG  TAGGTTG   TCTC
                                || ||||  |||||||   ||||
                                TC GTTC  GTTTAAT   AGAG
                                 _   GT     TAAA
GAM834  KIAA1814 3' GGACATGGCGTGCCTGGC   70363      TG AG  TG
                                GTCAGG  T  GT  CATGTCT
                                ||||||  |  ||  |||||||
                                CGGTCC  G  CG  GTACAGG
                                   GT __  __
GAM834  KIAA1829 3' GATCTGTTCTATACCTGGCT  61949          TT   T
                                AGTCAGGTGTAGG  GCA GTC
                                ||||||||||||  ||| |||
                                TCGGTCCATATCT  TGT TAG
                                       __  C
GAM834  KIAA1867 5' ACAGGCAGTTTGTGTCGGCT  94821     A  TG  GG   A
                                AGTC GG  TA  TTGC TGT
                                ||||  ||  ||  |||| |||
                                TCGG CT  GT  GACG ACA
                                  _  GT  TT   G
GAM834  KIAA1872 3' AGATATGTGGACCTCACT    62922     T  _ TG
                                GGTG AGG T  CATGTCT
                                ||||  ||| |  |||||||
                                TCAC TCC G  GTATAGA
                                  _  A GT
GAM834  KIAA1878 3' GACGTGCTTGTGGTCTGTGCTT 91712     TG   GT ____     TC
            GCT                   CAGG  TAG  T   GCATGTC
                                ||||  |||  |   |||||||
                                GTTC  GTC  G   CGTGCAG
                                  GT   TG TGTT
GAM834  KIAA1904 3' GCAGCCTTGCCTGGCT      73489         T
                                AGTCAGGTG AGGTTGC
                                |||||||||  |||||||
                                TCGGTCCGT TCCGACG
                                       _
GAM834  KIAA1951 3' AGGCATGCACAATCTGG     73757       GTAGGT
                                TCAGGT     TGCATGTCT
                                ||||||     |||||||||
                                GGTCTA     ACGTACGGA
                                   AC____
GAM834  KIAA1958 3' AGACAGATTGCGCTTGAT    81900          GTTGCA
                                GTCAGGTGTAG     TGTCT
                                ||||||||||     |||||
                                TAGTTCGCGTT     ACAGA
                                      AG____
GAM834  KIAA1979 3' GCCATCGTGGTGTGTGCTTGAC 88282       TG  G TT  _   TCTC
            T                   AGTCAGG  TA G  GC ATG
                                |||||||  || |  || |||
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                                TCAGTTC  GT T  TG TAC
                                    GT  G GG  C   CG
GAM834  KIF1C    3'  GGGGTGCTGCGTAGCCAGTGTT 61226      TG A  __   _ GT
            TGACT                   CAGG  T GGT  TGCA T  CTC
                                |||| | |||  |||| |  |||
                                GTTT  G CCG  GCGT G  GGG
                                  GT A   AT    C TG
GAM834  KLHL6    3'  GAGATTTCTGTTTATGCCAGAT 55304      A     GG TGCAT
            T                    AGTC GGTGTA  T    GTCTC
                                |||| ||||||  |    |||||
                                TTAG CCGTAT  G    TAGAG
                                  A     TT TCTT_
GAM834  KLHL8    3'  GAATCAATCTGCATTT      62855           CATG
                                AGGTGTAGGTTG   TC
                                ||||||||||||   ||
                                TTTACGTCTAAC   AG
                                       TA__
GAM834  KPNA6    3'  GGATCCTTGTACCTGGTT    24610   GT       TTGCAT
                                A  CAGGTGTAGG     GTCT
                                |  ||||||||||     ||||
                                T  GTCCATGTTC     TAGG
                                 TG        C_____
GAM834  KREMEN2  5'  GAGGGTGACCTATCCTTGGTT  44455   GT   TG    TG ATG
                                A  CAGG  TAGGT  C   TCTC
                                |  ||||  |||||  |  ||||
                                T  GTTC  ATCCA  G   GGAG
                                 TG   CT    GT ___
GAM834  LANO     3'  GATTTTAACCTGTGTCTTACT  36623     C   TG      CAT
                                AGT AGG  TAGGTTG   GTC
                                ||| |||  |||||||   |||
                                TCA TCT  GTCCAAT   TAG
                                  T   GT      TT_
GAM834  LBP-32   3'  GAGGCGGGGCTGCATCTGGCT  27275           G  GCA
                                AGTCAGGTGTAG TT   TGTCTC
                                ||||||||||| ||   ||||||
                                TCGGTCTACGTC GG   GCGGAG
                                       G  ___
GAM834  LDHL     3'  ATATATATGTAGTTGGCATTTG 52600    GT      AG       CTC
            GTT                   A  CAGGTGT  GTTGCATGT
                                |  |||||||  |||||||||
                                T  GTTTACG  TGATGTATA
                                 TG      GT       TATAT
GAM834  LEAP-2   5'  GAGGTATCTCATCCCTATGCCT 53743          T_  C_  GT
            G                    CAGGTGTAGG  TG  AT  CTC
                                ||||||||||  ||  ||  |||
                                GTCCGTATCC  AC  TA  GAG
                                      CT  TC  TG
GAM834  LENG5    3'  GAGAATGGGGCCTGGGTTTGAT 78483      GG G     G   G
            T                    AGTCA  T TAGGTT CAT TCTC
                                |||||  | |||||| ||| ||||
```

```
                                TTAGT  G GTCCGG GTA AGAG
                                  TT G     G  _
GAM834  LGALS8   5'  GGGATGTGCGGTGACCACCCTG 21450      T  A   ___
           G                     TCAGG GT GGTT   GCATGTCTC
                                 |||||| || ||||   |||||||||
                                 GGTCC CA CCAG   CGTGTAGGG
                                   _ _   TGG
GAM834  LHX6     3'  GGTATTCGATCTGTGCCATGAC 26860      _ TG      C  GT TC
           T                     AGTCA GG  TAGGTTG AT  C
                                 |||||| ||  ||||||| ||  |
                                 TCAGT CC  GTCTAGC TA  G
                                   A  GT      T  TG
GAM834  LRBA     3'  TGTAGTCTTTGCTTGACT    22054         T  GT
                                 AGTCAGGTG AG  TGCA
                                 |||||||||| ||  ||||
                                 TCAGTTCGT TC  ATGT
                                      T  TG
GAM834  LRP15    5'  GGGCAGCTCGGCTTGCAACTGG 53668   GT   G       CA_    C
           TT                     A  CAG TGTAGGTTG   TGTCT
                                 |  ||| |||||||||   |||||
                                 T  GTC ACGTTCGGC   ACGGG
                                  TG   A       TCG
GAM834  LW-1     5'  GGGCTTTGCTGTAGTTGTGCCT 32370      TG   GTT__   T_   C
           GGCT                    TCAGG  TAG    GCA  GTCT
                                 |||||  |||    |||  ||||
                                 GGTCC  GTT    CGT  CGGG
                                    GT   GATGT   TT
GAM834  LW-1     5'  GGGCTTTGCTGTAGTTGTGCCT 60261      TG   GTT__   T_   C
           GGCT                    TCAGG  TAG    GCA  GTCT
                                 |||||  |||    |||  ||||
                                 GGTCC  GTT    CGT  CGGG
                                    GT   GATGT   TT
GAM834  MAN1     3'  AGATATATACATATGGCT    26710      G    GGTTGC
                                 AGTCA GTGTA     ATGTCT
                                 ||||| |||||     ||||||
                                 TCGGT TACAT     TATAGA
                                    A    A_____
GAM834  MAN1     3'  TGTAATCTACAATTGGCT    26717       G
                                 AGTCAG TGTAGGTTGCA
                                 |||||| ||||||||||
                                 TCGGTT ACATCTAATGT
                                     A
GAM834  MAP2K4   3'  GAGACATTGCTCTATGTCTGCC 11550    T   TG   TT  _
           T                     AG CAGG  TAGG  GCA TGTCTC
                                 || ||||  ||||  ||| ||||||
                                 TC GTCT  ATCT  CGT ACAGAG
                                  C   GT   __   T
GAM834  MEGF10   3'  GAGGTGGTTTTCTCTGTTTGAC 50583      GG GT   TT  A GT
           T                     AGTCA  T  AGG  GC T  CTC
                                 |||||  |  |||  || |  |||
```

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                                TCAGT  G  TCT  TG G  GAG
                                   TT TC   TT  _ TG
GAM834  MEIS3    3' GACCCCCAGCCTCACACCTGGC 78281          _     CAT   TC
           T                    AGTCAGGTGT AGGTTG   GTC
                                |||||||||| ||||||   |||
                                TCGGTCCACA TCCGAC   CAG
                                     C      CCC
GAM834  MGC10200 3' GAGACAGTTTATCATCTGATT  58986         TAGGTT  A
                                AGTCAGGTG     GC TGTCTC
                                |||||||||     || ||||||
                                TTAGTCTAC     TG ACAGAG
                                     TATT__  _
GAM834  MGC10854 3' GGGGCGTGTGGTTTCCTG    50205      TGT GG TG
                                CAGG   A  T  CATGTCTC
                                ||||   |  |  ||||||||
                                GTCC   T  G  GTGCGGGG
                                  ___ TT GT
GAM834  MGC10966 5' GGGCGTGGCACCTGCACT    48898         T  _
                                GGTGTAGGT GC ATGTCT
                                ||||||||| || ||||||
                                TCACGTCCA CG TGCGGG
                                     _  G
GAM834  MGC10992 3' GGGACGGCATCGGCCTGCACCT 52627           ___   A
           GAC                    TCAGGTGTAGGT   TGC TGTCTC
                                  |||||||||||   ||| ||||||
                                  AGTCCACGTCCG   ACG GCAGGG
                                       GCT   _
GAM834  MGC11287 3' GAAAGCGCAGCCTGTACATGAC 48832       G          ATGTCTC
           T                     AGTCA GTGTAGGTTGC
                                 |||||  ||||||||||
                                 TCAGT CATGTCCGACG
                                    A          CGAAAG
GAM834  MGC12928 5' GAGAAAAGTTGACCTGTGCTGA 51836       G TG      _ ATG
           CT                     AGTCA G  TAGGTTG C   TCTC
                                  |||||  |  |||||||  |   ||||
                                  TCAGT C  GTCCAGT G   AGAG
                                    _ GT      T AAA
GAM834  MGC14595 5' GGGGCGTGCGTGAGGCGTTTAC 50332     C GG   AGGT
           T                     AGT A  TGT    TGCATGTCTC
                                 |||  |  |||    ||||||||||
                                 TCA T  GCG    GCGTGCGGGG
                                   _ TT   GAGT
GAM834  MGC15631 3' GAGGCATGGCCAGCATCTGCT  51264    T      A   TG
                                AG CAGGTGT GGT  CATGTCTC
                                || ||||||| |||  ||||||||
                                TC GTCTACG CCG  GTACGGAG
                                  _      A  ___
GAM834  MGC17330 3' GGGAAATTGCTCTGCATTTGAC 53529           TT   TG_
           T                     AGTCAGGTGTAGG  GCA   TCTC
                                 ||||||||||||  |||   ||||
```

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                                TCAGTTTACGTCT  CGT   AGGG
                                       __   TAA
GAM834  MGC17919  3'  GGCATGTCTGCAATTTACATTG 58222     G         ____    TC
          ACT                    CAG TGTAGGTTGCA    TGTC
                                 ||| ||||||||||    ||||
                                 GTT ACATTTAACGT    ACGG
                                   _          CTGT
GAM834  MGC19556  3'  GAGGAAAACTTGTCATCTGGCT 53229          _     GCATG
                                 AGTCAGGTG TAGGTT    TCTC
                                 |||||||||| ||||||    ||||
                                 TCGGTCTAC GTTCAA    GGAG
                                       T     AA___
GAM834  MGC20235  3'  ACAGATGTGAGCCTGTGCCTGG 58890        TG     G      C
          CT                     AGTCAGG  TAGGTT CATGTCT
                                 |||||||  |||||| |||||||
                                 TCGGTCC  GTCCGA GTGTAGA
                                    GT     _      CAT
GAM834  MGC20235  3'  GAGAGCTGTAGTTTTATCTGGC 58896         T GG     TG
          T                      AGTCAGGTG A  TTGCA  TCTC
                                 ||||||||| |  |||||  ||||
                                 TCGGTCTAT T  GATGT  AGAG
                                    _ TT    CG
GAM834  MGC2306   3'  GAGGCTGCCTCCGCACCTGACT 50960          A  TT   T
                                 AGTCAGGTGT GG  GCA GTCTC
                                 |||||||||| ||  ||| |||||
                                 TCAGTCCACG CC  CGT CGGAG
                                       _ TC  _
GAM834  MGC2474   3'  GCAACACTATGCCTGGTT    43725   GT       _
                                 A  CAGGTGTAG GTTGC
                                 |  ||||||||| |||||
                                 T  GTCCGTATC CAACG
                                  TG        A
GAM834  MGC25056  3'  GGGAAGCCCAGCCTGCATCTAG 79117    TC          CATG
          CT                     AG  AGGTGTAGGTTG    TCTC
                                 ||  ||||||||||||    ||||
                                 TC  TCTACGTCCGAC    AGGG
                                  GA           CCGA
GAM834  MGC2560   3'  GGTCATAGTTTTACATCTGATT 48784           TT  _   T
                                 AGTCAGGTGTAGG  GC ATG CT
                                 ||||||||||||  || ||| ||
                                 TTAGTCTACATTT  TG TAC GG
                                       __  A   T
GAM834  MGC27044  5'  GGGGTAGACCTTGTACCGGCT  58674     A  GT_    GC  G
                                 AGTC GGT   AGGTT  AT TC
                                 |||| |||   |||||  || ||
                                 TCGG CCA   TCCAG  TG GG
                                    _  TGT    A_  G
GAM834  MGC27434  3'  TAATCTCCATTTGGCT      58950          T
                                 AGTCAGGTG AGGTTG
                                 |||||||| ||||||
```

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                                TCGGTTTAC TCTAAT
                                     C
GAM834  MGC3047  3' GGGCTGGGGCTACATTTGGCT  50363          G  G  T
                                AGTCAGGTGTAG TT CA GTCT
                                |||||||||||| || || ||||
                                TCGGTTTACATC GG GT CGGG
                                      _  G  _
GAM834  MGC3130  3' GAGGTGTGGCCTATTGTACCT  43820     ___     TG   G  TC
                                AGGT   GTAGGT  CAT TC
                                ||||   ||||||  ||| ||
                                TCCA   TATCCG  GTG AG
                                  TGT     GT   G
GAM834  MGC3178  3' GGGATGTGGATACTTGGC    47990         AGG TG   G
                                GTCAGGTGT   T  CAT TC
                                |||||||||   |  ||| ||
                                CGGTTCATA   G  GTA GG
                                     ___ GT   G
GAM834  MGC3184  3' TTAGCATGCAATTGGTATTTGA 48236         TA        CTC
           CT                     AGTCAGGTG  GGTTGCATGT
                                |||||||||  ||||||||||
                                TCAGTTTAT  TTAACGTACG
                                     GG         ATTG
GAM834  MGC32043 3' GGGCACAGACCTGCATTTG   58054           GCA
                                CAGGTGTAGGTT   TGTCT
                                ||||||||||||   |||||
                                GTTTACGTCCAG   ACGGG
                                       AC_
GAM834  MGC4549  3' GGGGCCTGAACTGATCTCACTT 50465       TA___    G  T
           GGCT                    TCAGGTG     GGTT CA GTCTC
                                |||||||     |||| || |||||
                                GGTTCAC     TCAA GT CGGGG
                                     TCTAG    _  C
GAM834  MGC4655  3' GGGATATGCAAGGGGCTCTGGC 52803       T  AGG
                                GTCAGG GT   TTGCATGTCTC
                                ||||||  ||   ||||||||||
                                CGGTCT CG   AACGTATAGGG
                                    _  GGG
GAM834  MGC4796  3' GAGCAGCGAGCCTGCGTCTGTC 61487    T   GT      _  A  T
           T                     AG CAG  GTAGGTT GC TG CTC
                                || |||  ||||||| || || |||
                                TC GTC  CGTCCGA CG AC GAG
                                  T   TG      G  _  _
GAM834  MGC4796  3' GAGGCCTTTCTAGACCTGGCT  61488         G    TTGCAT
                                AGTCAGGT TAGG      GTCTC
                                ||||||||  ||||     |||||
                                TCGGTCCA ATCT      CGGAG
                                     G    TTC___
GAM834  MGC5590  3' GCATGTAGTCTGTCTCTGATT  43925       TG   GT
                                AGTCAGG  TAG  TGCATGT
                                |||||||  |||  |||||||
```

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                                TTAGTCT  GTC  ATGTACG
                                    CT   TG
GAM834  MGC9753   5'  CAGCCTGTACCTGCT      53047    T
                                AG CAGGTGTAGGTTG
                                || |||||||||||||
                                TC GTCCATGTCCGAC
                                 _
GAM834  MIL1      3'  GGGGCATTCACATTCATCTGAC 31094          TAG  T C
           T                     AGTCAGGTG   GT G ATGTCTC
                                 |||||||||   || | |||||||
                                 TCAGTCTAC   CA C TACGGGG
                                      TTA  _ T
GAM834  MMD       3'  GGGACATATACTTGACCTAGCT 59808    TC    G    TGC
                                AG  AGGT TAGGT   ATGTCTC
                                ||  |||| |||||   |||||||
                                TC  TCCA GTTCA   TACAGGG
                                 GA   _    TA_
GAM834  MO25      3'  GAGATGTATACATTTG      32810        GGT    G
                                CAGGTGTA   TGCAT TC
                                ||||||||   ||||| ||
                                GTTTACAT   ATGTA AG
                                    ___     G
GAM834  MR        5'  GGGGTGTGAGCTGCATTT    48322        G TG   G
                                AGGTGTAG T  CAT TC
                                |||||||| |  ||| ||
                                TTTACGTC A  GTG GG
                                     G GT   G
GAM834  MRPL10    3'  GGGAGTGTGTTTGTCACTTGGT 59154    GT     TAGGT    G
           T                     A  CAGGTG    TGCAT TCTC
                                 |  ||||||    ||||| ||||
                                 T  GTTCAC    GTGTG AGGG
                                  TG     TGTTT    _
GAM834  MRPL14    5'  GGGGCGAAGGCGGCGCTTGGCT 49503          AG   GCA
                                AGTCAGGTGT  GTT   TGTCTC
                                ||||||||||  |||   ||||||
                                TCGGTTCGCG  CGG   GCGGGG
                                     G_   AA_
GAM834  MRPL48    5'  GGGATATTGCTGCTGCACCTGG 32135          GTT   _
                                TCAGGTGTAG   GCA TGTCTC
                                ||||||||||   ||| ||||||
                                GGTCCACGTC   CGT ATAGGG
                                     GT_   T
GAM834  MVD       3'  GGGACATGTGGGTGGTGGCTTG 10144        GTAGG_ TG
           AC                     GTCAGGT     T  CATGTCTC
                                  |||||||     |  ||||||||
                                  CAGTTCG     G  GTACAGGG
                                      GTGGTG GT
GAM834  N4BP3     3'  GAGGCGTGTGCACTGTCTGCT  66262    T   TG   GT
                                AG CAGG  TAG  TGCATGTCTC
                                || ||||  |||  ||||||||||
```

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                                TC GTCT  GTC  GTGTGCGGAG
                                 _   __  AC
GAM834  NET-2    3'  TGTGTAGCCTGTGTATGACT  24707      G TG
                                AGTCA G  TAGGTTGCATG
                                ||||| |  ||||||||||
                                TCAGT T  GTCCGATGTGT
                                   A GT
GAM834  NICN1    3'  GGGGTGCTCTGTCTTCGCCTGG 50293        T  TT__   G  TC
           CT                    AGTCAGGTG AGG   GCAT TC
                                |||||||| |||   |||| ||
                                TCGGTCCGC TCT   CGTG GG
                                     T  GTCT   G
GAM834  NINJ2    3'  GGGACAGGGGTCTGGGTTTGGC 33287      GG G  GT GCA
           T                     AGTCA  T TAG  T  TGTCTC
                                ||||| | ||| |  ||||||
                                TCGGT  G GTC  G  ACAGGG
                                   TT G  TG GG_
GAM834  NIR3     3'  GGGGTCCAGCCTGCATCT    66243          C  G
                                AGGTGTAGGTTG AT TC
                                |||||||||||| || ||
                                TCTACGTCCGAC TG GG
                                       C  G
GAM834  NKX2C    3'  GACCCTGGCCGCGCTTGGTT  59220   GT     A    CAT
                                A  CAGGTGT GGTTG  GTC
                                |  ||||||| |||||  |||
                                T  GTTCGCG CCGGT  CAG
                                 TG      _    CC_
GAM834  NY-REN-60 5'  GACACAGCAGTCTAACATCTGG 67109   GT     _ GT  A_   TC
           TT                    A  CAGGTGT AG  TGC  TGTC
                                |  ||||||| ||  |||  ||||
                                T  GTCTACA TC  ACG  ACAG
                                 TG      A  TG  AC
GAM834  NYD-SP15  5'  GGGCCGAGATCATGTCTGACT  48111       TG A   GCAT
                                AGTCAGG  T GGTT   GTCT
                                |||||||  | ||||   ||||
                                TCAGTCT  A CTAG   CGGG
                                    GT _   AGC_
GAM834  PABPC5   3'  AGATTCTCTACATTTCACT   55070    C      TTGCAT
                                AGT AGGTGTAGG     GTCT
                                ||| |||||||||     ||||
                                TCA TTTACATCT     TAGA
                                  C       CT____
GAM834  PADI1    3'  GAGACATGCACAGGCAGGCTGG 61996   GT  G_  AG  T
           TT                    A  CAG  TGT  GT GCATGTCTC
                                |  |||  |||  || |||||||||
                                T  GTC  ACG  CA CGTACAGAG
                                 TG  GG  GA  _
GAM834  PAI-RBP1 3'  GGGACATGTTAAACTTTGATT  31585       T  AGGTT
                                AGTCAGG GT    GCATGTCTC
                                ||||||| ||    |||||||||
```

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                                TTAGTTT CA    TGTACAGGG
                                   _ AAT__
GAM834  PASK    5'  GGGATGTAGCACCATGCCTGGC 30723         A  T  _
          T                     AGTCAGGTGT GGT GC ATGTCTC
                                |||||||||| ||| || |||||||
                                TCGGTCCGTA CCA CG TGTAGGG
                                      _  _  A
GAM834  PCDH10  3'  CTTAAATGTAGTCAGTGTTTGA 51989       TG A GT    GTCTC
          TT                     AGTCAGG  T G  TGCAT
                                 |||||||  | |  |||||
                                 TTAGTTT  G C  ATGTA
                                    GT A TG    AATTCG
GAM834  PDE10A  3'  GGGGTGGGGGGGAACCTGCACCT 21865          GCA__ GT
          GG                     TCAGGTGTAGGTT    T  CTC
                                 ||||||||||||    |  |||
                                 GGTCCACGTCCAA    G  GGG
                                       GGGGG TG
GAM834  PDE2A   5'  GAGGTGCCACCTTAGTCTGGCT 10472       TGT   T   G
                                 AGTCAGG   AGGT GCAT TC
                                 |||||||   |||| |||| ||
                                 TCGGTCT   TCCA CGTG AG
                                    GAT   C   G
GAM834  PFTK1   3'  GAGGCATGACCTTTGTATTTCA 24757    C    T__   TG
          CT                     AGT AGGTG   AGGT  CATGTCTC
                                 ||| |||||   ||||  ||||||||
                                 TCA TTTAT   TCCA  GTACGGAG
                                   C    GTT   __
GAM834  PI4KII  3'  GAGATGTGCAGCCCTCTGG   37344      TGTA
                                 TCAGG   GGTTGCATGTCTC
                                 |||||   ||||||||||||
                                 GGTCT   CCGACGTGTAGAG
                                    C___
GAM834  PIP5K2B  3'  GGGATGTGCTGTGTGTGCACCT 13076   T      G TT__
          GCT                     G CAGGTGTA G   GCATGTCTC
                                 | ||||||| |   |||||||||
                                 C GTCCACGT T   CGTGTAGGG
                                 _      G GTGT
GAM834  PJA1    5'  GACTTGGTCTACACCTGAC   42323          TT CAT
                                 GTCAGGTGTAGG  G   GTC
                                 ||||||||||| |   |||
                                 CAGTCCACATCT  T   CAG
                                       GG T__
GAM834  PLP1    3'  GGGGCATCTGGCCTTACACCT  5008       _    C
                                 AGGTGTA GGTTG ATGTCTC
                                 ||||||| ||||| |||||||
                                 TCCACAT CCGGT TACGGGG
                                    T    C
GAM834  POLE3   3'  GTCAGCCTATGTTTGATT    33857       TG     _
                                 AGTCAGG  TAGGTTG C
                                 |||||||  ||||||| |
```

```
                                TTAGTTT  ATCCGAC G
                                    GT       T
GAM834  PREI3    3'  GAGTTAGTGGTGGCTTATACCT 66322          TG _  GT_
                                AGGTGTAGGT  C AT   CTC
                                ||||||||||  | ||   |||
                                TCCATATTCG  G TG   GAG
                                     GT G  ATT
GAM834  PRO0159  5'  ATGTAGCCTATTCTGACT    26109        T
                                AGTCAGG GTAGGTTGCAT
                                ||||||| ||||||||||
                                TCAGTCT TATCCGATGTA
                                   _
GAM834  PRO0159  3'  GAAAATCAGTCTATTGCCTGGC 26111          _  GT  CATG  TC
           T                     AGTCAGGTG TAG  TG    TC
                                |||||||| |||  ||    ||
                                TCGGTCCGT ATC  AC    AG
                                     T   TG  TAAA
GAM834  PRO0800  3'  GAGACAAACATTGCTTTGGCT  37740        T   _  GCA
                                AGTCAGG GTAG GTT   TGTCTC
                                ||||||| |||| |||   ||||||
                                TCGGTTT CGTT CAA   ACAGAG
                                   _   A   ___
GAM834  PRO0800  3'  GAGACAGGAATTACCTATATTT 37741    C        TGCA__
           CATT                   GT AGGTGTAGGT     TGTCTC
                                || ||||||||||     ||||||
                                TA TTTATATCCA     ACAGAG
                                 C         TTAAGG
GAM834  PRPF8    3'  GGAAGTTCTGCGTTTGACT   61193      GG     TTGCATG
                                AGTCA  TGTAGG      TCT
                                |||||  ||||||      |||
                                TCAGT  GCGTCT      AGG
                                   TT     TGA____
GAM834  QKI      3'  GGGATGCATTCATTTGATT   65445         TAGGT    G
                                AGTCAGGTG    TGCAT TC
                                |||||||||    ||||| ||
                                TTAGTTTAC    ACGTA GG
                                     TT___     G
GAM834  Rab11-FIP2 3'  GATTATTGACTTATAGTTGATT 29780        G        CAT
                                AGTCAG TGTAGGTTG   GTC
                                ||||||| |||||||||  |||
                                TTAGTT ATATTCAGT   TAG
                                   G        TAT
GAM834  RENT2    3'  GATGGTTCACTTGACT      54590         TAGGTT  A
                                AGTCAGGTG     GC TGTC
                                |||||||||     || ||||
                                TCAGTTCAC     TG GTAG
                                     T_____  _
GAM834  RENT2    3'  GATGGTTCACTTGACT      31419         TAGGTT  A
                                AGTCAGGTG     GC TGTC
                                |||||||||     || ||||
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                                TCAGTTCAC     TG GTAG
                                     T_____ _
GAM834  RHO6     5'  GAGGCAGGGAATCTGGCTTGAT 27123        G     GCA
           T                      AGTCAGGT TAGGTT   TGTCTC
                                  |||||||| ||||||   ||||||
                                  TTAGTTCG GTCTAA   ACGGAG
                                     _     GGG
GAM834  RPS27L   3'  GATAATGTAATTACATTTGGTT 31925   GT       G    _
                                  A  CAGGTGTAG TTGCAT GTC
                                  |  ||||||||| |||||| |||
                                  T  GTTTACATT AATGTA TAG
                                   TG       _     A
GAM834  SCAMP-4  5'  GGCTTCAGCCTGCGCTGGTT   54398   GT   G       CAT
                                  A  CAG TGTAGGTTG   GTC
                                  |  ||| |||||||||   |||
                                  T  GTC GCGTCCGAC   CGG
                                   TG  _       TT_
GAM834  SCAND2   3'  GAGATGTGATTATTGTCCTGGC 53316       TGTA   TG_
           T                      AGTCAGG    GGT   CATGTCTC
                                  |||||||    |||   ||||||||
                                  TCGGTCC    TTA   GTGTAGAG
                                     TG__    TTA
GAM834  SDCCAG8  3'  GAGATATTTACATTCATCTGGT 88586   GT     TAG  TGC
           T                      A  CAGGTG   GT   ATGTCTC
                                  |  ||||||   ||   |||||||
                                  T  GTCTAC   CA   TATAGAG
                                   TG     TTA  TT_
GAM834  SEC24D   3'  GGGAACAATCTGTTTCTGATT  29094       TG      CATG
                                  AGTCAGG  TAGGTTG    TCTC
                                  |||||||  |||||||    ||||
                                  TTAGTCT  GTCTAAC    AGGG
                                     TT      A___
GAM834  SEMA4F   3'  GGGGCCAGACCTTTGCCTGATT 14943         T    GCAT
                                  AGTCAGGTG AGGTT    GTCTC
                                  |||||||||| |||||    |||||
                                  TTAGTCCGT TCCAG    CGGGG
                                       T    AC__
GAM834  SHANK3   3'  GAGCCGTGTGTGTGCCTGATT  65498       TG  GGT     T
                                  AGTCAGG  TA   TGCATG CTC
                                  |||||||  ||   |||||| |||
                                  TTAGTCC  GT   GTGTGC GAG
                                     GT  ___     C
GAM834  SIAT8C   5'  GAGGCAGCCTCTCTTATTTGGT 31879   GT     TA  TT  A
           T                      A  CAGGTG  GG  GC TGTCTC
                                  |  ||||||  ||  || ||||||
                                  T  GTTTAT  TC  CG ACGGAG
                                   TG     TC  TC  _
GAM834  SIMRP7   3'  GAGGCAGCTGTTGTGTTTGGC  92365       TG   GTT  A
                                  GTCAGG  TAG   GC TGTCTC
                                  ||||||  |||   || ||||||
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                                CGGTTT  GTT   CG ACGGAG
                                   GT   GT_  _
GAM834  SIMRP7   3'  GGGCTCTGGCCTGCCCTGGCT  92370       T      CAT
                                AGTCAGG GTAGGTTG   GTCT
                                ||||||| ||||||||   ||||
                                TCGGTCC CGTCCGGT   CGGG
                                   _       CT_
GAM834  SIPL     3'  GAGATAGGATTATGCCT     36851         GTTGCA
                                AGGTGTAG     TGTCTC
                                |||||||||     ||||||
                                TCCGTATT     ATAGAG
                                    AGG___
GAM834  SMAP-5   3'  CATGCAGATTTACATTTGACT  47930             _
                                AGTCAGGTGTAGGT TGCATG
                                |||||||||||||| ||||||
                                TCAGTTTACATTTA ACGTAC
                                       G
GAM834  SMAP1    3'  GACCGTGTTGGTCTGTACTGAT 41652       G     TT _   _  TC
           T                     AGTCAG TGTAGG  G CATG TC
                                 |||||| ||||||  | |||| ||
                                 TTAGTC ATGTCT  T GTGC AG
                                    _     GG T    C
GAM834  SNTG1    3'  GAGGTGTGCAATTTACTCAGAT 38575      A  T         GT
           T                     AGTC GG GTAGGTTGCAT  CTC
                                 |||| || ||||||||||  |||
                                 TTAG CT CATTTAACGTG  GAG
                                   A  _          TG
GAM834  SPOP     3'  GAGACACCTGTCTGCATCTGAC 13093            TTGCA
           T                     AGTCAGGTGTAGG     TGTCTC
                                 ||||||||||||     ||||||
                                 TCAGTCTACGTCT     ACAGAG
                                       GTCC_
GAM834  SPTLC2   3'  GACCCTAGCCTGTCTCTGGCT  16802       TG      CAT
                                AGTCAGG  TAGGTTG   GTC
                                |||||||  |||||||   |||
                                TCGGTCT  GTCCGAT   CAG
                                    CT      CC_
GAM834  SQV7L    5'  GGGACACACCATTACACCTGGC 70577          __   TGCA
           T                     AGTCAGGTGTA  GGT    TGTCTC
                                 ||||||||||  |||    ||||||
                                 TCGGTCCACAT  CCA    ACAGGG
                                       TA   C___
GAM834  STAT5A   3'  GGGGTAAAAGCTGATCTGGTTT 12015     GG G     _  A__ GT
           GACT                    TCA  T TAGGTT GC   T  CTC
                                   |||  | |||||| ||   |  |||
                                   AGT  G GTCTAG CG   A  GGG
                                     TT _     T  AAA TG
GAM834  STC2     3'  GACATAGCCATACATCTGACT  13550          _    GC
                                AGTCAGGTGTA GGTT  ATGTC
                                |||||||||| ||||  |||||
```

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                                TCAGTCTACAT CCGA  TACAG
                                      A   __
GAM834  STHM     3'  GACACCCCAGCTTGTCCTTGGC 21297       TG      CA_   TC
              T                  AGTCAGG  TAGGTTG   TGTC
                                 |||||||  |||||||   ||||
                                 TCGGTTC  GTTCGAC   ACAG
                                     CT      CCC
GAM834  STI2     3'  GAGGCCTGCTCTGGTTTGACT  88967      GG G    TT   T
                                 AGTCA  T TAGG  GCA GTCTC
                                 |||||  | ||||  ||| |||||
                                 TCAGT  G GTCT  CGT CGGAG
                                    TT _   __   C
GAM834  STX12    3'  GAAAAACGATTTGCATTTGG   66352           CATG
                                 TCAGGTGTAGGTTG    TC
                                 ||||||||||||||    ||
                                 GGTTTACGTTTAGC    AG
                                       AAAA
GAM834  SUCLG2   3'  CAGCCTAAATCTGATT      65609        G
                                 AGTCAGGT TAGGTTG
                                 ||||||||  |||||||
                                 TTAGTCTA ATCCGAC
                                      A
GAM834  SYNPO2   3'  TAACCTATATTGACT       71896       G
                                 AGTCAG TGTAGGTTG
                                 ||||||  |||||||||
                                 TCAGTT ATATCCAAT
                                       _
GAM834  T2BP     3'  GAGGTGTGAGACAGACTTGACT 69996        GTAG  TG   GT
                                 AGTCAGGT    GT  CAT  CTC
                                 ||||||||    ||  |||  |||
                                 TCAGTTCA    CA  GTG  GAG
                                      GA__  GA   TG
GAM834  TBDN100  3'  GGCTTTAGCATCTGACT     46956          __
                                 AGTCAGGTGT  AGGTT
                                 ||||||||||  |||||
                                 TCAGTCTACG  TTCGG
                                       AT
GAM834  TGFB1I1  5'  GAGGCTGGGTTTGTGCTTGGCT 31931        TG  GG  G  T
                                 AGTCAGG  TA  TT CA GTCTC
                                 |||||||  ||  || || |||||
                                 TCGGTTC  GT  GG GT CGGAG
                                     GT  TT  _  _
GAM834  TNFSF13  3'  GAGGCATCTTCCTGGGTTTGGC 13742      GG G    TTGC
              T                  AGTCA  T TAGG    ATGTCTC
                                 |||||  | ||||    |||||||
                                 TCGGT  G GTCC    TACGGAG
                                    TT G    TTC_
GAM834  TRAD     3'  GGGATATTTTTGTGTCTACACC 22954        TTGC___
                                 GGTGTAGG      ATGTCTC
                                 ||||||||      |||||||
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                                CCACATCT      TATAGGG
                                    GTGTTTT
GAM834  TRIM5    3'  GGCGCCCAGCCTGTGCTT    52300     TG      CA
                                AGG  TAGGTTG  TGTC
                                |||  |||||||  ||||
                                TTC  GTCCGAC  GCGG
                                  GT      CC
GAM834  TRIM5    3'  GGCGCCCAGCCTGTGCTT    52367     TG      CA
                                AGG  TAGGTTG  TGTC
                                |||  |||||||  ||||
                                TTC  GTCCGAC  GCGG
                                  GT      CC
GAM834  TSCOT    3'  TGACCTGCTCTGGCT       52336       T
                                AGTCAGG GTAGGTTG
                                ||||||| ||||||||
                                TCGGTCT CGTCCAGT

                                    _
GAM834  UBE2G1   3'  GGACATGGTGTTTGATT     12484       TG AGGTTG
                                AGTCAGG  T     CATGTCT
                                |||||||  |     |||||||
                                TTAGTTT  G     GTACAGG
                                    GT _______
GAM834  UBXD2    3'  GATTCTTAATCTGACT      68344       G    TTGCAT
                                AGTCAGGT TAGG     GTC
                                |||||||| ||||     |||
                                TCAGTCTA ATTC     TAG
                                    _    T_____
GAM834  UPB1     3'  GTCAGCCTGACCTGATT     32889       G      _
                                AGTCAGGT TAGGTTG C
                                |||||||| ||||||| |
                                TTAGTCCA GTCCGAC G
                                    _      T
GAM834  VDU1     3'  GAGGCCACTTGCAACTTGATT  30418       _     TGCAT
                                AGTCAGGT GTAGGT    GTCTC
                                |||||||| ||||||    |||||
                                TTAGTTCA CGTTCA    CGGAG
                                    A     C____
GAM834  VRP      3'  TGTGCAATTGTATTTGGCT    22949       GTA
                                AGTCAGGT   GGTTGCATG
                                ||||||||   |||||||||
                                TCGGTTTA   TTAACGTGT
                                    TG_
GAM834  WASL     5'  GAGATGTGGCGCCTCTGACT   14141       T  AG  TG   G
                                AGTCAGG GT  GT  CAT TC
                                ||||||| ||  ||  ||| ||
                                TCAGTCT CG  CG  GTA AG
                                    C __ GT   G
GAM834  WBSCR21  5'  AGACTCCCTATGTCTGCCT   48473    T   TG    TTGCAT
                                AG CAGG  TAGG     GTCT
                                || ||||  ||||     ||||
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                                TC GTCT  ATCC     CAGA
                                 C   GT   CT____
GAM834  YAP1     3'  GACTAGTAGTTTATATTTCACT 20351     C      GG    AT
                                AGT AGGTGTA  TTGC  GTC
                                ||| |||||||  ||||  |||
                                TCA TTTATAT  GATG  CAG
                                  C      TT    AT
GAM834  YEA      5'  GGGACATGTAGTCTGGCCGGGG 51533      A_   G   GT
             CT                   AGTC  GGT TAG  TGCATGTCTC
                                ||||  ||| |||  ||||||||||
                                TCGG  CCG GTC  ATGTACAGGG
                                  GG   _   TG
GAM834  ZF5128   3'  GAGGCACACGGCCTGGCCTGGC 26804        G      CA
             T                    AGTCAGGT TAGGTTG  TGTCTC
                                |||||||| |||||||  ||||||
                                TCGGTCCG GTCCGGC  ACGGAG
                                     _      AC
GAM834  ZFP106   3'  GAGGCATGTGGATGATTTGG   42468       G  GG TG
                                TCAGGT TA  T  CATGTCTC
                                |||||| ||  |  ||||||||
                                GGTTTA GT  G  GTACGGAG
                                   _  A_ GT
GAM834  ZIC4     3'  GGGACATGTGTCAACTACATCT 49622    T       GT__
             GCT                    G CAGGTGTAG    TGCATGTCTC
                                | |||||||||    ||||||||||
                                C GTCTACATC    GTGTACAGGG
                                _        AACT
GAM834  LOC115131 3'  GGCATTGGCGTGTACCTGACT  59126          G    C
                                AGTCAGGTGTA GTTG ATGTC
                                |||||||||||| |||| |||||
                                TCAGTCCATGT CGGT TACGG
                                      G   _
GAM834  LOC115330 3'  GTCCCCGTGGCTGGCATCTGGC 56610          A   TG ATGTCTC
             T                    AGTCAGGTGT GGT  C
                                |||||||||| |||  |
                                TCGGTCTACG TCG  G
                                     G   GT CCCCTGG
GAM834  LOC116064 3'  GATAGTTTCACATTTGGCT    73721          A  TT  A
                                AGTCAGGTGT GG  GC TGTC
                                |||||||||| ||  || ||||
                                TCGGTTTACA CT  TG ATAG
                                     _  T_  _
GAM834  LOC116071 3'  GGGATGGGCTTGTACCTGAC   56626           G   G
                                GTCAGGTGTAGGTT CAT TC
                                |||||||||||||| ||| ||
                                CAGTCCATGTTCGG GTA GG
                                     _   G
GAM834  LOC116349 3'  GAGGCCCATGGCCAGCACTTGG 73831          A    CAT
             CT                   AGTCAGGTGT GGTTG   GTCTC
                                |||||||||| |||||   |||||
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                                TCGGTTCACG CCGGT   CGGAG
                                     A    ACC
GAM834  LOC119504 3' GTTAATGCACATTTGTACTTGG 73993   GT       _    GTCTC
           TT                  A  CAGGTGTAGGT TGCAT
                               |  |||||||||| |||||
                               T  GTTCATGTTTA ACGTA
                                TG        C    ATTG
GAM834  LOC121536 3' GATACATAGTTTGTACCTG   74088       GG   CA   TC
                               CAGGTGTA  TTG  TGTC
                               ||||||||  |||  ||||
                               GTCCATGT  GAT  ATAG
                                    TT   AC
GAM834  LOC122210 3' AGGAGTGCTGCATTTGACT   74116         GGTT   GT  C
                               AGTCAGGTGTA   GCAT  CT
                               ||||||||||    ||||  ||
                               TCAGTTTACGT   CGTG  GA
                                     ____    AG  T
GAM834  LOC123036 3' GAGGCAGATGACATTATACCTG 74191          _   CA
           ATT                   AGTCAGGTGTAG GTTG  TGTCTC
                               ||||||||||| ||||  ||||||
                               TTAGTCCATATT CAGT  ACGGAG
                                     A    AG
GAM834  LOC123346 5' GACTCTAATCTGCATTT     75608          CAT
                               AGGTGTAGGTTG   GTC
                               ||||||||||   |||
                               TTTACGTCTAAT   CAG
                                     CT_
GAM834  LOC127281 3' GGGTCAGTGCCTGTGTCTGG   74648      TG    TGCA  T
                               TCAGG  TAGGT    TG CTC
                               |||||  |||||    || |||
                               GGTCT  GTCCG    AC GGG
                                  GT    TG__  T
GAM834  LOC127687 3' GGCAGTGGCTGGTACTTGGCT  74689        TA   TG A
                               AGTCAGGTG  GGT  C TGTC
                               |||||||||  |||  | ||||
                               TCGGTTCAT  TCG  G ACGG
                                    GG   GT _
GAM834  LOC129198 3' GAGACAAATGCATGTCTGATT  76119       GT TAGGT   __
                               AGTCAG  G    TGCA  TGTCTC
                               ||||||  |    ||||  ||||||
                               TTAGTC  T    ACGT  ACAGAG
                                  TG _____    AA
GAM834  LOC130074 3' GGGGTATGTGGCCTATTTGG   76137     GT    TG   GT
                               TCAG  GTAGGT  CAT  CTC
                               ||||  ||||||  |||  |||
                               GGTT  TATCCG  GTA  GGG
                                 __     GT   TG
GAM834  LOC132949 3' ACTTGTCTACACTTGATT     75070          GTT   T
                               AGTCAGGTGTAG   GCA GT
                               ||||||||||||   ||| ||
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                                TTAGTTCACATC   TGT CA
                                    ___   T
GAM834   LOC133634 3'  GATTGTGTCAGCTTATATTTTA 75104     C          _   _ TC
              TT                    AGT AGGTGTAGGTTG CATG TC
                                    ||| |||||||||||| |||| ||
                                    TTA TTTATATTCGAC GTGT AG
                                      T          T   T
GAM834   LOC135154 3'  TAACTTATTTCTGATT      75221        T
                                    AGTCAGG GTAGGTTG
                                    ||||||| ||||||||
                                    TTAGTCT TATTCAAT
                                        T
GAM834   LOC135818 3'  GAGGTGCTCACTTGATT     75237         TAGGTT   G
                                    AGTCAGGTG     GCAT TC
                                    |||||||||     |||| ||
                                    TTAGTTCAC     CGTG AG
                                         T_____   G
GAM834   LOC136288 3'  GGGATGTGAAACACTTGGCT   75255          AGGTTG
                                    AGTCAGGTGT     CATGTCTC
                                    ||||||||||     ||||||||
                                    TCGGTTCACA     GTGTAGGG
                                         AA____
GAM834   LOC137492 3'  GAGACTGATTTTGTACCGATT  75268      A       TTG  T
                                    AGTC GGTGTAGG   CA GTCTC
                                    |||| ||||||||   || |||||
                                    TTAG CCATGTTT   GT CAGAG
                                      _       TA_  _
GAM834   LOC138389 3'  AGAAGTCAACACTTGGCT    76215          A GT GCATG
                                    AGTCAGGTGT G  T     TCT
                                    |||||||||| |  |     |||
                                    TCGGTTCACA C  A     AGA
                                         A TG _____
GAM834   LOC138515 5'  GGATTATCTGCATTTGG     75944           TGCAT
                                    TCAGGTGTAGGT    GTCT
                                    ||||||||||||    ||||
                                    GGTTTACGTCTA    TAGG
                                          T____
GAM834   LOC139322 3'  GAAGTATTAGCTTGCATTTGAT 75380             C   TC
                                    GTCAGGTGTAGGTTG ATG  TC
                                    |||||||||||||| |||  ||
                                    TAGTTTACGTTCGAT TAT  AG
                                          _  GA
GAM834   LOC139422 5'  GGAGCCACTGTACCTGGTT   75843   GT       GTT  ATG
                                    A  CAGGTGTAG   GC   TCT
                                    |  |||||||||   ||   |||
                                    T  GTCCATGTC   CG   AGG
                                     TG        AC_  ___
GAM834   LOC140219 5'  GAGAAGGTACTTGCATTTGCCT 75958    T         T  ATG
                                    AG CAGGTGTAGGT GC   TCTC
                                    || ||||||||||| ||   ||||
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                                TC GTTTACGTTCA TG   AGAG
                                 C          _  GA_
GAM834   LOC142820 3'  AGATGTGGGTATTTAGACT    76396     G     TG_
                                GGT TAGGT   CATGTCT
                                ||| |||||   |||||||
                                TCA ATTTA   GTGTAGA
                                  G     TGG
GAM834   LOC143188 5'  GAGGCAGCTAGCCATGTCTGGC 82898         TG A    _  A
            T                    AGTCAGG  T GGTT GC TGTCTC
                                |||||||  | |||| || ||||||
                                TCGGTCT  A CCGA CG ACGGAG
                                    GT _    T  _
GAM834   LOC143680 3'  GAGGCATGTATAAAATAGTTGG 82987    GT   G   AGGT
            TT                    A  CAG TGT    TGCATGTCTC
                                |  ||| |||    ||||||||||
                                T  GTT ATA    ATGTACGGAG
                                 TG   G   AAAT
GAM834   LOC143879 5'  GCAATCACACCTGATT      76654          A
                                AGTCAGGTGT GGTTGC
                                |||||||||| ||||||
                                TTAGTCCACA CTAACG
                                      _
GAM834   LOC144110 3'  GGGGTGCTGAGCCTGGCT    76675         GTAGGTT    G
                                AGTCAGGT      GCAT TC
                                ||||||||      |||| ||
                                TCGGTCCG      CGTG GG
                                    AGT_____    G
GAM834   LOC144165 5'  GCAGCCTGCGCTGACT      76680       G
                                AGTCAG TGTAGGTTGC
                                |||||| ||||||||||
                                TCAGTC GCGTCCGACG
                                    _
GAM834   LOC144587 5'  GGGGCATGTGGACCACCTGG   67028        TAGG TG
                                TCAGGTG    T  CATGTCTC
                                |||||||    |  ||||||||
                                GGTCCAC    G  GTACGGGG
                                    CA__ GT
GAM834   LOC144845 3'  GGGGCAGCTCTTCTACCTGGCT 56663          T   TT  A
                                AGTCAGGTG AGG  GC TGTCTC
                                |||||||| |||  || ||||||
                                TCGGTCCAT TTC  CG ACGGGG
                                    C   T_  _
GAM834   LOC144874 3'  GGGATCCTCTTACACCTTGCT  83194     C        TTGCAT
                                AGT AGGTGTAGG      GTCTC
                                ||| |||||||||      |||||
                                TCG TCCACATTC      TAGGG
                                  T        TCC___
GAM834   LOC145225 3'  GAGTCACAATGGCCTATGCTT  83305           CA_  T
                                AGGTGTAGGTTG   TG CTC
                                ||||||||||||   || |||
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                                TTCGTATCCGGT   AC GAG
                                       AAC  T
GAM834   LOC145225 3'  GGGGTATGCCTGTGTGCCTGGC 83306       TG  GGTT    GT
                                GTCAGG  TA    GCAT  CTC
                                ||||||  ||    ||||  |||
                                CGGTCC  GT    CGTA  GGG
                                   GT  GTC_   TG
GAM834   LOC145231 5'  GCACCTGTATCTACT      83287     C        T
                                AGT AGGTGTAGGT GC
                                ||| ||||||||| ||
                                TCA TCTATGTCCA CG
                                  _        _
GAM834   LOC145623 3'  GGGATGTCTTTGCATTTGCT   83399    T        TT    G
                                AG CAGGTGTAGG  GCAT TC
                                || ||||||||||  |||| ||
                                TC GTTTACGTTT  TGTA GG
                                 _        C_   G
GAM834   LOC145662 3'  GGGACCTAGCTATCTATACCTG 77322            T  AT_
            GCT                    AGTCAGGTGTAGGT GC   GTCTC
                                |||||||||||||| ||   |||||
                                TCGGTCCATATCTA CG   CAGGG
                                       T  ATC
GAM834   LOC145786 5'  GAGGTTTGCATCAGTTTGTCTT 83491       TGTAGGT__   TG
            GGCT                   GTCAGG       TGCA  TCTC
                                ||||||       ||||  ||||
                                CGGTTC        ACGT  GGAG
                                   TGTTTGACT    TT
GAM834   LOC146229 3'  GAGGTGAGGCTGCACTTCGCT  77752     C      G  G   G
                                AGT AGGTGTAG TT CAT TC
                                ||| |||||||| || ||| ||
                                TCG TTCACGTC GA GTG AG
                                  C       G  _   G
GAM834   LOC146268 3'  GGGACGGCCCGGTGCCTGGCT  77811        TG A  TT  A
                                AGTCAGG  T GG  GC TGTCTC
                                |||||||  | ||  || ||||||
                                TCGGTCC  G CC  CG GCAGGG
                                   GT G  __  _
GAM834   LOC146330 5'  GAGGCTTCGAGGGCTTCTGCCT 77836   GT    GT    GCAT__
            GGTT                    CAGGT  AGGTT     GTCTC
                                 |||||  |||||     |||||
                                 GTCCG  TTCGG     CGGAG
                                TG    TC    GAGCTT
GAM834   LOC146512 3'  GAACGTGGCAGCCTGCGTCTGC 77941    T  GT       _   CTC
            T                   AG CAG  GTAGGTTGC ATGT
                                || |||  ||||||||| ||||
                                TC GTC  CGTCCGACG TGCA
                                 _  TG       G   AG
GAM834   LOC147040 3'  GGGACTCTCCTGCACCTGACT  78235           TTGCAT
                                AGTCAGGTGTAGG     GTCTC
                                ||||||||||||     |||||
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                                TCAGTCCACGTCC     CAGGG
                                      TCT___
GAM834   LOC147136 3'  GGGGCTACATTCCAGTGCCTGA 78268       TG A  TTGCAT
           CT                   AGTCAGG  T GG     GTCTC
                                ||||||| | ||     |||||
                                TCAGTCC  G CC     CGGGG
                                   GT A  TTACAT
GAM834   LOC147515 3'  GAGAATGTGTCTATGTTGGCT  84023      G TG   GTT    G
                                AGTCA G  TAG   GCAT TCTC
                                ||||| |  |||   |||| ||||
                                TCGGT T  ATC   TGTA AGAG
                                  _ GT   TG_   _
GAM834   LOC147515 3'  GGGATGTGTAAGAAGCTGCTGG 84025   GT   GT  AGG
           TT                   A  CAG  GT   TTGCATGTCTC
                                |  |||  ||   ||||||||||
                                T  GTC  CG   AATGTGTAGGG
                                 TG   GT  AAG
GAM834   LOC147727 5'  GATGTACAATCTGTGCTTAACT 78468     C   TG      C
                                AGT AGG  TAGGTTG ATGTC
                                ||| |||  ||||||| |||||
                                TCA TTC  GTCTAAC TGTAG
                                  A   GT      A
GAM834   LOC148029 3'  GGGATTGGCCATTTATACTGGG 78621      A       T  AT
           CT                   AGTC GGTGTAGGT GC  GTCTC
                                |||| |||||||| ||  |||||
                                TCGG TCATATTTA CG  TAGGG
                                  G       C  GT
GAM834   LOC148137 3'  GGACCCACCTTATCTGGCT    58437        T    T CAT
                                AGTCAGGTG AGGT G   GTCT
                                ||||||||| |||| |   ||||
                                TCGGTCTAT TCCA C   CAGG
                                     _   _ C__
GAM834   LOC148293 5'  GAGGCATGTAAATGTATTT    78779       GG
                                AGGTGTA  TTGCATGTCTC
                                |||||||  ||||||||||
                                TTTATGT  AATGTACGGAG
                                   A_
GAM834   LOC148354 3'  GGGACAGGGCTGCATCTGA    78801         G  GCA
                                TCAGGTGTAG TT   TGTCTC
                                |||||||||| ||   ||||||
                                AGTCTACGTC GG   ACAGGG
                                     G  ___
GAM834   LOC148758 5'  GGGAAACTGTCTGTGCCTGCT  78973    T   TG   GTT   TG_
                                AG CAGG  TAG   GCA   TCTC
                                || ||||  |||   |||   ||||
                                TC GTCC  GTC   TGT   AGGG
                                 _   GT   ___   CAA
GAM834   LOC148932 3'  GGGGTGTGTGTGTGTGTGTGTG 79112      G TG  G TT_   GT
           ATT                  AGTCA G  TA G   GCAT  CTC
                                |||||  |  ||  |   ||||  |||
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                                TTAGT T  GT T   TGTG  GGG
                                   G GT  G GTG    TG
GAM834   LOC149127 3'  GAGGAGTAACCTGGTCTGACT  84346       GTG       ATG
                                AGTCAG   TAGGTTGC   TCTC
                                ||||||   ||||||||   ||||
                                TCAGTC   GTCCAATG   GGAG
                                   TG_       A__
GAM834   LOC149300 3'  GAGGTCTGCTTTGGCT      79286        T    GTTGC  G
                                AGTCAGG GTAG     AT TC
                                ||||||| ||||     || ||
                                TCGGTTT CGTC     TG AG
                                   _   _____  G
GAM834   LOC149421 5'  GGGCCTCCAATCTGCATTGATT 79362       G        CAT
                                AGTCAG TGTAGGTTG   GTCT
                                |||||| |||||||||   ||||
                                TTAGTT ACGTCTAAC   CGGG
                                   _       CTC
GAM834   LOC149464 3'  GAGAAAAGACTTCTGTCTGGCT 84429       GT T     GCATG
                                AGTCAG  G AGGTT     TCTC
                                ||||||  | |||||     ||||
                                TCGGTC  T TTCAG     AGAG
                                   TG C     AAA__
GAM834   LOC149606 3'  GAGGAGGGCCTGCACCCGGCT  79453      A        GCATG
                                AGTC GGTGTAGGTT     TCTC
                                |||| ||||||||||     ||||
                                TCGG CCACGTCCGG     GGAG
                                  C         GA___
GAM834   LOC149668 5'  ATCTGTGTGTGGCCTGTGTCTG 84533    T    TG     TG  TG CTC
         TCT                      AG CAGG  TAGGT  CA  T
                                || ||||  |||||  ||  |
                                TC GTCT  GTCCG  GT  G
                                 T   GT    GT  GT TCTAC
GAM834   LOC149821 5'  GGGGCACAGACTTGTGCCTCGC 84766     C   TG      GCA
         T                        AGT AGG  TAGGTT   TGTCTC
                                ||| |||  ||||||   ||||||
                                TCG TCC  GTTCAG   ACGGGG
                                  C   GT     AC_
GAM834   LOC149995 3'  GAGAATGTGTCTATGTTGGCT  84845      G TG   GTT    G
                                AGTCA G  TAG   GCAT TCTC
                                |||||  |  |||   |||| ||||
                                TCGGT T  ATC   TGTA AGAG
                                   _ GT   TG_   _
GAM834   LOC149995 3'  GGGGTGTGTAAGAAGCTGCTGG 84848   GT   GT  AGG     GT
         TT                       A  CAG  GT   TTGCAT  CTC
                                |  |||  ||   ||||||  |||
                                T  GTC  CG   AATGTG  GGG
                                 TG   GT  AAG     TG
GAM834   LOC150005 3'  GAGGTGTGCAAAGGTGTCCTGT 84821    T    TGTAGG     GT
         CT                       AG CAGG     TTGCAT  CTC
                                || ||||     ||||||  |||
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                                TC GTCC     AACGTG  GAG
                                 T   TGTGGA     TG
GAM834   LOC150005 3'  GGGGTGTGCAAAAGTACTTGGC 84822        TAGG     GT
                                GTCAGGTG    TTGCAT  CTC
                                ||||||||    ||||||  |||
                                CGGTTCAT    AACGTG  GGG
                                    GAA_     TG
GAM834   LOC150170 5'  GGTCACTGCTGGTTTACATTTG 79592        GG  _  _  T  C
           ATT                    GTCAGGTGTA  TT GCA TG CT
                                ||||||||||  || ||| || ||
                                TAGTTTACAT  GG CGT AC GG
                                     TT  T   C  T
GAM834   LOC150175 5'  GGTCACTGCTGGTTTACATTTG 79633        GG  _  _  T  C
           ATT                    GTCAGGTGTA  TT GCA TG CT
                                ||||||||||  || ||| || ||
                                TAGTTTACAT  GG CGT AC GG
                                     TT  T   C  T
GAM834   LOC150215 5'  GGTCACTGCTGGTTTACATTTG 79641        GG  _  _  T  C
           ATT                    GTCAGGTGTA  TT GCA TG CT
                                ||||||||||  || ||| || ||
                                TAGTTTACAT  GG CGT AC GG
                                     TT  T   C  T
GAM834   LOC150218 5'  GGTCACTGCTGGTTTACATTTG 79722        GG  _  _  T  C
           ATT                    GTCAGGTGTA  TT GCA TG CT
                                ||||||||||  || ||| || ||
                                TAGTTTACAT  GG CGT AC GG
                                     TT  T   C  T
GAM834   LOC150221 3'  GGGATGTGAGGGTGATCTGGCT 65277        GTAGGTTG
                                AGTCAGGT       CATGTCTC
                                ||||||||       ||||||||
                                TCGGTCTA       GTGTAGGG
                                    GTGGGA__
GAM834   LOC150291 3'  GAACCAATTTGCATTTGG    84946           CATG
                                TCAGGTGTAGGTTG    TC
                                ||||||||||||||    ||
                                GGTTTACGTTTAAC    AG
                                       CA__
GAM834   LOC150319 5'  GCAGCTTGCCTTGACT      79655        T
                                AGTCAGG GTAGGTTGC
                                ||||||| |||||||||
                                TCAGTTC CGTTCGACG
                                   _
GAM834   LOC150348 3'  GGGGCATGGATGCATTGTGACT 84945      _     GGTTG
                                AGTCA GGTGTA     CATGTCTC
                                |||||  ||||||    ||||||||
                                TCAGT TTACGT     GTACGGGG
                                   G     AG___
GAM834   LOC150378 5'  GAGGTGGCTATTCCACCTGGTT 79747    GT     T  GTT  A GT
                                A  CAGGTG AG   GC T  CTC
                                |  |||||| ||   || |  |||
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                                T  GTCCAC TT   CG G  GAG
                                 TG     C  AT_  _ TG
GAM834   LOC150538 3'  GAGGCGTGCGGTGGGCACTTGG 79935         AG TT
                                TCAGGTGT  G  GCATGTCTC
                                |||||||| |  |||||||||
                                GGTTCACG  T  CGTGCGGAG
                                     GG GG
GAM834   LOC150587 3'  GACCCAGTAATCTGCGTGTGAT 85061       GG        AT_   TC
           T                     AGTCA  TGTAGGTTGC   GTC
                                |||||  ||||||||||   |||
                                TTAGT  GCGTCTAATG   CAG
                                   GT         ACC
GAM834   LOC150759 3'  GGGATTATGTTCTTCATTTGAC 80007         T   TT    _
           T                     AGTCAGGTG AGG  GCATG TCTC
                                |||||||||| |||  ||||| ||||
                                TCAGTTTAC TTC  TGTAT AGGG
                                      _  T_    T
GAM834   LOC151094 3'  TAATCTCACGCTTGGTT     65294    GT      _
                                A  CAGGTGT AGGTTG
                                |  ||||||| ||||||
                                T  GTTCGCA TCTAAT
                                 TG      C
GAM834   LOC151103 3'  CCTTTTGTAACTTCACTTGGTT 85224    GT     T       TGTCTC
                                A  CAGGTG AGGTTGCA
                                |  |||||| ||||||||
                                T  GTTCAC TTCAATGT
                                 TG     _       TTTCCG
GAM834   LOC151176 5'  GGACCACCTGCGCCTGCT    85262    T         TGCAT
                                AG CAGGTGTAGGT    GTCT
                                || ||||||||||     ||||
                                TC GTCCGCGTCCA    CAGG
                                  _         C_____
GAM834   LOC151201 3'  GAAAAGCCATCTGTGCCTGGTT 85278    GT    TG    T  ATG
                                A  CAGG  TAGGT GC   TC
                                |  ||||  ||||| ||   ||
                                T  GTCC  GTCTA CG   AG
                                 TG   GT    C  AAA
GAM834   LOC151405 5'  GAGACGTGCGCTAACTTC    85338    T  A   T
                                GG GT GGT GCATGTCTC
                                || || ||| |||||||||
                                CT CA TCG CGTGCAGAG
                                  T  A   _
GAM834   LOC151475 5'  GGCTTGCAGCTGGTATCTGGTT 85414    GT     TA      T
                                A  CAGGTG  GGTTGCA GTC
                                |  ||||||  ||||||| |||
                                T  GTCTAT  TCGACGT CGG
                                 TG     GG      T
GAM834   LOC151742 3'  GGGCTGCAATCTGTCTTGATT  57669         TGT       T    C
                                AGTCAGG   AGGTTGCA GTCT
                                |||||||   |||||||| ||||
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                                TTAGTTC   TCTAACGT CGGG
                                   TG_      _    A
GAM834   LOC152283 5'  GAGGCATGTGGCCTGGAGAGGA 85682     AGGTG    TG
           C                    GTC     TAGGT  CATGTCTC
                                |||     |||||  ||||||||
                                CAG     GTCCG  GTACGGAG
                                  GAGAG     GT
GAM834   LOC152300 3'  GAGAATGCATTTCATGTCTGAT 80544       TG AG T    G
           T                    AGTCAGG  T  G TGCAT TCTC
                                |||||||  |  | ||||| ||||
                                TTAGTCT  A  T ACGTA AGAG
                                   GT CT T    _
GAM834   LOC152348 3'  GGCATCAGTTTGTGCTGATT   85696      G TG  GG   C
                                AGTCA G  TA  TTG ATGTC
                                |||||  |  ||  ||| |||||
                                TTAGT C  GT  GAC TACGG
                                  _ GT  TT  _
GAM834   LOC152348 3'  GTAGCCTATATTGACT      85697       G
                                AGTCAG TGTAGGTTGC
                                |||||| ||||||||||
                                TCAGTT ATATCCGATG
                                  _
GAM834   LOC152464 3'  GTCAGCTTGCATCTGCT     59987    T          _
                                AG CAGGTGTAGGTTG C
                                || ||||||||||||| |
                                TC GTCTACGTTCGAC G
                                 _          T
GAM834   LOC152502 3'  GGGACATGTTAAACTTTGATT  59315       T  AGGTT
                                AGTCAGG GT    GCATGTCTC
                                |||||||  ||    |||||||||
                                TTAGTTT CA    TGTACAGGG
                                   _  AAT__
GAM834   LOC152627 5'  AGAAGTTGATGCCTGGCT    80625         AGGTT  ATG
                                AGTCAGGTGT    GC   TCT
                                ||||||||||    ||   |||
                                TCGGTCCGTA    TG   AGA
                                     GT___  A__
GAM834   LOC152765 5'  GAGGCATGCAGTGGGTTGAT   80658      GTGTAGG
                                GTCAG      TTGCATGTCTC
                                |||||      ||||||||||
                                TAGTT      GACGTACGGAG
                                  GGGT___
GAM834   LOC152982 3'  GAGATGTCATCATCTTACATCA 80756     A       T  C__
           GACT                   GTC GGTGTAGG TG   ATGTCTC
                                  ||| |||||||| ||   |||||||
                                  CAG CTACATTC AC   TGTAGAG
                                    A       T  TAC
GAM834   LOC153163 3'  GACTCCTGGCTTGCTTTTGGCT 80771       T       CAT
                                AGTCAGG GTAGGTTG   GTC
                                ||||||| ||||||||   |||
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                                TCGGTTT CGTTCGGT   CAG
                                    T       CCT
GAM834   LOC153474 3'  GACCCTTGGGCCTGCATCTGAC 80845            G  T__   TC
             T                   AGTCAGGTGTAGGTT CA   GTC
                                 ||||||||||||||| ||   |||
                                 TCAGTCTACGTCCGG GT   CAG
                                          _  TCC
GAM834   LOC153811 3'  GGGACAAGGTGCCTATGTCTGC 80955    T    TG     TGCA
             T                   AG CAGG  TAGGT    TGTCTC
                                 || ||||  |||||    ||||||
                                 TC GTCT  ATCCG    ACAGGG
                                  _   GT    TGGA
GAM834   LOC154739 5'  AGAATTCTACACTTGACT    86223           TTGCATG
                                 AGTCAGGTGTAGG      TCT
                                 ||||||||||||       |||
                                 TCAGTTCACATCT      AGA
                                          TA_____
GAM834   LOC155004 3'  GAGGCATGCAAGCCTCTGCCT  81223      GT    _
                                 AGGT  AGGTT GCATGTCTC
                                 ||||  ||||| |||||||||
                                 TCCG  TCCGA CGTACGGAG
                                   TC    A
GAM834   LOC155032 3'  ATGTCTATGCTTGGCT      86319          GTT
                                 AGTCAGGTGTAG   GCAT
                                 ||||||||||||   ||||
                                 TCGGTTCGTATC   TGTA
                                            ___
GAM834   LOC155072 3'  GAGACATGACCATTTCTATCTG 86377         T    TG_
             GCT                    AGTCAGGTG AGGT   CATGTCTC
                                 ||||||||| ||||   ||||||||
                                 TCGGTCTAT TTTA   GTACAGAG
                                      C    CCA
GAM834   LOC155179 3'  GAGGCGTGCAGCCTCTGGGC   81315     A  TGT
                                 GTC GG   AGGTTGCATGTCTC
                                 ||| ||   ||||||||||||||
                                 CGG TC   TCCGACGTGCGGAG
                                   G  ___
GAM834   LOC155434 3'  TGTAACCTGCCTTGGCT     86409        T
                                 AGTCAGG GTAGGTTGCA
                                 ||||||| |||||||||
                                 TCGGTTC CGTCCAATGT
                                          _
GAM834   LOC157693 5'  GGGACACGTTTGCACTTGTCT  81556    T       GTT  A
                                 AG CAGGTGTAG   GC TGTCTC
                                 || |||||||||   || ||||||
                                 TC GTTCACGTT   TG ACAGGG
                                  T        ___  C
GAM834   LOC157858 5'  GACTTGACCTGCGTCTGAT    86592       GT      GCAT
                                 GTCAG  GTAGGTT    GTC
                                 |||||  |||||||    |||
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                                TAGTC  CGTCCAG    CAG
                                  TG      TT__
GAM834   LOC157858 3'  GGGATCGTTTTCTGTTTCTGGC 86598       TG    TT  AT
           T                     AGTCAGG  TAGG  GC  GTCTC
                                 |||||||  ||||  ||  |||||
                                 TCGGTCT  GTCT  TG  TAGGG
                                    TT    TT  C_
GAM834   LOC158293 5'  GGGATGCTGGCCGGCCGCGCCT 81864        A    _ AT__
           GGCT                    TCAGGTGT GGTTG C    GTCTC
                                 |||||||| ||||| |    |||||
                                 GGTCCGCG CCGGC G    TAGGG
                                    _    C GTCG
GAM834   LOC158337 3'  AGAGGATTTGCACTTGATT    86773            GCATG
                                 AGTCAGGTGTAGGTT     TCT
                                 ||||||||||||||     |||
                                 TTAGTTCACGTTTAG     AGA
                                       G____
GAM834   LOC158969 5'  GAGATGCTGGGCACTTGCACTG 82060    _       T  AT___
           TGACT                    A GGTGTAGGT GC     GTCTC
                                 | |||||||||  ||     |||||
                                 T TCACGTTCA CG     TAGAG
                                  G        _  GGTCG
GAM834   LOC162333 5'  GAGATGTGTAAGCAAGGCCTGC 87132    T    GTAG  _
           T                     AG CAGGT    GTT GCATGTCTC
                                 || |||||    ||| |||||||||
                                 TC GTCCG    CGA TGTGTAGAG
                                  _    GAA_   A
GAM834   LOC162461 3'  GAGGTATGCAAATCTTGACT   82361       TGTAGG     GT
                                 AGTCAGG     TTGCAT  CTC
                                 |||||||     ||||||  |||
                                 TCAGTTC     AACGTA  GAG
                                    TA____     TG
GAM834   LOC163255 5'  GAGAAAAGCTGTGACTCACACT 82449       AG  TG  TG___
           TGGTT                    CAGGTGT  GT  CA     TCTC
                                 |||||||  ||  ||    ||||
                                 GTTCACA  CA  GT    AGAG
                                    CT  GT  CGAAA
GAM834   LOC163341 3'  GGACATGGAGTGTCTGTCT    82121    T    TG AGGT G
                                 AG CAGG  T    T CATGTCT
                                 || ||||  |    | |||||||
                                 TC GTCT  G    A GTACAGG
                                  T    GT ____ G
GAM834   LOC169667 5'  GGGACTGCTGCCTGCATCTGG  82782          T   T
                                 TCAGGTGTAGGT GCA GTCTC
                                 |||||||||||| ||| |||||
                                 GGTCTACGTCCG CGT CAGGG
                                       T   _
GAM834   LOC170371 3'  GGGACATGATGGTACTTGGC   82837         AGGTTG
                                 GTCAGGTGT     CATGTCTC
                                 |||||||||     ||||||||
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                                CGGTTCATG     GTACAGGG
                                     GTA___
GAM834   LOC196214 3'  GGGATGTTCCTGCGCCTGGCT  89621          TT   G
                                AGTCAGGTGTAGG  GCAT TC
                                ||||||||||||  |||| ||
                                TCGGTCCGCGTCC  TGTA GG
                                   T_   G
GAM834   LOC196955 5'  GGCCATCAGCCTGTGCTTG   77385     TG     C  _
                                CAGG  TAGGTTG ATG TC
                                ||||  ||||||| ||| ||
                                GTTC  GTCCGAC TAC GG
                                  GT      _  C
GAM834   LOC199800 5'  GGGACTGGCCCTGGTACCTGGC 89860        TA  TT  AT
           T                     AGTCAGGTG  GG  GC  GTCTC
                                |||||||||  ||  ||  |||||
                                TCGGTCCAT  TC  CG  CAGGG
                                     GG  C_  GT
GAM834   LOC200138 3'  GAGATGAACCCTGCAGCCTGAC 89934       _     TTG   G  TC
           T                     AGTCAGG TGTAGG   CAT TC
                                |||||||  ||||||   ||| ||
                                TCAGTCC ACGTCC   GTA AG
                                    G     CAA   G
GAM834   LOC200282 3'  GAGCTGAGGCCTGTGCTTGG   88707      TG    TG  T T
                                TCAGG  TAGGT  CA G CTC
                                |||||  |||||  || | |||
                                GGTTC  GTCCG  GT C GAG
                                   GT    GA  _ _
GAM834   LOC200299 5'  AGAATATCTACGCTTG      89976          TGCATG
                                CAGGTGTAGGT     TCT
                                ||||||||||      |||
                                GTTCGCATCTA     AGA
                                     TA_____
GAM834   LOC200300 5'  AGAATATCTACGCTTG      89967          TGCATG
                                CAGGTGTAGGT     TCT
                                ||||||||||      |||
                                GTTCGCATCTA     AGA
                                     TA_____
GAM834   LOC200304 5'  AGAATATCTACGCTTG      89985          TGCATG
                                CAGGTGTAGGT     TCT
                                ||||||||||      |||
                                GTTCGCATCTA     AGA
                                     TA_____
GAM834   LOC200305 5'  AGAATATCTACGCTTG      89978          TGCATG
                                CAGGTGTAGGT     TCT
                                ||||||||||      |||
                                GTTCGCATCTA     AGA
                                     TA_____
GAM834   LOC200853 5'  GAGACACCTCCTGCTCTGACT  88913        T    TTGCA
                                AGTCAGG GTAGG     TGTCTC
                                |||||||  |||||     ||||||
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                                TCAGTCT CGTCC     ACAGAG
                                   _    TCC__
GAM834   LOC200853 5'  GAGACACTTTGAAATCAGTGTC 88914      TG A    G ___
              TGACT                 CAGG  T GGTT CA   TGTCTC
                                |||| | |||| ||   ||||||
                                GTCT  G CTAA GT   ACAGAG
                                  GT A    A  TTC
GAM834   LOC200933 3'  AGATGTGTTGTATTGACT    90192       GTGTAGGTT
                                AGTCAG        GCATGTCT
                                ||||||        ||||||||
                                TCAGTT        TGTGTAGA
                                   ATGT_____
GAM834   LOC201139 3'  GAGATGCTGGGCCTGGTT    88131    GT    G  GGTT    G
                                A  CAGGT TA    GCAT TC
                                |  ||||| ||    |||| ||
                                T  GTCCG GT    CGTA AG
                                 TG    G _____    G
GAM834   LOC201564 3'  GAGACAGCATCAGTATTTGACT 80436          TA   T  A
                                AGTCAGGTG  GGT GC TGTCTC
                                |||||||||  ||| || ||||||
                                TCAGTTTAT  CTA CG ACAGAG
                                     GA   _ _
GAM834   LOC201626 3'  GGGGTTTTATCTGCATTTGAC  88994            TGC  G
                                GTCAGGTGTAGGT   AT TC
                                ||||||||||||   || ||
                                CAGTTTACGTCTA   TG GG
                                       TTT  G
GAM834   LOC201696 3'  GAGATGAGGTCTGTGCCTGAT  63132        TG   GT G   G
                                GTCAGG  TAG  T CAT TC
                                ||||||  |||  | ||| ||
                                TAGTCC  GTC  G GTA AG
                                   GT   TG A   G
GAM834   LOC201706 5'  GTCAGCATATACTTGGTT    89522    GT       G   _
                                A  CAGGTGTA GTTG C
                                |  |||||||| |||| |
                                T  GTTCATAT CGAC G
                                 TG       A    T
GAM834   LOC201973 3'  TGCAGCCTGCTCTTGACT    89117         T
                                AGTCAGG GTAGGTTGCA
                                ||||||| ||||||||||
                                TCAGTTC CGTCCGACGT
                                     T
GAM834   LOC202460 5'  GGGATATGCAGTCTATCAATG  89185    GGT    GT
                                CA   GTAG  TGCATGTCTC
                                ||   ||||  ||||||||||
                                GT   TATC  ACGTATAGGG
                                 AAC    TG
GAM834   LOC202518 5'  GTGCTGACCTGAACCTGGTT   87486    GT    G     _
                                A  CAGGT TAGGTT GCAT
                                |  ||||| |||||| ||||
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                                T  GTCCA GTCCAG CGTG
                                 TG    A     T
GAM834   LOC202865 5'  GAGGCGCCCAGCCTGTGTCTGA 59255      TG      CA
                                TCAGG  TAGGTTG  TGTCTC
                                |||||  |||||||  ||||||
                                AGTCT  GTCCGAC  GCGGAG
                                   GT      CC
GAM834   LOC202868 3'  GAGACATGACCATTTCTATCTG 90375        T    TG_
           GCT                    AGTCAGGTG AGGT   CATGTCTC
                                |||||||||  ||||   ||||||||
                                TCGGTCTAT TTTA   GTACAGAG
                                     C    CCA
GAM834   LOC203248 3'  TGGCATGGAGCTTACACCTGAC 89314             G     TC
           T                     AGTCAGGTGTAGGTT CATGTC
                                ||||||||||||||| ||||||
                                TCAGTCCACATTCGA GTACGG
                                          G     TA
GAM834   LOC203504 3'  GGGGCCTCCTTGTGTCTGAT   90639       TG    TTGCAT
                                GTCAGG  TAGG     GTCTC
                                ||||||  ||||     |||||
                                TAGTCT  GTTC     CGGGG
                                   GT    CTC___
GAM834   LOC203952 5'  GGGATGTGCAAAAGCGCCGGCT 90654      A     AGG
                                AGTC GGTGT   TTGCATGTCTC
                                ||||  |||||   ||||||||||
                                TCGG CCGCG   AACGTGTAGGG
                                  _     AA_
GAM834   LOC219445 3'  GGCATTGGCGTGTACCTGACT  91576          G    C
                                AGTCAGGTGTA GTTG ATGTC
                                |||||||||| |||| |||||
                                TCAGTCCATGT CGGT TACGG
                                      G    _
GAM834   LOC219673 5'  GGGATGTGCCAGCATACTTGGC 93037          AG    _
           T                     AGTCAGGTGT  GTTG CATGTCTC
                                ||||||||||  |||| ||||||||
                                TCGGTTCATA  CGAC GTGTAGGG
                                      __    C
GAM834   LOC219793 3'  GGGGCCCTAACACTTGCACCTG 91373    T         TGCAT_
           CCT                     AG CAGGTGTAGGT     GTCTC
                                || ||||||||||      |||||
                                TC GTCCACGTTCA      CGGGG
                                 C          CAATCC
GAM834   LOC219848 3'  GGGACCCATTCTATGCCTGTCT 91494    T       GT  CAT
                                AG CAGGTGTAG  TG   GTCTC
                                || |||||||||  ||   |||||
                                TC GTCCGTATC  AC   CAGGG
                                 T        TT  C__
GAM834   LOC219899 3'  GGGATTTGCCTGCCACTTGGTT 91505    GT     _     TGCAT
                                A  CAGGTG TAGGT     GTCTC
                                |  |||||| |||||     |||||
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                                T  GTTCAC GTCCG    TAGGG
                                 TG     C    TT___
GAM834   LOC219920 3'  GAGTTGCCCTAGCCTCGTGCCT 93312     TG _    ___  TG  TC
              GACT                 CAGG  T AGGTT   GCA  TC
                                |||| | |||||  |||  ||
                                GTCC  G TCCGA   CGT  AG
                                  GT C    TCC   TG
GAM834   LOC220058 3'  GAGATGTGTGCGTCACCTGAC  91725       TAG  T
                                GTCAGGTG   GT GCATGTCTC
                                ||||||||  || |||||||||
                                CAGTCCAC   CG TGTGTAGAG
                                     TG_  _
GAM834   LOC220575 3'  GAACTGCTGGTTTGTACCTGGC 76309         GG  _   TG  TC
              T                   AGTCAGGTGTA  TT GCA  TC
                                ||||||||||  || |||  ||
                                TCGGTCCATGT  GG CGT  AG
                                      TT  T   CA
GAM834   LOC220575 3'  GAGGTGTGTGCATTTCTGACT  76311       TGTAG  T    GT
                                AGTCAGG    GT GCAT  CTC
                                |||||||    || ||||  |||
                                TCAGTCT    CG TGTG  GAG
                                    TTA__  _    TG
GAM834   LOC220883 3'  GAGGTGGTGGTTCTGGGTTTGA 91260      GG G   _ TT  A GT
              TT                   AGTCA  T TAG G  GC T  CTC
                                |||||  | ||| |  || |  |||
                                TTAGT  G GTC T  TG G  GAG
                                   TT G   T GG  _ TG
GAM834   LOC220936 3'  GACATGCAAGCTGGCT     91412     G   G
                                GGT TAG TTGCATGTC
                                ||| ||| |||||||||
                                TCG GTC AACGTACAG
                                  _   G
GAM834   LOC221042 3'  CAGCTTAACCTGATT       93181         G
                                AGTCAGGT TAGGTTG
                                |||||||| |||||||
                                TTAGTCCA ATTCGAC
                                      _
GAM834   LOC221178 5'  GGGACGTGTTGGACACGCTGAC 93537       _    AGGTT
              T                   AGTCAG GTGT    GCATGTCTC
                                |||||| ||||    |||||||||
                                TCAGTC CACA    TGTGCAGGG
                                   G   GGT__
GAM834   LOC221405 5'  GATAGTGATTGCGTTTGGCT   93884      GG    G TG A
                                AGTCA  TGTAG T  C TGTC
                                |||||  ||||| |  | ||||
                                TCGGT  GCGTT A  G ATAG
                                   TT    _ GT _
GAM834   LOC221895 3'  GGGATTCAATTTATGCCT    92525          CAT
                                AGGTGTAGGTTG   GTCTC
                                ||||||||||||   |||||
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                                TCCGTATTTAAC   TAGGG
                                       T__
GAM834   LOC222001 3'  GAGATGTGTAGTCAAGATGAC  92905     GGTGTA GT
                                GTCA     G  TGCATGTCTC
                                ||||     |  ||||||||||
                                CAGT     C  ATGTGTAGAG
                                  AGAA__ TG
GAM834   LOC222029 3'  GGGGTGTGTGGCTGGGCCCTGA 94040       T  A_   TG   GT
           C                     GTCAGG GT  GGT  CAT  CTC
                                ||||||  ||  |||  |||  |||
                                CAGTCC CG  TCG  GTG  GGG
                                   _ GG   GT   TG
GAM834   LOC222031 3'  GAGAGCTGAGGACCTGCACCAG 94022      A        G_  TG
           GCT                     AGTC GGTGTAGGTT  CA  TCTC
                                |||| ||||||||||  ||  ||||
                                TCGG CCACGTCCAG  GT  AGAG
                                  A        GA  CG
GAM834   LOC222865 3'  GATCAGCTCTGTATCTGGTT   92861    GT       _    CAT
                                A  CAGGTGTAG GTTG   GTC
                                |  |||||||||  ||||   |||
                                T  GTCTATGTC CGAC   TAG
                                 TG        T   ___
GAM834   LOC253018 5'  GAGGTCGCCTCTGTGCTGGCT  96006      G TG    TT  _  G
                                AGTCA G  TAGG  GC AT TC
                                |||||  |  ||||  || || ||
                                TCGGT C  GTCT  CG TG AG
                                  _ GT    C_  C  G
GAM834   LOC253681 3'  GGGACTCTCCTGCACCTGACT  95132           TTGCAT
                                AGTCAGGTGTAGG     GTCTC
                                ||||||||||||     |||||
                                TCAGTCCACGTCC     CAGGG
                                       TCT___
GAM834   LOC253782 3'  GGGAACAGTATTTGCATTTGTA 95697     _         T  A   _
           CT                     AGT CAGGTGTAGGT GC TGT CTC
                                ||| ||||||||||| || ||| |||
                                TCA GTTTACGTTTA TG ACA GGG
                                  T         _  _   A
GAM834   LOC253841 5'  GGGTTGAATGGCTTGCATCTGG 96343           TG   GT__
           CT                     AGTCAGGTGTAGGT  CAT    CTC
                                ||||||||||||||  |||    |||
                                TCGGTCTACGTTCG  GTA    GGG
                                       __   AGTT
GAM834   LOC254043 3'  GAAGTTTAGCGTATGTTTGACT 95071        TG  G    C  G
                                AGTCAGG  TA GTTG AT TC
                                |||||||  || |||| || ||
                                TCAGTTT  AT CGAT TG AG
                                    GT  G    T  A
GAM834   LOC254314 3'  ATGTATGTGACTTATATTTGGC 96476           TG   GTCTC
           T                      AGTCAGGTGTAGGT  CAT
                                ||||||||||||||  |||
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                                TCGGTTTATATTCA  GTA
                                      GT   TGTAA
GAM834   LOC254428 3'  GACATGGGGTTTGGCT      95459        TGTAGG  G
                                AGTCAGG     TT CATGTC
                                |||||||     || ||||||
                                TCGGTTT     GG GTACAG
                                   _______  G
GAM834   LOC254485 3'  AGTGAGGTGTGCCTGTGCCTGG 95012        TG    T   G  TC
           CT                     AGTCAGG  TAGGT GCAT TC
                                |||||||  ||||| |||| ||
                                TCGGTCC  GTCCG TGTG AG
                                   GT    _   G  TGAA
GAM834   LOC254485 3'  GAGGTGTGCCTGTGCCTGGCT  95014        TG    T   G
                                AGTCAGG  TAGGT GCAT TC
                                |||||||  ||||| |||| ||
                                TCGGTCC  GTCCG TGTG AG
                                   GT    _   G
GAM834   LOC254532 5'  GAGACTTGGATTGCATTTGGCT 96636           GTTG  T
                                AGTCAGGTGTAG    CA GTCTC
                                ||||||||||||   || |||||
                                TCGGTTTACGTT    GT CAGAG
                                      AG__  T
GAM834   LOC254820 3'  GGGATGTGTATATTCTTTTGAC 97345        TGTAGGT
           T                     AGTCAGG      TGCATGTCTC
                                |||||||      ||||||||||
                                TCAGTTT      ATGTGTAGGG
                                   TCTTAT_
GAM834   LOC255102 3'  GAGTGTGATGGCCTATGACTGG 96083   GT   GT      _   T
           TT                     A  CAG  GTAGGTTG CATG CTC
                                |  |||  |||||||| |||| |||
                                T  GTC  TATCCGGT GTGT GAG
                                 TG   AG       A   _
GAM834   LOC255995 3'  GAATTGCAGTTACATTTGGTT  96975   GT      GGT   TG
                                A  CAGGTGTA   TGCA  TC
                                |  ||||||||   ||||  ||
                                T  GTTTACAT   ACGT  AG
                                 TG       TG_   TA
GAM834   LOC256158 5'  GGGACGAGGGCATCTACACTTG 97675   _        T  AT__
           TGCT                    T CAGGTGTAGGT GC    GTCTC
                                | ||||||||||| ||    |||||
                                G GTTCACATCTA CG    CAGGG
                                 T         _  GGAG
GAM834   LOC256248 5'  AGGCATTCTTGCACCTG     96291          TTGC
                                CAGGTGTAGG    ATGTCT
                                ||||||||||    ||||||
                                GTCCACGTTC    TACGGA
                                      T____
GAM834   LOC256364 5'  GAGACTGGTCTCTGTGCTGACT 94799      G TG    TTG  T
                                AGTCA G  TAGG   CA GTCTC
                                ||||| |  ||||   || |||||
```

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                                TCAGT C  GTCT   GT CAGAG
                                  _ GT   CTG  _
GAM834   LOC256537 3'  GAGAGTGACTGACACTTGGTT  95227   GT      A   TG ATG
                                A  CAGGTGT GGT  C   TCTC
                                |  ||||||| |||  |   ||||
                                T  GTTCACA TCA  G   AGAG
                                 TG      G   GT ___
GAM834   LOC256691 3'  GAAATGATCTGCATTGGATT   96198      AG       TG   G
                                AGTC  GTGTAGGT  CAT TC
                                ||||  ||||||||  ||| ||
                                TTAG  TACGTCTA  GTA AG
                                  GT        __   A
GAM834   LOC256867 3'  TGCGGCCCGTGTTTGACT    94868        TG A
                                AGTCAGG  T GGTTGCA
                                |||||||  | |||||||
                                TCAGTTT  G CCGGCGT
                                     GT C
GAM834   LOC256946 3'  CACCACATGCAGTTTACATCTG 94545    T       GG       CTC
           TCT                    AG CAGGTGTA  TTGCATGT
                                || ||||||||  ||||||||
                                TC GTCTACAT  GACGTACA
                                 T       TT       CCACA
GAM834   LOC256974 5'  GGCAGTCGCAGCTTATATCTGC 97247    T           A__    TC
           T                     AG CAGGTGTAGGTTGC   TGTC
                                || ||||||||||||||   ||||
                                TC GTCTATATTCGACG   ACGG
                                 _            CTG
GAM834   LOC257169 5'  GGGGCCACGTTTTACCACTTGA 96150          _    T  CAT
           TT                     AGTCAGGTG TAGG TG   GTCTC
                                |||||||||| |||| ||   |||||
                                TTAGTTCAC ATTT GC   CGGGG
                                     C    T  AC_
GAM834   LOC257396 3'  GAGGCAGCTTTAGGCTTAACTT 97137       G     _____  A
           GATT                     CAGGT TAGGTT    GC TGTCTC
                                ||||| ||||||    || ||||||
                                GTTCA ATTCGG    CG ACGGAG
                                  _      ATTT  _
GAM834   LOC257428 5'  GAAGATGGGCTTGTATCTGGTT 94277    GT         G   G_
                                A  CAGGTGTAGGTT CAT  TC
                                |  ||||||||||| |||  ||
                                T  GTCTATGTTCGG GTA  AG
                                 TG          _   GA
GAM834   LOC257443 3'  GATTTTAACTTATGTTTGAT   95848       TG      CAT
                                GTCAGG  TAGGTTG   GTC
                                ||||||  |||||||   |||
                                TAGTTT  ATTCAAT   TAG
                                   GT      TT_
GAM834   LOC257468 3'  GACCCCCAGCCTCACACCTGGC 95188          _     CAT   TC
           T                     AGTCAGGTGT AGGTTG   GTC
                                |||||||||| ||||||   |||
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                                TCGGTCCACA TCCGAC   CAG
                                      C     CCC
GAM834  LOC257489 3'  CAGCCTAAATCTGATT      65612         G
                                AGTCAGGT TAGGTTG
                                |||||||| |||||||
                                TTAGTCTA ATCCGAC
                                   A
GAM834  LOC257548 5'  GAGGTCGCCTCTGTGCTGGCT  97740       G TG    TT  _  G
                                AGTCA G  TAGG  GC AT TC
                                ||||| |  ||||  || || ||
                                TCGGT C  GTCT  CG TG AG
                                   _ GT    C_  C  G
GAM834  LOC257610 5'  GAGGTCGCCTCTGTGCTGGCT  97856       G TG    TT  _  G
                                AGTCA G  TAGG  GC AT TC
                                ||||| |  ||||  || || ||
                                TCGGT C  GTCT  CG TG AG
                                   _ GT    C_  C  G
GAM834  LOC257619 5'  GTGCTGACCTGAACCTGGTT   97811    GT     G     _
                                A  CAGGT TAGGTT GCAT
                                |  ||||| |||||| ||||
                                T  GTCCA GTCCAG CGTG
                                 TG     A      T
GAM834  LOC51026  3'  GTACTTGCATTTGACT      32171             T
                                AGTCAGGTGTAGGT GC
                                |||||||||||||| ||
                                TCAGTTTACGTTCA TG
                                                _
GAM834  LOC51161  3'  GAGATGGGTCCCTGCACTTGGC 32514            TT  AT
                                GTCAGGTGTAGG  GC  GTCTC
                                ||||||||||||  ||  |||||
                                CGGTTCACGTCC  TG  TAGAG
                                      C_  GG
GAM834  LOC51231  3'  GGGACCCCTCCTACCCTTGACT 33171         T     TTGCAT
                                AGTCAGG GTAGG      GTCTC
                                ||||||| |||||      |||||
                                TCAGTTC CATCC      CAGGG
                                    C     TCCC__
GAM834  LOC80298  5'  GGACTCCCTGTGCCTTGCT    47290     C   TG    TTGCAT
                                AGT AGG  TAGG      GTCT
                                ||| |||  ||||      ||||
                                TCG TCC  GTCC      CAGG
                                  T   GT    CT____
GAM834  LOC89919  3'  ACATTGGCCTATGCCAGACT   60713      A         C
                                AGTC GGTGTAGGTTG ATGT
                                |||| |||||||||| ||||
                                TCAG CCGTATCCGGT TACA
                                  A          _
GAM834  LOC89941  3'  CAACTTGCTTTGATT       57056         T
                                AGTCAGG GTAGGTTG
                                ||||||| ||||||||
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                                TTAGTTT CGTTCAAC
                                      _
GAM834  LOC89944  3' GGGGCCCAGCCCAACACCTGGC 91549          A_    CAT
             T                   AGTCAGGTGT  GGTTG   GTCTC
                                 ||||||||||  |||||   |||||
                                 TCGGTCCACA  CCGAC   CGGGG
                                       AC    C__
GAM834  LOC90049  3' GAGGCATGTAAATGTATTT   61213        GG
                                 AGGTGTA  TTGCATGTCTC
                                 |||||||  ||||||||||
                                 TTTATGT  AATGTACGGAG
                                    A_
GAM834  LOC90355  3' GTCAGCCTACGCTTGGCT    52624              _
                                 AGTCAGGTGTAGGTTG C
                                 |||||||||||||||| |
                                 TCGGTTCGCATCCGAC G
                                           T
GAM834  LOC90631  3' GGATGTGTGAAGTCAGGCT   63636     AGG  TAGG TG
                                 AGTC   TG    T  CATGTCT
                                 ||||   ||    |  |||||||
                                 TCGG   AC    A  GTGTAGG
                                   ___  TGA_ GT
GAM834  LOC90768  5' GCGAGCTGGACCTGGCT     63957         G   G
                                 AGTCAGGT TAG TTGC
                                 ||||||||  ||| ||||
                                 TCGGTCCA GTC AGCG
                                      G   G
GAM834  LOC90906  3' GGGCACAGAGCCTACATTCGGT 64307    GT AG        GCA     C
             T                    A  C  GTGTAGGTT   TGTCT
                                  |  |  |||||||||   |||||
                                  T  G  TACATCCGA   ACGGG
                                  TG CT        GAC
GAM834  LOC91138  5' GCAACCTTGTCTGATT      65030        GT T
                                 AGTCAG  G AGGTTGC
                                 ||||||  | |||||||
                                 TTAGTC  T TCCAACG
                                    TG _
GAM834  LOC91263  3' GTCTTTGTAATTTATATTAGAT 65383      AG          TGTCTC
             T                    AGTC  GTGTAGGTTGCA
                                  ||||  ||||||||||||
                                  TTAG  TATATTTAATGT
                                    AT          TTCTGG
GAM834  LOC91397  3' GGACACCCTGTGCTGGCT    65911      G TG    TTGCA
                                 AGTCA G  TAGG    TGTCT
                                 |||||  |  ||||    |||||
                                 TCGGT C  GTCC    ACAGG
                                    _ GT    C_____
GAM834  LOC91445  3' AGACATGTGGCTTAACT     60546     G     TG
                                 GGT TAGGT  CATGTCT
                                 ||| |||||  |||||||
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                                TCA ATTCG  GTACAGA
                                  _    GT
GAM834  LOC91517  3' GAGGTGTGTGACAGGCAGTCTG 66309      _  AG  TG  GT
             ATT                  AGTCAGG TGT  GT  CAT  CTC
                                ||||||| |||  ||  |||  |||
                                TTAGTCT ACG  CA  GTG  GAG
                                   G   GA  GT   TG
GAM834  LOC91585  3' GAGATATCTTTGCCCTTGACT  66577      T    TTGC
                                AGTCAGG GTAGG   ATGTCTC
                                ||||||| |||||   |||||||
                                TCAGTTC CGTTT   TATAGAG
                                   C    C___
GAM834  LOC91585  5' GGACAAGGCCTAGCATTTGGCT 66579        _    GCA    C
                                AGTCAGGTGT AGGTT   TGTCT
                                |||||||||| |||||   |||||
                                TCGGTTTACG TCCGG   ACAGG
                                     A    A__    A
GAM834  LOC91812  5' GAGACAGGGTTCTGTGTTTGCT 67239   T   TG   TT  A_
                                AG CAGG  TAGG  GC  TGTCTC
                                || ||||  ||||  ||  ||||||
                                TC GTTT  GTCT  TG  ACAGAG
                                 _   GT   __ GG
GAM834  LOC91813  5' GAGACAGGGTTCTGTGTTTGCT 67251   T   TG   TT  A_
                                AG CAGG  TAGG  GC  TGTCTC
                                || ||||  ||||  ||  ||||||
                                TC GTTT  GTCT  TG  ACAGAG
                                 _   GT   __ GG
GAM834  LOC91960  5' GATATCTGTAGTTTTGCGTCTG 67664    GT _ GG    __   TC
             GCT                  TCAG  GT A  TTGCA  TGTC
                                ||||  || |  |||||  ||||
                                GGTC  CG T  GATGT  ATAG
                                  TG  T TT    CT
GAM834  LOC92080  3' CTGTGTGCAGCCTATGCCTGCT 68048   T          TG CTC
                                AG CAGGTGTAGGTTGCA  T
                                || ||||||||||||||  |
                                TC GTCCGTATCCGACGT  G
                                 _           GT TCT
GAM834  LOC92267  5' GGGCTGGGGCCGCGCCTGGCT  68623       A   G  T
                                AGTCAGGTGT GGTT CA GTCT
                                |||||||||| |||| || ||||
                                TCGGTCCGCG CCGG GT CGGG
                                     _   G  _
GAM834  LOC92299  5' GAGTCTGGCTTGCCGTTTGACT 68810     GG GTA  T_ ATGT
                                AGTCA  T   GGT  GC   CTC
                                |||||  |   |||  ||   |||
                                TCAGT  G   CCG  CG   GAG
                                  TT ____  TT  GTCT
GAM834  LOC92344  3' GGGGTATGTTTCACCTTGATT  69007     _   TAGGTT   GT
                                AGTCA GGTG    GCAT  CTC
                                ||||| ||||    ||||  |||
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                                TTAGT CCAC     TGTA  GGG
                                  T   TT____    TG
GAM834  LOC92360  5'  GAGACCTCACGTCTGGATCTGG 69074        G   TTGCAT
            CT                   AGTCAGGT TAGG     GTCTC
                                ||||||||  ||||     |||||
                                TCGGTCTA GTCT     CAGAG
                                   G   GCACTC
GAM834  LOC92391  3'  GTGTGGCCTGCACTGGGTT   69158   GT A       TG
                                A  C GGTGTAGGT  CAT
                                |  |  |||||||||  |||
                                T  G TCACGTCCG  GTG
                                 TG G        GT
GAM834  LOC92597  3'  TCAACTGTAATTTAAATTTGGC 69973        G       T  CTC
            T                    AGTCAGGT TAGGTTGCA GT
                                ||||||||  |||||||||  ||
                                TCGGTTTA ATTTAATGT CA
                                     A       _  ACTC
GAM834  LOC93268  5'  GAGGTGCCAGCTGTAGTCTGGT 71880   GT    GTA    _   G  TC
            T                    A  CAGGT   GGTTG CAT TC
                                |  |||||   ||||| ||| ||
                                T  GTCTG   TCGAC GTG AG
                                 TG    ATG    C   G
GAM834  LOC96597  5'  GGAAGAGCCTGTGCCTGCT   66915    T   TG     GCATG
                                AG CAGG  TAGGTT    TCT
                                || ||||  ||||||     |||
                                TC GTCC  GTCCGA     AGG
                                  _   GT     GA___
GAM834  LOC96597  3'  GTCGGTCTGCCCTGGCT     66920       T   GT  _
                                AGTCAGG GTAG  TG C
                                |||||||  ||||  || |
                                TCGGTCC CGTC  GC G
                                     _   TG  T
GAM835  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                ||||  |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM835  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   |||  ||  |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM835  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                ||||||||||||  |||
                                GTAAAGTGAAAG GAT
                                                _
GAM835  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                   CATTTCACTTTCACTGTCTGAGAT
                                ||||||||||||||||||||||||
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                                GTAAAGTGAAAGTGACAGACTCTA

GAM835  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM835  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM835  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM835  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM835  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_   CG_
GAM835  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM835  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                |||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM835  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||         |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM835  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM835  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
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                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM835  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM835  NIR3     3'  GCAGTGAAAGTGCAAT      66242      T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM835  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM835  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM835  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__   TT
GAM835  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM835  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM835  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM835  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM835  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
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                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM835  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                      _
GAM836  ABCA1    3'  GGAGACTGGTTTCCCGGTGA   18548          G  _
                                TCACTGGGAAA TA TCTCC
                                |||||||||| || |||||
                                AGTGGCCCTTT GT AGAGG
                                    G  C
GAM836  ACVR1    5'  GAGTACCCCAGTGA        6607         AAA   T
                                TCACTGGG   GTA CTC
                                ||||||||   ||| |||
                                AGTGACCC   CAT GAG
                                    ____  _
GAM836  ANXA8    3'  AGGTCATTTCCCAGTG      7892           GT
                                CACTGGGAAA  ATCT
                                ||||||||||  ||||
                                GTGACCCTTT  TGGA
                                    AC
GAM836  B4GALT4  3'  AGGTATGCCTTCCAGTGA    13669         AA_
                                TCACTGGGA   GTATCT
                                |||||||||   ||||||
                                AGTGACCTT   TATGGA
                                    CCG
GAM836  CALU     3'  AGAACCTCCCAGTAGA      6882     _     AA  A
                                TC ACTGGGA  GT TCT
                                || |||||||  || |||
                                AG TGACCCT  CA AGA
                                 A      C_ _
GAM836  CD44     3'  TCTGGGAGACACCAAAGGGTGA 5209       GGGAAA  A
                                TCACT     GT TCTCCCAGA
                                |||||     || ||||||||||
                                AGTGG     CA AGAGGGTCT
                                   GAAAC_  C
GAM836  COL11A2  3'  TCTGAGTCAGGACTTTCCTCAG 54765       _     A   CC__
          TGA                     TCACTG GGAAAGT TCT    CAGA
                                |||||| ||||||| |||    ||||
                                AGTGAC CCTTTCA GGA    GTCT
                                   T      _  CTGA
GAM836  COL11A2  3'  TCTGAGTCAGGACTTTCCTCAG 54767       _     A   CC__
          TGA                     TCACTG GGAAAGT TCT    CAGA
                                |||||| ||||||| |||    ||||
                                AGTGAC CCTTTCA GGA    GTCT
                                   T      _  CTGA
GAM836  CSPG3    3'  TCTGGGAGTGTGTCCCAGCTGA 15239     _     AAGTAT
                                TCA CTGGGA     CTCCCAGA
                                ||| ||||||     ||||||||
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                                AGT GACCCT     GAGGGTCT
                                  C     GTGT__
GAM836  DEC1     3'  TCTGGCATACTTTCC      33799         CTC
                                GGAAAGTAT   CCAGA
                                |||||||||   |||||
                                CCTTTCATA   GGTCT
                                     C__
GAM836  DNAJB1   3'  TCTGGGAGCCTGGCCTCAG   20448     _ AA  TAT
                                CTG GG  AG   CTCCCAGA
                                ||| ||  ||   ||||||||
                                GAC CC  TC   GAGGGTCT
                                  T  GG  C__
GAM836  DYRK1A   5'  TCTGAGGTTCTTTTCCAGTGA  55249          T    CC
                                TCACTGGGAAAG ATCTC  AGA
                                ||||||||||| |||||  |||
                                AGTGACCTTTTC TGGAG  TCT
                                       T    __
GAM836  DYT1     3'  CTGGAAGAGGAATCCAGTGA   3672         AAAGTA   C
                                TCACTGGG     TCT CCAG
                                ||||||||     ||| ||||
                                AGTGACCT     AGA GGTC
                                     AAGG__   A
GAM836  EPB42    5'  TCCAGGAGATACCAGCAGAGA  3692     A   GGAAA      CA
                                TC CTG    GTATCTCC  GA
                                || |||    ||||||||  ||
                                AG GAC    CATAGAGG  CT
                                 A   GAC__       AC
GAM836  ERBB2    3'  TCTGAGGCCCTGCCCAATGA   15476    C   AA  TA   CC
                                TCA TGGG  AG  TCTC  AGA
                                ||| ||||  ||  ||||  |||
                                AGT ACCC  TC  GGAG  TCT
                                  A   G_  CC   __
GAM836  FKRP     3'  CTGGGAGAGCCCTGTGA     44184      T   AAAGTA
                                TCAC GGG     TCTCCCAG
                                |||| |||     ||||||||
                                AGTG CCC     AGAGGGTC
                                   T   G_____
GAM836  FRK      5'  AGACACCTTCCTAGTGA     8959          A  A
                                TCACTGGGAA GT TCT
                                |||||||||| || |||
                                AGTGATCCTT CA AGA
                                      C  C
GAM836  FZD4     3'  AGATCTCTCCCAGTGA      24124         A  T
                                TCACTGGGA AG ATCT
                                ||||||||| || ||||
                                AGTGACCCT TC TAGA
                                      C  _
GAM836  GABRE    3'  CTGTAACTTTCCCAGTGA    41806           ATCTCC
                                TCACTGGGAAAGT     CAG
                                ||||||||||||      |||
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                                AGTGACCCTTTCA     GTC
                                      AT____
GAM836  GABRE    3'  CTGTAACTTTCCCAGTGA    41775          ATCTCC
                                TCACTGGGAAAGT     CAG
                                ||||||||||||      |||
                                AGTGACCCTTTCA     GTC
                                      AT____
GAM836  GABRE    3'  CTGTAACTTTCCCAGTGA    41784          ATCTCC
                                TCACTGGGAAAGT     CAG
                                ||||||||||||      |||
                                AGTGACCCTTTCA     GTC
                                      AT____
GAM836  GABRE    3'  CTGTAACTTTCCCAGTGA    17111          ATCTCC
                                TCACTGGGAAAGT     CAG
                                ||||||||||||      |||
                                AGTGACCCTTTCA     GTC
                                      AT____
GAM836  GRB10    5'  CTGGGTCCTCTCAGTGA     17977         AAGTATCT
                                TCACTGGGA       CCCAG
                                |||||||||       |||||
                                AGTGACTCT       GGGTC
                                     CCT_____
GAM836  HMG20A   3'  TCTGAAATGCTGTCTTTCCCAG 36543          TATCTCC__
          T                      ACTGGGAAAG        CAGA
                                 ||||||||||        ||||
                                 TGACCCTTTC        GTCT
                                       TGTCGTAAA
GAM836  IL18RAP  3'  AGATTTCCCAGTGG        13902          AGT
                                TCACTGGGAA   ATCT
                                ||||||||||   ||||
                                GGTGACCCTT   TAGA
                                      ___
GAM836  ITPR2    3'  TCTGGGAGATACTCTGCAAGT  9452      GGGAA
                                ACT    AGTATCTCCCAGA
                                |||    ||||||||||||||
                                TGA    TCATAGAGGGTCT
                                  ACGTC
GAM836  MAN2C1   5'  GAGACCTTCCCAGTGG      72918          A TA
                                TCACTGGGAA G  TCTC
                                |||||||||| |  ||||
                                GGTGACCCTT C  AGAG
                                      C __
GAM836  MAPK8IP1 3'  AGGACTTTCCAGTGA       18401        G    A
                                TCACTGG AAAGT TCT
                                ||||||| ||||| |||
                                AGTGACC TTTCA GGA
                                      _   _
GAM836  MN1      3'  TCTGTCTTTGACTTTCCCAG   10097          ATCTCC
                                CTGGGAAAGT     CAGA
                                ||||||||||     ||||
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                                GACCCTTTCA     GTCT
                                     GTTTCT
GAM836  NIPSNAP1  3'  TCTGGGGGTCTCCTCAGTGA  13294      _  AAGTAT
                                TCACTG GGA     CTCCCAGA
                                |||||| |||     ||||||||
                                AGTGAC CCT     GGGGGTCT
                                   T  CT____
GAM836  ODF2      3'  CTGGTGGTTTTCCTCTCCCAGT 10325        A  TAT__ TC
           GA                     TCACTGGGA AG    C  CCAG
                                |||||||||  ||    |  ||||
                                AGTGACCCT TC    G  GGTC
                                     C  CTTTT GT
GAM836  PAFAH1B1  3'  TCTGTGTGAACTTTCCCGGT  4734          A  TCC
                                ACTGGGAAAGT TC   CAGA
                                ||||||||||| ||   ||||
                                TGGCCCTTTCA AG   GTCT
                                      _  TGT
GAM836  PIG3      3'  CTGGAACTGCCCCAGTGA    16876        AA   ATCTC
                                TCACTGGG  AGT    CCAG
                                ||||||||  |||    ||||
                                AGTGACCC  TCA    GGTC
                                     CG   A____
GAM836  PKNOX1    3'  TCTGGAATTGATTTTTCCCA  15884        T   TC__
                                TGGGAAAG ATC    CCAGA
                                |||||||| |||    |||||
                                ACCCTTTT TAG    GGTCT
                                     _   TTAA
GAM836  PTGFRN    3'  CTGGAAGCAGATTCCCATTGA  67188     C     AGTAT  C
                                TCA TGGGAA     CT CCAG
                                ||| ||||||     || ||||
                                AGT ACCCTT     GA GGTC
                                  T     AGAC_  A
GAM836  PTPRG     3'  TCTGTATTACAGCTTTCCCAGT 11112          ATCTCC_
                                ACTGGGAAAGT      CAGA
                                ||||||||||       ||||
                                TGACCCTTTCG      GTCT
                                      ACATTAT
GAM836  RAB36     3'  CTGCACTCTTTCCCAGCGA    16959    A       TATCTCC
                                TC CTGGGAAAG      CAG
                                || |||||||||      |||
                                AG GACCCTTTC      GTC
                                  C        TCAC___
GAM836  RASD1     5'  CTGGGAGAACCCCAG       32222       AAA  A
                                CTGGG   GT TCTCCCAG
                                |||||   || ||||||||
                                GACCC   CA AGAGGGTC
                                     ___  _
GAM836  SMURF1    3'  AGAAGCCCGTTCCCCAGTGG  92446        _  A__  A
                                TCACTGGG AA   GT TCT
                                |||||||| ||   || |||
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                                GGTGACCC TT   CG AGA
                                    C  GCC  A
GAM836  SUFU     3'  AGCTGCTCCCCAGTGA     32406        AA    T
                                TCACTGGG  AGTA CT
                                ||||||||  |||| ||
                                AGTGACCC  TCGT GA
                                    C_    C
GAM836  TAZ      5'  GGCGACCGCTCCCCAGTGA   3677         AA   A_  T
                                TCACTGGG  AGT  TC CC
                                ||||||||  |||  || ||
                                AGTGACCC  TCG  AG GG
                                    C_   CC  C
GAM836  TM4SF6   3'  TCTGAACTGGCTCCTTCCCAGT 12327         __   ATCTCC
                                ACTGGGAA  AGT     CAGA
                                ||||||||  |||     ||||
                                TGACCCTT  TCG     GTCT
                                    CC   GTCAA_
GAM836  UBE2E3   3'  CTGGGAGACTCCCCA      20994     AA  TA
                                TGGG  AG  TCTCCCAG
                                ||||  ||  ||||||||
                                ACCC  TC  AGAGGGTC
                                  C_  __
GAM836  VCAM1    3'  CTGTGCAACTTTCCCAATG   54769    C       ATCTCC
                                CA TGGGAAAGT     CAG
                                || |||||||||     |||
                                GT ACCCTTTCA     GTC
                                 A        ACGT__
GAM836  VCAM1    3'  CTGTGCAACTTTCCCAATG   6545     C       ATCTCC
                                CA TGGGAAAGT     CAG
                                || |||||||||     |||
                                GT ACCCTTTCA     GTC
                                 A        ACGT__
GAM836  BART1    3'  CTGGGGGGCCCTTCCCCAG   23984      A   TA
                                CTGGG AAG  TCTCCCAG
                                ||||| |||  ||||||||
                                GACCC TTC  GGGGGGTC
                                   C   CC
GAM836  BTN3A1   3'  CTGAGGTTCTTTTCCCAGGA  22917    A       TATCT  _
                                TC CTGGGAAAG    CC CAG
                                || |||||||||    || |||
                                AG GACCCTTTT    GG GTC
                                 _       CTT__  A
GAM836  C20orf150 3'  CTGGGAGGTGTCCCACTGA   65398    C    AAG
                                TCA TGGGA   TATCTCCCAG
                                ||| |||||   ||||||||||
                                AGT ACCCT   GTGGAGGGTC
                                  C    ____
GAM836  C20orf183 3'  GGGAGGTGGAGCTTCCAGTGA 47809         AAG_
                                TCACTGGGA    TATCTCCC
                                |||||||||    ||||||||
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                                AGTGACCTT   GTGGAGGG
                                     CGAG
GAM836  CHERP    3'  CTGAGAGGAGGCCCAGTGA   21100       AAAGTA   C
                                TCACTGGG    TCTC CAG
                                |||||||     |||| |||
                                AGTGACCC    GGAG GTC
                                     GGA___   A
GAM836  CLIPR-59  3'  GAGATAGAGATTCCCAGT    31372       AG__
                                ACTGGGAA    TATCTC
                                ||||||||    ||||||
                                TGACCCTT    ATAGAG
                                     AGAG
GAM836  DJ726C3.2 5'  CTGGGTCCCTTCCCAGTGG   47445         AGTATCT
                                TCACTGGGAA      CCCAG
                                ||||||||||      |||||
                                GGTGACCCTT      GGGTC
                                      CCCT___
GAM836  DKFZP434A1319 3'  AGAGCACTCTTCCCAGT     49550       _   A_
                                ACTGGGAA AGT  TCT
                                |||||||| |||  |||
                                TGACCCTT TCA  AGA
                                     C   CG
GAM836  DKFZp434E0519 3'  CTGAATTCTCTCAGTGA     49987         A   ATCTCC
                                TCACTGGGA AGT     CAG
                                ||||||||| |||     |||
                                AGTGACTCT TTA     GTC
                                      C   A_____
GAM836  DKFZp434G0920 3'  TCTGGGGGATCCCCCAGCTGA  50014     _    AAAGT
                                TCA CTGGG    ATCTCCCAGA
                                ||| |||||    ||||||||||
                                AGT GACCC    TAGGGGGTCT
                                  C    CC___
GAM836  DKFZP434L0117 3'  TCTGGGGGATTCCCCCAGGGA  42922    A    AAAGT
                                TC CTGGG    ATCTCCCAGA
                                || |||||    ||||||||||
                                AG GACCC    TAGGGGGTCT
                                 G    CCT__
GAM836  DKFZp434N035 3'  CTGGGATAAATTTCCCAGGA   50049    A      GTATC
                                TC CTGGGAAA    TCCCAG
                                || ||||||||    ||||||
                                AG GACCCTTT    AGGGTC
                                 _       AAAT_
GAM836  DKFZp566D133 3'  GAGATTCTACCCAGTGA     71762        AA  T
                                TCACTGGG  AG ATCTC
                                ||||||||  || |||||
                                AGTGACCC  TC TAGAG
                                     A_  T
GAM836  DKFZp761G0313 3'  AGGTCACTTTCCCAGTGA    65813          _
                                TCACTGGGAAAGT ATCT
                                |||||||||||| ||||
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                                AGTGACCCTTTCA TGGA
                                       C
GAM836  DKFZP762D096 3'  TCTGACTGGCCCCCCAGTGA   65580        AAA  ATCTCC
                                TCACTGGG   GT     CAGA
                                ||||||||   ||     ||||
                                AGTGACCC   CG     GTCT
                                     CC_  GTCA__
GAM836  FLJ10751  3'  CTGGGAGACACTTGGCCT    36569     A_    A
                                GGG  AAGT TCTCCCAG
                                |||  |||| ||||||||
                                TCC  TTCA AGAGGGTC
                                  GG   C
GAM836  FLJ10751  3'  CTGGGAGACACTTGGCCT    36730     A_    A
                                GGG  AAGT TCTCCCAG
                                |||  |||| ||||||||
                                TCC  TTCA AGAGGGTC
                                  GG   C
GAM836  FLJ12526  3'  GATCACTTTCCCAGTGA     45562            _
                                TCACTGGGAAAGT ATC
                                |||||||||||| |||
                                AGTGACCCTTTCA TAG
                                       C
GAM836  FLJ12747  3'  TCTGAAAGAACTGGCCCAGTGG 49728         AA   A   CC
                                TCACTGGG  AGT TCT  CAGA
                                ||||||||  ||| |||  ||||
                                GGTGACCC  TCA AGA  GTCT
                                     GG   _   AA
GAM836  FLJ12891  3'  GGGCTTCCCGGTGA        46347          A TATCT
                                TCACTGGGAA G     CCC
                                ||||||||||  |     |||
                                AGTGGCCCTT C     GGG
                                          _ ______
GAM836  FLJ13117  3'  GATCTTTCCCAGTGA       43541            T
                                TCACTGGGAAAG ATC
                                |||||||||||| |||
                                AGTGACCCTTTC TAG
                                          _
GAM836  FLJ13158  3'  TCTGAATACTTTCCCA      46113           CTCC
                                TGGGAAAGTAT    CAGA
                                ||||||||||    ||||
                                ACCCTTTCATA    GTCT
                                       A___
GAM836  FLJ13955  3'  CTGGACCTCTCCCTAGTGA   45407      _    A  TATCTC
                                TCACT GGGA AG     CCAG
                                |||||  |||| ||     ||||
                                AGTGA CCCT TC     GGTC
                                   T    C  CA____
GAM836  FLJ14117  3'  CTGGGACTGCCACATCCCCAGT 42906         AAA___   TC
            GA                    TCACTGGG     GTA  TCCCAG
                                ||||||||     |||  ||||||
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                                AGTGACCC     CGT  AGGGTC
                                     CTACAC   C_
GAM836  FLJ14957  3'  TCTGAGACCTGTTCCCAGT   51764        AGTA    CC
                                ACTGGGAA    TCTC  AGA
                                ||||||||    ||||  |||
                                TGACCCTT    AGAG  TCT
                                     GTCC    __
GAM836  FLJ20452  3'  CTGAGGACCTTTCCCAG     35201         TATC  _
                                CTGGGAAAG    TCC CAG
                                |||||||||    ||| |||
                                GACCCTTTC    AGG GTC
                                     C___   A
GAM836  FLJ21986  5'  AGAACTGCAACTTCCAGTGA  46152         AA_  __
                                TCACTGGGA   GTA  TCT
                                |||||||||   |||  |||
                                AGTGACCTT   CGT  AGA
                                     CAA   CA
GAM836  FLJ22329  3'  CTGGGTAGGACATTTCCCAG  45067         _ A  _
                                CTGGGAAA GT TCT CCCAG
                                |||||||| || ||| |||||
                                GACCCTTT CA GGA GGGTC
                                     A  _   T
GAM836  FLJ30791  5'  GGACTACGTTTCCCAGCGG   58446    A       _   TC
                                TC CTGGGAAA GTA  TCC
                                || ||||||||  |||  |||
                                GG GACCCTTT CAT  AGG
                                 C       G   C_
GAM836  FLJ31121  3'  TCTGAGGCTGCTTTCCCA    58537          TCT  _
                                TGGGAAAGTA   CC CAGA
                                ||||||||||   || ||||
                                ACCCTTTCGT   GG GTCT
                                     C__  A
GAM836  FLJ32771  3'  AGCTACTTTCCTAATGA     58799     C        T
                                TCA TGGGAAAGTA CT
                                ||| ||||||||||  ||
                                AGT ATCCTTTCAT GA
                                  A         C
GAM836  GNB4      3'  TCTGAACATCTTTCCCAGTG   41273          TATCTCC
                                CACTGGGAAAG      CAGA
                                ||||||||||       ||||
                                GTGACCCTTTC      GTCT
                                      TACAA__
GAM836  GOLGA1    3'  GAGGCCGCTTCTCCAGTGA   9091        GA   A_
                                TCACTGG  AAGT  TCTC
                                |||||||  ||||  ||||
                                AGTGACC  TTCG  GGAG
                                     TC    CC
GAM836  HES2      3'  GGATCTGCCCCAGTGA      38855         AA  T
                                TCACTGGG  AG ATCT
                                ||||||||  || ||||
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                                AGTGACCC  TC TAGG
                                    CG  _
GAM836  HSPB7    3'  CTGGGAAATGCCTGCTGCCCCC 27027        AA_   TC____
            AGTGA                   TCACTGGG   AGTA     TCCCAG
                                |||||||||  ||||     ||||||
                                AGTGACCC   TCGT     AGGGTC
                                    CCG    CCGTAA
GAM836  ITPK1    3'  TCCGGGCTGTCCTCTGCCCAGT 26415        AA_  T  CT   A
            GA                    TCACTGGG   AG AT  CCC GA
                                |||||||||  || ||  ||| ||
                                AGTGACCC   TC TG  GGG CT
                                    GTC  C  TC   C
GAM836  KIAA0295 3'  GGAAGCTTTCCAGTGA     68106        G    A
                                TCACTGG AAAGT TCT
                                ||||||| ||||| |||
                                AGTGACC TTTCG AGG
                                    _    A
GAM836  KIAA0296 3'  TCTGGCTTCTTTCCCAAGGA   28120    AC      TATCTC
                                TC  TGGGAAAG     CCAGA
                                ||  |||||||||     |||||
                                AG  ACCCTTTC     GGTCT
                                 GA       TTC___
GAM836  KIAA0440 3'  AGACACTCCCTCCAGTGA    31454        _ AA   A
                                TCACTGG G  AGT TCT
                                ||||||| |  ||| |||
                                AGTGACC C  TCA AGA
                                    T CC   C
GAM836  KIAA0532 3'  TCTAAAAGATACTTCAAAGTGA 70779      GG   A     CCC
                                TCACT  GAA GTATCT   AGA
                                |||||  ||| ||||||   |||
                                AGTGA  CTT CATAGA   TCT
                                   AA   _     AAA
GAM836  KIAA0939 3'  CTGGGAGAGTGCCCCCA     62013      AAA  _
                                TGGG   GTA TCTCCCAG
                                ||||   ||| ||||||||
                                ACCC   CGT AGAGGGTC
                                  C__   G
GAM836  KIAA1045 3'  TCTGGGCCACATGCCCCAGTGA 71061        AAA   CT__
                                TCACTGGG   GTAT    CCCAGA
                                |||||||||  ||||    ||||||
                                AGTGACCC   CGTA    GGGTCT
                                    ____    CACC
GAM836  KIAA1277 3'  CTGGGAGGACAGCCCCAG    64454      AAA  A
                                CTGGG   GT TCTCCCAG
                                |||||   || ||||||||
                                GACCC   CA GGAGGGTC
                                   CGA  _
GAM836  KIAA1387 3'  CTGGGAGACAGCTTCTCAG    70872        A  A_
                                CTGGGAA GT  TCTCCCAG
                                ||||||| ||  ||||||||
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                                GACTCTT CG  AGAGGGTC
                                    _ AC
GAM836  KIAA1423  3'  CTGGATGCTTTCCCCGGTGA  61726       _     CTC
                                TCACTGGG AAAGTAT  CCAG
                                |||||||| |||||||  ||||
                                AGTGGCCC TTTCGTA  GGTC
                                    C     ____
GAM836  KIAA1613  3'  TCTGGACCATTTTCCCAATGG  64821    C       ATCTC
                                TCA TGGGAAAGT    CCAGA
                                ||| |||||||||    |||||
                                GGT ACCCTTTTA    GGTCT
                                  A       CCA__
GAM836  KIAA1679  3'  GGAGAAAACCTGCCCAGTGA  70154       AAA  A_
                                TCACTGGG  GT  TCTCC
                                ||||||||  ||  |||||
                                AGTGACCC  CA  AGAGG
                                    GTC  AA
GAM836  KIAA1719  3'  CTGACACCTTTCCCCAGTGA  68160       _   TATCTCC
                                TCACTGGG AAAG     CAG
                                |||||||| ||||     |||
                                AGTGACCC TTTC     GTC
                                    C   CACA___
GAM836  KR18    3'  CTGAGGCCATTACCCAGTGA  52744       A  GTATCT  _
                                TCACTGGG AA    CC CAG
                                |||||||| ||    || |||
                                AGTGACCC TT    GG GTC
                                    A  ACC___  A
GAM836  KRTAP4-14 3'  AGAATATCCTTCCCAGTGA  52341        A_   _
                                TCACTGGGAA  GTAT CT
                                ||||||||||  |||| ||
                                AGTGACCCTT  TATA GA
                                     CC   A
GAM836  MAP3K6  3'  AGGACTGGTTCCAGTGA    16244       A_  A
                                TCACTGGGA  AGT TCT
                                |||||||||  ||| |||
                                AGTGACCTT  TCA GGA
                                    GG  _
GAM836  METAP2  3'  CTAAGAGATACTTTTTGG    60169   TG G       CC
                                C  G AAAGTATCTC  AG
                                |  | ||||||||||  ||
                                G  T TTTCATAGAG  TC
                                 GT _        AA
GAM836  MGC10715 3'  CTGCCCTCACTCCCCAGTGA  44247       AA  ATCTCC
                                TCACTGGG  AGT    CAG
                                ||||||||  |||    |||
                                AGTGACCC  TCA    GTC
                                    C_  CTCCC_
GAM836  MGC13114 3'  TCTGGGAAATACCCCG    50417     AAA   C
                                TGGG  GTAT TCCCAGA
                                ||||  |||| |||||||
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                                GCCC  CATA AGGTCT
                                  ___   A
GAM836  MGC14161  3'  CTAGGAGGGTGTTTCCCAG  51842      GTA   C
                                CTGGGAAA  TCTCC AG
                                ||||||||  ||||| ||
                                GACCCTTT  GGAGG TC
                                    GTG   A
GAM836  MGC15677  3'  CTGGGTTATTTATTTTCCCA  51798       TCT__
                                TGGGAAAGTA   CCCAG
                                ||||||||||   |||||
                                ACCCTTTTAT   GGGTC
                                     TTATT
GAM836  MSP       3'  CTAGGAGATACTCAGGGA   49416   A  GGAA      C
                                TC CTG   AGTATCTCC AG
                                || |||   ||||||||| ||
                                AG GAC   TCATAGAGG TC
                                 G  ____      A
GAM836  OLIG1     3'  TCTGGGAGAGCGAGGCCGAG  95592   G  AAA_  A
                                CT GG   GT TCTCCCAGA
                                || ||   || |||||||||
                                GA CC   CG AGAGGGTCT
                                 G  GGAG  _
GAM836  P2RXL1    3'  CTGAAGGTCTCTCTCCCAGTG  18381      A  T_   CC
                                CACTGGGA AG  ATCT  CAG
                                |||||||| ||  ||||  |||
                                GTGACCCT TC  TGGA  GTC
                                    C  TC   A_
GAM836  P66       3'  CTGGGCTCCCCCAGTGG    40365      AA  TATCT
                                TCACTGGG  AG   CCCAG
                                ||||||||  ||   |||||
                                GGTGACCC  TC   GGGTC
                                    CC  _____
GAM836  PADI2     3'  TCTGAAGCCATCCCCAGTGA  23752      AAAGTAT  CC
                                TCACTGGG     CT  CAGA
                                ||||||||     ||  ||||
                                AGTGACCC     GA  GTCT
                                    CTACC__  A_
GAM836  PCDH16    3'  CTGGGTTCTCCTCAGTGA   13605      AA  TATCT
                                TCACTGGG  AG   CCCAG
                                ||||||||  ||   |||||
                                AGTGACTC  TC   GGGTC
                                    C_  TT___
GAM836  PIGQ      3'  CTGGGGGCTCCCCAGTGG   14849      AA  TAT
                                TCACTGGG  AG   CTCCCAG
                                ||||||||  ||   |||||||
                                GGTGACCC  TC   GGGGGTC
                                    C_  ___
GAM836  POLR3F    5'  CTGGAGTTCCTTTCCCAGTG  59939       TAT   C
                                CACTGGGAAAG   CTCC AG
                                ||||||||||   |||| ||
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                                GTGACCCTTTC  GAGG TC
                                     CTT   _
GAM836  PP1665   5'  GGAAACAGCTCTCCCAGTGA  47918        A  ATC_
                                TCACTGGGA AGT   TCC
                                ||||||||| |||   |||
                                AGTGACCCT TCG   AGG
                                     C  ACAA
GAM836  PPP1R16B 3'  CTGAGTGATGCTTTCCCAGGA  61384    A         TCC
                                TC CTGGGAAAGTATC  CAG
                                || ||||||||||||  |||
                                AG GACCCTTTCGTAG  GTC
                                 _         TGA
GAM836  PYPAF4   3'  GGAGATACAAATCATTGA   78579    C  GAAA
                                TCA TGG   GTATCTCC
                                ||| |||   ||||||||
                                AGT ACT   CATAGAGG
                                  T  AAA_
GAM836  PYY      3'  CTGGGAGATCTGCCAACCA   14777    GAA__  T
                                TGG    AG ATCTCCCAG
                                |||    || |||||||||
                                ACC    TC TAGAGGGTC
                                  AACCG  _
GAM836  RYBP     5'  TCTGAAAGATCCTCCTAGTGA  59471        AA T   CC
                                TCACTGGGA  G ATCT  CAGA
                                |||||||||  | ||||  ||||
                                AGTGATCCT  C TAGA  GTCT
                                     __ C   AA
GAM836  SCAND2   5'  AGATGGCTTCCCAGTGA    53313        AG
                                TCACTGGGAA  TATCT
                                ||||||||||  |||||
                                AGTGACCCTT  GTAGA
                                     CG
GAM836  SCAND2   5'  AGATGGCTTCCCAGTGA    53307        AG
                                TCACTGGGAA  TATCT
                                ||||||||||  |||||
                                AGTGACCCTT  GTAGA
                                     CG
GAM836  SCAND2   5'  AGATGGCTTCCCAGTGA    53308        AG
                                TCACTGGGAA  TATCT
                                ||||||||||  |||||
                                AGTGACCCTT  GTAGA
                                     CG
GAM836  SCAND2   5'  AGATGGCTTCCCAGTGA    53309        AG
                                TCACTGGGAA  TATCT
                                ||||||||||  |||||
                                AGTGACCCTT  GTAGA
                                     CG
GAM836  SCAND2   5'  AGATGGCTTCCCAGTGA    53306        AG
                                TCACTGGGAA  TATCT
                                ||||||||||  |||||
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                                AGTGACCCTT  GTAGA
                                      CG
GAM836  SCAND2   5'  AGATGGCTTCCCAGTGA     41885          AG
                                TCACTGGGAA  TATCT
                                ||||||||||  |||||
                                AGTGACCCTT  GTAGA
                                      CG
GAM836  SEI1     3'  CTGGAATTACCCCCTAGTGA  25378        AAA   TCTC
                                TCACTGGG   GTA   CCAG
                                ||||||||   |||   ||||
                                AGTGATCC   CAT   GGTC
                                     CC_   TAA_
GAM836  SIAT4A   3'  ATCTGAGAGACAGGACAGTTTC 11667       __ A___    C   III
            CCAGGA                  GGGAAA  GT   TCTC CAGA   T
                                ||||||  ||   |||| ||||  |
                                CCCTTT  CA   AGAG GTCT   A
                                    GA  GGAC   A   III
GAM836  SLC4A9   3'  TCTGGGAGTGGAGACCCCAGGA 66219    A    AAAGTAT
                                TC CTGGG      CTCCCAGA
                                || |||||      ||||||||
                                AG GACCC      GAGGGTCT
                                 _    CAGAGGT
GAM836  SOX7     3'  CTGAGAGTTGCTGTCTCCCAGT 48724         A__   T   C
            GG                    TCACTGGGA   AGTA CTC CAG
                                |||||||||   |||| ||| |||
                                GGTGACCCT   TCGT GAG GTC
                                      CTG   T   A
GAM836  TGOLN2   3'  CTGAGAGACACCCTCCTCTAGA 64048    ACT   AA  A   C
                                TC   GGGA  GT TCTC CAG
                                ||   ||||  || |||| |||
                                AG   TCCT  CA AGAG GTC
                                 ATC   CC  C   A
GAM836  TU3A     3'  TCTGGGAAAGCTTTTCCA    23193         ATC
                                TGGGAAAGT   TCCCAGA
                                |||||||||   |||||||
                                ACCTTTTCG   AGGGTCT
                                      AA_
GAM836  VPS33B   3'  CTGAACACATTCCTCAGTGA   37901       _   A  ATCTCC
                                TCACTG GGAA GT     CAG
                                |||||| |||| ||     |||
                                AGTGAC CCTT CA     GTC
                                   T   A  CAA___
GAM836  XYLT1    5'  CTGGGAAAGGCCCCGGTGA   77850        AAA  ATC
                                TCACTGGG   GT   TCCCAG
                                ||||||||   ||   ||||||
                                AGTGGCCC   CG   AGGGTC
                                     ___  GAA
GAM836  YEA      3'  GAGCTGATTCCCAGTGA     51530          AG  T
                                TCACTGGGAA  TA CTC
                                ||||||||||  || |||
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                                AGTGACCCTT  GT GAG
                                      A_  C
GAM836  LOC131870 3'  CTGGGAGATCAGAGCCACTGA  75018     C   GAAAGT
                                TCA TGG     ATCTCCCAG
                                ||| |||     |||||||||
                                AGT ACC     TAGAGGGTC
                                  C   GAGAC_
GAM836  LOC136442 3'  CTGCATGCTCCCTCCCAGTGA  54285         A__     CTCC
                                TCACTGGGA   AGTAT    CAG
                                |||||||||   |||||    |||
                                AGTGACCCT   TCGTA    GTC
                                      CCC     C___
GAM836  LOC142972 3'  AGGTCATTTCCCAGTG      65128          GT
                                CACTGGGAAA  ATCT
                                ||||||||||  ||||
                                GTGACCCTTT  TGGA
                                      AC
GAM836  LOC145813 5'  CTGGAGCCTGCCCTTACCCAGT 83507         A   TAT___    C
              GA                    TCACTGGG AAG      CTCC AG
                                ||||||||| |||      |||| ||
                                AGTGACCC TTC      GAGG TC
                                      A   CCGTCC    _
GAM836  LOC146669 5'  CTGGAAGACCCTCAGTGA    78057        AAAGTA   C
                                TCACTGGG     TCT CCAG
                                ||||||||     ||| ||||
                                AGTGACTC     AGA GGTC
                                      CC_____   A
GAM836  LOC148479 3'  CTGGGAGGCCCCTGTGA     78867      T   AAAGTA
                                TCAC GGG     TCTCCCAG
                                |||| |||     ||||||||
                                AGTG CCC     GGAGGGTC
                                  T   C______
GAM836  LOC150951 5'  AGAAGCAGGTCCTCCAGTGA   85165        __  AA_  A
                                TCACTGG  GA   GT TCT
                                |||||||  ||   || |||
                                AGTGACC  CT   CG AGA
                                     TC  GGA  A
GAM836  LOC152283 3'  TCTGGGAGTTTCTCCCAGAGA  85688    A     AAGTAT
                                TC CTGGGA     CTCCCAGA
                                || ||||||     ||||||||
                                AG GACCCT     GAGGGTCT
                                 A     CTTT__
GAM836  LOC157349 5'  CTGGGTTTCATTCCCAGTGA   81414          AGTATCT
                                TCACTGGGAA      CCCAG
                                ||||||||||      |||||
                                AGTGACCCTT      GGGTC
                                      ACTTT__
GAM836  LOC158801 3'  TCTGAAACAGACTCCAGTGA   86894        GAA   ATCTCC
                                TCACTGG   AGT     CAGA
                                |||||||   |||     ||||
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                                AGTGACC   TCA     GTCT
                                    ___   GACAAA
GAM836   LOC164397 5'  CTGGTGTCGGCTCCCCCAGTGA 82524         AA   ATCTC
                                TCACTGGG  AGT    CCAG
                                ||||||||  |||    ||||
                                AGTGACCC  TCG    GGTC
                                    CC   GCTGT
GAM836   LOC196955 5'  GAGACACTTTTCCTGGA     77376    ACT       A
                                TC   GGGAAAGT TCTC
                                ||   |||||||| ||||
                                AG   CCTTTTCA AGAG
                                 GT_       C
GAM836   LOC200942 5'  CTGTCATGCCTCCCCAGTGA   88947         AAA    CTCC
                                TCACTGGG   GTAT    CAG
                                ||||||||   ||||    |||
                                AGTGACCC   CGTA    GTC
                                    CTC    CT__
GAM836   LOC200982 3'  CTGAGCAGGACATTCCCCAGTG 90219         _  A  A   CC_
           A                     TCACTGGG AA GT TCT   CAG
                                ||||||||  ||  ||  |||   |||
                                AGTGACCC TT CA GGA   GTC
                                    C  A  _   CGA
GAM836   LOC202460 5'  TGGAGATTCAGTGA        89192         GAAAGT     C
                                TCACTGG     ATCTCC A
                                |||||||     |||||| |
                                AGTGACT     TAGAGG T
                                    _______     A
GAM836   LOC219700 5'  TCTGAAATAACCTTTCCCAGTG 93068           TATCTCC
           G                     TCACTGGGAAAG       CAGA
                                ||||||||||||       ||||
                                GGTGACCCTTTC       GTCT
                                      CAATAAA
GAM836   LOC221395 3'  CTAGGAAATACTTCAGTGA    92027         GAA    C   C
                                TCACTGG   AGTAT TCC AG
                                |||||||   ||||| ||| ||
                                AGTGACT   TCATA AGG TC
                                    ___     A   A
GAM836   LOC221416 3'  GACTGCCCTCCCAGTGA     93767          AA   _
                                TCACTGGGA  GTA TC
                                |||||||||  ||| ||
                                AGTGACCCT  CGT AG
                                     CC   C
GAM836   LOC221760 5'  CTGAATTCTTTCCCGTGA     93786      T      TATCTCC
                                TCAC GGGAAAG       CAG
                                ||||| |||||||      |||
                                AGTG CCCTTTC       GTC
                                  _      TTAA___
GAM836   LOC222182 3'  GGGTGTTCCACTTTTCCAGTGA 94193            ATCT__
                                TCACTGGGAAAGT      CCC
                                ||||||||||||       |||
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                                AGTGACCTTTTCA     GGG
                                      CCTTGT
GAM836  LOC253287 5'  CTAGGAAACCATCCAGTGG   97487       AAA  ATC   C
                                TCACTGGG   GT   TCC AG
                                ||||||||   ||   ||| ||
                                GGTGACCT   CA   AGG TC
                                     AC_  A__   A
GAM836  LOC253959 3'  GAGATTCTACCCAGTGA     94934       AA  T
                                TCACTGGG  AG ATCTC
                                ||||||||  || |||||
                                AGTGACCC  TC TAGAG
                                     A_  T
GAM836  LOC254219 5'  CTGGAGGAACCGCCCAGTGA  96549       AAA  A  TC
                                TCACTGGG   GT TC  CCAG
                                ||||||||   || ||  ||||
                                AGTGACCC   CA AG  GGTC
                                     GC_  _  GA
GAM836  LOC255540 5'  TCTGGGAAAGAGCCCTGTGA  97619     T   AAAGTATC
                                TCAC GGG       TCCCAGA
                                |||| |||       |||||||
                                AGTG CCC       AGGGTCT
                                  T   GAGAA___
GAM836  LOC257396 5'  TCTGAAAAACAATTTTCCCAG  97140         ATCTCC_
                                CTGGGAAAGT      CAGA
                                ||||||||||      ||||
                                GACCCTTTTA      GTCT
                                      ACAAAAA
GAM836  LOC51644  3'  TCTGGGAGTAAAGCTCCCAG   32139      AAGTAT
                                CTGGGA     CTCCCAGA
                                ||||||     ||||||||
                                GACCCT     GAGGGTCT
                                   CGAAAT
GAM836  LOC57086  3'  TCTAGGTTGAGGTTTTCCAGT  39781        GTA  TC  _
                                ACTGGGAAA   TC  CC AGA
                                |||||||||   ||  || |||
                                TGACCTTTT   AG  GG TCT
                                     GG_  TT  A
GAM836  LOC90246  3'  TCCAGGAGCTGGACCCCAGTGA 61909        AAAGTAT   CA
                                TCACTGGG      CTCC  GA
                                ||||||||      ||||  ||
                                AGTGACCC      GAGG  CT
                                     CAGGTC_    AC
GAM836  LOC91768  3'  CTGAGAGATACTGCATCA    67113     GAA      C
                                TGG   AGTATCTC CAG
                                |||   |||||||| |||
                                ACT   TCATAGAG GTC
                                  ACG       A
GAM837  ADH1B     3'  CTTAGACATAAAGTAAAAT   72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
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                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM837  AHR     3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM837  FDFT1   3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM837  JTB     3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM837  KLF4    3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM837  PHYH    3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM837  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                       T__    _
GAM837  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM837  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_    CG_
GAM837  CG012   5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM837  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
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                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM837  FLJ23462  3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
            G                     CATTTC        GTCTGAGAT
                                  ||||||        |||||||||
                                  GTAAAG        CAGACTCTA
                                     AAACATTT_
GAM837  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                  CATTTCA   TCACTGTCTGAGAT
                                  |||||||   ||||||||||||||
                                  GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM837  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                  TTCA TTTCACTG  TGAG
                                  |||| ||||||||  ||||
                                  AAGT AAAGTGAC  GTTT
                                    A       CT
GAM837  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                  TTTC CTG TCTGAGAT
                                  |||| ||| ||||||||
                                  AAAG GAC AGACTCTA
                                    _  G
GAM837  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                  ATT CACTTTCACTGT
                                  ||| ||||||||||||
                                  TAA GTGAAAGTGACG
                                   C
GAM837  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                  TTCACTTT  CT TCTGAGAT
                                  ||||||||  || ||||||||
                                  AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM837  PP35      3'  ATCTCAGACTGAAA       22814      CT
                                  TTTCA  GTCTGAGAT
                                  |||||  |||||||||
                                  AAAGT  CAGACTCTA
                                    __
GAM837  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148         TCAC  C_
                                  CATTTCACTT    TGT  TGAG
                                  ||||||||||    |||  ||||
                                  GTAAAGTGAA    ACG  ACTC
                                     TA__   TT
GAM837  SEP15     3'  TCCTACAGTAAGAGTGAAA    14934        C    CT
                                  TTTCACTTT ACTGT  GA
                                  ||||||||| |||||  ||
                                  AAAGTGAGA TGACA  CT
                                     A    TC
GAM837  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                  TTTCACTTT    TCTGAG
                                  |||||||||    ||||||
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                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM837  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM837  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM837  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226     A      GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM837  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM838  APOBEC1   3'  ACCACCAATCACGTGGAAGTTA 19699         CA   AC
                                TGACTTCCAT  GGT  TGGTGGT
                                ||||||||||  |||  |||||||
                                ATTGAAGGTG  CTA  ACCACCA
                                     CA   __
GAM838  FLJ22843  5'  AGTACTTGATAAAAGCCA    47223    A   CC
                                TG CTT  ATCAGGTACT
                                || |||  ||||||||||
                                AC GAA  TAGTTCATGA
                                 C   AA
GAM838  LEC3      3'  ACCACCAGCACCCAGACCGAA  30858     CA  A_   A
                                TTC  TC  GGT CTGGTGGT
                                |||  ||  ||| ||||||||
                                AAG  AG  CCA GACCACCA
                                  CC  AC   C
GAM838  LOC253281 3'  CATGGTACCTGATGGA      97344           G
                                TCCATCAGGTACTG TG
                                |||||||||||||| ||
                                AGGTAGTCCATGGT AC
                                          _
GAM839  CNGA1     3'  CAACTGATAATGTGCAAA    59507         GC   A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                     A_   _
GAM839  ESRRG     3'  TGGCAGTCTTATGTGCAAA   66396        TAGCT
                                TTTGCACAT    AGATTGCCA
                                |||||||||    |||||||||
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                                AAACGTGTA    TCTGACGGT
                                     T____
GAM839  KCNJ3    3'  GCAATAATGTGCAAA      9525          GCTAGA
                                TTTGCACATTA     TTGC
                                ||||||||||     ||||
                                AAACGTGTAAT     AACG
                                      _______
GAM839  SDC2     3'  GCAAATTAATGTGTAAA     67132          CTAGA
                                TTTGCACATTAG    TTGC
                                ||||||||||||    ||||
                                AAATGTGTAATT    AACG
                                     A____
GAM839  USP9X    3'  ATGGCCTGATGCTAATGTGTAA 16206          TAGATT
           A                     TTTGCACATTAGC     GCCAT
                                ||||||||||||     |||||
                                AAATGTGTAATCG     CGGTA
                                      TAGTC_
GAM839  AMOTL1   3'  GGCAAGTAATGTGCAAA     73650          G  AGAT
                                TTTGCACATTA CT    TGCC
                                |||||||||| ||    ||||
                                AAACGTGTAAT GA    ACGG
                                     _ ____
GAM839  BCAR3    3'  AGTAATAATGTGCAAA      13098          __
                                TTTGCACATTA  GCT
                                ||||||||||  |||
                                AAACGTGTAAT  TGA
                                     AA
GAM839  DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930          AGCTA    C
                                TTTGCACATT    GATTG CA
                                |||||||||     ||||| ||
                                AGACGTGTAA    TTAAC GT
                                     A____    A
GAM839  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                TTTGCACATTAG  AGA TG CAT
                                ||||||||||  ||| || |||
                                AGACGTGTAATC  TTT AC GTA
                                      __  T  A
GAM839  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
           AA                    TTTGCACATTAGCTAGATTGCCAT
                                ||||||||||||||||||||||||
                                AAACGTGTAATCGATCTAACGGTA

GAM840  AGL      5'  CCCAGCTGCCTCGGCGCT    5347     A    GA
                                AG TGCTG  GCAGCTGGG
                                || |||||  |||||||||
                                TC GCGGC  CGTCGACCC
                                 _    TC
GAM840  AOAH     5'  GCCTCAGCTCCAGCATC     91117          AGCT
                                GATGCTGGAGC    GGGC
                                ||||||||||    ||||
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                                CTACGACCTCG   TCCG
                                      AC__
GAM840  ARCN1   3'  CCCAGCTGCTCCTTTATT   7977     CT
                                GATG  GGAGCAGCTGGG
                                ||||  ||||||||||||
                                TTAT  CCTCGTCGACCC
                                  TT
GAM840  BCL11A  3'  CCCTACATTCCAGCATCTT   43161          CAGCT
                                AAGATGCTGGAG   GGG
                                ||||||||||||   |||
                                TTCTACGACCTT   CCC
                                      ACAT_
GAM840  CACNB1  3'  GCCCCTCCCCAGCATC     5572        AGC  CT
                                GATGCTGG   AG  GGGC
                                ||||||||   ||  ||||
                                CTACGACC   TC  CCCG
                                     CC_  __
GAM840  CDKN2D  5'  GCCCGGCTCCCAGCCCCT   8396    AT    AGC
                                AG  GCTGG   AGCTGGGC
                                ||  |||||   ||||||||
                                TC  CGACC   TCGGCCCG
                                 CC    C__
GAM840  CLDN5   3'  CTCACTCCAGCATCT      12345          CAGC
                                AGATGCTGGAG   TGGG
                                ||||||||||    ||||
                                TCTACGACCTC   ACTC
                                      ____
GAM840  COL9A2  3'  GCCCAGCTACAGTTCCA     8488        ___
                                TGGAGC   AGCTGGGC
                                ||||||   ||||||||
                                ACCTTG   TCGACCCG
                                   ACA
GAM840  CSTA    5'  CTTTGGTTCCAGCATCCTGTC  17806     A        AGCT
                                GACA GATGCTGGAGC   GG
                                |||| ||||||||||   ||
                                CTGT CTACGACCTTG   TC
                                  C         GTT_
GAM840  EPHA8   3'  GCCCAGCTGCCCAGC      40061      A
                                GCTGG GCAGCTGGGC
                                ||||| ||||||||||
                                CGACC CGTCGACCCG
                                      _
GAM840  ISL1    5'  GCCACAGCTCCAGCATC     9366          AGC  _
                                GATGCTGGAGC   TG GGC
                                ||||||||||   || |||
                                CTACGACCTCG   AC CCG
                                      ___  A
GAM840  MXI1    3'  CCCAGCTGCCACCTCTCCATC  19901     CT__  A_
                                GATG   GG  GCAGCTGGG
                                ||||   ||  |||||||||
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                                CTAC   CC  CGTCGACCC
                                  CTCT  AC
GAM840  MXI1     3'  CCCAGCTGCCACCTCTCCATC  55262     CT__  A_
                                GATG   GG  GCAGCTGGG
                                ||||   ||  |||||||||
                                CTAC   CC  CGTCGACCC
                                  CTCT  AC
GAM840  NEU3     3'  GCCCAGCTACTCCTTTACCTGT 21849     A A  CT   C
                                ACA G TG  GGAG AGCTGGGC
                                ||| | ||  |||| ||||||||
                                TGT C AT  CCTC TCGACCCG
                                  _ C  TT   A
GAM840  NTSR1    3'  GCCTGGTCTCCAGCACCT    10295    A      CA  TG
                                AG TGCTGGAG  GC  GGC
                                || ||||||||  ||  |||
                                TC ACGACCTC  TG  CCG
                                 C       __  GT
GAM840  PRODH    3'  CCCTTAGCCTCCAGCA      32924        CA  __
                                TGCTGGAG  GCT  GGG
                                ||||||||  |||  |||
                                ACGACCTC  CGA  CCC
                                     __   TT
GAM840  ROM1     5'  GCTGACTCAGCATCCTG     4383     A      AG
                                CA GATGCTGG  CAGC
                                || ||||||||  ||||
                                GT CTACGACT  GTCG
                                 C       CA
GAM840  SERPINI1 5'  GCTCCAGCATCCCGTC      17232     AA
                                GAC  GATGCTGGAGC
                                |||  ||||||||||
                                CTG  CTACGACCTCG
                                  CC
GAM840  SPN      3'  CCAGCCTCCAGCACCTT     11919     A      CA
                                AAG TGCTGGAG  GCTGG
                                ||| ||||||||  |||||
                                TTC ACGACCTC  CGACC
                                  C       __
GAM840  TAGLN    3'  CCCAGCCTGCCCCCTATC    59634     CT  A   _
                                GATG  GG GCAG CTGGG
                                ||||  || |||| |||||
                                CTAT  CC CGTC GACCC
                                   CC  _    C
GAM840  TBX2     3'  GCCCAGCTGCTCCCCTGC    19993    T__
                                GC   GGAGCAGCTGGGC
                                ||   ||||||||||||
                                CG   CCTCGTCGACCCG
                                 TCC
GAM840  USP11    5'  CCAGGACTCCAGCACCTT    16202     A      CAG
                                AAG TGCTGGAG   CTGG
                                ||| ||||||||   ||||
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                                TTC ACGACCTC   GACC
                                  C       AG_
GAM840  C20orf140 3'  CAGAAGCTCCAGCATTT     58243           AG
                                AGATGCTGGAGC  CTG
                                ||||||||||||  |||
                                TTTACGACCTCG  GAC
                                      AA
GAM840  CRA     3'  CTGCTCCAACTCTTGTC     21971        TGC
                                GACAAGA   TGGAGCAG
                                |||||||   ||||||||
                                CTGTTCT   ACCTCGTC
                                    CA_
GAM840  DDX12    3'  GCCCAGCTGTTTGCATCCTGC  59699    A  A    TG
                                G CA GATGC  GAGCAGCTGGGC
                                | || |||||  ||||||||||||
                                C GT CTACG  TTTGTCGACCCG
                                 _ C    __
GAM840  DKFZP434O047 5'  GCCCAGATGGCAGCATCT    31513        GAG  G
                                AGATGCTG   CA CTGGGC
                                ||||||||   || ||||||
                                TCTACGAC   GT GACCCG
                                     G__  A
GAM840  DKFZP761I2123 3'  CCCAGCCTGCTTCTTGTC    48760        TGCTGG    _
                                GACAAGA     AGCAG CTGGG
                                |||||||     ||||| |||||
                                CTGTTCT     TCGTC GACCC
                                    _______    C
GAM840  FLJ10079  3'  CCTCCTCCCCATCATCTTGTC  60201         C   AGC  CT
                                GACAAGATG TGG   AG  GG
                                |||||||||| |||   ||  ||
                                CTGTTCTAC ACC   TC  CC
                                      T   CC_  CT
GAM840  FLJ10110  5'  CCCCCTCCAGCGTCCTGTC   35819      A        CAGCT
                                GACA GATGCTGGAG     GGG
                                |||| ||||||||||     |||
                                CTGT CTGCGACCTC     CCC
                                  C        C____
GAM840  FLJ12650  3'  CTCTTCGCCCAGCATCCTG   44525    A      A  AGCT
                                CA GATGCTGG GC    GGG
                                || ||||||||  ||    |||
                                GT CTACGACC CG    CTC
                                 C       _  CTT_
GAM840  FLJ12788  3'  CTTGGGCTCCAGCATCTGTC   42547      A         AG TG
                                GACA GATGCTGGAGC  C  GG
                                |||| ||||||||||  |  ||
                                CTGT CTACGACCTCG  G  TC
                                  _          __ GT
GAM840  FLJ13590  5'  CCCAGCCACATTTATCCATC   45784      C_   GCA_
                                GATG  TGGA    GCTGGG
                                ||||  ||||    ||||||
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                                CTAC  ATTT   CGACCC
                                  CT   ACAC
GAM840  FLJ14327  3'  CCCAGCTGCCCTCAGC     46132     _ A
                                GCTG G GCAGCTGGG
                                |||| | |||||||||
                                CGAC C CGTCGACCC
                                  T C
GAM840  FLJ22362  3'  CCCAGCTGCCCCACATCTTG  43075       C   A
                                CAAGATG TGG GCAGCTGGG
                                ||||||| ||| |||||||||
                                GTTCTAC ACC CGTCGACCC
                                    _  C
GAM840  KIAA0773  3'  CCCAGGCTTCAGCATCT    28051          AG
                                AGATGCTGGAGC  CTGGG
                                ||||||||||||  |||||
                                TCTACGACTTCG  GACCC
                                              __
GAM840  KIAA1872  3'  GCCCAGCTGCCACGATTTGTC  62933       A  C  GA
                                GACAAG TG TG  GCAGCTGGGC
                                |||||| || ||  ||||||||||
                                CTGTTT GC AC  CGTCGACCCG
                                   A  _  __
GAM840  MGC4707   3'  CCCAGCCTCCTCTCCAGCACCT 44120     A      CA___
           TG                    CAAG TGCTGGAG    GCTGGG
                                |||| ||||||||    ||||||
                                GTTC ACGACCTC    CGACCC
                                  C       TCCTC
GAM840  MMP24    3'  CCCAGCTGCCAGCCTTCTGTC  21943     AG T   GA
                                GACA  A GCTG  GCAGCTGGG
                                ||||  | ||||  |||||||||
                                CTGT  T CGAC  CGTCGACCC
                                  CT C   __
GAM840  NMT1     3'  GCAAAGGCCCCAGCATCT    40784        A  AG  GG
                                AGATGCTGG GC  CT  GC
                                ||||||||| ||  ||  ||
                                TCTACGACC CG  GA  CG
                                     C  __  AA
GAM840  PHYHIP   3'  GCCCAGCTGCCCTCCCCTC   28611    TGCT_  A
                                GA    GG GCAGCTGGGC
                                ||    || ||||||||||
                                CT    CC CGTCGACCCG
                                 CCCCT  _
GAM840  RASSF2   3'  CCCAGCTGACAGCCTGTC    28432     AGAT   GAG
                                GACA   GCTG   CAGCTGGG
                                ||||   ||||  ||||||||
                                CTGT   CGAC   GTCGACCC
                                  C___   A__
GAM840  SES2     3'  CCCATCCCAGTATCTCATC   48808    CA      AGCAGC
                                GA  AGATGCTGG     TGGG
                                ||  |||||||||     ||||
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                                CT  TCTATGACC     ACCC
                                 AC        CT____
GAM840  SLC2A10   3'  CCATCTCCAGCATCCTG     47819    A        CAGC
                                CA GATGCTGGAG    TGG
                                || ||||||||||    |||
                                GT CTACGACCTC    ACC
                                 C         T___
GAM840  UBF-fl    3'  CCCAGCCACTGTTAGTGTC   51558         _  CA
                                GATGCTGG AG  GCTGGG
                                |||||||| ||  ||||||
                                CTGTGATT TC  CGACCC
                                     G  AC
GAM840  ZNF213    3'  GCCCAGCCACGGCACATCCTG 65100    A __    GAGCA
                                CA GA  TGCTG    GCTGGGC
                                || ||  |||||    |||||||
                                GT CT  ACGGC    CGACCCG
                                 C  AC    AC___
GAM840  LOC116150 3'  CCCAGCTACTTCCCTATT    56632     CT    C
                                GATG  GGAG AGCTGGG
                                ||||  |||| |||||||
                                TTAT  CTTC TCGACCC
                                  CC    A
GAM840  LOC128954 5'  CCCAGCTGCTCCCATC     75795     CT
                                GATG  GGAGCAGCTGGG
                                ||||  ||||||||||||
                                CTAC  CCTCGTCGACCC
                                  __
GAM840  LOC130951 3'  GCCCAGCTGCCCAGC      57144      A
                                GCTGG GCAGCTGGGC
                                ||||| ||||||||||
                                CGACC CGTCGACCCG
                                  _
GAM840  LOC144373 3'  GCCCAGCTGTTTGCATCCTGC  76820   A  A    TG
                                G CA GATGC  GAGCAGCTGGGC
                                | || |||||  ||||||||||||
                                C GT CTACG  TTTGTCGACCCG
                                 _  C    __
GAM840  LOC145501 3'  GCCCAGCTGCCCGTGTGCCT   77256    AT  _   A
                                AG  GC TGG GCAGCTGGGC
                                ||  || ||| ||||||||||
                                TC  TG GCC CGTCGACCCG
                                 CG  T  _
GAM840  LOC145676 5'  CATTGCTCCAGCATCTTTC   77337   C           C
                                A AAGATGCTGGAGCAG TG
                                | ||||||||||||||| ||
                                C TTCTACGACCTCGTT AC
                                 T           _
GAM840  LOC146712 5'  GCCCAGCTGCTCGGCTCCCTC  83719    CAA  T    G
                                GA   GA GCTG AGCAGCTGGGC
                                ||   || |||| ||||||||||
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                                CT   CT CGGC TCGTCGACCCG
                                 CC_  _    _
GAM840   LOC147515 3'  CCCAGCTGCTCCAAGC      84020     _
                                GCT GGAGCAGCTGGG
                                ||| ||||||||||||
                                CGA CCTCGTCGACCC
                                  A
GAM840   LOC148479 5'  GCCCCGCTCCAGCATC      78871          AGCT
                                GATGCTGGAGC    GGGC
                                ||||||||||    ||||
                                CTACGACCTCG    CCCG
                                       C___
GAM840   LOC148697 3'  CCCAGCTGCCTTACCTT     78922     ATGCT  A
                                AAG     GG GCAGCTGGG
                                |||     || |||||||||
                                TTC     TC CGTCGACCC
                                  CAT__  _
GAM840   LOC148709 5'  GCCCAGCTACTGCTTCACCA   78944    C      ___
                                TG TGGAGCA   GCTGGGC
                                || |||||||   |||||||
                                AC ACTTCGT   CGACCCG
                                 C       CAT
GAM840   LOC149426 3'  CCCAGCTGCCCCTGGCCTCT   84416     T   _  A
                                AGA GCT GG GCAGCTGGG
                                ||| ||| || |||||||||
                                TCT CGG CC CGTCGACCC
                                  C   T  C
GAM840   LOC149461 3'  GCCCCCTTGCCCAGCATC     79404         A    CT
                                GATGCTGG GCAG  GGGC
                                |||||||| ||||  ||||
                                CTACGACC CGTT  CCCG
                                      _    CC
GAM840   LOC149935 5'  GCCCAGCTGCTGTCTGGATC   60300     G TG  __
                                GAT C  GA  GCAGCTGGGC
                                ||| |  ||  ||||||||||
                                CTA G  CT  CGTCGACCCG
                                  _ GT  GT
GAM840   LOC149995 3'  CCCAGCTGCTCCAAGC      84842     _
                                GCT GGAGCAGCTGGG
                                ||| ||||||||||||
                                CGA CCTCGTCGACCC
                                  A
GAM840   LOC150421 3'  CCCGTTCCCAGCATC       85037         AGC   T
                                GATGCTGG   AGC GGG
                                ||||||||   ||| |||
                                CTACGACC   TTG CCC
                                      C__   _
GAM840   LOC151512 5'  CCTGCCTCCAGCATCT      85428           CA  T
                                AGATGCTGGAG  GC GG
                                ||||||||||  || ||
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                                TCTACGACCTC  CG CC
                                      __ T
GAM840   LOC153346 5'  CCCAGCTGCTGACCTTGTT   86023       ATGCTGG
                                GACAAG      AGCAGCTGGG
                                ||||||      ||||||||||
                                TTGTTC      TCGTCGACCC
                                   CAG____
GAM840   LOC154313 5'  GCCCAACTGCTCCGACCGTC  81064     C_      C
                                GATG  TGGAGCAG TGGGC
                                ||||  |||||||| |||||
                                CTGC  GCCTCGTC ACCCG
                                  CA       A
GAM840   LOC158061 3'  GCCCAGCTGCAGAAGGACCTC  81671    TG_  GGA_
                                GA   CT    GCAGCTGGGC
                                ||   ||    ||||||||||
                                CT   GG    CGTCGACCCG
                                 CCA  AAGA
GAM840   LOC158434 5'  GCCTCCTGCTCCAGCTC     86822    T        CT
                                GA GCTGGAGCAG  GGGC
                                || ||||||||||  ||||
                                CT CGACCTCGTC  TCCG
                                 _         C_
GAM840   LOC196985 5'  GCCCAGCTGCCTTTGTGATC   89663     _  T_  A
                                GAT GC  GG GCAGCTGGGC
                                ||| ||  || ||||||||||
                                CTA TG  TC CGTCGACCCG
                                  G  TT  _
GAM840   LOC196986 5'  GCCCAGCTGCCTTTGTGATC   89658     _  T_  A
                                GAT GC  GG GCAGCTGGGC
                                ||| ||  || ||||||||||
                                CTA TG  TC CGTCGACCCG
                                  G  TT  _
GAM840   LOC199986 5'  CCCGAAGCTCCAGCACCT     89902    A        AGC
                                AG TGCTGGAGC   TGGG
                                || |||||||||   ||||
                                TC ACGACCTCG   GCCC
                                 C         AA_
GAM840   LOC200575 5'  CCCAACTACTCGGGCCTC     88828    T   G   C  C
                                GA GCT GAG AG TGGG
                                || ||| ||| || ||||
                                CT CGG CTC TC ACCC
                                 C   G   A  A
GAM840   LOC220021 3'  CCACTCTCCAGCATCT       93392           C  C
                                AGATGCTGGAG AG TGG
                                |||||||||||  || |||
                                TCTACGACCTC TC ACC
                                      _ _
GAM840   LOC220739 3'  GCTTCACTCCAGCACCCTGTC  92933      AGA       C__
                                GACA   TGCTGGAG   AGC
                                ||||   ||||||||   |||
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                                CTGT   ACGACCTC   TCG
                                  CCC       ACT
GAM840  LOC221927 5'  GCCCAGCTGCTCCCGGCTCT   92650     T    _
                                AGA GCTGG AGCAGCTGGGC
                                ||| ||||| ||||||||||
                                TCT CGGCC TCGTCGACCCG
                                  _    C
GAM840  LOC254439 3'  CCCAACTGCCCTTCTTGTC    94746        TGCT  A    C
                                GACAAGA    GG GCAG TGGG
                                |||||||    || |||| ||||
                                CTGTTCT    CC CGTC ACCC
                                    T___ _    A
GAM840  LOC255031 5'  CCCAGCTGTGCATC        97233       TGGA
                                GATGC    GCAGCTGGG
                                |||||    |||||||||
                                CTACG    TGTCGACCC
                                  _____
GAM840  LOC255170 3'  CCCAGCTGCCACCCCTATCT   97519      CT  A_
                                AGATG  GG  GCAGCTGGG
                                |||||  ||  |||||||||
                                TCTAT  CC  CGTCGACCC
                                   CC  AC
GAM840  LOC56961  5'  GCCCCCCTCCCCAGCGTC    62908        AGC  CT
                                GATGCTGG   AG  GGGC
                                ||||||||   ||  ||||
                                CTGCGACC   TC  CCCG
                                     CC_  CC
GAM840  LOC89919  3'  CTGAGCCACCCCAGCATCCTGC 60721    A  A      AGCA   G
                                G CA GATGCTGG    GCT GG
                                | || ||||||||    ||| ||
                                C GT CTACGACC    CGA TC
                                 _ C       CCAC   G
GAM840  LOC92080  3'  CCCGACTCAGCATCCTGTC    68043     A      GAGC  C
                                GACA GATGCTG    AG TGGG
                                ||||| |||||||    || ||||
                                CTGT CTACGAC    TC GCCC
                                  C       _____  A
GAM841  ATRN      3'  TGTGTTTTCCCCATTTATG    57807       GTA       C
                                CATAAA   GGGAAAGC CA
                                ||||||   |||||||| ||
                                GTATTT   CCCTTTTG GT
                                   AC_       T
GAM841  DFFB      3'  GAAATGGGCATTTATTTTAT   87383          GAAA    C
                                ATAAAGTAGG    GCCCA TTC
                                ||||||||||    ||||| |||
                                TATTTTATTT    CGGGT AAG
                                      A___     A
GAM841  EPS8      3'  AAGTGGGGCCATTTTATG     15467         A  GAAAG
                                CATAAAGT GG    CCCACTT
                                |||||||| ||    |||||||
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                                GTATTTTA CC    GGGTGAA
                                   _ G____
GAM841  FRDA    5' AAGCAGGCTCTCCATTTTTG  3779      TAG  A   CA
                                TAAAG  GGA AGCC  CTT
                                |||||  ||| ||||  |||
                                GTTTT  CCT TCGG  GAA
                                   TA_  C   AC
GAM841  FZD4    3' AAATGGACCCTGCTTT     24119        AAAGC  C
                                AAAGTAGGG    CCA TT
                                |||||||||    ||| ||
                                TTTCGTCCC    GGT AA
                                     A____  A
GAM841  GCA     3' GAAGTGAACTGGACTACTTTA 24166       GGAA  CC
                                TAAAGTAG   AG  CACTTC
                                ||||||||   ||  ||||||
                                ATTTCATC   TC  GTGAAG
                                     AGG_  AA
GAM841  MDM1    3' AAGTAGGCCCTTACTT     39270        AAA  C
                                AAGTAGGG  GCC ACTT
                                ||||||||  ||| ||||
                                TTCATTCC  CGG TGAA
                                   ___  A
GAM841  PLAG1   3' AAGTAGGCTTTTCGCTCT   10604    T _     C
                                AG AG GGAAAGCC ACTT
                                || || |||||||| ||||
                                TC TC CTTTTCGG TGAA
                                 _ G      A
GAM841  ZNF35   3' GAAATGGACTTTTTCCTTACT 12779         C__  C
                                AGTAGGGAAAG  CCA TTC
                                ||||||||||  ||| |||
                                TCATTCCTTTT  GGT AAG
                                     TCA  A
GAM841  ATP6M8-9 3' GAAGTGGGTGAATTCTACTTT 19275        AAA
                                AAAGTAGGG  GCCCACTTC
                                |||||||||  |||||||||
                                TTTCATCTT  TGGGTGAAG
                                     AAG
GAM841  DAPK2   3' TGGGCTTTCCTCTGTCT    26742   _  _
                                AG TAG GGAAAGCCCA
                                || ||| ||||||||||
                                TC GTC CCTTTCGGGT
                                 T  T
GAM841  DKFZP761D0211 3' AGTGGGCCCTTCCCTG     49351       A_
                                TAGGGAA  GCCCACT
                                |||||||  |||||||
                                GTCCCTT  CGGGTGA
                                   CC
GAM841  DNAJA4  3' GAAGTGGGCGGTGACCCTAT  37755      AAA__
                                GTAGGG    GCCCACTTC
                                ||||||    |||||||||
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                                TATCCC    CGGGTGAAG
                                   AGTGG
GAM841  DRCTNNB1A 3'  GGCTCCCCTGACTTTATG    50841        _   AA
                                CATAAAGT AGGG  AGCC
                                |||||||| ||||  ||||
                                GTATTTCA TCCC  TCGG
                                     G   C_
GAM841  FLJ21432  3'  GAAATGGACCTTTCTCTGAC   44634    _      C_  C
                                GT AGGGAAAG  CCA TTC
                                || ||||||||  ||| |||
                                CA TCTCTTTC  GGT AAG
                                 G       CA  A
GAM841  FLJ22679  3'  GAAGTGGGCACAGCTCCCCAC  49922    A   AA___
                                GT GGGA    GCCCACTTC
                                || ||||    |||||||||
                                CA CCCT    CGGGTGAAG
                                 C   CGACA
GAM841  FLJ22679  3'  GAAGTGGGCACAGCTCCCCAC  34679    A   AA___
                                GT GGGA    GCCCACTTC
                                || ||||    |||||||||
                                CA CCCT    CGGGTGAAG
                                 C   CGACA
GAM841  IMP-2     3'  AAGCAGGCTTTTCTAGACTTTA 21566      A_       CA
                                TAAAGT  GGGAAAGCC  CTT
                                ||||||  |||||||||  |||
                                ATTTCA  TCTTTTCGG  GAA
                                   GA        AC
GAM841  KIAA0265  3'  GAAGTGAGCTCATTACTTTA   69879       GGAA   C
                                TAAAGTAG    AGC CACTTC
                                ||||||||    ||| ||||||
                                ATTTCATT    TCG GTGAAG
                                     AC__   A
GAM841  KIAA0377  3'  AAGTGGGCCTCCTCTG      27790     _  AA
                                TAG GGA  GCCCACTT
                                ||| |||  ||||||||
                                GTC CCT  CGGGTGAA
                                  T   C_
GAM841  KIAA0748  3'  TGAACTTTCTCCTATTTCATG  28944     A      _    CC
                                CAT AAGTAGG GAAAG  CA
                                ||| ||||||| |||||  ||
                                GTA TTTATCC CTTTC  GT
                                  C      T     AA
GAM841  KIAA1336  3'  AAATGAGCTTTCTCTAT     72320          C  C
                                GTAGGGAAAGC CA TT
                                |||||||||||| || ||
                                TATCTCTTTCG GT AA
                                       A  A
GAM841  KIAA1755  5'  GAAGCAGCCTGTGCTCCCTACT 61344        AA  C  _____
                                AGTAGGGA  GC CA    CTTC
                                ||||||||  || ||    ||||
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                                TCATCCCT  CG GT    GAAG
                                    __  T  CCGAC
GAM841  NESHBP   3'  GAAGCTGGCTCCCTATT    31252        AA   CA
                                AGTAGGGA  GCC  CTTC
                                ||||||||  |||  ||||
                                TTATCCCT  CGG  GAAG
                                    __  TC
GAM841  PFTK1    3'  TGGACTTTCCTGTGATTTG   24760     GTA_     C
                                TAAA   GGGAAAG CCA
                                ||||   ||||||| |||
                                GTTT   TCCTTTC GGT
                                  AGTG      A
GAM841  TP53INP1 3'  AAGTGGGCCTTCTATCTT    72949     TAG    A
                                AAG   GGAA GCCCACTT
                                |||   |||| ||||||||
                                TTC   TCTT CGGGTGAA
                                  TA_    C
GAM841  TP53INP1 3'  AAGTGGGCCTTCTATCTT    52722     TAG    A
                                AAG   GGAA GCCCACTT
                                |||   |||| ||||||||
                                TTC   TCTT CGGGTGAA
                                  TA_    C
GAM841  UBXD2    3'  AAGTGGGACTGCTTTAT     68340         GGAAAG
                                ATAAAGTAG     CCCACTT
                                |||||||||     |||||||
                                TATTTCGTC     GGGTGAA
                                    A_____
GAM841  LOC128077 3'  GGCTTCCTTCCCTACCTTAT   74716      A       ___
                                ATAA GTAGGGAA   AGCC
                                |||| ||||||||   ||||
                                TATT CATCCCTT   TCGG
                                  C       CCT
GAM841  LOC150889 3'  AAGTGAATTTTGATCTCTACTT 80022     A       ___   CC
           CATG                    CAT AAGTAGGGA   AAG  CACTT
                                ||| |||||||||   |||  |||||
                                GTA TTCATCTCT   TTT  GTGAA
                                  C        AGT   AA
GAM841  LOC200010 3'  GGCTCTCCTCTTACTTTG    89922        __    A
                                TAAAGTA  GGGA AGCC
                                |||||||  |||| ||||
                                GTTTCAT  TCCT TCGG
                                    TC    C
GAM841  LOC254753 3'  AAGTGGGCCTTCCCTGGGCTGT 96144      AAG      A
           G                     CATA   TAGGGAA GCCCACTT
                                ||||   ||||||| ||||||||
                                GTGT   GTCCCTT CGGGTGAA
                                  CGG      C
GAM841  LOC255042 3'  GAAGTGGGCTTGTTTCTCAC   95317    _  GG _
                                GT AG  A AAGCCCACTTC
                                || ||  | ||||||||||
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                                CA TC  T TTCGGGTGAAG
                                 C  TT G
GAM841  LOC51142  3'  GAAGTGGGGGTGTCCCTACTCT 32337     A       AAG_
              GT                  ATA AGTAGGGA    CCCACTTC
                                  ||| ||||||||    ||||||||
                                  TGT TCATCCCT    GGGTGAAG
                                    C       GTGG
GAM841  LOC90509  3'  AAGTGGGCCTCCTTTTCTT    63102     T_    AA
                                  AAG  AGGGA  GCCCACTT
                                  |||  |||||  ||||||||
                                  TTC  TTCCT  CGGGTGAA
                                    TT     C_
GAM842  LRAT      3'  CCACTATGAGAACTACCGT    60103         ACGTTG
                                  GCGGTAGTT     CATAGTGG
                                  |||||||||     ||||||||
                                  TGCCATCAA     GTATCACC
                                       GA____
GAM842  KIAA0628  3'  ACCACCTGTGTAACCACCACC  28860     A  TAC       _
                                  GGT GT   GTTGCATAG TGGT
                                  ||| ||   ||||||||| ||||
                                  CCA CA   CAATGTGTC ACCA
                                    C  C__        C
GAM842  NEDD5     3'  ACCACTATGCAAAGAACTCACC 15308     _    ACG
                                  GGT AGTT   TTGCATAGTGGT
                                  ||| ||||   ||||||||||||
                                  CCA TCAA   AACGTATCACCA
                                    C    GA_
GAM842  PROL3     3'  ACCACTACCCTTGTAACTACTG 21933           TTGCA
              C                    GCGGTAGTTACG     TAGTGGT
                                  ||||||||||||     |||||||
                                  CGTCATCAATGT     ATCACCA
                                         TCCC_
GAM843  HTR1D     3'  TGATTATAGAAAAGACCC     6004      A      T    C_
                                  GG GTCTTTT CTAT  TCA
                                  || ||||||| ||||  |||
                                  CC CAGAAAA GATA  AGT
                                   _      _    TT
GAM843  KAI1      3'  GGGACAGAAAGAGACTCC     9502             A
                                  GGAGTCTTTTTCT TCTC
                                  |||||||||||| ||||
                                  CCTCAGAGAAAGA AGGG
                                           C
GAM843  RALBP1    3'  TGAGCAATAGAAAAAAATTCC  22299       C        __
                                  GGAGT TTTTTCTAT  CTCA
                                  ||||| |||||||||  ||||
                                  CCTTA AAAAAGATA  GAGT
                                     A        AC
GAM843  TCF7L2    5'  AGGAGAAAAAGACCC       47737     A        A
                                  GG GTCTTTTTCT TCT
                                  || ||||||||| |||
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                                CC CAGAAAAAGA GGA
                                 _       _
GAM843  TFF3     3'  GGGCAGGAAAAGACTCC     63567           AT
                                GGAGTCTTTTTCT  CT
                                ||||||||||||  ||
                                CCTCAGAAAAGGA  GG
                                      CG
GAM843  BLR1     5'  TATGTAGGAAAAAACCTCC   52004     TC     ATCT
                                GGAG  TTTTTCT   CATA
                                ||||  |||||||   ||||
                                CCTC  AAAAAGG   GTAT
                                  CA      AT__
GAM843  DSCAML1  3'  TATGAAAAAAGACCC      40361    A      CTATC
                                GG GTCTTTTT    TCATA
                                || ||||||||    |||||
                                CC CAGAAAAA    AGTAT
                                 _      ______
GAM843  ERAP140  3'  TTTTATGAAAGCCAAAGACTGC 75207   G      TT  ATC
                                G AGTCTTT  CT   TCATAAAA
                                | |||||||  ||   ||||||||
                                C TCAGAAA  GA   AGTATTTT
                                 G      CC  A__
GAM843  KIAA0266 5'  ATGTCTGCAGAAAAGAGACTCC 41326          _  ATCT_
                                GGAGTCTTTTT CT    CAT
                                |||||||||| ||    |||
                                CCTCAGAGAAA GA    GTA
                                      A  CGTCT
GAM843  MGC2603  3'  AGATAGGAGGGAATCC     43857     G     T
                                GGA TCTTTT CTATCT
                                ||| |||||| ||||||
                                CCT AGGGAG GATAGA
                                  A     _
GAM843  MSTP032  3'  TGAGAAAAGACTCC       47444         TTCTA
                                GGAGTCTTT    TCTCA
                                |||||||||    |||||
                                CCTCAGAAA    AGAGT
                                      ______
GAM843  ZNF238   3'  TATGGACTGAAAAAGCCC    20968    A T      TA  T
                                GG G CTTTTTC  TC CATA
                                || | |||||||  || ||||
                                CC C GAAAAAG  AG GTAT
                                 _ _      TC  _
GAM843  LOC151361 3'  ATGAGACAAAGGGGCCC     85317    A      CTA
                                GG GTCTTTTT   TCTCAT
                                || ||||||||   ||||||
                                CC CGGGGAAA   AGAGTA
                                 _       C__
GAM843  LOC152220 3'  TGAGATAGAAAAAGATTCC    85591
                                GGAGTCTTTTTCTATCTCA
                                ||||||||||||||||||
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                                CCTTAGAAAAAGATAGAGT

GAM843  LOC222031 3'  GGACAGAAACAGACCC      94025    A   T    A
                                GG GTCT TTTCT TCT
                                || |||| |||||| |||
                                CC CAGA AAAGA AGG
                                 _   C    C
GAM844  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM844  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM844  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM844  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
           TG                     CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM844  KLF4     3'  TCCCAGACAGTGGATATG     14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM844  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM844  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM844  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM844  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
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                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM844  CG012    5' CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                     CT  __
GAM844  EIF2C2   3' ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM844  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC       GTCTGAGAT
                                ||||||       |||||||||
                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM844  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM844  KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM844  KLHL6    3' ATCTCAGAGCAGGAAA      55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM844  NIR3     3' GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM844  PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM844  PP35     3' ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM844  PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148         TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
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                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM844  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM844  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941        CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM844  LOC149703 3' ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM844  LOC154007 3' ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM844  LOC155004 3' TCATTTAAGTGAAAGGAAA    81226     A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM844  LOC222134 5' ACAGTGAAGTGAAATG       94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM845  APP      3'  TGCTTCTGCTATATTTGTG    4909          ATA
                                CACAAATATAG   AAGCA
                                ||||||||||   |||||
                                GTGTTTATATC   TTCGT
                                      GTC
GAM845  BCAT1    3'  CTTCATCTGTATTTATGGC    66203     C       A
                                GCCA AAATATAGAT AAG
                                |||| |||||||||| |||
                                CGGT TTTATGTCTA TTC
                                  A        C
GAM845  BTG2     3'  TGCTTTGTGTGTATGTGTGGC  22219       A    G
                                GCCACA ATATA ATAAAGCA
                                |||||| ||||| ||||||||
                                CGGTGT TATGT TGTTTCGT
                                   G    G
GAM845  COG3     3'  TGCTTTATATTATTTGGC     48702     CA    TAG
                                GCCA  AATA   ATAAAGCA
                                ||||  ||||   ||||||||
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                                CGGT  TTAT   TATTTCGT
                                  __   TA_
GAM845  DMD     5'  TGCTTTATCTGTGCTTGGC   14373     CAAA
                                GCCA   TATAGATAAAGCA
                                ||||   ||||||||||||
                                CGGT   GTGTCTATTTCGT
                                  TC__
GAM845  DMD     5'  TGCTTTATCTGTGCTTGGC   14381     CAAA
                                GCCA   TATAGATAAAGCA
                                ||||   ||||||||||||
                                CGGT   GTGTCTATTTCGT
                                  TC__
GAM845  DSC1    3'  TGCCTTATCTGTGGTTG     17062     A       A
                                CAA TATAGATAA GCA
                                ||| |||||||| |||
                                GTT GTGTCTATT CGT
                                  G       C
GAM845  DSC1    3'  TGCCTTATCTGTGGTTG     44331     A       A
                                CAA TATAGATAA GCA
                                ||| |||||||| |||
                                GTT GTGTCTATT CGT
                                  G       C
GAM845  ENTPD6  3'  TGCTGTAAACTATTTGTGGC  6972          TAGATAA
                                GCCACAAATA      AGCA
                                ||||||||||      ||||
                                CGGTGTTTAT      TCGT
                                     CAAATG_
GAM845  FACL3   3'  TGAGTTATCTATATTTGT    15500           AG
                                ACAAATATAGATAA  CA
                                ||||||||||||||  ||
                                TGTTTATATCTATT  GT
                                       GA
GAM845  FLRT2   5'  TGCTTTCATCTTTATATTTATG 25070     C     __   _
          GT                      GCCA AAATAT  AGAT AAAGCA
                                ||||| ||||||  |||| ||||||
                                TGGT TTTATA  TCTA TTTCGT
                                  A     TT    C
GAM845  HDAC4   3'  TGCTCTGGTGGATTTTTGTGGC 20118       T  AG  AA_
                                GCCACAAA AT  AT   AGCA
                                |||||||| ||  ||   ||||
                                CGGTGTTT TA  TG   TCGT
                                    T  GG  GTC
GAM845  HIC1    5'  TGCTCCCCTCTTTGTGGC    87317       ATAT   TAA_
                                GCCACAA    AGA    AGCA
                                |||||||    |||    ||||
                                CGGTGTT    TCT    TCGT
                                    _____  CCCC
GAM845  ITGB3   3'  TGCTTGCATTATATTTGT    3998          ATA
                                ACAAATATAG   AAGCA
                                ||||||||||   |||||
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                                TGTTTATATT  TTCGT
                                     ACG
GAM845  JRKL    3'  TGCTCATTGTGTTTGTG    13663         ATAA
                                CACAAATATAG   AGCA
                                ||||||||||   ||||
                                GTGTTTGTGTT   TCGT
                                     AC__
GAM845  LPIN1   3'  GCTTTATCTAGCTCATGGT   67393     CAAATA
                                GCCA    TAGATAAAGC
                                ||||    ||||||||||
                                TGGT    ATCTATTTCG
                                  ACTCG_
GAM845  MS4A1   3'  TGCTTTATTTAATTGTAGG   3751    _   ATA
                                CC ACAA  TAGATAAAGCA
                                || ||||  ||||||||||
                                GG TGTT  ATTTATTTCGT
                                 A   A__
GAM845  NDUFS3  3'  GCCTTATCTATGATTG     15845    A       A
                                CAA TATAGATAA GC
                                ||| ||||||||| ||
                                GTT GTATCTATT CG
                                  A       C
GAM845  POLK    3'  TTTTATTAATATTTGTG    32572         A
                                CACAAATAT GATAAAG
                                ||||||||| |||||||
                                GTGTTTATA TTATTTT
                                     A
GAM845  POLQ    3'  TGCCTCTTTCTGTTTGTGGC  21693       AT    TAAA_
                                GCCACAA  ATAGA    GCA
                                |||||||  |||||    |||
                                CGGTGTT  TGTCT    CGT
                                   __    TTCTC
GAM845  PRNP    3'  CTTTATATTTTCTATATTTGT  4335          _____
                                ACAAATATAGA    TAAAG
                                ||||||||||    |||||
                                TGTTTATATCT    ATTTC
                                     TTTAT
GAM845  PTGFRN  3'  TGCCGAAGGCTAATTTGTGGC  67194         A   ATAAA_
                                GCCACAAAT TAG     GCA
                                ||||||||| |||     |||
                                CGGTGTTTA ATC     CGT
                                   _  GGAAGC
GAM845  PTPRO   3'  TGCTTTGTAATATGTGGC    47700       AATATAG
                                GCCACA      ATAAAGCA
                                ||||||      ||||||||
                                CGGTGT      TGTTTCGT
                                   ATAA___
GAM845  PTPRO   3'  TGCTTTGTAATATGTGGC    47704       AATATAG
                                GCCACA      ATAAAGCA
                                ||||||      ||||||||
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                              CGGTGT     TGTTTCGT
                                 ATAA___
GAM845  PTPRO    3' TGCTTTGTAATATGTGGC   47709      AATATAG
                              GCCACA     ATAAAGCA
                              ||||||     ||||||||
                              CGGTGT     TGTTTCGT
                                 ATAA___
GAM845  PTPRO    3' TGCTTTGTAATATGTGGC   47718      AATATAG
                              GCCACA     ATAAAGCA
                              ||||||     ||||||||
                              CGGTGT     TGTTTCGT
                                 ATAA___
GAM845  PTPRO    3' TGCTTTGTAATATGTGGC   11136      AATATAG
                              GCCACA     ATAAAGCA
                              ||||||     ||||||||
                              CGGTGT     TGTTTCGT
                                 ATAA___
GAM845  RPS6KA2  3' CTTTGTAGATGCTGTGGC   40905       AA  AG
                              GCCACA  TAT  ATAAAG
                              ||||||  |||  ||||||
                              CGGTGT  GTA  TGTTTC
                                 C_   GA
GAM845  SERPINE2 3' TGTCTATATGTGCGGC     74924     A  A
                              GCC CA ATATAGATA
                              ||| || |||||||||
                              CGG GT TATATCTGT
                                C  G
GAM845  SLC25A15 3' TGCTTTATCTGAATAGGC   26513     ACAA  A
                              GCC    AT TAGATAAAGCA
                              |||    || ||||||||||
                              CGG    TA GTCTATTTCGT
                                A___   A
GAM845  SLC9A6   3' CTTTATCTGTATAGCAGGC  21003     ACAA
                              GCC    ATATAGATAAAG
                              |||    ||||||||||||
                              CGG    TATGTCTATTTC
                                ACGA
GAM845  SMPX     3' CTTTATCTTCATTTTTGGC   26760      C   AT
                              GCCA AAAT  AGATAAAG
                              |||| ||||  ||||||||
                              CGGT TTTA  TCTATTTC
                                T    CT
GAM845  STAU2    3' TGCTTTATAGTTGTTTGAGGC 26910     A     TAG
                              GCC CAAATA   ATAAAGCA
                              ||| ||||||   ||||||||
                              CGG GTTTGT   TATTTCGT
                                A     TGA
GAM845  TNFRSF10B 3' TGCTTTATTTATTTATTTGGGC 13884     A     __
                              GCC CAAATA  TAGATAAAGCA
                              ||| ||||||  ||||||||||
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                                CGG GTTTAT  ATTTATTTCGT
                                  _     TT
GAM845  TRIM37   3'  GCTATATATTTGTGG      30972          GATAA
                                CCACAAATATA    AGC
                                ||||||||||    |||
                                GGTGTTTATAT    TCG
                                      A____
GAM845  TRPC6    3'  TGCCCTATTTAGTTTGTGGC  16097        A     AA
                                GCCACAAAT TAGATA  GCA
                                ||||||||| ||||||  |||
                                CGGTGTTTG ATTTAT  CGT
                                      _     CC
GAM845  ARFD1    3'  TGCTTTAAAAAAATTTTGTGGC 7993         TATAGA_
                                GCCACAAA      TAAAGCA
                                ||||||||      |||||||
                                CGGTGTTT      ATTTCGT
                                     TAAAAAA
GAM845  BTBD3    3'  TGCTTTATTTACTTTTGT    30316      TA
                                ACAAA  TAGATAAAGCA
                                |||||  ||||||||||
                                TGTTT  ATTTATTTCGT
                                   TC
GAM845  C19orf7  3'  TGCTCTGTGGGATTTGTGG   61131        ATAG   A
                                CCACAAAT    ATA AGCA
                                ||||||||    ||| ||||
                                GGTGTTTA    TGT TCGT
                                     GGG_   C
GAM845  dA141H5.1 3'  TGCCCTTAGGTCTTTGTGGC  59108       ATAT    AAA___
                                GCCACAA    AGAT     GCA
                                |||||||    ||||     |||
                                CGGTGTT    TCTG     CGT
                                     _____   GATTCC
GAM845  ENPP4    3'  TGCCTATTGTATTTGTGGT   30051          ATAAA
                                GCCACAAATATAG    GCA
                                ||||||||||||    |||
                                TGGTGTTTATGTT    CGT
                                      ATC__
GAM845  FLJ10094  3'  TGCCTTTAGTTATATCTGTGGC 35809       A     A    _
                                GCCACA ATATAG TAAAG CA
                                |||||| |||||| ||||| ||
                                CGGTGT TATATT ATTTC GT
                                   C     G    C
GAM845  FLJ10716  3'  TGCTTTATCTACTTTAGGC   36488     ACA  TA
                                GCC   AA  TAGATAAAGCA
                                |||   ||  ||||||||||
                                CGG   TT  ATCTATTTCGT
                                  A__  TC
GAM845  FLJ11726  3'  CTTTTGGGACTGTATTTGTGGC 46412           AT___
                                GCCACAAATATAG    AAAG
                                ||||||||||||    ||||
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```
                                CGGTGTTTATGTC    TTTC
                                      AGGGT
GAM845  FLJ12994  3'  GCCATTTATATTTGTG     43127          AAA
                                CACAAATATAGAT  GC
                                ||||||||||||  ||
                                GTGTTTATATTTA  CG
                                      C__
GAM845  FLJ12994  3'  GCCATTTATATTTGTG     77477          AAA
                                CACAAATATAGAT  GC
                                ||||||||||||  ||
                                GTGTTTATATTTA  CG
                                      C__
GAM845  FLJ21106  3'  GCTTTATCGTGTGGC      46997       AATATA
                                GCCACA     GATAAAGC
                                ||||||     ||||||||
                                CGGTGT     CTATTTCG
                                   G_____
GAM845  FLJ21916  3'  TGCTATGTCTCTGTATTTGTGG 43646          __    A
              C                  GCCACAAATAT  AGATA AGCA
                                ||||||||||  ||||| ||||
                                CGGTGTTTATG  TCTGT TCGT
                                      TC    A
GAM845  FLJ22833  3'  CTTTAAATTATTTGTGG     43104         TAGA
                                CCACAAATA    TAAAG
                                |||||||||    |||||
                                GGTGTTTAT    ATTTC
                                     TAA_
GAM845  GABARAP   3'  TCTTAATGTTTGTGGC      23460          __
                                GCCACAAATAT  AGA
                                ||||||||||  |||
                                CGGTGTTTGTA  TCT
                                      AT
GAM845  GNG10     3'  GCTTTGTAGTTGTGGC      14676        ATATAG
                                GCCACAA     ATAAAGC
                                |||||||     |||||||
                                CGGTGTT     TGTTTCG
                                   GA____
GAM845  GTF2H3    3'  TGTCCATGTTTGTGGC      7709           A
                                GCCACAAATAT GATA
                                |||||||||| ||||
                                CGGTGTTTGTA CTGT
                                      C
GAM845  HMP19     3'  GCTTTATAATTTTGTGGT    87475        TATAG
                                GCCACAAA     ATAAAGC
                                ||||||||     |||||||
                                TGGTGTTT     TATTTCG
                                   TAA__
GAM845  HRIHFB2436 3'  TGCTTTGATTGTATTTTGGC  26798      C       A
                                GCCA AAATATAG TAAAGCA
                                |||| |||||||| |||||||
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                              CGGT TTTATGTT GTTTCGT
                                _      A
GAM845  HSPC019  3' TGCTTTATTATATTCAGGGC  25861    ACA    A
                              GCC   AATAT GATAAAGCA
                              |||   ||||| |||||||||
                              CGG   TTATA TTATTTCGT
                                GAC    _
GAM845  KIAA0211 3' TGCTTCTGTTATTTATGGC   27549     C    _   TAA
                              GCCA AAATA TAGA   AGCA
                              |||| ||||| ||||   ||||
                              CGGT TTTAT GTCT   TCGT
                                A    T   ____
GAM845  KIAA0459 3' CTTTATCTATGAAATGG     60995     CAAA
                              CCA    TATAGATAAAG
                              |||    ||||||||||
                              GGT    GTATCTATTTC
                                AAA_
GAM845  KIAA0483 3' TGCTTTATCTGCTCTCTGT   30793     AATA_
                              ACA    TAGATAAAGCA
                              |||    ||||||||||
                              TGT    GTCTATTTCGT
                                CTCTC
GAM845  KIAA0537 3' TGCTTTATTCACTTCTGTGG  29262      AATATA
                              CCACA     GATAAAGCA
                              |||||     |||||||||
                              GGTGT     TTATTTCGT
                                 CTTCAC
GAM845  KIAA1240 5' TGCTTTATCAATTTTTG     66740     T  A
                              CAAA AT GATAAAGCA
                              |||| || |||||||||
                              GTTT TA CTATTTCGT
                                T  A
GAM845  KIAA1336 3' TGCTCCTTTCTATCTGTGGT  72326      AAT    TAA_
                              GCCACA   ATAGA   AGCA
                              ||||||   |||||   ||||
                              TGGTGT   TATCT   TCGT
                                 C__    TTCC
GAM845  KIAA1437 3' TGCCTCTTCAGTATTTGTGGC 60594          A  TAAA
                              GCCACAAATAT GA   GCA
                              |||||||||| ||   |||
                              CGGTGTTTATG CT   CGT
                                     A  TCTC
GAM845  KIAA1765 3' TGCTTTATTTGTAGTAGC    70614    C  AAA
                              GC AC   TATAGATAAAGCA
                              || ||   ||||||||||||
                              CG TG   ATGTTTATTTCGT
                               A  ___
GAM845  MGC3178  3' TGCTGGACTATTTGTGGC    47992         TAGATAA
                              GCCACAAATA      AGCA
                              |||||||||       ||||
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                                CGGTGTTTAT      TCGT
                                     CAGG___
GAM845  P37NB    3'  TGCCTGTCCATTTGTGG     19507        ATA    AA
                                CCACAAAT   GATA  GCA
                                ||||||||   ||||  |||
                                GGTGTTTA   CTGT  CGT
                                    C__    C_
GAM845  PAIP1    3'  GCTTTATTTATATGGC      66925      CAAA
                                GCCA    TATAGATAAAGC
                                ||||    ||||||||||||
                                CGGT    ATATTTATTTCG
                                  ____
GAM845  PS-PLA1  3'  TGCTTTATCTCCTTGGGC    31908     A   ATAT
                                GCC CAA    AGATAAAGCA
                                ||| |||    ||||||||||
                                CGG GTT    TCTATTTCGT
                                  _  CC__
GAM845  PSPH     3'  CTTTATGTATATTTGTAGC    15915    C       G
                                GC ACAAATATA ATAAAG
                                || |||||||| ||||||
                                CG TGTTTATAT TATTTC
                                 A        G
GAM845  S164     5'  GCGGCTGTATTTGCGGC     60781     A       ATAAA
                                GCC CAAATATAG     GC
                                ||| |||||||||     ||
                                CGG GTTTATGTC     CG
                                  C        GG___
GAM845  SCDGF-B  3'  TGCTTTGTTAATGCCATGGC   52453     CAAA   A
                                GCCA    TAT GATAAAGCA
                                ||||    ||| |||||||||
                                CGGT    GTA TTGTTTCGT
                                  ACC_   A
GAM845  SCDGF-B  3'  TGCTTTGTTAATGCCATGGC   47381     CAAA   A
                                GCCA    TAT GATAAAGCA
                                ||||    ||| |||||||||
                                CGGT    GTA TTGTTTCGT
                                  ACC_   A
GAM845  TRIM36   3'  TGCTAAAGTCACATTTGTGGT  38017         ATA   AA_
                                GCCACAAAT   GAT   AGCA
                                |||||||||   |||   ||||
                                TGGTGTTTA   CTG   TCGT
                                     CA_   AAA
GAM845  TSPAN-2  3'  CTTTACTGTGTCTGTAGC    19165    C  A     A
                                GC ACA ATATAG TAAAG
                                || ||| |||||| |||||
                                CG TGT TGTGTC ATTTC
                                 A  C     _
GAM845  ZDHHC3   3'  TGTCTTATCTATATTT      33459           AG
                                AAATATAGATAA  CA
                                ||||||||||||  ||
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                                TTTATATCTATT  GT
                                      CT
GAM845  ZDHHC8   3'  TGCTTTATGCTCTTGTGG    63908      ATAT  _
                                CCACAA   AG ATAAAGCA
                                ||||||   || ||||||||
                                GGTGTT   TC TATTTCGT
                                   C___  G
GAM845  LOC121536 3'  TGCTTTATTCTGTATCTG    74091    A     _
                                CA ATATAGA TAAAGCA
                                || ||||||| |||||||
                                GT TATGTCT ATTTCGT
                                 C      T
GAM845  LOC150737 3'  GCTTTATTTACCCTTTGGC    79996     CAAATA
                                GCCA     TAGATAAAGC
                                ||||     ||||||||||
                                CGGT     ATTTATTTCG
                                  TTCCC_
GAM845  LOC151126 3'  TGCTACATAATTTTGTGGC    80132       TATAG  AA
                                GCCACAAA    AT  AGCA
                                ||||||||    ||  ||||
                                CGGTGTTT    TA  TCGT
                                     TAA__  CA
GAM845  LOC153505 3'  TGCTGACCATCTTTGTGGC    80850       ATAT   AA__
                                GCCACAA   AGAT   AGCA
                                |||||||   ||||   ||||
                                CGGTGTT   TCTA   TCGT
                                   _____   CCAG
GAM845  LOC158730 3'  TGCAGGTGTATATTTGTGGT   86891          G  AAA
                                GCCACAAATATA AT   GCA
                                ||||||||||||| ||   |||
                                TGGTGTTTATAT TG   CGT
                                      G  GA_
GAM845  LOC199675 3'  TGCCCTGTCACTATCTGTGGC  88270       A   TA   AA
                                GCCACA ATA  GATA  GCA
                                |||||| |||  ||||  |||
                                CGGTGT TAT  CTGT  CGT
                                   C   CA   CC
GAM845  LOC253512 3'  TGCTTCTTTATTTGTG      94914        T   TAA
                                CACAAATA AGA   AGCA
                                |||||||| |||   ||||
                                GTGTTTAT TCT   TCGT
                                     T  ___
GAM845  LOC253805 3'  TGCTTATCATATATTTGTG   96440         _    A
                                CACAAATATA GATAA GCA
                                |||||||||| ||||| |||
                                GTGTTTATAT CTATT CGT
                                      A    _
GAM845  LOC255040 3'  TGCTTTGTTTATTTGGTG    96384     AAAT
                                CAC    ATAGATAAAGCA
                                |||    ||||||||||||
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                                GTG   TATTTGTTTCGT
                                  GTT_
GAM845  LOC255041 3'  TGCTTTGTTTATTTGGTG    96389     AAAT
                                CAC   ATAGATAAAGCA
                                |||   ||||||||||||
                                GTG   TATTTGTTTCGT
                                  GTT_
GAM845  LOC51107  3'  TGCTTTGTCCTTTTGTG     32063       TATA
                                CACAAA   GATAAAGCA
                                ||||||   |||||||||
                                GTGTTT   CTGTTTCGT
                                   TC__
GAM845  LOC91628  3'  TCTTGGTATTTGTGGT      66763          __
                                GCCACAAATAT  AGA
                                ||||||||||  |||
                                TGGTGTTTATG  TCT
                                      GT
GAM846  CASQ2     3'  TACTGATGCCCTGAGGCACTGA 6939           AACT TG
                                TTAGTGCCTCAG   T  GTG
                                ||||||||||||   |  |||
                                AGTCACGGAGTC   A  CAT
                                      CCGT GT
GAM846  CHRM1     3'  ATATCAAGTCCCGAGGCA    94785       AGA   T
                                TGCCTC   ACTT GGTGT
                                ||||||   |||| |||||
                                ACGGAG   TGAA CTATA
                                   CCC   _
GAM846  CSF1R     3'  ACACCAAGCAGGAAGCAC    17800     C  AGAAC
                                GTGC TC    TTTGGTGT
                                |||| ||    ||||||||
                                CACG AG    GAACCACA
                                  A  GAC__
GAM846  DKFZP434C212 3'  ACACCAAAGCTTCAAGCAC   68901     CTCA  _
                                GTGC   GAA CTTTGGTGT
                                ||||   ||| |||||||||
                                CACG   CTT GAAACCACA
                                  AA__   C
GAM846  KIAA0376  3'  TACACTAGTGCTCCAGGGCAC  65602       CA  ACT
                                GTGCCT  GA   TTGGTGTA
                                ||||||  ||   ||||||||
                                CACGGG  CT   GATCACAT
                                   AC  CGT
GAM846  KIAA1013  3'  CAAACTCTAGGCACTAA     88886         C   AC
                                TTAGTGCCT AGA  TTTG
                                ||||||||| |||  ||||
                                AATCACGGA TCT  AAAC
                                      _  C_
GAM846  RASGRP4   3'  CACCTGAGCCCTGACAGCAC  53649      C_   AA   T
                                GTGC  TCAG  CTT GGTG
                                ||||  ||||  ||| ||||
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                                CACG  AGTC  GAG CCAC
                                  AC    CC   T
GAM846  LOC112817 3'  GCCTAGGTCTGAAACACTAA  56512       CC    A   T
                                TTAGTG  TCAGA CTT GGT
                                ||||||  ||||| ||| |||
                                AATCAC  AGTCT GGA CCG
                                   AA    _   T
GAM846  LOC149711 5'  TACCATGGGGCTTAAGGCAC  84688       C_  AA  T
                                GTGCCT  AG  CT TGGTG
                                ||||||  ||  || |||||
                                CACGGA  TC  GG ACCAT
                                   AT  GG  T
GAM846  LOC154743 3'  TACACCAATTGGAAATACTAA  81117       CC  AGAACT
                                TTAGTG  TC    TTGGTGTA
                                ||||||  ||    ||||||||
                                AATCAT  AG    AACCACAT
                                   AA  GTT___
GAM846  LOC200488 5'  ACACCAAAGCTTGAACAC    90077     CC   AA
                                GTG  TCAG  CTTTGGTGT
                                |||  ||||  |||||||||
                                CAC  AGTT  GAAACCACA
                                  A_   C_
GAM846  LOC203080 5'  TAGAGTCCAAGGCACTAA    89268        CA  A
                                TTAGTGCCT  GA CTTTG
                                |||||||||  || |||||
                                AATCACGGA  CT GAGAT
                                     AC  _
GAM846  LOC57105  3'  ACACCAAAGCTCTGAG      39812       A
                                CTCAGA CTTTGGTGT
                                |||||| |||||||||
                                GAGTCT GAAACCACA
                                   C
GAM847  ADD1     3'  CCACTGAGGCCCCTACTGA   26378     C   AGACACGA
                                TCA TAG       CTCAGTGG
                                ||| |||       ||||||||
                                AGT ATC       GAGTCACC
                                  C   CCCG____
GAM847  BCL2L2   3'  CCACACTGTGTCTCAGTGA   14465      A      ACTCA
                                TCACT GAGACACG    GTGG
                                ||||| ||||||||    ||||
                                AGTGA CTCTGTGT    CACC
                                   _       CA___
GAM847  BMPR2    3'  TCCACCTGGGTCATCTCCACTG 52913    CTA   CAC     _
          A                      TCA   GAGA   GACTCAG TGGA
                                 |||   ||||   ||||||| ||||
                                 AGT   CTCT   CTGGGTC ACCT
                                   CAC   A__      C
GAM847  BMPR2    3'  TCCACTGAATCGCTGGACTGTG 52914     T  AGA  _   C
          A                      TCAC AG   CA CGA TCAGTGGA
                                 |||| ||   || ||| ||||||||
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                                AGTG TC   GT GCT AGTCACCT
                                  _ AG_  C   A
GAM847  CISH     3'  TCCACTGATTTTTCTGTAATGA 59020     C  G   CAC  C
                                TCA TA AGA   GA TCAGTGGA
                                ||| || |||   || ||||||||
                                AGT AT TCT   TT AGTCACCT
                                  A  G   T__  T
GAM847  CISH     3'  TCCACTGATTTTTCTGTAATGA 25283     C  G   CAC  C
                                TCA TA AGA   GA TCAGTGGA
                                ||| || |||   || ||||||||
                                AGT AT TCT   TT AGTCACCT
                                  A  G   T__  T
GAM847  GASC1    5'  TCCACCGAGTCGTGCTCTC   64245      _       A
                                GAGA CACGACTC GTGGA
                                |||| |||||||| |||||
                                CTCT GTGCTGAG CACCT
                                  C       C
GAM847  KCNJ1    5'  TCCACTGACTGTCGCCTA    4028      A_    CGAC
                                TAG  GACA    TCAGTGGA
                                |||  ||||    ||||||||
                                ATC  CTGT    AGTCACCT
                                  CG    C___
GAM847  CDH24    3'  CCACTGGCCTCCAGCTGA    94929     _  A   ACACGAC
                                TCA CT GAG      TCAGTGG
                                ||| || |||      |||||||
                                AGT GA CTC      GGTCACC
                                  C  C   C_______
GAM847  CMG1     3'  TCCACTGAAAGTCTCTAAGGA  47023    AC      ACGAC
                                TC  TAGAGAC    TCAGTGGA
                                ||  |||||||    ||||||||
                                AG  ATCTCTG    AGTCACCT
                                 GA      AA___
GAM847  ITPK1    3'  TCCACCCCCTTGTCTCTAGTGG 26413           CGACTCA
                                TCACTAGAGACA      GTGGA
                                ||||||||||||      |||||
                                GGTGATCTCTGT      CACCT
                                       TCCCC__
GAM847  KIAA0682 3'  TCCACTGAGCTTCACTA     29370     A  CACGA
                                TAG GA    CTCAGTGGA
                                ||| ||    |||||||||
                                ATC CT    GAGTCACCT
                                  A  TC___
GAM847  KIAA1266 3'  CCACTGAGGGGTCCCTTCAG   66116    AG  AC  GA
                                CT  AG  AC  CTCAGTGG
                                ||  ||  ||  ||||||||
                                GA  TC  TG  GAGTCACC
                                 CT  CC  GG
GAM847  KIAA1364 3'  CCACTGACCCTGCAGTGA    63588      AG  ACACGAC
                                TCACT  AG      TCAGTGG
                                |||||  ||      |||||||
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                                AGTGA  TC      AGTCACC
                                  CG  CC_____
GAM847  RABL4    5'  CCACTCGCGTCTCTAG      22473         A   CTCA
                                CTAGAGAC CGA    GTGG
                                |||||||| |||    ||||
                                GATCTCTG GCT    CACC
                                    C   _____
GAM847  SDFR1    3'  TCCACTGAATGGGTATAATGA  24868     C  GAGA  CGAC
                                TCA TA    CA    TCAGTGGA
                                ||| ||    ||    ||||||||
                                AGT AT    GT    AGTCACCT
                                  A  ATGG  A___
GAM847  SDFR1    3'  TCCACTGAATGGGTATAATGA  33918     C  GAGA  CGAC
                                TCA TA    CA    TCAGTGGA
                                ||| ||    ||    ||||||||
                                AGT AT    GT    AGTCACCT
                                  A  ATGG  A___
GAM847  LOC144845 5'  CCACTGGGGGTCTCCAGTGG   56659       A    ACGA
                                TCACT GAGAC    CTCAGTGG
                                ||||| |||||    ||||||||
                                GGTGA CTCTG    GGGTCACC
                                   C    G___
GAM847  LOC150279 3'  CCACTGAGATTCTCTATGA    79666     C     CACGA
                                TCA TAGAGA     CTCAGTGG
                                ||| ||||||     ||||||||
                                AGT ATCTCT     GAGTCACC
                                  _     TA___
GAM847  LOC158156 3'  CCACTGAGATGCCTCTA     81725       A  CGA
                                TAGAG CA   CTCAGTGG
                                ||||| ||   ||||||||
                                ATCTC GT   GAGTCACC
                                   C  A__
GAM847  LOC51152  3'  TCCACTGACCTGGTCCCCATTG 32456     CTAGA   A  AC
            A                    TCA     GAC CG  TCAGTGGA
                                |||     ||| ||  ||||||||
                                AGT     CTG GT  AGTCACCT
                                  TACCC   _  CC
GAM847  LOC57228  5'  CCACTGAGGCCCTGTCCCCAG  39997    AGA   CGA_
                                CT   GACA   CTCAGTGG
                                ||   ||||   ||||||||
                                GA   CTGT   GAGTCACC
                                 CCC    CCCG
GAM847  LOC93496  3'  CCACCGAATGTTCTGGTGA   72431         A  CGAC  A
                                TCACTAGAG CA    TC GTGG
                                |||||||| ||    || ||||
                                AGTGGTCTT GT    AG CACC
                                     _ A___  C
GAM848  APBB1    3'  TAACACTGGAGTGGTAAC    6747     C   TTC
                                GT ACC   TTCCAGTGTTA
                                || |||   ||||||||||
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                                CA TGG   GAGGTCACAAT
                                 A   T__
GAM848  C14orf1   3'  ACATGGGAAGAAGACAACTAA  23171      CAC       A
                                TTGGT   CTTCTTCC GTGT
                                |||||   |||||||| ||||
                                AATCA   GAAGAAGG TACA
                                   ACA       G
GAM848  CALD1     3'  GTAACACTTTTTGAAAGTAACC 52465     C  C   TTCC
                                GGT AC TTC    AGTGTTAC
                                ||| || |||    ||||||||
                                CCA TG AAG    TCACAATG
                                  A  A   TTTT
GAM848  CALD1     3'  GTAACACTTTTTGAAAGTAACC 52469     C  C   TTCC
                                GGT AC TTC    AGTGTTAC
                                ||| || |||    ||||||||
                                CCA TG AAG    TCACAATG
                                  A  A   TTTT
GAM848  CALD1     3'  GTAACACTTTTTGAAAGTAACC 52529     C  C   TTCC
                                GGT AC TTC    AGTGTTAC
                                ||| || |||    ||||||||
                                CCA TG AAG    TCACAATG
                                  A  A   TTTT
GAM848  CCNF      3'  TAACATCTGAGGTGACCAA    8323          TCTTC  _
                                TTGGTCACCT    CAG TGTTA
                                ||||||||||    ||| |||||
                                AACCAGTGGA    GTC ACAAT
                                      _____   T
GAM848  CDK2AP1   3'  ACATCTGGAAGAAAATGACTAA 16172        CC       _
                                TTGGTCA  TTCTTCCAG TGT
                                |||||||  ||||||||| |||
                                AATCAGT  AAGAAGGTC ACA
                                   AA        T
GAM848  DLG5      5'  ACATCTGAGAAGAAGGCGGCCA 82908       A      _  _
          A                      TTGGTC CCTTCTTC CAG TGT
                                 ||||||| |||||||| ||| |||
                                 AACCGG GGAAGAAG GTC ACA
                                    C       A   T
GAM848  FLJ22865  3'  TTGGAAGAAAACAGCCAA    47074       CACC
                                TTGGT    TTCTTCCAG
                                |||||    |||||||||
                                AACCG    AAGAAGGTT
                                   ACAA
GAM848  GGA2      3'  ACAAGAAGAAGAAGGTGGCCAA 56866             CAG_
                                TTGGTCACCTTCTTC    TGT
                                ||||||||||||||    |||
                                AACCGGTGGAAGAAG    ACA
                                          AAGA
GAM848  KIAA0924  5'  AACACTGGAAGAATTGCAC    29711    _ CC
                                GT CA  TTCTTCCAGTGTT
                                || ||  ||||||||||||
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                                CA GT  AAGAAGGTCACAA
                                 C  T_
GAM848  KIAA1028  3'  CTGAAGAAAAAGGTGAC     91937        ___    C
                                GTCACCT   TCTTC AG
                                |||||||   ||||| ||
                                CAGTGGA   AGAAG TC
                                    AAA    _
GAM848  ZER6      3'  AACACTAGAAGAAGGTGTTAG  63373      T        C
                                TTGG CACCTTCTTC AGTGTT
                                |||| |||||||||| ||||||
                                GATT GTGGAAGAAG TCACAA
                                  _        A
GAM848  LOC146952 5'  TTGGAAGAAAATGCCAA     83878      T  CC
                                TTGG CA  TTCTTCCAG
                                |||| ||  |||||||||
                                AACC GT  AAGAAGGTT
                                  _ AA
GAM848  LOC220980 5'  ATTGAGAAGCAAGTGACCAA   93146         CTT   _
                                TTGGTCAC   CTTC CAGT
                                ||||||||   |||| ||||
                                AACCAGTG   GAAG GTTA
                                    AAC    A
GAM848  LOC56851  3'  AACACTGGGTGGCATCCAA    39338      TCA  TTCT
                                TTGG   CC    TCCAGTGTT
                                ||||   ||    |||||||||
                                AACC   GG    GGGTCACAA
                                  TAC  T___
GAM848  LOC93349  5'  GCAAGGAAGGAAAGTGACCAA  56458         C_      AG
                                TTGGTCAC  TTCTTCC  TGT
                                ||||||||  |||||||  |||
                                AACCAGTG  AGGAAGG  ACG
                                    AA      A_
GAM849  ARHGAP6   3'  TTACATTGTGCCAAAGGCTGAG 6770         G  ___  _
          GAA                    TTCCTCAG CTT   CA AGTGTGA
                                |||||||| |||   || |||||||
                                AAGGAGTC GAA   GT TTACATT
                                    G   ACC  G
GAM849  ARHGAP6   3'  TTACATTGTGCCAAAGGCTGAG 25521         G  ___  _
          GAA                    TTCCTCAG CTT   CA AGTGTGA
                                |||||||| |||   || |||||||
                                AAGGAGTC GAA   GT TTACATT
                                    G   ACC  G
GAM849  BCLG      3'  CATTGAGAACCTGAGGAA    47778         C   A_
                                TTCCTCAGG TTC  AGTG
                                ||||||||| |||  ||||
                                AAGGAGTCC AAG  TTAC
                                    _  AG
GAM849  BCLG      3'  CATTGAGAACCTGAGGAA    56974         C   A_
                                TTCCTCAGG TTC  AGTG
                                ||||||||| |||  ||||
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                                AAGGAGTCC AAG  TTAC
                                     _  AG
GAM849  BCLG    3'  CATTGAGAACCTGAGGAA    56980        C  A_
                                TTCCTCAGG TTC  AGTG
                                ||||||||| |||  ||||
                                AAGGAGTCC AAG  TTAC
                                     _  AG
GAM849  EHD4    3'  TCACATTGAAGCCTGAAGA   57692    C       G
                                TC TCAGGCTTCAA TGTGA
                                || |||||||||| |||||
                                AG AGTCCGAAGTT ACACT
                                 A         _
GAM849  EPB41L2 3'  ACCAGAAGCCTGAAGAA    7478     C       AA
                                TTC TCAGGCTTC  GT
                                ||| |||||||||  ||
                                AAG AGTCCGAAG  CA
                                  A        AC
GAM849  LGI1    3'  TATCACACTTGCAAATGA    17501    GGCTT
                                TCA    CAAGTGTGATA
                                |||    ||||||||||
                                AGT    GTTCACACTAT
                                  AAAC_
GAM849  MYO1D   3'  CACACTTGGGTCAGGAA    71766     CA   T
                                TTCCT  GGCT CAAGTGTG
                                |||||  |||| ||||||||
                                AAGGA  CTGG GTTCACAC
                                   __   _
GAM849  PYGB    3'  CATAGTGAAGCCTGGGAA    11172     T       AG
                                TTCC CAGGCTTCA  TGTG
                                |||| |||||||||  ||||
                                AAGG GTCCGAAGT  ATAC
                                  _       G_
GAM849  SYN3    3'  ATCCGCAACCTGAGGAA     56090        CTTCAA  T
                                TTCCTCAGG     GTG GAT
                                |||||||||     ||| |||
                                AAGGAGTCC     CGC CTA
                                     AA____   _
GAM849  SYN3    3'  ATCCGCAACCTGAGGAA     56096        CTTCAA  T
                                TTCCTCAGG     GTG GAT
                                |||||||||     ||| |||
                                AAGGAGTCC     CGC CTA
                                     AA____   _
GAM849  TPMT    3'  TTATGCTAAAGCCTGA      4548         CA
                                TCAGGCTT  AGTGTGA
                                ||||||||  |||||||
                                AGTCCGAA  TCGTATT
                                     A_
GAM849  CAMK2G  5'  CACAGGGACCTGAAGCCTGAG 68962          A ____
                                CTCAGGCTTCA GT   GTG
                                |||||||||| ||   |||
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                                GAGTCCGAAGT CA    CAC
                                      C  GGGA
GAM849  DKFZP434J1813 3'  TCATCCAGGAAAACCTGAGGGA 61790         C_   AAGT
                                TTCCTCAGG  TTC    GTGA
                                |||||||||  |||    ||||
                                AGGGAGTCC  AAG    TACT
                                     AA   GACC
GAM849  DKFZp434M0331 3'  TGTCAGCAAAACCTGGGGAA   34238         CTTCAAG  _
                                TTCCTCAGG      TG TGATA
                                |||||||||      || |||||
                                AAGGGGTCC      AC ACTGT
                                     AAA_____  G
GAM849  FLJ10201  3'  ACCCTGAGAGCCTGAGGAA   35890          CA  T
                                TTCCTCAGGCTT  AG GT
                                ||||||||||||  || ||
                                AAGGAGTCCGAG  TC CA
                                      AG  C
GAM849  FLJ11700  3'  TGCTTGAAACCCGGGAA     46041      CA  C
                                TTCCT  GG TTCAAGTG
                                |||||  || ||||||||
                                AAGGG  CC AAGTTCGT
                                   C_  A
GAM849  FLJ21945  3'  TTATCTTGAAGCCTAAAGAG   47319     ___        T
                                CTC   AGGCTTCAAG GTGA
                                |||   |||||||||| ||||
                                GAG   TCCGAAGTTC TATT
                                  AAA        _
GAM849  FLJ22558  5'  CTTGAAACTTGAGGAA      42738         C
                                TTCCTCAGG TTCAAG
                                ||||||||| ||||||
                                AAGGAGTTC AAGTTC
                                     A
GAM849  HH114     5'  CAGGCAGAGCCTGAGGAA    50685          CAA  G
                                TTCCTCAGGCTT   GT TG
                                ||||||||||||   || ||
                                AAGGAGTCCGAG   CG AC
                                      A__  G
GAM849  HUMGT198A 3'  TATCAAACCTGAGGAA      33332         CTTCAAGTG
                                TTCCTCAGG       TGATA
                                |||||||||       |||||
                                AAGGAGTCC       ACTAT
                                     AA_______
GAM849  HUMGT198A 3'  TATCAAACCTGAGGAA      25236         CTTCAAGTG
                                TTCCTCAGG       TGATA
                                |||||||||       |||||
                                AAGGAGTCC       ACTAT
                                     AA_______
GAM849  KIAA0210  5'  TTATCACATTTTAACGCTGA   28491      G _  C
                                TCAG C TT AAGTGTGATAA
                                |||| | || ||||||||||
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                                AGTC G AA TTTACACTATT
                                  _ C  T
GAM849  KIAA0355  3'  TCATCTTTGAAAAAGTCTGAG  28033        ___    T
                                CTCAGGCT   TCAAG GTGA
                                ||||||||   ||||| ||||
                                GAGTCTGA   AGTTT TACT
                                     AAA    C
GAM849  KIAA0590  3'  CACATTGTAAAGCCTGAG    28195        CA_
                                CTCAGGCTT   AGTGTG
                                |||||||||  ||||||
                                GAGTCCGAA   TTACAC
                                     ATG
GAM849  KIAA0643  3'  TTATCTTCTAAAACTTGAGGAA 45603        C  CA  TGT
                                TTCCTCAGG TT  AG   GATAA
                                ||||||||| ||  ||   |||||
                                AAGGAGTTC AA  TC   CTATT
                                     _  AA  TT_
GAM849  KIAA0884  5'  TCATGCAAGAGCCTGAAGAA   70206    C       CAA
                                TTC TCAGGCTT   GTGTGA
                                ||| ||||||||   ||||||
                                AAG AGTCCGAG   CGTACT
                                  A       AA_
GAM849  KIAA0976  3'  TTATCACAGCATAGCTCAAGGA 29897      CA    TCAAG
          A                      TTCCT  GGCT    TGTGATAA
                                |||||  ||||    ||||||||
                                AAGGA  TCGA    ACACTATT
                                   AC    TACG_
GAM849  KIAA1900  5'  GCTGAGAACCTGAGGAA     73248        C   A_
                                TTCCTCAGG TTC  AGT
                                ||||||||| |||  |||
                                AAGGAGTCC AAG  TCG
                                     _   AG
GAM849  ORMDL2    3'  TACACCTTTAAAGCCTGAG   26360        CAA__
                                CTCAGGCTT    GTGTG
                                |||||||||    |||||
                                GAGTCCGAA    CACAT
                                     ATTTC
GAM849  PHCA      3'  TACTTGAAACCTACAGAA    37180    CTC   C
                                TTC   AGG TTCAAGTG
                                |||   ||| ||||||||
                                AAG   TCC AAGTTCAT
                                  ACA   A
GAM849  PILR(ALPHA) 3'  TACTCTGAAGCCTGAGG     25549          _
                                CCTCAGGCTTCA AGTG
                                |||||||||||| ||||
                                GGAGTCCGAAGT TCAT
                                       C
GAM849  STAF65(gamma) 3'  GCTTGAAGCATAAGGAA     29440       CAG
                                TTCCT   GCTTCAAGT
                                |||||   |||||||||
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                                AAGGA  CGAAGTTCG
                                   ATA
GAM849  TFIP11   3'  TATTGTGAAGTCTGAGGAA  24056          AGT
                                TTCCTCAGGCTTCA  GTG
                                ||||||||||||||  |||
                                AAGGAGTCTGAAGT  TAT
                                      GT_
GAM849  LOC115131 3'  TCATCTACAGCCTGAG     59127       TCA  T
                                CTCAGGCT  AG GTGA
                                ||||||||  || ||||
                                GAGTCCGA  TC TACT
                                    CA_  _
GAM849  LOC142954 3'  TATTTTTTTAAAGCCTGA    76437       C  TGT
                                TCAGGCTT AAG  GATA
                                |||||||| |||  ||||
                                AGTCCGAA TTT  TTAT
                                    A  TT_
GAM849  LOC144240 5'  TCAGTCTGAGCCTGAG     76731       CA  TG
                                CTCAGGCTT  AG  TGA
                                |||||||||  ||  |||
                                GAGTCCGAG  TC  ACT
                                    __  TG
GAM849  LOC144438 3'  CAGTTGAAGCTGAGGAA    76832       G    G
                                TTCCTCAG CTTCAA TG
                                |||||||| |||||| ||
                                AAGGAGTC GAAGTT AC
                                   _    G
GAM849  LOC145173 3'  GCCTAAAGGCTGAGGAA    77041       G  CA  T
                                TTCCTCAG CTT  AG GT
                                |||||||| |||  || ||
                                AAGGAGTC GAA  TC CG
                                    G  A_  _
GAM849  LOC157506 3'  CACCTTAAAACTGAGGAA   81438       GC  C  T
                                TTCCTCAG  TT AAG GTG
                                ||||||||  || ||| |||
                                AAGGAGTC  AA TTC CAC
                                    AA  _  _
GAM849  LOC158332 3'  TCATAATCCTGAAGCCTGAGAG 81890   _       AG__
          A                      TC CTCAGGCTTCA   TGTGA
                                 || ||||||||||   |||||
                                 AG GAGTCCGAAGT   ATACT
                                  A         CCTA
GAM849  LOC159319 5'  CACACTCTGAGGAA       82189       GCTTCA
                                TTCCTCAG     AGTGTG
                                ||||||||     ||||||
                                AAGGAGTC     TCACAC
                                   ______
GAM849  LOC200812 3'  TCATCTACAGCCTGAG     88884       TCA  T
                                CTCAGGCT  AG GTGA
                                ||||||||  || ||||
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                                GAGTCCGA   TC TACT
                                     CA_  _
GAM849   LOC201411 3'  TTATGCTAAAGCCTGA      62965         CA
                                TCAGGCTT  AGTGTGA
                                ||||||||  |||||||
                                AGTCCGAA  TCGTATT
                                     A_
GAM849   LOC219347 3'  CACACAGAAGCCTGAGGAA    92981            AA
                                TTCCTCAGGCTTC  GTGTG
                                ||||||||||||  |||||
                                AAGGAGTCCGAAG  CACAC
                                       A_
GAM849   LOC220071 5'  CGCACGGCCGAAGCCTGAGGAA 93434            AA__
                                TTCCTCAGGCTTC    GTGTG
                                ||||||||||||    |||||
                                AAGGAGTCCGAAG    CACGC
                                       CCGG
GAM849   LOC221975 3'  ACTGAAGCCTGAGGAA      92602             A
                                TTCCTCAGGCTTCA GT
                                |||||||||||||| ||
                                AAGGAGTCCGAAGT CA
                                       _
GAM849   LOC255002 5'  TCACGGACCTGAAGCCTAAGGA 96779      C       A  __
                                TCCT AGGCTTCA GT  GTGA
                                |||| |||||||| ||  ||||
                                AGGA TCCGAAGT CA  CACT
                                  A       C  GG
GAM849   LOC255105 3'  TCATCTACAGCCTGAG      96067         TCA  T
                                CTCAGGCT   AG GTGA
                                ||||||||   || ||||
                                GAGTCCGA   TC TACT
                                     CA_  _
GAM849   LOC255524 3'  CAAACCCAGAAGCCTGAGGAA  96612            AA_  G
                                TTCCTCAGGCTTC   GT TG
                                ||||||||||||   || ||
                                AAGGAGTCCGAAG   CA AC
                                       ACC  A
GAM850   CACNA1F   3'  AACTGCTCAATAAACCTCCTG  17739      TA_   C
                                CAGG   TTTA TGAGCAGTT
                                ||||   |||| |||||||||
                                GTCC   AAAT ACTCGTCAA
                                  TCC    A
GAM850   NEBL      3'  AACTGAGGATAAAATACCTGCT 21116     A        ACTGAG
           CA                     TGA CAGGTATTT      CAGTT
                                ||| |||||||||      |||||
                                ACT GTCCATAAA      GTCAA
                                  C        ATAGGA
GAM850   OPHN1     3'  AACTGCTCAGTGTTTCATATTC 10351      CAGGTATT
           A                      TGAA       TACTGAGCAGTT
                                ||||       ||||||||||||
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                                ACTT       GTGACTCGTCAA
                                  ATACTTT_
GAM850  SRC      3'  ACTGCTCAGCTCTGGTCC    18283    T   TA__
                                GG ATT    CTGAGCAGT
                                || |||    |||||||||
                                CC TGG    GACTCGTCA
                                 _   TCTC
GAM850  C21orf108 3'  AACTGCCCAGTAAATG      88713          A
                                TATTTACTG GCAGTT
                                ||||||||| ||||||
                                GTAAATGAC CGTCAA
                                      C
GAM850  FLB6421   3'  AACTGCTCAGTAAACTCT    39222    TA
                                GG  TTTACTGAGCAGTT
                                ||  ||||||||||||||
                                TC  AAATGACTCGTCAA
                                 TC
GAM850  KIAA0237  3'  AACTGCTCAGCAGTTGGGCC   28518     AT__  A
                                GGT    TT CTGAGCAGTT
                                |||    || ||||||||||
                                CCG    GA GACTCGTCAA
                                  GGTT  C
GAM850  KIAA1582  5'  CAGTACAAATACCTCTTCA    65370      C      __
                                TGAA AGGTATT  TACTG
                                |||| |||||||  |||||
                                ACTT TCCATAA  ATGAC
                                   C       AC
GAM850  LOC146506 3'  AACTGCTCAAGACCCTGTGCCA 77930    A_     TATTTAC
                                TG  ACAGG      TGAGCAGTT
                                ||  |||||      |||||||||
                                AC  TGTCC      ACTCGTCAA
                                 CG    CAGA___
GAM850  LOC149935 3'  CTGCAACACCTGTTTA      60299          A  TACTGA
                                TGAACAGGT TT     GCAG
                                ||||||||| ||     ||||
                                ATTTGTCCA AA     CGTC
                                      C _______
GAM850  LOC155006 3'  AACTGCTCAGTGGCTCTTTCA  81228      CA   ATT
                                TGAA  GGT   TACTGAGCAGTT
                                ||||  |||   ||||||||||||
                                ACTT  TCG   GTGACTCGTCAA
                                   TC   ___
GAM850  LOC219513 5'  AGCAAATTCCTGTTCA      94325         T    A
                                TGAACAGG ATTT CT
                                |||||||| |||| ||
                                ACTTGTCC TAAA GA
                                      T    C
GAM851  ALDH1B1   3'  AAACATCCCAAATGTCCATC   5483       AAA   C
                                GGTG   ATT GGGATGTTT
                                ||||   ||| |||||||||
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                                CTAC   TAA CCCTACAAA
                                  CTG   A
GAM851  NDN      3'  ACAACCCCACCGTGA      10190        AAAATTC   A
                                TCACGGTG      GGG TGT
                                ||||||||      ||| |||
                                AGTGCCAC      CCC ACA
                                   ________   A
GAM851  RFX2     3'  CCAATTTTCACCATGA      5306      C        C
                                TCA GGTGAAAATT GG
                                ||| |||||||||| ||
                                AGT CCACTTTTAA CC
                                  A        _
GAM851  C7orf3   5'  AAACTGATTGGAACTTTCACCG 71476         A   G  AT_
                                CGGTGAAA TTC GG   GTTT
                                |||||||| ||| ||   ||||
                                GCCACTTT AAG TT   CAAA
                                     C   G  AGT
GAM851  FLJ13920 3'  TCGAAATTTCCATCGTGA    44656         _   A
                                TCACGGTG AAA TTCGG
                                |||||||| ||| |||||
                                AGTGCTAC TTT AAGCT
                                     C   A
GAM851  GW112    3'  AAACATTTTCTCTTTCACC    21182        ATTC
                                GGTGAAA    GGGATGTTT
                                |||||||    |||||||||
                                CCACTTT    TTTTACAAA
                                     CTC_
GAM851  KIAA1508 3'  AAACATCCATGGATTTCCC    61870    T    A   _
                                GG GAAA TTCG GGATGTTT
                                || |||| |||| ||||||||
                                CC CTTT AGGT CCTACAAA
                                  _   _    A
GAM851  KIAA1872 3'  AAACATTCTGCCCCCACC     62916      AAAATT
                                GGTG     CGGGATGTTT
                                ||||     ||||||||||
                                CCAC     GTCTTACAAA
                                   CCCC__
GAM851  LOC195977 3'  AACACCTGCCCCACTGTGA    87534         AAAATT    A
                                TCACGGTG     CGGG TGTT
                                ||||||||     |||| ||||
                                AGTGTCAC     GTCC ACAA
                                     CCC___   _
GAM852  LMAN1    5'  TAAAGCTTAGAGCCAA      18735       CGC  TAACC
                                TTGGC   CT    AGCTTTA
                                |||||   ||    |||||||
                                AACCG   GA    TCGAAAT
                                   A__  T_____
GAM852  PCDHGA2  5'  CTAAAGCTTCAGGACACCAA   38306      CCG   TAACC
                                TTGG   CCT    AGCTTTAG
                                ||||   |||    ||||||||
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                                AACC  GGA   TCGAAATC
                                  ACA  CT___
GAM852  PCDHGA2  5' CTAAAGCTTCAGGACACCAA  49267    CCG  TAACC
                                TTGG  CCT   AGCTTTAG
                                ||||  |||   ||||||||
                                AACC  GGA   TCGAAATC
                                  ACA  CT___
GAM852  CPEB1    3' AAAGCTGGCAGGTCAGGC   47594    __   TAA
                                GCC  GCCT  CCAGCTTT
                                |||  ||||  ||||||||
                                CGG  TGGA  GGTCGAAA
                                 AC   C__
GAM852  FLJ14957 3' CTGGAGCCAGACAGCCAA   51747     CGC  TAACCA
                                TTGGC  CT    GCTTTAG
                                |||||  ||    |||||||
                                AACCG  GA    CGAGGTC
                                   ACA  C_____
GAM852  PPP1R10  3' CTAAAGCTGGTTATCCTGGCGA 10732   G   CCT
            A                    TT GCCG  TAACCAGCTTTAG
                                || ||||  ||||||||||||
                                AA CGGT  ATTGGTCGAAATC
                                 G   CCT
GAM852  LOC115219 5' TCTAAAGCCCGGGGCAGCCAG  73322     C    AACCA
                                TTGGC GCCTT    GCTTTAGA
                                ||||| |||||    ||||||||
                                GACCG CGGGG    CGAAATCT
                                   A    CC___
GAM852  LOC253962 5' TCCAAAGCCAGGGCTGGGGCTG 96659     C    A_ A_   A
            CCAA                   TTGGC GCCTTA  CC  GCTTT GA
                                ||||| ||||||  ||  ||||| ||
                                AACCG CGGGGT  GG  CGAAA CT
                                   T    CG  AC    C
GAM853  APBA2    3' CCCAAACAGCTGCCTCTGC   18557    T   TGACAGA
                                GCAG GGCA     TTTGGG
                                |||| ||||     ||||||
                                CGTC CCGT     AAACCC
                                  T   CGAC___
GAM853  CACNA2D2  3' CCCAGTGGGACCACATGCCACT 20081          ACAGAT__
            GC                   GCAGTGGCATG      TTGGG
                                ||||||||||       |||||
                                CGTCACCGTAC      GACCC
                                      ACCAGGGT
GAM853  CALB2    3' CCGGTCCCCCATGCCAC    8210        ACA   T
                                GTGGCATG   GATT GG
                                ||||||||   |||| ||
                                CACCGTAC   CTGG CC
                                     CCC   _
GAM853  CAMLG    5' CCAACATCACCGCCACTGC   8234        A_   CAGAT
                                GCAGTGGC  TGA    TTGG
                                ||||||||  |||    ||||
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                                CGTCACCG ACT    AACC
                                     CC  AC___
GAM853  CEACAM5  3' CCAGATCGCACCACTGC    15157       CATGACA
                                GCAGTGG     GATTTGG
                                |||||||     |||||||
                                CGTCACC     CTAGACC
                                   ACG____
GAM853  COL1A1   3' CCCAAATCTGTCTCCCCA    3603     CAT
                                TGG  GACAGATTTGGG
                                |||  ||||||||||||
                                ACC  CTGTCTAAACCC
                                  CCT
GAM853  CRAT     3' CCCAAATCTACTGAGCCAC   5659      ATGAC
                                GTGGC    AGATTTGGG
                                |||||    |||||||||
                                CACCG    TCTAAACCC
                                   AGTCA
GAM853  CRAT     3' CCCAAATCTACTGAGCCAC   14351     ATGAC
                                GTGGC    AGATTTGGG
                                |||||    |||||||||
                                CACCG    TCTAAACCC
                                   AGTCA
GAM853  CX3CR1   3' CCCATCATTCATGCTACTGC  70645         CA  TT
                                GCAGTGGCATGA  GA  TGGG
                                ||||||||||||  ||  ||||
                                CGTCATCGTACT  CT  ACCC
                                      TA  __
GAM853  EGLN2    5' CCTCATCTTGCCACTGC     34098        TGAC   TT
                                GCAGTGGCA   AGAT  GG
                                |||||||||   ||||  ||
                                CGTCACCGT   TCTA  CC
                                     _____   CT
GAM853  GRB10    3' CCCAAATCCGCCCCACTG    17974       CA  ACA
                                CAGTGG  TG   GATTTGGG
                                ||||||  ||   ||||||||
                                GTCACC  GC   CTAAACCC
                                   CC  ___
GAM853  ICMT     3' CCGAGGCCACACGCCACTGC  24810        A  ACAGA
                                GCAGTGGC TG    TTTGG
                                ||||||||  ||    |||||
                                CGTCACCG AC    GAGCC
                                     C  ACCG_
GAM853  ITK      3' CCCAAATCTGTCTGACCGC   18678     _  T
                                GTGG CA GACAGATTTGGG
                                ||||  ||  ||||||||||||
                                CGCC GT CTGTCTAAACCC
                                  A  _
GAM853  MBD4     3' CCATGATCATGCCACTGC    14089          _  GATT
                                GCAGTGGCATGA CA    TGG
                                ||||||||||||  ||    |||
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                                CGTCACCGTACT GT   ACC
                                      A _____
GAM853  MTMR7   5' CCAAATCGGCCACGGC     69151   A   ATGACA
                                GC GTGGC    GATTTGG
                                || |||||    |||||||
                                CG CACCG    CTAAACC
                                 G   G_____
GAM853  MYEOV   5' CACGTCATGCCACGC      57048   A       AGATT
                                GC GTGGCATGAC   TG
                                || ||||||||||   ||
                                CG CACCGTACTG   AC
                                 _       C____
GAM853  PDE4C   3' CCGACATCATGCCACTGC   6231          CAGAT
                                GCAGTGGCATGA    TTGG
                                ||||||||||||    ||||
                                CGTCACCGTACT    AGCC
                                      AC___
GAM853  PODXL   3' CCATTTGCACCATGCCAC   18231       A__   TT
                                GTGGCATG  CAGA  TGG
                                ||||||||  ||||  |||
                                CACCGTAC  GTTT  ACC
                                    CAC   __
GAM853  PPP2R2B 5' CTGCCATCTCGCCACTGC   15908       ___  A
                                GCAGTGGC  ATG CAG
                                ||||||||  ||| |||
                                CGTCACCG  TAC GTC
                                    CTC   C
GAM853  PTGS1   3' CCCAAATCTGTCAGCATCTG  6350    TG  A
                                CAG  GC TGACAGATTTGGG
                                |||  || ||||||||||||
                                GTC  CG ACTGTCTAAACCC
                                  TA  _
GAM853  PTGS1   3' CCCAAATCTGTCAGCATCTG  54569    TG  A
                                CAG  GC TGACAGATTTGGG
                                |||  || ||||||||||||
                                GTC  CG ACTGTCTAAACCC
                                  TA  _
GAM853  SELPLG  3' CCCATCCCACACGCACTGC   59688     G A  ACA  TT
                                GCAGTG C TG   GA  TGGG
                                |||||| | ||   ||  ||||
                                CGTCAC G AC   CT  ACCC
                                   _ C  ACC  __
GAM853  SLC9A1  3' CCACGTACCAAGCCACCGC   70407   A    A  ACAG  T
                                GC GTGGC TG    AT TGG
                                || ||||| ||    || |||
                                CG CACCG AC    TG ACC
                                 C    A  CA__  C
GAM853  SLC9A5  3' CTGGGCTGCCATGTCAC     15982       A   A  TG
                                GTGGCATG CAG TT  G
                                |||||||| ||| ||  |
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                                CACTGTAC GTC GG  C
                                     C   _ GT
GAM853  SLC9A5   3'  CTGGGCTGCCATGTCAC     59769        A  A  TG
                                GTGGCATG CAG TT  G
                                |||||||| ||| ||  |
                                CACTGTAC GTC GG  C
                                     C   _ GT
GAM853  SOX10    3'  CCCAAATCCACATGTAACT   22683     G    ACA
                                AGT GCATG   GATTTGGG
                                ||| |||||   ||||||||
                                TCA TGTAC   CTAAACCC
                                  A    AC_
GAM853  TACC1    3'  CCATGATCATGCCACTGC    20795          _  GATT
                                GCAGTGGCATGA CA    TGG
                                |||||||||||| ||    |||
                                CGTCACCGTACT GT    ACC
                                       A _____
GAM853  AAK1     3'  CTGATCATGCCACTGC      29846          _
                                GCAGTGGCATGA CAG
                                |||||||||||| |||
                                CGTCACCGTACT GTC
                                       A
GAM853  ARTN     5'  CCCAAATCTGCACGTACCA   54037     C  A_
                                TGG ATG  CAGATTTGGG
                                ||| |||  ||||||||||
                                ACC TGC  GTCTAAACCC
                                  A  AC
GAM853  C20orf150 3'  CCATCCCATGCCATGC     65393     G     ACA  TT
                                GCA TGGCATG   GA  TGG
                                ||| |||||||   ||  |||
                                CGT ACCGTAC   CT  ACC
                                  _      C__  __
GAM853  DKFZP434H132 5'  CCCAAACCTGTCTACCGC    73604      CAT    A
                                GTGG   GACAG TTTGGG
                                ||||   ||||| ||||||
                                CGCC   CTGTC AAACCC
                                   AT_    C
GAM853  DKFZP564C196 3'  CCCAAATCCACCCCACCCGC   70065    A_   CA  ACA
                                GC  GTGG  TG   GATTTGGG
                                ||  ||||  ||   ||||||||
                                CG  CACC  AC   CTAAACCC
                                 CC    CC  ___
GAM853  EFA6R    3'  CCAGGCCATGCCACTGC     30981          ACAGA
                                GCAGTGGCATG    TTTGG
                                ||||||||||    |||||
                                CGTCACCGTAC    GGACC
                                       C_____
GAM853  FLJ10315  5'  CCCAAACTGTTGTGCCTCT   36017    T   TG   A
                                AG GGCA  ACAG TTTGGG
                                || ||||  |||| ||||||
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                                TC CCGT  TGTC AAACCC
                                 T   GT   _
GAM853  FLJ12409  3'  CCCATAATCATGCCACTGC   47045          CAGATT
                                GCAGTGGCATGA    TGGG
                                ||||||||||||    ||||
                                CGTCACCGTACT    ACCC
                                      AAT___
GAM853  FLJ13456  3'  CCAATATCATGCCACTGC    65935          CAGAT
                                GCAGTGGCATGA    TTGG
                                ||||||||||||    ||||
                                CGTCACCGTACT    AACC
                                      AT___
GAM853  FLJ20150  3'  CCCAAATCCACCATGCATCTGC 34646     TG    ACA
                                GCAG  GCATG   GATTTGGG
                                ||||  |||||   ||||||||
                                CGTC  CGTAC   CTAAACCC
                                  TA    CAC
GAM853  FLJ23519  3'  CCACTGTGACGCCACTGC    49965       ATG   ATT
                                GCAGTGGC   ACAG   TGG
                                ||||||||   ||||   |||
                                CGTCACCG   TGTC   ACC
                                    CAG   ___
GAM853  FYCO1     3'  CCTTCTTCATCATGCCACTG   44493         CA  TTT
                                CAGTGGCATGA  GA   GGG
                                ||||||||||  ||   |||
                                GTCACCGTACT  CT   TCC
                                      A_  TCT
GAM853  INE1      3'  CCGTGATCATGCCACTGC    13373          _  GATT
                                GCAGTGGCATGA CA    TGG
                                ||||||||||||  ||    |||
                                CGTCACCGTACT GT    GCC
                                      A  ____
GAM853  KIAA0022  3'  CCAAATTGTACCACT      29662      CATG   A
                                AGTGG    ACAG TTTGG
                                |||||    |||| |||||
                                TCACC    TGTT AAACC
                                  A___    _
GAM853  KIAA0447  3'  CCCAAATCCGGTGAGCTCTGC  71669     T   ATG  A_
                                GCAG GGC   AC  GATTTGGG
                                |||| |||   ||  ||||||||
                                CGTC TCG   TG  CTAAACCC
                                  _   AG_  GC
GAM853  KIAA0556  3'  CCCAAACCAGTGCCGCTGC   69081         GACAGA
                                GCAGTGGCAT     TTTGGG
                                ||||||||||     ||||||
                                CGTCGCCGTG     AAACCC
                                      ACC___
GAM853  KIAA0643  3'  CCGTGATCATGCCACTGC    45598          _  GATT
                                GCAGTGGCATGA CA    TGG
                                ||||||||||||  ||    |||
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                                CGTCACCGTACT GT   GCC
                                      A _____
GAM853  KIAA0953  3' CCCTTCTGCCATGCCAC    66783       A   TTT
                                GTGGCATG CAGA  GGG
                                |||||||| ||||  |||
                                CACCGTAC GTCT  CCC
                                    C   T__
GAM853  KIAA1649  5' CCATCATCATGCCACTGC    50252         CA  TT
                                GCAGTGGCATGA  GA  TGG
                                ||||||||||||  ||  |||
                                CGTCACCGTACT  CT  ACC
                                      A_  __
GAM853  KIAA1719  5' CCAGCCATGCCACCGC     68157    A      ACAGAT
                                GC GTGGCATG     TTGG
                                || ||||||||     ||||
                                CG CACCGTAC     GACC
                                 C      C_____
GAM853  KIAA1813  3' CCCACCGCTGCCAGTGCCACTG 70294        GA_  ATT
          C                      GCAGTGGCAT   CAG   TGGG
                                ||||||||||  |||  ||||
                                CGTCACCGTG   GTC   ACCC
                                      ACC   GCC
GAM853  KIAA1862  3' CCCTGCAGCCGCCATGCCACTG 68927         ACAGATTT_
          T                      GCAGTGGCATG       GGG
                                ||||||||||        |||
                                TGTCACCGTAC       CCC
                                      CGCCGACGT
GAM853  LIMR     3' CCAAATCTGTTTACAC     36188     GCAT
                                GTG   GACAGATTTGG
                                |||   ||||||||||
                                CAC   TTGTCTAAACC
                                  AT__
GAM853  MGC10812  3' CCAAATTTGACACCAC     48664     CA  A
                                GTGG  TG CAGATTTGG
                                ||||  || |||||||||
                                CACC  AC GTTTAAACC
                                   __ A
GAM853  MGC10999  3' CCACAGTCACGCCACTGC    50226       A   AGATT
                                GCAGTGGC TGAC    TGG
                                |||||||| ||||    |||
                                CGTCACCG ACTG    ACC
                                    C   AC___
GAM853  MRPL20   3' CCCTGCGTCGCCAGCCACCGC  35732    A    A  ACA  TT_
                                GC GTGGC TG   GAT   GGG
                                || ||||| ||   |||  |||
                                CG CACCG AC   CTG   CCC
                                 C    _ CG_   CGT
GAM853  NDUFC2   3' CCCAAATCTGGCCCACTGC   15828       CATGA
                                GCAGTGG    CAGATTTGGG
                                |||||||    ||||||||||
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                                CGTCACC    GTCTAAACCC
                                   CG___
GAM853  NRM     3' CCAAATCCATGGACTG     92025     GG   ACA
                                CAGT  CATG   GATTTGG
                                ||||  ||||   |||||||
                                GTCA  GTAC   CTAAACC
                                  G_   ___
GAM853  NRM     3' CCAAATCCATGGACTG     97764     GG   ACA
                                CAGT  CATG   GATTTGG
                                ||||  ||||   |||||||
                                GTCA  GTAC   CTAAACC
                                  G_   ___
GAM853  NRM     3' CCAAATCCATGGACTG     97890     GG   ACA
                                CAGT  CATG   GATTTGG
                                ||||  ||||   |||||||
                                GTCA  GTAC   CTAAACC
                                  G_   ___
GAM853  P5-1    3' CCCAAATCTTACCCCACCACTG 21916       CATGAC_
                                CAGTGG      AGATTTGGG
                                ||||||      |||||||||
                                GTCACC      TCTAAACCC
                                   ACCCCAT
GAM853  PLP1    3' CCCAAATCTGCCTATTGC    5006        CATGA
                                GCAGTGG    CAGATTTGGG
                                |||||||    ||||||||||
                                CGTTATC    GTCTAAACCC
                                   C____
GAM853  PP1665   3' CCACCTCATGCCACCGC     47911    A       CAGATT
                                GC GTGGCATGA     TGG
                                || |||||||||     |||
                                CG CACCGTACT     ACC
                                 C       CC____
GAM853  RNB6    3' GTCTGTCATGCACCAC     32930     __
                                GTG  GCATGACAGAT
                                |||  ||||||||||
                                CAC  CGTACTGTCTG
                                  CA
GAM853  SDC3    3' CCCAAATCTGCCCTGGCCG   27745     ATGA_
                                TGGC    CAGATTTGGG
                                ||||    ||||||||||
                                GCCG    GTCTAAACCC
                                  GTCCC
GAM853  SEPT3    3' CCTCTGCTGCCAGGCCACTGC  38892        A  A   ATTT
                                GCAGTGGC TG CAG    GG
                                |||||||| || |||    ||
                                CGTCACCG AC GTC    CC
                                     G  C   GTCT
GAM853  SIMRP7   3' CCAGGGCCAGCCACTGC     92361        A  ACAGA
                                GCAGTGGC TG    TTTGG
                                |||||||| ||    |||||
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                                CGTCACCG AC    GGACC
                                    _ CG___
GAM853  STK39    3'  CCCTGATCTGTCATGCC    25074          T
                                GGCATGACAGATT GGG
                                ||||||||||||| |||
                                CCGTACTGTCTAG CCC
                                     T
GAM853  THG-1    5'  CTGCGTGCCCCGCCACTGC   48185       _____  A
                                GCAGTGGC    ATG CAG
                                ||||||||    ||| |||
                                CGTCACCG    TGC GTC
                                    CCCCG  _
GAM853  VILL     5'  CAGGGCCACCAGGCCACTGC  68412       A  ACAGA
                                GCAGTGGC TG    TTTG
                                |||||||| ||    ||||
                                CGTCACCG AC    GGAC
                                    G  CACCG
GAM853  LOC126282 3'  CCGATGATCATGCCACTGC   74471         _  GAT
                                GCAGTGGCATGA CA   TTGG
                                |||||||||||| ||   ||||
                                CGTCACCGTACT GT   AGCC
                                     A  ___
GAM853  LOC129644 3'  CCCAAATCTGCTTGTTAT    74882      TGA
                                GTGGCA   CAGATTTGGG
                                ||||||   ||||||||||
                                TATTGT   GTCTAAACCC
                                   TC_
GAM853  LOC138428 3'  CCCACCAACCCAGCCACTGC  75334       A  ACAGATT
                                GCAGTGGC TG      TGGG
                                |||||||| ||      ||||
                                CGTCACCG AC      ACCC
                                    _ CCAACC_
GAM853  LOC142927 3'  CCCAGCGCATCATGCCACTG  76422         CAGAT
                                CAGTGGCATGA    TTGGG
                                ||||||||||    |||||
                                GTCACCGTACT    GACCC
                                     ACGC_
GAM853  LOC145216 3'  CCCAAAATACGTATGTCACT  83263        ACAGA
                                AGTGGCATG    TTTGGG
                                |||||||||    ||||||
                                TCACTGTAT    AAACCC
                                    GCATA
GAM853  LOC146728 5'  CCAAATCCATCTGCTG     83748     TG C   ACA
                                CAG  G ATG   GATTTGG
                                |||  | |||   |||||||
                                GTC  C TAC   CTAAACC
                                  GT _  ___
GAM853  LOC146822 3'  CCCAGGCTCTCCATGCCAC   78153       AC  _
                                GTGGCATG  AGA TTTGGG
                                ||||||||  ||| ||||||
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                                CACCGTAC  TCT GGACCC
                                     C_   C
GAM853   LOC146957 3'  CCAAATCTGCCCTCTG      78202     T  CATGA
                                CAG GG    CAGATTTGG
                                ||| ||    |||||||||
                                GTC CC    GTCTAAACC
                                  T  C____
GAM853   LOC148697 3'  GTCTGCCAGCCACTGC      78930        A  A
                                GCAGTGGC TG CAGAT
                                |||||||| || |||||
                                CGTCACCG AC GTCTG
                                     _ C
GAM853   LOC150378 3'  CCCTGCTGCACCATGCCACT   79744        A__   ATTT
                                AGTGGCATG   CAG    GGG
                                |||||||||   |||    |||
                                TCACCGTAC   GTC    CCC
                                     CAC   GT__
GAM853   LOC152518 5'  CCACTACCATGCCATGC     80612     G      AC  ATT
                                GCA TGGCATG  AG   TGG
                                ||| |||||||  ||   |||
                                CGT ACCGTAC  TC   ACC
                                  _      CA  ___
GAM853   LOC154214 3'  CCCAGTTCCATGCCGCT     81056         ACA  T
                                AGTGGCATG   GA TTGGG
                                |||||||||   || |||||
                                TCGCCGTAC   CT GACCC
                                     ___  T
GAM853   LOC158969 3'  CCCATCCCCACCGCCACTGC   82058        A_  ACA  TT
                                GCAGTGGC  TG   GA  TGGG
                                ||||||||  ||   ||  ||||
                                CGTCACCG  AC   CT  ACCC
                                     CC  CC_  __
GAM853   LOC160336 5'  CCCACGATTCCTGCCACTGC   82212        T  CAGATT
                                GCAGTGGCA GA     TGGG
                                ||||||||| ||     ||||
                                CGTCACCGT CT     ACCC
                                     C  TAGC__
GAM853   LOC199986 3'  CCCACTACAGTCATGCCAC    89901         AGATT
                                GTGGCATGAC     TGGG
                                ||||||||||     ||||
                                CACCGTACTG     ACCC
                                     ACATC
GAM853   LOC203611 5'  CAAGCTGTCATGCACCAC     60364     __       A
                                GTG  GCATGACAG TTTG
                                |||  ||||||||| ||||
                                CAC  CGTACTGTC GAAC
                                  CA       _
GAM853   LOC88745  3'  CTTCTGCCATGCCAC       92266        A   TTT
                                GTGGCATG CAGA   GG
                                |||||||| ||||   ||
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                                CACCGTAC GTCT   TC
                                    C   ___
GAM853  LOC90918  5' CCAGATCACACCATTGC    64353       CA  ACA
                                GCAGTGG  TG   GATTTGG
                                |||||||  ||   |||||||
                                CGTTACC  AC   CTAGACC
                                   __  A__
GAM853  LOC91464  3' CCCAAATCCCAGATCCTCTGC  66137     T  CA_  ACA
                                GCAG GG   TG   GATTTGGG
                                |||| ||   ||   ||||||||
                                CGTC CC   AC   CTAAACCC
                                  T  TAG  C__
GAM853  LOC93132  5' CCGACATCATGCCATTGC    71487          CAGAT
                                GCAGTGGCATGA    TTGG
                                ||||||||||||    ||||
                                CGTTACCGTACT    AGCC
                                      AC___
GAM854  ACP2    3' AGAAAGTTCTAGACTG     7851      GC  TC
                                CAGT  CT  AGAACTTTCT
                                ||||  ||  ||||||||||
                                GTCA  GA  TCTTGAAAGA
                                   __ __
GAM854  APTX    5' AAGAGAAAGAGATCAGGCA   34655      TCAGAA
                                TGCCT     CTTTCTCTT
                                |||||     |||||||||
                                ACGGA     GAAAGAGAA
                                   CTAGA_
GAM854  BCL7A   3' AGGCTGTCTCCTTAAGGCACTG 40637         C  A__  TT
                                CAGTGCCTT AG   AC  TCT
                                ||||||||| ||   ||  |||
                                GTCACGGAA TC   TG  GGA
                                      T  CTC  TC
GAM854  CLC     3' AAGAGAAAATACTGAAAGCACA 25105    A   C    AAC
            GG                    CC GTGC TTCAG   TTTCTCTT
                                || |||| |||||   ||||||||
                                GG CACG AAGTC   AAAGAGAA
                                 A   A    ATA
GAM854  CNK     3' AAGCCCTGAAGGCCTG     14517     T      AA
                                CAG GCCTTCAG  CTT
                                ||| ||||||||  |||
                                GTC CGGAAGTC  GAA
                                  _       CC
GAM854  COL4A3  3' AAGTGCAGGTTCTGAGGGCACC 48549    A           TCT
            GG                    CC GTGCCTTCAGAACTT   CTT
                                || ||||||||||||||   |||
                                GG CACGGGAGTCTTGGA   GAA
                                 C            CGT
GAM854  CSPG4   3' AAGAGAGACCTGGAGACAC   8570     C     AAC
                                GTG CTTCAG   TTTCTCTT
                                ||| ||||||   ||||||||
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                                CAC GAGGTC   AGAGAGAA
                                  A     C__
GAM854  CYP1B1   3'  AAGAGAAAAGAGAGAAACACTG 3651       CC   AGAAC
                                CAGTG  TTC    TTTCTCTT
                                |||||  |||    ||||||||
                                GTCAC  AAG    AAAGAGAA
                                   A_   AGAGA
GAM854  DLG3     3'  AAGAGAAAAGAGGAGGACTG   40880     G    AGAAC
                                CAGT CCTTC    TTTCTCTT
                                |||| |||||    ||||||||
                                GTCA GGAGG    AAAGAGAA
                                  _    AGA__
GAM854  DLG5     5'  AGGCAGACTCTGAAGGC     82909        A_  T
                                GCCTTCAGA  CT TCT
                                |||||||||  || |||
                                CGGAAGTCT  GA GGA
                                     CA  C
GAM854  FLT1     3'  AAGAGAAACCGGGAGAAGGCAT 8910        AGAAC_
                                GTGCCTTC     TTTCTCTT
                                ||||||||     ||||||||
                                TACGGAAG     AAAGAGAA
                                   AGGGCC
GAM854  GRB10    3'  AGAGAAAATGGCACCTGG    17971     _   TTCAGAAC
                                CCAG TGCC       TTTCTCT
                                |||| ||||       |||||||
                                GGTC ACGG       AAAGAGA
                                  C   TA_______
GAM854  LFG      3'  AAGAGAAAAGGAGCCAAGAACT 76711      GC   CAGAA   _
           GG                   CCAGT  CTT    CTTT CTCTT
                                |||||  |||    |||| |||||
                                GGTCA  GAA    GAAA GAGAA
                                  A_   CCGAG   A
GAM854  MAN2A2   3'  AAGAGAAAGTTCATTCAC    20391     CCTTCA
                                GTG     GAACTTTCTCTT
                                |||     ||||||||||||
                                CAC     CTTGAAAGAGAA
                                  TTA___
GAM854  NLGN3    3'  AAGAAAAGTTCTTAAAACACT  38596     CC  C       C
                                AGTG  TT AGAACTTT TCTT
                                ||||  || |||||||| ||||
                                TCAC  AA TCTTGAAA AGAA
                                  AA  T       _
GAM854  NPAS1    5'  AAGGTCTCCCGAGGGCACT   59879        A_  _
                                AGTGCCTTC  GA ACTTT
                                |||||||||  || |||||
                                TCACGGGAG  CT TGGAA
                                     CC  C
GAM854  PLAG1    3'  AGTGTGTTCCAAAGGCATT   10605        CA   TTT
                                AGTGCCTT  GAAC   CT
                                ||||||||  ||||   ||
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                                TTACGGAA  CTTG   GA
                                    AC    TGT
GAM854  PLXNA1   3'  AGAAAATGAAGGCAGTGG    72309     G       GAAC
                                CCA TGCCTTCA    TTTCT
                                ||| ||||||||    |||||
                                GGT ACGGAAGT    AAAGA
                                  G       A___
GAM854  PPP4R1   3'  AAGAGAAAGTACAGTAAACACT 17620      CCTTCAGA
                                AGTG       ACTTTCTCTT
                                ||||       ||||||||||
                                TCAC       TGAAAGAGAA
                                  AAATGACA
GAM854  ACYP2    3'  AAGAGAAAAATTGTAACACACT 56612       CC  _   AAC
           G                     CAGTG  TT CAG   TTTCTCTT
                                |||||  || |||   ||||||||
                                GTCAC  AA GTT   AAAGAGAA
                                   AC  T   AA_
GAM854  B3GNT6   3'  AGAAATCAGATGAAGGCAT   22503         GAAC_
                                GTGCCTTCA     TTTCT
                                |||||||||     |||||
                                TACGGAAGT     AAAGA
                                     AGACT
GAM854  BAG5     3'  AAGAGAAGGGATAAAGGAC   16835    G   CAGAA
                                GT CCTT     CTTTCTCTT
                                || ||||     |||||||||
                                CA GGAA     GGAAGAGAA
                                 _   ATAG_
GAM854  BIVM     3'  AAGAGAAAAGACTCAAGAAACT 34665      GC   C  AAC
           G                     CAGT  CTT AG   TTTCTCTT
                                ||||  ||| ||   ||||||||
                                GTCA  GAA TC   AAAGAGAA
                                  AA   C  AGA
GAM854  C15orf5  3'  AGAGAAAAGAAAGCAC      48195      C   AGAAC
                                GTGC TTC     TTTCTCT
                                |||| |||     |||||||
                                CACG AAG     AAAGAGA
                                  A   A____
GAM854  C20orf80  5'  AAGAGAAGAAGATGAAGAAAC  65282    GC    GAAC
                                GT  CTTCA    TTTCTCTT
                                ||  |||||    ||||||||
                                CA  GAAGT    GAAGAGAA
                                 AA     AGAA
GAM854  CLSTN1   3'  AGTTCTGAGGACACTGG     30103       C
                                CCAGTG CTTCAGAACT
                                |||||| ||||||||||
                                GGTCAC GGAGTCTTGA
                                   A
GAM854  DKFZP434P0111 3'  AAGAGAAAGTTTCTGCAC    67368      CTTCA
                                GTGC     GAACTTTCTCTT
                                ||||     ||||||||||||
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                                CACG    TTTGAAAGAGAA
                                  TC___
GAM854  DORFIN   5' AGAATTCTCTGAAGGAAC   31257   G      ACT
                                GT CCTTCAGA  TTCT
                                || ||||||||  ||||
                                CA GGAAGTCT  AAGA
                                 A       CTT
GAM854  FLJ10300 5' AAGAGAAAGATGAAGACTCTG 35997    TGC    GAA
                                CAG  CTTCA  CTTTCTCTT
                                |||  |||||  |||||||||
                                GTC  GAAGT  GAAAGAGAA
                                  TCA    A__
GAM854  FLJ20373 3' AAGAGAAGAAGGAAAGGCACAG 35070    A      _ AGAAC
           G                     CC GTGCCTT C    TTTCTCTT
                                || ||||||| |    ||||||||
                                GG CACGGAA G    GAAGAGAA
                                 A      A GAA__
GAM854  FLJ23511 5' AGAGAAAAACAAGGCAT    49956       CAGAAC
                                GTGCCTT     TTTCTCT
                                |||||||     |||||||
                                TACGGAA     AAAGAGA
                                    CAA___
GAM854  FLJ30681 3' AGAGAAGAAAGACCACTGG   91782      CCT  AGAAC
                                CCAGTG  TC    TTTCTCT
                                ||||||  ||    |||||||
                                GGTCAC  AG    GAAGAGA
                                   C__  AAA__
GAM854  HDAC11   3' GAGCTATAGGCACTGG     45717        TC  AACTTT
                                CCAGTGCCT  AG     CTC
                                |||||||||  ||     |||
                                GGTCACGGA  TC     GAG
                                     TA  _______
GAM854  IKKE     5' AGTGAGCCCTGAAAGCTCTGG  25745     T  C    AA   T
                                CCAG GC TTCAG  CTT CT
                                |||| || |||||  ||| ||
                                GGTC CG AAGTC  GAG GA
                                  T  A    CC   T
GAM854  KIAA0680 3' AGAGAAAATTGAAGCAT    28232     C    AAC
                                GTGC TTCAG   TTTCTCT
                                |||| |||||   |||||||
                                TACG AAGTT   AAAGAGA
                                  _    A__
GAM854  KIAA1228 3' AGGGGGTGATTCTGAGGCACTG 65035       T   ___   TT
                                CAGTGCCT CAGA   ACT  CT
                                |||||||| ||||   |||  ||
                                GTCACGGA GTCT   TGG  GA
                                    _   TAG   GG
GAM854  KIAA1300 5' AGGAACCCTGAAGGCA     62860        AAC
                                TGCCTTCAG   TTTCT
                                |||||||||   |||||
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                                ACGGAAGTC  AAGGA
                                     CC_
GAM854  KIAA1805  3'  AAGAGAAAGTAGAAGCAGCA  79966    __   AGA
                                TGC  CTTC  ACTTTCTCTT
                                |||  ||||  ||||||||||
                                ACG  GAAG  TGAAAGAGAA
                                  AC   A__
GAM854  LENG1    5'  AAGAGAAAGCTCTGGGCATCCT 84074    __   TT   A
          G                      CAG  TGCC  CAGA CTTTCTCTT
                                |||  ||||  |||| |||||||||
                                GTC  ACGG  GTCT GAAAGAGAA
                                  CT   __   C
GAM854  LHX6     3'  AAGAGAAAACTCTGGGGTCA  26854    C     AC
                                TG CTTCAGA  TTTCTCTT
                                ||  |||||||  ||||||||
                                AC GGGGTCT  AAAGAGAA
                                  T      CA
GAM854  N4BP3    3'  AGCTCCAGAAGGCACTGG    66250          A_  A
                                CCAGTGCCTTC  GA CT
                                ||||||||||  ||  ||
                                GGTCACGGAAG  CT GA
                                       AC  C
GAM854  NASP     3'  AGAGGGTGAAGAAACTG    67966     GC   AGA
                                CAGT  CTTC  ACTTTCT
                                ||||  ||||  |||||||
                                GTCA  GAAG  TGGGAGA
                                  AA  ____
GAM854  SMARCF1  3'  AAAATTCTGAAGGAC      57480    G      C
                                GT CCTTCAGAA TTT
                                ||  |||||||| |||
                                CA GGAAGTCTT AAA
                                  _       A
GAM854  SMARCF1  3'  AAAATTCTGAAGGAC      37430    G      C
                                GT CCTTCAGAA TTT
                                ||  |||||||| |||
                                CA GGAAGTCTT AAA
                                  _       A
GAM854  SMARCF1  3'  AAAATTCTGAAGGAC      20034    G      C
                                GT CCTTCAGAA TTT
                                ||  |||||||| |||
                                CA GGAAGTCTT AAA
                                  _       A
GAM854  TED      3'  AAGAGAAAGTCCAGGGACTGG  31630      G  TCA  A
                                CCAGT CCT   GA CTTTCTCTT
                                |||||  |||   ||  |||||||||
                                GGTCA GGA   CT GAAAGAGAA
                                   G  C__  _
GAM854  TGIF2    3'  AGAAGGGTGCTGAAGGC    41447        AA_
                                GCCTTCAG   CTTTCT
                                ||||||||   ||||||
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                                CGGAAGTC   GGAAGA
                                    GTG
GAM854  WBSCR20A  3'  AAGAGAAAGAAGAGACAGCA   35958     CT  AGAA
                                TGC  TC    CTTTCTCTT
                                |||  ||    |||||||||
                                ACG  AG    GAAAGAGAA
                                  AC  AGAA
GAM854  LOC115273 3'  AGAAAGTTCTGATGGCCAGG   73356     AGT   T
                                CC   GCC TCAGAACTTTCT
                                ||   ||| ||||||||||||
                                GG   CGG AGTCTTGAAAGA
                                 AC_   T
GAM854  LOC145761 5'  AAGAGAAAGTGGAAGGCATGG  83472      G      AGA
                                CCA TGCCTTC   ACTTTCTCTT
                                ||| |||||||   ||||||||||
                                GGT ACGGAAG   TGAAAGAGAA
                                  _     G__
GAM854  LOC146179 5'  AGAAAGTTTTGGGCCT      77700     T   TT
                                AG GCC  CAGAACTTTCT
                                || |||  ||||||||||||
                                TC CGG  GTTTTGAAAGA
                                 _  __
GAM854  LOC147072 3'  AAGAGAAAGTGAGAAGAAACTG 60407      GC    AGA
                                CAGT  CTTC   ACTTTCTCTT
                                ||||  ||||   ||||||||||
                                GTCA  GAAG   TGAAAGAGAA
                                  AA    AG_
GAM854  LOC148758 5'  AGAAAGTTCTGAGAAAC     78962     GCC
                                GT   TTCAGAACTTTCT
                                ||   ||||||||||||
                                CA   GAGTCTTGAAAGA
                                 AA_
GAM854  LOC148932 3'  AGGAATCTGAAGGCACTGG    79103             AC
                                CCAGTGCCTTCAGA  TTTCT
                                ||||||||||||||  |||||
                                GGTCACGGAAGTCT  AAGGA
                                          __
GAM854  LOC149386 5'  AAGTTTTGAAAGCACT      84400       C
                                AGTGC TTCAGAACTT
                                ||||| ||||||||||
                                TCACG AAGTTTTGAA
                                   A
GAM854  LOC150139 3'  AGAAAATAGAAAAAGGCGCTGG 79583          CAGAAC_
                                CCAGTGCCTT      TTTCT
                                ||||||||||      |||||
                                GGTCGCGGAA      AAAGA
                                      AAAGATA
GAM854  LOC152756 3'  AAGATGCAGTTCTGAAAACCTG 85871     TGCC        TTC
                                CAG    TTCAGAACT   TCTT
                                |||    |||||||||   ||||
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                                GTC   AAGTCTTGA  AGAA
                                  CAA_       CGT
GAM854  LOC162333 5'  AAGAGAAAGCGATGACACTG  87114     CCT  GAA
                                CAGTG  TCA  CTTTCTCTT
                                |||||  |||  |||||||||
                                GTCAC  AGT  GAAAGAGAA
                                   ___  AGC
GAM854  LOC199221 3'  AAGAGAAGCTCGAAAGCATGG  80347    G  C  A A  T
                                CCA TGC TTC GA CTT CTCTT
                                ||| ||| ||| || ||| |||||
                                GGT ACG AAG CT GAA GAGAA
                                  _  A  _ C  _
GAM854  LOC203339 3'  AGAGAAAATTGGGCCTG    90542    T  TCAGAAC
                                CAG GCCT     TTTCTCT
                                ||| ||||     |||||||
                                GTC CGGG     AAAGAGA
                                  _   TTA____
GAM854  LOC255017 3'  AGAAAGAGGAACTGG      94624     G  TCAGAA
                                CCAGT CCT    CTTTCT
                                ||||| |||    ||||||
                                GGTCA GGA    GAAAGA
                                   A  _______
GAM854  LOC256021 3'  AAGAGAAACAAAGACAACACTG 96512      CCT  AGAAC
          G                      CCAGTG  TC   TTTCTCTT
                                ||||||  ||   ||||||||
                                GGTCAC  AG   AAAGAGAA
                                   AAC  AAAC_
GAM854  LOC90139  3'  AGAATCCCGAAGGCAT    55396       A_  ACT
                                GTGCCTTC  GA  TTCT
                                ||||||||  ||  ||||
                                TACGGAAG  CT  AAGA
                                    CC  ___
GAM855  AQP3    3'  TTCACGATCCACCCTTTC    59593     T_  _
                                GAAA  GTGG TCGTGAA
                                ||||  |||| |||||||
                                CTTT  CACC AGCACTT
                                  CC   T
GAM855  ARSB    3'  TCACGACTCTTGTC       3502       AATGTG
                                GACAAGA    GTCGTGA
                                |||||||    |||||||
                                CTGTTCT    CAGCACT
                                          _______
GAM855  B4GALT5  3'  TTTTCACAAAAATAGTCCTTTG 16519      AAA_  GGTC
          TCA                    TGACAAG   TGT   GTGAAAA
                                |||||||   |||   |||||||
                                ACTGTTT   ATA   CACTTTT
                                   CCTG   AAAA
GAM855  CHRNA3   3'  TCGTTACCCATTTCTT     5610        T  CG
                                AAGAAATG GGT  TGA
                                |||||||| |||  |||
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                                TTCTTTAC CCA  GCT
                                     _  TT
GAM855  DRD1     3'  TTACAACCACATTTCTGGCCA  5840     ACA         C
                                TG   AGAAATGTGGT GTGA
                                ||   |||||||||||| ||||
                                AC   TCTTTACACCA CATT
                                 CGG          A
GAM855  FUT1     3'  TCTGATCACATCCCCTGTC   3798      AGAA        T
                                GACA   ATGTGGTCG GA
                                ||||   ||||||||| ||
                                CTGT   TACACTAGT CT
                                  CCCC        _
GAM855  IRF1     3'  GCCACATTTCTGATCA     64345     CA
                                TGA  AGAAATGTGGT
                                |||  ||||||||||
                                ACT  TCTTTACACCG
                                  AG
GAM855  MAP3K8   5'  TCACGACCACCTCATG      17791    A  AAT
                                CA GA   GTGGTCGTGA
                                || ||   ||||||||||
                                GT CT   CACCAGCACT
                                 A  C__
GAM855  NGFR     3'  TTCTGACCACACTTCCTGTC   10231      A   A       T
                                GACA GAA TGTGGTCG GAA
                                |||| ||| |||||||| |||
                                CTGT CTT ACACCAGT CTT
                                  C   C       _
GAM855  OLR1     3'  TTCACAACAGTTCTTGTTA    10341          ATGTG  C
                                TGACAAGAA     GT GTGAA
                                |||||||||     || |||||
                                ATTGTTCTT     CA CACTT
                                     GA___  A
GAM855  POU4F1   3'  CACTGAAAACATTTTTGTCA   20660          A   GG  _
                                TGACAAGAA TGT  TC GTG
                                ||||||||| |||  || |||
                                ACTGTTTTT ACA  AG CAC
                                     _  AA  T
GAM855  SMP1     3'  TTTCACATGAATAATTTTTGTC 26705          A   GGTC
           A                     TGACAAGAA TGT    GTGAAA
                                |||||||| |||    ||||||
                                ACTGTTTTT ATA    CACTTT
                                     A   AGTA
GAM855  ZNF264   3'  TTCTATTAACATTTCTTTTCA  12769     C        GGTCGT
                                TGA AAGAAATGT      GAA
                                ||| |||||||||      |||
                                ACT TTCTTTACA      CTT
                                  T        ATTAT_
GAM855  C20orf175 3'  CGAGCTCCACGTTTCCTGCCA  55063    A  A        ___
                                TG CA GAAATGTGG   TCG
                                || || |||||||||   |||
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                                AC GT CTTTGCACC   AGC
                                 C  C        TCG
GAM855  CAPNS2   3'  TTTCACAACCCTACATATTTCT 50323     CA      ____  C
            GATCA                   TGA  AGAAATGT    GGT GTGAAA
                                ||| ||||||||   ||| ||||||
                                ACT  TCTTTATA    CCA CACTTT
                                  AG       CATC   A
GAM855  CLDN6    3'  TTTACACTCACATTTTTATCA  41041     CA       _  C
                                TGA  AGAAATGTG GT GTGAA
                                |||  ||||||||| || |||||
                                ACT  TTTTTACAC CA CATTT
                                  A_       T  _
GAM855  DKFZP564L0864 3'  GCACCAATTTCTTGCCA     72555    A      G   C
                                TG CAAGAAAT TGGT GT
                                || |||||||| |||| ||
                                AC GTTCTTTA ACCA CG
                                 C      _   _
GAM855  DKFZP566B183 3'  TTTCCATAAACATTTCTTTTCA 31330     C       GGTCGT
                                TGA AAGAAATGT     GAAA
                                ||| |||||||||     ||||
                                ACT TTCTTTACA     CTTT
                                  T       AATAC_
GAM855  GTF2E1   3'  TACAGACCTCTTGTCA      18616        AATGT   _
                                TGACAAGA    GGTC GTG
                                ||||||||    |||| |||
                                ACTGTTCT    CCAG CAT
                                     _____   A
GAM855  KIAA0089  3'  TTTTAATTCACATTTCTT    69967          TCG
                                AAGAAATGTGG   TGAAA
                                ||||||||||   |||||
                                TTCTTTACACT   ATTTT
                                      TA_
GAM855  KIAA0373  5'  TTTTCAAAGTAACATTTCTT   28015         GGTCG
                                AAGAAATGT    TGAAAA
                                |||||||||    ||||||
                                TTCTTTACA    ACTTTT
                                     ATGAA
GAM855  KIAA1813  3'  TTTTCACACTGTAAATTTCTTG 70314         __ TG  C
            T                    ACAAGAAAT  G  GT GTGAAAA
                                |||||||||  |  || |||||||
                                TGTTCTTTA  T  CA CACTTTT
                                     AA GT  _
GAM855  KIAA1951  3'  TTCCAGGCTTCTCTTGTCA   73766        AATGT   GT
                                TGACAAGA    GGTC  GAA
                                ||||||||    ||||  |||
                                ACTGTTCT    TCGG  CTT
                                     CT___    AC
GAM855  MGC4170   3'  TTCACCATTTCTTGTC      44227          TGGTC
                                GACAAGAAATG    GTGAA
                                ||||||||||     |||||
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                                CTGTTCTTTAC    CACTT
                                      _____
GAM855  NRN1     3'  CACTGCACATTTCTCCTCA   33432    CA       GTC
                                TGA  AGAAATGTG   GTG
                                |||  |||||||||   |||
                                ACT  TCTTTACAC   CAC
                                  CC        GT_
GAM855  PLA2G12  3'  TTTTCACAACCACATTT    48028         C
                                AAATGTGGT GTGAAAA
                                ||||||||| |||||||
                                TTTACACCA CACTTTT
                                      A
GAM855  PPY2     3'  CACTCCACATTCCTGGCCA   40819    ACA  A      TC
                                TG   AG AATGTGG  GTG
                                ||   || |||||||  |||
                                AC   TC TTACACC  CAC
                                 CGG  C      T_
GAM855  ZNF31    3'  TTTGTAGACCACATTTCCTGTT 64992       A         _ TG
              A                  TGACA GAAATGTGGTC G  AA
                                |||||| |||||||||||  |  ||
                                ATTGT CTTTACACCAG T  TT
                                   C          A GT
GAM855  LOC115219 3'  CACGACAACGGGTCCTCA    73295     CAA  AA   G
                                TGA   GA  TGT GTCGTG
                                |||   ||  ||| ||||||
                                ACT   CT  GCA CAGCAC
                                  C__  GG   A
GAM855  LOC120376 5'  TTCAGAGCATTTCTTTCA    75986     C       GG  G
                                TGA AAGAAATGT  TC TGAA
                                ||| |||||||||  || ||||
                                ACT TTCTTTACG  AG ACTT
                                  _        __ _
GAM855  LOC133418 3'  TTTCATATACATTTTTTGCCA  75094    A         GTC
                                TG CAAGAAATGTG   GTGAAA
                                || ||||||||||   ||||||
                                AC GTTTTTTACAT   TACTTT
                                 C          A__
GAM855  LOC151199 3'  TTAAAACCACAGCTCTTGCCA  80174    A    AA     CG
                                TG CAAGA  TGTGGT  TGA
                                || |||||  ||||||  |||
                                AC GTTCT  ACACCA  ATT
                                 C    CG      AA
GAM855  LOC152317 5'  TCACACTGACTTTTGTCA    85649        AATG   C
                                TGACAAGA    TGGT GTGA
                                ||||||||    |||| ||||
                                ACTGTTTT    GTCA CACT
                                     CA__    _
GAM855  LOC152674 3'  TTCAACCCACCCTCTTGTCA   85841        AAT    TCG
                                TGACAAGA   GTGG   TGAA
                                ||||||||   ||||   ||||
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                                ACTGTTCT  CACC  ACTT
                                    CC_   CA_
GAM855  LOC152845 5'  CATGACCACATTTTTCA    60330    CAA
                                TGA  GAAATGTGGTCGTG
                                |||  |||||||||||||
                                ACT  TTTTACACCAGTAC
                                  ____
GAM855  LOC154743 3'  TTTAGTCCACATTGTCTTGTCA 81118       _     TCG
                                TGACAAGA AATGTGG  TGAA
                                |||||||| |||||||  ||||
                                ACTGTTCT TTACACC  ATTT
                                    G     TG_
GAM855  LOC165476 5'  TTCACGGCACCTTCT     87201     AT  G
                                AGAA  GTG TCGTGAA
                                ||||  ||| |||||||
                                TCTT  CAC GGCACTT
                                  C_  _
GAM855  LOC254266 5'  TTTTCGGTCACACATCTTATCA 97356    C   AA   GT  T
                                TGA AAGA  TGTG  CG GAA
                                ||| ||||  ||||  || |||
                                ACT TTCT  ACAC  GC TTT
                                  A   AC   TG  T
GAM855  LOC255919 3'  TTTCATTCTTACATTTCTAATC 95043    CA       TC
          A                      TGA  AGAAATGTGG  GTGAAA
                                |||  ||||||||||  ||||||
                                ACT  TCTTTACATT  TACTTT
                                  AA        CT
GAM855  LOC51754  5'  CACGGCCACATCTCTGTCA   71027     A  A
                                TGACA GA ATGTGGTCGTG
                                ||||| || ||||||||||
                                ACTGT CT TACACCGGCAC
                                   _ C
GAM855  LOC55862  3'  ACCTCATTTCTTGCCA     37485    A       T
                                TG CAAGAAATG GGT
                                || |||||||| |||
                                AC GTTCTTTAC CCA
                                 C        T
GAM855  LOC55954  3'  CACGTGGTCACTTTTCTCATCA 38877    CA    T  GT __
                                TGA  AGAAA GTG  C  GTG
                                |||  ||||| |||  |  |||
                                ACT  TCTTT CAC  G  CAC
                                  AC    T   TG TG
GAM856  ABCD2    5'  ACTTCTGTGGGTTTCT     17698        _
                                AGGAACTTA AGAAGT
                                |||||||| ||||||
                                TCTTTGGGT TCTTCA
                                     G
GAM856  ABCE1    3'  TCTAAATTTCTTGAGTTCCT   59521            A
                                AGGAACTTAAGAAGT TGGA
                                |||||||||||||| ||||
```

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                                TCCTTGAGTTCTTTA ATCT
                                          A
GAM856  AKAP2    3'  CTCTGTGCTCTTGAGTTTTT  23259          A
                                AGGAACTTAAGA GTATGGAG
                                |||||||||||| ||||||||
                                TTTTTGAGTTCT CGTGTCTC
                                          _
GAM856  ARF3     3'  TAATTTTATGCTTTCCCTGATT 8007       C   A__
            CC                    GGAA TTA   GAAGTATGGAGTTA
                                |||| |||   ||||||||||||||
                                CCTT AGT   TTTCGTATTTTAAT
                                  _  CCC
GAM856  ARHA     3'  TAATTCAAGGAATTTCTTAACT 70698      C        ATG__
            TCTT                    GGAA TTAAGAAGT     GAGTTA
                                |||| |||||||||     ||||||
                                TCTT AATTCTTTA     CTTAAT
                                  C        AGGAA
GAM856  ATP1B3   3'  TGAAAAATATTATCTTGGGTTC 8059            _     GGAGTTA
            TT                    AGGAACTTAAGA AGTAT
                                |||||||||||| |||||
                                TTCTTGGGTTCT TTATA
                                       A     AAAAGT
GAM856  AVPR1A   3'  AGCTTTATATTTTGTTGTT    5533      TTAA
                                AAC    GAAGTATGGAGTT
                                |||    ||||||||||||
                                TTG    TTTTATATTTCGA
                                  TTG_
GAM856  BAZ2A    3'  TAGCTTTGAATCTTAAGCTTCT 25610      A      AGTA GG
                                AGGA CTTAAGA    T  AGTTA
                                |||| |||||||    |  |||||
                                TCTT GAATTCT    G  TCGAT
                                  C      AA__ TT
GAM856  BAZ2A    3'  TGTTCCTGCTTTGTGTTCCT   25614       TTAA     T    TT
                                AGGAAC    GAAGTA GGAG  A
                                ||||||    |||||| ||||  |
                                TCCTTG    TTTCGT CCTT  T
                                   TG__      _    GG
GAM856  BCL11A   3'  TGATTTTGTACTTCTGTACCTG 35868   _ TTA___      TG
            TTTCCT                  A C     AGAAGTA  GAGTTA
                                | |     |||||||  ||||||
                                T G     TCTTCAT  TTTAGT
                                 T TCCATG      GT
GAM856  BCL11A   3'  TGATTTTGTACTTCTGTACCTG 56725   _ TTA___      TG
            TTTCCT                  A C     AGAAGTA  GAGTTA
                                | |     |||||||  ||||||
                                T G     TCTTCAT  TTTAGT
                                 T TCCATG      GT
GAM856  BCL6     5'  TGATTCTTAGAACTGGGGTTCT 8127         TA  AAGTAT
            T                    AGGAACT  AG     GGAGTTA
                                |||||||  ||     |||||||
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                                TTCTTGG  TC     TCTTAGT
                                    GG  AAGAT_
GAM856  BCRP2    3'  GTTCCCATTAGTCTTAAGTCTT 62406      A      AGT    AGTTA
                                AGGA CTTAAGA   ATGG
                                |||| |||||||   ||||
                                TTCT GAATTCT   TACC
                                  _      GAT    CTTGG
GAM856  BSN      3'  GGCTTCAAGCTAAGTTTCT    12926        AAGA   A
                                AGGAACTT    AGT TGGAGTT
                                ||||||||    ||| |||||||
                                TCTTTGAA    TCG ACTTCGG
                                    _____  A
GAM856  CD164    3'  TGAGCCATTAATTTTTGGGTTT 20051           GT_    AGTTA
           TT                     AGGAACTTAAGAA   ATGG
                                |||||||||||||   ||||
                                TTTTTGGGTTTTT   TACC
                                       AAT    GAGT
GAM856  CDC27    3'  TGACCTTCATTTCTAGGTTCTT 6992          A    AT  A
                                AGGAACTTA GAAGT  GG GTTA
                                ||||||||| |||||  || ||||
                                TTCTTGGAT CTTTA  TC CAGT
                                     _    CT  _
GAM856  CFL1     3'  TGACTCTGTGCTTGTCTGTTT  18575      TTAAG
                                GAAC    AAGTATGGAGTTA
                                ||||    ||||||||||||
                                TTTG    TTCGTGTCTCAGT
                                  TCTG_
GAM856  CHAC     3'  TAGCTTTGTATTGCATAGTTT  30830       TAAGA    TG
                                GAACT    AGTA  GAGTTA
                                |||||    ||||  ||||||
                                TTTGA    TTAT  TTCGAT
                                   TACG_   GT
GAM856  CKTSF1B1 3'  TGACTTTGTGTTTTTGTGCCCT 25372      ACTTA_     TG
           CCT                    AGGA     AGAAGTA  GAGTTA
                                ||||     |||||||  ||||||
                                TCCT     TTTTTGT  TTCAGT
                                  CCCGTG      GT
GAM856  CLECSF12 3'  TAATTTTGTATTTTTTTAGT   76697     T      TG
                                ACT AAGAAGTA  GAGTTA
                                ||| ||||||||  ||||||
                                TGA TTTTTTAT  TTTAAT
                                  T       GT
GAM856  CLN2     3'  TAACTTTGTGTTCCCAGGTCCT 4615      A   AA   G  TG
                                AGGA CTT  GAA TA  GAGTTA
                                |||| |||  ||| ||  ||||||
                                TCCT GGA  CTT GT  TTCAAT
                                  _  CC   _  GT
GAM856  CNTN3    3'  CAGGCTTTTTAGTTCCT     66693        T      A
                                AGGAACT AAGAAGT TG
                                ||||||| ||||||| ||
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                                TCCTTGA TTTTTCG AC
                                   _     G
GAM856  COL3A1   3'  AACTCCATATGTGTTCCT    3614       TTAAGAA
                                AGGAAC     GTATGGAGTT
                                ||||||     ||||||||||
                                TCCTTG     TATACCTCAA
                                   TG_____
GAM856  CRAT     3'  TGGTTCCACTCAGCTTGGTTCC 5662        T  AAGTA    TT
           T                     AGGAACT AAG    TGGAG  A
                                ||||||| |||    ||||| |
                                TCCTTGG TTC    ACCTT  T
                                   _  GACTC    GG
GAM856  CRAT     3'  TGGTTCCACTCAGCTTGGTTCC 14355       T  AAGTA    TT
           T                     AGGAACT AAG    TGGAG  A
                                ||||||| |||    ||||| |
                                TCCTTGG TTC    ACCTT  T
                                   _  GACTC    GG
GAM856  CSNK1A1  3'  ACTCTATAATGTTCTT     8547       TTAAGAAG
                                AGGAAC      TATGGAGT
                                ||||||      ||||||||
                                TTCTTG      ATATCTCA
                                   TA_______
GAM856  CUL3     3'  GGCATCATCTTAGGTTTCT   13164          AGTA  GA
                                AGGAACTTAAGA   TG  GTT
                                ||||||||||||   ||  |||
                                TCTTTGGATTCT   AC  CGG
                                      _____ TA
GAM856  DCK      3'  TAACTTCATATTAATATAAGTT 5794         AGA_
           TCT                    AGGAACTTA   AGTATGGAGTTA
                                |||||||||   ||||||||||||
                                TCTTTGAAT   TTATACTTCAAT
                                     ATAA
GAM856  DDX11    3'  GGCTTCGTGCCAGTTCCT    15301       TAAGAA
                                AGGAACT     GTATGGAGTT
                                |||||||     ||||||||||
                                TCCTTGA     CGTGCTTCGG
                                   C______
GAM856  DDX11    3'  GGCTTCGTGCCAGTTCCT    47659       TAAGAA
                                AGGAACT     GTATGGAGTT
                                |||||||     ||||||||||
                                TCCTTGA     CGTGCTTCGG
                                   C______
GAM856  DRD5     3'  TGGCTTTGTGCTTATGTCATTT 5849       CTTAAG    TG
           CT                     AGGAA     AAGTA  GAGTTA
                                |||||     |||||  ||||||
                                TCTTT     TTCGT  TTCGGT
                                   ACTGTA    GT
GAM856  DSG2     3'  TAATTTCATGTTTCCAATGTAC 8686      A  TTAA
           CT                     AGG AC    GAAGTATGGAGTTA
                                ||| ||    ||||||||||||||
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                                TCC TG    CTTTGTACTTTAAT
                                  A  TAAC
GAM856  EBAF     3'  TAACTTTATACTTAGCAAGTTA 65426    G    AAG
              CT                  AG AACTT   AAGTATGGAGTTA
                                || |||||   ||||||||||||||
                                TC TTGAA   TTCATATTTCAAT
                                  A    CGA
GAM856  ECH1     3'  TAACTTTATGACAATGAGTTTC 59877         AGAAG
              T                   AGGAACTTA    TATGGAGTTA
                                |||||||||    ||||||||||
                                TCTTTGAGT    GTATTTCAAT
                                     AACA_
GAM856  EFNA1    3'  TGATTTCTACAACTGGAGTTTT 15392        A  AA   T
              T                   AGGAACTT AG  GTA GGAGTTA
                                |||||||| ||  ||| |||||||
                                TTTTTGAG TC  CAT CTTTAGT
                                     G  AA  _
GAM856  ELOVL4   3'  ATATTTCTTAAGTATCT     42683     A
                                AGG ACTTAAGAAGTAT
                                ||| ||||||||||||
                                TCT TGAATTCTTTATA
                                  A
GAM856  EN2      3'  TGACTATAAAATATTTTTTTGA 7470          _  GG___
              GTTTTT                ACTTAAGAAG TAT    AGTTA
                                |||||||||| |||    |||||
                                TGAGTTTTTT ATA    TCAGT
                                      T   AAATA
GAM856  ETS2     3'  TAATCCCTGCTTTTTGTGTTTT 17879       T       T   GTTA
              T                   AGGAAC TAAGAAGTA GGA
                                |||||| ||||||||| |||
                                TTTTTG GTTTTTCGT CCT
                                   T       C   AAT
GAM856  FACL4    3'  AATTCCATGAATGTTCCT    15503       TTAAGAAG
                                AGGAAC       TATGGAGTT
                                ||||||       |||||||||
                                TCCTTG       GTACCTTAA
                                   TAA_____
GAM856  FACL4    3'  AATTCCATGAATGTTCCT    43393       TTAAGAAG
                                AGGAAC       TATGGAGTT
                                ||||||       |||||||||
                                TCCTTG       GTACCTTAA
                                   TAA_____
GAM856  FCMD     3'  TAGTTCCATGTTTCTTTTCT   22097     CTT         GT
                                GGAA   AAGAAGTATGGA  TA
                                ||||   ||||||||||||  ||
                                TCTT   TTCTTTGTACCT  AT
                                  ___          TG
GAM856  FZD4     3'  TGATTTCTGAGTTTTGAGTTCT 24154          AG  T
                                GGAACTTAAGA  TA GGAGTTA
                                ||||||||||  || |||||||
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                                TCTTGAGTTTT  GT CTTTAGT
                                      GA  _
GAM856  GAS41    3'  ATTTCTTCAAGTTCTT      21519         _
                                AGGAACTT AAGAAGT
                                |||||||| |||||||
                                TTCTTGAA TTCTTTA
                                    C
GAM856  GJA1     3'  TAACTGGTATTCTTGGGTTTT  3904            G   GG
                                GGAACTTAAGAA TAT  AGTTA
                                |||||||||||| |||  |||||
                                TTTTGGGTTCTT ATG  TCAAT
                                      _  G_
GAM856  HFE      3'  TAGGTTTCTGAGTTCCT     4656          A    TA
                                AGGAACTTA GAAG  TG
                                ||||||||| ||||  ||
                                TCCTTGAGT CTTT  AT
                                    _   GG
GAM856  HFE      3'  TAGGTTTCTGAGTTCCT     57323         A    TA
                                AGGAACTTA GAAG  TG
                                ||||||||| ||||  ||
                                TCCTTGAGT CTTT  AT
                                    _   GG
GAM856  HLCS     3'  TAATTCCAGAAACTTGTGGTTT 4676         _   AAGTA
          TT                     AGGAACT TAAG    TGGAGTTA
                                ||||||| ||||    ||||||||
                                TTTTTGG GTTC    ACCTTAAT
                                    T   AAAG_
GAM856  IRS1     3'  TAATTTTGTATTTTTTCCT   18666      CTTAA     TG
                                AGGAA    GAAGTA  GAGTTA
                                |||||    ||||||  ||||||
                                TCCTT    TTTTAT  TTTAAT
                                  _____     GT
GAM856  MAOB     3'  TGGCTTTGTGCTTGTTCTTCCT 60000      CTT  G    TG
                                AGGAA   AA AAGTA  GAGTTA
                                |||||   || |||||  ||||||
                                TCCTT   TT TTCGT  TTCGGT
                                  C__  G    GT
GAM856  MMP8     3'  TGACTTCATACATCCCTCAGTT 10065       TAA_  A
          TCT                    AGGAACT   GA GTATGGAGTTA
                                |||||||   || ||||||||||
                                TCTTTGA   CT CATACTTCAGT
                                    CTCC  A
GAM856  MSN      3'  TGTACTTTTTGGGTTTTT    60256
                                AGGAACTTAAGAAGTATG
                                ||||||||||||||||||
                                TTTTTGGGTTTTTCATGT

GAM856  MSN      3'  TTTTGTGTACTTTTTGGGTTTT 60257              G  TTA
          T                     AGGAACTTAAGAAGTATG AG
                                |||||||||||||||||| ||
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                                TTTTTGGGTTTTTCATGT TT
                                      G  TT
GAM856  MSR1    3'  ACTTCTATAGGTTTTT      56950          _
                    AGGAACTTA AGAAGT
                    ||||||||| ||||||
                    TTTTTGGAT TCTTCA
                          A
GAM856  MSR1    3'  ACTTCTATAGGTTTTT      56958          _
                    AGGAACTTA AGAAGT
                    ||||||||| ||||||
                    TTTTTGGAT TCTTCA
                          A
GAM856  MSX2    3'  CATATTTTTAAAGTTTTT    65571          A
                    AGGAACTT AGAAGTATG
                    |||||||| |||||||||
                    TTTTTGAA TTTTTATAC
                          A
GAM856  NAPB    3'  TTCTGCAGCTTGAGTCCT    70194      A     AA   T
                    AGGA CTTAAG  GTA GGA
                    |||| ||||||  ||| |||
                    TCCT GAGTTC  CGT CTT
                      _     GA  _
GAM856  NELL1   3'  GGTTGATGTATTTTTTGGGTTT 20476              GAGTTA
                    GAACTTAAGAAGTATG
                    ||||||||||||||||
                    TTTGGGTTTTTTATGT
                               AGTTGGT
GAM856  NLGN1    3'  TTATAGTTCTGAGTTCTT    30028          A   G
                    AGGAACTTA GAA TATGG
                    ||||||||| ||| |||||
                    TTCTTGAGT CTT ATATT
                          _  G
GAM856  NORE1    3'  GATTCCTCTTTGAGTTCT    48718          AAGTAT
                    GGAACTTAAG     GGAGTT
                    ||||||||||     ||||||
                    TCTTGAGTTT     CCTTAG
                          CT____
GAM856  NR2E3    3'  TTCCATGGAGTTCT        32974        AAGAAG
                    GGAACTT     TATGGAG
                    |||||||     |||||||
                    TCTTGAG     GTACCTT
                               _______
GAM856  P4HA1    3'  GCTTACTTTGTGGGTTCTT   6218          A     TGG
                    AGGAACTTA GAAGTA   AGT
                    ||||||||| ||||||   |||
                    TTCTTGGGT TTTCAT   TCG
                          G     ___
GAM856  PAX2     3'  TAATTCCGTGTTTTCGCTTTTT 14327      CTTAA_
              CC                  GGAA     GAAGTATGGAGTTA
                    ||||     ||||||||||||||
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                              CCTT     TTTTGTGCCTTAAT
                                TTTCGC
GAM856  PAX2     3'  TAATTCCGTGTTTTCGCTTTTT 14336      CTTAA_
            CC                   GGAA     GAAGTATGGAGTTA
                              ||||     ||||||||||||||
                              CCTT     TTTTGTGCCTTAAT
                                TTTCGC
GAM856  PCDHB16  3'  ATACTTTTCTTAAAGTTTCT  40549        _   __
                              AGGAACTT AAGA  AGTAT
                              |||||||| ||||  |||||
                              TCTTTGAA TTCT  TCATA
                                   A   TT
GAM856  PGAM1    3'  CCCTTCTGGGGTTTCT      76274        TA    TAT
                              AGGAACT  AGAAG   GG
                              |||||||  |||||   ||
                              TCTTTGG  TCTTC   CC
                                   GG    ___
GAM856  PIR51    3'  TAGTCACTTTTTGTTAAGTTCT 21365          G   TATG  GTTA
            T                   AGGAACTTAA AAG    GA
                              ||||||||||| |||    ||
                              TTCTTGAATT TTT    CT
                                    G   TTCA  GAT
GAM856  PPP1R2   3'  TTTTCTTGTTTCTGAGTTCTT  20699         A    TAT    TTA
                              AGGAACTTA GAAG   GGAG
                              |||||||| ||||   ||||
                              TTCTTGAGT CTTT   TCTT
                                   _   GT_   TTG
GAM856  RAI14    3'  AATTCCATGTTTTCTTCC    31477      CTTAA
                              GGAA    GAAGTATGGAGTT
                              ||||    ||||||||||||
                              CCTT    TTTTGTACCTTAA
                                C____
GAM856  RGR      3'  TGACTTTCTGTTTTTGAGTT   11324          G  TG
                              AACTTAAGAA TA  GAGTTA
                              |||||||||| ||  ||||||
                              TTGAGTTTTT GT  TTCAGT
                                    _ CT
GAM856  RNASE1   5'  TGGTTTCTGGCTCATAAGTTCC 11351          A  A  AT    TT
            T                   AGGAACTTA GA GT  GGAG  A
                              ||||||||| || ||  ||||  |
                              TCCTTGAAT CT CG  CTTT  T
                                   A  _  GT    GG
GAM856  RNTRE    3'  TGATTTCATGCTTTTGAACATC 28040      ACTTA
            TT                   AGGA    AGAAGTATGGAGTTA
                              ||||    ||||||||||||||||
                              TTCT    TTTTCGTACTTTAGT
                                ACAAG
GAM856  RPE      3'  GCTTGCTTGGGTTTCT      62185          _
                              AGGAACTTAAG AAGT
                              |||||||||| ||||
```

```
                                TCTTTGGGTTC TTCG
                                      G
GAM856  RSU1     3'  TGATTTTAATAAAATCTTGAGT 24854          AG_  _
            TT                   GAACTTAAGA   TAT GGAGTTA
                                 ||||||||||   ||| |||||||
                                 TTTGAGTTCT   ATA TTTTAGT
                                      AAA   A
GAM856  SALL2    3'  TGATTTTGTCTTTTTCTCTAAG 63863       _    T__ TG
            TTCTT                 AACTTA AGAAG   A  GAGTTA
                                  |||||| |||||   |  ||||||
                                  TTGAAT TCTTT   T  TTTAGT
                                     C     TTC GT
GAM856  SAR1     3'  TAACTTGCATATTTTTAATTTC 39325       C      G   _
            CT                    AGGAA TTAAGAA TATG GAGTTA
                                  ||||| ||||||| |||| ||||||
                                  TCCTT AATTTTT ATAC TTCAAT
                                     T      _   G
GAM856  SCO1     3'  CCTCTTCTTGAGTTCTT     15947             TAT
                                 AGGAACTTAAGAAG   GG
                                 ||||||||||||||   ||
                                 TTCTTGAGTTCTTC   CC
                                        T__
GAM856  SET      3'  TAACTTCGTATTTTTTGA    11559
                                 TTAAGAAGTATGGAGTTA
                                 ||||||||||||||||||
                                 AGTTTTTTATGCTTCAAT

GAM856  SGNE1    3'  AGAGCTTTTTTGTTTCTTGGGT 11585             T_     A
            TTTT                   GGAACTTAAGAAGTA  GGAGTT
                                   ||||||||||||||  ||||||
                                   TTTTGGGTTCTTTGT  TTTCGA
                                          TT     GAA
GAM856  SORBS1   3'  TAATTTCATTATTTTGGGTTTT 31161           AGT
            T                     AGGAACTTAAGA   ATGGAGTTA
                                  ||||||||||||   |||||||||
                                  TTTTTGGGTTTT   TACTTTAAT
                                        AT_
GAM856  SORCS1   3'  TAACTTTGTGTTTTTTTTCTTT 53587      CTT_       TG
            CC                     GGAA    AAGAAGTA  GAGTTA
                                   ||||    ||||||||  ||||||
                                   CCTT    TTTTTTGT  TTCAAT
                                     TCTT       GT
GAM856  SPG3A    3'  ACTTTTTAGAGTTCCT      31912         _
                                 AGGAACTT AAGAAGT
                                 |||||||| |||||||
                                 TCCTTGAG TTTTTCA
                                      A
GAM856  TADA2L   3'  TGGCTTTGTACTTTGCAGTCT  7639      A  TAA     TG
                                 GGA CT   GAAGTA  GAGTTA
                                 ||| ||   ||||||  ||||||
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```
                                TCT GA   TTTCAT  TTCGGT
                                  _ CG_     GT
GAM856  TGFBR2   5'  TGGTTCTACTTGCTTGGGTCCT 12271      A     _    T  GTTA
                                AGGA CTTAAG AAGTA GGA
                                |||| |||||| ||||| |||
                                TCCT GGGTTC TTCAT CTT
                                  _     G    _  GGT
GAM856  TIAL1    3'  TAGTTCTGCCTTTTTAAGTTTT 12288           TAT  GT
           T                     AGGAACTTAAGAAG  GGA  TA
                                |||||||||||||  |||  ||
                                TTTTTGAATTTTTC   TCT  AT
                                       CG_  TG
GAM856  TIAL1    3'  TAGTTCTGCCTTTTTAAGTTTT 42261           TAT  GT
           T                     AGGAACTTAAGAAG  GGA  TA
                                |||||||||||||  |||  ||
                                TTTTTGAATTTTTC   TCT  AT
                                       CG_  TG
GAM856  TLX1     5'  TGACTTCACCCTCCTTGGGTTT 18633         A  TA
                                GAACTTAAG AG  TGGAGTTA
                                ||||||||| ||  ||||||||
                                TTTGGGTTC TC  ACTTCAGT
                                     C  CC
GAM856  TOP2A    3'  TAAAACCTGATTTTTAAGTTCT 6532           GTAT  AG
           T                     AGGAACTTAAGAA   GG  TTA
                                ||||||||||||   ||  |||
                                TTCTTGAATTTTT   CC  AAT
                                       AGT_  AA
GAM856  TRPM6    3'  TGATTCTTGTAAGTTTGAGTTC 34549         AAGTAT
           C                     GGAACTTAAG     GGAGTTA
                                ||||||||||     |||||||
                                CCTTGAGTTT     TCTTAGT
                                     GAATGT
GAM856  UBE2L3   3'  TAATTCTATAACTTGAGATCTT 12505      A     AAG
                                AGGA CTTAAG   TATGGAGTTA
                                |||| ||||||   ||||||||||
                                TTCT GAGTTC   ATATCTTAAT
                                  A     A__
GAM856  USP18    3'  TAATTCCATATGAATCAAGT   63618      AAGAA
                                ACTT    GTATGGAGTTA
                                ||||    ||||||||||
                                TGAA    TATACCTTAAT
                                  CTAAG
GAM856  VAMP8    3'  TGGCTGCATTTCTTGGGTCCT  13647      A      GT   G
                                AGGA CTTAAGAA  ATG AGTTA
                                |||| ||||||||  ||| |||||
                                TCCT GGGTTCTT  TAC TCGGT
                                  _       __  G
GAM856  YES1     3'  TTCCATTCCAGTTTTTTAAAGT 18360         A    TA     TA
           TTCT                    AGGAACTT AGAAG  TGGAGT
                                |||||||| |||||  ||||||
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                                TCTTTGAA TTTTT  ACCTTA
                                    A    TG    CCTTA
GAM856  YWHAE    3'  TGGTCCCAGCTTTTAGGTTCTT 22198          A  A   AG
                                AGGAACTTAAGA GT TGG  TTA
                                |||||||||||| || |||  |||
                                TTCTTGGATTTT CG ACC  GGT
                                      _ _  CT
GAM856  ZFX      3'  TGATTCTATACCGAAGTTTT   12719       AAGAA
                                GGAACTT    GTATGGAGTTA
                                |||||||    ||||||||||
                                TTTTGAA    CATATCTTAGT
                                   GC___
GAM856  ZNF131   3'  TACTTGTTGGGTTTTT     70160         G
                                AGGAACTTAA AAGTA
                                |||||||||| |||||
                                TTTTTGGGTT TTCAT
                                     G
GAM856  ZNF215   5'  TGGCTTTGTGTCTAAAGTTTCT 25119        A   AG  TG
                                AGGAACTT AGA  TA  GAGTTA
                                |||||||| |||  ||  ||||||
                                TCTTTGAA TCT  GT  TTCGGT
                                   A  __ GT
GAM856  ABLIM    3'  GCATGTGCTTTTTAATTTCT   9770      C         GA
                                GGAA TTAAGAAGTATG  GT
                                |||| ||||||||||||  ||
                                TCTT AATTTTTCGTGT  CG
                                  T         A_
GAM856  ABLIM    3'  GCATGTGCTTTTTAATTTCT   22031     C         GA
                                GGAA TTAAGAAGTATG  GT
                                |||| ||||||||||||  ||
                                TCTT AATTTTTCGTGT  CG
                                  T         A_
GAM856  AKT3     3'  TAATTTTTTTTTTTTAAATTCC 18434      C       TAT
           T                     AGGAA TTAAGAAG   GGAGTTA
                                |||||  ||||||||   |||||||
                                TCCTT AATTTTTT   TTTTAAT
                                   A       TT_
GAM856  AMOT     3'  ATCTTTTGGGGTTCCT      55717        TA    T
                                AGGAACT  AGAAG AT
                                |||||||  |||||  ||
                                TCCTTGG  TTTTC TA
                                   GG    _
GAM856  AMSH     3'  TGATTTTGTATTTCAGGTTT   21320       AA     TG
                                GAACTT  GAAGTA  GAGTTA
                                ||||||  ||||||  ||||||
                                TTTGGA  CTTTAT  TTTAGT
                                   __     GT
GAM856  AP1S2    3'  TGGCTCTATATTTTTTAAAGCT 14043    AAC
                                GG   TTAAGAAGTATGGAGTTA
                                ||   ||||||||||||||||||
```

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                                TC  AATTTTTTATATCTCGGT
                                 GA_
GAM856  ARL8    3'  GTATTTTTTAGGTTTT     93198
                                GGAACTTAAGAAGTAT
                                ||||||||||||||||
                                TTTTGGATTTTTTATG

GAM856  ATIP1   3'  TGATTTTGTGTCTTAAGTCTT  40396     A     AG  TG
                                AGGA CTTAAGA  TA  GAGTTA
                                |||| |||||||  ||  ||||||
                                TTCT GAATTCT  GT  TTTAGT
                                  _     __ GT
GAM856  ATP6V1G3 3'  TGGCTTCGTATTTTTATGTT  55821    TTA
                                AAC  AGAAGTATGGAGTTA
                                |||  ||||||||||||||||
                                TTG  TTTTTATGCTTCGGT
                                  TA_
GAM856  ATP6V1G3 3'  TGGCTTCGTATTTTTATGTT  55713    TTA
                                AAC  AGAAGTATGGAGTTA
                                |||  ||||||||||||||||
                                TTG  TTTTTATGCTTCGGT
                                  TA_
GAM856  BAF53A  3'  TGGCTCTATAAATTAAGTTT  65431       GAAG
                                GAACTTAA   TATGGAGTTA
                                ||||||||   ||||||||||
                                TTTGAATT   ATATCTCGGT
                                    AA__
GAM856  BM-002  3'  TGGTTTTGAACATTGTAAGTTC 33527        A  A  A GG  TT
          CT                    AGGAACTTA GA GT T  AG  A
                                ||||||||| || || |  ||  |
                                TCCTTGAAT TT CA G  TT  T
                                    G  A  A TT  GG
GAM856  BM046   3'  TGATTTTGTGTTTAAGTTCC  37460        AAG  TG
                                GGAACTTAAG  TA  GAGTTA
                                ||||||||||  ||  ||||||
                                CCTTGAATTT  GT  TTTAGT
                                    ___ GT
GAM856  BMF     3'  TGGCTTTATGTGTTTATGTTCT 53165      T   AAG
          T                     AGGAAC TAAG  TATGGAGTTA
                                |||||| ||||  ||||||||||
                                TTCTTG ATTT  GTATTTCGGT
                                   T   GT_
GAM856  BOP     3'  AACTGTATTTTGAGTTTCT   85047         AGTA  G
                                AGGAACTTAAGA   TG AGTT
                                ||||||||||||   || ||||
                                TCTTTGAGTTTT   AT TCAA
                                    _____ G
GAM856  BOP     5'  TCTAGTTTCTCAGGTTCCT   85053       A   GTA
                                AGGAACTT AGAA  TGGA
                                |||||||| ||||  ||||
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                                TCCTTGGA TCTT   ATCT
                                    C    TG_
GAM856  C20orf21  3'  ATGCCGTCTTAAGTTTTT    35109          A_
                                AGGAACTTAAGA  GTAT
                                ||||||||||||  ||||
                                TTTTTGAATTCT  CGTA
                                     GC
GAM856  C20orf30  3'  TGGCCAGATTTTTTTGGGTCCT 26253     A       TA_   AGTTA
                                AGGA CTTAAGAAG   TGG
                                |||| |||||||||   |||
                                TCCT GGGTTTTTT   ACC
                                  _       TAG   GGT
GAM856  C20orf32  5'  TAGCTCCATAGAATTCAGTTTC 39787       T  GAAG
           T                     AGGAACT AA    TATGGAGTTA
                                |||||||  ||    ||||||||||
                                TCTTTGA TT    ATACCTCGAT
                                    C  AAG_
GAM856  CEACAM7   3'  TGACTTCATGCTGTGGACAGTT 22562       TAAGA_
           TT                     GGAACT     AGTATGGAGTTA
                                |||||||     ||||||||||||
                                TTTTGA     TCGTACTTCAGT
                                   CAGGTG
GAM856  CGR19     3'  TAACTTCATATTTGTATGGTAC 21642     A   TAAG
           TT                     AGG ACT    AAGTATGGAGTTA
                                |||  |||    ||||||||||||
                                TTC TGG    TTTATACTTCAAT
                                  A   TATG
GAM856  CHCR      3'  ATATTTCTGTAGGTTTCT     37235         _
                                AGGAACTTA AGAAGTAT
                                |||||||||  ||||||||
                                TCTTTGGAT TCTTTATA
                                     G
GAM856  CLL-1     5'  TAACTCACTCATCTTTTTGTGT 56368      T      T  ___
           TTTT                     GAAC TAAGAAG ATG   GAGTTA
                                |||| |||||||  |||   ||||||
                                TTTG GTTTTTC TAC   CTCAAT
                                  T      _   TCA
GAM856  D2S448    3'  ATAGCTTCACGTTAGACTTCTC 73515    A     A_____
           AGGTTTTT                  TT AGAAGT     TGGAGTTA   T
                                ||  ||||||     ||||||||   |
                                GA TCTTCA     ACTTCGAT   A
                                 C     GATTGC
GAM856  D6S2654E  3'  TGATTTCGTGACCTTGATTTCT 24050       C     AAG
           T                     AGGAA TTAAG   TATGGAGTTA
                                |||||  |||||   ||||||||||
                                TTCTT AGTTC   GTGCTTTAGT
                                   T    CA_
GAM856  DDX12     3'  GGCTTCGTGCCAGTTCCT     59701         TAAGAA
                                AGGAACT     GTATGGAGTT
                                |||||||     ||||||||||
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                                TCCTTGA     CGTGCTTCGG
                                   C_____
GAM856  DDX35    3'  TTTGTTTGCTTGGGTTCTT   41642          AAGT TG
                                AGGAACTTAAG   A  GA
                                ||||||||||   |  ||
                                TTCTTGGGTTC   T  TT
                                      GTT_ GT
GAM856  DEGS     3'  TGACTCTGTACTGCTCAGTTTC 13415       TA  A
                                GGAACT  AG AGTATGGAGTTA
                                ||||||  || ||||||||||||
                                CTTTGA  TC TCATGTCTCAGT
                                   C_  G
GAM856  DJ473B4  3'  GACTTTTTTTTAAGTTTTT   38960           TATG
                                AGGAACTTAAGAAG   GAGTT
                                ||||||||||||||   |||||
                                TTTTTGAATTTTTT   TTCAG
                                                 _____
GAM856  DKFZP564D172 3'  TAACTGTTCTTTTCTCGAGTTT 49390        TA    TATGG
           CT                    AGGAACT  AGAAG    AGTTA
                                |||||||  |||||    |||||
                                TCTTTGA  TCTTT    TCAAT
                                   GC    TCTTG
GAM856  DKFZp761B1514 3'  TACACTGTACTTTTTGGTGTTT 50147       _          A  TA
           TT                    AGGAAC TTAAGAAGTATGG GT
                                |||||| ||||||||||||| ||
                                TTTTTG GGTTTTTCATGTC CA
                                   T          A  T
GAM856  DKFZp761B1514 3'  TCATGCTTCTTGAGTTGCT   50148    G
                                AG AACTTAAGAAGTATGG
                                || ||||||||||||||||
                                TC TTGAGTTCTTCGTACT
                                 G
GAM856  DKFZp761B1514 3'  TGTCTCTCATGCTTCTTGAGTT 50149    G          _  TTA
           GCT                    AG AACTTAAGAAGTATG GAG
                                || |||||||||||||| |||
                                TC TTGAGTTCTTCGTAC CTC
                                 G           T  TGT
GAM856  DUSP10   5'  ACTGTCTTGAGTTCTT      23279          _
                                AGGAACTTAAGA AGT
                                |||||||||||| |||
                                TTCTTGAGTTCT TCA
                                      G
GAM856  EIF2B3   3'  AACTCTGTATTTATTTCC    39802      CTTAAG
                                GGAA     AAGTATGGAGTT
                                ||||     ||||||||||||
                                CCTT     TTTATGTCTCAA
                                  TA____
GAM856  EPN2     3'  TGGCTCTATGCTTGTGTACCT  30332     A  TTAAG
                                AGG AC     AAGTATGGAGTTA
                                ||| ||     ||||||||||||
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                                TCC TG    TTCGTATCTCGGT
                                  A  TG___
GAM856  EREG     3'  AGTAAGTATGTTTTTTATGTTC 7490       T        GAGTTA
                CT                  AGGAAC TAAGAAGTATG
                                    |||||| ||||||||||
                                    TCCTTG ATTTTTTGTAT
                                       T         GAATGAT
GAM856  FIGN     3'  CATTTTTCTTAATTTCCT    95640      C       T
                                    AGGAA TTAAGAAG ATG
                                    ||||| |||||||| |||
                                    TCCTT AATTCTTT TAC
                                       T       T
GAM856  FLJ10154 3'  TAGCTTCATGTTGAAGTGGTTT 35855       TAAGA
                TT                  AGGAACT    AGTATGGAGTTA
                                    |||||||    ||||||||||||
                                    TTTTTGG    TTGTACTTCGAT
                                        TGAAG
GAM856  FLJ10156 3'  TAGCTCTGTACCCGGGTGCCT  38694    A   AAGAA
                                    AGG ACTT    GTATGGAGTTA
                                    ||| ||||    ||||||||||
                                    TCC TGGG    CATGTCTCGAT
                                      G   CC___
GAM856  FLJ10326 3'  TGACTCTGTATTTAAATTCT   36031     CTTAAG
                                    GGAA     AAGTATGGAGTTA
                                    ||||     ||||||||||||
                                    TCTT     TTTATGTCTCAGT
                                      AAA___
GAM856  FLJ10468 3'  TTCAAGTTGTATTCTTTTAAGT 36151          _   TG AGTTA
                TCTT                  GGAACTTAAGA AGTA  G
                                    |||||||||| |||| |
                                    TCTTGAATTTT TTAT  T
                                          C   GT GAACTTG
GAM856  FLJ10545 3'  TACAGTATACTGTCTTGGGTTT 36264          _    GA  TA
                TT                  AGGAACTTAAGA AGTATG  GT
                                    |||||||||||| ||||||  ||
                                    TTTTTGGGTTCT TCATAT  CA
                                          G     GA  T
GAM856  FLJ10876 3'  ATCTCTTTAAGTTCCT     36790          GA  T
                                    AGGAACTTAA  AG AT
                                    |||||||||  || ||
                                    TCCTTGAATT  TC TA
                                          TC  _
GAM856  FLJ11320 3'  ATCCTCTCGTATTTCTGAGTTT 37240        A      _  TTA
                TT                  AGGAACTTA GAAGTATG GAG
                                    ||||||||| |||||||| |||
                                    TTTTTGAGT CTTTATGC CTC
                                          _       T   CTAT
GAM856  FLJ11539 3'  GAAGGACATACTTTTCAGGTTC 45378        A       GAGTTA
                CT                  AGGAACTT AGAAGTATG
                                    |||||||| |||||||||
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                                TCCTTGGA TTTTCATAC
                                    C        AGGAAGT
GAM856  FLJ11703  3'  TGATTCTATATGTGCAGGTCCT 46385      A   AAGAA
                                AGGA CTT     GTATGGAGTTA
                                |||| |||     ||||||||||
                                TCCT GGA     TATATCTTAGT
                                  _  CGTG_
GAM856  FLJ12838  3'  TAGCTTTCGTTTTGAGTTCT   44970          AGTAT
                                GGAACTTAAGA     GGAGTTA
                                ||||||||||     |||||||
                                TCTTGAGTTTT     TTTCGAT
                                      GC___
GAM856  FLJ12903  3'  TAATTTCATATTTTTTAGT    42779     T
                                ACT AAGAAGTATGGAGTTA
                                ||| ||||||||||||||||
                                TGA TTTTTTATACTTTAAT
                                  _
GAM856  FLJ13072  5'  TGGCTTTTGTGCTTTGGGTTTC 89831         AA     TG  _
          T                      AGGAACTT  GAAGTA  GA GTTA
                                 ||||||||  ||||||  || ||||
                                 TCTTTGGG  TTTCGT  TT CGGT
                                     __     GT  T
GAM856  FLJ13611  3'  TACTTTTTAGGTTGTT      46296    G
                                AG AACTTAAGAAGTA
                                || ||||||||||||
                                TT TTGGATTTTTCAT
                                 G
GAM856  FLJ13646  3'  TAGTTATATTTTTTTTGGGTTC 44729           __     AGTTA
          T                      GGAACTTAAGAA  GTATGG
                                 ||||||||||||  ||||||
                                 TCTTGGGTTTTT  TATATT
                                       TT     GAT
GAM856  FLJ14281  3'  TGGCTTTGTTCTTTGTTTAAGT 46216         __    T TG
          TTTT                    GGAACTTAA  GAAG A  GAGTTA
                                 |||||||||  |||| |  ||||||
                                 TTTTGAATT  TTTC T  TTCGGT
                                      TG    T GT
GAM856  FLJ14642  3'  TAGCTTCATGTTCAGAAGCTCC 51507      A   AA   G
          T                      AGGA CTT  GAA TATGGAGTTA
                                 |||| |||  ||| ||||||||||
                                 TCCT GAA  CTT GTACTTCGAT
                                   C   GA  _
GAM856  FLJ20034  3'  TAATTTTGTATTTTTTAGT    34383     T       TG
                                ACT AAGAAGTA  GAGTTA
                                ||| ||||||||  ||||||
                                TGA TTTTTTAT  TTTAAT
                                  _       GT
GAM856  FLJ20081  3'  TGATTTTATGCTTTTTAA    34509
                                TTAAGAAGTATGGAGTTA
                                ||||||||||||||||||
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```
                                AATTTTTCGTATTTTAGT

GAM856  FLJ20147  3'  TAACTTCATGTTTCTTATTCC  34642      CT
                                GGAA  TAAGAAGTATGGAGTTA
                                ||||  ||||||||||||||||
                                CCTT  ATTCTTTGTACTTCAAT
                                  __
GAM856  FLJ20298  3'  TAATAAATGCTTTTTTAAGTAC 34904      A       _   GGAGTTA
           CT                     AGG ACTTAAGAA GTAT
                                ||| ||||||||| ||||
                                TCC TGAATTTTT CGTA
                                  A       T   AATAAT
GAM856  FLJ20699  3'  GCACAGATGTTTTTCAAGTTCC 35563         A       GGAGTTA
           T                      AGGAACTT AGAAGTAT
                                |||||||| ||||||||
                                TCCTTGAA TTTTTGTA
                                     C       GACACGT
GAM856  FLJ21272  3'  AGGTTGATACTCTTAGGTTTTT 46733           A   G  G  A
                                AGGAACTTAAGA GTAT GA TT
                                |||||||||||| |||| || ||
                                TTTTTGGATTCT CATA TT GA
                                       _   G  G  G
GAM856  FLJ21551  3'  GACTCTGTGCTTTCTG      45629    AG
                                TA  AAGTATGGAGTT
                                ||  ||||||||||||
                                GT  TTCGTGTCTCAG
                                 CT
GAM856  FLJ22649  3'  TAGCTTTGTACTTTTTTTTTT  41637     CTT       TG
                                GAA   AAGAAGTA  GAGTTA
                                |||   ||||||||  ||||||
                                TTT   TTTTTCAT  TTCGAT
                                  TT_       GT
GAM856  FLJ23142  3'  ACACTAAGTATTTTTGAGTTCC 44725           G   GG   TA
           T                      AGGAACTTAAGAA TAT  AGT
                                |||||||||||| |||  |||
                                TCCTTGAGTTTTT ATG  TCA
                                       _   AA   CAA
GAM856  GIPC2     3'  TGATTTCAATAGCTTTGTAGTT 34483       TAA    A__
           TTT                    GGAACT   GAAGT   TGGAGTTA
                                ||||||   |||||   ||||||||
                                TTTTGA   TTTCG   ACTTTAGT
                                   TG_    ATA
GAM856  GNG10     3'  TGATTTTTGTATTCTTACGTTT 14677       T     GTAT
           CT                     AGGAAC TAAGAA    GGAGTTA
                                ||||||| ||||||    |||||||
                                TCTTTG ATTCTT    TTTTAGT
                                   C     ATGT
GAM856  GT650     5'  TGGCTCCGTGCTGCCGGGTTCC 53458        AAGA
                                GGAACTT    AGTATGGAGTTA
                                |||||||    ||||||||||||
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                                CCTTGGG   TCGTGCCTCGGT
                                    CCG_
GAM856  HABP4    3'  TGGCTCCAGTTCTAGAGTTCCT 70561       A   GTA
                                AGGAACTT AGAA   TGGAGTTA
                                |||||||| ||||  ||||||||
                                TCCTTGAG TCTT   ACCTCGGT
                                    A   G__
GAM856  HCRTR1   3'  TGGCTTCAGTCCTGGGTTTCT  7729        A  AGTA
                                AGGAACTTA GA    TGGAGTTA
                                ||||||||| ||    ||||||||
                                TCTTTGGGT CT    ACTTCGGT
                                    C  G___
GAM856  HGRG8    3'  ATGTTTCTTCAGTTTCT     32743       T
                                AGGAACT AAGAAGTAT
                                ||||||| |||||||||
                                TCTTTGA TTCTTTGTA
                                    C
GAM856  HSPC019  3'  CACAGTTTTATTTCTTAGGTTT 25857            TGGAGTTA
          TT                    AGGAACTTAAGAAGTA
                                ||||||||||||||||
                                TTTTTGGATTCTTTAT
                                        TTTGACACT
GAM856  HSPC177  5'  TTTGCTCTAGTGTTTGGGTTTC 33092         AAGTA     TA
          T                     AGGAACTTAAG     TGGAGT
                                ||||||||||     ||||||
                                TCTTTGGGTTT     ATCTCG
                                    GTG__     TTTT
GAM856  HSPCAL3  3'  ATGCTTTTTGAGTTTC      76557
                                GGAACTTAAGAAGTAT
                                ||||||||||||||||
                                CTTTGAGTTTTTCGTA

GAM856  HT002    3'  TGGTTTCATACTTTTTACCT  25949     AACT          TT
                                AGG    TAAGAAGTATGGAG  A
                                |||    |||||||||||||  |
                                TCC    ATTTTTCATACTTT  T
                                  _____          GG
GAM856  IMAGE:4907098 3'  GTATTTTTTAAGTTCCT     91665
                                AGGAACTTAAGAAGTAT
                                ||||||||||||||||
                                TCCTTGAATTTTTTATG

GAM856  ITGA10   3'  GACTTGACTTTTGAGTCCT   59379      A      A  ATG
                                AGGA CTTAAGA GT   GAGTT
                                |||| ||||||| ||   |||||
                                TCCT GAGTTTT CA   TTCAG
                                  _      _ G__
GAM856  KIAA0143 3'  TGCTTTGAGGTTCCT       64790         AA
                                AGGAACTT  GAAGTA
                                ||||||||  ||||||
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                                TCCTTGGA  TTTCGT
                                    G_
GAM856  KIAA0171  3'  TAATTTTATACTTTCTTTTCCT 27857      CTT    _
                                AGGAA   AAGAA GTATGGAGTTA
                                |||||   ||||| ||||||||||
                                TCCTT   TTCTT CATATTTTAAT
                                   ___    T
GAM856  KIAA0182  3'  TGACATGCAATCTCTTAAGTTT 72037          A___    GAGTTA
          TT                    GGAACTTAAGA    GTATG
                                ||||||||||    |||||
                                TTTTGAATTCT    CGTAC
                                      CTAA    AGT
GAM856  KIAA0285  3'  CCGTGCTTGAGATCTT      29015      A    AGA
                                AGGA CTTA   AGTATGG
                                |||| ||||   |||||||
                                TTCT GAGT   TCGTGCC
                                  A   ___
GAM856  KIAA0329  3'  TAGCTTCGTGCTTTGTACAGTT 29280       TAA_
          TT                    GGAACT    GAAGTATGGAGTTA
                                ||||||    ||||||||||||||
                                TTTTGA    TTTCGTGCTTCGAT
                                   CATG
GAM856  KIAA0493  3'  TAACTTTATATTTTGTTACCT  64281     _   TTAA
                                AGG AAC    GAAGTATGGAGTTA
                                ||| |||    ||||||||||||||
                                TCC TTG    TTTTATATTTCAAT
                                  A  _____
GAM856  KIAA0532  3'  TAGTTTTTGGGTTTCT      70777            G
                                AGGAACTTAAGAA TA
                                |||||||||||| ||
                                TCTTTGGGTTTTT AT
                                      G
GAM856  KIAA0551  3'  ACTTTGTTGAGTTCTT      66836          _
                                AGGAACTTAA GAAGT
                                |||||||||| |||||
                                TTCTTGAGTT TTTCA
                                      G
GAM856  KIAA0561  3'  TTCTGTACTTTTTAAGT     65901
                                ACTTAAGAAGTATGGAG
                                |||||||||||||||||
                                TGAATTTTTCATGTCTT

GAM856  KIAA0561  3'  TTTTCTGTACTTTTTAAGT    65902              TTA
                                ACTTAAGAAGTATGGAG
                                |||||||||||||||||
                                TGAATTTTTCATGTCTT
                                      TT
GAM856  KIAA0628  3'  TGAGGCCATATTTTGAGTTCTT 28877         AA        AG
                                AGGAACTT  GAAGTATGG  TTA
                                ||||||||  |||||||||  |||
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                                TTCTTGAG  TTTTATACC  AGT
                                   __        GG
GAM856  KIAA0644 3'  TGATGCATTACTTCTTATGTTT 29065       T       TGGA
            TT                   AGGAAC TAAGAAGTA    GTTA
                                 |||||| |||||||||    ||||
                                 TTTTTG ATTCTTCAT    TAGT
                                    T        TACG
GAM856  KIAA0668 3'  TGGTTCTTAAGTTTTT      66528           G
                                 AGGAACTTAAGAA TA
                                 |||||||||||| ||
                                 TTTTTGAATTCTT GT
                                        G
GAM856  KIAA0721 3'  TGTATTTCTTGAGTTTTT    41350
                                 AGGAACTTAAGAAGTATG
                                 ||||||||||||||||||
                                 TTTTTGAGTTCTTTATGT

GAM856  KIAA0721 3'  TGTATTTCTTGAGTTTTT    95978
                                 AGGAACTTAAGAAGTATG
                                 ||||||||||||||||||
                                 TTTTTGAGTTCTTTATGT

GAM856  KIAA0779 3'  CCGCACTTTTAAGGTTTTT    85725        A     A
                                 AGGAACTT AGAAGT TGG
                                 |||||||| |||||| |||
                                 TTTTTGGA TTTTCA GCC
                                      A     C
GAM856  KIAA0779 3'  TACTTTTGAGTTTCT       85731           A
                                 AGGAACTTAAGA GTA
                                 |||||||||||| |||
                                 TCTTTGAGTTTT CAT
                                           _
GAM856  KIAA0820 3'  TGGCTTTGTGCTAAATGTGGTT 69029       TAAGA_   TG
            TT                   GGAACT     AGTA  GAGTTA
                                 ||||||     ||||  ||||||
                                 TTTTGG     TCGT  TTCGGT
                                    TGTAAA    GT
GAM856  KIAA0825 3'  TGATTTTATACTTAGAATTCT  61033     C  AAG
                                 GGAA TT   AAGTATGGAGTTA
                                 |||| ||   ||||||||||||
                                 TCTT AA   TTCATATTTTAGT
                                   _  GA_
GAM856  KIAA0828 3'  TGATTCTGTATTTCAGAGTCAG 81200     TAA___
            TTTCT                AACT     GAAGTATGGAGTTA
                                 ||||     ||||||||||||||
                                 TTGA     CTTTATGTCTTAGT
                                   CTGAGA
GAM856  KIAA1014 3'  ATGGCTCCAAACACATAGTTTT 65351       G _______
            TAAGTTTTT              TAAGAA TA     TGGAGTTA   T
                                 |||||| ||     ||||||||   |
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                                ATTTTT AT     ACCTCGGT   A
                                   G  ACACAA
GAM856  KIAA1024  3'  TGGCTCCATTCCTTGATTTTCT 69067      C    AAGT
                                AGGAA TTAAG    ATGGAGTTA
                                ||||| |||||    |||||||||
                                TCTTT AGTTC    TACCTCGGT
                                   T    CT__
GAM856  KIAA1025  3'  TGTTTCATACTGGGGTTTCT   63979       TAAGA       TT
                                AGGAACT    AGTATGGAG  A
                                |||||||    |||||||||  |
                                TCTTTGG    TCATACTTT  T
                                    GG___       GG
GAM856  KIAA1040  3'  TACTTCTTAGTTTCCT     72232      C
                                AGGAA TTAAGAAGTA
                                ||||| ||||||||||
                                TCCTT GATTCTTCAT
                                   T
GAM856  KIAA1136  3'  TGCTTCCTAGGTTTCT     91322         A
                                AGGAACTTA GAAGTA
                                ||||||||| ||||||
                                TCTTTGGAT CTTCGT
                                     C
GAM856  KIAA1145  3'  TGTTCCTGCCTTCAAGTTCTT  65629        AA   TAT   TT
                                AGGAACTT  GAAG   GGAG  A
                                ||||||||  ||||   ||||  |
                                TTCTTGAA  CTTC   CCTT  T
                                    __   CGT    GG
GAM856  KIAA1200  3'  TGGTTTTATAATATCTTGGGTA 62384     A      AG_     TT
           TCT                    AGG ACTTAAGA   TATGGAG  A
                                |||  ||||||||   |||||||  |
                                TCT TGGGTTCT   ATATTTT  T
                                  A       ATA      GG
GAM856  KIAA1317  3'  TGACTCCGTATGCATGAGT   86034      AGAA
                                ACTTA   GTATGGAGTTA
                                |||||   ||||||||||||
                                TGAGT   TATGCCTCAGT
                                   ACG_
GAM856  KIAA1462  3'  AAAAGCAATATCTTTTAAGTTC 91379          AG   GGAGTTA
           CT                    AGGAACTTAAGA  TAT
                                ||||||||||||  |||
                                TCCTTGAATTTT  ATA
                                      CT   ACGAAAAT
GAM856  KIAA1557  3'  TGGCTTCCCACTTAGGTTTTT  61139         AAGTAT
                                AGGAACTTAAG     GGAGTTA
                                ||||||||||     |||||||
                                TTTTTGGATTC     CTTCGGT
                                      ACC___
GAM856  KIAA1573  3'  TGCTATTCTTAGGTTTCT    62691          __
                                AGGAACTTAAGA  AGTA
                                ||||||||||||  ||||
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                                TCTTTGGATTCT  TCGT
                                      TA
GAM856  KIAA1594  3'  TGGCTTTTAGCTTTTATGTTCC 72087       TTA     AT
            T                  AGGAAC   AGAAGT  GGAGTTA
                               ||||||   ||||||  |||||||
                               TCCTTG   TTTTCG  TTTCGGT
                                  TA_     AT
GAM856  KIAA1610  3'  TAATACCAATTTCTCTGAGTTT 67158         _     A   A
            CT                   AGGAACTTA AGAAGT TGG GTTA
                               |||||||||| |||||| ||| ||||
                               TCTTTGAGT TCTTTA ACC TAAT
                                    C     _  A
GAM856  KIAA1671  3'  TAATTTTGTACTGTGCTGTTTC 65688      CTTAAGA    TG
            CT                   AGGAA      AGTA  GAGTTA
                               |||||      ||||  ||||||
                               TCCTT      TCAT  TTTAAT
                                  TGTCGTG    GT
GAM856  KIAA1786  3'  TAGCTTTGTGCTTTTTAGATTC 66038      C        TG
            C                    GGAA TTAAGAAGTA  GAGTTA
                               |||| ||||||||||  ||||||
                               CCTT GATTTTTCGT  TTCGAT
                                  A        GT
GAM856  KIAA1894  3'  TAACTCTGTGAACAGTCTTGAC 73846    C     AG___
            TTTTT                 AA TTAAGA     TATGGAGTTA
                               || ||||||    ||||||||||
                               TT AGTTCT     GTGTCTCAAT
                                C     GACAA
GAM856  KIAA1915  3'  TGATTCTATATTTTGCTTTGTT 73284      TTAA_
            T                    GAAC     GAAGTATGGAGTTA
                               ||||     ||||||||||||||
                               TTTG     TTTTATATCTTAGT
                                  TTTCG
GAM856  KIAA1970  3'  TGAGATATGCTTCTTGGGGTCT 74298      A          GAGTTA
            T                    AGGA CTTAAGAAGTATG
                               |||| ||||||||||||
                               TTCT GGGTTCTTCGTAT
                                  G          AGAGT
GAM856  KIF4A     3'  TGACTTCTCTGGATTTCAGGTT 24594       AA     AT___
            TCT                    GAACTT  GAAGT     GGAGTTA
                               ||||||  |||||     |||||||
                               TTTGGA  CTTTA     CTTCAGT
                                  __     GGTCT
GAM856  KOC1      3'  TAATTCTATAATTGAGTTTT   91077         GAAG
                               GGAACTTAA    TATGGAGTTA
                               |||||||||    ||||||||||
                               TTTTGAGTT    ATATCTTAAT
                                    A___
GAM856  KOC1      3'  TGGCTTCAGGAGACTTCAGTTT 91079        T   AAGTA
            TT                     AGGAACT AAG     TGGAGTTA
                               ||||||| |||     ||||||||
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                                TTTTTGA TTC    ACTTCGGT
                                    C  AGAGG
GAM856  KPNA6    3'  TAACTCTTATCTTGGGTACTT  24613    A      AGTAT
                                AGG ACTTAAGA    GGAGTTA
                                ||| ||||||||    |||||||
                                TTC TGGGTTCT    TCTCAAT
                                  A       AT___
GAM856  LASP1    3'  TGACTTTATTGCTTAATTTCT  20463    C    AAGT
                                GGAA TTAAG    ATGGAGTTA
                                |||| |||||    |||||||||
                                TCTT AATTC    TATTTCAGT
                                  T    GT__
GAM856  LAT1-3TM  5'  AATTTTAGGGTGAGTTCCT    68597        AGAAGTA
                                AGGAACTTA      TGGAGTT
                                |||||||||      |||||||
                                TCCTTGAGT      ATTTTAA
                                     GGG_____
GAM856  LRP1B    3'  ACTTTTTCAGGTTCTT      37666        _
                                AGGAACTT AAGAAGT
                                |||||||| |||||||
                                TTCTTGGA TTTTTCA
                                    C
GAM856  MAEA     3'  GATTTCCCTGTGTTTTCAGTTT 19659       T   AG  T   TTA
            CT                    AGGAACT AAGA  TA GGAG
                                ||||||| ||||  || ||||
                                TCTTTGA TTTT  GT CCTT
                                    C   GT  C    TAGT
GAM856  MDS018    3'  CCTGCTTCTTGGTTTCCT    41530      C        T
                                AGGAA TTAAGAAGTA GG
                                ||||| |||||||||| ||
                                TCCTT GGTTCTTCGT CC
                                  T        _
GAM856  MGC10067  3'  TAATTTTATATTTTTTGA    58939
                                TTAAGAAGTATGGAGTTA
                                ||||||||||||||||||
                                AGTTTTTTATATTTTAAT

GAM856  MGC1127   3'  TAATTTCATTCCTTAACTTCCT 53217      C    AAGT
                                AGGAA TTAAG    ATGGAGTTA
                                ||||| |||||    |||||||||
                                TCCTT AATTC    TACTTTAAT
                                  C    CT__
GAM856  MGC13168  3'  TGGTTGCATTCTTCTGGGTTTC 51214        A   T   G  TT
            T                    AGGAACTTA GAAG ATG AG  A
                                ||||||||| |||| ||| ||  |
                                TCTTTGGGT CTTC TAC TT  T
                                     _   T   G  GG
GAM856  MGC2747   3'  TGCTTGTTGAGTTTTT      44089          G
                                AGGAACTTAA AAGTA
                                |||||||||| |||||
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                                TTTTTGAGTT TTCGT
                                      G
GAM856  MGC30052  3'  AATTTCATGTTACGTTCC    58531      T   GAAG
                                GGAAC TAA    TATGGAGTT
                                ||||| |||    |||||||||
                                CCTTG ATT    GTACTTTAA
                                  C  ____
GAM856  MGC3178   3'  TAACTAGAGTTCTAGAGTTTCT 47991        A    GTATGG
                                AGGAACTT AGAA     AGTTA
                                |||||||| ||||     |||||
                                TCTTTGAG TCTT     TCAAT
                                    A   GAGA__
GAM856  MGC5338   3'  TGACTTTGTATTGAGTTCTT   43942        AGAA   TG
                                AGGAACTTA   GTA  GAGTTA
                                |||||||||   |||  ||||||
                                TTCTTGAGT   TAT  TTCAGT
                                     ____  GT
GAM856  MGC5590   3'  TGATTTAGGGTTTAGGTTCCT  43930         AAGTATG
                                AGGAACTTAAG      GAGTTA
                                ||||||||||       ||||||
                                TCCTTGGATTT      TTTAGT
                                      GGGA___
GAM856  NS1-BP    3'  CATACTTTTTGGGTTT     72543
                                GAACTTAAGAAGTATG
                                ||||||||||||||||
                                TTTGGGTTTTTCATAC

GAM856  NUP160    3'  CCCTTCTTGAGTTTTT      87594            TAT
                                AGGAACTTAAGAAG   GG
                                ||||||||||||||   ||
                                TTTTTGAGTTCTTC   CC
                                          ___
GAM856  OLFM3     3'  TGATTTCATACAACTGAGTTAC 82147     G     A AA
            T                    AG AACTTA G  GTATGGAGTTA
                                || |||||| |  ||||||||||
                                TC TTGAGT C  CATACTTTAGT
                                 A     _ AA
GAM856  ORCTL4    5'  GGCTCCATGCTGGTCTCT    16650    GA   TAAGA
                                AG  ACT    AGTATGGAGTT
                                ||  |||    ||||||||||
                                TC  TGG    TCGTACCTCGG
                                 TC  ______
GAM856  P2RX1     3'  TAGCTTCGTGCTTCTCTCTCC  67170     ACTTA
                                GGA    AGAAGTATGGAGTTA
                                |||    ||||||||||||||
                                CCT    TCTTCGTGCTTCGAT
                                  CTC__
GAM856  PACSIN2   3'  GCTTCATGGTGTTCCT      23342        _   A
                                AGGAAC TTA GAAGT
                                |||||| ||| |||||
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                                TCCTTG GGT CTTCG
                                   T   A
GAM856  PAPOLG   3'  ATATTTTTTAAGTTTC      43171
                                GGAACTTAAGAAGTAT
                                ||||||||||||||||
                                CTTTGAATTTTTTATA

GAM856  PIP5K1C  3'  TGTTGGTTGTGTTTTTTGGTTC 70768        T       TG AGTTA
           CT                    AGGAACT AAGAAGTA  G
                                |||||||  ||||||||  |
                                TCCTTGG TTTTTTGT  T
                                   _       GT GGTTGTG
GAM856  PIP5K2B  3'  TGACTTCGTGGGTTTATTTGGG 13080        ___  AG
           TTTT                   AACTTAA   GA  TATGGAGTTA
                                |||||||   ||  ||||||||||
                                TTGGGTT   TT  GTGCTTCAGT
                                    TAT  GG
GAM856  PLSCR4   3'  AAATTTGTTTTTCTGAGTTTCT 39783         A    T TG  GTTA
                                AGGAACTTA GAAG A  GA
                                |||||||||  ||||  |  ||
                                TCTTTGAGT CTTT T  TT
                                   _   T GT  AAAT
GAM856  PRO0132  5'  TAATTTTGCTGACTTAAGTTTC 26105          A_    TG
                                GGAACTTAAG  AGTA  GAGTTA
                                ||||||||||  ||||  ||||||
                                CTTTGAATTC  TCGT  TTTAAT
                                    AG   __
GAM856  PRO1728  5'  TGATTTGTGCTTCTTTGGTTTT 37540        T       TG  GTTA
           T                     AGGAACT AAGAAGTA  GA
                                |||||||  ||||||||  ||
                                TTTTTGG TTCTTCGT  TT
                                    T       GT  AGT
GAM856  PRO2086  5'  TAATTTTCTACCTTTAGGTTCC 26071          AA   TG
                                GGAACTTAAG  GTA  GAGTTA
                                ||||||||||  |||  ||||||
                                CCTTGGATTT  CAT  TTTAAT
                                    C_   CT
GAM856  PRO2730  3'  GATTGTATTTGAGTTCCT    47417          GAAGT   G
                                AGGAACTTAA     ATG AGTT
                                ||||||||||     ||| ||||
                                TCCTTGAGTT     TAT TTAG
                                    _____   G
GAM856  RAB14    3'  GGACAACATGTTTTATTAAGTT 32873          _       GA   A
           CTT                    AGGAACTTAA GAAGTATG  GTT
                                ||||||||||  ||||||||  |||
                                TTCTTGAATT TTTTGTAC  CAG
                                    A       AA   GT
GAM856  SAD1     3'  TAACTTATGTCTTGAGTATCT  64023     A       AGTATG
                                AGG ACTTAAGA     GAGTTA
                                |||  ||||||||     ||||||
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                                TCT TGAGTTCT     TTCAAT
                                  A       GTA___
GAM856  SHANK3   3'  TGGTTCCGTTCAATTTGGGTTT 65507          AAGT     TT
            TT                   AGGAACTTAAG    ATGGAG  A
                                ||||||||||    ||||||  |
                                TTTTTGGGTTT    TGCCTT  T
                                      AACT     GG
GAM856  SLC11A2  3'  TAGCTCTATCAGGCTTAGGATT 5238       A     AAGT
            CT                   AGGA CTTAAG    ATGGAGTTA
                                |||| ||||||    |||||||||
                                TCTT GGATTC    TATCTCGAT
                                  A     GGAC
GAM856  SLC16A4  3'  CTTTCTTTGTATTACTTAGGTT 16280          A    TG   TTA
            CTT                   AGGAACTTAAG AGTA  GAG
                                ||||||||||| ||||  |||
                                TTCTTGGATTC TTAT  TTC
                                      A    GT   TTTCA
GAM856  SQV7L    5'  TGATTCCATGTTTTTGCTGTT  70581     TTA
                                AAC   AGAAGTATGGAGTTA
                                |||   ||||||||||||||||
                                TTG   TTTTTGTACCTTAGT
                                  TCG
GAM856  SQV7L    5'  TTTGTAATTTTAAGTTCT    70583          AG  TG
                                GGAACTTAAGA  TA  GA
                                ||||||||||  ||  ||
                                TCTTGAATTTT  AT  TT
                                      A_  GT
GAM856  STATI2   3'  CCTTGCCTTCTTAGGTTCTT   13921            _  T
                                AGGAACTTAAGAAG TA GG
                                |||||||||||||| || ||
                                TTCTTGGATTCTTC GT CC
                                        C  T
GAM856  STATI2   3'  CCTTGCCTTCTTAGGTTCTT   94551            _  T
                                AGGAACTTAAGAAG TA GG
                                |||||||||||||| || ||
                                TTCTTGGATTCTTC GT CC
                                        C  T
GAM856  STC2     3'  TGATTTTTCTTTTTTTTAAGTT 13552           TAT_
            CT                   GGAACTTAAGAAG    GGAGTTA
                                ||||||||||||    |||||||
                                TCTTGAATTTTTT    TTTTAGT
                                      TTCT
GAM856  SUPT4H1  3'  ATTTCCCTAAGTTCCT     12059         A_
                                AGGAACTTA  GAAGT
                                |||||||||  |||||
                                TCCTTGAAT  CTTTA
                                     CC
GAM856  SYNPO2   3'  GTGTTTCTTGAGTCCCT     71895     A
                                AGG ACTTAAGAAGTAT
                                ||| ||||||||||||
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                                TCC TGAGTTCTTTGTG
                                  C
GAM856  TOPBP1   3'  CCCTTCTTGAGTTTT      22839          TAT
                                GGAACTTAAGAAG  GG
                                |||||||||||||  ||
                                TTTTGAGTTCTTC  CC
                                       ___
GAM856  TP53INP1 3'  TGACTTCATATTTCTCTCTGCC 72958    AACTTA
           C                    GG     AGAAGTATGGAGTTA
                                ||     ||||||||||||||
                                CC     TCTTTATACTTCAGT
                                 CGTCTC
GAM856  TP53INP1 3'  TGACTTCATATTTCTCTCTGCC 52731    AACTTA
           C                    GG     AGAAGTATGGAGTTA
                                ||     ||||||||||||||
                                CC     TCTTTATACTTCAGT
                                 CGTCTC
GAM856  TRPM3    3'  TAATTTTATATTTTTTAA    64911
                                TTAAGAAGTATGGAGTTA
                                ||||||||||||||||||
                                AATTTTTTATATTTTAAT

GAM856  TUBGCP3  3'  GCTTCTTAAGCTTTCT      20894      _
                                AGGAA CTTAAGAAGT
                                ||||| ||||||||||
                                TCTTT GAATTCTTCG
                                   C
GAM856  UBCE7IP5 3'  CATTTTTTTGAGTTCCT     30150           T
                                AGGAACTTAAGAAG ATG
                                |||||||||||||| |||
                                TCCTTGAGTTTTTT TAC
                                       _
GAM856  WSB1     5'  GACTCCGTACTTTGGTCT    56146     ACTTAA
                                GGA     GAAGTATGGAGTT
                                |||     ||||||||||||
                                TCT     TTTCATGCCTCAG
                                  GG____
GAM856  WSB1     5'  GACTCCGTACTTTGGTCT    56140     ACTTAA
                                GGA     GAAGTATGGAGTT
                                |||     ||||||||||||
                                TCT     TTTCATGCCTCAG
                                  GG____
GAM856  XPO5     3'  TGACTTCATGCTAGAAATTTTC 91237      CTTAAGA
           T                    AGGAA      AGTATGGAGTTA
                                |||||      ||||||||||||
                                TCTTT      TCGTACTTCAGT
                                   TAAAGA_
GAM856  ZDHHC5   5'  TGGCTTCAAGGATTTTAAGTTT 91564          AGTA
           C                    GGAACTTAAGA    TGGAGTTA
                                ||||||||||    ||||||||
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                                CTTTGAATTTT   ACTTCGGT
                                      AGGA
GAM856  ZF      3'  TAAAGCTGCTTTGTTAGGTTCC 41091         _    TGGAGTTA
           T                   AGGAACTTAA GAAGTA
                               |||||||||| ||||||
                               TCCTTGGATT TTTCGT
                                     G     CGAAAT
GAM856  ZNF220  3'  TGCCTCTTAGGTTCTT     22228          A
                               AGGAACTTAAGA GTA
                               |||||||||||| |||
                               TTCTTGGATTCT CGT
                                      C
GAM856  LOC115207 3'  TAACTTACTGTTTTGAGTCCT  56606     A     AGTATG
                               AGGA CTTAAGA     GAGTTA
                               |||| |||||||     ||||||
                               TCCT GAGTTTT     TTCAAT
                                 _      GTCA__
GAM856  LOC115294 3'  CCATATTTTTTGTGTTTCT    73013      T
                               AGGAAC TAAGAAGTATGG
                               |||||| ||||||||||||
                               TCTTTG GTTTTTTATACC
                                  T
GAM856  LOC115297 3'  CCGTGTTCTTAGGTTCTT     72885          G
                               AGGAACTTAAGAA TATGG
                               |||||||||||| |||||
                               TTCTTGGATTCTT GTGCC
                                                _
GAM856  LOC115648 3'  TGGCAAACAACTCCTTAAGTTT 59304         A  A  GA_
           TT                    AGGAACTTAAG AGT TG   GTTA
                               |||||||||| ||| ||   ||||
                               TTTTTGAATTC TCA AC   CGGT
                                      C   _  AAA
GAM856  LOC121441 3'  TAGCTCACTAACTTTATGGGTT 74066        A    ATG_
           TCT                    AGGAACTTA GAAGT    GAGTTA
                               |||||||| |||||    ||||||
                               TCTTTGGGT TTTCA    CTCGAT
                                     A     ATCA
GAM856  LOC124599 3'  GATTCTGGGATGAGTTCCT    75652        AGAAGTA
                               AGGAACTTA      TGGAGTT
                               |||||||||      |||||||
                               TCCTTGAGT      GTCTTAG
                                     AGG_____
GAM856  LOC131368 3'  TGATTCTACGATTAAGTTCT   75862        GAA  AT
                               GGAACTTAA   GT  GGAGTTA
                               |||||||||   ||  |||||||
                               TCTTGAATT   CA  TCTTAGT
                                     AG_  ___
GAM856  LOC133022 3'  TTCGTGCTCTTCGGTTTTT    75921       T   A
                               AGGAACT AAGA GTATGGA
                               ||||||| |||| |||||||
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                                TTTTTGG TTCT CGTGCTT
                                   C   _
GAM856  LOC133121 3'  TAATTCTATACATAAAAGTTCC 75082        AAGAA
           T                    AGGAACTT    GTATGGAGTTA
                                ||||||||    ||||||||||
                                TCCTTGAA    CATATCTTAAT
                                    AATA_
GAM856  LOC135818 3'  TAATTTTGTATTTTTTTAGT  75241    T      TG
                                ACT AAGAAGTA  GAGTTA
                                ||| ||||||||  ||||||
                                TGA TTTTTTAT  TTTAAT
                                  T       GT
GAM856  LOC143154 3'  TACTTTTTGAGTCTT      76485     A
                                AGGA CTTAAGAAGTA
                                |||| ||||||||||
                                TTCT GAGTTTTTCAT

                                  _
GAM856  LOC144373 3'  GGCTTCGTGCCAGTTCCT    76821       TAAGAA
                                AGGAACT     GTATGGAGTT
                                |||||||     ||||||||||
                                TCCTTGA     CGTGCTTCGG
                                   C_____
GAM856  LOC144483 3'  CCCTTCTGGGGTTTCT     60177       TA    TAT
                                AGGAACT  AGAAG   GG
                                |||||||  |||||   ||
                                TCTTTGG  TCTTC   CC
                                   GG    ___
GAM856  LOC145739 3'  ATACTCTTAAGTTTTT      77439          A
                                AGGAACTTAAGA GTAT
                                |||||||||||| ||||
                                TTTTTGAATTCT CATA

                                     _
GAM856  LOC145757 5'  TGGTTTTGTGCTTCCTCTGTGC 77475     A  TTAA     TG   TT
           CT                     AGG AC    GAAGTA  GAG  A
                                ||| ||    ||||||  |||  |
                                TCC TG    CTTCGT  TTT  T
                                  G  TCTC     GT   GG
GAM856  LOC145815 5'  AACTTCATGCTGATTTCT    83514      CTTAAGA
                                AGGAA      AGTATGGAGTT
                                |||||      ||||||||||
                                TCTTT      TCGTACTTCAA
                                  AG_____
GAM856  LOC145824 5'  ACTCCTGTGAGTTTCT      77522         AGAAGTAT
                                AGGAACTTA       GGAGT
                                |||||||||       |||||
                                TCTTTGAGT       CCTCA
                                    GT_______
GAM856  LOC145826 3'  TAACTTTTTAGTGCTTGGGTTT 83532          AAG  TG
           TT                     AGGAACTTAAG   TA  GAGTTA
                                ||||||||||   ||  ||||||
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                                TTTTTGGGTTC   AT  TTCAAT
                                      GTG  TT
GAM856   LOC147991 3'  TAACTTTTAAAATTTTAAGTGC 78604     A       AGTAT
             CT                    AGG ACTTAAGA     GGAGTTA
                                   ||| ||||||||     |||||||
                                   TCC TGAATTTT     TTTCAAT
                                     G        AAAAT
GAM856   LOC148255 5'  GTATTTCTTGATGTTCTT     78756       _
                                   AGGAAC TTAAGAAGTAT
                                   |||||| ||||||||||
                                   TTCTTG AGTTCTTTATG
                                      T
GAM856   LOC148936 5'  TGGCTCTATAAGGGGGAGTTTC 84304         AAGAAG
             T                     AGGAACTT      TATGGAGTTA
                                   ||||||||      ||||||||||
                                   TCTTTGAG      ATATCTCGGT
                                        GGGGA_
GAM856   LOC148938 5'  TGGCTCTATAAGGGGGAGTTTC 84285         AAGAAG
             T                     AGGAACTT      TATGGAGTTA
                                   ||||||||      ||||||||||
                                   TCTTTGAG      ATATCTCGGT
                                        GGGGA_
GAM856   LOC149422 3'  TGGCTCCCAGGCTGGAGTTCCT 79352         A  AAGTAT
                                   AGGAACTT AG      GGAGTTA
                                   |||||||| ||      |||||||
                                   TCCTTGAG TC      CCTCGGT
                                        G  GGAC__
GAM856   LOC149464 5'  TGATTCTATGCAGAAGTTACTT 84436     _     AAGAA
                                   AGG AACTT     GTATGGAGTTA
                                   ||| |||||     ||||||||||
                                   TTC TTGAA     CGTATCTTAGT
                                     A     GA___
GAM856   LOC149705 3'  TGGCTTCATGTCTTGAATTTCT 84628       C      AG
                                   AGGAA TTAAGA  TATGGAGTTA
                                   ||||| ||||||  ||||||||||
                                   TCTTT AGTTCT  GTACTTCGGT
                                      A     __
GAM856   LOC150142 5'  TCATCTTCTTGTGTTTCT     79581        T      T
                                   AGGAAC TAAGAAG ATGG
                                   |||||| ||||||| ||||
                                   TCTTTG GTTCTTC TACT
                                      T     _
GAM856   LOC150157 5'  TGACAAACCCTTCTTAGTTCCT 84881         T     TAT  A__
                                   AGGAACT AAGAAG   GG   GTTA
                                   ||||||| ||||||   ||   ||||
                                   TCCTTGA TTCTTC   CC   CAGT
                                      _     ___  AAA
GAM856   LOC150468 3'  GACACTTGCTTCTTCAGTTCTT 79876         T       T  A   A
                                   AGGAACT AAGAAGTA GG GTT
                                   ||||||| |||||||| || |||
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                                TTCTTGA TTCTTCGT TC CAG
                                   C       _ A   G
GAM856  LOC150498 3'  TGGTCCCAGCTTTTAGGTTCTT 79907          A  A   AG
                                AGGAACTTAAGA GT TGG  TTA
                                |||||||||||| || |||  |||
                                TTCTTGGATTTT CG ACC  GGT
                                      _ _  CT
GAM856  LOC151201 3'  TAGTTCCTATACTTTTCTTAAT 85289     C     __    _  GT
          TCTT                    GAA TTAAGA  AGTAT GGA  TA
                                ||| ||||||  ||||| |||  ||
                                CTT AATTCT  TCATA CCT  AT
                                  _     TT    T  TG
GAM856  LOC152518 3'  TAACTTTGTGCTTTTTAA    80614          TG
                                TTAAGAAGTA  GAGTTA
                                ||||||||||  ||||||
                                AATTTTTCGT  TTCAAT
                                      GT
GAM856  LOC152941 3'  TAGTCTGTAGCTTTTTAGGTTC 80750            _    GTTA
          TT                     AGGAACTTAAGAAGT ATGGA
                                |||||||||||||| |||||
                                TTCTTGGATTTTTCG TGTCT
                                      A    GAT
GAM856  LOC152941 5'  TGACTTTGGTGTTTTAAGTTCT 80751          AGTA GG
                                GGAACTTAAGA    T  AGTTA
                                ||||||||||    |  |||||
                                TCTTGAATTTT    G  TCAGT
                                      GTG_ TT
GAM856  LOC153525 3'  TGCCCTATGTTTCTTAACTTCT 86047      C          A  TA
          T                      AGGAA TTAAGAAGTATGG GT
                                ||||| ||||||||||||| ||
                                TTCTT AATTCTTTGTATC CG
                                   C          C  T
GAM856  LOC154214 3'  TAACTCTGACCTTTGTGGTTCT 81058       TAA    TA
          T                      AGGAACT   GAAG  TGGAGTTA
                                |||||||   ||||  ||||||||
                                TTCTTGG   TTTC  GTCTCAAT
                                    TG_   CA
GAM856  LOC157624 5'  TAGCTCCAGGGTTAAGTTCCT  86500         GAAGTA
                                AGGAACTTAA     TGGAGTTA
                                ||||||||||     ||||||||
                                TCCTTGAATT     ACCTCGAT
                                      GGG___
GAM856  LOC158014 5'  TAATTCTAGTTTTAGGATTCCT 81658      _     AGTA
                                AGGAA CTTAAGA    TGGAGTTA
                                ||||| |||||||    ||||||||
                                TCCTT GGATTTT    ATCTTAAT
                                   A      G___
GAM856  LOC158187 3'  TGACTCCGAAGCTAGGTTTTT  86697         A AAGTA
                                AGGAACTTA G    TGGAGTTA
                                |||||||| |    ||||||||
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                                TTTTTGGAT C     GCCTCAGT
                                      _ GAA__
GAM856   LOC158402 5'  TAGCTCTGTGCTTTAGTCCCT  86810     A   TAA
                                AGG ACT   GAAGTATGGAGTTA
                                ||| |||   ||||||||||||||
                                TCC TGA   TTTCGTGTCTCGAT
                                  C  ___
GAM856   LOC158722 3'  TAACTCTGCTCTATTTGGTTTC 81996        T   A  TA
            T                    AGGAACT AAG AG  TGGAGTTA
                                ||||||| ||| ||  ||||||||
                                TCTTTGG TTT TC  GTCTCAAT
                                     _  A  TC
GAM856   LOC159065 5'  TGGTTTTATAAAGAGGAGTTCC 82084        AAGAAG      TT
                                GGAACTT     TATGGAG  A
                                |||||||     |||||||  |
                                CCTTGAG     ATATTTT  T
                                     GAGAA_      GG
GAM856   LOC163994 5'  TGTTCTAATTCTTATGTTCCT  87052       T     GTA    TT
                                AGGAAC TAAGAA   TGGAG  A
                                |||||| ||||||   |||||  |
                                TCCTTG ATTCTT   ATCTT  T
                                    T     A__     GG
GAM856   LOC166765 3'  TAATTTTGAATTTTTAAGTTCT 82663           GTA GG
                                GGAACTTAAGAA   T  AGTTA
                                ||||||||||||   |  |||||
                                TCTTGAATTTTT   G  TTAAT
                                       AA_ TT
GAM856   LOC196411 3'  TGACTTCATGTAAAGTTTCT   87689        AAGAAG
                                AGGAACTT     TATGGAGTTA
                                ||||||||     ||||||||||
                                TCTTTGAA     GTACTTCAGT
                                     AT_____
GAM856   LOC196890 5'  TGACAAACCCTTCTTAGTTCCT 89651        T     TAT  A__
                                AGGAACT AAGAAG   GG   GTTA
                                ||||||| ||||||   ||   ||||
                                TCCTTGA TTCTTC   CC   CAGT
                                   _     ___  AAA
GAM856   LOC199837 5'  ACTTCACTGAGTTTCT      88403          A_
                                AGGAACTTA  GAAGT
                                |||||||||  |||||
                                TCTTTGAGT  CTTCA
                                     CA
GAM856   LOC199926 5'  ATGCTTTTAAGGTTCCT     89877         A
                                AGGAACTT AGAAGTAT
                                |||||||| ||||||||
                                TCCTTGGA TTTTCGTA
                                     A
GAM856   LOC200261 3'  TGGCTTTGTGCTTCTCTTCC   88659      CTTA      TG
                                GGAA    AGAAGTA  GAGTTA
                                ||||    |||||||  ||||||
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                                CCTT    TCTTCGT  TTCGGT
                                  C___      GT
GAM856  LOC200933 3'  CTTTGTACTTCTGAGTTCTT   90197         A     TG
                                AGGAACTTA GAAGTA  GAG
                                ||||||||| ||||||  |||
                                TTCTTGAGT CTTCAT  TTC
                                     _     GT
GAM856  LOC201294 3'  TAGCTCTGAGTGCTTTGAGTTC 88218         AA      __
          TT                     AGGAACTT  GAAGTAT  GGAGTTA
                                ||||||||  |||||||  |||||||
                                TTCTTGAG  TTTCGTG  TCTCGAT
                                     __       AG
GAM856  LOC202316 5'  ATGCTTTTAAGGTTCCT     90337         A
                                AGGAACTT AGAAGTAT
                                |||||||| ||||||||
                                TCCTTGGA TTTTCGTA
                                     A
GAM856  LOC202934 5'  ATTTGTTCTTGCTTTTTGAGTT 90403              T   GTTA
          CCT                     AGGAACTTAAGAAGTA GGA
                                |||||||||||||||| |||
                                TCCTTGAGTTTTTCGT CTT
                                          T   GTTTAG
GAM856  LOC204804 3'  TGTTCCGTGTGCTGGTTCT    89489       TA  AAG      TT
                                GGAACT  AG   TATGGAG  A
                                ||||||  ||   |||||||  |
                                TCTTGG  TC   GTGCCTT  T
                                   __ GT_      GG
GAM856  LOC219376 3'  AATTCTGTGCTAGGTACTT    93894     A    AAGA
                                AGG ACTT    AGTATGGAGTT
                                ||| ||||    ||||||||||
                                TTC TGGA    TCGTGTCTTAA
                                  A   _____
GAM856  LOC219673 5'  TAGCTCTGTAACTGGGTCTCT  93040     GA     AGAAG
                                AG  ACTTA     TATGGAGTTA
                                ||  |||||     ||||||||||
                                TC  TGGGT     ATGTCTCGAT
                                 TC     CA___
GAM856  LOC220110 5'  TAACTGGCATTCTCTAAGTTTC 93465          _   GTATGG
          T                      AGGAACTTA AGAA      AGTTA
                                ||||||||| ||||      |||||
                                TCTTTGAAT TCTT      TCAAT
                                     C    ACGG__
GAM856  LOC220705 3'  TAGCTCCAATTTCTACTCTTAA 91230         A  ______
          GTTTCT                    CTTAAGA GTA     TGGAGTTA
                                ||||||| |||     ||||||||
                                GAATTCT CAT     ACCTCGAT
                                   _  CTTTA
GAM856  LOC221288 3'  TGATTTCGTGCTTCACCTCC   93621     ACTTAA
                                GGA     GAAGTATGGAGTTA
                                |||     ||||||||||||||
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                                CCT     CTTCGTGCTTTAGT
                                  CCA___
GAM856  LOC221550 5'  TTGTAGTCATATTTCTTAGTTC 92123       T        AGTTA
            TT                    AGGAACT AAGAAGTATGG
                                  ||||||| ||||||||||
                                  TTCTTGA TTCTTTATACT
                                     _        GATGTTT
GAM856  LOC221550 5'  TCCCAAATATTCTTTAAGTTCT 92121        GA   ___  GTTA
            T                     GGAACTTAA  AGTAT   GGA
                                  |||||||||  |||||   |||
                                  TCTTGAATT  TTATA   CCT
                                       TC    AAC     A
GAM856  LOC221662 3'  TAGTTTCATGCTTCCTCCT   92405     ACTTAA       GT
                                  AGGA    GAAGTATGGA  TA
                                  ||||    ||||||||||  ||
                                  TCCT    CTTCGTACTT  AT
                                    C_____        TG
GAM856  LOC221895 3'  CCATTCCTTAAGTTTTT     92523          AAGT
                                  AGGAACTTAAG   ATGG
                                  ||||||||||    ||||
                                  TTTTTGAATTC   TACC
                                        CT__
GAM856  LOC221968 3'  AACTCTGTGCCAAGTTTT    92567       AAGAA
                                  GGAACTT    GTATGGAGTT
                                  |||||||    ||||||||||
                                  TTTTGAA    CGTGTCTCAA
                                     C____
GAM856  LOC222008 3'  TGACTTTATCCTTCTTTAGGTT 94014         _   T
            TTT                     AGGAACTTAA GAAG ATGGAGTTA
                                  |||||||||| |||| |||||||||
                                  TTTTTGGATT CTTC TATTTCAGT
                                        T   C
GAM856  LOC253386 3'  ACTTCTTAAAGTTTCT      94938        _
                                  AGGAACTT AAGAAGT
                                  |||||||| |||||||
                                  TCTTTGAA TTCTTCA
                                       A
GAM856  LOC253386 5'  CCGGATTATTTGGGTTCCT   94939          A  A
                                  AGGAACTTAAG AGT TGG
                                  |||||||||| ||| |||
                                  TCCTTGGGTTT TTA GCC
                                        A  G
GAM856  LOC253912 3'  TAACTCCTCTAAACTTCAAGTT 97361       AA    AT___
            CCT                     GAACTT  GAAGT    GGAGTTA
                                  ||||||  |||||    |||||||
                                  CTTGAA  CTTCA    CCTCAAT
                                     __     AATCT
GAM856  LOC254082 5'  TGATTACATTTTTGGAGTTCCT 97205        A     ATGG
                                  AGGAACTT AGAAGT    AGTTA
                                  |||||||| ||||||    |||||
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                                TCCTTGAG TTTTTA    TTAGT
                                    G     CA__
GAM856   LOC254249 5'  ATGCTTCTTGGCTTCCT     95445       C
                                AGGAA TTAAGAAGTAT
                                ||||| ||||||||||
                                TCCTT GGTTCTTCGTA
                                   C
GAM856   LOC255465 5'  ATTTGTTCTTGCTTTTTGAGTT 97280              T   GTTA
           CCT                    AGGAACTTAAGAAGTA GGA
                                ||||||||||||||| |||
                                TCCTTGAGTTTTTCGT CTT
                                          T   GTTTAG
GAM856   LOC255533 5'  TAACTTTGTACTTATAGTTT   96980      TAAG    TG
                                GAACT    AAGTA  GAGTTA
                                |||||    |||||  ||||||
                                TTTGA    TTCAT  TTCAAT
                                   TA__     GT
GAM856   LOC256306 3'  GGCTTTGTGCGGTCTCCT    96695      _   TAAGAA   TG
                                AGGA ACT      GTA  GAGTT
                                |||| |||      |||  |||||
                                TCCT TGG      CGT  TTCGG
                                  C  _______   GT
GAM856   LOC256530 3'  TAATGGGGGCTTCTGGGTTTCT 96816          A    ATGGA
                                AGGAACTTA GAAGT     GTTA
                                |||||||| |||||     ||||
                                TCTTTGGGT CTTCG     TAAT
                                     _    GGGG_
GAM856   LOC256642 3'  TAACTCGAAGTTTTCTTAAGTT 96308             TATG_
           TCT                    AGGAACTTAAGAAG     GAGTTA
                                ||||||||||||||     ||||||
                                TCTTTGAATTCTTT     CTCAAT
                                       TGAAG
GAM856   LOC256777 3'  ATATTTATTGGGTTCCT     95136          G
                                AGGAACTTAA AAGTAT
                                |||||||||| ||||||
                                TCCTTGGGTT TTTATA
                                     A
GAM856   LOC256905 3'  TAACAAGGATGTATTTTGTGAG 96870        A       GA___
           TTTCT                   AACTTA GAAGTATG     GTTA
                                |||||| ||||||||     ||||
                                TTGAGT TTTTATGT     CAAT
                                   G       AGGAA
GAM856   LOC256974 5'  TGACTCTATGTGCCCCATTCCT 97248       CTTAAGAAG
                                AGGAA        TATGGAGTTA
                                |||||        ||||||||||
                                TCCTT        GTATCTCAGT
                                  ACCCCGT__
GAM856   LOC257495 5'  TCCCAAATATTCTTTAAGTTCT 97727          GA    ___   GTTA
           T                    GGAACTTAA  AGTAT   GGA
                                |||||||||  |||||   |||
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                                TCTTGAATT  TTATA   CCT
                                     TC     AAC      A
GAM856  LOC257495 5'  TTGTAGTCATATTTCTTAGTTC 97729        T         AGTTA
              TT                   AGGAACT AAGAAGTATGG
                                   ||||||| ||||||||||
                                   TTCTTGA TTCTTTATACT
                                      _         GATGTTT
GAM856  LOC257576 5'  TCCCAAATATTCTTTAAGTTCT 97884         GA    ___   GTTA
              T                    GGAACTTAA  AGTAT   GGA
                                   |||||||||  |||||   |||
                                   TCTTGAATT  TTATA   CCT
                                        TC     AAC      A
GAM856  LOC257576 5'  TTGTAGTCATATTTCTTAGTTC 97886        T         AGTTA
              TT                   AGGAACT AAGAAGTATGG
                                   ||||||| ||||||||||
                                   TTCTTGA TTCTTTATACT
                                      _         GATGTTT
GAM856  LOC51071  3'  TAACTTTGTGAAGAGTTTCT   31978        AAGAAG  TG
                                   AGGAACTT     TA  GAGTTA
                                   ||||||||     ||  ||||||
                                   TCTTTGAG     GT  TTCAAT
                                        AA____  GT
GAM856  LOC51097  3'  TAATTCTATATCTGTGACTAGG 32051       AGA__  _
              TTTTT                  AACTTA     AG TATGGAGTTA
                                   ||||||     || ||||||||||
                                   TTGGAT     TC ATATCTTAAT
                                      CAGTG  T
GAM856  LOC51292  3'  TAACTCTGTACTTCTCTATCT  33413     ACTTA
                                   GGA     AGAAGTATGGAGTTA
                                   |||     ||||||||||||||
                                   TCT     TCTTCATGTCTCAAT
                                     ATC__
GAM856  LOC81569  3'  GTATTTTTTAGGTTCT      61986
                                   GGAACTTAAGAAGTAT
                                   ||||||||||||||||
                                   TCTTGGATTTTTTATG

GAM856  LOC90624  3'  TAGCTTCATATTTAAATTTC   63607      CTTAAG
                                   GGAA      AAGTATGGAGTTA
                                   ||||      ||||||||||||
                                   CTTT      TTTATACTTCGAT
                                     AAA___
GAM856  LOC91431  5'  TGACAGAGTACTTCTTGGGCTT 56926      A          GGA
              CT                     AGGA CTTAAGAAGTAT   GTTA
                                   |||| ||||||||||||   ||||
                                   TCTT GGGTTCTTCATG   CAGT
                                     C          AGA
GAM856  LOC91796  3'  GCTTCCTTGGGTTCCT      67212          _
                                   AGGAACTTAAG AAGT
                                   |||||||||| ||||
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                                TCCTTGGGTTC TTCG
                                      C
GAM856  LOC92606  3'  TCTGTGTTTTTAAGTTTTT   69991          G
                                AGGAACTTAAGAA TATGGA
                                |||||||||||| ||||||
                                TTTTTGAATTTTT GTGTCT
                                      _
GAM857  ARNT2     3'  AAACAACCCGTGCATCCCTGC  29450    A   TTTTA
                                GTA GGAT    GGGTTGTTT
                                ||| ||||    |||||||||
                                CGT CCTA    CCCAACAAA
                                  C   CGTG_
GAM857  LCT       3'  AACCGTAAAAATCCTT     9697          G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
                                TTCCTAAAAAT CCAA
                                      G
GAM857  RPL15     3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM857  FBXO30    3'  AACTAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                  G        AA
GAM857  KIAA0494  3'  AACAACCCTTACTTAC      28736      GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM857  PRO0641   5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                   ___    C
GAM857  SMT3H2    3'  AACAACATAAAAATCCTTGC   22670          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM857  LOC120103 3'  AACCTATGAAAAATCCTTGC   74002          A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
                                CGTTCCTAAAAA   TCCAA
                                      GTA
GAM857  LOC129831 3'  AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
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                                CCTG  AA CCCAACAAA
                                  T_  C
GAM857  LOC133088 5'  AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                        GTA GGATTTTT     TTGTTT
                                   ||| ||||||||     ||||||
                                   CGT CCTAAAAA     AACAAA
                                     C       GATAA
GAM857  LOC148089 3'  GGCCCTAAAAATTCCTAC     78637     A
                                   GTA GGATTTTTAGGGTT
                                   ||| ||||||||||||||
                                   CAT CTTAAAAATCCCGG
                                     C
GAM857  LOC154547 3'  AACAACATAAAAATCCTTGC   76050           GG
                                   GTAAGGATTTTTA  GTTGTT
                                   ||||||||||||  ||||||
                                   CGTTCCTAAAAAT  CAACAA
                                           A_
GAM857  LOC158104 3'  ACAGCCAAAAATCCTTA      60313           AG
                                   TAAGGATTTTT  GGTTGT
                                   ||||||||||  ||||||
                                   ATTCCTAAAAA  CCGACA
                                           __
GAM857  LOC205880 5'  AAACAACCATCATCCTGAC    90709     A     TTTTAG
                                   GT AGGAT     GGTTGTTT
                                   || |||||     ||||||||
                                   CA TCCTA     CCAACAAA
                                    G    CTA___
GAM857  LOC221561 3'  AACAACATAAAAATCCTTGC   92130           GG
                                   GTAAGGATTTTTA  GTTGTT
                                   ||||||||||||  ||||||
                                   CGTTCCTAAAAAT  CAACAA
                                           A_
GAM857  LOC257591 3'  AACAACATAAAAATCCTTGC   97840           GG
                                   GTAAGGATTTTTA  GTTGTT
                                   ||||||||||||  ||||||
                                   CGTTCCTAAAAAT  CAACAA
                                           A_
GAM857  LOC51145  3'  AGCTAAAATCCTTAC        32393           TAG
                                   GTAAGGATTTT   GGTT
                                   ||||||||||   ||||
                                   CATTCCTAAAA   TCGA
                                           ___
GAM858  FZD4      3'  TAATTTATCACTGTACAAA    24148      C     A
                                   TTTG ACAGT ATAAGTTG
                                   |||| ||||| ||||||||
                                   AAAC TGTCA TATTTAAT
                                     A     C
GAM858  RAP1B     3'  GGTCATTATTATTGTACAAA   31600      C        GT
                                   TTTG ACAGTAATAA  TGACT
                                   |||| ||||||||||  |||||
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                                AAAC TGTTATTATT  ACTGG
                                  A        __
GAM858  STAC     3'  AGCAATCTCTGTGCAAA     11987         TAATAA    A
                                TTTGCACAG     GTTG CT
                                |||||||||     |||| ||
                                AAACGTGTC     TAAC GA
                                    TC_____   _
GAM858  VNN1     3'  CAGCCATGCACTGTGCAAA    16240          AATAA
                                TTTGCACAGT    GTTG
                                ||||||||||    ||||
                                AAACGTGTCA    CGAC
                                    CGTAC
GAM858  XRCC4    3'  TGAATTGAAACCATTGTGCAAA 42356          AATAAG TG C
                                TTTGCACAGT     T  A TCA
                                ||||||||||     |  | |||
                                AAACGTGTTA     A  T AGT
                                    CCAA__ GT A
GAM858  XRCC4    3'  TGAATTGAAACCATTGTGCAAA 42586          AATAAG TG C
                                TTTGCACAGT     T  A TCA
                                ||||||||||     |  | |||
                                AAACGTGTTA     A  T AGT
                                    CCAA__ GT A
GAM858  XRCC4    3'  TGAATTGAAACCATTGTGCAAA 12686          AATAAG TG C
                                TTTGCACAGT     T  A TCA
                                ||||||||||     |  | |||
                                AAACGTGTTA     A  T AGT
                                    CCAA__ GT A
GAM858  HSPC052  3'  TAATTTATTACTGCAAA     26260       CA
                                TTTGCA  GTAATAAGTTG
                                ||||||  ||||||||||
                                AAACGT  CATTATTTAAT
                                  __
GAM858  KIAA0876 3'  GTCTTACTCTGTGCAAA     64681         TAATA   T_
                                TTTGCACAG    AGT  GAC
                                |||||||||    |||  |||
                                AAACGTGTC    TCA  CTG
                                    _____  TT
GAM858  WDR7     3'  TCATTTATTACATGCAAA     30961       CA        T
                                TTTGCA  GTAATAAGT GA
                                ||||||  ||||||||| ||
                                AAACGT  CATTATTTA CT
                                  A_       _
GAM858  ZNF237   3'  CAGCTAAAATCACTTGTGCAAA 26473         _  A  A__
                                TTTGCACA GT AT   AGTTG
                                ||||||||| || ||   |||||
                                AAACGTGT CA TA   TCGAC
                                    T  C  AAA
GAM858  LOC153416 3'  GGTCATTATTATTGTACAAA   60540      C         GT
                                TTTG ACAGTAATAA  TGACT
                                ||||  ||||||||||  |||||
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                                AAAC TGTTATTATT  ACTGG
                                  A        __
GAM858  LOC154007 3'  AGTCAACTGCCATGCAGA    81013       CA  AATA
                                TTTGCA  GT    AGTTGACT
                                ||||||  ||    ||||||||
                                AGACGT  CG    TCAACTGA
                                   AC  ____
GAM858  LOC158237 5'  CAAATCTTTGCTGTGCAAA    60453           TAAG
                                TTTGCACAGTAA    TTG
                                ||||||||||||    |||
                                AAACGTGTCGTT    AAC
                                       TCTA
GAM858  LOC158427 3'  AGCCATTTGCCCACTGTGCAA  57676         AA_    T A
                                TTGCACAGT   TAAGT G CT
                                |||||||||   ||||| | ||
                                AACGTGTCA   GTTTA C GA
                                     CCC    _ C
GAM858  LOC220790 3'  GGTCATTATTATTGTACAAA   91233     C        GT
                                TTTG ACAGTAATAA  TGACT
                                |||| ||||||||||  |||||
                                AAAC TGTTATTATT  ACTGG
                                  A        __
GAM858  LOC56287  5'  TGAGTCAACCTGGTTAAGTACA 39031     C  AG    AA_
          AA                      TTTG AC  TAAT   GTTGACTCA
                                |||| ||  ||||   |||||||||
                                AAAC TG  ATTG   CAACTGAGT
                                  A  A_    GTC
GAM858  LOC90936  5'  CGAGTATTACTGTGCGAA    64434           AG
                                TTTGCACAGTAATA  TTG
                                ||||||||||||||  |||
                                AAGCGTGTCATTAT  AGC
                                       G_
GAM858  LOC91263  3'  AGTCAACTCATTAGCA      65376     ACAG    A
                                TGC    TAAT AGTTGACT
                                |||    |||| ||||||||
                                ACG    ATTA TCAACTGA
                                  _____    C
GAM859  ATP11B    3'  AGAGGCAAATCAACCCTAGG   80313    A  T    CACA   A
                                CC AG GTTGA    GCC TCT
                                || || |||||    ||| |||
                                GG TC CAACT    CGG AGA
                                 A  C    AAA_  _
GAM859  ATRN      3'  ATGGCTGTGCGGTGCGGGA    57795     AA TG   A
                                TCCC  G  TTG CACAGCCAT
                                ||||  |  ||| |||||||||
                                AGGG  C  GGC GTGTCGGTA
                                   __ GT   _
GAM859  FLG       3'  AGATGGCTCCAGACACCCCGGA 70876     CAA    GACAC
                                TCC   GTGTT    AGCCATCT
                                |||   |||||    ||||||||
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                                AGG   CACAG    TCGGTAGA
                                  CCC    ACC__
GAM859  GYG     3'  AGATGGCTGTATCAGTTCTT   14688    TG   C
                                AAG  TTGA ACAGCCATCT
                                |||  |||| ||||||||||
                                TTC  GACT TGTCGGTAGA
                                  TT   A
GAM859  H4F2    3'  GTGGCTGCAAACACTTGAGA   59357    C      GACA
                                TC CAAGTGTT   CAGCCAT
                                || ||||||||   |||||||
                                AG GTTCACAA   GTCGGTG
                                 A       AC__
GAM859  HNRPH1   3'  AGACGCAATACCAATACTTAGG 18628     C       ACACA  CA
            A                    TCC AAGTGTTG    GC  TCT
                                ||| ||||||||    ||  |||
                                AGG TTCATAAC    CG  AGA
                                  A       CATAA  C_
GAM859  IPP     3'  GATGGCTTGAACTCGGGA    19726     A   GTTGACAC
                                TCCC AGT       AGCCATC
                                |||| |||       |||||||
                                AGGG TCA       TCGGTAG
                                  C   AGT_____
GAM859  JTB     5'  AGATGGCTGCGTCGGGGGCGGG 21958     AAGTG    A
            A                    TCCC    TTGAC CAGCCATCT
                                ||||    ||||| |||||||||
                                AGGG    GGCTG GTCGGTAGA
                                  CGGG_    C
GAM859  LZTR1    3'  GGATATGTCAGCACCTGG    22242     A       CAG
                                CCA GTGTTGACA   CC
                                ||| |||||||||   ||
                                GGT CACGACTGT   GG
                                  C        ATA
GAM859  MUCDHL   3'  AGATGGCTACGTCTGCATT    48362      T   AC
                                AGTGT GAC  AGCCATCT
                                ||||| |||  ||||||||
                                TTACG CTG  TCGGTAGA
                                   T   CA
GAM859  MUCDHL   3'  AGATGGCTACGTCTGCATT    87297      T   AC
                                AGTGT GAC  AGCCATCT
                                ||||| |||  ||||||||
                                TTACG CTG  TCGGTAGA
                                   T   CA
GAM859  NFE2L1   3'  CTGTGTGAACACTTGGGA    12172          G
                                TCCCAAGTGTT ACACAG
                                |||||||||| ||||||
                                AGGGTTCACAA TGTGTC
                                       G
GAM859  PFKL    5'  GATGGCTGTGACCCTGGG    10518      A T  TGA
                                CCCA G GT   CACAGCCATC
                                |||| | ||   ||||||||||
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                                GGGT C CA   GTGTCGGTAG
                                  _ C ___
GAM859  PKIA     3'  ATGGCTGTGCTGCATTGCAGGA 22380     CA_    TGA
                                TCC   AGTGT   CACAGCCAT
                                |||   |||||   |||||||||
                                AGG   TTACG   GTGTCGGTA
                                  ACG    TC_
GAM859  PLGL     3'  ATGACTATGTTTGGGA      10635      AGTGTT   C  C
                                TCCCA     GACA AG CAT
                                |||||     |||| || |||
                                AGGGT     TTGT TC GTA
                                  _______   A  A
GAM859  SCNN1G   3'  CTGTGTCACTTTGCTTGGGG   6431          T__
                                TCCCAAGTG   TGACACAG
                                |||||||||   ||||||||
                                GGGGTTCGT   ACTGTGTC
                                     TTC
GAM859  TEM1     3'  ATGGGGTGTCAACCTT      39877     T      AG
                                AAG GTTGACAC  CCAT
                                ||| ||||||||  ||||
                                TTC CAACTGTG  GGTA
                                  _       G_
GAM859  APOL4    3'  GGCCAACACTTAGGG       47627     _      ACACA
                                CCC AAGTGTTG    GCC
                                ||| ||||||||    |||
                                GGG TTCACAAC    CGG
                                  A       _____
GAM859  C5orf5   3'  GCCATGTCAGTATGTAGGA   33467     CAA       CA
                                TCC   GTGTTGACA  GC
                                |||   |||||||||  ||
                                AGG   TATGACTGT  CG
                                  ATG       AC
GAM859  CCR8     3'  GTTGTTGCCAACACTT      17783         A  _
                                AAGTGTTG CA CAGC
                                |||||||| || ||||
                                TTCACAAC GT GTTG
                                     C  T
GAM859  EVI5     3'  AGATGAGTATCAACACTT    18988          C  AGC
                                AAGTGTTGA AC   CATCT
                                |||||||||  ||   |||||
                                TTCACAACT TG   GTAGA
                                     A  A__
GAM859  FLJ10704 3'  ATGGCTGTTGCGTATTGG    36450      GTGT  AC
                                CCAA    TG  ACAGCCAT
                                ||||    ||  ||||||||
                                GGTT    GC  TGTCGGTA
                                  AT__   GT
GAM859  FLJ12783 3'  AGACAGCCTCCAAGGTCAACAC 48674           ACA_____  CA
           TTGG                   CCAAGTGTTGAC      GC  TCT
                                ||||||||||||      ||  |||
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                                GGTTCACAACTG      CG  AGA
                                      GAACCTC  AC
GAM859  FLJ13055  3'  AGATGGCTAGAAGGACATTTAG 42708     C      GACAC
            GA                  TCC AAGTGTT     AGCCATCT
                                ||| |||||||     ||||||||
                                AGG TTTACAG     TCGGTAGA
                                  A      GAAGA
GAM859  FLJ14547  3'  GGCACCAAAACTTGGGA     51435         G   ACACA
                                TCCCAAGT TTG     GCC
                                |||||||| |||     |||
                                AGGGTTCA AAC     CGG
                                    A   CA___
GAM859  FLJ20004  3'  AGATGACATTTGAGTCAACACC 95284     A       A   C___
            TGG                   CCA GTGTTGAC CAG    CATCT
                                ||| |||||||| |||    |||||
                                GGT CACAACTG GTT    GTAGA
                                  C       A   TACA
GAM859  FLJ20651  5'  GACAGCTGTTACCAGGGA    35496     AA   TTGAC    CA
                                TCCC  GTG    ACAGC  TC
                                ||||  |||    |||||  ||
                                AGGG  CAT    TGTCG  AG
                                  AC  ______    AC
GAM859  FLJ22833  3'  AGATAGGAGCAACACTT     43097         ACACAG  _
                                AAGTGTTG     CC ATCT
                                ||||||||     || ||||
                                TTCACAAC     GG TAGA
                                    GA____  A
GAM859  FLJ23309  3'  AGATGGCTATGTAGCTTG    46060      GTTG   C
                                CAAGT    ACA AGCCATCT
                                |||||    ||| ||||||||
                                GTTCG    TGT TCGGTAGA
                                  A___   A
GAM859  FLJ23548  5'  AGATGGCTATGATATCTGGGA  44746       AG   TGA  C
                                TCCCA  TGT   CA AGCCATCT
                                |||||  |||   || ||||||||
                                AGGGT  ATA   GT TCGGTAGA
                                  CT   ___  A
GAM859  GT650     3'  AGATGGCTACATCCCTACT    53450     TT  CAC
                                AGTG  GA   AGCCATCT
                                ||||  ||   ||||||||
                                TCAT  CT   TCGGTAGA
                                  CC  ACA
GAM859  KIAA0140  5'  AGATGGCTGATACCCACCCTGG 27803      A_   TTGACA
            GA                  TCCCA  GTG     CAGCCATCT
                                |||||  |||     |||||||||
                                AGGGT  CAC     GTCGGTAGA
                                  CC   CCATA_
GAM859  KIAA0894  3'  AGATGGCCTGGACAC      29701       GACA  _
                                GTGTT    CAG CCATCT
                                |||||    ||| ||||||
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                                CACAG   GTC GGTAGA
                                  _____  C
GAM859  KIAA0998  3'  TGTTCTGTGTCAGCACCCAGGA 30587     CAA          C_
                                TCC   GTGTTGACACAG  CA
                                |||   ||||||||||||  ||
                                AGG   CACGACTGTGTC  GT
                                  ACC          TT
GAM859  KIAA1165  3'  AGATGAAAACAACACTTGTGA  67403    C       ACACAGC
                                TC CAAGTGTTG      CATCT
                                || |||||||||      |||||
                                AG GTTCACAAC      GTAGA
                                 T       AAAA___
GAM859  KIAA1958  3'  GGATGGCACCAATACTTGGGA  81907           ACACA
                                TCCCAAGTGTTG    GCCATCT
                                ||||||||||||    |||||||
                                AGGGTTCATAAC    CGGTAGG
                                       CA___
GAM859  SEC15B    3'  AGATGCTTCTCACCAACACTTT 66683    CC       ACAC__   C
           AGA                    TC  AAGTGTTG     AGC ATCT
                                ||  ||||||||     ||| ||||
                                AG  TTCACAAC     TCG TAGA
                                 AT       CACTCT  _
GAM859  STHM      3'  AGATGACTCTCAGAACACTGGG 21296      A    GACAC  C
           A                     TCCCA GTGTT    AG CATCT
                                |||||  |||||    || |||||
                                AGGGT CACAA    TC GTAGA
                                  _    GACTC  A
GAM859  USP24     3'  AGATGGAAGGGCCAGCACTT   91151        ACACAG
                                AAGTGTTG     CCATCT
                                ||||||||     ||||||
                                TTCACGAC     GGTAGA
                                     CGGGAA
GAM859  ZIM2      3'  CTGCGCCAACACTTTGGA    31085     C       ACA
                                TCC AAGTGTTG   CAG
                                ||| ||||||||   |||
                                AGG TTCACAAC   GTC
                                  T       CGC
GAM859  LOC129563 3'  GCCGATGTCAACACCTGG    74880     A       CA_
                                CCA GTGTTGACA   GC
                                ||| |||||||||   ||
                                GGT CACAACTGT   CG
                                  C        AGC
GAM859  LOC132338 5'  AGATGGCTACTTTCACCAGGA  75886     CAA   TTGACAC
                                TCC   GTG      AGCCATCT
                                |||   |||      ||||||||
                                AGG   CAC      TCGGTAGA
                                  AC_   TTTCA__
GAM859  LOC145988 5'  ATGGCCTGCTGTCAACACCCAG 77606     CAA       _  _
           GA                     TCC   GTGTTGACA CAG CCAT
                                |||   ||||||||| ||| ||||
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                                AGG   CACAACTGT GTC GGTA
                                  ACC       C   C
GAM859   LOC220883 3'  AGACGGCTGTGAATCCTGTGG  91258    _  TG  GA     A
                                CCA AG  TT  CACAGCC TCT
                                ||| ||  ||  ||||||| |||
                                GGT TC  AA  GTGTCGG AGA
                                  G  CT  __      C
GAM859   LOC256997 5'  GTGGCTGCCTACACTTGG    95336        TGACA
                                CCAAGTGT    CAGCCAT
                                ||||||||    |||||||
                                GGTTCACA    GTCGGTG
                                     TCC__
GAM859   LOC257358 3'  AGATGGCTATGGCTCTTGTGA  97097    C    T  TGA  C
                                TC CAAG GT   CA AGCCATCT
                                || |||| ||   || ||||||||
                                AG GTTC CG   GT TCGGTAGA
                                 T    T ___  A
GAM859   LOC90917  3'  AGAGGGTATCAACATTT     64333        CACA   A
                                AAGTGTTGA    GCC TCT
                                |||||||||    ||| |||
                                TTTACAACT    TGG AGA
                                     A___   G
GAM860   ADH4     3'  TGCACATGTACCCTGGA     5411      CTG  ACTCTC
                                TCC   AG     ACATGTGCA
                                |||   ||     |||||||||
                                AGG   TC     TGTACACGT
                                  ___  CCA___
GAM860   ADORA3   5'  TGCACATGGACCTCTGGGA   5443      T   ACTC  A
                                TCCC GAG    TC CATGTGCA
                                |||| |||    || ||||||||
                                AGGG CTC    AG GTACACGT
                                  T   C___  _
GAM860   COX7A2L   3'  CTGTGCTGAGGACCTCAGGGA  16349        AC    CAT TG
                                TCCCTGAG  TCTCA   G  CAG
                                ||||||||  |||||   |  |||
                                AGGGACTC  GGAGT   C  GTC
                                     CA     ___ GT
GAM860   DLG5     5'  CTGCACATCAACCTCAGTGGA  82914     _    ACTCTCAC
                                TCC CTGAG       ATGTGCAG
                                ||| |||||       ||||||||
                                AGG GACTC       TACACGTC
                                  T    CAAC_____
GAM860   ERBB2    3'  GTACTGAAAGCCTTAGGGA    15474        A  C   CAT
                                TCCCTGAG CT TCA   GTGC
                                |||||||| || |||   ||||
                                AGGGATTC GA AGT   CATG
                                     C  A   ___
GAM860   FAT2     3'  CACATGTGGGTGCCCATGGA   7543      C  AGACT
                                TCC TG    CTCACATGTG
                                ||| ||    ||||||||||
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                                AGG AC    GGGTGTACAC
                                  T  CCGT_
GAM860  FGF5    3'  TATTTGAAAGTCTCAGGGG   15548         C   C
                                TCCCTGAGACT TCA ATG
                                |||||||||| ||| |||
                                GGGGACTCTGA AGT TAT
                                      A   T
GAM860  FGF5    3'  TATTTGAAAGTCTCAGGGG   52493         C   C
                                TCCCTGAGACT TCA ATG
                                |||||||||| ||| |||
                                GGGGACTCTGA AGT TAT
                                      A   T
GAM860  GAD1    3'  CTGCACACATGGTTTCCAAGGG 25571     __     CTCACA
                                CCCT  GAGACT     TGTGCAG
                                ||||  ||||||     |||||||
                                GGGA  CTTTGG     ACACGTC
                                  AC     TAC___
GAM860  ID1     3'  CTGCACACCTACTAGTCACCAG 70031    C  A_   CTCACA
            AGA                   TC CTG  GACT     TGTGCAG
                                || |||  ||||     |||||||
                                AG GAC  CTGA     ACACGTC
                                 A   CA    TCATCC
GAM860  LIMD1   3'  CTGCAAGGCAAGTCTCAGG   26460         CTCACATG
                                CCTGAGACT       TGCAG
                                |||||||||       |||||
                                GGACTCTGA       ACGTC
                                      ACGGA___
GAM860  NHLH1   5'  TACCCCTGAGAGTCTAG    18804    G       CAT
                                CT AGACTCTCA   GTG
                                || |||||||||   |||
                                GA TCTGAGAGT   CAT
                                 _       CCC
GAM860  NTF5    3'  CTGGATGCTGAGAGACCTCAGG 20518        A_     CAT  G
            GA                    TCCCTGAG  CTCTCA   GT CAG
                                |||||||  ||||||   || |||
                                AGGGACTC  GAGAGT   TA GTC
                                     CA     CG_  G
GAM860  PDE7A   3'  CTGCACATGCGAGAAAAAGGTG 65521    _ GAGAC   A
            GA                    TCC CT    TCTC CATGTGCAG
                                ||| ||    |||| |||||||||
                                AGG GG    AGAG GTACACGTC
                                  T  AAAA_   C
GAM860  PPP1R12B 5'  CTGATTCTGAGAGTTCAGAGA  49469    C    A    CAT  G
                                TC CTGAG CTCTCA   GT CAG
                                || ||||| ||||||   || |||
                                AG GACTT GAGAGT   TA GTC
                                 A    _     CT_ _
GAM860  PPP1R12B 5'  CTGATTCTGAGAGTTCAGAGA  49480    C    A    CAT  G
                                TC CTGAG CTCTCA   GT CAG
                                || ||||| ||||||   || |||
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                                AG GACTT GAGAGT   TA GTC
                                 A    _     CT_ _
GAM860  PRX      3'  TGCCAAAAGTCTCAGAGA    40540    C      CTCACA  T
                                TC CTGAGACT     TG GCA
                                || ||||||||     || |||
                                AG GACTCTGA     AC CGT
                                 A       AA____  _
GAM860  SHANK2   3'  CTGCACCAGCAAACTCAGGGA  55736        ACTCTCACAT
                                TCCCTGAG        GTGCAG
                                ||||||||        ||||||
                                AGGGACTC        CACGTC
                                     AAACGAC___
GAM860  DKFZP434N178 3'  CTGTGCAGGACGGGAGTCTCAG 71904    C        ACA_  TG
             AGA                   TC CTGAGACTCTC    TG  CAG
                                || ||||||||||    ||  |||
                                AG GACTCTGAGGG    AC  GTC
                                 A          CAGG  GT
GAM860  FLJ12592  5'  TATAGTGAAAACTCAGGGA   49701        ACTC    A
                                TCCCTGAG    TCAC TGTG
                                ||||||||    |||| ||||
                                AGGGACTC    AGTG ATAT
                                     AAA_   _
GAM860  FLJ12800  5'  TGCGGAAAAGTTCAGGGA    43238        ACTC  ACATG
                                TCCCTGAG    TC     TGCA
                                ||||||||    ||     ||||
                                AGGGACTT    AG     GCGT
                                     GAAA  _____
GAM860  FLJ13189  3'  CACAAGAATTCAGGGA      45984        AC   CACA
                                TCCCTGAG  TCT    TGTG
                                ||||||||  |||    ||||
                                AGGGACTT  AGA    ACAC
                                     A_   ____
GAM860  GT650     3'  CTGCATTTCTAAGGAGTCTCAG 53453           CACAT_
             GGA                    TCCCTGAGACTCT     GTGCAG
                                ||||||||||||      ||||||
                                AGGGACTCTGAGG     TACGTC
                                       AATCTT
GAM860  KIAA1223  3'  CTGAGGCATGAAAATTCTCAGG 71144         CTCTCA    G_
             GA                     TCCCTGAGA     CATGT  CAG
                                |||||||||      |||||  |||
                                AGGGACTCT     GTACG  GTC
                                     TAAAA_    GA
GAM860  LGALS8    3'  TACAGAAAGTTTCAGG      21451         C  ACA
                                CCTGAGACT TC   TGTG
                                ||||||||| ||   ||||
                                GGACTTTGA AG   ACAT
                                     A  ___
GAM860  LIN-28    3'  GTACATGAGCAATCTCAGGGA  45150         CT_   CA
                                TCCCTGAGA   CTCA  TGTGC
                                |||||||||   ||||  |||||
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                                AGGGACTCT  GAGT  ACATG
                                     AAC   __
GAM860  MSTP043   3'  TATGTGAGAACCTAGG     49222     G  AC
                                CCT AG  TCTCACATG
                                ||| ||  |||||||||
                                GGA TC  AGAGTGTAT
                                  _  CA
GAM860  SSH2      3'  CACATGTGACTTTCTAG     62200    G   CTC
                                CT AGA   TCACATGTG
                                || |||   |||||||||
                                GA TCT   AGTGTACAC
                                  _  TTC
GAM860  TMLHE     3'  CACGAAAAGGGTCTCAGGGA  36513          CACA
                                TCCCTGAGACTCT   TGTG
                                ||||||||||||   ||||
                                AGGGACTCTGGGA   GCAC
                                       AAA_
GAM860  LOC138389 3'  CACTCTGAAAATCTCAGGG   76219       CTC   CAT
                                CCCTGAGA   TCA   GTG
                                ||||||||   |||   |||
                                GGGACTCT   AGT   CAC
                                     AAA   CT_
GAM860  LOC146512 3'  TGCACATGTATCCTGGA     77942     CT  GACTCTC
                                TCC  GA      ACATGTGCA
                                |||  ||      |||||||||
                                AGG  CT      TGTACACGT
                                  TC  A_______
GAM860  LOC149157 3'  TGCACATGTATCCCGG      79203     A  CTCTC
                                CTG GA     ACATGTGCA
                                ||| ||     |||||||||
                                GGC CT     TGTACACGT
                                  C  A____
GAM860  LOC152794 3'  TGCACATGGATCCCAG      80685     A  CTC  A
                                CTG GA   TC CATGTGCA
                                ||| ||   || ||||||||
                                GAC CT   AG GTACACGT
                                  C  ___  _
GAM860  LOC157623 5'  TGTGAGAATTCAAGGA      81502     C    AC
                                TCC TGAG  TCTCACA
                                ||| ||||  |||||||
                                AGG ACTT  AGAGTGT
                                  A   A_
GAM860  LOC159121 5'  CACACACAAGAGCTCAGGGA  86990        A   CACA
                                TCCCTGAG CTCT   TGTG
                                |||||||| ||||   ||||
                                AGGGACTC GAGA   ACAC
                                     _   ACAC
GAM860  LOC253291 5'  CACTTTGTAAGAGTCTC     96983        C   T_
                                GAGACTCT ACA  GTG
                                |||||||| |||  |||
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                                CTCTGAGA TGT  CAC
                                     A   TT
GAM860  LOC90936  5'  CACATCCCGAGAGTTTCAG   64431          AC_
                                CTGAGACTCTC   ATGTG
                                ||||||||||   |||||
                                GACTTTGAGAG   TACAC
                                      CCC
GAM861  ALDH1B1   3'  AAACATCCCAAATGTCCATC   5483      AAA   C
                                GGTG   ATT GGGATGTTT
                                ||||   ||| |||||||||
                                CTAC   TAA CCCTACAAA
                                  CTG   A
GAM861  NDN       3'  ACAACCCCACCGTGA       10190        AAAATTC   A
                                TCACGGTG      GGG TGT
                                ||||||||      ||| |||
                                AGTGCCAC      CCC ACA
                                   _______   A
GAM861  RFX2      3'  CCAATTTTCACCATGA      5306      C        C
                                TCA GGTGAAAATT GG
                                ||| ||||||||||  ||
                                AGT CCACTTTTAA CC
                                  A        _
GAM861  C7orf3    5'  AAACTGATTGGAACTTTCACCG 71476         A   G  AT_
                                CGGTGAAA TTC GG   GTTT
                                |||||||| ||| ||   ||||
                                GCCACTTT AAG TT   CAAA
                                     C   G  AGT
GAM861  FLJ13920  3'  TCGAAATTTCCATCGTGA    44656         _   A
                                TCACGGTG AAA TTCGG
                                |||||||| ||| |||||
                                AGTGCTAC TTT AAGCT
                                     C   A
GAM861  GW112     3'  AAACATTTTCTCTTTCACC   21182        ATTC
                                GGTGAAA    GGGATGTTT
                                |||||||    |||||||||
                                CCACTTT    TTTTACAAA
                                     CTC_
GAM861  KIAA1508  3'  AAACATCCATGGATTTCCC   61870    T   A   _
                                GG GAAA TTCG GGATGTTT
                                ||  |||| |||| ||||||||
                                CC CTTT AGGT CCTACAAA
                                  _   _   A
GAM861  KIAA1872  3'  AAACATTCTGCCCCCACC    62916     AAAATT
                                GGTG     CGGGATGTTT
                                ||||     ||||||||||
                                CCAC     GTCTTACAAA
                                  CCCC__
GAM861  LOC195977 3'  AACACCTGCCCCACTGTGA   87534         AAAATT   A
                                TCACGGTG     CGGG TGTT
                                ||||||||     |||| ||||
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                                AGTGTCAC     GTCC ACAA
                                     CCC___   _
GAM862  ABCB10   3'  ATGAACTGCTAGGTATTATT  23886        AG   A
                                AATAATAC  GGTA GTTCAT
                                ||||||||  |||| ||||||
                                TTATTATG  TCGT CAAGTA
                                     GA   _
GAM862  BPAG1    3'  GCACCTGTATCATTGAA     31429       A     _
                                TTCAAT ATACAGG GT
                                |||||| ||||||| ||
                                AAGTTA TATGTCC CG
                                   C      A
GAM862  EML1     3'  ACCATGTATTATTGAA      59728          G
                                TTCAATAATACA GGT
                                |||||||||||| |||
                                AAGTTATTATGT CCA
                                       A
GAM862  HEM1     5'  ATGAACTTCTCAACACCATTGA 18049      AATACA   T
                                TCAAT     GGG AAGTTCAT
                                |||||     ||| ||||||||
                                AGTTA     CTC TTCAAGTA
                                   CCACAA  _
GAM862  TTC3     5'  ATCCTTATTATTGAA       12416          C
                                TTCAATAATA AGGGT
                                |||||||||| |||||
                                AAGTTATTAT TCCTA
                                                _
GAM862  FLJ10468 3'  ATGTTTATCCCTGTTTACTGAA 36144     A   T     TAAGTT
                                TTCA TAA ACAGGG     CAT
                                |||| ||| ||||||     |||
                                AAGT ATT TGTCCC     GTA
                                  C  _     TATTT_
GAM862  KIAA1280 5'  AACTTACCCAGATTGAG     69707       AATACA
                                TTCAAT     GGGTAAGTT
                                ||||||     |||||||||
                                GAGTTA     CCCATTCAA
                                   GA____
GAM862  NEUROD6  5'  TGAAAACTGATTATTGAA    42688         A   GGTAAG
                                TTCAATAAT CAG     TTCA
                                |||||||| |||     ||||
                                AAGTTATTA GTC     AAGT
                                      _  AA____
GAM862  LOC144202 5'  TGAACTGCACATTGTTGAA   76710         ACAGG   A
                                TTCAATAAT    GTA GTTCA
                                |||||||||    ||| |||||
                                AAGTTGTTA    CGT CAAGT
                                     CA___  _
GAM862  LOC221552 3'  AACTTACCTATCATTTGAA   93804       TAATACA
                                TTCAA      GGGTAAGTT
                                |||||      |||||||||
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                                AAGTT      TCCATTCAA
                                   TACTA__
GAM862  LOC257493 3'  AACTTACCTATCATTTGAA   97799      TAATACA
                                TTCAA      GGGTAAGTT
                                |||||      |||||||||
                                AAGTT      TCCATTCAA
                                   TACTA__
GAM862  LOC257609 3'  AACTTACCTATCATTTGAA   97939      TAATACA
                                TTCAA      GGGTAAGTT
                                |||||      |||||||||
                                AAGTT      TCCATTCAA
                                   TACTA__
GAM862  LOC90768  5'  ATGAACTTACTGCGCCATTTGA 63951      TAATACAG
           A                     TTCAA      GGTAAGTTCAT
                                |||||      ||||||||||
                                AAGTT      TCATTCAAGTA
                                   TACCGCG_
GAM863  BAAT    3'  GGAATGTCTCCCCCAGCTG   8114      CA   AT
                                CAGC  GGG  GACATTCC
                                ||||  |||  ||||||||
                                GTCG  CCC  CTGTAAGG
                                  AC   CT
GAM863  BAPX1   3'  AATGTGAATATCCCTGGC    6810          ___
                                GCCAGGGATG   ACATT
                                ||||||||||   |||||
                                CGGTCCCTAT   TGTAA
                                      AAG
GAM863  CDR2    5'  CGATTGGACGAAGTCCCTG   76022       GACAT
                                CAGGGAT    TCCAATCG
                                |||||||    ||||||||
                                GTCCCTG    AGGTTAGC
                                    AAGC_
GAM863  DVL3    3'  ATGCCATCCCTGCCTG      15365     C      A
                                CAG CAGGGATG CAT
                                ||| |||||||| |||
                                GTC GTCCCTAC GTA
                                  C       C
GAM863  GJB1    3'  CGATCAAAACCTTCCTTCCCTG 59970         T_  CATTCCA_
           GCT                    AGCCAGGGA  GA       ATCG
                                |||||||||  ||       ||||
                                TCGGTCCCT  CT       TAGC
                                     TC  TCCAAAAC
GAM863  GPRC5B  3'  GATTTGCCTCCCTGGCTG    32664         TGA  TTCC
                                CAGCCAGGGA   CA    AATC
                                ||||||||||   ||    ||||
                                GTCGGTCCCT   GT    TTAG
                                      CC_  _____
GAM863  TEM8    3'  CGACTCAGTGTGTCATCCCCGG 49853      A        TCCAA_
           TT                     AGCC GGGATGACAT     TCG
                                |||| ||||||||||     |||
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                                TTGG CCCTACTGTG     AGC
                                  C         TGACTC
GAM863  TTN      3'  AATCTCTCCTTGGCT       55922          T  C
                                AGCCAGGGA GA ATT
                                ||||||||| || |||
                                TCGGTTCCT CT TAA
                                      _ C
GAM863  FLJ13949 3'  TGAAATGTCATCCTCAACTG  46893     CCA         C
                                CAG   GGGATGACATT CA
                                |||   |||||||||| ||
                                GTC   TCCTACTGTAA GT
                                  AAC         A
GAM863  KIAA0450 3'  GTGTCCCCCTGGCTG       27647          AT
                                CAGCCAGGG  GACAT
                                |||||||||  |||||
                                GTCGGTCCC  CTGTG
                                      C_
GAM863  KIAA0453 3'  GTGTCACTCCCTGGCTG     69050          _
                                CAGCCAGGGA TGACAT
                                |||||||||| ||||||
                                GTCGGTCCCT ACTGTG
                                      C
GAM863  MCM10    3'  ATGTCACCCTGGCTG       37569          A
                                CAGCCAGGG TGACAT
                                ||||||||| ||||||
                                GTCGGTCCC ACTGTA
                                      _
GAM863  MGC35521 3'  GGGCCATCATCCCTGAATG   59010    GC       CAT
                                CA  CAGGGATGA   TCC
                                ||  |||||||||   |||
                                GT  GTCCCTACT   GGG
                                  AA        ACC
GAM863  PLPL     3'  GGGTATCCTTGGCTG       39433          ACAT
                                CAGCCAGGGATG    TCC
                                ||||||||||||    |||
                                GTCGGTTCCTAT    GGG
                                      ____
GAM863  LOC113251 3'  GAATGCCATCTCTGACT     53523    C       A
                                AG CAGGGATG CATTC
                                || |||||||| |||||
                                TC GTCTCTAC GTAAG
                                  A       C
GAM863  LOC147081 5'  ATGCATCCCTGGCTG       78239          A
                                CAGCCAGGGATG CAT
                                |||||||||||| |||
                                GTCGGTCCCTAC GTA
                                      _
GAM863  LOC151720 3'  CGATCGAGACCATCCTGGCT  80339        G   ACA   CA
                                AGCCAGG ATG   TTC  ATCG
                                ||||||| |||   |||  ||||
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                                TCGGTCC TAC   GAG  TAGC
                                   _  CA_   C_
GAM863  LOC158490 3'  ATGTCACCACCTGGCTG     81933        GA_
                                CAGCCAGG   TGACAT
                                ||||||||   ||||||
                                GTCGGTCC   ACTGTA
                                    ACC
GAM863  LOC200868 5'  ATTGGAATGCCTTG        90704       ATGA
                                CAGGG    CATTCCAAT
                                |||||    |||||||||
                                GTTCC    GTAAGGTTA
                                   _____
GAM863  LOC51162  3'  TGTGAATCCACCCCTGGCT   32522        A  AC   _
                                AGCCAGGG TG  ATTC CA
                                |||||||| ||  |||| ||
                                TCGGTCCC AC  TAAG GT
                                    C  C_    T
GAM863  LOC51162  3'  TGTGAATCCACCCCTGGCT   65820        A  AC   _
                                AGCCAGGG TG  ATTC CA
                                |||||||| ||  |||| ||
                                TCGGTCCC AC  TAAG GT
                                    C  C_    T
GAM864  DLG5     5'  CCCCCAGCACCACTGTGAGCTC 82913           TTCTAG_
          CAT                    ATGGAGCTCACA      TGGGGG
                                ||||||||||||      ||||||
                                TACCTCGAGTGT      ACCCCC
                                      CACCACG
GAM864  IL12B    3'  CCAGAAAATATGGCTCCAT    9321         T  C   CTAG
                                ATGGAGC CA ATT    TGG
                                ||||||| || |||    |||
                                TACCTCG GT TAA    ACC
                                   _  A   AAG_
GAM864  RPIP8    3'  CCCCCACCAGACTGTGAGCTCC 21966           T   A
          AT                     ATGGAGCTCACA TCT GTGGGGG
                                ||||||||||| ||| |||||||
                                TACCTCGAGTGT AGA CACCCCC
                                      C   C
GAM864  SIM2     3'  CCCATGAATACACAACTCCA   17384       CTCAC_   TA
                                TGGAG     ATTC  GTGGG
                                |||||     ||||  |||||
                                ACCTC     TAAG  TACCC
                                   AACACA   __
GAM864  YWHAZ    3'  CTTTTAGAATGTAAGCTCC    12703        C       T
                                GGAGCT ACATTCTAG GG
                                |||||| ||||||||| ||
                                CCTCGA TGTAAGATT TC
                                   A        T
GAM864  AGPAT1   3'  CCCCACTCCAAAGTCCAT    21147       G  CACATTCT
                                ATGGA CT       AGTGGGG
                                ||||| ||       |||||||
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                                TACCT GA       TCACCCC
                                  _ AACC____
GAM864  AGPAT1   3' CCCCACTCCAAAGTCCAT    51233      G  CACATTCT
                                ATGGA CT       AGTGGGG
                                ||||| ||       |||||||
                                TACCT GA       TCACCCC
                                  _ AACC____
GAM864  CDIPT    3' CCCTCACTAGAATGTAAACTCC 20886       CTC
           AT                    ATGGAG   ACATTCTAGTGGGGG
                                ||||||  ||||||||||||||
                                TACCTC   TGTAAGATCACTCCC
                                   AAA
GAM864  CECR1    3' CCAGACTGTAAGCCCCAT    33809     A  C   T   AGT
                                ATGG GCT ACA TCT   GG
                                |||| ||| ||| |||   ||
                                TACC CGA TGT AGA   CC
                                  C   A   C   ___
GAM864  FLJ11099 3' CCCGTCTGAATAAAGCTCCAT  37044        CAC    T _
                                ATGGAGCT   ATTC AG TGGG
                                ||||||||   |||| || ||||
                                TACCTCGA   TAAG TC GCCC
                                    AA_    _ T
GAM864  FLJ14564 3' CCTGGAGAATGTGAGCCCC    76500    A         AG
                                GG GCTCACATTCT  TGGG
                                || ||||||||||  ||||
                                CC CGAGTGTAAGA  GTCC
                                 C          G_
GAM864  FLJ20113 3' CCCCCAGGCTGTGAGCTCC    34576          TT  AGT
                                GGAGCTCACA  CT   GGGGG
                                ||||||||||  ||   |||||
                                CCTCGAGTGT  GA   CCCCC
                                     CG  ___
GAM864  FLJ20527 3' CCCCATGCTAGGATGTAAACTC 35353       CTC         _
           CA                    TGGAG   ACATTCTAGTG GGGG
                                |||||   |||||||||| ||||
                                ACCTC   TGTAGGATCGT CCCC
                                   AAA         A
GAM864  FLJ21032 5' CCCCACCCTCGAGCTCCG    46087        ACATTCTA
                                TGGAGCTC       GTGGGG
                                ||||||||       ||||||
                                GCCTCGAG       CACCCC
                                    CTCC_____
GAM864  FOXH1    5' CCCCCACTAGAATGCTCTCT   14071      CTCA
                                GGAG    CATTCTAGTGGGGG
                                ||||    ||||||||||||||
                                TCTC    GTAAGATCACCCCC
                                  TC__
GAM864  KIAA1641 5' CCTCAAAACTGAGCTCCAT    80208          CATTCTAG
                                ATGGAGCTCA       TGGGG
                                ||||||||||       |||||
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                                TACCTCGAGT       ACTCC
                                     CAAA____
GAM864  MGC12538  3'  CCTCAAAACTGAGCTCCAT   51244          CATTCTAG
                                ATGGAGCTCA       TGGGG
                                ||||||||||       |||||
                                TACCTCGAGT       ACTCC
                                     CAAA____
GAM864  POF1B     3'  CTAAAATGTTAAGCTCCAT   46220        C_    C
                                ATGGAGCT  ACATT TAG
                                ||||||||  ||||| |||
                                TACCTCGA  TGTAA ATC
                                     AT    A
GAM864  URG4      3'  CCCCCAGACTGTGAGCTCC   35505         T   AGT
                                GGAGCTCACA TCT   GGGGG
                                |||||||||| |||   |||||
                                CCTCGAGTGT AGA   CCCCC
                                     C   ___
GAM864  LOC127428 3'  CCCAGAATGTAAGCTTCAT   74664        C      AGT
                                ATGGAGCT ACATTCT   GGG
                                |||||||| |||||||   |||
                                TACTTCGA TGTAAGA   CCC
                                     A     ___
GAM864  LOC145980 5'  CCCTTTAGAAACACACAGCTCC 83604        CACA__     T
           AT                     ATGGAGCT     TTCTAG GGG
                                |||||||      |||||| |||
                                TACCTCGA     AAGATT CCC
                                     CACACA     T
GAM864  LOC147700 3'  CCCCACTAGCTACTCCA     59195      CTCACATT
                                TGGAG       CTAGTGGGG
                                |||||       |||||||||
                                ACCTC       GATCACCCC
                                   ATC_____
GAM864  LOC163404 3'  CCCCCACTAGACTGTGAGCTCC 82125          T
                                GGAGCTCACA TCTAGTGGGGG
                                |||||||||| ||||||||||
                                CCTCGAGTGT AGATCACCCCC
                                     C
GAM864  LOC197342 3'  CCCACCAGAACGTGAGCTCC   87995         A   A
                                GGAGCTCAC TTCT GTGGG
                                |||||||| |||| |||||
                                CCTCGAGTG AAGA CACCC
                                     C   C
GAM864  LOC221398 3'  CCTATAGACTGTAAGCTCCAT  91018        C  T   G
                                ATGGAGCT ACA TCTA TGGG
                                |||||||| ||| |||| ||||
                                TACCTCGA TGT AGAT ATCC
                                     A  C   _
GAM864  LOC221688 5'  CCAAAGATTGTGAGCTCCAT   93677          T  AG
                                ATGGAGCTCACA TCT  TGG
                                |||||||||||| |||  |||
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                                TACCTCGAGTGT AGA  ACC
                                      T   A_
GAM864  LOC256714 3'  CTAGAATGTATACTCCA     96312      CTC
                                TGGAG   ACATTCTAG
                                |||||   |||||||||
                                ACCTC   TGTAAGATC
                                   ATA
GAM864  LOC257446 5'  CCTCAAAACTGAGCTCCAT    80000         CATTCTAG
                                ATGGAGCTCA      TGGGG
                                ||||||||||      |||||
                                TACCTCGAGT      ACTCC
                                     CAAA____
GAM864  LOC93496  3'  CTAGAATGTGAGCTCC     72433
                                GGAGCTCACATTCTAG
                                ||||||||||||||||
                                CCTCGAGTGTAAGATC

GAM865  CCNF     3'  CTGTAGACCCGTCCTGTC    8319      ACAA   AAA
                                GGCA    ATG   GTCTACAG
                                ||||    |||   ||||||||
                                CTGT    TGC   CAGATGTC
                                  CC__   C__
GAM865  CHD2     3'  AGCTGTAGCTGAGTAGCTGCC  7027      ACAA  GAA  T
                                GGCA    AT   AG CTACAGCT
                                ||||    ||   || ||||||||
                                CCGT    TG   TC GATGTCGA
                                  CGA_  AG_  _
GAM865  CYBB     3'  GCTTCATTTGTTGCT       76356           A
                                GGCAACAAATGAA GT
                                |||||||||||| ||
                                TCGTTGTTTACTT CG
                                          _
GAM865  GBAS     3'  AGCTGTAGAGTTTCTATGTGCC 7632      A  AAT    G
                                GGCA CA   GAAA TCTACAGCT
                                |||| ||   |||| |||||||||
                                CCGT GT   CTTT AGATGTCGA
                                  _ AT_    G
GAM865  NCALD    3'  AGACCCATCTTGTTGCC     49368        _   AAA
                                GGCAACAA ATG   GTCT
                                |||||||| |||   ||||
                                CCGTTGTT TAC   CAGA
                                     C   C__
GAM865  RGS9     3'  AGACTTTCCCTGCTGCC     13831      A  AAT
                                GGCA CA   GAAAGTCT
                                |||| ||   ||||||||
                                CCGT GT   CTTTCAGA
                                  C  CC_
GAM865  SNTB2    3'  CTACCCACTTGTTGCC      55611        A  AAA  CTAC
                                GGCAACAA TG   GT    AG
                                |||||||| ||   ||    ||
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                                CCGTTGTT AC   CA    TC
                                    C  C__  _____
GAM865  CHI3L2   3'  CTGTTGACTTGTTGCC      14347        AATGAA    T
                                GGCAACA     AGTC ACAG
                                |||||||     |||| ||||
                                CCGTTGT     TCAG TGTC
                                   _______   T
GAM865  CNOT3    5'  AGCTGCCAGTTTCATTTGTCTC 27215    CA        GTCTA
          C                      GG  ACAAATGAAA    CAGCT
                                ||  ||||||||||    |||||
                                CC  TGTTTACTTT    GTCGA
                                 TC        GACC_
GAM865  DCTD     3'  AGCCTGTCTCTCCTTGTTGCC  8620         AT  A  TCT   _
                                GGCAACAA  GA AG   ACAG CT
                                ||||||||  || ||   |||| ||
                                CCGTTGTT  CT TC   TGTC GA
                                    C_  C  ___    C
GAM865  FLJ20071  3'  CTGTAGAATTTATGCC     34480     ACAAA    AG
                                GGCA    TGAA  TCTACAG
                                ||||    ||||  |||||||
                                CCGT    ATTT  AGATGTC
                                  ______   A_
GAM865  KIAA0934  3'  GCTGCGTCGTTTGCCGCC    64222     AA      AAGTCTA
                                GGC  CAAATGA      CAGC
                                |||  |||||||      ||||
                                CCG  GTTTGCT      GTCG
                                  CC      GC_____
GAM865  KPNA5    3'  ACTCCTCTTTGTTGCC      9628          T  A_
                                GGCAACAAA GA  AGT
                                |||||||||  ||  |||
                                CCGTTGTTT CT  TCA
                                     _  CC
GAM865  SRF      3'  GACTTCATTTGTGCC       11948      A       A
                                GGCA CAAATGAA GTC
                                |||| ||||||||  |||
                                CCGT GTTTACTT CAG
                                  _       _
GAM865  ZF       3'  CTGTAAATGTTTTGTTGCT    41086         TGAAA  C
                                GGCAACAAA     GT TACAG
                                |||||||||     ||  |||||
                                TCGTTGTTT     TA ATGTC
                                     TG___  A
GAM865  LOC126549 5'  AGACTTTCATCCGTGCC     75706      ACAA
                                GGCA    ATGAAAGTCT
                                ||||    ||||||||||
                                CCGT    TACTTTCAGA
                                  GCC_
GAM865  LOC219914 5'  GGACTTTCGCCTATTGCC    93328       CAAA
                                GGCAA    TGAAAGTCT
                                |||||    |||||||||
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                                CCGTT   GCTTTCAGG
                                  ATCC
GAM865  LOC51077 3' ACTTTCTCTTGTTGCC     31992        AT
                                GGCAACAA  GAAAGT
                                ||||||||  ||||||
                                CCGTTGTT  CTTTCA
                                    CT
GAM865  LOC85569 5' AGCTGTAGGCACCTGTCGTC  52407    A   AATGAAA
                                GGC ACA      GTCTACAGCT
                                ||| |||      ||||||||||
                                CTG TGT      CGGATGTCGA
                                  C  CCA____
GAM865  LOC91548 5' CTGTAGACTCCTGCATAGCC  66412    AACAA   AA__
                                GGC    ATG    AGTCTACAG
                                |||    |||    |||||||||
                                CCG    TAC    TCAGATGTC
                                  A____   GTCC
GAM865  LOC93349 3' AGCTGCTTTTCATTTACGGCC 56451    AAC       TCTA
                                GGC   AAATGAAAG    CAGCT
                                |||   |||||||||    |||||
                                CCG   TTTACTTTT    GTCGA
                                  GCA       C___
GAM866  ADH1B    3' CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM866  AHR      3' ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM866  FDFT1    3' TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                                _
GAM866  JTB      3' ATCTCAGACAGTGAAAGTGAAA 21959
           TG                    CATTTCACTTTCACTGTCTGAGAT
                                ||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM866  KLF4     3' TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM866  PHYH     3' ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
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                                TAAAGTGAAA TGACA
                                     A
GAM866  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG   A
                                TTTCACTTTCA  TCTG GA
                                ||||||||||  |||| ||
                                AAAGTGAAAGT  GGAC CT
                                      T__   _
GAM866  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM866  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017        CA   CTG
                                TTTCACTTT  CTGT  AGAT
                                |||||||||  ||||  ||||
                                AAAGTGAAA  GACA  TCTA
                                     C_   CG_
GAM866  CG012   5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM866  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM866  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM866  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM866  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534     C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                   A       CT
GAM866  KLHL6   3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                   _  G
GAM866  NIR3    3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
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                                TAA GTGAAAGTGACG
                                  C
GAM866  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM866  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM866  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__    TT
GAM866  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A     TC
GAM866  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941          CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                     AAAGG
GAM866  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647       ACTTTCA
                                TTTC       CTGTCTGAGAT
                                ||||       ||||||||||||
                                AAAG       GACAGACTCTA
                                  GTTTGCC
GAM866  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM866  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM866  LOC222134 5'  ACAGTGAAGTGAAATG       94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                     _
GAM867  ADH4     3'  TAAAAAGATTTTTACTGGA    5408          CGT
                                TCCAGTGG   TCTTTTTA
                                ||||||||   ||||||||
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                                AGGTCATT  AGAAAAAT
                                    TTT
GAM867  B4GALT2  3'  AGTAAAAAACGTGAATGGA  47580    GTG   CT
                                TCCA  GCGTT  TTTTACT
                                ||||  |||||  |||||||
                                AGGT  TGCAA  AAAATGA
                                  AAG   __
GAM867  CTBP1    3'  AAAAAGAAAACCTGAAGGAG  67941    AGT_  CG
                                CTCC   GG  TTCTTTTT
                                ||||   ||  ||||||||
                                GAGG   CC  AAGAAAAA
                                  AAGT  AA
GAM867  ENPP3    3'  TAAAAAGAACAGCAGAGAG   17226    CAGTG  _
                                CTC    GC GTTCTTTTTA
                                |||    || ||||||||||
                                GAG    CG CAAGAAAAAT
                                  AGA__  A
GAM867  F8       3'  TAAAAAAATAAGTCAGGAGGA  3732      AG   GTTC_
                                TCCTCC  TGGC    TTTTTA
                                ||||||  ||||    ||||||
                                AGGAGG  ACTG    AAAAAT
                                   __   AATAA
GAM867  GK       3'  AGCAAAAAGAATGCTAT    3911          A
                                GTGGCGTTCTTTTT CT
                                |||||||||||||| ||
                                TATCGTAAGAAAAA GA
                                      C
GAM867  ID4      3'  GAAAAAAAGCCACCGGAGGA  7755      A   GTTC
                                TCCTCC GTGGC   TTTTT
                                |||||| |||||   |||||
                                AGGAGG CACCG   AAAAG
                                   C    AAA_
GAM867  PITX1    3'  GAAAAAGACGTCGGAG     10599    AGT   T    A
                                CTCC   GGCGT CTTTTT C
                                ||||   ||||| |||||| |
                                GAGG   CTGCA GAAAAA G
                                  ___    _     C
GAM867  TDG      3'  GAAAAAGATGCTGGAG     12191       GCGT     A
                                CTCCAGTG   TCTTTTT C
                                ||||||||   ||||||| |
                                GAGGTCGT   AGAAAAA G
                                     ____      C
GAM867  XRCC2    3'  AGCAAAAAGAACAAAGCTGGAG 18318       GGC      A
          G                   CCTCCAGT   GTTCTTTTT CT
                              ||||||||   ||||||||| ||
                              GGAGGTCG   CAAGAAAAA GA
                                   AAA       C
GAM867  DKFZP727M111 5'  AAAAGGAAAAGCCCTGAAG   31401   C  T  G_
                                CT CAG GGC  TTCTTTTT
                                || ||| |||  ||||||||
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                                GA GTC CCG  AAGGAAAA
                                 A  _  AA
GAM867  ELKS     3'  AGTGGTCAACGCCCTGGAAGA  30501    C    T     CTTT
                                TC TCCAG GGCGTT    TTACT
                                || ||||| ||||||    |||||
                                AG AGGTC CCGCAA    GGTGA
                                 A    _     CT__
GAM867  FLJ10648  3'  AGCAAAAAGAACAAAGTCCTGG 36378         T  ___       A
           AGGA                    TCCTCCAG GGC   GTTCTTTTT CT
                                ||||||||| |||   |||||||||| ||
                                AGGAGGTC CTG   CAAGAAAAA GA
                                     _  AAA        C
GAM867  FLJ20151  3'  AAAGACCCTGGAGGA       34648         T  CGT
                                TCCTCCAG GG   TCTTT
                                |||||||| ||   |||||
                                AGGAGGTC CC   AGAAA

                                   _  ____
GAM867  FLJ20435  3'  TAAAAAGAGCCATCTGGAGGA  35162         _   GT
                                TCCTCCAG TGGC  TCTTTTTA
                                |||||||| ||||  ||||||||
                                AGGAGGTC ACCG  AGAAAAAT
                                     T   ___
GAM867  MDS024    3'  AAAAAGAATTGCCAAGGA    41522     AG    _
                                TCC  TGGCG TTCTTTTT
                                |||  ||||| ||||||||
                                AGG  ACCGT AAGAAAAA
                                  A_    T
GAM867  ShrmL     5'  AGAGCGCCACTGAAGGA     40463      C
                                TCCT CAGTGGCGTTCT
                                |||| ||||||||||||
                                AGGA GTCACCGCGAGA
                                   A
GAM867  SIAT8C    5'  TAAAAAAGCCCCACAGAGGA   31883       CA    C   C
                                TCCTC  GTGG GTT TTTTTA
                                |||||  |||| ||| ||||||
                                AGGAG  CACC CGA AAAAAT
                                   A_    C   _
GAM867  VEST1     5'  AAAAAGATGCACTGGGGA    53678     T     G   T
                                TCC CCAGTG CGT CTTTTT
                                ||| |||||| ||| ||||||
                                AGG GGTCAC GTA GAAAAA

                                  _     _  _
GAM867  ZFD25     5'  AAAAAGAGCCCTGGA       32573       T   GT
                                TCCAG GGC  TCTTTTT
                                ||||| |||  |||||||
                                AGGTC CCG  AGAAAAA

                                   _  ___
GAM867  LOC124626 3'  AGTAAGACCAAACCACTGGA   74313         CGTTCT
                                TCCAGTGG     TTTTACT
                                ||||||||     |||||||
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                                AGGTCACC     AGAATGA
                                     AAACC_
GAM867  LOC144577 3'  TAAAAAGAAGCCACAAAGAG   76902     CA_    G
                                CTC   GTGGC TTCTTTTTA
                                |||   ||||| |||||||||
                                GAG   CACCG AAGAAAAAT
                                  AAA    _
GAM867  LOC145837 5'  AGCAAAAAGAACCAAAGAGGA  83542      CAG   CG      A
                                TCCTC   TGG  TTCTTTTT CT
                                |||||   |||  |||||||| ||
                                AGGAG   ACC  AAGAAAAA GA
                                   AA_  __       C
GAM867  LOC151194 3'  TAAAAAAACTGGGGA      59215     T    GGCGTTC
                                TCC CCAGT      TTTTTA
                                ||| |||||      ||||||
                                AGG GGTCA      AAAAAT
                                  _    A_______
GAM867  LOC154789 5'  AGTAAAATCTCAGGCCACTAGA 81131     C     GTTCT_
          G                      CTC AGTGGC     TTTTACT
                                ||| ||||||     |||||||
                                GAG TCACCG     AAAATGA
                                  A     GACTCT
GAM867  LOC197322 3'  AAAGACTCCACTGGAGGA    89736          C  T
                                TCCTCCAGTGG GT CTTT
                                |||||||||| || ||||
                                AGGAGGTCACC CA GAAA
                                       T  _
GAM867  LOC221596 3'  TAAAAACCTCACACTGGAGAGA 91980    _      GCGTTC
                                TC CTCCAGTG     TTTTTA
                                || ||||||||     ||||||
                                AG GAGGTCAC     AAAAAT
                                  A       ACTCC_
GAM867  LOC91796  3'  AGCAAAAAGAACAAGGCTGGA  67208       GGC       A
                                TCCAGT   GTTCTTTTT CT
                                ||||||   |||||||| ||
                                AGGTCG   CAAGAAAAA GA
                                    GAA       C
GAM867  LOC92539  5'  TAAAAAGTGTCACTG       69638        TT
                                CAGTGGCG  CTTTTTA
                                ||||||||  |||||||
                                GTCACTGT  GAAAAAT
                                          __
GAM868  BACH1     3'  AAGTAACTACACTACCTCA    6794         TA   TG
                                TGAGGTAGT  GGT  TGCTT
                                |||||||||  |||  |||||
                                ACTCCATCA  TCA  ATGAA
                                      CA   __
GAM868  CD80      3'  AAGCTGTTTTACCCACTACCTC 17765        TA   TGT___
          A                     TGAGGTAGT  GGT     GCTT
                                |||||||||  |||     ||||
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                                ACTCCATCA  CCA     CGAA
                                     C_   TTTTGT
GAM868  CEP1    3'  ACACCTCCACTACCTCA     22815         T_   T
                                TGAGGTAGT  AGGT GT
                                |||||||||  |||| ||
                                ACTCCATCA  TCCA CA
                                     CC   _
GAM868  CFTR    3'  AAGCATTCCAACTATCTCA    4925          A  TT
                                TGAGGTAGTT GG  GTGCTT
                                |||||||||| ||  ||||||
                                ACTCTATCAA CC  TACGAA
                                      _  T_
GAM868  CSF1R   3'  AGCACAAACTCCCCCA      17801    A  T   AGGT
                                TG GG AGTT    TGTGCT
                                || || ||||    ||||||
                                AC CC TCAA    ACACGA
                                 C  C   ____
GAM868  CYB5    3'  AAGCCATTGCTAACTACTTCA  8593           GT_  T
                                TGAGGTAGTTAG   TG GCTT
                                ||||||||||||   || ||||
                                ACTTCATCAATC   AC CGAA
                                       GTT  _
GAM868  DDEF1   3'  AAGCACAACTCCCAACCCA    59562    A   AGTTA
                                TG GGT     GGTTGTGCTT
                                || |||     ||||||||||
                                AC CCA     TCAACACGAA
                                 _   ACCC_
GAM868  DUSP5   3'  AAGCACAATTTCCACCTTA    15349       AGTT
                                TGAGGT    AGGTTGTGCTT
                                ||||||    ||||||||||||
                                ATTCCA    TTTAACACGAA
                                   CC__
GAM868  EGLN3   3'  AAGCACAGATCGCACTGCCTCA 41967          TA  _
                                TGAGGTAGT  GGT TGTGCTT
                                |||||||||  ||| |||||||
                                ACTCCGTCA  CTA ACACGAA
                                     CG   G
GAM868  MAFG    3'  AAGCACAACCTGTACCCCA    70092    A   GT
                                TG GGTA  TAGGTTGTGCTT
                                || ||||  ||||||||||||
                                AC CCAT  GTCCAACACGAA
                                 C   __
GAM868  PBX3    3'  CACAGCTTTATTACCTCA     20563         T
                                TGAGGTAGT AGGTTGTG
                                ||||||||| ||||||||
                                ACTCCATTA TTCGACAC
                                      T
GAM868  QARS    3'  AAGCACTGAACCTACCTCA    17309       AGTT    __
                                TGAGGT    AGGTT  GTGCTT
                                ||||||    |||||  ||||||
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                                ACTCCA   TCCAA  CACGAA
                                   ____    GT
GAM868  RRM2     3'  ACTGTGTAGCTACCTCA     6406          G TT
                                TGAGGTAGTTA G  GT
                                |||||||||||  |  ||
                                ACTCCATCGAT T  CA
                                      G GT
GAM868  SLC7A5   3'  AAGCACAACCCACCACA     13006    A   AGTTA
                                TG GGT    GGTTGTGCTT
                                || |||    ||||||||||
                                AC CCA    CCAACACGAA
                                 A  C____
GAM868  TXNIP    3'  AAGCAGTAGTAACTGCCCCA  21347    A      GGTTG
                                TG GGTAGTTA    TGCTT
                                || ||||||||    |||||
                                AC CCGTCAAT    ACGAA
                                 C       GATG_
GAM868  WIG1     3'  TGTGACCTACCTACCCCA    94471    A    T    TG
                                TG GGTAG TAGGT  TG
                                || ||||| |||||  ||
                                AC CCATC ATCCA  GT
                                 C    C    GT
GAM868  ZNF264   3'  AAGCAATTAACTGCCTCA    12739          GGTTG
                                TGAGGTAGTTA    TGCTT
                                ||||||||||    |||||
                                ACTCCGTCAAT    ACGAA
                                      TA___
GAM868  C20orf38 3'  AAGCACAAAGATCACCCA    37063    A  A   AGG
                                TG GGT GTT   TTGTGCTT
                                || ||| |||   ||||||||
                                AC CCA TAG   AACACGAA
                                 _  C  A__
GAM868  FLJ12619 3'  AAGCACAAGGTGATACTCA   48190     GTA   GG
                                TGAG  GTTA  TTGTGCTT
                                ||||  ||||  ||||||||
                                ACTC  TAGT  AACACGAA
                                  A__   GG
GAM868  FLJ20309 3'  ATGACCTAATCACCTCA     34921      A     TG
                                TGAGGT GTTAGGT  T
                                |||||| |||||||  |
                                ACTCCA TAATCCA  A
                                   C      GT
GAM868  FLJ21551 3'  ACTATTCTAATACCTCA     45625      G    TT_
                                TGAGGTA TTAGG  GT
                                ||||||| |||||  ||
                                ACTCCAT AATCT  CA
                                    _    TAT
GAM868  GNG3     3'  AAGCACAAGGCCCACCCTCA  24189     TA  TA  __
                                TGAGG  GT  GGT  TGTGCTT
                                |||||  ||  |||  |||||||
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                                ACTCC  CA  CCG  ACACGAA
                                  __  C_  GA
GAM868  HCA127   3' AAGCACAACCCCTCTCTCA   37946     GT  TTA
                                TGAG  AG   GGTTGTGCTT
                                ||||  ||   ||||||||||
                                ACTC  TC   CCAACACGAA
                                  TC  C__
GAM868  HPIP     3' AAGCACAGGGGACACCCCA   40046    A   A   AGG
                                TG GGT GTT   TTGTGCTT
                                || ||| |||   ||||||||
                                AC CCA CAG   GACACGAA
                                 C   _   GG_
GAM868  IMP-2    3' CACAGAAGAAGCTACCTCA   21569         AGG_
                                TGAGGTAGTT    TTGTG
                                ||||||||||    |||||
                                ACTCCATCGA    GACAC
                                      AGAA
GAM868  KIAA0982 3' AACCCATAACCACCTCA     25842       A   __
                                TGAGGT GTTA  GGTT
                                |||||| ||||  ||||
                                ACTCCA CAAT  CCAA
                                   C    AC
GAM868  KIAA1274 3' TACTTGCCTACCTACCTCA   91370        T    T_
                                TGAGGTAG TAGGT  GTG
                                |||||||| |||||  |||
                                ACTCCATC ATCCG  CAT
                                     C     TT
GAM868  KIAA1344 3' AAGCAGGAAACTACCT      72444        AGG  G
                                AGGTAGTT   TT TGCTT
                                ||||||||   || |||||
                                TCCATCAA   AG ACGAA
                                     ___  G
GAM868  KIAA1434 3' AGCTTACAGCTACCTCA     69608         __
                                TGAGGTAGT  TAGGTT
                                |||||||||  ||||||
                                ACTCCATCG  ATTCGA
                                      AC
GAM868  KIAA1443 3' AACCTGTTAACTACCTC     63823        ___
                                GAGGTAGT   TAGGTT
                                ||||||||   ||||||
                                CTCCATCA   GTCCAA
                                     ATT
GAM868  MGC5391  3' ACAAGGTTACCTACCTCA    51229        T   G  _
                                TGAGGTAG TAG TT GT
                                |||||||| ||| || ||
                                ACTCCATC ATT GA CA
                                     C   G  A
GAM868  NAP1L1   3' GTTTACCTAACTACCTCA    57622            TGT
                                TGAGGTAGTTAGGT   GC
                                ||||||||||||||   ||
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                                ACTCCATCAATCCA  TG
                                      TT_
GAM868  OAZ3    5'  ACACGTAACTACCTC      32448        G  T
                                GAGGTAGTTA GT GT
                                |||||||||| || ||
                                CTCCATCAAT CA CA
                                     G  _
GAM868  OMD     3'  ACACCAAACTATCTCA     17212         A  T
                                TGAGGTAGTT GGT GT
                                |||||||||| ||| ||
                                ACTCTATCAA CCA CA
                                     A  _
GAM868  PDZD2   5'  AAGCACAAAGCCCACTCC   80854   T  TA  __
                                GG AGT  GGT  TGTGCTT
                                || |||  |||  |||||||
                                CC TCA  CCG  ACACGAA
                                 _  C_  AA
GAM868  RGS20   3'  AAGCACAAGAATTTTATCTCA 13514       TTAGG
                                TGAGGTAG    TTGTGCTT
                                ||||||||    ||||||||
                                ACTCTATT    AACACGAA
                                     TTAAG
GAM868  RHOBTB1 3'  AAGCACAAGCTCACCATC   91436    A  T  G
                                GGT GT AG TTGTGCTT
                                ||| || || ||||||||
                                CTA CA TC AACACGAA
                                  C  C  G
GAM868  SEC61A1 3'  AAGCACAGGGCCACCGCC   25305   TA  TA  __
                                GG  GT  GGT  TGTGCTT
                                ||  ||  |||  |||||||
                                CC  CA  CCG  ACACGAA
                                 GC  __  GG
GAM868  TNRC3   3'  CACGGCACTACCTC       19657       TAG
                                GAGGTAGT   GTTGTG
                                ||||||||   ||||||
                                CTCCATCA   CGGCAC
                                     ___
GAM868  TNRC9   3'  AAGCACAGTTGTAACTACCT  71286        _ GT
                                AGGTAGTTA G  TGTGCTT
                                ||||||||| |  |||||||
                                TCCATCAAT T  ACACGAA
                                     G TG
GAM868  LOC121227 3' AAGCTTAACATACTACCTCA  74053        TAG   T
                                TGAGGTAGT   GTTG GCTT
                                |||||||||   |||| ||||
                                ACTCCATCA   CAAT CGAA
                                     TA_   T
GAM868  LOC135293 3' ACATATTAATTACCTCA    76169          GT
                                TGAGGTAGTTAG  TGT
                                ||||||||||||  |||
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                                ACTCCATTAATT  ACA
                                      AT
GAM868  LOC148823 3'  GTGACCTGACCACCTCA     59210       A      TG
                                TGAGGT GTTAGGT  T
                                |||||| |||||||  |
                                ACTCCA CAGTCCA  G
                                   C      GT
GAM868  LOC148930 3'  AAGCACAGAGTCCATCTCA    79089       AGTTAGG
                                TGAGGT      TTGTGCTT
                                ||||||      ||||||||
                                ACTCTA      GACACGAA
                                   CCTGA__
GAM868  LOC152274 3'  AAGCACAGGGCCCTCCTCA    80496      T  TTA  __
                                TGAGG AG   GGT  TGTGCTT
                                ||||| ||   |||  |||||||
                                ACTCC TC   CCG  ACACGAA
                                  _ ___   GG
GAM868  LOC157503 3'  ACATCTAACTACCTCA      86467           T
                                TGAGGTAGTTAGGT GT
                                |||||||||||||| ||
                                ACTCCATCAATCTA CA
                                              _
GAM868  LOC220000 5'  AAGCACAACCTCAACCCA    91596    A  AGTT
                                TG GGT    AGGTTGTGCTT
                                || |||    ||||||||||
                                AC CCA    TCCAACACGAA
                                  _   AC__
GAM868  LOC221087 3'  CACACCGACTGCCTCA      93239         A  T
                                TGAGGTAGTT GGT GTG
                                |||||||||| ||| |||
                                ACTCCGTCAG CCA CAC
                                          _  _
GAM868  LOC221272 3'  AACAGTAACTGCCTCA      93605         G_
                                TGAGGTAGTTA  GTT
                                ||||||||||  |||
                                ACTCCGTCAAT  CAA
                                      GA
GAM868  LOC221466 3'  AAGCACAACAGGAGACC     93681     AG  AG
                                GGT  TT  GTTGTGCTT
                                |||  ||  |||||||||
                                CCA  AG  CAACACGAA
                                  G_  GA
GAM868  LOC255721 5'  AAGCACAACCTCAACCCA    94830    A  AGTT
                                TG GGT    AGGTTGTGCTT
                                || |||    ||||||||||
                                AC CCA    TCCAACACGAA
                                  _   AC__
GAM868  LOC92578  5'  CACAACCTAAAGTTCCCA    69824    A  TAG_
                                TG GG    TTAGGTTGTG
                                || ||    ||||||||||
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                                AC CC    AATCCAACAC
                                 _ TTGA
GAM869  CD74     3'  GAACAGCAGATAACA       15129     CA
                                TGT  GTCTGCTGTTT
                                |||  ||||||||||
                                ACA  TAGACGACAAG
                                  A_
GAM869  MFAP4    3'  CCTGTCCCAACAGCTGACAG   69254       T   C  TTT
                                CTGTCAG CTG TG   GCAGG
                                ||||||| ||| ||   |||||
                                GACAGTC GAC AC   TGTCC
                                    _  A  CC_
GAM869  SLC20A1  3'  TGTTAACAGAAGACTGACA    59391         G    T
                                TGTCAGTCT CTGTT GCA
                                ||||||||| ||||| |||
                                ACAGTCAGA GACAA TGT
                                      A    T
GAM869  WNT14    3'  CCTGCAAGGACTGAGAG     12676    G     GCTGT
                                CT TCAGTCT    TTGCAGG
                                || |||||||    |||||||
                                GA AGTCAGG    AACGTCC
                                 G     _____
GAM869  ATF3     5'  CGCCCGCCGGCCAGACAAACAG 14431     CA    _  TTT  A
                                CTGT  GTCTG CTG   GC GGCG
                                ||||  ||||| |||   || ||||
                                GACA  CAGAC GGC   CG CCGC
                                  AA    C  ___  C
GAM869  CXorf9   3'  CGCCCTCCACCAGCGACTGACA 38623        T   TTTGCA
            G                    CTGTCAGTC GCTG     GGCG
                                |||||||||| ||||     ||||
                                GACAGTCAG CGAC     CCGC
                                    _   CACCTC
GAM869  FLJ20195 3'  CCAGCCCCAGCAGACCACAG   34708     CA      TTT  A
                                CTGT  GTCTGCTG   GC GG
                                ||||  ||||||||   || ||
                                GACA  CAGACGAC   CG CC
                                  C_       CC_  A
GAM869  MAP3K6   5'  CGCCTGCAGCGGAGACTGGACA 16245      _    G    T
            G                    CTGTC AGTCT CTGTT GCAGGCG
                                ||||| ||||| ||||| |||||||
                                GACAG TCAGA GGCGA CGTCCGC
                                   G    _    _
GAM869  SRF      5'  GCCCTAGCAGACGGACAG    11950      A      TTTGCA
                                CTGTC GTCTGCTG     GGC
                                ||||| ||||||||     |||
                                GACAG CAGACGAT     CCG
                                  G       C_____
GAM869  LOC115004 3'  CCTGCTGCTCAGACTGA     73174        CT  TT
                                TCAGTCTG  GT  GCAGG
                                ||||||||  ||  |||||
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                                AGTCAGAC  CG  CGTCC
                                    T_  T_
GAM869  LOC118611 5'  CACCCATGCAGACGACA     75470      A     _  TT
                                TGTC GTCTGC TG  TG
                                |||| |||||| ||  ||
                                ACAG CAGACG AC  AC
                                  _     T  CC
GAM869  LOC197342 3'  CCTGGGCTGCAGACAGACA   87998      A     T   TG
                                TGTC GTCTGC GTT  CAGG
                                |||| |||||| |||  ||||
                                ACAG CAGACG CGG  GTCC
                                  A     T  __
GAM869  LOC204084 5'  TTTGTACAGACTGACA      89450          CTGTT
                                TGTCAGTCTG    TGCAGG
                                ||||||||||    ||||||
                                ACAGTCAGAC    ATGTTT
                                              ______
GAM869  LOC83690  5'  CGCCCACCCTGGCAGACTAACG 48814     C       GTTTGCA
                                TGT AGTCTGCT      GGCG
                                ||| ||||||||      ||||
                                GCA TCAGACGG      CCGC
                                  A       TCCCAC_
GAM869  LOC90515  3'  CGCCTGCAACCTTGATCGACAG 63123       A   TGCTGT
                                CTGTC GTC     TTGCAGGCG
                                ||||| |||     |||||||||
                                GACAG TAG     AACGTCCGC
                                   C   TTCC__
GAM870  AQP8     5'  GATGTTTGTGCCATCTGA    6753      A  A
                                TCA ATG CACAGACATC
                                ||| ||| ||||||||||
                                AGT TAC GTGTTTGTAG
                                  C   C
GAM870  BCAT1    3'  GGGACAGACTGTTGCATTTGA  66205        AC    ACA
                                TCAAATG  ACAG   TCTGTCCC
                                |||||||  ||||   ||||||||
                                AGTTTAC  TGTC   AGACAGGG
                                    GT   ____
GAM870  CLCN4    3'  ACACTGACTGTGTCATTT    8440           A  TC
                                AAATGACACAG CA  TGT
                                |||||||||| ||  |||
                                TTTACTGTGTC GT  ACA
                                      A  C_
GAM870  COPS3    3'  GGACCAAGCCTGTGTCACCTGG 13331     AA       ACATCT
                                TCA  TGACACAG     GTCC
                                |||  ||||||||     ||||
                                GGT  ACTGTGTC     CAGG
                                  CC       CGAAC_
GAM870  DAZ      3'  ACATTTGTATCAGTATCATTTG 14547         C  AG__   TC
          A                      TCAAATGA AC    ACA  TGT
                                |||||||| ||    |||  |||
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                                AGTTTACT TG    TGT  ACA
                                    A  ACTA   TT
GAM870  DNAJB1   3'  GGAACAAATGTCTGTTCCCTGG 20445    AAAT  C      C  _
            A                    TC    GA ACAGACAT TGT CC
                                 ||    || |||||||| ||| ||
                                 AG    CT TGTCTGTA ACA GG
                                  GTCC  _       A   A
GAM870  DNMT2    3'  AGATGTATCTACCAGTGTCATT 15329        ____   __
                                 AATGACAC    AGA  CATCT
                                 ||||||||    |||  |||||
                                 TTACTGTG    TCT  GTAGA
                                     ACCA   AT
GAM870  DVL3     3'  GACAGGTGGATCACTTGA    15368      A  CACAGA
                                 TCAA TGA     CATCTGTC
                                 |||| |||     ||||||||
                                 AGTT ACT     GTGGACAG
                                   C   AG____
GAM870  EGLN3    3'  ACAGAGAAATTTGTGTCATCTG 52910     A        CA__
            A                    TCA ATGACACAGA    TCTGT
                                 ||| ||||||||||    |||||
                                 AGT TACTGTGTTT    AGACA
                                   C         AAAG
GAM870  EGLN3    3'  ACAGAGAAATTTGTGTCATCTG 41968     A        CA__
            A                    TCA ATGACACAGA    TCTGT
                                 ||| ||||||||||    |||||
                                 AGT TACTGTGTTT    AGACA
                                   C         AAAG
GAM870  KAL1     3'  GACTCGTGTCTGTATCAT    4015      C       CT
                                 ATGA ACAGACAT  GTC
                                 |||| ||||||||  |||
                                 TACT TGTCTGTG  CAG
                                   A       CT
GAM870  MGEA5    3'  GGACAAATGTGCATTTG     24213       A    GACATC
                                 CAAATG CACA     TGTCC
                                 |||||| ||||     |||||
                                 GTTTAC GTGT     ACAGG
                                    _    AA____
GAM870  NAV2     3'  GGGTATCTGTGTCCTTT     60159     T       C
                                 AAA GACACAGA ATCT
                                 ||| |||||||| ||||
                                 TTT CTGTGTCT TGGG
                                   C       A
GAM870  NFATC1   3'  AGACCACTGTGTCACCTGG   20482     AA       ACA
                                 TCA  TGACACAG   TCT
                                 |||  ||||||||   |||
                                 GGT  ACTGTGTC   AGA
                                   CC       ACC
GAM870  PCDH9    5'  AGAGGTCCCATTTCATTTGA  82790        CACA_   A
                                 TCAAATGA    GAC TCT
                                 ||||||||    ||| |||
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                                AGTTTACT    CTG AGA
                                    TTACC   G
GAM870  PLEK     3'  AGATTCTGTTTCATTTGA    10628        C    C
                                TCAAATGA ACAGA ATCT
                                |||||||| ||||| ||||
                                AGTTTACT TGTCT TAGA
                                    T    _
GAM870  TIM3     3'  ACTATGAGCTGTGTCACCTGA  51337     AA      A_   CT
                                TCA  TGACACAG  CAT  GT
                                |||  ||||||||  |||  ||
                                AGT  ACTGTGTC  GTA  CA
                                  CC       GA   T_
GAM870  TNFSF15  5'  GACATTGGTGTTATCATTTGA  17593        CACA     __
                                TCAAATGA   GACATC  TGTC
                                ||||||||   ||||||  ||||
                                AGTTTACT   TTGTGG  ACAG
                                    A___     TT
GAM870  AMSH     3'  GGGACAGCTTACTCCATTTGA  21318       ACAC  ACAT
                                TCAAATG   AG   CTGTCCC
                                |||||||   ||   |||||||
                                AGTTTAC   TC   GACAGGG
                                   C___  ATTC
GAM870  C1orf24  3'  GACTTGTATGTGTCATTTGA   53718         G   TCT
                                TCAAATGACACA ACA   GTC
                                |||||||||||| |||   |||
                                AGTTTACTGTGT TGT   CAG
                                      A   T__
GAM870  C20orf45 3'  AGGAGCTGTGTATCATTTGA   32105        __    ACA
                                TCAAATGA  CACAG   TCT
                                ||||||||  |||||   |||
                                AGTTTACT  GTGTC   GGA
                                    AT    GA_
GAM870  DKFZP566K0524 3'  GACAGATGTCTATTCAT     69351     CAC
                                ATGA   AGACATCTGTC
                                ||||   ||||||||||
                                TACT   TCTGTAGACAG
                                  TA_
GAM870  DKFZP727G051 3'  AGAGCCTGCATCATTTGG    69470        CA   ACA
                                TCAAATGA  CAG   TCT
                                ||||||||  |||   |||
                                GGTTTACT  GTC   AGA
                                    AC   CG_
GAM870  DKFZP727G051 3'  GGGTGTCTGCACCACCTGG   69474     AA  ACA
                                TCA  TG   CAGACATCT
                                |||  ||   |||||||||
                                GGT  AC   GTCTGTGGG
                                  CC  CAC
GAM870  FLJ10261  3'  GGACAGAGGTGTCCCTGA    35954     AAT    AGACA
                                TCA   GACAC    TCTGTCC
                                |||   |||||    |||||||
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                                AGT   CTGTG    AGACAGG
                                  CC_    G____
GAM870  FLJ13193  3'  GACAGGTAGATCATTTGA    49767        CACAGAC
                                TCAAATGA      ATCTGTC
                                ||||||||      |||||||
                                AGTTTACT      TGGACAG
                                    AGA____
GAM870  FLJ20343  3'  TGTCTGTGTTATCTGA      35002     A
                                TCA ATGACACAGACA
                                ||| ||||||||||||
                                AGT TATTGTGTCTGT
                                  C
GAM870  FLJ20542  3'  GGGACAGAGGCCTTGTGTCACC 49786    AA       ACA_
          TG                    CA  TGACACAG    TCTGTCCC
                                ||  ||||||||    ||||||||
                                GT  ACTGTGTT    AGACAGGG
                                 CC       CCGG
GAM870  FLJ23235  5'  GGAACACATTTGTGTCATGTGA 46307     A        CATCTG
                                TCA ATGACACAGA     TCC
                                ||| ||||||||||     |||
                                AGT TACTGTGTTT     AGG
                                  G        ACACA_
GAM870  FLJ23322  3'  GGGAGTCCCCGTCTGTGTCACT 88789     A        ATCTG_
          TG                    CAA TGACACAGAC     TCCC
                                ||| ||||||||||     ||||
                                GTT ACTGTGTCTG     AGGG
                                  C        CCCCTG
GAM870  FLJ23537  3'  GGACAGGTGGATCACCTGA    46026     AA   CACAGA
                                TCA  TGA     CATCTGTCC
                                |||  |||     |||||||||
                                AGT  ACT     GTGGACAGG
                                  CC   AG____
GAM870  HSPC228   3'  GACAAATGTCTGTTTTTATTTG 33227       C_      C
                                CAAATGA  ACAGACAT TGTC
                                |||||||  |||||||| ||||
                                GTTTATT  TGTCTGTA ACAG
                                    TT       A
GAM870  INE1      3'  ACAGATGTCTGGCCCAT     13371     ACA
                                ATG   CAGACATCTGT
                                |||   ||||||||||||
                                TAC   GTCTGTAGACA
                                  CCG
GAM870  KIAA0010  3'  GGACAGACACTGTGGTGTCATT 27895        AG   ___
                                AATGACAC  ACA   TCTGTCC
                                ||||||||  |||   |||||||
                                TTACTGTG  TGT   AGACAGG
                                    G_   CAC
GAM870  KIAA0451  3'  GACTCCACGTCTGTGTCACTGA 29108     AA        ATCT_
                                TCA  TGACACAGAC    GTC
                                |||  ||||||||||    |||
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                                AGT  ACTGTGTCTG    CAG
                                  C_        CACCT
GAM870  KIAA0471  3'  GGGACAGAGTATTTCATTT   29397       CACAG  A
                                AAATGA    AC TCTGTCCC
                                ||||||    || ||||||||
                                TTTACT    TG AGACAGGG
                                   TTA__  _
GAM870  KIAA0618  5'  GGAGGGGGCCAGTGTCATT   29171        AGACA   G
                                AATGACAC    TCT TCC
                                ||||||||    ||| |||
                                TTACTGTG    GGG AGG
                                     ACCG_   G
GAM870  KIAA0831  5'  GACAGGTGGATCACCTGA    29974     AA   CACAGA
                                TCA  TGA     CATCTGTC
                                |||  |||     ||||||||
                                AGT  ACT     GTGGACAG
                                  CC   AG____
GAM870  KIAA1028  3'  GGATGTCTGTGCCATGTGA    91942     A   A
                                TCA ATG CACAGACATCT
                                ||| ||| ||||||||||
                                AGT TAC GTGTCTGTAGG
                                  G   C
GAM870  KIAA1130  3'  GACAGGTGGATCACTTGA     62420      A   CACAGA
                                TCAA TGA     CATCTGTC
                                |||| |||     ||||||||
                                AGTT ACT     GTGGACAG
                                  C   AG____
GAM870  KIAA1391  3'  GACAGACTATATGTCATTT    67263        CAGACA
                                AAATGACA     TCTGTC
                                ||||||||     ||||||
                                TTTACTGT     AGACAG
                                     ATATC_
GAM870  KIAA1559  3'  GGACAAGGTGGGTGGATCACTT 73067      A   CA  GA    _
          GA                      TCAA TGA  CA  CATCT GTCC
                                |||| |||  ||  ||||| ||||
                                AGTT ACT  GT  GTGGA CAGG
                                  C   AG  GG    A
GAM870  KIAA1784  3'  GACAGTCGTGCTGTGTCA    65149        _  AT
                                TGACACAG AC  CTGTC
                                |||||||| ||  |||||
                                ACTGTGTC TG  GACAG
                                     G  CT
GAM870  KIAA1854  3'  GGACAGGCACATCATTTGG   71744        CACAGACA
                                TCAAATGA       TCTGTCC
                                ||||||||       |||||||
                                GGTTTACT       GGACAGG
                                     ACAC____
GAM870  KIAA1872  3'  GACAGGTGGATCACCTGA    62932     AA   CACAGA
                                TCA  TGA     CATCTGTC
                                |||  |||     ||||||||
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                                AGT  ACT     GTGGACAG
                                  CC   AG____
GAM870  PCF11    3'  GACAGACCGTTATTTGA     31892          ACAGACA
                                TCAAATGAC      TCTGTC
                                |||||||||      ||||||
                                AGTTTATTG      AGACAG
                                     CC_____
GAM870  RAB9A    5'  ACACTTTTCCCGTGTCGTTTGA 14911           A_  CATC
                                TCAAATGACAC  GA    TGT
                                ||||||||||  ||    |||
                                AGTTTGCTGTG  CT    ACA
                                      CC  TTTC
GAM870  TIGA1    3'  AGTTGCCTGGATCATTTGA   53799         CA   A  T
                                TCAAATGA  CAG CA CT
                                ||||||||  ||| || ||
                                AGTTTACT  GTC GT GA
                                     AG   C  T
GAM870  TONDU    5'  AGCTGTCACCTGTGTCATT   32755          ___   T
                                AATGACACA   GACA CT
                                |||||||||   |||| ||
                                TTACTGTGT   CTGT GA
                                     CCA    C
GAM870  TPD52L1  3'  TGTCTGTGTAATTCGA     12364    A   G
                                TC AAT ACACAGACA
                                || ||| |||||||||
                                AG TTA TGTGTCTGT
                                  C   A
GAM870  LOC125943 3'  GGGACAGATATCTTGT     74421     C   C
                                ACA AGA ATCTGTCCC
                                ||| ||| |||||||||
                                TGT TCT TAGACAGGG
                                  _   A
GAM870  LOC143038 3'  ACAGCACAGTGTTATTTGA   76451          AGACAT
                                TCAAATGACAC     CTGT
                                ||||||||||      ||||
                                AGTTTATTGTG     GACA
                                      ACAC__
GAM870  LOC145845 3'  GGGACAGACAAATGATCAGCTG 83554     AA   CA  GACA
           A                     TCA  TGA  CA    TCTGTCCC
                                |||  |||  ||    ||||||||
                                AGT  ACT  GT    AGACAGGG
                                  CG   A_  AAAC
GAM870  LOC152106 3'  GGACAGATCACTTGA      70063      A   CACAGACA
                                TCAA TGA       TCTGTCC
                                ||||  |||       |||||||
                                AGTT ACT       AGACAGG
                                  C  _________
GAM870  LOC153592 3'  GGAGCCTGTGATCATTTGA   86068         _    ACA
                                TCAAATGA CACAG   TCT
                                |||||||| |||||   |||
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                                AGTTTACT GTGTC   AGG
                                    A    CG_
GAM870  LOC159110 3'  GACAGGTGCATCAGTTGA    82099     A   CACAGA
                                TCAA TGA     CATCTGTC
                                |||| |||     ||||||||
                                AGTT ACT     GTGGACAG
                                  G   AC____
GAM870  LOC159116 3'  GACAGGTGCATCAGTTGA    82094     A   CACAGA
                                TCAA TGA     CATCTGTC
                                |||| |||     ||||||||
                                AGTT ACT     GTGGACAG
                                  G   AC____
GAM870  LOC167463 5'  GGACAGATGCCCTTGTTCA    82677     C    A__
                                TGA ACAG   CATCTGTCC
                                ||| ||||   |||||||||
                                ACT TGTT   GTAGACAGG
                                  _    CCC
GAM870  LOC199675 3'  ATGCCTGTGTCATGTGA     88261     A       A
                                TCA ATGACACAG CAT
                                ||| ||||||||| |||
                                AGT TACTGTGTC GTA
                                  G        C
GAM870  LOC219627 3'  GGGTGCTGTGTCATCTGA    92184     A       A
                                TCA ATGACACAG CATCT
                                ||| ||||||||| |||||
                                AGT TACTGTGTC GTGGG
                                  C        _
GAM870  LOC221362 3'  GGACAAGAATAATGTCCTTTGA 93761      T    CAGACA  _
                                TCAAA GACA     TCT GTCC
                                ||||| ||||     ||| ||||
                                AGTTT CTGT     AGA CAGG
                                   C    AATA__   A
GAM870  LOC257415 3'  GAATGTGTTATGTCATTTGA   96075         CA    CTG
                                TCAAATGACA  GACAT   TC
                                ||||||||||  |||||   ||
                                AGTTTACTGT  TTGTG   AG
                                      A_    TA_
GAM870  LOC89919  3'  ACAGATGGATGTCACATTGA   60712     A_    CAGA
                                TCAA  TGACA    CATCTGT
                                ||||  |||||    |||||||
                                AGTT  ACTGT    GTAGACA
                                  AC    AG__
GAM871  DLG5     5'  CAACAAGGACAAGAAGCAGG  82911    G    C  A_
                                CC TGTT CT  TCCTTGTTG
                                || |||| ||  |||||||||
                                GG ACGA GA  AGGAACAAC
                                 _   A  AC
GAM871  FLNB     3'  CAACAAGGACGGCACGG     62174       CCTA
                                CCGTGTT    TCCTTGTTG
                                |||||||    |||||||||
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                                GGCACGG   AGGAACAAC
                                   C___
GAM871  MBP      3'  CAAGGCACAGAGACACGGG   89780       TC  AT_
                                CCCGTGT  CT   CCTTG
                                |||||||  ||   |||||
                                GGGCACA  GA   GGAAC
                                   GA  CAC
GAM871  PSCD4    5'  CAAGCGACAGGAGCACGGGT  25401           A  _
                                ACCCGTGTTCCT TC CTTG
                                |||||||||||| || ||||
                                TGGGCACGAGGA AG GAAC
                                      C  C
GAM871  SH3BP2   3'  CAAGGACAGGAACACTGGT   11592     C       A
                                ACC GTGTTCCT TCCTTG
                                ||| |||||||| ||||||
                                TGG CACAAGGA AGGAAC
                                  T       C
GAM871  SORCS1   3'  CAACAGGGTATAACACAGG   53582    C    CCTAT
                                CC GTGTT    CCTTGTTG
                                || |||||    ||||||||
                                GG CACAA    GGGACAAC
                                 A    TAT__
GAM871  ANAPC11  3'  CAACAAGGTGGAAACAAGGG  33210     G   C  T
                                CCC TGTT CTA CCTTGTTG
                                ||| |||| ||| ||||||||
                                GGG ACAA GGT GGAACAAC
                                  A   A  _
GAM871  C20orf142 3'  AAGGAGCAGAAACACAGGT   74763     C    C  A_
                                ACC GTGTT CT  TCCTT
                                ||| ||||| ||  |||||
                                TGG CACAA GA  AGGAA
                                  A    A  CG
GAM871  CFLAR    5'  AACAAGGACCACGGG       13926       TTCCTA
                                CCCGTG     TCCTTGTT
                                ||||||     ||||||||
                                GGGCAC     AGGAACAA
                                   C_____
GAM871  CLSTN2   3'  CAACAAGGACAACAAGG     42121    G   CCTA
                                CC TGTT    TCCTTGTTG
                                || ||||    |||||||||
                                GG ACAA    AGGAACAAC
                                 A   C___
GAM871  CLSTN2   3'  CAACAAGGACACAACAC     42122      CCTA
                                GTGTT    TCCTTGTTG
                                |||||    |||||||||
                                CACAA    AGGAACAAC
                                   CAC_
GAM871  CLSTN2   3'  CAACAAGGACAGTCACAAC   42123    _  TC  A
                                GT GT  CT TCCTTGTTG
                                || ||  || |||||||||
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                                CA CA  GA AGGAACAAC
                                 A  CT  C
GAM871  CLSTN2   3'  CAACAAGGACAGTCACAACAAG 42124    CG__   TC  A
           G                     CC    TGT  CT TCCTTGTTG
                                 ||    |||  || |||||||||
                                 GG    ACA  GA AGGAACAAC
                                  AACA   CT  C
GAM871  ERp44    3'  CAACAAGGTAGCACACAGG   81691    C    TC   T
                                 CC GTGT  CTA CCTTGTTG
                                 || ||||  ||| ||||||||
                                 GG CACA  GAT GGAACAAC
                                  A   C_  _
GAM871  FLJ10101 5'  CGGGGAGACAGGAACACGGG   45264          A__
                                 CCCGTGTTCCT   TCCTTG
                                 ||||||||||   ||||||
                                 GGGCACAAGGA   AGGGGC
                                       CAG
GAM871  FLJ23306 5'  AACAAAGCCACACGGGT     44555        TC  ATCC
                                 ACCCGTGT  CT    TTGTT
                                 ||||||||  ||    |||||
                                 TGGGCACA  GA    AACAA
                                      CC  ____
GAM871  KIAA0391 3'  CAAGAGACAGGAACAC      27906         A  _
                                 GTGTTCCT TC CTTG
                                 |||||||| || ||||
                                 CACAAGGA AG GAAC
                                      C  A
GAM871  MGC13251 3'  GATGGAGACAGGGACACGGG   51148          A  C TG
                                 CCCGTGTTCCT TC T  TT
                                 |||||||||| || |  ||
                                 GGGCACAGGGA AG G  AG
                                       C  A GT
GAM871  SEMA3E   3'  CAACTTGGAGAAACAGGG    24879     G    CCTA   TT
                                 CCC TGTT    TCC  GTTG
                                 ||| ||||    |||  ||||
                                 GGG ACAA    AGG  CAAC
                                   _    AG__   TT
GAM871  SLC26A9  3'  CAACACAGGGAAAACGG     53617     G    ATCCT
                                 CCGT TTCCT     TGTTG
                                 |||| |||||     |||||
                                 GGCA AAGGG     ACAAC
                                   A     AC___
GAM871  SLC26A9  3'  CAACACAGGGAAAACGG     56178     G    ATCCT
                                 CCGT TTCCT     TGTTG
                                 |||| |||||     |||||
                                 GGCA AAGGG     ACAAC
                                   A     AC___
GAM871  LOC147639 3'  CAATAACAGGGACAC       78377         ATCC
                                 GTGTTCCT    TTGTTG
                                 ||||||||    ||||||
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                                CACAGGGA    AATAAC
                                     C___
GAM871   LOC148809 3'  CAAGGGTAAGAGCACGGG    79001         C
                                CCCGTGTTC TATCCTTG
                                ||||||||| ||||||||
                                GGGCACGAG ATGGGAAC
                                      A
GAM871   LOC150287 3'  CAACCTCTCAGGAACAGGG   79781     G      ATCCTT
                                CCC TGTTCCT     GTTG
                                ||| |||||||     ||||
                                GGG ACAAGGA     CAAC
                                  _      CTCTC_
GAM871   LOC157869 5'  CAACAAGGAGAGAACACG    81625        CTA
                                CGTGTTC   TCCTTGTTG
                                |||||||   |||||||||
                                GCACAAG   AGGAACAAC
                                     AG_
GAM871   LOC219743 3'  AGGGACAGAAACAGGAGT    93125    _ G    C  A
                                AC CC TGTT CT TCCTT
                                || || |||| || |||||
                                TG GG ACAA GA AGGGA
                                 A  _    A  C
GAM871   LOC221495 3'  CAACAAGGCCCAGGAAAC    93855    G     AT_
                                GT TTCCT   CCTTGTTG
                                || |||||   ||||||||
                                CA AAGGA   GGAACAAC
                                 _     CCC
GAM871   LOC221760 3'  CAACAAGGATACCAC       93782     TTCC
                                GTG    TATCCTTGTTG
                                |||    ||||||||||
                                CAC    ATAGGAACAAC
                                  C___
GAM871   LOC253289 5'  CAAGCAGGAACAGGGGT     96049      G      ATC
                                ACCC TGTTCCT   CTTG
                                |||| |||||||   ||||
                                TGGG ACAAGGA   GAAC
                                   G      C__
GAM871   LOC255652 3'  GGGATGGAACACAGG       96721     C      T
                                CC GTGTTCC ATCCT
                                || ||||||| |||||
                                GG CACAAGG TAGGG
                                 A      _
GAM871   LOC257206 5'  CAACGGCAGAAGCACGGG    97095         C  AT C
                                CCCGTGTT CT  C TTG
                                |||||||| ||  | |||
                                GGGCACGA GA  G AAC
                                     A  CG C
GAM871   LOC90342  5'  CAACAAGGACAAGGGCATCGCG 62353      T__    A_
                                CGTG   TCCT  TCCTTGTTG
                                ||||   ||||  |||||||||
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                                GCGC  GGGA  AGGAACAAC
                                  TAC   AC
GAM872  ANK1    3'  AGAGCCACCCCGGCCCGGCCTC 60385        A_  TT
          CA                    TGGAGGCTGG  TG  GGTGGCTCT
                                ||||||||||  ||  |||||||||
                                ACCTCCGGCC  GC  CCACCGAGA
                                     CG  C_
GAM872  HIVEP3  5'  GAGCCACCCCCAGCATCCA   44438     G    ATGTT
                                TGGA GCTGG    GGTGGCTC
                                |||| |||||    ||||||||
                                ACCT CGACC    CCACCGAG
                                  A    C____
GAM872  LNK     3'  AGAGCCATTCAGTACAACCCCC 18456    A  C  GA_  TT
          A                     TGG GG TG   TG  GGTGGCTCT
                                ||| || ||   ||  |||||||||
                                ACC CC AC   AC  TTACCGAGA
                                  C  A  ATG  __
GAM872  NDST1   3'  GAGGACTCCCAGCCTCCA   7744         AT   GGTGG
                                TGGAGGCTGG  GTT    CTC
                                ||||||||||  |||    |||
                                ACCTCCGACC  CAG    GAG
                                     CT   ______
GAM872  RFP     3'  ACCAGATGTCCACCTCCA    21490       C     _
                                TGGAGG TGGATGT TGGT
                                |||||| ||||||| ||||
                                ACCTCC ACCTGTA ACCA
                                   _      G
GAM872  TMPRSS3  3'  AGCCACCAACAGCCACTC    43788    GC   A
                                GAG  TGG TGTTGGTGGCT
                                |||  ||| ||||||||||
                                CTC  ACC ACAACCACCGA
                                  __   G
GAM872  TMPRSS3  3'  AGCCACCAACAGCCACTC    50501    GC   A
                                GAG  TGG TGTTGGTGGCT
                                |||  ||| ||||||||||
                                CTC  ACC ACAACCACCGA
                                  __   G
GAM872  TMPRSS3  3'  AGCCACCAACAGCCACTC    50521    GC   A
                                GAG  TGG TGTTGGTGGCT
                                |||  ||| ||||||||||
                                CTC  ACC ACAACCACCGA
                                  __   G
GAM872  XRCC3    3'  AGCATATCCCACCAACCTCCA  18334      C   A  TT   _
                                TGGAGG TGG TG  GGTG GCT
                                |||||| ||| ||  |||| |||
                                ACCTCC ACC AC  CTAT CGA
                                   A   _  C_   A
GAM872  ARHU    3'  AGAGCCACCAAAGTCACATCCA 41070     GGCTG   G
                                TGGA    GAT TTGGTGGCTCT
                                ||||    ||| ||||||||||
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                                ACCT    CTG AACCACCGAGA
                                  ACA__  A
GAM872  FBXO27   3'  CCTCCGATCCAGCCCCA    74507    A     TG   T
                                TGG GGCTGGA  TTGG GG
                                ||| |||||||  |||| ||
                                ACC CCGACCT  AGCC CC
                                  _     ___   T
GAM872  FLJ22174 5'  AGCCACCTGTCAACAAACCCCC 41673    A  C_  GA  TT_
           A                     TGG GG  TG  TG   GGTGGCT
                                ||| ||  ||  ||   |||||||
                                ACC CC  AC  AC   CCACCGA
                                  C  AA  A_  TGT
GAM872  GMPPB    3'  ACCAACACCCAACCTCC    95716      C   A
                                GGAGG TGG TGTTGGT
                                ||||| ||| |||||||
                                CCTCC ACC ACAACCA
                                   A   C
GAM872  JM4      3'  AGAGCCACCTACATCCAGCCCC 23300     A        T
           A                     TGG GGCTGGATGT GGTGGCTCT
                                ||| |||||||||| |||||||||
                                ACC CCGACCTACA CCACCGAGA
                                  _        T
GAM872  PIP5K2B  3'  AGCTGTCTTCCAGCCTCCA   13064          TGTT  TG
                                TGGAGGCTGGA   GG  GCT
                                ||||||||||    ||  |||
                                ACCTCCGACCT   CT  CGA
                                       T___  GT
GAM872  SOX7     3'  AGAGCCACCGCGCCCAGCCTAC 48723    G     A   T
           A                     TG AGGCTGG TGT GGTGGCTCT
                                || ||||||| ||| |||||||||
                                AC TCCGACC GCG CCACCGAGA
                                 A      C  _
GAM872  ZIC4     5'  GAACCACCACCACCTCCA    49620       C   ATGT     C
                                TGGAGG TGG    TGGTGG TC
                                ||||||  |||    ||||||  ||
                                ACCTCC ACC    ACCACC AG
                                   _  ____      A
GAM872  LOC149460 5'  AGAAGTGAACATCCAGCCCCA  84439     A         GG GG
                                TGG GGCTGGATGTT  T  CT
                                ||| ||||||||||  |  ||
                                ACC CCGACCTACAA  G  GA
                                  _         GT AA
GAM872  LOC153196 5'  GAGGACTCCCAGCCTCCA    85961          AT   GGTGG
                                TGGAGGCTGG  GTT    CTC
                                ||||||||||  |||    |||
                                ACCTCCGACC  CAG    GAG
                                       CT  _____
GAM872  LOC162333 5'  AGAGCCATGGGCACCCAGCCTC 87117          A    G
           C                     GGAGGCTGG TGTT GTGGCTCT
                                |||||||| |||| ||||||||
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                                CCTCCGACC ACGG TACCGAGA
                                     C   G
GAM872  LOC200734 3'  ACCTTCAGCCAGCCTCCA    88858          A  TT
                                TGGAGGCTGG TG  GGT
                                |||||||||| ||  |||
                                ACCTCCGACC AC  CCA
                                      G  TT
GAM872  LOC221751 5'  AGCCACCTGTCAACAAACCCCC 92046     A  C_  GA  TT_
          A                      TGG GG  TG  TG   GGTGGCT
                                 ||| ||  ||  ||   |||||||
                                 ACC CC  AC  AC   CCACCGA
                                   C  AA  A_  TGT
GAM872  LOC256032 5'  AGCCTGGGATCCAGCCCCC   97492    A       G TG TG
                                 GG GGCTGGAT T  G  GCT
                                 || ||||||||  |  |  |||
                                 CC CCGACCTA G  C  CGA
                                  C       G GT __
GAM872  LOC51762  3'  AGCACAGGTCACCCAGCCTC   33268        A  TTG_  G
                                 GAGGCTGG TG    GTG CT
                                 |||||||| ||    ||| ||
                                 CTCCGACC AC    CAC GA
                                      C  TGGA  _
GAM872  LOC96597  5'  AGCCCAGGACCCAGCATCCA   66906     G    AT   GGT
                                 TGGA GCTGG  GTT   GGCT
                                 |||| |||||  |||   ||||
                                 ACCT CGACC  CAG   CCGA
                                   A    __   GAC
GAM873  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                 ATTT ACTTT   TGTCTGAG
                                 |||| |||||   ||||||||
                                 TAAA TGAAA   ACAGATTC
                                   A    T__
GAM873  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                 CATTT   TTT AC GTCTGAGAT
                                 |||||   ||| || |||||||||
                                 GTAAA   AAA TG TAGACTCTA
                                    TA_   T  _
GAM873  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                 CATTTCACTTTC CTG
                                 |||||||||||| |||
                                 GTAAAGTGAAAG GAT
                                                _
GAM873  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
          TG                      CATTTCACTTTCACTGTCTGAGAT
                                  ||||||||||||||||||||||||
                                  GTAAAGTGAAAGTGACAGACTCTA

GAM873  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                 CA  TTCACTGTCTG GA
                                 ||  |||||||||| ||
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                                GT  AGGTGACAGAC CT
                                 AT         C
GAM873  PHYH    3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                     A
GAM873  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM873  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM873  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM873  CG012   5'  CTCACTCTGAAAGTGAA     83218          CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM873  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                |||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM873  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                |||||||       |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM873  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281         CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM873  KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM873  KLHL6   3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
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                                AAAG GAC AGACTCTA
                                  _  G
GAM873  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM873  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM873  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM873  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148         TCAC   C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM873  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM873  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM873  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM873  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM873  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||   |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM873  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
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                                GTAAAGTGAA GTGACA
                                      _
GAM874  OCRL     3'  ACACTAAGTTGGTGTACTGCCT 4255       ATA   TG  C   C
                                AGGCA   ATAT  GC TAG GT
                                |||||   ||||  || ||| ||
                                TCCGT   TGTG  TG ATC CA
                                   CA_   GT  A   A
GAM874  OCRL     3'  ACACTAAGTTGGTGTACTGCCT 7821       ATA   TG  C   C
                                AGGCA   ATAT  GC TAG GT
                                |||||   ||||  || ||| ||
                                TCCGT   TGTG  TG ATC CA
                                   CA_   GT  A   A
GAM874  GTF3C2   3'  GGATCCAATATTACTGCCT   7724       A       __
                                AGGCA TAATATTGG  CC
                                ||||| |||||||||  ||
                                TCCGT ATTATAACC  GG
                                   C        TA
GAM874  RAB40C   3'  GACGCCAGGCCAGTGCCGCCT  40979     AATAA       A
                                AGGC    TATTGGCCT GCGTC
                                ||||    ||||||||| |||||
                                TCCG    GTGACCGGA CGCAG
                                  CC___        C
GAM874  LOC127428 3'  GACGGGACTAACATTATTGCCT 74666         A   _  TAG
                                AGGCAATAAT TTGG CC   CGTC
                                |||||||||| |||| ||   ||||
                                TCCGTTATTA AATC GG   GCAG
                                      C   A  ___
GAM874  LOC150225 3'  GACGCTAGGACACCCTCTGCCT 84995      ATAATAT  G
                                AGGCA      TG CCTAGCGTC
                                |||||      || |||||||||
                                TCCGT      AC GGATCGCAG
                                   CTCCC__  A
GAM874  LOC152897 3'  GACAGTCCCAATATTATGCCT  80727      A       CCTA  _
                                AGGCA TAATATTGG    GC GTC
                                ||||| |||||||||    || |||
                                TCCGT ATTATAACC    TG CAG
                                   _       C___  A
GAM875  APM1     3'  TACCCTAAACTCTCTGGG    16600        ACTCA   T
                                TCCAGAGA    AGG GTG
                                ||||||||    ||| |||
                                GGGTCTCT    TCC CAT
                                     CAAA_  _
GAM875  APPBP2   3'  TTGCATTTAAGTTCCCTAGGA  21086    _  A    CA    TG
                                TCC AG GAACT  AGGTG  A
                                ||| || |||||  |||||  |
                                AGG TC CTTGA  TTTAC  T
                                  A  C    A_    GT
GAM875  AQP6     5'  CATGCTTGAGTCCCCTGGG   53915      AGA      G
                                TCCAG   ACTCAAG TGTG
                                |||||   ||||||| ||||
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                                GGGTC   TGAGTTC GTAC
                                  CCC     _
GAM875  ARAF1    3'  CACTCAGAACCTCTCTGGA   63937       AC_  AA
                                TCCAGAGA   TC  GGTG
                                ||||||||   ||  ||||
                                AGGTCTCT   AG  TCAC
                                    CCA  AC
GAM875  C8orf1   3'  TACTGGCTTGAATTTTCTGGA  15087       C    G _
                                TCCAGAGAA TCAAG T GTG
                                ||||||||| ||||| | |||
                                AGGTCTTTT AGTTC G CAT
                                     A    G T
GAM875  CA12     3'  CACTTCGGCTCTCTGGA     6875        A  CA
                                TCCAGAGA CT  AGGTG
                                |||||||| ||  |||||
                                AGGTCTCT GG  TTCAC
                                    C  C_
GAM875  CANX     3'  ATTCACACCTCTGTCCCTC   87480     A_  TCA
                                GAG  AC   AGGTGTGAAT
                                |||  ||   ||||||||||
                                CTC  TG   TCCACACTTA
                                  CC  TC_
GAM875  CEP1     5'  TAGACCCCGAACTCTTTGGA  22817       AC  AA   G
                                TCCAGAGA  TC  GGT TG
                                ||||||||  ||  ||| ||
                                AGGTTTCT  AG  CCA AT
                                    CA  CC   G
GAM875  FCAR     3'  TTCCTCGCTAGAGTTCTCCAGA 55807    CA      AA   T_
                                TC  GAGAACTC  GGTG  GAA
                                ||  ||||||||  ||||  |||
                                AG  CTCTTGAG  TCGC  CTT
                                  AC      A_   TC
GAM875  FCAR     3'  TTCCTCGCTAGAGTTCTCCAGA 55817    CA      AA   T_
                                TC  GAGAACTC  GGTG  GAA
                                ||  ||||||||  ||||  |||
                                AG  CTCTTGAG  TCGC  CTT
                                  AC      A_   TC
GAM875  HMGCR    3'  ATTCACACAGGGCTCTTGGA   5972      _  AA  CAAG
                                TCCA GAG  CT   GTGTGAAT
                                |||| |||  ||   ||||||||
                                AGGT CTC  GA   CACACTTA
                                  T   GG  ____
GAM875  MME      3'  TACTCTTGTTGAGTTCTATAGA 23490    CAG      __  T
                                TC   AGAACTCAA  GG GTG
                                ||   |||||||||  || |||
                                AG   TCTTGAGTT  TC CAT
                                  ATA       GT  T
GAM875  MME      3'  TACTCTTGTTGAGTTCTATAGA 6143     CAG      __  T
                                TC   AGAACTCAA  GG GTG
                                ||   |||||||||  || |||
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                                AG   TCTTGAGTT  TC CAT
                                 ATA        GT  T
GAM875  MME      3'  TACTCTTGTTGAGTTCTATAGA 23500    CAG        __  T
                                TC   AGAACTCAA  GG GTG
                                ||   |||||||||  || |||
                                AG   TCTTGAGTT  TC CAT
                                 ATA        GT  T
GAM875  MME      3'  TACTCTTGTTGAGTTCTATAGA 23512    CAG        __  T
                                TC   AGAACTCAA  GG GTG
                                ||   |||||||||  || |||
                                AG   TCTTGAGTT  TC CAT
                                 ATA        GT  T
GAM875  NEU3     3'  CACCTGAACTCTCTGGA     21846         AC   A
                                TCCAGAGA  TCA GGTG
                                ||||||||  ||| ||||
                                AGGTCTCT  AGT CCAC
                                     CA  _
GAM875  P53AIP1  3'  CACCCACTGAACTTTCTGGA   42080         AC   A_  T
                                TCCAGAGA  TCA  GG GTG
                                ||||||||  |||  || |||
                                AGGTCTTT  AGT  CC CAC
                                     CA   CA  _
GAM875  PAICS    3'  TACCTTTAGTTCTCTG      21260          C
                                CAGAGAACT AAGGTG
                                ||||||||| ||||||
                                GTCTCTTGA TTCCAT
                                      T
GAM875  PIR51    3'  CACTTTTTGTTAAGTTCTTTAG 21364    C       ___     T
            A                    TC AGAGAACT   CAAGG GTG
                                || ||||||||   ||||| |||
                                AG TTTCTTGA   GTTTT CAC
                                 A       ATT     T
GAM875  PLSCR1   5'  CATCGCCTGGCCCCGGCTCTCT 40856         A  CA____    _
            GGA                    TCCAGAGA CT     AGGTG TG
                                ||||||||  ||      ||||| ||
                                AGGTCTCT GG      TCCGC AC
                                     C  CCCCGG     T
GAM875  PTPN1    3'  TATTCACACCTCACGCTCTGGA 11050         AACTCA
                                TCCAGAG     AGGTGTGAATA
                                |||||||     ||||||||||||
                                AGGTCTC     TCCACACTTAT
                                     GCAC__
GAM875  RAP1A    3'  GTTTGCACAAGTTCCCTGGA   11248       A    CAAG   TG
                                TCCAG GAACT    GTG  AAT
                                ||||| |||||    |||  |||
                                AGGTC CTTGA    CAC  TTG
                                   C    A___   GT
GAM875  SYT4     3'  CACTATATTTGAGTTCTT     62435           GT__
                                GAGAACTCAAG    GTG
                                ||||||||||    |||
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                                TTCTTGAGTTT   CAC
                                      ATAT
GAM875  TCTA    3'  TAGGCCCTGAGTTTTCTG   42241          A  G
                                CAGAGAACTCA GGT TG
                                |||||||||| ||| ||
                                GTCTTTTGAGT CCG AT
                                      C   G
GAM875  VAT1    3'  CACCCTTCACTGAGTTCTCTGG 21044           ____  T
          A                     TCCAGAGAACTCA   AGG GTG
                                |||||||||||||   ||| |||
                                AGGTCTCTTGAGT   TCC CAC
                                       CACT  _
GAM875  ZFH4    5'  CACCTCAGCTCCCTGGA    45294      A  A  CA
                                TCCAG GA CT  AGGTG
                                ||||| || ||  |||||
                                AGGTC CT GA  TCCAC
                                   C  C  C_
GAM875  ZFP103  5'  TATTCCGAGCTCTCTGGA    19026       A  AA  T
                                TCCAGAGA CTC  GG GTG
                                |||||||| |||  || |||
                                AGGTCTCT GAG  CC TAT
                                     C   __  T
GAM875  ZNF202  3'  TTGCAGCCAAGTTCCCTGG   12913     A    CAA  _  TG
                                CCAG GAACT   GG TG  A
                                |||| |||||   || ||  |
                                GGTC CTTGA   CC AC  T
                                  C    A__  G  GT
GAM875  C1orf25 5'  ATTCACGTCAGTTCTCTG    72532        CAA GT
                                CAGAGAACT   G  GTGAAT
                                |||||||||   |  ||||||
                                GTCTCTTGA   C  CACTTA
                                     ___ TG
GAM875  C20orf177 3'  TACTTTTGAGTTCTC      62154          T
                                GAGAACTCAAGG GTG
                                |||||||||||| |||
                                CTCTTGAGTTTT CAT
                                          _
GAM875  CG012   3'  GCAGTCTGAGTTCTTCAGA   83221    CA       A  _
                                TC  GAGAACTCA GG TGT
                                ||  ||||||||| || |||
                                AG  TTCTTGAGT CT ACG
                                 AC        _  G
GAM875  CRK7    3'  TTCCATCCAGTTCTCTG     33256        CAA   T
                                CAGAGAACT   GGTG GAA
                                |||||||||   |||| |||
                                GTCTCTTGA   CTAC CTT
                                      C__   _
GAM875  DIO2    3'  ATTCACACTGTTGTCCTT    25678     A  TCAA
                                GAG AC    GGTGTGAAT
                                ||| ||    |||||||||
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                                TTC TG   TCACACTTA
                                  C TTG_
GAM875  DIO2     3' ATTCACACTGTTGTCCTT    5826     A TCAA
                                GAG AC   GGTGTGAAT
                                ||| ||   |||||||||
                                TTC TG   TCACACTTA
                                  C TTG_
GAM875  DKFZP434A043 3' CACACTTAAACTCTGTGGA   31187     G  ACTCA
                                TCCA AGA    AGGTGTG
                                |||| |||    |||||||
                                AGGT TCT    TTCACAC
                                  G  CAAA_
GAM875  DKFZp434F1819 3' TCACACCTCCTTTTTG      50009       ACTCA
                                CAGAGA    AGGTGTGA
                                ||||||    ||||||||
                                GTTTTT    TCCACACT
                                   CC___
GAM875  DPCR1    3' CATCTCTGAGTTCTCAGGA   55120    A       _
                                TCC GAGAACTCA AGGTG
                                ||| ||||||||| |||||
                                AGG CTCTTGAGT TCTAC
                                  A       C
GAM875  FLJ10898  3' ATTCACACTGATTTTGTCTGGA 59421       G  CTCAA
                                TCCAGA AA    GGTGTGAAT
                                |||||| ||    |||||||||
                                AGGTCT TT    TCACACTTA
                                   G  TTAG_
GAM875  FLJ11193  3' TATTTTGAATCTCTG      37154       AC
                                CAGAGA  TCAAGGTG
                                ||||||  ||||||||
                                GTCTCT  AGTTTTAT
                                   A_
GAM875  FLJ13769  3' CACTCAAGCTCTCTGGA    46603        A  CAA
                                TCCAGAGA CT   GGTG
                                |||||||| ||   ||||
                                AGGTCTCT GA   TCAC
                                     C  AC_
GAM875  FLJ13782  3' GCCTGAGCTTTCTGGA     46169        A   A
                                TCCAGAGA CTCA GGT
                                |||||||| |||| |||
                                AGGTCTTT GAGT CCG
                                     C   _
GAM875  FLJ20555  3' CAGACCTCAGCTCTCTGGA   35393        A  CA   G
                                TCCAGAGA CT  AGGT TG
                                |||||||| ||  |||| ||
                                AGGTCTCT GA  TCCA AC
                                     C  C_   G
GAM875  FLJ23142  3' TTTTGAGTTCCTAGA      44727    C  A
                                TC AG GAACTCAAGG
                                || || ||||||||||
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                                AG TC CTTGAGTTTT
                                 A  _
GAM875  FLJ30092  5'  TATTCACACCTCACTTCCTG  58691     A   CTCA
                                CAG GAA    AGGTGTGAATA
                                ||| |||    ||||||||||
                                GTC CTT    TCCACACTTAT
                                  _  CAC_
GAM875  GRID1     3'  TATTCAAGCAAGTTCTCTAGG  68501    _      CAAG  G
                                CC AGAGAACT    GT TGAATA
                                || ||||||||    || ||||||
                                GG TCTCTTGA    CG ACTTAT
                                 A       A___  A
GAM875  HPCAL4    3'  CATCTTGTGCCCTCTGGA    32732        AACT
                                TCCAGAG    CAAGGTG
                                |||||||    |||||||
                                AGGTCTC    GTTCTAC
                                    CCGT
GAM875  KIAA0229  3'  CATTTTGATTCTCTG       92423        C
                                CAGAGAA TCAAGGTG
                                ||||||| ||||||||
                                GTCTCTT AGTTTTAC
                                   _
GAM875  KIAA0295  3'  GCCTTGGGTTCTCCAGA     68105    CA
                                TC  GAGAACTCAAGGT
                                ||  |||||||||||||
                                AG  CTCTTGGGTTCCG
                                 AC
GAM875  KIAA0420  3'  TACCCTGCACTCTCTGGA    63366        ACTCA   T
                                TCCAGAGA     AGG GTG
                                ||||||||     ||| |||
                                AGGTCTCT     TCC CAT
                                    CACG_  _
GAM875  KIAA0565  3'  TATTTTTAAGTCTCTGGA    66897        ACTC
                                TCCAGAGA    AAGGTG
                                ||||||||    ||||||
                                AGGTCTCT    TTTTAT
                                    GAAT
GAM875  KIAA1036  3'  CATCTTGGTCCTCCGGA     29816     A   A  T
                                TCC GAG AC CAAGGTG
                                ||| ||| || |||||||
                                AGG CTC TG GTTCTAC
                                  C   C  _
GAM875  KIAA1240  3'  TATTCATGTTTGAGTTC     66737        G TG
                                GAACTCAA G  TGAATA
                                |||||||| |  ||||||
                                CTTGAGTT T  ACTTAT
                                    _ GT
GAM875  KIAA1297  5'  CACTGCAGCCCGAGTTCTCTGG 72170          AA  _____
                                CCAGAGAACTC  GGT    GTG
                                ||||||||||  |||    |||
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                                GGTCTCTTGAG  CCG    CAC
                                      C_   ACGT
GAM875  KIAA1579  3'  CACTTTGATTTCCCTGGA    36605      A   C
                                TCCAG GAA TCAAGGTG
                                ||||| ||| ||||||||
                                AGGTC CTT AGTTTCAC
                                   C   T
GAM875  MAB21L2   5'  TTCGCAGCTCTCTGGA      21233        ACTCAA G
                                TCCAGAGA     G TGTGAA
                                ||||||||     | ||||||
                                AGGTCTCT     C ACGCTT
                                     _______ G
GAM875  MAP2K6    5'  CATCTTGATTCCCTG       10868     A   C
                                CAG GAA TCAAGGTG
                                ||| ||| ||||||||
                                GTC CTT AGTTCTAC
                                  C   _
GAM875  MGC21688  3'  ATTCACGCAGAGCTCTCTG    58265       A   AAG
                                CAGAGA CTC   GTGTGAAT
                                |||||| |||   ||||||||
                                GTCTCT GAG   CGCACTTA
                                   C   A__
GAM875  MMPL1     3'  TATTCCTCTGTGTGTTCTCTGG 14722          T  A  TGT
          A                      TCCAGAGAAC CA GG   GAATA
                                ||||||||||| || ||   |||||
                                AGGTCTCTTG GT TC   CTTAT
                                      T  G  TC_
GAM875  NDUFB6    3'  ATTTACTGAATTTTCTGGA    10197         C   AGGT
                                TCCAGAGAA TCA    GTGAAT
                                ||||||||| |||    ||||||
                                AGGTCTTTT AGT    CATTTA
                                     A  _____
GAM875  SSB-4     3'  CACTGACTCACAGTTCTCTGGA 55097          CA_  GT_
                                TCCAGAGAACT   AG   GTG
                                ||||||||||   ||   |||
                                AGGTCTCTTGA   TC   CAC
                                      CAC  AGT
GAM875  STAM2     3'  TTCAAGCTAGTTCTCTG     19570         CAA   G
                                CAGAGAACT   GGT TGAA
                                |||||||||   ||| ||||
                                GTCTCTTGA   TCG ACTT
                                     ___   A
GAM875  SYT12     3'  TAGCTTGAGTTCCCTAGA    94740    C  A       G
                                TC AG GAACTCAAG TG
                                || || ||||||||| ||
                                AG TC CTTGAGTTC AT
                                 A  C        G
GAM875  TED       3'  TATTCACACCTTTCCATCCCTG 31643     A  ACTC
                                CAG GA    AAGGTGTGAATA
                                ||| ||    ||||||||||||
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                                GTC CT    TTCCACACTTAT
                                  C  ACCT
GAM875  TRAD     3'  CACTCCGTGCAGTTCTCTG   22951         _ A  T
                                CAGAGAACT CA GG GTG
                                ||||||||| || || |||
                                GTCTCTTGA GT CC CAC
                                     C  G  T
GAM875  TRIM22   3'  CATCTACAAGTTCTCTGGA   20286          CA_
                                TCCAGAGAACT   AGGTG
                                ||||||||||   |||||
                                AGGTCTCTTGA   TCTAC
                                      ACA
GAM875  TUB      3'  ATTCAGAACTTCAAGTTCTCTT 12425    C      CA   G_
            GA                    TC AGAGAACT  AGGT  TGAAT
                                || ||||||||  ||||  |||||
                                AG TCTCTTGA  TTCA  ACTTA
                                 T       AC    AG
GAM875  LOC120939 3'  CATCTCTCGAGTTCTTGGA   76250     G      A  GT
                                TCCA AGAACTC AG  GTG
                                |||| ||||||| ||  |||
                                AGGT TCTTGAG TC  TAC
                                  _      C  TC
GAM875  LOC122258 3'  CACGCCCACGTTCTCTG     59141        TCAA
                                CAGAGAAC    GGTGTG
                                ||||||||    ||||||
                                GTCTCTTG    CCGCAC
                                     CAC_
GAM875  LOC124842 3'  CACCTTCCTGAGTTCTCAGGA  75658     A       ___
                                TCC GAGAACTCA   AGGTG
                                ||| |||||||||   |||||
                                AGG CTCTTGAGT   TCCAC
                                  A        CCT
GAM875  LOC138050 5'  TCCATAATGAACTTCTCTGGA  75299         C_   AG   T
                                TCCAGAGAA  TCA  GTG GA
                                |||||||||  |||  ||| ||
                                AGGTCTCTT  AGT  TAC CT
                                     CA   AA  _
GAM875  LOC146839 5'  ATTCTCTTGAGTTTTCTAGA   83806    C          TGT
                                TC AGAGAACTCAAGG   GAAT
                                || ||||||||||||   ||||
                                AG TCTTTTGAGTTCT   CTTA
                                 A          ___
GAM875  LOC150095 5'  CACACCTTCCCTCTCTG     84855       ACTC
                                CAGAGA    AAGGTGTG
                                ||||||    ||||||||
                                GTCTCT    TTCCACAC
                                   CCC_
GAM875  LOC151094 3'  CACGCTTGGTTCCCT       65293    A    CA
                                AG GAACT  AGGTGTG
                                || |||||  |||||||
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                                TC CTTGG  TTCGCAC
                                 C    __
GAM875  LOC153603 3'  CATCTTCGAGCTCTCTGGA   80900        A  _
                                TCCAGAGA CTC AAGGTG
                                |||||||| ||| ||||||
                                AGGTCTCT GAG TTCTAC
                                     C   C
GAM875  LOC153811 3'  ATTCACACAGCTCCCTGGG   80942      A  A  CAAG
                                TCCAG GA CT   GTGTGAAT
                                ||||| || ||   ||||||||
                                GGGTC CT GA   CACACTTA
                                   C  C  ____
GAM875  LOC163341 3'  CATCTTGAGCCCCTTGGA    82119      AGAA
                                TCCAG   CTCAAGGTG
                                |||||   |||||||||
                                AGGTT   GAGTTCTAC
                                   CCCC
GAM875  LOC199800 5'  CACCCAGTGAGGTCTCTGGA  89856        A   A_  T
                                TCCAGAGA CTCA  GG GTG
                                |||||||| ||||  || |||
                                AGGTCTCT GAGT  CC CAC
                                     G   GA  _
GAM875  LOC254439 3'  TTCACAGCTCTCTGGA      94749        ACTCAA G
                                TCCAGAGA     G TGTGAA
                                ||||||||     | ||||||
                                AGGTCTCT     C ACACTT
                                     _______ G
GAM875  LOC255465 3'  GCCTTGAGTCTCTGGA      97289        A
                                TCCAGAGA CTCAAGGT
                                |||||||| ||||||||
                                AGGTCTCT GAGTTCCG
                                     _
GAM875  LOC256207 3'  TATTTTCAAGTCTCTGGA    95176        ACTC
                                TCCAGAGA   AAGGTG
                                ||||||||   ||||||
                                AGGTCTCT   TTTTAT
                                     GAAC
GAM875  LOC257354 3'  TACCCTGCACTCTCTGGA    95099        ACTCA  T
                                TCCAGAGA    AGG GTG
                                ||||||||    ||| |||
                                AGGTCTCT    TCC CAT
                                     CACG_  _
GAM875  LOC91308  3'  TGTGCCTTAAGTTCTCT     65568        C   TG
                                AGAGAACT AAGG  TG
                                |||||||| ||||  ||
                                TCTCTTGA TTCC  GT
                                     A   GT
GAM875  LOC91695  5'  TATTCCAATCAAGTTCTCTG  66971        CAAGG  T
                                CAGAGAACT    TG GAATA
                                |||||||||    || |||||
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                                GTCTCTTGA     AC CTTAT
                                      ACTA_ _
GAM875  LOC93259  5'  TACAGCCTTGAGTTCCTTGGA  71826       A        _
                                TCCAG GAACTCAAGG TGTG
                                ||||| |||||||||| ||||
                                AGGTT CTTGAGTTCC ACAT
                                   C         G
GAM876  USP14     3'  AGCCTGGCCACATGGTGAA    17655       _        A
                                TTCAC ATGTGGCCA GTT
                                ||||| ||||||||| |||
                                AAGTG TACACCGGT CGA
                                   G        C
GAM876  C1orf16   3'  CATGTCCCCAGCCACATGGGAA 29228      A       CAAGTTAT
                                TTC CATGTGGC       CATG
                                ||| ||||||||       ||||
                                AAG GTACACCG       GTAC
                                  G       ACCCCT__
GAM876  FLJ10702  3'  CATGATAAAGTCAGCACACA   36439      _  CAAG_
                                TGTG GC     TTATCATG
                                |||| ||     ||||||||
                                ACAC CG     AATAGTAC
                                  A  ACTGA
GAM876  FLJ14281  3'  CATGATCTGTTTGGCCACATG  46213           TT_
                                CATGTGGCCAAG   ATCATG
                                ||||||||||||   ||||||
                                GTACACCGGTTT   TAGTAC
                                      GTC
GAM876  HYPK      3'  AGCCTGGCCAACATGTGAA    33077         _    A
                                TTCACATGT GGCCA GTT
                                ||||||||| ||||| |||
                                AAGTGTACA CCGGT CGA
                                      A    C
GAM876  KIAA0445  5'  CATGATAACTCTGTGACATAGA 27951      AC    G  CA
           A                     TTC  ATGT GC  AGTTATCATG
                                |||  |||| ||  ||||||||||
                                AAG  TACA TG  TCAATAGTAC
                                  A_   G  TC
GAM876  KIAA1189  3'  TGGTAGCTACACATG       72048       GCCA
                                CATGTG    AGTTATCA
                                ||||||    ||||||||
                                GTACAC    TCGATGGT
                                   A___
GAM876  LIPI      5'  CATAATAACTTGTGCCA      79565      _      C
                                TGGC CAAGTTAT ATG
                                |||| |||||||| |||
                                ACCG GTTCAATA TAC
                                  T       A
GAM876  SEMA4F    3'  GACCTGGCCACATGTG       14941            A
                                CACATGTGGCCA GTT
                                |||||||||||| |||
```

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                                GTGTACACCGGT CAG
                                       C
GAM876  ZNF300   3'  CATGACCCCTAAAGCTACATGT 53475         CA_  TTA
                                ACATGTGGC   AG   TCATG
                                |||||||||   ||   |||||
                                TGTACATCG   TC   AGTAC
                                     AAA  CCC
GAM876  LOC149579 5'  CATGATAACTCTGTGACATAGA 71131     AC    G  CA
          A                      TTC  ATGT GC  AGTTATCATG
                                 |||  |||| ||  ||||||||||
                                 AAG  TACA TG  TCAATAGTAC
                                   A_    G  TC
GAM876  LOC92223  5'  CATGATAGTTCCCACATGGAA  68520     A      CCA GT
                                 TTC CATGTGG   A  TATCATG
                                 ||| |||||||   |  |||||||
                                 AAG GTACACC   T  ATAGTAC
                                   _      C__ TG
GAM877  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                 ATTT ACTTT   TGTCTGAG
                                 |||| |||||   ||||||||
                                 TAAA TGAAA   ACAGATTC
                                    A     T__
GAM877  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875        CAC   C  T
                                 CATTT   TTT AC GTCTGAGAT
                                 |||||   ||| || |||||||||
                                 GTAAA   AAA TG TAGACTCTA
                                    TA_   T  _
GAM877  FDFT1    3'  TAGGAAAGTGAAATG       15518            A
                                 CATTTCACTTTC CTG
                                 |||||||||||| |||
                                 GTAAAGTGAAAG GAT

                                        _
GAM877  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                  ||||||||||||||||||||||||
                                  GTAAAGTGAAAGTGACAGACTCTA

GAM877  KLF4     3'  TCCCAGACAGTGGATATG     14891     CT         A
                                 CA  TTCACTGTCTG GA
                                 ||  ||||||||||| ||
                                 GT  AGGTGACAGAC CT
                                   AT          C
GAM877  PHYH     3'  ACAGTAAAAGTGAAAT      20608           C
                                 ATTTCACTTT ACTGT
                                 |||||||||| |||||
                                 TAAAGTGAAA TGACA
                                       A
GAM877  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096           CTG    A
                                 TTTCACTTTCA   TCTG GA
                                 ||||||||||   |||| ||
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                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM877  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM877  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM877  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM877  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM877  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||         |||||||||
                                GTAAAG         CAGACTCTA
                                   AAACATTT_
GAM877  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM877  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM877  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM877  NIR3     3'  GCAGTGAAAGTGCAAT      66242      T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM877  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598         CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
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                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM877  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM877  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                     TA__    TT
GAM877  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A     TC
GAM877  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                     AAAGG
GAM877  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM877  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM877  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM877  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                     _
GAM878  ADAMTS8   5'  TCGGGCCGCCAGCACCTG    22886     _     ATAAG
                                CAG TGCTGGC     CTGA
                                ||| |||||||     ||||
                                GTC ACGACCG     GGCT
                                  C      CCG__
GAM878  BAP1     3'  TCAGGGACCCAGCACTGG     16219          CATAAG
                                CCAGTGCTGG     CTGA
                                ||||||||||     ||||
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                                GGTCACGACC     GACT
                                      CAGG__
GAM878  BF      5'  TTCAGCTTGGACACTG     8140       CTGGCA
                                CAGTG     TAAGCTGAA
                                |||||     |||||||||
                                GTCAC     GTTCGACTT
                                   AG_____
GAM878  C1QB    3'  TTCAACTCTGTGTCCCAGCACT 4923    A        __   _ C
           GGC                     G CCAGTGCTGG  CATA AG TGAA
                                | ||||||||||  |||| || ||||
                                C GGTCACGACC  GTGT TC ACTT
                                _         CT    C  A
GAM878  CHC1    3'  CAGCCCTGAGCACTGTGTC    7020     _      __ CATAA
                                GAC CAGTGCT  GG     GCTG
                                ||| |||||||  ||     ||||
                                CTG GTCACGA  CC     CGAC
                                  T       GT  _____
GAM878  CMRF35  5'  CAGAGCTGTCAGCACCGG    21929    A        TAAG
                                CC GTGCTGGCA    CTG
                                || |||||||||    |||
                                GG CACGACTGT    GAC
                                 C        CGA_
GAM878  EPHB6   3'  TCAGCCCTGGACACTGGTC    15466         _ TG CATAA
                                GACCAGTG C  G     GCTGA
                                |||||||| |  |     |||||
                                CTGGTCAC G  C     CGACT
                                     A GT C____
GAM878  EVPL    5'  CAGCCTGAGCCAGCACT     8803          A  A
                                AGTGCTGGC TA GCTG
                                ||||||||| || ||||
                                TCACGACCG GT CGAC
                                     A  C
GAM878  GARP    3'  CAGCCCAGCACTGG        18594          CATAA
                                CCAGTGCTGG    GCTG
                                ||||||||||    ||||
                                GGTCACGACC    CGAC
                                      _____
GAM878  GJB5    3'  CAGCTCGACGGCACTGG     17945          GCATA
                                CCAGTGCTG     AGCTG
                                |||||||||     |||||
                                GGTCACGGC     TCGAC
                                     AGC__
GAM878  GPR81   3'  CTTACCAGCATTAGTC      50757     C       CA
                                GAC AGTGCTGG  TAAG
                                ||| ||||||||  ||||
                                CTG TTACGACC  ATTC
                                  A       __
GAM878  IFI16   5'  AGCAAGCCAGCACTAGTC    71221     C        ATAA
                                GAC AGTGCTGGC    GCT
                                ||| |||||||||    |||
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                                CTG TCACGACCG    CGA
                                  A       AA__
GAM878  KRT4     3'  CAGCTGGGCCCAGCACTGGT  9635          _ ATA
                                ACCAGTGCTGG C   AGCTG
                                |||||||||||  |   |||||
                                TGGTCACGACC G   TCGAC
                                      C GG_
GAM878  MAP3K9   3'  TTCAGCTTCCCAAACACCAGT  60709    CA   C_   CAT
                                AC  GTG  TGG   AAGCTGAA
                                ||  |||  |||   ||||||||
                                TG  CAC  ACC   TTCGACTT
                                 AC   AA   C__
GAM878  MGAT5    5'  TCAGCTTACAGTTCCTG     10028     T_    GCA
                                CAG  GCTG   TAAGCTGA
                                |||  ||||   ||||||||
                                GTC  TGAC   ATTCGACT
                                  CT   ____
GAM878  MOCS1    3'  TTCAGCTTAACAGTTGCCCGGT 92037      A_   _   GCA
            C                    GACC  GTG CTG   TAAGCTGAA
                                ||||  ||| |||   |||||||||
                                CTGG  CGT GAC   ATTCGACTT
                                  CC   T   A__
GAM878  P23      3'  TCAGCTTATACCCGGGCT    21719     G    C_
                                AGT CTGG  ATAAGCTGA
                                ||| ||||  |||||||||
                                TCG GGCC  TATTCGACT
                                  _    CA
GAM878  PFKFB4   3'  TCAGCCACATGCAACACTGTGT 15874     _     CTG    AA_
            C                    GAC CAGTG   GCAT   GCTGA
                                ||| |||||   ||||   |||||
                                CTG GTCAC   CGTA   CGACT
                                  T    AA_    CAC
GAM878  PTPRK    3'  TTCAGCCTGTGGCCCAGCACTG 11125           __    A
            GTC                    GACCAGTGCTGG  CATA GCTGAA
                                ||||||||||||  |||| ||||||
                                CTGGTCACGACC  GTGT CGACTT
                                      CG    C
GAM878  RNPEPL1  3'  CGGATGCCAGCACCTG      36676     _       AAG
                                CAG TGCTGGCAT   CTG
                                |||  |||||||||   |||
                                GTC ACGACCGTA   GGC
                                  C       ___
GAM878  UBE2L3   3'  TCAGCCCTGGCACTGGC     12507    A      TG CATAA
                                G CCAGTGC  G    GCTGA
                                | |||||||  |    |||||
                                C GGTCACG  C    CGACT
                                 _      GT C____
GAM878  APXL2    5'  CAGCCTCAGCACTCATC     75185    CC       CATAA
                                GA  AGTGCTGG    GCTG
                                ||  ||||||||    ||||
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                                CT  TCACGACT    CGAC
                                 AC       C____
GAM878  ARHGEF9  3'  TTCAGCTTACCAAGCA     30824      _  CA
                                TGCT GG  TAAGCTGAA
                                |||| ||  |||||||||
                                ACGA CC  ATTCGACTT
                                  A  __
GAM878  CEGP1    3'  TTCAGCTTCCTCTAGCCCGG   40589    AGT    CAT
                                CC   GCTGG   AAGCTGAA
                                ||   |||||   ||||||||
                                GG   CGATC   TTCGACTT
                                 CC_    TCC
GAM878  DKFZp547D155 3'  CAGCCCTGAGACCACTGGTC   70435        CTGG  TAA
                                GACCAGTG    CA   GCTG
                                ||||||||    ||   ||||
                                CTGGTCAC    GT   CGAC
                                     CAGA  CC_
GAM878  DKFZP727G051 3'  TTCAGCCCATCAACCAGCATTG 69483           CATAA__
           GTC                    GACCAGTGCTGG      GCTGAA
                                ||||||||||||      ||||||
                                CTGGTTACGACC      CGACTT
                                      AACTACC
GAM878  DUSP14   5'  CACTGTCACCAGCACTGCTC   22834    C       CATA  C
                                GA CAGTGCTGG    AG TG
                                || |||||||||    || ||
                                CT GTCACGACC    TC AC
                                 C       ACTG  _
GAM878  FLJ10206  5'  CAGCTTATGCCAGGAGTC    35898     CAGTG
                                GAC    CTGGCATAAGCTG
                                |||    ||||||||||||||
                                CTG    GACCGTATTCGAC
                                  AG___
GAM878  FLJ20967  5'  GGCGCCCAGCACTGGTT     41962          CATAA
                                GACCAGTGCTGG    GCT
                                ||||||||||||    |||
                                TTGGTCACGACC    CGG
                                      CG___
GAM878  FLJ22569  3'  TTCAGCTTACTAAACTG     43679      GC   CA
                                CAGT  TGG  TAAGCTGAA
                                ||||  |||  |||||||||
                                GTCA  ATC  ATTCGACTT
                                  A_  __
GAM878  FOXN4    3'  TTCAGCTTGGACACACTGG    75574       C  GCA
                                CCAGTG TG   TAAGCTGAA
                                |||||| ||   |||||||||
                                GGTCAC AC   GTTCGACTT
                                   _ AG_
GAM878  GW112    3'  TTCAACTGAAGCCAGCACTGGT 21194           ATA  C
           T                    GACCAGTGCTGGC   AG TGAA
                                ||||||||||||||   || ||||
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                                TTGGTCACGACCG  TC ACTT
                                      AAG  A
GAM878  HOOK2    3'  CAGCTCACATGGCGCCCAGCAC 25256        _____  A__
            TGG                  CCAGTGCTGG   CAT  AGCTG
                                ||||||||||   |||  |||||
                                GGTCACGACC   GTA  TCGAC
                                     CGCG  CAC
GAM878  jdp2     3'  TTCAGCACAGCCAGCAT    55327       ATAA
                                GTGCTGGC   GCTGAA
                                ||||||||   ||||||
                                TACGACCG   CGACTT
                                    ACA_
GAM878  KIAA0767 3'  TCTGCTGCCAGCACAGG    60632    A      TAA  T
                                CC GTGCTGGCA  GC GA
                                || |||||||||  || ||
                                GG CACGACCGT  CG CT
                                 A       ___  T
GAM878  KIAA0923 3'  TCAGCTTGATGCATGGTC    25838     G   TGGCA
                                GACCA TGC    TAAGCTGA
                                ||||| |||    ||||||||
                                CTGGT ACG    GTTCGACT
                                   _  TA___
GAM878  KIAA0982 3'  TTCACTGTTTGCCAGCAC    25852       TA_  C
                                GTGCTGGCA  AG TGAA
                                |||||||||  || ||||
                                CACGACCGT  TC ACTT
                                     TTG  _
GAM878  KIAA1000 3'  TTCAGCTTTGCAAAGTACTGG  65281       G_  T
                                CCAGTGCT  GCA AAGCTGAA
                                ||||||||  ||| ||||||||
                                GGTCATGA  CGT TTCGACTT
                                    AA  _
GAM878  MAP3K3   3'  TCAGCCTGGGCGCTGGTC    9999        GG  TAA
                                GACCAGTGCT  CA  GCTGA
                                ||||||||||  ||  |||||
                                CTGGTCGCGG  GT  CGACT
                                     __  C__
GAM878  MGC16037 5'  CTTGTCCAGCACTAGTC    51821    C      C
                                GAC AGTGCTGG ATAAG
                                ||| |||||||| |||||
                                CTG TCACGACC TGTTC
                                  A      _
GAM878  MIDORI   3'  TCAGCTTATCCTGCAACT    73792    _  T  C
                                AGT GC GG ATAAGCTGA
                                ||| || || |||||||||
                                TCA CG CC TATTCGACT
                                  A  T  _
GAM878  MtFMT    5'  CAGTGGCGAGCACTGG      57651       G  ATAA
                                CCAGTGCT GC   GCTG
                                |||||||| ||   ||||
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                                GGTCACGA CG    TGAC
                                    G  G___
GAM878  PCDH16    5'  TCAGTTCCAACCACTGG     72826       C_   CATA
                                CCAGTG  TGG    AGCTGA
                                ||||||  |||    ||||||
                                GGTCAC  ACC    TTGACT
                                   CA   _____
GAM878  QKI       3'  CAGCTTATCAACTCGTC     65439     C   GCTGGC
                                GAC AGT     ATAAGCTG
                                ||| |||     ||||||||
                                CTG TCA     TATTCGAC
                                  C   AC____
GAM878  TNRC6     3'  CAACTTTTAGCACTG       70506         CAT   C
                                CAGTGCTGG   AAG TG
                                |||||||||   ||| ||
                                GTCACGATT   TTC AC
                                    ___   A
GAM878  TOB2      3'  CAGCCCAGGCCAGCACTG    95618          ATAA
                                CAGTGCTGGC    GCTG
                                ||||||||||    ||||
                                GTCACGACCG    CGAC
                                     GACC
GAM878  TU12B1-TY 3'  TCAGCCCACAGCACTGTC    33406     C      GCATAA
                                GAC AGTGCTG     GCTGA
                                ||| |||||||     |||||
                                CTG TCACGAC     CGACT
                                  _      ACC___
GAM878  TUSP      3'  TCAGCCTAAGAGCGCAGCACTG 39641         _  A__  A
                                CAGTGCTG GC   TA GCTGA
                                |||||||| ||   || |||||
                                GTCACGAC CG   AT CGACT
                                    G  AGA  C
GAM878  USP19     3'  TCAGCTTATGCATCTGGT    88959       TGCTG
                                ACCAG    GCATAAGCTGA
                                |||||    ||||||||||
                                TGGTC    CGTATTCGACT
                                   TA___
GAM878  ZD52F10   3'  CAGCCTGTGCCAGCCCTGG    52819     T       A
                                CCAG GCTGGCATA GCTG
                                |||| ||||||||| ||||
                                GGTC CGACCGTGT CGAC
                                   C       C
GAM878  LOC145268 3'  TCAGCTTACAAGAGCCACTG   77062      _ GGCA
                                CAGTG CT    TAAGCTGA
                                ||||| ||    ||||||||
                                GTCAC GA    ATTCGACT
                                   C  GAAC
GAM878  LOC149296 5'  CAGCTTATGGGCAGCA      79256       G_
                                TGCTG  CATAAGCTG
                                |||||  |||||||||
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                                ACGAC  GTATTCGAC
                                   GG
GAM878  LOC161877 5'  TCAGGGCAGGCCAGCGCTGG  82326          ATAAG
                                CCAGTGCTGGC    CTGA
                                ||||||||||    ||||
                                GGTCGCGACCG    GACT
                                     GACGG
GAM878  LOC163115 5'  TCAGCCCCTGACAGCACTGG  82413        G  TAA
                                CCAGTGCTG CA   GCTGA
                                ||||||||| ||   |||||
                                GGTCACGAC GT   CGACT
                                     A  CCC
GAM878  LOC196500 3'  TCAGCTCACTCAGTGGTC    87744     AGT    CATA
                                GACC   GCTGG    AGCTGA
                                ||||   |||||    |||||||
                                CTGG   TGACT    TCGACT
                                  ___    CAC_
GAM878  LOC197287 3'  TCAGCTCATGTGTTTTGCACTG 60865       T_     __
                                CAGTGC  GGCATA  AGCTGA
                                ||||||  ||||||  |||||||
                                GTCACG  TTGTGT  TCGACT
                                   TT     AC
GAM878  LOC200470 5'  TCAGCCTGCGGCGCTGG     90069        G  TAA
                                CCAGTGCTG CA   GCTGA
                                ||||||||| ||   |||||
                                GGTCGCGGC GT   CGACT
                                     _ C__
GAM878  LOC221584 3'  CAGCTTATGTGGCAC       93828       G
                                GTGCTG CATAAGCTG
                                |||||| |||||||||
                                CACGGT GTATTCGAC
                                  _
GAM878  LOC51716  3'  CAGCTCATGGCCCTAGCA    32787       ___  A
                                TGCTGG   CAT AGCTG
                                ||||||   ||| |||||
                                ACGATC   GTA TCGAC
                                   CCG   C
GAM878  LOC92196  5'  CAGAGCACCAGCACTGGC    68456   A       CATAAG
                                G CCAGTGCTGG     CTG
                                | ||||||||||     |||
                                C GGTCACGACC     GAC
                                _        ACGA__
GAM879  CD1A     5'  GAAGGAAATAACATCTGCAAA  71181          GCTAA
                                TTTGCAGATG    GTTTCCTTC
                                ||||||||||    |||||||||
                                AAACGTCTAC    TAAAGGAAG
                                     AA___
GAM879  CD1C     5'  GAAAGAAACATCTGCAAA    8329          GCTAAG
                                TTTGCAGATG     TTTC
                                ||||||||||     ||||
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                                AAACGTCTAC     AAAG
                                     AAAG__
GAM879  CPD      3'  GACCCAGCCATCTACAAG    7129      C       AA
                                TTTG AGATGGCT  GTT
                                |||| ||||||||  |||
                                GAAC TCTACCGA  CAG
                                  A       CC
GAM879  F13A1    3'  GGGAAACTTAACCACCTACAAG 91060     C  A   C
                                TTTG AG TGG TAAGTTTCCT
                                |||| || ||| ||||||||||
                                GAAC TC ACC ATTCAAAGGG
                                  A C   A
GAM879  GAGEB1   3'  AAGCTTTACAGCCTTCTGCAAA 13690        T   ___
                                TTTGCAGA GGCT   AAGTTT
                                |||||||| ||||   ||||||
                                AAACGTCT CCGA   TTCGAA
                                     T    CAT
GAM879  NR2E3    3'  AAGAAAACATCATTTGCAAA   32967         CTAA    C
                                TTTGCAGATGG    GTTT CTT
                                ||||||||||    |||| |||
                                AAACGTTTACT    CAAA GAA
                                      A___    A
GAM879  PABPN1   5'  GAAGGAAACAACATCCACAAA  16180     CA    GCTAA
                                TTTG  GATG    GTTTCCTTC
                                ||||  ||||    |||||||||
                                AAAC  CTAC    CAAAGGAAG
                                  AC    AA___
GAM879  AP3M1    3'  GATCTTAGCCATCCCAAA    23916     CA        TT
                                TTTG  GATGGCTAAG  TC
                                ||||  ||||||||||  ||
                                AAAC  CTACCGATTC  AG
                                  C_        T_
GAM879  BTBD3    3'  GATGCTTAGCTCATCTGCAAA  30310         _     T
                                TTTGCAGATG GCTAAGT TC
                                |||||||||| ||||||| ||
                                AAACGTCTAC CGATTCG AG
                                      T      T
GAM879  DKFZP564D166 3'  GAAGAAAACTTAGCCAT     47676          C
                                ATGGCTAAGTTT CTTC
                                |||||||||||| ||||
                                TACCGATTCAAA GAAG
                                       A
GAM879  ELF1     3'  GAAAAAAATGTCTTCTGCAAA  71458        T   TAAG_
                                TTTGCAGA GGC    TTTC
                                |||||||| |||    ||||
                                AAACGTCT CTG    AAAG
                                     T   TAAAA
GAM879  FBXO4    3'  AAGAAAACTTAGAAGCAAA   53111      AGATGG      C
                                TTTGC     CTAAGTTT CTT
                                |||||     |||||||| |||
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                                AAACG     GATTCAAA GAA
                                  AA____       A
GAM879  GAGE1    3'  AAGCTTTACAGCCTTCTGCAAA 7601         T   ___
                                TTTGCAGA GGCT   AAGTTT
                                |||||||| ||||   ||||||
                                AAACGTCT CCGA   TTCGAA
                                     T    CAT
GAM879  GAGE2    3'  AAGCTTTACAGCCTTCTGCAAA 7613         T   ___
                                TTTGCAGA GGCT   AAGTTT
                                |||||||| ||||   ||||||
                                AAACGTCT CCGA   TTCGAA
                                     T    CAT
GAM879  GAGE8    3'  AAGCTTTACAGCCTTCTGCAAA 24161        T   ___
                                TTTGCAGA GGCT   AAGTTT
                                |||||||| ||||   ||||||
                                AAACGTCT CCGA   TTCGAA
                                     T    CAT
GAM879  HTEX4    5'  AAGGAAACATATCTGTAAA   97718         GCTAA
                                TTTGCAGATG    GTTTCCTT
                                ||||||||||    ||||||||
                                AAATGTCTAT    CAAAGGAA
                                      A____
GAM879  LAT1-3TM 5'  AAATTTAGCTCATCTGCAAA  68596         _
                                TTTGCAGATG GCTAAGTTT
                                |||||||||| |||||||||
                                AAACGTCTAC CGATTTAAA
                                      T
GAM879  LAT1-3TM 3'  AAATTTAGCTCATCTGCAAA  48311         _
                                TTTGCAGATG GCTAAGTTT
                                |||||||||| |||||||||
                                AAACGTCTAC CGATTTAAA
                                      T
GAM879  NET-6    3'  GAAGGAAACACTATCTGGAAA  26938     G      CTAA
                                TTT CAGATGG    GTTTCCTTC
                                ||| |||||||    |||||||||
                                AAA GTCTATC    CAAAGGAAG
                                  G      A___
GAM879  RAB27B   5'  AAGGAAACCTCTCTG       14783      T  CTAA
                                CAGA GG    GTTTCCTT
                                |||| ||    ||||||||
                                GTCT TC    CAAAGGAA
                                  C  ____
GAM879  SEC24A   3'  GAAAGAAACTTGACTTCTG    82681      T  C       C
                                CAGA GG TAAGTTTC TTC
                                |||| || |||||||| |||
                                GTCT TC GTTCAAAG AAG
                                  _  A       A
GAM879  TIMM9    5'  AAGGAAACTCATGCATC      24943      G TA_
                                GATG C   AGTTTCCTT
                                |||| |   |||||||||
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                                CTAC G   TCAAAGGAA
                                  _ TAC
GAM879  TTTY11    5'  GAAGGAAATTTTCCATCTTACA 49187     C_     CT
              AA                  TTTG  AGATGG  AAGTTTCCTTC
                                  ||||  ||||||  ||||||||||
                                  AAAC  TCTACC  TTTAAAGGAAG
                                    AT     T_
GAM879  LOC124976 3'  GAAGCAGCTATCCACAAA    74381     CA     AA
                                  TTTG  GATGGCT  GTTTC
                                  ||||  |||||||  |||||
                                  AAAC  CTATCGA  CGAAG
                                    AC      __
GAM879  LOC145644 5'  GAAAATGAGCCATCTGCAAG   64660          AAG
                                  TTTGCAGATGGCT   TTTC
                                  ||||||||||||   ||||
                                  GAACGTCTACCGA   AAAG
                                          GTA
GAM879  LOC149830 3'  GAAACAGCCATCTGCA      84725          AA
                                  TGCAGATGGCT  GTTTC
                                  ||||||||||  |||||
                                  ACGTCTACCGA  CAAAG
                                             __
GAM879  LOC152582 5'  AAGGAAACTCAATTGTGA    85783   TG  A  GCTA
                                  T  CAG TG    AGTTTCCTT
                                  |  ||| ||    |||||||||
                                  A  GTT AC    TCAAAGGAA
                                   GT   A _____
GAM879  LOC152627 5'  GAAAGATGCCATCTGCA     80629         TAAG
                                  TGCAGATGGC    TTTC
                                  ||||||||||    ||||
                                  ACGTCTACCG    AAAG
                                        TAG_
GAM879  LOC154822 5'  GACCCAGCCATCTGTAAA    86261           AA
                                  TTTGCAGATGGCT  GTT
                                  ||||||||||||  |||
                                  AAATGTCTACCGA  CAG
                                          CC
GAM879  LOC197423 5'  AAATTTAGCTCATCTGCAAA   77855          _
                                  TTTGCAGATG GCTAAGTTT
                                  |||||||||| |||||||||
                                  AAACGTCTAC CGATTTAAA
                                        T
GAM879  LOC200488 5'  ACTTGAACCATCTGCAAA    90080          C_
                                  TTTGCAGATGG  TAAGT
                                  ||||||||||  |||||
                                  AAACGTCTACC  GTTCA
                                         AA
GAM879  LOC200742 3'  AAGGAGTGAGCCATGTGCAAA  88868       G     AAGT
                                  TTTGCA ATGGCT    TTCCTT
                                  ||||||  ||||||    ||||||
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                                AAACGT TACCGA    GAGGAA
                                   G     GT__
GAM879  LOC220565 5'  AAATTTAGCTCATCTGCAAA   90740          _
                                TTTGCAGATG GCTAAGTTT
                                |||||||||| |||||||||
                                AAACGTCTAC CGATTTAAA
                                      T
GAM879  LOC257475 3'  GAAGGAAACTTGCCGTTTCCA  72420    C      T
                                TG AGATGGC AAGTTTCCTTC
                                || ||||||| ||||||||||
                                AC TTTGCCG TTCAAAGGAAG
                                 C     _
GAM879  LOC91263  3'  GAAGAATGCCATCTGCAAG    65380           TAAG
                                TTTGCAGATGGC    TTTC
                                ||||||||||||    ||||
                                GAACGTCTACCG    GAAG
                                        TAA_
GAM880  LYPLA1    3'  ACAATATTAAGAATGCAT     20919          _    _
                                GTGCATTCT AGTGT GT
                                ||||||||| ||||| ||
                                TACGTAAGA TTATA CA
                                     A    A
GAM880  MPP1      3'  AAATGACACATCTGTGCA     10110       TCTA
                                TGCAT    GTGTGTCATTT
                                |||||    ||||||||||
                                ACGTG    TACACAGTAAA
                                   TC__
GAM880  EPB41L1   3'  TGAGCACACTGAACAC       70599     CA   T     _
                                GTG  TTC AGTGTG TCA
                                |||  ||| |||||| |||
                                CAC  AAG TCACAC AGT
                                  __  _     G
GAM880  HRIHFB2072 3'  AAATCATGTACTAAATGCAC   50723        C     TG C
                                GTGCATT TAGTG  T ATTT
                                ||||||| |||||  | ||||
                                CACGTAA ATCAT  A TAAA
                                     _    GT C
GAM880  KIAA0417  3'  ACACACTGAACGCAC       71240      A   T
                                GTGC TTC AGTGTGT
                                |||| ||| |||||||
                                CACG AAG TCACACA
                                  C   _
GAM880  KIAA1940  3'  GGGTGGTACACACTAGAATGC  79987            __
                                GCATTCTAGTGTGT  CATTT
                                ||||||||||||||  |||||
                                CGTAAGATCACACA  GTGGG
                                        TG
GAM880  MGC1842   3'  TGGTCTTCACACCAGATTGCAC 65663       T   A     TCATT
                                GTGCA TCT GTGTG     TCA
                                ||||| ||| |||||     |||
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                                CACGT AGA CACAC    GGT
                                  T  C    TTCT_
GAM880  STIP-1   3'  GAATTTCAACACTAGAATG   69664          GTCAT
                                CATTCTAGTGT    TTC
                                ||||||||||    |||
                                GTAAGATCACA    AAG
                                     ACTTT
GAM880  LOC257464 5'  TTGAAACAATACAATGAATGCA 89675        TAG    CA
          C                     GTGCATTC   TGTGT  TTTCAA
                                ||||||||   |||||  ||||||
                                CACGTAAG   ACATA  AAAGTT
                                    TA_    AC
GAM881  ABCC3    3'  GCGGTGGACTCTCATGTGGCC  39156      G      GAGA
                                GGCCA ATGAGAGT   CACCGC
                                ||||| ||||||||   ||||||
                                CCGGT TACTCTCA   GTGGCG
                                  G      G___
GAM881  ADCY2    3'  GCAGTGCACCTCTCATCAGCC  65018    CA      _  AGA   C
                                GGC  GATGAGAG TG   CAC GC
                                |||  |||||||| ||   ||| ||
                                CCG  CTACTCTC AC   GTG CG
                                 A_      C ___   A
GAM881  ARHA     3'  CGATGTCCAACCCGTCTGGCC  70695        AGAG  A    C
                                GGCCAGATG    TG GACA CG
                                |||||||||    || |||| ||
                                CCGGTCTGC    AC CTGT GC
                                     CCA_ _    A
GAM881  BIG1     3'  TTGATTCCCATCTGGC     21207        A    G
                                GCCAGATG GAGT AG
                                |||||||| |||| ||
                                CGGTCTAC CTTA TT
                                     C    G
GAM881  BMPR2    5'  GCTAGGTCCTCTCATCAGCC   6835     CA      TGA   ACC
                                GGC  GATGAGAG   GAC   GC
                                |||  ||||||||   |||   ||
                                CCG  CTACTCTC   CTG   CG
                                 A_       ___   GAT
GAM881  CLECSF5  3'  GGACACCGCGCAATCTCCATCT 25127       _  A_______   AGACAC
          GGCC                    CAGATG AG       GTG     C
                                |||||| ||       |||     |
                                GTCTAC TC       CGC     G
                                  C  TAACGIII   CACAGA
GAM881  COL4A5   3'  GCAGTGTCTCATTGTC     52969    G       C
                                GA AGTGAGACAC GC
                                || ||||||||| ||
                                CT TTACTCTGTG CG
                                 G        A
GAM881  COL4A5   3'  GCAGTGTCTCATTGTC     52973    G       C
                                GA AGTGAGACAC GC
                                || ||||||||| ||
```

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                                CT TTACTCTGTG CG
                                 G        A
GAM881  COL4A5   3'  GCAGTGTCTCATTGTC     4939     G        C
                                GA AGTGAGACAC GC
                                || |||||||||| ||
                                CT TTACTCTGTG CG
                                 G        A
GAM881  HLX1     5'  CTCGCTCTCATCCAGCC     41706     CA
                                GGC  GATGAGAGTGAG
                                |||  ||||||||||||
                                CCG  CTACTCTCGCTC
                                  AC
GAM881  ITGA7    3'  GTTTCCCCTCTCATCTGACC   9381     C        T_
                                GG CAGATGAGAG  GAGAC
                                || ||||||||||  |||||
                                CC GTCTACTCTC  CTTTG
                                 A         CC
GAM881  SEPN1    3'  GTCTCACTCCCCTCTGACC    66377    C    TGA
                                GG CAGA   GAGTGAGAC
                                || ||||   |||||||||
                                CC GTCT   CTCACTCTG
                                 A    CCC
GAM881  SERPINB9 3'  GTGCCTCACTCTGTC       14760     G       A
                                GAT AGAGTGAG CAC
                                ||| |||||||| |||
                                CTG TCTCACTC GTG
                                  _       C
GAM881  SIAH2    3'  GTGTCCCATCTGGCT       17374          AGAGTGA
                                GGCCAGATG      GACAC
                                |||||||||      |||||
                                TCGGTCTAC      CTGTG
                                     C_______
GAM881  ADAMTSL1 3'  GCAGTGTCTCACTGGTTGTAGC 53502     CA_   GAG        C
           T                     GGC   GAT   AGTGAGACAC GC
                                |||   |||   |||||||||| ||
                                TCG   TTG   TCACTCTGTG CG
                                  ATG   G__         A
GAM881  BTBD2    3'  GCAGTGTCCGTTCTCATCCACC 35106    CCA        A    C
                                GG   GATGAGAGTG GACAC GC
                                ||   |||||||||| ||||| ||
                                CC   CTACTCTTGC CTGTG CG
                                 AC_         _     A
GAM881  C14orf4  5'  GCGGTGCTGGCGGCCCCGTCTG 67337          AGA__  G  A
           GCC                    GGCCAGATG    GT AG CACCGC
                                |||||||||    || || ||||||
                                CCGGTCTGC    CG TC GTGGCG
                                     CCCGG  G  _
GAM881  CRSP3    3'  GCAGGTTGACACTCTCACCTG  60635     A       AGAC  _
                                CAG TGAGAGTG    ACC GC
                                ||| ||||||||    ||| ||
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                                GTC ACTCTCAC    TGG CG
                                  C       AGT_  A
GAM881  FLJ10713  3'  GTGTCTCACTGTTGCCCAGGC  36470     AGAT_  G
                                GCC     GA AGTGAGACAC
                                |||     || ||||||||||
                                CGG     TT TCACTCTGTG
                                  ACCCG  G
GAM881  FLJ12806  3'  CGTGTCAGTACCTGGCC     43086       ATGAGA  A_    C
                                GGCCAG     GTG  GACAC G
                                ||||||     |||  ||||| |
                                CCGGTC     CAT  CTGTG C
                                   _______  GA    A
GAM881  FLJ14327  3'  GCGGTACTTCTCTGCATCTGGC 46141          _   T   AC
            C                    GGCCAGATG AGAG GAG  ACCGC
                                |||||||| |||| |||  |||||
                                CCGGTCTAC TCTC TTC  TGGCG
                                     G   _  A_
GAM881  FLJ23499  3'  CGGTGCCATTGCTCTCCAGCC  42820     CAGAT    TG GA_
                                GGC    GAGAG  A   CACCG
                                |||    |||||  |   |||||
                                CCG    CTCTC  T   GTGGC
                                  AC___     GT ACC
GAM881  FLJ32894  3'  GCAGTGTCTCACTCTGTTGTCC 58340    C   ATG         C
                                GG CAG   AGAGTGAGACAC GC
                                || |||   |||||||||||| ||
                                CC GTT   TCTCACTCTGTG CG
                                 T  G__          A
GAM881  KCNT1    3'  CGATGCTTCTCATCTACC    61831    CC      GTG  A  C
                                GG  AGATGAGA   AG CA CG
                                ||  ||||||||   || || ||
                                CC  TCTACTCT   TC GT GC
                                 A_       ___  _  A
GAM881  KIAA1320  5'  GTATCTCACTCTTTC      69307    T        C
                                GA GAGAGTGAGA AC
                                || ||||||||||  ||
                                CT TTCTCACTCT TG
                                  _        A
GAM881  MGC33345  3'  CGGTGGCCCCTGCATCTGGCC  58275         AG  TGAGA
                                GGCCAGATG  AG    CACCG
                                |||||||||  ||    |||||
                                CCGGTCTAC  TC    GTGGC
                                     G_  CCCG_
GAM881  NMU2R    5'  CTCACTCTCTCCCAGCC     39400     CA_  T
                                GGC   GA GAGAGTGAG
                                |||   || |||||||||
                                CCG   CT CTCTCACTC
                                  ACC  _
GAM881  phospho1  3'  CGGTGTCTCCTTGCATCCCAGC 82370     CA_   AG  T
            C                    GGC   GATG  AG GAGACACCG
                                |||   ||||  || |||||||||
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                                CCG   CTAC  TC CTCTGTGGC
                                  ACC    GT  _
GAM881  SLC26A10  5'  GCGGTGTCTGCCTCCCTGGCC  56031       AT   A  G
                                GGCCAG  GAG GT AGACACCGC
                                ||||||  ||| || |||||||||
                                CCGGTC  CTC CG TCTGTGGCG
                                   C_   _ _
GAM881  LOC151031 5'  GTCTCATCCCATCCGGCC    87190      A    A  G
                                GGCC GATG GA TGAGAC
                                |||| |||| || ||||||
                                CCGG CTAC CT ACTCTG
                                  C    C  _
GAM881  LOC163231 3'  TGTTCACTCTCACCAGCC    82447     CAGA        A
                                GGC    TGAGAGTGAG CA
                                |||    |||||||||| ||
                                CCG    ACTCTCACTT GT
                                  ACC_         _
GAM881  LOC201616 3'  TCCACTCTCATCTGCC      90233     C          A
                                GGC AGATGAGAGTG GA
                                ||| |||||||||| ||
                                CCG TCTACTCTCAC CT
                                  _          _
GAM881  LOC204084 3'  CGGTGTCTCAAGAATTCGGCC  89445      AG  GAGAG
                                GGCC  AT    TGAGACACCG
                                ||||  ||    ||||||||||
                                CCGG  TA    ACTCTGTGGC
                                  CT  AGA__
GAM881  LOC222224 5'  GTCTCACTCTGTTACC      94201    CCA   G
                                GG   GAT AGAGTGAGAC
                                ||   ||| ||||||||||
                                CC   TTG TCTCACTCTG
                                 A__   _
GAM881  LOC253264 3'  TGTTTTACTCCTCTGACC    94692    C    TGA
                                GG CAGA   GAGTGAGACA
                                || ||||   ||||||||||
                                CC GTCT   CTCATTTTGT
                                 A    C__
GAM881  LOC255452 3'  CGGTGTCTCACTGCGGCC    97530      AGAT AG
                                GGCC    G  AGTGAGACACCG
                                ||||    |  ||||||||||||
                                CCGG    C  TCACTCTGTGGC
                                  _____ G_
GAM881  LOC90485  3'  CGGTGCCTGGCCAGCTGGCC   63013       A  AGA  G  A
                                GGCCAG TG   GT AG CACCG
                                |||||| ||   || || |||||
                                CCGGTC AC   CG TC GTGGC
                                   G  ___  G  C
GAM882  ARHGEF6   3'  CAAACTTGAAGCCAGGC     68197       ACCA
                                GCCTGG    CAAGTTTG
                                ||||||    ||||||||
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                              CGGACC   GTTCAAAC
                                 GAA_
GAM882  CNTN2    3'  GTCACAACCCAGGTGA     17411       ACCACAA  _
                              TCGCCTGG     GTT TGAC
                              ||||||||     ||| ||||
                              AGTGGACC     CAA ACTG
                                   _______  C
GAM882  CORO2A   3'  AAACTGTGGTCCAGAGA    12642   GC       A
                              TC  CTGGACCACA GTTT
                              ||  |||||||||| ||||
                              AG  GACCTGGTGT CAAA
                               A_       _
GAM882  CORO2A   3'  AAACTGTGGTCCAGAGA    53398   GC       A
                              TC  CTGGACCACA GTTT
                              ||  |||||||||| ||||
                              AG  GACCTGGTGT CAAA
                               A_       _
GAM882  GRLF1    3'  AGGTCAGAAAGTGGCCCAGG  78551     A   AAG
                              CCTGG CCAC   TTTGACCT
                              ||||| ||||   ||||||||
                              GGACC GGTG   AGACTGGA
                                 C   AA_
GAM882  LAPTM5   3'  AGGCTTGTGGTCAAGC     22199   CTG
                              GC   GACCACAAGTTT
                              ||   ||||||||||||
                              CG   CTGGTGTTCGGA
                               AA_
GAM882  POU2AF1  3'  AGATTTACAGTCCAGGC     20647       CAC
                              GCCTGGAC   AAGTTT
                              ||||||||   ||||||
                              CGGACCTG   TTTAGA
                                   ACA
GAM882  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  6355        C   TTT___
                              CTGGACCA AAG     GAC
                              |||||||| |||     |||
                              GACCTGGT TTC     CTG
                                   A   TGTCCT
GAM882  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  54574       C   TTT___
                              CTGGACCA AAG     GAC
                              |||||||| |||     |||
                              GACCTGGT TTC     CTG
                                   A   TGTCCT
GAM882  TRIM34   5'  AGGTCAAGTTGAGCCCAG    55224     ACCA   G
                              CTGG    CAA TTTGACCT
                              ||||    ||| ||||||||
                              GACC    GTT GAACTGGA
                                CGA_   _
GAM882  TRIM9    5'  AGGCCAGGCAAGTCCAGGC   30749       CACAA    A
                              GCCTGGAC    GTTTG CCT
                              ||||||||    ||||| |||
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                                CGGACCTG    CGGAC GGA
                                    AA___    C
GAM882  ABLIM    5'  GATATGTAACCCAGGCGG    22030        ACC   A
                                TCGCCTGG   ACA GTT
                                ||||||||   ||| |||
                                GGCGGACC   TGT TAG
                                    CAA   A
GAM882  AMOT     3'  AGGCATCTTCATGGTCCAGGGA 55716    G       C_   TT  A
                                TC CCTGGACCA  AAG  TG CCT
                                || |||||||||  |||  || |||
                                AG GGACCTGGT  TTC  AC GGA
                                 _       AC   T_ _
GAM882  DKFZp434D177 5'  TTAGACCCAGGCGA       79443        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                    ________
GAM882  DKFZp434D177 5'  TTAGACCCAGGCGA       50056        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                    ________
GAM882  FLJ23420  3'  CAAGTGGGTCCAGGC       46845         A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                    _ __
GAM882  HSA249128 5'  GGCGCGGTCCAGGCGG      34152          ACAA
                                TCGCCTGGACC    GTT
                                ||||||||||    |||
                                GGCGGACCTGG    CGG
                                      CG__
GAM882  MGC15668  5'  AGACCCGGTGGTCCAGACG    51277    C       AA_
                                CG CTGGACCAC   GTTT
                                || |||||||||   ||||
                                GC GACCTGGTG   CAGA
                                 A        GCC
GAM882  MGC22014  3'  AGGTCCCGAGTGTAACCCAGGT 64486        ACC   AGTTT
          GA                     TCGCCTGG   ACA    GACCT
                                ||||||||   |||    |||||
                                AGTGGACC   TGT    CTGGA
                                    CAA   GAGCC
GAM882  SDCCAG10  5'  AGAGTTGTGGTCCAAAGA    19641    GCC        G
                                TC   TGGACCACAA TTT
                                ||   |||||||||| |||
                                AG   ACCTGGTGTT AGA
                                 AA_         G
GAM882  LOC115442 3'  AGGTCAGGGATGGTCCAG    72676        CAAG
                                CTGGACCA    TTTGACCT
                                ||||||||    ||||||||
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                                GACCTGGT   GGACTGGA
                                    AG__
GAM882  LOC129011 5'  AGACCTGCGGTCCAGGC    74862        A  A
                                GCCTGGACC CA GTTT
                                ||||||||| || ||||
                                CGGACCTGG GT CAGA
                                     C  C
GAM882  LOC130536 5'  GCAAAGTCCAGGCG       75746        CACAAG   A
                                CGCCTGGAC    TTTG C
                                |||||||||    |||| |
                                GCGGACCTG    AAAC G
                                     _____   C
GAM882  LOC149108 3'  AGACTTCACTGTGGTCCA    84357        ____
                                TGGACCACA   AGTTT
                                |||||||||   |||||
                                ACCTGGTGT   TCAGA
                                     CACT
GAM882  LOC221688 5'  AGACTCGGGCCCAGACGA    93674    C   A  ACA
                                TCG CTGG CC   AGTTT
                                ||| |||| ||   |||||
                                AGC GACC GG   TCAGA
                                  A   C  GC_
GAM882  LOC256228 5'  AGACTTGTGGTCAAAGC     96233    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCAGA
                                 AAA
GAM882  LOC257441 5'  TTAGACCCAGGCGA        95566        ACCACAA
                                TCGCCTGG     GTTTGA
                                ||||||||     ||||||
                                AGCGGACC     CAGATT
                                     _______
GAM882  LOC91960  3'  AGGTGCCTCTCGTGGTCCAAGC 67657    C      A  TTTG
                                GC TGGACCAC AG    ACCT
                                || |||||||| ||    ||||
                                CG ACCTGGTG TC    TGGA
                                 A       C  TCCG
GAM882  LOC92840  3'  GTCCCTCGGGTCCAGGC     56435        ACA  TTT
                                GCCTGGACC   AG   GAC
                                |||||||||   ||   |||
                                CGGACCTGG   TC   CTG
                                     GC_  C__
GAM883  FUS2      5'  AGCTGAACCTGGATCCTGTG   24115    T   CA  _
                                CAC AGGA  CAG TTCAGCT
                                ||| ||||  ||| |||||||
                                GTG TCCT  GTC AAGTCGA
                                  _   AG   C
GAM883  GSTM4     3'  AGCCCTGAGCTGTCCCCGTGT  5951      TA    CA    __
                                ACAC  GGACA  GTTCA  GCT
                                ||||  |||||  |||||  |||
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                                TGTG  CCTGT  CGAGT  CGA
                                  CC    __    CC
GAM883  UNRIP    5'  AGCCCAGCCCTAGTGT     23198        ACACA   CA
                                ACACTAGG    GTT  GCT
                                ||||||||    |||  |||
                                TGTGATCC    CGA  CGA
                                     _____  CC
GAM883  C1orf34  3'  GGCTCACGTCCTAGTG     60676        ACA  TC
                                CACTAGGAC   GT  AGCT
                                |||||||||   ||  ||||
                                GTGATCCTG   CA  TCGG
                                     ___ C_
GAM883  C20orf151 3'  AGCTGAACCCACAGTG     88695      A_  ACACA
                                CACT  GG    GTTCAGCT
                                ||||  ||    ||||||||
                                GTGA  CC    CAAGTCGA
                                  CA  _____
GAM883  C9orf5   3'  CTTAGCTGAACCCTTTCTACTG 49275     C    CACA
           T                     ACA TAGGA    GTTCAGCTAAG
                                |||  |||||    ||||||||||
                                TGT ATCTT    CAAGTCGATTC
                                  C    TCC_
GAM883  EIF4B    3'  AGTGTTTTCTGTGTCCTAGT   75966          TTCA_
                                ACTAGGACACAG    GCT
                                ||||||||||||    |||
                                TGATCCTGTGTC    TGA
                                      TTTTG
GAM883  EREG     3'  AGCTGATGTGTCCTG      7489         GT
                                TAGGACACA  TCAGCT
                                |||||||||  ||||||
                                GTCCTGTGT  AGTCGA
                                     __
GAM883  FLJ12598 3'  CTGTAGACTGTGTCCCAGT   45397     A        __
                                ACT GGACACAGTT  CAG
                                |||  ||||||||||  |||
                                TGA CCTGTGTCAG  GTC
                                  C         AT
GAM883  FLJ12671 3'  AGGTGTTGTGTCCTGTGT    48277     T       TT  G
                                ACAC AGGACACAG  CA CT
                                ||||  |||||||||  ||  ||
                                TGTG TCCTGTGTT  GT GA
                                  _       __  G
GAM883  KIAA0159 3'  TAACTGAACTGCGTTGAGCTG  29510    _  AG   A      C
                                CA CT  GAC CAGTTCAG TA
                                ||  ||  |||  ||||||||  ||
                                GT GA  TTG GTCAAGTC AT
                                 C  G_   C       A
GAM883  KIAA0870 3'  AGTGGAACTGTGCCCTATGT   81466     C    A       A
                                ACA TAGG CACAGTTC GCT
                                |||  ||||  ||||||||  |||
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                                TGT ATCC GTGTCAAG TGA
                                  _   C       G
GAM883  KIAA1822  3'  GCTACTGTGTCCTATGT     67570     C         TC
                                ACA TAGGACACAGT  AGC
                                ||| ||||||||||  |||
                                TGT ATCCTGTGTCA  TCG
                                  _         __
GAM883  MGC16384  3'  AGCCATCAGAGCGTCCTGTGT  53864     T    ACA    A____
                                ACAC AGGAC   GTTC    GCT
                                |||| |||||   ||||    |||
                                TGTG TCCTG   CGAG    CGA
                                  _    ___   ACTAC
GAM883  MGC21621  3'  CTTGACTGTGTCCCAG      58796    A        C
                                CT GGACACAGTT AG
                                || ||||||||| ||
                                GA CCTGTGTCAG TC
                                 C         T
GAM883  PLA2G3    3'  TAGCTGAACTATGGTTTGGTGT 31687       GA  C
                                ACACTAG  CA AGTTCAGCTA
                                |||||||  || ||||||||||
                                TGTGGTT  GT TCAAGTCGAT
                                    TG  A
GAM883  PSMD12    3'  TTGTAACTGTGTCCCAGTG    11004      A        _
                                CACT GGACACAGTT CAG
                                |||| |||||||||| |||
                                GTGA CCTGTGTCAA GTT
                                  C         T
GAM883  SPTLC2    3'  TAGCTGAATTTTCTAGTGT    16810         CAC
                                ACACTAGGA   AGTTCAGCTA
                                |||||||||   ||||||||||
                                TGTGATCTT   TTAAGTCGAT
                                      ___
GAM883  STAG3     3'  AGCCTATTTTGTGTCCTAATG  24910    C        TTCA_
                                CA TAGGACACAG     GCT
                                || ||||||||||     |||
                                GT ATCCTGTGTT     CGA
                                 A         TTATC
GAM883  LOC139673 3'  GTTTTCTGTGTCCTAGT     75979           TTC
                                ACTAGGACACAG   AGC
                                ||||||||||||   |||
                                TGATCCTGTGTC   TTG
                                      TT_
GAM883  LOC147639 3'  CTTAGCTGTGTCATCACTAG   78381      ____       C
                                CTAG    GACACAGTT AG
                                ||||    ||||||||| ||
                                GATC    CTGTGTCGA TC
                                  ACTA        T
GAM883  LOC157958 3'  AGCTGAACCTTCAGGT      81638     A   CACA
                                ACT GGA    GTTCAGCT
                                ||| |||    ||||||||
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                                TGG CTT    CAAGTCGA
                                  A   C___
GAM883   LOC170063 3'  AGTGGACACATCCTAGTG    87244        CACA     G
                                CACTAGGA    GTTCA CT
                                ||||||||    ||||| ||
                                GTGATCCT    CAGGT GA
                                    ACA_    _
GAM883   LOC202347 3'  AGCTGAGCTTCCTAG       90344       CAC
                                CTAGGA   AGTTCAGCT
                                ||||||   |||||||||
                                GATCCT   TCGAGTCGA
                                   ___
GAM883   LOC203052 3'  AGCTGGGCCCTAAGGT      90450    AC    ACACA
                                AC  TAGG     GTTCAGCT
                                ||  ||||     ||||||||
                                TG  ATCC     CGGGTCGA
                                 GA   _____
GAM883   LOC254381 5'  AGCTCTGTGTCCCAG       97458    A       TTC
                                CT GGACACAG   AGCT
                                || ||||||||   ||||
                                GA CCTGTGTC   TCGA
                                 C      ___
GAM883   LOC254946 3'  TAGTACTACTGTGTCCTA    96043          TCA
                                TAGGACACAGT   GCTA
                                ||||||||||   ||||
                                ATCCTGTGTCA   TGAT
                                      TCA
GAM883   LOC256267 5'  AACTGTAATCCTAGTG      96791        C_
                                CACTAGGA  ACAGTT
                                ||||||||  ||||||
                                GTGATCCT  TGTCAA
                                    AA
GAM883   LOC92466  5'  AACTGTAATCCTAGTG      69416        C_
                                CACTAGGA  ACAGTT
                                ||||||||  ||||||
                                GTGATCCT  TGTCAA
                                    AA
GAM884   AQP6      3'  GCCCCAGCTTCTTACCCA    7951      ATATA      TA  A
                                TGG    AAGAAGT  TG GGC
                                |||    |||||||  || |||
                                ACC    TTCTTCG  AC CCG
                                  CA___      __  C
GAM884   AQP6      3'  GCCCCAGCTTCTTACCCA    53927     ATATA      TA  A
                                TGG    AAGAAGT  TG GGC
                                |||    |||||||  || |||
                                ACC    TTCTTCG  AC CCG
                                  CA___      __  C
GAM884   CDH6      3'  GCCTCATAGTTATTATCCA    17028       TAAAG  G
                                TGGATA    AA TTATGAGGC
                                ||||||    || |||||||||
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                                ACCTAT    TT GATACTCCG
                                   TA___ _
GAM884  CYP7A1   3'  TTTCAACTTCTTCTATATCCA  5765        _     TA
                                TGGATATA AAGAAGT  TGAGG
                                |||||||| |||||||  |||||
                                ACCTATAT TTCTTCA  ACTTT
                                     C     __
GAM884  PREP     3'  GCATACTTATCTATATCCA   10773       AAG   TATGAG
                                TGGATATA  AAGT    GC
                                ||||||||  ||||    ||
                                ACCTATAT  TTCA    CG
                                     CTA   TA____
GAM884  TEL2     5'  GCCGGTGGCTTCCTCACCTCCA 32327     TATAAA      GA
                                TGGA    GAAGTTAT  GGC
                                ||||    ||||||||  |||
                                ACCT    CTTCGGTG  CCG
                                  CCACTC      G_
GAM884  TMEM2    3'  GCCTCTACCTTTGTATCCA   25421         AAGTTAT
                                TGGATATAAAG     GAGGC
                                ||||||||||      |||||
                                ACCTATGTTTC     CTCCG
                                      CAT____
GAM884  C11orf23 3'  CCTGGTGGCTTCTCCATCC   37011     ATAA      G
                                GGAT   AGAAGTTAT AGG
                                ||||   ||||||||| |||
                                CCTA   TCTTCGGTG TCC
                                  CC__       G
GAM884  ESPL1    3'  GCCTCATAACTGTTCTACCTCC 24460     TATAAAGA
           A                     TGGA      AGTTATGAGGC
                                ||||      ||||||||||
                                ACCT      TCAATACTCCG
                                  CCATCTTG
GAM884  FLJ10620 3'  GCCCCATTCTTCATATC     36358     AAA   TT  A
                                GATAT  GAAG  ATG GGC
                                |||||  ||||  ||| |||
                                CTATA  CTTC  TAC CCG
                                   ___   T_  C
GAM884  FLJ13912 3'  GCCTCATACTCTATACTCA   42862   GA   A  AAGT
                                TG  TATA AG   TATGAGGC
                                ||  |||| ||   ||||||||
                                AC  ATAT TC   ATACTCCG
                                 TC   C ____
GAM884  FLJ20972 3'  GCCCCACCCTTATATCC     46726      AAGA  TTA  A
                                GGATATA   AG  TG GGC
                                |||||||   ||  || |||
                                CCTATAT   TC  AC CCG
                                    ____ CC_  C
GAM884  FLJ23476 3'  CCTCCACTATCCTTTATAGCCA 44959     A     A__   TAT
                                TGG TATAAAG  AGT  GAGG
                                ||| |||||||  |||  ||||
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                                ACC ATATTTC   TCA   CTCC
                                  G      CTA   C__
GAM884  ITGA8     5' GGCCTGTGCTCCTTTATATC   93226         A   TATG
                                GATATAAAG AGT    AGGCC
                                ||||||||| |||    |||||
                                CTATATTTC TCG    TCCGG
                                     C   TG__
GAM884  KIAA0217  3' GGCCTCATTGATTCACTTCCA  67040     TATAAA   GTT
                                TGGA     GAA   ATGAGGCC
                                ||||     |||   ||||||||
                                ACCT     CTT   TACTCCGG
                                  TCA___   AGT
GAM884  KIAA0252  3' GCTGTGTAACTTCCCCATTCC  62796     TATAAA       A
                                GGA     GAAGTTATG GGC
                                |||     ||||||||| |||
                                CCT     CTTCAATGT TCG
                                  TACCC_       G
GAM884  KIAA1199  3' GGCCTCATTTGCTCTTCATCCA 72517      ATA    A  T_
                                TGGAT   AAGA GT  ATGAGGCC
                                |||||   |||| ||  ||||||||
                                ACCTA   TTCT CG  TACTCCGG
                                   C__    _ TT
GAM884  KIAA1364  3' CCTAGGACTCCCTATATCCA   63590         AA  A   ATG
                                TGGATATA  GA GTT   AGG
                                ||||||||  || |||   |||
                                ACCTATAT  CT CAG   TCC
                                     CC  _   GA_
GAM884  KIAA1494  3' GCCTGTCTTTTTATATCCA    68460           AG TATG
                                TGGATATAAAGA  T    AGGC
                                ||||||||||||  |    ||||
                                ACCTATATTTTT  G    TCCG
                                       CT ____
GAM884  KIAA1915  3' AACTTCTTTTATCCA       73269        T
                                TGGATA AAAGAAGTT
                                |||||| |||||||||
                                ACCTAT TTTCTTCAA
                                   _
GAM884  SMT3H2    3' CCTGCTTCTTTACTCCA     22672      TA       TATG
                                TGGA  TAAAGAAGT    AGG
                                ||||  |||||||||    |||
                                ACCT  ATTTCTTCG    TCC
                                  C_        _____
GAM884  LOC132241 5' GGCCCAGCGCTCTTTATACCA  75051     A       A  TA  A
                                TGG TATAAAGA GT  TG GGCC
                                ||| |||||||| ||  || ||||
                                ACC ATATTTCT CG  AC CCGG
                                  _       _ CG  _
GAM884  LOC153139 5' CCTTTTTCTTTATTCCA     85924      T       TTAT
                                TGGA ATAAAGAAG    GAGG
                                |||| |||||||||    ||||
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                                ACCT TATTTCTTT   TTCC
                                  _      ____
GAM884  LOC158997 3'  CCTGCTTCTTTACTCCA    82080     TA       TATG
                                TGGA  TAAAGAAGT   AGG
                                ||||  |||||||||   |||
                                ACCT  ATTTCTTCG   TCC
                                  C_      ____
GAM884  LOC200939 3'  GCCCCATAGTTTTTATCCA   90204      TAAA   GT   A
                                TGGATA   GAA  TATG GGC
                                ||||||   |||  |||| |||
                                ACCTAT   TTT  ATAC CCG
                                   ____  TG   C
GAM884  LOC219404 3'  CCTGTATTCCTTCTTTATACTC 93492   GA       TT  _
          A                      TG  TATAAAGAAG  ATG AGG
                                ||  ||||||||||  ||| |||
                                AC  ATATTTCTTC  TAT TCC
                                 TC        CT   G
GAM884  LOC222019 3'  CCTGCTTCTTTACTCCA    94002     TA       TATG
                                TGGA  TAAAGAAGT   AGG
                                ||||  |||||||||   |||
                                ACCT  ATTTCTTCG   TCC
                                  C_      ____
GAM884  LOC253070 3'  GGCCTCGTGCCCTTACATCC   97011     ATA   AA  T
                                GGAT   AAG  GT ATGAGGCC
                                ||||   |||  || ||||||||
                                CCTA   TTC  CG TGCTCCGG
                                  CA_   C_  _
GAM884  LOC256990 3'  CCTGCTTCTTTACTCCA    96297     TA       TATG
                                TGGA  TAAAGAAGT   AGG
                                ||||  |||||||||   |||
                                ACCT  ATTTCTTCG   TCC
                                  C_      ____
GAM884  LOC89919  3'  GCAGGACCTCTCTGTATCCA  60724       A   A   ATGAG
                                TGGATATA AGA GTT    GC
                                |||||||| ||| |||    ||
                                ACCTATGT TCT CAG    CG
                                    C   C   GA___
GAM884  LOC90133  3'  GGCCTCACAACTCGTGACC   61606    A   AAA  A   A
                                GG TAT   GA GTT TGAGGCC
                                || |||   || ||| |||||||
                                CC GTG   CT CAA ACTCCGG
                                 A   ___  _   C
GAM885  BECN1     3'  TGACAGATACTTTCCAGAGCT  13649     G__       CA
                                AGT   GGAAAGTATC  TCA
                                |||   ||||||||||  |||
                                TCG   CCTTTCATAG  AGT
                                  AGA        AC
GAM885  DGKQ      3'  TGAAGTTACCTTCCCACTGGAA 7210      A       A   TCCA
                                TTC CAGTGGGAA GTA    TCA
                                ||| |||||||| |||    |||
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                                AAG GTCACCCTT CAT    AGT
                                  _       C   TGA_
GAM885  GPLD1    3'  ATGGATACTTAGGGTGA     92017      AGTGGGA
                                TCAC      AAGTATCCAT
                                ||||      ||||||||||
                                AGTG      TTCATAGGTA
                                  GGA_____
GAM885  GYS1     3'  TGCTCTGCCCACTGTGAA     88402           AA_
                                TTCACAGTGGG   AGTA
                                ||||||||||   ||||
                                AAGTGTCACCC   TCGT
                                      GTC
GAM885  NPTX2    3'  TGATGTTCCGCCCCACTGTGAA 92484           AAAGTATC
                                TTCACAGTGGG       CATCA
                                ||||||||||        |||||
                                AAGTGTCACCC       GTAGT
                                      CGCCTT__
GAM885  PSAP     3'  TGATGTAATTCCCACTGT     69359          AGTATC
                                ACAGTGGGAA     CATCA
                                ||||||||||     |||||
                                TGTCACCCTT     GTAGT
                                     AAT___
GAM885  FBXO26   3'  TGATGGCCATGACCCCCACCCT 46095      CA    AAA_  AT
           GAA                    TTCA  GTGGG    GT  CCATCA
                                ||||  |||||    ||  ||||||
                                AAGT  CACCC    TA  GGTAGT
                                  CC    CCAG  CC
GAM885  FLJ11113 3'  GATCCTTTCCCCATTGTGAA   37069          _   T
                                TTCACAGTGGG AAAG ATC
                                |||||||||| |||| |||
                                AAGTGTTACCC TTTC TAG
                                      C   C
GAM885  FLJ21276 3'  TGTCTACCTTCCCACTGGAA   44923     A       A   TC
                                TTC CAGTGGGAA GTA  CA
                                ||| |||||||| |||  ||
                                AAG GTCACCCTT CAT  GT
                                  _       C   CT
GAM885  KIAA0847 3'  ACTTTCCCACCCTGAA      77615      CA
                                TTCA  GTGGGAAAGT
                                ||||  ||||||||||
                                AAGT  CACCCTTTCA
                                  CC
GAM885  KIAA1161 3'  ACTTCTCCCACTTGAA      81731      C     _
                                TTCA AGTGGGA AAGT
                                |||| ||||||| ||||
                                AAGT TCACCCT TTCA
                                  _      C
GAM885  KIAA1870 3'  TGCTACCTCCCACTGTGAA    49663           A__
                                TTCACAGTGGGA   AGTA
                                ||||||||||||   ||||
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                                AAGTGTCACCCT   TCGT
                                       CCA
GAM885  MGC2487   5'  GATGACTGCAGCTCCCACTGTG 43736          AA_   TC
            A                   TCACAGTGGGA   GTA  CATC
                                ||||||||||   |||  ||||
                                AGTGTCACCCT   CGT  GTAG
                                      CGA   CA
GAM885  TA-KRP    3'  TGATGAATACTTTTACGTTGGA 50695     A    GG      C
            A                   TTC CAGTG  AAAGTAT CATCA
                                ||| |||||  ||||||| |||||
                                AAG GTTGC  TTTCATA GTAGT
                                  _    AT      A
GAM885  UAP1      3'  ATAGACCAACTGTGAA      11895         G  AAAGTA  C
                                TTCACAGT GG     TC AT
                                |||||||| ||     || ||
                                AAGTGTCA CC     AG TA
                                     A _______ A
GAM885  LOC116071 3'  GATGCCTCCCACTGTGA     56625          AA
                                TCACAGTGGGA  GTATC
                                ||||||||||  |||||
                                AGTGTCACCCT  CGTAG
                                      C_
GAM885  LOC127428 3'  GATGGATTTCACTGTGAA    74667         GG AAGTA
                                TTCACAGTG  A    TCCATC
                                |||||||||  |    ||||||
                                AAGTGTCAC  T    AGGTAG
                                     TT ______
GAM885  LOC132916 3'  TGATGAGTGTCCCACTGTGGA  75069          AAG  TC
                                TTCACAGTGGGA   TA  CATCA
                                ||||||||||||   ||  |||||
                                AGGTGTCACCCT   GT  GTAGT
                                       ___  GA
GAM885  LOC145009 3'  TGATGGATATTTTCCCATCGTG 60354       A
            AA                    TTCAC GTGGGAAAGTATCCATCA
                                |||||  ||||||||||||||||||
                                AAGTG TACCCTTTTATAGGTAGT
                                   C
GAM885  LOC150568 5'  TGATTTGGCCTCCCGCTGCGAA 85045     A       AA  ATCC
                                TTC CAGTGGGA  GT    ATCA
                                ||| ||||||||  ||    ||||
                                AAG GTCGCCCT  CG    TAGT
                                  C       C_  GTT_
GAM885  LOC158314 3'  GAGGTCTCCCCACTGTGAA    86769          AAAGTAT  A
                                TTCACAGTGGG      CC TC
                                ||||||||||       || ||
                                AAGTGTCACCC      GG AG
                                      CTCT___  _
GAM885  LOC197319 3'  ATGTCATTTTTCCCACTATGGA 87966      C         TATC
                                TTCA AGTGGGAAAG    CAT
                                |||| ||||||||||    |||
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                                AGGT TCACCCTTTT   GTA
                                  A        TACT
GAM885  LOC221178 3'  TGATTTTTGTTTCCCACTGT  93540         G  TCC
                                ACAGTGGGAAA TA  ATCA
                                |||||||||| ||  ||||
                                TGTCACCCTTT GT  TAGT
                                      _ TTT
GAM885  LOC253820 5'  TGGGCACCTTCCACTGTGAA  95715         AA  AT
                                TTCACAGTGGGA  GT  CCA
                                ||||||||||  ||  |||
                                AAGTGTCACCTT  CA  GGT
                                      C_  CG
GAM885  LOC51093  5'  GACACCTTCTCACTGTGAA   32044         A  A
                                TTCACAGTGGGAA GT TC
                                |||||||||||| || ||
                                AAGTGTCACTCTT CA AG
                                      C  C
GAM886  CDH12    5'  AGCCTTTTTAAAGCTTTGATG  14489        G   TTCTC
                                CATCAAAGCT TAG    GCT
                                |||||||||| |||    |||
                                GTAGTTTCGA ATT    CGA
                                     A  TTTC_
GAM886  DLG5     3'  TAGCGAGAAATCTTTGAT    82922       CTGTAG
                                ATCAAAG     TTCTCGCTA
                                |||||||     |||||||||
                                TAGTTTC     AAGAGCGAT
                                   TA_____
GAM886  IGFBP3   3'  AGCAGCTGGCTACAGCCTCGAT 5184     AAA       __ C
                                ATC   GCTGTAGTT  CT GCT
                                |||   |||||||||  || |||
                                TAG   CGACATCGG  GA CGA
                                  CTC       TC  _
GAM886  FER1L4   5'  AGGGGCAGCACAACTTTGATG  47331       C   A  _  G
                                CATCAAAG TGT GTT CTC CT
                                |||||||| ||| ||| ||| ||
                                GTAGTTTC ACA CGA GGG GA
                                     A  _  C  _
GAM886  FLJ12875  3'  AGCCCGTCGCAGCTTTGA    44608        AG TCTC
                                TCAAAGCTGT  T   GCT
                                |||||||||  |   |||
                                AGTTTCGACG  G   CGA
                                     CT CC__
GAM886  GIT2     3'  CTAGGGTGGCCACAGCTTTGAT 54080         A  TC  G
                                ATCAAAGCTGT GT  TC CTAG
                                |||||||||| ||  || ||||
                                TAGTTTCGACA CG  GG GATC
                                      C  GT  _
GAM886  GIT2     3'  CTAGGGTGGCCACAGCTTTGAT 54093         A  TC  G
                                ATCAAAGCTGT GT  TC CTAG
                                |||||||||| ||  || ||||
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                                TAGTTTCGACA CG  GG GATC
                                      C  GT  _
GAM886  GIT2     3'  CTAGGGTGGCCACAGCTTTGAT 28758          A  TC  G
                                ATCAAAGCTGT GT  TC CTAG
                                |||||||||||  ||  || ||||
                                TAGTTTCGACA CG  GG GATC
                                      C  GT  _
GAM886  GOLPH2   3'  CTAGCAAAGTAGCAACAGCTTT 33320        A  _  C_
                                AAAGCTGT GTT CT  GCTAG
                                ||||||||  ||| ||  |||||
                                TTTCGACA CGA GA  CGATC
                                     A   T  AA
GAM886  KIAA0303 5'  GGCTACAGCTCAGATG      69462      AA
                                CATC  AGCTGTAGTT
                                ||||  ||||||||||
                                GTAG  TCGACATCGG
                                  AC
GAM886  LOC146481 5'  AGCCTTCTACAGTTTGAT    77924       G     TTCTC
                                ATCAAA CTGTAG    GCT
                                ||||||  ||||||    |||
                                TAGTTT GACATC    CGA
                                   _     TTC__
GAM886  LOC154323 5'  CTAGCAAATAGCAGCCTTGGTG 86214       A    A   CTC
                                CATCAA GCTGT GTT   GCTAG
                                ||||||  |||||  |||   |||||
                                GTGGTT CGACG TAA   CGATC
                                   C    A   A__
GAM886  LOC200197 3'  AGTGACTCGCTTTGAT      88613         T T  TTC
                                ATCAAAGC G AG   TCGCT
                                ||||||||  | ||   |||||
                                TAGTTTCG C TC   AGTGA
                                     _ _  ____
GAM887  FTSJ2    3'  CCAAAAAGAGATGACAAAACT  25434       T       ACAA
                                AGTTTT TCATCTCT    TGG
                                ||||||  ||||||||    |||
                                TCAAAA AGTAGAGA    ACC
                                   C       AAA_
GAM887  LDHB     5'  CCATTTTGGAGATGAAGAAACT 9708              C
           GA                     TCAGTTTTTTCATCTCTA AATGG
                                ||||||||||||||||||  |||||
                                AGTCAAAGAAGTAGAGGT TTACC
                                        T
GAM887  MYCL1    3'  CCATTAACAGATGGAAAAACTG 18161            CTAC
           A                     TCAGTTTTTTCATCT    AATGG
                                ||||||||||||||||    |||||
                                AGTCAAAAAGGTAGA    TTACC
                                      CAA_
GAM887  NT5E     3'  CCACCTGTCAGATGAAAAAACT 10280            CT   A_
           GA                     TCAGTTTTTTCATCT  ACA  TGG
                                ||||||||||||||||  |||  |||
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                                AGTCAAAAAAGTAGA  TGT  ACC
                                        C_   CC
GAM887  PTGIS    3'  CCACTTCATAGATGAGAAAACT 6327              CTACAA
            GA                    TCAGTTTTTTCATCT     TGG
                                  ||||||||||||||     |||
                                  AGTCAAAAGAGTAGA     ACC
                                        TACTTC
GAM887  ZNF83    3'  TTGAGAGAAACAAAAACACTGA 36982      _    CA_    A
                                  TCAGT TTTTT   TCTCT CAA
                                  ||||| |||||   ||||| |||
                                  AGTCA AAAAA   AGAGA GTT
                                     C    CAA    _
GAM887  KIAA0040 5'  CCATTTTGGAGATGAAGAAACT 27782               C
            GA                    TCAGTTTTTTCATCTCTA AATGG
                                  |||||||||||||||||| |||||
                                  AGTCAAAGAAGTAGAGGT TTACC
                                           T
GAM887  KIAA1922 5'  CCTTTTAGAGATGAGAAAACTG 73623               C  T
            A                     TCAGTTTTTTCATCTCTA AA GG
                                  |||||||||||||||||| || ||
                                  AGTCAAAAGAGTAGAGAT TT CC
                                           T  _
GAM887  KRTAP1-3 3'  AGAAATGAAAAAGCCGA     48237    A        C
                                  TC GTTTTTTCAT TCT
                                  || ||||||||| |||
                                  AG CGAAAAAGTA AGA
                                    C         A
GAM887  SGP28    3'  AGTAATGAAAAAACTGA     20227            CT
                                  TCAGTTTTTTCAT  CT
                                  ||||||||||||  ||
                                  AGTCAAAAAAGTA  GA
                                        AT
GAM887  SIAT4A   5'  TGGAGATGAAGAAACTGA    11677
                                  TCAGTTTTTTCATCTCTA
                                  ||||||||||||||||||
                                  AGTCAAAGAAGTAGAGGT

GAM887  LOC113146 3'  AGAGATGCAAAAAACT      72970         _
                                  AGTTTTTT CATCTCT
                                  |||||||| |||||||
                                  TCAAAAAA GTAGAGA
                                       C
GAM887  LOC151720 5'  CCATTTACAGATGAAGAAACTG 80338              C  C
            A                     TCAGTTTTTTCATCT TA AATGG
                                  |||||||||||||| || |||||
                                  AGTCAAAGAAGTAGA AT TTACC
                                           C  _
GAM887  LOC152580 3'  CCAGGTTTAGATGAAAAACT   85775        T    CT  AA
                                  AGTTTTT CATCT  AC  TGG
                                  ||||||| |||||  ||  |||
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                                TCAAAAA GTAGA  TG  ACC
                                   _    TT  G_
GAM887  LOC158696 3'  CCATTGTATCTTGGAAATAACT 81972      T    ATCTC
                                AGTT TTTC     TACAATGG
                                |||| ||||     ||||||||
                                TCAA AAAG     ATGTTACC
                                  T    GTTCT
GAM887  LOC253805 3'  CCATTTTCCAGATGAAGAAACT 96427             CTAC
           GA                     TCAGTTTTTTCATCT    AATGG
                                |||||||||||||||    |||||
                                AGTCAAAGAAGTAGA    TTACC
                                         CCTT
GAM887  LOC92078  5'  CCATTTTACAGATGAGAAAACT 67979            C  C
           GA                     TCAGTTTTTTCATCT TA AATGG
                                |||||||||||||||| || |||||
                                AGTCAAAAGAGTAGA AT TTACC
                                         C  T
GAM888  ADAM17    3'  ATGCCTGTAATCCCAGCACTTG 41553    _ A          A
                                CA GT GCTGGGATTACAG CAT
                                || || |||||||||||||| |||
                                GT CA CGACCCTAATGTC GTA
                                 T _           C
GAM888  ADAM17    3'  ATGCCTGTAATCCCAGCACTTG 12081    _ A          A
                                CA GT GCTGGGATTACAG CAT
                                || || |||||||||||||| |||
                                GT CA CGACCCTAATGTC GTA
                                 T _           C
GAM888  ADAT1     3'  CTGTAATCCTAGCTACT     23898
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGATCCTAATGTC

GAM888  AICDA     3'  CTGTAATCCCAGCACT      40326     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  AK1       3'  ATGCCTGTAATCCCAGCACT   4879      A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM888  ALDH3A2   3'  ATGCCTGTAATCCCAGCACT   69270     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM888  ALDH3B1   3'  ATGCCTGTAATCCCAGCTACT  91520              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
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                                TCATCGACCCTAATGTC GTA
                                          C
GAM888  ALDH3B1  3' CTGTAATCCCAGCACT     91524    A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  ALDH8A1  3' ATGCCTATAATCCCAGCACT  42607    A       C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _       A  C
GAM888  ANKH     3' ATGCCTGTAATCCCAACACT  53987    AGC       A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_         C
GAM888  ANKH     3' CTGTAATCCCAGCTACT     53989
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  ARHGEF6  3' CTGTGGTCCCAGCTACTCA   68202   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||||
                                A TCATCGACCCTGGTGTC
                                 C
GAM888  ATM      3' CTATAATCCCAGCACT      56303    A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _       A
GAM888  ATM      3' CTGTAATCCCAGCACT      56295    A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  ATM      3' CTGTAATCCCAGCACT      3511     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  ATP1A2   3' ATGCCTGTAATCCCAGCACT  5521     A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  ATP1A2   3' CTGTAATCTCAGCTACTCA   5524    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||||
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                                A TCATCGACTCTAATGTC
                                 C
GAM888  BAAT    3'  ATGTCTCCCCCAGCTGC     8112          ATTAC
                                GTAGCTGGG    AGACAT
                                |||||||||    ||||||
                                CGTCGACCC    TCTGTA
                                     CC___
GAM888  BHMT2   3'  CTGCAATCCCAGCACT      34309     A       A
                                AGT GCTGGGATT CAG
                                ||| ||||||||| |||
                                TCA CGACCCTAA GTC
                                  _       C
GAM888  BRCA1   3'  CTGTAATCCCAGCACT      23518     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  BRCA1   3'  CTGTAATCCCAGCTACT     23519
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  BRCA1   3'  CTGTAATCCCAGCACT      23527     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  BRCA1   3'  CTGTAATCCCAGCTACT     23528
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  BRCA1   3'  CTGTAATCCCAGCACT      23535     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  BRCA1   3'  CTGTAATCCCAGCTACT     23536
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  BRCA1   3'  CTGTAATCCCAGCACT      23543     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  BRCA1   3'  CTGTAATCCCAGCTACT     23544
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
```

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                                TCATCGACCCTAATGTC

GAM888  BRCA1   3' CTGTAATCCCAGCACT     23551    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  BRCA1   3' CTGTAATCCCAGCTACT     23552
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  BRCA1   3' CTGTAATCCCAGCACT     23559    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  BRCA1   3' CTGTAATCCCAGCTACT     23560
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  BRCA1   3' CTGTAATCCCAGCACT     23568    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  BRCA1   3' CTGTAATCCCAGCTACT     23569
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  BRCA1   3' CTGTAATCCCAGCACT     23576    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  BRCA1   3' CTGTAATCCCAGCTACT     23577
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  BRCA1   3' CTGTAATCCCAGCACT     23584    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  BRCA1   3' CTGTAATCCCAGCTACT     23585
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
```

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                                TCATCGACCCTAATGTC

GAM888  BRCA1    3'  CTGTAATCCCAGCACT      23592     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  BRCA1    3'  CTGTAATCCCAGCTACT     23593
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  BRCA2    3'  ATGCCTGTAATCCCAACACTTT 3548      TAGC_         A
           G                     CAG     TGGGATTACAG CAT
                                |||     |||||||||||| |||
                                GTT     ACCCTAATGTC GTA
                                  TCACA          C
GAM888  C1orf1   3'  CTGTAATCCCAACACT      6859      AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  C5R1     3'  CTGTAATCCCAGAACT      8204      AG
                                AGT  CTGGGATTACAG
                                |||  ||||||||||||
                                TCA  GACCCTAATGTC
                                  A_
GAM888  CARKL    3'  ATGCCTGTAATCCCAGCTACT  25183              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                          C
GAM888  CASP10   3'  ATGCCTGTAATCCCAGTACTCT 52098     TA_           A
           G                     CAG   GCTGGGATTACAG CAT
                                |||   |||||||||||| |||
                                GTC   TGACCCTAATGTC GTA
                                  TCA           C
GAM888  CASP10   3'  ATGCCTGTAATCCCAGTACTCT 52116     TA_           A
           G                     CAG   GCTGGGATTACAG CAT
                                |||   |||||||||||| |||
                                GTC   TGACCCTAATGTC GTA
                                  TCA           C
GAM888  CASP6    3'  ATGCCTGCAATCCCAGCTACTT 52200     _          A   A
           G                     CA GTAGCTGGGATT CAG CAT
                                ||  |||||||||||| ||| |||
                                GT CATCGACCCTAA GTC GTA
                                 T          C   C
GAM888  CASP6    3'  CTGTAATCCCAGCACT      52203     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  CASP6    3'  CTGTAATCCCAGCACT      6910      A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  CASP6    3'  ATGCCTGCAATCCCAGCTACTT 6907     _          A  A
              G                  CA GTAGCTGGGATT CAG CAT
                                || |||||||||||| ||| |||
                                GT CATCGACCCTAA GTC GTA
                                 T          C  C
GAM888  CASP8    3'  ATGTCTATAATCCCAGCACT   6913      A        C
                                AGT GCTGGGATTA AGACAT
                                ||| |||||||||| ||||||
                                TCA CGACCCTAAT TCTGTA
                                  _        A
GAM888  CASP8    3'  ATGTCTATAATCCCAGCACT   52919     A        C
                                AGT GCTGGGATTA AGACAT
                                ||| |||||||||| ||||||
                                TCA CGACCCTAAT TCTGTA
                                  _        A
GAM888  CASP8    3'  ATGTCTATAATCCCAGCACT   52930     A        C
                                AGT GCTGGGATTA AGACAT
                                ||| |||||||||| ||||||
                                TCA CGACCCTAAT TCTGTA
                                  _        A
GAM888  CASP8    3'  ATGTCTATAATCCCAGCACT   52942     A        C
                                AGT GCTGGGATTA AGACAT
                                ||| |||||||||| ||||||
                                TCA CGACCCTAAT TCTGTA
                                  _        A
GAM888  CD68     3'  ATGCCTGTAATCCCAGCACT   59797     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  CHRNA5   3'  CTGTAATCCCAGCACT      59755     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  CHST5    3'  ATGCCTGTAATCCCAGCATTTT 24022     TA_          A
              G                  CAG   GCTGGGATTACAG CAT
                                |||   |||||||||||||| |||
                                GTT   CGACCCTAATGTC GTA
                                  TTA           C
GAM888  CHST5    3'  CTGTAATCCCAGCTACTTA    24025   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
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                                A TCATCGACCCTAATGTC
                                 T
GAM888  CNGB1    3'  ATGCCTATAATCCCAGTGCT  7110      G       C  A
                                AGTA CTGGGATTA AG CAT
                                |||| ||||||||| || |||
                                TCGT GACCCTAAT TC GTA
                                  _       A  C
GAM888  COG7     3'  CTGTAATCCCAGCACT     67622     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  COL16A1  3'  CTGTAATCCTAGCTATT    8500
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TTATCGATCCTAATGTC

GAM888  COPA     3'  CTGTAATCCCAGCACT     15187     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  CORO2A   3'  ATGCCTGTAATCCCAGCACTCT 53400     TA_          A
           G                     CAG   GCTGGGATTACAG CAT
                                |||   |||||||||||| |||
                                GTC   CGACCCTAATGTC GTA
                                  TCA           C
GAM888  CORO2A   3'  ATGCCTGTAATCCCAGCACTCT 12644     TA_          A
           G                     CAG   GCTGGGATTACAG CAT
                                |||   |||||||||||| |||
                                GTC   CGACCCTAATGTC GTA
                                  TCA           C
GAM888  CPT2     3'  ATGCCTGTAATCCCAGCATTTT 3641      TA_          A
           G                     CAG   GCTGGGATTACAG CAT
                                |||   |||||||||||| |||
                                GTT   CGACCCTAATGTC GTA
                                  TTA           C
GAM888  CRACC    3'  CTGTAATCCCAGCACT     41005     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  CTMP     3'  CTGTAATCCCAGCACTTTA   53876    C   A
                                TA AGT GCTGGGATTACAG
                                || ||| ||||||||||||
                                AT TCA CGACCCTAATGTC
                                 T   _
GAM888  CTMP     3'  CTGTAGTCCCAGCTACTCA   53877    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
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                                A TCATCGACCCTGATGTC
                                 C
GAM888  CTNNB1   3'  TCTGTAATGGTACTG      8581       G  GGG
                                CAGTA CT   ATTACAGA
                                ||||| ||   ||||||||
                                GTCAT GG   TAATGTCT
                                  _ ___
GAM888  CTSS     3'  ATGCCTGTAATCCCAGCTACTT 14540    _           A
            G                    CA GTAGCTGGGATTACAG CAT
                                || ||||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 T            C
GAM888  CTSS     3'  CTGTAATCCCAGTACTTG    14542   C   G
                                A AGTA CTGGGATTACAG
                                | |||| ||||||||||||
                                G TCAT GACCCTAATGTC
                                 T  _
GAM888  CYP4F3   3'  CTGTAATCCCAGCACTTTA   6115    C   A
                                TA AGT GCTGGGATTACAG
                                || ||| ||||||||||||
                                AT TCA CGACCCTAATGTC
                                 T  _
GAM888  DAPP1    3'  ATGCCTGTAATCCCAGGACT   26917    AG         A
                                AGT  CTGGGATTACAG CAT
                                |||  |||||||||||| |||
                                TCA  GACCCTAATGTC GTA
                                  G_         C
GAM888  DAPP1    3'  TGTAATCCCAGCTACTCA    26920   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  DBT      3'  CTGTAATCCCAGCACT      8610     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  DCLRE1C  3'  ATGCCTGTAATCCCAGCTAC  42524           A
                                GTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                CATCGACCCTAATGTC GTA
                                          C
GAM888  DDOST    3'  ATGCCTGTAATCCCAGCACT   17816    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _         C
GAM888  DFFA     3'  CTGTAATCCCAGCACTG     15302     A
                                CAGT GCTGGGATTACAG
                                |||| ||||||||||||
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                                GTCA CGACCCTAATGTC
                                   _
GAM888  DHFR    3'  ATGCCTGTAGTCCCAGCTACTC 5799    C           A
              A                  A AGTAGCTGGGATTACAG CAT
                                 | ||||||||||||||||| |||
                                 A TCATCGACCCTGATGTC GTA
                                  C             C
GAM888  DHFR    3'  CTGTAATCCCAGCGCT      5803     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCG CGACCCTAATGTC
                                   _
GAM888  DMC1    3'  CTGTAATCCCAGCACT      22972    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                   _
GAM888  DNASE2  3'  ATGCCTGTAGTCCCAGCCACTG 7263      A          A
                                 CAGT GCTGGGATTACAG CAT
                                 |||| |||||||||||| |||
                                 GTCA CGACCCTGATGTC GTA
                                    C          C
GAM888  DSC1    3'  CTGTAATCCCAGCTACTCA   17059   C
                                 A AGTAGCTGGGATTACAG
                                 | |||||||||||||||||
                                 A TCATCGACCCTAATGTC
                                  C
GAM888  DSC1    3'  CTGTAATCCCAGCTACTCA   44328   C
                                 A AGTAGCTGGGATTACAG
                                 | |||||||||||||||||
                                 A TCATCGACCCTAATGTC
                                  C
GAM888  DVL3    3'  GTCTGTAATCCCAGCACT    15373    A
                                 AGT GCTGGGATTACAGAC
                                 ||| ||||||||||||||
                                 TCA CGACCCTAATGTCTG
                                   _
GAM888  DYRK1A  3'  ATGTCTGTAACCAATAATGTA  55198     G  GCTG  A
                                 TACA TA   GG TTACAGACAT
                                 |||| ||   || ||||||||||
                                 ATGT AT   CC AATGTCTGTA
                                    A  AA__  _
GAM888  DYRK1A  3'  ATGTCTGTAACCAATAATGTA  55240     G  GCTG  A
                                 TACA TA   GG TTACAGACAT
                                 |||| ||   || ||||||||||
                                 ATGT AT   CC AATGTCTGTA
                                    A  AA__  _
GAM888  DYRK1A  3'  ATGTCTGTAACCAATAATGTA  7349      G  GCTG  A
                                 TACA TA   GG TTACAGACAT
                                 |||| ||   || ||||||||||
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                                ATGT AT    CC AATGTCTGTA
                                  A  AA__  _
GAM888  EFG2     5'  CTGTAATCCCAGCACT      50476     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  EGFL5    3'  CTGTAATCCCAGCACT      86618     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  EHHADH   3'  CTGTAATCCCAGCACT      8750      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  F2R      3'  CTGTAATCCCAGCACT      8837      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  F2RL3    3'  CTGCAATCCCAGCACT      14178     A       A
                                AGT GCTGGGATT CAG
                                ||| ||||||||| |||
                                TCA CGACCCTAA GTC
                                  _       C
GAM888  F2RL3    3'  CTGTAATCCCAGCACTTTA   14179     C   A
                                TA AGT GCTGGGATTACAG
                                || ||| ||||||||||||
                                AT TCA CGACCCTAATGTC
                                 T  _
GAM888  F2RL3    3'  TGTAATCCCAGCTACTCA    14197     C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  FANCD2   3'  CTGTAATCCCAGCACT      52355     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FCMD     3'  CTATAGTCCCAGCTAC      22091           C
                                GTAGCTGGGATTA AG
                                |||||||||||| ||
                                CATCGACCCTGAT TC
                                         A
GAM888  FGFR1    3'  CTGTAATCCCAGCACTTTA   43614     C   A
                                TA AGT GCTGGGATTACAG
                                || ||| ||||||||||||
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```
                                AT TCA CGACCCTAATGTC
                                 T  _
GAM888  FGFR1   3'  CTGTAATCCCAGCACTTTA   43621   C  A
                                TA AGT GCTGGGATTACAG
                                || ||| ||||||||||||||
                                AT TCA CGACCCTAATGTC
                                 T  _
GAM888  FGFR2   3'  ATGCCTGTAATCCCAGCACT  43376    A        A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _         C
GAM888  FGFR2   3'  ATGCCTGTAATCCCAGCACT  43382    A        A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _         C
GAM888  FKRP    3'  CTGTAATCCCAGCACT     44185    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLRT2   5'  GTCTGTAATCCCAGCGCTCTGT 25064     TA_
                                ACAG  GCTGGGATTACAGAC
                                ||||  ||||||||||||||||
                                TGTC  CGACCCTAATGTCTG
                                  TCG
GAM888  FUT6    3'  CTGTAATCCCAGCACT     3811     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  GALNT7  3'  CTGTAATCCCAGCTACTTG  54018   _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                 T
GAM888  GNE     3'  CTGTAATCCCAGCACT     18478    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  GP2     3'  ATGCCTGTAATCCCAGC     7680           A
                                GCTGGGATTACAG CAT
                                |||||||||||||| |||
                                CGACCCTAATGTC GTA
                                        C
GAM888  GP6     3'  ATGTCTGTAATCCTAGCACTGT 33030      A
            G                    TACAGT GCTGGGATTACAGACAT
                                ||||||| ||||||||||||||||
```

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                                GTGTCA CGATCCTAATGTCTGTA
                                     _
GAM888  GPRK7    3'  TCTATAATCCCAGTTAC     57629           C
                                GTAGCTGGGATTA AGA
                                |||||||||||| |||
                                CATTGACCCTAAT TCT
                                       A
GAM888  GRAF     3'  CTATAATCCCAGCACT      30556     A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM888  GRM6     3'  CTGTAATCCCAGCACT      5934      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  HFE      3'  CTGTAATCCCAGGGTGCTG   4651       G _
                                CAGTA C TGGGATTACAG
                                ||||| | ||||||||||
                                GTCGT G ACCCTAATGTC
                                   G G
GAM888  HIP1     3'  ATGCCTGTAATCCCAGAACT  18055     AG          A
                                AGT  CTGGGATTACAG CAT
                                |||  |||||||||||| |||
                                TCA  GACCCTAATGTC GTA
                                  A_          C
GAM888  HIP1     3'  CTGTAATCCCAGCACT      18059     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  HIP1     3'  GTAATCCCAGCTACTCA     18065   C
                                A AGTAGCTGGGATTAC
                                | ||||||||||||||
                                A TCATCGACCCTAATG
                                 C
GAM888  HLA-E    3'  ATGCCTGTAATCCCAGCACT  91021     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  HUNK     3'  CTGTAATCCCAGCACT      27449     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  IAPP     3'  GTGCCTGTAATCCCAGCTACTC 4696    C             A
              A                  A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
```

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                                A TCATCGACCCTAATGTC GTG
                                 C             C
GAM888  ICA1    3'  TGCAGTCCCAGCTACTCA    42257   C         A
                                A AGTAGCTGGGATT CA
                                | ||||||||||||| ||
                                A TCATCGACCCTGA GT
                                 C           C
GAM888  ICMT    3'  CTGTAATCCCAAAGTGCTG   24812      GC_
                                CAGTA   TGGGATTACAG
                                |||||   ||||||||||
                                GTCGT   ACCCTAATGTC
                                   GAA
GAM888  IFIT4   3'  ATGCCTGTAATCCCAGCACT   70920    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  IFNAR1  3'  CTGTAATCCCAGCACT     5284     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  IL10    3'  CTGTAATCCCAGCACT     5127     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  IL12RB2 3'  ATGCCTGTAATCCCAGCACT   7768     A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  IL17R   3'  CTGTAATCCCAGCAC      26776    A
                                GT GCTGGGATTACAG
                                || ||||||||||||
                                CA CGACCCTAATGTC
                                  _
GAM888  IL1R1   3'  CTATAATCCCAGCACT     6057     A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM888  IL1R1   3'  CTGTAATCCCAGCTAC     6058
                                GTAGCTGGGATTACAG
                                ||||||||||||||||
                                CATCGACCCTAATGTC

GAM888  IL4R    5'  ATGCCTATAATCCCAGCACT  4699     A       C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
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                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM888  IPP     3'  ATGCCTATAATCCCAGCACT  19724    A       C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM888  IRAK1   3'  CTGTAATCCCAGCACT     7808     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  ITGAL   3'  CTGTAATCCCAGCACT     9391     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  ITGAL   3'  CTGTAGTCCCAGCTACTCA  9392   C
                                A AGTAGCTGGGATTACAG
                                | |||||||||||||||||
                                A TCATCGACCCTGATGTC
                                 C
GAM888  JRK     3'  CTGTAATCCCAGCACTG    86526    A
                                CAGT GCTGGGATTACAG
                                |||| ||||||||||||
                                GTCA CGACCCTAATGTC

                                  _
GAM888  KAI1    3'  CTGTAATCCCAGCACT     9499     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  KCNA7   3'  ATGCCTGTGATCCCAGCTACTC 49049  C            A
          A                      A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACCCTAGTGTC GTA
                                 C             C
GAM888  KNSL1   3'  ATGCCTGTAATCCCAGCACT  15747    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| ||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LAMP2   3'  CTGTAATCCCAGCACT     25712    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LDLR    3'  CTGTAATCCCAGCACT     4985     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
```

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                                TCA CGACCCTAATGTC
                                  _
GAM888  LDLR    3'  CTGTAATCCCAGCACT      4986      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LEP     3'  CTGTAATCCCAGCACT      4048      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LRRC2   3'  GTAATCCCAGCTACTCA     44477     C
                                A AGTAGCTGGGATTAC
                                | ||||||||||||||
                                A TCATCGACCCTAATG
                                 C
GAM888  LRRC2   3'  CTATAATCCCAGCACT      44467     A         C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _         A
GAM888  LRRC2   3'  CTATAATCCCAGCACT      44468     A         C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _         A
GAM888  LRRC2   3'  CTGTAATCCCAGCACT      44469     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LUZP1   3'  ATGCCTGTAATCGCAGCTACTC 53296   C       G       A
              A                  A AGTAGCTG GATTACAG CAT
                                | |||||||| |||||||| |||
                                A TCATCGAC CTAATGTC GTA
                                 C       G       C
GAM888  LUZP1   3'  CTGTAATCCCAGCACT      53299     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  MAFF    3'  TCTGTAATCCCAGCACT      24654     A
                                AGT GCTGGGATTACAGA
                                ||| |||||||||||||
                                TCA CGACCCTAATGTCT
                                  _
GAM888  MCM4    3'  CTGTAATCCCAGCACT      61903     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
```

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                                TCA CGACCCTAATGTC
                                  _
GAM888  MIR16    3'  ATGCCTGTATTCCCAGCTACTC 33563   C        T    A
                A                A AGTAGCTGGGA TACAG CAT
                                 | |||||||||| ||||| |||
                                 A TCATCGACCCT ATGTC GTA
                                  C         T    C
GAM888  MOG      3'  CTGTAATCCCAGCACT     10102    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                  _
GAM888  MSH3     3'  ATGCCTGTAATCCCAGCACT  10118    A         A
                                 AGT GCTGGGATTACAG CAT
                                 ||| |||||||||||| |||
                                 TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  MTMR8    3'  CTGTAATCCCAGCACT     31292    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                  _
GAM888  MTNR1A   3'  CTGTAATCCCAGCTACT    19889
                                 AGTAGCTGGGATTACAG
                                 ||||||||||||||||
                                 TCATCGACCCTAATGTC

GAM888  NFKBIL2  3'  CTGTAATCCCAACACT     25525    AGC
                                 AGT   TGGGATTACAG
                                 |||   ||||||||||
                                 TCA   ACCCTAATGTC
                                   CA_
GAM888  NPHP1    3'  CTGTAATCCCAACACT     62479    AGC
                                 AGT   TGGGATTACAG
                                 |||   ||||||||||
                                 TCA   ACCCTAATGTC
                                   CA_
GAM888  NPHS1    3'  CTATAATCCCAGCACT     16190    A        C
                                 AGT GCTGGGATTA AG
                                 ||| |||||||||| ||
                                 TCA CGACCCTAAT TC
                                  _         A
GAM888  NT5C2    3'  ATGCCTGTAATCCCATCATCTA 24237      C___         A
                CT                 AGTAG    TGGGATTACAG CAT
                                   |||||    |||||||||| |||
                                   TCATC    ACCCTAATGTC GTA
                                     TACT          C
GAM888  NT5C2    3'  CTGTAATCCCAGCACT     24238    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
```

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                                TCA CGACCCTAATGTC
                                  _
GAM888  OASL    3' CTGTAATCCCAGAACT     13578    AG
                                AGT  CTGGGATTACAG
                                |||  ||||||||||||
                                TCA  GACCCTAATGTC
                                  A_
GAM888  OPTN    3' ATGCCTGTAATCCCAGCACT  41767    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  P2RX7   3' GTCTGTAATCCCAGCGCT   10374    A
                                AGT GCTGGGATTACAGAC
                                ||| ||||||||||||||
                                TCG CGACCCTAATGTCTG
                                  _
GAM888  PA2G4   3' CTGTAATCCCAGCACT     71299    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  PCDH11X 3' CTGTAATCCCAGCACT     52007    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  PCDH11X 3' CTGTAATCCCAGCACT     52008    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  PCDH11Y 3' CTGTAATCCCAGCACT     52060    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  PCDH11Y 3' CTGTAATCCCAGCACT     52066    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  PDE4C   3' ATGCCTATAATCCCAGCACT  6230     A       C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM888  PDE4C   3' TGCCTGTAATCCCGGTACT   6238     G         A
                                AGTA CTGGGATTACAG CA
                                |||| |||||||||||| ||
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                                TCAT GGCCCTAATGTC GT
                                  _          C
GAM888  PIK3R2   3'  ATGCCTGTAATCCCAGCACT  17256    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  PKD2     3'  CTGTAATCCCAGCACT     60092    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  PLA2G2D  3'  ATGCCTGTAATCCCAACACT  24786    AGC        A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_         C
GAM888  POLK     3'  CTGTAATCCCAGCTACT    32566
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  PSD      5'  CTGCAATCCCAGCACT      10927    A       A
                                AGT GCTGGGATT CAG
                                ||| ||||||||| |||
                                TCA CGACCCTAA GTC
                                  _       C
GAM888  PSMB2    3'  ATGCCTGTAATCCCAGCACT  10947    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  PSMB9    3'  CTATAATCCCAGCACT      10960    A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _       A
GAM888  PSMD5    3'  CTATAATCTCAGCTACTCA   17303   C          C
                                A AGTAGCTGGGATTA AG
                                | |||||||||||||| ||
                                A TCATCGACTCTAAT TC
                                 C          A
GAM888  PTAFR    3'  CTGTAGTCCCAGCTACTCA   6295    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTGATGTC
                                 C
GAM888  PTAFR    3'  CTGTAATCCCAGCACT      6294     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  RAB3B    3'  CTGTAATCCCAGCACT      11185     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  RAB7L1   3'  CTGTAATCCCAGCACT      14107     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  RAB7L1   3'  TGCCTGTAATCCCAGC      14110           A
                                GCTGGGATTACAG CA
                                |||||||||||| ||
                                CGACCCTAATGTC GT
                                        C
GAM888  RAD51L1  5'  CTGTAATCCCAGCGCT      56060     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCG CGACCCTAATGTC
                                  _
GAM888  RBBP5    3'  ATGCCTGTAATCCCAGCTAC   17332           A
                                GTAGCTGGGATTACAG CAT
                                |||||||||||||| |||
                                CATCGACCCTAATGTC GTA
                                        C
GAM888  RBBP5    3'  CTGTAATCCCAGCACT      17334     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  RBBP9    3'  ATGCCTGTAATCCCAGCACTGT 70128       A         A
          G                      TACAGT GCTGGGATTACAG CAT
                                |||||| |||||||||||| |||
                                GTGTCA CGACCCTAATGTC GTA
                                  _          C
GAM888  RBL1     3'  ATGCCTATAATCCCAGCTACTT 11260    _         C  A
          G                      CA GTAGCTGGGATTA AG CAT
                                || |||||||||||| || |||
                                GT CATCGACCCTAAT TC GTA
                                 T          A  C
GAM888  RBM3     3'  CTGTAATCCCAGTGACT      70487     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA TGACCCTAATGTC
                                  G
GAM888  RECQL5   3'  ATGTCTGTATTGGCTACTGT   14924        TG GAT
                                ACAGTAGC  G   TACAGACAT
                                ||||||||  |   |||||||||
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                                TGTCATCG  T   ATGTCTGTA
                                     GT ____
GAM888  RFC2     3'  CTGTAATCCCAACACT      11304     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  RPN1     5'  ATGCCTGTAATCCCAGCTACT  11389              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM888  SCD      3'  ATGTCTGTTTATTAACTACTG  17346       C   GATT
                                CAGTAG TGG    ACAGACAT
                                |||||| |||    ||||||||
                                GTCATC ATT    TGTCTGTA
                                    A   ATT_
GAM888  SCN2B    3'  CTGTAATCCCAGCACT      15938     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  SIM2     3'  CTGTAATCCCAGCACT      23783     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  SLC14A1  3'  CTGTAATCCCAGCACT      31839     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  SLC14A2  3'  CTGTAATCCCAGCACT      23132     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  SLC26A4  3'  ATGCCTGTAATCCCAGCACT  4783      A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM888  SLC28A2  3'  CTGTAATCCCAGCGCT      14869     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCG CGACCCTAATGTC
                                  _
GAM888  SLC2A3   3'  CTGTAATCCCAGCACT      22660     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                              TCA CGACCCTAATGTC
                                _
GAM888  SLC2A6   3'  CTGTAATCCCAGCACT     34157    A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM888  SLC31A1  3'  TGTAATCCCAGCTACTCA    8515    C
                              A AGTAGCTGGGATTACA
                              | ||||||||||||||||
                              A TCATCGACCCTAATGT
                               C
GAM888  SLC31A1  3'  ATGCCTGTAATCCCAGCACT   8511     A          A
                              AGT GCTGGGATTACAG CAT
                              ||| |||||||||||| |||
                              TCA CGACCCTAATGTC GTA
                                _          C
GAM888  SMG1     3'  CTGTAATCCCAGCACT      30651    A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM888  SRGAP1   5'  ATGCCTGTAGTCTCAGCTACTC 72259   C             A
          A                    A AGTAGCTGGGATTACAG CAT
                              | |||||||||||||||| |||
                              A TCATCGACTCTGATGTC GTA
                               C              C
GAM888  STAT3    3'  CTGTAATCCCAGCACT      57713    A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM888  STAT3    3'  CTGTAATCCCAGCACT      11998    A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM888  SULT1A2  3'  ATGTCTGCAATCCCAGCGATTT 72215    TA_       A
          G                    CAG   GCTGGGATT CAGACAT
                              |||   ||||||||| |||||||
                              GTT   CGACCCTAA GTCTGTA
                                TAG        C
GAM888  SULT1A3  3'  ATGTCTGCAATCCCAGCGATTT 12052    TA_       A
          G                    CAG   GCTGGGATT CAGACAT
                              |||   ||||||||| |||||||
                              GTT   CGACCCTAA GTCTGTA
                                TAG        C
GAM888  SULT2A1  3'  ATGTCTGTAATCCCAGCACT   71752    A
                              AGT GCTGGGATTACAGACAT
                              ||| ||||||||||||||||
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                                TCA CGACCCTAATGTCTGTA
                                  _
GAM888  SULT2A1   3'  ATGCCTGTAATCCCAGCACT   71751     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  SUV39H2   3'  CTGTAGTCCCAGCTACTCA    45136    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTGATGTC
                                 C
GAM888  SWAP70    3'  CTGTAATCCCAGCACT      71348     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  TBX6      3'  CTGTAATCCCAACTACTTG    54964    _    C
                                CA GTAG TGGGATTACAG
                                || |||| ||||||||||
                                GT CATC ACCCTAATGTC
                                 T    A
GAM888  TCF7      3'  CTGTAATCCCAGCACT      12161     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  TCTA      3'  CTGTAATCCCAACACT      42238     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  TEM7      3'  CTGTAATCCCAGCACT      39884     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  TKTL1     5'  ATGTCTGTCTTTCAGCCAC   24296    A   GG TT
                                GT GCTG  A  ACAGACAT
                                || ||||  |  ||||||||
                                CA CGAC  T  TGTCTGTA
                                 C    TT C_
GAM888  TM7SF3    3'  CTGTAATCCCAATACTG     59666      GC
                                CAGTA  TGGGATTACAG
                                |||||  ||||||||||
                                GTCAT  ACCCTAATGTC
                                   A_
GAM888  TNFRSF10A 3'  ATGCCTGTAATCCCAGCACT   13886     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  TNFRSF10D 3'  ATGCCTGTAATCCCAGCACT   13860     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  TNFSF15   3'  CTGTAATCCCAACACT      17592     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  TRIM14    3'  CTGTAATCCCAGCGCT      52635     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCG CGACCCTAATGTC

                                  _
GAM888  TRIM14    3'  ATGCCTGTAATCCCAGCTACT  28851              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                          C
GAM888  TRIM9     5'  ATGCCTGTAATCCCAGCTA    30752            A
                                TAGCTGGGATTACAG CAT
                                |||||||||||||| |||
                                ATCGACCCTAATGTC GTA
                                          C
GAM888  TRPM8     3'  TGTAATCCCAGCTACTCA     43987    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  TSN       3'  CTGTAATCCCAGCACACTG    16106      A_
                                CAGT  GCTGGGATTACAG
                                ||||  ||||||||||||
                                GTCA  CGACCCTAATGTC
                                   CA
GAM888  TSN       3'  TGCCTGTAATTCAGT        16111      G      A
                                GCTGG ATTACAG CA
                                ||||| ||||||| ||
                                TGACT TAATGTC GT
                                  _      C
GAM888  TSNAX     3'  CTGTAATCCCAGCACT       19998     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  TTF2      3'  TGCCTGTAATCCCGACACT    13176     AGC         A
                                AGT   TGGGATTACAG CA
                                |||   |||||||||| ||
```

```
                                TCA   GCCCTAATGTC GT
                                  CA_          C
GAM888  UBE2G2   3'  CTGCAATCCCAGCACT      64855     A       A
                                AGT GCTGGGATT CAG
                                ||| ||||||||| |||
                                TCA CGACCCTAA GTC
                                  _        C
GAM888  UBE2G2   3'  CTGTAGTCTCAGCTACTCA   64856   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACTCTGATGTC
                                 C
GAM888  UC28     3'  ATGCCTGTAATCCCAGCTACT  41288              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM888  UC28     3'  CTGTAATCCCAGCACT      41290     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  UPK1B    3'  ATGCCTGTAATCCCAGCACT   22715     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  USP14    3'  CTGTAATCCCAGCACT      17658     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  VDR      3'  TGTAATCCCAGCTACTCA    4574    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  VHL      3'  CTGTAATCCCAGCACT      5069      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  VHL      3'  TCTGTAATCCTAGCTACT    5090
                                AGTAGCTGGGATTACAGA
                                ||||||||||||||||||
                                TCATCGATCCTAATGTCT

GAM888  VHL      3'  ATGCCTGTAATCCCAGC     5058              A
                                GCTGGGATTACAG CAT
                                ||||||||||||| |||
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                                CGACCCTAATGTC GTA
                                        C
GAM888  VHL     3'  ATGCCTGTAATCCCAGCACT  5059     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  VHL     3'  ATGCCTGTAATCCTAGCTACTC 5060    C            A
          A                      A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGATCCTAATGTC GTA
                                 C            C
GAM888  VPS41   3'  ATGCCTGTAATCCCAGCTACT  26921              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                        C
GAM888  WIG1    3'  CTGTAATCCCAGCACT     94466    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  WSX1    3'  CTGTAATCCCAGCACT     16732    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  ZNF136  3'  CTGTAATCCCAGCACT     59888    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  ZNF137  3'  CTGTAATCCCAGCACT     12862    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  ZNF14   3'  ATGCCTCTAATCCCAGCTACTC 40713   C          C  A
          A                      A AGTAGCTGGGATTA AG CAT
                                | |||||||||||||| || |||
                                A TCATCGACCCTAAT TC GTA
                                 C           C  C
GAM888  ZNF36   3'  CTGTAATCCCAGCACT     93962    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  ZNF74   3'  CTGTAATCTTAACACTGTG  12795      AGC
                                TACAGT  TGGGATTACAG
                                ||||||  ||||||||||
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                                GTGTCA   ATTCTAATGTC
                                   CA_
GAM888  ZNF74    3'  ATGTCCCTGTGGTCCCAGCTAC 12790   C          __
              TCA                  A AGTAGCTGGGATTACA  GACAT
                                  | ||||||||||||||||  |||||
                                  A TCATCGACCCTGGTGT  CTGTA
                                   C             CC
GAM888  AF020591 3'  ATGCCTGTAATCCCAGCACTCT 27135    TA_         A
              G                   CAG   GCTGGGATTACAG CAT
                                  |||   |||||||||||||| |||
                                  GTC   CGACCCTAATGTC GTA
                                    TCA          C
GAM888  AF020591 3'  CTGTAATCCCAGCACT     27139    A
                                  AGT GCTGGGATTACAG
                                  ||| ||||||||||||
                                  TCA CGACCCTAATGTC
                                    _
GAM888  AF020591 3'  CTGTAGTCCCAGCTACTCA   27140   C
                                  A AGTAGCTGGGATTACAG
                                  | ||||||||||||||||
                                  A TCATCGACCCTGATGTC
                                   C
GAM888  AKAP11   3'  CTGTAATCCCAGAACTCTG   57831    TAG_
                                  CAG   CTGGGATTACAG
                                  |||   ||||||||||||
                                  GTC   GACCCTAATGTC
                                    TCAA
GAM888  AKR1D1   3'  ATGCCTATAATCCCAGCACT   19972    A       C  A
                                  AGT GCTGGGATTA AG CAT
                                  ||| |||||||||| || |||
                                  TCA CGACCCTAAT TC GTA
                                    _       A  C
GAM888  AKR1D1   3'  TGTAATCCCAGCTACTCA    19978   C
                                  A AGTAGCTGGGATTACA
                                  | ||||||||||||||||
                                  A TCATCGACCCTAATGT
                                   C
GAM888  APOF     3'  CTGTAATCCCAGCACTGTG   7909       A
                                  TACAGT GCTGGGATTACAG
                                  |||||| ||||||||||||
                                  GTGTCA CGACCCTAATGTC
                                     _
GAM888  APXL2    3'  CTGTAATCCCAGCACT     75189    A
                                  AGT GCTGGGATTACAG
                                  ||| ||||||||||||
                                  TCA CGACCCTAATGTC
                                     _
GAM888  ARNTL2   3'  ATGCCTGTAATCCCAGCACT   39454    A         A
                                  AGT GCTGGGATTACAG CAT
                                  ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  ARNTL2   3'  CTGTAATCCCAACTGCT     39462      C
                                AGTAG TGGGATTACAG
                                ||||| ||||||||||
                                TCGTC ACCCTAATGTC
                                   A
GAM888  ARNTL2   3'  CTGTAATCCCAGTACT      39463      G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC

                                  _
GAM888  BANP     3'  ATGCCTGTAATCCCAGC     66214            A
                                GCTGGGATTACAG CAT
                                |||||||||||| |||
                                CGACCCTAATGTC GTA
                                        C
GAM888  BFAR     3'  CTGTAATCCCAGCTACTTG   60771    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                 T
GAM888  BIA2     3'  CTGTAATCCCAGCACT      71281     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  BIRC1    3'  CTGTAATCCCAGCACT      15788     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  BLOV1    3'  ATGCCTGTAATCCCAGCTACT  76277              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                          C
GAM888  BLOV1    3'  CTGTAATCCCAGCACT      76280     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  BLOV1    3'  CTGTAATCCCAGCTACTTG   76281    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                 T
GAM888  BNIP-S   3'  GTCTGTAATCCCAGCACT    56274     A
                                AGT GCTGGGATTACAGAC
                                ||| ||||||||||||||
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                                TCA CGACCCTAATGTCTG
                                  _
GAM888  C13orf1   3'  CTGTAATCCCAGCACT      39969     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  C1orf24   3'  CTATAATCCCAGCACT      53714     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM888  C1QTNF2   3'  ATGCCTATAATCCCAGGACT   49124     AG       C  A
                                AGT  CTGGGATTA AG CAT
                                |||  ||||||||| || |||
                                TCA  GACCCTAAT TC GTA
                                  G_       A  C
GAM888  C20orf108 3'  CTGTAATCCCAGCACT      55045     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  C20orf12  3'  ATGCCTGTAATCCCAGTTACT  36321              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATTGACCCTAATGTC GTA
                                        C
GAM888  C20orf12  3'  CTGTAATCCCAGCACT      36322     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  C20orf130 3'  GTGGCTGTCCCAGCCAC     61758     A      TTA   A
                                GT GCTGGGA   CAG CAT
                                || |||||||   ||| |||
                                CA CGACCCT   GTC GTG
                                 C       ___   G
GAM888  C20orf142 3'  CTGTAATCCCAGCTACT     74775
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  C20orf175 3'  CTGTAATCCCAACACT      55064     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  C20orf177 3'  ATGCCTGTAATCCCAGCTACT  62143              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
```

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                                TCATCGACCCTAATGTC GTA
                                          C
GAM888  C20orf177 3'  CTGTAATCCCAGCACT     62146     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  C20orf183 3'  CTGTAATCCCAGCACT     47803     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  C20orf29  3'  CTGTAATCCCAGCACT     37126     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  C21orf108 3'  CTATAATCCCAGCACT     88720     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM888  C22orf19  3'  GTCTGTAATCCCAGCACT    13429     A
                                AGT GCTGGGATTACAGAC
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCTG
                                  _
GAM888  C22orf20  3'  ATGCCTGTAATCCCAGCTATT  47425               A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TTATCGACCCTAATGTC GTA
                                          C
GAM888  C2F       3'  CTGTAATCCCAGCACT      20928     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  C6orf10   5'  CTGTAATCCCATCATTTGCT   22289      C___
                                AGTAG   TGGGATTACAG
                                |||||   ||||||||||
                                TCGTT   ACCCTAATGTC
                                   TACT
GAM888  C6orf5    3'  CTGTAATCCCAGCACT      31346     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  C6orf5    3'  CTGTAATCCCAGCACT      31347     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  C8orf2   3'  CTGTAATCCCAGCACT     23163     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  C9orf5   3'  TCTGTAATCCCAGCACT     49284     A
                                AGT GCTGGGATTACAGA
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCT
                                  _
GAM888  CALN1    3'  CTATAATCCCAGCACT     48866     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM888  CAMKK2   5'  CTGTAATCCCAGCACT     21582     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  CBCIP2   3'  CTGTAATCCCAGCACT     51590     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  cerk     3'  CTGTAATCCCAGCACT     42846     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  CFLAR    3'  CTGTAATCCCAGCACT     13929     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  CG012    5'  CTGTAATCCCAGCTATTCGGCT 83219     _____
              G                  CAGT    AGCTGGGATTACAG
                                ||||    ||||||||||||||
                                GTCG    TCGACCCTAATGTC
                                  GCTTA
GAM888  CG012    5'  ATGCCTATATTCTAGCTACTCA 83214   C         TAC  A
                                A AGTAGCTGGGAT   AG CAT
                                | ||||||||||||   || |||
                                A TCATCGATCTTA   TC GTA
                                 C          TA_  C
GAM888  CG012    5'  ATGCCTGTAATCCCAACACT   83215     AGC         A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||| |||
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                                TCA   ACCCTAATGTC GTA
                                  CA_         C
GAM888  CGI-203   3'  TGTAATCCCAGCTACTCA    39904   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  CHRFAM7A  3'  ATGCTTGTAATCCCAGCTACTC 95017   C           GA
            A                    A AGTAGCTGGGATTACA  CAT
                                | ||||||||||||||||  |||
                                A TCATCGACCCTAATGT  GTA
                                 C             TC
GAM888  CLDN15    3'  ATGCCTGTAATCCCAGCACT   56558    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| ||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  CNNM4     3'  TCTGTTGTCAACTGCTGTA   39484        CTGG   T
                                TACAGTAG    GAT ACAGA
                                ||||||||    ||| |||||
                                ATGTCGTC    CTG TGTCT
                                     AA__   T
GAM888  COE2      3'  CTGTAATCCCAGCACT      64251     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  COE2      3'  ATGCCTGTAATCCCAGCTACTT 64247    _          A
            G                    CA GTAGCTGGGATTACAG CAT
                                || |||||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 T             C
GAM888  CPR2      3'  CTGTAATCCCAGCACT      48095     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  CPR2      3'  CTGTAATCCCAGCTACTCA   48096   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM888  CSAD      3'  CTGTAATCCCAGCACT      32028     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  D21S2056E 3'  ATGCCTGTAATCCCAGCTACT  13467            A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
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                                TCATCGACCCTAATGTC GTA
                                          C
GAM888  D21S2056E 3'  CTGTAATCCCAGCACT      13470     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM888  DCOHM    3'  CTGTAATCCCTGCACT      49600     A  T
                                AGT GC GGGATTACAG
                                ||| || ||||||||||
                                TCA CG CCCTAATGTC
                                  _  T
GAM888  DDX34    3'  CTGTAATCCCAGCACT      27982     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM888  DEGS     3'  ATGCCTGTAATCCCAGCTACAT 58613     _           A
           G                     CA GTAGCTGGGATTACAG CAT
                                || ||||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 A            C
GAM888  DEGS     3'  ATGCCTATAATCCCAGCACT   13409     A       C  A
                                AGT GCTGGGATTA AG CAT
                                ||| ||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                 _       A  C
GAM888  DEGS     3'  ATGCCTGTAATCCCAGCTACAT 13410     _           A
           G                     CA GTAGCTGGGATTACAG CAT
                                || ||||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 A            C
GAM888  DIS3     3'  ATGCCTGTAATCCCAGCTACTT 30227     _           A
           G                     CA GTAGCTGGGATTACAG CAT
                                || ||||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 T            C
GAM888  DKFZP434B168 3'  CTGTAATCCCAGCACT      31253     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM888  DKFZP434C171 3'  CTGTAATCCCAGCACT      31553     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM888  DKFZP434C1715 3'  CTGTAATCCCAGCAC      86148     A
                                GT GCTGGGATTACAG
                                || ||||||||||||
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                                CA CGACCCTAATGTC
                                  _
GAM888  DKFZp434E0519 3'  CTATAATCCCAGCACT      49986     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM888  DKFZp434E2220 5'  TGTAATCCCAGCTACTCA    34304    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  DKFZP434F091 3'  TGTAATCCCAACTACTCA    31284    C    C
                                A AGTAG TGGGATTACA
                                | ||||| ||||||||||
                                A TCATC ACCCTAATGT
                                 C    A
GAM888  DKFZp434G171 3'  ATGCCTGTAATCCCAGCACT   79431     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  DKFZp434G171 3'  TGTAATCCCAGCTACTCA    79440    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  DKFZP434I1735 3'  CTGTAATCCCAGCTACT     87801
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  DKFZP434L187 5'  CTGTAATCCCAGCTACT     68804
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  DKFZP434N1511 3'  ATGCCTGTAATCCCAGCACT   91415     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  DKFZP434N161 3'  GTCTGTAATCCCAGCACT    78522     A
                                AGT GCTGGGATTACAGAC
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCTG
                                  _
GAM888  DKFZp547C176 3'  CTGTAATCCCAGCACT      67222     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  DKFZp547I094 3'  CTGTAATCCCAGCACT      49639     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  DKFZp547I094 3'  CTGTAGTCACAGCTACT     49640         G
                                AGTAGCTG GATTACAG
                                |||||||| ||||||||
                                TCATCGAC CTGATGTC
                                     A
GAM888  DKFZP564B1023 3'  ATGCCTGTAATCCCAGCTACT  48536               A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM888  DKFZP564B1023 3'  CTGTAATCCCAGCACT      48538     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  DKFZP564I052 3'  CTGTAATCCCAGCACT      66707     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  DKFZP564M182 3'  CTGTAATCCCAGCACT      78033     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  DKFZP564M182 3'  CTGTAATCCCAGCTACT     78034
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  DKFZp566H0824 3'  CTGTAATCCCAGCACTTTA   34050    C   A
                                TA AGT GCTGGGATTACAG
                                || ||| ||||||||||||
                                AT TCA CGACCCTAATGTC
                                  T   _
GAM888  DKFZP586C1324 3'  ATGCCTGTAATCCCAGCACT   69796     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  DKFZP586M1120 3'  CTGTAATCCCAGCACT      48457     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  DKFZP667O116 3'  TGCCTATAATCCCGGCACT   94287    A       C  A
                                AGT GCTGGGATTA AG CA
                                ||| |||||||||| || ||
                                TCA CGGCCCTAAT TC GT
                                  _        A  C
GAM888  DKFZP761E2110 3'  ATGCCTGTAATCCCAGCAC   48224    A          A
                                GT GCTGGGATTACAG CAT
                                || |||||||||||| |||
                                CA CGACCCTAATGTC GTA
                                  _          C
GAM888  DKFZP761G1913 3'  ATGCCTGTAATCCCAGCACT  48909    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  DKFZP761G1913 3'  CTGTAATCCCAGCTACTTG   48913    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                 T
GAM888  DKFZp761J139 5'  CTGTAATCCCAGCACT     50108    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  DRF1     3'  CTATAATCCCAGCACT     47030    A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _       A
GAM888  DRF1     3'  CTGTAATCCCAGCACT     47032    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  DRF1     3'  TGTAATCCCAGCTACTCA   47038   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  FADS1    3'  ATGCCTGTAATCCCAACACT  25473    AGC        A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_         C
GAM888  FADS1    3'  CTGTAATCCCAGCTAC     25476
                                GTAGCTGGGATTACAG
                                ||||||||||||||||
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                                CATCGACCCTAATGTC

GAM888  FBXO27   3'  CTGTAATCCCTGCACT      74508     A  T
                                AGT GC GGGATTACAG
                                ||| || ||||||||||
                                TCA CG CCCTAATGTC
                                  _  T
GAM888  FBXO27   3'  ATGCCTGTAATCCCAGCACT   74504     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FBXO6    3'  CTGTAATCCCAGCACT      37383     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FBXO9    3'  ATGCCTATAATCCCAGCACT   53100     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM888  FBXO9    3'  CTATAATCCCAATACT      53102     GC       C
                                AGTA  TGGGATTA AG
                                ||||  |||||||| ||
                                TCAT  ACCCTAAT TC
                                  A_       A
GAM888  FKBP14   3'  ATGCCTGTAATCCCAGCACT   35622     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FKBP14   3'  ATGCCTGTAATCCCAGCACT   35623     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FKSG17   3'  CTGTAATCCCAGTTACTCA    49329    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||||
                                A TCATTGACCCTAATGTC
                                 C
GAM888  FLJ00060 3'  ATGTCTGTAATCCCAGCACTCT 61091     TA_
          G                      CAG   GCTGGGATTACAGACAT
                                |||   ||||||||||||||||||
                                GTC   CGACCCTAATGTCTGTA
                                  TCA
GAM888  FLJ10008 3'  GTCTGTAATCCCAGCACT     35729     A
                                AGT GCTGGGATTACAGAC
                                ||| ||||||||||||||
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                                TCA CGACCCTAATGTCTG
                                  _
GAM888  FLJ10043 3' CTGTAATCCCAGCACT     35758     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ10043 3' CTGTAATCCCAGCTACT     35759
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  FLJ10058 3' ATGCCTGTAATCCCAGCACT  35782     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ10244 3' ATGCCTGTAATCCCAGCTGCT 35940               A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCGTCGACCCTAATGTC GTA
                                           C
GAM888  FLJ10460 3' CTGTAATCCCAGCTACTTG   36129    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                 T
GAM888  FLJ10460 3' CTGTAATCCCAACACT      36127     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  FLJ10460 3' CTGTAATCCCAGCACT      36128     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ10547 3' CTGTAATCCCAGCACT      36267     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ10607 3' CTGTAATCCCAGCACT      77113     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ10607 3' CTGTAATCCCAGCTACTCA   77114    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
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                                A TCATCGACCCTAATGTC
                                 C
GAM888  FLJ10613  3'  GTCTGTAATCCCAGCACT    38825     A
                                AGT GCTGGGATTACAGAC
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCTG
                                  _
GAM888  FLJ10650  3'  CTGTAATCCCAGCACT      36382     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ10704  3'  ATGCCTGTAATCCCAGCTACT  36449               A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                          C
GAM888  FLJ10781  3'  CTGTAATCCCAGCACT      36631     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ10781  3'  TGTAATCCCAGCTACTCA    36638    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  FLJ10803  3'  CTGTAATCCCAGCACT      36664     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ10826  3'  ATGCCTGTAATCCCAGCTACT  36700               A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                          C
GAM888  FLJ10830  3'  ATGCCTGTAGTCCCAGCCACTC 36717    C   A          A
          A                      A AGT GCTGGGATTACAG CAT
                                | ||| |||||||||||| |||
                                A TCA CGACCCTGATGTC GTA
                                 C   C           C
GAM888  FLJ10830  3'  ATGCCTGTAGTTCCAGCTACTC 36718    C             A
          A                      A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGACCTTGATGTC GTA
                                 C             C
GAM888  FLJ10989  3'  CTGTAATCCCAGCACT      36949     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ10997 3' TGCCTGACCACCTACTGTA   36957       C  GATTA  A
                                TACAGTAG TGG    CAG CA
                                |||||||| |||    ||| ||
                                ATGTCATC ACC    GTC GT
                                     C  A____   C
GAM888  FLJ11029 3' CTGTAATCCCAGCACT     60975    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ11036 3' CTGCGGTTCCAGCTACTCA   36998   C        TA
                                A AGTAGCTGGGAT  CAG
                                | ||||||||||||  |||
                                A TCATCGACCTTG  GTC
                                 C          GC
GAM888  FLJ11042 3' ATGCCTGTAATCCCAGCACT  37004    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ11126 3' ATGCCTATAATCCCAGCAC   37083    A       C  A
                                GT GCTGGGATTA AG CAT
                                || |||||||||| || |||
                                CA CGACCCTAAT TC GTA
                                  _        A  C
GAM888  FLJ11136 3' CTGTAATCCCAGCACT      37093    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ11151 3' CTGTAATCCCAGCACT      67874    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ11151 3' CTGTAATCCCAGCTACT     67875
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  FLJ11267 3' ATGCCTGTAATCCCAGCACT  39003    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ11370 3' ATGCCTGTAATCCCAGCTACT 46370              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
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                                TCATCGACCCTAATGTC GTA
                                          C
GAM888  FLJ11637  3'  CTGTAATCCCAGCACT     46380     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM888  FLJ11700  3'  CTGTAATCCCAGCACT     46038     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM888  FLJ11700  3'  CTGTAATCCCAGCTACTCA   46039   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM888  FLJ11710  5'  ATGCCTGTAGTCCCAGCTACTC 45825   C            A
          A                      A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACCCTGATGTC GTA
                                 C             C
GAM888  FLJ11722  3'  ATGCCTGTAATCCCAGGACT   46389     AG         A
                                AGT  CTGGGATTACAG CAT
                                |||  |||||||||||| |||
                                TCA  GACCCTAATGTC GTA
                                  G_          C
GAM888  FLJ11722  3'  CTGTAATCCCAGCTACT     46391
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  FLJ11722  3'  TGTAATCCCAGCTACTCA    46401   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  FLJ11726  3'  CTGTAATCCCAGCACT     46411     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM888  FLJ11996  3'  ATGCCTGTAATCCCAGCTACT  46434             A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                          C
GAM888  FLJ12056  3'  ATGCCTATAATCCCAACACT   46251     AGC      C  A
                                AGT   TGGGATTA AG CAT
                                |||   |||||||| || |||
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                                TCA   ACCCTAAT TC GTA
                                  CA_       A  C
GAM888  FLJ12056  3'  ATGCCTGTAATCCCAGCTATT  46252              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TTATCGACCCTAATGTC GTA
                                        C
GAM888  FLJ12122  3'  CTGTAATCCCAGCACT      46462     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                _
GAM888  FLJ12178  3'  GTCTGTAATCCCAGCACT    47103     A
                                AGT GCTGGGATTACAGAC
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCTG

                                _
GAM888  FLJ12294  3'  CTATAATCCCAGCTACT     47012             C
                                AGTAGCTGGGATTA AG
                                |||||||||||||| ||
                                TCATCGACCCTAAT TC
                                        A
GAM888  FLJ12294  3'  CTGTAATCCCAGCACT      47013     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                _
GAM888  FLJ12331  3'  CTATAATCCCAGCACTTTA   46478    C   A         C
                                TA AGT GCTGGGATTA AG
                                || ||| |||||||||| ||
                                AT TCA CGACCCTAAT TC
                                  T   _         A
GAM888  FLJ12363  3'  CTGTAATCCCAGCACT      49679     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                _
GAM888  FLJ12547  3'  CTGTAATCCCAGCACTGTG   46491         A
                                TACAGT GCTGGGATTACAG
                                |||||| ||||||||||||
                                GTGTCA CGACCCTAATGTC

                                  _
GAM888  FLJ12606  3'  CTGTAATCCCAGCACT      45640     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                _
GAM888  FLJ12618  3'  ATGCCTGTAATCTCAGCTACTC 45994    C              A
              A                   A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
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                                A TCATCGACTCTAATGTC GTA
                                 C             C
GAM888  FLJ12660 3' CTGTAATCCCAGCACT     47141     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ12660 3' CTGTAATCCCAGCTACT     47142
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  FLJ12666 3' CTGTAATCCCAGCACT      44767     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ12800 3' CTGTAATCCCAGCACT      43232     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ12949 3' ATGCCTGTAGTCCCAGCTACTC 43442    C             A
          A                      A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACCCTGATGTC GTA
                                 C             C
GAM888  FLJ12949 3' CTGTAATCCCAGCACT      43445     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ12985 3' CTGTAATCCCAGCACT      46240     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ13117 3' ATGCCTGTAATCCCAGCACT  43539     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| ||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ13162 3' ATGCCTGTAATCCCAGCTACT 46550               A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM888  FLJ13162 3' CTGTAATCCCAGCACT      46556     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ13193 3' ATGCCTATAATCCCGGCTACT 49758          C A
                                AGTAGCTGGGATTA AG CAT
                                |||||||||||||| || |||
                                TCATCGGCCCTAAT TC GTA
                                      A  C
GAM888  FLJ13193 3' CTGTAATCCCAACACTTTA  49765   C  AGC
                                TA AGT  TGGGATTACAG
                                || |||  ||||||||||
                                AT TCA  ACCCTAATGTC
                                 T  CA_
GAM888  FLJ13193 3' CTGTAATCCCAGCACT    49766    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ13305 3' ATGCCTGTAATCCCAGC    90125         A
                                GCTGGGATTACAG CAT
                                |||||||||||| |||
                                CGACCCTAATGTC GTA
                                      C
GAM888  FLJ13448 3' CTGTAATCCCAGTTACT    47135
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATTGACCCTAATGTC

GAM888  FLJ13456 3' CTGTAATCCCAGCACT    65936    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ13456 3' CTGTAATCCCAGCTACTCA  65937  C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM888  FLJ13614 3' CTGTAATCCCAGCACT    57451    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ13659 3' ATGCCTGTAATCCCAGCTACT 47243           A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                      C
GAM888  FLJ13659 3' CTGTAATCCCAGCACT    47246    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ13769 3' ATGCCTATAATCCCAGCACT  46600    A       C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _       A  C
GAM888  FLJ13769 3' CTGTAATCCCAGCACT     46608    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ13848 3' CTGTAATCCCAGCACT     45465    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ13910 3' CTGCATTTTAGCTCTG     42927    T       TA
                                CAG AGCTGGGAT  CAG
                                ||| |||||||||  |||
                                GTC TCGATTTTA  GTC
                                  _       C_
GAM888  FLJ13952 3' ATGCCTGTAACCCCAGCTACT 45613        A    A
                                AGTAGCTGGG TTACAG CAT
                                |||||||||| |||||| |||
                                TCATCGACCC AATGTC GTA
                                      C     C
GAM888  FLJ13952 3' ATGCCTGTAATCCCAGCACT  45614    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _         C
GAM888  FLJ13984 3' CTGTGGTCCCAGCTACTCA   45448   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTGGTGTC
                                 C
GAM888  FLJ14100 3' CTGTAATCCCAGCACT     46679    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ14107 3' ATGCCTGTAATCCCAGCACT  46689    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _         C
GAM888  FLJ14117 3' CTGTAATCCCAGCACT     42908    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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```
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ14117 3' ATGCCTGTAGTCCCAGCTACTC 42901   C           A
              A                  A AGTAGCTGGGATTACAG CAT
                                 | |||||||||||||||| |||
                                 A TCATCGACCCTGATGTC GTA
                                  C            C
GAM888  FLJ14117 3' CTGTAATACCAGCTACTCA   42907   C      G
                                 A AGTAGCTGG ATTACAG
                                 | ||||||||| |||||||
                                 A TCATCGACC TAATGTC
                                  C       A
GAM888  FLJ14225 3' CTGTAATCCCAGCACT     45902    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                  _
GAM888  FLJ14251 3' CTGTAATCCCAGCACT     45970    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                  _
GAM888  FLJ14326 3' ATGCCTATAATCCCAGCTACT  49799          C  A
                                 AGTAGCTGGGATTA AG CAT
                                 |||||||||||||| || |||
                                 TCATCGACCCTAAT TC GTA
                                        A  C
GAM888  FLJ14326 3' ATGCCTGTAATCCCAGC     49800          A
                                 GCTGGGATTACAG CAT
                                 |||||||||||||| |||
                                 CGACCCTAATGTC GTA
                                        C
GAM888  FLJ14327 3' ATGCCTGTAATCCCAGCACT  46129    A         A
                                 AGT GCTGGGATTACAG CAT
                                 ||| |||||||||||| |||
                                 TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ14345 3' CTGTAATCCCAGCTACT     45335
                                 AGTAGCTGGGATTACAG
                                 ||||||||||||||||
                                 TCATCGACCCTAATGTC

GAM888  FLJ14345 3' CTGTAATCCCAGCACT      45334    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                  _
GAM888  FLJ14346 3' CTGTAATCCCAGCACT      46709    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ14346 3' CTGTAATCCCAGCACT     46710     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ14397 3' ATGCCTGTAACCCCAGCTACT 51323          A     A
                                AGTAGCTGGG TTACAG CAT
                                |||||||||| |||||| |||
                                TCATCGACCC AATGTC GTA
                                      C     C
GAM888  FLJ14397 3' CTATAATCCCAGCACT      51325     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM888  FLJ14621 3' CTGTAATCCCAGCACT      51470     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ14642 3' ATGCCTGTAATCCCAGCACT  51493     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ14642 3' CTGTAATCCCAGCACT      51499     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ14888 3' ATGCCTGTAATCCCAGCACT  51679     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ20004 3' CTGTAATCCCAGCACT      95292     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ20004 3' TGCCTGTAATCCCAGCTACT  95301               A
                                AGTAGCTGGGATTACAG CA
                                |||||||||||||||| ||
                                TCATCGACCCTAATGTC GT
                                           C
GAM888  FLJ20004 3' ATGCCTGTAATCCCAGCACT  34312     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
```

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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ20006 3' CTGTAATCCCAGCACT     34320     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ20006 3' CTGTAATCCCAGCTACT     34321
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  FLJ20034 3' CTGTAATCCCAGCACT      34371     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ20055 3' CTGAAGTCCCAGCTACTCA   34440   C         A
                                A AGTAGCTGGGATT CAG
                                | ||||||||||||| |||
                                A TCATCGACCCTGA GTC
                                 C          A
GAM888  FLJ20055 3' CTGTAATCCCAGCACTTTA   34441   C   A
                                TA AGT GCTGGGATTACAG
                                || ||| ||||||||||||
                                AT TCA CGACCCTAATGTC
                                 T  _
GAM888  FLJ20059 3' ATGCCTGTAATCCCAGCACT  34446    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| ||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ20071 3' ATGCCTATAATCCCAGCTACTT 34479   _         C  A
          G                      CA GTAGCTGGGATTA AG CAT
                                || |||||||||||| || |||
                                GT CATCGACCCTAAT TC GTA
                                 T          A  C
GAM888  FLJ20081 3' CTGTAATCCCAGCACT      34507     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ20139 3' CTGTAATCCCAACACT      34624     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  FLJ20174 3' CTGTAATCCCAAAGTGCTG   34688      GC_
                                CAGTA   TGGGATTACAG
                                |||||   ||||||||||
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                                GTCGT   ACCCTAATGTC
                                   GAA
GAM888  FLJ20200  3' TGCCTGTAATCCCTGCACT   34729     A  T        A
                                AGT GC GGGATTACAG CA
                                ||| || |||||||||| ||
                                TCA CG CCCTAATGTC GT
                                  _  T         C
GAM888  FLJ20211  3' CTGTAATCCCAGCACT      34751     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ20280  3' CTGTAATCCCAGCACT      34849     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ20280  3' CTGTAATCCCTGCTACT     34850       T
                                AGTAGC GGGATTACAG
                                |||||| ||||||||||
                                TCATCG CCCTAATGTC
                                   T
GAM888  FLJ20340  3' ATGCCTGTAATCCCAGCATTTT 34972     TA_          A
     G                   CAG   GCTGGGATTACAG CAT
                         |||   |||||||||||||| |||
                         GTT   CGACCCTAATGTC GTA
                           TTA           C
GAM888  FLJ20340  3' TGTAATCCCAGCTACTCA    34979    C
                         A AGTAGCTGGGATTACA
                         | ||||||||||||||||
                         A TCATCGACCCTAATGT
                          C
GAM888  FLJ20359  3' ATGCCTGTAATCCCAGCACT   35035     A          A
                         AGT GCTGGGATTACAG CAT
                         ||| |||||||||||| |||
                         TCA CGACCCTAATGTC GTA
                           _           C
GAM888  FLJ20452  3' ATGCCTGTAATCCCAGCACT   35196     A          A
                         AGT GCTGGGATTACAG CAT
                         ||| |||||||||||| |||
                         TCA CGACCCTAATGTC GTA
                           _           C
GAM888  FLJ20464  3' ATGCCTATAATCCGAGCTACT  35228        G     C  A
                         AGTAGCT GGATTA AG CAT
                         ||||||| |||||| || |||
                         TCATCGA CCTAAT TC GTA
                              G     A  C
GAM888  FLJ20464  3' ATGCCTGTAATCCCAGCACT   35229     A          A
                         AGT GCTGGGATTACAG CAT
                         ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ20464  3'  ATGCCTGTAATCTCAGCTACT  35230            A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACTCTAATGTC GTA
                                           C
GAM888  FLJ20627  3'  ATGCCTGTAATCCCAGCACT   35471    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ20627  3'  GTCATCTCAGCTACTCA     35475   C        T
                                A AGTAGCTGGGAT AC
                                | |||||||||||  ||
                                A TCATCGACTCTA TG
                                 C          C
GAM888  FLJ20695  3'  ATGCCTGTAATCCCAGCACT   35556    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ20700  3'  ATGCCTGTAATCCCAGCACT   35570    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ20783  3'  CTGTAATCCCAGCACT      35661    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ20825  3'  ATGCCTGTAATCCCAACTCTTG 35693    T  C        A
                                CAG AG TGGGATTACAG CAT
                                ||| || |||||||||| |||
                                GTT TC ACCCTAATGTC GTA
                                  C  A         C
GAM888  FLJ20825  3'  ATGCCTGTAATCCCAGCTACT  35694            A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM888  FLJ20825  3'  CTGTAATCCCAGCACT      35696    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ20972  3'  ATGCCTATAATCCCAGGTACT  46722     G       C  A
                                AGTA CTGGGATTA AG CAT
                                |||| ||||||||| || |||
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                                TCAT GACCCTAAT TC GTA
                                  G        A  C
GAM888  FLJ21106  3'  CTGTAATCCCAGCACT      46995     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ21144  3'  ATGCCTGTAATCCCAGCACT   42875     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ21162  3'  ATGCCTATAATCCCAGCACT   45892     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM888  FLJ21162  3'  CTATAAACCCAGCTACTCA    45894    C        A   C
                                A AGTAGCTGGG TTA AG
                                | |||||||||| ||| ||
                                A TCATCGACCC AAT TC
                                 C         A   A
GAM888  FLJ21240  3'  ATGCCTGTAATATCAGCTACTC 45837    C       GG      A
          A                      A AGTAGCTG  ATTACAG CAT
                                | ||||||||  ||||||| |||
                                A TCATCGAC  TAATGTC GTA
                                 C       TA      C
GAM888  FLJ21272  3'  ATGCCTGTAATCCCAGC     46735           A
                                GCTGGGATTACAG CAT
                                |||||||||||| |||
                                CGACCCTAATGTC GTA
                                        C
GAM888  FLJ21551  3'  CTGTAATCCCAGCTAC      45628
                                GTAGCTGGGATTACAG
                                ||||||||||||||||
                                CATCGACCCTAATGTC

GAM888  FLJ21657  3'  CTGTAATCCCAACACT      42509     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  FLJ21687  3'  CTGTAATCCCAGCACT      45857     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ21870  3'  ATGCCTGTAATCCCAGCACT   43458     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ22054  3'  CTGTAATCCAAGCTGC      94395       G
                                GTAGCT GGATTACAG
                                |||||| |||||||||
                                CGTCGA CCTAATGTC
                                   A
GAM888  FLJ22054  3'  CTGTAATCCCAGCACT      94396     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ22167  3'  ATGCCTGTAATCCCAGCATTTT 44565     TA_          A
          G                      CAG   GCTGGGATTACAG CAT
                                |||   |||||||||||| |||
                                GTT   CGACCCTAATGTC GTA
                                  TTA           C
GAM888  FLJ22167  3'  CTGTAATCCCAGCTACTTA    44572    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 T
GAM888  FLJ22313  3'  GTCTGTAATCCCAGCACT     42344     A
                                AGT GCTGGGATTACAGAC
                                ||| |||||||||||||
                                TCA CGACCCTAATGTCTG
                                  _
GAM888  FLJ22692  3'  CTGTAATCCCAGCACT       46802     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ23022  3'  TGCCTGTAATCCCTGCACT    46814     A  T        A
                                AGT GC GGGATTACAG CA
                                ||| || |||||||||| ||
                                TCA CG CCCTAATGTC GT
                                  _  T         C
GAM888  FLJ23042  3'  ATGCCTGTAATCCCAGCTACT  47170               A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM888  FLJ23042  3'  CTGTAATCCCAGCACT       47172     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ23120  3'  CTGTAATCCCAGCTACTCA    85148    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
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                                A TCATCGACCCTAATGTC
                                 C
GAM888  FLJ23235  3'  ATGCCTGTAATCCCAGCACT   46305     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ23323  3'  CTGTAATCCCAAAGTGCTG    45051      GC_
                                CAGTA   TGGGATTACAG
                                |||||   ||||||||||
                                GTCGT   ACCCTAATGTC
                                   GAA
GAM888  FLJ23447  3'  ATGCCTGTAATCCCAGCACT   45710     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ23476  3'  ATGCCTGTAATCCCAACATTCT 44958     TAGC_         A
          G                      CAG     TGGGATTACAG CAT
                                |||     |||||||||| |||
                                GTC     ACCCTAATGTC GTA
                                  TTACA          C
GAM888  FLJ23499  3'  ATGCCTGTAATCCCAGCACT   42816     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ23499  3'  ATGCCTGTAATCCCAGCACT   42817     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ23499  3'  CTGTAATCCCAGCTACT      42821
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  FLJ23537  3'  ATGCCTGCAATCCCAGCTACTT 46021     _          A  A
          G                      CA GTAGCTGGGATT CAG CAT
                                || |||||||||| ||| |||
                                GT CATCGACCCTAA GTC GTA
                                  T          C  C
GAM888  FLJ25012  3'  ATGCCTGTAATCCAGTACT    58088      G  G      A
                                AGTA CTGG ATTACAG CAT
                                |||| |||| ||||||| |||
                                TCAT GACC TAATGTC GTA
                                  _  _       C
GAM888  FLJ25012  3'  CTATGGTCCCAGCTACTCA    58089    C          C
                                A AGTAGCTGGGATTA AG
                                | |||||||||||||| ||
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                                A TCATCGACCCTGGT TC
                                 C           A
GAM888  FLJ25012  3'  CTGTAATCCCAGCACT      58090     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ25179  3'  ATGCCTGTAATCCCAGCACT   58354     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  FLJ30046  3'  CTGCAATGTTTGCTACTGTA   58100         TG G   A
                                TACAGTAGC  G ATT CAG
                                |||||||||  | ||| |||
                                ATGTCATCG  T TAA GTC
                                      TT G   C
GAM888  FLJ30092  3'  CTGTAATCCCAGCACT      58689     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ30681  3'  CTGTAATCCCAGCTACT     91786
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  FLJ31455  3'  CTGTAATCCCAGCACT      58623     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FLJ31737  3'  CTGTAATCCCAGCACT      58694     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  FUSIP1    3'  ATGCCTGTAATCTCAGCTACTC 53955   C              A
          A                      A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGACTCTAATGTC GTA
                                 C              C
GAM888  FUSIP1    3'  CTGTAATCCCAGCACT      53957     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  GALNT6    3'  ATGCCTGTAGTCGCAGCTACTC 23290   C       G       A
          A                      A AGTAGCTG GATTACAG CAT
                                | |||||||| |||||||| |||
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                                A TCATCGAC CTGATGTC GTA
                                 C       G       C
GAM888  GCN2     3'  ATGCCTGTAGTCCCAGCTACT  62768              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTGATGTC GTA
                                          C
GAM888  GLTP     3'  CTGTAATCCCAGCACT      33159     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  GLTP     3'  CTGTAGTTCCAGCTACTCA   33160   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCTTGATGTC
                                 C
GAM888  GP5      3'  CTGTAATCCCAGCACT      15645     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  HES2     3'  CTGTAATCCCAGCACT      38854     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  HSD17B7  3'  TGTAGTCCCAGCTACTCA    33037   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTGATGT
                                 C
GAM888  HSH2     3'  ATGCCTGTAATCCCAGCTACTT 51671   _            A
          G                      CA GTAGCTGGGATTACAG CAT
                                || |||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 T            C
GAM888  HSMPP8   3'  CTATAATCCCAGCGCT      93474     A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCG CGACCCTAAT TC
                                  _       A
GAM888  HSPC043  3'  ATGCCTGTAATCCCAGCACT  67719     A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  HSPC043  3'  CTGTAATCCCAGCTACT     67720
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
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                                TCATCGACCCTAATGTC

GAM888  ICAM4     3'  CTGTAATCCCAGCACT      42353     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  ICAM4     3'  CTGTAATCCCAGCACT      7749      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  IL10RB    3'  ATGCCTATAATCCCAGCTACT  5275            C  A
                                AGTAGCTGGGATTA AG CAT
                                |||||||||||||| || |||
                                TCATCGACCCTAAT TC GTA
                                         A  C
GAM888  IMAGE:4907098 3'  CTGTAATCCCAGCACT      91658     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  INE1      3'  CTGTAATCCCAGCTCTTTGT   13374     T_
                                ACAG  AGCTGGGATTACAG
                                ||||  ||||||||||||||
                                TGTT  TCGACCCTAATGTC
                                  TC
GAM888  ING1-like 3'  CTGTAATCCCAGCACT      54155     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  JAM1      3'  ATGCCTGTAATCCCAGCTGCT  33749           A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCGTCGACCCTAATGTC GTA
                                        C
GAM888  JAM1      3'  CTATAATCCCAGAGGCTG    33756     AG      C
                                CAGT  CTGGGATTA AG
                                ||||  ||||||||| ||
                                GTCG  GACCCTAAT TC
                                  GA       A
GAM888  JAM1      3'  ATGCCTGTAATCCCAGCTGCT  57887           A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCGTCGACCCTAATGTC GTA
                                        C
GAM888  JAM1      3'  CTATAATCCCAGAGGCTG    57894     AG      C
                                CAGT  CTGGGATTA AG
                                ||||  ||||||||| ||
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                                GTCG  GACCCTAAT TC
                                  GA        A
GAM888  JAM1     3'  ATGCCTGTAATCCCAGCTGCT  57915              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCGTCGACCCTAATGTC GTA
                                          C
GAM888  JAM1     3'  CTATAATCCCAGAGGCTG    57923     AG       C
                                CAGT  CTGGGATTA AG
                                ||||  ||||||||| ||
                                GTCG  GACCCTAAT TC
                                  GA        A
GAM888  JAM1     3'  ATGCCTGTAATCCCAGCTGCT  57942              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCGTCGACCCTAATGTC GTA
                                          C
GAM888  JAM1     3'  CTATAATCCCAGAGGCTG    57949     AG       C
                                CAGT  CTGGGATTA AG
                                ||||  ||||||||| ||
                                GTCG  GACCCTAAT TC
                                  GA        A
GAM888  KALI     3'  CTGTAATCCCAGTACT      53592     G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                  _
GAM888  KATII    3'  CTATAATCCCAGCACT      32646     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _         A
GAM888  KBRAS2   3'  ATGCCTGTAATCCCAGCTAC  34192              A
                                GTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                CATCGACCCTAATGTC GTA
                                          C
GAM888  KIAA0042 3'  CTGTAATCCCAGCACT      29610     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA0090 3'  ATGCCTGTAATCCCAGC      88438           A
                                GCTGGGATTACAG CAT
                                |||||||||||| |||
                                CGACCCTAATGTC GTA
                                        C
GAM888  KIAA0159 3'  CTGTAATCCCAGCACT      29507     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA0159 3' TGTAATCCCAGCTACTCA    29511    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  KIAA0184 3' CTGTAATCCCAGCACT      65194     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA0226 3' CTGTAATCCCAGCACT      63514     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA0226 3' CTGTAATCCCAGCTACTTG   63515    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                 T
GAM888  KIAA0252 3' CTGTAATCCCAGCACT      62791     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA0266 3' CTGTAATCCCAGCACT      41331     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA0266 3' CTGTAATCCCAGCACT      41332     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA0268 3' CTGTGTTTTAGCTAATGTA   70002      G         T
                                TACA TAGCTGGGAT ACAG
                                |||| |||||||||| ||||
                                ATGT ATCGATTTTG TGTC
                                   A       _
GAM888  KIAA0355 3' CTGTAATCCCAGCACT      28025     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA0391 3' ATGCCTGTGGTCCCAGCTACTC 27904   C              A
             A                   A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
```

```
                                A TCATCGACCCTGGTGTC GTA
                                 C             C
GAM888  KIAA0420 3' ATGCCTATAATCCCAACACT  63352    AGC      C  A
                                AGT   TGGGATTA AG CAT
                                |||   |||||||| || |||
                                TCA   ACCCTAAT TC GTA
                                  CA_       A  C
GAM888  KIAA0441 3' ATGCCTGTAATCCCAGCACT  28952    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  KIAA0445 5' CTGTAATCCCAGCACT     27953    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA0471 3' TCTGTAATCCCAGCACT    29400    A
                                AGT GCTGGGATTACAGA
                                ||| |||||||||||||
                                TCA CGACCCTAATGTCT
                                  _
GAM888  KIAA0472 3' ATGCCTGTAATCCAAGATACTC 71859  C   G  G       A
          A                      A AGTA CT GGATTACAG CAT
                                | |||| || ||||||||| |||
                                A TCAT GA CCTAATGTC GTA
                                 C   A  A        C
GAM888  KIAA0514 3' ATGCCTGTAATCCCAGCACT  28077    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  KIAA0547 3' TGTAATCCCAGCTACTCA    28918   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  KIAA0563 3' CTGTAATCCCAGCACT     29187    A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA0565 3' TCTGTAATTGCTATTG      66900       TGG
                                CAGTAGC   GATTACAGA
                                |||||||   |||||||||
                                GTTATCG   TTAATGTCT
                                    ____
GAM888  KIAA0618 3' ATGCCTGTAATCCCAGC     29161           A
                                GCTGGGATTACAG CAT
                                ||||||||||||| |||
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```
                                CGACCCTAATGTC GTA
                                        C
GAM888  KIAA0635 3' CTGTAATCCCAGCACT      27696     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM888  KIAA0694 3' ATGCCTATAATCCCAATACTTT 72579    C    GC       C  A
           A                     TA AGTA  TGGGATTA AG CAT
                                || ||||  |||||||| || |||
                                AT TCAT  ACCCTAAT TC GTA
                                 T    A_       A  C
GAM888  KIAA0694 3' CTGTAATCCCAGCACT      72580     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM888  KIAA0752 3' ATGCCTGCAATCCCAGCTACT  67048            A   A
                                AGTAGCTGGGATT CAG CAT
                                |||||||||||| ||| |||
                                TCATCGACCCTAA GTC GTA
                                        C   C
GAM888  KIAA0794 3' ATGCCTGTAATCCCAACACT   80409     AGC         A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_         C
GAM888  KIAA0794 3' CTGTAATCCCAGCTACTCA    80411    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM888  KIAA0795 3' CTATAATCCCAGCACT       46590     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _         A
GAM888  KIAA0825 3' CTGTAATCCCAGCACT       61025     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM888  KIAA0825 3' GTGCCTGCAATCCCAGCTACTC 61027    C          A   A
           A                     A AGTAGCTGGGATT CAG CAT
                                | |||||||||||| ||| |||
                                A TCATCGACCCTAA GTC GTG
                                 C           C   C
GAM888  KIAA0831 3' CTGTAATCCCAGCTACT      29972
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
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                                TCATCGACCCTAATGTC

GAM888  KIAA0831 3' CTGTAATCCCGGCACT     29973     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGGCCCTAATGTC
                                  _
GAM888  KIAA0852 5' CTGTAATCCCAGCACT     30077     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA0853 3' ATGTCTGTAGTCACAGCTACTC 30537   C       G
             A                   A AGTAGCTG GATTACAGACAT
                                | |||||||| ||||||||||||
                                A TCATCGAC CTGATGTCTGTA
                                 C       A
GAM888  KIAA0872 3' ATGCCTGTAATCCCAGCACT  30061     A           A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM888  KIAA0872 3' CTGTAATCCCAGCACT     30062     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA0889 3' ATGCCTGTAATCCCAGCACT  31129     A           A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM888  KIAA0907 3' CTGTAATCCCAGCACT     30173     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA0907 3' CTGTAATCCCAGCACT     30174     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA0912 3' CTGTAATCCCAGCACT     64409     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA0918 3' TCTGTAAGATGGGGCTACTGT  73136         GGGA_
                                ACAGTAGCT    TTACAGA
                                |||||||||    |||||||
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                                TGTCATCGG    AATGTCT
                                     GGTAG
GAM888  KIAA0930 3' CTGTAATCCCAGCACT     70542    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM888  KIAA1032 3' ATGCCTGTAGTCCCAGCTACTC 66151   C           A
          A                  A AGTAGCTGGGATTACAG CAT
                             | |||||||||||||||| |||
                             A TCATCGACCCTGATGTC GTA
                              C            C
GAM888  KIAA1056 3' CTGTAATCCCAGCACT     29695    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM888  KIAA1056 3' CTGTAATCCCAGCTGCT    29696
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCGTCGACCCTAATGTC

GAM888  KIAA1086 3' CTATAATCCCAGCACT     70744    A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                 _       A
GAM888  KIAA1086 3' CTGTAATCCCAGCACT     70745    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM888  KIAA1130 3' ATGCCTGTAATCCCAGCACT  62412    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                 _          C
GAM888  KIAA1130 3' ATGCCTGTAATCCCAGTGCT  62413    G         A
                                AGTA CTGGGATTACAG CAT
                                |||| |||||||||||| |||
                                TCGT GACCCTAATGTC GTA
                                   _        C
GAM888  KIAA1130 3' TGTAATCCCAGCTACTCA    62428   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  KIAA1164 3' ATGCCTGTAATCCCAGTACT  69503    G         A
                                AGTA CTGGGATTACAG CAT
                                |||| |||||||||||| |||
```

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                              TCAT GACCCTAATGTC GTA
                                _         C
GAM888  KIAA1191 3' CTGTAATCCCAGCACT     39954     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM888  KIAA1204 3' TCTGTAATCCCAACACT     69220     AGC
                              AGT   TGGGATTACAGA
                              |||   ||||||||||||
                              TCA   ACCCTAATGTCT
                                CA_
GAM888  KIAA1228 3' CTGTAATCCCAGCACT      65041     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM888  KIAA1244 3' CTGTAATCCCAGCACT      71989     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM888  KIAA1244 3' CTGTAATCCCAGCTACTTA   71990    C
                              A AGTAGCTGGGATTACAG
                              | ||||||||||||||||
                              A TCATCGACCCTAATGTC
                               T
GAM888  KIAA1253 3' ATGCCTGTGGTCCCAGCTACTG 91896                A
                              CAGTAGCTGGGATTACAG CAT
                              |||||||||||||||||| |||
                              GTCATCGACCCTGGTGTC GTA
                                          C
GAM888  KIAA1271 3' GTCTGTAATCCCAGCTATT   69551
                              AGTAGCTGGGATTACAGAC
                              ||||||||||||||||||
                              TTATCGACCCTAATGTCTG

GAM888  KIAA1271 3' CTGTAATCCCAGCACT      69542     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                _
GAM888  KIAA1276 3' CTGTAATCCCATCACT      66430     AGC
                              AGT   TGGGATTACAG
                              |||   ||||||||||
                              TCA   ACCCTAATGTC
                                CT_
GAM888  KIAA1277 3' ATGCCTATAATCCCAGCACT  64450     A        C  A
                              AGT GCTGGGATTA AG CAT
                              ||| |||||||||| || |||
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                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM888  KIAA1328 3' CTGTAATCCCAGGCTTTG    61646     T  _
                                CAG AGC TGGGATTACAG
                                ||| ||| ||||||||||
                                GTT TCG ACCCTAATGTC
                                  _  G
GAM888  KIAA1348 3' ATGCCTGTAATCCCAGCTACT  68571              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM888  KIAA1348 3' CTGTAATCCCAGCACTGTG    68575       A
                                TACAGT GCTGGGATTACAG
                                |||||| ||||||||||||
                                GTGTCA CGACCCTAATGTC
                                  _
GAM888  KIAA1364 3' ATGCCTGTAATCCCAGCACT   63586     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  KIAA1364 3' CTGTAATCCCAGCTACTTG    63593    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                 T
GAM888  KIAA1377 3' ATGCCTGTAATCCCAGCACT   67174     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  KIAA1404 3' CTGTAATCCCAGCACT       61987     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA1423 3' TAGTCCCAGCTACTCA       61728   C
                                A AGTAGCTGGGATTA
                                | ||||||||||||||
                                A TCATCGACCCTGAT
                                 C
GAM888  KIAA1456 3' ATGCCTGTAATCCCAGCACT   66988     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  KIAA1456 3' ATGCCTGTAATCCCAGCCACTT 66989    _ A          A
             G                   CA GT GCTGGGATTACAG CAT
                                || || |||||||||||| |||
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                                GT CA CGACCCTAATGTC GTA
                                 T C          C
GAM888  KIAA1473 3' ATGCCTGTAATCCCAGCTACT 70663            A
                                AGTAGCTGGGATTACAG CAT
                                ||||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM888  KIAA1473 3' CTGTAATCCCAGCACT     70667    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA1486 3' CTGTAATCCCAGCACTCTG   67379    TA_
                                CAG   GCTGGGATTACAG
                                |||   ||||||||||||
                                GTC   CGACCCTAATGTC
                                  TCA
GAM888  KIAA1554 3' CTGTAATCCCAGCTACCTG   95152    _
                                CAG TAGCTGGGATTACAG
                                ||| |||||||||||||
                                GTC ATCGACCCTAATGTC
                                  C
GAM888  KIAA1559 3' ATGCCTGTAATCCCAGCACT  73057    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  KIAA1559 3' ATGCCTGTAATCCCAGCTACTT 73058    _          A
           G                     CA GTAGCTGGGATTACAG CAT
                                || |||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 T           C
GAM888  KIAA1559 3' CTGTAATCCCAGCACT      73064    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA1586 5' CTGTAATCCCAGCACT      92329    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA1614 3' ATGCCTATAATCCCAGCTACTT 70117    _         C  A
           G                     CA GTAGCTGGGATTA AG CAT
                                || ||||||||||||| || |||
                                GT CATCGACCCTAAT TC GTA
                                 T          A  C
GAM888  KIAA1614 3' ATGCCTGTAATCCCAGAACT  70118    AG        A
                                AGT  CTGGGATTACAG CAT
                                |||  |||||||||||| |||
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                                TCA  GACCCTAATGTC GTA
                                  A_          C
GAM888  KIAA1630 3' ATGCCTGTAATCCCAGCACT   38030     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  KIAA1656 5' CTGTAATCCCAGCACT      65794     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA1674 3' CTGTAATCCCAGCACT      68777     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA1715 3' ATGCCTGTAATCCTAGCTACTC 68117    C             A
             A                   A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGATCCTAATGTC GTA
                                 C             C
GAM888  KIAA1735 3' CTGTAGTCCCAGCTACTCA    87627    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTGATGTC
                                 C
GAM888  KIAA1751 3' ATGCCTGTAATCCCAGAACT   71688     AG          A
                                AGT  CTGGGATTACAG CAT
                                |||  |||||||||||| |||
                                TCA  GACCCTAATGTC GTA
                                  A_          C
GAM888  KIAA1811 5' CTGTAATCCCAGCACT      64796     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  KIAA1829 3' TGTAATCCCAGCTACTCA     61958    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  KIAA1872 3' ATGCCTGTAATCCCAGCACTCT 62923     TA_          A
             G                   CAG   GCTGGGATTACAG CAT
                                |||   |||||||||||| |||
                                GTC   CGACCCTAATGTC GTA
                                  TCA          C
GAM888  KIAA1872 3' ATGCCTGTAATCCCAGCTACT  62924              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
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                                TCATCGACCCTAATGTC GTA
                                          C
GAM888  KIAA1872 3' CTATAATCCCAGCACT     62929    A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _       A
GAM888  KIAA1872 3' CTGTAATCCCAGACTTTG    62931    T _
                                CAG AG CTGGGATTACAG
                                ||| || ||||||||||||
                                GTT TC GACCCTAATGTC
                                  _ A
GAM888  KIAA1941 3' CTGTAATCCCAGCACT      74838    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  KIAA1948 5' ATGCCTATAATCCCAGCTACT 82399          C A
                                AGTAGCTGGGATTA AG CAT
                                |||||||||||||| || |||
                                TCATCGACCCTAAT TC GTA
                                        A  C
GAM888  KIAA1951 3' CTGTAATCCCAGCACT      73761    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  KIAA1954 3' CTGTAATCCCAGCACT      77719    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  KIAA1958 3' CTATAATCCCAGCACT      81902    A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _       A
GAM888  KIAA1979 3' CTGTAATCCCAGCACT      88278    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  KIAA1979 3' CTGTAATCCCAGCTACTCA   88279   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM888  KLHL6    3' CTGTAATCCCAGCCCTATG   55303   GTA_
                                CA   GCTGGGATTACAG
                                ||   ||||||||||||
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                                GT    CGACCCTAATGTC
                                 ATCC
GAM888  KLHL8    3'  CTGTAATTCCAGCTACTCA   62854   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||||
                                A TCATCGACCTTAATGTC
                                 C
GAM888  KR18     3'  CTGTAATCCCAGTACT      52745     G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC

                                  _
GAM888  KREMEN   3'  ATGCCTGTAATCCCAGCACT  49404     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  KREMEN   3'  CTGTAATCCCAGCTACT     49406
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  LHPP     5'  CTGTAATCCCAGCACT      42101     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LIAS     3'  CTGTAATCCCAGCACTTTA   70635    C   A
                                TA AGT GCTGGGATTACAG
                                || ||| ||||||||||||
                                AT TCA CGACCCTAATGTC
                                 T  _
GAM888  LIM      3'  CTGTAATCCCAGCTACTCA   21303    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM888  LIM      3'  CTGTAATCCCAGCACT      21302     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LRG      3'  CTGTAATCCCAGCACT      53750     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LRRFIP1  3'  TGCCTGTAATCTCAGTAC    16420     G          A
                                GTA CTGGGATTACAG CA
                                ||| |||||||||||| ||
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```
                                CAT GACTCTAATGTC GT
                                  _         C
GAM888  LRRFIP1  3'  TGTAATCCCAGCCACT     16421    A
                                AGT GCTGGGATTACA
                                ||| ||||||||||||
                                TCA CGACCCTAATGT
                                  C
GAM888  LSR68    3'  TGCCTATAATCCCAGCTACTCA 37937   C          C  A
                                A AGTAGCTGGGATTA AG CA
                                | |||||||||||||| || ||
                                A TCATCGACCCTAAT TC GT
                                 C           A  C
GAM888  LYSAL1   3'  CTGTAATCCCAGCACT     16918    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  MACF1    3'  CTGTAATCCCAGCACT     52316    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  MAWBP    3'  ATGCCTGTAATCCCAGCACT  42106    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _         C
GAM888  MCAM     3'  CTGTAATCCCAGCACT     21454    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  MESDC2   3'  CTGTAATCCCAGTACT     72492    G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                  _
GAM888  MESDC2   3'  TGTAATCCCAGCTACTCA   72503   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  METL     3'  ATGCCTGTAATCCCAGCCACT 37253    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  C           C
GAM888  MGC10765 3'  ATGCCTGTAATCCCAGCACT  44299    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  MGC10765  3'  CTGTAATCCCAGCTAC      44301
                                GTAGCTGGGATTACAG
                                ||||||||||||||||
                                CATCGACCCTAATGTC

GAM888  MGC10771  3'  ATGCCTGTAATCCCAGCACT   44451     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  MGC10814  3'  CTGTAATCCCAGCACT       51038     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  MGC10814  5'  ATGCCTGTAATCCCAGCACT   51036     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  MGC10999  3'  ATGCCTGTAATCCCAGCACTGT 50225       A          A
          G                      TACAGT GCTGGGATTACAG CAT
                                ||||||| |||||||||||||| |||
                                GTGTCA CGACCCTAATGTC GTA
                                    _          C
GAM888  MGC11287  5'  GTCTATAATCCCAGCACTGTG  48834       A        C
                                TACAGT GCTGGGATTA AGAC
                                ||||||| |||||||||| ||||
                                GTGTCA CGACCCTAAT TCTG
                                    _        A
GAM888  MGC11386  3'  CTATAATCCCAGCACT       51950     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM888  MGC13017  3'  TCTGTAATCCCAGCTACT     54694
                                AGTAGCTGGGATTACAGA
                                ||||||||||||||||||
                                TCATCGACCCTAATGTCT

GAM888  MGC13053  3'  CTGTAATCCCAGTACT       51131     G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                  _
GAM888  MGC13523  3'  TGCCTGTAATTTCACTA      53031     C  GG      A
                                TAG TG  ATTACAG CA
                                ||| ||  ||||||| ||
```

```
                                ATC AC  TAATGTC GT
                                  _ TT      C
GAM888  MGC14126 3' CTGTAATCCCAGCACT     51854     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  MGC14817 3' CTGTAATCCCAGCACT     50336     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  MGC15397 3' CTGTAATCCCAGCACT     54679     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  MGC15631 3' ATGCCTGTAATCCCAGTGCT  51259     G         A
                                AGTA CTGGGATTACAG CAT
                                |||| |||||||||||| |||
                                TCGT GACCCTAATGTC GTA
                                  _         C
GAM888  MGC15631 3' CTGTCATCCCAGCTAC      51263         T
                                GTAGCTGGGAT ACAG
                                |||||||||| ||||
                                CATCGACCCTA TGTC
                                       C
GAM888  MGC16142 3' ATGCCTATAATCCCAGCACT  51291    A       C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _       A  C
GAM888  MGC16142 3' ATGCCTATAATCCCAGCTACT 51292          C  A
                                AGTAGCTGGGATTA AG CAT
                                |||||||||||||| || |||
                                TCATCGACCCTAAT TC GTA
                                       A  C
GAM888  MGC16332 3' ATGCCTGTAATCCCAACACT  56774    AGC       A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_         C
GAM888  MGC16385 3' CTGTAATCCCAGCACT      58887     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  MGC16703 3' ATGCCTGTAATCCCAGCACT  73098     A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  MGC20235 3' CTGTAATCCCAGTACT     58894     G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                  _
GAM888  MGC20235 3' CTGTAGTCCCAGCTACTCA   58895   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTGATGTC
                                 C
GAM888  MGC22805 3' ATGCCTGTAATCCCAGCTACTT 58080   _           A
           G                     CA GTAGCTGGGATTACAG CAT
                                || |||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 T            C
GAM888  MGC2396  3' ATGCCTGTAATCCCAGCTACT  53460            A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM888  MGC2562  3' CTATAATCCCAGCACT     50437    A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM888  MGC2562  3' CTGTAATCCCAGCACT     50438    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  MGC26641 3' CTGTAATCCCAACTACTCA   58657   C   C
                                A AGTAG TGGGATTACAG
                                | ||||| ||||||||||
                                A TCATC ACCCTAATGTC
                                 C    A
GAM888  MGC2731  3' ATGCCTGTAATCCCAGCTACT  43948            A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM888  MGC29762 3' CTGTAATCCCAGCACT     58472    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  MGC29891 3' CTGTAATCCCAACACT     58204    AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
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                                TCA   ACCCTAATGTC
                                  CA_
GAM888  MGC29891  3'  CTGTAATCCCAGCACT      58205     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  MGC29937  3'  ATGCCTGTAATCCCAGCACT   58110     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM888  MGC29937  3'  ATGCCTGTAATCCCAGTTACTC 58111    C             A
              A                  A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATTGACCCTAATGTC GTA
                                 C              C
GAM888  MGC3207   3'  CTGTAATCCCAGCACT      62558     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  MGC39350  3'  CTGTAATCCCCAGCACT     58654     A     _
                                AGT GCTGGG ATTACAG
                                ||| |||||| |||||||
                                TCA CGACCC TAATGTC
                                  _     C
GAM888  MGC4248   3'  CTGTAATCCCAGCACT      50327     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  MGC4663   3'  CTATAATCCCAGCACTTTA    44505     C   A        C
                                TA AGT GCTGGGATTA AG
                                || ||| |||||||||| ||
                                AT TCA CGACCCTAAT TC
                                 T   _         A
GAM888  MGC5254   3'  CTGTAATCCCAGCACT      50410     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  MGC5384   3'  ATGCCTGTAATCCCAGCACT   48269     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM888  MKRN4     3'  CTGTAATCCCAGCACT      47746     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  MOST2    5'  CTGTAATCCCAGCACT      39684     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  MOST2    5'  ATGCCTGTAGTCCCAGCTACTC 39674    C             A
              A                  A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGACCCTGATGTC GTA
                                 C             C
GAM888  MRP63    3'  CTGTAATCCCAACACTTTA    43807    C   AGC
                                TA AGT   TGGGATTACAG
                                || |||   ||||||||||
                                AT TCA   ACCCTAATGTC
                                 T   CA_
GAM888  MRPL56   3'  CTGTAATCCCAACACT      51688     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  MRPS10   3'  CTGTAATCCCAGCACT      36292     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  MRPS10   3'  GTGCCTGTAATCCCAGCTACTC 36298    C             A
              A                  A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGACCCTAATGTC GTG
                                 C             C
GAM888  MT-ACT48 3'  ATGCCTGTAATCCCAGCACT   24686     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM888  N4BP2    3'  CTGTAATCCCAGCACT      36403     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  NDUFC2   3'  ATGCCTGTAATCCCAGCACT   15825     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM888  NDUFC2   3'  CTGCAATCCCAGCTACTCA    15832    C          A
                                A AGTAGCTGGGATT CAG
                                | |||||||||||| |||
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                                A TCATCGACCCTAA GTC
                                 C           C
GAM888  NMNAT    3'  CTGTAATCCCAGCACT      42956     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  NMT2     3'  CTGTAATCCCAGCACT      16664     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  NPTXR    3'  CTGTAATCCCAGCACT      26642     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  NPTXR    3'  CTGTAATCCCAGCACT      54178     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  OCLM     5'  ATGCCTATAATCCCAGCACT  42347     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _         A  C
GAM888  ORC6L    3'  ATGCCTGTAATCCCAGCTCCT  26722     T           A
                                AG AGCTGGGATTACAG CAT
                                || |||||||||||||| |||
                                TC TCGACCCTAATGTC GTA
                                 C           C
GAM888  ORC6L    3'  CTGTAATCCCAGCACT      26724     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  PAFAH2   3'  ATGCCTGTAATCCCAGCACT  4760      A           A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM888  PAFAH2   3'  CTATAATCCCAGCTACTCA   4762     C           C
                                A AGTAGCTGGGATTA AG
                                | |||||||||||||| ||
                                A TCATCGACCCTAAT TC
                                 C           A
GAM888  PB1      3'  CTGTAATCCCAGCACT      37021     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  PDCD7    3'  CTGTAATCCCAACACT      72138     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  phorbolin-1 3'  CTGTAATCCCAGCACT      88778     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  PILR(ALPHA) 3'  CTGTAATCCCAGCTACT     25546
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  PIWIL2   3'  CTGTAGTCCCAGCTACTCA   36055   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTGATGTC
                                 C
GAM888  PNPASE   3'  ATGCCTGTAATCCTAGCTACTC 70870   C            A
          A                      A AGTAGCTGGGATTACAG CAT
                                 | |||||||||||||||| |||
                                 A TCATCGATCCTAATGTC GTA
                                 C             C
GAM888  POFUT1   3'  ATGCCTGTAATCCCAGCACT   70465    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  POLYDOM  3'  ATGCCTGTAATTCCAGCTACTC 44424   C            A
          A                      A AGTAGCTGGGATTACAG CAT
                                 | |||||||||||||||| |||
                                 A TCATCGACCTTAATGTC GTA
                                 C             C
GAM888  POLYDOM  3'  CTGTAATCCCAGCACT     44425    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  PPP1R3B  3'  ATGCCTGTAATCCCAGCACT   44815    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  PPP1R3B  3'  TGCCTGTAATCCCTGCACT   44826    A  T       A
                                AGT GC GGGATTACAG CA
                                ||| || |||||||||| ||
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                                TCA CG CCCTAATGTC GT
                                  _ T         C
GAM888  PRDM14   3' ATGCCTGTGGTTCCAGCCACTC 44444   C   A          A
             A                   A AGT GCTGGGATTACAG CAT
                                 | ||| |||||||||||||| |||
                                 A TCA CGACCTTGGTGTC GTA
                                  C   C           C
GAM888  PRDM14   3' CTGTAATCCCAGCACT      44447     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                   _
GAM888  PRO0038  3' ATGCCTATAATCCCAACACCCT 26090     TAGC_       C  A
             G                    CAG     TGGGATTA AG CAT
                                 |||     |||||||| || |||
                                 GTC     ACCCTAAT TC GTA
                                   CCACA       A  C
GAM888  PRO0255  3' CTGTAATCTCAGCACT      26141     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACTCTAATGTC
                                   _
GAM888  PRO0478  3' ATGCCTGTAATCCCAGCACT   26183     A          A
                                 AGT GCTGGGATTACAG CAT
                                 ||| |||||||||||| |||
                                 TCA CGACCCTAATGTC GTA
                                   _           C
GAM888  PRO0478  5' CTGTAATCCCAGCACT      26187     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                   _
GAM888  PRO0478  3' CTGTAATCCCAGCCTG      26188     TA
                                 CAG  GCTGGGATTACAG
                                 |||  ||||||||||||
                                 GTC  CGACCCTAATGTC
                                   __
GAM888  PRO0478  5' CTGTAATCCCAGGTACT     26189      G
                                 AGTA CTGGGATTACAG
                                 |||| ||||||||||||
                                 TCAT GACCCTAATGTC
                                    G
GAM888  PRO0478  3' TGTAATCCCAGCTACTCA    26198    C
                                 A AGTAGCTGGGATTACA
                                 | ||||||||||||||||
                                 A TCATCGACCCTAATGT
                                  C
GAM888  PRO0611  3' ATGCCTGTAATCCCAGCACT   26007     A          A
                                 AGT GCTGGGATTACAG CAT
                                 ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  PRO0618  3' CTGTAATCCCAGCACTTTA   26200    C   A
                                TA AGT GCTGGGATTACAG
                                || ||| ||||||||||||||
                                AT TCA CGACCCTAATGTC
                                 T  _
GAM888  PRO1048  5' TCTGTAATCCCAGCACT     37525     A
                                AGT GCTGGGATTACAGA
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCT
                                  _
GAM888  PRO1496  3' ATGCCTGTAATCCCAGCACT  37757     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  PRO1580  5' ATGCCTTGTCCCAGCTTCT   37530    T       TAC  A
                                AG AGCTGGGAT   AG CAT
                                || |||||||||   || |||
                                TC TCGACCCTG   TC GTA
                                 T        T__  C
GAM888  PRO1777  3' ATGCCTGTAATCCCAGCATTCT 37762     TA_          A
          G                      CAG   GCTGGGATTACAG CAT
                                |||   |||||||||||||| |||
                                GTC   CGACCCTAATGTC GTA
                                  TTA           C
GAM888  PRO1853  3' ATGCCTGTAATCCCAGCACT   37771     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  PRO2015  3' CTGTAATCCCAGCACT      37557     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  PRO2198  5' CTGTAATCCCGGCACT      37791     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGGCCCTAATGTC
                                  _
GAM888  PRO2730  3' CTGTAATCCCAGCACT      47415     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  PRO2859  3' ATGCCTGTAATCCCAGCACT  37614     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||||| |||
```

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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  PRO2949  3' ATGCCTGTAATCCCAGCACT  37619    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  PSR      3' CTGTAATCCCAGCACT     65180    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  PTD012   3' ATGCCTATAATCCCAGCACT  25890    A       C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM888  PTK6     3' ATGCCTGTAATCCCAGCACT  19934    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  PTRF     3' ATGCCTGTAATCCCAGCTACT 63497              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM888  RAB4B    5' ATGCCTGTAATCCCAGCACT  32372    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  RAB4B    5' ATGCCTGTAATCCCAGCTACT 32373              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM888  RHOBTB3  3' CTGTAATCCCAGCTACT    29744
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  RNO2     5' CTGTAATCCCAGCACT     52769    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  RoXaN    3' ATGCCTGTAATCCCAGC    46632             A
                                GCTGGGATTACAG CAT
                                |||||||||||| |||
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                                CGACCCTAATGTC GTA
                                        C
GAM888  RoXaN    3'  CTATAATCCCAGCACTCTG   46641     TA_       C
                                CAG   GCTGGGATTA AG
                                |||   |||||||||| ||
                                GTC   CGACCCTAAT TC
                                  TCA         A
GAM888  RoXaN    3'  TCTGTAATCCCAGCTACTCA   46659    C
                                A AGTAGCTGGGATTACAGA
                                | ||||||||||||||||||
                                A TCATCGACCCTAATGTCT
                                 C
GAM888  Rpo1-2   3'  ATGCCTGTAGTTCCAGCTACTC 38697    C             A
              A                  A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACCTTGATGTC GTA
                                 C              C
GAM888  RRP4     3'  CTATAATCCCAGCACT      26563     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _         A
GAM888  SAMHD1   3'  ATGCCTGTAATCCCAGCACT   61308     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM888  SC65     3'  CTGTAATCCCAGCACTG     21288      A
                                CAGT GCTGGGATTACAG
                                |||| ||||||||||||
                                GTCA CGACCCTAATGTC
                                   _
GAM888  SCIN     3'  CTGTAATCCCAGCACT      52424     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  SCYA5    3'  CTGTAATCCCAGCTACT     11450
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  SEMA3E   3'  CTGTAATCCCAGCACT      24881     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  SEMA5A   3'  ATGCCTATAATCCCAGCACT  14252     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
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                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM888  SGKL    3'  ATGCCTATAATCCCAGCTACTT 25140    _          C  A
                G                  CA GTAGCTGGGATTA AG CAT
                                   || |||||||||||| || |||
                                   GT CATCGACCCTAAT TC GTA
                                    T          A  C
GAM888  SGKL    3'  ATGCCTTTAGTCCCAGCTACTC 25141   C          C  A
                A                  A AGTAGCTGGGATTA AG CAT
                                   | |||||||||||||| || |||
                                   A TCATCGACCCTGAT TC GTA
                                   C          T  C
GAM888  SGKL    3'  CTGTAATCCCAGCACT     25142    A
                                   AGT GCTGGGATTACAG
                                   ||| ||||||||||||
                                   TCA CGACCCTAATGTC
                                     _
GAM888  SLC7A11 3'  TCTGTAATCATATCTAC    26757     C  G
                                   GTAG TG GATTACAGA
                                   |||| || |||||||||
                                   CATC AT CTAATGTCT
                                     T  A
GAM888  SLC7A11 3'  TCTGTAATCCCAGCACT    26758     A
                                   AGT GCTGGGATTACAGA
                                   ||| ||||||||||||||
                                   TCA CGACCCTAATGTCT
                                     _
GAM888  SMAP-5  3'  CTGTAATCCCAGCACT     47931     A
                                   AGT GCTGGGATTACAG
                                   ||| ||||||||||||
                                   TCA CGACCCTAATGTC
                                     _
GAM888  SNAPC1  3'  ATGCCTGTAATCCCAGC    11838          A
                                   GCTGGGATTACAG CAT
                                   |||||||||||| |||
                                   CGACCCTAATGTC GTA
                                            C
GAM888  SPTLC2  3'  ATGCCTGTAATCCCAGCTAC  16797            A
                                   GTAGCTGGGATTACAG CAT
                                   |||||||||||||||| |||
                                   CATCGACCCTAATGTC GTA
                                             C
GAM888  SS18L1  3'  CTGTAATCCCAGCACT     65344     A
                                   AGT GCTGGGATTACAG
                                   ||| ||||||||||||
                                   TCA CGACCCTAATGTC
                                     _
GAM888  SS18L1  3'  CTGTAATCCCAGCTACT    65345
                                   AGTAGCTGGGATTACAG
                                   ||||||||||||||||
```

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                                TCATCGACCCTAATGTC

GAM888  TA-LRRP  3' ATGCCTATAATCCCAGCACT  31068     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM888  TACTILE  3' CTGTAATCCCAGCACT      19469     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  THEA     3' CTGTAATCCCAGCACT      66282     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  TIP47    3' CTGTAATCCCAGCACT      19479     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  TMG4     3' ATGCCTGTAATCCCAGCACT  43988     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  TRIAD3   3' ATGCCTATAATCCCAGGTACTC 94500   C   G       C  A
           A                     A AGTA CTGGGATTA AG CAT
                                | |||| ||||||||| || |||
                                A TCAT GACCCTAAT TC GTA
                                 C   G       A  C
GAM888  TRIM38   3' CTGTAATCCCAGAACTATGT  20986     GTAG_
                                ACA    CTGGGATTACAG
                                |||    ||||||||||||
                                TGT    GACCCTAATGTC
                                  ATCAA
GAM888  UBF-fl   3' CTGTAATCCCAGCACT      51564     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  VPS4B    3' ATGCCTGTAATCCCAGCACT  16821     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  VPS4B    3' TGTAATCCCAGCTACTCA    16826   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
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                              A TCATCGACCCTAATGT
                               C
GAM888  WBSCR21  3'  CTGTAATCCCAGCTACT     48476
                              AGTAGCTGGGATTACAG
                              ||||||||||||||||
                              TCATCGACCCTAATGTC

GAM888  WBSCR23  3'  CTGTAATCCCAGCACT      46759     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                 _
GAM888  WBSCR23  3'  CTGTAATCCCAGCTACT     46760
                              AGTAGCTGGGATTACAG
                              ||||||||||||||||
                              TCATCGACCCTAATGTC

GAM888  WBSCR23  3'  GTCTGTAGTCCCAGCTACTCA  46770    C
                              A AGTAGCTGGGATTACAGAC
                              | ||||||||||||||||||
                              A TCATCGACCCTGATGTCTG
                               C
GAM888  YEA      3'  ATGCCTGTAATCCCAGCTACTT 51528    _            A
          G                    CA GTAGCTGGGATTACAG CAT
                              || |||||||||||||| |||
                              GT CATCGACCCTAATGTC GTA
                               T            C
GAM888  YME1L1   3'  CTGTAATCCCAGCACT      26528     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                 _
GAM888  YME1L1   3'  TCTGTAATCCCAGCACT     26531     A
                              AGT GCTGGGATTACAGA
                              ||| |||||||||||||
                              TCA CGACCCTAATGTCT
                                 _
GAM888  YME1L1   3'  CTGTAATCCCAGCACT      57778     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
                              TCA CGACCCTAATGTC
                                 _
GAM888  YME1L1   3'  TCTGTAATCCCAGCACT     57781     A
                              AGT GCTGGGATTACAGA
                              ||| |||||||||||||
                              TCA CGACCCTAATGTCT
                                 _
GAM888  ZAK      3'  CTGTAATCCCAGCACT      56125     A
                              AGT GCTGGGATTACAG
                              ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  ZFP106   3'  CTGTAATCCCAGCTCT     42467    T
                                AG AGCTGGGATTACAG
                                || |||||||||||||
                                TC TCGACCCTAATGTC
                                  _
GAM888  ZFP106   3'  CTGTAATCCCAGCACT     42466    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  ZIM3     3'  ATGCCTGTAATCCCAGTACT  53536    G         A
                                AGTA CTGGGATTACAG CAT
                                |||| |||||||||||| |||
                                TCAT GACCCTAATGTC GTA
                                  _          C
GAM888  ZNF197   3'  ATGCCTGTAATCCCAGCACT  22763    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  ZNF197   3'  GTAATCCCAGCTACTCA    22766    C
                                A AGTAGCTGGGATTAC
                                | ||||||||||||||
                                A TCATCGACCCTAATG
                                 C
GAM888  ZNF271   3'  CTGTAATCCCAACACT     95250    AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  ZNF297B  5'  ATGCCTATAATCCCAACACTTT 25774   C   AGC      C  A
           A                     TA AGT   TGGGATTA AG CAT
                                || |||   |||||||| || |||
                                AT TCA   ACCCTAAT TC GTA
                                 T   CA_       A  C
GAM888  ZNF297B  5'  CTGTAATCCCAGCACT     25781    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  ZNF297B  3'  CTGTAATCCCAGCACT     25782    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  ZNF297B  3'  CTGTAATCCCAGCTACT    25783
                                AGTAGCTGGGATTACAG
                                |||||||||||||||||
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                                TCATCGACCCTAATGTC

GAM888  ZNF33A    3'  ATGCCTGTAATCCCAGCACT   91344     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM888  ZNF347    3'  ATGCCTGTAATCCCAACACT   50845     AGC        A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_         C
GAM888  LOC112687 3'  CTATAATCCCAGCACT      72859     A        C
                                AGT GCTGGGATTA AG
                                ||| ||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM888  LOC113201 3'  ATGCCTATAGTCCCAGCTACT  56549           C  A
                                AGTAGCTGGGATTA AG CAT
                                |||||||||||||| || |||
                                TCATCGACCCTGAT TC GTA
                                         A  C
GAM888  LOC115129 5'  CTATAATCCCAGCACT      73229     A        C
                                AGT GCTGGGATTA AG
                                ||| ||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM888  LOC115129 5'  CTGTAATCCCAGCTACT     73231
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  LOC115129 5'  CTGTAATCCCAGGTACT     73232      G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                  G
GAM888  LOC115273 3'  ATGCCTGTAATCCCAGTTACT  73357              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATTGACCCTAATGTC GTA
                                         C
GAM888  LOC115761 3'  ATGCCTGTAATCCCAGCACTGT 91737        A          A
          G                      TACAGT GCTGGGATTACAG CAT
                                ||||||| |||||||||||| |||
                                GTGTCA CGACCCTAATGTC GTA
                                  _           C
GAM888  LOC116228 3'  CTGTAATCCCAGCACT      73798     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC116349 3'  CTGTAATCCCAGCACT      73830     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC119504 5'  ATGCCTGTAATCCCAGCTACT  73989               A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                      C
GAM888  LOC119504 5'  CTGTAATCCCAGCACT      73990     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC122704 3'  CTGTAATCCCAGCACT      74139     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC122704 3'  TGTAATCCCAGCTACTCA    74145    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  LOC122970 3'  CTGTAATCCCAGTACT      74178     G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                  _
GAM888  LOC126282 3'  CTGTAATCCCAGCACT      74472     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC126282 3'  CTGTAATCCCAGCACT      74473     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC127262 3'  ATGCCTGTAATCCCAGC     76107           A
                                GCTGGGATTACAG CAT
                                |||||||||||| |||
                                CGACCCTAATGTC GTA
                                      C
GAM888  LOC127428 3'  ATGCCTATAATCCCAGCGCT  74662     A       C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
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                                TCG CGACCCTAAT TC GTA
                                  _        A  C
GAM888  LOC130162 3'  ATGTCTGTAATCCCAGCACT   74909     A
                                AGT GCTGGGATTACAGACAT
                                ||| ||||||||||||||||
                                TCA CGACCCTAATGTCTGTA
                                  _
GAM888  LOC130535 3'  ATGCCTGTAATCCCAGC      76147            A
                                GCTGGGATTACAG CAT
                                ||||||||||||| |||
                                CGACCCTAATGTC GTA
                                          C
GAM888  LOC130535 3'  CTGTAGTCCCAGCTACTCA    76151    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTGATGTC
                                 C
GAM888  LOC130589 3'  CTGTAATCCCAGCACT       57132     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC130951 3'  CTGTAATCCCAACACTTTG    57143     TAGC_
                                CAG     TGGGATTACAG
                                |||     ||||||||||
                                GTT     ACCCTAATGTC
                                  TCACA
GAM888  LOC131744 3'  ATGCCTGTAATCCCAGCACTGT 75868        A          A
          A                      TACAGT GCTGGGATTACAG CAT
                                ||||||| |||||||||||| |||
                                ATGTCA CGACCCTAATGTC GTA
                                    _           C
GAM888  LOC131965 3'  ATGCCTGTAATCCCAGCACT   75027     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| ||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM888  LOC131965 3'  TGTAATCCCAGCTACTCA     75034    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  LOC132625 3'  ATGCCTGTAATCCCAACACTTT 75898      TAGC_        A
          GT                      ACAG     TGGGATTACAG CAT
                                ||||     |||||||||||| |||
                                TGTT     ACCCTAATGTC GTA
                                  TCACA          C
GAM888  LOC132625 3'  CTGTGTTCCCAGCTACTCA    75906    C         T
                                A AGTAGCTGGGA TACAG
                                | |||||||||| |||||
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                                A TCATCGACCCT GTGTC
                                 C          T
GAM888  LOC133926 3'  ATGCCTGTAATCCCAGCGCT   75131     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCG CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC134147 3'  CTGTAATCCCAGCACT      57161     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC134147 3'  GTGCCTGTAATCCCAGCTACTC 57166    C              A
              A                  A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGACCCTAATGTC GTG
                                 C              C
GAM888  LOC137362 3'  ATGCCTGTAATCCCAACACTTT 75263     TAGC_         A
              G                  CAG     TGGGATTACAG CAT
                                |||     |||||||||| |||
                                GTT     ACCCTAATGTC GTA
                                  TCACA          C
GAM888  LOC138241 3'  CTGTAATCCCAACACT      75308     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  LOC138428 3'  ATGCCTGTAATCCCTGCTACT  75331       T         A
                                AGTAGC GGGATTACAG CAT
                                |||||| |||||||||| |||
                                TCATCG CCCTAATGTC GTA
                                    T         C
GAM888  LOC138428 3'  CTATAATCCCAGCACT      75335     A         C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _         A
GAM888  LOC143310 3'  CTGTAATCCCAGCACT      76532     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC143888 3'  CTGTAATCCCAGCACT      76659     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC143943 3'  ATGCCTGTAATCCCAGCACT   82994     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC144289 3'  CTGTAATCCCAGCTACT     83024
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  LOC144289 3'  TCTGTAATCCCAGCACT     83029     A
                                AGT GCTGGGATTACAGA
                                ||| |||||||||||||
                                TCA CGACCCTAATGTCT
                                  _
GAM888  LOC144465 3'  ATGCCTGTAATCCCAAAACT   76852     AGC          A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  AA_         C
GAM888  LOC144465 3'  ATGCCTGTAATCCCAGCTACT  76853               A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM888  LOC144465 3'  TGTAATCCCAGCTACTCA     76857    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  LOC144481 3'  ATGCCTGTAATCCCAATACT   83093      GC          A
                                AGTA  TGGGATTACAG CAT
                                ||||  |||||||||| |||
                                TCAT  ACCCTAATGTC GTA
                                   A_         C
GAM888  LOC144481 3'  ATGCCTGTAATCCCAGCTACT  83094               A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM888  LOC144486 3'  CTGTAATCCCAGCACGCTG    83083      A_
                                CAGT  GCTGGGATTACAG
                                ||||  ||||||||||||
                                GTCG  CGACCCTAATGTC
                                   CA
GAM888  LOC144524 3'  ATGCCTGTAGTCCCAGCTACTT 83121    C             A
          A                      A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGACCCTGATGTC GTA
                                 T             C
GAM888  LOC144817 3'  CTGTAATCCCAGCACT       76967     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC145216 3'  CTGTAATCCCAGCACT      83265     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC145216 3'  CTGTAATCCCAGCTACTCA    83266    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM888  LOC145231 3'  ATGCCTATAATCCCAGCACT   83278     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM888  LOC145231 3'  ATGCCTGTAATCCCAGCACT   83279     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC145231 3'  ATGCCTGTAATCCCAGCTACTT 83280     _            A
          G                      CA GTAGCTGGGATTACAG CAT
                                || ||||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 T             C
GAM888  LOC145299 3'  CTGTAATCCCAGCACT      83314     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC145333 3'  CTGTAATCCCAGCACT      83326     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC145387 3'  CTGTAATCCCAGCACT      83354     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC145438 3'  ATGCCTGTAGCCCCAGCTACTC 83334    C        AT    A
          A                      A AGTAGCTGGG  TACAG CAT
                                | ||||||||||  ||||| |||
                                A TCATCGACCC  ATGTC GTA
                                 C         CG    C
GAM888  LOC145438 3'  CTGTAATCCCAGCACT      83336     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC145453 3'  CTGTAATCTGAGCAC       77140    A   G
                                GT GCT GGATTACAG
                                || ||| |||||||||
                                CA CGA TCTAATGTC
                                  _   G
GAM888  LOC145482 3'  CTGTAATCCCAGCTACT     77229
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  LOC145483 3'  CTGTAATCCCAACACT      77242     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  LOC145663 3'  CTGTAATCCCAGCAATTG    83413     A
                                CAGT GCTGGGATTACAG
                                |||| ||||||||||||
                                GTTA CGACCCTAATGTC
                                   A
GAM888  LOC145757 3'  ATGCCTGTAATCCCAGCACT   77454     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC145757 3'  GTAGTCCCAGCTACTCA     77470    C
                                A AGTAGCTGGGATTAC
                                | ||||||||||||||
                                A TCATCGACCCTGATG
                                 C
GAM888  LOC145820 3'  CTGTAATCCCAGCACT       77513     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC145824 3'  ATGCCTGTAATCCCAGCACT   77523     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC145955 3'  ATGCCTGTAATCCCAACACT   83588     AGC        A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_         C
GAM888  LOC146059 3'  ATGCCTGTAATCCCAGCACT   77619     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC146059 3'  TGTAATCCCAGCTACTCA    77623   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  LOC146229 3'  CTGTAATCCCAGCACTCTG   77751     TA_
                                CAG   GCTGGGATTACAG
                                |||   ||||||||||||||
                                GTC   CGACCCTAATGTC
                                  TCA
GAM888  LOC146272 5'  CTGTAATCCCAGCACT      77787     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LOC146332 3'  CTGTAATCCCAACACT      77824     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  LOC146540 3'  CTGTAATCCCAGCACT      77974     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LOC146540 3'  ATGCCTGTAGTCCCAGCTACTC 77970   C             A
          A                      A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACCCTGATGTC GTA
                                 C              C
GAM888  LOC146667 3'  ATGCCTGTAATCCCAGCACT   83702     A           A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC146669 3'  CTGTAATCCAGCACTGTG     78058       A    G
                                TACAGT GCTGG ATTACAG
                                |||||| ||||| |||||||
                                GTGTCA CGACC TAATGTC

                                    _    _
GAM888  LOC146713 3'  CTGTAATCCCAGCACT       83725     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LOC146723 3'  CTGTAATCCCAGCTACT      78083
                                AGTAGCTGGGATTACAG
                                |||||||||||||||||
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                                TCATCGACCCTAATGTC

GAM888  LOC146728 3'  ATGCCTGTGGTCCCAGCTACTC 83746   C            A
                A                A AGTAGCTGGGATTACAG CAT
                                 | ||||||||||||||||| |||
                                 A TCATCGACCCTGGTGTC GTA
                                  C             C
GAM888  LOC146756 3'  CTGTAATCCCAGCACT     83776    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                   _
GAM888  LOC146756 3'  CTGTAATCCCAGCACT     83777    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                   _
GAM888  LOC146780 3'  ATGCCTGTAATCCCTGCACTTA 83786   C  A  T       A
                                 A AGT GC GGGATTACAG CAT
                                 | ||| || |||||||||| |||
                                 A TCA CG CCCTAATGTC GTA
                                  T  _  T        C
GAM888  LOC146901 3'  ATGCCTATAATCCCAGCTACT  83829           C  A
                                 AGTAGCTGGGATTA AG CAT
                                 |||||||||||||| || |||
                                 TCATCGACCCTAAT TC GTA
                                           A  C
GAM888  LOC146901 3'  CTGTAATCCCCGCACT     83839    A  T
                                 AGT GC GGGATTACAG
                                 ||| || ||||||||||
                                 TCA CG CCCTAATGTC
                                   _  C
GAM888  LOC146923 3'  CTGTAATCCCAGCACT     78192    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC
                                   _
GAM888  LOC146975 5'  CTATAATCCCAGCACT     78223    A       C
                                 AGT GCTGGGATTA AG
                                 ||| |||||||||| ||
                                 TCA CGACCCTAAT TC
                                   _        A
GAM888  LOC147057 3'  ATGCCTGTAATCCCAGCACT  83909    A         A
                                 AGT GCTGGGATTACAG CAT
                                 ||| |||||||||||| |||
                                 TCA CGACCCTAATGTC GTA
                                   _          C
GAM888  LOC147071 3'  CTGTAATCCCAGCACT     72998    A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC147599 3'  ATGCCTGTAATCCCAGCACCCT 84040     TA_          A
                G                  CAG   GCTGGGATTACAG CAT
                                   |||   |||||||||||||| |||
                                   GTC   CGACCCTAATGTC GTA
                                     CCA           C
GAM888  LOC147660 3'  CTGTAATCCCAGCAC       78392     A
                                   GT GCTGGGATTACAG
                                   || ||||||||||||||
                                   CA CGACCCTAATGTC
                                  _
GAM888  LOC147664 3'  ATGCCTGTAATCCCAGCTACTT 78403     _            A
                G                  CA GTAGCTGGGATTACAG CAT
                                   || |||||||||||||||| |||
                                   GT CATCGACCCTAATGTC GTA
                                    T             C
GAM888  LOC147664 3'  CTGTAATCCCAACACT      78408     AGC
                                   AGT   TGGGATTACAG
                                   |||   ||||||||||||
                                   TCA   ACCCTAATGTC
                                     CA_
GAM888  LOC147669 3'  CTGTAATCCCAGCACT      84061     A
                                   AGT GCTGGGATTACAG
                                   ||| ||||||||||||||
                                   TCA CGACCCTAATGTC
                                  _
GAM888  LOC147700 3'  ATGCCTGTAATCCCAGCTACT  59193              A
                                   AGTAGCTGGGATTACAG CAT
                                   |||||||||||||||| |||
                                   TCATCGACCCTAATGTC GTA
                                              C
GAM888  LOC147700 3'  CTGTAATCCCAACACT      59197     AGC
                                   AGT   TGGGATTACAG
                                   |||   ||||||||||||
                                   TCA   ACCCTAATGTC
                                     CA_
GAM888  LOC147727 5'  CTATAATCCCAGCTACTCA    78467    C          C
                                   A AGTAGCTGGGATTA AG
                                   | ||||||||||||||| ||
                                   A TCATCGACCCTAAT TC
                                    C             A
GAM888  LOC147837 3'  ATGCCTGTAATCCCAGCTACT  78512              A
                                   AGTAGCTGGGATTACAG CAT
                                   |||||||||||||||| |||
                                   TCATCGACCCTAATGTC GTA
                                              C
GAM888  LOC147837 3'  CTGTAATCCCAGCACT      78515     A
                                   AGT GCTGGGATTACAG
                                   ||| ||||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC147990 3'  CTGTAATCCCAGCACT      84092     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC147990 3'  CTGTAATCTCAGCTACTCA    84093    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACTCTAATGTC
                                 C
GAM888  LOC148147 3'  CTGTAATCCCAGCACT       78680     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC148198 3'  ATGCCTGTAATCCCAGCTACT  70676              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                          C
GAM888  LOC148198 3'  CTGTAATCCCAGCACT       70681     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC148254 3'  TGCCTGTAATCCCTGCACT    78760     A  T        A
                                AGT GC GGGATTACAG CA
                                ||| || |||||||||| ||
                                TCA CG CCCTAATGTC GT
                                  _  T         C
GAM888  LOC148343 3'  TGCCTGTAATCCCCGCACT    78796     A  T        A
                                AGT GC GGGATTACAG CA
                                ||| || |||||||||| ||
                                TCA CG CCCTAATGTC GT
                                  _  C         C
GAM888  LOC148397 3'  ATGCCTGTAATCCTAGCTATT  78812              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TTATCGATCCTAATGTC GTA
                                          C
GAM888  LOC148397 3'  CTGTAATCCCGGCACTGTG    78817       A
                                TACAGT GCTGGGATTACAG
                                |||||| ||||||||||||
                                GTGTCA CGGCCCTAATGTC
                                  _
GAM888  LOC148534 3'  ATGCCTGTAATCCCAGCACT   78894     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC148734 3'  CTGTAATCCCAGCACT      78954     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC148749 3'  CTGTAATCCCAGCACT      78960     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC148758 5'  ATGCCTATAATCCCAGCTACTT 78965    _          C  A
          G                    CA GTAGCTGGGATTA AG CAT
                               || |||||||||||| || |||
                               GT CATCGACCCTAAT TC GTA
                                T           A  C
GAM888  LOC148758 5'  ATGCCTGTAATCCCAGAACT   78966    AG         A
                               AGT  CTGGGATTACAG CAT
                               |||  |||||||||||| |||
                               TCA  GACCCTAATGTC GTA
                                A_          C
GAM888  LOC148809 3'  ATGCCTATAATCCCAGCTTCT  79000    T        C  A
                               AG AGCTGGGATTA AG CAT
                               || |||||||||| || |||
                               TC TCGACCCTAAT TC GTA
                                T          A  C
GAM888  LOC148809 5'  CTGTAATCCCAGCACT      79003     A
                               AGT GCTGGGATTACAG
                               ||| ||||||||||||
                               TCA CGACCCTAATGTC
                                  _
GAM888  LOC148918 5'  CTGTAATCCCAGCACT      79071     A
                               AGT GCTGGGATTACAG
                               ||| ||||||||||||
                               TCA CGACCCTAATGTC
                                  _
GAM888  LOC148936 3'  CTGTAATCCCAGCACT      84290     A
                               AGT GCTGGGATTACAG
                               ||| ||||||||||||
                               TCA CGACCCTAATGTC
                                  _
GAM888  LOC148938 3'  CTGTAATCCCAGCACT      84270     A
                               AGT GCTGGGATTACAG
                               ||| ||||||||||||
                               TCA CGACCCTAATGTC
                                  _
GAM888  LOC149073 3'  CTATAATCCCAGCACT      84324     A        C
                               AGT GCTGGGATTA AG
                               ||| |||||||||| ||
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                                TCA CGACCCTAAT TC
                                  _        A
GAM888  LOC149073 3'  GTGCCTGTAATCCCAGCTACTC 84331    C             A
                A                A AGTAGCTGGGATTACAG CAT
                                 | |||||||||||||||| |||
                                 A TCATCGACCCTAATGTC GTG
                                  C              C
GAM888  LOC149113 3'  CTGTAATCCCAGAACTTTA    79164    C   AG
                                 TA AGT  CTGGGATTACAG
                                 || |||  ||||||||||||
                                 AT TCA  GACCCTAATGTC
                                  T   A_
GAM888  LOC149113 3'  CTGTAATCCCAGCACT       79165     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC

                                  _
GAM888  LOC149194 5'  CTGTAATCCCAGCTACTCA    79225    C
                                 A AGTAGCTGGGATTACAG
                                 | ||||||||||||||||
                                 A TCATCGACCCTAATGTC
                                  C
GAM888  LOC149194 5'  GTCTGTAATCCCAGCACT     79229     A
                                 AGT GCTGGGATTACAGAC
                                 ||| |||||||||||||||
                                 TCA CGACCCTAATGTCTG

                                  _
GAM888  LOC149271 3'  CTGTAATCCCAGCACT       79240     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC

                                  _
GAM888  LOC149319 3'  GTCTGTAATCCCAGCACT     79301     A
                                 AGT GCTGGGATTACAGAC
                                 ||| |||||||||||||||
                                 TCA CGACCCTAATGTCTG

                                  _
GAM888  LOC149579 5'  CTGTAATCCCAGCACT       71133     A
                                 AGT GCTGGGATTACAG
                                 ||| ||||||||||||
                                 TCA CGACCCTAATGTC

                                  _
GAM888  LOC149606 3'  GTCTGTAGTCCCAGCTACTCA  79455    C
                                 A AGTAGCTGGGATTACAGAC
                                 | ||||||||||||||||||
                                 A TCATCGACCCTGATGTCTG
                                  C
GAM888  LOC149628 3'  CTATAATCCCAGCTACT      79462              C
                                 AGTAGCTGGGATTA AG
                                 |||||||||||||| ||
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                                TCATCGACCCTAAT TC
                                       A
GAM888  LOC149628 3'  CTGTAATCCCAGCACT      79463     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC149668 3'  ATGCCTGTAATCCCAGCACT   84534     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC149705 3'  CTGTAATCCCAACACTTTG    84623     TAGC_
                                CAG     TGGGATTACAG
                                |||     ||||||||||
                                GTT     ACCCTAATGTC
                                  TCACA
GAM888  LOC149837 3'  TGGAAATCCCAGCTAT       84747           A_
                                GTAGCTGGGATT  CA
                                ||||||||||||  ||
                                TATCGACCCTAA  GT
                                       AG
GAM888  LOC150139 3'  ATGCCTGTAATCCCAGCTG    79584             A
                                TAGCTGGGATTACAG CAT
                                |||||||||||||| |||
                                GTCGACCCTAATGTC GTA
                                       C
GAM888  LOC150185 3'  ATGCCTGTAATCCCAACACT   84905     AGC         A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_         C
GAM888  LOC150319 3'  ATGCCTGTAATCCCAGCACT   79647     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC150319 3'  ATGCCTGTAATCCCAGTTACTC 79648    C             A
          A                      A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATTGACCCTAATGTC GTA
                                 C             C
GAM888  LOC150343 3'  CTGTAATCCCAGCACT       79672     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC150358 3'  ATGCCTATAATCCCAGCACT   84920     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
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                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM888  LOC150358 3'  ATGCCTGTAATCCCAGCACT   84921     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC150358 3'  CTGTAATCCCAGGTACTCA    84922   C    G
                                A AGTA CTGGGATTACAG
                                | |||| ||||||||||||
                                A TCAT GACCCTAATGTC
                                 C    G
GAM888  LOC150372 3'  ATGCCTGTAATCCCAGC      79786            A
                                GCTGGGATTACAG CAT
                                |||||||||||| |||
                                CGACCCTAATGTC GTA
                                        C
GAM888  LOC150481 3'  CTGTAATCCCAGCACT       79884     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC150622 3'  CTGTAATCCCAACACT       79958     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  LOC150630 3'  ATGCCTATAATCCCAGCTACT  85099             C  A
                                AGTAGCTGGGATTA AG CAT
                                |||||||||||||| || |||
                                TCATCGACCCTAAT TC GTA
                                        A  C
GAM888  LOC150630 3'  ATGCCTGTAATCCCAGCACT   85100     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC150889 3'  ATGCCTGTAATCCCAGCACT   80024     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC150935 3'  ATGCCTGTAATCCCAGCGCT   80031     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCG CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC150998 3'  CTGTGGTCCCAGCTAC       85183
                                GTAGCTGGGATTACAG
                                ||||||||||||||||
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                                CATCGACCCTGGTGTC

GAM888  LOC151196 3'  CTGTAACCCCAGCTACTCA   85265   C        A
                                A AGTAGCTGGG TTACAG
                                | |||||||||| ||||||
                                A TCATCGACCC AATGTC
                                 C         C
GAM888  LOC151196 3'  CTGTAATCCCAGCACT      85266    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC151248 3'  CTGTAATCCCAGCACT      80186    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC151248 3'  TGTAATCCCAGCTACTCA    80193   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  LOC151429 3'  ATGCCTGTAATCCCAGC     85344           A
                                GCTGGGATTACAG CAT
                                |||||||||||| |||
                                CGACCCTAATGTC GTA
                                        C
GAM888  LOC151429 3'  CTGTAATCCCAGCACT      85352    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC151446 3'  ATGCCTGTAATCCCAGCTACTG 85375              A
                                CAGTAGCTGGGATTACAG CAT
                                |||||||||||||||||| |||
                                GTCATCGACCCTAATGTC GTA
                                           C
GAM888  LOC151556 3'  CTGTAATCCCAGTACT      80274     G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                  _
GAM888  LOC151556 3'  TGTAATCCCAGCTACTCA    80283   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  LOC151602 3'  CTGTAATCCCAACACT      80294    AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
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                                TCA   ACCCTAATGTC
                                  CA_
GAM888  LOC151602 3'  CTGTAATCCCAGCTACTCA    80295    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM888  LOC151614 3'  CTGTAATCCCAGCACT      80304     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

GAM888  LOC151623 3'  ATGCCTGTGGTCTCAGCTACTC 85456    C             A
              A                  A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGACTCTGGTGTC GTA
                                 C              C
GAM888  LOC151904 3'  CTGTAATCCCAGCACT      80390     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

GAM888  LOC152263 3'  CTGTAATCCCAGCACT      85674     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

GAM888  LOC152263 3'  TCCATAATCCTAGCTGCT    85676            CA
                                AGTAGCTGGGATTA  GA
                                ||||||||||||||  ||
                                TCGTCGATCCTAAT  CT
                                          AC
GAM888  LOC152316 3'  ATGCCTGTAATCCCAGCACTTT 85609    C  A          A
              A                  TA AGT GCTGGGATTACAG CAT
                                || ||| |||||||||||| |||
                                AT TCA CGACCCTAATGTC GTA
                                 T  _           C
GAM888  LOC152426 3'  CTGTAATCCCAGCACT      85714     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

GAM888  LOC152445 3'  ATGCCTGTAATCCCAACTACT  85746      C         A
                                AGTAG TGGGATTACAG CAT
                                ||||| |||||||||| |||
                                TCATC ACCCTAATGTC GTA
                                   A         C
GAM888  LOC152453 3'  ATGCCTGTAATCCCAGCACT   80592     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC152453 3'  ATGCCTGTAATCCCAGCTACT  80593            A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                        C
GAM888  LOC152453 3'  CTGTAATCCCAACACT     80595    AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  LOC152453 3'  CTGTAATCCCAGCACT     80596    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC152453 3'  CTGTAATCCCAGTTACTCA   80597   C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATTGACCCTAATGTC
                                 C
GAM888  LOC152627 5'  TGTAATCCCAGCTACTCA    80632   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  LOC152804 3'  ATGCCTGTAATCCCAGCTACT  85878            A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                        C
GAM888  LOC152860 3'  ATGTCTGTAATCCCAGCTACTG 80696
                                CAGTAGCTGGGATTACAGACAT
                                |||||||||||||||||||||
                                GTCATCGACCCTAATGTCTGTA

GAM888  LOC152860 3'  CTATAATCCCAGCACT     80701    A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM888  LOC152926 3'  ATGCCTGTAATCCCAGCACT  80744    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC153077 3'  CTATAATCCCAGCTACTCA   85909   C         C
                                A AGTAGCTGGGATTA AG
                                | ||||||||||||| ||
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                                A TCATCGACCCTAAT TC
                                 C           A
GAM888  LOC153260 3'  CTGTAATCCCAGCACT     80804     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC153561 3'  ATGCCTGTAATCCCAGCACT  80888     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC153579 3'  CTGTAATCCCAGTACT      80895     G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC
                                  _
GAM888  LOC153642 3'  CTATAGTCTCAGCTACTCA   80907   C          C
                                A AGTAGCTGGGATTA AG
                                | |||||||||||||| ||
                                A TCATCGACTCTGAT TC
                                 C           A
GAM888  LOC153642 3'  CTGTAATCCCAGGACT      80908     AG
                                AGT  CTGGGATTACAG
                                |||  ||||||||||||
                                TCA  GACCCTAATGTC
                                  G_
GAM888  LOC153682 3'  ATGCCTGTAATCCCAGCACT  86084     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC153688 3'  ATGCCTATAATCCCAGCACT  86095     A        C A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM888  LOC154092 3'  TCTGTAATCCCAGCACT     86161     A
                                AGT GCTGGGATTACAGA
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCT
                                  _
GAM888  LOC154215 3'  ATGTCTGTAATATACACACAC 81053    AGC  GG_
                                GT   TG   ATTACAGACAT
                                ||   ||   ||||||||||||
                                CA   AC   TAATGTCTGTA
                                 CAC  ATA
GAM888  LOC154403 3'  CTGTAATCCCAGAACTTTA   81071    C   AG
                                TA AGT  CTGGGATTACAG
                                || |||  ||||||||||||
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                                AT TCA  GACCCTAATGTC
                                 T   A_
GAM888  LOC154739 5'  ATGTCTATAATTCCAGCTACTC 86225    C           C
          A                     A AGTAGCTGGGATTA AGACAT
                                | ||||||||||||||| ||||||
                                A TCATCGACCTTAAT TCTGTA
                                 C            A
GAM888  LOC154791 3'  ATGCCTGTAATCCCAGCTACT  81154              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM888  LOC154791 3'  CTGTAATCCCAGCACT      81156     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC154992 3'  CTGTAATCCCAGAACTTTA    81215    C   AG
                                TA AGT  CTGGGATTACAG
                                || |||  ||||||||||||
                                AT TCA  GACCCTAATGTC
                                 T   A_
GAM888  LOC155006 3'  ATGCCTGTAATCCCAGCACT   81229     A           A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC155006 3'  ATGCCTGTAATCCCAGCACT   81230     A           A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC155006 3'  CTGTAATCCCAGCTACTTG    81237    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                 T
GAM888  LOC155072 3'  CTGTAATCCCAGCACT       86375     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC155072 3'  CTGTAATCCCAGCACT       86376     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC155438 3'  CTGTAATCCCAGTACCT      86393     TA
                                AG  GCTGGGATTACAG
                                ||  ||||||||||||
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                                TC  TGACCCTAATGTC
                                 CA
GAM888  LOC157278 3'  CTGTAATCCCAGCACT      86423     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC157292 5'  CTGTAATCTCAGTTACTCA    86413    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATTGACTCTAATGTC
                                 C
GAM888  LOC157464 5'  CTGTAATCCCAGCACT       86448     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC157657 3'  ATGCCTGTAATCCCAACTACT  81516       C          A
                                AGTAG TGGGATTACAG CAT
                                ||||| |||||||||||| |||
                                TCATC ACCCTAATGTC GTA
                                   A          C
GAM888  LOC157657 3'  CTGTAATCCCAGCACT       81518     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC157660 3'  CTGTAATCCCAGCACT       86507     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC158160 3'  TGTAGTCCCAACTACTCA     73082    C     C
                                A AGTAG TGGGATTACA
                                | ||||| ||||||||||
                                A TCATC ACCCTGATGT
                                 C     A
GAM888  LOC158187 3'  CTGTAGTCCCAGCTAC       86691
                                GTAGCTGGGATTACAG
                                ||||||||||||||||
                                CATCGACCCTGATGTC

GAM888  LOC158191 3'  CTGTAATCCCAGCACT       81775     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC158292 5'  ATGCCTGTAATCCCAGCACT   86728     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC158292 5'  TGTAATCCCAGCTACTCA    86732   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  LOC158310 3'  CTGTAATCCCAGCACT      86753    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC158819 5'  ATGCCTGTAATCCCAGCTTCT  86901    T          A
                                AG AGCTGGGATTACAG CAT
                                || |||||||||||||| |||
                                TC TCGACCCTAATGTC GTA
                                 T          C
GAM888  LOC158819 3'  CTGTAATCCCAGCACT      86903    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC158819 5'  CTGTAATCCCAGCACT      86904    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC158863 3'  CTGTAATCCCAACACT      86923    AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  LOC158987 3'  CTGTAATCCCAACACT      86961    AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  LOC159036 3'  ATGCCTGTAATCCCAGCACT  86969    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC159053 3'  CTGTAATCCCAGGACT      86978    AG
                                AGT  CTGGGATTACAG
                                |||  ||||||||||||
                                TCA  GACCCTAATGTC
                                  G_
GAM888  LOC161823 3'  ATGCCTGTAATCCCAGCACT  82300    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM888  LOC170395 3'  CTGTAATCCCAGCACT      76369     A
                                AGT GCTGGGATTACAG
                                ||| |||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LOC170395 3'  CTGCAGTCCCAGCTACTCA    76368    C          A
                                A AGTAGCTGGGATT CAG
                                | |||||||||||||| |||
                                A TCATCGACCCTGA GTC
                                 C           C
GAM888  LOC196047 5'  CTGTAATCCCAGTACT       89600      G
                                AGTA CTGGGATTACAG
                                |||| ||||||||||||
                                TCAT GACCCTAATGTC

                                  _
GAM888  LOC196528 3'  CTATAATCCCAGCACT       87764     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _         A
GAM888  LOC197196 3'  CTGTAATCCCAGCACT       89733     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LOC197201 3'  ATGCCTGTAATCTCAGCTACTC 87933    C              A
          A                      A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACTCTAATGTC GTA
                                 C              C
GAM888  LOC197201 3'  CTGTAATCCCAGCACT       87936     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LOC197319 3'  CTGTAATCCCAGCACT       87969     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LOC197319 3'  CTGTAATCCCAGCTCCT      87970     T
                                AG AGCTGGGATTACAG
                                || |||||||||||||
                                TC TCGACCCTAATGTC
                                 C
GAM888  LOC199733 3'  CTGAAATCCCAGCTACTG     89849           A
                                CAGTAGCTGGGATT CAG
                                |||||||||||||| |||
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                                GTCATCGACCCTAA GTC
                                       A
GAM888  LOC199786 3'  CTGTAATCCCAGCACT      88380     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM888  LOC200014 3'  CTGTAATCCCACCACT      88526     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CC_
GAM888  LOC200251 5'  CTGTAATCCCAGCTACTCA    88665    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM888  LOC200317 3'  CTGTAATCCCAGCTACTTG    88794    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                  T
GAM888  LOC200470 3'  CTGTAATCCCAACACT       90062     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  LOC200728 3'  CTGTAATCCCAGCACT       90115     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                 _
GAM888  LOC200803 3'  ATGCCTGTAATCCTAGCTACTC 88879    C              A
          A                      A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||||| |||
                                A TCATCGATCCTAATGTC GTA
                                 C              C
GAM888  LOC200803 3'  TGCCTGTAATCCCACCACT    88881     AGC         A
                                AGT   TGGGATTACAG CA
                                |||   |||||||||| ||
                                TCA   ACCCTAATGTC GT
                                  CC_          C
GAM888  LOC200918 3'  TGTAATCCCAGCTACTTA     88943    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 T
GAM888  LOC200940 3'  ATGCCTGTAATCCCAGCTACTT 88950    _              A
          G                      CA GTAGCTGGGATTACAG CAT
                                || ||||||||||||||||| |||
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                                GT CATCGACCCTAATGTC GTA
                                 T             C
GAM888  LOC201173 3'  CTGTAATCCCAGCACT      87328     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC201182 5'  ATGCCTGTAATCCCAGCTAC   89763              A
                                GTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                CATCGACCCTAATGTC GTA
                                           C
GAM888  LOC201220 3'  CTGTAATCCCAGCACT      87349     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC201252 3'  ATGCCTGTAATCCCAACTACT  88165       C          A
                                AGTAG TGGGATTACAG CAT
                                ||||| |||||||||||| |||
                                TCATC ACCCTAATGTC GTA
                                   A          C
GAM888  LOC201252 3'  CTGTAATCCCAGAACT       88168     AG
                                AGT  CTGGGATTACAG
                                |||  ||||||||||||
                                TCA  GACCCTAATGTC
                                  A_
GAM888  LOC201564 3'  ATGCCTGTAATCCCAGCTACTT 80435    _              A
          G                      CA GTAGCTGGGATTACAG CAT
                                || ||||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 T             C
GAM888  LOC201685 3'  ATGTCTATGGTCCCAGCTACTC 90239    C            C
          A                      A AGTAGCTGGGATTA AGACAT
                                | |||||||||||||| ||||||
                                A TCATCGACCCTGGT TCTGTA
                                 C            A
GAM888  LOC201685 3'  CTGTAATCCCAGCACT       90241     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC201689 3'  CTGTAATCCCAGCACT       67144     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC201868 3'  CTGTAATCCCAGCACT       89077     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC201868 3'  TGTAATCCCAGCTACTCA    89084   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  LOC201895 3'  CTGTAATCCCAGCACT      89087    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC201895 3'  GTGCCTGTAATCCCAGCTACTC 89091   C            A
          A                      A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACCCTAATGTC GTG
                                 C             C
GAM888  LOC201911 3'  CTGTAATCCCAGCACT      90261    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC202868 3'  CTGTAATCCCAGCACT      90373    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC202868 3'  CTGTAATCCCAGCACT      90374    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC203025 3'  ATGCCTGTAATCCCAACACTTT 89249    TAGC_        A
          G                      CAG    TGGGATTACAG CAT
                                |||    |||||||||| |||
                                GTT    ACCCTAATGTC GTA
                                  TCACA         C
GAM888  LOC203246 3'  CTGTAATCCCAGCACT      89304    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC203276 3'  GTCTATAATTCCAGCTACTCA  90487   C            C
                                A AGTAGCTGGGATTA AGAC
                                | |||||||||||||| ||||
                                A TCATCGACCTTAAT TCTG
                                 C            A
GAM888  LOC203305 3'  GTCTATAATTCCAGCTACTCA  90531   C            C
                                A AGTAGCTGGGATTA AGAC
                                | |||||||||||||| ||||
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                                  A TCATCGACCTTAAT TCTG
                                   C           A
GAM888  LOC203350 3'  ATGCCTGTAATCCCAGCACT   90560     A          A
                                  AGT GCTGGGATTACAG CAT
                                  ||| |||||||||||| |||
                                  TCA CGACCCTAATGTC GTA
                                    _          C
GAM888  LOC203350 3'  ATGCCTGTAGTTGCAGCTACTC 90561    C       G       A
          A                        A AGTAGCTG GATTACAG CAT
                                  | |||||||| |||||||| |||
                                  A TCATCGAC TTGATGTC GTA
                                   C       G       C
GAM888  LOC203378 3'  CTGTAATCCCGGCACT      90602     A
                                  AGT GCTGGGATTACAG
                                  ||| ||||||||||||
                                  TCA CGGCCCTAATGTC
                                    _
GAM888  LOC203378 3'  CTGTAGTTCCAGCTACTG    90603
                                  CAGTAGCTGGGATTACAG
                                  ||||||||||||||||||
                                  GTCATCGACCTTGATGTC

GAM888  LOC219406 3'  CTGCAATCCCAGCTACT     93559           A
                                  AGTAGCTGGGATT CAG
                                  |||||||||||| |||
                                  TCATCGACCCTAA GTC
                                         C
GAM888  LOC219406 3'  CTGTAATCCCAGCACT      93560     A
                                  AGT GCTGGGATTACAG
                                  ||| ||||||||||||
                                  TCA CGACCCTAATGTC
                                    _
GAM888  LOC219540 3'  CTGTAATCCCAGCTACTTG   93598    _
                                  CA GTAGCTGGGATTACAG
                                  || ||||||||||||||||
                                  GT CATCGACCCTAATGTC
                                   T
GAM888  LOC219627 3'  ATGCCTGTAATCCCAACACT  92175     AGC        A
                                  AGT   TGGGATTACAG CAT
                                  |||   |||||||||| |||
                                  TCA   ACCCTAATGTC GTA
                                    CA_         C
GAM888  LOC219627 3'  CTGTAATCCCAGCACT      92177     A
                                  AGT GCTGGGATTACAG
                                  ||| ||||||||||||
                                  TCA CGACCCTAATGTC
                                    _
GAM888  LOC219627 3'  GTGCCTGTAATCCCAGCTACTC 92185    C           A
          A                        A AGTAGCTGGGATTACAG CAT
                                  | |||||||||||||||| |||
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                                A TCATCGACCCTAATGTC GTG
                                 C              C
GAM888  LOC219649 3'  ATGCCTATAATCCCAGC     92950          C  A
                                GCTGGGATTA AG CAT
                                |||||||||| || |||
                                CGACCCTAAT TC GTA
                                      A  C
GAM888  LOC219649 3'  CTGTAATCCCAGCTACT     92956
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  LOC219649 3'  GTCTGTAATCCCAGCACT    92961     A
                                AGT GCTGGGATTACAGAC
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCTG

                                 _
GAM888  LOC219672 5'  ATGCCTGTAATCCCAGCACT  91328     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                 _           C
GAM888  LOC219673 3'  CTGTAATCCCAGCACT      93031     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                 _
GAM888  LOC219722 5'  CTGTAATCCCAGCACT      93081     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                 _
GAM888  LOC220370 3'  ATGCCTGTAATCCCAACACTCT 92824     T  C__         A
          G                      CAG AG   TGGGATTACAG CAT
                                ||| ||   |||||||||| |||
                                GTC TC   ACCCTAATGTC GTA
                                  _ ACA          C
GAM888  LOC220506 3'  CTATAATCCCAGCACTTTA    74077     C  A        C
                                TA AGT GCTGGGATTA AG
                                || ||| |||||||||| ||
                                AT TCA CGACCCTAAT TC
                                 T  _         A
GAM888  LOC220662 3'  CTGTAATCCCAGCACT      91169     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                 _
GAM888  LOC220662 3'  CTGTAATCCCAGCACT      91170     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC220662 3'  CTGTAATCCCAGCTACTTG   91171    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
                                GT CATCGACCCTAATGTC
                                 T
GAM888  LOC220662 3'  CTGTCATCCCAGCTACTCA   91172   C         T
                                A AGTAGCTGGGAT ACAG
                                | |||||||||||| ||||
                                A TCATCGACCCTA TGTC
                                 C          C
GAM888  LOC220906 3'  ATGCCTGTAATCCCAACACT  91396    AGC        A
                                AGT   TGGGATTACAG CAT
                                |||   |||||||||||| |||
                                TCA   ACCCTAATGTC GTA
                                  CA_         C
GAM888  LOC221042 3'  CTGTAATCCCAGCGCT     93185    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCG CGACCCTAATGTC
                                  _
GAM888  LOC221178 3'  ATGCCTGTAATCCCAGCACT  93527    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC221178 3'  ATGCCTGTAATCCCAGCTACTG 93528               A
                                CAGTAGCTGGGATTACAG CAT
                                |||||||||||||||||| |||
                                GTCATCGACCCTAATGTC GTA
                                           C
GAM888  LOC221271 3'  CTGTAATCCCAGCACT     91856    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC221271 3'  CTGTAATCCCAGCTACT    91857
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  LOC221474 3'  CTGTAATCCCAGCACT     92381    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC221474 3'  TGTAATCCCAGCTACTCA   92389   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
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                                A TCATCGACCCTAATGT
                                 C
GAM888  LOC221477 3'  CTGTAATCCCAGCTAC      92152
                                GTAGCTGGGATTACAG
                                ||||||||||||||||
                                CATCGACCCTAATGTC

GAM888  LOC221489 3'  CTGTAATCCCAGCACT      93641     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC221490 3'  CTGTAATCCCAGCACT      93658     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC221543 3'  CTGTAATCCCAGCACT      93740     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC221543 5'  CTGTAATCCCAGCACTCTG    93741     TA_
                                CAG   GCTGGGATTACAG
                                |||   ||||||||||||
                                GTC   CGACCCTAATGTC
                                  TCA
GAM888  LOC221931 3'  ATGCCTGTAATCCCAGCACT   93993     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM888  LOC221954 5'  CTGTAATCCCAGCACT      94000     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC221962 3'  CTGTAATCCCAGCACT      92681     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC222066 3'  CTGTAATCCCAGCTATT     92744
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TTATCGACCCTAATGTC

GAM888  LOC222160 5'  ATGCCTGTAATCCCAGCACT   94118     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC222160 3'  CTGTAATCCCAGCTACT     94125
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATCGACCCTAATGTC

GAM888  LOC222182 3'  CTGTAATCCCTTAGCTACTCA  94189   C     __
                                A AGTAGCT  GGGATTACAG
                                | |||||||  ||||||||||
                                A TCATCGA  CCCTAATGTC
                                 C      TT
GAM888  LOC222865 3'  CTGTAATCCCAGCACT      92860     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC253612 3'  CTGTAATCCCAACACT      96748     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  LOC253612 3'  GTCTGTAATCCCAGCTACT   96755
                                AGTAGCTGGGATTACAGAC
                                ||||||||||||||||||
                                TCATCGACCCTAATGTCTG

GAM888  LOC253639 3'  ATGCCTGTAATCCCAGCTACT 95818              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                            C
GAM888  LOC253927 3'  ATGCCTGTAATCCCAGCACT  95023     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| ||||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC254045 3'  ATGCCTGTAATCCCAATACT  96502     GC         A
                                AGTA  TGGGATTACAG CAT
                                ||||  |||||||||| |||
                                TCAT  ACCCTAATGTC GTA
                                   A_         C
GAM888  LOC254045 3'  ATGCCTGTAATCCCAGCTACT 96503              A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                            C
GAM888  LOC254243 3'  GTCTATAATTCCAGCTACTCA 97416   C          C
                                A AGTAGCTGGGATTA AGAC
                                | |||||||||||||| ||||
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                                A TCATCGACCTTAAT TCTG
                                 C           A
GAM888  LOC254249 5'  TGCTTGTCCCAGCTACTG    95449          TAC  A
                                CAGTAGCTGGGAT   AG CA
                                ||||||||||||   || ||
                                GTCATCGACCCTG   TC GT
                                       T__  _
GAM888  LOC254531 5'  ATGCCTGTAATCCCAGCTACTT 94980    _           A
          G                     CA GTAGCTGGGATTACAG CAT
                                || ||||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 T            C
GAM888  LOC254531 5'  CTGTAATCCCAGCACT      94985     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                 _
GAM888  LOC255042 3'  ATGCCTGTAATCCTAGCTACTC 95312   C           A
          A                     A AGTAGCTGGGATTACAG CAT
                                | ||||||||||||||| |||
                                A TCATCGATCCTAATGTC GTA
                                 C            C
GAM888  LOC255042 3'  CTGTAATCCCAGCACT      95315     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                 _
GAM888  LOC255042 3'  CTGTAATCCCAGCACT      95316     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                 _
GAM888  LOC255177 3'  CTGTAATCCCAGCACT      96605     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                 _
GAM888  LOC255196 5'  CTGTAATCCCAGCACT      97169     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                 _
GAM888  LOC255196 3'  ATGCCTATAATCCCAGCACT  97164     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                 _         A  C
GAM888  LOC255231 3'  CTGTAATCCCAGCACT      95373     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
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                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC255252 3'  ATGCCTATAATCCCAGCACT  95006    A       C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
                                TCA CGACCCTAAT TC GTA
                                  _       A  C
GAM888  LOC255326 3'  CTGTAATCCCAGACTGTG   96376      AG
                                TACAGT  CTGGGATTACAG
                                ||||||  ||||||||||||
                                GTGTCA  GACCCTAATGTC
                                   __
GAM888  LOC255328 3'  ATGTCTGTAATCCCAGCACT  96557    A
                                AGT GCTGGGATTACAGACAT
                                ||| ||||||||||||||||
                                TCA CGACCCTAATGTCTGTA
                                  _
GAM888  LOC255461 3'  CTGTAATCCCAGCACT     97319    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC255516 3'  CTGTAATCCCAGCACT     97332    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC255624 3'  CTGTAATCCCAGCACT     94523    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC255671 3'  CTGTAATCCCAGCTGCT    97255
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCGTCGACCCTAATGTC

GAM888  LOC255671 3'  TCTGTAATCCCAGCACT    97264    A
                                AGT GCTGGGATTACAGA
                                ||| ||||||||||||
                                TCA CGACCCTAATGTCT
                                  _
GAM888  LOC255937 3'  ATGCCTGTAATCCCAGCTACT  95987            A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                     C
GAM888  LOC255937 3'  CTGTAATCCCAGCTCT     95988    T
                                AG AGCTGGGATTACAG
                                || ||||||||||||||
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                                TC TCGACCCTAATGTC
                                  _
GAM888  LOC255971 3'  CTATAATCCCAGCACT      96533     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM888  LOC256073 3'  CTGTAATCCCAATGCT      96664     GC
                                AGTA  TGGGATTACAG
                                ||||  ||||||||||
                                TCGT  ACCCTAATGTC
                                  A_
GAM888  LOC256207 3'  TCTGTAATTGCTATTG      95179       TGG
                                CAGTAGC   GATTACAGA
                                |||||||   |||||||||
                                GTTATCG   TTAATGTCT
                                    ____
GAM888  LOC256267 3'  ATGCCTGTAATCCCAGCACT   96797     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC256277 3'  CTGTAATCCCAGCACT      94698     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC256520 3'  TGTAATCCCAGCTACTCA    95981    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  LOC256980 3'  TCTGTAATCCCAGCACTCTG   95223     TA_
                                CAG   GCTGGGATTACAGA
                                |||   ||||||||||||||
                                GTC   CGACCCTAATGTCT
                                  TCA
GAM888  LOC257354 3'  ATGCCTATAATCCCAACACT   95085     AGC       C  A
                                AGT   TGGGATTA AG CAT
                                |||   |||||||| || |||
                                TCA   ACCCTAAT TC GTA
                                  CA_       A  C
GAM888  LOC257480 3'  CTGTAATCCCAGCACT      77869     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC257539 3'  ATGCCTGTAATCCCAGCACT   97699     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC257578 3'  ATGCCTGTAATCCCAGCACT  97819    A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC257596 3'  CTGTAATCCCAGCACT     97933    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC257596 5'  CTGTAATCCCAGCACTCTG   97934    TA_
                                CAG   GCTGGGATTACAG
                                |||   ||||||||||||
                                GTC   CGACCCTAATGTC
                                  TCA
GAM888  LOC51145  3'  TGTAATCCCAGCTACTCA    32400   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  LOC51333  3'  CTGTAATCCCAGCACT      33567    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC51333  3'  CTGTAATCCCAGCTACTG    33568
                                CAGTAGCTGGGATTACAG
                                ||||||||||||||||||
                                GTCATCGACCCTAATGTC

GAM888  LOC51652  3'  ATGCCTATAATCCCAGTGCT  32191    G       C  A
                                AGTA CTGGGATTA AG CAT
                                |||| ||||||||| || |||
                                TCGT GACCCTAAT TC GTA
                                  _       A  C
GAM888  LOC51716  3'  TGCCTGTAATCCCTGC      32795   T       A
                                GC GGGATTACAG CA
                                || ||||||||| ||
                                CG CCCTAATGTC GT
                                  T        C
GAM888  LOC51759  3'  ATGCCTGTAATCCCAGCTGCT  72812            A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCGTCGACCCTAATGTC GTA
                                           C
GAM888  LOC55974  3'  ATGCCTGTAATCCCAGATACT  38130    G         A
                                AGTA CTGGGATTACAG CAT
                                |||| |||||||||||| |||
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                                TCAT GACCCTAATGTC GTA
                                  A          C
GAM888  LOC55974  3' CTGTAATCCCAGCACT     38131     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC57118  3' CTGTAATCCCAACACT     39867     AGC
                                AGT   TGGGATTACAG
                                |||   ||||||||||
                                TCA   ACCCTAATGTC
                                  CA_
GAM888  LOC63929  3' ATGCCTGTAATCCTGGCTACT  42041       TG        A
                                AGTAGC  GGATTACAG CAT
                                ||||||  |||||||| |||
                                TCATCG  CCTAATGTC GTA
                                   GT        C
GAM888  LOC64167  3' CTGTAATCCCAGCACT     42279     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC89890  3' CTGTAATCCCAGCTAC     60578
                                GTAGCTGGGATTACAG
                                ||||||||||||||||
                                CATCGACCCTAATGTC

GAM888  LOC90038  3' GTCTATAATTCCAGCTACTCA  61159   C           C
                                A AGTAGCTGGGATTA AGAC
                                | |||||||||||||| ||||
                                A TCATCGACCTTAAT TCTG
                                 C            A
GAM888  LOC90092  3' CTGTAATCCCAGCACT     61405     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC90092  3' CTGTAATCCCAGCACT     61406     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC90141  3' ATGCCTACAATCCCAGCACT  61625     A        AC  A
                                AGT GCTGGGATT  AG CAT
                                ||| |||||||||  || |||
                                TCA CGACCCTAA  TC GTA
                                  _        CA  C
GAM888  LOC90155  5' ATGCCTGTAATCCCAGCACT  61691     A           A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC90321  3' ATGCCTATAATCTCAGCAC   62260    A       C  A
                                GT GCTGGGATTA AG CAT
                                || |||||||||| || |||
                                CA CGACTCTAAT TC GTA
                                  _        A  C
GAM888  LOC90321  3' ATGCCTGCAATCCCAGCTACT  62261           A   A
                                AGTAGCTGGGATT CAG CAT
                                |||||||||||| ||| |||
                                TCATCGACCCTAA GTC GTA
                                       C   C
GAM888  LOC90408  5' ATGCCTGTAATCCCAGCACT   62656    A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC90509  3' CTGTAATCCCAGCACT     63104    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC90538  3' TCTGTAATCCCAGCACT    63196    A
                                AGT GCTGGGATTACAGA
                                ||| |||||||||||||
                                TCA CGACCCTAATGTCT
                                  _
GAM888  LOC90580  3' ATGTCTGTAATCCCAGC    63371
                                GCTGGGATTACAGACAT
                                |||||||||||||||||
                                CGACCCTAATGTCTGTA

GAM888  LOC90591  3' ATGCCTGTAATCCCAGCTACAT 63414   _           A
          G                      CA GTAGCTGGGATTACAG CAT
                                || ||||||||||||||| |||
                                GT CATCGACCCTAATGTC GTA
                                 A            C
GAM888  LOC90591  3' CTGTAATCCCAGCACT     63423    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC90591  3' CTGTAATCCCAGCACT     63424    A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC90624  3' CTGTAATCCCGCACT      63603    A  T
                                AGT GC GGGATTACAG
                                ||| || ||||||||||
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                                TCA CG CCCTAATGTC
                                  _ _
GAM888  LOC90639  3' CTGCAATCCCAGCACTTTA   63656    C  A       A
                                TA AGT GCTGGGATT CAG
                                || ||| ||||||||| |||
                                AT TCA CGACCCTAA GTC
                                 T  _       C
GAM888  LOC90777  3' CTATAATCTCAGCAC       63967    A       C
                                GT GCTGGGATTA AG
                                || |||||||||| ||
                                CA CGACTCTAAT TC
                                  _        A
GAM888  LOC90918  5' ATGCCTGTAATCCCAGCTACT  64350             A
                                AGTAGCTGGGATTACAG CAT
                                |||||||||||||||| |||
                                TCATCGACCCTAATGTC GTA
                                           C
GAM888  LOC90979  3' CTGTAATCCCAGCACT      64526     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC90982  5' ATGTCTCTTTCCAGCTCT    64537    T      TTAC
                                AG AGCTGGGA    AGACAT
                                || ||||||||    ||||||
                                TC TCGACCTT    TCTGTA
                                  _       TC__
GAM888  LOC91035  3' CTATAATCCCAGCACT      64669     A       C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _        A
GAM888  LOC91056  3' ATGCCTGTAATCCCAGCACT   94756     A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC91250  5' CTGTAATCCCAGTTACT     65323
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TCATTGACCCTAATGTC

GAM888  LOC91250  5' TCTGTAATCCCCGCACT     65330     A  T
                                AGT GC GGGATTACAGA
                                ||| || ||||||||||
                                TCA CG CCCTAATGTCT
                                  _ C
GAM888  LOC91286  3' ATGCCTGTAATCCTAGCCACT  65451     A         A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
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                                TCA CGATCCTAATGTC GTA
                                  C           C
GAM888  LOC91380  3'  CTGTAATCCCAACTAC      65860      C
                                GTAG TGGGATTACAG
                                |||| ||||||||||
                                CATC ACCCTAATGTC
                                  A
GAM888  LOC91380  3'  TGCCTGTAATCCCGGCACT    65864      A          A
                                AGT GCTGGGATTACAG CA
                                ||| |||||||||||| ||
                                TCA CGGCCCTAATGTC GT
                                  _           C
GAM888  LOC91380  3'  TGTAATCCCAGCTACTCA     65865    C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  LOC91574  3'  TCTGTAATCCCAGCACT      66521      A
                                AGT GCTGGGATTACAGA
                                ||| ||||||||||||||
                                TCA CGACCCTAATGTCT
                                  _
GAM888  LOC91664  3'  CTGTAATCCCAGCACT       66872      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC91750  3'  CTGTAATCCCAGCACT       67061      A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC91796  5'  ATGCCTGTAATCCCAGCACT   67210      A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM888  LOC91812  3'  GTGCCTGTAATCCCAGCTACTC 67242    C            A
          A                      A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACCCTAATGTC GTG
                                 C             C
GAM888  LOC91813  3'  GTGCCTGTAATCCCAGCTACTC 67259    C            A
          A                      A AGTAGCTGGGATTACAG CAT
                                | |||||||||||||||| |||
                                A TCATCGACCCTAATGTC GTG
                                 C             C
GAM888  LOC91963  5'  CTGTAATCCCAGCTACTTG    67694    _
                                CA GTAGCTGGGATTACAG
                                || ||||||||||||||||
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                                GT CATCGACCCTAATGTC
                                 T
GAM888  LOC92078 3' CTATAATCCCAGCACT      67980     A        C
                                AGT GCTGGGATTA AG
                                ||| |||||||||| ||
                                TCA CGACCCTAAT TC
                                  _         A
GAM888  LOC92078 3' TGTAATCCCAACTACTCA     67990   C    C
                                A AGTAG TGGGATTACA
                                | ||||| ||||||||||
                                A TCATC ACCCTAATGT
                                 C     A
GAM888  LOC92228 3' CTGTAATCCCAGCACT       68541     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LOC92267 3' CTGTAATCCCAGCACT       68613     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LOC92270 5' CTGTAATCCCAGCACT       68630     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LOC92270 5' TGTAATCCCAGCTACTCA     68637   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  LOC92283 3' ATGCCTGTAATCCCAGCACT   68744     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _           C
GAM888  LOC92299 3' CTGTAATCCCAGCACT       68809     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LOC92405 3' ATGTCTGTAATCCCAGCTACT  69192
                                AGTAGCTGGGATTACAGACAT
                                |||||||||||||||||||||
                                TCATCGACCCTAATGTCTGTA

GAM888  LOC92421 3' ATGCCTATAATCCCAGCACT   69212     A        C  A
                                AGT GCTGGGATTA AG CAT
                                ||| |||||||||| || |||
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                                TCA CGACCCTAAT TC GTA
                                  _        A  C
GAM888  LOC92465  5' ATGCCTGTAATCCCAGCACT   69402     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC92465  3' ATGTCTGTAGTCCCAGCCACTC 69403   C   A
             A                   A AGT GCTGGGATTACAGACAT
                                | ||| ||||||||||||||||
                                A TCA CGACCCTGATGTCTGTA
                                 C   C
GAM888  LOC92465  3' CTGTAATCCCAGCACT      69406     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LOC92465  5' TGTAATCCCAGCTACTCA    69415   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
                                A TCATCGACCCTAATGT
                                 C
GAM888  LOC92466  3' ATGCCTGTAATCCCAGCACT   69422     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC92482  3' CTGTAATCCCAGCACT      69488     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LOC92573  5' CTGTAATCCCAGCACT      69805     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC

                                  _
GAM888  LOC92573  5' TCTGTAATCCCAGCTTCT    69811    T
                                AG AGCTGGGATTACAGA
                                || ||||||||||||||
                                TC TCGACCCTAATGTCT
                                 T
GAM888  LOC92661  5' ATGCCTATAATCCCAGC     70078          C  A
                                GCTGGGATTA AG CAT
                                |||||||||| || |||
                                CGACCCTAAT TC GTA
                                      A  C
GAM888  LOC92771  3' TGTAATCCCAGCTACTCA    53078   C
                                A AGTAGCTGGGATTACA
                                | ||||||||||||||||
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                                A TCATCGACCCTAATGT
                                 C
GAM888  LOC93132  5'  CTGTAATCCCAGCACT      71488     A
                                AGT GCTGGGATTACAG
                                ||| ||||||||||||
                                TCA CGACCCTAATGTC
                                  _
GAM888  LOC93613  3'  ATGCCTGTAATCCCAGCACT   72694     A          A
                                AGT GCTGGGATTACAG CAT
                                ||| |||||||||||| |||
                                TCA CGACCCTAATGTC GTA
                                  _          C
GAM888  LOC93613  3'  CTGTAATCCCAGCTATT     72698
                                AGTAGCTGGGATTACAG
                                ||||||||||||||||
                                TTATCGACCCTAATGTC

GAM888  LOC96597  5'  CTGTAATCCCAGCTACTCA    66913    C
                                A AGTAGCTGGGATTACAG
                                | ||||||||||||||||
                                A TCATCGACCCTAATGTC
                                 C
GAM889  AF1Q      3'  GTTCTTCAGCTACATTGAG    22367      CAGA
                                CTCA    AGCTGAAGAAC
                                ||||    ||||||||||
                                GAGT    TCGACTTCTTG
                                  TACA
GAM889  BN51T     3'  GTTCTTGAATCTGTGAG      87497        AGCTG
                                CTCACAGA     AAGAAC
                                ||||||||     ||||||
                                GAGTGTCT     TTCTTG
                                     AAG__
GAM889  BSN       3'  CTTCTGTGCTCTGTGAG      12922        A_  T
                                CTCACAGA  GC GAAG
                                ||||||||  || ||||
                                GAGTGTCT  TG CTTC
                                     CG  T
GAM889  CELSR1    3'  TTCTTCAAATCAGGTGC      26490      CACA  AGC
                                GCACT    GA   TGAAGAA
                                |||||    ||   |||||||
                                CGTGG    CT   ACTTCTT
                                   A___  AA_
GAM889  CELSR3    3'  TCCCCAGTGGTGGGTGC      7404         AGAA    AA
                                GCACTCAC    GCTG  GA
                                ||||||||    ||||  ||
                                CGTGGGTG    TGAC  CT
                                     G___    CC
GAM889  GABRA2    3'  GCTCTGTTCATGAGTGCT     5864         _____     A
                                AGCACTC    ACAGA GC
                                |||||||    ||||| ||
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                                TCGTGAG   TGTCT CG
                                   TACT   _
GAM889  HOXC11   3'  TCCTCTGCGTGAGTGC     60175       AGAA  T  A
                                GCACTCAC   GC GA GA
                                ||||||||   || || ||
                                CGTGAGTG   CG CT CT
                                   _____  T  C
GAM889  IHPK1    3'  TCCTCAGCTTTGTGGCT    95764    ACT    A    A
                                AGC   CACAGA GCTGA GA
                                |||   |||||| ||||| ||
                                TCG   GTGTTT CGACT CT
                                  ____    _   C
GAM889  KIAA0857 3'  TCAGCTTTGGGGGC      66679    A  A   A
                                GC CTC CAGA GCTGA
                                || ||| |||| |||||
                                CG GGG GTTT CGACT
                                 _  _  _
GAM889  LY64     3'  CTTCTTACTCCTGTGAGT    18755       A  CT_
                                ACTCACAG AG   GAAG
                                |||||||| ||   ||||
                                TGAGTGTC TC   CTTC
                                    C  ATT
GAM889  MADH7    3'  TTTTCCTCCTGAGTGCTT    19749        CA  AGCT
                                AAGCACTCA  GA   GAAGA
                                |||||||||  ||   |||||
                                TTCGTGAGT  CT   CTTTT
                                    C_  C___
GAM889  MMP15    3'  TGGCCTCTGCGAGTGGTT    10078    G    A   A
                                AA CACTC CAGA GCTG
                                || ||||| |||| ||||
                                TT GTGAG GTCT CGGT
                                 G    C   C
GAM889  MYO1E    5'  GTTCCCATTGGCTCCTGTGAGT 17189          A   TG A__
            GCTT                   AAGCACTCACAG AGC  A   GAAC
                                |||||||||||| |||  |   ||||
                                TTCGTGAGTGTC TCG  T   CTTG
                                      C   GT ACC
GAM889  NME1     3'  TCTTGGAGCTGTGAGTTCT   4249     C      AAG  G
                                AG ACTCACAG   CT AAGA
                                || ||||||||   || ||||
                                TC TGAGTGTC   GG TTCT
                                 T       GA_  _
GAM889  NONO     3'  TCCTCAGCTTTCTCAGTGCT  82023       CACA      A
                                AGCACT    GAAGCTGA GA
                                ||||||    |||||||| ||
                                TCGTGA    TTTCGACT CT
                                   CTC_       C
GAM889  NR4A2    5'  GCTCCCTCCCTCCGTGAGTGTC 20532   A      A  ________
            C                    A GCACTCAC GA      AGC
                                | ||||||| ||      |||
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                                C TGTGAGTG CT      TCG
                                 C       C  CCCTCCC
GAM889  PHEMX    3'  TCTTCAGCTCCTTCCTGTGG   57371       A____
                                TCACAG     AGCTGAAGA
                                ||||||     |||||||||
                                GGTGTC     TCGACTTCT
                                   CTTCC
GAM889  PIK3R1   3'  TTCCTAAGCTGGAGTGCTT    68582        A  GAA   GAA
                                AAGCACTC CA   GCT   GAA
                                |||||||| ||   |||   |||
                                TTCGTGAG GT   CGA   CTT
                                     _ ___   ATC
GAM889  PIK3R3   3'  GGCCTCTGTGAGGCTT      61061      A       A
                                AAGC CTCACAGA GCT
                                |||| |||||||| |||
                                TTCG GAGTGTCT CGG
                                  _       C
GAM889  PIN4     3'  CTTGTATTCTGTGAAAGCT    20627     AC       GCTG
                                AGC  TCACAGAA    AAG
                                |||  ||||||||    |||
                                TCG  AGTGTCTT    TTC
                                  AA       ATG_
GAM889  POLR2A   3'  TTCCTGCTGTGAGTGGTT     6264     G        A  CTGAA
                                AA CACTCACAG AG     GAA
                                || |||||||| ||     |||
                                TT GTGAGTGTC TC     CTT
                                 G        G _____
GAM889  PYGO2    3'  GTTCTTCAACTTTCGGCGC    63990    A  CACA    C
                                GC CT    GAAG TGAAGAAC
                                || ||    |||| ||||||||
                                CG GG    TTTC ACTTCTTG
                                 C  C___    A
GAM889  SCNN1A   3'  TTACTTTTGTGAACGCTT     6427       AC        C
                                AAGC  TCACAGAAG TGA
                                ||||  ||||||||| |||
                                TTCG  AGTGTTTTC ATT
                                  CA       _
GAM889  SIGLEC6  5'  TTCCTCTTCTGTGAACAGC    59928    AC_       CT
                                GC   TCACAGAAG  GAA
                                ||   |||||||||  |||
                                CG   AGTGTCTTC  CTT
                                 ACA        TC
GAM889  SOCS4    3'  TTCTTCAGTAAAGCTGAATGTT 55115      C   CAGAA
                                AGCA TCA     GCTGAAGAA
                                |||| |||    |||||||||
                                TTGT AGT     TGACTTCTT
                                  A  CGAAA
GAM889  STARD4   3'  TCCCCTAATTCTGTGGGTGC   57518           GCTGAA
                                GCACTCACAGAA     GA
                                ||||||||||||     ||
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                                CGTGGGTGTCTT     CT
                                      AATCCC
GAM889  SYBL1    3'  GTTCCTTTTTCTTCTGTGA   18897        CT   _
                                TCACAGAAG  GAAG AAC
                                |||||||||  |||| |||
                                AGTGTCTTC  TTTC TTG
                                     TT    C
GAM889  TAPBP    3'  GTTCTTCAGCCCTAGATGGTGC 12132       CACAGAA
          T                      AGCACT      GCTGAAGAAC
                                |||||||      ||||||||||
                                TCGTGG      CGACTTCTTG
                                   TAGATCC
GAM889  TNFAIP2  3'  CTGACCTGCCTGTGAGTGC   20829         AA  TGA__
                                GCACTCACAG  GC    AG
                                |||||||||  ||    ||
                                CGTGAGTGTC  CG    TC
                                      __  TCCAG
GAM889  USH3A    3'  CAGTTCTGTAAGTCTT     53783     C   C     G
                                AAG ACT ACAGAA CTG
                                ||| ||| |||||| |||
                                TTC TGA TGTCTT GAC
                                  _   A     _
GAM889  BCDO     3'  TTCTTTCTGTGGGTGCTT    33826            CT
                                AAGCACTCACAGAAG  GAA
                                ||||||||||||||  |||
                                TTCGTGGGTGTCTTT  CTT
                                                 __
GAM889  CST9L    3'  TCTTCAGTGGCTGAGCAGCTT  54619      ACTCA   AA
                                AAGC    CAG  GCTGAAGA
                                ||||    |||  ||||||||
                                TTCG    GTC  TGACTTCT
                                  ACGA_   GG
GAM889  DKFZP564O0823 3'  GTTCTTTATTTATAAGTGCTT  59520        CACAG   C
                                AAGCACT    AAG TGAAGAAC
                                |||||||    ||| ||||||||
                                TTCGTGA    TTT ATTTCTTG
                                    ATA__   _
GAM889  DREV1    3'  TTCTGGAATCCGTGAGTGC   32073         A  AG  GA
                                GCACTCAC GA  CT  AGAA
                                |||||||| ||  ||  ||||
                                CGTGAGTG CT  GG  TCTT
                                     C  AA  __
GAM889  EVI5     3'  CTTCAGCTTCCCGAGT     19000      ACA
                                ACTC   GAAGCTGAAG
                                ||||   ||||||||||
                                TGAG   CTTCGACTTC
                                  CC_
GAM889  EZFIT    3'  TTCTTCATAGGTAGTGCTT   41114        C  AGAAGC
                                AAGCACT AC     TGAAGAA
                                ||||||| ||     |||||||
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                                TTCGTGA TG     ACTTCTT
                                   _ GAT___
GAM889  FLJ10040  3' CTCCAGCCCTGGAGGCTT   35752     A  A  AA   A
                                AAGC CTC CAG  GCTG AG
                                |||| ||| |||  |||| ||
                                TTCG GAG GTC  CGAC TC
                                  _  _  C_   C
GAM889  FLJ12150  3' TCTCCAGCAGGGCAGAGTGTTT 45352        ACAGAA   A
                                AAGCACTC     GCTG AGA
                                ||||||||     |||| |||
                                TTTGTGAG     CGAC TCT
                                     ACGGGA   C
GAM889  FLJ12704  5' TTTCCCTTCTGTGAG      46539         CT
                                CTCACAGAAG  GAAG
                                ||||||||||  ||||
                                GAGTGTCTTC  CTTT
                                      C_
GAM889  FLJ13912  3' TCCCTGGCTCTGTGAGTCTT  42866    C       A   AA
                                AAG ACTCACAGA GCTG  GA
                                ||| |||||||| ||||  ||
                                TTC TGAGTGTCT CGGT  CT
                                 _       _   CC
GAM889  FLJ14107  3' GTTCCTCAGCTTCCAGGATG  46698   C  ACA      A
                                CA TC   GAAGCTGA GAAC
                                || ||   |||||||| ||||
                                GT AG   CTTCGACT CTTG
                                 _ GAC       C
GAM889  FLJ14154  3' TCTTCAGCTCCCCTCCCTGCTT 45821      CTCACAGA
                                AAGCA       AGCTGAAGA
                                |||||       |||||||||
                                TTCGT       TCGACTTCT
                                   CCCTCCCC
GAM889  FLJ20123  5' CTGTCTCCTGGGAGTGCTT   34586       A  A  CTGA
                                AAGCACTC CAG AG    AG
                                |||||||| ||| ||    ||
                                TTCGTGAG GTC TC    TC
                                     G  C  TG__
GAM889  FLJ20345  3' TCCCCAGCCTGTGAGTCT    35024    C      AA   AA
                                AG ACTCACAG  GCTG  GA
                                || ||||||||  ||||  ||
                                TC TGAGTGTC  CGAC  CT
                                 _       ___   CC
GAM889  FLJ22548  5' TCTGCGGCTCTGTGAGCGC   42402    A      A   A
                                GC CTCACAGA GCTG AGA
                                || |||||||| |||| |||
                                CG GAGTGTCT CGGC TCT
                                 C       _   G
GAM889  FLJ23322  3' GCCTGTGGAGTGCTT       88788        _   AA
                                AAGCACTC ACAG  GC
                                |||||||| ||||  ||
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                                TTCGTGAG TGTC  CG
                                    G   __
GAM889  FLJ23467  3'  TTCCTTCCCAAGAGTGCTT   44712       ACA_   CT
                                AAGCACTC   GAAG  GAA
                                ||||||||   ||||  |||
                                TTCGTGAG   CTTC  CTT
                                    AACC   __
GAM889  GMEB2     3'  CTGAGCCCCTGTGAGTGC    24730        AA   GA
                                GCACTCACAG  GCT  AG
                                ||||||||||  |||  ||
                                CGTGAGTGTC  CGA  TC
                                     CC   G_
GAM889  GMEB2     3'  CTTCAGCTTGGGCTGCTT    24732      _   CAGA
                                AAGCA CTCA    AGCTGAAG
                                |||||| ||||    ||||||||
                                TTCGT GGGT    TCGACTTC
                                   C   ____
GAM889  H2AFJ     3'  TCAGCTTCTGTTAGTACTT   36843     C   C
                                AAG ACT ACAGAAGCTGA
                                ||| ||| ||||||||||
                                TTC TGA TGTCTTCGACT
                                  A   T
GAM889  KIAA0193  3'  TCCGTGGCCTCCCGTGAGTGC  28662        A_  A    AA
                                GCACTCAC  GA GCTG  GA
                                ||||||||  || ||||  ||
                                CGTGAGTG  CT CGGT  CT
                                     CC  C    GC
GAM889  KIAA1041  3'  TACCTTCTGTGAATGCTT    30138      C       C
                                AAGCA TCACAGAAG TG
                                ||||| ||||||||| ||
                                TTCGT AGTGTCTTC AT
                                   A       C
GAM889  KIAA1297  3'  CGGTCTCTATGAGTGCT     72177        C   AG
                                AGCACTCA AGA  CTG
                                |||||||| |||  |||
                                TCGTGAGT TCT  GGC
                                     A   CT
GAM889  KIAA1328  3'  CTTCAGCTTGCAGTG       61648      _  CAGA
                                CACT CA    AGCTGAAG
                                |||| ||    ||||||||
                                GTGA GT    TCGACTTC
                                  C  ____
GAM889  KIAA1373  3'  TTCTTCAGATTCAAAATGCTT  70958      CTCACA   G
                                AAGCA     GAA CTGAAGAA
                                |||||     ||| ||||||||
                                TTCGT     CTT GACTTCTT
                                   AAAA__   A
GAM889  KIAA1500  3'  GTTCTAGGCAGCTCTGTGAG   64122        A    A__
                                CTCACAGA GCTG   AGAAC
                                |||||||| ||||   |||||
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                                GAGTGTCT CGAC   TCTTG
                                    _   GGA
GAM889  KIAA1530  3'  GTTCCAGAGGGCTTCTGCGAGT 67958    C   A      GAA__
            CCT                   AG ACTC CAGAAGCT    GAAC
                                || |||| ||||||||    ||||
                                TC TGAG GTCTTCGG    CTTG
                                 C   C       GAGAC
GAM889  LRRFIP2   3'  GCAATTCTATGAGTGCT     34783        C   __
                                AGCACTCA AGAA  GC
                                |||||||| ||||  ||
                                TCGTGAGT TCTT  CG
                                    A   AA
GAM889  MACF1     3'  GTTCTTCAGCTCCGACCATGTT 23891     CTCACA  A
                                AGCA     GA GCTGAAGAAC
                                ||||     || ||||||||||
                                TTGT     CT CGACTTCTTG
                                  ACCAGC  _
GAM889  MAL2      3'  TCCTCATCTGAGAGTGCTT    53557        A   AGC   A
                                AAGCACTC CAGA   TGA GA
                                |||||||| ||||   ||| ||
                                TTCGTGAG GTCT   ACT CT
                                    A   ___   C
GAM889  MARCKS    3'  GTTCTAATTTTCTGTGAG    9869         CTGA
                                CTCACAGAAG   AGAAC
                                ||||||||||   |||||
                                GAGTGTCTTT   TCTTG
                                     TAA_
GAM889  MGC13138  3'  TCTCGGCTTCCGCAAGTGCT  53028      CACA      A
                                AGCACT   GAAGCTGA GA
                                ||||||   |||||||| ||
                                TCGTGA   CTTCGGCT CT
                                   ACGC      _
GAM889  MGC4268   3'  TCCCTAGCTGTGAGTGC     48748        GAA   AA
                                GCACTCACA   GCTG  GA
                                |||||||||   ||||  ||
                                CGTGAGTGT   CGAT  CT
                                    ___    CC
GAM889  NICN1     3'  TTCTCACCTGTGAGTTCTT   50296    C      AAGC   A
                                AAG ACTCACAG    TGA GAA
                                ||| ||||||||    ||| |||
                                TTC TGAGTGTC    ACT CTT
                                  T       C___   _
GAM889  PPP1R10   3'  CTTCAACTTTCTGTGA      10733        _ C
                                TCACAGAA G TGAAG
                                |||||||| | |||||
                                AGTGTCTT C ACTTC
                                     T A
GAM889  PPP1R10   3'  TGGCTTCTGTGAGGC       10740    A
                                GC CTCACAGAAGCTG
                                || ||||||||||||
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                                CG GAGTGTCTTCGGT
                                  _
GAM889  PTP4A1   3'  TCCCCCTTCTAGAGTGCTT   12943       AC    CT_
                                AAGCACTC  AGAAG   GA
                                ||||||||  |||||   ||
                                TTCGTGAG  TCTTC   CT
                                    A_    CCC
GAM889  SDC3     3'  TCCCTCCTGTGAGTCCTT    27763    C      A  CT
                                AAG ACTCACAG AG  GA
                                ||| |||||||| ||  ||
                                TTC TGAGTGTC TC  CT
                                  C       C  C_
GAM889  SNRPD1   3'  TCTTCATTCTGTGGC      22681    ACT     GC
                                GC   CACAGAA  TGAAGA
                                ||   |||||||  ||||||
                                CG   GTGTCTT  ACTTCT
                                 ____     __
GAM889  SRP9     3'  CTTGCATACTTCTGTGA     79191        C_ _
                                TCACAGAAG  TG AAG
                                |||||||||  || |||
                                AGTGTCTTC  AC TTC
                                     AT  G
GAM889  SSH2     3'  TGGCTGTCCTGTGAGTCCT   62217    C      A__
                                AG ACTCACAG   AGCTG
                                || ||||||||   |||||
                                TC TGAGTGTC   TCGGT
                                 C       CTG
GAM889  TXN2     3'  CTCCAGCCCTGAGTGCTT    25009        CAGAA   A
                                AAGCACTCA    GCTG AG
                                |||||||||    |||| ||
                                TTCGTGAGT    CGAC TC
                                     CC___    C
GAM889  USP15    3'  TTCACTCTGTGAGTGC      20884          A C
                                GCACTCACAGA G TGAA
                                |||||||||||| | ||||
                                CGTGAGTGTCT C ACTT
                                     _ _
GAM889  LOC125929 3'  TTTCAAGAACTTCTGTGAAGCT 75676     AC       C___
                                AGC  TCACAGAAG    TGAAG
                                |||  |||||||||   |||||
                                TCG  AGTGTCTTC    ACTTT
                                  A_        AAGA
GAM889  LOC126603 5'  CTTCAGCTTCTCTCTGACTG   75393    C   C__
                                CA TCA   AGAAGCTGAAG
                                || |||   ||||||||||
                                GT AGT   TCTTCGACTTC
                                 C   CTC
GAM889  LOC126669 3'  GTTCTCTGAGCTCTGAATGCT  75415     CTCA   A   GA_
                                AGCA    CAGA GCT   AGAAC
                                ||||    |||| |||   |||||
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                                TCGT   GTCT CGA  TCTTG
                                  AA__   _  GTC
GAM889  LOC139709 5'  TCTTGCCTGCTGTGAGTGC   75384        AA_  TG
                                GCACTCACAG  GC  AAGA
                                ||||||||||  ||  ||||
                                CGTGAGTGTC  CG  TTCT
                                     GTC  __
GAM889  LOC144705 3'  CAGACTTGCCTGTGAGTGC   83182        __  _
                                GCACTCACAG  AAG CTG
                                ||||||||||  ||| |||
                                CGTGAGTGTC  TTC GAC
                                     CG  A
GAM889  LOC145858 5'  GTTCCTGAATTTCTGTGACCGC 77547     AC       CTGAA
          TT                     AAGC  TCACAGAAG    GAAC
                                ||||  |||||||||    ||||
                                TTCG  AGTGTCTTT    CTTG
                                  CC       AAGTC
GAM889  LOC148046 3'  GTTCCCTGGTTCTGTGAG    84108        G  AA
                                CTCACAGAA CTG  GAAC
                                |||||||||  |||  ||||
                                GAGTGTCTT GGT  CTTG
                                     _  CC
GAM889  LOC148479 3'  TCTTCAGCAGTTCAAGTACTT  78880    C  CAC  AA
                                AAG ACT   AG  GCTGAAGA
                                |||  |||   ||  ||||||||
                                TTC TGA   TT  CGACTTCT
                                  A   AC_  GA
GAM889  LOC149668 3'  GGCTTCTGTAGGTGCT     84547      TC
                                AGCAC  ACAGAAGCT
                                |||||  |||||||||
                                TCGTG  TGTCTTCGG
                                   GA
GAM889  LOC150282 5'  CTTCCTTCTGTATATGCTT   79725      CTC      CT
                                AAGCA   ACAGAAG  GAAG
                                |||||   |||||||  ||||
                                TTCGT   TGTCTTC  CTTC
                                   ATA      __
GAM889  LOC151996 5'  TCGGGTGCTCCTGTGAGTG   85539        A  TGAA
                                CACTCACAG AGC    GA
                                |||||||||  |||    ||
                                GTGAGTGTC TCG    CT
                                     C   TGGG
GAM889  LOC152698 3'  TCCCCGGCTGTGGCGCTT    60427     A T    GAA    AA
                                AAGC C CACA   GCTG  GA
                                ||||  |  ||||   ||||  ||
                                TTCG G GTGT   CGGC  CT
                                  C _    ____    CC
GAM889  LOC152860 3'  TGGCCCCCGTGGGTGCTT    80705        AGAA
                                AAGCACTCAC    GCTG
                                ||||||||||    ||||
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                                TTCGTGGGTG   CGGT
                                     CCCC
GAM889  LOC157280 3'  TCCCCGGCTGTGGCGCTT   73913     A T   GAA   AA
                                AAGC C CACA  GCTG  GA
                                |||| | ||||  ||||  ||
                                TTCG G GTGT  CGGC  CT
                                  C _   ___   CC
GAM889  LOC157313 5'  CGGCTGCGGGTGCTT      81398       A  GAA
                                AAGCACTC CA  GCTG
                                |||||||| ||  ||||
                                TTCGTGGG GT  CGGC
                                     C ___
GAM889  LOC157376 3'  TCCCCTTCTGTGATGCT     81432     C       CT
                                AGCA TCACAGAAG  GA
                                |||| |||||||||  ||
                                TCGT AGTGTCTTC  CT
                                  _       CC
GAM889  LOC158293 3'  TTCCTCAGCTTCTGCTTCTGGT 81866    G  CTCA       A
          T                      AA CA   CAGAAGCTGA GAA
                                || ||   |||||||||| |||
                                TT GT   GTCTTCGACT CTT
                                 G  CTTC        C
GAM889  LOC196955 5'  TTCTTCAGTTTTGAG      77393     CAG
                                CTCA  AAGCTGAAGAA
                                ||||  ||||||||||
                                GAGT  TTTGACTTCTT
                                  ___
GAM889  LOC199704 5'  CAGCTCCTATGAGTGTT     88326       C  A
                                AGCACTCA AG AGCTG
                                |||||||| || |||||
                                TTGTGAGT TC TCGAC
                                     A  C
GAM889  LOC199858 3'  TTCTTCAGTTTTGAG      88426     CAG
                                CTCA  AAGCTGAAGAA
                                ||||  ||||||||||
                                GAGT  TTTGACTTCTT
                                  ___
GAM889  LOC200300 3'  TTCCCCTACTTTGAGTGCT   89970       C  A  CT
                                AGCACTCA AG AG  GAA
                                |||||||| || ||  |||
                                TCGTGAGT TC TC  CTT
                                     T  A  CC
GAM889  LOC200304 3'  TTCCCCTACTTTGAGTGCT   89988       C  A  CT
                                AGCACTCA AG AG  GAA
                                |||||||| || ||  |||
                                TCGTGAGT TC TC  CTT
                                     T  A  CC
GAM889  LOC200305 3'  TTCCCCTACTTTGAGTGCT   89982       C  A  CT
                                AGCACTCA AG AG  GAA
                                |||||||| || ||  |||
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                                TCGTGAGT TC TC  CTT
                                     T  A  CC
GAM889  LOC200895 3'  CTTCAGCTGAGCAGTT     88919     A_   CAGAA
                                AGC  CTCA    GCTGAAG
                                |||  ||||    |||||||
                                TTG  GAGT    CGACTTC
                                  AC   _____
GAM889  LOC202025 3'  TAGATTTCTGTGAGTCTT    90296     C         _
                                AAG ACTCACAGAAG CTG
                                ||| |||||||||| |||
                                TTC TGAGTGTCTTT GAT
                                  _         A
GAM889  LOC221301 5'  CTTCAGCTCTGTGCGTGTT   91888      T     A
                                AGCAC CACAGA GCTGAAG
                                ||||| |||||| |||||||
                                TTGTG GTGTCT CGACTTC
                                   C     _
GAM889  LOC221540 3'  TCATCTCCCTGAGTGCT     93841        CA  A C
                                AGCACTCA  GA G TGA
                                ||||||||  || | |||
                                TCGTGAGT  CT C ACT
                                     CC  _ T
GAM889  LOC254268 3'  CTTCCCTTCCTGTGAGTTCT  95407    C      _  CT
                                AG ACTCACAG AAG  GAAG
                                || ||||||| |||  ||||
                                TC TGAGTGTC TTC  CTTC
                                 T       C   C_
GAM889  LOC255448 3'  TCCCCGGCTGTGGCGCTT    94651     A T   GAA   AA
                                AAGC C CACA   GCTG  GA
                                |||| | ||||   ||||  ||
                                TTCG G GTGT   CGGC  CT
                                  C _    ___    CC
GAM889  LOC257451 3'  GTTCTTCAACTTTCGGCGC   95560    A  CACA   C
                                GC CT    GAAG TGAAGAAC
                                || ||    |||| ||||||||
                                CG GG    TTTC ACTTCTTG
                                 C  C___    A
GAM889  LOC257458 5'  CTGAAGTTGCATGAGTGCT   67792        CAGA   GA
                                AGCACTCA    AGCT  AG
                                ||||||||    ||||  ||
                                TCGTGAGT    TTGA  TC
                                     ACG_    AG
GAM889  LOC257476 3'  TCCTCAGCTTTGTGGCT     61259     ACT     A    A
                                AGC   CACAGA GCTGA GA
                                |||   |||||| ||||| ||
                                TCG   GTGTTT CGACT CT
                                  ___     _    C
GAM889  LOC257489 5'  CTGGAAGCTTCTGCAAGCCCT  65613    CA  CA      GA_
                                AG  CT  CAGAAGCT   AG
                                ||  ||  ||||||||   ||
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                                TC  GA  GTCTTCGA   TC
                                 CC  AC       AGG
GAM889  LOC257545 3'  TCATCTCCCTGAGTGCT     97809        CA  A C
                                AGCACTCA  GA G TGA
                                ||||||||  || | |||
                                TCGTGAGT  CT C ACT
                                    CC  _ T
GAM889  LOC257598 3'  TCATCTCCCTGAGTGCT     97924        CA  A C
                                AGCACTCA  GA G TGA
                                ||||||||  || | |||
                                TCGTGAGT  CT C ACT
                                    CC  _ T
GAM889  LOC90719  3'  TCAGCCTCTGTAAGTG      63889      C     A
                                CACT ACAGA GCTGA
                                |||| ||||| |||||
                                GTGA TGTCT CGACT
                                  A     C
GAM889  LOC91548  5'  GTTCTTCATTTGGTGA      66416      AG   C
                                TCAC  AAG TGAAGAAC
                                ||||  ||| ||||||||
                                AGTG  TTT ACTTCTTG
                                  G_  _
GAM889  LOC91796  3'  TCTTCAGCTCTGGATGT     67214     C  A    A
                                GCA TC CAGA GCTGAAGA
                                ||| || |||| ||||||||
                                TGT AG GTCT CGACTTCT
                                  _ _   _
GAM889  LOC92716  3'  CTGAAGCTCTGTGAGGC     70378    A       A   GA
                                GC CTCACAGA GCT  AG
                                || |||||||| |||  ||
                                CG GAGTGTCT CGA  TC
                                 _       _  AG
GAM889  LOC93587  5'  TCTTCAGCTCGAGGC       72650    A   ACA  A
                                GC CTC   GA GCTGAAGA
                                || |||   || ||||||||
                                CG GAG   CT CGACTTCT
                                 _  ____ _
GAM890  ABCA1     3'  GGATCTATTTTTGCACTGGA   18549    A   GGAG
                                TC CGG    AAAAATGGGTCC
                                || |||    ||||||||||||
                                AG GTC    TTTTTATCTAGG
                                 _  ACG_
GAM890  ABCB10    3'  GGTTTTGTATTTTCTTTTCTTG 23888        __      _  GG T
            TGG                   CACGGG  GAGAAAA AT  G CC
                                ||||||  ||||||| ||  | ||
                                GTGTTC  TTCTTTT TG  T GG
                                   TT      A  TT T
GAM890  ABL1      3'  CTTTTTCATTTTTTTCTCTCTG 23612     C           TCC
            G                     TCA GGGGAGAAAAATGGG
                                ||| ||||||||||||||
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                                GGT TCTCTTTTTTTACTT
                                  C           TTTCT
GAM890  ABL1    3'  CTTTTTCATTTTTTTCTCTCTG 17675    C          TCC
              G                   TCA GGGGAGAAAAATGGG
                                  ||| ||||||||||||||
                                GGT TCTCTTTTTTTACTT
                                  C           TTTCT
GAM890  ABL2    3'  GACTTGTTTTCCTGTG     23615       GAAA  TG
                                CACGGGGA   AA  GGTC
                                ||||||||   ||  ||||
                                GTGTCCTT   TT  TCAG
                                     ____  GT
GAM890  ABL2    3'  GACTTGTTTTCCTGTG     17681       GAAA  TG
                                CACGGGGA   AA  GGTC
                                ||||||||   ||  ||||
                                GTGTCCTT   TT  TCAG
                                     ____  GT
GAM890  ABP1    3'  GGACCTATAGACCTGTG    63112      GAGAAAA
                                CACGGG     ATGGGTCC
                                ||||||     ||||||||
                                GTGTCC     TATCCAGG
                                   AGA____
GAM890  ACADM   3'  GGGCTTTAACGTTTTTTCCAGT 3404      GG      AT___
              GA                  TCAC  GGAGAAAA    GGGTCC
                                  ||||  ||||||||    ||||||
                                AGTG  CCTTTTTT    TTCGGG
                                  A_      GCAAT
GAM890  ACADS   3'  GGGTCTGTCTTTTCCTTG    3409        AA   GT
                                CGGGGAGAA  ATGG  CC
                                |||||||||  ||||  ||
                                GTTCCTTTT  TGTC  GG
                                     C_    TG
GAM890  ACLY    5'  GGGTTCGTCGGGCCTGTGG   65061       GA_  AAAA  GG
                                TCACGGG   GA    TG  TCC
                                |||||||   ||    ||  |||
                                GGTGTCC   CT    GC  GGG
                                    GGG   ____  TT
GAM890  ADAM11  3'  GGGTCTTATCTCTCTGGGA   9970    A      AAAAT  GT
                                TC CGGGGAGA    GG  CC
                                || ||||||||    ||  ||
                                AG GTCTCTCT    TC  GG
                                  G       AT___  TG
GAM890  ADAM11  3'  GGGTCTTATCTCTCTGGGA   41218   A      AAAAT  GT
                                TC CGGGGAGA    GG  CC
                                || ||||||||    ||  ||
                                AG GTCTCTCT    TC  GG
                                  G       AT___  TG
GAM890  ADAM19  3'  GGTGCCTTTTTTCCTTGT    52711         AAT   _
                                ACGGGGAGAAA   GGGT CC
                                ||||||||||   |||| ||
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                                TGTTCCTTTTT  TCCG GG
                                      ___   T
GAM890  ADCY6   3'  GGGCCTGTCCACACCCTGGA  40620   A   AGAAAA
                                TC CGGGG    ATGGGTCC
                                || |||||    ||||||||
                                AG GTCCC    TGTCCGGG
                                  _   ACACC_
GAM890  ADCY6   3'  GGGCCTGTCCACACCCTGGA  30935   A   AGAAAA
                                TC CGGGG    ATGGGTCC
                                || |||||    ||||||||
                                AG GTCCC    TGTCCGGG
                                  _   ACACC_
GAM890  ADRA1A  3'  GGACTACACATTCTTCTGTGG  52789      G   AAATG
                                TCACGGG AGAA    GGTCC
                                ||||||| ||||    |||||
                                GGTGTCT TCTT    TCAGG
                                    _   ACACA
GAM890  ADRA2B  3'  GGATCTGTGGTTCCTTTG    5463      A  AA
                                CGGGG GAA  ATGGGTCC
                                ||||| |||  ||||||||
                                GTTTC CTT  TGTCTAGG
                                   _  GG
GAM890  ADRBK1  3'  GGGCCCGTTGTCTCCCTG    7870       AA
                                CGGGGAGA  AATGGGTCC
                                ||||||||  |||||||||
                                GTCCCTCT  TTGCCCGGG
                                    G_
GAM890  AF5Q31  3'  GGAATAGTTTTCTCCTCGT   27022         ATGGG
                                ACGGGGAGAAAA    TCC
                                ||||||||||||    |||
                                TGCTCCTCTTTT    AGG
                                      GATA_
GAM890  AIRE    5'  GGGCCTGGCCCCACTGCCCTGT 5398       _  AAAAA_
          GA                    TCACGGGG AG    TGGGTCC
                                |||||||| ||    |||||||
                                AGTGTCCC TC    GTCCGGG
                                    G  ACCCCG
GAM890  ALDH1A1 3'  GACAAAATTTTTCTTTTCTTGA 5481    C GG      GG_  C
                                TCA G  GAGAAAAAT  GTC
                                ||| |  |||||||||  |||
                                AGT C  TTCTTTTTA  CAG
                                  T TT       AAA
GAM890  AMFR    3'  GGCTCATGCACCCCTGA    57246    C   AGAAAA
                                TCA GGGG    ATGGGTC
                                ||| ||||    |||||||
                                AGT CCCC    TACTCGG
                                  _   ACG___
GAM890  AMFR    3'  GGCTCATGCACCCCTGA    6696     C   AGAAAA
                                TCA GGGG    ATGGGTC
                                ||| ||||    |||||||
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                                AGT CCCC     TACTCGG
                                  _   ACG___
GAM890  AMPD3    3'  GGGCCAGGATTTTCCCTG    4899         AAATG
                                CGGGGAGAA    GGTCC
                                |||||||||    |||||
                                GTCCCTTTT    CCGGG
                                     AGGA_
GAM890  ANK1     3'  GGGCCTGAGTTTCCCCG     40029        AAAA
                                CGGGGAGA   TGGGTCC
                                ||||||||   |||||||
                                GCCCCTTT   GTCCGGG
                                     GA__
GAM890  ANK1     3'  GGGCCTGAGTTTCCCCG     60391        AAAA
                                CGGGGAGA   TGGGTCC
                                ||||||||   |||||||
                                GCCCCTTT   GTCCGGG
                                     GA__
GAM890  ANK1     3'  GGGCCTGAGTTTCCCCG     3475         AAAA
                                CGGGGAGA   TGGGTCC
                                ||||||||   |||||||
                                GCCCCTTT   GTCCGGG
                                     GA__
GAM890  AP1S1    3'  GGACCCCCCTCTTTCTCCTTG  54033          AAT__
                                CGGGGAGAAA    GGGTCC
                                ||||||||||    ||||||
                                GTTCCTCTTT    CCCAGG
                                      CTCCC
GAM890  APBA1    3'  GGACTCTCCTCTTCGTGG    69918          AAAAAT
                                TCACGGGGAG     GGGTCC
                                ||||||||||     ||||||
                                GGTGCTTCTC     CTCAGG
                                      CT____
GAM890  APC      3'  TGTTTTTGTCCTTGTGA     3481           G
                                TCACGGGGA AAAAATG
                                ||||||||| |||||||
                                AGTGTTCCT TTTTTGT
                                     G
GAM890  APLP2    3'  GGTGTATTTTTATTTTCCTGTG 90897          __     G T
          A                      TCACGGGGAGA  AAAATG G CC
                                 ||||||||||  |||||| | ||
                                 AGTGTCCTTTT  TTTTAT T GG
                                       AT     G _
GAM890  APPBP2   3'  TATTTTTTCACTTGTGA     21081        GA
                                TCACGGG  GAAAAATG
                                |||||||  ||||||||
                                AGTGTTC  TTTTTTAT
                                    AC
GAM890  APPL     3'  GCCTTTTTTTTTCTTTG     23926          T
                                CGGGGAGAAAAA GGGT
                                |||||||||||| ||||
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                                GTTTCTTTTTTT TCCG
                                       T
GAM890  APTX     5' GGATCTGTTTTTCTAGTGA   34660     GGGG
                                TCAC   AGAAAAATGGGTCC
                                ||||   ||||||||||||||
                                AGTG   TCTTTTTGTCTAGG
                                  A___
GAM890  ARF4L    3' TTCTTATTTTTCTTCTCTGG  69817    C          TCC
                                TCA GGGGAGAAAAATGGG
                                ||| ||||||||||||||
                                GGT CTCTTCTTTTTATTC
                                  _          TTT
GAM890  ARHGEF7  3' GCCTTTTCTTTCTGTGG    14007      GG    AAT
                                TCACGG  AGAAA   GGGT
                                ||||||  |||||   ||||
                                GGTGTC  TCTTT   TCCG
                                   TT    ___
GAM890  ASNA1    3' GGGTCCATTCCCCCTGGTGG  62979     __   A  AAA   GT
                                TCAC  GGGG GA   ATGG  CC
                                ||||  |||| ||   ||||  ||
                                GGTG  CCCC CT   TACC  GG
                                  GT   _ ___    TG
GAM890  ASPH     3' GGATTTCTTTTTTCTTTTTGTG 50630           T_
          A                      TCACGGGGAGAAAAA  GGGTCC
                                 ||||||||||||||  ||||||
                                 AGTGTTTTTCTTTTT  TTTAGG
                                       TC
GAM890  ASPH     3' GGATTTCTTTTTTCTTTTTGTG 50618           T_
          A                      TCACGGGGAGAAAAA  GGGTCC
                                 ||||||||||||||  ||||||
                                 AGTGTTTTTCTTTTT  TTTAGG
                                       TC
GAM890  ASPH     3' GATTCATTATGCTGTGG     50617       GGAGAAA
                                TCACGG      AATGGGTC
                                ||||||      ||||||||
                                GGTGTC      TTACTTAG
                                   GTA____
GAM890  ASTN     3' TCCATTCATTTTTTTTTCCCTG 69336    C  GG         CC
          A                      TCA GG  AGAAAAATGGGT
                                 ||| ||  ||||||||||||
                                 AGT CC  TTTTTTTACTTA
                                   C  TT         CCTT
GAM890  ATP10C   3' GGATGTCTTTCTCCTCTGG   44412    C       A  GG
                                TCA GGGGAGAAA AT  GTCC
                                ||| |||||||| ||  ||||
                                GGT CTCCTCTTT TG  TAGG
                                  _       C __
GAM890  ATP6V1G2 3' GGATCCAATAATTTTCCTGTGA 55320          AAAA
                                TCACGGGGAGA   TGGGTCC
                                ||||||||||   |||||||
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                                AGTGTCCTTTT  ACCTAGG
                                     AATA
GAM890  ATP6V1G2  3'  GGATCCAATAATTTTCCTGTGA 56280        AAAA
                                TCACGGGGAGA  TGGGTCC
                                ||||||||||  |||||||
                                AGTGTCCTTTT  ACCTAGG
                                     AATA
GAM890  ATP7A   3'  GGATTTAGAAATTCCCTTGTGA 3527       A  AAA_
                                TCACGGGG GAA  TGGGTCC
                                |||||||| |||  |||||||
                                AGTGTTCC CTT  ATTTAGG
                                   _  AAAG
GAM890  ATP7A   3'  TTTGTTTTTTTCTCTG    3539          GG
                                CGGGGAGAAAAAT  G
                                ||||||||||||  |
                                GTCTCTTTTTTTG  T
                                      TT
GAM890  ATP8B2   5'  GGACAGTGCCTTCTTCTCTGG  65231    C     AAATGG
                                TCA GGGGAGAA    GTCC
                                ||| ||||||||    ||||
                                GGT CTCTTCTT    CAGG
                                  _     CCGTGA
GAM890  B3GALT5  5'  GGACTTGCTTTTTTCT    52580       AT
                                GGAGAAAA  GGGTCC
                                ||||||||  ||||||
                                TCTTTTTT  TTCAGG
                                    CG
GAM890  B3GAT1   3'  GGGCCCCTGCTCTTCCCGAGA  53977   A     AAAAT
                                TC CGGGGAGA    GGGTCC
                                || ||||||||    ||||||
                                AG GCCCTTCT    CCCGGG
                                 A      CGTC_
GAM890  B4GALT5  3'  GGATTCACTCTTCCC      16509       AAAA
                                GGGGAGA   TGGGTCC
                                |||||||   |||||||
                                CCCTTCT   ACTTAGG
                                   C___
GAM890  BAZ2A   3'  GGGCTCTGCTTTTTCCCCCTGG 25606    C      AAT
                                TCA GGGGAGAAA  GGGTCC
                                ||| |||||||||  ||||||
                                GGT CCCCTTTTT  CTCGGG
                                  C       CGT
GAM890  BCL9    3'  GGGCTTTATTTTTTTCTGTGT  15067    G       _
                                ACG GGAGAAAAATGG GTCC
                                ||| ||||||||||| ||||
                                TGT TCTTTTTTTATT CGGG
                                  G         T
GAM890  BCLG    3'  GGACTTCCTCATTCTTTGTGG  47780         AAAAAT
                                TCACGGGGAG    GGGTCC
                                ||||||||||    ||||||
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                                GGTGTTTCTT     TTCAGG
                                     ACTCC_
GAM890  BCLG    3'  GGACTTCCTCATTCTTTGTGG  56976         AAAAAT
                                TCACGGGGAG     GGGTCC
                                ||||||||||     ||||||
                                GGTGTTTCTT     TTCAGG
                                     ACTCC_
GAM890  BCLG    3'  GGACTTCCTCATTCTTTGTGG  56982         AAAAAT
                                TCACGGGGAG     GGGTCC
                                ||||||||||     ||||||
                                GGTGTTTCTT     TTCAGG
                                     ACTCC_
GAM890  BDNF    5'  GGACCCGTGAGGTTTGTGTGG  59601      G   GAAAA
                                TCACG GGA    ATGGGTCC
                                ||||| |||    ||||||||
                                GGTGT TTT    TGCCCAGG
                                   G   GGAG_
GAM890  BLAME   3'  GGACAGGGGTTTCTCTTTCTGG 39243     CG       AATGG
                                TCA  GGGAGAAA    GTCC
                                |||  ||||||||    ||||
                                GGT  TTCTCTTT    CAGG
                                  CT       GGGGA
GAM890  BMP8    3'  GGGCCCTCACTCTCTGTG    8168          AAAAAT
                                CACGGGGAG     GGGTCC
                                |||||||||     ||||||
                                GTGTCTCTC     CCCGGG
                                     ACT___
GAM890  BSG     3'  GTTTTTTTCCTTCTGA     67798     CG
                                TCA  GGGAGAAAAAT
                                |||  ||||||||||
                                AGT  TCCTTTTTTTG
                                  CT
GAM890  BTEB1   3'  GCCTTTTTATTCTTTGTGA   6846          A    T
                                TCACGGGGAG AAAA GGGT
                                |||||||||| |||| ||||
                                AGTGTTTCTT TTTT TCCG
                                     A   _
GAM890  BTG2    3'  GGGCACTGTTTTTTCTCCCTG  22216           _  _
                                CGGGGAGAAAAA TGG GTCC
                                |||||||||||| ||| ||||
                                GTCCCTCTTTTT GTC CGGG
                                       T   A
GAM890  C10orf2 3'  GGGCTCCTCTATCCTGTGG   41547        _   AAAAT
                                TCACGGGG AGA    GGGTCC
                                |||||||| |||    ||||||
                                GGTGTCCT TCT    CTCGGG
                                     A   C____
GAM890  C4BPA   5'  GGCAGTTTTCTTCTTTGA    5550      C        ATGG
                                TCA GGGGAGAAAA    GTC
                                ||| ||||||||||    |||
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                                AGT TTCTTCTTTT   CGG
                                  _       GA__
GAM890  CACNG6   5' GGGCCTTGTTTTTCCTCTGG  49102    C      AAT
                                TCA GGGGAGAAA  GGGTCC
                                ||| |||||||||  ||||||
                                GGT CTCCTTTTT  TCCGGG
                                  _       GT_
GAM890  CALU     3' GGGCATACATTTTTTTTCT   6890          G__
                                GGGAGAAAAATG  GTCC
                                ||||||||||||  ||||
                                TCTTTTTTTTAC  CGGG
                                       ATA
GAM890  CAPS     3' GGCCCCTTCTCTCCTGG    14481    C      AAAT
                                TCA GGGGAGAA   GGGTC
                                ||| ||||||||   |||||
                                GGT CCTCTCTT   CCCGG
                                  _      C___
GAM890  CAPZA1   5' GGGCTACCTGTTCTTTCGTGG 72628     GG A  AAATG
                                TCACG  G GAA    GGTCC
                                |||||  | |||    |||||
                                GGTGC  T CTT    TCGGG
                                   TT _  GTCCA
GAM890  CASP8    3' GGATTTAAACATATTTCCCTGT 52949         AAAA__
           GG                    TCACGGGGAGA    TGGGTCC
                                ||||||||||     |||||||
                                GGTGTCCCTTT    ATTTAGG
                                       ATACAA
GAM890  CBFA2T2  3' GGACCTGTTTTTTTTCTC   17475
                                GGGGAGAAAAATGGGTCC
                                |||||||||||||||||
                                CTCTTTTTTTTGTCCAGG

GAM890  CBFB    3' TCTATTTTTTTTTTTGT    43144
                                ACGGGGAGAAAAATGGG
                                |||||||||||||||||
                                TGTTTTTTTTTTTATCT

GAM890  CBFB    3' TCTATTTTTTTTTTTGT    8277
                                ACGGGGAGAAAAATGGG
                                |||||||||||||||||
                                TGTTTTTTTTTTTATCT

GAM890  CD33    3' TCTCCATTTTCTTCTCTGTGA 73780        GA      TCC
                                TCACGGGGA  AAAATGGG
                                |||||||||  ||||||||
                                AGTGTCTCT  TTTTACCT
                                      TC       CTG
GAM890  CD34    3' GGGCTCTTTTTTCTCCCTCTGG 8345     C        T
                                TCA GGGGAGAAAAA GGGTCC
                                ||| ||||||||||| ||||||
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                                GGT TCCCTCTTTTT CTCGGG
                                  C         T
GAM890  CDC25C   5'  GGTTTTGTTTTTCTCCTGGTGA 8368      G         GG T
                                TCAC GGGAGAAAAAT  G CC
                                |||| ||||||||||  | ||
                                AGTG TCCTCTTTTTG  T GG
                                  G         TT T
GAM890  CDC25C   5'  GGTTTTGTTTTTCTCCTGGTGA 43020     G         GG T
                                TCAC GGGAGAAAAAT  G CC
                                |||| ||||||||||  | ||
                                AGTG TCCTCTTTTTG  T GG
                                  G         TT T
GAM890  CELSR1   3'  GGGCCTGTCAGACCTGGTGA  26485     G   AGAAAA
                                TCAC GGG     ATGGGTCC
                                |||| |||     ||||||||
                                AGTG TCC     TGTCCGGG
                                  G   AGAC__
GAM890  CELSR2   3'  GGATTCATTTTTTTTATACG  7408     GG_
                                CG   GAGAAAAATGGGTCC
                                ||   ||||||||||||||
                                GC   TTTTTTTTACTTAGG
                                 ATA
GAM890  CENTD2   3'  GGGTTCACTGTCCTTGTGG   57558        GAAAAA  GG
                                TCACGGGGA     TG  TCC
                                |||||||||     ||  |||
                                GGTGTTCCT     AC  GGG
                                      GTC___  TT
GAM890  CENTD2   3'  GGGTTCACTGTCCTTGTGG   30874        GAAAAA  GG
                                TCACGGGGA     TG  TCC
                                |||||||||     ||  |||
                                GGTGTTCCT     AC  GGG
                                      GTC___  TT
GAM890  CHRNA3   3'  GGACTAGCTATCTCTGTGG   5607         GAAAAATG
                                TCACGGGGA       GGTCC
                                |||||||||       |||||
                                GGTGTCTCT       TCAGG
                                      ATCGA___
GAM890  CHRNA4   3'  GGGCTGGCTTCTCCCTGGA   5618     A       AAATG
                                TC CGGGGAGAA    GGTCC
                                || |||||||||    |||||
                                AG GTCCCTCTT    TCGGG
                                  _       CGG__
GAM890  CHRNB1   3'  GGACCCTAGTCATCTTCCTGGA 60535    A       AAAAT_
                                TC CGGGGAGA     GGGTCC
                                || ||||||||     ||||||
                                AG GTCCTTCT     CCCAGG
                                  _       ACTGAT
GAM890  CHRNB1   3'  GGACCGCCTCTTCCTGTGG   60536          AAAATG
                                TCACGGGGAGA     GGTCC
                                ||||||||||      |||||
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                                GGTGTCCTTCT     CCAGG
                                      CCG___
GAM890  CMAR    3'  GGGCCCATCTCCTTCCCTGA  17777    C     AAAA
                                TCA GGGGAG    ATGGGTCC
                                ||| ||||||    ||||||||
                                AGT CCCTTC    TACCCGGG
                                  _     CTC_
GAM890  CNTNAP2  3'  GATTCCATCCCCTGTGA     26230        A  AAAA   _
                                TCACGGGG GA    TGGG TC
                                |||||||| ||    |||| ||
                                AGTGTCCC CT    ACCT AG
                                     _ _____   T
GAM890  COLQ    3'  GGCCCAGTTCCCCGCGA     54497    A     GAAAAA
                                TC CGGGGA     TGGGTC
                                || ||||||     ||||||
                                AG GCCCCT     ACCCGG
                                 C     TG_____
GAM890  COPEB    3'  GGCCAACTTTTTTTTCCTTGTGG 82872            TG_   C
                                TCACGGGGAGAAAAA  GGTC
                                ||||||||||||||   ||||
                                GGTGTTCCTTTTTTT  CCGG
                                      CAA
GAM890  COX7A1   5'  GGGTCTGGACCGCCTCCTCCGT 8517       _   AAAAA_  GT
          GG                    TCACGG GGAG     TGG  CC
                                |||||| ||||     |||  ||
                                GGTGCC CCTC     GTC  GG
                                   T   CGCCAG   TG
GAM890  CPSF4    3'  GGGCTTAATTTTCTCTTGG   21956   G       A
                                C GGGAGAAAA TGGGTCC
                                | |||||||| |||||||
                                G TTCTCTTTT ATTCGGG
                                 G       A
GAM890  CREBL1   3'  GGGCTCCTCTCATTCCTGTGA  15209        GAAAAAT
                                TCACGGGGA      GGGTCC
                                |||||||||      ||||||
                                AGTGTCCTT      CTCGGG
                                      ACTCTC_
GAM890  CRYGS    3'  GGGCCATATTCTTCCTG     34078         AAATG
                                CGGGGAGAA     GGTCC
                                |||||||||     |||||
                                GTCCTTCTT     CCGGG
                                      ATA__
GAM890  CSHL1    3'  GGGCCCGCGTGGCATCCTGTGA 42624        AGAAAAA
                                TCACGGGG      TGGGTCC
                                ||||||||      |||||||
                                AGTGTCCT      GCCCGGG
                                     ACGGTGC
GAM890  CSHL1    3'  GGGCCCGCGTGGCATCCTGTGA 42622        AGAAAAA
                                TCACGGGG      TGGGTCC
                                ||||||||      |||||||
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                                AGTGTCCT      GCCCGGG
                                     ACGGTGC
GAM890  CSHL1    3'  GGGCCCGCGTGGCATCCTGTGA 42623         AGAAAAA
                                TCACGGGG      TGGGTCC
                                ||||||||      |||||||
                                AGTGTCCT      GCCCGGG
                                     ACGGTGC
GAM890  CSHL1    3'  GGGCCCGCGTGGCATCCTGTGA 7165          AGAAAAA
                                TCACGGGG      TGGGTCC
                                ||||||||      |||||||
                                AGTGTCCT      GCCCGGG
                                     ACGGTGC
GAM890  CSHL1    3'  GGGCCCGCGTGGCATCCTGTGA 42625         AGAAAAA
                                TCACGGGG      TGGGTCC
                                ||||||||      |||||||
                                AGTGTCCT      GCCCGGG
                                     ACGGTGC
GAM890  CSRP1    3'  GGATCTCAGAGATTCTCCTCTG 14535      _     AAA_ _
           TGG                     CACGG GGAGAA    TG GGTCC
                                |||||  ||||||    ||  |||||
                                GTGTC CCTCTT    AC CTAGG
                                   T     AGAG  T
GAM890  CTPS     3'  GGGTCCATTTTTCTTCCAGGA  88594    ACG          GT
                                TC   GGGAGAAAAATGG  CC
                                ||   ||||||||||||  ||
                                AG   CCTTCTTTTTACC  GG
                                 GA_           TG
GAM890  CYP4A11  3'  GGCTCGTGGCTCTGGA      5756     A     AGAAAA
                                TC CGGGG      ATGGGTC
                                || |||||      |||||||
                                AG GTCTC      TGCTCGG
                                 _    GG____
GAM890  CYP4F3   3'  GGATGGGGTTTTCTCCTGG    6121     G       ATGG
                                C GGGAGAAAA    GTCC
                                | |||||||||    ||||
                                G TCCTCTTTT    TAGG
                                 G        GGGG
GAM890  DAAM1    3'  GGACATCAATTTTTTCCCCTGA 30378     C        A  _
                                TCA GGGGAGAAAA TGG GTCC
                                ||| |||||||||| ||| ||||
                                AGT CCCCTTTTTT ACT CAGG
                                  _        A  A
GAM890  DBCCR1   5'  GGATTCATGCCTGTCCTCGGGA 27515     A     GAAAA
                                TC CGGGGA     ATGGGTCC
                                || ||||||     ||||||||
                                AG GCTCCT     TACTTAGG
                                 G     GTCCG
GAM890  DDX11    3'  GACCTTTGTTCCTGTGG      47653          G  AAAT
                                TCACGGGGA AA    GGGTC
                                |||||||| ||    |||||
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                                GGTGTCCTT TT    TCCAG
                                     G _____
GAM890  DDX11    3'  GGGCCCTGCTCCTCTCTGTGG  47660          AAAAAT
                                TCACGGGGAG     GGGTCC
                                ||||||||||     ||||||
                                GGTGTCTCTC     CCCGGG
                                     CTCGT_
GAM890  DDX11    3'  GACCTTTGTTCCTGTGG     15299          G  AAAT
                                TCACGGGGA AA    GGGTC
                                ||||||||| ||    |||||
                                GGTGTCCTT TT    TCCAG
                                     G _____
GAM890  DDX6     3'  TGCTCTTCTCTTTGTGG     15291           AAAT    CC
                                TCACGGGGAGAA    GGGT
                                ||||||||||||    ||||
                                GGTGTTTCTCTT    CTCG
                                      _____   TA
GAM890  DES      3'  GGGCTTGAAATTGTCCCCGTGG 72130         G  AAA
                                TCACGGGGA AA   TGGGTCC
                                ||||||||| ||   |||||||
                                GGTGCCCCT TT   GTTCGGG
                                     G  AAA
GAM890  DGKG     3'  GGATTTATTTTTCAAATTG    7206      GGA
                                CGG   GAAAAATGGGTCC
                                |||   ||||||||||||
                                GTT   CTTTTTATTTAGG
                                  AAA
GAM890  DHCR7    3'  GGGCCCGTGCGCCGTTTCTCCT 7236           A_____
           TG                     CGGGGAGAAA     ATGGGTCC
                                ||||||||||     ||||||||
                                GTTCCTCTTT     TGCCCGGG
                                     GCCGCG
GAM890  DHFR     5'  GGATTTCAGGCTTCCCGT     5807          AAAAA   _
                                ACGGGGAG    TGGG TCC
                                ||||||||    |||| |||
                                TGCCCTTC    ACTT AGG
                                     GG___    T
GAM890  DIAPH2   3'  GGGCCTGTAGCTCTTC      22069        AAAA
                                GGGGAG    ATGGGTCC
                                ||||||    ||||||||
                                CTTCTC    TGTCCGGG
                                   GA__
GAM890  DISC1    3'  AATTTCATTTTTTTTTTTGAGA 37865     A            TCC
                                TC CGGGGAGAAAAATGGG
                                || ||||||||||||||||
                                AG GTTTTTTTTTTTACTT
                                 A             TAAA
GAM890  DLEC1    3'  GGACTTTGGGACCTGCTTTGTG 23689         _  AAAAAT
           A                     TCACGGGG AG     GGGTCC
                                ||||||||  ||     ||||||
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                                AGTGTTTC TC     TTCAGG
                                    G  CAGGGT
GAM890  DLEC1    3'  GGACTTTGGGACCTGCTTTGTG 23703       _  AAAAAT
          A                      TCACGGGG AG     GGGTCC
                                 |||||||| ||     ||||||
                                AGTGTTTC TC     TTCAGG
                                    G  CAGGGT
GAM890  DLG4     3'  TTTATTTATTTTTTTCTTTTGA 7257     C          CC
                                TCA GGGGAGAAAAATGGGT
                                ||| ||||||||||||||||
                                AGT TTTCTTTTTTTATTTA
                                  _           TTTA
GAM890  DLG4     5'  GGGCTCAGCTTCTTTTTG    7254         AAA
                                CGGGGAGAA   TGGGTCC
                                |||||||||   |||||||
                                GTTTTTCTT   ACTCGGG
                                    CG_
GAM890  DLG5     3'  GGACTGTGTCTGCTCCGTGA  82916       _  AAAATG
                                TCACGGGG AGA     GGTCC
                                |||||||| |||     |||||
                                AGTGCCTC TCT     TCAGG
                                    G  GTG___
GAM890  DMD      3'  GGATTCCCAGCCCATCCCTGTG 14365       GAAAAA  __
          A                      TCACGGGGA    TGGG  TCC
                                 |||||||||    ||||  |||
                                AGTGTCCCT    ACCC  AGG
                                    ACCCG_   TT
GAM890  DMD      3'  GGATTCCCAGCCCATCCCTGTG 14412       GAAAAA  __
          A                      TCACGGGGA    TGGG  TCC
                                 |||||||||    ||||  |||
                                AGTGTCCCT    ACCC  AGG
                                    ACCCG_   TT
GAM890  DMD      3'  GGATTCCCAGCCCATCCCTGTG 14379       GAAAAA  __
          A                      TCACGGGGA    TGGG  TCC
                                 |||||||||    ||||  |||
                                AGTGTCCCT    ACCC  AGG
                                    ACCCG_   TT
GAM890  DMD      3'  GGATTCCCAGCCCATCCCTGTG 14408       GAAAAA  __
          A                      TCACGGGGA    TGGG  TCC
                                 |||||||||    ||||  |||
                                AGTGTCCCT    ACCC  AGG
                                    ACCCG_   TT
GAM890  DMD      3'  GGATTCCCAGCCCATCCCTGTG 3667        GAAAAA  __
          A                      TCACGGGGA    TGGG  TCC
                                 |||||||||    ||||  |||
                                AGTGTCCCT    ACCC  AGG
                                    ACCCG_   TT
GAM890  DMD      3'  GGATTCCCAGCCCATCCCTGTG 14385       GAAAAA  __
          A                      TCACGGGGA    TGGG  TCC
                                 |||||||||    ||||  |||
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                                AGTGTCCCT    ACCC  AGG
                                    ACCCG_   TT
GAM890  DMD     3'  GGATTCCCAGCCCATCCCTGTG 14390       GAAAAA  __
          A                      TCACGGGGA    TGGG  TCC
                                 |||||||||    ||||  |||
                                AGTGTCCCT    ACCC  AGG
                                    ACCCG_   TT
GAM890  DMD     3'  GGATTCCCAGCCCATCCCTGTG 14419       GAAAAA  __
          A                      TCACGGGGA    TGGG  TCC
                                 |||||||||    ||||  |||
                                AGTGTCCCT    ACCC  AGG
                                    ACCCG_   TT
GAM890  DMD     3'  GGATTCCCAGCCCATCCCTGTG 14359       GAAAAA  __
          A                      TCACGGGGA    TGGG  TCC
                                 |||||||||    ||||  |||
                                AGTGTCCCT    ACCC  AGG
                                    ACCCG_   TT
GAM890  DMD     3'  GGATTCCCAGCCCATCCCTGTG 14397       GAAAAA  __
          A                      TCACGGGGA    TGGG  TCC
                                 |||||||||    ||||  |||
                                AGTGTCCCT    ACCC  AGG
                                    ACCCG_   TT
GAM890  DMD     3'  GGATTCCCAGCCCATCCCTGTG 14403       GAAAAA  __
          A                      TCACGGGGA    TGGG  TCC
                                 |||||||||    ||||  |||
                                AGTGTCCCT    ACCC  AGG
                                    ACCCG_   TT
GAM890  DMD     3'  GGATTCCCAGCCCATCCCTGTG 14371       GAAAAA  __
          A                      TCACGGGGA    TGGG  TCC
                                 |||||||||    ||||  |||
                                AGTGTCCCT    ACCC  AGG
                                    ACCCG_   TT
GAM890  DMD     3'  GGATTCCCAGCCCATCCCTGTG 14426       GAAAAA  __
          A                      TCACGGGGA    TGGG  TCC
                                 |||||||||    ||||  |||
                                AGTGTCCCT    ACCC  AGG
                                    ACCCG_   TT
GAM890  DPEP1   5'  GTCTGTCTCCCTGGGA     15333    A      AAAA  GT
                                TC CGGGGAGA   TGG  C
                                || ||||||||   |||  |
                                AG GTCCCTCT   GTC  G
                                 G      ____   TG
GAM890  DPH2L2  3'  GGACCCATCTGTCTTCCTG   7279        AAA
                                CGGGGAGA  ATGGGTCC
                                ||||||||  ||||||||
                                GTCCTTCT  TACCCAGG
                                    GTC
GAM890  DPP6    3'  GGGCTTGCTACTTCCTGT    55451       AAAAAT
                                ACGGGGAG    GGGTCC
                                ||||||||    ||||||
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                                TGTCCTTC     TTCGGG
                                    ATCG__
GAM890  DRD2    3'  GGCTGAGTTTTCTCTTTGTGG  5845            ATG    C
                                TCACGGGGAGAAAA   GGTC
                                ||||||||||||||   ||||
                                GGTGTTTCTCTTTT   TCGG
                                      GAG
GAM890  DRG2    3'  GGGCCTGTTTGGGTCCCTGGA  7322     A     GAA
                                TC CGGGGA   AAATGGGTCC
                                || ||||||   ||||||||||
                                AG GTCCCT   TTTGTCCGGG
                                 _     GGG
GAM890  DRIL1   3'  GGAAATTTTTTTTTCTCTGT   17829           TGGG
                                ACGGGGAGAAAAA    TCC
                                ||||||||||||    |||
                                TGTCTCTTTTTTT    AGG
                                      TTAA
GAM890  DUSP6   3'  GGCTGCTTTCTTTGTG      65963         AAAATG
                                CACGGGGAGA     GGTC
                                ||||||||||     ||||
                                GTGTTTCTTT     TCGG
                                    CG____
GAM890  DYRK1A  3'  GGTCATTTTTTTTTTCTGTG   55247      GG      TG GT C
                                CACGG  AGAAAAA  G  C
                                |||||  |||||||  |  |
                                GTGTC  TTTTTTT  C  G
                                   TT      TA TG
GAM890  DYRK1A  3'  GGTCATTTTTTTTTTCTGTG   7354       GG      TG GT C
                                CACGG  AGAAAAA  G  C
                                |||||  |||||||  |  |
                                GTGTC  TTTTTTT  C  G
                                   TT      TA TG
GAM890  DYRK1A  3'  GGTCATTTTTTTTTTCTGTG   55205      GG      TG GT C
                                CACGG  AGAAAAA  G  C
                                |||||  |||||||  |  |
                                GTGTC  TTTTTTT  C  G
                                   TT      TA TG
GAM890  ECHS1   3'  GGGCCTGCGGGTCCTTGTG    14567        GAAAAAT
                                CACGGGGA      GGGTCC
                                ||||||||      ||||||
                                GTGTTCCT      TCCGGG
                                    GGGCG__
GAM890  ED1     3'  GACCTGTGGTCATGTGA     7371       GG  GAAAA
                                TCACG  GA    ATGGGTC
                                |||||  ||    |||||||
                                AGTGT  CT    TGTCCAG
                                   A_  GG___
GAM890  EGR1    3'  GGATTTCGTTTTTCTT      8742            _
                                GAGAAAAATGGG TCC
                                |||||||||||| |||
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                                TTCTTTTTGCTT AGG
                                       T
GAM890  EIF2C1   3'  GGACTTGCCTTCTCCCTG    24178         AAA
                                CGGGGAGAA   TGGGTCC
                                |||||||||   |||||||
                                GTCCCTCTT   GTTCAGG
                                     CC_
GAM890  EIF3S6   5'  GACTCCCTTTTCTTTG      7805          AAAT
                                CGGGGAGAA    GGGTC
                                |||||||||    |||||
                                GTTTCTTTT    CTCAG
                                     CC__
GAM890  EIF4A1   3'  CGGACATCTTGTCATTTTTTTT 7421           _______
           CTTTGA                  GGGAGAAAAATGG     GTCC   G
                                |||||||||||||      ||||  |
                                TCTTTTTTTTACT     CAGG   C
                                       GTTCTA
GAM890  EIF4EBP2 3'  CATTTTTTTCCTTTGTGG    14588       _
                                TCACGG GGAGAAAAATG
                                |||||| ||||||||||
                                GGTGTT CCTTTTTTTAC
                                   T
GAM890  EIF5A    3'  GGGCTTTACCCTTCCCTGCGG  8769     A      AAAAAT
                                TC CGGGGAG     GGGTCC
                                || |||||||     ||||||
                                GG GTCCCTT     TTCGGG
                                 C      CCCAT_
GAM890  ELF3     3'  GGGCTCCAGCACTTCTTTCTGG 15422    A  GG    AAA_  _
           A                     TC CGG  AGAA    TGG GTCC
                                || |||  ||||    ||| ||||
                                AG GTC  TCTT    ACC CGGG
                                 _   TT    CACG   T
GAM890  EMR1     3'  GGCCGTCTTCCTGTGG      8775           AAAATG
                                TCACGGGGAGA     GGTC
                                ||||||||||      ||||
                                GGTGTCCTTCT     CCGG
                                       G_____
GAM890  EPHA2    3'  GGGCCCTCTTTCCCTGCGA    15408    A      AAAAT
                                TC CGGGGAGA    GGGTCC
                                || ||||||||    ||||||
                                AG GTCCCTTT    CCCGGG
                                 C       CT___
GAM890  EPHA8    3'  GATCTGCCTCTCTGTGG     40059          AAAAA
                                TCACGGGGAG    TGGGTC
                                ||||||||||    ||||||
                                GGTGTCTCTC    GTCTAG
                                       C____
GAM890  EPHB6    3'  GGGCTCCAACAGCCTCTGTGA  15465        AGAAAAA  _
                                TCACGGGG      TGG GTCC
                                ||||||||      ||| ||||
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                                AGTGTCTC      ACC CGGG
                                     CGACA__   T
GAM890  ETF1    3'  GGAACCATTTCTCTCTTGG   16397   G     A     G
                                C GGGAGA AAATGG TCC
                                | |||||| |||||| |||
                                G TTCTCT TTTACC AGG
                                 G     C     A
GAM890  EVI2B   3'  TACAGTTTTTTTTCCCCTGA  21442    C        TGG  CC
                                TCA GGGGAGAAAAA   GT
                                ||| ||||||||||   ||
                                AGT CCCCTTTTTTT   CA
                                  _         TGA  TG
GAM890  FANCG   3'  GGCTGTCTCTCTGTGG      16142          AAAATG
                                TCACGGGGAGA     GGTC
                                ||||||||||      ||||
                                GGTGTCTCTCT     TCGG
                                      G_____
GAM890  FBLN5   5'  GGACCCCGGCGCTCTCCCCGTG 20917          AAAAT_
                                CACGGGGAGA     GGGTCC
                                ||||||||||     ||||||
                                GTGCCCCTCT     CCCAGG
                                     CGCGGC
GAM890  FGF12   3'  GGTCTGATTTTTTTGCTTTGTG 40722        _      G  T
          G                      TCACGGGG AGAAAAAT GG CC
                                 |||||||| |||||||| || ||
                                 GGTGTTTC TTTTTTTA TC GG
                                      G       G  T
GAM890  FKRP    5'  GGATTCATTTACCTTGTTTTGT 44186       __  AA
          GG                     TCACGGG  GAG  AAATGGGTCC
                                 |||||||  |||  ||||||||||
                                 GGTGTTT  TTC  TTTACTTAGG
                                     TG   CA
GAM890  FLRT1   5'  GATCCCCTCTCTGTG      59611         AAAAAT
                                CACGGGGAG     GGGTC
                                |||||||||     |||||
                                GTGTCTCTC     CCTAG
                                     C_____
GAM890  FOSB    3'  GGACATGAGATTTTATTTTTTG 22108        A    GG___
          TGA                     CACGGGGAG AAAAT     GTCC
                                  ||||||||| |||||     ||||
                                  GTGTTTTTT TTTTA     CAGG
                                       A    GAGTA
GAM890  FVT1    3'  GACCCATTGCCAGTGA     8968      GG  AGAAA
                                TCAC  GG    AATGGGTC
                                ||||  ||    ||||||||
                                AGTG  CC    TTACCCAG
                                  A_  G____
GAM890  FZD4    3'  GGATCCATCTTCTCTCCG    24146         AA
                                CGGGGAGAA  ATGGGTCC
                                |||||||||  ||||||||
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                                GCCTCTCTT  TACCTAGG
                                    C_
GAM890  FZD4    3'  GGGTTGTTTTTCTTTCTCTGA  24147    C  GG     TG G  C
                                TCA GG  AGAAAAA  G TC
                                ||| ||  |||||||  | ||
                                AGT TC  TCTTTTT  T GG
                                  C  TT      GT G
GAM890  GAC1    5'  GGACTCCAGACTCTTCTTGTGA 20944          AAAA  _
                                TCACGGGGAGA   TGG GTCC
                                ||||||||||    ||| ||||
                                AGTGTTCTTCT    ACC CAGG
                                      CAG_  T
GAM890  GADD45B  5'  GGATTTTGCAATTTCTCCCTG  31616         AAT__
                                CGGGGAGAAA    GGGTCC
                                |||||||||     ||||||
                                GTCCCTCTTT    TTTAGG
                                      AACGT
GAM890  GALNS   5'  GGGCTCCGCGGCTCCCGTGG   4966        G  AAAAAT
                                TCACGGG AG     GGGTCC
                                ||||||| ||     ||||||
                                GGTGCCC TC     CTCGGG
                                   _  GGCGC_
GAM890  GARP    3'  GGGTTCTCCTGTTCTCTCTGTG 18598          AAAT_ GG
                                CACGGGGAGAA    G  TCC
                                ||||||||||    |  |||
                                GTGTCTCTCTT    C  GGG
                                      GTCCT TT
GAM890  GATA2   5'  GGGCCCGTCGCCCTCG     9001       A_  AAAA
                                CGGGG  GA   TGGGTCC
                                |||||  ||   |||||||
                                GCTCC  CT   GCCCGGG
                                  CG  _____
GAM890  GFI1    3'  AACTTTTATTTTTTTCCTTCTG 17931     CG          TCC
          G                      TCA  GGGAGAAAAATGGG
                                |||  ||||||||||||||
                                GGT  TCCTTTTTTTTATTT
                                  CT           TCAAT
GAM890  GFRA2   3'  TGTTTTTCTCTCTGGA     7662     A
                                TC CGGGGAGAAAAATG
                                || ||||||||||||||
                                AG GTCTCTCTTTTTGT
                                 _
GAM890  GGT1    3'  GGACCGGCTTCCCCTGTGA   25523        A   AAATG
                                TCACGGGG GAA    GGTCC
                                |||||||| |||    |||||
                                AGTGTCCC CTT    CCAGG
                                   _  CGG__
GAM890  GGT1    3'  GGACCGGCTTCCCCTGTGA   25515        A   AAATG
                                TCACGGGG GAA    GGTCC
                                |||||||| |||    |||||
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                                AGTGTCCC CTT    CCAGG
                                    _  CGG__
GAM890  GGT1    3' GGACCGGCTTCCCCTGTGA  17939       A  AAATG
                                TCACGGGG GAA    GGTCC
                                |||||||| |||    |||||
                                AGTGTCCC CTT    CCAGG
                                    _  CGG__
GAM890  GM2A    3' GGGCTCATTTGAAGCCTGGA  67780   A   GAGAA
                                TC CGGG    AAATGGGTCC
                                || ||||    ||||||||||
                                AG GTCC    TTTACTCGGG
                                 _  GAAG_
GAM890  GNAI1   3' GGATCCTAAGAGCATTTTTGTG 9055        GAAAAAT_
          G                      TCACGGGGA      GGGTCC
                                |||||||||      ||||||
                                GGTGTTTTT      CCTAGG
                                     ACGAGAAT
GAM890  GNAI3   3' GTCCAATCTTTTTGGA     21444   A     AAAA  GT
                                TC CGGGGAGA   TGG  C
                                || ||||||||   |||  |
                                AG GTTTTTCT   ACC  G
                                 _      A___   TG
GAM890  GNLY    5' GGATCTGCGTTTCCTCG     25028       AAAA
                                CGGGGAGA   TGGGTCC
                                ||||||||   |||||||
                                GCTCCTTT   GTCTAGG
                                     GC__
GAM890  GPR23   5' GGGCTAACCTTTCCCTGT   60544       AAAATG
                                ACGGGGAGA     GGTCC
                                |||||||||     |||||
                                TGTCCCTTT     TCGGG
                                     CCAA__
GAM890  GPR44   3' GGACTTAAGATGCTACCTTGTG 16529       _ AAAAA
          A                     TCACGGGG AG    TGGGTCC
                                |||||||| ||    |||||||
                                AGTGTTCC TC    ATTCAGG
                                     A  GTAGA
GAM890  GPR56   3' GGGCCCTCAGCCTCTCCTGA  19072    C    AAAAAT
                                TCA GGGGAG     GGGTCC
                                ||| ||||||     ||||||
                                AGT CCTCTC     CCCGGG
                                 _     CGACT_
GAM890  GPRC5C  3' GGATCTTGCTCCTCTGTGA  37851      _  AAAAAT
                                TCACGG GGAG     GGGTCC
                                |||||| ||||     ||||||
                                AGTGTC CCTC     TCTAGG
                                   T   GT____
GAM890  GPRC5C  3' GGATCTTGCTCCTCTGTGA  41847      _  AAAAAT
                                TCACGG GGAG     GGGTCC
                                |||||| ||||     ||||||
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                                AGTGTC CCTC     TCTAGG
                                   T   GT____
GAM890  GPX3    3'  GGGCCCAAAGCCCTTGTGG   9123        AGAAAAA
                                TCACGGGG     TGGGTCC
                                ||||||||     |||||||
                                GGTGTTCC     ACCCGGG
                                    CGAA___
GAM890  GRB10   3'  GGATTTCTTTTTTCTGTG    17982      GG   AAAT
                                CACGG  AGAA   GGGTCC
                                |||||  ||||   ||||||
                                GTGTC  TTTT   TTTAGG
                                   TT   C___
GAM890  GSR     3'  GGACCCATAGATCTTCT     94514      AAA
                                GGGAGA   ATGGGTCC
                                ||||||   ||||||||
                                TCTTCT   TACCCAGG
                                   AGA
GAM890  GSTA4   3'  GGATCTCTTGTTCTCTCCTGA  7699     C      A  T
                                TCA GGGGAGAA AA GGGTCC
                                ||| |||||||| || ||||||
                                AGT CCTCTCTT TT TCTAGG
                                  _      G  C
GAM890  GUK1    5'  GGGCCTTCACTCCTCTGTGG   5969       _   AAAAAT
                                TCACGG GGAG     GGGTCC
                                |||||| ||||     ||||||
                                GGTGTC CCTC     TCCGGG
                                   T   ACT___
GAM890  HAS3    3'  GGGCTTGTTTTTCTTC      18040        TG
                                GGAGAAAAA  GGTCC
                                |||||||||  |||||
                                CTTCTTTTT  TCGGG
                                     GT
GAM890  HD      3'  GGACCACCTCGTCCTCGTGG   9188         _ AAAATG
                                TCACGGGGA GA     GGTCC
                                ||||||||| ||     |||||
                                GGTGCTCCT CT     CCAGG
                                     G  CCA___
GAM890  HDAC4   3'  GGACTTTGTTGTTTTTCTTTTT 20112          ____
            G                    CGGGGAGAAAAAT    GGGTCC
                                ||||||||||||    ||||||
                                GTTTTTCTTTTTG    TTCAGG
                                      TTGT
GAM890  HDGF    3'  GGGCTTGATGACTTTCTTTTTG 15683          AAT___
            T                    ACGGGGAGAAA     GGGTCC
                                ||||||||||     ||||||
                                TGTTTTTCTTT     TTCGGG
                                     CAGTAG
GAM890  HDLBP   3'  GATTCCACTTCCTGTG      67922        AAAAA   _
                                CACGGGGAG    TGGG TC
                                |||||||||    |||| ||
```

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                                GTGTCCTTC    ACCT AG
                                     _____   T
GAM890  HFE     3'  CCATTTTCTTTTTTTGTGG   4649          _
                                TCACGGGGAGA AAAATGG
                                |||||||||| |||||||
                                GGTGTTTTTTT TTTTACC
                                      C
GAM890  HFE     3'  GGACCCGTTCAACTTTTCCTTT 57321     C      AA__
            GA                    TCA GGGGAGA    AATGGGTCC
                                ||| |||||||    |||||||||
                                AGT TCCTTTT    TTGCCCAGG
                                  T      CAAC
GAM890  HFE     3'  CCATTTTCTTTTTTTGTGG   57317          _
                                TCACGGGGAGA AAAATGG
                                |||||||||| |||||||
                                GGTGTTTTTTT TTTTACC
                                      C
GAM890  HFE     3'  GGACCCGTTCAACTTTTCCTTT 4654      C      AA__
            GA                    TCA GGGGAGA    AATGGGTCC
                                ||| |||||||    |||||||||
                                AGT TCCTTTT    TTGCCCAGG
                                  T      CAAC
GAM890  HIS1    5'  GGACTTTAACCCCTTGTGG   21316        AGAAAAAT
                                TCACGGGG       GGGTCC
                                ||||||||       ||||||
                                GGTGTTCC       TTCAGG
                                     CCAAT___
GAM890  HIVEP1  3'  GGGTCTGTCCTCCTTGTG    9201         AAAA   GT
                                CACGGGGAG   ATGG  CC
                                |||||||||   ||||  ||
                                GTGTTCCTC   TGTC  GG
                                     C___    TG
GAM890  HLCS    5'  GGCCCTATTTCTTGTG      4671         AAAAAT
                                CACGGGGAG     GGGTC
                                |||||||||     |||||
                                GTGTTCTTT     CCCGG
                                     AT_____
GAM890  HMGCS2  3'  GGACTAGGGGTCCTTTGTGA  18627        A  AAAATG
                                TCACGGGG GA     GGTCC
                                |||||||| ||     |||||
                                AGTGTTTC CT     TCAGG
                                     _  GGGGA_
GAM890  HMX1    3'  GGCCTCAGCTCCTGTGG     38445       G  AAAAAT
                                TCACGGG AG     GGGTC
                                ||||||| ||     |||||
                                GGTGTCC TC     TCCGG
                                     _  GAC___
GAM890  HNF3G   3'  GGGTCTATTACTTACTGTGA  72342       GG  AAA    GT
                                TCACGG  AG   AATGG  CC
                                ||||||  ||   |||||  ||
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                                AGTGTC  TC   TTATC  GG
                                   AT  A__    TG
GAM890  HNRPDL   5'  GCCCCTTCGTTTTTCTCTTCTG 18427    C         ____    CC
            A                    CA GGGGAGAAAAAT    GGGT
                                || ||||||||||||    ||||
                                GT CTTCTCTTTTTG    CCCG
                                 _          CTTC
GAM890  HNRPF    3'  GGACCCATTTTGCACCATGA   17121     C  GGAGA
                                TCA GG    AAAATGGGTCC
                                ||| ||    ||||||||||
                                AGT CC    TTTTACCCAGG
                                  A  ACG__
GAM890  HOXD4    3'  GTTTTTTTCCCCCTGA      27530     C
                                TCA GGGGAGAAAAAT
                                ||| ||||||||||||
                                AGT CCCCTTTTTTTG
                                  C
GAM890  HPN      3'  GGGACGTTTTTCTTCTTG    9277            GG
                                CGGGGAGAAAAATG  TCC
                                ||||||||||||||  |||
                                GTTCTTCTTTTTGC  GGG
                                        A_   T
GAM890  HS3ST3A1  5'  GGATTCCGTTTCCCCGCGG   20152    A       AAAAT
                                TC CGGGGAGA    GGGTCC
                                || ||||||||    ||||||
                                GG GCCCCTTT    CTTAGG
                                 C       GC___
GAM890  HSPA1A   5'  GGACCGAGCTCTTCTCGCGG   18074    A       AAAATG
                                TC CGGGGAGA     GGTCC
                                || ||||||||     |||||
                                GG GCTCTTCT     CCAGG
                                 C       CGAG__
GAM890  HUNK     3'  TTAGTGTATTTATTTTCTTTGT 27464          _    GGTCC
              GG                   TCACGGGGAGAA AAATG
                                |||||||||||| |||||
                                GGTGTTTCTTTT TTTAT
                                       A    GTGATTG
GAM890  IAPP     3'  GACCTATATCTCAGTGG     4693      G   GAAAA
                                TCAC GGGA    ATGGGTC
                                |||| ||||    |||||||
                                GGTG CTCT    TATCCAG
                                  A   A____
GAM890  IGFBP4   5'  GGGCCGCCCCGTCTCCCCGCGG 7760     A       AAAATG
                                TC CGGGGAGA     GGTCC
                                || ||||||||     |||||
                                GG GCCCCTCT     CCGGG
                                 C       GCCCCG
GAM890  IGJ      3'  GGGCTTTTTTTTTTTTTTG   58315          TG
                                CGGGGAGAAAAA  GGTCC
                                ||||||||||||  |||||
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                                GTTTTTTTTTTT  TCGGG
                                      TT
GAM890  IHPK1    3'  GGGTTATATTTCTCTTTG    95761         A   G
                                CGGGGAGAAA ATGG TC
                                |||||||||| |||| ||
                                GTTTCTCTTT TATT GG
                                     A   G
GAM890  IHPK3    3'  GGGCTTATCTGGATTCTTCTGG 54026   G     AA___
                                C GGGAGAA    ATGGGTCC
                                | |||||||    ||||||||
                                G TCTTCTT    TATTCGGG
                                 G      AGGTC
GAM890  IKBKG    5'  TGACCCTACTCCTTGTG     13315        AAAAAT    C
                                CACGGGGAG     GGGTC
                                |||||||||     |||||
                                GTGTTCCTC     CCCAG
                                      AT____     TC
GAM890  IL13RA1  3'  GGATTTCCCATCCCCTGTGG   7775        A  AAAA   ___
                                TCACGGGG GA    TGGG   TCC
                                |||||||| ||    ||||   |||
                                GGTGTCCC CT    ACCC   AGG
                                     _ ____    TTT
GAM890  IL18RAP  5'  GGGCTCTCAATTCCTTCTGTGA 13904       GA   AAAT
                                TCACGGG  GAA    GGGTCC
                                |||||||  |||    ||||||
                                AGTGTCT  CTT    CTCGGG
                                    TC   AACT
GAM890  IL1F5    3'  GATCTATGGCCCTTGG     24379     C   AGAAAA
                                TCA GGGG     ATGGGTC
                                ||| ||||     |||||||
                                GGT TCCC     TATCTAG
                                  _   GG____
GAM890  IL21R    3'  GACCCACCCCCCGTGG      41427        AGAAAAA
                                TCACGGGG      TGGGTC
                                ||||||||      ||||||
                                GGTGCCCC      ACCCAG
                                     CC_____
GAM890  IL24     3'  GACCTCCCTCCCCCTGG     22444     C     AAAAAT
                                TCA GGGGAG     GGGTC
                                ||| ||||||     |||||
                                GGT CCCCTC     TCCAG
                                  C     CC____
GAM890  ILK      5'  GGGTTCATCCTCCTTCCCTGG  15725     C     AAAA   GG
                                TCA GGGGAG    ATG  TCC
                                ||| ||||||    |||  |||
                                GGT CCCTTC    TAC  GGG
                                  _     CTCC   TT
GAM890  IRF2     3'  TATTTTATTTTTTTCTCTCTGA 9357      C           TCC
                                TCA GGGGAGAAAAATGGG
                                ||| ||||||||||||||
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                                AGT TCTCTTTTTTTATTT
                                  C           TATG
GAM890  IRF2    3'  GGAATTTTTTATTCTTGTGA  9355        G    TGGG
                                TCACGGGGA AAAAA   TCC
                                ||||||||| |||||   |||
                                AGTGTTCTT TTTTT   AGG
                                     A    TA__
GAM890  ITGA5   3'  GGACTTATTTAAACTCTGT   61281      AGAA
                                ACGGGG   AAATGGGTCC
                                ||||||   ||||||||||
                                TGTCTC   TTTATTCAGG
                                   AAA_
GAM890  ITGBL1  3'  GGATTCTTATTTTTTCTG    16575    GG   A  T
                                CGG  AGAA AA GGGTCC
                                |||  |||| || ||||||
                                GTC  TTTT TT CTTAGG
                                  TT   A  _
GAM890  ITPKB   3'  GGATCTATAGAGTCTCTG    9433      GAAAA
                                CGGGGA    ATGGGTCC
                                ||||||    ||||||||
                                GTCTCT    TATCTAGG
                                   GAGA_
GAM890  ITPKB   3'  GGACTCTTGTTTCTCCTTG   9432        AAT
                                CGGGGAGAAA   GGGTCC
                                ||||||||||   ||||||
                                GTTCCTCTTT   CTCAGG
                                     GTT
GAM890  ITPR3   3'  CCGCTTGTTTTTCTCCTTTTGG 9454     CG       TG   CC
                                TCA  GGGAGAAAAA  GGT
                                |||  ||||||||||  |||
                                GGT  TCCTCTTTTT  TCG
                                  TT        GT   CCA
GAM890  JMJ     3'  GGATTCATCAATCCCGT     17132      AGAAAA
                                ACGGGG     ATGGGTCC
                                ||||||     ||||||||
                                TGCCCT     TACTTAGG
                                   AAC___
GAM890  JPH3    3'  GACGTTGTCCTCGTGG      40305        G  AAATGG
                                TCACGGGGA AA     GTC
                                ||||||||| ||     |||
                                GGTGCTCCT TT     CAG
                                     G  G_____
GAM890  JRK     3'  GGGCCCATTTCCTCTCTC    86535      A_
                                GGGAGA  AAATGGGTCC
                                ||||||  ||||||||||
                                CTCTCT  TTTACCCGGG
                                   CC
GAM890  JTB     5'  ATTTTTCTCGCTGTGG      21960       G
                                TCACGG GAGAAAAAT
                                |||||| |||||||||
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                                GGTGTC CTCTTTTTA
                                   G
GAM890  KCNA6    3'  GGGTCCACAGTCACTCTTTGTG 9516          AAAAA_  GT
                                CACGGGGAG     TGG  CC
                                |||||||||     |||  ||
                                GTGTTTCTC     ACC  GG
                                     ACTGAC   TG
GAM890  KCNJ15   3'  GGTCCCGTATCCCTGTGG    9545          GAAAA    T
                                TCACGGGGA     ATGGG CC
                                |||||||||     ||||| ||
                                GGTGTCCCT     TGCCC GG
                                     A____     T
GAM890  KIAA0442 5'  GGTGTCAATTTTTTTTTTGTGTG 31471       G        _  GT
             G                    TCACG GGAGAAAAAT GG  CC
                                |||||  ||||||||||  ||  ||
                                GGTGT TTTTTTTTTA CT  GG
                                   G         A  GT
GAM890  KIF3C    3'  GGGCATCTGCTCCCCGTGG    9608          AAAAATGG
                                TCACGGGGAG       GTCC
                                ||||||||||       ||||
                                GGTGCCCCTC       CGGG
                                     GTCTA___
GAM890  KIF5C    3'  GGGTTCAAAGTTTTCCTTCTGA 15738     CG      AAA  GG
                                TCA  GGGAGAA   TG  TCC
                                |||  |||||||   ||  |||
                                AGT  TCCTTTT   AC  GGG
                                  CT      GAA  TT
GAM890  KLK8     3'  GGCTCAGACCCCTGTGG     57962        AGAAAAA
                                TCACGGGG      TGGGTC
                                ||||||||      ||||||
                                GGTGTCCC      ACTCGG
                                     CAG_____
GAM890  KMO      3'  GGACCCATTGGTTTTGTCG    13452     G    AA
                                CGG GAGA  AATGGGTCC
                                ||| ||||  |||||||||
                                GCT TTTT  TTACCCAGG
                                  G   GG
GAM890  LBR      3'  CGGGTCTGTACTTTTTTTTTTC 59353         _______   GT
               TTTTTGA                GGGAGAAAA     ATGG  CC   G
                                |||||||||     ||||  ||  |
                                TTCTTTTTT     TGTC  GG   C
                                     TTTTCA    TG
GAM890  LDB3     3'  TTTTTCCAGTTTTGCTCTGTGG 76409         AG    A    TCC
                                TCACGGGG  AAAA TGGG
                                ||||||||  |||| ||||
                                GGTGTCTC  TTTT ACCT
                                     G_   G    TTTTG
GAM890  LDLR     3'  GGACTTCAGGTTCTTTCTG   4992      GG    AAA  _
                                CGG  AGAA   TGG GTCC
                                |||  ||||   ||| ||||
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                                GTC  TCTT   ACT CAGG
                                  TT    GG_   T
GAM890  LEP     3'  GGGCCAGGGGTCTCCCTGGA  4054     A       AAAATG
                                TC CGGGGAGA     GGTCC
                                || ||||||||     |||||
                                AG GTCCCTCT     CCGGG
                                  _       GGGGA_
GAM890  LFNG    3'  GGGCAGTTCTGCTCTGTGG   92644        _   AAATGG
                                TCACGGGG AGAA     GTCC
                                |||||||| ||||     ||||
                                GGTGTCTC TCTT     CGGG
                                     G    GA____
GAM890  LIMK1   3'  GATGTGTTCTCCTTTGG     33647     C      AAA   G
                                TCA GGGGAGA   ATG GTC
                                ||| |||||||   ||| |||
                                GGT TTCCTCT   TGT TAG
                                  _      ____  G
GAM890  LOX     5'  GCCCCGTTTTTATTTTCTGTGA 9793        GG  _       TCC
                                TCACGG  AG AAAAATGGG
                                ||||||  || |||||||||
                                AGTGTC  TT TTTTTGCCC
                                   TT  A        CG
GAM890  LSP1    5'  GGATCTGCCAGCACCCTGTGG  9811         AGAAAAAT
                                TCACGGGG       GGGTCC
                                ||||||||       ||||||
                                GGTGTCCC       TCTAGG
                                     ACGACCG_
GAM890  LTBR    3'  GGCACTTTCTCCCTTGA     9822      C       AATGG
                                TCA GGGGAGAAA     GTC
                                ||| |||||||||     |||
                                AGT TCCCTCTTT     CGG
                                  _       CA___
GAM890  LZTR1   3'  GACCCCTTTCTTGTTG      22239     G     AAT
                                CGG GAGAAA   GGGTC
                                ||| ||||||   |||||
                                GTT TTCTTT   CCCAG
                                  G     C__
GAM890  LZTR1   3'  GGGCTTGGCCTGGCTTCTGTGG 22243        G  AAAAA_
                                TCACGGG AG     TGGGTCC
                                ||||||| ||     |||||||
                                GGTGTCT TC     GTTCGGG
                                   _ GGTCCG
GAM890  LZTS1   3'  TTATTTTTCTCTTTGTGG    40700
                                TCACGGGGAGAAAAATGG
                                ||||||||||||||||||
                                GGTGTTTCTCTTTTTATT

GAM890  LZTS1   3'  CATAGTTATTTTTCTCTTTGTG 40683              GTCC
              G                  TCACGGGGAGAAAAATGG
                                 ||||||||||||||||||
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                                GGTGTTTCTCTTTTTATT
                                      GATACA
GAM890  MADD    3'  GGAGCAGTTTCACTCTGTGA  55334       A   AATGG _
                    TCACGGGG GAAA    G TCC
                    |||||||| ||||    | |||
                    AGTGTCTC CTTT    C AGG
                       A   GA___ G
GAM890  MADD    3'  GGAGCAGTTTCACTCTGTGA  13465       A   AATGG _
                    TCACGGGG GAAA    G TCC
                    |||||||| ||||    | |||
                    AGTGTCTC CTTT    C AGG
                       A   GA___ G
GAM890  MADD    3'  GGAGCAGTTTCACTCTGTGA  55356       A   AATGG _
                    TCACGGGG GAAA    G TCC
                    |||||||| ||||    | |||
                    AGTGTCTC CTTT    C AGG
                       A   GA___ G
GAM890  MADD    3'  GGAGCAGTTTCACTCTGTGA  55350       A   AATGG _
                    TCACGGGG GAAA    G TCC
                    |||||||| ||||    | |||
                    AGTGTCTC CTTT    C AGG
                       A   GA___ G
GAM890  MADD    3'  GGAGCAGTTTCACTCTGTGA  55340       A   AATGG _
                    TCACGGGG GAAA    G TCC
                    |||||||| ||||    | |||
                    AGTGTCTC CTTT    C AGG
                       A   GA___ G
GAM890  MADD    3'  GGAGCAGTTTCACTCTGTGA  55345       A   AATGG _
                    TCACGGGG GAAA    G TCC
                    |||||||| ||||    | |||
                    AGTGTCTC CTTT    C AGG
                       A   GA___ G
GAM890  MAGEC1   5'  GGACCTGAGGCATTTTGTGA  18422       AGAAAAAT
                    TCACGGGG      GGGTCC
                    ||||||||      ||||||
                    AGTGTTTT      TCCAGG
                       ACGGAG__
GAM890  MAN2B1   5'  GGGCTACAGCCTCTCTCCCGTG 4996       _   AAAATG
          A          TCACGGG GAGA     GGTCC
                    ||||||| ||||     |||||
                    AGTGCCC CTCT     TCGGG
                       T   CCGACA
GAM890  MAN2C1   3'  GGATCAGTCTTTTCTTGTGG  72920       AAAATG
                    TCACGGGGAGA     GGTCC
                    ||||||||||     |||||
                    GGTGTTCTTTT     CTAGG
                       CTGA__
GAM890  MAPT    3'  GGGCTAACCAGTTCTCTTTGT  19780       AAATG_
                    ACGGGGAGAA     GGTCC
                    ||||||||||     |||||
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                                TGTTTCTCTT     TCGGG
                                      GACCAA
GAM890  MAPT    3'  GGGCTAACCAGTTCTCTTTGT  33691          AAATG_
                                ACGGGGAGAA     GGTCC
                                ||||||||||     |||||
                                TGTTTCTCTT     TCGGG
                                      GACCAA
GAM890  MAPT    3'  GGGCTAACCAGTTCTCTTTGT  33700          AAATG_
                                ACGGGGAGAA     GGTCC
                                ||||||||||     |||||
                                TGTTTCTCTT     TCGGG
                                      GACCAA
GAM890  MAPT    3'  GGGCTAACCAGTTCTCTTTGT  33710          AAATG_
                                ACGGGGAGAA     GGTCC
                                ||||||||||     |||||
                                TGTTTCTCTT     TCGGG
                                      GACCAA
GAM890  MBL2    3'  GACTTGTCTTTTGGTGG     4115       G    AAAA TG
                                TCAC GGGAG    A  GGTC
                                |||| |||||    |  ||||
                                GGTG TTTTC    T  TCAG
                                  G     _____ GT
GAM890  MBTPS1  3'  GGCCTGCCCTCCTGTGA     13706        G  AAAAAT
                                TCACGGG AG     GGGTC
                                ||||||| ||     |||||
                                AGTGTCC TC     TCCGG
                                    _  CCG___
GAM890  MEF2C   3'  TGTTTTTTTCCCCTTGA     9991       C
                                TCA GGGGAGAAAAATG
                                ||| ||||||||||||
                                AGT CCCCTTTTTTTGT
                                  T
GAM890  MEN1    5'  GCCTTGTTTTTTTCCTTTTGG  93374     CG        TG  TCC
                                TCA  GGGAGAAAAA  GG
                                |||  ||||||||||  ||
                                GGT  TCCTTTTTTT  TC
                                  TT         GT  CG
GAM890  MEN1    5'  GGCCTGTTTGCCTGAGA     93375    A    G GAAA
                                TC CGGG A    AATGGGTC
                                || |||| |    ||||||||
                                AG GTCC T    TTGTCCGG
                                 A    G ____
GAM890  MGEA5   3'  GGACTCATTTTTTCATC     24214    GA
                                GG  GAAAAATGGGTCC
                                ||  ||||||||||||
                                CT  TTTTTTACTCAGG
                                 AC
GAM890  MKI67   3'  GATCGCTTCCTTGTGA      10045          AAAAATG
                                TCACGGGGAG      GGTC
                                ||||||||||      ||||
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                                AGTGTTCCTT      CTAG
                                      CG_____
GAM890  MLLT2    3'  GGGTTTTTTTTTTTCTCTG   19849          TG GT
                                CGGGGAGAAAAA  G  CC
                                ||||||||||||  |  ||
                                GTCTCTTTTTTT  T  GG
                                      TT TG
GAM890  MLLT2    3'  GGATGATTTTTTTTCTTTTGA  19846     CG        GG
                                TCA  GGGAGAAAAAT  GTCC
                                |||  ||||||||||  ||||
                                AGT  TCTTTTTTTTA  TAGG
                                  TT         G_
GAM890  MMP2     3'  ACTTTGTTTTTTTTCTTTG    15762          GG TCC
                                CGGGGAGAAAAAT  G
                                ||||||||||||  |
                                GTTTCTTTTTTTG  T
                                      TT CAC
GAM890  MPO      3'  GGGCCTGTTGCCCTTTCTGT   4203      GG  AAA
                                ACGG  AG   AATGGGTCC
                                ||||  ||   |||||||||
                                TGTC  TC   TTGTCCGGG
                                  TT  CCG
GAM890  MRPL49   3'  GGCCTGTTTTGTTTTTCTTTCC 69572   C  GG      _____    C
           TTGG                    GG  AGAAAAAT    GGGTC
                                ||  ||||||||    |||||
                                CC  TCTTTTTG    TCCGG
                                T  TT       TTTTG
GAM890  MS4A4A   3'  TTCTCATTTTTTTCCCTGGA   43786    A           TCC
                                TC CGGGGAGAAAAATGGG
                                || ||||||||||||||||
                                AG GTCCCTTTTTTTACTC
                                 _            TTG
GAM890  MTMR6    3'  GGAGCATTATTTTTCTTCTTGT 93550                 _ _
                                ACGGGGAGAAAAATGG G TCC
                                |||||||||||||||| | |||
                                TGTTCTTCTTTTTATT C AGG
                                      A G
GAM890  MTNR1A   3'  GGAACAATTTTTTTTCTGT   19891     GG     A  GG
                                ACGG  AGAAAA TG  TCC
                                ||||  ||||||  ||  |||
                                TGTC  TTTTTT AC  AGG
                                  TT     A  A_
GAM890  MYB      3'  GATCAGTATTTTTTCCTGTGA  59539           A  G    C
                                TCACGGGGAGAAA AT GGTC
                                |||||||||||||  || ||||
                                AGTGTCCTTTTTT TG CTAG
                                      A  A
GAM890  MYBPC2   3'  GGACTGTGTTCTTTCTGGA   15772    A   GG    AAATG
                                TC CGG  AGAA    GGTCC
                                ||  |||  ||||    |||||
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                                AG GTC  TCTT    TCAGG
                                 _  TT   GTG__
GAM890  MYCL2   3'  GGATTTTTTTTTTTTTTTTTGA 18184    CG       TG
                                TCA  GGGAGAAAAA  GGTCC
                                |||  ||||||||||  |||||
                                AGT  TTTTTTTTTT  TTAGG
                                  TT       TT
GAM890  NAGA    3'  GGCAATTTTCCTGTGG     4235          AAAATGG
                                TCACGGGGAGA     GTC
                                ||||||||||      |||
                                GGTGTCCTTTT     CGG
                                      AA_____
GAM890  NAPB    3'  GGAAAGTTTTGCTTTTTGTGG  70186         A    GGG
                                TCACGGGGAG AAAAT   TCC
                                |||||||||| |||||   |||
                                GGTGTTTTTC TTTTG   AGG
                                      G    AA_
GAM890  NAPB    3'  TGTTTTTGTCTTTGTGG    70193         G
                                TCACGGGGA AAAAATG
                                ||||||||| |||||||
                                GGTGTTTCT TTTTTGT
                                      G
GAM890  NDST1   5'  GGGCCTGTCCAGTGTCCTCTGG 7745     C    GAAAA_
                                TCA GGGGA     ATGGGTCC
                                ||| |||||     ||||||||
                                GGT CTCCT     TGTCCGGG
                                  _    GTGACC
GAM890  NDUFS6  3'  GGTCCCGCAGCATCCTGTGA   15847        AGAAAAA   T
                                TCACGGGG      TGGG CC
                                ||||||||      |||| ||
                                AGTGTCCT      GCCC GG
                                     ACGAC__    T
GAM890  NEBL    3'  GGCCATTTTCTTTTGTGA    21123        G    ATG
                                TCACGGG AGAAAA   GGTC
                                ||||||| ||||||   ||||
                                AGTGTTT TCTTTT   CCGG
                                   _     A__
GAM890  NEK6    3'  GGAAATCATTTTTTTCCGTGGA 26933    A  G         G_
                                TC CG GGAGAAAAATGG  TCC
                                || || ||||||||||||  |||
                                AG GT CCTTTTTTTACT  AGG
                                 _ G          AA
GAM890  NET1    3'  GACTTATTTGCCTTG       19615       AGAA
                                CGGGG    AAATGGGTC
                                |||||    |||||||||
                                GTTCC    TTTATTCAG
                                   G___
GAM890  NFYA    3'  GGACCTATTTCAGACTGTTGA  41352     _   GGAGAA
                                TCA CGG     AAATGGGTCC
                                ||| |||     ||||||||||
```

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                                AGT GTC     TTTATCCAGG
                                  T  AGAC__
GAM890  NFYA    3'  GGACCTATTTCAGACTGTTGA  10217     _  GGAGAA
                                TCA CGG     AAATGGGTCC
                                ||| |||     ||||||||||
                                AGT GTC     TTTATCCAGG
                                  T  AGAC__
GAM890  NGFR    3'  GACTGTTTTTTCCTG       10229          AATG
                                CGGGGAGAAA   GGTC
                                ||||||||||   ||||
                                GTCCTTTTTT   TCAG
                                     G___
GAM890  NLGN3   3'  GGACTTGGTCTTTTTTCTG   38601    GG   AAA
                                CGG  AGAA   TGGGTCC
                                |||  ||||   |||||||
                                GTC  TTTT   GTTCAGG
                                  TT   CTG
GAM890  NORE1   3'  GGGCCTGGCCTCCCCGT     48719        AAAAA
                                ACGGGGAG    TGGGTCC
                                ||||||||    |||||||
                                TGCCCCTC    GTCCGGG
                                    CG___
GAM890  NPTX2   3'  GGATTTGTTTTTTTTTTTTCCC 92483      ____      GG
                                GGGGA   GAAAAAT  GTCC
                                |||||   |||||||  ||||
                                CCCTT   TTTTTTG  TAGG
                                   TTTT      TT
GAM890  NRD1    5'  GGGTTCAGGCCTGTTCCCCGCG 10279    A      AAAAA_  GG
          G                      TC CGGGGAG     TG  TCC
                                || |||||||     ||  |||
                                GG GCCCCTT     AC  GGG
                                 C      GTCCGG  TT
GAM890  NRXN1   5'  GGACCCTTATTTCTTCGT    16632        AAAAT
                                ACGGGGAGA    GGGTCC
                                |||||||||    ||||||
                                TGCTTCTTT    CCCAGG
                                     ATT__
GAM890  NRXN2   3'  GGACCCTCTCCCTG       57015        AAAAT
                                CGGGGAGA    GGGTCC
                                ||||||||    ||||||
                                GTCCCTCT    CCCAGG
                                    _____     G
GAM890  NRXN2   3'  GGACCCTCTCCCTG       30629        AAAAT
                                CGGGGAGA    GGGTCC
                                ||||||||    ||||||
                                GTCCCTCT    CCCAGG
                                    _____     G
GAM890  NRXN2   3'  GGACCCTCTCCCTG       57026        AAAAT
                                CGGGGAGA    GGGTCC
                                ||||||||    ||||||
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                                GTCCCTCT    CCCAGG
                                   _____    G
GAM890  NSD1    3'  GGCTTATGGTTGTGTGA    42400      G  AGAAAA
                                TCACG GG    ATGGGTC
                                ||||| ||    |||||||
                                AGTGT TT    TATTCGG
                                   G  GG____
GAM890  OLIG2   3'  GATGTTCTCTCCGGGA     19411    A       AAATGG
                                TC CGGGGAGAA     GTC
                                || |||||||||     |||
                                AG GCCTCTCTT     TAG
                                 G       G_____
GAM890  OPCML   3'  GGGTTCACGTCTTTTCTTTCTG 10346   A  GG    A___  GG
            GGA                   C CGG  AGAAAA   TG  TCC
                                | |||  ||||||   ||  |||
                                G GTC  TCTTTT   AC  GGG
                                 G   TT    CTGC  TT
GAM890  ORC5L   3'  GGACTACATTTTGCTCTGTGA  10365       AGA    _
                                TCACGGGG   AAAATG GGTCC
                                ||||||||   |||||| |||||
                                AGTGTCTC   TTTTAC TCAGG
                                     G__     A
GAM890  OTOF    3'  CTGTTTTTCTTTTCTTGG    16643    C GG
                                TCA G  GAGAAAAATGG
                                ||| |  ||||||||||
                                GGT C  TTCTTTTTGTC
                                  T TT
GAM890  P2RY2   3'  GGGCTCAGGATATTCACTCTGT 10380       A  AAA__
            GG                    TCACGGGG GAA    TGGGTCC
                                |||||||| |||    |||||||
                                GGTGTCTC CTT    ACTCGGG
                                     A  ATAGG
GAM890  PACE    3'  GGATATATTTTCACTTTGTGA  10393       A    ATGG
                                TCACGGGG GAAAA   GTCC
                                |||||||| |||||   ||||
                                AGTGTTTC CTTTT   TAGG
                                     A    ATA_
GAM890  PACSIN1 3'  GGGCTCCCCCTCTCTGTG    92263        AAAAAT
                                CACGGGGAG     GGGTCC
                                |||||||||     ||||||
                                GTGTCTCTC     CTCGGG
                                      CCC___
GAM890  PAG     3'  GGAGACGTTTCTTCTGTGG   37404       G   AA  GG
                                TCACGGG AGAA  ATG  TCC
                                ||||||| ||||  |||  |||
                                GGTGTCT TCTT  TGC  AGG
                                   _   __  AG
GAM890  PARG    3'  GGACTAATGTTTCTTTTGTGG  13271       G    AATG
                                TCACGGG AGAAA   GGTCC
                                ||||||| |||||   |||||
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                                GGTGTTT TCTTT   TCAGG
                                   _    GTAA
GAM890  PBX2    3'  GGATCCATCTGTTTTTTTTTTT 10445          ____
              GT                  ACGGGGAGAAAA   ATGGGTCC
                                  ||||||||||||   ||||||||
                                  TGTTTTTTTTTT   TACCTAGG
                                     TGTC
GAM890  PCDH1   3'  GGCCTTGTTTTCCCGTGG    50564         AAAAT   C
                                  TCACGGGGAGA   GGGTC
                                  ||||||||||    |||||
                                  GGTGCCCTTTT   TCCGG
                                     GT___    A
GAM890  PCDHB4  3'  GGTCCTTTTCCTCTTGTGA   38436       GA   AT  GT
                                  TCACGGG  GAAAA  GG  C
                                  |||||||  |||||  ||  |
                                  AGTGTTC  CTTTT  CC  G
                                     TC    __  TG
GAM890  PCDHGA2 5'  GACCTGGGTCCCGTGA     49268       AGAAAAA
                                  TCACGGGG     TGGGTC
                                  ||||||||     ||||||
                                  AGTGCCCT     GTCCAG
                                     GG_____
GAM890  PCDHGA2 5'  GACCTGGGTCCCGTGA     38307       AGAAAAA
                                  TCACGGGG     TGGGTC
                                  ||||||||     ||||||
                                  AGTGCCCT     GTCCAG
                                     GG_____
GAM890  PCMT1   3'  GGAGTGGTTTTTCTTTTCTTGG 18224    C GG       GGG
                                  TCA G  GAGAAAAAT   TCC
                                  ||| |  |||||||||   |||
                                  GGT C  TTCTTTTTG   AGG
                                    T TT       GTG
GAM890  PDE4C   3'  GGCTTCTATCCCTGTGA     6236         GAAAAAT
                                  TCACGGGGA     GGGTC
                                  |||||||||     |||||
                                  AGTGTCCCT     TTCGG
                                     ATC____
GAM890  PFKFB4  3'  GGGCCTCTACCATCCTCTCTGT 15872         AAAAAT__
              GG                  TCACGGGGAG      GGGTCC
                                  ||||||||||      ||||||
                                  GGTGTCTCTC      TCCGGG
                                     CTACCATC
GAM890  PFN2    3'  GGACTTGGCTGTCTTGTGA   10528       AGAAAAA
                                  TCACGGGG     TGGGTCC
                                  ||||||||     |||||||
                                  AGTGTTCT     GTTCAGG
                                     GTCG___
GAM890  PFN2    3'  GGACTTGGCTGTCTTGTGA   53827       AGAAAAA
                                  TCACGGGG     TGGGTCC
                                  ||||||||     |||||||
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```
                                AGTGTTCT      GTTCAGG
                                    GTCG___
GAM890  PGC      3'  GGATTCAGCCTTCTTTTTCTGG 10531     CG      AAA
                                TCA  GGGAGAA   TGGGTCC
                                |||  |||||||   |||||||
                                GGT  TTTTCTT   ACTTAGG
                                  CT      CCG
GAM890  PIG8     3'  GGAACACTTTGTTTTTCTCCCT 16872           GG ____
            GTG                   ACGGGGAGAAAAAT  G    TCC
                                |||||||||||||| |    |||
                                TGTCCCTCTTTTTG  T    AGG
                                       TT CACA
GAM890  PIGN     3'  TTCATTTTTTTCCTTTGG    24675     C
                                TCA GGGGAGAAAAATGGG
                                ||| ||||||||||||||
                                GGT TTCCTTTTTTTACTT
                                 _
GAM890  PIK3C2B  3'  GGATTTTTTTTTTTTTTTTTGG 10573     CG        TG
                                TCA  GGGAGAAAAA  GGTCC
                                |||  ||||||||||  |||||
                                GGT  TTTTTTTTTT  TTAGG
                                  TT        TT
GAM890  PIK3C2B  3'  GACCCATGCTCTTTTGG     10566    G     AAA
                                C GGGAGA   ATGGGTC
                                | ||||||   |||||||
                                G TTTTCT   TACCCAG
                                 G     CG_
GAM890  PIK3R3   5'  GAGCTTTTCTCCCCGGA     61059    A       AAT  G
                                TC CGGGGAGAAA   GG TC
                                || ||||||||||   || ||
                                AG GCCCCTCTTT   TC AG
                                  _       ___  G
GAM890  PIK4CB   3'  GGGCCTTTCTTCTCCTTGT    10593         AAAT
                                ACGGGGAGAA    GGGTCC
                                ||||||||||    ||||||
                                TGTTCCTCTT    TCCGGG
                                      CTT_
GAM890  PIN1L    3'  GGGTTCCCCACTCCCTGT     20623        AAAAA   ___
                                ACGGGGAG    TGGG   TCC
                                ||||||||    ||||   |||
                                TGTCCCTC    ACCC   GGG
                                     _____   CTT
GAM890  PKHD1    5'  GATCATTTCTCCCTTGA     56914     C       AATG
                                TCA GGGGAGAAA    GGTC
                                ||| |||||||||    ||||
                                AGT TCCCTCTTT    CTAG
                                  _       A___
GAM890  PLA2G2D  3'  GGACAACTTTTTCCTATGA   24796     CG      AAATGG
                                TCA  GGGAGAA     GTCC
                                |||  |||||||     ||||
```

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                                AGT  CCTTTTT     CAGG
                                  AT      CAA___
GAM890  PLEK     3'  GGACCTGTCCACTTCTGTGA  10633       G  AAAA
                                TCACGGG AG    ATGGGTCC
                                ||||||| ||    ||||||||
                                AGTGTCT TC    TGTCCAGG
                                   _ ACC_
GAM890  PLXNA1   3'  GGTCCCGGCTCTTCCTGTG   72312         AAAA   T
                                CACGGGGAGA    TGGG CC
                                ||||||||||    |||| ||
                                GTGTCCTTCT    GCCC GG
                                     CG__    T
GAM890  PNN      3'  GGATTACCTTTCCTTGT     71112         AAAATG
                                ACGGGGAGA     GGTCC
                                |||||||||     |||||
                                TGTTCCTTT     TTAGG
                                     CCA___
GAM890  POP2     5'  GGATTCATTCATTTTCTG    42146     GG  AAA
                                CGG  AG   AATGGGTCC
                                |||  ||   |||||||||
                                GTC  TT   TTACTTAGG
                                  TT  AC_
GAM890  POP2     3'  GACTATCTTCTCTGTGG     42145         AAAAATG
                                TCACGGGGAG      GGTC
                                ||||||||||      ||||
                                GGTGTCTCTT      TCAG
                                     CTA_____
GAM890  PPARA    5'  GGGCCCTGTCTGCTCTGTGG   17275        _  AAAAT
                                TCACGGGG AGA    GGGTCC
                                |||||||| |||    ||||||
                                GGTGTCTC TCT    CCCGGG
                                    G   GT___
GAM890  PPAT     3'  GATTTTTTTTTTTTTCTG    10699     GG     TG
                                CGG  AGAAAAA  GGTC
                                |||  |||||||  ||||
                                GTC  TTTTTTT  TTAG
                                  TT      TT
GAM890  PPP2R5C  3'  GGATCTGTTTTTTCATCG    10760     GGA
                                CGG   GAAAAATGGGTCC
                                |||   ||||||||||||
                                GCT   TTTTTTGTCTAGG
                                  AC_
GAM890  PPP3R1   3'  GGAAGTATTTTTCTCTGTGA  76343     GG        GG
                                TCAC  GGAGAAAAATG  TCC
                                ||||  ||||||||||  |||
                                AGTG  TCTCTTTTTAT  AGG
                                   __         GA
GAM890  PRKACG   3'  GGGCCCCAGAGTTCCTTGT   10798        AAAAAT
                                ACGGGGAG     GGGTCC
                                ||||||||     ||||||
```

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                                TGTTCCTT     CCCGGG
                                     GAGAC_
GAM890  PRKCN    3'  GAAATGTTATTTTCCCTGTGA  19446          A   GG  C
                                TCACGGGGAGAA AATG  TC
                                |||||||||||| ||||  ||
                                AGTGTCCCTTTT TTGT  AG
                                       A    AA
GAM890  PRSS16   3'  GGATTCATGATTCTGGTGG   19630     G   GAAAA
                                TCAC GGGA    ATGGGTCC
                                |||| ||||    ||||||||
                                GGTG TCTT    TACTTAGG
                                  G   AG___
GAM890  PSEN1    5'  GGGTCTGATCTTTCTCCTTG  23625         A  _  GT
                                CGGGGAGAAA AT GG  CC
                                |||||||||| || ||  ||
                                GTTCCTCTTT TA TC  GG
                                       C  G  TG
GAM890  PSPHL    3'  GTTTTTTTCCCTTTGG     92908     C
                                TCA GGGGAGAAAAAT
                                ||| ||||||||||||
                                GGT TCCCTTTTTTTG
                                  T
GAM890  PVR      3'  GGGCCCGATCTTTCTTTGG   21481     C  GG   AAAA
                                TCA GG  AGA   TGGGTCC
                                ||| ||  |||   |||||||
                                GGT TC  TCT   GCCCGGG
                                  T  TT   A___
GAM890  RAB33A   5'  GACGTTCTCTTTGTG      16577          AAATGG
                                CACGGGGAGAA     GTC
                                ||||||||||      |||
                                GTGTTTCTCTT     CAG
                                       G_____
GAM890  RAG1     3'  TATTTTTCTCCTGTGA     4818         G
                                TCACGGG AGAAAAATG
                                ||||||| |||||||||
                                AGTGTCC TCTTTTTAT
                                      _
GAM890  RAG1     3'  GTTTTTCTTCCTTTGA     4817     C
                                TCA GGGGAGAAAAAT
                                ||| ||||||||||||
                                AGT TCCTTCTTTTTG
                                  T
GAM890  RASGRP2  3'  GGACTCATTCCTGCCTTGGA  19510    A    AGAAA
                                TC CGGGG    AATGGGTCC
                                || |||||    |||||||||
                                AG GTTCC    TTACTCAGG
                                 _    GTCC_
GAM890  RBBP5    3'  GGACTCATTTAAACTTTG    17338      AGAA
                                CGGGG   AAATGGGTCC
                                |||||   ||||||||||
```

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                                GTTTC   TTTACTCAGG
                                  AAA_
GAM890  RENT1   3' GGATTGACGGCTTTTTCCCG  11292       AAA __
                                CGGGGAGAA  TG GGTCC
                                |||||||||  || |||||
                                GCCCTTTTT  GC TTAGG
                                    CG_ AG
GAM890  RET     3' GGATCAGCTCTTCCTGTG   40177       AAAATG
                                CACGGGGAGA    GGTCC
                                ||||||||||    |||||
                                GTGTCCTTCT    CTAGG
                                    CGA___
GAM890  RET     3' GGATCAGCTCTTCCTGTG   40593       AAAATG
                                CACGGGGAGA    GGTCC
                                ||||||||||    |||||
                                GTGTCCTTCT    CTAGG
                                    CGA___
GAM890  REV3L   5' GGCTTCTCTCCTTGCGG    11297   A     AAAAT
                                TC CGGGGAGA   GGGTC
                                || ||||||||   |||||
                                GG GTTCCTCT   TTCGG
                                 C      C____
GAM890  RFP     3' GGATTCATTGACTTCTTG   21492      AAA
                                CGGGGAG  AATGGGTCC
                                |||||||  |||||||||
                                GTTCTTC  TTACTTAGG
                                   AG_
GAM890  RNF7    3' GATCTGTGGTCCTTTG     26481     A AAA
                                CGGGG GA  ATGGGTC
                                ||||| ||  |||||||
                                GTTTC CT  TGTCTAG
                                  _ GG_
GAM890  RP42    3' GGAATTTTTTTTTTTTCCTG  40202        TGGG_
                                CGGGGAGAAAAA   TCC
                                ||||||||||||   |||
                                GTCCTTTTTTTT   AGG
                                     TTTTA
GAM890  RPH3AL  3' GGGTCTGTTTAGTTTCTTTG  22753      A_    GT
                                CGGGGAGA  AAATGG  CC
                                ||||||||  ||||||  ||
                                GTTTCTTT  TTTGTC  GG
                                   GA     TG
GAM890  RUNX1   3' GGCTTCTTTCTCCCTG     8265        AAT
                                CGGGGAGAAA  GGGTC
                                ||||||||||  |||||
                                GTCCCTCTTT  TTCGG
                                     C__
GAM890  RUNX3   3' GACCCATGTCTCCTGG     15115   G    AAA
                                C GGGAGA  ATGGGTC
                                | ||||||  |||||||
```

```
                                G TCCTCT   TACCCAG
                                 G     G__
GAM890  SEZ6L    3'  GGGTTACGGGTTTTTTCCCCGG 40879    A        ATG__ GT
              A                   TC CGGGGAGAAAA    G  CC
                                  || ||||||||||    |  ||
                                  AG GCCCCTTTTTT    T  GG
                                   _         GGGCA TG
GAM890  SFTPA2   3'  GGATCCAAACCCATCTTCCTGG 22648    A      AAAA__
              A                   TC CGGGGAGA     TGGGTCC
                                  || ||||||||     |||||||
                                  AG GTCCTTCT     ACCTAGG
                                   _       ACCCAA
GAM890  SH3BP2   3'  GGACCCTAGAATCCTTGTGA   11608         GAAAAAT
                                  TCACGGGGA      GGGTCC
                                  |||||||||      ||||||
                                  AGTGTTCCT      CCCAGG
                                        AAGAT__
GAM890  SHC1     3'  GGACCTGTGTTCTTGCTG    11650     G    AA
                                  CGG GAGAA  ATGGGTCC
                                  ||| |||||  ||||||||
                                  GTC TTCTT  TGTCCAGG
                                    G    G_
GAM890  SIAH1    3'  GGGCCACTGCTTTTCCCTTTGT 11658      __      AAATG
              GA                    TCAC  GGGGAGAA    GGTCC
                                  ||||  ||||||||    |||||
                                  AGTG  TCCCTTTT    CCGGG
                                     TT       CGTCA
GAM890  SIAT1    3'  GGGCTTGCTCTCTCTGTG    11662          AAAA
                                  CACGGGGAGA    TGGGTCC
                                  ||||||||||    |||||||
                                  GTGTCTCTCT    GTTCGGG
                                        C___
GAM890  SLC16A1  3'  GGAATTTTTTTTTCCTGGA   11743    A         TGGG
                                  TC CGGGGAGAAAAA    TCC
                                  || ||||||||||||    |||
                                  AG GTCCTTTTTTTT    AGG
                                   _          TA__
GAM890  SLC25A13 3'  GGATAGTGCTGTCTTTTTGTGG 26503          AAAATGG
                                  TCACGGGGAGA      GTCC
                                  ||||||||||       ||||
                                  GGTGTTTTTCT      TAGG
                                        GTCGTGA
GAM890  SLC25A5  3'  ATTTTTCCCCCTGTGA     6712          A
                                  TCACGGGG GAAAAAT
                                  |||||||| |||||||
                                  AGTGTCCC CTTTTTA
                                       C
GAM890  SLC4A4   5'  GGGCTTTGATTTCTTTTTG   13640          AAT
                                  CGGGGAGAAA   GGGTCC
                                  ||||||||||   ||||||
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                                GTTTTTCTTT  TTCGGG
                                     AGT
GAM890  SLC6A8   3' GGCCTGCCTTTCCCTG     18852       AAAA
                                CGGGGAGA   TGGGTC
                                ||||||||   ||||||
                                GTCCCTTT   GTCCGG
                                    CC__
GAM890  SLC7A6   3' GGACTTCTGTTTTCTCCCTGTG 14311          AT_
           G                    TCACGGGGAGAAAA  GGGTCC
                                ||||||||||||||  ||||||
                                GGTGTCCCTCTTTT  TTCAGG
                                       GTC
GAM890  SMARCD1  3' GGACCAAACTTTTTTTTGT   11818        AAATG
                                ACGGGGAGAA    GGTCC
                                ||||||||||    |||||
                                TGTTTTTTTT    CCAGG
                                     CAAA_
GAM890  SMARCD1  3' GGACCAAACTTTTTTTTGT   57436        AAATG
                                ACGGGGAGAA    GGTCC
                                ||||||||||    |||||
                                TGTTTTTTTT    CCAGG
                                     CAAA_
GAM890  SMCX     5' GATCCGGTTTGTTGTGG     14826      G  GAAAAA
                                TCACGG GA     TGGGTC
                                |||||| ||     ||||||
                                GGTGTT TT     GCCTAG
                                   G  TG____
GAM890  SNTB2    3' GATCTGTCATCCTGGA      55612    A   GA  AAAA
                                TC CGGG  GA    TGGGTC
                                || ||||  ||    ||||||
                                AG GTCC  CT    GTCTAG
                                 _    TA  ____
GAM890  SORBS1   3' GGACGTCTGTTCTTTGTGG   31158        AAAAAT  _
                                TCACGGGGAG     GG GTCC
                                ||||||||||     || ||||
                                GGTGTTTCTT     CT CAGG
                                     GT____  G
GAM890  SORCS1   3' GGGCAATTTCCTCCTGTGA   53585       GA   AATGG
                                TCACGGG  GAAA    GTCC
                                |||||||  ||||    ||||
                                AGTGTCC  CTTT    CGGG
                                    TC   AA___
GAM890  SORCS3   3' GACTTTCTTTTTCCTTGTGG  30373          AAT
                                TCACGGGGAGAAA  GGGTC
                                ||||||||||||   |||||
                                GGTGTTCCTTTTT  TTCAG
                                       CT_
GAM890  SOX13    3' GGGCCTGGCCCCTTCTCCTCTG 19083    C      AAA__
           G                    TCA GGGGAGAA    TGGGTCC
                                ||| ||||||||    |||||||
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```
                                GGT CTCCTCTT    GTCCGGG
                                  _      CCCCG
GAM890  SOX13    3'  GGGCTCATCAGCCTTCCTG   19084       AAAA
                                CGGGGAG   ATGGGTCC
                                |||||||   ||||||||
                                GTCCTTC   TACTCGGG
                                    CGAC
GAM890  SPAG4    5'  GGGTCCGTGGGGTCCCCGCGG  11896   A    GAAAA   GT
                                TC CGGGGA    ATGG  CC
                                || ||||||    ||||  ||
                                GG GCCCCT    TGCC  GG
                                 C     GGGG_   TG
GAM890  STAU2    3'  GGATTGAGTTTCTTTTTATGA  26907    CG      AATG
                                TCA  GGGAGAAA   GGTCC
                                |||  ||||||||   |||||
                                AGT  TTTTCTTT   TTAGG
                                  AT       GAG_
GAM890  STC1     3'  GCTTTATTTTTCTTTTCCTGG  12031    C GG         TCC
                                TCA G  GAGAAAAATGGG
                                ||| |  ||||||||||||
                                GGT C  TTCTTTTTATTT
                                  C TT          CG
GAM890  STK10    3'  GTTTTGCTCTCTGTGG      19990         A
                                TCACGGGGAG AAAAT
                                |||||||||| |||||
                                GGTGTCTCTC TTTTG
                                      G
GAM890  STS      3'  GGATTCCACTGTTTTCTTTG   4453         AAA   _
                                CGGGGAGAA   TGGG TCC
                                |||||||||   |||| |||
                                GTTTCTTTT   ACCT AGG
                                      GTC    T
GAM890  STXBP1   3'  GGACGCCTTCTCCCCGT     12048         AAAT  _
                                ACGGGGAGAA    GG GTCC
                                ||||||||||    || ||||
                                TGCCCCTCTT    CC CAGG
                                      ____  G
GAM890  SURF4    3'  GGGTTCTCTTCTCCTGTGA    52544       G    AAAT GG
                                TCACGGG AGAA    G  TCC
                                ||||||| ||||    |  |||
                                AGTGTCC TCTT    C  GGG
                                    _    CT__ TT
GAM890  TARBP2   5'  GGGTTCTGTAGTTTTCTCGCGA 56169    A       AAAAT GG
                                TC CGGGGAGA     G  TCC
                                || ||||||||     |  |||
                                AG GCTCTTTT     C  GGG
                                 C       GATGT TT
GAM890  TARBP2   5'  GGGTTCTGTAGTTTTCTCGCGA 14809    A       AAAAT GG
                                TC CGGGGAGA     G  TCC
                                || ||||||||     |  |||
```

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                                AG GCTCTTTT    C  GGG
                                 C       GATGT TT
GAM890  TARBP2   5'  GGGTTCTGTAGTTTTCTCGCGA 56161    A       AAAAT GG
                                TC CGGGGAGA    G  TCC
                                || ||||||||    |  |||
                                AG GCTCTTTT    C  GGG
                                 C       GATGT TT
GAM890  TBL2     3'  GACTTCTCTCTTCGGGA    24928    A      AAAAT
                                TC CGGGGAGA    GGGTC
                                || ||||||||    |||||
                                AG GCTTCTCT    TTCAG
                                 G       C____
GAM890  TBL2     3'  GACTTCTCTCTTCGGGA    52185    A      AAAAT
                                TC CGGGGAGA    GGGTC
                                || ||||||||    |||||
                                AG GCTTCTCT    TTCAG
                                 G       C____
GAM890  TBX3     3'  GGATTCATGTCGTTCTTTG   33355       AAAA
                                CGGGGAG   ATGGGTCC
                                |||||||   ||||||||
                                GTTTCTT   TACTTAGG
                                    GCTG
GAM890  TBX5     5'  GGACTCCCACCTCCCTTCGTGA 54891      __    AAAAAT
                                TCACG  GGGAG    GGGTCC
                                |||||  |||||    ||||||
                                AGTGC  CCCTC    CTCAGG
                                   TT    CACC__
GAM890  TBX5     5'  GGACTCCCACCTCCCTTCGTGA 3959       __    AAAAAT
                                TCACG  GGGAG    GGGTCC
                                |||||  |||||    ||||||
                                AGTGC  CCCTC    CTCAGG
                                   TT    CACC__
GAM890  TBXA2R   5'  GGGCAATCCTTTTCCCGTGG  6500          AAAATGG
                                TCACGGGGAGA     GTCC
                                ||||||||||     ||||
                                GGTGCCCTTTT     CGGG
                                      CCTAA__
GAM890  TCF1     3'  GGGCCTATGGAGAGCCCTGGGA 5035    A    AGAAAA
                                TC CGGGG    ATGGGTCC
                                || |||||    ||||||||
                                AG GTCCC    TATCCGGG
                                 G    GAGAGG
GAM890  TCF19    3'  GGACTCATTCAGGGCCTGGA  97738    A   GAGAAA
                                TC CGGG    AATGGGTCC
                                || ||||    |||||||||
                                AG GTCC    TTACTCAGG
                                 _   GGGAC_
GAM890  TCF19    5'  GATTCATTGCCCTCGGA    97737    A    AGAAA
                                TC CGGGG    AATGGGTC
                                || |||||    ||||||||
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```
                                AG GCTCC    TTACTTAG
                                 _    CG___
GAM890  TCF19   3' GGACTCATTCAGGGCCTGGA  97868   A   GAGAAA
                                TC CGGG    AATGGGTCC
                                || ||||    |||||||||
                                AG GTCC    TTACTCAGG
                                 _   GGGAC_
GAM890  TCF19   5' GATTCATTGCCCTCGGA    97867   A    AGAAA
                                TC CGGGG   AATGGGTC
                                || |||||   ||||||||
                                AG GCTCC    TTACTTAG
                                 _    CG___
GAM890  TCF2    3' GGGCTTTGTGGATCTTTCTGCG 21383   A  GG   AAAAT_
          G                      TC CGG  AGA    GGGTCC
                                || |||  |||    ||||||
                                GG GTC  TCT    TTCGGG
                                 C   TT   AGGTGT
GAM890  TCL1B   3' GGACTTGGATGCCCTGTGG   16985      AGAAAAA
                                TCACGGGG     TGGGTCC
                                ||||||||     |||||||
                                GGTGTCCC     GTTCAGG
                                     GTAG___
GAM890  TCP10   3' GGGCCATTTCTGCCTTGTGA  16046       _    AATG
                                TCACGGGG AGAAA   GGTCC
                                |||||||| |||||   |||||
                                AGTGTTCC TCTTT   CCGGG
                                     G    A___
GAM890  TEC     3' GGGCCTTCCTTTTTGCCTTGTG 12220       AG   AT_
          A                     TCACGGGG  AAAA   GGGTCC
                                ||||||||  ||||   ||||||
                                AGTGTTCC  TTTT   TCCGGG
                                     GT   CCT
GAM890  TEGT    3' GGATCTCCAGCTCCTTCCTGTG 64625        AAAAA  __
          G                     TCACGGGGAG    TGG  GTCC
                                ||||||||||    |||  ||||
                                GGTGTCCTTC    ACC  TAGG
                                      CTCG_  TC
GAM890  TEM8    5' GGACCCTGCTCTCCCCG    49855       AAAAT
                                CGGGGAGA    GGGTCC
                                ||||||||    ||||||
                                GCCCCTCT    CCCAGG
                                     CGT__
GAM890  TEM8    5' GGACCCTGCTCTCCCCG    36330       AAAAT
                                CGGGGAGA    GGGTCC
                                ||||||||    ||||||
                                GCCCCTCT    CCCAGG
                                     CGT__
GAM890  TEM8    5' GGACCCTGCTCTCCCCG    53835       AAAAT
                                CGGGGAGA    GGGTCC
                                ||||||||    ||||||
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                                GCCCCTCT    CCCAGG
                                    CGT__
GAM890  TFDP1    5'  AAAATCATTTTTCTTCTCTGG  23046     C          GTCC
                                TCA GGGGAGAAAAATGG
                                ||| ||||||||||||||
                                GGT CTCTTCTTTTTACT
                                  _          AAAAA
GAM890  TGFA     3'  GGTTCACTTCCTCGTGA     12254         AAAAA  GG
                                TCACGGGGAG    TG  TC
                                |||||||||     ||  ||
                                AGTGCTCCTT    AC  GG
                                     C____  TT
GAM890  TGFBR3   5'  GGAGCTTTTTTTCCTTG     12275          AT  G
                                CGGGGAGAAAA  GG TCC
                                ||||||||||  ||  |||
                                GTTCCTTTTTT  TC AGG
                                    __  G
GAM890  TGM2     3'  GGGCCTTTGTTTCCTTGT    16055         AAAAT
                                ACGGGGAGA    GGGTCC
                                |||||||||    ||||||
                                TGTTCCTTT    TCCGGG
                                    GTT__
GAM890  TIA1     3'  GGATTTTTATCTTTCGTGA   41850       GG A  AAAAT
                                TCACG  G GA    GGGTCC
                                |||||  | ||    ||||||
                                AGTGC  T CT    TTTAGG
                                   TT _  ATT__
GAM890  TIA1     3'  GGATTTTTATCTTTCGTGA   42247       GG A  AAAAT
                                TCACG  G GA    GGGTCC
                                |||||  | ||    ||||||
                                AGTGC  T CT    TTTAGG
                                   TT _  ATT__
GAM890  TIC      3'  GGACAAACCTTGTTTCCCTGTG 24937           AAAATGG_
            G                    TCACGGGGAGA       GTCC
                                ||||||||||        ||||
                                GGTGTCCCTTT       CAGG
                                     GTTCCAAA
GAM890  TK1      5'  GGGTTCGTGAACTTCCCGGA  12306    A     AAAA   GG
                                TC CGGGGAG    ATG  TCC
                                || |||||||    |||  |||
                                AG GCCCTTC    TGC  GGG
                                  _      AAG_   TT
GAM890  TKT      3'  GGGTCTATACATTCCTGAGA  6513     A     GAAAA   GT
                                TC CGGGGA     ATGG  CC
                                || ||||||     ||||  ||
                                AG GTCCTT     TATC  GG
                                 A     ACA__    TG
GAM890  TLL1     3'  CTCTTTCATTTTTCTCTTCCTG 24950     C          TCC
            G                    TCA GGGGAGAAAAATGGG
                                ||| ||||||||||||||
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                                GGT CTTCTCTTTTTACTT
                                  C           TCTCT
GAM890  TMSB4Y   5'  GATCTGTCCTCTTTG      14843       AAAA
                                CGGGGAG   ATGGGTC
                                |||||||   |||||||
                                GTTTCTC   TGTCTAG
                                    C___
GAM890  TNC      3'  GGGCCTCACCTCCTCTGTGA  9289       _   AAAAAT
                                TCACGG GGAG     GGGTCC
                                |||||| ||||     ||||||
                                AGTGTC CCTC     TCCGGG
                                   T   CAC___
GAM890  TNFRSF17 5'  GCTCCCTTGTTTTCTTTTTGTG 6817           AT_   TCC
          A                     TCACGGGGAGAAAA   GGG
                                |||||||||||||   |||
                                AGTGTTTTTCTTTT   CCC
                                       GTT   TCG
GAM890  TNFSF15  5'  GATGTCTCTTCCTGTGG     17594          AAAATGG
                                TCACGGGGAGA      GTC
                                ||||||||||      |||
                                GGTGTCCTTCT      TAG
                                      CTG____
GAM890  TNFSF4   3'  GGGTCTTGCTTTTCTTTCTGT  12445     GG     AT_  GT
                                ACGG  AGAAAA   GG  CC
                                ||||  ||||||   ||  ||
                                TGTC  TCTTTT   TC  GG
                                  TT     CGT  TG
GAM890  TP63     3'  GGGCTTAATGGAGTTCTTGTGG 13569        GAAAAA
                                TCACGGGGA     TGGGTCC
                                |||||||||     |||||||
                                GGTGTTCTT     ATTCGGG
                                      GAGGTA
GAM890  TRIM37   3'  GGATTCATTACGTTCCTGG   30973   G    AAA
                                C GGGAG   AATGGGTCC
                                | |||||   |||||||||
                                G TCCTT   TTACTTAGG
                                 G    GCA
GAM890  TRIM39   3'  GGCCTCCTTCCCGTG       41174         AAAAAT
                                CACGGGGAG     GGGTC
                                |||||||||     |||||
                                GTGCCCTTC     TCCGG
                                      C_____
GAM890  TRIM9    3'  GGGCCTGTTGGCTGCTCCTGG  53760   G    AAA__
                                C GGGAG    AATGGGTCC
                                | |||||    |||||||||
                                G TCCTC    TTGTCCGGG
                                 G    GTCGG
GAM890  TRPM6    3'  GGGCTTGAGCGATTCTTGTG   34544        GAAAAAT
                                CACGGGGA      GGGTCC
                                ||||||||      ||||||
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                                GTGTTCTT     TTCGGG
                                    AGCGAG_
GAM890  TRPV1   3'  CTTTTTTTTTTTTCTGTGA   54869      GG     TG
                                TCACGG  AGAAAAA  GG
                                ||||||  |||||||  ||
                                AGTGTC  TTTTTTT  TC
                                   TT      TT
GAM890  TRPV1   3'  CTTTTTTTTTTTTCTGTGA   38084      GG     TG
                                TCACGG  AGAAAAA  GG
                                ||||||  |||||||  ||
                                AGTGTC  TTTTTTT  TC
                                   TT      TT
GAM890  TRRAP   5'  GGACCTGATACTTTTCTCTTGA 13023     C      AA  _
                                TCA GGGGAGAA  AT GGGTCC
                                |||  ||||||||  ||  ||||||
                                AGT TCTCTTTT  TA TCCAGG
                                  _      CA  G
GAM890  TSN     3'  GGACAGAATTTTTTTTGTTG   16108     G       GG_
                                CGG GAGAAAAAT   GTCC
                                |||  |||||||||   ||||
                                GTT TTTTTTTTA   CAGG
                                  G        AGA
GAM890  TYK2    3'  AACTTATTTTTCTTTCTTGG   59874     C  GG         CC
                                TCA GG  AGAAAAATGGGT
                                |||  ||  ||||||||||||
                                GGT TC  TCTTTTTATTCA
                                  _  TT          AG
GAM890  UBE4A   3'  TGCCTTTTTTTCTTTCTGTGA   16566       GG     T   CC
                                TCACGG  AGAAAAA GGGT
                                ||||||  ||||||| ||||
                                AGTGTC  TCTTTTT TCCG
                                   TT      _   TG
GAM890  UBQLN1  3'  TGTATTTTTCTTTTCTGG    25544     C GG        GGTCC
                                TCA G  GAGAAAAATG       G
                                |||  |  ||||||||||       |
                                GGT C  TTCTTTTTAT       T
                                  _ TT        G_______
GAM890  UCP3    3'  GGGCTCGTAAATATTCCCTG   12536       AAAA_
                                CGGGGAG    ATGGGTCC
                                |||||||    ||||||||
                                GTCCCTT    TGCTCGGG
                                    ATAAA
GAM890  UGT2B11 3'  GATTTCTTTCTTCCTGTGA   6537           AAT
                                TCACGGGGAGAAA   GGGTC
                                ||||||||||||   |||||
                                AGTGTCCTTCTTT   TTTAG
                                       C__
GAM890  UGT2B15 3'  GGATTTCCTTTTTCCTGTGA   60075          AAAT
                                TCACGGGGAGAA    GGGTCC
                                ||||||||||||   ||||||
```

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                                AGTGTCCTTTTT    TTTAGG
                                      CC__
GAM890  UGT2B28  3'  GATTTCTTTCTTCCTGTGA   53840          AAT
                                TCACGGGGAGAAA   GGGTC
                                |||||||||||||   |||||
                                AGTGTCCTTCTTT   TTTAG
                                      C__
GAM890  UNC13    3'  GGATCCAGGAGTATTTTCTTCT 21057         A_____
            TG                    CGGGGAGAAAA     TGGGTCC
                                |||||||||||     |||||||
                                GTTCTTCTTTT     ACCTAGG
                                      ATGAGG
GAM890  USH2A    3'  TATTTGTCTTTTTGTGA     23065          A
                                TCACGGGGAGA AAATG
                                |||||||||||| |||||
                                AGTGTTTTTCT TTTAT
                                      G
GAM890  USP6     5'  GGACTCAAAGGTTTTCTCCCTG 91148   A        A___
             AGA                    C CGGGGAGAAAA    TGGGTCC
                                | ||||||||||||    |||||||
                                G GTCCCTCTTTT    ACTCAGG
                                 A         GGAA
GAM890  VASP     3'  GGAAATTTTTTTTTCTCTTTG  12568          TGGG__
                                CGGGGAGAAAAA     TCC
                                ||||||||||||     |||
                                GTTTCTCTTTTT     AGG
                                      TTTTAA
GAM890  VCL      5'  GGATCCTACTTCTCTGT     12579        AAAAAT
                                ACGGGGAG     GGGTCC
                                ||||||||     ||||||
                                TGTCTCTT     CCTAGG
                                     CAT___
GAM890  VCL      5'  GGATCCTACTTCTCTGT     25738        AAAAAT
                                ACGGGGAG     GGGTCC
                                ||||||||     ||||||
                                TGTCTCTT     CCTAGG
                                     CAT___
GAM890  VDAC1    3'  GGACTTATTCCTTCTTGTG    12582        AAA
                                CACGGGGAG   AATGGGTCC
                                |||||||||   |||||||||
                                GTGTTCTTC   TTATTCAGG
                                     C__
GAM890  VPS41    3'  GGGTTTGGCTTTTTTCTGTG  26926      GG   AAA  GT
                                CACGG  AGAA   TGG  CC
                                |||||  ||||   |||  ||
                                GTGTC  TTTT   GTT  GG
                                   TT   CG_   TG
GAM890  VPS41    3'  GGGTTTGGCTTTTTTCTGTG  54657      GG   AAA  GT
                                CACGG  AGAA   TGG  CC
                                |||||  ||||   |||  ||
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                                GTGTC  TTTT   GTT  GG
                                   TT    CG_   TG
GAM890  VRK1     3'  GAACTGTTTTATTTTCCTGTGA 12621          _      G  C
                                TCACGGGGAGA AAAATGG TC
                                |||||||||||  |||||||  ||
                                AGTGTCCTTTT TTTTGTC AG
                                       A      A
GAM890  WHSC1    3'  GGGCTCATAGAGCTCTGCG   23666    G   AAAA
                                CG GGAG    ATGGGTCC
                                ||  ||||    ||||||||
                                GC TCTC    TACTCGGG
                                 G   GAGA
GAM890  WHSC1    3'  GGGCCTGTTTGCCGTCTGTGA  55848       GAGAA
                                TCACGGG    AAATGGGTCC
                                |||||||    ||||||||||
                                AGTGTCT    TTTGTCCGGG
                                    GCCG_
GAM890  WHSC1    3'  GGGCCTGTTTGCCGTCTGTGA  55831       GAGAA
                                TCACGGG    AAATGGGTCC
                                |||||||    ||||||||||
                                AGTGTCT    TTTGTCCGGG
                                    GCCG_
GAM890  WHSC1    3'  GGGCCTGTTTGCCGTCTGTGA  29913       GAGAA
                                TCACGGG    AAATGGGTCC
                                |||||||    ||||||||||
                                AGTGTCT    TTTGTCCGGG
                                    GCCG_
GAM890  WHSC1L1  5'  GGGCCTCCGTGTCTCTCCTGTG 43520       _   AAAAT
           A                    TCACGGG GAGA    GGGTCC
                                |||||||  ||||    ||||||
                                AGTGTCC CTCT    TCCGGG
                                    T   GTGCC
GAM890  WHSC1L1  5'  GGGCCTCCGTGTCTCTCCTGTG 35033       _   AAAAT
           A                    TCACGGG GAGA    GGGTCC
                                |||||||  ||||    ||||||
                                AGTGTCC CTCT    TCCGGG
                                    T   GTGCC
GAM890  WIF1     5'  GGACCTGTTTCTACCCTGGA   60180    A   _   AA
                                TC CGGGG AGAA  ATGGGTCC
                                ||  |||||  ||||  ||||||||
                                AG GTCCC TCTT  TGTCCAGG
                                 _    A   __
GAM890  WISP2    3'  GGACTGGCCATTTTTCT     13935         ___
                                AGAAAAATGG   GTCC
                                ||||||||||   ||||
                                TCTTTTTACC   CAGG
                                      GGT
GAM890  WNT3A    3'  GGATGAGGCTTCTTCCTGGA  52436    A       AAATGG
                                TC CGGGGAGAA     GTCC
                                ||  |||||||||     ||||
```

```
                                AG GTCCTTCTT      TAGG
                                 _        CGGAG_
GAM890  WNT5A    3'  GGAACCATTTTTTTTCCTGT   12670              G
                                ACGGGGAGAAAAATGG TCC
                                |||||||||||||||| |||
                                TGTCCTTTTTTTTACC AGG
                                      A
GAM890  XK       3'  GATCCACTTCTCTGT       40800         AAAAA
                                ACGGGGAG    TGGGTC
                                ||||||||    ||||||
                                TGTCTCTT    ACCTAG
                                    C____
GAM890  XRCC5    3'  GGTGTATTATTTTTTCTGTGG  40933       GG   A   G T
                                TCACGG  AGAA AATG G CC
                                ||||||  |||| |||| | ||
                                GGTGTC  TTTT TTAT T GG
                                   TT   A   G _
GAM890  ZFHX1B   3'  CGGCCTCAATTTTTTTTTTTTT 28923   GG     _____ _   C
             CTGTGA                 G  AGAAAAA    TG GGTC   G
                                |  |||||||    || ||||   |
                                C  TTTTTTT    AC CCGG   C
                                 TT      TTTTA  T      C
GAM890  ZHX1     3'  GACCCTTTCTTTTGTGA     23331        G    AAT    C
                                TCACGGG AGAAA   GGGTC
                                ||||||| |||||   |||||
                                AGTGTTT TCTTT   CCCAG
                                   _    ___     A
GAM890  ZNF137   3'  GGACTTGGGAGCTCTCTTTGA  12865     C     AAAAA
                                TCA GGGGAG    TGGGTCC
                                ||| ||||||    |||||||
                                AGT TCTCTC    GTTCAGG
                                  T     GAGG_
GAM890  ZNF16    3'  GGGCTTGTTTTTACAGCTTGTG 22724       GAG_    TG
                                CACGGG   AAAAA  GGTCC
                                ||||||   |||||  |||||
                                GTGTTC   TTTTT  TCGGG
                                   GACA    GT
GAM890  ZNF175   3'  GGATTATAAATTTTCTCCCCGG 23093    A        ATG__
             GA                   TC CGGGGAGAAAA    GGTCC
                                || ||||||||||    |||||
                                AG GCCCCTCTTTT    TTAGG
                                 G         AAATA
GAM890  ZNF216   3'  GGATCAGACCTTCTTTCCCGTG 20021         _  AAATG
             A                    TCACGGGGA GAA    GGTCC
                                |||||||||| |||    |||||
                                AGTGCCCTT CTT    CTAGG
                                      T  CCAGA
GAM890  ZNF22    3'  TCTTTTATTTCTTCTCCTTGTG 91466          _     TCC
             G                    TCACGGGGAGAA AAATGGG
                                ||||||||||| |||||||
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                                GGTGTTCCTCTT TTTATTT
                                      C      TCTG
GAM890  ZNF236   3' GGTTTTATTTTTTTTTCCTGA 23716    C  GG        T
                                TCA GG  AGAAAAATGGG CC
                                ||| ||  |||||||||||| ||
                                AGT CC  TTTTTTTATTT GG
                                  _  TT         T
GAM890  ZNF236   3' GGACCAATTCTCTCCATGA   23714    C      AAATG
                                TCA GGGGAGAA    GGTCC
                                ||| ||||||||    |||||
                                AGT CCTCTCTT    CCAGG
                                  A       AA___
GAM890  ZNF255   5' GACTTCTTTTCCTTTG     19321      A    AT
                                CGGGG GAAAA  GGGTC
                                ||||| |||||  |||||
                                GTTTC CTTTT  TTCAG
                                   _    C_
GAM890  ZNF257   5' GGCCCAGCCTCTGTGG     53098       AGAAAAA
                                TCACGGGG      TGGGTC
                                ||||||||      ||||||
                                GGTGTCTC      ACCCGG
                                     CG_____
GAM890  ZNF289   3' GGACTTGACTTTCTTTCTGGA 65334    A  GG    AA
                                TC CGG  AGAAA  TGGGTCC
                                || |||  |||||  |||||||
                                AG GTC  TCTTT  GTTCAGG
                                 _  TT    CA
GAM890  ZNF74    5' GGATCCTGCTCTTTCCCTG   12801       AAAAT
                                CGGGGAGA    GGGTCC
                                ||||||||    ||||||
                                GTCCCTTT    CCTAGG
                                     CTCGT
GAM890  AGMAT    3' ATTTTTTTTCCTTTGA     45404    C
                                TCA GGGGAGAAAAAT
                                ||| ||||||||||||
                                AGT TCCTTTTTTTTA
                                  T
GAM890  AGPAT1   3' GGACTCATCCATTCTTTGGA  21150    A     AAAA
                                TC CGGGGAG    ATGGGTCC
                                || |||||||    ||||||||
                                AG GTTTCTT    TACTCAGG
                                 _      ACC_
GAM890  AGPAT1   3' GACTCATCCATTTGTGA     51234       GA  AAAA
                                TCACGGG  GA    TGGGTC
                                |||||||  ||    ||||||
                                AGTGTTT  CT    ACTCAG
                                    AC  _____
GAM890  AGPAT1   3' GACTCATCCATTTGTGA     21149       GA  AAAA
                                TCACGGG  GA    TGGGTC
                                |||||||  ||    ||||||
```

```
                                AGTGTTT  CT    ACTCAG
                                   AC  _____
GAM890  AGPAT1   3'  GGACTCATCCATTCTTTGGA  51236    A      AAAA
                                TC CGGGGAG    ATGGGTCC
                                || |||||||    ||||||||
                                AG GTTTCTT    TACTCAGG
                                 _      ACC_
GAM890  AK5      3'  TCATTTTTTTTTCTTGA     23913     C  GG
                                TCA GG  AGAAAAATGG
                                ||| ||  ||||||||||
                                AGT TC  TTTTTTTACT
                                  _ TT
GAM890  ALDH9    5'  GGTCCCGCCCCTCCCGTGG   5514        G  AAAAA   T
                                TCACGGG AG    TGGG CC
                                ||||||| ||    |||| ||
                                GGTGCCC TC    GCCC GG
                                   _ CCC__    T
GAM890  AP4M1    3'  GGGCCCAGCCTTTCTGTGG   16359       GG  AAAAA
                                TCACGG  AG    TGGGTCC
                                ||||||  ||    |||||||
                                GGTGTC  TC    ACCCGGG
                                   TT  CG___
GAM890  APBA2BP  3'  GGCTTGTCTCCTCCTGG     48351     C     AAAA TG
                                TCA GGGGAG    A  GGTC
                                ||| ||||||    |  ||||
                                GGT CTCCTC    T  TCGG
                                  C     _____ GT
GAM890  APBA2BP  3'  GGCTTGTCTCCTCCTGA     48352     C     AAAA TG
                                TCA GGGGAG    A  GGTC
                                ||| ||||||    |  ||||
                                AGT CTCCTC    T  TCGG
                                  C     _____ GT
GAM890  APCL     5'  GGGCCTCGTTTCTCCCTCTGG  19681     C       AAT
                                TCA GGGGAGAAA   GGGTCC
                                ||| |||||||||   ||||||
                                GGT TCCCTCTTT   TCCGGG
                                  C       GC_
GAM890  ARHGEF11 3'  GGATCCCAACACTCCTCCCTGT 28806          AAAAA_   _
           GG                    TCACGGGGAG     TGGG TCC
                                ||||||||||     |||| |||
                                GGTGTCCCTC     ACCC AGG
                                     CTCACA    T
GAM890  ARHGEF9  5'  GGATTTTGCCTTTCCCGTGG  30813         AAAAAT
                                TCACGGGGAG     GGGTCC
                                ||||||||||     ||||||
                                GGTGCCCTTT     TTTAGG
                                     CCGT__
GAM890  ARHGEF9  3'  GAATCTTTTCTTTGTGG     30810          AAAT GG
                                TCACGGGGAGAA   G  TC
                                ||||||||||||   |  ||
```

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                                GGTGTTTCTTTT   C  AG
                                      ____ TA
GAM890  ARHGEF9  3' GGCAATTTTCCCTCTGA    30814    C      AAATGG
                                TCA GGGGAGAA    GTC
                                ||| ||||||||    |||
                                AGT TCCCTTTT    CGG
                                  C       AA____
GAM890  ARP5    5' GGACCCTCGGCTCTTCCTTGG 71572    C     AAAAT
                                TCA GGGGAGA    GGGTCC
                                ||| |||||||    ||||||
                                GGT TCCTTCT    CCCAGG
                                  _      CGGCT
GAM890  ATP1B4   3' TGTTTTTTCTCTTGTGG    23831       GA
                                TCACGGG  GAAAAATG
                                |||||||  ||||||||
                                GGTGTTC  TTTTTTGT
                                    TC
GAM890  B7-H1    3' GGGCTCATCGACGCCTGTGA  26237       GAGAAAA
                                TCACGGG      ATGGGTCC
                                |||||||      ||||||||
                                AGTGTCC      TACTCGGG
                                    GCAGC__
GAM890  BAD     3' GGATCCGTGCTGTCTCCTTTGG 15063    C     AAA_
                                TCA GGGGAGA    ATGGGTCC
                                ||| |||||||    ||||||||
                                GGT TTCCTCT    TGCCTAGG
                                  _      GTCG
GAM890  BAD     3' GGATCCGTGCTGTCTCCTTTGG 52190    C     AAA_
                                TCA GGGGAGA    ATGGGTCC
                                ||| |||||||    ||||||||
                                GGT TTCCTCT    TGCCTAGG
                                  _      GTCG
GAM890  BART1    3' GGACTCTGCAGTTTCTTCCTGT 23987         AAT__
                                ACGGGGAGAAA    GGGTCC
                                ||||||||||    ||||||
                                TGTCCTTCTTT    CTCAGG
                                      GACGT
GAM890  BART1    3' GACCTATTTATCCTG      23985      AGAA
                                CGGGG    AAATGGGTC
                                |||||    |||||||||
                                GTCCT    TTTATCCAG
                                  A___
GAM890  BCAS4    3' GACTATTTTCCTGTGG      35257          AAAATG
                                TCACGGGGAGA     GGTC
                                ||||||||||     ||||
                                GGTGTCCTTTT     TCAG
                                      A_____
GAM890  BCDO     3' ACTTATTCTTTCTGTGG     33824       GG  AAA
                                TCACGG  AGA   ATGGGT
                                ||||||  |||   ||||||
```

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                                GGTGTC  TCT   TATTCA
                                   TT  ___
GAM890  BCL2L1   3'  GACTAGTTTTTATTCCTTGTGA 56805        _    G   C
                                TCACGGGGAG AAAAAT GGTC
                                |||||||||| |||||| ||||
                                AGTGTTCCTT TTTTTG TCAG
                                     A     A
GAM890  BCMP1    3'  GGATCTCTGTTTTTCCTG    48736        AAAT
                                CGGGGAGAA   GGGTCC
                                |||||||||   ||||||
                                GTCCTTTTT   TCTAGG
                                     GTC_
GAM890  BIRC1    3'  GGATCCACATGAATCTTCTGTG 15789       _ GAAAAA
          G                      TCACGGG GA     TGGGTCC
                                ||||||| ||     |||||||
                                GGTGTCT CT     ACCTAGG
                                    T  AAGTAC
GAM890  BIRC2    5'  ATTTTTTACCTTGTGG      67200        A
                                TCACGGGG GAAAAAT
                                |||||||| |||||||
                                GGTGTTCC TTTTTTA
                                    A
GAM890  BIRC2    5'  GGACAAGTTTTATCTTGTGA   67201        AGA    GG
                                TCACGGGG   AAAAT  GTCC
                                ||||||||   |||||  ||||
                                AGTGTTCT   TTTTG  CAGG
                                    A__    AA
GAM890  BIRC4    3'  GGATTCTGTCCATTTTCTTGT  6748         AAAAT_
                                ACGGGGAGA     GGGTCC
                                |||||||||     ||||||
                                TGTTCTTTT     CTTAGG
                                     ACCTGT
GAM890  BIRC5    3'  GGGCTCATTTTTGCTGTTTTGA 6749     C   G  _
                                TCA GGG AG AAAAATGGGTCC
                                ||| ||| || ||||||||||||
                                AGT TTT TC TTTTTACTCGGG
                                  _  G  G
GAM890  BLP1     3'  GGATCCATGTTCCTCTTGTGA  54331       GA   AA
                                TCACGGG  GAA  ATGGGTCC
                                |||||||  |||  ||||||||
                                AGTGTTC  CTT  TACCTAGG
                                    TC   G_
GAM890  BLP1     3'  GGATCCATGTTCCTCTTGTGA  49199       GA   AA
                                TCACGGG  GAA  ATGGGTCC
                                |||||||  |||  ||||||||
                                AGTGTTC  CTT  TACCTAGG
                                    TC   G_
GAM890  BLP2     3'  GAAATATATTTTTTTCTGTGA  54334       GG    A   GG  C
                                TCACGG  AGAAA ATG  TC
                                ||||||  ||||| |||  ||
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                                AGTGTC  TTTTT TAT  AG
                                   TT    A   AA
GAM890  BLP2    3'  GAAATATATTTTTTTCTGTGA 47116      GG    A   GG  C
                                TCACGG  AGAAA ATG  TC
                                ||||||  ||||| |||  ||
                                AGTGTC  TTTTT TAT  AG
                                   TT    A   AA
GAM890  BM039    5'  GGGCCCATTTCCGTCCGT    37454     GA   AA
                                ACGGG  GAA  ATGGGTCC
                                |||||  |||  ||||||||
                                TGCCT  CTT  TACCCGGG
                                  GC  __
GAM890  BMF     3'  GGACCTTCTTTCTCTGT     53159        AAAAT
                                ACGGGGAGA    GGGTCC
                                |||||||||    ||||||
                                TGTCTCTTT    TCCAGG
                                     CT___
GAM890  BP75    5'  GGACTTCCCCATCCTGTGG   23990       AGAAAAAT
                                TCACGGGG      GGGTCC
                                ||||||||      ||||||
                                GGTGTCCT      TTCAGG
                                     ACCCC___
GAM890  BPES    3'  GGGCTCGTCTCTTTCCGGA   43536    A  GG   AAA
                                TC CGG  AGA   ATGGGTCC
                                || |||  |||   ||||||||
                                AG GCC  TCT   TGCTCGGG
                                 _   TT   C__
GAM890  BPNT1    3'  GGATTAGTTTATTCTTGTGG  64757        G   AATG
                                TCACGGGGA AAA    GGTCC
                                ||||||||| |||    |||||
                                GGTGTTCTT TTT    TTAGG
                                     A   GA__
GAM890  BRAG    3'  GGATTTTACAAATCTCTTTGCG 29475    A      AAAAT_
          G                      TC CGGGGAGA     GGGTCC
                                || ||||||||     ||||||
                                GG GTTTCTCT     TTTAGG
                                 C       AAACAT
GAM890  BRPF3    3'  GGGCCTATGTGTCTCTGTCG  92321    _    AAA
                                CGG GGAGA   ATGGGTCC
                                ||| |||||   ||||||||
                                GCT TCTCT   TATCCGGG
                                  G    GTG
GAM890  BTBD1    3'  ACATCCATTTTTTTCCCTTGA  47474    C           CC
                                TCA GGGGAGAAAAATGGGT
                                ||| ||||||||||||||||
                                AGT TCCCTTTTTTTACCTA
                                  _            CAA
GAM890  C11orf21  3'  GGGTTCACTCTTCTTGT     26244        AAAA  GG
                                ACGGGGAGA    TG  TCC
                                |||||||||    ||  |||
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                                TGTTCTTCT   AC  GGG
                                     C___  TT
GAM890  C11orf23  3'  GGATTTTTTTTTTTTTTTTTGG 37014    CG       TG
                                TCA  GGGAGAAAAA  GGTCC
                                |||  ||||||||||  |||||
                                GGT  TTTTTTTTTT  TTAGG
                                  TT        TT
GAM890  C1orf22   3'  ACTACTGTTTTTCTCCTTTGA  47252    C          GTCC
                                TCA GGGGAGAAAAATGG
                                ||| ||||||||||||||
                                AGT TTCCTCTTTTTGTC
                                  _           ATCAA
GAM890  C20orf102 3'  GGACCCAATTCTCCTCGGA   54617    A       AAA
                                TC CGGGGAGAA   TGGGTCC
                                || |||||||||   |||||||
                                AG GCTCCTCTT   ACCCAGG
                                 _       A__
GAM890  C20orf121 3'  GGATCCTGTTTTTGTTTGTGG  44276       G    AAT
                                TCACGGG AGAAA   GGGTCC
                                ||||||| |||||   ||||||
                                GGTGTTT TTTTT   CCTAGG
                                    G    GT_
GAM890  C20orf142 3'  GGCTGTTTTCTCTGT       74784          AAATG
                                ACGGGGAGAA    GGTC
                                ||||||||||    ||||
                                TGTCTCTTTT    TCGG
                                     G____
GAM890  C20orf150 3'  GGACTGCTGAGTTTTTCTTCAT 65400    G       G____
           G                     CG GGAGAAAAAT    GGTCC
                                || ||||||||||    |||||
                                GT CTTCTTTTTG    TCAGG
                                 A         AGTCG
GAM890  C20orf160 3'  GGGCTTGAGGGAATCTCCTGA  54650    C    GAAAAAT
                                TCA GGGGA      GGGTCC
                                ||| |||||      ||||||
                                AGT CCTCT      TTCGGG
                                  _    AAGGGAG
GAM890  C20orf21  3'  GTCTAATTTTTTTTCCTGTTGA 35116    _         GGGTCC
                                TCA CGGGGAGAAAAAT
                                ||| ||||||||||||
                                AGT GTCCTTTTTTTTA
                                  T          ATCTG
GAM890  C20orf36  3'  GGGCTTCAGTGTCTCTGTGG   36799        GAAAAA  _
                                TCACGGGGA     TGG GTCC
                                |||||||||     ||| ||||
                                GGTGTCTCT     ACT CGGG
                                     GTG___   T
GAM890  C21orf108 3'  GGGCTCTTGGGATCTGCTCTGT 88725       _  AAAAT_
           GG                    TCACGGGG AGA     GGGTCC
                                ||||||| |||     ||||||
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                                GGTGTCTC TCT     CTCGGG
                                     G  AGGGTT
GAM890  C21orf69  3'  GGACTTCCTCTCTCCGTGG   54213          AAAAT
                                TCACGGGGAGA    GGGTCC
                                ||||||||||    ||||||
                                GGTGCCTCTCT    TTCAGG
                                      CC___
GAM890  C22orf4   3'  GACCGGTTCCTCCGTGG    60642        A  AAA  G
                                TCACGGGG GA   AT GGTC
                                |||||||| ||   || ||||
                                GGTGCCTC CT   TG CCAG
                                     _  ___  G
GAM890  C22orf5   3'  GGGCCCAGCCGTCTTCCTG   24345        AAAA
                                CGGGGAGA    TGGGTCC
                                ||||||||    |||||||
                                GTCCTTCT    ACCCGGG
                                     GCCG
GAM890  C22orf5   3'  GGGTCCTCTCTCTCTTTGG   24346     C      AAAAT  GT
                                TCA GGGGAGA    GG  CC
                                ||| |||||||    ||  ||
                                GGT TCTCTCT    CC  GG
                                  T      CT___  TG
GAM890  C6.1A     3'  GACTCATTTTACCTG       44282      GAGA
                                CGGG    AAAATGGGTC
                                ||||    ||||||||||
                                GTCC    TTTTACTCAG
                                  A___
GAM890  C6orf26   3'  GGGCCCAGAGCTTCTTCCTTTG 47511     C       AAA_
             G                   TCA GGGGAGAA    TGGGTCC
                                ||| ||||||||    |||||||
                                GGT TCCTTCTT    ACCCGGG
                                  T       CGAG
GAM890  C7orf13   3'  GGACTCAGTATTTTTGTGG    50933         GAAAAA
                                TCACGGGGA     TGGGTCC
                                |||||||||     |||||||
                                GGTGTTTTT     ACTCAGG
                                      ATG___
GAM890  C8orf14   5'  GGCTCAACCTCTGTGA       54003         AGAAAAA
                                TCACGGGG      TGGGTC
                                ||||||||      ||||||
                                AGTGTCTC      ACTCGG
                                     CA_____
GAM890  CAMKK2    3'  GGACTGCAGATTTTTCTACTCT 21585       _       G___
             GTGA                    ACGGGG AGAAAAAT    GGTCC
                                ||||||| ||||||||    |||||
                                TGTCTC TCTTTTTA    TCAGG
                                   A       GACG
GAM890  CAP       3'  GGACCCTTTCTTTCTCTG    21023         A   T
                                CGGGGAGA AAA GGGTCC
                                |||||||| ||| |||||||
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                                GTCTCTTT TTT CCCAGG
                                    C   _
GAM890  CAT56    3'  GATCTTCTTTCCCGT      47516       _  AAAAT
                                ACGGGGA GA    GGGTC
                                ||||||| ||    |||||
                                TGCCCTT CT    TCTAG
                                   T ______
GAM890  CAT56    3'  GGATTTCATAGTTTCTCTGT  47517        AAA    _
                                ACGGGGAGA  ATGGG TCC
                                |||||||||  ||||| |||
                                TGTCTCTTT  TACTT AGG
                                     GA_    T
GAM890  CD84     3'  GGGCTGAATTCTCCCTCTGG  80690    C      AAATG
                                TCA GGGGAGAA    GGTCC
                                ||| ||||||||    |||||
                                GGT TCCCTCTT    TCGGG
                                  C       AAG__
GAM890  CED-6    5'  GTCCACCTTCTCGTGG     32854         AAAAA  GT
                                TCACGGGGAG    TGG  C
                                ||||||||||    |||  |
                                GGTGCTCTTC    ACC  G
                                     C____   TG
GAM890  CENTG1   3'  GGTTCCCAACCCTTTCCGTGA  28713      GG  AAAAA   T_
                                TCACGG  AG    TGGG  CC
                                ||||||  ||    ||||  ||
                                AGTGCC  TC    ACCC  GG
                                   TT  CCA__   TT
GAM890  ChGn     3'  ACTTTTTTTCCCTTGTGA    37194       A     T
                                TCACGGGG GAAAAA GGGT
                                |||||||| |||||| ||||
                                AGTGTTCC CTTTTT TTCA
                                    _     _
GAM890  CHSY1    3'  GGATTTGGCATTTTCTCTTCTT 29901     C       A__ GG
           GA                     TCA GGGGAGAAAA   T  GTCC
                                ||| ||||||||||  |  ||||
                                AGT CTTCTCTTTT   G  TAGG
                                  T        ACG TT
GAM890  CITED1   5'  GGGTCTGTCCTTCCTGGGA   14730    A     AAAA   GT
                                TC CGGGGAG    ATGG  CC
                                || |||||||    ||||  ||
                                AG GTCCTTC    TGTC  GG
                                 G     C___    TG
GAM890  CNNM1    3'  GGATCTCTGGTTTTTCTCCT   39774          ___
                                GGGAGAAAAAT   GGGTCC
                                ||||||||||   ||||||
                                TCCTCTTTTTG   TCTAGG
                                      GTC
GAM890  CNNM2    5'  GGGCTCCCGCCGCCCCCGTGG  34462        AGAAAAAT
                                TCACGGGG      GGGTCC
                                ||||||||      ||||||
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                                GGTGCCCC       CTCGGG
                                    CGCCGCC_
GAM890  CNOT8    3'  TGTTTTTTATTCCTGTGG    16533         _
                                TCACGGGGA GAAAAATG
                                ||||||||| ||||||||
                                GGTGTCCTT TTTTTTGT
                                    A
GAM890  COPS7A   3'  GGGTTTAATCTCCTTTTGTGA  32857      __     AAAA   GT
                                TCACG  GGGAGA   TGG  CC
                                |||||  ||||||   |||  ||
                                AGTGT  TCCTCT   ATT  GG
                                   TT     A___   TG
GAM890  COTL1    3'  GACCCTGCTTCCTGTG      87955         AAAAAT
                                CACGGGGAG     GGGTC
                                |||||||||     |||||
                                GTGTCCTTC     CCCAG
                                    GT_____
GAM890  CRNKL1   3'  GGATTTGTTTTTCCAACTG   33601     GGA      GG
                                CGG   GAAAAAT  GTCC
                                |||   |||||||  ||||
                                GTC   CTTTTTG  TAGG
                                  AAC      TT
GAM890  CSMD1    5'  GGATCTATCCTCACTCTGTGG  73126         A  AAA
                                TCACGGGG GA   ATGGGTCC
                                |||||||| ||   ||||||||
                                GGTGTCTC CT   TATCTAGG
                                    A  CC_
GAM890  CTAG2    5'  GGGCCCTGACCTTCTCTCTGAG 40651    A       AAAT_
            A                    TC CGGGGAGAA     GGGTCC
                                || |||||||||     ||||||
                                AG GTCTCTCTT     CCCGGG
                                 A        CCAGT
GAM890  CTNNBIP1 3'  GGAAACGGTTTTTTTCTTTG   39664           _ GG
                                CGGGGAGAAAAAT G  TCC
                                |||||||||||||  |  |||
                                GTTTCTTTTTTTG C  AGG
                                       G AA
GAM890  CXorf9   3'  GGCCCAGCCTCCCGTGG     38625        G  AAAAA
                                TCACGGG AG    TGGGTC
                                |||||||  ||    ||||||
                                GGTGCCC TC    ACCCGG
                                   _  CG___
GAM890  CXYorf1  3'  CCTTTTTCTTCCTGT       82045            T
                                ACGGGGAGAAAAA GG
                                |||||||||||||  ||
                                TGTCCTTCTTTTT CC
                                                _
GAM890  DC2      3'  ATTTTTTTTCCTGCTGG     64263     _
                                TCA CGGGGAGAAAAAT
                                |||  ||||||||||||
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                                GGT GTCCTTTTTTTTA
                                  C
GAM890  DC2      3'  GGACTAGAATTTCTTCTTG   64265          AATG
                                CGGGGAGAAA   GGTCC
                                ||||||||||   |||||
                                GTTCTTCTTT   TCAGG
                                     AAGA
GAM890  DCNP1    5'  GGGCTTACCTGTGCTCTGTGA  55624         AGAAAAA
                                TCACGGGG     TGGGTCC
                                ||||||||     |||||||
                                AGTGTCTC     ATTCGGG
                                    GTGTCC_
GAM890  DDX12    3'  GACCTTTGTTCCTGTGG     59697         G  AAAT
                                TCACGGGGA AA   GGGTC
                                ||||||||| ||   |||||
                                GGTGTCCTT TT   TCCAG
                                     G  _____
GAM890  DHODH    3'  GGACTCAGGCAAGCCTTTGTGG 7239          AGAAAAA
                                TCACGGGG     TGGGTCC
                                ||||||||     |||||||
                                GGTGTTTC     ACTCAGG
                                    CGAACGG
GAM890  DIP13B   3'  GGACCTAATAGCATTTCTTTGT 59660         AAAA__
           G                     CACGGGGAGA     TGGGTCC
                                ||||||||||     |||||||
                                GTGTTTCTTT     ATCCAGG
                                     ACGATA
GAM890  DJ971N18.2 3'  GGATCTGTTTGGAGACTGGGA  40959    A   GGAGAA
                                TC CGG     AAATGGGTCC
                                || |||     ||||||||||
                                AG GTC     TTTGTCTAGG
                                 G  AGAGG_
GAM890  DKFZp434B0417 3'  GACAATCTTCCTGTGA      25380          AAAATGG
                                TCACGGGGAGA      GTC
                                ||||||||||      |||
                                AGTGTCCTTCT      CAG
                                     AA_____
GAM890  DKFZp434B1222 5'  TGTTTTTTTCTCCTGA      34141     C
                                TCA GGGGAGAAAAATG
                                ||| ||||||||||||
                                AGT CCTCTTTTTTTGT
                                  _
GAM890  DKFZP434B205 5'  GGGCCTGGCGGGCTCCCCGT   75322        AAAAA
                                ACGGGGAG    TGGGTCC
                                ||||||||    |||||||
                                TGCCCCTC    GTCCGGG
                                    GGGCG
GAM890  DKFZp434F1719 3'  GGGCTGGTTTCTCCTCTTGG   50002     C       AA  G
                                TCA GGGGAGAA  AT GGTCC
                                ||| ||||||||  || |||||
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                                GGT CTCCTCTT  TG TCGGG
                                  T       __ G
GAM890  DKFZP434J154 3'  GATCTTGTTTTCCCTGTGG   31547          AAAT
                                TCACGGGGAGAA   GGGTC
                                ||||||||||||   |||||
                                GGTGTCCCTTTT   TCTAG
                                       GT__
GAM890  DKFZp434K1210 3'  GGATATACGGATTTTTCTCTTT 34275          GG____
          GTG                    ACGGGGAGAAAAAT     GTCC
                                ||||||||||||||     ||||
                                TGTTTCTCTTTTTA     TAGG
                                       GGCATA
GAM890  DKFZP434K2235 3'  GGATTTGATTTTTTTTTTCTG  83499     GG      __ GG
                                CGG  AGAAAAA  T  GTCC
                                |||  |||||||  |  ||||
                                GTC  TTTTTTT  G  TAGG
                                  TT      TA TT
GAM890  DKFZp434M0331 3'  GGAAGCATTCTCCCTGTGA   34234          AAA   GG
                                TCACGGGGAGA   ATG  TCC
                                ||||||||||   |||  |||
                                AGTGTCCCTCT   TAC  AGG
                                       ___   GA
GAM890  DKFZP434P0721 3'  GGACTCCGAATGTATTTTTGTG 63718          GAAAAA  _
          G                     TCACGGGGA      TGG GTCC
                                |||||||||      ||| ||||
                                GGTGTTTTT      GCC CAGG
                                      ATGTAA   T
GAM890  DKFZP434P211 3'  GGACCTCTCTCTCCTGTGG    27265        _    AAAAT
                                TCACGGG GAGA     GGGTCC
                                |||||||  ||||     ||||||
                                GGTGTCC CTCT     TCCAGG
                                    T    C____
GAM890  DKFZp434P2235 5'  GGACTCAAAGGTTTTCTCCCTG 50041    A         A___
          AGA                    C CGGGGAGAAAA    TGGGTCC
                                |  ||||||||||    |||||||
                                G GTCCCTCTTTT    ACTCAGG
                                 A          GGAA
GAM890  DKFZP564C1940 5'  GACACTTCCCCTGTGG      25902         A   AAATGG
                                TCACGGGG GAA      GTC
                                ||||||||  |||     |||
                                GGTGTCCC CTT      CAG
                                     _   CA____
GAM890  DKFZP564D0764 3'  GAATTTTTTTTTCCCTG     88242           TGGG
                                CGGGGAGAAAAA    TC
                                ||||||||||||    ||
                                GTCCCTTTTTTT    AG
                                       TTA_
GAM890  DKFZP564K0322 5'  GGATTTGGACGTCCTCGTGG   49361          GAAAAA GG
                                TCACGGGGA      T  GTCC
                                |||||||||      |  ||||
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                                GGTGCTCCT     G  TAGG
                                      GCAG__ TT
GAM890   DKFZP564O0423 3'  GGATCTTATATTTTTCCTGTG  91697          AAAT
                                CACGGGGAGAA    GGGTCC
                                ||||||||||    ||||||
                                GTGTCCTTTTT    TCTAGG
                                      ATAT
GAM890   DKFZP564O0463 3'  GGACTCCAGATCTTTCTCTG   26282        AAAA  _
                                CGGGGAGA    TGG GTCC
                                ||||||||    ||| ||||
                                GTCTCTTT    ACC CAGG
                                     CTAG   T
GAM890   DKFZP564O1664 3'  GGGCTTTAACTTCCTGGGA   47939    A      AAAAAT
                                TC CGGGGAG     GGGTCC
                                || |||||||     ||||||
                                AG GTCCTTC     TTCGGG
                                 G      AAT___
GAM890   DKFZP564O1863 3'  TTTATTTTTTTCTCTGT     68589
                                ACGGGGAGAAAAATGGG
                                |||||||||||||||||
                                TGTCTCTTTTTTTATTT

GAM890   DKFZp566D234 3'  CAATTTTCTTCCTTGTGA     61862          _    A
                                TCACGGGGA GAAAA TG
                                ||||||||| ||||| ||
                                AGTGTTCCT CTTTT AC
                                      T    A
GAM890   DKFZP566J091 3'  GGATCTTGGTCTGTTTTTCTTG 48124          AAAT___
           TGG                    CACGGGGAGAA      GGGTCC
                                ||||||||||       ||||||
                                GTGTTCTTTTT      TCTAGG
                                      GTCTGGT
GAM890   DKFZP566M114 3'  GGATTTGTTTTACTCTTTG    49543        A    GG
                                CGGGGAG AAAAT  GTCC
                                ||||||| |||||  ||||
                                GTTTCTC TTTTG  TAGG
                                     A    TT
GAM890   DKFZP566N034 3'  GGGTCCATTTTTGAGAGATGTG 80141      GGGAG_      GT
                                CACG     AAAAATGG  CC
                                ||||     ||||||||  ||
                                GTGT     TTTTTACC  GG
                                  AGAGAG       TG
GAM890   DKFZP586L151 3'  GGGTCTATTTTTTTATATGGA  63961    A  GGG        GT
                                TC CG   AGAAAAATGG  CC
                                || ||   ||||||||||  ||
                                AG GT   TTTTTTTATC  GG
                                 _ ATA        TG
GAM890   DKFZP586M1120 5'  GATCTGTTATCTGTGA      48458        GAGAAA
                                TCACGGG     AATGGGTC
                                |||||||     ||||||||
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                                AGTGTCT     TTGTCTAG
                                   A_____
GAM890  DKFZP727C091 5'  GGACTTCCTGTCTCTCTGTG   66211          AAAAT
                                CACGGGGAGA     GGGTCC
                                ||||||||||     ||||||
                                GTGTCTCTCT     TTCAGG
                                     GTCC_
GAM890  DKFZP761G1913 3'  CTATTTTTTCCTGTGG      48912           AA
                                TCACGGGGAGAA  ATGG
                                ||||||||||||  ||||
                                GGTGTCCTTTTT  TATC
                                      __
GAM890  DKFZp761G2113 3'  GGGCTCACGCTGTCCTGTGG   69908        _  AAAAA
                                TCACGGGG AG     TGGGTCC
                                |||||||| ||     |||||||
                                GGTGTCCT TC     ACTCGGG
                                     G  GC___
GAM890  DKFZp761K1423 5'  CGGATCCATATCACATTCTTTC 37331    _ GG    AA____
           TTGTGG                  G G  AGAA     ATGGGTCC   G
                                | |  ||||     |||||||||  |
                                T C  TCTT     TACCTAGG   C
                                 T TT    ACACTA
GAM890  DKFZp761O0113 5'  GGTCTCTCTATTTCTTCTCTTG 37281     C        AAT_   T
           A                     TCA GGGGAGAAA    GGG CC
                                ||| |||||||||    ||| ||
                                AGT CTCTTCTTT    CTC GG
                                  T       ATCT   T  G
GAM890  DKK2     5'  GGGCTTTGCGTCTTCCTG    27018         AAAAT
                                CGGGGAGA     GGGTCC
                                ||||||||     ||||||
                                GTCCTTCT     TTCGGG
                                     GCGT_
GAM890  DMWD     3'  GGACCTGTGTGTGTACTCTGTG 60880         AGAAAA_
           G                     TCACGGGG      ATGGGTCC
                                ||||||||      ||||||||
                                GGTGTCTC      TGTCCAGG
                                     ATGTGTG
GAM890  DTX2     3'  GGGCCCGTCTGTCCTCTG    71954       A  AAA
                                CGGGG GA   ATGGGTCC
                                ||||| ||   ||||||||
                                GTCTC CT   TGCCCGGG
                                   _  GTC
GAM890  E1B-AP5   3'  GGGCCAGGCATTTTTTTCT    58568          ___
                                GGAGAAAAATG   GGTCC
                                ||||||||||   |||||
                                TCTTTTTTTAC   CCGGG
                                      GGA
GAM890  E1B-AP5   3'  GGGCCAGGCATTTTTTTCT    22902          ___
                                GGAGAAAAATG   GGTCC
                                ||||||||||   |||||
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                                TCTTTTTTTTAC  CCGGG
                                      GGA
GAM890  EAT2    3'  GGCTACTCTCCTCCTGG    79279    C     AAAATG
                                TCA GGGGAGA    GGTC
                                ||| |||||||    ||||
                                GGT CTCCTCT    TCGG
                                  C     CA____
GAM890  EDG1    3'  GGATCCGTTTTTTGGAATTTG  59329     GA__
                                CGGG   GAAAAATGGGTCC
                                ||||   ||||||||||||
                                GTTT   TTTTTTGCCTAGG
                                  AAGG
GAM890  EDR2    3'  GGGCCTTTCATTTCTGTGG   60495      GG _  AAAT
                                TCACGG  A GAA   GGGTCC
                                ||||||  | |||   ||||||
                                GGTGTC  T CTT   TCCGGG
                                   TT A  ____
GAM890  EFA6R   3'  GGATAATTTATTTCCTGTGG  30986        AA   GG
                                TCACGGGGAG  AAAT  GTCC
                                ||||||||||  ||||  ||||
                                GGTGTCCTTT  TTTA  TAGG
                                      A_   A_
GAM890  EFNA5   5'  GGATCCCCGCTCTCTCCCCGGA 8733    A      AAAAT_
                                TC CGGGGAGA    GGGTCC
                                || ||||||||    ||||||
                                AG GCCCCTCT    CCTAGG
                                 _      CTCGCC
GAM890  ELAC1   3'  GACTCAGCCCTCGTGG     90970       AGAAAAA
                                TCACGGGG     TGGGTC
                                ||||||||     ||||||
                                GGTGCTCC     ACTCAG
                                     CG_____
GAM890  EPB41L1 3'  GGACCTGTTTCAGTTTTTG  70595      GAA
                                CGGGGA  AAATGGGTCC
                                ||||||  ||||||||||
                                GTTTTT  TTTGTCCAGG
                                   GAC
GAM890  EPHA7   3'  TTTTTCATTCTCGTGA     15436        _
                                TCACGGGGA GAAAAA
                                ||||||||| ||||||
                                AGTGCTCTT CTTTTT
                                      A
GAM890  EPSIN   5'  GGGCCTCTTTCTTCCTTGG   25299    C      AAT
                                TCA GGGGAGAAA  GGGTCC
                                ||| |||||||||  ||||||
                                GGT TCCTTCTTT  TCCGGG
                                  _       C__
GAM890  ERAL1   3'  GGGCCCAGAGTTTCTCCCTG  62625        AA_
                                CGGGGAGAAA  TGGGTCC
                                ||||||||||  |||||||
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                                GTCCCTCTTT  ACCCGGG
                                     GAG
GAM890  ERp44    3'  GGACTTAGGGATGTTTCCTGTG 81694       AAAAA_
                                CACGGGGAG    TGGGTCC
                                |||||||||    |||||||
                                GTGTCCTTT    ATTCAGG
                                     GTAGGG
GAM890  ESDN     3'  GGATTAAGTTTTTTCCTGT   55176         AATG
                                ACGGGGAGAAA   GGTCC
                                ||||||||||   |||||
                                TGTCCTTTTTT   TTAGG
                                      GAA_
GAM890  ESDN     3'  GGATTGCTTTTTCACTTTGTGA 55177       A    TG
                                TCACGGGG GAAAAA  GGTCC
                                |||||||| ||||||  |||||
                                AGTGTTTC CTTTTT  TTAGG
                                     A    CG
GAM890  FAM8A1   3'  GGATTTGTTCCCTTCAGTGA  32723     ___   GAAAA  GG
                                TCAC  GGGGA   AT  GTCC
                                ||||  |||||   ||  ||||
                                AGTG  TCCCT   TG  TAGG
                                   ACT    _____  TT
GAM890  FBXO25   3'  GGGCTCATAGTGAGTGTTCTGT 24095       AGAAAA__
           GA                    TCACGGGG      ATGGGTCC
                                 ||||||||      ||||||||
                                 AGTGTCTT      TACTCGGG
                                     GTGAGTGA
GAM890  FHOD2    3'  GATTTTGTCTTTCTGTGG   73826      GG  AAAAT
                                TCACGG  AGA   GGGTC
                                ||||||  |||   |||||
                                GGTGTC  TCT   TTTAG
                                   TT  GT___
GAM890  FLB6421  3'  GGATTCATTGTAACTCTCCTTG 39228        AA___
           TGA                   CACGGGGAGA    AATGGGTCC
                                 ||||||||||    |||||||||
                                 GTGTTCCTCT    TTACTTAGG
                                      CAATG
GAM890  FLB6421  3'  GGGCTCATCAAGTCACTCGTGA 39229      GA  AAA_
                                TCACGGG  GA   ATGGGTCC
                                |||||||  ||   ||||||||
                                AGTGCTC  CT   TACTCGGG
                                   A_  GAAC
GAM890  FLJ00001 3'  GGGCTGCCTCACTCTGTGG   81819       A  AAAATG
                                TCACGGGG GA    GGTCC
                                |||||||| ||    |||||
                                GGTGTCTC CT    TCGGG
                                   A  CCG___
GAM890  FLJ10060 3'  GGGCCTGAGACCTTTGTGG   35790       AGAAAAAT
                                TCACGGGG      GGGTCC
                                ||||||||      ||||||
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                                GGTGTTTC      TCCGGG
                                    CAGAG___
GAM890  FLJ10060 5' GGACCCCGGGTCCTCTGTGG  35789       A  AAAAT
                                TCACGGGG GA    GGGTCC
                                |||||||| ||    ||||||
                                GGTGTCTC CT    CCCAGG
                                    _ GGGC_
GAM890  FLJ10099 3' GGGCCTGGATGCTCTGTGA   35813       AGAAAAA
                                TCACGGGG     TGGGTCC
                                ||||||||     |||||||
                                AGTGTCTC     GTCCGGG
                                    GTAG___
GAM890  FLJ10139 3' GGCTTTTTTTTTTTTTTG    35842          TG
                                CGGGGAGAAAAA GGTC
                                |||||||||||| ||||
                                GTTTTTTTTTTT TCGG
                                      TT
GAM890  FLJ10193 3' GGGCCTGTTTTAAGGCTCTG  35887     AGA_
                                CGGGG   AAAATGGGTCC
                                |||||   ||||||||||
                                GTCTC   TTTTGTCCGGG
                                  GGAA
GAM890  FLJ10260 5' GGGCCTGCTCCCACCCTGTGG 35950       AGAAAAAT
                                TCACGGGG      GGGTCC
                                ||||||||      ||||||
                                GGTGTCCC      TCCGGG
                                    ACCCTCG_
GAM890  FLJ10276 3' GGATGGGGTTTTTCTCTTTGT 35965          GG_
                                ACGGGGAGAAAAAT  GTCC
                                |||||||||||||  ||||
                                TGTTTCTCTTTTTG  TAGG
                                      GGG
GAM890  FLJ10324 5' GGACCTGCTCTCCCTG     36029       AAAA
                                CGGGGAGA   TGGGTCC
                                ||||||||   |||||||
                                GTCCCTCT   GTCCAGG
                                    C___
GAM890  FLJ10376 3' GGATATTATTTTTTCCTCTGG 36077    C       ATGG
                                TCA GGGGAGAAAA   GTCC
                                ||| ||||||||||   ||||
                                GGT CTCCTTTTTT   TAGG
                                  _       ATTA
GAM890  FLJ10415 3' GGACTCTGGATCTTTGTGA   36098       GAAAAAT
                                TCACGGGGA     GGGTCC
                                |||||||||     ||||||
                                AGTGTTTCT     CTCAGG
                                    AGGT___
GAM890  FLJ10415 3' TTTTTCTTCCCCGTGA     36101        _
                                TCACGGGGA GAAAAA
                                ||||||||| ||||||
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                                AGTGCCCCT CTTTTT
                                      T
GAM890  FLJ10483  3' GGACTGTCTCTTCTTGT    36173        AAAATG
                                ACGGGGAGA    GGTCC
                                |||||||||    |||||
                                TGTTCTTCT    TCAGG
                                     CTG___
GAM890  FLJ10521  3' GGGCCTGTGGCCTTCCTG   36219      AAAA
                                CGGGGAG   ATGGGTCC
                                |||||||   ||||||||
                                GTCCTTC   TGTCCGGG
                                    CGG_
GAM890  FLJ10545  3' GATTTATTATCTCCT      36262      AA
                                GGGAGA  AATGGGTC
                                ||||||  ||||||||
                                TCCTCT  TTATTTAG
                                   A_
GAM890  FLJ10581  3' GGTTCTTTTTTCTCTTGG   36305   G       T GG
                                C GGGAGAAAAA G  TC
                                | ||||||||||  |  ||
                                G TTCTCTTTTT C  GG
                                 G        T TT
GAM890  FLJ10604  3' GGATCTGGCTTTTCCTGGA   36339   A      AAAA
                                TC CGGGGAGA   TGGGTCC
                                || ||||||||   |||||||
                                AG GTCCTTTT   GTCTAGG
                                 _       CG__
GAM890  FLJ10665  5' GACCTCTTTCTCCTGG     36392   G      AAT
                                C GGGAGAAA   GGGTC
                                | ||||||||   |||||
                                G TCCTCTTT   TCCAG
                                 G       C__
GAM890  FLJ10697  3' GGTTAGAATTTTTCTTTTTGT  36420          GGGT_
                                ACGGGGAGAAAAAT    CC
                                ||||||||||||||    ||
                                TGTTTTTCTTTTTA    GG
                                        AGATT  G
GAM890  FLJ10724  3' GGATTTTTTTTTTTTTTTTGG 36503    CG        TG
                                TCA  GGGAGAAAAA  GGTCC
                                |||  ||||||||||  |||||
                                GGT  TTTTTTTTTT  TTAGG
                                  TT        TT
GAM890  FLJ10737  3' GGGCCCCGGGCTTCCCGTG   36523        AAAAAT
                                CACGGGGAG     GGGTCC
                                |||||||||     ||||||
                                GTGCCCTTC     CCCGGG
                                     GGGC__
GAM890  FLJ10774  3' GGCCTGTGTGTCTGTGA     45084       GAGAAAA
                                TCACGGG      ATGGGTC
                                |||||||      |||||||
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                                AGTGTCT      TGTCCGG
                                   GTG____
GAM890  FLJ10774 3' GGGCCGCTGGGTCTCTCTTTGT 45085     __      AAAATG
            GG                   TCAC  GGGGAGA     GGTCC
                                ||||  |||||||     |||||
                                GGTG  TCTCTCT     CCGGG
                                  TT      GGGTCG
GAM890  FLJ10856 3' GGAGACTGTTTTCATTCTTGTG 36775         GA      G_
            A                    TCACGGGGA  AAAATGG  TCC
                                |||||||||  |||||||  |||
                                AGTGTTCTT  TTTTGTC  AGG
                                     AC      AG
GAM890  FLJ10874 5' GGACCCGTTTCGCCTCGCGG  36780    A    A   AA
                                TC CGGGG GAA  ATGGGTCC
                                || ||||| |||  ||||||||
                                GG GCTCC CTT  TGCCCAGG
                                 C    G  __
GAM890  FLJ10971 3' TATTTTTTTTCCCTGA     36929     C
                                TCA GGGGAGAAAAATG
                                ||| ||||||||||||
                                AGT CCCTTTTTTTTAT
                                 _
GAM890  FLJ11040 3' TTATTTTTCTTCTTATGA    37003     CG
                                TCA  GGGAGAAAAATGG
                                |||  ||||||||||||
                                AGT  TCTTCTTTTTATT
                                  AT
GAM890  FLJ12132 3' GGCCCTGTTTCCTTGGA     46471    A      AAAAT
                                TC CGGGGAGA    GGGTC
                                || ||||||||    |||||
                                AG GTTCCTTT    CCCGG
                                 _      GT___
GAM890  FLJ12221 3' GGACCCCCATTTCCTTG     62552        AAAAT
                                CGGGGAGA    GGGTCC
                                ||||||||    ||||||
                                GTTCCTTT    CCCAGG
                                     ACC__
GAM890  FLJ12229 5' GGACTCCAGCCCCTTCCTGT  45917        AAAAA  _
                                ACGGGGAG    TGG GTCC
                                ||||||||    ||| ||||
                                TGTCCTTC    ACC CAGG
                                     CCCG_  T
GAM890  FLJ12425 3' GGCTTTTATTTTTCTTTTTGT 85893           __   C
                                ACGGGGAGAAAAATG  GGTC
                                ||||||||||||||  ||||
                                TGTTTTTCTTTTTAT  TCGG
                                          TT
GAM890  FLJ12476 3' GGGCAATTTTTTTTTTCTGT   42952     GG      GG
                                ACGG  AGAAAAAT  GTCC
                                ||||  ||||||||  ||||
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                                TGTC  TTTTTTTA  CGGG
                                  TT       A_
GAM890  FLJ12687  3'  GGATCTGGACTGTTTCTTCCTG 46201          AA___
              T                   ACGGGGAGAAA    TGGGTCC
                                  ||||||||||    |||||||
                                  TGTCCTTCTTT    GTCTAGG
                                        GTCAG
GAM890  FLJ12700  3'  GGGCCCATTTCAAGGCTCTG   46120      AGAA_
                                  CGGGG    AAATGGGTCC
                                  |||||    ||||||||||
                                  GTCTC    TTTACCCGGG
                                     GGAAC
GAM890  FLJ12707  3'  GGCCCATTACCCATGG      41949     C   GAGAAA
                                  TCA GGG     AATGGGTC
                                  ||| |||     ||||||||
                                  GGT CCC     TTACCCGG
                                    A   A_____
GAM890  FLJ12750  3'  GGGCTTGCCATGTTCTGTGA   45124        AGAAAAAT
                                  TCACGGGG       GGGTCC
                                  ||||||||       ||||||
                                  AGTGTCTT       TTCGGG
                                       GTACCG__
GAM890  FLJ12891  3'  GGGCCTGCAGGCGCCCTTGTGG 46346        AGAAAAAT
                                  TCACGGGG       GGGTCC
                                  ||||||||       ||||||
                                  GGTGTTCC       TCCGGG
                                       CGCGGACG
GAM890  FLJ12973  3'  CGGACTTTTTTTTTTTTTT    46104          TG
                                  GGGGAGAAAAA  GGTCC   G
                                  ||||||||||  |||||   |
                                  TTTTTTTTTTT  TCAGG   C
                                         TT
GAM890  FLJ13102  3'  GGGCTGGCATCTCTCTTTGG   46016     C      AAAATG
                                  TCA GGGGAGA      GGTCC
                                  ||| |||||||      |||||
                                  GGT TCTCTCT      TCGGG
                                    T      ACGG__
GAM890  FLJ13102  3'  GGGCCTGTAGGCCCTGGTGA   46015      _   AGAAAA
                                  TCAC GGGG     ATGGGTCC
                                  |||| ||||     ||||||||
                                  AGTG TCCC     TGTCCGGG
                                    G    GGA___
GAM890  FLJ13110  3'  GGATTTATTTTTTTCCCC    43303
                                  GGGGAGAAAAATGGGTCC
                                  ||||||||||||||||||
                                  CCCCTTTTTTTATTTAGG

GAM890  FLJ13117  3'  GGAAGCTATTTTTTTTCCTTGA 43545     C           G_
                                  TCA GGGGAGAAAAATGG  TCC
                                  ||| ||||||||||||||  |||
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                                AGT TCCTTTTTTTTATC  AGG
                                  _           GA
GAM890  FLJ13150 3' GGATATAATTTCTCTTCTTG  45670       A   GG_
                                CGGGGAGA AAAT  GTCC
                                |||||||| ||||  ||||
                                GTTCTTCT TTTA  TAGG
                                    C   ATA
GAM890  FLJ13153 5' GACCTGTCGCTGTGTGG    45557     G  A  AAAA
                                TCACG GG GA   TGGGTC
                                ||||| || ||   ||||||
                                GGTGT TC CT   GTCCAG
                                  G  G  ____
GAM890  FLJ13154 3' GGGTCTGTCACCCTCTCTCCTT 44799    C     AAA__   GT
           GA                     TCA GGGGAGA    ATGG  CC
                                ||| |||||||    ||||  ||
                                AGT CCTCTCT    TGTC  GG
                                  T     CCCAC   TG
GAM890  FLJ13158 3' GGATCTGTTAGATCCTGGA   46112   A   AGAAA
                                TC CGGGG    AATGGGTCC
                                || |||||    |||||||||
                                AG GTCCT    TTGTCTAGG
                                 _    AGA__
GAM890  FLJ13441 3' GGGCCCTGGCCATCCTGTGG  43669       AGAAAAAT
                                TCACGGGG      GGGTCC
                                ||||||||      ||||||
                                GGTGTCCT      CCCGGG
                                    ACCGGT__
GAM890  FLJ13490 3' GGATTTGATTTTTCCTGT    46301        AAA GG
                                ACGGGGAGAA  T  GTCC
                                ||||||||||  |  ||||
                                TGTCCTTTTT  G  TAGG
                                     A__ TT
GAM890  FLJ13614 5' GGAAGGTTTTCTTCTTG     57452         ATGGG
                                CGGGGAGAAAA    TCC
                                ||||||||||    |||
                                GTTCTTCTTTT    AGG
                                     GGA__
GAM890  FLJ13769 3' GATCACTTTCTCTGGGA     46613   A      AAAATG
                                TC CGGGGAGA     GGTC
                                || ||||||||     ||||
                                AG GTCTCTTT     CTAG
                                 G      CA_____
GAM890  FLJ13782 3' GGGCCACTGTTCTCTTTG    46171        AAATG
                                CGGGGAGAA    GGTCC
                                |||||||||    |||||
                                GTTTCTCTT    CCGGG
                                     GTCA_
GAM890  FLJ13842 3' GGATTTTTAAATTCTTTCCTGA 44986    C  GG   AAAT_
                                TCA GG  AGAA    GGGTCC
                                ||| ||  ||||    ||||||
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                                AGT CC  TCTT    TTTAGG
                                  _ TT   AAATT
GAM890  FLJ14107  3' GGCTTGGTTCTCCCTG     46697        AAAT
                                CGGGGAGAA   GGGTC
                                |||||||||   |||||
                                GTCCCTCTT   TTCGG
                                     GG__
GAM890  FLJ14129  3' GGAATCGTTTTCTCTTTGAGA  48067    A        A  GG
                                TC CGGGGAGAAAA TG  TCC
                                || ||||||||||| ||  |||
                                AG GTTTCTCTTTT GC  AGG
                                 A         _ TA
GAM890  FLJ14166  3' GGTGCTTTTCTTTCCCTG    44686        AAAAT   _
                                CGGGGAGA    GGGT CC
                                ||||||||    |||| ||
                                GTCCCTTT    TTCG GG
                                     CTT__   T
GAM890  FLJ14213  3' GGATGTTTATTCTCTGTGG   45796         AA   GG
                                TCACGGGGAG  AAAT  GTCC
                                ||||||||||  ||||  ||||
                                GGTGTCTCTT  TTTG  TAGG
                                     A_   __
GAM890  FLJ14249  3' GGGCCTCTGCTCCTCGTGG   42406         AAAAAT
                                TCACGGGGAG     GGGTCC
                                ||||||||||     ||||||
                                GGTGCTCCTC     TCCGGG
                                     GTC___
GAM890  FLJ14249  3' GGGCCTCTGCTCCTCGTGG   55213         AAAAAT
                                TCACGGGGAG     GGGTCC
                                ||||||||||     ||||||
                                GGTGCTCCTC     TCCGGG
                                     GTC___
GAM890  FLJ14454  5' GGACTTGTTTTTCTGTTTTA  51382   C   G      TG
                                A GGG AGAAAAA  GGTCC
                                | ||| |||||||  |||||
                                A TTT TCTTTTT  TCAGG
                                 T   G      GT
GAM890  FLJ14457  3' GGCCTCTTTCCTGTGG      51386         AAAAAT
                                TCACGGGGAG     GGGTC
                                ||||||||||     |||||
                                GGTGTCCTTT     TCCGG
                                     C_____
GAM890  FLJ14566  3' GGGCCCATTAATCCCACTGTGG 51447       _  A  AA
                                TCACGG GG GA  AATGGGTCC
                                |||||| || ||  |||||||||
                                GGTGTC CC CT  TTACCCGGG
                                   A  _  AA
GAM890  FLJ14668  3' GGAGAGATATTTTCTCTTTGT  51513          ATGGG_
                                ACGGGGAGAAAA     TCC
                                ||||||||||||     |||
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                                TGTTTCTCTTTT     AGG
                                      ATAGAG
GAM890  FLJ14743  3'  GGGCCATTTTTCCTTTTGG   68066    CG      AATG
                                TCA  GGGAGAAA   GGTCC
                                |||  ||||||||   |||||
                                GGT  TCCTTTTT   CCGGG
                                  TT       A___
GAM890  FLJ14936  3'  GGATCCAGTTTTTCTTGGGA  51707    A       AAA
                                TC CGGGGAGAA   TGGGTCC
                                || |||||||||  |||||||
                                AG GTTCTTTTT   ACCTAGG
                                 G       G__
GAM890  FLJ14950  3'  GGCCATCTCTCTGTGA      51725          AAAATG
                                TCACGGGGAGA     GGTC
                                ||||||||||      ||||
                                AGTGTCTCTCT     CCGG
                                      A_____
GAM890  FLJ14966  3'  GATTTATCATCCCTGGA     51768    A     GAAAA
                                TC CGGGGA     ATGGGTC
                                || ||||||     |||||||
                                AG GTCCCT     TATTTAG
                                 _     AC___
GAM890  FLJ20004  3'  GGGCCTCTTTCTTCCCATGG   34315     C       AAT
                                TCA GGGGAGAAA   GGGTCC
                                ||| |||||||||   ||||||
                                GGT CCCTTCTTT   TCCGGG
                                  A       C__
GAM890  FLJ20040  3'  GGACTTACCTCCTTCTTTTTGT 38632          AAA__
                                ACGGGGAGAA     TGGGTCC
                                ||||||||||     |||||||
                                TGTTTTTCTT     ATTCAGG
                                      CCTCC
GAM890  FLJ20069  3'  TTTTTCTGTCTTGTGA      34471         _
                                TCACGGGG AGAAAAA
                                |||||||| |||||||
                                AGTGTTCT TCTTTTT
                                     G
GAM890  FLJ20093  3'  CCATTTTTCTTTTTGT      34553
                                ACGGGGAGAAAAATGG
                                ||||||||||||||||
                                TGTTTTTCTTTTTACC

GAM890  FLJ20094  3'  GAAACTATCTTTTCTCTCTGTG 34557            _   GTCC
          A                      TCACGGGGAGAAAA ATGG
                                 |||||||||||||| ||||
                                 AGTGTCTCTCTTTT TATC
                                       C    AAAG
GAM890  FLJ20147  3'  GATTATATTTTTTTCTCCAGTG 34638     _          _   C
          A                      TCAC GGGGAGAAAAATG GGTC
                                 |||| |||||||||||| ||||
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                                AGTG CCTCTTTTTTTAT TTAG
                                  A           A
GAM890  FLJ20152  5'  GTTTTTTTCCTCCTGA      38647     C
                                TCA GGGGAGAAAAAT
                                ||| ||||||||||||
                                AGT CTCCTTTTTTTG
                                  C
GAM890  FLJ20174  3'  GGGTTCTAGACTTCTTCCCTGA 34691     C       AAAT_ GG
                                TCA GGGGAGAA    G  TCC
                                ||| ||||||||    |  |||
                                AGT CCCTTCTT    C  GGG
                                  _       CAGAT TT
GAM890  FLJ20277  3'  GGGCCTGGATTTCTTTTTG   34835          AA
                                CGGGGAGAAA  TGGGTCC
                                ||||||||||  |||||||
                                GTTTTTCTTT  GTCCGGG
                                      AG
GAM890  FLJ20320  3'  GGCCCATGGCTTGTGG      34944        GAGAAAA
                                TCACGGG      ATGGGTC
                                |||||||      |||||||
                                GGTGTTC      TACCCGG
                                   GG_____
GAM890  FLJ20371  3'  GGCCTAAATTTTCCTG      35063        AAAA
                                CGGGGAGA    TGGGTC
                                ||||||||    ||||||
                                GTCCTTTT    ATCCGG
                                     AA__
GAM890  FLJ20373  3'  GGACCCAGTGAAGTTTCTCCGT 35072         AAAA__
                                ACGGGGAGA     TGGGTCC
                                |||||||||     |||||||
                                TGCCTCTTT     ACCCAGG
                                      GAAGTG
GAM890  FLJ20420  3'  GGAACATTTTTTTTCCTAGTGA 35142      _          GG
                                TCAC GGGGAGAAAAATG  TCC
                                |||| ||||||||||||  |||
                                AGTG TCCTTTTTTTTAC  AGG
                                  A           A_
GAM890  FLJ20485  3'  TTTATTTTTTTTTTCGAGA   38767    A  GG
                                TC CG  GAGAAAAATGGG
                                || ||  ||||||||||||
                                AG GC  TTTTTTTTATTT
                                 A  TT
GAM890  FLJ20507  3'  GGACCGAGACTTTCCTTGGA   35296    A       AAAATG
                                TC CGGGGAGA     GGTCC
                                || ||||||||     |||||
                                AG GTTCCTTT     CCAGG
                                  _       CAGAG_
GAM890  FLJ20507  3'  GGACCGAGACTTTCCTTGGA   60231    A       AAAATG
                                TC CGGGGAGA     GGTCC
                                || ||||||||     |||||
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                                AG GTTCCTTT     CCAGG
                                 _      CAGAG_
GAM890  FLJ20651  3'  GGAGCAGATTTTCTCCCTGGA  35498    A        A_  GG
                                TC CGGGGAGAAAA  TG  TCC
                                || ||||||||||  ||  |||
                                AG GTCCCTCTTTT  AC  AGG
                                 _        AG  G_
GAM890  FLJ20700  5'  GGATGCAGTCTCTTTGTGG   35581          AAAA  G
                                TCACGGGGAGA    TG GTCC
                                ||||||||||    || ||||
                                GGTGTTTCTCT    AC TAGG
                                      G___  G
GAM890  FLJ20898  5'  GGACTTGGCTTTCTCC      44806        AA
                                GGAGAAA  TGGGTCC
                                |||||||  |||||||
                                CCTCTTT  GTTCAGG
                                    CG
GAM890  FLJ21657  3'  GGATCCAATTTTCCTGAGA   42511    A      AAAA
                                TC CGGGGAGA    TGGGTCC
                                || ||||||||    |||||||
                                AG GTCCTTTT    ACCTAGG
                                 A       A___
GAM890  FLJ21657  3'  GGAGTTTTTTTTTTCTTGT   42510           T  G
                                ACGGGGAGAAAAA GG TCC
                                |||||||||||| || |||
                                TGTTCTTTTTTTT TT AGG
                                      _ G
GAM890  FLJ21742  3'  GACCCATGGTCTGTGG      49847        GAGAAAA
                                TCACGGG      ATGGGTC
                                |||||||      |||||||
                                GGTGTCT      TACCCAG
                                    GG_____
GAM890  FLJ21919  3'  GAGCTTTCTCCTCTGG      43457     C      AAAT  G
                                TCA GGGGAGAA    GG TC
                                ||| ||||||||    || ||
                                GGT CTCCTCTT    TC AG
                                 _      _____ G
GAM890  FLJ21940  3'  GGATGTTCTTTTTCTGTGA   43081       GG   AA   GG
                                TCACGG  AGA  AAT  GTCC
                                ||||||  |||  |||  ||||
                                AGTGTC  TTT  TTG  TAGG
                                   TT   C_   __
GAM890  FLJ22035  3'  GGACTAATATGTATCTTTCTGT 44538       GG   AAA   __
          GA                  TCACGG  AGA   ATG  GGTCC
                              ||||||  |||   |||  |||||
                              AGTGTC  TCT   TAT  TCAGG
                                 TT   ATG   AA
GAM890  FLJ22037  5'  GACCTCTCACTCCGTGA     93914        A  AAAAT
                                TCACGGGG GA    GGGTC
                                |||||||| ||    |||||
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                                AGTGCCTC CT    TCCAG
                                    A  C____
GAM890  FLJ22215  3'  GGACTTTGGGTTTCTCCT    96835       AAT_
                                GGGAGAAA   GGGTCC
                                ||||||||   ||||||
                                TCCTCTTT   TTCAGG
                                    GGGT
GAM890  FLJ22215  3'  GGGCCCATGCCTCTGTGA    96836       AGAAAA
                                TCACGGGG    ATGGGTCC
                                ||||||||    ||||||||
                                AGTGTCTC    TACCCGGG
                                    CG____
GAM890  FLJ22494  3'  GACTTGTCTCCCTCTGA    45675    C    AAAA TG
                                TCA GGGGAG   A  GGTC
                                ||| ||||||   |  ||||
                                AGT TCCCTC   T  TCAG
                                  C     ____ GT
GAM890  FLJ22558  5'  GACCTTTCATTTTTTTTTTCTT 42739    C GG       ___   C
          GA                    TCA G  GAGAAAAATG   GGTC
                                ||| |  ||||||||||   ||||
                                AGT C  TTTTTTTTAC   CCAG
                                  T TT        TTT
GAM890  FLJ22582  3'  GGGCTCCAGGACTCTCCCTG   46780       AAAA  _
                                CGGGGAGA   TGG GTCC
                                ||||||||   ||| ||||
                                GTCCCTCT   ACC CGGG
                                    CAGG   T
GAM890  FLJ22615  3'  GGACCCTCTCCTTTCTGTGA   68517      GG  AAAAAT
                                TCACGG  AG    GGGTCC
                                ||||||  ||    ||||||
                                AGTGTC  TC    CCCAGG
                                   TT  CTCT__
GAM890  FLJ22757  3'  GTTTTTTTCCTGGTGA     46070     G
                                TCAC GGGAGAAAAAT
                                |||| ||||||||||
                                AGTG TCCTTTTTTTG
                                  G
GAM890  FLJ22800  3'  GGACTTTTTTTTTTTTTTTTG 45606    CG       T_
          A                     TCA  GGGAGAAAAA  GGGTCC
                                |||  ||||||||||  ||||||
                                AGT  TTTTTTTTTT  TTCAGG
                                  TT        TT
GAM890  FLJ22938  3'  GGGCCCGTCCGGCTCTGCG   45164    G   AAAA
                                CG GGAG   ATGGGTCC
                                || ||||   ||||||||
                                GC TCTC   TGCCCGGG
                                 G   GGCC
GAM890  FLJ22938  3'  GGACTCCTGGGTGTCTTTGTGA 45162        GAAAAAT
                                TCACGGGGA     GGGTCC
                                |||||||||     ||||||
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                                AGTGTTTCT      CTCAGG
                                     GTGGGTC
GAM890  FLJ23027  3' GGGCCTGTCATCTTGATG    49932    GG    AAA
                                CG  GAGA   ATGGGTCC
                                ||  ||||   ||||||||
                                GT  TTCT   TGTCCGGG
                                  AG    AC_
GAM890  FLJ23033  3' AATTCATTTTTTTCCTCTGA   45195     C           CC
                                TCA GGGGAGAAAAATGGGT
                                ||| ||||||||||||||||
                                AGT CTCCTTTTTTTACTTA
                                  _            AC
GAM890  FLJ23074  3' GGGTTCATTTTGCCTTTCTG   46820     GG  A_     GG
                                CGG  AG  AAAATG  TCC
                                |||  ||  ||||||  |||
                                GTC  TC  TTTTAC  GGG
                                  TT  CG     TT
GAM890  FLJ23309  3' GGGCCTATTTTCTATCCCCGTG 46064         GA_
             G                   TCACGGGGA   AAAATGGGTCC
                                |||||||||   ||||||||||
                                GGTGCCCCT   TTTTATCCGGG
                                     ATC
GAM890  FLJ23403  3' GGGCCCGTGCACTTCCTGGA   41955    A      AAAA
                                TC CGGGGAG    ATGGGTCC
                                || |||||||    ||||||||
                                AG GTCCTTC    TGCCCGGG
                                 _      ACG_
GAM890  FLJ23510  3' GGCGCTTCCCTTGTGG      45284         A  AAAAT  _
                                TCACGGGG GA     GG GTC
                                |||||||| ||     || |||
                                GGTGTTCC CT     TC CGG
                                     _ _____  G
GAM890  FLJ23510  3' GGGCTCTTTCTTTCTGT     45286      GG    AAT
                                ACGG  AGAAA   GGGTCC
                                ||||  |||||   ||||||
                                TGTC  TCTTT   CTCGGG
                                  TT     ___
GAM890  FLJ23548  3' TGTTTCTTTTCCTGTGA     44750           A
                                TCACGGGGAGA AAATG
                                |||||||||| |||||
                                AGTGTCCTTTT TTTGT
                                       C
GAM890  FLJ30213  3' GGGCCAGTCTTTCCCGTGG    58769         _ AAAATG
                                TCACGGGGA GA      GGTCC
                                ||||||||| ||      |||||
                                GGTGCCCTT CT      CCGGG
                                     T  GA____
GAM890  FLJ30574  5' GGACCCAGATGGTTTTTTTTG  58247         AAA__
                                CGGGGAGAA     TGGGTCC
                                |||||||||     |||||||
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                                GTTTTTTTTT    ACCCAGG
                                      GGTAG
GAM890  FLJ30681  3'  GGAGAATTTTTTCCTTGTG   91787          ATGGG
                                CACGGGGAGAAAA    TCC
                                ||||||||||||    |||
                                GTGTTCCTTTTTT    AGG
                                     AAG__
GAM890  FLJ30681  3'  GGTAAATTTTTTCTCCTTG   91788          TGGGT
                                CGGGGAGAAAAA    CC
                                ||||||||||||    ||
                                GTTCCTCTTTTT    GG
                                      TAAAT
GAM890  FLJ30791  5'  GGCCCCGTCCCTGTGA     58447         GAAAAAT
                                TCACGGGGA     GGGTC
                                |||||||||     |||||
                                AGTGTCCCT     CCCGG
                                     GC_____
GAM890  FLJ30927  5'  GACCTATCAGCCCTTGA     58413    C   AGAAAA
                                TCA GGGG     ATGGGTC
                                ||| ||||     |||||||
                                AGT TCCC     TATCCAG
                                  _   GAC___
GAM890  FLJ32356  3'  GGGTTCATTTTTTTTTCTCTGG 58366    C  GG       GG
                                TCA GG  AGAAAAATG  TCC
                                ||| ||  |||||||||  |||
                                GGT TC  TTTTTTTAC  GGG
                                  C  TT       TT
GAM890  FLJ32468  3'  GGACCTCATCTTCCTG      59045        AAAA _
                                CGGGGAGA    TG GGTCC
                                ||||||||    || |||||
                                GTCCTTCT    AC CCAGG
                                     _____  T
GAM890  FLJ32499  5'  GGACTCATACTACGTTTCCCGT 58159         AAAA__
           GA                     TCACGGGGAG     ATGGGTCC
                                ||||||||||     ||||||||
                                AGTGCCCTTT     TACTCAGG
                                      GCATCA
GAM890  FLJ32670  5'  GGGCAGACATTCTCTTTGGA   58162    A       AAATGG
                                TC CGGGGAGAA     GTCC
                                || |||||||||     ||||
                                AG GTTTCTCTT     CGGG
                                  _       ACAGA_
GAM890  FLJ32783  3'  GATCACCTCTTCCTGGA     58643    A      AAAATG
                                TC CGGGGAGA     GGTC
                                || ||||||||     ||||
                                AG GTCCTTCT     CTAG
                                  _       CCA___
GAM890  FLJ32926  3'  GGGTCTCTGTCTTTTTCTCCCA 58024    G        T____  GT
           GTGG                    AC GGGAGAAAAA    GG  CC
                                || ||||||||||    ||  ||
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                                TG CCCTCTTTTT    TC  GG
                                 A        CTGTC  TG
GAM890  FOXP1    3'  GGACTTGTTTGGTACTTGGGA  51069    A   GAGAA   TG
                                TC CGGG    AAA  GGTCC
                                || ||||    |||  |||||
                                AG GTTC    TTT  TCAGG
                                 G   ATGG_   GT
GAM890  GBL      3'  GGACCTGATGGCCCCCTGTGG  42336       AGAAAAAT
                                TCACGGGG      GGGTCC
                                ||||||||      ||||||
                                GGTGTCCC      TCCAGG
                                    CCGGTAG_
GAM890  GDAP1L1  3'  GGTCTCACTTTCCTGTG    43834       AAAAA   T
                                CACGGGGAG    TGGG CC
                                |||||||||    |||| ||
                                GTGTCCTTT    ACTC GG
                                    C_____   T
GAM890  GDAP1L1  3'  GTTTTTCTACCCTGTGA    43835       _
                                TCACGGGG AGAAAAAT
                                |||||||| ||||||||
                                AGTGTCCC TCTTTTTG
                                    A
GAM890  GFR      3'  GGGCTTGAGTGCTCCTTGT   24473       AAAAAT
                                ACGGGGAG     GGGTCC
                                ||||||||     ||||||
                                TGTTCCTC     TTCGGG
                                    GTGAG_
GAM890  GGTL4    3'  GGACCGGCTTCCCCTGTGA   55076       A   AAATG
                                TCACGGGG GAA    GGTCC
                                |||||||| |||    |||||
                                AGTGTCCC CTT    CCAGG
                                    _  CGG__
GAM890  GGTLA4   3'  GGACAGGCTTCTCCTGTGA   55162       G   AAATGG
                                TCACGGG AGAA    GTCC
                                ||||||| ||||    ||||
                                AGTGTCC TCTT    CAGG
                                    _   CGGA__
GAM890  GMPPB    5'  GGATCCGTTCCCATTCCTG   95746       GAAA
                                CGGGGA   AATGGGTCC
                                ||||||   |||||||||
                                GTCCTT   TTGCCTAGG
                                   ACCC
GAM890  GOLGB1   3'  GGACCCTGATCTTTTGTGG   15634       G   AAAAT
                                TCACGGG AGA    GGGTCC
                                ||||||| |||    ||||||
                                GGTGTTT TCT    CCCAGG
                                    _  AGT__
GAM890  GPR51    3'  GGGCCCGGGGCCTCCCCCGTGA 18407        A  AAAA_
                                TCACGGGG GA    TGGGTCC
                                |||||||| ||    |||||||
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                                AGTGCCCC CT    GCCCGGG
                                    _ CCGGG
GAM890  GRIN3A   5' GGGCGCGCTTTCTCCCTGCGG 55971   A       AA  G
                                TC CGGGGAGAAA  TG GTCC
                                || ||||||||||  || ||||
                                GG GTCCCTCTTT  GC CGGG
                                 C        C_  G
GAM890  GRM5     3' GGCAGATTTTCTTCTAGTGG  62563     G       ATGG
                                TCAC GGGAGAAAA   GTC
                                |||| |||||||||   |||
                                GGTG TCTTCTTTT   CGG
                                  A       AGA_
GAM890  GRP3     3' GGGTCTATTTCTTCCATGA   31122    CG     AA   GT
                                TCA  GGGAGAA  ATGG  CC
                                |||  |||||||  ||||  ||
                                AGT  CCTTCTT  TATC  GG
                                 A_     __    TG
GAM890  GS3955   3' GATCTATGGCCTCTGG     41317    C   AGAAAA
                                TCA GGGG     ATGGGTC
                                ||| ||||     |||||||
                                GGT CTCC     TATCTAG
                                  _   GG____
GAM890  GZMK     3' GGGTCCATTTTTGCACTTGT  9169      GAG      GT
                                ACGGG   AAAAATGG  CC
                                |||||   ||||||||  ||
                                TGTTC   TTTTTACC  GG
                                   ACG       TG
GAM890  H2AFJ    3' GGATTCATCTTTCCTGTGA   36840        AAAA
                                TCACGGGGAG   ATGGGTCC
                                ||||||||||   ||||||||
                                AGTGTCCTTT   TACTTAGG
                                      C___
GAM890  H2AFL    5' ATTTTGTTTGTTTTCTCGTGA 13048         A   GG TCC
                                TCACGGGGAGA AAAT  G
                                |||||||||| ||||  |
                                AGTGCTCTTTT TTTG  T
                                       G   TT TAG
GAM890  HABP2    3' GGCCTTCTTCTTTTTG      14698        AAAT
                                CGGGGAGAA   GGGTC
                                |||||||||   |||||
                                GTTTTTCTT   TCCGG
                                     CT__
GAM890  HAND1    3' TTTATTTTATTTTTCTTTTTGT 16689            TCC
                                ACGGGGAGAAAAATGGG
                                |||||||||||||||||
                                TGTTTTTCTTTTTATTT
                                          TATTTT
GAM890  HARS2    3' GGACGTCATTCTCTCTG     55037        AAA   _
                                CGGGGAGA   ATGG GTCC
                                ||||||||   |||| ||||
```

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                                GTCTCTCT   TACT CAGG
                                   ___   G
GAM890  HBOA     3'  GGATCTGTCTGTCATTTCTCTG 22967        AAA___
              T                  ACGGGGAGA     ATGGGTCC
                                 |||||||||     ||||||||
                                 TGTCTCTTT     TGTCTAGG
                                     ACTGTC
GAM890  HCRTR2   5'  GGACGTAGCTTTCTCCTCCTGG 7732      C       AA  G
                                 TCA GGGGAGAAA  TG GTCC
                                 ||| |||||||||  || ||||
                                 GGT CTCCTCTTT  AT CAGG
                                   C       CG  G
GAM890  HEY1     3'  GGTCTGTTTTTCTCCTTGT   91251            GT
                                 ACGGGGAGAAAAATGG  C
                                 ||||||||||||||||  |
                                 TGTTCCTCTTTTTGTC  G
                                          TG
GAM890  HOMER-3  3'  GGCCCATTCGTCCTGGA     16715    A   GA  AAA
                                 TC CGGG  GA   ATGGGTC
                                 || ||||  ||   |||||||
                                 AG GTCC  CT   TACCCGG
                                  _   TG  ___
GAM890  HPRP8BP  3'  CGGATTTATTGCTGTCTTTTTT 59340   C_     AA__
              TTGA                 A  GGGGAGA   AATGGGTCC   G
                                 |  |||||||   |||||||||  |
                                 T  TTTTTCT   TTATTTAGG   C
                                  TT     GTCG
GAM890  HPRP8BP  3'  GGATTTTTTTTTTTTTTTGT  59341          T_
                                 ACGGGGAGAAAAA  GGGTCC
                                 ||||||||||||  ||||||
                                 TGTTTTTTTTTT  TTTAGG
                                         TT
GAM890  HRB2     3'  GGGCTTTTTTTTTTTTGGTGG 22906     G       TG
                                 TCAC GGGAGAAAAA  GGTCC
                                 |||| ||||||||||  |||||
                                 GGTG TTTTTTTTTT  TCGGG
                                   G        TT
GAM890  HRIHFB2122 3'  GGGTCCATTTTGTCCCCCTTGG 56837     C   A  _     GT
                                 TCA GGGG GA AAAATGG  CC
                                 ||| |||| || |||||||  ||
                                 GGT CCCC CT TTTTACC  GG
                                   T   _ G      TG
GAM890  HRIHFB2436 5'  GGGCCCGTCGCGGCTCCCCGT  26796        AAAA_
                                 ACGGGGAG    ATGGGTCC
                                 ||||||||    ||||||||
                                 TGCCCCTC    TGCCCGGG
                                     GGCGC
GAM890  HSPC065  3'  GGGCTTCCTGGGTCCCCCTGTG 26318        A  AAAAT_
              A                  TCACGGGG GA     GGGTCC
                                 |||||||| ||     ||||||
```

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                                AGTGTCCC CT     TTCGGG
                                    C  GGGTCC
GAM890  HSPC065  3' GGGCAGCATTTTTTTCTTT   26317          G_
                                GGGGAGAAAAATG  GTCC
                                |||||||||||||  ||||
                                TTTCTTTTTTTAC  CGGG
                                    GA
GAM890  HSPC072  5' GGACCCACAGACTCCCTG    26338       AAAAA
                                CGGGGAG    TGGGTCC
                                |||||||    |||||||
                                GTCCCTC    ACCCAGG
                                   AGAC_
GAM890  HSPC134  3' GGCTCCCTTCTCTTTG      26346        AAAT
                                CGGGGAGAA    GGGTC
                                |||||||||    |||||
                                GTTTCTCTT    CTCGG
                                     CC__
GAM890  HSPC232  3' ATTTTTTTTCCTGGA       33230    A
                                TC CGGGGAGAAAAAT
                                || ||||||||||||
                                AG GTCCTTTTTTTTA
                                 _
GAM890  HSPF2    5' GGACCTGTTTCAGCCCTGT   18643       AGAA
                                ACGGGG   AAATGGGTCC
                                ||||||   ||||||||||
                                TGTCCC   TTTGTCCAGG
                                   GAC_
GAM890  HSU54999 3' GGATTTATTTTTTTTCCT    25241
                                GGGGAGAAAAATGGGTCC
                                ||||||||||||||||||
                                TCCTTTTTTTTATTTAGG

GAM890  HSU79303 3' GGGCCTTCCTCCCCCGTGG   25251        A  AAAAT
                                TCACGGGG GA    GGGTCC
                                |||||||| ||    ||||||
                                GGTGCCCC CT    TCCGGG
                                    _ CCT__
GAM890  HTMP10   3' GGGCTGTATCTACTCTGTGG  52612        _  AAAATG
                                TCACGGGG AGA     GGTCC
                                |||||||| |||     |||||
                                GGTGTCTC TCT     TCGGG
                                    A  ATG___
GAM890  IL18BP   3' GATCCCCTCCCTTGTGA     19108      _    AAAAAT
                                TCACG GGGAG     GGGTC
                                ||||| |||||     |||||
                                AGTGT CCCTC     CCTAG
                                  T    C_____
GAM890  IL18BP   3' GGGCCCATCCGTCCTGGGA   19110    A    AGAAAA
                                TC CGGGG     ATGGGTCC
                                || |||||     ||||||||
```

```
                                AG GTCCT     TACCCGGG
                                 G    GCC___
GAM890  IMAGE145052 5'  GGGTTCGGCATTTTTCGTCG  26538    G    AA_  GG
                                CGG GAGAAA   TG  TCC
                                ||| ||||||   ||  |||
                                GCT CTTTTT   GC  GGG
                                  G     ACG  TT
GAM890  IMP13    5'  GGGCTCTCTCTCTCCCGTGA  27735       _   AAAAT
                                TCACGGG GAGA    GGGTCC
                                ||||||| ||||    ||||||
                                AGTGCCC CTCT    CTCGGG
                                    T   CT___
GAM890  IMPACT   3'  GGAGAGTTTCTTCTTGTGA   37391          AATGGG
                                TCACGGGGAGAAA     TCC
                                ||||||||||||     |||
                                AGTGTTCTTCTTT     AGG
                                       GAG___
GAM890  IPT      3'  GGAAAGCATTTTTTTTTTC   34453   GG       GG_
                                G  GAGAAAAATG   TCC
                                |  ||||||||||   |||
                                C  TTTTTTTTAC   AGG
                                 TT        GAA
GAM890  KCNH8    3'  TGATGTATTTTTCTTTTTGTGA 58259            G   C
                                TCACGGGGAGAAAAATG GTC
                                |||||||||||||||| |||
                                AGTGTTTTTCTTTTTAT TAG
                                       G   TC
GAM890  KCNMB2   3'  GGAATATTGCTCTTTGTGA   19540         AAA   GG
                                TCACGGGGAG   AATG  TCC
                                ||||||||||   ||||  |||
                                AGTGTTTCTC   TTAT  AGG
                                     G__    A_
GAM890  KIAA0063 5'  GGTTTTATTTTTTTCCTTTTGA 29639     CG          T
                                TCA  GGGAGAAAAATGGG CC
                                |||  |||||||||||||| ||
                                AGT  TCCTTTTTTTTATTT GG
                                  TT          T  G
GAM890  KIAA0077 3'  GGCTGTTTTTTCCCTGT     67020          ATG
                                ACGGGGAGAAAA   GGTC
                                ||||||||||||   ||||
                                TGTCCCTTTTTT   TCGG
                                       G__
GAM890  KIAA0087 3'  GTGCTCATTTTTTTTTTGTGG  28702       G         CC
                                TCACGGG AGAAAAATGGGT
                                ||||||| ||||||||||||
                                GGTGTTT TTTTTTTACTCG
                                    _         TGA
GAM890  KIAA0152 3'  GGATTGGTTCTCTCCTTG    28301        AA   G
                                CGGGGAGA  AAT GGTCC
                                ||||||||  ||| |||||
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                                GTTCCTCT  TTG TTAGG
                                    C_   G
GAM890  KIAA0153 3' GGCCCGTCGCCTTTGG     30703     C   GA  AAAA
                                TCA GGG  GA    TGGGTC
                                ||| |||  ||    ||||||
                                GGT TCC  CT    GCCCGG
                                  T   G_  ____
GAM890  KIAA0161 3' CAGCTTTCTCTCTGTGG     28499           AA
                                TCACGGGGAGAAA  TG
                                ||||||||||||  ||
                                GGTGTCTCTCTTT  AC
                                       CG
GAM890  KIAA0161 3' GGACCTGTGGCTTCTCTGA   28510     C     AAAA
                                TCA GGGGAG    ATGGGTCC
                                ||| ||||||    ||||||||
                                AGT CTCTTC    TGTCCAGG
                                  _     GG__
GAM890  KIAA0173 3' GGGTCTATGAACTTTGTGA   27670        AGAAAA    GT
                                TCACGGGG     ATGG  CC
                                ||||||||     ||||  ||
                                AGTGTTTC     TATC  GG
                                    AAG___    TG
GAM890  KIAA0184 3' GGACTCGCCCTTCCTGTG    65198         AAAAA
                                CACGGGGAG    TGGGTCC
                                |||||||||    |||||||
                                GTGTCCTTC    GCTCAGG
                                     CC___
GAM890  KIAA0186 3' GACCTGTTTTTCTCTCCTGA  40751     C
                                TCA GGGGAGAAAAATGGGTC
                                ||| ||||||||||||||||
                                AGT CCTCTCTTTTTGTCCAG
                                  _
GAM890  KIAA0210 3' GGACCTAGAGTCCCTTCTGTGG 28481       __  A  AAAA
                                TCACGG  GG GA    TGGGTCC
                                ||||||  || ||    |||||||
                                GGTGTC  CC CT    ATCCAGG
                                   TT  _  GAG_
GAM890  KIAA0210 5' GACTTTTTTTTTTTTTTG    28477           TG
                                CGGGGAGAAAAA  GGTC
                                ||||||||||||  ||||
                                GTTTTTTTTTTT  TCAG
                                       TT
GAM890  KIAA0229 3' GGGCTCATTTTGATTCTCTG  92431        A_
                                CGGGGAG  AAAATGGGTCC
                                |||||||  ||||||||||||
                                GTCTCTT  TTTTACTCGGG
                                    AG
GAM890  KIAA0229 3' GGACTCAGCTCTCTCTGCGG  92430    A       AAAA
                                TC CGGGGAGA    TGGGTCC
                                || ||||||||    |||||||
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```
                                GG GTCTCTCT    ACTCAGG
                                 C       CG__
GAM890  KIAA0232 3' TTTGTTTGTTTTCTTGTGG   72766          A   GG
                                TCACGGGGAGA AAAT  G
                                |||||||||| |||| |
                                GGTGTTCTTTT TTTG  T
                                      G   TT
GAM890  KIAA0232 3' GGGCTGAGATTGTTTTTCCCGT 72751          A  G__
           GG                   TCACGGGGAGAA AAT   GGTCC
                                |||||||||||| |||  |||||
                                GGTGCCCTTTTT TTA   TCGGG
                                      G   GAG
GAM890  KIAA0247 3' GGGTCTGTCCTGTTTCCTTTGA 28407    C     AAAA   GT
                                TCA GGGGAG   ATGG  CC
                                ||| ||||||   ||||  ||
                                AGT TCCTTT   TGTC  GG
                                  T     GTCC   TG
GAM890  KIAA0265 3' AAACCCATTTTTTTTTTGTGG  69873       G         CC
                                TCACGGG AGAAAAATGGGT
                                ||||||| ||||||||||||
                                GGTGTTT TTTTTTTACCCA
                                   _          AAA
GAM890  KIAA0286 3' GGTTCTTTTTCTTTGTGG    68329          AAT GG
                                TCACGGGGAGAAA   G  TC
                                ||||||||||||   |  ||
                                GGTGTTTCTTTTT   C  GG
                                      ___ TT
GAM890  KIAA0293 3' GGACCCGTGAACAACTTTGT   60608       AGAAAA
                                ACGGGG     ATGGGTCC
                                ||||||     ||||||||
                                TGTTTC     TGCCCAGG
                                   AACAAG
GAM890  KIAA0296 3' GGACCCATTCCATCTAGTGG   28115     GG   GAAA
                                TCAC  GGA    AATGGGTCC
                                ||||  |||   |||||||||
                                GGTG  TCT    TTACCCAGG
                                  A_   ACC_
GAM890  KIAA0310 3' GGATCCATTTGTCCTTGT    81679       GAA
                                ACGGGGA   AAATGGGTCC
                                |||||||   ||||||||||
                                TGTTCCT   TTTACCTAGG
                                   G__
GAM890  KIAA0323 3' GATATTTTCCCCTTGA      63264     C       AAATGG
                                TCA GGGGAGAA      GTC
                                ||| ||||||||      |||
                                AGT CCCCTTTT      TAG
                                  T       A_____
GAM890  KIAA0323 3' GGAGTTTTTTTTTTTCCTG   63268          TG G
                                CGGGGAGAAAAA  G TCC
                                ||||||||||||  | |||
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                                GTCCTTTTTTTT  T AGG
                                      TT G
GAM890  KIAA0329 3' GGGCTGCATCTCTCTGTG    29278        AAAA _
                                CACGGGGAGA    TG GGTCC
                                ||||||||||    || |||||
                                GTGTCTCTCT    AC TCGGG
                                     _____ G
GAM890  KIAA0335 3' GGCCATTTTTTTCTTCTTG    28994          TG_
                                CGGGGAGAAAAA   GGTC
                                ||||||||||||   ||||
                                GTTCTTCTTTTT   CCGG
                                      TTA
GAM890  KIAA0337 3' GACCCATGCGCCCCTGA     28832     C    AGAAAA
                                TCA GGGG     ATGGGTC
                                ||| ||||     |||||||
                                AGT CCCC     TACCCAG
                                  _   GCG___
GAM890  KIAA0337 3' GGACCTGTCAGGCTTTGT    28833       AGAAAA
                                ACGGGG     ATGGGTCC
                                ||||||     ||||||||
                                TGTTTC     TGTCCAGG
                                   GGAC__
GAM890  KIAA0349 3' GGATCCCAGCCCCTTTGTGG  92306     ___   AGAAAAAT
                                TCAC   GGGG      GGGTCC
                                ||||   ||||      ||||||
                                GGTG   CCCC      CCTAGG
                                  TTT    GAC_____
GAM890  KIAA0429 3' GGGCTTGTTTTTCTTTTC    28560   GG      TG
                                G  GAGAAAAA  GGTCC
                                |  ||||||||  |||||
                                C  TTCTTTTT  TCGGG
                                 TT       GT
GAM890  KIAA0445 5' GGGCTTGGTTGCCCTGTGG   27955        AGAAAAA
                                TCACGGGG      TGGGTCC
                                ||||||||      |||||||
                                GGTGTCCC      GTTCGGG
                                     GTTG___
GAM890  KIAA0453 3' TCATTTTTCTTCCTGTGG    69055
                                TCACGGGGAGAAAAATGG
                                ||||||||||||||||||
                                GGTGTCCTTCTTTTTACT

GAM890  KIAA0453 3' TCATCATTTTTCTTCCTGTGG 69054              GTCC
                                TCACGGGGAGAAAAATGG
                                ||||||||||||||||||
                                GGTGTCCTTCTTTTTACT
                                          ACTG
GAM890  KIAA0469 3' GGGTCCACCCCTTCTCTCTG  29342        AAA_  GT
                                CGGGGAGAA   TGG  CC
                                |||||||||   |||  ||
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                                GTCTCTCTT   ACC  GG
                                     CCCC   TG
GAM890  KIAA0515 3' GGACGCCTTTCTCCCGTGA   63812       G    AAT  _
                                TCACGGG AGAAA   GG GTCC
                                ||||||| |||||   || ||||
                                AGTGCCC TCTTT   CC CAGG
                                   _    ____ G
GAM890  KIAA0522 3' GGGCCTGTGTGAGCTCTCTGTG 71970         AAAA_
           A                     TCACGGGGAG    ATGGGTCC
                                 ||||||||||    ||||||||
                                 AGTGTCTCTC    TGTCCGGG
                                      GAGTG
GAM890  KIAA0523 3' GGGCCCTGTTCTCTCTG     67741         AAAT
                                 CGGGGAGAA    GGGTCC
                                 |||||||||    ||||||
                                 GTCTCTCTT    CCCGGG
                                      GT__
GAM890  KIAA0537 3' GGGTTTAGTCATCCTGTGG   29257       GA  AAAA   GT
                                 TCACGGG  GA    TGG  CC
                                 |||||||  ||    |||  ||
                                 GGTGTCC  CT    ATT  GG
                                     TA  G___   TG
GAM890  KIAA0546 3' TTTTTTTCTCCTGTGA      71317        _
                                 TCACGGG GAGAAAAA
                                 ||||||| ||||||||
                                 AGTGTCC CTTTTTTT
                                     T
GAM890  KIAA0553 3' GGACTCATTTTTCTTT      69894
                                 GGAGAAAAATGGGTCC
                                 ||||||||||||||||
                                 TTTCTTTTTACTCAGG

GAM890  KIAA0553 3' GGATTCCTGGGTTTCCCTG   69895         AAAAT
                                 CGGGGAGA    GGGTCC
                                 ||||||||    ||||||
                                 GTCCCTTT    CTTAGG
                                      GGGTC
GAM890  KIAA0555 5' GGATCATCTTTTCCCTGGA   60116    A       AAATG
                                 TC CGGGGAGAA    GGTCC
                                 || |||||||||    |||||
                                 AG GTCCCTTTT    CTAGG
                                   _       CTA__
GAM890  KIAA0596 3' GGGCCCAGCATTGTATTTCCCT 62835         AAAA____
           GTGA                    ACGGGGAGA       TGGGTCC
                                 |||||||||       |||||||
                                 TGTCCCTTT       ACCCGGG
                                      ATGTTACG
GAM890  KIAA0628 3' CCCATTTTTTTTTTTTGA    28867     C
                                 TCA GGGGAGAAAAATGGG
                                 ||| ||||||||||||||
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                                AGT TTTTTTTTTTTACCC
                                  _
GAM890  KIAA0672  3'  GGGCTGCTACCTTTTCCTTGGA 29415    A       AAATG_
                                TC CGGGGAGAA     GGTCC
                                || |||||||||     |||||
                                AG GTTCCTTTT     TCGGG
                                  _       CCATCG
GAM890  KIAA0683  5'  GGGTCCAGGTCGTCTTCCCGTG 32260          AAAA_  GT
          A                      TCACGGGGAGA    TGG  CC
                                ||||||||||    |||  ||
                                AGTGCCCTTCT    ACC  GG
                                       GCTGG   TG
GAM890  KIAA0703  5'  ATTTGTCTTTTTGTGA     29449          A
                                TCACGGGGAGA AAAT
                                |||||||||| ||||
                                AGTGTTTTTCT TTTA
                                       G
GAM890  KIAA0711  5'  GGACCAGTGTCCTCCCCGTGA  29524         AAAA  G
                                TCACGGGGAG    AT GGTCC
                                |||||||||    || |||||
                                AGTGCCCCTC    TG CCAGG
                                      CTG_  A
GAM890  KIAA0748  3'  GGAGTCCTATTTTTCTTCTTGA 28942    A           __
          GA                     TC CGGGGAGAAAAATGGG  TCC
                                || ||||||||||||||  |||
                                AG GTTCTTCTTTTTATCC  AGG
                                  A             TG
GAM890  KIAA0748  3'  GGACACATTTCTCCCCTGA    28941     C      AA   G
                                TCA GGGGAGAA  ATG GTCC
                                ||| ||||||||  ||| ||||
                                AGT CCCCTCTT  TAC CAGG
                                  _       __  A
GAM890  KIAA0767  3'  GGGCTCTGGGCTCCCCGTGG   60629         AAAAAT
                                TCACGGGGAG     GGGTCC
                                ||||||||||     ||||||
                                GGTGCCCCTC     CTCGGG
                                      GGGT__
GAM890  KIAA0779  3'  GGGTCTTTTATTTTTCCTTTGA 85729     C      A  T  GT
                                TCA GGGGAGAA AA GG  CC
                                ||| ||||||| || ||  ||
                                AGT TCCTTTTT TT TC  GG
                                  T       A  T  TG
GAM890  KIAA0795  5'  GGATCTGGTGCACTTCTCCGTG 46593         AAAAA_
                                CACGGGGAG     TGGGTCC
                                |||||||||     |||||||
                                GTGCCTCTT     GTCTAGG
                                      CACGTG
GAM890  KIAA0882  3'  GGACGATTTTTTCTTCT     82647          TGG
                                GGGAGAAAAA   GTCC
                                ||||||||||   ||||
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                                TCTTCTTTTT  CAGG
                                      TAG
GAM890  KIAA0884  5' ATTTTTTTATCCTGTGA    70201       _
                                TCACGGGG AGAAAAAT
                                |||||||| ||||||||
                                AGTGTCCT TTTTTTTA
                                     A
GAM890  KIAA0912  5' GGACTAGAGTTTCCTCGCGG  64411   A      AAAATG
                                TC CGGGGAGA    GGTCC
                                || ||||||||    |||||
                                GG GCTCCTTT    TCAGG
                                 C      GAGA__
GAM890  KIAA0914  3' GGGCCATGCTCTCCTTGGA  29680   A      AAAATG
                                TC CGGGGAGA    GGTCC
                                || ||||||||    |||||
                                AG GTTCCTCT    CCGGG
                                 _      CGTA__
GAM890  KIAA0945  5' GGACTTCCCATCTCTCTCTGTG 30212        AAA   ___
                                CACGGGGAGA  ATGGG  TCC
                                ||||||||||  |||||  |||
                                GTGTCTCTCT  TACCC  AGG
                                      C__    TTC
GAM890  KIAA0964  3' GGGCCCATTTCCAGCTTG   29765     GAGAA
                                CGGG   AAATGGGTCC
                                ||||   ||||||||||
                                GTTC   TTTACCCGGG
                                  GACC_
GAM890  KIAA0972  3' GGGCTTCAAGTCTCTCTCTGTG 30014        AAAA  _
          A                    TCACGGGGAGA   TGG GTCC
                               ||||||||||   ||| ||||
                               AGTGTCTCTCT   ACT CGGG
                                     CTGA  T
GAM890  KIAA0982  3' GGGCCTCACTTTTTCTCTTGG  25849   G       _ _
                               C GGGAGAAAAA TG GGTCC
                               | ||||||||| || |||||
                               G TTCTCTTTTT AC CCGGG
                                G        C  T
GAM890  KIAA0984  3' GGGCCTTCAGAGTCCCTGTGA  65531        GAAAAAT
                               TCACGGGGA     GGGTCC
                               |||||||||     ||||||
                               AGTGTCCCT     TCCGGG
                                     GAGACT_
GAM890  KIAA1007  5' GGACCCAGGAGTTTCCTGTG   93575       AAAAA
                               CACGGGGAG    TGGGTCC
                               |||||||||    |||||||
                               GTGTCCTTT    ACCCAGG
                                     GAGG_
GAM890  KIAA1023  3' GTCATTCTCTGTGG       34270        GAAAA   G
                               TCACGGGGA    ATGG T
                               |||||||||    |||| |
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                                GGTGTCTCT    TACT G
                                      _____  G
GAM890  KIAA1026 3' GGCCATATTTTGTCTTCTCGTG 71202         _    _   C
              G                  TCACGGGGAGA AAAATG GGTC
                                 |||||||||| |||||| ||||
                                 GGTGCTCTTCT TTTTAT CCGG
                                       G     A
GAM890  KIAA1030 3' GGACCTGTCCTTTCTGTGG   93338      GG  AAAA
                                 TCACGG  AG   ATGGGTCC
                                 ||||||  ||   ||||||||
                                 GGTGTC  TC   TGTCCAGG
                                    TT  C___
GAM890  KIAA1034 3' GCCTTTTTTTTTTTTTGTGA  62470           T
                                 TCACGGGGAGAAAAA GGGT
                                 |||||||||||||| ||||
                                 AGTGTTTTTTTTTT TCCG
                                           T
GAM890  KIAA1040 3' GGATTACAGTATTTTTCTTCT  72231          ____
                                 GGGAGAAAAATG   GGTCC
                                 ||||||||||||   |||||
                                 TCTTCTTTTTAT   TTAGG
                                       GACA
GAM890  KIAA1042 3' GGACAGTCGTTTCTTTTTTGA  30342    C       AATGG
                                 TCA GGGGAGAAA    GTCC
                                 ||| |||||||||    ||||
                                 AGT TTTTTCTTT    CAGG
                                   _       GCTGA
GAM890  KIAA1045 3' GGAAAGCTTTTTCCTCTG    71054      A     TGGG
                                 CGGGG GAAAAA   TCC
                                 ||||| ||||||   |||
                                 GTCTC CTTTTT   AGG
                                    _    CGAA
GAM890  KIAA1045 3' GGACCAAAGTCCCTTTGTGA  71055        A  AAAATG
                                 TCACGGGG GA    GGTCC
                                 |||||||| ||    |||||
                                 AGTGTTTC CT    CCAGG
                                      C  GAAA__
GAM890  KIAA1052 3' GACCCGATTTCTCTG      30250        AAAA
                                 CGGGGAGA   TGGGTC
                                 ||||||||   ||||||
                                 GTCTCTTT   GCCCAG
                                      A___
GAM890  KIAA1068 3' TCATTTTTTTTCCTGGA    31040    A
                                 TC CGGGGAGAAAAATGG
                                 || ||||||||||||||
                                 AG GTCCTTTTTTTTACT
                                  _
GAM890  KIAA1069 3' GGATCCCCTAATACTTCTCGTG 67939         AAAAAT_
              G                  TCACGGGGAG     GGGTCC
                                 ||||||||||     ||||||
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                                GGTGCTCTTC      CCTAGG
                                      ATAATCC
GAM890  KIAA1076 3' CTTCTCTATTTTTTTCCTCGT  65516             TCC
                                ACGGGGAGAAAAATGGG
                                |||||||||||||||||
                                TGCTCCTTTTTTTATCT
                                      CTTCT
GAM890  KIAA1078 3' TTTGCTATTTTTCTCTCCTGG  65126    C          GTCC
                                TCA GGGGAGAAAAATGG
                                ||| ||||||||||||||
                                GGT CCTCTCTTTTTATC
                                  _          GTTTG
GAM890  KIAA1086 3' GGTCAGTTTTTTTTTCTTTGG  70753    C  GG      G GT C
                                TCA GG  AGAAAAAT G  C
                                ||| ||  |||||||| |  |
                                GGT TC  TTTTTTTG C  G
                                  T  TT       A TG
GAM890  KIAA1126 3' GGGCTCGTGGCACCCTTGG   71932    C   GAGAAAA
                                TCA GGG      ATGGGTCC
                                ||| |||      ||||||||
                                GGT CCC      TGCTCGGG
                                  T   ACGG___
GAM890  KIAA1155 3' GGATTCCAACTTCCTGT     62236        AAAAA   _
                                ACGGGGAG    TGGG TCC
                                ||||||||    |||| |||
                                TGTCCTTC    ACCT AGG
                                     A____   T
GAM890  KIAA1157 3' GGATTTTTTTTTTTTTTTTTCG 72248     GG      T___
          TG                      CACG  GAGAAAAA   GGGTCC
                                ||||  ||||||||   ||||||
                                GTGC  TTTTTTTT   TTTAGG
                                  TT       TTTT
GAM890  KIAA1157 3' GGATCTATTTTGTGTGTTTTG  72247      AGA__
                                CGGGG    AAAATGGGTCC
                                |||||    ||||||||||
                                GTTTT    TTTTATCTAGG
                                   GTGTG
GAM890  KIAA1160 3' GGATCCATTTATTTTTATTGTG 40372       G    _
            G                    TCACGG GAGAA AAATGGGTCC
                                ||||||| ||||| ||||||||||
                                GGTGTT TTTTT TTTACCTAGG
                                   A    A
GAM890  KIAA1160 5' GGGCCTGTGGAGTTTCTTGGA  40374    A      AAAA
                                TC CGGGGAG    ATGGGTCC
                                || |||||||    ||||||||
                                AG GTTCTTT    TGTCCGGG
                                 _      GAGG
GAM890  KIAA1160 3' GGGTCTGTCCCTGGTCTTCCTG 40375        AAA___   GT
                                CGGGGAGA     ATGG  CC
                                ||||||||     ||||  ||
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                                GTCCTTCT     TGTC  GG
                                    GGTCCC    TG
GAM890  KIAA1163 3' GATTTGTTTCTTCCCGTGG   78901          AA  GG
                                TCACGGGGAGAA  AT  GTC
                                ||||||||||||  ||  |||
                                GGTGCCCTTCTT  TG  TAG
                                      __  TT
GAM890  KIAA1164 3' GGGTTTGTTTTTCCCGGGA   69507    A       AAA TG GT
                                TC CGGGGAGA   A  G  CC
                                || ||||||||   |  |  ||
                                AG GCCCTTTT   T  T  GG
                                 G       ___ GT TG
GAM890  KIAA1170 3' GGATTTTGCCTCTTTGTG    69858         AAAAAT
                                CACGGGGAG     GGGTCC
                                |||||||||     ||||||
                                GTGTTTCTC     TTTAGG
                                     CGT___
GAM890  KIAA1189 3' GGATAGTTTTATTTCTGTGG   72045       GG GA    GG
                                TCACGG  A  AAAAT  GTCC
                                ||||||  |  |||||  ||||
                                GGTGTC  T  TTTTG  TAGG
                                   TT A_    A_
GAM890  KIAA1196 3' GGGCCCCGCCCGCCTTGTGA  61477         AGAAAAAT
                                TCACGGGG       GGGTCC
                                ||||||||       ||||||
                                AGTGTTCC       CCCGGG
                                     GCCCGC__
GAM890  KIAA1203 3' GGACATCATTTTCCTTGT    71641         AAA   _
                                ACGGGGAGA   ATGG GTCC
                                |||||||||   |||| ||||
                                TGTTCCTTT   TACT CAGG
                                     ___    A
GAM890  KIAA1203 3' GGACTTGTCCTTACTGTGG   71642       GG  AAAA TG
                                TCACGG  AG    A  GGTCC
                                ||||||  ||    |  |||||
                                GGTGTC  TC    T  TCAGG
                                   AT  C___ GT
GAM890  KIAA1204 3' GGGCCTATTGTGGCCTCTGA  69218     C    AGAAA
                                TCA GGGG     AATGGGTCC
                                ||| ||||     |||||||||
                                AGT CTCC     TTATCCGGG
                                  _    GGTG_
GAM890  KIAA1223 3' TTTATTTTTTTTTCTTTTTGTG 71150            TG   CC
           G                     TCACGGGGAGAAAAA  GGT
                                 |||||||||||||||  |||
                                 GGTGTTTTTCTTTTT  TTA
                                       TT   TTTA
GAM890  KIAA1237 3' GGGCCTCTCTCTCTGTAGA   80475    _       AAAAT
                                TC ACGGGGAGA     GGGTCC
                                || |||||||||     ||||||
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                                AG TGTCTCTCT    TCCGGG
                                 A       C____
GAM890  KIAA1260 5' GGCTTTGTCTCCTTGGA    60026   A      AAAAT
                                TC CGGGGAGA    GGGTC
                                || ||||||||    |||||
                                AG GTTCCTCT    TTCGG
                                 _      GT___
GAM890  KIAA1266 3' GGACCTGCCTGCTCCTTTGG  66124    C     AAAAAT
                                TCA GGGGAG     GGGTCC
                                ||| ||||||     ||||||
                                GGT TTCCTC     TCCAGG
                                  _     GTCCG_
GAM890  KIAA1277 3' GACCTGACTCTTCTTG     64456       AAAA
                                CGGGGAGA   TGGGTC
                                ||||||||   ||||||
                                GTTCTTCT   GTCCAG
                                     CA__
GAM890  KIAA1280 5' ACTTTTTTTTCCTTG      69709          TG
                                CGGGGAGAAAAA GGT
                                |||||||||||  |||
                                GTTCCTTTTTTT TCA
                                      __
GAM890  KIAA1280 5' GGGCTTGGTTTTTCCTTGT  69727         AAT
                                ACGGGGAGAAA  GGGTCC
                                ||||||||||   ||||||
                                TGTTCCTTTTT  TTCGGG
                                      GG_
GAM890  KIAA1305 5' GGATCTTCAGCCTCCTGTGG  46932      G  AAAAAT
                                TCACGGG AG     GGGTCC
                                ||||||| ||     ||||||
                                GGTGTCC TC     TCTAGG
                                   _ CGACT_
GAM890  KIAA1317 5' GGGCTTAACTTTTTTTGCG   86030   G     AA
                                CG GGAGAAA  TGGGTCC
                                || |||||||  |||||||
                                GC TTTTTTT  ATTCGGG
                                 G      CA
GAM890  KIAA1332 3' GAAATGTTTTTTTCCTTGTGG 71167            GG  C
                                TCACGGGGAGAAAAATG  TC
                                ||||||||||||||||  ||
                                GGTGTTCCTTTTTTTGT  AG
                                          AA
GAM890  KIAA1348 3' GATCTATGCCTCTGGA     68576    A    AGAAAA
                                TC CGGGG     ATGGGTC
                                || |||||     |||||||
                                AG GTCTC     TATCTAG
                                 _    CG____
GAM890  KIAA1357 3' GGCTATTTTTTTTTCCTTG   71981          TG_
                                CGGGGAGAAAAA  GGTC
                                ||||||||||||  ||||
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                                GTTCCTTTTTTT  TCGG
                                      TTA
GAM890  KIAA1371 3' GGAGGCATTTTCTTCCCCTGA 89045    C    GA    GG
                                TCA GGGGA  AAAATG  TCC
                                ||| |||||  ||||||  |||
                                AGT CCCCT  TTTTAC  AGG
                                  _    TC    GG
GAM890  KIAA1387 3' GTCCATTTTTCCTGGA    70873    A     AAA   GT
                                TC CGGGGAGA  ATGG  C
                                || ||||||||  ||||  |
                                AG GTCCTTTT  TACC  G
                                  _     ___   TG
GAM890  KIAA1432 3' TATTTTTCTCCCCTTGG    66750    C
                                TCA GGGGAGAAAAATG
                                ||| ||||||||||||
                                GGT CCCCTCTTTTTAT
                                  T
GAM890  KIAA1434 3' GACTTCCTCTCTGTG      69611        AAAAAT
                                CACGGGGAG    GGGTC
                                |||||||||    |||||
                                GTGTCTCTC    TTCAG
                                     C_____
GAM890  KIAA1437 3' CTGGCCCCTTTTCTCCCTCTGA 60585    C       AT    C
                                TCA GGGGAGAAAA  GGGTC
                                ||| ||||||||||  |||||
                                AGT TCCCTCTTTT  CCCGG
                                  C       C_    TCG
GAM890  KIAA1443 3' CTGTTTTTTTCCCTTGG    63828    C
                                TCA GGGGAGAAAAATGG
                                ||| ||||||||||||||
                                GGT TCCCTTTTTTTGTC
                                  _
GAM890  KIAA1443 3' GGAATAGTTTCTCCTTGT    63837         AATGGG
                                ACGGGGAGAAA    TCC
                                ||||||||||    |||
                                TGTTCCTCTTT    AGG
                                      GATA__
GAM890  KIAA1450 3' GACAGTTCTTCCTTGG     65827    C     AAATGG
                                TCA GGGGAGAA    GTC
                                ||| ||||||||    |||
                                GGT TCCTTCTT    CAG
                                  _     GA____
GAM890  KIAA1464 3' GGGTTTTTAAATTTTTTTCTCC 68273   C        ____ GT
          TGA                    A GGGGAGAAAAAT   GG  CC
                                | ||||||||||||   ||  ||
                                T CCTCTTTTTTTA   TT  GG
                                _         AATT  TG
GAM890  KIAA1464 3' GGACTATCCCTTATCCCTGTGG 68270        GAAAAATG
                                TCACGGGGA      GGTCC
                                |||||||||      |||||
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                                GGTGTCCCT      TCAGG
                                     ATTCCCTA
GAM890  KIAA1467 3' GGCTAATTTTTTTTTTTGT   71614          G
                                ACGGGGAGAAAAAT GGTC
                                |||||||||||||| ||||
                                TGTTTTTTTTTTTA TCGG
                                       A
GAM890  KIAA1508 3' GGGTTTCTCATTTCCTCCTGTG 61888       GA  AA   ___
          G                      TCACGGG  GAA  ATGGG   TCC
                                 |||||||  |||  |||||   |||
                                 GGTGTCC  CTT  TACTC   GGG
                                     TC   __    TTT
GAM890  KIAA1509 3' GGATCTATTTATGTTCCAGTGG 61616     GG   AA_
                                TCAC  GGAG   AAATGGGTCC
                                ||||  ||||   ||||||||||
                                GGTG  CCTT   TTTATCTAGG
                                  A_   GTA
GAM890  KIAA1522 3' GGGCCACCGCTTCTTTCTTGA  64976    C  GG   AAATG
                                TCA GG  AGAA    GGTCC
                                ||| ||  ||||    |||||
                                AGT TC  TCTT    CCGGG
                                  _ TT   CGCCA
GAM890  KIAA1538 3' CCTGTTTTTTTTTCCTGA    71538    C  GG
                                TCA GG  AGAAAAATGGG
                                ||| ||  ||||||||||
                                AGT CC  TTTTTTTGTCC
                                  _ TT
GAM890  KIAA1538 3' TTTTTTTTCCTGATGG      71563    _
                                TCA CGGGGAGAAAAA
                                ||| ||||||||||||
                                GGT GTCCTTTTTTTT
                                  A
GAM890  KIAA1538 3' GGGCCTCCCTGCTCTGTGA   71550        AGAAAAAT
                                TCACGGGG       GGGTCC
                                ||||||||       ||||||
                                AGTGTCTC       TCCGGG
                                     GTCCC___
GAM890  KIAA1580 5' GACTTTTTTTTTTGGTGG    69445     G       ATG   C
                                TCAC GGGAGAAAA   GGTC
                                |||| |||||||||   ||||
                                GGTG TTTTTTTTT   TCAG
                                  G       ___    A
GAM890  KIAA1600 3' GATTCATAGCTTTTTG      71443        AAAA
                                CGGGGAG    ATGGGTC
                                |||||||    |||||||
                                GTTTTTC    TACTTAG
                                    GA__
GAM890  KIAA1613 3' GGTGTATTTTTTTTTCCTGT   64817          TGGGT
                                ACGGGGAGAAAAA    CC
                                ||||||||||||     ||
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                                TGTCCTTTTTTTT    GG
                                      TATGT
GAM890  KIAA1617 3' GACCTCCATTCCTGTGA    91427       GAAAAAT
                                TCACGGGGA     GGGTC
                                |||||||||     |||||
                                AGTGTCCTT     TCCAG
                                    ACC____
GAM890  KIAA1634 3' GGTTCATCTTGTTGTGA    63391      G   AAAA  GG
                                TCACGG GAGA   TG  TC
                                |||||| ||||   ||  ||
                                AGTGTT TTCT   AC  GG
                                   G   ____  TT
GAM890  KIAA1656 3' GATCTGGGTCTCGGTGG    65796     G   GAAAAA
                                TCAC GGGA     TGGGTC
                                |||| ||||     ||||||
                                GGTG CTCT     GTCTAG
                                  G   GG____
GAM890  KIAA1668 3' TTCATGTTTCTTTCTGTGG   66484      GG    A
                                TCACGG  AGAAA ATGGG
                                ||||||  ||||| |||||
                                GGTGTC  TCTTT TACTT
                                   TT    G
GAM890  KIAA1706 3' GGGCCTATTTTTCTCC     92791
                                GGAGAAAAATGGGTCC
                                ||||||||||||||||
                                CCTCTTTTTATCCGGG

GAM890  KIAA1728 3' CCATTTTTTTTCTTTGG    68417    C
                                TCA GGGGAGAAAAATGG
                                ||| ||||||||||||||
                                GGT TTCTTTTTTTTACC
                                 _
GAM890  KIAA1765 3' GGGTCTAAACTCCCCCTGTGA 70612       A  AAAA   GT
                                TCACGGGG GA   TGG  CC
                                |||||||| ||   |||  ||
                                AGTGTCCC CT   ATC  GG
                                     C  CAA_   TG
GAM890  KIAA1786 3' GGGTTGATTTCTTCTTGT    66035       AA  G GT
                                ACGGGGAGAA  AT G  CC
                                ||||||||||  || |  ||
                                TGTTCTTCTT  TA T  GG
                                     __  G TG
GAM890  KIAA1786 3' GGTCTCCATGATTTCCTGTGA 66036       AAAA   _ T
                                TCACGGGGAG   ATGG G CC
                                ||||||||||   |||| | ||
                                AGTGTCCTTT   TACC C GG
                                     AG__    T T
GAM890  KIAA1855 3' GACTCAGTTCTGGTGG     92341     G   GAAAAA
                                TCAC GGGA     TGGGTC
                                |||| ||||     ||||||
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                                GGTG TCTT     ACTCAG
                                  G   G_____
GAM890  KIAA1872 3' GGACCCCGACCCCTCCTCGT  62939       AAAAAT
                                ACGGGGAG     GGGTCC
                                ||||||||     ||||||
                                TGCTCCTC     CCCAGG
                                    CCCAGC
GAM890  KIAA1879 5' GGACCTGTTTCAGGCTGTGG  73571      GGAGAA
                                TCACGG     AAATGGGTCC
                                ||||||     ||||||||||
                                GGTGTC     TTTGTCCAGG
                                   GGAC__
GAM890  KIAA1884 3' GGGCCTGTGGAGATCTTTATGA 73339    CG   GAAAA
                                TCA  GGGA    ATGGGTCC
                                |||  ||||    ||||||||
                                AGT  TTCT    TGTCCGGG
                                  AT   AGAGG
GAM890  KIAA1889 5' GGGCTCACGCTCTTCTTCGTGG 73502        AAAAA
                                TCACGGGGAG    TGGGTCC
                                ||||||||||    |||||||
                                GGTGCTTCTT    ACTCGGG
                                     CTCGC
GAM890  KIAA1910 3' TATCTATTTTTCCCCTGTGG  73330       A        CC
                                TCACGGGG GAAAAATGGGT
                                |||||||| ||||||||||
                                GGTGTCCC CTTTTTATCTA
                                    _         TA
GAM890  KIAA1924 3' GGCTAATTTTTTTTTTTTGT  73684         TG_   C
                                ACGGGGAGAAAAA  GGTC
                                ||||||||||||  ||||
                                TGTTTTTTTTTTT  TCGG
                                      TAA
GAM890  KIAA1944 3' GGGTCTTTTTTCTCCCCCTGG 75564    C        T  GT
                                TCA GGGGAGAAAAA GG  CC
                                ||| |||||||||| ||  ||
                                GGT CCCCTCTTTTT TC  GG
                                  C         _ TG
GAM890  KIAA1950 3' GGGCTGAGGCTTCCTTGTGA  92595       AAAAATG
                                TCACGGGGAG     GGTCC
                                ||||||||||     |||||
                                AGTGTTCCTT     TCGGG
                                     CGGAG__
GAM890  KIAA1966 3' TATTTTTTTTTTTGTG     55895
                                CACGGGGAGAAAAATG
                                ||||||||||||||||
                                GTGTTTTTTTTTTTAT

GAM890  KIAA1979 3' GGAATATGTTTTTTCTCTGT  88285         ATGGG
                                ACGGGGAGAAAA    TCC
                                ||||||||||||    |||
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                                TGTCTCTTTTTT    AGG
                                      GTATA
GAM890  KIF13B   3'  GACCTGGCACTTCGTGG    82822       AGAAAAA
                                TCACGGGG     TGGGTC
                                ||||||||     ||||||
                                GGTGCTTC     GTCCAG
                                   ACG____
GAM890  KIF13B   3'  GACCTGGCACTTCGTGG    30908       AGAAAAA
                                TCACGGGG     TGGGTC
                                ||||||||     ||||||
                                GGTGCTTC     GTCCAG
                                   ACG____
GAM890  KOC1     5'  GGATCCATCCATCACCGTGG  91076      G  GAAAA
                                TCACGG GA    ATGGGTCC
                                |||||| ||    ||||||||
                                GGTGCC CT    TACCTAGG
                                   A  ACC__
GAM890  L3MBTL2  3'  GGGCTTGTATGTTCTTTTGG  88760   G     AA_ TG
                                C GGGAGAA   A  GGTCC
                                | |||||||   |  |||||
                                G TTTTCTT   T  TCGGG
                                 G      GTA GT
GAM890  LAGE2A   5'  GGGCCCTGACCTTCTCTCTGAG 71424    A       AAAT_
           A                     TC CGGGGAGAA    GGGTCC
                                 || |||||||||    ||||||
                                 AG GTCTCTCTT    CCCGGG
                                  A       CCAGT
GAM890  LAGE2A   5'  GGGCCCTGACCTTCTCTCTGAG 57684    A       AAAT_
           A                     TC CGGGGAGAA    GGGTCC
                                 || |||||||||    ||||||
                                 AG GTCTCTCTT    CCCGGG
                                  A       CCAGT
GAM890  LAMB4    3'  CTACTTCAGTTTTCTCTCTGTG 81174          A   TCC
           A                     TCACGGGGAGAAAA TGGG
                                 |||||||||||||| ||||
                                 AGTGTCTCTCTTTT ACTT
                                        G   CATCC
GAM890  LAP1B    3'  GGATTTGTGTCCTTTCTTATGA 64585    CG    AAAA  GG
                                 TCA  GGGAG   AT  GTCC
                                 |||  |||||   ||  ||||
                                 AGT  TCTTT   TG  TAGG
                                   AT    CCTG  TT
GAM890  LHX6     3'  GGGTCTATTCCTTGCGTGG   26859     __   GAAAA   GT
                                 TCACG  GGGA    ATGG  CC
                                 |||||  ||||    ||||  ||
                                 GGTGC  TCCT    TATC  GG
                                    GT   _____   TG
GAM890  LPAAT-delta 3'  GGGCTTTGGTTTTCTTTTTGTG 39290          AT_
                                 CACGGGGAGAAAA   GGGTCC
                                 ||||||||||||   ||||||
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                                GTGTTTTTCTTTT  TTCGGG
                                       GGT
GAM890  LRPPRC   3'  GGATTCATCATTTTCCAGTGA  55708     GG     AA
                                TCAC  GGAGAA  ATGGGTCC
                                ||||  ||||||  ||||||||
                                AGTG  CCTTTT  TACTTAGG
                                  A_     AC
GAM890  LYPLA2   3'  GGGCCCTGCCTCCCCGT     23430        AAAAAT
                                ACGGGGAG     GGGTCC
                                ||||||||     ||||||
                                TGCCCCTC     CCCGGG
                                     CGT___
GAM890  LYPLA3   3'  GGGCCCTGATTTCCTCGGA   24633    A       AAAAT
                                TC CGGGGAGA    GGGTCC
                                || ||||||||    ||||||
                                AG GCTCCTTT    CCCGGG
                                 _       AGT__
GAM890  LYSAL1   3'  TTTCTCCTCTTTATTTTCCTGT 16920          A   T   TCC
           GG                     TCACGGGGAGA AAA GGG
                                ||||||||||| ||| |||
                                GGTGTCCTTTT TTT TCC
                                      A   C   TCTTTG
GAM890  LZK1     3'  TGTTTCTCTTCCTGTGA     45755          A
                                TCACGGGGAGA AAATG
                                |||||||||| |||||
                                AGTGTCCTTCT TTTGT
                                      C
GAM890  M96      5'  GGATTGGTTGTTTTTTCCTGT  23738          _   G
                                ACGGGGAGAAA AAT GGTCC
                                |||||||||| ||| |||||
                                TGTCCTTTTTT TTG TTAGG
                                      G   G
GAM890  MAD3     3'  GGACTCATCAGGACCTCCCTG  48512        AAAA__
                                CGGGGAG     ATGGGTCC
                                |||||||     ||||||||
                                GTCCCTC     TACTCAGG
                                     CAGGAC
GAM890  MAD4     3'  GACCTGTCCCTCCGT       21277        A  AAAA
                                ACGGGG GA    TGGGTC
                                |||||| ||    ||||||
                                TGCCTC CT    GTCCAG
                                   C  _____
GAM890  MAP2K3   3'  GGGCCTGGATGCCCCCTGTGG  59030        AGAAAAA
                                TCACGGGG      TGGGTCC
                                ||||||||      |||||||
                                GGTGTCCC      GTCCGGG
                                     CCGTAG_
GAM890  MAP2K3   3'  GGGCCTGGATGCCCCCTGTGG  10862        AGAAAAA
                                TCACGGGG      TGGGTCC
                                ||||||||      |||||||
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                                GGTGTCCC      GTCCGGG
                                     CCGTAG_
GAM890  MAP2K6   5' GGATCTATTTTTTTTTCT    49246    GG
                                GG  AGAAAAATGGGTCC
                                ||  ||||||||||||||
                                TC  TTTTTTTATCTAGG
                                 TT
GAM890  MAPK8IP3  3' GGGCCCGCTCTTCTTCTCATGA 52991     C       AAA
                                TCA GGGGAGAA   TGGGTCC
                                ||| ||||||||   |||||||
                                AGT CTCTTCTT   GCCCGGG
                                  A       CTC
GAM890  MARCKS   5' GGATCTGTTGAGTTTCTTTGT  9868          AA_
                                ACGGGGAGA   AATGGGTCC
                                |||||||||   |||||||||
                                TGTTTCTTT   TTGTCTAGG
                                     GAG
GAM890  MBLL39   3' TCTGTTTTTTTCTTTGT     58612
                                ACGGGGAGAAAAATGGG
                                |||||||||||||||||
                                TGTTTCTTTTTTTGTCT

GAM890  MBLL39   3' GGATCTAAAACTATTTTTCTGT 58609      GG   AAAA__
                                ACGG  AGA     TGGGTCC
                                ||||  |||     |||||||
                                TGTC  TTT     ATCTAGG
                                  TT   ATCAAA
GAM890  MEF-2    3' GATATTTCCTTCGTGA      64385         A    AATGG
                                TCACGGGG GAAA     GTC
                                |||||||| ||||     |||
                                AGTGCTTC CTTT     TAG
                                     _    A____
GAM890  MGC10500  5' GGGCTCCCTCTGCTCCCCGTGG 48934          AAAAAT
                                TCACGGGGAG      GGGTCC
                                ||||||||||      ||||||
                                GGTGCCCCTC      CTCGGG
                                      GTCTCC
GAM890  MGC10765  3' TTTACTCATTTTTCTTCCCTGA 44305     C             CC
                                TCA GGGGAGAAAAATGGGT
                                ||| ||||||||||||||||
                                AGT CCCTTCTTTTTACTCA
                                  _             TTTG
GAM890  MGC10960  3' GGCCTCCCTCCCGTGG      51007        G  AAAAAT
                                TCACGGG AG     GGGTC
                                ||||||| ||     |||||
                                GGTGCCC TC     TCCGG
                                     _ CC_____
GAM890  MGC10981  3' GATCCGCTTTCTTTG       51019         AAAA
                                CGGGGAGA    TGGGTC
                                ||||||||    ||||||
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                                GTTTCTTT   GCCTAG
                                    C___
GAM890  MGC11115 3' GGACCCATGAGCTTCCTG    50242       AAAA
                                CGGGGAG   ATGGGTCC
                                |||||||   ||||||||
                                GTCCTTC   TACCCAGG
                                   GAG_
GAM890  MGC13138 3' TTATTTTTATTCTTGTGA    53029       G
                                TCACGGGGA AAAAATGG
                                ||||||||| ||||||||
                                AGTGTTCTT TTTTTATT
                                     A
GAM890  MGC14141 3' GGGCCTGTACACTCTGT     51933      AGAAAA
                                ACGGGG     ATGGGTCC
                                ||||||     ||||||||
                                TGTCTC     TGTCCGGG
                                   ACA___
GAM890  MGC15634 5' GGACCTTTGTTTTTTTTTGT   51273         AAT
                                ACGGGGAGAAA   GGGTCC
                                ||||||||||   ||||||
                                TGTTTTTTTTT   TCCAGG
                                      GTT
GAM890  MGC17330 3' GGGCTCATTAAGCCTTTTGG   53530    CG   AGAAA
                                TCA  GGG    AATGGGTCC
                                |||  |||    |||||||||
                                GGT  TCC    TTACTCGGG
                                  TT   GAA__
GAM890  MGC1842  3' GGATTTTTTTTTTTTTTTTTGA 65654    CG       TG
                                TCA  GGGAGAAAAA  GGTCC
                                |||  ||||||||||  |||||
                                AGT  TTTTTTTTTT  TTAGG
                                  TT        TT
GAM890  MGC1842  3' GGGCCCAAGTTTCTGTGG    65655      GG GAAAAA
                                TCACGG  A     TGGGTCC
                                ||||||  |     |||||||
                                GGTGTC  T     ACCCGGG
                                   TT GA____
GAM890  MGC20727 3' GGGCCTATCCATTCCATTGTGG 53462       _   AAAA
                                TCACGG GGAG    ATGGGTCC
                                |||||| ||||    ||||||||
                                GGTGTT CCTT    TATCCGGG
                                   A   ACC_
GAM890  MGC21621 3' GGGCCTCCTTCTCCCTG     58797        AAAT
                                CGGGGAGAA    GGGTCC
                                |||||||||    ||||||
                                GTCCCTCTT    TCCGGG
                                      CC__
GAM890  MGC2605  3' GGGCCTGCGTCCCTCCTCGTGA 50220         AAAAAT
                                TCACGGGGAG     GGGTCC
                                ||||||||||     ||||||
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                                AGTGCTCCTC     TCCGGG
                                      CCTGCG
GAM890  MGC2628  3' GACCGGCTCTTCCTGGA     43975    A      AAAATG
                                TC CGGGGAGA     GGTC
                                || ||||||||     ||||
                                AG GTCCTTCT     CCAG
                                 _       CGG___
GAM890  MGC2656  3' GGACCCGGACACCCTGTGG   44456        AGAAAAA
                                TCACGGGG      TGGGTCC
                                ||||||||      |||||||
                                GGTGTCCC      GCCCAGG
                                     ACAG___
GAM890  MGC29891 3' GGGCTCAGGAAGTTTCTCTGTG 58213          AAAA_
                                CACGGGGAGA    TGGGTCC
                                ||||||||||    |||||||
                                GTGTCTCTTT    ACTCGGG
                                      GAAGG
GAM890  MGC3222  3' GGATTTGTTTTCACTCTGGGA  44298    A    A    A GG
                                TC CGGGG GAAAA T  GTCC
                                || ||||| ||||| |  ||||
                                AG GTCTC CTTTT G  TAGG
                                 G    A    _ TT
GAM890  MGC3295  5' GGGCCCGCATTTCTCTGTG   47501         AAAA
                                CACGGGGAGA   TGGGTCC
                                ||||||||||   |||||||
                                GTGTCTCTTT   GCCCGGG
                                      AC__
GAM890  MGC4399  3' GATTCATGCTTTCTGGA    50288    A  GG  AAAA
                                TC CGG  AG   ATGGGTC
                                || |||  ||   |||||||
                                AG GTC  TC   TACTTAG
                                 _   TT  G___
GAM890  MGC4399  3' GATTCATGCTTTCTGGA    88502    A  GG  AAAA
                                TC CGG  AG   ATGGGTC
                                || |||  ||   |||||||
                                AG GTC  TC   TACTTAG
                                 _   TT  G___
GAM890  MGC4400  3' GGGCTGCTTTTCTTTTTGGA  51056    A        ATG
                                TC CGGGGAGAAAA   GGTCC
                                || ||||||||||   |||||
                                AG GTTTTTCTTTT   TCGGG
                                 _         CG_
GAM890  MGC5139  3' AAGTCTATTTTTTTTCCTGT  74102             GTCC
                                ACGGGGAGAAAAATGG
                                ||||||||||||||||
                                TGTCCTTTTTTTTATC
                                          TGAAA
GAM890  MGC5242  5' GGGCCCTGACTTTTCTTTGTGA 43824           AAAT
                                TCACGGGGAGAA   GGGTCC
                                ||||||||||||   ||||||
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                                AGTGTTTCTTTT  CCCGGG
                                      CAGT
GAM890  MGC5338  3' GATTCATTTGCTCTG     43940     AGAA
                                CGGGG  AAATGGGTC
                                |||||  |||||||||
                                GTCTC  TTTACTTAG
                                  G___
GAM890  MGC5508  3' GGCCACTTTTCCTTTGA   44039   C     AAATG
                                TCA GGGGAGAA  GGTC
                                ||| ||||||||  ||||
                                AGT TTCCTTTT  CCGG
                                  _     CA___
GAM890  moblak   3' GGACTCTTCTCTCCCTGGA  55508  A     AAAAT
                                TC CGGGGAGA  GGGTCC
                                || ||||||||  ||||||
                                AG GTCCCTCT  CTCAGG
                                 _     CTT__
GAM890  MPPE1    5' GGGCTCTGCAGTTTTCTCGTGG 43563        AAAAT
                                TCACGGGGAGA  GGGTCC
                                ||||||||||  ||||||
                                GGTGCTCTTTT  CTCGGG
                                      GACGT
GAM890  MSP      3' GGGCCCGTCAGAGTCTTTTGTG 49419      G  AAA__
           G                    TCACGGG AGA  ATGGGTCC
                                ||||||| |||  ||||||||
                                GGTGTTT TCT  TGCCCGGG
                                   _  GAGAC
GAM890  MYO3B    3' GGACCTGTCACTTTGGTGA  57308    G  G  AAAA
                                TCAC GG AG  ATGGGTCC
                                ||||  ||  ||  ||||||||
                                AGTG TT TC  TGTCCAGG
                                  G  _  AC__
GAM890  MYT1     3' GGATTTTGTTTTCCCTTGG  15777   C     AAAT
                                TCA GGGGAGAA  GGGTCC
                                ||| ||||||||  ||||||
                                GGT TCCCTTTT  TTTAGG
                                  _     GT__
GAM890  NDUFB5   3' TATTTTTGCTCTCCGTGA  10195       _
                                TCACGGGGAG AAAAATG
                                |||||||||| |||||||
                                AGTGCCTCTC TTTTTAT
                                      G
GAM890  NDUFC2   3' GGATCTATTGAGCCCTGGA  15839  A  AGAAA
                                TC CGGGG  AATGGGTCC
                                || |||||  |||||||||
                                AG GTCCC  TTATCTAGG
                                 _  GAG__
GAM890  NET-7    3' GGGCCCATTTCATCTCTG  24712     GAA
                                CGGGGA  AAATGGGTCC
                                ||||||  ||||||||||
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                                GTCTCT  TTTACCCGGG
                                  AC_
GAM890  NFASC   3' GGGCTCTGTCCTTCCGTGA  70347      GA  AAAAT
                                TCACGGG GA   GGGTCC
                                ||||||| ||   ||||||
                                AGTGCCT CT   CTCGGG
                                   TC GT___
GAM890  NFASC   3' GGACTCAATGCTCTTTGT   70346      AAAAA
                                ACGGGGAG   TGGGTCC
                                ||||||||   |||||||
                                TGTTTCTC   ACTCAGG
                                   GTA__
GAM890  NKX2B   3' GGGTCCAACTCCTTTCTTTGTG 10235        AAAA_  GT
          G                     TCACGGGGAGA   TGG CC
                                ||||||||||   ||| ||
                                GGTGTTTCTTT   ACC GG
                                      CCTCA  TG
GAM890  NLN     3' GGATTTGATTTCTTTTTATGA 40388    CG      AA GG
                                TCA GGGAGAAA T GTCC
                                ||| |||||||| | ||||
                                AGT TTTTCTTT G TAGG
                                  AT      A_ TT
GAM890  NPEPL1  3' GGGCTTGTTTCTGTTTGT   45092     G   AA TG
                                ACGGG AGAA A GGTCC
                                ||||| |||| | |||||
                                TGTTT TCTT T TCGGG
                                  G  __ GT
GAM890  NXPH3   3' GGGTCCATCCAACTTCCTCTGG 65768    C    AAAA   GT
                                TCA GGGGAG   ATGG CC
                                ||| ||||||   |||| ||
                                GGT TCCTTC   TACC GG
                                  C    AACC   TG
GAM890  NYD-SP17 5' GTACATTATTTCTTCCTGTGA 50878         _   GGTCC
                                TCACGGGGAGAAA AATG
                                |||||||||||| ||||
                                AGTGTCCTTCTTT TTAC
                                      A   ATG
GAM890  OLFM2   3' GGATGTCTTTTTCTTTTTATGG 54125    CG       TGG
                                TCA GGGAGAAAAA GTCC
                                ||| |||||||||| ||||
                                GGT TTTTCTTTTT TAGG
                                  AT       CTG
GAM890  OR2C3   3' GGATTCCAGGACGCTCCGTGG 75447       AGAAAAA  _
                                TCACGGGG     TGGG TCC
                                ||||||||     |||| |||
                                GGTGCCTC     ACCT AGG
                                   GCAGG__   T
GAM890  OSBPL1A 3' ATTTTTTTCCCTTGG     55742    C
                                TCA GGGGAGAAAAAT
                                ||| ||||||||||||
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                                GGT TCCCTTTTTTTA
                                  _
GAM890  OSBPL1A  3' ATTTTTTTCCCTTGG      35907     C
                                TCA GGGGAGAAAAAT
                                ||| ||||||||||||
                                GGT TCCCTTTTTTTA
                                  _
GAM890  OSBPL1A  3' ATTTTTTTCCCTTGG      54583     C
                                TCA GGGGAGAAAAAT
                                ||| ||||||||||||
                                GGT TCCCTTTTTTTA
                                  _
GAM890  OSBPL5   3' GGGCCTGTGGGGGCCCTGGA  72689    A    AGAAAA
                                TC CGGGG     ATGGGTCC
                                || |||||     ||||||||
                                AG GTCCC     TGTCCGGG
                                 _    GGGGG_
GAM890  PARVB    3' GGGCTGGGCTCTCCTTGGA   25293    A      AAAATG
                                TC CGGGGAGA     GGTCC
                                || ||||||||     |||||
                                AG GTTCCTCT     TCGGG
                                 _       CGGG__
GAM890  PCDH10   5' GATTTTTTTTTTGTTTCGTGG  51990      GG AG    TG
                                TCACG  G  AAAAA  GGTC
                                |||||  |  |||||  ||||
                                GGTGC  T  TTTTT  TTAG
                                   TT G_    TT
GAM890  PCDH10   5' GATTTTTTTTTTGTTTCGTGG  40425      GG AG    TG
                                TCACG  G  AAAAA  GGTC
                                |||||  |  |||||  ||||
                                GGTGC  T  TTTTT  TTAG
                                   TT G_    TT
GAM890  PCDH17   5' GACCCATAGACTTGTGG     27088       GAGAAAA
                                TCACGGG      ATGGGTC
                                |||||||      |||||||
                                GGTGTTC      TACCCAG
                                    AGA____
GAM890  PDGFC    5' GGATTTGTTTAAACCTTGGGA  32500    A    AGAA    GG
                                TC CGGGG    AAAT  GTCC
                                || |||||    ||||  ||||
                                AG GTTCC    TTTG  TAGG
                                 G    AAA_   TT
GAM890  PELI2    3' GGGCTCCACATCTTTTCCTTTG 41183     C      AAAA  _
           G                     TCA GGGGAGA    TGG GTCC
                                ||| |||||||    ||| ||||
                                GGT TCCTTTT    ACC CGGG
                                  T      CTAC   T
GAM890  PER3     3' GGAAAATACTTTTCTCCTTTGA 33680     C        A  GG_
                                TCA GGGGAGAAAA TG   TCC
                                ||| ||||||||| ||   |||
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                                AGT TTCCTCTTTT AT   AGG
                                  _        C  AAA
GAM890  PIGQ     3'  GGGTGCGGGTGTTCCCTGTGA  14851          AAAAA  G
                                TCACGGGGAG     TG GTCC
                                ||||||||||     || ||||
                                AGTGTCCCTT     GC TGGG
                                     GTGG_  G
GAM890  PIP3-E   5'  GATTTACTCTCTTTGT      66805          AAAA
                                ACGGGGAGA    TGGGTC
                                |||||||||    ||||||
                                TGTTTCTCT    ATTTAG
                                     C___
GAM890  PIP5K2B  3'  GGGCTGTTTTTCCTTGT     13077           AATG
                                ACGGGGAGAAA    GGTCC
                                ||||||||||    |||||
                                TGTTCCTTTTT    TCGGG
                                      G___
GAM890  PISD     5'  GGATTCATTTTCCTCCCTG    26772        A
                                CGGGGAG AAAATGGGTCC
                                ||||||| ||||||||||
                                GTCCCTC TTTTACTTAGG
                                    C
GAM890  PLAGL2   3'  GGTCACATTTTTCCCCCGTGG  70453        A       _ GT C
                                TCACGGGG GAAAAATG G  C
                                |||||||| |||||||| |  |
                                GGTGCCCC CTTTTTAC C  G
                                   _       A TG
GAM890  PLCL1    3'  GGGTCCGATAATATCTTTGTGA 20635         GAAAAA   GT
                                TCACGGGGA     TGG  CC
                                |||||||||     |||  ||
                                AGTGTTTCT     GCC  GG
                                     ATAATA   TG
GAM890  PP1628   5'  GGACCTATGTGTTTGTGTGG   47302       G   GAAAA
                                TCACG GGA     ATGGGTCC
                                ||||| |||     ||||||||
                                GGTGT TTT     TATCCAGG
                                   G   GTG__
GAM890  PP1665   5'  GATCCGTGGGTCCTGGA     47913     A    AGAAAA
                                TC CGGGG      ATGGGTC
                                || |||||      |||||||
                                AG GTCCT      TGCCTAG
                                 _    GGG___
GAM890  PP1665   3'  GGGCTCCACAGCCTCCTTGTGG 47919          AAAAA  _
                                TCACGGGGAG     TGG GTCC
                                ||||||||||     ||| ||||
                                GGTGTTCCTC     ACC CGGG
                                     CGAC_   T
GAM890  PP591    5'  GGGCCTCTGAACTTTCTCCG   47372        AAAAT_
                                CGGGGAGA      GGGTCC
                                ||||||||      ||||||
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                                GCCTCTTT     TCCGGG
                                    CAAGTC
GAM890  PPM1G    3'  GGGCTCATCACCGGTTCTGTG  10711       AGAAAA
                                CACGGGG     ATGGGTCC
                                |||||||     ||||||||
                                GTGTCTT     TACTCGGG
                                    GGCCAC
GAM890  PPP1R10  3'  GGACCTTCAACTTTCTGTGA   10735      GG  AAAAAT
                                TCACGG  AG     GGGTCC
                                ||||||  ||     ||||||
                                AGTGTC  TC     TCCAGG
                                   TT  AACT__
GAM890  PRAM-1   5'  GGTCCCACTCATCCCGTGG    69380       GA  AAAA   T
                                TCACGGG  GA    TGGG CC
                                |||||||  ||    |||| ||
                                GGTGCCC  CT    ACCC GG
                                    TA  C___    T
GAM890  PRDM15   3'  GGACCCGTGGCTCCGTG      61712       AGAAAA
                                CACGGGG     ATGGGTCC
                                |||||||     ||||||||
                                GTGCCTC     TGCCCAGG
                                    GG____
GAM890  PRO0386  5'  GGGTCCCTTCTCCCTGCGG    37688    A       AAAT  GT
                                TC CGGGGAGAA    GG  CC
                                || |||||||||    ||  ||
                                GG GTCCCTCTT    CC  GG
                                 C        C___  TG
GAM890  PRO0529  5'  GACTGTCTCCCCTGTGG      25993     _      AAAATG
                                TCAC GGGGAGA     GGTC
                                |||| |||||||     ||||
                                GGTG CCCCTCT     TCAG
                                  T      G_____
GAM890  PRO0529  5'  GGACTCATTTTTCTCATTG    25996     G
                                CGG GAGAAAAATGGGTCC
                                ||| ||||||||||||||
                                GTT CTCTTTTTACTCAGG
                                  A
GAM890  PRO0618  3'  GTAACCATTATTTTTTTTTACG 26203       GG        __  CC
           TGA                    TCACG  GAGAAAAATG  GGT
                                |||||  ||||||||||  |||
                                AGTGC  TTTTTTTTAT  CCA
                                   AT        TA   ATG
GAM890  PRO2133  3'  GGATTTCTAGTTTCTTGTGG   37790         AAAAAT
                                TCACGGGGAG     GGGTCC
                                ||||||||||     ||||||
                                GGTGTTCTTT     TTTAGG
                                     GATC__
GAM890  PRO2266  5'  GGACATCTTTTTCTTTG      37581         AATGG
                                CGGGGAGAAA     GTCC
                                ||||||||||     ||||
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                                GTTTCTTTTT    CAGG
                                     CTA__
GAM890  PRO2605  3' GGCCCCCCTCCCGTGG     94858       G  AAAAAT
                                TCACGGG AG    GGGTC
                                ||||||| ||    |||||
                                GGTGCCC TC    CCCGG
                                   _ CC____
GAM890  PRO2955  3' GGATTTCCCTTTTCTCTGT   37643        AAAT  ___
                                ACGGGGAGAA   GGG  TCC
                                ||||||||||   |||  |||
                                TGTCTCTTTT   CCC  AGG
                                     ____  TTT
GAM890  PROL3    3' GGACCTCCATTTTTCCCTGT  21935         AAT
                                ACGGGGAGAAA  GGGTCC
                                ||||||||||  ||||||
                                TGTCCCTTTTT  TCCAGG
                                      ACC
GAM890  PRPF8    5' GGGCCTGTGGGATTCTCCGGA 61196   A     AAAA
                                TC CGGGGAG   ATGGGTCC
                                || |||||||   ||||||||
                                AG GCCTCTT   TGTCCGGG
                                 _     AGGG
GAM890  PSKH1    3' GACCCGTAGCCCCTGG     68240    C   AGAAAA
                                TCA GGGG     ATGGGTC
                                ||| ||||     |||||||
                                GGT CCCC     TGCCCAG
                                  _   GA____
GAM890  PSTPIP2  3' GGATTTCCCTTTTCTCTGT   44395        AAAT  ___
                                ACGGGGAGAA   GGG  TCC
                                ||||||||||   |||  |||
                                TGTCTCTTTT   CCC  AGG
                                     ____  TTT
GAM890  PTGDR    3' TGTTTTTCACTCTGTGG     72455       A
                                TCACGGGG GAAAAATG
                                |||||||| ||||||||
                                GGTGTCTC CTTTTTGT
                                     A
GAM890  PTK6     3' GGATTTGTCTTCTCCCTTGTGA 19938     _     AA  GG
                                TCACG GGGAGAA  AT  GTCC
                                ||||| |||||||  ||  ||||
                                AGTGT CCCTCTT  TG  TAGG
                                   T      C_  TT
GAM890  Rab11-FIP3 3' GGGCCTGTGCTTCTCG      28126       AAAA
                                CGGGGAG   ATGGGTCC
                                |||||||   ||||||||
                                GCTCTTC   TGTCCGGG
                                     G___
GAM890  RAB33B   3' GGACTTATTTTTTAACTGT   48498     GGA
                                ACGG  GAAAAATGGGTCC
                                ||||  ||||||||||||
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                                TGTC   TTTTTTATTCAGG
                                  AA_
GAM890  RAB40C   3'  GGACCCAGGACCCCCCGTGG  40982        AGAAAAA
                                TCACGGGG      TGGGTCC
                                ||||||||      |||||||
                                GGTGCCCC      ACCCAGG
                                    CCAGG__
GAM890  RDHL     3'  GGACTCATTTAGATCGTG    60064      GGAGAA
                                CACGG     AAATGGGTCC
                                |||||     ||||||||||
                                GTGCT     TTTACTCAGG
                                  AGA___
GAM890  RFX4     3'  GACCTATTACCCTATGG     50662     CG   AGAAA
                                TCA  GGG    AATGGGTC
                                |||  |||    ||||||||
                                GGT  CCC    TTATCCAG
                                  AT   A____
GAM890  RGS11    3'  GGCCCAGTCTTCTGTGG     13825       G   AAAA
                                TCACGGG AGA    TGGGTC
                                ||||||| |||    ||||||
                                GGTGTCT TCT    ACCCGG
                                   _   G___
GAM890  RGS19    3'  GGACCCATGAGCCTCGCTG   19652     G   AAAA
                                CGG GAG    ATGGGTCC
                                ||| |||    ||||||||
                                GTC CTC    TACCCAGG
                                  G   CGAG
GAM890  RIP60    3'  GGGCTGGGGTCCTTCGTGG   25458        A  AAAATG
                                TCACGGGG GA     GGTCC
                                |||||||| ||     |||||
                                GGTGCTTC CT     TCGGG
                                   _  GGGG__
GAM890  RIS1     3'  GGCGTTTCTTCTTGT       80584          AATGG
                                ACGGGGAGAAA    GTC
                                ||||||||||     |||
                                TGTTCTTCTTT    CGG
                                     G____
GAM890  RNF8     3'  GACTTTGTCCTTTGTGG     14225        A  AAAAT
                                TCACGGGG GA    GGGTC
                                |||||||| ||    |||||
                                GGTGTTTC CT    TTCAG
                                   _  GT___
GAM890  RoXaN    3'  GATTCACTCTCTCCG       46645        AAAA
                                CGGGGAGA   TGGGTC
                                ||||||||   ||||||
                                GCCTCTCT   ACTTAG
                                    C___
GAM890  RPL41    3'  GGACCTGTGACATTCTGGA   40855    A    AGAAAA
                                TC CGGGG     ATGGGTCC
                                || |||||     ||||||||
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                                AG GTCTT     TGTCCAGG
                                 _    ACAG__
GAM890  SCMH1    3'  GGGCACTTTCTCTTTG      24256          AATGG
                                CGGGGAGAAA    GTCC
                                ||||||||||    ||||
                                GTTTCTCTTT    CGGG
                                      CA___
GAM890  SCOP     3'  GGATTCACTAATTTTCTCTGAG 91781    A       AAA_
              A                   TC CGGGGAGAA    TGGGTCC
                                || |||||||||   |||||||
                                AG GTCTCTTTT   ACTTAGG
                                 A        AATC
GAM890  SCYD1    3'  GGGCCCTGCCTCCTTTGTGA   90932       _   AAAAAT
                                TCACGG GGAG     GGGTCC
                                |||||| ||||     ||||||
                                AGTGTT CCTC     CCCGGG
                                    T    CGT___
GAM890  SDCCAG33 3'  GTTATTTTTCTTTTTCCGTGA  19365        __        GTCC
                                TCACGGG  GAGAAAAATGG
                                |||||||  ||||||||||
                                AGTGCCT  TTCTTTTTATT
                                     TT          G
GAM890  SDCCAG43 3'  GGGTCATTCTTCTCCTGG    70373   G      A    G
                                C GGGAGAA AATGG TC
                                | ||||||| ||||| ||
                                G TCCTCTT TTACT GG
                                 G      C    G
GAM890  SDCCAG8   5'  GGATTCTAGGCTCCCCTGTGA  88587      _     AAAAAT
                                TCAC GGGGAG     GGGTCC
                                |||| ||||||     ||||||
                                AGTG CCCCTC     CTTAGG
                                  T     GGAT__
GAM890  SEC22C   3'  GGATTCTTTGATTTTCTTTTGA 52058     CG     AA  T
                                TCA  GGGAGA  AA GGGTCC
                                |||  ||||||  || ||||||
                                AGT  TCTTTT  TT CTTAGG
                                  TT     AG  T
GAM890  SERF2    3'  TGTTTTTTATTCCTGTGG    19310         _
                                TCACGGGGA GAAAAATG
                                |||||||| ||||||||
                                GGTGTCCTT TTTTTTGT
                                      A
GAM890  SERPINB7 5'  GGAAACATTTTCTTTGTGA   13687          AAA   GG
                                TCACGGGGAGA   ATG  TCC
                                ||||||||||   |||  |||
                                AGTGTTTCTTT   TAC  AGG
                                      ___   AA
GAM890  SETBP1   3'  GCCTTTTTTTTTTTCTTG     31458           T
                                CGGGGAGAAAAA GGGT
                                ||||||||||| ||||
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                                GTTCTTTTTTTT TCCG
                                       T
GAM890  SFRS6    5'  GGGCTCGGCCGCCCCTGTGG  20783        AGAAAAA
                                TCACGGGG      TGGGTCC
                                ||||||||      |||||||
                                GGTGTCCC      GCTCGGG
                                    CGCCG__
GAM890  SHAPY    3'  GACCTGTTTGCTGGGA     57109    A   G  GAAAA
                                TC CGG GA     ATGGGTC
                                || ||| ||     |||||||
                                AG GTC TT     TGTCCAG
                                 G   G _____
GAM890  SIMRP7   3'  GGACTCATGGGCTTTGTGA   92368        AGAAAA
                                TCACGGGG     ATGGGTCC
                                ||||||||     ||||||||
                                AGTGTTTC     TACTCAGG
                                    GGG___
GAM890  SLC12A5  3'  GGACCCAGCCGCCTTCTCCGTG 40384         AAAAA_
                                CACGGGGAG     TGGGTCC
                                |||||||||     |||||||
                                GTGCCTCTT     ACCCAGG
                                    CCGCCG
GAM890  SLC12A5  3'  GGGTCCAACTTTTCCTGGA   40386    A      AAAA   GT
                                TC CGGGGAGA    TGG  CC
                                || ||||||||    |||  ||
                                AG GTCCTTTT    ACC  GG
                                 _       CA__   TG
GAM890  SLC17A6  3'  GGATTTATTTTTAGTGTTTGTG 39746       GAG_
                                CACGGG    AAAAATGGGTCC
                                ||||||    ||||||||||||
                                GTGTTT    TTTTTATTTAGG
                                   GTGA
GAM890  SLK      3'  GGATAATTTTCTTTTGGTGG   28227      G       ATGG
                                TCAC GGGAGAAAA    GTCC
                                |||| |||||||||    ||||
                                GGTG TTTTCTTTT    TAGG
                                  G        AA__
GAM890  SMARCF1  5'  GGGCCGGGTCTCTCCGCGG   20042    A      AAAATG
                                TC CGGGGAGA     GGTCC
                                || ||||||||     |||||
                                GG GCCTCTCT     CCGGG
                                 C       GGG___
GAM890  SMARCF1  5'  GGGCCGGGTCTCTCCGCGG   57488    A      AAAATG
                                TC CGGGGAGA     GGTCC
                                || ||||||||     |||||
                                GG GCCTCTCT     CCGGG
                                 C       GGG___
GAM890  SMARCF1  5'  GGGCCGGGTCTCTCCGCGG   37439    A      AAAATG
                                TC CGGGGAGA     GGTCC
                                || ||||||||     |||||
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                                GG GCCTCTCT     CCGGG
                                 C       GGG___
GAM890  SMOC1    3'  GGACTCCACGAGTTCTTTTCTG 42151     C GG    AAA_  _
                G                TCA G  GAGAA    TGG GTCC
                                 ||| |  |||||    ||| ||||
                                 GGT C  TTCTT    ACC CAGG
                                  _ TT    GAGC   T
GAM890  SMT3H2   5'  GGACCTGGTACCTCTTTTGTGA 22673       _  AAAAA
                                 TCACGGG GAG    TGGGTCC
                                 ||||||| |||    |||||||
                                 AGTGTTT CTC    GTCCAGG
                                     T   CATG_
GAM890  SNIP1    3'  GGACCAGGTGTTTTTCTTTTGG 45214     CG      AAATG
                                 TCA  GGGAGAA    GGTCC
                                 |||  |||||||    |||||
                                 GGT  TCTTTTT    CCAGG
                                   TT      GTGGA
GAM890  SNTG1    3'  GACTATTCTCCCTTGG     38574     C       AAATG
                                 TCA GGGGAGAA    GGTC
                                 ||| ||||||||    ||||
                                 GGT TCCCTCTT    TCAG
                                  _       A____
GAM890  SNX11    3'  GGGCTCCTTTCTTTTTGGA   25271    A        AAT
                                 TC CGGGGAGAAA   GGGTCC
                                 || ||||||||||   ||||||
                                 AG GTTTTTCTTT   CTCGGG
                                  _        C__
GAM890  SPEC1    3'  GGACAGTCTTTTTCCTTTGG   39610     C       A  GG
                                 TCA GGGGAGAAA AT  GTCC
                                 ||| |||||||| ||  ||||
                                 GGT TTCCTTTTT TG  CAGG
                                  _       C  A_
GAM890  STAT5A   3'  GGACTCCAGACTCTCTGTGA   12012         AAAAA  _
                                 TCACGGGGAG    TGG GTCC
                                 ||||||||||    ||| ||||
                                 AGTGTCTCTC    ACC CAGG
                                       AG___   T
GAM890  STATI2   5'  GGATCCGGTTTTCCCGTGA    13924          AAAA
                                 TCACGGGGAGA   TGGGTCC
                                 ||||||||||    |||||||
                                 AGTGCCCTTTT    GCCTAGG
                                       G___
GAM890  STHM     3'  GGACCATTTTTTTTTTTTTTG  21298          TG__
                                 CGGGGAGAAAAA   GGTCC
                                 ||||||||||||   |||||
                                 GTTTTTTTTTTT   CCAGG
                                       TTTA
GAM890  STI2     3'  GGACCCATACCATCCTTG    88968       GAAAA
                                 CGGGGA    ATGGGTCC
                                 ||||||    ||||||||
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                                GTTCCT    TACCCAGG
                                   ACCA_
GAM890  STRAIT11499 3'  GCTTTTTTTTTTTTCCTG    41145          T_
                                CGGGGAGAAAAA  GGGT
                                |||||||||||  ||||
                                GTCCTTTTTTTT  TTCG
                                      TT
GAM890  SULT1C2  3'  GGCTAATTTTTTTTTTTGT   21678           G
                                ACGGGGAGAAAAAT GGTC
                                |||||||||||||| ||||
                                TGTTTTTTTTTTTA TCGG
                                       A
GAM890  SV2     5'  GGACCTGTTTGCTCTTTTTTTT 29312         ____
           GTG                    ACGGGGAGAA    AAATGGGTCC
                                |||||||||    ||||||||||
                                TGTTTTTTTT    TTTGTCCAGG
                                     CTCG
GAM890  SZF1    5'  GGATTTGGACTCTCCTTGGGA  32233    A      AAAA GG
                                TC CGGGGAGA    T  GTCC
                                || ||||||||    |  ||||
                                AG GTTCCTCT    G  TAGG
                                 G       CAG_ TT
GAM890  TA-KRP   3'  CATTTTTTTTTCCTGG      50691     C  GG
                                TCA GG  AGAAAAATG
                                ||| ||  |||||||||
                                GGT CC  TTTTTTTAC
                                  _  TT
GAM890  TA-KRP   3'  GGATTTTCCTTCATCCTTGTGA 50693         _   AAAT
                                TCACGGGGA GAA    GGGTCC
                                |||||||||| |||    ||||||
                                AGTGTTCCT CTT    TTTAGG
                                      A   CCT_
GAM890  TBC1D2   5'  GGGCTCATTTGAGGGTGTGA   37320      GGGAGAA
                                TCACG      AAATGGGTCC
                                |||||      ||||||||||
                                AGTGT      TTTACTCGGG
                                   GGGAG__
GAM890  TCL6    5'  GGGCTTATTTTTATCCCTG    40086       G
                                CGGGGA AAAAATGGGTCC
                                |||||| ||||||||||||
                                GTCCCT TTTTTATTCGGG
                                   A
GAM890  TCL6    5'  GGGCTTATTTTTATCCCTG    40110       G
                                CGGGGA AAAAATGGGTCC
                                |||||| ||||||||||||
                                GTCCCT TTTTTATTCGGG
                                   A
GAM890  TCL6    5'  GGGCTTATTTTTATCCCTG    27003       G
                                CGGGGA AAAAATGGGTCC
                                |||||| ||||||||||||
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                                GTCCCT TTTTTATTCGGG
                                   A
GAM890  TCL6     5'  GGGCTTATTTTTATCCCTG   24987       G
                                CGGGGA AAAAATGGGTCC
                                |||||| ||||||||||||
                                GTCCCT TTTTTATTCGGG
                                   A
GAM890  TIP-1    3'  GGACCAGCTTTCTCTCCTGG  27505     C       AATG
                                TCA GGGGAGAAA   GGTCC
                                ||| |||||||||   |||||
                                GGT CCTCTCTTT   CCAGG
                                  _       CGA_
GAM890  TIX1     3'  GGATTTGTTGACTTCTTGGA  61746    A      AAA   GG
                                TC CGGGGAG   AAT  GTCC
                                || |||||||   |||  ||||
                                AG GTTCTTC   TTG  TAGG
                                 _      AG_   TT
GAM890  TOB2     3'  GGGTCATGAACTTTTTTCTTTA 95626   GG       TG_____ GT
             GTGA                   C  GGAGAAAAA      G  CC
                                |  |||||||||      |  ||
                                G  TTTCTTTTT      C  GG
                                 A_       TCAAGTA TG
GAM890  TOR2A    3'  GGCTCAGTCTTTTTG       55315        AAAA
                                CGGGGAGA    TGGGTC
                                ||||||||    ||||||
                                GTTTTTCT    ACTCGG
                                     G___
GAM890  TP53TG3  3'  GGCTATTTTTTCTCTGCTG   31107     _       TG
                                CGG GGAGAAAAA  GGTC
                                ||| |||||||||  ||||
                                GTC TCTCTTTTT  TCGG
                                  G        TA
GAM890  TRABID   5'  GGGTCTAAGATTTTTTCTTTGA 68519    A        A__   GT
             GA                   TC CGGGGAGAAAA   TGG  CC
                                || ||||||||||   |||  ||
                                AG GTTTCTTTTTT   ATC  GG
                                 A         AGA   TG
GAM890  TREX2    5'  GGACTTGCTATCCCCGTGG   54778        GAAAAAT
                                TCACGGGGA      GGGTCC
                                |||||||||      ||||||
                                GGTGCCCCT      TTCAGG
                                     ATCG___
GAM890  TREX2    5'  GGACTTGCTATCCCCGTGG   23277        GAAAAAT
                                TCACGGGGA      GGGTCC
                                |||||||||      ||||||
                                GGTGCCCCT      TTCAGG
                                     ATCG___
GAM890  TRIM11   3'  GGATCCTGGTCTTCCTG     72832        AAAAT
                                CGGGGAGA    GGGTCC
                                ||||||||    ||||||
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                                GTCCTTCT    CCTAGG
                                    GGT__
GAM890  TRIP13   3'  GATTGTTTGTCTCCTTGTGA  14896          A  TG G
                                TCACGGGGAGA AAA  G TC
                                |||||||||||| |||  | ||
                                AGTGTTCCTCT TTT  T AG
                                      G  GT _
GAM890  TU3A     3'  GGGCCTGGCTCTCCCTGGGA  23190    A      AAAA
                                TC CGGGGAGA   TGGGTCC
                                || ||||||||   |||||||
                                AG GTCCCTCT   GTCCGGG
                                 G      CG__
GAM890  TUSP     5'  GGATCAGCACGTTCTTCCTCTG 39638    C      AAATG_
           A                     TCA GGGGAGAA     GGTCC
                                ||| ||||||||     |||||
                                AGT TCCTTCTT     CTAGG
                                  C       GCACGA
GAM890  UBE2V2   3'  CACAATTTTTTTTCTCTTGA  12524    C        GG  CC
                                TCA GGGGAGAAAAAT  GT
                                ||| ||||||||||||  ||
                                AGT CTCTTTTTTTTA  CA
                                  T         A_  CG
GAM890  UBE3B    3'  GGGTCCATTCTTCCTGGTGA  76924     G    AAA    GT
                                TCAC GGGAG   AATGG  CC
                                |||| |||||   |||||  ||
                                AGTG TCCTT   TTACC  GG
                                  G    C__    TG
GAM890  UBN1     3'  GGGCCAGTTTCTCCTCGGA   33732    A       AATG
                                TC CGGGGAGAAA    GGTCC
                                || ||||||||||    |||||
                                AG GCTCCTCTTT    CCGGG
                                 _        GA__
GAM890  UGCGL2   5'  GGACTCGCGCTTTTCTCTCCGT 39237          A__
           G                     CACGGGGAGAAAA   TGGGTCC
                                ||||||||||||   |||||||
                                GTGCCTCTCTTTT   GCTCAGG
                                       CGC
GAM890  UNC5D    3'  GGATTTTTTTTTCCTTTG    55138      A     TG
                                CGGGG GAAAAA  GGTCC
                                ||||| ||||||  |||||
                                GTTTC CTTTTT  TTAGG
                                   _     TT
GAM890  UNC5D    3'  GGGCTCTACTATCTCCTTGGA  55139    A      AAAAT
                                TC CGGGGAGA    GGGTCC
                                || ||||||||    ||||||
                                AG GTTCCTCT    CTCGGG
                                 _       ATCAT
GAM890  USP22    3'  GGACCTTGGCTCCCTCCGTGG  68018       __   AAAAAT
                                TCACGG  GGAG     GGGTCC
                                ||||||  ||||     ||||||
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                                GGTGCC  CCTC     TCCAGG
                                   TC    GGT___
GAM890  VLCS-H1   5'  GGATCTGCGGTCTCCGTGG   25870        GAAAAAT
                                TCACGGGGA      GGGTCC
                                |||||||||      ||||||
                                GGTGCCTCT      TCTAGG
                                     GGCG___
GAM890  VMP       3'  TTTCTCCATTTTTTTTCCTTTG 54905     C           TCC
          A                      TCA GGGGAGAAAAATGGG
                                |||  ||||||||||||||
                                AGT TCCTTTTTTTTACCT
                                  T            CTTTT
GAM890  VPS33B    5'  GGGCCCATCTGGGGTCTCTGGA 37905    A     GAAAA_
                                TC CGGGGA     ATGGGTCC
                                || ||||||     ||||||||
                                AG GTCTCT     TACCCGGG
                                 _     GGGGTC
GAM890  WDR18     3'  GTTTTTCCTCTGTGA       65551         A
                                TCACGGGG GAAAAAT
                                |||||||| |||||||
                                AGTGTCTC CTTTTTG
                                      _
GAM890  WDR9      3'  GGGCCTATTTGACTTCT     38556       AA
                                GGGAG  AAATGGGTCC
                                |||||  ||||||||||
                                TCTTC  TTTATCCGGG
                                   AG
GAM890  XLKD1     3'  GGGTCCAAGTGTTTTCTCTG   21949         AAA_   GT
                                CGGGGAGAA    TGG  CC
                                |||||||||    |||  ||
                                GTCTCTTTT    ACC  GG
                                     GTGA   TG
GAM890  XT2       3'  GGGCCTGTGGTGCTCGTGG    42222        GAGAAAA
                                TCACGGG      ATGGGTCC
                                |||||||      ||||||||
                                GGTGCTC      TGTCCGGG
                                     GTGG___
GAM890  ZER6      3'  GGACCCATTTTTTTGCTC     63379     G
                                GGG AGAAAAATGGGTCC
                                |||  ||||||||||||||
                                CTC TTTTTTTACCCAGG
                                  G
GAM890  ZF5128    3'  GGGCCATTTGCTTCCTGTGG   26807          AA     G
                                TCACGGGGAG  AAATGG TCC
                                ||||||||||  |||||| |||
                                GGTGTCCTTC  TTTACC GGG
                                     G_     _
GAM890  ZFP100    5'  GGACTTGTCCTCCTCCTCCTGG 70055     C     AAAA TG
                                TCA GGGGAG    A  GGTCC
                                |||  ||||||    |  |||||
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                                GGT CTCCTC   T  TCAGG
                                  C     CTCC GT
GAM890  ZNF11B   3'  GGGCCTGTTGACATCCTG    73986      AGAAA
                                CGGGG    AATGGGTCC
                                |||||    |||||||||
                                GTCCT    TTGTCCGGG
                                   ACAG_
GAM890  ZNF212   3'  GGACTGAGTTCTTCCTG     24306        AAATG
                                CGGGGAGAA    GGTCC
                                |||||||||    |||||
                                GTCCTTCTT    TCAGG
                                     GAG__
GAM890  ZNF237   3'  ACATCTTGTTTGTCTCCCTGTG 26470          A   TG  TCC
           A                     TCACGGGGAGA AAA  GG
                                |||||||||| |||  ||
                                AGTGTCCCTCT TTT  TC
                                       G   GT  TACAT
GAM890  ZNF294   3'  GGATTGTGTTACTCCCCGTGA  70829         A  AATG
                                TCACGGGGAG AA   GGTCC
                                |||||||||| ||   |||||
                                AGTGCCCCTC TT    TTAGG
                                      A  GTG_
GAM890  ZNF297B  3'  GGACTTATTTAATATGTTGTGA 25785       GGAGAA
                                TCACGG     AAATGGGTCC
                                ||||||     ||||||||||
                                AGTGTT     TTTATTCAGG
                                   GTATAA
GAM890  ZNF396   3'  GGGCTCATTGTCTTTGT     75669       G AAA
                                ACGGGGA A   ATGGGTCC
                                |||||||  |  ||||||||
                                TGTTTCT T   TACTCGGG
                                    G ___
GAM890  LOC112476 3'  GGGCCCATCCCTCCCCTGG   59114     C     AAAA
                                TCA GGGGAG   ATGGGTCC
                                ||| ||||||   ||||||||
                                GGT CCCCTC   TACCCGGG
                                  _     CC__
GAM890  LOC112616 3'  GACCTGTGTTCCTGTG      56487        GAAAA
                                CACGGGGA    ATGGGTC
                                ||||||||    |||||||
                                GTGTCCTT    TGTCCAG
                                    G____
GAM890  LOC113523 3'  GGACCTATCTGTTCTTTGTGTG 73048      G     AA_
                                CACG GGAGAA   ATGGGTCC
                                |||| ||||||   ||||||||
                                GTGT TTTCTT   TATCCAGG
                                  G     GTC
GAM890  LOC113763 3'  GCCATATTTTTTTTTCTGGGA  56580    A   GG       _  CC
                                TC CGG  AGAAAAATG GGT
                                || |||  ||||||||| |||
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                                AG GTC  TTTTTTTAT CCG
                                 G   TT        A
GAM890   LOC114932 3'  GGGCTTAATTAAGTTGTTTTTG 72715        G  AAA___
            TGG                    CACGGGGA AA      TGGGTCC
                                   |||||||| ||      |||||||
                                   GTGTTTTT TT      ATTCGGG
                                      G  GAATTA
GAM890   LOC114971 3'  GGTAATTTTTCTTTCTCTGA   73153     C  GG       GGGT
                                   TCA GG  AGAAAAAT    CC
                                   ||| ||  ||||||||    ||
                                   AGT TC  TCTTTTTA    GG
                                     C  TT       AT__
GAM890   LOC115114 3'  GTCATTTATTTTTTTCTCTTGA 68759     C             CC
                                   TCA GGGGAGAAAAATGGGT
                                   ||| ||||||||||||||||
                                   AGT TCTCTTTTTTTATTTA
                                     _             CTGT
GAM890   LOC115297 3'  GGACCATAGTCCTCTTTGTGG  72887          AAAAATG
                                   TCACGGGGAG       GGTCC
                                   ||||||||||       |||||
                                   GGTGTTTCTC       CCAGG
                                         CTGATA_
GAM890   LOC115574 3'  GGACAGGTTTCTCCCTGGA    73466     A         AATGG
                                   TC CGGGGAGAAA     GTCC
                                   || ||||||||||     ||||
                                   AG GTCCCTCTTT     CAGG
                                    _         GGA__
GAM890   LOC116071 3'  GGGCTCTCCCCACTGCTTCGTG 56627         _  AAAAAT
            A                       TCACGGGG AG      GGGTCC
                                   |||||||| ||      ||||||
                                   AGTGCTTC TC      CTCGGG
                                      G  ACCCCT
GAM890   LOC119548 3'  GGGTTTGCTTTTTTTCTGTG   73996       GG     AAT  GT
                                   CACGG  AGAAA   GG  CC
                                   |||||  |||||   ||  ||
                                   GTGTC  TTTTT   TT  GG
                                      TT    CG_  TG
GAM890   LOC122439 3'  GGTCCCAAGCATTTCCTTG    74125         AAAA    T
                                   CGGGGAGA    TGGG CC
                                   ||||||||    |||| ||
                                   GTTCCTTT    ACCC GG
                                      ACGA    T
GAM890   LOC124944 3'  GGACCTGTGGATCTCCTGG    74374    G     AAA
                                   C GGGAGA   ATGGGTCC
                                   | ||||||   ||||||||
                                   G TCCTCT   TGTCCAGG
                                    G     AGG
GAM890   LOC125875 5'  GGGCCCATCCTGCCCTTGTGG  74418         AGAAAA
                                   TCACGGGG     ATGGGTCC
                                   ||||||||     ||||||||
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                                GGTGTTCC     TACCCGGG
                                     CGTCC_
GAM890  LOC127262 3'  GGACCCACGCACCTCCCTGT  76111        AAAAA
                                ACGGGGAG    TGGGTCC
                                ||||||||    |||||||
                                TGTCCCTC    ACCCAGG
                                     CACGC
GAM890  LOC127534 5'  GGGCCTTCACTTACTCTTTGTG 75439         AAAAAT_
          A                      TCACGGGGAG      GGGTCC
                                 ||||||||||      ||||||
                                 AGTGTTTCTC      TCCGGG
                                       ATTCACT
GAM890  LOC128272 3'  GGATAGTTTCTTCCTCTGA   74727    C       AATGG
                                TCA GGGGAGAAA    GTCC
                                ||| |||||||||    ||||
                                AGT TCCTTCTTT    TAGG
                                  C       GA___
GAM890  LOC128338 3'  GATTGTTTCTCCTTGGA    74742    A       AATGG
                                TC CGGGGAGAAA    GTC
                                || ||||||||||    |||
                                AG GTTCCTCTTT    TAG
                                 _       GT___
GAM890  LOC128954 5'  GACTTAGTCTCCCTG      75798        AAAA
                                CGGGGAGA   TGGGTC
                                ||||||||   ||||||
                                GTCCCTCT   ATTCAG
                                     G___
GAM890  LOC129080 3'  GGGCCTCAGTTTCCCTCTGTGA 55981        A   AAT
                                TCACGGGG GAAA   GGGTCC
                                |||||||| ||||   ||||||
                                AGTGTCTC CTTT   TCCGGG
                                     C   GAC
GAM890  LOC129138 3'  GGGCTTAGGCGGGCACCCTGTG 57124        AGAAAAA_
          G                     TCACGGGG       TGGGTCC
                                ||||||||       |||||||
                                GGTGTCCC       ATTCGGG
                                     ACGGGCGG
GAM890  LOC129181 5'  GGATCTATGGATTTTTCGTG   75807     GG   AAAA
                                CACG  GAG    ATGGGTCC
                                ||||  |||    ||||||||
                                GTGC  TTT    TATCTAGG
                                  TT   AGG_
GAM890  LOC129642 3'  GGGCTGTTTTTTTTTTTG    57127          TG
                                CGGGGAGAAAAA  GGTCC
                                ||||||||||||  |||||
                                GTTTTTTTTTTT  TCGGG
                                       TG
GAM890  LOC130471 5'  GGCTCCTTTCTCCGTCG     74942     _     AAT
                                CGG GGAGAAA   GGGTC
                                ||| |||||||   |||||
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                                GCT CCTCTTT   CTCGG
                                  G      C__
GAM890   LOC130644 3'  GGGCCCCCTTTCTCCCAGTGG  75754      G       AAT
                                TCAC GGGAGAAA   GGGTCC
                                |||| ||||||||   ||||||
                                GGTG CCCTCTTT   CCCGGG
                                  A       CC_
GAM890   LOC131034 3'  GGATCTGTTAAGCCCTTGT    55521       AGAAA
                                ACGGGG     AATGGGTCC
                                ||||||     |||||||||
                                TGTTCC     TTGTCTAGG
                                   CGAA_
GAM890   LOC132241 5'  GGGCTCCAGCCATCTTTGTGG  75052         GAAAAA   _
                                TCACGGGGA      TGG GTCC
                                |||||||||      ||| ||||
                                GGTGTTTCT      ACC CGGG
                                      ACCG__   T
GAM890   LOC133088 5'  GGGCTTGGTTTTTTTCCTTG   75077           G _
                                CGGGGAGAAAAAT G GTCC
                                |||||||||||| | ||||
                                GTTCCTTTTTTTG T CGGG
                                      G T
GAM890   LOC133686 3'  GGACTTTTTTTTTTTCCCCATG 75124      C         T_
           A                     TCA GGGGAGAAAAA  GGGTCC
                                 ||| ||||||||||  ||||||
                                 AGT CCCCTTTTTTT  TTCAGG
                                   A          TT
GAM890   LOC133923 3'  GGACTTCTTTCTTCCCTGA    75927     C       AAT
                                TCA GGGGAGAAA   GGGTCC
                                ||| |||||||||   ||||||
                                AGT CCCTTCTTT   TTCAGG
                                  _        C__
GAM890   LOC133923 3'  GGGCCTATACCTCTCTTGG    75928    G     AAA
                                C GGGAGA   ATGGGTCC
                                | ||||||   ||||||||
                                G TTCTCT   TATCCGGG
                                 G     CCA
GAM890   LOC134111 3'  ATCTCTGTTTTTCTTCCTGGA  75135    A            TCC
                                TC CGGGGAGAAAAATGGG
                                || ||||||||||||||||
                                AG GTCCTTCTTTTTGTCT
                                  _             CTAT
GAM890   LOC137964 3'  GGGCTTTGGATTTGTTCTTGTG 75285         G   AAT_
           A                     TCACGGGGA AAA    GGGTCC
                                 ||||||||| |||    ||||||
                                 AGTGTTCTT TTT    TTCGGG
                                       G   AGGT
GAM890   LOC143188 5'  GGACCTGCTGCCTCCCCTGTGA 82900      _     AAAAAT
                                TCAC GGGGAG      GGGTCC
                                |||| ||||||      ||||||
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                                AGTG CCCCTC      TCCAGG
                                  T      CGTCG_
GAM890   LOC143243 3'  GGGCTTTACCCTTCCCTGA   60308     C      AAAAAT
                                TCA GGGGAG      GGGTCC
                                ||| ||||||      ||||||
                                AGT CCCTTC      TTCGGG
                                  _      CCAT__
GAM890   LOC143287 3'  GACCTCACTCCCTGTG       82930          AAAAA  _
                                CACGGGGAG     TG GGTC
                                |||||||||     || ||||
                                GTGTCCCTC     AC CCAG
                                      _____  T
GAM890   LOC143452 3'  GACCTGTGCCCACGTGG      76570       _  AGAAAA
                                TCACG GGG      ATGGGTC
                                ||||| |||      |||||||
                                GGTGC CCC      TGTCCAG
                                   A   G_____
GAM890   LOC144058 5'  GGACACCGTGTTCCTCGTGG   76668          GAAAA   _
                                TCACGGGGA     ATGG GTCC
                                |||||||||     |||| ||||
                                GGTGCTCCT     TGCC CAGG
                                      TG___    A
GAM890   LOC144203 5'  GGATTTTCTCTTTCCTTGGA   76707    A       AAAAT
                                TC CGGGGAGA     GGGTCC
                                || ||||||||     ||||||
                                AG GTTCCTTT     TTTAGG
                                  _       CTCT_
GAM890   LOC144266 5'  GGGCCTGTCTCTCTCTTGA    76762     C      AAA
                                TCA GGGGAGA   ATGGGTCC
                                ||| |||||||   ||||||||
                                AGT TCTCTCT   TGTCCGGG
                                  _      C__
GAM890   LOC144347 3'  GGGCTTGAGCTCCCTCTGTGG  76816      __     AAAAAT
                                TCAC  GGGGAG     GGGTCC
                                ||||  ||||||     ||||||
                                GGTG  TCCCTC     TTCGGG
                                   TC     GAG___
GAM890   LOC144373 3'  GACCTTTGTTCCTGTGG      76819          G  AAAT
                                TCACGGGGA AA    GGGTC
                                ||||||||| ||    |||||
                                GGTGTCCTT TT    TCCAG
                                      G  _____
GAM890   LOC144395 3'  GGTCCATTTTTTTCTTCTGA   76827     C           GT
                                TCA GGGGAGAAAAATGG  C
                                ||| ||||||||||||||  |
                                AGT CTTCTTTTTTTACC  G
                                  _            TG
GAM890   LOC144519 5'  GACTTTATTCCTGTGG       76870          GAAAAAT
                                TCACGGGGA      GGGTC
                                |||||||||      |||||
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                                GGTGTCCTT      TTCAG
                                     AT_____
GAM890   LOC145127 3'  GACCTGTGCCCACGTGG     77001      _   AGAAAA
                                TCACG GGG     ATGGGTC
                                ||||| |||     |||||||
                                GGTGC CCC     TGTCCAG
                                   A   G_____
GAM890   LOC145387 5'  GGGCCCCTGACTTTTTCTCTG  83359          AAT__
                                CGGGGAGAAA    GGGTCC
                                ||||||||||    ||||||
                                GTCTCTTTTT    CCCGGG
                                     CAGTC
GAM890   LOC145508 3'  TATTTATTTGTCTTTTTGTGG  77259          A       CC
                                TCACGGGGAGA AAATGGGT
                                |||||||||| ||||||||
                                GGTGTTTTTCT TTTATTTA
                                      G       TT
GAM890   LOC145547 5'  GGGCCCAAGGCCTCTTCCTGGA 77267    A       AAAA_
                                TC CGGGGAGA    TGGGTCC
                                || ||||||||    |||||||
                                AG GTCCTTCT    ACCCGGG
                                 _       CCGGA
GAM890   LOC145566 5'  GGGCCTCAGTTTTTCTTTCTGT 77277      GG       __
                                ACGG  AGAAAAAT  GGGTCC
                                ||||  ||||||||  ||||||
                                TGTC  TCTTTTTG  TCCGGG
                                  TT       AC
GAM890   LOC145622 5'  GGCCCACTTTTCCTG       77308        AAAA
                                CGGGGAGA    TGGGTC
                                ||||||||    ||||||
                                GTCCTTTT    ACCCGG
                                     C___
GAM890   LOC145622 5'  GGCCTGCTTTTCCTG       77309        AAAA
                                CGGGGAGA    TGGGTC
                                ||||||||    ||||||
                                GTCCTTTT    GTCCGG
                                     C___
GAM890   LOC145622 5'  GGCTTGCTTTTCCTG       77310        AAAA
                                CGGGGAGA    TGGGTC
                                ||||||||    ||||||
                                GTCCTTTT    GTTCGG
                                     C___
GAM890   LOC145624 5'  GGATCTATTTTTTTAACATC   83407    GG__
                                GG    AGAAAAATGGGTCC
                                ||    ||||||||||||||
                                CT    TTTTTTTATCTAGG
                                 ACAA
GAM890   LOC145624 5'  GGATTTGTTCCCTACTTGCTGT 83408       G   AAA__   GG
            GG                    TCACGG GAG     AAT  GTCC
                                ||||||  |||     |||  ||||
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                                GGTGTC TTC    TTG  TAGG
                                   G   ATCCC   TT
GAM890   LOC145662 3'  GGATTTATTCATTCCTTGT   77321        AAA
                                ACGGGGAG   AATGGGTCC
                                ||||||||   |||||||||
                                TGTTCCTT   TTATTTAGG
                                     AC_
GAM890   LOC145693 5'  GGGCTCTAGTCTACTCTGTGA  77352        _   AAAAT
                                TCACGGGG AGA    GGGTCC
                                |||||||| |||    ||||||
                                AGTGTCTC TCT    CTCGGG
                                     A   GAT__
GAM890   LOC145757 5'  GGACCCATTGTGGTTTTGTG   77467       AGAAA
                                CACGGGG    AATGGGTCC
                                |||||||    |||||||||
                                GTGTTTT    TTACCCAGG
                                     GGTG_
GAM890   LOC145800 3'  GGGCCCATGGACAACTCCTGA  77502     C    AGAAAA
                                TCA GGGG     ATGGGTCC
                                ||| ||||     ||||||||
                                AGT CCTC     TACCCGGG
                                  _    AACAGG
GAM890   LOC145836 5'  GGGCTCACCGGCCTCTCCCTG  83548        AAAA__
                                CGGGGAGA     TGGGTCC
                                ||||||||     |||||||
                                GTCCCTCT     ACTCGGG
                                     CCGGCC
GAM890   LOC145845 3'  TTTGTTTTTCTTTTGTGA    83557        G       GG
                                TCACGGG AGAAAAAT  G
                                ||||||| ||||||||  |
                                AGTGTTT TCTTTTTG  T
                                     _       TT
GAM890   LOC146237 3'  GGGCCTGTTTGTGCATGTGA   83632      GGGAGAA
                                TCACG      AAATGGGTCC
                                |||||      ||||||||||
                                AGTGT      TTTGTCCGGG
                                   ACGTG__
GAM890   LOC146268 3'  GGGCCTACATTCTTCCCG    77812         AAA
                                CGGGGAGAA   TGGGTCC
                                |||||||||   |||||||
                                GCCCTTCTT   ATCCGGG
                                     AC_
GAM890   LOC146481 5'  GGATCTAGGCTGCTTTTCTTGT 77927          AAAA__
           GG                     TCACGGGGAGA     TGGGTCC
                                |||||||||||     |||||||
                                GGTGTTCTTTT     ATCTAGG
                                       CGTCGG
GAM890   LOC146520 5'  GGGCTAATTTTTCTTTTGGTGG 77956     G         G
                                TCAC GGGAGAAAAAT GGTCC
                                |||| |||||||||| |||||
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                                GGTG TTTTCTTTTTA TCGGG
                                  G         A
GAM890   LOC146667 5'  GGGCCTTTCCTTCTCTGTGA  83706          AAAAAT
                                TCACGGGGAG     GGGTCC
                                ||||||||||     ||||||
                                AGTGTCTCTT     TCCGGG
                                     CCTT__
GAM890   LOC146733 3'  GGGCTGTGGTCCCCTGTGA   83769        A  AAAATG
                                TCACGGGG GA     GGTCC
                                |||||||| ||     |||||
                                AGTGTCCC CT     TCGGG
                                    _  GGTG__
GAM890   LOC146733 5'  GGCAACATTTTTCTTCGTGA  83768           AATGG
                                TCACGGGGAGAAA    GTC
                                ||||||||||||     |||
                                AGTGCTTCTTTTT    CGG
                                       ACAA_
GAM890   LOC146756 3'  GGGTCTAGGCGTGTCTTTGTGG 83785         GAAAAA   GT
                                TCACGGGGA     TGG  CC
                                |||||||||     |||  ||
                                GGTGTTTCT     ATC  GG
                                     GTGCGG   TG
GAM890   LOC146774 3'  GGCTTTTTTTTTTCTTCTGG   78098     C         TG
                                TCA GGGGAGAAAAA  GGTC
                                ||| ||||||||||  ||||
                                GGT CTTCTTTTTTT  TCGG
                                  _         TT
GAM890   LOC146782 5'  GGACTCAAAGGTTTTCTCCCTG 76294    A         A___
           AGA                    C CGGGGAGAAAA    TGGGTCC
                                | ||||||||||    |||||||
                                G GTCCCTCTTTT    ACTCAGG
                                 A          GGAA
GAM890   LOC146795 5'  GCCAGTTTTTTTCTCTTGG    78133     C         G
                                TCA GGGGAGAAAAAT GGT
                                ||| ||||||||||| |||
                                GGT TCTCTTTTTTTG CCG
                                  _          A
GAM890   LOC146894 3'  GGATTCTGGCTTCTCTTTG    59192          AAAT
                                CGGGGAGAA    GGGTCC
                                |||||||||    ||||||
                                GTTTCTCTT    CTTAGG
                                     CGGT
GAM890   LOC146990 5'  GGCCGCATCCCTTGTGA     83888         A  AAAA  _
                                TCACGGGG GA    TG GGTC
                                |||||||| ||    || ||||
                                AGTGTTCC CT    AC CCGG
                                    _  _____  G
GAM890   LOC147123 5'  GGACTCAAAGGTTTTCTCCCTG 78255    A         A___
           AGA                    C CGGGGAGAAAA    TGGGTCC
                                | ||||||||||    |||||||
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                                G GTCCCTCTTTT   ACTCAGG
                                 A         GGAA
GAM890   LOC147165 3'  GGGCTGTTTTCTTACTGTGA  83980      GG     ATG
                                TCACGG  AGAAAA   GGTCC
                                ||||||  ||||||   |||||
                                AGTGTC  TCTTTT   TCGGG
                                   AT     G__
GAM890   LOC147165 3'  GGGCTGCTTTCTCTCTG     83979         AATG
                                CGGGGAGAAA    GGTCC
                                ||||||||||    |||||
                                GTCTCTCTTT    TCGGG
                                      CG__
GAM890   LOC147229 5'  GGACTCACCCTGACACCCTGTG 78322        AGAAAAA_
           A                     TCACGGGG       TGGGTCC
                                ||||||||       |||||||
                                AGTGTCCC       ACTCAGG
                                     ACAGTCCC
GAM890   LOC147341 3'  GGGCCCAGCCTTTTTTTTTGT  83995         AA_
                                ACGGGGAGAAA   TGGGTCC
                                ||||||||||   |||||||
                                TGTTTTTTTTT   ACCCGGG
                                      CCG
GAM890   LOC147515 3'  GGGCCACCTAGTTTCCCCTGTG 84026        A    AATG__
           G                     TCACGGGG GAAA     GGTCC
                                ||||||| ||||     |||||
                                GGTGTCCC CTTT     CCGGG
                                   _   GATCCA
GAM890   LOC147645 5'  GGACCCTCCATATCCTCGTGG  78423        GAAAAAT
                                TCACGGGGA      GGGTCC
                                |||||||||      ||||||
                                GGTGCTCCT      CCCAGG
                                     ATACCT_
GAM890   LOC147671 3'  GGGTCATGAAGTTTTTTCTTCA 78463    _       ATG___ GT
           GTGA                   AC GGGGAGAAAA     G  CC
                                || ||||||||||     |  ||
                                TG CTTCTTTTTT     C  GG
                                 A         GAAGTA TG
GAM890   LOC148014 3'  GGCCTCGCTTCCCCTGA     78608     C     AAAAAT
                                TCA GGGGAG     GGGTC
                                ||| ||||||     |||||
                                AGT CCCTTC     TCCGG
                                  C     GC____
GAM890   LOC148171 5'  GGGCCCAGCTCTTCTTCCTG   78699        AAA_
                                CGGGGAGAA    TGGGTCC
                                |||||||||    |||||||
                                GTCCTTCTT    ACCCGGG
                                     CTCG
GAM890   LOC148189 5'  GGACCCATTGGACCCCCG    78715      AGAAA
                                CGGGG    AATGGGTCC
                                |||||    |||||||||
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                                GCCCC    TTACCCAGG
                                   CAGG_
GAM890  LOC148479 3'  GGACCTGGGAGGCCCCTGTGA  78872        AGAAAAA
                                TCACGGGG      TGGGTCC
                                ||||||||      |||||||
                                AGTGTCCC      GTCCAGG
                                     CGGAGG_
GAM890  LOC148479 3'  GGGCTCCGGCTTTCTCT     78873        AA  _
                                GGAGAAA  TGG GTCC
                                |||||||  ||| ||||
                                TCTCTTT  GCC CGGG
                                    CG   T
GAM890  LOC148490 3'  GGGCCCATTGGTTCTT      78887       A_
                                GAGAA  AATGGGTCC
                                |||||  |||||||||
                                TTCTT  TTACCCGGG
                                   GG
GAM890  LOC148894 5'  ATTTTTTTCCCCATGG      84255     C
                                TCA GGGGAGAAAAAT
                                ||| ||||||||||||
                                GGT CCCCTTTTTTTA
                                  A
GAM890  LOC148930 3'  GGACTCATCGAGTCCCATGG   79098     C    AGAAAA
                                TCA GGGG     ATGGGTCC
                                ||| ||||     ||||||||
                                GGT CCCT     TACTCAGG
                                  A   GAGC__
GAM890  LOC148946 5'  GGGCTTGCTTATCTTGTGA    84311        AGAA  AT
                                TCACGGGG    AA  GGGTCC
                                ||||||||    ||  ||||||
                                AGTGTTCT    TT  TTCGGG
                                     A___   CG
GAM890  LOC148987 3'  GGACTCGTTCGAACATCGTGG  79121       GGAGAAA
                                TCACGG       AATGGGTCC
                                ||||||       |||||||||
                                GGTGCT       TTGCTCAGG
                                   ACAAGC_
GAM890  LOC149052 3'  ATTTTTTTCCTTTGA       79143     C
                                TCA GGGGAGAAAAAT
                                ||| ||||||||||||
                                AGT TTCCTTTTTTTA
                                  _
GAM890  LOC149111 3'  GGACCTGTTGAAAGCCTCGAGA 79183    A    AGAAA
                                TC CGGGG     AATGGGTCC
                                || |||||     |||||||||
                                AG GCTCC     TTGTCCAGG
                                  A    GAAAG
GAM890  LOC149124 5'  GGGCCCAGCTCTTCTTCCTG   79172        AAA_
                                CGGGGAGAA    TGGGTCC
                                |||||||||    |||||||
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                                GTCCTTCTT   ACCCGGG
                                    CTCG
GAM890  LOC149134 5'  GGACCTAGGACATTCTGTGA  84361       AGAAAAA
                                TCACGGGG     TGGGTCC
                                ||||||||     |||||||
                                AGTGTCTT     ATCCAGG
                                    ACAGG__
GAM890  LOC149149 3'  GGACCCGTCAGGGCCCCGTGA 84366       AGAAAA
                                TCACGGGG    ATGGGTCC
                                ||||||||    ||||||||
                                AGTGCCCC    TGCCCAGG
                                    GGGAC_
GAM890  LOC149276 5'  GGGCCTATTGTGCTGTCTTCCT 84388       AA____
          GTGA                    ACGGGGAGA    AATGGGTCC
                                ||||||||||   ||||||||||
                                TGTCCTTCT    TTATCCGGG
                                    GTCGTG
GAM890  LOC149422 3'  GGGCCTCTTTCTCCTCTTGA  79351    C       AAT
                                TCA GGGGAGAAA  GGGTCC
                                ||| |||||||||  ||||||
                                AGT CTCCTCTTT  TCCGGG
                                  T       C__
GAM890  LOC149448 3'  GGGCCCTGCCTCTTCCTG    84422       AAAAT
                                CGGGGAGA    GGGTCC
                                ||||||||    ||||||
                                GTCCTTCT    CCCGGG
                                    CCGT_
GAM890  LOC149579 5'  GGGCTTGGTTGCCCTGTGG   71137       AGAAAAA
                                TCACGGGG     TGGGTCC
                                ||||||||     |||||||
                                GGTGTCCC     GTTCGGG
                                    GTTG___
GAM890  LOC149722 5'  TCTGTTTTTTTTTTCTGA    84608    C GG
                                TCA G  GAGAAAAATGGG
                                ||| |  ||||||||||||
                                AGT C  TTTTTTTTGTCT
                                  _ TT
GAM890  LOC149837 5'  GGACCTCTCTCTGGA      84744    A      AAAATG
                                TC CGGGGAGA     GGTCC
                                || ||||||||     |||||
                                AG GTCTCTCT     CCAGG
                                  _      _______    A
GAM890  LOC149844 3'  GGGCTGCTCTTCCCCGTGG   79516         AAAAATG
                                TCACGGGGAG      GGTCC
                                ||||||||||      |||||
                                GGTGCCCCTT      TCGGG
                                    CTCG___
GAM890  LOC149995 3'  GGGCCACCTAGTTTCCCCTGTG 84847       A   AATG__
          G                      TCACGGGG GAAA     GGTCC
                                ||||||||| ||||     |||||
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                                GGTGTCCC CTTT     CCGGG
                                     _   GATCCA
GAM890   LOC150035 5'  GACCCCTCTTTTTGTGG     84809          AAAAT
                                TCACGGGGAGA    GGGTC
                                ||||||||||    |||||
                                GGTGTTTTTCT    CCCAG
                                      C____
GAM890   LOC150279 3'  GGACCTGTTAAACAATCTCTG  79669       GAAA__
                                CGGGGA     AATGGGTCC
                                ||||||     |||||||||
                                GTCTCT     TTGTCCAGG
                                   AACAAA
GAM890   LOC150282 5'  GGATTTGTTTCTCTTTTTCGT  79730     GG _ A   GG
                                ACG  GA GA AAAT  GTCC
                                |||  || || ||||  ||||
                                TGC  TT CT TTTG  TAGG
                                  TT  T  C    TT
GAM890   LOC150311 5'  GCCAACATTTTTTTTTCTTTGA 79755     C  GG       __  CC
                                TCA GG  AGAAAAATG  GGT
                                ||| ||  |||||||||  |||
                                AGT TC  TTTTTTTAC  CCG
                                  T  TT        AA
GAM890   LOC150319 3'  GGCCTAGTGCCTTGTGG     79659         AGAAAAA
                                TCACGGGG      TGGGTC
                                ||||||||      ||||||
                                GGTGTTCC      ATCCGG
                                     GTG____
GAM890   LOC150368 3'  GGACCCAGCTCTTCCTGAGA   79701    A       AAAA
                                TC CGGGGAGA    TGGGTCC
                                || ||||||||    |||||||
                                AG GTCCTTCT    ACCCAGG
                                 A       CG__
GAM890   LOC150368 3'  GGTCCCATCCTTTCTCCCTG   79702          A_    T
                                CGGGGAGAAA  ATGGG CC
                                ||||||||||  ||||| ||
                                GTCCCTCTTT  TACCC GG
                                       CC    T
GAM890   LOC150372 3'  GGGCCCATGGACTTCTTCTGG  79806   G      AA__
                                C GGGAGAA    ATGGGTCC
                                | |||||||    ||||||||
                                G TCTTCTT    TACCCGGG
                                 G      CAGG
GAM890   LOC150481 3'  GGACTCTAGACTCTCCCCTGG  79891     C      AAAAT
                                TCA GGGGAGA    GGGTCC
                                ||| |||||||    ||||||
                                GGT CCCCTCT    CTCAGG
                                  _      CAGAT
GAM890   LOC150519 3'  GGATTTGTTTTTGCATCCTGTG 79922         AG_     GG
            A                    TCACGGGG   AAAAAT  GTCC
                                ||||||||   ||||||  ||||
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                                AGTGTCCT  TTTTTG  TAGG
                                    ACG    TT
GAM890  LOC151056 3'  GGGCGCTCTTTTTCCTTTG   80110     A    T  _
                                CGGGG GAAAAA GG GTCC
                                ||||| |||||| || ||||
                                GTTTC CTTTTT TC CGGG
                                  _    C  G
GAM890  LOC151121 5'  GGACTCTCCTCTTTCTCCTGG  80120   G     AAT__
                                C GGGAGAAA    GGGTCC
                                | ||||||||    ||||||
                                G TCCTCTTT    CTCAGG
                                 G      CTCCT
GAM890  LOC151126 3'  GGATCACAAAGTTCTCTTTTTG 80128    CG     AAA  _
          G                      TCA  GGGAGAA   TG GGTCC
                                ||| |||||||  || |||||
                                GGT  TTCTCTT   AC CTAGG
                                  TT     GAA  A
GAM890  LOC151201 3'  TAACACTGTTTTTTTTCCTGGA 85287    A          _  CC
                                TC CGGGGAGAAAAATGG GT
                                || ||||||||||||||| ||
                                AG GTCCTTTTTTTTGTC CA
                                 _           A  ATC
GAM890  LOC151360 3'  GGACCCCAGCTTCCCTGTG   85313        AAAAAT
                                CACGGGGAG    GGGTCC
                                |||||||||    ||||||
                                GTGTCCCTT    CCCAGG
                                     CGAC__
GAM890  LOC151361 3'  GGACCCCAGCTTCCCTGTG   85326        AAAAAT
                                CACGGGGAG    GGGTCC
                                |||||||||    ||||||
                                GTGTCCCTT    CCCAGG
                                     CGAC__
GAM890  LOC151473 3'  GGGCCTGTAATATTTTTTTCTG 80258    GG    A___
                                CGG  AGAAA   ATGGGTCC
                                |||  |||||   ||||||||
                                GTC  TTTTT   TGTCCGGG
                                  TT    ATAA
GAM890  LOC151556 5'  GGACTTGGAAATTCTTTTTCTG 80279    CG     AAA_
          G                      TCA  GGGAGAA   TGGGTCC
                                ||| |||||||  |||||||
                                GGT  TTTTCTT   GTTCAGG
                                  CT     AAAG
GAM890  LOC151643 3'  GGATTTGTTTTTCCTG     80326       AAA  GG
                                CGGGGAGA   AT  GTCC
                                ||||||||   ||  ||||
                                GTCCTTTT   TG  TAGG
                                     ___  TT
GAM890  LOC151647 5'  GGAACTTTTCTTCTCCTGG   80333   G     A  T  G
                                C GGGAGAA AA GG TCC
                                | ||||||| || || |||
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                                G TCCTCTT TT TC AGG
                                 G      C  T  A
GAM890   LOC151790 3'  GGAAGTTTTCTCTTCATGG   80345     C        ATGGG
                                TCA GGGGAGAAAA     TCC
                                ||| ||||||||||     |||
                                GGT CTTCTCTTTT     AGG
                                  A         GA___
GAM890   LOC152059 3'  GGACCCTTTCTTTCTTTCTCTG 80447     C  GG     AAT_
           G                     TCA GG  AGAAA    GGGTCC
                                ||| ||  |||||    ||||||
                                GGT TC  TCTTT    CCCAGG
                                  C  TT     CTTT
GAM890   LOC152100 5'  GGCCCGTGTTTCTGTT      80458    G    A
                                GG AGAAA ATGGGTC
                                || ||||| |||||||
                                TT TCTTT TGCCCGG
                                 G    G
GAM890   LOC152195 5'  GGACCCTGGAATTCTCTCTG   85564         AAAT_
                                CGGGGAGAA     GGGTCC
                                |||||||||     ||||||
                                GTCTCTCTT     CCCAGG
                                     AAGGT
GAM890   LOC152274 5'  GACCCTTCCCTTGTGG      80508        A   AAAT    C
                                TCACGGGG GAA    GGGTC
                                |||||||| |||    |||||
                                GGTGTTCC CTT    CCCAG
                                   _   ____     C
GAM890   LOC152283 5'  GGATTCCCCGACCTTCCCGTG  85684         AAAAAT
                                CACGGGGAG      GGGTCC
                                |||||||||      ||||||
                                GTGCCCTTC      CTTAGG
                                     CAGCCC
GAM890   LOC152300 3'  GGACCTCAGTTTCTTTGT     80548         AAAAT
                                ACGGGGAGA     GGGTCC
                                |||||||||     ||||||
                                TGTTTCTTT     TCCAGG
                                     GAC__
GAM890   LOC152373 5'  GGATCTTCTTTTTCCTTG     80577          AAT
                                CGGGGAGAAA   GGGTCC
                                ||||||||||   ||||||
                                GTTCCTTTTT   TCTAGG
                                      CT_
GAM890   LOC152502 3'  GATTTGATTCTCGTGG      59314         GAAAAAT
                                TCACGGGGA      GGGTC
                                |||||||||      |||||
                                GGTGCTCTT      TTTAG
                                     AG_____
GAM890   LOC152519 3'  GGGTTTATTTCCTTTGCTGTGA 80610       G   AA     GT
                                TCACGG GAG  AAATGG  CC
                                |||||| |||  ||||||  ||
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                                AGTGTC TTT  TTTATT  GG
                                   G   CC     TG
GAM890   LOC152742 3'  GGGTCTATTGGGCTCTGTGG   85859        AGAAA    GT
                                TCACGGGG    AATGG  CC
                                ||||||||    |||||  ||
                                GGTGTCTC    TTATC  GG
                                    GGG__    TG
GAM890   LOC152762 5'  GGATCTCAGGTCTCTCTGAGA  80653    A       AAAA  _
                                TC CGGGGAGA    TG GGTCC
                                || |||||||||   || |||||
                                AG GTCTCTCT    AC CTAGG
                                 A       GG__  T
GAM890   LOC152765 3'  GGGCCTTAGAATTTTCTTTTTG 80662          AT___
                                CGGGGAGAAAA    GGGTCC
                                ||||||||||     ||||||
                                GTTTTTCTTTT    TCCGGG
                                      AAGAT
GAM890   LOC153454 5'  GGGCCCCATGGTATCCCTGTGA 80835         GAAAAAT
                                TCACGGGGA      GGGTCC
                                |||||||||      ||||||
                                AGTGTCCCT      CCCGGG
                                     ATGGTAC
GAM890   LOC153571 3'  GGGCTCGGGGTCTCCCCG    86051        AAAA
                                CGGGGAGA    TGGGTCC
                                ||||||||    |||||||
                                GCCCCTCT    GCTCGGG
                                    GGG_
GAM890   LOC153642 3'  TTTATTTTTCTTTTTATGA    80913     CG
                                TCA  GGGAGAAAAATGGG
                                |||  ||||||||||||||
                                AGT  TTTTCTTTTTATTT
                                  AT
GAM890   LOC153769 3'  GATCCCCACTCTCGTGG     80926        G  AAAAAT
                                TCACGGG AG     GGGTC
                                ||||||| ||     |||||
                                GGTGCTC TC     CCTAG
                                    _  ACC___
GAM890   LOC154282 5'  GGATTTTTTTTTTTTTTTTCCT 86206   A         T____
            GAGA                    CGGGGAGAAAAA    GGGTCC
                                    ||||||||||     ||||||
                                    GTCCTTTTTTTT    TTTAGG
                                    A          TTTTT
GAM890   LOC154547 5'  GGACCTGGTACCTCTTTTGTGA 76053        _   AAAAA
                                TCACGGG GAG    TGGGTCC
                                ||||||| |||    |||||||
                                AGTGTTT CTC    GTCCAGG
                                    T   CATG_
GAM890   LOC154761 3'  GGGCTCCTGTCTCCTTGT    81124         AAAAT
                                ACGGGGAGA    GGGTCC
                                |||||||||    ||||||
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                                TGTTCCTCT    CTCGGG
                                     GTC__
GAM890  LOC154789 3' GGAACTTTTTTCTTTCTGT   81137     GG     T  G
                                ACGG  AGAAAAA GG TCC
                                |||| ||||||| || |||
                                TGTC  TCTTTTT TC AGG
                                  TT      _  A
GAM890  LOC154790 5' GACCCGTTTGATCCGGA    81149    A   GAGAA
                                TC CGGG    AAATGGGTC
                                || ||||    |||||||||
                                AG GCCT    TTTGCCCAG
                                 _   AG___
GAM890  LOC155036 5' GGGCTAGATTTTCTCTTCTGG  86345    C        ATG
                                TCA GGGGAGAAAA   GGTCC
                                ||| ||||||||||   |||||
                                GGT CTTCTCTTTT   TCGGG
                                 _        AGA
GAM890  LOC155179 3' GTCATTCTCTGTGG       81324         GAAAA   G
                                TCACGGGGA    ATGG T
                                |||||||||    |||| |
                                GGTGTCTCT    TACT G
                                     _____   G
GAM890  LOC157254 3' GGGTTTGTTTTCTGTCTCCGTG 81389        GA_   TG GT
                                CACGGGGA   AAAA  G  CC
                                ||||||||   ||||  |  ||
                                GTGCCTCT   TTTT  T  GG
                                     GTC    GT TG
GAM890  LOC157254 5' GGCTTCCTTTTCCTGGA    81388    A      AAAAT
                                TC CGGGGAGA    GGGTC
                                || ||||||||    |||||
                                AG GTCCTTTT    TTCGG
                                 _      CC___
GAM890  LOC157556 3' GGACCTGGAGGGGTGCTCTGTG 86488        AGAAAAA_
           G                     TCACGGGG       TGGGTCC
                                ||||||||       |||||||
                                GGTGTCTC       GTCCAGG
                                     GTGGGGAG
GAM890  LOC157603 5' GGACCTCAGGCTTTCTTGTTG  86492    G     AA_  _
                                CGG GAGAAA   TG GGTCC
                                ||| ||||||   || |||||
                                GTT TTCTTT   AC CCAGG
                                  G     CGG  T
GAM890  LOC157653 5' GGATTCTGCATTTCTTTTTGTG 81526           AAT_
           G                     TCACGGGGAGAAA    GGGTCC
                                ||||||||||||||   ||||||
                                GGTGTTTTTCTTT    CTTAGG
                                         ACGT
GAM890  LOC157858 5' GGACTCATTTTTCTTTTCTGG  86597    C GG
                                TCA G  GAGAAAAATGGGTCC
                                ||| |  |||||||||||||||
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                                GGT C  TTCTTTTTACTCAGG
                                  _ TT
GAM890   LOC158191 3'  GGACTCTAGACTCTCCCCTGG  81778     C      AAAAT
                                TCA GGGGAGA     GGGTCC
                                ||| |||||||     ||||||
                                GGT CCCCTCT     CTCAGG
                                  _      CAGAT
GAM890   LOC158219 3'  ATTTTTTTTCCTATGG      81790     CG
                                TCA  GGGAGAAAAAT
                                |||  ||||||||||
                                GGT  CCTTTTTTTTA
                                  AT
GAM890   LOC158235 3'  ATTTTTTTCTCTGGA       86700     A
                                TC CGGGGAGAAAAAT
                                || ||||||||||||
                                AG GTCTCTTTTTTTA
                                 _
GAM890   LOC158263 5'  GGCCCTTCACCTTGTGG      81851         A   AAAT
                                TCACGGGG GAA    GGGTC
                                |||||||| |||    |||||
                                GGTGTTCC CTT    CCCGG
                                     A  ____
GAM890   LOC158563 5'  GGGCTTTGCTCCTCTGTGA    81951       _    AAAAAT
                                TCACGG GGAG     GGGTCC
                                |||||| ||||     ||||||
                                AGTGTC CCTC     TTCGGG
                                   T    GT____
GAM890   LOC158581 3'  GGGTCGTCAGTTTTCTCCGGTG 86870      _       AAATG GT
           G                     TCAC GGGGAGAA     G  CC
                                |||| ||||||||     |  ||
                                GGTG CCTCTTTT     C  GG
                                  G       GACTG TG
GAM890   LOC158654 5'  GGGTTCTGTTTCTCCCCTTGG  81967     C        AAT GG
                                TCA GGGGAGAAA   G  TCC
                                ||| |||||||||   |  |||
                                GGT CCCCTCTTT   C  GGG
                                  T       GT_ TT
GAM890   LOC158656 5'  GGACCCACGGCTTCTTGTGG   73038          AAAAA
                                TCACGGGGAG     TGGGTCC
                                ||||||||||     |||||||
                                GGTGTTCTTC     ACCCAGG
                                     GGC__
GAM890   LOC158819 5'  GGACTGTGATTTTCTTTGGA   86909     A       AAATG
                                TC CGGGGAGAA     GGTCC
                                || |||||||||     |||||
                                AG GTTTCTTTT     TCAGG
                                  _       AGTG_
GAM890   LOC158997 5'  GGACCTGGTACCTCTTTTGTGA 82081        _   AAAAA
                                TCACGGG GAG     TGGGTCC
                                ||||||| |||     |||||||
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                                AGTGTTT CTC    GTCCAGG
                                   T  CATG_
GAM890  LOC160418 5'  GACAGTTTCTCCGTGG     82213         AAAATGG
                                TCACGGGGAGA     GTC
                                ||||||||||      |||
                                GGTGCCTCTTT     CAG
                                   GA_____
GAM890  LOC161742 3'  GGAAATACTGTTTTTCCTTGTG 82292          AA_  GG
          A                      TCACGGGGAGAAA  TG  TCC
                                ||||||||||||  ||  |||
                                AGTGTTCCTTTTT  AT  AGG
                                    GTC  AA
GAM890  LOC162083 5'  GGCCCCCTCTCCCTGGA    82337   A      AAAAT
                                TC CGGGGAGA    GGGTC
                                || ||||||||    |||||
                                AG GTCCCTCT    CCCGG
                                 _      CC___
GAM890  LOC163404 3'  GGATTGTCTTTTTTTTTCTGTG 82128     GG     TG_
                                CACGG  AGAAAAA  GGTCC
                                |||||  |||||||  |||||
                                GTGTC  TTTTTTT  TTAGG
                                   TT     CTG
GAM890  LOC163590 3'  GATTTTTTTTTTTTCTTG    58860         TG
                                CGGGGAGAAAAA  GGTC
                                ||||||||||||  ||||
                                GTTCTTTTTTTT  TTAG
                                    TT
GAM890  LOC164390 5'  GGGCCTCATTGTCCTGTGG   82516       AGAAA   _
                                TCACGGGG    AATG GGTCC
                                ||||||||    |||| |||||
                                GGTGTCCT    TTAC CCGGG
                                    G____   T
GAM890  LOC164714 3'  GCCCGCTCCCCGTG       87233        AAAAA   T
                                CACGGGGAG    TGGG C
                                |||||||||    |||| |
                                GTGCCCCTC    GCCC G
                                    _____   T
GAM890  LOC165140 5'  GGACCTTCAACCTCCTCGT   82465       AAAAAT
                                ACGGGGAG     GGGTCC
                                ||||||||     ||||||
                                TGCTCCTC     TCCAGG
                                    CAACT_
GAM890  LOC165552 3'  GGGCTTTGCCTTTCCCTGCGG  82488   A      AAAAT
                                TC CGGGGAGA    GGGTCC
                                || ||||||||    ||||||
                                GG GTCCCTTT    TTCGGG
                                 C      CCGT_
GAM890  LOC167040 5'  GGGTTCAAATCCTCTGTGA   87268       A  AAAA  GG
                                TCACGGGG GA   TG  TCC
                                |||||||| ||   ||  |||
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                                AGTGTCTC CT    AC  GGG
                                    _  AA__  TT
GAM890   LOC169026 3'  GGGTGCATTTCTTTCTCTG   82726        A    G
                                CGGGGAGA AAATG GTCC
                                |||||||| ||||| ||||
                                GTCTCTTT TTTAC TGGG
                                    C    G
GAM890   LOC170261 3'  GTCTGTTTTCTGTGTG     82587     G    AAA   GT
                                CACG GGAGA   ATGG  C
                                |||| |||||   ||||  |
                                GTGT TCTTT   TGTC  G
                                  G    ___    TG
GAM890   LOC170261 5'  GGATCTGCGACCCCCTGTGG  82584        AGAAAAAT
                                TCACGGGG       GGGTCC
                                ||||||||       ||||||
                                GGTGTCCC       TCTAGG
                                    CCAGCG__
GAM890   LOC170281 5'  GGACCCACTCTTTTCCTGTG  87250         AAAA
                                CACGGGGAGA    TGGGTCC
                                ||||||||||    |||||||
                                GTGTCCTTTT    ACCCAGG
                                   CTC_
GAM890   LOC170394 5'  GGGCTTGGCTTTTCTCGTC   82855    G      A_
                                GG GAGAAAA  TGGGTCC
                                || |||||||  |||||||
                                CT CTCTTTT  GTTCGGG
                                 G      CG
GAM890   LOC170409 5'  GGCCTACACTCTGTGA      82865        AGAAAAA
                                TCACGGGG      TGGGTC
                                ||||||||      ||||||
                                AGTGTCTC      ATCCGG
                                    AC_____
GAM890   LOC196463 3'  GGCCCCTTCCTCGTG       87714         AAAAAT
                                CACGGGGAG     GGGTC
                                |||||||||     |||||
                                GTGCTCCTT     CCCGG
                                    C_____
GAM890   LOC196743 3'  GGACCCTCATTTCTTCT     87507        AAT
                                GGGAGAAA   GGGTCC
                                ||||||||   ||||||
                                TCTTCTTT   CCCAGG
                                    ACT
GAM890   LOC196761 3'  GGGCTTATGCCTCCGTGA    89555        AGAAAA
                                TCACGGGG     ATGGGTCC
                                ||||||||     ||||||||
                                AGTGCCTC     TATTCGGG
                                    CG____
GAM890   LOC196812 3'  GGGCTGTTTCTTTTTGT     89572          AATG
                                ACGGGGAGAAA    GGTCC
                                ||||||||||    |||||
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                                TGTTTTTCTTT   TCGGG
                                      G___
GAM890  LOC196892 3'  GGAAGATGTTTTCCCTGTGA  87805          AAATGGG
                                TCACGGGGAGAA      TCC
                                ||||||||||||      |||
                                AGTGTCCCTTTT      AGG
                                      GTAGA__
GAM890  LOC196985 5'  GGGCCCAGCTGCCTTTGTGA  89665        AGAAAAA
                                TCACGGGG      TGGGTCC
                                ||||||||      |||||||
                                AGTGTTTC      ACCCGGG
                                    CGTCG__
GAM890  LOC196986 5'  GGGCCCAGCTGCCTTTGTGA  89660        AGAAAAA
                                TCACGGGG      TGGGTCC
                                ||||||||      |||||||
                                AGTGTTTC      ACCCGGG
                                    CGTCG__
GAM890  LOC196988 3'  GGGCCCATGGACAACTCCTGA 87856     C   AGAAAA
                                TCA GGGG     ATGGGTCC
                                ||| ||||     ||||||||
                                AGT CCTC     TACCCGGG
                                  _   AACAGG
GAM890  LOC197201 3'  GGATGCAGCTCTCTCTGTGG  87940          AAAA  G
                                TCACGGGGAGA   TG GTCC
                                ||||||||||   || ||||
                                GGTGTCTCTCT   AC TAGG
                                      CG__  G
GAM890  LOC197285 3'  GACCTGTGCCCACGTGG     87792      _  AGAAAA
                                TCACG GGG     ATGGGTC
                                ||||| |||     |||||||
                                GGTGC CCC     TGTCCAG
                                   A  G_____
GAM890  LOC197414 3'  GGGCCTCCCTCTGCTCTGTGG 88068        _  AAAAT
                                TCACGGGG AGA    GGGTCC
                                |||||||| |||    ||||||
                                GGTGTCTC TCT    TCCGGG
                                    G  CCC__
GAM890  LOC199858 5'  GGTCCCCAGACTCATCCTGTGG 88423       GA  AAAAT  T
                                TCACGGG  GA    GGG CC
                                |||||||  ||    ||| ||
                                GGTGTCC  CT    CCC GG
                                   TA  CAGAC   T  G
GAM890  LOC200058 3'  GACTCCCTCTCTGTG      88557         AAAAAT
                                CACGGGGAG     GGGTC
                                |||||||||     |||||
                                GTGTCTCTC     CTCAG
                                    C_____
GAM890  LOC200081 3'  GGATTCTACTTCTTCCTGTG  88565          AAAT
                                CACGGGGAGAA   GGGTCC
                                ||||||||||   ||||||
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                                GTGTCCTTCTT  CTTAGG
                                     CAT_
GAM890  LOC200093 3'  CCTTTTTCTTCCTGT      63093          T
                                ACGGGGAGAAAAA GG
                                |||||||||||| ||
                                TGTCCTTCTTTTT CC
                                      _
GAM890  LOC200205 3'  GGGTTGTTTTCTCCCTGGA  88628   A      A TG G
                                TC CGGGGAGAAA A  G TC
                                || |||||||||| |  | ||
                                AG GTCCCTCTTT T  T GG
                                 _       _ GT G
GAM890  LOC200268 3'  TCATTTTTCTTCTGTGG    88693      G
                                TCACGGG AGAAAAATGG
                                ||||||| ||||||||||
                                GGTGTCT TCTTTTTACT
                                    _
GAM890  LOC200312 3'  GGGTTCTGGGAGCTCCCTGTGG 89995        AAAAAT GG
                                TCACGGGGAG    G  TCC
                                ||||||||||    |  |||
                                GGTGTCCCTC    C  GGG
                                     GAGGGT TT
GAM890  LOC200373 3'  GGAATATTTTTTCTCTTTGGA  88800   A        TGGG
                                TC CGGGGAGAAAAA   TCC
                                || ||||||||||||   |||
                                AG GTTTCTCTTTTT   AGG
                                 _         TATA
GAM890  LOC200420 5'  GACTTAGTTCTCCTTG     59249        AAA
                                CGGGGAGAA  TGGGTC
                                |||||||||  ||||||
                                GTTCCTCTT  ATTCAG
                                     G__
GAM890  LOC200845 5'  CTGTTTTTCTCCTCTTGA   88899    C
                                TCA GGGGAGAAAAATGG
                                ||| ||||||||||||||
                                AGT CTCCTCTTTTTGTC
                                  T
GAM890  LOC201283 3'  GGCTTATTCCTCCTTG     60416       AAA
                                CGGGGAG  AATGGGTC
                                |||||||  ||||||||
                                GTTCCTC  TTATTCGG
                                    C__
GAM890  LOC201292 5'  GGGTCCATTTGGAGGCTGTGG  88192       GGAGAA    GT
                                TCACGG    AAATGG  CC
                                ||||||    ||||||  ||
                                GGTGTC    TTTACC  GG
                                   GGAGG_    TG
GAM890  LOC201292 5'  GACTTAGCCCCCGTGG     88187        AGAAAAA
                                TCACGGGG     TGGGTC
                                ||||||||     ||||||
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                                GGTGCCCC      ATTCAG
                                    CG_____
GAM890  LOC201522 5'  GCTCACGTTTCTTTTTTCCGTG 88257       ___     AA    CC
          G                      TCACGGG   GAGAAA  TGGGT
                                 |||||||   ||||||  |||||
                                 GGTGCCT   TTCTTT  ACTCG
                                    TTT     GC
GAM890  LOC201549 3'  GGCTCAGCTTTTCCTG      90232        AAAA
                                 CGGGGAGA    TGGGTC
                                 ||||||||    ||||||
                                 GTCCTTTT    ACTCGG
                                    CG__
GAM890  LOC201696 3'  ATTTTTTTCCCTTGA       63129     C
                                 TCA GGGGAGAAAAAT
                                 ||| ||||||||||||
                                 AGT TCCCTTTTTTTA
                                  _
GAM890  LOC202460 5'  GGGTCTTTGCCCTCTCCCTTGT 89186       _     AAAAT_  GT
          GG                     TCACG GGGAGA     GG  CC
                                 ||||| ||||||     ||  ||
                                 GGTGT CCCTCT     TC  GG
                                    T     CCCGTT  TG
GAM890  LOC203052 3'  GGACCCCAGAGTGCCCTGTGG  90455        AGAAAAAT
                                 TCACGGGG       GGGTCC
                                 ||||||||       ||||||
                                 GGTGTCCC       CCCAGG
                                    GTGAGAC_
GAM890  LOC203248 3'  GGATATTTTTTTCTTGTGG    89312            ATGG
                                 TCACGGGGAGAAAA    GTCC
                                 ||||||||||||||    ||||
                                 GGTGTTCTTTTTTT    TAGG
                                         A___
GAM890  LOC203292 5'  GGGCTGGTTTCTCCTCTTGG   90512     C       AA  G
                                 TCA GGGGAGAA  AT GGTCC
                                 ||| ||||||||  || |||||
                                 GGT CTCCTCTT  TG TCGGG
                                   T       __  G
GAM890  LOC203378 5'  GGGCTTATTAGTAACTCTGTGA 90614        AGAAA
                                 TCACGGGG    AATGGGTCC
                                 ||||||||    |||||||||
                                 AGTGTCTC    TTATTCGGG
                                    AATGA
GAM890  LOC203378 5'  GGATTTGTGGTTCCTCTG    90611       A   AA  GG
                                 CGGGG GAA  AT  GTCC
                                 ||||| |||  ||  ||||
                                 GTCTC CTT  TG  TAGG
                                    _  GG  TT
GAM890  LOC203652 5'  GGGCCCATCCCCCTGTGA    90653         A  AAAA
                                 TCACGGGG GA    TGGGTCC
                                 |||||||| ||    |||||||
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                                AGTGTCCC CT    ACCCGGG
                                    C _____
GAM890  LOC204010 5'  GACAAATTTTTCTTTCTTTGTG 89443      __ GG       GG   C
            A                    TCAC  GG  AGAAAAAT  GTC
                                 ||||  ||  ||||||||  |||
                                 AGTG  TC  TCTTTTTA  CAG
                                   TT  TT       AA
GAM890  LOC205103 5'  GGATCCATGTGTCTTTCCTGG  89510     C  GG   AAA
                                 TCA GG  AGA   ATGGGTCC
                                 ||| ||  |||   ||||||||
                                 GGT CC  TCT   TACCTAGG
                                   _  TT   GTG
GAM890  LOC206804 5'  GGCATTCTCTCTGGGA      89542     A       AAATGG
                                 TC CGGGGAGAA      GTC
                                 || |||||||||      |||
                                 AG GTCTCTCTT      CGG
                                  G        A_____
GAM890  LOC219562 5'  GGACTCAAAGGTTTTCTCCCTG 90770    A         A___
            AGA                    C CGGGGAGAAAA    TGGGTCC
                                 | ||||||||||||    |||||||
                                 G GTCCCTCTTTT    ACTCAGG
                                  A          GGAA
GAM890  LOC219654 3'  GGGCCCATTTCAGCTCTGT    91308       AGAA
                                 ACGGGG    AAATGGGTCC
                                 ||||||    ||||||||||
                                 TGTCTC    TTTACCCGGG
                                    GAC_
GAM890  LOC219654 3'  GGGCTTATCCTTCTCT      91309       AA
                                 GGAGAA  ATGGGTCC
                                 ||||||  ||||||||
                                 TCTCTT  TATTCGGG
                                    CC
GAM890  LOC219699 5'  GGGCCTGTCACATCCTGCTGG  96355     CG    GAAAA
                                 TCA  GGGA    ATGGGTCC
                                 |||  ||||    ||||||||
                                 GGT  TCCT    TGTCCGGG
                                   CG   ACAC_
GAM890  LOC219722 5'  GGATCCATTTTGATGCCTTTTG 93084      __   AGA_
            TGG                    CACG  GGG    AAAATGGGTCC
                                 ||||  |||   ||||||||||||
                                 GTGT  TCC    TTTTACCTAGG
                                   TT   GTAG
GAM890  LOC219738 3'  GGGTCCGTTGGTTCCCGAGA   59258    A     GAAA    GT
                                 TC CGGGGA    AATGG  CC
                                 || ||||||    |||||  ||
                                 AG GCCCTT    TTGCC  GG
                                  A     GG__     TG
GAM890  LOC219854 3'  GGATTGCCAAATTGTCCCTGTG 91487         G  AAA   __
            G                      TCACGGGGA AA   TGG  GTCC
                                 |||||||||  ||   |||  ||||
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                                GGTGTCCCT TT   ACC  TAGG
                                     G  AA_   GT
GAM890   LOC219854 5'  GGAACTTTCTGTCTTGTGA    91486        _   AAAT  G
                                TCACGGGG AGAA    GG TCC
                                |||||||| ||||    || |||
                                AGTGTTCT TCTT    TC AGG
                                     G    ____  A
GAM890   LOC219899 3'  GGATTTTGTATATTTTTCCCCC 91504       A      _____
           TG                     CGGGG GAAAAATG     GGTCC
                                |||||| ||||||||     ||||||
                                GTCCC CTTTTTAT     TTAGG
                                   C       ATGTT
GAM890   LOC219920 5'  GGGCCTGTTATCTCCC      93319        AA
                                GGGAGA  AATGGGTCC
                                ||||||  |||||||||
                                CCCTCT  TTGTCCGGG
                                   A_
GAM890   LOC220370 3'  GGACCCAGGAGTCTCTCTG    92828         AAAA
                                CGGGGAGA    TGGGTCC
                                ||||||||    |||||||
                                GTCTCTCT    ACCCAGG
                                     GAGG
GAM890   LOC220370 3'  GGCTCCATCTCTCTGT      92832         AAAA  _
                                ACGGGGAGA    TGG GTC
                                |||||||||    ||| |||
                                TGTCTCTCT    ACC CGG
                                     ____   T
GAM890   LOC220739 3'  GGGTTCATTTGTCACCTTGGA  92936    A    A  A    GG
                                TC CGGGG GA AAATG  TCC
                                || ||||| || |||||  |||
                                AG GTTCC CT TTTAC  GGG
                                 _    A  G    TT
GAM890   LOC220883 3'  GGATCTGTCGGTCATTTCTGT  91263     GG _  AAA
                                ACGG  A GA   ATGGGTCC
                                ||||  | ||   ||||||||
                                TGTC  T CT   TGTCTAGG
                                   TT A  GGC
GAM890   LOC221035 5'  GGCCCAAGCCCCCGTGA     93167         AGAAAAA
                                TCACGGGG      TGGGTC
                                ||||||||      ||||||
                                AGTGCCCC      ACCCGG
                                     CGA____
GAM890   LOC221143 3'  GACCTAGCTCTCGTGG      93568         AGAAAAA
                                TCACGGGG      TGGGTC
                                ||||||||      ||||||
                                GGTGCTCT      ATCCAG
                                     CG_____
GAM890   LOC221241 3'  GGACTTTGGATTTTCTTTTTG  93585           AT__
                                CGGGGAGAAAA    GGGTCC
                                ||||||||||    ||||||
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                                GTTTTTCTTTT   TTCAGG
                                      AGGT
GAM890  LOC221296 3'  GGATTTAGTAAAATTTTTTTTT 91967    GG      _______
          CTG                   GG  AGAAAAAT     GGGTCC
                                ||  ||||||||     ||||||
                                TC  TTTTTTTA     TTTAGG
                                 TT       AAATGA
GAM890  LOC221300 3'  GATGTTTTCTTTGTGA      91926           AAATGG
                                TCACGGGGAGAA     GTC
                                ||||||||||||     |||
                                AGTGTTTCTTTT     TAG
                                      G_____
GAM890  LOC221337 3'  GGACTAGAGTTCCTTGTGG   92112          AAAAATG
                                TCACGGGGAG      GGTCC
                                ||||||||||      |||||
                                GGTGTTCCTT      TCAGG
                                      GAGA___
GAM890  LOC221405 5'  GGGTTCGTTTTTTTTTTT    93885           GG
                                GGGGAGAAAAATG  TCC
                                ||||||||||||  |||
                                TTTTTTTTTTTGC  GGG
                                       TT
GAM890  LOC221416 3'  GACTGTGTCTCCCCTGG     93768     C      AAAATG
                                TCA GGGGAGA     GGTC
                                ||| |||||||     ||||
                                GGT CCCCTCT     TCAG
                                  _      GTG___
GAM890  LOC221421 3'  GGACCTGTTTGGCCCATGA   92278     CG   AGAA
                                TCA  GGG   AAATGGGTCC
                                |||  |||   ||||||||||
                                AGT  CCC   TTTGTCCAGG
                                  A_   GG__
GAM890  LOC221561 5'  GGACCTGGTACCTCTTTTGTGA 92133        _   AAAAA
                                TCACGGG GAG    TGGGTCC
                                ||||||| |||    |||||||
                                AGTGTTT CTC    GTCCAGG
                                     T   CATG_
GAM890  LOC221562 5'  GGACCTGGTACCTCTTTTGTGA 91996        _   AAAAA
                                TCACGGG GAG    TGGGTCC
                                ||||||| |||    |||||||
                                AGTGTTT CTC    GTCCAGG
                                     T   CATG_
GAM890  LOC221641 5'  TTTTACCTGTTTTTCTTCCAGT 93732      G            CC
          GG                    TCAC GGGAGAAAAATGGGT
                                ||||| ||||||||||||||
                                GGTG CCTTCTTTTTGTCCA
                                  A             TTTTA
GAM890  LOC221656 3'  CCATGTTTTTCTTCTGTGA   92228        _     A
                                TCACGGG GAGAAA ATGG
                                |||||||  ||||||  ||||
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                                AGTGTCT CTTTTT TACC
                                    T     G
GAM890   LOC221955 3'  GGGCTGGGGTTTTCTCCTGG   57550   G       ATG_
                                C GGGAGAAAA   GGTCC
                                | |||||||||   |||||
                                G TCCTCTTTT   TCGGG
                                 G        GGGG
GAM890   LOC222019 5'  GGACCTGGTACCTCTTTTGTGA 94003       _   AAAAA
                                TCACGGG GAG    TGGGTCC
                                ||||||| |||    |||||||
                                AGTGTTT CTC    GTCCAGG
                                    T   CATG_
GAM890   LOC222057 3'  GGGCCCATCCCCTCCCTGT   92781        AAAA
                                ACGGGGAG   ATGGGTCC
                                ||||||||   ||||||||
                                TGTCCCTC   TACCCGGG
                                    CCC_
GAM890   LOC222070 5'  AGTAATGTGTTTTTTTCTCTGT 94149             G  CC
           GG                     TCACGGGGAGAAAAATG GT
                                ||||||||||||||||| ||
                                GGTGTCTCTTTTTTTGT TA
                                          G  ATGAG
GAM890   LOC222070 5'  GGGCTGCATTCCCTTTGTGA   94158     __    GAAAA  _
                                TCAC  GGGGA    ATG GGTCC
                                ||||  |||||    ||| |||||
                                AGTG  TCCCT    TAC TCGGG
                                  TT    _____  G
GAM890   LOC222174 3'  GGACTTGGGGTTCTTTGT    94116        AAAAA
                                ACGGGGAG    TGGGTCC
                                ||||||||    |||||||
                                TGTTTCTT    GTTCAGG
                                    GGG__
GAM890   LOC222182 3'  GGACCCATCACGGCCTGTGG   94191       GAGAAAA
                                TCACGGG     ATGGGTCC
                                |||||||     ||||||||
                                GGTGTCC     TACCCAGG
                                    GGCAC__
GAM890   LOC222865 3'  GGACTTGGGTTCCCTGTG    92864        AAAAA
                                CACGGGGAG    TGGGTCC
                                |||||||||    |||||||
                                GTGTCCCTT    GTTCAGG
                                     GG___
GAM890   LOC245728 5'  GGATCTGTGAGTCTTCTGG   91132   G    AAA
                                C GGGAGA   ATGGGTCC
                                | ||||||   ||||||||
                                G TCTTCT   TGTCTAGG
                                 G     GAG
GAM890   LOC253024 5'  GACTCCTTCTTTGTGA      97616         AAAAAT
                                TCACGGGGAG     GGGTC
                                ||||||||||     |||||
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                                AGTGTTTCTT     CTCAG
                                      C_____
GAM890   LOC253070 3'  GGGTCCGGGCTCCCCCTCGTGG 97013      ___     AAAAA   GT
                                TCAC   GGGGAG    TGG  CC
                                ||||   ||||||    |||  ||
                                GGTG   CCCCTC    GCC  GG
                                  CTC     GG___   TG
GAM890   LOC253264 5'  GGATCCATGCAGGTCTTGGA   94690    A    AGAAAA
                                TC CGGGG     ATGGGTCC
                                || |||||     ||||||||
                                AG GTTCT     TACCTAGG
                                 _    GGACG_
GAM890   LOC253641 3'  GGACCCTGTCTTCTCCTCG    97554         AAAT
                                CGGGGAGAA    GGGTCC
                                |||||||||    ||||||
                                GCTCCTCTT    CCCAGG
                                      CTGT
GAM890   LOC253891 3'  GGACCCTGACATCCCTGTGG   94415         GAAAAAT
                                TCACGGGGA      GGGTCC
                                |||||||||      ||||||
                                GGTGTCCCT      CCCAGG
                                      ACAGT__
GAM890   LOC253897 3'  GGGCTTTGGATTTGTTCTTGTG 96107         G   AAT_
           A                     TCACGGGGA AAA    GGGTCC
                                ||||||||| |||    ||||||
                                AGTGTTCTT TTT    TTCGGG
                                      G   AGGT
GAM890   LOC253943 3'  GGATTCATTAACTCTTTG     96139        AAA
                                CGGGGAG   AATGGGTCC
                                |||||||   |||||||||
                                GTTTCTC   TTACTTAGG
                                    AA_
GAM890   LOC253970 5'  GGATTTTAAATCTTCCTG     96542         AAAAT
                                CGGGGAGA    GGGTCC
                                ||||||||    ||||||
                                GTCCTTCT    TTTAGG
                                     AAAT_
GAM890   LOC254013 3'  GGGCTTTTTTTTTTTTTGAGA 94880    A          TG
                                TC CGGGGAGAAAAA  GGTCC
                                || ||||||||||||  |||||
                                AG GTTTTTTTTTTT  TCGGG
                                 A          TT
GAM890   LOC254015 3'  GGGTCTAGGCGTGTCTTTGTGG 96705         GAAAAA   GT
                                TCACGGGGA     TGG  CC
                                |||||||||     |||  ||
                                GGTGTTTCT     ATC  GG
                                      GTGCGG   TG
GAM890   LOC254181 5'  GGGCCTGAGTACCTTTTCTCCC 97585          AT_____
           TG                    CGGGGAGAAAA      GGGTCC
                                ||||||||||       ||||||
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                                GTCCCTCTTTT      TCCGGG
                                      CCATGAG
GAM890   LOC254182 3'  GACTCATTACTTCTGG     96035   G    AAA
                                C GGGAG   AATGGGTC
                                | |||||   ||||||||
                                G TCTTC   TTACTCAG
                                 G    A__
GAM890   LOC254228 3'  GGGCTCATCAGTCTCTGT    95954       GAAAA
                                ACGGGGA    ATGGGTCC
                                |||||||    ||||||||
                                TGTCTCT    TACTCGGG
                                    GAC__
GAM890   LOC254249 5'  GAATTATTTTTTTCTCTGT   95446            G  C
                                ACGGGGAGAAAAATGG TC
                                |||||||||||||||| ||
                                TGTCTCTTTTTTTATT AG
                                          A
GAM890   LOC254337 5'  GGATTTTTCTCTTTCCTTGA  96270    C  GG   AAAAT
                                TCA GG  AGA    GGGTCC
                                ||| ||  |||    ||||||
                                AGT CC  TCT    TTTAGG
                                  T  TT   CTT__
GAM890   LOC254381 5'  GGGCCTATTTCCTCTCG     97462     GA   AA
                                CGGG  GAA  ATGGGTCC
                                ||||  |||  ||||||||
                                GCTC  CTT  TATCCGGG
                                  TC   __
GAM890   LOC254532 5'  GGACCCGTTTTTTCTTCTG   96640      AG
                                CGGGG  AAAAATGGGTCC
                                |||||  ||||||||||||
                                GTCTT  TTTTTGCCCAGG
                                   CT
GAM890   LOC254742 3'  GGGTTCCTTTTCTCTGT     95782         AAAT GG
                                ACGGGGAGAA    G  TCC
                                ||||||||||    |  |||
                                TGTCTCTTTT    C  GGG
                                      C___ TT
GAM890   LOC255025 3'  GGGTCATTTTTCTTTGTGT   96993     G          G
                                ACG GGAGAAAAATGG TC
                                ||| ||||||||||| ||
                                TGT TTTCTTTTTACT GG
                                  G          G
GAM890   LOC255146 3'  GGCTCCTCACCTTGTGA     95602        A  AAAAT
                                TCACGGGG GA    GGGTC
                                |||||||| ||    |||||
                                AGTGTTCC CT    CTCGG
                                     A  C____
GAM890   LOC255349 3'  GGAACAGTTTTTTCTTCTGG  95613     C        A  GG
                                TCA GGGGAGAAAA TG  TCC
                                ||| ||||||||| ||  |||
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                                GGT CTTCTTTTTT AC  AGG
                                  _        G  A_
GAM890  LOC255374 3'  GGGCTCAGCTCCCTGTG     96062         AAAAA
                                CACGGGGAG    TGGGTCC
                                |||||||||    |||||||
                                GTGTCCCTC    ACTCGGG
                                     G____
GAM890  LOC255520 3'  CGGATTTGTATGTATTTTTTCT 95854   GG      _____  GG
          ACGTGA                  G  GAGAAAA    AT  GTCC   G
                                |  |||||||    ||  ||||  |
                                C  CTTTTTT    TG  TAGG   C
                                 AT      ATGTA  TT
GAM890  LOC255521 3'  GGATCTCAACCTTTCTTTG   96973         AAAAT
                                CGGGGAGA    GGGTCC
                                ||||||||    ||||||
                                GTTTCTTT    TCTAGG
                                     CCAAC
GAM890  LOC255527 5'  GGGCCTCTGTTTTCTCATCTGT 96854        _      AT_
          GA                      TCACGGG GAGAAAA   GGGTCC
                                ||||||| |||||||   ||||||
                                AGTGTCT CTCTTTT   TCCGGG
                                    A      GTC
GAM890  LOC255527 5'  GGGTCTAATCTCCTTGCGA   96855    A       AAAA   GT
                                TC CGGGGAGA    TGG  CC
                                || ||||||||    |||  ||
                                AG GTTCCTCT    ATC  GG
                                 C       A___   TG
GAM890  LOC255779 3'  GGGCTTATTGAAGGCCTGT    96014      GAGAAA
                                ACGGG     AATGGGTCC
                                |||||     |||||||||
                                TGTCC     TTATTCGGG
                                   GGAAG_
GAM890  LOC255855 5'  GGGTTGTTTGTTTTTTTCTTGT 96228            ATG__ GT
          GA                      TCACGGGGAGAAAA    G  CC
                                ||||||||||||||    |  ||
                                AGTGTTCTTTTTTT     T  GG
                                        GTTTG TG
GAM890  LOC256158 5'  GGACTTCCATCTCCTTGTG    97674         AAAA  __
                                CACGGGGAGA    TGG  GTCC
                                |||||||||    |||  ||||
                                GTGTTCCTCT    ACC  CAGG
                                      ____   TT
GAM890  LOC256221 3'  GGGTTGTTTTTTTTCTTGAGA  95212    A         TG G  C
                                TC CGGGGAGAAAAA  G TC
                                || ||||||||||||  | ||
                                AG GTTCTTTTTTTT  T GG
                                 A          GT G
GAM890  LOC256302 3'  GGGCCTGTGTCCTTTCTGGA   95193    A   GG  AAAA
                                TC CGG  AG    ATGGGTCC
                                || |||  ||    ||||||||
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                                AG GTC  TC    TGTCCGGG
                                 _   TT  CTG_
GAM890   LOC256310 5'  GGGCCCATTCACCTGCTGG   96349     _   GA  AAA
                                TCA CGGG  GA   ATGGGTCC
                                ||| ||||  ||   ||||||||
                                GGT GTCC  CT   TACCCGGG
                                  C   A_  ___
GAM890   LOC256346 5'  GGGCCCTCATTTTCTCTGGGA  97456    A        AAAT
                                TC CGGGGAGAA    GGGTCC
                                || |||||||||    ||||||
                                AG GTCTCTTTT    CCCGGG
                                 G        ACT_
GAM890   LOC256682 5'  TGAGCTATTTTCTCCCTGAGA  97580    A         A   G  C
                                TC CGGGGAGAAAA TGG TC
                                || |||||||||| ||| ||
                                AG GTCCCTCTTTT ATC AG
                                 A          _   G  TG
GAM890   LOC256849 5'  GGGCCGTCTTTCCCTGAGA    96951    A       AAAATG
                                TC CGGGGAGA      GGTCC
                                || ||||||||      |||||
                                AG GTCCCTTT      CCGGG
                                 A       CTG___
GAM890   LOC256866 5'  GGACCCGCATCGGTCTCTGTGA 96271          GAAAAA
                                TCACGGGGA      TGGGTCC
                                |||||||||      |||||||
                                AGTGTCTCT      GCCCAGG
                                     GGCTAC
GAM890   LOC256990 5'  GGACCTGGTACCTCTTTTGTGA 96298         _   AAAAA
                                TCACGGG GAG     TGGGTCC
                                ||||||| |||     |||||||
                                AGTGTTT CTC     GTCCAGG
                                    T   CATG_
GAM890   LOC257051 3'  GTCTGTTTTCTGTGTG      96321      G    AAA    GT
                                CACG GGAGA   ATGG  C
                                |||| |||||   ||||  |
                                GTGT TCTTT   TGTC  G
                                  G     ___    TG
GAM890   LOC257051 5'  GGATCTGCGACCCCCTGTGG   96318         AGAAAAAT
                                TCACGGGG       GGGTCC
                                ||||||||       ||||||
                                GGTGTCCC       TCTAGG
                                     CCAGCG__
GAM890   LOC257081 3'  GGCCTGGCACTTTGTGA     96785         AGAAAAA
                                TCACGGGG       TGGGTC
                                ||||||||       ||||||
                                AGTGTTTC       GTCCGG
                                     ACG_____
GAM890   LOC257106 3'  GGGCTCTCCTTTCTCCTTTGG  95389     C        AAT
                                TCA GGGGAGAAA   GGGTCC
                                ||| |||||||||   ||||||
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                                GGT TTCCTCTTT  CTCGGG
                                  _       CCT
GAM890  LOC257181 5'  GGACTCAAAGGTTTTCTCCCTG 94593   A        A___
                AGA                C CGGGGAGAAAA   TGGGTCC
                                | ||||||||||   |||||||
                                G GTCCCTCTTTT   ACTCAGG
                                 A         GGAA
GAM890  LOC257319 3'  TAAAACATTTTTTTTCCTGTG  95777             GGTCC
                                CACGGGGAGAAAAATG
                                ||||||||||||||||
                                GTGTCCTTTTTTTTAC
                                          AAAATC
GAM890  LOC257358 5'  GGATCTGTTCAACACCCTGTGG 97103        AGAAA
                                TCACGGGG    AATGGGTCC
                                ||||||||    |||||||||
                                GGTGTCCC    TTGTCTAGG
                                     ACAAC
GAM890  LOC257456 3'  GGACCGGCTTCCCCTGTGA   79779        A  AAATG
                                TCACGGGG GAA    GGTCC
                                |||||||| |||    |||||
                                AGTGTCCC CTT    CCAGG
                                     _  CGG__
GAM890  LOC257476 3'  GGGTTATATTTCTCTTTG    61256          A   G
                                CGGGGAGAAA ATGG TC
                                |||||||||| |||| ||
                                GTTTCTCTTT TATT GG
                                      A   G
GAM890  LOC257534 5'  GGACCTGGTACCTCTTTTGTGA 97712        _  AAAAA
                                TCACGGG GAG    TGGGTCC
                                ||||||| |||    |||||||
                                AGTGTTT CTC    GTCCAGG
                                    T  CATG_
GAM890  LOC257591 5'  GGACCTGGTACCTCTTTTGTGA 97843        _  AAAAA
                                TCACGGG GAG    TGGGTCC
                                ||||||| |||    |||||||
                                AGTGTTT CTC    GTCCAGG
                                    T  CATG_
GAM890  LOC257592 5'  GGACCTGGTACCTCTTTTGTGA 97899        _  AAAAA
                                TCACGGG GAG    TGGGTCC
                                ||||||| |||    |||||||
                                AGTGTTT CTC    GTCCAGG
                                    T  CATG_
GAM890  LOC50999  3'  GGACATGTTTTCTCTTTG    32101          ATGG
                                CGGGGAGAAAA   GTCC
                                ||||||||||   ||||
                                GTTTCTCTTTT   CAGG
                                      GTA_
GAM890  LOC51141  3'  GGATGCAGTTTTCCCCTTGA  68591    C      AAA  G
                                TCA GGGGAGAA  TG GTCC
                                ||| ||||||||  || ||||
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                                AGT CCCCTTTT   AC TAGG
                                  T       G__  G
GAM890  LOC51142  3' ATTTTATTCTTTGTGA      32336          A
                                TCACGGGGAG AAAAT
                                |||||||||| |||||
                                AGTGTTTCTT TTTTA
                                      A
GAM890  LOC51145  5' GGGCCCGGCCCGTTCCCTCTGG 32398     C     AAAAA
                                TCA GGGGAG    TGGGTCC
                                ||| ||||||    |||||||
                                GGT TCCCTT    GCCCGGG
                                  C     GCCCG
GAM890  LOC51145  3' GGACCTCCGCCTCTTGTGG    32397       G  AAAAAT
                                TCACGGG AG     GGGTCC
                                ||||||| ||     ||||||
                                GGTGTTC TC     TCCAGG
                                    _  CGCC__
GAM890  LOC51162  3' GGGCTGGGATCTTCTCTGTGA  32521          AAAAATG
                                TCACGGGGAG      GGTCC
                                ||||||||||      |||||
                                AGTGTCTCTT      TCGGG
                                      CTAGGG_
GAM890  LOC51162  3' GGGCTGGGATCTTCTCTGTGA  65819          AAAAATG
                                TCACGGGGAG      GGTCC
                                ||||||||||      |||||
                                AGTGTCTCTT      TCGGG
                                      CTAGGG_
GAM890  LOC51270  5' AGAATTGTTTTTCTTCTCTGG  60010     C         TG G  C
                                TCA GGGGAGAAAAA  G TC
                                ||| ||||||||||  | ||
                                GGT CTCTTCTTTTT  T AG
                                  _         GT A  AA
GAM890  LOC51725  3' GGGTCAAGATTTTTTTCTTCTG 69866     C          G__ GT
          A                      TCA GGGGAGAAAAAT   G  CC
                                ||| ||||||||||||  |  ||
                                AGT CTTCTTTTTTTA   C  GG
                                  _          GAA TG
GAM890  LOC54505  5' GGAAATCTTTTTGTTCCCTGTG 67839          _    TGGG
          A                      TCACGGGGAG AAAAA    TCC
                                |||||||||| |||||    |||
                                AGTGTCCCTT TTTTT    AGG
                                      G     CTAA
GAM890  LOC56181  5' GGGCTGGTTTTCTCCCCTGTGA 95540      _        A G
                                TCAC GGGGAGAAAA T GGTCC
                                |||| |||||||||| | |||||
                                AGTG CCCCTCTTTT G TCGGG
                                  T         _ G
GAM890  LOC56270  3' GGGTCCATGCAGTTCCCGCTGG 39021     _     GAAAA    GT
                                TCA CGGGGA     ATGG  CC
                                ||| ||||||     ||||  ||
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                                GGT GCCCTT    TACC  GG
                                  C     GACG_   TG
GAM890  LOC56920  3' GGGCCTTGTGGTTTCTCTGT  39390        AAAAT
                                ACGGGGAGA    GGGTCC
                                |||||||||    ||||||
                                TGTCTCTTT    TCCGGG
                                     GGTGT
GAM890  LOC56996  3' GGGCCAGGCCTCCTCTGTGA  39649      _   AAAAATG
                                TCACGG GGAG      GGTCC
                                |||||| ||||      |||||
                                AGTGTC CCTC      CCGGG
                                   T   CGGA___
GAM890  LOC57107  3' GGAATAGTCTGTTTTTCTTTCC 39839   C  GG        ____
           TGA                    A GG  AGAAAAATGGG    TCC
                                | ||  ||||||||||    |||
                                T CC  TCTTTTTGTCT    AGG
                                _ TT         GATA
GAM890  LOC57826  3' CAGTAACATTTTCCTTTCTGTG 41017      GG  A     GGTCC
           A                     TCACGG  AG AAAATG
                                ||||||  || ||||||
                                AGTGTC  TC TTTTAC
                                   TT  C     AATGACG
GAM890  LOC58512  3' GGGCCCGTCACACTCTCGTGG  64659       G  AAAA
                                TCACGGG AG    ATGGGTCC
                                ||||||| ||    ||||||||
                                GGTGCTC TC    TGCCCGGG
                                    _ ACAC
GAM890  LOC64150  5' GGATCTGTTGCTGTTTCTTG   67284       AAA_
                                CGGGGAG    AATGGGTCC
                                |||||||    |||||||||
                                GTTCTTT    TTGTCTAGG
                                    GTCG
GAM890  LOC64150  3' GGACCCAATAAACCTTTGTGA  67283        AGAAAAA
                                TCACGGGG      TGGGTCC
                                ||||||||      |||||||
                                AGTGTTTC      ACCCAGG
                                     CAAATA_
GAM890  LOC84549  3' GGATATGAATTTTTTTTTCCTG 50702   _         TGG___
           CTGG                    A CGGGGAGAAAAA     GTCC
                                | ||||||||||||     ||||
                                T GTCCTTTTTTTT     TAGG
                                 C          TAAGTA
GAM890  LOC89135  3' GGGCTGCTCTTCCCCGTGG    60317        AAAAATG
                                TCACGGGGAG      GGTCC
                                ||||||||||      |||||
                                GGTGCCCCTT      TCGGG
                                     CTCG___
GAM890  LOC90019  5' GGTCCCAGGCTCTTGTGG    56768       G  AAAAA   T
                                TCACGGG AG    TGGG CC
                                ||||||| ||    |||| ||
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                                GGTGTTC TC    ACCC GG
                                   _ GG___    T
GAM890  LOC90120  5' GACCCACCCTCCCCGT     61535        AAAAA
                                ACGGGGAG    TGGGTC
                                ||||||||    ||||||
                                TGCCCCTC    ACCCAG
                                   CC___
GAM890  LOC90288  3' GGCTGCTTTCCCTCTGA     62100     C      AAAATG
                                TCA GGGGAGA     GGTC
                                ||| |||||||     ||||
                                AGT TCCCTTT     TCGG
                                  C      CG____
GAM890  LOC90408  5' TTCATTTTTTTCTTTGAGA    62672    A
                                TC CGGGGAGAAAAATGGG
                                || ||||||||||||||||
                                AG GTTTCTTTTTTTACTT
                                 A
GAM890  LOC90410  5' GGACTTTATTCTTTCCTGA    62676     C  GG    AAAT
                                TCA GG  AGAA    GGGTCC
                                ||| ||  ||||    ||||||
                                AGT CC  TCTT    TTCAGG
                                  _  TT    AT__
GAM890  LOC90499  5' GGGCTGGTTTCTCCTCTTGG   63066     C       AA  G
                                TCA GGGGAGAA  AT GGTCC
                                ||| ||||||||  || |||||
                                GGT CTCCTCTT  TG TCGGG
                                  T       __  G
GAM890  LOC90529  3' GGGCTGCGCTTTTCCCTG     63163         AAATG
                                CGGGGAGAA     GGTCC
                                |||||||||     |||||
                                GTCCCTTTT     TCGGG
                                     CGCG_
GAM890  LOC90625  3' GGGTCCTCCTGTTTCTCCCCTG 63612      _        AAT__  GT
           TGG                    CAC GGGGAGAAA     GG  CC
                                ||| |||||||||     ||  ||
                                GTG CCCCTCTTT     CC  GG
                                  T       GTCCT  TG
GAM890  LOC90906  3' GGGCCTATTGAACTCTG      64308       AGAAA
                                CGGGG     AATGGGTCC
                                |||||     |||||||||
                                GTCTC     TTATCCGGG
                                   AAG__
GAM890  LOC91040  3' CCTTTTTCTTCCTGT       64715            T
                                ACGGGGAGAAAAA GG
                                |||||||||||| ||
                                TGTCCTTCTTTTT CC
                                             _
GAM890  LOC91050  3' GGGCCTGTTGAGCACCTTCTGA 64747     CG   AGAAA
                                TCA  GGG     AATGGGTCC
                                |||  |||     |||||||||
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                              AGT  TCC    TTGTCCGGG
                                CT   ACGAG
GAM890  LOC91450 3' GGACTTGTTTGCTGCTCTGT   66074       AGAA   TG
                              ACGGGG   AAA  GGTCC
                              ||||||   |||  |||||
                              TGTCTC   TTT  TCAGG
                                 GTCG   GT
GAM890  LOC91660 5' TCATTTTTTTTCCTGTG     66870
                              CACGGGGAGAAAAATGG
                              ||||||||||||||||
                              GTGTCCTTTTTTTTACT

GAM890  LOC91893 3' GGCTAATTTTTTTTTTTGT    67461            G
                              ACGGGGAGAAAAAT GGTC
                              |||||||||||||| ||||
                              TGTTTTTTTTTTTA TCGG
                                       A
GAM890  LOC91917 3' GACCTGTGCCCACGTGG     67529      _   AGAAAA
                              TCACG GGG     ATGGGTC
                              ||||| |||     |||||||
                              GGTGC CCC     TGTCCAG
                                 A   G_____
GAM890  LOC92078 5' GGGCCTGTCCTTCTGCCTGTGA 67986       G    AA
                              TCACGGG AGAA  ATGGGTCC
                              ||||||| ||||  ||||||||
                              AGTGTCC TCTT  TGTCCGGG
                                   G    CC
GAM890  LOC92080 5' GGACTGGCCTCTCCCCGTG    68053         AAAATG
                              CACGGGGAGA     GGTCC
                              ||||||||||     |||||
                              GTGCCCCTCT     TCAGG
                                    CCGG__
GAM890  LOC92379 3' GGGCTCACTCTCTCTTTGT    69149         AAAA
                              ACGGGGAGA    TGGGTCC
                              |||||||||    |||||||
                              TGTTTCTCT    ACTCGGG
                                    CTC_
GAM890  LOC92714 3' GGGCCTCGTGCCTTCTCTCTTG 70376     C       AA_  _
           G                   TCA GGGGAGAA   ATG GGTCC
                              ||| ||||||||   ||| |||||
                              GGT TCTCTCTT   TGC CCGGG
                                _       CCG   T
GAM890  LOC93052 5' GGGCTGGGGTTTCCCTGGA    71265    A       AAAATG
                              TC CGGGGAGA     GGTCC
                              || |||||||      |||||
                              AG GTCCCTTT     TCGGG
                                _       GGGG__
GAM890  LOC93052 5' GGACTGTTCATTCCTGTGG    71264          _  AAATG
                              TCACGGGGA GAA    GGTCC
                              ||||||||| |||    |||||
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                                GGTGTCCTT CTT    TCAGG
                                     A  G____
GAM890  LOC93166 3' GGACTTATTTTGTCCTGT   71625      AGA
                                ACGGGG  AAAATGGGTCC
                                ||||||  ||||||||||
                                TGTCCT  TTTTATTCAGG
                                   G__
GAM890  LOC93259 5' GGACAGAGCTTTTTCCTTG  71822        AATGG
                                CGGGGAGAAA   GTCC
                                ||||||||||   ||||
                                GTTCCTTTTT   CAGG
                                     CGAGA
GAM890  LOC93444 3' GGACCCATGGCTCTCTGTG  72388        AAAA
                                CACGGGGAG   ATGGGTCC
                                |||||||||   ||||||||
                                GTGTCTCTC   TACCCAGG
                                     GG__
GAM890  LOC93512 3' GGGCTGTTTTCTCACTGTGA 72461      G     ATG
                                TCACGG GAGAAAA  GGTCC
                                |||||| |||||||  |||||
                                AGTGTC CTCTTTT  TCGGG
                                   A     G__
GAM890  LOC95633 3' GGAGCCCTCTCTTCCTGTGG  59872         AAAAT  _
                                TCACGGGGAGA   GGG TCC
                                ||||||||||    ||| |||
                                GGTGTCCTTCT   CCC AGG
                                     CT___  G
GAM891  ASPH    3' CATCATTTTGAAAGG     50616     TA
                                CCTT  TCAGGATGATG
                                ||||  ||||||||||
                                GGAA  AGTTTTACTAC
                                   __
GAM891  ASPH    3' CATCATTTTGAAAGG     50629     TA
                                CCTT  TCAGGATGATG
                                ||||  ||||||||||
                                GGAA  AGTTTTACTAC
                                   __
GAM891  DDX6    5' CTGCATTGCAATAAAGG    15287       CAGGAT
                                CCTTTAT    GATGCAG
                                |||||||    |||||||
                                GGAAATA    TTACGTC
                                   ACG___
GAM891  TRIP15   3' CTGCAGTGTAGTAAAGGTTT  14893        CAGGATGA
                                AAACCTTTAT      TGCAG
                                ||||||||||      |||||
                                TTTGGAAATG      ACGTC
                                     ATGTG___
GAM891  FLJ13593 3' CAGACCTGGCAAAGGTTT   45503       AT   A_
                                AAACCTTT  CAGG  TG
                                ||||||||  ||||  ||
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                                TTTGGAAA GTCC AC
                                    CG  AG
GAM891  FLJ21988 3' CTGCATCATCCCCCAGCCAGGT 42554   A   TTATCA_
           CC                    A ACCT     GGATGATGCAG
                                | ||||     ||||||||||
                                C TGGA     CCTACTACGTC
                                 C  CCGACCC
GAM891  HIRIP5   5' CTGCATCAGTTTGTACAAAG  31653    AT_   A
                                CTTT  CAGG TGATGCAG
                                ||||  |||| ||||||||
                                GAAA  GTTT ACTACGTC
                                  CAT  G
GAM891  KIAA0547 3' TGCATCATCCCAGGTTT    28917      TTATCA
                                AAACCT    GGATGATGCA
                                ||||||    ||||||||||
                                TTTGGA    CCTACTACGT
                                  C_____
GAM891  KIAA1223 3' CTGCAGTTCCCTGATAAA   71145       ATGA
                                TTTATCAGG  TGCAG
                                |||||||||  |||||
                                AAATAGTCC  ACGTC
                                    CTTG
GAM891  KIAA1951 3' CTGCATCACCCTGGTG     73759       A
                                TATCAGG TGATGCAG
                                ||||||| ||||||||
                                GTGGTCC ACTACGTC
                                   C
GAM891  PFDN1    3' CTGCATCACCCTGAGCCCCATT 10511     CCTTTA   A
           TG                   CAAA    TCAGG TGATGCAG
                                ||||    ||||| ||||||||
                                GTTT    AGTCC ACTACGTC
                                  ACCCCG   C
GAM891  SLC22A6  3' CATCATTAAAAGGTTTG    16570       ATCAG
                                CAAACCTTT   GATGATG
                                |||||||||   |||||||
                                GTTTGGAAA   TTACTAC
                                    A____
GAM891  LOC90835 3' CATTTTCCCCAATAAAGGTCTG 64127   A     CA_  T
                                CA ACCTTTAT  GGA GATG
                                || ||||||||  ||| ||||
                                GT TGGAAATA  CCT TTAC
                                 C      ACC  T
GAM891  LOC92218 3' CTGCACTTTCTTGATAAATATT 68505    CC       TGA
           TG                   CAAA  TTTATCAGGA  TGCAG
                                ||||  ||||||||||  |||||
                                GTTT  AAATAGTTCT  ACGTC
                                  AT       TTC
GAM892  ARF3     3' GTTTCCAGGCCCTCAGACCAT  8006    C  GA  AA
                                GTG TT  AG  CCTGGAAAC
                                ||| ||  ||  |||||||||
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                                TAC AG  TC  GGACCTTTG
                                  C  AC  CC
GAM892  BTG2    3' CCAGGTTCTCCTCCCCAC   22211    CTT __
                                GTG  GA  AGAACCTGG
                                |||  ||  |||||||||
                                CAC  CT  TCTTGGACC
                                  CC_  CC
GAM892  CALB2   3' TTCCAGGTTCCATCCAC    8212     CT  AA
                                GTG  TG  GAACCTGGAA
                                |||  ||  ||||||||||
                                CAC  AC  CTTGGACCTT
                                  CT  __
GAM892  CNN2    3' TCCGCCTCCCCAAGCGCTGA  15178        AA  ACC
                                TCAGTGCTTG  GA  TGGA
                                ||||||||||  ||  ||||
                                AGTCGCGAAC  CT  GCCT
                                      CC  CC_
GAM892  CNTN2   3' TCTGCTCTCCCAGCACTGA  17413       TGA  ACC
                                TCAGTGCT  AGA  TGGA
                                ||||||||  |||  ||||
                                AGTCACGA  TCT  GTCT
                                    CCC  C__
GAM892  DMPK    5' TTCCCCCTACTCTAGCACTGA 15327       T  AGAACCT
                                TCAGTGCT GA     GGAA
                                |||||||| ||     ||||
                                AGTCACGA CT     CCTT
                                    T  CATCCC_
GAM892  EMX2    3' CAAGTTTTCAAGCACTGA   87564          ACC
                                TCAGTGCTTGAAGA  TG
                                ||||||||||||||  ||
                                AGTCACGAACTTTT  AC
                                       GA_
GAM892  FBXW1B  3' CCTAACTCTTCAAGTACCGA  53337   A       ACCT
                                TC GTGCTTGAAGA   GG
                                || ||||||||||   ||
                                AG CATGAACTTCT   CC
                                 C        CAAT
GAM892  FBXW1B  3' CCTAACTCTTCAAGTACCGA  24522   A       ACCT
                                TC GTGCTTGAAGA   GG
                                || ||||||||||   ||
                                AG CATGAACTTCT   CC
                                 C        CAAT
GAM892  FBXW1B  3' CCTAACTCTTCAAGTACCGA  53326   A       ACCT
                                TC GTGCTTGAAGA   GG
                                || ||||||||||   ||
                                AG CATGAACTTCT   CC
                                 C        CAAT
GAM892  FGF2    3' TTCATTTCTTCAACACCGA   8876    A  C     CC
                                TC GTG TTGAAGAA  TGGA
                                || ||| ||||||||  ||||
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                                AG CAC AACTTCTT  ACTT
                                 C  _       T_
GAM892  FTSJ2    3'  TTCACGCATTCTTCAAGCA   25437          CC  _
                                TGCTTGAAGAA  TG GAA
                                ||||||||||  || |||
                                ACGAACTTCTT  GC CTT
                                      AC  A
GAM892  GEM      3'  TTTCCAGGAAAAGCCTGA    17930      T   GAAGAA
                                TCAG GCTT     CCTGGAAA
                                |||| ||||     ||||||||
                                AGTC CGAA     GGACCTTT
                                  _   AA____
GAM892  LGALS3BP 3'  GTTTCCAGGTGGTAAGCAC   69320        AAGA
                                GTGCTTG    ACCTGGAAAC
                                |||||||    ||||||||||
                                CACGAAT    TGGACCTTTG
                                    GG__
GAM892  MAN2C1   5'  TCCAGGTTCTTTGGCCA     72921    C TG
                                TG T  AAGAACCTGGA
                                || |  ||||||||||
                                AC G  TTCTTGGACCT
                                 C GT
GAM892  MPP3     3'  TTCCCCTGTCTTCAAGCACT   8640           ACCT
                                AGTGCTTGAAGA   GGAA
                                ||||||||||   ||||
                                TCACGAACTTCT   CCTT
                                      GTCC
GAM892  NEDD4    3'  TTCCTTCTTCAAACATT     70013      C       CCT
                                AGTG TTGAAGAA   GGAA
                                |||| ||||||||   ||||
                                TTAC AACTTCTT   CCTT
                                  A       ___
GAM892  OTOF     5'  TCCAGGTTCTGAGAAC      16646    G   GA
                                GT CTT  AGAACCTGGA
                                || |||  ||||||||||
                                CA GAG  TCTTGGACCT
                                 A  __
GAM892  PKD2L2   3'  TCTCTGTACTCCTCAAGCACTG 26896          A  __  CT
           G                     TCAGTGCTTGA GA  AC  GGA
                                ||||||||||| ||  ||  |||
                                GGTCACGAACT CT  TG  TCT
                                      C  CA  TC
GAM892  PNOC     3'  TTCCTTCTTCCCCAAGGCACTG 20641         ____     CCT
           A                     TCAGTGCTT   GAAGAA   GGAA
                                |||||||||   ||||||  ||||
                                AGTCACGGA   CTTCTT   CCTT
                                     ACCC     ___
GAM892  PSEN1    3'  TTCTTCTTCTCAAGCACTGA   23629          A   CCT
                                TCAGTGCTTGA GAA   GGAA
                                |||||||||| |||   ||||
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                                AGTCACGAACT CTT   TCTT
                                      _  CT_
GAM892  PSEN1   3'  TTCTTCTTCTCAAGCACTGA  3427          A  CCT
                                TCAGTGCTTGA GAA   GGAA
                                |||||||||| |||   ||||
                                AGTCACGAACT CTT   TCTT
                                      _  CT_
GAM892  RAD52   3'  TCCAAACTTATAGCGCTGA   56199       TG  AACC
                                TCAGTGCT  AAG   TGGA
                                |||||||| |||   ||||
                                AGTCGCGA  TTC   ACCT
                                    TA  AA__
GAM892  RAD52   3'  TCCAAACTTATAGCGCTGA   56216       TG  AACC
                                TCAGTGCT  AAG   TGGA
                                |||||||| |||   ||||
                                AGTCGCGA  TTC   ACCT
                                    TA  AA__
GAM892  RAD52   3'  TCCAAACTTATAGCGCTGA   56208       TG  AACC
                                TCAGTGCT  AAG   TGGA
                                |||||||| |||   ||||
                                AGTCGCGA  TTC   ACCT
                                    TA  AA__
GAM892  RS1     3'  TTTCCAGGCCCCTTCCTGG   4399     TGCTT   AA_
                                TCAG    GAAG  CCTGGAAA
                                ||||    ||||  ||||||||
                                GGTC    CTTC  GGACCTTT
                                  _____   CCC
GAM892  RXRB    3'  CTAGGGCTCTCCAAGCACT   41760       A  A_
                                AGTGCTTG AGA  CCTGG
                                |||||||| |||  |||||
                                TCACGAAC TCT  GGATC
                                    C  CG
GAM892  SLC12A7  3'  GTTTCTGTACCTCAAGGCACTG 21708        GA  AACCT
           A                     TCAGTGCTT  AG    GGAAAC
                                |||||||||  ||    ||||||
                                AGTCACGGA  TC    TCTTTG
                                     AC  CATG_
GAM892  SLC7A8   3'  CCAAGCCCTTCAGGCCTGA   24277     T      AACC
                                TCAG GCTTGAAG   TGG
                                |||| ||||||||   |||
                                AGTC CGGACTTC   ACC
                                  _      CCGA
GAM892  SNRPN    5'  TTCCAGGCTGAACTGA     42995     GCTTGA  AA
                                TCAGT    AG  CCTGGAA
                                |||||    ||  |||||||
                                AGTCA    TC  GGACCTT
                                  AG____  __
GAM892  SNRPN    5'  TTCCAGGCTGAACTGA     43001     GCTTGA  AA
                                TCAGT    AG  CCTGGAA
                                |||||    ||  |||||||
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                              AGTCA     TC  GGACCTT
                                AG____  __
GAM892  SNRPN    5'  TTCCAGGCTGAACTGA      43009      GCTTGA  AA
                              TCAGT     AG  CCTGGAA
                              |||||     ||  |||||||
                              AGTCA     TC  GGACCTT
                                AG____  __
GAM892  SNRPN    5'  TTCCAGGCTGAACTGA      43016      GCTTGA  AA
                              TCAGT     AG  CCTGGAA
                              |||||     ||  |||||||
                              AGTCA     TC  GGACCTT
                                AG____  __
GAM892  SYN3     3'  TCCAGGTTCCTCAAAAC     56094    GC    A
                              GT  TTGA GAACCTGGA
                              ||  |||| |||||||||
                              CA  AACT CTTGGACCT
                               A_   C
GAM892  SYN3     3'  TCCAGGTTCCTCAAAAC     13019    GC    A
                              GT  TTGA GAACCTGGA
                              ||  |||| |||||||||
                              CA  AACT CTTGGACCT
                               A_   C
GAM892  SYN3     3'  TCCAGGTTCCTCAAAAC     56098    GC    A
                              GT  TTGA GAACCTGGA
                              ||  |||| |||||||||
                              CA  AACT CTTGGACCT
                               A_   C
GAM892  TEC      3'  CCAGATTCCCAAGCAC      12216       AA   C
                              GTGCTTG  GAA CTGG
                              |||||||  ||| ||||
                              CACGAAC  CTT GACC
                                  C_   A
GAM892  TNFSF12  3'  CCACTTCAGGCACT        13744          AACC
                              AGTGCTTGAAG   TGG
                              ||||||||||    |||
                              TCACGGACTTC   ACC
                                            ____
GAM892  VANGL2   3'  TCCAACTCTCTAAGCACT    71655        A   ACC
                              AGTGCTTG AGA   TGGA
                              |||||||| |||   ||||
                              TCACGAAT TCT   ACCT
                                  C   CA_
GAM892  ZNF146   5'  TCCAGGAAAGACTGA       23088      G   GAAGAA
                              TCAGT CTT     CCTGGA
                              ||||| |||     ||||||
                              AGTCA GAA     GGACCT
                                _   A_____
GAM892  ZNF35    3'  TCCATGGCCAAGCACT       12781        AAGAA  _
                              AGTGCTTG    CC TGGA
                              ||||||||    || ||||
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                                TCACGAAC    GG ACCT
                                    C____  T
GAM892  Apg4B    3'  CCAGCCCCCCAAGCATTGA   25284         AAGAAC
                                TCAGTGCTTG     CTGG
                                ||||||||||     ||||
                                AGTTACGAAC     GACC
                                     CCCCC_
GAM892  APOARGC  3'  TTCCAAACAAGCACTGA     44422         AAGAACC
                                TCAGTGCTTG     TGGAA
                                ||||||||||     |||||
                                AGTCACGAAC     ACCTT
                                     AA_____
GAM892  C20orf110 3'  GTTTCCAGGCCTCACAGC    79549    _   AGAA
                                GCT TGA    CCTGGAAAC
                                ||| |||    |||||||||
                                CGA ACT    GGACCTTTG
                                  C   CC__
GAM892  CYYR1    3'  TTCCTTGATCTTTAAGCACTGA 53676           ACCT
                                TCAGTGCTTGAAGA    GGAA
                                ||||||||||||||    ||||
                                AGTCACGAATTTCT    CCTT
                                      AGTT
GAM892  EPN2     3'  TCCTCCAAAGCACTGA      30329        GAA  ACCT
                                TCAGTGCTT   GA    GGA
                                |||||||||   ||    |||
                                AGTCACGAA   CT    CCT
                                     AC_  _____
GAM892  FLJ10261  3'  TCTGAAATTTCTCAAGCAC   35955       AG  CC_
                                GTGCTTGA  AA   TGGA
                                ||||||||  ||   ||||
                                CACGAACT  TT   GTCT
                                    CT  AAA
GAM892  FLJ10815  3'  TTCCAAAGGTAGCACTGA    36698       TGAAGA   __
                                TCAGTGCT     ACCT  GGAA
                                ||||||||     ||||  ||||
                                AGTCACGA     TGGA  CCTT
                                     _______    AA
GAM892  FLJ11117  3'  TTCCAGGTCCCTCACACT    37075     CT   AGA
                                AGTG  TGA   ACCTGGAA
                                ||||  |||   ||||||||
                                TCAC  ACT   TGGACCTT
                                   __   CCC
GAM892  FLJ12891  3'  TCCAGGTTCCAGGTAC      46348       AA
                                GTGCTTG  GAACCTGGA
                                |||||||  |||||||||
                                CATGGAC  CTTGGACCT
                                     __
GAM892  FLJ14640  5'  GTTTCCAGGCTCCCCTCCTGCA 51480      TT  A__  A
             C                   GTGC  GA   GA CCTGGAAAC
                                 ||||  ||   || |||||||||
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                                CACG  CT   CT GGACCTTTG
                                  TC  CCC  C
GAM892  FLJ23309 3' TTCCTTCCTCAGAGCACTGA  46065        _  A  CCT
                                TCAGTGCT TGA GAA  GGAA
                                |||||||| ||| |||  ||||
                                AGTCACGA ACT CTT  CCTT
                                     G  C  ___
GAM892  HCDI     3' TTCCAGGTTAGGCACTG     39494        AAGA
                                CAGTGCTTG   ACCTGGAA
                                |||||||||   ||||||||
                                GTCACGGAT   TGGACCTT
                                     ____
GAM892  HEMK     3' CCAGGTAGCACTGG       32429        TGAAGA
                                TCAGTGCT    ACCTGG
                                ||||||||    ||||||
                                GGTCACGA    TGGACC
                                     _______
GAM892  HEMK     3' TCCACTTCTTCAAGC      32439        CC
                                GCTTGAAGAA  TGGA
                                ||||||||||  ||||
                                CGAACTTCTT  ACCT
                                     C_
GAM892  HPCAL4   3' CCACATTTTCAAGCACT    32733          ACC
                                AGTGCTTGAAGA  TGG
                                ||||||||||||  |||
                                TCACGAACTTTT  ACC
                                     AC_
GAM892  KIAA0478 3' TCAGATCCTTTCAAGCACTGA 29557          AAC_
                                TCAGTGCTTGAAG   CTGG
                                ||||||||||||    ||||
                                AGTCACGAACTTT   GACT
                                     CCTA
GAM892  KIAA1450 3' TTCCAAGTTTAAGCAT     65829        AGA  C
                                GTGCTTGA  AC TGGAA
                                ||||||||  || |||||
                                TACGAATT  TG ACCTT
                                     ___  A
GAM892  KIAA1613 3' TCCAGGCTGATGCACTGG   64819       TTGA  AA
                                TCAGTGC   AG  CCTGGA
                                |||||||   ||  ||||||
                                GGTCACG   TC  GGACCT
                                     TAG_  __
GAM892  KIAA1831 3' TCTTACCTCCAAGCACTGA  63786         A  AACCT
                                TCAGTGCTTG AG    GGA
                                |||||||||| ||    |||
                                AGTCACGAAC TC    TCT
                                     C  CAT__
GAM892  LCE      3' TCCATCTCCAAGCACTG    44030        A   ACC
                                CAGTGCTTG AGA   TGGA
                                ||||||||| |||   ||||
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                                GTCACGAAC TCT   ACCT
                                     C  ___
GAM892  MFN1     3'  GTTTCTACCTTCAAGCAATGA  35545     G       AACC
                                TCA TGCTTGAAG    TGGAAAC
                                ||| |||||||||    |||||||
                                AGT ACGAACTTC    ATCTTTG
                                  A       C___
GAM892  MGC2541  5'  CCTTACTCTTCAAGCCCTGA   54748      T       ACCT
                                TCAG GCTTGAAGA    GG
                                |||| |||||||||    ||
                                AGTC CGAACTTCT    CC
                                  C       CATT
GAM892  MGC4293  5'  CCAGGTTTAGCCTGA       48522      T   TGAA
                                TCAG GCT    GAACCTGG
                                |||| |||    ||||||||
                                AGTC CGA    TTTGGACC
                                  _  ____
GAM892  MIC2L1   3'  TCCAGGAGCACTGA        48828         TGAAGAA     A
                                TCAGTGCT      CCTGG A
                                ||||||||      ||||| |
                                AGTCACGA      GGACC T
                                     ________    C
GAM892  NYD-SP11 3'  TTCCCAAGTGGTCTTCAAGCAC 49216           A  T____
                                GTGCTTGAAGA CC     GGAA
                                |||||||||| ||     ||||
                                CACGAACTTCT GG     CCTT
                                      _  TGAAC
GAM892  phorbolin-1 5'  TTCCAGGTTGCTCTGA      88785      T  TTGAAG
                                TCAG GC      AACCTGGAA
                                |||| ||      |||||||||
                                AGTC CG      TTGGACCTT
                                  T  _______
GAM892  PRO2266  3'  TTCTAATCTTCAAGCAT     37586           ACC
                                GTGCTTGAAGA   TGGAA
                                ||||||||||   |||||
                                TACGAACTTCT   ATCTT
                                      A__
GAM892  PTP4A1   5'  TTCATACTCAAAGCACTGA    12945         GA  AACC
                                TCAGTGCTT  AG    TGGA
                                |||||||||  ||    ||||
                                AGTCACGAA  TC    ACTT
                                     AC  AT__
GAM892  SSH2     3'  GTTTCCAGACCTGAGGCATCGA 62212     A     GA  AAC
                                TC GTGCTT  AG   CTGGAAAC
                                || ||||||  ||   ||||||||
                                AG TACGGA  TC   GACCTTTG
                                 C     G_  CA_
GAM892  LOC127534 5'  TCCAGGTTCCCCCAGGCCT    75441    T    AA_
                                AG GCTTG   GAACCTGGA
                                || |||||   |||||||||
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                                TC CGGAC   CTTGGACCT
                                 _    CCC
GAM892   LOC148824 3'  GTTTCCAGGCATACAACTACT  84227     C   AAGAA
                                AGTG TTG    CCTGGAAAC
                                |||| |||    |||||||||
                                TCAT AAC    GGACCTTTG
                                  C   ATAC_
GAM892   LOC150174 3'  TTTCCAGGTCCCATCCA    79613    CT  AA  A
                                TG  TG  GA CCTGGAAA
                                ||  ||  || ||||||||
                                AC  AC  CT GGACCTTT
                                 CT  C_  _
GAM892   LOC150271 5'  TTTCCAGGTTCTTCAGGAC   84959    G
                                GT CTTGAAGAACCTGGAAA
                                || ||||||||||||||||
                                CA GGACTTCTTGGACCTTT
                                 _
GAM892   LOC150935 5'  TTCCAGGTCCCCTTCTAGAC   80040    G  T   A__
                                GT CT GAAG   ACCTGGAA
                                || || ||||   ||||||||
                                CA GA CTTC   TGGACCTT
                                 _ T   CCC
GAM892   LOC151429 3'  CCAGGTTCTCAGGCCTGG    85348     T     A
                                TCAG GCTTGA GAACCTGG
                                |||| |||||| ||||||||
                                GGTC CGGACT CTTGGACC
                                  _    _
GAM892   LOC151742 3'  TCTTGATTTCTCCAAGCACT   57672        A   CCT_
                                AGTGCTTG AGAA   GGA
                                |||||||| ||||   |||
                                TCACGAAC TCTT   TCT
                                    C   TAGT
GAM892   LOC152426 5'  CCAGAGGCCCTTCAAGCCTGA  85712     T      AA  __
                                TCAG GCTTGAAG  CCT  GG
                                |||| ||||||||  |||  ||
                                AGTC CGAACTTC  GGA  CC
                                  _      CC   GA
GAM892   LOC158476 3'  TCCAGGTTCAGTACCTGA    86854     _   TGAA
                                TCAG TGCT   GAACCTGGA
                                |||| ||||   |||||||||
                                AGTC ATGA   CTTGGACCT
                                  C   _____
GAM892   LOC158581 5'  TTCCAGGTTCAGGACAC     86872    _   AGA
                                GTG CTTGA   ACCTGGAA
                                ||| |||||   ||||||||
                                CAC GGACT   TGGACCTT
                                 A    ____
GAM892   LOC196484 3'  CTGGATGCTCTTCAAGGACTGA 62872      G      AC__ TG
                                TCAGT CTTGAAGA   C  G
                                ||||| ||||||||   |  |
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                                AGTCA GAACTTCT   G  C
                                  G      CGTA GT
GAM892  LOC196812 3' GTTTCCAGACTCTGTTAC   89576    CTTGA  AC
                                GTG    AGA  CTGGAAAC
                                |||    |||  ||||||||
                                CAT    TCT  GACCTTTG
                                  TG___   CA
GAM892  LOC200312 3' CCTTTGGTCCTCAAGCACTGG  89993         A  A  T__
                                TCAGTGCTTGA GA CC   GG
                                |||||||||||| || ||   ||
                                GGTCACGAACT CT GG   CC
                                       C  _  TTT
GAM892  LOC203436 5' TTCCAGGTTCCACCAC     90701     CT  AA
                                GTG  TG  GAACCTGGAA
                                |||  ||  ||||||||||
                                CAC  AC  CTTGGACCTT
                                  C_  __
GAM892  LOC219412 5' TTCCAGGGCAAGCACTG     94344        AAGAA
                                CAGTGCTTG    CCTGGAA
                                |||||||||    |||||||
                                GTCACGAAC    GGACCTT
                                     G____
GAM892  LOC219673 3' TCTCAGCCTCCCAAAGCACTGA 93047        GAA  AC  _
                                TCAGTGCTT   GA  CTG GA
                                |||||||||   ||  ||| ||
                                AGTCACGAA   CT  GAC CT
                                      ACC  CC   T
GAM892  LOC220073 3' CTGGATGCTCTTCAAGTACTGA 93431           AC__ TG
                                TCAGTGCTTGAAGA   C  G
                                ||||||||||||||   |  |
                                AGTCATGAACTTCT   G  C
                                        CGTA GT
GAM892  LOC221421 3' TCCTGTCCCCAGCACTGA    92282        T AA  ACCT
                                TCAGTGCT G  GA   GGA
                                ||||||||  |  ||   |||
                                AGTCACGA C  CT   CCT
                                     _ CC  GT__
GAM892  LOC221773 3' CCAGGCTGGAGAGCACTG    91041        GA_  AA
                                CAGTGCTT   AG  CCTGG
                                ||||||||   ||  |||||
                                GTCACGAG   TC  GGACC
                                     AGG  __
GAM892  LOC221935 3' GTTTCTCCGTCTTCAAGAC   92627    G      ACCT
                                GT CTTGAAGA   GGAAAC
                                || ||||||||   ||||||
                                CA GAACTTCT   TCTTTG
                                  _      GCC_
GAM892  LOC255167 3' TCCCTCAGAGCACTGA      97163        GA  AACCT
                                TCAGTGCTT  AG    GGA
                                |||||||||  ||    |||
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                                AGTCACGAG  TC    CCT
                                     AC  _____
GAM892  LOC51629  3'  CCTTTTCCTCAGCACTGA    32059        T  A   CCT
                                TCAGTGCT GA GAA   GG
                                |||||||| || |||   ||
                                AGTCACGA CT CTT   CC
                                     _  C   TT_
GAM892  LOC51644  3'  CCAGTTCTCCAGCACTGA    32136        T  A    C
                                TCAGTGCT GA GAAC TGG
                                |||||||| || |||| |||
                                AGTCACGA CT CTTG ACC
                                     C  _    _
GAM892  LOC51759  3'  CTGGATTTTTCAAGCACT    72813           C TG
                                AGTGCTTGAAGAA C  G
                                |||||||||||| |  |
                                TCACGAACTTTTT G  C
                                       A GT
GAM892  LOC84548  3'  CCGTTTCTCCAAGCACTG    71253         A    CC
                                CAGTGCTTG AGAA  TGG
                                ||||||||| ||||  |||
                                GTCACGAAC TCTT  GCC
                                     C    T_
GAM892  LOC90538  3'  TCCAGGTTCTGGTGACTG    63195      _   TGA
                                CAGT GCT   AGAACCTGGA
                                |||| |||   ||||||||||
                                GTCA TGG   TCTTGGACCT
                                  G  ___
GAM892  LOC90768  5'  CCAGGTTCAAGCAC        63952         AGA
                                GTGCTTGA   ACCTGG
                                ||||||||   ||||||
                                CACGAACT   TGGACC
                                     ___
GAM892  LOC91069  3'  CTGGATGCTCTTCAAGTACTGA 64777             AC__ TG
                                TCAGTGCTTGAAGA    C  G
                                ||||||||||||||    |  |
                                AGTCATGAACTTCT    G  C
                                       CGTA GT
GAM892  LOC93097  5'  TTTCCAGGCAGAGAACACTG   71366       C  GAAGAA
                                CAGTG TT      CCTGGAAA
                                |||||  ||     ||||||||
                                GTCAC AG      GGACCTTT
                                   A  AGAC__
GAM893  ADH1B     3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM893  AHR       3'  ATCTCAGATGTTAAAATAAATG 7875        CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
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                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T _
GAM893  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM893  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                  CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM893  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||  ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM893  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM893  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM893  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM893  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_    CG_
GAM893  CG012    5'  CTCACTCTGAAAGTGAA     83218          CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM893  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM893  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
              G                   CATTTC        GTCTGAGAT
                                ||||||        |||||||||
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                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM893  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA  TCACTGTCTGAGAT
                                |||||||  ||||||||||||||
                                GTAAAGT  AGTGACAGACTCTA
                                   C__
GAM893  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM893  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM893  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM893  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM893  PP35      3'  ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM893  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148        TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM893  SEP15     3'  TCCTACAGTAAGAGTGAAA   14934       C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM893  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA  73941       CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM893  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
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                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM893  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM893  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM893  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA

                                      _
GAM894  GPR44    3'  ACTGAAGGCCTGGCCCACAGCA 16520     CATA  __    TCT
                                TGT   GGC  GGCCT   TCAGT
                                |||   |||  |||||   |||||
                                ACG   CCG  CCGGA   AGTCA
                                  ACAC   GT   ___
GAM894  OTOF     5'  ACTGAAGAACCCCCATGA    16638      A  C  CC
                                TCAT GG GG  TTCTTCAGT
                                |||| || ||  |||||||||
                                AGTA CC CC  AAGAAGTCA
                                  C  _  __
GAM894  PCDH11X  3'  ACTGAAGAAAACCACTAATAAC 52036     C  A  C  CC
          A                      TGT AT GG GG  TTCTTCAGT
                                |||  || || ||  |||||||||
                                ACA TA TC CC  AAGAAGTCA
                                  A  A  A  AA
GAM894  PCDH11X  3'  ACTGAAGAAAACCACTAATAAC 52014     C  A  C  CC
          A                      TGT AT GG GG  TTCTTCAGT
                                |||  || || ||  |||||||||
                                ACA TA TC CC  AAGAAGTCA
                                  A  A  A  AA
GAM894  PCDH11Y  3'  ACTGAAGAAAACCACTAATAAC 52072     C  A  C  CC
          A                      TGT AT GG GG  TTCTTCAGT
                                |||  || || ||  |||||||||
                                ACA TA TC CC  AAGAAGTCA
                                  A  A  A  AA
GAM894  STXBP1   3'  ACTGAAGAAACTGAATAAAACA 12045     CA  GG   CC
                                TGT  TA  CGG  TTCTTCAGT
                                |||  ||  |||  |||||||||
                                ACA  AT  GTC  AAGAAGTCA
                                  AA  AA   A_
GAM894  TMEPAI   3'  CTGAAGAAGCAGTGACA     39446       AGGCG  C
                                TGTCAT    GC TTCTTCAG
                                ||||||    || ||||||||
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                                ACAGTG    CG AAGAAGTC
                                  A____  _
GAM894  VMD2     3'  ACTGAAGAACATGTCCTACAAC 14817    CA   _ GCC
            A                    TGT  TAGG CG   TTCTTCAGT
                                 |||  |||| ||   |||||||||
                                 ACA  ATCC GT   AAGAAGTCA
                                   AC   T  AC_
GAM894  WW45     3'  CTGAAGAAATGTTGACA     41520      TAG   GCC
                                 TGTCA   GCG   TTCTTCAG
                                 |||||   |||   ||||||||
                                 ACAGT   TGT   AAGAAGTC
                                    ___   A__
GAM894  ZNF124   3'  ACTGAAGAAAATCCATATGA   12823      _  CGGCC
                                 TCATA GG    TTCTTCAGT
                                 |||||  ||    |||||||||
                                 AGTAT CC    AAGAAGTCA
                                    A  TAA__
GAM894  DKFZP564O0423 3'  AGAAGGCCACCCATGGCA    91676       A  C
                                 TGTCAT GG GGCCTTCT
                                 |||||| || ||||||||
                                 ACGGTA CC CCGGAAGA
                                    C  A
GAM894  FLJ20139  3'  CTGAAGAAACCATGA      34623      A  CGGCC
                                 TCAT GG    TTCTTCAG
                                 ||||  ||    ||||||||
                                 AGTA CC    AAGAAGTC
                                   _  A____
GAM894  KIAA1411  3'  ACTGAAGAAAGCTCTGTAGCA  40430    TC    GC   C
                                 TG  ATAG  GGC TTCTTCAGT
                                 ||  ||||  ||| |||||||||
                                 AC  TGTC  TCG AAGAAGTCA
                                  GA   __   A
GAM894  MKNK1    5'  ACTGAAGATTGCCACCTACGCA 13478     CA    C   CT
                                 TGT  TAGG GGC  TCTTCAGT
                                 |||  |||| |||  ||||||||
                                 ACG  ATCC CCG  AGAAGTCA
                                   C_   A   TT
GAM894  LOC133634 3'  ACTGAAGAAAAGACCTGTATAC 75102     C_    CGGCC
            A                    TGT  ATAGG    TTCTTCAGT
                                 |||  |||||    |||||||||
                                 ACA  TGTCC    AAGAAGTCA
                                   TA    AGAA_
GAM894  LOC150759 3'  ACTGAAGAAGGAGTGAGCAGAC 80001      ATAG  GG___
            A                    TGTC    GC    CCTTCTTCAGT
                                 ||||    ||    ||||||||||
                                 ACAG    CG    GGAAGAAGTCA
                                   A___  AGTGA
GAM894  LOC151323 3'  ACTGAAGAAGGAGTGAGCAGAC 80213      ATAG  GG___
            A                    TGTC    GC    CCTTCTTCAGT
                                 ||||    ||    ||||||||||
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                                ACAG    CG     GGAAGAAGTCA
                                  A___  AGTGA
GAM894  LOC164295 5'  ACCGAAGAAGGCCTCAGC    82507    ___        A
                                GC   GGCCTTCTTC GT
                                ||   |||||||||| ||
                                CG   CCGGAAGAAG CA
                                 ACT         C
GAM894  LOC200399 3'  ACTGAAGAAGGAGTGAGCAGAC 88804      ATAG  GG___
           A                     TGTC    GC     CCTTCTTCAGT
                                ||||    ||    ||||||||||
                                ACAG    CG     GGAAGAAGTCA
                                  A___  AGTGA
GAM895  D12S2489E 3'  CAAAAGAAGAGAGATCCTAA   23742      TGTTT       C
                                TTAG     GTCTCTCT CTTTTG
                                ||||     |||||||| ||||||
                                AATC     TAGAGAGA GAAAAC
                                  C____       A
GAM895  HMG20A    3'  CAAAAGGAAAGAGAGGTTCTGA 36532      TGTTTG     C
                                TTAG      TCTCT TCCTTTTG
                                ||||      ||||| ||||||||
                                AGTC      AGAGA AGGAAAAC
                                  TTGG__     A
GAM895  PPP2R5E   3'  AGAAAGACAAACACTAA     20720            C
                                TTAGTGTTTGTCT TCT
                                |||||||||||| |||
                                AATCACAAACAGA AGA
                                       A
GAM895  C20orf50  5'  CAAAAGGAAAGAAATGTCAC   70072     TT   C   C
                                GTG  TGT TCT TCCTTTTG
                                |||  ||| ||| ||||||||
                                CAC  GTA AGA AGGAAAAC
                                  T_   A   A
GAM895  C6orf37   3'  CAAAAAAAGAGAGACCTGTCAT 67475       TTT_       CC
           TA                     TAGTG    GTCTCTCT  TTTTG
                                |||||    ||||||||  |||||
                                ATTAC    CAGAGAGA  AAAAC
                                   TGTC       AA
GAM895  DKFZp434B0417 3'  AAAAGGAAAGAAAACA      25379       GTC   C
                                TGTTT   TCT TCCTTTT
                                |||||   ||| |||||||
                                ACAAA   AGA AGGAAAA
                                  ___   A
GAM895  EML4      3'  CAAAAGAAGAGAGATTCCAAGC 38808        ___      C
           A                     TGTTTG   TCTCTCT CTTTTG
                                ||||||   ||||||| ||||||
                                ACGAAC   AGAGAGA GAAAAC
                                   CTT      A
GAM895  FLJ12529  3'  CAAAAGGAAAAAAAACAC    45658       GTCTCTC
                                GTGTTT      TCCTTTTG
                                ||||||      ||||||||
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                                CACAAA      AGGAAAAC
                                   AAAA___
GAM895  KIAA0430  3'  AAAAGAAGAAAGCACTAA    38837        GTCTC   C
                                TTAGTGTTT    TCT CTTTT
                                |||||||||    ||| |||||
                                AATCACGAA    AGA GAAAA
                                     _____  A
GAM895  MGC13040  3'  AGAAGAAAGCAAACAC      51937        T  C   C
                                GTGTTTG CT TCT CT
                                ||||||| || ||| ||
                                CACAAAC GA AGA GA
                                    _ A  A
GAM895  PSK       3'  CAAAAAAAGAAAAAGACAAACA 32360         C__   CC
            C                    GTGTTTGTCT   TCT  TTTTG
                                ||||||||||   |||  |||||
                                CACAAACAGA   AGA  AAAAC
                                      AAA   AA
GAM895  VIT1      3'  GAAAGAGAAAACACTAA     37973         G     C
                                TTAGTGTTT TCTCT TC
                                ||||||||| ||||| ||
                                AATCACAAA AGAGA AG
                                     _    A
GAM896  ADH4      3'  TAAAAAGATTTTTACTGGA    5409         CGT
                                TCCAGTGG   TCTTTTTA
                                ||||||||   ||||||||
                                AGGTCATT   AGAAAAAT
                                     TTT
GAM896  ADRA2B    3'  GGGGGAACACACTAGAG     5465      C    GC
                                CTC AGTG  GTTCTTTT
                                ||| ||||  ||||||||
                                GAG TCAC  CAAGGGGG
                                  A   A_
GAM896  CTBP1     3'  AAAAAGAAAACCTGAAGGAG  67942      AGT_  CG
                                CTCC    GG  TTCTTTTT
                                ||||    ||  ||||||||
                                GAGG    CC  AAGAAAAA
                                   AAGT  AA
GAM896  EGFL5     5'  GTAAAAAGAAAAATATGGGGA 86626     T   GTGGCG
                                TCC CCA     TTCTTTTTAC
                                ||| |||     ||||||||||
                                AGG GGT     AAGAAAAATG
                                  _  ATAAA_
GAM896  ENPP3     3'  TAAAAAGAACAGCAGAGAG   17227     CAGTG  _
                                CTC    GC GTTCTTTTTA
                                |||    || ||||||||||
                                GAG    CG CAAGAAAAAT
                                  AGA__  A
GAM896  F8        3'  TAAAAAAATAAGTCAGGAGGA 3733        AG    GTTC_
                                TCCTCC  TGGC    TTTTTA
                                ||||||  ||||    ||||||
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                                AGGAGG  ACTG    AAAAAT
                                  __    AATAA
GAM896  ID4     3'  AAAAAAAGCCACCGGAGGA   7752        A    GTTC
                                TCCTCC GTGGC    TTTTT
                                |||||| |||||    |||||
                                AGGAGG CACCG    AAAAA
                                   C    AA__
GAM896  PITX1   3'  AAAAAGACGTCGGAG      10596     AGT    T
                                CTCC   GGCGT CTTTTT
                                ||||   ||||| ||||||
                                GAGG   CTGCA GAAAAA
                                  ___    _
GAM896  TDG     3'  AAAAAGATGCTGGAG       12184        GCGT
                                CTCCAGTG    TCTTTTT
                                ||||||||    |||||||
                                GAGGTCGT    AGAAAAA
                                  _____
GAM896  XRCC2   3'  AAAAAGAACAAAGCTGGAGG   18314        GGC
                                CCTCCAGT   GTTCTTTTT
                                ||||||||   |||||||||
                                GGAGGTCG   CAAGAAAAA
                                     AAA
GAM896  ABCA10  5'  AAAAAGAGACCAGTGGA     54406      G   CG
                                TCCA TGG  TTCTTTTT
                                |||| |||  ||||||||
                                AGGT ACC  GAGAAAAA
                                  G   A_
GAM896  ABCC13  3'  AAAAGTTTTCCACTGGGGA   56988     T      CGTT
                                TCC CCAGTGG    CTTTT
                                ||| |||||||    |||||
                                AGG GGTCACC    GAAAA
                                  _      TTTT
GAM896  ARFGAP1 3'  GGAACACCCTGGAAGA      36593    C     T  C
                                TC TCCAG GG GTTCT
                                || ||||| || |||||
                                AG AGGTC CC CAAGG
                                 A    _  A
GAM896  BA526D8.4 5'  TAAAAAAATTCATACTGGAGGG 70385          GCGTTC
                                TCCTCCAGTG     TTTTTA
                                ||||||||||     ||||||
                                GGGAGGTCAT     AAAAAT
                                     ACTTAA
GAM896  DKFZP727M111 5'  AAAAGGAAAAGCCCTGAAG   31402    C   T   G_
                                CT CAG GGC  TTCTTTTT
                                || ||| |||  ||||||||
                                GA GTC CCG  AAGGAAAA
                                 A   _   AA
GAM896  DKFZp761H079 3'  AAAAAGAGCCAATGGA      58727      G    GT
                                TCCA TGGC  TCTTTTT
                                |||| ||||  |||||||
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                                AGGT ACCG  AGAAAAA
                                  A   __
GAM896  FLJ10648  3'  AAAAAGAACAAAGTCCTGGAGG 36377        T  ___
              A                   TCCTCCAG GGC   GTTCTTTTT
                                  |||||||| |||   |||||||||
                                  AGGAGGTC CTG   CAAGAAAAA
                                      _   AAA
GAM896  FLJ20151  3'  AAAGACCCTGGAGGA       34649        T  CGT
                                  TCCTCCAG GG   TCTTT
                                  |||||||| ||   |||||
                                  AGGAGGTC CC   AGAAA
                                      _ ___
GAM896  FLJ20190  5'  AAAGGACACCATTGGAG     34702         C
                                  CTCCAGTGG GTTCTTT
                                  ||||||||| |||||||
                                  GAGGTTACC CAGGAAA
                                       A
GAM896  FLJ20435  3'  TAAAAAGAGCCATCTGGAGGA  35163        _   GT
                                  TCCTCCAG TGGC  TCTTTTTA
                                  |||||||| ||||  ||||||||
                                  AGGAGGTC ACCG  AGAAAAAT
                                       T   __
GAM896  FLJ22477  5'  GACACCATCTGGAGGA      45343        _  C
                                  TCCTCCAG TGG GTT
                                  |||||||| ||| |||
                                  AGGAGGTC ACC CAG
                                       T   A
GAM896  HNRPA3    3'  GTAAAAATCTGTCACAGAAGGA 19256     CCA     TTC
                                  TCCT   GTGGCG   TTTTTAC
                                  ||||   ||||||   |||||||
                                  AGGA   CACTGT   AAAAATG
                                    AGA     CT_
GAM896  KIAA1091  3'  GTAAAAAGAAAACTAGAGGA   69685      CAG   CG
                                  TCCTC   TGG  TTCTTTTTAC
                                  |||||   |||  ||||||||||
                                  AGGAG   ATC  AAGAAAAATG
                                     ___   AA
GAM896  KIAA1546  3'  AAAAAGAAGGTGGGGA      67900       CAGTG  G
                                  TCCTC    GC TTCTTTTT
                                  |||||    || ||||||||
                                  AGGGG    TG AAGAAAAA
                                     _____  G
GAM896  KIAA1956  3'  GTAAAACATAACACTGGAGGA  78439         GC  TCT
                                  TCCTCCAGTG  GT   TTTTAC
                                  ||||||||||  ||   ||||||
                                  AGGAGGTCAC  TA   AAAATG
                                       AA  C__
GAM896  MDS024    3'  AAAAAGAATTGCCAAGGA    41523     AG    _
                                  TCC  TGGCG TTCTTTTT
                                  |||  ||||| ||||||||
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                                AGG  ACCGT AAGAAAAA
                                  A_    T
GAM896  MEGF11   3'  AAAAGGAGACTGGGGA     50576     T    GGCG
                                TCC CCAGT    TTCTTTTT
                                ||| |||||    ||||||||
                                AGG GGTCA    GAGGAAAA
                                  _    _____
GAM896  MGC11082 5'  AAAAAAAAGGCGGAGGG     51098       AGTG  G  C
                                TCCTCC    GC TT TTTTT
                                ||||||    || || |||||
                                GGGAGG    CG AA AAAAA
                                   _____  G  A
GAM896  MGC13105 3'  AAAAAGTCACACTAGAGGA    71477      C    GCGTT
                                TCCTC AGTG     CTTTTT
                                ||||| ||||     ||||||
                                AGGAG TCAC     GAAAAA
                                   A    ACT__
GAM896  RPL13    3'  AAAAAGAGCCAAGGA       78080     AG    GT
                                TCC  TGGC  TCTTTTT
                                |||  ||||  |||||||
                                AGG  ACCG  AGAAAAA
                                  A_   __
GAM896  ShrmL    5'  AGAGCGCCACTGAAGGA     40464      C
                                TCCT CAGTGGCGTTCT
                                |||| ||||||||||||
                                AGGA GTCACCGCGAGA
                                  A
GAM896  SIAT8C   5'  TAAAAAAGCCCCACAGAGGA   31884      CA    C   C
                                TCCTC  GTGG GTT TTTTTA
                                |||||  |||| ||| ||||||
                                AGGAG  CACC CGA AAAAAT
                                   A_    C   _
GAM896  VEST1    5'  AAAAAGATGCACTGGGGA    53679     T     G   T
                                TCC CCAGTG CGT CTTTTT
                                ||| |||||| ||| ||||||
                                AGG GGTCAC GTA GAAAAA
                                  _     _   _
GAM896  ZFD25    5'  AAAAAGAGCCCTGGA       32574      T   GT
                                TCCAG GGC  TCTTTTT
                                ||||| |||  |||||||
                                AGGTC CCG  AGAAAAA
                                  _   __
GAM896  LOC124626 3'  GTAAGACCAAACCACTGGA   74315        CGTTCT
                                TCCAGTGG     TTTTAC
                                ||||||||     ||||||
                                AGGTCACC     AGAATG
                                    AAACC_
GAM896  LOC126302 3'  AAAAAGAAGCAGGAGGA     74486       AGTG  G
                                TCCTCC    GC TTCTTTTT
                                ||||||    || ||||||||
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                                AGGAGG   CG AAGAAAAA
                                   A___  _
GAM896  LOC132332 5'  AAAAAGAAGGCTGGA      76159     GTG  G
                                TCCA   GC TTCTTTTT
                                ||||   || ||||||||
                                AGGT   CG AAGAAAAA
                                  ___  G
GAM896  LOC144577 3'  TAAAAAGAAGCCACAAAGAG   76903    CA_    G
                                CTC   GTGGC TTCTTTTTA
                                |||   ||||| |||||||||
                                GAG   CACCG AAGAAAAAT
                                  AAA    _
GAM896  LOC145078 3'  GTAAAAATCTGCCACAGAAGGA 60292     CCA     TTC
                                TCCT   GTGGCG   TTTTTAC
                                ||||   ||||||   |||||||
                                AGGA   CACCGT   AAAAATG
                                   AGA     CT_
GAM896  LOC145837 5'  AAAAAGAACCAAAGAGGA    83540     CAG   CG
                                TCCTC   TGG  TTCTTTTT
                                |||||   |||  ||||||||
                                AGGAG   ACC  AAGAAAAA
                                   AA_  __
GAM896  LOC148753 3'  AAAAGGAGCACCAGGGA     84207     AG   C
                                TCC  TGG GTTCTTTTT
                                |||  ||| |||||||||
                                AGG  ACC CGAGGAAAA
                                  G_   A
GAM896  LOC148981 3'  GTAAAAATCTGCCACAGAAGGA 84317     CCA     TTC
                                TCCT   GTGGCG   TTTTTAC
                                ||||   ||||||   |||||||
                                AGGA   CACCGT   AAAAATG
                                   AGA     CT_
GAM896  LOC153711 5'  AAAAGCGTCCCGCCAGAGGA   86129      CA    C TT
                                TCCTC  GTGG G  CTTTT
                                |||||  |||| |  |||||
                                AGGAG  CGCC T  GAAAA
                                   AC    C GC
GAM896  LOC154789 5'  GTAAAATCTCAGGCCACTAGAG 81140     C     GTTCT_
                                CTC AGTGGC     TTTTAC
                                ||| ||||||     ||||||
                                GAG TCACCG     AAAATG
                                  A     GACTCT
GAM896  LOC197322 3'  AAAGACTCCACTGGAGGA    89737          C  T
                                TCCTCCAGTGG GT CTTT
                                |||||||||| || ||||
                                AGGAGGTCACC CA GAAA
                                       T  _
GAM896  LOC220988 3'  GTAAAAATCTGCCACAGAAGGA 90848     CCA     TTC
                                TCCT   GTGGCG   TTTTTAC
                                ||||   ||||||   |||||||
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                                AGGA   CACCGT   AAAAATG
                                  AGA     CT_
GAM896  LOC221596 3'  TAAAAACCTCACACTGGAGAGA 91981    _       GCGTTC
                                TC CTCCAGTG     TTTTTA
                                || ||||||||     ||||||
                                AG GAGGTCAC     AAAAAT
                                 A       ACTCC_
GAM896  LOC255190 3'  GTAAAAATCTGCCACAGAAGGA 97689      CCA     TTC
                                TCCT   GTGGCG   TTTTTAC
                                ||||   ||||||  |||||||
                                AGGA   CACCGT   AAAAATG
                                  AGA     CT_
GAM896  LOC91796  3'  AAAAAGAACAAGGCTGGA    67207       GGC
                                TCCAGT   GTTCTTTTT
                                ||||||   |||||||||
                                AGGTCG   CAAGAAAAA
                                   GAA
GAM896  LOC92539  5'  TAAAAAGTGTCACTG       69639         TT
                                CAGTGGCG  CTTTTTA
                                ||||||||  |||||||
                                GTCACTGT  GAAAAAT
                                          __
GAM896  LOC93444  3'  GAACCCACTGGAAGA       72387    C       C
                                TC TCCAGTGG GTTC
                                || |||||||| ||||
                                AG AGGTCACC CAAG
                                 A       _
GAM896  LOC93538  5'  GTAAAGCTTCAGCGACTGAAGG 72562      C    G  GTTCT
            A                    TCCT CAGT GC     TTTTAC
                                ||||| |||| ||     ||||||
                                AGGA GTCA CG     GAAATG
                                  A   G  ACTTC
GAM897  B4GALT1   3'  CAAGAGTCAGAACTGTAGA    7666          GTCAA  TG
                                TCTACAGT     TG  TCTTG
                                ||||||||     ||  |||||
                                AGATGTCA     AC  AGAAC
                                     AG___  TG
GAM897  DGKA      3'  CAAAACACATACATTG       7201         CA     C
                                CAGTGT  ATGTGT TTG
                                ||||||  |||||| |||
                                GTTACA  TACACA AAC
                                     __      A
GAM897  MTMR6     3'  CTCAAAACACAATTTGCACTGT 93549         C  _   C
            A                    TACAGTGT AAT GTGT TTGAG
                                ||||||||| ||| |||| |||||
                                ATGTCACG TTA CACA AACTC
                                     T   A    A
GAM897  SLC4A4    3'  CTCAAGACACAGACACCCACAG 13635     ACA_    AA
            A                    TCT    GTGTC  TGTGTCTTGAG
                                |||    |||||  ||||||||||
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                                AGA   CACAG  ACACAGAACTC
                                  CACC    __
GAM897  CUL4A    3'  CTCAAGACTTCAACCTGCAGA  13153     A   T  CAA  T_
                                TCT CAG GT   TG  GTCTTGAG
                                ||| ||| ||   ||  ||||||||
                                AGA GTC CA   AC  CAGAACTC
                                  C   _ ___  TT
GAM897  FLJ11301 3'  CAAGACACTAGCACTGTAGA   37226         CAAT
                                TCTACAGTGT   GTGTCTTG
                                ||||||||||   ||||||||
                                AGATGTCACG   CACAGAAC
                                      AT__
GAM897  GPR105   3'  GACACACCCACACCGTAGA   29655      A   CAA
                                TCTAC GTGT   TGTGTC
                                ||||| ||||   ||||||
                                AGATG CACA   ACACAG
                                   C   CCC
GAM897  LAP1B    5'  CTCAAGACACACCATGGGC   64584     AA___
                                GTC    TGTGTCTTGAG
                                |||    ||||||||||
                                CGG    ACACAGAACTC
                                  GTACC
GAM897  PRDM10   3'  CTCAAGACACATTGACACTGTA 39578
                GA                TCTACAGTGTCAATGTGTCTTGAG
                                  ||||||||||||||||||||||
                                  AGATGTCACAGTTACACAGAACTC

GAM897  SEMA3C   3'  CTCTTCTACATTGACAC     21061          TCTT
                                GTGTCAATGTG    GAG
                                ||||||||||    |||
                                CACAGTTACAT    CTC
                                      CTT_
GAM897  LOC255654 3'  GACATCCACACTGTAGA     96887         CAAT
                                TCTACAGTGT    GTGTC
                                ||||||||||    |||||
                                AGATGTCACA    TACAG
                                      CC__
GAM897  LOC96652  3'  CTCAAGACAGGACACTGCGGA  65467    TA     AATG
                                TC  CAGTGTC   TGTCTTGAG
                                ||  |||||||   |||||||||
                                AG  GTCACAG   ACAGAACTC
                                  GC      G___
GAM898  AP2A1    5'  CGGTCCCCGCTTGCCAGC    26387        T  T AA  A
                                GCTGGCAG GC G  GA CCG
                                |||||||| || |  || |||
                                CGACCGTT CG C  CT GGC
                                     _  _ CC  _
GAM898  AP2A1    5'  CGGTCCCCGCTTGCCAGC    55439        T  T AA  A
                                GCTGGCAG GC G  GA CCG
                                |||||||| || |  || |||
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                                CGACCGTT CG C  CT GGC
                                    _ _ CC  _
GAM898  APLP2    3'  TCTTCAGCCTCATTCACTG   90902     C   C__  T
                                CAG TGG   AG GCTGAAGA
                                ||| |||   || ||||||||
                                GTC ACT   TC CGACTTCT
                                  _   TAC  _
GAM898  AR       5'  CTTCAGCACTGCAGC       3492       G
                                GCTG CAGTGCTGAAG
                                |||| ||||||||||
                                CGAC GTCACGACTTC
                                  _
GAM898  CDH13    3'  TTTACACTGCCATCTG      6997      C       C
                                CAG TGGCAGTG TGAA
                                ||| |||||||| ||||
                                GTC ACCGTCAC ATTT
                                  T       _
GAM898  CHGA     5'  CGGCCCCACACCGCCAGCTG   7042          A   C  AAGAA
                                CAGCTGGC GTG TG    CCG
                                |||||||| ||| ||     |||
                                GTCGACCG CAC AC    GGC
                                    C   _  CCC__
GAM898  IL8      3'  TCTTGTCATTGCCAGCTG    94482           CTG
                                CAGCTGGCAGTG   AAGA
                                ||||||||||||   ||||
                                GTCGACCGTTAC   TTCT
                                       TG_
GAM898  NDUFV1   5'  GTTCCTCAGCCTCAGT      23024      GC  T    A
                                GCTG  AG GCTGA GAAC
                                ||||  || ||||| ||||
                                TGAC  TC CGACT CTTG
                                  __  _    C
GAM898  NRGN     3'  CAGCAACCTGCCAGCT      20512          __
                                AGCTGGCAG  TGCTG
                                |||||||||  |||||
                                TCGACCGTC  ACGAC
                                     CA
GAM898  PACSIN1  3'  CGGCTCTTCAGCAGATCCA   92259     CAG       A
                                TGG   TGCTGAAGA CCG
                                |||   ||||||||| |||
                                ACC   ACGACTTCT GGC
                                  TAG       C
GAM898  PCOLN3   3'  TCGGCCGCCCCTACCAGCTG  10913       C  T____
                                CAGCTGG AG    GCTGA
                                ||||||| ||    |||||
                                GTCGACC TC    CGGCT
                                    A  CCCGC
GAM898  PIM2     5'  CAGCCCTGGCTCCCCAGCTG  59990        _____  T
                                CAGCTGG    CAG GCTG
                                |||||||    ||| ||||
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                              GTCGACC    GTC CGAC
                                  CCTCG   C
GAM898  PSEN2    3'  TCTTTGGTGCCAGCTG     25032        AGT  TG
                              CAGCTGGC   GC  AAGA
                              ||||||||   ||  ||||
                              GTCGACCG   TG  TTCT
                                  ___  GT
GAM898  PSEN2    3'  TCTTTGGTGCCAGCTG     4808         AGT  TG
                              CAGCTGGC   GC  AAGA
                              ||||||||   ||  ||||
                              GTCGACCG   TG  TTCT
                                  ___  GT
GAM898  SERPINF2 3'  TCGAGATCCCAACACTGCCAGC 6259          C  AAGAAC
                              GCTGGCAGTG TG     CGA
                              |||||||||| ||     |||
                              CGACCGTCAC AC     GCT
                                    A  CCTAGA
GAM898  SLC7A6   3'  CGGCTCTTCAGCAGGCTGC   14301    T   AG       A
                              GC GGC  TGCTGAAGA CCG
                              || |||  |||||||||| |||
                              CG TCG  ACGACTTCT GGC
                               _  G_       C
GAM898  SLC7A8   3'  TCGGTTCTCCTCAGGACGCCAA 24284    C    A  G   __
           CT                   AG TGGC GT CTGA  AGAACCGA
                              || |||| || ||||  ||||||||
                              TC ACCG CA GACT  TCTTGGCT
                               A   _ G    CC
GAM898  SPI1     3'  CGGCTCCCGACGCCAGCTG   11907        AG  CTGAA  A
                              CAGCTGGC  TG    GA CCG
                              ||||||||  ||    || |||
                              GTCGACCG  GC    CT GGC
                                  CA  C____  C
GAM898  SPTAN1   5'  TCGGTCCTTCAGCACCCCTCGG 11939      CA_       A
           C                    GCTGG   GTGCTGAAG ACCGA
                              |||||   ||||||||| |||||
                              CGGCT   CACGACTTC TGGCT
                                 CCC       C
GAM898  STAM     5'  TCGGCTCCTTGCTGTTGCCGC  12962    T   GT_  TGAA  A
                              GC GGCA   GC    GA CCGA
                              || ||||   ||    || ||||
                              CG CCGT   CG    CT GGCT
                               _    TGT  TTC_  C
GAM898  TNFRSF6B 5'  TCAGCCCTGCTGCCAGC     33168         ___
                              GCTGGCAGT   GCTGA
                              |||||||||   |||||
                              CGACCGTCG   CGACT
                                    TCC
GAM898  TPM2     5'  CGGTCCTCACCGCCTGCCGGC  12370        T  __   A  A
                              GCTGGCAG GC  TGA GA CCG
                              |||||||| ||  ||| || |||
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                                CGGCCGTC CG  ACT CT GGC
                                     _ CC   C  _
GAM898  WFS1    5'  CGGCTCTTCAGCAGCGAGT   20008    G  AG       A
                                GCT GC  TGCTGAAGA CCG
                                ||| ||  ||||||||| |||
                                TGA CG  ACGACTTCT GGC
                                  G __        C
GAM898  7h3     3'  TCGGCCCTCTTGCTGCTGCCA  52276       _  TGA  AA
                                TGGCAGT GC   AG  CCGA
                                ||||||| ||   ||  ||||
                                ACCGTCG CG   TC  GGCT
                                    T  TTC  CC
GAM898  BC-2    5'  CTCCGGCCTGCCAGT      27085        T    A
                                GCTGGCAG GCTG AG
                                |||||||| |||| ||
                                TGACCGTC CGGC TC
                                     _   C
GAM898  BRI3    3'  TGGCACACGCCAGCTG     31149        A_
                                CAGCTGGC  GTGCTG
                                ||||||||  ||||||
                                GTCGACCG  CACGGT
                                     CA
GAM898  C12orf22  5'  CGGCCCTCTCTGCCTGCCGGCT 47977          T  T  _  AA
           G                     CAGCTGGCAG GC GA AG  CCG
                                 |||||||||| || || ||  |||
                                 GTCGGCCGTC CG CT TC  GGC
                                      _  T  C  CC
GAM898  C20orf162 5'  CAGCCCCCTGCCAGCTG    54598          T__
                                CAGCTGGCAG   GCTG
                                ||||||||||   ||||
                                GTCGACCGTC   CGAC
                                      CCC
GAM898  C20orf72  3'  TCAGCCCACTACCGCTG    53500      T  C  __
                                CAGC GG AGT  GCTGA
                                |||| || |||  |||||
                                GTCG CC TCA  CGACT
                                  _  A   CC
GAM898  C3IP1   5'  TCGGCTCCTCCCGAGCCGCCTG 41285     T   A  GCT_  A  A
           CT                     AGC GGC GT    GA GA CCGA
                                  ||| ||| ||    || || ||||
                                  TCG CCG CG    CT CT GGCT
                                    T   C  AGCC  C  C
GAM898  CCNE1   5'  CGACTCCCGGCGCCGCCGC   6949     T   A     AA  AC
                                GC GGC GTGCTG  GA  CG
                                || ||| ||||||  ||  ||
                                CG CCG CGCGGC  CT  GC
                                 _  C     C_  CA
GAM898  CDCA7   5'  TCGGCGCGCCCAGCCTGCCAGC 49205         T    AAGAA_
                                GCTGGCAG GCTG     CCGA
                                |||||||| ||||     ||||
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                                CGACCGTC CGAC     GGCT
                                   _   CCGCGC
GAM898  COE2     5'  GGAGGCAGCACTGCAGCTG   64255       G      AAGAA
                                CAGCTG CAGTGCTG    CC
                                |||||| ||||||||    ||
                                GTCGAC GTCACGAC    GG
                                   _       GGA__
GAM898  CPSF1    5'  TCGGCTCCAACTGCCAGC    64556        ____
                                GCTGGCAGT   GCTGA
                                |||||||||   |||||
                                CGACCGTCA   CGGCT
                                     ACCT
GAM898  DKFZP434K1772 5'  CGGCACCCAGCACCGCCAGCTG 67711        A     AAGAA
                                CAGCTGGC GTGCTG    CCG
                                |||||||| ||||||    |||
                                GTCGACCG CACGAC    GGC
                                     C     CCAC_
GAM898  DKFZp761F2014 3'  CAGTCCTATTTCTGCCAGTTG  39534         T_______
                                CAGCTGGCAG      GCTG
                                ||||||||||      ||||
                                GTTGACCGTC      TGAC
                                     TTTATCC
GAM898  DVL2     3'  TGGGCTCAGCCTACCAGCTG   15362       C  T    AGAA
                                CAGCTGG AG GCTGA   CCG
                                ||||||| || |||||   |||
                                GTCGACC TC CGACT   GGT
                                   A  _    CG__
GAM898  FLJ20435  3'  TCAGCACTCTGCCAGC     35164       __
                                GCTGGCA  GTGCTGA
                                |||||||  |||||||
                                CGACCGT  CACGACT
                                   CT
GAM898  FLJ20850  3'  CAGCCCTAACTGCCAGCTG   35721         _____
                                CAGCTGGCAGT   GCTG
                                ||||||||||   ||||
                                GTCGACCGTCA   CGAC
                                     ATCC
GAM898  FREQ     3'  TCGGCTCCCTGCTCAGCTG   26586      _   T__
                                CAGCTG GCAG   GCTGA
                                |||||| ||||   |||||
                                GTCGAC CGTC   CGGCT
                                   T   CCT
GAM898  HN1L     3'  TCAACAGCCCGCCAGCTG    58001       AGT   AA
                                CAGCTGGC   GCTG  GA
                                ||||||||   ||||  ||
                                GTCGACCG   CGAC  CT
                                   CC_    AA
GAM898  KIAA0057  3'  TCGGTCCCCCAGGGCCTGCC  24442      _ G   AAGA
                                GGCAG T CTG    ACCGA
                                ||||| | |||    |||||
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                                CCGTC G GAC    TGGCT
                                   C G   CCCC
GAM898  KIAA0397  3'  TCAGCAGCACTGCCACTG    61677     C         AA
                                CAG TGGCAGTGCTG  GA
                                ||| ||||||||||  ||
                                GTC ACCGTCACGAC  CT
                                  _         GA
GAM898  KIAA0937  3'  TCAGTGAGAACCCTGCCAGCTG 91590          _______
                                CAGCTGGCAG     TGCTGA
                                ||||||||||     ||||||
                                GTCGACCGTC     GTGACT
                                     CCAAGA
GAM898  KIAA1126  3'  GTTCCTCGCCAGCTG       71938         AGTGCT  A   C
                                CAGCTGGC     GA GAA C
                                ||||||||     || ||| |
                                GTCGACCG     CT CTT G
                                   _______ C   A
GAM898  KIAA1466  3'  TCAGCAACTGCCAGCT      71919          _
                                AGCTGGCAGT GCTGA
                                |||||||||| |||||
                                TCGACCGTCA CGACT
                                     A
GAM898  KIAA1856  3'  CGGCCCTCCAGGCTGCTGCTG  92663      T     G   A  AA
                                CAGC GGCAGT CTG AG  CCG
                                |||| |||||| ||| ||  |||
                                GTCG TCGTCG GAC TC  GGC
                                  _     _  C  CC
GAM898  MAPK8IP2  3'  TCGGTCCCCAGGGCGCAGCTG  24659       G A  G   AA  A
                                CAGCTG C GT CTG  GA CCGA
                                |||||| | || |||  || ||||
                                GTCGAC G CG GAC  CT GGCT
                                   _ _  G   CC  _
GAM898  MAPK8IP2  3'  TCGGTCCCCAGGGCGCAGCTG  33158       G A  G   AA  A
                                CAGCTG C GT CTG  GA CCGA
                                |||||| | || |||  || ||||
                                GTCGAC G CG GAC  CT GGCT
                                   _ _  G   CC  _
GAM898  MAPK8IP2  3'  TCGGTCCCCAGGGCGCAGCTG  57468       G A  G   AA  A
                                CAGCTG C GT CTG  GA CCGA
                                |||||| | || |||  || ||||
                                GTCGAC G CG GAC  CT GGCT
                                   _ _  G   CC  _
GAM898  MGC3146   5'  TCGGTTCTTCCAGACAAGCTG  48442      GGCAGTG  _
                                CAGCT      CTG AAGAACCGA
                                |||||      ||| |||||||||
                                GTCGA      GAC TTCTTGGCT
                                   ACA_____  C
GAM898  moblak    5'  GGTTGGTCAGCACCCCCAGC   55510      CA      AG
                                GCTGG  GTGCTGA  AACC
                                |||||  |||||||  ||||
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                                CGACC  CACGACT  TTGG
                                  CC      GG
GAM898  NAV1     3'  TTCCATCACCACTGCCA     39952        C   A_
                                TGGCAGTG TGA  GAA
                                |||||||| |||  |||
                                ACCGTCAC ACT  CTT
                                    C   AC
GAM898  NDP52    3'  TCAGCCCTGCTGCCGCT     19534     T     ___
                                AGC GGCAGT   GCTGA
                                ||| ||||||   |||||
                                TCG CCGTCG   CGACT
                                  _     TCC
GAM898  NPTXR    3'  TTCTTTAGCTCAGCT       26655       CAGT
                                AGCTGG    GCTGAAGAA
                                ||||||    |||||||||
                                TCGACT    CGATTTCTT
                                  ____
GAM898  NPTXR    3'  TTCTTTAGCTCAGCT       54191       CAGT
                                AGCTGG    GCTGAAGAA
                                ||||||    |||||||||
                                TCGACT    CGATTTCTT
                                  ____
GAM898  NTN4     5'  CGGCCCCTGGCTCCCAGCTG   62914        C  _____
                                CAGCTGG AGT    GCTG
                                ||||||| |||    ||||
                                GTCGACC TCG    CGGC
                                    C   GTCCC
GAM898  NXN      3'  TCAGCACTCTGCCAGC      42424        __
                                GCTGGCA  GTGCTGA
                                |||||||  |||||||
                                CGACCGT  CACGACT
                                    CT
GAM898  PDEF     5'  GTCCTCCAAGCCTGCTGCCAGC 24750          __  GA_  A
          T                      AGCTGGCAGT  GCT   AG AC
                                ||||||||||  |||   || ||
                                TCGACCGTCG  CGA   TC TG
                                      TC   ACC  C
GAM898  SHANK3   3'  CGGCCCCTCACTGCCACTG   65492     C      CTGA  AA_
                                CAG TGGCAGTG    AG   CCG
                                ||| ||||||||    ||   |||
                                GTC ACCGTCAC    TC   GGC
                                  _      ____  CCC
GAM898  WBSCR21  5'  CGGTTCTCTCCCACAGCCA   48475     A   CT  _
                                TGGC GTG  GA AGAACCG
                                |||| |||  || |||||||
                                ACCG CAC  CT TCTTGGC
                                  A   C_  C
GAM898  LOC116437 5'  CAGCCACACTGCCGCTG     73890      T     ___
                                CAGC GGCAGT   GCTG
                                |||| ||||||   ||||
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                                GTCG CCGTCA   CGAC
                                  _     CAC
GAM898   LOC118738 3'  CAGCAGGACCTGCCAGCTG   75487          ____
                                CAGCTGGCAG    TGCTG
                                ||||||||||    |||||
                                GTCGACCGTC    ACGAC
                                     CAGG
GAM898   LOC121793 5'  TCGGCCCCTTCATCTGTCAGCT 74115          TGC    AA_
           G                     CAGCTGGCAG   TGAAG   CCGA
                                ||||||||||   |||||  ||||
                                GTCGACTGTC   ACTTC   GGCT
                                      T__    CCC
GAM898   LOC126549 5'  TCGGCCCTTGCCGGCACCTGCC 75713       _   __  AA
           A                     TGGCAG TGCTG  AAG  CCGA
                                ||||||| |||||  |||  ||||
                                ACCGTC ACGGC  TTC  GGCT
                                   C    CG   CC
GAM898   LOC134301 5'  CGGTTCTCCGGGCAGCTGCCAC 75181     C    _   _ A
           TG                     CAG TGGCAG TGCT G AGAACCG
                                ||| ||||||| |||| | |||||||
                                GTC ACCGTC ACGG C TCTTGGC
                                  _     G   G C
GAM898   LOC149706 5'  CGGTTCTCCAACAGCC      84639     AG  C  A
                                GGC  TG TG AGAACCG
                                |||  || || |||||||
                                CCG  AC AC TCTTGGC
                                  __ A  C
GAM898   LOC150468 3'  TCAGTTCTTTGCTCAGCT     79878      _   T__
                                AGCTG GCAG   GCTGA
                                ||||| ||||   |||||
                                TCGAC CGTT   TGACT
                                   T    TCT
GAM898   LOC152742 3'  CTTTCTCATTGCCAACT      85858    C       CT
                                AG TGGCAGTG  GAAG
                                || ||||||||  ||||
                                TC ACCGTTAC  TTTC
                                 A       TC
GAM898   LOC153339 5'  CAGCTCTGCTGCCAACTG     86005     C      ___
                                CAG TGGCAGT   GCTG
                                ||| |||||||   ||||
                                GTC ACCGTCG   CGAC
                                  A      TCT
GAM898   LOC154789 3'  TCTTTCCAGCATACCAACT    81143    C   CA     __
                                AG TGG  GTGCTG  AAGA
                                || |||  ||||||  ||||
                                TC ACC  TACGAC  TTCT
                                 A  A_     CT
GAM898   LOC155066 3'  GTTCCTGGCTGGCCAGCTG    81283         AGT   GAA
                                CAGCTGGC   GCT   GAAC
                                ||||||||   |||   ||||
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                                GTCGACCG  CGG  CTTG
                                    GT_  TC_
GAM898  LOC158427 3'  TCAGTTCTGGCCGCTGCCA   57681       _ GA   C
                                TGGCAGTG CT  AGAAC GA
                                |||||||| ||  ||||| ||
                                ACCGTCGC GG  TCTTG CT
                                    C __    A
GAM898  LOC163231 5'  TCAGCTCACTGTCAGC     82444        __
                                GCTGGCAGT  GCTGA
                                |||||||||  |||||
                                CGACTGTCA  CGACT
                                     CT
GAM898  LOC200471 5'  CAGCCCCACGCTGCCAGGCTG  90050     _     _____
                                CAGC TGGCAGT    GCTG
                                |||| |||||||    ||||
                                GTCG ACCGTCG    CGAC
                                  G      CACCC
GAM898  LOC201952 5'  TCAGTTCCTGCTGCCAGT    90275       ____
                                GCTGGCAGT   GCTGA
                                |||||||||   |||||
                                TGACCGTCG   TGACT
                                     TCCT
GAM898  LOC220587 3'  TGGGCTCAGCCTACCAGCTG  90765       C  T    AGAA
                                CAGCTGG AG GCTGA   CCG
                                ||||||| || |||||   |||
                                GTCGACC TC CGACT   GGT
                                    A  _    CG__
GAM898  LOC221424 5'  TCAGCCCTGCCGCCTG     93629     C     T
                                CAG TGGCAG GCTGA
                                ||| |||||| |||||
                                GTC GCCGTC CGACT
                                  C     C
GAM898  LOC221749 3'  TCAGCTGTTCACTGCCAGCT  92008       _____
                                AGCTGGCAGT    GCTGA
                                ||||||||||    |||||
                                TCGACCGTCA    CGACT
                                     CTTGT
GAM898  LOC253216 3'  CGGCCCCAGCCTGCCCGC    94957    T    T   AAGAA
                                GC GGCAG GCTG    CCG
                                || ||||| ||||    |||
                                CG CCGTC CGAC    GGC
                                 C    _   CCC__
GAM898  LOC51644  3'  GTTCTCCAGCACTGAGGT    32138     GG      A
                                GCT  CAGTGCTG AGAAC
                                |||  |||||||| |||||
                                TGG  GTCACGAC TCTTG
                                  A_       C
GAM898  LOC91373  3'  CGACTCCCCCCAGACCTGCCAG 65838       TG   AA__  AC
            C                    GCTGGCAG  CTG   GA  CG
                                |||||||  |||   ||  ||
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                                CGACCGTC  GAC   CT  GC
                                    CA   CCCC  CA
GAM898  LOC95702  3'  CGGCCCCAGCCTGCCCGC    62640    T    T   AAGAA
                                GC GGCAG GCTG    CCG
                                || ||||| ||||    |||
                                CG CCGTC CGAC    GGC
                                 C    _   CCC__
GAM899  AQP6      3'  CAGAAGTTAAAATGCT      7941       C
                                AGTGT TTAACTTCTG
                                ||||| ||||||||||
                                TCGTA AATTGAAGAC
                                   A
GAM899  AQP6      3'  CAGAAGTTAAAATGCT      53912      C
                                AGTGT TTAACTTCTG
                                ||||| ||||||||||
                                TCGTA AATTGAAGAC
                                   A
GAM899  B3GALT2   5'  AGATGGACACTTTGGA      13683          TAACT
                                TTCAAAGTGTCT    TCT
                                ||||||||||||    |||
                                AGGTTTCACAGG    AGA
                                      T____
GAM899  CDH13     3'  GGAAACTAAGACACCTGAA   6995      AA       AC
                                TTCA  GTGTCTTA  TTCT
                                ||||  ||||||||  ||||
                                AAGT  CACAGAAT  AAGG
                                  C_       CA
GAM899  EDNRA     3'  AAGTCATTACACTTTGAA    64104         CTTA
                                TTCAAAGTGT    ACTT
                                ||||||||||    ||||
                                AAGTTTCACA    TGAA
                                      TTAC
GAM899  EIF2S3    3'  CAGAAGTTAAACATT       7414       C
                                AGTGT TTAACTTCTG
                                ||||| ||||||||||
                                TTACA AATTGAAGAC
                                  _
GAM899  EXTL2     3'  CAGAAGTTAAAACCCTTTG   7522       T  C
                                CAAAG GT TTAACTTCTG
                                ||||| || ||||||||||
                                GTTTC CA AATTGAAGAC
                                   C  A
GAM899  GPC5      3'  AGAAGTGACTTTGAA       15552        GTCTTA
                                TTCAAAGT     ACTTCT
                                ||||||||     ||||||
                                AAGTTTCA     TGAAGA
                                     G_____
GAM899  IFNAR2    3'  AAGTGGTGCACTTTGAA     6036          CTTA
                                TTCAAAGTGT    ACTT
                                ||||||||||    ||||
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                                AAGTTTCACG    TGAA
                                      TGG_
GAM899  NEB      3'  CAGAACAGACACTTT       15809         TAAC
                                AAAGTGTCT    TTCTG
                                |||||||||    |||||
                                TTTCACAGA    AAGAC
                                     C___
GAM899  PTPN11   3'  CAGAAGTTGTGCATT       54595       CT
                                AGTGT  TAACTTCTG
                                |||||  |||||||||
                                TTACG  GTTGAAGAC
                                   T_
GAM899  SULT1C1  3'  CAGAAGGAACACTTTGAG    6464          CTTAA
                                TTCAAAGTGT    CTTCTG
                                ||||||||||    ||||||
                                GAGTTTCACA    GAAGAC
                                      AG___
GAM899  ZNF133   3'  CAGAATGTTGACACTTTGA   12833         TT  _
                                TCAAAGTGTC  AAC TTCTG
                                ||||||||||  ||| |||||
                                AGTTTCACAG  TTG AAGAC
                                      __   T
GAM899  AKT3     3'  CAGATGTTGAAACTTTGAA   18432        GTC    T
                                TTCAAAGT   TTAAC TCTG
                                ||||||||   ||||| ||||
                                AAGTTTCA   AGTTG AGAC
                                     A__    T
GAM899  CDC14B   3'  CAGAAATCAGGGCACTT     52846         AAC
                                AAGTGTCTT   TTCTG
                                |||||||||   |||||
                                TTCACGGGA   AAGAC
                                      CTA
GAM899  CGI-127  3'  CAGAAGTTCAGCTGTTGAA   32153       AGT T  T
                                TTCAA   G CT AACTTCTG
                                |||||   | || ||||||||
                                AAGTT   C GA TTGAAGAC
                                   GT_ _  C
GAM899  DCTN4    3'  CAGAAACACAAAACACTTTGA  67786         CTTAAC_
                                TCAAAGTGT      TTCTG
                                |||||||||      |||||
                                AGTTTCACA      AAGAC
                                      AAACACA
GAM899  DDX25    5'  AGTAAAGACATTTGAA      25166       G     A
                                TTCAAA TGTCTT ACT
                                |||||| |||||| |||
                                AAGTTT ACAGAA TGA
                                   _     A
GAM899  DKFZP547E2110 3'  CAGATGTTAAACTTTGAA    90987         GTC    T
                                TTCAAAGT   TTAAC TCTG
                                ||||||||   ||||| ||||
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                                AAGTTTCA  AATTG AGAC
                                   ___    T
GAM899  DMTF1    3'  AAGTTAGCACTTTGAA     40935        CT
                                TTCAAAGTGT  TAACTT
                                ||||||||||  ||||||
                                AAGTTTCACG  ATTGAA
                                   __
GAM899  EFA6R    3'  CAGAAGTTTAGCTTTG     30980      GTCTT
                                CAAAGT    AACTTCTG
                                ||||||    ||||||||
                                GTTTCG    TTGAAGAC
                                  AT___
GAM899  ENAH     3'  CAGAAGTTTTACTAAAACTTTG 36613       GTCTT___
           AA                     TTCAAAGT      AACTTCTG
                                ||||||||      ||||||||
                                AAGTTTCA      TTGAAGAC
                                    AAATCATT
GAM899  FLJ12800 3'  CAGAAGCAGAGCCACTGTGAA  43228     A   T   AA
                                TTCA AGTG CTT  CTTCTG
                                |||| |||| |||  ||||||
                                AAGT TCAC GAG  GAAGAC
                                  G   C   AC
GAM899  H326     3'  AGAAACGCACTTTGGA      31702         CTTAAC
                                TTCAAAGTGT     TTCT
                                ||||||||||     ||||
                                AGGTTTCACG     AAGA
                                    CA_____
GAM899  HSU79252 5'  AAGTTGACTTATTTTGAA    25243        TC
                                TTCAAAGTG  TTAACTT
                                |||||||||  |||||||
                                AAGTTTTAT  AGTTGAA
                                    TC
GAM899  KIAA0746 3'  CAGTTATAAGGCACCTTGAA  69452      A      ACTT
                                TTCAA GTGTCTTA   CTG
                                ||||| ||||||||   |||
                                AAGTT CACGGAAT   GAC
                                  C      ATT_
GAM899  KIAA0997 3'  CAGAAGTTACATCATTT     30188      TCT
                                AAGTG   TAACTTCTG
                                |||||   |||||||||
                                TTTAC   ATTGAAGAC
                                  TAC
GAM899  KIAA1077 3'  CAGAAGTTAATCATTTGAA   72903      G  TC
                                TTCAAA TG  TTAACTTCTG
                                ||||||  ||  ||||||||||
                                AAGTTT AC  AATTGAAGAC
                                   _  T_
GAM899  KIAA1078 3'  CAGAAGTGAATGACACTTTGAG 65120          TTA_
                                TTCAAAGTGTC   ACTTCTG
                                ||||||||||    |||||||
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                                GAGTTTCACAG    TGAAGAC
                                      TAAG
GAM899  KIAA1627  3'  AGAAATTAAGAGACTTTGAA   80752        G     C
                                TTCAAAGT TCTTAA TTCT
                                |||||||| |||||| ||||
                                AAGTTTCA AGAATT AAGA
                                   G     A
GAM899  OSBPL2    3'  AGTGGAGCACTTTGAA      57851         T   A
                                TTCAAAGTG CTT ACT
                                ||||||||| ||| |||
                                AAGTTTCAC GAG TGA
                                   _  G
GAM899  OSBPL2    3'  AGTGGAGCACTTTGAA      29200         T   A
                                TTCAAAGTG CTT ACT
                                ||||||||| ||| |||
                                AAGTTTCAC GAG TGA
                                   _  G
GAM899  OSBPL3    3'  AGAAAACACTTTGAG       31434          CTTAAC
                                TTCAAAGTGT     TTCT
                                ||||||||||     ||||
                                GAGTTTCACA     AAGA
                                   A_____
GAM899  PDCD5     3'  CAGAAGTTAAGATCTGA     16301     AAGT
                                TCA    GTCTTAACTTCTG
                                |||    ||||||||||||
                                AGT    TAGAATTGAAGAC
                                  C___
GAM899  PPFIBP2   3'  CAGGAGGAAAGACACTT     76599         AA
                                AAGTGTCTT  CTTCTG
                                |||||||||  ||||||
                                TTCACAGAA  GAGGAC
                                   AG
GAM899  SYT13     3'  CAGAAATGAGATACATTTTGAA 93452        __       AC
                                TTCAAA  GTGTCTTA  TTCTG
                                ||||||  ||||||||  |||||
                                AAGTTT  CATAGAGT  AAGAC
                                   TA       A_
GAM899  TIX1      3'  CAGAGAACAGACACTTGGAA   61738     A       TAAC
                                TTC AAGTGTCT    TTCTG
                                ||| ||||||||    |||||
                                AAG TTCACAGA    GAGAC
                                  G       CAA_
GAM899  TTYH2     3'  CAGGTATGAACAGACACTTTGA 50993           TAACT__
          A                      TTCAAAGTGTCT      TCTG
                                ||||||||||||      ||||
                                AAGTTTCACAGA      GGAC
                                      CAAGTAT
GAM899  ZFP91     3'  CAGAAATTTGCACTTTGAA    53819          CTT  C
                                TTCAAAGTGT   AA TTCTG
                                ||||||||||   || |||||
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                                AAGTTTCACG   TT AAGAC
                                      T__  A
GAM899   LOC116068 3'  GGGTTTCACACTTTGAA     73727          CTT
                                TTCAAAGTGT   AACTT
                                ||||||||||   |||||
                                AAGTTTCACA   TTGGG
                                      CT_
GAM899   LOC122700 3'  AAGTGATACACTTTGAA     74147          CTTA
                                TTCAAAGTGT    ACTT
                                ||||||||||    ||||
                                AAGTTTCACA    TGAA
                                      TAG_
GAM899   LOC144871 3'  CAGAAGTTGTCTTTGA      83198        TGTCT
                                TCAAAG     TAACTTCTG
                                ||||||     |||||||||
                                AGTTTC     GTTGAAGAC
                                   T_____
GAM899   LOC145676 5'  CAGAAAGTGCACTTTGAG     77336          CTTA   _
                                TTCAAAGTGT    ACTT CTG
                                ||||||||||    |||| |||
                                GAGTTTCACG    TGAA GAC
                                      _____   A
GAM899   LOC145814 3'  CAGGAGAAAGAACACTCTGAA  77504      A    _   AA
                                TTCA AGTGT CTT  CTTCTG
                                |||| ||||| |||  ||||||
                                AAGT TCACA GAA  GAGGAC
                                  C    A   A_
GAM899   LOC148388 3'  CAGGTGAGAAGACATTTGAA   82122       G     AACT
                                TTCAAA TGTCTT    TCTG
                                ||||||| ||||||    ||||
                                AAGTTT ACAGAA    GGAC
                                   _     GAGT
GAM899   LOC151300 3'  AGGACAGCACTTTGAA       85304          T  TAAC
                                TTCAAAGTG CT    TTCT
                                ||||||||| ||    ||||
                                AAGTTTCAC GA    AGGA
                                      _ C___
GAM899   LOC151657 3'  CAGAAATAAAAGGACACTCTGA 85475      A       AAC__
           G                     TTCA AGTGTCTT     TTCTG
                                ||||  ||||||||     |||||
                                GAGT TCACAGGA     AAGAC
                                  C       AAATA
GAM899   LOC164684 3'  CAGAAGTTAAAAGATA      82550       __
                                TGTCT  TAACTTCTG
                                |||||  |||||||||
                                ATAGA  ATTGAAGAC
                                   AA
GAM899   LOC199692 3'  GTTAAGACACTGTGAA       59242      A
                                TTCA AGTGTCTTAAC
                                |||| ||||||||||
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                                AAGT TCACAGAATTG
                                  G
GAM899  LOC201229 5'  AGGAGCACACTTTGAA      88141          CTTAA
                                TTCAAAGTGT    CTTCT
                                ||||||||||    |||||
                                AAGTTTCACA    GAGGA
                                    C____
GAM899  LOC201477 5'  AGAAGAAAAGACACTCTGAA  89784     A       AA
                                TTCA AGTGTCTT  CTTCT
                                ||||  ||||||||  |||||
                                AAGT TCACAGAA  GAAGA
                                  C       AA
GAM899  LOC221463 3'  CAGAGTTCAAACATTTTGAA  92065         CTT    T
                                TTCAAAGTGT   AACT CTG
                                ||||||||||   ||||  |||
                                AAGTTTTACA   TTGA GAC
                                    AAC   _
GAM899  LOC222193 3'  AGGTTGGACACTTTGGA     94178           T
                                TTCAAAGTGTCT AACTT
                                ||||||||||||  |||||
                                AGGTTTCACAGG TTGGA
                                          _
GAM899  LOC255308 3'  CAGAAGTTAAGCATT       94530      T
                                AGTG CTTAACTTCTG
                                ||||  ||||||||||
                                TTAC GAATTGAAGAC
                                  _
GAM899  LOC51218  3'  CAGAAGTTAAATAGGAGCTTTG 33105        GT  ___
          GA                    TTCAAAGT  CT   TAACTTCTG
                                ||||||||  ||   |||||||||
                                AGGTTTCG  GA   ATTGAAGAC
                                    AG  TAA
GAM899  LOC91431  5'  CAGAACTGACTACTTTGAA   56923        _   TTAAC
                                TTCAAAGT GTC     TTCTG
                                ||||||||  |||    |||||
                                AAGTTTCA CAG     AAGAC
                                    T   TC___
GAM900  A1BG      3'  CCTCCCAAAGTGCTGGGATTA  55415            A
                                TAATCTCAGCACTTTG GGAGG
                                ||||||||||||||||  |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                          _
GAM900  ACADSB    3'  CCTCCCAAAGTGCTGGGATTA  7844             A
                                TAATCTCAGCACTTTG GGAGG
                                ||||||||||||||||  |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                          _
GAM900  ADAMTS4   3'  TCCCAAAGTGCTGGGATTA   17520            A
                                TAATCTCAGCACTTTG GGA
                                ||||||||||||||||  |||
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                                ATTAGGGTCGTGAAAC CCT
                                                _
GAM900  ADAMTS4  3' CCTCCCAAAGTGCTGGGATTA 17504          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  ADCY6    5' CCTCACAAAGTGCTGGGATTA 30925          AG
                                TAATCTCAGCACTTTG  GAGG
                                ||||||||||||||||  ||||
                                ATTAGGGTCGTGAAAC  CTCC
                                                A_
GAM900  ADRA1A   3' CCTCCCAAAGTGCTGGGATTA 52786          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  AIM1     3' CCTCCCAAAATGCTGGGATTA 91820        C  A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||| |||| |||||
                                ATTAGGGTCGT AAAC CCTCC
                                              A  _
GAM900  ALDH1B1  3' CCTCCCAAAGTGCTGGGATTA 5493           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  APAF1    3' CCTCCCAAAGTGCTGAGATTA 6727           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                                _
GAM900  APAF1    3' CCTCCCAAAGTGCTGAGATTA 25036          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                                _
GAM900  APM1     3' CCTCCCAAAGTGCTGGGATTA 16586          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  APM1     3' CCTCCCAAAGTGCTGGGATTA 16587          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  APOL1    3' CCTCCCAAAGTGCTGGGATTA 13344          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  APPL    3' CCTCCCAAAGTGCTGGGATTA 23924          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  AQP6    3' CCTCCCAAAGTGCTGGGATTA 7945           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  AQP6    3' CCTCCCAAAGTGCTGGGATTA 53919          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  ARSF    5' CCTCCCAAAGTGCTGGGATTA 64597          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  ATP7A   3' CCTCCCAAAGTGCTGGGATTA 3521          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  ATP8B2  3' CCTCCCAAAGTGCTGAGATTA 65221         A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                                 _
GAM900  AXL     3' CCTCCCAAAGTGCTGAGATTA 8096          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                                 _
GAM900  AXL     3' CCTCCCAAAGTGCTGAGATTA 41593         A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                                 _
GAM900  B4GALT5 3' CTTCCCAAAGTGCTGGGATTA 16500        A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTTC
                                                 _
GAM900  BAZ2B   5' CCTCCCAAAGTGCTGGGATTA 25619        A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC

                                          _
GAM900  BCL10    3'  CCTCCCAAAGTGCTGGGATTA  14057          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                          _
GAM900  CAMLG    3'  CCTCCCAAAGTGCTGGGATTA  8236           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                          _
GAM900  CASP8    3'  CCTCCCAAAGTGCTGGGATTA  6914           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                          _
GAM900  CASP8    3'  CCTCCCAAAGTGCTGGGATTA  52944          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                          _
GAM900  CASP8    3'  CCTCCCAAAGTGCTGGGATTA  52920          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                          _
GAM900  CASP8    3'  CCTCCCAAAGTGCTGGGATTA  52931          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                          _
GAM900  CBFA2T2  3'  CCTCCCAAAGTGCCAGGATTA  17461      CA      A
                                TAATCT  GCACTTTG GGAGG
                                ||||||  |||||||| |||||
                                ATTAGG  CGTGAAAC CCTCC
                                    AC       _
GAM900  CCNF     3'  TCCCAAAGTGCTGGGATTA   8328           A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT

                                          _
GAM900  CHRNB4   3'  CCTCCCAAAGTGCTGGGATTA  5630          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                          _
GAM900  CLECSF11 5'  CCTCCCAAAGTGCTGAGATTA  55275          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGAGTCGTGAAAC CCTCC
                                       _
GAM900  CLECSF12 3' CCTCCCAAAGTGCTGGGATTA 76685          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  CNN2     3' CCTCCCCAAGCGCTGAGATTA 15175       A  T A
                                TAATCTCAGC CTT G GGAGG
                                |||||||||| ||| | |||||
                                ATTAGAGTCG GAA C CCTCC
                                      C  _ C
GAM900  COX15    3' CTTCCCAAAGTGCTGAGATTA 54311         A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTTC
                                       _
GAM900  CR1      3' CCTCCCAAAGTGCTGCGATTA 5132      T    A
                                TAATC CAGCACTTTG GGAGG
                                ||||| |||||||||| |||||
                                ATTAG GTCGTGAAAC CCTCC
                                   C       _
GAM900  CXCL16   3' CCTCCCAAAGTGCTGGGATTA 41917         A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  CYP1A2   3' CCTCCCAAAGTGCTGGGATTA 5686          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  CYP1A2   3' CCTCCCAAAGTGCTGGGATTA 69106         A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  CYP2B6   3' CCTCCCAAAGTGCTGGGATTA 5727          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  CYP2B6   3' TTCCAAAGTGCTGATATTA  5747      C    A
                                TAAT TCAGCACTTTG GGA
                                |||| |||||||||| |||
                                ATTA AGTCGTGAAAC CTT
                                   T       _
GAM900  CYP4F3   3' CCTCCCAAAGTGCTGGGATTA 6114          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900  CYP51    3' CCTCCCAAAGTGCTGGGATTA 5782          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900  DFFB     3' TCCCAAAGTGCTGGGATTA  87398          A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                                  _
GAM900  DHFR     3' CCTCCCAAAGTGCTGGGATTA 5801          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900  DISC1    3' CTTCCCAAAGTGCTGAGATTA 37878         A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTTC
                                                  _
GAM900  DNASE1L1 5' CCTCCCAAAGTGCTGGGATTA 22074           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900  DSC3     3' CCTCCCAAAGTGCTGGGATTA 8674          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900  DSC3     3' CCTCCCAAAGTGCTGGGATTA 44339         A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900  DSCR3    3' CCTCCCAAAGTGCTGAGATTA 20175         A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                                  _
GAM900  DSCR3    3' CCTCCCAAAGTGCTGGGATTA 20176         A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900  EIF2S3   3' CCTCACAAAGTGCTGGGATTA 7416          AG
                                TAATCTCAGCACTTTG  GAGG
                                |||||||||||||||  ||||
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                                ATTAGGGTCGTGAAAC  CTCC
                                      A_
GAM900  EPB72   3'  CCTCCAAAGTGCTGGATTA   14601      T      GA
                                TAATC CAGCACTTT  GGAGG
                                ||||| |||||||||  |||||
                                ATTAG GTCGTGAAA  CCTCC
                                  _      __
GAM900  EVC     3'  CCTCCCCAAAGTGCTGAGATTA 27293           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                      C
GAM900  F2RL2   3'  CCTCCCAAAGTGCTGGATTA   14621      T      A
                                TAATC CAGCACTTTG GGAGG
                                ||||| |||||||||| |||||
                                ATTAG GTCGTGAAAC CCTCC
                                  _      _
GAM900  FANCF   3'  CCTCCCAAAGTGCTGGGATTA  42672           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  FCAR    3'  CCTCCCAAAGTGCTGAGATTA  8851            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                      _
GAM900  FCAR    3'  CCTCCCAAAGTGCTGAGATTA  55746           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                      _
GAM900  FCAR    3'  CCTCCCAAAGTGCTGAGATTA  55757           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                      _
GAM900  FCAR    3'  CCTCCCAAAGTGCTGAGATTA  55768           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                      _
GAM900  FCAR    3'  CCTCCCAAAGTGCTGAGATTA  55779           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                      _
GAM900  FCAR    3'  CCTCCCAAAGTGCTGGGATTA  55792           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  FEZ1    3'  CCTCCCAAAGTGCTGGGATTA  42570          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  FGF5    3'  CCTCCCCAAAGTGCTGGGATTA 52482          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      C
GAM900  FGF5    3'  CCTCCCCAAAGTGCTGGGATTA 15536          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      C
GAM900  FUT1    3'  CCTCCCAAAGTGCTGGGATTA  3787           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  FZD4    3'  CCTCCCAAAGTGCTGGGATTA  24133          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  GHR     3'  CCTCCCAAAGTGCTGGGATTA  3880           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  GLTSCR1 5'  CCTCCCAAAGTGCTGAGATTA  31670          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                                 _
GAM900  GPR4    3'  CCTCCCAAAGTGCTCAGATTA  59903      C   A
                                TAATCT AGCACTTTG GGAGG
                                |||||| ||||||||| |||||
                                ATTAGA TCGTGAAAC CCTCC
                                   C             _
GAM900  HCS     3'  CCTCCCAAAGTGCTGGGATTA  38464          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  HLCS    5'  CCTCCCAAAGTGCTGGGATTA  4662           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  HSD17B1  5' CCTCCCAAAGTGCTGGGATTA 4684          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  HTR1D    3' GCATCCCAAAGTGCTGGGATTA 5996        A  GG
                                TAATCTCAGCACTTTG GGA  GC
                                |||||||||||||||| |||  ||
                                ATTAGGGTCGTGAAAC CCT  CG
                                                _  A_
GAM900  HTR1E    5' CCTCCCAAAGTGCTGGAATTA 6013     CT      A
                                TAAT  CAGCACTTTG GGAGG
                                ||||  |||||||||| |||||
                                ATTA  GTCGTGAAAC CCTCC
                                  AG        _
GAM900  HUNK     3' CCTCCCAAAGTGCTGAGATTA 27447         A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                                _
GAM900  IL11     3' CCTCCCAAAGTGCTGGGATTA 5326          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  IMPA2    5' CCTTGCAAAGTGCTGGGATTA 95238         AG
                                TAATCTCAGCACTTTG  GAGG
                                ||||||||||||||||  ||||
                                ATTAGGGTCGTGAAAC  TTCC
                                                G_
GAM900  INMT     3' CCTCCCAAAGTGCTGGGATTA 22267         A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LNK      3' CCTCCCAAAGTGCTGGGATTA 18462         A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LTB4R    5' CCTCCCAAAGTGCTGGGATTA 5645          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LYZ      3' CCTCCCAAAGTGCTGGGATTA 4097          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LZTS1   3' CCTCCCAAAGTGCTGAGATTG 40688          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                GTTAGAGTCGTGAAAC CCTCC
                                                _
GAM900  MATN3   3' CCTCCCAAAGTGCTGGGATTA 9936           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  MDM2    3' CCTCCCAAAGTGCTGGGATTA 9971           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  MDM2    3' CCTCCCAAAGTGCTGGGATTA 22509          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  MDM2    3' CCTCCCAAAGTGCTGGGATTA 22513          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  MDM2    3' CCTCCCAAAGTGCTGGGATTA 22517          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  MDM2    3' CCTCCCAAAGTGCTGGGATTA 22521          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  MEFV    3' CCTCCCAAAGTGCTGGGATTA 4131           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  MHC2TA  3' CCTCCCAAAGTGCTGGGATTA 4168           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  MHC2TA  3' CCTCCCAAAGTGCTGGGATTA 4169           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  MICB     3'  GCATCCCAAAGTGCTGGGATTA 19826             A  GG
                                TAATCTCAGCACTTTG GGA  GC
                                |||||||||||||||| |||  ||
                                ATTAGGGTCGTGAAAC CCT  CG
                                          _  A_
GAM900  MLANA    3'  CCTCCCAAAGTGCTGGAATTA  18583     CT       A
                                TAAT  CAGCACTTTG GGAGG
                                ||||  |||||||||| |||||
                                ATTA  GTCGTGAAAC CCTCC
                                  AG        _
GAM900  MLF2     5'  CCCCCTGGAGCTGAGAT     18374        ACT  G   A
                                ATCTCAGC   TT AGG GGG
                                ||||||||   || ||| |||
                                TAGAGTCG   AG TCC CCC
                                    ___  G  _
GAM900  MPL      3'  CCTCCCAAAGTGCTGGGATTA  18137             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  MTR      3'  CCTCCCAAAATGCTGGGATTA  4210          C    A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||| |||| |||||
                                ATTAGGGTCGT AAAC CCTCC
                                      A   _
GAM900  NCOA6IP  3'  CCCTCCCCAAGTGCTGGAATTA 45736     CT       T A
                                TAAT  CAGCACTT G GGAGGG
                                ||||  |||||||| | ||||||
                                ATTA  GTCGTGAA C CCTCCC
                                  AG       _ C
GAM900  NDRG3    3'  CCTCCCAAAGTGCTGGGATTA  49295             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  NEU3     5'  GCCTTCCAAAGCGCTGAGATTG 21850          A   GA
                                TAATCTCAGC CTTT  GGAGGGC
                                |||||||||| ||||  |||||||
                                GTTAGAGTCG GAAA  CCTTCCG
                                      C   __
GAM900  NFRKB    5'  CCTCCCAAAGTACTGAGATTA  20496         C     A
                                TAATCTCAG ACTTTG GGAGG
                                ||||||||| |||||| |||||
                                ATTAGAGTC TGAAAC CCTCC
                                      A     _
GAM900  NONO     3'  CCTCCCAAAATGCTGGGATTA  82016          C    A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||| |||| |||||
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                                ATTAGGGTCGT AAAC CCTCC
                                      A   _
GAM900  NQO1     3'  CCTCCCAAAGTGCTGGGATTA  6155              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  PCDHA9   3'  CCTCCCAAAATGCTGGGATTA  25759          C   A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||| |||| |||||
                                ATTAGGGTCGT AAAC CCTCC
                                      A   _
GAM900  PCDHA9   3'  CCTCCCAAAGTGCTGGGATTA  25760             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  PCDHB11  3'  CCTCCCAAAGTGCTGGGATTA  38414             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  PCDHB11  3'  CCTCCCAAAGTGCTGTGATTA  38415      T      A
                                TAATC CAGCACTTTG GGAGG
                                ||||| |||||||||| |||||
                                ATTAG GTCGTGAAAC CCTCC
                                   T     _
GAM900  PER2     3'  CCTCCCAAAGTGCTGGGATTA  43030             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  PIGR     3'  CCTCCCAAAGTGCTGGGATTA  72594             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  PIGR     3'  CTTCTCAAAGTACTGGGATTA  72601         C
                                TAATCTCAG ACTTTGAGGAG
                                |||||||| ||||||||||
                                ATTAGGGTC TGAAACTCTTC
                                      A
GAM900  PIK3C2B  3'  CCTCCCAAAGTGCTGGGATTA  10563             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  PIK3CD   3'  CCTCCCAAAGTGCTGGGATTA  17242             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  PMCHL1   3'  CTTCCCAAAGTGCTGGGATTA  49071          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTTC

                                        _
GAM900  PPEF2    3'  CCTCCCAAAGTGCTGGGATTA  20667          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  PPID     3'  CCTCCCAAAGTGCTGGGATTA  87429          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  PRKR     3'  CCTCCCAAAGTGCTGGGATTA  10878          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  PSG6     3'  TCCCAAAGTGCTAGGATTA   10940     TC   A
                                TAATC  AGCACTTTG GGA
                                |||||  ||||||||| |||
                                ATTAG  TCGTGAAAC CCT
                                   GA       _
GAM900  PTGIS    3'  CCTCCCAAAGTGCTAGGATTA  6330      TC   A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900  PTGIS    3'  CCTCCCAAAGTGCTGGGATTA  6331          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  PTPN18   3'  CCTCCCAAAGTGCTGAGATTA  26863          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC

                                        _
GAM900  PVR      3'  CCTCCCAAAGTGCTGAATTA  21476     C    A
                                TAAT TCAGCACTTTG GGAGG
                                ||||  |||||||||| |||||
                                ATTA AGTCGTGAAAC CCTCC

                                     _      _
GAM900  RAB36    3'  CCTCCCAAAGTGCTGGGATTA  16953          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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```
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  RAB36    3'  CCTCCCAAAGTGCTGGGATTA  16954            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  RABL2A   3'  CCTCCCAAAGTGCTGGGATTA  25501            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  RABL2B   3'  CCTCCCAAAGTGCTGGGATTA  23000            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  RAD1     5'  CCTCCCAAAGCGCTGGGATTA  55912          A   A
                                TAATCTCAGC CTTTG GGAGG
                                |||||||||| ||||| |||||
                                ATTAGGGTCG GAAAC CCTCC
                                      C   _
GAM900  RGS9     5'  CCTCCCAAAGTGCTGGGATTA  13833            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  RHD      3'  CCTCCCAAAGTGCTGGA     32301    T      A
                                TC CAGCACTTTG GGAGG
                                || |||||||||| |||||
                                AG GTCGTGAAAC CCTCC

                                  _     _
GAM900  RHD      3'  CCTCCCAAAGTGCTGGGATTA  32302            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  RHD      3'  CCTCCCAAAGTGCTGGA     32610    T      A
                                TC CAGCACTTTG GGAGG
                                || |||||||||| |||||
                                AG GTCGTGAAAC CCTCC

                                  _     _
GAM900  RHD      3'  CCTCCCAAAGTGCTGGGATTA  32611            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  RPH3AL   3'  CCTCCCAAAGTGCTGGGATTA  22743            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC

                                          _
GAM900  RPP30    3' CCTCCCAAAGTGCTGGGATTA 21163            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                          _
GAM900  SCML2    3' CCTTGCAAAATGCTGGGATTA 20314          C   AG
                                TAATCTCAGCA TTTG  GAGG
                                |||||||||||| ||||  ||||
                                ATTAGGGTCGT AAAC  TTCC
                                      A   G_
GAM900  SEDL     3' CCTCCCAAAGTACTGGGATTA 27330        C    A
                                TAATCTCAG ACTTTG GGAGG
                                ||||||||| |||||| |||||
                                ATTAGGGTC TGAAAC CCTCC
                                      A    _
GAM900  SEDL     3' CCTCCCAAAGTGCTAGGATTA 27331      TC       A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900  SEDL     3' CCTCCCAAAGTGCTGGGATTA 27332           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                          _
GAM900  SEPN1    3' CCTCCCAAAGTGCTGGGATTA 66365           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                          _
GAM900  SERPINB9 3' CCTCCCAAAGTGCTGGGATTA 14752           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                          _
GAM900  SERPINB9 3' CCTCCCAAAGTGCTAGGATTA 14751      TC       A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900  SH3BP2   3' CCCTCCCATGTAGCTGGGATTA 11598        _ TT  A
                                TAATCTCAGC AC  TG GGAGGG
                                |||||||||| ||  || ||||||
                                ATTAGGGTCG TG  AC CCTCCC
                                      A  T_  _
GAM900  SH3BP2   3' CCTCCCAAAGTGCTGGGATTA 11599           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  SIL     5' CCTCCCAAAATGCTGGGATTA 11687        C   A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||| |||| |||||
                                ATTAGGGTCGT AAAC CCTCC
                                      A  _
GAM900  SLA2    3' CCTCCCAAAGTGCTGGGATTA 49897          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  SLC15A1 3' CAAAGTGCTGGGATTA     17397
                                TAATCTCAGCACTTTG
                                ||||||||||||||||
                                ATTAGGGTCGTGAAAC

GAM900  SLC17A5 3' CCTCACAAAGTGTTGAGA   24890          AG
                                TCTCAGCACTTTG  GAGG
                                ||||||||||||  ||||
                                AGAGTTGTGAAAC  CTCC
                                      A_
GAM900  SLC24A1 3' CCTCCCAAAGTGCTGGGATTA 16375           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  SNAP23  3' CCTCCCAAAGTACTGGGATTA 13808       C    A
                                TAATCTCAG ACTTTG GGAGG
                                ||||||||| |||||| |||||
                                ATTAGGGTC TGAAAC CCTCC
                                      A   _
GAM900  SNAP23  3' CCTCCCAAAGTACTGGGATTA 55461       C    A
                                TAATCTCAG ACTTTG GGAGG
                                ||||||||| |||||| |||||
                                ATTAGGGTC TGAAAC CCTCC
                                      A   _
GAM900  SNX15   3' TCCCAAAGTGCTGAGATTA   73751          A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGAGTCGTGAAAC CCT
                                       _
GAM900  SPN     3' CCTCCCAAAGTGCTGAGATTA 11920          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                       _
GAM900  SULT2B1 5' TCCCAAAGTGCTGGGATTA   16033          A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
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                                ATTAGGGTCGTGAAAC CCT
                                                _
GAM900  TAPBP    3'  CCTCCCAAAGTGCTGGGATTA  12121            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  TAPBP    3'  CCTCCCAAAGTGCTGGGATTA  12122            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  TBXA2R   3'  CCTCCCAAAGTGCTGGGAT   6486             A
                                ATCTCAGCACTTTG GGAGG
                                |||||||||||||| |||||
                                TAGGGTCGTGAAAC CCTCC
                                                _
GAM900  TERF1    3'  CCTCCCAAAGTGCTGAGATTA  33970            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                                _
GAM900  TERF2    3'  CCTCCCAAAGTGCTGGGATTA  18946            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  TES      3'  CCTCCCAAAGTGCTGGGATTA  72002            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  TIM3     3'  CCTCCCAAAGCACTGGGATTA  51339         CA   A
                                TAATCTCAG  CTTTG GGAGG
                                |||||||||  ||||| |||||
                                ATTAGGGTC  GAAAC CCTCC
                                      AC    _
GAM900  TIMM23   3'  CCTCCCAAAGTGCCGAGATTG  60139        A    A
                                TAATCTC GCACTTTG GGAGG
                                ||||||| |||||||| |||||
                                GTTAGAG CGTGAAAC CCTCC
                                     C      _
GAM900  TIRAP    3'  CCCAAAGTGCTGGGATTA    53568            A
                                TAATCTCAGCACTTTG GG
                                |||||||||||||||| ||
                                ATTAGGGTCGTGAAAC CC
                                                _
GAM900  TNFAIP1  5'  GCCCCCGGGGACGCACTGAGAT 40923         CAC_  GA  A
           TA                     TAATCTCAG   TTT  GG GGGC
                                |||||||||   |||  || ||||
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                                ATTAGAGTC   AGG  CC CCCG
                                     ACGC   GG  _
GAM900  TNFRSF11A 3'  CCTCCCAAAGTACTGGGATTA  13852        C     A
                                TAATCTCAG ACTTTG GGAGG
                                ||||||||| |||||| |||||
                                ATTAGGGTC TGAAAC CCTCC
                                     A    _
GAM900  TNFRSF9   3'  CCTCCCAAAGTGCTGGGATTA  7787             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TP53BP2   5'  CCTCCCAAAGTGCTGGATTA   18301      T        A
                                TAATC CAGCACTTTG GGAGG
                                ||||| |||||||||| |||||
                                ATTAG GTCGTGAAAC CCTCC
                                  _       _
GAM900  TPMT      3'  CCCAAAGTGCTAGGATTA    4536       TC       A
                                TAATC  AGCACTTTG GG
                                |||||  ||||||||| ||
                                ATTAG  TCGTGAAAC CC
                                   GA       _
GAM900  TPMT      3'  CCTCCCAAAGTGCTGGGATTA  4537             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TRAF5     3'  CCTCCCAAAGTGCTGAGATTA  16077            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                                 _
GAM900  TRPM6     3'  CTTCCCAAAGTGCTGGGATTA  34540            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTTC
                                                 _
GAM900  TRPV1     3'  CCTCCCAAAGTGCTGGGATTA  38074            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TRPV1     3'  CCTCCCAAAGTGCTGGGATTA  38075            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TRPV1     3'  CCTCCCAAAGTGCTGGGATTA  54795            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TRPV1   3' CCTCCCAAAGTGCTGGGATTA 54796          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TRPV1   3' CCTCCCAAAGTGCTGGGATTA 54828          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TRPV1   3' CCTCCCAAAGTGCTGGGATTA 54829          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TRPV1   3' CCTCCCAAAGTGCTGGGATTA 54860          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TRPV1   3' CCTCCCAAAGTGCTGGGATTA 54861          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TUFT1   3' CTTCCCAAAGTGCTAGGATTA 39260     TC     A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTTC
                                   GA        _
GAM900  UGDH    3' CCTCCCAAAGTGCTGGGATTA 12542          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  UMPS    3' TCTCAAAGTGCTGGGATTA  4560
                                TAATCTCAGCACTTTGAGG
                                ||||||||||||||||||
                                ATTAGGGTCGTGAAACTCT

GAM900  VENTX2  3' CCTCCCAAAGTGCTGGGATTA 27109           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  VHL     3' CCCTCCTGAGCTGGGATTA  5067        ACTT G
                                TAATCTCAGC   T AGGAGGG
                                |||||||||    | |||||||
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                                ATTAGGGTCG   A TCCTCCC
                                      ____ G
GAM900  VIPR2   3' CCTCCCAAAGTGCTGGGATTA 12607          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  WHSC1   5' CCTCCCAAAGTGCTGGGATTA 23657          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  WHSC1   5' CCTCCCAAAGTGCTGGGATTA 29908          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  WHSC1   5' CCTCCCAAAGTGCTGGGATTA 55826          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  WHSC1   5' CCTCCCAAAGTGCTGGGATTA 55843          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  XRCC2   3' CCTCCCAAAGTGCTAGGATTA 18319      TC      A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900  YES1    3' CCTCCCAAAGTGCTGGGATTA 18351          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  ZNF133  5' CCTCCCAAAATGCTGGGATTA 12834        C  A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||||| |||| |||||
                                ATTAGGGTCGT AAAC CCTCC
                                      A  _
GAM900  ZNF74   5' CCTCCCAAAGTGCTGGGATTA 12793          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  APOL2   3' CCTCCCAAAGTGCTGGGATTA 48045          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  ARHF     3'  CCTCCCAAAGTGCTGGGATTA  38739          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  ARHGAP11A 3'  CCTCCCAAAGTGCTGGGATTA  28794          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  ARHGAP5  5'  CCTCCCAAAGTGCTGCGATTA  77071     T    A
                                TAATC CAGCACTTTG GGAGG
                                ||||| |||||||||| |||||
                                ATTAG GTCGTGAAAC CCTCC
                                   C    _
GAM900  ARPP-19  3'  CCTCCCAAAGTGCTGGGATTA  21793          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  ASB16    3'  CCTCCCAAAGTGCTGGGATTA  69933          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  BA108L7.2 3'  CCTCCCAAAGCACTGGGATTA  48260     CA   A
                                TAATCTCAG  CTTTG GGAGG
                                |||||||||  ||||| |||||
                                ATTAGGGTC  GAAAC CCTCC
                                     AC    _
GAM900  BNIP-S   3'  CCTCCCAAAGTGCCGAGATTA  56258     A    A
                                TAATCTC GCACTTTG GGAGG
                                ||||||| |||||||| |||||
                                ATTAGAG CGTGAAAC CCTCC
                                    C     _
GAM900  BTN3A1   3'  TCCCAAAGTGCTGGGATTA   22927          A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                       _
GAM900  C13orf1  3'  CCTCCCAAAGTGCTGGAATTA  39966     CT   A
                                TAAT  CAGCACTTTG GGAGG
                                ||||  |||||||||| |||||
                                ATTA  GTCGTGAAAC CCTCC
                                  AG        _
GAM900  C1orf24  3'  CTTCCCAAAGTGCTGGGATTA  53715          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTTC

                                        _
GAM900  C1QTNF6  3'  GCCTCTCAAAATGCTGGGATTA 49146          C     GA
                                TAATCTCAGCA TTTGAG  GGGC
                                |||||||||| ||||||  ||||
                                ATTAGGGTCGT AAACTC  TCCG
                                      A    __
GAM900  C20orf142 3'  CCTCCCAAAGTGCTGGGATTA  74770            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  C22orf19  3'  CCTCCCAAAGTGCTAGGATTA  13419      TC       A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900  C2F       3'  TTCCCAAAGTGCTGGGATTA   20935           A
                                TAATCTCAGCACTTTG GGAG
                                |||||||||||||||| ||||
                                ATTAGGGTCGTGAAAC CCTT

                                        _
GAM900  C3F       3'  CCTCCCAAAGTGCTGGGATTA  19289           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  C6orf5    3'  CCTCCCAAAGTGCTAGGATTA  31344      TC       A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900  C6orf5    3'  CCTCCCAAAGTGCTGGGATTA  31345           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  C9orf9    3'  CCTCCCAAAGTGCTGGGATTA  38507           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  C9orf9    3'  CCTCCCAAAGTGCTGGGATTA  38508           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  CDC14B    3'  CCTCCCAAAGTGCTGGGATTA  52847           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                        _
GAM900  CECR1    3'  CCTCCCAAAGCACTGGGATTA  33810        CA    A
                                TAATCTCAG  CTTTG GGAGG
                                |||||||||  ||||| |||||
                                ATTAGGGTC  GAAAC CCTCC
                                     AC    _
GAM900  CECR1    3'  CTCCCAAAGTGCTGGAATTA  33812     CT       A
                                TAAT  CAGCACTTTG GGAG
                                ||||  |||||||||| ||||
                                ATTA  GTCGTGAAAC CCTC
                                  AG        _
GAM900  CIP29    3'  CCTCCCAAAGTGCTGGATTA  50403      T       A
                                TAATC CAGCACTTTG GGAGG
                                ||||| |||||||||| |||||
                                ATTAG GTCGTGAAAC CCTCC
                                      _       _
GAM900  COQ7     3'  CTTCCCAAAGTGCTGGGATTA  32331             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTTC
                                        _
GAM900  CPSF2    3'  CCTCCCAAAGTGCTGGGATTA  61576             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                        _
GAM900  CPSF2    3'  CCTCCCAAAGTGCTGGGATTA  61577             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                        _
GAM900  DCOHM    3'  CCTCCCAAAGTGCTGGGATTA  49594             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                        _
GAM900  DKFZp434A2417 3'  CCTCCCAAAGTGCTGGGATTA  66099              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                        _
GAM900  DKFZP434F0318 3'  CTTCCCAAAGTGCTGGGATTA  48010              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTTC
                                        _
GAM900  DKFZp434F1819 5'  CAAAGTGCTGGGATTA      50005
                                TAATCTCAGCACTTTG
                                ||||||||||||||||
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                                ATTAGGGTCGTGAAAC

GAM900  DKFZP434J037 3'  CCTCCCAAAGTGCTGGGATTA  48209              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  DKFZp547H025 3'  CCTCCCAAAGTGCTGGGATTA  39355              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  DKFZP564K0322 3'  CCTCCCAAAATGCTGGGATTA  49358          C   A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||| |||| |||||
                                ATTAGGGTCGT AAAC CCTCC
                                       A  _
GAM900  DKFZP566I1024 3'  CCTCCCAAAGTGCTGGGATTA  70099              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  DKFZp761J139 5'  CCTCCCAAAGTGCTGGGATTA  50106              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  DKFZp761N1114 3'  CCTCCCAAAGTGCTGGGATTA  79016             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  DRIM     3'  CCTCCCAAAGTGCTGGGATTA  27177                A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  DSCR6    3'  CCTCCCAAAGTGCTGGGATTA  38544                 A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  EVI5     3'  CCTCCCAAAGTGCTGGGATTA  18993                 A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  EVI5     3'  CCTCCCAAAGTGCTGGGATTA  18994                 A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FBP17    3' CCTCCCAAAGTGCTGAGATTA 72785          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                                _
GAM900  FER1L4   3' CCTCCCAAAGTGCTGGGATTA 47337          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLB6421  3' TCCCAAAGTGCTGGGATTA  39234          A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                                _
GAM900  FLJ00060 5' CCTCCCAAAGTGCTGGGATTA 61095          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ10298 3' CCTCCCAAAGTGCTGGGATTA 35986          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ10346 5' CCTCCCAAAGTGCTGGGATTA 36040          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ10535 3' CCTCCCAAAGTGCTGGGATTA 36236          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ10535 3' CCTCCCAAAGTGCTGGGATTA 36237          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ10560 3' CCTCCCAAAGTGCTGGGATTA 36276          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ10687 3' CCTCCCAAAGTGCTGAGATTA 36408          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGAGTCGTGAAAC CCTCC
                                       _
GAM900  FLJ10713 3' CCTCCCAAAATGCTGGGA    36466        C   A
                                TCTCAGCA TTTG GGAGG
                                |||||||| |||| |||||
                                AGGGTCGT AAAC CCTCC
                                    A   _
GAM900  FLJ10846 3' CCTCCCAAAGTGCTGGAATTA  36737      CT        A
                                TAAT  CAGCACTTTG GGAGG
                                ||||  |||||||||| |||||
                                ATTA  GTCGTGAAAC CCTCC
                                  AG        _
GAM900  FLJ10922 3' CCCAAAGTGCTGGAATTA    36873      CT        A
                                TAAT  CAGCACTTTG GG
                                ||||  |||||||||| ||
                                ATTA  GTCGTGAAAC CC
                                  AG        _
GAM900  FLJ10956 3' CCTCCCAAAGTGCTGGGATTA  36916              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  FLJ12610 3' CCTCCCAAAGTGCTGGGATTA  45512              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  FLJ12644 3' CCTCATGATGAGATTA       43556        G  CTT
                                TAATCTCA CA   TGAGG
                                |||||||| ||   |||||
                                ATTAGAGT GT   ACTCC
                                    A ____
GAM900  FLJ12747 3' CCTCCCAAAGTGCTGGGATTA  49715              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  FLJ12975 3' CCTCCCAAAGTGCTGAGATTA  69578              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                       _
GAM900  FLJ12975 3' CCTCCCAAAGTGCTGGGAT    69579             A
                                ATCTCAGCACTTTG GGAGG
                                |||||||||||||| |||||
                                TAGGGTCGTGAAAC CCTCC
                                       _
GAM900  FLJ13072 5' CCTCCCAAAGTGCTGGGATTA  89807              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC

                                       _
GAM900  FLJ13102  3' CCCTCCCAAAGTGCTGGGATTA 46006          A
                                TAATCTCAGCACTTTG GGAGGG
                                |||||||||||||||| ||||||
                                ATTAGGGTCGTGAAAC CCTCCC

                                       _
GAM900  FLJ13114  3' CCTCCCAAAGTGCTGGGATTA  44595          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                       _
GAM900  FLJ13193  3' CCTCCCAAAGTGCTGGGAT    49763        A
                                ATCTCAGCACTTTG GGAGG
                                |||||||||||||| |||||
                                TAGGGTCGTGAAAC CCTCC

                                       _
GAM900  FLJ13197  3' CCTCCCAAAGTGCTGGGATTA  44849          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                       _
GAM900  FLJ13305  5' CCCAAAGTGCTGGGATTA    90126        A
                                TAATCTCAGCACTTTG GG
                                |||||||||||||||| ||
                                ATTAGGGTCGTGAAAC CC

                                       _
GAM900  FLJ13952  3' CTTCCCAAAGTGCTGGGATTA  45615          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTTC

                                       _
GAM900  FLJ14351  3' CCTCCCAAAGTGCTAGGATTA  45322      TC      A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900  FLJ14442  3' CCTCCCAAAGTGCTGAGATTA  51365          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC

                                       _
GAM900  FLJ14824  3' CAAAGTGCTGGATTA       51640      T
                                TAATC CAGCACTTTG
                                ||||| ||||||||||
                                ATTAG GTCGTGAAAC

                                        _
GAM900  FLJ14950  3' CCTCCCAAAGTGCTGGGATTA  51717          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ14957  3'  CCTCCCAAAGTGCTGAGATTA  51745          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ20045  3'  CCTCCCAAAGTGCTGGGATTA  34417          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ20079  3'  CCTCCCAAAGTGCTGGGATTA  34491          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ20097  3'  CCTCCCAAAGTGCTGGGATTA  34561          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ20136  3'  CCTCCCAAAGTGCTGGGATTA  34610          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ20342  3'  CCTCCCAAAGTGCTGGGATTA  34988          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ20344  3'  CCTCCCAAAGTGCTGGGATTA  35008          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ20452  3'  GCCCTCCCAAAGTGCTGGGATT 35204           A
          A                      TAATCTCAGCACTTTG GGAGGGC
                                |||||||||||||||| |||||||
                                ATTAGGGTCGTGAAAC CCTCCCG
                                                _
GAM900  FLJ20507  3'  CCTCCCAAAGTGCTGGGATTA  35279          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ20507  3'  CCTCCCAAAGTGCTGGGATTA  60214          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ20671 3' CCTCCCAAAGTGCTGGGATTA 35520          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ20700 3' CCTCCCAAAGTGCTGGGATTA 35572          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ21302 3' CCTCCCAAAGTGCTGGGATTA 43213          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ22002 3' CCTCCCAAAGTGCTAGGATTA 45770     TC   A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900  FLJ22316 5' CCTCCCAAAGTGCTGGGATTA 46918          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ22969 3' CCTCCCAAAGTGCTGGGATTA 68648          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ23024 3' CCTCCCAAAGTGCTGGGATTA 46268          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  FLJ23209 3' TCCCAAAGTGCTAGGATTA   46056     TC   A
                                TAATC  AGCACTTTG GGA
                                |||||  ||||||||| |||
                                ATTAG  TCGTGAAAC CCT
                                   GA       _
GAM900  FLJ23323 3' TCCCAAAGTGCTGGGATTA   45058          A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                                _
GAM900  FLJ23356 3' CCTCCAAAGTGCTGGGATTA  49937          GA
                                TAATCTCAGCACTTT  GGAGG
                                |||||||||||||||  |||||
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                                ATTAGGGTCGTGAAA  CCTCC
                                                 __
GAM900  FLJ23392  3'  CCTCCCAAAGTGCTGGGATTA  45530          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  FLJ23392  3'  GCCTTAAAAAGTGCTGGGATTA 45535          GAGG
                                TAATCTCAGCACTTT   AGGGC
                                |||||||||||||||   |||||
                                ATTAGGGTCGTGAAA   TTCCG
                                                  AA__
GAM900  FLJ23556  3'  CCTCCCAAAGTGCTGGGATTA  45945          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  FLJ31101  3'  CCTCCCAAAGTGCTGGGATTA  35708          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  FLJ31153  3'  CCTCCCAAAGCGCTGGGATTA  58120        A   A
                                TAATCTCAGC CTTTG GGAGG
                                |||||||||| ||||| |||||
                                ATTAGGGTCG GAAAC CCTCC
                                      C    _
GAM900  FLJ32334  3'  CCTCCCAAAGTGCTGGGATTA  57982          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  FLJ32865  3'  CCTCCCAAAGTGCTGGGATTA  58171          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  FLJ32894  3'  CCTCCCAAAGTGCTGGGATTA  58338          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  GMPPB     5'  CTTCCCAAAGTGCTGGGATTA  95737          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTTC
                                                 _
GAM900  GNG4      3'  CCTCCCAAAGCGCTGGGATTA  15612        A   A
                                TAATCTCAGC CTTTG GGAGG
                                |||||||||| ||||| |||||
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                                ATTAGGGTCG GAAAC CCTCC
                                      C    _
GAM900  GOLGA3   3'  CCTCCCAAAGTGCTGGAATTA  19714     CT        A
                                TAAT  CAGCACTTTG GGAGG
                                ||||  |||||||||| |||||
                                ATTA  GTCGTGAAAC CCTCC
                                  AG        _
GAM900  GP5      3'  CCTCCCAAAGTGCTGGGATTA  15642             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  GREB1    3'  CCTCCCAAAGTGCTGGGATTA  27867              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                               _
GAM900  GTPBG3   3'  CCTCCCAAAGTGCTGGGAT   50896             A
                                ATCTCAGCACTTTG GGAGG
                                |||||||||||||| |||||
                                TAGGGTCGTGAAAC CCTCC
                                              _
GAM900  HARS2    3'  CCTCCCAAAGTGCTGGGATTA  55032             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                               _
GAM900  HRH4     3'  CCTCCCAAAGTGCTGGGATTA  41250             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                               _
GAM900  HSNOV1   3'  CCTCCCAAAGTGCTGGGATTA  34006             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                               _
GAM900  HSPC065  3'  GCCCTCTCAAAGTGCTGGGATT 26304               G
          A                      TAATCTCAGCACTTTGAG AGGGC
                                 |||||||||||||||||| |||||
                                 ATTAGGGTCGTGAAACTC TCCCG
                                                _
GAM900  ICK      3'  CCTCCCAAAGTACTGGGATTA  29925         C    A
                                TAATCTCAG ACTTTG GGAGG
                                ||||||||| |||||| |||||
                                ATTAGGGTC TGAAAC CCTCC
                                      A    _
GAM900  JM11     3'  CCTCCCAAAGTGCTGGGATTA  53255             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  KIAA0022 3' TCCCAAAGTGCTGGGATTA  29672          A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT

                                        _
GAM900  KIAA0063 3' CCTCCCAAAGTGCTGGGATTA 29620          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  KIAA0087 3' CCTCCCAAAATGCTGGGATTA 28696        C  A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||| |||| |||||
                                ATTAGGGTCGT AAAC CCTCC
                                      A  _
GAM900  KIAA0090 3' CCTCCCAAAGTGCCGGGATTA 88440      A    A
                                TAATCTC GCACTTTG GGAGG
                                ||||||| |||||||| |||||
                                ATTAGGG CGTGAAAC CCTCC
                                    C     _
GAM900  KIAA0161 3' CTTCCCAAAGTGCTGGAATTA 28505    CT     A
                                TAAT  CAGCACTTTG GGAGG
                                ||||  |||||||||| |||||
                                ATTA  GTCGTGAAAC CCTTC
                                  AG        _
GAM900  KIAA0186 3' CTTCTCAAAGTGTTGAGAT  40749
                                ATCTCAGCACTTTGAGGAG
                                ||||||||||||||||||
                                TAGAGTTGTGAAACTCTTC

GAM900  KIAA0210 5' CCTCCCAAAGTGCTGGGATTA 28474          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  KIAA0391 3' CCTCCCAAAGTGCTGGGATTA 27910          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  KIAA0459 3' CCTCCCAAAGTGCTAGGATTA 60987    TC    A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                  GA        _
GAM900  KIAA0469 3' CCTCCCAAAGTGCTAGGATTA 29325    TC    A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
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                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900  KIAA0469 3' CCTCCCAAAGTGCTGGGATTA 29326          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                         _
GAM900  KIAA0472 5' CCTCCCAAAGTGCTGGGATTA 71862          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                         _
GAM900  KIAA0478 3' CCTCCCAAAGTGCTAGGATTA 29545      TC  A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900  KIAA0495 3' CCTCCCAAAGTGCTGGGATTA 62578          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                         _
GAM900  KIAA0513 3' CCTCCCAAAGTGCTGGGATTA 28350          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                         _
GAM900  KIAA0544 3' CCTCCCAGAGTGCTGAGATTA 70901          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAGAC CCTCC
                                         _
GAM900  KIAA0555 3' CCTCCCAAAGTGCTAGGATTA 28881      TC  A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900  KIAA0557 3' CCTCCCAAAGTGCTGGGATTA 77994          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                         _
GAM900  KIAA0561 3' CCTCCCAAAGTGCTGGGATTA 65878          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                         _
GAM900  KIAA0562 3' CCTCCCAAAGTGCTGGAATTA 28150      CT  A
                                TAAT  CAGCACTTTG GGAGG
                                ||||  |||||||||| |||||
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                                ATTA  GTCGTGAAAC CCTCC
                                  AG        _
GAM900  KIAA0594 3' CCTCCCAAAGTGCTGGGATTA  64893           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                          _
GAM900  KIAA0599 3' CCTCCCAAAGTGCTGGGATTA  77174           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                          _
GAM900  KIAA0682 3' TCCCAAAGTGCTGAGATTA    29372          A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGAGTCGTGAAAC CCT
                                          _
GAM900  KIAA0737 3' CCTCCCAAAGTGCTGGGATTA  29133           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                          _
GAM900  KIAA0798 3' CCTCCCAAAGTGCTGGGATTA  27721           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                          _
GAM900  KIAA0831 5' CCTCCCAAAGTGCTGCGATTA  29969      T    A
                                TAATC CAGCACTTTG GGAGG
                                ||||| |||||||||| |||||
                                ATTAG GTCGTGAAAC CCTCC
                                  C       _
GAM900  KIAA0841 3' CCTCCCAAAGTGCTGGGATTA  71380           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                          _
GAM900  KIAA0861 3' CCTCCCAAAGTGCTGGGATTA  88921           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                          _
GAM900  KIAA0931 3' CCTCCCAAAGTGCTGTGATTA  67417      T    A
                                TAATC CAGCACTTTG GGAGG
                                ||||| |||||||||| |||||
                                ATTAG GTCGTGAAAC CCTCC
                                  T       _
GAM900  KIAA1010 3' CCCGCCTCCCTGCTGAGATTA  72071          CTTT  A
                                TAATCTCAGCA   GAGG GGG
                                ||||||||||    |||| |||
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                                ATTAGAGTCGT   CTCC CCC
                                      CC__   G
GAM900  KIAA1026 3' TCCCAAAGTGCTGGGATTA   71210          A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                                _
GAM900  KIAA1040 3' CCTCCCAAAGTGCTGACATTA  72224    C       A
                                TAAT TCAGCACTTTG GGAGG
                                |||| |||||||||| |||||
                                ATTA AGTCGTGAAAC CCTCC
                                  C       _
GAM900  KIAA1054 3' CCTCCCAAAATGCTGGGATTA  68432        C   A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||| |||| |||||
                                ATTAGGGTCGT AAAC CCTCC
                                      A  _
GAM900  KIAA1143 3' CCTCCCAAAGTGCTGGGATTA  68674          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  KIAA1155 3' CCTCCCAAAGTGCTGGGATTA  62230          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  KIAA1185 3' CCCCTCAAAGTGCTGGGATTA  62603            A
                                TAATCTCAGCACTTTGAGG GG
                                |||||||||||||||||| ||
                                ATTAGGGTCGTGAAACTCC CC
                                                _
GAM900  KIAA1185 3' CCTCCCAAAGTGCTGGGATTA  62604          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  KIAA1193 3' CCTCCCAAAGTGCTGGGATTA  67636          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  KIAA1198 3' CCCAAAGTGCTGGGATTA    63296          A
                                TAATCTCAGCACTTTG GG
                                |||||||||||||||| ||
                                ATTAGGGTCGTGAAAC CC
                                                _
GAM900  KIAA1198 3' CCTCCCAAAGTGCTGGGATTA  63298          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  KIAA1198 3' CCTCCCAAAGTGCTGGGATTA 63299        A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  KIAA1198 3' CCTCCCAAAGTGCTGGGATTA 63300        A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  KIAA1200 3' CCTCCCAAAGTGCTGGGATTA 62370        A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  KIAA1254 3' CCTCCCAAAGTGCTGGGATTA 70017        A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  KIAA1257 3' CCTCCCAAAGTGCTGGGATTA 62734        A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  KIAA1287 3' CCTCCCAAAGTGCTGGGATTA 78326        A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  KIAA1320 5' CCTCCCAAAGTGCTGGGATTA 69300        A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  KIAA1328 5' CCTCCCAAAGTGCTGGGATTA 61643        A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  KIAA1349 5' CCTCCCAAAGTGCTGAGATTA 70755        A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                                _
GAM900  KIAA1373 3' CCTCTCAAAGTGCTGGGATTA 70934         G
                                TAATCTCAGCACTTTGAG AGG
                                |||||||||||||||| |||
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                                ATTAGGGTCGTGAAACTC TCC

                                          _
GAM900  KIAA1373 3' CTTCCCAAAGTGCTGAGATTA 70936          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTTC

                                         _
GAM900  KIAA1432 5' TTCTCAAAACACTGAAATTG  66754    C   CAC
                                TAAT TCAG  TTTGAGGA
                                |||| ||||  ||||||||
                                GTTA AGTC  AAACTCTT
                                  A   ACA
GAM900  KIAA1443 3' CCTCCCAAAGTGCTGGGATTA 63827          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                         _
GAM900  KIAA1456 3' GCCCCCCACAGTGCTGGGATTA 66997         T A A
                                TAATCTCAGCACT TG GG GGGC
                                |||||||||||| || || ||||
                                ATTAGGGTCGTGA AC CC CCCG
                                       C _ _
GAM900  KIAA1467 3' CCTCCCAAAGTGCTGGGATTA 71604          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                         _
GAM900  KIAA1493 3' CCTCCCAAAGTGCTGGGATTA 64158          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                         _
GAM900  KIAA1508 3' CAAAGTGCTGGGATTA     61878
                                TAATCTCAGCACTTTG
                                ||||||||||||||||
                                ATTAGGGTCGTGAAAC

GAM900  KIAA1571 3' CCTCCCAAAGTGCTGGGATTA 60953          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                         _
GAM900  KIAA1615 3' CCTCCCAAAGTGCTGGGATTA 68703          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                         _
GAM900  KIAA1615 3' CCTCCCAAAGTGCTGGGATTA 68704          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  KIAA1655 3' CCTCCCAAAGTGCTGGGATTA 66603          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  KIAA1668 3' CCTCCCAAAGTGCTGGGATTA 66470          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  KIAA1671 3' CCTCCCAAAGTGCTGGGATTA 65670          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  KIAA1727 3' CCTCCCAAAGTGCTGGGATTA 64055          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  KIAA1755 3' CCTCCCAAAGTGCTGGGATTA 61341          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  KIAA1784 3' CCTCCCAAAGTGCTGGGAT   65146         A
                                ATCTCAGCACTTTG GGAGG
                                |||||||||||||| |||||
                                TAGGGTCGTGAAAC CCTCC

                                        _
GAM900  KIAA1821 3' CAAAGCACTGGGATTA     71777       CA
                                TAATCTCAG  CTTTG
                                |||||||||  |||||
                                ATTAGGGTC  GAAAC
                                      AC
GAM900  KIAA1829 3' CTCCCAAAGTGCTGGGATTA  61947          A
                                TAATCTCAGCACTTTG GGAG
                                |||||||||||||||| ||||
                                ATTAGGGTCGTGAAAC CCTC

                                        _
GAM900  KIAA1829 3' CTTCCCAAAGTGCTGAGATTA 61948          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTTC

                                        _
GAM900  KIAA1922 5' CCTCCCAAAATGCTGAGATTA 73621        C  A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||| |||| |||||
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                                ATTAGAGTCGT AAAC CCTCC
                                      A   _
GAM900  KIAA1924 3' CCTCCCAAAGTGCTGGGAT   73668          A
                                ATCTCAGCACTTTG GGAGG
                                ||||||||||||| |||||
                                TAGGGTCGTGAAAC CCTCC
                                                _
GAM900  KIAA1971 3' CTCCCAAAGTGCTGGGATTA  74215           A
                                TAATCTCAGCACTTTG GGAG
                                |||||||||||||||| ||||
                                ATTAGGGTCGTGAAAC CCTC
                                                _
GAM900  KIAA1975 5' CCTCCCAAAGTGCTAGGATTA 73970      TC      A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900  KLK7     3' CCTCCCAAAGTGCTGGGATTA 17290          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  KLK7     3' CCTCCCAAAGTGCTGGGATTA 57730          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LAMP3    3' CCTCCCAAAGTGCTGGGATTA 59488          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LY75     3' CCTCCCAAAGTGCTGGGATTA 9836           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  MAIL     3' TCCCAAAATGCTGGGATTA   48654        C  A
                                TAATCTCAGCA TTTG GGA
                                |||||||||| |||| |||
                                ATTAGGGTCGT AAAC CCT
                                      A   _
GAM900  MCLC     3' CCTCCCAAAGTGCTGGGATTA 30679          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  MGC10200 3' CCTCCCAAAGTGCTGGGATTA 58983          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  MGC11386 3' CCTCAAAGTATTGAGATTA  51949       C
                                TAATCTCAG ACTTTGAGG
                                ||||||||| |||||||||
                                ATTAGAGTT TGAAACTCC
                                    A
GAM900  MGC12518 3' CCTCCCAAAGTGCTGGGATTA 64079           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  MGC21675 3' CTCCCAAAGTGCTGAGATTA  53481           A
                                TAATCTCAGCACTTTG GGAG
                                |||||||||||||||| ||||
                                ATTAGAGTCGTGAAAC CCTC
                                      _
GAM900  MGC21738 3' CCTCCCAAAGTGCTGGGATTA 58916           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  MGC2474  3' CCTCCCAAAGTGCTGGGATTA 43718           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  MGC2474  3' CCTCCCAAAGTGCTGGGATTA 43719           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  MGC2477  5' CCTCCCAAAGTGCTGGGATTA 44061           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  MGC2603  3' CCTCCCAAAGTGCTGAGATTA 43858           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                      _
GAM900  MGC29898 3' CTTCCAAAGTGCTGGGATTA  58927           A
                                TAATCTCAGCACTTTG GGAG
                                |||||||||||||||| ||||
                                ATTAGGGTCGTGAAAC CTTC
                                      _
GAM900  MGC4766  5' CCTCCCAAAGTGCTGGGATTA 48775           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  MGC5149  3' TCCCAAAGCGCTGGGATTA  72301        A   A
                                TAATCTCAGC CTTTG GGA
                                |||||||||| ||||| |||
                                ATTAGGGTCG GAAAC CCT
                                     C  _
GAM900  MKRN4    3' CCTTCCAAAGTGCTGGGATTA 47740           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CTTCC

                                        _
GAM900  MLZE     5' CCTCCCAAAGTGCTGGGATTA 48617           A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                       _
GAM900  moblak   3' CCTCCCAAAGTGCTGGA    55493   T       A
                                TC CAGCACTTTG GGAGG
                                || |||||||||| |||||
                                AG GTCGTGAAAC CCTCC

                                 _      _
GAM900  moblak   3' CCTCCCAAAGTGCTGGGATTA 55494          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  MRPL20   3' GCCCTCCCAAAGTGCTGGGATT 35735          A
          A                      TAATCTCAGCACTTTG GGAGGGC
                                |||||||||||||||| |||||||
                                ATTAGGGTCGTGAAAC CCTCCCG

                                       _
GAM900  MRPL44   3' CCTCCCAAAGTGCTGGGATTA 43315          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  MtFMT    3' CCTCCCAAAGTGCTATGATTA 57652      TC      A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   TA       _
GAM900  MYO5C    3' CCTCCCAAAGTGCTAGGATTA 38106      TC      A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900  NDP52    3' GCCGTCCAAAGTGCTGGGATTA 19531          GA  G
                                TAATCTCAGCACTTT  GGA GGC
                                |||||||||||||||  ||| |||
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                                ATTAGGGTCGTGAAA  CCT CCG
                                      __  G
GAM900  NINJ2    3'  CCTCCCAAAGTGCTGGGATTA  33280            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  Nup43    3'  CCTCCAAAGTGCTGTGATTA  44996      T      GA
                                TAATC CAGCACTTT  GGAGG
                                ||||| |||||||||  |||||
                                ATTAG GTCGTGAAA  CCTCC
                                   T      __
GAM900  Nup43    3'  CCTCCCAAAATGCTGGGATTA  44997          C   A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||| |||| |||||
                                ATTAGGGTCGT AAAC CCTCC
                                      A  _
GAM900  NXN      3'  CCTCCCAAAGTGCTGGGATTA  42417            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  OSBPL2   3'  CCTCCCAAAGTGCTGGGATTA  29209            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  OSBPL2   3'  CCTCCCAAAGTGCTGGGATTA  57860            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                      _
GAM900  PASK     5'  TCCCAAAGTGCTGGGATTA   30727            A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                      _
GAM900  PCDH16   3'  GCCCCCTCAGAGTACTAGGA  13607   TC  C      A
                                TC  AG ACTTTGAGG GGGC
                                ||  || ||||||||| ||||
                                AG  TC TGAGACTCC CCCG
                                  GA  A       _
GAM900  PDE10A   3'  CCTAAAGGGCTGAGAT     21861       A   G
                                ATCTCAGC CTTT AGG
                                |||||||| |||| |||
                                TAGAGTCG GGAA TCC
                                      _   A
GAM900  PELI1    5'  CCTCCCAAAGTGCTGGGATTA  40259            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  PELI1    5' CTTCCCAAAGTGCTGGAATTA 40266     CT       A
                                TAAT  CAGCACTTTG GGAGG
                                ||||  |||||||||| |||||
                                ATTA  GTCGTGAAAC CCTTC
                                  AG        _
GAM900  PRO0245  5' CCTCCCAAAGTGCTGAGATTA 26127             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                                 _
GAM900  PRO0365  5' CCTCCCAAAGTGCTGGGATTA 26155             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  PRO1992  3' CCTCCCAAAGTGCTGGGATTA 26055             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  PRO2955  3' CCTCCCAAAGTGCTGGGATTA 37634             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  PSPH     3' CCTCCCAAAGTGCTGGGATTA 15913              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  PSTPIP2  3' CCTCCCAAAGTGCTGGGATTA 44386             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  RAB14    3' CCCTTTTCAGTGTAAGAT    32872     CA    TT
                                ATCT  GCACT  GAGGAGGG
                                ||||  |||||  ||||||||
                                TAGA  TGTGA  CTTTTCCC
                                  A_    __
GAM900  RAB21    3' CCTCCCAAAGTGCTGGGATTA 30384             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  RAB33B   3' CTTCCCAAAGTGCTGGGATTA 48493             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTTC
                                                _
GAM900  RAB39    3'  CCTCCAAAGTGCTGGAATTA  76631     CT       GA
                                TAAT  CAGCACTTT  GGAGG
                                ||||  |||||||||  |||||
                                ATTA  GTCGTGAAA  CCTCC
                                  AG        __
GAM900  RAP140   3'  CCTCCCAAAGTGCTGGGATTA  30842            A
                                TAATCTCAGCACTTTG GGAGG
                                ||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  RNF8     3'  CCTCCCAAAGTGCTGAGATTA  14221            A
                                TAATCTCAGCACTTTG GGAGG
                                ||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                                _
GAM900  RNO2     5'  CCTCCCAAAGTGCTGGGATTA  52767            A
                                TAATCTCAGCACTTTG GGAGG
                                ||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  SC4MOL   3'  CCTCCCAAAGTGCTGGGATTA  22154             A
                                TAATCTCAGCACTTTG GGAGG
                                ||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  SCYA22   3'  CCTCCCAAAGTGCTGGGATTA  90940            A
                                TAATCTCAGCACTTTG GGAGG
                                ||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  SCYA22   3'  CCTCCCAAAGTGCTGGGATTA  90941            A
                                TAATCTCAGCACTTTG GGAGG
                                ||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  SCYA22   3'  CTCCCAAAGTGCTGAGATTA  90944            A
                                TAATCTCAGCACTTTG GGAG
                                ||||||||||||||| ||||
                                ATTAGAGTCGTGAAAC CCTC
                                                _
GAM900  SEC22C   5'  GCCCTCCCGGTCGGCTAAGATT 52057      C  ACT  A
          G                      TAATCT AGC  TTG GGAGGGC
                                 |||||| |||  ||| |||||||
                                 GTTAGA TCG  GGC CCTCCCG
                                    A  GCT  _
GAM900  SEC22C   5'  GCCCTCCCGGTCGGCTAAGATT 14852      C  ACT  A
          G                      TAATCT AGC  TTG GGAGGGC
                                 |||||| |||  ||| |||||||
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                                GTTAGA TCG   GGC CCTCCCG
                                   A  GCT  _
GAM900  SERF1B   3'  CCTCCCAAAGTGCTGGGATTA  43414            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                                 _
GAM900  SIRPB1   3'  CCTCCCAAAGTGCTGGGATTA  20247            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                                 _
GAM900  SLC12A8  3'  CCTCCCAAAGTACTGGGATTA  44897        C   A
                                TAATCTCAG ACTTTG GGAGG
                                ||||||||| |||||| |||||
                                ATTAGGGTC TGAAAC CCTCC
                                      A     _
GAM900  SLC19A3  3'  CCTCCCAAAGAGCTGAGATTA  47483        A   A
                                TAATCTCAGC CTTTG GGAGG
                                |||||||||| ||||| |||||
                                ATTAGAGTCG GAAAC CCTCC
                                      A    _
GAM900  SLC5A7   3'  GCCCTGTTCAAAGTACT    41513    C      G
                                AG ACTTTGAG AGGGC
                                || |||||||| |||||
                                TC TGAAACTT TCCCG
                                  A       G
GAM900  SLC6A14  3'  CCTCCTAAAGTGCTGAGATTA  23349            G
                                TAATCTCAGCACTTT AGGAGG
                                |||||||||||||| ||||||
                                ATTAGAGTCGTGAAA TCCTCC

                                                 _
GAM900  SNAPC1   3'  CCTCCCAAAGTACTGGGATTA  11840        C   A
                                TAATCTCAG ACTTTG GGAGG
                                ||||||||| |||||| |||||
                                ATTAGGGTC TGAAAC CCTCC
                                      A     _
GAM900  SQV7L    5'  CCTCCCAAAGTGCTGTGATTA  70573      T       A
                                TAATC CAGCACTTTG GGAGG
                                ||||| |||||||||| |||||
                                ATTAG GTCGTGAAAC CCTCC
                                   T        _
GAM900  STAF65(gamma) 3'  CTCCCAAAGTGCTGGGATTA  29433              A
                                TAATCTCAGCACTTTG GGAG
                                |||||||||||||||| ||||
                                ATTAGGGTCGTGAAAC CCTC

                                                 _
GAM900  SYT13    3'  CCTCCCAAAGTACTGGGATTA  93453        C   A
                                TAATCTCAG ACTTTG GGAGG
                                ||||||||| |||||| |||||
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                                ATTAGGGTC TGAAAC CCTCC
                                     A     _
GAM900  SYTL4   5' CCTCCCAAAGTGCTGGGATTA 54940          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TADA3L  3' CCTCCCAAAGTGCCGGGATTA 55990      A    A
                                TAATCTC GCACTTTG GGAGG
                                ||||||| |||||||| |||||
                                ATTAGGG CGTGAAAC CCTCC
                                    C      _
GAM900  TCL6    5' CCTCCCAAAGTGCTGGGATTA 24976          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TCL6    3' CCTCCCAAAGTGCTGGGATTA 24977          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TCL6    5' CCTCCCAAAGTGCTGGGATTA 26992          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TCL6    3' CCTCCCAAAGTGCTGGGATTA 26993          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TCL6    5' CCTCCCAAAGTGCTGGGATTA 40080          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TCL6    5' CCTCCCAAAGTGCTGGGATTA 40096          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TCL6    5' CTTCTCAAAGTGCTGGGATTA 40132
                                TAATCTCAGCACTTTGAGGAG
                                |||||||||||||||||||||
                                ATTAGGGTCGTGAAACTCTTC

GAM900  TCL6    5' CTTCTCAAAGTGCTGGGATTA 40157
                                TAATCTCAGCACTTTGAGGAG
                                |||||||||||||||||||||
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                                ATTAGGGTCGTGAAACTCTTC

GAM900  THEA     3'  TCCCAAAGTGCTGGGATTA   66299            A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                                 _
GAM900  TRIM16   3'  CCTCCCAAAGTGCTGGGATTA  21336             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900  TRIM5    3'  CCTCCCAAAGTGCTGGGATTA  52296             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900  TRIM5    3'  CCTCCCAAAGTGCTGGGATTA  52365             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  TRIM6    3'  TCCCAAAGTGCTGGGATTA   54147            A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                                 _
GAM900  TUCAN    3'  CCTCCCAAAGTGCTGGGATTA  30273             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900  TUSP     3'  CCTCCCAAAGTGCTGGGATTA  39629             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900  UBF-fl   3'  CTCCCAAAGTGCTGAAATTA   51563     C      A
                                TAAT TCAGCACTTTG GGAG
                                |||| |||||||||| ||||
                                ATTA AGTCGTGAAAC CCTC
                                  A              _
GAM900  USP22    3'  TCCCAAAGTGCTGGGATTA   68027            A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                                 _
GAM900  VDU1     3'  CCTCCCAAAGTGCTGGGATTA  30416             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                        _
GAM900  WBSCR23  3'  CTTCCCAAAGTACTGGGATTA  46761        C     A
                                TAATCTCAG ACTTTG GGAGG
                                ||||||||| |||||| |||||
                                ATTAGGGTC TGAAAC CCTTC
                                      A     _
GAM900  YAP      5'  CCTCCCAAAGTGCTGGAATTA  36786      CT       A
                                TAAT  CAGCACTTTG GGAGG
                                ||||  |||||||||| |||||
                                ATTA  GTCGTGAAAC CCTCC
                                  AG        _
GAM900  ZNF17    3'  CCTCCCAAAGTGCTGGGATTA  82388             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                        _
GAM900  ZNF338   3'  CCTCCCAAAGTGCTGGGATTA  42010             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                        _
GAM900  ZTL1     3'  CCTCACAAAGTGCTAGGATTA  43913       TC       AG
                                TAATC  AGCACTTTG  GAGG
                                |||||  |||||||||  ||||
                                ATTAG  TCGTGAAAC  CTCC
                                   GA        A_
GAM900  LOC112687 3'  CCTCCCAAAGTGCTGGGATTA  72857              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                        _
GAM900  LOC112817 3'  CCTCCCAAAGTGCTGGGATTA  56508              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                        _
GAM900  LOC113026 3'  GCATTCCAAAGTGCTGGGATTA 55903              A  GG
                                TAATCTCAGCACTTTG GGA  GC
                                |||||||||||||||| |||  ||
                                ATTAGGGTCGTGAAAC CTT  CG
                                        _  A_
GAM900  LOC113523 5'  CTCCCAAAGTGCTGGGATTA  73044              A
                                TAATCTCAGCACTTTG GGAG
                                |||||||||||||||| ||||
                                ATTAGGGTCGTGAAAC CCTC
                                        _
GAM900  LOC115548 3'  CTTCCCAAAGTGCTGGGATTA  73461              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTTC

                                          _
GAM900  LOC116411 5'  CCTCCCAAAGTGCCGAGATTG  73857       A      A
                                TAATCTC GCACTTTG GGAGG
                                ||||||| |||||||| |||||
                                GTTAGAG CGTGAAAC CCTCC
                                    C      _
GAM900  LOC120114 3'  CCTCCCAAAGTGCTGGGATTA  75523              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                          _
GAM900  LOC120224 5'  GCCCTCCCAAAGTGCTGGGATT 57099              A
          A                      TAATCTCAGCACTTTG GGAGGGC
                                |||||||||||||||| |||||||
                                ATTAGGGTCGTGAAAC CCTCCCG

                                          _
GAM900  LOC120939 3'  CCTCCCAAAGTGCTGGAATTA  76251      CT      A
                                TAAT  CAGCACTTTG GGAGG
                                ||||  |||||||||| |||||
                                ATTA  GTCGTGAAAC CCTCC
                                  AG       _
GAM900  LOC124216 3'  CCTCCCAAAGTGCTGGGATTA  74261              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                          _
GAM900  LOC124871 3'  CTTCTCAAAGTACCAGGATTA  74346       CAGC
                                TAATCT   ACTTTGAGGAG
                                ||||||   ||||||||||
                                ATTAGG   TGAAACTCTTC
                                   ACCA
GAM900  LOC125194 5'  CCTCCCAAAGTGCTGGGATTA  74396              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                          _
GAM900  LOC126272 3'  CCTCCCAAAGTGCTGGGATTA  76088              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                          _
GAM900  LOC126661 3'  GCCCTCCCAAAGTGCTGGGATT 74552              A
          A                      TAATCTCAGCACTTTG GGAGGGC
                                |||||||||||||||| |||||||
                                ATTAGGGTCGTGAAAC CCTCCCG

                                          _
GAM900  LOC127534 5'  CAAAGTGCAAGATTA       75436       CA
                                TAATCT  GCACTTTG
                                ||||||  ||||||||
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                                ATTAGA  CGTGAAAC
                                   A_
GAM900   LOC128077 3'  CCTCCCAAAGTGCTGGGATTA  74710          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900   LOC128989 3'  CCTCCCAAAGTGCTGGGATTA  74808          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900   LOC130813 3'  CCTCCCAAAGCACTGGGATTA  75768       CA   A
                                TAATCTCAG  CTTTG GGAGG
                                |||||||||  ||||| |||||
                                ATTAGGGTC  GAAAC CCTCC
                                      AC    _
GAM900   LOC130813 3'  CCTCCCAAAGTGCTGGGATTA  75769          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900   LOC132625 3'  CCTCCCAAAGTGCTGGGATTA  75903          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900   LOC142820 5'  CTTCCCAAAGTGCTGGGATTA  76398          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTTC
                                                _
GAM900   LOC142927 5'  CCTCCCAAAGTGCTGGGATTA  76423          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900   LOC143153 3'  TCCCAAAGTGCTGGGATTA    76470          A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                                _
GAM900   LOC143154 3'  TCCCAAAGTGCTGGGATTA    76487          A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                                _
GAM900   LOC144317 5'  CCTCCCAAAGTGCTGGGATTA  76786          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC144524 5'  CCTCCCAAAGTGCTGGGATTA  83124          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC145009 3'  CCTCCCAAAGTGCTGGGATTA  60347          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC145082 5'  CCCCTCAAAGTGCTGGGATTA  83237           A
                                TAATCTCAGCACTTTGAGG GG
                                |||||||||||||||||| ||
                                ATTAGGGTCGTGAAACTCC CC

                                       _
GAM900  LOC145622 3'  CCTCCCAAAGTGCTGGGATTA  77297          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC145873 5'  CCTCCCAAAGTGCTAGGATTA  77553      TC      A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900  LOC146050 3'  CCTCCCAAAGTGCTGGGATTA  77634          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC146050 3'  TCCCAAAGTGCTGGGATTA   77651           A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT

                                        _
GAM900  LOC146229 3'  CCCTCCCGAGTCACTGGGATTA 77735       CAC   A
                                TAATCTCAG   TTTG GGAGGG
                                |||||||||   |||| ||||||
                                ATTAGGGTC   GAGC CCTCCC
                                      ACT   _
GAM900  LOC146229 3'  CCTCCCAAAGTGCTGGGATTA  77736          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC146229 3'  CCTCCCAAAGTGCTGGGATTA  77737          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900   LOC146429 5'  CCTCCCAAAGTGCTGGGATTA  83670          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900   LOC146443 5'  CCTCCCAAAGTGCTGGGATTA  77882          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900   LOC146455 3'  CCTCCCAAAATGCTGGGATTA  77903        C  A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||| |||| |||||
                                ATTAGGGTCGT AAAC CCTCC
                                       A  _
GAM900   LOC146599 5'  CCTCCCAAAGTGCTAGGATTA  78023       TC     A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900   LOC146784 5'  CCTCCCAAAGTGCTGGGATTA  78106          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900   LOC146909 3'  CCTCCCAAAGTGCTGGGATTA  78169          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900   LOC146909 3'  CTTCCCAAAGTGCTGAGATTA  78171          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTTC

                                        _
GAM900   LOC147080 5'  CCTCCCAAAGTGCTGGGATTA  83932          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900   LOC147160 5'  CCTCCCAAAGTGCTGGGATTA  83963          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900   LOC147166 3'  CCTCCCAAAGTGCTGGGATTA  78285          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900   LOC147429 3'  CCTCCCAAAGTGCTGGGATTA  78356            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900   LOC147817 3'  CCTCCAAAATGCTGGGATTA   78494          C  GA
                                TAATCTCAGCA TTT  GGAGG
                                |||||||||| |||  |||||
                                ATTAGGGTCGT AAA  CCTCC
                                      _  A_
GAM900   LOC147817 3'  CCTCCCAAAGTGCTGGGATTA  78495            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900   LOC147990 3'  CCTCCCAAAGTGCTGGGATTA  84091            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900   LOC148147 3'  CCCAAAGTGCTGGGATTA     78677           A
                                TAATCTCAGCACTTTG GG
                                |||||||||||||||| ||
                                ATTAGGGTCGTGAAAC CC
                                                _
GAM900   LOC148189 5'  TCCCAAAGTGCTGGGATTA    78724           A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                                _
GAM900   LOC148195 3'  GCCTGGCAAAATGCTGGGATTA 84130          C   AGGA
                                TAATCTCAGCA TTTG   GGGC
                                |||||||||| ||||   ||||
                                ATTAGGGTCGT AAAC   TCCG
                                      A  GG__
GAM900   LOC148443 3'  GCCTCTCAAAATGCTGGGATTA 78857          C    GA
                                TAATCTCAGCA TTTGAG  GGGC
                                |||||||||| ||||||  ||||
                                ATTAGGGTCGT AAACTC  TCCG
                                      A    __
GAM900   LOC148887 5'  CCTCCCAAAGTGCTGGGATTA  84234            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900   LOC149171 5'  CCTCCAAAGTGCTGGAATTA   79217     CT     GA
                                TAAT  CAGCACTTT  GGAGG
                                ||||  |||||||||  |||||
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                                ATTA  GTCGTGAAA  CCTCC
                                  AG        __
GAM900   LOC149421 3'  CCTCCCAAAGTGCTGGGATTA  79357              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900   LOC149478 3'  CCTCCCAAAGTGCTGGGATTA  79375              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900   LOC149577 3'  CCTCCCAAAATGCTGGGATTA  84505           C  A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||| |||| |||||
                                ATTAGGGTCGT AAAC CCTCC
                                       A  _
GAM900   LOC149577 3'  CCTCCCAAAGTGCTGGGATTA  84506              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900   LOC149684 5'  TCCCAAAGTGCTGGGATTA   84619              A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                                 _
GAM900   LOC149692 3'  CCTCCCGAAGTGCTAAGATTA  84581        C     A
                                TAATCT AGCACTTTG GGAGG
                                |||||| ||||||||| |||||
                                ATTAGA TCGTGAAGC CCTCC
                                   A        _
GAM900   LOC149703 5'  CCTCCCAAAGTGCTGGGATTA  84651              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900   LOC149821 5'  CCTCCCAAAGTGCTGGGATTA  84762              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900   LOC150054 5'  CCTCCCAAAGTGCTGGGATTA  84827              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900   LOC150166 5'  TCCCAAAGTGCTGGGATTA   84891              A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
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                                ATTAGGGTCGTGAAAC CCT

                                        _
GAM900  LOC150212 5'  CCTCCCAAAGTGCTGGAATTA  79706     CT        A
                      TAAT  CAGCACTTTG GGAGG
                      ||||  |||||||||| |||||
                      ATTA  GTCGTGAAAC CCTCC
                        AG        _
GAM900  LOC150225 3'  CCTCCCAAAGTGCTGGGATTA  84987              A
                      TAATCTCAGCACTTTG GGAGG
                      |||||||||||||||| |||||
                      ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC150397 3'  TCCCAAAGTGCTGGGATTA   79853              A
                      TAATCTCAGCACTTTG GGA
                      |||||||||||||||| |||
                      ATTAGGGTCGTGAAAC CCT

                                        _
GAM900  LOC150407 3'  CCTCCCAAAGTACTGGGATTA  79820         C    A
                      TAATCTCAG ACTTTG GGAGG
                      ||||||||| ||||||| |||||
                      ATTAGGGTC TGAAAC CCTCC
                            A     _
GAM900  LOC150407 3'  CCTCCCAAAGTGCTGGGATTA  79821              A
                      TAATCTCAGCACTTTG GGAGG
                      |||||||||||||||| |||||
                      ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC150630 5'  CCTCCCAAAGTGCTGGGATTA  85102              A
                      TAATCTCAGCACTTTG GGAGG
                      |||||||||||||||| |||||
                      ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC150960 3'  CCTCCCAAAGTGCTGTAATTA  80056     CT        A
                      TAAT  CAGCACTTTG GGAGG
                      ||||  |||||||||| |||||
                      ATTA  GTCGTGAAAC CCTCC
                        AT        _
GAM900  LOC151201 3'  CCTCCCCAAAGTGCTGGGATTA 85275              A
                      TAATCTCAGCACTTTG GGAGG
                      |||||||||||||||| |||||
                      ATTAGGGTCGTGAAAC CCTCC
                                C
GAM900  LOC151475 5'  CCTCCCAAAGTGCTGGGATTA  85399              A
                      TAATCTCAGCACTTTG GGAGG
                      |||||||||||||||| |||||
                      ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC151826 3'  CCTCCCAAAGTGCTGGGATTA  80356              A
                      TAATCTCAGCACTTTG GGAGG
                      |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900   LOC151979 5'  CCTCCCAAAGTGCTGGGATTA  80422              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900   LOC152343 3'  TCCCAAAGTGCTGGGATTA   80572             A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT

                                        _
GAM900   LOC152348 3'  CCTCCCAAAGTGCTGGGATTA  85692              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900   LOC152445 3'  CCTCCCAAAGTGCTGGGATTA  85750              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900   LOC152620 3'  CCTCCCAAAGTGCTGAGATTA  60080              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC

                                        _
GAM900   LOC152851 3'  CCTCCCAAAGTGCTGGGATTA  80706              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900   LOC153606 5'  CTCCCAAAGTGCTGGGATTA   86072             A
                                TAATCTCAGCACTTTG GGAG
                                |||||||||||||||| ||||
                                ATTAGGGTCGTGAAAC CCTC

                                        _
GAM900   LOC153688 3'  CCTCCCAAAGTGCTAGGATTA  86100      TC      A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900   LOC153811 3'  TCTCAAAGTGCTGGGATTA   80959
                                TAATCTCAGCACTTTGAGG
                                ||||||||||||||||||
                                ATTAGGGTCGTGAAACTCT

GAM900   LOC154141 5'  CCTCCCAAAGTGCTGGGATTA  86168              A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC154282 5'  CCTCCCAAAGTGCTGGGATTA  86194          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC154726 5'  CCTCCCAAAGTGCTGGGATTA  81104          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC154877 3'  CCTCCCAAAGTGCTGGATTA   86287     T    A
                                TAATC CAGCACTTTG GGAGG
                                ||||| |||||||||| |||||
                                ATTAG GTCGTGAAAC CCTCC

                                  _     _
GAM900  LOC154877 3'  CCTCCCAAAGTGCTGGGATTA  86288          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC155372 3'  CCTCCCAAAGTGCTGAGATTA  81342          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC

                                        _
GAM900  LOC157247 5'  CCTCCCAAAGTGCTGGGATTA  81363          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC157506 3'  CCTCCCAAAGTGCTGGGATTA  81439          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC157507 5'  CCTCCCAAAGTGCTGGGATTA  81455          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC157681 5'  CCTCCCAAAGTGCTGGGA     81542             A
                                TCTCAGCACTTTG GGAGG
                                |||||||||||| |||||
                                AGGGTCGTGAAAC CCTCC

                                        _
GAM900  LOC158310 5'  CCTCCCAAAGTGCTGGGATTA  86751          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900   LOC158402 5'  CCTCCCAAAGTGCTGGAATTA  86802     CT        A
                       TAAT  CAGCACTTTG GGAGG
                       ||||  |||||||||| |||||
                       ATTA  GTCGTGAAAC CCTCC
                         AG         _
GAM900   LOC158476 3'  CCTCCCAAAGTGCTGGGATTA  86842               A
                       TAATCTCAGCACTTTG GGAGG
                       |||||||||||||||| |||||
                       ATTAGGGTCGTGAAAC CCTCC
                                 _
GAM900   LOC158668 3'  CCTCCCAAAGTGCTGAGATTA  69367               A
                       TAATCTCAGCACTTTG GGAGG
                       |||||||||||||||| |||||
                       ATTAGAGTCGTGAAAC CCTCC
                                 _
GAM900   LOC158709 3'  CCTCCCAAAGTGCTGGGATTA  81979               A
                       TAATCTCAGCACTTTG GGAGG
                       |||||||||||||||| |||||
                       ATTAGGGTCGTGAAAC CCTCC
                                 _
GAM900   LOC160646 3'  CCTCCCAAAGTGCTGGGATTA  82225               A
                       TAATCTCAGCACTTTG GGAGG
                       |||||||||||||||| |||||
                       ATTAGGGTCGTGAAAC CCTCC
                                 _
GAM900   LOC161829 3'  CTTCCAAAGTGCTGGGATTA   82313              A
                       TAATCTCAGCACTTTG GGAG
                       |||||||||||||||| ||||
                       ATTAGGGTCGTGAAAC CTTC
                                 _
GAM900   LOC163590 5'  CCTCCCAAAGTGCTGGGATTA  58859               A
                       TAATCTCAGCACTTTG GGAGG
                       |||||||||||||||| |||||
                       ATTAGGGTCGTGAAAC CCTCC
                                 _
GAM900   LOC170082 5'  CCTCCCAAAGTGCTGGGATTA  82559               A
                       TAATCTCAGCACTTTG GGAGG
                       |||||||||||||||| |||||
                       ATTAGGGTCGTGAAAC CCTCC
                                 _
GAM900   LOC170409 5'  CCTCCCAAAGTGCTGGGATTA  82860               A
                       TAATCTCAGCACTTTG GGAGG
                       |||||||||||||||| |||||
                       ATTAGGGTCGTGAAAC CCTCC
                                 _
GAM900   LOC196047 5'  CCTCCCAAAGTGCTGCGATTA  89596      T        A
                       TAATC CAGCACTTTG GGAGG
                       ||||| |||||||||| |||||
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                                ATTAG GTCGTGAAAC CCTCC
                                   C        _
GAM900   LOC197358 3'  CCTCCCAAAGTACTGGGATTA  88028        C     A
                                TAATCTCAG ACTTTG GGAGG
                                ||||||||| |||||| |||||
                                ATTAGGGTC TGAAAC CCTCC
                                    A     _
GAM900   LOC197358 3'  CCTCCCAAAGTGCTGGGATTA  88029             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900   LOC199699 3'  CCTCCCAAAGTGCTGGGAT    88301           A
                                ATCTCAGCACTTTG GGAGG
                                ||||||||||||| |||||
                                TAGGGTCGTGAAAC CCTCC
                                               _
GAM900   LOC199725 5'  CCTCCCAAAGTGCTGGGATTA  89836             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                               _
GAM900   LOC199775 5'  CCTCCCAAAGTGCTGGGATTA  88355             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                               _
GAM900   LOC199786 3'  CAAAGTGCTGGGATTA      88367
                                TAATCTCAGCACTTTG
                                ||||||||||||||||
                                ATTAGGGTCGTGAAAC

GAM900   LOC199786 3'  CCTCCCAAAGTGCTAGGATTA  88374       TC      A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA        _
GAM900   LOC199786 3'  CCTCCCAAAGTGCTGGGATTA  88375             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                               _
GAM900   LOC200014 3'  CCTCCCAAAGTGCTGGGATTA  88522             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                               _
GAM900   LOC200169 5'  CCTCCCAAAGTGCTGGGATTA  89946             A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900   LOC200301 5'  CCTCCCAAAGTGCTGGGATTA  88741          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900   LOC200310 3'  CCTCCCAAAGTGCTAGGATTA  65731     TC   A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA          _
GAM900   LOC200314 3'  CCTCCCAAAGTGCTGGGATTA  90006          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900   LOC200316 5'  CCTCCCAAAGTGCTGGGATTA  88767          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900   LOC200316 3'  TCCCAAAGTGCTGGGATTA    88776        A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                                  _
GAM900   LOC200845 5'  CCTCCCAAAGTGCTGGGATTA  88897          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900   LOC200860 3'  CCTCCCAAAGTGCTGGGATTA  90161          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900   LOC201164 3'  CCTCCCAAAGTGCTGGGATTA  88114          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900   LOC201294 3'  CCTCCCAAAGTGCTGGGATTA  88206          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                  _
GAM900   LOC201411 3'  CCTCCCAAAGTGCTGGGATTA  62954          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC201627 3'  CCTCCCAAAGTGCTGGGATTA  89007          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC201705 5'  TCCCAAAGTGCTGGGATTA   90256          A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                                _
GAM900  LOC202460 5'  TCCCAAAGTGCTGGGATTA   89189          A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                                _
GAM900  LOC203197 3'  CTCCCAAAGTGCTGGGATTA  89287          A
                                TAATCTCAGCACTTTG GGAG
                                |||||||||||||||| ||||
                                ATTAGGGTCGTGAAAC CCTC
                                                _
GAM900  LOC203232 3'  CCCTCCTCATCAGCAAGAT   71411     CA  ACTT
                                ATCT  GC   TGAGGAGGG
                                ||||  ||   |||||||||
                                TAGA  CG   ACTCCTCCC
                                  A_  ACT_
GAM900  LOC203369 3'  CCTCCCAAAGTGCTGGGATTA  89337          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC203378 3'  CCTCCCAAAGTGCTGGGATTA  90598          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC205251 5'  CCTCCCAAAGTGCTGGGATTA  90668          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC219294 3'  TCCCAAAGTGCTGGGATTA   93012          A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                                _
GAM900  LOC219295 3'  TCCCAAAGTGCTGGGATTA   92997          A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
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                                ATTAGGGTCGTGAAAC CCT
                                                _
GAM900   LOC219673 5'  CCTCCCAAAGTGCTAGGATTA  93023      TC       A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900   LOC219894 3'  CCTCCCAAAGTGCTGGGATTA  93280            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900   LOC220074 3'  CCTCCCAAAGTGCTAGGATTA  59268      TC       A
                                TAATC  AGCACTTTG GGAGG
                                |||||  ||||||||| |||||
                                ATTAG  TCGTGAAAC CCTCC
                                   GA       _
GAM900   LOC220074 3'  CCTCCCAAAGTGCTGGGATTA  59269            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900   LOC221271 3'  CCTCCCAAAGTGTTGAGATTA  91852            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTTGTGAAAC CCTCC
                                                _
GAM900   LOC221540 3'  CCTCCCAAAATGCTGAGATTA  93835          C   A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||||| |||| |||||
                                ATTAGAGTCGT AAAC CCTCC
                                      A    _
GAM900   LOC221663 5'  CCTCCCAAAGTGCCGGGATTA  93812       A      A
                                TAATCTC GCACTTTG GGAGG
                                ||||||| |||||||| |||||
                                ATTAGGG CGTGAAAC CCTCC
                                    C       _
GAM900   LOC221964 3'  GCATCCCAAAGTGCTGGGATTA 93981            A  GG
                                TAATCTCAGCACTTTG GGA  GC
                                |||||||||||||||| |||  ||
                                ATTAGGGTCGTGAAAC CCT  CG
                                                _  A_
GAM900   LOC222070 5'  CCTCCCAAAGTGCTGGGATTA  94153            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900   LOC253842 5'  CCTCCCAAAGTGCTGGGATTA  97384            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900   LOC254100 3'  CCTCCCAAAGTGCTGGGATTA  96413            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900   LOC254295 5'  CCTCCAAAGTGCTGGGATTA   96174           GA
                                TAATCTCAGCACTTT  GGAGG
                                |||||||||||||||  |||||
                                ATTAGGGTCGTGAAA  CCTCC

                                        __
GAM900   LOC254672 3'  CTTCCCAAAGTGCTGGGATTA  94644            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTTC

                                        _
GAM900   LOC255196 5'  CCTCCCTAAGTGCTGAGATTA  97165           TGA
                                TAATCTCAGCACTT   GGAGG
                                ||||||||||||||   |||||
                                ATTAGAGTCGTGAA   CCTCC
                                        TC_
GAM900   LOC255308 3'  CCTCACAAAGTGCCGGGATTA  94534       A       AG
                                TAATCTC GCACTTTG  GAGG
                                ||||||| ||||||||  ||||
                                ATTAGGG CGTGAAAC  CTCC
                                    C       A_
GAM900   LOC255338 5'  TCCCAAAGTGCTGGGATTA    95934           A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT

                                        _
GAM900   LOC255465 3'  TCTCAAAGTGCTGGGATTA    97304
                                TAATCTCAGCACTTTGAGG
                                ||||||||||||||||||
                                ATTAGGGTCGTGAAACTCT

GAM900   LOC255707 3'  CCTCCCAAAGTGCTGGGATTA  96957            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900   LOC256221 3'  CCTCCCAAAGTGCTGGGATTA  95209            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC

                                        _
GAM900   LOC256360 5'  TCCCAAAGTGCTGAGATTA    96553           A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
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                                ATTAGAGTCGTGAAAC CCT
                                                _
GAM900  LOC256364 5'  CCTCCCAAAGTGCTGGGATTA  94797            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC257128 5'  GCATCCCAAAATGCTGGGATTA 96087        C   A  GG
                                TAATCTCAGCA TTTG GGA  GC
                                |||||||||| |||| |||  ||
                                ATTAGGGTCGT AAAC CCT  CG
                                      A   _  A_
GAM900  LOC257463 3'  CCTCCCAAAGTGCTGGGATTA  71068            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC257465 3'  CCTCCCAAAGTGCTGGGATTA  81591            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC257545 3'  CCTCCCAAAATGCTGAGATTA  97803        C   A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||| |||| |||||
                                ATTAGAGTCGT AAAC CCTCC
                                      A   _
GAM900  LOC257598 3'  CCTCCCAAAATGCTGAGATTA  97918        C   A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||| |||| |||||
                                ATTAGAGTCGT AAAC CCTCC
                                      A   _
GAM900  LOC51008  5'  CCTCCCAAAGTGCTGGGATTA  31961            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC51193  5'  CCTCCCAAAGTGCTGGGATTA  32904            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC51219  5'  CCTCCCAAAGTGCTGGGATTA  33115            A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC51275  5'  CCTCCCAAAGTACTGGGATTA  33290        C   A
                                TAATCTCAG ACTTTG GGAGG
                                ||||||||| |||||| |||||
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                                ATTAGGGTC TGAAAC CCTCC
                                     A     _
GAM900  LOC51696 3' CCTCCCAAAGTGCTGGGATTA 32545          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC56181 5' CCTCCCAAAGTGCTGGGATTA 95533          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC56920 3' CCAGAAGCACTGAGATTA    39383      CA  GA
                                TAATCTCAG  CTTT  GG
                                |||||||||  ||||  ||
                                ATTAGAGTC  GAAG  CC
                                     AC    A_
GAM900  LOC57107 3' CCTCCCAAAGTGCTGGGATTA 39832          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC57146 3' CCTCCCAAAGTGCTGGGATTA 39916          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC81034 3' CCTCCCAAAGTGCTGGGATTA 47848          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC89231 3' CCTCCCAAAGTGCTGGGATTA 92730          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC89932 3' CCTCCCAAAATGCTGGGATTA 60794        C  A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||||  |||| |||||
                                ATTAGGGTCGT AAAC CCTCC
                                      A     _
GAM900  LOC89932 3' CCTCCCAAAGTGCTGGGATTA 60795          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                _
GAM900  LOC90110 5' CCTCCCAAAGTGCTGGGATTA 61508          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  LOC90288 3' CCTCCCAAAGTGCTGGGATTA 62086          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  LOC90333 3' CCTCCCAAAGTGCTGAGATTA 62287          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGAGTCGTGAAAC CCTCC
                                       _
GAM900  LOC90408 5' CCTCCCAAAGTACTGGGATTA 62659       C  A
                                TAATCTCAG ACTTTG GGAGG
                                ||||||||| |||||| |||||
                                ATTAGGGTC TGAAAC CCTCC
                                      A  _
GAM900  LOC90485 3' CCTCCCAAAGTGCTGGGATTA 63010          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  LOC90485 3' GCATCCCAAAGTGCTGGGA  63017         A  GG
                                TCTCAGCACTTTG GGA  GC
                                |||||||||||| |||  ||
                                AGGGTCGTGAAAC CCT  CG
                                      _  A_
GAM900  LOC90591 3' TCCCAAAGTGCTGGGATTA  63445          A
                                TAATCTCAGCACTTTG GGA
                                |||||||||||||||| |||
                                ATTAGGGTCGTGAAAC CCT
                                       _
GAM900  LOC90918 3' CCTCCCAAAGTGCCGGGATTA 64354       A  A
                                TAATCTC GCACTTTG GGAGG
                                ||||||| |||||||| |||||
                                ATTAGGG CGTGAAAC CCTCC
                                     C  _
GAM900  LOC91115 3' CCTCCCAAAGTGCTGGGATTA 64929          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  LOC91250 5' CCTCCCAAAGTGCTGGGATTA 65322          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                       _
GAM900  LOC91308 3' CCTCCCAAAGTGCTGGGATTA 65557          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
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                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  LOC91373  3' CCTCCCAAAGTGCTGGGATTA  65837          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  LOC91893  3' CCTCCCAAAGTGCTGGGATTA  67460          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  LOC92303  3' CCTCCCAAAGTGCTGGGATTA  68822          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  LOC92661  5' CCTCCCAAAGTGCTGGGATTA  70080          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  LOC92689  3' CCTCCCAAAGTGCTGGGATTA  70222          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  LOC92841  3' CCTCCCAAAGTGCTGGGATTA  70707          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  LOC93356  3' CCTCCCAAAATGCTGGGATTA  72076        C  A
                                TAATCTCAGCA TTTG GGAGG
                                |||||||||| |||| |||||
                                ATTAGGGTCGT AAAC CCTCC
                                      A  _
GAM900  LOC93408  5' CCTCCCAAAGTGCTGGGATTA  56476          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM900  LOC93496  3' CCTCCCAAAGTGCTGGGATTA  72432          A
                                TAATCTCAGCACTTTG GGAGG
                                |||||||||||||||| |||||
                                ATTAGGGTCGTGAAAC CCTCC
                                                 _
GAM901  ADORA3    5' CTGCACATGGACCTCTGGGA  5442     T  ACTC
                                TCCC GAG   TCTGTGTGCAG
                                |||| |||   ||||||||||
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                                AGGG CTC    AGGTACACGTC
                                  T  C___
GAM901  ARHGAP6  3'  GCCACACTCCAAGTCTCAG   20406        CTCT    _
                                CTGAGACT    GTGTG C
                                ||||||||    ||||| |
                                GACTCTGA    CACAC G
                                    ACCT    C
GAM901  ARHGAP6  3'  GCCACACTCCAAGTCTCAG   25516        CTCT    _
                                CTGAGACT    GTGTG C
                                ||||||||    ||||| |
                                GACTCTGA    CACAC G
                                    ACCT    C
GAM901  ATP8B2   3'  CACACCCAGCTCAGGGA     65213        A  CTCT
                                TCCCTGAG CT    GTGTG
                                |||||||| ||    |||||
                                AGGGACTC GA    CACAC
                                    _  CC__
GAM901  CA12     3'  CTGCACAGACCTTAGGGA     6878         AC   CTGT
                                TCCCTGAG  TCT    GTGCAG
                                ||||||||  |||    ||||||
                                AGGGATTC  AGA    CACGTC
                                    C_  _____
GAM901  CD34     3'  CTGCACACACCTCAGAGG     8344     _    ACTCTC
                                CC CTGAG      TGTGTGCAG
                                || |||||      |||||||||
                                GG GACTC      ACACACGTC
                                 A    C_____
GAM901  DLG5     5'  GCTGCACATCAACCTCAGTGGA 82915     _    ACTCTCT
                                TCC CTGAG       GTGTGCAGC
                                ||| |||||       |||||||||
                                AGG GACTC       TACACGTCG
                                  T    CAAC___
GAM901  ELK1     5'  GCTACACACAGGTACCCCTGGG 17841      TGAGACT T      C
          A                      TCCC       C CTGTGTG AGC
                                 ||||       | ||||||| |||
                                 AGGG       G GACACAC TCG
                                   TCCCCAT _       A
GAM901  HSD11B2  3'  CTACACACCCCCAAGCCACAGG 3971        AGA  CTCT_    C
          GA                     TCCCTG   CT    GTGTG AG
                                 ||||||   ||    ||||| ||
                                 AGGGAC   GA    CACAC TC
                                    ACC  ACCCC     A
GAM901  IL24     3'  GCTGTGAAGAGTCTACAGAGA  22446    C  _     CTGTG
                                TC CTG AGACTCT     TGCAGC
                                || ||| |||||||     ||||||
                                AG GAC TCTGAGA     GTGTCG
                                 A  A      A_____
GAM901  KCNA7    3'  ACAACAGAGTCTCAGGGA     49044          CTG
                                TCCCTGAGACTCT   TGT
                                ||||||||||||   |||
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                                AGGGACTCTGAGA  ACA
                                       CA_
GAM901  LDHB    5'  CACACAGACATTTCAGG    9703       CTC
                                CCTGAGA  TCTGTGTG
                                |||||||  ||||||||
                                GGACTTT  AGACACAC
                                    AC_
GAM901  NCOR2   3'  GCCACACACAGGCGGCCAGGG  20880     AGA  C     CA
                                CCCTG  CT TCTGTGTG  GC
                                |||||  || ||||||||  ||
                                GGGAC  GG GGACACAC  CG
                                   C__  C      AC
GAM901  NHLH1   5'  GCTACCCCTGAGAGTCTAG   18802   G     TGT_  _
                                CT AGACTCTC   GT GC
                                || ||||||||   || ||
                                GA TCTGAGAG   CA CG
                                 _      TCCC  T
GAM901  NTF5    3'  GCTGAGAGACCTCAGGGA    20519       A_    T
                                TCCCTGAG  CTCTC GT
                                ||||||||  ||||| ||
                                AGGGACTC  GAGAG CG
                                     CA    T
GAM901  OLR1    3'  GCTGCACACAATCTAGCAGG  10336     AGACTCTC
                                CCTG      TGTGTGCAGC
                                ||||      ||||||||||
                                GGAC      ACACACGTCG
                                  GATCTA__
GAM901  PCDH11X 3'  TTGTAGAGAAACTCAGG    52033      AC    GTGT
                                CCTGAG  TCTCT   GCAG
                                ||||||  |||||   ||||
                                GGACTC  AGAGA   TGTT
                                   AA   _____
GAM901  PCDH11X 3'  TTGTAGAGAAACTCAGG    52055      AC    GTGT
                                CCTGAG  TCTCT   GCAG
                                ||||||  |||||   ||||
                                GGACTC  AGAGA   TGTT
                                   AA   _____
GAM901  PCDH11Y 3'  TTGTAGAGAAACTCAGG    52089      AC    GTGT
                                CCTGAG  TCTCT   GCAG
                                ||||||  |||||   ||||
                                GGACTC  AGAGA   TGTT
                                   AA   _____
GAM901  PDE4B   5'  GCAGAGAGAGTCTGAG     10479   G      G
                                CT AGACTCTCT TGT
                                || |||||||| |||
                                GA TCTGAGAGA ACG
                                 G       G
GAM901  PPP5C   3'  GCCATAGGAAGACCCCCAGAGA 20732   C  AGA__  CT    T
                                TC CTG    CT  CTGTG GC
                                || |||    ||  ||||| ||
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                                AG GAC    GA  GATAC CG
                                 A  CCCCA  AG    _
GAM901  PRX      3'  CTGCCAAAAGTCTCAGAGA   40531    C      CTCTG  T
                                TC CTGAGACT    TG GCAG
                                || ||||||||    || ||||
                                AG GACTCTGA    AC CGTC
                                 A       AA___  _
GAM901  TNR      3'  GCCCAGAGAAAAGAGCCTCAG  12354      A  ___  G  T
                                CTGAG CTC   TCT TG GC
                                ||||| |||   ||| || ||
                                GACTC GAG   AGA AC CG
                                   C   AAA   G  C
GAM901  ADG-90   5'  GCTGCTCTTGGAGAGTCCCAGG 52352       A       TGT
           GG                     TCCCTG GACTCTCTG   GCAGC
                                ||||||| |||||||||   |||||
                                GGGGAC CTGAGAGGT   CGTCG
                                   C        TCT
GAM901  AMAC     5'  CACCTCAGGAGAGTTCCAGGGA 53996       AG      GT__
                                TCCCTG  ACTCTCT    GTG
                                ||||||  |||||||    |||
                                AGGGAC  TGAGAGG    CAC
                                   CT      ACTC
GAM901  BCKDK    3'  GCTGCATCTTGGGTCTCAGGGA 59796          TCTGT
                                TCCCTGAGACTC    GTGCAGC
                                ||||||||||||    |||||||
                                AGGGACTCTGGG    TACGTCG
                                      TTC__
GAM901  C1orf19  5'  CTGCAGCTGCGAGCCTCGGGGA 68191        A   TCT  G
                                TCCCTGAG CTC   GT TGCAG
                                |||||||| |||   || |||||
                                AGGGGCTC GAG   CG ACGTC
                                    C   CGT  _
GAM901  DKFZP586I2223 3'  GCTGCAGAGGCCCAGGGA    31270       AGAC      T
                                TCCCTG    TCTCTGTG GC
                                ||||||    |||||||| ||
                                AGGGAC    GGAGACGT CG
                                   CC__       _
GAM901  FLJ11715  3'  GCAGTGCAGAGACTCCCAGGGA 44673       A  C      _
                                TCCCTG GA TCTCTGTG TGC
                                |||||| || |||||||| |||
                                AGGGAC CT AGAGACGT ACG
                                   C  C       G
GAM901  FLJ12484  3'  GCAACAGAAAGCCCCAGG    42857     AGA  C    G
                                CCTG   CT TCTGT TGC
                                ||||   || ||||| |||
                                GGAC   GA AGACA ACG
                                  CCC  A    _
GAM901  FLJ12484  3'  GCAACAGAAAGCCCCAGG    69654     AGA  C    G
                                CCTG   CT TCTGT TGC
                                ||||   || ||||| |||
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                                GGAC   GA AGACA ACG
                                  CCC  A    _
GAM901  FLJ12800  5'  CTGCGGAAAAGTTCAGGGA   43231        ACTC   GTGT
                                TCCCTGAG   TCT   GCAG
                                ||||||||   |||   ||||
                                AGGGACTT   AGG   CGTC
                                    GAAA  ____
GAM901  FLJ13189  3'  CACAAGAATTCAGGGA     45983        AC   C
                                TCCCTGAG  TCT TGTG
                                ||||||||  ||| ||||
                                AGGGACTT  AGA ACAC
                                    A_  _
GAM901  FLJ20033  5'  GCTGCGTAAAATCTCTAAGGA  34347    CT_   CTCTCTG
                                TCC   GAGA     TGTGCAGC
                                |||   ||||     ||||||||
                                AGG   CTCT     ATGCGTCG
                                  AAT   AAA____
GAM901  FLJ20294  3'  GCCCTGGACAGAGAGCCTCCAG 34876    C   _  A      G  CA
          AGA                     TC CTG AG CTCTCTGT TG  GC
                                || ||| || |||||||| ||  ||
                                AG GAC TC GAGAGACA GT  CG
                                 A   C  C       G  CC
GAM901  FLJ31709  5'  CTGCAAGGTCTCAGGGA     58271          T  CTGTG
                                TCCCTGAGAC CT    TGCAG
                                |||||||||| ||    |||||
                                AGGGACTCTG GA    ACGTC
                                          _  _____
GAM901  GAB3      3'  TTGCAAAGAGTCTCAGG     54637          CTGTG
                                CCTGAGACTCT    TGCAG
                                ||||||||||    |||||
                                GGACTCTGAGA    ACGTT
                                     A____
GAM901  GTPBP5    3'  CTGCAGAGGAGCCCCAGGG   65356      AGACT   GTG
                                CCCTG    CTCT   TGCAG
                                |||||    ||||   |||||
                                GGGAC    GAGG   ACGTC
                                   CCC__    AG_
GAM901  H963      5'  GCTACACAACCTTGGAGTCTTA 25254         CTG__   C
          G                      CTGAGACTCT    TGTG AGC
                                |||||||||    |||| |||
                                GATTCTGAGG    ACAC TCG
                                     TTCCA    A
GAM901  H963      5'  GCTACACAACCTTGGAGTCTTA 94635         CTG__   C
          G                      CTGAGACTCT    TGTG AGC
                                |||||||||    |||| |||
                                GATTCTGAGG    ACAC TCG
                                     TTCCA    A
GAM901  HPIP      5'  GCCACAGCAGCCTCAGGGA   40049        A  CT    T
                                TCCCTGAG CT  CTGTG GC
                                |||||||| ||  ||||| ||
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                                AGGGACTC GA  GACAC CG
                                     C  C_    _
GAM901  HRD1     3'  CACACAACTCAGGGA       69557         ACTCTC
                                TCCCTGAG     TGTGTG
                                ||||||||     ||||||
                                AGGGACTC     ACACAC
                                     A_____
GAM901  IBTK     3'  GCTGTGGAAAAGAGTCTTAGAG 67490    C        CTGTGT
              A                   TC CTGAGACTCT     GCAGC
                                || ||||||||||     |||||
                                AG GATTCTGAGA     TGTCG
                                 A        AAAGG_
GAM901  KIAA0040 5'  CACACAGACATTTCAGG     27778        CTC
                                CCTGAGA   TCTGTGTG
                                |||||||   ||||||||
                                GGACTTT   AGACACAC
                                     AC_
GAM901  KIAA0318 3'  GCTACACACAGAAAATGTTT   68956      TC__       C
                                AGAC    TCTGTGTG AGC
                                ||||    |||||||| |||
                                TTTG    AGACACAC TCG
                                  TAAA       A
GAM901  KIAA0494 3'  GCTGCACTTTATAGAGACTCAG 28745       AC      ___
                                CTGAG  TCTCTGT   GTGCAGC
                                |||||  |||||||   |||||||
                                GACTC  AGAGATA   CACGTCG
                                   __      TTT
GAM901  KIAA0618 5'  GCTGTACGGTGAGCCCCAGGGA 29170        AGA   T  GT
                                TCCCTG   CTC CT  GTGCAGC
                                ||||||   ||| ||  |||||||
                                AGGGAC   GAG GG  CATGTCG
                                   CCC   T  __
GAM901  KIAA1280 5'  GCTGCGTGGGCAGAGCCACAAA 69724    GAGACT     G__
              G                   CT     CTCTGT   TGCAGC
                                ||     ||||||   ||||||
                                GA     GAGACG   GCGTCG
                                 AACACC     GGT
GAM901  KIAA1582 5'  CACACACAGGGTCGAG      65368    GA     C
                                CT  GACTCT TGTGTG
                                ||  |||||| ||||||
                                GA  CTGGGA ACACAC
                                 G_     C
GAM901  KIAA1764 5'  CTGCACACAGGAGTT       69288       T
                                GACTC CTGTGTGCAG
                                ||||| ||||||||||
                                TTGAG GACACACGTC
                                     _
GAM901  KIAA1786 3'  GCAGCAGAGACCTCAGGGA    66032         AC      G
                                TCCCTGAG  TCTCTGT TGC
                                ||||||||  ||||||| |||
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                                AGGGACTC  AGAGACG ACG
                                    C_      _
GAM901  KIAA1841  3'  GCCAGGCAGAAAGAGTGCTCAG 80047        _   __     G  _
          GGA                     TCCCTGAG ACTC  TCTGT TG C
                                ||||||||| ||||  ||||| || |
                                AGGGACTC TGAG  AGACG AC G
                                    G    AA    G  C
GAM901  KIAA1854  3'  GCTAAGTATAAACCTCAGGGA  71743         ACTCTCTG    __
                                TCCCTGAG       TGTGC  AGC
                                ||||||||       |||||  |||
                                AGGGACTC       ATATG  TCG
                                    CAA_____     AA
GAM901  KIAA1893  3'  GCCAGAGGGTCTCAGG      73215             T
                                CCTGAGACTCTCTG GT
                                |||||||||||||| ||
                                GGACTCTGGGAGAC CG
                                                _
GAM901  KIAA1893  3'  GCTGAGAGAGAGTCACAG    73216     A       GTGTG
                                CTG GACTCTCT     CAGC
                                ||| ||||||||     ||||
                                GAC CTGAGAGA     GTCG
                                  A       GA___
GAM901  KIAA1944  5'  GCCACAGGGACCCCAGG     75562      AGAC       T
                                CCTG    TCTCTGTG GC
                                ||||    |||||||| ||
                                GGAC    AGGGACAC CG
                                  CCC_       _
GAM901  KNTC1     5'  CTCAGGAAGACAGTCTCAG   28178         C   GTG  C
                                CTGAGACT TCT   TG AG
                                |||||||| |||   || ||
                                GACTCTGA AGA   AC TC
                                    C   AGG  _
GAM901  LGALS8    3'  GCCTACAGAAAGTTTCAGG   21448         C      T
                                CCTGAGACT TCTGTG GC
                                ||||||||| |||||| ||
                                GGACTTTGA AGACAT CG
                                    A     C
GAM901  MAD4      3'  GCCACCCAGCGTCTCAGGGA  21280          T  CT   T
                                TCCCTGAGAC CT  GTG GC
                                |||||||||| ||  ||| ||
                                AGGGACTCTG GA  CAC CG
                                    C  CC   _
GAM901  MGC4840   3'  GCTGCACACTCAAGTTCAGG  71567       A  CTCT
                                CCTGAG CT    GTGTGCAGC
                                |||||| ||    |||||||||
                                GGACTT GA    CACACGTCG
                                   _ ACT_
GAM901  NSE1      3'  GCGGCAGGAAGTCTCAGG    59074         CT    G
                                CCTGAGACT  CTGT TGC
                                |||||||||  |||| |||
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                                GGACTCTGA  GACG GCG
                                     AG   _
GAM901  OSR2     3'  GCCGCACCTGCAGCTCCAGGGA 53806       A  CTCT   __   A
                                TCCCTG GA   CTGT  GTGC GC
                                |||||| ||   ||||  |||| ||
                                AGGGAC CT   GACG  CACG CG
                                   _ C___   TC   C
GAM901  PEG10    3'  GCCACACACAGAGATGTAAGAG 30527     GAG _       CA
           G                     CCT   AC TCTCTGTGTG  GC
                                |||   || ||||||||||  ||
                                GGA   TG AGAGACACAC  CG
                                  GAA  T         AC
GAM901  PRO1580  5'  GCCGCAGGAATTCAGAGA    37533    C    AC  T    T
                                TC CTGAG  TC CTGTG GC
                                || |||||  || ||||| ||
                                AG GACTT  AG GACGC CG
                                 A    A_ _    _
GAM901  SH3BGRL2 3'  CACACTTAGCTCAGAGA     48885    C    A  CTCT
                                TC CTGAG CT   GTGTG
                                || ||||| ||   |||||
                                AG GACTC GA   CACAC
                                 A    _ TT__
GAM901  TED      3'  GCCAGAGGGCCTCAGGGA     31639        A      T
                                TCCCTGAG CTCTCTG GT
                                |||||||| ||||||| ||
                                AGGGACTC GGGAGAC CG
                                     C     _
GAM901  TMLHE    3'  CACGAAAAGGGTCTCAGGGA   36512           CTG
                                TCCCTGAGACTCT   TGTG
                                ||||||||||||   ||||
                                AGGGACTCTGGGA   GCAC
                                       AAA
GAM901  TOMM40   3'  GCCAGACAACCTCAGGGA    20371        ACTC   T
                                TCCCTGAG   TCTG GT
                                ||||||||   |||| ||
                                AGGGACTC   AGAC CG
                                     CAAC   _
GAM901  LOC115129 5'  GCGACAGAGAGACTCA      73234      A      G
                                TGAG CTCTCTGT TGC
                                |||| |||||||| |||
                                ACTC GAGAGACA GCG
                                  A      _
GAM901  LOC132880 3'  CTGCACACAAATGAGGCAG    75067     AGA  TC_
                                CTG   CTC   TGTGTGCAG
                                |||   |||   |||||||||
                                GAC   GAG   ACACACGTC
                                  G__   TAA
GAM901  LOC137362 3'  CACAGAGAGCTCAGAGA     75264    C    A
                                TC CTGAG CTCTCTGTG
                                || ||||| |||||||||
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                                AG GACTC GAGAGACAC
                                 A    _
GAM901   LOC143146 3'  GCTACTTTAGAAGAGTCACAGA 60134    C   A     _   T_ _
                GA                TC CTG GACTCT CTG  GT GC
                                  || ||| |||||| |||  || ||
                                  AG GAC CTGAGA GAT  CA CG
                                   A  A     A  TT  T
GAM901   LOC144110 3'  GCTGTCTGTCAAAAGTCTCACA 76674    CC      CTC  TGT_
                GA                TC  TGAGACT   TG    GCAGC
                                  ||  |||||||   ||    |||||
                                  AG  ACTCTGA   AC    TGTCG
                                   AC      AA_  TGTC
GAM901   LOC145468 3'  GCCAGACAACCTCAGGGA    73821        ACTC    T
                                  TCCCTGAG    TCTG GT
                                  ||||||||    |||| ||
                                  AGGGACTC    AGAC CG
                                       CAAC    _
GAM901   LOC146520 5'  GCCACTCGGAAAACCTCAGGGA 77954        ACTC    T  _
                                  TCCCTGAG    TCTG GTG C
                                  ||||||||    |||| ||| |
                                  AGGGACTC    AGGC CAC G
                                       CAAA    T   C
GAM901   LOC146713 5'  CTGCAAAGGCCTCAGGGA    83724        ACTCT  GTG
                                  TCCCTGAG    CT   TGCAG
                                  |||||||     ||   |||||
                                  AGGGACTC    GG   ACGTC
                                       C_____  AA_
GAM901   LOC146741 5'  CACCTCAGGAGAGTTCCAGGGA 76286       AG      GT__
                                  TCCCTG  ACTCTCT    GTG
                                  ||||||  |||||||    |||
                                  AGGGAC  TGAGAGG    CAC
                                     CT      ACTC
GAM901   LOC146802 3'  GCTGCATGTGAGACCCAAGG   78136     GAGAC    T TG
                                  CCT     TCTC G  TGCAGC
                                  |||     ||||  |  ||||||
                                  GGA     AGAG T  ACGTCG
                                    ACCC_    _ GT
GAM901   LOC146861 5'  CACCTCAGGAGAGTTCCAGGGA 76296       AG      GT__
                                  TCCCTG  ACTCTCT    GTG
                                  ||||||  |||||||    |||
                                  AGGGAC  TGAGAGG    CAC
                                     CT      ACTC
GAM901   LOC148710 3'  ACACAGAAGTCCCAGGGA    84190        A    C
                                  TCCCTG GACT TCTGTGT
                                  |||||| |||| |||||||
                                  AGGGAC CTGA AGACACA
                                     C    _
GAM901   LOC150155 3'  GCCAGACAACCTCAGGGA    70852        ACTC    T
                                  TCCCTGAG    TCTG GT
                                  ||||||||    |||| ||
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                                AGGGACTC    AGAC CG
                                     CAAC    _
GAM901   LOC150157 5'  GCTGCACGTGAGCTCCAG    84878     _ A   TCTG
                                CTG AG CTC    TGTGCAGC
                                ||| || |||    ||||||||
                                GAC TC GAG    GCACGTCG
                                  C  _   T___
GAM901   LOC151304 3'  ACCGGGGAGCCTCAGGGA    85308        A      T
                                TCCCTGAG CTCTCTG GT
                                |||||||| ||||||| ||
                                AGGGACTC GAGGGGC CA
                                     C      _
GAM901   LOC170394 5'  GCTGGACAGAGAGTCCCGGG   82852      A        GTG
                                CCTG GACTCTCTGT   CAGC
                                |||| ||||||||||   ||||
                                GGGC CTGAGAGACA   GTCG
                                  C        G__
GAM901   LOC196741 3'  GCTGCACAGGAGCCCACAG    82836     AGACT    G
                                CTG    CTCT TGTGCAGC
                                |||    |||| ||||||||
                                GAC    GAGG ACACGTCG
                                  ACCC_   _
GAM901   LOC196890 5'  GCTGCACGTGAGCTCCAG    89648     _ A   TCTG
                                CTG AG CTC    TGTGCAGC
                                ||| || |||    ||||||||
                                GAC TC GAG    GCACGTCG
                                  C  _   T___
GAM901   LOC196892 3'  GCTAGAAGTCTCAG        87804         C    TGT
                                CTGAGACT TCTG   GC
                                |||||||| ||||   ||
                                GACTCTGA AGAT   CG
                                     _   ____
GAM901   LOC199958 3'  CTCACGTAGGGAGCCCCAGG   89886      AGA         C
                                CCTG   CTCTCTGTGTG AG
                                ||||   ||||||||||| ||
                                GGAC   GAGGGATGCAC TC
                                  CCC          _
GAM901   LOC200488 5'  GCTGCACACACAGCTTCCCAGT 90087    C   A  CT  C
           GA                     TC CTG GA  CT TGTGTGCAGC
                                || ||| ||  || ||||||||||
                                AG GAC CT  GA ACACACGTCG
                                 T   C  TC  C
GAM901   LOC202781 5'  GCTGGAGGAGAGTCCCAG    90366     A       GTGTG
                                CTG GACTCTCT     CAGC
                                ||| ||||||||     ||||
                                GAC CTGAGAGG     GTCG
                                  C       AG___
GAM901   LOC203025 3'  CACAGAGAGCTCAGAGA     89250    C     A
                                TC CTGAG CTCTCTGTG
                                || ||||| |||||||||
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                                AG GACTC GAGAGACAC
                                 A    _
GAM901  LOC219690 5'  GCCACAGGAATCTCACAGA   93073    CC    C T    T
                                TC  TGAGA TC CTGTG GC
                                ||  ||||| || ||||| ||
                                AG  ACTCT AG GACAC CG
                                 AC    A _    _
GAM901  LOC221354 3'  CTGTGGAAAGCCGCAGGGA   92411       AGA  C   GTGT
                                TCCCTG   CT TCT    GCAG
                                ||||||   || |||    ||||
                                AGGGAC   GA AGG    TGTC
                                   GCC  A  _____
GAM901  LOC58525  3'  GCCCCCCCAAAGAGCCTCAGGGG 78648         A    C  TGT_
                                TCCCTGAG CTCT TG    GC
                                |||||||| |||| ||    ||
                                GGGGACTC GAGA AC    CG
                                     C    A  CCCC
GAM901  LOC85479  5'  CTGAAAACAGAGTCTCAG    52404          CT  GTG
                                CTGAGACTCT  GT   CAG
                                ||||||||||  ||   |||
                                GACTCTGAGA  CA   GTC
                                      __  AAA
GAM901  LOC92482  3'  GCTACACACAGAGACAAGGA   69490     C  AGAC        C
                                TCC TG    TCTCTGTGTG AGC
                                ||| ||    |||||||||| |||
                                AGG AC    AGAGACACAC TCG
                                  A _____         A
GAM902  ARHGEF7   3'  ATTGCAGCACCGTGG       14001     _  AGAA
                                CCA GG    TGCTGCAAT
                                ||| ||    |||||||||
                                GGT CC    ACGACGTTA
                                  G  _____
GAM902  BFSP2     3'  AGCTTTCTCCTGAGCT      13111     C       T
                                AGC CAGGAGAA GCT
                                ||| |||||||| |||
                                TCG GTCCTCTT CGA
                                  A       T
GAM902  C21orf33  3'  ATTGCAGCTCCTCAGC      16196    CC    GAAT
                                GC  AGGA    GCTGCAAT
                                ||  ||||    ||||||||
                                CG  TCCT    CGACGTTA
                                 AC    _____
GAM902  CCND2     3'  GCACACTCTCCTGGGC      8290           A  C
                                GCCCAGGAGA TG TGC
                                |||||||||| || |||
                                CGGGTCCTCT AC ACG
                                      C  _
GAM902  CDH11     5'  GCTGCATTCTCCTGTGC     53363    C         T
                                GC CAGGAGAATGC GC
                                || ||||||||||| ||
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                                CG GTCCTCTTACG CG
                                 T         T
GAM902  EPHA2    3'  TTGCTTTCCTGGGC       15410          ATGCT
                                GCCCAGGAGA    GCAA
                                ||||||||||    ||||
                                CGGGTCCTTT    CGTT
                                      _____
GAM902  F2RL3    3'  GATTGCGCCACTGGACT     14181    C    GAGAAT  T
                                AG CCAG     GC GCAATC
                                || ||||     || ||||||
                                TC GGTC     CG CGTTAG
                                 A   AC____ _
GAM902  GLP1R    3'  CACATTCTCCTGTGC       9029     C        C
                                GC CAGGAGAATG TG
                                || ||||||||||  ||
                                CG GTCCTCTTAC AC
                                 T        _
GAM902  HAS3     3'  GTAGCCTCCTCCTGGGCT    18041          AAT
                                AGCCCAGGAG   GCTGC
                                ||||||||||   |||||
                                TCGGGTCCTC   CGATG
                                      CTC
GAM902  HOXA7    3'  AGATATTCTCCCAGCTT     22570      CCA       _
                                AAGC   GGAGAATG CT
                                ||||   |||||||| ||
                                TTCG   CCTCTTAT GA
                                  AC_       A
GAM902  IFI16    5'  AGATTACAACATCCTGCGGTT  71220      _    GAA  C  C
                                AGCC CAGGA   TG TG AATCT
                                |||| |||||   || || |||||
                                TTGG GTCCT   AC AC TTAGA
                                  C     ___  A  A
GAM902  IFIT4    3'  GATTGCGCCCCTGCACT     70921    CC    AGAAT  T
                                AG  CAGG    GC GCAATC
                                ||  ||||    || ||||||
                                TC  GTCC    CG CGTTAG
                                 AC   C____ _
GAM902  LILRB4   3'  AGACTCAGTTCTCCTAGG    22430    C     AT    CAA
                                CC AGGAGA  GCTG   TCT
                                || ||||||  ||||   |||
                                GG TCCTCT  TGAC   AGA
                                 A     __    TC_
GAM902  MHC2TA   3'  AGATTGCAACAGGCTGGGCTT  4162         GAGAA  C
                                AAGCCCAG    TG TGCAATCT
                                ||||||||    || ||||||||
                                TTCGGGTC    AC ACGTTAGA
                                     GG___  A
GAM902  PCDHA9   5'  GATTGCAACTCCTGG       25762        AATGC
                                CCAGGAG    TGCAATC
                                |||||||    |||||||
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                              GGTCCTC    ACGTTAG
                                 A____
GAM902  PCDHA9   5'  GATTGCAACTCCTGG      49015       AATGC
                              CCAGGAG    TGCAATC
                              |||||||    |||||||
                              GGTCCTC    ACGTTAG
                                 A____
GAM902  PTK7     3'  AGATCCCTGTCCTCCTGGGC  11014        AAT  TGCA
                              GCCCAGGAG  GC   ATCT
                              |||||||||  ||   ||||
                              CGGGTCCTC  TG   TAGA
                                   C__  TCCC
GAM902  TNXB     5'  ATTCTCCCCTGGGCTT     50638       __
                              AAGCCCA  GGAGAAT
                              |||||||  |||||||
                              TTCGGGT  CCTCTTA
                                 CC
GAM902  WHSC1L1  3'  AGACTTGTTTCTCCATGGGCT  35028      _    TGCT   _
                              AGCCCA GGAGAA   GCAA TCT
                              |||||| ||||||   |||| |||
                              TCGGGT CCTCTT   TGTT AGA
                                 A    _____   C
GAM902  C8orf14  5'  TGGTCTCTGCCTGGGCT    54006       _  AT
                              AGCCCAGG AGA  GCTG
                              |||||||| |||  ||||
                              TCGGGTCC TCT  TGGT
                                   G  C_
GAM902  CIDEB    5'  AGACCGACATCCTTCTGGGC  27041        A  C  CAA
                              GCCCAGGAG ATG TG   TCT
                              ||||||||| ||| ||   |||
                              CGGGTCTTC TAC GC   AGA
                                   C  A  C__
GAM902  DKFZP434C0826 3'  AGATCCTTCTTTCCCTGGGCTT 84032        A   TGCTGCA
                              AAGCCCAGG GAA      ATCT
                              ||||||||| |||      ||||
                              TTCGGGTCC CTT      TAGA
                                   _  TCTTCC_
GAM902  DKFZP434H132 5'  TGGAGCATCCCCTGGGCTT   73611        A  A   G
                              AAGCCCAGG GA TGCT CA
                              ||||||||| || |||| ||
                              TTCGGGTCC CT ACGA GT
                                   C  _   G
GAM902  DKFZp434O0515 5'  ATTGCAGCACTCTTGAATGCT  65926    C__    AA
                              AGC   CAGGAG  TGCTGCAAT
                              |||   ||||||  |||||||||
                              TCG   GTTCTC  ACGACGTTA
                                TAA     __
GAM902  FLJ10759  3'  AGACCACAACCTCCTGGG    36574       AA  C  CAA
                              CCCAGGAG  TG TG   TCT
                              ||||||||  || ||   |||
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                                GGGTCCTC  AC AC   AGA
                                    CA  _  C__
GAM902  FLJ11117  3'  AGATTGCCTCTCTCCCAGCT  37071    CCA    ATGCT
                                AGC  GGAGA    GCAATCT
                                |||  |||||    |||||||
                                TCG  CCTCT    CGTTAGA
                                  AC_    CTC__
GAM902  FLJ12572  3'  GATTGCAGCACAGGGC     43251     AGGAGAA
                                GCCC     TGCTGCAATC
                                ||||     ||||||||||
                                CGGG     ACGACGTTAG
                                  AC_____
GAM902  FLJ13782  3'  AGACTGGGGCTTCCTCCTGGGC 46159        AAT  G  A
                                GCCCAGGAG  GCT CA TCT
                                |||||||||  ||| || |||
                                CGGGTCCTC  CGG GT AGA
                                     CTT  G  C
GAM902  FLJ20034  5'  TGAACATCTCCTGGGTT    34388         A  CTG
                                AGCCCAGGAGA TG  CA
                                |||||||||||  ||  ||
                                TTGGGTCCTCT AC  GT
                                     _  AA_
GAM902  FLJ20195  3'  GGACTAAGCCTCCTGGGC    34712        AAT  GCAA
                                GCCCAGGAG  GCT   TCT
                                |||||||||  |||   |||
                                CGGGTCCTC  CGA   AGG
                                    ___  ATC_
GAM902  FLJ22169  3'  AGACTGAGGTCTTCCTGGGC  43997        AAT  G  A
                                GCCCAGGAG  GCT CA TCT
                                |||||||||  ||| || |||
                                CGGGTCCTT  TGG GT AGA
                                     C__  A  C
GAM902  GRIN3A   5'  AGACCGCTCCAGCTCCTGGG  55966        AA  CT  AA
                                CCCAGGAG  TG  GC  TCT
                                ||||||||  ||  ||  |||
                                GGGTCCTC  AC  CG  AGA
                                    G_  CT  CC
GAM902  HERPUD1  3'  GATTGCCTCTCCTGG      28018        ATGCT
                                CCAGGAGA    GCAATC
                                ||||||||    ||||||
                                GGTCCTCT    CGTTAG
                                    C_____
GAM902  KCND1    5'  AGACAGCCACATTCTCCT    17140        CT  AA
                                AGGAGAATG  GC  TCT
                                |||||||||  ||  |||
                                TCCTCTTAC  CG  AGA
                                     AC  AC
GAM902  KIAA0174  3'  GCACAACACTCCCTCTGGGCT  78594       ___   AA_  C
                                AGCCCA  GGAG  TG TGC
                                ||||||  ||||  || |||
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                                TCGGGT  CCTC  AC ACG
                                   CTC   ACA  _
GAM902  KIAA0295  3'  TAGTATTCCCCCCAGCTT   68109     CCA  A
                                AAGC  GG GAATGCTG
                                ||||  || ||||||||
                                TTCG  CC CTTATGAT
                                  ACC  C
GAM902  KIAA0523  3'  AGATTGGCCTTACCTCTGGACT 67727    C    AG_  T  TG
           T                     AAG CCAGG  AA GC  CAATCT
                                ||| |||||  || ||  ||||||
                                TTC GGTCT  TT CG  GTTAGA
                                  A   CCA  C  __
GAM902  KIAA0676  3'  CAGATTCCCTGGGC       30450       A   G
                                GCCCAGG GAAT CTG
                                ||||||| |||| |||
                                CGGGTCC CTTA GAC
                                   _   _
GAM902  KIAA1318  5'  AGATTTTCTTGCCTCCTGGGCT 67305         AAT  TGC__
                                AGCCCAGGAG  GC   AATCT
                                ||||||||||  ||   |||||
                                TCGGGTCCTC  CG   TTAGA
                                     ___  TTCTT
GAM902  KIAA1336  3'  AGACCGCAACACCTGAATCCTG 72321         GAA___  C  AA
           GGTTT                  AAGCCCAGGA    TG TGC  TCT
                                ||||||||||    || |||  |||
                                TTTGGGTCCT    AC ACG  AGA
                                     AAGTCC  A  CC
GAM902  KIAA1548  3'  ATTGCACTTTTCCTGACTT   40500    CC      TGC
                                AAG  CAGGAGAA  TGCAAT
                                |||  ||||||||  ||||||
                                TTC  GTCCTTTT  ACGTTA
                                  A_      C__
GAM902  Kv6.3    3'  GCTAACATTCTCCTGGGC    56038          CT_
                                GCCCAGGAGAATG  GC
                                ||||||||||||  ||
                                CGGGTCCTCTTAC  CG
                                       AAT
GAM902  MAP3K3   3'  AGACTGTGTGTGCCCTCTGGGC 9997        AGA_   T  A
           T                     AGCCCAGG   ATGC GCA TCT
                                |||||||   |||| ||| |||
                                TCGGGTCT   TGTG TGT AGA
                                    CCCG   _  C
GAM902  MGC13183  3'  AGAGGCTGCCTTTCTCCTGAGC 50388    C      T_  T  AA
           T                     AGC CAGGAGAA  GC GC  TCT
                                ||| ||||||||  || ||  |||
                                TCG GTCCTCTT  CG CG  AGA
                                  A      TC  T  G_
GAM902  MGC2560   5'  GGCCACCTCTCCTGGGCTT   48783          AT__
                                AAGCCCAGGAGA   GCT
                                ||||||||||||   |||
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                                TTCGGGTCCTCT   CGG
                                      CCAC
GAM902  PHYHIP   3' AGACCTGCCCACCTCCTGGGCT 28604        AA  CT  A_
                                AGCCCAGGAG  TG  GCA  TCT
                                ||||||||||  ||  |||  |||
                                TCGGGTCCTC  AC  CGT  AGA
                                     C_  C_  CC
GAM902  PP1201   3' CAGCATCTCCCCTGGGCTT   42188        A  _
                                AAGCCCAGG GA ATGCTG
                                ||||||||| || ||||||
                                TTCGGGTCC CT TACGAC
                                     C  C
GAM902  RALGPS1A 3' TGTTGCACTCTCCTGGGCT   27611         A   T
                                AGCCCAGGAGA TGC GCA
                                |||||||||| ||| |||
                                TCGGGTCCTCT ACG TGT
                                      C   T
GAM902  SLC12A8  5' CAGCATTCCCCTGGGCT    44896        A
                                AGCCCAGG GAATGCTG
                                |||||||| ||||||||
                                TCGGGTCC CTTACGAC
                                     C
GAM902  STAG3    3' TGAAGCATTCCCCCAGGCTT  24912      CA  A     G
                                AAGCC  GG GAATGCT CA
                                |||||  || ||||||| ||
                                TTCGG  CC CTTACGA GT
                                   AC  C      A
GAM902  SYT12    3' AGATTGCAGCAGAGGAGTGGGC 94721      GGAGAA
                                GCCCA     TGCTGCAATCT
                                |||||     ||||||||||
                                CGGGT     ACGACGTTAGA
                                   GAGGAG
GAM902  LOC112724 3' AGGTGAGCACTGCCCTGGGCT  56491        AGAA   G  A
                                AGCCCAGG    TGCT CA TCT
                                ||||||||    |||| || |||
                                TCGGGTCC    ACGA GT GGA
                                     CGTC   _  _
GAM902  LOC124930 5' CACCACACTCCTGGGCTT    74354         AA  C
                                AAGCCCAGGAG  TG TG
                                ||||||||||  || ||
                                TTCGGGTCCTC  AC AC
                                      AC  C
GAM902  LOC149108 3' AGATCACTCCAACTCCTGGG   84358        AA  CTGCA
                                CCCAGGAG  TG    ATCT
                                ||||||||  ||    ||||
                                GGGTCCTC  AC    TAGA
                                     A_  CTCAC
GAM902  LOC151414 3' AGATCACAATGTTTTCTGAGCT 80233     CCA     GC  CA
           T                     AAGC   GGAGAAT  TG  ATCT
                                ||||   |||||||  ||  ||||
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                                TTCG   TCTTTTG  AC  TAGA
                                  AG_      TA  AC
GAM902  LOC152941 3'  AGATTGCAATATGCTT     80749     A   C
                                GAG ATG TGCAATCT
                                ||| ||| ||||||||
                                TTC TAT ACGTTAGA
                                  G   A
GAM902  LOC153339 5'  TGCCTCTTGGGCTT       86017          AATGCT
                                AAGCCCAGGAG     GCA
                                ||||||||||     |||
                                TTCGGGTTCTC     CGT
                                          _______
GAM902  LOC154222 5'  AGCGTCACCTCCTCCCAGGCT  86187     C___    A__
                                AGCC    AGGAG   ATGCT
                                ||||    |||||   |||||
                                TCGG    TCCTC   TGCGA
                                  ACCC     CAC
GAM902  LOC169026 3'  TAGCATTCTGCTGAGCTT    82728     C   G
                                AAGC CAG AGAATGCTG
                                |||| ||| |||||||||
                                TTCG GTC TCTTACGAT
                                  A   G
GAM902  LOC199780 5'  AGACCCACGCTTCTCTGGGCT  78731       G   T _  CAA
                                AGCCCAG AGAA GC TG   TCT
                                ||||||| |||| || ||   |||
                                TCGGGTC TCTT CG AC   AGA
                                   _   _  C  CC_
GAM902  LOC201109 3'  AGACTCGGTCCTCCCTGGGCT  89758       A  AT   CAA
                                AGCCCAGG GA  GCTG   TCT
                                |||||||| ||  ||||   |||
                                TCGGGTCC CT  TGGC   AGA
                                     _ CC    TC_
GAM902  LOC202266 3'  GGCCCTCTCCTGGGCTT     90331          AT
                                AAGCCCAGGAGA  GCT
                                ||||||||||||  |||
                                TTCGGGTCCTCT  CGG
                                       CC
GAM902  LOC221922 5'  AGAAGGCCATTCTCCTGAGCT  92686     C       CT  AA
                                AGC CAGGAGAATG  GC  TCT
                                ||| ||||||||||  ||  |||
                                TCG GTCCTCTTAC  CG  AGA
                                  A        __  GA
GAM902  LOC222189 3'  CACATCTCCCCTGGGTCC    94170   A     A  _  C
                                A GCCCAGG GA ATG TG
                                | ||||||| || ||| ||
                                C TGGGTCC CT TAC AC
                                 C      C  C  _
GAM902  LOC245787 3'  CACATCTCCCCTGGGTCC    81345   A     A  _  C
                                A GCCCAGG GA ATG TG
                                | ||||||| || ||| ||
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                                C TGGGTCC CT TAC AC
                                 C      C  C  _
GAM902  LOC253609 5'  TGATGGCATTTTCCCGGGCT   96764       A         _
                                AGCCC GGAGAATGCTG CA
                                ||||| |||||||||||| ||
                                TCGGG CCTTTTACGGT GT
                                   C          A
GAM902  LOC253815 3'  CAGAACCCTCCTGGGCTT    95597           AATG
                                AAGCCCAGGAG    CTG
                                ||||||||||    |||
                                TTCGGGTCCTC    GAC
                                      CCAA
GAM902  LOC64102  5'  GCAGCACAGGAGTCCCCTGGGC 42174         A  A_____
              T                  AGCCCAGG GA     TGCTGC
                                ||||||||| ||     ||||||
                                TCGGGTCC CT     ACGACG
                                     C  GAGGAC
GAM902  LOC89919  5'  AGATCAGTCCACCTCTCCTGGG 60714    A        AT___    CA
              TCC                  A GCCCAGGAGA     GCTG  ATCT
                                | ||||||||||    ||||  ||||
                                C TGGGTCCTCT    TGAC  TAGA
                                 C         CCACC   __
GAM902  LOC92689  3'  AGTGGCTGCTTCTCCTGAGCT  70217     C       T  T  AAT
                                AGC CAGGAGAA GC GC   CT
                                ||| ||||||| || ||   ||
                                TCG GTCCTCTT CG CG   GA
                                  A       _  T  GT_
GAM903  ASPH     5'  TGGATTGAAGAAATCAA     39396     GC       _
                                TTG  TTCTTCAA CCA
                                |||  |||||||| |||
                                AAC  AAGAAGTT GGT
                                  TA       A
GAM903  ASPH     5'  TGGATTGAAGAAATCAA     50626     GC       _
                                TTG  TTCTTCAA CCA
                                |||  |||||||| |||
                                AAC  AAGAAGTT GGT
                                  TA       A
GAM903  ASPH     5'  TGGATTGAAGAAATCAA     50634     GC       _
                                TTG  TTCTTCAA CCA
                                |||  |||||||| |||
                                AAC  AAGAAGTT GGT
                                  TA       A
GAM903  FOS      5'  GCGAGCAACTGAGAAGCCAA   17906         T  ACCA  A_
                                TTGGCTTCT CA    GC  GT
                                ||||||||| ||    ||  ||
                                AACCGAAGA GT    CG  CG
                                      _  CAA_  AG
GAM903  FSTL1    3'  ATACTGCTAGTTAACCCAG    23010      C  CTTC   C
                                TTGG TT    AAC AGCAGTAT
                                |||| ||    ||| ||||||||
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                                GACC AA    TTG TCGTCATA
                                  C _____  A
GAM903  NR4A2    3'  TGAGTTGAAGAAGGCAA     20535     G        _
                                TTG CTTCTTCAAC CA
                                ||| |||||||||| ||
                                AAC GAAGAAGTTG GT
                                  G         A
GAM903  NXF5     3'  CTGGCTGACCAAGAAGCCAA   51966          ___  A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
                                AACCGAAGA   AGT GGTC
                                     ACC   C
GAM903  NXF5     3'  CTGGCTGACCAAGAAGCCAA   52508          ___  A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
                                AACCGAAGA   AGT GGTC
                                     ACC   C
GAM903  NXF5     3'  CTGGCTGACCAAGAAGCCAA   52513          ___  A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
                                AACCGAAGA   AGT GGTC
                                     ACC   C
GAM903  NXF5     3'  CTGGCTGACCAAGAAGCCAA   52517          ___  A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
                                AACCGAAGA   AGT GGTC
                                     ACC   C
GAM903  NXF5     3'  CTGGCTGACCAAGAAGCCAA   52521          ___  A
                                TTGGCTTCT   TCA CCAG
                                |||||||||   ||| ||||
                                AACCGAAGA   AGT GGTC
                                     ACC   C
GAM903  POLG     5'  GCCAGTAAAAGAAGCCAA     10680          CA  CA
                                TTGGCTTCTT  AC  GC
                                ||||||||||  ||  ||
                                AACCGAAGAA  TG  CG
                                     AA  AC
GAM903  FLJ12377 3'  TGTTGGATAAAGAAGCCAA    46487           CAA
                                TTGGCTTCTT   CCAGCA
                                ||||||||||   ||||||
                                AACCGAAGAA   GGTTGT
                                     ATA
GAM903  FLJ13102 3'  ACGGCGATTGAGAAGCCAA    46002          T   CCA  A
                                TTGGCTTCT CAA   GC GT
                                ||||||||| |||   || ||
                                AACCGAAGA GTT   CG CA
                                     _  AG_  G
GAM903  FLJ23120 3'  CATACTAAATGAAAGAAGCCAG 85145          CAAC  GC_
                                TTGGCTTCTT   CA   AGTATG
                                ||||||||||   ||   ||||||
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                                GACCGAAGAA   GT  TCATAC
                                     A___  AAA
GAM903  FREQ     3'  GCGGCCAAGAAGCCAA     26582        CAA  A
                                TTGGCTTCTT   CC GC
                                ||||||||||  || ||
                                AACCGAAGAA   GG CG
                                     CC_  _
GAM903  KIAA0232 3'  TTGCTAACTGAAGAAGCCAA  72764          ACC
                                TTGGCTTCTTCA  AGCAG
                                ||||||||||||  |||||
                                AACCGAAGAAGT  TCGTT
                                      CAA
GAM903  KIAA0987 3'  GCAATTAAAGAGGCCAA    24563        C  CCA
                                TTGGCTTCTT AA  GC
                                |||||||||| ||  ||
                                AACCGGAGAA TT  CG
                                     A  AA_
GAM903  PPFIA2   5'  ATTGATCAATTGAAGAAGC   13261        CCAG_
                                GCTTCTTCAA    CAGT
                                ||||||||||    ||||
                                CGAAGAAGTT    GTTA
                                     AACTA
GAM903  SNPH     3'  ACAGCTTACTGAAAAAGCCAG  28236      C   ACC  A
                                TTGGCTT TTCA  AGC GT
                                ||||||| ||||  ||| ||
                                GACCGAA AAGT  TCG CA
                                    A   CAT  A
GAM903  LOC134957 3'  ACGTGACAGATGAAGAAACCAA 57661     C     ACCAG  _
                                TTGG TTCTTCA    CA GT
                                |||| |||||||    || ||
                                AACC AAGAAGT    GT CA
                                  A     AGACA  G
GAM903  LOC136895 5'  CTGCCAAAGAAGCCAA     57168        CAACCA
                                TTGGCTTCTT     GCAG
                                ||||||||||     ||||
                                AACCGAAGAA     CGTC
                                     AC____
GAM903  LOC162333 5'  ACTAAGCTGAAGAGGCCAA   87115          ACCA  __
                                TTGGCTTCTTCA   GC  AGT
                                ||||||||||||   ||  |||
                                AACCGGAGAAGT   CG  TCA
                                       ____  AA
GAM903  LOC253227 5'  ACTACTGGTAAGAAGCCA    97506        CA   C
                                TGGCTTCTT  ACCAG AGT
                                |||||||||  ||||| |||
                                ACCGAAGAA  TGGTC TCA
                                     __    A
GAM903  LOC255452 3'  GCAGCCGAAGAAGCCA      97538        AACCA  A
                                TGGCTTCTTC    GC GT
                                ||||||||||    || ||
```

```
                                ACCGAAGAAG    CG CG
                                      C____  A
GAM904  ADH1B   3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||  ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM904  AHR     3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM904  FDFT1   3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT

                                      _
GAM904  JTB     3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM904  KLF4    3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM904  PHYH    3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM904  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM904  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM904  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_   CG_
GAM904  CG012   5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
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                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM904  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                |||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM904  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
          G                      CATTTC       GTCTGAGAT
                                 ||||||       |||||||||
                                 GTAAAG       CAGACTCTA
                                    AAACATTT_
GAM904  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM904  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                   A       CT
GAM904  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                   _  G
GAM904  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM904  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM904  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM904  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG 48148         TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM904  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
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                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM904  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM904  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM904  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                     TTTCC_  A
GAM904  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM904  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                                _
GAM905  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM905  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875        CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM905  FDFT1    3'  TAGGAAAGTGAAATG       15518            A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                                _
GAM905  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                ||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM905  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
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                                GT  AGGTGACAGAC CT
                                 AT         C
GAM905  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM905  PKD2     3'  TCCAGGTTGAAAGTGAAA     60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM905  WRN      3'  GGGCAGTGAAAATGAAA      5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM905  ZNF216   3'  ATCTGCACAGCAAAGTGAAA   20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_   CG_
GAM905  CG012    5'  CTCACTCTGAAAGTGAA      83218          CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM905  EIF2C2   3'  ATCTTCTGAGAGTGAAAG     71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM905  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM905  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281         CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM905  KIAA0984 3'  TTTGTCCAGTGAAAATGAA    65534      C       TC
                                TTCA TTTCACTG  TGAG
                                ||||  ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM905  KLHL6    3'  ATCTCAGAGCAGGAAA       55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
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                                AAAG GAC AGACTCTA
                                  _  G
GAM905  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM905  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM905  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM905  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148         TCAC   C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM905  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM905  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM905  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM905  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM905  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||   |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM905  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
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                                GTAAAGTGAA GTGACA
                                        _
GAM906  AASS    3'  TTTTGTTGTTGTTGTT     19269       TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT
GAM906  AASS    3'  TTTTTTTTTTGTTGTTGTTGTT 19270       TG    CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT    TTTTTTG
GAM906  ABCC5   3'  TGGTGTCACTTACTGTTTCT  19096   C     CAG
                                AG AGCAGTGA   GACATCA
                                || ||||||||   |||||||
                                TC TTGTCATT   CTGTGGT
                                 T      CA_
GAM906  ABH     3'  GGTGTTTTGTTACTGTT    59751           A
                                AGCAGTGACAGGACATC
                                |||||||||||||||||
                                TTGTCATTGTTTTGTGG
                                          G
GAM906  ACCN1   3'  TGATGTTCTGAGGTTTGCT   6587      TGA_
                                AGCAG   CAGGACATCA
                                |||||   ||||||||||
                                TCGTT   GTCTTGTAGT
                                   TGGA
GAM906  ACP5    3'  TTCTGTTACTGATGTT     7858     G
                                AGCA CAGTGACAGGA
                                |||| ||||||||||
                                TTGT GTCATTGTCTT
                                  A
GAM906  ADARB1  3'  TGGTGAGACCACGTGCTGCT  31727       _  ACAGGA
                                AGCAGCA GTG     CATCA
                                ||||||| |||     |||||
                                TCGTCGT CAC     GTGGT
                                    G   CAGA__
GAM906  ADARB1  3'  TGGTGAGACCACGTGCTGCT  6634        _  ACAGGA
                                AGCAGCA GTG     CATCA
                                ||||||| |||     |||||
                                TCGTCGT CAC     GTGGT
                                    G   CAGA__
GAM906  ADRB3   3'  TGGTTCCCTTATTACTGCT   3439        C_  AC
                                AGCAGTGA  AGG  ATCA
                                ||||||||  |||  ||||
                                TCGTCATT  TCC  TGGT
                                    AT   CT
GAM906  AKAP13  3'  TGATGTTTCATCTGCT     89690      _  CAG
                                AGCAG TGA   GACATCA
                                ||||| |||   |||||||
```

```
                                TCGTC ACT   TTGTAGT
                                  T  ____
GAM906  ALG6    3'  TGGTGAAAAGTCATTGTTGT  25314          AGGA
                                GCAGCAGTGAC   CATCA
                                ||||||||||   |||||
                                TGTTGTTACTG   GTGGT
                                     AAAA
GAM906  ANKH    3'  GTCTTTACTGTTGCT      53993          CA
                                AGCAGCAGTGA  GGAC
                                ||||||||||  ||||
                                TCGTTGTCATT  TCTG
                                     __
GAM906  ANXA7   5'  TGGGCTGTGACGCTGCTGCT  14454          __   GA  TCA
                                AGCAGCAGTG  ACAG  CA
                                |||||||||  ||||  ||
                                TCGTCGTCGC  TGTC  GT
                                     AG   GG
GAM906  ANXA7   5'  TGGGCTGTGACGCTGCTGCT  6722           __   GA  TCA
                                AGCAGCAGTG  ACAG  CA
                                |||||||||  ||||  ||
                                TCGTCGTCGC  TGTC  GT
                                     AG   GG
GAM906  APLP2   3'  TGATGTCGATGCTCACTGCTTC 90903   C      _  G_
          T                      AG AGCAGTGA CA  GACATCA
                                || ||||||| ||  |||||||
                                TC TCGTCACT GT  CTGTAGT
                                 T      C  AG
GAM906  APLP2   3'  GGTGTCCGCTGCTGCT     90898        GACA     A
                                AGCAGCAGT   GGACATC
                                |||||||||   |||||||
                                TCGTCGTCG   CCTGTGG
                                    ____     G
GAM906  APM1    3'  ATGTCTTTTTGTTGTTGTTGTT 16584       TG  ___   TCA
                                AGCAGCAG  ACA   GGACA
                                ||||||||  |||   |||||
                                TTGTTGTT  TGT   TCTGT
                                     GT   TTT      AC
GAM906  APM1    3'  TTTGTCTTTTTGTTGTTGTT  16606       TG C     TCA
                                AGCAGCAG  A AGGACA
                                ||||||||  | ||||||
                                TTGTTGTT  T TTCTGT
                                     GT T     TT
GAM906  ARCN1   3'  TGTCTGCTGCTGTTGCT    7990         GA   G
                                AGCAGCAGT  CAG ACA
                                |||||||||  ||| |||
                                TCGTTGTCG  GTC TGT
                                     TC  _
GAM906  ARG2    3'  TGGTCTTGTTGCTGTTGTT   6756        TG      ATCA
                                AGCAGCAG  ACAGGAC
                                ||||||||  |||||||
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                                TTGTTGTC  TGTTCTG
                                    GT      GT
GAM906  ARHGDIA   3' GGTGTGCTGCTGCTGCT     15044        TGA  G    A
                                AGCAGCAG   CAG ACATC
                                ||||||||   ||| |||||
                                TCGTCGTC   GTC TGTGG
                                    ___  G    G
GAM906  ARHGDIB   3' TTTTGTGGTTGTTGCT      6775         TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TCGTTGTT  TGTTTT
                                    GG
GAM906  ARHGEF12  3' AAAAAGTTGTTGTTGTTGTT 30993         TG   _  ATCA
           T                     AGCAGCAG  ACAG GAC
                                ||||||||  |||| |||
                                TTGTTGTT  TGTT TTG
                                    GT   G   AAAAAT
GAM906  ARHGEF7   3' TGATGCTACACTGTTGT     14013         ACA  A
                                GCAGCAGTG   GG CATCA
                                |||||||||   || |||||
                                TGTTGTCAC   TC GTAGT
                                    A__ _
GAM906  ARHI      3' TGGTTGATTTTGTGCTGTTGTT 16250         G    _ _
                                AGCAGCAGT ACAGGA CA TCA
                                ||||||||| |||||| || |||
                                TTGTTGTCG TGTTTT GT GGT
                                    _    A  T
GAM906  ASB1      3' TGAGTGCTGTGCTGCTGCT   32269         G   G  A
                                AGCAGCAGT ACAG AC TCA
                                ||||||||| |||| || |||
                                TCGTCGTCG TGTC TG AGT
                                    _   G  _
GAM906  ATP11A    3' GAAGTCCCTGTTGTT       77029         TGACA   A  A
                                AGCAGCAG    GGAC TC
                                ||||||||    |||| ||
                                TTGTTGTC    CCTG AG
                                    _____   A  G
GAM906  ATP5A1    3' GTTTTGTCATTGTTCT      66245    C
                                AG AGCAGTGACAGGAC
                                || ||||||||||||||
                                TC TTGTTACTGTTTTG
                                 _
GAM906  ATP6V1A1  3' TGTTTTTTTGTTGTTGTTGTT  8082         TG     CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT     TTTGT
GAM906  ATP6V1A1  3' TTTGTTTTTTTGTTGTTGTT   8083         TG C     TCA
                                AGCAGCAG  A AGGACA
                                ||||||||  | ||||||
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                                TTGTTGTT  T TTTTGT
                                    GT T     TT
GAM906  ATP7A   3'  TGTTGTTGTTGTTGTTGTTGTT 3533        TG   _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                    GT   G   T
GAM906  ATP7A   3'  TGTTGTTGTTGTTGTTGTTGTT 3534        TG   _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                    GT   G   T
GAM906  ATP7A   3'  TGTTTGTTGTTGTTGTT    3536        TG   G
                                AGCAGCAG  ACAG ACA
                                ||||||||  |||| |||
                                TTGTTGTT  TGTT TGT
                                    GT   _
GAM906  ATP7A   3'  TGTTTGTTGTTGTTGTTGTTGT 3537        TG   _   TCA
          T                      AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                    GT   G   TTGT
GAM906  ATP7A   3'  TGTTGTTGTTGTTGTTGTTGTT 3535        TG   _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                    GT   G   T
GAM906  BAT1    5'  TCCTTCGTCGCTGTTGCT    54587          __
                                AGCAGCAGTGAC  AGGA
                                ||||||||||||  ||||
                                TCGTTGTCGCTG  TCCT
                                      CT
GAM906  BAT1    5'  TCCTTCGTCGCTGTTGCT    16164          __
                                AGCAGCAGTGAC  AGGA
                                ||||||||||||  ||||
                                TCGTTGTCGCTG  TCCT
                                      CT
GAM906  BAT4    5'  TGGTTTTTGTTGTTGTTGT   52584       TG    C
                                GCAGCAG  ACAGGA ATCA
                                |||||||  |||||| ||||
                                TGTTGTT  TGTTTT TGGT
                                    GT    _
GAM906  BCL2    3'  TCTTGTCACTGTAGTT     5305     A
                                AGC GCAGTGACAGGA
                                |||  ||||||||||||
                                TTG TGTCACTGTTCT
                                  A
GAM906  BCL9    3'  TGATGTTTTAAGCTGCT     15069      GAC
                                AGCAGT   AGGACATCA
                                ||||||   |||||||||
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                                TCGTCG  TTTTGTAGT
                                   AA_
GAM906  BECN1   3'  GGTGTTTGATACTGTT     13648       ACA
                                AGCAGTG  GGACATC
                                |||||||  |||||||
                                TTGTCAT  TTTGTGG
                                   AG_
GAM906  BHLHB3  3'  TGATGTCTGACATGCT     47767     G  ACA
                                AGCA TG  GGACATCA
                                ||||  ||  ||||||||
                                TCGT AC  TCTGTAGT
                                  _ AG_
GAM906  BHLHB3  3'  TGGTGCATTTGCTGCTGCTGTT 47768        GA   A_
                                AGCAGCAGT  CAGG  CATCA
                                |||||||||  ||||  |||||
                                TTGTCGTCG  GTTT  GTGGT
                                     TC   AC
GAM906  BMP6    3'  TGTCTCAGTCATTGCTGTT   8166          A_
                                AGCAGCAGTGAC  GGACA
                                ||||||||||||  |||||
                                TTGTCGTTACTG  TCTGT
                                      AC
GAM906  C11orf8 3'  CAATGTTTTGTTGTTGTTGTT  7816        TG       CA
                                AGCAGCAG  ACAGGACAT
                                ||||||||  |||||||||
                                TTGTTGTT  TGTTTTGTA
                                     GT       ACT
GAM906  CALCR   3'  TCTTGGTACTGTTGCT     8223          A
                                AGCAGCAGTG CAGGA
                                |||||||||| |||||
                                TCGTTGTCAT GTTCT
                                      G
GAM906  CBFB    3'  GGTGTTTTATGTTACT     8276        __
                                AGTGACA  GGACATC
                                |||||||  |||||||
                                TCATTGT  TTTGTGG
                                   AT
GAM906  CBFB    3'  GGTGTTTTATGTTACT     43143       __
                                AGTGACA  GGACATC
                                |||||||  |||||||
                                TCATTGT  TTTGTGG
                                   AT
GAM906  CCND2   3'  GCTCTTTTTGTTGTTGTTGTT  8295        TG     CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                     GT     TCTCGT
GAM906  CCND2   3'  AACTTGCTCTTTTTGTTGTTGT 8284         TG C   _  TCA
           T                     AGCAGCAG  A AGGA CA
                                ||||||||  | |||| ||
```

```
                                TTGTTGTT  T TTCT GT
                                    GT T   C  TCAAG
GAM906  CD1A    3'  TAAAAATTTTGTTATTTTTGCT 71183      C       CATCA
                                AGCAG AGTGACAGGA
                                ||||| ||||||||||
                                TCGTT TTATTGTTTT
                                   T        AAAAATG
GAM906  CDC6    3'  GTTTTTTTTGTTGTTGTTGTT  6986        TG    CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT     TTTTGT
GAM906  CDH11   3'  TGAACATTGTACTGTTGCT   53366         A  GACA
                                AGCAGCAGTG CAG   TCA
                                |||||||||| |||   |||
                                TCGTTGTCAT GTT   AGT
                                     _  ACA_
GAM906  CDH12   3'  CTTTGTTTTGTTGTTTTGTT  14492     C  TG      TCA
                                AGCAG AG  ACAGGACA
                                ||||| ||  ||||||||
                                TTGTT TT  TGTTTTGT
                                   _ GT       TTCG
GAM906  CDH5    3'  TGGTGTTCTGTCTGGGCT   8389     AGT
                                AGC   GACAGGACATCA
                                |||   ||||||||||||
                                TCG   CTGTCTTGTGGT
                                  GGT
GAM906  CELSR2  3'  GTAGCGTTTTGTTGTTGTTGTT 7409        TG      ATCA
                                AGCAGCAG  ACAGGAC
                                ||||||||  |||||||
                                TTGTTGTT  TGTTTTG
                                    GT     CGATGG
GAM906  CENTD1  3'  GTCCTGTTGTTTTGTT     57564      C  TG
                                AGCAG AG  ACAGGAC
                                ||||| ||  |||||||
                                TTGTT TT  TGTCCTG
                                   _ GT
GAM906  CENTD1  3'  GTCCTGTTGTTTTGTT     30854      C  TG
                                AGCAG AG  ACAGGAC
                                ||||| ||  |||||||
                                TTGTT TT  TGTCCTG
                                   _ GT
GAM906  CHIC2   5'  TGTTGTTGTTATTGCT     23997          _
                                AGCAGTGACAG GACA
                                |||||||||| ||||
                                TCGTTATTGTT TTGT
                                      G
GAM906  CLASP1  3'  GTACCTCACTGCTGCT     65307          CA _
                                AGCAGCAGTGA  GG AC
                                ||||||||||  || ||
```

```
                                TCGTCGTCACT  CC TG
                                      __ A
GAM906  CLNS1A   5'  TGGTGCACGCATTGCTGT    7099          ACAGGA
                                GCAGCAGTG     CATCA
                                |||||||||     |||||
                                TGTCGTTAC     GTGGT
                                    GCAC__
GAM906  CNTNAP2  3'  GTTATTATTGCTGTT      26233          CAG
                                AGCAGCAGTGA   GAC
                                ||||||||||   |||
                                TTGTCGTTATT   TTG
                                      A__
GAM906  COL16A1  3'  TTTTGTTGTTGTTGTT     8503         TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT
GAM906  COL16A1  3'  TTTTTTTTTTTGTTGTTGTTGT 8504         TG     CATCA
           T                     AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT     TTTTTTTT
GAM906  COL4A3   3'  TCCTTGTCACTGCTGTT     48560           _
                                AGCAGCAGTGACA GGA
                                |||||||||||| |||
                                TTGTCGTCACTGT CCT
                                      T
GAM906  COL4A3   3'  TCCTTGTCACTGCTGTT     3625            _
                                AGCAGCAGTGACA GGA
                                |||||||||||| |||
                                TTGTCGTCACTGT CCT
                                      T
GAM906  COL4A3   3'  TCCTTGTCACTGCTGTT     48571           _
                                AGCAGCAGTGACA GGA
                                |||||||||||| |||
                                TTGTCGTCACTGT CCT
                                      T
GAM906  COMT     5'  TGGTGGTGCTGCTGCTGCT   23603         GA  GGA
                                AGCAGCAGT  CA   CATCA
                                |||||||||  ||   |||||
                                TCGTCGTCG  GT   GTGGT
                                    TC  G__
GAM906  CORT     3'  TGATGTTCATTATGGTGCT    7119       G  GTGACA
                                AGCA CA     GGACATCA
                                ||||  ||     ||||||||
                                TCGT GT     CTTGTAGT
                                  G  ATTA__
GAM906  COX7A2L  3'  TGATGTTTTGGTTTGTT     16354       TGA
                                AGCAG   CAGGACATCA
                                |||||   ||||||||||
```

```
                                TTGTT  GTTTTGTAGT
                                  TG_
GAM906  CPA3    3'  CCATGTTACTGCTGTT     8521          _
                                AGCAGCAGTGACA GG
                                |||||||||||| ||
                                TTGTCGTCATTGT CC
                                       A
GAM906  CPS1    3'  TGATGTTTGTGTATTGCTTCT  8531    C     ACA
                                AG AGCAGTG  GGACATCA
                                || |||||||  ||||||||
                                TC TCGTTAT  TTTGTAGT
                                 T     GTG
GAM906  CRIM1   3'  TCACTGTTTGTTGTTGCT    33178       TG _  _
                                AGCAGCAG  A CAG GA
                                ||||||||  | ||| ||
                                TCGTTGTT  T GTC CT
                                     GT T  A
GAM906  CSNK2A2 3'  TGTTGGTTACTGTTGCT    8569          AG
                                AGCAGCAGTGAC  GACA
                                ||||||||||||  ||||
                                TCGTTGTCATTG  TTGT
                                       G_
GAM906  CTPS    3'  TGGTGTCTGCCTGTTGC     88598       TGACA
                                GCAGCAG    GGACATCA
                                |||||||    ||||||||
                                CGTTGTC    TCTGTGGT
                                    CG___
GAM906  CUL4B   3'  TGATGTTCTGTTACACTG    13145    CA
                                CAG  GTGACAGGACATCA
                                |||  ||||||||||||||
                                GTC  CATTGTCTTGTAGT
                                  A_
GAM906  DAPK1   3'  TGATCAGTGTTGTTGCTCT   17050    C    TG  G_  CA
                                AG AGCAG  ACA  GA  TCA
                                || |||||  |||  ||  |||
                                TC TCGTT  TGT  CT  AGT
                                 _    GT   GA  __
GAM906  DAPK1   3'  GATGGTCATTGCAGTT      17048     A      AGGA
                                AGC GCAGTGAC    CATC
                                ||| ||||||||    ||||
                                TTG CGTTACTG    GTAG
                                  A       ____
GAM906  DBY     3'  TGATGTCCTGTTGGCT      16229     AGT
                                AGC   GACAGGACATCA
                                |||   ||||||||||||
                                TCG   TTGTCCTGTAGT
                                  G__
GAM906  DDOST   3'  TGGTGGTTTTGTTTTGCT    17821      T      _
                                AGCAG GACAGGAC ATCA
                                ||||| |||||||| ||||
```

```
                                TCGTT TTGTTTTG TGGT
                                  _       G
GAM906  DDX3    3'  TGATGTCCTGTTGGCT     7227     AGT
                                AGC   GACAGGACATCA
                                |||   ||||||||||||
                                TCG   TTGTCCTGTAGT
                                  G__
GAM906  DGKG    3'  TGGTGTCTACATGTTTGCT   7208      CA   ACA
                                AGCAG  GTG   GGACATCA
                                |||||  |||   ||||||||
                                TCGTT  TAC   TCTGTGGT
                                   TG   A__
GAM906  DLG5    3'  GGTGTTCAGCTGTGCT     82921     G    GACA
                                AGCA CAGT    GGACATC
                                |||| ||||    |||||||
                                TCGT GTCG    CTTGTGG
                                  _    A___
GAM906  DMD     3'  GTTTGGTTTTTGTTGCT     14413       T   AG
                                AGCAGCAG GAC  GAC
                                |||||||| |||  |||
                                TCGTTGTT TTG  TTG
                                     T   GT
GAM906  DMD     3'  GTTTGGTTTTTGTTGCT     14404       T   AG
                                AGCAGCAG GAC  GAC
                                |||||||| |||  |||
                                TCGTTGTT TTG  TTG
                                     T   GT
GAM906  DMD     3'  GCATGTTTTGTCATTGTT    14418           CA
                                AGCAGTGACAGGACAT
                                ||||||||||||||||
                                TTGTTACTGTTTTGTA
                                        CGG
GAM906  DMD     3'  GTTTGGTTTTTGTTGCT     14386       T   AG
                                AGCAGCAG GAC  GAC
                                |||||||| |||  |||
                                TCGTTGTT TTG  TTG
                                     T   GT
GAM906  DMD     3'  GCATGTTTTGTCATTGTT    14370           CA
                                AGCAGTGACAGGACAT
                                ||||||||||||||||
                                TTGTTACTGTTTTGTA
                                        CGG
GAM906  DMD     3'  GCATGTTTTGTCATTGTT    14402           CA
                                AGCAGTGACAGGACAT
                                ||||||||||||||||
                                TTGTTACTGTTTTGTA
                                        CGG
GAM906  DMD     3'  GCATGTTTTGTCATTGTT    14358           CA
                                AGCAGTGACAGGACAT
                                ||||||||||||||||
```

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                                TTGTTACTGTTTTGTA
                                     CGG
GAM906  DMD     3' GCATGTTTTGTCATTGTT   14384          CA
                                AGCAGTGACAGGACAT
                                ||||||||||||||||
                                TTGTTACTGTTTTGTA
                                     CGG
GAM906  DMD     3' GCATGTTTTGTCATTGTT   14364          CA
                                AGCAGTGACAGGACAT
                                ||||||||||||||||
                                TTGTTACTGTTTTGTA
                                     CGG
GAM906  DMD     3' GTTTGGTTTTTGTTGCT    14372       T  AG
                                AGCAGCAG GAC  GAC
                                |||||||| |||  |||
                                TCGTTGTT TTG  TTG
                                     T   GT
GAM906  DMD     3' GCATGTTTTGTCATTGTT   14389          CA
                                AGCAGTGACAGGACAT
                                ||||||||||||||||
                                TTGTTACTGTTTTGTA
                                     CGG
GAM906  DMD     3' GTTTGGTTTTTGTTGCT    14360       T  AG
                                AGCAGCAG GAC  GAC
                                |||||||| |||  |||
                                TCGTTGTT TTG  TTG
                                     T   GT
GAM906  DMD     3' GTTTGGTTTTTGTTGCT    14421       T  AG
                                AGCAGCAG GAC  GAC
                                |||||||| |||  |||
                                TCGTTGTT TTG  TTG
                                     T   GT
GAM906  DMD     3' GCATGTTTTGTCATTGTT   14407          CA
                                AGCAGTGACAGGACAT
                                ||||||||||||||||
                                TTGTTACTGTTTTGTA
                                     CGG
GAM906  DMD     3' GCATGTTTTGTCATTGTT   14378          CA
                                AGCAGTGACAGGACAT
                                ||||||||||||||||
                                TTGTTACTGTTTTGTA
                                     CGG
GAM906  DMD     3' GTTTGGTTTTTGTTGCT    14391       T  AG
                                AGCAGCAG GAC  GAC
                                |||||||| |||  |||
                                TCGTTGTT TTG  TTG
                                     T   GT
GAM906  DMD     3' GTTTGGTTTTTGTTGCT    14366       T  AG
                                AGCAGCAG GAC  GAC
                                |||||||| |||  |||
```

```
                                TCGTTGTT TTG  TTG
                                    T   GT
GAM906  DMD    3' GTTTGGTTTTTGTTGCT    14428       T   AG
                                AGCAGCAG GAC  GAC
                                |||||||| |||  |||
                                TCGTTGTT TTG  TTG
                                    T   GT
GAM906  DMD    3' GCATGTTTTGTCATTGTT    14425           CA
                                AGCAGTGACAGGACAT
                                ||||||||||||||||
                                TTGTTACTGTTTTGTA
                                      CGG
GAM906  DMD    3' GCATGTTTTGTCATTGTT    14411           CA
                                AGCAGTGACAGGACAT
                                ||||||||||||||||
                                TTGTTACTGTTTTGTA
                                      CGG
GAM906  DMD    3' GTTTGGTTTTTGTTGCT    14409       T   AG
                                AGCAGCAG GAC  GAC
                                |||||||| |||  |||
                                TCGTTGTT TTG  TTG
                                    T   GT
GAM906  DMD    3' GCATGTTTTGTCATTGTT    14396           CA
                                AGCAGTGACAGGACAT
                                ||||||||||||||||
                                TTGTTACTGTTTTGTA
                                      CGG
GAM906  DMD    3' GTTTGGTTTTTGTTGCT    14399       T   AG
                                AGCAGCAG GAC  GAC
                                |||||||| |||  |||
                                TCGTTGTT TTG  TTG
                                    T   GT
GAM906  DMD    3' GTTTGGTTTTTGTTGCT    14380       T   AG
                                AGCAGCAG GAC  GAC
                                |||||||| |||  |||
                                TCGTTGTT TTG  TTG
                                    T   GT
GAM906  DMD    3' GCATGTTTTGTCATTGTT    3666            CA
                                AGCAGTGACAGGACAT
                                ||||||||||||||||
                                TTGTTACTGTTTTGTA
                                      CGG
GAM906  DMD    3' GTTTGGTTTTTGTTGCT    3668        T   AG
                                AGCAGCAG GAC  GAC
                                |||||||| |||  |||
                                TCGTTGTT TTG  TTG
                                    T   GT
GAM906  DPP6   5' GCTTGCCTGCTGCTGCTGCT  55450       GA   A  TCA
                                AGCAGCAGT  CAGG CA
                                |||||||||  |||| ||
```

```
                                TCGTCGTCG  GTCC GT
                                    TC   _ TCGG
GAM906  DPYSL2   3'  GGGTTTTTTGTTGTTGTTGTT  7301        TG     C   A
                                AGCAGCAG  ACAGGA ATC
                                ||||||||  |||||| |||
                                TTGTTGTT  TGTTTT TGG
                                    GT     T   GT
GAM906  DTR      3'  TTTTGTTGTTGTTGTT      8694         TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT
GAM906  DTR      3'  TTTTGTTGTTGTTGTT      8693         TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT
GAM906  DUSP4    3'  TGGTGTCTTGTAGATATGT   7338      GCAGTG
                                GCA     ACAGGACATCA
                                |||     ||||||||||
                                TGT     TGTTCTGTGGT
                                  ATAGA_
GAM906  DUSP4    3'  TGGTGTCTTGTAGATATGT   54058     GCAGTG
                                GCA     ACAGGACATCA
                                |||     ||||||||||
                                TGT     TGTTCTGTGGT
                                  ATAGA_
GAM906  DUSP4    3'  TGTCCCTTTGTTGTCGTTGTT  54059       A TG  ___    TCA
                                AGCAGC G  ACA   GGACA
                                ||||||  |  |||   |||||
                                TTGTTG T  TGT   CCTGT
                                   C GT   TTC
GAM906  DUSP4    3'  TGTCCCTTTGTTGTCGTTGTT  7339        A TG  ___    TCA
                                AGCAGC G  ACA   GGACA
                                ||||||  |  |||   |||||
                                TTGTTG T  TGT   CCTGT
                                   C GT   TTC
GAM906  DUSP5    3'  TGTCTGTCTCTGTTGCT     15357        T    G
                                AGCAGCAG GACAG ACA
                                |||||||| ||||| |||
                                TCGTTGTC CTGTC TGT
                                    T    _
GAM906  DUSP5    3'  TGTTACTGGTTGTTGTTGTT  15358        TG  AG__   TCA
                                AGCAGCAG  AC    GACA
                                ||||||||  ||    ||||
                                TTGTTGTT  TG    TTGT
                                    GT  GTCA
GAM906  DUT      3'  GGTGTTTTGCACTTCT      8697     C    A
                                AG AGTG CAGGACATC
                                || |||| |||||||||
```

```
                                TC TCAC GTTTTGTGG
                                 T   _
GAM906  DVL3     3'  TGATGTCCTCAATTGCTGCT   15377        GAC
                                AGCAGCAGT   AGGACATCA
                                |||||||||   |||||||||
                                TCGTCGTTA   TCCTGTAGT
                                     AC_
GAM906  DXF68S1E 3'  TGATGTCCTTGAGCTACT    60009    C   GAC
                                AG AGT   AGGACATCA
                                || |||   |||||||||
                                TC TCG   TCCTGTAGT
                                 A   AGT
GAM906  EBF      3'  TGATGTTTTTAAAGCTGT    66048      AG   CA
                                GCAGC  TGA  GGACATCA
                                |||||  |||  ||||||||
                                TGTCG  ATT  TTTGTAGT
                                   AA   __
GAM906  EDAR     3'  TGTCTGTTTGCTGCTGTT    42269        TG CA
                                AGCAGCAG  A  GGACA
                                ||||||||  |  |||||
                                TTGTCGTC  T  TCTGT
                                     GT TG
GAM906  EGF      3'  TTTTGTTTTTGTTGTT      8736         T
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
                                TTGTTGTT TTGTTTT
                                     T
GAM906  EIF4A2   3'  GGATGCAGTGCTCGCTGTTGCT 8756          _ GGA   A
                                AGCAGCAGTGA CA   CATC
                                |||||||||||| ||   ||||
                                TCGTTGTCGCT GT   GTAG
                                      C  GAC   GT
GAM906  EIF4EBP2 3'  TGGTGTCCTGGGAATTTCT   14591    C   GA_
                                AG AGT   CAGGACATCA
                                || |||   ||||||||||
                                TC TTA   GTCCTGTGGT
                                 T   AGG
GAM906  EIF4EL3  3'  GAGTCTGTTGTTCTGTT     16751      C  TG   G  A  A
                                AGCAG AG  ACAG AC TC
                                |||||  ||  |||| || ||
                                TTGTC TT  TGTC TG AG
                                   _  GT   _ _  G
GAM906  ELL      3'  ATCCCATTTGTTGCTGCTGCT  21522        TG  ____   CATCA
                                AGCAGCAG  ACA   GGA
                                ||||||||  |||   |||
                                TCGTCGTC  TGT   CCT
                                     GT   TTAC     AC
GAM906  ELMO2    3'  TGGTGCCAAGACGTTGCTGCT  55676         ACA_  A
                                AGCAGCAGTG   GG CATCA
                                ||||||||||   || |||||
```

```
                                TCGTCGTTGC   CC GTGGT
                                     AGAA  _
GAM906  EMD     3'  TGGTCCTCTTTGTCATTTTGTT 3686      C     ____   ATCA
                                AGCAG AGTGACA   GGAC
                                ||||| |||||||   ||||
                                TTGTT TTACTGT   CCTG
                                  _     TTCT   GT
GAM906  EPHB2   3'  TGGCTCCTGTCCCTGCTGCT  15451       T     CATCA
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
                                TCGTCGTC CTGTCCT
                                     C      CGGT
GAM906  EPHB2   3'  TGGCTCCTGTCCCTGCTGCT  33890       T     CATCA
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
                                TCGTCGTC CTGTCCT
                                     C      CGGT
GAM906  ESRRA   3'  TGATGCTTTTGCTGCTGCT   15483       TG C   A
                                AGCAGCAG  A AGG CATCA
                                ||||||||  | ||| |||||
                                TCGTCGTC  T TTC GTAGT
                                     GT _  _
GAM906  ETV6    3'  TGGTGTTTTTGTTTTTGTT   8800      T     _
                                AGCAG GACAGGA CATCA
                                ||||| ||||||| |||||
                                TTGTT TTGTTTT GTGGT
                                   T      T
GAM906  EYA1    3'  TGAAGTTGTGTGTTGCTGCT  4957       GT A  G   A
                                AGCAGCA  G CA GAC TCA
                                |||||||  | || ||| |||
                                TCGTCGT  T GT TTG AGT
                                     TG _  G   A
GAM906  FASN    3'  TGGTGTTTGTCTGTGTTTGTT  14636     _ GT    G
                                AGCAG CA  GACAG ACATCA
                                ||||| ||  ||||| ||||||
                                TTGTT GT  CTGTT TGTGGT
                                   T  GT    _
GAM906  FBN2    3'  TGATGTTTAGTTTGCT     8849      GT   AG
                                AGCA  GAC  GACATCA
                                ||||  |||  |||||||
                                TCGT  TTG  TTGTAGT
                                  __   AT
GAM906  FBXL7   3'  TCATTGTTTGTTGTTGTTGTT  24554       TG   G   TCA
                                AGCAGCAG  ACAG ACA
                                ||||||||  |||| |||
                                TTGTTGTT  TGTT TGT
                                     GT   _  TACTC
GAM906  FBXL7   3'  TGTTTGTTGTTGTTGTT    24557       TG   G
                                AGCAGCAG  ACAG ACA
                                ||||||||  |||| |||
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```
                                TTGTTGTT  TGTT TGT
                                    GT   _
GAM906  FBXW1B   3'  TGGTGTCAGCTGCTGCT    53333        GACAG
                                AGCAGCAGT    GACATCA
                                |||||||||    |||||||
                                TCGTCGTCG    CTGTGGT
                                    A____
GAM906  FBXW1B   3'  TGGTGTCAGCTGCTGCT    53344        GACAG
                                AGCAGCAGT    GACATCA
                                |||||||||    |||||||
                                TCGTCGTCG    CTGTGGT
                                    A____
GAM906  FBXW1B   3'  TGGTGTCAGCTGCTGCT    24529        GACAG
                                AGCAGCAGT    GACATCA
                                |||||||||    |||||||
                                TCGTCGTCG    CTGTGGT
                                    A____
GAM906  FGF13    3'  GTCAAGTTATTGTGCT     53320     G     AG
                                AGCA CAGTGAC  GAC
                                ||||  |||||||  |||
                                TCGT GTTATTG  CTG
                                  _      AA
GAM906  FGF2     3'  TGATGTTCTGTCATTGT     8875
                                GCAGTGACAGGACATCA
                                |||||||||||||||||
                                TGTTACTGTCTTGTAGT

GAM906  FKBP1A   3'  TGGTGAGAAATCGTTGCTGC  5859          CAGGA
                                GCAGCAGTGA    CATCA
                                ||||||||||    |||||
                                CGTCGTTGCT    GTGGT
                                    AAAGA
GAM906  FLRT2    3'  TGATGATTTGTTATTGTT    25068          A
                                AGCAGTGACAGG CATCA
                                ||||||||||| |||||
                                TTGTTATTGTTT GTAGT
                                      A
GAM906  FMO2     3'  TGGGCCTTCTTGCTGTTGTT  7587         TG C_  A_  TCA
                                AGCAGCAG  A  AGG  CA
                                ||||||||  |  |||  ||
                                TTGTTGTC  T  TCC  GT
                                    GT CT   GG
GAM906  FPGS     3'  TGGTGTCCTGAAGCTGCTG   17091        GA
                                CAGCAGT  CAGGACATCA
                                |||||||  ||||||||||
                                GTCGTCG  GTCCTGTGGT
                                    AA
GAM906  FRDA     3'  TGAGGTGTGTTTTTTGTTGTTG 3781        TG   ____    A
            TTGTT                GCAGCAG  ACAGG   ACATC
                                |||||||  |||||   |||||
```

```
                                TGTTGTT  TGTTT   TGTGG
                                   GT    TTTG    AGT
GAM906  FRDA    3'  TGTTTTTTGTTGTTGTTGTT  3782        TG    CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                   GT     TTGT
GAM906  FST     3'  AGCTGCTTCTGCGCTGTTGTT  20955         A   _  TCA
                                AGCAGCAGTG CAGGA CA
                                |||||||||| ||||| ||
                                TTGTTGTCGC GTCTT GT
                                      _    C  CGAG
GAM906  FUT5    3'  GTTTTATTGCTGTTGTT    8967         TG C
                                AGCAGCAG  A AGGAC
                                ||||||||  | |||||
                                TTGTTGTC  T TTTTG
                                   GT A
GAM906  FZD4    3'  TGGTGCGCTGTCTGCTGTT   24155       GT    GA
                                AGCAGCA  GACAG  CATCA
                                |||||||  |||||  |||||
                                TTGTCGT  CTGTC  GTGGT
                                   __    GC
GAM906  FZD4    3'  TGGTGTCTTGGGAGTTGT    24156      AGTGA
                                GCAGC    CAGGACATCA
                                |||||    ||||||||||
                                TGTTG    GTTCTGTGGT
                                  AGG__
GAM906  GABRP   3'  TGTCATTCTGTCATTGCTGCT  26403           ___   TCA
                                AGCAGCAGTGACAG   GACA
                                ||||||||||||||   ||||
                                TCGTCGTTACTGTC   CTGT
                                      TTA      A
GAM906  GAD1    3'  TGGTGTTCTCAATGCT     5876      G   CA
                                AGCA TGA  GGACATCA
                                |||| |||  ||||||||
                                TCGT ACT  CTTGTGGT
                                  A  __
GAM906  GAS1    3'  GTTTTTTTGTCATTTTTGTT  8994       C        CATCA
                                AGCAG AGTGACAGGA
                                ||||| ||||||||||
                                TTGTT TTACTGTTTT
                                   T         TTTGT
GAM906  GDF8    3'  TGGTTTACTGTCATTGTGTT  17927     G       GAC
                                AGCA CAGTGACAG   ATCA
                                |||| |||||||||   ||||
                                TTGT GTTACTGTC   TGGT
                                  _       ATT
GAM906  GDI2    3'  TGTGCTGCTGCTGCT      7656         TGA   G
                                AGCAGCAG   CAG ACA
                                ||||||||   ||| |||
```

```
                                TCGTCGTC  GTC TGT
                                   ___  G
GAM906  GHR     3'  TTTTGTTGTTGTTGTT     3894        TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                   GT
GAM906  GHR     3'  TTTGTTGTTGTTGTTGTTGTT  3893        TG  _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                   GT   G   TT
GAM906  GHR     3'  TCATTTTTGTTGTTGTTGTT  3888        TG    CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                   GT    TACT
GAM906  GNB1    3'  TGTCCACTTCTCGTTGCTGCT  9072          CA___    TCA
                                AGCAGCAGTGA    GGACA
                                ||||||||||    |||||
                                TCGTCGTTGCT    CCTGT
                                   CTTCA
GAM906  GNB1    3'  TGATGTCACAGATCATTGTTGC 9071          CAG__
                                GCAGCAGTGA    GACATCA
                                ||||||||||    |||||||
                                CGTTGTTACT    CTGTAGT
                                   AGACA
GAM906  GNE     3'  TTTTGTTACTGTTCT      18486    C
                                AG AGCAGTGACAGGA
                                || ||||||||||||
                                TC TTGTCATTGTTTT
                                 _
GAM906  GNRH1   5'  TGATGTCCTGTCCTTCACTGT  5885      C__  T
                                GCAG   AG GACAGGACATCA
                                ||||   || ||||||||||||
                                TGTC   TC CTGTCCTGTAGT
                                  ACT  _
GAM906  GPR23   3'  GAGTTTTTATTGCTGTT     60543         CA   A  A
                                AGCAGCAGTGA  GGAC TC
                                ||||||||||  |||| ||
                                TTGTCGTTATT  TTTG AG
                                   __   _ A
GAM906  GPR63   5'  TGGGACCTGATACTGCTGTT  47891         A   ACA
                                AGCAGCAGTG CAGG   TCA
                                ||||||||| ||||   |||
                                TTGTCGTCAT GTCC   GGT
                                   A   AG_
GAM906  GRAF    3'  TGAGTCAGTTGCTGTGCT    30579     G   TG  AG   A
                                AGCA CAG  AC  GAC TCA
                                |||| |||  ||  ||| |||
```

```
                                TCGT GTC  TG  CTG AGT
                                  _  GT  A_  _
GAM906  GRB10    3'  TGATGTTCTGTTTCTTGT    17987     T_
                                GCAG  GACAGGACATCA
                                ||||  ||||||||||||
                                TGTT  TTGTCTTGTAGT
                                  CT
GAM906  GRIN2A   3'  GGAGGTATTTTGTTGTTGTTGT 5897        TG    C   A
           T                     AGCAGCAG  ACAGGA ATC
                                ||||||||  |||||| |||
                                TTGTTGTT  TGTTTT TGG
                                    GT     A   AGGG
GAM906  GRIN2A   3'  TTTTGTTGTTGTTGTT     5901         TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT
GAM906  GYG      3'  TGAGAAAAGTCTGTTACAGTTG 14692       A      ACA___
           CT                    AGCAGC GTGACAGG     TCA
                                ||||||| ||||||||     |||
                                TCGTTG CATTGTCT     AGT
                                   A       GAAAAG
GAM906  H3F3B    3'  TGATGTGAGCACTGTTGCT    18025         ACAGG
                                AGCAGCAGTG    ACATCA
                                ||||||||||    ||||||
                                TCGTTGTCAC    TGTAGT
                                    GAG__
GAM906  HADHSC   3'  TGCACCATGCTCACTGTTGCT  18033          _ _  ACATCA
                                AGCAGCAGTGA CA GG
                                |||||||||||  || ||
                                TCGTTGTCACT GT CC
                                     C  A  ACGT
GAM906  HCFC1    3'  ATGTCCCTTTTTTGTTGTTGTT 70989      TG  _______    TCA
           AGCT                   AGCAG  ACA     GGACA
                                |||||  |||     |||||
                                TTGTT  TGT     CCTGT
                                  GT   TTTTTC       AC
GAM906  HD       3'  TGGTGTCTTGGCACTGTT    9194         A
                                AGCAGTG CAGGACATCA
                                |||||||  ||||||||||
                                TTGTCAC GTTCTGTGGT
                                   G
GAM906  HGF      3'  GGGTGTTTTCTGTTGTTTTGTT 94235      C  TG   __     A
                                AGCAG AG  ACAG  GACATC
                                |||||  ||  ||||  ||||||
                                TTGTT TT  TGTC  TTGTGG
                                  _  GT    TT     GT
GAM906  HLF      3'  ATGTGTTCGGTTTTGTTGTT   9217         T   A     CA
                                AGCAGCAG GAC GGACAT
                                |||||||| ||| ||||||
```

```
                                TTGTTGTT TTG CTTGTG
                                    _  G     TAG
GAM906  HMGA2   3'  GGACTGTTCTTTGCTGTTGTT  13001       TG C    _ A
                                AGCAGCAG  A AGGACA TC
                                |||||||| | |||||| ||
                                TTGTTGTC  T TCTTGT AG
                                    GT _    C  GA
GAM906  HNF3B   3'  TGATTTTTTTGTTGTTGTTGTT 41414       TG    C_
                                AGCAGCAG  ACAGGA  ATCA
                                ||||||||  ||||||  ||||
                                TTGTTGTT  TGTTTT  TAGT
                                    GT     TT
GAM906  HNRPDL  3'  TGGCCTCTTTTTTGCTGCTGTT 18430       TG C_   CA
                                AGCAGCAG  A  AGGA  TCA
                                ||||||||  |  ||||  |||
                                TTGTCGTC  T  TTCT  GGT
                                    GT TT   CC
GAM906  HOXB5   3'  TGGTTATCTTGTTATTATTGTT 9266      C       C_
                                AGCAG AGTGACAGGA  ATCA
                                ||||| ||||||||||  ||||
                                TTGTT TTATTGTTCT  TGGT
                                   A        AT
GAM906  HPS1    3'  TGATGTCTTTCAAAGCTTCT  3970    C  AG  C
                                AG AGC  TGA AGGACATCA
                                || |||  ||| |||||||||
                                TC TCG  ACT TTCTGTAGT
                                 T  AA  _
GAM906  HRH1    3'  TGATGTTTTGTATTTTGTGTT  5988     G  TG_
                                AGCA CAG   ACAGGACATCA
                                |||| |||   ||||||||||
                                TTGT GTT   TGTTTTGTAGT
                                  _  TTA
GAM906  HUNK    3'  ATAGATTTTTGTTGTTGTTGTT 27441       TG    C  A
                                AGCAGCAG  ACAGGA ATC
                                ||||||||  |||||| |||
                                TTGTTGTT  TGTTTT TAG
                                    GT    _  ATAG
GAM906  ICOS    3'  TGGTGTTCTGTTTTCAGCT   23907    AGT_
                                AGC   GACAGGACATCA
                                |||   ||||||||||||
                                TCG   TTGTCTTGTGGT
                                  ACTT
GAM906  IDH3B   3'  TGAGGCTGTCATTGCTGC    22580          GACA
                                GCAGCAGTGACAG   TCA
                                ||||||||||||   |||
                                CGTCGTTACTGTC   AGT
                                       GG__
GAM906  IL13RA1 3'  TGTTCTACTTTGTTCTGCTGTT 7781       T  _____   TCA
                                GCAGCAG GACA    GGACA
                                ||||||| ||||    |||||
```

```
                                TGTCGTC TTGT    CTTGT
                                   _   TTCAT      A
GAM906  IL1R1   3'  TGGTGTTCTGAGTACT     6065      A_
                                AGTG  CAGGACATCA
                                ||||  ||||||||||
                                TCAT  GTCTTGTGGT
                                  GA
GAM906  IMMP2L  3'  TGATGTATTTGTCACTTGCTGT 50731       _      _
          T                      AGCAGCA GTGACAGG ACATCA
                                 ||||||| |||||||| ||||||
                                 TTGTCGT CACTGTTT TGTAGT
                                    T       A
GAM906  IMPA2   3'  TGGTGTTTAGCTGTTTCT    95242    C     GACAG
                                AG AGCAGT    GACATCA
                                || ||||||    |||||||
                                TC TTGTCG    TTGTGGT
                                 T     AT___
GAM906  INPP5A  3'  TGTCTTTTGTTACTGTT     18659          __
                                AGCAGTGACA  GGACA
                                ||||||||||  |||||
                                TTGTCATTGT  TCTGT
                                      TT
GAM906  ISLR    3'  GGTGCTCATTGCTGCT      18670          CAG A
                                AGCAGCAGTGA   G CATC
                                ||||||||||   | ||||
                                TCGTCGTTACT   C GTGG
                                      ___ _
GAM906  ITGA6   3'  TGTAGTGCCACTGTTGTT    3988          A  GG
                                AGCAGCAGTG CA  ACA
                                |||||||||| ||  |||
                                TTGTTGTCAC GT  TGT
                                      C  GA
GAM906  ITGAV   3'  TGTTGTTGTTGTTGTTGTTGTT 9400         TG   _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                     GT   G   T
GAM906  ITGAV   3'  TGTTGTTGTTGTTGTTGTTGTT 9401         TG   _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                     GT   G   T
GAM906  ITGAV   3'  TGTTGTTGTTGTTGTTGTTGTT 9399         TG   _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                     GT   G   T
GAM906  ITGAV   3'  TTTGTTGTTGTTGTTGTTGTT  9402         TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
```

```
                                TTGTTGTT  TGTT TTGT
                                    GT   G   TT
GAM906  KCNJ3   3'  TGATGTTTTGTTCAAAGTTGT  9528      AG  _
                                GCAGC  TGA CAGGACATCA
                                |||||  ||| ||||||||||
                                TGTTG  ACT GTTTTGTAGT
                                   AA   T
GAM906  KCNN2   5'  GTCCTGCTGCTGCTGCT    41219       GA
                                AGCAGCAGT  CAGGAC
                                |||||||||  ||||||
                                TCGTCGTCG  GTCCTG
                                     TC
GAM906  KERA    3'  TCTTGTAGCTGTTGTT     22872       G
                                AGCAGCAGT ACAGGA
                                ||||||||| ||||||
                                TTGTTGTCG TGTTCT
                                     A
GAM906  KIN     3'  TGTCCTTGTTATTTTTGTT   24596     C    _
                                AGCAG AGTGACA GGACA
                                ||||| ||||||| |||||
                                TTGTT TTATTGT CCTGT
                                   T     T
GAM906  KNSL1   3'  ATGATGAAACTTTTTGTTGTTG 15746     TG    _____
          CTTGTT                 AGCAG  ACAGGA   CATCA  T
                                |||||  ||||||   |||||  |
                                TCGTT  TGTTTT   GTAGT  A
                                   GT    TCAAA
GAM906  LAMP1   3'  TGATGTTTTGCCGTGGCT   18708    AG  A
                                AGC  TG CAGGACATCA
                                |||  || ||||||||||
                                TCG  GC GTTTTGTAGT
                                  GT  C
GAM906  LAMP2   3'  TGGTGTTCTGTTTTCAATGT  9686    GCAGT
                                GCA    GACAGGACATCA
                                |||    ||||||||||||
                                TGT    TTGTCTTGTGGT
                                  AACTT
GAM906  LAMP2   5'  TGGTGTTGCAGCTGTTGTT  25720       GACAG
                                AGCAGCAGT    GACATCA
                                |||||||||    |||||||
                                TTGTTGTCG    TTGTGGT
                                     ACG__
GAM906  LAMP2   5'  TGGTGTTGCAGCTGTTGTT  9687        GACAG
                                AGCAGCAGT    GACATCA
                                |||||||||    |||||||
                                TTGTTGTCG    TTGTGGT
                                     ACG__
GAM906  LBR     3'  TGAAATTGTCATTGTT     59354         GACA
                                AGCAGTGACAG    TCA
                                ||||||||||    |||
```

```
                                TTGTTACTGTT   AGT
                                      AA__
GAM906  LFG     3'  TCCTGTCAGCTGCTGTT    76728       _
                                AGCAGCAG TGACAGGA
                                |||||||| ||||||||
                                TTGTCGTC ACTGTCCT
                                    G
GAM906  LIFR    3'  TTCTGTTCTGTTGTT      9750        T
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
                                TTGTTGTC TTGTCTT
                                      _
GAM906  LILRB4  3'  TGGTTTCTTGCTGTTGCT   22437       TGA   C
                                AGCAGCAG   CAGGA ATCA
                                ||||||||   ||||| ||||
                                TCGTTGTC   GTTCT TGGT
                                     ___    T
GAM906  LILRB4  3'  TGATGTCTTCCTGGCTGT   22435     _ T  CA
                                GCAGC AG GA  GGACATCA
                                ||||| || ||  ||||||||
                                TGTCG TC CT  TCTGTAGT
                                  G  _ __
GAM906  LIMD1   3'  TGATGGAATTCATTCTGTT   26467     C    CAGGA
                                AGCAG AGTGA    CATCA
                                ||||| |||||    |||||
                                TTGTC TTACT    GTAGT
                                  _    TAAG_
GAM906  LIPE    3'  TGCCTTTTGCTGCTGCT    18088       TG C   A  TCA
                                AGCAGCAG  A AGG CA
                                ||||||||  | ||| ||
                                TCGTCGTC  T TCC GT
                                    GT T  _
GAM906  LOXL1   3'  TGTTGTTTTGTTGTTGTTG   60191      TG      T
                                CAGCAG  ACAGGACA CA
                                ||||||  |||||||| ||
                                GTTGTT  TGTTTTGT GT
                                   GT      T
GAM906  LPL     3'  TGATGTATGATTTGTTGTT   4092        TGA  GG
                                AGCAGCAG   CA  ACATCA
                                ||||||||   ||  ||||||
                                TTGTTGTT   GT  TGTAGT
                                    TA_  A_
GAM906  LPL     3'  TGAGGGTTGTTATTTGTTGTT  4091        _    GACA
                                AGCAGCAG TGACAG    TCA
                                |||||||| ||||||    |||
                                TTGTTGTT ATTGTT    AGT
                                    T     GGG_
GAM906  LZTFL1  3'  TGGTTTGTCATTTTTGTTGTTG 39758       TG   ____   TCA
            TTGTT                GCAGCAG  ACAG   GACA
                                |||||||  ||||   ||||
```

```
                                TGTTGTT  TGTT   CTGT
                                   GT   TTTA   TTGGT
GAM906  LZTFL1   3'  TGTTGTTGTTGTTGTTGTTGTT 39759       TG   _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                   GT   G   T
GAM906  LZTFL1   3'  TTTGTTGTTGTTGTTGTTGTT  39762       TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                   GT   G   TT
GAM906  LZTFL1   3'  ATGTCATTTTTGTTGTTGTTGT 39752       TG   ____   TCA
           T                    GCAGCAG  ACAG   GACA
                                |||||||  ||||   ||||
                                TGTTGTT  TGTT   CTGT
                                   GT   TTTA     AC
GAM906  MAB21L1  3'  TGGTGTTTTGTGATTTGGT   18762    AGC   G
                                GC   AGT ACAGGACATCA
                                ||   ||| ||||||||||||
                                TG   TTA TGTTTTGTGGT
                                 GT_   G
GAM906  MADH9    3'  TGATGTCACTTTTAGTGCTGTT 19752       G   C   _
                                AGCAGCA TGA AG GACATCA
                                ||||||| ||| || |||||||
                                TTGTCGT ATT TC CTGTAGT
                                   G   T  A
GAM906  MAN2A2   3'  TTCTGTTTATTGCTGCT     20402          _
                                AGCAGCAGTGA CAGGA
                                |||||||||||| |||||
                                TCGTCGTTATT GTCTT
                                      T
GAM906  MAN2A2   3'  TGTTTATTGCTGCTGCT     20401        TG CA
                                AGCAGCAG  A  GGACA
                                ||||||||  |  |||||
                                TCGTCGTC  T  TTTGT
                                   GT A_
GAM906  MAP3K7IP2 3'  TGGTGTTCTGCTAATGTT    30664      G  A
                                AGCA TG CAGGACATCA
                                |||| || ||||||||||
                                TTGT AT GTCTTGTGGT
                                  A  C
GAM906  MAP7     3'  TGAAGTCTGTATGTTGCTGCT  14288        TG_   G  A
                                AGCAGCAG   ACAG AC TCA
                                ||||||||   |||| || |||
                                TCGTCGTT   TGTC TG AGT
                                   GTA   _  A
GAM906  MAPT     3'  TGATGTCTTGAGAGCGCT    19781     A  GA_
                                AGC GT   CAGGACATCA
                                ||| ||   ||||||||||
```

```
                              TCG CG   GTTCTGTAGT
                                _ AGA
GAM906  MAPT    3' TGATGTCTTGAGAGCGCT    33692     A  GA_
                              AGC GT   CAGGACATCA
                              ||| ||   ||||||||||
                              TCG CG   GTTCTGTAGT
                                _ AGA
GAM906  MAPT    3' TGATGTCTTGAGAGCGCT    33711     A  GA_
                              AGC GT   CAGGACATCA
                              ||| ||   ||||||||||
                              TCG CG   GTTCTGTAGT
                                _ AGA
GAM906  MAPT    3' TGATGTCTTGAGAGCGCT    33701     A  GA_
                              AGC GT   CAGGACATCA
                              ||| ||   ||||||||||
                              TCG CG   GTTCTGTAGT
                                _ AGA
GAM906  MDM1    3' GATGATCATTGTTGC       39272          CAGGA
                              GCAGCAGTGA    CATC
                              ||||||||||    ||||
                              CGTTGTTACT    GTAG
                                    A____
GAM906  MEN1    5' TGTCCTTGCACTGCTGTT    93385          AC
                              AGCAGCAGTG  AGGACA
                              ||||||||||  ||||||
                              TTGTCGTCAC  TCCTGT
                                    GT
GAM906  MLLT2   5' TGGCCCGCGTTGTGCTGTTGCT 19855         __  A_  A_  TCA
                              AGCAGCAGT  GAC  GG  CA
                              |||||||||  |||  ||  ||
                              TCGTTGTCG  TTG  CC  GT
                                   TG   CG  CG    A
GAM906  MLLT3   3' TGATTTTTTGTTCTTGTTGTT  15759        T      C
                              AGCAGCAG GACAGGA ATCA
                              |||||||| ||||||| ||||
                              TTGTTGTT TTGTTTT TAGT
                                   C      T
GAM906  MMP16    3' TGATGCACAGTATCTGCTGTT  19878        TG  AGGA
                              AGCAGCAG  AC    CATCA
                              ||||||||  ||    |||||
                              TTGTCGTC  TG    GTAGT
                                   TA  ACAC
GAM906  MNT     3' TGTGCTGCTGCTGCT       39719         TGA   G
                              AGCAGCAG   CAG ACA
                              ||||||||   ||| |||
                              TCGTCGTC   GTC TGT
                                   ___   G
GAM906  MS4A1   3' TTTTGTTTCTGCTGCT      3752          T
                              AGCAGCAG GACAGGA
                              |||||||| |||||||
```

```
                                TCGTCGTC TTGTTTT
                                     T
GAM906  MTF1    3'  TGTATGTCACTTTTGCT    19886      C      GG
                                AGCAG AGTGACA  ACA
                                ||||| |||||||  |||
                                TCGTT TCACTGT  TGT
                                   T      A_
GAM906  MTMR8   3'  TTTGTTGTTGTTGTTGTTGTT  31302        TG   _    TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                     GT   G   TT
GAM906  MTMR8   3'  TGTTGTTGTTGTTGTTGTTGTT 31300        TG   _    T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                     GT   G   T
GAM906  MTMR8   3'  ATGATAAAGTTTTGTTGTTGTT 31288        TG     ___
            GTT                   GCAGCAG  ACAGGAC   ATCA   T
                                |||||||  |||||||   ||||  |
                                TGTTGTT  TGTTTTG   TAGT   A
                                   GT      AAA
GAM906  MX2     3'  TGGTTCACTGTCATTGTGTT   10151      G       _ C
                                AGCA CAGTGACAG GA ATCA
                                |||| |||||||| || ||||
                                TTGT GTTACTGTC CT TGGT
                                  _       A _
GAM906  MYBL1   3'  TGGTTTTTTGTTGTTGTTGTT  64076        TG     C
                                AGCAGCAG  ACAGGA ATCA
                                ||||||||  |||||| ||||
                                TTGTTGTT  TGTTTT TGGT
                                     GT     T
GAM906  MYOM2   3'  TGGTGTCCTGTGTGGGCTG   14271      AGTG
                                CAGC   ACAGGACATCA
                                ||||   ||||||||||
                                GTCG   TGTCCTGTGGT
                                  GGTG
GAM906  NAGA    3'  TGATGTCTTGAGGCTGTTG   4238        GA
                                CAGCAGT  CAGGACATCA
                                |||||||  ||||||||||
                                GTTGTCG  GTTCTGTAGT
                                     GA
GAM906  NBEA    3'  TGAATTCCTTCTTCACTGTTGT 94913          C__   CA
            T                    AGCAGCAGTGA   AGGA  TCA
                                ||||||||||   ||||  |||
                                TTGTTGTCACT   TCCT  AGT
                                      TCT   TA
GAM906  NCALD   3'  TGTTCATTGTCATTGCTGT   49381          __    TCA
                                GCAGCAGTGACA  GGACA
                                ||||||||||  |||||
```

```
                                TGTCGTTACTGT  CTTGT
                                      TA
GAM906  NCAM2   3'  TTTGTTATTGTTGTTGTTGTT  15808       TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                    GT   A   TT
GAM906  NCAM2   3'  TCCCTTTTGTTATTGTTGTT   15803           CATCA
                                AGCAGCAGTGACAGGA
                                ||||||||||||||||
                                TTGTTGTTATTGTTTT
                                        CCCT
GAM906  NCAM2   3'  TGTTGTTGTTGTTGCTGTTGTT 15804       TG   _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTC  TGTT TTGT GT
                                    GT   G   T
GAM906  NCAM2   3'  TTATTGTTGTTGTTGTTGCTGT 15805       TG   _   TCA
          T                      AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTCGTT  TGTT TTGT
                                    GT   G   TATTG
GAM906  NDP     3'  TGGTCTAAGGTTGCCATTGCTG 4246        A _____   ATCA
          CT                     CAGCAGTG CA    GGAC
                                ||||||||  ||    ||||
                                GTCGTTAC GT    TCTG
                                    C  TGGAA   GT   A
GAM906  NEO1    3'  TGGTGTTCTCCACAAGTGGTT  10206    A  A_   AC
                                AGC GC  GTG  AGGACATCA
                                |||  ||  |||  |||||||||
                                TTG TG  CAC  TCTTGTGGT
                                  G  AA   C_
GAM906  NESH    3'  TGATGTCCTGTGACTGC     33148      G
                                GCAGT ACAGGACATCA
                                |||||  ||||||||||
                                CGTCA TGTCCTGTAGT
                                   G
GAM906  NLGN1   3'  TGGTGGCTGTGCTGCTG     30027       G   GA
                                CAGCAGT ACAG  CATCA
                                |||||||  ||||  |||||
                                GTCGTCG TGTC  GTGGT
                                    _   G_
GAM906  NLGN3   3'  GGTGTTTTTTGTTGTTGTT   38602       TG C      A
                                AGCAGCAG  A AGGACATC
                                ||||||||  |  ||||||||
                                TTGTTGTT  T TTTTGTGG
                                    GT _      C
GAM906  NOL3    3'  TCATTGTCATTACTGTT     14158      C      _
                                AGCAG AGTGACAG GA
                                |||||  ||||||||  ||
```

```
                                TTGTC TTACTGTT CT
                                   A       A
GAM906  NONO    3'  TGTCTATGATGTTGCTGTT   82026       GT A  _
                                AGCAGCA  G CA GGACA
                                |||||||  | || |||||
                                TTGTCGT  T GT TCTGT
                                    TG A  A
GAM906  NR5A2   3'  TTCTGCTACTGTTGCT     13793         A
                                AGCAGCAGTG CAGGA
                                |||||||||| |||||
                                TCGTTGTCAT GTCTT
                                      C
GAM906  NRAS    3'  GTTATTATTGCTGTT      10275         CAG
                                AGCAGCAGTGA   GAC
                                ||||||||||   |||
                                TTGTCGTTATT   TTG
                                      A__
GAM906  NRG1    3'  TGGTGCTGCTTTCTTGTTGCT  25651       T  CA__  A
                                AGCAGCAG GA    GG CATCA
                                |||||||| ||    || |||||
                                TCGTTGTT CT    TC GTGGT
                                    _  TTCG  _
GAM906  NRG1    3'  TGGTGCTGCTTTCTTGTTGCT  25657       T  CA__  A
                                AGCAGCAG GA    GG CATCA
                                |||||||| ||    || |||||
                                TCGTTGTT CT    TC GTGGT
                                    _  TTCG  _
GAM906  NRG1    3'  TGGTGCTGCTTTCTTGTTGCT  25649       T  CA__  A
                                AGCAGCAG GA    GG CATCA
                                |||||||| ||    || |||||
                                TCGTTGTT CT    TC GTGGT
                                    _  TTCG  _
GAM906  NT5C3   3'  TGGTGTTTACAATGTTGCT   33238       G  ACA
                                AGCAGCA TG   GGACATCA
                                ||||||| ||   ||||||||
                                TCGTTGT AC   TTTGTGGT
                                    A  A__
GAM906  NTSR1   3'  TGATGTCTTGATGCTCCT    10299    C   GTGA
                                AG AGCA    CAGGACATCA
                                || ||||    ||||||||||
                                TC TCGT    GTTCTGTAGT
                                 C    A___
GAM906  NXF3    3'  TGGTGTCTTGTTATGTCA    41903   A   G
                                C GCA TGACAGGACATCA
                                | ||| ||||||||||||
                                A TGT ATTGTTCTGTGGT
                                 C  _
GAM906  ODC1    5'  TGAGATTGTCACTGCTGTT   10322           GACA
                                AGCAGCAGTGACAG    TCA
                                ||||||||||||||   |||
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```
                                TTGTCGTCACTGTT   AGT
                                      AG__
GAM906  OSR1    5'  TTCTGTCGCTGCTGCT     17571
                    AGCAGCAGTGACAGGA
                    ||||||||||||||||
                    TCGTCGTCGCTGTCTT

GAM906  OSR1    5'  TTCTGTCGCTGCTGCT     17570
                    AGCAGCAGTGACAGGA
                    ||||||||||||||||
                    TCGTCGTCGCTGTCTT

GAM906  OTX1    3'  GTCCCGATCCTGTTGCTGCTGC 27308       TG     CATCA
          T          AGCAGCAG  ACAGGA
                    ||||||||  ||||||
                    TCGTCGTC  TGTCCT
                        GT     AGCCCTGG
GAM906  PAICS   3'  TGATCTCAGTTCACTGCTGCT  21264         CAG  C
                    AGCAGCAGTGA   GA ATCA
                    ||||||||||   || ||||
                    TCGTCGTCACT   CT TAGT
                          TGA  C
GAM906  PAIP2   3'  TCTTGTCACTGTGTT      33222      G
                    AGCA CAGTGACAGGA
                    |||| ||||||||||
                    TTGT GTCACTGTTCT
                      _
GAM906  PBX2    3'  TTTTTTTTTTGTTGTTGTTGTT 10449       TG     CATCA
                    AGCAGCAG  ACAGGA
                    ||||||||  ||||||
                    TTGTTGTT  TGTTTT
                        GT     TTTTTTT
GAM906  PBX2    3'  TTTTGTTGTTGTTGTT      10448       TG
                    AGCAGCAG  ACAGGA
                    ||||||||  ||||||
                    TTGTTGTT  TGTTTT
                        GT
GAM906  PCDH11X 3'  TTTCAGTTTTTTTGTTGTTGTT 52056       TG C    ATCA
                    AGCAGCAG  A AGGAC
                    ||||||||  | |||||
                    TTGTTGTT  T TTTTG
                        GT T    ACTTTT
GAM906  PCDH11X 3'  TTTCAGTTTTTTTGTTGTTGTT 52034       TG C    ATCA
                    AGCAGCAG  A AGGAC
                    ||||||||  | |||||
                    TTGTTGTT  T TTTTG
                        GT T    ACTTTT
GAM906  PCDH11Y 3'  TTTTCAGTTTTTTTGTTGTTGT 52090       TG C    ATCA
          T          AGCAGCAG  A AGGAC
                    ||||||||  | |||||
```

```
                                TTGTTGTT  T TTTTG
                                    GT T    ACTTTTG
GAM906  PCDHA2   3'  TGGTGGGTTTTTTGTTGTTGTT 48984       TG C   A_
                                AGCAGCAG  A AGG  CATCA
                                ||||||||  | |||  |||||
                                TTGTTGTT  T TTT  GTGGT
                                    GT T   GG
GAM906  PDGFRA   3'  TGATGTCAGCTGCTGTT    20598        GACAG
                                AGCAGCAGT    GACATCA
                                |||||||||    |||||||
                                TTGTCGTCG    CTGTAGT
                                    A____
GAM906  PGM1     3'  GCCCTCCTGCATTGCTGCT   10538        A    CATCA
                                AGCAGCAGTG CAGGA
                                |||||||||| |||||
                                TCGTCGTTAC GTCCT
                                    _    CCCGT
GAM906  PIK3C2B  3'  TTTTGTTATTGTTGTT     10584
                                AGCAGCAGTGACAGGA
                                ||||||||||||||||
                                TTGTTGTTATTGTTTT

GAM906  PIK3C2B  3'  TGTTATTGTTGTTGTTGTT   10581       TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                    GT   A
GAM906  PIK3C2B  3'  TTTTGTTATTGTTGTT     10583
                                AGCAGCAGTGACAGGA
                                ||||||||||||||||
                                TTGTTGTTATTGTTTT

GAM906  PIK3C2B  3'  TTTGTTATTGTTGTTGTTGTT 10582       TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                    GT   A   TT
GAM906  PIP5K1A  3'  TGGTGAGGTCATTGCTGT    13059         AGGA
                                GCAGCAGTGAC   CATCA
                                ||||||||||    |||||
                                TGTCGTTACTG   GTGGT
                                    GA__
GAM906  PKNOX1   3'  TGTTCTCTTGTACGTTGTTGCT 15885         _    CATCA
                                AGCAGCAGTG ACAGGA
                                |||||||||| ||||||
                                TCGTTGTTGC TGTTCT
                                    A    CTTGT
GAM906  PLAB     5'  TGATGTTACAGATGTTGTT   65857       GTGACAG
                                AGCAGCA     GACATCA
                                |||||||     |||||||
```

```
                                TTGTTGT      TTGTAGT
                                    AGACA__
GAM906  PLCG1    3'  GATGTTATTACTGTT      10620        CAG
                                AGCAGTGA   GACATC
                                ||||||||   ||||||
                                TTGTCATT   TTGTAG
                                    A__
GAM906  PODXL    3'  TGATTCAGAGGTTACTGCT    18241        AG__  C
                                AGCAGTGAC    GA ATCA
                                |||||||||    || ||||
                                TCGTCATTG    CT TAGT
                                    GAGA  _
GAM906  PODXL    3'  TGAGAGTTTTGTTATAGTTGTT 18240       A        A_
                                AGCAGC GTGACAGGAC  TCA
                                ||||||| ||||||||||  |||
                                TTGTTG TATTGTTTTG  AGT
                                    A         AG
GAM906  POMZP3   3'  TGGTGTCCCTGACTCTGACTGC 24244      _   TGA   _
            T                    AGCAG CAG   CAGG ACATCA
                                |||||| |||   |||| ||||||
                                TCGTC GTC   GTCC TGTGGT
                                   A   TCA    C
GAM906  PPL      3'  TAGTGGATTGTGCTGCTGTT   10705        G   GA   CA
                                AGCAGCAGT ACAG  CAT
                                |||||||||| ||||  |||
                                TTGTCGTCG TGTT  GTG
                                    _   AG   ATA
GAM906  PPP1R12A 3'  GGGGTGTTTTTGTTGTTGTTG  10180       TG    _   A
                                CAGCAG  ACAGGA CATC
                                ||||||  |||||| ||||
                                GTTGTT  TGTTTT GTGG
                                   GT     T    GGT
GAM906  PPP1R2   3'  TTCTGTCATTTGCTGCT     20698        _
                                AGCAGCAG TGACAGGA
                                |||||||| ||||||||
                                TCGTCGTT ACTGTCTT
                                    T
GAM906  PPP2R2B  3'  TGCCTTGTTACTCTTGCT    15910      C       A
                                AGCAG AGTGACAGG CA
                                ||||| |||||||||  ||
                                TCGTT TCATTGTTC GT
                                   C        C
GAM906  PPT2     3'  TGGCTGCTTTTGCTGCTGCTGC 56967        GA   _ _
            T                    AGCAGCAGT  CAGGA CA TCA
                                |||||||||  |||||  || |||
                                TCGTCGTCG  GTTTT GT GGT
                                    TC     C  C
GAM906  PPT2     3'  TGGCTGCTTTTGCTGCTGCTGC 17671        GA   _ _
            T                    AGCAGCAGT  CAGGA CA TCA
                                |||||||||  |||||  || |||
```

```
                                TCGTCGTCG  GTTTT GT GGT
                                     TC    C  C
GAM906  PRDM4   3'  TGGTGGGAAGGTTTTGCTGCT  24828       T   AGGA_
                                AGCAGCAG GAC    CATCA
                                |||||||| |||    |||||
                                TCGTCGTT TTG    GTGGT
                                    _  GAAGG
GAM906  PRex1   3'  GGATTTTTTGTTGTTGGTGTT  40432     G   TG    C   A
                                AGCA CAG  ACAGGA ATC
                                |||| |||  |||||| |||
                                TTGT GTT  TGTTTT TAG
                                  G   GT    T   GG
GAM906  PRKCB1  3'  TGGGGTTTTGTTTCTGTTGTT  70515       T      AT
                                AGCAGCAG GACAGGAC  CA
                                |||||||| ||||||||  ||
                                TTGTTGTC TTGTTTTG  GT
                                     T      GG
GAM906  PRKCM   3'  TGTGTCCCATTGGTGTT    10815     G    ACA    CA
                                AGCA CAGTG   GGACAT
                                |||| |||||   ||||||
                                TTGT GTTAC   CCTGTG
                                  G    ___     TG
GAM906  PRKCN   5'  TTCTTTACTGCTGTT      19451         C
                                AGCAGCAGTGA AGGA
                                |||||||||||| ||||
                                TTGTCGTCATT TCTT
                                          _
GAM906  PSEN1   5'  GTGTTTGCTGCTGCT      23626         GACA
                                AGCAGCAGT    GGACAT
                                |||||||||    ||||||
                                TCGTCGTCG    TTTGTG
                                         ____
GAM906  PSMB9   3'  TGTTATTGTTACTATTGTT   10964      C      _
                                AGCAG AGTGACAG GACA
                                ||||| |||||||| ||||
                                TTGTT TCATTGTT TTGT
                                  A       A
GAM906  PSMD5   3'  TGTCAGATGTTACTTTGTT   17304      C     G__
                                AGCAG AGTGACA   GACA
                                ||||| |||||||   ||||
                                TTGTT TCATTGT   CTGT
                                  _      AGA
GAM906  PSMD9   3'  TGGTGTCCTGTCAGCT     10991     AG
                                AGC  TGACAGGACATCA
                                |||  ||||||||||||
                                TCG  ACTGTCCTGTGGT
                                  __
GAM906  PTER    3'  GATGGGCACTGCTGCT      47696         ACAGGA
                                AGCAGCAGTG     CATC
                                |||||||||      ||||
```

```
                                TCGTCGTCAC     GTAG
                                     GG____
GAM906  PTPN18   3'  TGATGCCCCGGTGCTGCT    26872       G  ACA  A
                                AGCAGCA TG   GG CATCA
                                ||||||| ||   || |||||
                                TCGTCGT GC   CC GTAGT
                                   G  C__  _
GAM906  PTPRA    5'  TGGTGTTCACGGTGTTGCTGC  11097     TG  ____
                                GCAG  ACA    GGACATCA
                                ||||  |||   ||||||||
                                CGTC  TGT    CTTGTGGT
                                  GT   GGCA
GAM906  RAB36    3'  TGATGGCTTGTTTGTTGTT    16979       GT     A
                                AGCAGCA  GACAGG CATCA
                                |||||||  |||||| |||||
                                TTGTTGT  TTGTTC GTAGT
                                   __     G
GAM906  RABL2A   3'  TGGTGTTTTTGTTTTTGTT    25507      T     _
                                AGCAG GACAGGA CATCA
                                ||||| ||||||| |||||
                                TTGTT TTGTTTT GTGGT
                                   T      T
GAM906  RABL2B   3'  TGGTGTTTTTGTTTTTGTT    23008      T     _
                                AGCAG GACAGGA CATCA
                                ||||| ||||||| |||||
                                TTGTT TTGTTTT GTGGT
                                   T      T
GAM906  RAD23B   3'  TGATGGTTAATTGTTGCT     11219        GACAGGA
                                AGCAGCAGT      CATCA
                                |||||||||      |||||
                                TCGTTGTTA      GTAGT
                                     ATTG___
GAM906  RAD51L3  3'  TGCCTTTGCTGCTGCT       56084        TG C   A
                                AGCAGCAG  A AGG CA
                                ||||||||  | ||| ||
                                TCGTCGTC  T TCC GT
                                     GT _   _
GAM906  RAD51L3  3'  TGCCTTTGCTGCTGCT       56077        TG C   A
                                AGCAGCAG  A AGG CA
                                ||||||||  | ||| ||
                                TCGTCGTC  T TCC GT
                                     GT _   _
GAM906  RAD51L3  3'  TGACCTGTGCTGTTGTT      56083         G     A
                                AGCAGCAGT ACAGG CA
                                ||||||||| ||||| ||
                                TTGTTGTCG TGTCC GT
                                     _     A
GAM906  RAD51L3  3'  TGACCTGTGCTGTTGTT      56070         G     A
                                AGCAGCAGT ACAGG CA
                                ||||||||| ||||| ||
```

```
                                TTGTTGTCG TGTCC GT
                                    _    A
GAM906  RAD51L3  3'  TGCCTTTGCTGCTGCT     11237       TG C   A
                                AGCAGCAG  A AGG CA
                                |||||||| | ||| ||
                                TCGTCGTC  T TCC GT
                                    GT _  _
GAM906  RAD51L3  3'  TGCCTTTGCTGCTGCT     56071       TG C   A
                                AGCAGCAG  A AGG CA
                                |||||||| | ||| ||
                                TCGTCGTC  T TCC GT
                                    GT _  _
GAM906  RAI2     5'  TGTATGTTCTGTTGTT     41417       T   GG
                                AGCAGCAG GACA  ACA
                                |||||||| ||||  |||
                                TTGTTGTC TTGT  TGT
                                    _   A_
GAM906  RANBP2L1 3'  TGGTGTCTTTCCAGGCTCT   17315   C   AG  AC
                                AG AGC  TG  AGGACATCA
                                || |||  ||  |||||||||
                                TC TCG  AC  TTCTGTGGT
                                 _  G_  CT
GAM906  RBBP5    3'  TGATGCTTAGTTATGTTGCT   17340       G   _   A
                                AGCAGCA TGAC AGG CATCA
                                ||||||| |||| ||| |||||
                                TCGTTGT ATTG TTC GTAGT
                                    _   A   _
GAM906  RBM6     3'  TGTTACTGTTCTTGCTGCT    19330       T    _
                                AGCAGCAG GACAG GACA
                                |||||||| ||||| ||||
                                TCGTCGTT TTGTC TTGT
                                    C    A
GAM906  RBM6     3'  TTTTGTTACTGTTCT      19331    C
                                AG AGCAGTGACAGGA
                                || ||||||||||||
                                TC TTGTCATTGTTTT
                                 _
GAM906  RENT1    3'  TGATGGGGTGATTGCTGCT   11294        G  AGGA
                                AGCAGCAGT AC    CATCA
                                ||||||||| ||    |||||
                                TCGTCGTTA TG    GTAGT
                                     G  GG__
GAM906  RGS14    3'  TGATGTATGATACTGTT     21370       A  GG
                                AGCAGTG CA  ACATCA
                                ||||||| ||  ||||||
                                TTGTCAT GT  TGTAGT
                                    A  A_
GAM906  RGS16    3'  TGTTATTGTTGGTGCTGTT   11342       G    _
                                AGCAGCA TGACAG GACA
                                ||||||| |||||| ||||
```

```
                                TTGTCGT GTTGTT TTGT
                                   G     A
GAM906  RGS9     5'  GTTTTGTCATGTTGCT      13835        G
                                AGCAGCA TGACAGGAC
                                ||||||| |||||||||
                                TCGTTGT ACTGTTTTG
                                   _
GAM906  RLN2     3'  TGATGTCAGAATTTGTTGCT   17341         TGACAG
                                AGCAGCAG     GACATCA
                                ||||||||     |||||||
                                TCGTTGTT     CTGTAGT
                                    TAAGA_
GAM906  RNF28    3'  TGATGTCTTCTCTCTGCT     50863       T  C
                                AGCAG GA AGGACATCA
                                ||||| || |||||||||
                                TCGTC CT TTCTGTAGT
                                   T  C
GAM906  RNTRE    3'  TGATGTTTCTTCCTGTTGC    28039        T  CA
                                GCAGCAG GA  GGACATCA
                                ||||||| ||  ||||||||
                                CGTTGTC CT  TTTGTAGT
                                    _  TC
GAM906  RPH3AL   3'  TTTTGTCCTTGCTGCT      22760         T
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
                                TCGTCGTT CTGTTTT
                                    C
GAM906  RSN      3'  TGGTGTTTTGTTTATTAGTT   11398     _    _
                                AGC AGTGA CAGGACATCA
                                ||| ||||| ||||||||||
                                TTG TTATT GTTTTGTGGT
                                  A    T
GAM906  SAR1     3'  TGTCCCTTGTCACTTTGTT    39327       C      __
                                AGCAG AGTGACA  GGACA
                                ||||| |||||||  |||||
                                TTGTT TCACTGT  CCTGT
                                   _      TC
GAM906  SBF1     5'  TGCTCGATGTGATTGTTGCT   65460         G   G_  CATCA
                                AGCAGCAGT ACA  GA
                                ||||||||| |||  ||
                                TCGTTGTTA TGT  CT
                                     G   AG  CGT
GAM906  SBF1     5'  TCCTGGCACTGCTGTT       65459          A
                                AGCAGCAGTG CAGGA
                                |||||||||| |||||
                                TTGTCGTCAC GTCCT
                                     G
GAM906  SCML2    3'  TGGTGTTCTGTTCATGTTCT   20326     C    GT
                                AG AGCA  GACAGGACATCA
                                || ||||  ||||||||||||
```

```
                                TC TTGT  TTGTCTTGTGGT
                                 _   AC
GAM906  SDC4    3'  TGGTGTTCTTTGGTTTGCT   11484      TGAC_
                                AGCAG    AGGACATCA
                                |||||    |||||||||
                                TCGTT    TCTTGTGGT
                                   TGGTT
GAM906  SDC4    3'  TGGTGTTTCCAGTTTGATGTTG 11485       GT_  A  __
           CT                    AGCAGCA   GAC GGA  CATCA
                                |||||||   ||| |||  |||||
                                TCGTTGT   TTG CCT  GTGGT
                                    AGT   A   TT
GAM906  SELENBP1  3'  TGACCACTGTTGCTTGTTGCT  14155       _ TG   GACA
                                AGCAGCA G  ACAG   TCA
                                ||||||| |  ||||   |||
                                TCGTTGT C  TGTC   AGT
                                    T GT   ACC_
GAM906  SEPN1   3'  TGATGTCTTTGCAGCTGC    66382      A TG CA
                                GCAGC G  A  GGACATCA
                                ||||| |  |  ||||||||
                                CGTCG C  T  TCTGTAGT
                                   A GT __
GAM906  SERPINB13 3'  TGCCATGGCATTGCTGCT    24774         A  _  A
                                AGCAGCAGTG CA GG CA
                                |||||||||| || || ||
                                TCGTCGTTAC GT CC GT
                                     G  A  _
GAM906  SERPINE2  3'  TTTTTGTTGTTGTTGTTGTT 74927        TG   _   TCA
           T                     AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                    GT   G   TTTTG
GAM906  SERPINE2  3'  TGTTGTTGTTGTTGTTGTT 74926        TG   _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                    GT   G   T
GAM906  SERPINE2  3'  TGTGTTTTTGTTGTTGTTGTT  74925       TG    _  CA
                                AGCAGCAG  ACAGGA CAT
                                ||||||||  |||||| |||
                                TTGTTGTT  TGTTTT GTG
                                    GT    T  T
GAM906  SERPINI1  3'  TGTTTGTGTGCTGTTGTT    17237        ACA
                                AGCAGCAGTG   GGACA
                                ||||||||||   |||||
                                TTGTTGTCGT   TTTGT
                                     GTG
GAM906  SERPINI1  3'  TGTTATGTCATTGTGTT     17236     G      G
                                AGCA CAGTGACA GACA
                                |||| |||||||| ||||
```

```
                                TTGT GTTACTGT TTGT
                                  _      A
GAM906  SET7    3'  TGATGTTCTTTGGTG      47639    G   TGAC
                                CA CAG    AGGACATCA
                                || |||    |||||||||
                                GT GTT    TCTTGTAGT
                                 G  ____
GAM906  SH2D2A  3'  GTCCAATGCTGCTGTT     14274         ACA
                                AGCAGCAGTG   GGAC
                                ||||||||||   ||||
                                TTGTCGTCGT   CCTG
                                      AA_
GAM906  SIP     3'  TGATGTGGAAATACTGATGTT  26977     G    ACAGG
                                AGCA CAGTG    ACATCA
                                |||| |||||    ||||||
                                TTGT GTCAT    TGTAGT
                                  A    AAAGG
GAM906  SIRT1   3'  TGAAATATTTGCCATTGTTGTT 24266         A   ACA_
                                AGCAGCAGTG CAGG   TCA
                                |||||||||| ||||   |||
                                TTGTTGTTAC GTTT   AGT
                                      C   ATAA
GAM906  SLC13A1 3'  TTCTGCATTGTTGTT      42382         A
                                AGCAGCAGTG CAGGA
                                |||||||||| |||||
                                TTGTTGTTAC GTCTT
                                      _
GAM906  SLC26A4 3'  TGGTGTTATAATACGCTGCTG 4790        ACAG__
                                CAGCAGTG     GACATCA
                                ||||||||     |||||||
                                GTCGTCGC     TTGTGGT
                                     ATAATA
GAM906  SLC2A3  3'  TGCACTGTCACTTTGCT     22666      C      GA
                                AGCAG AGTGACAG  CA
                                ||||| ||||||||  ||
                                TCGTT TCACTGTC  GT
                                  _      AC
GAM906  SLC7A9  5'  TGCGTCTTGTCTGCTGCTGCT  26544        _      ATCA
                                AGCAGCAGT GACAGGAC
                                ||||||||| ||||||||
                                TCGTCGTCG CTGTTCTG
                                      T      CGT
GAM906  SLC9A6  3'  TGATGTTGTGTGTTCTGTT   21010      TG_  G
                                AGCAG   ACA GACATCA
                                |||||   ||| |||||||
                                TTGTC   TGT TTGTAGT
                                   TTG   G
GAM906  SMARCC1 3'  TTCTGTTATTATTGTT      11803      C
                                AGCAG AGTGACAGGA
                                ||||| ||||||||||
```

```
                                TTGTT TTATTGTCTT
                                  A
GAM906  SMARCD2  3'  GATTCCTTGTTGCT       11823       GTGAC   C   A
                                AGCAGCA    AGGA ATC
                                |||||||    |||| |||
                                TCGTTGT    TCCT TAG
                                   _____   _  G
GAM906  SNAP23   3'  GAGGTGTTTTTTGTTGTTGTT  13809        TG C      A
                                AGCAGCAG  A AGGACATC
                                ||||||||  | ||||||||
                                TTGTTGTT  T TTTTGTGG
                                    GT _      AGA
GAM906  SNAP23   3'  GAGGTGTTTTTTGTTGTTGTT  55462        TG C      A
                                AGCAGCAG  A AGGACATC
                                ||||||||  | ||||||||
                                TTGTTGTT  T TTTTGTGG
                                    GT _      AGA
GAM906  SNCA     3'  TTTTGTTGCTGTTGTT     4435        TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTC  TGTTTT
                                    GT
GAM906  SNCA     3'  TTTTGTTGCTGTTGTT     4434        TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTC  TGTTTT
                                    GT
GAM906  SNCA     3'  TTTTGTTGCTGTTGTT     23597       TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTC  TGTTTT
                                    GT
GAM906  SNCA     3'  TTTTGTTGCTGTTGTT     23598       TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTC  TGTTTT
                                    GT
GAM906  SNX9     3'  TGATGAGAAGCGCTGCTGT   32594         ACAGGA
                                GCAGCAGTG     CATCA
                                |||||||||     |||||
                                TGTCGTCGC     GTAGT
                                    GAAGA_
GAM906  SNX9     3'  TGATTTTTGTTGTTGTTGTT  32595        TG     C
                                AGCAGCAG  ACAGGA ATCA
                                ||||||||  |||||| ||||
                                TTGTTGTT  TGTTTT TAGT
                                    GT     _
GAM906  SOCS5    3'  TGCCTTGTTATGGCTGCT    25802       A       A
                                AGCAGC GTGACAGG CA
                                ||||||  |||||||| ||
```

```
                                TCGTCG TATTGTTC GT
                                   G       C
GAM906  SOCS5    3'  TGATGTGCAGTCTAATTGTTGT 25800         __   AGG
             T                   AGCAGCAGT  GAC   ACATCA
                                 |||||||||  |||   ||||||
                                 TTGTTGTTA  CTG   TGTAGT
                                      AT   ACG
GAM906  SOCS5    3'  TGATGTTCTAACTGTAGTT   25801     A    GAC
                                 AGC GCAGT   AGGACATCA
                                 ||| |||||   |||||||||
                                 TTG TGTCA   TCTTGTAGT
                                   A    A__
GAM906  SORBS1   3'  TTTTGTTGTTGTTGTT      31165        TG
                                 AGCAGCAG  ACAGGA
                                 ||||||||  ||||||
                                 TTGTTGTT  TGTTTT
                                      GT
GAM906  SORBS1   3'  TTTTGTTGTTGTTGTT      31164        TG
                                 AGCAGCAG  ACAGGA
                                 ||||||||  ||||||
                                 TTGTTGTT  TGTTTT
                                      GT
GAM906  SORCS2   5'  TCCTGCTGCTGCTGCT      40422         GA
                                 AGCAGCAGT  CAGGA
                                 |||||||||  |||||
                                 TCGTCGTCG  GTCCT
                                       TC
GAM906  SOX4     3'  TGATTGTTGTTATTGATGTT   11881      G       GAC
                                 AGCA CAGTGACAG   ATCA
                                 |||| |||||||||   ||||
                                 TTGT GTTATTGTT   TAGT
                                   A        GT_
GAM906  SPOCK    3'  GATGTTTGTTCCTGTT      62817       TG    G
                                 AGCAG  ACAG ACATC
                                 |||||  |||| |||||
                                 TTGTC  TGTT TGTAG
                                    CT    _
GAM906  SRD5A1   3'  TGCTTTCTGTTTTGCTGTTGTT 6459          __      CATCA
                                 AGCAGCAGT  GACAGGA
                                 |||||||||  |||||||
                                 TTGTTGTCG  TTGTCTT
                                       TT       TCGT
GAM906  SRGAP2   3'  TGGGCCTGTTCTGTTGCT    74609        T     A_
                                 AGCAGCAG GACAGG  CA
                                 |||||||| ||||||  ||
                                 TCGTTGTC TTGTCC  GT
                                      _     GG
GAM906  SSX3     3'  TGAAGTGTGTCATTCTGTT    40671       C      GG  A
                                 AGCAG AGTGACA  AC TCA
                                 ||||| |||||||  || |||
```

```
                                TTGTC TTACTGT  TG AGT
                                  _     G_  A
GAM906  STARD4   3'  TGTCTACTGTTTTGTTGTT   57520       T   __
                                AGCAGCAG GACAG  GACA
                                |||||||| |||||  ||||
                                TTGTTGTT TTGTC  CTGT
                                   _    AT
GAM906  STAT3    3'  TTTTGTTATTGTTGTT     57719
                                AGCAGCAGTGACAGGA
                                ||||||||||||||||
                                TTGTTGTTATTGTTTT

GAM906  STAT3    3'  TTTTGTTATTGTTGTT     12004
                                AGCAGCAGTGACAGGA
                                ||||||||||||||||
                                TTGTTGTTATTGTTTT

GAM906  STAT3    3'  TTTGTTATTGTTGTTGTTGTT  12003       TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                    GT   A   TT
GAM906  STAT3    3'  TGTTATTGTTGTTGTTGTT   57717       TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                    GT   A
GAM906  STAT3    3'  TTTGTTATTGTTGTTGTTGTT  57718       TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                    GT   A   TT
GAM906  STAT3    3'  TGTTATTGTTGTTGTTGTT   12002       TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                    GT   A
GAM906  SYT4     3'  TTTTGTTGTTGTTGTT     62441       TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT
GAM906  SYT4     3'  ACCTTTTTGTTGTTGTTGTT  62433       TG    CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT    TCCAT
GAM906  SYT4     3'  TTTGTTGTTGTTGTTGTTGCT  62440       TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
```

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                                TCGTTGTT  TGTT TTGT
                                    GT   G   TT
GAM906  TAF7L   3'  TGATTCCTTGCTGCTGCT   45997       TG CA  C
                                AGCAGCAG  A  GGA ATCA
                                ||||||||  |  ||| ||||
                                TCGTCGTC  T  CCT TAGT
                                    GT __  _
GAM906  TAL1    3'  TGGTGCCATCATTGCTGT   12115        CA  A
                                GCAGCAGTGA  GG CATCA
                                ||||||||||  || |||||
                                TGTCGTTACT  CC GTGGT
                                     A_ _
GAM906  TARBP1  3'  TGAACTGCTGCTGCTGTT   18921        GA  GA
                                AGCAGCAGT  CAG  CA
                                |||||||||  |||  ||
                                TTGTCGTCG  GTC  GT
                                     TC  AA
GAM906  TBL1X   3'  TGCTTTGTTCTTGTTGCT   18938       T   GA
                                AGCAGCAG GACAG  CA
                                ||||||||| |||||  ||
                                TCGTTGTT TTGTT  GT
                                    C    TC
GAM906  TBX3    5'  TGAATTATGTGCTGCTGTT   33356       G  GGACA
                                AGCAGCAGT ACA    TCA
                                |||||||||| |||    |||
                                TTGTCGTCG TGT    AGT
                                    _  ATTA_
GAM906  TBX3    3'  TGATGTTTTCAGAGCCGCT   33357    A  AG  CA
                                AGC GC  TGA  GGACATCA
                                ||| ||  |||  ||||||||
                                TCG CG  ACT  TTTGTAGT
                                  C  AG  __
GAM906  TBX3    5'  TGAATTATGTGCTGCTGTT   19995       G  GGACA
                                AGCAGCAGT ACA    TCA
                                |||||||||| |||    |||
                                TTGTCGTCG TGT    AGT
                                    _  ATTA_
GAM906  TCF8    3'  TCCTGCTGCTGCTGCT    47731       GA
                                AGCAGCAGT  CAGGA
                                |||||||||  |||||
                                TCGTCGTCG  GTCCT
                                     TC
GAM906  TCTE1L  3'  TGTTTTTTATTATTGTTGTT  70974        C__    TCA
                                AGCAGCAGTGA  AGGACA
                                ||||||||||||  ||||||
                                TTGTTGTTATT  TTTTGT
                                      ATT
GAM906  TDG     3'  TGATGTACTGTACTGCTGTT  12194        A  G
                                AGCAGCAGTG CAG ACATCA
                                |||||||||| ||| ||||||
```

```
                                TTGTCGTCAT GTC TGTAGT
                                      _  A
GAM906  TFCP2   5' TGGTTTGCGTTACTCCTGTT  18953     C    A_   ATCA
                                AGCAG AGTGAC  GGAC
                                ||||| ||||||  ||||
                                TTGTC TCATTG  TTTG
                                   C     CG   GT
GAM906  TGFA    3' TGATGTCTGTATATGTTGC   12256      GTG   G
                                GCAGCA   ACAG ACATCA
                                ||||||   |||| ||||||
                                CGTTGT   TGTC TGTAGT
                                   ATA   _
GAM906  TGFA    3' TGATGTATGTGTTGCTGACT  12255   _  TG  GG_
                                AG CAG  ACA   ACATCA
                                || |||  |||   ||||||
                                TC GTC  TGT   TGTAGT
                                 A  GT   GTA
GAM906  THBD    3' TGAATTTTGTTGCTGTT    4496      TG    CA
                                AGCAG  ACAGGA  TCA
                                |||||  ||||||  |||
                                TTGTC  TGTTTT  AGT
                                   GT     A_
GAM906  TIMP3   3' TGATGTTTTGGGATTGT    4521      GA
                                GCAGT  CAGGACATCA
                                |||||  ||||||||||
                                TGTTA  GTTTTGTAGT
                                   GG
GAM906  TIRAP   3' TGATTATGATGTCACTGCTGT 53571         GGAC_
                                GCAGCAGTGACA    ATCA
                                ||||||||||||    ||||
                                TGTCGTCACTGT    TAGT
                                      AGTAT
GAM906  TLL1    3' TGTCGATCTGTTATTGTTGT  24959         ___   TCA
                                GCAGCAGTGACAG   GACA
                                ||||||||||||   ||||
                                TGTTGTTATTGTC   CTGT
                                      TAG      A
GAM906  TLL1    3' TGGTGTCTAATTATTGCAGTT 24958    A     CA
                                AGC GCAGTGA  GGACATCA
                                ||| |||||||  ||||||||
                                TTG CGTTATT  TCTGTGGT
                                  A      AA
GAM906  TM4SF6  3' TGGTGTCGGAATTGTTGT    12328       GACAG
                                GCAGCAGT    GACATCA
                                ||||||||    |||||||
                                TGTTGTTA    CTGTGGT
                                    AGG__
GAM906  TMEM2   3' GGTTTTTTGTTATTGTT    25423          C  A
                                AGCAGTGACAGGA ATC
                                |||||||||||| |||
```

```
                                TTGTTATTGTTTT TGG
                                      T  G
GAM906  TMEPAI   3'  TGTCGTTGTTGTTGTT     39450        TG  AG
                                AGCAGCAG  AC  GACA
                                ||||||||  ||  ||||
                                TTGTTGTT  TG  CTGT
                                    GT  __
GAM906  TNC      3'  TTCTGTTTTGTTGTT      9290         T
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
                                TTGTTGTT TTGTCTT
                                    _
GAM906  TNFRSF10B 3'  TGGTGTCCTTTCATGCTTCT   13885    C   G   C
                                AG AGCA TGA AGGACATCA
                                || |||| ||| |||||||||
                                TC TCGT ACT TCCTGTGGT
                                 T   _  T
GAM906  TNFSF4   3'  TGTCTATGTTCTTGTTGCT    12448        T   _
                                AGCAGCAG GACA GGACA
                                |||||||| |||| |||||
                                TCGTTGTT TTGT TCTGT
                                    C   A
GAM906  TNFSF9   3'  TGGTGCTGGGTCCCTGCTGCT  13758         T  A_  A
                                AGCAGCAG GAC  GG CATCA
                                |||||||| |||  || |||||
                                TCGTCGTC CTG  TC GTGGT
                                    C  GG  _
GAM906  TOX      3'  TGATGTTTTAACTTTTGCT   28291      C  GACA
                                AGCAG AGT   GGACATCA
                                ||||| |||   ||||||||
                                TCGTT TCA   TTTGTAGT
                                   T  AT__
GAM906  TRDN     3'  TGATGTTTTGTCCACAGT    20282    A  _
                                GC GTG ACAGGACATCA
                                || ||| ||||||||||
                                TG CAC TGTTTTGTAGT
                                 A  C
GAM906  TRIM37   3'  TGATGTCTTGCTGAATGCTGT  30974      GTGA_
                                GCAGCA    CAGGACATCA
                                ||||||    ||||||||||
                                TGTCGT    GTTCTGTAGT
                                   AAGTC
GAM906  TRIM9    5'  GGTTGTTCTGTTTTGTTGTT   30764        T       TCA
                                AGCAGCAG GACAGGACA
                                |||||||| |||||||||
                                TTGTTGTT TTGTCTTGT
                                    _       TGGG
GAM906  TRIP15   3'  TGGTTTGTGTTTTGCTGCT   14894        T   G  C
                                AGCAGCAG GACA GA ATCA
                                |||||||| |||| || ||||
```

```
                                TCGTCGTT TTGT TT TGGT
                                    _   G _
GAM906  TRPS1    3'  TGATGTTCTGTTCTAAACTGTT 26082   C     ____
             CT                   G AGCAGT   GACAGGACATCA
                                | ||||||   ||||||||||||
                                C TTGTCA   TTGTCTTGTAGT
                                _     AATC
GAM906  TSG101   5'  TGGTGCCGACTTCCTGTTGTT  20841       T  CA__  A
                                AGCAGCAG GA   GG CATCA
                                |||||||| ||   || |||||
                                TTGTTGTC CT   CC GTGGT
                                    _ TCAG _
GAM906  TUFT1    3'  TGGTTGCTGCCATTGCTGCT   39269        A  _  ATCA
                                AGCAGCAGTG CAG GAC
                                |||||||||| ||| |||
                                TCGTCGTTAC GTC TTG
                                     C  G  GT
GAM906  TYR      3'  TGTCTTTGTCTTGCTGTT    4549        T   _
                                AGCAGCAG GACAG GACA
                                |||||||| ||||| ||||
                                TTGTCGTT CTGTT CTGT
                                    _    T
GAM906  UBE2B    3'  TGATGCGACTTGTTTTGCTGCT 12477       T    A__
                                AGCAGCAG GACAGG   CATCA
                                |||||||| ||||||   |||||
                                TCGTCGTT TTGTTC   GTAGT
                                    _    AGC
GAM906  UBE2V1   3'  TGGTTTTGGTGCTGCTGCT   41798       GA    ATCA
                                AGCAGCAGT  CAGGAC
                                |||||||||  ||||||
                                TCGTCGTCG  GTTTTG
                                     TG    GT
GAM906  UBE2V1   3'  CCTTGGTTTTGGTGCTGCTGCT 12517       GA    ATCA
                                AGCAGCAGT  CAGGAC
                                |||||||||  ||||||
                                TCGTCGTCG  GTTTTG
                                     TG    GTTCCG
GAM906  UBE2V1   3'  CCTTGGTTTTGGTGCTGCTGCT 42369       GA    ATCA
                                AGCAGCAGT  CAGGAC
                                |||||||||  ||||||
                                TCGTCGTCG  GTTTTG
                                     TG    GTTCCG
GAM906  UBE2V1   3'  CCTTGGTTTTGGTGCTGCTGCT 41792       GA    ATCA
                                AGCAGCAGT  CAGGAC
                                |||||||||  ||||||
                                TCGTCGTCG  GTTTTG
                                     TG    GTTCCG
GAM906  UBE2V1   3'  TGGTTTTGGTGCTGCTGCT   42375       GA    ATCA
                                AGCAGCAGT  CAGGAC
                                |||||||||  ||||||
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                                TCGTCGTCG  GTTTTG
                                     TG     GT
GAM906  UBE2V1   3'  TGGTTTTGGTGCTGCTGCT   12523        GA     ATCA
                                AGCAGCAGT  CAGGAC
                                |||||||||  ||||||
                                TCGTCGTCG  GTTTTG
                                     TG     GT
GAM906  UBE3A    3'  TGATGCAATTACTGCTGTT   55594         CAGGA
                                AGCAGCAGTGA    CATCA
                                ||||||||||     |||||
                                TTGTCGTCATT    GTAGT
                                      AAC__
GAM906  UBE3A    3'  TTTTGTTCTTGTTGTT      55597        T
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
                                TTGTTGTT TTGTTTT
                                     C
GAM906  UBE3A    3'  TTTTGTTCTTGTTGTT      55584        T
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
                                TTGTTGTT TTGTTTT
                                     C
GAM906  UBE3A    3'  TGATGCAATTACTGCTGTT   55581         CAGGA
                                AGCAGCAGTGA    CATCA
                                ||||||||||     |||||
                                TTGTCGTCATT    GTAGT
                                      AAC__
GAM906  UBE3A    3'  TGATGCAATTACTGCTGTT   4869          CAGGA
                                AGCAGCAGTGA    CATCA
                                ||||||||||     |||||
                                TTGTCGTCATT    GTAGT
                                      AAC__
GAM906  UBE3A    3'  TTTTGTTCTTGTTGTT      4872         T
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
                                TTGTTGTT TTGTTTT
                                     C
GAM906  VANGL2   3'  TGGTGTGTGATTGTTGT     71656        G  AGG
                                GCAGCAGT AC   ACATCA
                                |||||||| ||   ||||||
                                TGTTGTTA TG   TGTGGT
                                     G  ___
GAM906  VAPB     3'  TGAACTGGTATTGCTGCT    16441         A   GA
                                AGCAGCAGTG CAG  CA
                                |||||||||| |||  ||
                                TCGTCGTTAT GTC  GT
                                      G   AA
GAM906  VHL      3'  GGGTTTTTTTGTTGTTGTTGTT 5078         TG     CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
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                                TTGTTGTT  TGTTTT
                                    GT     TTTGGGT
GAM906  VHL     3'  TTGGGTTTTTTTGTTGTTGTT  5092         TG C    A
                                AGCAGCAG  A AGGAC TCA
                                ||||||||  | ||||| |||
                                TTGTTGTT  T TTTTG GGT
                                    GT T    _   TT
GAM906  WEE1    5'  TGGTGGGCAACTGTGCTGCTGT 12655         G   GA___
          T                      AGCAGCAGT ACAG    CATCA
                                |||||||||| ||||    ||||||
                                TTGTCGTCG TGTC    GTGGT
                                    _   AACGG
GAM906  WHSC1L1  3'  TGGTGTCTGGTTTTTGTT    43522      T   A
                                AGCAG GAC GGACATCA
                                ||||| ||| ||||||||
                                TTGTT TTG TCTGTGGT
                                   T   G
GAM906  WWP2    3'  AGGTTTTTTGTTACGCTGCT   61086      A       C   A
                                AGCAGC GTGACAGGA ATC
                                |||||| ||||||||| |||
                                TCGTCG CATTGTTTT TGG
                                   _       T   AC
GAM906  ZNF10   5'  TCTGTTTTGCTGTTGCTGCT   31181       GT A     TCA
                                AGCAGCA  G CAGGACA
                                |||||||  | |||||||
                                TCGTCGT  T GTTTTGT
                                    TG C      CT
GAM906  ZNF14   3'  GTTCTTTTGTTGTTGTT     40717        TG C
                                AGCAGCAG  A AGGAC
                                ||||||||  | |||||
                                TTGTTGTT  T TCTTG
                                    GT T
GAM906  ZNF236  3'  TGATTTTTTTGTTGTTGTTGTT 23718        TG     C_
                                AGCAGCAG  ACAGGA  ATCA
                                ||||||||  ||||||  ||||
                                TTGTTGTT  TGTTTT  TAGT
                                    GT     TT
GAM906  ZNF264  3'  GTCCTCACTGATTGTT      12762      _     CA
                                AGCAG CAGTGA  GGAC
                                |||||  ||||||  ||||
                                TTGTT GTCACT  CCTG
                                   A     __
GAM906  ZNF278  3'  TGATGTTTGGGTTCTGTAGCT  49446     A   T   A_
                                AGC GCAG GAC  GGACATCA
                                |||  |||| |||  ||||||||
                                TCG TGTC TTG  TTTGTAGT
                                  A   _  GG
GAM906  ZNF278  3'  TGATGTTTGGGTTCTGTAGCT  26731     A   T   A_
                                AGC GCAG GAC  GGACATCA
                                |||  |||| |||  ||||||||
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                                TCG TGTC TTG  TTTGTAGT
                                  A   _  GG
GAM906  ZNF278   3'  TGATGTTTGGGTTCTGTAGCT  49438     A   T  A_
                                AGC GCAG GAC  GGACATCA
                                ||| |||| |||  ||||||||
                                TCG TGTC TTG  TTTGTAGT
                                  A   _  GG
GAM906  ZP3A     3'  TGGTGTCCCTGACTCTGACTGC 23122       _  TGA   _
           T                     AGCAG CAG   CAGG ACATCA
                                ||||| |||   |||| ||||||
                                TCGTC GTC   GTCC TGTGGT
                                   A  TCA   C
GAM906  ACAA2    5'  TGTTTGTAGTTGCTGCT     91771         TG   G
                                AGCAGCAG  ACAG ACA
                                ||||||||  |||| |||
                                TCGTCGTT  TGTT TGT
                                     GA   _
GAM906  ACTR2    3'  TGGTGTTTTGTTAATGCTTCT  19153    C   G
                                AG AGCA TGACAGGACATCA
                                || |||| ||||||||||||
                                TC TCGT ATTGTTTTGTGGT
                                 T   A
GAM906  AKAP10   3'  TGATCTGTCACTGTTGTT    23254             A
                                AGCAGCAGTGACAGG CA
                                |||||||||||||| ||
                                TTGTTGTCACTGTCT GT
                                          A
GAM906  ALS2CR19 3'  TGATGTCTTGGCAGATGTTGTT 54114        G_  A
                                AGCAGCA  TG CAGGACATCA
                                |||||||  || ||||||||||
                                TTGTTGT  AC GTTCTGTAGT
                                    AG  G
GAM906  AP1S2    3'  ATGATGTCTTGTCAGTATTACT 14038      _______
           GTT                    GCAGT     GACAGGACATCA   T
                                |||||     ||||||||||||  |
                                TGTCA     CTGTTCTGTAGT   A
                                   TTATGA
GAM906  APEG1    3'  TGTGCTACTGCTGCT       72134         GAC  G
                                AGCAGCAGT   AG ACA
                                |||||||||   || |||
                                TCGTCGTCA   TC TGT
                                     ___  G
GAM906  Apg4B    3'  TCGCTGCTGCTGCTGCT     25288         GA  _
                                AGCAGCAGT  CAG GA
                                |||||||||  ||| ||
                                TCGTCGTCG  GTC CT
                                      TC   G
GAM906  ARHF     3'  TGGTGTCTGGGGCCTGCGGCT  38753     A   TGACA
                                AGC GCAG    GGACATCA
                                ||| ||||    ||||||||
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                                TCG CGTC    TCTGTGGT
                                  G   CGGGG
GAM906  ARHGDIG  3'  TGTACTGCTGCTGCTGCT   6782        GA  G
                                AGCAGCAGT  CAG ACA
                                |||||||||  ||| |||
                                TCGTCGTCG  GTC TGT
                                     TC   A
GAM906  ASAH     3'  GTTCTAACTGCTGTT      15050       GAC
                                AGCAGCAGT   AGGAC
                                |||||||||   |||||
                                TTGTCGTCA   TCTTG
                                     A__
GAM906  ASB16    5'  TGATTGGATTCGTTACTGCT  69949       _  GA  _
                                AGCAGTGAC AG  CA TCA
                                ||||||||| ||  || |||
                                TCGTCATTG TT  GT AGT
                                     C  AG  T
GAM906  ATP6V1B2 3'  TGGGCTGTGCTGCTGCT    8086        G   GA
                                AGCAGCAGT ACAG  CA
                                ||||||||| ||||  ||
                                TCGTCGTCG TGTC  GT
                                     _   GG
GAM906  BDG-29   5'  TGGTGTCGCTGGCGCTGCT  72357       A  _
                                AGCAGTG CAG GACATCA
                                ||||||| ||| |||||||
                                TCGTCGC GTC CTGTGGT
                                    G   G
GAM906  BHC80    5'  TGGTGGTGCTCGCTGCTGCT  33536         CAGGA
                                AGCAGCAGTGA    CATCA
                                ||||||||||     |||||
                                TCGTCGTCGCT    GTGGT
                                     CGTG_
GAM906  BIA2     3'  TGATTCGTTGTTGCTGT    71284       TG  AG  C
                                GCAGCAG  AC  GA ATCA
                                |||||||  ||  || ||||
                                TGTCGTT  TG  CT TAGT
                                    GT  __  _
GAM906  BLR1     3'  TGTCCCCTTTTATTGCTGCT  52005        CA__    TCA
                                AGCAGCAGTGA   GGACA
                                ||||||||||    |||||
                                TCGTCGTTATT   CCTGT
                                     TTCC
GAM906  BLR1     3'  TGTCCCCTTTTATTGCTGCT  8159         CA__    TCA
                                AGCAGCAGTGA   GGACA
                                ||||||||||    |||||
                                TCGTCGTTATT   CCTGT
                                     TTCC
GAM906  BRD1     5'  TCTCTGCCTGTTACTGCTGCT 27418           A  TCA
                                AGCAGCAGTGACAGG CA
                                |||||||||||||| ||
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                                TCGTCGTCATTGTCC GT
                                       _ CTCTC
GAM906  BRD2     5' GATTCTTCGCTGCTGCT     17536          CA  C  A
                                AGCAGCAGTGA  GGA ATC
                                ||||||||||  ||| |||
                                TCGTCGTCGCT  TCT TAG
                                     __  _  A
GAM906  BZW2     5' TGCCGCCACTGCTGCT      25885         ACA  A  TCA
                                AGCAGCAGTG   GG CA
                                |||||||||   || ||
                                TCGTCGTCAC   CC GT
                                    CG_ _    A
GAM906  C(27)-3BETA-HSD 3' TGATGTTCCCATTGTT      47276        ACA
                                AGCAGTG   GGACATCA
                                |||||||   ||||||||
                                TTGTTAC   CTTGTAGT
                                   C__
GAM906  C11orf15  3' TTTTGTTGTTGTTGTT      40224        TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                     GT
GAM906  C11orf15  3' GGGTTTTTGTTGTTGTTGTT   40222        TG     C   A
                                AGCAGCAG  ACAGGA ATC
                                ||||||||  ||||||  |||
                                TTGTTGTT  TGTTTT TGG
                                     GT     _  GA
GAM906  C11orf23  3' GACGTCTGCTGCTGCT      37012        GACA    A
                                AGCAGCAGT    GGAC TC
                                |||||||||    ||||  ||
                                TCGTCGTCG    TCTG AG
                                     _____   C
GAM906  C15orf5   3' AGCAGTCTTCATTGTTGTT   48196          CA    ATCA
                                AGCAGCAGTGA  GGAC
                                ||||||||||  ||||
                                TTGTTGTTACT  TCTG
                                      __    ACGAC
GAM906  C1orf25   3' TGATGTTTATGTTTTCCTGTT  72540      CAGT   _
                                AGCAG    GACA GGACATCA
                                |||||    |||| ||||||||
                                TTGTC    TTGT TTTGTAGT
                                   CTT_    A
GAM906  C1orf25   3' GGGTTGTTTTTTTGTTGTTGCT 72537        TG C     TCA
                                AGCAGCAG  A AGGACA
                                ||||||||  | ||||||
                                TCGTTGTT  T TTTTGT
                                     GT T     TGGGG
GAM906  C1orf35   3' TGGACCCTGCTCACTGCTGTT  44234          _   ACATCA
                                AGCAGCAGTGA CAGG
                                |||||||||| ||||
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                                TTGTCGTCACT GTCC
                                      C    CAGGT
GAM906  C20orf21  3'  TGATGTCCAGTGGATTTTTGTT 35118      C  G_  A
                                AGCAG AGT  AC GGACATCA
                                ||||| |||  || ||||||||
                                TTGTT TTA  TG CCTGTAGT
                                   T   GG  A
GAM906  C20orf31  5'  TGGTTGCAGTGGCTGCTGCT  36641        G  AG_  ATCA
                                AGCAGCAGT AC   GAC
                                ||||||||| ||   |||
                                TCGTCGTCG TG   TTG
                                     G  ACG   GT
GAM906  C22orf4   3'  TGTATTTCACTGCTGCT    60647          CAGG
                                AGCAGCAGTGA    ACA
                                ||||||||||    |||
                                TCGTCGTCACT    TGT
                                      TTA_
GAM906  C6orf32   5'  GTTCTGCTGCTGTTGTT    31833        GA
                                AGCAGCAGT  CAGGAC
                                |||||||||  ||||||
                                TTGTTGTCG  GTCTTG
                                     TC
GAM906  CAPN6     3'  TGAAACCTCTCGCTGCTGCT  26608          C  ACA
                                AGCAGCAGTGA AGG   TCA
                                |||||||||| |||   |||
                                TCGTCGTCGCT TCC   AGT
                                      C   AA_
GAM906  CBLN1     3'  TAAAGTTTTGTTGTTGTTGTT  15125        TG     ATCA
                                AGCAGCAG  ACAGGAC
                                ||||||||  |||||||
                                TTGTTGTT  TGTTTTG
                                    GT      AAAT
GAM906  CBLN1     3'  TGCCTTGTCATTGTTTCT    15126    C         A
                                AG AGCAGTGACAGG CA
                                || ||||||||||| ||
                                TC TTGTTACTGTTC GT
                                 T          C
GAM906  CBX6      3'  TGTACGTTTGTTCTGCTGCT  26633        T    ACAT
                                AGCAGCAG GACAGG    CA
                                |||||||| ||||||    ||
                                TCGTCGTC TTGTTT    GT
                                     _     GCAT
GAM906  CCNE2     3'  TGGTGTTCAACCTGTGCT    16293      G  TGACA
                                AGCA CAG    GGACATCA
                                |||| |||    ||||||||
                                TCGT GTC    CTTGTGGT
                                  _  CAA__
GAM906  CCNE2     3'  TGGTGTTCAACCTGTGCT    54121      G  TGACA
                                AGCA CAG    GGACATCA
                                |||| |||    ||||||||
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                                TCGT GTC    CTTGTGGT
                                  _  CAA__
GAM906  CDC14A   3'  TGATGTTCTGCATTTGTTTCT  52810    C    _ A
                                AG AGCAG TG CAGGACATCA
                                || ||||| || ||||||||||
                                TC TTGTT AC GTCTTGTAGT
                                 T    T _
GAM906  CDK5RAP3 5'  TGATAAATGTTATTGTCGCT  47285    A       GGAC
                                AGC GCAGTGACA   ATCA
                                ||| |||||||||   ||||
                                TCG TGTTATTGT   TAGT
                                  C       AAA_
GAM906  CDK5RAP3 5'  TGTTATTGTCGCTGTT     47286         _
                                AGCAGTGACAG GACA
                                |||||||||| ||||
                                TTGTCGCTGTT TTGT
                                       A
GAM906  CENPH    3'  TTTGTTTTTTTGTTGTTGTT  43283       TG C     TCA
                                AGCAGCAG  A AGGACA
                                ||||||||  | ||||||
                                TTGTTGTT  T TTTTGT
                                     GT T     TT
GAM906  CENPH    3'  TGTTTTTTTGTTGTTGTTGTT 43279       TG     CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                     GT     TTTGT
GAM906  CG012    5'  TGATGTGAACTCTGTTGTTGC 83228     TG    ____
                                GCAG  ACAGG   ACATCA
                                ||||  |||||   ||||||
                                CGTT  TGTCT   TGTAGT
                                  GT    CAAG
GAM906  CHORDC1  3'  TGTTTTGTTGTTGTGTT    24020     G   TG
                                AGCA CAG  ACAGGACA
                                |||| |||  ||||||||
                                TTGT GTT  TGTTTTGT
                                  _  GT
GAM906  CHORDC1  3'  TGGTGGCTTGCTGCTGT    24019       TGA   A
                                GCAGCAG   CAGG CATCA
                                |||||||   |||| |||||
                                TGTCGTC   GTTC GTGGT
                                     ___   G
GAM906  CHPT1    3'  CTATCTCTTGCTGCTGCTGTT 39620       GA    CATCA
                                AGCAGCAGT  CAGGA
                                |||||||||  |||||
                                TTGTCGTCG  GTTCT
                                     TC    CTATCG
GAM906  CPR2     3'  TGGTGTTTTGTGACTGGCT   48106    AG   G
                                AGC  CAGT ACAGGACATCA
                                |||  |||| ||||||||||
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                                TCG  GTCA TGTTTTGTGGT
                                  __   G
GAM906  CPSF2    3'  GATGTTTTGTTTTGT      61586     T
                                GCAG GACAGGACATC
                                |||| ||||||||||
                                TGTT TTGTTTTGTAG
                                  _
GAM906  CUL2     3'  TGACAAACATGATACTGCTGCT 13170          A  GGACA_
                                AGCAGCAGTG CA     TCA
                                |||||||||| ||     |||
                                TCGTCGTCAT GT     AGT
                                     A  ACAAAC
GAM906  CUL4A    3'  TGGTGTCCGCCCTGCTGC    13156       TGACA
                                GCAGCAG    GGACATCA
                                |||||||    ||||||||
                                CGTCGTC    CCTGTGGT
                                    CCG__
GAM906  CYorf15B 5'  TGACCTGTCATTGTTGC     50819            A
                                GCAGCAGTGACAGG CA
                                |||||||||||||| ||
                                CGTTGTTACTGTCC GT
                                       A
GAM906  CYP2A13  3'  TGATGTCCTTCAGAGCTGT   5718       AG   C
                                GCAGC  TGA AGGACATCA
                                |||||  ||| |||||||||
                                TGTCG  ACT TCCTGTAGT
                                  AG  _
GAM906  DGKD     3'  TGGCTTCTTGTCGCCTGCTGCT 59412        _      CA
                                AGCAGCAG TGACAGGA  TCA
                                |||||||| ||||||||  |||
                                TCGTCGTC GCTGTTCT  GGT
                                    C       TC
GAM906  DHRS2    5'  TGATAAATCTTGCTGCTGCT   19383        TGA    C__
                                AGCAGCAG   CAGGA   ATCA
                                ||||||||   |||||   ||||
                                TCGTCGTC   GTTCT   TAGT
                                   ___     AAA
GAM906  DICER1   3'  TGATGTTCCCGGTCGCTGTTGC 47610          A_  _
                                GCAGCAGTGAC  GGA CATCA
                                ||||||||||  ||| |||||
                                CGTTGTCGCTG  CCT GTAGT
                                      GC   T
GAM906  DKFZP434A1315 3'  GCTCTTTTGTCATTGTGCT    67705     G        CATCA
                                AGCA CAGTGACAGGA
                                |||| ||||||||||
                                TCGT GTTACTGTTTT
                                  _         CTCGG
GAM906  DKFZp434D177 3'  TGAGAGATGTCATTGCTGC    50055           GGACA
                                GCAGCAGTGACA     TCA
                                ||||||||||||     |||
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                                CGTCGTTACTGT    AGT
                                      AGAG_
GAM906  DKFZP434I0714 3'  TGTAATCTGTTGTTCTTGCT  85802      C  TG    __   TCA
                                AGCAG AG  ACAGG  ACA
                                ||||| ||  |||||  |||
                                TCGTT TT  TGTCT  TGT
                                   C  GT    AA
GAM906  DKFZp434I1916 3'  TGCCTTTTTGTTGTTGTTGTT  49978        TG     CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                     GT     TCCGT
GAM906  DKFZp434I1916 3'  AATTTGCCTTTTTGTTGTTGTT 49976        TG C_   A  TCA
                                AGCAGCAG  A  AGG CA
                                ||||||||  |  ||| ||
                                TTGTTGTT  T  TCC GT
                                     GT TT   _  TTAAG
GAM906  DKFZP434J154 3'  TTTGTGCATTGCTGCT      32053          _
                                AGCAGCAGTG ACAGG
                                |||||||||| |||||
                                TCGTCGTTAC TGTTT
                                      G
GAM906  DKFZP434J154 3'  TTTGTGCATTGCTGCT      31548          _
                                AGCAGCAGTG ACAGG
                                |||||||||| |||||
                                TCGTCGTTAC TGTTT
                                      G
GAM906  DKFZp434O0320 3'  TGGTCCGTCATTGTGACTGCTG 83699         G   _  __
           CT                    AGCAGCAGT ACAG GAC  ATCA
                                |||||||| |||| |||  ||||
                                TCGTCGTCA TGTT CTG  TGGT
                                     G   A   CC
GAM906  DKFZP434O047 5'  TGGTGGGAGTGTCGTTGCTTCT 31518    C        GGA_
                                AG AGCAGTGACA    CATCA
                                || ||||||||||    |||||
                                TC TCGTTGCTGT    GTGGT
                                 T         GAGG
GAM906  DKFZp547D155 3'  TGTCATTGTTGCTCTGCT    70439      C  TG   _
                                AGCAG AG  ACAG GACA
                                ||||| ||  |||| ||||
                                TCGTC TC  TGTT CTGT
                                   _ GT    A
GAM906  DKFZP564B1162 5'  TTTTGTCATTGTTCCT      48534    C
                                AG AGCAGTGACAGGA
                                || ||||||||||||
                                TC TTGTTACTGTTTT
                                 C
GAM906  DKFZP564I122 3'  TGGGAATTCTGTACTGCTGCT  63177          A    CA_
                                AGCAGCAGTG CAGGA   TCA
                                |||||||||| |||||   |||
```

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                                TCGTCGTCAT GTCTT   GGT
                                      _     AAG
GAM906  DKFZP564K0822 3'  TGTCTCCTCTGTTGCTTCTGTT 94051      C  TG   ____   TCA
                                AGCAG AG  ACAG    GACA
                                ||||| ||  ||||    ||||
                                TTGTC TC  TGTC    CTGT
                                   T  GT    TCCT      A
GAM906  DKFZp566H0824 5'  TGGTTCCAGTGTTTTGCTGTT  34060        T   __  C
                                AGCAGCAG GACA  GGA ATCA
                                |||||||| ||||  ||| ||||
                                TTGTCGTT TTGT  CCT TGGT
                                      _    GA  _
GAM906  DKFZP566I1024 3'  TGATGGGATCTCGCTCTGTT   70110      C    CAGGA
                                AGCAG AGTGA    CATCA
                                ||||| |||||    |||||
                                TTGTC TCGCT    GTAGT
                                   _    CTAGG
GAM906  DKFZP566K1924 3'  TGGTGTTTTGTTTCCAAGTT   73776     AGT__
                                AGC    GACAGGACATCA
                                |||    ||||||||||||
                                TTG    TTGTTTTGTGGT
                                  AACCT
GAM906  DKFZP586A011 3'  GGGTTTTTGTTGTTGCTGTT   31219        TG    C   A
                                AGCAGCAG  ACAGGA ATC
                                ||||||||  |||||| |||
                                TTGTCGTT  TGTTTT TGG
                                      GT    _  GT
GAM906  DKFZP586C1619 3'  CAGCTCTTGTTTTGCTGCT   61933        T     CATCA
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
                                TCGTCGTT TTGTTCT
                                      _     CGACT
GAM906  DKFZP727G051 3'  GTTTTTAATTGCTGCT     69479         GAC
                                AGCAGCAGT   AGGAC
                                |||||||||   |||||
                                TCGTCGTTA   TTTTG
                                      AT_
GAM906  DKFZp761D0614 3'  TTTTGTTATCTGTTGTT    87559        _
                                AGCAGCAG TGACAGGA
                                |||||||| ||||||||
                                TTGTTGTC ATTGTTTT
                                      T
GAM906  DKFZp761D081 3'  TGATTCAGTTTTTGCTGCT   34282        T   AG  C
                                AGCAGCAG GAC  GA ATCA
                                |||||||| |||  || ||||
                                TCGTCGTT TTG  CT TAGT
                                      T   A_  _
GAM906  DKFZP761E1824 3'  GAGGATGCACTGCTGCT    66438         A  GGACA  A
                                AGCAGCAGTG CA    TC
                                |||||||||| ||    ||
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                                TCGTCGTCAC GT    AG
                                      _ AGG__  G
GAM906  DKFZp761F2014 3'  TGTTAGCGTTGCTGCTGTT   39543       TG  AG_
                                AGCAGCAG  AC   GACA
                                ||||||||  ||   ||||
                                TTGTCGTC  TG   TTGT
                                    GT  CGA
GAM906  DKFZp761H079 5'  TGATGGCCAGTTGCTGCGGCT  58739    A   TG  A  A
                                AGC GCAG  AC GG CATCA
                                ||| ||||  || || |||||
                                TCG CGTC  TG CC GTAGT
                                  G   GT  A  G
GAM906  DKFZp761J139 5'  GTTTTGTTGTTTTTGTT    50117      C  TG
                                AGCAG AG  ACAGGAC
                                |||||  ||  |||||||
                                TTGTT TT  TGTTTTG
                                   T  GT
GAM906  DKFZp761N0624 3'  TGATGATTTTTGCTGTTGTT   50182       TG C   A
                                AGCAGCAG  A AGG CATCA
                                ||||||||  | ||| |||||
                                TTGTTGTC  T TTT GTAGT
                                    GT _   A
GAM906  DKFZp761O0113 5'  TGTTTGTTGTTGTTGTT    37283       TG   G
                                AGCAGCAG  ACAG ACA
                                ||||||||  |||| |||
                                TTGTTGTT  TGTT TGT
                                    GT   _
GAM906  DKFZp761O0113 5'  GTTTGTTGTTGTTGTTGTTGTT 37282       TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                    GT   G   TTGT
GAM906  DKFZp762K2015 3'  TGTTATTGTTGTTGTTGTT   72478       TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                    GT   A
GAM906  DKFZp762K2015 3'  TGTTGTTATTGTTGTTGTTGTT 72479       TG   _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                    GT   A   T
GAM906  DKFZp762P2111 3'  GTTTTTTTTTTGTTGTTGTTGT 86362       TG    CATCA
          T                      AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT    TTTTTTGG
GAM906  DNAJA3   3'  TGAAGCCCTGCCACTGTTGCT  60488         A   ACA
                                AGCAGCAGTG CAGG   TCA
                                |||||||||| ||||  |||
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                                TCGTTGTCAC GTCC   AGT
                                      C    CGA
GAM906  DNAJC5   3'  TGATGTCCCTGTGCTGGCT   61456    AG   G    _
                                AGC  CAGT ACAGG ACATCA
                                |||  |||| ||||| ||||||
                                TCG  GTCG TGTCC TGTAGT
                                  __   _    C
GAM906  DSCR1L1  3'  TGGTGTCTGAATGATTGTT   19501      GACA_
                                AGCAGT    GGACATCA
                                ||||||    ||||||||
                                TTGTTA    TCTGTGGT
                                   GTAAG
GAM906  DUSP9    3'  GGTGGGCTGTTTTGTT     7343       T    GA
                                AGCAG GACAG  CATC
                                ||||| |||||  ||||
                                TTGTT TTGTC  GTGG
                                  _    GG
GAM906  EBRP     3'  TGTTTTTGTATTGTTGCT    50794         AC
                                AGCAGCAGTG  AGGACA
                                ||||||||||  ||||||
                                TCGTTGTTAT  TTTTGT
                                      GT
GAM906  EIF4B    3'  TGTTGTTTTGTTGTTGTT    75974      TG      T
                                AGCAG  ACAGGACA CA
                                |||||  |||||||| ||
                                TTGTT  TGTTTTGT GT
                                   GT       T
GAM906  EIF4B    3'  TGATGTCTTGGGCATT      75972      A_
                                AGTG  CAGGACATCA
                                ||||  ||||||||||
                                TTAC  GTTCTGTAGT
                                  GG
GAM906  ELAC1    3'  TGCCCAGCTTTATTGCTGCT   90972          CA__  A  TCA
                                AGCAGCAGTGA    GG CA
                                ||||||||||    || ||
                                TCGTCGTTATT    CC GT
                                      TCGA  C
GAM906  ELKS     5'  TTTTGTTGTTGTTGTT      30507        TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                     GT
GAM906  ELKS     5'  CCCATTTTTGTTGTTGTTGTT 30503        TG     CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                     GT     TACCCT
GAM906  EML4     3'  TGATGGAGAATCACTGTTG   38812         CAGGA
                                CAGCAGTGA    CATCA
                                |||||||||    |||||
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                                GTTGTCACT    GTAGT
                                     AAGAG
GAM906  EMR2    3'  TTTTGTTTTTGTTGTT     25583        T
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
                                TTGTTGTT TTGTTTT
                                     T
GAM906  EPB41L1 3'  TCCTTGCACTGCTGCT     70598         AC
                                AGCAGCAGTG  AGGA
                                ||||||||||  ||||
                                TCGTCGTCAC  TCCT
                                      GT
GAM906  ESDN    3'  GAGGTTTTTGTTGTTGTTGTT  55172        TG     C   A
                                AGCAGCAG  ACAGGA ATC
                                ||||||||  |||||| |||
                                TTGTTGTT  TGTTTT TGG
                                     GT     _  AGG
GAM906  FBXO26  3'  TGAATCTGCTTGCTGCTGCT   46094        TG _   ACA
                                AGCAGCAG  A CAGG   TCA
                                ||||||||  | ||||   |||
                                TCGTCGTC  T GTCT   AGT
                                     GT C    A__
GAM906  FIBL-6  3'  GGTGCTACACTCTGTT     72915      C    ACA  A
                                AGCAG AGTG   GG CATC
                                ||||| ||||   || ||||
                                TTGTC TCAC   TC GTGG
                                   _    A__  _
GAM906  FIGN    3'  TGATTCCATTCTGCTGTT    95645        TGACA   C
                                AGCAGCAG    GGA ATCA
                                ||||||||    ||| ||||
                                TTGTCGTC    CCT TAGT
                                     TTA__   _
GAM906  FLJ00060 3' TGATTCCACGTCTTTGCTGTT  61106        T   A_   C
                                AGCAGCAG GAC  GGA ATCA
                                |||||||| |||  ||| ||||
                                TTGTCGTT CTG  CCT TAGT
                                     T   CA   _
GAM906  FLJ10094 3' TGGTGTAGCAATGATTGTTGCT 35810         GACAGG_
                                AGCAGCAGT      ACATCA
                                |||||||||      ||||||
                                TCGTTGTTA      TGTGGT
                                      GTAACGA
GAM906  FLJ10404 5' GGAAGTTCTGTGACTGCTGCT  38798         G      A  A
                                AGCAGCAGT ACAGGAC TC
                                ||||||||| ||||||| ||
                                TCGTCGTCA TGTCTTG AG
                                     G      A  GG
GAM906  FLJ10483 3' TGGTGTCTTGTTTAATGATCTG 36176       __  GT_
             TT                   AGCAG  CA   GACAGGACATCA
                                |||||  ||   ||||||||||||
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                                TTGTC  GT   TTGTTCTGTGGT
                                   TA  AAT
GAM906  FLJ10540 3' TGATCTTTATTGCTGCT     36259          C   A
                                AGCAGCAGTGA AGG CA
                                |||||||||||  ||| ||
                                TCGTCGTTATT TCT GT
                                      _   A
GAM906  FLJ10546 3' TGTTTTTGTTGTTGTTGTT    59482        TG     CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                     GT     TGT
GAM906  FLJ10546 3' GAGTTGTTTTTGTTGTTGTTGT 59476        TG     _  TCA
          T                      AGCAGCAG  ACAGGA CA
                                ||||||||  ||||||  ||
                                TTGTTGTT  TGTTTT GT
                                     GT     T  TGAGA
GAM906  FLJ10560 3' GGTGCTATTGCTGCT       36283        GACA  A    A
                                AGCAGCAGT    GG CATC
                                |||||||||    ||  ||||
                                TCGTCGTTA    TC GTGG
                                     ____  _    A
GAM906  FLJ10604 3' GGATGCTGTTGTGATTGCTGTT 36340         G  __  A    A
                                AGCAGCAGT ACA  GG CATC
                                |||||||||  |||  ||  ||||
                                TTGTCGTTA TGT  TC GTAG
                                     G   TG  _    GT
GAM906  FLJ10607 3' TAGCCTTTTGTTGTTGTTGTT  77125        TG     CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                     GT     CCGAT
GAM906  FLJ10701 3' TGTTATTGTTGTTATTGTTGTT 36433            ____    TCA
                                AGCAGCAGTGACAG    GACA
                                ||||||||||||||    ||||
                                TTGTTGTTATTGTT    TTGT
                                       GTTA      A
GAM906  FLJ10701 3' TGTTCTTTTGTTATTGTTGTT  36434           ___    TCA
                                AGCAGCAGTGACA   GGACA
                                ||||||||||||   |||||
                                TTGTTGTTATTGT   CTTGT
                                       TTT       A
GAM906  FLJ10715 3' TGTCATGTTTTGTTGCT     36478        T   G
                                AGCAGCAG GACA GACA
                                |||||||| |||| ||||
                                TCGTTGTT TTGT CTGT
                                     _   A
GAM906  FLJ10774 3' TGATGTTGTCTTGTGCTGTT  45087       GT_   GG
                                AGCAGCA   GACA  ACATCA
                                |||||||   ||||  ||||||
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                                TTGTCGT  CTGT  TGTAGT
                                   GTT   __
GAM906  FLJ10932  3'  TGATGAGTTCACTGCTTCT   36899   C     CAGGA
                                AG AGCAGTGA    CATCA
                                || ||||||||    |||||
                                TC TCGTCACT    GTAGT
                                 T      TGA__
GAM906  FLJ10971  3'  TGATGTTCTTGTTCTTGGTGTT 36931    G  T    _
                                AGCA CAG GACAGGA CATCA
                                |||| ||| ||||||| |||||
                                TTGT GTT TTGTTCT GTAGT
                                  G  C     T
GAM906  FLJ10996  3'  TCTGTTGGCTGCTGTT     38778       _
                                AGCAGCAGT GACAGG
                                ||||||||| ||||||
                                TTGTCGTCG TTGTCT
                                     G
GAM906  FLJ11011  3'  GGAGGGTTTTGTTTTGTTGTT  36977       T     A_  A
                                AGCAGCAG GACAGGAC  TC
                                |||||||| ||||||||  ||
                                TTGTTGTT TTGTTTTG  AG
                                    _      GG  GT
GAM906  FLJ11078  3'  TGATGTCTTGTCTCTGT    37034    T
                                GCAG GACAGGACATCA
                                |||| ||||||||||||
                                TGTC CTGTTCTGTAGT
                                  T
GAM906  FLJ11149  3'  TATCTGTTTGTTGTTGTTGTT  37113       TG   G  TCA
                                AGCAGCAG  ACAG ACA
                                ||||||||  |||| |||
                                TTGTTGTT  TGTT TGT
                                    GT   _  CTATC
GAM906  FLJ11149  3'  TGTTTGTTGTTGTTGTT    37114       TG   G
                                AGCAGCAG  ACAG ACA
                                ||||||||  |||| |||
                                TTGTTGTT  TGTT TGT
                                    GT   _
GAM906  FLJ11259  5'  GGTGTCTTTAGTGCT     37190    G  CA
                                AGCA TGA  GGACATC
                                |||| |||  |||||||
                                TCGT ATT  TCTGTGG
                                  G  __
GAM906  FLJ11259  3'  AAACCATCCTTTATTGTTGCT  37184        C   CATCA
                                AGCAGCAGTGA AGGA
                                |||||||||||| ||||
                                TCGTTGTTATT TCCT
                                      _   ACCAAAA
GAM906  FLJ11269  3'  GATGTTTTGTTTGCT     72630    GT
                                AGCA  GACAGGACATC
                                ||||  ||||||||||
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                                TCGT  TTGTTTTGTAG
                                  __
GAM906  FLJ11383 3' TGGACCTCCTTGTTGACTGCTG 46284        _   _  CA  A
              TT                  AGCAGCAGT GACA GGA  TC
                                  ||||||||| |||| |||  ||
                                  TTGTCGTCA TTGT CCT  AG
                                      G    T   CC  GT
GAM906  FLJ11413 3' TTTTCTTACTGTTGCT      44644          C
                                  AGCAGCAGTGA AGGA
                                  |||||||||| ||||
                                  TCGTTGTCATT TTTT
                                        C
GAM906  FLJ11795 3' GTTTTTTTGTTATTGTTCT   45132    C         CATCA
                                  AG AGCAGTGACAGGA
                                  || ||||||||||||
                                  TC TTGTTATTGTTTT
                                   _          TTTGT
GAM906  FLJ12076 3' TGCCATGTGCTGTTGCT     47236        G  _  A
                                  AGCAGCAGT ACA GG CA
                                  ||||||||| ||| || ||
                                  TCGTTGTCG TGT CC GT
                                      _  A  _
GAM906  FLJ12076 5' TGGTGTTGGGCCGGTGCTGCT  47237       G  ACAG
                                  AGCAGCA TG    GACATCA
                                  ||||||| ||    |||||||
                                  TCGTCGT GC    TTGTGGT
                                     G  CGGG
GAM906  FLJ12078 3' TGATGTGGAAATGCTGTT    46456       GTGA AGG
                                  AGCAGCA    C   ACATCA
                                  |||||||    |  ||||||
                                  TTGTCGT    G   TGTAGT
                                     AAAG ___
GAM906  FLJ12331 3' TGGTCACATTGTCTTTGCTGTT 46481        T    ___  ATCA
                                  AGCAGCAG GACAG   GAC
                                  |||||||| |||||   |||
                                  TTGTCGTT CTGTT   CTG
                                       T    ACA   GT
GAM906  FLJ12529 3' TGTAATGTGGTTGCTGCT    45662        TG   GG
                                  AGCAGCAG  ACA  ACA
                                  ||||||||  |||  |||
                                  TCGTCGTT  TGT  TGT
                                       GG   AA
GAM906  FLJ12568 3' TGGTGTTTGACTGTTGT     46501        GACA
                                  GCAGCAGT    GGACATCA
                                  ||||||||    ||||||||
                                  TGTTGTCA    TTTGTGGT
                                       G___
GAM906  FLJ12747 3' TGATATTTTTTTGTTGTTGTT  49729        TG C    C
                                  AGCAGCAG  A AGGA ATCA
                                  ||||||||  | |||| ||||
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                                TTGTTGTT  T TTTT TAGT
                                    GT T   A
GAM906  FLJ12888  5' CAAATCCTGTGCTGCTGTT   46316       G    CATCA
                                AGCAGCAGT ACAGGA
                                ||||||||| ||||||
                                TTGTCGTCG TGTCCT
                                    _     AAACT
GAM906  FLJ13052  3' TGGTGTCCTGGTTACTGCTGC  43475         _
                                GCAGCAGTGAC AGGACATCA
                                |||||||||| |||||||||
                                CGTCGTCATTG TCCTGTGGT
                                      G
GAM906  FLJ13057  3' GTGTTTATTGCTGTT      42457          CAGG
                                AGCAGCAGTGA   ACAT
                                ||||||||||   ||||
                                TTGTCGTTATT   TGTG
                                     ____
GAM906  FLJ13456  3' TGATGTTTTGGGGGTTTCT   65946   C  AGTGA
                                AG AGC    CAGGACATCA
                                || |||    ||||||||||
                                TC TTG    GTTTTGTAGT
                                 T  GGG__
GAM906  FLJ13842  3' TGGTGTCTTGTAGCCTG     44991    CA  G
                                CAG  GT ACAGGACATCA
                                |||  || ||||||||||
                                GTC  CG TGTTCTGTGGT
                                  __  A
GAM906  FLJ13962  3' TGGTGTTTCATCAGCTCTTGTT 45871      C  _  CA
                                AGCAG AG TGA  GGACATCA
                                ||||| || |||  ||||||||
                                TTGTT TC ACT  TTTGTGGT
                                   C  G   AC
GAM906  FLJ13984  3' TTTTGTCTTGTTGTT      45456        T
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
                                TTGTTGTT CTGTTTT
                                     _
GAM906  FLJ14054  3' TGATTTAATTTATTGCTGTT  44662         CAG  C
                                AGCAGCAGTGA   GA ATCA
                                ||||||||||   || ||||
                                TTGTCGTTATT   TT TAGT
                                      TAA  _
GAM906  FLJ14124  3' TGTTTGTAGCTGCTGCT     45890        G   G
                                AGCAGCAGT ACAG ACA
                                ||||||||| |||| |||
                                TCGTCGTCG TGTT TGT
                                     A   _
GAM906  FLJ14166  3' TGTCATGTGCTGCTGCT     44687        G  G
                                AGCAGCAGT ACA GACA
                                ||||||||| ||| ||||
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```
                                TCGTCGTCG TGT CTGT
                                     _  A
GAM906  FLJ14525  3' GAAGTTCTTGTTGCT      51416       GTGAC    A
                                AGCAGCA    AGGAC TC
                                |||||||    ||||| ||
                                TCGTTGT    TCTTG AG
                                   _____    A
GAM906  FLJ14917  3' TGGTGTTCTGTTTCTTCT    51697    C  T
                                AG AG GACAGGACATCA
                                || || ||||||||||||
                                TC TC TTGTCTTGTGGT
                                 T  T
GAM906  FLJ14936  3' TGGGATTTGTGCTGCTGCT   51708        G    ACA
                                AGCAGCAGT ACAGG   TCA
                                ||||||||| |||||   |||
                                TCGTCGTCG TGTTT   GGT
                                     _    AG_
GAM906  FLJ20033  3' TGGTGTCCTGTCACTTTGTT  34349      C
                                AGCAG AGTGACAGGACATCA
                                ||||| ||||||||||||||||
                                TTGTT TCACTGTCCTGTGGT
                                  _
GAM906  FLJ20174  5' TTTTATTATTGCTGTT      34692          C
                                AGCAGCAGTGA AGGA
                                |||||||||| ||||
                                TTGTCGTTATT TTTT
                                      A
GAM906  FLJ20298  5' TCTTGTTATTGGTGTT      34905      G
                                AGCA CAGTGACAGGA
                                |||| ||||||||||
                                TTGT GTTATTGTTCT
                                  G
GAM906  FLJ20312  3' TGATGTTTTGTTTTTGTT    34929       T
                                AGCAG GACAGGACATCA
                                ||||| ||||||||||||
                                TTGTT TTGTTTTGTAGT
                                   T
GAM906  FLJ20343  3' GGTGTTCCTGTGCGCT      34999      _    _
                                AGTG ACAGGA CATC
                                |||| |||||| ||||
                                TCGC TGTCCT GTGG
                                  G     T
GAM906  FLJ20366  3' TTCTGTCGTTTTGCT       35051      C
                                AGCAG AGTGACAGGA
                                ||||| ||||||||||
                                TCGTT TTGCTGTCTT
                                  _
GAM906  FLJ20396  3' TGGAGTCATGTGCTGCTGCT   35122        G  G  AT
                                AGCAGCAGT ACA GAC  CA
                                ||||||||| ||| |||  ||
```

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                                TCGTCGTCG TGT CTG  GT
                                      _  A   AG
GAM906  FLJ20396 3' TAAATGATTCTGTCATTCTGTT 35121      C        _  CA
                                AGCAG AGTGACAGGA CAT
                                ||||| |||||||||| |||
                                TTGTC TTACTGTCTT GTA
                                  _        A   AATA
GAM906  FLJ20425 3' ACTTCTTCCTTTCACTGCTGTT 35150          C   CATCA
                                AGCAGCAGTGA AGGA
                                |||||||||| ||||
                                TTGTCGTCACT TCCT
                                       T   TCTTCAG
GAM906  FLJ20435 3' TGAGCTGTTGACACTGTTGTT  35165          ___   GACATCA
                                AGCAGCAGTG   ACAG
                                |||||||||   ||||
                                TTGTTGTCAC   TGTC
                                      AGT   GAGT
GAM906  FLJ20445 3' TGAATCTGTTGTGTTGTT    35181       G      ACA
                                AGCAGCA TGACAGG   TCA
                                ||||||| |||||||   |||
                                TTGTTGT GTTGTCT   AGT
                                  _      A__
GAM906  FLJ20651 3' TGAGGACCTTTGCTGCTGTT   35499        TG C   ACA
                                AGCAGCAG  A AGG   TCA
                                ||||||||  | |||   |||
                                TTGTCGTC  T TCC   AGT
                                     GT _   AGG
GAM906  FLJ20666 5' TGGTCAGACGCTGTCATTGATG 35512    G       _____  ATCA
           CT                    CA CAGTGACAG    GAC
                                || |||||||||    |||
                                GT GTTACTGTC    CTG
                                 A       GCAGA   GT   A
GAM906  FLJ20718 3' TGATGAGTTATTGCTGT     35608          AGGA
                                GCAGCAGTGAC    CATCA
                                ||||||||||    |||||
                                TGTCGTTATTG    GTAGT
                                      A___
GAM906  FLJ20736 3' TCCATTTTGTCATTTTTGTT   35632      C        CATCA
                                AGCAG AGTGACAGGA
                                ||||| ||||||||||
                                TTGTT TTACTGTTTT
                                   T        ACCT
GAM906  FLJ20783 5' TGGTGTTCTCCACGCTG     35665     A   AC
                                CAGC GTG  AGGACATCA
                                |||| |||  |||||||||
                                GTCG CAC  TCTTGTGGT
                                  _  C_
GAM906  FLJ20986 5' TCTTGTTCTGCTGTT       44547         T
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
```

```
                                TTGTCGTC TTGTTCT
                                        _
GAM906  FLJ21125 3' TGGTGTTCTGAAGCAGGCTCCT 44893    C   A_  GA
                                AG AGC  GT  CAGGACATCA
                                || |||  ||  ||||||||||
                                TC TCG  CG  GTCTTGTGGT
                                 C   GA  AA
GAM906  FLJ21276 3' TTGACGTTTTTGCTGTTGTT   44924        TG CA    A
                                AGCAGCAG  A  GGAC TCA
                                ||||||||  |  |||| |||
                                TTGTTGTC  T  TTTG AGT
                                     GT __    C   TT
GAM906  FLJ21313 3' TTATGTTTTGTTTTGTTGCT   43694        T        CA
                                AGCAGCAG GACAGGACAT
                                |||||||| ||||||||||
                                TCGTTGTT TTGTTTTGTA
                                     _        TTT
GAM906  FLJ21432 3' TGGTGTCCTCAGTAGGTGTT   44639     GTG  ___
                                AGCA   AC  AGGACATCA
                                ||||   ||  |||||||||
                                TTGT   TG  TCCTGTGGT
                                  GGA  AC
GAM906  FLJ21736 5' TCGTTGTTGTTGTTGTT     46233        TG   _
                                AGCAGCAG  ACAG GA
                                ||||||||  |||| ||
                                TTGTTGTT  TGTT CT
                                     GT    G
GAM906  FLJ22167 5' TGATGACAACAATTGCTGTT   44584         GACAGGA
                                AGCAGCAGT      CATCA
                                |||||||||      |||||
                                TTGTCGTTA      GTAGT
                                     ACAACA_
GAM906  FLJ22174 3' TGGTGTCGCATCTGTTGT     41677        _ ACAG
                                GCAGCAG TG    GACATCA
                                ||||||| ||    |||||||
                                TGTTGTC AC    CTGTGGT
                                    T  G___
GAM906  FLJ22202 3' TTTTGTATTGTTGTT       45993          A
                                AGCAGCAGTG CAGGA
                                |||||||||| |||||
                                TTGTTGTTAT GTTTT
                                        _
GAM906  FLJ22283 3' TGATGGAACTTTTCTGCTGTT  49917        T  C  GA_
                                AGCAGCAG GA AG   CATCA
                                |||||||| || ||   |||||
                                TTGTCGTC TT TC   GTAGT
                                     _  T  AAG
GAM906  FLJ22477 3' TGATGCCTCCACTGCTGT     45347         AC   A
                                GCAGCAGTG  AGG CATCA
                                |||||||||  ||| |||||
```

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                                TGTCGTCAC  TCC GTAGT
                                    C_   _
GAM906  FLJ22679  3'  TGGTGTCCATTTTGTGTT    49925     G   TGACA
                                AGCA CAG    GGACATCA
                                |||| |||    ||||||||
                                TTGT GTT    CCTGTGGT
                                  _   TTA__
GAM906  FLJ22679  3'  TGGTGTCCATTTTGTGTT    34681     G   TGACA
                                AGCA CAG    GGACATCA
                                |||| |||    ||||||||
                                TTGT GTT    CCTGTGGT
                                  _   TTA__
GAM906  FLJ22843  3'  GATGTCTTTGACTGTT      47228       GAC
                                AGCAGT   AGGACATC
                                ||||||   ||||||||
                                TTGTCA   TTCTGTAG
                                   GT_
GAM906  FLJ23878  3'  TGGTGTTTAAACTGTTGC    58712        GACA
                                GCAGCAGT    GGACATCA
                                ||||||||    ||||||||
                                CGTTGTCA    TTTGTGGT
                                    AA__
GAM906  FLJ25082  3'  TGATGTGTTTATTGCT      58330        CA G
                                AGCAGTGA  G ACATCA
                                ||||||||  | ||||||
                                TCGTTATT  T TGTAGT
                                   __ G
GAM906  FRAT1     3'  TGAGACTGTGCTGTTGTT    18495        G    GACA
                                AGCAGCAGT ACAG    TCA
                                ||||||||| ||||    |||
                                TTGTTGTCG TGTC    AGT
                                    _    AG__
GAM906  FREQ      3'  TGGTTGTTAACTGTTGCTGCTG 26592        TG   __   _
          C                      GCAGCAG  ACAG  GACA TCA
                                |||||||  ||||  |||| |||
                                CGTCGTC  TGTC  TTGT GGT
                                    GT    AA    T
GAM906  FREQ      3'  GAATTCTTGCTGCTGCT     26576        TGA    CA
                                AGCAGCAG   CAGGA  TC
                                ||||||||   |||||  ||
                                TCGTCGTC   GTTCT  AG
                                   ___     TA
GAM906  FSD1      3'  TCTGTCACTTGCTGCT      44289        _
                                AGCAGCA GTGACAGG
                                ||||||| ||||||||
                                TCGTCGT CACTGTCT
                                    T
GAM906  FUBP3     3'  TGATGAAGAACTGTTGTT    63734        GACAGGA
                                AGCAGCAGT      CATCA
                                |||||||||      |||||
```

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                                TTGTTGTCA      GTAGT
                                     AGAA___
GAM906  FUSIP1   3'  CTTAGTTTTCTTACTGCTGTT  53958          C     ATCA
                                AGCAGCAGTGA AGGAC
                                |||||||||| |||||
                                TTGTCGTCATT TTTTG
                                      C     ATTCG
GAM906  FZD9     3'  TGATGTAATTTATTGTTGC   13047          CAGG
                                GCAGCAGTGA   ACATCA
                                ||||||||||   ||||||
                                CGTTGTTATT   TGTAGT
                                      TAA_
GAM906  G2       3'  TGATGTCCAGTGTGTGCTGCT  66664        GTG  A
                                AGCAGCA  AC GGACATCA
                                |||||||  || ||||||||
                                TCGTCGT  TG CCTGTAGT
                                    GTG  A
GAM906  GAB3     3'  TTTTGTTTTTGCTGTT      54638         T
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
                                TTGTCGTT TTGTTTT
                                     T
GAM906  GABARAPL1 3'  GATATTTTTTGCTGCT     48601         TGAC   C
                                AGCAGCAG   AGGA ATC
                                ||||||||   |||| |||
                                TCGTCGTT   TTTT TAG
                                     ____   A
GAM906  GALNT11  3'  TGATGTTTGAGCTGCTGTT   42007         GACA
                                AGCAGCAGT   GGACATCA
                                |||||||||   ||||||||
                                TTGTCGTCG   TTTGTAGT
                                     AG__
GAM906  GFR      3'  TGGTGTTTTGAATTTGCTCT  24477   C    TGA
                                AG AGCAG  CAGGACATCA
                                || |||||  ||||||||||
                                TC TCGTT  GTTTTGTGGT
                                 _    TAA
GAM906  GIT2     3'  TGTTATGTTGCTGTCGCT    28763    A   TG  G
                                AGC GCAG  ACA GACA
                                ||| ||||  ||| ||||
                                TCG TGTC  TGT TTGT
                                  C   GT  A
GAM906  GIT2     3'  GATGTTCGGTTGTGTT      54095     G   A
                                AGCA TGAC GGACATC
                                |||| |||| |||||||
                                TTGT GTTG CTTGTAG
                                  _   G
GAM906  GIT2     3'  GATGTTCGGTTGTGTT      28760     G   A
                                AGCA TGAC GGACATC
                                |||| |||| |||||||
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                                TTGT GTTG CTTGTAG
                                  _   G
GAM906  GIT2    3'  TGTTATGTTGCTGTCGCT    54098    A   TG  G
                                AGC GCAG  ACA GACA
                                ||| ||||  ||| ||||
                                TCG TGTC  TGT TTGT
                                  C   GT  A
GAM906  GIT2    3'  TGTTATGTTGCTGTCGCT    54085    A   TG  G
                                AGC GCAG  ACA GACA
                                ||| ||||  ||| ||||
                                TCG TGTC  TGT TTGT
                                  C   GT  A
GAM906  GIT2    3'  GATGTTCGGTTGTGTT     54082     G   A
                                AGCA TGAC GGACATC
                                |||| |||| |||||||
                                TTGT GTTG CTTGTAG
                                  _   G
GAM906  GNA13   3'  TGATGTTTTCTGTTTGTTTTGT 21651     CAGT   __
          T                      AGCAG   GACAG  GACATCA
                                |||||   |||||  |||||||
                                TTGTT   TTGTC  TTGTAGT
                                   TTGT    TT
GAM906  GNG4    3'  TTTTTTTTTTGTTGTTGTTGTT 15630       TG    CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                     GT    TTTTTTG
GAM906  GNG4    3'  TTTTGTTGTTGTTGTT     15629       TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                     GT
GAM906  GORASP2 3'  TTTTGTAACTGCTGCT     31384       G
                                AGCAGCAGT ACAGGA
                                ||||||||| ||||||
                                TCGTCGTCA TGTTTT
                                     A
GAM906  GORASP2 3'  TGTAACTGCTGCTGTTGCT  31383       GA  G_
                                AGCAGCAGT  CAG  ACA
                                |||||||||  |||  |||
                                TCGTTGTCG  GTC  TGT
                                     TC   AA
GAM906  GPR88   5'  TGGACCACTGATGCTGTTGCT 41882       A  GACA
                                AGCAGCAGTG CAG   TCA
                                |||||||||| |||   |||
                                TCGTTGTCGT GTC   GGT
                                     A  ACCA
GAM906  GPT2    3'  TGAATCTGTTATTGTT     55960         ACA
                                AGCAGTGACAGG  TCA
                                ||||||||||||  |||
```

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                                TTGTTATTGTCT  AGT
                                      A__
GAM906  H-plk   5'  GTTTTCTTTTTGTTGTTGTTGT 31811       TG    CATCA
              T                  AGCAGCAG  ACAGGA
                                 ||||||||  ||||||
                                 TTGTTGTT  TGTTTT
                                     GT    TCTTTTGG
GAM906  HAK     3'  TGGTGTCTAATACGCTATTGTT 53643     C   ACA_
                                 AGCAG AGTG   GGACATCA
                                 ||||| ||||   ||||||||
                                 TTGTT TCGC   TCTGTGGT
                                    A   ATAA
GAM906  HCDI    3'  TCCCATTGTTCTGTTGCT    39492       T   ___
                                 AGCAGCAG GACA  GGA
                                 |||||||| ||||  |||
                                 TCGTTGTC TTGT  CCT
                                     _   TAC
GAM906  HCGIV.9 3'  GGTTTTTTGTTGTTGTTGTT  38613       TG    C  A
                                 AGCAGCAG  ACAGGA ATC
                                 ||||||||  |||||| |||
                                 TTGTTGTT  TGTTTT TGG
                                     GT    T  G
GAM906  HCGIV.9 3'  TTTTGTTGTTGTTGTT     38615       TG
                                 AGCAGCAG  ACAGGA
                                 ||||||||  ||||||
                                 TTGTTGTT  TGTTTT
                                     GT
GAM906  HIC2    3'  TGGGCCTGTGTTGCTGTT    65270       GT A   A_  TCA
                                 AGCAGCA  G CAGG  CA
                                 |||||||  | ||||  ||
                                 TTGTCGT  T GTCC  GT
                                    TG _   GG
GAM906  HN1L    3'  CCTGTCCACTGCTGCT     57994        _
                                 AGCAGCAGTG ACAGG
                                 |||||||||| |||||
                                 TCGTCGTCAC TGTCC
                                       C
GAM906  HNRPA3  3'  TGAGTATGTGTCCTGCTGTT  19262       T   GG_  A
                                 AGCAGCAG GACA  AC TCA
                                 |||||||| ||||  || |||
                                 TTGTCGTC CTGT  TG AGT
                                     _   GTA  _
GAM906  HRB2    3'  TGATGTCCCAGCATTTGATGTT 22907     GC_   ACA
                                 AGCA  AGTG  GGACATCA
                                 ||||  ||||  ||||||||
                                 TTGT  TTAC  CCTGTAGT
                                   AGT   GAC
GAM906  HSJ1    3'  TGACCGTCTCTGTTGCT     22139       T  A  A
                                 AGCAGCAG GAC GG CA
                                 |||||||| ||| || ||
```

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                                TCGTTGTC CTG CC GT
                                     T  _  A
GAM906  HSPC019  3' GTTGAGTCATTGCTCT     25859    C       AG
                                AG AGCAGTGAC  GAC
                                || |||||||||  |||
                                TC TCGTTACTG  TTG
                                  _       AG
GAM906  HSPC065  3' TGGTGTTTGTTTCTGTT     26332      T    G
                                AGCAG GACAG ACATCA
                                ||||| ||||| ||||||
                                TTGTC TTGTT TGTGGT
                                   T    _
GAM906  HSPC129  5' GTTCTGTTGCTGCTGC      33071        TG
                                GCAGCAG  ACAGGAC
                                |||||||  |||||||
                                CGTCGTC  TGTCTTG
                                     GT
GAM906  HSPC129  3' TGATTTAGTTACTGCTGC    33073          AG  CA
                                GCAGCAGTGAC  GA  TCA
                                ||||||||||  ||  |||
                                CGTCGTCATTG  TT  AGT
                                       AT  __
GAM906  HSPC189  3' TGGGGCTTCTGCGCTGTTGTT  95279          A    CA_
                                AGCAGCAGTG CAGGA   TCA
                                |||||||||| |||||   |||
                                TTGTTGTCGC GTCTT   GGT
                                     _    CGG
GAM906  HUMNPIIY20 3'  TGGACCGTTACTGCGCT     83349     A       A  A_
                                AGC GCAGTGAC GG  CA
                                ||| ||||||| ||  ||
                                TCG CGTCATTG CC  GT
                                  _       _ AG
GAM906  HYA22    3'  TGACATCCTGTCACTTCTGCT  19431      C        CA
                                AGCAG AGTGACAGGA  TCA
                                ||||| ||||||||||  |||
                                TCGTC TCACTGTCCT  AGT
                                   T        AC
GAM906  HYPH     3'  TGATGTTCAAAATTGCTGTT   94900         GACA
                                AGCAGCAGT    GGACATCA
                                |||||||||    ||||||||
                                TTGTCGTTA    CTTGTAGT
                                      AAA_
GAM906  ILKAP    5'  AGTGTCTGTCGCTGCTGC    47782           G   CA
                                GCAGCAGTGACAG ACAT
                                |||||||||||| ||||
                                CGTCGTCGCTGTC TGTG
                                       _   AG
GAM906  ITPK1    3'  TGGTGTCTGGGCTGTGCT    26416      G   GA  G
                                AGCA CAGT  CAG ACATCA
                                |||| ||||  ||| ||||||
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                                TCGT GTCG  GTC TGTGGT
                                  _   G_  _
GAM906  KIAA0057 3' GTGTTCTGTTTTGTT      24440      T
                                AGCAG GACAGGACAT
                                ||||| ||||||||||
                                TTGTT TTGTCTTGTG
                                  _
GAM906  KIAA0062 3' TGTCATTATTATTGTTGTT   70246          CAG_
                                AGCAGCAGTGA   GACA
                                ||||||||||   ||||
                                TTGTTGTTATT   CTGT
                                      ATTA
GAM906  KIAA0063 3' GAGGTTTTTTGTTGTTGTT   29626      TG    C  A
                                AGCAG  ACAGGA ATC
                                |||||  |||||| |||
                                TTGTT  TGTTTT TGG
                                   GT     T  AGG
GAM906  KIAA0121 3' TGTTGTTGTTACTGTT      72665          _
                                AGCAGTGACAG GACA
                                |||||||||| ||||
                                TTGTCATTGTT TTGT
                                      G
GAM906  KIAA0143 3' GGGTTTTTGTTACTGTT     64789           C  A
                                AGCAGTGACAGGA ATC
                                |||||||||||| |||
                                TTGTCATTGTTTT TGG
                                      _  GG
GAM906  KIAA0240 3' GTGTGTTTTGTTGTTATTGTT 92439      C TG       CA
                                AGCAG AG  ACAGGACAT
                                ||||| ||  |||||||||
                                TTGTT TT  TGTTTTGTG
                                   A  GT       TGT
GAM906  KIAA0247 3' TGTTTGTTGTTGGTGTT     28413     G  TG   G
                                AGCA CAG  ACAG ACA
                                |||| |||  |||| |||
                                TTGT GTT  TGTT TGT
                                  G  GT   _
GAM906  KIAA0252 3' TGGTGATTCTGTTTTGCTGCT 62801        T     _
                                AGCAGCAG GACAGGA CATCA
                                |||||||| ||||||| |||||
                                TCGTCGTT TTGTCTT GTGGT
                                     _     A
GAM906  KIAA0254 3' TGATGTTGGGATTGTTGCT   28603        GA  GG
                                AGCAGCAGT  CA  ACATCA
                                |||||||||  ||  ||||||
                                TCGTTGTTA  GT  TGTAGT
                                      GG  __
GAM906  KIAA0265 3' TGGTCGTGCTCTTTGTTGTTGC 69887       TG ____  G  ATCA
           T                   AGCAGCAG  A   CA GAC
                               ||||||||  |   || |||
```

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                              TCGTTGTT  T    GT CTG
                                   GT TCTC  G   GT
GAM906  KIAA0268 3' TGTATGTCTTGTCACTGTTGT  70005              _
                              GCAGCAGTGACAGGACAT CA
                              |||||||||||||||||| ||
                              TGTTGTCACTGTTCTGTA GT
                                        T
GAM906  KIAA0275 3' TGTTTGTTTGTTGCTGTT    28689        TG CA
                              AGCAGCAG  A  GGACA
                              ||||||||  |  |||||
                              TTGTCGTT  T  TTTGT
                                   GT TG
GAM906  KIAA0276 3' TGATTATGTGTATATTGCTGTT 70969          _  GGAC
                              AGCAGCAGTG ACA    ATCA
                              |||||||||| |||    ||||
                              TTGTCGTTAT TGT    TAGT
                                    A   GTAT
GAM906  KIAA0310 3' GAGCCCTGACGCTGCTGTT   81677          A    ACA  A
                              AGCAGCAGTG CAGG   TC
                              |||||||||| ||||   ||
                              TTGTCGTCGC GTCC   AG
                                    A   CG_  G
GAM906  KIAA0329 3' TGGTGTTTAACTAATGCTGCT  29281        GTGACA
                              AGCAGCA     GGACATCA
                              |||||||     ||||||||
                              TCGTCGT     TTTGTGGT
                                  AATCAA
GAM906  KIAA0332 3' TGGGAATGTGCTGCTGTT    62706         G   GGACA
                              AGCAGCAGT ACA     TCA
                              ||||||||| |||     |||
                              TTGTCGTCG TGT     GGT
                                    _  AAG__
GAM906  KIAA0336 3' TGGTGTCTTTCCAGGCTCT   27590    C   AG  AC
                              AG AGC  TG  AGGACATCA
                              || |||  ||  |||||||||
                              TC TCG  AC  TTCTGTGGT
                               _  G_  CT
GAM906  KIAA0376 3' TGAGTTGTGTTTTTGTTGCT  65604        T   G   A
                              AGCAGCAG GACA GAC TCA
                              |||||||| |||| ||| |||
                              TCGTTGTT TTGT TTG AGT
                                   T   G  _
GAM906  KIAA0436 3' TGATAGTTGTTATTGTGGTT  60059     A        GAC
                              AGC GCAGTGACAG   ATCA
                              ||| ||||||||||   ||||
                              TTG TGTTATTGTT   TAGT
                                G        GA_
GAM906  KIAA0438 3' TGATGTATATAGTCACTGTTGT 29073           AGG__
                              GCAGCAGTGAC    ACATCA
                              ||||||||||     ||||||
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                                TGTTGTCACTG    TGTAGT
                                      ATATA
GAM906  KIAA0469 3' TGGATGTCATTGCTGT     29359          GGA
                                GCAGCAGTGACA   CA
                                ||||||||||||  ||
                                TGTCGTTACTGT   GT
                                      AG_
GAM906  KIAA0471 3' TGATGTTTTCAATGCT     29403     G   CA
                                AGCA TGA  GGACATCA
                                |||| |||  ||||||||
                                TCGT ACT  TTTGTAGT
                                  A  __
GAM906  KIAA0471 3' TCTTTCATTGTTGTT      29401          C
                                AGCAGCAGTGA AGGA
                                |||||||||| ||||
                                TTGTTGTTACT TTCT

                                      _
GAM906  KIAA0513 3' TGATGTTCTACAAACTCTGTT  28382      C   GAC_
                                AGCAG AGT    AGGACATCA
                                ||||| |||    |||||||||
                                TTGTC TCA    TCTTGTAGT
                                   _  AACA
GAM906  KIAA0514 3' GGCCAGTTCTGTTGCTGTGGCT 28089     A    TG     ATCA
                                AGC GCAG  ACAGGAC
                                ||| ||||  |||||||
                                TCG TGTC  TGTCTTG
                                  G   GT      ACCGGG
GAM906  KIAA0514 5' TGGTGTCTTGTCACTGC     28098
                                GCAGTGACAGGACATCA
                                ||||||||||||||||
                                CGTCACTGTTCTGTGGT

GAM906  KIAA0530 3' TGGTGAGCCCACTGTT      70868       ACA  A_
                                AGCAGTG   GG  CATCA
                                |||||||   ||  |||||
                                TTGTCAC   CC  GTGGT
                                    ___  GA
GAM906  KIAA0537 3' TGATGTCTGCCTTGCTCT    29261    C    TGACA
                                AG AGCAG    GGACATCA
                                || |||||    ||||||||
                                TC TCGTT    TCTGTAGT
                                  _    CCG__
GAM906  KIAA0537 3' TGGTGTTTTGGCTTATGC    29263     GC   GA
                                GCA  AGT  CAGGACATCA
                                |||  |||  ||||||||||
                                CGT  TCG  GTTTTGTGGT
                                  AT  __
GAM906  KIAA0546 3' TTTTGTTGTTGTTGTT      71316        TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
```

```
                                TTGTTGTT  TGTTTT
                                    GT
GAM906  KIAA0546 3' TTTTTTTTTTGTTGTTGTTGTT 71318       TG     CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT     TTTTTTG
GAM906  KIAA0555 5' TGATGCTGCTGCTGCTGCTGCT 60117        GA   GA_
                                AGCAGCAGT  CAG   CATCA
                                |||||||||  |||   |||||
                                TCGTCGTCG  GTC   GTAGT
                                     TC   GTC
GAM906  KIAA0570 3' TGGTGAGTTGGGCTCATTGCTG 28181         ___   GA
          TT                    AGCAGCAGTGA   CAG  CATCA
                                ||||||||||   |||  |||||
                                TTGTCGTTACT   GTT  GTGGT
                                      CGG   GA
GAM906  KIAA0664 3' TGGTCTGGCTGCTGCT     64289        GA   GA
                                AGCAGCAGT  CAG  CA
                                |||||||||  |||  ||
                                TCGTCGTCG  GTC  GT
                                    __   TG
GAM906  KIAA0673 3' GTTATCGCTGTTGCT      62271         CAG
                                AGCAGCAGTGA   GAC
                                ||||||||||   |||
                                TCGTTGTCGCT   TTG
                                      A__
GAM906  KIAA0716 3' TGTTCATGTTGGTTGCTGCT   28169       GT_   _    TCA
                                AGCAGCA   GACA GGACA
                                |||||||   |||| |||||
                                TCGTCGT   TTGT CTTGT
                                    TGG    A
GAM906  KIAA0721 3' TGATGTTTACAGGCCTGCT   95976      _ AG  ACA
                                AGCAG C  TG   GGACATCA
                                ||||| |  ||   ||||||||
                                TCGTC G  AC   TTTGTAGT
                                   C G_  A__
GAM906  KIAA0721 3' TGATGTTTACAGGCCTGCT   41348      _ AG  ACA
                                AGCAG C  TG   GGACATCA
                                ||||| |  ||   ||||||||
                                TCGTC G  AC   TTTGTAGT
                                   C G_  A__
GAM906  KIAA0738 3' CATCTTGTTATTGTTGCT    28217            CATCA
                                AGCAGCAGTGACAGGA
                                ||||||||||||||||
                                TCGTTGTTATTGTTCT
                                          ACT
GAM906  KIAA0738 3' TGTTATTGTTGCTGTTGTT   28222        TG   _    TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
```

```
                                TTGTTGTC  TGTT TTGT
                                    GT    A
GAM906  KIAA0738 3' AAAATTTCTTGTTATTGTTGCT 28213              CATCA
                                AGCAGCAGTGACAGGA
                                ||||||||||||||||
                                TCGTTGTTATTGTTCT
                                        TTAAAAA
GAM906  KIAA0738 3' TCTTGTTATTGTTGCT      28220
                                AGCAGCAGTGACAGGA
                                ||||||||||||||||
                                TCGTTGTTATTGTTCT

GAM906  KIAA0757 3' TGTTTTGTTTTGTTGTT     20137         T        TCA
                                AGCAGCAG GACAGGACA
                                |||||||| |||||||||
                                TTGTTGTT TTGTTTTGT
                                    _          A
GAM906  KIAA0757 3' TTTTGTTTTGTTTTGTTGTT   20138         T        TCA
                                AGCAGCAG GACAGGACA
                                |||||||| |||||||||
                                TTGTTGTT TTGTTTTGT
                                    _        TTTG
GAM906  KIAA0826 3' TGGTGTTCTGGTACTGT     82643        A
                                GCAGTG CAGGACATCA
                                |||||| ||||||||||
                                TGTCAT GTCTTGTGGT
                                   G
GAM906  KIAA0826 3' TGCCATGCACTGTTGTT     82642          A _ A
                                AGCAGCAGTG CA GG CA
                                |||||||||| || || ||
                                TTGTTGTCAC GT CC GT
                                    _ A _
GAM906  KIAA0836 3' GATTTCCTTGCTGTT       64563        GTGAC    C
                                AGCAGCA     AGGA ATC
                                |||||||     |||| |||
                                TTGTCGT     TCCT TAG
                                    _____    T
GAM906  KIAA0843 3' AAGGGCTTTTGTTATTGTTGTT 30108              CA  A
                                AGCAGCAGTGACAGGA  TC
                                ||||||||||||||||  ||
                                TTGTTGTTATTGTTTT  GG
                                        CG  AAG
GAM906  KIAA0876 3' TGTTTTTTTGTTGTTGTT     64684         TG C     TCA
                                AGCAGCAG  A AGGACA
                                ||||||||  | ||||||
                                TTGTTGTT  T TTTTGT
                                    GT T
GAM906  KIAA0876 3' CGCTGTTTTTTTGTTGTTGTT  64678         TG C     TCA
                                AGCAGCAG  A AGGACA
                                ||||||||  | ||||||
```

```
                                TTGTTGTT  T TTTTGT
                                    GT T     CGCT
GAM906  KIAA0977 3' TGGTGTTCTGTCCCTACT    29751    C  T
                                AG AG GACAGGACATCA
                                || || ||||||||||||
                                TC TC CTGTCTTGTGGT
                                 A  C
GAM906  KIAA0981 3' TGGGAATCCTGTCATGTTGTT  61427       G      CA_
                                AGCAGCA TGACAGGA   TCA
                                ||||||| ||||||||   |||
                                TTGTTGT ACTGTCCT   GGT
                                   _      AAG
GAM906  KIAA1012 3' TGACTTGTCATTTTGTT     30060      C       A
                                AGCAG AGTGACAGG CA
                                ||||| ||||||||| ||
                                TTGTT TTACTGTTC GT
                                   _       A
GAM906  KIAA1017 5' TGATGATTATGTTGCTGTAGCT 23305     A   TG  G _
                                AGC GCAG  ACA GA CATCA
                                ||| ||||  ||| || |||||
                                TCG TGTC  TGT TT GTAGT
                                  A   GT   A A
GAM906  KIAA1034 3' TGTTTGTTGTTGCTGTT     62474        TG   G
                                AGCAGCAG  ACAG ACA
                                ||||||||  |||| |||
                                TTGTCGTT  TGTT TGT
                                    GT   _
GAM906  KIAA1034 3' TGTTTGTTGTTGCTGTT     62475        TG   G
                                AGCAGCAG  ACAG ACA
                                ||||||||  |||| |||
                                TTGTCGTT  TGTT TGT
                                    GT   _
GAM906  KIAA1041 3' TCTCTGTACTGCTGTT      30142         A  _
                                AGCAGCAGTG CAG GA
                                |||||||||| ||| ||
                                TTGTCGTCAT GTC CT
                                    _  T
GAM906  KIAA1052 3' TGATGTTTGTTCCGTTGTT   30253       AGT    G
                                AGCAGC   GACAG ACATCA
                                ||||||   ||||| ||||||
                                TTGTTG   TTGTT TGTAGT
                                   CC_    _
GAM906  KIAA1068 3' TGCTCTCTGCTTGCTGTTGTT 31041        TG _  _ CATCA
                                AGCAGCAG  A CAG GA
                                ||||||||  | ||| ||
                                TTGTTGTC  T GTC CT
                                    GT C   T  CGT
GAM906  KIAA1140 5' TGGTGCTGCTGCTGCTGCT   62777        GA   G  ATCA
                                AGCAGCAGT  CAG AC
                                |||||||||  ||| ||
```

```
                                TCGTCGTCG  GTC TG
                                     TC   G  GT
GAM906  KIAA1140 5' GGAGCTGCTGGTGCTGCTGCT  62775        GA   GACA  A
                                AGCAGCAGT  CAG   TC
                                |||||||||  |||   ||
                                TCGTCGTCG  GTC   AG
                                     TG   GTCG  GG
GAM906  KIAA1184 3' TGGTGTCCTGAGACTCTGC   42619     C   GA
                                GCAG AGT  CAGGACATCA
                                |||| |||  ||||||||||
                                CGTC TCA  GTCCTGTGGT
                                  _  GA
GAM906  KIAA1185 3' TGATGTTCAGTCATGCTGCT  62611       G    A
                                AGCAGCA TGAC GGACATCA
                                ||||||| |||| ||||||||
                                TCGTCGT ACTG CTTGTAGT
                                   _   A
GAM906  KIAA1198 3' TGGTGTCTCACTCTGTTGC   63343       TGACA
                                GCAGCAG    GGACATCA
                                |||||||    ||||||||
                                CGTTGTC    TCTGTGGT
                                    TCAC_
GAM906  KIAA1199 3' TGTCCTCCTTGTTATTTCTGTT 72521      C     ____    TCA
                                AGCAG AGTGACA    GGACA
                                ||||| |||||||    |||||
                                TTGTC TTATTGT    CCTGT
                                  T      TCCT       A
GAM906  KIAA1219 3' GAGGTAATTTGACACTGCTGCT 61367         A   AC   A
                                AGCAGCAGTG CAGG  ATC
                                |||||||||| ||||  |||
                                TCGTCGTCAC GTTT  TGG
                                     A   AA   AGG
GAM906  KIAA1229 3' TGATGTTTTGTTAAACCTG   62070    CAG
                                CAG   TGACAGGACATCA
                                |||   ||||||||||||
                                GTC   ATTGTTTTGTAGT
                                  CAA
GAM906  KIAA1266 3' TGGCATGTCACTGTGGTT    66129    A       GGA
                                AGC GCAGTGACA   CA
                                ||| |||||||||   ||
                                TTG TGTCACTGT   GT
                                  G        ACG
GAM906  KIAA1266 3' TGGTGTTCTGCCCGGCTCT   66130    C   AGTGA
                                AG AGC    CAGGACATCA
                                || |||    ||||||||||
                                TC TCG    GTCTTGTGGT
                                 _  GCCC_
GAM906  KIAA1266 3' TGGTGTTTATGCCCCACTGCTG 66131        A__  _
           T                     GCAGCAGTG   CA GGACATCA
                                 |||||||||   || ||||||||
```

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                                TGTCGTCAC  GT TTTGTGGT
                                     CCC  A
GAM906  KIAA1376 3' TACTTATTTTGTTGTTGTTGTT 63624       TG    CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT    ATTCATG
GAM906  KIAA1376 3' TTTGTTGTTGTTGTTGTTGTT  63626       TG  _  TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                    GT   G   TT
GAM906  KIAA1384 3' TGTCAACTGTCACTGTTTCT  64580   C       __  TCA
                                AG AGCAGTGACAG  GACA
                                || ||||||||||  ||||
                                TC TTGTCACTGTC  CTGT
                                 T        AA
GAM906  KIAA1396 3' TGGTGTCTTTCTATGTTGC   62996     GT  C
                                GCAGCA  GA AGGACATCA
                                ||||||  || |||||||||
                                CGTTGT  CT TTCTGTGGT
                                   AT  _
GAM906  KIAA1437 3' TGGTGTCTTGTTTTCT    60596   T_
                                AG  GACAGGACATCA
                                ||  ||||||||||||
                                TC  TTGTTCTGTGGT
                                 TT
GAM906  KIAA1449 3' TGATGTCCTGGCTTTGT    40454    TGA
                                GCAG   CAGGACATCA
                                ||||   ||||||||||
                                TGTT   GTCCTGTAGT
                                  TCG
GAM906  KIAA1458 3' TGATGACAGTTGTATTGTTGCT 69006        A  GA__
                                AGCAGCAGTG CAG   CATCA
                                |||||||||| |||   |||||
                                TCGTTGTTAT GTT   GTAGT
                                      _  GACA
GAM906  KIAA1467 3' TGATGTCCTTATCCTGCTGT  71618      T  C_
                                GCAGCAG GA  AGGACATCA
                                |||||||  ||  |||||||||
                                TGTCGTC CT  TCCTGTAGT
                                   _  AT
GAM906  KIAA1486 3' TGGTGAAACTTTCTTTGCTGTT 67386       T  C  GA_
                                AGCAGCAG GA AG   CATCA
                                |||||||| || ||   |||||
                                TTGTCGTT CT TC   GTGGT
                                     T  T  AAA
GAM906  KIAA1576 3' TGTTGATCACTGTTGTT    65905         CAG
                                AGCAGCAGTGA   GACA
                                ||||||||||   ||||
```

```
                                TTGTTGTCACT  TTGT
                                      AG_
GAM906  KIAA1594  3'  GGAGCTGTTTTGTTGTTGTTGT 72084       TG      TCA
          T                    AGCAGCAG  ACAGGACA
                               ||||||||  ||||||||
                               TTGTTGTT  TGTTTTGT
                                   GT       CGAGGA
GAM906  KIAA1610  3'  TGTACATTCACTGTTGTT    67159         CAGG
                               AGCAGCAGTGA   ACA
                               ||||||||||   |||
                               TTGTTGTCACT   TGT
                                      TACA
GAM906  KIAA1615  3'  TGATGTTTGTATTATTGCTCT  68738   C      CA_
                               AG AGCAGTGA  GGACATCA
                               || ||||||||  ||||||||
                               TC TCGTTATT  TTTGTAGT
                                _      ATG
GAM906  KIAA1655  5'  TGGTGGACTTCCTGCTGCT   66636       T  C  GA
                               AGCAGCAG GA AG  CATCA
                               |||||||| || ||  |||||
                               TCGTCGTC CT TC  GTGGT
                                   _ _  AG
GAM906  KIAA1674  3'  TGCCATTGATGCTGTTGCT   68796        A  __  A
                               AGCAGCAGTG CA  GG CA
                               |||||||||| ||  || ||
                               TCGTTGTCGT GT  CC GT
                                     A  TA  _
GAM906  KIAA1674  3'  TGTTCATTGTTATTTGTTGCT  68798       _    __    TCA
                               AGCAGCAG TGACA  GGACA
                               |||||||| |||||  |||||
                               TCGTTGTT ATTGT  CTTGT
                                    T    TA
GAM906  KIAA1691  3'  TGTACTGTCGCTGTGTT    92566     G       G
                               AGCA CAGTGACAG ACA
                               |||| ||||||||| |||
                               TTGT GTCGCTGTC TGT
                                 _       A
GAM906  KIAA1712  3'  TGGAGTTTCGCTGTTGTT    67543         CAG   AT
                               AGCAGCAGTGA   GAC  CA
                               ||||||||||   |||  ||
                               TTGTTGTCGCT   TTG  GT
                                     ___   AG
GAM906  KIAA1715  3'  TGATGTCAGTTATTGCT    68128        AG
                               AGCAGTGAC  GACATCA
                               |||||||||  |||||||
                               TCGTTATTG  CTGTAGT
                                     A_
GAM906  KIAA1786  3'  TGATGAACTGCTGTTG     66041       TGA   GA
                               CAGCAG   CAG  CATCA
                               ||||||   |||  |||||
```

```
                                GTTGTC  GTC  GTAGT
                                   ___  AA
GAM906  KIAA1795 3' GTTTTTTTTTGTTGTTGTTGTT 72155       TG    CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT    TTTTTGT
GAM906  KIAA1798 3' GTTTTTTGTTGCTGTT     60623       TG C
                                AGCAGCAG  A AGGAC
                                ||||||||  | |||||
                                TTGTCGTT  T TTTTG
                                    GT _
GAM906  KIAA1858 3' GTCTTGCTGCTGTTGCT    67136       GA
                                AGCAGCAGT  CAGGAC
                                |||||||||  ||||||
                                TCGTTGTCG  GTTCTG
                                    TC
GAM906  KIAA1877 3' TGTTGTTGTTGTTGTTGTTGTT 66185       TG  _  T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                    GT   G   T
GAM906  KIAA1877 3' TGTTGTTGTTGTTGTTGTTGTT 66180       TG  _  T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                    GT   G   T
GAM906  KIAA1877 3' TGTTGTTGTTGTTGTTGTTGTT 66183       TG  _  T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                    GT   G   T
GAM906  KIAA1877 3' TGTTGTTGTTGTTGTTGTTGTT 66184       TG  _  T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                    GT   G   T
GAM906  KIAA1877 3' TGTTGTTGTTGTTGTTGTTGTT 66182       TG  _  T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                    GT   G   T
GAM906  KIAA1877 3' TGTTGTTGTTGTTGTTGTTGTT 66181       TG  _  T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                    GT   G   T
GAM906  KIAA1877 3' TGTTGTTGTTGTTGTTGTTGTT 66186       TG  _  T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
```

```
                                TTGTTGTT  TGTT TTGT GT
                                    GT   G   T
GAM906  KIAA1877 3'  TGTTGTTGTTGTTGTTGTTGTT 66187       TG   _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                    GT   G   T
GAM906  KIAA1912 3'  TCTCTGTTGTTGTTGTT    73367       TG   _
                                AGCAGCAG  ACAG GA
                                ||||||||  |||| ||
                                TTGTTGTT  TGTC CT
                                    GT   T
GAM906  KIAA1915 5'  GATGTCTTTTAGTGTT     73281     G   C
                                AGCA TGA AGGACATC
                                |||| ||| ||||||||
                                TTGT ATT TTCTGTAG
                                  G  _
GAM906  KIAA1946 3'  TGTATTTATTGCTGTT     82474         CAGG
                                AGCAGCAGTGA   ACA
                                ||||||||||   |||
                                TTGTCGTTATT   TGT
                                     TA__
GAM906  KLK11    3'  TGGTGTTTGGTTCCTGTT    58616      TG  AG
                                AGCAG  AC  GACATCA
                                |||||  ||  |||||||
                                TTGTC  TG  TTGTGGT
                                   CT  GT
GAM906  KLK7     3'  TGAGACAGAGTCTCTGTTGCT  17300       T   AGGACA
                                AGCAGCAG GAC     TCA
                                |||||||| |||     |||
                                TCGTTGTC CTG     AGT
                                    T   AGACAG
GAM906  KLK7     3'  TGAGACAGAGTCTCTGTTGCT  57740       T   AGGACA
                                AGCAGCAG GAC     TCA
                                |||||||| |||     |||
                                TCGTTGTC CTG     AGT
                                    T   AGACAG
GAM906  KRTAP4-7 3'  GTTTTGTCACTGATGTT     52343     G
                                AGCA CAGTGACAGGAC
                                |||| ||||||||||||
                                TTGT GTCACTGTTTTG
                                  A
GAM906  LAT1-3TM 3'  TGGTGTTTTGCTCGGCAGCT   48316    A  AG  _
                                AGC GC  TGA CAGGACATCA
                                ||| ||  ||| ||||||||||
                                TCG CG  GCT GTTTTGTGGT
                                  A  __  C
GAM906  LATS1    3'  GATGCCACCTGTTGCT      60276        TGACA  A
                                AGCAGCAG    GG CATC
                                ||||||||    || ||||
```

```
                                TCGTTGTC    CC GTAG
                                    CA___  _
GAM906  LBP-9    3'  TGGTCTGTCACTCCTGCT    27283      C      GA
                                AGCAG AGTGACAG  CA
                                ||||| ||||||||  ||
                                TCGTC TCACTGTC  GT
                                   C       TG
GAM906  LHFPL2   3'  TGTATGTTTTGTTGTTTTGTT  69956      C  TG      _
                                AGCAG AG  ACAGGACAT CA
                                ||||| ||  |||||||||  ||
                                TTGTT TT  TGTTTTGTA GT
                                   _  GT       T
GAM906  LHX6     3'  TGGTTAACCTGTTATGTTGCT  26862       G      AC_
                                AGCAGCA TGACAGG   ATCA
                                |||||||  |||||||   ||||
                                TCGTTGT ATTGTCC   TGGT
                                   _      AAT
GAM906  LIP8     3'  TTTGTTCTCTCATTGTTGTT   88153         C     TCA
                                AGCAGCAGTGA AGGACA
                                ||||||||||| ||||||
                                TTGTTGTTACT TCTTGT
                                      C     TT
GAM906  LSM5     3'  TGGTTAACTGTCATTTTGTT   24640      C      GAC
                                AGCAG AGTGACAG   ATCA
                                ||||| ||||||||   ||||
                                TTGTT TTACTGTC   TGGT
                                   _      AAT
GAM906  MAGEE1   5'  TGATACGTTTACCTGCTGCT   32716       TGACA   __
                                AGCAGCAG    GGAC  ATCA
                                ||||||||    ||||  ||||
                                TCGTCGTC    TTTG  TAGT
                                    CA___    CA
GAM906  MANBAL   3'  TGATCAGTCACCTTTGTTGCTG 41981       TG CAG_  __
            CT                   AGCAGCAG  A    GAC  ATCA
                                |||||||| |    |||  ||||
                                TCGTCGTT  T    CTG  TAGT
                                    GT TCCA   AC
GAM906  MAP2K4   3'  TGATGTGATATTCTGTTGCT   11552       TGACAGG
                                AGCAGCAG      ACATCA
                                ||||||||      ||||||
                                TCGTTGTC      TGTAGT
                                    TTATAG_
GAM906  MARCKS   5'  TCCTGTGCTGCTGCT       9873         G
                                AGCAGCAGT ACAGGA
                                ||||||||| ||||||
                                TCGTCGTCG TGTCCT
                                          _
GAM906  MATR3    3'  TGTTAATGTCATGCTGTT    38117       G    G_
                                AGCAGCA TGACA  GACA
                                ||||||| |||||  ||||
```

```
                                TTGTCGT ACTGT  TTGT
                                   _    AA
GAM906  MED6    3'  TGATGGCTTTGTTGCAGCT   18438    A TG    A_
                                AGC G  ACAGG  CATCA
                                ||| |  |||||  |||||
                                TCG C  TGTTT  GTAGT
                                  A GT    CG
GAM906  MEF-2   3'  GTATGCTTGTTCCTGCTGCT  64392       TG    A   CA
                                AGCAGCAG  ACAGG CAT
                                ||||||||  ||||| |||
                                TCGTCGTC  TGTTC GTA
                                     CT    _  TGG
GAM906  MEGF10  3'  TGATTTGCCATTGCTGTT   50586        A   A
                                AGCAGCAGTG CAGG CA
                                |||||||||| |||| ||
                                TTGTCGTTAC GTTT GT
                                      C   A
GAM906  MESDC2  3'  TGATGTCTGATTTTGCCGTT  72501    A   TGACA
                                AGC GCAG    GGACATCA
                                ||| ||||    ||||||||
                                TTG CGTT    TCTGTAGT
                                  C   TTAG_
GAM906  MESDC2  3'  TGATGTGCTACTGTTG     72502      GAC  G
                                CAGCAGT   AG ACATCA
                                |||||||   || ||||||
                                GTTGTCA   TC TGTAGT
                                    ___  G
GAM906  MFN1    3'  TGATGTTTTAAAAAAGCTGTTG 35546       GAC___
          TT                    AGCAGCAGT    AGGACATCA
                                |||||||||    |||||||||
                                TTGTTGTCG    TTTTGTAGT
                                     AAAAAA
GAM906  MFN1    3'  TGATGTTTTAAAAAAGCTGTTG 53204       GAC___
          TT                    AGCAGCAGT    AGGACATCA
                                |||||||||    |||||||||
                                TTGTTGTCG    TTTTGTAGT
                                     AAAAAA
GAM906  MGC10870 5' TGACTCAGTGCTGCTGCT   50209        ACAG  CA
                                AGCAGCAGTG   GA  TCA
                                ||||||||||   ||  |||
                                TCGTCGTCGT   CT  AGT
                                     GA__  C_
GAM906  MGC10871 3' TGGGGGTTTTGTTGTTTTGTT  94780     C  TG     A_
                                AGCAG AG  ACAGGAC  TCA
                                ||||| ||  |||||||  |||
                                TTGTT TT  TGTTTTG  GGT
                                   _ GT     GG
GAM906  MGC11082 5' TGACTCATTCATTGCTGTT   51103        CAG  CA
                                AGCAGCAGTGA   GA  TCA
                                ||||||||||   ||  |||
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```
                                TTGTCGTTACT  CT  AGT
                                      TA_  C_
GAM906  MGC12992  3'  TCACTGTTTACTGTTGTT   50346          _  _
                                AGCAGCAGTGA CAG GA
                                |||||||||| ||| ||
                                TTGTTGTCATT GTC CT
                                      T   A
GAM906  MGC14353  3'  TGATGTCCTGATTTGTTCT   51195   C    TGA
                                AG AGCAG   CAGGACATCA
                                || |||||   ||||||||||
                                TC TTGTT   GTCCTGTAGT
                                 _    TA_
GAM906  MGC14407  5'  TGATGGCATTTTGTTTGCTGTT 51881        TG _    ___
           GCT                    GCAGCAG  A CAGGA   CATCA
                                |||||||  | |||||   |||||
                                CGTTGTC  T GTTTT   GTAGT
                                    GT T    ACG
GAM906  MGC15606  3'  TTTTTTTTTTGTTGTTGTTGTT 58884        TG     CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT     TTTTTTT
GAM906  MGC15606  3'  TTTTGTTGTTGTTGTT     58883        TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT
GAM906  MGC15606  3'  TTTGTTGTTGTTGTTGTTGTT  58882        TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                    GT   G   TT
GAM906  MGC15634  5'  TTTTTGTTGTTGTTGTTGTT 51276        TG   _   TCA
           T                     AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                    GT   G   TTTTG
GAM906  MGC15634  5'  ATGTTTTGTTTTTGTTGTT   51271        T       TCA
                                AGCAGCAG GACAGGACA
                                |||||||| |||||||||
                                TTGTTGTT TTGTTTTGT
                                    T          AC
GAM906  MGC15634  5'  TTTTGTTTTGTTTTTGTTGTT  51275        T       TCA
                                AGCAGCAG GACAGGACA
                                |||||||| |||||||||
                                TTGTTGTT TTGTTTTGT
                                    T       TTTG
GAM906  MGC15634  5'  TGTTGTTGTTGTTGTTGTTGTT 51274        TG   _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
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```
                                TTGTTGTT  TGTT TTGT GT
                                    GT   G   T
GAM906  MGC16386 3' TGGTGTCCTGTCTCTTGT   54737    GC  T
                                GCA  AG GACAGGACATCA
                                |||  || ||||||||||||
                                TGT  TC CTGTCCTGTGGT
                                  __  T
GAM906  MGC19556 5' TGGAGTTCATTGTCCTGTTGCT 53232       T   __   AT
                                AGCAGCAG GACA  GGAC  CA
                                |||||||| ||||  ||||  ||
                                TCGTTGTC CTGT  CTTG  GT
                                    _   TA   AG
GAM906  MGC21738 3' TGATGCCTTATCTGCTGCT   58922       TGAC   A
                                AGCAGCAG   AGG CATCA
                                ||||||||   ||| |||||
                                TCGTCGTC   TCC GTAGT
                                    TAT_  _
GAM906  MGC22014 3' TGAGCTTTCTCAGTCATTGTTG 64500         __   CA_
          CT                   AGCAGCAGTGAC  AGGA   TCA
                               ||||||||||||  ||||   |||
                               TCGTTGTTACTG  TCTT   AGT
                                     AC   TCG
GAM906  MGC23937 3' TGGTGTTCTGAAATCTGCT   58957     TGA_
                               AGCAG   CAGGACATCA
                               |||||   ||||||||||
                               TCGTC   GTCTTGTGGT
                                 TAAA
GAM906  MGC2477  5' TGAGGAGCTGCTGCTGCT   44072       TGA  GACA
                               AGCAGCAG   CAG   TCA
                               ||||||||   |||   |||
                               TCGTCGTC   GTC   AGT
                                    ___  GAGG
GAM906  MGC2477  5' TGGTTTTGTTGTTGTTGTT   44074       TG    ATCA
                               AGCAGCAG  ACAGGAC
                               ||||||||  |||||||
                               TTGTTGTT  TGTTTTG
                                    GT     GT
GAM906  MGC26651 3' TGGTGTTTTGTGGCTCT    58307   C  G
                               AG AGT ACAGGACATCA
                               || ||| ||||||||||
                               TC TCG TGTTTTGTGGT
                                _  G
GAM906  MGC26954 3' TGTTGTTTATTGCTGCT    58841        CAG
                               AGCAGCAGTGA  GACA
                               ||||||||||  ||||
                               TCGTCGTTATT  TTGT
                                     TG_
GAM906  MGC2747  5' TGATGTTCTGCATGATTGT   44088    CA  A
                               GCAG  GTG CAGGACATCA
                               ||||  ||| ||||||||||
```

```
                                TGTT  TAC GTCTTGTAGT
                                  AG  _
GAM906  MGC2963  3' TGGTTGAATTCGCTGCTTGTT 48511     _     CAG_  ATCA
                                AGCA GCAGTGA   GAC
                                |||| |||||||   |||
                                TTGT CGTCGCT   TTG
                                  T      TAAG  GT
GAM906  MGC3035  5' TGGTGGCCTCACTGCTCT   44153   C      CA  A
                                AG AGCAGTGA  GG CATCA
                                || ||||||||  || |||||
                                TC TCGTCACT  CC GTGGT
                                 _      __ G
GAM906  MGC3279  5' TGGTGTCCTGCCTGCGCT   43816    A   TGA
                                AGC GCAG   CAGGACATCA
                                ||| ||||   ||||||||||
                                TCG CGTC   GTCCTGTGGT
                                  _   C__
GAM906  MGC4161  3' TGGTTTGTGTTGCTGTTCT   44191   C    TG  G  C
                                AG AGCAG  ACA GA ATCA
                                || |||||  ||| || ||||
                                TC TTGTC  TGT TT TGGT
                                 _    GT  G  _
GAM906  MGC4172  3' TGGTGTCCCTAATTGTT    44204      GACA
                                AGCAGT   GGACATCA
                                ||||||   ||||||||
                                TTGTTA   CCTGTGGT
                                   ATC_
GAM906  MGC4342  3' TGGTGTCTGTTGCTGT     44271     TG   G
                                GCAG  ACAG ACATCA
                                ||||  |||| ||||||
                                TGTC  TGTC TGTGGT
                                  GT   _
GAM906  MGC5370  3' TGATGTTCATCTGCAGCT    51228    A   TGACA
                                AGC GCAG    GGACATCA
                                ||| ||||    ||||||||
                                TCG CGTC    CTTGTAGT
                                  A   TA___
GAM906  MGC9753  5' TGGTGGTCTTGCTGCTGC    53059      TGA    _
                                GCAGCAG   CAGGAC ATCA
                                |||||||   |||||| ||||
                                CGTCGTC   GTTCTG TGGT
                                    ___     G
GAM906  MKNK1    3' TGGTGTTTTTAACCATGCTGT  13480      GTGAC_
                                GCAGCA     AGGACATCA
                                ||||||     |||||||||
                                TGTCGT     TTTTGTGGT
                                   ACCAAT
GAM906  MKNK1    3' TGTTTGTGATTGCTGCT     13482        G   G
                                AGCAGCAGT ACAG ACA
                                ||||||||| |||| |||
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```
                                TCGTCGTTA TGTT TGT
                                     G   _
GAM906  MKP-7    3'  TGTAAGTGTCGCTAGTTGCT  66423       _     GG_  TCA
                                AGCAGC AGTGACA  ACA
                                |||||| |||||||  |||
                                TCGTTG TCGCTGT  TGT
                                   A      GAA
GAM906  MKRN1    3'  TTTGTGTTTTGTTGCTCTGTT  25580      C  TG       CA
                                AGCAG AG  ACAGGACAT
                                ||||| ||  |||||||||
                                TTGTC TC  TGTTTTGTG
                                   _ GT       TTTC
GAM906  MMPL1    3'  GGTGTCCTGCTGTT       14720      TGA
                                AGCAG   CAGGACATC
                                |||||   |||||||||
                                TTGTC   GTCCTGTGG

                                  ___
GAM906  MO25     3'  TGGTGTCCTGGCTTTGT     32817     TGA
                                GCAG   CAGGACATCA
                                ||||   ||||||||||
                                TGTT   GTCCTGTGGT
                                  TCG
GAM906  MPPE1    5'  TGATGGATTTGTTGTTGCT   43564      TG    A_
                                AGCAG  ACAGG  CATCA
                                |||||  |||||  |||||
                                TCGTT  TGTTT  GTAGT
                                   GT    AG
GAM906  MPZL1    3'  TGTACCCATTGTCTTGCTGTT  14205        T   ___ _  TCA
                                AGCAGCAG GACA   GG ACA
                                |||||||| ||||   || |||
                                TTGTCGTT CTGT   CC TGT
                                     _   TAC  A
GAM906  MRPL1    3'  TGATGTCTTGTTATTG     39592
                                CAGTGACAGGACATCA
                                ||||||||||||||||
                                GTTATTGTTCTGTAGT

GAM906  MRPL20   3'  CCTAGTCGCTGCTGCT      35733          _
                                AGCAGCAGTGAC AGG
                                |||||||||||| |||
                                TCGTCGTCGCTG TCC
                                       A
GAM906  NCKX3    5'  TGGCCTCGGTGGCGCTGCTGCT 40356         AC____  A  TCA
                                AGCAGCAGTG     AGG CA
                                ||||||||||     ||| ||
                                TCGTCGTCGC     TCC GT
                                     GGTGGC   G    A
GAM906  NEDD5    3'  TGCCCTTCACTGTTGCT     15314          C   A
                                AGCAGCAGTGA AGG CA
                                |||||||||| ||| ||
```

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                                TCGTTGTCACT TCC GT
                                      _  C
GAM906  NEIL1    5'  TTTTGTTGTTGTTGTT     44831        TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT
GAM906  NEIL1    5'  TTTTGTTGTTGTTGTT     44830        TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT
GAM906  NEIL1    5'  TGGCTCGTCGCTGCTGTT    44829          AG A
                                AGCAGCAGTGAC  G CA
                                ||||||||||||  | ||
                                TTGTCGTCGCTG  C GT
                                      CT G
GAM906  NIN283   3'  TGATGTTTACAGCTTGCTGTT  50077       _ GACA
                                AGCAGCA GT    GGACATCA
                                |||||||  ||    ||||||||
                                TTGTCGT CG    TTTGTAGT
                                    T  ACA_
GAM906  NISCH    3'  CCAGTCCTTTGTTGCTGTT   23211        TG C    ATCA
                                AGCAGCAG  A AGGAC
                                ||||||||  | |||||
                                TTGTCGTT  T TCCTG
                                    GT _    ACCT
GAM906  NISCH    3'  TCCTTTGTTGCTGTTGCT    23215        TG  __
                                AGCAGCAG  ACA  GGA
                                ||||||||  |||  |||
                                TCGTTGTC  TGT  CCT
                                    GT   TT
GAM906  NISCH    3'  TTGCTGTTGCTGTTGCTGTTGC 23217        TG   _   TCA
          T                      AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TCGTTGTC  TGTC TTGT
                                    GT   G   CGTTG
GAM906  NISCH    3'  TTGCTGTTGCTGTTGCTGTTGC 23216        TG   _   TCA
          T                      AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TCGTTGTC  TGTC TTGT
                                    GT   G   CGTTG
GAM906  NISCH    3'  TTTGTTGCTGTTGCTGTTGCT  23218        TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TCGTTGTC  TGTC TTGT
                                    GT   G   TT
GAM906  NLI-IF   3'  TGGTGATGTCGTTGTGCT    41053     G      GGA
                                AGCA CAGTGACA   CATCA
                                ||||  ||||||||   |||||
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                                TCGT GTTGCTGT   GTGGT
                                  _      A__
GAM906  NLP_1    3'  TGATGTTTAAAATTGCT     23709       GACA
                                AGCAGT    GGACATCA
                                ||||||    ||||||||
                                TCGTTA    TTTGTAGT
                                   AAA_
GAM906  NPTXR    3'  TGATGTGTTTCTGTTATTGTT  54189           ___
                                AGCAGTGACAGG   ACATCA
                                ||||||||||||   ||||||
                                TTGTTATTGTCT   TGTAGT
                                       TTG
GAM906  NPTXR    3'  TGATGTGTTTCTGTTATTGTT  26653           ___
                                AGCAGTGACAGG   ACATCA
                                ||||||||||||   ||||||
                                TTGTTATTGTCT   TGTAGT
                                       TTG
GAM906  NRBF-2   5'  TGGTGAGGTTGTTGCTCCT    47761    C    TG  AGGA
                                AG AGCAG  AC    CATCA
                                || |||||  ||    |||||
                                TC TCGTT  TG    GTGGT
                                 C    GT  GA__
GAM906  NSG-X    3'  TGGTAGGCCTCACTGCTCT    26973    C      CA  AC_
                                AG AGCAGTGA  GG   ATCA
                                || ||||||||  ||   ||||
                                TC TCGTCACT  CC   TGGT
                                 _      __  GGA
GAM906  NTT5     3'  TGATGTCTACCAGTCCTGCT   25882      T   A___
                                AGCAG GAC    GGACATCA
                                ||||| |||    ||||||||
                                TCGTC CTG    TCTGTAGT
                                   _   ACCA
GAM906  NXN      3'  TGAGCTGTTGACACTGTTGTT  42428          ___    GACATCA
                                AGCAGCAGTG   ACAG
                                ||||||||||   ||||
                                TTGTTGTCAC   TGTC
                                      AGT    GAGT
GAM906  OATL1    3'  TTCTGTTTCTGTTGTT      70494         T
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
                                TTGTTGTC TTGTCTT
                                     T
GAM906  OAZIN    5'  TGGTGTCAAGTGGGCTGTTGCT 31876         G_  AG
                                AGCAGCAGT  AC  GACATCA
                                |||||||||  ||  |||||||
                                TCGTTGTCG  TG  CTGTGGT
                                      GG  AA
GAM906  OLFM3    5'  TGTTATTGCTACTGCTGCT    82149         A  _
                                AGCAGCAGTG CAG GACA
                                |||||||||| ||| ||||
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                                TCGTCGTCAT GTT TTGT
                                      C   A
GAM906  OR2C3    3'  TCCTTGCGTTGTTGTT      75449          AC
                                AGCAGCAGTG  AGGA
                                ||||||||||  ||||
                                TTGTTGTTGC  TCCT
                                      GT
GAM906  OSBPL2   3'  TTTTGTTACTGTTTCT      29226    C
                                AG AGCAGTGACAGGA
                                || ||||||||||||||
                                TC TTGTCATTGTTTT
                                 T
GAM906  OSBPL2   3'  TTTTGTTACTGTTTCT      57877    C
                                AG AGCAGTGACAGGA
                                || ||||||||||||||
                                TC TTGTCATTGTTTT
                                 T
GAM906  OSBPL3   3'  TGATGTTCTTGCTTTGT     31440     C  TG CA
                                GCAG AG  A  GGACATCA
                                |||| ||  |  ||||||||
                                TGTT TC  T  CTTGTAGT
                                  _  GT __
GAM906  P1P373C6 3'  TGATGTGGGGGGCTGCTGCT   38905         GACAGG
                                AGCAGCAGT     ACATCA
                                |||||||||     ||||||
                                TCGTCGTCG     TGTAGT
                                      GGGGG_
GAM906  P450RAI-2 3'  TGATGTTCTGAACTGCT     39106       GA
                                AGCAGT  CAGGACATCA
                                ||||||  ||||||||||
                                TCGTCA  GTCTTGTAGT
                                   A_
GAM906  PAI-RBP1 3'  AATACTTTTGTATTGCTGCT   31583          A    CATCA
                                AGCAGCAGTG CAGGA
                                |||||||||| |||||
                                TCGTCGTTAT GTTTT
                                      _    CATAAG
GAM906  PARG1    3'  CAGGGTTTTTTTGTTGTTGTT  16680         TG C    ATCA
                                AGCAGCAG  A AGGAC
                                ||||||||  | |||||
                                TTGTTGTT  T TTTTG
                                     GT T    GGACT
GAM906  PB1      3'  TGGTAGAGCTTCCACTGCTGTT 36371          AC  AC__
                                AGCAGCAGTG  AGG   ATCA
                                ||||||||||  |||   ||||
                                TTGTCGTCAC  TTC   TGGT
                                      C_  GAGA
GAM906  PCDH19   3'  TGATGACACTATTACTGTT   63710         C  GA_
                                AGCAGTGA AG   CATCA
                                |||||||| ||   |||||
```

```
                                TTGTCATT TC   GTAGT
                                     A  ACA
GAM906  PCNT2    3'  TGGCTTCCTGTTGTTTTGTT   20092      C  TG     CA
                                AGCAG AG  ACAGGA  TCA
                                ||||| ||  ||||||  |||
                                TTGTT TT  TGTCCT  GGT
                                  _ GT     TC
GAM906  PDIR     3'  TGATACCTGTTTTGTTGTT    22339        T     AC
                                AGCAGCAG GACAGG  ATCA
                                |||||||| ||||||  ||||
                                TTGTTGTT TTGTCC  TAGT
                                     _     A_
GAM906  PELI1    3'  TGATGTATCAGTAACTGCTGTT 40293         G  A  _
                                AGCAGCAGT AC GG ACATCA
                                ||||||||| || || ||||||
                                TTGTCGTCA TG CT TGTAGT
                                     A  A  A
GAM906  PELI2    3'  TGATATAGTCATTGTTGT    41186          AGGAC
                                GCAGCAGTGAC    ATCA
                                ||||||||||     ||||
                                TGTTGTTACTG    TAGT
                                      ATA__
GAM906  PELI2    3'  TACTCTTGATTGCTGCTGCT   41184        TG _    CATCA
                                AGCAGCAG  A CAGGA
                                ||||||||  | |||||
                                TCGTCGTC  T GTTCT
                                     GT A    CAT
GAM906  PFTK1    3'  TGTCAGCTGTCACTGTTGTT   24761            __    TCA
                                AGCAGCAGTGACAG  GACA
                                ||||||||||||||  ||||
                                TTGTTGTCACTGTC  CTGT
                                       GA
GAM906  PIPPIN   3'  GATGTGTGGCTGTTGCT     79696         G  AGG    A
                                AGCAGCAGT AC   ACATC
                                ||||||||| ||   |||||
                                TCGTTGTCG TG   TGTAG
                                     G ____    A
GAM906  PLPL     5'  TGGTGTCTGAGACAGTGTTGCT 39435        G  ACA_
                                AGCAGCA TG    GGACATCA
                                ||||||| ||    ||||||||
                                TCGTTGT AC    TCTGTGGT
                                    G  AGAG
GAM906  PM5      3'  GACCCTCCTGTCACTCTGCT   26596      C         CATCA
                                AGCAG AGTGACAGGA
                                ||||| ||||||||||
                                TCGTC TCACTGTCCT
                                  _        CCCAGG
GAM906  PMAIP1   3'  TGCATTGTTGTTGTTGCT    40893         TG   GA  TCA
                                AGCAGCAG  ACAG  CA
                                ||||||||  ||||  ||
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                                TCGTTGTT  TGTT  GT
                                    GT    AC
GAM906  PNMA1    3'  TGTTCTGTTTTGTTGTT     20074        T
                                AGCAGCAG GACAGGACA
                                |||||||| |||||||||
                                TTGTTGTT TTGTCTTGT
                                                _
GAM906  PNMA5    3'  TCTGCTCACTGCTGTT      73600          _
                                AGCAGCAGTGA CAGG
                                |||||||||||| ||||
                                TTGTCGTCACT GTCT
                                      C
GAM906  POLR2B   3'  TGGTGTCTTGTTTCTATTGT  6266      C  T
                                GCAG AG GACAGGACATCA
                                |||| || ||||||||||||
                                TGTT TC TTGTTCTGTGGT
                                  A  T
GAM906  POPX1    3'  TGATTAAAGTTACTGTTGC    29803          AGGAC
                                GCAGCAGTGAC    ATCA
                                ||||||||||     ||||
                                CGTTGTCATTG    TAGT
                                      AAAT_
GAM906  PORIMIN  3'  ATGTAGGTTTTTTTGTTGTTGT 53599        TG C    ATCA
          T                      AGCAGCAG  A AGGAC
                                ||||||||  | |||||
                                TTGTTGTT  T TTTTG
                                    GT T    GATGTAA
GAM906  PP1628   3'  TGTACTGTCACTTTGTT     47309      C       G
                                AGCAG AGTGACAG ACA
                                ||||| |||||||| |||
                                TTGTT TCACTGTC TGT
                                  _       A
GAM906  PP2447   5'  TGATGCAGATGCTGCTGCT   47323        GACAGGA
                                AGCAGCAGT      CATCA
                                |||||||||      |||||
                                TCGTCGTCG      GTAGT
                                     TAGAC__
GAM906  PPAP2B   5'  GGTGTGTGGCTGCTGTT     13546        G  AGG
                                AGCAGCAGT AC   ACATC
                                ||||||||| ||   |||||
                                TTGTCGTCG TG   TGTGG
                                     G ____
GAM906  PPP2R2A  3'  TGGTGTTCTCCATGTCTGCT  10748      CA   AC
                                AGCAG  GTG  AGGACATCA
                                |||||  |||  |||||||||
                                TCGTC  TAC  TCTTGTGGT
                                   TG   C_
GAM906  PPP4R1L  5'  TGGTGATATTTGTCATGCTGTT 79506       G      A__
                                AGCAGCA TGACAGG   CATCA
                                ||||||| |||||||   |||||
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                                TTGTCGT ACTGTTT  GTGGT
                                   _     ATA
GAM906  PRKCL2   3'  TGAGTTTTTTGTTGTTGTTGTT 20742       TG    CA_
                                AGCAGCAG  ACAGGA  TCA
                                ||||||||  ||||||  |||
                                TTGTTGTT  TGTTTT  AGT
                                   GT     TTG
GAM906  PRO0082  3'  GTTTACTTTTGTTCCTGTTGTT 37736       TG    CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTC  TGTTTT
                                   CT     CATTTGA
GAM906  PRO0233  3'  TGGTGTCCACTTTGATTGCT  26118     _  TGACA
                                AGCAG CAG    GGACATCA
                                |||||  |||    ||||||||
                                TCGTT GTT    CCTGTGGT
                                   A  TCA__
GAM906  PRO0529  5'  TTTTCTCATTGCTGCT     26004         C
                                AGCAGCAGTGA AGGA
                                |||||||||||  ||||
                                TCGTCGTTACT TTTT
                                      C
GAM906  PRO1598  5'  AAGTGCCCTTTGCTGCTGCT  37535       TG C  A  CA
                                AGCAGCAG  A AGG CAT
                                ||||||||  |  ||| |||
                                TCGTCGTC  T TCC GTG
                                   GT _  C  AAG
GAM906  PRO1635  3'  TGATGTTCTGTTATGTT    37731     G
                                AGCA TGACAGGACATCA
                                ||||  ||||||||||||
                                TTGT ATTGTCTTGTAGT
                                  _
GAM906  PTDSS1   3'  TTTGGTTACTGTTGTT     28573         AG
                                AGCAGCAGTGAC  GA
                                ||||||||||||  ||
                                TTGTTGTCATTG  TT
                                      GT
GAM906  PTPNS1   3'  TGGTGTTTTGTTTTGTT    55003     T
                                AGCAG GACAGGACATCA
                                |||||  ||||||||||||
                                TTGTT TTGTTTTGTGGT
                                  _
GAM906  PXR2b    3'  TGGAGTTTTGTTTTGTTGCT  33341       T     AT
                                AGCAGCAG GACAGGAC  CA
                                ||||||||  ||||||||  ||
                                TCGTTGTT TTGTTTTG  GT
                                   _     AG
GAM906  RAB40A   5'  GTTTTGTTATTTTGTT     82071     C
                                AGCAG AGTGACAGGAC
                                |||||  ||||||||||
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```
                                TTGTT TTATTGTTTTG
                                   _
GAM906  RBBP4    3'  ATGGTGTTTTTTTTTTTGTTGT 18824        T_  C
                T                   AGCAGCAG  GA AGGACATCA   T
                                    ||||||||  || |||||||||   |
                                    TTGTTGTT  TT TTTTGTGGT   A
                                        TT  T
GAM906  RES4-25  3'  TGTAGAATTTACTGTTGTT    64654          CAGG_
                                    AGCAGCAGTGA     ACA
                                    ||||||||||     |||
                                    TTGTTGTCATT     TGT
                                          TAAGA
GAM906  RFX4     3'  GTACACATTCTGTATGCTGCTG 11318          _     CATCA
                TT                   AGCAGCAGTG ACAGGA
                                    |||||||||| ||||||
                                    TTGTCGTCGT TGTCTT
                                          A     ACACATGG
GAM906  RGS12    3'  TGGTGTCCTGAGAGGCTCT    11335    C   AGTGA
                                    AG AGC     CAGGACATCA
                                    || |||     ||||||||||
                                    TC TCG     GTCCTGTGGT
                                     _  GAGA_
GAM906  RHOBTB1  3'  TGGTGTTCGGATTGCTGT    91443        GACA
                                    GCAGCAGT    GGACATCA
                                    ||||||||    ||||||||
                                    TGTCGTTA    CTTGTGGT
                                        GG__
GAM906  RICH1    3'  TTTTGTCCCTGCTGTT      36008         T
                                    AGCAGCAG GACAGGA
                                    |||||||| |||||||
                                    TTGTCGTC CTGTTTT
                                        C
GAM906  RNAC     3'  TGGAGTCTGTTACTGTTCT    19315    C        G  AT
                                    AG AGCAGTGACAG AC  CA
                                    || ||||||||||| ||  ||
                                    TC TTGTCATTGTC TG  GT
                                     _         _  AG
GAM906  RNF24    3'  TGGTGTCTGTATGGCTGCT    23322       AGTG    G
                                    AGCAGC    ACAG ACATCA
                                    ||||||    |||| ||||||
                                    TCGTCG    TGTC TGTGGT
                                       GTA_   _
GAM906  RNF8     3'  TCCTGCTTGCTGCTGCT      14243         TG _
                                    AGCAGCAG  A CAGGA
                                    ||||||||  | |||||
                                    TCGTCGTC  T GTCCT
                                        GT C
GAM906  RNF8     3'  TGTTGTTGTTACTGTT      14246           _
                                    AGCAGTGACAG GACA
                                    |||||||||| ||||
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                                TTGTCATTGTT TTGT
                                      G
GAM906  RPC32   3' AAGATCTTGTTTCTGTTGTT  21333       T     CATCA
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
                                TTGTTGTC TTGTTCT
                                     T      AGAAT
GAM906  RRN3    3' GGTTTTTTTTGTTGTTGTTGTT 37358       TG    CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                     GT     TTTTGGG
GAM906  SART3   3' TGGTGTCCTGAGATAGTT   28172     A  GA
                                AGC GT  CAGGACATCA
                                ||| ||  ||||||||||
                                TTG TA  GTCCTGTGGT
                                  A  GA
GAM906  SCYA11  3' TGAAAATGTCATTGTTCT   11456    C       GGACA
                                AG AGCAGTGACA    TCA
                                || ||||||||||    |||
                                TC TTGTTACTGT    AGT
                                 _       AAA__
GAM906  SCYA4   3' TGGTCCACTGTCACTGTTTCT  11448    C       __   ATCA
                                AG AGCAGTGACA  GGAC
                                || ||||||||||  ||||
                                TC TTGTCACTGT  CCTG
                                 T       CA   GT
GAM906  SEC22C  3' TGATGTCAAACTTCTGCTGCT  14853       TGACAG
                                AGCAGCAG     GACATCA
                                ||||||||     |||||||
                                TCGTCGTC     CTGTAGT
                                     TTCAAA
GAM906  SEC24D  3' GAAACTTCTCTGTCATTGATGT 29093      G       _ CATCA
           T                     AGCA CAGTGACAG GA
                                ||||  |||||||||  ||
                                TTGT GTTACTGTC CT
                                  A       T  TCAAAGT
GAM906  SENP2   3' GTCATTTACTGCTGCT      76345          CAG
                                AGCAGCAGTGA   GAC
                                ||||||||||   |||
                                TCGTCGTCATT   CTG
                                      TA_
GAM906  SEPW1   3' TGATGTTCTCGTGGCTGCTGTT 11543         G _
                                AGCAGCAGT AC AGGACATCA
                                ||||||||| || |||||||||
                                TTGTCGTCG TG TCTTGTAGT
                                     G  C
GAM906  Sfmbt   3' TGCTTCATTGTCATTGTGTT  32899      G       _ CATCA
                                AGCA CAGTGACAG GA
                                |||| |||||||| ||
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                                TTGT GTTACTGTT CT
                                  _       A  TCGT
GAM906  SHANK3   3'  GAATCGTCCTGTTTGCTGTTGC 65497        TG _     ATCA
            T                    AGCAGCAG  A CAGGAC
                                 ||||||||  | ||||||
                                 TCGTTGTC  T GTCCTG
                                     GT T     CTAAGT
GAM906  SHANK3   3'  TGGTGAATCCCTGCTGCT    65506        TGACA  __
                                 AGCAGCAG    GGA  CATCA
                                 ||||||||    |||  |||||
                                 TCGTCGTC    CCT  GTGGT
                                     _____  AA
GAM906  SLC17A6  3'  TGGACTGTCATTTTGTT     39748      C       GA
                                 AGCAG AGTGACAG  CA
                                 ||||| ||||||||  ||
                                 TTGTT TTACTGTC  GT
                                   _       AG
GAM906  SLC21A11  5'  GATGTACTTGCTGCT       64467       GTGAC  G
                                 AGCAGCA     AG ACATC
                                 |||||||     || |||||
                                 TCGTCGT     TC TGTAG
                                     _____  A
GAM906  SLC26A10  5'  GTCCTGTCGGTGCTGCT     56033        G
                                 AGCAGCA TGACAGGAC
                                 ||||||| |||||||||
                                 TCGTCGT GCTGTCCTG
                                     G
GAM906  SMAP1    3'  TCACTGTGCTGTTGTT      41654         G   _
                                 AGCAGCAGT ACAG GA
                                 ||||||||| |||| ||
                                 TTGTTGTCG TGTC CT
                                     _   A
GAM906  SNRK     3'  TGGTGTCTTACTCCTTTGTT   34772      C  T  C_
                                 AGCAG AG GA  AGGACATCA
                                 ||||| || ||  |||||||||
                                 TTGTT TC CT  TTCTGTGGT
                                   _ _  CA
GAM906  SOX17    3'  TGGGTTTTTGTTGTTGCTGTT  42398        TG     C   A
                                 AGCAGCAG  ACAGGA ATC
                                 ||||||||  |||||| |||
                                 TTGTCGTT  TGTTTT TGG
                                     GT     _  GT
GAM906  SOX6     3'  ATGTTATTGTTATTGTTGTT   52826           _   TCA
                                 AGCAGCAGTGACAG GACA
                                 |||||||||||||| ||||
                                 TTGTTGTTATTGTT TTGT
                                         A      AC
GAM906  SOX6     3'  TGTTGTTATTGTTATTGTTGTT 52828           _   T
                                 AGCAGCAGTGACAG GACA CA
                                 |||||||||||||| |||| ||
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                                TTGTTGTTATTGTT TTGT GT
                                       A   T
GAM906  SOX6    3'  TGTTATTGTTGTTGTTGTT   52827       TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                    GT   A      A
GAM906  SP192   3'  TTTTGTTATTGTTCT      41313    C
                                AG AGCAGTGACAGGA
                                || ||||||||||||
                                TC TTGTTATTGTTTT
                                 _
GAM906  SQV7L   5'  TGATTCCATGTTTTTGCTGTT  70581       T   _  C
                                AGCAGCAG GACA GGA ATCA
                                |||||||| |||| ||| ||||
                                TTGTCGTT TTGT CCT TAGT
                                    T   A  _
GAM906  SRPK1   3'  TGGACTGTTTCTGTTGTT    11967       T    GA
                                AGCAGCAG GACAG  CA
                                |||||||| |||||  ||
                                TTGTTGTC TTGTC  GT
                                    T    AG
GAM906  SSB     5'  GTCGTTGTTGTTGCTGTT    11978       TG   _
                                AGCAGCAG  ACAG GAC
                                ||||||||  |||| |||
                                TTGTCGTT  TGTT CTG
                                    GT   G
GAM906  SSR1    3'  GTGTCCATTGTTGCT       11982        GACA    T
                                AGCAGCAGT   GGACA C
                                |||||||||   ||||| |
                                TCGTTGTTA   CCTGT G
                                    ____    T
GAM906  STAM2   3'  GCAGTATTGTCACTTTTGCT  19563      C      G  ATCA
                                AGCAG AGTGACAG AC
                                ||||| |||||||| ||
                                TCGTT TCACTGTT TG
                                  T      A  ACGT
GAM906  STK39   3'  TCCTTTCATTGTTGTT      25078          C
                                AGCAGCAGTGA AGGA
                                |||||||||| ||||
                                TTGTTGTTACT TCCT
                                     T
GAM906  STRAIT11499 3'  TGATGAAGGGTTCCACTGTTGT 41148         __  AGGA
          T                      AGCAGCAGTG  AC   CATCA
                                 ||||||||||  ||   |||||
                                 TTGTTGTCAC  TG   GTAGT
                                      CT  GGAA
GAM906  STX12   3'  CATCTTGTTGTTGTTGTT    66351       TG    CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
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                                TTGTTGTT  TGTTCT
                                   GT       ACT
GAM906  STX12    3'  ATGATTTAATCTTGTTGTTGTT 66347       TG     C___
             GTT                  GCAGCAG  ACAGGA   ATCA   T
                                |||||||  ||||||   ||||  |
                                TGTTGTT  TGTTCT   TAGT   A
                                   GT     AATT
GAM906  STX12    3'  TGTTGTTGTTGTTGTTGTTGTT 66355       TG   _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                   GT   G   T
GAM906  SUCLG2   3'  TGATGTCCAATTTTGTTGT   65610       TGACA
                                GCAGCAG    GGACATCA
                                |||||||    ||||||||
                                TGTTGTT    CCTGTAGT
                                   TTAA_
GAM906  SYNJ2    3'  TTTTGTTCCTGCTGTT     61771       TG
                                AGCAGCAG  ACAGGA
                                |||||||  ||||||
                                TTGTCGTC  TGTTTT
                                   CT
GAM906  SYTL2    5'  TGATGCTCTGATGCTGCT    51962       GTGA   GA
                                AGCAGCA   CAG  CATCA
                                |||||||   |||  |||||
                                TCGTCGT   GTC  GTAGT
                                   A___   TC
GAM906  TA-PP2C  3'  TGGGTTGTTACTGTGCT     57762     G       GA
                                AGCA CAGTGACAG  CA
                                ||||  |||||||||  ||
                                TCGT GTCATTGTT  GT
                                  _       GG
GAM906  TAF9L    3'  TATGTTTTGATCACTGCTGCT  32007         _      CA
                                AGCAGCAGTGA CAGGACAT
                                |||||||||||  ||||||||
                                TCGTCGTCACT GTTTTGTA
                                      A       T
GAM906  TCL6     5'  TGGTGTGGGGCTGTGCTGCT   40165       G   G___
                                AGCAGT ACAG    ACATCA
                                ||||||  ||||    ||||||
                                TCGTCG TGTC    TGTGGT
                                   _   GGGG
GAM906  TCL6     5'  TGGTGTGGGGCTGTGCTGCT   40151       G   G___
                                AGCAGT ACAG    ACATCA
                                ||||||  ||||    ||||||
                                TCGTCG TGTC    TGTGGT
                                   _   GGGG
GAM906  TDRKH    3'  TGATGGGTTCTTTGTCATTCTG 22485      C      _ ___
             TT                   GCAG AGTGACAG GA   CATCA
                                ||||  |||||||| ||   |||||
```

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                                TGTC TTACTGTT CT   GTAGT
                                  _       T  TGG
GAM906  TEB4     3'  TGATGTCCTAGCAGCTCT    60658    C   AG  AC
                                AG AGC  TG  AGGACATCA
                                || |||  ||  |||||||||
                                TC TCG  AC  TCCTGTAGT
                                 _  __  GA
GAM906  TIGD1    5'  TGATGTTGCTATTGTCATTGTT 88870          ____
                                AGCAGTGACAG   GACATCA
                                ||||||||||   |||||||
                                TTGTTACTGTT   TTGTAGT
                                      ATCG
GAM906  TJP4     3'  ACAAGTTTTGTTATTTTGTT   54607      C        ATCA
                                AGCAG AGTGACAGGAC
                                ||||| ||||||||||
                                TTGTT TTATTGTTTTG
                                  _         AACAC
GAM906  TRIM36   3'  GGTTGTCCTTGTTGTT      38015       GTGAC    _
                                AGCAGCA    AGGACA TC
                                |||||||    ||||||  ||
                                TTGTTGT    TCCTGT GG
                                   _____     T
GAM906  TRIM38   3'  TGATGATCGTATGTTGCT    20991       GTGACA  A
                                AGCAGCA     GG CATCA
                                |||||||     ||  |||||
                                TCGTTGT     CT GTAGT
                                    ATG___  A
GAM906  TRIM4    3'  TGATGTTTGGTTTTCTGTT    52256      T_   AG
                                AGCAG  GAC  GACATCA
                                |||||  |||  |||||||
                                TTGTC  TTG  TTGTAGT
                                   TT   GT
GAM906  TRIP-Br2 3'  GGGATGTTTTGTTGTTGTTGTT 28585        TG        A
                                AGCAGCAG  ACAGGACATC
                                ||||||||  ||||||||||
                                TTGTTGTT  TGTTTTGTAG
                                     GT        GGT
GAM906  TSPAN-3  3'  TGAGCAGGTCTGCTGCTGTT   19161         _  AGGACA
                                AGCAGCAGT GAC     TCA
                                |||||||||  |||     |||
                                TTGTCGTCG CTG     AGT
                                      T   GACG__
GAM906  TU3A     3'  TGATGTTCCCACCTGCTTCT   23194    C    _  ACA
                                AG AGCAG TG   GGACATCA
                                || |||||  ||   ||||||||
                                TC TCGTC AC   CTTGTAGT
                                 T    C  C__
GAM906  TUSP     3'  TGTTGTTTTTTGTTGTTGTT   39645        TG C     TCA
                                AGCAGCAG  A AGGACA
                                ||||||||  |  ||||||
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                                TTGTTGTT  T TTTTGT
                                    GT _     TGTT
GAM906  TUSP    3'  GTGTTTTTTGTTGTTGTT    39639        TG C
                                AGCAGCAG  A AGGACAT
                                ||||||||  | |||||||
                                TTGTTGTT  T TTTTGTG
                                    GT _
GAM906  UCK1    3'  TGATGTTTTGTTGACAGT    48704    A  _
                                GC GT GACAGGACATCA
                                || || ||||||||||||
                                TG CA TTGTTTTGTAGT
                                 A  G
GAM906  UQCRH   5'  TGGGTTAGGTGCCGCTGTTGCT 74660          __ AG   A
                                AGCAGCAGTG  AC  GAC TCA
                                ||||||||||  ||  ||| |||
                                TCGTTGTCGC  TG  TTG GGT
                                     CG  GA  _
GAM906  USP22   3'  TGACCAAGTTCTGCTGTT    68031        T   A_  A
                                AGCAGCAG GAC  GG CA
                                ||||||||  |||  || ||
                                TTGTCGTC TTG  CC GT
                                    _  AA  A
GAM906  USP29   3'  TGGTGTATTTTGCTACTGTT  40496      C  TG CAGG
                                AGCAG AG  A   ACATCA
                                |||||  ||  |   ||||||
                                TTGTC TC  T   TGTGGT
                                   A  GT TTA_
GAM906  VAV3    3'  TGGTGTTTAGTCTTCCTGTT  20366      CAGT   AG
                                AGCAG   GAC  GACATCA
                                |||||   |||  |||||||
                                TTGTC   CTG  TTGTGGT
                                   CTT_  AT
GAM906  VEZATIN 3'  TTCTGTTGTTGCTGCT     34231        TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TCGTCGTT  TGTCTT
                                    GT
GAM906  VEZATIN 3'  TTCTGTTGTTGCTGCT     34230        TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TCGTCGTT  TGTCTT
                                    GT
GAM906  VMP     3'  TGATGTTTTTGTGGCTGT    54904      G    _
                                GCAGT ACAGGA CATCA
                                ||||| |||||| |||||
                                TGTCG TGTTTT GTAGT
                                   G     T
GAM906  WDR7    3'  TGGTGAACGTGCTGTTGT    30963        G  AGGA
                                GCAGCAGT AC   CATCA
                                |||||||| ||   |||||
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                                TGTTGTCG TG   GTGGT
                                    _ CAA_
GAM906  YAP1     3'  TGCTCTTCCTTGTCCATTGCTG 20359         _  _  CATCA
            CT                   AGCAGCAGTG ACA GGA
                                ||||||||||| ||| |||
                                TCGTCGTTAC TGT CCT
                                     C   T   TCTCGT
GAM906  YWHAQ    3'  TGGTGTGCAGTACTGCTGT   22397        ACAGG
                                GCAGCAGTG    ACATCA
                                |||||||||    ||||||
                                TGTCGTCAT    TGTGGT
                                     GACG_
GAM906  ZAK      3'  TGGTGAAACCCTGTTGCTACT  56132    C  TG    A___
                                AG AG  ACAGG   CATCA
                                || ||  |||||   |||||
                                TC TC  TGTCC   GTGGT
                                 A  GT    CAAA
GAM906  ZID      3'  TGGTGTTCTGAGCCATAGTT   21778    A   A__
                                AGC GTG   CAGGACATCA
                                ||| |||   ||||||||||
                                TTG TAC   GTCTTGTGGT
                                  A   CGA
GAM906  ZNF262   3'  TGACCTTCACTGCTGTT     17490          C   A
                                AGCAGCAGTGA AGG CA
                                |||||||||||| ||| ||
                                TTGTCGTCACT TCC GT
                                     _   A
GAM906  ZNF31    3'  TGGTGTTTATTGAGCTGTTGCT 64991        GACA_
                                AGCAGCAGT    GGACATCA
                                |||||||||    ||||||||
                                TCGTTGTCG    TTTGTGGT
                                     AGTTA
GAM906  ZNF313   3'  TCGCGCTTGTACACTGCTGCT  37943         _    ACATCA
                                AGCAGCAGTG ACAGG
                                |||||||||| |||||
                                TCGTCGTCAC TGTTC
                                     A    GCGCT
GAM906  ZNF384   3'  TGATGTTTTGTTTATTTTTGT  55987     C    _
                                GCAG AGTGA CAGGACATCA
                                |||| ||||| ||||||||||
                                TGTT TTATT GTTTTGTAGT
                                  T    T
GAM906  ZNF387   3'  ATGATGTATTCCACTGTTATTA 27994    C      G_____
            CTGTT                AG AGTGACAG     ACATCA   T
                                || ||||||||     ||||||  |
                                TC TTATTGTC     TGTAGT   A
                                 A       ACCTTA
GAM906  LOC112714 5'  TGGGCAGGTCATTGCAGTT   72873     A      AGGACA
                                AGC GCAGTGAC     TCA
                                ||| ||||||||     |||
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                                TTG CGTTACTG      GGT
                                  A       GACG__
GAM906   LOC113146 3'  TCCTGCTGCTGCTGCT      72972          GA
                                AGCAGCAGT  CAGGA
                                |||||||||  |||||
                                TCGTCGTCG  GTCCT
                                     TC
GAM906   LOC113828 5'  GAGCCCTCTTGTCGTTTTTGTT 56584       C         CATCA
                                AGCAG AGTGACAGGA
                                ||||| ||||||||||
                                TTGTT TTGCTGTTCT
                                   T         CCCGAGG
GAM906   LOC115196 3'  TGTATTTTGTTGTTGTTGTT   73268         TG     CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                     GT      ATGT
GAM906   LOC116437 3'  GATGACTTCTGCTGCT      73892         TGAC   A
                                AGCAGCAG    AGG CATC
                                ||||||||    ||| ||||
                                TCGTCGTC    TTC GTAG
                                     _____   A
GAM906   LOC120534 3'  GAATGTTGTTCTTGCTGCT    74019         T    GG    CA
                                AGCAGCAG GACA  ACAT
                                |||||||| ||||  ||||
                                TCGTCGTT TTGT  TGTA
                                     C    __    AGG
GAM906   LOC120856 3'  TGATGTTTTGTAATGTTACT   74031     C    GTG
                                AG AGCA   ACAGGACATCA
                                || ||||   ||||||||||
                                TC TTGT   TGTTTTGTAGT
                                  A    AA_
GAM906   LOC123096 3'  TGGCCACGTCATTGTGCT     74204      G       A_  A
                                AGCA CAGTGAC  GG CA
                                |||| |||||||  || ||
                                TCGT GTTACTG  CC GT
                                   _       CA  G
GAM906   LOC123624 3'  TGTGCTCACTGCTGTT       75617           CA G
                                AGCAGCAGTGA  G ACA
                                ||||||||||  | |||
                                TTGTCGTCACT  C TGT
                                     __ G
GAM906   LOC124470 3'  TGATTTCTCTTGTCTCTGCTGC 75643         T      C__
            T                    AGCAGCAG GACAGGA   ATCA
                                ||||||||| |||||||   ||||
                                TCGTCGTC CTGTTCT   TAGT
                                     T      CTT
GAM906   LOC126006 5'  TGGGGTCCAGTCATTGCTGCT  74430           A    AT
                                AGCAGCAGTGAC GGAC  CA
                                |||||||||||| ||||  ||
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                                TCGTCGTTACTG CCTG  GT
                                      A    GG
GAM906   LOC126364 3'  GTTTTTTTTTGTTGTTGTTGTT 75697        TG     CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT     TTTTTGT
GAM906   LOC126669 3'  TCTGTTATTGGCTGTT      75421       _
                                AGCAGC AGTGACAGG
                                |||||| |||||||||
                                TTGTCG TTATTGTCT
                                   G
GAM906   LOC126917 3'  TGATTCTTGTTGTTATTGTTGT 74594           ___   C
           T                     AGCAGCAGTGACA   GGA ATCA
                                ||||||||||||   ||| ||||
                                TTGTTGTTATTGT   TCT TAGT
                                      TGT  _
GAM906   LOC126917 3'  TGGTGCATGTTGTTGCTG    74597       TG   GGA
                                CAGCAG  ACA   CATCA
                                ||||||  |||   |||||
                                GTCGTT  TGT   GTGGT
                                   GT   AC_
GAM906   LOC126969 3'  TGTCTTTGTCATTATTGTT    74632       C       _
                                AGCAG AGTGACAG GACA
                                ||||| |||||||| ||||
                                TTGTT TTACTGTT CTGT
                                  A       T
GAM906   LOC128387 3'  TGATGGAGTTTCGCTGTTGTT  74755          CAGGA
                                AGCAGCAGTGA     CATCA
                                ||||||||||     |||||
                                TTGTTGTCGCT     GTAGT
                                      TTGAG
GAM906   LOC129305 5'  TGCCTGATCATTGCTGCT    75724          _   A
                                AGCAGCAGTGA CAGG CA
                                |||||||||| |||| ||
                                TCGTCGTTACT GTCC GT
                                      A   _
GAM906   LOC132422 5'  TGGTGCGGGTCACCGTTGCT   75889       A    AGGA
                                AGCAGC GTGAC    CATCA
                                |||||| |||||    |||||
                                TCGTTG CACTG    GTGGT
                                   C    GGC_
GAM906   LOC132720 3'  TGTATTTTACTGTTGTT     75065          CAGG
                                AGCAGCAGTGA    ACA
                                ||||||||||    |||
                                TTGTTGTCATT    TGT
                                      TTA_
GAM906   LOC133584 3'  TCACTGTCATTTTTGTT     75101       C       _
                                AGCAG AGTGACAG GA
                                ||||| |||||||| ||
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                                TTGTT TTACTGTC CT
                                   T       A
GAM906  LOC134288 3'  GGTGTTCTATGTTGT       75177       GTGAC
                                GCAGCA    AGGACATC
                                ||||||    ||||||||
                                TGTTGT    TCTTGTGG
                                   A____
GAM906  LOC135138 3'  GGATCATCTGTCTCTGTTGCT  75208        T     AC   A
                                AGCAGCAG GACAGG  ATC
                                |||||||| ||||||  |||
                                TCGTTGTC CTGTCT  TAG
                                     T     AC   GG
GAM906  LOC137964 5'  GTTTTTCTGTCATTCTGTT   75286      C        CATCA
                                AGCAG AGTGACAGGA
                                ||||| ||||||||||
                                TTGTC TTACTGTCTT
                                   _        TTTGT
GAM906  LOC138050 5'  TGGCCGCGCTGCTGCT      75300          ACA  A
                                AGCAGCAGTG   GG CA
                                ||||||||||   || ||
                                TCGTCGTCGC   CC GT
                                     G__  G
GAM906  LOC139673 3'  TGATGTCTTGGGCATT      75981      A_
                                AGTG  CAGGACATCA
                                ||||  ||||||||||
                                TTAC  GTTCTGTAGT
                                  GG
GAM906  LOC142955 3'  TGAGGACTTCTGTGCTGCTGCT 76449         G     CA__
                                AGCAGCAGT ACAGGA    TCA
                                |||||||| ||||||    |||
                                TCGTCGTCG TGTCTT    AGT
                                     _     CAGG
GAM906  LOC143098 3'  TGGTCTCAGGTGTGGCTGCTGC 76458         G  ____    ATCA
           T                   AGCAGCAGT ACA    GGAC
                               ||||||||| |||    ||||
                               TCGTCGTCG TGT    TCTG
                                     G   GGAC    GT
GAM906  LOC144524 5'  TTTTGTTGTTGTCTGTT     83143       _   TG
                                AGCAG CAG  ACAGGA
                                ||||| |||  ||||||
                                TTGTC GTT  TGTTTT
                                   T   GT
GAM906  LOC144962 3'  TGATAATGTCATTGCTGTT    76974           GGAC
                                AGCAGCAGTGACA    ATCA
                                ||||||||||||    ||||
                                TTGTCGTTACTGT    TAGT
                                       AA__
GAM906  LOC145216 3'  TGAGCCAAGGTCGTGCTGCT   83270        G    AGGACA
                                AGCAGCA TGAC      TCA
                                |||||||| ||||      |||
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                                TCGTCGT GCTG     AGT
                                    _   GAACCG
GAM906  LOC145225 3'  TGGTGTCCTGGGCCTCTCT   83311    C  C  TGA
                                AG AG AG   CAGGACATCA
                                || || ||   ||||||||||
                                TC TC TC   GTCCTGTGGT
                                 _ _  CGG
GAM906  LOC145231 3'  TGCTTTGTTATGCTGTT     83297       G     GA
                                AGCAGCA TGACAG  CA
                                ||||||| ||||||  ||
                                TTGTCGT ATTGTT  GT
                                    _     TC
GAM906  LOC145231 3'  TGGTGTCTTACAATTGCTGTT  83298         GAC
                                AGCAGCAGT   AGGACATCA
                                |||||||||   |||||||||
                                TTGTCGTTA   TTCTGTGGT
                                      ACA
GAM906  LOC145268 3'  TGGTGTTTTAAGTGCTAGCT   77064     _   GTGAC
                                AGC AGCA    AGGACATCA
                                ||| ||||    |||||||||
                                TCG TCGT    TTTTGTGGT
                                  A   GAA__
GAM906  LOC145483 5'  TGTCACTGTCGCTGCTGC    77249           _
                                GCAGCAGTGACAG GACA
                                |||||||||||| ||||
                                CGTCGTCGCTGTC CTGT
                                       A
GAM906  LOC145483 5'  TCGCTGTCACTGTCGCT     77248     A        _
                                AGC GCAGTGACAG GA
                                ||| ||||||||| ||
                                TCG TGTCACTGTC CT
                                  C        G
GAM906  LOC145497 5'  TGGTGTCCAACATGGCTGTT   77219       A   ACA
                                AGCAGC GTG   GGACATCA
                                |||||| |||   ||||||||
                                TTGTCG TAC   CCTGTGGT
                                   G   AA_
GAM906  LOC145608 5'  TATGTTGTTACTGCT       83386          GG    CA
                                AGCAGTGACA  ACAT
                                ||||||||||  ||||
                                TCGTCATTGT  TGTA
                                      __    TT
GAM906  LOC145676 5'  TGGTGTCAGGCTGCTGT     77341         GACAG
                                GCAGCAGT    GACATCA
                                ||||||||    |||||||
                                TGTCGTCG    CTGTGGT
                                     GA___
GAM906  LOC145758 5'  TGTTCTGTATTGCTGCT     83487          A
                                AGCAGCAGTG CAGGACA
                                |||||||||| |||||||
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                                TCGTCGTTAT GTCTTGT
                                          _
GAM906  LOC145781 3'  TGGGAAGGGTGACTGTTGTT  77493        G  AGGACA
                                AGCAGCAGT AC     TCA
                                ||||||||| ||     |||
                                TTGTTGTCA TG     GGT
                                     G  GGAAG_
GAM906  LOC145814 5'  GAAGTTTTGTTGTTTTGCT   77507      C  TG      A  A
                                AGCAG AG  ACAGGAC TC
                                ||||| ||  ||||||| ||
                                TCGTT TT  TGTTTTG AG
                                   _ GT      A  G
GAM906  LOC145900 3'  TGCCTATGTTCTGCTGTT    77567        T   __  A
                                AGCAGCAG GACA  GG CA
                                |||||||| ||||  || ||
                                TTGTCGTC TTGT  CC GT
                                     _   AT  _
GAM906  LOC146315 5'  GTTCTGCCATTGCTGCT     60890          A
                                AGCAGCAGTG CAGGAC
                                |||||||||| ||||||
                                TCGTCGTTAC GTCTTG
                                     C
GAM906  LOC146455 3'  TGTCTATGATACTGCTGTT   77911          A  _
                                AGCAGCAGTG CA GGACA
                                |||||||||| || |||||
                                TTGTCGTCAT GT TCTGT
                                     A  A
GAM906  LOC146901 3'  TGGTTTTTGTTGTTGGTGTT  83852     G   TG     C
                                AGCA CAG  ACAGGA ATCA
                                |||| |||  |||||| ||||
                                TTGT GTT  TGTTTT TGGT
                                  G   GT     _
GAM906  LOC146909 3'  TGTTAATGTGCTGCTGTT    78188        G   G_
                                AGCAGCAGT ACA  GACA
                                ||||||||| |||  ||||
                                TTGTCGTCG TGT  TTGT
                                     _  AA
GAM906  LOC147004 3'  TGGATGTCATTGCTGC      83908          GGA
                                GCAGCAGTGACA   CA
                                ||||||||||||   ||
                                CGTCGTTACTGT   GT
                                       AG_
GAM906  LOC147343 3'  TGTATCTGTCACTGTGTT    84005      G        _
                                AGCA CAGTGACAGG ACA
                                |||| |||||||||| |||
                                TTGT GTCACTGTCT TGT
                                  _        A
GAM906  LOC147429 5'  TGGTGTCTCACCCTGTTGC   78367        TGACA
                                GCAGCAG    GGACATCA
                                |||||||    ||||||||
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                                CGTTGTC    TCTGTGGT
                                    CCAC_
GAM906  LOC147515 3'  TGGTGTTCTTATGTTGT    84030      GTGAC
                                GCAGCA    AGGACATCA
                                ||||||    |||||||||
                                TGTTGT    TCTTGTGGT
                                   AT___
GAM906  LOC148255 5'  TGATGTCCTAGGTGCTGC    78757      GTGAC
                                GCAGCA    AGGACATCA
                                ||||||    |||||||||
                                CGTCGT    TCCTGTAGT
                                   GGA__
GAM906  LOC148371 5'  TGTCCTAATTGTTGCTGCTG  78808      TG  ____    TCA
                                CAGCAG  ACA   GGACA
                                ||||||  |||   |||||
                                GTCGTC  TGT   CCTGT
                                   GT   TAAT      A
GAM906  LOC149372 3'  TGATGTAGGATTGCTGC     79330      GACAGG
                                GCAGCAGT     ACATCA
                                ||||||||     ||||||
                                CGTCGTTA     TGTAGT
                                    GGA___
GAM906  LOC149420 3'  TCTTCGTTGTTGTTGTT     79372      TG _
                                AGCAGCAG  AC AGGA
                                ||||||||  || ||||
                                TTGTTGTT  TG TTCT
                                    GT  C
GAM906  LOC149706 5'  GATTTCTCTGCTGTT       84644      TGACA   C
                                AGCAGCAG    GGA ATC
                                ||||||||    ||| |||
                                TTGTCGTC    TCT TAG
                                   _____  T
GAM906  LOC149770 3'  TGATGTTTTCAAGGTGCT    79509     G AG   CA
                                AGCA C  TGA  GGACATCA
                                |||| |  |||  ||||||||
                                TCGT G  ACT  TTTGTAGT
                                  _ GA  __
GAM906  LOC149995 3'  TGGTGTTCTTATGTTGT     84852      GTGAC
                                GCAGCA    AGGACATCA
                                ||||||    |||||||||
                                TGTTGT    TCTTGTGGT
                                   AT___
GAM906  LOC150184 3'  TGATGTTATTATTGCTGTT   84912        CAG
                                AGCAGCAGTGA   GACATCA
                                ||||||||||   |||||||
                                TTGTCGTTATT   TTGTAGT
                                      A__
GAM906  LOC150185 3'  TGATGTTATTATTGCTGTT   84909        CAG
                                AGCAGCAGTGA   GACATCA
                                ||||||||||   |||||||
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                                TTGTCGTTATT   TTGTAGT
                                      A__
GAM906   LOC150503 3'  TGATGTGGAAATACTGATGTT  79909     G    ACAGG
                                AGCA CAGTG    ACATCA
                                |||| |||||    ||||||
                                TTGT GTCAT    TGTAGT
                                  A    AAAGG
GAM906   LOC150504 3'  TGATGTGGAAATACTGATGTT  59349     G    ACAGG
                                AGCA CAGTG    ACATCA
                                |||| |||||    ||||||
                                TTGT GTCAT    TGTAGT
                                  A    AAAGG
GAM906   LOC150587 3'  GTTTTGTTGTTACTGCT     85065      C  TG
                                AGCAG AG  ACAGGAC
                                ||||| ||  |||||||
                                TCGTC TT  TGTTTTG
                                   A  GT
GAM906   LOC150606 3'  TTTGTTGTTGTTGTTGTTGTT  85096       TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                     GT   G   TT
GAM906   LOC150606 3'  TGTTGTTGTTGTTGTTGTTGTT 85093       TG   _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                     GT   G   T
GAM906   LOC150606 3'  TCCATAGTTTTGTTGTTGTTGT 85092       TG     ATCA
            T                    AGCAGCAG  ACAGGAC
                                ||||||||  |||||||
                                TTGTTGTT  TGTTTTG
                                     GT     ATACCTG
GAM906   LOC150696 3'  TGTCGTTGTTGTTGTT     58490       TG  AG
                                AGCAGCAG  AC  GACA
                                ||||||||  ||  ||||
                                TTGTTGTT  TG  CTGT
                                     GT  __
GAM906   LOC150848 5'  AGGCTGGTTTTGTTGTTGTTGT 85125       TG     ATCA
            T                    AGCAGCAG  ACAGGAC
                                ||||||||  |||||||
                                TTGTTGTT  TGTTTTG
                                     GT     GTCGGAA
GAM906   LOC150848 5'  TGTTGTTGTTGTTGTTGTTGTT 85136       TG   _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                     GT   G   T
GAM906   LOC150848 5'  TGTTGTTGTTGTTGTTGTTGTT 85137       TG   _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
```

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                                TTGTTGTT  TGTT TTGT GT
                                    GT    G    T
GAM906   LOC150848 5'  TGTTGTTGTTGTTGTTGTTGTT 85138        TG    _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                    GT    G    T
GAM906   LOC151315 5'  TGCTTTGCTCGTTGTTGCT    80222          _  GA
                                AGCAGCAGTGA CAG  CA
                                ||||||||||| |||  ||
                                TCGTTGTTGCT GTT  GT
                                      C   TC
GAM906   LOC151360 3'  ATGTTTTCGTTGTTGTTGTT   85310        TG _     TCA
                                AGCAGCAG  AC AGGACA
                                ||||||||  || ||||||
                                TTGTTGTT  TG TTTTGT
                                    GT  C        AC
GAM906   LOC151360 3'  CCGGTTGTTTTCGTTGTTGTTG 85312        TG _     TCA
           TT                     AGCAGCAG  AC AGGACA
                                ||||||||  || ||||||
                                TTGTTGTT  TG TTTTGT
                                    GT  C     TGGCCA
GAM906   LOC151361 3'  CCGGTTGTTTTCGTTGTTGTTG 85323        TG _     TCA
           TT                     AGCAGCAG  AC AGGACA
                                ||||||||  || ||||||
                                TTGTTGTT  TG TTTTGT
                                    GT  C     TGGCCA
GAM906   LOC151361 3'  ATGTTTTCGTTGTTGTTGTT   85318        TG _     TCA
                                AGCAGCAG  AC AGGACA
                                ||||||||  || ||||||
                                TTGTTGTT  TG TTTTGT
                                    GT  C        AC
GAM906   LOC151391 3'  TGATGTTCTTGTCTCTGTCGCT 85333     A    T     _
                                AGC GCAG GACAGGA CATCA
                                ||| |||| ||||||| |||||
                                TCG TGTC CTGTTCT GTAGT
                                  C   T      T
GAM906   LOC151521 3'  TGGTGTCTGACGGTGATGCT   85441      G  G  ACA
                                AGCA CA TG   GGACATCA
                                |||| || ||   ||||||||
                                TCGT GT GC   TCTGTGGT
                                  A  G  AG_
GAM906   LOC151623 5'  TGATGTCTTGAGTACTG     85460       A_
                                CAGTG  CAGGACATCA
                                |||||  ||||||||||
                                GTCAT  GTTCTGTAGT
                                   GA
GAM906   LOC152328 5'  GTCTCGTCCTCTTGCTGCTGCT 80527        TG C     ATCA
                                AGCAGCAG  A AGGAC
                                ||||||||  | |||||
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                                TCGTCGTC  T TCCTG
                                    GT C    CTCTGG
GAM906  LOC152502 3'  AATACTTTTGTATTGCTGCT  59312         A    CATCA
                                AGCAGCAGTG CAGGA
                                |||||||||| |||||
                                TCGTCGTTAT GTTTT
                                      _    CATAAG
GAM906  LOC152503 5'  TGATGTTCTGGACAGAGTT   85771    AG  A_
                                AGC  TG  CAGGACATCA
                                |||  ||  ||||||||||
                                TTG  AC  GTCTTGTAGT
                                  AG  AG
GAM906  LOC152580 3'  TGGGCTGGTCGTTGCTGTT   85781          _ GA
                                AGCAGCAGTGAC AG  CA
                                ||||||||||| ||  ||
                                TTGTCGTTGCTG TC  GT
                                       G  GG
GAM906  LOC153020 3'  TGCCTGCTGCTGCTGCT    80765        GA   A
                                AGCAGCAGT  CAGG CA
                                |||||||||  |||| ||
                                TCGTCGTCG  GTCC GT
                                     TC   _
GAM906  LOC153114 5'  GGTGTCTCGTTCTGTT     85922      T  AG
                                AGCAG GAC  GACATC
                                ||||| |||  ||||||
                                TTGTC TTG  CTGTGG
                                   _  CT
GAM906  LOC153196 5'  TGGTGGAGCATCCTGCTGCT  85982       T  CAGGA
                                AGCAGCAG GA    CATCA
                                |||||||| ||    |||||
                                TCGTCGTC CT    GTGGT
                                     _ ACGAG
GAM906  LOC153205 5'  TCTTGCTGCTGCTGCT     85947        GA
                                AGCAGCAGT  CAGGA
                                |||||||||  |||||
                                TCGTCGTCG  GTTCT
                                     TC
GAM906  LOC153914 5'  TGGTGCTTTTTTGTTGTTGTT  80992       TG C_  A
                                AGCAGCAG  A  AGG CATCA
                                ||||||||  |  ||| |||||
                                TTGTTGTT  T  TTC GTGGT
                                     GT TT  _
GAM906  LOC154790 5'  TGGTGGTCACTGTTGCTGCTG  81152      TG  _  _
                                CAGCAG  ACAG GAC ATCA
                                ||||||  |||| ||| ||||
                                GTCGTC  TGTC CTG TGGT
                                   GT   A  G
GAM906  LOC154860 5'  TGAGCAGGTCGCTGCAGCT   86276    A      AGGACA
                                AGC GCAGTGAC     TCA
                                ||| ||||||||     |||
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                                TCG CGTCGCTG     AGT
                                  A       GACG__
GAM906   LOC154877 3'  TCCTGTTGCTTGCTGCT     86314        _ TG
                                AGCAGCA G  ACAGGA
                                ||||||| |  ||||||
                                TCGTCGT C  TGTCCT
                                   T GT
GAM906   LOC155006 3'  GTTTGGTCACTGCTCT      81242    C       AG
                                AG AGCAGTGAC  GAC
                                || |||||||||  |||
                                TC TCGTCACTG  TTG
                                 _       GT
GAM906   LOC155434 3'  TGACCGTGTGTTACTGCT     86407          ___  A  TCA
                                AGCAGTGACA   GG CA
                                ||||||||||   || ||
                                TCGTCATTGT   CC GT
                                      GTG  A
GAM906   LOC157507 5'  TGGTGTTTTCACAGCTGT     81463       A    CA
                                GCAGC GTGA  GGACATCA
                                ||||| ||||  ||||||||
                                TGTCG CACT  TTTGTGGT
                                  A   __
GAM906   LOC157660 3'  CATGAGGATTTTGTTGTTGTTG 86505         TG     CA_
            TT                    AGCAGCAG  ACAGGA   TCA   TG
                                ||||||||  ||||||   |||   ||
                                TTGTTGTT  TGTTTT   AGT   AC
                                     GT     AGG
GAM906   LOC157660 3'  TGTTGTTGTTGTTGTTGTTGTT 86513         TG   _    T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                     GT   G    T
GAM906   LOC157660 3'  TGAGATTCTGTTGTTTTGTT   86512       C  TG     CA
                                AGCAG AG  ACAGGA  TCA
                                ||||| ||  ||||||  |||
                                TTGTT TT  TGTCTT  AGT
                                  _ GT     AG
GAM906   LOC157753 3'  TAACATCTTGTTATTGCTGTT  81587              CATCA
                                AGCAGCAGTGACAGGA
                                ||||||||||||||||
                                TTGTCGTTATTGTTCT
                                        ACAAT
GAM906   LOC158014 5'  GATTTTGTTTTTTGTTGTTGTT 81650         TG   __    TCA
            GTT                   AGCAGCAG  ACAG  GACA
                                ||||||||  ||||  ||||
                                TTGTTGTT  TGTT  TTGT
                                     GT   TT    TTTAGT
GAM906   LOC158088 3'  GGTTTTCTTGCTGCT       86683        GTGAC    C
                                AGCAGCA     AGGA ATC
                                |||||||     |||| |||
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                                TCGTCGT    TCTT TGG
                                   _____   T
GAM906  LOC158117 3'  GATGTTGGCTGTTGC      81706        GACAG
                                GCAGCAGT    GACATC
                                ||||||||    ||||||
                                CGTTGTCG    TTGTAG
                                    G____
GAM906  LOC158293 3'  TGCTTTTTGTTTTTGTTGCT  81865        T      CATCA
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
                                TCGTTGTT TTGTTTT
                                    T      TCGT
GAM906  LOC158332 3'  TTTTGTCGTTGTTGTT     81892
                                AGCAGCAGTGACAGGA
                                ||||||||||||||||
                                TTGTTGTTGCTGTTTT

GAM906  LOC158332 3'  TTTTGTCGTTGTTGTT     81891
                                AGCAGCAGTGACAGGA
                                ||||||||||||||||
                                TTGTTGTTGCTGTTTT

GAM906  LOC158363 3'  TGACATTGTGCTGTTGCT    86778        G   GACA
                                AGCAGCAGT ACAG   TCA
                                ||||||||| ||||   |||
                                TCGTTGTCG TGTT   AGT
                                    _   AC__
GAM906  LOC158476 3'  TTTTTGTTTTTTTGTTGTTGTT 86859       TG C    TCA
                                AGCAGCAG  A AGGACA
                                ||||||||  | ||||||
                                TTGTTGTT  T TTTTGT
                                    GT T     TTTTT
GAM906  LOC158527 3'  TGGTGTTACCCACCCTTGCTGT 81946       ___  ACAG
          T                      AGCAGCA  GTG   GACATCA
                                |||||||  |||   |||||||
                                TTGTCGT  CAC   TTGTGGT
                                    TCC  CCA_
GAM906  LOC158572 3'  AAGGAATCCTGCTGCTGCTGCT 81953        GA    CATCA
                                AGCAGCAGT  CAGGA
                                |||||||||  |||||
                                TCGTCGTCG  GTCCT
                                    TC    AAGGAAG
GAM906  LOC158654 3'  TGATCTAGTTGTTGTTGCT   81968        TG  A   CA
                                AGCAGCAG  AC GGA  TCA
                                ||||||||  || |||  |||
                                TCGTTGTT  TG TCT  AGT
                                    GT  A  __
GAM906  LOC159121 5'  TGGTGTTATCTTTGTTGC    87000        T  CAG
                                GCAGCAG GA   GACATCA
                                |||||||  ||   |||||||
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                                CGTTGTT CT   TTGTGGT
                                    T  A__
GAM906   LOC159963 3'  TGAGGAAGGTGCTGTTGTT   82201        G  AGGACA
                                AGCAGCAGT AC     TCA
                                ||||||||| ||     |||
                                TTGTTGTCG TG     AGT
                                    _  GAAGG_
GAM906   LOC161742 3'  ATGTTTTGTTGTTGTTGTT   82290        TG       TCA
                                AGCAGCAG  ACAGGACA
                                ||||||||  ||||||||
                                TTGTTGTT  TGTTTTGT
                                    GT         AC
GAM906   LOC161742 3'  TTTTTGTTTTGTTGTTGTTGTT 82296        TG       TCA
                                AGCAGCAG  ACAGGACA
                                ||||||||  ||||||||
                                TTGTTGTT  TGTTTTGT
                                    GT       TTTTG
GAM906   LOC161829 5'  TGGTGTCTTCGAGGGTGTGCT  82323     _  AG_   CA
                                AGCA GC   TGA  GGACATCA
                                |||| ||   |||  ||||||||
                                TCGT TG   GCT  TCTGTGGT
                                  G  GGA  __
GAM906   LOC162333 5'  TGTACCTGGTGCTGCTGCT    87143        GA   _
                                AGCAGCAGT  CAGG ACA
                                |||||||||  |||| |||
                                TCGTCGTCG  GTCC TGT
                                    TG    A
GAM906   LOC162427 3'  TGAGGAGGTGCTGCTGTT    82354        G  AGGACA
                                AGCAGCAGT AC     TCA
                                ||||||||| ||     |||
                                TTGTCGTCG TG     AGT
                                    _  GAGG__
GAM906   LOC164295 3'  TGATTGTTGTCAGTGCTGTT   82512        G     GAC
                                AGCAGCA TGACAG   ATCA
                                ||||||| ||||||   ||||
                                TTGTCGT ACTGTT   TAGT
                                    G     GT_
GAM906   LOC165568 5'  TGGTGTCTTTGGTGGCTGTT   82501       G  __
                                AGCAGT AC  AGGACATCA
                                |||||| ||  |||||||||
                                TTGTCG TG  TTCTGTGGT
                                   G  GT
GAM906   LOC196411 3'  TGGTGTTTTAAGTTGCTGT    87690      TG  __
                                GCAG  AC  AGGACATCA
                                ||||  ||  |||||||||
                                TGTC  TG  TTTTGTGGT
                                  GT  AA
GAM906   LOC196478 5'  TGTCAAGGTTTATTGTTGCT   87727          _ AG_   TCA
                                AGCAGCAGTGA C   GACA
                                |||||||||| |   ||||
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                                TCGTTGTTATT G   CTGT
                                      T GAA
GAM906   LOC196996 3'  GTTTATGCTGCTGCT      87862         ACA
                                AGCAGCAGTG   GGAC
                                ||||||||||   ||||
                                TCGTCGTCGT   TTTG
                                     A__
GAM906   LOC197201 3'  TGGTGACCATTGATTGCTGCT  87948        GACA  A
                                AGCAGCAGT    GG CATCA
                                |||||||||    || |||||
                                TCGTCGTTA    CC GTGGT
                                     GTTA  A
GAM906   LOC197423 5'  TGGTGTTTTGCTCGGCAGCT   77864     A  AG  _
                                AGC GC  TGA CAGGACATCA
                                ||| ||  ||| ||||||||||
                                TCG CG  GCT GTTTTGTGGT
                                  A __  C
GAM906   LOC199232 3'  TGGTTTTGTTTTTTTTGTTGTT 88974        T___      ATCA
                                AGCAGCAG    GACAGGAC
                                ||||||||    ||||||||
                                TTGTTGTT    TTGTTTTG
                                     TTTT       GT   A
GAM906   LOC199907 3'  TGTTTGTTGTTGCTGTT     88470        TG    G
                                AGCAGCAG  ACAG ACA
                                ||||||||  |||| |||
                                TTGTCGTT  TGTT TGT
                                     GT   _
GAM906   LOC199907 3'  AGAGGTCTGTTTGTTGTTGCT  88459        TG CA    A  A
                                AGCAGCAG  A  GGAC TC
                                ||||||||  |  |||| ||
                                TCGTTGTT  T  TCTG AG
                                     GT TG    G  AT
GAM906   LOC199907 3'  TGTAGTGCTATTGCTGTT    88468         A  GG
                                AGCAGCAGTG CA  ACA
                                ||||||||||  ||  |||
                                TTGTCGTTAT GT  TGT
                                      C  GA
GAM906   LOC199907 3'  TGTTTGTTGTTGCTGTT     88469        TG    G
                                AGCAGCAG  ACAG ACA
                                ||||||||  |||| |||
                                TTGTCGTT  TGTT TGT
                                     GT   _
GAM906   LOC200014 3'  GTCTTTCCTGTTGTT       88538        T  C
                                AGCAGCAG GA AGGAC
                                |||||||| || |||||
                                TTGTTGTC CT TTCTG
                                     _ _
GAM906   LOC200227 3'  TAGTTGTTGTTGTTGTTGTT   88647        TG   _   ATCA
                                AGCAGCAG  ACAG GAC
                                ||||||||  |||| |||
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                                TTGTTGTT  TGTT TTG
                                    GT    G   AT
GAM906   LOC200227 3'  GTCCTAGTTGTTGTTGTT    88645        TG  _
                                AGCAGCAG  AC AGGAC
                                ||||||||  || |||||
                                TTGTTGTT  TG TCCTG
                                    GT  A
GAM906   LOC200583 3'  CCATGTCCTGTAGCTGCTGCT  88833         G        CA
                                AGCAGCAGT ACAGGACAT
                                ||||||||| |||||||||
                                TCGTCGTCG TGTCCTGTA
                                     A        CCT
GAM906   LOC200609 5'  GTTATTTTTTGTTGTTGTTGTT 90103         TG     CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT     TTATTGT
GAM906   LOC200609 5'  TTTGTTGTTGTTGTTGTTGTT  90107         TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                    GT    G    TT
GAM906   LOC200931 5'  TGGTGTCTGTGCTGTGCTGCT  88945        GTGACA
                                AGCAGCA     GGACATCA
                                |||||||     ||||||||
                                TCGTCGT     TCTGTGGT
                                   GTCGTG
GAM906   LOC200982 3'  TTCTGTCACTGTTTCT      90228    C
                                AG AGCAGTGACAGGA
                                || ||||||||||||
                                TC TTGTCACTGTCTT
                                 T
GAM906   LOC201595 3'  TGAGAATGTTACTGCTG      88980          GGACA
                                CAGCAGTGACA     TCA
                                ||||||||||     |||
                                GTCGTCATTGT     AGT
                                      AAG__
GAM906   LOC201595 3'  TGACACATTATTACTGCTGTT  88979          C  GACA
                                AGCAGCAGTGA AG    TCA
                                |||||||||| ||    |||
                                TTGTCGTCATT TT    AGT
                                      A  ACAC
GAM906   LOC201627 3'  GTTAGCTTTTGTTGTTGTTGTT 89023         TG     CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT     CGATTGG
GAM906   LOC201696 3'  TGTCAACTGTCATTTTGCT    63139       C       __
                                AGCAG AGTGACAG  GACA
                                ||||| ||||||||  ||||
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                                TCGTT TTACTGTC  CTGT
                                  _       AA
GAM906   LOC201725 3'  TGAAGACTGTCATTGTTTCT   89038    C         GACA
                                AG AGCAGTGACAG    TCA
                                || ||||||||||    |||
                                TC TTGTTACTGTC    AGT
                                 T         AGA_
GAM906   LOC202126 3'  TGGTGCCCATGCGCTGCT    90317        A _ A
                                AGCAGTG CA GG CATCA
                                ||||||| || || |||||
                                TCGTCGC GT CC GTGGT
                                   _ A  C
GAM906   LOC202934 5'  TGGGTCTCTTTTTTTGTTGTT  90433         T  C  _   A
                                AGCAGCAG GA AG GAC TCA
                                |||||||| || || ||| |||
                                TTGTTGTT TT TC CTG GGT
                                     T  T  T  _
GAM906   LOC203275 3'  GATGTTGGCTGTTGC       89322         GACAG
                                GCAGCAGT    GACATC
                                ||||||||    ||||||
                                CGTTGTCG    TTGTAG
                                    G____
GAM906   LOC203411 3'  TGCGTTGTCACTTTGTT     90631       C       GA
                                AGCAG AGTGACAG  CA
                                ||||| ||||||||  ||
                                TTGTT TCACTGTT  GT
                                  _       GC
GAM906   LOC204301 3'  TGCCTATGTTCTGCTGTT    89463         T   __  A
                                AGCAGCAG GACA  GG CA
                                |||||||| ||||  || ||
                                TTGTCGTC TTGT  CC GT
                                    _   AT  _
GAM906   LOC205418 5'  TGACACCTGTTATTTTTGCT   90689       C        ACA
                                AGCAG AGTGACAGG   TCA
                                ||||| |||||||||   |||
                                TCGTT TTATTGTCC   AGT
                                  T        AC_
GAM906   LOC219688 3'  TGCTTTTTTGTTGTTGTTGTT  93056         TG     CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                    GT      TTCGT
GAM906   LOC219818 3'  TGCCTGTTAATTGCTGCT    90891          _     A
                                AGCAGCAGT GACAGG CA
                                ||||||||| |||||| ||
                                TCGTCGTTA TTGTCC GT
                                     A     _
GAM906   LOC219842 3'  TGGTGTCTCTGTGCTCCT    93271    C  G   _
                                AG AGT ACAG GACATCA
                                || ||| |||| |||||||
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                                TC TCG TGTC CTGTGGT
                                 C  _   T
GAM906  LOC219855 3'  GGTGCCATCTGCTGCT     91516       TGACA  A
                                AGCAGCAG    GG CATC
                                ||||||||    || ||||
                                TCGTCGTC    CC GTGG
                                    TA___  _
GAM906  LOC219857 3'  TGGGCTTGCCGCTGCTGCT   91511         A   A_
                                AGCAGCAGTG CAGG  CA
                                |||||||||| ||||  ||
                                TCGTCGTCGC GTTC  GT
                                      C   GG
GAM906  LOC219894 3'  TGGTGTTCTCCTCTTGTTG   93290       T  C_
                                CAGCAG GA  AGGACATCA
                                |||||| ||  |||||||||
                                GTTGTT CT  TCTTGTGGT
                                   _ CC
GAM906  LOC219920 3'  GGTGGCCCTGCTGTT       93320       TGACA  A
                                AGCAGCAG    GG CATC
                                ||||||||    || ||||
                                TTGTCGTC    CC GTGG
                                    _____ G
GAM906  LOC220074 3'  TGGCTAATTTTGTTGTTGTTGT 59289       TG     CATCA
          T                      AGCAGCAG  ACAGGA
                                 ||||||||  ||||||
                                 TTGTTGTT  TGTTTT
                                      GT     AATCGGT
GAM906  LOC220074 3'  TTTGTTGTTGTTGTTGTTGTT  59290       TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                     GT   G   TT
GAM906  LOC220370 3'  TGACTTTTGTCATTGTT     92835          CA
                                AGCAGTGACAGGA  TCA
                                ||||||||||||  |||
                                TTGTTACTGTTTT  AGT
                                       C_
GAM906  LOC220477 3'  TGTCCATTTGTTATTGTGTT   75983     G      ___    TCA
                                AGCA CAGTGACA   GGACA
                                |||| ||||||||   |||||
                                TTGT GTTATTGT   CCTGT
                                  _       TTA
GAM906  LOC220692 3'  TGGTGTCTTTCCAGGCTCT   91222    C   AG  AC
                                AG AGC  TG  AGGACATCA
                                || |||  ||  |||||||||
                                TC TCG  AC  TTCTGTGGT
                                 _  G_  CT
GAM906  LOC220776 3'  TGGTTTTGTTGTTGTTGTT   68397       TG     ATCA
                                AGCAGCAG  ACAGGAC
                                ||||||||  |||||||
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                                TTGTTGTT  TGTTTTG
                                    GT      GT
GAM906  LOC220776 3'  TTTGGTTTTGTTGTTGTTGTT  68399        TG      ATCA
                                AGCAGCAG  ACAGGAC
                                ||||||||  |||||||
                                TTGTTGTT  TGTTTTG
                                    GT      GTTTG
GAM906  LOC220846 3'  TGGTTCCCTTATTACTGCT   90821        C_   AC
                                AGCAGTGA  AGG  ATCA
                                ||||||||  |||  ||||
                                TCGTCATT  TCC  TGGT
                                    AT   CT
GAM906  LOC220963 3'  GACTATTCTGTTTTGCTGTT   91449        T      CATCA
                                AGCAGCAG GACAGGA
                                ||||||||  |||||||
                                TTGTCGTT TTGTCTT
                                    _      ATCAGG
GAM906  LOC221288 5'  TGATGGATCTTCTTTATTGCTG 93619          C_   __
          TT                     AGCAGCAGTGA  AGGA  CATCA
                                ||||||||||  ||||  |||||
                                TTGTCGTTATT  TTCT  GTAGT
                                      TC    AG
GAM906  LOC221288 5'  TGATGTTTTGTGTGTGTT    93620      GTG
                                AGCA   ACAGGACATCA
                                ||||   ||||||||||
                                TTGT   TGTTTTGTAGT
                                  GTG
GAM906  LOC221337 3'  TGCTTGTTGCTTTGCT      92116      C  TG    A
                                AGCAG AG  ACAGG CA
                                |||||  ||  |||||  ||
                                TCGTT TC  TGTTC GT
                                   _  GT    _
GAM906  LOC221398 3'  TTCTGTTACTTTGCT       91019      C
                                AGCAG AGTGACAGGA
                                |||||  ||||||||||
                                TCGTT TCATTGTCTT
                                   _
GAM906  LOC221405 5'  TTTTGTTTTTGTTGTT      93893        T
                                AGCAGCAG GACAGGA
                                |||||||  |||||||
                                TTGTTGTT TTGTTTT
                                    T
GAM906  LOC221468 3'  TGTCTTCTGTTGATGCTGCT   59293       GT    __   TCA
                                AGCAGCA  GACAG  GACA
                                |||||||  |||||  ||||
                                TCGTCGT  TTGTC  CTGT
                                    AG    TT
GAM906  LOC221491 5'  TCCTGTCCGCTGTTGCT     92013         _
                                AGCAGCAGTG ACAGGA
                                ||||||||||  ||||||
```

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                                TCGTTGTCGC TGTCCT
                                      C
GAM906  LOC221495 3'  TTCAGTTATTGCTGTT      93866           A
                                AGCAGCAGTGAC GGA
                                |||||||||||| |||
                                TTGTCGTTATTG CTT
                                      A
GAM906  LOC221576 3'  TGGTGTTTTCAAATGTTG    93707      G_  CA
                                CAGCA  TGA  GGACATCA
                                |||||  |||  ||||||||
                                GTTGT  ACT  TTTGTGGT
                                   AA  __
GAM906  LOC221692 3'  TGATGTTTTGTGGCGGCT    92244     A  G
                                AGC GT ACAGGACATCA
                                ||| || ||||||||||
                                TCG CG TGTTTTGTAGT
                                  G  G
GAM906  LOC221751 3'  TGGTGTCGCATCTGTTGT    92052       _  ACAG
                                GCAGCAG TG    GACATCA
                                ||||||| ||    |||||||
                                TGTTGTC AC    CTGTGGT
                                    T  G___
GAM906  LOC221810 3'  TCTTCACTGCTGTT       93933          CA
                                AGCAGCAGTGA  GGA
                                ||||||||||  |||
                                TTGTCGTCACT  TCT
                                          __
GAM906  LOC221838 5'  TGTGCTGTCCTGATTGTTGCTG 92545        TG _      TCA
           CT                     AGCAGCAG  A CAGGACA
                                ||||||||  | |||||||
                                TCGTCGTT  T GTCCTGT
                                    GT A      CGTGTC
GAM906  LOC221839 5'  TGTGCTGTCCTGATTGTTGCTG 92498        TG _      TCA
           CT                     AGCAGCAG  A CAGGACA
                                ||||||||  | |||||||
                                TCGTCGTT  T GTCCTGT
                                    GT A      CGTGTC
GAM906  LOC221882 3'  TGGTGCTGGTTTATTTGTTGTT 92502        T__   A  A
                                AGCAGCAG   GAC GG CATCA
                                ||||||||   ||| || |||||
                                TTGTTGTT   TTG TC GTGGT
                                    TAT   G  _
GAM906  LOC221968 3'  GATGTTCTTTGCCGTT     92568     A    TGAC
                                AGC GCAG    AGGACATC
                                ||| ||||    ||||||||
                                TTG CGTT    TCTTGTAG
                                  C   ____
GAM906  LOC222060 5'  TGTTATTGTCATATGCTGCT   94113        _      _   TCA
                                AGCAGCA GTGACAG GACA
                                ||||||| ||||||| ||||
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                                TCGTCGT TACTGTT TTGT
                                   A      A
GAM906   LOC222662 3'  TTTGTTTTCTTATTGCTGCT   92847          C     TCA
                                AGCAGCAGTGA AGGACA
                                |||||||||||| ||||||
                                TCGTCGTTATT TTTTGT
                                      C     TT
GAM906   LOC222803 5'  TGTCATTCTGTCGTTCTGTT   94357      C       ___   TCA
                                AGCAG AGTGACAG   GACA
                                ||||| ||||||||   ||||
                                TTGTC TTGCTGTC   CTGT
                                  _       TTA
GAM906   LOC222865 3'  TGAAATACTGCCATTGTTGCT  92870         A   GACA
                                AGCAGCAGTG CAG    TCA
                                |||||||||| |||    |||
                                TCGTTGTTAC GTC    AGT
                                      C   ATAA
GAM906   LOC253187 5'  TGGTGTTCATAATATGCAGTT  97120     A   GTGACA
                                AGC GCA      GGACATCA
                                ||| |||      ||||||||
                                TTG CGT      CTTGTGGT
                                  A   ATAATA
GAM906   LOC253187 5'  TGAGACTGTTCTTGTTGTT    97119        T    GACA
                                AGCAGCAG GACAG    TCA
                                |||||||| |||||    |||
                                TTGTTGTT TTGTC    AGT
                                     C     AG__
GAM906   LOC253233 5'  TGCTTGTTGTTGCGCT      95634     A    TG    A
                                AGC GCAG  ACAGG CA
                                ||| ||||  ||||| ||
                                TCG CGTT  TGTTC GT
                                  _    GT    _
GAM906   LOC253351 5'  TGGTGTTCAGCTGTGGCT    96295     A    GACA
                                AGC GCAGT    GGACATCA
                                ||| |||||    ||||||||
                                TCG TGTCG    CTTGTGGT
                                  G    A___
GAM906   LOC253461 3'  TGGTGTACAATTGTAGCTGCTG 96285         G   GG___
            TT                    AGCAGCAGT ACA     ACATCA
                                |||||||| |||     ||||||
                                TTGTCGTCG TGT     TGTGGT
                                     A   TAACA
GAM906   LOC253573 3'  TACCTTTTGTCACGGTTGCT   97052       A       CATCA
                                AGCAGC GTGACAGGA
                                |||||| |||||||||
                                TCGTTG CACTGTTTT
                                   G        CCAT
GAM906   LOC253596 5'  TCCTGTCACTGCTCT       95480    C
                                AG AGCAGTGACAGGA
                                || ||||||||||||
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                                TC TCGTCACTGTCCT
                                  _
GAM906  LOC253664 3'  TTTTTGTTTTGTTTTGTTGTT  94819        T       TCA
                                AGCAGCAG GACAGGACA
                                |||||||| |||||||||
                                TTGTTGTT TTGTTTTGT
                                     _       TTTTT
GAM906  LOC253664 3'  TGTTTTGTTTTGTTGTT     94817        T       TCA
                                AGCAGCAG GACAGGACA
                                |||||||| |||||||||
                                TTGTTGTT TTGTTTTGT
                                     _         A
GAM906  LOC253752 3'  TGTCTTTGTCTTGCTGTT     94714        T    _
                                AGCAGCAG GACAG GACA
                                |||||||| ||||| ||||
                                TTGTCGTT CTGTT CTGT
                                     _    T
GAM906  LOC254358 3'  TGCCTATGTTCTGCTGTT     94975        T   __ A
                                AGCAGCAG GACA  GG CA
                                |||||||| ||||  || ||
                                TTGTCGTC TTGT  CC GT
                                     _   AT  _
GAM906  LOC254531 3'  TGAATTTTGTTATTGTTGTT   94989             CA
                                AGCAGCAGTGACAGGA  TCA
                                |||||||||||||||  |||
                                TTGTTGTTATTGTTTT  AGT
                                       A_
GAM906  LOC254552 5'  TGAGGACAATGTCAGTGTTGCT 94778        G    GGACA_
                                AGCAGCA TGACA     TCA
                                |||||||| |||||     |||
                                TCGTTGT ACTGT     AGT
                                   G    AACAGG
GAM906  LOC254659 5'  TGGTGCATTCTTGCTGCT     95114        T  CAGGA
                                AGCAGCAG GA     CATCA
                                |||||||| ||    |||||
                                TCGTCGTT CT     GTGGT
                                     _  TAC__
GAM906  LOC254967 5'  TGCATTCTCTGTCACTGCTGT  96266           _  CATCA
                                GCAGCAGTGACAG GA
                                |||||||||||| ||
                                TGTCGTCACTGTC CT
                                       T  TACGT
GAM906  LOC255177 3'  TGGTGTTTTGTTTTTTTGTT   96610      CAGT
                                AGCAG   GACAGGACATCA
                                |||||   ||||||||||||
                                TTGTT   TTGTTTTGTGGT
                                   TTT_
GAM906  LOC255290 3'  TGGTGTCTTAGCAGCTGC     95611      AG  AC
                                GCAGC  TG  AGGACATCA
                                |||||  ||  |||||||||
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                                CGTCG  AC  TTCTGTGGT
                                  __  GA
GAM906   LOC255461 5'  TGATGTCTTGAGTACTG     97322       A_
                                CAGTG  CAGGACATCA
                                |||||  ||||||||||
                                GTCAT  GTTCTGTAGT
                                   GA
GAM906   LOC255465 5'  TCCTGTCATTTTGTT       97302       C
                                AGCAG AGTGACAGGA
                                ||||| ||||||||||
                                TTGTT TTACTGTCCT
                                  _
GAM906   LOC255475 5'  TGGTGTTGCCATCACTGTTCT  97618    C       CAG_
                                AG AGCAGTGA    GACATCA
                                || ||||||||    |||||||
                                TC TTGTCACT    TTGTGGT
                                 _       ACCG
GAM906   LOC255515 3'  TGATAGGAACTTACTTGCTGCT 96099         _    CAGGAC
                                AGCAGCA GTGA      ATCA
                                ||||||| ||||      ||||
                                TCGTCGT CATT      TAGT
                                    T    CAAGGA
GAM906   LOC255516 5'  TGATGTCTTGAGTACTG     97335       A_
                                CAGTG  CAGGACATCA
                                |||||  ||||||||||
                                GTCAT  GTTCTGTAGT
                                   GA
GAM906   LOC255598 5'  TGGTGCCCACATTGTTG     97482         ACA  A
                                CAGCAGTG   GG CATCA
                                ||||||||   || |||||
                                GTTGTTAC   CC GTGGT
                                     AC_  _
GAM906   LOC256440 3'  TCTTGTTAATGCTGTT      95568         G
                                AGCAGCA TGACAGGA
                                ||||||| ||||||||
                                TTGTCGT ATTGTTCT
                                    A
GAM906   LOC257443 3'  TGATGACAGTTGTATTGTTGCT 95850           A   GA__
                                AGCAGCAGTG CAG    CATCA
                                |||||||||| |||    |||||
                                TCGTTGTTAT GTT    GTAGT
                                      _   GACA
GAM906   LOC257490 5'  TGGTGTCTGGGTTCTGTGCT   97715      G   T   A_
                                AGCA CAG GAC  GGACATCA
                                |||| ||| |||  ||||||||
                                TCGT GTC TTG  TCTGTGGT
                                  _  _  GG
GAM906   LOC257515 3'  TGGTGTTTTCAAATGTTG    97787       G_   CA
                                CAGCA  TGA  GGACATCA
                                |||||  |||  ||||||||
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                                GTTGT  ACT  TTTGTGGT
                                  AA   __
GAM906  LOC257572 3'  TGGTGTTTTCAAATGTTG    97916      G_  CA
                                CAGCA  TGA  GGACATCA
                                |||||  |||  ||||||||
                                GTTGT  ACT  TTTGTGGT
                                  AA   __
GAM906  LOC51003  5'  GGTGTCTTCGTTTGTT      32149      GT  _
                                AGCA  GAC AGGACATC
                                ||||  ||| ||||||||
                                TTGT  TTG TTCTGTGG
                                  __   C
GAM906  LOC51018  3'  TGGTGTTTTTTGCTTTGT    32126      C  TG C
                                GCAG AG  A AGGACATCA
                                |||| ||  | |||||||||
                                TGTT TC  T TTTTGTGGT
                                  _  GT _
GAM906  LOC51191  3'  TGTTGTTGTTGTTGTTGTTGTT 32878        TG   _   T
                                AGCAGCAG  ACAG GACA CA
                                ||||||||  |||| |||| ||
                                TTGTTGTT  TGTT TTGT GT
                                    GT   G   T
GAM906  LOC51191  3'  TTATCGTTGTTGTTGTTGTTGT 32879        TG   _  ATCA
          T                      AGCAGCAG  ACAG GAC
                                ||||||||  |||| |||
                                TTGTTGTT  TGTT TTG
                                    GT   G   CTATTG
GAM906  LOC51191  3'  CGTTGTTGTTGTTGTTGTTGTT 32877        TG   _   TCA
                                AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                    GT   G   TGCT
GAM906  LOC51202  3'  TGATGTCAAGACTGTTACTGTT 33018   C        ____
          CT                     G AGCAGTGACAG   GACATCA
                                | ||||||||||   |||||||
                                C TTGTCATTGTC   CTGTAGT
                                _        AGAA
GAM906  LOC51580  3'  TGGTGTCTGGGCTGTT     31866       AGTGACA
                                AGCAGC      GGACATCA
                                ||||||      ||||||||
                                TTGTCG      TCTGTGGT
                                  GG_____
GAM906  LOC51652  3'  TGCTCTGTGGTTGCTGCT    32196        TG   GA
                                AGCAGCAG  ACAG  CA
                                ||||||||  ||||  ||
                                TCGTCGTT  TGTC  GT
                                    GG   TC
GAM906  LOC51696  3'  TGATACCTTACTGTTG      32562        AC   AC
                                CAGCAGTG  AGG  ATCA
                                ||||||||  |||  ||||
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                                GTTGTCAT  TCC  TAGT
                                   __   A_
GAM906  LOC51716 3' GGTGTCTTGTGTCTCT     32794    C  TG
                                AG AG  ACAGGACATC
                                || ||  ||||||||||
                                TC TC  TGTTCTGTGG
                                 _  TG
GAM906  LOC51725 3' TGGATGATACTGCTGTT     69869         A  GGA
                                AGCAGCAGTG CA   CA
                                |||||||||| ||   ||
                                TTGTCGTCAT GT   GT
                                      A  AG_
GAM906  LOC54505 5' GGTATGTTTTTTGTTGTTGTT  67840        TG C      CA
                                AGCAGCAG  A AGGACAT
                                ||||||||  | |||||||
                                TTGTTGTT  T TTTTGTA
                                     GT _      TGGA
GAM906  LOC54505 5' TGTTTTTTGTTGTTGTTGTT   67841        TG     CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                     GT     TTGT
GAM906  LOC54518 3' ACACATTCTGTCAGTGCTGTT  38769       G      CATCA
                                AGCAGCA TGACAGGA
                                ||||||| ||||||||
                                TTGTCGT ACTGTCTT
                                    G       ACACAT
GAM906  LOC56996 3' TGATGTTTTCGTTCTGTT    39650      T  _
                                AGCAG GAC AGGACATCA
                                ||||| ||| |||||||||
                                TTGTC TTG TTTTGTAGT
                                   _  C
GAM906  LOC57019 3' TGGTGTGTAGTGCTGCTGT   39726        G  AGG
                                GCAGCAGT AC   ACATCA
                                |||||||| ||   ||||||
                                TGTCGTCG TG   TGTGGT
                                    _ ATG
GAM906  LOC57086 3' TGGGTTGTTTATTGTTGTT   39782          _  GA  TCA
                                AGCAGCAGTGA CAG  CA
                                |||||||||| |||  ||
                                TTGTTGTTATT GTT  GT
                                      T  GG    A
GAM906  LOC58489 3' ATGATTGCCAGTTTGTGTACTG 72527        _  ____  AC
           TTGCT                AGCAGTG ACA   GG  ATCA   T
                                ||||||| |||   ||  ||||  |
                                TTGTCAT TGT   CC  TAGT   A
                                   G   TTGA  GT
GAM906  LOC58525 3' CCTTTTCACTGTTGCT      78644          C_
                                AGCAGCAGTGA  AGG
                                ||||||||||  |||
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                                TCGTTGTCACT  TCC
                                      TT
GAM906  LOC63929  3' AATAGTATGTTACTGCAGCT   42038     A       GG  ATCA
                                AGC GCAGTGACA  AC
                                ||| |||||||||  ||
                                TCG CGTCATTGT  TG
                                  A       A_  ATAAG
GAM906  LOC64150  5' TGGGGATCTGTTGCTGTTTCT  67285    C     TG    ACA
                                AG AGCAG  ACAGG   TCA
                                || |||||  |||||   |||
                                TC TTGTC  TGTCT   GGT
                                 T    GT    AGG
GAM906  LOC90110  5' TGAAACCTTTGCTGCTGCT    61515        TG C   ACA
                                AGCAGCAG  A AGG   TCA
                                ||||||||  | |||   |||
                                TCGTCGTC  T TCC   AGT
                                     GT _   AA_
GAM906  LOC90120  5' TGTCGGTGCTGCTGCT      61545        G  AG
                                AGCAGCAGT AC  GACA
                                |||||||||  ||  ||||
                                TCGTCGTCG TG  CTGT
                                     _ G_
GAM906  LOC90190  3' CCGTTGTTGTTGTTGTTGTGT 61776        TG   _    TCA
          T                      AGCAGCAG  ACAG GACA
                                ||||||||  |||| ||||
                                TTGTTGTT  TGTT TTGT
                                     GT   G    TGCCT
GAM906  LOC90249  5' GTCCTGCTGCTGCT       61924        TGA
                                AGCAGCAG   CAGGAC
                                ||||||||   ||||||
                                TCGTCGTC   GTCCTG
                                     ___
GAM906  LOC90459  3' CCCTATTTTGTTGTTGTTGTT  62884        TG     CATCA
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                     GT     ATCCCA
GAM906  LOC90459  3' TTTTGTTGTTGTTGTT      62895        TG
                                AGCAGCAG  ACAGGA
                                ||||||||  ||||||
                                TTGTTGTT  TGTTTT
                                     GT
GAM906  LOC90494  5' TGGTGTTCTGCTTGGCTGT    63058      AGTGA
                                GCAGC    CAGGACATCA
                                |||||    ||||||||||
                                TGTCG    GTCTTGTGGT
                                   GTTC_
GAM906  LOC90573  5' TGAGAAGGTAGCTGCTGCT    63277        G  AGGACA
                                AGCAGCAGT AC     TCA
                                |||||||||  ||     |||
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                                TCGTCGTCG TG      AGT
                                    A  GAAG__
GAM906  LOC90736 3' TGTACTGTCACTCTGCT     63904       C       G
                                AGCAG AGTGACAG ACA
                                ||||| |||||||| |||
                                TCGTC TCACTGTC TGT
                                  _       A
GAM906  LOC90925 3' TCTTGTTTTTGTTGTT      64428         T
                                AGCAGCAG GACAGGA
                                |||||||| |||||||
                                TTGTTGTT TTGTTCT
                                    T
GAM906  LOC91523 3' TCCTTTTGTTCATTGCTGTT   56394           _     CATCA
                                AGCAGCAGTGA CAGGA
                                |||||||||| |||||
                                TTGTCGTTACT GTTTT
                                      T    CCT
GAM906  LOC91549 3' TGTATATGTTACTGATGCT    66428      G       GG_
                                AGCA CAGTGACA   ACA
                                |||| ||||||||   |||
                                TCGT GTCATTGT   TGT
                                  A       ATA
GAM906  LOC91661 3' TGGGATACTGTTCTGCTGCT   56406         T    GACA
                                AGCAGCAG GACAG    TCA
                                |||||||| |||||    |||
                                TCGTCGTC TTGTC    GGT
                                    _    ATAG
GAM906  LOC91768 3' ACATTGTTTTGTTACTGCTCCT 67110    C            TCA
                                AG AGCAGTGACAGGACA
                                || ||||||||||||||
                                TC TCGTCATTGTTTTGT
                                 C            TACAG
GAM906  LOC91923 5' TGGTTGTTTGTTGTTGTTGC   67555        TG    AC
                                GCAGCAG  ACAGG  ATCA
                                |||||||  |||||  ||||
                                CGTTGTT  TGTTT  TGGT
                                    GT    GT
GAM906  LOC92303 3' TGATGTTTTTTTTTCTGCT    68830      T_  C
                                AGCAG  GA AGGACATCA
                                |||||  || |||||||||
                                TCGTC  TT TTTTGTAGT
                                  TT  T
GAM906  LOC92360 5' TGTTTTGTTGTTGTTGT     69076        TG
                                GCAGCAG  ACAGGACA
                                |||||||  ||||||||
                                TGTTGTT  TGTTTTGT
                                    GT
GAM906  LOC92360 5' GAATGTATTGTTATTATTGTT  69073      C       G    CA
                                AGCAG AGTGACAG ACAT
                                ||||| |||||||| ||||
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                                TTGTT TTATTGTT TGTA
                                  A       A   AGT
GAM906  LOC92573  5' GTTGTGTTTTGTTGCTGCTGT  69810       TG       CA
                                GCAGCAG  ACAGGACAT
                                |||||||  |||||||||
                                TGTCGTC  TGTTTTGTG
                                   GT       TTGG
GAM906  LOC92578  5' TGGTGGGTTTTGTTGC     69833       T   AGGA
                                GCAGCAG GAC    CATCA
                                ||||||| |||    |||||
                                CGTTGTT TTG    GTGGT
                                   _  G___
GAM906  LOC92606  3' TGGAATGTCATTGTAGTT    69993     A       GGA
                                AGC GCAGTGACA   CA
                                ||| |||||||||   ||
                                TTG TGTTACTGT   GT
                                  A       AAG
GAM906  LOC93206  3' AGTTTTTTGTTGTTGTT     71724       TG C    ATCA
                                AGCAGCAG  A AGGAC
                                ||||||||  | |||||
                                TTGTTGTT  T TTTTG
                                   GT _    A_____
GAM906  LOC93589  3' TGATGTCCCCAAACTGCTGCT  72672        GACA
                                AGCAGCAGT    GGACATCA
                                |||||||||    ||||||||
                                TCGTCGTCA    CCTGTAGT
                                     AACC
GAM907  AP2B1     3' GAGCCTGTCAGCACCAAAGCT  7062      C         AA
                                AGCT TGGTGTTGATG  TTC
                                |||| ||||||||||  |||
                                TCGA ACCACGACTGT  GAG
                                  A         CC
GAM907  CELSR3    3' AGGGAATTCAAGACCCAGA   7395      T   GA
                                TCTGG GTT  TGAATTCCCT
                                ||||| |||  ||||||||||
                                AGACC CAG  ACTTAAGGGA
                                   _  A_
GAM907  HFL1      3' GGATGGTCACCAACACCAAAGT 59311     C       A   AT_
                                GCT TGGTGTTG TGA   TCC
                                ||| |||||||| |||   |||
                                TGA ACCACAAC ACT   AGG
                                  A       C   GGT
GAM907  JJAZ1     3' AGGGAATTCATCCTCTAAGA   31076     GGTGTT
                                TCT     GATGAATTCCCT
                                |||     ||||||||||||
                                AGA     CTACTTAAGGGA
                                  ATCTC_
GAM907  PDE4C     3' AATTTTCAGCACCAAAGCT    6229      C       T
                                AGCT TGGTGTTGA GAATT
                                |||| ||||||||| |||||
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                                TCGA ACCACGACT TTTAA
                                  A       _
GAM907  XT3     3' AGGGAACTCAGAGGCCAGCGC  39518    T    G  GA   A
                                GC CTGGT TT  TGA TTCCCT
                                || ||||| ||  ||| ||||||
                                CG GACCG AG  ACT AAGGGA
                                 C    G __   C
GAM907  C20orf38  3' AGGAAATTCATCACCAAAAGAT 37064    C   GG  T       C
           CT                    AG TCT  TG TGATGAATT CCT
                                || |||  || ||||||||| |||
                                TC AGA  AC ACTACTTAA GGA
                                 T   AA  C       A
GAM907  FLJ12891  3' GAATTCATCTGAAGAGC     46339      GGTGTT
                                GCTCT     GATGAATTC
                                |||||     |||||||||
                                CGAGA     CTACTTAAG
                                   AGT___
GAM907  FLJ13490  3' GGAAAGTAAACATCAGAACT   46300    C       GATGAA
                                AG TCTGGTGTT     TTCC
                                || |||||||||     ||||
                                TC AGACTACAA     AAGG
                                 A       ATGA__
GAM907  FLJ20154  3' GGAAACCCACAGAGGCCCAGGG 72930        T   GA  AA___
           CT                    AGCTCTGG GTT  TG     TTCC
                                ||||||| |||  ||    ||||
                                TCGGGACC CGG  AC     AAGG
                                     _  AG  ACCCA
GAM907  FLJ22795  3' GGAAATCCACACACCCAGAGC  46944        _  TGAT  A
                                GCTCTGG TGT    GA TTCC
                                ||||||| |||    || ||||
                                CGAGACC ACA    CT AAGG
                                    C   CAC_  A
GAM907  GFRA4    3' GGAATCCATCGGACAAGA    42157     G  G     A
                                TCT GT TTGATG ATTCC
                                ||| || |||||| |||||
                                AGA CA GGCTAC TAAGG
                                  A  _     C
GAM907  GRWD     3' GAACTCGGTTTAACCAGGGCT  48965         GTTGA   A
                                AGCTCTGGT     TGA TTC
                                |||||||||     ||| |||
                                TCGGGACCA     GCT AAG
                                     ATTTG   C
GAM907  KIAA0152  3' GAATTCCAGTCAGCCAGAGC   28300        GT   __
                                GCTCTGGT  TGAT  GAATTC
                                ||||||||  ||||  ||||||
                                CGAGACCG  ACTG  CTTAAG
                                     __    AC
GAM907  KIAA0298  3' AGAGAACCAGAGCATCAGAGC  76575          GA  AA   C
                                GCTCTGGTGTT  TG  TTC CT
                                ||||||||||  ||  ||| ||
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                                CGAGACTACGA  AC  AAG GA
                                      G_  C_   A
GAM907  KIAA0674  5'  GGAAATCAGGCAACACCA    60614        A_  A
                                TGGTGTTG  TGA TTCC
                                ||||||||  ||| ||||
                                ACCACAAC  ACT AAGG
                                    GG   A
GAM907  KIAA1229  3'  AGGGAACATCACACACCAGGGC 62062          _    AA
                                GCTCTGGTGT TGATG  TTCCCT
                                |||||||||| |||||  ||||||
                                CGGGACCACA ACTAC  AAGGGA
                                      C    __
GAM907  KIAA1649  3'  AGAGAATCCAGGCTGGCAGAGC 66973       G _  GA  A   C
          T                    AGCTCTG T GTT  TG ATTC CT
                               ||||||| | |||  || |||| ||
                               TCGAGAC G CGG  AC TAAG GA
                                   G T  __ C   A
GAM907  KIAA1649  3'  AGAGAATCCAGGCTGGCAGAGC 50244       G _  GA  A   C
          T                    AGCTCTG T GTT  TG ATTC CT
                               ||||||| | |||  || |||| ||
                               TCGAGAC G CGG  AC TAAG GA
                                   G T  __ C   A
GAM907  KR19    3'  AGAGAATTCATATTGGACAGA  81164     GTGTTG      C
                               TCTG     ATGAATTC CT
                               ||||     |||||||| ||
                               AGAC     TACTTAAG GA
                                 AGGTTA       A
GAM907  MGC11257  3'  TCACCAGCACCAGAGC      50373          A
                               GCTCTGGTGTTG TGA
                               |||||||||||| |||
                               CGAGACCACGAC ACT
                                      C
GAM907  MGC2749   3'  GGTTCCCAGACACCAGAGC   43956          GAT
                               GCTCTGGTGTT   GAATT
                               ||||||||||   |||||
                               CGAGACCACAG   CTTGG
                                      ACC
GAM907  RNP24    3'  GGAAATCAGCACAAAGC    22358    CTG      GAA
                               GCT   GTGTTGAT   TTCC
                               |||   ||||||||   ||||
                               CGA   CACGACTA   AAGG
                                 AA_      ___
GAM907  SV2B    3'  GGAAAAACATCAGAACT    29298    C       GATGAA
                               AG TCTGGTGTT     TTCC
                               || |||||||||     ||||
                               TC AGACTACAA     AAGG
                                A       A_____
GAM907  TTYH2    3'  AGTTCACAACACCAGAGC    50992          A
                               GCTCTGGTGTTG TGAATT
                               |||||||||||| ||||||
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                                CGAGACCACAAC ACTTGA
                                           _
GAM907  LOC145216 3'  AGAGAATTCCTGAGCCAGAGC  83262        GTTGAT     C
                                GCTCTGGT     GAATTC CT
                                ||||||||     |||||| ||
                                CGAGACCG     CTTAAG GA
                                     AGTC__     A
GAM907  LOC145717 3'  GGAAATCCACACACCCAGAGC  66829        _  TGAT  A
                                GCTCTGG TGT    GA TTCC
                                ||||||| |||    || ||||
                                CGAGACC ACA    CT AAGG
                                    C   CAC_  A
GAM907  LOC145725 5'  GGAAATCCACACACCCAGAGC  77411        _  TGAT  A
                                GCTCTGG TGT    GA TTCC
                                ||||||| |||    || ||||
                                CGAGACC ACA    CT AAGG
                                    C   CAC_  A
GAM907  LOC145732 5'  GGAAATCCACACACCCAGAGC  77433        _  TGAT  A
                                GCTCTGG TGT    GA TTCC
                                ||||||| |||    || ||||
                                CGAGACC ACA    CT AAGG
                                    C   CAC_  A
GAM907  LOC149041 3'  GGAAATTCACCAGAG       79141         TTGAT  A
                                CTCTGGTG     GA TTCC
                                ||||||||     || ||||
                                GAGACCAC     TT AAGG
                                     _____  A
GAM907  LOC149465 3'  GGAATTCAATGAGTACCAGGC  79394    T      G  _
                                GC CTGGTGTT AT GAATTCC
                                || |||||||| || |||||||
                                CG GACCATGA TA CTTAAGG
                                 _      G  A
GAM907  LOC151760 5'  AATTCATCAATGAAAAAGA    85492     GG__
                                TCT    TGTTGATGAATT
                                |||    ||||||||||||
                                AGA    GTAACTACTTAA
                                  AAAA
GAM907  LOC161528 3'  GGAAATCCACACACCCAGAGC  82278        _  TGAT  A
                                GCTCTGG TGT    GA TTCC
                                ||||||| |||    || ||||
                                CGAGACC ACA    CT AAGG
                                    C   CAC_  A
GAM907  LOC196957 5'  GGAAATCCACACACCCAGAGC  87827        _  TGAT  A
                                GCTCTGG TGT    GA TTCC
                                ||||||| |||    || ||||
                                CGAGACC ACA    CT AAGG
                                    C   CAC_  A
GAM907  LOC196961 5'  GGAAATCCACACACCCAGAGC  87848        _  TGAT  A
                                GCTCTGG TGT    GA TTCC
                                ||||||| |||    || ||||
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                                CGAGACC ACA   CT AAGG
                                    C  CAC_ A
GAM907  LOC197138 5'  GGAAATCCACACACCCAGAGC  87921       _  TGAT  A
                                GCTCTGG TGT   GA TTCC
                                ||||||| |||   || ||||
                                CGAGACC ACA   CT AAGG
                                    C  CAC_ A
GAM907  LOC201626 5'  GGAACTCACCGGCTACAACGC  88993   TC  GT   A  A
                                GC  TG  GTTG TGA TTCC
                                ||  ||  |||| ||| ||||
                                CG  AC  CGGC ACT AAGG
                                 CA  AT   C  C
GAM907  LOC202759 3'  AGAGAATTCATATTGGACAGA  73511     GTGTTG      C
                                TCTG     ATGAATTC CT
                                ||||     |||||||| ||
                                AGAC     TACTTAAG GA
                                  AGGTTA       A
GAM907  LOC203111 5'  AGAGAATGTAACACCAGAAGT  90466    _       ATGA   C
                                GCT CTGGTGTTG   ATTC CT
                                ||| |||||||||   |||| ||
                                TGA GACCACAAT   TAAG GA
                                  A       G___   A
GAM907  LOC220537 3'  GGAAATCCACACACCCAGAGC  90730       _  TGAT  A
                                GCTCTGG TGT   GA TTCC
                                ||||||| |||   || ||||
                                CGAGACC ACA   CT AAGG
                                    C  CAC_ A
GAM907  LOC221477 3'  GGAAATCCAGACCCAAAGT   92157    C   T   GAT  A
                                GCT TGG GTT   GA TTCC
                                ||| ||| |||   || ||||
                                TGA ACC CAG   CT AAGG
                                  A  _  AC_  A
GAM907  LOC245727 5'  GGAAATCCACACACCCAGAGC  91127       _  TGAT  A
                                GCTCTGG TGT   GA TTCC
                                ||||||| |||   || ||||
                                CGAGACC ACA   CT AAGG
                                    C  CAC_ A
GAM908  NHLH1    5'  TGAGTGTGGCTGGCCCCAGT   18806     AAT   TT
                                ACTG   GCT  GCCACACTCA
                                ||||   |||  ||||||||||
                                TGAC   CGG  CGGTGTGAGT
                                  CC_   T_
GAM908  PRAME    3'  TGAGGAAAAAACATTCAG    20373       C   GCCACA
                                CTGAATG TTT     CTCA
                                ||||||| |||     ||||
                                GACTTAC AAA     GAGT
                                    A  AAG___
GAM908  RARB     3'  TGGCAAAGACCCAGTCA     32366       AATG
                                TGACTG    CTTTGCCA
                                ||||||    ||||||||
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                                ACTGAC   GAAACGGT
                                   CCA_
GAM908  RARB     3'  TGGCAAAGACCCAGTCA     6374        AATG
                                TGACTG   CTTTGCCA
                                ||||||   ||||||||
                                ACTGAC   GAAACGGT
                                   CCA_
GAM908  SLC25A12  3'  TGAGTGTGGCAAAATGGCG   13527     ___
                                TGCT   TTGCCACACTCA
                                ||||   ||||||||||||
                                GCGG   AACGGTGTGAGT
                                  TAA
GAM908  DKFZP434C212 3'  TGAGTGTGAAGGTCACTAAGTC 68920      GAA _   GC
           A                     TGACT   TG CTTT  CACACTCA
                                |||||   || ||||  ||||||||
                                ACTGA   AC GGAA  GTGTGAGT
                                   ATC  T   __
GAM908  DKFZP434L1123 3'  GAGAACACAAACATTCAGTCA  49584         C   CCACA
                                TGACTGAATG TTTG    CTC
                                |||||||||| ||||    |||
                                ACTGACTTAC AAAC    GAG
                                      _   ACAA_
GAM908  DKFZP434N093 3'  GAGTGCGGCCTTTTAGTCA   79944        TGCTTT   A
                                TGACTGAA     GCC CACTC
                                ||||||||     ||| |||||
                                ACTGATTT     CGG GTGAG
                                     TC____   C
GAM908  DKFZP434N1511 3'  GTGCAACTTGCTTCAGTCA   91422        T  T__   C
                                TGACTGAA GC   TTGC AC
                                |||||||| ||   |||| ||
                                ACTGACTT CG   AACG TG
                                     _ TTC   _
GAM908  DKFZp564O1278 3'  AGTGTGTCATCAATCA      63722     C   ATGCTT  C
                                TGA TGA     TG CACACT
                                ||| |||     || ||||||
                                ACT ACT     AC GTGTGA
                                  A  _______  T
GAM908  ENPP4    3'  AGTGTTTTTAATTCAGTCA   30045         GCTTTGCC
                                TGACTGAAT       ACACT
                                |||||||||       |||||
                                ACTGACTTA       TGTGA
                                     ATTTT___
GAM908  FLJ10891  3'  TGTGGCAAGTTTTTCAG     36807      T_   T
                                CTGAA  GCTT GCCACA
                                |||||  |||| ||||||
                                GACTT  TGAA CGGTGT
                                   TT   _
GAM908  FLJ11191  3'  TGTGGCAAGGTTTTCAGTCA   37152         T
                                TGACTGAA GCTTTGCCACA
                                |||||||| ||||||||||
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                                ACTGACTT TGGAACGGTGT
                                     T
GAM908  FLJ12488  5'  TGTGGCAAAGCCTTTA      48331      T
                                TGAA GCTTTGCCACA
                                |||| ||||||||||
                                ATTT CGAAACGGTGT
                                  C
GAM908  FLJ12969  5'  GGACAAAACTTCAGTCA     43113         TGC   _
                                TGACTGAA   TTTG CC
                                ||||||||   |||| ||
                                ACTGACTT   AAAC GG
                                     CA_   A
GAM908  FLJ12985  3'  TGAATGTGGCAAGGTTTTTAAT 46243     C   T         C
          CA                      TGA TGAA GCTTTGCCACA TCA
                                ||| |||| |||||||||| |||
                                ACT ATTT TGGAACGGTGT AGT
                                  A   T         A
GAM908  FLJ14457  3'  TGAGTGTGGCAAGCCTTCAGTT 51389         T   T
          A                       TGACTGAA GCTT GCCACACTCA
                                |||||||| |||| ||||||||||
                                ATTGACTT CGAA CGGTGTGAGT
                                     C   _
GAM908  FLJ22774  3'  AGTGTGTCATCAATCA      63724     C   ATGCTT  C
                                TGA TGA      TG CACACT
                                ||| |||      || ||||||
                                ACT ACT      AC GTGTGA
                                  A  _______  T
GAM908  FLJ23510  3'  GAGTCAGTAAGCATTCATTCA  45283     C       T  CAC
                                TGA TGAATGCTT GC   ACTC
                                ||| ||||||||| ||   ||||
                                ACT ACTTACGAA TG   TGAG
                                  T        _  AC_
GAM908  H-plk     3'  TGAATGTGGCAAAGCTTC     31814     T         C
                                GAA GCTTTGCCACA TCA
                                ||| |||||||||| |||
                                CTT CGAAACGGTGT AGT
                                  _         A
GAM908  HGC6.1.1  3'  TGAGTGTGTCCGGCCCCAGCCA 26833    A   AAT   TTGC
                                TG CTG   GCT    CACACTCA
                                || |||   |||    ||||||||
                                AC GAC   CGG    GTGTGAGT
                                 C   CC_   CCT_
GAM908  KIAA1126  3'  TGAGTGTGTCTGCGCCCAGCCA 71942    A   AA   TTTGC
                                TG CTG  TGC     CACACTCA
                                || |||  |||     ||||||||
                                AC GAC  GCG     GTGTGAGT
                                 C   CC   TCT__
GAM908  KIAA1199  3'  TGAGCACAGAGGAATTCAGTC  72519         G_    CCACA
                                GACTGAAT  CTTTG     CTCA
                                ||||||||  |||||     ||||
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                                CTGACTTA  GAGAC    GAGT
                                    AG    AC___
GAM908  KIAA1979  3'  TGAGTGTGGCAAAACCTTCCAT 88291    CT   TGC
          CA                      TGA  GAA   TTTGCCACACTCA
                                  |||  |||   ||||||||||||
                                  ACT  CTT   AAACGGTGTGAGT
                                    AC   CCA
GAM908  KIAA1979  3'  TGAGTGTGGCAAAACCTTTCA  88292     TGC_
                                  TGAA   TTTGCCACACTCA
                                  ||||   ||||||||||||
                                  ACTT   AAACGGTGTGAGT
                                    TCCA
GAM908  KIAA1979  5'  TGAGTGTGGCAAGACCTTTAGT 88293       TGC
          CA                      TGACTGAA   TTTGCCACACTCA
                                  ||||||||   ||||||||||||
                                  ACTGATTT   GAACGGTGTGAGT
                                      CCA
GAM908  MGC5384   5'  TGAGTGTGGCAAAGCCTTTGGC 48274    A TG  T
          A                        TG C  AA GCTTTGCCACACTCA
                                  || |  || ||||||||||||||
                                  AC G  TT CGAAACGGTGTGAGT
                                   _ GT  C
GAM908  PCSK7    5'  TGAGTGTGACGTGGTTAGCCA  16339    A   AAT   T  C
                                  TG CTG   GCT TG CACACTCA
                                  || |||   ||| || ||||||||
                                  AC GAT   TGG GC GTGTGAGT
                                   C   ___   T  A
GAM908  PPP2R2A   3'  AGTGAAAGCCTTCAGTCA    10745        T    GCCA
                                  TGACTGAA GCTTT    CACT
                                  |||||||| |||||    ||||
                                  ACTGACTT CGAAA    GTGA
                                      C    _____
GAM908  ZNF271    5'  TGAGTGTGGGAAAGCCTTCAGT 95257        T    G
          CA                      TGACTGAA GCTTT CCACACTCA
                                  |||||||| ||||| |||||||||
                                  ACTGACTT CGAAA GGTGTGAGT
                                      C    G
GAM908  LOC115297 3'  TGTGAGATTCAGTCA       72890         G  TTGC
                                  TGACTGAAT CT    CACA
                                  ||||||||| ||    ||||
                                  ACTGACTTA GA    GTGT
                                        _ _____
GAM908  LOC124842 5'  TGGGGCAAAGCACTCA      75661     A       A
                                  TGA TGCTTTGCC CA
                                  ||| ||||||||| ||
                                  ACT ACGAAACGG GT
                                    C        G
GAM908  LOC130412 5'  TGGAACAAAGCATCCAGCA   75741    A  A      __
                                  TG CTG ATGCTTTG  CCA
                                  || ||| ||||||||  |||
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                                AC GAC TACGAAAC  GGT
                                 _  C       AA
GAM908  LOC132948 3'  TGTGGCAAGGTTTCTCAGTC   59175       AT_
                                GACTGA   GCTTTGCCACA
                                ||||||   ||||||||||
                                CTGACT   TGGAACGGTGT
                                   CTT
GAM908  LOC145623 3'  GGGAAAGCATTCAGTC      83398            G
                                GACTGAATGCTTT CC
                                |||||||||||| ||
                                CTGACTTACGAAA GG
                                      G
GAM908  LOC147660 3'  TGTGGCAAATTTTTCAG     78400       TGC
                                CTGAA   TTTGCCACA
                                |||||   |||||||||
                                GACTT   AAACGGTGT
                                   TTT
GAM908  LOC147660 3'  TGAGTGTGGCAAAGCCTTTAGT 78399       T
                                ACTGAA GCTTTGCCACACTCA
                                |||||| ||||||||||||||
                                TGATTT CGAAACGGTGTGAGT
                                   C
GAM908  LOC148266 5'  TGAGTGTGGAAAAGCATTCAGC 78770    A         G
           CA                     TG CTGAATGCTTT CCACACTCA
                                || |||||||||| |||||||||
                                AC GACTTACGAAA GGTGTGAGT
                                 C          A
GAM908  LOC151178 3'  TGGCCTGGAAGATTCAGTCA   80150         G   ___
                                TGACTGAAT CTTT   GCCA
                                ||||||||| ||||   ||||
                                ACTGACTTA GAAG   CGGT
                                      _   GTC
GAM908  LOC161829 3'  TGTAGTAATGCTTCAGTCA    82324        T  T    C
                                TGACTGAA GC TTGC ACA
                                |||||||| || |||| |||
                                ACTGACTT CG AATG TGT
                                     _ T    A
GAM908  LOC163081 3'  TGAATGTGGTAAATCATTCAGT 82408          C        C
           CA                     TGACTGAATG TTTGCCACA TCA
                                |||||||||| ||||||||| |||
                                ACTGACTTAC AAATGGTGT AGT
                                      T        A
GAM908  LOC163861 5'  GAGCACAGTCTGCATTCAGTCA 87045           TTT  CACA
                                TGACTGAATGC   GC    CTC
                                ||||||||||   ||    |||
                                ACTGACTTACG   TG    GAG
                                       TC_  ACAC
GAM908  LOC200953 5'  AGTGTGGCAAAGACAGGACCAG 90207      AA__  _
                                CTG    TG CTTTGCCACACT
                                |||    || ||||||||||||
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                                GAC    AC GAAACGGTGTGA
                                  CAGG  A
GAM908  LOC219401 3'  TGAGTGTGGGAAAGCTCTCAGC 92818    A    AT     G
          CA                      TG CTGA  GCTTT CCACACTCA
                                || ||||  ||||| |||||||||
                                AC GACT  CGAAA GGTGTGAGT
                                 C    CT     G
GAM908  LOC221191 3'  GAGTGCCAGGCATTCA      93574          T  CAC
                                TGAATGCTT GC   ACTC
                                ||||||||| ||   ||||
                                ACTTACGGA CG   TGAG
                                      C ___
GAM908  LOC221596 3'  TGTGGCAAAGCCTTTAG     91983       T
                                CTGAA GCTTTGCCACA
                                ||||| ||||||||||
                                GATTT CGAAACGGTGT
                                   C
GAM908  LOC255624 3'  TGAATGTGGCAAGGTTTTTAAT 94526     C    T         C
          CA                      TGA TGAA GCTTTGCCACA TCA
                                ||| |||| |||||||||| |||
                                ACT ATTT TGGAACGGTGT AGT
                                  A   T          A
GAM908  LOC257115 3'  TGAGCTAAGCATCCAGTC    96526       A     T _
                                GACTG ATGCTT GC CA
                                ||||| |||||| || ||
                                CTGAC TACGAA CG GT
                                   C     T  A
GAM908  LOC90317  5'  TGAATGTGGCAAAGCCTTTA   62251      T         C
                                TGAA GCTTTGCCACA TCA
                                |||| |||||||||| |||
                                ATTT CGAAACGGTGT AGT
                                  C          A
GAM908  LOC90317  3'  TGAATGTGGCAAAGCCTTTAAT 62252     C    T         C
          CA                      TGA TGAA GCTTTGCCACA TCA
                                ||| |||| |||||||||| |||
                                ACT ATTT CGAAACGGTGT AGT
                                  A   C          A
GAM908  LOC90317  3'  TGAATGTGGCAAGGTATTCAG  62253               C
                                CTGAATGCTTTGCCACA TCA
                                |||||||||||||||| |||
                                GACTTATGGAACGGTGT AGT
                                          A
GAM908  LOC90317  5'  TGAATGTGGCAAGGTCTTCAGT 62254        T         C
                                ACTGAA GCTTTGCCACA TCA
                                |||||| |||||||||| |||
                                TGACTT TGGAACGGTGT AGT
                                   C          A
GAM908  LOC90317  5'  TGAGTGTGGCAAAGCCTTTCA  62255      T_
                                TGAA  GCTTTGCCACACTCA
                                ||||  ||||||||||||||
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                                ACTT  CGAAACGGTGTGAGT
                                  TC
GAM908  LOC90322  5' TGTGGCAAGGTCTTCAATC   62267    C   T
                                GA TGAA GCTTTGCCACA
                                || |||| ||||||||||
                                CT ACTT TGGAACGGTGT
                                 A   C
GAM908  LOC90333  3' TGAATGTGGCAAGGTTTTTAAT 62304    C   T       C
          CA                     TGA TGAA GCTTTGCCACA TCA
                                ||| |||| |||||||||| |||
                                ACT ATTT TGGAACGGTGT AGT
                                  A   T        A
GAM908  LOC90333  3' TGAGTGTGGCAAGACCTTCCAT 62305    CT  TGC
          CA                     TGA  GAA   TTTGCCACACTCA
                                ||| |||  ||||||||||||
                                ACT  CTT   GAACGGTGTGAGT
                                  AC   CCA
GAM908  LOC90333  3' TGTGGCAAATTTTTCAG    62307     TGC
                                CTGAA   TTTGCCACA
                                |||||  |||||||||
                                GACTT   AAACGGTGT
                                   TTT
GAM908  LOC90485  3' GAGTGCGGCAAAGCTTTCAGCC 63015   A   T     A
          A                     TG CTGAA GCTTTGCC CACTC
                                || ||||| |||||||| |||||
                                AC GACTT CGAAACGG GTGAG
                                 C    T      C
GAM908  LOC90485  3' GAGTGCGGCAAGGCCTTCAGCA 63016   A   T     A
                                TG CTGAA GCTTTGCC CACTC
                                || ||||| |||||||| |||||
                                AC GACTT CGGAACGG GTGAG
                                 _    C      C
GAM908  LOC91664  3' GAGTGTGGCAAAGCCTTTA   66873    T
                                TGAA GCTTTGCCACACTC
                                |||| ||||||||||||||
                                ATTT CGAAACGGTGTGAG
                                  C
GAM908  LOC91664  3' TGTGGCAAATTTTTCAG    66875     TGC
                                CTGAA   TTTGCCACA
                                |||||  |||||||||
                                GACTT   AAACGGTGT
                                   TTT
GAM909  CENTD2   3' GCATGGGAAACTGCACCC   30870       GTG
                                GGGTGCAGT   CTCATGC
                                |||||||||  |||||||
                                CCCACGTCA   GGGTACG
                                     AA_
GAM909  CENTD2   3' GCATGGGAAACTGCACCC   57555       GTG
                                GGGTGCAGT   CTCATGC
                                |||||||||  |||||||
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                                CCCACGTCA  GGGTACG
                                     AA_
GAM909  GM2A    3'  GCATGAGCCACTACACCCAG  67777      C   T
                                CTGGGTG AGTG GCTCATGC
                                ||||||| |||| ||||||||
                                GACCCAC TCAC CGAGTACG
                                   A  _
GAM909  LPIN1   3'  CATGACTATAACCCAGTGA   67392       GCAG   C
                                TCACTGGGT   TGTG TCATG
                                |||||||||   |||| |||||
                                AGTGACCCA   ATAT AGTAC
                                     ____  C
GAM909  LRPAP1  3'  GCAGTCACCACCCCAGTGA   9807       _ CA  __
                                TCACTGGG TG  GTG  TGC
                                |||||||| ||  |||  |||
                                AGTGACCC AC  CAC  ACG
                                   C  __  TG
GAM909  PLD1    3'  CACACTGCACACAGTGA     10624      G
                                TCACTG GTGCAGTGTG
                                |||||| ||||||||||
                                AGTGAC CACGTCACAC
                                  A
GAM909  TAPBP   3'  GCCACCACACCCAGTGA     12126       CA  T
                                TCACTGGGTG  GTG GC
                                ||||||||||  ||| ||
                                AGTGACCCAC  CAC CG
                                     AC  _
GAM909  ATP10B  3'  GCACATCTGCACCCAG      63368        _
                                CTGGGTGCAG TGTGC
                                |||||||||| |||||
                                GACCCACGTC ACACG
                                     T
GAM909  BMF     3'  GCATGCTACCCCAGTGA     53158       TGC
                                TCACTGGG   AGTGTGC
                                ||||||||   |||||||
                                AGTGACCC   TCGTACG
                                   CA_
GAM909  C1orf34 3'  CACACCACACCCAGTGA     60665       CA
                                TCACTGGGTG  GTGTG
                                ||||||||||  |||||
                                AGTGACCCAC  CACAC
                                     AC
GAM909  CECR1   3'  GCATGTGCCACCACACCCAGCT 33815    _     CA  T  T
          GA                     TCA CTGGGTG  GTG GC CATGC
                                ||| |||||||  ||| || |||||
                                AGT GACCCAC  CAC CG GTACG
                                  C      AC  _ T
GAM909  FLJ10535 3' GCATGAGCCACCACACCCAGCG 36241    A     CA  T
          A                      TC CTGGGTG  GTG GCTCATGC
                                || |||||||  ||| ||||||||
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                                AG GACCCAC  CAC CGAGTACG
                                 C      AC  _
GAM909  FLJ10687  3'  CACACACACCCAATGA      36407     C     CA
                                TCA TGGGTG  GTGTG
                                ||| ||||||  |||||
                                AGT ACCCAC  CACAC
                                  A     A_
GAM909  FLJ12363  3'  GCACCTGTCACCACACCCAG   49680       _______  T
                                CTGGGTG     CAG GTGC
                                |||||||     ||| ||||
                                GACCCAC     GTC CACG
                                    ACCACT  _
GAM909  FLJ12747  3'  GCATGCGCCACCACACCCAG   49717       CA   T  T
                                CTGGGTG  GTG GC CATGC
                                |||||||  ||| || |||||
                                GACCCAC  CAC CG GTACG
                                    AC   _  C
GAM909  FLJ20584  3'  GCACCACCACACCCAGTGG    35428        CA  _
                                TCACTGGGTG  GTG TGC
                                ||||||||||  ||| |||
                                GGTGACCCAC  CAC ACG
                                     AC   C
GAM909  HEMK      3'  GCATAAGCAGCTCACTCCCAGT 32432        TGC   ___   C
          GA                      TCACTGGG   AGTG   TGCT ATGC
                                |||||||   ||||   |||| ||||
                                AGTGACCC   TCAC   ACGA TACG
                                    ___    TCG    A
GAM909  HSMPP8    3'  GCATGAGCCACCGCACCCAG   93476       A   T
                                CTGGGTGC GTG GCTCATGC
                                |||||||| ||| ||||||||
                                GACCCACG CAC CGAGTACG
                                    C   _
GAM909  ICK       3'  GCATGAGCCACTGCACCCAG   29930         T
                                CTGGGTGCAGTG GCTCATGC
                                |||||||||||| ||||||||
                                GACCCACGTCAC CGAGTACG
                                          _
GAM909  KIAA0599  3'  GCATGAGCCACCACACCCAG   77180       CA   T
                                CTGGGTG  GTG GCTCATGC
                                |||||||  ||| ||||||||
                                GACCCAC  CAC CGAGTACG
                                    AC   _
GAM909  MGC3101   3'  CACAAGCACAGCCCAGTGG    43880        GCAG     CA
                                TCACTGGGT    TGTGCT  TG
                                |||||||||    ||||||  ||
                                GGTGACCCG    ACACGA  AC
                                     _____      AC
GAM909  PEPP3     5'  CACATTTCTACACCCAGTGA   30037         C___
                                TCACTGGGTG    AGTGTG
                                ||||||||||    ||||||
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                                AGTGACCCAC    TTACAC
                                      ATCT
GAM909  RAB33B   3'  GCACTACCACACCCAGCTGA   48494     _      CA  _
                                TCA CTGGGTG  GT GTGC
                                ||| |||||||  || ||||
                                AGT GACCCAC  CA CACG
                                  C      AC  T
GAM909  SEMA4G   3'  CCATGCACCAACACTGCACTCA 35433   C        T________  TCAT
           ATGA                    TGGGTGCAGTG      GC   G
                                ||||||||||       ||   |
                                ACTCACGTCAC      CG   C
                                A         AACCAIII  TACT
GAM909  SEMA4G   3'  CCATGCACCAACACTGCACTCA 94674   C        T________  TCAT
           ATGA                    TGGGTGCAGTG      GC   G
                                ||||||||||       ||   |
                                ACTCACGTCAC      CG   C
                                A         AACCAIII  TACT
GAM909  SIRPB1   3'  GCATGTACCACCACACCCAG   20254       CA   TGCT
                                CTGGGTG  GTG   CATGC
                                |||||||  |||   |||||
                                GACCCAC  CAC   GTACG
                                    AC   CAT_
GAM909  TU12B1-TY 3'  GCATGCACTACCACACCCAG   33387       CA  _   TC
                                CTGGGTG  GT GTGC  ATGC
                                |||||||  || ||||  ||||
                                GACCCAC  CA CACG  TACG
                                    AC  T   __
GAM909  LOC132241 3'  GCATGCGCCACCACACCCAG   75048       CA   T  T
                                CTGGGTG  GTG GC CATGC
                                |||||||  ||| || |||||
                                GACCCAC  CAC CG GTACG
                                    AC   _  C
GAM909  LOC146136 5'  CATGAGTAAAGCACCAAGT   72941     G    AGTG
                                ACT GGTGC    TGCTCATG
                                |||  |||||    ||||||||
                                TGA CCACG    ATGAGTAC
                                  A     AA__
GAM909  LOC155036 5'  GCATGAGGACACATCCAGT    86343       GCA    G
                                ACTGGGT   GTGT CTCATGC
                                |||||||   |||| |||||||
                                TGACCTA   CACA GAGTACG
                                    ___    G
GAM909  LOC169611 3'  GCACCCACCACCACACCCAG   82764       CA   _  CTCA
                                CTGGGTG  GTG TG    TGC
                                |||||||  ||| ||    |||
                                GACCCAC  CAC AC    ACG
                                    AC   C  CC__
GAM909  LOC196264 3'  GCATGCGCCACCACACCCAG   87606       CA   T  T
                                CTGGGTG  GTG GC CATGC
                                |||||||  ||| || |||||
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                                GACCCAC  CAC CG GTACG
                                    AC   _  C
GAM909  LOC220565 3'  CATGAGTAAAGCACCAAGT   90747     G    AGTG
                                ACT GGTGC   TGCTCATG
                                ||| |||||   ||||||||
                                TGA CCACG   ATGAGTAC
                                  A    AA__
GAM909  LOC220575 3'  GCATGGGCCACCACACCCAGCT 76313     _      CA   T
           GA                     TCA CTGGGTG  GTG GCTCATGC
                                ||| |||||||  ||| ||||||||
                                AGT GACCCAC  CAC CGGGTACG
                                  C      AC  _
GAM909  LOC92267  3'  GCACCTGACACCACACCCAG   68614        _______  T
                                CTGGGTG     CAG GTGC
                                |||||||     ||| ||||
                                GACCCAC     GTC CACG
                                    ACCACA  _
GAM910  ARNT2    3'  AAACAACCCGTGCATCCCTGC  29450     A   TTTTA
                                GTA GGAT    GGGTTGTTT
                                ||| ||||    |||||||||
                                CGT CCTA    CCCAACAAA
                                  C   CGTG_
GAM910  LCT      3'  AACCGTAAAAATCCTT      9697           G
                                AAGGATTTTTA GGTT
                                |||||||||||| ||||
                                TTCCTAAAAAT CCAA
                                       G
GAM910  RPL15    3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM910  FBXO30   3'  AACTAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                 G        AA
GAM910  KIAA0494  3'  AACAACCCTTACTTAC      28736      GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM910  PRO0641   5'  AAACAACCCCAAAACTTG    26210     GAT   A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                   ___   C
GAM910  SMT3H2   3'  AACAACATAAAAATCCTTGC   22670           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
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                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM910  LOC120103 3'  AACCTATGAAAAATCCTTGC   74002          A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||  |||||
                                CGTTCCTAAAAA   TCCAA
                                      GTA
GAM910  LOC129831 3'  AAACAACCCCAATGTCC     74889     TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM910  LOC133088 5'  AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                      GTA GGATTTTT     TTGTTT
                                ||| ||||||||     ||||||
                                CGT CCTAAAAA     AACAAA
                                  C       GATAA
GAM910  LOC148089 3'  GGCCCTAAAAATTCCTAC    78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM910  LOC154547 3'  AACAACATAAAAATCCTTGC   76050          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM910  LOC158104 3'  ACAGCCAAAAATCCTTA     60313          AG
                                TAAGGATTTTT  GGTTGT
                                ||||||||||  ||||||
                                ATTCCTAAAAA  CCGACA
                                      __
GAM910  LOC205880 5'  AAACAACCATCATCCTGAC    90709    A    TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM910  LOC221561 3'  AACAACATAAAAATCCTTGC   92130          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM910  LOC257591 3'  AACAACATAAAAATCCTTGC   97840          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM910  LOC51145  3'  AGCTAAAATCCTTAC       32393          TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
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                              CATTCCTAAAA   TCGA
                                    ___
GAM911  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644      C    CAC
                              ATTT ACTTT   TGTCTGAG
                              |||| |||||   ||||||||
                              TAAA TGAAA   ACAGATTC
                                A    T__
GAM911  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                              CATTT   TTT AC GTCTGAGAT
                              |||||   ||| || |||||||||
                              GTAAA   AAA TG TAGACTCTA
                                 TA_   T  _
GAM911  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                              CATTTCACTTTC CTG
                              |||||||||||| |||
                              GTAAAGTGAAAG GAT
                                    _
GAM911  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
           TG                   CATTTCACTTTCACTGTCTGAGAT
                              |||||||||||||||||||||||||
                              GTAAAGTGAAAGTGACAGACTCTA

GAM911  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                              CA  TTCACTGTCTG GA
                              ||  |||||||||| ||
                              GT  AGGTGACAGAC CT
                               AT         C
GAM911  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                              ATTTCACTTT ACTGT
                              |||||||||| |||||
                              TAAAGTGAAA TGACA
                                    A
GAM911  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                              TTTCACTTTCA   TCTG GA
                              ||||||||||   |||| ||
                              AAAGTGAAAGT   GGAC CT
                                    T__   _
GAM911  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                              TTTCA TTTCACTGTCT
                              ||||| ||||||||||
                              AAAGT AAAGTGACGGG
                                 A
GAM911  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                              TTTCACTTT  CTGT   AGAT
                              |||||||||  ||||   ||||
                              AAAGTGAAA  GACA   TCTA
                                   C_   CG_
GAM911  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                              TTCACTTTCA  GT  GAG
                              |||||||||  ||  |||
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                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM911  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                |||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM911  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC       GTCTGAGAT
                                |||||||       |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM911  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                    C__
GAM911  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM911  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM911  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM911  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM911  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM911  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148         TCAC   C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM911  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
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                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM911  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941        CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM911  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM911  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM911  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226     A      GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM911  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                                _
GAM912  CARPX    3'  CTGTCAAGAAATCAATAAATGT 39421     TGT__
           G                     CAC     TTGATTTCTTGACAG
                                |||     ||||||||||||||||
                                GTG    AACTAAAGAACTGTC
                                  TAAAT
GAM912  ELK4     3'  TTATAAAACAAACAGTGAT   41419         A  CT
                                ATCACTGTTTG TTT  TGA
                                |||||||||| |||  |||
                                TAGTGACAAAC AAA  ATT
                                      _  AT
GAM912  KCNK6    3'  TGTCCCCAGACAGTGATG    16698          ATTTCTT
                                CATCACTGTTTG      GACA
                                ||||||||||||      ||||
                                GTAGTGACAGAC      CTGT
                                      CC_____
GAM912  LRAT     3'  CTGTCAAGAATCACAAA     60104     AT_
                                TTTG   TTCTTGACAG
                                ||||   ||||||||||
                                AAAC   AAGAACTGTC
                                  ACT
GAM912  MAN2A2   3'  CTGTTTCAGAAACCAACAGTGA 20396         T A    T_
           TG                    CATCACTGTT G TTTCT  GACAG
                                |||||||||| | |||||  |||||
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                                GTAGTGACAA C AAAGA  TTGTC
                                      _ C    CT
GAM912  PCP4     3'  CTGTCAAGAAATTAAAAG    20572    G
                                CT TTTGATTTCTTGACAG
                                || ||||||||||||||||
                                GA AAATTAAAGAACTGTC
                                 _
GAM912  PHTF1    3'  TCAAGGAAAGTGATG       21732        GTTTGA
                                CATCACT     TTTCTTGA
                                |||||||     ||||||||
                                GTAGTGA     AAGGAACT
                                  _______
GAM912  XPR1     3'  CTGTCAAGAAACAGCAGT    16426       T A
                                ACTGTT G TTTCTTGACAG
                                |||||| | ||||||||||
                                TGACGA C AAAGAACTGTC
                                  _ _
GAM912  C9orf5   3'  AAATTAGCAGCAGTGATG    49271         __
                                CATCACTGTT  TGATTT
                                ||||||||||  ||||||
                                GTAGTGACGA  ATTAAA
                                      CG
GAM912  FHX      3'  TCAAGGGTGAAAGTGATG    37306       GTTTGAT
                                CATCACT      TTCTTGA
                                |||||||      |||||||
                                GTAGTGA      GGGAACT
                                     AAGT___
GAM912  FLJ12643 3'  GTCAAGAAAGAAAATA      82786      GA
                                TGTTT  TTTCTTGAC
                                |||||  |||||||||
                                ATAAA  AAAGAACTG
                                   AG
GAM912  FLJ13031 5'  TCAAAAAAACGAAACAGTGAT  45198          _ A   C
                                ATCACTGTTT G TTT TTGA
                                |||||||||| | ||| ||||
                                TAGTGACAAA C AAA AACT
                                      G A   A
GAM912  FLJ22833 3'  AGTAATCAAACAGTGATG    43098             T
                                CATCACTGTTTGATT CT
                                |||||||||||||| ||
                                GTAGTGACAAACTAA GA
                                         T
GAM912  KIAA1559 3'  GTCAAGAAAAAGGAAACA    73072       GA__
                                TGTTT    TTTCTTGAC
                                |||||    |||||||||
                                ACAAA    AAAGAACTG
                                   GGAA
GAM912  KIAA1958 3'  AAGAAACCAAACATGAT     81896      C     A
                                ATCA TGTTTG TTTCTT
                                |||| |||||| ||||||
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                                TAGT ACAAAC AAAGAA
                                  _     C
GAM912  LOC149711 5'  CTGCCAAAAAATGAGATAGTG  84680        G   C   A
                                CACTGTTT ATTT TTG CAG
                                |||||||| |||| ||| |||
                                GTGATAGA TAAA AAC GTC
                                    G   A   C
GAM912  LOC201799 3'  CTGCCAAGAAGACACAGTGA   89060       TT A     A
                                TCACTGT  G TTTCTTG CAG
                                |||||||  | ||||||| |||
                                AGTGACA  C GAAGAAC GTC
                                   __ A     C
GAM912  LOC253263 3'  CTGCCATCCCCCAAACAGTGA  97031         ATTTCT  A
                                TCACTGTTTG     TG CAG
                                ||||||||||     || |||
                                AGTGACAAAC     AC GTC
                                      CCCCT_  C
GAM912  LOC56959  5'  TGTCTATCAAACAGTG      81928          TTCTT
                                CACTGTTTGAT    GACA
                                ||||||||||     ||||
                                GTGACAAACTA    CTGT
                                      T_____
GAM913  ESRRG     3'  ACTCCAATCAGTTCAGATGTG  66385         TAT
                                CACATCTGAG   GTTGGAGT
                                |||||||||   ||||||||
                                GTGTAGACTT   TAACCTCA
                                      GAC
GAM913  RPH3AL    5'  ACCCCCATCTCAGATGTGA   22737          T   TT  A
                                TCACATCTGAG ATG  GG GT
                                |||||||||||| |||  || ||
                                AGTGTAGACTC TAC  CC CA
                                      _   C_  _
GAM913  EML4      3'  CTTCAATACTCAGAAATGATG  38809      CA       GT
                                CATCA  TCTGAGTAT  TGGAG
                                |||||  |||||||||  |||||
                                GTAGT  AGACTCATA  ACTTC
                                   AA        __
GAM913  FLJ13962  3'  ACTCCAACAATGACGAT     45869     TGA  A
                                ATC   GT TGTTGGAGT
                                |||   || |||||||||
                                TAG   TA ACAACCTCA
                                  CAG  _
GAM913  FLJ21324  5'  CCGAGCACTCAGATGGATG   91195      A       ATG
                                CATC CATCTGAGT   TTGG
                                ||||| |||||||||  ||||
                                GTAG GTAGACTCA   AGCC
                                   _       CG_
GAM913  KIAA0552  5'  CCCGCGACCCAGATGTG     28309        A  A   T
                                CACATCTG GT TGT GG
                                |||||||| || ||| ||
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                                GTGTAGAC CA GCG CC
                                     C _  C
GAM913  KIAA0922  5'  ACTCCAACACTAAAAGCATGAT 30832      CAT  GAGTA
          G                   CATCA  CT    TGTTGGAGT
                              |||||  ||    |||||||||
                              GTAGT  GA    ACAACCTCA
                                AC_  AAATC
GAM913  KIAA1058  3'  TCCAACAAGCACAATG     82256     C  A  A
                              CAT TG GT TGTTGGA
                              ||| || || |||||||
                              GTA AC CG ACAACCT
                                _  A  A
GAM913  MBD2      3'  CTTAGTGCATCAGATGT     31717        _   GTT
                              ACATCTGA GTAT   GG
                              |||||||| ||||   ||
                              TGTAGACT CGTG   TC
                                   A    AT_
GAM913  LOC121838 5'  ACCCCAAGTACCAAATGTGA   75994      C  A   G   A
                              TCACAT TG GTAT TTGG GT
                              |||||| || |||| |||| ||
                              AGTGTA AC CATG AACC CA
                                 A  _   _   C
GAM913  LOC122970 3'  ACTCGAGACTCAGATGGGA   74174    A       ATG  G
                              TC CATCTGAGT   TT GAGT
                              || |||||||||   || ||||
                              AG GTAGACTCA   GA CTCA
                               G       ____  G
GAM913  LOC150819 5'  ACTCCAGTCTGGACTCAGATG  85117        ATG__
                              CATCTGAGT    TTGGAGT
                              |||||||||    |||||||
                              GTAGACTCA    GACCTCA
                                   GGTCT
GAM914  ABCC1     3'  CTGGCCCAAAGCAGTGTT    17180        C   A_
                              AACGCTGCT TGG  CAG
                              ||||||||| |||  |||
                              TTGTGACGA ACC  GTC
                                   A   CG
GAM914  ABCC1     3'  CTGGCCCAAAGCAGTGTT    39125        C   A_
                              AACGCTGCT TGG  CAG
                              ||||||||| |||  |||
                              TTGTGACGA ACC  GTC
                                   A   CG
GAM914  ABCC1     3'  CTGGCCCAAAGCAGTGTT    39133        C   A_
                              AACGCTGCT TGG  CAG
                              ||||||||| |||  |||
                              TTGTGACGA ACC  GTC
                                   A   CG
GAM914  ACPP      3'  CTGCCCAGAGCAGGGT      66848    G       A
                              AC CTGCTCTGG CAG
                              || ||||||||| |||
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                                TG GACGAGACC GTC
                                 G       C
GAM914  ARF1    3'  CCATCTGTCCCTCGGTCGC   70658   T  CT_
                                GC GCT   GGACAGATGG
                                || |||   ||||||||||
                                CG TGG   CCTGTCTACC
                                 C   CTC
GAM914  CCNK    5'  CCGACTGAGGGCAGCG     77283        GGA  A
                                CGCTGCTCT   CAG TGG
                                |||||||||   ||| |||
                                GCGACGGGA   GTC GCC
                                     ___  A
GAM914  CRABP2  3'  CCAGCCCAGAGCAGGGT    8536    G       ACAGA
                                AC CTGCTCTGG    TGG
                                || |||||||||    |||
                                TG GACGAGACC    ACC
                                 G       CG___
GAM914  DCN     5'  CTAGTCACAGAGCAGC     8617         _  _
                                GCTGCTCTG GAC AG
                                ||||||||| ||| ||
                                CGACGAGAC CTG TC
                                     A  A
GAM914  DUSP5   3'  CCTCTTCTCAGAGCA      15351       _ C  T
                                TGCTCTG GA AGA GG
                                ||||||| || ||| ||
                                ACGAGAC CT TCT CC
                                    T _  _
GAM914  ENO2    3'  CCAGCTGCACCAGAGCA    8776        A_  A
                                TGCTCTGG  CAG TGG
                                ||||||||  ||| |||
                                ACGAGACC  GTC ACC
                                     AC  G
GAM914  ESR1    3'  CCATCTTTTCAGTAGCGTT   3702         CT  C
                                AACGCTGCT  GGA AGATGG
                                |||||||||  ||| ||||||
                                TTGCGATGA  CTT TCTACC
                                     __  T
GAM914  ETF1    3'  CCATCTGTTTGCAG       16393     TCT
                                CTGC   GGACAGATGG
                                ||||   ||||||||||
                                GACG   TTTGTCTACC
                                   ___
GAM914  EXTL3   3'  CCATCTGTGTGCAGC      7529       TCT G
                                GCTGC   G ACAGATGG
                                |||||   | ||||||||
                                CGACG   T TGTCTACC
                                   ___ G
GAM914  FANCG   5'  CCATCTGTCCTGGAAAGC   16141    GC  _
                                GCT  TCT GGACAGATGG
                                |||  ||| ||||||||||
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                                CGA  AGG CCTGTCTACC
                                  A_   T
GAM914  GAA     3'  CCATCTGTTCCCAGCACCG   3839     C    CT
                                CG TGCT  GGACAGATGG
                                || ||||  ||||||||||
                                GC ACGA  CTTGTCTACC
                                 C    CC
GAM914  GNB1    3'  CCAGTGTTCAGCAGCAGCGTT  9069          _      GA
                                AACGCTGCT CTGGACA  TGG
                                ||||||||| |||||||  |||
                                TTGCGACGA GACTTGT  ACC
                                      C      G_
GAM914  GPRC5B  3'  CCATCTGTCCTGAGCAAGT   32663    GC    T
                                AC  TGCTC GGACAGATGG
                                ||  ||||| ||||||||||
                                TG  ACGAG CCTGTCTACC
                                 A_    T
GAM914  GRIN2A  3'  CCATCTGTCTGCCGAAGGC   5895     GC  T__
                                GCT  TC   GGACAGATGG
                                |||  ||   ||||||||||
                                CGG  AG   TCTGTCTACC
                                  A_  CCG
GAM914  HMG20A  3'  CCATCTGTTGACAATGT     36536     C  C  TG
                                ACG TG TC  GACAGATGG
                                ||| || ||  |||||||||
                                TGT AC AG  TTGTCTACC
                                  A  _  __
GAM914  HS3ST3B1 5'  CCACCTGGGGAAGAGCAGC   20148        GGA_   A
                                GCTGCTCT    CAG TGG
                                ||||||||    ||| |||
                                CGACGAGA    GTC ACC
                                     AGGG   C
GAM914  KCNJ10  5'  CCATCTGTCCCGCTGC      9535     T  TCT
                                GC GC   GGACAGATGG
                                || ||   ||||||||||
                                CG CG   CCTGTCTACC
                                 T  C__
GAM914  LIF     3'  CCATCTGTCCATCCCAACAGC  9734      CTC___
                                GCTG     TGGACAGATGG
                                ||||     ||||||||||
                                CGAC     ACCTGTCTACC
                                  AACCCT
GAM914  LZTS1   3'  CCATCTGTCCAGCTGGGGC   40685     GCT_
                                GCT    CTGGACAGATGG
                                |||    ||||||||||||
                                CGG    GACCTGTCTACC
                                  GGTC
GAM914  MNT     3'  CCACCTGTCCGGCCCAGTG   39706      CT       A
                                CGCTG  CTGGACAG TGG
                                |||||  |||||||| |||
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                                GTGAC  GGCCTGTC ACC
                                  CC       C
GAM914  NKX2H    5'  CCATCCGTAGGAGCGGCGT   26843         GG  A
                                ACGCTGCTCT  AC GATGG
                                ||||||||||  || |||||
                                TGCGGCGAGG  TG CTACC
                                     A_  C
GAM914  S100A1   5'  CCATCTGTCCAGAACCTGC   20776    TGC_
                                GC   TCTGGACAGATGG
                                ||   ||||||||||||||
                                CG   AGACCTGTCTACC
                                 TCCA
GAM914  SCML2    3'  CCACCTGCCCAGCCATGTT   20312     C  CT   A   A
                                AACG TG  CTGG CAG TGG
                                |||| ||  |||| ||| |||
                                TTGT AC  GACC GTC ACC
                                  _ C_   C   C
GAM914  SDC4     3'  CCATCTGTTGGACAGC      11476     C  TG A
                                GCTG TC  G CAGATGG
                                |||| ||  | |||||||
                                CGAC AG  T GTCTACC
                                  _ GT _
GAM914  SELPLG   3'  CCATCTGTTTTGGCA       59687     CT
                                TGCT  GGACAGATGG
                                ||||  ||||||||||
                                ACGG  TTTGTCTACC
                                  T_
GAM914  SNTB1    3'  CCATCTGTAGTGAGCAGCG   40703        TGG
                                CGCTGCTC   ACAGATGG
                                ||||||||   ||||||||
                                GCGACGAG   TGTCTACC
                                     TGA
GAM914  SQSTM1   3'  CCATTTGTAAGAACAATGC   14015    __  C   GG
                                GC  TG TCT  ACAGATGG
                                ||  || |||  ||||||||
                                CG  AC AGA  TGTTTACC
                                 TA  A   A_
GAM914  TNFRSF6B 3'  CCAGCTCAGAGCAGTG      51981          ACAGA
                                CGCTGCTCTGG    TGG
                                ||||||||||     |||
                                GTGACGAGACT    ACC
                                      CG___
GAM914  TRPM4    3'  CCATCTGGAGGCTGCAGGGT   34405    G   T_  GGA
                                AC CTGC  CT   CAGATGG
                                || ||||  ||   |||||||
                                TG GACG  GG   GTCTACC
                                 G   TC  AG_
GAM914  TSG      3'  CCAAGACAAAGCAGTGTT    40232         C  GACAGA
                                AACGCTGCT TG     TGG
                                ||||||||| ||     |||
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                                TTGTGACGA AC     ACC
                                     A  AGA___
GAM914  TTN     3'  CCTATGCCAGAGCAGTG    55919         A  GAT
                                CGCTGCTCTGG CA   GG
                                |||||||||| ||   ||
                                GTGACGAGACC GT   CC
                                      _  AT_
GAM914  TTN     3'  CCTATGCCAGAGCAGTG    55937         A  GAT
                                CGCTGCTCTGG CA   GG
                                |||||||||| ||   ||
                                GTGACGAGACC GT   CC
                                      _  AT_
GAM914  TTN     3'  CCTATGCCAGAGCAGTG    55949         A  GAT
                                CGCTGCTCTGG CA   GG
                                |||||||||| ||   ||
                                GTGACGAGACC GT   CC
                                      _  AT_
GAM914  APCL    5'  CATCTGTCCTGCCGTT     19667     CT  TCT
                                AACG  GC   GGACAGATG
                                ||||  ||   |||||||||
                                TTGC  CG   CCTGTCTAC
                                  __  T__
GAM914  ATP10D  5'  CCAGACACCAGAGCAGGT   73141    G       ACAGA
                                AC CTGCTCTGG    TGG
                                || |||||||||    |||
                                TG GACGAGACC    ACC
                                 _       ACAG_
GAM914  BRPF3   3'  CCATCTGTCCACATGGATGT  92313    _  CTC
                                ACG CTG   TGGACAGATGG
                                ||| |||   ||||||||||
                                TGT GGT   ACCTGTCTACC
                                  A   AC_
GAM914  C1orf14 5'  CCACCTAGCTCTGAGCAGCG  48180       T_  AC  A
                                CGCTGCTC  GG  AG TGG
                                ||||||||  ||  || |||
                                GCGACGAG  TC  TC ACC
                                     TC  GA  C
GAM914  C20orf160 3'  CCATCTGTCCAGTGAGC    54647    GCT
                                GCT   CTGGACAGATGG
                                |||   ||||||||||||
                                CGA   GACCTGTCTACC
                                  GT_
GAM914  C20orf36  3'  CCATCCTCAGAGCAGGT    36796    G       ACA
                                AC CTGCTCTGG   GATGG
                                || |||||||||   |||||
                                TG GACGAGACT   CTACC
                                 _       C__
GAM914  C22orf5   3'  CCATCTGTCCCACACGC    24341    _  CTCT
                                GC TG    GGACAGATGG
                                || ||    ||||||||||
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                                CG AC   CCTGTCTACC
                                 C  AC__
GAM914  CENTG2   5' CCAGGAGCCCAGAGCAGCG   29877         ACAGA
                                CGCTGCTCTGG    TGG
                                ||||||||||    |||
                                GCGACGAGACC    ACC
                                     CGAGG
GAM914  CPLX1    3' CCATCCGTCTCTGTCCGCGT  21835     T_ TCT   A
                                ACGC  GC   GGAC GATGG
                                ||||  ||   |||| |||||
                                TGCG  TG   TCTG CTACC
                                  CC  TC_   C
GAM914  DKFZP434A0131 3' CCAGGAGTCCCAGAGCAGC   38627         _ AGA
                                GCTGCTCTGG AC   TGG
                                |||||||||| ||   |||
                                CGACGAGACC TG   ACC
                                     C  AGG
GAM914  FLJ00007 3' CCATCAATGATCCAGAGCA   71275        _ __
                                TGCTCTGGA CA  GATGG
                                ||||||||| ||  |||||
                                ACGAGACCT GT  CTACC
                                     A  AA
GAM914  FLJ00060 5' CCATCTATCGGAGCGGT    61093         AC
                                GCTGCTCTGG  AGATGG
                                ||||||||||  ||||||
                                TGGCGAGGCT  TCTACC
                                     A_
GAM914  FLJ10620 3' CCATCTGTATCAGCGCA    36357    T   _
                                TGC CTGG ACAGATGG
                                ||| |||| ||||||||
                                ACG GACT TGTCTACC
                                  C   A
GAM914  FLJ10932 3' CCATCTGTCTGCTTCAG    36892    CTC
                                CTG   TGGACAGATGG
                                |||   ||||||||||
                                GAC   GTCTGTCTACC
                                  TTC
GAM914  FLJ12476 5' CCATTACACCCAGAGCAGC   42948         ACA_
                                GCTGCTCTGG   GATGG
                                ||||||||||   |||||
                                CGACGAGACC   TTACC
                                     CACA
GAM914  FLJ13710 3' CCATCAGTAGGGCAGC     45680        GACA
                                GCTGCTCTG   GATGG
                                |||||||||   |||||
                                CGACGGGAT   CTACC
                                     GA__
GAM914  FLJ14154 3' CCATCTGTCTTGTAGGGC   45812      ___
                                GCTCT   GGACAGATGG
                                |||||   ||||||||||
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                                CGGGA  TCTGTCTACC
                                   TGT
GAM914  FLJ20303  3'  CCAAATCCAGAGCAGC     34910          CAGA
                                GCTGCTCTGGA   TGG
                                ||||||||||   |||
                                CGACGAGACCT   ACC
                                      AA__
GAM914  FLJ20457  3'  CCACTTATAGAGCAGGTT    35219    G      GAC  A
                                AAC CTGCTCTG  AG TGG
                                ||| ||||||||  || |||
                                TTG GACGAGAT  TC ACC
                                  _      AT_ _
GAM914  FLJ21438  5'  CCATCTGCAGGACAACGT    61519    C  CT   GA
                                ACG TG  CTG  CAGATGG
                                ||| ||  |||  |||||||
                                TGC AC  GAC  GTCTACC
                                  A  AG  __
GAM914  FLJ22242  5'  CCACAATGGAGGCAGCGTT   46866        CTGGA  GA_
                                AACGCTGCT    CA   TGG
                                |||||||||    ||   |||
                                TTGCGACGG    GT   ACC
                                     AG___  AAC
GAM914  GGTLA1    5'  CCATCTGTCCAATTACCTGTG  14658    TGCTC__
                                CGC      TGGACAGATGG
                                |||      ||||||||||
                                GTG      ACCTGTCTACC
                                  TCCATTA
GAM914  GGTLA1    5'  CCATCTGTCCATCTGGCAGC   14659      C__
                                GCTGCT   TGGACAGATGG
                                ||||||   ||||||||||
                                CGACGG   ACCTGTCTACC
                                   TCT
GAM914  GPR72     3'  CCATCTGTGGGGCAGC      69760       GG
                                GCTGCTCT  ACAGATGG
                                ||||||||  ||||||||
                                CGACGGGG  TGTCTACC
                                          __
GAM914  GSA7      3'  CCATCGCCAGAGCAG       21130        ACA
                                CTGCTCTGG   GATGG
                                |||||||||   |||||
                                GACGAGACC   CTACC
                                     G__
GAM914  H2AFY2    3'  CCATCTGTAAGGAAGCAGGT  37842    G    _  GG
                                AC CTGCT CT  ACAGATGG
                                || ||||| ||  ||||||||
                                TG GACGA GG  TGTCTACC
                                  _    A  AA
GAM914  HABP2     3'  CCATCTGCTTTCAGAGT     14696        __
                                GCTCTGGA  CAGATGG
                                ||||||||  |||||||
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                                TGAGACTT  GTCTACC
                                    TC
GAM914  HAND1    3'  CCTTCGCCAAAGCAGTGT    16687        C   ACA  T
                                ACGCTGCT TGG   GA GG
                                |||||||| |||   || ||
                                TGTGACGA ACC   CT CC
                                    A   G__  T
GAM914  HSPC055  3'  CCATCTGTTGAACAG      26268     C  TG
                                CTG TC  GACAGATGG
                                ||| ||  |||||||||
                                GAC AG  TTGTCTACC
                                  A  __
GAM914  HTCD37   3'  CCATCTGTAAAACAGGGT    67673       G___
                                GCTCTG    ACAGATGG
                                ||||||    ||||||||
                                TGGGAC    TGTCTACC
                                   AAAA
GAM914  HTGN29   5'  CCGGTTTCCAGAGCACGT    39506     C       CAGA
                                ACG TGCTCTGGA    TGG
                                ||| |||||||||    |||
                                TGC ACGAGACCT    GCC
                                  _       TTG_
GAM914  KIAA0337 3'  CCACTTGAGAGCAGC       28830        GGA   A
                                GCTGCTCT   CAG TGG
                                ||||||||   ||| |||
                                CGACGAGA   GTT ACC
                                    ___   C
GAM914  KIAA0376 3'  CCACCTGTCCGGATCCAGC    65598      C_       A
                                GCTG  TCTGGACAG TGG
                                ||||  ||||||||| |||
                                CGAC  AGGCCTGTC ACC
                                  CT        C
GAM914  KIAA0513 3'  CCATGGTCACGAAGCAGCGTT  28347         C  _   AG
                                AACGCTGCT TG GAC  ATGG
                                ||||||||| || |||  ||||
                                TTGCGACGA GC CTG  TACC
                                    A  A   G_
GAM914  KIAA0544 3'  CCATCTGGGGACAGCG      70899      CT  GGA
                                CGCTG  CT   CAGATGG
                                |||||  ||   |||||||
                                GCGAC  GG   GTCTACC
                                  AG  ___
GAM914  KIAA0545 3'  CCATCTCTCCGAGCAGCG    63146        T   C
                                CGCTGCTC GGA AGATGG
                                |||||||| ||| ||||||
                                GCGACGAG CCT TCTACC
                                    _  C
GAM914  KIAA0546 3'  CCATCTGTCCTTAGCATGT   71308     C    CT
                                ACG TGCT  GGACAGATGG
                                ||| ||||  ||||||||||
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                                TGT ACGA  CCTGTCTACC
                                  _   TT
GAM914  KIAA0595  5'  CCAGCGATCAGAGCAGCG    30499          ACAGA
                                CGCTGCTCTGG    TGG
                                ||||||||||    |||
                                GCGACGAGACT    ACC
                                      AGCG_
GAM914  KIAA0763  3'  CCACCTGTCAGAGCCACAGC  29532    ___    G   A
                                GCT   GCTCTG ACAG TGG
                                |||   |||||| |||| |||
                                CGA   CGAGAC TGTC ACC
                                  CAC     _   C
GAM914  KIAA1023  3'  CCATCTACCACTTCAGGGT   34257   G  CTC  AC
                                AC CTG   TGG  AGATGG
                                || |||   |||  ||||||
                                TG GAC   ACC  TCTACC
                                 G   TTC   A_
GAM914  KIAA1297  5'  CCACCGCATCCAGAGCAGCG  72172          CAGA_
                                CGCTGCTCTGGA    TGG
                                ||||||||||    |||
                                GCGACGAGACCT    ACC
                                      ACGCC
GAM914  KIAA1405  3'  CCACCTGCCACACAGCG    61039     CTC  A  A
                                CGCTG   TGG CAG TGG
                                |||||   ||| ||| |||
                                GCGAC   ACC GTC ACC
                                   AC_  _   C
GAM914  KIAA1463  5'  CCATCTGTCCGTGCGC     72273   T  TC
                                GC GC  TGGACAGATGG
                                || ||  ||||||||||
                                CG CG  GCCTGTCTACC
                                 _  T_
GAM914  KIAA1522  3'  CCACCTGTCTAGGCAAGC    64973    _ T      A
                                GCT GC CTGGACAG TGG
                                ||| || |||||||| |||
                                CGA CG GATCTGTC ACC
                                  A  _       C
GAM914  LASP1     3'  CCATCTGTCTTCAGCA     20450     CT
                                TGCT  GGACAGATGG
                                ||||  ||||||||||
                                ACGA  TCTGTCTACC
                                  CT
GAM914  LGALS12   3'  CCATCTGCCTTCAGGGC     52389       __
                                GCTCTGGA  CAGATGG
                                ||||||||  |||||||
                                CGGGACTT  GTCTACC
                                     CC
GAM914  MAP2K3    3'  CCATCTGCGGGGGCAGTG    10861        GGA
                                CGCTGCTCT   CAGATGG
                                |||||||||   |||||||
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                              GTGACGGGG  GTCTACC
                                   GC_
GAM914  MAP2K3   3' CCATCTGCGGGGGCAGTG   59029       GGA
                              CGCTGCTCT  CAGATGG
                              |||||||||  |||||||
                              GTGACGGGG  GTCTACC
                                   GC_
GAM914  MED8     5' CCATCTGTCCTGGACAGC   53521     CT T
                              GCTG  C GGACAGATGG
                              ||||  | ||||||||||
                              CGAC  G CCTGTCTACC
                                AG T
GAM914  MGC15631 5' CCATCTGTCCCGCTGC     51262    T  TCT
                              GC GC   GGACAGATGG
                              || ||   ||||||||||
                              CG CG   CCTGTCTACC
                               T  C__
GAM914  MGC2376  3' CCATCTGTCCCTGGCATGT   43702    C    CT
                              ACG TGCT  GGACAGATGG
                              ||| ||||  ||||||||||
                              TGT ACGG  CCTGTCTACC
                                _   TC
GAM914  NXPH3    3' CCATCTGTCTCCAGCCAGGC  65756    __   CT
                              GCT  GCT  GGACAGATGG
                              |||  |||  ||||||||||
                              CGG  CGA  TCTGTCTACC
                                AC   CC
GAM914  PCBP3    5' CCATCTGTCCTTCCTCACAGC 40069     CTCT___
                              GCTG      GGACAGATGG
                              ||||      ||||||||||
                              CGAC      CCTGTCTACC
                                ACTCCTT
GAM914  PDEF     3' CATTTCCAGAGCAG       24747         CA
                              CTGCTCTGGA  GATG
                              ||||||||||  ||||
                              GACGAGACCT  TTAC
                                          __
GAM914  PIP5K2B  3' CCACCTGCCTTCGGAGC     13067        __  A
                              GCTCTGGA  CAG TGG
                              ||||||||  ||| |||
                              CGAGGCTT  GTC ACC
                                   CC   C
GAM914  PRO1843  5' CCATTATTCTAGAGCA      37542        CA
                              TGCTCTGGA  GATGG
                              |||||||||  |||||
                              ACGAGATCT  TTACC
                                   TA
GAM914  RAB35    3' CCATCTTACTGCAAGCAGCGT 22477       CT_ AC
                              ACGCTGCT   GG  AGATGG
                              ||||||||   ||  ||||||
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                                TGCGACGA  TC  TCTACC
                                    ACG  AT
GAM914  SRp25    3'  CCATCTGAAAGAGCAGC    33558       GGA
                                GCTGCTCT  CAGATGG
                                ||||||||  |||||||
                                CGACGAGA  GTCTACC
                                    AA_
GAM914  SRp25    3'  CCATCTGAAAGAGCAGC    37979       GGA
                                GCTGCTCT  CAGATGG
                                ||||||||  |||||||
                                CGACGAGA  GTCTACC
                                    AA_
GAM914  TNKS1BP1 3'  CCACCTCTGAGGAGCGT    53003      G  T  CA A
                                ACGCT CTC GGA  G TGG
                                ||||| ||| |||  | |||
                                TGCGA GAG TCT  C ACC
                                   G  _  __ C
GAM914  TPD52L1  5'  CCATCTGCTCTGGGAAGC    12362    GC  TG  _
                                GCT  TC  GA CAGATGG
                                |||  ||  || |||||||
                                CGA  GG  CT GTCTACC
                                  A_  GT  C
GAM914  TReP-132 5'  CCACCTGTCCAGCAGC     37291      CT    A
                                GCTGCT  GGACAG TGG
                                ||||||  |||||| |||
                                CGACGA  CCTGTC ACC
                                    __     C
GAM914  TReP-132 5'  CCACCTGTCCAGCAGC     53138      CT    A
                                GCTGCT  GGACAG TGG
                                ||||||  |||||| |||
                                CGACGA  CCTGTC ACC
                                    __     C
GAM914  TReP-132 5'  CCACCTGTCCAGCAGC     53147      CT    A
                                GCTGCT  GGACAG TGG
                                ||||||  |||||| |||
                                CGACGA  CCTGTC ACC
                                    __     C
GAM914  ZNF185   3'  CCATCTGTGGGCCCAGC    23110    __   TGG
                                GCT  GCTC  ACAGATGG
                                |||  ||||  ||||||||
                                CGA  CGGG  TGTCTACC
                                  CC  ____
GAM914  LOC113026 5'  CCGGGCCAGAGCGGCG     55900         ACAGA
                                CGCTGCTCTGG    TGG
                                ||||||||||    |||
                                GCGGCGAGACC    GCC
                                      GG___
GAM914  LOC114984 5'  CCACCCAGCCAGGGCAGCG   73168         ACAGA
                                CGCTGCTCTGG    TGG
                                ||||||||||    |||
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                                GCGACGGGACC    ACC
                                      GACCC
GAM914  LOC124753 3'  CCATCTGTTCTCAGGGTT    74320    G  CTCT
                                AAC CTG   GGACAGATGG
                                ||| |||   ||||||||||
                                TTG GAC   CTTGTCTACC
                                  G  T___
GAM914  LOC130074 3'  CCATCTGTTAAGAACGTT    76131    CTGC  G
                                AACG   TCT GACAGATGG
                                ||||   ||| |||||||||
                                TTGC   AGA TTGTCTACC
                                  A___  A
GAM914  LOC142955 3'  CCATCTGCCCCAGAGCGC    76444    T     A_
                                GC GCTCTGG  CAGATGG
                                || |||||||  |||||||
                                CG CGAGACC  GTCTACC
                                 _     CC
GAM914  LOC143497 5'  CCATCTGTGATCCACTGCA    76588    TC   ___
                                TGC  TGGA   CAGATGG
                                |||  ||||   |||||||
                                ACG  ACCT   GTCTACC
                                  TC   AGT
GAM914  LOC144114 5'  CAGGCTTCCAGAGCAGC     82209         C  A_
                                GCTGCTCTGGA AG  TG
                                |||||||||||  ||  ||
                                CGACGAGACCT TC  AC
                                      _  GG
GAM914  LOC144563 5'  CCATCTGTCCTGGCACACGTT  76887     C_   CT
                                AACG  TGCT  GGACAGATGG
                                ||||  ||||  ||||||||||
                                TTGC  ACGG  CCTGTCTACC
                                  AC   T_
GAM914  LOC146177 3'  CCACCTGCAAGCTCAGGGCAGC 77692         A____  A
                                GCTGCTCTGG    CAG TGG
                                ||||||||||    ||| |||
                                CGACGGGACT    GTC ACC
                                      CGAAC   C
GAM914  LOC147136 3'  CCATCTGGCCACAGC       78260     CTC   A
                                GCTG   TGG CAGATGG
                                ||||   ||| |||||||
                                CGAC   ACC GTCTACC
                                  ___   G
GAM914  LOC148223 3'  CCAATGTCAGAGCAGC      78735        G   GA
                                GCTGCTCTG ACA  TGG
                                ||||||||| |||  |||
                                CGACGAGAC TGT  ACC
                                      _  A_
GAM914  LOC150378 5'  CCATCCGCAGGCAGCGT     79743       T   GACA
                                ACGCTGC CTG   GATGG
                                ||||||| |||   |||||
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                                TGCGACG GAC    CTACC
                                   _   GC__
GAM914   LOC151632 5'  CCATCTGTCCTGGCACACGTT  85467      C_    CT
                                AACG  TGCT  GGACAGATGG
                                ||||  ||||  ||||||||||
                                TTGC  ACGG  CCTGTCTACC
                                  AC    T_
GAM914   LOC155006 3'  CCATCTGTCCCCCAGC      81234      CTCT
                                GCTG    GGACAGATGG
                                ||||    ||||||||||
                                CGAC    CCTGTCTACC
                                  CC__
GAM914   LOC155179 3'  CCATCTACCACTTCAGGGT   81313    G   CTC   AC
                                AC CTG   TGG  AGATGG
                                || |||   |||  ||||||
                                TG GAC   ACC  TCTACC
                                 G   TTC   A_
GAM914   LOC162083 5'  CCATCTGTAGTCAGCAGC    82336       CTGG
                                GCTGCT    ACAGATGG
                                ||||||    ||||||||
                                CGACGA    TGTCTACC
                                   CTGA
GAM914   LOC199678 5'  CCGTCCCCAGAGCAGGT     89790    G        ACA
                                AC CTGCTCTGG   GATGG
                                || |||||||||   |||||
                                TG GACGAGACC   CTGCC
                                 _        C__
GAM914   LOC199704 5'  CCATCTCTTCAGAGCAGC    88328           C
                                GCTGCTCTGGA AGATGG
                                |||||||||||| ||||||
                                CGACGAGACTT TCTACC
                                       C
GAM914   LOC199899 3'  CCACCTGTCTGGTAG       89872       CT     A
                                CTGCT  GGACAG TGG
                                |||||  ||||||  |||
                                GATGG  TCTGTC ACC
                                   __      C
GAM914   LOC200339 3'  TGTCCATAGCAGCGTT      90041          C
                                AACGCTGCT TGGACA
                                |||||||||  ||||||
                                TTGCGACGA ACCTGT
                                      T
GAM914   LOC200904 5'  CCATCTGTCCTGGCA       90186      CT
                                TGCT  GGACAGATGG
                                ||||  ||||||||||
                                ACGG  CCTGTCTACC
                                  T_
GAM914   LOC201191 3'  CCATCTGCCCAGACAGAGCGGC 89768          GA____
                                GCTGCTCTG     CAGATGG
                                |||||||||     |||||||
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                                CGGCGAGAC     GTCTACC
                                     AGACCC
GAM914  LOC201952 5'  CCATCTGTCATAGCGTT     90270       CTCTG
                                AACGCTG    GACAGATGG
                                |||||||    |||||||||
                                TTGCGAT    CTGTCTACC
                                   A_____
GAM914  LOC220011 5'  CCACCTACCGGGGCATCGTT   91641     C      AC  A
                                AACG TGCTCTGG  AG TGG
                                |||| ||||||||  || |||
                                TTGC ACGGGGCC  TC ACC
                                  T       A_  C
GAM914  LOC220758 5'  CCATCTGTCCGGCTGGCGGT   90784       __
                                GCTGCT  CTGGACAGATGG
                                ||||||  ||||||||||||
                                TGGCGG  GGCCTGTCTACC
                                   TC
GAM914  LOC221795 5'  CCATCTGTCCTGGCACACGTT  92476     C_   CT
                                AACG  TGCT  GGACAGATGG
                                ||||  ||||  ||||||||||
                                TTGC  ACGG  CCTGTCTACC
                                  AC   T_
GAM914  LOC222029 5'  CCATCTATGGAGCAGC      94037        GAC
                                GCTGCTCTG   AGATGG
                                |||||||||   ||||||
                                CGACGAGGT   TCTACC
                                     A__
GAM914  LOC222166 3'  CCATCTGTGCTTCAGTA     94092     CT  _
                                TGCT  GG ACAGATGG
                                ||||  || ||||||||
                                ATGA  TC TGTCTACC
                                  CT  G
GAM914  LOC222962 3'  CCATCTGTGTCCAGCGGC    92872       CT    __
                                GCTGCT  GGACA  GATGG
                                ||||||  |||||  |||||
                                CGGCGA  CCTGT  CTACC
                                   __    GT
GAM914  LOC253148 3'  CCATCACCGCCCAGAGCAGC   96874          ACA__
                                GCTGCTCTGG    GATGG
                                ||||||||||    |||||
                                CGACGAGACC    CTACC
                                     CGCCA
GAM914  LOC254431 3'  CCACCTGGGAGCAGC       96850        GGA   A
                                GCTGCTCT   CAG TGG
                                ||||||||   ||| |||
                                CGACGAGG   GTC ACC
                                     ___   C
GAM914  LOC255146 3'  CCATCTGCAGACCGGACAACGT 95600      C  C    A___
           T                     AACG TG TCTGG    CAGATGG
                                ||||  ||  |||||    |||||||
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                                TTGC AC AGGCC   GTCTACC
                                  A _    AGAC
GAM914  LOC255290 5'  CCATCTGTCCAATTACCTGTG  95608    TGCTC__
                                CGC     TGGACAGATGG
                                |||     ||||||||||
                                GTG     ACCTGTCTACC
                                  TCCATTA
GAM914  LOC255290 5'  CCATCTGTCCATCTGGCAGC  95609      C__
                                GCTGCT  TGGACAGATGG
                                ||||||  ||||||||||
                                CGACGG  ACCTGTCTACC
                                   TCT
GAM914  LOC256158 5'  CCATCCTCAACAGCAGCGT   97653       CTG  CA
                                ACGCTGCT  GA  GATGG
                                ||||||||  ||  |||||
                                TGCGACGA  CT  CTACC
                                    CAA  C_
GAM914  LOC256515 5'  CCATCTGTCCTGGCACACGTT  96461     C_   CT
                                AACG  TGCT  GGACAGATGG
                                ||||  ||||  ||||||||||
                                TTGC  ACGG  CCTGTCTACC
                                  AC   T_
GAM914  LOC256594 5'  CCATCTGTCCTGGCACACGTT  97076     C_   CT
                                AACG  TGCT  GGACAGATGG
                                ||||  ||||  ||||||||||
                                TTGC  ACGG  CCTGTCTACC
                                  AC   T_
GAM914  LOC256987 3'  CCATCTTTTGAACAGTGT    95946      C  TGGAC
                                ACGCTG TC    AGATGG
                                ||||||  ||    ||||||
                                TGTGAC AG    TCTACC
                                   A  TTT__
GAM914  LOC51219  3'  CCACCCCTGGAGGGAGCAGCGT 33113          GGA   A__
          T                      AACGCTGCTCT   CAG   TGG
                                ||||||||||   |||   |||
                                TTGCGACGAGG   GTC   ACC
                                      GAG   CCC
GAM914  LOC64116  5'  CCTCTGACTCGGAGCAGCG   42198         _ A    T
                                CGCTGCTCTG G CAGA GG
                                |||||||||| | |||| ||
                                GCGACGAGGC C GTCT CC
                                     T A   _
GAM914  LOC90371  5'  CCATCTGTCCATCCATTCAGC  62496     CTC___
                                GCTG     TGGACAGATGG
                                ||||     ||||||||||
                                CGAC     ACCTGTCTACC
                                  TTACCT
GAM914  LOC91409  3'  CCACCTGGTGCCCAGAGCA   65954        A___   A
                                TGCTCTGG    CAG TGG
                                ||||||||    ||| |||
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                                ACGAGACC   GTC ACC
                                    CGTG  C
GAM914  LOC92080  3'  CCACCCTGCGGGAGAGCAGC  68041       GGA_  A_
                                GCTGCTCT   CAG  TGG
                                ||||||||   |||  |||
                                CGACGAGA   GTC  ACC
                                    GGGC   CC
GAM915  IRTA1     3'  ATTACCAACCCCTTAGCAATA  48418        AATTCA
                                TATTGCTAAG     GGTAGT
                                ||||||||||     ||||||
                                ATAACGATTC     CCATTA
                                     CCCAA_
GAM915  EFNA5     3'  GCCTGAATTCTAAGCAA     8732       A
                                TTGCT AGAATTCAGGT
                                ||||| ||||||||||
                                AACGA TCTTAAGTCCG
                                   A
GAM915  FLJ11827  3'  GACTACTCCCCAGCAATA    46984       AAGAATTCA
                                TATTGCT        GGTAGTC
                                |||||||        |||||||
                                ATAACGA        TCATCAG
                                    CCCC_____
GAM915  NAALAD2   3'  AGACTACTTACTACTCAGCAAT 18440       A  AATTC
           A                     TATTGCT AG    AGGTAGTCT
                                ||||||| ||    |||||||||
                                ATAACGA TC    TTCATCAGA
                                    C  ATCA_
GAM915  P114-RHO-GEF 3'  ACCTGATTCTAGCAATA     31020       A   T
                                TATTGCTA GAAT CAGGT
                                |||||||| |||| |||||
                                ATAACGAT CTTA GTCCA
                                    _   _
GAM915  SQV7L     5'  AGACCACCTGAATTCT      70568          A
                                AGAATTCAGGT GTCT
                                |||||||||| ||||
                                TCTTAAGTCCA CAGA
                                      C
GAM915  STAB2     3'  ACTGTGAATTCTCAGCA     34112      A      GG
                                TGCT AGAATTCA  TAGT
                                |||| ||||||||  ||||
                                ACGA TCTTAAGT  GTCA
                                  C       __
GAM915  ZDHHC5    5'  AGACTACCTAAAAGAGACAA   91558     _  AAGAATTC
                                TTG CT       AGGTAGTCT
                                ||| ||       |||||||||
                                AAC GA       TCCATCAGA
                                  A  GAAAA___
GAM915  LOC144952 5'  ACCACCTGAATCTAGCA     87074      A  A      A
                                TGCTA GA TTCAGGT GT
                                ||||| || ||||||| ||
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                                ACGAT CT AAGTCCA CA
                                  _ _     C
GAM915  LOC196337 3'  AGACTATAAAATCCCTAGCAAT 87644       A_  ATTCAG
            A                    TATTGCTA  GA    GTAGTCT
                                 ||||||||  ||    |||||||
                                 ATAACGAT  CT    TATCAGA
                                     CC  AAAA__
GAM915  LOC220573 5'  GACCCACTGCTTAGCAA    69602       AATT  GTA
                                 TTGCTAAG   CAG  GTC
                                 ||||||||   |||  |||
                                 AACGATTC   GTC  CAG
                                     ____  ACC
GAM916  CLCN5    5'  TGAAATACCTAAGCTGCTCCAA 3595        _______
                                 TTGGAGCAG     GTTTCA
                                 |||||||||     ||||||
                                 AACCTCGTC     TAAAGT
                                      GAATCCA
GAM916  FLRT2    5'  ATTGAAAAATGAGGTCTGC   25056    GT    CTC
                                 GCAG  TTCATT   CAAT
                                 ||||  ||||||   ||||
                                 CGTC  GAGTAA   GTTA
                                   TG     AAA
GAM916  IL17     3'  TGGGGAAAATGAAACCCTCC  9333     CA     __
                                 GGAG  GGTTTCAT  TCTCCA
                                 ||||  ||||||||  ||||||
                                 CCTC  CCAAAGTA  AGGGGT
                                   __      AA
GAM916  NLGN1    5'  TGAAGATGCTGCTCCAA    30026       G__
                                 TTGGAGCAG   TTTCA
                                 |||||||||   |||||
                                 AACCTCGTC   GAAGT
                                      GTA
GAM916  POLG     3'  GTGATAAACCTGCTCCAA   10682         __
                                 TTGGAGCAGGTT  TCAT
                                 ||||||||||||  ||||
                                 AACCTCGTCCAA  AGTG
                                       AT
GAM916  TPK1     3'  GGAGAACCTGTCCAA      42384     G    TTCAT
                                 TTGGA CAGGT    TCTCC
                                 ||||| |||||    |||||
                                 AACCT GTCCA    AGAGG
                                   _    _____
GAM916  C1orf8   5'  GAGAATGAAACCCTC      16832    CA
                                 GAG  GGTTTCATTCTC
                                 |||  ||||||||||||
                                 CTC  CCAAAGTAAGAG
                                   __
GAM916  CLIC6    3'  TGGAGAACATGTTCCAA    82536       G  TTCAT
                                 TTGGAGCA GT    TCTCCA
                                 |||||||| ||    ||||||
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                                AACCTTGT CA    AGAGGT
                                   A _____
GAM916  CLIPR-59 3'  TGGAGAATTTCAATGCCCCGA 31374     A  GGTTTC
                                TTGG GCA     ATTCTCCA
                                |||| |||     ||||||||
                                AGCC CGT     TAAGAGGT
                                  C  AACTT_
GAM916  DKFZP547L112 3'  TGGAGAACTCTTGCTCCA   66532        TTTCA
                                TGGAGCAGG    TTCTCCA
                                |||||||||    |||||||
                                ACCTCGTTC    AAGAGGT
                                     TC___
GAM916  EPS8R3   5'  GGACCACCTGCTCCAA     55701          TTCATTC
                                TTGGAGCAGGT     TCC
                                ||||||||||      |||
                                AACCTCGTCCA     AGG
                                      CC_____
GAM916  EPS8R3   5'  GGACCACCTGCTCCAA     57404          TTCATTC
                                TTGGAGCAGGT     TCC
                                ||||||||||      |||
                                AACCTCGTCCA     AGG
                                      CC_____
GAM916  FLJ20552 3'  AGAACAAAACTGCTCCAA   35389        G  CA
                                TTGGAGCAG TTT  TTCT
                                ||||||||| |||  ||||
                                AACCTCGTC AAA  AAGA
                                     _  AC
GAM916  FLJ22865 5'  TGGAGAAAACTGCTCTAA   47071        GTTTCA
                                TTGGAGCAG     TTCTCCA
                                |||||||||     |||||||
                                AATCTCGTC     AAGAGGT
                                      AA____
GAM916  KIAA0372 5'  ATTGAAATTTGTTACCTACTCC 27663      C   TT  TTCTC
           AA                    TTGGAG AGGT  CA    CAAT
                                |||||| ||||  ||    ||||
                                AACCTC TCCA  GT    GTTA
                                   A   TT  TTAAA
GAM916  PRO0132  5'  ATGAAACCACTCCAA      26101       CA
                                TTGGAG  GGTTTCAT
                                ||||||  ||||||||
                                AACCTC  CCAAAGTA
                                   A_
GAM916  TEX27    3'  AGAGTGGAACCCGCTGCAA   41658     G  A
                                TTG AGC GGTTTCATTCT
                                ||| ||| ||||||||||
                                AAC TCG CCAAGGTGAGA
                                  G  C
GAM916  LOC149373 3'  ATTGGGGTGATGATACCCACCC 79312     AGCA  T   _
           CAA                    TTGG   GGT TCATT CTCCAAT
                                ||||   ||| ||||| |||||||
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                                AACC    CCA AGTAG GGGGTTA
                                  CCAC   T    T
GAM916  LOC152687 3'  TTGGAGAATATTGCTCC     80643        GTTTC
                                GGAGCAG     ATTCTCCAA
                                |||||||     |||||||||
                                CCTCGTT     TAAGAGGTT
                                   A____
GAM916  LOC51202  3'  ATTGGAGAATGAAACCTGCTCC 33017
           AA                    TTGGAGCAGGTTTCATTCTCCAAT
                                 ||||||||||||||||||||||||
                                 AACCTCGTCCAAAGTAAGAGGTTA

GAM917  CD36     5'  CTAATTCACCTCCTGAACA   3569     A   A       G
                                TG TCAG AGGTGAGT AG
                                || |||| |||||||| ||
                                AC AGTC TCCACTTA TC
                                 A   C       A
GAM917  CXorf6   3'  CACTCACCTTCTGGCCA     18512    AT
                                TG  CAGAAGGTGAGTG
                                ||  ||||||||||||
                                AC  GTCTTCCACTCAC
                                 CG
GAM917  GPR56    3'  CATTGCCCTTGCTCACCCTGAC 19067    A    AA     TG __
           CA                    TG TCAG  GGTGAG  A  GCAATG
                                 || ||||  ||||||  |  ||||||
                                 AC AGTC  CCACTC  T  CGTTAC
                                  C   __      GT CC
GAM917  HKE4     5'  TGCCTCTGTCCCTCTGGTCA   22733        A  T  GT   _
                                TGATCAGA GG GA  GAG CA
                                |||||||| || ||  ||| ||
                                ACTGGTCT CC CT  CTC GT
                                     _ _  GT   C
GAM917  IL22RA2  3'  TTACTCAATCCTTCTGGCCA   53696    AT      __
                                TG  CAGAAGG  TGAGTGA
                                ||  |||||||  |||||||
                                AC  GTCTTCC  ACTCATT
                                 CG      TA
GAM917  KRT6A    3'  ATTGCTCACCATCAGATCA    18693      AGAA    A
                                TGATC    GGTG GTGAGCAAT
                                |||||    |||| |||||||||
                                ACTAG    CTAC CACTCGTTA
                                   A___    _
GAM917  MAPK1    3'  CACTTCACCTTTTGACCA    10820    A         _
                                TG TCAGAAGGTGA GTG
                                || ||||||||||| |||
                                AC AGTTTTCCACT CAC
                                 C         T
GAM917  PDE4A    3'  CACCTTCCACACTCTGATCA   20581         AG   A___
                                TGATCAGA  GTG    GTG
                                ||||||||  |||    |||
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                                ACTAGTCT  CAC    CAC
                                     CA   CTTC
GAM917  PTMS     3'  CATTGTTCCACCTCCTGA    11033      A     AGT
                                TCAG AGGTG   GAGCAATG
                                |||| |||||   ||||||||
                                AGTC TCCAC   CTTGTTAC
                                  C    ___
GAM917  TCN2     5'  TGCTCACCCACCTGCT      4483     A     A
                                AG AGGTG GTGAGCA
                                || ||||| |||||||
                                TC TCCAC CACTCGT
                                 G    C
GAM917  C20orf100 3'  TGCTCTCCTTTTAATCA     51815      C      T
                                TGAT AGAAGG GAGTG
                                |||| |||||| |||||
                                ACTA TTTTCC CTCGT
                                  A     T
GAM917  CNOT4    3'  TGCTCTGGGGCCATCTGATCA  25259         A   GAGT
                                TGATCAGA GGT    GAGCA
                                |||||||| |||    |||||
                                ACTAGTCT CCG    CTCGT
                                     A   GGGT
GAM917  DKFZP434N093 3'  TGCTCACTTGCAACCTTATCA  79947      C  AAG TG
                                TGAT AG   G  AGTGAGCA
                                |||| ||   |  ||||||||
                                ACTA TC   C  TCACTCGT
                                  T  CAA GT
GAM917  FLJ10581  3'  TCACTCACAGCTGATCA     36306        AAG
                                TGATCAG   GTGAGTGA
                                |||||||   ||||||||
                                ACTAGTC   CACTCACT
                                    GA_
GAM917  RALGPS1A  3'  CACTCCACCTCTGATCA     27597         A   _
                                TGATCAGA GGTG AGTG
                                |||||||| |||| ||||
                                ACTAGTCT CCAC TCAC
                                     _   C
GAM917  RASD2    3'  TGCCTGAGCCTTCTGAGCA   26689    A       GAGTGA
                                TG TCAGAAGGT     GCA
                                || |||||||||     |||
                                AC AGTCTTCCG     CGT
                                 G        AGTC__
GAM917  LOC145990 3'  GCTCAGCACGCCTTCTAATTA  77603      C       A _
                                TGAT AGAAGGTG G TGAGC
                                |||| |||||||| | |||||
                                ATTA TCTTCCGC C ACTCG
                                  A       A G
GAM917  LOC157740 3'  CACCGCCCACTTCTGACA    81562    A     ___    A
                                TG TCAGAA   GGTG GTG
                                || ||||||   |||| |||
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                                AC AGTCTT   CCGC CAC
                                 _     CAC   _
GAM917  LOC220929 5'  CACCATCACGCTCTGATCA   91401        AG   __
                                TGATCAGA  GTGA  GTG
                                ||||||||  ||||  |||
                                ACTAGTCT  CACT  CAC
                                     CG    AC
GAM918  MEN1     5'  AATGGAAGCCACTGCCAGC   93366        TGAAAAA
                                GCTGGCAGT      TTCATT
                                |||||||||      ||||||
                                CGACCGTCA      AGGTAA
                                     CCGA___
GAM918  IFRG28   3'  ATGAACTGGCTGCCACTT    60067    C       AAAAA
                                AAG TGGCAGTTG     TTCAT
                                ||| |||||||||     |||||
                                TTC ACCGTCGGT     AAGTA
                                  _       C____
GAM918  KIAA0461 3'  ATTTTTCACTGCCAGCTT    70837          T
                                AAGCTGGCAGT GAAAAAT
                                |||||||||| |||||||
                                TTCGACCGTCA CTTTTTA
                                           _
GAM918  KIAA0828 3'  TTTTCAGCACCTGCTT      81206      T  CA
                                AAGC GG  GTTGAAAA
                                |||| ||  ||||||||
                                TTCG CC  CGACTTTT
                                  T  A_
GAM918  LOC146952 5'  AATGAATCTCTTAATTGCAGCT 83855       G      AAA
           T                     AAGCTG CAGTTGA   ATTCATT
                                ||||||| |||||||   |||||||
                                TTCGAC GTTAATT   TAAGTAA
                                   _      CTC
GAM918  LOC148438 3'  TTTTCAACTGCCTGCT      84160     T
                                AGC GGCAGTTGAAAA
                                ||| ||||||||||||
                                TCG CCGTCAACTTTT
                                  T
GAM918  LOC152580 5'  ATGAATTTCTCCACAGCCA    85773      A  T  A
                                TGGC GT GA AAATTCAT
                                |||| || || ||||||||
                                ACCG CA CT TTTAAGTA
                                  A  C  C
GAM918  LOC170396 3'  AATGAATTTCTCAGATGAGCCA 82842      AG__    A
                                TGGC    TTGA AAATTCATT
                                ||||    |||| |||||||||
                                ACCG    GACT TTTAAGTAA
                                  AGTA    C
GAM918  LOC221477 5'  GTGGTTTCCGAACTGCCAGCT  92162          __    AAT
                                AGCTGGCAGTT  GAAA   TCAT
                                ||||||||||  ||||   ||||
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                                TCGACCGTCAA CTTT  GGTG
                                      GC   ___
GAM918  LOC92606 3' AATGAATTTTTCCTTATTCCA 69985    C  T__
                                TGG AGT  GAAAAATTCATT
                                ||| |||  ||||||||||||
                                ACC TTA  CTTTTTAAGTAA
                                  _  TTC
GAM919  SLC1A4   3' AACTTAGATTCTGAGGTCAAAG 11711   G      A ___
                                CT TGACCTCA GA  TGAGTT
                                || |||||||| ||  ||||||
                                GA ACTGGAGT CT  ATTCAA
                                 A       _ TAG
GAM919  SSA1     3' AACTCATCTTGATCA      11974    CC
                                TGA  TCAAGATGAGTT
                                |||  ||||||||||||
                                ACT  AGTTCTACTCAA
                                  __
GAM919  AP3M2    3' AACTCATCCTGTTTCAAGGGAA 22312      G  CCT  A
                                TTCCCT TGA  CA GATGAGTT
                                |||||| |||  || ||||||||
                                AAGGGA ACT  GT CTACTCAA
                                   _  TT_  C
GAM919  ATF3     3' AACTCAGTTCCAAAGTCACAGG 14429       CTCAAGA_
                                CCTGTGAC       TGAGTT
                                ||||||||       ||||||
                                GGACACTG       ACTCAA
                                     AAACCTTG
GAM919  BRAG     3' TCTTGGAAGTCACAGGGAA   29478         C_
                                TTCCCTGTGAC  TCAAGA
                                ||||||||||  ||||||
                                AAGGGACACTG  GGTTCT
                                       AA
GAM919  CHST8    5' GTCCCCACGGCCACAGGGAA  42440        A  TCAA_
                                TTCCCTGTG CC    GAT
                                ||||||||| ||    |||
                                AAGGGACAC GG    CTG
                                      C  CACCC
GAM919  FLJ10420 3' AACTCATCTTTGCAAAAGGAA 36103     CTG  ACCTC
                                TTCC  TG    AAGATGAGTT
                                ||||  ||    ||||||||||
                                AAGG  AC    TTCTACTCAA
                                  AAA  GT___
GAM919  FLJ23462 3' AACTCACCCCAAGGTCACACGG 45800    C       CAAGA
                                CC TGTGACCT    TGAGTT
                                || ||||||||    ||||||
                                GG ACACTGGA    ACTCAA
                                 C       ACCCC
GAM919  FLJ31300 3' AACTCATCCTAAACAGAGAA  58283    C   GACCTCAA
                                TTC CTGT       GATGAGTT
                                ||| ||||       ||||||||
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                                AAG GACA       CTACTCAA
                                  A    AATC____
GAM919  KIAA0475  3'  ACTCATCCTACAGGGGA     29482         ACCTCAA
                                TTCCCTGTG      GATGAGT
                                |||||||||      |||||||
                                AGGGGACAT      CTACTCA
                                     C_______
GAM919  KIAA1655  3'  AATTTGTCCAAGGTCACCAAGA 66584     CCT      CAA  TG
              A                   TTC   GTGACCT   GA  AGTT
                                  |||   |||||||   ||  ||||
                                  AAG   CACTGGA   CT  TTAA
                                    AAC      AC_  GT
GAM919  MGC10715  3'  AACTCACTCTCAGCCACAGGGA 44244         AC  CA   _
              G                   TTCCCTGTG  CT  AGA TGAGTT
                                  |||||||||  ||  ||| ||||||
                                  GAGGGACAC  GA  TCT ACTCAA
                                       C_  C_   C
GAM919  SV2B      3'  AACTTGGTGTTTGAGGTCCCAG 29292      T       AT__
              G                    CCTG GACCTCAAG    GAGTT
                                  |||| |||||||||    |||||
                                  GGAC CTGGAGTTT    TTCAA
                                    C        GTGG
GAM919  LOC130120 3'  TGTCTTGAGATCTCAGAGAA   74908     C   T  C
                                  TTC CTG GA CTCAAGATG
                                  ||| ||| || |||||||||
                                  AAG GAC CT GAGTTCTGT
                                    A   T  A
GAM919  LOC157313 5'  GTCCCCGAGGTCACAAGG     81399    C       AA_
                                  CC TGTGACCTC   GAT
                                  || |||||||||   |||
                                  GG ACACTGGAG   CTG
                                   A        CCC
GAM919  LOC163682 3'  GTCCTGAAATCACAGGG      87039        CC   A
                                  CCCTGTGA  TCA GAT
                                  ||||||||  ||| |||
                                  GGGACACT  AGT CTG
                                       AA   C
GAM919  LOC196808 5'  AACTCATCCTATTACAGG     87520        CCTCAA
                                  CCTGTGA      GATGAGTT
                                  |||||||      ||||||||
                                  GGACATT      CTACTCAA
                                      ATC____
GAM919  LOC222361 5'  AACTCATCTGGCTCCAAGGAA  92819      C  T  _  TCA
                                  TTCC TG GA CC   AGATGAGTT
                                  |||| || || ||   |||||||||
                                  AAGG AC CT GG   TCTACTCAA
                                    A  _  C  ____
GAM919  LOC254295 5'  CTCAGAGTCACAGGGAA      96175          C  AAGA
                                  TTCCCTGTGAC TC    TGAG
                                  |||||||||| ||    ||||
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                                AAGGGACACTG AG    ACTC
                                      _ ____
GAM919  LOC255974 5'  ATCTTAGGCCACAGGGAA    97477         A   C
                                TTCCCTGTG CCT AAGAT
                                ||||||||| ||| |||||
                                AAGGGACAC GGA TTCTA
                                     C   _
GAM920  ABCB9    3'  GCCCCTGCTTCTCCCGGTGGGG 39035         __      T___
          C                      GCCCCATC  GAGAAGC    GC
                                ||||||||  |||||||    ||
                                CGGGGTGG  CTCTTCG    CG
                                     CC      TCCC
GAM920  ADAMTS13  3'  CAGCTTCCTCGATGGG      57372         _
                                CCCATCGAG AAGCTG
                                ||||||||| ||||||
                                GGGTAGCTC TTCGAC
                                     C
GAM920  ADCY3    3'  CTCCACTTCAGACAGGGC    14456     CA  GA    C  C
                                GCCC  TC  GAAG TG AG
                                ||||  ||  |||| || ||
                                CGGG  AG  CTTC AC TC
                                  AC  A_   _ C
GAM920  ADRA2A   3'  GGCTCTGCAGCCTCCTGCGGGC 5456      _ TC   AA      A
                                GCCC CA  GAG  GCTGCAGA CC
                                |||| ||  |||  |||||||| ||
                                CGGG GT  CTC  CGACGTCT GG
                                  C  C_  __       C
GAM920  AKR1A1   3'  TCTGCAGCTAATGAGGT    20267    C   CGAGA
                                GCC CAT    AGCTGCAGA
                                ||| |||    |||||||||
                                TGG GTA    TCGACGTCT
                                 A   A____
GAM920  BMP1     3'  TCTGCAGCCCCCTCGGGG    20413     ATC   AA_
                                CCCC   GAG   GCTGCAGA
                                ||||   |||   ||||||||
                                GGGG   CTC   CGACGTCT
                                  ___   CCC
GAM920  BMP1     3'  TCTGCAGCCCCCTCGGGG    20416     ATC   AA_
                                CCCC   GAG   GCTGCAGA
                                ||||   |||   ||||||||
                                GGGG   CTC   CGACGTCT
                                  ___   CCC
GAM920  BMP1     3'  TCTGCAGCCCCCTCGGGG    20420     ATC   AA_
                                CCCC   GAG   GCTGCAGA
                                ||||   |||   ||||||||
                                GGGG   CTC   CGACGTCT
                                  ___   CCC
GAM920  BMP1     3'  TCTGCAGCCCCCTCGGGG    20425     ATC   AA_
                                CCCC   GAG   GCTGCAGA
                                ||||   |||   ||||||||
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                                GGGG  CTC  CGACGTCT
                                  ___  CCC
GAM920  CBFA2T2  3'  GCCTGCAGCTCCAGGGC    17469     CATCGA  A     AA
                                GCCC    GA GCTGCAG  C
                                ||||    || |||||||  |
                                CGGG    CT CGACGTC  G
                                  AC____ _     CC
GAM920  CD83     5'  TCTGCAGCTCGTGGCAGCGGC  14885    ____  T  GAA
                                GCC   CCA CGA  GCTGCAGA
                                |||   ||| |||  ||||||||
                                CGG   GGT GCT  CGACGTCT
                                  CGAC  _  ___
GAM920  DAZL     3'  GGTACATAAGCTTCTCAATG  68141    C      GCAGA
                                CAT GAGAAGCT    ACC
                                ||| ||||||||    |||
                                GTA CTCTTCGA    TGG
                                  A       ATACA
GAM920  DGCR2    3'  GGCTCTGCAGCCCAGCTCTGTG 17628     C  AA__      A
            G                    CCAT GAG   GCTGCAGA CC
                                ||||| |||   |||||||| ||
                                GGTG CTC   CGACGTCT GG
                                  T  GACC      C
GAM920  DKK1     5'  TCTGCAGCCGAACCGGC    24270    CCA  AGAA
                                GCC  TCG   GCTGCAGA
                                |||  |||   ||||||||
                                CGG  AGC   CGACGTCT
                                  CCA  _____
GAM920  EDAR     3'  GTTCTGCAGCGCAAATGAGAGC 42268   CCCA  AGAA_
                                GC   TCG   GCTGCAGAAC
                                ||   |||   ||||||||||
                                CG   AGT   CGACGTCTTG
                                 AG__  AAACG
GAM920  FMNL     3'  TTCTGCAGGGGTGTGGGGC   19706      T  AGAAG
                                GCCCCA CG    CTGCAGAA
                                |||||| ||    ||||||||
                                CGGGGT GT    GACGTCTT
                                   _  GGG__
GAM920  FSTL1    3'  GTTCTGCAGCTTCTGTG    23014    CG
                                CAT  AGAAGCTGCAGAAC
                                |||  ||||||||||||||
                                GTG  TCTTCGACGTCTTG
                                  __
GAM920  GAC1     5'  GCTGCCCCTGATGGGGC    20943       G  AA  T
                                GCCCCATC AG  GC GC
                                |||||||| ||  || ||
                                CGGGGTAG TC  CG CG
                                     _  CC  T
GAM920  GCGR     5'  GGCCCTGAGGCTCAAAGGGGC  3857      ATCGA  A  G  AA
                                GCCCC    GA GCT CAG  CC
                                |||||    || ||| |||  ||
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                              CGGGG    CT CGG GTC  GG
                                AAA__ _   A   CC
GAM920  GCN5L2   3'  CTGCAGCTCTTTCTGG     59840     TC    A
                              CCA  GAGA GCTGCAG
                              |||  |||| |||||||
                              GGT  TTCT CGACGTC
                                CT   _
GAM920  GGT2     5'  GTCTGCAGTGGATGCAGC    73712    CC    GAGAA      A
                              GC  CATC    GCTGCAGA C
                              ||  ||||    |||||||| |
                              CG  GTAG    TGACGTCT G
                               AC   G____      C
GAM920  GRN      3'  TCTGCAGCCCTCGGG      9132      ATC   AA
                              CCC   GAG  GCTGCAGA
                              |||   |||  ||||||||
                              GGG   CTC  CGACGTCT
                                ___   C_
GAM920  HSF4     5'  TCTGCAGCTCCGCGGC      59777     CCAT  A  A
                              GCC    CG GA GCTGCAGA
                              |||    || || ||||||||
                              CGG    GC CT CGACGTCT
                                C___  _  _
GAM920  MYCL2    3'  TCTGCAGCTCCACGTGG     18190     T  AGA
                              CCA CG   AGCTGCAGA
                              ||| ||   |||||||||
                              GGT GC   TCGACGTCT
                                _  ACC
GAM920  NEK6     3'  GGTTCTGCAACTTCCTAGCGTG 26934    T  A___    C
                              CA CG    GAAG TGCAGAACC
                              || ||    |||| |||||||||
                              GT GC    CTTC ACGTCTTGG
                               _  GATC    A
GAM920  PIK3CD   3'  TCTGCAGATGGGGC       17252         GAGAAGC
                              GCCCCATC      TGCAGA
                              ||||||||      ||||||
                              CGGGGTAG      ACGTCT
                                            _______
GAM920  PRKAB1   3'  GTCTGCAGCCTTAAGGC     20738     CCATC   AA      A
                              GCC    GAG  GCTGCAGA C
                              |||    |||  |||||||| |
                              CGG    TTC  CGACGTCT G
                                AA___   __       C
GAM920  PTAFR    3'  AGTTCTCCCCGATGGGGC    6292          A_  _
                              GCCCCATCG  GA AGCT
                              |||||||||  || ||||
                              CGGGGTAGC  CT TTGA
                                    CC  C
GAM920  RAB18    3'  TTCCACAGCTTTTCTGGG    41169      TC       CA
                              CCCA  GAGAAGCTG  GAA
                              ||||  |||||||||  |||
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                                GGGT  CTTTTCGAC  CTT
                                  __        AC
GAM920  TEAD3    3'  TCTGCAGTGTGGAGTGGAGC   12211    C   CGAGAA
                                GC CCAT     GCTGCAGA
                                || ||||     ||||||||
                                CG GGTG     TGACGTCT
                                 A   AGGTG_
GAM920  A4GALT   3'  CTGCTCCTGATGGGGC      33836         A  AGCT
                                GCCCCATCG GA   GCAG
                                ||||||||| ||   ||||
                                CGGGGTAGT CT   CGTC
                                     C ____
GAM920  APH2     3'  TCTTGGCTTCTCAACAGGGC   50320     CATC       C
                                GCCC   GAGAAGCTG AGA
                                ||||   ||||||||| |||
                                CGGG   CTCTTCGGT TCT
                                  ACAA       _
GAM920  C20orf160 3'  GGCTCTGCAGCCGCATAATGG  54649      CGAGAA      A
                                CCAT     GCTGCAGA CC
                                ||||     |||||||| ||
                                GGTA     CGACGTCT GG
                                  ATACGC       C
GAM920  C20orf29  3'  TTCTGCAGCTCCTTTTGTGC   37130    CC  TC   A
                                GC  CA  GAG AGCTGCAGAA
                                ||  ||  ||| ||||||||||
                                CG  GT  TTC TCGACGTCTT
                                 T_  T_   C
GAM920  C20orf80  5'  GGTCCTGCAGCTCCGGCGGGAG 65289    _   AT  A  A      A
           C                     GC CCC  CG GA GCTGCAG ACC
                                || |||  || || ||||||| |||
                                CG GGG  GC CT CGACGTC TGG
                                 A  CG  _ _      C
GAM920  CSR1     3'  CTGCAGCTTTGGGC       32687      CATCGA
                                GCCC     GAAGCTGCAG
                                ||||     ||||||||||
                                CGGG     TTTCGACGTC
                                  _______
GAM920  DKFZp434N035 3'  GTCCTGCAGGTGTGACGGGC   50051      CA   AGAAG     A
                                GCCC  TCG    CTGCAG AC
                                ||||  |||    |||||| ||
                                CGGG  AGT    GACGTC TG
                                  C_   GTG__     C
GAM920  DKFZP761I2123 3'  CTGTGCTCGATGGG       48762         AAGC
                                CCCATCGAG    TGCAG
                                |||||||||    |||||
                                GGGTAGCTC    GTGTC
                                     _____
GAM920  FLJ10900  5'  GTTCTGCAGCCACTCGGT    65593       AA
                                ATCGAG  GCTGCAGAAC
                                ||||||  ||||||||||
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                                TGGCTC  CGACGTCTTG
                                   AC
GAM920  FLJ12505  5'  GTCTGCAGCCATGAAGC    45390   CC  CGAGAA     A
                                GC  CAT    GCTGCAGA C
                                ||  |||    |||||||| |
                                CG  GTA    CGACGTCT G
                                 AA  C_____      C
GAM920  FLJ13710  3'  TCTGCAGCCTGGGC      45684    CATCG  AA
                                GCCC   AG  GCTGCAGA
                                ||||   ||  ||||||||
                                CGGG   TC  CGACGTCT
                                  _____  __
GAM920  FLJ14596  5'  GCCTGCAGCTGGTGAAGG   51461   A  AGA     AA
                                CC TCG   AGCTGCAG  C
                                || |||   ||||||||  |
                                GG AGT   TCGACGTC  G
                                 A  GG_     CC
GAM920  FLJ20045  5'  TTCCCGGCTTCTCGA      34433        CA
                                TCGAGAAGCTG  GAA
                                ||||||||||  |||
                                AGCTCTTCGGC  CTT
                                      C_
GAM920  FLJ20507  3'  TCTGCAGCTCCTCTCG     35303     __
                                CGAGA  AGCTGCAGA
                                |||||  |||||||||
                                GCTCT  TCGACGTCT
                                   CC
GAM920  FLJ20507  3'  TCTGCAGCTCCTCTCG     60238     __
                                CGAGA  AGCTGCAGA
                                |||||  |||||||||
                                GCTCT  TCGACGTCT
                                   CC
GAM920  FLJ22625  5'  TTCTGCACCTCGATGGG    45262       AAGC
                                CCCATCGAG   TGCAGAA
                                |||||||||   |||||||
                                GGGTAGCTC   ACGTCTT
                                      C___
GAM920  FLJ32884  5'  TCTGCACGCGGTGGGGC    58460       AGAAGC
                                GCCCCATCG    TGCAGA
                                |||||||||    ||||||
                                CGGGGTGGC    ACGTCT
                                      GC_____
GAM920  H17739    3'  GTTCTGCAGTGTAATGGAGG  54757   _  CGAGAA
                                CC CCAT    GCTGCAGAAC
                                || ||||    ||||||||||
                                GG GGTA    TGACGTCTTG
                                 A   ATG___
GAM920  H2BFQ     3'  GTTCTGCCGTGCGATGGGGC  59359       AGAA  T
                                GCCCCATCG   GC GCAGAAC
                                |||||||||   || |||||||
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                                CGGGGTAGC   TG CGTCTTG
                                     G___  C
GAM920  HCNGP    3'  GTTCTCACCCCTTCCTCGATGG 25153          _  C__  C
             GGC                   GCCCCATCGAG AAG   TG AGAAC
                                |||||||||| |||  || |||||
                                CGGGGTAGCTC TTC   AC TCTTG
                                      C  CCC  _
GAM920  HIC2     3'  GGTTCTGCAGGGAACAGGTG  65268     GAGAAG
                                CATC     CTGCAGAACC
                                ||||     ||||||||||
                                GTGG     GACGTCTTGG
                                  ACAAGG
GAM920  HTGN29   3'  TCTGCAGCTTGCAGTGG     39508     CGAG
                                CCAT    AAGCTGCAGA
                                ||||    ||||||||||
                                GGTG    TTCGACGTCT
                                  ACG_
GAM920  KIAA0337 3'  CAGCCTGATGGGGC        28829        G  AA
                                GCCCCATC AG  GCTG
                                |||||||| ||  ||||
                                CGGGGTAG TC  CGAC
                                     _  __
GAM920  KIAA0574 3'  GTTCTGCAGGAGAGAGGC    69284     CCA  GAGAAG
                                GCC   TC     CTGCAGAAC
                                |||   ||     |||||||||
                                CGG   AG     GACGTCTTG
                                  AG_  AG____
GAM920  KIAA0720 3'  GCCCTTCTCGACGGCGC     62322    C  A      CT
                                GC CC TCGAGAAG  GC
                                || || ||||||||  ||
                                CG GG AGCTCTTC  CG
                                 C  C       C_
GAM920  KIAA0937 3'  CAGTTCTGATGGGGC       91584        G   G
                                GCCCCATC AGAA CTG
                                |||||||| |||| |||
                                CGGGGTAG TCTT GAC
                                     _   _
GAM920  KIAA1305 5'  GGCTTCCTCTCCTCTGATGGGG 46933        _______  _
             C                   GCCCCATC     GAG AAGCT
                                |||||||      ||| |||||
                                CGGGGTAG     CTC TTCGG
                                     TCTCCT   C
GAM920  KIAA1373 3'  GCCTGCAGTTAGATGAGC    70939    CC    GAGAA      AA
                                GC  CATC    GCTGCAG  C
                                ||  ||||    |||||||  |
                                CG  GTAG    TGACGTC  G
                                 A_    AT___      CC
GAM920  KIAA1813 3'  TCTGCAGCCTCTCTCCTGG   70311     TC_   A
                                CCA   GAGA GCTGCAGA
                                |||   |||| ||||||||
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                                GGT   CTCT CGACGTCT
                                  CCT    C
GAM920  KIAA1924  3'  GCCTGCAGCTCTGGGC      73679      CATCG   A      AA
                                GCCC     AGA GCTGCAG  C
                                ||||     ||| |||||||  |
                                CGGG     TCT CGACGTC  G
                                  _____  _      CC
GAM920  LBP-9     3'  TAGCTTCTAAATGGAGC     27281     C    CG
                                GC CCAT  AGAAGCTG
                                || ||||  ||||||||
                                CG GGTA  TCTTCGAT
                                 A    AA
GAM920  MGC3178   3'  GGCTCTGCAGCCCTGCTGAAGG 47989      CA  G  AA__       A
              GC                  GCCC  TC AG    GCTGCAGA CC
                                ||||  || ||    |||||||| ||
                                CGGG  AG TC    CGACGTCT GG
                                  A_  _  GTCC       C
GAM920  NUDE1     3'  GTCCTGCAGCTTCTTCTTCGA  34569      ____        A
                                TCGA    GAAGCTGCAG AC
                                ||||    |||||||||| ||
                                AGCT    CTTCGACGTC TG
                                  TCTT         C
GAM920  NXPH3     3'  TCTCCTTCTCGATGAAGC    65770    CC        CTGC
                                GC  CATCGAGAAG    AGA
                                ||  ||||||||||    |||
                                CG  GTAGCTCTTC    TCT
                                 AA         C___
GAM920  PDGFC     3'  GCAGCTTCCTGATAAAGC    32498    CCC    A
                                GC   ATCG GAAGCTGC
                                ||   |||| ||||||||
                                CG   TAGT CTTCGACG
                                 AAA    C
GAM920  PEG10     3'  GGTTCTGTTAATTCTCAAGGAG 30529    C  ATC    GCT
              C                   GC CC   GAGAA   GCAGAACC
                                || ||   |||||   ||||||||
                                CG GG   CTCTT   TGTCTTGG
                                 A  AA_    AAT
GAM920  PP1628    3'  GCAGCTTCCGATAGG       47299    C    A
                                CC ATCG GAAGCTGC
                                || |||| ||||||||
                                GG TAGC CTTCGACG
                                 A   _
GAM920  SCYA26    3'  GGCTCTGCAGCCCTCTGGGG   20281      TC   AA      A
                                CCCCA  GAG  GCTGCAGA CC
                                |||||  |||  |||||||| ||
                                GGGGT  CTC  CGACGTCT GG
                                   __   C_       C
GAM920  SPRY4     5'  CTGCAGCTCCTCAAAGGC    48234     CCATC   A
                                GCC     GAG AGCTGCAG
                                |||     ||| ||||||||
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                                CGG     CTC TCGACGTC
                                  AAA__   C
GAM920  UBF-fl   5' GGCTCTGCAGCCCCGTGACGGC 51569     CCA   AGAA       A
                                GCC   TCG    GCTGCAGA CC
                                |||   |||    |||||||| ||
                                CGG   AGT    CGACGTCT GG
                                  C__   GCCC       C
GAM920  UHRF1    3' GCACTTCTCGACAGGC      25219     CCA       C
                                GCC   TCGAGAAG TGC
                                |||   |||||||| |||
                                CGG   AGCTCTTC ACG
                                  AC_       _
GAM920  LOC116173 3' TGTGGCTTCTCATGAAGC    56643    CC   C      TG
                                GC  CAT GAGAAGC  CA
                                ||  ||| |||||||  ||
                                CG  GTA CTCTTCG  GT
                                  AA   _      GT
GAM920  LOC123904 3' GGCTCTGCAGAGCGCAGCAGGG 74248      CAT__  AGAAG      A
             C                    GCCC     CG     CTGCAGA CC
                                ||||     ||     ||||||| ||
                                CGGG     GC     GACGTCT GG
                                  ACGAC  GA___       C
GAM920  LOC142937 5' GTTCTGCAGCTGGCGGGC    56656      CATC AGA
                                GCCC    G   AGCTGCAGAAC
                                ||||    |   ||||||||||
                                CGGG    C   TCGACGTCTTG
                                  _____ GG_
GAM920  LOC145195 5' GGCTCCTGGCCTCGACGGAGC  83273    C  A     AA   GCA  A
                                GC CC TCGAG  GCT   GA CC
                                || || |||||  |||   || ||
                                CG GG AGCTC  CGG   CT GG
                                 A  C     __   TC_  C
GAM920  LOC147687 5' GGCTCTGCAGCCCCGTGACGGC 64045     CCA   AGAA       A
                                GCC   TCG    GCTGCAGA CC
                                |||   |||    |||||||| ||
                                CGG   AGT    CGACGTCT GG
                                  C__   GCCC       C
GAM920  LOC149373 3' TTCTCACTCTCGATGTGGC    79316     C       A C  C
                                GCC CATCGAGA G TG AGAA
                                ||| |||||||| | || ||||
                                CGG GTAGCTCT C AC TCTT
                                  T       _ _  _
GAM920  LOC158297 5' GCAGCTTCCTGGGGC       81868        TCGA
                                GCCCCA    GAAGCTGC
                                ||||||    ||||||||
                                CGGGGT    CTTCGACG
                                   C___
GAM920  LOC199796 5' GGTTCTGCGCCTCAACCGGGC  74457      CATC   AA  T
                                GCCC    GAG  GC GCAGAACC
                                ||||    |||  || ||||||||
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                                CGGG   CTC  CG CGTCTTGG
                                  CCAA  __  _
GAM920  LOC200470 5'  CTGACCGGCTCGGTGGGGC   90061          AAGCTG
                                GCCCCATCGAG     CAG
                                ||||||||||     |||
                                CGGGGTGGCTC     GTC
                                      GGCCA_
GAM920  LOC203286 3'  TTCTGCAGCCAGAATGAAGG  90507    A  AGAA_
                                CC TCG    GCTGCAGAA
                                || |||    |||||||||
                                GG AGT    CGACGTCTT
                                 A  AAGAC
GAM920  LOC219406 3'  GCCCATCCTTCTCGAGGGGC  93561      A      CT___
                                GCCCC TCGAGAAG    GC
                                ||||| ||||||||    ||
                                CGGGG AGCTCTTC    CG
                                  _       CTACC
GAM920  LOC219690 5'  TTCTGCAGCTGCTTCAGGC   93076    CCATC  A
                                GCC    GAG AGCTGCAGAA
                                |||    ||| ||||||||||
                                CGG    TTC TCGACGTCTT
                                 AC___   G
GAM920  LOC219920 5'  CTCGGCTCCCTGATGGGGC   93310        AGA    C
                                GCCCCATCG   AGCTG AG
                                |||||||||   ||||| ||
                                CGGGGTAGT   TCGGC TC
                                      CCC    _
GAM920  LOC221552 3'  TAGCTTCTCACGGGGC     93805      ATC
                                GCCCC   GAGAAGCTG
                                |||||   |||||||||
                                CGGGG   CTCTTCGAT
                                   CA_
GAM920  LOC221975 5'  GTAGCTTCTCCATGGAGC    92608    C   C
                                GC CCAT GAGAAGCTGC
                                || |||| ||||||||||
                                CG GGTA CTCTTCGATG
                                 A   C
GAM920  LOC253767 3'  TCTGCAGCTCCGCGGC     94403    CCAT  A  A
                                GCC    CG GA GCTGCAGA
                                |||    || || ||||||||
                                CGG    GC CT CGACGTCT
                                 C___  _  _
GAM920  LOC256940 5'  GTTCTGCTCCACATAGGGC   96494     C  CGA  AGCT
                                GCCC AT   GA    GCAGAAC
                                |||| ||   ||    |||||||
                                CGGG TA   CT    CGTCTTG
                                  A  CAC  _____
GAM920  LOC257054 3'  GGCCCTGCAGCTCATGCAGC  95666    CC   C  GAA     AA
                                GC  CAT GA   GCTGCAG  CC
                                ||  ||| ||   |||||||  ||
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                                CG  GTA CT   CGACGTC  GG
                                 AC   _ ___     CC
GAM920  LOC257493 3'  TAGCTTCTCACGGGGC     97800      ATC
                                GCCCC   GAGAAGCTG
                                |||||   |||||||||
                                CGGGG   CTCTTCGAT
                                   CA_
GAM920  LOC257609 3'  TAGCTTCTCACGGGGC     97940      ATC
                                GCCCC   GAGAAGCTG
                                |||||   |||||||||
                                CGGGG   CTCTTCGAT
                                   CA_
GAM920  LOC96597  5'  GGTTCCAGCCCCTGATGGGGC  66919        G  AA   CA
                                GCCCCATC AG  GCTG  GAACC
                                ||||||||  ||  ||||  |||||
                                CGGGGTAG TC  CGAC  CTTGG
                                     _  CC   __
GAM921  ALCAM     3'  ATCAGCAATGCCCCAAACTTTC 7889       AGA  TT
           T                     AGAAA   TG  GGCATTGCTGAT
                                |||||   ||  ||||||||||||
                                TCTTT   AC  CCGTAACGACTA
                                   CAA  C_
GAM921  CDK10     3'  ATGCCAACACCCTTCTC     53775     A   A_
                                GA AAG  TGTTGGCAT
                                ||  |||  |||||||||
                                CT TTC  ACAACCGTA
                                 C   CC
GAM921  COL1A1    3'  TGGCTCTTGCAACATCT     3609         G  TT_
                                AGATGTTG CA   GCTG
                                ||||||||  ||   ||||
                                TCTACAAC GT   CGGT
                                     _  TCT
GAM921  DNAI1     3'  ATCAGGTCCCAGCATCTTCCCT 24058     AA        C  TG
                                AG  AAGATGTTGG AT  CTGAT
                                ||  ||||||||||  ||  |||||
                                TC  TTCTACGACC TG  GACTA
                                 CC         C  __
GAM921  IL17      3'  ATCAACAGACCAACATTTTTCT 9329       A      CA   C
                                AGAAA GATGTTGG  TTG TGAT
                                |||||  ||||||||  |||  ||||
                                TCTTT TTACAACC  GAC ACTA
                                   _       A_   A
GAM921  KLRF1     3'  AATGCCAAAATCTCTTCT    33264      A   G
                                AGAA AGAT TTGGCATT
                                ||||  ||||  ||||||||
                                TCTT TCTA AACCGTAA
                                  C   A
GAM921  MEL       3'  ATCAGCAATAGTCTGCTCT   18120     T  T  _
                                AGA GT GGC ATTGCTGAT
                                |||  ||  |||  |||||||||
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                                TCT CG CTG TAACGACTA
                                  _ T  A
GAM921  SHC1    3'  CAGGGATGCCAACACCTT    11645    A       G
                                AAG TGTTGGCATT CTG
                                ||| |||||||||| |||
                                TTC ACAACCGTAG GAC
                                  C        G
GAM921  TFAP2C  3'  ATCAACAATACCTTTTTTTTC  12230       TGTT  C   C
                                GAAAAGA   GG ATTG TGAT
                                |||||||   || |||| ||||
                                CTTTTTT   CC TAAC ACTA
                                    TT__  A   A
GAM921  TGFA    3'  CAGCCCAACATCTT       12249         CATT
                                AAGATGTTGG   GCTG
                                ||||||||||   ||||
                                TTCTACAACC   CGAC

                                     ____
GAM921  TYRO3   3'  TAGTGCCAACTTCCCCTCT   20846    AAA  T
                                AGA  GA GTTGGCATTG
                                |||  || ||||||||||
                                TCT  CT CAACCGTGAT
                                  CCC  T
GAM921  WNT5A   3'  ATCAGCAATGTTTCTCTTTTCT 12662       TGTT
                                AGAAAAGA   GGCATTGCTGAT
                                ||||||||   ||||||||||||
                                TCTTTTCT   TTGTAACGACTA
                                    CT__
GAM921  BAGE    3'  ATCAGTATTCAACATCTTTT  6806          CAT
                                AAAAGATGTTGG  TGCTGAT
                                ||||||||||||  |||||||
                                TTTTCTACAACT  ATGACTA
                                       T__
GAM921  FLJ10342 3' CAGCAATGCCAATACCCCTTCT 36036     AAGA
                                AGAA   TGTTGGCATTGCTG
                                ||||   ||||||||||||||
                                TCTT   ATAACCGTAACGAC
                                  CCCC
GAM921  FLJ12903 3' ATCAGCAATGAAGGTC     42770    G  GG
                                GAT TT  CATTGCTGAT
                                ||| ||  ||||||||||
                                CTG AA  GTAACGACTA
                                  G  __
GAM921  FLJ13215 3' ATCAGCAACCTGCATCTTTT  46566       T  CA
                                AAAAGATGT GG  TTGCTGAT
                                |||||||| ||  ||||||||
                                TTTTCTACG CC  AACGACTA
                                      T  __
GAM921  FLJ20048 3' CAAGGGCAACATCTTTTCT   34436          G A_
                                AGAAAAGATGTTG C  TTG
                                |||||||||||| |  |||
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                                TCTTTTCTACAAC G  AAC
                                       _ GG
GAM921  FLJ20340  5'  CAGATCACCAACATCTTTTC   34974          CATTG
                                GAAAAGATGTTGG    CTG
                                ||||||||||||    |||
                                CTTTTCTACAACC    GAC
                                       ACTA_
GAM921  HSRNAFEV  3'  AGTGCCAAATCTTTTC     34019       G
                                GAAAAGAT TTGGCATT
                                |||||||| ||||||||
                                CTTTTCTA AACCGTGA
                                      _
GAM921  ILF2      3'  GATACCAACATTTCTTC     66940     A       C
                                GAA AGATGTTGG ATT
                                ||| ||||||||| |||
                                CTT TTTACAACC TAG
                                  C       A
GAM921  KIAA0179  3'  ATCAGCAATACCATAGTTTTTC 64824       ATGT   C
           T                     AGAAAAG   TGG ATTGCTGAT
                                |||||||   ||| |||||||||
                                TCTTTTT   ACC TAACGACTA
                                    GAT_  A
GAM921  KIAA0819  3'  CAGCAATGATAGACTCTT    63575     T   GG_
                                AAGA GTT   CATTGCTG
                                |||| |||   ||||||||
                                TTCT CAG   GTAACGAC
                                  _  ATA
GAM921  KIAA1493  3'  ATCAGCAGCCTCAGCATCT   64152        CA
                                AGATGTTGG  TTGCTGAT
                                |||||||||  ||||||||
                                TCTACGACT  GACGACTA
                                     CC
GAM921  KIAA1727  3'  ATCAGCAAGGACCCATCT    64053      TT  CA_
                                AGATG  GG   TTGCTGAT
                                |||||  ||   ||||||||
                                TCTAC  CC   AACGACTA
                                   __  AGG
GAM921  MGC32043  3'  CAGCCCCAACATCCTTC     58046     AA      CATT
                                GAA  GATGTTGG    GCTG
                                |||  ||||||||    ||||
                                CTT  CTACAACC    CGAC
                                  C_       C___
GAM921  NAV1      3'  CACTGCCAACAACTCCTC    39951    AA  A       T
                                GA  AG TGTTGGCA TG
                                ||  || |||||||| ||
                                CT  TC ACAACCGT AC
                                 CC  A       C
GAM921  TCL6      3'  ATCAGCAATTTCTGATTTTCT  24975       GATGTT  C
                                AGAAAA     GG ATTGCTGAT
                                ||||||     || |||||||||
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                                TCTTTT     CT TAACGACTA
                                   AGT___  T
GAM921  TCL6     3'  ATCAGCAATTTCTGATTTTCT  26991       GATGTT  C
                                AGAAAA     GG ATTGCTGAT
                                ||||||     || |||||||||
                                TCTTTT     CT TAACGACTA
                                   AGT___  T
GAM921  ZDHHC2   3'  ATCAACGGGGAAAACATCTTCT 33007    A      GGCA   C
          C                      GA AAGATGTT    TTG TGAT
                                || ||||||||    ||| ||||
                                CT TTCTACAA    GGC ACTA
                                 C       AAGG   A
GAM921  LOC131368 3'  CAGCACATGTTAACTCTCCTC  75859    AA   T      _
                                GA  AGA GTTGGCAT TGCTG
                                ||  ||| |||||||| |||||
                                CT  TCT CAATTGTA ACGAC
                                 CC  _      C
GAM921  LOC147299 3'  GTTCTGCCAACACCCTTTC    78348     AGA      TT
                                GAAA   TGTTGGCA  GC
                                ||||   ||||||||  ||
                                CTTT   ACAACCGT  TG
                                  CCC       CT
GAM921  LOC148418 3'  TGCCAACACCCTTTTT      78851       A_
                                GAAAAG  TGTTGGCA
                                ||||||  ||||||||
                                TTTTTC  ACAACCGT
                                   CC
GAM921  LOC159121 5'  TCCTGCTGCAACATCTTCTC   86999    A       G  TT  T_
                                GA AAGATGTTG CA  GC  GA
                                || |||||||| ||  ||  ||
                                CT TTCTACAAC GT  CG  CT
                                 C       _  __  TC
GAM921  LOC221296 3'  ATCAGCAATGAGTATGCCTT   91956     AT  TGG
                                AAG  GT   CATTGCTGAT
                                |||  ||   ||||||||||
                                TTC  TA   GTAACGACTA
                                  CG  TGA
GAM921  LOC255330 5'  CAGCCCTGCCAACATC      95812          TT
                                GATGTTGGCA  GCTG
                                |||||||||  ||||
                                CTACAACCGT  CGAC
                                     CC
GAM921  LOC91974  3'  ATCAGCCTGTAACATTTCTTCT 67752      A       G  TT
                                AGAA AGATGTTG CA  GCTGAT
                                |||| |||||||| ||  ||||||
                                TCTT TTTACAAT GT  CGACTA
                                  C       _  C_
GAM922  AHCY     3'  TCCAGCTGCTGTCCTTGCC    5476       GACCT    _
                                GGCAA    GGGCA CAGCTGGA
                                |||||    ||||| ||||||||
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                                CCGTT    CCTGT GTCGACCT
                                  _____    C
GAM922  ATP2B3   5'  CTCACCGCCGCCAAACCTTGCC 41692      ACCTG  ACA  TG_
                                GGCAAG    GGC  GC  GAG
                                ||||||    |||  ||  |||
                                CCGTTC    CCG  CG  CTC
                                   CAAA_  C__  CCA
GAM922  BAZ2A    3'  CAGTGCATCCAGGTCCTGCC  25598     A      CACA
                                GGCA GACCTGGG   GCTG
                                |||| ||||||||   ||||
                                CCGT CTGGACCT   TGAC
                                  C       ACG_
GAM922  BGN      3'  CCAGCCTGCCCTGCTCAGGCCT 8141       A      ___  _
           TGCC                   GGCAAG CCTGGGCA  CAG CTGG
                                |||||| ||||||||  ||| ||||
                                CCGTTC GGACTCGT  GTC GACC
                                   C       CCC  C
GAM922  BRF1     3'  TCCAGCTGTGGCCCTGC     7715     AGACCT   _
                                GCA     GGGC ACAGCTGGA
                                |||     |||| |||||||||
                                CGT     CCCG TGTCGACCT
                                 _______   G
GAM922  CALB1    5'  CCCGCGCCCAGGTCTCC     17023    CA       ACA  T
                                GG  AGACCTGGGC  GC GG
                                ||  ||||||||||  || ||
                                CC  TCTGGACCCG  CG CC
                                 __        ___  C
GAM922  CHRM1    3'  CCAGGGCCCTGCTCAGGCCTCA 94787    CA  A      CA  __
           CC                     GG  AG CCTGGGCA  GCT  GG
                                ||  || ||||||||  |||  ||
                                CC  TC GGACTCGT  CGG  CC
                                 AC  C       CC   GA
GAM922  DES      3'  CCAGCTGTGAGCCTTGG     72123    T   __
                                CC GGGC  ACAGCTGG
                                || ||||  ||||||||
                                GG TCCG  TGTCGACC
                                 T   AG
GAM922  DMRT1    5'  CTCCAGCTGCGCCTCCGGCTGC 41698     A A  T _  A
                                GCA G CC G GGC CAGCTGGAG
                                ||| | || | ||| |||||||||
                                CGT C GG C CCG GTCGACCTC
                                 _ _  C T   C
GAM922  DSCR4    3'  TTGTGCCCAGGCCTTGC     19639      A
                                GCAAG CCTGGGCACAG
                                ||||| ||||||||||
                                CGTTC GGACCCGTGTT
                                   C
GAM922  ELAVL3   3'  CCCCTTGCCCAGGCCTCCCC   7426     CA  A      C  CT
                                GG  AG CCTGGGCA AG  GG
                                ||  || |||||||| ||  ||
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                                CC  TC GGACCCGT TC  CC
                                 CC  C       _ C_
GAM922  ELK1     3'  CTCCAGCCAGTACTCCAGGTCT 17840     CA       _ C  A_
              CC                  GG  AGACCTGG G AC  GCTGGAG
                                ||  |||||||| | ||  |||||||
                                CC  TCTGGACC C TG  CGACCTC
                                 __       T A  AC
GAM922  FBXL7    5'  CTGCAGCTGTGCCCGGCCCCGC 24549     AAGAC          G
              C                   GGC     CTGGGCACAGCTG AG
                                |||     |||||||||||||| ||
                                CCG     GGCCCGTGTCGAC TC
                                  CCCC_           G
GAM922  FE65L2   3'  TTGTGCCCAGATCTTGTC    55682        C
                                GGCAAGA CTGGGCACAG
                                ||||||| ||||||||||
                                CTGTTCT GACCCGTGTT
                                    A
GAM922  FE65L2   3'  TTGTGCCCAGATCTTGTC    55686        C
                                GGCAAGA CTGGGCACAG
                                ||||||| ||||||||||
                                CTGTTCT GACCCGTGTT
                                    A
GAM922  FZD1     3'  CCATGCCCAGGCCTCGGC    13033    A_  A       CAGC
                                GC  AG CCTGGGCA    TGG
                                ||  || ||||||||    |||
                                CG  TC GGACCCGT    ACC
                                 GC  C       _____
GAM922  HD       3'  TCCTTGCCCAGGTCTCACT    9193     CA         CAGCT
                                GG  AGACCTGGGCA     GGA
                                ||  ||||||||||     |||
                                TC  TCTGGACCCGT     CCT
                                 AC          T_____
GAM922  HOXB3    5'  CCACTGCCCAGGCCTCACC    9259     CA  A       CAGC
                                GG  AG CCTGGGCA    TGG
                                ||  || ||||||||    |||
                                CC  TC GGACCCGT    ACC
                                 AC  C       C___
GAM922  KLHL1    5'  CCACGCCCAGGTCCTGC     40485     A        ACAGC
                                GCA GACCTGGGC     TGG
                                ||| |||||||||     |||
                                CGT CTGGACCCG     ACC
                                  C        C_____
GAM922  MN1      3'  CTCGCAAATGCCCAGGCCCTGC 10090     AGA       CA_  T
                                GCA   CCTGGGCA   GC GG
                                |||   ||||||||   || ||
                                CGT   GGACCCGT   CG TC
                                  CCC       AAA  C
GAM922  MPP2     3'  TTGTGCCCAGGTGCTGCC    59833      AG
                                GGCA  ACCTGGGCACAG
                                ||||  ||||||||||||
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                                CCGT  TGGACCCGTGTT
                                  CG
GAM922  OFD1    5'  CTCCAGCCGCCTTTGAGTCGTG 13217     A  CT__   ACA
            CC                    GGCA GAC   GGGC  GCTGGAG
                                  |||| |||   ||||  |||||||
                                  CCGT CTG   TCCG  CGACCTC
                                    G  AGTT   C__
GAM922  OPHN1   5'  TCCAGCTCTAACCTCGCC    10361     AA  CCT  GCAC
                                  GGC  GA   GG   AGCTGGA
                                  |||  ||   ||   |||||||
                                  CCG  CT   CC   TCGACCT
                                    __  ___  AATC
GAM922  PDE1B   3'  CCACCCCAGATCTTAGC     6242     _   C    CACAGC
                                  GC AAGA CTGGG     TGG
                                  || |||| |||||     |||
                                  CG TTCT GACCC     ACC
                                   A   A    C_____
GAM922  PDGFB   5'  CTGCGCCCAGGTCCTCC     10499    CAA       A
                                  GG   GACCTGGGC CAG
                                  ||   ||||||||| |||
                                  CC   CTGGACCCG GTC
                                   TC_       C
GAM922  PDGFRB  3'  CCAGCCTGCAGCCCTTGCC   65973      GACCT   A_  _
                                  GGCAA    GGGC  CAG CTGG
                                  |||||    ||||  ||| ||||
                                  CCGTT    CCCG  GTC GACC
                                     _____   AC   C
GAM922  PHF1    3'  CCATCCCCAGGTCTTCC     10542    C       CACAGC
                                  GG AAGACCTGGG     TGG
                                  || ||||||||||     |||
                                  CC TTCTGGACCC     ACC
                                   _        CT____
GAM922  PRG2    5'  CCAACTACAGCATAGGCCTGTG 10780     _ A   G  AC_  C
            CC                    GGCA AG CCTG GC   AG TGG
                                  |||| || |||| ||   || |||
                                  CCGT TC GGAT CG   TC ACC
                                    G  C    A  ACA  A
GAM922  PRX     3'  CCAGCCGTGGGAATCCAGGTCC 40524    CAA      ____  A
            CC                    GG   GACCTGGG    CAC GCTGG
                                  ||   ||||||||    ||| |||||
                                  CC   CTGGACCT    GTG CGACC
                                   C__       AAGG   C
GAM922  RUNX3   3'  CTCCAGCTATGCCCAGTGCTGC 15114    A AC     C
                                  GCA G  CTGGGCA AGCTGGAG
                                  ||| |  ||||||| ||||||||
                                  CGT C  GACCCGT TCGACCTC
                                    _ GT      A
GAM922  SECTM1  3'  TCCACCCCCCAGGTCTTCC   11531    C       CACAGC
                                  GG AAGACCTGGG     TGGA
                                  || ||||||||||     ||||
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                                CC TTCTGGACCC     ACCT
                                 _        CCC___
GAM922  TBL2     3'  CCAACGCCCAGGTCTTGGC   52180   G         ACAGC
                                G CAAGACCTGGGC    TGG
                                | ||||||||||||    |||
                                C GTTCTGGACCCG    ACC
                                 G          CA___
GAM922  TMSB4Y   5'  TCCAGCTGCAGCCTCCGCC   14844    AAGACCT   A_
                                GGC      GGGC  CAGCTGGA
                                |||      ||||  ||||||||
                                CCG      TCCG  GTCGACCT
                                  CC_____    AC
GAM922  WNT7A    3'  CCAGACACAGCCCAGGTCCC  16120   CAA       ACAG_
                                GG   GACCTGGGC    CTGG
                                ||   |||||||||    ||||
                                CC   CTGGACCCG    GACC
                                 ___        ACACA
GAM922  ZAP70    3'  CCACCCCAGGTCCTGC      70819     A       CACAGC
                                GCA GACCTGGG      TGG
                                ||| ||||||||      |||
                                CGT CTGGACCC      ACC
                                  C       C_____
GAM922  C11orf15 5'  CCAGCCGGGTCCCAAGCCTGTG 40221      AGACC_   _ ACA
           CC                     GGCA     TGGG C   GCTGG
                                ||||     |||| |   |||||
                                CCGT     ACCC G   CGACC
                                  GTCCGA    T GGC
GAM922  C20orf177 5' CCAGCTGTCATCATCTTCC   62145    C    CC   GC
                                GG AAGA  TGG  ACAGCTGG
                                || ||||  |||  ||||||||
                                CC TTCT  ACT  TGTCGACC
                                 _   __  AC
GAM922  C20orf3  3'  CTCGAGGATGCCCGGGCCCC  68072    CAAGA      CAG  G
                                GG    CCTGGGCA   CT GAG
                                ||    ||||||||   || |||
                                CC    GGGCCCGT   GA CTC
                                 CC___       AG_  G
GAM922  C22orf4  3'  TCCAGCTCAGATCATGCC    60645     A  C   GGCAC
                                GGCA GA CTG     AGCTGGA
                                |||| || |||     |||||||
                                CCGT CT GAC     TCGACCT
                                  A  A  ______
GAM922  DECR2    3'  CTCCAGCTGCCCACAAGGTCCG 40335     AA    ___    CA
           CC                     GGC  GACCT   GGGCA  GCTGGAG
                                |||  |||||   |||||  |||||||
                                CCG  CTGGA   CCCGT  CGACCTC
                                  C_    ACA    __
GAM922  DKFZP434H132 5'  CTCCAGCCGTAGCTGTGGCCTC 31317    CA  A  TG   _  A
           CCC                      GG  AG CC  GGC AC GCTGGAG
                                ||  || ||  ||| || |||||||
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                                CC  TC GG  TCG TG CGACCTC
                                 CC  C  TG   A  C
GAM922  DMTF1    5'  CTCCAGCTGCAGCCACTCTCGC 40939     A   CCTG   A_
            C                    GGC AGA    GGC  CAGCTGGAG
                                |||  |||    |||  |||||||||
                                CCG TCT    CCG  GTCGACCTC
                                  C   CA__   AC
GAM922  FLJ12688 3'  GTGCCCAGGTCTTCC      73179    C
                                GG AAGACCTGGGCAC
                                ||  ||||||||||||
                                CC TTCTGGACCCGTG
                                 _
GAM922  FLJ13055 3'  CCAGCCATGTGTTCGTCGCC   42710     AA   CT      __
                                GGC  GAC  GGGCACA  GCTGG
                                |||  |||  |||||||  |||||
                                CCG  CTG  CTTGTGT  CGACC
                                  __   __      AC
GAM922  FLJ20315 3'  TCCAGCTCCAGACCTTGTC   34936       AC    GCAC
                                GGCAAG  CTGG    AGCTGGA
                                ||||||  ||||    |||||||
                                CTGTTC  GACC    TCGACCT
                                   CA    _____
GAM922  FLJ20337 3'  CCACCGCCCAGGTCTT      34964           ACAGC
                                AAGACCTGGGC     TGG
                                ||||||||||     |||
                                TTCTGGACCCG     ACC
                                      CC___
GAM922  FLJ20359 3'  CCAGCCCCCAGGTCCTCC    35037    CAA      CACA
                                GG   GACCTGGG   GCTGG
                                ||   ||||||||   |||||
                                CC   CTGGACCC   CGACC
                                 TC_       C___
GAM922  FLJ21438 3'  AGTCTGTCCAGGCCCTGCC   61517     AGA      CA
                                GGCA   CCTGGGCA  GCT
                                ||||   ||||||||  |||
                                CCGT   GGACCTGT  TGA
                                  CCC       C_
GAM922  FLJ21820 3'  CCAACTGTGCCTCCTGCC    41622     A  CCTG     C
                                GGCA GA    GGCACAG TGG
                                |||| ||    ||||||| |||
                                CCGT CT    CCGTGTC ACC
                                  C _____      A
GAM922  GPR9     3'  CCAGCACCACCAGGTCTCC    7685     CA      GCACA
                                GG  AGACCTGG    GCTGG
                                ||  ||||||||    |||||
                                CC  TCTGGACC    CGACC
                                 __       ACCA_
GAM922  GTF3C1   3'  CTCCTTGAGTGCCCAGGTGCC  7719      AAG        AGCT
                                GGC   ACCTGGGCAC   GGAG
                                |||   ||||||||||   ||||
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                                CCG  TGGACCCGTG   CCTC
                                  ___        AGTT
GAM922  HN1L     3'  CTCTGAAGTGCCCAGTTCCTGC 57995     A  C      AGC
            C                    GGCA GA CTGGGCAC   TGGAG
                                ||||  ||  ||||||||   |||||
                                CCGT CT GACCCGTG   GTCTC
                                  C  T       AA_
GAM922  KIAA0210 3'  CCACAGTGCCCAGTCCTGCC  28473     A   C      AGC
                                GGCA GAC TGGGCAC   TGG
                                ||||  |||  |||||||   |||
                                CCGT CTG ACCCGTG   ACC
                                  C   _      AC_
GAM922  KIAA0350 3'  CCACCTCACCCAGGTCTCAGC  61170    A_       CAC  C
                                GC  AGACCTGGG   AG TGG
                                ||  |||||||||   || |||
                                CG  TCTGGACCC   TC ACC
                                 AC        AC_  C
GAM922  KIAA0450 5'  CCTGCATGCCCAGGCCGC    27633    AAGA      CA  T
                                GC    CCTGGGCA  GC GG
                                ||    ||||||||  || ||
                                CG    GGACCCGT  CG CC
                                 CC__       A_  T
GAM922  KIAA0523 5'  TCCAGCCAGGAGCCCTGCT    67743     AGACCT    ACA__
                                GGCA     GGGC     GCTGGA
                                ||||     ||||     ||||||
                                TCGT     CCCG     CGACCT
                                  _______    AGGAC
GAM922  KIAA0537 5'  CTGTGCCCGGTCTTGCC     29249         T
                                GGCAAGACC GGGCACAG
                                ||||||||| ||||||||
                                CCGTTCTGG CCCGTGTC
                                     _
GAM922  KIAA0632 3'  CTCCAGCTACCTTTGTGTGTC  31425     AG  CT   CAC
                                GGCA  AC  GGG   AGCTGGAG
                                ||||  ||  |||   ||||||||
                                CTGT  TG  TCC   TCGACCTC
                                  G_  TT   A__
GAM922  KIAA0638 3'  CTCCAGCTGTCTGGCCTCGCC  72395     A  A  TG  C
                                GGC AG CC  GG ACAGCTGGAG
                                ||| || ||  || ||||||||||
                                CCG TC GG  TC TGTCGACCTC
                                  C  C  __  _
GAM922  KIAA0676 3'  CCAACCACTGCTTAGGCCTCC  30451    CA  A      CAGC_
                                GG  AG CCTGGGCA     TGG
                                ||  || ||||||||     |||
                                CC  TC GGATTCGT     ACC
                                 __  C       CACCA
GAM922  KIAA0934 3'  TCCAGCTGCGTCGTTTGCC    64224     A   CTG   A
                                GGCA GAC   GGC CAGCTGGA
                                ||||  |||   |||  ||||||||
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                                CCGT TTG   CTG GTCGACCT
                                  _  ___   C
GAM922  KIAA1100 3' CTCCAGCCAGGGCCCAACTCCC 29753    CAA  CC    ACA_
                                GG   GA  TGGGC    GCTGGAG
                                ||   ||  |||||    |||||||
                                CC   CT  ACCCG    CGACCTC
                                 ___  CA    GGAC
GAM922  KIAA1157 3' CTGTGTCCAAGTCCC      72244    CAA   C
                                GG   GAC TGGGCACAG
                                ||   ||| |||||||||
                                CC   CTG ACCTGTGTC
                                 ___   A
GAM922  KIAA1193 3' CCAGCCCTGCAGGTCTTCC   67635    C      GG   CA
                                GG AAGACCT  GCA  GCTGG
                                || |||||||  |||  |||||
                                CC TTCTGGA  CGT  CGACC
                                 _     __   CC
GAM922  KIAA1196 3' CCTGCTGTGCTCAGGCCCTGCC 61464      AGA          T
                                GGCA   CCTGGGCACAGC GG
                                ||||   |||||||||||| ||
                                CCGT   GGACTCGTGTCG CC
                                  CCC          T
GAM922  KIAA1297 3' CTCCAGCTGTCAGGCCACGCC  72179     AAGA    GGC
                                GGC    CCTG   ACAGCTGGAG
                                |||    ||||   ||||||||||
                                CCG    GGAC   TGTCGACCTC
                                 CACC   ___
GAM922  KIAA1656 3' TCCAGCTGCTGCACCTGCC    65808     AGACCT  _   _
                                GGCA     GG GCA CAGCTGGA
                                ||||     || ||| ||||||||
                                CCGT     CC CGT GTCGACCT
                                  _______  A   C
GAM922  KIAA1870 3' CCAGCTGTTGTCTGCC      49659      A   CTGGGC
                                GGCA GAC     ACAGCTGG
                                |||| |||     ||||||||
                                CCGT CTG     TGTCGACC
                                  _   T_____
GAM922  LY6G5B   5' CCGGTAGTGCCCAGGTATTACC 41130    C  G         A
                                GG AA ACCTGGGCAC GCTGG
                                || || |||||||||| |||||
                                CC TT TGGACCCGTG TGGCC
                                 A  A         A
GAM922  MGC16332 5' CTGGGTGCCCAGGCCCTGGC   56775    A  A_       AG TG
                                GC AG  CCTGGGCAC  C  G
                                || ||  |||||||||  |  |
                                CG TC  GGACCCGTG  G  C
                                 G  CC         __ GT
GAM922  MGC2474  5' CCGCATGCCCAGGCCTGGCC   43717     A  A       CA  T
                                GGC AG CCTGGGCA  GC GG
                                ||| || ||||||||  || ||
```

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                                CCG TC GGACCCGT  CG CC
                                  G  C       A_  _
GAM922  MGC4368   3'  AGTGTACCCAGGTCCTCC    44458    CAA       C   G
                                GG   GACCTGGG ACA CT
                                ||   |||||||| ||| ||
                                CC   CTGGACCC TGT GA
                                 TC_       A   _
GAM922  MUC16     5'  TCAGCGGCCCAGGTCTGCC    60530     A        ACA
                                GGCA GACCTGGGC   GCTGG
                                |||| |||||||||   |||||
                                CCGT CTGGACCCG   CGACT
                                  _       G__
GAM922  OBTP      5'  CCAGGATCCAGGTCCACC    34243    CAA       CACAG
                                GG   GACCTGGG    CTGG
                                ||   ||||||||    ||||
                                CC   CTGGACCT    GACC
                                 AC_       AG___
GAM922  PIB5PA    3'  CTCCAGCTGTATCTGCACCTGC 66053      AGACCT  GC
              C                  GGCA     GG  ACAGCTGGAG
                                ||||     ||  ||||||||||
                                CCGT     TC  TGTCGACCTC
                                  CCACG_  TA
GAM922  PTDSS2    3'  CCACGTGCCCGGCCTTGCC    47885       A  T     AGC
                                GGCAAG CC GGGCAC   TGG
                                |||||| || ||||||   |||
                                CCGTTC GG CCCGTG   ACC
                                   C  _     C__
GAM922  RAB20     5'  CTCCAGCTGCGCCCAGGGCGC  35154    AAGA      A
                                GC    CCTGGGC CAGCTGGAG
                                ||    ||||||| |||||||||
                                CG    GGACCCG GTCGACCTC
                                 CG__      C
GAM922  RALGPS1A  5'  CTCCAGCTGCGCCTGGCCCGGC 27601     AAGAC TG   A
              C                  GGC    C  GGC CAGCTGGAG
                                |||    |  ||| |||||||||
                                CCG    G  CCG GTCGACCTC
                                  GCCC_ GT   C
GAM922  SLC26A1   3'  CTCCCTATGCCCAGGCCTGCC  41865      A A       C  CT
                                GGCA G CCTGGGCA AG  GGAG
                                |||| | |||||||| ||  ||||
                                CCGT C GGACCCGT TC  CCTC
                                  _ C       A  __
GAM922  STRN3     5'  CCAGCTGTCGGCGTCTCGCC   27407     A   _   GGC
                                GGC AGAC CTG   ACAGCTGG
                                ||| |||| |||   ||||||||
                                CCG TCTG GGC   TGTCGACC
                                  C   C  ____
GAM922  LOC112868 3'  CCAGCCCCTCATGTCTTGCC   72892         C    CACA
                                GGCAAGAC TGGG    GCTGG
                                |||||||| ||||    |||||
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                                CCGTTCTG ACTC    CGACC
                                     T    CC__
GAM922   LOC146325 5'  CCATGGTGCCCGGCCCTGCC   59177      A AC       AGC
                                GGCA G  CTGGGCAC   TGG
                                |||| |  ||||||||   |||
                                CCGT C  GGCCCGTG   ACC
                                  _ CC       GT_
GAM922   LOC148490 3'  CCAGGCCCAGGTCT        78884          ACAG
                                AGACCTGGGC    CTGG
                                ||||||||||    ||||
                                TCTGGACCCG    GACC
                                      _____
GAM922   LOC148753 5'  CTCCAGCTGTTTCACGTCGCC  84216     AA   C    C
                                GGC  GAC TGGG ACAGCTGGAG
                                |||  ||| |||| ||||||||||
                                CCG  CTG ACTT TGTCGACCTC
                                  __   C    _
GAM922   LOC149464 5'  CTCCAGCTGGTTGGGACCCC   84427    CAAGA  TG G A
                                GG     CC  G C CAGCTGGAG
                                ||     ||  | | ||||||||||
                                CC     GG  T G GTCGACCTC
                                 CCA__  GT _ _
GAM922   LOC197335 5'  CCACAGTGCCCAGGTCCTGGC  87975    G  A         AGC
                                G CA GACCTGGGCAC   TGG
                                | || ||||||||||   |||
                                C GT CTGGACCCGTG   ACC
                                 G  C          AC_
GAM922   LOC197342 3'  CCAGCTGTCCTCATCCCTGCC  87992      A_  CC    C
                                GGCA  GA  TGGG ACAGCTGG
                                ||||  ||  |||| ||||||||
                                CCGT  CT  ACTC TGTCGACC
                                  CC  __    C
GAM922   LOC199786 3'  CTCTGGTGCCCAGATCCAGCC  88378     AA  C     ACA  TG
                                GGC  GA CTGGGC   GC  GAG
                                |||  || ||||||   ||  |||
                                CCG  CT GACCCG   TG  CTC
                                  AC  A      ___  GT
GAM922   LOC200081 3'  TCCAGCTGCTGCCCCAGCC    88568     AAGACCT    _
                                GGC       GGGCA CAGCTGGA
                                |||       ||||| ||||||||
                                CCG       CCCGT GTCGACCT
                                  AC_____     C
GAM922   LOC204970 3'  TCAGGTGCGCCCAGACCGTGCC 89418       AGAC     A  G
                                GGCA    CTGGGC CA CTGG
                                ||||    |||||| || ||||
                                CCGT    GACCCG GT GACT
                                  GCCA     C  G
GAM922   LOC220070 3'  CTCCAGCCAATGTCAGCCCAGG 59260   CAA        __   ___
            TCCCC                    GACCTGGGC  ACA   GCTGGAG
                                    |||||||||  |||   |||||||
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                                  CTGGACCCG  TGT   CGACCTC
                                C__       AC   AAC
GAM922  LOC222031 3'  CTCCAGCCACCCCAGGTCTCAG 94020    A_       CACA
          C                      GC  AGACCTGGG    GCTGGAG
                                 ||  |||||||||    |||||||
                                 CG  TCTGGACCC    CGACCTC
                                  AC        CAC_
GAM922  LOC253069 3'  CTGTGCCCCGGTCTTACC    95711    C     T
                                 GG AAGACC GGGCACAG
                                 || |||||| ||||||||
                                 CC TTCTGG CCCGTGTC
                                  A     C
GAM922  LOC253092 5'  TCCAGCTGCGCCTCTGCC    97469      A  CCTG   A
                                 GGCA GA    GGC CAGCTGGA
                                 |||| ||    ||| ||||||||
                                 CCGT CT    CCG GTCGACCT
                                   _ _____   C
GAM922  LOC255975 5'  CTAGACAGGCCCAGGTCTTGCC 95891            ACAG
                                 GGCAAGACCTGGGC    CTGG
                                 ||||||||||||||    ||||
                                 CCGTTCTGGACCCG    GATC
                                         GACA
GAM922  LOC51667  3'  CTCCAGCTGTGGCTCCATCTGC 32273      A  CCT  G
          C                      GGCA GA   GG CACAGCTGGAG
                                 |||| ||   || ||||||||||
                                 CCGT CT   TC GTGTCGACCTC
                                   _ ACC  G
GAM922  LOC90019  3'  CCCGCTGAGCCCAGGCACTTGC 56757       A_      A    T
          C                      GGCAAG  CCTGGGC CAGC GG
                                 ||||||  ||||||| |||| ||
                                 CCGTTC  GGACCCG GTCG CC
                                    AC      A   C
GAM922  LOC90019  5'  CTAGGCTGCCCAGGCCCTGCC  56760      AGA       CAG
                                 GGCA   CCTGGGCA   CTGG
                                 ||||   ||||||||   ||||
                                 CCGT   GGACCCGT   GATC
                                   CCC       CG_
GAM922  LOC90522  3'  CTCCAGCTGCACAGGCCACCGC 63154     AAGA_   GGCA
          C                      GGC    CCTG    CAGCTGGAG
                                 |||    ||||    |||||||||
                                 CCG    GGAC    GTCGACCTC
                                   CCACC    AC__
GAM922  LOC90826  5'  CTCGCGGCCCAGGTCCCGCC   64091     AA       ACA  T
                                 GGC  GACCTGGGC   GC GG
                                 |||  |||||||||   || ||
                                 CCG  CTGGACCCG   CG TC
                                   CC        G__  C
GAM922  LOC91035  5'  CCTCAGTGCCCAGGTCCACC   64668    CAA        AGCT
                                 GG   GACCTGGGCAC    GG
                                 ||   ||||||||||    ||
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                                CC  CTGGACCCGTG  CC
                                 AC_        ACT_
GAM923  ADRA2A  5' GCAGCAGGCCCAGGCCA    5453        ATC   AA
                                TGGCCTGG  CCTG TGC
                                ||||||||  |||| |||
                                ACCGGACC  GGAC ACG
                                    C__   G_
GAM923  CIT     5' GCTGAAGAGGAGATCCAGGC  69747        _  GAAT_
                                GCCTGGATC CCT   GC
                                ||||||||| |||   ||
                                CGGACCTAG GGA   CG
                                     A  GAAGT
GAM923  CYP19   3' AGTTGATTAGAAAGACCAGGCC 48335       A C__  ATG
           A                     TGGCCTGG TC  CTGA  CAACT
                                ||||||||  ||  ||||  |||||
                                ACCGGACC AG  GATT  GTTGA
                                    _ AAA   A__
GAM923  CYP19   3' AGTTGATTAGAAAGACCAGGCC 3647        A C__  ATG
           A                     TGGCCTGG TC  CTGA  CAACT
                                ||||||||  ||  ||||  |||||
                                ACCGGACC AG  GATT  GTTGA
                                    _ AAA   A__
GAM923  FPGS    3' GCCAAAGGCATCCAGGCCA   17086        C  GAAT
                                TGGCCTGGAT CCT   GC
                                ||||||||| |||   ||
                                ACCGGACCTA GGA   CG
                                     C  AAC_
GAM923  GPR17   3' GTTGAAGAGACACAGGCCA   17957      GA  C  GAATG
                                TGGCCTG  TC CT   CAAC
                                |||||||  || ||   ||||
                                ACCGGAC  AG GA   GTTG
                                   AC  A  A____
GAM923  KIF3B   3' GCATTTGGATCCAGGCC    16608        CT
                                GGCCTGGATCC  GAATGC
                                ||||||||||  ||||||
                                CCGGACCTAGG  TTTACG
                                      __
GAM923  LFG     3' GCTCCAGGGACCCAGGCCA   76724       A    AAT
                                TGGCCTGG TCCCTG  GC
                                |||||||| ||||||  ||
                                ACCGGACC AGGGAC  CG
                                    C    CT_
GAM923  MMP11   3' TGTTCTCCAGAATCCAGGCCA 19875        CC  AAT_
                                TGGCCTGGAT  CTG   GCA
                                ||||||||||  |||   |||
                                ACCGGACCTA  GAC   TGT
                                     A_  CTCT
GAM923  MMP19   5' TGCACCCAGATGATGTGGC   42976    T G  C_  AA
                                GCC G ATC  CTG  TGCA
                                ||| | |||  |||  ||||
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                                CGG T TAG  GAC  ACGT
                                  _ G   TA   CC
GAM923  MMP19    5'  TGCACCCAGATGATGTGGC   42986     T G   C_   AA
                                GCC G ATC  CTG  TGCA
                                ||| | |||  |||  ||||
                                CGG T TAG  GAC  ACGT
                                  _ G   TA   CC
GAM923  MMP2     5'  GCCGGGCAAACCCCAGGCCA  15768        ATC___    AAT
                                TGGCCTGG     CCTG   GC
                                ||||||||     ||||   ||
                                ACCGGACC     GGGC   CG
                                     CCAAAC   ___
GAM923  MSF      3'  GCGCCAGGGCCCAGGCCA    88086        AT    AA
                                TGGCCTGG  CCCTG  TGC
                                ||||||||  |||||  |||
                                ACCGGACC  GGGAC  GCG
                                     C_    C_
GAM923  RNASE1   5'  TGCAGATCCAGGTCA       11350          CCTGAA
                                TGGCCTGGATC     TGCA
                                ||||||||||     ||||
                                ACTGGACCTAG     ACGT
                                               _______
GAM923  SMG1     3'  TGCACTCAGGGATACGCC    30657     CTGG       A
                                GGC    ATCCCTGA TGCA
                                |||    |||||||| ||||
                                CCG    TAGGGACT ACGT
                                  CA__       C
GAM923  SMURF1   3'  ATTCCAAAAGTCCAGGCCA   92447         CCCT_
                                TGGCCTGGAT    GAAT
                                ||||||||||    ||||
                                ACCGGACCTG    CTTA
                                      AAAAC
GAM923  STK18    5'  TCCGGAGAACCCAGGCCA    26535        A_  _  T
                                TGGCCTGG  TC CC GA
                                ||||||||  || || ||
                                ACCGGACC  AG GG CT
                                     CA  A  C
GAM923  TFE3     3'  TCAGTAGGACCAGGCCA     21512        A   __
                                TGGCCTGG TCC  CTGA
                                |||||||| |||  ||||
                                ACCGGACC AGG  GACT
                                     _   AT
GAM923  CCNE2    5'  GCCCAGATAATCCAGGCCA   16291         CC_   AAT
                                TGGCCTGGAT   CTG   GC
                                ||||||||||   |||   ||
                                ACCGGACCTA   GAC   CG
                                      ATA   C__
GAM923  DKFZP586M1120 3'  GCTCCAGAGGGAACCAGGCCA  48461         A     GAAT_
                                TGGCCTGG TCCCT    GC
                                |||||||| |||||    ||
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                                ACCGGACC AGGGA    CG
                                    A    GACCT
GAM923  FLJ10300  5'  GCCGAGGTGCAGGGATCCCGAC 36002    CCT      AAT____
          CA                  TGG  GGATCCCTG     GC
                              |||  |||||||||     ||
                              ACC  CCTAGGGAC     CG
                                AGC       GTGGAGC
GAM923  FLJ10315  5'  GCTGCCAGTCCAGGCCA    36020       TCC  AAT
                              TGGCCTGGA  CTG  GC
                              |||||||||  |||  ||
                              ACCGGACCT  GAC  CG
                                   ___  CGT
GAM923  FLJ10743  3'  TCGGCCCGAGACCCAGGCCA  36553       A  C____
                              TGGCCTGG TC    CTGA
                              |||||||| ||    ||||
                              ACCGGACC AG    GGCT
                                   C  AGCCC
GAM923  FLJ23420  3'  GCCAAGTGGGTCCAGGCCA   46847         _  GAAT
                              TGGCCTGGATCC CT   GC
                              |||||||||||| ||   ||
                              ACCGGACCTGGG GA   CG
                                     T  AC__
GAM923  FYCO1     3'  TGGGTCAGGGACTCCAGGCCA  44500       _     A G
                              TGGCCTGGA TCCCTGA T CA
                              ||||||||| ||||||| | ||
                              ACCGGACCT AGGGACT G GT
                                   C      _ G
GAM923  GK001     3'  TTCAGGGACCCAGAACA    39502    GC   A
                              TG  CTGG TCCCTGAA
                              ||  |||| ||||||||
                              AC  GACC AGGGACTT
                               AA   C
GAM923  HS6ST     3'  TGCCCCAGCTCCAGGCCA    62032       TCC  AAT
                              TGGCCTGGA  CTG  GCA
                              |||||||||  |||  |||
                              ACCGGACCT  GAC  CGT
                                   C__  CC_
GAM923  HS6ST1    3'  TGCCCCAGCTCCAGGCCA    16662       TCC  AAT
                              TGGCCTGGA  CTG  GCA
                              |||||||||  |||  |||
                              ACCGGACCT  GAC  CGT
                                   C__  CC_
GAM923  KIAA0534  3'  TGGGGACACCAGGCCA     71436       A_
                              TGGCCTGG  TCCCTG
                              ||||||||  ||||||
                              ACCGGACC  AGGGGT
                                   AC
GAM923  KIAA1045  3'  TGCCTGGCAAGGCCCCAGGCCA 71062       AT  C  AAT_
                              TGGCCTGG  CC TG   GCA
                              ||||||||  || ||   |||
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                                ACCGGACC  GG AC   CGT
                                    CC  A  GGTC
GAM923  KIAA1100  5'  GCTCTTAAAGGATCCAGACA  29755   GC     C_  AT
                                TG  CTGGATCC  TGA  GC
                                ||  ||||||||  |||  ||
                                AC  GACCTAGG  ATT  CG
                                 A_      AA   CT
GAM923  KIAA1789  5'  AGTCACATTCAAAGACACCTTG 67097      __ A_ CC    CA
          GGCCA                   TGGCCT  GG  TC  TGAATG  ACT
                                ||||||  ||  ||  ||||||  |||
                                ACCGGG  CC  AG  ACTTAC  TGA
                                   TT  AC  AA    AC
GAM923  MGC10715  5'  AGTTACATTCAGGGATGT   44246   G       C
                                G ATCCCTGAATG AACT
                                | ||||||||||| ||||
                                T TAGGGACTTAC TTGA
                                 G        A
GAM923  MGC3036   5'  TGCCAGGGCCCAGGCCA    43749       AT   AAT
                                TGGCCTGG  CCCTG  GCA
                                ||||||||  |||||  |||
                                ACCGGACC  GGGAC  CGT
                                    C_   ___
GAM923  OBSCN     3'  GCCGGAGGCAGAACCAGGCCA  70655       A __  GAAT
                                TGGCCTGG TC  CCT   GC
                                ||||||||  ||  |||   ||
                                ACCGGACC AG  GGA   CG
                                    A  AC   GGC_
GAM923  PPP1R16B  3'  AGGGGCTCCTGGAATCCAGGCC 61378        C  TGAAT  AA
          A                   TGGCCTGGAT CC    GC  CT
                                ||||||||||  ||    ||  ||
                                ACCGGACCTA GG    CG  GA
                                     A  TCCT_  GG
GAM923  PTPNS1    3'  GCCACAGTGACCCAGCCA    55000     C   A  C   AAT
                                TGGC TGG TC CTG   GC
                                ||||  |||  ||  |||   ||
                                ACCG ACC AG GAC   CG
                                  _   C  T   AC_
GAM923  SCAMP-4   3'  TCGGGGACCCAGGCCA     54402       A
                                TGGCCTGG TCCCTGA
                                ||||||||  |||||||
                                ACCGGACC AGGGGCT
                                    C
GAM923  SYT12     3'  GCTATGGAGACCCAGGCCA   94733       A  _  TGAAT
                                TGGCCTGG TC CC    GC
                                ||||||||  ||  ||    ||
                                ACCGGACC AG GG    CG
                                    C  A  TAT__
GAM923  TCL6      5'  TTGCATTCAGAAGTGCACCA  40120    CC  G  CC
                                TGG  TG AT  CTGAATGCAA
                                |||  ||  ||  ||||||||||
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                                ACC  AC TG  GACTTACGTT
                                  __  G  AA
GAM923  TCL6     5'  TTGCATTCAGAAGTGCACCA  40091    CC  G  CC
                                TGG  TG AT  CTGAATGCAA
                                |||  || ||  ||||||||||
                                ACC  AC TG  GACTTACGTT
                                  __  G  AA
GAM923  TCL6     5'  TTGCATTCAGAAGTGCACCA  24994    CC  G  CC
                                TGG  TG AT  CTGAATGCAA
                                |||  || ||  ||||||||||
                                ACC  AC TG  GACTTACGTT
                                  __  G  AA
GAM923  TCL6     5'  TTGCATTCAGAAGTGCACCA  27010    CC  G  CC
                                TGG  TG AT  CTGAATGCAA
                                |||  || ||  ||||||||||
                                ACC  AC TG  GACTTACGTT
                                  __  G  AA
GAM923  ZNF238   3'  TTGCACAAAACCCATGCCA  20973     C  ATCCC  AA
                                TGGC TGG    TG  TGCAA
                                |||| |||    ||  |||||
                                ACCG ACC    AC  ACGTT
                                  T  CAAA_  __
GAM923  LOC115051 3'  TGCCCCAGCTCCAGGCCA   60043       TCC  AAT
                                TGGCCTGGA  CTG  GCA
                                |||||||||  |||  |||
                                ACCGGACCT  GAC  CGT
                                     C__  CC_
GAM923  LOC129138 3'  GCCACAGAGTCCAGGCCA   57122       CC  AAT
                                TGGCCTGGAT  CTG  GC
                                ||||||||||  |||  ||
                                ACCGGACCTG  GAC  CG
                                     A_  AC_
GAM923  LOC137964 5'  TTGCCAAGAACCCAGGTCA  75289       ATCC  GAAT
                                TGGCCTGG   CT   GCAA
                                ||||||||   ||   ||||
                                ACTGGACC   GA   CGTT
                                    CAA_  AC__
GAM923  LOC138515 5'  TGCATCCAACCTCCAGGTCA  75945       TCCC  A
                                TGGCCTGGA   TG ATGCA
                                |||||||||   || |||||
                                ACTGGACCT   AC TACGT
                                     CCA_  C
GAM923  LOC146315 5'  GCTCAGAGCCCAGGCCA    60889       ATCC  AT
                                TGGCCTGG   CTGA  GC
                                ||||||||   ||||  ||
                                ACCGGACC   GACT  CG
                                    CGA_   __
GAM923  LOC147004 3'  GTTCAGAGATCCAGGCC    83906        C
                                GGCCTGGATC CTGAAT
                                |||||||||| ||||||
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                                CCGGACCTAG GACTTG
                                      A
GAM923  LOC148029 5'  GTTTAAGAAGTCCAGGCCA   78622          CC  GAAT
                                TGGCCTGGAT  CT    GC
                                ||||||||||  ||    ||
                                ACCGGACCTG  GA    TG
                                      AA  ATT_
GAM923  LOC148413 3'  GTCTGCAGGGACCAGGCCA   78831         A     AAT
                                TGGCCTGG TCCCTG   GC
                                ||||||||  ||||||   ||
                                ACCGGACC AGGGAC   TG
                                     _     GTC
GAM923  LOC149194 3'  GTTACAAGGTCCCAGGCCA   79230         AT  C  AAT
                                TGGCCTGG  CC TG   GC
                                ||||||||  || ||   ||
                                ACCGGACC  GG AC   TG
                                     CT  A  AT_
GAM923  LOC151124 5'  TCACTGGCCAGAACCAGGCCA  85233         A ____ __
                                TGGCCTGG TC   CC  TGA
                                ||||||||  ||   ||  |||
                                ACCGGACC AG   GG  ACT
                                     A  ACC  TC
GAM923  LOC164537 5'  AGTCACACTCAGGAAGGGGGGC 87218       GGATC    A  CA
          C                    GGCCT    CCTGA TG  ACT
                               |||||    ||||| ||  |||
                               CCGGG    GGACT AC  TGA
                                  GGGAA    C  AC
GAM923  LOC196074 5'  GTCGTTTGGAAACCCCAGGCCA 87583         ATCC_ TG   _
                                TGGCCTGG    C  AATG C
                                ||||||||    |  |||| |
                                ACCGGACC    G  TTGC G
                                     CCAAA GT   T
GAM923  LOC197320 5'  GCTGGAAATAGGGATCCAGCCA 87965      C        AAT___
                                TGGC TGGATCCCTG     GC
                                |||| ||||||||||     ||
                                ACCG ACCTAGGGAT     CG
                                  _        AAAGGT
GAM923  LOC221143 3'  ATTCAGAGACCCAGGCCA    93564         A  C
                                TGGCCTGG TC CTGAAT
                                ||||||||  || ||||||
                                ACCGGACC AG GACTTA
                                     C  A
GAM923  LOC221584 3'  TATCCAGAATTCCAGGCCA   93832         TCC   A
                                TGGCCTGGA   CTG ATG
                                |||||||||   ||| |||
                                ACCGGACCT   GAC TAT
                                      TAA   C
GAM923  LOC256211 5'  GCCTAAGGATCCAGCCCA    96706     C       C  AAT
                                TGG CTGGATCC TG   GC
                                ||| ||||||||  ||   ||
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                                ACC GACCTAGG AT   CG
                                  C       A  C__
GAM924  AICDA    5'  GCCTGAGACTTGCAGGGAGGCA 40329     C       ATTTGC__
            AGAA                   TTC TGCCTCCCT       CAGGC
                                |||  |||||||||       |||||
                                AAG ACGGAGGGA       GTCCG
                                  A        CGTTCAGA
GAM924  ANK1     3'  GCCTCCGGCCCAGGGAGGCCAG 40027     CT      ATTT  __
            AA                     TTC  GCCTCCCT    GCC  AGGC
                                |||  ||||||||   |||  ||||
                                AAG  CGGAGGGA    CGG  TCCG
                                  AC       CC__   CC
GAM924  ANK1     3'  GCCTCCGGCCCAGGGAGGCCAG 3473      CT      ATTT  __
            AA                     TTC  GCCTCCCT    GCC  AGGC
                                |||  ||||||||   |||  ||||
                                AAG  CGGAGGGA    CGG  TCCG
                                  AC       CC__   CC
GAM924  EIF2C1   3'  CCCAAATCCAGAGGAAGCAAGG 24170      _  C  _  __    CCA
            A                      TCCT GC TCC CT  ATTTG   GG
                                ||||  ||  |||  ||  |||||   ||
                                AGGA CG AGG GA  TAAAC   CC
                                  A  A   A  CC    ___
GAM924  IKBKG    3'  CCCGGCACTGGGGAAGTCAAGA 94663     C  _ C     TT    A
            A                      TTC TG C TCCCTA  TGCC GG
                                |||  ||  |  ||||||  ||||  ||
                                AAG AC G AGGGGT  ACGG CC
                                  A  T A     C_    C
GAM924  IKBKG    3'  CCCGGCACTGGGGAAGTCAAGA 13311     C  _ C     TT    A
            A                      TTC TG C TCCCTA  TGCC GG
                                |||  ||  |  ||||||  ||||  ||
                                AAG AC G AGGGGT  ACGG CC
                                  A  T A     C_    C
GAM924  LY9      3'  AAATAAAAGGCAGGAA      71680          CCC
                                TTCCTGCCT   TATTT
                                |||||||||   |||||
                                AAGGACGGA   ATAAA
                                      AA_
GAM924  MAFF     3'  TGGCAAATAGGGAGACAAGGA  24655      GC_
                                TCCT   CTCCCTATTTGCCA
                                ||||   ||||||||||||||
                                AGGA   GAGGGATAAACGGT
                                  ACA
GAM924  MC1R     5'  GCCCAGATGGAAGGAGGCAGG  9954          __      CCA
                                CCTGCCTCC  CTATTTG   GGC
                                |||||||||  |||||||   |||
                                GGACGGAGG  GGTAGAC   CCG
                                      AA      ___
GAM924  MYO15A   3'  GCCTGAGGGAGGAGGCAGGAG  32671           _  ATTTGC
                                TTCCTGCCTCC CT     CAGGC
                                ||||||||||| ||     |||||
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                                GAGGACGGAGG GG     GTCCG
                                      A  GA____
GAM924  NRG1     3'  GCAAATAGAAAACAGGAA    25646       CCTCC
                                TTCCTG    CTATTTGC
                                ||||||    ||||||||
                                AAGGAC    GATAAACG
                                   AAAA_
GAM924  NRG1     3'  GCAAATAGAAAACAGGAA    25659       CCTCC
                                TTCCTG    CTATTTGC
                                ||||||    ||||||||
                                AAGGAC    GATAAACG
                                   AAAA_
GAM924  SEPN1    3'  GCCTGGCAGAGGAAGAAGGAA  66369      GC  C   AT
                                TTCCT  CT CCT  TTGCCAGGC
                                |||||  || |||  |||||||||
                                AAGGA  GA GGA  GACGGTCCG
                                   A_  A   __
GAM924  SMURF1   3'  GCCTAACCCGCGGGAGGCGGAA 92453      T      TATTTGCC
                                TTCC GCCTCCC       AGGC
                                |||| |||||||       ||||
                                AAGG CGGAGGG       TCCG
                                  _      CGCCCAA_
GAM924  STAT6    3'  GCCTAGGACGGATAGGCAGGAA 12021         CCCT    _ _
                                TTCCTGCCT    ATTTG CC AGGC
                                |||||||||    ||||| || ||||
                                AAGGACGGA    TAGGC GG TCCG
                                     _____    A  A
GAM924  TFF3     3'  GCCCAGGCCTCAAGGGCAGGAA 63566         CCCTATTT   A_
                                TTCCTGCCT       GCC  GGC
                                |||||||||       |||  |||
                                AAGGACGGG       CGG  CCG
                                     AACTC___   AC
GAM924  TOP3B    5'  GCCCGGCGGCTCAGAAAGGCGG 14129         CC  AT_    A
           GAA                    TTCCTGCCT  CT   TTGCC GGC
                                |||||||||  ||   ||||| |||
                                AAGGGCGGA  GA   GGCGG CCG
                                     AA  CTC    C
GAM924  VAV1     3'  GCCTTGGCAGAGAGACGAG    18305     C_  A      _
                                CTC  CT TTTGCCA GGC
                                |||  || ||||||| |||
                                GAG  GA AGACGGT CCG
                                  CA  G      T
GAM924  YWHAB    5'  GCTGTGGATAGAGAAGCAGGAA 12692        C  C     TG CA
                                TTCCTGC TC CTATT  C  GGC
                                ||||||| || |||||  |  |||
                                AAGGACG AG GATAG  G  TCG
                                   A  A    GT __
GAM924  AF020591 3'  GCCTGGCAAACATGGCA     27141      TCCCTA
                                TGCC     TTTGCCAGGC
                                ||||     ||||||||||
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                                ACGG     AAACGGTCCG
                                  TAC___
GAM924  BCL2L1   3'  CCTCAGGCAGGAAGGGCAGGAA 56804        CC  ATT   __
                                TTCCTGCCT  CT   TGCC  AGG
                                |||||||||  ||   ||||  |||
                                AAGGACGGG  GG   ACGG  TCC
                                     AA  ___    AC
GAM924  BNIP-S   5'  TAAAGAAGGAGGCAGGAA    56263         CTA
                                TTCCTGCCTCC   TTTG
                                ||||||||||   ||||
                                AAGGACGGAGG   AAAT
                                      AAG
GAM924  BTBD3    5'  GCAAATAAGAGAAACAGGAA   30311      C__   CC
                                TTCCTG   CTC  TATTTGC
                                ||||||   |||  |||||||
                                AAGGAC   GAG  ATAAACG
                                   AAA   A_
GAM924  C20orf28  3'  GCCTGAGACGGGAGGCAGGAA  31224          TAT  GC
                                TTCCTGCCTCCC   TT  CAGGC
                                ||||||||||||   ||  |||||
                                AAGGACGGAGGG   AG  GTCCG
                                      C__  A_
GAM924  CHODL    5'  CCCGGCAGGGAGGCAGGGA    46310          ATTT   A
                                TTCCTGCCTCCCT    GCC GG
                                ||||||||||||    ||| ||
                                AGGGACGGAGGGA    CGG CC
                                      _____  C
GAM924  D2S448   3'  CCTGAAGGGAAGCAGG      73519      C    ATTTGC
                                CCTGC TCCCT     CAGG
                                |||||  |||||     ||||
                                GGACG AGGGA     GTCC
                                  A    A_____
GAM924  DKFZP434K1772 3'  GCCTTACTCAGGAAGGCAGGAG 67714          C   ATTTGCC
                                TTCCTGCCT CCT      AGGC
                                |||||||||  |||      ||||
                                GAGGACGGA GGA      TCCG
                                     A   CTCAT__
GAM924  DKFZp547I094 3'  CCTGGCAACCTGAGGGAGG    49637       AT__
                                CCTCCCT    TTGCCAGG
                                |||||||    ||||||||
                                GGAGGGA    AACGGTCC
                                    GTCC
GAM924  DKFZP547L112 3'  CCTGGATATAGCAAGGCAGGAA 66529         CC    TTG
                                TTCCTGCCT  CTAT   CCAGG
                                |||||||||  ||||   |||||
                                AAGGACGGA  GATA   GGTCC
                                     AC    TA_
GAM924  FABP7    5'  CAAATAAGAAGGCAGGAG    7542          CCC
                                TTCCTGCCT   TATTTG
                                |||||||||   ||||||
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                                GAGGACGGA  ATAAAC
                                     AGA
GAM924  FLJ14957  3'  CCCAAAGTGGGAGGCAGGGA  51744          TA   CCA
                                TTCCTGCCTCCC  TTTG  GG
                                ||||||||||||  ||||  ||
                                AGGGACGGAGGG  AAAC  CC
                                      TG   ___
GAM924  FLJ20343  3'  CCTGGCAAACTGACCAG    34998    CC  CCTA
                                CTG  TC   TTTGCCAGG
                                |||  ||   |||||||||
                                GAC  AG   AAACGGTCC
                                  C_  TC__
GAM924  FLJ23185  3'  CCTGGCAGGATGAGGCAGAGA  46830   _     CCTA
                                TC CTGCCTC   TTTGCCAGG
                                || |||||||   |||||||||
                                AG GACGGAG   GGACGGTCC
                                 A     TA__
GAM924  GGA2    3'  GCCTGATGGGTGGGAGAAGGAA 30468     GC   T   GC
                                TTCCT  CTCCC ATTT  CAGGC
                                |||||  ||||| ||||  |||||
                                AAGGA  GAGGG TGGG  GTCCG
                                   A_    _   TA
GAM924  GGA2    3'  GCCTGATGGGTGGGAGAAGGAA 56882     GC   T   GC
                                TTCCT  CTCCC ATTT  CAGGC
                                |||||  ||||| ||||  |||||
                                AAGGA  GAGGG TGGG  GTCCG
                                   A_    _   TA
GAM924  HDAC11   3'  GCCCATAGGTCCAGGGAGGCAG 45718         ATTT  A___
          G                     CCTGCCTCCCT   GCC   GGC
                                ||||||||||   |||   |||
                                GGACGGAGGGA   TGG   CCG
                                      CC__  ATAC
GAM924  IKKE    5'  CACAAGGAGGCAGGGA     25746         CTAT  CCA
                                TTCCTGCCTCC   TTG  G
                                ||||||||||   |||  |
                                AGGGACGGAGG   AAC  C
                                     ____  A__
GAM924  IL1F10   3'  CAAGAAGGAGGCAGGAA    50771         CTA
                                TTCCTGCCTCC  TTTG
                                ||||||||||  ||||
                                AAGGACGGAGG  GAAC
                                     AA_
GAM924  KIAA0370  5'  GCCCAGCAAATAGGAGCCTGGA 73209     T_ CTC       CA
          G                     TTCC  GC  CCTATTTGC  GGC
                                ||||  ||  |||||||||  |||
                                GAGG  CG  GGATAAACG  CCG
                                  TC  A__       AC
GAM924  KIAA0551  3'  GCCTGGTTGAGAAGGAGAG   66839    _  A_  T
                                CTC CCT  TT GCCAGGC
                                ||| |||  || |||||||
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                                GAG GGA  AG TGGTCCG
                                  A   AG  T
GAM924  KIAA1183  3'  CCCGGATGGGAGGAGGAA    62530      G     TATTTG  A
                                TTCCT CCTCCC     CC GG
                                ||||| ||||||     || ||
                                AAGGA GGAGGG     GG CC
                                   _     TA_____  C
GAM924  KIAA1464  3'  CCTGACCCATGGAGGCAGGAG  68264          CTATTTGC
                                TTCCTGCCTCC       CAGG
                                ||||||||||        ||||
                                GAGGACGGAGG       GTCC
                                      TACCCA__
GAM924  MAPK8IP3  3'  GCCTGGTAGATGAAGCAG    52987      C  CCT
                                CTGC TC   ATTTGCCAGGC
                                |||| ||   ||||||||||
                                GACG AG   TAGATGGTCCG
                                  A  ___
GAM924  MGC2306   3'  GCCTGGCAGGGGGTGAAGGCAG 50963          ___    AT
            GAG                   TTCCTGCCT   CCCT  TTGCCAGGC
                                |||||||||   ||||  |||||||||
                                GAGGACGGA   GGGG  GACGGTCCG
                                     AGT    __
GAM924  MGC2865   5'  GCCTGGCAAACCGAAGCAAGAA 50451     C   C  CCTA
                                TTC TGC TC    TTTGCCAGGC
                                ||| ||| ||    ||||||||||
                                AAG ACG AG    AAACGGTCCG
                                  A   A  CC__
GAM924  MGC9753   3'  GCCTGATTTTGGGGAGGAGGAA 53049       G       TTTGC
                                TTCCT CCTCCCTA     CAGGC
                                ||||| ||||||||     |||||
                                AAGGA GGAGGGGT     GTCCG
                                   _       TTTA_
GAM924  PALM      3'  GCCTGGTAGGAGAGAGACAGGA 10414       C   C  A
                                TCCTG CTC CT TTTGCCAGGC
                                ||||| ||| || ||||||||||
                                AGGAC GAG GA GGATGGTCCG
                                   A   A  _
GAM924  PDZD2     5'  CCTGGCACGGAAGGAGGAA    80866      G   C  TATT
                                TTCCT CCT CC    TGCCAGG
                                ||||| ||| ||    |||||||
                                AAGGA GGA GG    ACGGTCC
                                   _   A  C___
GAM924  PLPL      3'  CCTGGAGGGGGAGGCAGGAG   39431           ATTTG
                                TTCCTGCCTCCCT     CCAGG
                                ||||||||||||     |||||
                                GAGGACGGAGGGG     GGTCC
                                      GA___
GAM924  RABEX5    3'  GCCTGGAATGGAAGGCGGGAA  27186         C  TATTTG
                                TTCCTGCCT CC      CCAGGC
                                |||||||| ||      ||||||
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                                AAGGGCGGA GG     GGTCCG
                                     A  TAA___
GAM924  SHANK3   5'  GCCTGCTCGCAGGGAGGCAGAG 65500   _       ATTT  C
          A                   TC CTGCCTCCCT   GC AGGC
                              || ||||||||||   || ||||
                              AG GACGGAGGGA   CG TCCG
                               A        CGCT  _
GAM924  SRF      5'  CCGGGCCACAGGGGCAGGAA  11944        CCTATTT  A
                              TTCCTGCCTC      GCC GG
                              ||||||||||      ||| ||
                              AAGGACGGGG      CGG CC
                                   ACAC___  G
GAM924  TREX1    5'  CCCAGCAGAGGGAGGCAG   53280        AT   CA
                              CTGCCTCCCT  TTGC  GG
                              ||||||||||  ||||  ||
                              GACGGAGGGA  GACG  CC
                                   __   AC
GAM924  TREX1    5'  CCCAGCAGAGGGAGGCAG   53290        AT   CA
                              CTGCCTCCCT  TTGC  GG
                              ||||||||||  ||||  ||
                              GACGGAGGGA  GACG  CC
                                   __   AC
GAM924  URG4     3'  GCCCCCAGGGTAGGGAGACA  35506   C       GCCA
                              TG CTCCCTATTT   GGC
                              || ||||||||||   |||
                              AC GAGGGATGGG   CCG
                               A        ACCC
GAM924  LOC124222 3'  CCTGACAAACAGGCAGGGA   74271        CCCTA   C
                              TTCCTGCCT    TTTG CAGG
                              |||||||||    |||| ||||
                              AGGGACGGA    AAAC GTCC
                                   C____   A
GAM924  LOC131873 5'  CCCGGAGGAGAGGCAGGGA   75877        _  ATTTG  A
                              TTCCTGCCTC CCT    CC GG
                              |||||||||| |||    || ||
                              AGGGACGGAG GGA    GG CC
                                   A  _____  C
GAM924  LOC144348 5'  CCTTCCGTAGAAAGACAGGCA  76806     CC  A   C__
                              TGCCT  CT TTTGC   AGG
                              |||||  || |||||   |||
                              ACGGA  GA AGATG   TCC
                                 CA  A    CCT
GAM924  LOC146316 5'  CTTCGAGAGGCAGGAA     60872        CCTAT   CC
                              TTCCTGCCTC    TTG  AG
                              ||||||||||    |||  ||
                              AAGGACGGAG    AGC  TC
                                   _____  T_
GAM924  LOC148529 5'  CCTGGCAGACAGGAAGACA   84167   C  C   A
                              TG CT CCT TTTGCCAGG
                              || || ||| |||||||||
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                                AC GA GGA AGACGGTCC
                                 A  A   C
GAM924   LOC149606 3'  GCCCGCGGAGCAGGGAG     79454        A_    CA
                                CTCCCT  TTTGC  GGC
                                ||||||  |||||  |||
                                GAGGGA  AGGCG  CCG
                                    CG    C_
GAM924   LOC151057 3'  CCAGGAAAGAAGGCAGGAA    85209         CCCTA   G  A
                                TTCCTGCCT    TTT CC GG
                                |||||||||    ||| || ||
                                AAGGACGGA    AAA GG CC
                                     AG___   _  A
GAM924   LOC153346 5'  CCCAGATGGAAGGCA       86022       CC      CCA
                                TGCCT  CTATTTG   GG
                                |||||  |||||||   ||
                                ACGGA  GGTAGAC   CC
                                   A_      ___
GAM924   LOC196418 5'  CCTTCCGTAGAAAGACAGGCA  87696       CC  A    C__
                                TGCCT  CT TTTGC   AGG
                                |||||  || |||||   |||
                                ACGGA  GA AGATG   TCC
                                   CA  A    CCT
GAM924   LOC199786 3'  GCCTGGCAGCTGAGGCAGAGA  88386    _      CCTAT
                                TC CTGCCTC    TTGCCAGGC
                                || |||||||    |||||||||
                                AG GACGGAG    GACGGTCCG
                                 A      TC___
GAM924   LOC200058 3'  CCTGAAGGATGGGAAGCCAGGA 88556       C  C      GC
            A                    TTCCTG CT CCTATTT  CAGG
                                ||||||| || |||||||  ||||
                                AAGGAC GA GGGTAGG  GTCC
                                   C  A      AA
GAM924   LOC204579 5'  CCCGGCTATGAGGCAGGAA   89465         CCTATTT   A
                                TTCCTGCCTC      GCC GG
                                ||||||||||      ||| ||
                                AAGGACGGAG      CGG CC
                                     TAT_____   C
GAM924   LOC219700 5'  GCCTGGCAGTCCAAAGACCAAG 93064     C  CCTCCCTAT
            AA                    TTC TG        TTGCCAGGC
                                ||| ||        |||||||||
                                AAG AC        GACGGTCCG
                                  A  CAGAAACCT
GAM924   LOC253181 5'  GCCTGGCAAACAGCACAGGA   97558       CCTCC  A
                                TCCTG    CT TTTGCCAGGC
                                |||||    || ||||||||||
                                AGGAC    GA AAACGGTCCG
                                   AC____  C
GAM924   LOC253296 3'  GCCTGGGGCCACAGGAAAGGCA 94490         C_   ATTTG_
            GGAA                    TTCCTGCCT  CCT     CCAGGC
                                |||||||||  |||     ||||||
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                                AAGGACGGA  GGA     GGTCCG
                                     AA   CACCGG
GAM924   LOC253298 5'  GCCTGGGGCCACAGGAAAGGCA 97215         C_   ATTTG_
            GGAA                  TTCCTGCCT  CCT     CCAGGC
                                |||||||||  |||     ||||||
                                AAGGACGGA  GGA     GGTCCG
                                     AA   CACCGG
GAM924   LOC254107 5'  CCCAGAGGGCAGGAA      94384         CCCTA    CCA
                                TTCCTGCCT    TTTG   G
                                |||||||||    ||||   |
                                AAGGACGGG    AGAC   C
                                     _____   C__
GAM924   LOC255189 5'  CTGACCAAGGCAGGAA      96589         CCCTATT  C_
                                TTCCTGCCT      TG  CAG
                                |||||||||      ||  |||
                                AAGGACGGA      AC  GTC
                                     ________  CA
GAM924   LOC257160 3'  CCTGACTGGGGAGGAAG     94846    G       TTTGC
                                CT CCTCCCTA     CAGG
                                || ||||||||     ||||
                                GA GGAGGGGT     GTCC
                                  A       CA___
GAM924   LOC257570 3'  GCCTGGGGCCACAGGAAAGGCA 97833         C_   ATTTG_
            GGAA                  TTCCTGCCT  CCT     CCAGGC
                                |||||||||  |||     ||||||
                                AAGGACGGA  GGA     GGTCCG
                                     AA   CACCGG
GAM924   LOC257571 5'  GCCTGGGGCCACAGGAAAGGCA 97945         C_   ATTTG_
            GGAA                  TTCCTGCCT  CCT     CCAGGC
                                |||||||||  |||     ||||||
                                AAGGACGGA  GGA     GGTCCG
                                     AA   CACCGG
GAM925   CASP3    3'  ACATACTCCTTCCATCA     15095    C     A
                                TG ATGGAA GAGTATGT
                                || |||||| ||||||||
                                AC TACCTT CTCATACA
                                  _     C
GAM925   CASP3    3'  ACATACTCCTTCCATCA     52191    C     A
                                TG ATGGAA GAGTATGT
                                || |||||| ||||||||
                                AC TACCTT CTCATACA
                                  _     C
GAM925   MSL3L1   3'  AAGAATACTCAGATTTCCAT   54359        GAGTAT
                                ATGGAAA     GTATTCTT
                                |||||||     ||||||||
                                TACCTTT     CATAAGAA
                                     AGACT_
GAM925   SACM1L   3'  GCATACTTTTCCACACA     25824    CA    A
                                TG  TGGAA GAGTATGT
                                ||  ||||| ||||||||
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                                AC  ACCTT TTCATACG
                                 AC    _
GAM925  SURF6    3'  TAAGAATACATACTCTTTCCAT 22192                  III
            GCA                   GCATGGAAAGAGTATGTATTCTT   A
                                  ||||||||||||||||||||||  |
                                  CGTACCTTTCTCATACATAAGAA   T
                                                    III
GAM925  UCHL1    3'  AATATATACCCCCCCATGCA   14814       AAAGA
                                  TGCATGG    GTATGTATT
                                  |||||||    |||||||||
                                  ACGTACC    CATATATAA
                                      CCCC_
GAM925  DYRK4    5'  AAGAATACGGTAAGCTTCCCA  64225     A   AG   _
                                  TGG AAG  TAT GTATTCTT
                                  ||| |||  ||| ||||||||
                                  ACC TTC  ATG CATAAGAA
                                    C   GA   G
GAM925  FLJ10276 3'  ACATACTCTGTCCATACA    35961    C    A
                                  TG ATGGA AGAGTATGT
                                  || ||||| |||||||||
                                  AC TACCT TCTCATACA
                                   A    G
GAM925  KIAA0678 3'  AAGAATATTTCCCTCTCCTGCA 66851     T   AA   TAT_
                                  TGCA GGA  GAG    GTATTCTT
                                  |||| |||  |||    ||||||||
                                  ACGT CCT  CTC    TATAAGAA
                                    _  __   CCTT
GAM925  SGKL     3'  AAGAACAAGCATCCCTTCCATG 25138         A_  _  A   AT
            TA                    TGCATGGAA  GA GT TGT  TCTT
                                  |||||||||  || || |||  ||||
                                  ATGTACCTT  CT CG ACA  AGAA
                                       CC  A  A   __
GAM925  LOC148638 3'  CACTCTCTTTCCACGCA     78919     A       TA
                                  TGC TGGAAAGAG  TG
                                  ||| |||||||||  ||
                                  ACG ACCTTTCTC  AC
                                    C        TC
GAM925  LOC196385 3'  ATCTCTTTCCATACA       87654    C        T
                                  TG ATGGAAAGAG AT
                                  || ||||||||||  ||
                                  AC TACCTTTCTC TA
                                   A        _
GAM925  LOC221178 3'  ATACTCCTTCATGCA       93526         AA
                                  TGCATGGA  GAGTAT
                                  ||||||||  ||||||
                                  ACGTACTT  CTCATA
                                       C_
GAM925  LOC221405 3'  AGAATTGCTTTCCATGCA    93880           AGTATGT
                                  TGCATGGAAAG      ATTCT
                                  ||||||||||       |||||
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                                ACGTACCTTTC      TAAGA
                                      GT_____
GAM926  PCDH9    5'  ATTTTCAACCAGCCTGT     82792          CTT
                                ACAGGCTGGTT   GAT
                                ||||||||||   |||
                                TGTCCGACCAA   TTA
                                      CTT
GAM926  CHERP    3'  CAGGAAACCAGCCTAAGA    21097    AC       _
                                TC  AGGCTGGTT CTTG
                                ||  ||||||||| ||||
                                AG  TCCGACCAA GGAC
                                 AA        A
GAM926  DKFZp762K2015 3'  CATCAATGGGCCTGTGA     72475         G   CT
                                TCACAGGCT GTT  TG
                                ||||||||| |||  ||
                                AGTGTCCGG TAA  AC
                                      G   CT
GAM926  FLJ13194  3'  GATATCAAAATAGACTTTGAT  47128      C  G   GTTC
                                ATCA AG CTG    TTGATATC
                                |||| || |||    ||||||||
                                TAGT TC GAT    AACTATAG
                                  T  A   AA__
GAM926  INA      3'  ATATCCCAAACTGTGATG    51186        GC   TTCTT
                                CATCACAG  TGG    GATAT
                                ||||||||  |||    |||||
                                GTAGTGTC  ACC    CTATA
                                     AA  _____
GAM926  KIAA0443  5'  AAGAAACAAACCTGTGA     28183        C_  G
                                TCACAGG  TG TTCTT
                                |||||||  || |||||
                                AGTGTCC  AC AAGAA
                                     AA  A
GAM926  OR7C1    5'  GAGAACCAGCCCCTGA      82430     CA
                                TCA  GGCTGGTTCTT
                                |||  ||||||||||
                                AGT  CCGACCAAGAG
                                  CC
GAM926  PAK6     5'  CAAGCACCAGCCTGCAGTG    39405     CA        T
                                CAT  CAGGCTGGT CTTG
                                |||  ||||||||| ||||
                                GTG  GTCCGACCA GAAC
                                  AC        C
GAM926  PGRMC2   3'  ATCAAGGGACTCCTGTG     20891       CT    _
                                CACAGG  GGTTC TTGAT
                                ||||||  ||||| |||||
                                GTGTCC  TCAGG AACTA
                                    __    G
GAM926  PRPF8    3'  ATCAAGAACCGCTTG       61183       T
                                CAGGC GGTTCTTGAT
                                ||||| ||||||||||
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                                GTTCG CCAAGAACTA
                                   _
GAM926  SCMH1     5' ATATCAAGAAGCTGCTGA    24252     CA    GGT
                                TCA  GGCT   TCTTGATAT
                                |||  ||||   |||||||||
                                AGT  TCGA   AGAACTATA
                                  CG   ___
GAM926  LOC114928 5' AAGAAACAAACCTGTGA     56590       C_  G
                                TCACAGG  TG TTCTT
                                |||||||  || |||||
                                AGTGTCC  AC AAGAA
                                    AA  A
GAM926  LOC144603 3' AAGAAGCCAGCCCATGA     60365     CA      _
                                TCA  GGCTGGTT CTT
                                |||  |||||||| |||
                                AGT  CCGACCGA GAA
                                  AC       A
GAM926  LOC145790 3' ATATCAAGAACACCT       77484     CTG
                                AGG   GTTCTTGATAT
                                |||   ||||||||||||
                                TCC   CAAGAACTATA
                                  A__
GAM926  LOC150372 5' ATGGAGAACCAGCCTGTGA   79787             G
                                TCACAGGCTGGTTCTT AT
                                |||||||||||||||| ||
                                AGTGTCCGACCAAGAG TA
                                        G
GAM926  LOC170425 5' ATATCTTACCAGCCTATG    76378    C       TCTT
                                CA AGGCTGGT    GATAT
                                || ||||||||    |||||
                                GT TCCGACCA    CTATA
                                 A       TT__
GAM926  LOC221042 3' ATCAGGAAGCCTGT        93180        GGT
                                ACAGGCT   TCTTGAT
                                |||||||   |||||||
                                TGTCCGA   AGGACTA
                                   ___
GAM926  LOC222031 3' CATTGCCAGGCTGTGATG    94018         G    TCT
                                CATCACAG CTGGT   TG
                                |||||||| |||||   ||
                                GTAGTGTC GACCG   AC
                                     G    TT_
GAM926  LOC222193 3' ATACCAAGAACTATGAT     94179     CAGGC       A
                                ATCA     TGGTTCTTG TAT
                                ||||     ||||||||| |||
                                TAGT     ATCAAGAAC ATA
                                  _____         C
GAM926  LOC255042 3' TCAAAACCAGCCTGGA      95325    A        C
                                TC CAGGCTGGTT TTGA
                                || ||||||||| ||||
```

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                                AG GTCCGACCAA AACT
                                  _      _
GAM926  LOC90643  3' GAGAACCAAGCTGTGAT    63690       GC
                                ATCACAG  TGGTTCTT
                                |||||||  ||||||||
                                TAGTGTC  ACCAAGAG
                                   GA
GAM926  LOC91818  3' GAGAACCAAGCTGTGAT    67270       GC
                                ATCACAG  TGGTTCTT
                                |||||||  ||||||||
                                TAGTGTC  ACCAAGAG
                                   GA
GAM926  LOC93052  5' ATTAGCAGAACCAAACTGTGAT 71258        GC     __
          G                    CATCACAG  TGGTTCT  TGAT
                               ||||||||  |||||||  ||||
                               GTAGTGTC  ACCAAGA  ATTA
                                    AA     CG
GAM927  ARHGAP6   5' CCCGGGCCAGCCCCGCCT   6761     AA   GTT  A_
                                AGGC  GGCT   GGC  GGG
                                ||||  ||||   |||  |||
                                TCCG  CCGA   CCG  CCC
                                  CC    ___   GG
GAM927  ARHGAP6   5' CCCGGGCCAGCCCCGCCT   20405    AA   GTT  A_
                                AGGC  GGCT   GGC  GGG
                                ||||  ||||   |||  |||
                                TCCG  CCGA   CCG  CCC
                                  CC    ___   GG
GAM927  COL4A3    5' CGAGCCCTACAAAACCCGCC  3619    AA  CTG   GC
                                GGC  GG   TTG  AGGGCTCG
                                |||  ||   |||  ||||||||
                                CCG  CC   AAC  TCCCGAGC
                                  C_   AA_   A_
GAM927  COL4A3    5' CGAGCCCTACAAAACCCGCC  48553    AA  CTG   GC
                                GGC  GG   TTG  AGGGCTCG
                                |||  ||   |||  ||||||||
                                CCG  CC   AAC  TCCCGAGC
                                  C_   AA_   A_
GAM927  COL4A3    5' CGAGCCCTACAAAACCCGCC  48565    AA  CTG   GC
                                GGC  GG   TTG  AGGGCTCG
                                |||  ||   |||  ||||||||
                                CCG  CC   AAC  TCCCGAGC
                                  C_   AA_   A_
GAM927  CTNNB1    3' CCCTAGCCTTGCTT      8578         GTTGGC
                                AGGCAAGGCT    AGGG
                                ||||||||||    ||||
                                TTCGTTCCGA    TCCC
                                          _______
GAM927  GAS7     3' AGACCCACAGCCCTGCC    13319     A    TGGCA  _
                                GGCA GGCTGT    GGG CT
                                ||||  ||||||    |||  ||
```

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                                CCGT CCGACA    CCC GA
                                  C     _____  A
GAM927  KCNA6    3'  CTTTGCCAACAGCCTCACT   9513     CA
                                GG  AGGCTGTTGGCAGGG
                                ||  ||||||||||||||
                                TC  TCCGACAACCGTTTC
                                 AC
GAM927  LANGERIN 3'  GAGCCCTGCCTTCCACC     31690    C  TT_
                                GG TG   GGCAGGGCTC
                                || ||   ||||||||||
                                CC AC   CCGTCCCGAG
                                 _  CTT
GAM927  MASP1    3'  CCCTGCCAAGTGCTGCTT    8537       AG  TG
                                AGGCA  GC  TTGGCAGGG
                                |||||  ||  |||||||||
                                TTCGT  CG  AACCGTCCC
                                  __  TG
GAM927  NRG1     5'  CGAGCCCTTGGACCAAACTCGC 15690     A  GC  TTGGC
          CT                      AGGC AG  TG    AGGGCTCG
                                |||| ||  ||    ||||||||
                                TCCG TC  AC    TCCCGAGC
                                  C  AA  CAGGT
GAM927  NRG1     5'  CGAGCCCTTGGACCAAACTCGC 25645     A  GC  TTGGC
          CT                      AGGC AG  TG    AGGGCTCG
                                |||| ||  ||    ||||||||
                                TCCG TC  AC    TCCCGAGC
                                  C  AA  CAGGT
GAM927  NRG1     5'  CGAGCCCTTGGACCAAACTCGC 25656     A  GC  TTGGC
          CT                      AGGC AG  TG    AGGGCTCG
                                |||| ||  ||    ||||||||
                                TCCG TC  AC    TCCCGAGC
                                  C  AA  CAGGT
GAM927  NRG1     5'  CGAGCCCTTGGACCAAACTCGC 25658     A  GC  TTGGC
          CT                      AGGC AG  TG    AGGGCTCG
                                |||| ||  ||    ||||||||
                                TCCG TC  AC    TCCCGAGC
                                  C  AA  CAGGT
GAM927  NRG1     5'  CGAGCCCTTGGACCAAACTCGC 25647     A  GC  TTGGC
          CT                      AGGC AG  TG    AGGGCTCG
                                |||| ||  ||    ||||||||
                                TCCG TC  AC    TCCCGAGC
                                  C  AA  CAGGT
GAM927  NRG1     5'  CGAGCCCTTGGACCAAACTCGC 25648     A  GC  TTGGC
          CT                      AGGC AG  TG    AGGGCTCG
                                |||| ||  ||    ||||||||
                                TCCG TC  AC    TCCCGAGC
                                  C  AA  CAGGT
GAM927  NRG1     5'  CGAGCCCTTGGACCAAACTCGC 25654     A  GC  TTGGC
          CT                      AGGC AG  TG    AGGGCTCG
                                |||| ||  ||    ||||||||
```

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                                TCCG TC  AC    TCCCGAGC
                                  C  AA  CAGGT
GAM927  PACE    5'  CGAGCCCTGCCCGTCTCGGCC  10390      TT___
                                GGCTG    GGCAGGGCTCG
                                |||||    ||||||||||
                                CCGGC    CCGTCCCGAGC
                                   TCTGC
GAM927  PGF     5'  GCCACAGCCTTACCT      10535    C      T
                                AGG AAGGCTGT GGC
                                ||| |||||||| |||
                                TCC TTCCGACA CCG
                                  A      _
GAM927  XRCC3   3'  CTGCACAACAGCCCTGCCT   18338      A      _
                                AGGCA GGCTGTTG GCAG
                                ||||| |||||||| ||||
                                TCCGT CCGACAAC CGTC
                                   C       A
GAM927  C1QTNF6  3'  CCCCAGGGGGCCTTGGCC    49141    _    G  GGCA
                                GGC AAGGCT TT    GGG
                                ||| |||||| ||    |||
                                CCG TTCCGG GG    CCC
                                  G     G  AC__
GAM927  C4orf6   5'  AGCCCTGCCAGCCTCCTACCT  19238    CA   CT
                                AGG  AGG  GTTGGCAGGGCT
                                |||  |||  ||||||||||||
                                TCC  TCC  CGACCGTCCCGA
                                  A_   TC
GAM927  DKFZP434P211 5'  AGCCCTGCCTTCCTTCCT    27259    C   CTGTT
                                AGG AAGG    GGCAGGGCT
                                ||| ||||    |||||||||
                                TCC TTCC    CCGTCCCGA
                                  _   TT___
GAM927  DKFZP586N0721 3'  AGCCCCACTCCCTTGCT     31199       CT  TGGCA
                                GGCAAGG  GT    GGGCT
                                |||||||  ||    |||||
                                TCGTTCC  CA    CCCGA
                                    CT  C____
GAM927  DKFZP761G1913 3'  GAGCCCCTGAGCCTTGC     48914       GTTGG    _
                                GCAAGGCT    CAGGG CTC
                                ||||||||    ||||| |||
                                CGTTCCGA    GTCCC GAG
                                     _____    C
GAM927  DKFZP761I2123 3'  TGTCACCACAGCCCTGCC    48770     A    __
                                GGCA GGCTGT  TGGCA
                                |||| ||||||  |||||
                                CCGT CCGACA  ACTGT
                                  C     CC
GAM927  DOCK3    3'  AGCCCTACCACCCCCGCCT   66493     AA  CTGT   C
                                AGGC  GG    TGG AGGGCT
                                ||||  ||    ||| ||||||
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                              TCCG  CC   ACC TCCCGA
                                CC  C___  A
GAM927  FLJ10474 3' CGAGCCGCTCACGCCCTGCC  36152     A  T T  AG
                              GGCA GGC GT GGC  GGCTCG
                              |||| ||| || |||  ||||||
                              CCGT CCG CA TCG  CCGAGC
                                C  _ C  __
GAM927  FLJ10922 3' CGAGCCCCCGCAAGCCACGCC 36874    AA  GT  CA
                              GGC  GGCT  TGG  GGGCTCG
                              |||  ||||  |||  |||||||
                              CCG  CCGA  GCC  CCCGAGC
                                CA   AC  __
GAM927  FLJ12505 5' AGCCCCAGCAGCCCCAGCC   45384    AA_      CAG
                              GGC  GGCTGTTGG  GGCT
                              |||  |||||||||  ||||
                              CCG  CCGACGACC  CCGA
                                ACC       ___
GAM927  FLJ13868 3' CCACCATCAGCCCTGCCT   42729     A   T  CA
                              AGGCA GGCTG TGG  GG
                              ||||| ||||| |||  ||
                              TCCGT CCGAC ACC  CC
                                 C    T  A_
GAM927  FLJ14640 5' GAGCCCTATGCCACCACCT   51479    C  T   __
                              AGG TG TGGCA  GGGCTC
                              ||| || |||||  ||||||
                              TCC AC ACCGT  CCCGAG
                                _ C    AT
GAM927  FLJ30473 3' AGCCCTGCCTCTTCTCCCT   58462    CA  CTGTT
                              AGG  AGG   GGCAGGGCT
                              |||  |||   |||||||||
                              TCC  TCT   CCGTCCCGA
                                C_  TCT__
GAM927  KIAA0125 3' AGCCCTGCCTGCCTCC    60502    CA   TGTT
                              GG AGGC   GGCAGGGCT
                              ||  ||||  |||||||||
                              CC  TCCG  CCGTCCCGA
                                __   T___
GAM927  KIAA0125 5' AGCCCTGCCTGCCTCC    28894    CA   TGTT
                              GG AGGC   GGCAGGGCT
                              ||  ||||  |||||||||
                              CC  TCCG  CCGTCCCGA
                                __   T___
GAM927  KIAA0700 3' CGAGCCCTGGGGCTCAGCCCC  72054   CAA   TTGG_
                              GG  GGCTG   CAGGGCTCG
                              ||  |||||   |||||||||
                              CC  CCGAC   GTCCCGAGC
                                ___   TCGGG
GAM927  KLK15   3' AGCTGGCCAGCAGCCCCGCCT  56745     AA       AG
                              AGGC  GGCTGTTGGC  GGCT
                              ||||  ||||||||||  ||||
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                                TCCG  CCGACGACCG  TCGA
                                  CC        G_
GAM927  KLK15    3'  AGCTGGCCAGCAGCCCCGCCT  56747     AA        AG
                                AGGC  GGCTGTTGGC  GGCT
                                ||||  ||||||||||  ||||
                                TCCG  CCGACGACCG  TCGA
                                  CC        G_
GAM927  KLK15    3'  AGCTGGCCAGCAGCCCCGCCT  43434     AA        AG
                                AGGC  GGCTGTTGGC  GGCT
                                ||||  ||||||||||  ||||
                                TCCG  CCGACGACCG  TCGA
                                  CC        G_
GAM927  KLK15    3'  AGCTGGCCAGCAGCCCCGCCT  33998     AA        AG
                                AGGC  GGCTGTTGGC  GGCT
                                ||||  ||||||||||  ||||
                                TCCG  CCGACGACCG  TCGA
                                  CC        G_
GAM927  PTPRN2   3'  CGAACCCTGCCAGGCCCCCGCT 55602     AA_   GT      C
                                GGC   GGCT  TGGCAGGG TCG
                                |||   ||||  |||||||| |||
                                TCG   CCGG  ACCGTCCC AGC
                                  CCC   __      A
GAM927  PTPRN2   3'  CGAACCCTGCCAGGCCCCCGCT 55606     AA_   GT      C
                                GGC   GGCT  TGGCAGGG TCG
                                |||   ||||  |||||||| |||
                                TCG   CCGG  ACCGTCCC AGC
                                  CCC   __      A
GAM927  RIN1     3'  AGCCCCACCCAGGGCCCTGTC  15025     A   G   CA_
                                GGCA GGCT TTGG   GGGCT
                                |||| |||| ||||   |||||
                                CTGT CCGG GACC   CCCGA
                                  C   _   CAC
GAM927  RNPS1    5'  AGCCCCCAACGCCAGGCCCTGC 22006     A   ____    CA
          C                      GGCA GGCT   GTTGG  GGGCT
                                ||||  ||||   |||||  |||||
                                CCGT CCGG   CAACC  CCCGA
                                  C   ACCG   __
GAM927  SERPINA6 5'  AGCCAGCAGAAACAGCCTCAGC 8280     A_      G__  AG
          C                      GGC  AGGCTGTT   GC  GGCT
                                |||  ||||||||   ||  ||||
                                CCG  TCCGACAA   CG  CCGA
                                  AC       AGA  A_
GAM927  LOC147650 3'  CGAGCCCTGGAGGCCCAGCCT  78387     AA   GTTGG
                                AGGC  GGCT    CAGGGCTCG
                                ||||  ||||    |||||||||
                                TCCG  CCGG    GTCCCGAGC
                                  AC   AG___
GAM927  LOC147791 5'  AGCCCTGCCCCCAGCT     84069      TT
                                GGCTG  GGCAGGGCT
                                |||||  |||||||||
```

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                                TCGAC  CCGTCCCGA
                                   CC
GAM927  LOC148887 3'  CCGCCAGCAGCCCCGCCT    84232     AA       A
                                AGGC  GGCTGTTGGC GG
                                ||||  |||||||||| ||
                                TCCG  CCGACGACCG CC
                                  CC        _
GAM927  LOC148887 3'  CCGCCAGCAGCCCCGCCT    84233     AA       A
                                AGGC  GGCTGTTGGC GG
                                ||||  |||||||||| ||
                                TCCG  CCGACGACCG CC
                                  CC        _
GAM927  LOC150174 5'  AGCCCTGCCTTCCTTCCT    79603     C   CTGTT
                                AGG AAGG    GGCAGGGCT
                                ||| ||||    |||||||||
                                TCC TTCC    CCGTCCCGA
                                  _   TT___
GAM927  LOC150213 5'  AGCCCTGCCTTCCTTCCT    74849     C   CTGTT
                                AGG AAGG    GGCAGGGCT
                                ||| ||||    |||||||||
                                TCC TTCC    CCGTCCCGA
                                  _   TT___
GAM927  LOC150236 5'  AGCCCTGCCTTCCTTCCT    79681     C   CTGTT
                                AGG AAGG    GGCAGGGCT
                                ||| ||||    |||||||||
                                TCC TTCC    CCGTCCCGA
                                  _   TT___
GAM927  LOC199986 5'  AGCCCTGCCCTCCTGACCT   89895     CA  CTGTT
                                AGG  AGG    GGCAGGGCT
                                |||  |||    |||||||||
                                TCC  TCC    CCGTCCCGA
                                  AG   TC___
GAM927  LOC221421 3'  GGGACCCAACTGCCCTGCCT   92280      A  T    CAGGG
                                AGGCA GGC GTTGG    CTC
                                ||||| ||| |||||    |||
                                TCCGT CCG CAACC    GGG
                                   C   T    CA___
GAM927  LOC254099 5'  GAGCCCCGCCAGAACCCCT    96846     CAA  CTG    A
                                AGG   GG   TTGGC GGGCTC
                                |||   ||   ||||| ||||||
                                TCC   CC   GACCG CCCGAG
                                  ___  AA_    C
GAM927  LOC90750  5'  GCAAACAGCCTGCCT       63921      A     G
                                AGGCA GGCTGTT GC
                                ||||| ||||||| ||
                                TCCGT CCGACAA CG
                                   _     A
GAM928  HPGD     3'  ACAATGACAAATATTTCAC    5976      CATC   GC
                                GTG   GTG  TTGTCATTGT
                                |||   |||  ||||||||||
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                                CAC   TAT  AACAGTAACA
                                  TT__   A_
GAM928  MGAM     3'  ACAATGACCCCACGACAC    72359     CA     CTT
                                GTG  TCGTGG   GTCATTGT
                                |||  ||||||   ||||||||
                                CAC  AGCACC   CAGTAACA
                                 __     C__
GAM928  BRAG     3'  CAATTCCAAAACACAATGCAC  29472       C   GC   TC
                                GTGCAT GTG  TTG  ATTG
                                ||||||| |||  |||  ||||
                                CACGTA CAC  AAC  TAAC
                                    A   AA   CT
GAM928  HT002    3'  TGACAGGATGCAACCACAACAC 25947     CATC    C    CA_
                                GTG    GTGG TTGT   TTGTCA
                                |||    |||| ||||   ||||||
                                CAC    CACC AACG   GACAGT
                                  AA__    _    TAG
GAM928  LOC144347 3'  ACAAGCCAGGATGCAC      76808        G
                                GTGCATC TGGCTTGT
                                |||||||| ||||||||
                                CACGTAG ACCGAACA
                                    G
GAM928  LOC144519 3'  TGACAGGCGTGAGCCACAGCAC 76875      ATC     TG CA
                                GTGC   GTGGCT  T  TTGTCA
                                ||||   ||||||  |  ||||||
                                CACG   CACCGA  G  GACAGT
                                  A__     GT CG
GAM928  LOC144698 3'  TGACAAGGGGAGCCACGATG   76911          G  A
                                CATCGTGGCTT TC TTGTCA
                                |||||||||||| || ||||||
                                GTAGCACCGAG GG AACAGT
                                      G  _
GAM929  HOXC13   3'  ACAAAGACTCCAGCCA      59680        _  C
                                TGGCTGGA TCT TGT
                                |||||||| ||| |||
                                ACCGACCT AGA ACA
                                     C   A
GAM929  C22orf19  3'  CAATCACATACAGAGATACAG  13417     G         CA
                                CTG ATCTCTGTATG  ATTG
                                ||| ||||||||||  ||||
                                GAC TAGAGACATAC  TAAC
                                  A          AC
GAM929  LOC151719 3'  GTGACAAAAATCCAGCCA    80343         CTC   A
                                TGGCTGGAT   TGT TGC
                                |||||||||   ||| |||
                                ACCGACCTA   ACA GTG
                                     AAA  _
GAM930  NPEPPS   3'  GACTGTAAGCCTGTGTGTG   20876      _    GAACC
                                TACAC CGGGT    TACAGTC
                                ||||| |||||    |||||||
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                                GTGTG GTCCG    ATGTCAG
                                  T    A____
GAM930  STIM1    3' AGAACTGTAGGTTATAAGG   60143   GG   A     C
                                CC  GTGA CCTACAGT CT
                                ||  |||| |||||||| ||
                                GG  TATT GGATGTCA GA
                                 AA   _      A
GAM930  CLIC4    3' AGGACTGTAAACTTTTGTG   25630    C_   GAACC
                                CAC  GGGT    TACAGTCCT
                                |||  ||||    |||||||||
                                GTG  TTCA    ATGTCAGGA
                                  TT   A____
GAM930  CTPS2    5' GCGTGGAGTTCACCCG      39088        _   A
                                CGGGTGAAC CTAC GT
                                ||||||||| |||| ||
                                GCCCACTTG GGTG CG
                                     A   _
GAM930  FLJ12750 3' AGAACTGTAGGTCAGTGGTG  45121      GG   A      C
                                CACCG  TGA CCTACAGT CT
                                |||||  ||| |||||||| ||
                                GTGGT  ACT GGATGTCA GA
                                  G_   _      A
GAM930  LOC130412 5' GCTGGTTCACCAGTG      75740     CG      TAC
                                CAC  GGTGAACC   AGT
                                |||  ||||||||   |||
                                GTG  CCACTTGG   TCG
                                  A_      ____
GAM930  LOC137964 5' GACTGTAGCTCTCCAGGT    75282     G  T  AC
                                ACC GG GA  CTACAGTC
                                ||| || ||  ||||||||
                                TGG CC CT  GATGTCAG
                                  A  T  C_
GAM930  LOC158709 3' AGGACTGTAGACTGAGG     81978    G_   GAAC
                                CC  GGT    CTACAGTCCT
                                ||  |||    ||||||||||
                                GG  TCA    GATGTCAGGA
                                 AG   _____
GAM930  LOC197117 3' GACAGGCCACCCGGTG      89717         AA   ACA
                                CACCGGGTG  CCT   GTC
                                |||||||||  |||   |||
                                GTGGCCCAC  GGA   CAG
                                     C_   ___
GAM930  LOC200301 3' GACTGTGGATTCACCCATGTA  88743      CC      C
                                TACA  GGGTGAA CTACAGTC
                                ||||  ||||||| ||||||||
                                ATGT  CCCACTT GGTGTCAG
                                  A_      A
GAM931  MXI1     3' TCCATGCATGACAGCCTCT    19902       CA   AGGT
                                AGAGGT  TGT    TGCATGGA
                                ||||||  |||    ||||||||
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                                TCTCCG  ACA    ACGTACCT
                                   __   GT__
GAM931  MXI1     3'  TCCATGCATGACAGCCTCT   55263       CA   AGGT
                                AGAGGT  TGT    TGCATGGA
                                ||||||  |||    ||||||||
                                TCTCCG  ACA    ACGTACCT
                                   __   GT__
GAM931  SOX12    3'  CCACGCGCACCACCTCT     22694       CATGTA  _  A
                                AGAGGT     GGT TGC TGG
                                ||||||     ||| ||| |||
                                TCTCCA     CCA GCG ACC
                                   _______  C   C
GAM931  TCF7     3'  GTCCATGTATTCACACACCCCT 12162    A   CA   A GT
                                AG GGT  TGT G  TGCATGGAC
                                || |||  ||| |  |||||||||
                                TC CCA  ACA C  ATGTACCTG
                                 C   C_   _ TT
GAM931  CDCA4    3'  TCCATGTCATTCATAACCCCT  35657    A   C   TA   T
                                AG GGT ATG  GGT GCATGGA
                                || ||| |||  ||| |||||||
                                TC CCA TAC  TTA TGTACCT
                                 C   A   __   C
GAM931  DGS-A    3'  GTCCATGCATTGTAATGTCCCC 84901    A  T   GTAGGT
           T                     AG GG CAT     TGCATGGAC
                                || || |||     |||||||||
                                TC CC GTA     ACGTACCTG
                                 C  T   ATGTT_
GAM931  DKFZP434L187 5'  CCACCTCCCACATGACCTT    68803          A  TTGCA
                                GAGGTCATGT GG     TGG
                                |||||||||| ||     |||
                                TTCCAGTACA CC     ACC
                                      C  TCC__
GAM931  DKFZp564I1922 3'  CCATGAATAATACACGACCT   31234       A    GGTTG
                                AGGTC TGTA     CATGG
                                ||||| ||||     |||||
                                TCCAG ACAT     GTACC
                                   C    AATAA
GAM931  EZFIT    3'  GCCCTGACCTCATGACCTC    41109         T    ____
                                GAGGTCATG AGGTT   GC
                                ||||||||| |||||   ||
                                CTCCAGTAC TCCAG   CG
                                      _    TCC
GAM931  FLJ13842  3'  GCCGACCTACAAACCTC     44985       CA       _
                                GAGGT  TGTAGGTTG C
                                |||||  ||||||||| |
                                CTCCA  ACATCCAGC G
                                   A_        C
GAM931  FLJ14855  3'  GTCACCTACATAACCCT     52619    A   C       T
                                AG GGT ATGTAGGT GC
                                || ||| |||||||| ||
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                                TC CCA TACATCCA TG
                                 _  A      C
GAM931  KIAA0057  3'  GCCCACTTGCCATAACCTCT  24432      C  _   T_
                                AGAGGT ATG TAGGT  GC
                                |||||| ||| |||||  ||
                                TCTCCA TAC GTTCA  CG
                                   A  C    CC
GAM931  MGC19556  3'  GTCCATGCCAACATAACCTCT  53231      C   A GTT
                                AGAGGT ATGT G  GCATGGAC
                                |||||| |||| |  ||||||||
                                TCTCCA TACA C  CGTACCTG
                                   A  A ___
GAM931  MGC3413   3'  CCATAGGACACATAACCTT   51047     C   AG  GC
                                GAGGT ATGT  GTT  ATGG
                                ||||| ||||  |||  ||||
                                TTCCA TACA  CAG  TACC
                                   A   __  GA
GAM931  VCY2IP1   3'  TCCATGCAGGATGACGCCT   36394     CATG  GG
                                AGGT   TA  TTGCATGGA
                                ||||   ||  |||||||||
                                TCCG   GT  GACGTACCT
                                  CA__  AG
GAM931  ZNF263    3'  CCAGCCGACCAAATGACCTCT  19225       GTA   CA
                                AGAGGTCAT  GGTTG  TGG
                                |||||||||  |||||  |||
                                TCTCCAGTA  CCAGC  ACC
                                     AA_   CG
GAM931  LOC125268 3'  CCCAGCCTACACCACCTC    76072     CA      CAT
                                GAGGT  TGTAGGTTG  GG
                                |||||  |||||||||  ||
                                CTCCA  ACATCCGAC  CC
                                   CC       ___
GAM931  LOC149837 3'  CCAGAGCATACATGACCTCT  84730         GGT  A_
                                AGAGGTCATGTA  TGC  TGG
                                ||||||||||||  |||  |||
                                TCTCCAGTACAT  ACG  ACC
                                      ___  AG
GAM931  LOC200982 5'  CCACACGGTTGCATGACCTT  90218         G TT CA
                                GAGGTCATGTA G  G  TGG
                                |||||||||| |  |  |||
                                TTCCAGTACGT T  C  ACC
                                     _ GG AC
GAM931  LOC205143 5'  CCACACAACCTGCCTC     90665     CATGT    CA
                                GAGGT   AGGTTG  TGG
                                |||||   ||||||  |||
                                CTCCG   TCCAAC  ACC
                                  _____    AC
GAM931  LOC221922 5'  CCACACCATGACCCT      92688   A    GTA  TGCA
                                AG GGTCAT  GGT   TGG
                                || ||||||  |||   |||
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                                TC CCAGTA  CCA   ACC
                                 _    ___  C___
GAM932  ACADS    3'  ACCACTGTGCCTCAAGTTCC  3406      AAGACA
                                GGAG     GGGCACAGTGGT
                                ||||     ||||||||||||
                                CCTT     TCCGTGTCACCA
                                  GAAC__
GAM932  AIPL1    3'  ACCCCTCCCTGTCTCCCCA   59849     A A      CAC  T
                                TGG GA GACAGGG  AG GGT
                                ||| || |||||||  || |||
                                ACC CT CTGTCCC  TC CCA
                                  C _      ___ C
GAM932  B3GAT1   5'  TGCTCTGTCCTCTCCA     53979       A
                                TGGAGA GACAGGGCA
                                |||||| |||||||||
                                ACCTCT CTGTCTCGT
                                    C
GAM932  COG5     3'  TGTACCCTGCTTCCCC     20954    A   A    C
                                GG GAAG CAGGG ACA
                                || |||| ||||| |||
                                CC CTTC GTCCC TGT
                                 C   _    A
GAM932  CRTAP    3'  ACCTTCATCCCTGTCTTCCTCA 21028    GA        CACAGT
                                TG  GAAGACAGGG     GGT
                                ||  ||||||||||     |||
                                AC  CTTCTGTCCC     CCA
                                 TC        TACTT_
GAM932  EPB72    3'  ACCACAACCAGCTTCTCCA   14594        ACA  GCACA
                                TGGAGAAG  GG    GTGGT
                                ||||||||  ||    |||||
                                ACCTCTTC  CC    CACCA
                                     GA_  AA___
GAM932  GAB2     3'  TACCACTGTCCTCTGCCCCCA  24502     AGAAGA    C
                                TGG     CAGGG ACAGTGGTA
                                |||     ||||| |||||||||
                                ACC     GTCTC TGTCACCAT
                                  CCC___    C
GAM932  GAB2     3'  TACCACTGTCCTCTGCCCCCA  54459     AGAAGA    C
                                TGG     CAGGG ACAGTGGTA
                                |||     ||||| |||||||||
                                ACC     GTCTC TGTCACCAT
                                  CCC___    C
GAM932  GPD1     3'  TGCCCTGTCCCTCTCCA     59672       A_
                                TGGAGA  GACAGGGCA
                                ||||||  |||||||||
                                ACCTCT  CTGTCCCGT
                                    CC
GAM932  GSTT1    3'  ACCATCCCCACCCTGTCTTCCA 73457    GA        CACA_
            CA                    TG  GAAGACAGGG    GTGGT
                                ||  ||||||||||    |||||
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                                AC  CTTCTGTCCC    TACCA
                                 AC        ACCCC
GAM932  MATN1    3'  ACCACTGTGGCCTCTCCA    9916       AGACA  G
                                TGGAGA    GG CACAGTGGT
                                ||||||    || |||||||||
                                ACCTCT    CC GTGTCACCA
                                   _____  G
GAM932  MAZ      3'  TGCCCTGTCTTCCCA      73390     A
                                TGG GAAGACAGGGCA
                                ||| ||||||||||||
                                ACC CTTCTGTCCCGT
                                  _
GAM932  NR1D1    3'  ACCACTCTGTCTCCCCCA    41361     AGA     GGCAC
                                TGG   AGACAG    AGTGGT
                                |||   ||||||    ||||||
                                ACC   TCTGTC    TCACCA
                                  CCC     _____
GAM932  OTOF     3'  CACACCCTGTCTTCCCA     16639     A       CACA
                                TGG GAAGACAGGG    GTG
                                ||| ||||||||||    |||
                                ACC CTTCTGTCCC    CAC
                                  _        A___
GAM932  PCTP     3'  ACCACTGTTCAGCCTTCCCC   41094    A   ACAG  C
                                GG GAAG    GG ACAGTGGT
                                || ||||    || ||||||||
                                CC CTTC    CT TGTCACCA
                                 C    CGA_  _
GAM932  PPP2R1A  3'  CACCTCCCGTCCTCCCCA    26442     A  A   A   CACA
                                TGG GA GAC GGG    GTG
                                ||| || ||| |||    |||
                                ACC CT CTG CCC    CAC
                                  C  C   _   TC__
GAM932  PPP2R4   3'  TGTGCCTGCCTTCCCCA     60563     A   ACA
                                TGG GAAG   GGGCACA
                                ||| ||||   |||||||
                                ACC CTTC   TCCGTGT
                                  C    CG_
GAM932  SH3BP2   3'  CACGCCCTGTTCCCTCCA    11595      AA      ACA
                                TGGAG  GACAGGGC   GTG
                                |||||  ||||||||   |||
                                ACCTC  TTGTCCCG   CAC
                                   CC       ___
GAM932  SMAC     3'  CACTGCCCTGTCTCCCCA    39111     A  A       CA
                                TGG GA GACAGGGCA  GTG
                                ||| || |||||||||  |||
                                ACC CT CTGTCCCGT  CAC
                                  C  _        __
GAM932  SMAC     3'  CACTGCCCTGTCTCCCCA    57195     A  A       CA
                                TGG GA GACAGGGCA  GTG
                                ||| || |||||||||  |||
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                                ACC CT CTGTCCCGT  CAC
                                  C _       __
GAM932  SMAC     3'  CACTGCCCTGTCTCCCCA    57205     A  A       CA
                                TGG GA GACAGGGCA  GTG
                                ||| || |||||||||  |||
                                ACC CT CTGTCCCGT  CAC
                                  C _       __
GAM932  UVRAG    3'  TACTGTCGCCCCATCTTCTCC  12562        CA   _
                                GGAGAAGA  GGGC ACAGTG
                                ||||||||  |||| ||||||
                                CCTCTTCT  CCCG TGTCAT
                                     AC   C
GAM932  XPA      3'  ACCACTGTACCCCAGGTTCT   4596      GACA  C
                                AGAA   GGG ACAGTGGT
                                ||||   ||| ||||||||
                                TCTT   CCC TGTCACCA
                                  GGAC  A
GAM932  ZNF261   3'  CCATTCCCTGCCTTCTCTA   17493        A    CAC
                                TGGAGAAG CAGGG  AGTGG
                                |||||||| |||||  |||||
                                ATCTCTTC GTCCC  TTACC
                                     C   ___
GAM932  B3GNT7   3'  ACCGCACCCTGCTTCTCCA   71123        A    CACA
                                TGGAGAAG CAGGG   GTGGT
                                |||||||| |||||   |||||
                                ACCTCTTC GTCCC   CGCCA
                                     _   A___
GAM932  CBCIP2   3'  CACCTTTCCCCTCTTCTCCA  51589        CA  CACA
                                TGGAGAAGA  GGG   GTG
                                |||||||||  |||   |||
                                ACCTCTTCT  CCC   CAC
                                     C_  TTTC
GAM932  DKFZP434P1750 3'  GCCCTCCCTGTCTCCCCCA   31377     AGA      CAC  T
                                TGG  AGACAGGG  AG GGT
                                |||  ||||||||  || |||
                                ACC  TCTGTCCC  TC CCG
                                  CCC      ___ _
GAM932  DKFZp547I094 5'  ACCCCTGTTGCCCTGCCTTCTT 49629        A     _  T
           CA                    TGGAGAAG CAGGGCA CAG GGT
                                |||||||| ||||||| ||| |||
                                ACTTCTTC GTCCCGT GTC CCA
                                     C      T  C
GAM932  DKFZp564I1922 3'  ACCACTGTTATATTACCTTCTC 31232        AC  GGC_
           CA                    TGGAGAAG  AG   ACAGTGGT
                                ||||||||  ||   ||||||||
                                ACCTCTTC  TT   TGTCACCA
                                     CA  ATAT
GAM932  DUSP9    3'  CACCTCCCTGTTTCTCCA    7341       A     CACA
                                TGGAGA GACAGGG   GTG
                                ||||||| |||||||   |||
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                                ACCTCT TTGTCCC   CAC
                                   _     TC__
GAM932  FLJ14708  3'  ACCACTGTGGGCCCTCCTTC  51538     AC   __
                                GAAG  AGGGC  ACAGTGGT
                                ||||  |||||  ||||||||
                                CTTC  TCCCG  TGTCACCA
                                  C_    GG
GAM932  FLJ23120  3'  ACCACTGCACCACTGTACTCCA 85143      AAG   _ CA
                                TGGAG   ACAG GG  CAGTGGT
                                |||||   |||| ||  |||||||
                                ACCTC   TGTC CC  GTCACCA
                                   A__    A  AC
GAM932  IMAGE:4907098 3'  ACCACTGTGGTCCCCTCCA   91656      AA   AGGG
                                TGGAG  GAC   CACAGTGGT
                                |||||  |||   |||||||||
                                ACCTC  CTG   GTGTCACCA
                                   CC  ____
GAM932  KIAA0416  3'  ACCACTACCCACTCCA     31462      AAGACA   CAC
                                TGGAG     GGG   AGTGGT
                                |||||     |||   ||||||
                                ACCTC     CCC   TCACCA
                                   A_____   A__
GAM932  KIAA0545  3'  CCACGCTGTTCCTCCA     63144      AAGACA    CA
                                TGGAG     GGGCA  GTGG
                                |||||     |||||  ||||
                                ACCTC     CTTGT  CACC
                                   ______    CG
GAM932  KIAA0924  3'  TGCCCTGTCCTCTGCA     29724    G   A
                                TG AGA GACAGGGCA
                                || ||| |||||||||
                                AC TCT CTGTCCCGT
                                 G   C
GAM932  KIAA1111  3'  CATCCTGCCTGCCTTCTCCA  96206        ACA    CA
                                TGGAGAAG   GGGCA  GTG
                                ||||||||   |||||  |||
                                ACCTCTTC   TCCGT  TAC
                                     CG_    CC
GAM932  KIAA1184  3'  TGTGCCCCTCCCCTCCA     42620      AA  CA
                                TGGAG  GA  GGGCACA
                                |||||  ||  |||||||
                                ACCTC  CT  CCCGTGT
                                   CC  C_
GAM932  MGC13138  3'  TACCACCATGCCTGGCTTC   53022     ACA    CA
                                GAAG   GGGCA  GTGGTA
                                ||||   |||||  ||||||
                                CTTC   TCCGT  CACCAT
                                  GG_    AC
GAM932  MGC5590   5'  TACCACTGTCAGCACTCTCCA 43927       AGACAGG __
                                TGGAGA     GC  ACAGTGGTA
                                ||||||     ||  |||||||||
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                                ACCTCT     CG  TGTCACCAT
                                   CA_____  AC
GAM932  moblak   3'  CCACACCTCTGTCTCCCCCA  55490    AGA      CACA
                                TGG  AGACAGGG   GTGG
                                |||  ||||||||   ||||
                                ACC  TCTGTCTC   CACC
                                  CCC      CA__
GAM932  NR6A1    3'  ACCACTGCGAACTTTCCA   52878     AAGAC  GGCA
                                TGGAG   AG   CAGTGGT
                                |||||   ||   |||||||
                                ACCTT   TC   GTCACCA
                                   _____ AAGC
GAM932  NR6A1    3'  ACCACTGCGAACTTTCCA   52866     AAGAC  GGCA
                                TGGAG   AG   CAGTGGT
                                |||||   ||   |||||||
                                ACCTT   TC   GTCACCA
                                   _____ AAGC
GAM932  NR6A1    3'  ACCACTGCGAACTTTCCA   7641      AAGAC  GGCA
                                TGGAG   AG   CAGTGGT
                                |||||   ||   |||||||
                                ACCTT   TC   GTCACCA
                                   _____ AAGC
GAM932  PEG10    3'  TACCACTGCCGGATGTATTCTC 30530       G  G__   CA
          CA                     TGGAGAA ACA  GGCA  GTGGTA
                                |||||||  |||  ||||  ||||||
                                ACCTCTT TGT  CCGT  CACCAT
                                   A  AGG  __
GAM932  STMN3    3'  TACCACTGCAGCATCCCCCACT 31902       ACA  CA____
          TCTCCA                  GGAGAAG  GGG    CAGTGGTA
                                |||||||  |||    ||||||||
                                CCTCTTC  CCC    GTCACCAT
                                   ACC  TACGAC
GAM932  LOC126964 3'  ACCACTGTGTGCGCCTCCA   74610     AAGACAGG
                                TGGAG      GCACAGTGGT
                                |||||      ||||||||||
                                ACCTC      TGTGTCACCA
                                  CGCG____
GAM932  LOC145837 5'  CATCTGCCCTGTCTCTCCA   83543      A       CA
                                TGGAGA GACAGGGCA  GTG
                                ||||||  |||||||||  |||
                                ACCTCT CTGTCCCGT  TAC
                                   _       C_
GAM932  LOC148930 3'  GCTTTGCCCTGTGTTCTCCA  79097       G      C
                                TGGAGAA ACAGGGCA AGT
                                |||||||  ||||||||  |||
                                ACCTCTT TGTCCCGT TCG
                                   G       T
GAM932  LOC150372 3'  TACCACTGTGCCCTGGCCCA  79808    AGAAGA
                                TGG    CAGGGCACAGTGGTA
                                |||    ||||||||||||||
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                                ACC     GTCCCGTGTCACCAT
                                  CG____
GAM932  LOC151162 5'  GCCACCCCATTTCTCCA     85244        ACA   CACA
                                TGGAGAAG   GGG    GTGGT
                                ||||||||   |||    |||||
                                ACCTCTTT   CCC    CACCG
                                    A__    ____
GAM932  LOC154761 3'  ACCACACCCACTTCTCCA     81120        ACA   CACA
                                TGGAGAAG   GGG    GTGGT
                                ||||||||   |||    |||||
                                ACCTCTTC   CCC    CACCA
                                    A__    A___
GAM932  LOC199964 3'  TGCCGTGCCTTCTCCA      89891        A  G
                                TGGAGAAG CA GGCA
                                |||||||| || ||||
                                ACCTCTTC GT CCGT
                                    C  G
GAM932  LOC203377 5'  GCCACCCCATTTCTCCA     90582        ACA   CACA
                                TGGAGAAG   GGG    GTGGT
                                ||||||||   |||    |||||
                                ACCTCTTT   CCC    CACCG
                                    A__    ____
GAM932  LOC203504 5'  ACCCCTCCCCAGTCTTCTCCA  90635         A   CAC  T
                                TGGAGAAGAC GGG   AG GGT
                                |||||||||| |||   || |||
                                ACCTCTTCTG CCC   TC CCA
                                     A   C__  C
GAM932  LOC219654 3'  CGTTGTTCCCCGTCTTCTCCA  91302         A   C
                                TGGAGAAGAC GGG ACAGTG
                                |||||||||| ||| ||||||
                                ACCTCTTCTG CCC TGTTGC
                                     C   T
GAM932  LOC221416 3'  TGGCACCCTATCTTCTCCA    93772         C    CA_
                                TGGAGAAGA AGGG   CA
                                ||||||||| ||||   ||
                                ACCTCTTCT TCCC   GT
                                    A    ACG
GAM932  LOC221491 5'  ACCACTGTGCCCAATGCCCCCC 92010     AGAAGACA
          A                      TGG       GGGCACAGTGGT
                                 |||       ||||||||||||
                                 ACC       CCCGTGTCACCA
                                   CCCCGTAA
GAM932  LOC222001 3'  ACCACTAATTAAGTTTTCTCCA 92903         AGGGCAC
                                TGGAGAAGAC      AGTGGT
                                ||||||||||      ||||||
                                ACCTCTTTTG      TCACCA
                                     AATTAA_
GAM932  LOC255975 5'  TACCACCCGGCAGCCTCTCCA  95897       AGACAGG  ACA
                                TGGAGA      GC   GTGGTA
                                ||||||      ||   ||||||
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                                ACCTCT     CG  CACCAT
                                   CCGA___  GCC
GAM932  LOC256901 3'  ACCACTTCCCCCTTCTCCA   96619       ACA  CAC
                                TGGAGAAG  GGG  AGTGGT
                                ||||||||  |||  ||||||
                                ACCTCTTC  CCC  TCACCA
                                    C__   T__
GAM932  LOC54550  3'  ACCACTGTGCCCAGGCGCCA  77688    AGAAGACA
                                TGG      GGGCACAGTGGT
                                |||      ||||||||||||
                                ACC      CCCGTGTCACCA
                                  GCGGA___
GAM932  LOC93097  3'  ACCACCAGCATTTCCTCCA   71357     AA  CAGG  ACA
                                TGGAG  GA   GC   GTGGT
                                |||||  ||   ||  |||||
                                ACCTC  CT   CG   CACCA
                                   __  TTA_  AC_
GAM932  LOC96652  3'  ACCACCTGCACCAGCTTCTCCA 65462       ACA  _   CA
                                TGGAGAAG  GG GCA  GTGGT
                                ||||||||  || |||  |||||
                                ACCTCTTC  CC CGT  CACCA
                                    GA_  A  C_
GAM933  ADAM20   5'  CAGCACTGCAGCTCTGA    13764    A      AT  C
                                TCA AGCTGCAG  TGC TG
                                ||| ||||||||  ||| ||
                                AGT TCGACGTC  ACG AC
                                  C       __  _
GAM933  E2F1     3'  CAATCTGCACTTTGA      84794      C
                                TCAAAG TGCAGATTG
                                |||||| |||||||||
                                AGTTTC ACGTCTAAC
                                    _
GAM933  E2F1     3'  TCACCTTGTCTCTGCAGCCCTG 84803    AA      TTGCCT
           G                     TCA  GCTGCAGA     GTGA
                                |||  ||||||||     ||||
                                GGT  CGACGTCT     CACT
                                  CC       CTGTTC
GAM933  FPRL1    5'  CACTGCATTTGCAGCCTTGA   7589      A       T  CT
                                TCAA GCTGCAGAT GC  GTG
                                |||| |||||||| ||  |||
                                AGTT CGACGTTTA CG  CAC
                                  C       _  T_
GAM933  FSHPRH1  5'  TCACGGCTCTCTGCAGC     22116       TT   T
                                GCTGCAGA  GCC GTGA
                                ||||||||  ||| ||||
                                CGACGTCT  CGG CACT
                                    CT  _
GAM933  GPR44    3'  CACAGGGTCTGCACT      16522    C     TG
                                AG TGCAGAT  CCTGTG
                                || |||||||  ||||||
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                                TC ACGTCTG  GGACAC
                                 _     __
GAM933  IL10RA   3'  CACAGGCATGGAAGCTGTGA   59640     A    GCAGAT
                                TCA AGCT     TGCCTGTG
                                ||| ||||     ||||||||
                                AGT TCGA     ACGGACAC
                                  G    AGGT__
GAM933  ITGA2    3'  ATCACAGACACTACATATCTAA 9371     GC   _______ C     III
            AGCTTTGA                CT  AGAT     TG CTGTGA   T
                                ||  ||||     || ||||||  |
                                GA  TCTA     AC GACACT   A
                                 AA    TACATC  A     III
GAM933  LZTFL1   3'  ACAATGCAGCTTTGG       39750          GATTGCC
                                TCAAAGCTGCA      TGT
                                ||||||||||       |||
                                GGTTTCGACGT      ACA
                                       A_______
GAM933  MLC1     3'  CACCTCCCTGCAGCTTTGA   57588          ATTGCCT
                                TCAAAGCTGCAG      GTG
                                ||||||||||||      |||
                                AGTTTCGACGTC      CAC
                                       CCTC___
GAM933  MLC1     3'  CACCTCCCTGCAGCTTTGA   30776          ATTGCCT
                                TCAAAGCTGCAG      GTG
                                ||||||||||||      |||
                                AGTTTCGACGTC      CAC
                                       CCTC___
GAM933  MPP3     3'  TCACAGGCAAGCTGACCCT   8638     CTG   A
                                AG   CAG TTGCCTGTGA
                                ||   ||| ||||||||||
                                TC   GTC AACGGACACT
                                 CCA   G
GAM933  OCM      3'  CACAGGCAATGCCTCT     20545    CT   GA
                                AG  GCA  TTGCCTGTG
                                ||  |||  |||||||||
                                TC  CGT  AACGGACAC
                                 TC   __
GAM933  PACE4    3'  GGGAATCCACAGCTCTGG    56347     A    CA    G
                                TCA AGCTG  GATT CC
                                ||| |||||  |||| ||
                                GGT TCGAC  CTAA GG
                                  C    AC    G
GAM933  PACE4    3'  GGGAATCCACAGCTCTGG    10402     A    CA    G
                                TCA AGCTG  GATT CC
                                ||| |||||  |||| ||
                                GGT TCGAC  CTAA GG
                                  C    AC    G
GAM933  PIGK     3'  TCATGGAATCCTGCAGCTTT   66702          _   G  T
                                AAAGCTGCAG ATT CC GTGA
                                |||||||||| ||| || ||||
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                                TTTCGACGTC TAA GG TACT
                                      C  _ _
GAM933  RNMT     3'  CACCACCTGCAGCTTGA     13711      A      AT  CCT
                                TCAA GCTGCAG  TG   GTG
                                |||| |||||||  ||   |||
                                AGTT CGACGTC  AC   CAC
                                  _      C_ ____
GAM933  STARD4   3'  TCACAGCTCACTGCAGCTTTGA 57517           ATT  C
                                TCAAAGCTGCAG   GC TGTGA
                                ||||||||||||   || |||||
                                AGTTTCGACGTC   CG ACACT
                                       ACT  _
GAM933  TUFT1    3'  CAGTGAACCTAAGCTTTGA   39255        GC  A  GC
                                TCAAAGCT  AG TT  CTG
                                ||||||||  || ||  |||
                                AGTTTCGA  TC AA  GAC
                                     A_  C  GT
GAM933  C11orf9  3'  CACTCATTCTCAGCTTTGA   25206        C   T  CCT
                                TCAAAGCTG AGA TG   GTG
                                |||||||||| ||| ||   |||
                                AGTTTCGAC TCT AC   CAC
                                      _  T  T__
GAM933  C20orf98 3'  CACAGGCAATTACTAGC     71511      CA
                                GCTG  GATTGCCTGTG
                                ||||  ||||||||||||
                                CGAT  TTAACGGACAC
                                  CA
GAM933  C5orf5   5'  CACAGCCGTAGCTTT       33465        AGATT C
                                AAAGCTGC     G CTGTG
                                ||||||||     | |||||
                                TTTCGATG     C GACAC
                                     _____ C
GAM933  C6orf5   3'  CAGCTCACTGCAGCTTTGA   31342           ATT  C
                                TCAAAGCTGCAG   GC TG
                                ||||||||||||   || ||
                                AGTTTCGACGTC   CG AC
                                       ACT  _
GAM933  CHST3    3'  CACAGACAATCTGCCGT     14969    T      C
                                GC GCAGATTG CTGTG
                                || |||||||| |||||
                                TG CGTCTAAC GACAC
                                 C       A
GAM933  FLJ12331 3'  CACAATCAGTGCAGTTTGA   46476      G    GA   CC
                                TCAAA CTGCA  TTG  TGTG
                                ||||| |||||  |||  ||||
                                AGTTT GACGT  GAC  ACAC
                                   _    __   TA
GAM933  FLJ12650 3'  CACAGGCATGGAGCT       44523      G  GAT
                                AGCT CA   TGCCTGTG
                                |||| ||   ||||||||
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                                TCGA GT   ACGGACAC
                                  G ___
GAM933  FLJ14082  5'  CACATGGAGAGCTGCAGCT   46669       ATTG _
                                AGCTGCAG   CC TGTG
                                ||||||||   || ||||
                                TCGACGTC   GG ACAC
                                    GAGA  T
GAM933  FLJ14326  5'  CACATCCTGCCCCAGCTTTGA  49802       ___   ATTGCC
                                TCAAAGCT   GCAG    TGTG
                                ||||||||   ||||    ||||
                                AGTTTCGA   CGTC    ACAC
                                    CCC   CT____
GAM933  FLJ23185  3'  CACAGGCCACCGGCTCCAGCTT 46827       C  ATT___
           TGA                   TCAAAGCTG AG    GCCTGTG
                                |||||||||  ||    |||||||
                                AGTTTCGAC TC    CGGACAC
                                    C  GGCCAC
GAM933  FLJ23563  5'  TCACGGTCACCCACAGCTTTGA 67598       CAGAT  C
                                TCAAAGCTG    TG CTGTGA
                                |||||||||    || ||||||
                                AGTTTCGAC    AC GGCACT
                                    ACCC_  T
GAM933  HRH4      3'  ACAGATCTGCACTTTGA     41242       C      TGC
                                TCAAAG TGCAGAT   CTGT
                                ||||||  |||||||   ||||
                                AGTTTC ACGTCTA   GACA
                                  _     ___
GAM933  KIAA1348  3'  CACAAAAATCTGCAAATTTGA  68573      GC      GCC
                                TCAAA  TGCAGATT   TGTG
                                |||||  ||||||||   ||||
                                AGTTT  ACGTCTAA   ACAC
                                   AA       AA_
GAM933  KIAA1579  3'  TCACAAATTGCTGCAGTCTGA  36611     AA      ATTGCC
                                TCA  GCTGCAG     TGTGA
                                |||  |||||||     |||||
                                AGT  TGACGTC     ACACT
                                  C_      GTTAA_
GAM933  MGC11034  3'  TCATTAGAATCCAAGCTTTGA  48789       GCA   GCCT
                                TCAAAGCT   GATT    GTGA
                                ||||||||   ||||    ||||
                                AGTTTCGA   CTAA    TACT
                                    AC_    GAT_
GAM933  MGC20258  5'  CAGGAATCTGCAGCCTGGA   58149    AAA       G
                                TC   GCTGCAGATT CCTG
                                ||   |||||||||| ||||
                                AG   CGACGTCTAA GGAC
                                  GTC        _
GAM933  MGC4832   3'  CACTCTGCAGCTTGGA      59000    A       T
                                TC AAGCTGCAGA TG
                                || |||||||||| ||
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                                AG TTCGACGTCT AC
                                 G        C
GAM933  MIC2L1   3'  CACTGGAATCTGCAGC     48819          G  T
                                GCTGCAGATT CC GTG
                                |||||||||| || |||
                                CGACGTCTAA GG CAC
                                      _  T
GAM933  MYO5C    3'  CACAGGTGACAGCTGTGA    38105     A    CAGA TG
                                TCA AGCTG   T  CCTGTG
                                ||| |||||   |  ||||||
                                AGT TCGAC   A  GGACAC
                                 G    ____ GT
GAM933  NSE1     3'  CACCGTCCACAGCTTTGG    59023         CA   TGCCT
                                TCAAAGCTG  GAT    GTG
                                |||||||||  |||    |||
                                GGTTTCGAC  CTG    CAC
                                     AC   C____
GAM933  TOLLIP   3'  TCACAAGTGATGCACTTT    38688      C    GA TG C
                                AAAG TGCA  T  C TGTGA
                                |||| ||||  |  | |||||
                                TTTC ACGT  A  G ACACT
                                  _   __ GT A
GAM933  LOC124976 3'  CGATCTGCAGCTTTGA     74378
                                TCAAAGCTGCAGATTG
                                ||||||||||||||||
                                AGTTTCGACGTCTAGC

GAM933  LOC130471 3'  CAGCACTGCAGCTCTGA    74939     A       AT   C
                                TCA AGCTGCAG  TGC TG
                                ||| ||||||||  ||| ||
                                AGT TCGACGTC  ACG AC
                                 C       __  _
GAM933  LOC146819 3'  TCACATTATTTTGCAGCTCTGA 78152     A        TTGCC
                                TCA AGCTGCAGA     TGTGA
                                ||| |||||||||     |||||
                                AGT TCGACGTTT     ACACT
                                 C        TATT_
GAM933  LOC146821 3'  TCACATTATTTTGCAGCTCTGA 78144     A        TTGCC
                                TCA AGCTGCAGA     TGTGA
                                ||| |||||||||     |||||
                                AGT TCGACGTTT     ACACT
                                 C        TATT_
GAM933  LOC149372 3'  TCAAAGGATCCTGCAGCTTT   79329          ATTG   G
                                AAAGCTGCAG    CCT TGA
                                ||||||||||    ||| |||
                                TTTCGACGTC    GGA ACT
                                      CTA_   A
GAM933  LOC149910 3'  CACGCCTCTCTGCAGCT     79530          TT_  CT
                                AGCTGCAGA   GC  GTG
                                |||||||||   ||  |||
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                                TCGACGTCT   CG  CAC
                                     CTC  __
GAM933   LOC165283 5'  TCAACCCTAATCTGCAGC    87194          CCTG
                                GCTGCAGATTG    TGA
                                ||||||||||    |||
                                CGACGTCTAAT    ACT
                                     CCCA
GAM933   LOC168667 3'  TCACCCTCGTATCTGCAGCCTG 92759     AA       _  CCT
           A                     TCA  GCTGCAGAT TG   GTGA
                                |||  |||||||| ||   ||||
                                AGT  CGACGTCTA GC   CACT
                                  C_        T  TCC
GAM933   LOC201324 3'  CACATCAGCTGCAGCT      68560         A   CC
                                AGCTGCAG TTG  TGTG
                                |||||||| |||  ||||
                                TCGACGTC GAC  ACAC
                                     _   T_
GAM933   LOC219818 3'  CAGTCTTATTACAGCTTTGA   90886         C____
                                TCAAAGCTG     AGATTG
                                |||||||||     ||||||
                                AGTTTCGAC     TCTGAC
                                     ATTAT
GAM933   LOC220980 3'  CACATACTGCAGTTTGA     93147       G     ATTGCC
                                TCAAA CTGCAG     TGTG
                                ||||| ||||||     ||||
                                AGTTT GACGTC     ACAC
                                   _     AT____
GAM933   LOC221583 3'  CACAGATTTGCAGGCTT     92142       _      TGC
                                AAGC TGCAGAT   CTGTG
                                |||| |||||||   |||||
                                TTCG ACGTTTA   GACAC
                                  G      ___
GAM933   LOC254962 3'  TCACAGGCAATCTTGCTTCT   96616     CT   _
                                AG  GCA GATTGCCTGTGA
                                ||  ||| ||||||||||||
                                TC  CGT CTAACGGACACT
                                 TT   T
GAM933   LOC255299 5'  CAGCAACCTGGAGCTTTGA    97466         G   A    C
                                TCAAAGCT CAG TTGC TG
                                |||||||| ||| |||| ||
                                AGTTTCGA GTC AACG AC
                                     G   C   _
GAM933   LOC256940 3'  CACAGGTTTTCTGCAGT      96491         TT
                                GCTGCAGA  GCCTGTG
                                ||||||||  |||||||
                                TGACGTCT  TGGACAC
                                     TT
GAM933   LOC51075  3'  CACAAGCCTGAGGTGCAGCTTT 31988          GA  __  C
                                AAAGCTGCA  TT  GC TGTG
                                |||||||||  ||  || ||||
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                                TTTCGACGT  AG  CG ACAC
                                     GG  TC  A
GAM934  ADCY7    3'  ACTGTGCTGTGCTCAGAT    6635            __
                                ATCTGGGCACAGT  GGT
                                ||||||||||||  |||
                                TAGACTCGTGTCG  TCA
                                      TG
GAM934  APM1     3'  GCATGAGCCACCATGCCCAGTC 16593    AT     CA
           GA                    TC  CTGGGCA  GTGGTTCATGC
                                 ||  |||||||  ||||||||||
                                 AG  GACCCGT  CACCGAGTACG
                                  CT      AC
GAM934  ASTN     3'  CATGAACCACTGTAATAG    69331    GGC
                                 CTG   ACAGTGGTTCATG
                                 |||   ||||||||||||
                                 GAT   TGTCACCAAGTAC
                                   AA_
GAM934  C7       3'  CATGAACCACCACGCCTGGCTG 5156     T TG   ACA
           G                     TCA C  GGC   GTGGTTCATG
                                 ||| |  |||   ||||||||||
                                 GGT G  CCG   CACCAAGTAC
                                   C GT   CAC
GAM934  CDH17    3'  GCATGAACCACTGCACCCA   14504     CA
                                 TGGG  CAGTGGTTCATGC
                                 ||||  ||||||||||||
                                 ACCC  GTCACCAAGTACG
                                   AC
GAM934  COX15    3'  GCATGGACATCTACCCAGAT   54313       CAC  TG
                                 ATCTGGG   AG  GTTCATGC
                                 |||||||   ||  ||||||||
                                 TAGACCC   TC  CAGGTACG
                                     A__   TA
GAM934  F3       3'  GCGTGAACCACCATGCCCAGCC 67080    AT     CA
           GA                    TC  CTGGGCA  GTGGTTCATGC
                                 ||  |||||||  ||||||||||
                                 AG  GACCCGT  CACCAAGTGCG
                                  CC      AC
GAM934  GM2A     3'  GCATGAGCCACTACACCCAGCC 67778    AT    CAC
           GA                    TC  CTGGG   AGTGGTTCATGC
                                 ||  |||||   ||||||||||||
                                 AG  GACCC   TCACCGAGTACG
                                  CC    ACA
GAM934  GNAI1    5'  GCCACTGTACCCAGAGA     9053     A     C
                                 TC TCTGGG ACAGTGGT
                                 || |||||| ||||||||
                                 AG AGACCC TGTCACCG
                                  _     A
GAM934  PCDHB13  3'  GCAGATGCCTGTGCCCA     38427        GT   TCA
                                 TGGGCACA  GGT   TGC
                                 ||||||||  |||   |||
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                                ACCCGTGT  CCG   ACG
                                     __  TAG
GAM934  SCNN1G   3' GCACAAGCCACCGTGCCCAG  6432        A     CA
                                CTGGGCAC GTGGTT  TGC
                                |||||||| ||||||  |||
                                GACCCGTG CACCGA  ACG
                                     C     AC
GAM934  SEDL     3' GCATGAACCACCGTGCCCGG  27336       A
                                CTGGGCAC GTGGTTCATGC
                                |||||||| ||||||||||
                                GGCCCGTG CACCAAGTACG
                                     C
GAM934  SLC39A1  3' GTGTCCCATGCCCAGATGA   27053         CAG   TT
                                TCATCTGGGCA   TGG  CAT
                                ||||||||||   |||  |||
                                AGTAGACCCGT   ACC  GTG
                                       ___  CT
GAM934  TACC1    3' CATGAACCACTCCA       20794     GCAC
                                TGG    AGTGGTTCATG
                                |||    ||||||||||
                                ACC    TCACCAAGTAC
                                 ____
GAM934  TBXA2R   3' GCATGAACCACCACACCTGG   6491    TG  CACA
                                C  GG    GTGGTTCATGC
                                |  ||    ||||||||||
                                G  CC    CACCAAGTACG
                                 GT  ACAC
GAM934  ZNF133   5' GCATGAGCCACTGCGCCCAGCC 12837    AT     A
           GA                     TC  CTGGGC CAGTGGTTCATGC
                                ||  |||||| ||||||||||||
                                AG  GACCCG GTCACCGAGTACG
                                 CC     C
GAM934  ANKRD6   3' ACCTGCTGTGCCTAGA      30084           _
                                TCTGGGCACAGT GGT
                                |||||||||||| |||
                                AGATCCGTGTCG CCA
                                       T
GAM934  C20orf59 3' CACAAACCACTGTGGAGCCTGA 41990    T  ___       CA
                                TC GGGC   ACAGTGGTT  TG
                                || ||||   |||||||||  ||
                                AG TCCG   TGTCACCAA  AC
                                 _   AGG        AC
GAM934  CECR1    3' GCATGCACCACCATGCCCGGAT 33814         CA    T
                                ATCTGGGCA  GTGGT CATGC
                                |||||||||  ||||| |||||
                                TAGGCCCGT  CACCA GTACG
                                      AC    C
GAM934  CSL4     3' GCATGAACCACTGTGCTTGG  32112   TG
                                C  GGCACAGTGGTTCATGC
                                |  ||||||||||||||||
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                              G  TCGTGTCACCAAGTACG
                               GT
GAM934  FLJ10535  3'  GCATGAGCCACCACACCCAG  36239      CACA
                              CTGGG   GTGGTTCATGC
                              |||||   ||||||||||
                              GACCC   CACCGAGTACG
                                 ACAC
GAM934  FLJ12294  5'  GCCACTGCACTCCAGATGA   47014        CA_
                              TCATCTGGG  CAGTGGT
                              |||||||||  |||||||
                              AGTAGACCT  GTCACCG
                                   CAC
GAM934  FLJ13305  5'  GCATGAACCACTGTGCCTGG  90127   TG
                              C  GGCACAGTGGTTCATGC
                              |  ||||||||||||||||
                              G  CCGTGTCACCAAGTACG
                               GT
GAM934  FLJ20507  3'  GCATGAACCACCGTGCCTGG  60222   TG    A
                              C  GGCAC GTGGTTCATGC
                              |  ||||| ||||||||||
                              G  CCGTG CACCAAGTACG
                               GT    C
GAM934  FLJ20507  3'  GCATGCGCCACTATGCCCAGAT 35289        C     T
                              ATCTGGGCA AGTGGT CATGC
                              ||||||||| |||||| |||||
                              TAGACCCGT TCACCG GTACG
                                   A     C
GAM934  FLJ20507  3'  GCATGCGCCACTATGCCCAGAT 60224        C     T
                              ATCTGGGCA AGTGGT CATGC
                              ||||||||| |||||| |||||
                              TAGACCCGT TCACCG GTACG
                                   A     C
GAM934  FLJ20507  3'  GCATGAACCACCGTGCCTGG  35287   TG    A
                              C  GGCAC GTGGTTCATGC
                              |  ||||| ||||||||||
                              G  CCGTG CACCAAGTACG
                               GT    C
GAM934  HSMPP8    3'  GCATGAGCCACCGCACCCAG  93476      CACA
                              CTGGG   GTGGTTCATGC
                              |||||   ||||||||||
                              GACCC   CACCGAGTACG
                                 ACGC
GAM934  ICK       3'  GCATGAGCCACTGCACCCAG  29930      CA
                              CTGGG  CAGTGGTTCATGC
                              |||||  ||||||||||||
                              GACCC  GTCACCGAGTACG
                                 AC
GAM934  IL18BP    3'  AGTCACATGGCCAGATGA    19103        G  CA  GT
                              TCATCTGG CA  GTG  T
                              |||||||| ||  |||  |
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                                AGTAGACC GT  CAC  A
                                     G  A_   TG
GAM934  KIAA0599  3'  GCATGAGCCACCACACCCAG   77180      CACA
                                CTGGG    GTGGTTCATGC
                                |||||    ||||||||||
                                GACCC    CACCGAGTACG
                                   ACAC
GAM934  KIAA1349  5'  GCATGAGCCACTGTGCCCAGCT 70756     T
            GA                    TCA CTGGGCACAGTGGTTCATGC
                                ||| ||||||||||||||||||
                                AGT GACCCGTGTCACCGAGTACG
                                  C
GAM934  KIAA1364  3'  CCACTGTGCCCAGATGA     63589
                                TCATCTGGGCACAGTGG
                                ||||||||||||||||
                                AGTAGACCCGTGTCACC

GAM934  KIAA1671  3'  GCCACCATGCCCAGCTGA    65675     T      CA
                                TCA CTGGGCA  GTGGT
                                ||| |||||||  |||||
                                AGT GACCCGT  CACCG
                                  C      AC
GAM934  LGI3      3'  GCACACCATGTGCCCAAATGG  57744      C       G    TCA
                                TCAT TGGGCACA TGGT   TGC
                                |||| |||||||| ||||   |||
                                GGTA ACCCGTGT ACCA   ACG
                                  A       _    C__
GAM934  MAN1      3'  CATGAACTTGCACAGAT     26712       G   CAGT
                                ATCTG GCA    GGTTCATG
                                ||||| |||    ||||||||
                                TAGAC CGT    TCAAGTAC
                                   A  _____
GAM934  MGC21675  3'  GCATGAACCACTGTGCCCAGCC 53483    AT
            GA                    TC  CTGGGCACAGTGGTTCATGC
                                ||  ||||||||||||||||||
                                AG  GACCCGTGTCACCAAGTACG
                                 CC
GAM934  MGC3222   3'  CGCTGTATACCTAGATGA    44295         C__
                                TCATCTGGG   ACAGTG
                                |||||||||   ||||||
                                AGTAGATCC   TGTCGC
                                     ATA
GAM934  UBCE7IP5  3'  CACGGCGCTCCCAGATGA    30149         CAC    GT  A
                                TCATCTGGG   AGTG  TC TG
                                |||||||||   ||||  || ||
                                AGTAGACCC   TCGC  GG AC
                                     ____   __  C
GAM934  LOC142949 5'  CCACCGTGCCCAGCTGA     82893     T       A
                                TCA CTGGGCAC GTGG
                                ||| |||||||| ||||
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                                AGT GACCCGTG CACC
                                  C       C
GAM934   LOC145946 3'  CATACATGCCCAGCATGA    83568      _      CA_
                                TCAT CTGGGCA   GTG
                                |||| |||||||   |||
                                AGTA GACCCGT   TAC
                                  C       ACA
GAM934   LOC146784 5'  GCATGAGCCACCACGCCCAG   78115       ACA
                                CTGGGC   GTGGTTCATGC
                                ||||||   ||||||||||
                                GACCCG   CACCGAGTACG
                                   CAC
GAM934   LOC147160 5'  CACGTGTGCCCAGTCGA     83959    AT       _
                                TC  CTGGGCACA GTG
                                ||  ||||||||| |||
                                AG  GACCCGTGT CAC
                                 CT        G
GAM934   LOC150407 3'  CATAAGCCACTGTGCCCAG    79818             C
                                CTGGGCACAGTGGTT ATG
                                |||||||||||||| |||
                                GACCCGTGTCACCGA TAC
                                          A
GAM934   LOC153883 5'  GCATGAACCACTGCATCT    80981     CA
                                GGG  CAGTGGTTCATGC
                                |||  ||||||||||||
                                TCT  GTCACCAAGTACG
                                  AC
GAM934   LOC155046 3'  CATAAATGCCCAGATGA     81286          CA_
                                TCATCTGGGCA   GTG
                                ||||||||||   |||
                                AGTAGACCCGT   TAC
                                       AAA
GAM934   LOC157247 5'  GCATGAACCACCGTGCCCGG   81366        A
                                CTGGGCAC GTGGTTCATGC
                                |||||||| ||||||||||
                                GGCCCGTG CACCAAGTACG
                                     C
GAM934   LOC159089 5'  CACAAACCACTGTGTACA    86986    GG        CA
                                TG  CACAGTGGTT  TG
                                ||  ||||||||||  ||
                                AC  GTGTCACCAA  AC
                                 AT         AC
GAM934   LOC200473 5'  ATGAGCACCCAGAGA       90073    A     CACAGTG
                                TC TCTGGG      GTTCAT
                                || ||||||      ||||||
                                AG AGACCC      CGAGTA
                                 _     A_______
GAM934   LOC219918 5'  CAAGACCAAGCCCAGAT     91538        ACAG    CA
                                ATCTGGGC    TGGTT  TG
                                ||||||||    |||||  ||
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                                TAGACCCG   ACCAG  AC
                                   A___    A_
GAM934  LOC220575 3'  GCATGGGCCACCACACCCAGCT 76313    T    CACA
          GA                     TCA CTGGG   GTGGTTCATGC
                                 ||| |||||   ||||||||||
                                 AGT GACCC   CACCGGGTACG
                                   C    ACAC
GAM934  LOC221663 5'  GCATGAGCCACTGCACCCAGA  93814      CA
                                 TCTGGG  CAGTGGTTCATGC
                                 ||||||  ||||||||||||
                                 AGACCC  GTCACCGAGTACG
                                    AC
GAM934  LOC253842 5'  GCCACTGCACCCAGCCGA   97387   AT   CA
                                 TC  CTGGG  CAGTGGT
                                 ||  |||||  |||||||
                                 AG  GACCC  GTCACCG
                                  CC    AC
GAM934  LOC255991 3'  GCCACTGTGCCCAGCTGA   97249    T
                                 TCA CTGGGCACAGTGGT
                                 ||| ||||||||||||||
                                 AGT GACCCGTGTCACCG
                                   C
GAM935  AMFR    3'  GAGAGACAGCGCATGCTGGTGC 57244   A   G   __
          AG                     CT CACC AGCA  CGCTGTCTCTC
                                 || |||| ||||  ||||||||||
                                 GA GTGG TCGT  GCGACAGAGAG
                                  C   _   AC
GAM935  GAC1    5'  AGAAGTGACGCCCGGTGTAGA  20940        A  A_   G
                                 TCTACACCG GC  CGCT TCT
                                 |||||||||  ||  |||| |||
                                 AGATGTGGC CG  GTGA AGA
                                      C  CA   _
GAM935  IL18RAP  5'  AGAGACAGCTGAAGGTGTAG   13901       GAG  C
                                 CTACACC   CA GCTGTCTCT
                                 |||||||   || |||||||||
                                 GATGTGG   GT CGACAGAGA
                                    AA_  _
GAM935  KRT10   3'  AGAGGTGGCGCCCGACGGTAGA 4705      AC_  A  AC  TG
                                 TCTAC   CG GC  GC  TCTCT
                                 |||||   || ||  ||  |||||
                                 AGATG   GC CG  CG  GGAGA
                                    GCA  C  __  GT
GAM935  XK      3'  GAGACAGCCCAGTGTAGA    40799       CGAGCAC
                                 TCTACAC      GCTGTCTC
                                 |||||||      ||||||||
                                 AGATGTG      CGACAGAG
                                    ACC____
GAM935  AD-020   3'  GAGAGGCATAGTGCTC     39309       GC
                                 GAGCAC  TGTCTCTC
                                 ||||||  ||||||||
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                                CTCGTG  ACGGAGAG
                                   AT
GAM935  AD-020   3'  GAGAGGCATAGTGCTC     59385       GC
                                GAGCAC  TGTCTCTC
                                ||||||  ||||||||
                                CTCGTG  ACGGAGAG
                                   AT
GAM935  ARL8     3'  GAAATTGGCATCAGTGTAGA  93196       C  _  A  CTG
                                TCTACAC GA GC CG   TC
                                ||||||| || || ||   ||
                                AGATGTG CT CG GT   AG
                                    A  A  _  TAA
GAM935  DKFZp434D177 3'  GAGAGACAACGAGTGGCGCTG  79441    C  A_  A  C
                                CA CG  GC CG TGTCTCTC
                                || ||  || || ||||||||
                                GT GC  TG GC ACAGAGAG
                                 C  GG  A  A
GAM935  FLJ20125  3'  GAGAGACAACACTGGGGTTAGA 34589     CA  G  CACGC
                                TCTA  CC AG    TGTCTCTC
                                ||||  || ||    ||||||||
                                AGAT  GG TC    ACAGAGAG
                                  TG  G  ACA__
GAM935  KIAA0285  3'  GAGAGGTGGGCACCCGGTGCCG 29017    TA    A__  A   G
          A                      TC  CACCG   GC CGCT TCTC
                                ||  |||||   || |||| ||||
                                AG  GTGGC   CG GTGG AGAG
                                 CC    CCA  G   _
GAM935  KIAA0705  3'  AGAGACAGTGCAGTGTAG    24532       CGA  AC
                                CTACAC   GC  GCTGTCTCT
                                ||||||   ||  |||||||||
                                GATGTG   CG  TGACAGAGA
                                   A__  __
GAM935  KIAA1297  3'  AGCGCTCACGCTCGGTGCAGG  72165     A       A____
                                TCT CACCGAGC     CGCT
                                ||| ||||||||     ||||
                                GGA GTGGCTCG     GCGA
                                  C       CACTC
GAM935  KPNB3    3'  AGAACAGTTACTCAGCGTAGA  9633       ACC   CAC    C
                                TCTAC   GAG   GCTGT TCT
                                |||||   |||   ||||| |||
                                AGATG   CTC   TGACA AGA
                                   CGA   AT_    _
GAM935  MGC4607   3'  AGAGGCGCCCGGTGCAGA    48739     A    A  ACGCT
                                TCT CACCG GC     GTCTCT
                                ||| ||||| ||     ||||||
                                AGA GTGGC CG     CGGAGA
                                  C    C  _____
GAM935  MKRN1    3'  GAGAGGCATAACATCAATGCAG 25574     A  CC  GCACGC
          A                      TCT CA  GA     TGTCTCTC
                                ||| ||  ||     ||||||||
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                                AGA GT  CT     ACGGAGAG
                                  C  AA  ACAAT_
GAM935  PLEKHA4   5' GAGAGACAGCAGCTAAGAGA  40498    ACACCG   AC
                                TCT     AGC  GCTGTCTCTC
                                |||     |||  ||||||||||
                                AGA     TCG  CGACAGAGAG
                                  GAA___   A_
GAM935  PRO0899   3' GAGAGACAACTCAGGAACAGA  37696    ACA  _   CACGC
                                TCT   CC GAG    TGTCTCTC
                                |||   || |||    ||||||||
                                AGA   GG CTC    ACAGAGAG
                                  CAA  A   A____
GAM935  LOC119151 5' GAGAAACAGCCCCGGTGTGGA  73961         AGCAC    C
                                TCTACACCG    GCTGT TCTC
                                |||||||||    ||||| ||||
                                AGGTGTGGC    CGACA AGAG
                                      CC___    A
GAM935  LOC119188 5' GAGAAACAGCCCGGGTGTGGA  73962        GAGCAC    C
                                TCTACACC     GCTGT TCTC
                                ||||||||     ||||| ||||
                                AGGTGTGG     CGACA AGAG
                                     GCC___    A
GAM935  LOC143107 5' GAGAAACAGCCCGGGTGTGGA  76459        GAGCAC    C
                                TCTACACC     GCTGT TCTC
                                ||||||||     ||||| ||||
                                AGGTGTGG     CGACA AGAG
                                     GCC___    A
GAM935  LOC147495 3' GAGACACAGGTGTAGA      84014        GAGCACGC
                                TCTACACC       TGTCTC
                                ||||||||       ||||||
                                AGATGTGG       ACAGAG
                                     AC_______
GAM935  LOC148710 3' GAGAGAGGCTCAGGCAGA    84194     ACA  _   ACG  G
                                TCT   CC GAGC   CT TCTC
                                |||   || ||||   || ||||
                                AGA   GG CTCG   GA AGAG
                                  C__  A    ___  G
GAM935  LOC196746 3' AGACAGTGCTCAGTG       87511     C    AC
                                CAC GAGC  GCTGTCT
                                ||| ||||  |||||||
                                GTG CTCG  TGACAGA
                                  A   __
GAM935  LOC257017 5' AGAGACAGCGTGACGATG    97372    C  AG
                                CA CG  CACGCTGTCTCT
                                || ||  ||||||||||||
                                GT GC  GTGCGACAGAGA
                                 A  A_
GAM935  LOC257441 3' GAGAGACAACGAGTGGCGCTG  95564    C  A_  A  C
                                CA CG  GC CG TGTCTCTC
                                || ||  || || ||||||||
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                                GT GC  TG GC ACAGAGAG
                                 C  GG  A  A
GAM935  LOC57146  5'  AGAGACAGAGCGACATGAGA   39910     A  CCGA  ACG
                                TCT CA    GC   CTGTCTCT
                                ||| ||    ||   ||||||||
                                AGA GT    CG   GACAGAGA
                                  _  ACAG  A__
GAM935  LOC90589  3'  GAGAGACACACCTCCAGTAAGA 59104     _  ACC   CACGC
                                TCT AC   GAG    TGTCTCTC
                                ||| ||   |||    ||||||||
                                AGA TG   CTC    ACAGAGAG
                                  A  AC_   CAC__
GAM936  ARNT2     3'  AAACAACCCGTGCATCCCTGC  29450     A    TTTTA
                                GTA GGAT    GGGTTGTTT
                                ||| ||||    |||||||||
                                CGT CCTA    CCCAACAAA
                                  C   CGTG_
GAM936  LCT       3'  AACCGTAAAAATCCTT      9697           G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
                                TTCCTAAAAAT CCAA
                                       G
GAM936  RPL15     3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM936  FBXO30    3'  AACTAAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                 G        AA
GAM936  KIAA0494  3'  AACAACCCTTACTTAC      28736       GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM936  PRO0641   5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                   ___    C
GAM936  SMT3H2    3'  AACAACATAAAAATCCTTGC   22670           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM936  LOC120103 3'  AACCTATGAAAAATCCTTGC   74002           A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
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                                CGTTCCTAAAAA  TCCAA
                                      GTA
GAM936  LOC129831 3'  AAACAACCCCAATGTCC     74889      TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM936  LOC133088 5'  AAACAAAATAGAAAAATCCCTG 75075     A       AGGG_
          C                      GTA GGATTTTT    TTGTTT
                                ||| ||||||||    ||||||
                                CGT CCTAAAAA    AACAAA
                                  C       GATAA
GAM936  LOC148089 3'  GGCCCTAAAAATTCCTAC    78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM936  LOC154547 3'  AACAACATAAAAATCCTTGC   76050           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM936  LOC158104 3'  ACAGCCAAAAATCCTTA     60313          AG
                                TAAGGATTTTT  GGTTGT
                                ||||||||||  ||||||
                                ATTCCTAAAAA  CCGACA
                                      __
GAM936  LOC205880 5'  AAACAACCATCATCCTGAC   90709    A    TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM936  LOC221561 3'  AACAACATAAAAATCCTTGC   92130           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM936  LOC257591 3'  AACAACATAAAAATCCTTGC   97840           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM936  LOC51145  3'  AGCTAAAATCCTTAC       32393          TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
                                CATTCCTAAAA   TCGA
                                      ___
GAM937  BACE     3'  CAGGGCATAAAACTCA      23976       CGCC
                                TGGGT    TTATGCCCTG
                                |||||    ||||||||||
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                                ACTCA   AATACGGGAC
                                  A___
GAM937  BACE    3'  CAGGGCATAAAACTCA     57286      CGCC
                                TGGGT   TTATGCCCTG
                                |||||   ||||||||||
                                ACTCA   AATACGGGAC
                                  A___
GAM937  BCAT2   3'  CCAAAGCCGTAAGGGCCGACCC 6814          __     _ CC
            AGGCA                 TGCCTGGGTCG  CCTTATG C  TGG
                                ||||||||||  ||||||| |  |||
                                ACGGACCCAGC  GGAATGC G  ACC
                                      CG      C AA
GAM937  CYR61   3'  AGGGCACACCTAGACA     7767    C     CGCCTTA
                                TG CTGGGT      TGCCCT
                                || ||||||      ||||||
                                AC GATCCA      ACGGGA
                                 A     C_______
GAM937  DDX11   3'  CCAGAGCGCTGCCAGGACCCAG 47650         ___  CTTA   C
            GCA                   TGCCTGGGTC   GC    TGC CTGG
                                ||||||||||   ||    ||| ||||
                                ACGGACCCAG   CG    GCG GACC
                                      GAC  TC__   A
GAM937  GAB2    3'  CAAGCTGGGCGACCAAGCA   54445    CTG      TAT  CC
                                TGC   GGTCGCCT   GC  TG
                                |||   ||||||||   ||  ||
                                ACG   CCAGCGGG   CG  AC
                                  AA_       T__  A_
GAM937  GAB2    3'  CAAGCTGGGCGACCAAGCA   24488    CTG      TAT  CC
                                TGC   GGTCGCCT   GC  TG
                                |||   ||||||||   ||  ||
                                ACG   CCAGCGGG   CG  AC
                                  AA_       T__  A_
GAM937  LYPLA1  3'  TATAAGACGACCCAGG     20925        C
                                CCTGGGTCG CTTATG
                                ||||||||| ||||||
                                GGACCCAGC GAATAT
                                      A
GAM937  NR2E3   5'  CCAGGCTCAGCAACCCAGGC   32970        C  CTTAT   C
                                GCCTGGGT GC    GCC TGG
                                |||||||| ||    ||| |||
                                CGGACCCA CG    CGG ACC
                                     A  ACT__   _
GAM937  CHRAC1  3'  AGGGAAAGCGACCCAGACA   33865    C       CTTATG
                                TG CTGGGTCGC     CCCT
                                || |||||||||     ||||
                                AC GACCCAGCG     GGGA
                                 A       AAA___
GAM937  DDX12   3'  CCAGAGCGCTGCCGGGACCCAG 59694         G  TTA__   C
            GCA                   TGCCTGGGTC CC    TGC CTGG
                                ||||||||||  ||    ||| ||||
```

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                                ACGGACCCAG GG    GCG GACC
                                      _ CCGTC   A
GAM937  DGKD     3'  CAGAACAAGCCCCAGGCA    59398        TC  CTTA  CC
                                TGCCTGGG  GC   TG  CTG
                                ||||||||  ||   ||  |||
                                ACGGACCC  CG   AC  GAC
                                    __  A___  AA
GAM937  DKFZP564K0822 3'  CCAGGCCGAGCATCCCAGGCA  94044        TC  CTTA  C
                                TGCCTGGG  GC   TG CCTGG
                                ||||||||  ||   || |||||
                                ACGGACCC  CG   GC GGACC
                                     TA  A___  C
GAM937  KIAA1077  3'  CCAAGGCATAAGGTTGGG    72904     GGTC        C
                                CCTG   GCCTTATGCC TGG
                                ||||   |||||||||| |||
                                GGGT   TGGAATACGG ACC
                                  _____        A
GAM937  LANCL2    3'  CAGAACATTTACCCAGGTA    37994        CGCCTT   CC
                                TGCCTGGGT    ATG  CTG
                                |||||||||    |||  |||
                                ATGGACCCA    TAC  GAC
                                     TT_____  AA
GAM937  NR6A1     3'  CCAGGACACAAAGCCCAAGGC  52868     _   CGCC  A  C
                                GCCT GGGT   TT TG CCTGG
                                |||| ||||   || || |||||
                                CGGA CCCG   AA AC GGACC
                                  A   A___  C  A
GAM937  NR6A1     3'  CCAGGACACAAAGCCCAAGGC  52880     _   CGCC  A  C
                                GCCT GGGT   TT TG CCTGG
                                |||| ||||   || || |||||
                                CGGA CCCG   AA AC GGACC
                                  A   A___  C  A
GAM937  NR6A1     3'  CCAGGACACAAAGCCCAAGGC  7643      _   CGCC  A  C
                                GCCT GGGT   TT TG CCTGG
                                |||| ||||   || || |||||
                                CGGA CCCG   AA AC GGACC
                                  A   A___  C  A
GAM937  ZNF183    5'  AAGTGCAACCCAGGCA      22729         C  _
                                TGCCTGGGT GC CTT
                                ||||||||| || |||
                                ACGGACCCA CG GAA
                                     A  T
GAM937  LOC219920 5'  CAGGGCAGGACCCTGGCA    93305      T    GCCTTA
                                TGCC GGGTC    TGCCCTG
                                |||| |||||    |||||||
                                ACGG CCCAG    ACGGGAC
                                  T    G_____
GAM937  LOC220370 3'  CCAGGGCAAGCAACCCAAGCA  92826     C    C  CTTA
                                TGC TGGGT GC   TGCCCTGG
                                ||| ||||| ||   ||||||||
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                              ACG ACCCA CG    ACGGGACC
                                A    A  A___
GAM937  LOC220595 5'  CCAGGAAGAAGGCAAGCCCAGG 91141        C_    ATGC
          CA                   TGCCTGGGT  GCCTT   CCTGG
                              |||||||||  |||||   |||||
                              ACGGACCCG  CGGAA   GGACC
                                   AA    GAA_
GAM937  LOC257355 3'  CCAGGGCACCTGCAACCCTAGC 94404    CT   C  CTTA
          A                    TGC  GGGT GC   TGCCCTGG
                              |||  |||| ||   ||||||||
                              ACG  CCCA CG   ACGGGACC
                                AT    A  TCC_
GAM937  LOC51172  3'  CCAGGGCACCTGCAACCCTAGC 63346    CT   C  CTTA
          A                    TGC  GGGT GC   TGCCCTGG
                              |||  |||| ||   ||||||||
                              ACG  CCCA CG   ACGGGACC
                                AT    A  TCC_
GAM938  ABCA3    3'  GGGCAGGCCGGGCA      6563       GGTC   TAT
                              TGCCTG   GCCT   GCCC
                              ||||||   ||||   ||||
                              ACGGGC   CGGA   CGGG
                                  ____   ____
GAM938  ABCB6    3'  GGGTATGGTGCTAGC     19098    C   GT   TT
                              GC TGG  CGCC  ATGCCC
                              || |||  ||||  ||||||
                              CG ATC  GTGG  TATGGG
                                _  __   __
GAM938  ADAM12   3'  TATGAGATGTGGCTTGGGCA   12972     TG    __
                              TGCC  GGTCGC  CTTATG
                              ||||  ||||||  ||||||
                              ACGG  TCGGTG  GAGTAT
                                GT     TA
GAM938  ADAM19   3'  CGGGGCATGGCCATTGGGG   52705    G   C   TT
                              CCT GGT GCC  ATGCCCTG
                              ||| ||| |||  ||||||||
                              GGG TTA CGG  TACGGGGC
                                G   C  __
GAM938  ADAMTS4  5'  CTAGGGTGTGGAGGACTTGG   17506   TG   G_  TT
                              C  GGTC  CC  ATGCCCTGG
                              |  ||||  ||  |||||||||
                              G  TCAG  GG  TGTGGGATC
                               GT   GA  __
GAM938  ADAMTS9  3'  TCAGGGCACTTTGGGCTTGGC  39671    TGGGTC   TA__
                              GCC    GCCT   TGCCCTGG
                              |||    ||||   ||||||||
                              CGG    CGGG   ACGGGACT
                                TT____   TTTC
GAM938  ADAR     3'  CTAGGGTGTGAGAGAGGTAGGT 31748     GG  GC
                              GCCTG  TC  CTTATGCCCTGG
                              |||||  ||  ||||||||||||
```

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                              TGGAT  AG  GAGTGTGGGATC
                                GG  A_
GAM938  ADAR    3'  TTAGGGTGTGTCATACTAGG  31753     GTCGCCT
                              CCTGG     TATGCCCTGG
                              |||||     ||||||||||
                              GGATC     GTGTGGGATT
                                ATACT__
GAM938  ADAR    3'  CTAGGGTGTGAGAGAGGTAGGT 31758     GG  GC
                              GCCTG  TC  CTTATGCCCTGG
                              |||||  ||  ||||||||||||
                              TGGAT  AG  GAGTGTGGGATC
                                GG  A_
GAM938  ADAR    3'  TTAGGGTGTGTCATACTAGG  31763     GTCGCCT
                              CCTGG     TATGCCCTGG
                              |||||     ||||||||||
                              GGATC     GTGTGGGATT
                                ATACT__
GAM938  ADAR    3'  CTAGGGTGTGAGAGAGGTAGGT 6623      GG  GC
                              GCCTG  TC  CTTATGCCCTGG
                              |||||  ||  ||||||||||||
                              TGGAT  AG  GAGTGTGGGATC
                                GG  A_
GAM938  ADAR    3'  TTAGGGTGTGTCATACTAGG  6628      GTCGCCT
                              CCTGG     TATGCCCTGG
                              |||||     ||||||||||
                              GGATC     GTGTGGGATT
                                ATACT__
GAM938  ADAT1   3'  CCAGGCTTGGTGGCTCAGGC  23897         TTAT  C
                              GCCTGGGTCGCC   GCC TGG
                              ||||||||||||   ||| |||
                              CGGACTCGGTGG   CGG ACC
                                    TT__  _
GAM938  ADCY8   5'  CCGGGGGCGTGGCTTGGCGC  6651    _ TG    CTTATG
                              GC C  GGTCGC    CCCTGG
                              || |  ||||||    ||||||
                              CG G  TCGGTG    GGGGCC
                               C GT    CG____
GAM938  ADRA1A  3'  CCAGGTAGCTGGAGACCTAGGC 52792        G  TTA   C
          A                    TGCCTGGGTC CC   TGCC TGG
                              ||||||||| ||   |||| |||
                              ACGGATCCAG GG   ATGG ACC
                                   A  TCG   _
GAM938  AGRN    3'  CCAGGGCCGATCTGGGT    78834    TG    CCTTAT
                              GCC  GGTCG    GCCCTGG
                              |||  |||||    |||||||
                              TGG  CTAGC    CGGGACC
                               GT    _______
GAM938  ALPL    3'  CCAGGAAGCCGGTGCCTGGGT  4892    TG  T   TTAT __
                              GCC  GG CGCC   GC  CCTGG
                              |||  || ||||   ||  |||||
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                                TGG  CC GTGG   CG  GGACC
                                  GT  _   C___  AA
GAM938  ALPPL2   3'  CCATATCCTGAGGTGGATCAGG 68838       GT     TGCCC
           CA                     TGCCTGG  CGCCTTA    TGG
                                  |||||||  |||||||    |||
                                  ACGGACT  GTGGAGT    ACC
                                     AG      CCTAT
GAM938  ANK1     5'  CTGGGCAGAAGGGCACTTGGGC 40031    TG  C    A_    TGG
                                  GCC  GGT GCCTT  TGCCC
                                  |||  ||| |||||  |||||
                                  CGG  TCA CGGGA  ACGGG
                                    GT  _    AG    TC
GAM938  ANK1     5'  CTGGGCAGAAGGGCACTTGGGC 40034    TG  C    A_    TGG
                                  GCC  GGT GCCTT  TGCCC
                                  |||  ||| |||||  |||||
                                  CGG  TCA CGGGA  ACGGG
                                    GT  _    AG    TC
GAM938  ANK1     5'  CTGGGCAGAAGGGCACTTGGGC 40037    TG  C    A_    TGG
                                  GCC  GGT GCCTT  TGCCC
                                  |||  ||| |||||  |||||
                                  CGG  TCA CGGGA  ACGGG
                                    GT  _    AG    TC
GAM938  ANKRD3   3'  TGGGGTGTGGCCCCAGG     40200      TC  TT    TG
                                  CCTGGG  GCC  ATGCCC  G
                                  ||||||  |||  ||||||  |
                                  GGACCC  CGG  TGTGGG  T
                                     __   __     GT
GAM938  ANKRD3   3'  CCAGGTGAAGCTGGCTCAGGT  40197        C  ATGC
                                  GCCTGGGTCG CTT   CCTGG
                                  ||||||||||| |||   |||||
                                  TGGACTCGGT GAA   GGACC
                                        C  GT__
GAM938  AOC3     3'  CCAGGGTGTGAGGGATGGGGAG 13585    _ GG  G
           CA                     TGC CT  GTC CCTTATGCCCTGG
                                  |||  ||  |||  ||||||||||||
                                  ACG GG  TAG GGAGTGTGGGACC
                                    A  GG  _
GAM938  APBA1    3'  GGCAGGTGGCCAGGCA      69919        G     TAT
                                  TGCCTGG TCGCCT   GCC
                                  |||||||  ||||||   |||
                                  ACGGACC GGTGGA   CGG
                                     _     ____
GAM938  AQP3     3'  CCAGGGTGTGTATGTTTCAGG  59590       T  CCT
                                  CCTGGG CG   TATGCCCTGG
                                  ||||||  ||   ||||||||||
                                  GGACTT GT   GTGTGGGACC
                                     T  AT_
GAM938  ARSA     3'  TGTGGGGGAGGCTCAGGT    4914         G_
                                  GCCTGGGTC  CCTTATG
                                  |||||||||  |||||||
```

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                              TGGACTCGG  GGGGTGT
                                   AG
GAM938  ARVCF    3'  GGGCAGGGCCCAGG       8028        CG   TAT
                              CCTGGGT  CCT   GCCC
                              |||||||  |||   ||||
                              GGACCCG  GGA   CGGG
                                       __   ____
GAM938  ATP5B    5'  CTGGTTTTGGAGGTGGCCCAGC 59661     C        AT__  CTGG
          A                    TGC TGGGTCGCCTT    GCC
                              ||| ||||||||||    |||
                              ACG ACCCGGTGGAG    TGG
                                _        GTTT   TC
GAM938  ATP8B2   3'  CCGGCTGTGGGGTGGTTTGGG  65218    TG GT      _  CTGG
                              CC  G  CGCCTTAT GCC
                              ||  |  |||||||| |||
                              GG  T  GTGGGGTG CGG
                               GT TG       T   CC
GAM938  ATSV     3'  TCAGGGCGACGGTCTAGGT    15059       GT  CCTTA
                              GCCTGG  CG    TGCCCTGG
                              ||||||  ||    ||||||||
                              TGGATC  GC    GCGGGACT
                                 TG  A____
GAM938  B3GAT1   5'  CAGGGCAGCGGTCTAGG     37826       GT   CTTA
                              CCTGG  CGC    TGCCCTG
                              |||||  |||   |||||||
                              GGATC  GCG    ACGGGAC
                                 TG  ____
GAM938  B3GAT1   3'  CTGGGGTGAGGGTGGCACCCAG 37831         __     A    TG
          GCA                    GCCTGGGT  CGCCTT TGCCC  G
                              ||||||||  |||||| |||||  |
                              CGGACCCA  GTGGGA GTGGG  C
                                   CG     _    GT
GAM938  B3GAT1   5'  CAGGGCAGCGGTCTAGG     53971       GT   CTTA
                              CCTGG  CGC    TGCCCTG
                              |||||  |||   |||||||
                              GGATC  GCG    ACGGGAC
                                 TG  ____
GAM938  B3GAT1   3'  CTGGGGTGAGGGTGGCACCCAG 53975         __     A    TG
          GCA                    GCCTGGGT  CGCCTT TGCCC  G
                              ||||||||  |||||| |||||  |
                              CGGACCCA  GTGGGA GTGGG  C
                                   CG     _    GT
GAM938  B4GALT7  3'  CGGGGTGTGTCCTGTCCGGG   23413       T  CCT      TG
                              CCTGGG CG   TATGCCC  G
                              ||||||  ||  |||||||  |
                              GGGCCT GT   GTGTGGG  C
                                 _ CCT      GT
GAM938  BACH1    3'  TCAGGGTGTAGGGGGAGG    6802     TGGG  G
                              CC   TC CCTTATGCCCTGG
                              ||   || ||||||||||||
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                                GG   AG GGGATGTGGGACT
                                 ____ G
GAM938  BAK1    5'  CGGGGCAAGGCCCAGGT    91989        GCCTTA
                                GCCTGGGTC    TGCCCTG
                                |||||||||    |||||||
                                TGGACCCGG    ACGGGGC
                                     A_____
GAM938  BAK1    3'  CTGGGGTGTGGGGATTGGTGGG 91991     GGGTCG       TG
              T                  GCCT    CCTTATGCCC  G
                                 ||||    ||||||||||  |
                                 TGGG    GGGGTGTGGG  C
                                   TGGTTA       GT
GAM938  BCAT2   3'  AGGGCCGACCCAGGCA     6813         CCTTAT
                                TGCCTGGGTCG    GCCCT
                                ||||||||||    |||||
                                ACGGACCCAGC    CGGGA
                                      _______
GAM938  BCL11B  3'  GCATGGGTGACCCAGCCG    43192    C        T
                                TG CTGGGTCGCCT ATGC
                                || |||||||||| ||||
                                GC GACCCAGTGGG TACG
                                 C        _
GAM938  BCL7A   3'  TGGGGCGTTTAGGACTGGGC   40645    TG GTCG   T_    TG
                                GCC  G   CCT  ATGCCC  G
                                |||  |   |||  ||||||  |
                                CGG  C   GGA  TGCGGG  T
                                  GT A___   TT     GT
GAM938  BCR     3'  AAGGACAGGTGGCCTGGGCA  41204     TG      TAT C   GG
                                TGCC  GGTCGCCT   G CCT
                                ||||  ||||||||   | |||
                                ACGG  CCGGTGGA   C GGA
                                  GT       ___ A   AG
GAM938  BCR     3'  AAGGACAGGTGGCCTGGGCA  15073     TG      TAT C   GG
                                TGCC  GGTCGCCT   G CCT
                                ||||  ||||||||   | |||
                                ACGG  CCGGTGGA   C GGA
                                  GT       ___ A   AG
GAM938  BLTR2   5'  GGGCAGGGCCTGAGGCA    39044     G  TC   TA
                                TGCCT GG  GCCT  TGCCC
                                ||||| ||  ||||  |||||
                                ACGGA TC  CGGG  ACGGG
                                  G __   __
GAM938  BMPR1B  3'  CAGGGAGCGACCTGGGCA    6833     TG     CTTATG
                                TGCC  GGTCGC    CCCTG
                                ||||  ||||||    |||||
                                ACGG  CCAGCG    GGGAC
                                  GT     A_____
GAM938  BNC     3'  TGGGGCGAGTCAGGCA     8161        G
                                TGCCTGG TCGCCTTA
                                ||||||| ||||||||
```

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                                ACGGACT AGCGGGGT
                                    G
GAM938  BSN      5'  CCGGGAGCCGCCGGCCCGGGC  12918          CCTTAT  _
                                GCCTGGGTCG     GC CCTGG
                                ||||||||||     || |||||
                                CGGGCCCGGC     CG GGGCC
                                    CGC___  A
GAM938  BTEB1    5'  GCGTCGGGGTGATCGGGT    6847        G      _
                                GCCTGG TCGCCTT ATGC
                                |||||| ||||||| ||||
                                TGGGCT AGTGGGG TGCG
                                   _      C
GAM938  BZRP     3'  CAGGGCCTTGGCCCAGG     5548          CCTTAT
                                CCTGGGTCG     GCCCTG
                                |||||||||     ||||||
                                GGACCCGGT     CGGGAC
                                    TC_____
GAM938  BZRP     3'  CAGGGCCTTGGCCCAGG     23604         CCTTAT
                                CCTGGGTCG     GCCCTG
                                |||||||||     ||||||
                                GGACCCGGT     CGGGAC
                                    TC_____
GAM938  C10orf2  3'  GGCGAAGGGGACCCAGGCA   41545          G    A
                                TGCCTGGGTC CCTT TGCC
                                |||||||||| |||| ||||
                                ACGGACCCAG GGAA GCGG
                                    G   _
GAM938  CACNG6   3'  CTGGGGTGTGGGGTTGGGG   49101     G GTC         TG
                                CCT G   GCCTTATGCCC  G
                                ||| |   ||||||||||| |
                                GGG T   TGGGGTGTGGG  C
                                  G ___         GT
GAM938  CAPN10   3'  CCAGGGGGCTGCGGCCTAGG   43591          CTTATG
                                CCTGGGTCGC     CCCTGG
                                ||||||||||     ||||||
                                GGATCCGGCG     GGGACC
                                    TCGG__
GAM938  CAPN10   3'  CCAGGGGGCTGCGGCCTAGG   43592          CTTATG
                                CCTGGGTCGC     CCCTGG
                                ||||||||||     ||||||
                                GGATCCGGCG     GGGACC
                                    TCGG__
GAM938  CAPN10   3'  CCAGGGGGCTGCGGCCTAGG   43593          CTTATG
                                CCTGGGTCGC     CCCTGG
                                ||||||||||     ||||||
                                GGATCCGGCG     GGGACC
                                    TCGG__
GAM938  CAPN10   3'  CCAGGGGGCTGCGGCCTAGG   43594          CTTATG
                                CCTGGGTCGC     CCCTGG
                                ||||||||||     ||||||
```

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                                GGATCCGGCG     GGGACC
                                     TCGG__
GAM938  CAPN10   3'  CCAGGGGGCTGCGGCCTAGG  43599         CTTATG
                                CCTGGGTCGC     CCCTGG
                                ||||||||||     ||||||
                                GGATCCGGCG     GGGACC
                                     TCGG__
GAM938  CAPN10   3'  CCAGGGGGCTGCGGCCTAGG  41165         CTTATG
                                CCTGGGTCGC     CCCTGG
                                ||||||||||     ||||||
                                GGATCCGGCG     GGGACC
                                     TCGG__
GAM938  CAPN7    5'  GCTGGGGCCGCGAAGTGGGGCG 26662   G       _______   TG
           GCCGGGT                  TCGCCTTAT     GCCC  G   C
                                    |||||||||     ||||  |   |
                                    GGCGGGGTG     CGGG  C   G
                                _       AAGCGC    GT
GAM938  CAPS     3'  CCAGGAAGCCAGGTGACCCCAG 14478       _     TAT  __
           GT                     CCTGGG TCGCCT   GC  CCTGG
                                ||||||  ||||||   ||  |||||
                                GGACCC AGTGGA   CG  GGACC
                                   C     C__  AA
GAM938  CAPZA1   5'  GGGCGCGGGCGCGGGC     72627      GGT    TA
                                GCCTG   CGCCT  TGCCC
                                |||||   |||||  |||||
                                CGGGC   GCGGG  GCGGG
                                   ____    C_
GAM938  CCND3    3'  GGCTGGTGGCCCAGG      8308          TTAT
                                CCTGGGTCGCC    GCC
                                ||||||||||    |||
                                GGACCCGGTGG    CGG
                                     T___
GAM938  CD59     3'  CTGGTAGAAAGGCAGTTCAGGT 5214         TC    A_   CTGG
           A                     TGCCTGGG  GCCTT  TGCC
                                ||||||||  |||||  ||||
                                ATGGACTT  CGGAA  ATGG
                                     GA    AG    TC
GAM938  CDC34    3'  CCAGCCTGGGAGGCCCAGGT   15138         G   TATGCC
                                GCCTGGGTC CCT     CTGG
                                |||||||| |||     ||||
                                TGGACCCGG GGG     GACC
                                     A   TCC___
GAM938  CDC7L1   5'  GGAGACGGCGACCCAGGCA    13030           TTATG
                                TGCCTGGGTCGCC    CC
                                ||||||||||||     ||
                                ACGGACCCAGCGG    GG
                                     CAGA_
GAM938  CDKN2A   5'  CCAACCTGGGGCGACTTCAGGT 3577        _       TGCCCTGG
                                GCCTGG GTCGCCTTA
                                ||||||  |||||||||
```

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                                TGGACT CAGCGGGGT
                                   T       CCAACC
GAM938  CDKN2A   5'  CCAACCTGGGGCGACTTCAGGT 54235       _       TGCCCTGG
                                GCCTGG GTCGCCTTA
                                |||||| |||||||||
                                TGGACT CAGCGGGGT
                                   T       CCAACC
GAM938  CDS1     5'  GGTGCGGGAGGCCCGGGCA   7004          G   TAT _
                                TGCCTGGGTC CCT   GC CC
                                |||||||||| |||   || ||
                                ACGGGCCCGG GGG   CG GG
                                      A   ___  T
GAM938  CDX1     3'  CCGGGGGACCTGGGGACTCGGG 8403          G  TTATG
           T                     GCCTGGGTC CC    CCCTGG
                                |||||||| ||    ||||||
                                TGGGCTCAG GG    GGGGCC
                                     G  TCCAG
GAM938  CEP2     3'  TGGGGTGGGCTTGGCA     22286     T  G
                                TGCC GG TCGCCTTA
                                |||| || ||||||||
                                ACGG TC GGTGGGGT
                                  T  G
GAM938  CLC      3'  TTGGGGTGTAGGGTGGC     25111            TG
                                GTCGCCTTATGCCC  G
                                |||||||||||||  |
                                CGGTGGGATGTGGG  T
                                      GT
GAM938  CST      5'  CTGGGAGTTGGACGTGGCTCAG 16789          C  AT  _  TG
          GCA                    TGCCTGGGTCGC TT  GC CC  G
                                |||||||||||| ||  || ||  |
                                ACGGACTCGGTG AG  TG GG  C
                                      C  GT  A  GT
GAM938  CYP51    3'  AGGGGGGATCTAGGTA      5780          G  TTATG
                                TGCCTGGGTC CC    CCCT
                                |||||||||| ||    ||||
                                ATGGATCTAG GG    GGGA
                                      _ _____
GAM938  DBH      3'  CCGGGGTGTGGAATCACCGGG  5790       GTCG_  TT
                                CCTGG    CC  ATGCCCTGG
                                |||||    ||  |||||||||
                                GGGCC    GG  TGTGGGGCC
                                   ACTAA  __
GAM938  DBH      3'  TTAGGGAGTGTGCCTTGGGC   5792     TG  T  _  TATG
                                GCC  GG CGC CT   CCCTGG
                                |||  || ||| ||   ||||||
                                CGG  TC GTG GA   GGGATT
                                  GT  C   T  ____
GAM938  DBP      5'  GGGCAGGTGCCAGGC      7216        GT    TAT
                                GCCTGG  CGCCT   GCCC
                                ||||||  |||||   ||||
```

```
                              CGGACC  GTGGA   CGGG
                                __    ___
GAM938  DDX10    3'  GGGGGCACTTAGGTA      15296        C   TTATG
                              TGCCTGGGT GCC    CCC
                              |||||||| |||    |||
                              ATGGATTCA CGG    GGG
                                 _  _____
GAM938  DHCR24   3'  GGGGGCATCCAGGCA      28631        C   TTATG
                              TGCCTGGGT GCC    CCC
                              |||||||| |||    |||
                              ACGGACCTA CGG    GGG
                                 _  _____
GAM938  DLG4     5'  CTAGGGTGTGAGTACCCTAAGT 7252     CT_   CGC
                              GC   GGGT   CTTATGCCCTGG
                              ||   ||||   ||||||||||||
                              TG   CCCA   GAGTGTGGGATC
                                AAT    T__
GAM938  DLX4     5'  CAGGGGGCGATCCTGGT     8652      T      TTATG   _
                              GCC GGGTCGCC    CCCT G
                              ||| ||||||||    |||| |
                              TGG CCTAGCGG    GGGA C
                                T       _____   A
GAM938  DMN      3'  TGGGGTGTTTTGTCCAGG    62368       T  CCTT     TG
                              CCTGGG CG    ATGCCC  G
                              |||||| ||    ||||||  |
                              GGACCT GT    TGTGGG  T
                                 _ TT__     GT
GAM938  DNASE1L1 5'  CGGGGTCTCACTCAGGCA    22075         CGCCTTAT
                              TGCCTGGGT       GCCCTG
                              |||||||||       ||||||
                              ACGGACTCA       TGGGGC
                                   CTC_____
GAM938  DNMT3B   5'  CGGGGTTAAGTGGCCCAAGTA  22564     C       C   T    TG
                              TGC TGGGTCGC TTA GCCC  G
                              ||| |||||||| ||| ||||  |
                              ATG ACCCGGTG AAT TGGG  C
                                A       _   _    GT
GAM938  DRIL1    3'  GGGCAGGGGGTCCAGGT     17830       GT G   TAT
                              GCCTGG  C CCT   GCCC
                              ||||||  | |||   ||||
                              TGGACC  G GGA   CGGG
                                 TG G   ___
GAM938  DUSP7    5'  CTGGGGCCCGCGCGGCCGGGGC 65433      G     CTTAT    TG
                              GCCT GGTCGC     GCCC  G
                              |||| ||||||     ||||  |
                              CGGG CCGGCG     CGGG  C
                                G     CGCC_    GT
GAM938  DUSP7    5'  GGGGGCACCCGGGC       65434        C   TTATG
                              GCCTGGGT GCC    CCC
                              |||||||| |||    |||
```

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                                CGGGCCCA CGG    GGG
                                   _  _____
GAM938  DVL1    3'  CCAGGCCCCCAGGGTGGTCCAT 59334    C  GT    ATGC_
            GC                    GC TGG  CGCCTT    CCTGG
                                  || |||  ||||||    |||||
                                  CG ACC  GTGGGA    GGACC
                                   T  TG    CCCCC
GAM938  DXYS155E  3'  CCAGAGAAGAGGTGCCCGGGC  17451       T    ATGCC
                                  GCCTGGG CGCCTT    CTGG
                                  ||||||| ||||||    ||||
                                  CGGGCCC GTGGAG    GACC
                                      _     AAGA_
GAM938  DYRK1B   5'  CAGGGCGTGGGGGGGCC    16328     G
                                  GGTC CCTTATGCCCTG
                                  |||| ||||||||||||
                                  CCGG GGGGTGCGGGAC
                                    G
GAM938  EBAG9    5'  GGAGCGGGACCCAGGC      14871        G  TTAT  _
                                  GCCTGGGTC CC    GC CC
                                  |||||||| ||    || ||
                                  CGGACCCAG GG    CG GG
                                       _ _____ A
GAM938  EDAR    3'  TTGGGGCAGGTAGGGTTCAGGT 42272      GG  __    TAT    TG
                                  GCCTG  TC  GCCT   GCCC  G
                                  |||||  ||  ||||   ||||  |
                                  TGGAC  GG  TGGA   CGGG  T
                                     TT  GA    ___    GT
GAM938  EFNB1    3'  CAGGGTGGAGACCTAAGC    15393    C     G  TTAT
                                  GC TGGGTC CC    GCCCTG
                                  || |||||| ||    ||||||
                                  CG ATCCAG GG    TGGGAC
                                   A     A  ____
GAM938  EFNB1    5'  CCGTGCCAGGGCGGCCCAGTCG 15396    C          AT  CC
                                  TG CTGGGTCGCCTT  GC  TGG
                                  || ||||||||||||  ||  |||
                                  GC GACCCGGCGGGA  CG  GCC
                                   T          C_  T_
GAM938  EGLN2    5'  GCGCAGGGCGGCTGGGCA    54929      TG G      A
                                  TGCC  G TCGCCTT TGC
                                  ||||  | ||||||| |||
                                  ACGG  C GGCGGGA GCG
                                    GT _      C
GAM938  EIF2C1   3'  TTAGGGTTGAGCTATTTGGGTA 24182      TG   C  C   T
                                  TGCC  GGT GC TTA GCCCTGG
                                  ||||  ||| || ||| |||||||
                                  ATGG  TTA CG AGT TGGGATT
                                    GT   T  _  _
GAM938  ELK1     3'  GGGGGTTGGTGATTTGGG    17843    TG      TT  G
                                  CC  GGTCGCC  AT CCC
                                  ||  |||||||  || |||
```

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                                GG  TTAGTGG  TG GGG
                                 GT      T_  G
GAM938  EN2     5'  GCCCCGGGCGGCCCAGGC    7465           TAT
                                GCCTGGGTCGCCT   GC
                                ||||||||||||   ||
                                CGGACCCGGCGGG   CG
                                     CCC
GAM938  EN2     5'  GGAGCCGGCCCGGGC      7467          CCTTAT  C
                                GCCTGGGTCG     GC CT
                                ||||||||||     || ||
                                CGGGCCCGGC     CG GG
                                     _______ A
GAM938  ENSA    3'  CCAGGGGTCAGGAGGTGGCTCG 15424            A  __
            GGT                   GCCTGGGTCGCCTT TG  CCCTGG
                                ||||||||||||||  ||  ||||||
                                TGGGCTCGGTGGAG AC  GGGACC
                                       G  TG
GAM938  ENTPD6  3'  CAGGGCCATGTCTTAGGT    6968        T  CCTTAT
                                GCCTGGG CG     GCCCTG
                                |||||||  ||     ||||||
                                TGGATTC GT     CGGGAC
                                   T  AC_____
GAM938  EP300   5'  CCGGGGCGCACGGGCTGAGGC  7475      G    GCCTTA
                                GCCT GGTC     TGCCCTGG
                                ||||  ||||     ||||||||
                                CGGA TCGG     GCGGGGCC
                                  G    GCAC__
GAM938  EPHB2   3'  GGGAAGGTGACCTGGC      15445     T        ATG
                                GCC GGGTCGCCTT   CCC
                                |||  ||||||||||   |||
                                CGG TCCAGTGGAA   GGG
                                  _        ____
GAM938  EPHB2   3'  GGGAAGGTGACCTGGC      33887     T        ATG
                                GCC GGGTCGCCTT   CCC
                                |||  ||||||||||   |||
                                CGG TCCAGTGGAA   GGG
                                  _        ____
GAM938  ESRRA   3'  CTGGGGCGGAGCTGGGGTCTGG 15482     TG GT G  TTA__     TG
            GCA                   GCC  G  C CC    TGCCC  G
                                |||  |  | ||    |||||  |
                                CGG  C  G GG    GCGGG  C
                                  GT TG _  TCGAG    GT
GAM938  EXTL1   5'  AGGGCTGCTCAGGCA       15492         CGCCTTAT
                                TGCCTGGGT      GCCCT
                                |||||||||       |||||
                                ACGGACTCG      CGGGA
                                     T________
GAM938  EZH1    3'  CGGGGTGGATGACTTATGC   8818     C      _  TTAT   TG
                                GC TGGGTCG CC    GCCC  G
                                || |||||| ||    ||||  |
```

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                                CG ATTCAGT GG   TGGG  C
                                 T      A ____    GT
GAM938  F2RL3    3'  TCGGGGTGTGGCAGGCCGCGGT 14194     TG   _  TT
                                GCC  GGTC GCC  ATGCCCTGG
                                |||  |||| |||  |||||||||
                                TGG  CCGG CGG  TGTGGGGCT
                                  CG    A  __
GAM938  FECH     5'  GGGCCGAGGCTGCCCAGGCA  3756          C    AT
                                TGCCTGGGT GCCTT  GCCC
                                |||||||||| |||||  ||||
                                ACGGACCCG CGGAG  CGGG
                                      T    C_
GAM938  FLNB     3'  CCAAATGTGTAGTGTGGTCTGG 62177     TG GT   C     CC_
           GCA                    TGCC  G  CGC TTATGC   TGG
                                ||||  |  ||| ||||||   |||
                                ACGG  C  GTG GATGTG   ACC
                                  GT TG   T     TAA
GAM938  FLOT2    3'  CTAGGGCTGCACTGTCCTGGGT 15573     TG  T  CCTTAT
                                GCC  GG CG     GCCCTGG
                                |||  || ||     |||||||
                                TGG  CC GT     CGGGATC
                                  GT  T  CACGT_
GAM938  FLRT2    3'  CTGGCCAAATGAGGTGACTCAG 25059           ___  CTGG
                                CTGGGTCGCCTTAT   GCC
                                ||||||||||||||   |||
                                GACTCAGTGGAGTA   CGG
                                       AAC   TC
GAM938  FOXD2    5'  GGCCCGGTGGCCCGGGC     15567          TTAT
                                GCCTGGGTCGCC    GCC
                                ||||||||||||    |||
                                CGGGCCCGGTGG    CGG
                                       CC__
GAM938  FOXD2    3'  CAGGGCGACAGGCCCGGG    15563        GCCTTA
                                CCTGGGTC     TGCCCTG
                                ||||||||     |||||||
                                GGGCCCGG     GCGGGAC
                                     ACA___
GAM938  FOXD2    5'  CGGGGCAGCAGCCCAGGCA    15564        C  CTTA
                                TGCCTGGGT GC    TGCCCTG
                                ||||||||| ||    |||||||
                                ACGGACCCG CG    ACGGGGC
                                     A  ____
GAM938  FOXM1    3'  GCAGGGTGGTCCGTGTA     41705     C   GT    TA
                                TGC TGG  CGCCT  TGC
                                ||| |||  |||||  |||
                                ATG GCC  GTGGG  ACG
                                  T   TG    __
GAM938  FRAT2    3'  TGGTGGTGGGTGGCTTGGCA  23882      T       TAT  _ TG
                                TGCC GGGTCGCCT   GCC C  G
                                |||| |||||||||   ||| |  |
```

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                                ACGG TTCGGTGGG   TGG G  T
                                  _       ___   T GT
GAM938  FUT7     3'  GGGCGGGGCCCAGG        15586         G  TTAT
                                CCTGGGTC CC    GCCC
                                |||||||| ||    ||||
                                GGACCCGG GG    CGGG
                                   _ _____
GAM938  GAA      3'  CCGGAGAAGGGGGTGCTCAGGT 3840         T     ATGCC
                                GCCTGGG CGCCTT    CTGG
                                ||||||| ||||||    ||||
                                TGGACTC GTGGGG    GGCC
                                   _     GAAGA
GAM938  GAS7     3'  CAGAAGGGTGACCCGGACA   13320    C          ATGCC
                                TG CTGGGTCGCCTT    CTG
                                || ||||||||||||    |||
                                AC GGCCCAGTGGGA    GAC
                                 A          A_____
GAM938  GNA11    3'  GCACAAGGTGACCTGGC     76099     T        A
                                GCC GGGTCGCCTT TGC
                                ||| |||||||||| |||
                                CGG TCCAGTGGAA ACG
                                  _        C
GAM938  GNL1     5'  GGCGGAGGGCGGGCCAGGT   92039       G      A
                                GCCTGG TCGCCTT TGCC
                                |||||| ||||||| ||||
                                TGGACC GGCGGGA GCGG
                                   G      G
GAM938  GNL1     5'  GGCGGAGGGCGGGCCAGGT   97888       G      A
                                GCCTGG TCGCCTT TGCC
                                |||||| ||||||| ||||
                                TGGACC GGCGGGA GCGG
                                   G      G
GAM938  GORASP1  5'  CTGGCGCCGGGTCGGTCCGGGT 49110        GT  _   TA   CTGG
           A                     TGCCTGG  CG CCT  TGCC
                                |||||||  || |||  ||||
                                ATGGGCC  GC GGG  GCGG
                                    TG  T   CC    TC
GAM938  GPR30    3'  GCTCCGGGGTGGTTCAGTCA  7694     C  GG      AT_
                                TG CTG  TCGCCTT   GC
                                || |||  |||||||   ||
                                AC GAC  GGTGGGG   CG
                                 T   TT      CCT
GAM938  GRB10    5'  GAGGGTGGGCGCCCAGGC    17979        T    TAT    GG
                                GCCTGGG CGCCT   GCCCT
                                ||||||| |||||   |||||
                                CGGACCC GCGGG   TGGGA
                                   _    ___     GG
GAM938  GTF2F1   5'  GGGTCCTCGCTCAGGCA     9153          T  CCTTAT
                                TGCCTGGG CG     GCCC
                                |||||||| ||     ||||
```

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                                ACGGACTC GC     TGGG
                                    _ TCC___
GAM938  HIP1    3' CAAGGGGTGGCCGGGCA    18056       G    TA
                                TGCCTGG TCGCCT  TG
                                ||||||| ||||||  ||
                                ACGGGCC GGTGGG  AC
                                    _     GA
GAM938  HLA-DMB  5' TTGGGGGGTCAAGGGACCCGGG 9208         G   _ G   TG
           CA                    TGCCTGGGTC CCTT AT CCC  G
                                 |||||||||| |||| || |||  |
                                 ACGGGCCCAG GGAA TG GGG  T
                                     _   C  G   GT
GAM938  HOXD1   5' GGAGAGGGCAGCTCGGGTA   44430        C    ATG
                                TGCCTGGGT GCCTT   CC
                                ||||||||| |||||   ||
                                ATGGGCTCG CGGGA   GG
                                     A    GA_
GAM938  HPN     3' CCAGGGCCCGAGGTGATCCCGG 9273     T       AT
           T                    GCC GGGTCGCCTT  GCCCTGG
                                ||| ||||||||||  |||||||
                                TGG CCTAGTGGAG  CGGGACC
                                  C         CC
GAM938  HR      5' CCGGGAGGGGGCCGGCCCAGGC 17640         _   ATG   T
                                GCCTGGGTCG CCTT   CCC GG
                                |||||||||| ||||   ||| ||
                                CGGACCCGGC GGGG   GGG CC
                                     C   GA_  _
GAM938  HR      5' GGCAGGCGCCCGGGT      17643       T    TAT
                                GCCTGGG CGCCT   GCC
                                ||||||| |||||   |||
                                TGGGCCC GCGGA   CGG
                                    _   ___
GAM938  HTR1D   5' CCAGGGCATTGCCCACCTGGGT 5994     TG   C_  CTT
                                GCC  GGT  GC   ATGCCCTGG
                                |||  |||  ||   |||||||||
                                TGG  CCA  CG   TACGGGACC
                                  GT   CC  T__
GAM938  HUNK    5' CGGGTGCGGAGACCCAGGC   27448       G  TTAT  _  TG
                                GCCTGGGTC CC    GC CC  G
                                |||||||| ||    || ||  |
                                CGGACCCAG GG    CG GG  C
                                     A  ____  T  GT
GAM938  IARS    5' CTGGCCCGCGGGGCTGTCCAGG 25512       TC    TA  CC TG
           CA                    TGCCTGGG  GCCT  TG  C  G
                                 ||||||||  ||||  ||  |  |
                                 ACGGACCT  CGGG  GC  G  C
                                     GT    GC  CC GT
GAM938  IARS    5' CTGGCCCGCGGGGCTGTCCAGG 9292        TC    TA  CC TG
           CA                    TGCCTGGG  GCCT  TG  C  G
                                 ||||||||  ||||  ||  |  |
```

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                                ACGGACCT  CGGG  GC  G  C
                                    GT    GC  CC GT
GAM938  IKBKG    5'  TCAGGACCCAGGTTACTTGGGC 13314     TG   C    TATGC
                                GCC  GGT GCCT    CCTGG
                                |||  ||| ||||    |||||
                                CGG  TCA TGGA    GGACT
                                  GT   T   CCCA_
GAM938  IL10RA   3'  TTAGGCACGAGGCAGTCTGGGC 59647     TG  TC    TA   CTGG
          A                      TGCC  GG  GCCT  TGCC
                                ||||  ||  ||||  ||||
                                ACGG  CT  CGGA  ACGG
                                  GT  GA   GC   ATT
GAM938  IL1RAPL2  5'  CTGGGAGGCAGGCGACTTAGG  33792          TATG   TGG
                                CCTGGGTCGCCT   CCC
                                ||||||||||||   |||
                                GGATTCAGCGGA   GGG
                                       CGGA   TC
GAM938  IL21R    3'  TCAGGGCATTGCCTGTGACTGA 41434      G     CTT__
          GGC                    GCCT GGTCGC    ATGCCCTGG
                                |||| ||||||    |||||||||
                                CGGA TCAGTG    TACGGGACT
                                  G     TCCGT
GAM938  IL9R     5'  TCAGATGTGGGCGGCCTGTGT  9318     C        TATGCC
                                GC TGGGTCGCCT     CTGG
                                || ||||||||||     ||||
                                TG GTCCGGCGGG     GACT
                                 T         TGTA__
GAM938  IRS2     5'  GGGCGGGCGGCCGGGC      59722       G     TAT
                                GCCTGG TCGCCT   GCCC
                                |||||| ||||||   ||||
                                CGGGCC GGCGGG   CGGG
                                   _     ____
GAM938  ITGA5    3'  CCAGGGTGTGCTGGAACTCAGC 61279    C    CG  T_
                                GC TGGGT  CC  TATGCCCTGG
                                || |||||  ||  ||||||||||
                                CG ACTCA  GG  GTGTGGGACC
                                 _    A_  TC
GAM938  ITGAL    3'  TCAGGGCGTGGGACATCTAG   9395        CG   T
                                CTGGGT  CCT ATGCCCTGG
                                ||||||  ||| |||||||||
                                GATCTA  GGG TGCGGGACT
                                   CA  _
GAM938  ITGAM    3'  GGGGCTGTGGCTCACGT     5289     C       CTTAT
                                GC TGGGTCGC     GCCCT
                                || ||||||||     |||||
                                TG ACTCGGTG     CGGGG
                                 C       T_____
GAM938  ITPKB    3'  AGGGCTGCTCAGGCA       9419           CGCCTTAT
                                TGCCTGGGT       GCCCT
                                |||||||||       |||||
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                                ACGGACTCG       CGGGA
                                     T_______
GAM938  ITPR3    3'  GGGTTGGGTGGCCCAGCCA   9457     C         TAT
                                TG CTGGGTCGCCT   GCCC
                                || ||||||||||   ||||
                                AC GACCCGGTGGG   TGGG
                                 C         T__
GAM938  JRK      3'  CACGGGTGTGGCTCGGGT    86522          CTTAT   _
                                GCCTGGGTCGC    GCCC TG
                                ||||||||||     |||| ||
                                TGGGCTCGGTG    TGGG AC
                                      _____   C
GAM938  JUN      5'  CGGGCTGGTGGTTCGGG     9477      GG    TTAT    T
                                CCTG  TCGCC    GCCC G
                                ||||  |||||    |||| |
                                GGGC  GGTGG    CGGG C
                                  TT    T___   _
GAM938  KCNF1    5'  CCGGGGGTGAGTGCCCCGGGC   9521        TC  _   AT
                                GCCTGGG  GC CTT  GCCCTGG
                                |||||||  || |||  |||||||
                                CGGGCCC  CG GAG  TGGGGCC
                                    __ T   __
GAM938  KCNK3    5'  GGGGGGCCGGCGGCGGCCCGGG 9552           TTAT    GG
              C                  GCCTGGGTCGCC    GCCCT
                                 ||||||||||||    |||||
                                 CGGGCCCGGCGG    CGGGG
                                       CGGC     GGC
GAM938  KCNK6    3'  GGGACTGAGGGGTCCAGGC    16695       GT G    TG
                                GCCTGG  C CCTTA  CCC
                                ||||||  | |||||  |||
                                CGGACC  G GGAGT  GGG
                                   TG _     CA
GAM938  KCNMB1   5'  TTGGGGTGGGGGCGGGGGTCCA 14711        ___      A    TG
              GGCA                  CCTGGG   TCGCCTT TGCCC  G
                                    ||||||   ||||||| |||||  |
                                    GGACCT   GGCGGGG GTGGG  T
                                       GGG      _     GT
GAM938  KCNS2    3'  CATGGGGGGTGACTGGGTA   68302      TG G     TATG  _
                                TGCC  G TCGCCT    CCC TG
                                ||||  | ||||||    ||| ||
                                ATGG  C AGTGGG    GGG AC
                                  GT _     _____   T
GAM938  KCNS3    3'  TCAGGGTGTACCTTTCAGCCA  9589     C    TCGCCT
                                TG CTGGG     TATGCCCTGG
                                || |||||     ||||||||||
                                AC GACTT     ATGTGGGACT
                                 C    TCC___
GAM938  KIF3B    3'  TCAGGAAGGTGGCGACTCAGGT 16612           TTATGC
                                GCCTGGGTCGCC     CCTGG
                                ||||||||||||     |||||
```

```
                                TGGACTCAGCGG     GGACT
                                      TGGAA_
GAM938  KIF5C    5'  GCAGGAGGCGGCCTAGC     15736    C         A
                                GC TGGGTCGCCTT TGC
                                || |||||||||| |||
                                CG ATCCGGCGGAG ACG
                                 _         G
GAM938  KIFAP3   5'  GGCTTAGGCGACTCTGGGC   30364     TG _      TAT
                                GCC  G GTCGCCT   GCC
                                |||  | |||||||   |||
                                CGG  C CAGCGGA   CGG
                                  GT T      TT_
GAM938  KLK5     5'  GGTGAGGGTGGCTCAGCA    24860     C         A
                                TGC TGGGTCGCCTT TGCC
                                ||| |||||||||| ||||
                                ACG ACTCGGTGGGA GTGG
                                 _         _
GAM938  KRT3     3'  CCAGGTGTGGCCTAGGC     54032           CTTATGC
                                GCCTGGGTCGC      CCTGG
                                ||||||||||       |||||
                                CGGATCCGGTG      GGACC
                                      T_______
GAM938  LAMA4    5'  CCAGGGAGAGGAGGTGGCCTAG 9666     C         ATG_
          C                      GC TGGGTCGCCTT    CCCTGG
                                || |||||||||    ||||||
                                CG ATCCGGTGGAG    GGGACC
                                 _         GAGA
GAM938  LARS2    3'  CTGGGGTGAAGGTGAGCTGGGC 31056      TG G      A    TG
          A                      TGCC  G TCGCCTT TGCCC  G
                                ||||  | ||||||| |||||  |
                                ACGG  C AGTGGAA GTGGG  C
                                  GT G      _    GT
GAM938  LENG4    3'  GGGCCGTGACTTAGGCA     44168           CTTAT
                                TGCCTGGGTCGC     GCCC
                                ||||||||||||     ||||
                                ACGGATTCAGTG     CGGG
                                      C____
GAM938  LGALS3BP 5'  CCAGGATCTGGGCATCCAGGCA 69317         C    TATGC
                                TGCCTGGGT GCCT     CCTGG
                                |||||||| ||||     |||||
                                ACGGACCTA CGGG     GGACC
                                     _    TCTA_
GAM938  LHX3     3'  GGGTGGGCGGCTCGGG      27377           TAT
                                CCTGGGTCGCCT   GCCC
                                ||||||||||||   ||||
                                GGGCTCGGCGGG   TGGG
                                       ___
GAM938  LIF      3'  TAGGTTGGGACTTAGGT     9739          G  TTATGC
                                GCCTGGGTC CC     CCTG
                                |||||||| ||     ||||
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                                TGGATTCAG GG     GGAT
                                    _ TT____
GAM938  LIMD1    3'  CTAGATTGAGGTGATTCAG   26458          TGCC
                                CTGGGTCGCCTTA   CTGG
                                ||||||||||||   ||||
                                GACTTAGTGGAGT   GATC
                                    TA__
GAM938  LMO2     5'  CCAGGGGCTCCGGGCGGCCGGG 18740      G     TAT   _
          C                      GCCTGG TCGCCT   GCCC TGG
                                ||||||| ||||||   |||| |||
                                CGGGCC GGCGGG   CGGG ACC
                                   _     CCT    G
GAM938  LPHH1    5'  CGGGGCCTCTGGCTCGGT    24537     T     CCTTAT
                                GCC GGGTCG     GCCCTG
                                ||| ||||||     ||||||
                                TGG CTCGGT     CGGGGC
                                  _     CTC___
GAM938  LSS      3'  GGGTCGGCCCTGGGCA      9820       _     CCTTAT
                                TGCCT GGGTCG     GCCC
                                ||||| ||||||     ||||
                                ACGGG CCCGGC     TGGG
                                   T     _______
GAM938  LZTR1    5'  CGGGGCTGCGGCCTGGCA    22234      T      CTTAT
                                TGCC GGGTCGC    GCCCTG
                                |||| |||||||    ||||||
                                ACGG TCCGGCG    CGGGGC
                                  _      T_____
GAM938  MAFG     3'  CGGGGCTCCTCGTCCCAGGCA  70095        T  CCTTAT   TG
                                TGCCTGGG CG     GCCC  G
                                |||||||| ||     ||||  |
                                ACGGACCC GC     CGGG  C
                                     T  TCCT__    GT
GAM938  MAGEC1   5'  CCACAGCAGAGGAGGCCCAGGC 18420         G    A   CC
          A                      TGCCTGGGTC CCTT TGC  TGG
                                |||||||||| |||| |||  |||
                                ACGGACCCGG GGAG ACG  ACC
                                      A   _   AC
GAM938  MAP3K9   3'  GAAAGCAAGGTGGCCCAGTGT  60706    _        TA   CCTGG
                                GC CTGGGTCGCCT  TGC
                                || ||||||||||  |||
                                TG GACCCGGTGGA  ACG
                                 T          __   AAAGT
GAM938  MAPK14   3'  TGAGAGTTGGCTCAGGCA    57336          _ _
                                TGCCTGGGTCG C CTTA
                                |||||||||| | ||||
                                ACGGACTCGGT G GAGT
                                       T A
GAM938  MAPK14   3'  TGAGAGTTGGCTCAGGCA    57347          _ _
                                TGCCTGGGTCG C CTTA
                                |||||||||| | ||||
```

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                                ACGGACTCGGT G GAGT
                                      T A
GAM938  MAPK14   3'  TGAGAGTTGGCTCAGGCA    7162          _ _
                                TGCCTGGGTCG C CTTA
                                |||||||||| | ||||
                                ACGGACTCGGT G GAGT
                                      T A
GAM938  MASP1    3'  GGGCATGAGCTGGGCG     57473     TG GTCGC
                                TGCC  G    CTTATGCCC
                                ||||  |    |||||||||
                                GCGG  C    GAGTACGGG
                                  GT _____
GAM938  MEF2D    3'  CCAGGGTGTAATCTTGTTCATG 96911    C  GG CGCC
           CA                     TGC TG  T    TTATGCCCTGG
                                ||| ||  |    ||||||||||
                                ACG AC  G    AATGTGGGACC
                                  T  TT TTCT
GAM938  MEN1     5'  TTGGGGTGTGGGTGTTATCAAG 93387    C   GT_    T     TG
           T                     GC TGG   CGCCT ATGCCC  G
                                || |||   ||||| ||||||  |
                                TG ACT   GTGGG TGTGGG  T
                                 A  ATT    _     GT
GAM938  METTL1   3'  GGGTCTGGAGATCCGGGT    43510        G  TTAT
                                GCCTGGGTC CC    GCCC
                                ||||||||| ||    ||||
                                TGGGCCTAG GG    TGGG
                                     A  TC__
GAM938  MLC1     3'  TAGGGTACAGCCCAGGC     57597        CGCCTTA
                                GCCTGGGT      TGCCCTG
                                ||||||||      |||||||
                                CGGACCCG      ATGGGAT
                                    AC_____
GAM938  MLC1     3'  TAGGGTCTGTCCCGGGTA    57598        T  CCTTAT
                                TGCCTGGG CG     GCCCTG
                                |||||||| ||     ||||||
                                ATGGGCCC GT     TGGGAT
                                     T  C_____
GAM938  MLC1     3'  TAGGGTCTGTCCCGGGTA    30786        T  CCTTAT
                                TGCCTGGG CG     GCCCTG
                                |||||||| ||     ||||||
                                ATGGGCCC GT     TGGGAT
                                     T  C_____
GAM938  MLC1     3'  TAGGGTACAGCCCAGGC     30785        CGCCTTA
                                GCCTGGGT      TGCCCTG
                                ||||||||      |||||||
                                CGGACCCG      ATGGGAT
                                    AC_____
GAM938  MME      3'  AGGGTGACCTTGGGTA      23484        _
                                TGCCTG GGTCGCCTT
                                |||||| |||||||||
```

```
                                ATGGGT CCAGTGGGA
                                   T
GAM938  MME     3'  AGGGTGACCTTGGGTA     23494       _
                                TGCCTG GGTCGCCTT
                                |||||| |||||||||
                                ATGGGT CCAGTGGGA
                                   T
GAM938  MME     3'  AGGGTGACCTTGGGTA     6137        _
                                TGCCTG GGTCGCCTT
                                |||||| |||||||||
                                ATGGGT CCAGTGGGA
                                   T
GAM938  MME     3'  AGGGTGACCTTGGGTA     23504       _
                                TGCCTG GGTCGCCTT
                                |||||| |||||||||
                                ATGGGT CCAGTGGGA
                                   T
GAM938  MNT     3'  GGTGAAGGTGGCCCAGGC    39717           A
                                GCCTGGGTCGCCTT TGCC
                                |||||||||||||| ||||
                                CGGACCCGGTGGAA GTGG
                                          _
GAM938  MNT     3'  GGGCAGGGGCTGGGC       39716       GGTC    A
                                GCCTG   GCCTT TGCCC
                                |||||   ||||| |||||
                                CGGGT   CGGGG ACGGG
                                  _____   _
GAM938  MPP2    3'  CTGGCAGCCAGGCAGGCCCGGG 59822         _   TA_   CTGG
          T                      GCCTGGGTC GCCT   TGCC
                                |||||||||| ||||  ||||
                                TGGGCCCGG CGGA   ACGG
                                     A   CCG   TC
GAM938  MPP4    5'  TCGGGAGCAGTGAGGTGACTTT 52348     TG       _  _
          GGCA                    GCC  GGTCGCCTTA TGC CCTGG
                                |||  |||||||||| ||| |||||
                                CGG  TCAGTGGAGT ACG GGGCT
                                  TT        G  A
GAM938  MRPS12  5'  CAGGGACGGCCCAGGT      40866          CCTTATG
                                GCCTGGGTCG      CCCTG
                                ||||||||||      |||||
                                TGGACCCGGC      GGGAC
                                   A_______
GAM938  MSX2    3'  CACAGATTGCAAAGGTGATTTG 65570    TG       A  C__  G
          GGT                     CC  GGTCGCCTT TGC   CTG
                                ||  |||||||| |||   |||
                                GG  TTAGTGGAA ACG   GAC
                                 GT        _  TTA   ACT
GAM938  MYC     5'  CTAGGGTGGAAGAGCCGGGC  10159       G  G_  TTAT
                                GCCTGG TC  CC    GCCCTGG
                                |||||| ||  ||   |||||||
```

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                                CGGGCC AG  GG   TGGGATC
                                   G  AA  ____
GAM938  MYEOV    5'  TCAGCTGCTGGGTGACTCGGGT 57053          TAT  C_
                                GCCTGGGTCGCCT   GC  CTGG
                                ||||||||||||   ||  ||||
                                TGGGCTCAGTGGG   CG  GACT
                                      T__  TC
GAM938  MYO10    5'  TTAGGGACTTGGGTTTGGGC   24702    TG GTC   TATG
                                GCC  G   GCCT   CCCTGG
                                |||  |   ||||   ||||||
                                CGG  T   TGGG   GGGATT
                                  GT ___   TTCA
GAM938  MYO5A    5'  GGGCGGCCGCCCAGGC     59765       C   TTAT
                                GCCTGGGT GCC   GCCC
                                |||||||| |||   ||||
                                CGGACCCG CGG   CGGG
                                    C  ____
GAM938  NAB2     5'  CCGGGAAGGGCAGCCCGGGT   19914       C    ATGC
                                GCCTGGGT GCCTT   CCTGG
                                |||||||| |||||   |||||
                                TGGGCCCG CGGGA   GGGCC
                                    A    A___
GAM938  NDST1    3'  GGGGAGCACCCAGGC      7746        C  C  ATG
                                GCCTGGGT GC TT   CCC
                                |||||||| || ||   |||
                                CGGACCCA CG AG   GGG
                                    _  _  ___
GAM938  NEBL     3'  CTAGTAAATAAGCGATTTAGGT 21121         C   GCC
                                GCCTGGGTCGC TTAT   CTGG
                                |||||||||| ||||   ||||
                                TGGATTTAGCG AATA   GATC
                                      _   AAT
GAM938  NEURL    3'  TTAGGTACCTCAGGTGGCCCAG 14867         TA__   CTGG
            G                    CCTGGGTCGCCT   TGCC
                                ||||||||||||   ||||
                                GGACCCGGTGGA   ATGG
                                      CTCC   ATT
GAM938  NGB      5'  CGGGGTGGGGCGGCTCTGGC   41187    T       AT    G
                                GCC GGGTCGCCTT  GCCCTG
                                ||| ||||||||||  ||||||
                                CGG CTCGGCGGGG  TGGGGC
                                  T        __     G
GAM938  NLGN3    5'  TTGGCCTGGAGGCGATATGGGT 38603      G      AT_  CTGG
                                GCCTG GTCGCCTT   GCC
                                |||||  ||||||||   |||
                                TGGGT TAGCGGAG   CGG
                                   A       GTC   TT
GAM938  NMI      5'  CCGGGGGTTCGCGTTTCAGGC  16264       T   CTT  G
                                GCCTGGG CGC   AT CCCTGG
                                |||||||  |||   || ||||||
```

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                                CGGACTT GCG   TG GGGGCC
                                    T   CT_  _
GAM938  NOS1    3'  TCAGGGCATGGGGAGAGG    5254     TGGG  G
                                CC    TC CCTTATGCCCTGG
                                ||    || ||||||||||||
                                GG    AG GGGGTACGGGACT
                                 ____  A
GAM938  NQO1    3'  TTAGGGTACAGTTGGCTAGGTA 6172         G   C  TA
                                TGCCTGG TCG CT  TGCCCTGG
                                ||||||| ||| ||  ||||||||
                                ATGGATC GGT GA  ATGGGATT
                                    _  T  C_
GAM938  NR4A1   5'  CGGGGCGCCAGTCCGGGCA   9236         TCGC  TA
                                TGCCTGGG    CT  TGCCCTG
                                ||||||||    ||  |||||||
                                ACGGGCCT    GA  GCGGGGC
                                     _____  CC
GAM938  NRAS    5'  CCGGGGCGGGGACTCAGGC    10269         G  TTAT
                                GCCTGGGTC CC    GCCCTGG
                                ||||||||| ||    |||||||
                                CGGACTCAG GG    CGGGGCC
                                     G  _____
GAM938  NRBP    3'  GCTGGGGCGGCCGGGGC     25432      G         T
                                GCCT GGTCGCCTTA GC
                                |||| |||||||||| ||
                                CGGG CCGGCGGGGT CG
                                  G         _
GAM938  NT5M    3'  CCAGGAACCCGGCGACTGAGGT 39510      G      TTATGC
                                GCCT GGTCGCC      CCTGG
                                |||| |||||||      |||||
                                TGGA TCAGCGG      GGACC
                                  G      CCCAA_
GAM938  OPHN1   5'  GGGCGGGGCGCAGGC       10359       GGT     TA
                                GCCTG   CGCCT  TGCCC
                                |||||   |||||  |||||
                                CGGAC   GCGGG  GCGGG
                                  ____    __
GAM938  OSBP    5'  GTGTGGGGCGCTCCGGGC    10368        GT
                                GCCTGG  CGCCTTATGC
                                ||||||  ||||||||||
                                CGGGCC  GCGGGGTGTG
                                    TC
GAM938  OSM     3'  CCAGGCCCAGTGGGGTGGCCGG 40074        G        GC__
          GC                    GCCTGG TCGCCTTAT    CCTGG
                                |||||| |||||||||    |||||
                                CGGGCC GGTGGGGTG    GGACC
                                   _        ACCC
GAM938  PACE    3'  GGGCGTGGGGAGGGCC      10395      G_
                                GGTC  CCTTATGCCC
                                ||||  ||||||||||
```

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                                CCGG  GGGGTGCGGG
                                  GA
GAM938  PACSIN3  3'  GGGTGGGCTTGGGGT      32586     G  TC    TAT
                                GCCT GG  GCCT   GCCC
                                |||| ||  ||||   ||||
                                TGGG TT  CGGG   TGGG
                                  G __   ___
GAM938  PAK4     3'  GCGGGGTGGCCCTGGCA     19689     T       TA
                                TGCC GGGTCGCCT  TGC
                                |||| |||||||||  |||
                                ACGG CCCGGTGGG  GCG
                                  T       __
GAM938  PAWR     5'  GGTGGGCGGCCTGAGGT     10431     _       TAT
                                GCCT GGGTCGCCT   GCC
                                |||| |||||||||   |||
                                TGGA TCCGGCGGG   TGG
                                  G       ___
GAM938  PAX9     5'  TAGGGCGTGTCCCCAG      20561      TCGCCT
                                CTGGG     TATGCCCTG
                                |||||     |||||||||
                                GACCC     GTGCGGGAT
                                   CT____
GAM938  PCK1     3'  TCAAATTTAAGGTTACTCAGGC 59946         C     TGCCCTGG
          A                      TGCCTGGGT GCCTTA
                                |||||||| ||||||
                                ACGGACTCA TGGAAT
                                      T     TTAAACT
GAM938  PDE1B    3'  GGGCTGGCCCAGGT       6244          CCTTAT
                                GCCTGGGTCG     GCCC
                                ||||||||||     ||||
                                TGGACCCGGT     CGGG
                                          _______
GAM938  PFKFB4   3'  CAGAGAGGCAGCCTGGGCA   15866     TG   C    ATGCC
                                TGCC  GGT GCCTT    CTG
                                ||||  ||| |||||    |||
                                ACGG  CCG CGGAG    GAC
                                  GT   A    A____
GAM938  PGF      3'  CTGGGGCCGCCACGGCCTGGC  10534    T    CCTTAT   TG
                                GCC GGGTCG     GCCC  G
                                ||| ||||||     ||||  |
                                CGG TCCGGC     CGGG  C
                                  _     ACCGC_    GT
GAM938  PIK3R3   3'  CCAGGGGCCCTGTGGTCCAGG  61056      GT   CTTATG
                                CCTGG  CGC     CCCTGG
                                |||||  |||     ||||||
                                GGACC  GTG     GGGACC
                                   TG   TCCCG_
GAM938  PITX3    3'  CCAGGGTCTGAAAGGGGTGTTT 17266   TG  T     AT____
          GGGCA                    GG CGCCTT     GCCCTGG
                                  || ||||||     |||||||
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                                TT GTGGGG     TGGGACC
                               GT _     AAAGTC
GAM938  PKIG     3'  GCGAGCGGCCCGGGCA      22962          CTTA
                               TGCCTGGGTCGC    TGC
                               ||||||||||||    |||
                               ACGGGCCCGGCG    GCG
                                      A___
GAM938  PLA2G10  5'  CCGGGGCGTGACAGCCGGGGT  13084      G   CGCC
                               GCCT GGT    TTATGCCCTGG
                               |||| |||    ||||||||||
                               TGGG CCG    AGTGCGGGGCC
                                 G  AC__
GAM938  PLA2G2D  3'  CCAACACTTAGGGTGGCTGAGG 24787      G        TGCCC
           CA                    TGCCT GGTCGCCTTA     TGG
                               ||||| ||||||||||     |||
                               ACGGA TCGGTGGGAT     ACC
                                  G         TCACA
GAM938  PMP22    3'  GGTGGGTGACCCAG        4330          TAT
                               CTGGGTCGCCT   GCC
                               ||||||||||   |||
                               GACCCAGTGGG   TGG
                                      ___
GAM938  POLH     5'  CGGGGACGGTTGCCCGGGCA   21463        C   TTATG   TG
                               TGCCTGGGT GCC    CCC  G
                               ||||||||| |||    |||  |
                               ACGGGCCCG TGG    GGG  C
                                     T   CA___   GT
GAM938  POLR2E   3'  CCAGGAAGCTGAGGTGGCCCAG 59917           T __
           G                    CCTGGGTCGCCTTA GC  CCTGG
                               |||||||||||||| ||  |||||
                               GGACCCGGTGGAGT CG  GGACC
                                      _ AA
GAM938  POP2     3'  ATGAGTTGATTTAGGTA     42144          C
                               TGCCTGGGTCG CTTAT
                               |||||||||| |||||
                               ATGGATTTAGT GAGTA
                                      T
GAM938  PPARGC1  3'  TGGGGTATGATGTTTGGGT    25164     TG GTC  C      TG
                               GCC  G   GC TTATGCCC  G
                               |||  |   || ||||||||  |
                               TGG  T   TG AGTATGGG  T
                                 GT ___  T       GT
GAM938  PPID     5'  CTGGAGTTTGGGCGGCCCGGGC 87432          TAT  _  TGG
                               GCCTGGGTCGCCT   GC CC
                               ||||||||||||   || ||
                               CGGGCCCGGCGGG   TG GG
                                      TT_  A  TC
GAM938  PPP1R8   5'  CCAGGGCTAGAGTGGCCCGGC  56740     T      C   T
                               GCC GGGTCGC TTA GCCCTGG
                               ||| ||||||| ||| |||||||
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                                CGG CCCGGTG GAT CGGGACC
                                  _     A  _
GAM938  PPP1R8   5'  CCAGGGCTAGAGTGGCCCGGC  10723     T     C   T
                                GCC GGGTCGC TTA GCCCTGG
                                ||| ||||||| ||| |||||||
                                CGG CCCGGTG GAT CGGGACC
                                  _     A  _
GAM938  PPT2     3'  GGGGCAGGTTGCCTGGGCA   57232     TG   C    TAT
                                TGCC  GGT GCCT   GCCCT
                                ||||  ||| ||||   |||||
                                ACGG  CCG TGGA   CGGGG
                                  GT   T   ___
GAM938  PRKAA2   3'  TCAATGTAAGGGTGGTTTGGCA 20733     T  GT     A   CC
                                TGCC GG  CGCCTT TGC  TGG
                                |||| ||  |||||| |||  |||
                                ACGG TT  GTGGGA ATG  ACT
                                  _ TG     _  TA
GAM938  PRKACA   3'  GGGTGGGGCCCCGGGT     10793       TC    AT
                                GCCTGGG  GCCTT  GCCC
                                |||||||  |||||  ||||
                                TGGGCCC  CGGGG  TGGG
                                   __    __
GAM938  PRKCABP  3'  CAGGGTCATGGCCTGGG    24829    TG   GCCTT  _
                                CC  GGTC    ATG CCCTG
                                ||  ||||    ||| |||||
                                GG  CCGG    TAC GGGAC
                                 GT   ______  T
GAM938  PRKCH    5'  CCAGTCGAGGGGCGCTTAGGC  20741       T    TA  CC
                                GCCTGGG CGCCT  TG  CTGG
                                ||||||| |||||  ||  ||||
                                CGGATTC GCGGG  GC  GACC
                                   _    GA  T_
GAM938  PRKRA    5'  CCGGGGACCAGCGACCCGGG   13495         CTTATG
                                CCTGGGTCGC     CCCTGG
                                ||||||||||     ||||||
                                GGGCCCAGCG     GGGGCC
                                     ACCA__
GAM938  PRODH    3'  CCAGAGTATGGGCACTCAGGT  32922        C   T   C
                                GCCTGGGT GCCT ATGC CTGG
                                |||||||| |||| |||| ||||
                                TGGACTCA CGGG TATG GACC
                                   _   _   A
GAM938  PRX      3'  CCAGGGCAGCAGGCTCAGAGTA 40525     _     _ CTTA
                                TGC CTGGGTC GC    TGCCCTGG
                                ||| ||||||| ||    ||||||||
                                ATG GACTCGG CG    ACGGGACC
                                  A      A  ____
GAM938  PRX      3'  TCGGGGCCAAAGGTGGCTAAGG 40539      G       AT
             CA                   TGCCT GGTCGCCTT  GCCCTGG
                                |||||| |||||||||  |||||||
```

```
                                ACGGA TCGGTGGAA  CGGGGCT
                                  A       AC
GAM938  PSD     5'  GGGTGGGCTCAAGGCA     10933      G  TC   TAT
                                TGCCT GG  GCCT   GCCC
                                ||||| ||  ||||   ||||
                                ACGGA CT  CGGG   TGGG
                                  A __   ___
GAM938  PTK7    3'  GCTCAGGATGGCCTGGGCA   11018     TG   _  TAT
                                TGCC  GGTCG CCT   GC
                                ||||  ||||| |||   ||
                                ACGG  CCGGT GGA   CG
                                  GT    A  CT_
GAM938  PTPN2   3'  TTGGGGTAGATTATGATTTAGG 11056        CCTTA    TG
                                CCTGGGTCG    TGCCC  G
                                |||||||||    |||||  |
                                GGATTTAGT    ATGGG  T
                                     ATTAG    GT
GAM938  PTPN6   5'  CCGGGGGTGGTGAGGCGGCCCG 11062     T        G__
           GCA                   GCC GGGTCGCCTTAT   CCCTGG
                                ||| ||||||||||||   ||||||
                                CGG CCCGGCGGAGTG   GGGGCC
                                  _         GTG
GAM938  PTPN6   5'  CCGGGGGTGGTGAGGCGGCCCG 54511     T        G__
           GCA                   GCC GGGTCGCCTTAT   CCCTGG
                                ||| ||||||||||||   ||||||
                                CGG CCCGGCGGAGTG   GGGGCC
                                  _         GTG
GAM938  PTPRH   3'  GGGTCGGCAGCCCAGGCA    11115        C   TTAT
                                TGCCTGGGT GCC    GCCC
                                ||||||||| |||    ||||
                                ACGGACCCG CGG    TGGG
                                     A  C___
GAM938  PTPRN   3'  CTGGGGCATCCCAGAGCCCAGG 11131       CGCCTT     TG
                                CCTGGGT     ATGCCC  G
                                |||||||     ||||||  |
                                GGACCCG     TACGGG  C
                                    AGACCC     GT
GAM938  PTTG1IP 3'  CTGGCTCGAGGGTGGTCTGAGC 15091     CT  GT     AT_  CTGG
           A                    TGC  GG  CGCCTT   GCC
                                |||  ||  ||||||   |||
                                ACG  TC  GTGGGA   CGG
                                  AG  TG     GCT   TC
GAM938  PUNC    5'  TCGGGGTGGAGGGCATCCAGGT 89654        C    A
                                GCCTGGGT GCCTT TGCCCTGG
                                |||||||| ||||| ||||||||
                                TGGACCTA CGGGA GTGGGGCT
                                    _    G
GAM938  RAB18   5'  CCGGAGAGGCGCACCCGGGC   41167        _     ATGCC
                                GCCTGGGT CGCCTT    CTGG
                                |||||||| ||||||    ||||
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                                CGGGCCCA GCGGAG    GGCC
                                    C     A____
GAM938  RAD50    5'  GCAGGGCGGCCGAGGCA     19195      G      TA
                                TGCCT GGTCGCCT  TGC
                                ||||| ||||||||  |||
                                ACGGA CCGGCGGG  ACG
                                   G      __
GAM938  RAD50    5'  GCAGGGCGGCCGAGGCA     56009      G      TA
                                TGCCT GGTCGCCT  TGC
                                ||||| ||||||||  |||
                                ACGGA CCGGCGGG  ACG
                                   G      __
GAM938  RARG     5'  CGGGGCAGTGGGCATGGGCA  6379       GG  C   TA    TG
                                TGCCT  GT GCCT  TGCCC  G
                                |||||  || ||||  |||||  |
                                ACGGG  TA CGGG  ACGGG  C
                                   __ _   TG    GT
GAM938  RASAL1   3'  TCAGGGCATGGAAGCCCTTTGG 16226     T__   CG  TT
            CA                    TGCC   GGGT  CC  ATGCCCTGG
                                ||||   ||||  ||  |||||||||
                                ACGG   CCCG  GG  TACGGGACT
                                   TTT    AA  __
GAM938  RECQL5   3'  CCAGGGGCTGGGGTCCAGGCA  14927       GT G  TTATG
                                TGCCTGG  C CC    CCCTGG
                                |||||||  | ||    ||||||
                                ACGGACC  G GG    GGGACC
                                    TG _  TCG__
GAM938  RENT1    3'  CGGGGCTGCGGCCAGGGC    11287     G     CTTAT
                                GCCT GGTCGC    GCCCTG
                                |||| ||||||    ||||||
                                CGGG CCGGCG    CGGGGC
                                   A     T____
GAM938  RFXAP    5'  TCGGGGCGCCTTCCCGGTATAG 5017       GG   CCTTA_
            GC                    GCCTG  TCG     TGCCCTGG
                                |||||  |||     ||||||||
                                CGGAT  GGC     GCGGGGCT
                                   AT   CCTTCC
GAM938  RIMS1    5'  CTGGGCTGCGGGAGGCGGCCGG 72631      G      AT___    TGG
            GC                    CCTGG TCGCCTT    GCCC
                                ||||| |||||||    ||||
                                GGGCC GGCGGAG    CGGG
                                   _      GGCGT    TC
GAM938  ROM1     5'  TCAGGGTATTGGGGTCAGGGT  4386      G GT G  TT
                                GCCT G  C CC  ATGCCCTGG
                                |||| |  | ||  |||||||||
                                TGGG C  G GG  TATGGGACT
                                   A TG _  T_
GAM938  RPL10    3'  TAGGTGGGTGGCCTGAGCA   20031     CT       TATGC
                                TGC  GGGTCGCCT    CCTG
                                |||  |||||||||    ||||
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                                ACG  TCCGGTGGG    GGAT
                                  AG       T____
GAM938  RPS6KA2  3'  GAGGGCTGGGGTGACCTGGCA  40906     T        T    GG
                                TGCC GGGTCGCCTTA GCCCT
                                |||| |||||||||| |||||
                                ACGG TCCAGTGGGGT CGGGA
                                  _        _    GA
GAM938  RXRA     3'  GGGCTGGCGGCCTGGT     11413     T      TTAT
                                GCC GGGTCGCC   GCCC
                                ||| ||||||||   ||||
                                TGG TCCGGCGG   CGGG
                                  _      T___
GAM938  RXRA     3'  GGGTGCGTGATCTGGT     11414     T     CTTA
                                GCC GGGTCGC   TGCCC
                                ||| |||||||   |||||
                                TGG TCTAGTG   GTGGG
                                  _      C___
GAM938  RYR1     3'  CGGGGGAGAGGTGACCTAG   5022          ATG   TG
                                CTGGGTCGCCTT   CCC  G
                                ||||||||||||   |||  |
                                GATCCAGTGGAG   GGG  C
                                       AG_   GT
GAM938  SCNN1A   3'  CTAGGGCTAGAGCAGACCCGGG 6423          _  C   T
          TA                      TGCCTGGGTC GC TTA GCCCTGG
                                |||||||||| || ||| |||||||
                                ATGGGCCCAG CG GAT CGGGATC
                                       A  A  _
GAM938  SCNN1G   3'  TTGGGGCATGGGTGGCTCCAGG 6437       _     T     TG
                                CCTGG GTCGCCT ATGCCC  G
                                ||||| ||||||| ||||||  |
                                GGACC CGGTGGG TACGGG  T
                                   T      _     GT
GAM938  SEPN1    3'  AGGGTCACTCAGGTA       66360         CGCCTTAT
                                TGCCTGGGT       GCCCT
                                |||||||||       |||||
                                ATGGACTCA       TGGGA
                                     C________
GAM938  SFRP1    3'  CCAGGGTAGCCATGGCCGGGTA 11566        G   CCTTA
                                TGCCTGG TCG    TGCCCTGG
                                ||||||| |||    ||||||||
                                ATGGGCC GGT    ATGGGACC
                                    _  ACCG_
GAM938  SHMT2    3'  TAGGGCAAGAGCCAGGTA    18271        G  GCCTTA
                                TGCCTGG TC     TGCCCTG
                                ||||||| ||     |||||||
                                ATGGACC AG     ACGGGAT
                                    G  A_____
GAM938  SHOX     5'  GTGTGGGGGGCTCGGGC     22542         G
                                GCCTGGGTC CCTTATGC
                                ||||||||| ||||||||
```

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                                CGGGCTCGG GGGGTGTG
                                          _
GAM938  SHOX     5'  GTGTGGGGGGCTCGGGC     4838          G
                                GCCTGGGTC CCTTATGC
                                ||||||||| ||||||||
                                CGGGCTCGG GGGGTGTG
                                          _
GAM938  SLC13A3  3'  CCAGGGTAAAATGTCTCAGGCA 60467         T  CC  A
                                TGCCTGGG CG  TT TGCCCTGG
                                |||||||| ||  || ||||||||
                                ACGGACTC GT  AA ATGGGACC
                                     T __  A
GAM938  SLC22A11 3'  TCAGAGCGTGGAGGCGAGTTGG 37490     TG G      _    C
           GC                     GCC  G TCGCCTT ATGC CTGG
                                  |||  | ||||||| |||| ||||
                                  CGG  T AGCGGAG TGCG GACT
                                    GT G      G    A
GAM938  SLC22A12 3'  GGCAGGAGGTGACCCAG     58072           A
                                CTGGGTCGCCTT TGCC
                                |||||||||||| ||||
                                GACCCAGTGGAG ACGG
                                       G
GAM938  SLC22A2  5'  GCTGGGGTGGCTTACGCA    59535     C         T
                                TGC TGGGTCGCCTTA GC
                                ||| |||||||||||| ||
                                ACG ATTCGGTGGGGT CG
                                  C          _
GAM938  SLC25A1  3'  CCGGGGTGCCCGTGTGGCCTGG 19963     TG     CTTAT_
           GT                     GCC  GGTCGC     GCCCTGG
                                  |||  ||||||     |||||||
                                  TGG  CCGGTG     TGGGGCC
                                    GT     TGCCCG
GAM938  SLC2A4   3'  CTGGGGGAAGGGTGGTCTGAGC 6442      CT  GT     ATG   TG
           A                       TGC  GG  CGCCTT   CCC  G
                                  |||  ||  ||||||   |||  |
                                  ACG  TC  GTGGGA   GGG  C
                                    AG  TG     AG_   GT
GAM938  SLC4A1   3'  CCAGAGAGAGGCGTCCTGGGT  4425      TG  T     ATGCC
                                GCC  GG CGCCTT    CTGG
                                |||  || ||||||    ||||
                                TGG  CC GCGGAG    GACC
                                  GT  T     AGA__
GAM938  SLC7A5   3'  GGAGGGGGTGGGGGATCTGGGC 13011      TG   G     G   GG
           A                       TGCC  GGTC CCTTAT CCCT
                                  ||||  |||| |||||| ||||
                                  ACGG  CTAG GGGGTG GGGA
                                    GT   _     G   GGG
GAM938  SLC8A2   3'  GGGCCAAGGGATCTGGGT    66334     TG   G   AT
                                GCC  GGTC CCTT  GCCC
                                |||  |||| ||||  ||||
```

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                                TGG  CTAG GGAA  CGGG
                                  GT   _   C_
GAM938  SMARCD1  5'  CCGGGAAGATGGCGGCCCGGGC 57431          TTATG  T
                                GCCTGGGTCGCC    CCC GG
                                ||||||||||||    ||| ||
                                CGGGCCCGGCGG    GGG CC
                                      TAGAA  _
GAM938  SMARCD1  5'  CCGGGAAGATGGCGGCCCGGGC 11813          TTATG  T
                                GCCTGGGTCGCC    CCC GG
                                ||||||||||||    ||| ||
                                CGGGCCCGGCGG    GGG CC
                                      TAGAA  _
GAM938  SMG1     5'  TCGGCGGCGGCCGGTTCGGGC  30656      GG  _  TTAT  _
                                GCCTG  TCG CC   GCC CTGG
                                |||||  ||| ||   ||| ||||
                                CGGGC  GGC GG   CGG GGCT
                                   TT   C  ____  C
GAM938  SPAG11   3'  TGACCGCAGGGTGGCCCAGGT  54248          TA  CCTGG
                                GCCTGGGTCGCCT  TGC
                                ||||||||||||  |||
                                TGGACCCGGTGGG  ACG
                                      __  CCAGTG
GAM938  SPAG11   3'  TGACCGCAGGGTGGCCCAGGT  54242          TA  CCTGG
                                GCCTGGGTCGCCT  TGC
                                ||||||||||||  |||
                                TGGACCCGGTGGG  ACG
                                      __  CCAGTG
GAM938  SPHK2    3'  CTAGGGGGTGTGGCCTGGC   39246    T     CTT  G
                                GCC GGGTCGC   AT CCCTGG
                                |||  |||||||   ||  ||||||
                                CGG TCCGGTG   TG GGGATC
                                  _     ___  G
GAM938  SRC      3'  TCAGGGTAAAAGGTGCAGGT   18288      GGT     A
                                GCCTG   CGCCTT TGCCCTGG
                                |||||   |||||| ||||||||
                                TGGAC   GTGGAA ATGGGACT
                                   ___      A
GAM938  SRR      3'  CAGGGTACTGGTTCTGGTA   41686     T   TC   TTA
                                TGCC GGG  GCC   TGCCCTG
                                ||||  |||  |||   |||||||
                                ATGG TCT  TGG   ATGGGAC
                                  _  __  TC_
GAM938  STARD4   3'  TGAGGCAATTCAGGTA     57519         C
                                TGCCTGGGT GCCTTA
                                |||||||||  ||||||
                                ATGGACTTA CGGAGT
                                      A
GAM938  STAT1    5'  CCGAGCAGAGGCGACCCAGC   57694    C        A   CC
                                GC TGGGTCGCCTT TGC  TGG
                                ||  ||||||||||  |||  |||
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                                CG ACCCAGCGGAG ACG  GCC
                                 _        _  A_
GAM938  STAT1   5'  CCGAGCAGAGGCGACCCAGC  23617   C       A  CC
                                GC TGGGTCGCCTT TGC  TGG
                                || |||||||||| |||  |||
                                CG ACCCAGCGGAG ACG  GCC
                                 _        _  A_
GAM938  SURF4   3'  TAGGGCCTGATTCGGG     52545        CCTTAT
                                CCTGGGTCG    GCCCTG
                                |||||||||    ||||||
                                GGGCTTAGT    CGGGAT
                                     C_____
GAM938  TAF7    5'  GGGTAGGCGACCCGG      18911         TAT
                                CTGGGTCGCCT  GCCC
                                ||||||||||  ||||
                                GGCCCAGCGGA  TGGG
                                    ___
GAM938  TAL1    3'  GGCTGGGGTGGCCTGTGT   12110   C       T
                                GC TGGGTCGCCTTA GCC
                                || ||||||||||| |||
                                TG GTCCGGTGGGGT CGG
                                 T        _
GAM938  TBX5    5'  GGGTATGCCTGGTA       54892     T   CGCCTT
                                TGCC GGGT    ATGCCC
                                |||| ||||    ||||||
                                ATGG TCCG    TATGGG
                                  _  _______
GAM938  TBX5    5'  GGGTATGCCTGGTA       3960      T   CGCCTT
                                TGCC GGGT    ATGCCC
                                |||| ||||    ||||||
                                ATGG TCCG    TATGGG
                                  _  _______
GAM938  TBX6    3'  CCAGGTGTGGTGGCTCACGCA  54963    C       TTAT _
                                TGC TGGGTCGCC   GC CCTGG
                                ||| |||||||||   || |||||
                                ACG ACTCGGTGG   TG GGACC
                                  C       ____ T
GAM938  TCF1    3'  TGGGGTGACCCGGCA      5038      T
                                TGCC GGGTCGCCTTA
                                |||| ||||||||||
                                ACGG CCCAGTGGGGT
                                  _
GAM938  TCF7    3'  TCAGAGACAGGTGGCCTAGCA  12163    C       TATGCC
                                TGC TGGGTCGCCT    CTGG
                                ||| ||||||||||    ||||
                                ACG ATCCGGTGGA    GACT
                                  _       CAGA__
GAM938  TCL1B   3'  TTAGGGCAGCTGGCCTGG   16987   TG  _  CTTA
                                C  GGTC GC   TGCCCTGG
                                |  |||| ||   ||||||||
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                              G  CCGG CG    ACGGGATT
                               GT    T _____
GAM938  TEC      3'  CGGGGCAGAAGGATCAGGT   12217       GTCG    A     TG
                              GCCTGG    CCTT TGCCC  G
                              ||||||    |||| |||||  |
                              TGGACT    GGAA ACGGG  C
                                 A___    G     GT
GAM938  TMEM1    3'  TCAGCGGTGAGGTGGTTTAGG  12340      GT     AT  _
                              CCTGG  CGCCTT  GCC CTGG
                              |||||  ||||||  ||| ||||
                              GGATT  GTGGAG  TGG GACT
                                 TG     __  C
GAM938  TMPRSS3  5'  CCGGGCACCGGACGGCTCGGGT 50534          _ TTA    T
           A                   TGCCTGGGTCG CC   TGCCC GG
                              ||||||||||| ||   ||||| ||
                              ATGGGCTCGGC GG   ACGGG CC
                                    A  CC_    _
GAM938  TMPRSS3  5'  CCGGGCACCGGACGGCTCGGGT 43792          _ TTA    T
           A                   TGCCTGGGTCG CC   TGCCC GG
                              |||||||||||  ||   ||||| ||
                              ATGGGCTCGGC GG   ACGGG CC
                                    A  CC_    _
GAM938  TNFRSF11A 3'  GGCAGAGGCACTCAGGTA    13854        C     A
                              TGCCTGGGT GCCTT TGCC
                              |||||||| ||||| ||||
                              ATGGACTCA CGGAG ACGG
                                       _    _
GAM938  TOP3A    5'  CGGGGAGCGGCTCCGGGC    16071       _    CTTATG
                              GCCTGG GTCGC     CCCTG
                              |||||| |||||     |||||
                              CGGGCC CGGCG     GGGGC
                                 T    A_____
GAM938  TRPV1    5'  CTGGGGTGTGCCTGCGTCTAGC 38083    C    T   CT_     TG
                              GC TGGG CGC   TATGCCC  G
                              || |||| |||   |||||||  |
                              CG ATCT GCG   GTGTGGG  C
                               _   _  TCC      GT
GAM938  TSSC4    3'  CTGGGGTGTGGGGTGTGGGC   19122      GGT         TG
                              GCCTG   CGCCTTATGCCC  G
                              |||||   ||||||||||||  |
                              CGGGT   GTGGGGTGTGGG  C
                                 ___          GT
GAM938  TXNRD2   3'  GGACAGGTGGCCCGTGT     21236    C        TATG
                              GC TGGGTCGCCT    CC
                              || ||||||||||    ||
                              TG GCCCGGTGGA    GG
                               T         CA__
GAM938  UFD1L    5'  CTGGGGCGTACCGGCTTGGCGC 73286    _ TG    CCT      TG
                              GC C  GGTCG   TATGCCC  G
                              || |  |||||   |||||||  |
```

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                                CG G  TCGGC   ATGCGGG  C
                                 C GT    C__      GT
GAM938  UNC13    5'  GGGCGGGTCCGAGGCA     21058      G  TC    TAT
                                TGCCT GG  GCCT   GCCC
                                |||||  ||  ||||   ||||
                                ACGGA CC  TGGG   CGGG
                                  G  __    ___
GAM938  UNRIP    5'  TCAGGGCGGGGGCCTGGAGCA  23204     _ TG    G  TTAT
                                TGC C  GGTC CC    GCCCTGG
                                |||  |  ||||  ||    |||||||
                                ACG G  CCGG GG    CGGGACT
                                  A GT    G  ____
GAM938  UTY      5'  AGATGTGATCCAGGTA      23068           CTTATGCC
                                TGCCTGGGTCGC       CT
                                ||||||||||||       ||
                                ATGGACCTAGTG       GA
                                       TA_______
GAM938  VEGFB    5'  GGCGGGCGGCCCCGGC      12590     T       TAT
                                GCC GGGTCGCCT   GCC
                                |||  |||||||||   |||
                                CGG CCCGGCGGG   CGG
                                  C       ___
GAM938  VGF      3'  GAGGGCGGGTGGTTTGTGC   12593    C   GT    TAT    GG
                                GC TGG  CGCCT   GCCCT
                                ||  |||  |||||   |||||
                                CG GTT  GTGGG   CGGGA
                                 T   TG     ___     GG
GAM938  VIPR2    3'  TTGGGGCGCCCACCCGGCCCGG 12620     T     CCTTA_    TG
            C                    GCC GGGTCG     TGCCC  G
                                |||  ||||||     |||||  |
                                CGG CCCGGC     GCGGG  T
                                  _     CCACCC     GT
GAM938  WEE1     5'  CCGGCTTTCGGGTCGGCTTAGG 12650          _   TAT_   CTGG
            C                    GCCTGGGTCG CCT    GCC
                                ||||||||||  |||    |||
                                CGGATTCGGC GGG    CGG
                                       T   CTTT   CC
GAM938  WHSC1    3'  TCAGGGACCTAGGCAACCTGGG 23668     TG   C    TATG
            C                    GCC  GGT GCCT    CCCTGG
                                |||  |||  ||||    ||||||
                                CGG  CCA CGGA    GGGACT
                                  GT   A    TCCA
GAM938  WNT6     3'  TCAGGGCACCGGCACCGGGC   21515       _    CCTTA
                                GCCTGG GTCG     TGCCCTGG
                                ||||||  ||||    ||||||||
                                CGGGCC CGGC     ACGGGACT
                                   A    C____
GAM938  WT1      5'  CGGGACGGCAGCCCAGGC     44351         C   TTAT C
                                GCCTGGGT GCC    G CCTG
                                ||||||||  |||    |  ||||
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                                CGGACCCG CGG    C GGGC
                                    A  ____ A
GAM938  WT1     5'  CGGGACGGCAGCCCAGGC    44361        C   TTAT C
                                GCCTGGGT GCC    G CCTG
                                |||||||| |||    | ||||
                                CGGACCCG CGG    C GGGC
                                    A  ____ A
GAM938  WT1     5'  CGGGACGGCAGCCCAGGC    44371        C   TTAT C
                                GCCTGGGT GCC    G CCTG
                                |||||||| |||    | ||||
                                CGGACCCG CGG    C GGGC
                                    A  ____ A
GAM938  WT1     5'  CGGGACGGCAGCCCAGGC    4586         C   TTAT C
                                GCCTGGGT GCC    G CCTG
                                |||||||| |||    | ||||
                                CGGACCCG CGG    C GGGC
                                    A  ____ A
GAM938  WWOX    3'  GGGCTGGGCTAGGCA      33046       GGTC    TAT
                                TGCCTG    GCCT   GCCC
                                ||||||    ||||   ||||
                                ACGGAT    CGGG   CGGG
                                   ____    T__
GAM938  XK      3'  GGGGGTGTCCAGGCA      40802        T    TTATG
                                TGCCTGGG CGCC     CCC
                                |||||||| ||||     |||
                                ACGGACCT GTGG     GGG
                                   _   _____
GAM938  XKRY    3'  GCAACCAAGGTGGTCGGGCA   16257      G GT     A__
                                TGCCT G  CGCCTT   TGC
                                ||||| |  ||||||   |||
                                ACGGG C  GTGGAA   ACG
                                   _ TG     CCA
GAM938  XKRY    3'  GCAACCAAGGTGGTCGGGCA   60019      G GT     A__
                                TGCCT G  CGCCTT   TGC
                                ||||| |  ||||||   |||
                                ACGGG C  GTGGAA   ACG
                                   _ TG     CCA
GAM938  ZNF134  5'  CCAGGGTCCCGCGACCTGGG   12847    TG     CTTAT
                                CC  GGTCGC    GCCCTGG
                                ||  ||||||    |||||||
                                GG  CCAGCG    TGGGACC
                                 GT     CCC__
GAM938  ZNF261  3'  TCAGGGTGACAGGCCCAGG    17497        GCCTTAT
                                CCTGGGTC      GCCCTGG
                                ||||||||      |||||||
                                GGACCCGG      TGGGACT
                                    ACAG___
GAM938  ZNF74   5'  CCGGGGCGTGAGTGCGCCGAGC 12792     C G  T  _
            A                    TGC T GG CGC CTTATGCCCTGG
                                ||| | || ||| ||||||||||||
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                                ACG A CC GCG GAGTGCGGGGCC
                                  _ G  _  T
GAM938  20D7-FC4  3'  CTGGGGTTCAGCAGGGGTGACC 60900          AT____   TG
          CAGG                    TGGGTCGCCTT     GCCC  G
                                ||||||||||      ||||  |
                                ACCCAGTGGGG     TGGG  C
                                      ACGACT    GT
GAM938  20D7-FC4  3'  GGGTCTCGTTCAGGCA      60906        T  CCTTAT
                                TGCCTGGG CG     GCCC
                                |||||||| ||     ||||
                                ACGGACTT GC     TGGG
                                    _  TC____
GAM938  ACTR2     3'  CTGGGATGGGGGGGTGGTTCGGG 19150      GG      ATG_  TGG
                                CCTG  TCGCCTT    CCC
                                ||||  |||||||    |||
                                GGGC  GGTGGGG    GGG
                                  TT      GGTA   TC
GAM938  ACTR3     5'  CCGGACGGTGAAGGCGGCCCAG 19146    C         A   __
          C                      GC TGGGTCGCCTT TGCC  CTGG
                                || ||||||||||| ||||  ||||
                                CG ACCCGGCGGAA GTGG  GGCC
                                 _         _   CA
GAM938  ADAMTS10  5'  CCAGAGAGGGAGGCCCAGGT   48231         G   ATGCC
                                GCCTGGGTC CCTT    CTGG
                                |||||||| ||||    ||||
                                TGGACCCGG GGGA    GACC
                                     A   GA___
GAM938  AF093680  5'  TCGGCTCCGGGGGCGGCTTAGG 25091           AT__  CTGG
                                CCTGGGTCGCCTT   GCC
                                ||||||||||||    |||
                                GGATTCGGCGGGG   CGG
                                      GCCT  CT
GAM938  AGS3      5'  CCAGGGCGACAGGCTCAGGC   73111         GCCTTA
                                GCCTGGGTC     TGCCCTGG
                                |||||||||     ||||||||
                                CGGACTCGG     GCGGGACC
                                     ACA___
GAM938  ALOXE3    5'  CCAGGGCATCAGTCCGGGC    41262        TCGC  T
                                GCCTGGG   CT ATGCCCTGG
                                |||||||   || |||||||||
                                CGGGCCT   GA TACGGGACC
                                    ____  C
GAM938  ALTE      3'  GGGCGGTGGCCGGGC       16391        G    TTAT
                                GCCTGG TCGCC   GCCC
                                |||||| |||||   ||||
                                CGGGCC GGTGG   CGGG
                                   _   ____
GAM938  APBA3     5'  GGGACGCGGCCCGGGC      16883          CTTATG
                                GCCTGGGTCGC    CCC
                                ||||||||||     |||
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                              CGGGCCCGGCG     GGG
                                    CA____
GAM938  APELIN   3'  GGCCAGGGTACTCTAATAGGGG 33786       A_______
            CGGCTCAGGCA              CGCCTT      TGCCCTGG   CC
                              ||||||      ||||||||   ||
                              GCGGGG      ATGGGACC   GG
                                 ATAATCTC
GAM938  ARFGAP1  5'  GGTGGGCGACCGGGC      36594       G     TAT
                              GCCTGG TCGCCT   GCC
                              |||||| ||||||   |||
                              CGGGCC AGCGGG   TGG
                                 _    ___
GAM938  ARHGEF2  3'  GGGTATATTCAGGC       16363        CGCCTT
                              GCCTGGGT     ATGCCC
                              ||||||||     ||||||
                              CGGACTTA     TATGGG
                                   _______
GAM938  ARHGEF4  5'  CCAGGGTCCGCGCGGCTTGGGC 52208     TG     CTTAT
            A                   TGCC  GGTCGC    GCCCTGG
                              ||||  ||||||    |||||||
                              ACGG  TCGGCG    TGGGACC
                                GT     CGCC_
GAM938  ARL5     5'  CCGGGGGAAGCCAGGCGGCCCG 23938           TATG__
            GGT                  GCCTGGGTCGCCT     CCCTGG
                              ||||||||||||||     ||||||
                              TGGGCCCGGCGGA     GGGGCC
                                    CCGAAG
GAM938  ATP6V0A1 3'  TCAGGAGGGGTGTCCTGGGCA  17732     TG  T     ATGC
                              TGCC  GG CGCCTT    CCTGG
                              ||||  || ||||||    |||||
                              ACGG  CC GTGGGG    GGACT
                                GT  T     A___
GAM938  ATP9A    3'  GGGTAGGCTGGGCA       62049       GGTC    TAT
                              TGCCTG    GCCT   GCCC
                              ||||||    ||||   ||||
                              ACGGGT    CGGA   TGGG
                                   ____    ___
GAM938  B7       3'  GCGAAGGCGGCTGGGGT     22767      G       A
                              GCCT GGTCGCCTT TGC
                              |||| ||||||||| |||
                              TGGG TCGGCGGAA GCG
                                G       _
GAM938  BLCAP    3'  CTGGACTCCGAGGTGGTTCAGA 21979    C   GG      ATG__  CTGG
            CA                    TG CTG  TCGCCTT    CC
                              || |||  |||||||    ||
                              AC GAC  GGTGGAG    GG
                               A  TT      CCTCA  TC
GAM938  BLR1     3'  CTGGGGTGTGGGAGGCCCGTCC 8158     ___     GC       TG
            GGCA                   CC   TGGGTC  CTTATGCCC  G
                              ||   ||||||  |||||||||  |
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                              GG  GCCCGG  GGGTGTGGG  C
                               CCT     A_       GT
GAM938  BLR1     3'  CTGGGGTGTGGGAGGCCCGTCC 52003    ___     GC       TG
            GGCA                  CC  TGGGTC  CTTATGCCC  G
                              ||  ||||||  |||||||||  |
                              GG  GCCCGG  GGGTGTGGG  C
                               CCT     A_       GT
GAM938  BPES     3'  GGCAGCGGCCGACCTAGGC   43533         _ TTA
                              GCCTGGGTCG CC   TGCC
                              ||||||||||  ||   ||||
                              CGGATCCAGC GG   ACGG
                                    C  CG_
GAM938  BPESC1   3'  GAGGTGATGTTAGGTA     41473        _
                              TGCCTGG GTCGCCTT
                              |||||||  ||||||||
                              ATGGATT TAGTGGAG
                                  G
GAM938  BRE      5'  GGGGCGCGCTCGGGTA     16916        T   CTTAT
                              TGCCTGGG CGC    GCCCT
                              ||||||||  |||    |||||
                              ATGGGCTC GCG    CGGGG
                                    _  _____
GAM938  BRP44l   5'  CGGGGGGTTGGCCTGGGT    32243     TG    _ TTATG
                              GCC  GGTCG CC    CCCTG
                              |||  |||||  ||    |||||
                              TGG  CCGGT GG    GGGGC
                               GT    T  _____
GAM938  BTBD1    5'  CCGGCCTCCGGAGGCGGCCTGG 47475    TG       AT___   CTGG
            GC                    CC  GGTCGCCTT    GCC
                              ||  |||||||||    |||
                              GG  CCGGCGGAG    CGG
                               GT       GCCTC   CC
GAM938  BTBD3    3'  CTGGGGTGTGTGTGTGCCTGCG 30308     C    _  CT     TG
            CA                    TGC TGGGT CGC  TATGCCC  G
                              |||  |||||  |||  |||||||  |
                              ACG GTCCG GTG  GTGTGGG  C
                               C    T  T_     GT
GAM938  BTEB5    3'  AGGGTGGGTCCAGGCA     56910       GTC   TAT
                              TGCCTGG   GCCT   GCCCT
                              |||||||   ||||   |||||
                              ACGGACC   TGGG   TGGGA
                                    ___   ___
GAM938  C11orf21 3'  GCTTAGGGTGGTTTGAGGT   26241     _ GT     T
                              GCCT GG  CGCCTTA GC
                              ||||  ||  |||||||  ||
                              TGGA TT  GTGGGAT CG
                                G  TG      T
GAM938  C11orf9  3'  CCAGGGACCAGGGGTGCCCAGG 25208         T     ATG_
            CA                    TGCCTGGG CGCCTT    CCCTGG
                              ||||||||  ||||||    ||||||
```

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                                ACGGACCC GTGGGG   GGGACC
                                    _     ACCA
GAM938  C17orf31  5'  CTGGGGCGTAAGGTCAGAGGT  34122     GGGTC        TG
                                GCCT    GCCTTATGCCC  G
                                ||||    ||||||||||  |
                                TGGA    TGGAATGCGGG  C
                                  GAC__         GT
GAM938  C1QR1     3'  TCAGGGTGTGAGGAGGCTGGGG 23844     G   G
                                CCT GGTC CCTTATGCCCTGG
                                ||| |||| ||||||||||||
                                GGG TCGG GGAGTGTGGGACT
                                  G   A
GAM938  C1QTNF7   3'  CCAGACAGAGGGGCGGCCGGGC 49157       G     A_  CC
           A                     TGCCTGG TCGCCTT  TG  CTGG
                                ||||||| |||||||  ||  ||||
                                ACGGGCC GGCGGGG  AC  GACC
                                    _     AG  A_
GAM938  C20orf102 3'  GGAGAAGGTGGCCCTGGGCA   54618      _       ATG
                                TGCCT GGGTCGCCTT   CC
                                ||||| ||||||||||   ||
                                ACGGG CCCGGTGGAA   GG
                                   T        GA_
GAM938  C20orf150 3'  CAGGGTGGAGATCTGGGT    65391     TG   G  TTAT
                                GCC  GGTC CC    GCCCTG
                                |||  |||| ||    ||||||
                                TGG  CTAG GG    TGGGAC
                                  GT    A  ____
GAM938  C20orf172 3'  AAGGTGATTTTAGGTA      46209        _
                                TGCCTGGG TCGCCTT
                                |||||||| |||||||
                                ATGGATTT AGTGGAA
                                     T
GAM938  C20orf18  5'  GGGTGGTGTCCGGGC       48343       T   TTAT
                                GCCTGGG CGCC    GCCC
                                ||||||| ||||    ||||
                                CGGGCCT GTGG    TGGG
                                    _   ____
GAM938  C20orf18  5'  GGGTGGTGTCCGGGC       48348       T   TTAT
                                GCCTGGG CGCC    GCCC
                                ||||||| ||||    ||||
                                CGGGCCT GTGG    TGGG
                                    _   ____
GAM938  C20orf28  5'  GGGCGGGACCCGGCA       31228     T    G  TTAT
                                TGCC GGGTC CC    GCCC
                                |||| ||||| ||    ||||
                                ACGG CCCAG GG    CGGG
                                  _    _ ____
GAM938  C20orf30  5'  CTGGGTGTGCGGGCGGCCTGGC 26250     T       _      TGG
                                GCC GGGTCGCCT TATGCCC
                                ||| ||||||||| |||||||
```

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                                CGG TCCGGCGGG GTGTGGG
                                  _       C      TC
GAM938  C20orf42  3'  TGGGGTGTAAGGATAAGGCA  34582      GGGTCG       TG
                                TGCCT     CCTTATGCCC  G
                                |||||     ||||||||||  |
                                ACGGA     GGAATGTGGG  T
                                   ATA___        GT
GAM938  C20orf44  3'  CCAGGGCCTGCTGTGGCCTAGG 36760         CT  T
                                CCTGGGTCGC  TA GCCCTGG
                                ||||||||||  || |||||||
                                GGATCCGGTG  GT CGGGACC
                                      TC  C
GAM938  C20orf55  3'  GGCAGCTGGCCTAGGT      48660         _ CTTA
                                GCCTGGGTC GC    TGCC
                                |||||||| ||    ||||
                                TGGATCCGG CG    ACGG
                                     T _____
GAM938  C20orf64  5'  CCGGGGTGGACGCATTCGGGTA 53220         _ _  TTAT
                                TGCCTGGGT CG CC    GCCCTGG
                                |||||||| || ||    |||||||
                                ATGGGCTTA GC GG    TGGGGCC
                                     C  A _____
GAM938  C21orf69  3'  GGGGGTCCTGGCGGCCTGGGC  54214     TG     TTAT    GG
                                GCC  GGTCGCC    GCCCT
                                |||  |||||||    |||||
                                CGG  CCGGCGG    TGGGG
                                  GT      TCC_    GT
GAM938  C22orf4   3'  TCGGGGTGTGCTGTCTGG    60646   TG  TC  CTT
                                C  GG  GC   ATGCCCTGG
                                |  ||  ||   |||||||||
                                G  CT  CG   TGTGGGGCT
                                 GT  GT  ___
GAM938  C5orf3    5'  GGGGCAGGGCCCGGGCA     37963        CG   TAT
                                TGCCTGGGT  CCT   GCCCT
                                |||||||||  |||   |||||
                                ACGGGCCCG  GGA   CGGGG
                                           __   ___
GAM938  C8orf14   5'  AGGGCAGGACCGGGCA      53997        GT GCCTTA
                                TGCCTGG  C     TGCCCT
                                |||||||  |     ||||||
                                ACGGGCC  G     ACGGGA
                                    AG _______
GAM938  CACNA1H   3'  CGGGGTGGAGGCCCAGGCA   40841         G  TTAT   TG
                                TGCCTGGGTC CC    GCCC  G
                                |||||||||| ||    ||||  |
                                ACGGACCCGG GG    TGGG  C
                                      A _____    GT
GAM938  CAMKK2    3'  TGGGGTATGAGGAAACCAGG  21589      GTCG       TG
                                CCTGG    CCTTATGCCC  G
                                |||||    ||||||||||  |
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                                GGACC   GGAGTATGGG  T
                                  AAA_       GT
GAM938  CARD14   3'  GGGTGGGGCGCCTGGGT    44107    TG  T    AT
                                GCC  GG CGCCTT  GCCC
                                |||  || ||||||  ||||
                                TGG  CC GCGGGG  TGGG
                                  GT  _    __
GAM938  CARD9    3'  CTGGCCGTGGAGGGCAGGCTCA 42287       _   AT___  CTGG
           GGC                   CTGGGTC GCCTT    GCC
                                |||||||  |||||    |||
                                GACTCGG CGGGA    CGG
                                   A    GGTGC   TC
GAM938  CBARA1   3'  ATGAGGATGACCTAGGCA    20290          _
                                TGCCTGGGTCG CCTTAT
                                ||||||||||| ||||||
                                ACGGATCCAGT GGAGTA
                                      A
GAM938  CCR6     3'  CTAGGGTATATATCCGCCTGGC 15167     T   CGCCT
           A                    TGCC GGGT    TATGCCCTGG
                                |||| ||||    ||||||||||
                                ACGG TCCG    ATATGGGATC
                                  _   CCTAT
GAM938  CCR6     3'  CTAGGGTATATATCCGCCTGGC 48582     T   CGCCT
           A                    TGCC GGGT    TATGCCCTGG
                                |||| ||||    ||||||||||
                                ACGG TCCG    ATATGGGATC
                                  _   CCTAT
GAM938  CDIPT    3'  CGGGGTGCCGGGACCGGGCA   20888      G  G  TTA    TG
                                TGCCTGG TC CC   TGCCC  G
                                |||||||  || ||   |||||  |
                                ACGGGCC AG GG   GTGGG  C
                                   _ _  CC_    GT
GAM938  CECR7    5'  CTGGGGAGCCCGGTGACCCAGG 79620          TTATG   TG
           CA                     TGCCTGGGTCGCC    CCC  G
                                ||||||||||||    |||  |
                                ACGGACCCAGTGG    GGG  C
                                      CCCGA   GT
GAM938  CENTA1   3'  CGTGGGGTGTTTGGGT     22494     TG  T
                                GCC  GG CGCCTTATG
                                |||  || |||||||||
                                TGG  TT GTGGGGTGC
                                  GT  _
GAM938  CLDN4    3'  CAGAGAGGCGGCTCAGGT    7135           ATGCC
                                GCCTGGGTCGCCTT    CTG
                                ||||||||||||||    |||
                                TGGACTCGGCGGAG    GAC
                                      A____
GAM938  CNNM2    5'  GGGGGCAAGGGTGGCTCGGG   34463          A     GG
                                CCTGGGTCGCCTT TGCCCT
                                |||||||||||| ||||||
```

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                                GGGCTCGGTGGGA ACGGGG
                                      _     GC
GAM938  COE2     5'  CTAGGGTGGAGTGGCTGAGGC  64250     G     _  TAT
                                GCCT GGTCGC CT   GCCCTGG
                                |||| |||||| ||   |||||||
                                CGGA TCGGTG GG   TGGGATC
                                  G     A ___
GAM938  CRA      3'  CCAGGGCTGCTGCTGCCTGGGT 21970     TG   C  CTTAT
           A                     TGCC  GGT GC    GCCCTGG
                                ||||  ||| ||    |||||||
                                ATGG  CCG CG    CGGGACC
                                  GT   T  TCGT_
GAM938  CRK7     3'  GCAGGCGACTTAGG       33254          TAT
                                CCTGGGTCGCCT   GC
                                ||||||||||||   ||
                                GGATTCAGCGGA   CG
                                      ___
GAM938  CTNNBIP1  5'  CCGGGTCGGGCGGCCCAGG   39662         TAT   T
                                CCTGGGTCGCCT   GCCC GG
                                ||||||||||||   |||| ||
                                GGACCCGGCGGG   TGGG CC
                                      C__   _
GAM938  CX46.6   3'  CCAGGGTGCCTGGTATGGGCA  39943      GGTC   TTA
                                TGCCTG   GCC   TGCCCTGG
                                ||||||   |||   ||||||||
                                ACGGGT   TGG   GTGGGACC
                                   A___   TCC
GAM938  CXYorf1   5'  CCAGGAGCCAGGGGGTGACTGG 82042     G       AT_  _
           GGT                    GCCT GGTCGCCTT   GC CCTGG
                                |||| |||||||||   || |||||
                                TGGG TCAGTGGGG   CG GGACC
                                  G       GAC  A
GAM938  CXYorf1   5'  CCAGGGCATCAGACACAGGTA  82043      G   GCCTT
                                TGCCTG GTC    ATGCCCTGG
                                |||||| |||    |||||||||
                                ATGGAC CAG    TACGGGACC
                                   A   AC___
GAM938  CXYorf1   5'  CGGGGTGGCTCGGCTCGGG   82046       __   TTAT   TG
                                CCTGGGTC  GCC   GCCC  G
                                ||||||||  |||   ||||  |
                                GGGCTCGG  CGG   TGGG  C
                                     CT   _____   GT
GAM938  CYB5-M   3'  CTAGGTGTGGTGGCTCAGGC   94564         TTAT  _
                                GCCTGGGTCGCC   GC CCTGG
                                ||||||||||||   || |||||
                                CGGACTCGGTGG   TG GGATC
                                      _____  T
GAM938  CYB5-M   3'  CTAGGTGTGGTGGCTCAGGC   47567         TTAT  _
                                GCCTGGGTCGCC   GC CCTGG
                                ||||||||||||   || |||||
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                                CGGACTCGGTGG   TG GGATC
                                      _____  T
GAM938  D21S2056E 3'  CAGCTGGGCGGCCGGGGCA   13469      G      TATGCC
                                TGCCT GGTCGCCT     CTG
                                ||||| ||||||||     |||
                                ACGGG CCGGCGGG     GAC
                                   G       TC_____
GAM938  DC-TM4F2  3'  GGGCATTTGTCTAGC      48172    C    T  CCTT
                                GC TGGG CG    ATGCCC
                                || |||| ||    ||||||
                                CG ATCT GT    TACGGG
                                 _    _  T___
GAM938  DDM36     3'  GGGAAACCGTGGCCCAGGCA   40575          CTTATG
                                TGCCTGGGTCGC     CCC
                                ||||||||||||     |||
                                ACGGACCCGGTG     GGG
                                      CCAAA_
GAM938  DDR1      3'  CAGGGAGCGATCCAGG      25695         CTTATG
                                CCTGGGTCGC     CCCTG
                                ||||||||||     |||||
                                GGACCTAGCG     GGGAC
                                     A_____
GAM938  DDR1      3'  CAGGGAGCGATCCAGG      25704         CTTATG
                                CCTGGGTCGC     CCCTG
                                ||||||||||     |||||
                                GGACCTAGCG     GGGAC
                                     A_____
GAM938  DDR1      3'  CAGGGAGCGATCCAGG      8722          CTTATG
                                CCTGGGTCGC     CCCTG
                                ||||||||||     |||||
                                GGACCTAGCG     GGGAC
                                     A_____
GAM938  DDX18     3'  GTAAAAGGTGACCTAG      22264           A
                                CTGGGTCGCCTT TGC
                                |||||||||||| |||
                                GATCCAGTGGAA ATG
                                      A
GAM938  DDX39     3'  GCACCGGGTGGCCCGGGC    57313           TA
                                GCCTGGGTCGCCT  TGC
                                ||||||||||||  |||
                                CGGGCCCGGTGGG  ACG
                                      CC
GAM938  DGCR8     5'  GGCTGCGGGCGGCTTGGGCA  42667      TG      TAT
                                TGCC  GGTCGCCT   GCC
                                ||||  ||||||||   |||
                                ACGG  TCGGCGGG   CGG
                                  GT       CGT
GAM938  DGS-A     3'  GGGTGATGGCCAGGGCA     84900      G    CCTTA
                                TGCCT GGTCG    TGCCC
                                ||||| |||||    |||||
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                                ACGGG CCGGT    GTGGG
                                  A    A____
GAM938  DHRS2    3'  AGGGGGTGTCTAGGT      19379       T   TTATG
                                GCCTGGG CGCC    CCCT
                                ||||||| ||||    ||||
                                TGGATCT GTGG    GGGA
                                  _   _____
GAM938  DJ1042K10.2 3'  GCGTCTGAGGTGGCCCAGG   31667          __
                                CCTGGGTCGCCTT  ATGC
                                ||||||||||||  ||||
                                GGACCCGGTGGAG  TGCG
                                      TC
GAM938  DJ473B4   3'  CCAGATACCAGGTGATTTATGT 38959    C       TATGCC
                                GC TGGGTCGCCT     CTGG
                                || ||||||||||     ||||
                                TG ATTTAGTGGA     GACC
                                 T        CCATA_
GAM938  DKFZP434A0225 5'  CCGGGTGGGTGGGGCGGGCTGG 93909     TG G       __   T
          GTA                    GCC  G TCGCCTTAT  GCCC GG
                                |||  | |||||||||  |||| ||
                                TGG  C GGCGGGGTG  TGGG CC
                                 GT G        GG   _
GAM938  DKFZP434B172 3'  CGGGGCAAAGGGTATGGGCA   70035       GGTC    A    TG
                                TGCCTG    GCCTT TGCCC  G
                                ||||||    ||||| |||||  |
                                ACGGGT    TGGGA ACGGG  C
                                   A___     A    GT
GAM938  DKFZp434C0923 3'  CCAGGGGGCGTGGCTTGGGCA  34211     TG    _ TATG
                                TGCC  GGTCGC CT    CCCTGG
                                ||||  |||||| ||    ||||||
                                ACGG  TCGGTG GG    GGGACC
                                  GT     C _____
GAM938  DKFZp434E0519 3'  CAGGGTAAGATTTGGGT     49984     TG    GCCTTA
                                GCC  GGTC     TGCCCTG
                                |||  ||||     |||||||
                                TGG  TTAG     ATGGGAC
                                  GT    A_____
GAM938  DKFZp434G171 5'  GGGTGTGGCCCAGCA       79438     C       CTTAT
                                TGC TGGGTCGC    GCCC
                                ||| ||||||||    ||||
                                ACG ACCCGGTG    TGGG
                                  _       _____
GAM938  DKFZP434I216 3'  CCAGGGTGTGGCTGACACCTGG 77724     _ _  _   TT
          GC                     CCT GG GTC GCC  ATGCCCTGG
                                ||| || ||| |||  |||||||||
                                GGG CC CAG CGG  TGTGGGACC
                                  T  A   T   __
GAM938  DKFZP434K028 3'  GGGCAGAGGCTGGGGCA     93236       G    GCCTTA
                                TGCCT GGTC     TGCCC
                                ||||| ||||     |||||
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                                ACGGG TCGG     ACGGG
                                  G   AG____
GAM938  DKFZP434N014 3'  TGGGGCTGCATGGCCAGGGT  60602     G    CCTTAT   TG
                                GCCT GGTCG     GCCC  G
                                |||| |||||     ||||  |
                                TGGG CCGGT     CGGG  T
                                  A    ACGT__   GT
GAM938  DKFZp434N2030 5'  GGCGAGGGCGGCTGGGC     65524     TG G      A
                                GCC  G TCGCCTT TGCC
                                |||  | ||||||| ||||
                                CGG  C GGCGGGA GCGG
                                  GT _      _
GAM938  DKFZp434P0531 3'  TCACAGCTGGGGTGGCCTGGG  92207    TG         T  CC
                                CC  GGTCGCCTTA GC  TGG
                                ||  |||||||||| ||  |||
                                GG  CCGGTGGGGT CG  ACT
                                 GT         _  AC
GAM938  DKFZP434P211 3'  TCAGTGAAGAGGGGCTCAGGCA 27269          G    ATGCC
                                TGCCTGGGTC CCTT     CTGG
                                |||||||||| ||||     ||||
                                ACGGACTCGG GGAG     GACT
                                       _    AAGT_
GAM938  DKFZP547E1010 5'  TCGGGGTATGATAGGTCGGGG  66938     G GT GCC
                                CCT G  C   TTATGCCCTGG
                                ||| |  |  ||||||||||
                                GGG C  G   AGTATGGGGCT
                                  G TG AT_
GAM938  DKFZP547E1010 5'  TCGGGGTATGATAGGTCGGGG  31545     G GT GCC
                                CCT G  C   TTATGCCCTGG
                                ||| |  |  ||||||||||
                                GGG C  G   AGTATGGGGCT
                                  G TG AT_
GAM938  DKFZp547M072 5'  GGGCCCGGCGGCCGAGGC     61083      G      TTAT
                                GCCT GGTCGCC    GCCC
                                |||| |||||||    ||||
                                CGGA CCGGCGG    CGGG
                                  G      CC__
GAM938  DKFZP564I1171 5'  GGGTGAGAGGTGGCCTGGC    71590     T        A
                                GCC GGGTCGCCTT TGCCC
                                ||| |||||||||| |||||
                                CGG TCCGGTGGAG GTGGG
                                  _         A
GAM938  DKFZP564K0822 3'  CCAGGGCATTCTCAGGCCCGGG 94045         GCCTT
                                CCTGGGTC     ATGCCCTGG
                                ||||||||     |||||||||
                                GGGCCCGG     TACGGGACC
                                     ACTCT
GAM938  DKFZP564O0423 3'  GGGCTGCAGGTGACTCAG     91698           TAT
                                CTGGGTCGCCT   GCCC
                                ||||||||||   ||||
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                                GACTCAGTGGA  CGGG
                                      CGT
GAM938  DKFZP566M1046 3'  TCAGGGCCATGGGTGGCCCGGG 49539          TAT
          C                    GCCTGGGTCGCCT  GCCCTGG
                               ||||||||||||  |||||||
                               CGGGCCCGGTGGG  CGGGACT
                                     TAC
GAM938  DKFZP566M114 3'  TGGGGCATAACTCATTAGCA  49544    C__   CGCCT    TG
                               TGC  TGGGT   TATGCCC  G
                               |||  |||||   |||||||  |
                               ACG  ACTCA   ATACGGG  T
                                 ATT    _____     GT
GAM938  DKFZP586I2223 3'  GGGCTGGCCGGGGCA     31271     G   CCTTAT
                               TGCCT GGTCG    GCCC
                               ||||| |||||    ||||
                               ACGGG CCGGT    CGGG
                                  G   _______
GAM938  DKFZP586I2223 3'  GGGCTGGCCGGGGCA     54912     G   CCTTAT
                               TGCCT GGTCG    GCCC
                               ||||| |||||    ||||
                               ACGGG CCGGT    CGGG
                                  G   _______
GAM938  DKFZP586I2223 3'  GGGCTGGCCGGGGCA     54921     G   CCTTAT
                               TGCCT GGTCG    GCCC
                               ||||| |||||    ||||
                               ACGGG CCGGT    CGGG
                                  G   _______
GAM938  DKFZP586J1624 3'  GGTAGGGGCAGTCTGGGCA   31397    TG  TC   A
                               TGCC  GG  GCCTT TGCC
                               ||||  ||  ||||| ||||
                               ACGG  CT  CGGGG ATGG
                                 GT  GA   _
GAM938  DKFZP586J1624 3'  CCAGCACCAGGGTGGCCCGTGT 31391    C       A_  CC
                               GC TGGGTCGCCTT  TGC  TGG
                               || ||||||||||  |||  |||
                               TG GCCCGGTGGGA  ACG  ACC
                                T         CC  __
GAM938  DKFZp761A132 3'  CCAGGGTGTGGCCATCCCCAGC 50184    C   TC__  TT
          A                    TGC TGGG   GCC  ATGCCCTGG
                               |||  ||||   |||  |||||||||
                               ACG ACCC   CGG  TGTGGGACC
                                 _   CTAC  __
GAM938  DKFZp761F2014 3'  CCAGGGGTCCGTGGTCCAGCA  39535    C  GT  CTTATG
                               TGC TGG  CGC    CCCTGG
                               ||| |||  |||    ||||||
                               ACG ACC  GTG    GGGACC
                                 _  TG  CCTG__
GAM938  DKFZp761O17121 5'  CCAGCCAAGGCTGTTCAGGT  50137     GG C   ATGCC
                               GCCTG  T GCCTT    CTGG
                               |||||  | |||||   ||||
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                                TGGAC  G CGGAA    GACC
                                   TT T    CC___
GAM938  DKFZp761O17121 3'  TTGGGGTGTAGGGCCTTCCACG 50145    C   TC        TG
           T                    GC TGGG  GCCTTATGCCC  G
                                || ||||  ||||||||||  |
                                TG ACCT  CGGGATGTGGG  T
                                 C   TC         GT
GAM938  DKFZp762A227 5'  CCAGGGCACCATAGTGTCTGGG 26035    TG  T   CTTA_
           T                    GCC  GG CGC    TGCCCTGG
                                |||  || |||    ||||||||
                                TGG  CT GTG    ACGGGACC
                                  GT  _   ATACC
GAM938  DKFZp762P2111 3'  GGGCTAGGAGATCTGGGT    86360    TG   G   TAT
                                GCC  GGTC CCT   GCCC
                                |||  |||| |||   ||||
                                TGG  CTAG GGA   CGGG
                                  GT    A   T__
GAM938  DLAT    5'  TTGGGGTGTGGGGGGTTGGTGG 67469     TG_ GT G       TG
           CA                   TGCC   G  C CCTTATGCCC  G
                                ||||   |  | ||||||||||  |
                                ACGG   T  G GGGGTGTGGG  T
                                   TGG TG _        GT
GAM938  DMTF1    3'  CTGGCAGTGGGAGCTGATTTAG 40940        _ _   _   CTGG
           GCA                    CCTGGGTC GC CTTA TGCC
                                |||||||| || |||| ||||
                                GGATTTAG CG GGGT ACGG
                                     T  A   G   TC
GAM938  DNAJC5   3'  CCGGTTCACGAGGGGGTCCGGG 61451       GT G   TA  CC
           CA                   TGCCTGG  C CCT  TG  CTGG
                                |||||||  | |||  ||  ||||
                                ACGGGCC  G GGA  AC  GGCC
                                    TG G   GC  TT
GAM938  DNAL4    3'  CAGGGTGTGGACGGGGCA    19213      GG   GCCT
                                TGCCT  GTC   TATGCCCTG
                                |||||  |||   |||||||||
                                ACGGG  CAG   GTGTGGGAC
                                   G_  _____
GAM938  DNCI2    5'  GGTGTTGGGGGCTTAGGC    60966        G   T
                                GCCTGGGTC CCT ATGCC
                                ||||||||| ||| |||||
                                CGGATTCGG GGG TGTGG
                                      _  T
GAM938  DTX2     3'  GGCTGGGTGGCCAGGCA     71952       G     TAT
                                TGCCTGG TCGCCT   GCC
                                ||||||| ||||||   |||
                                ACGGACC GGTGGG   CGG
                                   _     T__
GAM938  ECE2     5'  CGGGGCCGCGGCCCGGG     28066         CTTAT
                                CCTGGGTCGC    GCCCTG
                                ||||||||||    ||||||
```

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                                GGGCCCGGCG    CGGGGC
                                     C____
GAM938  EFS2    5'  CCGGGGCGCCCCCGCGGCCTAG 19620         CTTA_
            G                    CCTGGGTCGC    TGCCCTGG
                                 ||||||||||    ||||||||
                                 GGATCCGGCG    GCGGGGCC
                                      CCCCC
GAM938  EHM2    5'  GCGAGAGGCGGCGCGGGC    38916      G      A
                                 GCCTG GTCGCCTT TGC
                                 ||||| |||||||| |||
                                 CGGGC CGGCGGAG GCG
                                    G       A
GAM938  ELF4    3'  CTAGGGCATATGCTTTTGGCA  7432      TGGGTC  CT
                                 TGCC     GC  TATGCCCTGG
                                 ||||     ||  ||||||||||
                                 ACGG     CG  ATACGGGATC
                                   TTTT__  T_
GAM938  EMILIN  3'  CCGGGGCGCGCCGGCTCAGG   22908         CCTTA
                                 CCTGGGTCG    TGCCCTGG
                                 |||||||||    ||||||||
                                 GGACTCGGC    GCGGGGCC
                                      CGC__
GAM938  ETR101  3'  CTGGGAGAAGGGAGGCTTGGGT 72366     TG   G_   ATG   TGG
                                 GCC  GGTC  CCTT   CCC
                                 |||  ||||  ||||   |||
                                 TGG  TCGG  GGAA   GGG
                                   GT    AG    GA_   TC
GAM938  ETR101  3'  CTGGGGCGTGCACCCGCCCTGG 72367     TG  T  CCT_     TG
            GCA                    TGCC  GG CG    TATGCCC  G
                                 ||||  || ||    ||||||| |
                                 ACGG  CC GC    GTGCGGG  C
                                   GT  C  CCAC      GT
GAM938  EZFIT   3'  GGGTGGGGACTCGGG      41111         G  TTAT
                                 CCTGGGTC CC    GCCC
                                 |||||||| ||    ||||
                                 GGGCTCAG GG    TGGG
                                      G  ____
GAM938  FAM10A6 3'  TAGGGTATTCATTCAG      72318       CGCCTT
                                 CTGGGT     ATGCCCTG
                                 ||||||     ||||||||
                                 GACTTA     TATGGGAT
                                    CT____
GAM938  FAM10A7 3'  TAGGGTATTCATTCAG      81246       CGCCTT
                                 CTGGGT     ATGCCCTG
                                 ||||||     ||||||||
                                 GACTTA     TATGGGAT
                                    CT____
GAM938  FBXO2   5'  CTGGGACTGCGGGGCGGCCGGG 24087       G      ATG__   TGG
            C                     GCCTGG TCGCCTT    CCC
                                 |||||| |||||||    |||
```

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                                CGGGCC GGCGGGG    GGG
                                   _     CGTCA   TC
GAM938  FBXW2    5' CGGGGCGCTCGCTCAGGTA   24085        C_  CTTAT
                                TGCCTGGGT  GC    GCCCTG
                                |||||||||  ||    ||||||
                                ATGGACTCG  CG    CGGGGC
                                     CT  _____
GAM938  FKSG28   3' GGGTGGGGGCCTGAGCA    48177    CT    G  TTAT
                                TGC  GGGTC CC    GCCC
                                |||  ||||| ||    ||||
                                ACG  TCCGG GG    TGGG
                                  AG    G  ____
GAM938  FLJ10038 5' GGCGGGGTCGGCCTGGGC    35750    TG    _  TA
                                GCC  GGTCG CCT  TGCC
                                |||  ||||| |||  ||||
                                CGG  CCGGC GGG  GCGG
                                  GT    T  __
GAM938  FLJ10154 3' CCAGGGTATTACTGGACCTATG 35853    C     GCCTT
           T                     GC TGGGTC    ATGCCCTGG
                                || ||||||    |||||||||
                                TG ATCCAG    TATGGGACC
                                 T     GTCAT
GAM938  FLJ10565 5' CTGAGCGAGGAGGCGGTTCGGG 36286      GG      A_  CCTGG
           C                     GCCTG  TCGCCTT  TGC
                                |||||  |||||||  |||
                                CGGGC  GGCGGAG  GCG
                                   TT      GA   AGTC
GAM938  FLJ10656 3' TCAGCAAAAGTGGGGATGACCC 36389        _     GCC__
           AGGCA                   CTGGGTCG CCTTAT    CTGG
                                |||||||| ||||||    ||||
                                GACCCAGT GGGGTG    GACT
                                     A     AAAAC
GAM938  FLJ10709 3' CAGGGCCAGACCCAGGT     36462         GCCTTAT
                                GCCTGGGTC      GCCCTG
                                |||||||||      ||||||
                                TGGACCCAG      CGGGAC
                                     AC_____
GAM938  FLJ10709 3' CCGGGGCAGCAGGAGCCAGGCA 36463       GTCG   TA
                                TGCCTGG   CCT  TGCCCTGG
                                |||||||   |||  ||||||||
                                ACGGACC   GGA  ACGGGGCC
                                    GA__   CG
GAM938  FLJ10874 5' TGGGGCGGTCTCAGGT     36782       _
                                GCCTGGG TCGCCTTA
                                ||||||| ||||||||
                                TGGACTC GGCGGGGT
                                     T
GAM938  FLJ10925 5' CCGGCACCGGGGGCGGCCCGGG 36883            A__   CTGG
           C                     GCCTGGGTCGCCTT   TGCC
                                ||||||||||||||   ||||
```

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                                CGGGCCCGGCGGGG  ACGG
                                      GCC   CC
GAM938  FLJ10936 5' CTGACCCTAGGGCGGCTTGCGC 36907    C        TGCCCTGG
           A                   TGC TGGGTCGCCTTA
                               ||| ||||||||||||
                               ACG GTTCGGCGGGAT
                                 C          CCCAGTC
GAM938  FLJ10956 3' TTAGGGTGTATTTCCCAGGT  36921       TCGCCT
                               GCCTGGG    TATGCCCTGG
                               |||||||    ||||||||||
                               TGGACCC    ATGTGGGATT
                                  TTT___
GAM938  FLJ10996 3' CAGCAGGTGGCCCAGG     38775         TATGCC
                               CCTGGGTCGCCT    CTG
                               ||||||||||||    |||
                               GGACCCGGTGGA    GAC
                                     C_____
GAM938  FLJ11125 3' GGAGAGAGGGACCCAGGCA   59582        G   ATG
                               TGCCTGGGTC CCTT  CC
                               |||||||||| ||||  ||
                               ACGGACCCAG GGAG  GG
                                     _   AGA
GAM938  FLJ11171 3' CTAGGGTATATACACCCACAGG 37131      _ TCGCCT
           CA                    TGCCTG GG    TATGCCCTGG
                               |||||| ||    ||||||||||
                               ACGGAC CC    ATATGGGATC
                                  A  CACAT_
GAM938  FLJ11193 3' TTGGTATCAAGGTGGTCTGGT  37156    T  GT    _   CTGG
                               GCC GG  CGCCTT ATGCC
                               ||| ||  |||||| |||||
                               TGG TC  GTGGAA TATGG
                                 _ TG    C    TT
GAM938  FLJ11710 3' TCAGGGCAGACCTGATACAGGT 45832     GG  CCTTA
                               GCCTG  TCG    TGCCCTGG
                               |||||  |||    ||||||||
                               TGGAC  AGT    ACGGGACT
                                  AT   CCAG_
GAM938  FLJ11773 5' CCAGGGCGTGAGGAGGAGG   41647    GGG  G
                               CCT   TC CCTTATGCCCTGG
                               |||   || ||||||||||||
                               GGA   GG GGAGTGCGGGACC
                                 ___  A
GAM938  FLJ12287 3' GGCTGGGCGGCCCAAGCA    42317    C       TAT
                               TGC TGGGTCGCCT   GCC
                               ||| ||||||||||   |||
                               ACG ACCCGGCGGG   CGG
                                 A        T__
GAM938  FLJ12443 3' CTGGGGTGTGAGGGCAGAGG  45727    GG  CG       TG
                               CCT  GT  CCTTATGCCC  G
                               |||  ||  ||||||||||  |
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                                GGA  CG  GGAGTGTGGG  C
                                  GA  __        GT
GAM938  FLJ12455  3'  GCGGGAGGTGGCTTGGGT    41984     TG        A
                                GCC  GGTCGCCTT TGC
                                |||  |||||||| |||
                                TGG  TCGGTGGAG GCG
                                  GT        G
GAM938  FLJ12541  3'  CCAGGGCAGCCACATCCAGGC  42328         CGCCTTA
                                GCCTGGGT      TGCCCTGG
                                ||||||||      ||||||||
                                CGGACCTA      ACGGGACC
                                     CACCG__
GAM938  FLJ12606  5'  GGCTCTGGGAGGCCCAGGT   45642         G   TAT
                                GCCTGGGTC CCT   GCC
                                ||||||||| |||   |||
                                TGGACCCGG GGG   CGG
                                     A   TCT
GAM938  FLJ12747  3'  TGGGGTGTGGCAGTTGGGCA  49730     TG GTC   TT     TG
                                TGCC  G   GCC  ATGCCC  G
                                ||||  |   |||  ||||||  |
                                ACGG  T   CGG  TGTGGG  T
                                  GT GA_  __     GT
GAM938  FLJ13055  5'  TGGGGTGCTGGACCCAGAGT   42713    _      __ CTTAT    TG
                                GC CTGGGTC  GC    GCCC  G
                                || |||||||  ||    ||||  |
                                TG GACCCAG  CG    TGGG  T
                                 A      GT  _____    GT
GAM938  FLJ13154  3'  CCAGTAGAGGGCAGCCTGGGCA 44791     TG   C    ATGCC
                                TGCC  GGT GCCTT    CTGG
                                ||||  ||| |||||    ||||
                                ACGG  CCG CGGGA    GACC
                                  GT   A    GAT__
GAM938  FLJ13189  3'  GGGGGGTGACTTAG       45986          TATG
                                CTGGGTCGCCT    CCC
                                ||||||||||    |||
                                GATTCAGTGGG    GGG
                                          ____
GAM938  FLJ13330  3'  GGGCACGTGGCCCAGGC     46977          CTTA
                                GCCTGGGTCGC    TGCCC
                                ||||||||||    |||||
                                CGGACCCGGTG    ACGGG
                                      C___
GAM938  FLJ13441  3'  CGGGGTGTGGGTGGTGGGT   43661      GG     T     TG
                                GCCTG  TCGCCT ATGCCC  G
                                |||||  |||||| ||||||  |
                                TGGGT  GGTGGG TGTGGG  C
                                   __     _     GT
GAM938  FLJ13441  3'  TGGGGGGTTGTGGTCTGTGT  43674    C   GT   CTT  G   TG
                                GC TGG  CGC   AT CCC  G
                                || |||  |||   || |||  |
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                                TG GTC  GTG   TG GGG  T
                                 T   TG   T__  G   GT
GAM938  FLJ13544  3'  TCAGGCTTGGTGGCTGGGGT   46578     G     TTAT   C
                                GCCT GGTCGCC    GCC TGG
                                |||| |||||||    ||| |||
                                TGGG TCGGTGG    CGG ACT
                                  G      TT__   _
GAM938  FLJ13782  3'  CTGGGGCATAGGACTCCAGAGT 46167    _    TCG   T     TG
            A                    TGC CTGGG   CCT ATGCCC  G
                                |||| |||||   ||| ||||||  |
                                ATG GACCT   GGA TACGGG  C
                                  A    CA_  _     GT
GAM938  FLJ13852  3'  CCAGGGCAGGCTGACTCAG    43575       _   TAT
                                CTGGGTC GCCT   GCCCTGG
                                ||||||| ||||   |||||||
                                GACTCAG CGGA   CGGGACC
                                    T   ___
GAM938  FLJ13855  3'  CAGGGTGTGGGAGTGGGGG    43582    GGG   _
                                CCT   TCGC CTTATGCCCTG
                                |||   |||| ||||||||||
                                GGG   GGTG GGGTGTGGGAC
                                  ___    A
GAM938  FLJ14129  5'  GGGTGTCGATTCGGG       48070         CCTT
                                CCTGGGTCG    ATGCCC
                                |||||||||    ||||||
                                GGGCTTAGC    TGTGGG
                                      _____
GAM938  FLJ14442  3'  GGGGTATGGTGTCCAGGTA    51371        T    TT
                                TGCCTGGG CGCC  ATGCCCT
                                |||||||| ||||  |||||||
                                ATGGACCT GTGG  TATGGGG
                                    _   __
GAM938  FLJ14486  5'  CGGGAAGCTGGCCTGGGC    51396     TG    C   ATGC
                                GCC  GGTCG CTT    CCTG
                                |||  ||||| |||    ||||
                                CGG  CCGGT GAA    GGGC
                                  GT    C   ____
GAM938  FLJ14490  3'  CCAGGAGGGAGGTGGCTTAGG  51398           ATGC
                                CCTGGGTCGCCTT    CCTGG
                                ||||||||||||    |||||
                                GGATTCGGTGGAG    GGACC
                                       GGA_
GAM938  FLJ14596  5'  CTGGGGCGTGGATGGTGCCTGG 51460    TG  T   __      TG
            G                    CC  GG CGCC  TTATGCCC  G
                                ||  || ||||  ||||||||  |
                                GG  CC GTGG  GGTGCGGG  C
                                 GT  _   TA      GT
GAM938  FLJ14642  3'  CTGGGCCATCAGGTTGTTCAGG 51498      GG C    T   _   TGG
            T                    GCCTG  T GCCT ATG CCC
                                |||||  | |||| ||| |||
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                                TGGAC  G TGGA TAC GGG
                                   TT T    C   C   TC
GAM938  FLJ14810  3'  GGGCACCAGACCAGGCA     51629       G  GCCTTA
                                TGCCTGG TC     TGCCC
                                ||||||| ||     |||||
                                ACGGACC AG     ACGGG
                                   _  ACC___
GAM938  FLJ14810  3'  GGGCTGGGGCCTAGGCA     51630         G  TTAT
                                TGCCTGGGTC CC    GCCC
                                |||||||||| ||    ||||
                                ACGGATCCGG GG    CGGG
                                      _  T___
GAM938  FLJ14834  5'  GGGAGGGGCCGCCCGGGC     51655        C    TATG
                                GCCTGGGT GCCT    CCC
                                |||||||| ||||    |||
                                CGGGCCCG CGGG    GGG
                                     C    GA__
GAM938  FLJ20006  5'  GGGCCTGGGACCCAGGT      34324        G  TTAT
                                GCCTGGGTC CC    GCCC
                                ||||||||| ||    ||||
                                TGGACCCAG GG    CGGG
                                     _  TC__
GAM938  FLJ20006  3'  GGGCGCGGTGGCTCGGGC     34325          TTA
                                GCCTGGGTCGCC   TGCCC
                                ||||||||||||   |||||
                                CGGGCTCGGTGG   GCGGG
                                       C__
GAM938  FLJ20079  5'  GCCCTGAGGCGATCTTGGCA   34494     T         T_
                                TGCC GGGTCGCCTTA  GC
                                |||| ||||||||||  ||
                                ACGG TCTAGCGGAGT  CG
                                   T         CC
GAM938  FLJ20195  3'  GTAGAGGCGGCCCACGC      34713    C         A
                                GC TGGGTCGCCTT TGC
                                || |||||||||| |||
                                CG ACCCGGCGGAG ATG
                                 C         _
GAM938  FLJ20257  5'  GGCGGGGAGGCGCTTGGGC    38998     TG  T     A_
                                GCC  GG CGCCTT  TGCC
                                |||  || ||||||  ||||
                                CGG  TC GCGGAG  GCGG
                                  GT  _     GG
GAM938  FLJ20257  3'  TTAGGGCATGGGAGGTGG     39002        __
                                TCGCCTT  ATGCCCTGG
                                |||||||  |||||||||
                                GGTGGAG  TACGGGATT
                                     GG
GAM938  FLJ20273  3'  TGGGGTGTGCACATCCAGG    38732        C_  CTT     TG
                                CCTGGGT  GC   ATGCCC  G
                                |||||||  ||   ||||||  |
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                                GGACCTA  CG   TGTGGG  T
                                    CA  ___     GT
GAM938  FLJ20321  3'  CCAGGGCCAGGTGGGGTGGACT 34946   TG GT      ___
             GGGC                   C  G  CGCCTTAT   GCCCTGG
                                |  |  ||||||||   |||||||
                                G  C  GTGGGGTG   CGGGACC
                                 GT AG       GAC
GAM938  FLJ20321  3'  CGGGGCATGGCCATCGGGT   34948      GTC   TT    TG
                                GCCTGG   GCC  ATGCCC  G
                                ||||||   |||  ||||||  |
                                TGGGCT   CGG  TACGGG  C
                                   AC_   __     GT
GAM938  FLJ20378  3'  TCAGAGGAAAGGTGGCTTTAGG 35097        _       ATG  _
             CA                   TGCCTGG GTCGCCTT   CC CTGG
                                |||||||  ||||||||   || ||||
                                ACGGATT CGGTGGAA   GG GACT
                                    T       A__  A
GAM938  FLJ20424  5'  CTGGGGTGTAGACGCTGCTGGC 35149    TG   C  C_      TG
                                GCC  GGT GC  TTATGCCC  G
                                |||  ||| ||  ||||||||  |
                                CGG  TCG CG  GATGTGGG  C
                                  __   T  CA       GT
GAM938  FLJ20546  3'  CCAGGGCTCCTTGCCTTAGGT  35366       TC  CTTAT
                                GCCTGGG  GC    GCCCTGG
                                |||||||  ||    |||||||
                                TGGATTC  CG    CGGGACC
                                   __  TTCCT
GAM938  FLJ20552  3'  CAGGGCAGGACCCGGGC     35390         GCCTTA
                                GCCTGGGTC     TGCCCTG
                                |||||||||     |||||||
                                CGGGCCCAG     ACGGGAC
                                     G_____
GAM938  FLJ20686  3'  CCGGGCACGGTGGCTCAGGC   35534           TTA    T
                                GCCTGGGTCGCC   TGCCC GG
                                ||||||||||||   ||||| ||
                                CGGACTCGGTGG   ACGGG CC
                                      C__    _
GAM938  FLJ20979  5'  CCACGCGGAGCCGGCTTGGGC  44146    TG    C   A   CC
                                GCC  GGTCG CTT TGC  TGG
                                |||  ||||| ||| |||  |||
                                CGG  TCGGC GAG GCG  ACC
                                  GT    C   _   C_
GAM938  FLJ20986  3'  AAGGAATGAGGTGTTTAGGT   44542       T      GC   GG
                                GCCTGGG CGCCTTAT  CCT
                                |||||||  ||||||||  |||
                                TGGATTT GTGGAGTA  GGA
                                   _       A_   AA
GAM938  FLJ21313  5'  GGGGCAGAGCCAGGC       43687       G  GCCTTA
                                GCCTGG TC     TGCCCT
                                ||||||  ||     ||||||
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                                CGGACC AG     ACGGGG
                                   G _______
GAM938  FLJ21477  3'  TCAGGGCAGGTCTGTGTCTAGG 47148        T   CTTA_
              T                    GCCTGGG CGC     TGCCCTGG
                                   ||||||| |||     ||||||||
                                   TGGATCT GTG     ACGGGACT
                                      _   TCTGG
GAM938  FLJ21870  3'  CCAGGGCGCAAAGCCTCGGGCA 43459         TC  C  A
                                   TGCCTGGG  GC TT TGCCCTGG
                                   ||||||||  || || ||||||||
                                   ACGGGCTC  CG AA GCGGGACC
                                        __  A  C
GAM938  FLJ21988  3'  CCAGGTGGGGTGGGGTGGCCCA 42553              G  __
              GGCA                     GCCTGGGTCGCCTTAT CC  CTGG
                                   |||||||||||||||| ||  ||||
                                   CGGACCCGGTGGGGTG GG  GACC
                                            G  TG
GAM938  FLJ22283  5'  CCGGGGTGTGGCTGCCGGGT   49915       GTC   TT
                                   GCCTGG   GCC  ATGCCCTGG
                                   ||||||   |||  |||||||||
                                   TGGGCC   CGG  TGTGGGGCC
                                      GT_   __
GAM938  FLJ22313  3'  CCAGCTACTTGGGGGGCTCAGG 42339          G   TATGCC
              CA                     TGCCTGGGTC CCT      CTGG
                                   |||||||||| |||     ||||
                                   ACGGACTCGG GGG     GACC
                                         G   TTCATC
GAM938  FLJ22329  3'  CTGGGGCACTGCCCGTGGCCTG 45066     TG     CTTA__    TG
              GGTA                     GCC  GGTCGC     TGCCC  G
                                   |||  ||||||     |||||  |
                                   TGG  CCGGTG     ACGGG  C
                                     GT     CCCGTC     GT
GAM938  FLJ22390  5'  GGCCCGGGTGGCTCGGG     42737           TAT
                                   CCTGGGTCGCCT   GCC
                                   ||||||||||||   |||
                                   GGGCTCGGTGGG   CGG
                                          CC_
GAM938  FLJ22457  3'  GCAGAGGTGACACAGGTA    46084       G       A
                                   TGCCTG GTCGCCTT TGC
                                   |||||| |||||||| |||
                                   ATGGAC CAGTGGAG ACG
                                      A       _
GAM938  FLJ22477  5'  CCGGGGTCGGGGGCGGCTTGTG 45340    C         AT
              C                     GC TGGGTCGCCTT  GCCCTGG
                                   || ||||||||||  |||||||
                                   CG GTTCGGCGGGG  TGGGGCC
                                     T         GC
GAM938  FLJ22501  5'  TCAGGGCACTCTGGCCTGTGT  45371    C      CCTTA
                                   GC TGGGTCG     TGCCCTGG
                                   || |||||||     ||||||||
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                                TG GTCCGGT    ACGGGACT
                                 T     CTC__
GAM938  FLJ22679  3'  CGGGGTGTAGTGCTGGGC   49921    TG GT  CT     TG
                                GCC  G  CGC  TATGCCC  G
                                |||  |  |||  |||||||  |
                                CGG  C  GTG  ATGTGGG  C
                                  GT __  __     GT
GAM938  FLJ23323  3'  GGGCATGGTGGCTCATGCA   45055    C      TT
                                TGC TGGGTCGCC  ATGCCC
                                |||  |||||||||  ||||||
                                ACG ACTCGGTGG  TACGGG
                                  T       __
GAM938  FLJ25467  5'  CCGGAGGAGGTGACCTAGCCG  58527    C        TATG  _
                                TG CTGGGTCGCCT    CC CTGG
                                ||  ||||||||||    ||  ||||
                                GC GATCCAGTGGA    GG GGCC
                                 C          _____  A
GAM938  FLJ32332  3'  CTAGTGCCCGGGTGTGGTCTGG  58304     TG GT  _  AT  C
          GCA                     TGCC  G  CGC CTT  GC CTGG
                                ||||  |  |||  |||  ||  ||||
                                ACGG  C  GTG  GGG  CG GATC
                                  GT TG   T   CC  T
GAM938  FLJ32356  3'  TCGGGGCTCCTGGCCTGGGC   58367    TG    CCTTAT
                                GCC  GGTCG     GCCCTGG
                                |||  |||||     |||||||
                                CGG  CCGGT     CGGGGCT
                                  GT    CCT___
GAM938  FLJ32919  3'  TTAGCCATGAGCTGGCTCAGGC  58078          C     CC
          A                      TGCCTGGGTCG  CTTATG  CTGG
                                ||||||||||  ||||||  ||||
                                ACGGACTCGGT  GAGTAC  GATT
                                       C     C_
GAM938  FLT3LG   5'  CGGGGCAAGCCTGACCCGGC   7584     T     CCTTA    TG
                                GCC  GGGTCG     TGCCC  G
                                |||  ||||||     |||||  |
                                CGG  CCCAGT     ACGGG  C
                                  _      CCGA_     GT
GAM938  FOXD4    5'  CCGGGGCTGCAGGTGGCCCGGT  82745     T       TAT
                                GCC  GGGTCGCCT   GCCCTGG
                                |||  |||||||||   |||||||
                                TGG  CCCGGTGGA   CGGGGCC
                                  _        CGT
GAM938  FSD1     5'  CCGGGCCGGGGTGACCTGGGC  44288     TG       AT   T
                                GCC  GGTCGCCTT  GCCC GG
                                |||  |||||||||  ||||  ||
                                CGG  CCAGTGGGG  CGGG CC
                                  GT       C_   _
GAM938  FXYD3    5'  TTAGGGCGTGGCAGCTTCGG   41588    TG   C   TT
                                CC  GGT GCC  ATGCCCTGG
                                ||  |||  |||  |||||||||
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                                GG  TCG CGG  TGCGGGATT
                                 CT   A  __
GAM938  FXYD3    3'  GGGTGGGGCTTGGGGCA    41587     G  TC    AT
                                TGCCT GG  GCCTT  GCCC
                                ||||| ||  |||||  ||||
                                ACGGG TT  CGGGG  TGGG
                                  G __    __
GAM938  FXYD3    3'  GGGTGGGGCTTGGGGCA    19927     G  TC    AT
                                TGCCT GG  GCCTT  GCCC
                                ||||| ||  |||||  ||||
                                ACGGG TT  CGGGG  TGGG
                                  G __    __
GAM938  FXYD3    5'  TTAGGGCGTGGCAGCTTCGG  19928    TG   C   TT
                                CC  GGT GCC  ATGCCCTGG
                                ||  ||| |||  |||||||||
                                GG  TCG CGG  TGCGGGATT
                                 CT   A  __
GAM938  GAP1IP4BP 5'  GGGCGAGGCTCGGC      23755     T  GTC    AT
                                GCC GG   GCCTT  GCCC
                                ||| ||   |||||  ||||
                                CGG CT   CGGAG  CGGG
                                  _ ___    __
GAM938  GBL      3'  GGTGCAGGTGGCCTGGC     42338     T       TAT _
                                GCC GGGTCGCCT   GC CC
                                ||| |||||||||   || ||
                                CGG TCCGGTGGA   CG GG
                                  _       ___  T
GAM938  GDBR1    5'  CCGGGGCGGGGCGGCGGCCCAG 32420    C       _ TA
          C                      GC TGGGTCGCC T  TGCCCTGG
                                || |||||||||  |  ||||||||
                                CG ACCCGGCGG G  GCGGGGCC
                                 _       C GG
GAM938  GIT1     3'  CCGGGGTCCCCGACTCAGC   25865    C      CCTTAT
                                GC TGGGTCG     GCCCTGG
                                || |||||||     |||||||
                                CG ACTCAGC     TGGGGCC
                                 _      CCC___
GAM938  GMPPB    5'  GGCGTCAGGGCGACCGGGC   25304       G     _
                                GCCTGG TCGCCTT ATGCC
                                |||||| ||||||| |||||
                                CGGGCC AGCGGGA TGCGG
                                   _      C
GAM938  GMPPB    5'  GGCGTCAGGGCGACCGGGC   41748       G     _
                                GCCTGG TCGCCTT ATGCC
                                |||||| ||||||| |||||
                                CGGGCC AGCGGGA TGCGG
                                   _      C
GAM938  GMPPB    5'  GGCGTCAGGGCGACCGGGC   95748       G     _
                                GCCTGG TCGCCTT ATGCC
                                |||||| ||||||| |||||
```

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                                CGGGCC AGCGGGA TGCGG
                                   _      C
GAM938  GPR      5'  GGCAGGCGGCCGGGC      23337       G     TAT
                                GCCTGG TCGCCT   GCC
                                |||||| ||||||   |||
                                CGGGCC GGCGGA   CGG
                                   _     ____
GAM938  GPR72    3'  GGGTGTGGTGACCCAG      69762          TT
                                CTGGGTCGCC  ATGCCC
                                ||||||||||  ||||||
                                GACCCAGTGG  TGTGGG
                                     __
GAM938  GPS2     5'  CCGGGGCAGGCGGTGGTGGCCC 15664          TTA___
             AGG                   CCTGGGTCGCC     TGCCCTGG
                                ||||||||||      ||||||||
                                GGACCCGGTGG     ACGGGGCC
                                      TGGCGG
GAM938  GPS2     3'  CAGGTGGCGTTCCAGGT     87153       GT    TTATGC
                                GCCTGG  CGCC     CCTG
                                ||||||  ||||     ||||
                                TGGACC  GCGG     GGAC
                                   TT    T_____
GAM938  GPS2     5'  CCGGGGTCCAACGGGGGTCTGG 87155      TG GT G  _  AT
             GCA                   TGCC  G  C CC TT  GCCCTGG
                                ||||  |  | || ||  |||||||
                                ACGG  C  G GG AA  TGGGGCC
                                  GT TG G  C  CC
GAM938  GRID1    3'  GGGGAGGTGCCCAGGT      68499        T     ATG
                                GCCTGGG CGCCTT   CCC
                                |||||||  ||||||   |||
                                TGGACCC GTGGAG   GGG
                                   _     ____
GAM938  GSK3A    5'  GGGCAGCCCGGGCA       95273         CGCCTTA
                                TGCCTGGGT      TGCCC
                                |||||||||      |||||
                                ACGGGCCCG      ACGGG
                                   ________
GAM938  H17      3'  CGGGGCAGCCTGGCTCAGGT   34087         CCTTA    TG
                                GCCTGGGTCG    TGCCC  G
                                ||||||||||    |||||  |
                                TGGACTCGGT    ACGGG  C
                                     CCG__    GT
GAM938  HCA127   3'  TTAGGAAGAGATGTGGTTCAGG 37952       GG    C  ATGC
             T                   GCCTG  TCGC TT    CCTGG
                                |||||  |||| ||    |||||
                                TGGAC  GGTG AG    GGATT
                                   TT    T  AGAA
GAM938  HCGIX    3'  CCAGGCGCGGTGGCTCAGGC   19572          TTAT  _
                                GCCTGGGTCGCC    GC CCTGG
                                ||||||||||||    || |||||
```

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                                CGGACTCGGTGG   CG GGACC
                                      ____ C
GAM938  HDCMA18P  3'  TCAGTGTCAGGTGATTTAG   33593         TAT  C
                                CTGGGTCGCCT   GC CTGG
                                ||||||||||   || ||||
                                GATTTAGTGGA   TG GACT
                                      C__  T
GAM938  HE3-BETA  5'  GTAGGGCGGCCCCGGT     42299     T
                                GCC GGGTCGCCTTAT
                                ||| ||||||||||||
                                TGG CCCGGCGGGATG
                                  C
GAM938  HIC2      3'  GGGTGAGGCCTGGGCA      65266      TG GTC     AT
                                TGCC  G   GCCTT  GCCC
                                ||||  |   |||||  ||||
                                ACGG  C   CGGAG  TGGG
                                  GT ____    __
GAM938  HIF3A     5'  TCAGCCAACGGGGGCCTGGGC  42413     TG    G  TTA  CC
                                GCC  GGTC CC   TG  CTGG
                                |||  |||| ||   ||  ||||
                                CGG  CCGG GG   AC  GACT
                                  GT    G  CA_  C_
GAM938  HIP-55    3'  TCAGGGCTCCCTCCGGCTTGGC 25930      T     CCTTAT
          A                      TGCC GGGTCG     GCCCTGG
                                ||||  ||||||     |||||||
                                ACGG TTCGGC     CGGGACT
                                  _     CTCCCT
GAM938  HOOK3     5'  CCGGGGTGTCAGGCTGCAGGTA 50547       GGTC    T
                                TGCCTG    GCCT ATGCCCTGG
                                ||||||    |||| |||||||||
                                ATGGAC    CGGA TGTGGGGCC
                                   GT__    C
GAM938  HRH3      3'  CAGAGGAGGTGCCCGGGCA    23365        T    TATG  _
                                TGCCTGGG CGCCT    CC CTG
                                |||||||| |||||    || |||
                                ACGGGCCC GTGGA    GG GAC
                                     _    ____ A
GAM938  HSPC049   3'  GGCAAGGAGGCTCAGGT     71921         G   TA
                                GCCTGGGTC CCT  TGCC
                                ||||||||| |||  ||||
                                TGGACTCGG GGA  ACGG
                                     A  __
GAM938  HSPC111   3'  CCAGGGTGTAAGGCAAGGAGGT 33066      GGGTC
                                GCCT    GCCTTATGCCCTGG
                                ||||    ||||||||||||||
                                TGGA    CGGAATGTGGGACC
                                  GGAA_
GAM938  HSPC121   3'  TAAAGTGACTCAGGCA      59760           C
                                TGCCTGGGTCGC TTA
                                |||||||||||| |||
```

```
                                ACGGACTCAGTG AAT
                                      A
GAM938  HSPC189  3'  CCGGGCTGCCGGGTGCCCCAGG 95276       T    TAT_   T
            TA                   TGCCTGGG CGCCT    GCCC GG
                                 |||||||| |||||    |||| ||
                                 ATGGACCC GTGGG    CGGG CC
                                     C     CCGT   _
GAM938  HSRNAFEV 5'  TCAGGGCACATGGCCCGGGC  34025         CCTTA
                                 GCCTGGGTCG    TGCCCTGG
                                 ||||||||||    ||||||||
                                 CGGGCCCGGT    ACGGGACT
                                       AC___
GAM938  HT002    5'  CCAGGTGCTGGGGGCGACTCGG 25934    C         AT  _
            ACA                    TG CTGGGTCGCCTT  GC CCTGG
                                 || ||||||||||||  || |||||
                                 AC GGCTCAGCGGGG  CG GGACC
                                   A          GT  T
GAM938  HT007    5'  GCCAAGGGATTCAGGT     37487         G    AT
                                 GCCTGGGTC CCTT  GC
                                 |||||||| ||||  ||
                                 TGGACTTAG GGAA  CG
                                       _   C_
GAM938  HT021    5'  GAGGCGGGCTCGGGCA      40349          _
                                 TGCCTGGGTC GCCTT
                                 |||||||||| |||||
                                 ACGGGCTCGG CGGAG
                                       G
GAM938  HTF9C    5'  CCAGGACGAGGTGGCCAGGC  42687       G      AT C
                                 GCCTGG TCGCCTT  G CCTGG
                                 |||||| |||||||  | |||||
                                 CGGACC GGTGGAG  C GGACC
                                    _      __ A
GAM938  HUMAGCGB 5'  GGGTGGGTGGCCTGGG     25233    TG       TAT
                                 CC  GGTCGCCT   GCCC
                                 ||  ||||||||   ||||
                                 GG  CCGGTGGG   TGGG
                                   GT       ____
GAM938  IMAGE:4907098 3'  GGGTGGACCCAGACA       91664    C      GCCTTA
                                 TG CTGGGTC     TGCCC
                                 || |||||||     |||||
                                 AC GACCCAG     GTGGG
                                   A     _______
GAM938  jdp2     3'  CTGGGTGTCGGGGGTGGCCAGG 55325      G        __      TGG
            GC                     GCCT GGTCGCCTT  ATGCCC
                                 |||| |||||||||  ||||||
                                 CGGG CCGGTGGGG  TGTGGG
                                   A        GC     TC
GAM938  KBRAS2   3'  CCAGAAAAAGGGTGTCCAGGTA 34193         T     ATGCC
                                 TGCCTGGG CGCCTT    CTGG
                                 |||||||| ||||||    ||||
```

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                                ATGGACCT GTGGGA    GACC
                                   _     AAAA_
GAM938  KCNH6    3'  GGGAGGTGGCCGGGT      47837       G     TATG
                                GCCTGG TCGCCT    CCC
                                |||||| ||||||    |||
                                TGGGCC GGTGGA    GGG
                                   _     _____
GAM938  KCNJ9    3'  CCAGGGTGCATGGCTTGGG   17152    TG    CCTTAT
                                CC  GGTCG     GCCCTGG
                                ||  |||||     |||||||
                                GG  TCGGT     TGGGACC
                                 GT    ACG___
GAM938  KCNT1    3'  GGGCAGCCGGCGGCCCAGCA  61838     C       TTA
                                TGC TGGGTCGCC   TGCCC
                                ||| |||||||||   |||||
                                ACG ACCCGGCGG   ACGGG
                                  _       CCG
GAM938  KIAA0014 3'  CCAGGGCTCCCGGCTCTAGGC 27838       TC   TTAT
                                GCCTGGG  GCC    GCCCTGG
                                |||||||  |||    |||||||
                                CGGATCT  CGG    CGGGACC
                                   __   CCCT
GAM938  KIAA0084 5'  GCGTGGAGGTGACCGGGC    68143       G     _
                                GCCTGG TCGCCTT ATGC
                                |||||| ||||||| ||||
                                CGGGCC AGTGGAG TGCG
                                   _      G
GAM938  KIAA0152 3'  TAGGGTATTGAGTCAGGCA   28304       G   CCTT
                                TGCCTGG TCG    ATGCCCTG
                                ||||||| |||    ||||||||
                                ACGGACT AGT    TATGGGAT
                                    G   ____
GAM938  KIAA0193 3'  GTACTGGGTGGTTCAGCA    28658     C  GG     TA
                                TGC TG  TCGCCT  TGC
                                ||| ||  ||||||  |||
                                ACG AC  GGTGGG  ATG
                                  _ TT     TC
GAM938  KIAA0215 3'  CAGGGTATTTGCTCAG      28417       CGCCTT
                                CTGGGT     ATGCCCTG
                                ||||||     ||||||||
                                GACTCG     TATGGGAC
                                   TT____
GAM938  KIAA0232 3'  TGGGGTGTGGGGTCGTATGC   72760    G _ _       TG
                                G GT CG CCTTATGCCC  G
                                | || || ||||||||||  |
                                C TA GC GGGGTGTGGG  T
                                 G  T  T        GT
GAM938  KIAA0276 5'  GGGCGGCGAGCCGGGT      70966       G    TTAT
                                GCCTGG TCGCC    GCCC
                                |||||| |||||    ||||
```

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                                TGGGCC AGCGG   CGGG
                                   G   ____
GAM938  KIAA0326 3' CTAGGGTGTAGCATATTTAG  64326      C_ CT
                                CTGGGT  GC  TATGCCCTGG
                                ||||||  ||  ||||||||||
                                GATTTA  CG  ATGTGGGATC
                                   TA  __
GAM938  KIAA0370 3' CGCGGGGTGGCCCATGCA   73207    C       TA
                                TGC TGGGTCGCCT  TG
                                ||| ||||||||||  ||
                                ACG ACCCGGTGGG  GC
                                  T       GC
GAM938  KIAA0376 3' GGGTGGGTTCCGGT      65601    T  TC   TAT
                                GCC GGG  GCCT   GCCC
                                ||| |||  ||||   ||||
                                TGG CCT  TGGG   TGGG
                                  _  __   ___
GAM938  KIAA0423 5' CCGGAGTTGGGGGCGGCCTGGC 87807    T       AT  C
                                GCC GGGTCGCCTT  GC CTGG
                                ||| ||||||||||  || ||||
                                CGG TCCGGCGGGG  TG GGCC
                                  _       GT  A
GAM938  KIAA0436 5' CCAGCTCTAGGCGGCTCTGGGT 60055    TG _    TAT  CC
           A                     TGCC  G GTCGCCT   GC  TGG
                                ||||  | |||||||   ||  |||
                                ATGG  C CGGCGGA   CG  ACC
                                  GT T     TCT  __
GAM938  KIAA0444 3' CCAGCCAGGGTGGCCCCGGC  62339    T       ATGCC
                                GCC GGGTCGCCTT    CTGG
                                ||| ||||||||||    ||||
                                CGG CCCGGTGGGA    GACC
                                  C       CC___
GAM938  KIAA0449 3' CGGGGATGTGTGGCCTGGGCA 34199    TG    CT  G  TG
                                TGCC  GGTCGC  TAT CCC  G
                                ||||  ||||||  ||| |||  |
                                ACGG  CCGGTG  GTA GGG  C
                                  GT    T_  _  GT
GAM938  KIAA0450 5' CAGGGCTGGCTTTGGGCA   27622    TG  TC  TTAT
                                TGCC  GG  GCC   GCCCTG
                                ||||  ||  |||   ||||||
                                ACGG  TT  CGG   CGGGAC
                                  GT  __  T___
GAM938  KIAA0451 3' GGGCATGCCCTGGGCA    29111    TG  TC  CTT
                                TGCC  GG  GC   ATGCCC
                                ||||  ||  ||   ||||||
                                ACGG  CC  CG   TACGGG
                                  GT  __  ___
GAM938  KIAA0469 3' CTGGGCAGGAGGTGGCTTTGGT 29330    TG      A   TGG
                                GCC  GGTCGCCTT TGCCC
                                |||  ||||||||| |||||
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                                TGG  TCGGTGGAG ACGGG
                                  TT       G    TC
GAM938  KIAA0470 3' TTGGGGTGTATCTTAATTCAG  29057      CGCCT     TG
                                CTGGGT    TATGCCC  G
                                ||||||    |||||||  |
                                GACTTA    ATGTGGG  T
                                   ATTCT      GT
GAM938  KIAA0523 3' CAGTGGGTGGGTTTGGGCA   67732     TG GTC    TATG  _
                                TGCC  G   GCCT    CC CTG
                                ||||  |   ||||    || |||
                                ACGG  T   TGGG    GG GAC
                                  GT ___    TG__  T
GAM938  KIAA0527 5' GGGCAGTGGCCTGGGCA    95805     TG     CTTA
                                TGCC  GGTCGC    TGCCC
                                ||||  ||||||    |||||
                                ACGG  CCGGTG    ACGGG
                                  GT     _____
GAM938  KIAA0527 5' CCGGGAGTTCGGCGGCCCAGGC 95797           TTAT  _
                                GCCTGGGTCGCC    GC CCTGG
                                ||||||||||||    || |||||
                                CGGACCCGGCGG    TG GGGCC
                                       CT__  A
GAM938  KIAA0544 3' GGGCCTGGTGACCCAGG     70906          TTAT
                                CCTGGGTCGCC    GCCC
                                ||||||||||    ||||
                                GGACCCAGTGG    CGGG
                                       TC__
GAM938  KIAA0552 3' CTGGCGCCCTGAGGTGGCTCAG 28314    C         ___    CTGG
           CA                     GC TGGGTCGCCTTA   TGCC
                                || ||||||||||||   ||||
                                CG ACTCGGTGGAGT   GCGG
                                 _         CCC    TC
GAM938  KIAA0562 5' TTGGGGTGCAAGGCGGCCTGGG 28161    TG       AT    TG
                                CC  GGTCGCCTT  GCCC  G
                                ||  |||||||||  ||||  |
                                GG  CCGGCGGAA  TGGG  T
                                 GT       CG    GT
GAM938  KIAA0574 3' GGGGGCGGTGTGGGCA      69283       GG    TTATG
                                TGCCTG  TCGCC    CCC
                                ||||||  |||||    |||
                                ACGGGT  GGCGG    GGG
                                   GT    ______
GAM938  KIAA0594 5' CTGGGTGGATGGGCGCTTGGGC 64895     TG  T    TA_    TGG
                                GCC  GG CGCCT   TGCCC
                                |||  || |||||   |||||
                                CGG  TC GCGGG   GTGGG
                                  GT  _    TAG    TC
GAM938  KIAA0596 3' CGGGGCATCAGCCTGAGT    62829    CT    CGCCTT
                                GC  GGGT     ATGCCCTG
                                ||  ||||     ||||||||
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                              TG  TCCG     TACGGGGC
                               AG   AC____
GAM938  KIAA0599  3'  ATGAAACATAAGGCACCCGGGT 77167         C       CCCTGG
          A                    TGCCTGGGT GCCTTATG
                               |||||||| ||||||||
                               ATGGGCCCA CGGAATAC
                                    _       AAAGTAT
GAM938  KIAA0607  3'  CGGGGCAGACAGGCCTGGT   72569    T    GCCTTA    TG
                               GCC GGGTC     TGCCC  G
                               ||| |||||     |||||  |
                               TGG TCCGG     ACGGG  C
                                 _    ACAG__    GT
GAM938  KIAA0618  3'  GCCTGGGGTGGCACAGGCA   29167       G       T
                               TGCCTG GTCGCCTTA GC
                               |||||| ||||||||| ||
                               ACGGAC CGGTGGGGT CG
                                  A        C
GAM938  KIAA0645  3'  CCGGGGCGGAGGATTCCAGGCA 27819         TCG    A
                               TGCCTGGG   CCTT TGCCCTGG
                               ||||||||   |||| ||||||||
                               ACGGACCT   GGAG GCGGGGCC
                                    TA_   _
GAM938  KIAA0672  5'  CGGGAGCAGGCAGCCCGGGC   29407        C    TAT  _  TG
                               GCCTGGGT GCCT   GC CC  G
                               |||||||| ||||   || ||  |
                               CGGGCCCG CGGA   CG GG  C
                                    A   ___  A  GT
GAM938  KIAA0711  3'  CGGGGTGTGGAGCCGCTAGG   29517      GTC  CT     TG
                               CCTGG   GC  TATGCCC  G
                               |||||   ||  |||||||  |
                               GGATC   CG  GTGTGGG  C
                                  GC_  AG      GT
GAM938  KIAA0711  3'  TCAGGGCAGCTGTTGTGATCTG 29526    C       CTTA__
          TGTA                   GC TGGGTCGC     TGCCCTGG
                               || ||||||||     ||||||||
                               TG GTCTAGTG     ACGGGACT
                                T       TTGTCG
GAM938  KIAA0720  3'  TTGGGGCCCAGTGACTCGGGGC 62333       _      CTTAT    TG
          A                    TGCCT GGGTCGC    GCCC  G
                               ||||| |||||||    ||||  |
                               ACGGG CTCAGTG    CGGG  T
                                  G      ACC__    GT
GAM938  KIAA0766  5'  GCTGAGGTGATCTGGC     29006     T        T
                               GCC GGGTCGCCTTA GC
                               ||| ||||||||||| ||
                               CGG TCTAGTGGAGT CG
                                 _        _
GAM938  KIAA0821  3'  CCAGGGGCTGGTGGCCCAGGC  29943          TTATG
                               GCCTGGGTCGCC    CCCTGG
                               ||||||||||||    ||||||
```

```
                                CGGACCCGGTGG    GGGACC
                                      TCG__
GAM938  KIAA0870 3' GGGTGTGTCTCAGGCA     81469        T  CTTAT
                                TGCCTGGG CGC    GCCC
                                |||||||| |||    ||||
                                ACGGACTC GTG    TGGG
                                     T  _____
GAM938  KIAA0937 3' CTAGGGTATGGGCAGTGCTTAG 91585        C__   T
           GCA                   GCCTGGGT   GCCT ATGCCCTGG
                                |||||||   |||| |||||||||
                                CGGATTCG   CGGG TATGGGATC
                                     TGA   _
GAM938  KIAA0939 3' CTGGGGTGTGGGTGTGGCCTGG 62014    TG    _       TG
           G                    CC  GGTCGC CTTATGCCC  G
                                ||  |||||| |||||||||  |
                                GG  CCGGTG GGGTGTGGG  C
                                 GT     T       GT
GAM938  KIAA0940 3' GTACAAAATAAGATGGCCTGGG 29872     TG    C    GCCCTGG
           CA                    TGCC  GGTCG CTTAT
                                ||||  ||||| |||||
                                ACGG  CCGGT GAATA
                                  GT    A    AAACATGT
GAM938  KIAA0964 5' CCGGGAGAGGTGACCCGGGC   29760           ATGC
                                GCCTGGGTCGCCTT   CCTGG
                                ||||||||||||||   |||||
                                CGGGCCCAGTGGAG   GGGCC
                                      A___
GAM938  KIAA0977 5' CCGGGGCTGGAGCGGCTCGGGC 29748          CT  T
                                GCCTGGGTCGC  TA GCCCTGG
                                ||||||||||  || |||||||
                                CGGGCTCGGCG  GT CGGGGCC
                                      AG  _
GAM938  KIAA0987 3' CAGGCGCTGGCTCAGGCA    24560          CCTTAT  _
                                TGCCTGGGTCG     GC CCTG
                                ||||||||||     || ||||
                                ACGGACTCGGT     CG GGAC
                                      _______  C
GAM938  KIAA0998 3' CATCAGGGTGACCTGAGT    30586    CT        _
                                GC  GGGTCGCCTT ATG
                                ||  |||||||||| |||
                                TG  TCCAGTGGGA TAC
                                 AG         C
GAM938  KIAA1055 3' GCTTGGGGCAGGCTTGGGT   66063     TG   _     T
                                GCC  GGTC GCCTTA GC
                                |||  |||| |||||| ||
                                TGG  TCGG CGGGGT CG
                                  GT   A     T
GAM938  KIAA1076 3' CGGGGCACCACTGACCCGGT  65514     T     CCTTA    TG
                                GCC GGGTCG    TGCCC  G
                                ||| ||||||    |||||  |
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                              TGG CCCAGT    ACGGG  C
                                _     CACC_    GT
GAM938  KIAA1094  5' GGGGGGTGGCCGGGC      29806       G     TATG
                              GCCTGG TCGCCT    CCC
                              |||||| ||||||    |||
                              CGGGCC GGTGGG    GGG
                                 _    _____
GAM938  KIAA1126  3' CGGGGCGGTGATGTTCGGGT   71925       __     TTAT   TG
                              GCCTGG  GTCGCC   GCCC  G
                              ||||||  ||||||   ||||  |
                              TGGGCT  TAGTGG   CGGG  C
                                 TG     _____   GT
GAM938  KIAA1126  3' GGTCCGGGGGGGCCTGGGCA   71934     TG   G   TAT
                              TGCC  GGTC CCT   GCC
                              ||||  |||| |||   |||
                              ACGG  CCGG GGG   TGG
                                GT   G   CC_
GAM938  KIAA1161  5' CATGAGGTGACTTGGGT    81742     TG
                              GCC  GGTCGCCTTATG
                              |||  ||||||||||||
                              TGG  TCAGTGGAGTAC
                                GT
GAM938  KIAA1169  5' TGGGGCAACTGGGCCCATGT   35452    C    CG  TTA    TG
                              GC TGGGT  CC   TGCCC  G
                              || |||||  ||   |||||  |
                              TG ACCCG  GG   ACGGG  T
                               T    __  TCA    GT
GAM938  KIAA1190  3' TCAGAATGAGGCGACTAGGGCA 71105      G         GCC
                              TGCCT GGTCGCCTTAT   CTGG
                              ||||| ||||||||||   ||||
                              ACGGG TCAGCGGAGTA   GACT
                                 A         A__
GAM938  KIAA1193  3' GGGTAGAGGTGGTCGGGGCA   67645      G GT     A
                              TGCCT G  CGCCTT TGCCC
                              ||||| |  |||||| |||||
                              ACGGG C  GTGGAG ATGGG
                                 G TG     _
GAM938  KIAA1196  3' CCAGGGCGTGGGTCTCTGGG   61462    TG  TC    T
                              CC  GG  GCCT ATGCCCTGG
                              ||  ||  |||| |||||||||
                              GG  CT  TGGG TGCGGGACC
                               GT  C_   _
GAM938  KIAA1196  3' GGGCGGGGGCCTAGGT      61478         G  TTAT
                              GCCTGGGTC CC    GCCC
                              |||||||| ||    ||||
                              TGGATCCGG GG    CGGG
                                    G  _____
GAM938  KIAA1229  3' TCAGGGCGTGGGGGGCTAGGG  62069     G   G
                              CCT GGTC CCTTATGCCCTGG
                              ||| |||| ||||||||||||
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                                GGG TCGG GGGGTGCGGGACT
                                  A   _
GAM938  KIAA1237 3' CGGGGTGTGTGATTCACGT   80467   C      CTT     TG
                                GC TGGGTCGC   ATGCCC  G
                                || ||||||||   ||||||  |
                                TG ACTTAGTG   TGTGGG  C
                                 C       ___      GT
GAM938  KIAA1396 3' GGGCGGCCATTCGGGCA     62991         C   TTAT
                                TGCCTGGGT GCC    GCCC
                                ||||||||| |||    ||||
                                ACGGGCTTA CGG    CGGG
                                     C  ____
GAM938  KIAA1464 3' GGGTGAGGCTGTCCAGGCA   68272        TC    AT
                                TGCCTGGG  GCCTT  GCCC
                                ||||||||  |||||  ||||
                                ACGGACCT  CGGAG  TGGG
                                    GT    __
GAM938  KIAA1530 5' CAGGGCGTGTCCCGTGT     67946    C   T  CTTAT
                                GC TGGG CGC     GCCCTG
                                || |||| |||     ||||||
                                TG GCCC GTG     CGGGAC
                                 T   T  _____
GAM938  KIAA1530 5' GGCCCTGGGTATCCGGGCA   67956         C    TAT
                                TGCCTGGGT GCCT   GCC
                                ||||||||| ||||   |||
                                ACGGGCCTA TGGG   CGG
                                     _   TCC
GAM938  KIAA1548 3' CGGGGCATTTACCTCAGGCA  40501       _  CGCCTT     TG
                                TGCCTG GGT     ATGCCC  G
                                |||||| |||     ||||||  |
                                ACGGAC CCA     TACGGG  C
                                   T  TT____     GT
GAM938  KIAA1615 5' CTGGCGAGTCGAGGTGACCCGG 68709           A___   CTGG
          GC                  CCTGGGTCGCCTT   TGCC
                              ||||||||||||    ||||
                              GGGCCCAGTGGAG   GCGG
                                     CTGA   TC
GAM938  KIAA1622 5' CCGGGGCCGCTCCGGCCCGGGC 40559         CCTTAT
                              GCCTGGGTCG     GCCCTGG
                              |||||||||      |||||||
                              CGGGCCCGGC     CGGGGCC
                                   CTCGC_
GAM938  KIAA1622 5' CCGGGGCCGCTCCGGCCCGGGC 54260         CCTTAT
                              GCCTGGGTCG     GCCCTGG
                              |||||||||      |||||||
                              CGGGCCCGGC     CGGGGCC
                                   CTCGC_
GAM938  KIAA1649 5' CAGTGGAGGTGCCTGGGT    50249     TG  T    TATG  _
                              GCC  GG CGCCT    CC CTG
                              |||  || |||||    || |||
```

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                                TGG  CC GTGGA    GG GAC
                                  GT  _    ____  T
GAM938  KIAA1649 3' CAGTGGAGGTGCCTGGGT    66976     TG  T    TATG  _
                                GCC  GG CGCCT    CC CTG
                                |||  || |||||    || |||
                                TGG  CC GTGGA    GG GAC
                                  GT  _    ____  T
GAM938  KIAA1666 3' TTGGGATGTGAGGGTGATCTGG 65253     T        ATG__   TGG
            C                    GCC GGGTCGCCTT    CCC
                                |||  ||||||||||    |||
                                CGG TCTAGTGGGA    GGG
                                  _        GTGTA   TT
GAM938  KIAA1679 3' TCAGGGTGGACGGCTTGGACA  70157    C TG    _  TTAT
                                TG C  GGTCG CC    GCCCTGG
                                || |  ||||| ||    |||||||
                                AC G  TCGGC GG    TGGGACT
                                 A GT    A  ____
GAM938  KIAA1706 3' CCAGGGCTCAGTGGCCCAGG   92785          CTTAT
                                CCTGGGTCGC    GCCCTGG
                                ||||||||||    |||||||
                                GGACCCGGTG    CGGGACC
                                      ACT__
GAM938  KIAA1715 3' GGTGGGTGACTTGGC      68125     T       TAT
                                GCC GGGTCGCCT   GCC
                                |||  |||||||||   |||
                                CGG TTCAGTGGG   TGG
                                  _       ___
GAM938  KIAA1719 3' TCAGGGCCTCTCGGCTTGGG   68172    TG    CCTTAT
                                CC  GGTCG     GCCCTGG
                                ||  |||||     |||||||
                                GG  TCGGC     CGGGACT
                                 GT    TCTC__
GAM938  KIAA1804 3' TTGGGGAGTGTATGTGATCTGG 69794     TG     CT_  G   TG
            GT                    GCC  GGTCGC   TAT CCC  G
                                |||  ||||||   ||| |||  |
                                TGG  CTAGTG   GTG GGG  T
                                  GT     TAT   A   GT
GAM938  KIAA1811 3' GGTTGGGGTGGCTTAGCA    64798     C         T
                                TGC TGGGTCGCCTTA GCC
                                |||  |||||||||||| |||
                                ACG ATTCGGTGGGGT TGG
                                  _         _
GAM938  KIAA1813 5' CCGGGTCTGGGAGGCGGCCTGG 70295    TG       AT__    T
            G                    CC  GGTCGCCTT    GCCC GG
                                ||  |||||||||    |||| ||
                                GG  CCGGCGGAG    TGGG CC
                                 GT       GGTC   _
GAM938  KIAA1821 3' GGGCGTGCTTCAGGC      71791        TC  CTT
                                GCCTGGG  GC   ATGCCC
                                |||||||  ||   ||||||
```

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                              CGGACTT  CG   TGCGGG
                                 __  ___
GAM938  KIAA1822 3' CTGGCACCAGGGGTGGCTGGGC 67566     TG G     A__   CTGG
            A                    TGCC  G TCGCCTT   TGCC
                              ||||  | |||||||   ||||
                              ACGG  C GGTGGGG   ACGG
                                GT _      ACC    TC
GAM938  KIAA1904 3' GGGGAAGGGTCCAGGC      73496       GTC    ATG
                              GCCTGG   GCCTT   CCC
                              ||||||   |||||   |||
                              CGGACC   TGGGA   GGG
                                 ___     AG_
GAM938  KIAA1924 3' CCAGGGCTCCCTGGCCCAG   73666        CCTTAT
                              CTGGGTCG     GCCCTGG
                              ||||||||     |||||||
                              GACCCGGT     CGGGACC
                                   CCCT__
GAM938  KIAA1924 5' CTGGGCGCGCGGAGGCCTAGGC 73671         G  TTA    TGG
                              GCCTGGGTC CC   TGCCC
                              ||||||||| ||   |||||
                              CGGATCCGG GG   GCGGG
                                   A  CGC    TC
GAM938  KIAA1924 3' GGGCACCGGCCAGGT       73685       G   CCTTA
                              GCCTGG TCG    TGCCC
                              |||||| |||    |||||
                              TGGACC GGC    ACGGG
                                 _  C_____
GAM938  KIAA1932 3' CTGGTGATTGAGGTGCCCAGGC 73445        T      __   CTGG
                              GCCTGGG CGCCTTA  TGCC
                              ||||||| |||||||  ||||
                              CGGACCC GTGGAGT  GTGG
                                   _      TA   TC
GAM938  KIAA1937 3' CCATGCCAGGGAGATCTGGGCA 73697     TG   G   AT  CC
                              TGCC  GGTC CCTT  GC  TGG
                              ||||  |||| ||||  ||  |||
                              ACGG  CTAG GGGA  CG  ACC
                                GT   A   C_  T_
GAM938  KIAA1939 3' CATAAAGTGATTCGGGCA    45763          C
                              TGCCTGGGTCGC TTATG
                              |||||||||||| |||||
                              ACGGGCTTAGTG AATAC
                                     A
GAM938  KIAA1940 3' CCAGACCTAGGGGCCTGGGCA  79979     TG   G   TATGCC
                              TGCC  GGTC CCT     CTGG
                              ||||  |||| |||     ||||
                              ACGG  CCGG GGA     GACC
                                GT   _  TCCA__
GAM938  KIAA1949 5' GGGTATCGCTGAGGCA      92085      G  T  CCTT
                              TGCCT GG CG   ATGCCC
                              ||||| || ||   ||||||
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                                ACGGA TC GC    TATGGG
                                  G  _  _____
GAM938  KIAA1949  5'  GGGTATCGCTGAGGCA      97753      G  T  CCTT
                                TGCCT GG CG    ATGCCC
                                |||||| || ||    ||||||
                                ACGGA TC GC    TATGGG
                                  G  _  _____
GAM938  KIAA1949  5'  GGGTATCGCTGAGGCA      97875      G  T  CCTT
                                TGCCT GG CG    ATGCCC
                                |||||| || ||    ||||||
                                ACGGA TC GC    TATGGG
                                  G  _  _____
GAM938  KIAA1950  3'  GGGTGGTGGCTCAGGC      92596          TTAT
                                GCCTGGGTCGCC    GCCC
                                ||||||||||||    ||||
                                CGGACTCGGTGG    TGGG
                                                _____
GAM938  KIAA1958  3'  GGGACACGATGATTTAGGCA   81909          CC TA  _
                                TGCCTGGGTCG  T  TG CCC
                                ||||||||||  |  || |||
                                ACGGATTTAGT  A  AC GGG
                                       __ GC  A
GAM938  KIAA1969  3'  CCGGGTGCGGTGGCTTATGCA  78730     C        TTAT  _
                                TGC TGGGTCGCC    GC CCTGG
                                ||| |||||||||    || |||||
                                ACG ATTCGGTGG    CG GGGCC
                                  T        _____  T
GAM938  KIAA1981  3'  GCAAGAGGCGGCCCAGC     88344    C         A
                                GC TGGGTCGCCTT TGC
                                || ||||||||||| |||
                                CG ACCCGGCGGAG ACG
                                  _          A
GAM938  KNSL6     3'  TTGGGTACCTGGTGGGTCTAGG 22427        GT _   TTA     TGG
            CA                    TGCCTGG  C GCC   TGCCC
                                |||||||  | |||   |||||
                                ACGGATC  G TGG   ATGGG
                                     TG G   TCC     TT
GAM938  KPTN      3'  CCAGACCTGGGGCGACTCATGG 73411     _          TGCC
            C                     GCC TGGGTCGCCTTA    CTGG
                                ||| ||||||||||||    ||||
                                CGG ACTCAGCGGGGT    GACC
                                  T          CCA_
GAM938  LAGY      5'  CCAGGGAGGGAGGCCCGGGT   50674         G    ATG
                                GCCTGGGTC CCTT   CCCTGG
                                |||||||| ||||   ||||||
                                TGGGCCCGG GGGA   GGGACC
                                     A    ___
GAM938  LGALS9    3'  CTGGGGTGTGGGGCAGTCTGGG 23790     TG  TC         TG
            T                     GCC  GG  GCCTTATGCCC  G
                                |||  ||  ||||||||||  |
```

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                                TGG  CT  CGGGGTGTGGG  C
                                  GT  GA         GT
GAM938  LGALS9    3'  CTGGGGTGTGGGGCAGTCTGGG 9722      TG  TC        TG
            T                    GCC  GG  GCCTTATGCCC  G
                                 |||  ||  ||||||||||| |
                                TGG  CT  CGGGGTGTGGG  C
                                  GT  GA         GT
GAM938  LGI3     5'  GCGCGGGGTGGCCCAGCCG   57746    C        TA
                                TG CTGGGTCGCCT  TGC
                                || ||||||||||  |||
                                GC GACCCGGTGGG  GCG
                                 C         GC
GAM938  LIG-1    5'  CCGGGTGCTCCGGAGCGGCCCG 63894          _  TAT  _
            GGCA                    GCCTGGGTCGC CT   GC CCTGG
                                ||||||||||| ||   || |||||
                                CGGGCCCGGCG GG   CG GGGCC
                                      A  CCT  T
GAM938  LRPPRC   5'  GCTCAGGTGGCCTAGGT     55707           TAT
                                GCCTGGGTCGCCT   GC
                                ||||||||||||   ||
                                TGGATCCGGTGGA   CG
                                       CT_
GAM938  LSFR2    3'  CTGGGCCGGGGTGGCCTGGGT  60566     TG       AT   TGG
                                GCC  GGTCGCCTT  GCCC
                                |||  |||||||||  ||||
                                TGG  CCGGTGGGG  CGGG
                                  GT       C_   TC
GAM938  LSFR2    3'  GGCATGGGCACCTGGGT     60567     TG   C   T
                                GCC  GGT GCCT ATGCC
                                |||  ||| |||| |||||
                                TGG  CCA CGGG TACGG
                                  GT  _   _
GAM938  LY6G5B   5'  CCAGGGTATTTGAGAGTGACCC 41129         _  __
            AG                    CTGGGTCGC CTT  ATGCCCTGG
                                |||||||||  |||  |||||||||
                                GACCCAGTG GAG  TATGGGACC
                                     A   TT
GAM938  MAD4     5'  CCGGGGCGGACGGGCGCGGGC  21270      GGT    TA_
                                GCCTG   CGCCT   TGCCCTGG
                                |||||   |||||   ||||||||
                                CGGGC   GCGGG   GCGGGGCC
                                   ____    CAG
GAM938  MAPK8IP3  3'  CCAGGGTGTCAGGGGCTCAGGC 52978         G   T
                                GCCTGGGTC CCT ATGCCCTGG
                                ||||||||| ||| |||||||||
                                CGGACTCGG GGA TGTGGGACC
                                      _  C
GAM938  MAST205  5'  CGGGGTCGGTGGCTTAGG    30667          TTAT   TG
                                CCTGGGTCGCC   GCCC  G
                                ||||||||||   ||||  |
```

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                                GGATTCGGTGG   TGGG  C
                                      C___    GT
GAM938  MBD2     5'  CGGGGCCACGCCCCGGGCA   31716        T  CCTTAT
                                TGCCTGGG CG     GCCCTG
                                |||||||| ||     ||||||
                                ACGGGCCC GC     CGGGGC
                                     C  AC____
GAM938  MDS018   3'  GGCGGGGTGCCCAGGT     41536        T    TA
                                GCCTGGG CGCCT  TGCC
                                ||||||| |||||  ||||
                                TGGACCC GTGGG  GCGG
                                   _    __
GAM938  MEF-2    3'  CAGGCTGGTAATTCGGGTA   64380         CG  TTATGC
                                TGCCTGGGT  CC     CCTG
                                |||||||||  ||     ||||
                                ATGGGCTTA  GG     GGAC
                                      AT  TC____
GAM938  MEF-2    5'  GCTCAGGCGGCCGAGGC     64389      G       TAT
                                GCCT GGTCGCCT   GC
                                |||| ||||||||   ||
                                CGGA CCGGCGGA   CG
                                  G       CT_
GAM938  MESDC2   3'  CTGGGGTGGGAGTGGTCTCAGG 72491         _   _  AT   TG
          CA                      TGCCTGGG TCGC CTT  GCCC  G
                                ||||||| |||| |||  ||||  |
                                ACGGACTC GGTG GGG  TGGG  C
                                     T   A  __   GT
GAM938  MGC10818 5'  CAGGGAGTGGCCCAGGC     47536          CTTATG
                                GCCTGGGTCGC     CCCTG
                                ||||||||||      |||||
                                CGGACCCGGTG     GGGAC
                                      A_____
GAM938  MGC11287 3'  CCGGGGCGTGGGACCGACCTGG 48831    TG    C_
          G                      CC  GGTCG  CTTATGCCCTGG
                                ||  |||||  ||||||||||||
                                GG  CCAGC  GGGTGCGGGGCC
                                 GT    CA
GAM938  MGC11303 3'  CAGGGTGGGGACTCAGC     50703    C     G  TTAT
                                GC TGGGTC CC    GCCCTG
                                || |||||| ||    ||||||
                                CG ACTCAG GG    TGGGAC
                                 _     G  ____
GAM938  MGC11352 5'  GGGCATTTGTCTAGC       64805    C    T  CCTT
                                GC TGGG CG    ATGCCC
                                || |||| ||    ||||||
                                CG ATCT GT    TACGGG
                                 _   _  T___
GAM938  MGC1136  3'  GGAGATAGGAGGCCCAGGT   43803         G   TATG
                                GCCTGGGTC CCT    CC
                                |||||||| |||    ||
```

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                                TGGACCCGG GGA   GG
                                     A  TAGA
GAM938  MGC12966 3' CCGGAGGAGGTGACTCGGACA 51124   C       TATG _
                                TG CTGGGTCGCCT   CC CTGG
                                || ||||||||||   || ||||
                                AC GGCTCAGTGGA   GG GGCC
                                 A        ____ A
GAM938  MGC13064 5' TCAGGGTTAGGAGGTCTGGGC 50355    TG GT G  TAT
                                GCC  G  C CCT   GCCCTGG
                                |||  |  | |||   |||||||
                                CGG  C  G GGA   TGGGACT
                                  GT TG A  T__
GAM938  MGC14161 5' CGGGGTGATGGTGCAGGT   51841     GGT   TTA
                                GCCTG   CGCC   TGCCCTG
                                |||||   ||||   |||||||
                                TGGAC   GTGG   GTGGGGC
                                   ___   TA_
GAM938  MGC14859 3' CCAGGGTATGGGGCATGTGCCC 61917   C    C___
            AGCA                  C TGGGT   GCCTTATGCCCTGG
                                | |||||   ||||||||||||||
                                G ACCCG   CGGGGTATGGGACC
                                _    TGTA
GAM938  MGC15631 3' TCAGGCAGGAGGTGACCCAAGT 51270    C        A   C
            A                   TGC TGGGTCGCCTT TGCC TGG
                                ||| |||||||||| |||| |||
                                ATG ACCCAGTGGAG ACGG ACT
                                  A        G   _
GAM938  MGC15854 5' CCAGGTTTGAGGGCGGTCAGGC 58847     G GT     ATGC
                                GCCT G  CGCCTT   CCTGG
                                |||| |  ||||||   |||||
                                CGGA C  GCGGGA   GGACC
                                  _ TG    GTTT
GAM938  MGC16186 5' GGGCGGGGGGCACCCGGGCA   50431        C   A
                                TGCCTGGGT GCCTT TGCCC
                                ||||||||| ||||| |||||
                                ACGGGCCCA CGGGG GCGGG
                                      _   _
GAM938  MGC16279 5' CCAGGGTGACAGTGGCCCAGC  51887   C      CTTAT
                                GC TGGGTCGC    GCCCTGG
                                || ||||||||    |||||||
                                CG ACCCGGTG    TGGGACC
                                 _      ACAG_
GAM938  MGC16386 3' TCAGGGTGTGGCCACCAGGT   54736      GTC   TT
                                GCCTGG   GCC  ATGCCCTGG
                                ||||||   |||  |||||||||
                                TGGACC   CGG  TGTGGGACT
                                   AC_   __
GAM938  MGC1842  5' GCTGGGGCGGCGCTTGGGGCGG 65653         _____    TG
            CCCAGCCG               GGTCGCCTTA    TGCCC  G   C
                                |||||||||    |||||  |   |
```

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                              CCGGCGGGGT    GCGGG  C   G
                                    TCGCG    GT
GAM938  MGC19556 5' TTAGGGTATGGGGAAAGGC   53234     GGGTCG
                              GCCT     CCTTATGCCCTGG
                              ||||     ||||||||||||
                              CGGA     GGGGTATGGGATT
                                AA____
GAM938  MGC19570 5' CCAGGTGAAGGGTGACTTGGC  59006    T       A   C
                              GCC GGGTCGCCTT TGCC TGG
                              ||| |||||||||| |||| |||
                              CGG TTCAGTGGGA GTGG ACC
                                _       A   _
GAM938  MGC20486 5' TCGGGGTTGCGAGCGGCCCGGG 53429         CTTAT
                              CCTGGGTCGC    GCCCTGG
                              ||||||||||    |||||||
                              GGGCCCGGCG    TGGGGCT
                                    AGCGT
GAM938  MGC21688 3' CCAGGGTGTTAATGCCCACGTA 58266    C    CGCCTT
                              TGC TGGGT     ATGCCCTGG
                              ||| |||||     |||||||||
                              ATG ACCCG     TGTGGGACC
                                C    TAAT__
GAM938  MGC21738 3' CCAGACACAGGTGGCCAGGT   58915      G     TA  CC
                              GCCTGG TCGCCT  TG  CTGG
                              |||||| ||||||  ||  ||||
                              TGGACC GGTGGA  AC  GACC
                                 _     C_  A_
GAM938  MGC2488  5' GCCGAGATGACCTGGGCA    43871     TG    C   AT
                              TGCC  GGTCG CTT  GC
                              ||||  ||||| |||  ||
                              ACGG  CCAGT GAG  CG
                                GT    A  C_
GAM938  MGC2541  5' CTGGCATCTATGCGGCTCAGGC 54749          CTT_    CTGG
           A                   TGCCTGGGTCGC    ATGCC
                              ||||||||||||   |||||
                              ACGGACTCGGCG    TACGG
                                     TATC    TC
GAM938  MGC3038  3' CTGGGGGAGGGATGGTTTGGGC 48275     TG GT  _   ATG   TG
           A                   TGCC  G  CG CCTT   CCC  G
                              ||||  |  || ||||   |||  |
                              ACGG  T  GT GGGA   GGG  C
                                GT TG  A    G__   GT
GAM938  MGC4342  3' GGTGAAGGGACCCGGGCA    44269         G    A
                              TGCCTGGGTC CCTT TGCC
                              |||||||||| |||| ||||
                              ACGGGCCCAG GGAA GTGG
                                        _   _
GAM938  MGC4638  3' TTAGGGTGATGGTCCAGAGCA  48944     _   GT  CCTTA
                              TGC CTGG  CG    TGCCCTGG
                              ||| ||||  ||    ||||||||
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                                ACG GACC  GT    GTGGGATT
                                  A   TG  A____
GAM938  MGC4663  3'  GGTCTAGGTGCCCGGGC    44508       T    TAT
                                GCCTGGG CGCCT   GCC
                                ||||||| |||||   |||
                                CGGGCCC GTGGA   TGG
                                   _    TC_
GAM938  MRAS     5'  CTAGGAGGGGGCGGCCTGAGT  24226    CT       ATGC
                                GC  GGGTCGCCTT   CCTGG
                                ||  ||||||||||   |||||
                                TG  TCCGGCGGGG   GGATC
                                 AG        GA__
GAM938  MSE55    3'  CAGGGCCCCACCTAGGT     22941        CGCCTTAT
                                GCCTGGGT      GCCCTG
                                ||||||||      ||||||
                                TGGATCCA      CGGGAC
                                    CCC_____
GAM938  MSP      3'  CCAGGGGCCCCAGGGAGGTCCA 49414       GT G    AT_   _
            GGT                   GCCTGG  C CCTT   GCCC TGG
                                ||||||  | ||||   |||| |||
                                TGGACC  G GGGA   CGGG ACC
                                   TG A    CCC    G
GAM938  MUC13    3'  TCGGGGTGTAGGTTTCTGAGGT 52331     G  TC    T
                                GCCT GG  GCCT ATGCCCTGG
                                |||| ||  |||| |||||||||
                                TGGA TC  TGGA TGTGGGGCT
                                  G  TT   _
GAM938  MYO3B    3'  CCGGGTGCGGTGGCTCAGGC   57304          TTAT  _
                                GCCTGGGTCGCC    GC CCTGG
                                ||||||||||||    || |||||
                                CGGACTCGGTGG    CG GGGCC
                                       _____  T
GAM938  MYOM1    3'  GGCCTGTGTGACTTGGGT    13737     TG     CT  T
                                GCC  GGTCGC  TA GCC
                                |||  ||||||  || |||
                                TGG  TCAGTG  GT CGG
                                  GT     T_  C
GAM938  N4BP3    3'  GGCAGGTGGGGGCTTAGGCA   66267         G  TTA
                                TGCCTGGGTC CC   TGCC
                                |||||||||| ||   ||||
                                ACGGATTCGG GG   ACGG
                                     G  TGG
GAM938  NAG14    3'  AGGGGGTGGTATGGGT      42162      GG    TTATG
                                GCCTG  TCGCC    CCCT
                                |||||  |||||    ||||
                                TGGGT  GGTGG    GGGA
                                  AT    _____
GAM938  NFAT5    3'  TAGGGTGACCTAGCA       21712     C
                                TGC TGGGTCGCCTTA
                                ||| ||||||||||||
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```
                                ACG ATCCAGTGGGAT
                                  _
GAM938  NICE-3   5'  CCGGGGAGCTCCAGGGGACCCA 31276        G   TATG__
            GGC                  GCCTGGGTC CCT     CCCTGG
                                ||||||||| |||     ||||||
                                CGGACCCAG GGA     GGGGCC
                                   G   CCTCGA
GAM938  NMT1     3'  GGGCTGACCCTGGGCA      40787      _     CCTTAT
                                TGCCT GGGTCG     GCCC
                                ||||| ||||||     ||||
                                ACGGG CCCAGT     CGGG
                                  T     _______
GAM938  NMT1     3'  TGGGGTGGCTAGGCA       40791        G
                                TGCCTGG TCGCCTTA
                                ||||||| ||||||||
                                ACGGATC GGTGGGGT
                                  _
GAM938  NPC1L1   3'  TGAGGTATCCAGGCA       25417         C
                                TGCCTGGGT GCCTTA
                                ||||||||| ||||||
                                ACGGACCTA TGGAGT
                                   _
GAM938  NPD002   3'  CCAGGGTGTGAGGTGGGTGGGG 25913     GGG
                                CCT   TCGCCTTATGCCCTGG
                                |||   ||||||||||||||||
                                GGG   GGTGGAGTGTGGGACC
                                  GTG
GAM938  NPEPL1   5'  CCGGGGCGTGGGCCGGCAGG   45089     GG    C
                                CCT  GTCG CTTATGCCCTGG
                                |||  |||| ||||||||||||
                                GGA  CGGC GGGTGCGGGGCC
                                  __    C
GAM938  NR5A1    3'  GGGGCGGGGCCTGGGC      17103     TG    G  TTAT
                                GCC  GGTC CC    GCCCT
                                |||  |||| ||    |||||
                                CGG  CCGG GG    CGGGG
                                  GT   _ _____
GAM938  NUBP2    3'  GCAGGGGCAGGCCCAGGCA   64232          _    A
                                TGCCTGGGTC GCCTT TGC
                                |||||||||| ||||| |||
                                ACGGACCCGG CGGGG ACG
                                     A    _
GAM938  NXN      3'  GGGTGTGGAATCAGCA      42422     C   GTCG  TT
                                TGC TGG    CC  ATGCCC
                                ||| |||    ||  ||||||
                                ACG ACT    GG  TGTGGG
                                  _   AA__  __
GAM938  OBSCN    3'  CTAGTGCTGGTGATCCGGGC   70653           TTAT  C
                                GCCTGGGTCGCC    GC CTGG
                                ||||||||||||    || ||||
```

```
                                CGGGCCTAGTGG   CG GATC
                                      T___  T
GAM938  OBTP    5'  GGGTGGGGACCGGGT      34249       G  G  TTAT
                                GCCTGG TC CC   GCCC
                                |||||| || ||   ||||
                                TGGGCC AG GG   TGGG
                                   _ G ____
GAM938  OIP5    5'  GGGCGGGGCCTGGC       62784     T    G  TTAT
                                GCC GGGTC CC   GCCC
                                ||| ||||| ||   ||||
                                CGG TCCGG GG   CGGG
                                  _   _ ____
GAM938  OMD     3'  GTAAGAGGCCATCCAGGTA   17214         C    A
                                TGCCTGGGT GCCTT TGC
                                ||||||||| ||||| |||
                                ATGGACCTA CGGAG ATG
                                     C    A
GAM938  OSBPL1A  5'  GCAAAGGTGACTTAGG     35908          A
                                CCTGGGTCGCCTT TGC
                                |||||||||||| |||
                                GGATTCAGTGGAA ACG
                                          _
GAM938  PADI3   3'  CTGGGGCGGGCATTGGCCAGGT 32658       G ___   TAT   TG
                                GCCTGG TC   GCCT   GCCC  G
                                |||||| ||   ||||   ||||  |
                                TGGACC GG   CGGG   CGGG  C
                                   _ TTA    ___    GT
GAM938  PAIP1   3'  GGTATGGTGATTTAGCA     66926     C       TT
                                TGC TGGGTCGCC  ATGCC
                                ||| |||||||||  |||||
                                ACG ATTTAGTGG  TATGG
                                  _       __
GAM938  PAK7    5'  TCAGTAGCTGGGGGAGGTTTGG 69650     TG GT G_    T  C_
           GT                     GCC  G  C  CCTTA GC  CTGG
                                ||| | | ||||| ||  ||||
                                TGG  T  G  GGGGT CG  GACT
                                  GT TG AG    _  AT
GAM938  PANX2   3'  CTGGGGTGGGGAAAGGTGGCCC 53425          A___    TG
           AG                     CTGGGTCGCCTT   TGCCC  G
                                ||||||||||||   |||||  |
                                GACCCGGTGGAA   GTGGG  C
                                      AGGG    GT
GAM938  PCDH20  3'  GGGTATTGTACTTGGCA     43130     T   C  CTT
                                TGCC GGGT GC   ATGCCC
                                |||| |||| ||   ||||||
                                ACGG TTCA TG   TATGGG
                                  _   _  T__
GAM938  PCTAIRE2BP 5'  CGCGGGGCGGCTCCGGT     70601     T       TA
                                GCC GGGTCGCCT  TG
                                ||| |||||||||  ||
```

```
                                TGG CTCGGCGGG  GC
                                  C       GC
GAM938  PDE2A    5'  TGGGGTGTTGAGTCCAGGC   10474       _  CCTT    TG
                                GCCTGGG TCG   ATGCCC  G
                                ||||||| |||   ||||||  |
                                CGGACCT AGT   TGTGGG  T
                                   G  ____    GT
GAM938  PEPP3    3'  GGTGTGGGGATCTGGGT    30041    TG   G  T
                                GCC  GGTC CCT ATGCC
                                |||  |||| ||| |||||
                                TGG  CTAG GGG TGTGG
                                  GT  _  _
GAM938  PIP5K1C  3'  TGTGGGGTGACTCGGAGCA   70767    _
                                TGC CTGGGTCGCCTTATG
                                ||| ||||||||||||||
                                ACG GGCTCAGTGGGGTGT
                                  A
GAM938  PIP5K2B  5'  GGCGTTGGGGGGCCCGGGC   13075       G  T
                                GCCTGGGTC CCT ATGCC
                                ||||||||| ||| |||||
                                CGGGCCCGG GGG TGCGG
                                     G  T
GAM938  PIP5K2B  5'  GGCGTTGGGGGGCCCGGGC   56894       G  T
                                GCCTGGGTC CCT ATGCC
                                ||||||||| ||| |||||
                                CGGGCCCGG GGG TGCGG
                                     G  T
GAM938  PISD     3'  CATGAGGCCATCCAGGTA    26770       C
                                TGCCTGGGT GCCTTATG
                                ||||||||| ||||||||
                                ATGGACCTA CGGAGTAC
                                     C
GAM938  PLA2G12  5'  GCCCGAGGCGGTTCACGTA   48025    C  GG     AT
                                TGC TG  TCGCCTT  GC
                                ||| ||  |||||||  ||
                                ATG AC  GGCGGAG  CG
                                  C  TT     CC
GAM938  PLEKHA3  5'  GGCGGAGGGGGCCCGGGC    38864       G  A
                                GCCTGGGTC CCTT TGCC
                                ||||||||| |||| ||||
                                CGGGCCCGG GGAG GCGG
                                     G  _
GAM938  POR1     3'  CCAGGGTGTGGGAGATTGGACA 24804    _ TG   GC
                                TG CC  GGTC  CTTATGCCCTGG
                                || ||  ||||  ||||||||||||
                                AC GG  TTAG  GGGTGTGGGACC
                                 A  __   A_
GAM938  PP3501   3'  GGGGGTGACTAGGT       41373       G    TTATG
                                GCCTGG TCGCC    CCC
                                |||||| |||||    |||
```

```
                                TGGATC AGTGG    GGG
                                  _   _____
GAM938  PPAP2B   5'  TCGGCCAGGAGGCGACCCGGGC 13547           AT_  CTGG
                                GCCTGGGTCGCCTT  GCC
                                |||||||||||||  |||
                                CGGGCCCAGCGGAG  CGG
                                     GAC  CT
GAM938  PPIL3    5'  GCTTGAGGTTGCCCAGGTA   55659       C     T
                                TGCCTGGGT GCCTTA GC
                                ||||||||| |||||| ||
                                ATGGACCCG TGGAGT CG
                                    T     T
GAM938  PPP1R3B  3'  CCAGGGACATGGACTTGGGT  44816    TG   GCCT   _
                                GCC  GGTC   TATG CCCTGG
                                |||  ||||   |||| ||||||
                                TGG  TCAG   GTAC GGGACC
                                  GT   ____   A
GAM938  PTDSS2   3'  CCAGCCATGGTGTGGTCCAGGC 47886       GT  C    CC
           A                     TGCCTGG  CGC TTATG  CTGG
                                |||||||  ||| |||||  ||||
                                ACGGACC  GTG GGTAC  GACC
                                   TG  T    C_
GAM938  PTR4     5'  GGGGGCGGTGCGGGC      74055      G     TTATG
                                GCCTG GTCGCC    CCC
                                ||||| ||||||    |||
                                CGGGC TGGCGG    GGG
                                  G    _____
GAM938  RAB24    5'  TCGGGGTCTGAGGCTTGGGC  55393    TG GTC     T
                                GCC  G  GCCTTA GCCCTGG
                                |||  |  |||||| |||||||
                                CGG  T  CGGAGT TGGGGCT
                                  GT ___     C
GAM938  RACGAP1  5'  CGAAGTGAAGGGTGGCCCAGGT 25195           A  CCTGG
                                GCCTGGGTCGCCTT TGC
                                |||||||||||||| |||
                                TGGACCCGGTGGGA GTG
                                       A  AAGC
GAM938  RASAL2   3'  TCAGGGCATAAGGCGGCGACTT 16724    _____
           CCA                   TGG    GTCGCCTTATGCCCTGG
                                |||    ||||||||||||||||
                                ACC    CGGCGGAATACGGGACT
                                  TTCAG
GAM938  RASSF2   3'  CCAGGGCCTGGTGGCCTGGT  28431    T      TTAT
                                GCC GGGTCGCC   GCCCTGG
                                ||| ||||||||   |||||||
                                TGG TCCGGTGG   CGGGACC
                                  _      TC__
GAM938  RDH-E2   5'  CTAGGGAGAGTGTCCTGGGT  57270    TG  T  _  TATG
                                GCC  GG CGC CT   CCCTGG
                                |||  || ||| ||   ||||||
```

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                                TGG  CC GTG GA    GGGATC
                                  GT  T   A  ____
GAM938   RGS7     5'  CAGCGAGGCGGCCCAGG     11329           ATGCC
                                CCTGGGTCGCCTT    CTG
                                ||||||||||||    |||
                                GGACCCGGCGGAG    GAC
                                       C____
GAM938   RIPK2    5'  TCGTGCAGGGGCGTATCTGGGC 13786     TG  _    A  CCTGG
                                GCC  GGT CGCCTT TGC
                                |||  ||| |||||| |||
                                CGG  CTA GCGGGG ACG
                                  GT   T     _  TGCT
GAM938   RNF8     3'  CCAGAAACATGGGGTGTCCTAG 14219        T       CC_
            GTA                    TGCCTGGG CGCCTTATG   CTGG
                                |||||||| |||||||||   ||||
                                ATGGATCC GTGGGGTAC   GACC
                                     T       AAA
GAM938   RoXaN    3'  GGGTGATGGCATGGGCA     46655      GG  C   TTA
                                TGCCT  GT GCC   TGCCC
                                |||||  || |||   |||||
                                ACGGG  TA CGG   GTGGG
                                   __  _   TA_
GAM938   RPIA     5'  CCGGGGCGTGCACAGTCTGGG  57965    TG  TCGCCT
                                CC  GG     TATGCCCTGG
                                ||  ||     ||||||||||
                                GG  CT     GTGCGGGGCC
                                 GT  GACAC_
GAM938   RPL13    5'  CGGGGCGGAGGCCCGGG     52680        G  TTAT
                                CCTGGGTC CC    GCCCTG
                                ||||||||  ||    ||||||
                                GGGCCCGG GG    CGGGGC
                                     A  ____
GAM938   SARM     3'  CCAGGGTGTTCTGCTTGGC    30601     T    CGCCTT
                                GCC GGGT     ATGCCCTGG
                                ||| ||||     |||||||||
                                CGG TTCG     TGTGGGACC
                                  _    TCT___
GAM938   SARM     3'  CTGGGGTGGGCTGGTCCAGGTA 30605        GT _   TAT   TG
                                TGCCTGG  C GCCT   GCCC  G
                                |||||||  | ||||   ||||  |
                                ATGGACC  G CGGG   TGGG  C
                                     TG T    ___    GT
GAM938   SARM     3'  GGGTGGGGCCTAGG       30611         G  TTAT
                                CCTGGGTC CC    GCCC
                                ||||||||  ||    ||||
                                GGATCCGG GG    TGGG
                                       _  _____
GAM938   SARM     3'  TTGGGGCATTGCTGATCTAGCC 30620    C      _ CTT     TG
            G                    TG CTGGGTC GC   ATGCCC  G
                                || |||||||  ||   ||||||  |
```

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                                GC GATCTAG CG   TACGGG  T
                                 C      T  T__     GT
GAM938  SCAMP5   3'  CCAGCACAGTGAGGCATTTAGG 57254         C      GCC_
           TA                     TGCCTGGGT GCCTTAT    CTGG
                                |||||||||  |||||||    ||||
                                ATGGATTTA CGGAGTG    GACC
                                      _      ACAC
GAM938  SCAMP5   3'  TTGGTCACAGGGCGGTTCTGGG 57264       _ GG      A  C  TGG
           CA                     TGCCT G  TCGCCTT TG CC
                                |||||  |  |||||||  ||  ||
                                ACGGG C  GGCGGGA AC GG
                                  T TT      C  T  TT
GAM938  SCYD1    3'  CAGGGCCTGGCTCAGGT     90926          CCTTAT
                                GCCTGGGTCG     GCCCTG
                                ||||||||||     ||||||
                                TGGACTCGGT     CGGGAC
                                      C_____
GAM938  SDC3     3'  TTAGGGCATTGCATGCAGGT   27770       G  C  CTT
                                GCCTG GT GC   ATGCCCTGG
                                |||||  ||  ||   |||||||||
                                TGGAC TA CG   TACGGGATT
                                  G  _  T__
GAM938  SDC3     3'  GTGAGACGGCCTGGGCA     27761      TG    C
                                TGCC  GGTCG CTTAT
                                ||||  |||||  |||||
                                ACGG  CCGGC GAGTG
                                  GT     A
GAM938  SDFR1    3'  GTAAGGGTGATCTAGCCA    24867    C         A
                                TG CTGGGTCGCCTT TGC
                                ||  ||||||||||||  |||
                                AC GATCTAGTGGGA ATG
                                 C          _
GAM938  SDFR1    3'  GTAAGGGTGATCTAGCCA    33917    C         A
                                TG CTGGGTCGCCTT TGC
                                ||  ||||||||||||  |||
                                AC GATCTAGTGGGA ATG
                                 C          _
GAM938  SDOS     3'  TCAGGCAGAGCAGGGTGGTCCG 50369      GT    TA  _____
           GGCA                    CTGG  CGCCT  TGC    CCTGG
                                ||||  |||||  |||   |||||
                                GGCC  GTGGG  ACG    GGACT
                                  TG    __   AGAC
GAM938  SDS3     3'  CCAGGGTGTTTTCATTCATGC  69225    C    CGCCTT
                                GC TGGGT     ATGCCCTGG
                                ||  |||||     |||||||||
                                CG ACTTA     TGTGGGACC
                                 T    CTTT__
GAM938  SEC24C   3'  CGGGGTATAGCCCATAGGT   16996      __   CGCCT      TG
                                GCCT  GGGT    TATGCCC  G
                                ||||  ||||    |||||||  |
```

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                                TGGA  CCCG    ATATGGG  C
                                  TA   _____     GT
GAM938  SEMA5A   5'  CCGTGCAGGGGCGGCCCGGC   14254    T       A   CC
                                GCC GGGTCGCCTT TGC  TGG
                                ||| |||||||||| |||  |||
                                CGG CCCGGCGGGG ACG  GCC
                                  _       _   T_
GAM938  SIAT4B   3'  CGGGGCTCCGGCCCGGG    22655        CCTTAT
                                CCTGGGTCG    GCCCTG
                                |||||||||    ||||||
                                GGGCCCGGC    CGGGGC
                                     CT____
GAM938  SLC16A8  3'  GGGTGGGGTGGCCCAG     25335          AT
                                CTGGGTCGCCTT  GCCC
                                ||||||||||||  ||||
                                GACCCGGTGGGG  TGGG
                                      __
GAM938  SLC26A8  5'  GGCAGGTACCCAGGTA     56968        C   TAT
                                TGCCTGGGT GCCT   GCC
                                ||||||||| ||||   |||
                                ATGGACCCA TGGA   CGG
                                      _   ___
GAM938  SLC2A12  5'  CTGGGAGCGGGGGTGGTCGGGG 59079     G GT     A  _  TG
           C                     GCCT G  CGCCTT TGC CC  G
                                ||||  |  |||||| ||| ||  |
                                CGGG C  GTGGGG GCG GG  C
                                  G TG     _   A  GT
GAM938  SLC4A11  3'  TCAGGCCTGGGGCATCTGGGCA 49341     TG   C     T   C
                                TGCC  GGT GCCTTA GCC TGG
                                ||||  ||| |||||| ||| |||
                                ACGG  CTA CGGGGT CGG ACT
                                  GT   _     C   _
GAM938  SLC5A6   3'  AGGGCCTGATTCAGG      40830         CCTTAT
                                CCTGGGTCG    GCCCT
                                |||||||||    |||||
                                GGACTTAGT    CGGGA
                                     C_____
GAM938  SLC5A7   5'  CCAGGGGGCGGCGGCCCCGGGC 41507        _    TTATG
                                GCCTGGG TCGCC    CCCTGG
                                ||||||| |||||    ||||||
                                CGGGCCC GGCGG    GGGACC
                                    C    CGG__
GAM938  SMOC2    5'  CTGGGGCGTGAGGAGGGCGCGG 72372     T G   G_       TG
           T                     GCC G GTC  CCTTATGCCC  G
                                ||| | |||  ||||||||||  |
                                TGG C CGG  GGAGTGCGGG  C
                                  _ G   GA        GT
GAM938  SNT-2    3'  CTGGGGAGAGAAGGGTGACCAG 21841       G      ATG__   TG
           GC                    GCCTGG TCGCCTT    CCC  G
                                ||||||| |||||||    |||  |
```

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                                CGGACC AGTGGGA    GGG  C
                                   _     AGAGA   GT
GAM938  SP140    3'  ATGAGGTCACTTGGGCA    23375     TG   C
                                TGCC  GGT GCCTTAT
                                ||||  ||| |||||||
                                ACGG  TCA TGGAGTA
                                  GT   C
GAM938  SRF      3'  CGGGGCATGGCAAATCAGG   11945     GTC   TT    TG
                                CCTGG   GCC  ATGCCC  G
                                |||||   |||  ||||||  |
                                GGACT   CGG  TACGGG  C
                                  AAA   __     GT
GAM938  SRF      3'  CGGGGTATGTGTGTGTGGGT   11946     G T   CT     TG
                                GCCTG G CGC  TATGCCC  G
                                ||||| | |||  |||||||  |
                                TGGGT T GTG  GTATGGG  C
                                  G _   T_     GT
GAM938  SSH2     3'  TCAGTTCTGAAGTGATCTAGGC 62214          C   TGCC
           A                     TGCCTGGGTCGC TTA    CTGG
                                ||||||||||| |||    ||||
                                ACGGATCTAGTG AGT    GACT
                                      A  CTT_
GAM938  ST13     3'  TAGGGTATTCATTCAG     14118       CGCCTT
                                CTGGGT     ATGCCCTG
                                ||||||     ||||||||
                                GACTTA     TATGGGAT
                                   CT____
GAM938  TAO1     3'  TTGGGGCTGGCCAGTGGCCCAG 16549         CTTAT_   TG
           G                     CCTGGGTCGC     GCCC  G
                                ||||||||||     ||||  |
                                GGACCCGGTG     CGGG  T
                                     ACCGGT    GT
GAM938  TBX4     3'  CTGGGGTGTGAGGACTCTGTGC 37493     CT_   CG       TG
           A                     TGC   GGGT  CCTTATGCCC  G
                                |||   ||||  ||||||||||  |
                                ACG   CTCA  GGAGTGTGGG  C
                                  TGT   __        GT
GAM938  TIAF1    3'  CCAGGGCCTGTGGCTGCCTGGG 54327     TG   C   T  T
           CA                    TGCC  GGT GCC TA GCCCTGG
                                ||||  ||| ||| || |||||||
                                ACGG  CCG CGG GT CGGGACC
                                  GT   T   T  C
GAM938  TIGA1    5'  GCAGAGGTGACTCGGGC     53802            A
                                GCCTGGGTCGCCTT TGC
                                ||||||||||||| |||
                                CGGGCTCAGTGGAG ACG
                                                _
GAM938  TIX1     3'  CTAGGCAGCTGGGGCGGCCCAG 61742             T  __
           GC                    GCCTGGGTCGCCTTA GC  CCTGG
                                |||||||||||||| ||  |||||
```

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                                CGGACCCGGCGGGGT CG  GGATC
                                        _ AC
GAM938  TOLLIP   3' GGTGTCCAGGCGCCCAGGT   38687       T    T_
                                GCCTGGG CGCCT  ATGCC
                                ||||||| |||||  |||||
                                TGGACCC GCGGA  TGTGG
                                   _    CC
GAM938  TOLLIP   3' GGGGGCTTCGGTGTCCAGGC   38686       T   TTAT    GG
                                GCCTGGG CGCC   GCCCT
                                ||||||| ||||   |||||
                                CGGACCT GTGG   CGGGG
                                   _   CTT_    GT
GAM938  TRIAD3   3' TTAGGGAGACAGGTGACCCTGG 94510      _       TATG
           GT                    GCCT GGGTCGCCT   CCCTGG
                                ||||| |||||||||   ||||||
                                TGGG CCCAGTGGA   GGGATT
                                  T       CAGA
GAM938  TRIM11   3' GGGAGGTGCCTGGGCA     72834     TG  T    TATG
                                TGCC  GG CGCCT   CCC
                                ||||  || |||||   |||
                                ACGG  CC GTGGA   GGG
                                  GT  _    ____
GAM938  TSCOT    3' CCAGGGAACTGGTGACCTAAGC 52334     C       TTATG
           A                     TGC TGGGTCGCC    CCCTGG
                                ||| |||||||||    ||||||
                                ACG ATCCAGTGG    GGGACC
                                  A       TCAA_
GAM938  TSPEAR   3' CTAGGGCATCCCGGGCCTGGGC 58720     TG   GCCTT
           A                     TGCC  GGTC    ATGCCCTGG
                                ||||  ||||    |||||||||
                                ACGG  CCGG    TACGGGATC
                                  GT   GCCC_
GAM938  TTY7     3' GGGTGGGTGTCTGGGT     49181     TG  T    TAT
                                GCC  GG CGCCT   GCCC
                                |||  || |||||   ||||
                                TGG  CT GTGGG   TGGG
                                  GT  _    ___
GAM938  UBP1     3' GGAAATAGGTGACCCAAGTA   27225     C       TATG
                                TGC TGGGTCGCCT    CC
                                ||| ||||||||||    ||
                                ATG ACCCAGTGGA    GG
                                  A        TAAA
GAM938  ULK2     3' TAGGGTGTAGCTGGGTA     28007     TG GTCGCC
                                TGCC  G     TTATGCCCTG
                                ||||  |     ||||||||||
                                ATGG  C     GATGTGGGAT
                                  GT _______
GAM938  VIT1     5' GGGGGAGGCCCAGGT      37978         G  TTATG
                                GCCTGGGTC CC    CCC
                                ||||||||| ||    |||
```

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                                TGGACCCGG GG    GGG
                                     A _____
GAM938  YEA      5' GGGTAGCGGTACAGGC     51534      GG   CTTA
                                GCCTG  TCGC   TGCCC
                                |||||  ||||   |||||
                                CGGAC  GGCG   ATGGG
                                  AT   ____
GAM938  ZDHHC2   5' GCGAGGTGGCCCGAGC     33009    C        AT
                                GC TGGGTCGCCTT  GC
                                || ||||||||||  ||
                                CG GCCCGGTGGAG  CG
                                 A        __
GAM938  ZDHHC5   5' TCAGGGTGTGGGAGTGGTGGCA 91560     TGGG   _
                                TGCC   TCGC CTTATGCCCTGG
                                ||||   |||| ||||||||||||
                                ACGG   GGTG GGGTGTGGGACT
                                  T___   A
GAM938  ZIN      3' CTGGGGTGTAGGGCCGGGCA  25490      GGTC       TG
                                TGCCTG   GCCTTATGCCC  G
                                ||||||   ||||||||||| |
                                ACGGGC   CGGGATGTGGG  C
                                   ____        GT
GAM938  ZNF185   3' TTAGGGTGTATAGATCCCAGCA 23118    C   _ GCCT
                                TGC TGGG TC   TATGCCCTGG
                                ||| |||| ||   ||||||||||
                                ACG ACCC AG   ATGTGGGATT
                                  _   T  AT__
GAM938  ZNF263   3' CAAGGTGCGATTTGGGCA   19223    TG    CTTAT  C
                                TGCC  GGTCGC   GCC TG
                                ||||  ||||||   ||| ||
                                ACGG  TTAGCG   TGG AC
                                  GT    _____  A
GAM938  ZNF282   3' GGGGGCGGCCTGAGCA    89217    CT     TTATG
                                TGC  GGGTCGCC   CCC
                                |||  ||||||||   |||
                                ACG  TCCGGCGG   GGG
                                  AG     _____
GAM938  ZNF338   5' TGGGGCGCCGGGCCCGGC   42019    T GTC   TA   TG
                                GCC GG  GCCT  TGCCC  G
                                ||| ||  ||||  ||||| |
                                CGG CC  CGGG  GCGGG  T
                                  _ ___   CC   GT
GAM938  LOC112473 5' GGTACCGGGGGTTCAGGCA   73203      GG  G   TA
                                TGCCTG  TC CCT  TGCC
                                ||||||  || |||  ||||
                                ACGGAC  GG GGG  ATGG
                                   TT  _  CC
GAM938  LOC112868 3' GGGCGGGGTCCTGGGTA    72894     TG  TC   TA
                                TGCC  GG  GCCT  TGCCC
                                ||||  ||  ||||  |||||
```

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                                ATGG  CC  TGGG  GCGGG
                                  GT  __   __
GAM938  LOC115110 5'  GGGCAGCCCCAGGC       71721        TC  CTTA
                                GCCTGGG  GC   TGCCC
                                |||||||  ||   |||||
                                CGGACCC  CG   ACGGG
                                   __  ____
GAM938  LOC115265 5'  GGCGCAGGGTGGCCCGGG    73354           A
                                CCTGGGTCGCCTT TGCC
                                |||||||||||| ||||
                                GGGCCCGGTGGGA GCGG
                                       C
GAM938  LOC115399 3'  CGGGGGTGCGGTCCAGGC    73430       GT   CTTATG
                                GCCTGG  CGC     CCCTG
                                ||||||  |||     |||||
                                CGGACC  GCG     GGGGC
                                   TG   TG____
GAM938  LOC115704 3'  CGCGGGGGGCGCCCGGGCA   73542        T    TATG  _
                                TGCCTGGG CGCCT    CCC TG
                                |||||||| |||||    ||| ||
                                ACGGGCCC GCGGG    GGG GC
                                   _    ____  C
GAM938  LOC115708 3'  CGGGGTGTCATGAACTGGGT   73549     TG G   CCTT     TG
                                GCC  G TCG    ATGCCC  G
                                |||  | |||   ||||||  |
                                TGG  C AGT    TGTGGG  C
                                  GT A   AC__     GT
GAM938  LOC115708 3'  CTGGGGTTGGGGTGGTCCAGG  73551      GT      T   TG
                                CCTGG  CGCCTTA GCCC  G
                                |||||  ||||||| ||||  |
                                GGACC  GTGGGGT TGGG  C
                                   TG      _   GT
GAM938  LOC116068 3'  TTAGGGTAAACAGGCCAGGT   73729     GGTC   TA_
                                GCCTG   GCCT   TGCCCTGG
                                |||||   ||||   ||||||||
                                TGGAC   CGGA   ATGGGATT
                                   _____   CAA
GAM938  LOC123242 5'  CCACTGTGAGGTGGTTCAGGC  75594      GG        CCC
                                GCCTG  TCGCCTTATG   TGG
                                |||||  ||||||||||   |||
                                CGGAC  GGTGGAGTGT   ACC
                                   TT        C__
GAM938  LOC123643 5'  CGGGGCTCATGGCTCCAGGC   76017       TC   TTAT    TG
                                GCCTGGG  GCC    GCCC  G
                                |||||||  |||    ||||  |
                                CGGACCT  CGG    CGGG  C
                                   __  TACT    GT
GAM938  LOC124446 5'  CCGGGGAGGGGGTGCTCAGGT  74288       T     ATG
                                GCCTGGG CGCCTT   CCCTGG
                                ||||||| ||||||   ||||||
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                                TGGACTC GTGGGG  GGGGCC
                                   _    GA_
GAM938  LOC124739 3'  GGCCAGGGGCCTGGGCA    74330     TG   G  TAT
                                TGCC  GGTC CCT  GCC
                                |||| |||| |||  |||
                                ACGG  CCGG GGA  CGG
                                  GT   _  C__
GAM938  LOC124753 3'  CCAGGCGTCTGGGACCCAGGT  74319        G  TT   C
                                GCCTGGGTC CC  ATGCC TGG
                                ||||||||| ||  ||||| |||
                                TGGACCCAG GG  TGCGG ACC
                                     _ TC    _
GAM938  LOC124930 3'  AGGGCGGAGCCAGGC      74353      G  GCCTTA
                                GCCTGG TC     TGCCCT
                                |||||| ||     ||||||
                                CGGACC AG     GCGGGA
                                   G _______
GAM938  LOC124976 3'  CTGCAATCAAGGTGGTTCTGGT 74379     T GG     A__  CCTGG
                                GCC G  TCGCCTT  TGC
                                ||| |  |||||||  |||
                                TGG C  GGTGGAA  ACG
                                  T TT     CTA  TC
GAM938  LOC125268 3'  TTAGTTCATGGCGACCCAGGCA 76084          TT  CC
                                TGCCTGGGTCGCC  ATG  CTGG
                                |||||||||||||  |||  ||||
                                ACGGACCCAGCGG  TAC  GATT
                                      __  TT
GAM938  LOC126392 5'  GGCCGCAGGTGTCCAGGT    75703       T    TAT
                                GCCTGGG CGCCT  GCC
                                ||||||| |||||  |||
                                TGGACCT GTGGA  CGG
                                   _    CGC
GAM938  LOC126669 3'  CGGGTGCGGTGGCTCATGCA  75402    C       TTAT  _  TG
                                TGC TGGGTCGCC   GC CC  G
                                ||| |||||||||   || ||  |
                                ACG ACTCGGTGG   CG GG  C
                                  T       ____  T  GT
GAM938  LOC127281 3'  TGGGGCGGCCGGCCCGGG    74651        _  TTAT   TG
                                CCTGGGTCG CC   GCCC  G
                                ||||||||| ||   ||||  |
                                GGGCCCGGC GG   CGGG  T
                                     C ____   GT
GAM938  LOC127281 3'  TTGGGGTGCATGGGGGTGCCCC 74652       T    _   _  GG
           GGGCA                  CCTGGG CGCCTT ATGC CCT
                                ||||||| |||||| |||| |||
                                GGGCCC GTGGGG TACG GGG
                                   C    G   T  GTT
GAM938  LOC127687 3'  CTGGCCTGCTATGGGGGATCCA 74688        G    _  C__ TG
           GGT                    CCTGGGTC CCTTAT GC   C  G
                                ||||||||| |||||| ||   |  |
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                                GGACCTAG GGGGTA CG   G  C
                                    _     T  TCC GT
GAM938  LOC127702 3'  TGGGGCACAGACCTGGGGCA   75463     _ TG    GCCTTA    TG
                                TGC C  GGTC     TGCCC  G
                                ||| |  ||||     |||||  |
                                ACG G  CCAG     ACGGG  T
                                  G GT    AC____    GT
GAM938  LOC129052 5'  CGGGGCTCCTGGCCGGGC    75805      GGTC   TTAT
                                GCCTG   GCC   GCCCTG
                                |||||   |||   ||||||
                                CGGGC   CGG   CGGGGC
                                   ____  TCCT
GAM938  LOC130074 3'  TTGGGGCGAGGGGGGTGGTTTA 76143    C   GT     AT__   TG
            TGT                   GC TGG  CGCCTT   GCCC  G
                                || |||  ||||||   ||||  |
                                TG ATT  GTGGGG   CGGG  T
                                 T   TG     GGAG   GT
GAM938  LOC130595 5'  CAGGGCACTGATTGGGCA    75749      TG G   CCTTA
                                TGCC  G TCG    TGCCCTG
                                ||||  | |||    |||||||
                                ACGG  T AGT    ACGGGAC
                                  GT _   C____
GAM938  LOC130612 5'  GTCAGGGCATGGGGCCGCGGTT 74960    TC_____
            CTGGGGC                GG      GCCTTATGCCCTGG   T
                                ||      ||||||||||||||  |
                                TC      CGGGGTACGGGACT   G
                                 TTGGCGC
GAM938  LOC130814 5'  GGCCGGGTGGTCCCGGGC    74985       _     TAT
                                GCCTGGG TCGCCT   GCC
                                ||||||| ||||||   |||
                                CGGGCCC GGTGGG   CGG
                                    T     C__
GAM938  LOC131744 5'  GGGAAAAGGCATCCAGGC    75872        C    ATG
                                GCCTGGGT GCCTT   CCC
                                |||||||| |||||   |||
                                CGGACCTA CGGAA   GGG
                                    _    AA_
GAM938  LOC133728 5'  GCTGGGAGGCGGCCTGGGC    75926     TG       AT_
                                GCC  GGTCGCCTT   GC
                                |||  |||||||||   ||
                                CGG  CCGGCGGAG   CG
                                  GT       GGT
GAM938  LOC134553 3'  CAGGGCATGAGCAGCGGC    75197      __
                                GTCGC  CTTATGCCCTG
                                |||||  ||||||||||
                                CGGCG  GAGTACGGGAC
                                   AC
GAM938  LOC135892 5'  GAGGCTGGCCCGGGCA      75245          _
                                TGCCTGGGTC GCCTT
                                |||||||||| |||||
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                                ACGGGCCCGG CGGAG
                                      T
GAM938  LOC135932 5'  CTGGGGTATGGGCTGCCTCGGG 76198      _  C   T    TG
            T                  GCCTG GGT GCCT ATGCCC  G
                               ||||| ||| |||| ||||||  |
                               TGGGC CCG CGGG TATGGG  C
                                  T  T   _    GT
GAM938  LOC139322 3'  ATGAGGAGACTTAGGTA    75379         G
                               TGCCTGGGTC CCTTAT
                               |||||||||| ||||||
                               ATGGATTCAG GGAGTA
                                      A
GAM938  LOC139840 5'  CCAGGGCAGGGATCTTGGGTA  76267     TG  TCG   TA
                               TGCC  GG   CCT  TGCCCTGG
                               ||||  ||   |||  ||||||||
                               ATGG  TC   GGG  ACGGGACC
                                 GT  TA_  __
GAM938  LOC143308 5'  GCATAAGTGGCCTAGGCA    82938          C
                               TGCCTGGGTCGC TTATGC
                               |||||||||||| ||||||
                               ACGGATCCGGTG AATACG
                                        _
GAM938  LOC143381 3'  TGGGGCGAGACCGGGT      76551       G_
                               GCCTGG  TCGCCTTA
                               ||||||  ||||||||
                               TGGGCC  AGCGGGGT
                                  AG
GAM938  LOC143666 5'  GGGCTGGGGCCCGGGT      82973         G  TTAT
                               GCCTGGGTC CC    GCCC
                               ||||||||| ||    ||||
                               TGGGCCCGG GG    CGGG
                                     _ T___
GAM938  LOC143909 5'  CCAGGGATTGCAGGCCTGGGC  82997     TG   _  CTTATG
                               GCC  GGTC GC     CCCTGG
                               |||  |||| ||     ||||||
                               CGG  CCGG CG     GGGACC
                                 GT    A  TTA___
GAM938  LOC144231 5'  GGGCAAGGCGCTCAGGCA    83018        T    TA
                               TGCCTGGG CGCCT  TGCCC
                               |||||||| |||||  |||||
                               ACGGACTC GCGGA  ACGGG
                                        _    __
GAM938  LOC144278 3'  CCAGGGTCTCCACGGTGAACTT 76768   TG  _   TTAT__
            GGGC                  C  GGT CGCC     GCCCTGG
                               |  ||| ||||     |||||||
                               G  TCA GTGG     TGGGACC
                                GT   A    CACCTC
GAM938  LOC144305 3'  CGGGGTGTGGGTGATGGGGG  83032     GG     T     TG
                               CCT  GTCGCCT ATGCCC  G
                               |||  ||||||| ||||||  |
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                                GGG  TAGTGGG TGTGGG  C
                                  GG      _     GT
GAM938   LOC144698 3'  TCAGAACAGGTGTGACTCAGGC 76910          _  TA  CC
             A                    TGCCTGGGTCGC CT  TG  CTGG
                                  ||||||||||| ||  ||  ||||
                                  ACGGACTCAGTG GG  AC  GACT
                                         T  __  AA
GAM938   LOC145323 5'  GGGAAGGAGGCCTGGGC     77091     TG   G   ATG
                                  GCC  GGTC CCTT   CCC
                                  |||  |||| ||||   |||
                                  CGG  CCGG GGAA   GGG
                                    GT   A   ___
GAM938   LOC145333 5'  CTAGGTTGGGTGACCTAGGT   83325          TATGC
                                  GCCTGGGTCGCCT    CCTGG
                                  ||||||||||||     |||||
                                  TGGATCCAGTGGG    GGATC
                                         TT___
GAM938   LOC145483 3'  GTGGGGAGGCTCAGGT      77247         G
                                  GCCTGGGTC CCTTAT
                                  ||||||||| ||||||
                                  TGGACTCGG GGGGTG
                                       A
GAM938   LOC145652 5'  CAGGCTGGTAATTCGGGTA   83410         CG  TTATGC
                                  TGCCTGGGT  CC     CCTG
                                  |||||||||  ||     ||||
                                  ATGGGCTTA  GG     GGAC
                                       AT  TC____
GAM938   LOC145786 5'  GGTTCCAGGGATTTGGGCA   83492     TG   G   TAT
                                  TGCC  GGTC CCT   GCC
                                  ||||  |||| |||   |||
                                  ACGG  TTAG GGA   TGG
                                    GT   _  CCT
GAM938   LOC145786 3'  GTGAGTGGTTTAGGCA      83493       GT   C
                                  TGCCTGG  CGC TTAT
                                  |||||||  ||| ||||
                                  ACGGATT  GTG AGTG
                                       TG  _
GAM938   LOC145858 5'  GGGTATGGCCCGGGCA      77546         GCCTT
                                  TGCCTGGGTC    ATGCCC
                                  ||||||||||    ||||||
                                  ACGGGCCCGG    TATGGG
                                                _____
GAM938   LOC145980 5'  CCAGTGCCGGGCAGTTCAGGT  83603       TC    TAT  C
                                  GCCTGGG  GCCT   GC CTGG
                                  |||||||  ||||   || ||||
                                  TGGACTT  CGGG   CG GACC
                                       GA   C__  T
GAM938   LOC145981 5'  CCAGGGCGCCGGGCCCGGG   60310      GTC   TA
                                  CCTGG   GCCT  TGCCCTGG
                                  |||||   ||||  ||||||||
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                                GGGCC  CGGG  GCGGGACC
                                   ___   CC
GAM938  LOC145981 5'  TCGGGTGGCGGCCGGCCCAGGC 60312        _ TTA    TGG
                                GCCTGGGTCG CC  TGCCC
                                |||||||||| ||  |||||
                                CGGACCCGGC GG  GTGGG
                                     C  CG_    CT
GAM938  LOC146223 5'  CCAGCCGCGCGAGGCGGCCCGG 77708          TA  C_
          GC                     GCCTGGGTCGCCT  TGC  CTGG
                                |||||||||||||  |||  ||||
                                CGGGCCCGGCGGA  GCG  GACC
                                       GC  CC
GAM938  LOC146381 5'  CCGGGTACCAGGGATTCAGGCA 77866        G  TA    T
                                TGCCTGGGTC CCT  TGCCC GG
                                |||||||||| |||  ||||| ||
                                ACGGACTTAG GGA  ATGGG CC
                                     _  CC    _
GAM938  LOC146443 3'  GGGCAGCAGGCTCAGCA    77884    C    _ CTTA
                                TGC TGGGTC GC   TGCCC
                                ||| |||||| ||   |||||
                                ACG ACTCGG CG   ACGGG
                                  _    A ____
GAM938  LOC146520 5'  CCAGGGGTGATCTGGGCA    77953     TG     TTATGC
                                TGCC  GGTCGCC    CCTGG
                                ||||  |||||||    |||||
                                ACGG  CTAGTGG    GGACC
                                  GT     _______
GAM938  LOC146733 5'  CATAGGGTGACCAGGT     83757      G
                                GCCTGG TCGCCTTATG
                                |||||| ||||||||||
                                TGGACC AGTGGGATAC
                                   _
GAM938  LOC146733 3'  CCAGAGCCTAGGGCAGTCCAGG 83758       TC    T  C
          CA                     TGCCTGGG  GCCTTA GC CTGG
                                |||||||  |||||| || ||||
                                ACGGACCT  CGGGAT CG GACC
                                     GA    C  A
GAM938  LOC146756 3'  CGGGGTGGGGTGGTCAGGGT  83775    G GT    AT   TG
                                GCCT G  CGCCTT  GCCC  G
                                |||| |  ||||||  ||||  |
                                TGGG C  GTGGGG  TGGG  C
                                  A TG    __   GT
GAM938  LOC146784 5'  CTAGGGTATGGAGTCCACGT  78110   C   TCG  TT
                                GC TGGG  CC  ATGCCCTGG
                                || ||||  ||  |||||||||
                                TG ACCT  GG  TATGGGATC
                                 C   GA_ __
GAM938  LOC146802 5'  CTGGCCGTGCAGGCGCTCAGGC 78135       T   _   C  TGG
                                GCCTGGG CGCCT TATG CC
                                ||||||| ||||| |||| ||
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                                CGGACTC GCGGA GTGC GG
                                   _    C   C  TC
GAM938  LOC146818 5'  TTGTAATAAGGCGCATCCAGGT 78146        _      GCCCTGG
          A                     TGCCTGGGT CGCCTTAT
                                |||||||| ||||||||
                                ATGGACCTA GCGGAATA
                                    C       ATGTT
GAM938  LOC147080 3'  CCAGGTGTGGTGGCTCAGGC  83931          TTAT  _
                                GCCTGGGTCGCC   GC CCTGG
                                ||||||||||||   || |||||
                                CGGACTCGGTGG   TG GGACC
                                      _____ T
GAM938  LOC147124 3'  CGGGGTGTGGGGCAGTCGGGG  76301    G  TC        TG
                                CCT GG  GCCTTATGCCC  G
                                ||| ||  ||||||||||| |
                                GGG CT  CGGGGTGTGGG  C
                                  G  GA         GT
GAM938  LOC147160 5'  TCAGGGCCTCCTGGTGGGCCTG 83973    TG   _  TTAT_
          GGTA                    GCC  GGTC GCC    GCCCTGG
                                ||| |||| |||    |||||||
                                TGG  CCGG TGG    CGGGACT
                                  GT   G   TCCTC
GAM938  LOC147166 3'  TTGCATTTTAGGGTGATTTGGG 78293    TG       ___  CCTGG
                                CC  GGTCGCCTTA   TGC
                                ||  ||||||||||  |||
                                GG  TTAGTGGGAT   ACG
                                 GT        TTT   TT
GAM938  LOC147639 3'  GGCAAGGGGCGGCCTGGC    78383    T       TA
                                GCC GGGTCGCCT  TGCC
                                ||| |||||||||  ||||
                                CGG TCCGGCGGG  ACGG
                                  _       GA
GAM938  LOC148193 5'  CCGGCGCGGGTGGCCGAGGC  60336     G      TAT  C
                                GCCT GGTCGCCT   GC CTGG
                                |||| ||||||||   || ||||
                                CGGA CCGGTGGG   CG GGCC
                                  G       ___  C
GAM938  LOC148223 3'  TCGGGGCCTGCAGGCTTGGGCA 78744     TG   _  CTTAT
                                TGCC  GGTC GC    GCCCTGG
                                ||||  |||| ||    |||||||
                                ACGG  TCGG CG    CGGGGCT
                                  GT    A  TC___
GAM938  LOC148426 5'  TCAGGCCAGGAGGTGCCCCAGG 84152       T     A  C
          T                     GCCTGGG CGCCTT TG CCTGG
                                ||||||| |||||| || |||||
                                TGGACCC GTGGAG AC GGACT
                                    C     G  C
GAM938  LOC148709 5'  CAGGGCATGATGGTGGGCA   78936     TGGGT   _
                                TGCC    CGCC TTATGCCCTG
                                ||||    |||| ||||||||||
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                                ACGG    GTGG AGTACGGGAC
                                  _____   T
GAM938  LOC148764 5'  GGGCATGGCACTCAGCA     78987     C    C   TT
                                TGC TGGGT GCC  ATGCCC
                                ||| ||||| |||  ||||||
                                ACG ACTCA CGG  TACGGG
                                  _    _  __
GAM938  LOC148764 5'  GGGCATGGCTGAGGT       78988      G   GCCTT
                                GCCT GGTC    ATGCCC
                                |||| ||||    ||||||
                                TGGA TCGG    TACGGG
                                  G  _____
GAM938  LOC148894 3'  CCAGGGCAAAGCAGTGGCTCAG 84257          __  A
           G                     CCTGGGTCGC  CTT TGCCCTGG
                                ||||||||||  ||| ||||||||
                                GGACTCGGTG  GAA ACGGGACC
                                      AC  _
GAM938  LOC149052 3'  TAGGGTATTCATTCAG      79144       CGCCTT
                                CTGGGT     ATGCCCTG
                                ||||||     ||||||||
                                GACTTA     TATGGGAT
                                   CT____
GAM938  LOC149153 3'  TTGGCCATTGGGCGTATCTGGG 84372      TG  _    T   C  TGG
           CA                     TGCC  GGT CGCCT ATG CC
                                ||||  ||| ||||| ||| ||
                                ACGG  CTA GCGGG TAC GG
                                  GT   T    T   C  TT
GAM938  LOC149267 3'  CAGAGGAGGCGGCTTGGG    56675    TG      TATG  _
                                CC  GGTCGCCT    CC CTG
                                ||  ||||||||    || |||
                                GG  TCGGCGGA    GG GAC
                                 GT       _____  A
GAM938  LOC149276 5'  CCAGGAACTTGGGGGTGGTCTT 84383     T  GT     ATGC__
           GGCA                    GCC GG  CGCCTT     CCTGG
                                ||| ||  ||||||     |||||
                                CGG TC  GTGGGG     GGACC
                                  T  TG     GTTCAA
GAM938  LOC149386 5'  CGGGGCTGGTGGTCCAGG    84405      GT    TTAT    TG
                                CCTGG  CGCC    GCCC  G
                                |||||  ||||    ||||  |
                                GGACC  GTGG    CGGG  C
                                   TG    T___    GT
GAM938  LOC149461 3'  CTGGGGCATAGGATGGGCATAG 79402       G   GC_       TG
           GT                     GCCTG GTC   CTTATGCCC  G
                                |||||  |||   |||||||||  |
                                TGGAT CGG   GGATACGGG  C
                                   A   GTA       GT
GAM938  LOC149464 5'  TCGGCCGCTGGGTGACTTCGGT 84435     TG      TAT_  CTGG
                                GCC  GGTCGCCT    GCC
                                |||  ||||||||    |||
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                                TGG  TCAGTGGG    CGG
                                  CT       TCGC   CT
GAM938   LOC149535 5'  GTAGGGGCGACACAGGTA    79418       G       A
                                TGCCTG GTCGCCTT TGC
                                ||||||| |||||||| |||
                                ATGGAC CAGCGGGG ATG
                                   A       _
GAM938   LOC149576 3'  CCGGGCCTGAGGGGCGTCCCGG 79426        T     AT__    T
           GC                     GCCTGGG CGCCTT    GCCC GG
                                ||||||| ||||||    |||| ||
                                CGGGCCC GCGGGG    CGGG CC
                                   T     AGTC    _
GAM938   LOC149576 5'  TATAAGCCGGCCCAGGCA    79428           C
                                TGCCTGGGTCG CTTATG
                                |||||||||| ||||||
                                ACGGACCCGGC GAATAT
                                      C
GAM938   LOC149619 5'  GCAGAGGTGACACAGGTA    84529       G       A
                                TGCCTG GTCGCCTT TGC
                                ||||||| |||||||| |||
                                ATGGAC CAGTGGAG ACG
                                   A       _
GAM938   LOC149668 5'  CAAGGGTGGGGCTGGCCTGGGC 84535      TG    _    AT    GG
           A                     TGCC  GGTC GCCTT  GCCCT
                                ||||  |||| |||||  |||||
                                ACGG  CCGG CGGGG  TGGGA
                                  GT    T     __     ACA
GAM938   LOC149803 5'  CAGGACAGGCATTCAGGCA    79537         C    TAT C
                                TGCCTGGGT GCCT   G CCTG
                                ||||||||| ||||   | ||||
                                ACGGACTTA CGGA   C GGAC
                                      _    ___ A
GAM938   LOC149837 3'  TTAGGGTAAACAACGGTTAAGG 84749      G GT  CCTTA
           CA                     TGCCT G  CG     TGCCCTGG
                                ||||| |  ||     ||||||||
                                ACGGA T  GC     ATGGGATT
                                   A TG  AACAA
GAM938   LOC149944 3'  CAGATGGGTGACTTAAGT     84771     C         TATGCC
                                GC TGGGTCGCCT      CTG
                                || ||||||||||      |||
                                TG ATTCAGTGGG      GAC
                                 A         TA____
GAM938   LOC150067 5'  CCAGGGCTTTCCGGGCTTAGGT 60340          GCCTTAT
                                GCCTGGGTC       GCCCTGG
                                |||||||||       |||||||
                                TGGATTCGG       CGGGACC
                                     GCCTTT_
GAM938   LOC150067 5'  CGTGGGGGCGGCTCGGC      60341     T       TTATG  _
                                GCC GGGTCGCC     CCC TG
                                ||| ||||||||     ||| ||
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                                CGG CTCGGCGG    GGG GC
                                  _      _____  T
GAM938  LOC150155 5' GCTGAGAGGCGGCCTGGGC   70853    TG      AT_
                                GCC  GGTCGCCTT   GC
                                |||  |||||||||   ||
                                CGG  CCGGCGGAG   CG
                                  GT       AGT
GAM938  LOC150157 5' AGGGGTCTAGTGGTCTGTGCA  84871    C   GT   CT  T    GG
                                TGC TGG  CGC  TA GCCCT
                                ||| |||  |||  || |||||
                                ACG GTC  GTG  AT TGGGG
                                  T  TG   __ C    AT
GAM938  LOC150157 5' CAGCAGTGTGGCTCAGGT    84872         CTTA   CC
                                GCCTGGGTCGC    TGC  TG
                                ||||||||||    |||  ||
                                TGGACTCGGTG    ACG  AC
                                       TG__   __
GAM938  LOC150174 3' TCAGTGAAGAGGGGCTCGGGCA 79611         G    ATGCC
                                TGCCTGGGTC CCTT    CTGG
                                |||||||||| ||||    ||||
                                ACGGGCTCGG GGAG    GACT
                                      _   AAGT_
GAM938  LOC150213 3' TCAGTGAAGAGGGGCTCGGGCA 74859         G    ATGCC
                                TGCCTGGGTC CCTT    CTGG
                                |||||||||| ||||    ||||
                                ACGGGCTCGG GGAG    GACT
                                      _   AAGT_
GAM938  LOC150221 3' TTGGGATGTGAGGGTGATCTGG 65278    T       ATG__   TGG
          C                      GCC GGGTCGCCTT    CCC
                                |||  ||||||||||    |||
                                CGG TCTAGTGGGA    GGG
                                  _       GTGTA   TT
GAM938  LOC150236 5' CCAGGAGCGGTTACCTGGGCA  79685    TG   C   TTAT  _
                                TGCC  GGT GCC    GC CCTGG
                                ||||  ||| |||    || |||||
                                ACGG  CCA TGG    CG GGACC
                                  GT   T  ____  A
GAM938  LOC150236 5' TCAGTGAAGAGGGGCTCGGGCA 79690         G    ATGCC
                                TGCCTGGGTC CCTT    CTGG
                                |||||||||| ||||    ||||
                                ACGGGCTCGG GGAG    GACT
                                      _   AAGT_
GAM938  LOC150271 3' CCATGCTGGGGTGGCTCAGG   84950          T  CC
                                CCTGGGTCGCCTTA GC  TGG
                                |||||||||||||| ||  |||
                                GGACTCGGTGGGGT CG  ACC
                                       _  T_
GAM938  LOC150378 5' AGGTGGGACCCAGGC       79739         G  TTATGC
                                GCCTGGGTC CC     CCT
                                |||||||| ||     |||
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                                CGGACCCAG GG     GGA
                                    _ T_____
GAM938  LOC150465 5'  GGCGGGCGCCCGGGC      79873       T    TAT
                                GCCTGGG CGCCT   GCC
                                ||||||| |||||   |||
                                CGGGCCC GCGGG   CGG
                                   _    ___
GAM938  LOC150481 5'  GGGAGGGGCCCAGGT      79895        G   TATG
                                GCCTGGGTC CCT    CCC
                                ||||||||| |||    |||
                                TGGACCCGG GGA    GGG
                                   _  _____
GAM938  LOC150577 3'  GCAAGAGGAGGCTCAGGT    85075        G    A
                                GCCTGGGTC CCTT TGC
                                ||||||||| |||| |||
                                TGGACTCGG GGAG ACG
                                     A    A
GAM938  LOC150759 3'  GGTGGAGGGTGGGCTGGGCA   80009     TG G     A
                                TGCC  G TCGCCTT TGCC
                                ||||  | ||||||| ||||
                                ACGG  C GGTGGGA GTGG
                                  GT G      G
GAM938  LOC151009 5'  CAGCAGGTGGCGCAGGC     85192      G     TATGCC
                                GCCTG GTCGCCT     CTG
                                ||||| |||||||     |||
                                CGGAC CGGTGGA     GAC
                                  G      C_____
GAM938  LOC151121 5'  GGGTATTGTGACCTGGGT    80121     TG     CTT
                                GCC  GGTCGC   ATGCCC
                                |||  ||||||   ||||||
                                TGG  CCAGTG   TATGGG
                                  GT     T__
GAM938  LOC151176 3'  CTAGAAGTACTGGGCTGGCCTG 85261     TG   _   TA   C_
          GGTA                    GCC  GGTC GCCT  TGC  CTGG
                                |||  |||| ||||  |||  ||||
                                TGG  CCGG CGGG  ATG  GATC
                                  GT    T    TC   AA
GAM938  LOC151323 3'  GGTGGAGGGTGGGCTGGGCA   80221     TG G     A
                                TGCC  G TCGCCTT TGCC
                                ||||  | ||||||| ||||
                                ACGG  C GGTGGGA GTGG
                                  GT G      G
GAM938  LOC151429 3'  GGGAGGTGGCTCAGC      85358    C       TATG
                                GC TGGGTCGCCT    CCC
                                || ||||||||||    |||
                                CG ACTCGGTGGA    GGG
                                   _       _____
GAM938  LOC151556 3'  GCTGGGTGACCTTGGGCA    80277       _       TAT
                                TGCCTG GGTCGCCT   GC
                                |||||| ||||||||   ||
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                                ACGGGT CCAGTGGG   CG
                                   T       T__
GAM938   LOC152313 3'  TGGGGGCAATGGGTGTTCTAGG 85669       GT    TA     GG
            T                    GCCTGG  CGCCT  TGCCCT
                                 ||||||  |||||  ||||||
                                 TGGATC  GTGGG  ACGGGG
                                    TT     TA     GTC
GAM938   LOC152316 3'  ATGAGGTCATTTGGGCA     85607      TG   C
                                 TGCC  GGT GCCTTAT
                                 ||||  ||| |||||||
                                 ACGG  TTA TGGAGTA
                                   GT   C
GAM938   LOC152343 3'  CCAGTCTGGAGGTGATCTGGGC 80559     TG        ATGCC
                                 GCC  GGTCGCCTT    CTGG
                                 |||  |||||||||    ||||
                                 CGG  CTAGTGGAG    GACC
                                   GT        GTCT_
GAM938   LOC152633 5'  CTGGGGGTGGGGTGGCCCCAGG 85809         _       G   TGG
            CA                     TGCCTGGG TCGCCTTAT CCC
                                 ||||||||| ||||||||| |||
                                 ACGGACCC GGTGGGGTG GGG
                                      C        G   TC
GAM938   LOC153196 5'  GGGGAGCACCCAGGC       85967         C  C  ATG
                                 GCCTGGGT GC TT   CCC
                                 |||||||| || ||   |||
                                 CGGACCCA CG AG   GGG
                                      _  _  ___
GAM938   LOC153218 5'  GGGTGTTACCCAGGC       80778         C  CTTAT
                                 GCCTGGGT GC     GCCC
                                 |||||||| ||     ||||
                                 CGGACCCA TG     TGGG
                                      T  _____
GAM938   LOC153243 5'  CTGCTTTCGGGGTGGCCTGGGC 80797      TG        AT__  CCTGG
            G                     TGCC  GGTCGCCTT    GC
                                 ||||  |||||||||    ||
                                 GCGG  CCGGTGGGG    CG
                                   GT        CTTT  TC
GAM938   LOC153688 3'  CCAGTTGCCCAGGTTGTCCAGG 86099        TC    TAT  C_
            C                     GCCTGGG  GCCT   GC  CTGG
                                 |||||||  ||||   ||  ||||
                                 CGGACCT  TGGA   CG  GACC
                                      GT    CC_  TT
GAM938   LOC154760 5'  CTGGGGTATGGGCTGCCTCGGG 86245      _  C    T     TG
            T                     GCCTG GGT GCCT ATGCCC  G
                                 |||||  ||| |||| ||||||  |
                                 TGGGC CCG CGGG TATGGG  C
                                   T  T   _     GT
GAM938   LOC154789 5'  GGGCGGCTGCTCAGGCA     81138         C   TTAT
                                 TGCCTGGGT GCC    GCCC
                                 |||||||||  |||    ||||
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                                ACGGACTCG CGG    CGGG
                                     T  ____
GAM938  LOC154789 5'  GGGCGTGGCTTAGGT      81139          CTTAT
                                GCCTGGGTCGC    GCCC
                                ||||||||||    ||||
                                TGGATTCGGTG    CGGG
                                      _____
GAM938  LOC154789 5'  TGGGGTGGAAGATTTAGGC   81144        G_ TTAT   TG
                                GCCTGGGTC CC   GCCC G
                                |||||||| ||   |||| |
                                CGGATTTAG GG   TGGG T
                                     AA ____   GT
GAM938  LOC155032 3'  TGGCAGAGGTAGTGAGGTGATT 86325           _  _  G
          CAGGTA                  CCTGGGTCGCCTTA TGCC CTG
                                ||||||||||||| |||| |||
                                GGACTTAGTGGAGT ATGG GAC
                                     G   A  GGTT
GAM938  LOC155064 5'  TCGGGCGAGGCGGGGCGGCTCG 81252          A___    TGG
          GGC                    CCTGGGTCGCCTT   TGCCC
                                ||||||||||||   |||||
                                GGGCTCGGCGGGG   GCGGG
                                     CGGA    CT
GAM938  LOC155066 5'  TCAGGTTCGGGGCGGCCCAGGC 81284          AT  C
                                GCCTGGGTCGCCTT  GCC TGG
                                ||||||||||||  ||| |||
                                CGGACCCGGCGGGG  TGG ACT
                                     CT  _
GAM938  LOC155081 5'  CTGAGCCTGAGGAGACCTGGGT 81291     TG   G    T  CCTGG
          A                     TGCC  GGTC CCTTA GC
                                ||||  |||| ||||| ||
                                ATGG  CCAG GGAGT CG
                                  GT   A    C  AGTC
GAM938  LOC157306 3'  GGGGACGGAGGCTCGGGT    81396        G  TTATG
                                GCCTGGGTC CC    CCCT
                                ||||||||| ||    ||||
                                TGGGCTCGG GG    GGGG
                                     A  CA___
GAM938  LOC157567 5'  TAGGGCTGTGGTCCGGG     81484      GT   CTTAT
                                CCTGG  CGC    GCCCTG
                                |||||  |||    ||||||
                                GGGCC  GTG    CGGGAT
                                   TG   T____
GAM938  LOC157697 5'  GGGAGGCAATCTAGGT      81552        C   TATG
                                GCCTGGGT GCCT   CCC
                                |||||||| ||||   |||
                                TGGATCTA CGGA   GGG
                                     A   ____
GAM938  LOC158267 3'  CCAGCTGGGTGATCTTGGGCA  81827      TG  _     TATGCC
                                TGCC  GG TCGCCT     CTGG
                                ||||  || ||||||     ||||
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                                ACGG  TC AGTGGG     GACC
                                  GT  T     TC____
GAM938   LOC158288 5'  GCCTGGGCGACCTGGC      86717     T       TAT
                                GCC GGGTCGCCT   GC
                                ||| |||||||||   ||
                                CGG TCCAGCGGG   CG
                                  _       TC_
GAM938   LOC158292 5'  CCGGGCACGGTGGCTCAGGC   86729           TTA     T
                                GCCTGGGTCGCC   TGCCC GG
                                ||||||||||||   ||||| ||
                                CGGACTCGGTGG   ACGGG CC
                                       C__    _
GAM938   LOC158308 3'  CGGGGTGTGGGGGGGC      86743     G
                                GTC CCTTATGCCCTG
                                ||| ||||||||||||
                                CGG GGGGTGTGGGGC
                                  G
GAM938   LOC158435 5'  TTAGGGCATGAGGATGTTGGG  56719     TG GTCG
                                CC  G    CCTTATGCCCTGG
                                ||  |    ||||||||||||
                                GG  T    GGAGTACGGGATT
                                 GT GTA_
GAM938   LOC158563 3'  CCAGAAAGGAGGTGGCCCAGTC 81950     C          ATGCC
           A                     TG CTGGGTCGCCTT     CTGG
                                || ||||||||||||     ||||
                                AC GACCCGGTGGAG     GACC
                                 T          GAAA_
GAM938   LOC158886 3'  TAGGGTATTCATTCAG      82835       CGCCTT
                                CTGGGT      ATGCCCTG
                                ||||||      ||||||||
                                GACTTA      TATGGGAT
                                   CT____
GAM938   LOC158972 3'  CTGGCAGGTGAGGAGATCCAGG 86950          G    __    CTGG
           CA                     TGCCTGGGTC CCTTA  TGCC
                                |||||||||| |||||  ||||
                                ACGGACCTAG GGAGT  ACGG
                                      A     GG    TC
GAM938   LOC159193 5'  CCAGGGCAGCTGTGCGGCCTGG 82176     T      CTTA_
           C                      GCC GGGTCGC     TGCCCTGG
                                ||| |||||||     ||||||||
                                CGG TCCGGCG     ACGGGACC
                                  _       TGTCG
GAM938   LOC159723 5'  GCTTGGGGCCGCTCGGGTA    82193          C     T
                                TGCCTGGGT GCCTTA GC
                                ||||||||| |||||| ||
                                ATGGGCTCG CGGGGT CG
                                      C     T
GAM938   LOC159766 5'  CCAGGGTGTCCTCGCCTGGC   82199     T   T  CCTT
                                GCC GGG CG    ATGCCCTGG
                                ||| ||| ||    |||||||||
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                                CGG TCC GC    TGTGGGACC
                                  _  _  TCC_
GAM938  LOC161176 5'  GGAGCAGGTGGCCCGGG     82261          TAT  _
                                CCTGGGTCGCCT   GC CC
                                ||||||||||||  || ||
                                GGGCCCGGTGGA   CG GG
                                      ____  A
GAM938  LOC162333 5'  GGAACAGGTGGCCCAGG     87135          TATG
                                CCTGGGTCGCCT    CC
                                ||||||||||||    ||
                                GGACCCGGTGGA    GG
                                      CAA_
GAM938  LOC162417 5'  CGGGGCGCCGGCTCAGCA    82347     C      CCTTA
                                TGC TGGGTCG     TGCCCTG
                                ||| |||||||     |||||||
                                ACG ACTCGGC     GCGGGGC
                                  _       C_____
GAM938  LOC163126 5'  GGGTGTCCGCCGGGCA      82416       GT  CCTT
                                TGCCTGG  CG    ATGCCC
                                |||||||  ||    ||||||
                                ACGGGCC  GC    TGTGGG
                                   __  C___
GAM938  LOC163682 5'  CCACAATGGGGGCTGTCCAGGC 87026        TC     ATGCCC
          A                      TGCCTGGG  GCCTT      TGG
                                 ||||||||  |||||      |||
                                 ACGGACCT  CGGGG      ACC
                                      GT     GTAAC_
GAM938  LOC164397 3'  TTGGGGCTAAAGCTGACTTGGG 82535      TG   _ C   T    TG
          CA                     TGCC  GGTC GC TTA GCCC  G
                                 ||||  |||| || ||| ||||  |
                                 ACGG  TCAG CG AAT CGGG  T
                                   GT    T  A   _    GT
GAM938  LOC164584 5'  TCAACGTGAGGGTGGTGCAGGT 82546       G     _     CCCTGG
                                 GCCTG GTCGCC TTATG
                                 ||||| |||||| |||||
                                 TGGAC TGGTGG AGTGC
                                    G      G     AACT
GAM938  LOC164684 3'  TCAGGATAAGGAGGACGACTCA 82551          _    ATGC_
          GGTA                     GCCTGGGTCG CCTT     CCTGG
                                   |||||||||| ||||     |||||
                                   TGGACTCAGC GGAG     GGACT
                                        A    GAATA
GAM938  LOC164714 5'  CATGAAGGTGGCCCAGG     87224          _
                                 CCTGGGTCGCCT TATG
                                 |||||||||||| ||||
                                 GGACCCGGTGGA GTAC
                                       A
GAM938  LOC164944 5'  GCAGAGGGACTTGGGCA     87183      TG   G    A
                                 TGCC  GGTC CCTT TGC
                                 ||||  |||| |||| |||
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                                ACGG  TCAG GGAG ACG
                                  GT   _   _
GAM938   LOC165476 5'  CTAGGGTCCCCGCGGCCTGGC  87197     T      CTTAT
                                GCC GGGTCGC    GCCCTGG
                                ||| |||||||    |||||||
                                CGG TCCGGCG    TGGGATC
                                  _      CCCC_
GAM938   LOC165693 3'  GCAAAGGAGATTCGGGT     82598         G    A
                                GCCTGGGTC CCTT TGC
                                ||||||||| |||| |||
                                TGGGCTTAG GGAA ACG
                                     A   _
GAM938   LOC168544 3'  CTGGGGTGAGCAAGGCGACCTG 82717     TG       A__    TG
           GGC                    GCC  GGTCGCCTT   TGCCC  G
                                |||  |||||||||   |||||  |
                                CGG  CCAGCGGAA   GTGGG  C
                                  GT       CGA    GT
GAM938   LOC196489 3'  GGGCGTGGGGGGCCCGGGT   87737         G
                                GCCTGGGTC CCTTATGCCC
                                ||||||||| ||||||||||
                                TGGGCCCGG GGGGTGCGGG
                                     _
GAM938   LOC196890 5'  AGGGGTCTAGTGGTCTGTGCA  89644    C   GT   CT  T    GG
                                TGC TGG  CGC  TA GCCCT
                                ||| |||  |||  || |||||
                                ACG GTC  GTG  AT TGGGG
                                  T   TG  __  C     AT
GAM938   LOC196906 5'  GAGAGCTGGCCCGGGC      87806          _  _
                                GCCTGGGTC GC CTT
                                ||||||||| || |||
                                CGGGCCCGG CG GAG
                                     T  A
GAM938   LOC197125 5'  AGGGGTAGAGGAGGTTCAGGCA 87897       GG  G    A     GG
                                TGCCTG  TC CCTT TGCCCT
                                ||||||  || |||| ||||||
                                ACGGAC  GG GGAG ATGGGG
                                    TT  A    _     AT
GAM938   LOC197202 5'  GGTACCGGGGGTTCAGGCA   87961       GG  G   TA
                                TGCCTG  TC CCT  TGCC
                                ||||||  || |||  ||||
                                ACGGAC  GG GGG  ATGG
                                    TT  _   CC
GAM938   LOC197319 3'  CCAGGTGTGGTGGCTCAGGC   87968           TTAT  _
                                GCCTGGGTCGCC    GC CCTGG
                                ||||||||||||    || |||||
                                CGGACTCGGTGG    TG GGACC
                                       _____  T
GAM938   LOC197342 3'  CCAGGGCACATGACCTGTGGTA 87994      _      CCTTA
                                TGCC TGGGTCG    TGCCCTGG
                                |||| |||||||    ||||||||
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                                ATGG GTCCAGT    ACGGGACC
                                  T      AC___
GAM938  LOC197342 3'  TTGGGGTGTGGCACCCTCAGC  88009    CT_   C   TT     TG
                                GC   GGGT GCC  ATGCCC  G
                                ||   |||| |||  ||||||  |
                                CG   CCCA CGG  TGTGGG  T
                                 ACT    _  __      GT
GAM938  LOC197358 3'  GCAGGAGTGGTCCAGGCA    88036       GT   C  A
                                TGCCTGG  CGC TT TGC
                                |||||||  ||| || |||
                                ACGGACC  GTG AG ACG
                                    TG   _  G
GAM938  LOC197423 5'  GGCGGCGGCCGGTTCGGGC    77861      GG   _  TTA
                                GCCTG  TCG CC   TGCC
                                |||||  ||| ||   ||||
                                CGGGC  GGC GG   GCGG
                                   TT   C  CG_
GAM938  LOC197439 5'  CCGGGTACCAGGGATTCAGGCA 88074         G   TA    T
                                TGCCTGGGTC CCT  TGCCC GG
                                ||||||||||| |||  ||||| ||
                                ACGGACTTAG GGA  ATGGG CC
                                      _   CC    _
GAM938  LOC200093 5'  CCAGGGCATCAGACACAGGTA  63092       G   GCCTT
                                TGCCTG GTC    ATGCCCTGG
                                |||||| |||    |||||||||
                                ATGGAC CAG    TACGGGACC
                                   A   AC___
GAM938  LOC200170 3'  CCGGGGTGGCCACAGGCA    88590       _   GCCTTAT
                                TGCCTG GGTC      GCCCTGG
                                |||||| ||||      |||||||
                                ACGGAC CCGG      TGGGGCC
                                   A   ________
GAM938  LOC200205 3'  GGGCATTGGATCAGGT      88627       GTCG  TT
                                GCCTGG   CC  ATGCCC
                                ||||||   ||  ||||||
                                TGGACT   GG  TACGGG
                                   A___  T_
GAM938  LOC200399 3'  GGTGGAGGGTGGGCTGGGCA   88812     TG G      A
                                TGCC  G TCGCCTT TGCC
                                ||||  | ||||||| ||||
                                ACGG  C GGTGGGA GTGG
                                  GT G      G
GAM938  LOC200515 5'  GGTGGGTGCTCCAGGCA     90091       GT    TAT
                                TGCCTGG  CGCCT   GCC
                                |||||||  |||||   |||
                                ACGGACC  GTGGG   TGG
                                    TC    ___
GAM938  LOC200634 3'  GGTGGTGGCCCGGGTA      88847           TTAT
                                TGCCTGGGTCGCC    GCC
                                ||||||||||||    |||
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                                ATGGGCCCGGTGG  TGG
                                      ____
GAM938  LOC200862 5'  CCGGGGTGTGGGGGGCGGCGGG 90181      G_  G
            C                   GCCTG  GTC CCTTATGCCCTGG
                                ||||||  ||| ||||||||||||
                                CGGGC  CGG GGGGTGTGGGGCC
                                  GG  _
GAM938  LOC200953 5'  GGGCAGAGGCCCTGGCA    90208     T    GCCTTA
                                TGCC GGGTC     TGCCC
                                |||| |||||     |||||
                                ACGG CCCGG     ACGGG
                                  T    AG____
GAM938  LOC201522 5'  CGGGGCATGTCCCCGGG    88256       TCGCCT
                                CCTGGG     TATGCCCTG
                                ||||||     |||||||||
                                GGGCCC     GTACGGGGC
                                   CT____
GAM938  LOC201952 5'  CAGGGCATTCTGCCCAGCA   90269     C    CGCCTT
                                TGC TGGGT     ATGCCCTG
                                ||| |||||     ||||||||
                                ACG ACCCG     TACGGGAC
                                  _    TCT___
GAM938  LOC202279 5'  GGCGGGGGCGGCCCAGGC    89161            A
                                GCCTGGGTCGCCTT TGCC
                                |||||||||||||| ||||
                                CGGACCCGGCGGGG GCGG
                                      _
GAM938  LOC202802 5'  CTGAGCCTGAGGAGACCTGGGT 89205     TG   G    T  CCTGG
            A                    TGCC  GGTC CCTTA GC
                                ||||  |||| ||||| ||
                                ATGG  CCAG GGAGT CG
                                  GT   A    C  AGTC
GAM938  LOC202915 3'  GGCAGGCACCCAGGT       90394        C   TAT
                                GCCTGGGT GCCT   GCC
                                |||||||| ||||   |||
                                TGGACCCA CGGA   CGG
                                     _   ___
GAM938  LOC202915 3'  TCAGGGCACCTGATGGCCCTGG 90397     T     CCTTA
            CA                    TGCC GGGTCG    TGCCCTGG
                                |||| ||||||    ||||||||
                                ACGG CCCGGT    ACGGGACT
                                  T     AGTCC
GAM938  LOC203052 3'  GGGCATAAGGACAGG       90457     GGTCG
                                CCTG    CCTTATGCCC
                                ||||    ||||||||||
                                GGAC    GGAATACGGG
                                  A____
GAM938  LOC203209 5'  CACAAGGGGGCCCAGGCA    89297         G   A
                                TGCCTGGGTC CCTT TG
                                |||||||||| |||| ||
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                                ACGGACCCGG GGAA AC
                                      G   C
GAM938  LOC203286 3'  AGGGCAGGTTTAGGCA     90492       GTC   TAT
                                TGCCTGG  GCCT  GCCCT
                                |||||||  ||||  |||||
                                ACGGATT  TGGA  CGGGA
                                   ___   ___
GAM938  LOC203636 3'  CGGGGCAGCAGGCCCAGGC   89423        _ CTTA   TG
                                GCCTGGGTC GC   TGCCC  G
                                |||||||||  ||   |||||  |
                                CGGACCCGG CG   ACGGG  C
                                      A ____    GT
GAM938  LOC204161 5'  AGGAAGCTGACCTGGGCA    90656     TG    C  ATGC
                                TGCC  GGTCG CTT   CCT
                                ||||  ||||| |||   |||
                                ACGG  CCAGT GAA   GGA
                                  GT    C  ____
GAM938  LOC204161 5'  CCAGTAGTGGGTGACCTGGT  90657     T       T  GCC
                                GCC GGGTCGCCT AT  CTGG
                                ||| |||||||| ||  ||||
                                TGG TCCAGTGGG TG  GACC
                                 _       _ AT_
GAM938  LOC204579 5'  TTAGCGCGGAGGCGACCCGGC  89466     T       A  C
                                GCC GGGTCGCCTT TGC CTGG
                                ||| |||||||||| ||| ||||
                                CGG CCCAGCGGAG GCG GATT
                                 _       _  C
GAM938  LOC205313 5'  TCGGGGCACACAGGCCTGGGT  90677     TG   GCCTTA
                                GCC  GGTC     TGCCCTGG
                                |||  ||||     ||||||||
                                TGG  CCGG     ACGGGGCT
                                  GT   ACAC__
GAM938  LOC205327 3'  GGGTATGGGGGGAAGCA     89502    GG  G
                                TG  TC CCTTATGCCC
                                ||  || ||||||||||
                                AC  AG GGGGTATGGG
                                 GA  G
GAM938  LOC207061 5'  CCAGGTGCCGGCGGCCCGGGC  89512          TTAT  _
                                GCCTGGGTCGCC   GC CCTGG
                                ||||||||||||   || |||||
                                CGGGCCCGGCGG   CG GGACC
                                       C___  T
GAM938  LOC219513 5'  TGGGGTGTTACATTCTGGCA  94336     T   CGCCTT    TG
                                TGCC GGGT     ATGCCC  G
                                |||| ||||     ||||||  |
                                ACGG CTTA     TGTGGG  T
                                  T   CAT___     GT
GAM938  LOC219537 3'  CCAGAGCCAGGGGCTTAGGCA  91557         G  TAT  C
                                TGCCTGGGTC CCT   GC CTGG
                                |||||||||| |||   || ||||
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                                ACGGATTCGG GGA   CG GACC
                                      _  C__  A
GAM938  LOC219649 5'  GGGGCCTGCGATCCGGC     92960     T      CTTAT
                                GCC GGGTCGC     GCCCT
                                ||| |||||||     |||||
                                CGG CCTAGCG     CGGGG
                                  _      TC___
GAM938  LOC219700 5'  GGGTGCGGCCTGGC       93066     T      CTTAT
                                GCC GGGTCGC     GCCC
                                ||| |||||||     ||||
                                CGG TCCGGCG     TGGG
                                  _     _____
GAM938  LOC219700 5'  TGGAGGCGGGTGGCCTGGC    93069     T       TAT   _ TG
                                GCC GGGTCGCCT   GCC C  G
                                ||| |||||||||   ||| |  |
                                CGG TCCGGTGGG   CGG G  T
                                  _       ___   A GT
GAM938  LOC219842 5'  TCAGAACAGCACAGGGTGATTT 93270    TG       A   C___
            GGGTA                    C  GGTCGCCTT TGC    CTGG
                                |  |||||||| |||    ||||
                                G  TTAGTGGGA ACG    GACT
                                 GT        C   ACAA
GAM938  LOC219855 3'  CAGGGCCAGCACTCGGGC    91513        C  CTTAT
                                GCCTGGGT GC     GCCCTG
                                |||||||| ||     ||||||
                                CGGGCTCA CG     CGGGAC
                                     _  AC___
GAM938  LOC219920 5'  CAGGGCAGGACCCTGGCA    93305     T    GCCTTA
                                TGCC GGGTC      TGCCCTG
                                |||| |||||      |||||||
                                ACGG CCCAG      ACGGGAC
                                  T    G_____
GAM938  LOC219940 3'  TGGGGTGGGTGACTTAGG    93361          TAT    TG
                                CCTGGGTCGCCT   GCCC  G
                                ||||||||||||   ||||  |
                                GGATTCAGTGGG   TGGG  T
                                       ___    GT
GAM938  LOC220565 5'  GGCAGCGGCCGGTTCGGGC    90751      GG   _  TTA
                                GCCTG  TCG CC   TGCC
                                |||||  ||| ||   ||||
                                CGGGC  GGC GG   ACGG
                                   TT   C  CG_
GAM938  LOC220581 5'  TCAGCTACCGGGGTGGTCCGGG 76288       GT     ATGCC
            C                    GCCTGG  CGCCTT     CTGG
                                ||||||  ||||||     ||||
                                CGGGCC  GTGGGG     GACT
                                   TG     CCATC
GAM938  LOC220705 5'  CCGGGGCCAGGTGTCCCGGGC  91226        T    TAT
                                GCCTGGG CGCCT   GCCCTGG
                                |||||||  |||||   |||||||
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                                CGGGCCC GTGGA  CGGGGCC
                                   T   C__
GAM938  LOC220766 3'  TTGGGGTGTATCTTAATTCAG  90802      CGCCT     TG
                                CTGGGT   TATGCCC  G
                                ||||||   |||||||  |
                                GACTTA   ATGTGGG  T
                                   ATTCT     GT
GAM938  LOC221466 5'  GGGTCAGGGTGACTGAGGCA  93690      G       AT
                                TGCCT GGTCGCCTT  GCCC
                                ||||| |||||||||  ||||
                                ACGGA TCAGTGGGA  TGGG
                                   G       C_
GAM938  LOC221496 5'  CCGGGCCTGCGGGCGACTCGAG 91997    C       _ T   T
           C                     GC TGGGTCGCCT TA GCCC GG
                                || ||||||||||  || |||| ||
                                CG GCTCAGCGGG GT CGGG CC
                                 A        C  C   _
GAM938  LOC221496 3'  CTGGGGCATGGCCACGCCAGG  92000      _ C   TT     TG
                                CCTGG GT GCC  ATGCCC  G
                                ||||| || |||  ||||||  |
                                GGACC CA CGG  TACGGG  C
                                   G  C   __     GT
GAM938  LOC221509 3'  TTAGGGCATAATTTTTGGTTTA 92421      GT  CC__
           GGC                    GCCTGG  CG    TTATGCCCTGG
                                ||||||  ||    ||||||||||
                                CGGATT  GT    AATACGGGATT
                                   TG  TTTT
GAM938  LOC221787 5'  GGTGGAGGCGGCTTGGC     92470     T       A
                                GCC GGGTCGCCTT TGCC
                                ||| |||||||||| ||||
                                CGG TTCGGCGGAG GTGG
                                  _        _
GAM938  LOC221935 3'  CCAGGGCAGAGATTCCAGGCA  92620        _  GCCTTA
                                TGCCTGGG TC     TGCCCTGG
                                |||||||| ||     ||||||||
                                ACGGACCT AG     ACGGGACC
                                     T  AG____
GAM938  LOC221975 5'  CCAATCCTGAGCGCGACCCGGG 92603          _   TGCCC
           CA                     TGCCTGGGTCGC CTTA     TGG
                                ||||||||||| ||||     |||
                                ACGGGCCCAGCG GAGT     ACC
                                      C    CCTA_
GAM938  LOC222169 5'  CCAGCAGGAAGGGGCGACTCAG 94084           ATG  __
           GT                     GCCTGGGTCGCCTT   CC  CTGG
                                ||||||||||||||   ||  ||||
                                TGGACTCAGCGGGG   GG  GACC
                                      AA_  AC
GAM938  LOC222228 5'  CTGAGCCTGAGGAGACCTGGGT 94296     TG   G    T  CCTGG
           A                      TGCC  GGTC CCTTA GC
                                ||||  |||| ||||| ||
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                                ATGG  CCAG GGAGT CG
                                  GT    A     C  AGTC
GAM938   LOC222832 5'  CCGGGGACGCGGCGGCCTCGGC 92859     T       TTATG
                                GCC GGGTCGCC     CCCTGG
                                ||| ||||||||     ||||||
                                CGG TCCGGCGG     GGGGCC
                                  C       CGCA_
GAM938   LOC245726 5'  GCCGGGTGACCCAGG       74126            TAT
                                CCTGGGTCGCCT   GC
                                ||||||||||||   ||
                                GGACCCAGTGGG   CG
                                       C__
GAM938   LOC253001 5'  CCACTGTGAGGTGGTTCAGGC  96252       GG        CCC
                                GCCTG  TCGCCTTATG   TGG
                                |||||  ||||||||||   |||
                                CGGAC  GGTGGAGTGT   ACC
                                   TT        C__
GAM938   LOC253070 3'  GCGTGGGGCGGTGCGGGC    97010      G
                                GCCTG GTCGCCTTATGC
                                ||||| ||||||||||||
                                CGGGC TGGCGGGGTGCG
                                   G
GAM938   LOC253148 5'  CAAGGGGCGCTCGGGC      96873        T     TA
                                GCCTGGG CGCCT  TG
                                ||||||| |||||  ||
                                CGGGCTC GCGGG  AC
                                    _     GA
GAM938   LOC253150 5'  CCAGCCAAGGGTGCTCCAGGCA 95515        GT     A  CC
                                TGCCTGG  CGCCTT TG  CTGG
                                |||||||  |||||| ||  ||||
                                ACGGACC  GTGGGA AC  GACC
                                    TC      _ C_
GAM938   LOC253187 5'  TCAGGGCGTGGGGATACAG   97118     GGTCG
                                CTG    CCTTATGCCCTGG
                                |||    ||||||||||||
                                GAC    GGGGTGCGGGACT
                                  ATA__
GAM938   LOC254124 3'  CCGGGGGCAAGGGGCGGCCGGG 96648       G     TA     _
           C                     GCCTGG TCGCCT  TGCCCT GG
                                ||||||| ||||||  |||||| ||
                                CGGGCC GGCGGG  ACGGGG CC
                                   _     GA     G
GAM938   LOC254359 3'  GGGCCGTGACTTAGGCA     94782           CTTAT
                                TGCCTGGGTCGC    GCCC
                                ||||||||||||    ||||
                                ACGGATTCAGTG    CGGG
                                       C____
GAM938   LOC254528 3'  TATGGTGGAGGTGGTCTGGGT  95054     TG GT     A    CTGG
                                GCC  G  CGCCTT TGCC
                                |||  |  |||||| ||||
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                                TGG  C  GTGGAG GTGG
                                  GT TG     _    TATT
GAM938  LOC254559 5'  CGGGGCGCAGTCGGCCCAGC   96595    C      C  TA    TG
                                GC TGGGTCG CT  TGCCC  G
                                || ||||||| ||  |||||  |
                                CG ACCCGGC GA  GCGGG  C
                                  _      T  C_    GT
GAM938  LOC254873 3'  CTGGGGGAAGGGTGGTCTGAGC 94572     CT  GT     ATG   TG
              A                   TGC  GG  CGCCTT   CCC  G
                                ||| ||  ||||||   |||  |
                                ACG  TC  GTGGGA   GGG  C
                                  AG  TG     AG_   GT
GAM938  LOC255040 3'  CCGGGGCGCGCGGCCTAGGC   96380          CTTA
                                GCCTGGGTCGC    TGCCCTGG
                                ||||||||||    ||||||||
                                CGGATCCGGCG    GCGGGGCC
                                      C___
GAM938  LOC255041 3'  CCGGGGCGCGCGGCCTAGGC   96386          CTTA
                                GCCTGGGTCGC    TGCCCTGG
                                ||||||||||    ||||||||
                                CGGATCCGGCG    GCGGGGCC
                                      C___
GAM938  LOC255056 5'  GGGTCAGACGATCCAGGTA    97628          C  TAT
                                TGCCTGGGTCG CT   GCCC
                                |||||||||| ||   ||||
                                ATGGACCTAGC GA   TGGG
                                      A  C__
GAM938  LOC255090 5'  GGGTATGGGCTGGGGC      96247      G    GCCT
                                GCCT GGTC    TATGCCC
                                |||| ||||    |||||||
                                CGGG TCGG    GTATGGG
                                  G   ____
GAM938  LOC255146 3'  CTGGGACCAAGGGTGGCTGGGG 95601      G        ATG_   TGG
              T                   GCCT GGTCGCCTT    CCC
                                |||| |||||||||    |||
                                TGGG TCGGTGGGA    GGG
                                  G        ACCA   TC
GAM938  LOC255196 5'  CTAGAAATGAAGGGTGACTTAG 97167     C         ATGCC_
              CA                    TGC TGGGTCGCCTT     CTGG
                                ||| ||||||||||      ||||
                                ACG ATTCAGTGGGA     GATC
                                  _         AGTAAA
GAM938  LOC255271 3'  GGGCAGGGACTCGGGCA     95502          G   TAT
                                TGCCTGGGTC CCT   GCCC
                                |||||||||| |||   ||||
                                ACGGGCTCAG GGA   CGGG
                                      _  ___
GAM938  LOC255326 3'  CCAGACTGTGGGAGGCCCAGGC 96375          GC     CC
                                GCCTGGGTC  CTTATG  CTGG
                                |||||||||  ||||||  ||||
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                                CGGACCCGG  GGGTGT  GACC
                                     A_     CA
GAM938  LOC255426 5'  CGGGAGCCGGGCGGTCGGGC  97159     G GT    TAT  _  TG
                                GCCT G  CGCCT   GC CC  G
                                |||| |  |||||   || ||  |
                                CGGG C  GCGGG   CG GG  C
                                  _ TG    C__  A  GT
GAM938  LOC255452 3'  CCAGGGTCCGCGCGGCTTGGGC 97528     TG     CTTAT
          A                      TGCC  GGTCGC    GCCCTGG
                                 ||||  ||||||    |||||||
                                 ACGG  TCGGCG    TGGGACC
                                   GT     CGCC_
GAM938  LOC255452 3'  CTAGCAGTGAGGGGACCCAGGT 97532        G     GCC
                                GCCTGGGTC CCTTAT   CTGG
                                ||||||||| ||||||   ||||
                                TGGACCCAG GGAGTG   GATC
                                     G     AC_
GAM938  LOC255452 3'  CTGGGGCATTTCTGTCCAGGCA 97534        T  CCTT     TG
                                TGCCTGGG CG    ATGCCC  G
                                |||||||| ||    ||||||  |
                                ACGGACCT GT    TACGGG  C
                                     _  CTT_     GT
GAM938  LOC255452 3'  GCGGGTGGCCCAGGC       97539           TAT
                                GCCTGGGTCGCCT   GC
                                ||||||||||||   ||
                                CGGACCCGGTGGG   CG
                                          ___
GAM938  LOC255506 5'  CAGGCTGGCCATCCAGGT    97039        C   TTATGC
                                GCCTGGGT GCC     CCTG
                                |||||||| |||     ||||
                                TGGACCTA CGG     GGAC
                                     C   TC____
GAM938  LOC255520 5'  CCAGAGCCCTGGGGTGCTCAGG 95853        T      T_  C
          C                      GCCTGGG CGCCTTA  GC CTGG
                                 |||||||  |||||||  || ||||
                                 CGGACTC GTGGGGT  CG GACC
                                     _      CC  A
GAM938  LOC255837 5'  GGGAAAAGGCGACTTAG     97602           ATG
                                CTGGGTCGCCTT   CCC
                                ||||||||||||   |||
                                GATTCAGCGGAA   GGG
                                       AA_
GAM938  LOC256158 5'  GCCCAGCGTGGTTCGGGCA   97669       GG   _  TAT
                                TGCCTG  TCGC CT   GC
                                ||||||  |||| ||   ||
                                ACGGGC  GGTG GA   CG
                                   TT    C  CC_
GAM938  LOC256158 5'  CGGGGCAGCATGACTGGGGT   97662     G    CCTTA    TG
                                GCCT GGTCG    TGCCC  G
                                |||| |||||    |||||  |
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                                TGGG TCAGT    ACGGG  C
                                  G    ACG__    GT
GAM938  LOC256273 3'  GGGCATGAGGGAGG       96407    TGGG  G
                                CC    TC CCTTATGCCC
                                ||    || ||||||||||
                                GG    AG GGAGTACGGG
                                 ____  _
GAM938  LOC256789 3'  GGGCAGGGCCACTTAGGCA   97450         C    TA
                                TGCCTGGGT GCCT  TGCCC
                                ||||||||| ||||  |||||
                                ACGGATTCA CGGG  ACGGG
                                      C   __
GAM938  LOC256848 5'  CCAGAGCTATGAGGCAATTCGG 97514         C      _  C
           GCA                    TGCCTGGGT GCCTTAT GC CTGG
                                ||||||||| ||||||| || ||||
                                ACGGGCTTA CGGAGTA CG GACC
                                      A      T  A
GAM938  LOC257041 5'  CGGGGTCTCCGGTCCGGCA   97493     T  GT  CCTTAT
                                TGCC GG  CG     GCCCTG
                                |||| ||  ||     ||||||
                                ACGG CC  GC     TGGGGC
                                  _  TG  CTC___
GAM938  LOC257106 5'  GGGGAGGTGGCCCAGGCA    95390             ATG
                                TGCCTGGGTCGCCTT   CCC
                                ||||||||||||||   |||
                                ACGGACCCGGTGGAG   GGG
                                                 ___
GAM938  LOC257203 5'  GGACAGGCGGCCCAGGC     96933            TATG
                                GCCTGGGTCGCCT    CC
                                ||||||||||||    ||
                                CGGACCCGGCGGA    GG
                                       CA__
GAM938  LOC257358 3'  CGGGGTTGGGCTCAGGC     97098         GCCTTAT
                                GCCTGGGTC      GCCCTG
                                |||||||||      ||||||
                                CGGACTCGG      TGGGGC
                                      GT_____
GAM938  LOC257472 3'  CCAGGGTGTGGCTGACACCTGG 95101     _ _  _  TT
           GC                     CCT GG GTC GCC  ATGCCCTGG
                                ||| || ||| |||  |||||||||
                                GGG CC CAG CGG  TGTGGGACC
                                  T  A   T   __
GAM938  LOC257541 5'  GGCGGAGGGCGGGCCAGGT    97762       G      A
                                GCCTGG TCGCCTT TGCC
                                |||||| ||||||| ||||
                                TGGACC GGCGGGA GCGG
                                   G      G
GAM938  LOC257554 5'  GGGTGTGGCCTTGGT       97695     T      CTTAT
                                GCC GGGTCGC    GCCC
                                ||| |||||||    ||||
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                                TGG TCCGGTG    TGGG
                                  T    _____
GAM938  LOC51003  3' CTGGGGCATGGGGTAGGGGTGG 32146     GG  _       TG
             GC                   GCCTG  TC GCCTTATGCCC  G
                                  |||||  || ||||||||||  |
                                  CGGGT  GG TGGGGTACGGG  C
                                    GG  A        GT
GAM938  LOC51063  3' CTGGGGTGTGGACAGACCCAG  31918      GCC      TG
                                  CTGGGTC   TTATGCCC  G
                                  |||||||   ||||||||  |
                                  GACCCAG   GGTGTGGG  C
                                     ACA      GT
GAM938  LOC51072  5' CGTGGGGGCGGCTCGGC    31979    T      TTATG  _
                                  GCC GGGTCGCC    CCC TG
                                  ||| ||||||||    ||| ||
                                  CGG CTCGGCGG    GGG GC
                                   _      _____  T
GAM938  LOC51104  5' GGCCCGGGCCGCTCAGGT    32058       C   TAT
                                  GCCTGGGT GCCT   GCC
                                  |||||||| ||||   |||
                                  TGGACTCG CGGG   CGG
                                     C   CC_
GAM938  LOC51112  5' CCAACAGCGAGGGCGACGCGGG 32084     G      A  CC_
             C                     GCCTG GTCGCCTT TGC   TGG
                                   ||||| |||||||| |||   |||
                                   CGGGC CAGCGGGA GCG   ACC
                                     G       _  ACA
GAM938  LOC51333  3' TTGGGGTTCTCCAGGCTCAGGT 33571        GCCTTAT   TG
                                  GCCTGGGTC      GCCC  G
                                  |||||||||      ||||  |
                                  TGGACTCGG      TGGG  T
                                       ACCTCT_   GT
GAM938  LOC54466  5' CTAGGAGGAGGTGGCCCAGCCA 38653    C         ATGC
                                  TG CTGGGTCGCCTT    CCTGG
                                  || ||||||||||||    |||||
                                  AC GACCCGGTGGAG    GGATC
                                   C          GA__
GAM938  LOC54557  5' CGGGGTCTACGGCCTAGG    72828        CCT  T   TG
                                  CCTGGGTCG   TA GCCC  G
                                  |||||||||   || ||||  |
                                  GGATCCGGC   AT TGGG  C
                                       ___  C   GT
GAM938  LOC55833  3' GGTTCAAGGCTGTTTGGGTA   64914     TG  TC    AT
                                  TGCC  GG  GCCTT  GCC
                                  ||||  ||  |||||  |||
                                  ATGG  TT  CGGAA  TGG
                                    GT  GT    CT
GAM938  LOC56920  3' CTGGGGTGGTCAGGGCTCAGGC 39386         ___   TTAT   TG
                                  GCCTGGGTC   GCC   GCCC  G
                                  |||||||||   |||   ||||  |
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                                CGGACTCGG  TGG   TGGG  C
                                    GAC  ____   GT
GAM938  LOC56963  3' GGGCTTGGCCCCAGGCA    71457       TC  TTAT
                                TGCCTGGG  GCC   GCCC
                                ||||||||  |||   ||||
                                ACGGACCC  CGG   CGGG
                                   __  TT__
GAM938  LOC57109  5' CCAGGGCGCCGGGCCCGGG   39849     GTC   TA
                                CCTGG  GCCT  TGCCCTGG
                                |||||  ||||  ||||||||
                                GGGCC  CGGG  GCGGGACC
                                  ___  CC
GAM938  LOC57109  5' TCGGGTGGCCGCCGGCCCAGGC 39854        CCTTA    TGG
                                GCCTGGGTCG    TGCCC
                                ||||||||||    |||||
                                CGGACCCGGC    GTGGG
                                     CGCCG    CT
GAM938  LOC63928  5' GAAGGAGGAGGTGGCTCAGGT  42035          ATGC   GG
                                GCCTGGGTCGCCTT   CCT
                                ||||||||||||||   |||
                                TGGACTCGGTGGAG   GGA
                                       GA__  AGC
GAM938  LOC64182  5' CGGGGTGGCCAGGCCCAGG   42295       __  TTAT   TG
                                CCTGGGTC  GCC   GCCC  G
                                ||||||||  |||   ||||  |
                                GGACCCGG  CGG   TGGG  C
                                    AC  ____   GT
GAM938  LOC89941  5' CGGGGAGCGGCTCCGGGC    57059      _   CTTATG
                                GCCTGG GTCGC     CCCTG
                                ||||||| |||||     |||||
                                CGGGCC CGGCG     GGGGC
                                   T    A_____
GAM938  LOC89985  3' CTGGGGCCAGTGGTGCCTCAGG 61019       T   TTAT   TG
          CA                    TGCCTGGG CGCC   GCCC  G
                                ||||||||  ||||   ||||  |
                                ACGGACTC GTGG   CGGG  C
                                    C   TGAC   GT
GAM938  LOC90019  3' CTGGGCAGCTGGGTGGGCCTGG 56761    TG   _   TA_   TGG
          GCA                   GCC  GGTC GCCT   TGCCC
                                |||  |||| ||||   |||||
                                CGG  CCGG TGGG   ACGGG
                                  GT   G   TCG    TC
GAM938  LOC90019  3' GGGCTGGGTGGGCCTGGGCA  56767    TG   _   TAT
                                TGCC  GGTC GCCT   GCCC
                                ||||  |||| ||||   ||||
                                ACGG  CCGG TGGG   CGGG
                                  GT   G   T__
GAM938  LOC90019  3' TCGGGGCATGAGCCCCTGGGT  56772    TG  TC  C
                                GCC  GG  GC TTATGCCCTGG
                                |||  ||  || ||||||||||
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                                TGG  CC  CG AGTACGGGGCT
                                  GT  C_  _
GAM938  LOC90092  5' CGGGGCTTGTGTGGCTCAGG   61404         CT  T    TG
                                CCTGGGTCGC  TA GCCC  G
                                ||||||||||  || ||||  |
                                GGACTCGGTG  GT CGGG  C
                                      T_  T    GT
GAM938  LOC90110  3' TACGGGGTGACTTAGCA     61513     C        TA
                                TGC TGGGTCGCCT  TG
                                ||| ||||||||||  ||
                                ACG ATTCAGTGGG  AT
                                  _        GC
GAM938  LOC90133  5' TGGGGTGGCCTGGGCG      61610      TG
                                TGCC  GGTCGCCTTA
                                ||||  ||||||||||
                                GCGG  CCGGTGGGGT
                                  GT
GAM938  LOC90170  5' GGCAGGCAGACCCAGGCA    61709          _    TAT
                                TGCCTGGGTC GCCT   GCC
                                |||||||||| ||||   |||
                                ACGGACCCAG CGGA   CGG
                                      A   ___
GAM938  LOC90231  5' CCGGGGTGGGCGCCGCGGTCCG 61866       GT   CTTA__
           GGC                    GCCTGG  CGC     TGCCCTGG
                                |||||| |||     ||||||||
                                CGGGCC  GCG     GTGGGGCC
                                   TG   CCGCGG
GAM938  LOC90246  5' CCAGGGTGGACTGTCTCAGGT  61907        T  CCTTA
                                GCCTGGG CG     TGCCCTGG
                                ||||||| ||     ||||||||
                                TGGACTC GT     GTGGGACC
                                   T  CAG__
GAM938  LOC90573  5' GGGTTGGCATTTAGGT      63274         C   TTAT
                                GCCTGGGT GCC    GCCC
                                |||||||| |||    ||||
                                TGGATTTA CGG    TGGG
                                     _   T___
GAM938  LOC90631  3' TTGGTCGCTGAGGCGACCAGGC 63639       G       T  __  TGG
                                GCCTGG TCGCCTTA GC  CC
                                |||||| |||||||| ||  ||
                                CGGACC AGCGGAGT CG  GG
                                   _       _ CT  TT
GAM938  LOC90777  3' TTGGGGCCTATTAGGTGATTCG 63971    C         TAT__   TG
           GTCA                   G CTGGGTCGCCT    GCCC  G
                                | ||||||||||     ||||  |
                                C GGCTTAGTGGA    CGGG  T
                                 T         TTATC    GT
GAM938  LOC90784  5' GGCAGGGTACCTGGGTA     64004      TG   C    TA
                                TGCC  GGT GCCT  TGCC
                                ||||  ||| ||||  ||||
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                                ATGG  CCA TGGG  ACGG
                                  GT  _   __
GAM938  LOC90784  5'  TTGGCCTGGAGTGTGGCCTAGG 64008          _  AT_  CTGG
                CA                  TGCCTGGGTCGC CTT  GCC
                                    ||||||||||| |||  |||
                                    ACGGATCCGGTG GAG  CGG
                                          T  GTC  TT
GAM938  LOC90835  5'  CTGGAAGAGAGGGCGCCCAGGT 64129       T    ATG__ CTGG
                                    GCCTGGG CGCCTT    CC
                                    ||||||| ||||||    ||
                                    TGGACCC GCGGGA    GG
                                       _    GAGAA  TC
GAM938  LOC90957  3'  CCAGGGCATGAAGCCCAAGGCA 64463     _  CGCC
                                    TGCCT GGGT   TTATGCCCTGG
                                    ||||| ||||   ||||||||||
                                    ACGGA CCCG   AGTACGGGACC
                                      A   A___
GAM938  LOC91035  5'  AGGGCAAGGCCTGGCA     64665     T   GCCTTA
                                    TGCC GGGTC    TGCCCT
                                    |||| |||||    ||||||
                                    ACGG TCCGG    ACGGGA
                                      _    A_____
GAM938  LOC91040  5'  CCAGGAGCCAGGGGGTGACTGG 64711     G      AT_ _
                GGT                 GCCT GGTCGCCTT  GC CCTGG
                                    |||| |||||||||  || |||||
                                    TGGG TCAGTGGGG  CG GGACC
                                      G       GAC  A
GAM938  LOC91040  5'  CCAGGGCATCAGACACAGGTA  64713      G  GCCTT
                                    TGCCTG GTC    ATGCCCTGG
                                    |||||| |||    |||||||||
                                    ATGGAC CAG    TACGGGACC
                                       A  AC___
GAM938  LOC91040  5'  CGGGGTGGCTCGGCTCGGG   64717       __  TTAT   TG
                                    CCTGGGTC  GCC   GCCC  G
                                    ||||||||  |||   ||||  |
                                    GGGCTCGG  CGG   TGGG  C
                                         CT  _____   GT
GAM938  LOC91050  5'  TCGGGGCCGCGCGGGGCCCGGG 64753       G  TTAT_
                C                    GCCTGGGTC CC    GCCCTGG
                                    |||||||||  ||    |||||||
                                    CGGGCCCGG GG    CGGGGCT
                                         _  CGCGC
GAM938  LOC91069  3'  CAGGGAGTGTGGCTCGGT    64774    T    _  TATG
                                    GCC GGGTCGC CT   CCCTG
                                    ||| ||||||| ||   |||||
                                    TGG CTCGGTG GA   GGGAC
                                      _     T  _____
GAM938  LOC91137  5'  TTAGGTCGTGGTGGCCCCGGT  57067    T     TT  C
                                    GCC GGGTCGCC  ATG CCTGG
                                    ||| ||||||||  ||| |||||
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                                TGG CCCGGTGG  TGC GGATT
                                  C       __  T
GAM938  LOC91355  5' CCAGGGCATGAGGGATGCTCTG 65712   TG ___  G
                GGC                C  G  GTC CCTTATGCCCTGG
                                   | |  ||| ||||||||||||||
                                   G  C  TAG GGAGTACGGGACC
                                    GT TCG  _
GAM938  LOC91355  5' CTGGGGTGCAGCAGAGACCCAG 65713        GCC_ AT   TG
                GT                  GCCTGGGTC   TT  GCCC  G
                                    |||||||||   ||  ||||  |
                                    TGGACCCAG   GA  TGGG  C
                                        AGAC  CG   GT
GAM938  LOC91431  5' TTAGCTAGTGAGTTGATTCAGG 56927         C    GCC
                TA                  TGCCTGGGTCG CTTAT  CTGG
                                    |||||||||||| |||||  ||||
                                    ATGGACTTAGT GAGTG  GATT
                                          T    ATC
GAM938  LOC91450  5' CCAGGGCATGTGCCCTTGGGC  66073    TG  TC  CT
                                    GCC  GG  GC  TATGCCCTGG
                                    |||  ||  ||  ||||||||||
                                    CGG  TC  CG  GTACGGGACC
                                      GT  C_  T_
GAM938  LOC91565  5' CCAGGGCACATGGCTTGGG   66460    TG    CCTTA
                                    CC  GGTCG    TGCCCTGG
                                    ||  |||||    ||||||||
                                    GG  TCGGT    ACGGGACC
                                     GT    AC___
GAM938  LOC91759  5' TCAGGGAACTGTGGCCCAGCCG 67090    C       CTTATG
                                    TG CTGGGTCGC     CCCTGG
                                    || |||||||||     ||||||
                                    GC GACCCGGTG     GGGACT
                                     C       TCAA__
GAM938  LOC91807  5' CTGGGGCATGGGGGGCTGCCAG 67233      __  G       TG
                G                   CCTGG  GTC CCTTATGCCC  G
                                    |||||  ||| ||||||||||  |
                                    GGACC  CGG GGGGTACGGG  C
                                       GT  _        GT
GAM938  LOC91813  5' CTAGGGCGTGGGGTGCTGGGGC 67250      G  T
                A                   TGCCT GG CGCCTTATGCCCTGG
                                    ||||| || ||||||||||||||||
                                    ACGGG TC GTGGGGTGCGGGATC
                                       G  _
GAM938  LOC92017  3' CCAGGGTCTCCCGGCTCTAGGC 67887       _   CCTTAT
                A                   TGCCTGG GTCG     GCCCTGG
                                    ||||||| ||||     |||||||
                                    ACGGATC CGGC     TGGGACC
                                        T   CCTC__
GAM938  LOC92078  5' GGTGGGGGGTGGTCTAGG     67987      GT     A
                                    CCTGG  CGCCTT TGCC
                                    |||||  |||||| ||||
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                                GGATC  GTGGGG GTGG
                                  TG     _
GAM938  LOC92080  3' CGGGGTAGGCCCGACTCAGCA  68047    C     __   TAT   TG
                                TGC TGGGTC  GCCT   GCCC  G
                                ||| ||||||  ||||   ||||  |
                                ACG ACTCAG  CGGA   TGGG  C
                                  _     CC    ___    GT
GAM938  LOC92228  5' CCAGGGTGAGGGCTGCCCGGGT 68539        C    A
                                GCCTGGGT GCCTT TGCCCTGG
                                |||||||| ||||| ||||||||
                                TGGGCCCG CGGGA GTGGGACC
                                     T    _
GAM938  LOC92305  3' CCAGGGTACAAGTCCTGGGCA  56415     TG  TCGC   A
                                TGCC  GG    CTT TGCCCTGG
                                ||||  ||    ||| ||||||||
                                ACGG  CC    GAA ATGGGACC
                                  GT  T___   C
GAM938  LOC92340  3' GGAAAAAAGGTGGCCCAGG    68995          ATG_
                                CCTGGGTCGCCTT    CC
                                ||||||||||||    ||
                                GGACCCGGTGGAA    GG
                                       AAAA
GAM938  LOC92340  3' TTGGGGAGGAGGTGGCCTGGC  69001     T        ATG   TG
                                GCC GGGTCGCCTT   CCC  G
                                ||| ||||||||||   |||  |
                                CGG TCCGGTGGAG   GGG  T
                                  _        GA_   GT
GAM938  LOC92719  3' TCAGGGTATGGGGAGGGAGGG  70383    GGG  G
                                CCT   TC CCTTATGCCCTGG
                                |||   || ||||||||||||
                                GGG   GG GGGGTATGGGACT
                                  AG_  A
GAM938  LOC92799  3' GGTCCTGGGGGACTCAGGT    56430         G   TAT
                                GCCTGGGTC CCT   GCC
                                ||||||||| |||   |||
                                TGGACTCAG GGG   TGG
                                     G   TCC
GAM938  LOC92841  5' GGTAGCGGGTGGCTGGGCA    70718     TG G     TA
                                TGCC  G TCGCCT  TGCC
                                ||||  | ||||||  ||||
                                ACGG  C GGTGGG  ATGG
                                  GT _     CG
GAM938  LOC93017  5' CCGGGGCTCCTGCCCCGGGC   71152        TC  CTTAT
                                GCCTGGG  GC    GCCCTGG
                                |||||||  ||    |||||||
                                CGGGCCC  CG    CGGGGCC
                                   __  TCCT_
GAM938  LOC93070  5' CTGACCCTAGGGCGGCTTGCGC 71292     C          TGCCCTGG
          A                     TGC TGGGTCGCCTTA
                                ||| ||||||||||||
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                                ACG GTTCGGCGGGAT
                                  C          CCCAGTC
GAM938  LOC93129  3'  GTAGAGGGATTTGGGT     71468     TG   G   A
                                GCC  GGTC CCTT TGC
                                |||  |||| |||| |||
                                TGG  TTAG GGAG ATG
                                  GT   _   _
GAM938  LOC93134  5'  GGCCTGAGGTGATCTTGGCA  71521     T        T
                                TGCC GGGTCGCCTTA GCC
                                |||| |||||||||| |||
                                ACGG TCTAGTGGAGT CGG
                                  T         C
GAM938  LOC93259  5'  CGGGTGCAGGGGCTCAGGCA  71813         G   TAT  _  TG
                                TGCCTGGGTC CCT   GC CC  G
                                |||||||||| |||   || ||  |
                                ACGGACTCGG GGA   CG GG  C
                                      _  ___  T  GT
GAM938  LOC93259  5'  CTAGGAGTGGGGAGGCCTGGGT 71814     TG   G     GC
          A                      TGCC  GGTC CCTTAT  CCTGG
                                |||| |||| ||||||  |||||
                                ATGG  CCGG GGGGTG  GGATC
                                  GT   A     A_
GAM938  LOC93268  5'  GGGTGAAGGTCCGGG      71885      GTC    A
                                CCTGG   GCCTT TGCCC
                                |||||   ||||| |||||
                                GGGCC   TGGAA GTGGG
                                   ___    _
GAM938  LOC93626  3'  GCACAAGGTGACCTGGC     72770     T        A
                                GCC GGGTCGCCTT TGC
                                ||| ||||||||| |||
                                CGG TCCAGTGGAA ACG
                                  _        C
GAM939  ATP11A    3'  GCCACGCCGGCAGCTTC     77030         A  T  TCTA
                                GAAGTTGCC GC GT    GC
                                ||||||||| || ||    ||
                                CTTCGACGG CG CA    CG
                                     C  _  C___
GAM939  CD28      3'  GCCAGCCGGCTGGCAGC     20439          TT  A
                                GTTGCCAGCTG  CT GC
                                ||||||||||  || ||
                                CGACGGTCGGC  GA CG
                                      C_  C
GAM939  GATA4     3'  GCAGCTGGCAACTTCT      9006
                                AGAAGTTGCCAGCTGT
                                ||||||||||||||||
                                TCTTCAACGGTCGACG

GAM939  GUCY1B2   3'  AACAGCTGGAACTTC       14682       G
                                GAAGTT CCAGCTGTT
                                |||||| |||||||||
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                                CTTCAA GGTCGACAA
                                     _
GAM939  LNK     3'  GGCCCCAGCCGGCAACTTCTA  18467          A   TTCTA
                                TAGAAGTTGCC GCTG    GCC
                                |||||||||| ||||    |||
                                ATCTTCAACGG CGAC    CGG
                                      C   CC___
GAM939  PCLO    3'  AACAGTCAACTTCTA      94220         CCA
                                TAGAAGTTG  GCTGTT
                                |||||||||  ||||||
                                ATCTTCAAC  TGACAA
                                     ___
GAM939  PRG3    3'  GCTAGAAATGCAACTTGTA   51408   G     CAGCTG
                                TA AAGTTGC     TTCTAGC
                                || |||||||     |||||||
                                AT TTCAACG     AAGATCG
                                 G      TA____
GAM939  C16orf44 3'  GACCAGCAGCAACTTCT    45315        CA   T
                                AGAAGTTGC  GCTG TC
                                |||||||||  |||| ||
                                TCTTCAACG  CGAC AG
                                     A_   C
GAM939  FLJ11125 3'  GGCTAGACTTGGAGC      59583    G   CTGT
                                GTT CCAG   TCTAGCC
                                ||| ||||   |||||||
                                CGA GGTT   AGATCGG
                                  _   C___
GAM939  FLJ12132 3'  GGCTGGAGAGCCGGCAACT   46472       A  G
                                AGTTGCC GCT TTCTAGCC
                                ||||||| ||| ||||||||
                                TCAACGG CGA GAGGTCGG
                                    C  _
GAM939  FLJ12747 3'  GCTAGGATTTGACAAATTC   49720    G  C  CT
                                GAA TTG CAG  GTTCTAGC
                                ||| ||| |||  ||||||||
                                CTT AAC GTT  TAGGATCG
                                 A  A  __
GAM939  FLJ20254 5'  GCCAAAGAAGGTGGCAACTCCT 34792   A      G  GTTCTA
                                AG AGTTGCCA CT     GC
                                || |||||||| ||     ||
                                TC TCAACGGT GA     CG
                                 C      G  AGAAAC
GAM939  KIAA0286 3'  CTATAGGCTGCAACTTC     68324        C   GTTC
                                GAAGTTGC AGCT   TAG
                                |||||||| ||||   |||
                                CTTCAACG TCGG   ATC
                                     _   AT__
GAM939  KIAA0662 3'  GGCCACAGGCTGGCAGCCTC  81856   A       GTTCTA
                                GA GTTGCCAGCT     GCC
                                || ||||||||||     |||
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                                CT CGACGGTCGG     CGG
                                 C         ACAC__
GAM939  MFN1     3'  CTATAGGCTGGAAACTCCTA  35542     A   G     GTTC
                                TAG AGTT CCAGCT    TAG
                                ||| |||| ||||||    |||
                                ATC TCAA GGTCGG    ATC
                                  C    A     AT__
GAM939  MGC2474  3'  GACTCACTGCAACTTC      43723        C  C  T_
                                GAAGTTGC AG TG  TC
                                |||||||| || ||  ||
                                CTTCAACG TC AC  AG
                                     _ _  TC
GAM939  MRF2     5'  GACCAGCCGGCAACTTTTA   76521          A   T
                                TAGAAGTTGCC GCTG TC
                                |||||||||| |||| ||
                                ATTTTCAACGG CGAC AG
                                       C   C
GAM939  NFX1     3'  GGCCAGGCTTCCAGCAACTTC  10216        C___   GTTCTA
                                GAAGTTGC   AGCT    GCC
                                ||||||||   ||||    |||
                                CTTCAACG   TCGG    CGG
                                     ACCT   AC____
GAM939  PL6      3'  AGAACAGCTCCAGCT      22831      CC
                                AGTTG  AGCTGTTCT
                                |||||  |||||||||
                                TCGAC  TCGACAAGA
                                  C_
GAM939  PTP4A1   3'  GCTAGACAGATTTGGCAACCTC 12938     A      __   T
           TG                     TAGA GTTGCCAG  CTGT CTAGC
                                |||| ||||||||  |||| |||||
                                GTCT CAACGGTT  GACA GATCG
                                  C       TA   _
GAM939  RAI17    3'  AGGAGCGGCAACTTCTA     91274          A  G
                                TAGAAGTTGCC GCT TT
                                |||||||||| ||| ||
                                ATCTTCAACGG CGA GA
                                       _  G
GAM939  LOC127294 3'  GGCTTGGAGCTGGTAACCTC  74659    A       GT  T
                                GA GTTGCCAGCT  TC AGCC
                                || ||||||||||  || ||||
                                CT CAATGGTCGA  GG TCGG
                                 C        __  T
GAM939  LOC143524 3'  GGCCGAAGCTAGCAACTTCTA  76596         C   GTTCTA
                                TAGAAGTTGC AGCT     GCC
                                |||||||||| ||||     |||
                                ATCTTCAACG TCGA     CGG
                                      A   AGC___
GAM939  LOC144817 3'  CTGGAACTGGCGACCCCTA   76966     AA      GCT
                                TAG  GTTGCCA   GTTCTAG
                                |||  |||||||   |||||||
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                                ATC  CAGCGGT   CAAGGTC
                                  CC      ___
GAM939  LOC146316 5'  GGCCAAGGGCTGGAACCTC   60873    A   G     G  CTA
                                GA GTT CCAGCT TT   GCC
                                || ||| |||||| ||   |||
                                CT CAA GGTCGG AA   CGG
                                 C   _     G  C__
GAM939  LOC146990 5'  GGCCAACATTGGCAATTCCTA  83887     A       C    CTA
                                TAG AGTTGCCAG TGTT   GCC
                                ||| ||||||||| ||||   |||
                                ATC TTAACGGTT ACAA   CGG
                                  C        _    C__
GAM939  LOC199858 5'  CTAAAATTCGGGGAACTTCTA  88418        G  AGCT   C
                                TAGAAGTT CC    GTT TAG
                                |||||||| ||    ||| |||
                                ATCTTCAA GG    TAA ATC
                                     G  GCT_   A
GAM939  LOC201799 3'  GCCAGAACAGCCAAGCCTC    89064    A   GCCA      A
                                GA GTT    GCTGTTCT GC
                                || |||    |||||||| ||
                                CT CGA    CGACAAGA CG
                                 C   AC__       C
GAM939  LOC219914 5'  AGTTCAACTAACAACTTCTA   93325         CC  C  TT
                                TAGAAGTTG  AG TG  CT
                                |||||||||  || ||  ||
                                ATCTTCAAC  TC AC  GA
                                      AA  A  TT
GAM939  LOC219918 5'  GGCCGAAGCTAGCAACTTCTA  91542         C    GTTCTA
                                TAGAAGTTGC AGCT     GCC
                                |||||||||| ||||     |||
                                ATCTTCAACG TCGA     CGG
                                      A    AGC___
GAM939  LOC221766 3'  GGCCACAGCTGGCAACGCCTA  93778     AA          TCTA
                                TAG  GTTGCCAGCTGT    GCC
                                |||  ||||||||||||    |||
                                ATC  CAACGGTCGACA    CGG
                                  CG          C___
GAM939  LOC255515 3'  GGCCCAAGCTAGCAACTTCTA  96098         C    GTTCTA
                                TAGAAGTTGC AGCT     GCC
                                |||||||||| ||||     |||
                                ATCTTCAACG TCGA     CGG
                                      A    ACC___
GAM939  LOC91049  5'  GCAGCTGGCAACTTCT      64737
                                AGAAGTTGCCAGCTGT
                                ||||||||||||||||
                                TCTTCAACGGTCGACG

GAM939  LOC91181  3'  GCCTAACAGCAACTTCTA    65171          CAGC   CTA
                                TAGAAGTTGC    TGTT   GC
                                |||||||||    ||||   ||
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                                ATCTTCAACG   ACAA  CG
                                     _____   TC_
GAM940  ADAM21   3'  CTACATCCTTCCCTC      13762     AA      C
                                GAGG  GAAGGATG AG
                                ||||  |||||||| ||
                                CTCC  CTTCCTAC TC
                                  __      A
GAM940  ADCY8    5'  CCGTGACCCCCTCCTCCTC   6652      A  A  ATG  GAG
                                GAGGA GA GG   CA   TGG
                                ||||| || ||   ||   |||
                                CTCCT CT CC   GT   GCC
                                   C  C  CCA  ___
GAM940  ADORA3   3'  CCCACTCCACTACTCTCTTCCT 5440         AG ATGCA
           C                     GAGGAAGA  G    GAGTGGG
                                ||||||||  |    |||||||
                                CTCCTTCT  C    CTCACCC
                                     CT ATCAC
GAM940  ADSS     5'  CTCTGGCTCCTTCTTCCTCT   71758          T  _
                                AGAGGAAGAAGGA GC AGAG
                                ||||||||||||| || ||||
                                TCTCCTTCTTCCT CG TCTC
                                       _ G
GAM940  AP2B1    3'  CTGCATCCCCCCTCCTCT    7060       AGAA
                                AGAGGA   GGATGCAG
                                ||||||   ||||||||
                                TCTCCT   CCTACGTC
                                   CCCC
GAM940  AR       5'  CCCACTCTCTCTCCACCTCCTC 3489       A AA   TGC
                                GAGGA G  GGA   AGAGTGGG
                                ||||| |  |||   ||||||||
                                CTCCT C  CCT   TCTCACCC
                                  _ CA   CTC
GAM940  ATP2A3   3'  CCCAAGGGCACCCGCTCTCCCT 17722     A  A_  A  AGAG
           C                     GAGG AGA  GG TGC   TGGG
                                |||| |||  || |||   ||||
                                CTCC TCT  CC ACG   ACCC
                                  C   CG  C   GGA_
GAM940  BGLAP    3'  CCAGGCACCCTTCTTTCCTCT  5544        _    A  AGAG
                                AGAGGAA GAAGG TGC   TGG
                                ||||||| ||||| |||   |||
                                TCTCCTT CTTCC ACG   ACC
                                    T    C   G___
GAM940  C14orf1  3'  CCCACTGTGTCTCCTTCCCCT  23176    AA    T  G
                                AGG  GAAGGA GCA AGTGGG
                                |||  |||||| ||| ||||||
                                TCC  CTTCCT TGT TCACCC
                                  C_     C  G
GAM940  CAPZA1   3'  CATTCATCCTTCTCCCTCT   72625      A      GCA
                                AGAGG AGAAGGAT   GAGTG
                                |||||  ||||||||   |||||
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                                TCTCC TCTTCCTA   CTTAC
                                  C      ___
GAM940  CARD15   3'  CTGCACACGCTCCTTCCTCT  42213        A  GA__
                                AGAGGAAG AG    TGCAG
                                |||||||| ||    |||||
                                TCTCCTTC TC    ACGTC
                                    C  GCAC
GAM940  CD4      3'  CCCACTCTCCACCCCTGCTCCC 5224     A   AGA   A_  C
            CT                    AG GGA   AGG  TG AGAGTGGG
                                || |||   |||  || ||||||||
                                TC CCT   TCC  AC TCTCACCC
                                 C   CG_   CC  C
GAM940  CD97     5'  CCACTCACTCTTTCCCCT    8359      AA     TGCA
                                AGG  GAAGGA    GAGTGG
                                |||  ||||||    ||||||
                                TCC  CTTTCT    CTCACC
                                  C_     CA__
GAM940  CD97     5'  CCACTCACTCTTTCCCCT    54347     AA     TGCA
                                AGG  GAAGGA    GAGTGG
                                |||  ||||||    ||||||
                                TCC  CTTTCT    CTCACC
                                  C_     CA__
GAM940  CDKN1A   3'  CCAGCTACCCTTCTTCT     54294         AT_  AGAG
                                GGAAGAAGG   GC    TGG
                                |||||||||   ||    |||
                                TCTTCTTCC   CG    ACC
                                     CAT  _____
GAM940  CHAD     3'  CCAGGATCATCCTTCCTCT    7011        AGA     CAGAG
                                AGAGGA   AGGATG     TGG
                                ||||||   ||||||     |||
                                TCTCCT   TCCTAC     ACC
                                   ___     TAGG_
GAM940  CHD2     3'  CACTCTCTCTTCTTCT      7028          ATGC
                                GGAAGAAGG    AGAGTG
                                |||||||||    ||||||
                                TCTTCTTCT    TCTCAC
                                     C___
GAM940  CHRNE    3'  CCCACCCTGCCCCTTTCTTCC  3584          AT   A
                                GGAAGAAGG  GCAG GTGGG
                                |||||||||  |||| |||||
                                CCTTCTTTC  CGTC CACCC
                                     CC   C
GAM940  CKMT1    5'  CCGGTTGCATCCTCCCTC    40631      AAGA       AG
                                GAGG   AGGATGCAG  TGG
                                ||||   |||||||||  |||
                                CTCC   TCCTACGTT  GCC
                                  C___       G_
GAM940  CST3     3'  CCCACCCCCTGTATTCCCACCC 3643      AAGAA      A__
            CT                    AGG    GGATGCAG   GTGGG
                                |||    ||||||||   |||||
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                                TCC    CTTATGTC   CACCC
                                  CCACC      CCC
GAM940  CYP4A11  3'  CCCACCTTCCCTTCTTCC    5754         ATGC  A
                                GGAAGAAGG    AG GTGGG
                                |||||||||    || |||||
                                CCTTCTTCC    TC CACCC
                                     CT__  _
GAM940  DAG1     3'  CCCACTCTGCTTCGATTCTCCT 15278      A   G_  T
          C                      GAGGA GAA  GA GCAGAGTGGG
                                |||||  |||  || ||||||||||
                                CTCCT CTT  CT CGTCTCACCC
                                   _  AG  T
GAM940  EBAF     5'  CCCACTCTGCCTCCTGCTCCC  65424    A  A    T
                                GG AG AGGA GCAGAGTGGG
                                || || |||| ||||||||||
                                CC TC TCCT CGTCTCACCC
                                 C  G    C
GAM940  ERBB4    3'  CCCACCCCCCTCTCTTTCTCT  17874         _  ATGCAGA
                                AGAGGAAGA AGG      GTGGG
                                ||||||||| |||      |||||
                                TCTCTTTCT TCC      CACCC
                                     C   CCC____
GAM940  GAP43    3'  CCACTAGCCCTCTTTCTCT    8983          A  AT  AG
                                AGAGGAAGA GG  GC  AGTGG
                                ||||||||| ||  ||  |||||
                                TCTCTTTCT CC  CG  TCACC
                                     _  __  A_
GAM940  GAS11    3'  CTGCCCCCTCTTCCTCT     7625          A  AT
                                AGAGGAAGA GG  GCAG
                                ||||||||| ||  ||||
                                TCTCCTTCT CC  CGTC
                                     _  CC
GAM940  GPLD1    3'  CACTCTGCCCACCTCT      92018       AAGAA  AT
                                AGAGG    GG  GCAGAGTG
                                |||||    ||  ||||||||
                                TCTCC    CC  CGTCTCAC
                                   A____  __
GAM940  GPR86    3'  CCAATCACCCCCTCCTCT    43650       A AA  A  CAGAG
                                AGAGGA G  GG TG    TGG
                                |||||| |  || ||    |||
                                TCTCCT C  CC AC    ACC
                                   _ CC  _  TA___
GAM940  GRIK5    3'  CTCAAAGCCCCTTCTTCCCCT  9135     A       AT  AGAG
                                AG GGAAGAAGG  GC    TGGG
                                || |||||||||  ||    ||||
                                TC CCTTCTTCC  CG    ACTC
                                 C       C_  AA__
GAM940  HCFC1    3'  CCCACCTCTTCTACCCTCCCCC 70990       AA  A  ATGC   _
          TCT                    AGAGG  GA GG    AGAG TGGG
                                |||||  || ||    |||| ||||
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                                TCTCC  CT CC    TCTC ACCC
                                   CC  C  ATCT    C
GAM940  HDAC5    3'  CCCACCCTGCGATTCTCCACCC 57606     AAGA    _    A
           T                    AGG    AGGAT GCAG GTGGG
                                |||    ||||| |||| |||||
                                TCC    TCTTA CGTC CACCC
                                  CACC     G    C
GAM940  HDGF     3'  CCCACCCCAACCTGCTCTCCTC 15680       _  A   A  CAGA
           T                    AGAGGA AG AGG TG    GTGGG
                                ||||||  || ||| ||    |||||
                                TCTCCT TC TCC AC    CACCC
                                   C  G   A  CC__
GAM940  HLA-G    3'  CCCACCATGACCCTCTTCCTC  9224         A  ATG  GA
                                GAGGAAGA GG   CA  GTGGG
                                ||||||||  ||   ||  |||||
                                CTCCTTCT CC   GT  CACCC
                                     _  CA_  AC
GAM940  IGSF8    3'  CTGGACACCCTCTCCCTCT    53504      A   A  A  __
                                AGAGG AGA GG TG  CAG
                                |||||  ||| ||  ||  |||
                                TCTCC TCT CC AC  GTC
                                   C   C  _  AG
GAM940  IL1F8    5'  CCCACTCTGTCTTTCTCACCTC 27055       A_     AT
           T                    AGAGG  AGAAGG  GCAGAGTGGG
                                |||||  ||||||  ||||||||||
                                TCTCC  TCTTTC  TGTCTCACCC
                                   AC     __
GAM940  INPP5B   3'  CCCACTCTGAGCCTCTCTCTC  95524     GA   A  ATG
                                GAG  AGA GG   CAGAGTGGG
                                |||  ||| ||   |||||||||
                                CTC  TCT CC   GTCTCACCC
                                  TC   _  GA_
GAM940  KCNJ10   3'  CCACTCCCCCATTCCTCT    9534         GAA  ATGCA
                                AGAGGAA   GG    GAGTGG
                                |||||||   ||    ||||||
                                TCTCCTT   CC    CTCACC
                                    ACC  _____
GAM940  KCNN4    3'  CCACTCTGCATACCCTC     9567       AAGAAGG
                                GAGG      ATGCAGAGTGG
                                ||||      ||||||||||
                                CTCC      TACGTCTCACC
                                  CA_____
GAM940  LASS2    3'  CTGCATCCTCCCTCCTT     67685       AGA
                                GAGGA   AGGATGCAG
                                |||||   |||||||||
                                TTCCT   TCCTACGTC
                                   CCC
GAM940  LEF1     5'  CCCACCCTTGAGTTACCCCTCT 32756       AAGAAG   GC_  A
                                AGAGG     GAT   AG GTGGG
                                |||||     |||   || |||||
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                                TCTCC    TTG  TC CACCC
                                   CCA___  AGT  C
GAM940  LLGL1   3' CCACACACCATCCTTCCCCC  66877   AA     CAGA
                                GG  GAAGGATG   GTGG
                                ||  ||||||||   ||||
                                CC  CTTCCTAC   CACC
                                 CC      CACA
GAM940  LTB4R   5' CCACACCCCTCTTTCCTCT   5644       GA  ATGCAGA
                                AGAGGAA  AGG     GTGG
                                |||||||  |||     ||||
                                TCTCCTT  TCC     CACC
                                    TC  CCA____
GAM940  MATK    5' CCCACTCCCCGACCCTTCTTC  57817       A_  CA
                                GAAGAAGG  TG  GAGTGGG
                                ||||||||  ||  |||||||
                                CTTCTTCC  GC  CTCACCC
                                     CA  CC
GAM940  MATK    5' CCCACTCCCCGACCCTTCTTC  57820       A_  CA
                                GAAGAAGG  TG  GAGTGGG
                                ||||||||  ||  |||||||
                                CTTCTTCC  GC  CTCACCC
                                     CA  CC
GAM940  MEOX1   3' CCCAATCCCACCTTCACCCTCT 15753     AA   A  CA  G
                                AGAGG  GAAGG TG  GA TGGG
                                |||||  ||||| ||  || ||||
                                TCTCC  CTTCC AC  CT ACCC
                                   CA    _  C_  A
GAM940  MEOX1   3' CCCACCTTCACCCTCTTCCTT  15754       A  A  C  A
                                GAGGAAGA GG TG AG GTGGG
                                |||||||| || || || |||||
                                TTCCTTCT CC AC TC CACCC
                                     C  _  T  _
GAM940  MEOX1   3' CCCAATCCCACCTTCACCCTCT 25727     AA   A  CA  G
                                AGAGG  GAAGG TG  GA TGGG
                                |||||  ||||| ||  || ||||
                                TCTCC  CTTCC AC  CT ACCC
                                   CA    _  C_  A
GAM940  MEOX1   3' CCCACCTTCACCCTCTTCCTT  25728       A  A  C  A
                                GAGGAAGA GG TG AG GTGGG
                                |||||||| || || || |||||
                                TTCCTTCT CC AC TC CACCC
                                     C  _  T  _
GAM940  MFNG    3' CCCACTCCTGCCTCCCTCATCT 10003    A  A   T   _
                                GGA GA GGA GCAG AGTGGG
                                ||| || ||| |||| ||||||
                                TCT CT CCT CGTC TCACCC
                                  A  C   C   C
GAM940  MPP3    5' CCCACCTCCACCCCCTTCTTCC 8636        A__  C  A
                                GGAAGAAGG   TG AG GTGGG
                                |||||||||   || || |||||
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                                CCTTCTTCC  AC TC CACCC
                                     CCC  C  _
GAM940  MUC3B   3'  CCCAAATCCCATCCTTCTCCTT 94268      A      CAGAG
                                GAGGA GAAGGATG    TGGG
                                ||||| ||||||||    ||||
                                TTCCT CTTCCTAC    ACCC
                                  _      CCTAA
GAM940  MYOZ1   3'  CCCACTCCACGCATCCTTCCTC 41150      AGA     A__
                                GAGGA  AGGATGC  GAGTGGG
                                |||||  |||||||  |||||||
                                CTCCT  TCCTACG  CTCACCC
                                   ___     CAC
GAM940  NESH    5'  CCCTGGCTTCCCCCTTCCTCT  33145       AA  T  AGAGT
                                AGAGGAAG  GGA GC    GGG
                                ||||||||  ||| ||    |||
                                TCTCCTTC  CCT CG    CCC
                                     CC   T  GT___
GAM940  NR2F2   5'  CCCACTCGCTCTCCTGTCCCCT 40664    AAGA   T_  A
                                AGG   AGGA  GC GAGTGGG
                                |||   ||||  || |||||||
                                TCC   TCCT  CG CTCACCC
                                  CCTG   CT  _
GAM940  NRXN2   3'  CCCACGGGCTCCCTGCTCCC  57011    A  A   AT  AGA
                                GG AG AGG  GC   GTGGG
                                || || |||  ||   |||||
                                CC TC TCC  CG   CACCC
                                 C  G   CT  GG_
GAM940  NRXN2   3'  CCCACGGGCTCCCTGCTCCC  57022    A  A   AT  AGA
                                GG AG AGG  GC   GTGGG
                                || || |||  ||   |||||
                                CC TC TCC  CG   CACCC
                                 C  G   CT  GG_
GAM940  NRXN2   3'  CCCACGGGCTCCCTGCTCCC  30625    A  A   AT  AGA
                                GG AG AGG  GC   GTGGG
                                || || |||  ||   |||||
                                CC TC TCC  CG   CACCC
                                 C  G   CT  GG_
GAM940  PABPN1  3'  CCCACCCCACCCCTCTTTCTC  16176        A  A  CAGA
                                GAGGAAGA GG TG    GTGGG
                                |||||||| || ||    |||||
                                CTCTTTCT CC AC    CACCC
                                     C  C  CC__
GAM940  PACSIN1 3'  CCCACTCTCGTCTCCTTCCCCT 92255     AA     T  _
          C                      GAGG  GAAGGA GC AGAGTGGG
                                ||||  |||||| || ||||||||
                                CTCC  CTTCCT TG TCTCACCC
                                  C_     C  C
GAM940  PAX5    3'  CCTGAAGCTCCCCTCTTCCTCT 33633         A  AT  AGAG
                                AGAGGAAGA GG  GC    TGGG
                                ||||||||| ||  ||    ||||
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                                TCTCCTTCT CC  CG   GTCC
                                    C  CT  AA__
GAM940  PBX2     3' CCCACTTTCCCTTCCCC    10444   AA   ATGC
                                GG  GAAGG   AGAGTGGG
                                ||  |||||   ||||||||
                                CC  CTTCC   TTTCACCC
                                 C_    C___
GAM940  PCDHGA1  3' CCCACCCCACCCTCTTCCT   38283      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
                                TCCTTCT CC AC   CACCC
                                    C  _  CC__
GAM940  PCDHGA10 3' CCCACCCCACCCTCTTCCT   38290      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
                                TCCTTCT CC AC   CACCC
                                    C  _  CC__
GAM940  PCDHGA11 3' CCCACCCCACCCTCTTCCT   38297      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
                                TCCTTCT CC AC   CACCC
                                    C  _  CC__
GAM940  PCDHGA11 3' CCCACCCCACCCTCTTCCT   49461      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
                                TCCTTCT CC AC   CACCC
                                    C  _  CC__
GAM940  PCDHGA12 3' CCCACCCCACCCTCTTCCT   13593      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
                                TCCTTCT CC AC   CACCC
                                    C  _  CC__
GAM940  PCDHGA2  3' CCCACCCCACCCTCTTCCT   38305      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
                                TCCTTCT CC AC   CACCC
                                    C  _  CC__
GAM940  PCDHGA3  3' CCCACCCCACCCTCTTCCT   38314      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
                                TCCTTCT CC AC   CACCC
                                    C  _  CC__
GAM940  PCDHGA4  3' CCCACCCCACCCTCTTCCT   38321      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
                                TCCTTCT CC AC   CACCC
                                    C  _  CC__
GAM940  PCDHGA5  3' CCCACCCCACCCTCTTCCT   38328      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
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                                TCCTTCT CC AC   CACCC
                                   C  _  CC__
GAM940  PCDHGA6  3' CCCACCCCACCCTCTTCCT  38335      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
                                TCCTTCT CC AC   CACCC
                                   C  _  CC__
GAM940  PCDHGA7  3' CCCACCCCACCCTCTTCCT  38342      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
                                TCCTTCT CC AC   CACCC
                                   C  _  CC__
GAM940  PCDHGA8  3' CCCACCCCACCCTCTTCCT  49453      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
                                TCCTTCT CC AC   CACCC
                                   C  _  CC__
GAM940  PCDHGA9  3' CCCACCCCACCCTCTTCCT  38349      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
                                TCCTTCT CC AC   CACCC
                                   C  _  CC__
GAM940  PCDHGB1  3' CCCACCCCACCCTCTTCCT  38356      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
                                TCCTTCT CC AC   CACCC
                                   C  _  CC__
GAM940  PCDHGB2  3' CCCACCCCACCCTCTTCCT  38363      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
                                TCCTTCT CC AC   CACCC
                                   C  _  CC__
GAM940  PCDHGB3  3' CCCACCCCACCCTCTTCCT  38370      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
                                TCCTTCT CC AC   CACCC
                                   C  _  CC__
GAM940  PCDHGB4  3' CCCACCCCACCCTCTTCCT  13600      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
                                TCCTTCT CC AC   CACCC
                                   C  _  CC__
GAM940  PCDHGB5  3' CCCACCCCACCCTCTTCCT  38377      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
                                TCCTTCT CC AC   CACCC
                                   C  _  CC__
GAM940  PCDHGB6  3' CCCACCCCACCCTCTTCCT  38384      A  A  CAGA
                                AGGAAGA GG TG   GTGGG
                                ||||||| || ||   |||||
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                                TCCTTCT CC AC    CACCC
                                    C  _  CC__
GAM940  PCDHGB7  3'  CCCACCCCACCCTCTTCCT   38391       A  A  CAGA
                                AGGAAGA GG TG    GTGGG
                                ||||||| || ||    |||||
                                TCCTTCT CC AC    CACCC
                                    C  _  CC__
GAM940  PCDHGC3  3'  CCCACCCCACCCTCTTCCT   10454       A  A  CAGA
                                AGGAAGA GG TG    GTGGG
                                ||||||| || ||    |||||
                                TCCTTCT CC AC    CACCC
                                    C  _  CC__
GAM940  PCDHGC3  3'  CCCACCCCACCCTCTTCCT   50517       A  A  CAGA
                                AGGAAGA GG TG    GTGGG
                                ||||||| || ||    |||||
                                TCCTTCT CC AC    CACCC
                                    C  _  CC__
GAM940  PCDHGC4  3'  CCCACCCCACCCTCTTCCT   38398       A  A  CAGA
                                AGGAAGA GG TG    GTGGG
                                ||||||| || ||    |||||
                                TCCTTCT CC AC    CACCC
                                    C  _  CC__
GAM940  PCDHGC5  3'  CCCACCCCACCCTCTTCCT   38405       A  A  CAGA
                                AGGAAGA GG TG    GTGGG
                                ||||||| || ||    |||||
                                TCCTTCT CC AC    CACCC
                                    C  _  CC__
GAM940  PCSK5    5'  CCACTCAGCCTCCTCCT     20575      AGAA   T  A
                                AGGA    GGA GC GAGTGG
                                ||||    ||| || ||||||
                                TCCT    CCT CG CTCACC
                                  _____   C  A
GAM940  PFN1     3'  CCCACAGCTTTGCACCCCTTTC 17228        AA  A       ___
            CTC                    GAGGAAG  GG TGCAGAGT   GGG
                                ||||||| || ||||||||  |||
                                CTCCTTT  CC ACGTTTCG   CCC
                                    CC  _       ACA
GAM940  PGR      5'  CCACTTTCTCCTCCCTCT    6245       AAGA    TGC
                                AGAGG    AGGA   AGAGTGG
                                |||||    ||||   |||||||
                                TCTCC    TCCT   TTTCACC
                                  C___    C__
GAM940  PI3      3'  CCCACACTGTCCATTCTTCCTC 10545          _  AT    A
                                GAGGAAGAA GG  GCAG GTGGG
                                ||||||||| ||  |||| |||||
                                CTCCTTCTT CC  TGTC CACCC
                                     A  __   A
GAM940  PIK3CD   3'  CCCACCCTGTGTATCCTCCCT  17241     AAGA       G __
                                AGG    AGGATGCA A  GTGGG
                                |||    |||||||| |  |||||
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                                TCC   TCCTATGT T  CACCC
                                  C___      G CC
GAM940  PKD2L1   5' CTCTGCTCCCTCTTCCTCT   32263        A   T
                                AGAGGAAGA GGA GCAGAG
                                ||||||||| ||| ||||||
                                TCTCCTTCT CCT CGTCTC
                                    C   _
GAM940  PLEK     3' CTGCATTCCTCCTCCCCT    10631    A   A  A
                                AG GGA GA GGATGCAG
                                || ||| || ||||||||
                                TC CCT CT CTTACGTC
                                 C   C  C
GAM940  PMX1     5' CCACCCCTTCTTCTCTCT    42659     _      ATGCAGA
                                AGAG GAAGAAGG      GTGG
                                |||| ||||||||      ||||
                                TCTC CTTCTTCC      CACC
                                  T       C_______
GAM940  PMX1     5' CCACCCCTTCTTCTCTCT    22591     _      ATGCAGA
                                AGAG GAAGAAGG      GTGG
                                |||| ||||||||      ||||
                                TCTC CTTCTTCC      CACC
                                  T       C_______
GAM940  POU3F1   3' CCCACCCCGCTTTCCCCTTTCT 59309       AA   T_  AGA
          C                      GAGGAAG  GGA  GC   GTGGG
                                 |||||||  |||  ||   |||||
                                 CTCTTTC  CCT  CG   CACCC
                                     C_   TT  CCC
GAM940  RAMP1    3' CCCACAATGCCCCCCTTCTTCC 19582        AT_   GA
                                GGAAGAAGG   GCA  GTGGG
                                |||||||||   |||  |||||
                                CCTTCTTCC   CGT  CACCC
                                     CCC   AA
GAM940  RUNX1    3' CCCACTTTCTCCCTCCTCCTTT 8262       A  A   TGC
                                AGAGGA GA GGA   AGAGTGGG
                                |||||| || |||   ||||||||
                                TTTCCT CT CCT   TTTCACCC
                                   C  C   C__
GAM940  SALL2    3' CCCTGGTGTGACCCTTCTTCC  63859        AT_   GAGT
                                GGAAGAAGG   GCA    GGG
                                |||||||||   |||    |||
                                CCTTCTTCC   TGT    CCC
                                     CAG   GGT_
GAM940  SALL2    3' CTGTACATTCCTTCTTCCTC   63861          ___
                                GAGGAAGAAGGA   TGCAG
                                ||||||||||||   |||||
                                CTCCTTCTTCCT   ATGTC
                                       TAC
GAM940  SH3BP2   3' CTGCAGCCCCCTTCCCCT    11602    A    AA  A
                                AG GGAAG  GG TGCAG
                                || |||||  || |||||
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                                TC CCTTC  CC ACGTC
                                 C    CC  G
GAM940  SHMT2   3'  CCCACTCTGGGGACCCCTCTCC 18262     A  A  ATG__
            T                    AGGA GA GG    CAGAGTGGG
                                 |||| || ||    |||||||||
                                 TCCT CT CC    GTCTCACCC
                                   _  C  CAGGG
GAM940  SIRT2   3'  CCCACTCTGTCTCCTGCCCC  47590   AAGA   T
                                 GG   AGGA GCAGAGTGGG
                                 ||   |||| ||||||||||
                                 CC   TCCT TGTCTCACCC
                                  CCG_   C
GAM940  SIRT2   3'  CCCACTCTGTCTCCTGCCCC  24260   AAGA   T
                                 GG   AGGA GCAGAGTGGG
                                 ||   |||| ||||||||||
                                 CC   TCCT TGTCTCACCC
                                  CCG_   C
GAM940  SMCX    3'  CACTCTCCTCCCCTCT     14823      AAGAA   TGC
                                 AGAGG    GGA   AGAGTG
                                 |||||    |||   ||||||
                                 TCTCC    CCT   TCTCAC
                                    _____  CC_
GAM940  SNAI1   3'  CCCTCGAGGCTCCCTCTTCCTC 19967         A   T  A__   T
            T                    AGAGGAAGA GGA GC   GAG GG
                                 ||||||||| ||| ||   ||| ||
                                 TCTCCTTCT CCT CG   CTC CC
                                       C   _  GAG   _
GAM940  SOX4    3'  CCCAGCGCACCCCTCCCCCCCT 11875    A  AA  A  A   AGAG
                                 AG GG  GA GG TGC    TGGG
                                 || ||  || || |||    ||||
                                 TC CC  CT CC ACG    ACCC
                                  C  CC  C  C   CG__
GAM940  SUFU    3'  TTGCCCCCTCTTCCTCT     32416          A  AT
                                 AGAGGAAGA GG  GCAG
                                 |||||||||  ||  ||||
                                 TCTCCTTCT CC  CGTT
                                       _  CC
GAM940  TIMP3   3'  CCCCTCTTGCTTCTTCCCC   4505     AA     T  _  T
                                 GG  GAAGGA GCA GAG GGG
                                 ||  |||||| ||| ||| |||
                                 CC  CTTCTT CGT CTC CCC
                                  C_     _   T   _
GAM940  TLE2    5'  CCCACTTCAGCCTCCCCCACTC 12308      GAAGAA   T  A_
            T                    AGAG     GGA GC  GAGTGGG
                                 ||||     ||| ||  |||||||
                                 TCTC     CCT CG  TTCACCC
                                   ACCC__   C  AC
GAM940  UGCG    5'  CCCCTCCGCCCTTTCCTCT   12540        GA   AT  A   T
                                 AGAGGAA  AGG  GC GAG GGG
                                 |||||||  |||  || ||| |||
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                                TCTCCTT  TCC  CG CTC CCC
                                   __  __  C  _
GAM940  USP5    3'  CCACCCTGTCTCTTCCTT    12991        A GAT   A
                                GAGGAAGA G   GCAG GTGG
                                |||||||| |   |||| ||||
                                TTCCTTCT C   TGTC CACC
                                   _ ___   C
GAM940  VAMP1   3'  CCACCCTGTACCCTCTTCT   33677       A  A    A
                                GGAAGA GG TGCAG GTGG
                                |||||| || ||||| ||||
                                TCTTCT CC ATGTC CACC
                                   C  _    C
GAM940  WAS     3'  CCACCCTCCACTCTCCTCT   4580        AGAA GA  C  A
                                AGAGGA   G  TG AG GTGG
                                ||||||   |  || || ||||
                                TCTCCT   C  AC TC CACC
                                   ____ TC  C  C
GAM940  ZNF179  3'  CCCTTAAACACATCCTTTCTCC 23101    A   AG      CAGAGT_
            CCT                   AG GGA  AAGGATG      GGG
                                || |||  |||||||      |||
                                TC CCT  TTCCTAC      CCC
                                 C   CT      ACAAATT
GAM940  A4GALT  3'  CCCACCCCATCCTTCTTCCTCT 33835             CAGA
                                AGAGGAAGAAGGATG   GTGGG
                                ||||||||||||||   |||||
                                TCTCCTTCTTCCTAC   CACCC
                                      CC__
GAM940  ATP6V0A1  3'  CCCACCCTGCACTCCCATCCTT 17728       AA___  _    A
            TCCTCT                 GAGGAAG    GGA TGCAG GTGGG
                                |||||||    ||| ||||| |||||
                                CTCCTTT    CCT ACGTC CACCC
                                   CCTAC   C    C
GAM940  C17orf31  3'  CCCTCACCCTTCTTCCCCT   34120    A       ATGCA   T
                                AG GGAAGAAGG    GAG GG
                                || |||||||||    ||| ||
                                TC CCTTCTTCC    CTC CC
                                 C       CA___  _
GAM940  C4.4A   3'  CCCACTCTAAGCACTGCCTCCC 26942    A  A  AA  A  __
            CT                   AG GG AG  GG TGC  AGAGTGGG
                                || || ||  || |||  ||||||||
                                TC CC TC  TC ACG  TCTCACCC
                                 _  C  CG  _   AA
GAM940  CBX6    3'  CCAAGCTCCCTCTTCCTC    26611        A   T  AGAG
                                GAGGAAGA GGA GC   TGG
                                |||||||| ||| ||   |||
                                CTCCTTCT CCT CG   ACC
                                   C   _  A___
GAM940  D2S448  3'  CTCTGAACTCCTCCTTCCTCT  73522        A   TG_
                                AGAGGAAG AGGA   CAGAG
                                |||||||| ||||   |||||
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                                TCTCCTTC TCCT   GTCTC
                                     C    CAA
GAM940   DKFZP434C0826 5'  TTGCATCCCTTCCCTCT     84039       _   AA
                                AGAGG AAG  GGATGCAG
                                ||||| |||  ||||||||
                                TCTCC TTC  CCTACGTT
                                  C   __
GAM940   DKFZP564K0822 3'  CCAAACACTCCTCTTCCTC    94043         A   _  CAGAG
                                GAGGAAGA GGA TG     TGG
                                |||||||| ||| ||     |||
                                CTCCTTCT CCT AC     ACC
                                     _   C  AA___
GAM940   DKFZP566C243 3'  CCCACCTACCCCTTCCTTCCTC 31167          _    ATGC  A
           T                     AGAGGAAG AAGG    AG GTGGG
                                |||||||| ||||    || |||||
                                TCTCCTTC TTCC    TC CACCC
                                     C    CCA_  _
GAM940   DKFZp761B0514 3'  CCCACCCTTTCTCCTCCTCCTT 50153         A    TGC   ____
             CCTCT                   GAGGAAG AGGA   AGA    GTGGG
                                ||||||| ||||   |||    |||||
                                CTCCTTC TCCT   TCT    CACCC
                                     C    CC_   TTCC
GAM940   DKFZp761K1824 3'  CCTTCCCCTTCCTCCCCT    34207    A   A    ATGCA   T
                                AG GGA GAAGG     GAG GG
                                || ||| |||||     ||| ||
                                TC CCT CTTCC     CTT CC
                                 C   C    C____   _
GAM940   DOCK3     3'  CCCAGGCAAGCCCTTCTTCCTC 66501           A__   AGAG
                                GAGGAAGAAGG   TGC    TGGG
                                ||||||||||   |||    ||||
                                CTCCTTCTTCC   ACG    ACCC
                                       CGA   G___
GAM940   EMR2      5'  CCACTCACTCTTTCCCCT    25581     AA     TGCA
                                AGG  GAAGGA    GAGTGG
                                |||  ||||||    ||||||
                                TCC  CTTTCT    CTCACC
                                  C_     CA__
GAM940   EPB41L1   3'  CCCACCCCACACCCTTCACCCT 70587       AA     A  CAGA
             CT                   AGAGG  GAAGG TG    GTGGG
                                |||||  ||||| ||    |||||
                                TCTCC  CTTCC AC    CACCC
                                   CA    C  ACCC
GAM940   FLJ10156  3'  CCCACTCTCATCCCTCCTTTCC 38693    A   __ A    C
             CT                    AG GGAA  GA GGATG AGAGTGGG
                                || ||||  || ||||| ||||||||
                                TC CCTT  CT CCTAC TCTCACCC
                                 _   TC  C    _
GAM940   FLJ10376  3'  TTGCATCCCTCTCCCTT     36078      A   A
                                GAGG AGA GGATGCAG
                                |||| ||| ||||||||
```

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                                TTCC TCT CCTACGTT
                                  C   C
GAM940  FLJ10613  3'  CCCACTGTGTGTCTTCTCCCCC 38822    A A    G    G
              T                   AG GG AGAAG ATGCA AGTGGG
                                  || || ||||| ||||| ||||||
                                  TC CC TCTTC TGTGT TCACCC
                                   C C    _    G
GAM940  FLJ12089  3'  CCCACCCGCCCTTCTTCCCT   44642    A       AT  AGA
                                  AG GGAAGAAGG  GC   GTGGG
                                  || |||||||||  ||   |||||
                                  TC CCTTCTTCC  CG   CACCC
                                   _       __ CC_
GAM940  FLJ12587  3'  CCACACATCCTTTCCCTC    42495     AA      CAGA
                                  GAGG  GAAGGATG    GTGG
                                  ||||  ||||||||    ||||
                                  CTCC  TTTCCTAC    CACC
                                    C_      A___
GAM940  FLJ14431  5'  CCCACTCTCTACCTTCTTTCCT 51353       _    A  C
              C                   GAGGAA GAAGG TG AGAGTGGG
                                  |||||| ||||| || ||||||||
                                  CTCCTT CTTCC AT TCTCACCC
                                     T    _ C
GAM940  FLJ21916  3'  GCAACCCCTCTTCCTCT     43643         A_  A
                                  AGAGGAAGA  GG TGC
                                  |||||||||  || |||
                                  TCTCCTTCT  CC ACG
                                       CC  A
GAM940  FLJ22341  3'  CCACCATGCCCCTTCCTCT   44802        AA  AT   GA
                                  AGAGGAAG  GG  GCA  GTGG
                                  ||||||||  ||  |||  ||||
                                  TCTCCTTC  CC  CGT  CACC
                                       __  __   AC
GAM940  FLJ22644  3'  CCCACATGCCCTCTTTCCTCT  47001       GA   AT   GA
                                  AGAGGAA  AGG  GCA  GTGGG
                                  |||||||  |||  |||  |||||
                                  TCTCCTT  TCC  CGT  CACCC
                                      TC   __   A_
GAM940  GABBR1    3'  TGCATCCTCCCCTCT      41577      AA  A
                                  AGAGG  GA GGATGCA
                                  |||||  || |||||||
                                  TCTCC  CT CCTACGT
                                    C_  _
GAM940  GABBR1    3'  TGCATCCTCCCCTCT      7612       AA  A
                                  AGAGG  GA GGATGCA
                                  |||||  || |||||||
                                  TCTCC  CT CCTACGT
                                    C_  _
GAM940  GFR       3'  CCACTGCCTCACCTCCCCT   24469    A  A  AAG  T   GA
                                  AG GG AG   GA GCA  GTGG
                                  || || ||   || |||  ||||
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                                TC CC TC   CT CGT  CACC
                                 _ C  CA_  C  __
GAM940  GIT1     3'  CCACTCTCGCCCCTTCTCT   25864     A    AT  _
                                GGA GAAGG  GC AGAGTGG
                                ||| |||||  || |||||||
                                TCT CTTCC  CG TCTCACC
                                  _    C_  C
GAM940  GP5      3'  CCCACTCCTCCTCTCTTCTTCC 15641          _  TGCA
             TCT                   AGAGGAAGAAG GA    GAGTGGG
                                |||||||||||  ||    |||||||
                                TCTCCTTCTTC CT    CTCACCC
                                      T  CCTC
GAM940  H326     3'  CCAGATCATTCTTCCTC     31703         G   GCAGAG
                                GAGGAAGAA GAT     TGG
                                |||||||||  |||     |||
                                CTCCTTCTT CTA     ACC
                                     A  G_____
GAM940  HNRPA0   5'  CCCTTCCCTCCCCCTTCCTCT  22321        AA   TGCA   T
                                AGAGGAAG  GGA    GAG GGG
                                ||||||||  |||    ||| |||
                                TCTCCTTC  CCT    CTT CCC
                                    CC   CC__   _
GAM940  IL-17RE  3'  CCCGCGCGCGTCCCTCTTCCTC 58291         A     AGA
                                GAGGAAGA GGATGC   GTGGG
                                |||||||| ||||||   |||||
                                CTCCTTCT CCTGCG   CGCCC
                                     C     CG_
GAM940  KIAA0169 5'  CCAGCAACCTTCTCCCTC    72816     A     A  AGAG
                                GAGG AGAAGG TGC    TGG
                                |||| |||||| |||    |||
                                CTCC TCTTCC ACG    ACC
                                  C     A  ____
GAM940  KIAA0222 3'  CCCACTCTTTGCCTCCCCGCCC 27680    A  AAGAA   T  __
             CT                   AG GG    GGA GCA  GAGTGGG
                                || ||    ||| |||  |||||||
                                TC CC    CCT CGT  CTCACCC
                                 C  GCC__   C   TT
GAM940  KIAA0247 5'  CCCACCTCCTCCCTCCCTC   28393     AA  A   TGC  A
                                GAGG  GA GGA   AG GTGGG
                                ||||  || |||   || |||||
                                CTCC  CT CCT   TC CACCC
                                  __  C   CC_  _
GAM940  KIAA0350 3'  CCCACCGGCACCTCTTTCTTCC 61172          __   AGA
             TCT                   AGAGGAAGAAGGA  TGC   GTGGG
                                ||||||||||||  |||   |||||
                                TCTCCTTCTTTCT  ACG   CACCC
                                       CC   GC_
GAM940  KIAA0415 3'  CCACTCTGGCTCCGCCCC    92576    AAGAA   T  _
                                GG    GGA GC AGAGTGG
                                ||    ||| || |||||||
```

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                                CC    CCT CG TCTCACC
                                 CCG__  _ G
GAM940  KIAA0446 3' CCCACCCTGCCAGCCCTTCTTC 68861        AT__   A
            T                    GGAAGAAGG   GCAG GTGGG
                                 ||||||||||  |||| |||||
                                 TCTTCTTCC   CGTC CACCC
                                      CGAC   C
GAM940  KIAA0964 3' CCCAATTATCCTTCTCTCTCT 29758     GA       CAGAG
                                 AGAG AGAAGGATG    TGGG
                                 ||||  |||||||||    ||||
                                 TCTC  TCTTCCTAT    ACCC
                                   TC       TA___
GAM940  KIAA1465 3' CCCACCTCGACCCCTCCTCCTC 60825     A A_ A C A
                                 GAGGA GA  GG TG AG GTGGG
                                 |||||  ||  || || || |||||
                                 CTCCT CT  CC GC TC CACCC
                                    C  CC  A  _ _
GAM940  KIAA1828 5' CCCTCCCTCCCTCTTCCTC   73778       A  TGCA  T
                                 GAGGAAGA GGA   GAG GG
                                 |||||||| |||   ||| ||
                                 CTCCTTCT CCT   CTC CC
                                      C  CC__  _
GAM940  KIAA1872 5' CCTGCGAGCATCCTCTTCCTC 62927       A    AGA TG
                                 GAGGAAGA GGATGC  G  GG
                                 |||||||| ||||||  |  ||
                                 CTCCTTCT CCTACG  C  CC
                                      _    AG_ GT
GAM940  KIAA1887 5' CCCACCCCTGGCCCTTCCCACT 76773    GAA   ATG  A_
            CT                    AGAG  GAAGG  CAG  GTGGG
                                  ||||  |||||  |||  |||||
                                  TCTC  CTTCC  GTC  CACCC
                                    ACC   CG_  CC
GAM940  KIAA1904 3' CTGCTCCTCCTTCCTCT    73485       A   T
                                 AGAGGAAG AGGA GCAG
                                 ||||||||  |||| ||||
                                 TCTCCTTC TCCT CGTC
                                      C   _
GAM940  KIAA1944 3' CTTTACTCCTTCTTCCTCT   75560          TGC
                                 AGAGGAAGAAGGA  AGAG
                                 ||||||||||||  ||||
                                 TCTCCTTCTTCCT  TTTC
                                        CA_
GAM940  LEFTB    5' CCCACTCTGCCTCTTGCTCCTC 40653     AGA   T
                                 GAGGA  AGGA GCAGAGTGGG
                                 |||||  |||| ||||||||||
                                 CTCCT  TTCT CGTCTCACCC
                                   CG_   C
GAM940  MESDC1   3' CCCACCCCCATACCCCTTCTTC 42594        ___  CAGA
            C                    GGAAGAAGG  ATG   GTGGG
                                 |||||||||  |||   |||||
```

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                                CCTTCTTCC  TAC   CACCC
                                     CCA  CCC_
GAM940  MGC20255 3'  CCCACCCTGTCTCCTGCCTCT  53442     AAGA   T   A
                                AGAGG   AGGA GCAG GTGGG
                                |||||   |||| |||| |||||
                                TCTCC   TCCT TGTC CACCC
                                   G___   C   C
GAM940  MGC2541  3'  CCCACTCTGGGGCCTGCCCCT  54746    AAGA  ATG
                                AGG   AGG  CAGAGTGGG
                                |||   |||  |||||||||
                                TCC   TCC  GTCTCACCC
                                  CCG_  GGG
GAM940  MGC2941  3'  CCCACCCTATCCTTCCTCC   44157    A     GC  A
                                GGA GAAGGAT  AG GTGGG
                                ||| |||||||  || |||||
                                CCT CTTCCTA  TC CACCC
                                  C      __ C
GAM940  MSTP032  3'  CCCACCTTGCCCCTGTTCCTC  47440      GA  AT   A
                                GAGGAA  AGG  GCAG GTGGG
                                ||||||  |||  |||| |||||
                                CTCCTT  TCC  CGTT CACCC
                                   G_  C_   C
GAM940  NPTXR    3'  CCCACCCATGCCTCCCTCTTCC 54176       A  T  GA_
           TC                    GAGGAAGA GGA GCA   GTGGG
                                |||||||| ||| |||   |||||
                                CTCCTTCT CCT CGT   CACCC
                                     C   C   ACC
GAM940  NPTXR    3'  CCCACCCATGCCTCCCTCTTCC 26640       A  T  GA_
           TC                    GAGGAAGA GGA GCA   GTGGG
                                |||||||| ||| |||   |||||
                                CTCCTTCT CCT CGT   CACCC
                                     C   C   ACC
GAM940  OBSCN    3'  CCTTGAGGGCACCTCCTTCCTC 70652       A  A  AGAGT
           T                     AGAGGAAG AGG TGC    GGG
                                |||||||| ||| |||    |||
                                TCTCCTTC TCC ACG    TCC
                                     C   _  GGAGT
GAM940  OSBPL3   3'  CCCACCCCGTTTTTTGTCCCTC 31435     AA_      CAGA
                                GAGG   GAAGGATG   GTGGG
                                ||||   ||||||||   |||||
                                CTCC   TTTTTTGC   CACCC
                                  CTG      CC__
GAM940  p25      3'  CCCACGCCCCCACTCTCCCTC  22848     A  A_  AT  AGA
                                GAGG AGA  GG  GC   GTGGG
                                |||| |||  ||  ||   |||||
                                CTCC TCT  CC  CG   CACCC
                                  C   CA  CC  ___
GAM940  PCDH19   3'  CACCCCACCTTCTCCT     63698     A    A  CAGA
                                AGGA GAAGG TG   GTG
                                |||| ||||| ||   |||
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                                TCCT CTTCC AC    CAC
                                  _    _ CC__
GAM940  PLAGL2   3'  CCCACTCCTGTGTCCTCCCATC 70445    _ AAGA      _
          T                      AGA GG    AGGATGCAG AGTGGG
                                 ||| ||    ||||||||| ||||||
                                 TCT CC    TCCTGTGTC TCACCC
                                   A  C___       C
GAM940  PPP1R13B 3'  CCCACACATGATCCTTCTTCCC 31007    A        G  GA_
          T                      AG GGAAGAAGGAT CA   GTGGG
                                 || ||||||||||| ||   |||||
                                 TC CCTTCTTCCTA GT   CACCC
                                  _         _ ACA
GAM940  PTPRU    3'  CCCACTCAGCCTGCCCCCTCT  55688      AAGA   ATGCA
                                 AGAGG    AGG    GAGTGGG
                                 |||||    |||    |||||||
                                 TCTCC    TCC    CTCACCC
                                    CCCG   GA___
GAM940  PTPRU    3'  CCCACTCAGCCTGCCCCCTCT  55694      AAGA   ATGCA
                                 AGAGG    AGG    GAGTGGG
                                 |||||    |||    |||||||
                                 TCTCC    TCC    CTCACCC
                                    CCCG   GA___
GAM940  PTPRU    3'  CCCACTCAGCCTGCCCCCTCT  19115      AAGA   ATGCA
                                 AGAGG    AGG    GAGTGGG
                                 |||||    |||    |||||||
                                 TCTCC    TCC    CTCACCC
                                    CCCG   GA___
GAM940  RAB1B    3'  CCCACTCTGCACCCAGGATCCT 48285     AGAA  A
                                 AGGA    GG TGCAGAGTGGG
                                 ||||    || ||||||||||
                                 TCCT    CC ACGTCTCACCC
                                   AGGA  C
GAM940  REPRIMO  3'  CCCACTCTTCTCCTGCTCCC   39053    A  A    TGC
                                 GG AG AGGA   AGAGTGGG
                                 || || ||||   ||||||||
                                 CC TC TCCT   TCTCACCC
                                  C  G    CT_
GAM940  RoXaN    3'  CACCCTGCCTTTCTCT      46636         AAGGAT    A
                                 AGAGGAAG     GCAG GTG
                                 ||||||||     |||| |||
                                 TCTCTTTC     CGTC CAC
                                      _______    C
GAM940  SCYA22   3'  CCCAGATTCACCTTTCTTCC   90939         A  C  AG
                                 GGAAGAAGG TG AG  TGGG
                                 ||||||||| || ||  ||||
                                 CCTTCTTTC AC TT  ACCC
                                       C  _  AG
GAM940  SLC19A3  3'  CACTCTCTCTTTCTCC      47482     A     TGC
                                 GGA GAAGGA   AGAGTG
                                 ||| ||||||   ||||||
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                                CCT CTTTCT   TCTCAC
                                  _     C__
GAM940  SNPH     3'  CCGTCATCCCTTTCCTCT    28240        AA    CAGAG
                                AGAGGAAG  GGATG    TGG
                                ||||||||  |||||    |||
                                TCTCCTTT  CCTAC    GCC
                                    C_    T____
GAM940  STIM2    3'  CCCACCCTCCACTCCCCACCT  40473    AAGAA  _  C  A
                                AGG    GGA TG AG GTGGG
                                |||    ||| || || |||||
                                TCC    CCT AC TC CACCC
                                  ACC__   C  C  C
GAM940  STX3A    3'  CCCACCCAGCTTTCTTCCTC   14803          A  CAGA
                                GAGGAAGAAGG TG    GTGGG
                                ||||||||||| ||    |||||
                                CTCCTTCTTTC AC    CACCC
                                      G  C___
GAM940  TXNL     5'  CCTGAGCATCTCTCCTTCCTCT 16552        A  _    AGAGT
                                AGAGGAAG AG GATGC    GG
                                |||||||| || |||||    ||
                                TCTCCTTC TC CTACG    CC
                                    C  T    AGT__
GAM940  WIRE     3'  CTGCATCCATCCTTCCTC    78303       AA_
                                GAGGAAG   GGATGCAG
                                |||||||   ||||||||
                                CTCCTTC   CCTACGTC
                                    CTA
GAM940  LOC121838 5'  CCCACTAGCAGACCCTTCTTCC 75998          A__   AG
          TC                    GAGGAAGAAGG   TGC  AGTGGG
                                ||||||||||   |||  ||||||
                                CTCCTTCTTCC   ACG  TCACCC
                                      CAG   A_
GAM940  LOC123242 5'  CCCACTCTGTACCTTCTCC    75596     A    A
                                GGA GAAGG TGCAGAGTGGG
                                ||| ||||| ||||||||||
                                CCT CTTCC ATGTCTCACCC
                                  _    _
GAM940  LOC123775 3'  CCCACTCTCTCTTTCTCTCCTC 75622       _      TGC
                                GAGGA AGAAGGA   AGAGTGGG
                                |||||  |||||||   ||||||||
                                CTCCT TCTTTCT   TCTCACCC
                                   C      C__
GAM940  LOC126695 3'  CCCACTCTGGCTCCTCCTGCC  75428    A  A    T  _
                                GG AG AGGA GC AGAGTGGG
                                || || |||| || ||||||||
                                CC TC TCCT CG TCTCACCC
                                 G  C    _  G
GAM940  LOC145945 5'  TGCACCCTCTCTCCCCT     83580    A  A   _   A
                                AG GG AGA AGG TGCA
                                || || ||| ||| ||||
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                                TC CC TCT TCC ACGT
                                 _ C   C   C
GAM940   LOC147160 5'  CCCACCACGTCCCTTCTCACTC 83961      GA     _   CAGA
           T                     AGAG  AGAAGG ATG    GTGGG
                                 ||||  |||||| |||    |||||
                                 TCTC  TCTTCC TGC    CACCC
                                   AC     C   AC__
GAM940   LOC147804 3'  CCCACCCTGCTGCTGCTCCTTC 78484         A  GAT__    A
           CTCT                    AGAGGAAG AG     GCAG GTGGG
                                 ||||||||| ||     |||| |||||
                                 TCTCCTTC TC     CGTC CACCC
                                      C  GTCGT    C
GAM940   LOC150319 3'  CCACTCTGCCTCCGCCTC     79650      AAGAA   T
                                 GAGG     GGA GCAGAGTGG
                                 ||||     ||| |||||||||
                                 CTCC     CCT CGTCTCACC
                                   G_____   C
GAM940   LOC150605 5'  CCCACTCTGCAAGCACTCCCCC 85082     AA  A GA__
                                 GG  GA G    TGCAGAGTGGG
                                 ||  || |    ||||||||||
                                 CC  CT C    ACGTCTCACCC
                                  CC  _ ACGA
GAM940   LOC151512 5'  CCAGGAGCTCCTCCTTCCTCT  85426         A    T  AGAG
                                 AGAGGAAG AGGA GC    TGG
                                 |||||||| |||| ||    |||
                                 TCTCCTTC TCCT CG    ACC
                                      C    _  AGG_
GAM940   LOC152794 5'  CCCACCTTTTCCTTTTCCTCT  80674          A   TGC  A
                                 AGAGGAAGA GGA   AG GTGGG
                                 ||||||||| |||   || |||||
                                 TCTCCTTTT CCT   TC CACCC
                                       _   TT_  _
GAM940   LOC153196 5'  CCCACCTGCACCCCTTTCTTCC 85957          A__     A
                                 GGAAGAAGG   TGCAG GTGGG
                                 |||||||||   ||||| |||||
                                 CCTTCTTTC   ACGTC CACCC
                                       CCC    _
GAM940   LOC153364 5'  CTGCGTCCTTCCTCCTC      80812       A
                                 GAGGA GAAGGATGCAG
                                 ||||| ||||||||||
                                 CTCCT CTTCCTGCGTC
                                    C
GAM940   LOC158364 5'  TTTTGCATCCCTCTTACCCT   81879     A  _    A
                                 AG GG AAGA GGATGCAGAG
                                 || || |||| ||||||||||
                                 TC CC TTCT CCTACGTTTT
                                  _ A   C
GAM940   LOC162333 5'  CCCACTCTGCCACCCCCATCC  87128      AGAA  AT
                                 GGA    GG  GCAGAGTGGG
                                 |||    ||  ||||||||||
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                                CCT   CC  CGTCTCACCC
                                  ACCC  AC
GAM940  LOC166341 3'  CCCACTCTGGCTCTCCCACTCT 82630     GAA  AG ATG
                                AGAG   GA  G   CAGAGTGGG
                                ||||   ||  |   |||||||||
                                TCTC   CT  C   GTCTCACCC
                                  ACC  CT G__
GAM940  LOC200812 5'  CCCACCCCCATGTACTTCTTCC 88882          GA   GA___
          TCT                   AGAGGAAGAAG  TGCA    GTGGG
                                ||||||||||  ||||    |||||
                                TCTCCTTCTTC  ATGT    CACCC
                                      __   ACCCC
GAM940  LOC201510 3'  TGATCCTCCTTCCTCT     88252        A    G
                                AGAGGAAG AGGAT CA
                                |||||||| ||||| ||
                                TCTCCTTC TCCTA GT
                                    C    _
GAM940  LOC201911 3'  CCGGGCTCCTTCTTCCTC    90259          T  AGAG
                                GAGGAAGAAGGA GC   TGG
                                ||||||||||| ||   |||
                                CTCCTTCTTCCT CG   GCC
                                      _  G___
GAM940  LOC202546 3'  CCACTGCCTTCTTCTCCT    90358     A    T   GA
                                AGGA GAAGGA GCA  GTGG
                                |||| |||||| |||  ||||
                                TCCT CTTCTT CGT  CACC
                                  _     C  __
GAM940  LOC219688 5'  CCCGCTGCCCCCCTCCTCCTC  93051      A  A  AT   GA
                                GAGGA GA GG  GCA  GTGGG
                                ||||| || ||  |||  |||||
                                CTCCT CT CC  CGT  CGCCC
                                   C  C  CC   __
GAM940  LOC219818 3'  CCCACAAGCCCTTCTTCCT   90888         AT  AGA
                                AGGAAGAAGG  GC   GTGGG
                                ||||||||||  ||   |||||
                                TCCTTCTTCC  CG   CACCC
                                      __  AA_
GAM940  LOC220020 5'  CCCAGCACCCCTCCCCACTCT  93418     GAA_  A  A   AGAG
                                AGAG    GA GG TGC    TGGG
                                ||||    || || |||    ||||
                                TCTC    CT CC ACG    ACCC
                                  ACCC  C  C   _____
GAM940  LOC222070 5'  CACCCCTTCTTCCCCT      94150    A       ATGCAGA
                                AG GGAAGAAGG      GTG
                                || |||||||||      |||
                                TC CCTTCTTCC      CAC
                                 C        C_______
GAM940  LOC222159 5'  CTCACATCTCCTTCCTCT    94078        AA    CA
                                AGAGGAAG  GGATG  GAG
                                ||||||||  |||||  |||
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                                TCTCCTTC  TCTAC  CTC
                                   C_     A_
GAM940  LOC253001 5'  CCCACTCTGTACCTTCTCC    96254     A    A
                                GGA GAAGG TGCAGAGTGGG
                                ||| ||||| ||||||||||
                                CCT CTTCC ATGTCTCACCC
                                  _    _
GAM940  LOC253609 5'  CCCTCCAGTCCTTCTCCCTC   96759      A      GCA   T
                                GAGG AGAAGGAT   GAG GG
                                |||| ||||||||   ||| ||
                                CTCC TCTTCCTG   CTC CC
                                  C       AC_  _
GAM940  LOC255271 3'  CACTCTCCCTTCTCCT      95499      A    ATGC
                                AGGA GAAGG    AGAGTG
                                |||| |||||    ||||||
                                TCCT CTTCC    TCTCAC
                                  _    C___
GAM940  LOC255386 5'  CCGGTTGCATCCTCCCTC     95001      AAGA       AG
                                GAGG    AGGATGCAG  TGG
                                ||||    |||||||||  |||
                                CTCC    TCCTACGTT  GCC
                                  C___        G_
GAM940  LOC255446 3'  CCCGTGGACCTCCCCCTTCCTC 97153         AA   TGCAGA
          T                      AGAGGAAG  GGA     GTGGG
                                ||||||||  |||     |||||
                                TCTCCTTC  CCT     TGCCC
                                    CC   CCAGG_
GAM940  LOC257054 5'  CCCACCATGTCCTTCCCTC    95658     AA    AT   GA
                                GAGG  GAAGG  GCA  GTGGG
                                ||||  |||||  |||  |||||
                                CTCC  CTTCC  TGT  CACCC
                                  __    __   AC
GAM940  LOC257054 5'  CCCACCGTGTCCTTCCCTC    95659      AA       AGA
                                GAGG  GAAGGATGC   GTGGG
                                ||||  |||||||||   |||||
                                CTCC  CTTCCTGTG   CACCC
                                  __        C__
GAM940  LOC90538  3'  CCCACCCTGCTTTGGCTCACCC 63189      A__  AA   T    A
          TC                     GAGG   AG  GGA GCAG GTGGG
                                ||||   ||  ||| |||| |||||
                                CTCC   TC  TTT CGTC CACCC
                                  CAC  GG   _    C
GAM940  LOC90785  3'  CCCACCCTGCTCTCCTCCCCT  64014     AA  A   T_    A
                                AGG  GA GGA  GCAG GTGGG
                                |||  || |||  |||| |||||
                                TCC  CT CCT  CGTC CACCC
                                  C_  _   CT    C
GAM940  LOC90786  5'  CCCACCTAAACCTTCTTGCTCT 64030      G      ATGC  A
                                AGAG AAGAAGG    AG GTGGG
                                |||| |||||||    || |||||
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                                TCTC TTCTTCC    TC CACCC
                                  G      AAA_ _
GAM940  LOC91373  3' CCCACTCGAGGGCTGCCCCCTC 65836      AAGAA  ATGCA
             T                   AGAGG    GG    GAGTGGG
                                 |||||    ||    |||||||
                                 TCTCC    TC    CTCACCC
                                   CCCG_  GGGAG
GAM940  LOC91397  5' CCCACGTCACTGCCCCTCCCCC 65906    AA  A  AT   A___
                                 GG  GA GG  GCAG    GTGGG
                                 ||  || ||  ||||    |||||
                                 CC  CT CC  CGTC    CACCC
                                  CC  _  C_    ACTG
GAM940  LOC91397  5' CCTCCCCCCCCTTCCTCT     65907        AA  ATGCA   T
                                 AGAGGAAG  GG    GAG G
                                 ||||||||  ||    ||| |
                                 TCTCCTTC  CC    CTC C
                                      CC  C_____  _
GAM940  LOC91445  3' CCCACTCCCCCTCTTCTTCCTC 60548          ATGCA
             T                   AGAGGAAGAAGG    GAGTGGG
                                 ||||||||||||    |||||||
                                 TCTCCTTCTTCT    CTCACCC
                                       CCCC_
GAM940  LOC91963  5' CCCACTCTCACCTCTCCTC   67690      A  A  A  C
                                 GAGGA GA GG TG AGAGTGGG
                                 ||||| || || || ||||||||
                                 CTCCT CT CC AC TCTCACCC
                                    _  _  _  _
GAM940  LOC92299  5' CCACTCCTCCCTCCTC      68808      AGAA   TGCA
                                 GAGGA   GGA   GAGTGG
                                 |||||   |||   ||||||
                                 CTCCT   CCT   CTCACC
                                   C___   C___
GAM941  ATP1B1    3' TGTTTTCTACTTTATG     8044
                                 CATAAAGTAGAAAGCA
                                 ||||||||||||||||
                                 GTATTTCATCTTTTGT

GAM941  ATR       5' TGCTTTCTATTTATG      94464       G
                                 CATAAA TAGAAAGCA
                                 |||||| |||||||||
                                 GTATTT ATCTTTCGT
                                    _
GAM941  EPB41L2   3' GTGACTTTCTACTTTTA     7483    T        _
                                 A AAAGTAGAAAG CAC
                                 | ||||||||||| |||
                                 A TTTCATCTTTC GTG
                                  T         A
GAM941  FGF7      3' GTTAGCACATGCTTTCTACT   8886          CTA_
                                 AGTAGAAAGCA   CTAAC
                                 ||||||||||    |||||
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                                TCATCTTTCGT   GATTG
                                      ACAC
GAM941  NUFIP1   3' GTATGGTTTCTACTTTATG   24720          G  C
                                CATAAAGTAGAAA CA TAC
                                |||||||||||| || |||
                                GTATTTCATCTTT GT ATG
                                     G  _
GAM941  RSN      3' AGTAGTGCCTTTACTT     11397       AA
                                AAGTAGA  GCACTACT
                                |||||||  ||||||||
                                TTCATTT  CGTGATGA
                                   C_
GAM941  SLC17A5  3' TAGGACTTCTACTTTA     24896         A CA
                                TAAAGTAGAA G  CTA
                                |||||||||| |  |||
                                ATTTCATCTT C  GAT
                                      _ AG
GAM941  TCF8     3' GTGAACTTTCTGCTTCATG   47728     A       __
                                CAT AAGTAGAAAG  CAC
                                ||| ||||||||||  |||
                                GTA TTCGTCTTTC  GTG
                                  C        AA
GAM941  DIO2     3' TTAGTAACTGTTCCTACTTTGT 5838         AA   C_
                                ATAAAGTAG  AGCA  TACTAA
                                |||||||||  ||||  ||||||
                                TGTTTCATC  TTGT  ATGATT
                                     C_   CA
GAM941  DIO2     3' TTAGTAACTGTTCCTACTTTGT 25690        AA   C_
                                ATAAAGTAG  AGCA  TACTAA
                                |||||||||  ||||  ||||||
                                TGTTTCATC  TTGT  ATGATT
                                     C_   CA
GAM941  FLJ12121 3' TGGTGCTTCCACTCCATG    46459    AA  A  A
                                CAT  AGT GAA GCACTA
                                |||  ||| ||| ||||||
                                GTA  TCA CTT CGTGGT
                                  CC   C  _
GAM941  FLJ12800 3' AGCAGTGCTTTCTGTATG    43227     AAG       A
                                CATA   TAGAAAGCACT CT
                                ||||   |||||||||||| ||
                                GTAT   GTCTTTCGTGA GA
                                   ___         C
GAM941  FPGT     3' TAGTCTGTGCTACTTTATG   13849       AGAA   T_
                                CATAAAGT   AGCAC  ACTA
                                ||||||||   |||||  ||||
                                GTATTTCA   TCGTG  TGAT
                                     ____    TC
GAM941  KIAA0368 3' GCTTTATTTTACTTTATG    65166         ___
                                CATAAAGTAGAA   AGC
                                ||||||||||||   |||
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                                GTATTTCATTTT  TCG
                                      ATT
GAM941  KIAA0721  3'  TGGGCTTCATACTTTATG    95977        GA   A
                                CATAAAGTA  AAGC CTA
                                |||||||||  |||| |||
                                GTATTTCAT  TTCG GGT
                                     AC   _
GAM941  KIAA0721  3'  TGGGCTTCATACTTTATG    41349        GA   A
                                CATAAAGTA  AAGC CTA
                                |||||||||  |||| |||
                                GTATTTCAT  TTCG GGT
                                     AC   _
GAM941  KIAA1046  3'  TGCTTCCTACTTTATG      30000         A
                                CATAAAGTAG AAGCA
                                |||||||||| |||||
                                GTATTTCATC TTCGT
                                      C
GAM941  KIAA1204  3'  GTTAGAAGGCCTCCTCTTTATG 69219       TA  AA  A  A
                                CATAAAG  GA  GC CT CTAAC
                                |||||||  ||  || || |||||
                                GTATTTC  CT  CG GA GATTG
                                    TC  C_  _  A
GAM941  KIAA1911  3'  TAGTGCCCTCTACTTTTA    73509   T      AA
                                A AAAGTAGA  GCACTA
                                | ||||||||  ||||||
                                A TTTCATCT  CGTGAT
                                 T       CC
GAM941  LRPPRC    3'  TAGGCTTCTTACTTTAT     55710        GA   A
                                ATAAAGTA  AAGC CTA
                                ||||||||  |||| |||
                                TATTTCAT  TTCG GAT
                                     TC   _
GAM941  MAL2      3'  GTTAGTTTCACTTGTCTACTTT 53554         _  CACT
          AT                     ATAAAGTAGA AAG   ACTAAC
                                ||||||||||  |||   ||||||
                                TATTTCATCT TTC    TGATTG
                                      G   ACTT
GAM941  MEGF10    3'  TTAGTAGTCCACTTTATG    50588        A  AAGCA
                                CATAAAGT GA    CTACTAA
                                |||||||| ||    |||||||
                                GTATTTCA CT    GATGATT
                                     C  _____
GAM941  MGC15563  3'  TGCTTCCTACCTTTATG     51796        _  A
                                CATAAAG TAG AAGCA
                                ||||||| ||| |||||
                                GTATTTC ATC TTCGT
                                    C   C
GAM941  NMU2R     3'  GTGCTGTTCTACTTTAT     39401          _
                                ATAAAGTAGAA AGCAC
                                |||||||||| |||||
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                                TATTTCATCTT TCGTG
                                      G
GAM941  PDE4DIP  5'  AGTAGTGCTTTCTGCT     27687
                                AGTAGAAAGCACTACT
                                ||||||||||||||||
                                TCGTCTTTCGTGATGA

GAM941  RNF38    3'  TAGTAATGCTTTACTA     42939    _    C
                                TAG AAAGCA TACTA
                                ||| |||||| |||||
                                ATC TTTCGT ATGAT
                                  A     A
GAM941  ZDHHC3   3'  TGCCTTGTACTTTATG     33458        G  A
                                CATAAAGTA AA GCA
                                ||||||||| || |||
                                GTATTTCAT TT CGT
                                      G  C
GAM941  LOC121506 3'  AGTATCTACTTTATG      74094          AAGCAC
                                CATAAAGTAGA     TACT
                                ||||||||||      ||||
                                GTATTTCATCT     ATGA
                                                _______
GAM941  LOC152098 3'  GGTAACTTTCTACTTCAT    80461    A       CAC
                                AT AAGTAGAAAG   TACT
                                || ||||||||||   ||||
                                TA TTCATCTTTC   ATGG
                                 C        A__
GAM941  LOC51015  3'  GTAGTGCTTTTACTTTA     32120          A
                                TAAAGTAGAA GCACTAC
                                |||||||||| |||||||
                                ATTTCATTTT CGTGATG
                                                _
GAM942  AK1      3'  TAGCAGAAGACAAGGCA     4887        CTCC  GC
                                TGCCTTG    CT  CTGCTA
                                |||||||    ||  ||||||
                                ACGGAAC    GA  GACGAT
                                     A___  A_
GAM942  APBB1    3'  ATGGTAACAAGAGGAGCAGGAA 6745      C    _  GC____    III
            GCAAGGC                  GCT CCTGC CT     TACCA   T
                                ||| ||||| ||     |||||  |
                                CGA GGACG GG     ATGGT   A
                                  A     A  AGAACA    III
GAM942  EPHA1    3'  GGTGCAAGGAGCAAGG      17860         C  _
                                CCTTGCTCC TGC CT
                                ||||||||| ||| ||
                                GGAACGAGG ACG GG
                                      A   T
GAM942  EPHA8    3'  GGCAGCAGGCAGGGCGGC    40062     _        A
                                GCT CCCTGCCTGCT CC
                                ||| ||||||||||| ||
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                                CGG GGGACGGACGA GG
                                  C         C
GAM942  FCMD     3'  AGCAGTTTGAGAAGCTAAGGCA 22087       _  _ CCTGC
                                TGCCTT GCT C     CTGCT
                                ||||||| ||| |    |||||
                                ACGGAA CGA G     GACGA
                                   T   A AGTTT
GAM942  FSTL3    3'  GGCAGCTCAGAGCAGGGCA   19611         C___
                                TGCCTTGCTC   CTGCC
                                ||||||||||   |||||
                                ACGGGACGAG   GACGG
                                      ACTC
GAM942  FZD4     3'  AGCATCTAGCAGAAAGCCAGGC 24125      T  CC   C___
          A                      TGCCT GCT  CTGC   TGCT
                                ||||| |||  ||||   ||||
                                ACGGA CGA  GACG   ACGA
                                   C   AA   ATCT
GAM942  GAB2     3'  CAGGACAAGGAGAAAGCA    54448    C  G   C  _
                                TGC TT CTCC TG CCTG
                                ||| || |||| || ||||
                                ACG AA GAGG AC GGAC
                                  A  _   A  A
GAM942  GAB2     3'  TGGCAGGAGAGAAGCAAGGC  54462       _ C  G
                                GCCTTGCT C CT CCTGCTA
                                |||||||| | || |||||||
                                CGGAACGA G GA GGACGGT
                                     A A  _
GAM942  GAB2     3'  CAGGACAAGGAGAAAGCA    24491    C  G   C  _
                                TGC TT CTCC TG CCTG
                                ||| || |||| || ||||
                                ACG AA GAGG AC GGAC
                                  A  _   A  A
GAM942  GAB2     3'  TGGCAGGAGAGAAGCAAGGC  24505       _ C  G
                                GCCTTGCT C CT CCTGCTA
                                |||||||| | || |||||||
                                CGGAACGA G GA GGACGGT
                                     A A  _
GAM942  GCNT1    3'  CAGAGCAGGTAGCAAGGCA   7653         C    _
                                TGCCTTGCT CCTGC CTG
                                ||||||||| ||||| |||
                                ACGGAACGA GGACG GAC
                                      T    A
GAM942  HNRPDL   3'  CGGGCAGAGCGCAAGGCA   18425        TCC
                                TGCCTTGC  CTGCCTG
                                ||||||||  |||||||
                                ACGGAACG  GACGGGC
                                     CGA
GAM942  IFI16    5'  TAGCAGAATAGGAGCAAGCCA 71224    C      CTGC
                                TG CTTGCTCC   CTGCTA
                                || ||||||||   ||||||
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                                AC GAACGAGG    GACGAT
                                 C       ATAA
GAM942  ITGA3    3'  TAGCAGCAGGCTCAGGCA    18540      T CTC    C
                                TGCCT G   CCTGC TGCTA
                                |||||| |   ||||| |||||
                                ACGGA C   GGACG ACGAT
                                  _ TC_    _
GAM942  ITGA3    3'  TAGCAGCAGGCTCAGGCA    9378       T CTC    C
                                TGCCT G   CCTGC TGCTA
                                |||||| |   ||||| |||||
                                ACGGA C   GGACG ACGAT
                                  _ TC_    _
GAM942  ITPKB    3'  CAGGCAGGAAGAAGGCA     9423       G  C
                                TGCCTT CT CCTGCCTG
                                |||||| || ||||||||
                                ACGGAA GA GGACGGAC
                                  _ A
GAM942  KCNK5    3'  CGGGCAGGAAGCAAGTCA    13611    C     C
                                TG CTTGCT CCTGCCTG
                                || |||||| ||||||||
                                AC GAACGA GGACGGGC
                                 T     A
GAM942  KIAA0857 3'  TGGGCAGGGAGCAGGCA     66680      T
                                TGCCT GCTCCCTGCCTG
                                ||||| ||||||||||||
                                ACGGA CGAGGGACGGGT
                                  _
GAM942  MGA      3'  CAGCCAAGGAGCAGGCA     62806      T    C  C
                                TGCCT GCTCC TG CTG
                                ||||| ||||| || |||
                                ACGGA CGAGG AC GAC
                                  _    A  C
GAM942  MMP3     5'  CAGGCAAGACAGCAAGGCA   10063        CC  _
                                TGCCTTGCT  CT GCCTG
                                |||||||||  || |||||
                                ACGGAACGA  GA CGGAC
                                     CA  A
GAM942  MOCS1    3'  TGGGCAGGAAGCCAGACA    92035    C  T   C
                                TG CT GCT CCTGCCTG
                                || || ||| ||||||||
                                AC GA CGA GGACGGGT
                                 A  C   A
GAM942  MTCP1    5'  TAGGCAGAAAGCAAGTCA    26434    C     CC
                                TG CTTGCT  CTGCCTG
                                || ||||||  |||||||
                                AC GAACGA  GACGGAT
                                 T     AA
GAM942  NPR2L    3'  TAGTAACAGGGCTGAGCAAGGC 21563          ___     CC
           A                     TGCCTTGCT   CCCTG  TGCTA
                                |||||||||   |||||  |||||
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                                ACGGAACGA   GGGAC  ATGAT
                                     GTC    A_
GAM942  NRXN2    3'  AGCAGGGAAGAGGGAGCAAGGC 30622          G___
          A                   TGCCTTGCTCCCT   CCTGCT
                              ||||||||||||    ||||||
                              ACGGAACGAGGGA   GGACGA
                                    GAAG
GAM942  NRXN2    3'  AGCAGGGAAGAGGGAGCAAGGC 57008          G___
          A                   TGCCTTGCTCCCT   CCTGCT
                              ||||||||||||    ||||||
                              ACGGAACGAGGGA   GGACGA
                                    GAAG
GAM942  NRXN2    3'  AGCAGGGAAGAGGGAGCAAGGC 57019          G___
          A                   TGCCTTGCTCCCT   CCTGCT
                              ||||||||||||    ||||||
                              ACGGAACGAGGGA   GGACGA
                                    GAAG
GAM942  OLR1     3'  GTGCAGGCAGAGAGCAA     10337       C      T
                              TTGCTC CTGCCTGC AC
                              |||||| |||||||| ||
                              AACGAG GACGGACG TG
                                 A      _
GAM942  PROK1    3'  GGGACAGGGAGCAGGGCA    50556           _
                              TGCCTTGCTCCCTG CCT
                              |||||||||||||| |||
                              ACGGGACGAGGGAC GGG
                                    A
GAM942  RPP30    5'  TGGTAGATGAAAGCAAAGCA  21175    C    CCCTGCCTG
                              TGC TTGCT       CTACCA
                              ||| |||||       ||||||
                              ACG AACGA       GATGGT
                                A    AAGTA____
GAM942  SHMT2    3'  GTAGCAGGCAGGGGTGGGTAGG 18269      T  ___
          CA                    TGCCT GCT   CCCTGCCTGCTAC
                              |||||| |||   ||||||||||||
                              ACGGA TGG   GGGACGGACGATG
                                 _  GTG
GAM942  SIAH1    3'  GGTAGGTGGAAGCTAGACA   11659    C  T   C  T
                              TG CT GCT CC GCCTGCT
                              || || ||| || |||||||
                              AC GA CGA GG TGGATGG
                               A  T   A  _
GAM942  SPINK2   5'  CAGACCGCAGGGGCAAGACA  40876    C    T    ___
                              TG CTTGC CCCTGC   CTG
                              || ||||| ||||||   |||
                              AC GAACG GGGACG   GAC
                               A    _      CCA
GAM942  TCF2     3'  TGGAGGGACAGGGAGCAGGGCA 21387           _  G
                              TGCCTTGCTCCCTG CCT CTA
                              |||||||||||||| ||| |||
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                                ACGGGACGAGGGAC GGG GGT
                                       A  A
GAM942  TNFSF7   3' TGGCAGGACAAGAGAAGGCA  6979       G  CC _
                                TGCCTT CTC  TG CCTGCTA
                                |||||| |||  || |||||||
                                ACGGAA GAG  AC GGACGGT
                                   _  A_  A
GAM942  USP7     3' TGGTAACCACAGTGCAAGGCA 12955       TCC  CCTGC
                                TGCCTTGC  CTG   TACCA
                                ||||||||  |||   |||||
                                ACGGAACG  GAC   ATGGT
                                    T__  ACCA_
GAM942  ZNF174   3' AGTCTCTGCAGAGAGCAAGG  12896       C   CT__
                                CCTTGCTC CTGC   GCT
                                |||||||| ||||   |||
                                GGAACGAG GACG   TGA
                                    A   TCTC
GAM942  AP1GBP1  3' GTAGCAGGCAGGTGAGGGCA  23397     TTG  _
                                TGCC  CTC CCTGCCTGCTAC
                                ||||  ||| ||||||||||||
                                ACGG  GAG GGACGGACGATG
                                  ___  T
GAM942  AP1GBP1  3' GTAGCAGGCAGGTGAGGGCA  54522     TTG  _
                                TGCC  CTC CCTGCCTGCTAC
                                ||||  ||| ||||||||||||
                                ACGG  GAG GGACGGACGATG
                                  ___  T
GAM942  AQP10    3' AGAGACAGAGAGCAAGGC    54430       C  C  G
                                GCCTTGCTC CTG CT CT
                                ||||||||| ||| || ||
                                CGGAACGAG GAC GA GA
                                     A  A  _
GAM942  ATP9A    3' TGGCAGCTTTCAGAACAAGG  62053      CTCC  CCT  A
                                CCTTG   CTG  GCT CCA
                                |||||   |||  ||| |||
                                GGAAC   GAC  CGA GGT
                                  AA__  TTT  C
GAM942  CAMK1G   3' GGCAGAGGGAGGAAGGCA   39947      G    GC
                                TGCCTT CTCCCT  CTGCT
                                |||||| ||||||  |||||
                                ACGGAA GAGGGA  GACGG
                                   G    __
GAM942  CASKIN1  3' TGGCAGCCACGTGGAAGCAGGG 40403        _  C__  C
           CA                    TGCCTTGCT CC   TG CTGCTA
                                |||||||| ||   || ||||||
                                ACGGGACGA GG   AC GACGGT
                                     A  TGC  C
GAM942  DAP13    5' CAGAAGGGGAGCGAGGCA    38121          GC
                                TGCCTTGCTCCCT  CTG
                                ||||||||||||  |||
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                                ACGGAGCGAGGGG  GAC
                                       AA
GAM942  DKFZP566J2046 3'  AGAGAAGGGAGCAAGACA    48306    C        GC  G
                                TG CTTGCTCCCT  CT CT
                                || ||||||||||  || ||
                                AC GAACGAGGGA  GA GA
                                 A        A_  _
GAM942  DKFZp586I021 3'  GGCCGCCGAGAGCAAGGCA    50090          CCT  CT
                                TGCCTTGCTC   GC  GCT
                                ||||||||||   ||  |||
                                ACGGAACGAG   CG  CGG
                                      AGC  C_
GAM942  EAP30    3'  AGCAGGCAGGGAGGAGGC    23381       G
                                GCCTT CTCCCTGCCTGCT
                                ||||| ||||||||||||
                                CGGAG GAGGGACGGACGA
                                  _
GAM942  FLJ10008  3'  AGCAGGCAGGGCAGCGCA    35723     CTT  _
                                TGC   GCT CCCTGCCTGCT
                                |||   ||| ||||||||||
                                ACG   CGA GGGACGGACGA
                                  ___  C
GAM942  FLJ10853  3'  TGGCAGCTCAGAAACAAGG    36772       CTCC  C_
                                CCTTG    CTG  CTGCTA
                                |||||    |||  ||||||
                                GGAAC    GAC  GACGGT
                                   AAA_  TC
GAM942  FLJ11807  3'  GGTACCCAGGGAGCAGGCA    46352       T       CC
                                TGCCT GCTCCCTG  TGCT
                                ||||| ||||||||  ||||
                                ACGGA CGAGGGAC  ATGG
                                   _       CC
GAM942  FLJ12783  3'  TGATAGCAGATTGAGGGAGGAA 48686    G     GC__     C
                                TT CTCCCT    CTGCTA CA
                                || ||||||    |||||| ||
                                AA GAGGGA    GACGAT GT
                                 G     GTTA     A
GAM942  FLJ20257  5'  AGCAGGCAGCCGGAGGGA    38991    G   __
                                TT CTCC  CTGCCTGCT
                                || ||||  |||||||||
                                AG GAGG  GACGGACGA
                                 G   CC
GAM942  FLJ20373  5'  TGGTAGCAGACAGGTGGT    35074    TC   C
                                GC  CCTG CTGCTACCA
                                ||  |||| |||||||||
                                TG  GGAC GACGATGGT
                                 GT   A
GAM942  FLJ20699  3'  GGGCAGGAAGCAGGCA      35564       T   C
                                TGCCT GCT CCTGCCT
                                ||||| ||| |||||||
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                                ACGGA CGA GGACGGG
                                  _  A
GAM942  FLJ22794  5'  TGGCAGGCAGGACAAAGCA   91615    C  CTC
                                TGC TTG  CCTGCCTGCTA
                                ||| |||  ||||||||||
                                ACG AAC  GGACGGACGGT
                                  A  A__
GAM942  FLJ23121  3'  AGCAGGCAATGCAAAAGGC   45199    __  TCCC
                                GCCT  TGC   TGCCTGCT
                                ||||  |||   ||||||||
                                CGGA  ACG   ACGGACGA
                                  AA  TA__
GAM942  FLJ25082  3'  AGCAGAGTAGGAGAGCAAGG  58329      _   _
                                CCTTGCTC CCTGC CTGCT
                                |||||||| ||||| |||||
                                GGAACGAG GGATG GACGA
                                     A    A
GAM942  FOXH1    3'  GTTGACAGGGAGCAAGG    14074         CCT
                                CCTTGCTCCCTG  GC
                                ||||||||||||  ||
                                GGAACGAGGGAC  TG
                                      AGT
GAM942  HIC2     3'  AGCAGCAGGGGCAAG      65255     T    C
                                CTTGC CCCTGC TGCT
                                ||||| |||||| ||||
                                GAACG GGGACG ACGA
                                  _    _
GAM942  HSP105B  5'  GGCAGGAGAAGCAGGCA    21820     T  _ _
                                TGCCT GCT C CCTGCC
                                ||||| ||| | ||||||
                                ACGGA CGA G GGACGG
                                  _  A A
GAM942  HT002    3'  AGACACGCAGGGAGAAGGCA  25932      G     C  _
                                TGCCTT CTCCCTGC TG CT
                                |||||| |||||||| || ||
                                ACGGAA GAGGGACG AC GA
                                  _      C  A
GAM942  KIAA0628 3'  GTAGGGGCAGGGAGAAGACA  28875   C  G      G
                                TG CTT CTCCCTGCCT CTAC
                                || ||| |||||||||| ||||
                                AC GAA GAGGGACGGG GATG
                                 A  _       _
GAM942  KIAA0716 3'  AGCAGGCGAGCAAGACA    28163   C     CCT
                                TG CTTGCTC  GCCTGCT
                                || |||||||  |||||||
                                AC GAACGAG  CGGACGA
                                 A     ___
GAM942  KIAA1239 3'  GGTAGCCCAGAGAAGGCA   71333      G  CC  CCT
                                TGCCTT CTC  TG  GCTACC
                                |||||| |||  ||  ||||||
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                                ACGGAA GAG  AC   CGATGG
                                  _  __ C__
GAM942  KIAA1300 3' GGTAGGGAAGCAGGCA     62865      T  _
                                TGCCT GCT CCCTGCC
                                ||||| ||| |||||||
                                ACGGA CGA GGGATGG
                                  _  A
GAM942  KIAA1363 3' AGTAGCTTAGGCAAGGCA    69259        CCCT  C
                                TGCCTTGCT   GC TGCT
                                |||||||||   || ||||
                                ACGGAACGG   CG ATGA
                                    ATT_ _
GAM942  KIAA1399 3' CAGAGGGAGCAGGCA      70248      T     GC
                                TGCCT GCTCCCT  CTG
                                ||||| |||||||  |||
                                ACGGA CGAGGGA  GAC
                                  _     __
GAM942  KIAA1656 3' CAGAGCCAGGGAGCAAGGCA  65781           _ _
                                TGCCTTGCTCCCTG C CTG
                                |||||||||||||| | |||
                                ACGGAACGAGGGAC G GAC
                                        C A
GAM942  KIAA1656 3' GGCAGCAGGCAGATGCA     65800     TCC       A
                                TGC   CTGCCTGCT CC
                                |||   ||||||||| ||
                                ACG   GACGGACGA GG
                                  TA_       C
GAM942  KIAA1765 5' AGTTGCAGGATGCAAGGCA   70609        TC    CT
                                TGCCTTGC  CCTGC  GCT
                                ||||||||  |||||  |||
                                ACGGAACG  GGACG  TGA
                                    TA    T_
GAM942  KIAA1853 3' AGCAGCAGGACAGGGCA     69388       CTC    C
                                TGCCTTG   CCTGC TGCT
                                |||||||   ||||| ||||
                                ACGGGAC   GGACG ACGA
                                  A__    _
GAM942  KIAA1944 5' GGTAGAGGAACATAGGCA    75565      _  C  _
                                TGCCT TG TCC CTGCC
                                ||||| || ||| |||||
                                ACGGA AC AGG GATGG
                                  T  A   A
GAM942  LHX6     3' GGGCAAAGAGCAGGCA      26858      T   CC
                                TGCCT GCTC  TGCCT
                                ||||| ||||  |||||
                                ACGGA CGAG  ACGGG
                                  _   AA
GAM942  MBLL39   3' AGGAGGAGGCAAGGCA      58604        TC   G
                                TGCCTTGC  CCT CCT
                                ||||||||  ||| |||
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                                ACGGAACG  GGA GGA
                                    GA  _
GAM942  MGC15416 3'  TGGCAGCAGGTGCAACAGCA  56545    C_   TC    C
                                TGC  TTGC  CCTGC TGCTA
                                |||  ||||  ||||| |||||
                                ACG  AACG  GGACG ACGGT
                                  AC   T_   _
GAM942  MGC5442  5'  GGTAGCGCGGCGGGCAAGGCA  48711         C   CT
                                TGCCTTGCTC CTGC  GCTACC
                                |||||||||| ||||  ||||||
                                ACGGAACGGG GGCG  CGATGG
                                      C   __
GAM942  MRAS     3'  TGGGCAGGGAGCAAGACA    24228    C
                                TG CTTGCTCCCTGCCTG
                                || ||||||||||||||
                                AC GAACGAGGGACGGGT
                                 A
GAM942  NKD2     3'  GGGCAGGGAGCAGAGCA     52419     C
                                TGC TTGCTCCCTGCCT
                                ||| ||||||||||||
                                ACG GACGAGGGACGGG
                                  A
GAM942  PHRET1   3'  GGGCAGGGAGCAAGACA     41061    C
                                TG CTTGCTCCCTGCCT
                                || ||||||||||||||
                                AC GAACGAGGGACGGG
                                 A
GAM942  PMI      3'  AGTAGAACAGGGAGCGAAGCA  13919     C        C_
                                TGC TTGCTCCCTG  CTGCT
                                ||| ||||||||||  |||||
                                ACG AGCGAGGGAC  GATGA
                                  A         AA
GAM942  PRDM15   3'  TGGCAGCAGGCAGCAGGG    61713       C    C
                                CCTTGCT CCTGC TGCTA
                                ||||||| ||||| |||||
                                GGGACGA GGACG ACGGT
                                    C    _
GAM942  RES4-22  5'  AGCAACAAGAGTAAGGCA    13516         CC  CC
                                TGCCTTGCTC  TG  TGCT
                                ||||||||||  ||  ||||
                                ACGGAATGAG  AC  ACGA
                                      A_  A_
GAM942  SYT12    3'  AGTAGGAGGAGAGCAGGCA   94723      T   _   G
                                TGCCT GCTC CCT CCTGCT
                                ||||| |||| ||| ||||||
                                ACGGA CGAG GGA GGATGA
                                   _    A   _
GAM942  LOC120087 5'  AGCAGCAGGCAGCAG       75511       C    C
                                TTGCT CCTGC TGCT
                                ||||| ||||| ||||
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                                GACGA GGACG ACGA
                                  C    _
GAM942  LOC128239 3'  TAGTCCTGCAGGGAGGAAGGCA 74724       G       CT_
                                TGCCTT CTCCCTGC   GCTA
                                |||||| ||||||||   ||||
                                ACGGAA GAGGGACG   TGAT
                                   G       TCC
GAM942  LOC131870 3'  AGCAGAAGGGCAGGGCA     75012        TC   GC
                                TGCCTTGC  CCT  CTGCT
                                |||||||||  |||  |||||
                                ACGGGACG  GGA  GACGA
                                     __   A_
GAM942  LOC143146 5'  AGCAATTGCAGAAGCAGGCA   60132      T   CC    C__
                                TGCCT GCT  CTGC   TGCT
                                ||||| |||  ||||   ||||
                                ACGGA CGA  GACG   ACGA
                                  _   A_    TTA
GAM942  LOC144893 5'  TGATAGCTGAAGGAGCCAGGCA 83190      T    CTGCCT    C
                                TGCCT GCTCC      GCTA CA
                                ||||| |||||      |||| ||
                                ACGGA CGAGG      CGAT GT
                                  C     AAGT__    A
GAM942  LOC145078 3'  TAGCAGGAGAGAGAGCAAGG   60293        C  G_
                                CCTTGCTC CT  CCTGCTA
                                |||||||| ||  |||||||
                                GGAACGAG GA  GGACGAT
                                     A  GA
GAM942  LOC146520 5'  AGCAAGCAGGCAGCCAG     77950    T   C     C
                                CT GCT CCTGC TGCT
                                || ||| ||||| ||||
                                GA CGA GGACG ACGA
                                 C   C     A
GAM942  LOC148304 5'  TGGCAGCAGGCAGGAAGCCGCA 78790     CTT   C        A
                                TGC   GCT CCTGCCTGCT CCA
                                |||   ||| |||||||||| |||
                                ACG   CGA GGACGGACGA GGT
                                  C__   A         C
GAM942  LOC149773 5'  TGGCAGCTCAGAAGCGAGGCA  79478         CC   C_
                                TGCCTTGCT  CTG  CTGCTA
                                |||||||||  |||  ||||||
                                ACGGAGCGA  GAC  GACGGT
                                     A_   TC
GAM942  LOC151174 5'  GGGCAGGGAGGAAGACA     85253    C   G
                                TG CTT CTCCCTGCCT
                                || ||| ||||||||||
                                AC GAA GAGGGACGGG
                                 A   G
GAM942  LOC151363 5'  CAGTAGGAGCAGGCA       80231       T    C   C
                                TGCCT GCTCC TGC TG
                                ||||| ||||| ||| ||
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                                ACGGA CGAGG ATG AC
                                  _    _  _
GAM942  LOC153688 3'  CAGCAAGGGGCAAGCA      86097     C      C  C
                                TGC TTGCTCC TGC TG
                                ||| ||||||| ||| ||
                                ACG AACGGGG ACG AC
                                  _      A  _
GAM942  LOC155061 3'  AGCAGAGCTGGGAGCAAAGC  81264     C       T _
                                GC TTGCTCCC GC CTGCT
                                || |||||||| || |||||
                                CG AACGAGGG CG GACGA
                                 A       T  A
GAM942  LOC157753 3'  AGCAGCAAGAGGCAAGGCA   81585          CCC  C
                                TGCCTTGCT   TGC TGCT
                                |||||||||   ||| ||||
                                ACGGAACGG   ACG ACGA
                                      AGA  _
GAM942  LOC163682 3'  TGGACGTGCAGGGAGCAGAGCA 87042     C         C _
                                TGC TTGCTCCCTGC TG CTA
                                ||| ||||||||||| || |||
                                ACG GACGAGGGACG GC GGT
                                  A         T  A
GAM942  LOC199745 3'  AGCCTCAGAGCAGAGCA     88350     C     CC  CCT
                                TGC TTGCTC  TG   GCT
                                ||| ||||||  ||   |||
                                ACG GACGAG  AC   CGA
                                  A     __  TC_
GAM942  LOC200731 3'  AGCAATTTGGGAGACCAAGGCA 90121         __     TGCC
                                TGCCTTG  CTCCC    TGCT
                                |||||||  |||||    ||||
                                ACGGAAC  GAGGG    ACGA
                                    CA    TTTA
GAM942  LOC202754 3'  TAGCAGCAGAAGCAGGCA    82709       T  CC    C
                                TGCCT GCT  CTGC TGCTA
                                ||||| |||  |||| |||||
                                ACGGA CGA  GACG ACGAT
                                   _  A_   _
GAM942  LOC219347 3'  AGGCAGCAAGCAAGGCA     92979          CC
                                TGCCTTGCT  CTGCCT
                                |||||||||  ||||||
                                ACGGAACGA  GACGGA
                                      AC
GAM942  LOC220045 5'  GGTGGCAGGAAGCAG       93412       CCCTG
                                TTGCT    CCTGCTACC
                                |||||    |||||||||
                                GACGA    GGACGGTGG
                                   A____
GAM942  LOC221608 3'  TGGCAAGTATGGAAGCAGAGGC 92188       _   _ C  C
              A                  TGCCT TGCT CC TGC TGCTA
                                |||||  |||| || ||| |||||
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                                ACGGA ACGA GG ATG ACGGT
                                   G   A T  A
GAM942  LOC222112 5'  TGGCAGCAGGCAGTGGCAGCAG 92807      T  _ _       A
          GCA                     TGCCT GCT CC CTGCCTGCT CCA
                                |||||| ||| || ||||||||| |||
                                ACGGA CGA GG GACGGACGA GGT
                                   _  C  T       C
GAM942  LOC222112 5'  TGGCAGCAGGCAGTGGCCCAGG 92808      T CT  _       A
          CA                      TGCCT G  CC CTGCCTGCT CCA
                                |||||| |  || ||||||||| |||
                                ACGGA C  GG GACGGACGA GGT
                                   _ CC  T       C
GAM942  LOC253148 5'  GGCAAGAGGAGCAAGAGCA   96878    _      _ _
                                TGC CTTGCTCC CT GCC
                                ||| |||||||| || |||
                                ACG GAACGAGG GA CGG
                                  A       A  A
GAM942  LOC256158 5'  CAGACACAGGAGCAAGACA   97650    C      C_  C
                                TG CTTGCTCC  TG CTG
                                || ||||||||  || |||
                                AC GAACGAGG  AC GAC
                                 A       AC  A
GAM942  LOC51333  3'  GGCAGAGCTCCAGTGAGCAAGG 33570          C  ___  _
          CA                      TGCCTTGCTC CT   GC CTGCT
                                |||||||||| ||   || |||||
                                ACGGAACGAG GA   CG GACGG
                                      T  CCT  A
GAM942  LOC57795  5'  AGTAAAGCGGGGAGCAAG    69321          C_
                                CTTGCTCCCTGC  TGCT
                                ||||||||||||  ||||
                                GAACGAGGGGCG  ATGA
                                       AA
GAM942  LOC86651  5'  AGCAGACATAAGCAAGGCA   68754         CCC  C
                                TGCCTTGCT   TG CTGCT
                                |||||||||   || |||||
                                ACGGAACGA   AC GACGA
                                      AT_  A
GAM942  LOC90589  3'  GTAGCCCAGGAGCAA       59106        C  CCT
                                TTGCTCC TG   GCTAC
                                ||||||| ||   |||||
                                AACGAGG AC   CGATG
                                   _  C__
GAM942  LOC90906  5'  GGCCAGGAAGCAAGGTA     64306         C   _
                                TGCCTTGCT CCTG CC
                                ||||||||| |||| ||
                                ATGGAACGA GGAC GG
                                      A   C
GAM942  LOC93082  3'  GGCAGAGAGAGGAAGGCA    56447       G  C__
                                TGCCTT CTC   CTGCC
                                |||||| |||   |||||
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                                ACGGAA GAG   GACGG
                                   G   AGA
GAM943  HHLA1    5'  CCAAGCCATCGCAACCCCTGTG 19128    G   AGA    A__    GT
              AC                    GT ACA   GTTGC   GGCT  TGG
                                    || |||   |||||   ||||  |||
                                    CA TGT   CAACG   CCGA  ACC
                                     G   CCC    CTA   __
GAM943  MYC      5'  CCAGCGGTCCGCAACCCTTGCC 10158     A    A    A
              GC                    GTG CAAG GTTGC GGCTGTTGG
                                    ||| |||| ||||| |||||||||
                                    CGC GTTC CAACG CTGGCGACC
                                      C    C    C
GAM943  FLJ14810  5'  CAACAGCGCCCTGGTCAC    51622       A  A  TGCAG
                                    GTGAC AG GT    GCTGTTG
                                    ||||| || ||    |||||||
                                    CACTG TC CG    CGACAAC
                                       G  C  _____
GAM943  FYCO1    3'  CCAGCAGCCACAACCTCAC    44490      CAA A    CA
                                    GTGA   G GTTG  GGCTGTTGG
                                    ||||   | ||||  |||||||||
                                    CACT   C CAAC  CCGACGACC
                                      ___ _   A_
GAM943  GGA2     3'  CCAACAGCCAGCCCTTGCCA   56875    A    A   GCA
                                    TG CAAG GTT   GGCTGTTGG
                                    || |||| |||   |||||||||
                                    AC GTTC CGA   CCGACAACC
                                     C    C   ___
GAM943  GGA2     3'  CCAACAGCCAGCCCTTGCCA   30461    A    A   GCA
                                    TG CAAG GTT   GGCTGTTGG
                                    || |||| |||   |||||||||
                                    AC GTTC CGA   CCGACAACC
                                     C    C   ___
GAM943  KIAA1458  3'  CCAACAGCCCAGAATTGTCAC  69003        GAG   CA
                                    GTGACAA   TTG  GGCTGTTGG
                                    |||||||   |||  |||||||||
                                    CACTGTT   GAC  CCGACAACC
                                        AA_   __
GAM943  LHX6     3'  CCTGCTACAACTCTTCCAC   26855     AC      ___
                                    GTG  AAGAGTT   GCAGG
                                    |||  |||||||   |||||
                                    CAC  TTCTCAA   CGTCC
                                      C_      CAT
GAM943  PGLYRP    3'  CCAACAGCCCCTCTGCCCTCAC 53574      CA__    TTGCA
                                    GTGA    AGAG    GGCTGTTGG
                                    ||||    ||||    |||||||||
                                    CACT    TCTC    CCGACAACC
                                      CCCG    C____
GAM943  LOC257443 3'  CCAACAGCCCAGAATTGTCAC  95847        GAG   CA
                                    GTGACAA   TTG  GGCTGTTGG
                                    |||||||   |||  |||||||||
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                                CACTGTT  GAC  CCGACAACC
                                   AA_  __
GAM944  NEUROD1  5' CAGGACCTACTAACAACA   10210    C      T  G
                                TGT GTTAGTAG TT TG
                                ||| |||||||| || ||
                                ACA CAATCATC AG AC
                                  A       C  G
GAM944  FLJ13081  3' GAGCAAACTAACAACAG    45750    C    AGTTTG
                                CTGT GTTAGT     TGCTC
                                |||| ||||||     |||||
                                GACA CAATCA     ACGAG
                                  A     A_____
GAM944  FLJ21438  3' GAGCACAACCTAACAAGC   61521    AG_  T
                                GTT   TAG TTGTGCTC
                                |||   ||| ||||||||
                                CGA   ATC AACACGAG
                                  ACA   C
GAM944  HSPC171   3' GAGCACAATGAGAAACGGCAG  26370       AGTAGT
                                CTGTCGTT     TTGTGCTC
                                ||||||||     ||||||||
                                GACGGCAA     AACACGAG
                                     AGAGT_
GAM944  KIAA1165  3' AGACTACTAATAACAG     67402     CG
                                CTGT  TTAGTAGTTT
                                ||||  ||||||||||
                                GACA  AATCATCAGA
                                  AT
GAM944  MGC16291  3' GCTCAAACCACAAACAACAG  51306     C  A A    T
                                CTGT GTT GT GTTTG GC
                                |||| ||| || ||||| ||
                                GACA CAA CA CAAAC CG
                                  A  A C    T
GAM944  PMVK     3' TGGAGCACACTCTCAAAAC   21612    AGT  TT
                                GTT   AG  TGTGCTCCA
                                |||   ||  |||||||||
                                CAA   TC  ACACGAGGT
                                  AAC  TC
GAM944  SEZ6     3' GGAGCACAAGCATCAAC     74365    A  A
                                GTT GT GTTTGTGCTCC
                                ||| || ||||||||||
                                CAA TA CGAACACGAGG
                                  C  _
GAM944  LOC134121 3' TGGAGCACAGGCATAACACAG  75155     C   GTA
                                CTGT GTTA   GTTTGTGCTCCA
                                |||| ||||   ||||||||||||
                                GACA CAAT   CGGACACGAGGT
                                  _    A__
GAM944  LOC144817 5' AGCACAAGACAAACACA     76963     C  A  AG
                                TGT GTT GT  TTTGTGCT
                                ||| ||| ||  ||||||||
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                                ACA CAA CA  GAACACGA
                                  _  A  __
GAM944  LOC149041 3'  CACCACTACTAAAAACA     79140     CG       TT
                                TGT  TTAGTAGT  GTG
                                |||  ||||||||  |||
                                ACA  AATCATCA  CAC
                                  AA       C_
GAM944  LOC51313  3'  GAAAGAGAACTACTAACAAC   33510    C         GTGC
                                GT GTTAGTAGTTT    TC
                                || ||||||||||    ||
                                CA CAATCATCAAG    AG
                                 A          AGAA
GAM945  ARHGEF6   3'  CAAACTTGAAGCCAGGC     68197       ACCA
                                GCCTGG    CAAGTTTG
                                ||||||    ||||||||
                                CGGACC    GTTCAAAC
                                    GAA_
GAM945  CNTN2     3'  GTCACAACCCAGGTGA      17411        ACCACAA  _
                                TCGCCTGG      GTT TGAC
                                ||||||||      ||| ||||
                                AGTGGACC      CAA ACTG
                                     ________  C
GAM945  CORO2A    3'  AAACTGTGGTCCAGAGA     53398    GC        A
                                TC  CTGGACCACA GTTT
                                ||  ||||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_         _
GAM945  CORO2A    3'  AAACTGTGGTCCAGAGA     12642    GC        A
                                TC  CTGGACCACA GTTT
                                ||  ||||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_         _
GAM945  GRLF1     3'  AGGTCAGAAAGTGGCCCAGG   78551      A    AAG
                                CCTGG CCAC   TTTGACCT
                                ||||| ||||   ||||||||
                                GGACC GGTG   AGACTGGA
                                   C    AA_
GAM945  LAPTM5    3'  AGGCTTGTGGTCAAGC      22199    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCGGA
                                 AA_
GAM945  POU2AF1   3'  AGATTTACAGTCCAGGC     20647        CAC
                                GCCTGGAC   AAGTTT
                                ||||||||   ||||||
                                CGGACCTG   TTTAGA
                                     ACA
GAM945  PTGS1     3'  GTCTCCTGTCTTATGGTCCAG  54574         C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
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                                GACCTGGT TTC     CTG
                                    A   TGTCCT
GAM945  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  6355        C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                    A   TGTCCT
GAM945  TRIM34   5'  AGGTCAAGTTGAGCCCAG    55224     ACCA   G
                                CTGG   CAA TTTGACCT
                                ||||   ||| ||||||||
                                GACC   GTT GAACTGGA
                                  CGA_  _
GAM945  TRIM9    5'  AGGCCAGGCAAGTCCAGGC   30749       CACAA    A
                                GCCTGGAC    GTTTG CCT
                                ||||||||    ||||| |||
                                CGGACCTG    CGGAC GGA
                                    AA___    C
GAM945  ABLIM    5'  GATATGTAACCCAGGCGG    22030       ACC   A
                                TCGCCTGG   ACA GTT
                                ||||||||   ||| |||
                                GGCGGACC   TGT TAG
                                    CAA   A
GAM945  AMOT     3'  AGGCATCTTCATGGTCCAGGGA 55716    G       C_   TT  A
                                TC CCTGGACCA  AAG  TG CCT
                                || |||||||||  |||  || |||
                                AG GGACCTGGT  TTC  AC GGA
                                 _       AC   T_ _
GAM945  DKFZp434D177 5'  TTAGACCCAGGCGA       50056        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                    ________
GAM945  DKFZp434D177 5'  TTAGACCCAGGCGA       79443        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                    ________
GAM945  FLJ23420  3'  CAAGTGGGTCCAGGC       46845         A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                    _ __
GAM945  HSA249128 5'  GGCGCGGTCCAGGCGG      34152          ACAA
                                TCGCCTGGACC    GTT
                                ||||||||||    |||
                                GGCGGACCTGG    CGG
                                      CG__
GAM945  MGC15668  5'  AGACCCGGTGGTCCAGACG   51277    C       AA_
                                CG CTGGACCAC   GTTT
                                || |||||||||   ||||
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                                GC GACCTGGTG   CAGA
                                 A        GCC
GAM945  MGC22014  3'  AGGTCCCGAGTGTAACCCAGGT 64486         ACC   AGTTT
           GA                     TCGCCTGG   ACA    GACCT
                                |||||||||   |||    |||||
                                AGTGGACC   TGT    CTGGA
                                    CAA   GAGCC
GAM945  SDCCAG10  5'  AGAGTTGTGGTCCAAAGA    19641    GCC        G
                                TC   TGGACCACAA TTT
                                ||   |||||||||| |||
                                AG   ACCTGGTGTT AGA
                                 AA_        G
GAM945  LOC115442 3'  AGGTCAGGGATGGTCCAG    72676        CAAG
                                CTGGACCA    TTTGACCT
                                ||||||||    ||||||||
                                GACCTGGT    GGACTGGA
                                    AG__
GAM945  LOC129011 5'  AGACCTGCGGTCCAGGC     74862         A  A
                                GCCTGGACC CA GTTT
                                ||||||||| || ||||
                                CGGACCTGG GT CAGA
                                    C  C
GAM945  LOC130536 5'  GCAAAGTCCAGGCG        75746         CACAAG    A
                                CGCCTGGAC     TTTG C
                                |||||||||     |||| |
                                GCGGACCTG     AAAC G
                                    _______   C
GAM945  LOC149108 3'  AGACTTCACTGTGGTCCA    84357         ____
                                TGGACCACA    AGTTT
                                |||||||||    |||||
                                ACCTGGTGT    TCAGA
                                    CACT
GAM945  LOC221688 5'  AGACTCGGGCCCAGACGA    93674     C    A  ACA
                                TCG CTGG CC   AGTTT
                                ||| |||| ||   |||||
                                AGC GACC GG   TCAGA
                                  A   C  GC_
GAM945  LOC256228 5'  AGACTTGTGGTCAAAGC     96233     CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCAGA
                                 AAA
GAM945  LOC257441 5'  TTAGACCCAGGCGA        95566         ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                    _______
GAM945  LOC91960  3'  AGGTGCCTCTCGTGGTCCAAGC 67657     C       A  TTTG
                                GC TGGACCAC AG    ACCT
                                || |||||||| ||    ||||
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                                CG ACCTGGTG TC    TGGA
                                 A       C  TCCG
GAM945  LOC92840  3'  GTCCCTCGGGTCCAGGC     56435         ACA  TTT
                                GCCTGGACC   AG   GAC
                                |||||||||   ||   |||
                                CGGACCTGG   TC   CTG
                                     GC_  C__
GAM946  ACPT      3'  AGCACCCTGCTGGCCCTC     54979    T      AGA
                                GA GGCTAGCA   TGCT
                                || ||||||||   ||||
                                CT CCGGTCGT   ACGA
                                 C       CCC
GAM946  ACPT      3'  AGCACCCTGCTGGCCCTC     54985    T      AGA
                                GA GGCTAGCA   TGCT
                                || ||||||||   ||||
                                CT CCGGTCGT   ACGA
                                 C       CCC
GAM946  COPA      5'  TGCCGTAGCCATCTTGCC     15189           __
                                GGCAAGATGGCTA  GCA
                                ||||||||||||  |||
                                CCGTTCTACCGAT  CGT
                                       GC
GAM946  DUSP4     3'  CAGCATCTCACTATGTTGCC   7336       G    CTAGCA
                                GGCAA ATGG     AGATGCTG
                                ||||| ||||     ||||||||
                                CCGTT TATC     TCTACGAC
                                   G    AC____
GAM946  DUSP4     3'  CAGCATCTCACTATGTTGCC   54055      G    CTAGCA
                                GGCAA ATGG     AGATGCTG
                                ||||| ||||     ||||||||
                                CCGTT TATC     TCTACGAC
                                   G    AC____
GAM946  EYA2      3'  CAGCATCTCCACCTGCCATCT  17884        TAGCA_
                                AGATGGC     AGATGCTG
                                |||||||     ||||||||
                                TCTACCG     TCTACGAC
                                     TCCACC
GAM946  NPR2L     3'  CAGCATCTCACCAGGAGCTTTG 21558      GAT    AGCA___
           TC                     GGCAA   GGCT      AGATGCTG
                                |||||   ||||      ||||||||
                                CTGTT   TCGA      TCTACGAC
                                   ___    GGACCAC
GAM946  SMAC      5'  CATGTTGCCAGCCATGTTGCC  57207      G     A    G
                                GGCAA ATGGCT GCAA ATG
                                ||||| |||||| |||| |||
                                CCGTT TACCGA CGTT TAC
                                   G     C    G
GAM946  C6orf28   5'  AGCACCCTGCTGTCTTCC     40992    C      T  CAAGA
                                GG AAGATGGC AG     TGCT
                                || |||||||| ||     ||||
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                                CC TTCTGTCG TC    ACGA
                                 _      _ CC___
GAM946  DKFZp547I094 5'  AGCATCTTCCCATCCTCC    49630    CAA    CTAGC
                                GG  GATGG    AAGATGCT
                                ||  |||||    ||||||||
                                CC  CTACC    TTCTACGA
                                 TC_    C____
GAM946  EBF2     3'  CAGCATCTTACTTGGTC     42644      _ C
                                GGCTA G AAGATGCTG
                                ||||| | |||||||||
                                CTGGT C TTCTACGAC
                                   T A
GAM946  FLJ10008  5'  CAGCATCTTATCTCACCCTGC  35725    AGAT  CT  C_
                                GCA   GG  AG  AAGATGCTG
                                |||   ||  ||  |||||||||
                                CGT   CC  TC  TTCTACGAC
                                  C___  AC  TA
GAM946  FLJ13102  3'  CAGCATCTCACCCTGTCCTGGC 46004   G  A    CTAGCA
                                G CA GATGG     AGATGCTG
                                | || |||||     ||||||||
                                C GT CTGTC     TCTACGAC
                                 G  C    CCAC__
GAM946  KIAA0445  5'  CAGCATCTCGCCACCCTGCC   27950     AGA   TAGCA
                                GGCA   TGGC    AGATGCTG
                                ||||   ||||    ||||||||
                                CCGT   ACCG    TCTACGAC
                                  CCC    C____
GAM946  MLL4     3'  CGTCGCTGCCATCTTGCC    28286          T   AA
                                GGCAAGATGGC AGC  GATG
                                |||||||||||  |||  ||||
                                CCGTTCTACCG TCG  CTGC
                                       _  __
GAM946  VIAAT    5'  CAGACCTGCTGCCATCTTGCC  54538          T    A ATG
                                GGCAAGATGGC AGCA G   CTG
                                |||||||||||  ||||  |   |||
                                CCGTTCTACCG TCGT C   GAC
                                       _   _ CA_
GAM946  WDR7     3'  CAGCATTTTTAGCCATCTCAAC 30957    CA_       GC
             C                   GG   AGATGGCTA  AAGATGCTG
                                ||   |||||||||  |||||||||
                                CC   TCTACCGAT  TTTTACGAC
                                 AAC        __
GAM946  YKT6     3'  CAGCACCCCACCTATGGTCTTG 21599        GGC   CAAGA_
             CC                   GGCAAGAT   TAG     TGCTG
                                ||||||||   |||     |||||
                                CCGTTCTG   ATC     ACGAC
                                    GT_   CACCCC
GAM946  LOC118668 5'  AGCATCTCACCATCCTCC    75478    CAA    CTAGCA
                                GG   GATGG     AGATGCT
                                ||   |||||     |||||||
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                                CC   CTACC     TCTACGA
                                 TC_     AC____
GAM946   LOC120224 3'  CAGCATCCTGTGTATCTTGC   57093        G TA   A
                                GCAAGATG C  GCA GATGCTG
                                |||||||| |  ||| |||||||
                                CGTTCTAT G  TGT CTACGAC
                                    _ __   C
GAM946   LOC146177 3'  GCACCTCCATCTTGC       77693         CTAGCA  A
                                GCAAGATGG     AG TGC
                                |||||||||     || |||
                                CGTTCTACC     TC ACG
                                      _______ C
GAM946   LOC149301 3'  CGGCTGCCAGCCATCTGGCC   79250     A       A   AGAT
                                GGC AGATGGCT GCA    GCTG
                                ||| |||||||| |||    ||||
                                CCG TCTACCGA CGT    CGGC
                                  G       C  _____
GAM946   LOC149579 5'  CAGCATCTCGCCACCCTGCC   71130     AGA    TAGCA
                                GGCA   TGGC    AGATGCTG
                                ||||   ||||    ||||||||
                                CCGT   ACCG    TCTACGAC
                                  CCC    C____
GAM946   LOC149707 5'  AGCATAGAGCCATCTTCC     79484    C       AGCAAG
                                GG AAGATGGCT     ATGCT
                                || |||||||||     |||||
                                CC TTCTACCGA     TACGA
                                 _       GA____
GAM946   LOC151475 5'  CATCTCAGGCCTGACCTTGACC 85398    _   AT__    AGCA
                                GG CAAG    GGCT    AGATG
                                || ||||    ||||    |||||
                                CC GTTC    CCGG    TCTAC
                                 A    CAGT    AC__
GAM946   LOC200227 5'  AGCATAGAGCCATCTTCC     88641    C       AGCAAG
                                GG AAGATGGCT     ATGCT
                                || |||||||||     |||||
                                CC TTCTACCGA     TACGA
                                 _       GA____
GAM946   LOC220692 5'  CAGCATCTTACTTGGCTTGGC  91219    AAGAT    _ C
                                GC     GGCTA G AAGATGCTG
                                ||     ||||| | |||||||||
                                CG     TCGGT C TTCTACGAC
                                 GT___     T A
GAM946   LOC256568 5'  AGCACCTGCCATCTTGCC     94841          TAGCA  A
                                GGCAAGATGGC     AG TGCT
                                ||||||||||     || ||||
                                CCGTTCTACCG     TC ACGA
                                      _____ C
GAM947   ADH1B     3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
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                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM947  AHR     3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM947  FDFT1   3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM947  JTB     3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM947  KLF4    3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM947  PHYH    3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM947  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                       T__    _
GAM947  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM947  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_    CG_
GAM947  CG012   5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM947  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
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                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM947  FLJ23462  3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
            G                     CATTTC        GTCTGAGAT
                                  ||||||        |||||||||
                                  GTAAAG        CAGACTCTA
                                     AAACATTT_
GAM947  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                  CATTTCA   TCACTGTCTGAGAT
                                  |||||||   ||||||||||||||
                                  GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM947  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                  TTCA TTTCACTG  TGAG
                                  |||| ||||||||  ||||
                                  AAGT AAAGTGAC  GTTT
                                    A       CT
GAM947  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                  TTTC CTG TCTGAGAT
                                  |||| ||| ||||||||
                                  AAAG GAC AGACTCTA
                                    _  G
GAM947  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                  ATT CACTTTCACTGT
                                  ||| ||||||||||||
                                  TAA GTGAAAGTGACG
                                   C
GAM947  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                  TTCACTTT  CT TCTGAGAT
                                  ||||||||  || ||||||||
                                  AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM947  PP35      3'  ATCTCAGACTGAAA       22814      CT
                                  TTTCA  GTCTGAGAT
                                  |||||  |||||||||
                                  AAAGT  CAGACTCTA
                                     __
GAM947  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148         TCAC  C_
                                  CATTTCACTT    TGT  TGAG
                                  ||||||||||    |||  ||||
                                  GTAAAGTGAA    ACG  ACTC
                                     TA__   TT
GAM947  SEP15     3'  TCCTACAGTAAGAGTGAAA    14934        C    CT
                                  TTTCACTTT ACTGT  GA
                                  ||||||||| |||||  ||
                                  AAAGTGAGA TGACA  CT
                                     A    TC
GAM947  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                  TTTCACTTT    TCTGAG
                                  |||||||||    ||||||
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                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM947  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM947  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM947  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM947  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM948  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM948  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM948  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM948  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                ||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM948  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM948  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
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                                TAAAGTGAAA TGACA
                                      A
GAM948  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                       T__   _
GAM948  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM948  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_   CG_
GAM948  CG012   5'  CTCACTCTGAAAGTGAA     83218          CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                       CT  __
GAM948  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                      G  TC
GAM948  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                    CATTTC        GTCTGAGAT
                                ||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM948  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM948  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                   A       CT
GAM948  KLHL6   3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                   _  G
GAM948  NIR3    3'  GCAGTGAAAGTGCAAT      66242      T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
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                                TAA GTGAAAGTGACG
                                  C
GAM948  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM948  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM948  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148         TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__    TT
GAM948  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A     TC
GAM948  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                      AAAGG
GAM948  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC       CTGTCTGAGAT
                                ||||       ||||||||||||
                                AAAG       GACAGACTCTA
                                  GTTTGCC
GAM948  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT      GT TGAGAT
                                |||||||      || ||||||
                                AAAGTGA      CA ACTCTA
                                     TTTCC_  A
GAM948  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM948  LOC222134 5'  ACAGTGAAGTGAAATG       94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM949  BCL3     3'  CCCCTCTTCTGAGCACAGA    17734     A  CA       CTTT
                                TC TG  CTCAGAAG    GG
                                || ||  ||||||||    ||
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                                AG AC  GAGTCTTC    CC
                                 _ AC       TCC_
GAM949  BUB3     3'  CTTCTTAAGTGCATGA      16369          C_
                                TCATGCACT  AGAAG
                                |||||||||  |||||
                                AGTACGTGA  TCTTC
                                     AT
GAM949  CHC1     5'  CATCCAAAAGAGGAGTCCATGA 7021        C    AGAAGC
                                TCATG ACTC     TTTGGATG
                                ||||| ||||     ||||||||
                                AGTAC TGAG     AAACCTAC
                                   C    GAGA__
GAM949  PLS3     3'  CATGCTCCCAGGTGCATGA    17271         CAGA   TT
                                TCATGCACT    AGC  TG
                                |||||||||    |||  ||
                                AGTACGTGG    TCG  AC
                                     ACCC   T_
GAM949  TTC3     3'  CATCCAGCCGTGCTGAGCACA  12417    CA    AAGCT
                                TG  CTCAG    TTGGATG
                                ||  |||||    |||||||
                                AC  GAGTC    GACCTAC
                                 AC    GTGCC
GAM949  EDG2     5'  CATCCACCTATCTGAGTACCTG 54064     TGC      _ CTT
           A                     TCA   ACTCAGA AG   TGGATG
                                |||   ||||||| ||   ||||||
                                AGT   TGAGTCT TC   ACCTAC
                                  CCA      A  C__
GAM949  FLJ13154 3'  ATCCTCCCTGAGTGCTGA    44790     T      AAGCTTT
                                TCA GCACTCAG      GGAT
                                ||| ||||||||      ||||
                                AGT CGTGAGTC      CCTA
                                  _      CCT_____
GAM949  HSA277841 5'  CATCCAGGACTGAGTGTATGA  37657           AAGC
                                TCATGCACTCAG    TTTGGATG
                                ||||||||||||    ||||||||
                                AGTATGTGAGTC    GGACCTAC
                                       A___
GAM949  KIAA1729 3'  CCGTTTTCTGAGTACAT     89127     C       CTT
                                ATG ACTCAGAAG   TGG
                                ||| |||||||||   |||
                                TAC TGAGTCTTT   GCC
                                  A       T__
GAM949  NYD-SP11 5'  GGAGCTCCTGAGTGCA      49213         A
                                TGCACTCAG AGCTTT
                                ||||||||| ||||||
                                ACGTGAGTC TCGAGG
                                     C
GAM949  WAC      3'  CATCCAAAACTAATCAATGCTG 55187     T   CTCAGA  C
           A                     TCA GCA     AG TTTGGATG
                                ||| |||      || ||||||||
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                                AGT CGT     TC AAACCTAC
                                  _  AACTAA  A
GAM949  WAC      3'  CATCCAAAACTAATCAATGCTG 55193     T   CTCAGA  C
              A                   TCA GCA     AG TTTGGATG
                                  ||| |||     || ||||||||
                                AGT CGT     TC AAACCTAC
                                  _  AACTAA  A
GAM949  WAC      3'  CATCCAAAACTAATCAATGCTG 33553     T   CTCAGA  C
              A                   TCA GCA     AG TTTGGATG
                                  ||| |||     || ||||||||
                                AGT CGT     TC AAACCTAC
                                  _  AACTAA  A
GAM949  LOC145438 3'  CATCCAAAGATGAATATATGA  83335      CAC   GAAG
                                TCATG   TCA   CTTTGGATG
                                |||||   |||   |||||||||
                                AGTAT   AGT   GAAACCTAC
                                   ATA   A___
GAM949  LOC155434 3'  CTAACTTCTGAGGTGCAT    86404       _     CT
                                ATGCAC TCAGAAG  TTGG
                                |||||| |||||||  ||||
                                TACGTG AGTCTTC  AATC
                                   G     __
GAM949  LOC255299 5'  CACTGGCCTCTGAGTGCAGA   97465    A       A   T_
                                TC TGCACTCAGA GCT  TG
                                || ||||||||||  |||  ||
                                AG ACGTGAGTCT CGG  AC
                                 _       C   TC
GAM949  LOC256476 5'  CCCAGGCTGGAGTGCATGA   96818         AGA    T
                                TCATGCACTC   AGCTT GG
                                ||||||||||   ||||| ||
                                AGTACGTGAG   TCGGA CC
                                      G__    C
GAM949  LOC57826  3'  ATCTATTTAAGTGCAT      41013        C   AGCTT
                                ATGCACT AGA    TGGAT
                                ||||||| |||    |||||
                                TACGTGA TTT    ATCTA
                                   A  _____
GAM949  LOC63928  3'  CATCCAAAGCCCCCATGGACGC 42032     AC   GAA__
              A                   TGC  TCA    GCTTTGGATG
                                  |||  |||    ||||||||||
                                ACG  GGT    CGAAACCTAC
                                  CA   ACCCC
GAM949  LOC90591  3'  CAACTTCTGGTGCATGA     63415        T     CT
                                TCATGCAC CAGAAG  TTG
                                |||||||| ||||||  |||
                                AGTACGTG GTCTTC  AAC
                                      _    __
GAM949  LOC91151  5'  AGCTTTCTGAGTGCAT      52615          _
                                ATGCACTCAGAA GCT
                                |||||||||||| |||
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                                TACGTGAGTCTT CGA
                                       T
GAM950  GLRB     3'  TTGTAATAAAACTGTGGCAC  5881       ACTGTG     C
                                GTGC     TAGTTT ATTACAA
                                ||||     ||||||| |||||||
                                CACG     GTCAAA TAATGTT
                                  GT____     A
GAM950  MATN2    3'  AATGAACGCAGTGCA       9929           AGTT
                                TGCACTGTGT    TCATT
                                ||||||||||    |||||
                                ACGTGACGCA    AGTAA
                                      _____
GAM950  MTMR8    3'  TTGTAATAAAACTGAGTTGTAC 31301       CTGTG     C
                                GTGCA     TAGTTT ATTACAA
                                |||||     ||||||| |||||||
                                CATGT     GTCAAA TAATGTT
                                   TGA__     A
GAM950  SRGAP1   3'  TGTAATGAAGGCAACAC     72267      A _
                                GTGT GT TTCATTACA
                                |||| || |||||||||
                                CACA CG AAGTAATGT
                                  A  G
GAM950  TBR1     3'  TGTAATGAAACTCTTCAC    21685     T__
                                GTG   AGTTTCATTACA
                                |||   ||||||||||||
                                CAC   TCAAAGTAATGT
                                  TTC
GAM950  ANKRD6   3'  TAATGAAATATAAACACAG   30089       A___
                                CTGTGT    GTTTCATTA
                                ||||||    |||||||||
                                GACACA    TAAAGTAAT
                                   AATA
GAM950  BIRC8    5'  TGTACTACACAGGCAC      52906      A       TT
                                GTGC CTGTGTAGT  CA
                                |||| |||||||||  ||
                                CACG GACACATCA  GT
                                  _       T_
GAM950  CLDN15   3'  ATGGCGCACACACACAGTGCAC 56559           A___  T
                                GTGCACTGTGT    GT TCAT
                                ||||||||||    || ||||
                                CACGTGACACA    CG GGTA
                                       CACA  C
GAM950  DKFZP564K0822 3'  TGTAATGAAAAAGCACA     94050       AG
                                TGTGT  TTTCATTACA
                                |||||  ||||||||||
                                ACACG  AAAGTAATGT
                                   AA
GAM950  DKFZP564O0423 5'  ATGGGCACCAACAGTGCAC    91680          GTA  _
                                GTGCACTGT   GT TTCAT
                                |||||||||   || |||||
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                                CACGTGACA   CA GGGTA
                                     AC_  C
GAM950  FLJ20171  3'  ATGAACTACACAGCGTAC    34676      A        T
                                GTGC CTGTGTAGTT CAT
                                |||| |||||||||| |||
                                CATG GACACATCAA GTA
                                  C        _
GAM950  FLJ21870  3'  TGTAATGAAACTACATTGTAT  43468       CT
                                GTGCA  GTGTAGTTTCATTACA
                                |||||  ||||||||||||||||
                                TATGT  TACATCAAAGTAATGT
                                   __
GAM950  KIAA0321  3'  TGTAATGAAACTACTAG     62399     T
                                CTG GTAGTTTCATTACA
                                ||| ||||||||||||||
                                GAT CATCAAAGTAATGT
                                  _
GAM950  KIAA0493  3'  GTAATGACACGTACAC      64279       _  T
                                GTGTA GT TCATTAC
                                ||||| || |||||||
                                CACAT CA AGTAATG
                                   G  C
GAM950  KIAA0970  3'  TAATGAAACTATCTACA     29966     __
                                TGT  GTAGTTTCATTA
                                |||  ||||||||||||
                                ACA  TATCAAAGTAAT
                                  TC
GAM950  PRO1580   5'  GAAAAGCACATTGCAC      37532       C    AG
                                GTGCA TGTGT  TTTC
                                ||||| |||||  ||||
                                CACGT ACACG  AAAG
                                   T    A_
GAM950  LOC118851 5'  TGTAACATTACCTCCACACAAC 75507       C_    A___  TTCA
           TGCAC                   GTGCA  TGTGT    GT    TTACA
                                |||||  |||||   ||   |||||
                                CACGT  ACACA    CA    AATGT
                                   CA    CCTC  TTAC
GAM950  LOC253573 3'  TGTAATGAGATAGCACAATGCA 97053      C    A
                                TGCA TGTGT GTTTCATTACA
                                |||| ||||| ||||||||||
                                ACGT ACACG TAGAGTAATGT
                                  A    A
GAM951  ASH1      3'  AAGCACTTGTAACTGCTGC   37497       TTG
                                GCAGCA   TACAGGTGCTT
                                ||||||   ||||||||||
                                CGTCGT   ATGTTCACGAA
                                   CA_
GAM951  CASP3     3'  AGGTGCTACAATGCCCCT    52192    CA     ACA  TG
                                AG  GCATTGT   GG  CTT
                                ||  |||||||   ||  |||
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                                TC  CGTAACA   TC  GGA
                                 CC       ___  GT
GAM951  CASP3    3'  AGGTGCTACAATGCCCCT    15096    CA      ACA  TG
                                AG  GCATTGT   GG  CTT
                                ||  |||||||   ||  |||
                                TC  CGTAACA   TC  GGA
                                 CC       ___  GT
GAM951  CDC25A   5'  AGCACCCGTGCCTGT       8363      CATT    A
                                GCAG    GTAC GGTGCT
                                ||||    |||| ||||||
                                TGTC    CGTG CCACGA
                                  ____    C
GAM951  CFTR     3'  CATATATTACAATGCTGT     4928           CAG_
                                GCAGCATTGTA    GTG
                                ||||||||||    |||
                                TGTCGTAACAT    TAC
                                      TATA
GAM951  COL14A1  5'  ATGTGTACAATGTTGC      69077           G
                                GCAGCATTGTACA GT
                                |||||||||||| ||
                                CGTTGTAACATGT TA
                                       G
GAM951  COLQ     3'  ACCGGCTACAATGCTCT     19047    C       CA_
                                AG AGCATTGTA   GGT
                                || |||||||||   |||
                                TC TCGTAACAT   CCA
                                 _       CGG
GAM951  COLQ     3'  ACCGGCTACAATGCTCT     54494    C       CA_
                                AG AGCATTGTA   GGT
                                || |||||||||   |||
                                TC TCGTAACAT   CCA
                                 _       CGG
GAM951  COLQ     3'  ACCGGCTACAATGCTCT     54482    C       CA_
                                AG AGCATTGTA   GGT
                                || |||||||||   |||
                                TC TCGTAACAT   CCA
                                 _       CGG
GAM951  COLQ     3'  ACCGGCTACAATGCTCT     54470    C       CA_
                                AG AGCATTGTA   GGT
                                || |||||||||   |||
                                TC TCGTAACAT   CCA
                                 _       CGG
GAM951  COLQ     3'  ACCGGCTACAATGCTCT     54476    C       CA_
                                AG AGCATTGTA   GGT
                                || |||||||||   |||
                                TC TCGTAACAT   CCA
                                 _       CGG
GAM951  COLQ     3'  ACCGGCTACAATGCTCT     54488    C       CA_
                                AG AGCATTGTA   GGT
                                || |||||||||   |||
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                                TC TCGTAACAT   CCA
                                 _       CGG
GAM951  CYP7A1   3'  TGCCTGTGTACAACAATGCT  5764        _____
                                AGCATTGT    ACAGGTG
                                ||||||||    |||||||
                                TCGTAACA    TGTCCGT
                                    ACATG
GAM951  DDX11    5'  AGCGTAGCAATGCTGC     15298         ACAGG
                                GCAGCATTGT    TGCT
                                ||||||||||    ||||
                                CGTCGTAACG    GCGA
                                      AT___
GAM951  DGKA     3'  AGGCTCTGTACATTGCTGC   7200       T      T
                                GCAGCA TGTACAGG GCTT
                                |||||| |||||||| ||||
                                CGTCGT ACATGTCT CGGA
                                   T      _
GAM951  HAT1     3'  TCTGTACAATGTGCT      13318     G
                                AGCA CATTGTACAGG
                                |||| ||||||||||
                                TCGT GTAACATGTCT
                                  _
GAM951  HNF3B    3'  AAGCACCTGCAGATTCTG    41413     C   GTA
                                CAG ATT   CAGGTGCTT
                                ||| |||   |||||||||
                                GTC TAG   GTCCACGAA
                                  T   AC_
GAM951  IFNAR2   3'  AAGCACCTACAGGGTTCT    6035     C   A    AC
                                AG AGC TTGT  AGGTGCTT
                                || ||| ||||  ||||||||
                                TC TTG GACA  TCCACGAA
                                 _   G   __
GAM951  IL1RN    3'  AAGCACCTAGCCTCGCTCT   5140     C   ATT  AC
                                AG AGC   GT  AGGTGCTT
                                || |||   ||  ||||||||
                                TC TCG   CG  TCCACGAA
                                 _   CTC  A_
GAM951  ITPR1    3'  AAGCACCTGATTTGC       9441      TT  A
                                GCA  GT CAGGTGCTT
                                |||  || |||||||||
                                CGT  TA GTCCACGAA
                                  T_  _
GAM951  JJAZ1    3'  AGGATCAATGCTGCT       31074          TACAG  G
                                AGCAGCATTG    GT CT
                                ||||||||||    || ||
                                TCGTCGTAAC    TA GA
                                      _____  G
GAM951  KCNN4    3'  CACTCTCACTATGCTGCT    9566         T  ACA
                                AGCAGCAT GT   GGTG
                                |||||||| ||   ||||
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                                TCGTCGTA CA   TCAC
                                    T  CTC
GAM951  MADD    3'  AGTGCACGATGCTGCT     55336          ACAG TG
                                AGCAGCATTGT   G  CT
                                ||||||||||    |  ||
                                TCGTCGTAGCA   C  GA
                                      ____ GT
GAM951  MADD    3'  AGTGCACGATGCTGCT     55341          ACAG TG
                                AGCAGCATTGT   G  CT
                                ||||||||||    |  ||
                                TCGTCGTAGCA   C  GA
                                      ____ GT
GAM951  MADD    3'  AGTGCACGATGCTGCT     55346          ACAG TG
                                AGCAGCATTGT   G  CT
                                ||||||||||    |  ||
                                TCGTCGTAGCA   C  GA
                                      ____ GT
GAM951  MADD    3'  AGTGCACGATGCTGCT     55329          ACAG TG
                                AGCAGCATTGT   G  CT
                                ||||||||||    |  ||
                                TCGTCGTAGCA   C  GA
                                      ____ GT
GAM951  MADD    3'  AGTGCACGATGCTGCT     13461          ACAG TG
                                AGCAGCATTGT   G  CT
                                ||||||||||    |  ||
                                TCGTCGTAGCA   C  GA
                                      ____ GT
GAM951  MADD    3'  AGTGCACGATGCTGCT     55352          ACAG TG
                                AGCAGCATTGT   G  CT
                                ||||||||||    |  ||
                                TCGTCGTAGCA   C  GA
                                      ____ GT
GAM951  MAT1A   3'  AAGCACCTGTAATGTGC     90824      TG
                                GCAT  TACAGGTGCTT
                                ||||  ||||||||||
                                CGTG  ATGTCCACGAA
                                  TA
GAM951  MGAT5   3'  AGCCCTGCACCATGCTGCT   10021        T  A   T
                                AGCAGCAT GT CAGG GCT
                                |||||||| || |||| |||
                                TCGTCGTA CA GTCC CGA
                                    C  C   _
GAM951  MME     3'  ATGTGTCCAATGCTGC      23505         T   G
                                GCAGCATTG ACA GT
                                ||||||||| ||| ||
                                CGTCGTAAC TGT TA
                                     C   G
GAM951  MME     3'  ATGTGTCCAATGCTGC      23495         T   G
                                GCAGCATTG ACA GT
                                ||||||||| ||| ||
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                                CGTCGTAAC TGT TA
                                     C   G
GAM951  MME     3'  ATGTGTCCAATGCTGC     23485        T   G
                                GCAGCATTG ACA GT
                                ||||||||| ||| ||
                                CGTCGTAAC TGT TA
                                     C   G
GAM951  MME     3'  ATGTGTCCAATGCTGC     6138         T   G
                                GCAGCATTG ACA GT
                                ||||||||| ||| ||
                                CGTCGTAAC TGT TA
                                     C   G
GAM951  NOTCH2  3'  TTTGTAAATGCTGCT      44318        G
                                AGCAGCATT TACAGG
                                ||||||||| ||||||
                                TCGTCGTAA ATGTTT
                                          _
GAM951  OLR1    3'  AAGTGTCACAATGCTCCT    10334    C      ACA  TG
                                AG AGCATTGT   GG  CTT
                                || ||||||||   ||  |||
                                TC TCGTAACA   CT  GAA
                                 C       ___  GT
GAM951  PKHD1   5'  AAGCACAAAAGCTATGCTGCT 56911        T  ACAG
                                AGCAGCAT GT    GTGCTT
                                |||||||| ||    ||||||
                                TCGTCGTA CG    CACGAA
                                     T  AAAA
GAM951  POP2    3'  AAGCACCTAGCACATGCCGT  42143    A   _   AC
                                GC GCAT TGT  AGGTGCTT
                                || |||| |||  ||||||||
                                TG CGTA ACG  TCCACGAA
                                 C   C  A_
GAM951  RUNX3   3'  AAGCACCTACAGACCGGCT   15107    AGCA    AC
                                AGC    TTGT  AGGTGCTT
                                |||    ||||  ||||||||
                                TCG    GACA  TCCACGAA
                                  GCCA   __
GAM951  SH3BP2  3'  CACACAATGCTGCT       11594         ACAG
                                AGCAGCATTGT    GTG
                                ||||||||||    |||
                                TCGTCGTAACA    CAC
                                          ____
GAM951  SLC1A3  3'  AAGCACCTGCCCTCTGTT    14796      CATTGTA
                                AGCAG      CAGGTGCTT
                                |||||      |||||||||
                                TTGTC      GTCCACGAA
                                   TCCC___
GAM951  SLC20A2 3'  ACTATGGAAATGCTGCT     22174        GTA  _
                                AGCAGCATT   CA GGT
                                |||||||||   || |||
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                                TCGTCGTAA  GT TCA
                                     AG_  A
GAM951  SRM     3'  AAGCCCCAGAATGCTGC    11955       GTACA  T
                                GCAGCATT   GG GCTT
                                ||||||||   || ||||
                                CGTCGTAA   CC CGAA
                                    GAC__  _
GAM951  SUOX    5'  AGGTCTGCTACAATGCTGCT  4851          _  GT
                                AGCAGCATTGTA CAG  GCTT
                                |||||||||||| |||  ||||
                                TCGTCGTAACAT GTC  TGGA
                                      C  __
GAM951  TJP1    3'  ATTTGTGATACAATGCTGT   12295         ___
                                GCAGCATTGT  ACAGGT
                                ||||||||||  ||||||
                                TGTCGTAACA  TGTTTA
                                      TAG
GAM951  UTY     3'  AAGCAACTGGACACAGTGCTGC 23066         A__  G
                                GCAGCATTGT  CAG TGCTT
                                ||||||||||  ||| |||||
                                CGTCGTGACA  GTC ACGAA
                                     CAG  A
GAM951  WNT7A   3'  CACCCAATGCTGCT      16119         TACA
                                AGCAGCATTG   GGTG
                                ||||||||||   ||||
                                TCGTCGTAAC   CCAC
                                     _____
GAM951  AKAP11  3'  ATTTGCCAATGCTGC      32701         TA
                                GCAGCATTG  CAGGT
                                |||||||||  |||||
                                CGTCGTAAC  GTTTA
                                     C_
GAM951  ANKRD6  3'  TTGTAATAAAATGCTGCT   30093        G___
                                AGCAGCATT   TACAG
                                |||||||||   |||||
                                TCGTCGTAA   ATGTT
                                     AATA
GAM951  C1orf19 3'  ACTTGTCAACACTGCT     68187      CA  T
                                AGCAG  TTG ACAGGT
                                |||||  ||| ||||||
                                TCGTC  AAC TGTTCA
                                   AC  _
GAM951  CDC14B  3'  AAGCACCTGCCAGCACCGC  52841    AT  A__
                                GC  TGT  CAGGTGCTT
                                ||  |||  |||||||||
                                CG  ACG  GTCCACGAA
                                 CC  ACC
GAM951  D15Wsu75e 3'  TGTAGACAATGCTGCT    66650         __
                                AGCAGCATTGT  ACA
                                ||||||||||  |||
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                                TCGTCGTAACA  TGT
                                      GA
GAM951  EDG2     3'  AGCAAACAATGCTCT      7378     C      ACAGG
                                AG AGCATTGT    TGCT
                                || ||||||||    ||||
                                TC TCGTAACA    ACGA
                                 _      A____
GAM951  EDG2     3'  AGCAAACAATGCTCT      54061    C      ACAGG
                                AG AGCATTGT    TGCT
                                || ||||||||    ||||
                                TC TCGTAACA    ACGA
                                 _      A____
GAM951  EPHA7    3'  GCATAGAATGCTGCT      15434        G ACAG
                                AGCAGCATT T   GTGC
                                ||||||||| |   ||||
                                TCGTCGTAA A   TACG
                                      G ____
GAM951  FADS1    3'  AAGCACCTGAACCACTGT    25468     CATT  A
                                GCAG   GT CAGGTGCTT
                                ||||   || |||||||||
                                TGTC   CA GTCCACGAA
                                  AC__  A
GAM951  FLJ10246 3'  TGCCACAATGCTGCT      35944         ACA
                                AGCAGCATTGT   GGTG
                                ||||||||||   ||||
                                TCGTCGTAACA   CCGT
                                       ___
GAM951  FLJ10307 3'  AGCTAACGATGCTGCT     36004         ACAGGT
                                AGCAGCATTGT    GCT
                                ||||||||||     |||
                                TCGTCGTAGCA    CGA
                                      AT____
GAM951  FLJ11155 5'  AAGCACCTGCCTCAGCTG   37116     AT  TA_
                                CAGC  TG   CAGGTGCTT
                                ||||  ||   |||||||||
                                GTCG  AC   GTCCACGAA
                                  __  TCC
GAM951  FLJ13848 3'  AAGCACCTAACAGCT      45457    AT   AC
                                AGC  TGT  AGGTGCTT
                                |||  |||  ||||||||
                                TCG  ACA  TCCACGAA
                                 __   A_
GAM951  FLJ20128 3'  AAGCACCTCAGCGCACTTGC  34595     CAT   AC
                                GCAG   TGT  AGGTGCTT
                                ||||   |||  ||||||||
                                CGTT   GCG  TCCACGAA
                                  CAC   AC
GAM951  FLJ20281 5'  AAGCACCTTGAGTTACTGGCT 90976    ATT  _ ___
                                AGC   GTA C   AGGTGCTT
                                |||   ||| |   ||||||||
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                                TCG   CAT G   TCCACGAA
                                  GT_   T AGT
GAM951   FLJ20716  3'  AAGTGTTACAATGCCGCT    35598     A       CAG TG
                                AGC GCATTGTA   G  CTT
                                ||| ||||||||   |  |||
                                TCG CGTAACAT   T  GAA
                                  C       ___ GT
GAM951   FLJ21709  3'  AAGCACCTAGAGCAGCTCT    77917    C   AT   AC_
                                AG AGC  TGT   AGGTGCTT
                                || |||  |||   ||||||||
                                TC TCG  ACG   TCCACGAA
                                 _  __  AGA
GAM951   FLJ22626  3'  GCTTTACAGTGCTACT      44553    C       C
                                AG AGCATTGTA AGGT
                                || ||||||||| ||||
                                TC TCGTGACAT TTCG
                                 A       _
GAM951   FLJ23056  3'  ACCACAATGCTGCT        44720          ACA
                                AGCAGCATTGT   GGT
                                ||||||||||   |||
                                TCGTCGTAACA   CCA
                                          ___
GAM951   HEF1      3'  AAGCACCTTCTAATGCTGC    21134         TAC
                                GCAGCATTG   AGGTGCTT
                                |||||||||   ||||||||
                                CGTCGTAAT   TCCACGAA
                                     CT_
GAM951   HEMK      3'  AAGCTCCAACACAAATGCTGC  32423         _  ACA  T
                                GCAGCATT GT   GG GCTT
                                |||||||| ||   || ||||
                                CGTCGTAA CA   CC CGAA
                                    A  CAA  T
GAM951   HRH3      3'  AAGCACCTGGGTGTGCT      23363       TGTA
                                AGCAT    CAGGTGCTT
                                |||||    |||||||||
                                TCGTG    GTCCACGAA
                                   TGG_
GAM951   HSA243666 3'  AGTCCCACTCAATGCTGCT    34145          TACA  TG
                                AGCAGCATTG    GG  CT
                                ||||||||||    ||  ||
                                TCGTCGTAAC    CC  GA
                                     TCA_  CT
GAM951   IMAGE:4907098 5'  AAGCACCTGCACTTGCT     91655      TT  A
                                AGCA  GT CAGGTGCTT
                                ||||  || |||||||||
                                TCGT  CA GTCCACGAA
                                  T_  C
GAM951   KCNMB2    5'  ACCTTGGTATAAATGCTGCT   19538          _    __
                                AGCAGCATT GTAC  AGGT
                                ||||||||| ||||  ||||
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                                TCGTCGTAA TATG  TCCA
                                     A    GT
GAM951  KIAA0276 3' AAGCACACAGACAGTGCTACT 70960    C       ACAG
                                AG AGCATTGT    GTGCTT
                                || ||||||||    ||||||
                                TC TCGTGACA    CACGAA
                                 A       GACA
GAM951  KIAA0472 5' AGATCTTAAATGCTGC      71852        GTAC    G
                                GCAGCATT    AGGT CT
                                ||||||||    |||| ||
                                CGTCGTAA    TCTA GA
                                     AT__    _
GAM951  KIAA0513 3' AGCAAACAGTGCTGCT      28337           ACAGG
                                AGCAGCATTGT     TGCT
                                ||||||||||     ||||
                                TCGTCGTGACA     ACGA
                                      A____
GAM951  KIAA0555 3' AAGCTACTTTGTACAATGCTCT 60110    C          _ _
                                AG AGCATTGTACAG GT GCTT
                                || ||||||||||| || ||||
                                TC TCGTAACATGTT CA CGAA
                                 _          T  T
GAM951  KIAA0779 3' AAGTCTTGCTGTAAATGCTGC  85722        G     GT__
                                GCAGCATT TACAG    GCTT
                                |||||||| |||||    ||||
                                CGTCGTAA ATGTC    TGAA
                                     _    GTTC
GAM951  KIAA1265 3' ACTTGTACAATGCTGT      70786
                                GCAGCATTGTACAGGT
                                ||||||||||||||||
                                TGTCGTAACATGTTCA

GAM951  KIAA1878 3' CACCTGTCCAATGCTGCT     91709          T
                                AGCAGCATTG ACAGGTG
                                |||||||||| |||||||
                                TCGTCGTAAC TGTCCAC
                                      C
GAM951  KIAA1879 5' AAGCAGGAGCTGGACAATGCTG 73558          A   G___
          CT                     AGCAGCATTGT CAG    TGCTT
                                ||||||||||| |||    |||||
                                TCGTCGTAACA GTC    ACGAA
                                      G   GAGG
GAM951  KIAA1958 3' AAGACTCAACCAATGCTGC    81897         TACA   G
                                GCAGCATTG    GGT CTT
                                |||||||||    ||| |||
                                CGTCGTAAC    TCA GAA
                                     CAAC   _
GAM951  KRTHB5   3' AAGCACCTGCCTGCCTGC     9651       _  TTGTA
                                GCAG CA     CAGGTGCTT
                                |||| ||     |||||||||
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                                CGTC GT    GTCCACGAA
                                  C  CC___
GAM951  LRRN3    3'  AAGCTTCACCAATGCTGCT   69437        TACA  T
                                AGCAGCATTG   GG GCTT
                                ||||||||||   || ||||
                                TCGTCGTAAC   CT CGAA
                                     CA__  T
GAM951  MGC12945 5'  AAGTGTGTACCATGCTGCT   50297       T    GG
                                AGCAGCAT GTACA  TGCTT
                                |||||||| |||||  |||||
                                TCGTCGTA CATGT  GTGAA
                                    C    __
GAM951  MGC1842  3'  AAGCACCTGCTGGCTGCT   65633      ATTGTA
                                AGCAGC     CAGGTGCTT
                                ||||||     |||||||||
                                TCGTCG     GTCCACGAA
                                   GTC___
GAM951  MGC20470 3'  GGGACACCAATGCTGCT    58964        GTACA   _
                                AGCAGCATT    GGTG CTT
                                |||||||||    |||| |||
                                TCGTCGTAA    CCAC GGG
                                     _____   A
GAM951  MGC23980 3'  AAGCACTTAGAACAGTGC   58757       AC_
                                GCATTGT   AGGTGCTT
                                |||||||   ||||||||
                                CGTGACA   TTCACGAA
                                    AGA
GAM951  MGC26914 3'  AGCACGTAACAATGCT     58664        _ AG
                                AGCATTGT AC  GTGCT
                                |||||||| ||  |||||
                                TCGTAACA TG  CACGA
                                    A  __
GAM951  MGC33887 5'  AGCTTCACAATGCTGT     58872        ACA  T
                                GCAGCATTGT   GG GCT
                                ||||||||||   || |||
                                TGTCGTAACA   CT CGA
                                     ___  T
GAM951  PAK2     5'  AAGCACCTGCAGTAGTG    66534      TA_
                                CATTG   CAGGTGCTT
                                |||||   |||||||||
                                GTGAT   GTCCACGAA
                                   GAC
GAM951  PARVA    3'  AAGCAAATGTACAATATGCT  36648     GC      GG
                                AGCA  ATTGTACA  TGCTT
                                ||||  ||||||||  |||||
                                TCGT  TAACATGT  ACGAA
                                  A_       AA
GAM951  PLAC3    3'  GTTCCACACATGCTGCT     69346        _  ACA  T
                                AGCAGCAT TGT   GG GC
                                |||||||| |||   || ||
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                                TCGTCGTA ACA   CC TG
                                     C  ___  T
GAM951  PP1665   5'  AAGCACTTGGAACAATGC    47909       A_
                                GCATTGT  CAGGTGCTT
                                |||||||  |||||||||
                                CGTAACA  GTTCACGAA
                                   AG
GAM951  Rab11-FIP2 3'  AAGGATCACAGTGCTGCT    29778          ACA  G
                                AGCAGCATTGT   GGT CTT
                                ||||||||||   ||| |||
                                TCGTCGTGACA   CTA GAA
                                      ___  G
GAM951  SLC6A14  3'  CACATACAGTGCTGCT     23347          CAG
                                AGCAGCATTGTA   GTG
                                ||||||||||||   |||
                                TCGTCGTGACAT   CAC
                                      A__
GAM951  SMCR5    3'  AAGTCATCTGCACAAGGCT   58588    A   A    _
                                AGC TTGT CAGGTG CTT
                                ||| |||| |||||| |||
                                TCG AACA GTCTAC GAA
                                  G   C     T
GAM951  WAP1     3'  ATCCGTACATGCTGCT     79512       T   A
                                AGCAGCAT GTAC GGT
                                |||||||| |||| |||
                                TCGTCGTA CATG CTA
                                     _   C
GAM951  ZNF323   3'  AAGTTATCTAAATGCTGCT   48075       GTAC   _
                                AGCAGCATT   AGGTG CTT
                                |||||||||   ||||| |||
                                TCGTCGTAA   TCTAT GAA
                                      A___    T
GAM951  LOC115442 5'  ACTTGTATAAATGCTGCT    72675        _
                                AGCAGCATT GTACAGGT
                                ||||||||| ||||||||
                                TCGTCGTAA TATGTTCA
                                      A
GAM951  LOC122553 3'  AAGCACCTGAATTGTGCTTCT  74128   C    T  A
                                AG AGCAT GT CAGGTGCTT
                                || ||||| || |||||||||
                                TC TCGTG TA GTCCACGAA
                                  T    T  A
GAM951  LOC124045 3'  AAGCACCTTTGCATGGC     76030    AT   C
                                GC  TGTA AGGTGCTT
                                ||  |||| ||||||||
                                CG  ACGT TCCACGAA
                                  GT   T
GAM951  LOC144481 3'  AAGCACCTGTACACAAGC    83091    AT_
                                GC   TGTACAGGTGCTT
                                ||   ||||||||||||
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                                CG   ACATGTCCACGAA
                                 AAC
GAM951   LOC144559 5'  TGTTTGTATAATGCCACT    76884    CA        GT
                                AG  GCATTGTACAG  G
                                ||  ||||||||||  |
                                TC  CGTAATATGTT  T
                                 AC          TG
GAM951   LOC145601 3'  CACCCAGTGCTGCT        83363          TACA
                                AGCAGCATTG    GGTG
                                ||||||||||    ||||
                                TCGTCGTGAC    CCAC
                                      ____
GAM951   LOC149050 3'  AGCTCCTTGTACAACACGC    60428    AGCA      _  T
                                GC    TTGTACA GG GCT
                                ||    ||||||| || |||
                                CG    AACATGT CC CGA
                                 CAC_      T  T
GAM951   LOC149175 3'  AAGCACCTTCCTATGTGCT    79205      G   TGTAC
                                AGCA CAT     AGGTGCTT
                                |||| |||     ||||||||
                                TCGT GTA     TCCACGAA
                                  _   TCCT_
GAM951   LOC149351 5'  GAGTAGCACAGTGCTGCT     79307           ACAGG
                                AGCAGCATTGT     TGCTT
                                ||||||||||     |||||
                                TCGTCGTGACA     ATGAG
                                       CG___
GAM951   LOC196411 3'  TCTGTACAAGGCTGCT      87688        A
                                AGCAGC TTGTACAGG
                                |||||| |||||||||
                                TCGTCG AACATGTCT
                                   G
GAM951   LOC200583 3'  AAGCAATTAACAGTGCTACT   88831     C       ACAGG
                                AG AGCATTGT     TGCTT
                                || ||||||||     |||||
                                TC TCGTGACA     ACGAA
                                 A       ATTA_
GAM951   LOC201304 3'  CACTTCATGCTGCT        88228         T TAC
                                AGCAGCAT G   AGGTG
                                ||||||||  |   |||||
                                TCGTCGTA C   TTCAC
                                     _ ____
GAM951   LOC219918 5'  TGTTTGTATAATGCCACT    91543    CA        GT
                                AG  GCATTGTACAG  G
                                ||  ||||||||||  |
                                TC  CGTAATATGTT  T
                                 AC          TG
GAM951   LOC220071 5'  TGTTTGTATAATGCCACT    93438    CA        GT
                                AG  GCATTGTACAG  G
                                ||  ||||||||||  |
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                                TC  CGTAATATGTT  T
                                 AC          TG
GAM951   LOC220766 5'  AAGCACCTAAACAGGT      90789     A    AC
                                GC TTGT  AGGTGCTT
                                || ||||  ||||||||
                                TG GACA  TCCACGAA
                                 _    AA
GAM951   LOC221773 3'  AAGCACCTAGTAAGTGCCTGCT 91033       _    G   _
                                AGCAG CATT TAC AGGTGCTT
                                ||||| |||| ||| ||||||||
                                TCGTC GTGA ATG TCCACGAA
                                   C    _   A
GAM951   LOC253517 3'  AAGCACCTTTGCATGGC     95103     AT    C
                                GC  TGTA AGGTGCTT
                                ||  |||| ||||||||
                                CG  ACGT TCCACGAA
                                 GT    T
GAM951   LOC254045 3'  AAGCACCTGTACACAAGC    96500     AT_
                                GC   TGTACAGGTGCTT
                                ||   ||||||||||||
                                CG   ACATGTCCACGAA
                                 AAC
GAM951   LOC254173 3'  TCTGTACATGCTGCT       96845         T
                                AGCAGCAT GTACAGG
                                |||||||| |||||||
                                TCGTCGTA CATGTCT
                                      _
GAM951   LOC254611 5'  AAGCACCTATCCAAACTGT   97604      CA   TAC
                                GCAG  TTG   AGGTGCTT
                                ||||  |||   ||||||||
                                TGTC  AAC   TCCACGAA
                                  A_   CTA
GAM951   LOC255736 5'  ACTTAGTGTACAATGCTGT   95332           ___
                                GCAGCATTGTACA   GGT
                                ||||||||||||   |||
                                TGTCGTAACATGT   TCA
                                       GAT
GAM951   LOC255855 3'  AGCAACTATGCTGCT       96224         T  ACAGG
                                AGCAGCAT GT     TGCT
                                |||||||| ||     ||||
                                TCGTCGTA CA     ACGA
                                     T _____
GAM951   LOC257438 3'  AGCTAACGATGCTGCT      93969           ACAGGT
                                AGCAGCATTGT     GCT
                                ||||||||||      |||
                                TCGTCGTAGCA     CGA
                                       AT____
GAM951   LOC57826  3'  ATTTGCACAGATGCTGCT    41015         _   A
                                AGCAGCAT TGT CAGGT
                                |||||||| ||| |||||
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                                TCGTCGTA ACA GTTTA
                                     G   C
GAM951  LOC64744  3'  CACCTGTATGGCTGC      61796      ATT
                                GCAGC   GTACAGGTG
                                |||||   |||||||||
                                CGTCG   TATGTCCAC
                                   G__
GAM951  LOC90906  3'  AAGCACCTGATCTTGT      64290     TT  A
                                GCA  GT CAGGTGCTT
                                |||  || |||||||||
                                TGT  TA GTCCACGAA
                                  TC  _
GAM951  LOC90906  3'  TGTTTGTATAATGCTACT    64316    C          GT
                                AG AGCATTGTACAG  G
                                || ||||||||||||  |
                                TC TCGTAATATGTT  T
                                 A           TG
GAM951  LOC93268  5'  AAGCACCTAGGTAGCAGC    71874    A  ATTG   __
                                GC GC    TAC  AGGTGCTT
                                || ||    |||  |||||||||
                                CG CG    ATG  TCCACGAA
                                 A  _____   GA
GAM952  ADCY2     3'  TTGATCCTGTAATCACA     65023      TTCGTG
                                TGTG     ACAGGATCAA
                                ||||     ||||||||||
                                ACAC     TGTCCTAGTT
                                  TAA___
GAM952  CAPNS1    3'  GATCCTGTCTGCAGTCACAT   8252       TTC  _
                                GTGTG   GT GACAGGATC
                                |||||   || |||||||||
                                TACAC   CG CTGTCCTAG
                                   TGA  T
GAM952  CDK6      3'  TGATCCTGCGGAGAACACCCTT 7000      T     G_  A
                                AAG GTGTTC  TG CAGGATCA
                                ||| ||||||  || ||||||||
                                TTC CACAAG  GC GTCCTAGT
                                  C     AG  _
GAM952  CTNNA1    3'  CCATAATCAGAACACACTTT   65918          G   CA__
                                AAAGTGTGTTC TGA    GG
                                |||||||||| |||    ||
                                TTTCACACAAG ACT    CC
                                      _   AATA
GAM952  FLRT2     3'  GATCCTGTTCCACTTT      25062       TGTTCGT
                                AAAGTG      GACAGGATC
                                ||||||      |||||||||
                                TTTCAC      TTGTCCTAG
                                   C_______
GAM952  HGF       3'  CTGGTACACGAACACACTTT   94233            _  A
                                AAAGTGTGTTCGTG AC GG
                                |||||||||||||| || ||
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                                TTTCACACAAGCAC TG TC
                                       A  G
GAM952  MASP1    3'  CCGGCTCATCAAACACACTCC  57471    A      C_   CA_
                                A AGTGTGTT  GTGA   GG
                                | ||||||||  ||||   ||
                                C TCACACAA  TACT   CC
                                 C       AC    CGG
GAM952  NAGA     3'  TTGATCCTATCTCTTCACCCTT 4239      T   TTCGT  C
                                AAG GTG    GA AGGATCAA
                                ||| |||    || ||||||||
                                TTC CAC    CT TCCTAGTT
                                  C   TTCT_  A
GAM952  SAR1     3'  TGATCCTATTCACAGC      39326     C    C_
                                GTT GTGA  AGGATCA
                                ||| ||||  |||||||
                                CGA CACT  TCCTAGT
                                  _    TA
GAM952  TAC3     5'  TTGATCCTGCCAGACCAC    25124     T  G  A
                                GTG TC TG CAGGATCAA
                                ||| || || |||||||||
                                CAC AG AC GTCCTAGTT
                                  C  _  C
GAM952  TSTA3    3'  TGATCCTGCATCCCAC      12407     TTC   A
                                GTG   GTG CAGGATCA
                                |||   ||| ||||||||
                                CAC   TAC GTCCTAGT
                                  CC_   _
GAM952  ZNF2     3'  TGATCCTGTCACCAACCAT    40808     T   C
                                GTG GTT GTGACAGGATCA
                                ||| ||| ||||||||||||
                                TAC CAA CACTGTCCTAGT
                                  _   C
GAM952  DKFZP564O0463 3'  TGCTCACACACACACTTT    26283         TC   _
                                AAAGTGTGT  GTGA CA
                                |||||||||  |||| ||
                                TTTCACACA  CACT GT
                                      CA    C
GAM952  EPB41L1  3'  CTGAGCACACTGAACACAC    70592         _  A___
                                GTGTGTTC GTG    CAG
                                |||||||| |||    |||
                                CACACAAG CAC    GTC
                                     T   ACGA
GAM952  FLJ10900 3'  GTCTCACAAACACACTTT    65592          C   CAG
                                AAAGTGTGTT GTGA   GAT
                                |||||||||| ||||   |||
                                TTTCACACAA CACT   CTG
                                      A   ___
GAM952  FLJ10900 3'  GTCTCACAAACACACTTT    36815          C   CAG
                                AAAGTGTGTT GTGA   GAT
                                |||||||||| ||||   |||
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                                TTTCACACAA CACT   CTG
                                     A   ___
GAM952  FLJ32783  3'  CCTGTTACAGCACTCT     58642    T    C
                                AG GTGTT GTGACAGG
                                || ||||| ||||||||
                                TC CACGA CATTGTCC
                                 T    _
GAM952  H326    3'  TGATCCTGCCTGGGCA     31711       TGA
                                TGTTCG   CAGGATCA
                                ||||||   ||||||||
                                ACGGGT   GTCCTAGT
                                   CC_
GAM952  MGC17299  3'  ATCCTGTCCTGTAACAT     58235      _  T
                                GTGTT CG GACAGGAT
                                ||||| || ||||||||
                                TACAA GT CTGTCCTA
                                   T  C
GAM952  MGC3101   3'  TGACCCAGCAGACACACTT   43886       TC  GACA  A
                                AAGTGTGT  GT    GG TCA
                                ||||||||  ||    || |||
                                TTCACACA  CG    CC AGT
                                     GA  AC__  _
GAM952  PLAGL2    3'  CTGATTCAGAAACACACTT   70447        CG  __
                                AAGTGTGTT  TGA  CAG
                                |||||||||  |||  |||
                                TTCACACAA  ACT  GTC
                                      AG   TA
GAM952  PTBP2     3'  CCTTTTCGTACACACT     41034       T  T  C
                                AGTGTGT CG GA AGG
                                ||||||| || || |||
                                TCACACA GC TT TCC
                                     T  _  T
GAM952  RASSF2    3'  ATCTCACACAACACACTT    28427        C   ACA
                                AAGTGTGTT GTG   GGAT
                                ||||||||| |||   ||||
                                TTCACACAA CAC   TCTA
                                      _   AC_
GAM952  SMBP      3'  ATCCTGTCTGGGACAC     72158       GT
                                GTGTTC  GACAGGAT
                                ||||||  ||||||||
                                CACAGG  CTGTCCTA
                                   GT
GAM952  LOC126364 3'  ATCCTGTCATCACCCTCC    75682   A  T   TTC
                                A AG GTG   GTGACAGGAT
                                | || |||   ||||||||||
                                C TC CAC   TACTGTCCTA
                                 C  C   ___
GAM952  LOC145719 5'  ATCCCACAACACACTT     83446        C   ACA
                                AAGTGTGTT GTG   GGAT
                                ||||||||| |||   ||||
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                                TTCACACAA CAC   CCTA
                                    _  ___
GAM952  LOC145720 5'  ATCCCACAACACACTT     83428        C   ACA
                                AAGTGTGTT GTG   GGAT
                                ||||||||| |||   ||||
                                TTCACACAA CAC   CCTA
                                    _  ___
GAM952  LOC197114 5'  ATCCCACAACACACTT     89698        C   ACA
                                AAGTGTGTT GTG   GGAT
                                ||||||||| |||   ||||
                                TTCACACAA CAC   CCTA
                                    _  ___
GAM952  LOC197117 5'  ATCCCACAACACACTT     89714        C   ACA
                                AAGTGTGTT GTG   GGAT
                                ||||||||| |||   ||||
                                TTCACACAA CAC   CCTA
                                    _  ___
GAM952  LOC221692 3'  CCCCACAACACACTT      92237        C   ACA
                                AAGTGTGTT GTG   GG
                                ||||||||| |||   ||
                                TTCACACAA CAC   CC
                                    _  C__
GAM952  LOC253558 3'  TGATATTCACGAACCACTT   95674      T      CAGG
                                AAGTG GTTCGTGA   ATCA
                                ||||| ||||||||   ||||
                                TTCAC CAAGCACT   TAGT
                                   _      TA__
GAM952  LOC51754  5'  CCTGCATACACACTT      71028       TC   A
                                AAGTGTGT  GTG CAGG
                                ||||||||  ||| ||||
                                TTCACACA  TAC GTCC
                                    __  _
GAM952  LOC91050  3'  TTGATCCTGTCACAGATATA  64754      TC
                                TGTGT  GTGACAGGATCAA
                                |||||  ||||||||||||
                                ATATA  CACTGTCCTAGTT
                                   GA
GAM953  ADRA2A    3'  CCGGGCGCTGCCTGCTCTG   5450        A    A
                                CAGAGCAG CAGCG CTTGG
                                ||||||||| ||||| |||||
                                GTCTCGTC GTCGC GGGCC
                                     C    _
GAM953  B4GALT6   3'  TCACCCGTCCTCCCTGCTCTGA 59867        AC  C   TT  C
                                TCAGAGCAG  AG GAC  GG GA
                                |||||||||  || |||  || ||
                                AGTCTCGTC  TC CTG  CC CT
                                      CC  _   C_  A
GAM953  BN51T     3'  CCACGGCTGCTGCCTGCTC    87493       A    A  _
                                GAGCAG CAGCG CT TGG
                                |||||| ||||| || |||
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                                CTCGTC GTCGT GG ACC
                                   C    C  C
GAM953  CACNG7   3'  TCGTTCTCCACCTGCTCTGA  49098        AC____
                                TCAGAGCAG    AGCGA
                                |||||||||    |||||
                                AGTCTCGTC    TTGCT
                                     CACCTC
GAM953  GNB5     5'  TCACCTCTCACCATCTGCTCTG 32468        CAGC  CTT  C
                                CAGAGCAGA   GA  GG GA
                                |||||||||   ||  || ||
                                GTCTCGTCT   CT  CC CT
                                     ACCA  CT_  A
GAM953  KLHL3    3'  TCACCAAAGCCAATCTGCTCT  87466       CA_  GAC   C
                                AGAGCAGA   GC   TTGG GA
                                ||||||||   ||   |||| ||
                                TCTCGTCT   CG   AACC CT
                                     AAC  A__   A
GAM953  LAMP2    5'  CGCCGTCGCCGCCTGCTCTG   25710       ACA    TT
                                CAGAGCAG   GCGAC  GGCG
                                ||||||||   |||||  ||||
                                GTCTCGTC   CGCTG  CCGC
                                     CGC    __
GAM953  LAMP2    5'  CGCCGTCGCCGCCTGCTCTG   9683        ACA    TT
                                CAGAGCAG   GCGAC  GGCG
                                ||||||||   |||||  ||||
                                GTCTCGTC   CGCTG  CCGC
                                     CGC    __
GAM953  NAPB     3'  TCGCCAAGTCTGTGTTGCTGTG 70190     G    A  GC
           A                     TCA AGCAG CA  GACTTGGCGA
                                |||  |||||  ||  ||||||||||
                                AGT TCGTT GT  CTGAACCGCT
                                  G    _  GT
GAM953  PCSK2    3'  CCCAGCTGCTGCTCTGA     10465         A   GACT   C
                                TCAGAGCAG CAGC    TGG G
                                ||||||||| ||||    ||| |
                                AGTCTCGTC GTCG    ACC C
                                     _   _____   A
GAM953  PLIN     3'  CCAGAGCCGCAGCCTGCTCTGA 10641        ACA   A  _
                                TCAGAGCAG   GCG CT TGG
                                |||||||||   ||| || |||
                                AGTCTCGTC   CGC GA ACC
                                     CGA   C  G
GAM953  PPP1R2   3'  CCCAATGTCTGCTCTG      20687          GCGAC    C
                                CAGAGCAGACA     TTGG G
                                ||||||||||     |||| |
                                GTCTCGTCTGT     AACC C
                                      _____    A
GAM953  PTMA     5'  CCACTGGCTGCTCTGA      11030         A   CGACT
                                TCAGAGCAG CAG     TGG
                                |||||||||  |||     |||
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                                AGTCTCGTC GTC    ACC
                                     G  _____
GAM953  RECQL    5'  TCACTGCCCTGCTCTGA    11284        A_  C
                                TCAGAGCAG  CAG GA
                                |||||||||  ||| ||
                                AGTCTCGTC  GTC CT
                                     CC   A
GAM953  C20orf18  3'  CCACGTCAACTGCCTGCTCTG  48338       A  C_  T
                                CAGAGCAG CAG  GAC TGG
                                |||||||| |||  ||| |||
                                GTCTCGTC GTC  CTG ACC
                                     C  AA  C
GAM953  C20orf59  5'  TCATGAGTCGCCATCTGCCCTG 41997     A    CA      GC
          A                      TCAG GCAGA  GCGACTTG  GA
                                |||| |||||  ||||||||  ||
                                AGTC CGTCT  CGCTGAGT  CT
                                  C    AC       A_
GAM953  C9orf9   5'  TCGCGCGGGTCGCCCCCGC   38529    AGACA      _
                                GC    GCGACTTG GCGA
                                ||    |||||||| ||||
                                CG    CGCTGGGC CGCT
                                 CCCC_       G
GAM953  CLIPR-59  5'  CCAGCGCTGTCTGC       31370         A  T
                                GCAGACAGCG CT GG
                                |||||||||| || ||
                                CGTCTGTCGC GA CC
                                     _  _
GAM953  CXYorf1   3'  CAGGGCCGCTGCCCGCCCTGG  82039     A  AGA    A_
                                TCAG GC   CAGCG  CTTG
                                |||| ||   |||||  ||||
                                GGTC CG   GTCGC  GGAC
                                  C  CCC    CG
GAM953  DNAJC6   3'  GTCAGTATCTGCTCTGA    28847         CA  _
                                TCAGAGCAGA  GC GAC
                                ||||||||||  || |||
                                AGTCTCGTCT  TG CTG
                                     A_  A
GAM953  FLJ10656  3'  GCCAGTATCTGCTCT      36388        CAGCG   T
                                AGAGCAGA    ACT GGC
                                ||||||||    ||| |||
                                TCTCGTCT    TGA CCG
                                    A____   _
GAM953  FLJ10901  3'  GCTATGCTTCTGCTCTGA    36827         C    ACT
                                TCAGAGCAGA AGCG   TGGC
                                |||||||||| ||||   ||||
                                AGTCTCGTCT TCGT   ATCG
                                     _   ____
GAM953  FLJ12056  3'  TCCTGCCTGCTCTGA      46257         A  C
                                TCAGAGCAG CAG GA
                                |||||||| ||| ||
```

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                                AGTCTCGTC GTC CT
                                     C  _
GAM953  FLJ14154  3'  CGCCTTCCTGTCCATCTGA   45816     GCA    C  CTT
                                TCAGA  GACAG GA  GGCG
                                |||||  ||||| ||  ||||
                                AGTCT  CTGTC CT  CCGC
                                  AC_    _ T__
GAM953  HRH3    5'  CGGCACCGCCTGCTCTGG    23367       ACA  ACT  G
                                TCAGAGCAG  GCG  TG CG
                                |||||||||  |||  || ||
                                GGTCTCGTC  CGC  AC GC
                                     ___  C__  G
GAM953  HSU79266  3'  CGCCTGTTCCGTCTGCTC   25250       AGC  TT
                                GAGCAGAC  GAC  GGCG
                                ||||||||  |||  ||||
                                CTCGTCTG  TTG  CCGC
                                     CC_  T_
GAM953  KIAA0355  3'  CGGCACCGCCTTGCTCTGA   28024       ACA  ACT  G
                                TCAGAGCAG  GCG  TG CG
                                |||||||||  |||  || ||
                                AGTCTCGTT  CGC  AC GC
                                     C__  C__  G
GAM953  MGC10500  3'  CCAGTGCACCGTCTGCTCTG  48933       A__  G  T
                                CAGAGCAGAC  GC ACT GG
                                ||||||||||  || ||| ||
                                GTCTCGTCTG  CG TGA CC
                                     CCA  _  _
GAM953  MGC3178  3'  CCACTTATACTGTCTGTCTGA  47984     G     CGACT_
                                TCAGA CAGACAG    TGG
                                ||||| |||||||     |||
                                AGTCT GTCTGTC    ACC
                                  _     ATATTC
GAM953  MIG2    3'  TCACCAGCATAATCACTGTCTG 72425   A     C  C____   C
          CCT                   AG GCAGACAG GA    TTGG GA
                                || |||||||| ||    |||| ||
                                TC CGTCTGTC CT    GACC CT
                                 _      A  AATAC   A
GAM953  PIGQ    3'  GCCAGCCATCTGCTCTG    14850       CA  GACT
                                CAGAGCAGA  GC   TGGC
                                |||||||||  ||   ||||
                                GTCTCGTCT  CG   ACCG
                                     AC  ____
GAM953  RASGRP4  3'  CCAGCGCCATCTGCTC     53650       CA  A  T
                                GAGCAGA  GCG CT GG
                                |||||||  ||| || ||
                                CTCGTCT  CGC GA CC
                                     AC  _  _
GAM953  SLC2A11  5'  CGCCAAGTCTCTCGCTCTG   47964      _  CAGC
                                CAGAGC AGA   GACTTGGCG
                                ||||||  |||   |||||||||
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                                GTCTCG TCT    CTGAACCGC
                                   C  ____
GAM953   LOC138307 3'  CCCTGCACCTGCTCTGA     75313         ACA   ACTT  C
                                TCAGAGCAG   GCG    GG G
                                |||||||||   |||    || |
                                AGTCTCGTC   CGT    CC C
                                     CA_   ____  A
GAM953   LOC144266 5'  TCACTCCCTCGCTGTCTCTCTG 76764       C       CTT  C
           A                     TCAGAG AGACAGCGA   GG GA
                                |||||| |||||||||   || ||
                                AGTCTC TCTGTCGCT   TC CT
                                   _       CCC  A
GAM953   LOC145123 5'  CCACTGGCTGCTCTGA      67526         A   CGACT
                                TCAGAGCAG CAG     TGG
                                ||||||||| |||     |||
                                AGTCTCGTC GTC     ACC
                                     G  _____
GAM953   LOC145226 3'  CGAATCCTGCCTGCTCTGA    77047         A   C  C
                                TCAGAGCAG CAG GA TTG
                                ||||||||| ||| || |||
                                AGTCTCGTC GTC CT AGC
                                     C   _  A
GAM953   LOC145725 3'  TCGCCATGTGCTCTGA      77416       AGACAGCG  T
                                TCAGAGC       AC TGGCGA
                                |||||||       || ||||||
                                AGTCTCG       TG ACCGCT
                                   _________  T
GAM953   LOC145732 3'  TCGCCATGTGCTCTGA      77438       AGACAGCG  T
                                TCAGAGC       AC TGGCGA
                                |||||||       || ||||||
                                AGTCTCG       TG ACCGCT
                                   _________  T
GAM953   LOC196411 3'  CGTCATCATCTGCTCTGA    87671         CAGC  CT
                                TCAGAGCAGA    GA  TGGCG
                                ||||||||||    ||  |||||
                                AGTCTCGTCT    CT  ACTGC
                                     A___  __
GAM953   LOC196961 3'  TCGCCATGTGCTCTGA      87853       AGACAGCG  T
                                TCAGAGC       AC TGGCGA
                                |||||||       || ||||||
                                AGTCTCG       TG ACCGCT
                                   _________  T
GAM953   LOC197138 3'  TCGCCATGTGCTCTGA      87926       AGACAGCG  T
                                TCAGAGC       AC TGGCGA
                                |||||||       || ||||||
                                AGTCTCG       TG ACCGCT
                                   _________  T
GAM953   LOC219920 5'  CCACCATCTTCCTGCTCTGA  93306         AC  CGACT
                                TCAGAGCAG  AG    TGG
                                |||||||||  ||    |||
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                                AGTCTCGTC  TC    ACC
                                     CT  TACC_
GAM953  LOC255043 3'  CGCCCCCTGCTGCTGCTCTGA  95329        A    ACTT
                                TCAGAGCAG CAGCG   GGCG
                                ||||||||| |||||   ||||
                                AGTCTCGTC GTCGT   CCGC
                                     _    CCC_
GAM953  LOC257468 5'  TCGCCAAGCAGGTTCGCTCTGA 95189       AG  AGCGA
                                TCAGAGC  AC    CTTGGCGA
                                |||||||  ||    ||||||||
                                AGTCTCG  TG    GAACCGCT
                                    CT  GAC__
GAM954  GJB3    5'  CAAAGCACATCTTTCCACC   43764      T  TT
                                GGTGG AG  GTGTGCTTTG
                                ||||| ||  ||||||||||
                                CCACC TT  TACACGAAAC
                                   _ TC
GAM954  DKFZP566M114 5'  AAAACCCACCCACCCTAA    49541        TAGTT   TGC
                                TTAGGGTGG    GTG   TTT
                                |||||||||    |||  |||
                                AATCCCACC    CAC   AAA
                                     _____  CCA
GAM954  HSPB7    5'  CAAAACACACAATAAACCC   27023     GGTA      C
                                GGGT   GTTGTGTG TTTG
                                ||||   |||||||| ||||
                                CCCA   TAACACAC AAAC
                                  AA__      A
GAM955  AP2B1    3'  AGGGCAAGCAGACAAC      7056     A  C
                                GTT TC GCTTGCCTT
                                ||| || |||||||||
                                CAA AG CGAACGGGA
                                  C  A
GAM955  C5R1     3'  AGGCTAAGGTGGGTGGATCACC 8199       T     TG
           TG                     CAGGT ATCCGCT  CCTTAGCCT
                                |||||  |||||||  |||||||||
                                GTCCA TAGGTGG  GGAATCGGA
                                   C      GT
GAM955  EGFL5    3'  AGGGAGTACAAGCAAATAATCT 86611       CC    C_  AG
                                AGGTTAT  GCTTG  CTT  CCT
                                |||||||  |||||  |||  |||
                                TCTAATA  CGAAC  GAG  GGA
                                    AA    AT  __
GAM955  HTR2A    3'  AGGCCAAGAGTTTGAGACCAAC 5257       ATCCG  __ _  A
           CTG                    CAGGTT    CTT  GC CTT GCCT
                                ||||||    |||  || ||| ||||
                                GTCCAA    GAG  TG GAA CGGA
                                   CCA__   TT  A   C
GAM955  ITGAL    3'  AGGCCAAGGAGGGTGGATCACC 9384       T     TG   A
           TG                     CAGGT ATCCGCT  CCTT GCCT
                                |||||  |||||||  |||| ||||
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                                GTCCA TAGGTGG  GGAA CGGA
                                  C      GA   C
GAM955  MSH3    3'  AGGCCAAGGTAGGCAGATCACC 10117      T  C       A
          TG                      CAGGT ATC GCTTGCCTT GCCT
                                  ||||| ||| |||||||||| ||||
                                GTCCA TAG CGGATGGAA CGGA
                                  C  A       C
GAM955  PPAT    3'  GCTCAGCAAGTAACCTG     10700       ATCC     CTT
                                CAGGTT   GCTTGC  AGC
                                ||||||   ||||||  |||
                                GTCCAA   TGAACG  TCG
                                   ____     AC_
GAM955  PSMB9   3'  AGGCCAAGGCAGGCGGATCACC 10957      T          A
          TG                      CAGGT ATCCGCTTGCCTT GCCT
                                  ||||| |||||||||||||| ||||
                                GTCCA TAGGCGGACGGAA CGGA
                                  C           C
GAM955  RBBP5   3'  AGGCCAAGGCGGGTGGATCACC 17330     T          A
                                GGT ATCCGCTTGCCTT GCCT
                                  ||| |||||||||||||| ||||
                                CCA TAGGTGGGCGGAA CGGA
                                  C           C
GAM955  ROCK2   3'  AGGCCAAGACGGGCGGATCACC 66007      T       C  A
          TG                      CAGGT ATCCGCTTG CTT GCCT
                                  ||||| ||||||||| ||| ||||
                                GTCCA TAGGCGGGC GAA CGGA
                                  C        A  C
GAM955  SIM2    3'  AGGCCAAGGTGGGCGGATCACC 23780      T     TG   A
          TG                      CAGGT ATCCGCT  CCTT GCCT
                                  ||||| |||||||  |||| ||||
                                GTCCA TAGGCGG  GGAA CGGA
                                  C      GT   C
GAM955  SLC2A6  3'  AGGCCAAAGCAGGTGGATTACC 34156     T       C  A
                                GGT ATCCGCTTGC TT GCCT
                                  ||| |||||||||| || ||||
                                CCA TAGGTGGACG AA CGGA
                                  T        A  C
GAM955  SRGAP1  5'  AGGCCAAGGCGGGTGGATTACC 72257      T          A
          TG                      CAGGT ATCCGCTTGCCTT GCCT
                                  ||||| |||||||||||||| ||||
                                GTCCA TAGGTGGGCGGAA CGGA
                                  T           C
GAM955  TDG     5'  AGGCCAAGGCAGGCGGACCACC 12186      TA         A
          TG                      CAGGT  TCCGCTTGCCTT GCCT
                                  |||||  |||||||||||| ||||
                                GTCCA  AGGCGGACGGAA CGGA
                                  CC          C
GAM955  TNFSF14 3'  AGGCCAAGGCAGGCGGATCACC 13740      T          A
          TG                      CAGGT ATCCGCTTGCCTT GCCT
                                  ||||| |||||||||||||| ||||
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                                GTCCA TAGGCGGACGGAA CGGA
                                  C           C
GAM955  TRIM9    5'  AGGCTAAGGCAGGCGGACCACC 30750       TA
           TG                     CAGGT  TCCGCTTGCCTTAGCCT
                                  |||||  |||||||||||||||||
                                  GTCCA  AGGCGGACGGAATCGGA
                                    CC
GAM955  ZNF36    3'  AGGCTAATCTTACGGATAATC  93959          CTTGCC
                                  GGTTATCCG     TTAGCCT
                                  |||||||||     |||||||
                                  CTAATAGGC     AATCGGA
                                       ATTCT_
GAM955  ASTN2    3'  AGGCCAAAGCAAACGGTTTCTC 73181      TTAT_  C    C  A
           CTG                     CAGG    CCG TTGC TT GCCT
                                  ||||    ||| |||| || ||||
                                  GTCC    GGC AACG AA CGGA
                                    TCTTT   A    A  C
GAM955  C1orf27  5'  GCTAAGTTGGATAACTTG    35265          CTTGC
                                  CAGGTTATCCG    CTTAGC
                                  ||||||||||    ||||||
                                  GTTCAATAGGT    GAATCG
                                        T____
GAM955  C21orf108 3'  AGGCCAAGGCGGGTGAATCACC 88715       T  C        A
           TG                     CAGGT AT CGCTTGCCTT GCCT
                                  ||||| || |||||||||| ||||
                                  GTCCA TA GTGGGCGGAA CGGA
                                    C  A         C
GAM955  C8orf2   3'  AGGCCAAGGCAGGCGGATCACC 23156       T          A
           TG                     CAGGT ATCCGCTTGCCTT GCCT
                                  ||||| |||||||||||| ||||
                                  GTCCA TAGGCGGACGGAA CGGA
                                    C           C
GAM955  DEGS     3'  AGGCCAAGGTGGGTGGATCACC 13408       T      TG    A
           TG                     CAGGT ATCCGCT  CCTT GCCT
                                  ||||| |||||||  |||| ||||
                                  GTCCA TAGGTGG  GGAA CGGA
                                    C      GT    C
GAM955  DKFZP434C1715 3'  GCTAAGGTGGGAGGATCACCTG 86149       T    G  TG
                                  CAGGT ATCC CT  CCTTAGC
                                  ||||| |||| ||  |||||||
                                  GTCCA TAGG GG  GGAATCG
                                    C    A  GT
GAM955  DKFZp434G171 3'  AGGCCAAGGTGGGTGGATCACC 79430       T      TG    A
           TG                     CAGGT ATCCGCT  CCTT GCCT
                                  ||||| |||||||  |||| ||||
                                  GTCCA TAGGTGG  GGAA CGGA
                                    C      GT    C
GAM955  DKFZP434K2235 3'  AAGCCAGAGCAGATAACTTG   83496         C    GC_
                                  CAGGTTATC GCTT   CTT
                                  |||||||| ||||   |||
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                                GTTCAATAG CGAG   GAA
                                    A    ACC
GAM955  DKFZp547G183 3'  AGGCCAAGGTGAGCGGATCACC 38022      T     TG    A
           TG                    CAGGT ATCCGCT  CCTT GCCT
                                 ||||| |||||||  |||| ||||
                                 GTCCA TAGGCGA  GGAA CGGA
                                   C      GT    C
GAM955  FBXO9    3'  AGGCTAAGACAGGCAGATCACC 53099      T  C    C
           TG                    CAGGT ATC GCTTG CTTAGCCT
                                 ||||| ||| ||||| ||||||||
                                 GTCCA TAG CGGAC GAATCGGA
                                   C  A    A
GAM955  FLJ10547  3'  AGGCCAAGGTGAGTGGATCACC 36265      T     TG    A
           TG                    CAGGT ATCCGCT  CCTT GCCT
                                 ||||| |||||||  |||| ||||
                                 GTCCA TAGGTGA  GGAA CGGA
                                   C      GT    C
GAM955  FLJ10826  3'  AGGCCAAGGCAGGCGGATCACC 36699      T         A
           TG                    CAGGT ATCCGCTTGCCTT GCCT
                                 ||||| |||||||||||| ||||
                                 GTCCA TAGGCGGACGGAA CGGA
                                   C          C
GAM955  FLJ11370  3'  AGGCCAAGGCAGGCAGATCACC 46368      T  C       A
           TG                    CAGGT ATC GCTTGCCTT GCCT
                                 ||||| ||| ||||||||| ||||
                                 GTCCA TAG CGGACGGAA CGGA
                                   C  A       C
GAM955  FLJ13441  3'  GCCAAGGTTGGGGACACCCT   43664     TTA  G  T    A
                                 AGG   TCC CT GCCTT GC
                                 |||   ||| || ||||| ||
                                 TCC   AGG GG TGGAA CG
                                   CAC   _  T    C
GAM955  FLJ13952  3'  AGGCCAAGATGGGTGGATCACC 45612      T     GC   A
           TG                    CAGGT ATCCGCTT  CTT GCCT
                                 ||||| ||||||||  ||| ||||
                                 GTCCA TAGGTGGG  GAA CGGA
                                   C       TA   C
GAM955  FLJ20004  3'  AGGCCAAGATGGGCGGATCACC 95285      T     GC   A
           TG                    CAGGT ATCCGCTT  CTT GCCT
                                 ||||| ||||||||  ||| ||||
                                 GTCCA TAGGCGGG  GAA CGGA
                                   C       TA   C
GAM955  FLJ20694  3'  GCCAAGGTGGGCGGATCACCTG 35550      T     TG    A
                                 CAGGT ATCCGCT  CCTT GC
                                 ||||| |||||||  |||| ||
                                 GTCCA TAGGCGG  GGAA CG
                                   C      GT    C
GAM955  FLJ20695  3'  AGGCCAAGGTGGGTGAATCACC 35555      T  C   TG    A
           TG                    CAGGT AT CGCT  CCTT GCCT
                                 ||||| || ||||  |||| ||||
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                                GTCCA TA GTGG  GGAA CGGA
                                  C A   GT   C
GAM955  FLJ20972  3'  AGGCCAAGGTGGGCGGATCACC 46721     T     TG   A
            TG                    CAGGT ATCCGCT  CCTT GCCT
                                  ||||| |||||||  |||| ||||
                                GTCCA TAGGCGG  GGAA CGGA
                                  C      GT   C
GAM955  FLJ32915  5'  AGGCCAAGGCGGGCAGATCACC 58790     T  C       A
            TG                    CAGGT ATC GCTTGCCTT GCCT
                                  ||||| ||| ||||||||| ||||
                                GTCCA TAG CGGGCGGAA CGGA
                                  C  A       C
GAM955  GALNT6    3'  AGGCCAAGGCAGGTGGATCACC 23288     T         A
            TG                    CAGGT ATCCGCTTGCCTT GCCT
                                  ||||| |||||||||||| ||||
                                GTCCA TAGGTGGACGGAA CGGA
                                  C          C
GAM955  KIAA0419  3'  AGGCCAAGGTGGGTGGATCACC 28186     T     TG   A
            TG                    CAGGT ATCCGCT  CCTT GCCT
                                  ||||| |||||||  |||| ||||
                                GTCCA TAGGTGG  GGAA CGGA
                                  C      GT   C
GAM955  KIAA0565  3'  AGGCCAAGGTGGGTGGATCACC 66885     T     TG   A
            TG                    CAGGT ATCCGCT  CCTT GCCT
                                  ||||| |||||||  |||| ||||
                                GTCCA TAGGTGG  GGAA CGGA
                                  C      GT   C
GAM955  KIAA0618  3'  AGGCCAAGGTGGGCAGATCACC 29160     T  C  TG   A
            TG                    CAGGT ATC GCT  CCTT GCCT
                                  ||||| ||| |||  |||| ||||
                                GTCCA TAG CGG  GGAA CGGA
                                  C  A  GT   C
GAM955  KIAA0795  3'  AGGCCAAGGAGGGCGGATCACC 46586     T     TG   A
            T                      AGGT ATCCGCT  CCTT GCCT
                                  |||| |||||||  |||| ||||
                                TCCA TAGGCGG  GGAA CGGA
                                  C      GA   C
GAM955  KIAA0831  5'  AGGCCAAGACAGGTGGATCACC 29967     T      C  A
            TG                    CAGGT ATCCGCTTG CTT GCCT
                                  ||||| |||||||| ||| ||||
                                GTCCA TAGGTGGAC GAA CGGA
                                  C        A  C
GAM955  KIAA0907  3'  AGGCCAAGGTGGGCGGATAACC 30170          TG   A
            TG                    CAGGTTATCCGCT  CCTT GCCT
                                  |||||||||||||  |||| ||||
                                GTCCAATAGGCGG  GGAA CGGA
                                       GT   C
GAM955  KIAA0953  3'  AGGCCAAGGCAGGTGGATCACC 66779     T         A
            TG                    CAGGT ATCCGCTTGCCTT GCCT
                                  ||||| |||||||||||| ||||
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                                GTCCA TAGGTGGACGGAA CGGA
                                  C           C
GAM955  KIAA1191  3'  AGGCCAAGGTAGGTGGATACCT 39953       T           A
            G                    CAGGT ATCCGCTTGCCTT GCCT
                                ||||| |||||||||||||| ||||
                                GTCCA TAGGTGGATGGAA CGGA
                                  _           C
GAM955  KIAA1244  3'  AGGCCAAGGTGGGCAGATAACC 71986         C   TG    A
            TG                   CAGGTTATC GCT  CCTT GCCT
                                ||||||||| |||  |||| ||||
                                GTCCAATAG CGG  GGAA CGGA
                                    A  GT   C
GAM955  KIAA1956  3'  AGACTAAGGCAAGAACATCCTG 78428      TTATCCG        C
                                CAGG      CTTGCCTTAG CT
                                ||||      |||||||||| ||
                                GTCC      GAACGGAATC GA
                                  TACAA__         A
GAM955  KR18      3'  AGGCCAAGGCAAGCAGATCACC 52738       T   C        A
            TG                   CAGGT ATC GCTTGCCTT GCCT
                                ||||| ||| ||||||||| ||||
                                GTCCA TAG CGAACGGAA CGGA
                                  C   A        C
GAM955  LAP1B     3'  AGGCCAAGGCAGGTGGATCACC 64583       T           A
            TG                   CAGGT ATCCGCTTGCCTT GCCT
                                ||||| |||||||||||||| ||||
                                GTCCA TAGGTGGACGGAA CGGA
                                  C           C
GAM955  LIAS      3'  AGGCCAAGGCGGGTGGATCACC 70634       T           A
            TG                   CAGGT ATCCGCTTGCCTT GCCT
                                ||||| |||||||||||||| ||||
                                GTCCA TAGGTGGGCGGAA CGGA
                                  C           C
GAM955  LRRFIP1   3'  AGGCCAAGGCAGGTGGATCACC 16417       T           A
            TG                   CAGGT ATCCGCTTGCCTT GCCT
                                ||||| |||||||||||||| ||||
                                GTCCA TAGGTGGACGGAA CGGA
                                  C           C
GAM955  MAWBP     3'  AGGCCAAGGTGGGTGGATCACC 42105       T      TG    A
            TG                   CAGGT ATCCGCT  CCTT GCCT
                                ||||| |||||||  |||| ||||
                                GTCCA TAGGTGG  GGAA CGGA
                                  C      GT   C
GAM955  MGC16142  3'  AGGCCAAGGTGGGAGGATCACC 51290       T   G  TG    A
            TG                   CAGGT ATCC CT  CCTT GCCT
                                ||||| |||| ||  |||| ||||
                                GTCCA TAGG GG  GGAA CGGA
                                  C   A  GT   C
GAM955  MGC2396   3'  AGGCCAAGGTGGGAGGATCACC 53459       T   G  TG    A
            TG                   CAGGT ATCC CT  CCTT GCCT
                                ||||| |||| ||  |||| ||||
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                                GTCCA TAGG GG  GGAA CGGA
                                  C    A GT    C
GAM955  MGC2562   3'  AGGCCAAGGCAAGCAAATCACT 50433      T  CC       A
           TG                     CAGGT AT  GCTTGCCTT GCCT
                                  |||||| ||  |||||||||| ||||
                                  GTTCA TA  CGAACGGAA CGGA
                                    C  AA        C
GAM955  MGC29762  3'  AGGCCAAGGCGGGTCAATCACC 58467      T  CC       A
           TG                     CAGGT AT  GCTTGCCTT GCCT
                                  |||||| ||  |||||||||| ||||
                                  GTCCA TA  TGGGCGGAA CGGA
                                    C  AC        C
GAM955  MGC39350  3'  AGGCCAAGGCGGGCGGATCACC 58651      T          A
           TG                     CAGGT ATCCGCTTGCCTT GCCT
                                  |||||| |||||||||||||| ||||
                                  GTCCA TAGGCGGGCGGAA CGGA
                                    C           C
GAM955  My015     3'  AGGCCAAAGCAGGCGGATCACC 66652      T        C  A
           TG                     CAGGT ATCCGCTTGC TT GCCT
                                  |||||| |||||||||| || ||||
                                  GTCCA TAGGCGGACG AA CGGA
                                    C         A  C
GAM955  NAG14     3'  AGGCTAAGGGGAAGATAGACCT 42161       _  CGC  G
           G                      CAGGTT ATC   TT CCTTAGCCT
                                  |||||| |||   || |||||||||
                                  GTCCAG TAG   AG GGAATCGGA
                                     A   A__  G
GAM955  ORC6L     3'  AGGCCAAGGTGGGTGGATCACC 26721      T      TG    A
           TG                     CAGGT ATCCGCT  CCTT GCCT
                                  ||||| |||||||  |||| ||||
                                  GTCCA TAGGTGG  GGAA CGGA
                                    C      GT    C
GAM955  PB1       3'  AGGCCAAGATGGGTGGATTACC 37019      T      GC   A
           TG                     CAGGT ATCCGCTT  CTT GCCT
                                  ||||| ||||||||  ||| ||||
                                  GTCCA TAGGTGGG  GAA CGGA
                                    T       TA   C
GAM955  RRP4      3'  AGGCCAAGGCGGGCAGATCACC 26561      T  C       A
           TG                     CAGGT ATC GCTTGCCTT GCCT
                                  ||||| ||| |||||||||| ||||
                                  GTCCA TAG CGGGCGGAA CGGA
                                    C  A        C
GAM955  SEMA5A    3'  AGGCCAAGGTGGGCGGATCACC 14251      T      TG    A
           TG                     CAGGT ATCCGCT  CCTT GCCT
                                  ||||| |||||||  |||| ||||
                                  GTCCA TAGGCGG  GGAA CGGA
                                    C      GT    C
GAM955  TNFAIP3   3'  AGGCTAAATAATAATAACCTG  20822        CCGC   CC
                                  CAGGTTAT    TTG  TTAGCCT
                                  ||||||||    |||  |||||||
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                                GTCCAATA   AAT  AATCGGA
                                   AT__   A_
GAM955  YME1L1   3'  AGGCCAAGGCGGGCAAATCACC 26525      T  CC       A
           TG                    CAGGT AT  GCTTGCCTT GCCT
                                 |||||| ||  |||||||||| ||||
                                 GTCCA TA  CGGGCGGAA CGGA
                                   C  AA        C
GAM955  YME1L1   3'  AGGCCAAGGCGGGCAAATCACC 57775      T  CC       A
           TG                    CAGGT AT  GCTTGCCTT GCCT
                                 |||||| ||  |||||||||| ||||
                                 GTCCA TA  CGGGCGGAA CGGA
                                   C  AA        C
GAM955  ZAK      3'  AGGCCAAGGTGGGCGGATCACC 56117      T     TG   A
           TG                    CAGGT ATCCGCT  CCTT GCCT
                                 ||||| |||||||  |||| ||||
                                 GTCCA TAGGCGG  GGAA CGGA
                                   C      GT   C
GAM955  ZFD25    3'  AGGCCAAGGTGGGTGGATCACC 32575      T     TG   A
           TG                    CAGGT ATCCGCT  CCTT GCCT
                                 ||||| |||||||  |||| ||||
                                 GTCCA TAGGTGG  GGAA CGGA
                                   C      GT   C
GAM955  LOC119504 5'  AGGCCAAGGCAGGTGGATCACC 73988      T          A
           TG                    CAGGT ATCCGCTTGCCTT GCCT
                                 ||||| ||||||||||||| ||||
                                 GTCCA TAGGTGGACGGAA CGGA
                                   C           C
GAM955  LOC127294 3'  AGGCCAAGGCGGGCAGATCACC 74653      T  C       A
           TG                    CAGGT ATC GCTTGCCTT GCCT
                                 ||||| ||| |||||||||| ||||
                                 GTCCA TAG CGGGCGGAA CGGA
                                   C  A        C
GAM955  LOC134147 3'  AGGCCAAAGTGGGTGGATCACC 57157      T     TG C  A
           TG                    CAGGT ATCCGCT  C TT GCCT
                                 ||||| |||||||  | || ||||
                                 GTCCA TAGGTGG  G AA CGGA
                                   C      GT A  C
GAM955  LOC138241 3'  AGGCCAAGGAGGGTGGATCACC 75307      T     TG   A
           TG                    CAGGT ATCCGCT  CCTT GCCT
                                 ||||| |||||||  |||| ||||
                                 GTCCA TAGGTGG  GGAA CGGA
                                   C      GA   C
GAM955  LOC144486 3'  AGGCCAAGGCAGGTGGATCACC 83079      T          A
           TG                    CAGGT ATCCGCTTGCCTT GCCT
                                 ||||| ||||||||||||| ||||
                                 GTCCA TAGGTGGACGGAA CGGA
                                   C           C
GAM955  LOC145453 3'  AGGCCAAGGCAGGTGGATCACC 77133      T          A
           TG                    CAGGT ATCCGCTTGCCTT GCCT
                                 ||||| |||||||||||| ||||
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                                GTCCA TAGGTGGACGGAA CGGA
                                  C           C
GAM955  LOC145955 3'  AGGCCAAGGCAGGTGGATCACC 83587      T          A
          TG                    CAGGT ATCCGCTTGCCTT GCCT
                                ||||| |||||||||||| ||||
                                GTCCA TAGGTGGACGGAA CGGA
                                  C           C
GAM955  LOC146713 3'  AGGCCAAGGTGGGCAGATCACC 83721      T  C  TG   A
          TG                    CAGGT ATC GCT  CCTT GCCT
                                ||||| ||| |||  |||| ||||
                                GTCCA TAG CGG  GGAA CGGA
                                  C  A  GT   C
GAM955  LOC148918 5'  AAGGTGGGCAGATCACCTG   79052      T  C  TG
                                CAGGT ATC GCT  CCTT
                                ||||| ||| |||  ||||
                                GTCCA TAG CGG  GGAA
                                  C  A  GT
GAM955  LOC148918 5'  AGGCCAAGGCAGGCAGATCACC 79059      T  C       A
          TG                    CAGGT ATC GCTTGCCTT GCCT
                                ||||| ||| |||||||| ||||
                                GTCCA TAG CGGACGGAA CGGA
                                  C  A       C
GAM955  LOC149194 5'  AGGCCAAGGCGGGTGGATCACC 79221      T          A
          TG                    CAGGT ATCCGCTTGCCTT GCCT
                                ||||| |||||||||||| ||||
                                GTCCA TAGGTGGGCGGAA CGGA
                                  C           C
GAM955  LOC149464 3'  AGGCCAAGGTGGGTGGATCACC 84425      T     TG   A
          TG                    CAGGT ATCCGCT  CCTT GCCT
                                ||||| |||||||  |||| ||||
                                GTCCA TAGGTGG  GGAA CGGA
                                  C      GT   C
GAM955  LOC149668 3'  AGGCTAAGGTGGGCGGATCACC 84532      T     TG
          TG                    CAGGT ATCCGCT  CCTTAGCCT
                                ||||| |||||||  |||||||||
                                GTCCA TAGGCGG  GGAATCGGA
                                  C      GT
GAM955  LOC152445 3'  AGGCCAAGGCAGGCGGATCACC 85742      T          A
          TG                    CAGGT ATCCGCTTGCCTT GCCT
                                ||||| |||||||||||| ||||
                                GTCCA TAGGCGGACGGAA CGGA
                                  C           C
GAM955  LOC153688 3'  AAGGCGGGTGGATCACCTG   86089      T
                                CAGGT ATCCGCTTGCCTT
                                ||||| ||||||||||||
                                GTCCA TAGGTGGGCGGAA
                                  C
GAM955  LOC154791 3'  AGGCCAAGGCAGGCGGATCACC 81153      T          A
          TG                    CAGGT ATCCGCTTGCCTT GCCT
                                ||||| |||||||||||| ||||
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                                GTCCA TAGGCGGACGGAA CGGA
                                  C           C
GAM955  LOC159053 3'  AGGCCAAGGCGGGCAGATCACC 86976      T  C       A
          TG                      CAGGT ATC GCTTGCCTT GCCT
                                  ||||| ||| |||||||||| ||||
                                GTCCA TAG CGGGCGGAA CGGA
                                  C  A       C
GAM955  LOC221178 3'  AGGCCAAGGCAGGTGGATCACC 93525      T          A
          TG                      CAGGT ATCCGCTTGCCTT GCCT
                                  ||||| |||||||||||||| ||||
                                GTCCA TAGGTGGACGGAA CGGA
                                  C           C
GAM955  LOC221943 5'  AGGCCAAGGCGGGTGGATCACC 93986      T          A
          TG                      CAGGT ATCCGCTTGCCTT GCCT
                                  ||||| |||||||||||||| ||||
                                GTCCA TAGGTGGGCGGAA CGGA
                                  C           C
GAM955  LOC254531 5'  AGGCCAAGGCGGGTGGATCACC 94979      T          A
          TG                      CAGGT ATCCGCTTGCCTT GCCT
                                  ||||| |||||||||||||| ||||
                                GTCCA TAGGTGGGCGGAA CGGA
                                  C           C
GAM955  LOC254778 3'  GCTAAGGCACCTAACTT     96128       TCCGCT      C
                                AGGTTA     TGCCTTAG C
                                ||||||     |||||||| |
                                TTCAAT     ACGGAATC G
                                   CC____       A
GAM955  LOC255042 3'  AGGCCGAGGCAAGCAGATCACC 95311      T  C       TA
          TG                      CAGGT ATC GCTTGCCT  GCCT
                                  ||||| ||| ||||||||  ||||
                                GTCCA TAG CGAACGGA  CGGA
                                  C  A       GC
GAM955  LOC256207 3'  AGGCCAAGGTGGGTGGATCACC 95165      T     TG   A
          TG                      CAGGT ATCCGCT  CCTT GCCT
                                  ||||| |||||||  |||| ||||
                                GTCCA TAGGTGG  GGAA CGGA
                                  C      GT   C
GAM955  LOC90591  3'  AAGGCAGGCAGATCACCTG    63404      T  C
                                CAGGT ATC GCTTGCCTT
                                ||||| ||| |||||||||
                                GTCCA TAG CGGACGGAA
                                  C  A
GAM955  LOC90785  3'  AGGCCAAAGTGGGCGGATCACC 64010      T     TG C  A
          TG                      CAGGT ATCCGCT  C TT GCCT
                                  ||||| |||||||  | || ||||
                                GTCCA TAGGCGG  G AA CGGA
                                  C      GT A  C
GAM955  LOC91574  3'  AGGCTAAGACAGGAAGATCACC 66517      T  CG   C
          TG                      CAGGT ATC  CTTG CTTAGCCT
                                  ||||| |||  |||| ||||||||
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                                GTCCA TAG  GGAC GAATCGGA
                                  C  AA   A
GAM955  LOC92270  5'  AGGCCAAGGGAGTGGATCACCT 68627      T      G   A
          G                      CAGGT ATCCGCTT CCTT GCCT
                                 ||||| |||||||| |||| ||||
                                 GTCCA TAGGTGAG GGAA CGGA
                                   C      _   C
GAM955  LOC92736  3'  AGGCCGAGGCAAGCAGATCACC 70425      T  C      TA
          TG                     CAGGT ATC GCTTGCCT  GCCT
                                 ||||| ||| ||||||||  ||||
                                 GTCCA TAG CGAACGGA  CGGA
                                   C  A      GC
GAM955  LOC93132  5'  AGGCCAAGGCGGGTGGATACCC 71481      T          A
          TG                     CAGG TATCCGCTTGCCTT GCCT
                                 |||| |||||||||||||| ||||
                                 GTCC ATAGGTGGGCGGAA CGGA
                                   C          C
GAM956  BGN      3'  CCTGCTCTCCCACCACAGC   8142      CA  T  AAG
                                 GCTG  GTG GA   GGGCAGG
                                 ||||  ||| ||   |||||||
                                 CGAC  CAC CT   CTCGTCC
                                   AC  C  ___
GAM956  CACNA2D2  3'  CCTGCCCCTTTCAGGCCTACAG 20082      CA_  G
          C                      GCTG  GT TGAAAGGGGCAGG
                                 ||||  || ||||||||||||
                                 CGAC  CG ACTTTCCCCGTCC
                                   ATC  G
GAM956  CACNB1   3'  CCTGCCCCTTCCTCCCAGCT   5570       CAGTGT  A
                                 AGCTG     GAA GGGGCAGG
                                 |||||     ||| ||||||||
                                 TCGAC     CTT CCCCGTCC
                                   CCTC__  _
GAM956  CEP2     5'  TGCCCCCACACTGTAGC     22285          AAA
                                 GCTGCAGTGTG   GGGGCA
                                 ||||||||||   ||||||
                                 CGATGTCACAC   CCCCGT
                                      ___
GAM956  DCN      5'  CCTCCTCCTTTCCACAC     8616       _     C
                                 GTGTG AAAGGGG AGG
                                 ||||| ||||||| |||
                                 CACAC TTTCCTC TCC
                                   C      C
GAM956  DDX11    3'  CCTGCCCCTTGTCATCTGCAGC 47651        T   _
                                 GCTGCAG GTGA AAGGGGCAGG
                                 ||||||| |||| ||||||||||
                                 CGACGTC TACT TTCCCCGTCC
                                     _   G
GAM956  DRPLA    5'  CCTGCTTCCCAGACCACAGCTG 8669        CA  G  AAA
                                 CAGCTG  GT TG   GGGGCAGG
                                 ||||||  || ||   ||||||||
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                                GTCGAC  CA AC   CTTCGTCC
                                   AC  G  C__
GAM956  ED1     5'  CCCACCCCTCGGAGTAGAGCTG 7364       __  AG  TGAA    CA
                                CAGCT  GC  TG   AGGGG  GG
                                |||||  ||  ||   |||||  ||
                                GTCGA  TG  GC   TCCCC  CC
                                   GA  AG  ____    AC
GAM956  EGR1    5'  CCTGCCCCAGCCTCCGCAGC   8741       __  T  GAAA
                                GCTGC  AG GT   GGGGCAGG
                                |||||  || ||   ||||||||
                                CGACG  TC CG   CCCCGTCC
                                   CC  _  A___
GAM956  EIF5A   3'  CCTGCCCCCTCCTCAGGCATCT 8766     C   AG  TGAAA
          G                      CAG TGC  TG    GGGGCAGG
                                ||| |||  ||    ||||||||
                                GTC ACG  AC    CCCCGTCC
                                  T   G_  TCCTC
GAM956  ENSA    3'  CCTGCCCCTTCCTGCTTTTGCA 15425       T_   A_
          GC                     GCTGCAG  GTG  AAGGGGCAGG
                                |||||||  |||  ||||||||||
                                CGACGTT  CGT  TTCCCCGTCC
                                   TT   CC
GAM956  EPHA8   3'  CCTGCCCCCCCCTCCCCATAGC  40056    A   T_  AA_
                                GC GTG  GA   GGGGCAGG
                                || |||  ||   ||||||||
                                CG TAC  CT   CCCCGTCC
                                 A   CC  CCC
GAM956  FAAH    3'  CCTGCCCCTTCCTCCTCGTA   44194     _  TGT   A
                                TGC AG   GAA GGGGCAGG
                                ||| ||   ||| ||||||||
                                ATG TC   CTT CCCCGTCC
                                  C  CTC   _
GAM956  FGFR1   3'  CCAAACCCCACACTGCGCTG   43637     T      AAA   GCA
                                CAGC GCAGTGTG   GGG   GG
                                |||| ||||||||   |||   ||
                                GTCG CGTCACAC   CCC   CC
                                  _      ___   AAA
GAM956  FGFR2   5'  CTGAGCCCACCGCAGCTG    43390       A   TGAAA  GG
                                CAGCTGC GTG    GG  CAG
                                ||||||| |||    ||  |||
                                GTCGACG CAC    CC  GTC
                                   C   _____  GA
GAM956  FGFR2   5'  CTGAGCCCACCGCAGCTG    43488       A   TGAAA  GG
                                CAGCTGC GTG    GG  CAG
                                ||||||| |||    ||  |||
                                GTCGACG CAC    CC  GTC
                                   C   _____  GA
GAM956  FGFR2   5'  CTGAGCCCACCGCAGCTG    43498       A   TGAAA  GG
                                CAGCTGC GTG    GG  CAG
                                ||||||| |||    ||  |||
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                                GTCGACG CAC    CC  GTC
                                   C  _____  GA
GAM956  GNA11    5'  GCCCCCACACCGCAGC      76103      A    AAA
                                GCTGC GTGTG   GGGGC
                                ||||| |||||   |||||
                                CGACG CACAC   CCCCG
                                   C   ___
GAM956  GRM6     5'  CCCGCCCCTCTGTCTCCCCGCA 5930       AGTGT  A__     A
              GC                  GCTGC    GA   AGGGGC GG
                                ||||||    ||   |||||| ||
                                CGACG    CT   TCCCCG CC
                                   CCCCT  GTC     C
GAM956  H1F0     3'  CCACCCCCTTTTTTTAAACAAGT 18014     GCAG  T       CA
                                GCT    TG GAAAGGGG  GG
                                |||    || ||||||||  ||
                                TGA    AT TTTTCCCC  CC
                                  ACAA  T       CA
GAM956  HAP1     3'  CCTGCCCCCCTTCACACAGCA  14166     A      A_
                                TGC GTGTGAA  GGGGCAGG
                                ||| |||||||  ||||||||
                                ACG CACACTT  CCCCGTCC
                                  A      CC
GAM956  HMOX2    3'  CTACCCCTTTCTCCAGC     65157      CAGTGT       C
                                GCTG     GAAAGGGG AG
                                ||||     |||||||| ||
                                CGAC     CTTTCCCC TC
                                   CT_____       A
GAM956  HOXC4    5'  CCTGCCCCCTTCTTGCAACT   27516    C    TGT   A
                                AG TGCAG   GAA GGGGCAGG
                                || |||||   ||| ||||||||
                                TC ACGTT   CTT CCCCGTCC
                                  A    ___   C
GAM956  HPCAL1   5'  CCTGGGGTCCTCACTGCAGCTG 56185          TGAA    G__
                                CAGCTGCAGTG    AGGG   CAGG
                                ||||||||||    ||||   ||||
                                GTCGACGTCAC    TCCT   GTCC
                                      _____    GGG
GAM956  KRT8     3'  TCCCCTCCTGCGCTG       9639       T    TGTGAA    C
                                CAGC GCAG      AGGGG A
                                |||| ||||      ||||| |
                                GTCG CGTC      TCCCC T
                                   _    C_____     A
GAM956  LTBP2    3'  CCATGGCCTCACACTGCAG    4721           AAG  G  _
                                CTGCAGTGTGA   GG CA GG
                                ||||||||||   || || ||
                                GACGTCACACT   CC GT CC
                                      ___  G  A
GAM956  MAPK3    3'  CCTGCCCCTCTCCCGCCAGACT 73384     _   CA   T  A
              G                  CAG CTG  GTG GA AGGGGCAGG
                                ||| |||  ||| || |||||||||
```

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                                GTC GAC  CGC CT TCCCCGTCC
                                  A  __  C  C
GAM956  MPG     5'  CTGCCCCCAGCAGCAGC     10109      AG   GAAA
                                GCTGC  TGT   GGGGCAG
                                |||||  |||   |||||||
                                CGACG  ACG   CCCCGTC
                                   __  AC__
GAM956  MSF     3'  CCCACCCCTTCGACATGCTGC  88079        A__     CA
                                GCAGTGTG  AAGGGG  GG
                                ||||||||  ||||||  ||
                                CGTCGTAC  TTCCCC  CC
                                     AGC    AC
GAM956  MUC4    5'  CTCCTCACACTGCAGCTG    56324           AA
                                CAGCTGCAGTGTGA  GGGG
                                ||||||||||||||  ||||
                                GTCGACGTCACACT  CCTC
                                          __
GAM956  MUC4    5'  CTCCTCACACTGCAGCTG    37271           AA
                                CAGCTGCAGTGTGA  GGGG
                                ||||||||||||||  ||||
                                GTCGACGTCACACT  CCTC
                                          __
GAM956  NAP1L4  3'  CACCCCTCCTGCAGTTG     19918         TGTGAA    CA
                                CAGCTGCAG     AGGGG  G
                                |||||||||     |||||  |
                                GTTGACGTC     TCCCC  C
                                     C_____    AC
GAM956  NFKB2   5'  CTGCCCCTTCCCCGGC      10213      CAGTGT   A
                                GCTG     GAA GGGGCAG
                                ||||     ||| |||||||
                                CGGC     CTT CCCCGTC
                                  CC____  _
GAM956  NGFR    3'  CCTGCCCCCTTCTCCCACACTG 10225        ____  A
          C                      GCAGTGT   GAA GGGGCAGG
                                |||||||   ||| ||||||||
                                CGTCACA   CTT CCCCGTCC
                                    CCCT  C
GAM956  NR1I2   5'  CCTGCCCCCCTCTTACAT    13966       AA__
                                GTGTGA   GGGGCAGG
                                ||||||   ||||||||
                                TACATT   CCCCGTCC
                                   CTCC
GAM956  OTC     5'  TTTGCTCCCTCACTGCAACTG  5001     C      TGAA   _
                                CAG TGCAGTG   AGGG GCAGG
                                ||| |||||||   |||| |||||
                                GTC ACGTCAC   TCCC CGTTT
                                  A      ____   T
GAM956  PDGFB   5'  CCTGCCCCCCCAGCGACGGAGC  10496    GCAG   GAAA
                                GCT   TGT   GGGGCAGG
                                |||   |||   ||||||||
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                                CGA   GCG   CCCCGTCC
                                  GGCA  ACC_
GAM956  PEA15    3'  CCTGCCCCTCTGGCCACTGC  13651      TGAA_
                                GCAGTG    AGGGGCAGG
                                ||||||    |||||||||
                                CGTCAC    TCCCCGTCC
                                   CGGTC
GAM956  PPP2R5D  3'  CCTGCTCCTCACCCACAGCT  20717      CAGT   AA
                                AGCTG   GTGA  GGGGCAGG
                                |||||   ||||  ||||||||
                                TCGAC   CACT  CCTCGTCC
                                  ACC_   __
GAM956  PPP2R5E  5'  CGCCCCCGCTGCGGC      20724        TGAAA    A
                                GCTGCAGTG    GGGGC G
                                |||||||||    ||||| |
                                CGGCGTCGC    CCCCG C
                                     _____    C
GAM956  PRODH    3'  CCCGCCCAGGCCATCACCACAG 32923      CA  _  AAAG   A
           CTG                    CAGCTG  GTG TG   GGGC GG
                                ||||||  ||| ||   |||| ||
                                GTCGAC  CAC AC   CCCG CC
                                   AC   T  CGGA   C
GAM956  RAB36    3'  CCTGGCACACTGCAGCTG    16956          AA
                                CAGCTGCAGTGTG  AGG
                                ||||||||||||  |||
                                GTCGACGTCACAC  TCC
                                       GG
GAM956  RCN1     3'  CCTGCCCCCCCCCGCAACAGCT  11271      CAG   AAA
                                AGCTG   TGTG   GGGGCAGG
                                |||||   ||||   ||||||||
                                TCGAC   ACGC   CCCCGTCC
                                  A__    CCC
GAM956  SLC25A1  3'  CCTGCCCTGGCCTACCACAGCT 19964      CA   TGAAA
           G                    CAGCTG  GTG    GGGGCAGG
                                ||||||  |||    ||||||||
                                GTCGAC  CAT    TCCCGTCC
                                   AC   CCGG_
GAM956  SLC29A1  3'  CTGCCCCTTCCTTCTGC    17074     TGT   A
                                GCAG   GAA GGGGCAG
                                ||||   ||| |||||||
                                CGTC   CTT CCCCGTC
                                  TTC   _
GAM956  SLC9A6   3'  CCACGATCGTTCCACACTGCA  21001        A  G  GCA_
                                TGCAGTGTG AA GG    GG
                                |||||||||  || ||    ||
                                ACGTCACAC TT CT    CC
                                     C  G  AGCA
GAM956  SORCS1   3'  TGCCCCAACTGCAGT      53589        GTGAAA
                                GCTGCAGT     GGGGCA
                                ||||||||     ||||||
```

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                                TGACGTCA     CCCCGT
                                   A_____
GAM956  SYT1     3'  CCTATTATCCCACACTGCATCT 18900    C       AAA   GC__
                                AG TGCAGTGTG   GGG    AGG
                                || |||||||||   |||    |||
                                TC ACGTCACAC   CCT    TCC
                                 T        ___   ATTA
GAM956  TACC1    5'  CCTGCCCCTAGGAGCTGGAGC  20796     G   GTGAA
                                GCT CAGT     AGGGGCAGG
                                ||| ||||     |||||||||
                                CGA GTCG     TCCCCGTCC
                                  G    AGGA_
GAM956  TARDBP   3'  CCTACCCCTTTGTCAACTGC   23771      GTG_     C
                                GCAGT    AAAGGGG AGG
                                |||||    ||||||| |||
                                CGTCA    TTTCCCC TCC
                                   ACTG      A
GAM956  TKTL1    3'  CCATCCCACCTGCAGCTG    24297        T   AAAG
                                CAGCTGCAG GTG    GG
                                ||||||||| |||    ||
                                GTCGACGTC CAC    CC
                                     _   CCTA
GAM956  TTF2     3'  CCTGCAGCCACCCTGCAGC    13174       T   AAAGGG
                                GCTGCAG GTG     GCAGG
                                ||||||| |||     |||||
                                CGACGTC CAC     CGTCC
                                    C   CGA___
GAM956  ARHGEF9  5'  CCACCTGGAACACTACAGT    30806     C    GAA   _
                                GCTG AGTGT   AGG GG
                                |||| |||||   ||| ||
                                TGAC TCACA   TCC CC
                                  A     AGG   A
GAM956  BICD2    3'  CCTGTCACACTGCAGC      70391          A
                                GCTGCAGTGTGA AGG
                                |||||||||||| |||
                                CGACGTCACACT TCC
                                       G
GAM956  C11orf11 3'  CCCACCCCCAAGGCTGCAGC   93252        G_  AAA    CA
                                GCTGCAGT  TG   GGGG  GG
                                ||||||||  ||   ||||  ||
                                CGACGTCG  AC   CCCC  CC
                                     GA  ___    AC
GAM956  C16orf7  3'  CGCCCATCGCTGCAGCTG    16939          TGAAAG    A
                                CAGCTGCAGTG     GGGC G
                                ||||||||||      |||| |
                                GTCGACGTCGC     CCCG C
                                       TA_____    C
GAM956  C20orf124 3'  CTGCCCCCTCCAATGC      45485     G  T  AA
                                GCA TG GA  GGGGCAG
                                ||| || ||  |||||||
```

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                                CGT AC CT  CCCCGTC
                                  A  _  C_
GAM956  C20orf151 3'  CCTACCCCTGCTGTGCACTGCA 88700          AA__    C
            GC                    GCTGCAGTGTG    AGGGG AGG
                                  ||||||||||    ||||| |||
                                  CGACGTCACGT    TCCCC TCC
                                        GTCG    A
GAM956  Cab45    5'  CTGCCCCTCCCAGCACCTG   32447    C   AGTG  AA
                                  CAG TGC    TG  AGGGGCAG
                                  ||| |||    ||  ||||||||
                                  GTC ACG    AC  TCCCCGTC
                                    C  _____  CC
GAM956  Cab45    5'  CTGCCCCTCCCAGCACCTG   33318    C   AGTG  AA
                                  CAG TGC    TG  AGGGGCAG
                                  ||| |||    ||  ||||||||
                                  GTC ACG    AC  TCCCCGTC
                                    C  _____  CC
GAM956  CASKIN1  3'  CTGCCCCCTCCAAGAAGT    40398    GCAG  T  AA
                                  GCT    TG GA  GGGGCAG
                                  |||    || ||  |||||||
                                  TGA    AC CT  CCCCGTC
                                    AGA_  _  C_
GAM956  COPS7A   3'  CCTGTCACACTACAGTCA    32856   A   C      A
                                  C GCTG AGTGTGA AGG
                                  | |||| ||||||| |||
                                  A TGAC TCACACT TCC
                                   C    A      G
GAM956  DKFZp434J1015 3'  CCTGCCCCTCTCCCCCCAGCTG 92634        CAGTGT  A
                                  CAGCTG      GA AGGGGCAGG
                                  ||||||      || |||||||||
                                  GTCGAC      CT TCCCCGTCC
                                      CCCC__  C
GAM956  DKFZp762E1312 5'  CCTGCCCCCGGATACTGCAGT  37284          GAAA
                                  GCTGCAGTGT    GGGGCAGG
                                  ||||||||||    ||||||||
                                  TGACGTCATA    CCCCGTCC
                                        GGC_
GAM956  FAM10A7  3'  CCTACCCCTCTCCCCCAAATGC 81245         GTGT___  A    C
            AGCTG                   CAGCTGCA      GA AGGGG AGG
                                  ||||||||      || ||||| |||
                                  GTCGACGT      CT TCCCC TCC
                                       AAACCCC  C    A
GAM956  FER1L4   3'  CCTGCCCCTGAATACCGAGC   47338    GCA   GAA
                                  GCT   GTGT   AGGGGCAGG
                                  |||   ||||   |||||||||
                                  CGA   CATA   TCCCCGTCC
                                    GC_   AG_
GAM956  FLJ10261  3'  CCTGCCCCCATCACACCAAGC  35953    GCA    AA
                                  GCT   GTGTGA  GGGGCAGG
                                  |||   ||||||  ||||||||
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                                CGA  CACACT  CCCCGTCC
                                  AC_    AC
GAM956  FLJ10713 3' CTGCCACCACACCCAGCT   36468     CA   AAAGG
                                AGCTG  GTGTG   GGCAG
                                |||||  |||||   |||||
                                TCGAC  CACAC   CCGTC
                                  C_    CA___
GAM956  FLJ10853 3' TCTGTACCTCACACTGCA   36771       AA  GG
                                TGCAGTGTGA  GG  CAGG
                                ||||||||||  ||  ||||
                                ACGTCACACT  CC  GTCT
                                      __ AT
GAM956  FLJ11099 3' CCTGCCCCTTCAAGGGCAGC  37045     AGTG   A
                                GCTGC   TGAA GGGGCAGG
                                |||||   |||| ||||||||
                                CGACG   ACTT CCCCGTCC
                                  GGA_   _
GAM956  FLJ12960 3' CCTGCCCTGGCAGTGCAGC   44947     G   GAAA
                                GCTGCA TGT   GGGGCAGG
                                ||||||| |||   ||||||||
                                CGACGT ACG   TCCCGTCC
                                   G  G___
GAM956  FLJ13055 3' CTGCCCCCCAAGCCAGC    42712    CA  G  AAA
                                GCTG  GT TG  GGGGCAG
                                ||||  || ||  |||||||
                                CGAC  CG AC  CCCCGTC
                                  __ A  C__
GAM956  FLJ13322 3' CACCCCTCCCTGCAGCT    45296      TGTGAA   CA
                                AGCTGCAG    AGGGG  G
                                ||||||||    |||||  |
                                TCGACGTC    TCCCC  C
                                    CC_____   AC
GAM956  FLJ13782 3' CCTACCCCTCTCTCTCCAGC  46165    C  TGT  A   C
                                GCTG AG   GA AGGGG AGG
                                |||| ||   || ||||| |||
                                CGAC TC   CT TCCCC TCC
                                  C  T__  C    A
GAM956  FLJ14154 3' CCTGCCCCCCTGCGCATGCA  45814    G   AAA_
                                TGCA TGTG   GGGGCAGG
                                |||| ||||   ||||||||
                                ACGT ACGC   CCCCGTCC
                                  _   GTCC
GAM956  FLJ14154 3' CCTGCCCCTAATCACTGCAGT 45815       TGAA
                                GCTGCAGTG   AGGGGCAGG
                                |||||||||   |||||||||
                                TGACGTCAC   TCCCCGTCC
                                     TAA_
GAM956  FLJ14936 3' GCTCTCCCACACTGCGCT    50133    T     AAA
                                AGC GCAGTGTG   GGGGC
                                ||| ||||||||   |||||
```

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                                TCG CGTCACAC   TCTCG
                                  _      CC_
GAM956  FLJ14950  3'  CCTGCCCCCTCCCAGCAGC   51718     AG  T  AA
                                GCTGC  TG GA  GGGGCAGG
                                |||||  || ||  ||||||||
                                CGACG  AC CT  CCCCGTCC
                                  __  C  C_
GAM956  FLJ20507  3'  CCTGCCCCCTTCACATTCA   60215    C      A
                                TG AGTGTGAA GGGGCAGG
                                || |||||||| ||||||||
                                AC TTACACTT CCCCGTCC
                                  _      C
GAM956  FLJ20507  3'  CCTGCCCCCTTCACATTCA   35280    C      A
                                TG AGTGTGAA GGGGCAGG
                                || |||||||| ||||||||
                                AC TTACACTT CCCCGTCC
                                  _      C
GAM956  FLJ22169  3'  CACCCCTCACCCAGCTG    44000      CA   TGAA    CA
                                CAGCTG  GTG   AGGGG  G
                                ||||||  |||   |||||  |
                                GTCGAC  CAC   TCCCC  C
                                   C_  ____    AC
GAM956  H326    3'  CCTGCCCCTTTCCCAGCAGCT  31705      AG  T
                                AGCTGC  TG GAAAGGGGCAGG
                                ||||||  || ||||||||||||
                                TCGACG  AC CTTTCCCCGTCC
                                   __  C
GAM956  HRI     3'  CCTGCCCCTTTCACACTGCAGC 26982
            TG                    CAGCTGCAGTGTGAAAGGGGCAGG
                                ||||||||||||||||||||||||
                                GTCGACGTCACACTTTCCCCGTCC

GAM956  HTATIP   3'  CGCCCCCACTGCAGCT     21106         TGAAA    A
                                AGCTGCAGTG    GGGGC G
                                ||||||||||    ||||| |
                                TCGACGTCAC    CCCCG C
                                     _____    C
GAM956  HYA22    3'  CTGCTCTCACACTACTGC    19425      _  AAA
                                GCAGT GTG   GGGGCAG
                                ||||| |||   |||||||
                                CGTCA CAC   TCTCGTC
                                   T   AC_
GAM956  ITM3    3'  CCTGCCCCCCCAGGAGCACAAGC 48163    GCA   GAAA__
                                GCT   GTGT    GGGGCAGG
                                |||   ||||    ||||||||
                                CGA   CACG    CCCCGTCC
                                  A__   AGGACC
GAM956  KIAA0169 3'  CCTACCCCTCTCCACCAGC   72818    CA  T  A   C
                                GCTG  GTG GA AGGGG AGG
                                ||||  ||| || ||||| |||
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                                CGAC  CAC CT TCCCC TCC
                                  __  _ C    A
GAM956  KIAA0329 3' CCACCCCACACCGCACTG    29271    C  A    AAA  GCA
                                CAG TGC GTGTG  GGG  G
                                ||| ||| |||||  |||  |
                                GTC ACG CACAC  CCC  C
                                  _  C    ___  ACA
GAM956  KIAA0367 3' CTACTTTCACACTACAGC    67298     C       GG
                                GCTG AGTGTGAAAG  G
                                |||| ||||||||||  |
                                CGAC TCACACTTTC  C
                                  A        AT
GAM956  KIAA0537 5' CTGCCCCCTCCCCCAGCT    29248      CAGTGT  AA
                                AGCTG     GA  GGGGCAG
                                |||||     ||  |||||||
                                TCGAC     CT  CCCCGTC
                                   CCC___  C_
GAM956  KIAA0562 3' CCCGCCCCTTCCACATCCATGT 28149     TGCA    A     A
           TG                    CAGC    GTGTG AAGGGGC GG
                                ||||    ||||| ||||||| ||
                                GTTG    TACAC TTCCCCG CC
                                  TACC    C      C
GAM956  KIAA0657 5' CCTGCCCCCCCCACCGTTCGCCG 72197     T  AGT__   AAA
           CTG                    CAGC GC    GTG   GGGGCAGG
                                |||| ||    |||  ||||||||
                                GTCG CG    CAC   CCCCGTCC
                                  C  CTTGC   CC_
GAM956  KIAA0676 3' TCTGTGCTCCACACTGCGGC   30454          AAA  G
                                GCTGCAGTGTG   GG GCAGG
                                ||||||||||   || |||||
                                CGGCGTCACAC   TC TGTCT
                                      C__  G
GAM956  KIAA0789 3' CCTGCCCCTTTCTATCCATGCT 63683     TGCA   T
           G                     CAGC    GTG GAAAGGGGCAGG
                                ||||    ||| ||||||||||||
                                GTCG    TAT CTTTCCCCGTCC
                                  TACC   _
GAM956  KIAA0852 3' CCTGCCCCTCAACCCTGTAGCT 30076         T  GAA
           G                     CAGCTGCAG GT   AGGGGCAGG
                                |||||||| ||   |||||||||
                                GTCGATGTC CA   TCCCCGTCC
                                     C  AC_
GAM956  KIAA1110 5' CCTGCCCCCGGCCCACAGCGG  61843     A  TGAAA
                                CTGC GTG    GGGGCAGG
                                |||| |||    ||||||||
                                GGCG CAC    CCCCGTCC
                                  A  CCGGC
GAM956  KIAA1297 5' CTACCCCACCATCAGCTG    72178       CAGT   AAA   C
                                CAGCTG   GTG   GGGG AG
                                ||||||   |||   |||| ||
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                                GTCGAC   TAC  CCCC TC
                                   ____  CA_   A
GAM956  KIAA1372  3'  CCTGCCCCCTTACCAAGCGC  91650   T  AGT   AA
                                GC GC  GTGA  GGGGCAGG
                                || ||  ||||  ||||||||
                                CG CG  CATT  CCCCGTCC
                                 _ AAC   C_
GAM956  KIAA1493  3'  CTGCCACCACACCCAGCT   64161     CA    AAAGG
                                AGCTG  GTGTG   GGCAG
                                |||||  |||||   |||||
                                TCGAC  CACAC   CCGTC
                                  C_   CA___
GAM956  KIAA1538  5'  CTGCCACCACCACAGCTG   71543     CA   TGAAAGG
                                CAGCTG  GTG    GGCAG
                                ||||||  |||    |||||
                                GTCGAC  CAC    CCGTC
                                   AC   CA_____
GAM956  KIAA1656  3'  CCTGCCCCTTTCACTAGGCA  65788    AGT
                                TGC   GTGAAAGGGGCAGG
                                |||   ||||||||||||||
                                ACG   CACTTTCCCCGTCC
                                  GAT
GAM956  KIAA1771  5'  CCTGCCCCCCCCCACCAACTG  79135     __  AAA
                                CAGT  GTG   GGGGCAGG
                                ||||  |||   ||||||||
                                GTCA  CAC   CCCCGTCC
                                  AC   CCC
GAM956  LLGL2    3'  CCGGCTTCCACAATGCAGCTG  15751       G   AAA    A
                                CAGCTGCA TGTG   GGGGC GG
                                |||||||| ||||   ||||| ||
                                GTCGACGT ACAC   CTTCG CC
                                    A   ___    G
GAM956  MAGE-E1   5'  CCCGCCCCCTCCCCCTGCAGCT 47944        TGT  AA    A
           G                     CAGCTGCAG   GA  GGGGC GG
                                |||||||||   ||  ||||| ||
                                GTCGACGTC   CT  CCCCG CC
                                     CCC  C_    C
GAM956  MCF2L    3'  CCTGCCCCTGCCTCACTGCACT 60842     C      TGAA
           G                     CAG TGCAGTG    AGGGGCAGG
                                ||| |||||||    |||||||||
                                GTC ACGTCAC    TCCCCGTCC
                                  _      TCCG
GAM956  MFN2     3'  CCTGCCCCCTGGCCACTGC   29599       TGAAA
                                GCAGTG    GGGGCAGG
                                ||||||    ||||||||
                                CGTCAC    CCCCGTCC
                                   CGGTC
GAM956  MGC:13379 3'  CTGCCCCTTCTCAGAAC     33245    G_  _
                                GT  TGA AAGGGGCAG
                                ||  ||| |||||||||
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                                CA  ACT TTCCCCGTC
                                 AG   C
GAM956  MGC10646 3' CCTACTCACACTACGCTG    51106     T C     AA
                                CAGC G AGTGTGA  GGG
                                |||| | |||||||  |||
                                GTCG C TCACACT  TCC
                                  _ A      CA
GAM956  MGC10981 3' CCTGTAAATCCCCACACTGCAG 51016          AAA  ____
           C                     GCTGCAGTGTG   GGG   GCAGG
                                ||||||||||  |||   |||||
                                CGACGTCACAC   CCC   TGTCC
                                      ___  TAAA
GAM956  MGC13114 3' CTGCCCCCCGCCCAGC     50413     CAGT   AAA
                                GCTG   GTG   GGGGCAG
                                ||||   |||   |||||||
                                CGAC   CGC   CCCCGTC
                                  C___   C__
GAM956  MGC15677 3' CCTGCCCCTTTGGGGCTGC   51797      GTG
                                GCAGT   AAAGGGGCAGG
                                |||||  ||||||||||
                                CGTCG   TTTCCCCGTCC
                                   GGG
GAM956  MGC16179 3' CCTGCCCCTCCCAGTTCTGCGG 51302        TG_  AA
           CTG                    CAGCTGCAG   TG  AGGGGCAGG
                                |||||||||   ||  |||||||||
                                GTCGGCGTC   AC  TCCCCGTCC
                                     TTG  CC
GAM956  MGC20470 3' CCTGCCCCCAGCTGCAGCT   58963        GTGAAA
                                AGCTGCAGT     GGGGCAGG
                                |||||||||     ||||||||
                                TCGACGTCG     CCCCGTCC
                                     AC_____
GAM956  MGC2474  3' CCTGTCCCCCGAGCTG     43720      G  AAA
                                CAGT TG   GGGGCAGG
                                |||| ||   ||||||||
                                GTCG GC   CCCTGTCC
                                  A  C__
GAM956  MGC2752  5' CCCAGGAGGCCACACTGCAGGC 78446    _       AAAG___
                                GC TGCAGTGTG      GGG
                                || |||||||||      |||
                                CG ACGTCACAC      CCC
                                 G        CGGAGGA
GAM956  MGC3113  3' CCCACCCCCTTCGCCAGCAGCT 43843       AGT    A    CA
                                AGCTGC   GTGAA GGGG  GG
                                ||||||   ||||| ||||  ||
                                TCGACG   CGCTT CCCC  CC
                                   AC_    C    AC
GAM956  MGC4604  3' CCTGCCCCTTTCTCTACTGAGC 48977      G    T_
           T                     AGCT CAGTG  GAAAGGGGCAGG
                                ||||| |||||  ||||||||||||
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                                TCGA GTCAT  CTTTCCCCGTCC
                                  _    CT
GAM956  OASIS    3'  CCTGCCCCCACACCTGCA    53463      _   AAA
                                TGCAG TGTG   GGGGCAGG
                                ||||| ||||  ||||||||
                                ACGTC ACAC   CCCCGTCC
                                  C   ___
GAM956  OATPRP4  5'  CCTGCCCCCTGTGGCACGCGGC 48232       A   GAAA_
           TG                    CAGCTGC GTGT    GGGGCAGG
                                ||||||| ||||    ||||||||
                                GTCGGCG CACG    CCCCGTCC
                                   _   GTGTC
GAM956  PADI1    3'  CCTGCTGAGACCTCACACTGAG 61994    G      AA ____
           C                     GCT CAGTGTGA  GG   GGCAGG
                                ||| ||||||||  ||   ||||||
                                CGA GTCACACT  CC   TCGTCC
                                  _      __ AGAG
GAM956  PP1057   5'  CCCTCCAAACTGCAGCTG    48433         G  AA
                                CAGCTGCAGT TG  AGGG
                                |||||||||| ||  ||||
                                GTCGACGTCA AC  TCCC
                                     A  C_
GAM956  PPM1G    3'  CCCTCCACACTGCAGC      10709          AA
                                GCTGCAGTGTG  AGGG
                                ||||||||||  ||||
                                CGACGTCACAC  TCCC
                                     C_
GAM956  PRDX2    3'  CCTGCCCCTCCAAACTCCACAG 59881     C__   G  AA
           T                     GCTG   AGT TG  AGGGGCAGG
                                ||||   ||| ||  |||||||||
                                TGAC   TCA AC  TCCCCGTCC
                                  ACC   A  C_
GAM956  RAI15    3'  CTCCCCCCCACCACAGCTG    66669       CA   TGAAA   C
                                CAGCTG  GTG    GGGG AG
                                ||||||  |||    |||| ||
                                GTCGAC  CAC    CCCC TC
                                   AC  _____   C
GAM956  SDC3     3'  CCTGCTTCCTCCCCACCGCAGC 27747       A   TGAA   _
           TG                    CAGCTGC GTG    AGGG GCAGG
                                ||||||| |||    |||| |||||
                                GTCGACG CAC    TCCT CGTCC
                                   C   CCC_    T
GAM956  SDS3     3'  CCTACCCCCTTTTCCCTG    69227     TGT      C_
                                CAG   GAAAGGGG  AGG
                                |||   ||||||||  |||
                                GTC   TTTTCCCC  TCC
                                  CC_       CA
GAM956  SPINLW1  3'  CTGCCCCCTCAACAGTCC    39870   A   CAGTG   AA
                                C GCTG    TGA  GGGGCAG
                                | ||||    |||  |||||||
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                                C TGAC    ACT  CCCCGTC
                                 C   A____   C_
GAM956  SR-BP1   3'  CCCTTCACCTGCAGCT     19632        T    A
                                AGCTGCAG GTGAA GGG
                                |||||||| ||||| |||
                                TCGACGTC CACTT CCC
                                      _    _
GAM956  ST13     3'  CCTACCCCTCTCCCCCAAATGC 14116        GTGT___ A    C
            AGCTG                   CAGCTGCA      GA AGGGG AGG
                                |||||||       || ||||| |||
                                GTCGACGT      CT TCCCC TCC
                                      AAACCCC  C    A
GAM956  TEB4     3'  CCTCTCTTTTCCACAC      60655       _      C
                                GTGTG AAAGGGG AGG
                                ||||| ||||||| |||
                                CACAC TTTTCTC TCC
                                   C      _
GAM956  TNFRSF19L 3'  CTGCCCCTCCCCCAGCTG    51776       CAGTGTGAA
                                CAGCTG        AGGGGCAG
                                ||||||        ||||||||
                                GTCGAC        TCCCCGTC
                                    CCCC_____
GAM956  TNFRSF19L 3'  CCCGCCCCTGGCCCTGCTGC   51774    T    T  GAA     A
                                GC GCAG GT   AGGGGC GG
                                || |||| ||   |||||| ||
                                CG CGTC CG   TCCCCG CC
                                 T    C  G__     C
GAM956  TRIM16   3'  CTGCCACCACACCCAGCT    21338      CA    AAAGG
                                AGCTG  GTGTG    GGCAG
                                |||||  |||||    |||||
                                TCGAC  CACAC    CCGTC
                                   C_    CA___
GAM956  WBSCR20A  5'  TGCCCCTCCACATCTG      49658     _    AA
                                CAG TGTG  AGGGGCA
                                ||| ||||  |||||||
                                GTC ACAC  TCCCCGT
                                  T    C_
GAM956  ZF       3'  CCCCTCACAATGCAGCTG    41085         G    AA
                                CAGCTGCA TGTGA  GGGG
                                |||||||| |||||  ||||
                                GTCGACGT ACACT  CCCC
                                     A    __
GAM956  ZNF221   3'  CGCCACCACACCCAGCT     25337      CA    AAAGG   A
                                AGCTG  GTGTG    GGC G
                                |||||  |||||    ||| |
                                TCGAC  CACAC    CCG C
                                   C_    CA___   C
GAM956  LOC112817 3'  CCTGCCCTCCACACTGCAAGCT 56509       _       AAA
            G                    CAGCT GCAGTGTG   GGGGCAGG
                                ||||| ||||||||   ||||||||
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                                GTCGA CGTCACAC   TCCCGTCC
                                  A       C__
GAM956  LOC115708 3'  CCTGCCCCTCCTGGCCACAGC  73547     CA  GTGAA
                                GCTG  GT    AGGGGCAGG
                                |||| ||    |||||||||
                                CGAC  CG    TCCCCGTCC
                                  AC  GTCC_
GAM956  LOC121274 5'  CCTAGAACCCACACTGCAGT   74062          AAA  GGC_
                                GCTGCAGTGTG   GG    AGG
                                ||||||||||  ||    |||
                                TGACGTCACAC   CC    TCC
                                      ___  AAGA
GAM956  LOC124930 3'  CCCACCCCTTCCCACCAGCTGC 74355     T    __   A_     CA
          TGCT                    AGC GCAGT  GTG  AAGGGG  GG
                                ||| |||||  |||  ||||||  ||
                                TCG CGTCG  CAC  TTCCCC  CC
                                  T    AC   CC     AC
GAM956  LOC128402 3'  CCTGCCCCTCAGTCATGCAGCT 75780       G  TGAA
                                AGCTGCA TG    AGGGGCAGG
                                ||||||| ||    |||||||||
                                TCGACGT AC    TCCCCGTCC
                                   _  TGAC
GAM956  LOC129450 3'  CCACCCCCTTTTCAACCAC    74873     __       CA_
                                GTG  TGAAAGGGG   GG
                                |||  |||||||||   ||
                                CAC  ACTTTTCCC   CC
                                  CA        CCA
GAM956  LOC130639 3'  CTGCCTGACACTGCACTG     74973     C       GAAAG
                                CAG TGCAGTGT     GGGCAG
                                ||| ||||||||     ||||||
                                GTC ACGTCACA     TCCGTC
                                  _       G____
GAM956  LOC143243 3'  CCTGCCCCCTCCTCAGGCATCT 60305     C   AG  TGAAA
          G                      CAG TGC  TG    GGGGCAGG
                                ||| |||  ||    ||||||||
                                GTC ACG  AC    CCCCGTCC
                                  T   G_  TCCTC
GAM956  LOC144563 5'  CCTGCCCCTCTCTGTCGTAGCT 76888       AG  T  A
                                AGCTGC  TG GA AGGGGCAGG
                                ||||||  || || |||||||||
                                TCGATG  GT CT TCCCCGTCC
                                   CT  _  C
GAM956  LOC146229 3'  CACCTCCACACCCAGCT     77732      CA    AAA    CA
                                AGCTG  GTGTG   GGGG  G
                                |||||  |||||   ||||  |
                                TCGAC  CACAC   CTCC  C
                                  C_     ___    AC
GAM956  LOC146988 3'  CCACCCCCTCAAAATCACCCCA 83891       CA   TGAA__    CA
          GCTG                    CAGCTG  GTG     AGGGG  GG
                                ||||||  |||     |||||  ||
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                                GTCGAC  CAC     TCCCC  CC
                                   CC   TAAAAC    CA
GAM956  LOC147111 3'  CCTGCCCCTCTCCCACAGC   83947    A   T  A
                                GC GTG GA AGGGGCAGG
                                || ||| || |||||||||
                                CG CAC CT TCCCCGTCC
                                 A   C  C
GAM956  LOC147166 3'  CTGCCACCACACCCAGCT    78286      CA    AAAGG
                                AGCTG  GTGTG    GGCAG
                                |||||  |||||    |||||
                                TCGAC  CACAC    CCGTC
                                   C_    CA___
GAM956  LOC147645 5'  CCTGCCCCCCGGGGCCCCACAG 78422      CAGT  GAAA_
           T                     GCTG    GT    GGGGCAGG
                                ||||    ||    ||||||||
                                TGAC    CG    CCCCGTCC
                                   ACCC  GGGCC
GAM956  LOC147858 3'  CCTGCCCCTGGTGCCCAGC   78570     CAGT   AA
                                GCTG    GTG  AGGGGCAGG
                                ||||    |||  |||||||||
                                CGAC    CGT  TCCCCGTCC
                                   C___   GG
GAM956  LOC149461 3'  CCTGCCCCCGACCCCACAGCT  79401      CAGT  GAAA
                                AGCTG    GT    GGGGCAGG
                                |||||    ||    ||||||||
                                TCGAC    CA    CCCCGTCC
                                   ACCC  GC__
GAM956  LOC149478 5'  CTGCCCCAAACTACAGCT    79376      C   GTGAAA
                                AGCTG AGT     GGGGCAG
                                ||||| |||     |||||||
                                TCGAC TCA     CCCCGTC
                                   A   AA____
GAM956  LOC149501 3'  TGCCCCTTCTGCGCTG      75276       GA
                                CAGTGT  AAGGGGCA
                                ||||||  ||||||||
                                GTCGCG  TTCCCCGT
                                    TC
GAM956  LOC149668 5'  CCTGCCCCTCTCCCTCAGCT   84537      C  TGT  A
                                AGCTG AG   GA AGGGGCAGG
                                ||||| ||   || |||||||||
                                TCGAC TC   CT TCCCCGTCC
                                   _  C__  C
GAM956  LOC150142 5'  CTGCCCCCTTCCAGC       79576      CAGTGT   A
                                GCTG     GAA GGGGCAG
                                ||||     ||| |||||||
                                CGAC     CTT CCCCGTC
                                   _______  C
GAM956  LOC150445 3'  CCTGCCCCCCCTTGGCAC     79870      G  A_
                                GTGT AA  GGGGCAGG
                                |||| ||  ||||||||
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                                CACG TT  CCCCGTCC
                                  G  CC
GAM956  LOC150886 5'  CTGCCCCTTCCACCATGT    85152     GT   A
                                GCA  GTG AAGGGGCAG
                                |||  ||| |||||||||
                                TGT  CAC TTCCCCGTC
                                  AC   C
GAM956  LOC151568 5'  CCCAGAGCCACACTGCAGC   56691          AAAG_
                                GCTGCAGTGTG    GGG
                                ||||||||||    |||
                                CGACGTCACAC    CCC
                                      CGAGA
GAM956  LOC151632 5'  CCTGCCCCTCTCTGTCATAGCT 85469       CAGTGT  A
                                AGCTG     GA AGGGGCAGG
                                |||||     || |||||||||
                                TCGAT     CT TCCCCGTCC
                                   ACTGT_  C
GAM956  LOC151742 5'  CCCAGTCTCAGACTGCAGCTG  57666          G   AAG_
                                CAGCTGCAGT TGA   GGG
                                |||||||||| |||   |||
                                GTCGACGTCA ACT   CCC
                                     G   CTGA
GAM956  LOC152220 3'  CGCCACCACACCCAGCT     85581       CA    AAAGG   A
                                AGCTG  GTGTG    GGC G
                                |||||  |||||    ||| |
                                TCGAC  CACAC    CCG C
                                   C_    CA___   C
GAM956  LOC152271 3'  CCTGCCCCTCTTTGTCGTAGCT 80516       AGT TG  _
                                AGCTGC   G  AA AGGGGCAGG
                                ||||||   |  || |||||||||
                                TCGATG   T  TT TCCCCGTCC
                                   C__ GT  C
GAM956  LOC153243 3'  TCCCCTCCTGCGCTG       80799      T    TGTGAA    C
                                CAGC GCAG     AGGGG A
                                |||| ||||     ||||| |
                                GTCG CGTC     TCCCC T
                                  _   C_____    A
GAM956  LOC158373 5'  CCCACCCCAGCACTGCAGGC   71042    _      GAAA   CA
                                GC TGCAGTGT   GGGG  GG
                                || ||||||||   ||||  ||
                                CG ACGTCACG   CCCC  CC
                                 G       A___    AC
GAM956  LOC158886 3'  CCTACCCCTCTCCCCCAAATGC 82834         GTGT___  A    C
           AGCTG                   CAGCTGCA      GA AGGGG AGG
                                ||||||||      || ||||| |||
                                GTCGACGT      CT TCCCC TCC
                                     AAACCCC  C    A
GAM956  LOC158972 3'  CCACCCCCTCCCATGAAGCGCT 86946      T  AG   AA    CA
           G                    CAGC GC  TGTG  AGGGG  GG
                                |||| ||  ||||  |||||  ||
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                                GTCG CG  GTAC  TCCCC  CC
                                  _ AA   CC    CA
GAM956  LOC165140 5'  CCTGCCCCTCCGCGTGGACT  82463   _ TG A  T  AA
                                AG C  C GTG GA  GGGGCAGG
                                || |  | ||| ||  ||||||||
                                TC G  G CGC CT  CCCCGTCC
                                 A GT _  _  __
GAM956  LOC196337 5'  CCTGCCCCTGCTCACTAAGCTG 87647     GC   TGAA
                                CAGCT  AGTG   AGGGGCAGG
                                |||||  ||||   |||||||||
                                GTCGA  TCAC   TCCCCGTCC
                                   A_   TCG_
GAM956  LOC196955 3'  CCTGCCCCCTTCTGTCCAGC  77373    CAGTGT  A
                                GCTG    GAA GGGGCAGG
                                ||||    ||| ||||||||
                                CGAC    CTT CCCCGTCC
                                  CTGT__  C
GAM956  LOC199906 5'  CCCACCCCTTTCTCTGGGACAG 88477    ___  TGT     CA
          T                      GCTG  CAG  GAAAGGGG  GG
                                ||||  |||  ||||||||  ||
                                TGAC  GTC  CTTTCCCC  CC
                                  AGG  T__      AC
GAM956  LOC199989 3'  CCCGCCCCTCCCGCTGCAGC  89893       T  AA   A
                                GCTGCAGTG GA  GGGGC GG
                                |||||||||  ||  ||||| ||
                                CGACGTCGC CT  CCCCG CC
                                     C  __    C
GAM956  LOC200301 3'  CTGCCCCTCCTCAAACT    88742    G  A_
                                AGT TGA  AGGGGCAG
                                ||| |||  ||||||||
                                TCA ACT  TCCCCGTC
                                 A  CC
GAM956  LOC200734 3'  CCTGCCGCCCACACTGCAGC  88862        AAA  _
                                GCTGCAGTGTG  GG GGCAGG
                                ||||||||||  || ||||||
                                CGACGTCACAC  CC CCGTCC
                                      ___  G
GAM956  LOC200958 3'  CCACCGACAGACTGCAGCTG  65924        G  AAA  _
                                CAGCTGCAGT TG  GG GG
                                |||||||||| ||  || ||
                                GTCGACGTCA AC  CC CC
                                     G  AG_  A
GAM956  LOC201252 3'  CCTGCCTGAGAAACTGCAGCT  88167       GTGAAAG
                                AGCTGCAGT     GGGCAGG
                                |||||||||     |||||||
                                TCGACGTCA     TCCGTCC
                                     AAGAG__
GAM956  LOC203083 5'  CCTGCCCCTCTCTGTCATAGCT 90462     CAGTGT  A
                                AGCTG    GA AGGGGCAGG
                                |||||    || |||||||||
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                                TCGAT     CT TCCCCGTCC
                                   ACTGT_  C
GAM956   LOC220469 5'  TGCCCCCTCGCCACTG      76388       _   AA
                                CAGTG TGA  GGGGCA
                                ||||| |||  ||||||
                                GTCAC GCT  CCCCGT
                                   C   C_
GAM956   LOC220827 3'  CCCATTTTCACACTACACT    91240    C  C        _
                                AG TG AGTGTGAAAG GGG
                                || || |||||||||| |||
                                TC AC TCACACTTTT CCC
                                 _ A         A
GAM956   LOC221795 5'  CCTGCCCCTCTCTGTCGTAGCT 92477        AG  T  A
                                AGCTGC  TG GA AGGGGCAGG
                                ||||||  || || |||||||||
                                TCGATG  GT CT TCCCCGTCC
                                   CT  _  C
GAM956   LOC245718 3'  CCTACCCCTCTCCCCCAAATGC 90720         GTGT___  A     C
            AGCTG                   CAGCTGCA       GA AGGGG AGG
                                |||||||||       || ||||| |||
                                GTCGACGT       CT TCCCC TCC
                                     AAACCCC  C     A
GAM956   LOC253573 3'  CTGCCCCCTGATGCTGC     97050         GAAA
                                GCAGTGT    GGGGCAG
                                |||||||    |||||||
                                CGTCGTA    CCCCGTC
                                     GTC_
GAM956   LOC254057 3'  CCTTCTTCCTCACTGCAGC    96998          T_   AG
                                GCTGCAGTG  GAA  GGG
                                |||||||||  |||  |||
                                CGACGTCAC  CTT  TCC
                                      TC   CT
GAM956   LOC254176 5'  CCTGCCCCTCTCTGTCATAGCT 97339       CAGTGT  A
                                AGCTG      GA AGGGGCAGG
                                |||||      || |||||||||
                                TCGAT     CT TCCCCGTCC
                                   ACTGT_  C
GAM956   LOC256094 3'  CCTGCCCCCCCACACCACACCTG 94891     C  CA     AAA
                                CAG TG  GTGTG   GGGGCAGG
                                ||| ||  |||||   ||||||||
                                GTC AC  CACAC   CCCCGTCC
                                  C  AC    C__
GAM956   LOC256515 5'  CCTGCCCCTCTCTGTCGTAGCT 96462        AG  T  A
                                AGCTGC  TG GA AGGGGCAGG
                                ||||||  || || |||||||||
                                TCGATG  GT CT TCCCCGTCC
                                   CT  _  C
GAM956   LOC256594 5'  CCTGCCCCTCTCTGTCGTAGCT 97077        AG  T  A
                                AGCTGC  TG GA AGGGGCAGG
                                ||||||  || || |||||||||
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                                TCGATG  GT CT TCCCCGTCC
                                   CT  _  C
GAM956  LOC257153 5'  CCTGCCTCTTCGCACCACAGC  95767     CA      A
                                GCTG  GTGTGAA GGGGCAGG
                                ||||  ||||||| ||||||||
                                CGAC  CACGCTT CTCCGTCC
                                  AC      _
GAM956  LOC257438 3'  CCAGCAGGATTCCACTGCAGCT 93971          T   AGGG  A
          G                     CAGCTGCAGTG GAA    GC GG
                                ||||||||||| |||    || ||
                                GTCGACGTCAC CTT    CG CC
                                      _   AGGA  A
GAM956  LOC51195  3'  CCTGCCCCCTCCCTGCTACTG  32939    CT    TGT  AA
                                CAG  GCAG   GA  GGGGCAGG
                                |||  ||||   ||  ||||||||
                                GTC  CGTC   CT  CCCCGTCC
                                  AT    C__  C_
GAM956  LOC51200  3'  CCTGCCCCTCTCCAGCCAGCT  32994     CAG  T  A
                                AGCTG   TG GA AGGGGCAGG
                                |||||   || || |||||||||
                                TCGAC   AC CT TCCCCGTCC
                                   CG_  _  C
GAM956  LOC56834  3'  TCTGCTTCCACACCGGAGC   39343    GCA    AAA
                                GCT   GTGTG   GGGGCAGG
                                |||   |||||   ||||||||
                                CGA   CACAC   CTTCGTCT
                                  GGC    ___
GAM956  LOC56920  3'  CTGCCCCCACACCGCTACTG   39385    CT  A    AAA
                                CAG  GC GTGTG   GGGGCAG
                                |||  || |||||   |||||||
                                GTC  CG CACAC   CCCCGTC
                                  AT  C    ___
GAM956  LOC56963  3'  CTGCCCCTTCCACCCTGT    71454     T   A
                                GCAG GTG AAGGGGCAG
                                |||| ||| |||||||||
                                TGTC CAC TTCCCCGTC
                                  C   C
GAM956  LOC56965  3'  CCTACACCAAACTGCAGCTG   39528         G  AAAG
                                CAGCTGCAGT TG    GGG
                                |||||||||| ||    |||
                                GTCGACGTCA AC    TCC
                                      A  CACA
GAM956  LOC87769  5'  CCTGGGTTCTCACTGCAGCTG  71322          T   AGGGG
                                CAGCTGCAGTG GAA    CAGG
                                |||||||||| |||    ||||
                                GTCGACGTCAC CTT    GTCC
                                      T  GG___
GAM956  LOC90557  3'  CCCACCAACCTGCAGCTG    57062         T  GAAA
                                CAGCTGCAG GT    GGG
                                |||||||| ||    |||
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                                GTCGACGTC CA   CCC
                                     _ ACCA
GAM956  LOC91409  3'  CCCACCAACCTGCAGCTG    65955        T  GAAA
                                CAGCTGCAG GT   GGG
                                ||||||||| ||   |||
                                GTCGACGTC CA   CCC
                                     _ ACCA
GAM956  LOC92841  3'  CGCCACCACACCCAGCT     70709      CA    AAAGG  A
                                AGCTG  GTGTG    GGC G
                                |||||  |||||    ||| |
                                TCGAC  CACAC    CCG C
                                   C_    CA___   C
GAM957  ABCC1     3'  TGATGTGGGGTAAATATTAAGG 17183     CA       AAA  C
          A                      TCC  AATATTTAC   GC ATCA
                                 |||  |||||||||   || ||||
                                 AGG  TTATAAATG   TG TAGT
                                   AA        GGG  _
GAM957  ABCC1     3'  TGATGTGGGGTAAATATTAAGG 39128     CA       AAA  C
          A                      TCC  AATATTTAC   GC ATCA
                                 |||  |||||||||   || ||||
                                 AGG  TTATAAATG   TG TAGT
                                   AA        GGG  _
GAM957  ABCC1     3'  TGATGTGGGGTAAATATTAAGG 39136     CA       AAA  C
          A                      TCC  AATATTTAC   GC ATCA
                                 |||  |||||||||   || ||||
                                 AGG  TTATAAATG   TG TAGT
                                   AA        GGG  _
GAM957  ASIC4     3'  TTTGTAAATATTTAGGG     37924     _
                                 CCC AAATATTTACAAA
                                 ||| |||||||||||||
                                 GGG TTTATAAATGTTT
                                   A
GAM957  CREBBP    3'  GATAACTTTGTGATGTTTCGGG 15207     _      T     CC
          A                      TCCC AAATATT ACAAAG  ATC
                                 |||| ||||||| ||||||  |||
                                 AGGG TTTGTAG TGTTTC  TAG
                                   C       _      AA
GAM957  CTSS      3'  TGATGGCTTAAAAATA      14545       ACA
                                 TATTT   AAGCCATCA
                                 |||||   |||||||||
                                 ATAAA   TTCGGTAGT
                                    AA_
GAM957  EYA1      5'  GATGGCTCCGAGTTTGGGG    4954         ATTTACAA
                                 TCCCAAAT       AGCCATC
                                 ||||||||       |||||||
                                 GGGGTTTG       TCGGTAG
                                      AGCC____
GAM957  FBXW1B    3'  TGACAGCTTTGTACTGTGG    24527     AATATT       CA
                                 CCA     TACAAAGC  TCA
                                 |||     ||||||||  |||
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                                GGT     ATGTTTCG  AGT
                                  GTC___       AC
GAM957  FBXW1B   3'  TGACAGCTTTGTACTGTGG   53331     AATATT      CA
                                CCA     TACAAAGC  TCA
                                |||     ||||||||  |||
                                GGT     ATGTTTCG  AGT
                                  GTC___       AC
GAM957  FBXW1B   3'  TGACAGCTTTGTACTGTGG   53342     AATATT      CA
                                CCA     TACAAAGC  TCA
                                |||     ||||||||  |||
                                GGT     ATGTTTCG  AGT
                                  GTC___       AC
GAM957  GCN5L2   3'  TGATGGCTTCAGGGGTTGG   59841     ATA   ACA
                                CCAA   TTT   AAGCCATCA
                                ||||   |||   |||||||||
                                GGTT   GGA   TTCGGTAGT
                                  GG_   C__
GAM957  GSPT1    3'  GCTTTGTAAGTGATGTGG    9143     AA_
                                CCA   TATTTACAAAGC
                                |||   ||||||||||||
                                GGT   GTGAATGTTTCG
                                  GTA
GAM957  PTPN11   3'  TGATGAGAAGAAATGATTTGGG 11085        _    ACAAAGC
          A                      TCCCAAAT ATTT      CATCA
                                ||||||||  ||||      |||||
                                AGGGTTTA TAAA      GTAGT
                                     G    GAAGA__
GAM957  RNMT     3'  TGATAGCTTTGTAGGTACAGGA 13725     CAAA          C
                                TCC    TATTTACAAAGC ATCA
                                |||    ||||||||||||| ||||
                                AGG    ATGGATGTTTCG TAGT
                                  AC__          A
GAM957  ROR2     3'  TGACAGCTTTGTATTTGGTGA  15855    _    TATT      CA
                                TC CCAAA    TACAAAGC  TCA
                                || |||||    ||||||||  |||
                                AG GGTTT    ATGTTTCG  AGT
                                 T     _____       AC
GAM957  STAM     3'  TTGTAATTATTTGGGA      12964          T
                                TCCCAAATA TTACAA
                                |||||||||  ||||||
                                AGGGTTTAT AATGTT
                                      T
GAM957  TGFBR2   3'  CTTTATAAATATTTGG      12267           C
                                CCAAATATTTA AAAG
                                ||||||||||| ||||
                                GGTTTATAAAT TTTC
                                       A
GAM957  ZNF14    3'  TGTAAGACATTTGGGA      40718         A_
                                TCCCAAAT  TTTACA
                                ||||||||  ||||||
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                                AGGGTTTA  GAATGT
                                     CA
GAM957  DKFZP434L1123 5'  TGGTTTGTAAATATTTG     49585            G
                                CAAATATTTACAAA CCA
                                ||||||||||||| |||
                                GTTTATAAATGTTT GGT
                                          _
GAM957  DKFZP434O047 5'  TGATGGCTCCACATCTTGGGG  31517       ATATTTACAA
                                TCCCAA         AGCCATCA
                                ||||||         ||||||||
                                GGGGTT         TCGGTAGT
                                   CTACACC___
GAM957  DKFZP564G092 5'  TGGACAGTAAATATTTG     31539          AAAG
                                CAAATATTTAC    CCA
                                ||||||||||    |||
                                GTTTATAAATG    GGT
                                      ACA_
GAM957  DKFZP564O0823 3'  ATGGCTGTAAAATGTTT     59519        ACAA
                                AAATATTT    AGCCAT
                                ||||||||    ||||||
                                TTTGTAAA    TCGGTA
                                     ATG_
GAM957  FLJ10036  3'  GCTTTGTAAATATTTCAGA   94950    CC
                                TC  AAATATTTACAAAGC
                                ||  |||||||||||||||
                                AG  TTTATAAATGTTTCG
                                 AC
GAM957  FLJ11267  5'  TGATGGCTCTAGAATGTCTAGG 39007     CAA     ACAA
           A                     TCC   ATATTT    AGCCATCA
                                |||   ||||||   ||||||||
                                AGG   TGTAAG    TCGGTAGT
                                  ATC     ATC_
GAM957  FLJ11730  3'  TGGAGGCTGTAAATATCTGG   42798     A       AA   AT
                                CCA ATATTTACA  GCC  CA
                                ||| |||||||||  |||  ||
                                GGT TATAAATGT  CGG  GT
                                  C        __   AG
GAM957  FLJ13194  3'  TGATAACTTTGTAAGATGGGA  47131      AATA       CC
                                TCCCA   TTTACAAAG  ATCA
                                |||||   |||||||||  ||||
                                AGGGT   GAATGTTTC  TAGT
                                   A___        AA
GAM957  FLJ14564  3'  ATGGGGAAAATATTTGGGA   76499          ACAAAG
                                TCCCAAATATTT     CCAT
                                ||||||||||||     ||||
                                AGGGTTTATAAA     GGTA
                                      AGG___
GAM957  FLJ22596  5'  TGATGGCTTGATGGTATCTGG  46964     A    TACA
                                CCA ATATT    AAGCCATCA
                                ||| |||||    |||||||||
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                                GGT TATGG    TTCGGTAGT
                                  C    TAG_
GAM957  FLJ25200  5'  TGATGGCTTCATTAACTATCTG 58514    A  T  CA_
          G                      CCA ATA TTA   AAGCCATCA
                                 ||| ||| |||   |||||||||
                                 GGT TAT AAT   TTCGGTAGT
                                   C  C  TAC
GAM957  FRAT1    3'  TGAGGGCCAAAATATTTGG   18496        ACAAA  A
                                 CCAAATATTT    GCC TCA
                                 ||||||||||    ||| |||
                                 GGTTTATAAA    CGG AGT
                                       AC___   G
GAM957  GLUC     3'  ATGGCCTTTATTTGTATTTGG  40586       TTAC   _
                                 CCAAATAT    AAAG CCAT
                                 ||||||||    |||| ||||
                                 GGTTTATG    TTTC GGTA
                                      TTTA   C
GAM957  GPR      3'  GGATTGTAAATTCTTGG     23336     AT      AG
                                 CCAA  ATTTACAA  CC
                                 ||||  ||||||||  ||
                                 GGTT  TAAATGTT  GG
                                   CT      A_
GAM957  GSPT2    3'  GCTTTGTAAGTGATGTGG    36120     AA_
                                 CCA   TATTTACAAAGC
                                 |||   ||||||||||||
                                 GGT   GTGAATGTTTCG
                                   GTA
GAM957  KIAA0453 3'  GTGTGTTTGTAAATATATAGGA 69051    CAA        GC
                                 TCC   ATATTTACAAA  CAT
                                 |||   ||||||||||  |||
                                 AGG   TATAAATGTTT  GTG
                                   ATA         GT
GAM957  KIAA0746 3'  GCTTTGTAAATTGG       69454    AAT
                                 CCA   ATTTACAAAGC
                                 |||   ||||||||||
                                 GGT   TAAATGTTTCG
                                       ___
GAM957  KIAA0884 3'  TGATTATTGTAAATATTTTGGA 70207    C          AGCC
                                 TCC AAATATTTACAA    ATCA
                                 ||| ||||||||||||    ||||
                                 AGG TTTATAAATGTT    TAGT
                                   T          AT__
GAM957  KIAA0930 3'  TGATGGCTTTGCCCTGGGCTGG 70554      AATATTTA
          GA                     TCCCA       CAAAGCCATCA
                                 |||||       ||||||||||||
                                 AGGGT       GTTTCGGTAGT
                                    CGGGTCCC
GAM957  KIAA1052 3'  TGATGGCTTTTATCCTCCTGGG 30252      AATATT  C
          A                      TCCCA     TA AAAGCCATCA
                                 |||||     || ||||||||||
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                                AGGGT     AT TTTCGGTAGT
                                   CCTCCT  _
GAM957  KIAA1557  3'  TTGTAAATATTTGTGA      61140    C
                                TC CAAATATTTACAA
                                || ||||||||||||
                                AG GTTTATAAATGTT
                                 T
GAM957  KIAA1587  3'  TGATAGCTCTATAAAATGTTTT 40512     C       ACAA_  C
           GGA                    TCC AAATATTT     AGC ATCA
                                ||| ||||||||     ||| ||||
                                AGG TTTGTAAA     TCG TAGT
                                  T       ATATC   A
GAM957  LIPI      3'  ATGACTTTGTAAATATTT     79564             C
                                AAATATTTACAAAG CAT
                                |||||||||||||| |||
                                TTTATAAATGTTTC GTA
                                        A
GAM957  MARCKS    3'  GTTTTGTAAATACTGGAGA    9870     _   AA
                                TC CCA  TATTTACAAAGC
                                || |||  ||||||||||||
                                AG GGT  ATAAATGTTTTG
                                 A   C_
GAM957  MED6      3'  TGATGGCTTTGTTGCAGCTGAG 18439    C  AATATTT
           A                     TC CA      ACAAAGCCATCA
                                || ||      ||||||||||||
                                AG GT      TGTTTCGGTAGT
                                 A  CGACGT_
GAM957  MGC17330  3'  GTTTTTAAAATATTTGGGA   53531           AC
                                TCCCAAATATTT  AAAGC
                                ||||||||||||  |||||
                                AGGGTTTATAAA  TTTTG
                                        AT
GAM957  OR51E2    3'  ATGGCTTTGTACTTGTGATG   47790    A_   TT
                                CA  ATA  TACAAAGCCAT
                                ||  |||  ||||||||||||
                                GT  TGT  ATGTTTCGGTA
                                 AG   TC
GAM957  PSTPIP2   3'  CTTTCACAAATATTTGGG    44389          AC_
                                CCCAAATATTT   AAAG
                                ||||||||||   ||||
                                GGGTTTATAAA   TTTC
                                       CAC
GAM957  PURG      3'  ATGGCTTTGCTATGG       25336     AATATT  _
                                CCA     TA CAAAGCCAT
                                |||     || |||||||||
                                GGT     AT GTTTCGGTA
                                  _______  C
GAM957  VDU1      3'  TGATGGCTTTGTTTTGGTTTGG 30431         ATTT
           GG                     TCCCAAAT    ACAAAGCCATCA
                                ||||||||    ||||||||||||
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                                GGGGTTTG   TGTTTCGGTAGT
                                    GTTT
GAM957  ZNF294   3'  GCTTTGTAAATGTTTGG    70828
                                CCAAATATTTACAAAGC
                                |||||||||||||||||
                                GGTTTGTAAATGTTTCG

GAM957  LOC127162 3'  TGATGGCTACATATACTAGGGA 74638     AAA   TTACAA
                                TCCC   TAT     AGCCATCA
                                ||||   |||     ||||||||
                                AGGG   ATA     TCGGTAGT
                                  ATC   TACA__
GAM957  LOC148936 5'  TGATGGCTCTATAAGGGGGA   84303     AAA   TTACAA
                                TCCC   TAT     AGCCATCA
                                ||||   |||     ||||||||
                                AGGG   ATA     TCGGTAGT
                                  GGA   TC____
GAM957  LOC148938 5'  TGATGGCTCTATAAGGGGGA   84284     AAA   TTACAA
                                TCCC   TAT     AGCCATCA
                                ||||   |||     ||||||||
                                AGGG   ATA     TCGGTAGT
                                  GGA   TC____
GAM957  LOC152084 5'  GATGGCTTTCCTCAGCCTGGGA 85553      AATATTTAC
                                TCCCA       AAAGCCATC
                                |||||       |||||||||
                                AGGGT       TTTCGGTAG
                                   CCGACTCC_
GAM957  LOC152573 3'  GATGACTATATATTTGGG    80618        TTACAA  C
                                CCCAAATAT     AG CATC
                                |||||||||     || ||||
                                GGGTTTATA     TC GTAG
                                     TA____  A
GAM957  LOC152627 5'  ATGGCTTCTAAGTATTCAGG   80627    CA      CA
                                CC  AATATTTA  AAGCCAT
                                ||  ||||||||  |||||||
                                GG  TTATGAAT  TTCGGTA
                                 AC       C_
GAM957  LOC200301 3'  GCTTGTTATTTGGGG      88748        TTT    A
                                TCCCAAATA   ACAA GC
                                |||||||||   |||| ||
                                GGGGTTTAT   TGTT CG
                                      ___    _
GAM958  DAZ      3'  CTCCAAGAAGTACCTGTGAA   14549       ACTGAG
                                TTCACGG     TTCTTGGAG
                                |||||||     |||||||||
                                AAGTGTC     AAGAACCTC
                                   CATG__
GAM958  ITGA1    3'  CCAAACTCAGTACATGAAT   63529      CGG      CT
                                ATTCA   ACTGAGTT  TGG
                                |||||   ||||||||  |||
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                                TAAGT  TGACTCAA  ACC
                                  ACA      __
GAM958  DAZ2     3'  CTCCAAGAAGTACCTGTGAA  39799       ACTGAG
                                TTCACGG    TTCTTGGAG
                                |||||||    |||||||||
                                AAGTGTC    AAGAACCTC
                                    CATG__
GAM958  FOXJ1    5'  CCGGCTCAGCCCGTGGATG  7572         A    TCT
                                CATTCACGG CTGAGT  TGG
                                |||||||| ||||||  |||
                                GTAGGTGCC GACTCG  GCC
                                     C    ___
GAM958  TU3A     3'  TCCAAGAGGCTCCTGAATG  23191       C  _  GAGT
                                CATTCA GGA CT   TCTTGGA
                                |||||| ||| ||   |||||||
                                GTAAGT CCT GG   AGAACCT
                                   _  C ____
GAM958  LOC124817 5'  CCAAGAGGCTCGTGAAT    74343       GA  GAGT
                                ATTCACG  CT   TCTTGG
                                |||||||  ||   ||||||
                                TAAGTGC  GG   AGAACC
                                    TC ____
GAM958  LOC200531 5'  CTCCAAGAACTATCATAGGAA  88821     ACGGACTG
                                TTC       AGTTCTTGGAG
                                |||       ||||||||||
                                AAG       TCAAGAACCTC
                                  GATACTA_
GAM959  GCN1L1   3'  GGTCAGACTGTGGGTTC    69755
                                GAACTCACAGTCTGATT
                                |||||||||||||||||
                                CTTGGGTGTCAGACTGG

GAM959  TRAF1    3'  CCCAGTCACTGTGAGCTC    18971    A      CT   A
                                GA CTCACAGT  GATT GG
                                || ||||||||  |||| ||
                                CT GAGTGTCA  CTGA CC
                                 C       __   C
GAM959  DKFZP434A043 3'  ATCCTAATTCAGTAAGTTCT  31183       CACAGT   _
                                AGAACT     CTGA TTAGGAT
                                ||||||     |||| |||||||
                                TCTTGA     GACT AATCCTA
                                   AT____    T
GAM959  DKFZP434G072 5'  CAGACTTGAGTTCTT      49588         C
                                AAGAACTCA AGTCTG
                                |||||||| ||||||
                                TTCTTGAGT TCAGAC
                                          _
GAM959  E2F6     3'  CCATTAGACTGTGAGCTC    8712     A         TA
                                GA CTCACAGTCTGAT  GG
                                || ||||||||||||  ||
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                                CT GAGTGTCAGATTA  CC
                                 C         __
GAM959  FLJ12668  3'  TCAGATTGTGAGCCCTT    46526    AA
                                AAG  CTCACAGTCTGA
                                |||  ||||||||||||
                                TTC  GAGTGTTAGACT
                                  CC
GAM959  KIAA0410  3'  ATTAGATATGAGTTCTT    28772        CA
                                AAGAACTCA  GTCTGAT
                                |||||||||  |||||||
                                TTCTTGAGT  TAGATTA
                                     A_
GAM959  KIAA1305  3'  CCTTGCAGTGAGTGTGAGTTC  46928        G  __  ATT
                                GAACTCACA TC  TG   AGG
                                |||||||||  ||  ||   |||
                                CTTGAGTGT AG  AC   TCC
                                     G  TG  GT_
GAM959  SEMA4F    3'  TCCCAGCCTCTGAGTTCT    14945       C  T   ATTA
                                AGAACTCA AG CTG    GGA
                                ||||||||  ||  |||    |||
                                TCTTGAGT TC GAC    CCT
                                     C  C  _____
GAM959  LOC115110 3'  CCTAGGGGGCTGTGG      71715        GA
                                TCACAGTCT  TTAGG
                                |||||||||  |||||
                                GGTGTCGGG  GATCC
                                     G_
GAM959  LOC145547 3'  CCTTGCAGTGAGTGTGAGTTC  77264        G  __  ATT
                                GAACTCACA TC  TG   AGG
                                |||||||||  ||  ||   |||
                                CTTGAGTGT AG  AC   TCC
                                     G  TG  GT_
GAM959  LOC152926 3'  TCCTAAAATGCGAGTTTTT   80747        A  GTCTGA
                                AAGAACTC CA     TTAGGA
                                ||||||||  ||     ||||||
                                TTTTTGAG GT     AATCCT
                                     C  AA_____
GAM959  LOC153592 3'  ATCAGACTCCAAGTTCTT    86065       CAC
                                AAGAACT   AGTCTGAT
                                |||||||   ||||||||
                                TTCTTGA   TCAGACTA
                                    ACC
GAM959  LOC170395 3'  ATCAGACTCCAAGTTCTT    76367       CAC
                                AAGAACT   AGTCTGAT
                                |||||||   ||||||||
                                TTCTTGA   TCAGACTA
                                    ACC
GAM959  LOC199704 3'  ATCCTAAGTTATGTGAGTTGTT 88325    G       GTCTGA
                                AA AACTCACA     TTAGGAT
                                ||  ||||||||     |||||||
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                                TT TTGAGTGT     AATCCTA
                                 G       ATTG__
GAM959  LOC199858 3'  ATCAGACTCCAAGTTCTT    88417       CAC
                                AAGAACT   AGTCTGAT
                                |||||||   ||||||||
                                TTCTTGA   TCAGACTA
                                    ACC
GAM959  LOC221416 3'  TCCCCTCAGACTGGAGCTC   93770    A  A      TTA
                                GA CTC CAGTCTGA   GGA
                                || ||| ||||||||   |||
                                CT GAG GTCAGACT   CCT
                                 C  _       CC_
GAM959  LOC221692 3'  CCTGGGAGACTACAGGTCCTT  92239     A  CAC    GA
                                AAG ACT   AGTCT  TTAGG
                                ||| |||   |||||  |||||
                                TTC TGG   TCAGA  GGTCC
                                  C  ACA    G_
GAM959  LOC51246  3'  CCTGGCAACTGTGAGT      33215        C  A
                                ACTCACAGT TG TTAGG
                                |||||||||| || |||||
                                TGAGTGTCA AC GGTCC
                                      _ _
GAM960  ABCC11    3'  TTAACTTACATGCTGAATAATT 52507      CG       _   AGA
           TTA                    TGAGAT  TTCAGTATG AAGT
                                |||||| |||||||| ||||
                                ATTTTA  AAGTCGTAC TTCA
                                   AT       A   ATTT
GAM960  ABCD4     5'  CTGCAGATACTGAAGGTTTT   39736      G      GAA   A
                                GAGATC TTCAGTAT   GTAG
                                |||||| ||||||||   ||||
                                TTTTGG AAGTCATA   CGTC
                                   _      GA_   C
GAM960  ABCG2     5'  TGCACATGCTTGGTGGTCTT   16702       TC     AA
                                GAGATCGT  AGTATG  GTA
                                ||||||||  ||||||  |||
                                TTCTGGTG  TCGTAC  CGT
                                     GT     A_
GAM960  ACVR1     5'  TTCAGAGATATTGGGCGGCTCA 6612      A        GAAGTAGA
                                TGAG TCGTTCAGTAT
                                |||| ||||||||||
                                ACTC GGCGGGTTATA
                                  _         GAGACTTT
GAM960  ADD1      3'  TCTGCTCAGTGATCTCA     26374         C   T
                                TGAGATCGTT AGTA GA
                                |||||||||| |||| ||
                                ACTCTAGTGA TCGT CT
                                      C   _
GAM960  ADD1      3'  TCTGCTCAGTGATCTCA     26380         C   T
                                TGAGATCGTT AGTA GA
                                |||||||||| |||| ||
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                                ACTCTAGTGA TCGT CT
                                      C   _
GAM960  AKAP13   3'  TCTGCTTCGGCCATGATTT   22145       TCA  A
                                AGATCGT   GT TGAAGTAGA
                                |||||||   || |||||||||
                                TTTAGTA   CG GCTTCGTCT
                                    C__  _
GAM960  AKAP13   3'  TCTGCTTCGGCCATGATTT   23249       TCA  A
                                AGATCGT   GT TGAAGTAGA
                                |||||||   || |||||||||
                                TTTAGTA   CG GCTTCGTCT
                                    C__  _
GAM960  AKAP13   3'  TCTGCTTCGGCCATGATTT   58581       TCA  A
                                AGATCGT   GT TGAAGTAGA
                                |||||||   || |||||||||
                                TTTAGTA   CG GCTTCGTCT
                                    C__  _
GAM960  AKAP2    3'  TTACAAAGTTTTGAGCGGTTTT 23272          T  GAA    A
                                GAGATCGTTCAG AT   GTAG
                                |||||||||||| ||   ||||
                                TTTTGGCGAGTT TG   CATT
                                      T  AAA
GAM960  ALEX2    3'  TTTAAGCTGAACCATTTTA   28792       C      A
                                TGAGAT GTTCAGT TGAA
                                |||||| ||||||| ||||
                                ATTTTA CAAGTCG ATTT
                                    C      A
GAM960  AMD1     3'  TCTACTTCATACTGATGTTTTT 7902      T   T
                                GAGA CGT CAGTATGAAGTAGA
                                |||| ||| ||||||||||||||
                                TTTT GTA GTCATACTTCATCT
                                  T  _
GAM960  APC      3'  TTTGTTTGAAGGGTCTT     3484        G    T TG
                                GAGATC TTCAG A  AA
                                |||||| ||||| |  ||
                                TTCTGG AAGTT T  TT
                                    G    _ GT
GAM960  APPBP2   3'  TCAGTAGAATGATTTCA     21084          AGTA
                                TGAGATCGTTC    TGA
                                ||||||||||    |||
                                ACTTTAGTAAG    ACT
                                      ATG_
GAM960  ASH2L    3'  TCTGGGAATAATACTGGGGGTT 71523       G       GAAG__
          TT                    GAGATC TTCAGTAT     TAGA
                                |||||| ||||||||     ||||
                                TTTTGG GGGTCATA     GTCT
                                   _       ATAAGG
GAM960  ASH2L    3'  TTGTTTTTGTTTTTGAACTGTC 71524       C     T_ TG   TAGA
          TCA                     TGAGAT GTTCAG  A  AAG
                                |||||| ||||||  |  |||
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                                ACTCTG CAAGTT  T  TTT
                                   T     TT GT   TGTTT
GAM960  ATP7B    3'  CTACTTCAAAAACATTTCA   3541        C   CAGTA
                                TGAGAT GTT     TGAAGTAG
                                ||||||| |||    ||||||||
                                ACTTTA CAA     ACTTCATC
                                   _   AA___
GAM960  BAZ1A    3'  TTTATTTTGTTATTGATGATTT 25585        T   _ TG
                                AGATCGT CAGT A  AAGTAGA
                                ||||||| |||| |  |||||||
                                TTTAGTA GTTA T  TTTATTT
                                   _    T GT
GAM960  BLAME    3'  CTGCCCCTGAATGATTCT    39242     _      TATGAA
                                AGA TCGTTCAG     GTAG
                                ||| ||||||||     ||||
                                TCT AGTAAGTC     CGTC
                                  T       CC_____
GAM960  CAPN2    3'  TTTACTTAAACGGATGATC    8248         A  ATG
                                GATCGTTC GT   AAGTAGA
                                |||||||| ||   |||||||
                                CTAGTAGG CA   TTCATTT
                                   _ AA_
GAM960  CCNDBP1  3'  TGTAAAGATGTTGATGGTCTCA 24053         T     GAAGTAGA
                                TGAGATCGT CAGTAT
                                ||||||||| ||||||
                                ACTCTGGTA GTTGTA
                                   _     GAAATGTT
GAM960  CCNDBP1  3'  TGTAAAGATGTTGATGGTCTCA 53373         T     GAAGTAGA
                                TGAGATCGT CAGTAT
                                ||||||||| ||||||
                                ACTCTGGTA GTTGTA
                                   _     GAAATGTT
GAM960  CDC5L    3'  TTTATTTTAAATGATATCGATC 6982         T__   GTA
           TTA                    GAGATCG   TCA   TGAAGTAGA
                                ||||||| |||  |||||||||
                                TTCTAGC   AGT   ATTTTATTT
                                   TAT   AA_
GAM960  CDS2     3'  TCTGCTTTATAAGATGGGTTCA 13778      AT   CAG
                                TGAG  CGTT   TATGAAGTAGA
                                ||||  ||||   ||||||||||
                                ACTT  GTAG   ATATTTCGTCT
                                  GG    A__
GAM960  CHAC     3'  TTTATTTTACTTGGAATGTTTC 30831      T    AGTA
           A                     TGAGA CGTTC    TGAAGTAGA
                                ||||| |||||    |||||||||
                                ACTTT GTAAG    ATTTTATTT
                                   _    GTTC
GAM960  CHRNA2   5'  TCTATTTCTGGGGTGACTT   5604      A   TT AGTAT
                                GAG TCG  C     GAAGTAGA
                                ||| |||  |     ||||||||
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                                TTC AGT  G    CTTTATCT
                                  _  GG GT___
GAM960  CLASP2   3'  TTTATTTTAACTTTAGACGGTC 64595        C__  A
            TT                   GAGATCGTT  AGT TGAAGTAGA
                                 |||||||||  ||| |||||||||
                                 TTCTGGCAG  TCA ATTTTATTT
                                     ATT  _
GAM960  CLN5     3'  TCTGTTTTTCAGGGGGTGATTT 21433        TT AGTA   __
            TA                   TGAGATCG  C   TGAAG  TAGA
                                 |||||||| |   |||||  ||||
                                 ATTTTAGT  G   ACTTT  GTCT
                                     GG GG__    TT
GAM960  CNTN3    3'  TTTGTTTCATATTGAAAAGT  66700    CG
                                 AT  TTCAGTATGAAGTAGA
                                 ||  ||||||||||||||||
                                 TG  AAGTTATACTTTGTTT
                                  AA
GAM960  DAP3     3'  TCTGCTTTATGCTGGAC     53354
                                 GTTCAGTATGAAGTAGA
                                 ||||||||||||||||
                                 CAGGTCGTATTTCGTCT

GAM960  DAP3     3'  TCTGCTTTATGCTGGAC     16152
                                 GTTCAGTATGAAGTAGA
                                 ||||||||||||||||
                                 CAGGTCGTATTTCGTCT

GAM960  DBH      3'  TTTCCCTGCTGAGTGGCTC   5793      A        T_
                                 GAG TCGTTCAGTA  GAAG
                                 ||| ||||||||||  ||||
                                 CTC GGTGAGTCGT  CTTT
                                   _        CC
GAM960  DIO3     3'  TCTGCTTCTGTAACTGTCTCA  7246        C  _  GTAT
                                 TGAGAT GTT CA    GAAGTAGA
                                 |||||| ||| ||    ||||||||
                                 ACTCTG CAA GT    CTTCGTCT
                                    T   T  _____
GAM960  DMN      3'  TCTTGCTAAATGATTTCA    62367          C    T
                                 TGAGATCGTT AGTA GA
                                 |||||||||| |||| ||
                                 ACTTTAGTAA TCGT CT
                                     A    T
GAM960  DMXL1    3'  TCTGTTTTGTGCTGTACCTTTT 18578      TC  T    TG
            C                    GAGA  GT CAGTA  AAGTAGA
                                 ||||  || |||||  |||||||
                                 CTTT  CA GTCGT  TTTGTCT
                                   TC  T    GT
GAM960  E48      3'  TTTATTTTGTACTCAAATCTC  13508      CG  C    TG
                                 GAGAT  TT AGTA  AAGTAGA
                                 |||||  || ||||  |||||||
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                                CTCTA  AA TCAT  TTTATTT
                                  __ C    GT
GAM960  EFG1     3'  TTTATTTCAGTTTGTGGTTTC  94632        TT   TA
                                GAGATCG  CAG  TGAAGTAGA
                                |||||||  |||  |||||||||
                                CTTTGGT  GTT  ACTTTATTT
                                   __   TG
GAM960  EGF      3'  CATGCTGATGATTTT       8735          T
                                GAGATCGT CAGTATG
                                |||||||| |||||||
                                TTTTAGTA GTCGTAC
                                  _
GAM960  EIF1A    3'  TTATGTGAATGGTTTT      88607           G
                                GAGATCGTTCA TATGA
                                |||||||||| |||||
                                TTTTGGTAAGT GTATT
                                   _
GAM960  F13B     3'  AAATTATTTGTGCTGAACATTT 8842         C       TG  GTAGA
           CA                    TGAGAT GTTCAGTA  AA
                                |||||| ||||||||  ||
                                ACTTTA CAAGTCGT  TT
                                  _       GT  ATTAAAT
GAM960  F8A      3'  TTTGTTTCATAGTGAGGATTTT 24059        G   G
           A                     TGAGATC TTCA TATGAAGTAGA
                                ||||||| |||| ||||||||||
                                ATTTTAG GAGT ATACTTTGTTT
                                   _   G
GAM960  FZD5     5'  TTTATCTTTGGACGGTTTT   60061           T_
                                GAGATCGTTCAG  ATGAA
                                ||||||||||||  |||||
                                TTTTGGCAGGTT  TATTT
                                      TC
GAM960  G6PC     3'  TTTATCTTTGAATGGTCTT   3837            T_
                                GAGATCGTTCAG  ATGAA
                                ||||||||||||  |||||
                                TTCTGGTAAGTT  TATTT
                                      TC
GAM960  GATA6    3'  TCTGCTTTTGTGCAGCGGTCCA 17919    A     CA   TG  _
                                TG GATCGTT  GTA  AA GTAGA
                                || |||||||  |||  || |||||
                                AC CTGGCGA  CGT  TT CGTCT
                                  _      __   GT  T
GAM960  GNPI     3'  CTGCTTCAGCCATGGTTCA   18446    G    TCA  A
                                TGA ATCGT   GT TGAAGTAG
                                ||| |||||   || ||||||||
                                ACT TGGTA   CG ACTTCGTC
                                  _    C__  _
GAM960  GUCY1A2  3'  TTCATATGAGTGGTTTT    5962           G
                                GAGATCGTTCA TATGAA
                                |||||||||| ||||||
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                                TTTTGGTGAGT ATACTT
                                            _
GAM960  HCS      3'  CATACTGAATTATTTCA     38461       C
                                TGAGAT GTTCAGTATG
                                |||||| ||||||||||
                                ACTTTA TAAGTCATAC
                                    T
GAM960  HLA-DOB  5'  TCTGAAGAGGCTGACGATTTTA 9211          T   ATGAAG
                                TGAGATCGT CAGT     TAGA
                                ||||||||| ||||     ||||
                                ATTTTAGCA GTCG     GTCT
                                      _   GAGAA_
GAM960  HLF      3'  TTTGCTTCATGTTCGAGC    9222      _
                                GTTC AGTATGAAGTAGA
                                |||| ||||||||||||
                                CGAG TTGTACTTCGTTT
                                  C
GAM960  HS3ST4   3'  TCTGCTTTATAGGGGTTCTCA  73472      TC TT AG
                                TGAGA  G  C  TATGAAGTAGA
                                |||||  |  |  ||||||||||
                                ACTCT  T  G  ATATTTCGTCT
                                   __ GG G_
GAM960  HSD11B1  3'  CATGCTGAGGGATTTT      18639       G
                                GAGATC TTCAGTATG
                                |||||| |||||||||
                                TTTTAG GAGTCGTAC
                                    G
GAM960  HUS1     3'  TTTGTTTTGTTTGAGACGGTCT 91103         _   T TG
            CA                    TGAGATCGT TCAG A  AAGTAGA
                                |||||||||| |||| |  |||||||
                                ACTCTGGCA AGTT T  TTTGTTT
                                     G   _ GT
GAM960  IL19     3'  ACACATTGTACTGAGTGGTTTT 25359            TG A  AGA
                                GAGATCGTTCAGTA  A GT
                                ||||||||||||||  | ||
                                TTTTGGTGAGTCAT  T CA
                                        GT A  CAT
GAM960  IL1RAPL2 5'  TCTGAGACCTGCTGGACGTTTT 33796      T       TGAAG
                                GAGA CGTTCAGTA     TAGA
                                |||| |||||||||     ||||
                                TTTT GCAGGTCGT     GTCT
                                  _        CCAGA
GAM960  IMPA1    3'  TTTATTTTAATAAGACGATC   18651       CA  A
                                GATCGTT  GT TGAAGTAGA
                                |||||||  || |||||||||
                                CTAGCAG  TA ATTTTATTT
                                    AA  _
GAM960  ISL1     3'  TCTATTTTGCCACAAGCGTCTC 9369      T   CAGTAT
                                GAGA CGTT     GAAGTAGA
                                |||| ||||     ||||||||
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                                CTCT GCGA     TTTTATCT
                                  _   ACACCG
GAM960  ITPR3    3'  CATGATGGACGATCTT     9453          G
                                GAGATCGTTCA TATG
                                |||||||||| ||||
                                TTCTAGCAGGT GTAC
                                     A
GAM960  JAK2     3'  CTATTTTATTATGGTTTC    17126        TCAGT
                                GAGATCGT    ATGAAGTAG
                                ||||||||    |||||||||
                                CTTTGGTA    TATTTTATC
                                    T____
GAM960  JMJ      3'  TTTGTTTCTCTGGGCGGTT   17137         TAT
                                GATCGTTCAG   GAAGTAGA
                                ||||||||||   ||||||||
                                TTGGCGGGTC   CTTTGTTT
                                     T__
GAM960  KCNJ3    3'  TCTGTTTTGTATATGATCT   9527        TCA   TG
                                AGATCGT   GTA  AAGTAGA
                                |||||||   |||  |||||||
                                TCTAGTA   TAT  TTTGTCT
                                   ___  GT
GAM960  LDB2     5'  TCTACTTTGTACTGGG      7094        TG
                                TTCAGTA  AAGTAGA
                                |||||||  |||||||
                                GGGTCAT  TTCATCT
                                   GT
GAM960  LILRB4   3'  TTTAAATTGAATGATC      22439          A
                                GATCGTTCAGT TGAA
                                |||||||||| ||||
                                CTAGTAAGTTA ATTT
                                     A
GAM960  LPP      3'  TTTGCTTTTGTCACTAAACGGT 18751         C   AT__
            TTT                   GAGATCGTT AGT    GAAGTAGA
                                |||||||| |||    ||||||||
                                TTTTGGCAA TCA    TTTCGTTT
                                     A   CTGT
GAM960  LRRC2    3'  TCTACTACTTGAATGATTTT   44479          _  ATGA
                                GAGATCGTTCA GT    AGTAGA
                                |||||||||| ||    ||||||
                                TTTTAGTAAGT CA    TCATCT
                                     T  _____
GAM960  LTA4H    3'  CGTATTGATGATTTTA      6101          T
                                TGAGATCGT CAGTATG
                                ||||||||| |||||||
                                ATTTTAGTA GTTATGC
                                    _
GAM960  MAGEA4   3'  TCTATTTTGTTGGATGACTT  9883      A      GT TG
                                GAG TCGTTCA  A  AAGTAGA
                                ||| |||||||  |  |||||||
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                                TTC AGTAGGT  T  TTTATCT
                                  _      __ GT
GAM960  MASP1    3'  TCTGTTTTATAGAAATTGATCT 8539         TTCAG
                T                  GAGATCG    TATGAAGTAGA
                                   |||||||    ||||||||||
                                   TTCTAGT    ATATTTTGTCT
                                      TAAAG
GAM960  MPP1     3'  TATGCTGGGTATTTCA      10111        C TT
                                   TGAGAT G  CAGTATG
                                   |||||| |  |||||||
                                   ACTTTA T  GTCGTAT
                                      _ GG
GAM960  MYBL1    3'  TCATACTGGATCATTTCA    64075        C
                                   TGAGAT GTTCAGTATGA
                                   |||||| ||||||||||
                                   ACTTTA TAGGTCATACT
                                      C
GAM960  MYD88    3'  ATACTGGGCATTTTA       10163        C
                                   TGAGAT GTTCAGTAT
                                   |||||| |||||||||
                                   ATTTTA CGGGTCATA
                                      _
GAM960  NEUROD1  3'  CATGCTGAATTATTTT      10211        C
                                   GAGAT GTTCAGTATG
                                   ||||| ||||||||||
                                   TTTTA TAAGTCGTAC
                                     T
GAM960  NKTR     3'  TCTACTTCATGCTTTGGTGCTT 18203     _    TTC
                                   GAG ATCG   AGTATGAAGTAGA
                                   ||| ||||   ||||||||||||
                                   TTC TGGT   TCGTACTTCATCT
                                     G   T__
GAM960  NOV      3'  TTTACTTTGTAGACTGTTTCA  10244        C   CAG  TG
                                   TGAGAT GTT   TA  AAGTAGA
                                   |||||| |||   ||  |||||||
                                   ACTTTG CAG   AT  TTCATTT
                                      T   ___  GT
GAM960  NQO1     3'  TCTACTTCTGGAAGTCATCTCA 6170        CG_   AGTAT
                                   TGAGAT   TTC    GAAGTAGA
                                   ||||||   |||    ||||||||
                                   ACTCTA   AAG    CTTCATCT
                                      CTG   GT___
GAM960  OPA1     3'  TTGTTTTATACTGTTTGA    55538     TT
                                   TCG  CAGTATGAAGTAG
                                   |||  ||||||||||||
                                   AGT  GTCATATTTTGTT
                                     TT
GAM960  OPA1     3'  TTGTTTTATACTGTTTGA    55547     TT
                                   TCG  CAGTATGAAGTAG
                                   |||  ||||||||||||
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                                AGT  GTCATATTTTGTT
                                  TT
GAM960  OPA1     3'  TTGTTTTATACTGTTTGA    55556     TT
                                TCG  CAGTATGAAGTAG
                                |||  ||||||||||||
                                AGT  GTCATATTTTGTT
                                  TT
GAM960  OPA1     3'  TTGTTTTATACTGTTTGA    55565     TT
                                TCG  CAGTATGAAGTAG
                                |||  ||||||||||||
                                AGT  GTCATATTTTGTT
                                  TT
GAM960  OPA1     3'  TTGTTTTATACTGTTTGA    55574     TT
                                TCG  CAGTATGAAGTAG
                                |||  ||||||||||||
                                AGT  GTCATATTTTGTT
                                  TT
GAM960  OXCT     3'  TATATTGATATGATTTT     4755        _
                                GAGATCGT TCAGTATG
                                |||||||| ||||||||
                                TTTTAGTA AGTTATAT
                                     T
GAM960  P29      3'  CTACTTTGTATACATTCT    31312     TC  TCA   TG
                                AGA  GT   GTA  AAGTAG
                                |||  ||   |||  ||||||
                                TCT  CA   TAT  TTCATC
                                  TA  ___  GT
GAM960  PAFAH1B1 3'  TTTATTTCATTTTGGTCTTA  4736        TTCAGT
                                TGAGATCG     ATGAAGTAGA
                                ||||||||     ||||||||||
                                ATTCTGGT     TACTTTATTT
                                     TT____
GAM960  PDE6D    3'  CTATTTCATACATTCTCA    10490      TCGTTCA
                                TGAGA      GTATGAAGTAG
                                |||||      ||||||||||
                                ACTCT      CATACTTTATC
                                   TA_____
GAM960  PFKFB3   3'  TTTGTTTCGTTTCTGTGATCTC 82876       TT  T_
                                GAGATCG  CAG  ATGAAGTAGA
                                |||||||  |||  ||||||||||
                                CTCTAGT  GTC  TGCTTTGTTT
                                     __  TT
GAM960  PITPNB   3'  TTTATTTCTGGATGGTC     24783         T_
                                GATCGTTCAG  ATGAA
                                ||||||||||  |||||
                                CTGGTAGGTC  TATTT
                                      TT
GAM960  PRKAR2B  3'  TTTGCTTTTAAATGAGTGATTT 10807          GTAT
           CA                     TGAGATCGTTCA   GAAGTAGA
                                  ||||||||||||   ||||||||
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                                ACTTTAGTGAGT   TTTCGTTT
                                      AAAT
GAM960  PRKR    5'  TTTGCTTCTCTGGCGGTCTT  10890       T  TAT
                                GAGATCGT CAG  GAAGTAGA
                                |||||||| |||  ||||||||
                                TTCTGGCG GTC  CTTCGTTT
                                    _  T__
GAM960  PSMB9   3'  CGTACTGAATGATTTT     10959
                                GAGATCGTTCAGTATG
                                ||||||||||||||||
                                TTTTAGTAAGTCATGC

GAM960  PTER    3'  CTTCTACTGAAATGATTTT   47695        _   T
                                GAGATCGTT CAGTA GAAG
                                ||||||||| ||||| ||||
                                TTTTAGTAA GTCAT CTTC
                                    A   _
GAM960  PTP4A2  3'  TCTGCCAGGATTGAATTATTTT 54416     C     ATGAA
                                GAGAT GTTCAGT    GTAGA
                                ||||| |||||||    |||||
                                TTTTA TAAGTTA    CGTCT
                                   T     GGAC_
GAM960  PTP4A2  3'  TCTGCCAGGATTGAATTATTTT 12988     C     ATGAA
                                GAGAT GTTCAGT    GTAGA
                                ||||| |||||||    |||||
                                TTTTA TAAGTTA    CGTCT
                                   T     GGAC_
GAM960  RAB18   3'  TTTACTTCATGTTGGGTTCTTT 41170     TC TT
          C                     GAGA  G  CAGTATGAAGTAGA
                                ||||  |  ||||||||||||||
                                CTTT  T  GTTGTACTTCATTT
                                  CT GG
GAM960  RAD51L1 3'  TCTACTTTGTTGCTATGGCTTT 56061     AT  TC  _ TG
          A                     TGAG  CGT  AGT A  AAGTAGA
                                ||||  |||  ||| |  |||||||
                                ATTT  GTA  TCG T  TTCATCT
                                  CG  __   T GT
GAM960  RAD51L1 3'  TCTACTTTGTTGCTATGGCTTT 11231     AT  TC  _ TG
          A                     TGAG  CGT  AGT A  AAGTAGA
                                ||||  |||  ||| |  |||||||
                                ATTT  GTA  TCG T  TTCATCT
                                  CG  __   T GT
GAM960  RANBP2  3'  TTTGCTTTATACAAGATT    20768     GTTCA
                                GATC    GTATGAAGTAGA
                                ||||    ||||||||||||
                                TTAG    CATATTTCGTTT
                                  AA___
GAM960  RDS     3'  TCTGCTTCTGACCGATGGTGTT 4364     G     CA  AT
                                GA ATCGTT  GT  GAAGTAGA
                                || ||||||  ||  ||||||||
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                                TT TGGTAG  CA  CTTCGTCT
                                 G     C_  GT
GAM960  RNF14    3'  TCTGTTTGTAAGGATGATTTTA 15024          AG  TG  G
                                TGAGATCGTTC  TA  AA TAGA
                                |||||||||||  ||  || ||||
                                ATTTTAGTAGG  AT  TT GTCT
                                      A_  GT  _
GAM960  RNGTT    3'  TCTACTGCGTGGATGGTTACA  13732    A       _  ATGA
                                TG GATCGTTCA GT    AGTAGA
                                || |||||||||  ||    ||||||
                                AC TTGGTAGGT CG    TCATCT
                                 A       G  ____
GAM960  RPE      3'  TCTATTTCATGTTATTGTGATT 62187       TT    ___
           T                     AGATCG  CAGTA   TGAAGTAGA
                                ||||||  |||||   |||||||||
                                TTTAGT  GTTAT   ACTTTATCT
                                   __    TGT
GAM960  SCN3A    3'  TTTACTTTATGCTTTTGC    22634    TC_
                                GT   AGTATGAAGTAGA
                                ||   ||||||||||||
                                CG   TCGTATTTCATTT
                                 TTT
GAM960  SFRS7    3'  CTACTCTCAATGGTCTT     59446         C  TATGA
                                GAGATCGTT AG    AGTAG
                                |||||||||  ||    |||||
                                TTCTGGTAA TC    TCATC
                                     C  ______
GAM960  SHANK2   3'  TTGCTTCCAATGGTTTC     24592         CAGTAT
                                GAGATCGTT     GAAGTAG
                                |||||||||     |||||||
                                CTTTGGTAA     CTTCGTT
                                     C_____
GAM960  SLA2     3'  TCTATTTCATTTTGTGGCTTA  49910      A   TT   T
                                TGAG TCG  CAG ATGAAGTAGA
                                ||||  |||  |||  ||||||||||
                                ATTC GGT  GTT TACTTTATCT
                                  _  __   T
GAM960  SLC12A7  3'  TCTGCTTTGTAGGTTGTGGTC  21709      TTCAG  TG
                                GATCG    TA  AAGTAGA
                                |||||    ||  |||||||
                                CTGGT    AT  TTCGTCT
                                   GTTGG  GT
GAM960  SLC19A2  3'  TTTGCTTAAAATTGCTAGTGAT 68982         C    TG___
           TTCA                   AGATCGTT AGTA    AAGTAGA
                                ||||||||  ||||    |||||||
                                TTTAGTGA TCGT    TTCGTTT
                                     _   TAAAA
GAM960  SLC22A3  3'  TCTGCTTTATATGTTATATTC  41764    TC  TCA
                                GA  GT   GTATGAAGTAGA
                                ||  ||   ||||||||||||
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                                CT  TA   TATATTTCGTCT
                                 TA  TTG
GAM960  SLC24A1  3'  TCTGTGGTTTATGAATGATCTT 16381          GTATGAA
            A                    TGAGATCGTTCA      GTAGA
                                 ||||||||||||      |||||
                                 ATTCTAGTAAGT      TGTCT
                                       ATTTGG_
GAM960  SLC7A5   3'  TTTGTTTTGTGCTAACGTCTTA 13015      T   C   TG
                                 TGAGA CGTT AGTA  AAGTAGA
                                 ||||| |||| ||||  |||||||
                                 ATTCT GCAA TCGT  TTTGTTT
                                    _   _   GT
GAM960  SMARCA2  5'  TACTCTGGGTGACTCA     11783     A   TT   TATGA
                                 TGAG TCG  CAG    AGTA
                                 |||| |||  |||    ||||
                                 ACTC AGT  GTC    TCAT
                                   _   GG  _____
GAM960  SMT3H1   3'  TTTGCTTCTGATGAATGATT   59963        GTAT
                                 GATCGTTCA   GAAGTAGA
                                 |||||||||   ||||||||
                                 TTAGTAAGT   CTTCGTTT
                                      AGT_
GAM960  SOX9     3'  TTTATTTTGTAAGGAGAGGTTT 4441        G   AG  TG
            TA                    TGAGATC TTC  TA  AAGTAGA
                                 |||||||  |||  ||  |||||||
                                 ATTTTGG GAG  AT  TTTATTT
                                     A   GA  GT
GAM960  SPS2     5'  TTGCTTCATATTAATCT     24289     CGTTC
                                 AGAT    AGTATGAAGTAG
                                 ||||    ||||||||||||
                                 TCTA    TTATACTTCGTT
                                   A____
GAM960  SVIL     5'  TTTACTTTGTGCTTAGAAT   41412     __   TG
                                 GTTC  AGTA  AAGTAGA
                                 ||||  ||||  |||||||
                                 TAAG  TCGT  TTCATTT
                                   AT   GT
GAM960  TAF9     3'  CATGCTGGATGTTTTCA     12096      T
                                 TGAGA CGTTCAGTATG
                                 ||||| ||||||||||
                                 ACTTT GTAGGTCGTAC
                                    T
GAM960  TBL2     3'  TTTGCTTTCTCCAACGACTCA  52188     A    CAGTAT
                                 TGAG TCGTT     GAAGTAGA
                                 |||| |||||     ||||||||
                                 ACTC AGCAA     TTTCGTTT
                                   _    CCTC__
GAM960  TCF8     3'  TCTGCTTCATGTATCAGTTTTA 47732       CGTTCAG
                                 TGAGAT      TATGAAGTAGA
                                 ||||||      ||||||||||
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```
                                ATTTTG      GTACTTCGTCT
                                   ACTAT__
GAM960  TCF8    3'  TTTACCATAACTGAATTATTTT 47735       C      _  AA
            A                   TGAGAT GTTCAGT ATG  GTAGA
                                |||||| ||||||| |||  |||||
                                ATTTTA TAAGTCA TAC  CATTT
                                   T      A  __
GAM960  TGFB3   3'  TTGGGGCATCCTGGATGATTTC 12263           T   AAGTAGA
            A                   TGAGATCGTTCAG ATG
                                |||||||||||| |||
                                ACTTTAGTAGGTC TAC
                                       C   GGGGTTT
GAM960  TGFBR2  5'  TCTATTTTATATAATTTGATTC 12269     A   TTCA
            A                   TGAG TCG    GTATGAAGTAGA
                                |||| |||    ||||||||||||
                                ACTT AGT    TATATTTTATCT
                                  _   TTAA
GAM960  TIRAP   3'  TTTACTTTGTGCTTTTTGTGTT 53572       _ TTC    TG
            TTA                   TGAGAT CG   AGTA  AAGTAGA
                                |||||| ||   ||||  |||||||
                                ATTTTG GT   TCGT  TTCATTT
                                   T  TTT    GT
GAM960  TMPRSS2 3'  TCAGCTGCTGGATGACTT    18967     A        __
                                GAG TCGTTCAGTA  TGA
                                ||| ||||||||||  |||
                                TTC AGTAGGTCGT  ACT
                                  _         CG
GAM960  TOP2A   3'  CTGCTTTGTCTGTGTTTT    6530       CGTT   T TG
                                GAGAT    CAG A  AAGTAG
                                |||||    ||| |  ||||||
                                TTTTG    GTC T  TTCGTC
                                   T___   _ GT
GAM960  TP63    3'  TTTACTTGTTTTGGATGGCTT  13571     A       T  G
                                GAG TCGTTCAG AT AAGTAGA
                                ||| |||||||| || |||||||
                                TTC GGTAGGTT TG TTCATTT
                                  _       T  _
GAM960  TRAM    3'  TTGCTATTGTACGGTTTCA    26659         T    ATGA
                                TGAGATCGT CAGT    AGTAG
                                |||||||||| ||||    |||||
                                ACTTTGGCA GTTA    TCGTT
                                      T   _____
GAM960  TRDN    3'  TTGATGCTTAATGATTTTA    20283          C    G
                                TGAGATCGTT AGTAT AA
                                |||||||||| ||||| ||
                                ATTTTAGTAA TCGTA TT
                                       T    G
GAM960  TREM2   3'  CTGAATATTGGACATTTTA    38569       C       GA
                                TGAGAT GTTCAGTAT  AG
                                |||||| |||||||||  ||
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                                ATTTTA CAGGTTATA  TC
                                  _       AG
GAM960  TRPM8    3'  CATGGTGGATGATTTTA     43983           G
                                TGAGATCGTTCA TATG
                                |||||||||||| ||||
                                ATTTTAGTAGGT GTAC
                                      G
GAM960  TRPS1    3'  TTTCATATGGAATGATTTCA   26087          A
                                TGAGATCGTTC GTATGAAG
                                |||||||||||| ||||||||
                                ACTTTAGTAAG TATACTTT
                                      G
GAM960  UGT2B15  3'  TTTATTTCAGCATGGAGGGTTT 60076       G   GTA
           TA                     TGAGATC TTCA   TGAAGTAGA
                                |||||||| ||||   |||||||||
                                ATTTTGG AGGT   ACTTTATTT
                                    G   ACG
GAM960  UPK1B    3'  TTTGCCCTGAATGGTCTCA    22721          TA
                                TGAGATCGTTCAG  TGAA
                                |||||||||||||  ||||
                                ACTCTGGTAAGTC  GTTT
                                       CC
GAM960  UVRAG    3'  TTTGCTTTTCGGGCCTGATGAT 12564        CA  AT__
           TTTA                   GAGATCGTT  GT   GAAGTAGA
                                |||||||||  ||   ||||||||
                                TTTTAGTAG  CG   TTTCGTTT
                                     TC  GGCT
GAM960  ZNF20    3'  TCTACTTTGTATTGCAAGC    63401    __    TG
                                GTT  CAGTA  AAGTAGA
                                |||  |||||  |||||||
                                CGA  GTTAT  TTCATCT
                                  AC    GT
GAM960  ZNF20    3'  TCTAGAAGAACTTGGATGGTTT 63402          TATGAAG
           C                     GAGATCGTTCAG      TAGA
                                ||||||||||||      ||||
                                CTTTGGTAGGTT      ATCT
                                       CAAGAAG
GAM960  ZNF265   3'  TTTGCTTCATTTAAAACCATTT 18400       C  CAGT
           CA                     TGAGAT GTT    ATGAAGTAGA
                                ||||||| |||    ||||||||||
                                ACTTTA CAA    TACTTCGTTT
                                   C   AATT
GAM960  24432    5'  TCACACGGTGCTGAAATGGTTT 43311        _    GAAGTAGA
           C                     GAGATCGTT CAGTAT
                                |||||||||| ||||||
                                CTTTGGTAA GTCGTG
                                     A     GCACACT
GAM960  ALS2CR3  5'  TTTCATTATTGAATGGCTT   30489    A       _
                                GAG TCGTTCAGTA TGAAG
                                ||| ||||||||| |||||
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                                TTC GGTAAGTTAT ACTTT
                                  _       T
GAM960  AQP9     3'  CATTTGGGTGGTTTCA     40607       TT  T
                                TGAGATCG  CAG ATG
                                ||||||||  ||| |||
                                ACTTTGGT  GTT TAC
                                     GG  _
GAM960  ATP10D   3'  TTTATTTTACTAGGAGATCTTA 73145       G  _  TG
                                TGAGATC TTC AGTA  AAGTAGA
                                ||||||| ||| ||||  |||||||
                                ATTCTAG AGG TCAT  TTTATTT
                                     _  A   __
GAM960  BIRC2    3'  TCTGCTTTGGTACTAATAATCT 67203      CG  C   _
           T                     GAGAT  TT AGTAT GAAGTAGA
                                |||||  || ||||| ||||||||
                                TTCTA  AA TCATG TTTCGTCT
                                   AT  _    G
GAM960  BIVM     3'  TTATGGTGGGTGATTTCA    34669       TT  G
                                TGAGATCG  CA TATGA
                                ||||||||  || |||||
                                ACTTTAGT  GT GTATT
                                     GG  G
GAM960  C14orf3  3'  TTTCTGCTGGGTGGGTTCA   23998     AT  TT    T
                                TGAG  CG  CAGTA GAAG
                                ||||  ||  ||||| ||||
                                ACTT  GT  GTCGT CTTT
                                  GG  GG    _
GAM960  C15orf15 3'  TTATGCTGGACTGTTTT    32834      C
                                GAGAT GTTCAGTATGA
                                ||||| ||||||||||
                                TTTTG CAGGTCGTATT
                                   T
GAM960  C1orf9   3'  TTGCTTTGTATTGGCTAC    32640    __     TG
                                GT  TCAGTA  AAGTAG
                                ||  ||||||  ||||||
                                CA  GGTTAT  TTCGTT
                                 TC     GT
GAM960  C20orf170 3'  ATATTGAATGATGTTA     61823     G
                                TGA ATCGTTCAGTAT
                                ||| ||||||||||||
                                ATT TAGTAAGTTATA
                                  G
GAM960  C20orf46  3'  TCTGTTTTGTAGCTGAGGTTTT 37149       GT    _ TG
                                GAGATC  TCAGT A  AAGTAGA
                                ||||||  ||||| |  |||||||
                                TTTTGG  AGTCG T  TTTGTCT
                                   __     A GT
GAM960  C21orf7  3'  TTTGCTTCATGCCATGTGACCT 39335     A   TTCA
           CA                     TGAG TCG    GTATGAAGTAGA
                                |||| |||    ||||||||||||
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                                ACTC AGT   CGTACTTCGTTT
                                  C  GTAC
GAM960  C5orf4   3'  ATGCTGGTGATCTCA      50488        T
                                TGAGATCGT CAGTAT
                                ||||||||| ||||||
                                ACTCTAGTG GTCGTA
                                          _
GAM960  C5orf4   5'  ATGCTGGTGATCTCA      32978        T
                                TGAGATCGT CAGTAT
                                ||||||||| ||||||
                                ACTCTAGTG GTCGTA
                                          _
GAM960  C6orf37  3'  TTTCTGTGGAATGATCTT   67484        AG  T
                                GAGATCGTTC  TA GAAG
                                ||||||||||  || ||||
                                TTCTAGTAAG  GT CTTT
                                      GT  _
GAM960  C8orf6   3'  TCTATTTCATATTTACCATTTT 89270     C  TC
                                GAGAT GT  AGTATGAAGTAGA
                                ||||| ||  ||||||||||||
                                TTTTA CA  TTATACTTTATCT
                                   C  T_
GAM960  C8orf6   5'  TTGCTTCTTAATGGTTTC    89271        CAGTAT
                                GAGATCGTT     GAAGTAG
                                |||||||||     |||||||
                                CTTTGGTAA     CTTCGTT
                                      TT_____
GAM960  CARD6    5'  TTTACTTATTCATTAGGATGAT 50859        AGT   ___
           TTCA                   AGATCGTTC   ATGA   AGTAGA
                                ||||||||||  ||||  ||||||
                                TTTAGTAGG   TACT   TCATTT
                                      AT_   TAT
GAM960  CDV-1    3'  TTTGTTTTGTAGAGATGTGGTC 48907       GT_  AG  TG
           TCA                    TGAGATC   TC  TA  AAGTAGA
                                |||||||   ||  ||  |||||||
                                ACTCTGG   AG  AT  TTTGTTT
                                     TGT  AG  GT
GAM960  CECR1    3'  TTTCCTGGGTGGTCTCA     33823        TT   TAT
                                TGAGATCG  CAG   GAAG
                                ||||||||  |||   ||||
                                ACTCTGGT  GTC   CTTT
                                     GG   ___
GAM960  cerk     3'  TCTATATTTATTGAACATCTT  42852      C      TGAA
                                GAGAT GTTCAGTA    GTAGA
                                ||||| ||||||||    |||||
                                TTCTA CAAGTTAT    TATCT
                                   _      TTA_
GAM960  CL24751  3'  TCTATTTCTGGGTGAAGGGTCT 64688       G   GTAT
           T                    GAGATC TTCA    GAAGTAGA
                                |||||| ||||    ||||||||
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                                TTCTGG AAGT    CTTTATCT
                                   G    GGGT
GAM960  COASTER   3'  TTTATTTCATGTGAAGTGTTTT 31450       T _    G
              CA                    TGAGA CG TTCA TATGAAGTAGA
                                    ||||| || |||| ||||||||||
                                    ACTTT GT AAGT GTACTTTATTT
                                      T  G   _
GAM960  COVA1     3'  TTTACTTCATGCTGAATGTTTG 73263     AGAT
              CA                    TG    CGTTCAGTATGAAGTAGA
                                    ||    ||||||||||||||||||
                                    AC    GTAAGTCGTACTTCATTT
                                     GTTT
GAM960  CSTF3     3'  TTTATTTTAAAAACTGGATGGC 7178      A       A__
              TTA                   GAG TCGTTCAGT   TGAAGTAGA
                                    ||| |||||||||   |||||||||
                                    TTC GGTAGGTCA   ATTTTATTT
                                     _       AAA
GAM960  CTHRC1    3'  TTTGCTTCAATCAAAAGTGGTT 56622         TTCAGTA_
              TCA                   TGAGATCG       TGAAGTAGA
                                    ||||||||       |||||||||
                                    ACTTTGGT       ACTTCGTTT
                                       GAAAACTA
GAM960  CXorf1    3'  TTTGCTTCTCACAATGATT    16305        CA  AT
                                    GATCGTT  GT  GAAGTAGA
                                    |||||||  ||  ||||||||
                                    TTAGTAA  CA  CTTCGTTT
                                       __  CT
GAM960  DKFZP434H0820 3'  CTTCTGTGGGATGATCTCA    63849          AG  T
                                    TGAGATCGTTC  TA GAAG
                                    ||||||||||||  || ||||
                                    ACTCTAGTAGG  GT CTTC
                                          GT  _
GAM960  DKFZP434N093 3'  TCTATTTTATATTAAGACTTCA 79946      A  GTTC
                                    TGAG TC    AGTATGAAGTAGA
                                    |||| ||    ||||||||||||
                                    ACTT AG    TTATATTTTATCT
                                      C  AA__
GAM960  DKFZP564B1162 3'  TTTGCTTTTGCGAGGCGATTT  48533         CA   T
                                    AGATCGTT  GTA GAAGTAGA
                                    ||||||||  ||| ||||||||
                                    TTTAGCGG  CGT TTTCGTTT
                                       AG  _
GAM960  DKFZP566M1046 3'  TTTATTTCAGATGAATGTTTTA 49540       T     GTA
                                    TGAGA CGTTCA   TGAAGTAGA
                                    ||||| ||||||   |||||||||
                                    ATTTT GTAAGT   ACTTTATTT
                                      _     AG_
GAM960  DKFZP761C169 5'  TGTACTGAGTAGTTTCA     67811        CG
                                    TGAGAT  TTCAGTATG
                                    ||||||  |||||||||
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                                ACTTTG  GAGTCATGT
                                   AT
GAM960  DKFZp761D112 3'  TTTGCTTTTGGAGAATGTATCT 50194       _    AGTAT
           TA                    TGAGAT CGTTC    GAAGTAGA
                                 |||||| |||||    ||||||||
                                 ATTCTA GTAAG    TTTCGTTT
                                    T    AGGT_
GAM960  DKFZp762K2015 3'  TTTACCATGATGCTGGATATCT 72480       C       GAA_
           TA                    TGAGAT GTTCAGTAT   GTAGA
                                 |||||| |||||||||   |||||
                                 ATTCTA TAGGTCGTA   CATTT
                                    _       GTAC
GAM960  DKFZp762P2111 3'  TTTGTTTTGTGCAGAGATCTC  86367       GT  A   TG
                                 GAGATC  TC GTA  AAGTAGA
                                 ||||||  || |||  |||||||
                                 CTCTAG  AG CGT  TTTGTTT
                                    __  A   GT
GAM960  DREV1    3'  TTTGTTTTTTTCTGGACAATCT 32074       C     TAT
           CA                    TGAGAT GTTCAG   GAAGTAGA
                                 |||||| ||||||   ||||||||
                                 ACTCTA CAGGTC   TTTTGTTT
                                    A     TTT
GAM960  DRIL2    3'  TCTATTTCTTATGGGGCCATCT 21330      C    A   T
           T                     GAGAT GTTC GTA GAAGTAGA
                                 ||||| |||| ||| ||||||||
                                 TTCTA CGGG TAT CTTTATCT
                                    C    G   T
GAM960  EDIL3    3'  TCTGTAGGAAACTGAATGGTTT 19126           ATGAAG
           T                     GAGATCGTTCAGT     TAGA
                                 ||||||||||||||     ||||
                                 TTTTGGTAAGTCA     GTCT
                                       AAGGAT
GAM960  EIF4B    3'  TCTAGAATAATGGATGGTCTT  75971          G   GAAG
                                 GAGATCGTTCA TAT    TAGA
                                 |||||||||||| |||    ||||
                                 TTCTGGTAGGT ATA    ATCT
                                       A   AG__
GAM960  ELKS     3'  TCTGCTTTGGATGTGGTCTC   30506       TT  GTA
                                 GAGATCG  CA   TGAAGTAGA
                                 |||||||  ||   |||||||||
                                 CTCTGGT  GT   GTTTCGTCT
                                    __  AG_
GAM960  FBXO4    3'  TTTGCTTTATGCTTCTGCATCT 53114      C  TC_
           T                     GAGAT GT   AGTATGAAGTAGA
                                 ||||| ||   ||||||||||||
                                 TTCTA CG   TCGTATTTCGTTT
                                    _ TCT
GAM960  FKSG14   3'  TTTGTTTCATATATACTGTCTT 67808       C  TCA
           A                     TGAGAT GT   GTATGAAGTAGA
                                 |||||| ||   ||||||||||||
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                                ATTCTG CA   TATACTTTGTTT
                                   T  TA_
GAM960   FLJ10462  3'  TCTATTTTATGCCCTTGCGTAT 36139     _   TCA_
            T                   GAT CGT    GTATGAAGTAGA
                                ||| |||    ||||||||||||
                                TTA GCG    CGTATTTTATCT
                                  T   TTCC
GAM960   FLJ10604  3'  TCTGCTAGGACCAGGGTGATTT 36341        TT A_  ATGA
            CA                    TGAGATCG  C  GT    AGTAGA
                                ||||||||  |  ||    ||||||
                                ACTTTAGT  G  CA    TCGTCT
                                     GG AC  GGA_
GAM960   FLJ10761  3'  TCTGCTTTGTGCTGTGGCTTA  36585     A   TT    TG
                                TGAG TCG  CAGTA  AAGTAGA
                                |||| |||  |||||  |||||||
                                ATTC GGT  GTCGT  TTCGTCT
                                  _  __     GT
GAM960   FLJ10824  3'  TATGCTGATGGTCTTA      72576         T
                                TGAGATCGT CAGTATG
                                ||||||||| |||||||
                                ATTCTGGTA GTCGTAT
                                     _
GAM960   FLJ10846  3'  TCTTGGCTGAATGGTCTTA    36744           AT_
                                TGAGATCGTTCAGT   GA
                                ||||||||||||||   ||
                                ATTCTGGTAAGTCG   CT
                                       GTT
GAM960   FLJ11210  3'  TTTGTCATGACTGAACGAATTT 59578     A       _    AGTAGA
                                GAG TCGTTCAGT ATGA
                                ||| ||||||||| ||||
                                TTT AGCAAGTCA TACT
                                  A        G    GTTT
GAM960   FLJ11730  3'  TTTGTTTTATGCTGAA      42799
                                TTCAGTATGAAGTAGA
                                ||||||||||||||||
                                AAGTCGTATTTTGTTT

GAM960   FLJ11795  3'  GGTTGTTTTTTTGCTGAATGAT 45130             T    TAGA
            TTTA                   TGAGATCGTTCAGTA GAAG
                                ||||||||||||||| ||||
                                ATTTTAGTAAGTCGT TTTT
                                       T    TGTTGGT
GAM960   FLJ12085  3'  TTTACCATGCAGTATTGCATGA 42869       T     GAA___
            TTTTA                  GATCGT CAGTAT     GTAGA
                                ||||||| ||||||     |||||
                                TTAGTA GTTATG     CATTT
                                   C     ACGTAC
GAM960   FLJ12377  3'  TCTACTTCAATAGTATCATTTC 46486       C  TCAGTA
            A                   TGAGAT GT     TGAAGTAGA
                                |||||| ||     |||||||||
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                                ACTTTA TA     ACTTCATCT
                                   C  TGATA_
GAM960  FLJ12389 3' ATTGCACAGACTGAATGGCTTT 60265     AT       A  AA    A
            A                   TGAG  CGTTCAGT TG  GTAG
                                ||||  |||||||| ||  ||||
                                ATTT  GTAAGTCA AC  CGTT
                                  CG       G  A_    AT
GAM960  FLJ12783 3' TCTATTTCAGGTTGTGGCTC   48684    A   TT   TA
                                GAG TCG  CAG  TGAAGTAGA
                                ||| |||  |||  ||||||||||
                                CTC GGT  GTT  ACTTTATCT
                                  _  __   GG
GAM960  FLJ12783 3' TTTGGCCATGACTGGCTGATCT 48687       TT   _   AAGTAGA
            T                   GAGATCG  CAGT ATG
                                |||||||  |||| |||
                                TTCTAGT  GTCA TAC
                                    CG   G   CGGTTT
GAM960  FLJ12888 3' TCATAGATTATATTGAATGATT 46322             AGTAGA
            T                   AGATCGTTCAGTATGA
                                ||||||||||||||||
                                TTTAGTAAGTTATATT
                                         AGATACTT
GAM960  FLJ12910 3' TCTACGTGCACTGGATGATTTT 44705           ATGAA
                                GAGATCGTTCAGT    GTAGA
                                ||||||||||||    |||||
                                TTTTAGTAGGTCA    CATCT
                                      CGTG_
GAM960  FLJ13150 3' TCTACTTTTTCTGGATGATTTC 45671           TAT
                                GAGATCGTTCAG   GAAGTAGA
                                ||||||||||||  ||||||||
                                CTTTAGTAGGTC   TTTCATCT
                                      TT_
GAM960  FLJ14957 3' TCTGCTTTAGGGTATGGTTT   51765       TCAGTA
                                AGATCGT     TGAAGTAGA
                                |||||||     |||||||||
                                TTTGGTA     ATTTCGTCT
                                    TGGG__
GAM960  FLJ20010 3' TTTACTTTATATTTGTAATTTT 38718       CG TC
            A                   TGAGAT  T  AGTATGAAGTAGA
                                ||||||  |  ||||||||||||
                                ATTTTA  G  TTATATTTCATTT
                                   AT T_
GAM960  FLJ20051 3' TCTATTTTCCTCTGGTCATTTC 38851       CGT    TAT
            A                   TGAGAT   TCAG   GAAGTAGA
                                ||||||   ||||   ||||||||
                                ACTTTA   GGTC   TTTTATCT
                                   CT_    TCC
GAM960  FLJ20079 3' TCTATTTCACCCCTGCAGTCTC 34504       C  TCAGTA
                                GAGAT GT     TGAAGTAGA
                                ||||| ||     |||||||||
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                                CTCTG CG     ACTTTATCT
                                   A  TCCCC_
GAM960  FLJ20156  3'  TTTATTTTATGTCATGATTTCA 34654         TCAG
                                TGAGATCGT    TATGAAGTAGA
                                |||||||||    ||||||||||
                                ACTTTAGTA    GTATTTTATTT
                                     CT__
GAM960  FLJ20254  3'  CCCCATCATGCTGGGGGTCTT  34789       G        AGTAGA
                                GAGATC TTCAGTATGA
                                |||||| ||||||||||
                                TTCTGG GGGTCGTACT
                                   _        ACCCCT
GAM960  FLJ20793  3'  TCTATTTTATATATTGAGATTT 91808       GTTCA
           C                     GAGATC     GTATGAAGTAGA
                                ||||||     ||||||||||||
                                CTTTAG     TATATTTTATCT
                                    AGTTA
GAM960  FLJ21628  3'  TTTATTTGGTAAATGAATGATT 47605          G_   G
           TT                    GAGATCGTTCA  TAT AAGTAGA
                                ||||||||||  ||| |||||||
                                TTTTAGTAAGT  ATG TTTATTT
                                      AA   G
GAM960  FLJ22595  3'  TTGTTATCACATTGGATGACTT 46785     A        A   AGTAGA
                                GAG TCGTTCAGT TGA
                                ||| ||||||||| |||
                                TTC AGTAGGTTA ACT
                                  _       C   ATTGTTT
GAM960  FLJ23053  3'  CTTGCAGAGTGATGAATGATTT 43262           G   GAA    A
           TA                    TGAGATCGTTCA TAT   GTAG
                                ||||||||||| |||   ||||
                                ATTTTAGTAAGT GTG   CGTT
                                      A   AGA    CT
GAM960  FLJ23112  5'  TCAGCTCTGTAGGGTGGTCTT  46249       TT AG   GA   AGA
                                GAGATCG  C  TAT  AGT
                                |||||||  |  |||  |||
                                TTCTGGT  G  ATG  TCG
                                    GG __   TC   ACTG
GAM960  FLJ23189  3'  TTTACAATCTGGATGGCTTCA  46842     AT      TATGAA
                                TGAG  CGTTCAG     GTAGA
                                ||||  |||||||     |||||
                                ACTT  GTAGGTC     CATTT
                                  CG      TAA___
GAM960  FLJ23506  3'  TTACCTGTGTTGATTGATTTCA 45749        T      GAA
                                TGAGATCG TCAGTAT   GTAG
                                |||||||| |||||||   ||||
                                ACTTTAGT AGTTGTG   CATT
                                     T      TC_
GAM960  FNBP3     5'  CAAGTTTTATGTTGAGGATCTT 80151        G          AGA
           A                     TGAGATC TTCAGTATGAAGT
                                ||||||| ||||||||||||
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                                ATTCTAG GAGTTGTATTTTG
                                   _          AACT
GAM960  GLUC     3'  TCTGCTTTGGTGATGATCTT  40588        T  G AT
                                GAGATCGT CA T  GAAGTAGA
                                |||||||| || |  ||||||||
                                TTCTAGTA GT G  TTTCGTCT
                                   _ G __
GAM960  GPA33    3'  TTTGCTTCATTCCAAATGCTTT 19461      T    CAGT
           CA                    TGAGA CGTT    ATGAAGTAGA
                                |||||| ||||   ||||||||||
                                ACTTT GTAA    TACTTCGTTT
                                  C    ACCT
GAM960  GPR105   3'  TCTATTTCATGCTTTACTGTCT 29656     C  TC
                                AGAT GT  AGTATGAAGTAGA
                                |||| ||  ||||||||||||
                                TCTG CA  TCGTACTTTATCT
                                  T  TT
GAM960  H_GS165L15.1 5'  TTTATTTCTGAGACGATCTCA  16927         _    T_
                                TGAGATCGT TCAG  ATGAA
                                |||||||| ||||  |||||
                                ACTCTAGCA AGTC  TATTT
                                     G    TT
GAM960  HCNGP    3'  TAAAACCAGTTGAGTGGTCTCA 25154           GTA  AAGTAGA
                                TGAGATCGTTCA   TG
                                ||||||||||||   ||
                                ACTCTGGTGAGT   AC
                                       TG_  CAAAATT
GAM960  HEY1     3'  TTTACTTTGTAAACCAGAATGA 91254   G      AG___  TG
           TTCCG                   ATCGTTC    TA  AAGTAGA
                                |||||||    ||  |||||||
                                TAGTAAG    AT  TTCATTT
                                T      ACCAA  GT
GAM960  HEYL     3'  TTTGCTTCGTGGACTGGCTCA  27401      ATC    GTA
                                TGAG   GTTCA   TGAAGTAGA
                                ||||   |||||  |||||||||
                                ACTC   CAGGT   GCTTCGTTT
                                  GGT    ___
GAM960  HPCL2    5'  TTTGCCTTGCTGGATGATTCCG 24324    AG        TGAA
                                TG  ATCGTTCAGTA    GTAGA
                                ||  ||||||||||    |||||
                                GC  TAGTAGGTCGT    CGTTT
                                 CT         TC__
GAM960  IL1RAPL1 5'  TCTGCTTTTATGGTGAAC    26547      G     _
                                GTTCA TATGAA GTAGA
                                ||||| |||||| |||||
                                CAAGT GTATTT CGTCT
                                   G     T
GAM960  IRX1     3'  TCTGTATATAGAGTGGTTTCA  85939          A    AAG
                                TGAGATCGTTC GTATG   TAGA
                                |||||||||| |||||   ||||
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                                ACTTTGGTGAG TATAT   GTCT
                                      A    ___
GAM960  JWA      3' CCTGCCAATTGAATGATTTC  21140          A  AA   A
                                GAGATCGTTCAGT TG  GTAG
                                |||||||||||| ||  ||||
                                CTTTAGTAAGTTA AC  CGTC
                                      _ __   CG
GAM960  KIAA0010 3' GACCTGTTGCTGGGTGATTTTA 27894        TT    TGA  TAGA
                                TGAGATCG  CAGTA   AG
                                ||||||||  |||||   ||
                                ATTTTAGT  GTCGT   TC
                                     GG    TG_  CAGT
GAM960  KIAA0026 5' TTACAGAATCTTGGATGATTTC 24410           T  GAA   A
           A                     TGAGATCGTTCAG AT   GTAG
                                |||||||||||| ||   ||||
                                ACTTTAGTAGGTT TA   CATT
                                      C  AGA
GAM960  KIAA0042 5' CTGCGGGCGGGTGGTCTTA   29609        TT A  ATGAA
                                TGAGATCG  C GT    GTAG
                                ||||||||  | ||    ||||
                                ATTCTGGT  G CG    CGTC
                                     GG _  GG___
GAM960  KIAA0179 3' TAAATTAATGCTGGTGATCTTA 64831         T     GAAGTAGA
                                TGAGATCGT CAGTAT
                                |||||||| ||||||
                                ATTCTAGTG GTCGTA
                                     _     ATTAAATT
GAM960  KIAA0193 3' TCAGTACTGGGTGGTTCA    28660     G   TT    _
                                TGA ATCG  CAGTA TGA
                                ||| ||||  ||||| |||
                                ACT TGGT  GTCAT ACT
                                  _   GG    G
GAM960  KIAA0193 3' TCTAAAATCTCACTGAGTGATT 28663           AT  AG_
           TCA                    TGAGATCGTTCAGT  GA   TAGA
                                |||||||||||||  ||   ||||
                                ACTTTAGTGAGTCA  CT   ATCT
                                      CT  AAA
GAM960  KIAA0205 3' TTTATTTTATACAGATGGGTTT 29593       GT  A
           T                    GAGATC  TC GTATGAAGTAGA
                                ||||||  || ||||||||||||
                                TTTTGG  AG CATATTTTATTT
                                   GT  A
GAM960  KIAA0252 3' CTGCTTTGTACTTCCTCA    62790     ATCGTTC   TG
                                TGAG      AGTA  AAGTAG
                                ||||      ||||  ||||||
                                ACTC      TCAT  TTCGTC
                                  CT_____    GT
GAM960  KIAA0261 3' TTTGCTTTTTTGTTGAATGATT 68186    AG        T_
           CCA                    TG  ATCGTTCAGTA  GAAGTAGA
                                ||  ||||||||||  ||||||||
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                                AC  TAGTAAGTTGT  TTTCGTTT
                                 CT         TT
GAM960  KIAA0332 3' TTTGTTTTGTGCCTGAACGGTC 62709          _ TG
              T                  AGATCGTTCAG TA  AAGTAGA
                                 ||||||||||| ||  |||||||
                                 TCTGGCAAGTC GT  TTTGTTT
                                       C  GT
GAM960  KIAA0335 3' TTTATTTCAGATGTAGATTTT  28995       GTT  GTA
                                 GAGATC   CA   TGAAGTAGA
                                 ||||||   ||   |||||||||
                                 TTTTAG   GT   ACTTTATTT
                                    AT_  AG_
GAM960  KIAA0352 3' TCTTCTGAATGGTTTT      29158           TAT
                                 GAGATCGTTCAG   GA
                                 ||||||||||||   ||
                                 TTTTGGTAAGTC   CT
                                        TT_
GAM960  KIAA0408 3' TTTACTTCTACATAGGTGATTT 28142         TTCA_   T
              TA                  TGAGATCG    GTA GAAGTAGA
                                  ||||||||    ||| ||||||||
                                  ATTTTAGT    CAT CTTCATTT
                                       GGATA  _
GAM960  KIAA0441 3' TTTGTATTGAGCATTTCA    28962       C       TG
                                 TGAGAT GTTCAGTA  AA
                                 |||||| ||||||||  ||
                                 ACTTTA CGAGTTAT  TT
                                    _       GT
GAM960  KIAA0451 3' TCTATTTCTACAGAATCATTTC 29116       C    A   T
              A                   TGAGAT GTTC GTA GAAGTAGA
                                  |||||| |||| ||| ||||||||
                                  ACTTTA TAAG CAT CTTTATCT
                                     C   A  _
GAM960  KIAA0451 3' TGTTTTCATGCAGGACATTTTA 29119       C    A       TAGA
                                 TGAGAT GTTC GTATGAAG
                                 |||||| |||| ||||||||
                                 ATTTTA CAGG CGTACTTT
                                    _   A       TGTT
GAM960  KIAA0459 3' CTGTTTTGTACTGCTTGA    60992     TT    TG
                                 TCG  CAGTA  AAGTAG
                                 |||  |||||  ||||||
                                 AGT  GTCAT  TTTGTC
                                   TC    GT
GAM960  KIAA0475 3' ATTTGTTTTGTGTTCTGGCAAA 29484   T____   __ TG
              GTGATCTCA               G    TCAG  TA  AAGTAGA  T
                                 |    ||||  ||  |||||||  |
                                 T    GGTC  GT  TTTGTTT   A
                                  GAAAC    TT  GT
GAM960  KIAA0648 3' TTTGCTTTTGTCTGATGGTCT  82661        T   TAT
                                 AGATCGT CAG   GAAGTAGA
                                 ||||||| |||   ||||||||
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                                TCTGGTA GTC   TTTCGTTT
                                   _  TGT
GAM960  KIAA0861 5' TTTATTTATACGGAATGGTTTT 88936         A      GTAGA
                                GAGATCGTTC GTATGAA
                                |||||||||| |||||||
                                TTTTGGTAAG CATATTT
                                     G      ATTT
GAM960  KIAA0882 3' ATTTGCTTTTTACAGATGTTGG 82645      _______  T
           ACGATTTT               GTTCA     GTA GAAGTAGA   T
                                |||||     ||| ||||||||  |
                                CAGGT     CAT TTTCGTTT   A
                                   TGTAGA   T
GAM960  KIAA0882 3' TCTATTTACAGGATGATTTT   82648         A   TGA
                                GAGATCGTTC GTA   AGTAGA
                                |||||||||| |||   ||||||
                                TTTTAGTAGG CAT   TTATCT
                                     A  ___
GAM960  KIAA0895 3' TTTATATGTTGAGGGATTTTA  92728       G   __
                                TGAGATC TTCA  GTATGAA
                                ||||||| ||||  |||||||
                                ATTTTAG GAGT  TATATTT
                                    G   TG
GAM960  KIAA0907 3' TTTGCTTTATATTGGGAGCT   30185    ATCG
                                AG   TTCAGTATGAAGTAGA
                                ||   ||||||||||||||||
                                TC   GGGTTATATTTCGTTT
                                 GA__
GAM960  KIAA0976 5' TTTGCTTCAGATACTGATATCT 29898       CGT     __
           CA                    TGAGAT   TCAGTA  TGAAGTAGA
                                ||||||   ||||||  |||||||||
                                ACTCTA   AGTCAT  ACTTCGTTT
                                   T__     AG
GAM960  KIAA0981 3' TCTACTTTGGTTCTAGCTATTT 61426       C   C  TA_
           TA                    TGAGAT GTT AG   TGAAGTAGA
                                |||||| ||| ||   |||||||||
                                ATTTTA CGA TC   GTTTCATCT
                                   T  _  TTG
GAM960  KIAA0992 3' TCTGACCAGACTTGATGGTTTT 32209         C   A  AAG
           A                     TGAGATCGTT AGT TG   TAGA
                                |||||||||| ||| ||   ||||
                                ATTTTGGTAG TCA AC   GTCT
                                     T   G  CA_
GAM960  KIAA1026 3' TCTATTTTGTGCTTTTTCT   71213     TCGTTC   TG
                                AGA     AGTA  AAGTAGA
                                |||     ||||  |||||||
                                TCT     TCGT  TTTATCT
                                  TTT___   GT
GAM960  KIAA1026 3' TCTGTTTTATACTGGTGC    71215    _
                                GT TCAGTATGAAGTAGA
                                || ||||||||||||||
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                              CG GGTCATATTTTGTCT
                               T
GAM960  KIAA1033 3' TTTATATTAATGATCTT     64520         C
                              GAGATCGTT AGTATGAA
                              ||||||||| ||||||||
                              TTCTAGTAA TTATATTT
                                    _
GAM960  KIAA1041 3' TCATACTGAGTGATTT      30141
                              AGATCGTTCAGTATGA
                              ||||||||||||||||
                              TTTAGTGAGTCATACT

GAM960  KIAA1041 3' TTGCTATTGCACGATTTCA   30146         T   ATGA
                              TGAGATCGT CAGT   AGTAG
                              ||||||||| ||||   |||||
                              ACTTTAGCA GTTA   TCGTT
                                    C  _____
GAM960  KIAA1143 3' TCTACTTCATATTCATCTT   68691       CGTTC
                              GAGAT    AGTATGAAGTAGA
                              |||||    ||||||||||||||
                              TTCTA    TTATACTTCATCT
                                 C_____
GAM960  KIAA1145 3' TTTAAGCGTACAATTGAGTGGT 65632          ___    AAG
           TTTA                  AGATCGTTCA  GTATG  TAGA
                              |||||||||   |||||  ||||
                              TTTGGTGAGT  CATGC  ATTT
                                    TAA   GA_
GAM960  KIAA1161 5' CTGAGGCTGGATGATCT     81748          ATGAAG
                              AGATCGTTCAGT     TAG
                              ||||||||||||     |||
                              TCTAGTAGGTCG     GTC
                                    GA_____
GAM960  KIAA1239 3' GCTCATATTGAATGTTTTTA  71331       T         A
                              TGAGA CGTTCAGTATGA GT
                              ||||| |||||||||||| ||
                              ATTTT GTAAGTTATACT CG
                                 T         _
GAM960  KIAA1240 3' TTTGAATCTTGTTGAGTGATTT 66743           T  AG
           C                   GAGATCGTTCAGTA GA  TAGA
                              |||||||||||||| ||  ||||
                              CTTTAGTGAGTTGT CT  GTTT
                                       T  AA
GAM960  KIAA1327 3' TTTACTTTGTATCTGAAC    72270       _ TG
                              GTTCAG TA  AAGTAGA
                              |||||| ||  |||||||
                              CAAGTC AT  TTCATTT
                                 T  GT
GAM960  KIAA1344 3' TGTATTAGATGGTCTTA     72452         TC
                              TGAGATCGT  AGTATG
                              |||||||||  ||||||
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                                ATTCTGGTA  TTATGT
                                     GA
GAM960  KIAA1399 3' TTTATTTTATAGTGATTTGGTT 70256     G    T_  G
            CA                    TGA ATCG  TCA TATGAAGTAGA
                                  ||| ||||  ||| ||||||||||
                                  ACT TGGT  AGT ATATTTTATTT
                                    _   TT   G
GAM960  KIAA1456 3' TTTACTTTATGCTGGATGA    67011
                                  TCGTTCAGTATGAAGTAGA
                                  ||||||||||||||||||
                                  AGTAGGTCGTATTTCATTT

GAM960  KIAA1462 3' TTTATCTAGAATGATCTT    91393          _ T
                                  GAGATCGTTC AG ATGAA
                                  |||||||||| || |||||
                                  TTCTAGTAAG TC TATTT
                                       A  _
GAM960  KIAA1727 3' TCTATCATGGATGCTGGGTGAC 64068     A   TT     GAA__
            TT                     GAG TCG  CAGTAT    GTAGA
                                  ||| |||  ||||||    |||||
                                  TTC AGT  GTCGTA    TATCT
                                    _  GG     GGTAC
GAM960  KIAA1754 3' TTTGCTTCATACCATTGGGATC 63243      GTTCA_
            T                      AGATC     GTATGAAGTAGA
                                  |||||     ||||||||||||
                                  TCTAG     CATACTTCGTTT
                                     GGTTAC
GAM960  KIAA1804 3' CTACCTTTGAACTGTTTCA    69788       C     TATGAA
                                  TGAGAT GTTCAG     GTAG
                                  |||||| ||||||     ||||
                                  ACTTTG CAAGTT     CATC
                                     T     TC____
GAM960  KIAA1813 5' TCTGCTGAGTGAATTCA     70312      A        T
                                  TGAG TCGTTCAGTA GA
                                  |||| |||||||||| ||
                                  ACTT AGTGAGTCGT CT
                                    A        _
GAM960  KIAA1858 5' TCTGCTGATGTGATTTCA    67140       GT_     T
                                  TGAGATC   TCAGTA GA
                                  |||||||   |||||| ||
                                  ACTTTAG   AGTCGT CT
                                      TGT     _
GAM960  KIAA1878 3' TCTGTGTCACTGGTCGATTTT  91717       TT   AT  AG
                                  GAGATCG  CAGT  GA  TAGA
                                  |||||||  ||||  ||  ||||
                                  TTTTAGC  GTCA  CT  GTCT
                                      TG    __  GT
GAM960  KIAA1894 3' TTTACTTCATTGAATACGATC  73847       TCAGT
                                  GATCGT    ATGAAGTAGA
                                  ||||||    ||||||||||
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                                CTAGCA    TACTTCATTT
                                   TAAGT
GAM960  KIAA1908 5' TTGATACTGGACGGTTCT    73407    _       G
                                AGA TCGTTCAGTAT AA
                                ||| |||||||||| ||
                                TCT GGCAGGTCATA TT
                                  T        G
GAM960  KIAA1944 5' TTTATTTGGGGAATGATCTC  75569        AGTATG
                                GAGATCGTTC    AAGTAGA
                                ||||||||||    |||||||
                                CTCTAGTAAG    TTTATTT
                                      GGG___
GAM960  KRTAP1-5 3' TTGCCTGCTGGATATTTCA   49228      C      TGAA
                                TGAGAT GTTCAGTA   GTAG
                                |||||| ||||||||   ||||
                                ACTTTA TAGGTCGT   CGTT
                                   _      C___
GAM960  LASP1    3' TTATATTGGGCGATTT     20465
                                AGATCGTTCAGTATGA
                                ||||||||||||||||
                                TTTAGCGGGTTATATT

GAM960  LRRFIP1  3' TTTACTTTGTAAGAGATTTTA 16422      GTTCAG  TG
                                TGAGATC    TA  AAGTAGA
                                |||||||    ||  |||||||
                                ATTTTAG    AT  TTCATTT
                                    AGA___  GT
GAM960  MANBAL   3' TCTGCTTCTGTGACGGTTT   41980      T  GTAT
                                AGATCGT CA   GAAGTAGA
                                ||||||| ||   ||||||||
                                TTTGGCA GT   CTTCGTCT
                                   _ GT__
GAM960  MAPK8IP3 3' TTTATTTTATGCTCTAGGTTTT 53000     GTTC
                                GAGATC   AGTATGAAGTAGA
                                ||||||   ||||||||||||
                                TTTTGG   TCGTATTTTATTT
                                   ATC_
GAM960  MGC10067 3' TCTAAATTCTGAGCGGTCTCA  58941          TATGAAG
                                TGAGATCGTTCAG      TAGA
                                ||||||||||||      ||||
                                ACTCTGGCGAGTC      ATCT
                                      TTAA___
GAM960  MGC12966 3' TCTACATTTTGTAGAATGATTT 51127        AG  T  A
           T                    GAGATCGTTC  TA GA GTAGA
                                ||||||||||  || || |||||
                                TTTTAGTAAG  GT TT CATCT
                                      AT  T  A
GAM960  MGC12992 3' TCTGCTTTGTGTTAGAGC    50348    _   TG
                                GTTC AGTA  AAGTAGA
                                |||| ||||  |||||||
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                                CGAG TTGT  TTCGTCT
                                  A    GT
GAM960  MGC29956 3'  TCTGCTTTGTGTATGGTACTT  58281     _    TCAG  TG
                                GAG ATCGT    TA  AAGTAGA
                                ||| |||||    ||  |||||||
                                TTC TGGTA    GT  TTCGTCT
                                  A    T___  GT
GAM960  MGC30052 3'  TTGCTTCATGACTATTTC    58535      C   CAGT
                                GAGAT GTT    ATGAAGTAG
                                ||||| |||    |||||||||
                                CTTTA CAG    TACTTCGTT
                                   T  _____
GAM960  MGC32043 3'  CATCTGGATGGTTTCA      58047           T
                                TGAGATCGTTCAG ATG
                                |||||||||||| |||
                                ACTTTGGTAGGTC TAC

                                          _
GAM960  MGC34923 3'  CTACACACTGGGTGGCTT    58520     A   TT    ATGAA
                                GAG TCG  CAGT    GTAG
                                ||| |||  ||||    ||||
                                TTC GGT  GTCA    CATC
                                  _  GG   CA___
GAM960  MGC4734  3'  TTTGTTTCTCTTTGAATGTCTT 58952      T      TAT
                                GAGA CGTTCAG   GAAGTAGA
                                |||| |||||||   ||||||||
                                TTCT GTAAGTT   CTTTGTTT
                                  _      TCT
GAM960  N4BP2    3'  TCTGCTTTGTATATGACCTT   36406     A   TCA   TG
                                GAG TCGT   GTA  AAGTAGA
                                ||| ||||   |||  |||||||
                                TTC AGTA   TAT  TTCGTCT
                                  C    ___   GT
GAM960  NECL1    3'  TCTGCTTTGGGTGCGGTTTT   41027        TCAGTA
                                GAGATCGT     TGAAGTAGA
                                ||||||||     |||||||||
                                TTTTGGCG     GTTTCGTCT
                                     TGG___
GAM960  NUCKS    3'  TTTATTTCATCACTTGTTATCT 42699       CG TC  _
            CA                    TGAGAT  T  AGT ATGAAGTAGA
                                ||||||  |  ||| ||||||||||
                                ACTCTA  G  TCA TACTTTATTT
                                   TT T_  C
GAM960  Nup43    3'  TCTGCTTTGTGTTGGGACGCTT 45012     T    AG_  TG
            T                     AGA CGTTC   TA  AAGTAGA
                                ||| |||||   ||  |||||||
                                TTT GCAGG   GT  TTCGTCT
                                  C    GTT  GT
GAM960  OCLM     3'  TTTACTGGCAATTGGGTGGCCT 42351     AT  TT    A  A_
            T                     GAG  CG  CAGT TG  AGTAGA
                                |||  ||  |||| ||  ||||||
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                                TTC  GT  GTTA AC  TCATTT
                                  CG  GG   _ GG
GAM960  OSBPL3   3'  TTTATCATGAGTGATCTT    31443          GT
                                GAGATCGTTCA  ATGAA
                                ||||||||||  |||||
                                TTCTAGTGAGT  TATTT
                                      AC
GAM960  PIK3R4   3'  TTTATTTTGTATTGAAAAAGAT 62182     G__      TG
                                ATC   TTCAGTA  AAGTAGA
                                |||   |||||||  |||||||
                                TAG   AAGTTAT  TTTATTT
                                  AAA      GT
GAM960  PKNOX2   3'  TTTATAATCTGGGTGATCCA   90880    A    TT   __
                                TG GATCG  CAG  TATGAA
                                || |||||  |||  ||||||
                                AC CTAGT  GTC  ATATTT
                                 _    GG   TA
GAM960  PMAIP1   3'  TTTATTTCAGCAGGAATAATTT 40894       CG   AGTA
           TA                     TGAGAT  TTC    TGAAGTAGA
                                |||||||  |||   |||||||||
                                ATTTTA  AAG    ACTTTATTT
                                   AT   GACG
GAM960  PNMA5    3'  TCTGCTTTGCCGGTGTAGATCT 73601       GT__  A  AT
           C                     GAGATC    TC GT  GAAGTAGA
                                ||||||    || ||  ||||||||
                                CTCTAG    GG CG  TTTCGTCT
                                   ATGT  C  __
GAM960  PPP2R3A  3'  TTTACTTCATGTTGAAAACAAT 10751     GATCG
           TA                     TGA     TTCAGTATGAAGTAGA
                                |||     ||||||||||||||||
                                ATT     AAGTTGTACTTCATTT
                                  AACAA
GAM960  PRO0641  5'  TTTACTTTGTGCCCAACTGTCT 26212       C   CA   TG
           CA                     TGAGAT GTT  GTA  AAGTAGA
                                ||||||| |||  |||  |||||||
                                ACTCTG CAA  CGT  TTCATTT
                                   T   CC   GT
GAM960  PRO1880  5'  TCTATTTTGTCTCCATGATTTT 26043        TC  T TG
                                GAGATCGT  AG A  AAGTAGA
                                ||||||||  || |  |||||||
                                TTTTAGTA  TC T  TTTATCT
                                     CC  _ GT
GAM960  QKI      3'  TTATATTGGGTGTCTT      65449      T  TT
                                GAGA CG  CAGTATGA
                                ||||  ||  ||||||||
                                TTCT GT  GTTATATT
                                  _  GG
GAM960  QKI      3'  TTTATTTCATTAAATGATTTT  65450          CAGT
                                GAGATCGTT    ATGAAGTAGA
                                |||||||||    ||||||||||
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                                TTTTAGTAA   TACTTTATTT
                                     AT__
GAM960  Rab11-FIP2 3'  TTTATTCATACATGAGTGATTT 29785         _     GTAGA
                                AGATCGTTCA GTATGAA
                                |||||||||| |||||||
                                TTTAGTGAGT CATACTT
                                     A      ATTT
GAM960  RAD51    3'  TCTGTCTGAATGATCTT    56020          TAT
                                GAGATCGTTCAG  GA
                                ||||||||||||  ||
                                TTCTAGTAAGTC  CT
                                      TGT
GAM960  RAD51    3'  TCTGTCTGAATGATCTT    11226          TAT
                                GAGATCGTTCAG  GA
                                ||||||||||||  ||
                                TTCTAGTAAGTC  CT
                                      TGT
GAM960  RALGPS1A  3'  TCTGGGCTGGATGTTTCA   27610     T      AT_
                                TGAGA CGTTCAGT  GA
                                ||||| ||||||||  ||
                                ACTTT GTAGGTCG  CT
                                   _      GGT
GAM960  RNASE3L   3'  TCTGTTTTTAGCTGGATGGTCT 25082          AT
           T                     GAGATCGTTCAGT  GAAGTAGA
                                ||||||||||||  ||||||||
                                TTCTGGTAGGTCG  TTTTGTCT
                                      AT
GAM960  RNF8     3'  TCTACTTTGTATTGTGGTC   14244      TT    TG
                                GATCG  CAGTA  AAGTAGA
                                |||||  |||||  |||||||
                                CTGGT  GTTAT  TTCATCT
                                   __     GT
GAM960  RNP24    3'  TTTGCTTTAAAACTACGACTCA 22361     A   TC   A_
                                TGAG TCGT  AGT  TGAAGTAGA
                                |||| ||||  |||  |||||||||
                                ACTC AGCA  TCA  ATTTCGTTT
                                   _   __   AA
GAM960  SCYB10   3'  TGTGCTGAATGGTTTT     7799
                                GAGATCGTTCAGTATG
                                ||||||||||||||||
                                TTTTGGTAAGTCGTGT

GAM960  SFXN5    3'  TTTGCTTTGTCTCCCGGATGAT 58042         ___  T TG
           TTC                    AGATCGTTC   AG A  AAGTAGA
                                |||||||||   || |  |||||||
                                TTTAGTAGG   TC T  TTCGTTT
                                      CCC  _ GT
GAM960  SH3BGRL2  3'  TCAGCACTGAACGATTTCA   48890           A_
                                TGAGATCGTTCAGT  TGA
                                ||||||||||||||  |||
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                                ACTTTAGCAAGTCA  ACT
                                       CG
GAM960  SLC2A9   3'  TCTACATGGATGATCTCA    39172          _  T
                                TGAGATCGTTCA GTA GA
                                |||||||||||| ||| ||
                                ACTCTAGTAGGT CAT CT
                                       A  _
GAM960  SLC38A1  3'  CTGTTTTATATTGAGTATTTTA 47723      C           A
                                TGAGAT GTTCAGTATGAAGTAG
                                |||||| ||||||||||||||||
                                ATTTTA TGAGTTATATTTTGTC
                                   _           C
GAM960  SNIP1    3'  TTTCAGAACAGTCTCA     45217      C   AGTA
                                TGAGAT GTTC   TGAAG
                                |||||| ||||   |||||
                                ACTCTG CAAG   ACTTT
                                   A  _____
GAM960  SNRK     3'  TTTGTTTATAAGTGAATGATT  34776        G_    GTAGA
                                GATCGTTCA  TATGAA
                                |||||||||  ||||||
                                TTAGTAAGT  ATATTT
                                      GA     GTTT
GAM960  Spir-1   3'  TTTATGATAGTGTATTGGATGA 64706           AA___
           TTT                  GATCGTTCAGTATG    GTAGA
                                ||||||||||||||    |||||
                                TTAGTAGGTTATGT    TATTT
                                       GATAG
GAM960  STIM2    3'  TCTATTTTATATTGTTATATTT 40480      TC  T_
           TTA                   TGAGA  GT  CAGTATGAAGTAGA
                                |||||  ||  ||||||||||||||
                                ATTTT  TA  GTTATATTTTATCT
                                   TA  TT
GAM960  SYPL     3'  TCTGTTTCATGAGATATGATCT 92912       TCAG
                                AGATCGT   TATGAAGTAGA
                                |||||||   ||||||||||
                                TCTAGTA   GTACTTTGTCT
                                     TAGA
GAM960  TANK     3'  TTTATTTTTCTGAAGTGATCT  56012       _   TAT
                                AGATCG TTCAG   GAAGTAGA
                                |||||| |||||   ||||||||
                                TCTAGT AAGTC   TTTTATTT
                                   G    T__
GAM960  TOLLIP   3'  TCGTGCTGGGAGGTCTCA    38689       G
                                TGAGATC TTCAGTATGA
                                ||||||| ||||||||||
                                ACTCTGG GGGTCGTGCT
                                     A
GAM960  TP53INP1 3'  TATCTTGGATGGTTTCA     52729          T
                                TGAGATCGTTCAG ATG
                                |||||||||||| |||
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                                ACTTTGGTAGGTT TAT
                                      C
GAM960  TP53INP1  3'  TATCTTGGATGGTTTCA     72956           T
                                TGAGATCGTTCAG ATG
                                ||||||||||||| |||
                                ACTTTGGTAGGTT TAT
                                      C
GAM960  TPD52     3'  TTTACTTCAGTATAAATTATCT 17428       C   CAGTA
          TA                    TGAGAT GTT     TGAAGTAGA
                                |||||| |||     |||||||||
                                ATTCTA TAA     ACTTCATTT
                                   T   ATATG
GAM960  TRIM4     3'  TATCCTGGATGGTCCA      52255    A        T
                                TG GATCGTTCAG ATG
                                || ||||||||| |||
                                AC CTGGTAGGTC TAT
                                 _        C
GAM960  TRIM5     5'  TCTGAAGGTGTATTGAGTGATT 52307             AAG_
          TT                    GAGATCGTTCAGTATG    TAGA
                                |||||||||||||||    ||||
                                TTTTAGTGAGTTATGT    GTCT
                                      GGAA
GAM960  TRIM5     5'  TCTGAAGGTGTATTGAGTGATT 52364             AAG_
          TT                    GAGATCGTTCAGTATG    TAGA
                                |||||||||||||||    ||||
                                TTTTAGTGAGTTATGT    GTCT
                                      GGAA
GAM960  TRIM5     5'  TCTGAAGGTGTATTGAGTGATT 52370             AAG_
          TT                    GAGATCGTTCAGTATG    TAGA
                                |||||||||||||||    ||||
                                TTTTAGTGAGTTATGT    GTCT
                                      GGAA
GAM960  UCK1      3'  TCTGACAACTGTAACGGTTTT  48703         _   A  AAG
                                GAGATCGTT CAGT TG   TAGA
                                ||||||||| |||| ||   ||||
                                TTTTGGCAA GTCA AC   GTCT
                                     T   _  A__
GAM960  UST       3'  CATGTTGGGCAGTCTCA     19135        C
                                TGAGAT GTTCAGTATG
                                |||||| ||||||||||
                                ACTCTG CGGGTTGTAC
                                   A
GAM960  VIT       3'  GTGCTGGAGATTTTA       53903        G
                                TGAGATC TTCAGTAT
                                ||||||| ||||||||
                                ATTTTAG AGGTCGTG
                                  _
GAM960  VMP       3'  TCTACTACCTGTGTGATCTT   54903        TT   TATGA
                                GAGATCG  CAG    AGTAGA
                                |||||||  |||    ||||||
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                                TTCTAGT  GTC    TCATCT
                                   GT   CA___
GAM960  WIRE     3'  TCTGCTTTATTTTTGGGGGT   78309    G    T_
                                ATC TTCAG  ATGAAGTAGA
                                ||| |||||  ||||||||||
                                TGG GGGTT  TATTTCGTCT
                                  _    TT
GAM960  ZFD25    3'  ATATTGAGTGATCCA      32576    A
                                TG GATCGTTCAGTAT
                                || ||||||||||||
                                AC CTAGTGAGTTATA
                                 _
GAM960  ZNF238   3'  TTTACCCAGTTGAGCGTTCTTA 20975      T     GTA  AA
                                TGAGA CGTTCA   TG  GTAGA
                                ||||| ||||||   ||  |||||
                                ATTCT GCGAGT   AC  CATTT
                                   T     TG_  C_
GAM960  ZNF306   3'  TCTACTGGGTGGATGGTT    92246        GTATGA
                                GATCGTTCA     AGTAGA
                                |||||||||     ||||||
                                TTGGTAGGT     TCATCT
                                     GGG___
GAM960  LOC112687 3'  TCTATTTCACAAGGAGTGGCTC 72870     A     AGTA
           A                     TGAG TCGTTC    TGAAGTAGA
                                |||| ||||||    |||||||||
                                ACTC GGTGAG    ACTTTATCT
                                  _     GAAC
GAM960  LOC113251 3'  TATATTGAACTGTTTT      53524      C
                                GAGAT GTTCAGTATG
                                ||||| ||||||||||
                                TTTTG CAAGTTATAT
                                   T
GAM960  LOC113612 3'  TTTATTTCAAGATGATCATCA  73085    _     CAGTA
                                TGA GATCGTT    TGAAGTAGA
                                ||| |||||||    |||||||||
                                ACT CTAGTAG    ACTTTATTT
                                  A      A____
GAM960  LOC116071 3'  TCTGCTTCAAGAGGGGGTTTTA 56628       G   AGTA
                                TGAGATC TTC    TGAAGTAGA
                                ||||||| |||    |||||||||
                                ATTTTGG GGG    ACTTCGTCT
                                     _   AGA_
GAM960  LOC123872 5'  TCTGCAGAAACTGGATGCTCTT 74239      T       ATGAA
           A                     TGAGA CGTTCAGT     GTAGA
                                ||||| ||||||||     |||||
                                ATTCT GTAGGTCA     CGTCT
                                   C       AAGA_
GAM960  LOC124842 3'  TCTGGGCGGCTGAATTGATTTT 75660       _     A  AAG
                                GAGATCG TTCAGT TG   TAGA
                                ||||||| |||||| ||   ||||
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                                TTTTAGT AAGTCG GC   GTCT
                                    T     _ GG_
GAM960  LOC125893 3'  TTTACTTCATGTTCACACCTCA 75673     ATC  TC
                                TGAG   GT  AGTATGAAGTAGA
                                ||||   ||  ||||||||||||
                                ACTC   CA  TTGTACTTCATTT
                                  CA_  C_
GAM960  LOC126964 3'  TCTACTTTTGGAGAATGAACTT 74623     A     AGTAT
          A                      TGAG TCGTTC    GAAGTAGA
                                |||| ||||||    ||||||||
                                ATTC AGTAAG    TTTCATCT
                                  A     AGGT_
GAM960  LOC128344 3'  ATCTGTTGGGTGCTGAGTTGGG 74735    _____       GA
          TGATTTCA                CG    TTCAGTAT  AGTAGA   T
                                ||    ||||||||  ||||||  |
                                GT    GAGTCGTG  TTGTCT   A
                                 GGGTT       GG
GAM960  LOC128553 3'  CTGCTTATGGGCGGT       74761        GTATG
                                ATCGTTCA    AAGTAG
                                ||||||||    ||||||
                                TGGCGGGT    TTCGTC
                                    A____
GAM960  LOC132241 3'  TTTACTTTGGCCAGGCTGGTCT 75055        TT AGTA
          TA                     TGAGATCG  C    TGAAGTAGA
                                ||||||||  |    |||||||||
                                ATTCTGGT  G    GTTTCATTT
                                    CG ACCG
GAM960  LOC134218 3'  TCTGCTTTATTTTCTGAATTTC 75158    TC     T__
                                GA  GTTCAG   ATGAAGTAGA
                                ||  ||||||   ||||||||||
                                CT  TAAGTC   TATTTCGTCT
                                 T_     TTT
GAM960  LOC139673 3'  TCTAGAATAATGGATGGTCTT  75980          G   GAAG
                                GAGATCGTTCA TAT    TAGA
                                |||||||||||  |||    ||||
                                TTCTGGTAGGT ATA    ATCT
                                      A   AG__
GAM960  LOC145314 3'  TTTGCTTCTCTGGGAAAGGTCT 77090        G   AGTAT
          TA                     TGAGATC TTC    GAAGTAGA
                                |||||||  |||    ||||||||
                                ATTCTGG AAG    CTTCGTTT
                                    A   GGTCT
GAM960  LOC145645 3'  CATATTTCATGTTGGATGGTTT 77325                GA
          C                      GAGATCGTTCAGTATGAAGTA
                                |||||||||||||||||||||
                                CTTTGGTAGGTTGTACTTTAT
                                           ACT
GAM960  LOC145739 3'  TCTGCTTCATGCAGATCTC   77445       GTTCA
                                GAGATC    GTATGAAGTAGA
                                ||||||    ||||||||||||
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                                CTCTAG    CGTACTTCGTCT
                                  A____
GAM960  LOC145761 5'  TGCTTTCGGGCTGGGTGGTTTC 83477       TT   AT_    GA
          A                    TGAGATCG  CAGT   GAAGTA
                               ||||||||  ||||  ||||||
                               ACTTTGGT  GTCG   TTTCGT
                                  GG   GGC
GAM960  LOC145871 3'  TTTGCTTTTTCAGGACATTTCA 83565      C   AGTAT
                               TGAGAT GTTC    GAAGTAGA
                               ||||||  ||||    ||||||||
                               ACTTTA CAGG    TTTCGTTT
                                  _   ACTT_
GAM960  LOC146506 3'  TTTACTTCATTTAACAACGTAT 77938      _   CAGT_
          CTT                    GAGAT CGTT    ATGAAGTAGA
                               |||||  ||||    ||||||||||
                               TTCTA GCAA    TACTTCATTT
                                  T   CAATT
GAM960  LOC146603 5'  TCTGCTTTTTGTGGGTGGTTTT 78022       TT  G  T
                               GAGATCG  CA TA GAAGTAGA
                               |||||||  || || ||||||||
                               TTTTGGT  GT GT TTTCGTCT
                                  GG  _  T
GAM960  LOC146713 3'  CATGTTGAACATCTT      83722      C
                               GAGAT GTTCAGTATG
                               |||||  ||||||||||
                               TTCTA CAAGTTGTAC
                                  _
GAM960  LOC147180 5'  ATTTCGTGGAAGATTGGGTGGT 83983     TT   _____    TAGA
          CTCA                   ATCG  CAGT    ATGAAG
                               ||||  ||||    ||||||
                               TGGT  GTTA    TGCTTT
                                 GG   GAAGG       AG
GAM960  LOC147429 3'  TCTATTTTGTTTATGGTC    78365       TCAGT TG
                               GATCGT    A  AAGTAGA
                               ||||||    |  |||||||
                               CTGGTA    T  TTTATCT
                                  TT___ GT
GAM960  LOC147632 5'  TTTAGTCATGGATGGTCTC   56671         GTA_
                               GAGATCGTTCA   TGAA
                               ||||||||||    ||||
                               CTCTGGTAGGT   ATTT
                                     ACTG
GAM960  LOC147660 3'  TTTACTTCATGTTCACACCTCA 78402     ATC  TC
                               TGAG   GT  AGTATGAAGTAGA
                               ||||   ||  ||||||||||||
                               ACTC   CA  TTGTACTTCATTT
                                 CA_  C_
GAM960  LOC147804 5'  TCTATAGTTGATTGAATGCTCT 78486     T      ATGAA
          TA                     TGAGA CGTTCAGT    GTAGA
                               |||||  ||||||||    |||||
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                                ATTCT GTAAGTTA    TATCT
                                  C       GTTGA
GAM960   LOC147817 3'  TTTCACCATATTGGCTGGTCTC 78510        TT      AAGTAGA
           A                     TGAGATCG  CAGTATG
                                 ||||||||  |||||||
                                 ACTCTGGT  GTTATAC
                                     CG      CACTTT
GAM960   LOC148293 3'  TTACTTATGTATGATCTTA   78787        TCA   TGA
                                 TGAGATCGT   GTA   AGTAG
                                 |||||||||   |||   |||||
                                 ATTCTAGTA   TAT   TCATT
                                      TG_   ___
GAM960   LOC149041 3'  TCTGTTTGATTAATTGTATGAT 79142        T   __  G
           CTTA                    GAGATCGT CAGT  AT AAGTAGA
                                 |||||||| ||||  || |||||||
                                 TTCTAGTA GTTA  TA TTTGTCT
                                      T    AT  G
GAM960   LOC149373 3'  TTTGTTTTATACTGAAGGCT   79317    A  G
                                 AG TC TTCAGTATGAAGTAGA
                                 || || ||||||||||||||||
                                 TC GG AAGTCATATTTTGTTT
                                  _ _
GAM960   LOC149421 5'  TCTGCTGAGCAATCTT      79365       C       T
                                 GAGAT GTTCAGTA GA
                                 ||||| |||||||| ||
                                 TTCTA CGAGTCGT CT
                                    A       _
GAM960   LOC149483 5'  TCTGCAGGTCTTGGCTGGTTTC 79387        TT   T  GAA
           A                     TGAGATCG  CAG AT   GTAGA
                                 ||||||||  ||| ||   |||||
                                 ACTTTGGT  GTT TG   CGTCT
                                      CG   C  GA_
GAM960   LOC149711 3'  ATATTGAATGATGTTA      84669     G
                                 TGA ATCGTTCAGTAT
                                 ||| ||||||||||||
                                 ATT TAGTAAGTTATA
                                   G
GAM960   LOC150051 3'  TCTGCGCTCCCGGGGTGATCTT 84806        TT AGTAT  A_
                                 GAGATCG  C    GA  GTAGA
                                 |||||||  |    ||  |||||
                                 TTCTAGT  G    CT  CGTCT
                                     GG GCC__  CG
GAM960   LOC150084 5'  TTTATTTGGTGAATGGTTTC   79562          G  TGA
                                 GAGATCGTTCA TA   AGTAGA
                                 |||||||||||  ||   ||||||
                                 CTTTGGTAAGT GT   TTATTT
                                        G  ___
GAM960   LOC150406 5'  TTTGCTTATTCTGGGCATTTCA 79862        C     TATG
                                 TGAGAT GTTCAG    AAGTAGA
                                 |||||| ||||||    |||||||
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                                ACTTTA CGGGTC    TTCGTTT
                                   _     TTA_
GAM960   LOC151201 3'  TCTGTTTCATATTGGACTTTTT 85296      TC
           A                    TGAGA  GTTCAGTATGAAGTAGA
                                |||||  ||||||||||||||||
                                ATTTT  CAGGTTATACTTTGTCT
                                  T_
GAM960   LOC151521 3'  TCTAAAGCTATGGATGGTTTCA 85439          GTATGAAG
                                TGAGATCGTTCA       TAGA
                                ||||||||||||       ||||
                                ACTTTGGTAGGT       ATCT
                                       ATCGAA__
GAM960   LOC151614 3'  TCTATTTCATAAAGATCTCA   80311       GTTCAG
                                TGAGATC     TATGAAGTAGA
                                |||||||     ||||||||||
                                ACTCTAG     ATACTTTATCT
                                   AA_____
GAM960   LOC151647 3'  TCTGCTTCGTGATTTTATTTCA 80334       CGTTCAG
                                TGAGAT      TATGAAGTAGA
                                ||||||      ||||||||||
                                ACTTTA      GTGCTTCGTCT
                                   TTTTA__
GAM960   LOC152348 5'  TTTGCTTTGTACTAGTGATTT  85702        C    TG
                                AGATCGTT AGTA  AAGTAGA
                                |||||||| ||||  |||||||
                                TTTAGTGA TCAT  TTCGTTT
                                   _    GT
GAM960   LOC154007 3'  TTTGTTTCAAATTGTGATTTCA 81028        TT    A
                                TGAGATCG  CAGT TGAAGTAGA
                                ||||||||  |||| |||||||||
                                ACTTTAGT  GTTA ACTTTGTTT
                                   __    A
GAM960   LOC154562 3'  TCTATTTTGTGTTGAACTTGCT 81094    ATC       TG
                                AG   GTTCAGTA  AAGTAGA
                                ||   ||||||||  |||||||
                                TC   CAAGTTGT  TTTATCT
                                 GTT       GT
GAM960   LOC154739 5'  TCTATATGCTTGGATGGCTTC  86241     AT     _    GAA
                                GAG  CGTTCA GTAT   GTAGA
                                |||  |||||| ||||   |||||
                                CTT  GTAGGT CGTA   TATCT
                                  CG     T   ___
GAM960   LOC155038 3'  TCTTGGAGGTTCTGAATGATTT 81262          TATGAAGT
           TA                    TGAGATCGTTCAG       AGA
                                 ||||||||||||       |||
                                 ATTTTAGTAAGTC       TCT
                                        TTGGAGGT
GAM960   LOC157627 3'  TCTACTCTGTGGGTGGTTTCA  81507        TT  GTAT  A
                                TGAGATCG  CA    GA GTAGA
                                ||||||||  ||    || |||||
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                                ACTTTGGT  GT    CT CATCT
                                    GG  GT__  _
GAM960   LOC158014 5'  TCTGCTTTGAATGGGATTTC   81660       GT   GTA
                                GAGATC  TCA   TGAAGTAGA
                                ||||||  |||   |||||||||
                                CTTTAG  GGT   GTTTCGTCT
                                   __   AA_
GAM960   LOC158947 3'  CTATAGCTGGACCATTTTA    82055       C      ATGAA
                                TGAGAT GTTCAGT    GTAG
                                |||||| |||||||     ||||
                                ATTTTA CAGGTCG    TATC
                                   C      A____
GAM960   LOC160646 3'  TTTCAATGCTGAATATTTTA   82234       C       _
                                TGAGAT GTTCAGTAT GAAG
                                |||||| ||||||||| ||||
                                ATTTTA TAAGTCGTA CTTT
                                   _       A
GAM960   LOC161190 5'  TTGCAGGTACTGGGTGCTCTT  82265     T  TT     GAA
                                GAGA CG  CAGTAT   GTAG
                                ||||  ||  ||||||   ||||
                                TTCT GT  GTCATG   CGTT
                                  C  GG     GA_
GAM960   LOC164971 5'  TTGATATTGACATGGTTTTA   82462         _     G
                                TGAGATCGT TCAGTAT AA
                                ||||||||| ||||||| ||
                                ATTTTGGTA AGTTATA TT
                                     C      G
GAM960   LOC165693 5'  TTTACTTTGCTGGGATGTTTC  82600      CG     AT
                                GAGAT  TTCAGT  GAAGTAGA
                                |||||  ||||||  ||||||||
                                CTTTG  GGGTCG  TTTCATTT
                                   TA     __
GAM960   LOC170425 5'  CTAGTGCTGAATGATCCCA    76379    A          GA
                                TG GATCGTTCAGTAT  AG
                                || ||||||||||||  ||
                                AC CTAGTAAGTCGTG  TC
                                 C          A_
GAM960   LOC196411 3'  CTAAAGCTGAGTGATTTT     87672           ATGAAG
                                GAGATCGTTCAGT     TAG
                                ||||||||||||      |||
                                TTTTAGTGAGTCG     ATC
                                      AA_____
GAM960   LOC196540 5'  TCTGCTTCGGGCTAAATATCTT 89637       C   C   A
           A                     TGAGAT GTT AGT TGAAGTAGA
                                ||||||| ||| ||| |||||||||
                                ATTCTA TAA TCG GCTTCGTCT
                                   _  A  G
GAM960   LOC199982 3'  TTTATTTTTTAAAGTATGGTTT 88510         TCAG  T
           CA                     TGAGATCGT    TA GAAGTAGA
                                |||||||||    || ||||||||
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                                ACTTTGGTA   AT TTTTATTT
                                      TGAA  T
GAM960   LOC200301 3'  TCTGCTTTATGTTGCACCTATG 88755      T____
            ATTTC                  ATCGT    CAGTATGAAGTAGA
                                   ||||||   ||||||||||||||
                                   TAGTA    GTTGTATTTCGTCT
                                     TCCAC
GAM960   LOC200609 5'  TTTGCTTCATATGCTTTAGTGG 90106       TTCA___
            TCT                    AGATCG     GTATGAAGTAGA
                                   ||||||     ||||||||||||
                                   TCTGGT     TATACTTCGTTT
                                     GATTTCG
GAM960   LOC200627 3'  TTTATTTTATTCAAAAGGGTTT 88846       G  CAGT
            CA                     TGAGATC TT   ATGAAGTAGA
                                   ||||||| ||   ||||||||||
                                   ACTTTGG AA   TATTTTATTT
                                      G  AACT
GAM960   LOC201626 3'  AAAGTACCATTTGAATGATCTT 88982           T   AAGTAGA
            A                       TGAGATCGTTCAG ATG
                                    |||||||||||||| |||
                                    ATTCTAGTAAGTT TAC
                                           _  CATGAAAT
GAM960   LOC201696 5'  GTACTGGATGTGTTTTA     63136       _
                                   TGAGAT CGTTCAGTAT
                                   |||||| ||||||||||
                                   ATTTTG GTAGGTCATG
                                      T
GAM960   LOC203378 5'  TTGTTTCATACTGTTCG     90622    TT
                                   CG  CAGTATGAAGTAG
                                   ||  |||||||||||||
                                   GC  GTCATACTTTGTT
                                    TT
GAM960   LOC219294 3'  TCTATTTCATCAAATTATTTCA 93014       C   CAGT
                                   TGAGAT GTT   ATGAAGTAGA
                                   |||||| |||   ||||||||||
                                   ACTTTA TAA   TACTTTATCT
                                      T  AC__
GAM960   LOC219672 3'  CATGTTGAGCTGTTTCA     91329       C
                                   TGAGAT GTTCAGTATG
                                   |||||| ||||||||||
                                   ACTTTG CGAGTTGTAC
                                      T
GAM960   LOC220021 5'  CTCTATATTGAGTGGTCT     93393            A
                                   AGATCGTTCAGTATG AG
                                   |||||||||||||||| ||
                                   TCTGGTGAGTTATAT TC
                                             C
GAM960   LOC220064 3'  TTTGGAGTGTATTGGCGCGATC 93430        _      AAGTAGA
            TC                      GAGATCGT TCAGTATG
                                    |||||||| ||||||||
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                                CTCTAGCG GGTTATGT
                                    C       GAGGTTT
GAM960   LOC220074 3'  TCTGTTTTATATGCTGGGATTC 59287     TCG       __
             T                   AGA   TTCAGTAT  GAAGTAGA
                                 |||   ||||||||  ||||||||
                                 TCT   GGGTCGTA  TTTTGTCT
                                   TA_       TA
GAM960   LOC221288 3'  TTTACTTTAACAGGGGTGATT  93623       TT AGTA
                                 GATCG  C    TGAAGTAGA
                                 |||||  |    |||||||||
                                 TTAGT  G    ATTTCATTT
                                    GG GACA
GAM960   LOC221405 3'  TTTGCTCTTTAGACGGTCTCA  93891          CAGTAT  A
                                 TGAGATCGTT     GA GTAGA
                                 ||||||||||     || |||||
                                 ACTCTGGCAG     CT CGTTT
                                       ATTT__  _
GAM960   LOC221490 5'  TTTGCCACAACTGTGTGATTTT 93672         TT    A  AA
             A                   TGAGATCG  CAGT TG  GTAGA
                                 ||||||||  |||| ||  |||||
                                 ATTTTAGT  GTCA AC  CGTTT
                                      GT    _  AC
GAM960   LOC221662 3'  TTTATACTTGAACAATTTCA   92408       C     _
                                 TGAGAT GTTCA GTATGAA
                                 ||||||| ||||| |||||||
                                 ACTTTA CAAGT CATATTT
                                    A     T
GAM960   LOC221830 3'  TCTACTTTGTATAACACATTCT 92511     TC  TCA   TG
                                 AGA  GT   GTA  AAGTAGA
                                 |||  ||   |||  |||||||
                                 TCT  CA   TAT  TTCATCT
                                   TA  CAA   GT
GAM960   LOC253451 3'  TTTATTTTATACTAGGTCCTCA 96022      _  GTTC
                                 TGAG ATC    AGTATGAAGTAGA
                                 |||| |||    ||||||||||||
                                 ACTC TGG    TCATATTTTATTT
                                   C   A___
GAM960   LOC253967 5'  TTTACTTCATATTTTTCTT    96267      TCGTTC
                                 GAGA      AGTATGAAGTAGA
                                 ||||      ||||||||||||
                                 TTCT      TTATACTTCATTT
                                   TT_____
GAM960   LOC254013 5'  TTTACTTCCGAGGGCGGTGTCA 94881     G      AGTAT
                                 TGA ATCGTTC     GAAGTAGA
                                 ||| |||||||     ||||||||
                                 ACT TGGCGGG     CTTCATTT
                                   G       AGC__
GAM960   LOC255328 3'  TCTAGCAGTGTTGGACATCTCA 96565        C        GAAG
                                 TGAGAT GTTCAGTAT    TAGA
                                 |||||| |||||||||    ||||
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                                ACTCTA CAGGTTGTG    ATCT
                                   _       ACG_
GAM960   LOC255623 3'  TTTACTTCATGTTCACACCTCA 94853     ATC  TC
                                TGAG   GT  AGTATGAAGTAGA
                                ||||   ||  ||||||||||||
                                ACTC   CA  TTGTACTTCATTT
                                  CA_  C_
GAM960   LOC255811 3'  TCTGGGAATAATACTGGGGGTT 94652       G       GAAG__
           TT                    GAGATC TTCAGTAT     TAGA
                                ||||||| ||||||||     ||||
                                TTTTGG GGGTCATA     GTCT
                                   _       ATAAGG
GAM960   LOC255811 3'  TTGTTTTTGTTTTTGAACTGTC 94653       C     T_ TG   TAGA
           TCA                   TGAGAT GTTCAG  A  AAG
                                |||||| ||||||  |  |||
                                ACTCTG CAAGTT  T  TTT
                                   T     TT GT   TGTTT
GAM960   LOC256073 3'  TTGAATTCTATTTGAATGGTTT 96670           TAT   GTAGA
           T                     GAGATCGTTCAG   GAA
                                ||||||||||||   |||
                                TTTTGGTAAGTT   CTT
                                      TAT   AAGTTT
GAM960   LOC256267 3'  TCTGTCACCAAGCTGGACGATC 96811            A  AAG_
           TCA                   TGAGATCGTTCAGT TG    TAGA
                                |||||||||||||| ||    ||||
                                ACTCTAGCAGGTCG AC    GTCT
                                      A  CACT
GAM960   LOC256568 3'  TCTACTTTATATTTTATTGTCT 94844      C  TC
                                AGAT GT  AGTATGAAGTAGA
                                |||| ||  ||||||||||||
                                TCTG TA  TTATATTTCATCT
                                  T  TT
GAM960   LOC256812 5'  TCTGCTTCGCGGAGGCGGTGTC 97549    G    _  A  AT
                                GA ATCGT TC GT  GAAGTAGA
                                || ||||| || ||  ||||||||
                                CT TGGCG AG CG  CTTCGTCT
                                 G    G  G  __
GAM960   LOC256846 5'  TCTGCAGGTCTTGGCTGGTTTC 95424        TT   T  GAA
           A                     TGAGATCG  CAG AT   GTAGA
                                |||||||  ||| ||   |||||
                                ACTTTGGT  GTT TG   CGTCT
                                     CG   C  GA_
GAM960   LOC257017 5'  TTTATTTTATTTTTAGGGGTCT 97381       G  C  T
           C                     GAGATC TT AG ATGAAGTAGA
                                |||||| || || ||||||||||
                                CTCTGG GA TT TATTTTATTT
                                   G  T  T
GAM960   LOC257463 3'  TTTATTTTTAGAGCGATTT    71073         AGTAT
                                AGATCGTTC    GAAGTAGA
                                |||||||||    ||||||||
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                                TTTAGCGAG    TTTTATTT
                                     AT___
GAM960  LOC51018  3' TTTGCTTTGTGTTGGGAAGTT  32127    CG     TG
                                GAT  TTCAGTA  AAGTAGA
                                |||  |||||||  |||||||
                                TTG  GGGTTGT  TTCGTTT
                                  AA      GT
GAM960  LOC51580  3' TTTATATTTTGAGTGATTTCA  31872          __
                                TGAGATCGTTCA  GTATGAA
                                ||||||||||||  |||||||
                                ACTTTAGTGAGT  TATATTT
                                       TT
GAM960  LOC51608  3' TCTGTTTCTGTGCGGCGGCTCA 63676     A    CA   _
                                TGAG TCGTT  GTAT GAAGTAGA
                                |||| |||||  |||| ||||||||
                                ACTC GGCGG  CGTG CTTTGTCT
                                  _    __    T
GAM960  LOC56270  3' TCTATTTTATGGTTTTGATTTC 39023        TTCAG
           A                     TGAGATCG    TATGAAGTAGA
                                |||||||||    ||||||||||
                                ACTTTAGT    GTATTTTATCT
                                     TTTG_
GAM960  LOC56920  3' TCTGTTTTATGCTAAATGGATT 39393     A    C
           TA                    TGAG TCGTT AGTATGAAGTAGA
                                |||| ||||| ||||||||||||
                                ATTT GGTAA TCGTATTTTGTCT
                                  A    A
GAM960  LOC89919  5' ATACTGAGTGTTTTCA     60718      T
                                TGAGA CGTTCAGTAT
                                ||||| ||||||||||
                                ACTTT GTGAGTCATA
                                   T
GAM960  LOC90288  3' TCTTGCAGAATGATCTCA    62110          A  T
                                TGAGATCGTTC GTA GA
                                |||||||||||  ||| ||
                                ACTCTAGTAAG CGT CT
                                       A  T
GAM960  LOC90378  3' TTTATTTTGGTGGGTGGTCTT  62525       TT  G AT
                                GAGATCG  CA T  GAAGTAGA
                                |||||||  || |  ||||||||
                                TTCTGGT  GT G  TTTTATTT
                                    GG  G __
GAM960  LOC90639  5' TTGTATGGGGCGGTTTTA    63666          A  TG
                                TGAGATCGTTC GTA  A
                                ||||||||||| |||  |
                                ATTTTGGCGGG TAT  T
                                       G  GT
GAM960  LOC90639  3' TTTGTTTTTTGCGTGGACGATT 63668    _     _  T
           CT                    AGA TCGTTCA GTA GAAGTAGA
                                ||| ||||||| ||| ||||||||
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                                TCT AGCAGGT CGT TTTTGTTT
                                  T      G   T
GAM960  LOC91252  3'  GTCTGGATGGTTTTA      65341           T
                                TGAGATCGTTCAG AT
                                |||||||||||| ||
                                ATTTTGGTAGGTC TG
                                          _
GAM960  LOC91694  3'  TCTTGCTGAACTGTCTT     66965      C       T
                                GAGAT GTTCAGTA GA
                                ||||| |||||||| ||
                                TTCTG CAAGTCGT CT
                                   T       T
GAM960  LOC91828  5'  TCTGGCCGAGCTGGGTGGCTT  67279     A   TT    A  AAG
                                GAG TCG  CAGT TG   TAGA
                                ||| |||  |||| ||   ||||
                                TTC GGT  GTCG GC   GTCT
                                  _  GG    A  CG_
GAM960  LOC92249  5'  TTTACTTCATACCTTGTCTCA  68569       CGTTCA
                                TGAGAT     GTATGAAGTAGA
                                ||||||     ||||||||||||
                                ACTCTG     CATACTTCATTT
                                    TTC___
GAM960  LOC92466  3'  TCTGTCACCAAGCTGGACGATC 69436            A  AAG_
           TCA                    TGAGATCGTTCAGT TG    TAGA
                                ||||||||||||| ||    ||||
                                ACTCTAGCAGGTCG AC    GTCT
                                      A  CACT
GAM960  LOC92606  3'  TCTTTTGAATGGTTTCA     69992           TAT
                                TGAGATCGTTCAG   GA
                                ||||||||||||   ||
                                ACTTTGGTAAGTT   CT
                                      TT_
GAM961  EGFL5     5'  CAGCAGCTACCATGACAGCAT  86614       GA  ___
                                ATGCTG  CA   TAGCTGCTG
                                ||||||  ||   |||||||||
                                TACGAC  GT   ATCGACGAC
                                   A_  ACC
GAM961  GAB2      3'  CAGCCGTATCTAGCATAT    24490         C TA
                                ATATGCTGGA A  GCTG
                                |||||||||| |  ||||
                                TATACGATCT T  CGAC
                                      A GC
GAM961  GAB2      3'  CAGCCGTATCTAGCATAT    54447         C TA
                                ATATGCTGGA A  GCTG
                                |||||||||| |  ||||
                                TATACGATCT T  CGAC
                                      A GC
GAM961  LHX3      3'  CAGCCCAGCCCAGCATA     27372        ACATA  __
                                TATGCTGG    GCT  GCTG
                                ||||||||    |||  ||||
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                                ATACGACC    CGA  CGAC
                                      _____  CC
GAM961  MYD88    3'  CAGCAGCTGGACATCACATTTC 10166      A  C  GACA
                                GAAAT TG TG    TAGCTGCTG
                                ||||| || ||    |||||||||
                                CTTTA AC AC    GTCGACGAC
                                   C  T  AG__
GAM961  PSMD9    3'  GGCTTTGACCAACATATTTC   10988        C   A  T
                                GAAATATG TGG CA AGCT
                                |||||||| ||| || ||||
                                CTTTATAC ACC GT TCGG
                                     A   A  T
GAM961  TRPM1    5'  CAGTTCACCAACCAGCATAT   10056         ACAT__
                                ATATGCTGG     AGCTG
                                |||||||||     |||||
                                TATACGACC     TTGAC
                                      AACCAC
GAM961  WBP2     3'  CAGTGCTGCCCAGCGTA     73026        ACA    T
                                TATGCTGG   TAGC GCTG
                                ||||||||   |||| ||||
                                ATGCGACC   GTCG TGAC
                                     C__    _
GAM961  ZNF192   3'  CAGCACTCCAGCATTTTTC    20853     T      CATA
                                GAAA ATGCTGGA    GCTG
                                |||| ||||||||    ||||
                                CTTT TACGACCT    CGAC
                                  T       CA__
GAM961  DKFZp761K1423 5'  CAGCAGCTCTCCAGCAT     37330         CAT
                                ATGCTGGA   AGCTGCTG
                                ||||||||   ||||||||
                                TACGACCT   TCGACGAC
                                     C__
GAM961  GL009    3'  CAGCTATGAAACAAATTTC    72635      A  CTGGA
                                GAAAT TG    CATAGCTG
                                ||||| ||    ||||||||
                                CTTTA AC    GTATCGAC
                                   A  AAA__
GAM961  HYPC     5'  CAGCAGCTGCCACAGACA    64609    _  GACA
                                TG CTG    TAGCTGCTG
                                || |||    |||||||||
                                AC GAC    GTCGACGAC
                                 A   ACC_
GAM961  KIAA1128 3'  AGCAACTCAGCATAT       68470        GACAT  C
                                ATATGCTG    AG TGCT
                                ||||||||    || ||||
                                TATACGAC    TC ACGA
                                     _____  A
GAM961  KIAA1855 3'  CAGCAGCTTGGGCAGC      92337      GA  T
                                GCTG  CA AGCTGCTG
                                ||||  || ||||||||
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                                CGAC  GT TCGACGAC
                                  GG  _
GAM961  REA      3'  CAGCCAGGGGTCCAGCA     23445        ATAG  _
                                TGCTGGAC    CTG CTG
                                ||||||||    ||| |||
                                ACGACCTG    GAC GAC
                                    GG__   C
GAM961  UGT2B10  3'  AGCAGCTAAGGCATGTT     6539         GGACA
                                AATATGCT    TAGCTGCT
                                ||||||||    ||||||||
                                TTGTACGG    ATCGACGA
                                    A____
GAM961  ZFP36L2  3'  CAGCAGCTACCAACCACCAT   22552     C   ACA_
                                ATG TGG    TAGCTGCTG
                                ||| |||    |||||||||
                                TAC ACC    ATCGACGAC
                                  C   AACC
GAM961  LOC151103 5'  CAGCAGCTACCAACCACCAT   85222     C   ACA_
                                ATG TGG    TAGCTGCTG
                                ||| |||    |||||||||
                                TAC ACC    ATCGACGAC
                                  C   AACC
GAM961  LOC199729 3'  CAGCCATAGCTCAGCATA     73031        GACAT   ___
                                TATGCTG    AGCT   GCTG
                                |||||||    ||||   ||||
                                ATACGAC    TCGA   CGAC
                                    _____   TAC
GAM961  LOC90288  3'  TTATGTCCAGCACATTTT     62112      A
                                GAAAT TGCTGGACATAG
                                ||||| ||||||||||||
                                TTTTA ACGACCTGTATT
                                   C
GAM961  LOC92181  3'  CAACTATGTAATGGCTATATTT 68402        _  GG_     C
            C                    GAAATAT GCT   ACATAG TG
                                ||||||| |||   |||||| ||
                                CTTTATA CGG   TGTATC AC
                                    T   TAA     A
GAM962  ABCC1    3'  GGGCCTGGCCCAAAGCAGTGTT 17182         C   CAA  _
                                AACACTGTT TGG   GCT GGTTT
                                ||||||||| |||   ||| |||||
                                TTGTGACGA ACC   CGG CCGGG
                                    A   ___   T
GAM962  ABCC1    3'  GGGCCTGGCCCAAAGCAGTGTT 39127         C   CAA  _
                                AACACTGTT TGG   GCT GGTTT
                                ||||||||| |||   ||| |||||
                                TTGTGACGA ACC   CGG CCGGG
                                    A   ___   T
GAM962  ABCC1    3'  GGGCCTGGCCCAAAGCAGTGTT 39135         C   CAA  _
                                AACACTGTT TGG   GCT GGTTT
                                ||||||||| |||   ||| |||||
```

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                                TTGTGACGA ACC   CGG CCGGG
                                     A  ___  T
GAM962  ADAM17   3'  CTGCAGCGTCAGAATCGTGTT  41555      T      AA   GTTT
                                AACAC GTTCTGGC  GCTG
                                ||||| ||||||||  ||||
                                TTGTG TAAGACTG  CGAC
                                  C       __   GTCA
GAM962  ADAMTS4  3'  GGGCTAGGAAATCCAGGGTGGT 17515    TG    CAAG_
          G                      CAC  TTCTGG    CTGGTTT
                                 |||  ||||||    |||||||
                                 GTG  GGGACC    GATCGGG
                                   GT     TAAAG
GAM962  ADH5     3'  ACATGAGTATGGAATGGTGTT  5414         TGG  A   G  TT
                                 AACACTGTTC   CA GCT GT
                                 ||||||||||   || ||| ||
                                 TTGTGGTAAG   GT TGA TA
                                      ___  A   G  CAT
GAM962  ADRA1D   3'  GGACCAGAGAGGCGGGCTGGTG 5446       GTT  G  AAG_
          TT                     AACACT   CT GC    CTGGTTT
                                 ||||||   || ||    |||||||
                                 TTGTGG   GG CG    GACCAGG
                                    TC_  G  GAGA
GAM962  ALK      5'  AGGCTGGGCCCGGAGAGCAGTG 73380        ___   A_   GGTTT
          T                      CACTGTTCT   GGC  AGCT
                                 |||||||||   |||  ||||
                                 GTGACGAGA   CCG  TCGG
                                      GGC   GG    A   T
GAM962  AMD1     3'  AAATCAAGTGGTTGGAACACTG 7898      C    TG  AA  _
          TT                     AACA TGTTC  GC  GCT GGTTT
                                 |||| |||||  ||  ||| |||||
                                 TTGT ACAAG  TG  TGA CTAAA
                                   C    GT  G_   A
GAM962  ANXA9    5'  AGGCCACACCGGAGCAGTG    13101          CAAGC
                                 CACTGTTCTGG     TGGTTT
                                 ||||||||||     ||||||
                                 GTGACGAGGCC     ACCGGA
                                       AC___
GAM962  APG5L    5'  GAGCCATAGCTTGGAGTAGGTT 16760     A     TGG     __
                                 AAC CTGTTC   CAAGCT  GGTTT
                                 |||  ||||||   ||||||  |||||
                                 TTG GATGAG   GTTCGA  CCGAG
                                   _     ___      TA
GAM962  ATF7     3'  AGATCATCCCCCAGGGTGGGGT 22461     A TG     CAAGC
          T                      AAC C  TTCTGG     TGGTTT
                                 |||  |  ||||||     ||||||
                                 TTG G  GGGACC     ACTAGA
                                   G GT     CCCT_
GAM962  ATP6IP1  3'  GGGTTGAGGGTGGGACGGTGT  6791          GG___   G
                                 ACACTGTTCT     CAA CT
                                 ||||||||||     ||| ||
```

```
                                TGTGGCAGGG    GTT GG
                                     TGGGA   G
GAM962  AXIN1    3'  GAGTTTGACTGTGGGGTGGTGT 60854     TG   __ _     GGTTT
              T                   ACAC  TTCT  GG CAAGCT
                                  ||||  ||||  || ||||||
                                  TGTG  GGGG  TC GTTTGA
                                    GT    TG  A     G   T
GAM962  BAZ1B    3'  GGATCTGGCCAGAGGGGTGTT  50539       G      AAGCT
                                  AACACT TTCTGGC    GGTTT
                                  |||||| |||||||    |||||
                                  TTGTGG GAGACCG    CTAGG
                                     G      GT___
GAM962  BAZ2A    3'  AGTGGGGGCTGGAGCGGGGTT  25591     A     TG  AA__
                                  AAC CTGTTC  GC    GCT
                                  ||| ||||||  ||    |||
                                  TTG GGCGAG  CG    TGA
                                    G     GT  GGGG
GAM962  BCHE     3'  AAACCCAAATGGCTAGAACATG 3547       C        AAGCT_
              TT                   AACA TGTTCTGGC      GGTTT
                                  |||| |||||||||      |||||
                                  TTGT ACAAGATCG      CCAAA
                                    _       GTAAAC
GAM962  BCL11A   3'  AGCTTTAGGTGGTGTT      56722       TG T   GC
                                  AACAC  T CTG  AAGCT
                                  |||||  | |||  |||||
                                  TTGTG  G GAT  TTCGA
                                     GT _   __
GAM962  BCL11A   3'  AGCTTTAGGTGGTGTT      35865       TG T   GC
                                  AACAC  T CTG  AAGCT
                                  |||||  | |||  |||||
                                  TTGTG  G GAT  TTCGA
                                     GT _   __
GAM962  BIRC7    5'  AAACCTGGTCAGAGCCAGTGTT 42207         _      AAGCT
                                  AACACTG TTCTGGC    GGTTT
                                  ||||||| |||||||    |||||
                                  TTGTGAC GAGACTG    CCAAA
                                     C      GT___
GAM962  BIRC7    5'  AAACCTGGTCAGAGCCAGTGTT 57788         _      AAGCT
                                  AACACTG TTCTGGC    GGTTT
                                  ||||||| |||||||    |||||
                                  TTGTGAC GAGACTG    CCAAA
                                     C      GT___
GAM962  BLK      5'  TGGACTGGCTTTTGCTTTAGGA 8155        __   __  TG
              TGGTGTT                 TGTTCT  GGCA  AGC  GTTT  G
                                  ||||||  ||||  |||  ||||  |
                                  GTAGGA  TCGT  TCG  CAGG   T
                                     TT    TT   GT
GAM962  BPGM     3'  GAGCTAGGCTGTGGAGTAGAGT 8175      A       G  AG
              T                   AAC CTGTTCTG CA  CTGGTTT
                                  ||| |||||||| ||  |||||||
```

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                                TTG GATGAGGT GT  GATCGAG
                                  A       _ CG
GAM962  BRCA1   3' GAACCGGTTTCCAAAGACAGT 23521      C_  C
                                ACTGTT  TGG AAGCTGGTTT
                                ||||||  ||| ||||||||||
                                TGACAG  ACC TTTGGCCAAG
                                   AA  _
GAM962  BRCA1   3' GAACCGGTTTCCAAAGACAGT 23530      C_  C
                                ACTGTT  TGG AAGCTGGTTT
                                ||||||  ||| ||||||||||
                                TGACAG  ACC TTTGGCCAAG
                                   AA  _
GAM962  BRCA1   3' GAACCGGTTTCCAAAGACAGT 23538      C_  C
                                ACTGTT  TGG AAGCTGGTTT
                                ||||||  ||| ||||||||||
                                TGACAG  ACC TTTGGCCAAG
                                   AA  _
GAM962  BRCA1   3' GAACCGGTTTCCAAAGACAGT 23546      C_  C
                                ACTGTT  TGG AAGCTGGTTT
                                ||||||  ||| ||||||||||
                                TGACAG  ACC TTTGGCCAAG
                                   AA  _
GAM962  BRCA1   3' GAACCGGTTTCCAAAGACAGT 23554      C_  C
                                ACTGTT  TGG AAGCTGGTTT
                                ||||||  ||| ||||||||||
                                TGACAG  ACC TTTGGCCAAG
                                   AA  _
GAM962  BRCA1   3' GAACCGGTTTCCAAAGACAGT 23562      C_  C
                                ACTGTT  TGG AAGCTGGTTT
                                ||||||  ||| ||||||||||
                                TGACAG  ACC TTTGGCCAAG
                                   AA  _
GAM962  BRCA1   3' GAACCGGTTTCCAAAGACAGT 23571      C_  C
                                ACTGTT  TGG AAGCTGGTTT
                                ||||||  ||| ||||||||||
                                TGACAG  ACC TTTGGCCAAG
                                   AA  _
GAM962  BRCA1   3' GAACCGGTTTCCAAAGACAGT 23579      C_  C
                                ACTGTT  TGG AAGCTGGTTT
                                ||||||  ||| ||||||||||
                                TGACAG  ACC TTTGGCCAAG
                                   AA  _
GAM962  BRCA1   3' GAACCGGTTTCCAAAGACAGT 23587      C_  C
                                ACTGTT  TGG AAGCTGGTTT
                                ||||||  ||| ||||||||||
                                TGACAG  ACC TTTGGCCAAG
                                   AA  _
GAM962  BRCA1   3' GAACCGGTTTCCAAAGACAGT 23595      C_  C
                                ACTGTT  TGG AAGCTGGTTT
                                ||||||  ||| ||||||||||
```

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                                TGACAG  ACC TTTGGCCAAG
                                   AA  _
GAM962  BRF1     3'  GGCTGGCAGTGTGGTGTT    7714       TG T   G  A
                                AACAC  T CTG CA GCT
                                ||||||  | ||| || |||
                                TTGTG  G GAC GT CGG
                                   GT T   G  _
GAM962  C10orf2  3'  GGGCCTAACCTAGAGCAGGTT  41546     A       CAAGCT
                                AAC CTGTTCTGG     GGTTT
                                ||| |||||||||     |||||
                                TTG GACGAGATC     CCGGG
                                  _       CAAT__
GAM962  CACNG1   3'  GAGCCAGCAGGTGGACAGGTGT 5584       _    TG  AA
           T                     AACAC TGTTC  GC  GCTGGTTT
                                |||||  |||||  ||  ||||||||
                                TTGTG ACAGG  TG  CGACCGAG
                                   G     __  GA
GAM962  CASP2    3'  GGCCAGGAAGAATGGTGT    6902          GGCAAG
                                ACACTGTTCT     CTGGTT
                                ||||||||||     ||||||
                                TGTGGTAAGA     GACCGG
                                     AG____
GAM962  CASP2    3'  GGCCAGGAAGAATGGTGT    52144         GGCAAG
                                ACACTGTTCT     CTGGTT
                                ||||||||||     ||||||
                                TGTGGTAAGA     GACCGG
                                     AG____
GAM962  CASP2    3'  GGCCAGGAAGAATGGTGT    52158         GGCAAG
                                ACACTGTTCT     CTGGTT
                                ||||||||||     ||||||
                                TGTGGTAAGA     GACCGG
                                     AG____
GAM962  CASP2    3'  GGCCAGGAAGAATGGTGT    52173         GGCAAG
                                ACACTGTTCT     CTGGTT
                                ||||||||||     ||||||
                                TGTGGTAAGA     GACCGG
                                     AG____
GAM962  CDC27    3'  GGTTCTTCAAGAATGGTGTT   6989          _ CA
                                AACACTGTTCT GG  AGCT
                                |||||||||| ||  ||||
                                TTGTGGTAAGA CT  TTGG
                                     A  TC
GAM962  CHRNA3   3'  AACCTTTAGAACAGGGTT    5605      A       CAAGCT
                                AAC CTGTTCTGG     GGTT
                                ||| |||||||||     ||||
                                TTG GACAAGATT     CCAA
                                  G       T_____
GAM962  CHS1     3'  AAATTAGTCCCCTATTAGAATA 3587    A       CAA___
              GGGTT                  CTGTTCTGG     GCTGGTTT
                                |||||||||     ||||||||
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                                GATAAGATT     TGATTAAA
                                G       ATCCCC
GAM962  CHST6   3'  GAGCTGGTCTGGGAACTGTGTT 41229      T    GG  AG TG
                                AACAC GTTCT  CA  C  GTTT
                                ||||| |||||  ||  |  ||||
                                TTGTG CAAGG  GT  G  CGAG
                                   T    __  CT GT
GAM962  CLCN6   3'  GGCTGCACTCCGAGCAGTGTT  41390        TG___   A
                                AACACTGTTC    GCA GCT
                                ||||||||||    ||| |||
                                TTGTGACGAG    CGT CGG
                                      CCTCA  _
GAM962  CLCN6   3'  GGCTGCACTCCGAGCAGTGTT  41405        TG___   A
                                AACACTGTTC    GCA GCT
                                ||||||||||    ||| |||
                                TTGTGACGAG    CGT CGG
                                      CCTCA  _
GAM962  CLCN6   3'  GGCTGCACTCCGAGCAGTGTT  7083         TG___   A
                                AACACTGTTC    GCA GCT
                                ||||||||||    ||| |||
                                TTGTGACGAG    CGT CGG
                                      CCTCA  _
GAM962  CREM    3'  CCAGTTTGGATTAGTGTT    8540       T  TGG
                                AACACTG TC   CAAGCTGG
                                ||||||| ||   ||||||||
                                TTGTGAT AG   GTTTGACC
                                   T  ____
GAM962  CSNK1E  3'  GAGCCCCCATTGGACCAGTGTT 8552       T  TG CAAGCT
                                AACACTG TC  G     GGTTT
                                ||||||| ||  |     |||||
                                TTGTGAC AG  T     CCGAG
                                    C  GT ACCC__
GAM962  CSPG3   3'  GGCTGGGGATGCAGTGTT    15233       _  GGCA
                                AACACTGT TCT    AGCT
                                |||||||| |||    ||||
                                TTGTGACG AGG    TCGG
                                     T   GG__
GAM962  CSRP1   3'  GGACCCCAAAGTCAGGATGTTG 14533     CT      AAGCT
          TT                     AACA  GTTCTGGC    GGTTT
                                ||||  ||||||||    |||||
                                TTGT  TAGGACTG    CCAGG
                                  TG       AAACC
GAM962  CTSB    3'  AAATCAGAGGAGAGACGGTGTT 64724       _  GGCAAG
                                AACACTGT TCT     CTGGTTT
                                |||||||| |||     |||||||
                                TTGTGGCA AGA     GACTAAA
                                     G   GGA___
GAM962  CUL3    3'  AGTCCAGGACAGTGTT      13159          CAA
                                AACACTGTTCTGG   GCT
                                ||||||||||||   |||
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                                TTGTGACAGGACC  TGA
                                    ___
GAM962  CUL3    3'  GGATTGTATAGGGTGGTGTT  13163     TG   _  G
                                AACAC  TTCTG GCAA CT
                                |||||  ||||| |||| ||
                                TTGTG  GGGAT TGTT GG
                                   GT    A   A
GAM962  CYP8B1  3'  AGGTTCTAGAACAGTGT    15256         C  G
                                ACACTGTTCTGG AA CT
                                |||||||||||| || ||
                                TGTGACAAGATC TT GA
                                      _ G
GAM962  DAAM2   3'  GATCAGCTCTGGTAGG     92288     G  _
                                TCTG CA AGCTGGTT
                                |||| || ||||||||
                                GGAT GT TCGACTAG
                                  G  C
GAM962  DDX11   3'  CGGTACGGAGCAGTGTT    47652         GCAA
                                AACACTGTTCTG   GCTG
                                ||||||||||||   ||||
                                TTGTGACGAGGC   TGGC
                                      A___
GAM962  DGUOK   3'  GAGCTGGTTTGTTAATTATTGT 55157    C  TTC     TG
          T                      AACA TG   TGGCAAGC  GTTT
                                |||| ||   ||||||||  ||||
                                TTGT AT   ATTGTTTG  CGAG
                                  T  TA_      GT
GAM962  DGUOK   3'  GAGCTGGTTTGTTAATTATTGT 55158    C  TTC     TG
          T                      AACA TG   TGGCAAGC  GTTT
                                |||| ||   ||||||||  ||||
                                TTGT AT   ATTGTTTG  CGAG
                                  T  TA_      GT
GAM962  DGUOK   3'  GAGCTGGTTTGTTAATTATTGT 55159    C  TTC     TG
          T                      AACA TG   TGGCAAGC  GTTT
                                |||| ||   ||||||||  ||||
                                TTGT AT   ATTGTTTG  CGAG
                                  T  TA_      GT
GAM962  DGUOK   3'  GAGCTGGTTTGTTAATTATTGT 8633     C  TTC     TG
          T                      AACA TG   TGGCAAGC  GTTT
                                |||| ||   ||||||||  ||||
                                TTGT AT   ATTGTTTG  CGAG
                                  T  TA_      GT
GAM962  DGUOK   3'  GAGCTGGTTTGTTAATTATTGT 55160    C  TTC     TG
          T                      AACA TG   TGGCAAGC  GTTT
                                |||| ||   ||||||||  ||||
                                TTGT AT   ATTGTTTG  CGAG
                                  T  TA_      GT
GAM962  DIAPH2  5'  GAGTCAGCGCGGGGCAGTGT  23601        G AA   GT
                                ACACTGTTCTG C  GCTG  TT
                                |||||||||| |  ||||  ||
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                                TGTGACGGGGC G  CGAC  AG
                                      _ __   TG
GAM962  DIAPH2   5'  GAGTCAGCGCGGGGCAGTGT  22068        G AA   GT
                                ACACTGTTCTG C  GCTG  TT
                                |||||||||||  |  ||||  ||
                                TGTGACGGGGC G  CGAC  AG
                                      _ __   TG
GAM962  DMRT1    3'  AGTTCCTGAGTGGTGTT    41696      TG   T  CA
                                AACAC  TTC GG  AGCT
                                |||||  ||| ||  ||||
                                TTGTG  GAG CC  TTGA
                                   GT   T  __
GAM962  DYRK3    5'  AGTTGGGGGATGGTGT     13122         GGCA
                                ACACTGTTCT    AGCT
                                ||||||||||    ||||
                                TGTGGTAGGG    TTGA
                                     GG__
GAM962  E2F3     3'  AGCTGTCAAACAGTGTT     8698          C     A
                                AACACTGTT TGGCA GCT
                                |||||||||  ||||| |||
                                TTGTGACAA ACTGT CGA
                                      _     _
GAM962  EFEMP1   3'  AAGTCAGCCAAAGAATATTGTT 14638      C     GGCAA    GT
                                AACA TGTTCT    GCTG  TT
                                ||||  ||||||    ||||  ||
                                TTGT ATAAGA    CGAC  AA
                                  T     AAC__    TG
GAM962  EFEMP1   3'  AAGTCAGCCAAAGAATATTGTT 38153      C     GGCAA    GT
                                AACA TGTTCT    GCTG  TT
                                ||||  ||||||    ||||  ||
                                TTGT ATAAGA    CGAC  AA
                                  T     AAC__    TG
GAM962  EGR1     3'  AGCATGTGTCAGAGTGTT    8738       TGT      A__
                                AACAC   TCTGGCA   GCT
                                |||||   |||||||   |||
                                TTGTG   AGACTGT   CGA
                                   ___      GTA
GAM962  EIF2C1   3'  GGCTGGTGGGACAGT      24179         G  A
                                ACTGTTCTG CA GCT
                                |||||||||  || |||
                                TGACAGGGT GT CGG
                                     G  _
GAM962  EMD      3'  GGGCCTAGCCCAGAGTAGTG  3682           CAA  _
                                CACTGTTCTGG   GCT GGTTT
                                ||||||||||   ||| |||||
                                GTGATGAGACC   CGA CCGGG
                                      ___  T
GAM962  EPHB3    3'  AAGCCAGCTTGCACCTCCAGT  15453      TTCTG
                                ACTG    GCAAGCTGGTTT
                                ||||    ||||||||||||
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                                TGAC    CGTTCGACCGAA
                                  CTCCA
GAM962  ESR1    5' AGTTGTGCCTGGAGTGATGTT 3698      C GT  _   _
                                AACA T  TCT GGCA AGCT
                                |||| |  ||| |||| ||||
                                TTGT G  AGG CCGT TTGA
                                  A TG   T   G
GAM962  EXO1    5' TAGGGGCGTCGGAGCGGGTT  55231     A       AA  GGTTT
                                AAC CTGTTCTGGC  GCT
                                ||| ||||||||||  |||
                                TTG GGCGAGGCTG  CGG
                                  _       __  GGATT
GAM962  EZH1    3' GATTGGCCTGGGAGTGTT    8821       GT  TG CAA  TG
                                AACACT  TC  G   GC  GTT
                                ||||||  ||  |   ||  |||
                                TTGTGA  GG  C   CG  TAG
                                   __  GT ___  GT
GAM962  EZH1    3' GGTGAGTTAGAATATGTT    8824      C       AA
                                AACA TGTTCTGGC  GCT
                                |||| |||||||||  |||
                                TTGT ATAAGATTG  TGG
                                  _       AG
GAM962  FBXL5   3' AATTGGCTTCTGAGTGTT    53200      GTTC  C   TG
                                AACACT   TGG AAGC  GTT
                                ||||||   ||| ||||  |||
                                TTGTGA   GTC TTCG  TAA
                                   ____  _   GT
GAM962  FBXL5   3' AATTGGCTTCTGAGTGTT    24075      GTTC  C   TG
                                AACACT   TGG AAGC  GTT
                                ||||||   ||| ||||  |||
                                TTGTGA   GTC TTCG  TAA
                                   ____  _   GT
GAM962  FCMD    3' AGTCAGCTAGGATGCTGTT   22088     CT      AA
                                AACA  GTTCTGGC  GCT
                                ||||  ||||||||  |||
                                TTGT  TAGGATCG  TGA
                                  CG       AC
GAM962  FGFR1   3' AGGCCAGGTTGGGGGCAGTGTT 5201          GG  G
                                AACACTGTTCT  CAA CTGGTTT
                                ||||||||||  ||| |||||||
                                TTGTGACGGGG  GTT GACCGGA
                                      __  G
GAM962  FGFR1   3' AGGCCAGGTTGGGGGCAGTGTT 43627         GG  G
                                AACACTGTTCT  CAA CTGGTTT
                                ||||||||||  ||| |||||||
                                TTGTGACGGGG  GTT GACCGGA
                                      __  G
GAM962  FGFR1   3' AGGCCAGGTTGGGGGCAGTGTT 31794         GG  G
                                AACACTGTTCT  CAA CTGGTTT
                                ||||||||||  ||| |||||||
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                                TTGTGACGGGG  GTT GACCGGA
                                      __   G
GAM962   FOLR1    5'  GGCTGGGGTCGGGACAGGTT   33613     A        A__
                                AAC CTGTTCTGGC   AGCT
                                ||| ||||||||||   ||||
                                TTG GACAGGGCTG   TCGG
                                  _        GGG
GAM962   FOXI1    3'  GGATCAGTGAGAGGAGTGGTGT 24109      TG    GGCAA
                                ACAC  TTCT    GCTGGTTT
                                ||||  ||||    ||||||||
                                TGTG  GAGG    TGACTAGG
                                  GT    AGAG_
GAM962   FRG1     5'  GGCTGTCAGGGAGTGTT     15579       G       A
                                AACACT TTCTGGCA GCT
                                |||||| |||||||| |||
                                TTGTGA GGGACTGT CGG
                                  _       _
GAM962   FUT5     3'  AGGCTGGTTTGCTTGTGGT    8964     TG TCT      TG
                                AC  T   GGCAAGC  GTTT
                                ||  |   |||||||  ||||
                                TG  G   TCGTTTG  CGGA
                                 GT T__       GT
GAM962   FZD4     3'  AGTTCTGGAGCTAGTGTT    24126       _    TG CA
                                AACACT GTTC  G  AGCT
                                |||||| ||||  |  ||||
                                TTGTGA CGAG  C  TTGA
                                   T    GT __
GAM962   GCNT3    3'  CTTGCTGGGACAGTGT      16457         TG
                                ACACTGTTC  GCAAG
                                |||||||||  |||||
                                TGTGACAGG  CGTTC
                                     GT
GAM962   GDF8     3'  GGCAGTCAAATGGTGTT     17926         C    AA
                                AACACTGTT TGGC  GCT
                                ||||||||| ||||  |||
                                TTGTGGTAA ACTG  CGG
                                     _    A_
GAM962   GJA5     3'  GGACCATTCCTCGGAGTAGTG  17942          CA  C
                                CACTGTTCTGG  AG TGGTTT
                                ||||||||||  || ||||||
                                GTGATGAGGCT  TT ACCAGG
                                      CC  _
GAM962   GNRH1     5'  GGACTAACTACTTTGAACAGTG 5884          TGGCA  C
           TT                    AACACTGTTC    AG TGGTTT
                                ||||||||||    || ||||||
                                TTGTGACAAG    TC ATCAGG
                                      TTTCA  A
GAM962   HEPH     5'  GGCTTCCTGGGGCCAGTGTT   28965        _   TG C
                                AACACTG TTC  G AAGCT
                                ||||||| |||  | |||||
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```
                                TTGTGAC GGG  C TTCGG
                                   C   GT C
GAM962  HK1     5'  GAACTGTTCCCCAGAGCATTGT 53123     C      CA   T
             T                   AACA TGTTCTGG  AGC GGTTT
                                 |||| ||||||||  ||| |||||
                                 TTGT ACGAGACC  TTG TCAAG
                                   T       CC   _
GAM962  HK1     5'  GAACTGTTCCCCAGAGCATTGT 53127     C      CA   T
             T                   AACA TGTTCTGG  AGC GGTTT
                                 |||| ||||||||  ||| |||||
                                 TTGT ACGAGACC  TTG TCAAG
                                   T       CC   _
GAM962  HK1     5'  GAACTGTTCCCCAGAGCATTGT 53132     C      CA   T
             T                   AACA TGTTCTGG  AGC GGTTT
                                 |||| ||||||||  ||| |||||
                                 TTGT ACGAGACC  TTG TCAAG
                                   T       CC   _
GAM962  HOXD3   3'  GAACTAGTTGAGAGAGTAGT   22575        GG   G
                                 ACTGTTCT  CAA CTGGTTT
                                 ||||||||  ||| |||||||
                                 TGATGAGA  GTT GATCAAG
                                     GA   _
GAM962  HSPA4   3'  GACTGCTTTTTGGGGCAGTGTT 89170         TG C    T
                                 AACACTGTTC  G AAGC GGTT
                                 ||||||||||  | |||| ||||
                                 TTGTGACGGG  T TTCG TCAG
                                     GT T    _
GAM962  HTR4    3'  TAAGCTGTGAGATCTTGAATAG 6030     _______  G   A   GGTTT
             TGTT                  TGT     TCT GCA GCT
                                 |||     ||| ||| |||
                                 ATA     AGA TGT CGA
                                   AGTTCT   G   _   A   TT
GAM962  HUNK    3'  GAGCTGGTCTGGAGCAGAGTT  27452     A     TG CAA  TG
                                 AAC CTGTTC  G   GC  GTTT
                                 ||| ||||||  |   ||  ||||
                                 TTG GACGAG  C   TG  CGAG
                                   A     GT ___  GT
GAM962  IHH     3'  GAGCTGGCGAGGGGATGGTTGT 72112      _      GGCAA  TG
             T                   AACA CTGTTCT     GC  GTTT
                                 |||| |||||||     ||  ||||
                                 TTGT GGTAGGG     CG  CGAG
                                   T      GAG__  GT
GAM962  IL12B   3'  AGACTTCCTGGAGATGGTGTT  9320         _  TG C   _
                                 AACACTGT TC  G AAG CT
                                 |||||||| ||  | ||| ||
                                 TTGTGGTA AG  C TTC GA
                                     G  GT C   A
GAM962  IRAK4   3'  GGCTGTTGCAGGACAGTG    61199          G  __
                                 CACTGTTCTG CA  AGCT
                                 |||||||||| ||  ||||
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                                GTGACAGGAC GT  TCGG
                                      _ TG
GAM962  ITCH     3'  TCTCACTTGGGAGTAGTGTT  48949          GG   C  TTT
                                AACACTGTTCT  CAAG TGG
                                ||||||||||  |||| |||
                                TTGTGATGAGG  GTTC ACT
                                     __   _  CTG
GAM962  ITGA6    3'  CAGGTTATAACAGTGTT     3984          C   AAG
                                AACACTGTT TGGC   CTG
                                |||||||| ||||   |||
                                TTGTGACAA ATTG   GAC
                                     T   ___
GAM962  ITIH2    3'  GAACCAGATATCAGGGTGGT  9413     TG     CAAG
                                AC  TTCTGG   CTGGTTT
                                ||  ||||||   |||||||
                                TG  GGGACT   GACCAAG
                                 GT     ATA_
GAM962  ITM2A    5'  AGACCTCGGCTTGCAGTAGTGT 16819        TT   G    __
              T                  AACACTG  CTG CAAGCT  GGTTT
                                |||||||  ||| ||||||  |||||
                                TTGTGAT  GAC GTTCGG  CCAGA
                                   __  _     CT
GAM962  ITPKB    3'  AGCCAGCTTGGCTGTGTT    9418       T  TCTGG
                                AACAC GT    CAAGCTGGTT
                                ||||| ||    ||||||||||
                                TTGTG CG    GTTCGACCGA
                                   T _____
GAM962  IVD      3'  GGATTGTTGGGACAGGTT    9464      A     TG   G
                                AAC CTGTTC  GCAA CT
                                ||| ||||||  |||| ||
                                TTG GACAGG  TGTT GG
                                  _     GT   A
GAM962  JUP      3'  GGTCTTTCTTGGGATAGTGTT  9489          TG C_  _
                                AACACTGTTC  G  AAG CT
                                ||||||||||  |  ||| ||
                                TTGTGATAGG  T  TTC GG
                                      GT CT   T
GAM962  KCNA7    3'  AGTTTCCTAGGTCAGTGTT   49048       TT   C
                                AACACTG  CTGG AAGCT
                                |||||||  |||| |||||
                                TTGTGAC  GATC TTTGA
                                    TG   C
GAM962  KCNJ15   3'  AGCTGTGCTCTGGACAGTGTT  9541          T_   _
                                AACACTGTTC  GGCA AGCT
                                ||||||||||  |||| ||||
                                TTGTGACAGG  TCGT TCGA
                                      TC   G
GAM962  KCNMB3   5'  AAACCCTGTTCAGGACGCTGTT 26960      C       CAA  T_
                                AACA TGTTCTGG   GC  GGTTT
                                |||| ||||||||   ||  |||||
```

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                                TTGT GCAGGACT   TG  CCAAA
                                  C       ___  TC
GAM962  KCNMB3   5'  TTTGCTGGAGCAGGTT     26962     A     TG
                                AAC CTGTTC  GCAAG
                                ||| ||||||  |||||
                                TTG GACGAG  CGTTT
                                  _     GT
GAM962  KCNN4    3'  GGGCCCTGGCTTGGAGTGGGTT 9569      A TG   TGG     __
                                AAC C  TTC   CAAGCT  GGTTT
                                ||| |  |||   ||||||  |||||
                                TTG G  GAG   GTTCGG  CCGGG
                                  _ GT   ___      TC
GAM962  KIFC3    3'  GAACCATGGGGACTGGGGTGGG 18687     A TG   TG CAAGC_
             TT                   AAC C  TTC  G     TGGTTT
                                ||| |  |||  |     ||||||
                                TTG G  GGG  C     ACCAAG
                                  _ GT   GT AGGGGT
GAM962  KPNB2    5'  GGCTCTGGGATGGTGT      9630          TG CA
                                ACACTGTTC  G  AGCT
                                |||||||||  |  ||||
                                TGTGGTAGG  C  TCGG
                                     GT __
GAM962  LAMC2    3'  AAGCTGGAAGAAGTGAGCAGTG 18709          TGGCAAG TG
             TT                   AACACTGTTC      C  GTTT
                                ||||||||||      |  ||||
                                TTGTGACGAG      G  CGAA
                                     TGAAGAA GT
GAM962  LAMC2    3'  GGCTGGTGGGACAGTG      18713          G  A
                                CACTGTTCTG CA GCT
                                |||||||||| || |||
                                GTGACAGGGT GT CGG
                                     G  _
GAM962  LAPTM5   3'  AGTCATTTAGAATAGTG     22200          CAA
                                CACTGTTCTGG   GCT
                                ||||||||||   |||
                                GTGATAAGATT   TGA
                                      TAC
GAM962  LEP      3'  AAGCCATTTGTTGGGGCAGTG  4044         TG    C
                                CACTGTTC  GCAAG TGGTTT
                                |||||||  ||||| ||||||
                                GTGACGGG  TGTTT ACCGAA
                                     GT    _
GAM962  LHX4     3'  AGACCACACTAGGGCATTGTT  52908      C       CAAGC
                                AACA TGTTCTGG    TGGTTT
                                |||| ||||||||    ||||||
                                TTGT ACGGGATC    ACCAGA
                                  T       AC___
GAM962  LIF      3'  TTGGGGCAGCTGCTCAGAGCAG 9742           _  A   G
             TGTT                   ACACTGTTCTG GCA GCTG TTT
                                |||||||||| ||| |||| |||
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                                TGTGACGAGAC CGT CGAC GGG
                                      T  _   G  TTG
GAM962  LIG3    3'  AAGTCAGTTTGTCTTGCTGGTT 25665    ACT  TCT      GT
                                AAC  GT  GGCAAGCTG  TT
                                |||  ||  |||||||||  ||
                                TTG  CG  CTGTTTGAC  AA
                                  GT_  TT_      TG
GAM962  LRRC2   3'  GGCTGGCTTCTACATGTT   44476    C  TCT  A
                                AACA TGT  GGC AGCT
                                |||| |||  ||| ||||
                                TTGT ACA  TCG TCGG
                                  _  TCT  G
GAM962  MAD2L2  3'  TCCCCGCCTAGGGCAGTG   20949        CAA  T  TTT
                                CACTGTTCTGG  GC GG
                                ||||||||||  || ||
                                GTGACGGGATC  CG CC
                                      ___  C  CTA
GAM962  MAFF    3'  GAGCCGGCTTAGAGAACAGCTG 24648    _    GGC
          TT                    AACA CTGTTCT  AAGCTGGTTT
                                |||| |||||||  ||||||||||
                                TTGT GACAAGA  TTCGGCCGAG
                                  C     GA_
GAM962  MAL     3'  GAGCTGAAAACCCAGATGGTGT 42360      T  CA____  GGTTT
          T                     CACTGT CTGG    AGCT
                                ||||||  ||||    ||||
                                GTGGTA GACC    TCGA
                                   _  CAAAAG  G  T
GAM962  MAL     3'  GAGCTGAAAACCCAGATGGTGT 42362      T  CA____  GGTTT
          T                     CACTGT CTGG    AGCT
                                ||||||  ||||    ||||
                                GTGGTA GACC    TCGA
                                   _  CAAAAG  G  T
GAM962  MAL     3'  GAGCTGAAAACCCAGATGGTGT 42364      T  CA____  GGTTT
          T                     CACTGT CTGG    AGCT
                                ||||||  ||||    ||||
                                GTGGTA GACC    TCGA
                                   _  CAAAAG  G  T
GAM962  MAL     3'  GAGCTGAAAACCCAGATGGTGT 9891       T  CA____  GGTTT
          T                     CACTGT CTGG    AGCT
                                ||||||  ||||    ||||
                                GTGGTA GACC    TCGA
                                   _  CAAAAG  G  T
GAM962  MANBA   3'  GAATCTGTGCCAGGACTGTGTT 19772     T      AGCT
                                AACAC GTTCTGGCA   GGTTT
                                |||||  |||||||||   |||||
                                TTGTG CAGGACCGT   CTAAG
                                  T       GT__
GAM962  MAOB    3'  AATTGGCTTGTTTAAGGTT   59998    A  GTTCT    TG
                                AAC CT    GGCAAGC  GTT
                                |||  ||    |||||||  |||
```

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                                TTG GA    TTGTTCG  TAA
                                  _ AT___      GT
GAM962  MAP3K4   3'  GAACCGTGACATCAGCGTAGTG 22047       TT   CAA_ T
           TT                    AACACTG  CTGG   GC GGTTT
                                 ||||||| ||||   || |||||
                                 TTGTGAT  GACT   TG CCAAG
                                    GC   ACAG  _
GAM962  MAP3K4   3'  GAACCGTGACATCAGCGTAGTG 19799       TT   CAA_ T
           TT                    AACACTG  CTGG   GC GGTTT
                                 ||||||| ||||   || |||||
                                 TTGTGAT  GACT   TG CCAAG
                                    GC   ACAG  _
GAM962  MAT2A    3'  AGCTCTTTGTCAGGGAGTGTT  19784       G      ___
                                 AACACT TTCTGGCA   AGCT
                                 |||||| ||||||||   ||||
                                 TTGTGA GGGACTGT   TCGA
                                    _      TTC
GAM962  MEIS2    3'  CTCCAGCTTCAGAATGTGTT   39320      T     CA     TTT
                                 AACAC GTTCTGG  AGCTGG
                                 ||||| |||||||  ||||||
                                 TTGTG TAAGACT  TCGACC
                                    _     __     TCA
GAM962  MEST     3'  AATTGGTGAACAGTGT      69897        TGGCAA  TG
                                 ACACTGTTC     GC  GTT
                                 |||||||||     ||  |||
                                 TGTGACAAG     TG  TAA
                                       _______  GT
GAM962  MTMR8    3'  AAACCATCATCTAGAATAGAGT 31285     A       CAAGC
           T                     AAC CTGTTCTGG    TGGTTT
                                 ||| |||||||||    ||||||
                                 TTG GATAAGATC    ACCAAA
                                   A       TACT_
GAM962  MXI1     3'  AAACTCAGCCTGGGACAGT   55257       TG CAA   _
                                 ACTGTTC  G   GCTG GTTT
                                 |||||||  |   |||| ||||
                                 TGACAGG  C   CGAC CAAA
                                    GT ___    T
GAM962  MXI1     3'  AAACTCAGCCTGGGACAGT   19896       TG CAA   _
                                 ACTGTTC  G   GCTG GTTT
                                 |||||||  |   |||| ||||
                                 TGACAGG  C   CGAC CAAA
                                    GT ___    T
GAM962  NELL1    3'  AAGTTTCCACCTGAGGACGGTG 20474        _____ C    GGTTT
           TT                    ACTGTTCT    GG AAGCT
                                 ||||||||    || |||||
                                 TGGCAGGA    CC TTTGA
                                    GTCCA  _    A  T
GAM962  NOLA1    5'  GGCTGTTTTGGAACCAGTGTT  38607       _   TG CA_
                                 AACACTG TTC  G   AGCT
                                 ||||||| |||  |   ||||
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                                TTGTGAC AAG  T   TCGG
                                    C   GT TTG
GAM962  NOTCH3   3'  GGGCCAGGGGTCGGGGGAGTGT 4748       G      AAG
           T                     AACACT TTCTGGC   CTGGTTT
                                 |||||| |||||||   |||||||
                                 TTGTGA GGGGCTG   GACCGGG
                                    G      GG_
GAM962  NPTX1    3'  AGCACTGTTGAGGCAGTGTT   10257        TC    A_
                                 AACACTGT  TGGCA  GCT
                                 ||||||||  |||||  |||
                                 TTGTGACG  GTTGT  CGA
                                     GA    CA
GAM962  NPTX2    3'  AGACCAGGGCTGGGGCAGTGT  92482         TG  AAG
                                 ACACTGTTC  GC   CTGGTTT
                                 |||||||||  ||   |||||||
                                 TGTGACGGG  CG   GACCAGA
                                      GT  G__
GAM962  OCRL     3'  AGACTGAGAGCAGAACAGGTT  4256      A      GCAAG  _
                                 AAC CTGTTCTG    CT GGTTT
                                 ||| ||||||||    || |||||
                                 TTG GACAAGAC    GA TCAGA
                                   _       GA___  G
GAM962  OCRL     3'  AGACTGAGAGCAGAACAGGTT  7822      A      GCAAG  _
                                 AAC CTGTTCTG    CT GGTTT
                                 ||| ||||||||    || |||||
                                 TTG GACAAGAC    GA TCAGA
                                   _       GA___  G
GAM962  OGG1     5'  GGGCTCTGGGGCCGGAGCTGTG 10331     T      A____    GGTTT
           TT                     CAC GTTCTGGC     AGCT
                                  ||| ||||||||     ||||
                                  GTG CGAGGCCG     TCGG
                                    T       GGGTC    G   T
GAM962  OGG1     5'  GGGCTCTGGGGCCGGAGCTGTG 33661     T      A____    GGTTT
           TT                     CAC GTTCTGGC     AGCT
                                  ||| ||||||||     ||||
                                  GTG CGAGGCCG     TCGG
                                    T       GGGTC    G   T
GAM962  OGG1     5'  GGGCTCTGGGGCCGGAGCTGTG 33667     T      A____    GGTTT
           TT                     CAC GTTCTGGC     AGCT
                                  ||| ||||||||     ||||
                                  GTG CGAGGCCG     TCGG
                                    T       GGGTC    G   T
GAM962  OSR1     3'  ACACCATGTCCCAGGACAGTGT 17563          CAA  _   TT
           T                      AACACTGTTCTGG   GC TGGT
                                  ||||||||||||||  || ||||
                                  TTGTGACAGGACC   TG ACCA
                                         C__  T   CAG
GAM962  OXTR     3'  GGACCAGCTTGTCAGAGGGT   6212      G
                                 ACT TTCTGGCAAGCTGGTTT
                                 ||| ||||||||||||||||
```

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                                TGG GAGACTGTTCGACCAGG
                                  _
GAM962  PCDH11Y  5' AGATCACATACCAGAGCGGT  52059        CAAGC
                                ACTGTTCTGG    TGGTTT
                                ||||||||||    ||||||
                                TGGCGAGACC    ACTAGA
                                     ATAC_
GAM962  PDCL     3' AGTAGCTGGGCACGGTGTT   18209       _ TG  AA
                                AACACTGT TC  GC  GCT
                                |||||||| ||  ||  |||
                                TTGTGGCA GG  CG  TGA
                                    C  GT  A_
GAM962  PDGFRB   3' GGCCTAGCCTTGAGCAGTGTT 65978        T_  AA_
                                AACACTGTTC  GGC   GCT
                                ||||||||||  |||   |||
                                TTGTGACGAG  CCG   CGG
                                     TT   ATC
GAM962  PDHA1    3' GGCTACCAGACAGTGTT    4295        T   CA
                                AACACTGT CTGG  AGCT
                                |||||||| ||||  ||||
                                TTGTGACA GACC  TCGG
                                    _   A_
GAM962  PDX1     3' AAGCCATATGTTTAGGGTGGT 12975    TG    _ AGC
                                AC  TTCTGG CA   TGGTTT
                                ||  ||||||  ||   ||||||
                                TG  GGGATT GT   ACCGAA
                                 GT     T  AT_
GAM962  PHYH     3' GAGTTAGTTTTGCAGCACAATG 20609      C __    _ GG
           GTGTT                 ACTGTT TG  GCAAG CT  TTT
                                ||||||  ||  |||||  ||  |||
                                TGGTAA AC  CGTTT GA  GAG
                                   C  GA    T  TT
GAM962  PIGA     3' GGCTTTACTTCAGAATGGT   10554        C___
                                ACTGTTCTGG   AAGCT
                                ||||||||||   |||||
                                TGGTAAGACT   TTCGG
                                     TCAT
GAM962  PIGA     3' GGCTTTACTTCAGAATGGT   40006        C___
                                ACTGTTCTGG   AAGCT
                                ||||||||||   |||||
                                TGGTAAGACT   TTCGG
                                     TCAT
GAM962  PIGA     3' GGCTTTACTTCAGAATGGT   40015        C___
                                ACTGTTCTGG   AAGCT
                                ||||||||||   |||||
                                TGGTAAGACT   TTCGG
                                     TCAT
GAM962  PIK3R3   3' AAGCTTTCATCACAGAACAGTG 61046        GC____   GGTTT
           TT                    CACTGTTCTG    AAGCT
                                ||||||||||    |||||
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```
                                GTGACAAGAC     TTCGA
                                     ACTACT    A  T
GAM962  PIK3R3   3'  AGTTGGTGCTTGTATGGTGTT  61050       TCT   __
                                AACACTGT   GGCA  AGCT
                                ||||||||   ||||  ||||
                                TTGTGGTA   TCGT  TTGA
                                    TGT    GG
GAM962  PIN1L    3'  GATGAGCGGGACAGTGTT    20622        GGCAA   G
                                AACACTGTTCT    GCT GTT
                                ||||||||||     ||| |||
                                TTGTGACAGGG    CGA TAG
                                      _____    G
GAM962  PLA2G2D  3'  AGCCCTCAGAGGTGGTGTT   24784      TG _    CAA
                                AACAC  T TCTGG   GCT
                                |||||  | |||||   |||
                                TTGTG  G AGACT   CGA
                                   GT G    CC_
GAM962  PLAB     5'  TCCCAGGCTGGAATGGTGT   65856       TG  AAG    TTT
                                ACACTGTTC  GC   CTGG
                                |||||||||  ||   ||||
                                TGTGGTAAG  CG   GACC
                                     GT  ___    CTC
GAM962  PMM2     3'  GGCTGTGAGTGGGGCAGTGT   72092         G_  _
                                ACACTGTTCTG  CA AGCT
                                ||||||||||  || ||||
                                TGTGACGGGGT  GT TCGG
                                      GA  G
GAM962  PPP1R12A 3'  GGCTACTCCATGATAGTGTT   10179        C   CA_
                                AACACTGTT TGG   AGCT
                                |||||||||  |||   ||||
                                TTGTGATAG ACC   TCGG
                                     T   TCA
GAM962  PPP3CC   5'  AGGTCGGTGCCGAAGCGGTGTT 18815        C    AA    GT
                                AACACTGTT TGGC  GCTG  TT
                                |||||||||  ||||  ||||  ||
                                TTGTGGCGA GCCG  TGGC  GA
                                     A    __    TG
GAM962  PPP5C    3'  AGGCCCCGCCCCAGGGCAATGT 20731     C       CAA  T_
           T                     AACA TGTTCTGG   GC  GGTTT
                                ||||  ||||||||   ||  |||||
                                TTGT ACGGGACC   CG  CCGGA
                                  A       C__   CC
GAM962  PPT2     3'  GGGCCTGGGTCAGAGCGGTG   57231          AAGCT
                                CACTGTTCTGGC    GGTTT
                                ||||||||||||    |||||
                                GTGGCGAGACTG    CCGGG
                                       GGT__
GAM962  PRDM16   3'  GGATTGGTCTTGAGAACACTGT 42086     C     GG   _ TG
           T                     AACA TGTTCT  CAAG C  GTTT
                                ||||  ||||||  ||||  |  ||||
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                                TTGT ACAAGA  GTTC G  TAGG
                                  C     __   T GT
GAM962  PRKCB1   3'  GACTAGAGTGACAGTGTT    70513        TCTGG  AG
                                AACACTGT    CA  CTGGTT
                                ||||||||    ||  ||||||
                                TTGTGACA    GT  GATCAG
                                    _____  GA
GAM962  PRKCQ    3'  GGCCAGCCCTGGATAGGTT   20743     A     T  CAA
                                AAC CTGTTC GG   GCTGGTT
                                ||| |||||| ||   |||||||
                                TTG GATAGG CC   CGACCGG
                                  _     T ___
GAM962  PROK1    3'  GGATCAGCCCTGAGAGCAGGTT 50555     A      __ CAA
                                AAC CTGTTCT  GG   GCTGGTTT
                                ||| |||||||  ||   ||||||||
                                TTG GACGAGA  CC   CGACTAGG
                                  _      GT  ___
GAM962  PTP4A2   3'  AGCTAAGATAGATGGTGTT   12981        T  GCA_
                                AACACTGT CTG    AGCT
                                |||||||| |||    ||||
                                TTGTGGTA GAT    TCGA
                                    _  AGAA
GAM962  PTPRC    3'  AGATAGTTTTGCCAGAACAGT  11099           _  GTTT
                                ACTGTTCTGGCAAG CTG
                                |||||||||||||| |||
                                TGACAAGACCGTTT GAT
                                       T  AGA
GAM962  PTPRC    3'  AGATAGTTTTGCCAGAACAGT  55164           _  GTTT
                                ACTGTTCTGGCAAG CTG
                                |||||||||||||| |||
                                TGACAAGACCGTTT GAT
                                       T  AGA
GAM962  PXN      3'  AACTGGTTGAAGAGTGTT    11157      G  TGGCA  TG
                                AACACT TTC    AGC  GTT
                                |||||| |||    |||  |||
                                TTGTGA AAG    TTG  CAA
                                   G  _____  GT
GAM962  PYGB     3'  GGGCCATGGGGGTCAGGGTGGT 11176    TG     AAGC_
                                AC  TTCTGGC    TGGTTT
                                ||  |||||||    ||||||
                                TG  GGGACTG    ACCGGG
                                 GT      GGGGT
GAM962  RAB36    3'  GGCCTCCAGGATATGTT     16968     C      CAA
                                AACA TGTTCTGG   GCT
                                ||||  ||||||||  |||
                                TTGT ATAGGACC   CGG
                                  _      TC_
GAM962  RAB7L1   3'  AAATTATCTCTAGGATGGTG  14100         CA  C
                                CACTGTTCTGG  AG TGGTTT
                                ||||||||||  || ||||||
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                                GTGGTAGGATC  TC ATTAAA
                                      __ T
GAM962  RAD52   3' AAATTGGCTTTTCATAGTG   11238     TTC  C   TG
                                CACTG  TGG AAGC  GTTT
                                |||||  ||| ||||  ||||
                                GTGAT  ACT TTCG  TAAA
                                   ___  T   GT
GAM962  RAD52   3' AAATTGGCTTTTCATAGTG   56192     TTC  C   TG
                                CACTG  TGG AAGC  GTTT
                                |||||  ||| ||||  ||||
                                GTGAT  ACT TTCG  TAAA
                                   ___  T   GT
GAM962  RAD52   3' AAATTGGCTTTTCATAGTG   56200     TTC  C   TG
                                CACTG  TGG AAGC  GTTT
                                |||||  ||| ||||  ||||
                                GTGAT  ACT TTCG  TAAA
                                   ___  T   GT
GAM962  RAD52   3' AAATTGGCTTTTCATAGTG   56209     TTC  C   TG
                                CACTG  TGG AAGC  GTTT
                                |||||  ||| ||||  ||||
                                GTGAT  ACT TTCG  TAAA
                                   ___  T   GT
GAM962  RAD9    5' GTCGCGGAGAGCTGGGCAGTGT 15935       T TG  AAG   GTTT
           T                    AACACTGT C  GC   CTG
                                |||||||| |  ||   |||
                                TTGTGACG G  CG   GGC
                                    _ GT  AGA   GCTGG
GAM962  RANBP17  3' GGTCTCAGGACAGTG      43180         CAA
                                CACTGTTCTGG   GCT
                                ||||||||||   |||
                                GTGACAGGACT   TGG
                                      C__
GAM962  RARA    3' GGCCCCGGGACAGAGTT     6368     A       CAA
                                AAC CTGTTCTGG   GCT
                                ||| |||||||||   |||
                                TTG GACAGGGCC   CGG
                                  A       C__
GAM962  RASGRP1  3' GAACTAGCTTGTAGTTAGTGTT 19206       TT   G
                                AACACTG  CTG CAAGCTGGTTT
                                |||||||  ||| ||||||||||
                                TTGTGAT  GAT GTTCGATCAAG
                                   T_  _
GAM962  RBBP5   5' AAGCCGGCCGGGGAGAAGGTGT 17326      GT___    AA  GGTTT
           T                    ACACT    TCTGGC  GCT
                                |||||    ||||||  |||
                                TGTGG    GGGCCG  CGA
                                  AAGAG    GC  A   T
GAM962  RCN1    3' AGCCAAACGGAGTGGAGTT   59628    A TG    GCAAGC
                                AAC C  TTCTG     TGGTT
                                ||| |  |||||     |||||
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                                TTG G  GAGGC     ACCGA
                                  A GT    AA____
GAM962  RCN1    3'  AGCCAAACGGAGCGGGGTT   11269     A      GCAAGC
                                AAC CTGTTCTG     TGGTT
                                ||| ||||||||     |||||
                                TTG GGCGAGGC     ACCGA
                                  G       AA____
GAM962  RET     3'  GCTAGCTAGCTGTGTT     40176      TGTTCT   A
                                AACAC     GGC AGCTGGT
                                |||||     ||| |||||||
                                TTGTG     TCG TCGATCG
                                  _______  A
GAM962  RET     3'  GCTAGCTAGCTGTGTT     40592      TGTTCT   A
                                AACAC     GGC AGCTGGT
                                |||||     ||| |||||||
                                TTGTG     TCG TCGATCG
                                  _______  A
GAM962  RFX2    3'  GGCTCCCGGGGTCAGTGTT   5312        _     CA
                                AACACTG TTCTGG  AGCT
                                ||||||| ||||||  ||||
                                TTGTGAC GGGGCC  TCGG
                                    T     C_
GAM962  SCAMP1   3'  AAATTGGCTTGCTTTTTAGCTG 16815     _  TTCT      TG
           TT                    AACA CTG    GGCAAGC  GTTT
                                ||||| |||   |||||||  ||||
                                TTGT GAT    TCGTTCG  TAAA
                                  C   TTT_      GT
GAM962  SEC22L1  5'  GGCCTTCCGGGCCAGTGTT   16889       TT    CAA
                                AACACTG  CTGG   GCT
                                |||||||  ||||   |||
                                TTGTGAC  GGCC   CGG
                                    CG    TTC
GAM962  SET     3'  AGGTCAGCAAAGGGGTGGGGTT 11555     A TG    GGCAA    GT
                                AAC C  TTCT    GCTG  TT
                                ||| |  ||||    ||||  ||
                                TTG G  GGGG    CGAC  GA
                                  G GT    AAA__    TG
GAM962  SH3BP2   3'  AGGTCAGGCCAGGGCAGTG    11591          AAG   GT
                                CACTGTTCTGGC   CTG  TT
                                ||||||||||||   |||  ||
                                GTGACGGGACCG   GAC  GA
                                       ___   TG
GAM962  SH3BP5   3'  GGGCTGGTTTTTCAGAGCAGAG 16743     A       C    TG
           TT                    AAC CTGTTCTGG AAGC  GTTT
                                ||| |||||||| ||||  ||||
                                TTG GACGAGACT TTTG  CGGG
                                  A        T    GT
GAM962  SH3GL1   3'  GAGCCCCTGCTGCCAGGGCGGT 11623            A  T__
           GT                    ACACTGTTCTGGCA GC   GGTTT
                                |||||||||||||| ||   |||||
```

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                                TGTGGCGGGACCGT CG   CCGAG
                                        _ TCC
GAM962  SLC14A1  5' AGCCAGCTAGAGTGGT     31834    TG   GGCA
                                AC  TTCT   AGCTGGTT
                                ||  ||||   ||||||||
                                TG  GAGA   TCGACCGA
                                 GT   ____
GAM962  SLC1A3   3' AAACTTTCAGCTGGAGTGGGGT 14795    A TG   TG  AAGCT
           T                     AAC C  TTC  GC    GGTTT
                                ||| |  |||  ||    |||||
                                TTG G  GAG  CG    TCAAA
                                  G GT   GT  ACTT_
GAM962  SLC22A1LS 5' GGGCTGCAGGGGCTGGGGTGT  23026      ___    G   A   GGTTT
                                ACACT   GTTCT GCA GCT
                                |||||   ||||| ||| |||
                                TGTGG   CGGGG CGT CGG
                                   GGT    A  _  G   T
GAM962  SLC25A13  3' AGATCAGCCCTGGGATAGTG   26500        TG CAA
                                CACTGTTC  G   GCTGGTTT
                                ||||||||  |   ||||||||
                                GTGATAGG  C   CGACTAGA
                                     GT C__
GAM962  SLC4A1AP  5' AAGCTGGTTTGTTGATTAGTG  36362      T  T     TG
                                CACTG TC GGCAAGC  GTTT
                                ||||| || |||||||  ||||
                                GTGAT AG TTGTTTG  CGAA
                                   T  _      GT
GAM962  SLC4A2   3' GGCTGGTGGGATGGGTT     11725     A      G  A
                                AAC CTGTTCTG CA GCT
                                ||| ||||||| || |||
                                TTG GGTAGGGT GT CGG
                                  _       G  _
GAM962  SLC7A6   3' GGTCACCGGGACAGTGT     14312          CAA
                                ACACTGTTCTGG   GCT
                                ||||||||||||   |||
                                TGTGACAGGGCC   TGG
                                       AC_
GAM962  SMARCC2  3' GGCTGGTGAAAGGTGTT     11806       G   TG  A
                                AACACT TTC  GC AGCT
                                ||||||  |||  ||  ||||
                                TTGTGG AAG  TG TCGG
                                   A   __  G
GAM962  SMARCC2  3' GGCTGGTGAAAGGTGTT     57409       G   TG  A
                                AACACT TTC  GC AGCT
                                ||||||  |||  ||  ||||
                                TTGTGG AAG  TG TCGG
                                   A   __  G
GAM962  SMARCD1  3' ACCTCTAGATAGTGTT      57428         T   CAAGCT
                                AACACTGT CTGG     GGT
                                ||||||||  ||||     |||
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                                TTGTGATA GATC     CCA
                                   _   T_____
GAM962  SMARCD1  3'  ACCTCTAGATAGTGTT     11810        T   CAAGCT
                                AACACTGT CTGG     GGT
                                |||||||| ||||     |||
                                TTGTGATA GATC     CCA
                                   _   T_____
GAM962  SMARCD2  3'  GGCTGGGAGGACTGGTGTT   11825      _    GG  A
                                AACACT GTTCT  CA GCT
                                |||||| |||||  || |||
                                TTGTGG CAGGA  GT CGG
                                   T    GG  _
GAM962  SMG1     3'  CCAGACTAGAATAGGGTT    30650     A       CAAG
                                AAC CTGTTCTGG    CTGG
                                ||| |||||||||    ||||
                                TTG GATAAGATC    GACC
                                  G        A___
GAM962  SORBS1   3'  GTCCTATTGCTAGAATAGGTT  31160     A         GCT  TTT
                                AAC CTGTTCTGGCAA   GG
                                ||| ||||||||||||   ||
                                TTG GATAAGATCGTT   CC
                                  _          AT_  TGA
GAM962  STAU2    3'  GAACTAGTTTGCTTGTGTGT   26905     TGTTCT
                                ACAC     GGCAAGCTGGTTT
                                ||||     |||||||||||||
                                TGTG     TCGTTTGATCAAG
                                  TGT___
GAM962  STK19    3'  AGGCTGGTGAAGGAGGGCAGGG 50593     A      GGCAA  TG
           TT                     AAC CTGTTCT     GC  GTTT
                                ||| |||||||     ||  ||||
                                TTG GACGGGA     TG  CGGA
                                  G      GGAAG  GT
GAM962  STK19    3'  AGGCTGGTGAAGGAGGGCAGGG 14836     A      GGCAA  TG
           TT                     AAC CTGTTCT     GC  GTTT
                                ||| |||||||     ||  ||||
                                TTG GACGGGA     TG  CGGA
                                  G      GGAAG  GT
GAM962  SURF4    3'  AGACTGGCTTGTCTCAGTGTT  52540       TTCT      TG
                                AACACTG    GGCAAGC  GTTT
                                |||||||    |||||||  ||||
                                TTGTGAC    CTGTTCG  CAGA
                                   T___       GT
GAM962  SURF5    3'  GGCTCTGAGCAGTGTT      56104          T  CA
                                AACACTGTTC GG  AGCT
                                |||||||||| ||  ||||
                                TTGTGACGAG TC  TCGG
                                   _  __
GAM962  SURF5    3'  GGCTCTGAGCAGTGTT      22185          T  CA
                                AACACTGTTC GG  AGCT
                                |||||||||| ||  ||||
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                                TTGTGACGAG TC  TCGG
                                      _  __
GAM962  SYNGR1   3'  GGACCAGCATGGGGGCAGGTT  16319     A      GG  A
                                AAC CTGTTCT  CA GCTGGTTT
                                ||| |||||||  || ||||||||
                                TTG GACGGGG  GT CGACCAGG
                                  _     __ A
GAM962  TARDBP   3'  AATTGGTTTGTTCAGTGT    23769       TTCT     TG
                                ACACTG   GGCAAGC  GTT
                                ||||||   |||||||  |||
                                TGTGAC   TTGTTTG  TAA
                                    ____      GT
GAM962  TCF19    3'  AACCAGCTACAGCAGT     97730     TT   GCA
                                ACTG  CTG   AGCTGGTT
                                ||||  |||   ||||||||
                                TGAC  GAC   TCGACCAA
                                  __  A__
GAM962  TCF19    3'  AACCAGCTACAGCAGT     97860     TT   GCA
                                ACTG  CTG   AGCTGGTT
                                ||||  |||   ||||||||
                                TGAC  GAC   TCGACCAA
                                  __  A__
GAM962  TEC      3'  AGCAGCCAGCATGGTGTT    12214        T    AA
                                AACACTGT CTGGC  GCT
                                |||||||| |||||  |||
                                TTGTGGTA GACCG  CGA
                                     C    A_
GAM962  TEM5     3'  AGCTGCAGGTGGTGTT     51317      TG T   G  A
                                AACAC  T CTG CA GCT
                                |||||  | ||| || |||
                                TTGTG  G GAC GT CGA
                                   GT _  _ _
GAM962  TFCP2    5'  AGATTAGTTGTGCACAGAGCAG 18952          _  _
            TG                    CACTGTTCTG GCA AGCTGGTTT
                                ||||||||||| ||| |||||||||
                                GTGACGAGAC CGT TTGATTAGA
                                     A  G
GAM962  TGM2     3'  AGCTGGGTGGGGACAGTG    16052         G  A_
                                CACTGTTCT GC  AGCT
                                |||||||| ||  ||||
                                GTGACAGGG TG  TCGA
                                     G  GG
GAM962  TIMP3    3'  TACTATTTCCAGAATAGTGTT  4518           C   C    TT
                                AACACTGTTCTGG AAG TGGT
                                |||||||||||| ||| ||||
                                TTGTGATAAGACC TTT ATCA
                                       _  _   TA
GAM962  TNFRSF14 3'  GGTTGGCTGCAGTGTGGTGTT  13785      TG T   G  A  TG TT
                                AACAC  T CTG CA GC  G  T
                                |||||  | ||| || ||  |  |
```

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                                TTGTG  G GAC GT CG  T  G
                                  GT T  _ _  GT GG
GAM962  TOP2A    3'  AGCTAAAACTAGAGCAGT    6529          CA__
                                ACTGTTCTGG   AGCT
                                ||||||||||   ||||
                                TGACGAGATC   TCGA
                                     AAAA
GAM962  TRADD    3'  GACCTGCTGGGGCAGAGTT   13698    A     TG   AGCT
                                AAC CTGTTC  GCA   GGTT
                                ||| ||||||  |||   ||||
                                TTG GACGGG  CGT   CCAG
                                  A     GT  _____
GAM962  TRPM6    3'  GAGTCAGCTGGGAATATTGTT  34541     C     GGCA    GT
                                AACA TGTTCT   AGCTG  TT
                                |||| ||||||   |||||  ||
                                TTGT ATAAGG   TCGAC  AG
                                  T     G___     TG
GAM962  TRPM7    3'  AGCTGTTTAAATAGTGTT    62126         CT    A
                                AACACTGTT  GGCA GCT
                                |||||||||  |||| |||
                                TTGTGATAA  TTGT CGA
                                     AT   _
GAM962  UBE3A    3'  GGGCCAGCCTTTAGAACACTGT 55580      C       CAA
          T                      AACA TGTTCTGG   GCTGGTTT
                                 |||| ||||||||   ||||||||
                                 TTGT ACAAGATT   CGACCGGG
                                   C       TC_
GAM962  UBE3A    3'  GGGCCAGCCTTTAGAACACTGT 55593      C       CAA
          T                      AACA TGTTCTGG   GCTGGTTT
                                 |||| ||||||||   ||||||||
                                 TTGT ACAAGATT   CGACCGGG
                                   C       TC_
GAM962  UBE3A    3'  GGGCCAGCCTTTAGAACACTGT 4868       C       CAA
          T                      AACA TGTTCTGG   GCTGGTTT
                                 |||| ||||||||   ||||||||
                                 TTGT ACAAGATT   CGACCGGG
                                   C       TC_
GAM962  UNC119   3'  GGGCCCAAGTTTCAGAATAGTG 17646           CA   __
          TT                      AACACTGTTCTGG  AGCT  GGTTT
                                  ||||||||||||  ||||  |||||
                                  TTGTGATAAGACT  TTGA  CCGGG
                                       __    AC
GAM962  UNC119   3'  GGGCCCAAGTTTCAGAATAGTG 54015           CA   __
          TT                      AACACTGTTCTGG  AGCT  GGTTT
                                  ||||||||||||  ||||  |||||
                                  TTGTGATAAGACT  TTGA  CCGGG
                                       __    AC
GAM962  USH2A    3'  AGTATGTGCCAGGACATGTT   23063      C        A__
                                AACA TGTTCTGGCA   GCT
                                |||| ||||||||||   |||
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                                TTGT ACAGGACCGT   TGA
                                  _       GTA
GAM962  VAPB     3'  AGCTGCCAGGAAGTGTT     16438       G      A
                                AACACT TTCTGGCA GCT
                                |||||| |||||||| |||
                                TTGTGA AGGACCGT CGA
                                  _      _
GAM962  WBSCR14  3'  GGCTGCAGGATGGT       51972        G  A
                                ACTGTTCTG CA GCT
                                ||||||||| || |||
                                TGGTAGGAC GT CGG
                                  _ _
GAM962  WBSCR14  3'  GGCTGCAGGATGGT       51977        G  A
                                ACTGTTCTG CA GCT
                                ||||||||| || |||
                                TGGTAGGAC GT CGG
                                  _ _
GAM962  WBSCR5   3'  AGCTGATTAAACAGTGTT    50608        C   CA
                                AACACTGTT TGG  AGCT
                                ||||||||| |||  ||||
                                TTGTGACAA ATT  TCGA
                                  _  AG
GAM962  WBSCR5   3'  AGCTGATTAAACAGTGTT    41854        C   CA
                                AACACTGTT TGG  AGCT
                                ||||||||| |||  ||||
                                TTGTGACAA ATT  TCGA
                                  _  AG
GAM962  WBSCR5   3'  AGCTGATTAAACAGTGTT    26254        C   CA
                                AACACTGTT TGG  AGCT
                                ||||||||| |||  ||||
                                TTGTGACAA ATT  TCGA
                                  _  AG
GAM962  WIF1     5'  GGACTAGAGGGAGAGCAGTGT  60181         GGCAAG
                                ACACTGTTCT     CTGGTTT
                                ||||||||||     |||||||
                                TGTGACGAGA     GATCAGG
                                    GGGA__
GAM962  WNT1     3'  GGTCGGCTCCTGATGGTGT    18312       CT  CA     TT
                                ACACTGTT  GG  AGCTGG  T
                                ||||||||  ||  ||||||  |
                                TGTGGTAG  CC  TCGGCT  G
                                   T_ __     GG
GAM962  ZNF193   3'  AGTTGTGTGGGGCAGGTT    20858     A   T  G  _
                                AAC CTGT CT GCA AGCT
                                ||| |||| || ||| ||||
                                TTG GACG GG TGT TTGA
                                  _   _  G   G
GAM962  ABCA6    5'  GAACTGGTTTTGACAGTGTT  54412        CTGGC   TG
                                AACACTGTT    AAGC  GTTT
                                |||||||||    ||||  ||||
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                                TTGTGACAG    TTTG  CAAG
                                     T____   GT
GAM962  ABIN-2   5' GGACGCGCTGCTGGAGCAGGTT 44208    A    TG  A  TG
                                AAC CTGTTC  GCA GC  GTTT
                                ||| ||||||  ||| ||  ||||
                                TTG GACGAG  CGT CG  CAGG
                                  _    GT  _  CG
GAM962  AGTRL2   5' AGGCTGGCTTTACTAACAGGTT 17689    A   CTGGC   TG
                                AAC CTGTT    AAGC  GTTT
                                ||| |||||    ||||  ||||
                                TTG GACAA    TTCG  CGGA
                                  _   TCAT_   GT
GAM962  AGTRL2   5' GGTTAGCCAGGAGCAGTGT   17695        _   A
                                ACACTGTTC TGGC AGCT
                                ||||||||| |||| ||||
                                TGTGACGAG ACCG TTGG
                                     G   A
GAM962  ALTE     3' GGCTGGGGAGGACGGTGT    16390        GGCA
                                ACACTGTTCT   AGCT
                                ||||||||||   ||||
                                TGTGGCAGGA   TCGG
                                     GGGG
GAM962  AP3D1    3' GAACCGTGGACGGGGTGGGTT  14137    A TG    GCAA  T
                                AAC C  TTCTG   GC GGTTT
                                ||| |  |||||   || |||||
                                TTG G  GGGGC   TG CCAAG
                                  _ GT    AGG_  _
GAM962  AP3M1    3' GGACCAGTTTGTTTTCCAAGTG 23917     GTTCT
           T                     ACACT    GGCAAGCTGGTTT
                                |||||    ||||||||||||||
                                TGTGA    TTGTTTGACCAGG
                                   ACCTT
GAM962  AP3S2    3' GGGCTAGATCTCAGGTGTGGTG 19522     TG _    CAAG
           TT                     AACAC  T TCTGG   CTGGTTT
                                |||||  | |||||   |||||||
                                TTGTG  G GGACT   GATCGGG
                                   GT T    CTA_
GAM962  APCL     3' AAGCCCCGCCCAGACGGTGTT  19660       T   CAA  T_
                                AACACTGT CTGG   GC  GGTTT
                                |||||||| ||||   ||  |||||
                                TTGTGGCA GACC   CG  CCGAA
                                     _   ___  CC
GAM962  AQP10    3' TCTCTTGGCTTCTTAGGACAGT 54433          C   TG TTT
           GTT                     AACACTGTTCTGG AAGC  G
                                |||||||||||| ||||  |
                                TTGTGACAGGATT TTCG  T
                                       C   GT CTCTC
GAM962  ARHGAP5  3' AGGCCATGCTTGGGATGTTGTT 77069     CT   TGG   _
                                AACA  GTTC   CAAGC TGGTTT
                                ||||  ||||   ||||| ||||||
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                                TTGT  TAGG   GTTCG ACCGGA
                                  TG    ___     T
GAM962  ASP      5'  GAACTGCAGGGTCTAGGGTGTT 49166     CT TT    _ AA_  T
             GTT                    ACA  G  CTGG C   GC GGTTT
                                ||| |  |||| |   || |||||
                                TGT  T  GATC G   CG TCAAG
                                  TG GG    T GGA  _
GAM962  ATPW     5'  GAGCCGGGCGGGACTAGGGTGG 31629     TG     CAA_  _
             TG                    CAC  TTCTGG    GCT GGTTT
                                ||| ||||||   ||| |||||
                                GTG  GGGATC    CGG CCGAG
                                  GT     AGGG   G
GAM962  BBP      3'  AGCTGTATAATAGTGTT     49320          CTG   A
                                AACACTGTT   GCA GCT
                                |||||||||   ||| |||
                                TTGTGATAA   TGT CGA
                                     TA_   _
GAM962  BCAA     3'  GGTGGGTCAGAACATGTT    33048      C        AA
                                AACA TGTTCTGGC  GCT
                                |||| |||||||||  |||
                                TTGT ACAAGACTG  TGG
                                  _       GG
GAM962  BCCIP    3'  GATTAGAAGGAACAGTG     54305          GGCAAG
                                CACTGTTCT     CTGGTT
                                |||||||||     ||||||
                                GTGACAAGG     GATTAG
                                     AA_____
GAM962  BIRC8    5'  CCGGCTTAGGGCAGGGTT    52905     A       GCA
                                AAC CTGTTCTG   AGCTGG
                                ||| ||||||||   ||||||
                                TTG GACGGGAT   TCGGCC
                                  G      ___
GAM962  C11orf11  3'  GGCTTGGCTCAGGATGTGTT   93255      T     _ _
                                AACAC GTTCTG GC AAGCT
                                ||||| |||||| || |||||
                                TTGTG TAGGAC CG TTCGG
                                  _     T  G
GAM962  C11orf25  5'  AAATCGAGCATCGTGGGTAGTG 48635        TT _   CAA   _
             TT                    AACACTG  C TGG   GCT GGTTT
                                |||||||  | |||   ||| |||||
                                TTGTGAT  G GCT   CGA CTAAA
                                    GG T   A__   G
GAM962  C20orf110 3'  AGGTCAGCGTGCAGAGCAGTG  79542          G  A    GT
                                CACTGTTCTG CA GCTG  TT
                                |||||||||| || ||||  ||
                                GTGACGAGAC GT CGAC  GA
                                     _ G    TG
GAM962  C20orf124 3'  GGCTCCGGGATAGT       45489          CA
                                ACTGTTCTGG  AGCT
                                ||||||||||  ||||
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                                TGATAGGGCC  TCGG
                                          __
GAM962  C20orf139 3'  GAACTGGGACTAGGACAGTGT  84757          CAAG TG
                                ACACTGTTCTGG   C  GTTT
                                ||||||||||||   |  ||||
                                TGTGACAGGATC   G  CAAG
                                      AG__ GT
GAM962  C20orf21  3'  AACCAGTTTCTTACATGTT   35108     C   TCT  C
                                AACA TGT   GG AAGCTGGTT
                                |||| |||   || |||||||||
                                TTGT ACA   TC TTTGACCAA
                                  _   T__  _
GAM962  C20orf3   3'  AGGCCAGCGGTGAGAGCCGTGT 68071      T    G  AA
           T                     AACAC GTTCT GC  GCTGGTTT
                                |||||  |||||  ||  ||||||||
                                TTGTG CGAGA TG  CGACCGGA
                                   C    G  G_
GAM962  C20orf80  5'  AGACCTACGCTGTCAGGGAGTG 65283       G      A  T__
           TT                     AACACT TTCTGGCA GC   GGTTT
                                |||||||  ||||||||  ||   |||||
                                TTGTGA GGGACTGT CG   CCAGA
                                  _       _ CAT
GAM962  C5orf3    3'  AGTCTCTTCAGGATGTGTT   37962      T     CA  _
                                AACAC GTTCTGG  AG CT
                                |||||  |||||||  || ||
                                TTGTG TAGGACT  TC GA
                                  _      TC  T
GAM962  C5orf4    5'  AGATGGTCAGGATGGTG     32975          AAG
                                CACTGTTCTGGC   CT
                                ||||||||||||   ||
                                GTGGTAGGACTG   GA
                                      GTA
GAM962  C5orf4    3'  AGATGGTCAGGATGGTG     50485          AAG
                                CACTGTTCTGGC   CT
                                ||||||||||||   ||
                                GTGGTAGGACTG   GA
                                      GTA
GAM962  C8orf2    3'  GGGCCAGCTTGCTCAGAA    23168      _
                                TTCTG GCAAGCTGGTTT
                                |||||  ||||||||||||
                                AAGAC CGTTCGACCGGG
                                   T
GAM962  CAT56     3'  GGTCCAGAGTGGTGTT      47518      TG     CAA
                                AACAC  TTCTGG   GCT
                                |||||  ||||||   |||
                                TTGTG  GAGACC   TGG
                                   GT     ____
GAM962  CBX6      3'  GGGCTGGTGAGTGGGCAGT   26620       TG  AA  TG
                                ACTGTTC  GC  GC  GTTT
                                |||||||  ||  ||  ||||
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                                TGACGGG  TG  TG  CGGG
                                   __  AG  GT
GAM962  CCR6    3'  GATTGGCCGGCTAGTGTT    48583      GTTCT   AA  TG
                                AACACT    GGC  GC  GTT
                                ||||||    |||  ||  |||
                                TTGTGA    TCG  CG  TAG
                                   _____  GC  GT
GAM962  CCR6    3'  GATTGGCCGGCTAGTGTT    15168      GTTCT   AA  TG
                                AACACT    GGC  GC  GTT
                                ||||||    |||  ||  |||
                                TTGTGA    TCG  CG  TAG
                                   _____  GC  GT
GAM962  CED-6   5'  AGGCTGGTTTTCTTGGAATGTG 32852      T    TG C_   TG
           TT                    AACAC GTTC  G  AAGC  GTTT
                                |||||  ||||  |  ||||  ||||
                                TTGTG TAAG  T  TTTG  CGGA
                                   _   GT CT    GT
GAM962  CENPJ   5'  GGCTTCACGGAGCGGTGTT   37450          GC
                                AACACTGTTCTG  AAGCT
                                ||||||||||||  |||||
                                TTGTGGCGAGGC  TTCGG
                                      AC
GAM962  CG012   5'  AGGCAGCCTGTCAGGGCAGTG  83213          A    GTTT
                                CACTGTTCTGGCA GCTG
                                ||||||||||||| ||||
                                GTGACGGGACTGT CGAC
                                      C    GGA
GAM962  CGI-203 5'  AGTTCGTTCAGAATAGTG    39902          _ A
                                CACTGTTCTGG C AGCT
                                |||||||||||  | ||||
                                GTGATAAGACT G TTGA
                                      T C
GAM962  CIP29   3'  GGGCTGTAGCACAGGATGGAGT 50406    A      _  A__   GGTTT
           T                     AC CTGTTCTG GC   AGCT
                                || ||||||||  ||   ||||
                                TG GGTAGGAC CG   TCGG
                                 A       A  ATG    G   T
GAM962  CMG2    3'  GGATCGGTTTGATGTGGTG   54164     TG TCTGG
                                CAC  T    CAAGCTGGTTT
                                |||  |    ||||||||||
                                GTG  G    GTTTGGCTAGG
                                  GT TA___
GAM962  COL12A1 3'  GGTCAGATAGAGCAGTGT    15182          GCAA
                                ACACTGTTCTG    GCT
                                ||||||||||    |||
                                TGTGACGAGAT    TGG
                                      AGAC
GAM962  COL12A1 3'  GGTCAGATAGAGCAGTGT    54664          GCAA
                                ACACTGTTCTG    GCT
                                ||||||||||    |||
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                                TGTGACGAGAT   TGG
                                      AGAC
GAM962  CPR2     3'  GGCCTGTTAGGAAGTGTT    48100       G       A
                                AACACT TTCTGGCA GCT
                                |||||| |||||||| |||
                                TTGTGA AGGATTGT CGG
                                   _       C
GAM962  CSEN     3'  GGGCTGGCAGAGGGGACAGAGT 25533     A      GGCAA  TG
          T                      AAC CTGTTCT     GC  GTTT
                                 ||| |||||||     ||  ||||
                                 TTG GACAGGG     CG  CGGG
                                   A      GAGA_  GT
GAM962  CTCF     3'  TGCTGAGGACAGTGTT      21636          _
                                AACACTGTTCT GGCA
                                |||||||||| ||||
                                TTGTGACAGGA TCGT
                                      G
GAM962  CYorf14  3'  AAATTAGTTGGTCATGGTGGTG 37604       TG TC    A
          TT                     AACAC  T  TGGC AGCTGGTTT
                                 |||||  |  |||| |||||||||
                                 TTGTG  G  ACTG TTGATTAAA
                                    GT GT    G
GAM962  CYP2A7   3'  GGCGGGGTCAGGGCGGGGTT   47585     A        AA_
                                AAC CTGTTCTGGC   GCT
                                ||| ||||||||||   |||
                                TTG GGCGGGACTG   CGG
                                  G         GGG
GAM962  CYP2A7   3'  GGCGGGGTCAGGGCGGGGTT   5714      A        AA_
                                AAC CTGTTCTGGC   GCT
                                ||| ||||||||||   |||
                                TTG GGCGGGACTG   CGG
                                  G         GGG
GAM962  D2S448   3'  GGGCCAGTCACAAGGAATTGTG 73528       T    GGCAA
          TT                     AACAC GTTCT     GCTGGTTT
                                 ||||| |||||     ||||||||
                                 TTGTG TAAGG     TGACCGGG
                                    T     AACAC
GAM962  DJ122O8.2 3'  AAATTAGCTTGGTGTGGTG    39991     TG TCT G
                                CAC  T   G CAAGCTGGTTT
                                |||  |   | ||||||||||
                                GTG  G   T GTTCGATTAAA
                                  GT ___ G
GAM962  DKFZp434B1222 5'  GGGCTAGGCACTGGGATGGTGT 34140          TG CAAG
                                ACACTGTTC  G    CTGGTTT
                                |||||||||  |   |||||||
                                TGTGGTAGG  C    GATCGGG
                                      GT ACG_
GAM962  DKFZp434C0923 3'  GGTCAGTTTGGGCAGCAGGTT  34217     A    _  GG       TT
                                AAC CTGTT CT  CAAGCTGG  T
                                ||| ||||| ||  ||||||||  |
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                                TTG GACGA GG  GTTTGACT  G
                                  _    C  __      GG
GAM962  DKFZP434C171 3'  GGCTGGAGAATGGTGT     31559         GGCA
                                ACACTGTTCT   AGCT
                                ||||||||||   ||||
                                TGTGGTAAGA   TCGG
                                     GG__
GAM962  DKFZP434N093 3'  AGTCATCAGAATAGTGT     79942          CAA
                                ACACTGTTCTGG  GCT
                                ||||||||||||  |||
                                TGTGATAAGACT  TGA
                                      AC_
GAM962  DKFZP564C186 3'  GGCTGGTGGCCAGTGTT     72409       TT TG  A
                                AACACTG  C  GC AGCT
                                |||||||  |  || ||||
                                TTGTGAC  G  TG TCGG
                                    CG __  G
GAM962  DKFZP564I052 3'  AAGTCAGTTTTGGCATACAGT  66704      TC  G   _  GT
                                ACTGT  TG CAAG CTG  TT
                                |||||  || |||| |||  ||
                                TGACA  AC GTTT GAC  AA
                                   T_  G   T   TG
GAM962  DKFZp566H0824 5'  AGACTTAGCCCCTGGAACAGTG 34041         TG CAA   _
           T                     ACACTGTTC  G   GCTG GTTT
                                 |||||||||  |   |||| ||||
                                 TGTGACAAG  C   CGAT CAGA
                                      GT CC_   T
GAM962  DKFZp566H0824 5'  AGCTGGTGGAAGTGTT     34046       GT   G  A
                                AACACT  TCTG CA GCT
                                ||||||  |||| ||  |||
                                TTGTGA  AGGT GT CGA
                                   __   G  _
GAM962  DKFZP727M111 5'  GGACCGGCTAGCAGGCAGTGT  31411        T   G A
                                ACACTGT CTG C AGCTGGTTT
                                ||||||| ||| | |||||||||
                                TGTGACG GAC G TCGGCCAGG
                                   _  _ A
GAM962  DKFZp761B0514 3'  GATCAGCTGAAGTGTGTT    50155       TG   TGGCA
                                AACAC  TTC    AGCTGGTT
                                |||||  |||    ||||||||
                                TTGTG  AAG    TCGACTAG
                                   TG  _____
GAM962  DKFZP761D0211 3'  GAACTGGCTGTGGAATGCGTGT 49353      _     G  A  TG
           T                     AACAC TGTTCTG CA GC  GTTT
                                 |||||  ||||||| || ||  ||||
                                 TTGTG GTAAGGT GT CG  CAAG
                                   C       _  _  GT
GAM962  DKFZp761K1423 5'  GAGCTAAGCTCTTAGGAATAGT 37333          GGCA   _
           GTT                     AACACTGTTCT    AGCT GGTTT
                                   ||||||||||    |||| |||||
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                                TTGTGATAAGG    TCGA TCGAG
                                       ATTC    A
GAM962  DKFZp762P2111 3'  GGCTCTGGGGCAGAGTT     86359     A     TG CA
                                AAC CTGTTC  G  AGCT
                                ||| ||||||  |  ||||
                                TTG GACGGG  C  TCGG
                                  A     GT __
GAM962  DOCK3    3'  AAACTATAAAGCAGAGCAGTG  66492         G AAGC
                                CACTGTTCTG C    TGGTTT
                                |||||||||| |    ||||||
                                GTGACGAGAC G    ATCAAA
                                       _ AAAT
GAM962  DOCK3    3'  GGCTGGCAGGAGGGTAGTT    66505     _   G    G  A
                                AAC ACT TTCTG CA GCT
                                ||| ||| ||||| || |||
                                TTG TGG AGGAC GT CGG
                                  A  G    G  _
GAM962  DUSP14   3'  AAATTAACATTTTGGAATAGTG 22833         TG CAAGC
             TT                   AACACTGTTC  G    TGGTTT
                                ||||||||||  |    ||||||
                                TTGTGATAAG  T    ATTAAA
                                       GT TTACA
GAM962  EIF4B    3'  GGATCAGCTTGGTAGACAGT   75970      T   G
                                ACTGT CTG CAAGCTGGTTT
                                ||||| ||| ||||||||||
                                TGACA GAT GTTCGACTAGG
                                  _  G
GAM962  ELOVL1   3'  GGACTGCACCTTAGGGCAGTGT 43061          CAA  T
                                ACACTGTTCTGG   GC GGTTT
                                ||||||||||||   || |||||
                                TGTGACGGGATT   CG TCAGG
                                       CCA  _
GAM962  EPB41L1  3'  AAGCTAGAATCTAGGGCACTGT 70585      C       CAAG
             T                    AACA TGTTCTGG    CTGGTTT
                                |||| ||||||||    |||||||
                                TTGT ACGGGATC    GATCGAA
                                  C       TAA_
GAM962  ERp44    3'  TAGACTTGGGACTGGGACAGT  81698       TG ___    _  GGTTT
                                ACTGTTC  G   CAAG CT
                                |||||||  |   |||| ||
                                TGACAGG  C   GTTC GA
                                    GT AGG    A     TT
GAM962  FAM3D    5'  AAGCTGGCCCAGGGTGGTG   57149     TG     CAA  TG
                                CAC  TTCTGG   GC  GTTT
                                |||  ||||||   ||  ||||
                                GTG  GGGACC   CG  CGAA
                                  GT      ___  GT
GAM962  FLJ10300 3'  AGTTATTTTTAGAACAGT    35999          CA__
                                ACTGTTCTGG    AGCT
                                ||||||||||    ||||
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                                TGACAAGATT    TTGA
                                      TTTA
GAM962  FLJ10420  3'  AAGCCAGACGGAACAGTGTT   36104          GCAAG
                                AACACTGTTCTG     CTGGTTT
                                ||||||||||||    |||||||
                                TTGTGACAAGGC     GACCGAA
                                      A_____
GAM962  FLJ10468  3'  AAGTCTGCTTGTGGAGCAGTGT 36141          G     T GT
          T                     AACACTGTTCTG CAAGC G  TT
                                |||||||||||| ||||| |  ||
                                TTGTGACGAGGT GTTCG C  AA
                                      _     T TG
GAM962  FLJ10724  3'  AGGCCAGTCATGAGGATGGTGT 36499          GGCAA
                                ACACTGTTCT     GCTGGTTT
                                ||||||||||     ||||||||
                                TGTGGTAGGA     TGACCGGA
                                      GTAC_
GAM962  FLJ10895  3'  TAAAATACGCTTGCTAGGGTGT 38848       T TT        TGGTTT
          GTT                     AACAC G  CTGGCAAGC
                                |||||| |  |||||||||
                                TTGTG T  GATCGTTCG
                                  _ GG        CATAAAATT
GAM962  FLJ10904  5'  AGGCCGAGCCTGGGGCGGAGTT 36846     A      TG CAA   _
                                AAC CTGTTC  G   GCT GGTTT
                                ||| ||||||  |   ||| |||||
                                TTG GGCGGG  C   CGA CCGGA
                                  A     GT ___   G
GAM962  FLJ10956  3'  AGATTCGTCTAGAGCAGTG    36915          CAA  TG
                                CACTGTTCTGG   GC  GTTT
                                ||||||||||   ||  ||||
                                GTGACGAGATC   TG  TAGA
                                      ___  CT
GAM962  FLJ10971  5'  GAACTGGTTGTCTTCTTGGGCG 36926       T____     G TG
          GTGTT                     CTGTTC    GGCAA C  GTTT
                                ||||||    ||||| |  ||||
                                GGCGGG    CTGTT G  CAAG
                                    TTCTT    _ GT
GAM962  FLJ10980  3'  AAACCCCCAGTTAGATTAGTGT 64648       T     AAGCT
          T                     AACACTG TCTGGC     GGTTT
                                ||||||| ||||||     |||||
                                TTGTGAT AGATTG     CCAAA
                                    T     ACCC_
GAM962  FLJ11715  3'  GGCTTTGGGGCAGTGT      44677         TG CA
                                ACACTGTTC  G  AGCT
                                |||||||||  |  ||||
                                TGTGACGGG  T  TCGG
                                      GT __
GAM962  FLJ11726  3'  GGGCTGGTTAGCCAGTAGTGT  46418       TT    A   TG
                                ACACTG  CTGGC AGC  GTTT
                                ||||||  ||||| |||  ||||
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                                TGTGAT  GACCG TTG  CGGG
                                  __    A   GT
GAM962  FLJ12476  3'  AAATTGGTTTGCTTTGTGT   42946     TGTTCT     TG
                                ACAC     GGCAAGC  GTTT
                                ||||     |||||||  ||||
                                TGTG     TCGTTTG  TAAA
                                  TT____      GT
GAM962  FLJ12921  3'  AGACTGAAGGGCCAGGACAGT  45906          AAGCT
                                ACTGTTCTGGC    GGTTT
                                ||||||||||     |||||
                                TGACAGGACCG    TCAGA
                                      GGAAG
GAM962  FLJ12998  3'  AGACCGGCTCTGGGAGAATGGG 42834     A      GG  _
          TT                     AAC CTGTTCT  CA AGCTGGTTT
                                ||| |||||||  || |||||||||
                                TTG GGTAAGA  GT TCGGCCAGA
                                  _      GG  C
GAM962  FLJ13052  3'  GGCTGGAAGACGGCAGTGTT   43472        __  GGCA
                                AACACTGT  TCT    AGCT
                                ||||||||  |||    ||||
                                TTGTGACG  AGA    TCGG
                                     GC   AGG_
GAM962  FLJ13096  3'  GGTTTTTTAGAATACTGTT    46540      C       C
                                AACA TGTTCTGG AAGCT
                                |||| |||||||| |||||
                                TTGT ATAAGATT TTTGG
                                  C       T
GAM962  FLJ13110  3'  GGCTCTAGAATGGT        43306          CA
                                ACTGTTCTGG  AGCT
                                ||||||||||  ||||
                                TGGTAAGATC  TCGG
                                      __
GAM962  FLJ13194  3'  GGCTGGTTGTTAGCAGGTT    47129     A   TT      G TG
                                AAC CTG  CTGGCAA C  GTT
                                ||| |||  ||||||| |  |||
                                TTG GAC  GATTGTT G  CGG
                                  _  __       _ GT
GAM962  FLJ13310  5'  AGTGTGTCAGGATGGGTT    47083     A         A
                                AAC CTGTTCTGGCA GCT
                                ||| ||||||||||| |||
                                TTG GGTAGGACTGT TGA
                                  _         G
GAM962  FLJ13315  3'  GGATCAATAATTTGGGGGAGTG 46570        G   TG CAAGC
          TT                     AACACT TTC  G     TGGTTT
                                |||||| |||  |    ||||||
                                TTGTGA GGG  T     ACTAGG
                                   G   GT TAATA
GAM962  FLJ13391  3'  GGTCTCGGAATGGTG       49791           CAA
                                CACTGTTCTGG   GCT
                                ||||||||||   |||
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                                GTGGTAAGGCT   TGG
                                      C__
GAM962  FLJ13456  3' GAGCTGGTTTGTTAGTTCACTG 65940    C  TT       TG
                                CA TG  CTGGCAAGC  GTTT
                                || ||  |||||||||  ||||
                                GT AC  GATTGTTTG  CGAG
                                 C  TT       GT
GAM962  FLJ13842  3' AACCTCCTGTGATGGTGTT   44982        CTG   A CT
                                AACACTGTT   GCA G  GGTT
                                |||||||||   ||| |  ||||
                                TTGTGGTAG   TGT C  CCAA
                                      ___   _ CT
GAM962  FLJ14075  5' ACCCGGGACTTGAACAGTGTT  46047         T  CAAG    TTT
                                AACACTGTTC GG    CTGG
                                |||||||||| ||    ||||
                                TTGTGACAAG TC    GGCC
                                      T  AG__    CAG
GAM962  FLJ14146  3' AGGCTGGGTGGCTGGGACAGGT 45240     A     TG  AAG TG
           T                     AAC CTGTTC  GC   C  GTTT
                                ||| ||||||  ||   |  ||||
                                TTG GACAGG  CG   G  CGGA
                                  _     GT  GTG GT
GAM962  FLJ14249  3' AGATCGGCTGTCTGGAGTGTT  42404       GT  T    A
                                AACACT  TC GGCA GCTGGTTT
                                ||||||  || |||| ||||||||
                                TTGTGA  GG CTGT CGGCTAGA
                                   __  T    _
GAM962  FLJ14249  3' AGATCGGCTGTCTGGAGTGTT  55211       GT  T    A
                                AACACT  TC GGCA GCTGGTTT
                                ||||||  || |||| ||||||||
                                TTGTGA  GG CTGT CGGCTAGA
                                   __  T    _
GAM962  FLJ14326  3' AAGTCAGCTTTGCCTGTGGT   49796    TG TCT    _    GT
                                AC  T   GGCAA GCTG  TT
                                ||  |   ||||| ||||  ||
                                TG  G   CCGTT CGAC  AA
                                 GT T__     T    TG
GAM962  FLJ14442  3' AGGCCAGGTGTTAGAGCAATGT 51358      C         AG
           T                     AACA TGTTCTGGCA  CTGGTTT
                                |||| ||||||||||  |||||||
                                TTGT ACGAGATTGT  GACCGGA
                                  A        G_
GAM962  FLJ14936  3' AAACTGGTTTGTAGCAGT    51706       CTG     TG
                                ACTGTT   GCAAGC  GTTT
                                ||||||   ||||||  ||||
                                TGACGA   TGTTTG  CAAA
                                   ___     GT
GAM962  FLJ20015  3' GAGCTCTGAGACGGGACAGTGT 38638          G__  _   GGTTT
           T                     ACACTGTTCTG   CA AGCT
                                ||||||||||   || ||||
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                                TGTGACAGGGC   GT TCGA
                                      AGA  C    G   T
GAM962   FLJ20060  5'  AGGTTGCCAGAGCAGT      34448            G
                                ACTGTTCTGGCAA CT
                                |||||||||||| ||
                                TGACGAGACCGTT GA
                                   G
GAM962   FLJ20136  3'  GAATCAATTCAGGACAGT     34611          CAAGC
                                ACTGTTCTGG    TGGTTT
                                ||||||||||    ||||||
                                TGACAGGACT    ACTAAG
                                      TA___
GAM962   FLJ20190  5'  GGCTGGCTGGGCAGTGT      34706        T TG  A
                                ACACTGT C  GC AGCT
                                ||||||| |  || ||||
                                TGTGACG G  CG TCGG
                                    _ GT  G
GAM962   FLJ20254  5'  GAACTGGACAAGAGCCAGAGTG 34791     TGT     AAG___ TG
            TGTT                   CAC   TCTGGC     C  GTTT
                                |||   ||||||     |  ||||
                                GTG   AGACCG     G  CAAG
                                  TG_     AGAACA GT
GAM962   FLJ20297  3'  AGGTTGGCAGAGTGGGTT     34894     A TG     G   G
                                AAC C  TTCTG CAA CT
                                ||| |  ||||| ||| ||
                                TTG G  GAGAC GTT GA
                                  _ GT     G   G
GAM962   FLJ20297  3'  GGCTTCTGGAGCGGGGTT     34896     A      TG C
                                AAC CTGTTC  G AAGCT
                                ||| ||||||  | |||||
                                TTG GGCGAG  C TTCGG
                                  G      GT _
GAM962   FLJ20297  3'  AGGTTGGCAGAGTGGGTT     35635     A TG     G   G
                                AAC C  TTCTG CAA CT
                                ||| |  ||||| ||| ||
                                TTG G  GAGAC GTT GA
                                  _ GT     G   G
GAM962   FLJ20297  3'  GGCTTCTGGAGCGGGGTT     35636     A      TG C
                                AAC CTGTTC  G AAGCT
                                ||| ||||||  | |||||
                                TTG GGCGAG  C TTCGG
                                  G      GT _
GAM962   FLJ20309  3'  AGCCTTCCCAGGACAGT      34920          C   _
                                ACTGTTCTGG AAG CT
                                |||||||||| ||| ||
                                TGACAGGACC TTC GA
                                      C   C
GAM962   FLJ20421  5'  GAGTCAGGCGCGCGGGGCGGCG 35146     A       _  AAG   GT
            TT                    AAC CTGTTCTG GC   CTG  TT
                                ||| |||||||| ||   |||  ||
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                                TTG GGCGGGGC CG   GAC  AG
                                  C       G  CG_   TG
GAM962  FLJ20456  3'  ATTGGCTGGACGTGTT      35211       T   TGGCA   TG
                                AACAC GTTC     AGC  GT
                                ||||| ||||     |||  ||
                                TTGTG CAGG     TCG  TA
                                  _   _____   GT
GAM962  FLJ21276  3'  AGTTGGAAGTAGCAGTGTT    44915         _  GGCA
                                AACACTGTT CT    AGCT
                                |||||||||  ||    ||||
                                TTGTGACGA GA    TTGA
                                     T  AGG_
GAM962  FLJ21596  3'  GGTTGGGCTAGATCAGTGTT   45702        T     A_
                                AACACTG TCTGGC  AGCT
                                |||||||  ||||||  ||||
                                TTGTGAC AGATCG  TTGG
                                    T     GG
GAM962  FLJ21736  3'  GGACCTGGAGCTAGGGGGTGTT 46230       G      AAGCT
                                AACACT TTCTGGC     GGTTT
                                ||||||  |||||||     |||||
                                TTGTGG GGGATCG     CCAGG
                                  _      AGGT_
GAM962  FLJ22160  3'  GGCTTTGCAGGACAGTGTT    44735          G  _
                                AACACTGTTCTG CAA GCT
                                ||||||||||||  ||| |||
                                TTGTGACAGGAC GTT CGG
                                     _  T
GAM962  FLJ22378  3'  GGTGGGGCTGGGACGCTGTT   46904     C    TG  AA_
                                AACA TGTTC  GC   GCT
                                ||||  |||||  ||   |||
                                TTGT GCAGG  CG   TGG
                                  C    GT  GGG
GAM962  FLJ22479  3'  AGTTGACTCAGGATGGT     46071          CA_
                                ACTGTTCTGG   AGCT
                                ||||||||||   ||||
                                TGGTAGGACT   TTGA
                                     CAG
GAM962  FLJ22672  3'  GGTTGGCGGGGGGAGGTGTT   46067       G_   G  A
                                AACACT  TTCT GC AGCT
                                ||||||  |||| ||  ||||
                                TTGTGG  GGGG CG TTGG
                                   AG   G  G
GAM962  FLJ22833  3'  GGACCAGTGGGAAATGGTGTT  43105         CTGGCAA
                                AACACTGTT      GCTGGTTT
                                |||||||||      ||||||||
                                TTGTGGTAA      TGACCAGG
                                     AGGG___
GAM962  FLJ23129  3'  GGCTCCTGGAATGTGTT     45430      T   TG CA
                                AACAC GTTC  G  AGCT
                                |||||  ||||  |  ||||
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                                TTGTG TAAG  C  TCGG
                                  _   GT C_
GAM962  FLJ23510 3' AGCTACCAGATGGTGTT    45280       T   CA
                                AACACTGT CTGG  AGCT
                                |||||||| ||||  ||||
                                TTGTGGTA GACC  TCGA
                                    _   A_
GAM962  FLJ23556 3' AAATTAGCTGGGGGTGGTG   45938    TG   GGCA
                                CAC  TTCT   AGCTGGTTT
                                |||  ||||   |||||||||
                                GTG  GGGG   TCGATTAAA
                                  GT   G___
GAM962  FLJ23590 3' AGTTCCCAGGGCAGTG     45015         CA
                                CACTGTTCTGG  AGCT
                                ||||||||||  ||||
                                GTGACGGGACC  TTGA
                                      C_
GAM962  FLJ31168 3' AAATTAGCTGGGCATGGTGTT 58499       TCTG  A_
                                AACACTGT   GC  AGCTGGTTT
                                ||||||||   ||  |||||||||
                                TTGTGGTA   CG  TCGATTAAA
                                    ____ GG
GAM962  FPGT    3' GGTCTTCAGAGTAGTGT    13847         CAA
                                ACACTGTTCTGG   GCT
                                ||||||||||||  |||
                                TGTGATGAGACT   TGG
                                      TC_
GAM962  FUBP1   3' AAATTGGTTTGTTTTTAGT   14018     TTCT     TG
                                ACTG   GGCAAGC  GTTT
                                ||||   |||||||  ||||
                                TGAT   TTGTTTG  TAAA
                                  TT__     GT
GAM962  FUK     5' AGATCCCTGCTGGGACGCTGTT 58970     C    TG   AGCT
                                AACA TGTTC  GCA   GGTTT
                                |||| |||||  |||   |||||
                                TTGT GCAGG  CGT   CTAGA
                                  C    GT   CC__
GAM962  FYCO1   3' ATCAGCTTGTTCACTGTT    44486     C  TTCT      GT
                                AACA TG   GGCAAGCTG  T
                                |||| ||   |||||||||  |
                                TTGT AC   TTGTTCGAC  A
                                  C  ____       TG
GAM962  GFR     3' AGGCCTCTTCAGAATAGGGTT  24466     A       CA  CT
                                AAC CTGTTCTGG  AG  GGTTT
                                ||| |||||||||  ||  |||||
                                TTG GATAAGACT  TC  CCGGA
                                  G       __ T_
GAM962  GPT2    3' AGCCGCTGGAATGGTGT     55952        TG  AA
                                ACACTGTTC  GC  GCT
                                |||||||||  ||  |||
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                                TGTGGTAAG  CG  CGA
                                     GT  C_
GAM962  HEMGN    3'  AGGTCGGGGAGAGGATAGTG  37376        GGCAAG   GT
                                CACTGTTCT     CTG  TT
                                |||||||||     |||  ||
                                GTGATAGGA     GGC  GA
                                     GAGG__   TG
GAM962  HM74     3'  GGACTGAGCTAAACAGTGTT  20057        C    A_ _
                                AACACTGTT TGGC  AG CT
                                ||||||||| ||||  || ||
                                TTGTGACAA ATCG  TC GG
                                     _   AG  A
GAM962  HSA250839 3'  AAATCAGCTTGTCAGA     37257
                                TCTGGCAAGCTGGTTT
                                ||||||||||||||||
                                AGACTGTTCGACTAAA

GAM962  HTMP10   3'  AGACCTGGCACTGGAACAGGGT 52605     A     TG CAA  _
          T                      AAC CTGTTC  G   GCT GGTTT
                                ||| ||||||  |   ||| |||||
                                TTG GACAAG  C   CGG CCAGA
                                  G     GT A__   T
GAM962  KALI     3'  AGATGGCCAGAGTAATGTT   53590      C       AAG
                                AACA TGTTCTGGC   CT
                                |||| |||||||||   ||
                                TTGT ATGAGACCG   GA
                                   A        GTA
GAM962  KIAA0036  3'  GAACTAAACTTAGCATAGTGTT 27676        T    CAAGC
                                AACACTGT CTGG     TGGTTT
                                |||||||| ||||     ||||||
                                TTGTGATA GATT     ATCAAG
                                     C    CAA__
GAM962  KIAA0090  3'  AAACTAGTTTGTTTTAGT    88434      TTCT
                                ACTG    GGCAAGCTGGTTT
                                ||||    ||||||||||||
                                TGAT    TTGTTTGATCAAA
                                   T___
GAM962  KIAA0140  3'  GGCGGCCAGGGCAGTTGTT    27815      _        AA
                                AACA CTGTTCTGGC  GCT
                                |||| ||||||||||  |||
                                TTGT GACGGGACCG  CGG
                                   T        G_
GAM962  KIAA0153  3'  GGTCAGAGCAGGACAGTG    30704         GCAAG    TT
                                CACTGTTCTG    CTGG  T
                                ||||||||||    ||||  |
                                GTGACAGGAC    GACT  G
                                     GA___    GG
GAM962  KIAA0215  3'  AGGCTAACTTGTGGATAGTGTT 28415          TG    C
                                AACACTGTTC  GCAAG TGGTTT
                                ||||||||||  ||||| ||||||
```

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                                TTGTGATAGG  TGTTC ATCGGA
                                    __     A
GAM962  KIAA0227 3' GGGCCAAGGTTTGGGACAGGTT 60699     A     TGG     __
                                AAC CTGTTC   CAAGCT  GGTTT
                                ||| ||||||   ||||||  |||||
                                TTG GACAGG   GTTTGG  CCGGG
                                  _     ___      AA
GAM962  KIAA0286 3' AAGCTGGACATTGGAGCCGTGT 68315      T    TG CAAG TG
              T                  AACAC GTTC  G    C  GTTT
                                 ||||| ||||  |    |  ||||
                                 TTGTG CGAG  T    G  CGAA
                                    C    GT ACA_ GT
GAM962  KIAA0295 3' GGCTGGAGGGGCAGTGTT    68107          GGCA
                                AACACTGTTCT    AGCT
                                ||||||||||    ||||
                                TTGTGACGGGG    TCGG
                                      AGG_
GAM962  KIAA0296 3' GAGCCAGTTTGCCAGGGCTGG  28112    _
                                CT GTTCTGGCAAGCTGGTTT
                                || ||||||||||||||||||
                                GG CGGGACCGTTTGACCGAG
                                 T
GAM962  KIAA0303 3' AAACTGTTACCAGATAGTGTT  69459        T    CA   T
                                AACACTGT CTGG  AGC GGTTT
                                |||||||| ||||  ||| |||||
                                TTGTGATA GACC  TTG TCAAA
                                    _    A_   _
GAM962  KIAA0318 3' AGTGGCCAGAACGTGTT     68948       T       AA
                                AACAC GTTCTGGC  GCT
                                ||||| ||||||||  |||
                                TTGTG CAAGACCG  TGA
                                   _       G_
GAM962  KIAA0329 3' TGTCTTTGGAATGGTGTT    29282           ___
                                AACACTGTTCT   GGCA
                                ||||||||||   ||||
                                TTGTGGTAAGG   CTGT
                                      TTT
GAM962  KIAA0335 3' GGATTGGAACATGTTAGAATAG 28993           AG__ TG
              T                  ACTGTTCTGGCA    C  GTTT
                                 ||||||||||||    |  ||||
                                 TGATAAGATTGT    G  TAGG
                                       ACAA GT
GAM962  KIAA0420 3' GAACTGGCCTGTGGGTGGTGT  63356     TG   TG   A  TG
                                ACAC  TTC  GCA GC  GTTT
                                ||||  |||  ||| ||  ||||
                                TGTG  GGG  TGT CG  CAAG
                                  GT   __   C  GT
GAM962  KIAA0441 3' AACTGGGCAGAATGGT      28948          G AAG TG
                                ACTGTTCTG C   C  GTT
                                |||||||| |   |  |||
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                                TGGTAAGAC G   G  CAA
                                    _ ___ GT
GAM962  KIAA0441 3' AATGATGTTGCTAGTGCAGTGT 28949        T      GCTGGTTT
           T                    AACACTGT CTGGCAA
                                |||||||| |||||||
                                TTGTGACG GATCGTT
                                    T      GTAGTAAA
GAM962  KIAA0444 3' TACTAGAGTCAGAGCGGGTT  62347     A        AAG     TT
                                AAC CTGTTCTGGC   CTGGT
                                ||| ||||||||||   |||||
                                TTG GGCGAGACTG   GATCA
                                  _        A__     TC
GAM962  KIAA0475 3' GGATTGGCTCTGGAGCATGTGT 29500       _    TG CA   TG
           T                    AACAC TGTTC  G  AGC  GTTT
                                ||||| |||||  |  |||  ||||
                                TTGTG ACGAG  C  TCG  TAGG
                                   T    GT __   GT
GAM962  KIAA0478 3' GTTGGAGTCTGCTGGTGCGGTG 29556        T TG   AG  GGTTT
           TT                    AACACTGT C  GCA  CT
                                ||||||||  |  |||  ||
                                TTGTGGCG G  CGT  GA
                                     T GT   CT  GGTTGG
GAM962  KIAA0514 3' AGGCCCTGCTCTGGGAGGTGTT 28075       G   TG CA   T_
                                AACACT TTC  G  AGC  GGTTT
                                |||||| |||  |  |||  |||||
                                TTGTGG AGG  C  TCG  CCGGA
                                    _  GT __   TC
GAM962  KIAA0514 3' GGGCCGGCTGAGCCGAGGGTGT 28093       G  CT   A_
           T                    AACACT TT  GGC  AGCTGGTTT
                                |||||| ||  |||  |||||||||
                                TTGTGG AG  CCG  TCGGCCGGG
                                   G  __   AG
GAM962  KIAA0530 3' AAACTAGTAGTGTGGAGCAGTG 70863          G  A_
           T                    ACACTGTTCTG CA  GCTGGTTT
                                |||||||||| ||  ||||||||
                                TGTGACGAGGT GT  TGATCAAA
                                      _ GA
GAM962  KIAA0547 3' AGGCTAGCTTGCCAGGGC    28907
                                GTTCTGGCAAGCTGGTTT
                                ||||||||||||||||||
                                CGGGACCGTTCGATCGGA

GAM962  KIAA0556 3' GAGCTGGCTGAGAGGTTGGGGT 69084     TT TG  A____   TG
           AGT                    CTG  C  GC    AGC  GTTT
                                ||| | ||    |||  ||||
                                GAT  G  TG    TCG  CGAG
                                  GG GT  GAGAG   GT
GAM962  KIAA0557 3' AGTTGAACTTGGAACAGAGTT  77989     A     TG CA__
                                AAC CTGTTC  G    AGCT
                                ||| ||||||  |    ||||
```

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                                TTG GACAAG  T    TTGA
                                  A     GT CAAG
GAM962  KIAA0662 3' GGCTTATTCAGAACTGGTGTT  81858       _     C_
                                AACACT GTTCTGG  AAGCT
                                |||||| |||||||  |||||
                                TTGTGG CAAGACT  TTCGG
                                   T      TA
GAM962  KIAA0759 3' GGGCTGTAGGCCTGGGGCAGGT 67328     A     _  AA  T
           T                     AAC CTGTTCT GGC  GC GGTTT
                                ||| ||||||| |||  || |||||
                                TTG GACGGGG CCG  TG TCGGG
                                  _     T  GA  _
GAM962  KIAA0830 3' GAATTTGAAAGCTGGAATAGT  69698       TG  AAGCT
                                ACTGTTC  GC    GGTTT
                                |||||||  ||    |||||
                                TGATAAG  CG    TTAAG
                                    GT  AAAGT
GAM962  KIAA0831 3' AGTTGCAGAACGGAGTT    29968     A      G   G
                                AAC CTGTTCTG CAA CT
                                ||| |||||||| ||| ||
                                TTG GGCAAGAC GTT GA
                                  A      _  _
GAM962  KIAA0931 3' GGGTTGTAGAATAGTG      67423         G   G
                                CACTGTTCTG CAA CT
                                |||||||||| ||| ||
                                GTGATAAGAT GTT GG
                                      _  G
GAM962  KIAA1028 3' TCGGGGGCACCGGAGCAGGGTT 91949     A       CAA   GGTTT
                                AAC CTGTTCTGG   GCT
                                ||| |||||||||   |||
                                TTG GACGAGGCC   CGG
                                  G       A__   GGGCTG
GAM962  KIAA1029 3' GGACTTACCGGGGTGATGTT   23478     CT TT   C  _
                                AACA  G  CTGG AAG CT
                                ||||  |  |||| ||| ||
                                TTGT  T  GGCC TTC GG
                                  AG GG   A  A
GAM962  KIAA1040 3' AGTTATGGAACAGTGTT     72219          GCAA
                                AACACTGTTCTG    GCT
                                ||||||||||||   |||
                                TTGTGACAAGGT    TGA
                                      AT__
GAM962  KIAA1040 3' GAATTAGCATAAGTTATGGAAC 72226       __  AA__
           AGTGTT                 CTGTTCT  GGC    GCTGGTTT
                                |||||||  |||   ||||||||
                                GACAAGG  TTG   CGATTAAG
                                    TA   AATA
GAM962  KIAA1089 3' GGCTGGCTTTTGGAGTGTT   68846      TGT  TG C   TG
                                AACAC   TC  G AAGC  GTT
                                |||||   ||  | ||||  |||
```

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                                TTGTG   AG  T TTCG  CGG
                                   ___  GT _   GT
GAM962  KIAA1118  5'  GGCCTCGGGGCAGTGTT     69607          CAA
                                AACACTGTTCTGG   GCT
                                ||||||||||||   |||
                                TTGTGACGGGGCT   CGG
                                     C__
GAM962  KIAA1126  3'  AGACCAGTTACCAAACTAGGAT 71923   C      CA____
            AATGTT                 TGTTCTGG     AGCTGGTTT
                                ||||||||     |||||||||
                                ATAGGATC     TTGACCAGA
                                A       AAACCA
GAM962  KIAA1145  3'  GAATCACAGGCTTGGGCAGTGT 65623         T   AAGC
            T                   AACACTGTTC GGC    TGGTTT
                                ||||||||||| |||    ||||||
                                TTGTGACGGG TCG    ACTAAG
                                     T   GAC_
GAM962  KIAA1323  3'  AGTTGTCATTGAGTAGTGTT   63038          __     G
                                AACACTGTTC  TGGCAA CT
                                ||||||||||  |||||| ||
                                TTGTGATGAG  ACTGTT GA
                                     TT     _
GAM962  KIAA1328  3'  GAACCATCTCTACTTGCCAGAG 61650          C_____
            TATGTT                 TGTTCTGGCAAG     TGGTTT
                                ||||||||||||     ||||||
                                ATGAGACCGTTC     ACCAAG
                                     ATCTCT
GAM962  KIAA1332  3'  AAGCTGGTGCTGTGAGTGATGT 71157     CTGTT  G   A_  TG
            T                   AACA     CT GCA  GC  GTTT
                                ||||     || |||  ||  ||||
                                TTGT     GA TGT  TG  CGAA
                                  AGT__  G   CG  GT
GAM962  KIAA1332  3'  CAGCAGAGCGGGTT       71162     A      GGCAA
                                AAC CTGTTCT     GCTG
                                ||| |||||||     ||||
                                TTG GGCGAGA     CGAC
                                  _     _____
GAM962  KIAA1361  5'  AGCTTTGGAGCAGTGT      62194          TG CA
                                ACACTGTTC  G  AGCT
                                |||||||||  |  ||||
                                TGTGACGAG  T  TCGA
                                     GT __
GAM962  KIAA1371  3'  AGTTTTAAGACAGTGTT     89040         T  GGC
                                AACACTGT CT   AAGCT
                                ||||||||| ||   |||||
                                TTGTGACA GA   TTTGA
                                     _ AT_
GAM962  KIAA1376  3'  AAACTGGCACATACTCAGAGCA 63619          CAA___  TG
            GT                    ACTGTTCTGG     GC  GTTT
                                ||||||||||     ||  ||||
```

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                                TGACGAGACT     CG  CAAA
                                     CATACA  GT
GAM962  KIAA1430  3'  GGTGTGTCGGACAGTGTT    80767        T     A
                                AACACTGT CTGGCA GCT
                                |||||||| |||||| |||
                                TTGTGACA GGCTGT TGG
                                    _     G
GAM962  KIAA1464  3'  TAGGCTTTTGCAGCTGGAATGG 68275       TG _____    GGTTT
          GGTT                    CTGTTC  GC    AAGCT
                                |||||| ||    |||||
                                GGTAAG  CG    TTCGG
                                   GT  ACGTT    A   TT
GAM962  KIAA1500  3'  ATGCACACTTGTTAAATAGTGT 64116         C      C  _  TT
          T                      AACACTGTT TGGCAAG TG GT
                                ||||||||| ||||||| || ||
                                TTGTGATAA ATTGTTC AC CG
                                    _     _  A  TAG
GAM962  KIAA1554  3'  GGGCTGGCTTGCTGAA      95153     T      TG
                                TTC GGCAAGC  GTTT
                                ||| |||||||  ||||
                                AAG TCGTTCG  CGGG
                                  _      GT
GAM962  KIAA1577  5'  GCCACATCGGACAGTGTT    64479          ____
                                AACACTGTTC    TGGC
                                ||||||||||    ||||
                                TTGTGACAGG    ACCG
                                     CTAC
GAM962  KIAA1582  5'  AGTCAGTGGGGGCAGTG     65366         G  AA
                                CACTGTTCT GC  GCT
                                ||||||||| ||  |||
                                GTGACGGGG TG  TGA
                                     G  AC
GAM962  KIAA1796  5'  GGCTTCAGAGTGGGTT      91455     A TG     CA
                                AAC C  TTCTGG  AGCT
                                ||| |  ||||||  ||||
                                TTG G  GAGACT  TCGG
                                  _ GT     __
GAM962  KIAA1813  5'  AGACCAGCATTGGGCAGTGT   70286         TGGCAA
                                ACACTGTTC     GCTGGTTT
                                |||||||||     ||||||||
                                TGTGACGGG     CGACCAGA
                                     TTA___
GAM962  KIAA1879  5'  AGACCAGAAAAGATGGGGCGGG 73560     A       GCAAG_
          GTT                     AAC CTGTTCTG     CTGGTTT
                                ||| ||||||||     |||||||
                                TTG GGCGGGGT     GACCAGA
                                  G       AGAAAA
GAM962  KIAA1894  3'  AGCTATGGGGTAGTGTT     73841        TT   GCA
                                AACACTG  CTG   AGCT
                                |||||||  |||   ||||
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                                TTGTGAT  GGT   TCGA
                                    GG   A__
GAM962  KIAA1915  3'  AGCCTTTCAGGACATGTT    73273      C       CAA
                                AACA TGTTCTGG   GCT
                                |||| ||||||||   |||
                                TTGT ACAGGACT   CGA
                                  _       TTC
GAM962  KIAA1975  5'  AGGCTAGAAAAAGAACAGTG   73969         GGCAAG
                                CACTGTTCT     CTGGTTT
                                |||||||||     |||||||
                                GTGACAAGA     GATCGGA
                                     AAAA__
GAM962  KNSL6     3'  GGTCTGAGCTGGGACAGGTT   22426     A     TG  A_  _
                                AAC CTGTTC  GC  AG CT
                                ||| ||||||  ||  || ||
                                TTG GACAGG  CG  TC GG
                                  _     GT  AG  T
GAM962  L3MBTL    3'  GGGCTGGCTTGAGTGCATGTT  69529      C   TCTGG    TG
                                AACA TGT    CAAGC  GTTT
                                |||| |||    |||||  ||||
                                TTGT ACG    GTTCG  CGGG
                                  _  TGA__    GT
GAM962  LANCL2    3'  AAGTCAGTTTAAGATAAGTGTT 37991       GT   GGC     GT
                                AACACT  TCT   AAGCTG  TT
                                ||||||  |||   ||||||  ||
                                TTGTGA  AGA   TTTGAC  AA
                                   AT   A__     TG
GAM962  LHFP      3'  GGCTAGTAGAAACAGTGTT    19338         _  G A
                                AACACTGTT CTG C AGCT
                                ||||||||| ||| | ||||
                                TTGTGACAA GAT G TCGG
                                     A  _ A
GAM962  M9        5'  CGCCGTGCCGGGTCAGTGTT   61679       TT     AGC    TT
                                AACACTG  CTGGCA   TGGT
                                |||||||  ||||||   ||||
                                TTGTGAC  GGCCGT   GCCG
                                   TG     ___    CA
GAM962  MAP2K4    3'  ATGCAGCTACTGGAATGGTGTT 11545         TG CA    GTTT
                                AACACTGTTC  G  AGCTG
                                ||||||||||  |  |||||
                                TTGTGGTAAG  C  TCGAC
                                     GT A_    GTAG
GAM962  MDS018    3'  AAGCCAGGAGAGCAAGCAGTGT 41528        TCTG  AAG_
           T                     AACACTGT    GC    CTGGTTT
                                 ||||||||    ||    |||||||
                                 TTGTGACG    CG    GACCGAA
                                     AA__  AGAG
GAM962  MEIS3     3'  AAACCAGGCATGCTTAGAATAG 78274         _   A  _
           T                     ACTGTTCTG GCA GC TGGTTT
                                 ||||||||| ||| || ||||||
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                                TGATAAGAT CGT CG ACCAAA
                                     T   A  G
GAM962  MGC11386 3' AAATTAGCCTGATGTGGTGTT  51945      TG TCTGG  A
                                AACAC  T    CA GCTGGTTT
                                ||||| |    || ||||||||
                                TTGTG  G    GT CGATTAAA
                                   GT TA___  C
GAM962  MGC12992 5' AGTTCCAGGATGGT       50343         CA
                                ACTGTTCTGG  AGCT
                                ||||||||||  ||||
                                TGGTAGGACC  TTGA
                                     __
GAM962  MGC13168 3' AGCGGTCAGAACAGT       51208          AA
                                ACTGTTCTGGC  GCT
                                ||||||||||  |||
                                TGACAAGACTG  CGA
                                      G_
GAM962  MGC14141 3' GGCTCTCCCTGGGGTGGTGTT 51932      TG   __  CA
                                AACAC  TTCT  GG  AGCT
                                |||||  ||||  ||  ||||
                                TTGTG  GGGG  CC  TCGG
                                   GT    TC  TC
GAM962  MGC14421 5' GGTCGCCACCGGATAGTGTT   51874         __   AA
                                AACACTGTTC  TGGC  GCT
                                ||||||||||  ||||  |||
                                TTGTGATAGG  ACCG  TGG
                                      CC    C_
GAM962  MGC15482 5' GAGCTAGCGACGAGCAGTCGTT 51794     _      T GCAA
                                AAC ACTGTTC G    GCTGGTTT
                                ||| ||||||| |    ||||||||
                                TTG TGACGAG C    CGATCGAG
                                  C      _ AG__
GAM962  MGC1842  3' AGTCTGCTCAGGACAGTG    65643          _  AG
                                CACTGTTCTG GCA  CT
                                |||||||||| |||  ||
                                GTGACAGGAC CGT  GA
                                      T   CT
GAM962  MGC22688 5' GGCTTCGGGACATGTT      58756      C       CA
                                AACA TGTTCTGG  AGCT
                                |||| ||||||||  ||||
                                TTGT ACAGGGCT  TCGG
                                   _       __
GAM962  MGC2628  3' GGCCTGTTGGGGCGGGGTT   43977     A     TG   A
                                AAC CTGTTC  GCA GCT
                                ||| ||||||  ||| |||
                                TTG GGCGGG  TGT CGG
                                  G     GT   C
GAM962  MGC26954 3' GGCCACAGAAAGGTGTT     58838       G    GCAA
                                AACACT TTCTG    GCT
                                ||||||| |||||    |||
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                                TTGTGG AAGAC   CGG
                                   A    AC__
GAM962  MGC2742   5' CCGGCTTGGGACATTGTT   43745     C    TGG
                                AACA TGTTC  CAAGCTGG
                                |||| |||||  ||||||||
                                TTGT ACAGG  GTTCGGCC
                                  T    ___
GAM962  MGC27434  3' AAATTGGCTTCCGTTGGTGTT  58944       TTC  C   TG
                                AACACTG  TGG AAGC  GTTT
                                |||||||  ||| ||||  ||||
                                TTGTGGT  GCC TTCG  TAAA
                                   T__  _   GT
GAM962  MGC29956  3' CAGCTGCAGCAGTGTT     58278        CTG  A
                                AACACTGTT  GCA GCTG
                                |||||||||  ||| ||||
                                TTGTGACGA  CGT CGAC
                                     ___  _
GAM962  MGC5149   3' AGACCAGGAGGGCGTGGTGTT  72284      TG TCTG  AAG_
                                AACAC  T   GC   CTGGTTT
                                |||||  |   ||   |||||||
                                TTGTG  G   CG   GACCAGA
                                   GT _____  GGAG
GAM962  MGC9912   3' AAACTAGTTTCTATAGCTGTT  54711     CT  C  C
                                AACA  GTT TGG AAGCTGGTTT
                                ||||  ||| ||| ||||||||||
                                TTGT  CGA ATC TTTGATCAAA
                                  __  T  _
GAM962  MRF2      3' GGATTGGTGAAGGAACACTGTT 76523     C     GGCAA  TG
                                AACA TGTTCT    GC  GTTT
                                |||| ||||||    ||  ||||
                                TTGT ACAAGG    TG  TAGG
                                  C     AAG__  GT
GAM962  MRPS27    3' GGATTGGCTTCTCCATCGTGTT 30641      TGTTC  C_   TG
                                AACAC    TGG  AAGC  GTTT
                                |||||    |||  ||||  ||||
                                TTGTG    ACC  TTCG  TAGG
                                   CT___   TC   GT
GAM962  MSC       3' AGATCCGCGTCGGGACAGGGTT 76348     A        AA  T
                                AAC CTGTTCTGGC  GC GGTTT
                                ||| ||||||||||  || |||||
                                TTG GACAGGGCTG  CG CTAGA
                                  G         __ C
GAM962  MSP       3' AGCTGCTGGGGCGGGTT     49411     A     TG   A
                                AAC CTGTTC  GCA GCT
                                ||| ||||||  ||| |||
                                TTG GGCGGG  CGT CGA
                                  _     GT   _
GAM962  My015     3' AAATTAGCCAGGGGTGGTG   66651     TG   GGCAA
                                CAC  TTCT    GCTGGTTT
                                |||  ||||    ||||||||
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                                GTG  GGGG    CGATTAAA
                                  GT   AC___
GAM962  NDST3    5'  TACTGGGCCAGGACTGGTGTT  16550       _       AAG TG  TT
                                AACACT GTTCTGGC   C  GT
                                |||||| ||||||||   |  ||
                                TTGTGG CAGGACCG   G  CA
                                   T       ___ GT  TG
GAM962  NSE1     3'  GGCTAAGCCAGACAGTGTT    59075        T    A_
                                AACACTGT CTGGC  AGCT
                                |||||||| |||||  ||||
                                TTGTGACA GACCG  TCGG
                                     _    AA
GAM962  OSBPL2   3'  AGCTGGAAGCGATGGTGTT   29198         CTG  AAG TG
                                AACACTGTT   GC   C  GTT
                                |||||||||   ||   |  |||
                                TTGTGGTAG   CG   G  CGA
                                     ___  AA_ GT
GAM962  OSBPL2   3'  AGCTGGAAGCGATGGTGTT   57849         CTG  AAG TG
                                AACACTGTT   GC   C  GTT
                                |||||||||   ||   |  |||
                                TTGTGGTAG   CG   G  CGA
                                     ___  AA_ GT
GAM962  OSTF1    3'  AAACTTTGTCTTTGCCAGAAAA 24724     G       __  T_
           GTGTT                   ACT TTCTGGCAA  GC  GGTTT
                                |||  |||||||||  ||  |||||
                                TGA AAGACCGTT  TG  TCAAA
                                  A        TC  TT
GAM962  OTEX     3'  GAGCTAGTTTGGAGATGGGT   82004     GT   GG
                                ACT  TCT  CAAGCTGGTTT
                                |||  |||  ||||||||||
                                TGG  AGA  GTTTGATCGAG
                                  GT   G_
GAM962  p25      3'  AAACCAGGAGAGAGGGACAGGT 22841     A      GGCAAG
           T                     AAC CTGTTCT     CTGGTTT
                                |||  |||||||     |||||||
                                TTG GACAGGG     GACCAAA
                                  _      AGAGAG
GAM962  PAPOLG   5'  AGCCGGTTTTGTGGTGTT    43170       GTTCTG    _
                                AACACT     GCAAG CTGGTT
                                ||||||     ||||| ||||||
                                TTGTGG     TGTTT GGCCGA
                                     _______    T
GAM962  PCYT1B   3'  GTCACAGGGTTGCCTGGGTGGT 16749       TG   T    G  G  TT
           GTT                     AACAC  TTC GGCAA CT GT
                                |||||  ||| ||||| || ||
                                TTGTG  GGG CCGTT GG CA
                                   GT   T    G  A  CTGA
GAM962  PEX12    3'  GAGCTGGTTTCAGCATGGT    4297       T   CA   TG
                                ACTGT CTGG  AGC  GTTT
                                ||||| ||||  |||  ||||
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                                TGGTA GACT  TTG  CGAG
                                  C    __   GT
GAM962  PLA2G3   3'  ATCCAGGATTGGGGTGGGTGTT 31683      GT   GG   G_   TTT
                                AACACT  TCT  CAA  CTGG
                                ||||||  |||  |||  ||||
                                TTGTGG  GGG  GTT  GACC
                                   GT   __   AG    TAA
GAM962  PLAA     3'  AAGCCAGTTGGTAAGCTGTGTT 14914      T  TCTG  A
                                AACAC GT    GC AGCTGGTTT
                                ||||| ||    || |||||||||
                                TTGTG CG    TG TTGACCGAA
                                   T  AA__  G
GAM962  PLAC3    3'  AGTTGGCAGGGATACTGTT    69341     C     G  A
                                AACA TGTTCT GC AGCT
                                ||||| |||||| || ||||
                                TTGT ATAGGG CG TTGA
                                  C     A  G
GAM962  PLPL     3'  GGGCTGGATTCCTTTGGGAGCA 39432       ____  C  G TG
            GTGTT                  CTGTTCT    GG AA C  GTTT
                                |||||||    || || |  ||||
                                GACGAGG    CC TT G  CGGG
                                    GTTT  _  A GT
GAM962  POLE3    3'  AAATCAGCAGTGTGGAATGGT  33853        G  A_
                                ACTGTTCTG CA  GCTGGTTT
                                |||||||||  ||  ||||||||
                                TGGTAAGGT GT  CGACTAAA
                                     _  GA
GAM962  POPX1    3'  AGTTAGTTAGAAGCATGTT    29793     C   _    A
                                AACA TGTT CTGGC AGCT
                                |||| |||| ||||| ||||
                                TTGT ACGA GATTG TTGA
                                  _    A    A
GAM962  PPP1R1A  3'  AGCTTCAGGATGTGTT      22146      T     CA
                                AACAC GTTCTGG  AGCT
                                ||||| |||||||  ||||
                                TTGTG TAGGACT  TCGA
                                  _     ___
GAM962  PRO0971  3'  AGACTCAGATTTAGAATAGTGT 37702          CAAG  _
            T                   AACACTGTTCTGG    CTG GTTT
                                ||||||||||||    ||| ||||
                                TTGTGATAAGATT    GAC CAGA
                                       TA__   T
GAM962  PRO1728  5'  GAATTGGCTTGTATGGCAGT   37539      CTG     TG
                                ACTGTT   GCAAGC  GTTT
                                ||||||   ||||||  ||||
                                TGACGG   TGTTCG  TAAG
                                   TA_     GT
GAM962  PRO2032  5'  GAACCTGCCCTTGGAATATGTT 37780     C    TG CAA  T
                                AACA TGTTC  G   GC GGTTT
                                |||| |||||  |   || |||||
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                                TTGT ATAAG  T   CG CCAAG
                                  _     GT CC_  T
GAM962  PRO2955  5'  CTTTTAGAGCAGTGTT      37637           C
                                AACACTGTTCTGG AAG
                                |||||||||||| |||
                                TTGTGACGAGATT TTC
                                          _
GAM962  PTPN9    3'  GGACTAGCTTGGGTTGGTG    11079      TT  GG
                                CACTG  CT  CAAGCTGGTTT
                                |||||  ||  ||||||||||
                                GTGGT  GG  GTTCGATCAGG
                                  T_  __
GAM962  QSCN6    3'  GTTTGGCTTCAGGGTGGGGTT  11040     A TG     CA   TG TTT
                                AAC C  TTCTGG  AGC  G
                                ||| |  ||||||  |||  |
                                TTG G  GGGACT  TCG  T
                                  G GT      __   GT TGG
GAM962  RAB35    3'  AGTTCAACACCAGGATGTGTT  22475      T      CA___
                                AACAC GTTCTGG     AGCT
                                ||||| |||||||     ||||
                                TTGTG TAGGACC     TTGA
                                  _       ACAAC
GAM962  RAP140   3'  GTCAGTAATAGCAGTGTT    30846         ____
                                AACACTGTT    CTGGC
                                |||||||||    |||||
                                TTGTGACGA    GACTG
                                     TAAT
GAM962  RDC1     3'  GGCTCTGGGACGGGTT      72402     A     TG CA
                                AAC CTGTTC  G  AGCT
                                ||| ||||||  |  ||||
                                TTG GGCAGG  C  TCGG
                                  _     GT __
GAM962  RINZF    3'  AGGCTAGTTTGTACTAGTAGAG 43697     A   TTCTG
           TT                     AAC CTG     GCAAGCTGGTTT
                                ||| |||     ||||||||||||
                                TTG GAT     TGTTTGATCGGA
                                  A   GATCA
GAM962  RPL26L1  3'  AGATTTTGAGGCTAGGGTGTGT 32237      T TT     AAGCT
           T                      AACAC G  CTGGC     GGTTT
                                |||||  |  |||||     |||||
                                TTGTG T  GATCG     TTAGA
                                  _ GG     GAGTT
GAM962  RYK      3'  AAGCCAGTCCCTGGAGTACTGT 82611      C     TG CAA
           T                      AACA TGTTC  G   GCTGGTTT
                                ||||  |||||  |   ||||||||
                                TTGT ATGAG  C   TGACCGAA
                                  C     GT CC_
GAM962  RYK      3'  TTGACAAAGCAGTGTT      82622          C  G
                                AACACTGTT TG CAA
                                |||||||||  ||  |||
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                                TTGTGACGA AC GTT
                                     A  A
GAM962  SBBI31   3'  AAACTGAACCGGGGCGGTG   25874          CAAGCT
                                CACTGTTCTGG     GGTTT
                                ||||||||||      |||||
                                GTGGCGGGGCC     TCAAA
                                      AAG___
GAM962  SELM     3'  GGCCAGCAGGGATGGGGTT   54436     A      GGCAA
                                AAC CTGTTCT     GCTGGTT
                                ||| |||||||     |||||||
                                TTG GGTAGGG     CGACCGG
                                  G      A____
GAM962  SEMA4B   3'  AGGTTGGTGGAACAGTG     69035          G   G
                                CACTGTTCTG CAA CT
                                |||||||||| ||| ||
                                GTGACAAGGT GTT GA
                                      G   G
GAM962  SEMA4F   3'  GGGTGATTTGCTGGAATGGAGT 14944     A     TG     CTGGTTT
          T                      AAC CTGTTC  GCAAG
                                ||| ||||||  |||||
                                TTG GGTAAG  CGTTT
                                  A     GT     AGTGGG
GAM962  SH3BGRL2 3'  AGACCAGTCTCGAGTGGTG   48882     TG   T  CAA
                                CAC  TTC GG   GCTGGTTT
                                |||  ||| ||   ||||||||
                                GTG  GAG TC   TGACCAGA
                                  GT   C  ___
GAM962  SIAT4A   3'  AGACGTGCCAGGCGGTGTT   11666        T     AG_
                                AACACTGT CTGGCA   CT
                                |||||||| ||||||   ||
                                TTGTGGCG GACCGT   GA
                                     _     GCA
GAM962  SIMRP7   3'  GAGTCAGGTTTAGAATGGT   92366        GC  G   GT
                                ACTGTTCTG  AA CTG  TT
                                |||||||||  || |||  ||
                                TGGTAAGAT  TT GAC  AG
                                     __  G   TG
GAM962  SLC2A12  5'  GGTGGTCGGGGCGGT       59082          AA
                                ACTGTTCTGGC  GCT
                                ||||||||||  |||
                                TGGCGGGGCTG  TGG
                                      G_
GAM962  SLC38A4  5'  AGTTGGACAGAAGGAGGTGTT  35874       G__    GCA
                                AACACT   TTCTG   AGCT
                                ||||||   |||||   ||||
                                TTGTGG   AAGAC   TTGA
                                   AGG    AGG
GAM962  SLC38A4  3'  GGTTTTGCTAGAGCAGTGT   35875             _
                                ACACTGTTCTGGCAAG CT
                                |||||||||||||||| ||
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                                TGTGACGAGATCGTTT GG
                                        T
GAM962  SMC4L1   3'  GAGCCAGTAAATTAGGACAGTG 18528          CAA
           TT                  AACACTGTTCTGG  GCTGGTTT
                               ||||||||||||  ||||||||
                               TTGTGACAGGATT  TGACCGAG
                                     AAA
GAM962  SMCR5    3'  GAACTAGGCAGGTGAGGTGGTG 58594     TG T  G  AA  _
           TT                  AACAC  T CT GC  GC TGGTTT
                               |||||  | || ||  || ||||||
                               TTGTG  G GA TG  CG ATCAAG
                                 GT _  G  GA  G
GAM962  SNRPD1   3'  TATCAGTTATGAGCAGTGTT  22680        TGGCA     TT
                               AACACTGTTC    AGCTGGT
                               ||||||||||    |||||||
                               TTGTGACGAG    TTGACTA
                                     TA___     TT
GAM962  SNX10    3'  AAATCAGCTTCAACAAATGGT  25262      C  GC_
                               ACTGTT TG   AAGCTGGTTT
                               ||||||  ||  ||||||||||
                               TGGTAA AC   TTCGACTAAA
                                  _  AAC
GAM962  SSH2     3'  AGACTGAAATCCCAGAACATTG 62199     C      CAAGCT
           TT                  AACA TGTTCTGG     GGTTT
                               |||| ||||||||     |||||
                               TTGT ACAAGACC     TCAGA
                                 T       CTAAAG
GAM962  STK29    3'  AGGCCGCTGGGCTGGGATCAGT 87574      _  TG  A_  T
           GTT                   ACACTG TTC  GC  AGC GGTTT
                               ||||||| |||  ||  ||| |||||
                               TGTGAC AGG  CG  TCG CCGGA
                                  T  GT  GG  _
GAM962  SYNCOILIN 3'  GCCAGAGACTGGTGTT     47897       _ _
                               AACACT GT TCTGGC
                               |||||| || ||||||
                               TTGTGG CA AGACCG
                                  T  G
GAM962  TAF9L    3'  AAGTTTCATCTTAGGATAGTGT 32001          C___    GGTTT
           T                   ACACTGTTCTGG   AAGCT
                               ||||||||||||   |||||
                               TGTGATAGGATT   TTTGA
                                     CTAC    A  T
GAM962  TBC1D1   3'  AAACCGGCTTGCCAGCAAGT  64662    GTT
                               ACT  CTGGCAAGCTGGTTT
                               |||  ||||||||||||||
                               TGA  GACCGTTCGGCCAAA
                                 AC_
GAM962  TLK2     3'  AGGCTCAGCTGGGGATGGTGTT 22448          GGCA   _
                               AACACTGTTCT   AGCTG GTTT
                               ||||||||||   ||||| ||||
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                                TTGTGGTAGGG   TCGAC CGGA
                                      G___    T
GAM962  TLK2    3'  AGGCTCAGCTGGGGATGGTGTT 78197          GGCA   _
                                AACACTGTTCT   AGCTG GTTT
                                |||||||||||   ||||| ||||
                                TTGTGGTAGGG   TCGAC CGGA
                                      G___    T
GAM962  TLN2    3'  AACTGGACAGACAGTGTT    61684        T  GCAAG TG
                                AACACTGT CTG    C  GTT
                                |||||||| |||    |  |||
                                TTGTGACA GAC    G  CAA
                                     _  A____ GT
GAM962  TLN2    5'  GGACCCTCGCTGGGGCGGTGT  61688        TG  A  CT
                                ACACTGTTC  GC AG  GGTTT
                                |||||||||  || ||  |||||
                                TGTGGCGGG  CG TC  CCAGG
                                      GT  C  __
GAM962  TNFAIP3  5'  GGATCGCGGGGCCCGGAGAGGT 20825      G    _ AA_  T
            GTT                   ACACT TTCTGG C   GC GGTTT
                                |||||| ||||||  |   || |||||
                                TGTGG GAGGCC G   CG CTAGG
                                   A     C GGG  _
GAM962  TRIM29   3'  GGCCAGCTTGCAGGGGT    54222   TT  G
                                G  CT GCAAGCTGGTT
                                |  || ||||||||||
                                T  GG CGTTCGACCGG
                                 GG  A
GAM962  TRIM29   3'  GGCCAGCTTGCAGGGGT    23960   TT  G
                                G  CT GCAAGCTGGTT
                                |  || ||||||||||
                                T  GG CGTTCGACCGG
                                 GG  A
GAM962  TRIM35   3'  AGACTTATCAGGGCGGAGTT  60837    A      GC  _
                                AAC CTGTTCTG  AAG CT
                                ||| ||||||||  ||| ||
                                TTG GGCGGGAC  TTC GA
                                  A       TA   A
GAM962  TUSP    5'  GACTAGTGGTGTGGTGTT    39635      GTTCTG  A_
                                AACACT     GCA  GCTGGTT
                                ||||||     |||  |||||||
                                TTGTGG     TGT  TGATCAG
                                     _______  GG
GAM962  ULK2    3'  GGTTCATCAGAGCAGTGT    28005          CA
                                ACACTGTTCTGG  AGCT
                                ||||||||||||  ||||
                                TGTGACGAGACT  TTGG
                                       AC
GAM962  USP19   5'  GAACCGGAACGGAGAGCGGGTT 88957    A      GGCAAG
                                AAC CTGTTCT     CTGGTTT
                                ||| |||||||     |||||||
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                                TTG GGCGAGA     GGCCAAG
                                  _      GGCAA_
GAM962  VIAAT    3'  GGGCCAGCTTGCCTGCCGGT   54540      TTCT
                                ACTG    GGCAAGCTGGTTT
                                ||||    ||||||||||||
                                TGGC    CCGTTCGACCGGG
                                  CGT_
GAM962  VPS33B   3'  GAGCCGGGAGCATGGAACGTGT 37902       T     _  AAG
           T                     AACAC GTTCTG GC   CTGGTTT
                                 ||||| |||||| ||   |||||||
                                 TTGTG CAAGGT CG   GGCCGAG
                                   _     A  AG_
GAM962  WIT-1    3'  GGCTGCAGGGCAAGTGTT    31828       _     G  A
                                 AACACT GTTCTG CA GCT
                                 |||||| |||||| || |||
                                 TTGTGA CGGGAC GT CGG
                                    A     _ _
GAM962  WNT16    3'  GAATCTAAATCAGAATAGTG   32227          CAAGCT
                                 CACTGTTCTGG     GGTTT
                                 ||||||||||      |||||
                                 GTGATAAGACT     CTAAG
                                       AAAT__
GAM962  WNT16    3'  GAATCTAAATCAGAATAGTG   54072          CAAGCT
                                 CACTGTTCTGG     GGTTT
                                 ||||||||||      |||||
                                 GTGATAAGACT     CTAAG
                                       AAAT__
GAM962  YKT6     3'  AGCTTCTGCTGGGATGGTGT   21597         TG   __
                                 ACACTGTTC  GCA  AGCT
                                 |||||||||  |||  ||||
                                 TGTGGTAGG  CGT  TCGA
                                      GT   CT
GAM962  ZAK      3'  AGTAAAGCCTGAGCAGTGTT   56118         T   AA_
                                 AACACTGTTC GGC   GCT
                                 |||||||||| |||   |||
                                 TTGTGACGAG CCG   TGA
                                       T   AAA
GAM962  ZER6     3'  AGGCCAGTTCCAAAGAGTGTT  63375       G  C   CA
                                 AACACT TT TGG  AGCTGGTTT
                                 |||||| || |||  |||||||||
                                 TTGTGA AA ACC  TTGACCGGA
                                    G  _  ___
GAM962  ZNF185   3'  GGATTGGCATAGGCTAGTGTT  23115        TT   GCAA  TG
                                 AACACTG  CTG   GC  GTTT
                                 |||||||  |||   ||  ||||
                                 TTGTGAT  GAT   CG  TAGG
                                     CG   A___  GT
GAM962  LOC115123 3'  GAGTTAGTTTGTTTCTCAGT   73220      TTCT      GG
                                 ACTG   GGCAAGCT  TTT
                                 ||||   ||||||||  |||
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                                TGAC    TTGTTTGA  GAG
                                  TCT_       TT
GAM962   LOC118812 5'  GGGCCAATGCGGAGTGGCGTT  73932     A TG    G  AGC
                                AAC C  TTCTG CA   TGGTTT
                                ||| |  ||||| ||   ||||||
                                TTG G  GAGGC GT   ACCGGG
                                  C GT     _ A__
GAM962   LOC121274 3'  GGTTCTATTAAGGCAGTGTT   74063        TC   CA_
                                AACACTGT  TGG   AGCT
                                ||||||||  |||   ||||
                                TTGTGACG  ATT   TTGG
                                     GA   ATC
GAM962   LOC122553 3'  AAGTTGGTTTGTTAGACA    74129     T        GG
                                TGT CTGGCAAGCT  TTT
                                ||| ||||||||||  |||
                                ACA GATTGTTTGG  GAA
                                  _        TT
GAM962   LOC126282 3'  GAACTGGGGGAAGGGAAGTGTT 74474       G    GGCAAG TG
                                AACACT TTCT     C  GTTT
                                |||||| ||||     |  ||||
                                TTGTGA AGGG     G  CAAG
                                   _   AAGGG_ GT
GAM962   LOC130412 5'  AAGTTTGTGTCCAGGGCAGTGT 75739          ___     GGTTT
            T                    ACACTGTTCTGG   CAAGCT
                                ||||||||||||   ||||||
                                TGTGACGGGACC   GTTTGA
                                       TGT     A   T
GAM962   LOC132166 3'  TAAGCTGGTTTTATGAGTTGTG 75041     CT  _____   TG
            ACAGTGTT                GTT  GGC    AAGC  GTTT   A
                                |||  |||    ||||  ||||  |
                                CAG  TTG    TTTG  CGAA   T
                                  TG   AGTAT    GT
GAM962   LOC132241 3'  ATCAATGAACAGTGTT     75046         TGGCAAGC
                                AACACTGTTC       TGGT
                                ||||||||||       ||||
                                TTGTGACAAG       ACTA
                                     TA_______
GAM962   LOC134288 3'  TCTCCTCCGGAACAGT      75179         CA  CT
                                ACTGTTCTGG  AG  GG
                                ||||||||||  ||  ||
                                TGACAAGGCC  TC  CT
                                     __  CT
GAM962   LOC138389 5'  GAGTCGGTTTGCTAGTGACTGT 76227     T  _        GT
            G                    CAC GTT CTGGCAAGCTG  TT
                                ||| ||| ||||||||||  ||
                                GTG CAG GATCGTTTGGC  AG
                                  T  T         TG
GAM962   LOC138428 3'  GGACCAGTCCATTTCTGGAGTA 75337    A     TG C  ___
            GGTT                   C CTGTTC  G AA   GCTGGTTT
                                | ||||||  | ||   ||||||||
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                                G GATGAG  C TT   TGACCAGG
                                _     GT T  ACC
GAM962   LOC139410 5'  GAGCTGAATGTCGGGGTACTGT 75833     C  TT     ___    GGTTT
             T                   ACA TG  CTGGCA   AGCT
                                ||| ||  ||||||   ||||
                                TGT AT  GGCTGT   TCGA
                                  C  GG     AAG    G   T
GAM962   LOC142955 5'  AGATCAGCTGGCAGATGTGTT  76440      TGT    G  A
                                AACAC   TCTG CA GCTGGTTT
                                |||||   |||| || ||||||||
                                TTGTG   AGAC GT CGACTAGA
                                   T__    G  _
GAM962   LOC144319 5'  AAGCCACTGCATTTGGGGTG   83055     GTTCTG   A C
                                CACT     GCA G TGGTTT
                                ||||     ||| | ||||||
                                GTGG     CGT C ACCGAA
                                  GGTTTA  _ _
GAM962   LOC144395 3'  AAACCAGTTCTGAAGCAGT    76824       CT  CA
                                ACTGTT  GG  AGCTGGTTT
                                ||||||  ||  |||||||||
                                TGACGA  TC  TTGACCAAA
                                   AG  __
GAM962   LOC144453 3'  AGCTCTCAGGACAGCTGTT    76844      _       CA
                                AACA CTGTTCTGG  AGCT
                                |||| |||||||||  ||||
                                TTGT GACAGGACT  TCGA
                                  C        C_
GAM962   LOC144501 3'  TTTGCCAGGACATGTT      83113      C
                                AACA TGTTCTGGCAAG
                                |||| ||||||||||||
                                TTGT ACAGGACCGTTT
                                  _
GAM962   LOC144997 3'  AAACCAGCAAAGAGAGTAGGGT 83208     A      GGCAA
             T                   AAC CTGTTCT    GCTGGTTT
                                ||| |||||||    ||||||||
                                TTG GATGAGA    CGACCAAA
                                  G      GAAA_
GAM962   LOC145082 5'  GGGCCGTGGTGGGCCAGGATGG 83245          AA  __
             T                   ACTGTTCTGGC  GCT  GGTTT
                                ||||||||||  |||  |||||
                                TGGTAGGACCG  TGG  CCGGG
                                      GG   TG
GAM962   LOC145241 3'  GGCTATGGGGGCAGTGTT    62869          GG  _
                                AACACTGTTCT  CA AGCT
                                ||||||||||  || ||||
                                TTGTGACGGGG  GT TCGG
                                      __ A
GAM962   LOC145255 3'  GGCTTCCGGGATGCTGTT    83313      CT      C
                                AACA  GTTCTGG AAGCT
                                ||||  ||||||| |||||
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                                TTGT  TAGGGCC TTCGG
                                  CG      _
GAM962   LOC145438 5'  GGCTGGCCGGGGGCGGCTGTT  83343      _      _  A
                                AACA CTGTTCT GGC AGCT
                                |||| ||||||| ||| ||||
                                TTGT GGCGGGG CCG TCGG
                                  C      G   G
GAM962   LOC145608 5'  AGCCCGCCTGAGCAGTGTT    83380          T   AA
                                AACACTGTTC GGC  GCT
                                |||||||||| |||  |||
                                TTGTGACGAG CCG  CGA
                                      T   CC
GAM962   LOC145748 3'  AGGCCAGTGGGGGCGTTGGGAC 83461        TG  AA____
            GGT                   CTGTTC  GC     GCTGGTTT
                                ||||||  ||     ||||||||
                                GGCAGG  TG     TGACCGGA
                                   GT  CGGGGG
GAM962   LOC145814 3'  GAACTAGCTTCAGTTATGGT   77506       T_   CA
                                ACTGT  CTGG  AGCTGGTTT
                                |||||  ||||  |||||||||
                                TGGTA  GACT  TCGATCAAG
                                   TT   __
GAM962   LOC145815 5'  GGTGGCCAGACGGTGTT     83521         T    AA
                                AACACTGT CTGGC  GCT
                                |||||||| |||||  |||
                                TTGTGGCA GACCG  TGG
                                     _    G_
GAM962   LOC145842 5'  ATCAGCTTAGACACTGTT    77530      C   T   GCA    GT
                                AACA TGT CTG   AGCTG  T
                                |||| ||| |||   |||||  |
                                TTGT ACA GAT   TCGAC  A
                                  C   _  ___     TG
GAM962   LOC146315 5'  AAGCTGAGCACTGGAGTGGAGT 60884     A TG   TG CAA  _
            T                    AAC C  TTC  G   GCT GGTTT
                                ||| |  |||  |   ||| |||||
                                TTG G  GAG  C   CGA TCGAA
                                  A GT   GT A__   G
GAM962   LOC146515 3'  TTTGACTTAAACAGTGTT    77967         CT  _
                                AACACTGTT  GG CAAG
                                |||||||||  || ||||
                                TTGTGACAA  TC GTTT
                                     AT  A
GAM962   LOC146667 5'  AGTGTGAGTCAGGGTAGTGT   83701       TT    AA__
                                ACACTG  CTGGC    GCT
                                ||||||  |||||   |||
                                TGTGAT  GACTG    TGA
                                   GG    AGTG
GAM962   LOC147118 5'  GGCCTGCCAGGACGGTGTT   83952             A
                                AACACTGTTCTGGCA GCT
                                ||||||||||||||| |||
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                                TTGTGGCAGGACCGT CGG
                                       C
GAM962  LOC147276 3'  GGATTGAAATGGAGCAGTG   78339        GG__  G
                                CACTGTTCT   CAA CT
                                |||||||||   ||| ||
                                GTGACGAGG   GTT GG
                                     TAAA  A
GAM962  LOC148089 3'  GGCCCCGGGGCAGTGT     78636         CAA
                                ACACTGTTCTGG  GCT
                                ||||||||||||  |||
                                TGTGACGGGGCC  CGG
                                      C__
GAM962  LOC148936 5'  GGACTGTTGGGATGGTGT    84295        TG  AG
                                ACACTGTTC  GCA  CT
                                |||||||||  |||  ||
                                TGTGGTAGG  TGT  GG
                                     GT   CA
GAM962  LOC148938 5'  GGACTGTTGGGATGGTGT    84277        TG  AG
                                ACACTGTTC  GCA  CT
                                |||||||||  |||  ||
                                TGTGGTAGG  TGT  GG
                                     GT   CA
GAM962  LOC149073 5'  GGGCTAAAGGGCAGGCAGTGTT 84328        T  G AAGC
                                AACACTGT CTG C    TGGTTT
                                ||||||||| ||| |   ||||||
                                TTGTGACG GAC G    ATCGGG
                                     _  _ GGAA
GAM962  LOC149073 5'  GGTTAGTAGCAGAACAGGTT  84329     A      __  A
                                AAC CTGTTCTG  GC AGCT
                                ||| ||||||||  || ||||
                                TTG GACAAGAC  TG TTGG
                                  _       GA  A
GAM962  LOC149302 5'  GAGCTGCTGCTTGGTGGTAGTG 79269       TT  G    T__
           TT                    AACACTG  CTG CAAGC   GGTTT
                                |||||||  ||| |||||  |||||
                                TTGTGAT  GGT GTTCG   TCGAG
                                     __  G    TCG
GAM962  LOC149464 5'  AAATTAGCTGAGTGTGGTGTT  84424      TG T  GGCA
                                AACAC  T CT    AGCTGGTTT
                                |||||  | ||   |||||||||
                                TTGTG  G GA    TCGATTAAA
                                   GT T  G___
GAM962  LOC149935 3'  GGCTCCAGAAGGTGTT      60302       G     CA
                                AACACT TTCTGG  AGCT
                                ||||||| ||||||  ||||
                                TTGTGG AAGACC  TCGG
                                     _     __
GAM962  LOC150208 5'  AGACTCTGCCTAGAAACAGTGT 84913         _  _   AGCT
           T                     AACACTGTT CT GGCA    GGTTT
                                |||||||||  || ||||    |||||
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                                TTGTGACAA GA CCGT    TCAGA
                                     A  T    C___
GAM962   LOC150225 3'  GGCTGGGAGCACAGTGTT    85004        T  GG  A
                                AACACTGT CT  CA GCT
                                ||||||||  ||  ||  |||
                                TTGTGACA GA  GT CGG
                                    C  GG  _
GAM962   LOC150343 5'  GGTGAGCTGGGAGGTGTT    79677       G   TG  AA
                                AACACT TTC  GC  GCT
                                ||||||  |||  ||  |||
                                TTGTGG AGG  CG  TGG
                                   _  GT  AG
GAM962   LOC150776 3'  GGCTTCTGGAGCGGGGTT    63224     A     TG C
                                AAC CTGTTC  G AAGCT
                                |||  ||||||  |  |||||
                                TTG GGCGAG  C TTCGG
                                  G     GT _
GAM962   LOC151098 5'  GGACGCAGCTAAAGTAGTGTT  80115       TT  GGCA    _
                                AACACTG  CT    AGCTG GTTT
                                |||||||  ||    |||||  ||||
                                TTGTGAT  GA    TCGAC CAGG
                                   __  AA__     G
GAM962   LOC151248 3'  AAATTAGCCAGGGGTGGTG   80181     TG    GGCAA
                                CAC  TTCT    GCTGGTTT
                                |||  ||||    ||||||||
                                GTG  GGGG    CGATTAAA
                                  GT    AC___
GAM962   LOC151438 3'  GGCTGGCTGTAGCAGTGT    85367        CT   A
                                ACACTGTT  GGC AGCT
                                ||||||||  |||  ||||
                                TGTGACGA  TCG TCGG
                                    TG   G
GAM962   LOC152220 3'  AAATCAGTTTTTTGATAGTGT  85576        CTGGC
                                ACACTGTT    AAGCTGGTTT
                                ||||||||    ||||||||||
                                TGTGATAG    TTTGACTAAA
                                    TTT__
GAM962   LOC153514 3'  AGGTCAGTTTTAGAACATGTT  80852     C      GC     GT
                                AACA TGTTCTG  AAGCTG  TT
                                ||||  |||||||  ||||||  ||
                                TTGT ACAAGAT  TTTGAC  GA
                                  _      __      TG
GAM962   LOC153811 3'  AGCTCCTCTGGGGCATTGTT   80939     C     TG CA_
                                AACA TGTTC  G   AGCT
                                ||||  |||||  |   ||||
                                TTGT ACGGG  C   TCGA
                                  T    GT TCC
GAM962   LOC154043 3'  GGTTATTTGTGTGGGGTGGTGT 81029       TG    _    CTGGTTT
            T                    AACAC  TTCTG GCAAG
                                |||||  |||||  |||||
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                                TTGTG  GGGGT TGTTT
                                  GT    G    ATTGG
GAM962  LOC154184 3'  AGTTCCAGGATAGGTT     86178     A       CA
                                AAC CTGTTCTGG  AGCT
                                ||| |||||||||  ||||
                                TTG GATAGGACC  TTGA
                                  _       __
GAM962  LOC157773 5'  TCAGCTCCTGACGGGTT     81610     A    CT  CA
                                AAC CTGTT  GG  AGCTGG
                                ||| |||||  ||  ||||||
                                TTG GGCAG  CC  TCGACT
                                  _    T_ __
GAM962  LOC158314 3'  GGCTCCTTTCCTAGAACAGTGT 86770           C   CT    T
          T                     AACACTGTTCTGG AAG  GGTT
                                |||||||||||| |||  ||||
                                TTGTGACAAGATC TTT  TCGG
                                       C   CC
GAM962  LOC158835 3'  AGCTGTAACAGAATGGGTT    82007     A      GCA_
                                AAC CTGTTCTG    AGCT
                                ||| ||||||||    ||||
                                TTG GGTAAGAC    TCGA
                                  _       AATG
GAM962  LOC163132 5'  GGGCCGCGGCCCAGGATGGGTT 87180     A       CAA  T
                                AAC CTGTTCTGG   GC GGTTT
                                ||| |||||||||   || |||||
                                TTG GGTAGGACC   CG CCGGG
                                  _       CGG  _
GAM962  LOC164386 5'  AACTGGCTGATGAAGTGTT    87207       GT  TGG  A  TG
                                AACACT  TC   CA GC  GTT
                                ||||||  ||   || ||  |||
                                TTGTGA  AG   GT CG  CAA
                                   __  TA_  _  GT
GAM962  LOC196527 3'  GGCTTCACTGGGATGCTGTT   87757     CT    TG C_
                                AACA  GTTC  G  AAGCT
                                ||||  ||||  |  |||||
                                TTGT  TAGG  C  TTCGG
                                  CG    GT AC
GAM962  LOC196812 3'  GGTTGGTGGGAACAGAGTT    89573     A     G  A
                                AAC CTGTTCT GC AGCT
                                ||| ||||||| || ||||
                                TTG GACAAGG TG TTGG
                                  A      G  G
GAM962  LOC199883 3'  GGCTGGTTCTGGACAGT     89871        T_  A
                                ACTGTTC  GGC AGCT
                                |||||||  ||| ||||
                                TGACAGG  TTG TCGG
                                    TC   G
GAM962  LOC200420 5'  AAATTGGAAGAGGACAGTG    59247          GGCAAG TG
                                CACTGTTCT     C  GTTT
                                |||||||||     |  ||||
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                                GTGACAGGA     G  TAAA
                                     GAA___ GT
GAM962   LOC200583 3'  AGACCAGCTTCTTCACAGGTT  88832     A    TCT  C
                                AAC CTGT   GG AAGCTGGTTT
                                ||| ||||   || ||||||||||
                                TTG GACA   TC TTCGACCAGA
                                  _    CT_  _
GAM962   LOC200689 5'  GGCTAAGCCAGACAGTGTT    90109        T     A_
                                AACACTGT CTGGC  AGCT
                                |||||||| |||||  ||||
                                TTGTGACA GACCG  TCGG
                                     _     AA
GAM962   LOC202052 3'  ATTTAGCCTTTGGAACATGTT  90306     C     TG CAA     TTT
                                AACA TGTTC  G   GCTGG
                                |||| |||||  |   |||||
                                TTGT ACAAG  T   CGATT
                                  _     GT TC_     TAG
GAM962   LOC203052 3'  GGCTGGCTTGAACTGGTGTT   90456       _   T   A
                                AACACT GTTC GGC AGCT
                                |||||| |||| ||| ||||
                                TTGTGG CAAG TCG TCGG
                                   T    T   G
GAM962   LOC203276 3'  CAGGCCAGGACAGTG       90478          AAG
                                CACTGTTCTGGC   CTG
                                ||||||||||||   |||
                                GTGACAGGACCG   GAC
                                       ___
GAM962   LOC203305 3'  CAGGCCAGGACAGTG       90522          AAG
                                CACTGTTCTGGC   CTG
                                ||||||||||||   |||
                                GTGACAGGACCG   GAC
                                       ___
GAM962   LOC203378 5'  AAGCCAGCTTACATGAGTGTT  90588       GTTC  GC
                                AACACT    TG  AAGCTGGTTT
                                ||||||    ||  ||||||||||
                                TTGTGA    AC  TTCGACCGAA
                                   GT__  A_
GAM962   LOC203414 3'  AGGCCAGCTTTCAAAAATGGT  89355       C_   C
                                ACTGTT  TGG AAGCTGGTTT
                                ||||||  ||| ||||||||||
                                TGGTAA  ACT TTCGACCGGA
                                   AA   _
GAM962   LOC204285 3'  TCACCCACAGCCAGGGCAGGTT 89460     A         AAGCT   TT
                                AAC CTGTTCTGGC     GGT
                                ||| ||||||||||     |||
                                TTG GACGGGACCG     CCA
                                  _         ACAC_   CTG
GAM962   LOC206078 5'  AGCTCCAGGGCATTGTT     90711      C       CA
                                AACA TGTTCTGG  AGCT
                                |||| ||||||||  ||||
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                                TTGT ACGGGACC  TCGA
                                  T      __
GAM962  LOC219513 5'  AAGCCGGAAGAGACTGGAACAG 94322        TG CAAG__
                T                  ACTGTTC  G     CTGGTTT
                                   |||||||  |     |||||||
                                   TGACAAG  C     GGCCGAA
                                      GT AGAGAA
GAM962  LOC219667 3'  GAACTAGCTTTAAAACGGGGTT 91312     A    C  GC
                                   AAC CTGTT TG  AAGCTGGTTT
                                   ||| ||||| ||  ||||||||||
                                   TTG GGCAA AT  TTCGATCAAG
                                     G    A __
GAM962  LOC219744 5'  ATTCAGACCCAGCACAGTGTT  91356        T   CAAG   TTT
                                   AACACTGT CTGG    CTGG
                                   |||||||| ||||    ||||
                                   TTGTGACA GACC    GACT
                                        C    CA__    TAA
GAM962  LOC220846 3'  GGCTGGCTGTGGCAGGTT    90818     A   TC   A
                                   AAC CTGT  TGGC AGCT
                                   ||| ||||  |||| ||||
                                   TTG GACG  GTCG TCGG
                                     _   GT    G
GAM962  LOC221272 3'  GGCTGACAGAGCAGGTT     93607     A      GCA
                                   AAC CTGTTCTG   AGCT
                                   ||| ||||||||   ||||
                                   TTG GACGAGAC   TCGG
                                     _       AG_
GAM962  LOC221416 3'  GGCTCCCTCAGGACAGCGTT   93769     A      _ CA
                                   AAC CTGTTCTG G  AGCT
                                   ||| ||||||||  |  ||||
                                   TTG GACAGGAC C  TCGG
                                     C       T CC
GAM962  LOC221486 5'  GGCAGCCGGGACAGTGTT     91014           AA
                                   AACACTGTTCTGGC  GCT
                                   ||||||||||||||  |||
                                   TTGTGACAGGGCCG  CGG
                                            A_
GAM962  LOC221496 3'  GGTGGGGCAGGGATGGTGTT   92002          G  AA_
                                   AACACTGTTCT GC   GCT
                                   ||||||||||| ||   |||
                                   TTGTGGTAGGG CG   TGG
                                         A  GGG
GAM962  LOC221543 5'  AGATTGGTTTGATCAGGTGTT  93734      TGTT   _    TG
                                   AACAC    CTGG CAAGC  GTTT
                                   |||||    |||| |||||  ||||
                                   TTGTG    GACT GTTTG  TAGA
                                      _____    A     GT
GAM962  LOC221576 3'  AGATTTCTATAGCAGTGTT    93702         C   C   _
                                   AACACTGTT TGG AAG CT
                                   ||||||||| ||| ||| ||
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                                TTGTGACGA ATC TTT GA
                                     T  _  A
GAM962  LOC221583 5'  GAGCTGCTGGTGCTGGAGCAGT 92144       TG  __  T
                                ACTGTTC  GCA  AGC GGTTT
                                |||||||  |||  ||| |||||
                                TGACGAG  CGT  TCG TCGAG
                                   GT   GG  _
GAM962  LOC221601 3'  AGTTCCAGGATAGGTT     93646     A       CA
                                AAC CTGTTCTGG  AGCT
                                ||| |||||||||  ||||
                                TTG GATAGGACC  TTGA
                                  _       __
GAM962  LOC222057 5'  AAACTGGCTGGGCAACATGTT  92762     C   CTG  A_  TG
                                AACA TGTT   GC  AGC  GTTT
                                |||| ||||   ||  |||  ||||
                                TTGT ACAA   CG  TCG  CAAA
                                  _   ___  GG   GT
GAM962  LOC222256 3'  AAATTAGCTTGGTGTGGTG   94259     TG TCT G
                                CAC  T   G CAAGCTGGTTT
                                |||  |   | ||||||||||
                                GTG  G   T GTTCGATTAAA
                                  GT ___ G
GAM962  LOC245727 5'  AGCTGCGGGGCAGGTGTT    91121      _     G  A
                                AACAC TGTTCTG CA GCT
                                ||||| ||||||| || |||
                                TTGTG ACGGGGC GT CGA
                                   G     _ _
GAM962  LOC253148 3'  AGGCCGTGTGCGGGTCGGTGTT 96872       TT  G   A  T
                                AACACTG  CT GCA GC GGTTT
                                |||||||  || ||| || |||||
                                TTGTGGC  GG CGT TG CCGGA
                                   T_  G   G  _
GAM962  LOC253392 5'  GGCTTGGGATGGTGTT      96450         TGG
                                AACACTGTTC   CAAGCT
                                ||||||||||   ||||||
                                TTGTGGTAGG   GTTCGG
                                      ___
GAM962  LOC253782 3'  GGTTAGTCAGAATGCTGTT   95698     CT      A
                                AACA  GTTCTGGC AGCT
                                ||||  |||||||| ||||
                                TTGT  TAAGACTG TTGG
                                  CG       A
GAM962  LOC254014 3'  GGCCCTCCAGAATGGAGTT   95206     A       CAA
                                AAC CTGTTCTGG   GCT
                                ||| |||||||||   |||
                                TTG GGTAAGACC   CGG
                                  A        TCC
GAM962  LOC254243 3'  CAGGCCAGGACAGTG       97407          AAG
                                CACTGTTCTGGC   CTG
                                ||||||||||||   |||
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                                GTGACAGGACCG   GAC
                                    ___
GAM962   LOC254387 3'  GGGCCAGGGGCAGCCAGGGCAG 94910    A        AAG__
            AGTT                    AC CTGTTCTGGC    CTGGTTT
                                || ||||||||||    |||||||
                                TG GACGGGACCG    GACCGGG
                                 A         ACGGG
GAM962   LOC254531 5'  GGGCCGGCTGAAGGTGGCGTT  94988    A TG T  GGCA
                                AAC C  T CT    AGCTGGTTT
                                ||| |  | ||    |||||||||
                                TTG G  G GA    TCGGCCGGG
                                  C GT _  AG__
GAM962   LOC254659 5'  AGCTCACCAGAACAGAGTT    95110    A        CA
                                AAC CTGTTCTGG  AGCT
                                ||| |||||||||  ||||
                                TTG GACAAGACC  TCGA
                                  A        AC
GAM962   LOC254700 5'  GATTGGTCCAGAACAGT     96221          CAA  TG
                                ACTGTTCTGG   GC  GTT
                                ||||||||||   ||  |||
                                TGACAAGACC   TG  TAG
                                      ___  GT
GAM962   LOC255057 3'  GGCTGGGGCAGAGCAGGGTT   95352    A       GCA_
                                AAC CTGTTCTG    AGCT
                                ||| ||||||||    ||||
                                TTG GACGAGAC    TCGG
                                  G       GGGG
GAM962   LOC255486 3'  GGCGCCGGGGCAGTGT      95207           AA
                                ACACTGTTCTGGC  GCT
                                ||||||||||||  |||
                                TGTGACGGGGCCG  CGG
                                      __
GAM962   LOC255533 5'  TATTAGAGTTAGGGTAGT    96981      TT    AAG    TT
                                ACTG  CTGGC   CTGGT
                                ||||  |||||   |||||
                                TGAT  GATTG   GATTA
                                   GG    A__    TA
GAM962   LOC255649 3'  AAACCAGTTTCATCAATACTGT 96454      C    CTGGC
            T                    AACA TGTT    AAGCTGGTTT
                                ||||| ||||    ||||||||||
                                TTGT ATAA    TTTGACCAAA
                                  C    CTAC_
GAM962   LOC256113 5'  AGATCAAGATGTAAGCAGTGTT 96768        TCTG   AGC
                                AACACTGT    GCA   TGGTTT
                                ||||||||    |||   ||||||
                                TTGTGACG    TGT   ACTAGA
                                     AA__   AGA
GAM962   LOC256730 3'  GGCTTAGTCCAGAGTGGGTT   95232     A TG     _ _
                                AAC C  TTCTGG C AAGCT
                                ||| |  |||||| | |||||
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                                TTG G  GAGACC G TTCGG
                                  _ GT     T A
GAM962   LOC256789 3'  GGCCTTCCATGGGGCAGTGTT  97448          __ CAA
                                AACACTGTTCT  GG   GCT
                                ||||||||||  ||   |||
                                TTGTGACGGGG  CC   CGG
                                      TA  TTC
GAM962   LOC257000 3'  GACCCTCAGGGCAGTGT     96783           CAAGCT
                                ACACTGTTCTGG     GGTT
                                ||||||||||||     ||||
                                TGTGACGGGACT     CCAG
                                       C_____
GAM962   LOC257041 5'  GGCTGGCAGAGCGGT       97494         G  A
                                ACTGTTCTG CA GCT
                                ||||||||| || |||
                                TGGCGAGAC GT CGG
                                     G  _
GAM962   LOC257153 5'  GAATGGGCTGAGAGTGGTGTT  95768      TG   GGCA   G
                                AACAC  TTCT   AGCT GTTT
                                |||||  ||||   |||| ||||
                                TTGTG  GAGA   TCGG TAAG
                                   GT   G___   G
GAM962   LOC257319 3'  AGTTGGTGGGACACTGTT    95773      C      G  G
                                AACA TGTTCTG CAA CT
                                |||| ||||||| ||| ||
                                TTGT ACAGGGT GTT GA
                                  C      G  _
GAM962   LOC257354 3'  GAACTGGCCTGTGGGTGGTGT  95089      TG  TG  A  TG
                                ACAC  TTC  GCA GC  GTTT
                                ||||  |||  ||| ||  ||||
                                TGTG  GGG  TGT CG  CAAG
                                  GT   __   C  GT
GAM962   LOC257415 3'  GAGCTGGCTACCAGCAGT    96076      TT   CA   TG
                                ACTG  CTGG  AGC  GTTT
                                ||||  ||||  |||  ||||
                                TGAC  GACC  TCG  CGAG
                                  __   A_   GT
GAM962   LOC257463 5'  GGACTGGTTTGTACAGATATGT 71070      CTGT   _     TG
           T                     AACA   TCTG GCAAGC  GTTT
                                ||||   |||| ||||||  ||||
                                TTGT   AGAC TGTTTG  CAGG
                                  AT__   A     GT
GAM962   LOC257465 3'  AGATTGGGTGCATTTGGAGTGG 81590   A TG    ___   AG TG
           CGTT                   C C  TTCTG   GCA  C  GTTT
                                | |  |||||   |||  |  ||||
                                G G  GAGGT   CGT  G  TAGA
                                 C GT    TTA   G_ GT
GAM962   LOC257468 3'  AAACCGGCATGCTTAGAATAGT 95181         _  A
                                ACTGTTCTG GCA GCTGGTTT
                                ||||||||| ||| ||||||||
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                                TGATAAGAT CGT CGGCCAAA
                                     T   A
GAM962  LOC257515 3'  AGATTTCTATAGCAGTGTT   97782        C   C   _
                                AACACTGTT TGG AAG CT
                                ||||||||| ||| ||| ||
                                TTGTGACGA ATC TTT GA
                                     T   _   A
GAM962  LOC257572 3'  AGATTTCTATAGCAGTGTT   97911        C   C   _
                                AACACTGTT TGG AAG CT
                                ||||||||| ||| ||| ||
                                TTGTGACGA ATC TTT GA
                                     T   _   A
GAM962  LOC257596 5'  AGATTGGTTTGATCAGGTGTT  97927      TGTT   _    TG
                                AACAC   CTGG CAAGC  GTTT
                                |||||   |||| |||||  ||||
                                TTGTG   GACT GTTTG  TAGA
                                  _____   A    GT
GAM962  LOC51001  5'  GACCAGCAAGAACACTGTT   31951     C     GGCAA
                                AACA TGTTCT    GCTGGTT
                                |||| ||||||    |||||||
                                TTGT ACAAGA    CGACCAG
                                  C     A_____
GAM962  LOC51157  5'  TGATTGTCTGCTGGGGTGGGTT 32492    A TG   TG   AG T   T
                                AAC C  TTC  GCA  C GGTT
                                ||| |  |||  |||  | ||||
                                TTG G  GGG  CGT  G TTAG
                                  _ GT   GT   CT _   TT
GAM962  LOC51301  3'  AAACCACCCATTTCAGAGTAGT 33436          CAAGC_
           GTT                    AACACTGTTCTGG     TGGTTT
                                ||||||||||||     ||||||
                                TTGTGATGAGACT     ACCAAA
                                      TTACCC
GAM962  LOC51315  5'  TGTCTGTGGAGTAGTGTT    33532         ___
                                AACACTGTTCT   GGCA
                                ||||||||||   ||||
                                TTGTGATGAGG   CTGT
                                      TGT
GAM962  LOC51339  3'  AGTCTTCAGGGCAGTGT     33596          CAA
                                ACACTGTTCTGG   GCT
                                ||||||||||||   |||
                                TGTGACGGGACT   TGA
                                      TC_
GAM962  LOC51652  3'  AATCATACAGAATAGGTT    32187     A      GCAAGC
                                AAC CTGTTCTG     TGGTT
                                ||| ||||||||     |||||
                                TTG GATAAGAC     ACTAA
                                  _       AT_____
GAM962  LOC56181  5'  AGATTGGCATGAGCTGGTGTT  95531       _   _ G   G
                                AACACT GTTC TG CAA CT
                                |||||| |||| || ||| ||
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                                TTGTGG CGAG AC GTT GA
                                   T   T G   A
GAM962  LOC56959  5' AGCTGTCTATCAAACAGTGTT  81924        CT___   A
                                AACACTGTT    GGCA GCT
                                |||||||||    |||| |||
                                TTGTGACAA    CTGT CGA
                                     ACTAT   _
GAM962  LOC63904  5' AACTAGCTTGGTAAGTGTT   41974      GTTC  G
                                AACACT   TG CAAGCTGGTT
                                ||||||   || ||||||||||
                                TTGTGA   AT GTTCGATCAA
                                   ____  G
GAM962  LOC84524  3' AGACTGGTGATTTGGAGTAGT  50668       TG CAA  TG
                                ACTGTTC  G   GC  GTTT
                                |||||||  |   ||  ||||
                                TGATGAG  T   TG  CAGA
                                    GT TAG  GT
GAM962  LOC89890  3' TTGCTAGATAGTGTT      60580        T
                                AACACTGT CTGGCAA
                                |||||||| |||||||
                                TTGTGATA GATCGTT
                                   _
GAM962  LOC90038  3' CAGGCCAGGACAGTG      61151          AAG
                                CACTGTTCTGGC   CTG
                                ||||||||||||   |||
                                GTGACAGGACCG   GAC
                                   ___
GAM962  LOC90393  3' GAATCACTGTTGGGGCAGTGT  62622        TG   A C
                                ACACTGTTC  GCA G TGGTTT
                                |||||||||  ||| | ||||||
                                TGTGACGGG  TGT C ACTAAG
                                     GT  _ _
GAM962  LOC90494  5' AAGCTATAAAGGGTTATAGTGG 63049     TG  C    AAGC__
           TGTT                   ACAC  TT TGGC     TGGTTT
                                ||||  || ||||     ||||||
                                TGTG  GA ATTG     ATCGAA
                                  GT  T    GGAAAT
GAM962  LOC90538  3' AGGCTGGTGATGGAGCAGTGT  63186          GCAA  TG
                                ACACTGTTCTG    GC  GTTT
                                ||||||||||    ||  ||||
                                TGTGACGAGGT    TG  CGGA
                                     AG__  GT
GAM962  LOC90906  3' GGATTGATGGGACAGGGTT   64305     A      GG   G
                                AAC CTGTTCT  CAA CT
                                ||| |||||||  ||| ||
                                TTG GACAGGG  GTT GG
                                  G      TA   A
GAM962  LOC92080  5' AAACTGGTTTGAGCTTTTAGAG 68036     A   TTCTGG    TG
           TT                    AAC CTG     CAAGC  GTTT
                                ||| |||     |||||  ||||
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                                TTG GAT     GTTTG  CAAA
                                  A   TTTCGA    GT
GAM962  LOC92283  3'  AGACTTTTAGACAGTGTT    68743        T    C  _
                                AACACTGT CTGG AAG CT
                                |||||||| |||| ||| ||
                                TTGTGACA GATT TTC GA
                                    _   _  A
GAM962  LOC92340  3'  GGGCCAGGTGGGAACAGTGT   68997         G  AAG
                                ACACTGTTCT GC   CTGGTTT
                                |||||||||| ||   |||||||
                                TGTGACAAGG TG   GACCGGG
                                     G  ___
GAM962  LOC92345  5'  AGTTGGGCCCAGGCAGTGTT   56421         CT   A_
                                AACACTGTT  GGC  AGCT
                                |||||||||  |||  ||||
                                TTGTGACGG  CCG  TTGA
                                     AC   GG
GAM962  LOC93333  5'  GCAGTTAAAGCAGTGTT     72066         C    AA
                                AACACTGTT TGGC  GC
                                |||||||||  ||||  ||
                                TTGTGACGA ATTG  CG
                                     A    A_
GAM962  LOC93538  3'  AATCAGCAAAGGCAGTGTT    72558         T  GGCAA
                                AACACTGT CT    GCTGGTT
                                |||||||| ||    |||||||
                                TTGTGACG GA    CGACTAA
                                    _  AA___
GAM962  LOC93538  5'  GAGCCGAGGCAGGACAGTGT   72561          G AAGC
                                ACACTGTTCTG C    TGGTTT
                                |||||||||||  |    ||||||
                                TGTGACAGGAC G    GCCGAG
                                     _ GA__
GAM963  FLJ22672  3'  AACCAGGCCGAGAGGCCAC    46066       ___
                                GTGGTC   CGGCCTGGTT
                                ||||||   ||||||||||
                                CACCGG   GCCGGACCAA
                                   AGA
GAM963  RBT1      3'  AACCAGGCCGGACCACGTGCAA 25348
          TA                    TATTGCACGTGGTCCGGCCTGGTT
                                ||||||||||||||||||||||||
                                ATAACGTGCACCAGGCCGGACCAA

GAM964  ABCC12    5'  TCCCAACCAAAACCACAC     52648       ATGG
                                GTGTGG   TTGGTTGGGA
                                ||||||   ||||||||||
                                CACACC   AACCAACCCT
                                   AA__
GAM964  CYP1A2    3'  CCCAAGTTATCCACCTGC     69105     T     GG TGG
                                GCAG GTGGAT  T   TTGGG
                                |||| ||||||  |   |||||
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                                CGTC CACCTA  G   AACCC
                                  _     TT ____
GAM964  CYP1A2   3'  CCCAAGTTATCCACCTGC    5685      T     GG TGG
                                GCAG GTGGAT  T   TTGGG
                                |||| ||||||  |   |||||
                                CGTC CACCTA  G   AACCC
                                  _     TT ____
GAM964  EFNB1    3'  CCACCTCCACACTGC      15395          T   T
                                GCAGTGTGGA GGT GG
                                |||||||||| ||| ||
                                CGTCACACCT CCA CC
                                      _  _
GAM964  HRC      5'  CCCAACGTTTGTCCACATTGC  9279          TG TTG
                                GCAGTGTGGA  G   GTTGGG
                                ||||||||||  |   ||||||
                                CGTTACACCT  T   CAACCC
                                      GT TG_
GAM964  MAFF     3'  CCCAACACTGTCCACACTGC   24644           TG
                                GCAGTGTGGATGGT  GTTGGG
                                ||||||||||||||  ||||||
                                CGTCACACCTGTCA  CAACCC
                                      __
GAM964  ODF2     5'  TCCCAAGTTTTCATCCAACTGC 10327       G      TTGG
                                GCAGT TGGATGG    TTGGGA
                                ||||| |||||||    ||||||
                                CGTCA ACCTACT    AACCCT
                                  _      TTTG
GAM964  PODXL    3'  TCCATTTGCACCATGCCACACT 18238          _    TGGT_
           GCT                    AGCAGTGTGG ATGGT    TGGG
                                ||||||||||  |||||    ||||
                                TCGTCACACC TACCA    ACCT
                                      G    CGTTT
GAM964  ARSDR1   3'  TCCCAACCAACCAGTCTTCACT 32076      T  _
                                AGTG GGA TGGTTGGTTGGGA
                                |||| ||| ||||||||||||
                                TCAC TCT ACCAACCAACCCT
                                  T  G
GAM964  CBARA1   3'  TCAGGGAACCATCCACAC    20293          GG
                                GTGTGGATGGTT  TTGG
                                ||||||||||||  ||||
                                CACACCTACCAA  GACT
                                      GG
GAM964  CYP2S1   3'  CCCAACCACTTGTCCACACAGC 47613     A      TG T
           T                    AGC GTGTGGA  G TGGTTGGG
                                ||| |||||||  | ||||||||
                                TCG CACACCT  T ACCAACCC
                                  A      GT C
GAM964  DKFZP434J193 3'  CCCAACCAGGGCACCCAC    71003      A  G _
                                GTGG TG T TGGTTGGG
                                |||| || | ||||||||
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                                CACC AC G ACCAACCC
                                  C  G G
GAM964  DKFZP566G1424 5'  CCCATCCAGCCACACCAC    84781      A_      T
                                GTGG  TGGTTGG TGGG
                                ||||  ||||||| ||||
                                CACC  ACCGACC ACCC
                                  AC      T
GAM964  GAL3ST-4  3'  CCCAAGGCAGATCCACAT    44935        G_  GG
                                GTGTGGAT  GTT  TTGGG
                                ||||||||  |||  |||||
                                TACACCTA  CGG  AACCC
                                    GA  __
GAM964  KIAA1280  5'  CAAACAACCATCCACACTGC   69711             G
                                GCAGTGTGGATGGTTG TTG
                                |||||||||||||||| |||
                                CGTCACACCTACCAAC AAC
                                          A
GAM964  KIAA1957  3'  CCCTTTGCCCCTCCACACTGC  75716         T  TT   T__
                                GCAGTGTGGA GG  GGT   GGG
                                |||||||||| ||  |||   |||
                                CGTCACACCT CC  CCG   CCC
                                      _ __   TTT
GAM964  PARD6A    3'  CCCATGCCACTCCACACTGCT  33769          _    TGGT
                                AGCAGTGTGGA TGGT    TGGG
                                |||||||||| ||||    ||||
                                TCGTCACACCT ACCG    ACCC
                                      C    T___
GAM964  PRKRI     5'  CCCAGCTCACCCACCCAC    20755      A   T  _
                                GTGG TGG TG GTTGGG
                                |||| ||| || ||||||
                                CACC ACC AC CGACCC
                                  C   C  T
GAM964  SDC3      3'  CCCAAATACACCCACACTCT   27744    C      A  GTTGG
                                AG AGTGTGG TG    TTGGG
                                || ||||||| ||    |||||
                                TC TCACACC AC    AACCC
                                 _      C  ATA__
GAM964  WIT-1     5'  CCCAACGGATCCACATGC    31822     G     TGG  G
                                GCA TGTGGA   TT GTTGGG
                                ||| ||||||   || ||||||
                                CGT ACACCT   AG CAACCC
                                  _     ___  G
GAM964  LOC148753 3'  CCCGCACACACACCCACACTGC 84215          A  GT  GT
          T                      AGCAGTGTGG TG  TG  TGGG
                                ||||||||||  ||  ||  ||||
                                TCGTCACACC AC  AC  GCCC
                                      C  AC  AC
GAM964  LOC149345 3'  CCCAATATCCACTCTAC     79306       _   TTG
                                GTGGA TGG   GTTGGG
                                ||||| |||   ||||||
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                                CATCT ACC   TAACCC
                                  C   TA_
GAM964  LOC200597 3'  TCCCAACCCCACCCCAC     88844     T  A   TT
                                GTG GG TGG  GGTTGGGA
                                ||| || |||  ||||||||
                                CAC CC ACC  CCAACCCT
                                  _ C   __
GAM964  LOC255990 5'  CCCAACCAACCAGAGC      96235    GGA
                                GT   TGGTTGGTTGGG
                                ||   ||||||||||||
                                CG   ACCAACCAACCC
                                 AG_
GAM964  LOC93259  5'  CCCGTAGCCACCACCACACTGC 71811          A    T   __
           T                     AGCAGTGTGG TGGT GGT  TGGG
                                ||||||||||| |||| |||  ||||
                                TCGTCACACC ACCA CCG  GCCC
                                      _   _  AT
GAM965  ARHGEF6   3'  CAAACTTGAAGCCAGGC     68197       ACCA
                                GCCTGG    CAAGTTTG
                                ||||||    ||||||||
                                CGGACC    GTTCAAAC
                                   GAA_
GAM965  CNTN2     3'  GTCACAACCCAGGTGA      17411        ACCACAA   _
                                TCGCCTGG      GTT TGAC
                                ||||||||      ||| ||||
                                AGTGGACC      CAA ACTG
                                     ________  C
GAM965  CORO2A    3'  AAACTGTGGTCCAGAGA     53398    GC        A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM965  CORO2A    3'  AAACTGTGGTCCAGAGA     12642    GC        A
                                TC  CTGGACCACA GTTT
                                ||  |||||||||| ||||
                                AG  GACCTGGTGT CAAA
                                 A_        _
GAM965  GRLF1     3'  AGGTCAGAAAGTGGCCCAGG   78551      A    AAG
                                CCTGG CCAC   TTTGACCT
                                ||||| ||||   ||||||||
                                GGACC GGTG   AGACTGGA
                                   C    AA_
GAM965  LAPTM5    3'  AGGCTTGTGGTCAAGC      22199    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCGGA
                                 AA_
GAM965  POU2AF1   3'  AGATTTACAGTCCAGGC     20647        CAC
                                GCCTGGAC   AAGTTT
                                ||||||||   ||||||
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                                CGGACCTG   TTTAGA
                                     ACA
GAM965  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  54574        C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM965  PTGS1    3'  GTCTCCTGTCTTATGGTCCAG  6355         C   TTT___
                                CTGGACCA AAG     GAC
                                |||||||| |||     |||
                                GACCTGGT TTC     CTG
                                     A   TGTCCT
GAM965  TRIM34   5'  AGGTCAAGTTGAGCCCAG    55224      ACCA   G
                                CTGG    CAA TTTGACCT
                                ||||    ||| ||||||||
                                GACC    GTT GAACTGGA
                                  CGA_   _
GAM965  TRIM9    5'  AGGCCAGGCAAGTCCAGGC   30749        CACAA    A
                                GCCTGGAC    GTTTG CCT
                                ||||||||    ||||| |||
                                CGGACCTG    CGGAC GGA
                                     AA___    C
GAM965  ABLIM    5'  GATATGTAACCCAGGCGG    22030        ACC   A
                                TCGCCTGG   ACA GTT
                                ||||||||   ||| |||
                                GGCGGACC   TGT TAG
                                     CAA   A
GAM965  AMOT     3'  AGGCATCTTCATGGTCCAGGGA 55716    G       C_   TT  A
                                TC CCTGGACCA  AAG  TG CCT
                                || |||||||||  |||  || |||
                                AG GGACCTGGT  TTC  AC GGA
                                  _       AC   T_ _
GAM965  DKFZp434D177 5'  TTAGACCCAGGCGA       50056        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                              _______
GAM965  DKFZp434D177 5'  TTAGACCCAGGCGA       79443        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
                                AGCGGACC      CAGATT
                                              _______
GAM965  FLJ23420  3'  CAAGTGGGTCCAGGC       46845         A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                           _ __
GAM965  HSA249128 5'  GGCGCGGTCCAGGCGG      34152          ACAA
                                TCGCCTGGACC    GTT
                                ||||||||||    |||
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                                GGCGGACCTGG   CGG
                                      CG__
GAM965  MGC15668  5'  AGACCCGGTGGTCCAGACG   51277    C       AA_
                                CG CTGGACCAC   GTTT
                                || |||||||||   ||||
                                GC GACCTGGTG   CAGA
                                 A       GCC
GAM965  MGC22014  3'  AGGTCCCGAGTGTAACCCAGGT 64486        ACC   AGTTT
           GA                    TCGCCTGG   ACA    GACCT
                                |||||||||   |||    |||||
                                AGTGGACC   TGT    CTGGA
                                     CAA   GAGCC
GAM965  SDCCAG10  5'  AGAGTTGTGGTCCAAAGA    19641    GCC       G
                                TC   TGGACCACAA TTT
                                ||   |||||||||| |||
                                AG   ACCTGGTGTT AGA
                                 AA_        G
GAM965  LOC115442 3'  AGGTCAGGGATGGTCCAG    72676       CAAG
                                CTGGACCA    TTTGACCT
                                ||||||||    ||||||||
                                GACCTGGT    GGACTGGA
                                     AG__
GAM965  LOC129011 5'  AGACCTGCGGTCCAGGC     74862        A  A
                                GCCTGGACC CA GTTT
                                ||||||||| || ||||
                                CGGACCTGG GT CAGA
                                      C  C
GAM965  LOC130536 5'  GCAAAGTCCAGGCG        75746        CACAAG    A
                                CGCCTGGAC     TTTG C
                                |||||||||     |||| |
                                GCGGACCTG     AAAC G
                                      _______   C
GAM965  LOC149108 3'  AGACTTCACTGTGGTCCA    84357        _____
                                TGGACCACA    AGTTT
                                |||||||||    |||||
                                ACCTGGTGT    TCAGA
                                      CACT
GAM965  LOC221688 5'  AGACTCGGGCCCAGACGA    93674    C    A  ACA
                                TCG CTGG CC   AGTTT
                                ||| |||| ||   |||||
                                AGC GACC GG   TCAGA
                                  A   C  GC_
GAM965  LOC256228 5'  AGACTTGTGGTCAAAGC     96233    CTG
                                GC   GACCACAAGTTT
                                ||   ||||||||||||
                                CG   CTGGTGTTCAGA
                                 AAA
GAM965  LOC257441 5'  TTAGACCCAGGCGA        95566        ACCACAA
                                TCGCCTGG      GTTTGA
                                ||||||||      ||||||
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                                AGCGGACC      CAGATT
                                        _______
GAM965  LOC91960  3'  AGGTGCCTCTCGTGGTCCAAGC 67657    C       A  TTTG
                                GC TGGACCAC AG    ACCT
                                || |||||||| ||    ||||
                                CG ACCTGGTG TC    TGGA
                                 A       C  TCCG
GAM965  LOC92840  3'  GTCCCTCGGGTCCAGGC     56435         ACA  TTT
                                GCCTGGACC   AG   GAC
                                |||||||||   ||   |||
                                CGGACCTGG   TC   CTG
                                     GC_  C__
GAM966  AMPD3     3'  CTGGTGATTTTGGTTGC     4898      _
                                GTG CTAAGATTACCAG
                                ||| ||||||||||||
                                CGT GGTTTTAGTGGTC
                                  T
GAM966  ARF1      3'  ACTGGTCTATTTGGTGTCGTGG 70657       A TG     ATT
              AA                  TTCCAC G  CTAAG   ACCAGT
                                ||||||  |  |||||   ||||||
                                AAGGTG T  GGTTT   TGGTCA
                                   C GT     ATC
GAM966  ASTN      3'  GTCTCCATTTTAGTGTTGAGGA 69335      A   TG      TACCAGT
              A                   TTCC CAG  CTAAGAT
                                ||||  |||  |||||||
                                AAGG GTT  GATTTTA
                                  A  GT      CCTCTG
GAM966  B4GALT5   3'  GCTGGTGACACTTGTGTGCTGT 16508        TG _   A_
              GGG                   TCCACAG  C TAAG  TTACCAGT
                                |||||||  | ||||  ||||||||
                                GGGTGTC  G GTTC  AGTGGTCG
                                    GT T    AC
GAM966  BCAT1     3'  ATTGGTGATCTGAAATCTTGGG 66200      C  TGCTA
              A                   TTCCA AG    AGATTACCAGT
                                |||||  ||    ||||||||||
                                AGGGT TC    TCTAGTGGTTA
                                   _  TAAAG
GAM966  BDP1      5'  GCTGGTGGTGTGGCTTTGTGGG 37366        T    AG
                                TCCACAG GCTA  ATTACCAGT
                                ||||||| ||||  |||||||||
                                GGGTGTT CGGT  TGGTGGTCG
                                    T   G_
GAM966  BIG1      3'  ACTGGTAATCATCCTGTG    21201       TGCTAA
                                CACAG     GATTACCAGT
                                |||||     ||||||||||
                                GTGTC     CTAATGGTCA
                                   CTA___
GAM966  BLAME     3'  TCTTGGCACTTGGGA       39244       C
                                TTCCA AGTGCTAAGA
                                ||||| ||||||||||
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                                AGGGT TCACGGTTCT
                                    _
GAM966  CA11    5'  CTGCTTTGGCATTTGGG    6871      C       ATTAC
                                TCCA AGTGCTAAG    CAG
                                |||| |||||||||    |||
                                GGGT TTACGGTTT    GTC
                                  _       C____
GAM966  CARKL   3'  ATTGGTAGGGATGGCTGTGGG 25184      GT   AGA
                                TCCACA  GCTA   TTACCAGT
                                ||||||  ||||   ||||||||
                                GGGTGT  CGGT   GATGGTTA
                                   __   AGG
GAM966  CD164   3'  ACTGGTGATTCATTTGTG    20049      _ CTAA
                                CACAG TG   GATTACCAGT
                                ||||| ||   ||||||||||
                                GTGTT AC   TTAGTGGTCA
                                  T ____
GAM966  CNTN2   3'  GCTGGTGTGTCCTGGTATTGGG 17410     A      A  _
            AG                    TTCC CAGTGCTA GAT TACCAGT
                                |||| |||||||| ||| |||||||
                                GAGG GTTATGGT CTG GTGGTCG
                                  _       C  T
GAM966  CROT    3'  CCTATAATCTTAGCACTTTGGG 40948      C          CCAGT
            A                    TTCCA AGTGCTAAGATTA
                                ||||| ||||||||||||
                                AGGGT TCACGATTCTAAT
                                  T          ATCCG
GAM966  DGKB    3'  TAATTAAGCATTGTGGAG    92534          AA
                                TTCCACAGTGCT  GATTA
                                ||||||||||||  |||||
                                GAGGTGTTACGA  TTAAT
                                      A_
GAM966  DMBT1   3'  TCTTAGCACTGTTGAG     15317     C
                                TTC ACAGTGCTAAGA
                                ||| ||||||||||||
                                GAG TGTCACGATTCT
                                  T
GAM966  E2F3    3'  CTGGAAATGCACTGTGGG    8699          TAAG  A
                                TCCACAGTGC    ATT CCAG
                                ||||||||||    ||| ||||
                                GGGTGTCACG    TAA GGTC
                                      ____   A
GAM966  FCAR    3'  ATTGAAAACTTAGTCTGTGGAG 55790        T    A  AC
                                TTCCACAG GCTAAG TT  CAGT
                                |||||||| ||||||  ||  ||||
                                GAGGTGTC TGATTC AA  GTTA
                                      _     _ AA
GAM966  FCAR    3'  ATTGAAAACTTAGTCTGTGGAG 55809        T    A  AC
                                TTCCACAG GCTAAG TT  CAGT
                                |||||||| ||||||  ||  ||||
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                                GAGGTGTC TGATTC AA  GTTA
                                   _     _ AA
GAM966  FNTB     3'  GCTGGTGGTGGCAGCGTGGG  8953       AG    AAG
                                TCCAC  TGCT   ATTACCAGT
                                |||||  ||||   |||||||||
                                GGGTG  ACGG   TGGTGGTCG
                                  CG   ____
GAM966  GP6      3'  CTGTAATCCTAGCACTGTGGGA 33031           A     C  T
                                TTCCACAGTGCTA GATTAC AG
                                |||||||||||| |||||| ||
                                AGGGTGTCACGAT CTAATG TC
                                       C      _ T
GAM966  HCFC1    3'  TCATTGTAATTTTAGCGTGTGG 70999       G          CAGT
             G                   TCCACA TGCTAAGATTAC
                                |||||| ||||||||||||
                                GGGTGT GCGATTTTAATG
                                   _          TTACTT
GAM966  IGFBP4   3'  TCCTCTGATTTTGGCATGTGGA 7764        G         CCAGT
             G                   TTCCACA TGCTAAGATTA
                                |||||||| ||||||||||
                                GAGGTGT ACGGTTTTAGT
                                   _          CTCCTT
GAM966  IL6R     3'  TTGGTGGGGGGCCTCGGTGTGGA 5125        G  CTAAGA     GT
             G                   TTCCACA TG     TTACCA
                                |||||||  ||     ||||||
                                GAGGTGT GC     GGTGGT
                                    G  TCCGGG     TG
GAM966  INPP5D   3'  TCTTGGTACTTGGGA       82811       C
                                TTCCA AGTGCTAAGA
                                |||||  ||||||||||
                                AGGGT TCATGGTTCT

                                   _
GAM966  ITGA1    3'  GCTGCTCATTTTAGCACTGTGG 63535              TAC
             AA                   TTCCACAGTGCTAAGAT   CAGT
                                |||||||||||||||||   ||||
                                AAGGTGTCACGATTTTA   GTCG
                                          CTC
GAM966  KCNAB2   3'  GCTGGTGGGCTTGGGTTTTGTG 13306        TG_    A
             GAG                    TTCCACAG   CTAAG TTACCAGT
                                |||||||   ||||| ||||||||
                                GAGGTGTT   GGTTC GGTGGTCG
                                     TTG    G
GAM966  KIAA0442 3'  GCTGGTGATCAAGTCTGGGAA  31470      A   T   AA
                                TTCC CAG GCT  GATTACCAGT
                                ||||  ||| |||  ||||||||||
                                AAGG GTC TGA  CTAGTGGTCG
                                   _  _  A_
GAM966  LEP      3'  TTGGAAGGTTTGGTGTGTGGAG 4061         G      ATTA   GT
                                TTCCACA TGCTAAG    CCA
                                |||||||  |||||||    |||
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                              GAGGTGT GTGGTTT   GGT
                                 _     GGAA  TG
GAM966  LTA4H    3'  TGGTGATTTTACTG       6103       CTA
                              CAGTG  AGATTACCA
                              |||||  |||||||||
                              GTCAT  TTTAGTGGT
                                 ___
GAM966  MLH1     3'  GTTATTTATGCACTGTGGGA  4200          TA   T
                              TTCCACAGTGC  AGAT AC
                              ||||||||||  |||| ||
                              AGGGTGTCACG  TTTA TG
                                    TA   T
GAM966  MTRR     5'  GTGGAAGTCGCGTTGTG     10134        TAA   A  GT
                              CACAGTGC  GATT CCA
                              ||||||||  |||| |||
                              GTGTTGCG  CTGA GGT
                                 ___   A  GG
GAM966  NAB1     3'  ACTGGTACGGTAGTCTGTGGAA 19905        T   AGAT
                              TTCCACAG GCTA   TACCAGT
                              ||||||| ||||   |||||||
                              AAGGTGTC TGAT   ATGGTCA
                                 _   GGC_
GAM966  NFRKB    5'  ACTGAGATTAGTACCTGTGGAG 20492        _    GATTAC
                              TTCCACAG TGCTAA    CAGT
                              |||||||| ||||||     ||||
                              GAGGTGTC ATGATT     GTCA
                                 C     AGA___
GAM966  PCDH11X  3'  ATGTTTGTATTGTGGGA     52018         T  G
                              TTCCACAGTGC AA AT
                              |||||||||| || ||
                              AGGGTGTTATG TT TA
                                    T  G
GAM966  PCDH11X  3'  ATGTTTGTATTGTGGGA     52040         T  G
                              TTCCACAGTGC AA AT
                              |||||||||| || ||
                              AGGGTGTTATG TT TA
                                    T  G
GAM966  PCDH11Y  3'  ATGTTTGTATTGTGGGA     52075         T  G
                              TTCCACAGTGC AA AT
                              |||||||||| || ||
                              AGGGTGTTATG TT TA
                                    T  G
GAM966  PCDHAC1  5'  TTGGTGTAGCGTGTTGGTGGAA 49041      AG___   AGAT   GT
                              TCCAC    TGCTA   TACCA
                              |||||    |||||   |||||
                              AGGTG    GCGAT   GTGGT
                                 GTTGT    ____    TG
GAM966  PCDHAC1  5'  TTGGTGTAGCGTGTTGGTGGAA 38170      AG___   AGAT   GT
                              TCCAC    TGCTA   TACCA
                              |||||    |||||   |||||
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                                AGGTG    GCGAT    GTGGT
                                  GTTGT    ____     TG
GAM966  PFKFB2   3'  TGGTGAAGTGTTGGGGGA    20605      A   TG  AAGA
                                TTCC CAG  CT    TTACCA
                                |||| |||  ||    ||||||
                                AGGG GTT  GA    AGTGGT
                                  G   GT  ____
GAM966  PITPNB   3'  ACTGGTGGACATCTGACTGTGG 24777         GCTA   ___
          GA                      TCCACAGT    AGAT   TACCAGT
                                |||||||||    ||||   |||||||
                                GGGTGTCA    TCTA   GTGGTCA
                                    G___    CAG
GAM966  PROML1   3'  ATTGACTTCTTGGTGCTGTTGA 20053     C    TG     TTAC
          A                      TTC ACAG  CTAAGA    CAGT
                                ||| ||||  ||||||    ||||
                                AAG TGTC  GGTTCT    GTTA
                                  T   GT     TCA_
GAM966  PRV1     3'  ACTGGCCCTAGCGCTGTGG    73531          AGATTA
                                CCACAGTGCTA     CCAGT
                                ||||||||||      |||||
                                GGTGTCGCGAT     GGTCA
                                     CCC___
GAM966  PTPRC    3'  ATTTTACTACTGTGGAA     55166          C
                                TTCCACAGTG TAAGAT
                                |||||||||| ||||||
                                AAGGTGTCAT ATTTTA
                                     C
GAM966  PTPRC    3'  ATTTTACTACTGTGGAA     11101          C
                                TTCCACAGTG TAAGAT
                                |||||||||| ||||||
                                AAGGTGTCAT ATTTTA
                                     C
GAM966  RAG1     3'  TTTTACCACTGTGGAA      4820           C
                                TTCCACAGTG TAAGA
                                |||||||||| |||||
                                AAGGTGTCAC ATTTT
                                     C
GAM966  RFC1     3'  ACTGGTAGTCTTGTTTGGGTG  11300     AGT_  T
                                CAC    GC AAGATTACCAGT
                                |||    || ||||||||||||
                                GTG    TG TTCTGATGGTCA
                                  GGTT  _
GAM966  RGS16    3'  TGGTGGGGCTCTCTGTGGG   11341        T__   AAGA
                                TCCACAG   GCT    TTACCA
                                |||||||   |||    ||||||
                                GGGTGTC   CGG    GGTGGT
                                    TCT   ____
GAM966  SERPINH2 3'  GTCTGGCGTTGTGGG       6944            A
                                TCCACAGTGCTA GAT
                                |||||||||||| |||
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                                GGGTGTTGCGGT CTG
                                          _
GAM966  SMN1    3'  ATTGGTAATTTTATGGCCTGTG 4430    _    T   __
            AGAA                  C CACAG GCTA  AGATTACCAGT
                                  | ||||| ||||  ||||||||||
                                  G GTGTC CGGT  TTTAATGGTTA
                                   A    _   AT
GAM966  SMN1    3'  ATTGGTAATTTTATGGCCTGTG 43154   _    T   __
            AGAA                  C CACAG GCTA  AGATTACCAGT
                                  | ||||| ||||  ||||||||||
                                  G GTGTC CGGT  TTTAATGGTTA
                                   A    _   AT
GAM966  SPO11   3'  ATTGGCAAATACTATTGTGGAA 24907         C  AGATTA
                                  TTCCACAGTG TA     CCAGT
                                  ||||||||||  ||     |||||
                                  AAGGTGTTAT AT     GGTTA
                                        C  AAAC__
GAM966  SRGAP2  3'  ATTGGTAGTTAGGTCTATGGAA 74604      C  T   AA
                                  TTCCA AG GCT  GATTACCAGT
                                  |||||  ||  |||  ||||||||||
                                  AAGGT TC TGG  TTGATGGTTA
                                     A  _  A_
GAM966  TCF8    3'  TCTTATTGCTGTGGAA     47733         GC
                                  TTCCACAGT  TAAGA
                                  |||||||||  |||||
                                  AAGGTGTCG  ATTCT
                                        TT
GAM966  USH3A   5'  GCTGGCTGCTTTAGTGCTGTG  53785      TG    ATTA
                                  CACAG  CTAAG    CCAGT
                                  |||||  |||||   |||||
                                  GTGTC  GATTT    GGTCG
                                     GT    CGTC
GAM966  WHSC1   3'  ACTGGTAACAGCTTTTGTGGGA 23652        T_  AAGA
                                  TTCCACAG  GCT    TTACCAGT
                                  ||||||||  |||   ||||||||
                                  AGGGTGTT  CGA    AATGGTCA
                                       TT   C___
GAM966  ZNF239  5'  GCTGAGATCATTGGCACTGTGG 19041            _   AC
            AG                    TTCCACAGTGCTAA GATT  CAGT
                                  ||||||||||||||  ||||  ||||
                                  GAGGTGTCACGGTT CTAG  GTCG
                                           A   A_
GAM966  ZNF74   3'  CTGTAATCTTAACACTGTGGGA 12796          C       C  T
                                  TTCCACAGTG TAAGATTAC AG
                                  ||||||||||  |||||||||  ||
                                  AGGGTGTCAC ATTCTAATG TC
                                        A       _  C
GAM966  ACAS2L  3'  TTTTATATTGTGGAA      68079          C
                                  TTCCACAGTG TAAGA
                                  |||||||||  |||||
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                                AAGGTGTTAT ATTTT
                                     _
GAM966  ALY     3' CTGGTTGCTGTTGTGGAG    19349       GT  TA  ATT
                                TTCCACA  GC  AG   ACCAG
                                |||||||  ||  ||   |||||
                                GAGGTGT  TG  TC   TGGTC
                                   __  __  GT_
GAM966  C5orf7   5' TGGTGGTGGCTGTTGGGG   63872      _   GCTAAG
                                TTCCA CAGT     ATTACCA
                                ||||| ||||     |||||||
                                GGGGT GTCG     TGGTGGT
                                   T   G_____
GAM966  CEP3     5' ACTGGGGGGTGGCGCTGGGGA 21246     A      AGATTA
                                TTCC CAGTGCTA     CCAGT
                                |||| ||||||||     |||||
                                AGGG GTCGCGGT     GGTCA
                                  _       GGGG__
GAM966  DEPC-1   3' TTGGTAATAGGTCTACTGTGGG 57549         CTAAG      GT
           A                     TTCCACAGTG     ATTACCA
                                 ||||||||||     |||||||
                                 AGGGTGTCAT     TAATGGT
                                       CTGGA      TG
GAM966  DKFZP434G072 3' TTTTGGTATTGAGGAA      49589      A
                                TTCC CAGTGCTAAGA
                                |||| ||||||||||
                                AAGG GTTATGGTTTT
                                  A
GAM966  DLAD     5' GCTGGTAGAAATGTTGTGGG   54289       GT  TAAGA
                                TCCACA  GC    TTACCAGT
                                ||||||  ||    ||||||||
                                GGGTGT  TG    GATGGTCG
                                   __  TAAA_
GAM966  FLJ10154 3' TGGTGATTGCATTGGGAA    35857     A     TAA
                                TTCC CAGTGC   GATTACCA
                                |||| ||||||   ||||||||
                                AAGG GTTACG   TTAGTGGT
                                   _    ____
GAM966  FLJ10159 3' TGGTGAGACAGTTGTGGAG   35863       GT   AAGA
                                TTCCACA  GCT   TTACCA
                                |||||||  |||   ||||||
                                GAGGTGT  TGA   AGTGGT
                                   __  CAG_
GAM966  FLJ10607 3' GCTGGTGGGACATGCTGTG   77121       GCTAAGA
                                CACAGT      TTACCAGT
                                ||||||      ||||||||
                                GTGTCG      GGTGGTCG
                                   TACAG__
GAM966  FLJ10971 3' ATTGGTAATCTTTTCTGTG   36924      TGCT
                                CACAG   AAGATTACCAGT
                                |||||   ||||||||||||
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                                GTGTC    TTCTAATGGTTA
                                   TT__
GAM966  FLJ12229  5'  TGGTTGGCCTTGTGGG      45921        T    AGATT
                                TCCACAG GCTA    ACCA
                                ||||||| ||||    ||||
                                GGGTGTT CGGT    TGGT
                                    C   _____
GAM966  FLJ14681  3'  CTGGTGAACTTTGTGGAA    51525        GTGCT   A
                                TTCCACA    AAG TTACCAG
                                |||||||    ||| |||||||
                                AAGGTGT    TTC AGTGGTC
                                    _____  A
GAM966  FLJ14803  3'  GCTGGTAGTTTTAATTTGGG  51618    A   TGC
                                CC CAG   TAAGATTACCAGT
                                || |||   ||||||||||||
                                GG GTT   ATTTTGATGGTCG
                                 _   TA_
GAM966  FLJ20019  3'  ATCTTAGCACTTTGGGA     34344       C
                                TTCCA AGTGCTAAGAT
                                ||||| ||||||||||
                                AGGGT TCACGATTCTA
                                   T
GAM966  FLJ20343  3'  TGGTATGCCTGTGGG       35001        T  TAAGAT
                                TCCACAG GC     TACCA
                                ||||||| ||     |||||
                                GGGTGTC CG     ATGGT
                                    _  T_____
GAM966  FLJ20671  3'  ACTGGGACCCTTGTGCTGTGGA 35515        TG T   ATTA
          G                      TTCCACAG  C AAG    CCAGT
                                ||||||||  | |||    |||||
                                GAGGTGTC  G TTC    GGTCA
                                    GT _   CCAG
GAM966  FLJ21047  5'  TTGGTGAAGCTGGTGCTGTGGG 44692        TG   AGA     GT
                                TCCACAG  CTA   TTACCA
                                |||||||  |||   ||||||
                                GGGTGTC  GGT   AGTGGT
                                    GT   CGA     TG
GAM966  FLJ21687  3'  ACTGTGCTAGGTACTGTGGAG  45855          A  ATTAC
                                TTCCACAGTGCT AG     CAGT
                                |||||||||||| ||     ||||
                                GAGGTGTCATGG TC     GTCA
                                      A  GT___
GAM966  FLJ22477  3'  CTGGTGGTTTTCTCGGGAA    45342      AC  TGCT
                                TTCC  AG    AAGATTACCAG
                                ||||  ||    ||||||||||
                                AAGG  TC    TTTTGGTGGTC
                                  GC  ____
GAM966  FLJ30294  5'  TTGGTTTAATGGGATTGTGGAA 58251         G   AGATT    GT
                                TTCCACAGT CTA     ACCA
                                ||||||||| |||     ||||
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                                AAGGTGTTA GGT    TGGT
                                     G  AATT_   TG
GAM966  FLJ30567  3'  GCTGGTGGTTGGAGAGTTTGGG 58827   A  TG_  AA
                                CC CAG  CT  GATTACCAGT
                                || |||  ||  ||||||||||
                                GG GTT  GA  TTGGTGGTCG
                                 _  TGA  GG
GAM966  FLN29    3'  ACTGCCCCTTGGTGCTGTG   21982     TG    ATTAC
                                CACAG  CTAAG    CAGT
                                |||||  |||||    ||||
                                GTGTC  GGTTC    GTCA
                                   GT    CCC__
GAM966  G4       3'  GCTGGTAGCTCAGGCAGTGTGG 90994      G   A_  A
            G                    TCCACA TGCT  AG TTACCAGT
                                ||||||| ||||  || ||||||||
                                GGGTGT ACGG  TC GATGGTCG
                                   G   AC  _
GAM966  GS3955   3'  TGGTGACATGCATGGTGGG   41321     A   TAAGA
                                TCCAC GTGC    TTACCA
                                |||||| ||||    ||||||
                                GGGTG TACG    AGTGGT
                                   G   TAC__
GAM966  HEMK     3'  TGGTGAAATTGCTGTGGGG   32445       GCT  GA
                                TTCCACAGT   AA  TTACCA
                                |||||||||   ||  ||||||
                                GGGGTGTCG   TT  AGTGGT
                                     ___  AA
GAM966  ITGB5    3'  TGGTGATGGGGCTGTTGAG   59500    C    G  AAG
                                TTC ACAGT CT   ATTACCA
                                ||| ||||| ||   |||||||
                                GAG TGTCG GG   TAGTGGT
                                  T    G  ___
GAM966  KIAA0459 3'  TAAACTTAGTATTGTGGAA   61004           A
                                TTCCACAGTGCTAAG TTA
                                |||||||||||||| |||
                                AAGGTGTTATGATTC AAT
                                        A
GAM966  KIAA0514 3'  CTGGTGCAGTTTGTGGAA    28081       T  AAGAT
                                TTCCACAG GCT    TACCAG
                                |||||||| |||    ||||||
                                AAGGTGTT TGA    GTGGTC
                                     _  C_____
GAM966  KIAA0596 3'  GTCATCTTGGTGCTGTGAGA  62837   _    TG     T
                                TC CACAG  CTAAGAT AC
                                || |||||  ||||||| ||
                                AG GTGTC  GGTTCTA TG
                                 A    GT     C
GAM966  KIAA0618 3'  GCTGGTGCACGTAGCACTGTGG 29169          AGAT
                                CCACAGTGCTA   TACCAGT
                                ||||||||||   |||||||
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                                GGTGTCACGAT   GTGGTCG
                                      GCAC
GAM966  KIAA0630  3'  GTAATTTTGGTACTTGGAA   89394      C
                                TTCCA AGTGCTAAGATTAC
                                ||||| ||||||||||||||
                                AAGGT TCATGGTTTTAATG
                                  _
GAM966  KIAA0870  3'  TTGGTGATAACCTCTGCTGGGA 81474     A   GCTAAG_     GT
          G                      TTCC CAGT      ATTACCA
                                |||| ||||      |||||||
                                GAGG GTCG      TAGTGGT
                                  _   TCTCCAA      TG
GAM966  KIAA1023  3'  TGGATTCTGTCACTGTGGAG   34271         CTA   TTA
                                TTCCACAGTG   AGA   CCA
                                ||||||||||   |||   |||
                                GAGGTGTCAC   TCT   GGT
                                      TG_   TA_
GAM966  KIAA1272  5'  TGGTGGTGGTGCTGTG     70176      TG  AAG
                                CACAG  CT   ATTACCA
                                |||||  ||   |||||||
                                GTGTC  GG   TGGTGGT
                                   GT  ___
GAM966  KIAA1281  3'  GTTTGTACTTGTGTATTGTGGA 89153          _   ATTACCAGT
          A                      TTCCACAGTGC TAAG
                                ||||||||||| ||||
                                AAGGTGTTATG GTTC
                                      T   ATGTTTG
GAM966  KIAA1328  5'  TTCAATGATATTGGTGCTGTGG 61659        TG   G   CCAGT
          AG                     TTCCACAG  CTAA ATTA
                                ||||||||  |||| ||||
                                GAGGTGTC  GGTT TAGT
                                    GT   A   AACTTG
GAM966  KIAA1492  5'  CTGGTGATTTTAGTTGT     64504     GT
                                ACA  GCTAAGATTACCAG
                                |||  ||||||||||||||
                                TGT  TGATTTTAGTGGTC
                                  __
GAM966  KIAA1514  3'  ACTGGCCTTGGCACTGTGGGA  38817            ATTA
                                TTCCACAGTGCTAAG   CCAGT
                                ||||||||||||||   |||||
                                AGGGTGTCACGGTTC   GGTCA
                                         C___
GAM966  KIAA1535  3'  TCTTGGTGTGTGGGA      79414        G
                                TTCCACA TGCTAAGA
                                ||||||| ||||||||
                                AGGGTGT GTGGTTCT
                                  _
GAM966  KIAA1872  3'  ACTGGTGGTATTTAGTGCTGAG 62921     A  TG   _
          GG                     TCC CAG  CTAAG ATTACCAGT
                                ||| |||  ||||| |||||||||
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                                GGG GTC  GATTT TGGTGGTCA
                                  A  GT    A
GAM966  LMOD1    3'  GCTGCCACCCCTTGGCACTGTG 24045            ATTAC_
            GAA                   TTCCACAGTGCTAAG     CAGT
                                  ||||||||||||||     ||||
                                  AAGGTGTCACGGTTC     GTCG
                                         CCCACC
GAM966  LY75     3'  TTTTAGCACTGGGGAA      9845       A
                                  TTCC CAGTGCTAAGA
                                  |||| ||||||||||
                                  AAGG GTCACGATTTT
                                    G
GAM966  MGC10999 3'  TAATCTTAGCACTTTGGGA    50228      C
                                  TTCCA AGTGCTAAGATTA
                                  ||||| ||||||||||||
                                  AGGGT TCACGATTCTAAT
                                     T
GAM966  MGC21854 3'  TGGTCAGCCTGTGGAG      53494        T   AAGATT
                                  TTCCACAG GCT     ACCA
                                  |||||||| |||     ||||
                                  GAGGTGTC CGA     TGGT
                                       _   C_____
GAM966  MGC27434 3'  ATTGGCTTCCGTTGGTGTTTGG 58945      C  TG   __  TTA
            AA                    TTCCA AG  CTAA  GA   CCAGT
                                  ||||| ||  ||||  ||   |||||
                                  AAGGT TT  GGTT  CT   GGTTA
                                    _ GT    GC  TC_
GAM966  MGC4368  5'  CTGGCCTGGGCTGTGGGA    44459        G   A ATTA
                                  TTCCACAGT CTA G    CCAG
                                  ||||||||| ||| |    ||||
                                  AGGGTGTCG GGT C    GGTC
                                       _   _ C____
GAM966  MGC4796  3'  GGTCTTGTGCTGTGGG      61494        TG T
                                  TCCACAG  C AAGATT
                                  |||||||  | ||||||
                                  GGGTGTC  G TTCTGG
                                      GT _
GAM966  MGC9753  5'  GCTGGCCTGGTGCCTGTGGAA  53051        T  TA_  ATTA
                                  TTCCACAG GC   AG    CCAGT
                                  |||||||| ||   ||    |||||
                                  AAGGTGTC CG   TC    GGTCG
                                       _  TGG  C____
GAM966  MP1      5'  TTGGTGGAGGTTGTACTGTGG  30359        TAAGA     GT
                                  CCACAGTGC     TTACCA
                                  |||||||||     ||||||
                                  GGTGTCATG     GGTGGT
                                        TTGGA     TG
GAM966  NCKX3    3'  GTTGTTTGGCATTTGGG     40354      C        ATT
                                  TCCA AGTGCTAAG   AC
                                  |||| |||||||||   ||
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                                GGGT TTACGGTTT   TG
                                  _       GT_
GAM966  NXPH3    3'  GCTGGTGACCTTGCATTGTGG  65764         T   A
                                CCACAGTGC AAG TTACCAGT
                                ||||||||| ||| ||||||||
                                GGTGTTACG TTC AGTGGTCG
                                     _  C
GAM966  PDE3A    3'  GCTTTTGCTCTTAGTACTGAGG 6227       A         T  CC
          GA                      TTCC CAGTGCTAAGA TA  AGT
                                |||| |||||||||| ||  |||
                                AGGG GTCATGATTCT GT  TCG
                                  A         C  TT
GAM966  PIP5K1C  3'  TTGGTGATGGCTGTGGGA    70770         GCTAAG
                                TTCCACAGT     ATTACCAG
                                |||||||||     ||||||||
                                AGGGTGTCG     TAGTGGTT
                                     G_____
GAM966  POLD3    3'  GCTGGTGATTTTGCACAGTG   91645     A   T
                                CAC GTGC AAGATTACCAGT
                                ||| |||| ||||||||||||
                                GTG CACG TTTTAGTGGTCG
                                  A   _
GAM966  PPFIA4   3'  GCTGGGGTTTCCTGGTATTGTG 70326           A  TTA_
          GAG                     TTCCACAGTGCTA GA    CCAGT
                                |||||||||||| ||    |||||
                                GAGGTGTTATGGT CT    GGTCG
                                     C  TTGG
GAM966  PRO2012  3'  ATTGGTCCAACCACTGTGGAA  37778         CTAAGATT
                                TTCCACAGTG       ACCAGT
                                ||||||||||       ||||||
                                AAGGTGTCAC       TGGTTA
                                     CAACC___
GAM966  PROZ     3'  GCTGGCACTGCCACTGTGGAG  13980         CTA  ATTA
                                TTCCACAGTG   AG    CCAGT
                                ||||||||||   ||    |||||
                                GAGGTGTCAC   TC    GGTCG
                                     CG_  AC__
GAM966  PTPN9    5'  TCTGTGGCGCTGTGGAG     11082           _
                                TTCCACAGTGCTA AGA
                                |||||||||||| |||
                                GAGGTGTCGCGGT TCT
                                     G
GAM966  REPRIMO  3'  GTTACAGTTTTGTCATTGTGGG 39055         C      ACCAGT
          A                      TTCCACAGTG TAAGATT
                                |||||||||| |||||||
                                AGGGTGTTAC GTTTTGA
                                     T      CATTG
GAM966  RoXaN    3'  AGTCTTAGCATTGGGAA     46630      A
                                TTCC CAGTGCTAAGATT
                                |||| ||||||||||||
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                                AAGG GTTACGATTCTGA
                                    _
GAM966  SERPINH1  3'  GTCTGGCGTTGTGGG      15127          A
                                TCCACAGTGCTA GAT
                                |||||||||||| |||
                                GGGTGTTGCGGT CTG
                                      _
GAM966  SLC21A6   3'  ATTTAAGTATTGTGGAA    21241          A
                                TTCCACAGTGCT AGAT
                                |||||||||||| ||||
                                AAGGTGTTATGA TTTA
                                       A
GAM966  SLC26A10  5'  CTGGTGGATGCTGGTGGGA   56030      AGT  TAAGA
                                TTCCAC   GC    TTACCAG
                                ||||||   ||    |||||||
                                AGGGTG   CG    GGTGGTC
                                   GT_  TA___
GAM966  THEA      3'  GCTTGTAATTTTAGCACTTTGG 66294      C          C
              GA                  TTCCA AGTGCTAAGATTAC AGT
                                |||||| |||||||||||||| |||
                                AGGGT TCACGATTTTAATG TCG
                                   T          T
GAM966  TIMM22    3'  GTTGTTTGGTGTTGTGGG    78315       TG    ATT
                                TCCACAG  CTAAG   AC
                                |||||||  |||||   ||
                                GGGTGTT  GGTTT   TG
                                    GT    GT_
GAM966  TOB2      3'  ACTGGTTTGCAGACTGTGGAA  95616        G  AA  TT
                                TTCCACAGT CT  GA  ACCAGT
                                ||||||||| ||  ||  ||||||
                                AAGGTGTCA GA  TT  TGGTCA
                                      _ CG  __
GAM966  USP29     3'  TGGTAATGTGTGGAG      40495       GTGCTAAG
                                TTCCACA       ATTACCA
                                |||||||       |||||||
                                GAGGTGT       TAATGGT
                                    G________
GAM966  ZAK       3'  ACTGTTTTTGGTGCTCTGGAA  56116      C  TG     TTAC
                                TTCCA AG  CTAAGA    CAGT
                                ||||| ||  ||||||    ||||
                                AAGGT TC  GGTTTT    GTCA
                                   C  GT     T___
GAM966  ZFP91     3'  GTTTTTGTGTTGTGGAA     53820        TG T
                                TTCCACAG  C AAGAT
                                ||||||||  | |||||
                                AAGGTGTT  G TTTTG
                                     GT T
GAM966  LOC118668 5'  TGGTGGCTGATGTGGAG     75485       GT_   AAGATT
                                TTCCACA   GCT     ACCA
                                |||||||   |||     ||||
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                                GAGGTGT   CGG     TGGT
                                    AGT   _______
GAM966   LOC124977 5'  ACTGGTGAAGCTGCCGTGGG   76055      A _   AAGA
                                TCCAC GT GCT    TTACCAGT
                                ||||| || |||    ||||||||
                                GGGTG CG CGA    AGTGGTCA
                                   C  T   ____
GAM966   LOC131377 3'  CTGGCCTGGCCTTGTGGG     76270       T    A ATTA
                                TCCACAG GCTA G    CCAG
                                ||||||| |||| |    ||||
                                GGGTGTT CGGT C    GGTC
                                    C    _ C___
GAM966   LOC138046 3'  GCTGTTGTCTTGTGCTGTGGAA 75295        TG T     TAC
                                TTCCACAG  C AAGAT   CAGT
                                ||||||||  | |||||   ||||
                                AAGGTGTC  G TTCTG   GTCG
                                    GT _    TT_
GAM966   LOC143943 3'  TGGTGATCATTGTGGGA     82996         GCTAA
                                TTCCACAGT    GATTACCA
                                |||||||||    ||||||||
                                AGGGTGTTA    CTAGTGGT
                                     _____
GAM966   LOC145384 3'  ACTGGTTCAACCATTGTGGAA  77195         CTAA  TT
                                TTCCACAGTG   GA  ACCAGT
                                ||||||||||   ||  ||||||
                                AAGGTGTTAC   CT  TGGTCA
                                     CAA_  __
GAM966   LOC145645 3'  TTTTGGTACTGGGGGA      77328      A
                                TTCC CAGTGCTAAGA
                                |||| ||||||||||
                                AGGG GTCATGGTTTT
                                  G
GAM966   LOC145826 5'  ATTGGTGATGGTAAATGTGGG  83528       G_   AAG
                                TCCACA  TGCT   ATTACCAGT
                                ||||||  ||||   ||||||||
                                GGGTGT  ATGG   TAGTGGTTA
                                   AA   ___
GAM966   LOC146307 5'  GCTGGTGCTGGCCGCTGTGGG  83657         _   AGAT
                                TCCACAGTG CTA    TACCAGT
                                ||||||||| |||    |||||||
                                GGGTGTCGC GGT    GTGGTCG
                                    C   C___
GAM966   LOC146435 3'  TGGTGATGTTTGGAA       77900       CAGTGCT  G
                                TTCCA      AA ATTACCA
                                |||||      || |||||||
                                AAGGT      TT TAGTGGT
                                  _______  G
GAM966   LOC146774 3'  TCTTGGTACTGGGAG       78100      A
                                TTCC CAGTGCTAAGA
                                |||| ||||||||||
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                                GAGG GTCATGGTTCT
                                     _
GAM966  LOC146856 3'  CTGGAAATGCACTGTGGG    82801         TAAG  A
                                TCCACAGTGC   ATT CCAG
                                ||||||||||   ||| ||||
                                GGGTGTCACG   TAA GGTC
                                     _____   A
GAM966  LOC149276 5'  TGATTTGGTTTTGTGGG     84390       T   A
                                TCCACAG GCTA GATTA
                                ||||||| |||| |||||
                                GGGTGTT TGGT TTAGT
                                    T   _
GAM966  LOC149464 5'  CTGTAATCTTAGCACTTTGGGA 84428      C          C  T
                                TTCCA AGTGCTAAGATTAC AG
                                ||||| |||||||||||||| ||
                                AGGGT TCACGATTCTAATG TC
                                   T          _  C
GAM966  LOC150378 3'  TTGGTAGTCCCTGGATTTGGGA 79750    A  TG  A_     GT
                                TCC CAG  CTA  GATTACCA
                                ||| |||  |||  ||||||||
                                AGG GTT  GGT  CTGATGGT
                                  _  TA  CC      TG
GAM966  LOC151103 3'  GATCTTGATGCTGTGGAA    85225        GC
                                TTCCACAGT  TAAGATT
                                |||||||||  |||||||
                                AAGGTGTCG  GTTCTAG
                                      TA
GAM966  LOC151959 5'  GTTTGAGTATTGTGGG      85526          A
                                TCCACAGTGCT AGAT
                                |||||||||||| ||||
                                GGGTGTTATGA TTTG
                                       G
GAM966  LOC151987 5'  TGGTGGTAGCGGCTTGGG    67468    A  T  AAG
                                CC CAG GCT   ATTACCA
                                || ||| |||   |||||||
                                GG GTT CGG   TGGTGGT
                                 _  _  CGA
GAM966  LOC155179 3'  TGGATTCTGTCACTGTGGAG  81325         CTA  TTA
                                TTCCACAGTG   AGA   CCA
                                ||||||||||   |||   |||
                                GAGGTGTCAC   TCT   GGT
                                      TG_   TA_
GAM966  LOC158267 5'  TAGTCTTGGCCCTGTGGAG   81838        T
                                TTCCACAG GCTAAGATTA
                                |||||||| ||||||||||
                                GAGGTGTC CGGTTCTGAT
                                     C
GAM966  LOC158332 3'  ACTGCACCTTGGTGCTTGGAG  81885      C  TG    ATTAC
                                TTCCA AG  CTAAG    CAGT
                                ||||| ||  |||||    ||||
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                                GAGGT TC  GGTTC    GTCA
                                  _ GT    CAC__
GAM966  LOC163682 5'  GCCAGATCTTGGCAGTTGTGGA 87035       _       ACCAGT
          G                      TTCCACAG TGCTAAGATT
                                 |||||||| ||||||||||
                                 GAGGTGTT ACGGTTCTAG
                                     G        ACCG
GAM966  LOC169426 3'  CTGGTGGTTTTTGTAGGA   87286    ACAG  T
                                 TCC   TGC AAGATTACCAG
                                 |||   ||| ||||||||||
                                 AGG   ATG TTTTGGTGGTC
                                   ____  T
GAM966  LOC197135 5'  ACTGGTGATGTCGGTTGGGAA  87890     A  GT   AAG
                                 TTCC CA  GCT   ATTACCAGT
                                 |||| ||  |||   |||||||||
                                 AAGG GT  TGG   TAGTGGTCA
                                   _ __  CTG
GAM966  LOC200251 5'  ACTGGATGCTGTGGTGCTGTGG 88662       TG   AGATTA
          AA                     TTCCACAG  CTA     CCAGT
                                 ||||||||  |||     |||||
                                 AAGGTGTC  GGT     GGTCA
                                     GT   GTCGTA
GAM966  LOC200261 3'  GCTGACAGGATTGTTGGTGCTG 88657      TG   _   AC__
          TGGG                     CACAG  CTAA GATT    CAGT
                                 |||||  |||| ||||    ||||
                                 GTGTC  GGTT TTAG    GTCG
                                   GT    G    GACA
GAM966  LOC200854 5'  GCTGGTGGTAGCGGCTTGGG   87422    A   T   AAG
                                 CC CAG GCT   ATTACCAGT
                                 || ||| |||   |||||||||
                                 GG GTT CGG   TGGTGGTCG
                                  _  _  CGA
GAM966  LOC201522 3'  GCTGGTGACCCTGGTGCTGTGG 88258       TG   AGA
          AA                     TTCCACAG  CTA   TTACCAGT
                                 ||||||||  |||   ||||||||
                                 AAGGTGTC  GGT   AGTGGTCG
                                     GT   CCC
GAM966  LOC201931 3'  CTGTAATCTTAGTACTTTGGGA 89111      C          C  T
                                 TTCCA AGTGCTAAGATTAC AG
                                 ||||| |||||||||||||| ||
                                 AGGGT TCATGATTCTAATG TC
                                   T           _ C
GAM966  LOC220827 3'  GCTGGAAGTTGGTGCTTGGAA  91243      C  TG   GA  A
                                 TTCCA AG  CTAA  TT CCAGT
                                 ||||| ||  ||||  || |||||
                                 AAGGT TC  GGTT  AA GGTCG
                                   _ GT   G_  _
GAM966  LOC221474 5'  GCTGGTGGGGATGGTGTGGG   92383      AGT   AGA
                                 TCCAC   GCTA   TTACCAGT
                                 |||||   ||||   ||||||||
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                                GGGTG  TGGT  GGTGGTCG
                                  ___   AGG
GAM966  LOC222234 3'  CTGGTGAACTGTTTTGGGA   94245    A  T  TA  A
                                TCC CAG GC  AG TTACCAG
                                ||| ||| ||  || |||||||
                                AGG GTT TG  TC AGTGGTC
                                  _  T  __  A
GAM966  LOC257554 3'  GCTGGTAGCTCAGGCAGTGTGG 97694      G   A_  A
          G                      TCCACA TGCT  AG TTACCAGT
                                |||||| ||||  || ||||||||
                                GGGTGT ACGG  TC GATGGTCG
                                   G   AC  _
GAM966  LOC51218  3'  TTGGTGATTTTAGTTGGTCTGG 33107    CAGT_         GT
                                CCA    GCTAAGATTACCA
                                |||    ||||||||||||
                                GGT    TGATTTTAGTGGT
                                  CTGGT          TG
GAM966  LOC59346  3'  GTCTTGGACTGTGGGA     41277        G
                                TTCCACAGT CTAAGAT
                                ||||||||| |||||||
                                AGGGTGTCA GGTTCTG
                                      _
GAM966  LOC90719  3'  CTGGTGATGGAGTGTGGG    63883     AGT  AAG
                                TCCAC  GCT  ATTACCAG
                                |||||  |||  ||||||||
                                GGGTG  TGA  TAGTGGTC
                                  ____  GG_
GAM966  LOC91156  5'  ACTGGTGGTCAAGGCTGGGAA  65111    A   G  AA
                                TTCC CAGT CT  GATTACCAGT
                                |||| |||| ||  ||||||||||
                                AAGG GTCG GA  CTGGTGGTCA
                                  _   _  A_
GAM966  LOC92552  5'  ATTTTAGCCCTGTGGAA     69665        T
                                TTCCACAG GCTAAGAT
                                |||||||| ||||||||
                                AAGGTGTC CGATTTTA
                                     C
GAM966  LOC92578  5'  GTTGCAGTTTAGCTGCTGTGGA 69830         _    ATTACCAGT
          G                      TTCCACAGT GCTAAG
                                |||||||| ||||||
                                GAGGTGTCG CGATTT
                                     T     GACGTTG
GAM966  LOC92935  3'  ACTGGTGGTTTTACAGGGGGA  70959     ACAG  C
                                TTCC    TG TAAGATTACCAGT
                                ||||    || ||||||||||||
                                AGGG    AC ATTTTGGTGGTCA
                                  GG__  _
GAM967  ABL1      3'  AAAACAGGGTGCTAAAGC    17672     GCTC
                                GCT    AGCACCCTGTTTT
                                |||    ||||||||||||
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                                CGA   TCGTGGGACAAAA
                                  AA__
GAM967  ABL1     3'  AAAACAGGGTGCTAAAGC    23610     GCTC
                                GCT   AGCACCCTGTTTT
                                |||   ||||||||||||
                                CGA   TCGTGGGACAAAA
                                  AA__
GAM967  CUL3     3'  AAAATTATACATGAGCAGCT   13157         GCACCCT
                                AGCTGCTCA     GTTTT
                                |||||||||     |||||
                                TCGACGAGT     TAAAA
                                     ACATAT_
GAM967  PRG2     5'  AAAACAGGGAGCTACAGT    10776     CTC   A
                                GCTG   AGC CCCTGTTTT
                                ||||   ||| |||||||||
                                TGAC   TCG GGGACAAAA
                                  A__   A
GAM967  TDGF1    3'  AAAACAAAATGGGTTACTTGA  12197      CT    GCACCC
                                TCAAG  GCTCA     TGTTTT
                                |||||  |||||     ||||||
                                AGTTC  TGGGT     ACAAAA
                                   AT    AAA___
GAM967  DKFZp547G183 3'  AAAACAAGACATGGGGCAGCTG 38020     A      AGCACCC
           A                     TCA GCTGCTC      TGTTTT
                                ||| |||||||      ||||||
                                AGT CGACGGG      ACAAAA
                                  _      GTACAGA
GAM967  EBF2     3'  AAAACAGGGTACCAGC      42640      CTCAGC
                                GCTG     ACCCTGTTTT
                                ||||     ||||||||||
                                CGAC     TGGGACAAAA
                                  CA____
GAM967  EVI5     3'  AAAACAGGATGCCTGTCACTGA 18984     A C  CT   _  C
                                TCA G TG  CAG CA CCTGTTTT
                                ||| | ||  ||| || ||||||||
                                AGT C AC  GTC GT GGACAAAA
                                  _ _  T_   C  A
GAM967  FLJ20069  3'  AAAACAAAAAAGATAAGCAGCT 34465         CAGCACCC_
           T                     AAGCTGCT        TGTTTT
                                ||||||||        ||||||
                                TTCGACGA        ACAAAA
                                     ATAGAAAAA
GAM967  GRIP1    5'  AAACAGAGAGGCAGCTTG    70623         CAGCACC
                                CAAGCTGCT      CTGTTT
                                |||||||||      ||||||
                                GTTCGACGG      GACAAA
                                     AGA____
GAM967  KIAA0172  5'  AAAACAGGGAATGCGGAACAGC 64965     A   C  A   __
           TGA                     TCA GCTG TC GCA  CCCTGTTTT
                                ||| |||| || |||  |||||||||
```

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                                AGT CGAC AG CGT  GGGACAAAA
                                  _   A  G   AA
GAM967  KIAA1641  3'  AAAACAGGATGACCAAATTGA  80204     GC  C   GCAC
                                TCAA  TG TCA   CCTGTTTT
                                ||||  || |||   ||||||||
                                AGTT  AC AGT   GGACAAAA
                                  AA  C   A___
GAM967  MGC14161  5'  AGATGCTGAGCAGGTTGA    51837     G        CC
                                TCAA CTGCTCAGCA  CT
                                |||| ||||||||||  ||
                                AGTT GACGAGTCGT  GA
                                  G        A_
GAM967  NYD-SP21  3'  AGGGCATGCTGAGCACT     50872    C       __
                                AG TGCTCAGCA  CCCT
                                || |||||||||  ||||
                                TC ACGAGTCGT  GGGA
                                 _       AC
GAM967  LOC126917 3'  AAAACAAACAACAAAAGCAGCT 74577         CAGCACCC_
            TG                    CAAGCTGCT       TGTTTT
                                |||||||||       ||||||
                                GTTCGACGA       ACAAAA
                                     AAACAACAA
GAM967  LOC134121 5'  GCTGGCGCTGAGCAACCTGA   75154     AGC      A  CT
                                TCA   TGCTCAGC CC  GT
                                |||   |||||||| ||  ||
                                AGT   ACGAGTCG GG  CG
                                  CCA       C  T_
GAM967  LOC153396 3'  AACAGTGGCACTGAGCAGCTT  80818          CA  _
                                AAGCTGCTCAG  CC CTGTT
                                ||||||||||  || |||||
                                TTCGACGAGTC  GG GACAA
                                      AC  T
GAM968  FLNA     3'  GCCCGCCTGTCACTGCAG    7580             A_
                                CTGCAGTGACAGGC  GC
                                ||||||||||||||  ||
                                GACGTCACTGTCCG  CG
                                       CC
GAM968  Nrap     3'  ACTTAGCATGCCCTTCACTGCA 43346          CA   _  CTT
            GT                    ACTGCAGTGA  GGCA GC   AGT
                                |||||||||  |||| ||   |||
                                TGACGTCACT  CCGT CG   TCA
                                     TC    A  AT_
GAM968  Nrap     3'  ACTTAGCATGCCCTTCACTGCA 57633          CA   _  CTT
            GT                    ACTGCAGTGA  GGCA GC   AGT
                                |||||||||  |||| ||   |||
                                TGACGTCACT  CCGT CG   TCA
                                     TC    A  AT_
GAM968  ZFX      5'  GCCCGCCTGTCACTGCCGT   12718    T         A_
                                AC GCAGTGACAGGC  GC
                                || ||||||||||||  ||
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                                TG CGTCACTGTCCG  CG
                                 C          CC
GAM968  C19orf7   3' GCTATGCCTGCACTGCAG    61129        A     __
                                CTGCAGTG CAGGCA  GC
                                |||||||| ||||||  ||
                                GACGTCAC GTCCGT  CG
                                     _     AT
GAM968  FLJ10604  3' ACTAAGGCCACTGTGCCACTGT 36334       __   GCA
                                GCAGTG  ACAG   GCCTTAGT
                                ||||||  ||||   ||||||||
                                TGTCAC  TGTC   CGGAATCA
                                   CG    AC_
GAM968  FLJ12363  3' AGGCACCTGTCACCACA     49670    CA      CA
                                TG  GTGACAGG  GCCT
                                ||  ||||||||  ||||
                                AC  CACTGTCC  CGGA
                                 AC       A_
GAM968  FLJ14525  3' ACCAAGGCTGCCCAGTG     51411    G  ACA       A
                                CA TG   GGCAGCCTT GT
                                || ||   |||||||||  ||
                                GT AC   CCGTCGGAA CA
                                 G  ___        C
GAM968  GTF2E1    3' TTGCTGTCACTACAGT      18621      C       G
                                ACTG AGTGACAG CAG
                                |||| |||||||| |||
                                TGAC TCACTGTC GTT
                                  A       _
GAM968  HYPC      5' GGTGCCTGTCACCGCAG     64610      A        G
                                CTGC GTGACAGGCA CC
                                |||| ||||||||||  ||
                                GACG CACTGTCCGT GG
                                  C        _
GAM968  KIAA0937  3' CTGCCTGTCACCCAGT      91586      CA
                                ACTG  GTGACAGGCAG
                                ||||  ||||||||||
                                TGAC  CACTGTCCGTC
                                  C_
GAM968  KIAA1010  3' GTTGCCTGCCACCCAG      72073     CA   A
                                CTG  GTG CAGGCAGC
                                |||  ||| ||||||||
                                GAC  CAC GTCCGTTG
                                  C_   C
GAM968  KIAA1301  3' ACTAAAGGCACGTACTGCAGT  66340         ACAGGCA    _
                                ACTGCAGTG      GCCTT AGT
                                |||||||||      ||||| |||
                                TGACGTCAT      CGGAA TCA
                                     GCA____     A
GAM968  KIAA1393  3' ACTAAGGCTACCAAATAC     72095     ACA  C
                                GTG   GG AGCCTTAGT
                                |||   || |||||||||
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                                CAT   CC TCGGAATCA
                                  AAA  A
GAM968  LMOD1    3'  TTGCCTGTCACCCCAGT     24048      CA
                                ACTG  GTGACAGGCAG
                                ||||  ||||||||||
                                TGAC  CACTGTCCGTT
                                  CC
GAM968  PTDSS2   3'  GCTCCCTGTCACCCAG      47889     CA       C
                                CTG  GTGACAGG AGC
                                |||  |||||||| |||
                                GAC  CACTGTCC TCG
                                  C_       C
GAM968  LOC125704 5'  GCTGCCTGCACTACA       74410    C    A
                                TG AGTG CAGGCAGC
                                || |||| ||||||||
                                AC TCAC GTCCGTCG
                                 A   _
GAM968  LOC131368 3'  ACTAAACTATGTGTGACTGCAG 75855         G   GGC  CC
          T                      ACTGCAGT ACA   AG  TTAGT
                                ||||||||| |||   ||  |||||
                                TGACGTCA TGT   TC  AATCA
                                     G   GTA  A_
GAM968  LOC145719 5'  GCCGTACCTGTCACGCAGT    83452       A       CA__
                                ACTGC GTGACAGG    GC
                                ||||| ||||||||    ||
                                TGACG CACTGTCC    CG
                                   _       ATGC
GAM968  LOC145720 5'  GCCGTACCTGTCACGCAGT    83434       A       CA__
                                ACTGC GTGACAGG    GC
                                ||||| ||||||||    ||
                                TGACG CACTGTCC    CG
                                   _       ATGC
GAM968  LOC158402 3'  CTAAAGTTTGTCACCGCA     86803      A        AGCC
                                TGC GTGACAGGC    TTAG
                                ||| |||||||||    ||||
                                ACG CACTGTTTG    AATC
                                  C        A___
GAM968  LOC161176 5'  GCTGCCCATCACGCAG      82260      A    CA
                                CTGC GTGA  GGCAGC
                                |||| ||||  ||||||
                                GACG CACT  CCGTCG
                                   _    AC
GAM968  LOC197114 5'  GCCGTACCTGTCATGCAGT    89706       G       CA__
                                ACTGCA TGACAGG    GC
                                ||||||| |||||||    ||
                                TGACGT ACTGTCC    CG
                                   _       ATGC
GAM968  LOC197117 5'  GCCGTACCTGTCATGCAGT    89720       G       CA__
                                ACTGCA TGACAGG    GC
                                ||||||| |||||||    ||
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                                TGACGT ACTGTCC   CG
                                   _     ATGC
GAM968  LOC199796 5'  ACCAAGGTGAAGCCACTGC   74448     GACA  A__    A
                                GCAGT   GGC  GCCTT GT
                                |||||   |||  ||||| ||
                                CGTCA   CCG  TGGAA CA
                                   _____  AAG    C
GAM968  LOC203080 5'  ACTAAGGCCGCTGAGCCACAGT 89264     CA  GACA  A
                                ACTG  GT   GGC GCCTTAGT
                                ||||  ||   ||| ||||||||
                                TGAC  CG   TCG CGGAATCA
                                  AC  AG__  C
GAM969  CYP2S1   3'  CTACAAGGGCCACAAAGCA   47614       A    CAT
                                TGCTTTGT GTTCT  TGTAG
                                |||||||| |||||  |||||
                                ACGAAACA CGGGA  ACATC
                                     C   ___
GAM969  FLJ11222  3'  TACAACACTACAGAGCACT   37172          TCTCA
                                AGTGCTTTGTAGT   TTGTA
                                ||||||||||||    |||||
                                TCACGAGACATCA   AACAT
                                       C____
GAM969  KIAA1229  3'  CAAGGAGAACTACAAACCACT  62064     C         A
                                AGTG TTTGTAGTTCTC TTG
                                |||| |||||||||||| |||
                                TCAC AAACATCAAGAG AAC
                                  C         G
GAM969  KIAA1582  5'  ACAATGAAGGAAGCACT    65364       TGTAG TC
                                AGTGCTT    T  TCATTGT
                                |||||||    |  |||||||
                                TCACGAA    G  AGTAACA
                                   _____ GA
GAM969  MGC32104  3'  CTACAATGAGAATTACAAAGCA 58406
                                TGCTTTGTAGTTCTCATTGTAG
                                |||||||||||||||||||||
                                ACGAAACATTAAGAGTAACATC

GAM969  LOC55885  3'  AGAATACAAAGCACT      37814          G
                                AGTGCTTTGTA TTCT
                                |||||||||| ||||
                                TCACGAAACAT AAGA
                                      _
GAM970  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT  TGTCTGAG
                                |||| |||||  ||||||||
                                TAAA TGAAA  ACAGATTC
                                  A    T__
GAM970  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875      CAC  C  T
                                CATTT  TTT AC GTCTGAGAT
                                |||||  ||| || |||||||||
```

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                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T _
GAM970  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                                _
GAM970  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                  CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM970  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||  ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM970  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM970  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM970  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM970  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_    CG_
GAM970  CG012    5'  CTCACTCTGAAAGTGAA     83218          CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM970  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM970  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
              G                   CATTTC        GTCTGAGAT
                                ||||||        |||||||||
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                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM970  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA  TCACTGTCTGAGAT
                                |||||||  ||||||||||||||
                                GTAAAGT  AGTGACAGACTCTA
                                   C__
GAM970  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM970  KLHL6     3'  ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM970  NIR3      3'  GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                 C
GAM970  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM970  PP35      3'  ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM970  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148        TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM970  SEP15     3'  TCCTACAGTAAGAGTGAAA   14934       C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM970  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA  73941       CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM970  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
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                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM970  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM970  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM970  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA

                                      _
GAM971  AGXT     3'  AGGCAGCCCTTTTCCCTCCAGT 3458         __     A__  A
           GG                     TCACTGG  GGAAAA   CT CCT
                                |||||||  ||||||   || |||
                                GGTGACC  CCTTTT   GA GGA
                                    TC     CCC  C
GAM971  CACNG1   3'  CTCAGGCTTCTTCCCCAGGA   5583     A       A  CTA   A
                                TC CTGGGGAA AA   CCT AG
                                || ||||||| ||   ||| ||
                                AG GACCCCTT TT   GGA TC
                                 _       C  C__   C
GAM971  CHAC     3'  TCTCAGTAGTTTCCCCCA    52794       AA      CTA
                                TGGGG  AAACTAC   AGA
                                |||||  |||||||   |||
                                ACCCC  TTTGATG   TCT
                                  C_      AC_
GAM971  ED1      3'  AGTGTTATTTATTCCCCAGTGA 7362           _  CT  _
                                TCACTGGGGAA AAA  AC CT
                                |||||||||| |||  || ||
                                AGTGACCCCTT TTT  TG GA
                                      A   AT  T
GAM971  HOXC13   3'  CTTAGGCAAGATTTCCCAGT   59684         AAACTA
                                ACTGGGGAA     CCTAAG
                                |||||||||     ||||||
                                TGACCCTTT     GGATTC
                                    AGAAC_
GAM971  IFNA7    5'  TAGGTAGCCTAGTGA       40740         GAAAAA     A
                                TCACTGGG     CTACCT A
                                ||||||||     |||||| |
                                AGTGATCC     GATGGA T
                                    _______      C
GAM971  MAPK4    3'  TGGGCGTCCTACCCCAGTGA   10831         AAAA  TA
                                TCACTGGGG    AC  CCTA
                                |||||||||    ||  ||||
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                                AGTGACCCC   TG  GGGT
                                     ATCC  C_
GAM971  PIGN    3'  GGCAGCTCTTCCCAGTGA   24671        AAAA  A
                                TCACTGGGGA   CT CC
                                ||||||||||   || ||
                                AGTGACCCTT   GA GG
                                     CTC_  C
GAM971  PPP2R5E  5'  TCTTCGGATTCTTCCCCAG   20729       A  CTA  T
                                CTGGGGAA AA   CC AAGA
                                |||||||| ||   || ||||
                                GACCCCTT TT   GG TTCT
                                     C  A__  C
GAM971  PTPRH   3'  CTCTGGTTTCCCCAGGA    11114    A      AAACT   TA
                                TC CTGGGGAA    ACC  AG
                                || ||||||||    |||  ||
                                AG GACCCCTT    TGG  TC
                                 _     _____  TC
GAM971  RNASE1   5'  TCTTAAGACCTTCCCCAGAGA  11349    A      AAA  ACC
                                TC CTGGGGAA   CT   TAAGA
                                || ||||||||   ||   |||||
                                AG GACCCCTT   GA   ATTCT
                                 A      CCA  ___
GAM971  SNRPN   3'  TCTCAGTCACTTTTTCCCC   42994        CTAC  A
                                GGGGAAAAA   CT AGA
                                |||||||||   || |||
                                CCCCTTTTT   GA TCT
                                     CACT  C
GAM971  SNRPN   3'  TCTCAGTCACTTTTTCCCC   43000        CTAC  A
                                GGGGAAAAA   CT AGA
                                |||||||||   || |||
                                CCCCTTTTT   GA TCT
                                     CACT  C
GAM971  SNRPN   3'  TCTCAGTCACTTTTTCCCC   43008        CTAC  A
                                GGGGAAAAA   CT AGA
                                |||||||||   || |||
                                CCCCTTTTT   GA TCT
                                     CACT  C
GAM971  SNRPN   3'  TCTCAGTCACTTTTTCCCC   43015        CTAC  A
                                GGGGAAAAA   CT AGA
                                |||||||||   || |||
                                CCCCTTTTT   GA TCT
                                     CACT  C
GAM971  TSG     3'  TCTGTTAGTTTTTCCCC    40240          CCTA
                                GGGGAAAAACTA   AGA
                                ||||||||||||   |||
                                CCCCTTTTTGAT   TCT
                                       TG__
GAM971  AKT3    3'  TCTTTTAGTTTTTCCCTCAGTG 18436       _        CCT
           A                     TCACTG GGGAAAAACTA   AAGA
                                ||||||| ||||||||||   ||||
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                                AGTGAC CCCTTTTTGAT   TTCT
                                   T         T__
GAM971  CALN1    3'  CTTAGGCAAACCCAGTGG    48868        GAAAAACTA
                                TCACTGGG        CCTAAG
                                ||||||||        ||||||
                                GGTGACCC        GGATTC
                                     AAAC_____
GAM971  DCTN4    3'  TCTTAATTTTTTTCCCAGT    67789           CTACC
                                ACTGGGGAAAAA    TAAGA
                                ||||||||||||    |||||
                                TGACCCTTTTTT    ATTCT
                                       TA___
GAM971  DKFZP564K0822 3'  CTCAGGCAGCTCCAGTGG    94046         AAAAA  A   A
                                TCACTGGGG    CT CCT AG
                                |||||||||    || ||| ||
                                GGTGACCTC    GA GGA TC
                                     _____  C   C
GAM971  DKFZp564K142 3'  TCTTAACCTTCTCTTCCCAGTG 49525          AAAACTACC
           A                     TCACTGGGGA        TAAGA
                                ||||||||||        |||||
                                AGTGACCCTT        ATTCT
                                      CTCTTCCA_
GAM971  FLJ12270  3'  TGGGTTCGTCCCCAGTGA    47575          AAAACT
                                TCACTGGGGA     ACCTA
                                ||||||||||     |||||
                                AGTGACCCCT     TGGGT
                                      GCT___
GAM971  FLJ20871  3'  CTTGGAAGCTTTCCCCAGTGA  42028           AA  A  T
                                TCACTGGGGAAA  CT CC AAG
                                ||||||||||||  || || |||
                                AGTGACCCCTTT  GA GG TTC
                                       C_  A  _
GAM971  KIAA0057  3'  AGTTCTCCCCAGTGA      24417          AA
                                TCACTGGGGA  AACT
                                ||||||||||  ||||
                                AGTGACCCCT  TTGA
                                      C_
GAM971  KIAA0161  3'  TCTTGCCATCATTCCCCAGT   28516         AAACTACC
                                ACTGGGGAA       TAAGA
                                |||||||||       |||||
                                TGACCCCTT       GTTCT
                                     ACTACC__
GAM971  KIAA0222  3'  GTAGTTTCCCCACAGTGA    27683       _  AA
                                TCACTG GGG  AAACTAC
                                ||||||  |||  |||||||
                                AGTGAC CCC  TTTGATG
                                   A   C_
GAM971  KIAA0472  3'  AGTTTTTTCCCCAGTGG     71856            _
                                TCACTGGGGAAAAA CT
                                |||||||||||||| ||
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                                GGTGACCCCTTTTT GA
                                       T
GAM971  KIAA0711 3' TCTTAGGTAACTTCCT     29528      AAAC
                                GGGAA   TACCTAAGA
                                |||||   |||||||||
                                TCCTT   ATGGATTCT
                                  CA__
GAM971  KIAA0852 5' TTAGATAGTCTTTCCCCA    30083        A   C
                                TGGGGAAA ACTA CTAA
                                |||||||| |||| ||||
                                ACCCCTTT TGAT GATT
                                     C   A
GAM971  KIAA1010 3' TCTTAAGATCTTCCCCAG    72074        AAA  ACC
                                CTGGGGAA  CT  TAAGA
                                ||||||||  ||  |||||
                                GACCCCTT  GA  ATTCT
                                     CTA  ___
GAM971  KIAA1145 3' GTATCTTCTCCCCAGTGA    65626         A  AC
                                TCACTGGGGA AA  TAC
                                |||||||||| ||  |||
                                AGTGACCCCT TT  ATG
                                      C  CT
GAM971  KIAA1161 5' AGGCGGTTTCCCCAGGA     81734    A      AA  TA
                                TC CTGGGGAA  AC  CCT
                                || ||||||||  ||  |||
                                AG GACCCCTT  TG  GGA
                                 _      __  GC
GAM971  KIAA1238 3' TCTGCTGGCTTTTCTCCAATGA 71080     C       A   CCTA
                                TCA TGGGGAAAA CTA    AGA
                                ||| ||||||||| |||    |||
                                AGT ACCTCTTTT GGT    TCT
                                  A       C   CG__
GAM971  KIAA1649 5' CTTATTTTGTTCCCCAGTGA   50260          AAACTACC
                                TCACTGGGGAA       TAAG
                                ||||||||||        ||||
                                AGTGACCCCTT       ATTC
                                      GTTTT___
GAM971  KIAA1735 3' AGTTTTTCCCCAGGA       87624    A
                                TC CTGGGGAAAAACT
                                || ||||||||||||
                                AG GACCCCTTTTTGA
                                 _
GAM971  KIAA1908 5' TGGCTTTTCCCCACCGA     73405    AC       A
                                TC  TGGGGAAAA CTA
                                ||  ||||||||| |||
                                AG  ACCCCTTTT GGT
                                 CC        C
GAM971  MAD4     3' GTGTTGCCCTCCCCAGTGG   21283          AA__   T
                                TCACTGGGGA    AAC AC
                                ||||||||||    ||| ||
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                                GGTGACCCCT   TTG TG
                                     CCCG  _
GAM971  MGC22014  3'  TCTTAGTCATCTCCCCAGTG  64499       AAAACTAC
                                CACTGGGGA      CTAAGA
                                |||||||||      ||||||
                                GTGACCCCT      GATTCT
                                     CTACT___
GAM971  PLA2G12   3'  TCTCAGGTATCTTCCCCAG   48026       AAAC    A
                                CTGGGGAA   TACCT AGA
                                ||||||||   ||||| |||
                                GACCCCTT   ATGGA TCT
                                     CT__    C
GAM971  RAB3D     3'  CTCAGGCAGCCCCGGTGG    15008       AAAAA  A   A
                                TCACTGGGG    CT CCT AG
                                |||||||||    || ||| ||
                                GGTGGCCCC    GA GGA TC
                                     _____  C   C
GAM971  SMT3H2    3'  TCCTAGATAGTTTTCCCT    22675       A   C   A
                                GGGGAAAA CTA CTA GA
                                |||||||| ||| ||| ||
                                TCCCTTTT GAT GAT CT
                                     _   A   C
GAM971  SNURF     3'  TCTCAGTCACTTTTTCCCC   19054       CTAC  A
                                GGGGAAAAA   CT AGA
                                |||||||||   || |||
                                CCCCTTTTT   GA TCT
                                     CACT  C
GAM971  TA-NFKBH  3'  TAGTCCTTTCCCCACTGA    51172    C      A_
                                TCA TGGGGAAA  ACTA
                                ||| ||||||||  ||||
                                AGT ACCCCTTT  TGAT
                                  C       CC
GAM971  U5-116KD  3'  CTTACTCTGTTCTCCCCCAGTG 14908       AAA   TACC
           A                     TCACTGGGG   AAC    TAAG
                                |||||||||   |||    ||||
                                AGTGACCCC   TTG    ATTC
                                     CTC   TCTC
GAM971  LOC149535 5'  CTCAGGCCTGTGCTCCCCAGT  79417       AAA  TA_   A
                                ACTGGGGA   AC   CCT AG
                                ||||||||   ||   ||| ||
                                TGACCCCT   TG   GGA TC
                                     CG_  TCC   C
GAM971  LOC153810 5'  TCTCAGGTAGTTCTTTGTAG   80936    G   AA      A
                                CTG GGA  AACTACCT AGA
                                ||| |||  |||||||| |||
                                GAT TTT  TTGATGGA TCT
                                  G   C_       C
GAM971  LOC154547 3'  TCCTAGATAGTTTTCCCT    76054       A   C   A
                                GGGGAAAA CTA CTA GA
                                |||||||| ||| ||| ||
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                                TCCCTTTT GAT GAT CT
                                    _  A  C
GAM971  LOC165257 3'  CTCAGACAGCCTCCTCCCAGTG 82480        AAAAA  AC  A
                                CACTGGGG    CT  CT AG
                                ||||||||    ||  || ||
                                GTGACCCT    GA  GA TC
                                    CCTCC  CA  C
GAM971  LOC221561 3'  TCCTAGATAGTTTTCCCT    92134        A   C   A
                                GGGGAAAA CTA CTA GA
                                |||||||| ||| ||| ||
                                TCCCTTTT GAT GAT CT
                                    _  A  C
GAM971  LOC254393 5'  TAGGTACTCCAGTGA       97126         AAAAAC    A
                                TCACTGGGG     TACCT A
                                |||||||||     ||||| |
                                AGTGACCTC     ATGGA T
                                    _______    C
GAM971  LOC256596 5'  TCTGTGTGTTCTGCCCCAGTGA 96956         AAA   T  CTA
                                TCACTGGGG   AAC AC   AGA
                                |||||||||   ||| ||   |||
                                AGTGACCCC   TTG TG   TCT
                                    GTC   _  TG_
GAM971  LOC257591 3'  TCCTAGATAGTTTTCCCT    97844        A   C   A
                                GGGGAAAA CTA CTA GA
                                |||||||| ||| ||| ||
                                TCCCTTTT GAT GAT CT
                                    _  A  C
GAM971  LOC51289  5'  TCTTAGGTCTTGTCCCCCAG   33349       AAAAACT
                                CTGGGG      ACCTAAGA
                                ||||||      ||||||||
                                GACCCC      TGGATTCT
                                   CTGTTC_
GAM971  LOC90494  5'  TCTTAGGCAGTCTTTTCTGG   63057    TG GG  AA   A
                                C  G  AA  ACT CCTAAGA
                                |  |  ||  ||| |||||||
                                G  C  TT  TGA GGATTCT
                                 GT TT  C_   C
GAM972  ABCC3    3'  GCGGTGGACTCTCATGTGGCC  39156      G       GAGA
                                GGCCA ATGAGAGT    CACCGC
                                ||||| ||||||||    ||||||
                                CCGGT TACTCTCA    GTGGCG
                                   G       G___
GAM972  ADCY2    3'  GCAGTGCACCTCTCATCAGCC  65018     CA      _  AGA   C
                                GGC  GATGAGAG TG   CAC GC
                                |||  |||||||| ||   ||| ||
                                CCG  CTACTCTC AC   GTG CG
                                  A_       C ___   A
GAM972  ARHA     3'  CGATGTCCAACCCGTCTGGCC  70695         AGAG  A   C
                                GGCCAGATG    TG GACA CG
                                |||||||||    || |||| ||
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                                CCGGTCTGC    AC CTGT GC
                                     CCA_ _    A
GAM972  BIG1     3'  TTGATTCCCATCTGGC      21207         A    G
                                GCCAGATG GAGT AG
                                |||||||| |||| ||
                                CGGTCTAC CTTA TT
                                     C    G
GAM972  BMPR2    5'  GCTAGGTCCTCTCATCAGCC   6835      CA       TGA   ACC
                                GGC  GATGAGAG   GAC   GC
                                |||  ||||||||   |||   ||
                                CCG  CTACTCTC   CTG   CG
                                  A_        ___   GAT
GAM972  CLECSF5  3'  GGACACCGCGCAATCTCCATCT 25127        _ A________   AGACAC
            GGCC                    CAGATG AG       GTG     C
                                |||||| ||       |||     |
                                GTCTAC TC       CGC     G
                                    C  TAACGIII   CACAGA
GAM972  COL4A5   3'  GCAGTGTCTCATTGTC      52969    G        C
                                GA AGTGAGACAC GC
                                || |||||||||| ||
                                CT TTACTCTGTG CG
                                  G         A
GAM972  COL4A5   3'  GCAGTGTCTCATTGTC      52973    G        C
                                GA AGTGAGACAC GC
                                || |||||||||| ||
                                CT TTACTCTGTG CG
                                  G         A
GAM972  COL4A5   3'  GCAGTGTCTCATTGTC      4939     G        C
                                GA AGTGAGACAC GC
                                || |||||||||| ||
                                CT TTACTCTGTG CG
                                  G         A
GAM972  HLX1     5'  CTCGCTCTCATCCAGCC     41706     CA
                                GGC  GATGAGAGTGAG
                                |||  ||||||||||||
                                CCG  CTACTCTCGCTC
                                  AC
GAM972  ITGA7    3'  GTTTCCCCTCTCATCTGACC   9381     C        T_
                                GG CAGATGAGAG  GAGAC
                                || ||||||||||  |||||
                                CC GTCTACTCTC  CTTTG
                                  A         CC
GAM972  SEPN1    3'  GTCTCACTCCCCTCTGACC    66377    C    TGA
                                GG CAGA   GAGTGAGAC
                                || ||||   |||||||||
                                CC GTCT   CTCACTCTG
                                  A   CCC
GAM972  SERPINB9 3'  GTGCCTCACTCTGTC       14760     G       A
                                GAT AGAGTGAG CAC
                                ||| |||||||| |||
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                                CTG TCTCACTC GTG
                                  _      C
GAM972  SIAH2    3'  GTGTCCCATCTGGCT      17374         AGAGTGA
                                GGCCAGATG     GACAC
                                |||||||||     |||||
                                TCGGTCTAC     CTGTG
                                    C_______
GAM972  ADAMTSL1 3'  GCAGTGTCTCACTGGTTGTAGC 53502    CA_  GAG       C
           T                     GGC  GAT  AGTGAGACAC GC
                                |||  |||  |||||||||| ||
                                TCG  TTG  TCACTCTGTG CG
                                  ATG  G__       A
GAM972  BTBD2    3'  GCAGTGTCCGTTCTCATCCACC 35106    CCA       A    C
                                GG  GATGAGAGTG GACAC GC
                                ||  |||||||||| ||||| ||
                                CC  CTACTCTTGC CTGTG CG
                                 AC_        _    A
GAM972  C14orf4  5'  GCGGTGCTGGCGGCCCCGTCTG 67337         AGA__  G  A
           GCC                    GGCCAGATG    GT AG CACCGC
                                |||||||||    || || ||||||
                                CCGGTCTGC    CG TC GTGGCG
                                     CCCGG  G  _
GAM972  CRSP3    3'  GCAGGTTGACACTCTCACCTG  60635    A      AGAC  _
                                CAG TGAGAGTG   ACC GC
                                ||| ||||||||   ||| ||
                                GTC ACTCTCAC   TGG CG
                                  C       AGT_  A
GAM972  FLJ10713 3'  GTGTCTCACTGTTGCCCAGGC  36470    AGAT_  G
                                GCC    GA AGTGAGACAC
                                |||    || ||||||||||
                                CGG    TT TCACTCTGTG
                                  ACCCG  G
GAM972  FLJ12806 3'  CGTGTCAGTACCTGGCC     43086      ATGAGA  A_   C
                                GGCCAG     GTG  GACAC G
                                ||||||     |||  ||||| |
                                CCGGTC     CAT  CTGTG C
                                   _______  GA    A
GAM972  FLJ14327 3'  GCGGTACTTCTCTGCATCTGGC 46141         _   T  AC
           C                     GGCCAGATG AGAG GAG  ACCGC
                                |||||||| |||| |||  |||||
                                CCGGTCTAC TCTC TTC  TGGCG
                                     G   _  A_
GAM972  FLJ23499 3'  CGGTGCCATTGCTCTCCAGCC  42820    CAGAT    TG GA_
                                GGC    GAGAG  A   CACCG
                                |||    |||||  |   |||||
                                CCG    CTCTC  T   GTGGC
                                  AC___     GT ACC
GAM972  FLJ32894 3'  GCAGTGTCTCACTCTGTTGTCC 58340    C  ATG         C
                                GG CAG   AGAGTGAGACAC GC
                                || |||   |||||||||||| ||
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                                CC GTT   TCTCACTCTGTG CG
                                 T  G__         A
GAM972  KCNT1    3'  CGATGCTTCTCATCTACC    61831    CC      GTG  A  C
                                GG  AGATGAGA   AG CA CG
                                ||  ||||||||   || || ||
                                CC  TCTACTCT   TC GT GC
                                 A_       ___  _  A
GAM972  KIAA1320 5'  GTATCTCACTCTTTC      69307    T       C
                                GA GAGAGTGAGA AC
                                || ||||||||||  ||
                                CT TTCTCACTCT TG
                                 _        A
GAM972  MGC33345 3'  CGGTGGCCCCTGCATCTGGCC  58275         AG  TGAGA
                                GGCCAGATG  AG    CACCG
                                |||||||||  ||    |||||
                                CCGGTCTAC  TC    GTGGC
                                     G_  CCCG_
GAM972  NMU2R    5'  CTCACTCTCTCCCAGCC     39400     CA_  T
                                GGC   GA GAGAGTGAG
                                |||   || |||||||||
                                CCG   CT CTCTCACTC
                                  ACC  _
GAM972  phospho1 3'  CGGTGTCTCCTTGCATCCCAGC 82370     CA_   AG  T
           C                     GGC   GATG  AG GAGACACCG
                                |||   ||||  || |||||||||
                                CCG   CTAC  TC CTCTGTGGC
                                  ACC    GT  _
GAM972  SLC26A10 5'  GCGGTGTCTGCCTCCCTGGCC  56031       AT   A  G
                                GGCCAG  GAG GT AGACACCGC
                                ||||||  ||| || |||||||||
                                CCGGTC  CTC CG TCTGTGGCG
                                   C_   _  _
GAM972  LOC151031 5'  GTCTCATCCCATCCGGCC    87190      A    A  G
                                GGCC GATG GA TGAGAC
                                |||| |||| || ||||||
                                CCGG CTAC CT ACTCTG
                                  C    C  _
GAM972  LOC163231 3'  TGTTCACTCTCACCAGCC    82447     CAGA        A
                                GGC    TGAGAGTGAG CA
                                |||    |||||||||| ||
                                CCG    ACTCTCACTT GT
                                  ACC_         _
GAM972  LOC201616 3'  TCCACTCTCATCTGCC      90233     C         A
                                GGC AGATGAGAGTG GA
                                ||| ||||||||||| ||
                                CCG TCTACTCTCAC CT
                                  _         _
GAM972  LOC204084 3'  CGGTGTCTCAAGAATTCGGCC  89445     AG  GAGAG
                                GGCC  AT    TGAGACACCG
                                ||||  ||    ||||||||||
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                                CCGG  TA    ACTCTGTGGC
                                  CT  AGA__
GAM972  LOC222224 5'  GTCTCACTCTGTTACC      94201    CCA   G
                                GG   GAT AGAGTGAGAC
                                ||   ||| ||||||||||
                                CC   TTG TCTCACTCTG
                                 A__   _
GAM972  LOC253264 3'  TGTTTTACTCCTCTGACC    94692    C    TGA
                                GG CAGA   GAGTGAGACA
                                || ||||   ||||||||||
                                CC GTCT   CTCATTTTGT
                                 A    C__
GAM972  LOC255452 3'  CGGTGTCTCACTGCGGCC    97530      AGAT AG
                                GGCC    G  AGTGAGACACCG
                                ||||    |  ||||||||||||
                                CCGG    C  TCACTCTGTGGC
                                  _____ G_
GAM972  LOC90485  3'  CGGTGCCTGGCCAGCTGGCC   63013       A  AGA  G  A
                                GGCCAG TG   GT AG CACCG
                                |||||| ||   || || |||||
                                CCGGTC AC   CG TC GTGGC
                                   G  ___  G  C
GAM973  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM973  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM973  FDFT1    3'  TAGGAAAGTGAAATG       15518            A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                                _
GAM973  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM973  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  ||||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM973  PHYH     3'  ACAGTAAAAGTGAAAT      20608           C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
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                                TAAAGTGAAA TGACA
                                      A
GAM973  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__   _
GAM973  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM973  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_   CG_
GAM973  CG012   5'  CTCACTCTGAAAGTGAA     83218          CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM973  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946         G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                      G  TC
GAM973  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802        ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM973  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281         CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                      C__
GAM973  KIAA0984 3'  TTTGTCCAGTGAAAATGAA    65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                   A       CT
GAM973  KLHL6   3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                   _  G
GAM973  NIR3    3'  GCAGTGAAAGTGCAAT      66242      T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
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                                TAA GTGAAAGTGACG
                                  C
GAM973  PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                    CC  G
GAM973  PP35     3' ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                  __
GAM973  PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148          TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM973  SEP15    3' TCCTACAGTAAGAGTGAAA   14934         C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM973  SFXN2    3' CTCAGGGGAAAAAAGTGAAA  73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM973  LOC149703 3' ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM973  LOC154007 3' ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM973  LOC155004 3' TCATTTAAGTGAAAGGAAA   81226     A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM973  LOC222134 5' ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                     _
GAM974  ABCB1    5' CCAGAACATTCCTCCTGGAA  6247       CTGT  CT
                                TTCC   GG  ATGTTCTGG
                                ||||   ||  |||||||||
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                                AAGG   CC  TACAAGACC
                                  TCCT  T_
GAM974  AGT     3'  CCAGAACACAGTGCCTGGCA  3454     __  TA__
                                TGT  GGC   TGTTCTGG
                                |||  |||   ||||||||
                                ACG  CCG   ACAAGACC
                                  GT   TGAC
GAM974  ALDOB   3'  CCAGAATACCCACCCAAGAA  68087    CCT_   CTA
                                TTC   GTGG   TGTTCTGG
                                |||   ||||   ||||||||
                                AAG   CACC   ATAAGACC
                                  AACC   C__
GAM974  ARL4    3'  CCAGAACACAGTTGTGGGAA  19198     T TG   A
                                TTCCC G  GCT TGTTCTGG
                                ||||| |  ||| ||||||||
                                AAGGG T  TGA ACAAGACC
                                   _ GT   C
GAM974  B3GAT1  3'  CCAGAACAAAGGACAGAGAA  37827    C   GG  A
                                TTC CTGT  CT TGTTCTGG
                                ||| ||||  || ||||||||
                                AAG GACA  GA ACAAGACC
                                  A   G_  A
GAM974  B3GAT1  3'  CCAGAACAAAGGACAGAGAA  53972    C   GG  A
                                TTC CTGT  CT TGTTCTGG
                                ||| ||||  || ||||||||
                                AAG GACA  GA ACAAGACC
                                  A   G_  A
GAM974  CD79B   3'  CCAGAAGAGCCACAGG     5271        ATG
                                CCTGTGGCT   TTCTGG
                                |||||||||   ||||||
                                GGACACCGA   AAGACC
                                     G__
GAM974  CD79B   3'  CCAGAAGAGCCACAGG     41207       ATG
                                CCTGTGGCT   TTCTGG
                                |||||||||   ||||||
                                GGACACCGA   AAGACC
                                     G__
GAM974  CDH3    3'  CCAAACGTCAGGCCACAG    8380        __   C
                                CTGTGGCT  ATGTT TGG
                                ||||||||  ||||| |||
                                GACACCGG  TGCAA ACC
                                    AC    _
GAM974  COL5A1  5'  GCCAGAACAGCCGCCGCCACAA 3634   CC    TA____     III
          AGAA                    C  TGTGGC    TGTTCTGG  C
                                |  ||||||    ||||||||  |
                                G  ACACCG    ACAAGACC  G
                                 AA    CCGCCG      III
GAM974  CRIM1   3'  CCAGAACAAAGGCAG      33173     GG  A
                                CTGT  CT TGTTCTGG
                                ||||  || ||||||||
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                                GACG  GA ACAAGACC
                                  __ A
GAM974  DIAPH2   3'  CCAAAACAAGTCTAGCAGGGAA 22063        __   A   C
                                TTCCCTGT  GGCT TGTT TGG
                                ||||||||  |||| |||| |||
                                AAGGGACG  CTGA ACAA ACC
                                    AT   _   A
GAM974  DMD      3'  AGAAAATATAGTCACAGG    14414          __
                                CCTGTGGCTATGT  TCT
                                ||||||||||||  |||
                                GGACACTGATATA  AGA
                                      AA
GAM974  ED1      3'  TTGGAACAATCACAGGGAA   7376         CTA    TG
                                TTCCCTGTGG   TGTTC  G
                                ||||||||||   |||||  |
                                AAGGGACACT   ACAAG  T
                                    A__    GT
GAM974  EXTL3    3'  CCAAAACATGCCGCAGGGAG  7528          T    C
                                TTCCCTGTGGC ATGTT TGG
                                |||||||||||  ||||| |||
                                GAGGGACGCCG TACAA ACC
                                      _    A
GAM974  FCRH3    3'  CCAGAGTGGCCCACAGG     53630       _   GT
                                CCTGTGG CTAT  TCTGG
                                |||||||  ||||  |||||
                                GGACACC GGTG  AGACC
                                    C   __
GAM974  FECH     3'  CGTGGTGCCACAGGGAA     3753          __
                                TTCCCTGTGGC  TATG
                                ||||||||||  ||||
                                AAGGGACACCG  GTGC
                                      TG
GAM974  FGFRL1   3'  CCAGAACATACAAGGA      41619     C   GGCT
                                TCC TGT    ATGTTCTGG
                                |||  |||    |||||||||
                                AGG ACA    TACAAGACC
                                  A  _____
GAM974  GATA4    3'  CCAGAACAACAACTGGGAA    9004       T  GGCTA
                                TTCCC GT     TGTTCTGG
                                |||||  ||    ||||||||
                                AAGGG CA     ACAAGACC
                                   T  ACA__
GAM974  GNRH1    5'  CCATCACCAGCCACAGAGA    5883     C      AT  TC
                                TC CTGTGGCT  GT  TGG
                                ||  ||||||||  ||  |||
                                AG GACACCGA  CA  ACC
                                 A       C_  CT
GAM974  HAMP     3'  CCAGAACATAGGTCTTGGAA   40991      CTGT  _
                                TTCC    GGC TATGTTCTGG
                                ||||    ||| ||||||||||
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                                AAGG    CTG ATACAAGACC
                                  TT__   G
GAM974  IPP     3'  TAGTTTGAGCCACAGAGAA   19729     C      ATGTT
                                TTC CTGTGGCT    CTG
                                ||| ||||||||    |||
                                AAG GACACCGA    GAT
                                  A       GTTT_
GAM974  ITGB1   3'  CCAGTGTGGCCCAGGGAA    53369       T     GTT
                                TTCCCTG GGCTAT   CTGG
                                ||||||| ||||||   ||||
                                AAGGGAC CCGGTG   GACC
                                    _     T__
GAM974  KCNQ1   3'  CCAGCTGCTGAGCCGCAGAGAA 4021      C       AT  T_
                                TTC CTGTGGCT  GT  CTGG
                                ||| ||||||||  ||  ||||
                                AAG GACGCCGA  CG  GACC
                                  A       GT  TC
GAM974  KDR     3'  CAGAATACCACAAAGAA     9591      CC    CTA
                                TTC  TGTGG   TGTTCTG
                                |||  |||||   |||||||
                                AAG  ACACC   ATAAGAC
                                  AA    ___
GAM974  LEP     3'  CCAGGGGCCCACAGGGAA    4047          _  ATGT
                                TTCCCTGTGG CT    TCTGG
                                |||||||||| ||    |||||
                                AAGGGACACC GG    GGACC
                                      C  _____
GAM974  MKI67   3'  CCAGTGACCAGCCACAGGAGA  10041    _       AT  _
                                TC CCTGTGGCT  GTT CTGG
                                || |||||||||  ||| ||||
                                AG GGACACCGA  CAG GACC
                                  A       C_  T
GAM974  NEFH    3'  CCGGAACAGCCAAAG      40780    G    AT
                                CT TGGCT  GTTCTGG
                                || |||||  |||||||
                                GA ACCGA  CAAGGCC
                                  A    __
GAM974  NXF2    5'  CCAGAACATCACCAAG     35136    G   CT
                                CT TGG  ATGTTCTGG
                                || |||  |||||||||
                                GA ACC  TACAAGACC
                                  _   AC
GAM974  PDE6D   3'  CCAGCATACACACAGGGAA   10489        GC    TT
                                TTCCCTGTG  TATG  CTGG
                                |||||||||  ||||  ||||
                                AAGGGACAC  ATAC  GACC
                                      AC   __
GAM974  PHEMX   5'  CCAGCTGGAAACCACAGGGAG  57359          CTATGTT
                                TTCCCTGTGG      CTGG
                                ||||||||||      ||||
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                                GAGGGACACC      GACC
                                     AAAGGTC
GAM974  PHEMX    5'  CCAGCTGGAAACCACAGGGAG  57364          CTATGTT
                                TTCCCTGTGG      CTGG
                                ||||||||||      ||||
                                GAGGGACACC      GACC
                                     AAAGGTC
GAM974  PODXL    3'  CCAGAATGACACAAAGGA    18230     C_   GCTAT
                                TCC  TGTG    GTTCTGG
                                |||  ||||    |||||||
                                AGG  ACAC    TAAGACC
                                  AA   AG___
GAM974  PRODH    3'  CTGGGACAGCCACTGGAA    32925      CT    AT   TG
                                TTCC  GTGGCT  GTTC  G
                                ||||  ||||||  ||||  |
                                AAGG  CACCGA  CAGG  C
                                  T_     __    GT
GAM974  RANBP2L1 3'  CCAGAATAAAACCACCAGGAA 17313      CT   CTA
                                TTCC  GTGG   TGTTCTGG
                                ||||  ||||   ||||||||
                                AAGG  CACC   ATAAGACC
                                  AC    AAA
GAM974  REGL     3'  CCAGAACATGAATTCAGG    21486      TGGC
                                CCTG    TATGTTCTGG
                                ||||    ||||||||||
                                GGAC    GTACAAGACC
                                  TTAA
GAM974  SLC19A1  5'  CCAGAATGCATCCAGAGGGAA 11755       G   CTA
                                TTCCCT TGG   TGTTCTGG
                                ||||||  |||   ||||||||
                                AAGGGA ACC   GTAAGACC
                                   G   TAC
GAM974  ST14     3'  CCAGAACATACACTGTGAA   41765     CCT   GC
                                TTC   GTG  TATGTTCTGG
                                |||   |||  ||||||||||
                                AAG   CAC  ATACAAGACC
                                  TGT   __
GAM974  TBL2     3'  CCAGAACAACCTAGAGAA    24926     C   T  CTA
                                TTC CTG GG   TGTTCTGG
                                ||| ||| ||   ||||||||
                                AAG GAT CC   ACAAGACC
                                  A   _  A__
GAM974  TBL2     3'  CCAGAACAACCTAGAGAA    52182     C   T  CTA
                                TTC CTG GG   TGTTCTGG
                                ||| ||| ||   ||||||||
                                AAG GAT CC   ACAAGACC
                                  A   _  A__
GAM974  TCFL4    3'  CCAGGATAAGACCACAGGGAA 63461          _  A
                                TTCCCTGTGG CT TGTTCTGG
                                |||||||||| || ||||||||
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                                AAGGGACACC GA ATAGGACC
                                      A  _
GAM974  TFAP4    3'  CCGGGGCAGCCACAGGGAG   12237          AT
                                TTCCCTGTGGCT  GTTCTGG
                                ||||||||||||  |||||||
                                GAGGGACACCGA  CGGGGCC
                                              __
GAM974  UBE2L6   3'  CCAGGGGGAGCCACGG     14873        ATG
                                CTGTGGCT   TTCTGG
                                ||||||||   ||||||
                                GGCACCGA   GGGACC
                                     GG_
GAM974  UBQLN3   3'  CAAAACATAGTGGAG      33926     CTGTG      C
                                TTCC    GCTATGTT TG
                                ||||    |||||||| ||
                                GAGG    TGATACAA AC
                                  _____       A
GAM974  UMOD     3'  CCAGTGCTCCAGCCACAG    12548        AT_  T
                                CTGTGGCT   GT CTGG
                                ||||||||   || ||||
                                GACACCGA   CG GACC
                                     CCT  T
GAM974  WBSCR5   3'  CCAGAACAGGGCAGAG     26256    G  G  A
                                CT TG CT TGTTCTGG
                                || || || ||||||||
                                GA AC GG ACAAGACC
                                 G  G  _
GAM974  WBSCR5   3'  CCAGAACAGGGCAGAG     41856    G  G  A
                                CT TG CT TGTTCTGG
                                || || || ||||||||
                                GA AC GG ACAAGACC
                                 G  G  _
GAM974  WBSCR5   3'  CCAGAACAGGGCAGAG     50610    G  G  A
                                CT TG CT TGTTCTGG
                                || || || ||||||||
                                GA AC GG ACAAGACC
                                 G  G  _
GAM974  ZNF134   3'  CAGTTTAAGCCACAGGGAA   12846          A  TT
                                TTCCCTGTGGCT TG  CTG
                                |||||||||||| ||  |||
                                AAGGGACACCGA AT  GAC
                                      _  TT
GAM974  ZNF36    3'  CCTTCGTAGCCACAAGG     93960    C        TTCT
                                CC TGTGGCTATG    GG
                                || ||||||||||    ||
                                GG ACACCGATGC    CC
                                 A        TT__
GAM974  ABCA9    5'  CAGAACATGCAGAGA       54410    C    GGCT
                                TC CTGT    ATGTTCTG
                                || ||||    ||||||||
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                                AG GACG    TACAAGAC
                                 A   _____
GAM974  ADAMTSL1  3'  CCTCAAATAGCACAGGGAA    57686          G    GTTCT
                                TTCCCTGTG CTAT     GG
                                ||||||||| ||||     ||
                                AAGGGACAC GATA     CC
                                     _    AACT_
GAM974  BAIAP1    3'  CCAGAACGGCAGCAGG      16449       G   AT
                                CCTGT GCT  GTTCTGG
                                ||||| |||  |||||||
                                GGACG CGG  CAAGACC
                                   A   __
GAM974  BCKDK     3'  CCAGAACTTGGAGCAGGGAA   59793         GG   T
                                TTCCCTGT  CTA GTTCTGG
                                ||||||||  ||| |||||||
                                AAGGGACG  GGT CAAGACC
                                     A_   T
GAM974  C11orf25  3'  CCAAATTAGGGCCACAG     48639         AT_   C
                                CTGTGGCT   GTT TGG
                                ||||||||   ||| |||
                                GACACCGG   TAA ACC
                                     GAT   _
GAM974  C20orf112 3'  CCAGTGCTGCCACAGGGA    54640          TAT  T
                                TCCCTGTGGC   GT CTGG
                                ||||||||||   || ||||
                                AGGGACACCG   CG GACC
                                      T__  T
GAM974  C6orf26   3'  CCAAAACACAGAGCAGG     47509       GG  A    C
                                CCTGT  CT TGTT TGG
                                |||||  || |||| |||
                                GGACG  GA ACAA ACC
                                   A_  C    A
GAM974  CGGBP1    5'  CTGGCACCACAGGGAA      13362          CTA    CT
                                TTCCCTGTGG   TGTT  G
                                ||||||||||   ||||  |
                                AAGGGACACC   ACGG  C
                                     ____    T_
GAM974  DKFZP566G1424 5'  CCAGTGCTGCCACAGGGA    84779          TAT  T
                                TCCCTGTGGC   GT CTGG
                                ||||||||||   || ||||
                                AGGGACACCG   CG GACC
                                      T__  T
GAM974  DKFZp586I021 5'  CCAGACGTCACCACAGGGA    50088         CT    T
                                TCCCTGTGG  ATGT CTGG
                                |||||||||  |||| ||||
                                AGGGACACC  TGCA GACC
                                     AC    _
GAM974  DKFZP727M111 5'  CCAATCTGGTCACAGGGAA    31407           T  TC
                                TTCCCTGTGGCTA GT  TGG
                                |||||||||||| ||  |||
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                                AAGGGACACTGGT TA  ACC
                                      C  __
GAM974  ELF4     3'  CCGTGGATCAGCCACAGGGA  7431          AT   _
                                TCCCTGTGGCT  GTTC TGG
                                ||||||||||  |||| |||
                                AGGGACACCGA  TAGG GCC
                                      C_   T
GAM974  ERG-1    3'  CCAGGATGCCAAAGG      41842     G   TAT
                                CCT TGGC   GTTCTGG
                                ||| ||||   |||||||
                                GGA ACCG   TAGGACC
                                  A   ___
GAM974  FLJ00058 5'  CCAGAAATGCCAGCAGGGAA  78765       _   TATG
                                TTCCCTG TGGC    TTCTGG
                                ||||||| ||||    ||||||
                                AAGGGAC ACCG    AAGACC
                                    G   TA__
GAM974  FLJ12816 3'  CCAGAACAGGACGACAGTGAA  41932     C   GGCTA
                                TTC CTGT    TGTTCTGG
                                ||| ||||    ||||||||
                                AAG GACA    ACAAGACC
                                  T   GCAGG
GAM974  FLJ13315 3'  CCAGAACATAATACA       46568     GC
                                TGTG  TATGTTCTGG
                                ||||  ||||||||||
                                ACAT  ATACAAGACC
                                  A_
GAM974  FLJ20010 3'  CCAGAACGATTGGAACAGG    38716     GG  __
                                CCTGT  CTA  TGTTCTGG
                                |||||  |||  ||||||||
                                GGACA  GGT  GCAAGACC
                                   A_   TA
GAM974  FLJ22369 5'  ATGGCGCGACAGGGAA      49918       _ _
                                TTCCCTGT G GCTAT
                                |||||||| | |||||
                                AAGGGACA C CGGTA
                                     G G
GAM974  FLJ23563 3'  CCAGAATGCTACAAAAGAA   67593    CC_    TAT
                                TTC   TGTGGC   GTTCTGG
                                |||   ||||||   |||||||
                                AAG   ACATCG   TAAGACC
                                  AAA    ___
GAM974  FLJ32332 3'  CACAGCACACAGGGAA      58299       _  A
                                TTCCCTGTG GCT TG
                                ||||||||| ||| ||
                                AAGGGACAC CGA AC
                                      A  C
GAM974  GRIN3A   3'  CCAAGTGAAGCAGCCACAGGGA 55968         ATG  ___
                                TCCCTGTGGCT   TTC   TGG
                                ||||||||||   |||   |||
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                                AGGGACACCGA  AAG  ACC
                                     CG_  TGA
GAM974  HSPC166  3' CCAGAACACATGGAGGGAA  26366      G  GCTA
                                TTCCCT TG   TGTTCTGG
                                |||||| ||   ||||||||
                                AAGGGA GT   ACAAGACC
                                   G  AC__
GAM974  HSPC251  3' CCAGGCTAGAGCCACAGAGA  33249   C      A  TT
                                TC CTGTGGCT TG  CTGG
                                || |||||||| ||  ||||
                                AG GACACCGA AT  GACC
                                 A       G  CG
GAM974  IGF2AS   3' CCAGGGTGCAACAGAGAA   33095    C   G  TAT TT
                                TTC CTGT GC   G  CTGG
                                ||| |||| ||   |  ||||
                                AAG GACA CG   T  GACC
                                  A   A  ___ GG
GAM974  ILF3     3' CCAAAACACGCTGGGAA    15722     T  GCTA   C
                                TTCCC GTG   TGTT TGG
                                ||||| |||   |||| |||
                                AAGGG CGC   ACAA ACC
                                   T  ____   A
GAM974  KIAA0040 3' CCAAAGTTTCCAGCAGGGAA  27780       _  CT  GTTC
                                TTCCCTG TGG  AT   TGG
                                ||||||| |||  ||   |||
                                AAGGGAC ACC  TG   ACC
                                    G  TT  AA__
GAM974  KIAA0254 3' CAGACAGTCACAGGGAA    28596         ATGT
                                TTCCCTGTGGCT   TCTG
                                ||||||||||||   ||||
                                AAGGGACACTGA   AGAC
                                       C___
GAM974  KIAA0336 3' CCAGAATAAAACCACCAGGAA 27589     CT   CTA
                                TTCC  GTGG  TGTTCTGG
                                ||||  ||||  ||||||||
                                AAGG  CACC  ATAAGACC
                                  AC   AAA
GAM974  KIAA0494 3' CCAGAACACATTTGGG     28740    T_  GCTA
                                CCC  GTG   TGTTCTGG
                                |||  |||   ||||||||
                                GGG  TAC   ACAAGACC
                                  TT  ____
GAM974  KIAA0537 3' CCAGAACAGCCTACAGGGGA  29244       _   AT
                                TTCCCTGT GGCT  GTTCTGG
                                |||||||| ||||  |||||||
                                AGGGGACA CCGA  CAAGACC
                                     T   __
GAM974  KIAA0774 5' CGGGATGCCACAAGGAA    91752     C    TAT   TG
                                TTCC TGTGGC   GTTC  G
                                |||| ||||||   ||||  |
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                                AAGG ACACCG   TAGG  C
                                  A     ___    GT
GAM974  KIAA0828  3'  CCATGAAAGCCACAGAGGA   81194    _      ATG  _
                                TCC CTGTGGCT   TTC TGG
                                ||| ||||||||   ||| |||
                                AGG GACACCGA   AAG ACC
                                  A       ___   T
GAM974  KIAA1118  3'  CCAGAGGCCCACAGGGA     69606        _ ATGT
                                TCCCTGTGG CT    TCTGG
                                ||||||||| ||    |||||
                                AGGGACACC GG    AGACC
                                     C ____
GAM974  KIAA1742  3'  CAGATCCACAGGGAG       77657         CTATGT
                                TTCCCTGTGG     TCTG
                                ||||||||||     ||||
                                GAGGGACACC     AGAC
                                     T_____
GAM974  KIAA1944  5'  CCAACCTAGCCACAGGGA    75558          T  TC
                                TCCCTGTGGCTA GT  TGG
                                |||||||||||| ||  |||
                                AGGGACACCGAT CA  ACC
                                      C __
GAM974  KIAA1981  3'  CGGAACAGCACAAGGAA     88342     C   G  AT   TG
                                TTCC TGTG CT  GTTC  G
                                |||| |||| ||  ||||  |
                                AAGG ACAC GA  CAAG  C
                                  A   _ __    GT
GAM974  NXPH3     3'  ACGGAGCCACAGAGAG      65747     C       A
                                TTC CTGTGGCT TGT
                                ||| |||||||| |||
                                GAG GACACCGA GCA
                                  A       G
GAM974  PP5395    3'  TCAGGATAGCACAGGGAA     72110         G  AT
                                TTCCCTGTG CT  GTTCTGG
                                ||||||||| ||  |||||||
                                AAGGGACAC GA  TAGGACT
                                      _ __
GAM974  PRDM7     3'  CCAGAAGGGCCACAGAGAA   53788     C       ATG
                                TTC CTGTGGCT   TTCTGG
                                ||| ||||||||   ||||||
                                AAG GACACCGG   AAGACC
                                  A       G__
GAM974  PRDM9     3'  CCAGAAGGGCCACAGAGAA   39575     C       ATG
                                TTC CTGTGGCT   TTCTGG
                                ||| ||||||||   ||||||
                                AAG GACACCGG   AAGACC
                                  A       G__
GAM974  PXR2b     3'  ATATAGCCCAAGGAA       33337      C  T
                                TTCC TG GGCTATGT
                                |||| || ||||||||
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                                AAGG AC CCGATATA
                                  A  _
GAM974  RAB33B   3'  CCAGCTTAGCCACAAAGAA   48490    CC      TGTT
                                TTC  TGTGGCTA   CTGG
                                |||  ||||||||   ||||
                                AAG  ACACCGAT   GACC
                                  AA       TC__
GAM974  SH120    3'  CCAGAACATGAGAGGGAG    94606      GTGGC
                                TTCCCT    TATGTTCTGG
                                ||||||    ||||||||||
                                GAGGGA    GTACAAGACC
                                   GA___
GAM974  SH120    3'  CCAGAACATGAGAGGGAG    32920      GTGGC
                                TTCCCT    TATGTTCTGG
                                ||||||    ||||||||||
                                GAGGGA    GTACAAGACC
                                   GA___
GAM974  SLC2A12  3'  CCAGAACACACAGTGTGGA   59078    ___    GCTA
                                TCC   CTGTG   TGTTCTGG
                                |||   |||||   ||||||||
                                AGG   GACAC   ACAAGACC
                                  TGT    _____
GAM974  SP329    3'  CCAGAGTGCTCCACAGGGA   47924       CTA GT
                                TCCCTGTGG   T  TCTGG
                                |||||||||   |  |||||
                                AGGGACACC   G  AGACC
                                      TC_ TG
GAM974  SSH2     3'  TCAGTAAGCCCACAGGGAA   62213        _  ATGTT
                                TTCCCTGTGG CT    CTGG
                                |||||||||| ||    ||||
                                AAGGGACACC GA    GACT
                                      C  AT___
GAM974  SYTL4    5'  CCAGTCAGCCACAGGGAA    54939         ATGTT
                                TTCCCTGTGGCT    CTGG
                                ||||||||||||    ||||
                                AAGGGACACCGA    GACC
                                      CT___
GAM974  TNRC4    3'  CCAGTCAGCCACAGAGA     23221    C      ATGTT
                                TC CTGTGGCT    CTGG
                                || ||||||||    ||||
                                AG GACACCGA    GACC
                                  A       CT___
GAM974  UBE3B    3'  CCAGACTGTCAGCACAGGGAA  76919       G  _  GT
                                TTCCCTGTG CT AT  TCTGG
                                ||||||||| || ||  |||||
                                AAGGGACAC GA TG  AGACC
                                      _  C  TC
GAM974  VPS4A    3'  CCTTGCAGCCACAGAGA     25102    C      AT  TCT
                                TC CTGTGGCT  GT   GG
                                || ||||||||  ||   ||
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                                AG GACACCGA  CG   CC
                                 A       __  TT_
GAM974  XYLT1    5'  CCAACAGCAGCCACGGGAA   77847      T     A_   TC
                                TTCCC GTGGCT  TGT  TGG
                                ||||| ||||||  |||  |||
                                AAGGG CACCGA  ACA  ACC
                                   _     CG   __
GAM974  ZFP100   3'  CCAGAAAGCCAAAAAGAA    70050     CCTG    ATG
                                TTC    TGGCT   TTCTGG
                                |||    |||||   ||||||
                                AAG    ACCGA   AAGACC
                                  AAAA    ____
GAM974  ZNF213   5'  CAGCTACCACAGGGGA      65091          C  TGTT
                                TTCCCTGTGG TA    CTG
                                |||||||||| ||    |||
                                AGGGGACACC AT    GAC
                                      _  C___
GAM974  LOC112609 3'  CCAGTGTGGCACAGGGAA    72837         G    GTT
                                TTCCCTGTG CTAT   CTGG
                                ||||||||| ||||   ||||
                                AAGGGACAC GGTG   GACC
                                      _    T__
GAM974  LOC115073 5'  CCAGGCGTCAAACCACAGGGA  73204         CT__    T
                                TCCCTGTGG    ATGT CTGG
                                |||||||||    |||| ||||
                                AGGGACACC    TGCG GACC
                                     AAAC    _
GAM974  LOC122962 5'  CCAGACAGTGGCCACTGAGAA  75587     CCT       GT
                                TTC   GTGGCTAT  TCTGG
                                |||   ||||||||  |||||
                                AAG   CACCGGTG  AGACC
                                  AGT       AC
GAM974  LOC124044 3'  CCAGAACACTCAGAGGGA    76025      G   CTA
                                TCCCT TGG   TGTTCTGG
                                ||||| |||   ||||||||
                                AGGGA ACT   ACAAGACC
                                   G   C__
GAM974  LOC143308 5'  CCAAATTTGGCCACAG      82936         T   C
                                CTGTGGCTA GTT TGG
                                ||||||||| ||| |||
                                GACACCGGT TAA ACC
                                     T   _
GAM974  LOC145314 3'  CCAGAACACATCACCTGAG   77086     CCT    CTA
                                TTC   GTGG   TGTTCTGG
                                |||   ||||   ||||||||
                                GAG   CACT   ACAAGACC
                                  TC_    AC_
GAM974  LOC146420 3'  CCAGAACCAGTTACAG      83667         AT
                                CTGTGGCT  GTTCTGG
                                ||||||||  |||||||
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                                GACATTGA  CAAGACC
                                    C_
GAM974   LOC146445 3'  CCAGAGCCACCACAGGGA    83678        CTAT
                                TCCCTGTGG   GTTCTGG
                                |||||||||   |||||||
                                AGGGACACC   CGAGACC
                                    AC__
GAM974   LOC147178 3'  CCAGCCAGCCACGGAGAA    61323    C      ATGTT
                                TTC CTGTGGCT    CTGG
                                ||| ||||||||    ||||
                                AAG GGCACCGA    GACC
                                  A       CC___
GAM974   LOC148529 5'  CACAGCCACAGGAGAA     84166    _       A
                                TTC CCTGTGGCT TG
                                ||| |||||||| ||
                                AAG GGACACCGA AC
                                  A       C
GAM974   LOC148930 5'  CCAGGGGCAGACCACGGGGAA  79093         CTA    _
                                TTCCCTGTGG   TGTTC TGG
                                ||||||||||   ||||| |||
                                AAGGGGCACC   ACGGG ACC
                                    AG_    G
GAM974   LOC149950 5'  CCAGAACATGATCTCAGG    79551     T GC
                                CCTG G  TATGTTCTGG
                                |||| |  ||||||||||
                                GGAC C  GTACAAGACC
                                  T TA
GAM974   LOC150378 5'  CCAGAAACAAGCCACGGGAA  79742     T     ATG
                                TTCCC GTGGCT   TTCTGG
                                ||||| ||||||   ||||||
                                AAGGG CACCGA   AAGACC
                                   _     ACA
GAM974   LOC150951 5'  CCAGGGCCACACAGGGAA    85167        GCTAT
                                TTCCCTGTG    GTTCTGG
                                |||||||||    |||||||
                                AAGGGACAC    CGGGACC
                                    AC___
GAM974   LOC151429 3'  CCAGGAGACCACAGGGA     85347        _ ATGT
                                TCCCTGTGG CT    TCTGG
                                ||||||||| ||    |||||
                                AGGGACACC GA    GGACC
                                    A  ____
GAM974   LOC158434 3'  CCAGAATAAACCACTGGGAA  86819     T   CTA
                                TTCCC GTGG   TGTTCTGG
                                ||||| ||||   ||||||||
                                AAGGG CACC   ATAAGACC
                                   T    AA_
GAM974   LOC170106 5'  CCAAGGCAGTCAGCCACAGG  82571        A__   TC
                                CCTGTGGCT   TGT  TGG
                                |||||||||   |||  |||
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                                GGACACCGA  ACG  ACC
                                     CTG  GA
GAM974  LOC196446 3' CGGAAAGCCACAGAGAA    87708    C      ATG  TG
                                TTC CTGTGGCT  TTC  G
                                ||| ||||||||  |||  |
                                AAG GACACCGA  AAG  C
                                  A       ___  GT
GAM974  LOC197136 3' CCAGAACACTCAGAGGGA    89728      G  CTA
                                TCCCT TGG  TGTTCTGG
                                ||||| |||  ||||||||
                                AGGGA ACT  ACAAGACC
                                   G  C__
GAM974  LOC197342 3' CCAGGAGAAGCCACAGGGGA  87993          ATG
                                TTCCCTGTGGCT  TTCTGG
                                ||||||||||||  ||||||
                                AGGGGACACCGA  AGGACC
                                       AG_
GAM974  LOC200734 3' CCATCCGCAGCCACAGGGGA  88860          A  TTC
                                TTCCCTGTGGCT TG  TGG
                                |||||||||||| ||  |||
                                AGGGGACACCGA GC  ACC
                                       C  CT_
GAM974  LOC201102 3' CCTGACCAGCCACAGGAGA   88090   _      AT  CT
                                TC CCTGTGGCT  GTT  GG
                                || |||||||||  |||  ||
                                AG GGACACCGA  CAG  CC
                                 A       C_  T_
GAM974  LOC201283 3' CCAGAACACAGTCGTGAGGA  60413    CT    A
                                TCC  GTGGCT TGTTCTGG
                                |||  |||||| ||||||||
                                AGG  TGCTGA ACAAGACC
                                  AG    C
GAM974  LOC202915 3' CCACACGCCAGCCACAGGGGA 90388          A_  TC
                                TTCCCTGTGGCT  TGT  TGG
                                ||||||||||||  |||  |||
                                AGGGGACACCGA  GCA  ACC
                                       CC  C_
GAM974  LOC204965 5' CAGAGTGCACAGAGAA      90647    C    G TATG
                                TTC CTGTG C   TTCTG
                                ||| ||||| |   |||||
                                AAG GACAC G   GAGAC
                                  A    _ T___
GAM974  LOC205418 3' CACAGCCAGCAGGGAA      90681       _    A
                                TTCCCTG TGGCT TG
                                ||||||| ||||| ||
                                AAGGGAC ACCGA AC
                                    G    C
GAM974  LOC220692 3' CCAGAATAAAACCACCAGGAA 91220     CT   CTA
                                TTCC  GTGG  TGTTCTGG
                                ||||  ||||  ||||||||
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                                AAGG  CACC   ATAAGACC
                                  AC   AAA
GAM974  LOC222631 5'  CCAGAACACAGCTGGAA    92838     CTGT   A
                                TTCC   GGCT TGTTCTGG
                                ||||   |||| ||||||||
                                AAGG   TCGA ACAAGACC
                                  ____   C
GAM974  LOC253039 3'  CCAAATACATCTACAGGGAA  96153        CT   TC_
                                TTCCCTGTGG  ATGT   TGG
                                ||||||||||  ||||   |||
                                AAGGGACATC  TACA   ACC
                                      __    TAA
GAM974  LOC253841 5'  CCAGAATGTAGCCACAG    96342
                                CTGTGGCTATGTTCTGG
                                ||||||||||||||||
                                GACACCGATGTAAGACC

GAM974  LOC254028 3'  CCAGAACAGAAGCACCAAGAA 96539    CC  TG   A_
                                TTC  TG  GCT  TGTTCTGG
                                |||  ||  |||  ||||||||
                                AAG  AC  CGA  ACAAGACC
                                  A_  CA   AG
GAM974  LOC257449 3'  CAGATCCACAGGGAG      62718        CTATGT
                                TTCCCTGTGG     TCTG
                                ||||||||||     ||||
                                GAGGGACACC     AGAC
                                     T_____
GAM974  LOC89231  3'  GGACAGCACAGGGAA      92733        G  AT
                                TTCCCTGTG CT  GTTC
                                |||||||||  ||  ||||
                                AAGGGACAC GA  CAGG
                                      _  __
GAM974  LOC90550  3'  CCAGAACACAAATCAGAGGGA  73090      G   CTA_
                                TCCCT TGG    TGTTCTGG
                                ||||| |||    ||||||||
                                AGGGA ACT    ACAAGACC
                                   G   AAAC
GAM974  LOC91373  3'  CCAGCAAGGCCACAG      65834        A  TT
                                CTGTGGCT TG  CTGG
                                ||||||||  ||  ||||
                                GACACCGG AC  GACC
                                     A  __
GAM974  LOC91445  3'  CCAGAACCTGCCACAGG     60547        TAT
                                CCTGTGGC   GTTCTGG
                                ||||||||   |||||||
                                GGACACCG   CAAGACC
                                     TC_
GAM975  PMX1      3'  CAAACAATACAAAAAGCAA   22589      AAGA
                                TTGT   TGTATTGTTTG
                                ||||   ||||||||||
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                                AACG    ACATAACAAAC
                                  AAAA
GAM975  PMX1     3'  CAAACAATACAAAAAGCAA    42657      AAGA
                                TTGT    TGTATTGTTTG
                                ||||    ||||||||||
                                AACG    ACATAACAAAC
                                  AAAA
GAM975  SIX6     3'  CAAACAATAAAACAAC      23768       AAGATG
                                GTTGT     TATTGTTTG
                                |||||     |||||||||
                                CAACA     ATAACAAAC
                                  AA____
GAM975  ARHU     3'  CCAAAGTCACATCCACAACTAA 41071         AA     ATTG
                                TTAGTTGT  GATGT    TTTGG
                                ||||||||  |||||    |||||
                                AATCAACA  CTACA    AAACC
                                     C_     CTG_
GAM975  MGC12837 3'  CCATACCGACATCTACAACTAA 51183         A     ATT  T
                                TTAGTTGTA GATGT   GT TGG
                                |||||||||| |||||   || |||
                                AATCAACAT CTACA   CA ACC
                                      _    GC_  T
GAM975  POT1     3'  GCTATTACAACTTACAACTAA  31279          A    TT_
                                TTAGTTGTAAG TGTA   GT
                                |||||||||||| ||||   ||
                                AATCAACATTC ACAT   CG
                                       A    TAT
GAM976  ABCG5    3'  GAGCACCACTGCTACAGA    42359    CA       CAC
                                TC  TAGCAGTG   GTTT
                                ||  ||||||||   ||||
                                AG  ATCGTCAC   CGAG
                                 AC       CA_
GAM976  ADAMTS3  3'  AAAGAAACACAAAAGCTATAGA 26475    C     AG_  CAC
                                TC ATAGC   TG   GTTTCTTT
                                || |||||   ||   ||||||||
                                AG TATCG   AC   CAAAGAAA
                                 A    AAA  A__
GAM976  BACH1    3'  AAAGAGACACTTCTATAGA    6793     C    C   GCAC
                                TC ATAG AGT    GTTTCTTT
                                || |||| |||    ||||||||
                                AG TATC TCA    CAGAGAAA
                                 A    T  _____
GAM976  BACH2    3'  GAAAAAAGCATTGCTATG     41487          ACG
                                CATAGCAGTGC   TTTC
                                ||||||||||   ||||
                                GTATCGTTACG   AAAG
                                       AAA
GAM976  BAZ2B    3'  AAAGAAACTTTACTGT      25616       CAC
                                GCAGTG   GTTTCTTT
                                ||||||   ||||||||
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                                TGTCAT   CAAAGAAA
                                   TT_
GAM976  GALNT7   3'  AAAGAAATGACCATATGGA   33800      GCA  GCA
                                TCCATA   GT   CGTTTCTTT
                                ||||||   ||   |||||||||
                                AGGTAT   CA   GTAAAGAAA
                                   AC_  ___
GAM976  GAS1     3'  AAGCTCTGCACTGCCATG    8990     A      C_
                                CAT GCAGTGCA  GTTT
                                ||| ||||||||  ||||
                                GTA CGTCACGT  CGAA
                                  C       CT
GAM976  IRTA2    3'  GAAAGAAACTATGCTATTGGA  48406     _    GTGCAC
                                TCCA TAGCA     GTTTCTTTC
                                |||| |||||     |||||||||
                                AGGT ATCGT     CAAAGAAAG
                                   T    AT_____
GAM976  KCNAB1   3'  GAAAGAGAGGGCTACACTGCTA 60926          CACG__
           TGGA                   TCCATAGCAGTG     TTTCTTTC
                                ||||||||||||     ||||||||
                                AGGTATCGTCAC     AGAGAAAG
                                      ATCGGG
GAM976  KCNJ1    5'  AAAGAAATCAGTCTGC      4024       T  AC
                                GCAG GC  GTTTCTTT
                                |||| ||  ||||||||
                                CGTC TG  TAAAGAAA
                                  _  AC
GAM976  LAMC1    3'  GAAAGAAACCTATTATCATGGA 9675       AGC    CAC
                                TCCAT   AGTG   GTTTCTTTC
                                |||||   ||||   |||||||||
                                AGGTA   TTAT   CAAAGAAAG
                                   CTA    C__
GAM976  MATN3    3'  GAAAGAAATGTACTACTA    9937     C     CG
                                TAG AGTGCA  TTTCTTTC
                                ||| ||||||  ||||||||
                                ATC TCATGT  AAAGAAAG
                                  A     __
GAM976  MEN1     5'  GAAGATAACTGCTATAGA    93370    C      GCACG
                                TC ATAGCAGT     TTTC
                                || ||||||||     ||||
                                AG TATCGTCA     GAAG
                                  A       ATA__
GAM976  MN1      3'  AAAGAAACTTGTCTGC      10087      T   C
                                GCAG GCA GTTTCTTT
                                |||| ||| ||||||||
                                CGTC TGT CAAAGAAA
                                  _   T
GAM976  MPP2     3'  GAGGCGTGCACTGCCAGGGA   59823     ATA
                                TCC   GCAGTGCACGTTTC
                                |||   ||||||||||||||
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                                AGG  CGTCACGTGCGGAG
                                  GAC
GAM976  PDE4A    3'  GAAAGAAACACAGCAACTGT  20585     _ AC_
                                GCAGT GC  GTTTCTTTC
                                ||||| ||  |||||||||
                                TGTCA CG  CAAAGAAAG
                                   A  ACA
GAM976  PRKG1    3'  AAGCACAACTGCTATAGA   20745   C     GCAC
                                TC ATAGCAGT   GTTT
                                || ||||||||   ||||
                                AG TATCGTCA   CGAA
                                 A      ACA_
GAM976  SCO1     3'  ACGTGCACTCTACAGA     15944   CA  C
                                TC  TAG AGTGCACGT
                                ||  ||| |||||||||
                                AG  ATC TCACGTGCA
                                 AC  _
GAM976  TWIST    3'  GAAAGGCATCACTATGGA   4878      CA   ACG
                                TCCATAG  GTGC  TTTC
                                |||||||  ||||  ||||
                                AGGTATC  TACG  AAAG
                                    AC   G__
GAM976  VHL      3'  AAAGAAATGTATCACT     5047     C_
                                AGTG  ACGTTTCTTT
                                ||||  ||||||||||
                                TCAC  TGTAAAGAAA
                                  TA
GAM976  WHSC1L1  3'  AAAGAAGAGACTGCTA     43516      GCACG
                                TAGCAGT    TTTCTTT
                                |||||||    |||||||
                                ATCGTCA    GAAGAAA
                                    GA___
GAM976  ACAA2    5'  GAAAGACTTCACTGCTACTG  91767   _     CACGTT
                                CA TAGCAGTG    TCTTTC
                                || ||||||||    ||||||
                                GT ATCGTCAC    AGAAAG
                                 C      TTC___
GAM976  B3GNT7   3'  AAGGGGACAGCGCTACTGCTAT 71122         _ AC_ TT
          GGA                    TCCATAGCAGT GC  GT  CTTT
                                ||||||||||| ||  ||  ||||
                                AGGTATCGTCA CG  CA  GGAA
                                      T  CGA  GG
GAM976  FLJ11113 3'  AAAGAAACAGTGATAC     59393    _  _
                                GTG CAC GTTTCTTT
                                ||| ||| ||||||||
                                CAT GTG CAAAGAAA
                                  A  A
GAM976  FLJ23563 3'  AAAGAAATCACAGCTGCTA  67579      GCAC
                                TAGCAGT   GTTTCTTT
                                |||||||   ||||||||
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                                ATCGTCG    TAAAGAAA
                                    ACAC
GAM976  KIAA1210  3'  GAAAACATTTGCACTGCTGT   96329          CG___
                                ATAGCAGTGCA     TTTC
                                ||||||||||     ||||
                                TGTCGTCACGT     AAAG
                                      TTACA
GAM976  KIAA1219  3'  AAAGAAACATGTATTG      61360        C
                                CAGTGCA GTTTCTTT
                                ||||||| ||||||||
                                GTTATGT CAAAGAAA
                                    A
GAM976  KIAA1854  3'  AAGAAACCGCTTTGGA      71734      T   AGTGCAC
                                TCCA AGC      GTTTCTT
                                |||| |||      |||||||
                                AGGT TCG      CAAAGAA
                                  T   C_______
GAM976  KIAA1911  5'  GAAAGAAACGTGTTAGC     73506     AGT
                                GC   GCACGTTTCTTTC
                                ||   |||||||||||||
                                CG   TGTGCAAAGAAAG
                                 AT_
GAM976  RANBP6    3'  AAAAAAATGTCATTGCTACAGA 61633     CA       C     C
                                TC  TAGCAGTG ACGTTT TTT
                                ||  |||||||| |||||| |||
                                AG  ATCGTTAC TGTAAA AAA
                                 AC        _     A
GAM976  TPD52     3'  AACATGCATTGCCATG      17417     A       C
                                CAT GCAGTGCA GTT
                                ||| |||||||| |||
                                GTA CGTTACGT CAA
                                  C       A
GAM976  ZNF213    5'  GAGGGCGCGCGCACTGCTAGGA 65099     A        A   T
                                TCC TAGCAGTGC CGT TCTTT
                                ||| ||||||||| ||| |||||
                                AGG ATCGTCACG GCG GGGAG
                                  _        C   C
GAM976  LOC128977 3'  GAAATGCACACAGCTACAGA   74823    CA    A   CA
                                TC  TAGC GTG  CGTTTC
                                ||  |||| |||  ||||||
                                AG  ATCG CAC  GTAAAG
                                 AC    A   AC
GAM976  LOC130733 3'  GAAAGAAGAAACTGCAATGGA  74980       A    GCACG
                                TCCAT GCAGT     TTTCTTTC
                                ||||| |||||     ||||||||
                                AGGTA CGTCA     GAAGAAAG
                                   A     AA___
GAM976  LOC144535 3'  GAAGTAATTCACTGCTAT     76876          CAC   T
                                ATAGCAGTG   GTT CTTT
                                |||||||||   ||| ||||
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                                TATCGTCAC   TAA GAAG
                                     T__   T
GAM976  LOC153810 5'  GAAGTGTGGCACTGCTAT    80935          _
                                ATAGCAGTGC ACGTTTC
                                |||||||||| |||||||
                                TATCGTCACG TGTGAAG
                                      G
GAM976  LOC158288 5'  GAAAGAAACGTGTCAGGC    86714    AGT
                                GC   GCACGTTTCTTTC
                                ||   ||||||||||||
                                CG   TGTGCAAAGAAAG
                                 GAC
GAM976  LOC203523 3'  AAAGAAACATAGTTTGTTAT   89372        TGCAC
                                ATAGCAG    GTTTCTTT
                                |||||||    ||||||||
                                TATTGTT    CAAAGAAA
                                    TGATA
GAM976  LOC257486 3'  AAACATTTGCACTGCTGT    69239          C__
                                ATAGCAGTGCA   GTTT
                                ||||||||||   ||||
                                TGTCGTCACGT   CAAA
                                      TTA
GAM976  LOC51652  3'  GAAAGAAATCCATCTGCTCATG 32192     _    _ CAC
                                CAT AGCAG TG   GTTTCTTTC
                                ||| ||||| ||   |||||||||
                                GTA TCGTC AC   TAAAGAAAG
                                  C    T  C__
GAM976  LOC91947  3'  GAAAGAAACAAACTCCAGTATG 67613       GC__   GCAC
           GA                     TCCATA    AGT    GTTTCTTTC
                                ||||||   |||   |||||||||
                                AGGTAT    TCA    CAAAGAAAG
                                   GACC   AA__
GAM977  ADARB1    3'  GCCCAGCATCGCCGCCT     6633      AA_      T
                                AGG   CGATGCTG GGT
                                |||   |||||||| |||
                                TCC   GCTACGAC CCG
                                  GCC       _
GAM977  ADARB1    3'  GCCCAGCATCGCCGCCT     31726     AA_      T
                                AGG   CGATGCTG GGT
                                |||   |||||||| |||
                                TCC   GCTACGAC CCG
                                  GCC       _
GAM977  AP3S1     3'  ATCACAAGTGCAGCATTCCTT  7069        CGA   ___
                                AAGGAA   TGC   TGTGGT
                                ||||||   |||   ||||||
                                TTCCTT   ACG   ACACTA
                                   ACG   TGA
GAM977  BAZ2A     3'  GTCACCTTGTGGCATCTCC    25608     AC      TG TA
                                GGA  GATGCTG  G  TGAC
                                |||  |||||||  |  ||||
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                                CCT  CTACGGT  T  ACTG
                                  __      GT CC
GAM977  BCL9    3'  GGTCATGTGTTGCACCGTTCT  15068       A   TGTGG
                                GGAACG TGC    TATGACC
                                ||||||| |||    |||||||
                                TCTTGC ACG    GTACTGG
                                   C   TTGT_
GAM977  DLEC1   3'  GGCCACACCACAGCAGAGACC  23690    AACGA       A  A
                                GG    TGCTGTGGT TG CC
                                ||    ||||||||| || ||
                                CC    ACGACACCA AC GG
                                 AGAG_       C  C
GAM977  DLEC1   3'  GGCCACACCACAGCAGAGACC  23693    AACGA       A  A
                                GG    TGCTGTGGT TG CC
                                ||    ||||||||| || ||
                                CC    ACGACACCA AC GG
                                 AGAG_       C  C
GAM977  DLEC1   3'  GGCCACACCACAGCAGAGACC  23704    AACGA       A  A
                                GG    TGCTGTGGT TG CC
                                ||    ||||||||| || ||
                                CC    ACGACACCA AC GG
                                 AGAG_       C  C
GAM977  DLEC1   3'  GGCCACACCACAGCAGAGACC  94629    AACGA       A  A
                                GG    TGCTGTGGT TG CC
                                ||    ||||||||| || ||
                                CC    ACGACACCA AC GG
                                 AGAG_       C  C
GAM977  ENG     5'  GGTCATACCACAGCCTTC    3691     T_
                                GA  GCTGTGGTATGACC
                                ||  ||||||||||||||
                                CT  CGACACCATACTGG
                                 TC
GAM977  FACL5   3'  TCATACCAAACATTTCCT    64188      AC    CTG
                                AGGA  GATG   TGGTATGA
                                ||||  ||||   ||||||||
                                TCCT  TTAC   ACCATACT
                                  __    AA_
GAM977  MTMR8   3'  CCACAGCATCTTCCTT      31290        C
                                AAGGAA GATGCTGTGG
                                |||||| ||||||||||
                                TTCCTT CTACGACACC
                                   _
GAM977  OCRL    3'  GGTCATACCACAGGGAAATACC 4263       AACGATG
          TT                     AAGG      CTGTGGTATGACC
                                 ||||      ||||||||||||
                                 TTCC      GACACCATACTGG
                                   ATAAAGG
GAM977  OCRL    3'  GGTCATACCACAGGGAAATACC 7829       AACGATG
          TT                     AAGG      CTGTGGTATGACC
                                 ||||      ||||||||||||
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                                TTCC      GACACCATACTGG
                                  ATAAAGG
GAM977  PLA2G10  5'  GCCCTGCAGCACCGTCCC    13087    A  A     __
                                GG ACG TGCTGT  GGT
                                || ||| ||||||  |||
                                CC TGC ACGACG  CCG
                                 C  C     TC
GAM977  PTMA     5'  GCCATCTTTGCATTGTTCCT   11031          T___
                                AGGAACGATGC    GTGGT
                                ||||||||||    |||||
                                TCCTTGTTACG    TACCG
                                       TTTC
GAM977  RASA1    5'  GGCCATACCGTTGACCGCTCCT 42637      A  ATGCTG      A
                                AGGA CG     TGGTATG CC
                                |||| ||     ||||||| ||
                                TCCT GC     GCCATAC GG
                                  C  CAGTT_      C
GAM977  SFRS7    3'  ACCAAGAAGCAGTCGTTCC   59445        _   G__
                                GGAACGA TGCT   TGGT
                                ||||||| ||||   ||||
                                CCTTGCT ACGA   ACCA
                                    G    AGA
GAM977  SHC1     3'  GGCCACACCACAGCAAGCCGGC 11651    AA  A__       A  A
           CC                     GG  CG   TGCTGTGGT TG CC
                                ||  ||   |||||||| || ||
                                CC  GC   ACGACACCA AC GG
                                 CG  CGA        C  C
GAM977  SLC13A4  3'  ACCACAAACACATCGTTC    24918        C___
                                GAACGATG    TGTGGT
                                ||||||||    ||||||
                                CTTGCTAC    ACACCA
                                     ACAA
GAM977  SLC18A2  3'  GTCATACCATCCATCCCT    11752     AAC    CT
                                AGG   GATG  GTGGTATGAC
                                |||   ||||  ||||||||||
                                TCC   CTAC  TACCATACTG
                                  ___    C_
GAM977  SLC8A2   3'  GCCGCACACCGTTCCTT     66333         A  C
                                AAGGAACG TG TGTGGT
                                |||||||| || ||||||
                                TTCCTTGC AC ACGCCG
                                     C  _
GAM977  SOX15    3'  ATCCAGCAGCATCCCCT     22690     AAC      _  T
                                AGG   GATGCTG TGG AT
                                |||   ||||||| ||| ||
                                TCC   CTACGAC ACC TA
                                  C__      G  _
GAM977  ZNF135   3'  GCCATAGCTCATCCCTT     12853      AAC  T
                                AAGG   GA GCTGTGGT
                                ||||   || ||||||||
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                                TTCC   CT CGATACCG
                                  CTA  _
GAM977  BRAG     3'  TCATACCACATTCACTT     29476     _  CGATGC
                                AAG GAA     TGTGGTATGA
                                ||| |||     ||||||||||
                                TTC CTT     ACACCATACT
                                  A  _______
GAM977  C1QR1    3'  GCCACATGCCATCTTCC     23841      C   _ _
                                GGAA GATG C TGTGGT
                                |||| |||| | ||||||
                                CCTT CTAC G ACACCG
                                  _   C T
GAM977  C5orf5   3'  TCATACCACATGCTGCCT    33469     AACGAT  _
                                AGG     GC TGTGGTATGA
                                |||     || ||||||||||
                                TCC     CG ACACCATACT
                                  GT_____  T
GAM977  CAMTA1   3'  CATACAGCAGCATCCCTT    67914      AAC       G
                                AAGG   GATGCTGT GTATG
                                ||||   |||||||| |||||
                                TTCC   CTACGACG CATAC
                                  ___       A
GAM977  CED-6    3'  TCATACTTTTATGTTCCTT    32855       G   CTGT
                                AAGGAAC ATG    GGTATGA
                                ||||||| |||    |||||||
                                TTCCTTG TAT    TCATACT
                                    _   TT__
GAM977  DKFZP586M1120 3'  ATCACATCTTCCATTGTTCCTT 48452          C____
                                AAGGAACGATG     TGTGGT
                                ||||||||||     ||||||
                                TTCCTTGTTAC     ACACTA
                                      CTTCT
GAM977  DKFZP761I2123 5'  ACCCCAAGCAGCAGCGTCCCTT 48753      A   A     ____
                                AAGG ACG TGCTGT    GGT
                                |||| ||| ||||||    |||
                                TTCC TGC ACGACG    CCA
                                  C   G     AACC
GAM977  DRG1     3'  ACCACAACAGCGTTCC      14731       A  C
                                GGAACG TG TGTGGT
                                |||||| || ||||||
                                CCTTGC AC ACACCA
                                   G  A
GAM977  FLJ10933  3'  GCAGACAGCATCTACTCCTT   36902      AC_      G_
                                AAGGA   GATGCTGT  GT
                                |||||   ||||||||  ||
                                TTCCT   CTACGACA  CG
                                  CAT       GA
GAM977  FLJ14326  3'  CATACCATACCCTTGTCCC    49803    A    TGC
                                GG ACGA   TGTGGTATG
                                || ||||   |||||||||
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                              CC TGTT   ATACCATAC
                               C   CCC
GAM977  FLJ20695 3' GCTACAGCTCGCTCC      35557    A  T
                              GGA CGA GCTGTGGT
                              ||| ||| ||||||||
                              CCT GCT CGACATCG
                                C  _
GAM977  KIAA0690 5' GGTCATTTAAGCTCATTCCT  30795     C  T  GTGGT
                              AGGAA GA GCT    ATGACC
                              ||||| || |||    ||||||
                              TCCTT CT CGA    TACTGG
                                 A  _  ATT__
GAM977  KIAA0852 5' ACCAGTAACTCGTTCCTT    30075        __   GT
                              AAGGAACGA  TGCT  GGT
                              |||||||||  ||||  |||
                              TTCCTTGCT  ATGA  CCA
                                   CA   __
GAM977  KIAA0853 3' TCATACCACCAACTTCCT    30544     CGA  CT
                              AGGAA   TG  GTGGTATGA
                              |||||   ||  |||||||||
                              TCCTT   AC  CACCATACT
                                 CA_ __
GAM977  KIAA1030 3' GCCACCCGAAGCTCGCTCC   93335    A  T  ____
                              GGA CGA GCT    GTGGT
                              ||| ||| |||    |||||
                              CCT GCT CGA    CACCG
                                C  _  AGCC
GAM977  KIAA1553 3' CACACCACAGCATGACC     91915    AACG       A
                              GG    ATGCTGTGGT TG
                              ||    |||||||||| ||
                              CC    TACGACACCA AC
                               AG__        C
GAM977  KIAA1644 5' GCCACGGCATCCTCCTT     85028      AC
                              AAGGA  GATGCTGTGGT
                              |||||  ||||||||||
                              TTCCT  CTACGGCACCG
                                 C_
GAM977  MGC14376 5' GCCACAGCATCTCC        51849     AC
                              GGA  GATGCTGTGGT
                              |||  ||||||||||
                              CCT  CTACGACACCG
                                   __
GAM977  MGLL     5' ATCGCAGCGCCGCTCC      23465     A  A
                              GGA CG TGCTGTGGT
                              ||| || |||||||||
                              CCT GC GCGACGCTA
                                C  C
GAM977  PP1201   3' CATGGAACAGCATCTCC     42189     AC      GG
                              GGA  GATGCTGT  TATG
                              |||  ||||||||  ||||
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                                CCT  CTACGACA  GTAC
                                  __       AG
GAM977  PP1628   5' CATCCACAGCACTGCCCC    47294    AA  A      T
                                GG  CG TGCTGTGG ATG
                                ||  || |||||||| |||
                                CC  GT ACGACACC TAC
                                 CC  C       _
GAM977  SRCRB4D  3' GTCAATAAAGCATTGTCCC    54956    A      GTG  A
                                GG ACGATGCT   GT TGAC
                                || ||||||||   || ||||
                                CC TGTTACGA   TA ACTG
                                 C       AA_ _
GAM977  TCL6     3' GTTTCCATAGCACCATTCCT   40112      CGA      TAT
                                AGGAA   TGCTGTGG   GAC
                                |||||   ||||||||   |||
                                TCCTT   ACGATACC   TTG
                                   ACC       T__
GAM977  TCL6     3' GTTTCCATAGCACCATTCCT   40143      CGA      TAT
                                AGGAA   TGCTGTGG   GAC
                                |||||   ||||||||   |||
                                TCCTT   ACGATACC   TTG
                                   ACC       T__
GAM977  TUB      3' GCCATGGCATGCTCCTT     12427      A G
                                AAGGA C ATGCTGTGGT
                                ||||| | ||||||||||
                                TTCCT G TACGGTACCG
                                   C _
GAM977  LOC113230 5' GGTCCAGGGGCAGCATCCCCCT 72987     AAC      GGTAT
                                AGG   GATGCTGT    GACC
                                |||   ||||||||    ||||
                                TCC   CTACGACG    CTGG
                                  CC_      GGGAC
GAM977  LOC120114 3' GTGTTACAGCATCAGTCCTT   75537      AC      GG
                                AAGGA  GATGCTGT  TAT
                                |||||  ||||||||  |||
                                TTCCT  CTACGACA  GTG
                                   GA       TT
GAM977  LOC132166 3' GGTCATCCCGCAGCATCGTTCC 75039              T
           TT                     AAGGAACGATGCTGTGG ATGACC
                                |||||||||||||||| ||||||
                                TTCCTTGCTACGACGCC TACTGG
                                          C
GAM977  LOC145123 5' GCCATCTTTGCATTGTTCCT   67527          T___
                                AGGAACGATGC    GTGGT
                                ||||||||||    |||||
                                TCCTTGTTACG    TACCG
                                       TTTC
GAM977  LOC147054 5' TCATCTCCATATCATCCCTT   83925     AAC   C    T_
                                AAGG   GATG TGTGG  ATGA
                                ||||   |||| |||||  ||||
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                                TTCC   CTAC ATACC  TACT
                                  ___   T    TC
GAM977  LOC147063 3'  ATCACAGTCTCATTCC      83927      C  T
                                GGAA GA GCTGTGGT
                                |||| || ||||||||
                                CCTT CT TGACACTA
                                  A  C
GAM977  LOC151742 3'  GCCACAATACCATGATTCCTT  57668       CG   C___
                                AAGGAA  ATG    TGTGGT
                                ||||||  |||    ||||||
                                TTCCTT  TAC    ACACCG
                                   AG   CATA
GAM977  LOC152503 5'  ACCAGAACATCGTTCTT     85766          CTG
                                AGGAACGATG   TGGT
                                ||||||||||   ||||
                                TTCTTGCTAC   ACCA
                                      AAG
GAM977  LOC158288 5'  GCCACAGCCCCGCTCCTT    86715      A  AT
                                AAGGA CG  GCTGTGGT
                                |||||  ||  ||||||||
                                TTCCT GC  CGACACCG
                                   C  CC
GAM977  LOC165476 5'  GTTCCTACAGCACCGCACC    87198    AA  A       TAT
                                GG  CG TGCTGTGG   GAC
                                ||  || ||||||||   |||
                                CC  GC ACGACATC   TTG
                                 AC  C       C__
GAM977  LOC199786 3'  GGTCATACCTCACTATGCCCCC 88390     AACG   C  T
           T                     AGG    ATG TG GGTATGACC
                                |||    ||| || |||||||||
                                TCC    TAT AC CCATACTGG
                                  CCCG   C  T
GAM977  LOC201562 3'  GTCCTTTTCACAGCACCATTCT 88976      CGA       TAT_
                                GGAA   TGCTGTGG    GAC
                                ||||   ||||||||    |||
                                TCTT   ACGACACT    CTG
                                   ACC       TTTC
GAM977  LOC219612 5'  CACACAACAGCATTCCCT    94279     AAC       G  A
                                AGG   GATGCTGT GT TG
                                |||   |||||||| || ||
                                TCC   TTACGACA CA AC
                                  C__       A  C
GAM977  LOC253289 3'  ACCCCAACCTCGTTCCTT    96048          TGC  T
                                AAGGAACGA   TG GGT
                                |||||||||   || |||
                                TTCCTTGCT   AC CCA
                                      CCA  C
GAM977  LOC256073 3'  GTCACATGGCATCACTTCCT   96667       C_       GTA
                                AGGAA  GATGCTGTG   TGAC
                                |||||  |||||||||   ||||
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                                TCCTT CTACGGTAC  ACTG
                                  CA      ___
GAM977  LOC91812 5' TCACCACACAGCATCATCGCC 67243   AAC_     GTA
                                GG  GATGCTGTG  TGA
                                ||  |||||||||  |||
                                CC  CTACGACAC  ACT
                                 GCTA      ACC
GAM977  LOC91813 5' TCACCACACAGCATCATCGCC 67260   AAC_     GTA
                                GG  GATGCTGTG  TGA
                                ||  |||||||||  |||
                                CC  CTACGACAC  ACT
                                 GCTA      ACC
GAM977  LOC92840 3' GGCCACACCACAGGCCCCCGT 56434    AT_ _    A A
                                ACG  GC TGTGGT TG CC
                                |||  || |||||| || ||
                                TGC  CG ACACCA AC GG
                                 CCC  G    C  C
GAM978  CNGA1    3' CAACTGATAATGTGCAAA    59507        GC  A
                                TTTGCACATTA  TAG TTG
                                ||||||||||  ||| |||
                                AAACGTGTAAT  GTC AAC
                                      A_  _
GAM978  ESRRG    3' TGGCAGTCTTATGTGCAAA   66396       TAGCT
                                TTTGCACAT    AGATTGCCA
                                |||||||||    |||||||||
                                AAACGTGTA    TCTGACGGT
                                     T____
GAM978  KCNJ3    3' GCAATAATGTGCAAA      9525         GCTAGA
                                TTTGCACATTA     TTGC
                                ||||||||||     ||||
                                AAACGTGTAAT     AACG
                                      _______
GAM978  SDC2     3' GCAAATTAATGTGTAAA    67132         CTAGA
                                TTTGCACATTAG    TTGC
                                ||||||||||||    ||||
                                AAATGTGTAATT    AACG
                                      A____
GAM978  USP9X    3' ATGGCCTGATGCTAATGTGTAA 16206         TAGATT
          A                      TTTGCACATTAGC     GCCAT
                                ||||||||||||     |||||
                                AAATGTGTAATCG     CGGTA
                                      TAGTC_
GAM978  AMOTL1   3' GGCAAGTAATGTGCAAA    73650        G  AGAT
                                TTTGCACATTA CT   TGCC
                                ||||||||||| ||   ||||
                                AAACGTGTAAT GA   ACGG
                                      _ ____
GAM978  BCAR3    3' AGTAATAATGTGCAAA     13098         __
                                TTTGCACATTA  GCT
                                ||||||||||  |||
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                                AAACGTGTAAT  TGA
                                      AA
GAM978  DKFZP434B044 3'  TGACAATTAAATGTGCAGA   48930         AGCTA    C
                                TTTGCACATT    GATTG CA
                                ||||||||||    ||||| ||
                                AGACGTGTAA    TTAAC GT
                                      A____    A
GAM978  MGC3184  3'  ATGACATTTTCTAATGTGCAGA 48235          CT   T  C
                                TTTGCACATTAG  AGA TG CAT
                                ||||||||||||  ||| || |||
                                AGACGTGTAATC  TTT AC GTA
                                       __  T  A
GAM978  PTD012   3'  ATGGCAATCTAGCTAATGTGCA 25891
           AA                    TTTGCACATTAGCTAGATTGCCAT
                                ||||||||||||||||||||||||||
                                AAACGTGTAATCGATCTAACGGTA

GAM979  CRHR2    3'  ATGGAGCCAGCAGCCAGGCA   8541       A  AC     G
                                TGCCTG CT  CTGGCT CCAT
                                ||||||  ||  ||||||  ||||
                                ACGGAC GA  GACCGA GGTA
                                   C  C_    _
GAM979  ITK      3'  CAGCTGGCAGTCAAGC     18675    C    A  T
                                GC TGACT CC GGCTG
                                ||  |||||  ||  |||||
                                CG ACTGA GG TCGAC
                                 A    C  _
GAM979  ME1      5'  CAGCTGCAGTCAGCA      9985     C    ACC
                                TGC TGACT   TGGCTG
                                |||  |||||   ||||||
                                ACG ACTGA   GTCGAC
                                  _    C__
GAM979  TOP1     5'  GCCCGGCAGTCAGGCA     12358         A  T
                                TGCCTGACT CC GGC
                                |||||||||  ||  |||
                                ACGGACTGA GG CCG
                                      C  C
GAM979  WT1      5'  CTACAGCAGCCAGAGCAGCAGG 4587      A  AC_      CA
                                CCTG CT   CTGGCTGC  TAG
                                ||||  ||   ||||||||  |||
                                GGAC GA   GACCGACG  ATC
                                  _  CGA       AC
GAM979  WT1      5'  CTACAGCAGCCAGAGCAGCAGG 44352     A  AC_      CA
                                CCTG CT   CTGGCTGC  TAG
                                ||||  ||   ||||||||  |||
                                GGAC GA   GACCGACG  ATC
                                  _  CGA       AC
GAM979  WT1      5'  CTACAGCAGCCAGAGCAGCAGG 44362     A  AC_      CA
                                CCTG CT   CTGGCTGC  TAG
                                ||||  ||   ||||||||  |||
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                                GGAC GA   GACCGACG  ATC
                                  _ CGA       AC
GAM979  WT1      5'  CTACAGCAGCCAGAGCAGCAGG 44372      A  AC_       CA
                                CCTG CT   CTGGCTGC  TAG
                                |||| ||   ||||||||  |||
                                GGAC GA   GACCGACG  ATC
                                  _ CGA       AC
GAM979  CCNI     5'  CTACAGCAAGCTGGGTAGCAGG 22419       A    TG  _ CA
             CA                   TGCCTG CTACC  GCT GC  TAG
                                |||||| |||||  ||| ||  |||
                                ACGGAC GATGG  CGA CG  ATC
                                   _    GT   A  AC
GAM979  FLJ23537 3'  ATGGCAGCAGAACCAGG     87522      ACTAC   G
                                CCTG     CTG CTGCCAT
                                ||||     ||| |||||||
                                GGAC     GAC GACGGTA
                                  CAA__   _
GAM979  FLJ23537 3'  ATGGCAGCAGAACCAGG     46022      ACTAC   G
                                CCTG     CTG CTGCCAT
                                ||||     ||| |||||||
                                GGAC     GAC GACGGTA
                                  CAA__   _
GAM979  FLJ32389 3'  CCAGGCCAGTCAGGCA      58190         A_
                                TGCCTGACT  CCTGG
                                |||||||||  |||||
                                ACGGACTGA  GGACC
                                     CC
GAM979  HIF1AN   3'  CACCCTCAATAGTCAGGGCA   61969      _     CCT_  C
                                TGCC TGACTA    GG TG
                                |||| ||||||    || ||
                                ACGG ACTGAT    CC AC
                                  G     AACT  C
GAM979  KIAA1024 3'  TAGCTGGAGAGGTAGTCAG    69064          _____
                                CTGACTACCT    GGCTG
                                ||||||||||    |||||
                                GACTGATGGA    TCGAT
                                     GAGG
GAM979  KIAA1110 3'  ATGGCCTGCGCAGTCAGGC    61841         ACCTG  T_
                                GCCTGACT    GC  GCCAT
                                ||||||||    ||  |||||
                                CGGACTGA    CG  CGGTA
                                   CG___  TC
GAM979  KIAA1553 3'  CTATGGCATCCACAGACAGGCA 91918       A  ACC   C
                                TGCCTG CT   TGG TGCCATAG
                                |||||| ||   ||| ||||||||
                                ACGGAC GA   ACC ACGGTATC
                                   A  C__   T
GAM979  KIAA1656 3'  CTATGGCAGCCAAGAGAGAGGC 65791      GA  ACC
                                GCCT  CT   TGGCTGCCATAG
                                ||||  ||   ||||||||||||
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                                CGGA  GA   ACCGACGGTATC
                                  GA  GA_
GAM979  MGC11082  3'  ATGGCAGCTGCAGTGAAGCA   51100     CTG   ACC
                                TGC   ACT   TGGCTGCCAT
                                |||   |||   ||||||||||
                                ACG   TGA   GTCGACGGTA
                                  AAG   C__
GAM979  MGC8974   3'  CTATGGCATTAGCATAGTAAGC 53634     CTG   C_   C
          A                      TGC   ACTA  CTGG TGCCATAG
                                |||   ||||  |||| ||||||||
                                ACG   TGAT  GATT ACGGTATC
                                  AA_   AC   _
GAM979  NCKX3     3'  GGTGCCAGGCAGTCA      40353      A     T
                                TGACT CCTGGC GCC
                                ||||| |||||| |||
                                ACTGA GGACCG TGG
                                   C     _
GAM979  SCAM-1    3'  ATGGCAACTTGGAGCCAGCCA 19324    C   A  A  T  C
                                TG CTG CT CC GG TGCCAT
                                || ||| || || || ||||||
                                AC GAC GA GG TC ACGGTA
                                 C   C  _  T  A
GAM979  LOC122704 3'  TGGCCAGGCAGTCAAGC     74144    C    A
                                GC TGACT CCTGGCTG
                                || ||||| ||||||||
                                CG ACTGA GGACCGGT
                                 A    C
GAM979  LOC126302 3'  CAGCCAGGCACCAGGCA     74491       ACTA
                                TGCCTG    CCTGGCTG
                                ||||||    ||||||||
                                ACGGAC    GGACCGAC
                                   CAC_
GAM979  LOC134285 5'  GCAGCGCGGTCAGCCAGGC    76165      A  AC   _
                                GCCTG CT  CTG GCTGC
                                ||||| ||  ||| |||||
                                CGGAC GA  GGC CGACG
                                   C  CT   G
GAM979  LOC145858 5'  ATGGCAGCCCCTCTCAGGC    77542       CTACCT
                                GCCTGA     GGCTGCCAT
                                ||||||     |||||||||
                                CGGACT     CCGACGGTA
                                   CTCC__
GAM979  LOC146280 5'  AGCCAGGTAGCAGACA      77817    C   A
                                TG CTG CTACCTGGCT
                                || ||| ||||||||||
                                AC GAC GATGGACCGA
                                 A   _
GAM979  LOC150397 3'  ATGGCAGCCTTCAGG       79837       CTACCT
                                CCTGA     GGCTGCCAT
                                |||||     |||||||||
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                                GGACT     CCGACGGTA
                                  T_____
GAM979  LOC152503 5'  GCACCTCAGACAGTCAGGCA   85770         AC  _ C
                                TGCCTGACT  CTG G TGC
                                |||||||||  ||| | |||
                                ACGGACTGA  GAC C ACG
                                     CA   T C
GAM979  LOC158125 5'  TGGGAGCCAAGCAGCCAGGC   81719      A  ACC    G
                                GCCTG CT   TGGCT CCA
                                |||||  ||   ||||| |||
                                CGGAC GA   ACCGA GGT
                                   C  CGA    G
GAM979  LOC164397 5'  TGGCACATCCAGGCAGTCAAGC 82531     C    A    C__
          A                      TGC TGACT CCTGG   TGCCA
                                ||| ||||| |||||   |||||
                                ACG ACTGA GGACC   ACGGT
                                  A    C    TAC
GAM979  LOC220581 5'  AGCCAGGCAGCCAAGGCA    76287      GA_  A
                                TGCCT   CT CCTGGCT
                                |||||   ||  |||||||
                                ACGGA   GA GGACCGA
                                   ACC  C
GAM979  LOC221583 5'  TGTGCAAACAATTCAGGCA    92145       CTACC  GC  _
                                TGCCTGA    TG  TGC CA
                                |||||||    ||  ||| ||
                                ACGGACT    AC  ACG GT
                                     TA___  AA   T
GAM979  LOC222008 5'  CAGCCAGGCAGCCGAGACA   94007    C  _ A  A
                                TG CT G CT CCTGGCTG
                                || || | || ||||||||
                                AC GA C GA GGACCGAC
                                 A  G C  C
GAM979  LOC253687 3'  CAGCCGGAACAGCCAGGC    95495      A  AC_
                                GCCTG CT   CTGGCTG
                                |||||  ||   |||||||
                                CGGAC GA   GGCCGAC
                                   C  CAA
GAM979  LOC51001  5'  TAGCTCAAGTAGTCAGG     31952         C  _
                                CCTGACTAC TG GCTG
                                ||||||||| || ||||
                                GGACTGATG AC CGAT
                                     A  T
GAM979  LOC91145  3'  AGTCAAGGAGTCAGGCA     65055         A  _
                                TGCCTGACT CCT GGCT
                                ||||||||| ||| ||||
                                ACGGACTGA GGA CTGA
                                     _  A
GAM980  ATP8A2    3'  GCTGAAGAAAGAAAGGAGAC   93512        G   CTC
                                GTCTTTT TCT   TCTTCAGC
                                ||||||| |||   ||||||||
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                                CAGAGGA AGA   AGAAGTCG
                                    A   A__
GAM980  BCL11A   3'  GAGAGAGAAAAAGAC      43164       G
                                GTCTTTT TCTCTCTC
                                ||||||| ||||||||
                                CAGAAAA AGAGAGAG
                                    _
GAM980  DCT      5'  CTGAAAAGAAAAGACTGAAAGA 8624       _   C_  C
                                TCTTTT GTCT  TCT TTCAG
                                |||||| ||||  ||| |||||
                                AGAAAG CAGA  AGA AAGTC
                                   T   AA  A
GAM980  ESRRG    3'  CTGAAGAGAGATGGAAGC    66392   T   TG     CT
                                G CTTT  TCTCTCT  TCAG
                                | ||||  |||||||  ||||
                                C GAAG  AGAGAGA  AGTC
                                _   GT      __
GAM980  HOXD4    5'  GCTGAAAAGAAAGAAAGAC   27526      TTG  C  C
                                GTCTT   TCT TCT TTCAGC
                                |||||   ||| ||| ||||||
                                CAGAA   AGA AGA AAGTCG
                                   ___  A  A
GAM980  MBNL     3'  CTGTCAAAAGTCAAAAGACT  40728        T  CTCTCTT
                                AGTCTTTTG CT      CAG
                                ||||||||| ||      |||
                                TCAGAAAAC GA      GTC
                                     T  AAACT__
GAM980  MYH8     3'  GCTGAAGAAAGGCACAAAA   59843       C  C
                                TTTTGT TCT TCTTCAGC
                                |||||| ||| ||||||||
                                AAAACA GGA AGAAGTCG
                                   C   A
GAM980  NIPSNAP1 3'  AGAGATGACAAAAGAC     13288         _
                                GTCTTTTGTC TCTCT
                                |||||||||| |||||
                                CAGAAAACAG AGAGA
                                     T
GAM980  NUP62    5'  GCTGAAGAAAGAAGGTGGGAGC 33328   T   TG  _  C
                                G CTTT  TCT CT TCTTCAGC
                                | ||||  ||| || ||||||||
                                C GAGG  GGA GA AGAAGTCG
                                _   GT  A  A
GAM980  PDE4C    3'  CTGAAGAGAGCTATGACTG   6232      TTTTGTCT
                                CAGTC       CTCTCTTCAG
                                |||||       ||||||||||
                                GTCAG       GAGAGAAGTC
                                  TATC____
GAM980  RP42     3'  TGAAAAGAGAAGACTG     40207       TTTGTC    C
                                CAGTCT     TCTCT TTCA
                                ||||||     ||||| ||||
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                                GTCAGA     AGAGA AAGT
                                   _______    A
GAM980  SLC4A10  3'  GCCGAAAAGAGAAGAAAGCTG  41912     T    G    CTC   A
                                CAG CTTTT TCTCT   TTC GC
                                ||| |||||| ||||||  ||| ||
                                GTC GAAAG AGAGA   AAG CG
                                  _    A    A__   C
GAM980  WT1      3'  GCTGAAGAAAGAATCAGAACT  44354     CT   TC   C
                                AGT  TTTG  TCT TCTTCAGC
                                |||  ||||  ||| ||||||||
                                TCA  AGAC  AGA AGAAGTCG
                                  __   TA   A
GAM980  WT1      3'  GCTGAAGAAAGAATCAGAACT  44364     CT   TC   C
                                AGT  TTTG  TCT TCTTCAGC
                                |||  ||||  ||| ||||||||
                                TCA  AGAC  AGA AGAAGTCG
                                  __   TA   A
GAM980  WT1      3'  GCTGAAGAAAAAATCAGAACT  44374     CT   TCTCTC
                                AGT  TTTG     TCTTCAGC
                                |||  ||||     ||||||||
                                TCA  AGAC     AGAAGTCG
                                  __   TAAAAA
GAM980  WT1      3'  GCTGAAGAAAGAATCAGAACT  4589      CT   TC   C
                                AGT  TTTG  TCT TCTTCAGC
                                |||  ||||  ||| ||||||||
                                TCA  AGAC  AGA AGAAGTCG
                                  __   TA   A
GAM980  ZNF141   3'  CTGAAGAGAAACTGCAAA    12873      CTC_
                                TTTGT    TCTCTTCAG
                                |||||    |||||||||
                                AAACG    AGAGAAGTC
                                   TCAA
GAM980  CLECSF9  5'  GAGAGAAACAAAAAAC     26840    C     C
                                GT TTTTGT TCTCTC
                                || |||||| ||||||
                                CA AAAACA AGAGAG
                                 A     A
GAM980  FLJ10188 3'  GCTCAGTAAAGAGACAAAAGC  35871   T        CT_  TC
                                G CTTTTGTCTCT   CT  AGC
                                | ||||||||||   ||  |||
                                C GAAAACAGAGA   GA  TCG
                                _         AAT  C_
GAM980  FLJ12700 3'  GCTGAAAAGACGCACAAAGA   46118      _  C   CTC
                                TCTTT TGT TCT   TTCAGC
                                ||||| ||| |||   ||||||
                                AGAAA ACG AGA   AAGTCG
                                   C   C   A__
GAM980  FLJ13386 3'  AAGAGAGAGTGAAAAGAC    95709       GT
                                GTCTTTT  CTCTCTCTT
                                |||||||  |||||||||
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                                CAGAAAA  GAGAGAGAA
                                    GT
GAM980  KIAA0293  3'  GCTAAAAAGAGAAAGTCCAAAA 60607         T_  C     C__
              GACT                  AGTCTTTTG  CT TCTCTT   AGC
                                |||||||||  || ||||||   |||
                                TCAGAAAAC  GA AGAGAA   TCG
                                     CT  A     AAA
GAM980  KIAA0934  3'  CTGAAGAAACAAAGGCTG    64219         T  CTCTC
                                CAGTCTTT GT    TCTTCAG
                                |||||||| ||    |||||||
                                GTCGGAAA CA    AGAAGTC
                                     _  A____
GAM980  KIAA1028  3'  CTGAAGAGAGTAACAACTG   91938      CTTT   CT
                                CAGT    TGT  CTCTCTTCAG
                                ||||    |||  ||||||||||
                                GTCA    ACA  GAGAGAAGTC
                                  ____   AT
GAM980  KIAA1323  3'  CTGAAGAGAAAAAAAAAAC   63041    C    GTCTC
                                GT TTTT     TCTCTTCAG
                                || ||||     |||||||||
                                CA AAAA     AGAGAAGTC
                                 A    AAA__
GAM980  KIAA1634  3'  GCTGACAAAAACAAAGAGACTG 63390          GTCTCTCTCT
                                CAGTCTTTT         TCAGC
                                |||||||||         |||||
                                GTCAGAGAA         AGTCG
                                     ACAAAAAC__
GAM980  KIAA1765  3'  GCTGAATGAAAGAAGAAAAAAA 70610         G__   _  C  _
              AGACT                 AGTCTTTT   TCT CT TC TTCAGC
                                |||||||||   ||| || || ||||||
                                TCAGAAAA   AGA GA AG AAGTCG
                                     AAA   A  A  T
GAM980  KIAA1813  5'  GCCGAAGAGAGAAGGAAAC    70302    C    GTC       A
                                GT TTTT   TCTCTCTTC GC
                                || ||||   ||||||||| ||
                                CA AGGA   AGAGAGAAG CG
                                 A   ___        C
GAM980  KIAA1906  3'  CTGAAGAGCCAGACAACAAACT 73192     CTT     CT
                                AGT   TTGTCT  CTCTTCAG
                                |||   ||||||  ||||||||
                                TCA   AACAGA  GAGAAGTC
                                  AAC     CC
GAM980  KIF4A     3'  CTGAAGAGAGAACCAACTG   24593     CTTT  TC
                                CAGT    TG  TCTCTCTTCAG
                                ||||    ||  ||||||||||
                                GTCA    AC  AGAGAGAAGTC
                                  ____  CA
GAM980  MAAT1     5'  GCTGAAGAAAGTGTGGAAGC  21218   T    TG CT  C
                                G CTTT  T  CT TCTTCAGC
                                | ||||  |  || ||||||||
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                                C GAAG  G  GA AGAAGTCG
                                 _    GT T_  A
GAM980  NASP     3'  CTGACAGAAACAAAAGAT    67969         C   CTCT
                                GTCTTTTGT TCT    TCAG
                                ||||||||| |||    ||||
                                TAGAAAACA AGA    AGTC
                                     A   C___
GAM980  NNT      3'  CTGAAGAAAGCAAAGCAAAAAC 24714      C     CT__  C
              TG                   CAGT TTTTGT    CT TCTTCAG
                                |||| ||||||    || |||||||
                                GTCA AAAACG    GA AGAAGTC
                                  _     AAAC  A
GAM980  PSIP1    3'  CTGAAAAGAGAATACAAG    40934       C_    C
                                TTTGT  TCTCT TTCAG
                                |||||  ||||| |||||
                                GAACA  AGAGA AAGTC
                                   TA     A
GAM980  RAB5EP   3'  CTGAAGAAAGAGAAGTCACAAC 16295    CTTTTG_    C
                                GT      TCTCT TCTTCAG
                                ||      ||||| |||||||
                                CA      AGAGA AGAAGTC
                                 ACACTGA     A
GAM980  RASSF2   3'  CTGAAAAGCACAAAAGAT    28433         CTCT  C
                                GTCTTTTGT    CT TTCAG
                                |||||||||    || |||||
                                TAGAAAACA    GA AAGTC
                                     C___  A
GAM980  SNTG1    3'  AAGTGGAGACAAAAGA      38571           CT
                                TCTTTTGTCTCT  CTT
                                ||||||||||||  |||
                                AGAAAACAGAGG  GAA
                                       T_
GAM980  TED      3'  GCTGGGCCTCAAAACAAAAGGC 31640           CTCTCTC
              TG                   CAGTCTTTTGT      TTCAGC
                                ||||||||||      ||||||
                                GTCGGAAAACA      GGGTCG
                                      AAACTCC
GAM980  ZNF263   3'  GCTGAAGGTCAACAAAAGACTG 19228          CTCT T
                                CAGTCTTTTGT    C CTTCAGC
                                ||||||||||    | |||||||
                                GTCAGAAAACA    G GAAGTCG
                                      ACT_ _
GAM980  LOC123926 3'  AGAGCAAGAGACAAAGAACT   74250     CT       __
                                AGT  TTTGTCTCT  CTCT
                                |||  |||||||||  ||||
                                TCA  AAACAGAGA  GAGA
                                  AG        AC
GAM980  LOC145902 3'  CTGAAGAAAGCATAAGAT    77561       T  T  CTC
                                GTCTT TG CT   TCTTCAG
                                ||||| || ||   |||||||
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                                TAGAA AC GA   AGAAGTC
                                  T  _  A__
GAM980  LOC158327 3'  CTGAAATTACAAAAGAT     81880         CTCTCTC
                                GTCTTTTGT      TTCAG
                                |||||||||      |||||
                                TAGAAAACA      AAGTC
                                    TTA____
GAM981  CKTSF1B1  3'  ACAACTAAACAGGAGCCAT   25361        CCTCAACC  C
                                ATGGCTCC       AG TTGT
                                ||||||||       || ||||
                                TACCGAGG       TC AACA
                                    ACAAA___  _
GAM981  GPR61     5'  ATCAGCTGAGAGGAGCTAT   78909        C   ACCA   T
                                ATGGCTCC CTCA    GCT GT
                                |||||||| ||||    ||| ||
                                TATCGAGG GAGT    CGA TA
                                    A   _____   C
GAM981  SDC4      3'  GCGGTGAGGGGAACCA      11480     C      A  A
                                TGG TCCCCTCA CC GC
                                ||| |||||||| || ||
                                ACC AGGGGAGT GG CG
                                  A       _  _
GAM981  TRPS1     3'  TTGGTTGAAAGGCACCAT    26086      CT  CC
                                ATGG  CC  TCAACCAG
                                ||||  ||  ||||||||
                                TACC  GG  AGTTGGTT
                                  AC  AA
GAM981  C20orf139 3'  CATGTCTTGATGAGGGGAACCA 84754     C       AC   CT
                                TGG TCCCCTCA  CAG  TGTG
                                ||| ||||||||  |||  ||||
                                ACC AGGGGAGT  GTT  GTAC
                                  A       A_   CT
GAM981  COL12A1   3'  ACAGCCATGAGGAGCCAT    54662        CC   ACCA   T
                                ATGGCTCC  TCA    GCT GT
                                ||||||||  |||    ||| ||
                                TACCGAGG  AGT    CGA CA
                                    __   AC__   _
GAM981  COL12A1   3'  ACAGCCATGAGGAGCCAT    15180        CC   ACCA   T
                                ATGGCTCC  TCA    GCT GT
                                ||||||||  |||    ||| ||
                                TACCGAGG  AGT    CGA CA
                                    __   AC__   _
GAM981  DKFZP434L1435 5'  CACAAGCTGTGGTGGAG     92168      _  TCAAC
                                CTCC CC     CAGCTTGTG
                                |||| ||     |||||||||
                                GAGG GG     GTCGAACAC
                                  T  T_____
GAM981  FLJ14326  3'  CACAAGCTGGCCAAGAGC    49801      CCCTCAA
                                GCTC       CCAGCTTGTG
                                ||||       ||||||||||
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                                CGAG      GGTCGAACAC
                                  AACC___
GAM981  KIAA0233  3'  CAGGCCGGGGGAGCCA      28493          CAACCA
                                TGGCTCCCCT     GCTTG
                                ||||||||||     |||||
                                ACCGAGGGGG     CGGAC
                                     C_____
GAM981  MGC15873  3'  ATAAGTTGTGGAAAGCCA    51899      CC  TCAAC
                                TGGCT  CC     CAGCTTGT
                                |||||  ||     ||||||||
                                ACCGA  GG     GTTGAATA
                                  AA  T____
GAM981  PPP1R12C  3'  AGAGCCGAGGGGGCCA      34278      T     AACCA    G
                                TGGC CCCCTC     GCTT T
                                |||| ||||||     |||| |
                                ACCG GGGGAG     CGAG A
                                  _     C____    G
GAM981  RASSF2    3'  CACAAGCTGTGGTGGGAAACCC 28428    C__    C   AC
                                GG   TCCC TCA  CAGCTTGTG
                                ||   |||| |||  |||||||||
                                CC   AGGG GGT  GTCGAACAC
                                 CAA    T   __
GAM981  SDR1      3'  CACAAACTGGTTGAACGGC    16462     CCCC       C
                                GCT    TCAACCAG TTGTG
                                |||    |||||||| |||||
                                CGG    AGTTGGTC AACAC
                                  CA__       A
GAM981  ZNF145    5'  TGAGCCGAGGGGAGC       20014          AACCA
                                GCTCCCCTC     GCTTG
                                |||||||||     |||||
                                CGAGGGGAG     CGAGT
                                     C____
GAM981  LOC120939 3'  CACTGCCACCTAGAGGAGCCAT 76247         C  CAACCA  TT
                                ATGGCTCC CT     GC  GTG
                                |||||||| ||     ||  |||
                                TACCGAGG GA     CG  CAC
                                     A  TCCAC_  T_
GAM981  LOC124977 5'  CAGGCTAGATCAAGGGGACCA  76057     C     CAACC_
                                TGG TCCCCT     AGCTTG
                                ||| ||||||     ||||||
                                ACC AGGGGA     TCGGAC
                                  _     ACTAGA
GAM981  LOC147077 3'  CACAAGAAAAAGGAAGCCA    78248      CC   CAACCAG
                                TGGCT  CCT     CTTGTG
                                |||||  |||     ||||||
                                ACCGA  GGA     GAACAC
                                  A_   AAAA___
GAM981  LOC148018 5'  CACCTGGTCACAGGGAGCCA   82417        CTCA    CTT
                                TGGCTCCC    ACCAG   GTG
                                ||||||||    |||||   |||
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                                ACCGAGGG   TGGTC  CAC
                                    ACAC    ___
GAM981  LOC154386 3'  CACACCTCTCAGGGGAGCCAT  81081          CAACC  CT
                                ATGGCTCCCCT    AG  TGTG
                                ||||||||||    ||  ||||
                                TACCGAGGGGA    TC  ACAC
                                      CTC__  C_
GAM981  LOC257407 5'  CACAAATGCATGAGGGGGCCA  96986     T     AC  GC
                                TGGC CCCCTCA  CA  TTGTG
                                |||| |||||||  ||  |||||
                                ACCG GGGGAGT  GT  AACAC
                                  _      AC  A_
GAM981  LOC54103  5'  AGAAAGTAGAAGGGAGCCAT  94210         C  A  CAG
                                ATGGCTCCC TC AC   CT
                                ||||||||| || ||   ||
                                TACCGAGGG AG TG   GA
                                      A  A  AAA
GAM981  LOC92997  3'  CACAAATGCATGAGGGGGCCA  71087     T     AC  GC
                                TGGC CCCCTCA  CA  TTGTG
                                |||| |||||||  ||  |||||
                                ACCG GGGGAGT  GT  AACAC
                                  _      AC  A_
GAM982  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM982  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM982  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM982  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM982  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM982  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
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                                TAAAGTGAAA TGACA
                                     A
GAM982  PKD2    3'  TCCAGGTTGAAAGTGAAA    60096          CTG   A
                                TTTCACTTTCA  TCTG GA
                                ||||||||||  |||| ||
                                AAAGTGAAAGT  GGAC CT
                                      T__   _
GAM982  WRN     3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM982  ZNF216  3'  ATCTGCACAGCAAAGTGAAA  20017        CA   CTG
                                TTTCACTTT  CTGT  AGAT
                                |||||||||  ||||  ||||
                                AAAGTGAAA  GACA  TCTA
                                     C_   CG_
GAM982  CG012   5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM982  EIF2C2  3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM982  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM982  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                     C__
GAM982  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534     C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                   A       CT
GAM982  KLHL6   3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                   _  G
GAM982  NIR3    3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
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                                TAA GTGAAAGTGACG
                                  C
GAM982  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM982  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM982  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148          TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__    TT
GAM982  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                      A     TC
GAM982  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941          CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                      AAAGG
GAM982  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647       ACTTTCA
                                TTTC       CTGTCTGAGAT
                                ||||       ||||||||||||
                                AAAG       GACAGACTCTA
                                  GTTTGCC
GAM982  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT      GT TGAGAT
                                |||||||      || ||||||
                                AAAGTGA      CA ACTCTA
                                     TTTCC_  A
GAM982  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM982  LOC222134 5'  ACAGTGAAGTGAAATG       94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM983  LRRC2    3'  AAACCTTGTTTCACTGTC     44464          G  TT
                                GACAGTGAAG CA  GTTT
                                |||||||||| ||  ||||
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                                CTGTCACTTT GT  CAAA
                                      _  TC
GAM983  LOC158364 5'  AAACAATGCCATTTAT     81871      _
                                GTGAA GGCATTGTTT
                                ||||| ||||||||||
                                TATTT CCGTAACAAA
                                   A
GAM983  LOC221895 3'  AAATAATACCTTCATTATC   92519    C      C
                                GA AGTGAAGG ATTGTTT
                                || |||||||| |||||||
                                CT TTACTTCC TAATAAA
                                 A       A
GAM984  CTPS    3'  ACCCTCTCATATATAGACAGCT 88592      _ CAGT  GA   A
           T                     AAGCTG CT    TG  AGA GGT
                                ||||||  ||    ||  ||| |||
                                TTCGAC GA    AT  TCT CCA
                                    A  TAT_  AC   C
GAM984  EYA3    3'  GACTGGAACCAACTGAGAACTT 8811     CTG       AAGAA
                                AAG   CTCAGTTGG    GGTC
                                |||   |||||||||    ||||
                                TTC   GAGTCAACC    TCAG
                                 AA_       AAGG_
GAM984  FUT7    3'  GACCCTCCCCACCCTGAACA   15583    C    T_   AA  A
                                TG TCAG  TGG  GA GGTC
                                || ||||  |||  || ||||
                                AC AGTC  ACC  CT CCAG
                                 A   CC   C_  C
GAM984  GPR85   3'  ACCTTCTCTGCTGAGCA     38576        T   A
                                TGCTCAGT GGA GAAGGT
                                |||||||| ||| ||||||
                                ACGAGTCG TCT CTTCCA
                                      _  _
GAM984  PACSIN1  3'  ACCCCCTCCGTCCTGAGCAGC  92251         T_    A AA
                                GCTGCTCAG  TGGA G  GGT
                                |||||||||  |||| |  |||
                                CGACGAGTC  GCCT C  CCA
                                     CT    _ CC
GAM984  CHST8   5'  TCTCCCAACAAGCAGCTT    42442        CA    A
                                AAGCTGCT  GTTGG AGA
                                ||||||||  ||||| |||
                                TTCGACGA  CAACC TCT
                                    A_    C
GAM984  DKFZp761N1114 3'  ACCTCCTCATAAGCGGCTT   79008        CAGTT   AGAA
                                AAGCTGCT    GGA   GGT
                                ||||||||    |||   |||
                                TTCGGCGA    CCT   CCA
                                    ATACT  _____
GAM984  ENDO180  3'  GACCCCCTTCTTTGCAGAGC   20144      A  T_    AA
                                GCTC GT  GGAAG  GGTC
                                |||| ||  |||||  ||||
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                                CGAG CG  TCTTC  CCAG
                                  A  TT    CC
GAM984  FLJ13909  5'  GACCCCCTTCCAGCATGCA   47066    TCA      AA
                                TGC  GTTGGAAG  GGTC
                                |||  ||||||||  ||||
                                ACG  CGACCTTC  CCAG
                                  TA_      CC
GAM984  FLJ23040  3'  GACCTTCTAGGCTCAAGCAGTC 47197   A    C_   GGA
          C                      A GCTGCT  AGTT   AGAAGGTC
                                | ||||||  ||||  ||||||||
                                C TGACGA  TCGG   TCTTCCAG
                                 C     AC    A__
GAM984  FLJ30681  3'  TTTCCAATGAGCAGCTT    91793         G
                                AAGCTGCTCA TTGGAAG
                                |||||||||| |||||||
                                TTCGACGAGT AACCTTT
                                          _
GAM984  KIAA0286  3'  ACCTTCTTTAGGAGCTGCT   68317    T   AGTTG
                                AGC GCTC    GAAGAAGGT
                                ||| ||||    |||||||||
                                TCG CGAG    TTTCTTCCA
                                  T   GA___
GAM984  KIAA0450  5'  GACCCCCTGCCCGGGCAGCT   27639       AGTT  A  AA
                                AGCTGCTC    GG AG  GGTC
                                ||||||||    || ||  ||||
                                TCGACGGG    CC TC  CCAG
                                     C___   G  CC
GAM984  KIAA0843  3'  ACCCTCACTGAGCACCT    30109    C      TGGAA  A
                                AG TGCTCAGT    GA GGT
                                || ||||||||    || |||
                                TC ACGAGTCA    CT CCA
                                 C       _____  C
GAM984  KIAA1024  3'  ACCTTCTTCCTTGCACTT    69059    C   TCAGTT
                                AAG TGC     GGAAGAAGGT
                                ||| |||     ||||||||||
                                TTC ACG     CCTTCTTCCA
                                  _   TT_____
GAM984  PALM      3'  GACCCCCCATGTCACGGCAGCT 10413       CAGT__   AAGAA
          T                     AAGCTGCT     TGG    GGTC
                                |||||||      |||    ||||
                                TTCGACGG     ACC    CCAG
                                     CACTGT   CC___
GAM984  PIP5K2B   3'  ACCTCCTCCCAGGCACT     13062    C   CAGT   A  A
                                AG TGCT    TGG AG AGGT
                                || ||||    ||| || ||||
                                TC ACGG    ACC TC TCCA
                                 _   _____  C  C
GAM984  RASGRP4   3'  CTCCCAATGAGCAGC       53652        G   A
                                GCTGCTCA TTGG AG
                                |||||||| |||| ||
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                                CGACGAGT AACC TC
                                   _   C
GAM984  SIMRP7   3' ACCTTCTGCGTGCAGC     92358      TCA  TGGA
                                GCTGC   GT    AGAAGGT
                                |||||   ||    |||||||
                                CGACG   CG    TCTTCCA
                                  TG_  _____
GAM984  LOC115286 3' ACCCTCTTCCGCTGAGCAGCT  73370          T     A
                                AGCTGCTCAGT GGAAGA GGT
                                |||||||||||| |||||| |||
                                TCGACGAGTCG CCTTCT CCA
                                      _     C
GAM984  LOC150383 3' GACCTCCTTCAGCAGGGCAGCT 79814         A    G   A
                                AGCTGCTC GTTG AAG AGGTC
                                |||||||| |||| ||| |||||
                                TCGACGGG CGAC TTC TCCAG
                                     A   _  C
GAM984  LOC150606 3' ACCCTCTATTTTTCCAAACTAG 85086       CTCAG       _____
           CTT                    AGCTG     TTGGAAGAA     GGT
                                |||||     |||||||||     |||
                                TCGAT     AACCTTTTT     CCA
                                  CA___         ATCTC
GAM984  LOC196540 5' ACCTTCCTTCAGCAGC      89632       CAGTT   A
                                GCTGCT     GGA GAAGGT
                                ||||||     ||| ||||||
                                CGACGA     CTT CTTCCA
                                   _____   C
GAM984  LOC197342 3' GACCTTCCTGTTACCTGAGCAG 88001         T   AA_
                                CTGCTCAG TGG   GAAGGTC
                                |||||||| |||   |||||||
                                GACGAGTC ATT   CTTCCAG
                                     C   GTC
GAM984  LOC253983 3' GACCTCCTGGTCATGAGCAGC  96625         GT   A_  A
                                GCTGCTCA  TGG  AG AGGTC
                                ||||||||  |||  || |||||
                                CGACGAGT  ACT  TC TCCAG
                                     __   GG  C
GAM984  LOC255779 3' ACCCTCCGGATGTGAGCAGTCC 96012    A       G__     AGAA
                                A GCTGCTCA   TTGGA    GGT
                                | ||||||||   |||||    |||
                                C TGACGAGT   GGCCT    CCA
                                 C       GTA    C___
GAM984  LOC257282 5' GACCCCCTGGGCTGAGCAGC   96399          TGGA  AA
                                GCTGCTCAGT    AG  GGTC
                                ||||||||||    ||  ||||
                                CGACGAGTCG    TC  CCAG
                                      GG__  CC
GAM985  ACADS    3' CACTGTGCCTCAAGTTCCT    3407         AA  A   GG
                                AGGAACTT  GA GTAT  AGTG
                                ||||||||  || ||||  ||||
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                                TCCTTGAA  CT CGTG  TCAC
                                   __  C   __
GAM985  ATP2A3   3'  CACCGACATCCTCAGGTTCCT  17720       A  AAGT   GA_
                                AGGAACTT AG   ATG   GTG
                                |||||||| ||   |||  |||
                                TCCTTGGA TC   TAC   CAC
                                   C  C___   AGC
GAM985  CASP10   3'  CATACTTCTAAAATTCC     52091     C  A
                                GGAA TT AGAAGTATG
                                |||| || |||||||||
                                CCTT AA TCTTCATAC
                                  A  A
GAM985  CTSK     3'  CTCACTTCCTAAGTTCC     4622        A    ATG
                                GGAACTTA GAAGT   GAG
                                |||||||| |||||   |||
                                CCTTGAAT CTTCA   CTC
                                   C    ___
GAM985  DUOX2    3'  CACTTCGTCTCCCCTAGCTCCT 26020     A  TAAGA  T
                                AGGA CT    AG ATGGAGTG
                                |||| ||    || ||||||||
                                TCCT GA    TC TGCTTCAC
                                  C  TCCCC  _
GAM985  GRIK5    3'  CACTCCTTCCCAGGCTCC    9133     A   AA   GTAT
                                GGA CTT  GAA   GGAGTG
                                ||| |||  |||   ||||||
                                CCT GGA  CTT   CCTCAC
                                  C   CC  ____
GAM985  MLF2     3'  CACTCCATCTTCAAACCCCCT  18373    AACTTAA   T
                                AGG      GAAG ATGGAGTG
                                |||      |||| ||||||||
                                TCC      CTTC TACCTCAC
                                  CCCAAA_   _
GAM985  RAD1     5'  TCACTGCAGTTTCAAGTTCCT  55913       AA   GTA  G
                                AGGAACTT  GAA   TG AGTGA
                                ||||||||  |||   || |||||
                                TCCTTGAA  CTT   AC TCACT
                                   __  TG_  G
GAM985  UBE2V1   3'  CTCCTCCTCAAGTTCCT    41793       A  AAGTAT
                                AGGAACTT AG    GGAG
                                |||||||| ||    ||||
                                TCCTTGAA TC    CCTC
                                   C  CT____
GAM985  UBE2V1   3'  CTCCTCCTCAAGTTCCT    42370       A  AAGTAT
                                AGGAACTT AG    GGAG
                                |||||||| ||    ||||
                                TCCTTGAA TC    CCTC
                                   C  CT____
GAM985  UBE2V1   3'  CTCCTCCTCAAGTTCCT    12518       A  AAGTAT
                                AGGAACTT AG    GGAG
                                |||||||| ||    ||||
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                                TCCTTGAA TC     CCTC
                                    C  CT____
GAM985  VIPR1    3'  TCACCATTGCTGTCAAGTTCCT 16116        AAGA   TGGA
                                AGGAACTT   AGTA   GTGA
                                ||||||||   ||||   ||||
                                TCCTTGAA   TCGT   CACT
                                    CTG_   TAC_
GAM985  ZNF142   3'  CACTCCATCAAAGTCCCT   17432    A   AAGAAGT
                                AGG ACTT      ATGGAGTG
                                ||| ||||      ||||||||
                                TCC TGAA      TACCTCAC
                                  C   AC_____
GAM985  ZNF266   3'  CACTCCATATTTGTAAGCCCT  88322    AA   AG
                                AGG  CTTA  AAGTATGGAGTG
                                |||  ||||  ||||||||||||
                                TCC  GAAT  TTTATACCTCAC
                                  C_   G_
GAM985  AMOTL2   3'  CTCCTCCTCAAGTTCCT    32482        A  AAGTAT
                                AGGAACTT AG     GGAG
                                |||||||| ||     ||||
                                TCCTTGAA TC     CCTC
                                    C  CT____
GAM985  BCL2L1   3'  CACCCCACACTTGTTCC    56803      TTAAG   A   A
                                GGAAC    AAGT TGG GTG
                                |||||    |||| ||| |||
                                CCTTG    TTCA ACC CAC
                                   _____   C   C
GAM985  C(27)-3BETA-HSD 3'  CACCTCTCTACCTAAGTTCCT  47270         AGAA   T   _
                                AGGAACTTA   GTA GGAG TG
                                |||||||||   ||| |||| ||
                                TCCTTGAAT   CAT TCTC AC
                                     C___   C   C
GAM985  C21orf69  3'  TCACCCCATACTCTGTCACTGC 54215   AACTTA_  A    A
            C                    GG      AGA GTATGG GTGA
                                ||      ||| |||||| ||||
                                CC      TCT CATACC CACT
                                 GTCACTG  _     C
GAM985  CLSTN2   3'  CACTTCTGCCCTAAGTTCC   42129        AGAA   T
                                GGAACTTA   GTA GGAGTG
                                ||||||||   ||| ||||||
                                CCTTGAAT   CGT CTTCAC
                                    CC__   _
GAM985  DKFZP434J037 3'  CACTCCACACTCTTGAGTCTCT 48206    GA       A  A
                                AG  ACTTAAGA GT TGGAGTG
                                ||  |||||||| || |||||||
                                TC  TGAGTTCT CA ACCTCAC
                                 TC       _ C
GAM985  DKFZP566I1024 3'  TCACTCTAGCCTTGAATTCCT  70107       C    AAGTA
                                AGGAA TTAAG    TGGAGTGA
                                ||||| |||||    ||||||||
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                                TCCTT AGTTC    ATCTCACT
                                  A    CG___
GAM985  ERN1     3'  TCAGACTTTTTAAATTCCT   7519       C       A
                                AGGAA TTAAGAAGT TGG
                                ||||| ||||||||| |||
                                TCCTT AATTTTTCA ACT
                                  A       G
GAM985  FLJ10292 3'  TCACTTCAGTTTCCCAGTTCCT 35976       TAA   GTA
                                AGGAACT   GAA   TGGAGTGA
                                |||||||   |||   ||||||||
                                TCCTTGA   CTT   ACTTCACT
                                   CC_   TG_
GAM985  FLJ10925 3'  CCAGTATTCCCCGAGTTCCT   36882       AA_   GTA
                                AGGAACTT   GAA   TGG
                                ||||||||   |||   |||
                                TCCTTGAG   CTT   ACC
                                    CCC   ATG
GAM985  FLJ14082 3'  CACTCCTGAGACCCAAGGTTCC 46671       AAGAAGTAT
          T                      AGGAACTT       GGAGTG
                                ||||||||       ||||||
                                TCCTTGGA       CCTCAC
                                    ACCCAGAGT
GAM985  FLJ20275 3'  CCAACCCTTAAGTTCCT     34820         AA  A
                                AGGAACTTAAG  GT TGG
                                ||||||||||  || |||
                                TCCTTGAATTC  CA ACC
                                   C_  _
GAM985  FLJ21742 3'  CACCCTGGCCCTCAGGTTCCT  49844       A  AA  AT  A
                                AGGAACTT AG  GT  GG GTG
                                |||||||| ||  ||  || |||
                                TCCTTGGA TC  CG  CC CAC
                                    C  C_  GT  _
GAM985  FLJ23071 3'  CACTCCCTTCCCAAGTTCCT   47263       AA    TAT
                                AGGAACTT  GAAG   GGAGTG
                                ||||||||  ||||   ||||||
                                TCCTTGAA  CTTC   CCTCAC
                                    CC    ___
GAM985  KIAA0255 3'  CACCCCACACCTGAGTTCTT   28465       AGAA  A   A
                                AGGAACTTA    GT TGG GTG
                                |||||||||    || ||| |||
                                TTCTTGAGT    CA ACC CAC
                                    C___  C   C
GAM985  KIAA0444 3'  CCACCTTCCGAAGCTCCT    62338     A   AA    TA
                                AGGA CTT  GAAG  TGG
                                |||| |||  ||||  |||
                                TCCT GAA  CTTC  ACC
                                  C   GC    C_
GAM985  KIAA1319 3'  CCATACCCCTCCAGTTCCT   40405       TA  AA
                                AGGAACT  AG  GTATGG
                                |||||||  ||  ||||||
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                                TCCTTGA  TC  CATACC
                                   CC  CC
GAM985  KIAA1535  3'  CATACTTCTAAGTTCC      79410         A
                                GGAACTTA GAAGTATG
                                |||||||| ||||||||
                                CCTTGAAT CTTCATAC
                                        _
GAM985  KIAA1671  3'  TCACTCCAGCCTCCAACTCCT  65692      ACTTAA  A  A
                                AGGA     GA GT TGGAGTGA
                                ||||     || || ||||||||
                                TCCT     CT CG ACCTCACT
                                  CAAC__  C  _
GAM985  KIAA1856  3'  TCACTCTGGGCTTCCCAAGCAC 92671    AA   AA    A
            C                    GG  CTT  GAAGT TGGAGTGA
                                ||  |||  ||||| ||||||||
                                CC  GAA  CTTCG GTCTCACT
                                 AC   CC    G
GAM985  MGC1127   3'  TCACTCCATTTGGCAAGCTCT  53218     A   AAGAAGT
                                GGA CTT      ATGGAGTGA
                                ||| |||      |||||||||
                                TCT GAA      TACCTCACT
                                  C   CGGTT__
GAM985  MMPL1    3'  TCACCCCACCGCCCTCTTAAGT 14723           A_  A_   A
            TTCT                   AGGAACTTAAGA  GT  TGG GTGA
                                ||||||||||||  ||  ||| ||||
                                TCTTTGAATTCT  CG  ACC CACT
                                       CC  CC   C
GAM985  NESCA    3'  CACTCCATCCCTCCCAAGTTGC 26743    _    AA  AGT
            C                    GG AACTT  GA   ATGGAGTG
                                || |||||  ||   ||||||||
                                CC TTGAA  CT   TACCTCAC
                                 G    CC  CCC
GAM985  RNF32    3'  CACTCCTTAAGTTCC       48187         GAAGTAT
                                GGAACTTAA      GGAGTG
                                |||||||||      ||||||
                                CCTTGAATT      CCTCAC
                                        _______
GAM985  SCMH1    5'  CCAAACTTCTTAACCCCT    24253     AAC       A
                                AGG   TTAAGAAGT TGG
                                |||   ||||||||| |||
                                TCC   AATTCTTCA ACC
                                  CC_       A
GAM985  SEMA4G   5'  CACTCCATACCCTTCTCC    94672     ACTT   AA
                                GGA    AAG  GTATGGAGTG
                                |||    |||  ||||||||||
                                CCT    TTC  CATACCTCAC
                                  C___   C_
GAM985  TRAP95   3'  CACCCACCTCAAGTTCCT    65536        A  AAGTA   A
                                AGGAACTT AG    TGG GTG
                                |||||||| ||    ||| |||
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                                TCCTTGAA TC     ACC CAC
                                    C  C____   _
GAM985  ZAK      3'  TCTCTTCCTAAGTTCC      33604          A    TAT
                                GGAACTTA GAAG   GGA
                                |||||||| ||||   |||
                                CCTTGAAT CTTC   TCT
                                    C   ___
GAM985  LOC149506 3'  CACTCCTACAAATTCC      84452      C  AAGAA   T
                                GGAA TT     GTA GGAGTG
                                |||| ||     ||| ||||||
                                CCTT AA     CAT CCTCAC
                                  A _____  _
GAM985  LOC152674 3'  CACTCCACACTTTATTAGCAAA 85833       ____  TAA     A
           TTCCT                    AGGAA    CT   GAAGT TGGAGTG
                                |||||    ||   ||||| |||||||
                                TCCTT    GA   TTTCA ACCTCAC
                                   AAAC  TTA     C
GAM985  LOC255096 5'  CACTCCATCCTCAACTCC     97622      ACTTAA  A T
                                GGA      GA G ATGGAGTG
                                |||      || | ||||||||
                                CCT      CT C TACCTCAC
                                  CAA___  _ C
GAM985  LOC257415 3'  TCACTCTTGCTGTCTTAAGTTC 96078          _    T
                                GAACTTAAGA AGTA GGAGTGA
                                |||||||||| |||| |||||||
                                CTTGAATTCT TCGT TCTCACT
                                     G   _
GAM986  CD74     3'  GAACAGCAGATAACA       15129      CA
                                TGT  GTCTGCTGTTT
                                |||  ||||||||||
                                ACA  TAGACGACAAG
                                  A_
GAM986  MFAP4    3'  CCTGTCCCAACAGCTGACAG   69254        T   C  TTT
                                CTGTCAG CTG TG   GCAGG
                                ||||||| ||| ||   |||||
                                GACAGTC GAC AC   TGTCC
                                    _   A  CC_
GAM986  SLC20A1   3'  TGTTAACAGAAGACTGACA    59391          G     T
                                TGTCAGTCT CTGTT GCA
                                |||||||| ||||| |||
                                ACAGTCAGA GACAA TGT
                                     A     T
GAM986  WNT14    3'  CCTGCAAGGACTGAGAG      12676     G      GCTGT
                                CT TCAGTCT     TTGCAGG
                                || |||||||     |||||||
                                GA AGTCAGG     AACGTCC
                                 G      _____
GAM986  ATF3     5'  CGCCCGCCGGCCAGACAAACAG 14431      CA     _   TTT  A
                                CTGT  GTCTG CTG   GC GGCG
                                ||||  ||||| |||   || ||||
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                                GACA  CAGAC GGC   CG CCGC
                                  AA    C  ___  C
GAM986  CXorf9    3'  CGCCCTCCACCAGCGACTGACA 38623         T   TTTGCA
            G                    CTGTCAGTC GCTG     GGCG
                                 ||||||||| ||||     ||||
                                 GACAGTCAG CGAC     CCGC
                                      _   CACCTC
GAM986  FLJ20195  3'  CCAGCCCCAGCAGACCACAG   34708      CA       TTT  A
                                 CTGT  GTCTGCTG   GC GG
                                 ||||  ||||||||   || ||
                                 GACA  CAGACGAC   CG CC
                                   C_       CC_  A
GAM986  MAP3K6    5'  CGCCTGCAGCGGAGACTGGACA 16245       _    G    T
            G                    CTGTC AGTCT CTGTT GCAGGCG
                                 ||||| ||||| ||||| |||||||
                                 GACAG TCAGA GGCGA CGTCCGC
                                   G    _    _
GAM986  SRF       5'  GCCCTAGCAGACGGACAG    11950       A       TTTGCA
                                 CTGTC GTCTGCTG     GGC
                                 ||||| ||||||||     |||
                                 GACAG CAGACGAT     CCG
                                   G       C_____
GAM986  LOC115004 3'  CCTGCTGCTCAGACTGA     73174         CT  TT
                                 TCAGTCTG  GT  GCAGG
                                 ||||||||  ||  |||||
                                 AGTCAGAC  CG  CGTCC
                                      T_  T_
GAM986  LOC118611 5'  CACCCATGCAGACGACA     75470      A     _  TT
                                 TGTC GTCTGC TG  TG
                                 |||| |||||| ||  ||
                                 ACAG CAGACG AC  AC
                                   _     T  CC
GAM986  LOC197342 3'  CCTGGGCTGCAGACAGACA    87998      A     T   TG
                                 TGTC GTCTGC GTT  CAGG
                                 |||| |||||| |||  ||||
                                 ACAG CAGACG CGG  GTCC
                                   A     T  __
GAM986  LOC204084 5'  TTTGTACAGACTGACA      89450          CTGTT
                                 TGTCAGTCTG    TGCAGG
                                 ||||||||||    ||||||
                                 ACAGTCAGAC    ATGTTT
                                               _____
GAM986  LOC83690  5'  CGCCCACCCTGGCAGACTAACG 48814     C       GTTTGCA
                                 TGT AGTCTGCT      GGCG
                                 ||| ||||||||      ||||
                                 GCA TCAGACGG      CCGC
                                   A       TCCCAC_
GAM986  LOC90515  3'  CGCCTGCAACCTTGATCGACAG 63123       A   TGCTGT
                                 CTGTC GTC     TTGCAGGCG
                                 ||||| |||     |||||||||
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                                GACAG TAG     AACGTCCGC
                                  C   TTCC__
GAM987  BLTR2    5'  GCTCAAGAATACAGGATCACCT 39042         G   TGCCATC
            G                    CAGGTGATC TGT      GAGC
                                |||||||||  |||      ||||
                                GTCCACTAG ACA      CTCG
                                     G   TAAGAA_
GAM987  DKFZP434A043 3'  CTCTCAACATGACCACC     31190      A       CCATC
                                GGTG TCGTGTTG    GAG
                                ||||  ||||||||    |||
                                CCAC AGTACAAC    CTC
                                  C       T____
GAM987  PDZD2    3'  CTCAATAGGTTATTGATCACC  80868         TGTT  _  C
                                GGTGATCG   GCC AT GAG
                                ||||||||   ||| || |||
                                CCACTAGT   TGG TA CTC
                                     TAT_   A  A
GAM987  SLC12A8  3'  CTCTGCAACACGACACC     44899      A       CATC
                                GGTG TCGTGTTGC   GAG
                                ||||  |||||||||   |||
                                CCAC AGCACAACG   CTC
                                  _       T___
GAM987  SLK      3'  GCTCATGAAGACAATCACCTG  28226         CG   GC   C
                                CAGGTGAT  TGTT  CAT GAGC
                                ||||||||  ||||  ||| ||||
                                GTCCACTA  ACAG  GTA CTCG
                                     __    AA  _
GAM987  LOC253574 5'  CAACCACGACCACTCTG     97473     _  A    _
                                CAG GTG TCGTG TTG
                                ||| ||| ||||| |||
                                GTC CAC AGCAC AAC
                                  T  C    C
GAM988  AF1Q     3'  TCTGACTCGACATCTTGTCCC  22369            CGCATG
                                GGGACAAGATGTTG     CAGA
                                ||||||||||||||     ||||
                                CCCTGTTCTACAGC     GTCT
                                       TCA___
GAM988  EN2      5'  CTGCATGCGCGCAGCTCTCGCC 7461      ACA  T  __
            C                    GGG   AGA GT  TGCGCATGCAG
                                |||   ||| ||  ||||||||||
                                CCC   TCT CG  GCGCGTACGTC
                                  GC_   _  AC
GAM988  SLC22A12 3'  CGCACTGCCACTTGTCCC    58068         ATGT  C   _  A
                                GGGACAAG    TG GCA TGC G
                                ||||||||    || ||| ||| |
                                CCCTGTTC    AC CGT ACG C
                                     _____  _   C   C
GAM988  ZNF76    3'  TCTGCATGGCCACTCTTGCCC  12813     A    T  T  G
                                GGG CAAGA GT GC CATGCAGA
                                ||| ||||| || || ||||||||
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                                CCC GTTCT CA CG GTACGTCT
                                  _    _ C _
GAM988  C9orf7   3' CTGGGTCAGCAGCATCCCACCC 34171    ACAA      GC  G
                                GGG   GATGTTGC  AT CAG
                                |||   |||||||| || |||
                                CCC   CTACGACG  TG GTC
                                  ACC_      AC  G
GAM988  CAMK2G   3' CTGCATGCAGCCCTCCCGCCC  68964    ACAA  TGTT  _
                                GGG   GA   GC GCATGCAG
                                |||   ||   || ||||||||
                                CCC   CT   CG CGTACGTC
                                  GCC_  CC__  A
GAM988  DDX34    3' CTGCATGCGCCCCTCACGCCC  27981    ACAA  TGTT
                                GGG   GA   GCGCATGCAG
                                |||   ||   ||||||||||
                                CCC   CT   CGCGTACGTC
                                  GCA_  CCC_
GAM988  DKFZp547E052 3' TCTGCTATAACACATCTTGCCC 50100    A      TGCGCAT
                                GGG CAAGATGT      GCAGA
                                ||| ||||||||      |||||
                                CCC GTTCTACA      CGTCT
                                  _       CAATAT_
GAM988  FBXO21   3' TCTGCATGCAGTATTCTCACCC 53242    ACA   TGT  _
                                GGG   AGA   TGC GCATGCAGA
                                |||   |||   ||| |||||||||
                                CCC   TCT   ATG CGTACGTCT
                                  AC_   T__   A
GAM988  FEM-2    3' CTGCATGCCCAGCCTTACCCC  27578    AC   AT   C
                                GGG  AAG  GTTG GCATGCAG
                                |||  |||  |||| ||||||||
                                CCC  TTC  CGAC CGTACGTC
                                  CA   __    C
GAM988  FLJ12681 3' CAGGCCAACCCTTGTCCC    42872       AT   C  A
                                GGGACAAG  GTTG GC TG
                                ||||||||  |||| || ||
                                CCCTGTTC  CAAC CG AC
                                     C_    _ G
GAM988  GNB4     3' CTGCATCTGAACATCTTTCCC  41268     C      G  C
                                GGGA AAGATGTT CG ATGCAG
                                |||| |||||||| || ||||||
                                CCCT TTCTACAA GT TACGTC
                                  _       _ C
GAM988  HSJ1     3' TCTGCATGCTGAGCCCCATC   22138     TT ___
                                GATG  GC   GCATGCAGA
                                ||||  ||   |||||||||
                                CTAC  CG   CGTACGTCT
                                  CC  AGT
GAM988  NYD-SP17 5' TCTGTTTTCCAACACCTTGCCT 50879     A   A    CGCAT
                                GGG CAAG TGTTG    GCAGA
                                ||| |||| |||||    |||||
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                                TCC GTTC ACAAC    TGTCT
                                  _   C    CTTT_
GAM988  SLC17A6  3'  GCACAACATCTCATCCT    39744     CA      C
                                GGGA  AGATGTTG GC
                                ||||  |||||||| ||
                                TCCT  TCTACAAC CG
                                  AC       A
GAM988  TRPV5    5'  CTGCATGCACACACACCACC   39047    GACAAGA  _  C
                                GG      TGT TG GCATGCAG
                                ||      ||| || ||||||||
                                CC      ACA AC CGTACGTC
                                 ACC____   C  A
GAM988  LOC148987 3'  TGGGCAGCATCCTATCCC    79122     CAA      G
                                GGGA   GATGTTGC CA
                                ||||   |||||||| ||
                                CCCT   CTACGACG GT
                                  ATC       G
GAM988  LOC152641 5'  TCTGCATGCGCATTCCTCGCGC 80635    ACAA  TGT_
          C                      GG    GA    TGCGCATGCAGA
                                ||    ||    ||||||||||||
                                CC    CT    ACGCGTACGTCT
                                 GCG_  CCTT
GAM988  LOC253980 3'  GCCAACACTTGTCCC      95072        A    C
                                GGGACAAG TGTTG GC
                                |||||||| ||||| ||
                                CCCTGTTC ACAAC CG
                                      _    _
GAM988  LOC254556 3'  TGCCTAACATCTGCCC     94619     A  A     C
                                GGG CA GATGTTG GCA
                                ||| || ||||||| |||
                                CCC GT CTACAAT CGT
                                  _ _      C
GAM989  APPBP2   3'  AAACACTAACAATCTTTAC   21064        TTTAG
                                GTAAGGATT    GGTGTTT
                                |||||||||    |||||||
                                CATTTCTAA    TCACAAA
                                     CAA__
GAM989  COG3     3'  AAACACTCAAACACCTTAC   48696      ATT   A
                                GTAAGG   TTT GGGTGTTT
                                ||||||   ||| ||||||||
                                CATTCC   AAA CTCACAAA
                                   AC_   _
GAM989  GALNT3   3'  AAACACAATAAAAAATCCT   15602        _ GG
                                AGGATTTTT A  GTGTTT
                                ||||||||| |  ||||||
                                TCCTAAAAA T  CACAAA
                                     A AA
GAM989  GNA11    5'  AAACACCCTGGGCCCT     76092     ATT
                                AGG   TTTAGGGTGTTT
                                |||   ||||||||||||
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                                TCC   GGGTCCCACAAA
                                  C__
GAM989  GNRH1    3'  ATTTCAGAAATCCTTAC     5882           AG
                                GTAAGGATTTTT  GGT
                                |||||||||||  |||
                                CATTCCTAAAGA  TTA
                                      CT
GAM989  GRM6     3'  AAACACCAAAAAAACCC     5923     A     AG
                                GG TTTTT  GGTGTTT
                                || |||||  |||||||
                                CC AAAAA  CCACAAA
                                 C     AA
GAM989  POU3F1   3'  AAACACCCGGACGACCCT    59307     A  T  A
                                AGG TT TT GGGTGTTT
                                ||| || || ||||||||
                                TCC AG AG CCCACAAA
                                  C  C  G
GAM989  RPL15    3'  AAACAACCCTAAAAATCCTTAC 11382              _
                                GTAAGGATTTTTAGGGT GTTT
                                |||||||||||||||| ||||
                                CATTCCTAAAAATCCCA CAAA
                                           A
GAM989  SLC26A4  3'  AAACACCTTATCCCTAAC    4781     A   ATTTT
                                GT AGG     TAGGGTGTTT
                                || |||     ||||||||||
                                CA TCC     ATTCCACAAA
                                 A  CT___
GAM989  TTC3     5'  ACTATAAAAATCCTTAT      12412            G
                                GTAAGGATTTTTA GGT
                                |||||||||||| |||
                                TATTCCTAAAAAT TCA
                                       A
GAM989  DKFZp762L0311 3'  AACATGCTAGAAAATCCTCAC  38049     A       _  G
                                GT AGGATTTTT AG GTGTT
                                || |||||||| || |||||
                                CA TCCTAAAAG TC TACAA
                                 C        A  G
GAM989  EPB41L1  3'  AACACCGCATCCTTGC      70584         TTTTAG
                                GTAAGGAT     GGTGTT
                                ||||||||     ||||||
                                CGTTCCTA     CCACAA
                                     CG____
GAM989  FLJ10656 3'  AAACATCTTGAAAATCC     36384
                                GGATTTTTAGGGTGTTT
                                |||||||||||||||||
                                CCTAAAAGTTCTACAAA

GAM989  FLJ13263 3'  AAACACCTTACCCTCAC     47088     A   ATTTT
                                GT AGG     TAGGGTGTTT
                                || |||     ||||||||||
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                                CA TCC    ATTCCACAAA
                                 C  C____
GAM989  KIAA0870  3'  AAACACATGAATCCTTAT    81465        TTAGG
                                GTAAGGATTT    GTGTTT
                                ||||||||||    ||||||
                                TATTCCTAAG    CACAAA
                                      TA___
GAM989  KIAA0907  3'  ACCACAAAAATCCTTAT     30168         AG
                                GTAAGGATTTTT  GGT
                                ||||||||||||  |||
                                TATTCCTAAAAA  CCA
                                       CA
GAM989  KIAA1467  3'  AAACACCCTCCCTTTTCCTTA  71601       TTTTT_
                                TAAGGA     AGGGTGTTT
                                ||||||     |||||||||
                                ATTCCT     TCCCACAAA
                                    TTTCCC
GAM989  NICE-3    3'  AAGCTTCTTAAAAATCTTCAC  31274    A         T
                                GT AGGATTTTTAGGG GTTT
                                || ||||||||||||| ||||
                                CA TTCTAAAAATTCT CGAA
                                 C          T
GAM989  PRO1430   3'  AAATATTATAAAAATCCT    37747        GG
                                AGGATTTTTA  GTGTTT
                                ||||||||||  ||||||
                                TCCTAAAAAT  TATAAA
                                      AT
GAM989  SEMA4G    3'  AAACACCCTTTTTCCCCAC   35432    AA   TTTTT
                                GT  GGA    AGGGTGTTT
                                ||  |||    |||||||||
                                CA  CCT    TCCCACAAA
                                 CC   TTT__
GAM989  SEMA5A    3'  AAACACCCTCCCTCAC      14250    A   ATTTTT
                                GT AGG     AGGGTGTTT
                                || |||     |||||||||
                                CA TCC     TCCCACAAA
                                 C  C_____
GAM989  SH3BGRL   3'  AAACACCCTTCCCTCCTT    61938      TTTTT
                                AAGGA    AGGGTGTTT
                                |||||    |||||||||
                                TTCCT    TCCCACAAA
                                   CCCT_
GAM989  SMT3H2    3'  ACATAAAAATCCTTGC      22671          GG
                                GTAAGGATTTTTA  GT
                                ||||||||||||  ||
                                CGTTCCTAAAAAT  CA
                                       A_
GAM989  SV2B      3'  AAACACCCAGGTTCCT      29289      TT   A
                                AGGA  TTT GGGTGTTT
                                ||||  ||| ||||||||
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                                TCCT  GGA CCCACAAA
                                  T_  _
GAM989  THEG     3'  AAACACCCTCAGGCACCCTAAC 33427    A  AT_  T
                                GT AGG   TTT AGGGTGTTT
                                || |||   ||| |||||||||
                                CA TCC   GGA TCCCACAAA
                                 A   CAC   C
GAM989  TRAP-1   3'  AAACCCCTAAAAATCC      14920          T
                                GGATTTTTAGGG GTTT
                                |||||||||||| ||||
                                CCTAAAAATCCC CAAA
                                          _
GAM989  WIT-1    3'  AAACACCCCAAAGCGCT     31818    AT   A
                                GG  TTTT GGGTGTTT
                                ||  |||| ||||||||
                                TC  GAAA CCCACAAA
                                 GC    C
GAM989  LOC116441 3'  AAACACCCCAAAATTCT     57089        TA
                                AGGATTTT  GGGTGTTT
                                ||||||||  ||||||||
                                TCTTAAAA  CCCACAAA
                                     C_
GAM989  LOC120103 3'  ACCTATGAAAAATCCTTGC   74003          A__
                                GTAAGGATTTTT   GGGT
                                ||||||||||||   ||||
                                CGTTCCTAAAAA   TCCA
                                       GTA
GAM989  LOC124302 3'  AAACACCTTCATCCCCAC    74275    AA   TTTT
                                GT  GGAT    AGGGTGTTT
                                ||  ||||    |||||||||
                                CA  CCTA    TTCCACAAA
                                 CC    C___
GAM989  LOC145955 5'  AAACACCCCAGGCTTCT     83582     TT   A
                                GGA  TTT GGGTGTTT
                                |||  ||| ||||||||
                                TCT  GGA CCCACAAA
                                  TC   C
GAM989  LOC147942 3'  AAACACTGACCTAATCCTTGC  78576         TTTAG
                                GTAAGGATT    GGTGTTT
                                |||||||||    |||||||
                                CGTTCCTAA    TCACAAA
                                     TCCAG
GAM989  LOC148089 3'  CCCTAAAAATTCCTAC      78631     A
                                GTA GGATTTTTAGGG
                                ||| ||||||||||||
                                CAT CTTAAAAATCCC
                                  C
GAM989  LOC150225 5'  AAACTACAAAAAAATCCTTA   84974          AGG  _
                                TAAGGATTTTT   GT GTTT
                                ||||||||||   || ||||
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                                ATTCCTAAAAA   CA CAAA
                                      AA_  T
GAM989  LOC150381 3'  AAACACCAGACAGAGATCC   79812        AG__
                                GGATTTTT   GGTGTTT
                                ||||||||   |||||||
                                CCTAGAGA   CCACAAA
                                    CAGA
GAM989  LOC154547 3'  ACATAAAAATCCTTGC     76051          GG
                                GTAAGGATTTTTA  GT
                                ||||||||||||  ||
                                CGTTCCTAAAAAT  CA
                                       A_
GAM989  LOC158997 3'  ACATAAAAATCCTTGC     82079          GG
                                GTAAGGATTTTTA  GT
                                ||||||||||||  ||
                                CGTTCCTAAAAAT  CA
                                       A_
GAM989  LOC202347 3'  AAACACCCTGTTGATCC    90341      TT
                                GGATT  TAGGGTGTTT
                                |||||  ||||||||||
                                CCTAG  GTCCCACAAA
                                   TT
GAM989  LOC221561 3'  ACATAAAAATCCTTGC     92131          GG
                                GTAAGGATTTTTA  GT
                                ||||||||||||  ||
                                CGTTCCTAAAAAT  CA
                                       A_
GAM989  LOC221895 3'  GTGCCAAGAAATCCTCAC   92526   A      AG  TG
                                GT AGGATTTTT  GG  T
                                || |||||||||  ||  |
                                CA TCCTAAAGA  CC  G
                                 C       A_  GT
GAM989  LOC255650 3'  AAACACCTTAAATTCTCAC   96708   A     TT
                                GT AGGATT  TAGGGTGTTT
                                || ||||||  ||||||||||
                                CA TCTTAA  ATTCCACAAA
                                 C     __
GAM989  LOC257591 3'  ACATAAAAATCCTTGC     97841          GG
                                GTAAGGATTTTTA  GT
                                ||||||||||||  ||
                                CGTTCCTAAAAAT  CA
                                       A_
GAM989  LOC91250  5'  AAACACCCTAAAGATC     65317
                                GATTTTTAGGGTGTTT
                                ||||||||||||||||
                                CTAGAAATCCCACAAA

GAM990  ADAM20    3'  GGAAAAAGAAGGAGACT     13768          C_
                                AGTCTCTTTCT  TTCC
                                ||||||||||  ||||
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                                TCAGAGGAAGA  AAGG
                                      AA
GAM990  APOL1   3'  GGAAAAGAAAGAGCTGA     13351      T       C
                                TCAG CTCTTTCT TTCC
                                |||| |||||||| ||||
                                AGTC GAGAAAGA AAGG
                                  _       A
GAM990  AQP6    5'  CAGGTGAGACTGGGAAAGG   53914        T_  C
                                TCTTTCTC  TC CACCTG
                                ||||||||  || ||||||
                                GGAAAGGG  AG GTGGAC
                                     TC  A
GAM990  CDH1    3'  GGGAAAAAAAAAGAGACTGG   15149          CTC
                                TCAGTCTCTTT   TTCCC
                                ||||||||||   |||||
                                GGTCAGAGAAA   AAGGG
                                      AAA
GAM990  DIO3    3'  GGGAGAGAGAAAAAGCTGA   7245       T  C      _
                                TCAG CT TTTCTCT TCCC
                                |||| || ||||||| ||||
                                AGTC GA AAAGAGA AGGG
                                  _ A      G
GAM990  DUOX2   3'  TGAGAAAAGGCAGGAGACT   26022         _  C   C
                                AGTCTCTT TCT TTC CA
                                |||||||| ||| ||| ||
                                TCAGAGGA GGA AAG GT
                                     C   A   A
GAM990  EDNRA   3'  AAGAGAAAAAGATCGA      64103     A    C
                                TC GTCT TTTCTCTT
                                || |||| ||||||||
                                AG TAGA AAAGAGAA
                                 C    A
GAM990  EHD3    3'  GAAGAGAAAAAAATTGA     27478       CTC
                                TCAGT   TTTCTCTTC
                                |||||   |||||||||
                                AGTTA   AAAGAGAAG
                                   AAA
GAM990  FGF7    5'  CAGATAGGAAGAGGTCAATGA  8883      GTCTCTT       CAC
                                TCA      TCTCTTCC   CTG
                                |||      ||||||||   |||
                                AGT      GGAGAAGG   GAC
                                  AACT___       ATA
GAM990  GRIN2B  5'  GAGAAGAAGGGACTGG      5903          TC
                                TCAGTCTCTT  TCTT
                                ||||||||||  ||||
                                GGTCAGGGAA  AGAG
                                      GA
GAM990  IRS2    3'  GGAAAGAAAGAAACTGA     59719       C      C
                                TCAGT TCTTTCT TTCC
                                ||||| ||||||| ||||
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                                AGTCA AGAAAGA AAGG
                                  A     _
GAM990  NOS1    3'  CAGGCAGTTCCCAGAAAGAGAC 5243          CTTCCCA_
                                GTCTCTTTCT      CCTG
                                ||||||||||      ||||
                                CAGAGAAAGA      GGAC
                                     CCCTTGAC
GAM990  PSCD4   3'  CAGGTGGGACCCTCAAGAAAAT 25402    GTC   TCTCT
          GA                      TCA  TCTT    TCCCACCTG
                                  |||  ||||    |||||||||
                                  AGT  AGAA    AGGGTGGAC
                                    AAA   CTCCC
GAM990  TRPC1   3'  CAGGTGGGAAGAAAATATGGA  12385    CT_  C
                                  TCT  TT TCTTCCCACCTG
                                  |||  || ||||||||||||
                                  AGG  AA AGAAGGGTGGAC
                                    TAT  A
GAM990  WRN     5'  CAGGTGGGAAGATGGGAATGA  5095     G   TTTC
                                  TCA TCTC   TCTTCCCACCTG
                                  ||| ||||   ||||||||||||
                                  AGT AGGG   AGAAGGGTGGAC
                                    A   T___
GAM990  APOL2   3'  GGAAAAGAAAGAGCTGA    48052     T     C
                                  TCAG CTCTTTCT TTCC
                                  |||| |||||||| ||||
                                  AGTC GAGAAAGA AAGG
                                    _      A
GAM990  APOL3   3'  GGAAAAGAAAGAGCTGA    26814     T     C
                                  TCAG CTCTTTCT TTCC
                                  |||| |||||||| ||||
                                  AGTC GAGAAAGA AAGG
                                    _      A
GAM990  APOL4   3'  GGAAAAGAAAGAGCTGA    47626     T     C
                                  TCAG CTCTTTCT TTCC
                                  |||| |||||||| ||||
                                  AGTC GAGAAAGA AAGG
                                    _      A
GAM990  C12orf3 3'  CAGTGTGTAAAAAGAAAGAGCC 39808     T     C  CC  _
          TGA                     TCAG CTCTTTCT TT  CAC CTG
                                  |||| |||||||| ||  ||| |||
                                  AGTC GAGAAAGA AA  GTG GAC
                                    C      A  AT   T
GAM990  C20orf82 3' GGGGGAAAGAGACTGA     84714
                                  TCAGTCTCTTTCTCTT
                                  ||||||||||||||||
                                  AGTCAGAGAAAGGGGG

GAM990  C9orf4  3'  GGCAGAGAAGGAACT      81894    C      T
                                  AGT TCTTTCTCT CC
                                  ||| ||||||||| ||
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                                TCA AGGAAGAGA GG
                                  _       C
GAM990  CDC14A   3' GGAGAGAAAAAACTGA     13394      CTC
                                TCAGT   TTTCTCTTC
                                |||||   |||||||||
                                AGTCA   AAAGAGAGG
                                   AA_
GAM990  COASTER  3' GTGGCCTTGAAGAGACTGA   31448          CTCTTC
                                TCAGTCTCTTT     CCAC
                                ||||||||||     ||||
                                AGTCAGAGAAG     GGTG
                                      TTCC__
GAM990  FLJ00007 3' CAGGCAGGGGAAGGAGAAGAGA 71273          CT     A__
           CTGA                   TCAGTCTCTTT  CTTCCC   CCTG
                                ||||||||||  ||||||   ||||
                                AGTCAGAGAAG  GAAGGG   GGAC
                                      AG     GAC
GAM990  FLJ10081 3' GTGGGAAGATGATTGA      35801       TCTTTC
                                TCAGTC     TCTTCCCAC
                                ||||||     |||||||||
                                AGTTAG     AGAAGGGTG
                                   T_____
GAM990  FLJ10352 3' CAGGTGAGAAGAGAGTTCTG   49558     TCTCT      C
                                CAG     TTCTCTTC CACCTG
                                |||     |||||||| ||||||
                                GTC     GAGAGAAG GTGGAC
                                  TT___       A
GAM990  FLJ10898 5' CAGGTGAGAATTCGACAAGAGA 59424          _  TC_   C
           TTGA                   TCAGTCTCTT TC   TTC CACCTG
                                ||||||||||  ||   |||  ||||||
                                AGTTAGAGAA AG   AAG GTGGAC
                                      C  CTT   A
GAM990  FLJ22569 5' CAGGTGAGCAGCCCAGAAAGAG 43677          ___  TCC
           AC                     GTCTCTTTCT   CT   CACCTG
                                ||||||||||   ||   ||||||
                                CAGAGAAAGA   GA   GTGGAC
                                      CCC  CGA
GAM990  FLJ22595 5' GAGAGAAAAAGGCTGA      46784        C
                                TCAGTCT TTTCTCTT
                                |||||||  ||||||||
                                AGTCGGA AAAGAGAG
                                   A
GAM990  KIAA1376 3' GTGGGAAAAAAAGAGAT     63623        CTC
                                GTCTCTTT   TTCCCAC
                                ||||||||   |||||||
                                TAGAGAAA   AAGGGTG
                                   AA_
GAM990  KIAA1389 3' AGGCTCAGAAGAGACTGA    69765          T  CTTCCCA
                                TCAGTCTCTT CT      CCT
                                ||||||||||  ||      |||
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                                AGTCAGAGAA GA      GGA
                                      _ CTC____
GAM990  KIAA1463  3'  GAATGAGATGAGACTGA     72276        TT   _
                                TCAGTCTC  TCTC TTC
                                ||||||||  |||| |||
                                AGTCAGAG  AGAG AAG
                                     T_   T
GAM990  MGC10814  5'  AGATGAGCAGAGACTGA     51035         _  _
                                TCAGTCTCT TTC TCT
                                ||||||||| ||| |||
                                AGTCAGAGA GAG AGA
                                      C   T
GAM990  MGC11061  3'  CAGATGGAAAGGGAAG      50285        C   C
                                TTTCTCTT CCA CTG
                                |||||||| ||| |||
                                GAAGGGAA GGT GAC
                                     A   A
GAM990  MGC14407  3'  GGAAAATAAAAAGACTGA    51877        C   CTC
                                TCAGTCT TTT   TTCC
                                ||||||| |||   ||||
                                AGTCAGA AAA   AAGG
                                    A   TAA
GAM990  MGC3040   3'  AGGTGAGGTAAGAGACTGA    66842          TCTCTT  _
                                TCAGTCTCTT     CC CACCT
                                ||||||||||     || |||||
                                AGTCAGAGAA     GG GTGGA
                                      T_____  A
GAM990  MYLE      3'  GAAGAAAAAGAAGCTGA     25813      TC     C
                                TCAG  TCTTT TCTTC
                                ||||  ||||| |||||
                                AGTC  AGAAA AGAAG
                                  GA     A
GAM990  PCDH19    3'  CAGGAAGAAGAGAAAGAAAC  63699    C         CCA
                                GT TCTTTCTCTTC   CCTG
                                || ||||||||||   ||||
                                CA AGAAAGAGAAG   GGAC
                                 A          AA_
GAM990  PLAC3     5'  GAAGAGAAAGAAATGA      69343     GTC
                                TCA   TCTTTCTCTTC
                                |||   ||||||||||
                                AGT   AGAAAGAGAAG
                                  AA_
GAM990  PLEKHA4   5'  CAGAGAGAAAGAGGAAGAGACT 40497              CCCAC
           GA                    TCAGTCTCTTTCTCTT    CTG
                                 ||||||||||||||||    |||
                                 AGTCAGAGAAGGAGAA    GAC
                                       AGAGA
GAM990  PPY2      3'  CAGGTATGGAGAAAGAGAC    40820           TCCC
                                GTCTCTTTCTCT    ACCTG
                                ||||||||||||   |||||
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                                CAGAGAAAGAGG   TGGAC
                                       TA__
GAM990  SDC3     3'  GTGGAAAAAAGAGAC      27762        CTC  C
                                GTCTCTTT   TT CCAC
                                ||||||||   || ||||
                                CAGAGAAA   AA GGTG
                                    ____  A
GAM990  TIGD4    5'  AAGAGAAAAAGACTGA      89066        C
                                TCAGTCT TTTCTCTT
                                ||||||| ||||||||
                                AGTCAGA AAAGAGAA
                                    A
GAM990  TLN2     5'  CAGATTGGAGAGAATGAGACTG 61686        T       CCAC
          A                      TCAGTCTC TTCTCTTC    CTG
                                ||||||||| ||||||||    |||
                                AGTCAGAG AAGAGAGG    GAC
                                     T       TTA_
GAM990  LOC148756 5'  CAGAAAGAAGAGAAAAGACTGA 84221        C        CCAC
                                TCAGTCT TTTCTCTTC    CTG
                                ||||||| |||||||||    |||
                                AGTCAGA AAAGAGAAG    GAC
                                   _        AAA_
GAM990  LOC148918 5'  CAGGTAAAAGAGAAAAGAC    79066      C       CCC
                                GTCT TTTCTCTT   ACCTG
                                |||| ||||||||   |||||
                                CAGA AAAGAGAA   TGGAC
                                  _       AA_
GAM990  LOC150759 3'  GGCAAGGGAAAGAAAC      80006     C        C
                                GT TCTTTCTCTT CC
                                || ||||||||||  ||
                                CA AGAAAGGGAA GG
                                 A         C
GAM990  LOC151323 3'  GGCAAGGGAAAGAAAC      80219     C        C
                                GT TCTTTCTCTT CC
                                || ||||||||||  ||
                                CA AGAAAGGGAA GG
                                 A         C
GAM990  LOC151556 5'  GGTGGGAAAAATAAAGAGACTG 80282           CTC_
          A                      TCAGTCTCTTT    TTCCCACC
                                ||||||||||    ||||||||
                                AGTCAGAGAAA    AAGGGTGG
                                       TAAA
GAM990  LOC158038 5'  TGTGGAAGAGAAAGAGCT     81664     T          _
                                AG CTCTTTCTCTTCC CA
                                || ||||||||||||  ||
                                TC GAGAAAGAGAAGG GT
                                 _           T
GAM990  LOC158267 3'  GAGGGAAAAAGCTGA       81830      T  C
                                TCAG CT TTTCTCTT
                                |||| ||  ||||||||
```

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                                AGTC GA AAAGGGAG
                                  _ A
GAM990  LOC165904 3'  TGGAAAAAGAAAGGTCTGG   82609     T T    C  C
                                TCAG C CTTTCT TT CCA
                                |||| | |||||| || |||
                                GGTC G GAAAGA AA GGT
                                  T _    A  A
GAM990  LOC167040 5'  AGGTGAGGAAAAAGAGACTGA  87267          CTC   _
                                TCAGTCTCTTT   TTCC CACCT
                                ||||||||||   |||| ||||||
                                AGTCAGAGAAA   AAGG GTGGA
                                      ___   A
GAM990  LOC200399 3'  GGCAAGGGAAAGAAAC     88810    C       C
                                GT TCTTTCTCTT CC
                                || ||||||||||  ||
                                CA AGAAAGGGAA GG
                                 A        C
GAM990  LOC200488 5'  CAGTGTCTGATAAAAAGAGACT 90084          CTCT  CC  _
          GA                     TCAGTCTCTTT   TC  AC CTG
                                ||||||||||   ||  || |||
                                AGTCAGAGAAA   AG  TG GAC
                                      AAT_  TC  T
GAM990  LOC203069 5'  CAGGCAGGAAGAATGGGGGCTG 89259         TTC     CA
          A                      TCAGTCTCT   TCTTCC  CCTG
                                |||||||||   ||||||  ||||
                                AGTCGGGGGG   AGAAGG  GGAC
                                     TA_     AC
GAM990  LOC220906 3'  CAGATGGAAATGGGGAAAGA   91397        TC__   C
                                TCTTTCTCT    CCA CTG
                                |||||||||    ||| |||
                                AGAAAGGGG    GGT GAC
                                     TAAA   A
GAM990  LOC254249 3'  GTGGGAAGAAAGCAGC     95447    CT     CT
                                GT  CTTTCT  TCCCAC
                                ||  ||||||  ||||||
                                CG  GAAAGA  AGGGTG
                                 AC     __
GAM990  LOC90288  3'  AGGTGGGAAGGCAGCTGA    62078     T  CTTTC
                                TCAG CT    TCTTCCCACCT
                                |||| ||    ||||||||||
                                AGTC GA    GGAAGGGTGGA
                                  _ C_____
GAM990  LOC92078  3'  CAGGCAGGAGAAAAGAAATGA  67978     GTC    C   T  CA
                                TCA   TCTTT TCT CC  CCTG
                                |||   ||||| ||| ||  ||||
                                AGT   AGAAA AGA GG  GGAC
                                  AA_    _  _  AC
GAM991  ALDH3A2   3'  TTCATTCTTCCTCATTCA    69276      T  TAAA
                                TGGAT AG    GAAGAATGAA
                                ||||| ||    ||||||||||
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                                ACTTA TC    CTTCTTACTT
                                  C ____
GAM991  COL4A5   3'  TTTTCACGGTGCTACTAATCC  4940         AA  AAGAA
                                GGATTAGT  AG    TGAAAA
                                ||||||||  ||    ||||||
                                CCTAATCA  TC    ACTTTT
                                    __  GTGGC
GAM991  COL4A5   3'  TTTTCACGGTGCTACTAATCC  52970        AA  AAGAA
                                GGATTAGT  AG    TGAAAA
                                ||||||||  ||    ||||||
                                CCTAATCA  TC    ACTTTT
                                    __  GTGGC
GAM991  COL4A5   3'  TTTTCACGGTGCTACTAATCC  52974        AA  AAGAA
                                GGATTAGT  AG    TGAAAA
                                ||||||||  ||    ||||||
                                CCTAATCA  TC    ACTTTT
                                    __  GTGGC
GAM991  DAAM2    3'  CATCCTGTCTACTAATCCA   92285         AAGA  A
                                TGGATTAGTA   AG ATG
                                ||||||||||   || |||
                                ACCTAATCAT   TC TAC
                                     CTG_  C
GAM991  ESRRG    3'  CATTCTCCTTTATTTTCT    66389     TT      A
                                GGA  AGTAAAG AGAATG
                                |||  ||||||| ||||||
                                TCT  TTATTTC TCTTAC
                                  T_      C
GAM991  HOXB5    3'  TTTTCATTCTCCTCCTCCTCC  9267      TT  TAA  A
                                GGA  AG   AG AGAATGAAAA
                                |||  ||   || ||||||||||
                                CCT  TC   TC TCTTACTTTT
                                  CC  C__  C
GAM991  IL22RA2  3'  TTCATTCTTCTAATAC      53697     A_
                                GTA  AGAAGAATGAA
                                |||  ||||||||||
                                CAT  TCTTCTTACTT
                                  AA
GAM991  PHB      3'  TTTCATTCTTCTCACATCCA   10541       TA  AA
                                TGGAT  GT  AGAAGAATGAAA
                                |||||  ||  ||||||||||||
                                ACCTA  CA  TCTTCTTACTTT
                                   __  C_
GAM991  RASGRP1  3'  TTTTCATTCTTCCTCCTCTCCA 19210      TT  TAAA
                                TGGA  AG   GAAGAATGAAAA
                                ||||  ||   ||||||||||||
                                ACCT  TC   CTTCTTACTTTT
                                  C_  CTC_
GAM991  SUFU     3'  TTTCATTCTCCACTCCTAATCC 32417        TAAAGA
                                GGATTAG     AGAATGAAA
                                |||||||     |||||||||
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                                CCTAATC     TCTTACTTT
                                    CTCACC
GAM991  TRPS1    3'  TCATTCTTCCTTTTCT     26079     TT  TAAA
                                GGA  AG   GAAGAATGA
                                |||  ||   |||||||||
                                TCT  TC   CTTCTTACT
                                  TT  ____
GAM991  AKAP12   3'  TTTTTCTTTCTAACCCA     57845     A   T
                                TGG TTAG AAAGAAGAA
                                ||| |||| |||||||||
                                ACC AATC TTTCTTTTT
                                  C   _
GAM991  AKAP12   3'  TTTTTCTTTCTAACCCA     17525     A   T
                                TGG TTAG AAAGAAGAA
                                ||| |||| |||||||||
                                ACC AATC TTTCTTTTT
                                  C   _
GAM991  ALK7     3'  TGTTCTTCATAATCCA      75744       GTAAA
                                TGGATTA    GAAGAATG
                                |||||||    ||||||||
                                ACCTAAT    CTTCTTGT
                                    A____
GAM991  C6orf33  3'  CTTCTGCACTAATCCA      55880        AA
                                TGGATTAGT  AGAAG
                                |||||||||  |||||
                                ACCTAATCA  TCTTC
                                     CG
GAM991  DKFZp434J1015 3'  TTCTCCTTTACTAACACA    92636    GA       A
                                TG  TTAGTAAAG AGAA
                                ||  ||||||||| ||||
                                AC  AATCATTTC TCTT
                                  AC       C
GAM991  DKFZp547I224 5'  TTTTCATTCCCCTTTACCTTTC 39562     TTA     AA
           C                     GGA   GTAAAG  GAATGAAAA
                                |||   ||||||  |||||||||
                                CCT   CATTTC  CTTACTTTT
                                  TTC     CC
GAM991  DKFZp566H0824 5'  TTTTCATTCCCCTTTATCCCG  34062     ATTA     AA
                                TGG    GTAAAG  GAATGAAAA
                                |||    ||||||  |||||||||
                                GCC    TATTTC  CTTACTTTT
                                  C___     CC
GAM991  DKFZp761A132 3'  TTTTCATTCTTCCAAAGCATC  50185     TAGTAAA
                                GAT      GAAGAATGAAAA
                                |||      ||||||||||||
                                CTA      CTTCTTACTTTT
                                  CGAAAC_
GAM991  FAM10A6  3'  TTTTTCTTTACTAATC     72319
                                GATTAGTAAAGAAGAA
                                ||||||||||||||||
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                              CTAATCATTTCTTTTT

GAM991  FAM10A7  3' TTTTTCTTTACTAATC     81247
                              GATTAGTAAAGAAGAA
                              ||||||||||||||||
                              CTAATCATTTCTTTTT

GAM991  FLJ21458 5' TCTTCTCTCTAATCCA     45845        TAA
                              TGGATTAG   AGAAGA
                              ||||||||   ||||||
                              ACCTAATC   TCTTCT
                                   TC_
GAM991  KIAA0286 3' CATTCTTCCTTACCCTGCC   68322    ATTA   A
                              GG    GTAA GAAGAATG
                              ||    |||| ||||||||
                              CC    CATT CTTCTTAC
                                GTCC    C
GAM991  KIAA0825 3' TTTCATTCCCCCTTTGCCGTCC 61037      TA     AA_
           A                   TGGAT  GTAAAG   GAATGAAA
                              |||||  ||||||   ||||||||
                              ACCTG  CGTTTC   CTTACTTT
                                 C_     CCC
GAM991  KIAA0828 3' TTCTGCTGTCTTTCTAATCCA  81203        T    _  AAT
                              TGGATTAG AAAGA AG   GAA
                              |||||||| ||||| ||   |||
                              ACCTAATC TTTCT TC   CTT
                                   _    G  GT_
GAM991  KIAA0931 3' TTTTCATTCTTCTCTAC     67430     A
                              GTA AGAAGAATGAAAA
                              ||| ||||||||||||
                              CAT TCTTCTTACTTTT
                                C
GAM991  KIAA1750 3' TCATTCTTCTTTCCTCCC    68256    ATT  T
                              GG   AG AAAGAAGAATGA
                              ||   || ||||||||||||
                              CC   TC TTTCTTCTTACT
                               C__  C
GAM991  KPNA6    3' TTTCATTCTTCCCGGTCC    24616      AGTAAA
                              GGATT     GAAGAATGAAA
                              |||||     ||||||||||
                              CCTGG     CTTCTTACTTT
                                 CC____
GAM991  PDE1C    3' TTCATTCTCCTTCTTCTCC   17222     TT  TA   A
                              GGA  AG  AAG AGAATGAA
                              |||  ||  ||| ||||||||
                              CCT  TC  TTC TCTTACTT
                                CT  __   C
GAM991  PEG10    3' CATTCTTCCCTGTCGTCC    30521      __   TAAA
                              GGAT  TAG   GAAGAATG
                              ||||  |||   ||||||||
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                                CCTG  GTC   CTTCTTAC
                                  CT  C___
GAM991  PIP3-E   3'  TCTTCCCTTACTAATC     66814        A_
                                GATTAGTAA  GAAGA
                                |||||||||  |||||
                                CTAATCATT  CTTCT
                                     CC
GAM991  PP3501   5'  TTTCACTCTTCTTTTTCA    41375     TTAGT      A
                                TGGA    AAAGAAGA TGAAA
                                ||||    |||||||| |||||
                                ACTT    TTTCTTCT ACTTT
                                  _____      C
GAM991  PRO0800  5'  TTTTCATTCTCCTCTCAAAATC 37746      AGTAA  A
          C                      GGATT    AG AGAATGAAAA
                                |||||    || ||||||||||
                                CCTAA    TC TCTTACTTTT
                                   AACTC  C
GAM991  PRO1855  3'  TTTCATTCCTCCCTGGGAATC  37549     AG  AA  A
                                GATT  TA  GA GAATGAAA
                                ||||  ||  || ||||||||
                                CTAA  GT  CT CTTACTTT
                                  GG  CC  C
GAM991  SPTLC2   3'  TCATTCCTCTTTTTATTCA   16811      TAGT    A
                                TGGAT    AAAGA GAATGA
                                |||||    ||||| ||||||
                                ACTTA    TTTCT CTTACT
                                   TT__    C
GAM991  ST13     3'  TTTTTCTTTACTAATC      14120
                                GATTAGTAAAGAAGAA
                                ||||||||||||||||
                                CTAATCATTTCTTTTT

GAM991  STK39    3'  TTTATTCTCTAGCAATCCA   25079       A  AA   A
                                TGGATT GT  AGA GAATGAA
                                |||||| ||  ||| |||||||
                                ACCTAA CG  TCT CTTATTT
                                   _  A_  _
GAM991  LOC113386 3'  TTTTCATTCCTCTTTAT     57083        A
                                GTAAAGA GAATGAAAA
                                ||||||| |||||||||
                                TATTTCT CTTACTTTT
                                    C
GAM991  LOC131873 3'  TTTATTAATTTTCACTAATCCA 75884         A   AG
                                TGGATTAGT AAGA  AATGAA
                                ||||||||| ||||  ||||||
                                ACCTAATCA TTTT  TTATTT
                                     C   AA
GAM991  LOC144920 3'  TTTTCATTCTTCCTCTGCCA   83193     AT   TAAA
                                TGG  TAG   GAAGAATGAAAA
                                |||  |||   ||||||||||||
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                                ACC  GTC    CTTCTTACTTTT
                                  __   TC__
GAM991   LOC149052 3'  TTTTTCTTTACTAATC      79145
                                GATTAGTAAAGAAGAA
                                ||||||||||||||||
                                CTAATCATTTCTTTTT

GAM991   LOC149699 5'  TCATCTCTCTTCTAATCCA    79508        TA   _   A
                                TGGATTAG  AAGA AGA TGA
                                ||||||||  |||| ||| |||
                                ACCTAATC  TTCT TCT ACT
                                     __    C   _
GAM991   LOC196812 3'  TTCATGCATTCACTAATTCA   89577         AAA   GA_
                                TGGATTAGT   GAA   ATGAA
                                |||||||||   |||   |||||
                                ACTTAATCA   CTT   TACTT
                                     ___   ACG
GAM991   LOC90333  3'  TTCATTCACAAATCCA      62310       A  AAAGAA
                                TGGATT GT     GAATGAA
                                ||||||  ||     |||||||
                                ACCTAA CA     CTTACTT
                                   A  _______
GAM991   LOC92228  3'  TTTTCATTCTTCTTTTGTGGTC 68544        GT
            CA                    TGGATTA  AAAGAAGAATGAAAA
                                |||||||  ||||||||||||||||
                                ACCTGGT  TTTCTTCTTACTTTT
                                   GT
GAM992   DPH2L1    3'  AAGTCATCCCCTCTCA      7276       AGTA  TTGT
                                TGAGA    GG    GTGACTT
                                |||||    ||    |||||||
                                ACTCT    CC    TACTGAA
                                   _____  CC__
GAM992   FLNB      3'  AAAGTCTCCTACTTC       62168         TTGTGT
                                GAAGTAGG     GACTTT
                                ||||||||     ||||||
                                CTTCATCC     CTGAAA
                                     T_____
GAM992   POPX1     3'  TACACAACCCCCTTCCCA    29801     A    TA
                                TG GAAG  GGTTGTGTG
                                || ||||  |||||||||
                                AC CTTC  CCAACACAT
                                 C    CC
GAM992   LOC145624 5'  ACACAACCCCTTCCCA      83404     A    TA
                                TG GAAG  GGTTGTGT
                                || ||||  ||||||||
                                AC CTTC  CCAACACA
                                 C    C_
GAM992   LOC257428 3'  AAAGTCATCCACGCCTCA    94275    T    _  TG
                                G AGGT TG  TGACTTT
                                | |||| ||  |||||||
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                                A TCCG AC  ACTGAAA
                                 C   C  CT
GAM993  ALDH3B1  3' CTGTACGCCTTCTCCA     91525        CA  C
                                TGGAGAAG  CG ACAG
                                ||||||||  || ||||
                                ACCTCTTC  GC TGTC
                                    C_  A
GAM993  ARHGDIB  3' ACCTGCTCCCTCTGATCCTCCA 6772       AAG  CGCACA
                                TGGAG   CA    GAGCAGGT
                                |||||   ||    ||||||||
                                ACCTC   GT    CTCGTCCA
                                  CTA  CTCC__
GAM993  BAIAP3   3' ACCTGCTCCACGACCCTTCCA  14121      AAGCA  CACA
                                TGGAG    CG   GAGCAGGT
                                |||||    ||   ||||||||
                                ACCTT    GC   CTCGTCCA
                                  CCCA_  AC__
GAM993  CARD15   5' ACCCGCAGATGCCATGCCTGCT 42210     AA_  C_  CAGA  A
           CC                    GGAG   GCA  GCA   GC GGT
                                ||||   |||  |||   || |||
                                CCTC   CGT  CGT   CG CCA
                                  GTC   AC   AGA_  C
GAM993  DACH     5' TTTTGTGCGTTCCTCTCCA   54977       AGC
                                TGGAGA   ACGCACAGAG
                                ||||||   ||||||||||
                                ACCTCT   TGCGTGTTTT
                                   CCT
GAM993  EGFL5    5' CCTGGCTGCGACTTCTCCA   86616        CA   CA AG
                                TGGAGAAG  CGCA  G  CAGG
                                ||||||||  ||||  |  ||||
                                ACCTCTTC  GCGT  C  GTCC
                                    A_    __ G_
GAM993  LZTR1    5' CCTGCTCCGGGGCTCCCCA   22233     A  A  A_  CACA
                                TGG GA GC  CG   GAGCAGG
                                ||| || ||  ||   |||||||
                                ACC CT CG  GC   CTCGTCC
                                  C  _  GG  ____
GAM993  NPR1     3' ACCTGCTCCCCCGACCCCCTCC 87368      AAGCA  CACA
           A                     TGGAG    CG   GAGCAGGT
                                |||||    ||   ||||||||
                                ACCTC    GC   CTCGTCCA
                                  CCCCA  CCC_
GAM993  OAS3     3' ACCTGCTCTGCCAAGTTGTCCA 20537     GA   ACGCA
                                TGGA  AGC    CAGAGCAGGT
                                ||||  |||    ||||||||||
                                ACCT  TTG    GTCTCGTCCA
                                  G_   AACC_
GAM993  PTMS     3' ACCTGCTCCATCTGAGCTCTCC 11032       A  A  CACA
           A                     TGGAGA GC CG   GAGCAGGT
                                ||||||  ||  ||   ||||||||
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                                ACCTCT CG GT   CTCGTCCA
                                   _ A  CTAC
GAM993  RARG    3'  ACCTGCTCTGCCCTCTCC   6375      AGCACGCA
                                GGAGA      CAGAGCAGGT
                                |||||      ||||||||||
                                CCTCT      GTCTCGTCCA
                                   CCC_____
GAM993  WAS     3'  ACCTGCTCTGTGCCCACCCTCC 4579      AAGCAC
           A                    TGGAG     GCACAGAGCAGGT
                                |||||     ||||||||||||
                                ACCTC     CGTGTCTCGTCCA
                                   CCACC_
GAM993  WWOX    3'  ACCCGCCCTGTGTGTGTCCCCT 33044    AA_       A  A
           C                    GAG   GCACGCACAG GC GGT
                                |||   |||||||||| || |||
                                CTC   TGTGTGTGTC CG CCA
                                  CCC        C  C
GAM993  ZNF277  5'  CCCGCCCTGCGGCCCTCC    41814     AA  A    CA A  A
                                GGAG  GC CGCA  G GC GG
                                ||||  || ||||  | || ||
                                CCTC  CG GCGT  C CG CC
                                  C_ _   __ C  C
GAM993  AP4S1   3'  ACCTGCTCTACGCGTGAAGGTA 22992    GAGAAG    AC
           CA                   TG     CACGC  AGAGCAGGT
                                ||     |||||  |||||||||
                                AC     GTGCG  TCTCGTCCA
                                 ATGGAA    CA
GAM993  C20orf18 3'  CCTGCCCTGTGTGTTTCCA   48341      AAGC      A
                                TGGAG    ACGCACAG GCAGG
                                |||||    |||||||| |||||
                                ACCTT    TGTGTGTC CGTCC
                                   _____       C
GAM993  CLSTN2  3'  CTGTGCGTCTCCTCCA     42132      A  C
                                TGGAG AG ACGCACAG
                                ||||| || ||||||||
                                ACCTC TC TGCGTGTC
                                   C  _
GAM993  DCNP1   3'  CTGTACGAACTTCTCCA     55621        CA  C
                                TGGAGAAG  CG ACAG
                                ||||||||  || ||||
                                ACCTCTTC  GC TGTC
                                     AA  A
GAM993  EPB41L1 3'  CTCTGTGCCACCTCTCCA    70591      AGCAC
                                TGGAGA    GCACAGAG
                                ||||||    ||||||||
                                ACCTCT    CGTGTCTC
                                   CCAC_
GAM993  FLJ13162 3'  CCTGCTCTGCGCCCTGC    46553     C_  A
                                GCA  GC CAGAGCAGG
                                |||  || |||||||||
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                                CGT  CG GTCTCGTCC
                                  CC  C
GAM993  FLJ20730  5' CCTACTGTAGCTTCTCCA    35618        ACGC    AGC
                                TGGAGAAGC   ACAG   AGG
                                |||||||||   ||||  |||
                                ACCTCTTCG   TGTC   TCC
                                     A___   A__
GAM993  FLJ21742  3' CCTGCTCCGACTTCTGCA    49845    G    CA  CACA
                                TG AGAAG  CG   GAGCAGG
                                || |||||  ||   |||||||
                                AC TCTTC  GC   CTCGTCC
                                 G    A_ ____
GAM993  KIAA0562  3' ACCTTGCTGGATGCTTCTCCA  28148         CGCA   AGC
                                TGGAGAAGCA   CAG   AGGT
                                ||||||||||   |||  ||||
                                ACCTCTTCGT   GTC   TCCA
                                     AG__   GT_
GAM993  KIAA0673  5' CCTGCACCCGCTTCTCCA    62268        ACGCACAGA
                                TGGAGAAGC       GCAGG
                                |||||||||       |||||
                                ACCTCTTCG       CGTCC
                                     CCCA_____
GAM993  KIAA1102  3' ACCTACTCTCCTCCATTCTCCA 69010       GCACGCAC   C
                                TGGAGAA      AGAG AGGT
                                |||||||      |||| ||||
                                ACCTCTT      TCTC TCCA
                                    ACCTCC__   A
GAM993  KIAA1656  3' CTGCTGCACCTGCTCCTCCA   65793     A   C__   CAGA
                                TGGAG AGCA   GCA   GCAG
                                ||||| ||||   |||   ||||
                                ACCTC TCGT   CGT   CGTC
                                   C   CCA  ____
GAM993  MDS018    3' CCTGCTCTGAGCCTGCCCA   41529    AGAA   C  A
                                TGG   GCA GC CAGAGCAGG
                                |||   ||| || |||||||||
                                ACC   CGT CG GTCTCGTCC
                                  ____  C  A
GAM993  MGC10986  5' ACCCAGCGGGTGCCGCTTCTCC 47561        AC   AGA  A_
          A                    TGGAGAAGC  GCAC   GC  GGT
                               |||||||||  ||||   ||  |||
                               ACCTCTTCG  CGTG   CG  CCA
                                    C_   GG_  AC
GAM993  MGC14832  3' CTCTCCATGAACACTTCTCCA  50339       CACG  CA   C
                                TGGAGAAG   CA  GAG AG
                                ||||||||   ||  ||| ||
                                ACCTCTTC   GT  CTC TC
                                    ACAA  AC  _
GAM993  MGC20470  5' ACCTGCTCCCCATCTGCCCACC 58958    AGAA   CGCACA
          CA                   TGG   GCA    GAGCAGGT
                               |||   |||    ||||||||
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                                ACC   CGT    CTCGTCCA
                                  CACC  CTACCC
GAM993  MGC32043  3'  GCTTCCGTGCAGGCTTCTCCA  58053        AC   A_
                                TGGAGAAGC  GCAC  GAGC
                                |||||||||  ||||  ||||
                                ACCTCTTCG  CGTG  TTCG
                                     GA   CC
GAM993  MGC5149   3'  ACCTGCTTGCTTGCACCCCTCT 72281      AA__  C  CAG
          A                      TGGAG   GCA GCA  AGCAGGT
                                |||||   ||| |||  |||||||
                                ATCTC   CGT CGT  TCGTCCA
                                   CCCA  T  ___
GAM993  PIP3-E    3'  TGTGGGTACTTCTCCA     66816        C  G
                                TGGAGAAG AC CACA
                                |||||||| || ||||
                                ACCTCTTC TG GTGT
                                     A  G
GAM993  SCYA4     3'  ACCTGAGCCCGGATGCTTCTCC 11447         CGCACAGAG
          A                      TGGAGAAGCA       CAGGT
                                ||||||||||       |||||
                                ACCTCTTCGT       GTCCA
                                     AGGCCCGA_
GAM993  TOMM34    3'  ACCTGCTCTGTGCCCGCTCC  22331     AAGCAC
                                GGAG    GCACAGAGCAGGT
                                ||||    ||||||||||||
                                CCTC    CGTGTCTCGTCCA
                                  GCC___
GAM993  YEA       5'  CTCTGTGCGCTTGCTTCCCCA  51529    A    __
                                TGG GAAGCA  CGCACAGAG
                                ||| ||||||  |||||||||
                                ACC CTTCGT  GCGTGTCTC
                                  C     TC
GAM993  LOC148014 3'  ACCTGCTCAGTCACTTCCC   78606    A   CAC  ACA
                                GG GAAG   GC   GAGCAGGT
                                || ||||   ||   ||||||||
                                CC CTTC   TG   CTCGTCCA
                                 _   AC_  A__
GAM993  LOC149498 5'  ACCTGCTCCCCACTCCTTCTCC 79406        CACGCACA
          A                      TGGAGAAG       GAGCAGGT
                                ||||||||       ||||||||
                                ACCTCTTC       CTCGTCCA
                                     CTCACCC_
GAM993  LOC159319 5'  CCTGCAGCTGCTTCTCCA    82190         C  ACAGA
                                TGGAGAAGCA GC    GCAGG
                                |||||||||| ||    |||||
                                ACCTCTTCGT CG    CGTCC
                                     _  A_____
GAM993  LOC160484 3'  ACCCCGTGGTGTACTACTTCTC 82215        CAC_   AGAGCA
          CA                     TGGAGAAG   GCAC     GGT
                                ||||||||   ||||     |||
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                                ACCTCTTC  TGTG    CCA
                                    ATCA  GTGCC_
GAM993  LOC96597  5'  CCTGCTCTGTTCCCTCC    66911     AAGCACGC
                                GGAG      ACAGAGCAGG
                                ||||      ||||||||||
                                CCTC      TGTCTCGTCC
                                  CCT_____
GAM993  LOC96652  3'  CCTGCACCAGCTTCTCCA   65466       ACGCACAGA
                                TGGAGAAGC      GCAGG
                                |||||||||      |||||
                                ACCTCTTCG      CGTCC
                                    ACCA_____
GAM994  ADAM2     5'  ACTGCCCTGTAACCACCA    7594      A        C
                                TGGT GTTGCAGGGCA GT
                                |||| |||||||||| ||
                                ACCA CAATGTCCCGT CA
                                  C        _
GAM994  CTNS      3'  GAAGGCCTTGCCCCAAACTACC 17043        ____      ACG
          A                      TGGTAGTT   GCAGGGC  TC
                                |||||||   |||||||  ||
                                ACCATCAA   CGTTCCG  AG
                                    ACCC     GA_
GAM994  MLLT2     3'  AATAACGTGCCAGCTATCA   19839       GCAG     C
                                TGGTAGTT   GGCACGT ATT
                                |||||||   ||||||| |||
                                ACTATCGA   CCGTGCA TAA
                                    ____       A
GAM994  ORM1      5'  GACTGCACCCTGCAGCCACCA  5208      A      __  C
                                TGGT GTTGCAGG  GCA GTC
                                |||| ||||||||  ||| |||
                                ACCA CGACGTCC  CGT CAG
                                  C       CA  _
GAM994  SH3BP2    3'  ACGATCTGCAACCACCA     11588     A      GCA
                                TGGT GTTGCAGG  CGT
                                |||| ||||||||  |||
                                ACCA CAACGTCT  GCA
                                  C       A__
GAM994  SLC1A1    3'  AATAACAGTGGCAAGCTACC  14791      _   AGGG  _  C
                                GGTAG TTGC   CAC GT ATT
                                ||||| ||||   ||| || |||
                                CCATC AACG   GTG CA TAA
                                  G   ____  A  A
GAM994  FLJ10718  5'  GAGTGCCCTACAACTACC    36491       C      G
                                GGTAGTTG AGGGCAC TC
                                |||||||| ||||||| ||
                                CCATCAAC TCCCGTG AG
                                    A      _
GAM994  LOC200169 3'  ATGAGCTGCAACTCCA      89942     T      GGCACG
                                TGG AGTTGCAG     TCAT
                                ||| ||||||||     ||||
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                                ACC TCAACGTC      AGTA
                                  _       G_____
GAM994   LOC221495 3'  GAACACACCCTGCAACTAC    93856           CACG_
                                GTAGTTGCAGGG     TC
                                ||||||||||||     ||
                                CATCAACGTCCC     AG
                                       ACACA
GAM995   ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A     T__
GAM995   AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM995   FDFT1    3'  TAGGAAAGTGAAATG       15518            A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM995   JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM995   KLF4     3'  TCCCAGACAGTGGATATG     14891     CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||  ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM995   PHYH     3'  ACAGTAAAAGTGAAAT      20608           C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                       A
GAM995   PKD2     3'  TCCAGGTTGAAAGTGAAA    60096           CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                       T__    _
GAM995   WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM995   ZNF216   3'  ATCTGCACAGCAAAGTGAAA   20017         CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
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                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM995  CG012    5' CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                     CT  __
GAM995  EIF2C2   3' ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM995  FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC       GTCTGAGAT
                                ||||||       |||||||||
                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM995  FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM995  KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM995  KLHL6    3' ATCTCAGAGCAGGAAA      55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM995  NIR3     3' GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM995  PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM995  PP35     3' ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM995  PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148         TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
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                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM995  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                      A    TC
GAM995  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941        CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                      AAAGG
GAM995  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM995  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                     TTTCC_  A
GAM995  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226     A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM995  LOC222134 5'  ACAGTGAAGTGAAATG      94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                      _
GAM996  FLJ10922  3'  ACCACCAGCAGCCTGTGCAA   36863        A  A  AAA
                                TTGCATAG CT CT   GTGGT
                                |||||||| || ||   |||||
                                AACGTGTC GA GA   CACCA
                                     C  C  C__
GAM996  FLJ13576  3'  ACCACTATCTATGCAG      42514         CTACTAA
                                TTGCATAGA      AGTGGT
                                |||||||||      ||||||
                                GACGTATCT      TCACCA
                                      A_______
GAM996  NYD-SP18  3'  CACTGGGGAGAATCTATGCAA  50876         __  A  AA
                                TTGCATAGA  CT CT  AGTG
                                |||||||||  || ||  ||||
                                AACGTATCT  GA GG  TCAC
                                      AA  _  GG
GAM996  SDFR1    3'  CATGGTAATATTCTATGCAA   24865        C  C  AA
                                TTGCATAGA TA TA  GTG
                                ||||||||| || ||  |||
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                                AACGTATCT AT AT  TAC
                                     T  A  GG
GAM996  SDFR1    3'  CATGGTAATATTCTATGCAA  33915        C  C  AA
                                TTGCATAGA TA TA  GTG
                                |||||||||  ||  ||  |||
                                AACGTATCT AT AT  TAC
                                     T  A  GG
GAM996  STIM2    3'  TACCACTTTAAAAATATGCAA  40479       GACTAC
                                TTGCATA     TAAAGTGGTA
                                |||||||     ||||||||||
                                AACGTAT     ATTTCACCAT
                                   AAAA__
GAM996  LOC144438 3'  ATTTAAGCAGTCTATGCAA   76831          A  A
                                TTGCATAGACT CT AAGT
                                ||||||||||| ||  ||||
                                AACGTATCTGA GA TTTA
                                      C  A
GAM996  LOC222160 5'  TTAGTGGTCTATGCAA     94135
                                TTGCATAGACTACTAA
                                ||||||||||||||||
                                AACGTATCTGGTGATT

GAM997  ENPP2    3'  CAATGCACAGTTGCCACATTTA 20600         A_  AA
          GT                    ACTAAATGTG  GAC  TGCATTG
                                ||||||||||  |||  |||||||
                                TGATTTACAC  TTG  ACGTAAC
                                     CG   AC
GAM997  TGFBI    3'  AATGTGTCTCACAT       4488          AAT
                                ATGTGAGAC   GCATT
                                |||||||||   |||||
                                TACACTCTG   TGTAA
                                     ___
GAM997  ZNF148   3'  CAATGCATTACTTGTTTTAG   41737      T TG  AC
                                CTAAA G  AG  AATGCATTG
                                ||||| |  ||  |||||||||
                                GATTT T  TC  TTACGTAAC
                                   _ GT  A_
GAM997  CPR2     3'  GTTGTCTCACACTTAG     48104     A
                                CTAA TGTGAGACAAT
                                ||||  ||||||||||
                                GATT ACACTCTGTTG
                                  C
GAM997  FLJ10035  3'  CAATGGGACCCTCACATTTG   35746         ACAATG
                                TAAATGTGAG     CATTG
                                ||||||||||     |||||
                                GTTTACACTC     GTAAC
                                     CCAGG_
GAM997  NAG73    3'  AATGCATGCACATGCAGTA   50805     AA    AGACA
                                TACT  ATGTG    ATGCATT
                                ||||  |||||    |||||||
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                                ATGA  TACAC    TACGTAA
                                  CG    G____
GAM997  PSMD12    3'  CAATGCATTGGTCACA      10996       GA
                                TGTGA  CAATGCATTG
                                |||||  ||||||||||
                                ACACT  GTTACGTAAC
                                   G_
GAM997  LOC143162 3'  GCATCTCACATTTA        76496          CAA
                                TAAATGTGAGA   TGC
                                ||||||||||   |||
                                ATTTACACTCT   ACG
                                          ___
GAM997  LOC146050 3'  CAATGCATTAGTTTGCTTTA   77631      T TG  AC
                                TAAA G  AG  AATGCATTG
                                ||||  |  ||  |||||||||
                                ATTT C  TT  TTACGTAAC
                                  _ GT  GA
GAM997  LOC196738 3'  GCATCTCACATTTA        87504          CAA
                                TAAATGTGAGA   TGC
                                ||||||||||   |||
                                ATTTACACTCT   ACG
                                          ___
GAM997  LOC90918  5'  CAATGCAGAAAACACATTTG   64351         AGACAA
                                TAAATGTG     TGCATTG
                                ||||||||     |||||||
                                GTTTACAC     ACGTAAC
                                     AAAAG_
GAM998  TNFAIP1   3'  CATCAGCTGAGGACAGCAAACT 40917     AG     G
           CC                     GGA  TTGCTG CTTCAGCTGATG
                                |||  |||||| ||||||||||||
                                CCT  AACGAC GGAGTCGACTAC
                                  CA     A
GAM998  C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 21681     AA       _ ___
           CCC                     GG  GTTGCTGG CT   TCAGCTG
                                ||  ||||||||  ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM998  C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 94622     AA       _ ___
           CCC                     GG  GTTGCTGG CT   TCAGCTG
                                ||  ||||||||  ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM998  C20orf59  3'  CATCCCTAGCCAGCAGCTCC   41992     A        TC  CT
                                GGA GTTGCTGGCT  AG  GATG
                                ||| ||||||||||  ||  ||||
                                CCT CGACGACCGA  TC  CTAC
                                  _        __ C_
GAM998  FLJ20079  3'  CATTCTGGTAAACCAGCAGCCT 34490     A       CT__    CT
           CC                     GGA GTTGCTGG    TCAG  GATG
                                ||| ||||||||    ||||  ||||
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                                CCT CGACGACC    GGTC  TTAC
                                  C       AAAT   __
GAM998  SSAT2    3'  CATCAGCTGAAGCACTCTTC  56041      TTGCTG
                                GAAG     GCTTCAGCTGATG
                                ||||     |||||||||||||
                                CTTC     CGAAGTCGACTAC
                                  TCA___
GAM998  SYNJ2    3'  ATCAGCTTAAGCAATTCC    61763      GTTGCTG   C
                                GGAA      GCTT AGCTGAT
                                ||||      |||| |||||||
                                CCTT      CGAA TCGACTA
                                  AA_____   T
GAM998  LOC162333 5'  CTGAAGCCAGCAATTCC     87131      G
                                GGAA TTGCTGGCTTCAG
                                |||| ||||||||||||
                                CCTT AACGACCGAAGTC
                                  _
GAM998  LOC222060 5'  CACCTCCCACCAGCAACCCCC  94104    AA       CTTC  C
                                GG  GTTGCTGG    AG TG
                                ||  ||||||||    || ||
                                CC  CAACGACC    TC AC
                                 CC       ACCC  C
GAM998  LOC255650 3'  CATCAGCCCCAGGCAACTTCC  96711         _  CTTCA
                                GGAAGTTGC TGG     GCTGATG
                                ||||||||| |||     |||||||
                                CCTTCAACG ACC     CGACTAC
                                     G   C____
GAM999  B3GALT3   3'  GTGGTCCCATAAAATTATAATG 13681         C     T
                                CATTATAAT TTATGG ACCGC
                                ||||||||| |||||| |||||
                                GTAATATTA AATACC TGGTG
                                     A     C
GAM999  SLC16A1   3'  GTGTCATAAAGATTATAAT    11744          _  GT
                                ATTATAATCTT ATG  AC
                                |||||||||| |||  ||
                                TAATATTAGAA TAC  TG
                                      A   TG
GAM999  DKFZp762K2015 3'  ATGCAGCTGTATAGATTATA   72473        _     ACC
                                TATAATCT TATGGT   GCAT
                                |||||||| ||||||   ||||
                                ATATTAGA ATGTCG   CGTA
                                     T     A__
GAM999  GPCR150   3'  GCTGTCATAAGATCATAAT    26878       A       GT CC
                                ATTAT ATCTTATG  A  GC
                                ||||| ||||||||  |  ||
                                TAATA TAGAATAC  T  CG
                                  C       TG __
GAM999  GPR74     3'  TGGTCATAAGATCATAA     53838       A       GT
                                TTAT ATCTTATG  ACCG
                                |||| ||||||||  ||||
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                                AATA TAGAATAC  TGGT
                                  C       __
GAM999   NPGPR    3'  TGGTCATAAGATCATAA     16880      A       GT
                                TTAT ATCTTATG  ACCG
                                |||| ||||||||  ||||
                                AATA TAGAATAC  TGGT
                                  C       __
GAM999   TNRC6    3'  ATGCAGGCCAATATTATAATG  70505         CTTA    ACC
                                CATTATAAT    TGGT   GCAT
                                |||||||||    ||||   ||||
                                GTAATATTA    ACCG   CGTA
                                     TA__    GA_
GAM999   LOC90918 5'  TGCTATAAGATTATAA      64364
                                TTATAATCTTATGGTA
                                ||||||||||||||||
                                AATATTAGAATATCGT

GAM1000  ACCN2    3'  GCTGCCTCCTCACATCTGCC   39169        C   CA   A
                                GGCAGATG TGG  GAG CAGC
                                |||||||| |||  ||| ||||
                                CCGTCTAC ACT  CTC GTCG
                                     _  C_  C
GAM1000  ADRBK2   3'  GTCCCAGCAGCATCTGCC    17685          G AGA
                                GGCAGATGCTG C   GAC
                                |||||||||| |   |||
                                CCGTCTACGAC G   CTG
                                      _ ACC
GAM1000  APBA2    3'  GCTGCCTCTGCCACTGACTGC  18561      A GC       A
                                GCAG T  TGGCAGAG CAGC
                                |||| |  |||||||| ||||
                                CGTC G  ACCGTCTC GTCG
                                  A TC       C
GAM1000  ARHGEF7  3'  GGCACTGCCGCATCCACC    14009    CA     T     AGACA
                                GG  GATGC GGCAG    GCC
                                ||  ||||| |||||     |||
                                CC  CTACG CCGTC    CGG
                                 AC     _     A____
GAM1000  ARVCF    3'  GGGGCTGCCGCATCTGCC    8029          T     AGACAG
                                GGCAGATGC GGCAG     CC
                                ||||||||| |||||     ||
                                CCGTCTACG CCGTC     GG
                                     _    GG____
GAM1000  BAG1     3'  GGCGCCACCAGCTCTGCC    94516       T     CAGAGACA
                                GGCAGA GCTGG       GCC
                                |||||| |||||       |||
                                CCGTCT CGACC       CGG
                                   _    ACCG____
GAM1000  BCL7B    3'  TGTCCTGCCAGCTCTGCC    8137        T       A
                                GGCAGA GCTGGCAG GACA
                                |||||| |||||||| ||||
```

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                                CCGTCT CGACCGTC CTGT
                                  _      _
GAM1000 BSN      3'  GCTGCCTGGGTGAAGCATCTGC 12924          G_  AG  A
              T                   GGCAGATGCT  GC  AG CAGC
                                  ||||||||||  ||  || ||||
                                  TCGTCTACGA  TG  TC GTCG
                                        AG  GG  C
GAM1000 BTG2     3'  TCCTGCCAGCTCTGCC      22218       T      A
                                  GGCAGA GCTGGCAG GA
                                  |||||| |||||||| ||
                                  CCGTCT CGACCGTC CT
                                    _      _
GAM1000 CAPN10   3'  TGGCTGTCCCCAGCACCTTCC  43597    C  A     CAGA
                                  GG AG TGCTGG    GACAGCCA
                                  || || ||||||    ||||||||
                                  CC TC ACGACC    CTGTCGGT
                                   T  C     C___
GAM1000 CAPN10   3'  TGGCTGTCCCCAGCACCTTCC  43605    C  A     CAGA
                                  GG AG TGCTGG    GACAGCCA
                                  || || ||||||    ||||||||
                                  CC TC ACGACC    CTGTCGGT
                                   T  C     C___
GAM1000 CLCN6    3'  GCTTCCTGCCAGCACGTGCC   41387      GA       A  C
                                  GGCA  TGCTGGCAG GA AGC
                                  ||||  ||||||||| || |||
                                  CCGT  ACGACCGTC CT TCG
                                    GC       _ _
GAM1000 CLCN6    3'  GCTTCCTGCCAGCACGTGCC   41402      GA       A  C
                                  GGCA  TGCTGGCAG GA AGC
                                  ||||  ||||||||| || |||
                                  CCGT  ACGACCGTC CT TCG
                                    GC       _ _
GAM1000 CLCN6    3'  GCTTCCTGCCAGCACGTGCC   7080       GA       A  C
                                  GGCA  TGCTGGCAG GA AGC
                                  ||||  ||||||||| || |||
                                  CCGT  ACGACCGTC CT TCG
                                    GC       _ _
GAM1000 CTF1     3'  GCTGTCTCCATTGCCTCGGCC  7182      A  TGCT   ___
                                  GGC GA   GGCA   GAGACAGC
                                  ||| ||   ||||   ||||||||
                                  CCG CT   CCGT   CTCTGTCG
                                    G ____   TAC
GAM1000 EGLN2    5'  GCCACCTCTACCACTGCC    54928      ATGC   C   ACA
                                  GGCAG   TGG AGAG   GC
                                  |||||   ||| ||||  ||
                                  CCGTC   ACC TCTC   CG
                                    ____  A   CAC
GAM1000 EMP1     5'  GGCTGCTGCCAGCACCTGCC   7446       A       AGA
                                  GGCAG TGCTGGCAG   CAGCC
                                  ||||| |||||||||   |||||
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                                CCGTC ACGACCGTC   GTCGG
                                  C       ___
GAM1000  FLRT2    3'  CTGTCCCTGGGGATTCTGCT  25060      TG  GG   A
                                GGCAGA  CT  CAG GACAG
                                ||||||  ||  ||| |||||
                                TCGTCT  GG  GTC CTGTC
                                   TA  G_   C
GAM1000  GDI1     3'  TGGCCGCCCCCAGCCCCTGCT  59982      AT    CAGAGACA
                                GGCAG  GCTGG      GCCA
                                |||||  |||||      ||||
                                TCGTC  CGACC      CGGT
                                  CC    CCCGC___
GAM1000  GJA5     3'  TGGAATTCCTGCCAACATCTGT 17944        C     A  CAG
              C                  GGCAGATG TGGCAG GA   CCA
                                ||||||||  ||||||  ||   |||
                                CTGTCTAC ACCGTC CT   GGT
                                    A     _  TAA
GAM1000  GNS      3'  TGGCTGTCTCTGGTCTCTTCC  9085     C   T  TGG
                                GG AGA GC   CAGAGACAGCCA
                                || ||| ||   ||||||||||||
                                CC TCT TG   GTCTCTGTCGGT
                                 T   C  ___
GAM1000  GPX3     3'  TTGGGGCCAGCATCTCC     9128     C        AGAGA
                                GG AGATGCTGGC     CAG
                                || ||||||||||     |||
                                CC TCTACGACCG     GTT
                                 _         GG___
GAM1000  HIVEP3   3'  CTGCTTCAGCATCTGGC     44437    G        __
                                G CAGATGCTG  GCAG
                                | |||||||||  ||||
                                C GTCTACGAC  CGTC
                                 G        TT
GAM1000  HR       5'  CTGCCCCTGCCAGCTCTGGC   17641    G    T       AGA
                                G CAGA GCTGGCAG   CAG
                                | |||| ||||||||   |||
                                C GTCT CGACCGTC   GTC
                                 G   _       CCC
GAM1000  IL1R1    3'  TGGCTGTCTCTGTCCCTCACTG 6064       A  CT  _
              CC                  GGCAG TG  GG CAGAGACAGCCA
                                ||||| ||  || ||||||||||||
                                CCGTC AC  CC GTCTCTGTCGGT
                                   _  TC  T
GAM1000  KLK8     3'  TGGCGTCTATACCAACATCTGC 57964        C   CAG    A
              C                  GGCAGATG TGG   AGAC GCCA
                                ||||||||  |||   |||| ||||
                                CCGTCTAC ACC   TCTG CGGT
                                    A   ATA   _
GAM1000  MAG      3'  GCTGCCCCTCCCTGCCAGCACC 54593    CAGA       A  _____
              CC                  GG    TGCTGGCAG GA    CAGC
                                ||   |||||||||  ||    ||||
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                                CC   ACGACCGTC CT   GTCG
                                 CC__       C  CCCC
GAM1000  MAG     3'  GCTGCCCCTCCCTGCCAGCACC 9881    CAGA       A ____
                CC                GG   TGCTGGCAG GA   CAGC
                                ||   ||||||||| ||   ||||
                                CC   ACGACCGTC CT   GTCG
                                 CC__       C  CCCC
GAM1000  MAP3K1  3'  TGGCTATAAAATCAGTATCTGC 67817          CAGAGAC
                C                 GGCAGATGCTGG     AGCCA
                                |||||||||||      |||||
                                CCGTCTATGACT     TCGGT
                                      AAAATA_
GAM1000  MAPK4   3'  GGCCGCCTCCGCCCTCTCTGCT 10830      TGCT   A   ACA
                                GGCAGA   GGC GAG   GCC
                                ||||||   ||| |||   |||
                                TCGTCT   CCG CTC   CGG
                                   CTC_   C   CGC
GAM1000  MGAT3   5'  GGCGGACGCCAGCATCTCC   10019    C       AGAGACA
                                GG AGATGCTGGC     GCC
                                || ||||||||||      |||
                                CC TCTACGACCG     CGG
                                 _        CAGG___
GAM1000  NPTX1   3'  GCTCCCTGCCAGCACCTCC   10264    C  A       A  CA
                                GG AG TGCTGGCAG GA  GC
                                || || ||||||||| ||  ||
                                CC TC ACGACCGTC CT  CG
                                 _ C       C  __
GAM1000  PHEMX   3'  CTGACCAGCATCGGCC     57368     A      _
                                GGC GATGCTGG CAG
                                ||| |||||||| |||
                                CCG CTACGACC GTC
                                  G       A
GAM1000  PVR     3'  GCCACTTTCTGCCAGCATCTGC 21479            CA_
                                GCAGATGCTGGCAGAGA   GC
                                ||||||||||||||||   ||
                                CGTCTACGACCGTCTTT   CG
                                          CAC
GAM1000  PVR     3'  GCCACTTTCTGCCAGCATCTGC 21480            CA_
                                GCAGATGCTGGCAGAGA   GC
                                ||||||||||||||||   ||
                                CGTCTACGACCGTCTTT   CG
                                          CAC
GAM1000  REV3L   5'  GGCTGCCCCCGCCTCCTCTGCT 11296      TGCT   AGAGA
                                GGCAGA   GGC    CAGCC
                                ||||||   |||    |||||
                                TCGTCT   CCG    GTCGG
                                   CCT_   CCCCC
GAM1000  RGL     3'  CTCTGCCTGCATCTGCC     30733         T
                                GGCAGATGC GGCAGAG
                                ||||||||| |||||||
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                                CCGTCTACG CCGTCTC
                                     T
GAM1000 RNPEPL1  3' GCCCCGGATGCCAGCACCTGCC 36677      A      GAGACA
                                GGCAG TGCTGGCA     GC
                                ||||| ||||||||     ||
                                CCGTC ACGACCGT     CG
                                   C       AGGCCC
GAM1000 RPL4     5' TGGCTGTCTCCTCTCTCCGCC  6385     A  TGCT  CA
                                GGC GA    GG  GAGACAGCCA
                                ||| ||    ||  ||||||||||
                                CCG CT    TC  CTCTGTCGGT
                                  C  C___  TC
GAM1000 SCGB1A1  3' CTGCTCCAGCCTCTGCC     12539       T    CAG  A
                                GGCAGA GCTGG   AG CAG
                                |||||| |||||   || |||
                                CCGTCT CGACC   TC GTC
                                   C    ___  _
GAM1000 SLC17A4  3' GGCCATCTTGACTTCTGCC   18526       TGCT  CA   CA
                                GGCAGA   GG  GAGA  GCC
                                ||||||   ||  ||||  |||
                                CCGTCT   TC  TTCT  CGG
                                   ____  AG   AC
GAM1000 SLC19A2  3' TGTTCTAACAGCATCTGCC   68981          GC   A
                                GGCAGATGCTG  AGAG CA
                                ||||||||||  |||| ||
                                CCGTCTACGAC  TCTT GT
                                      AA   _
GAM1000 SOD3     3' GCTGTTTCGCATCCACC     11864    CA    TGGCA
                                GG  GATGC    GAGACAGC
                                ||  |||||    ||||||||
                                CC  CTACG    CTTTGTCG
                                 AC    ______
GAM1000 TIMP3    3' TCTCCCAGCATCCGCC      4519      A      CA
                                GGC GATGCTGG  GAGA
                                ||| ||||||||  ||||
                                CCG CTACGACC  CTCT
                                  C       __
GAM1000 VIL2     3' GGCGCTGCCAGCCCCGCC    12599     AGAT      AGACA
                                GGC   GCTGGCAG    GCC
                                |||   ||||||||    |||
                                CCG   CGACCGTC    CGG
                                  CCC_       G____
GAM1000 WARS     5' TGGCCACCTCTGCAGTGTCTTC 67289    C      G    ACA
            C                    GG AGATGCTG CAGAG   GCCA
                                || |||||||| |||||   ||||
                                CC TCTGTGAC GTCTC   CGGT
                                 T       _    CAC
GAM1000 ZNF16    3' TGGCCATTGTCTCAGCCTCTGC 22725       TGCT   A    ___
            C                    GGCAGA   GGC GAGACA   GCCA
                                ||||||   ||| ||||||   ||||
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                                CCGTCT   CCG CTCTGT  CGGT
                                   ____  A     TAC
GAM1000 AIF1    5' CTCTACCAGCATCTGCT    7886          C
                                GGCAGATGCTGG AGAG
                                |||||||||||| ||||
                                TCGTCTACGACC TCTC
                                      A
GAM1000 AMOT    3' TCTGCCATCATCTGCC     55727        C
                                GGCAGATG TGGCAGA
                                |||||||| |||||||
                                CCGTCTAC ACCGTCT
                                     T
GAM1000 ARFRP1  3' GGCTGTCTCCGCCCCATC   12243     CT  A
                                GATG  GGC GAGACAGCC
                                ||||  ||| |||||||||
                                CTAC  CCG CTCTGTCGG
                                  C_  C
GAM1000 ARTN    5' CTCCCAGCATCTACC      54040   C       CA
                                GG AGATGCTGG  GAG
                                || |||||||||  |||
                                CC TCTACGACC  CTC
                                 A       __
GAM1000 ASB13   3' GTTGTGCCCAGCATTGCC   45221     A    _ GA
                                GGCAG TGCTGG CA  GAC
                                ||||| |||||| ||  |||
                                CCGTT ACGACC GT  TTG
                                   _     C  G_
GAM1000 BICD2   3' GCTGTCCGCCTCAGCTCCC  70397   C  A  CT   AGA
                                GG AG TG  GGC   GACAGC
                                || || ||  |||   ||||||
                                CC TC AC  CCG   CTGTCG
                                 C  G  T_  C__
GAM1000 C11orf11 3' TGGCTGTCCTGGGAGCCCCTGC 93262      AT   GG   A
            C                    GGCAG  GCT  CAG GACAGCCA
                                |||||  |||  ||| ||||||||
                                CCGTC  CGA  GTC CTGTCGGT
                                   CC   GG  _
GAM1000 CAPN13  3' GGCCACCTCCCACCAACCTGGC 58015   G   A_  C   CA   ACA
                                G CAG  TG TGG  GAG   GCC
                                | |||  || |||  |||   |||
                                C GTC  AC ACC  CTC   CGG
                                 G   CA  C   __   CAC
GAM1000 CDC14B  5' CTCCCGCCGGGCTCTGCC   52849      T   _   A_
                                GGCAGA GCT GGC  GAG
                                |||||| ||| |||  |||
                                CCGTCT CGG CCG  CTC
                                   _  G   CC
GAM1000 CDC14B  5' CTCCCGCCGGGCTCTGCC   52832      T   _   A_
                                GGCAGA GCT GGC  GAG
                                |||||| ||| |||  |||
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                                CCGTCT CGG CCG  CTC
                                   _  G  CC
GAM1000 CDC14B   5' CTCCCGCCGGGCTCTGCC    13385       T  _  A_
                                GGCAGA GCT GGC  GAG
                                |||||| ||| |||  |||
                                CCGTCT CGG CCG  CTC
                                   _  G  CC
GAM1000 CLPTM1   3' GCCATCTCGCCCTGCC     7101       ATGCT  A   CA
                                GGCAG    GGC GAGA  GC
                                |||||    ||| ||||  ||
                                CCGTC    CCG CTCT  CG
                                  _____  _   AC
GAM1000 COX4I2   3' GCTGTCTCCCTGAGGCTCCGCC 50891     A  T  GG  __
                                GGC GA GCT  CA  GAGACAGC
                                ||| || |||  ||  ||||||||
                                CCG CT CGG  GT  CTCTGTCG
                                  C  _  A_  CC
GAM1000 DDX31    3' CTGTCCCTTGGCATCCTCC   56829    CA    TG CA A
                                GG  GATGC  G  G GACAG
                                ||  |||||  |  | |||||
                                CC  CTACG  T  C CTGTC
                                 TC    GT __ C
GAM1000 DKFZp434J0226 5' TCTGCCAGCCCTGCC      72336      AT
                                GGCAG  GCTGGCAGA
                                |||||  |||||||||
                                CCGTC  CGACCGTCT
                                   C_
GAM1000 DKFZP586M0122 3' CTACCCCGGCACCATCTGCC  31249      ___     CAG
                                GGCAGA  TGCTGG  AG
                                ||||||  ||||||  ||
                                CCGTCT  ACGGCC  TC
                                   ACC    CCA
GAM1000 EIF2C2   3' TGTTCTGCCAGCACCGCC    71948    AGA        A
                                GGC  TGCTGGCAGAG CA
                                |||  |||||||||| ||
                                CCG  ACGACCGTCTT GT
                                  CC_        _
GAM1000 ET(B)R-LP-2 5' TGGCTGTCTCCTGCTCATCCAG 16483    A_   CT    _
            CC                    GGC  GATG  GGCAG AGACAGCCA
                                ||| ||||  ||||| |||||||||
                                CCG  CTAC  TCGTC TCTGTCGGT
                                  AC   __    C
GAM1000 EVI5     3' TGACTGCTTTCAGCATCT    19018        CA  A  C
                                AGATGCTGG  GAG CAG CA
                                |||||||||  ||| ||| ||
                                TCTACGACT  TTC GTC GT
                                     __  _  A
GAM1000 FASTK    3' GGCTACCAGCTCCTGCC    46993      AT    CAGAGAC
                                GGCAG  GCTGG     AGCC
                                |||||  |||||     ||||
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                              CCGTC  CGACC      TCGG
                                CT    A_______
GAM1000  FLJ10379  3'  TCTACTTGCCAACATCTGCC   36082        C    _ _
                              GGCAGATG TGGCA G AGA
                              |||||||| ||||| | |||
                              CCGTCTAC ACCGT C TCT
                                   A    T A
GAM1000  FLJ11017  3'  TGATTCTGCCAGCATGC     36989     GA        A
                              GCA  TGCTGGCAGAG CA
                              |||  |||||||||||  ||
                              CGT  ACGACCGTCTT GT
                                __         A
GAM1000  FLJ11149  5'  GGCTGTCTCCGCTGCCCTCC   37110    C  AT  T   A
                              GG AG  GC GGC GAGACAGCC
                              || ||  || ||| |||||||||
                              CC TC  CG TCG CTCTGTCGG
                               _ C_ _   C
GAM1000  FLJ14225  3'  GCTGTCCCAGCATCTGCT    45904          CAGA
                              GGCAGATGCTGG    GACAGC
                              ||||||||||||    ||||||
                              TCGTCTACGACC    CTGTCG
                                              _____
GAM1000  FLJ20005  5'  GGCCGCTCCACCAGCATC    34318        CA   ACA
                              GATGCTGG  GAG   GCC
                              ||||||||  |||   |||
                              CTACGACC  CTC   CGG
                                   AC   GC_
GAM1000  FLJ20034  3'  GGCCAGGGGCCCAGCATCCAGC 34377     A_       _ AGAGACA
            C                  GGC  GATGCTGG C      GCC
                              |||  |||||||| |      |||
                              CCG  CTACGACC G      CGG
                                AC       C GGGAC__
GAM1000  FLJ20154  3'  GTCCTGCCAGCACCC       72932     CAGA       A
                              GG    TGCTGGCAG GAC
                              ||    ||||||||| |||
                              CC    ACGACCGTC CTG
                               C___        _
GAM1000  FLJ20343  3'  GTTTGCTACCAGCATCCAGC   35000    A_      C  _
                              GC  GATGCTGG AG AGAC
                              ||  |||||||| || ||||
                              CG  CTACGACC TC TTTG
                               AC       A  G
GAM1000  FLJ21324  5'  TGGCTGTCCCTGCAGGCGCCTC 91213    C  A    G    A
            C                  GG AG TGCT GCAG GACAGCCA
                              || || |||| |||| ||||||||
                              CC TC GCGG CGTC CTGTCGGT
                               _ C   A   C
GAM1000  FLJ23120  3'  TCCTGCCTGCACCTGCC     85150      A  T    A
                              GGCAG TGC GGCAG GA
                              ||||| ||| ||||| ||
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                                CCGTC ACG CCGTC CT
                                  C  T   _
GAM1000 FLJ30213 5' GTCTCTGCGGGGGCTGC    58770     ATG  G
                                GCAG  CT GCAGAGAC
                                ||||  || ||||||||
                                CGTC  GG CGTCTCTG
                                  GG_  G
GAM1000 GAL3ST-4 5' GCTGTCTCTGCCCCTCTTCC  44939   C  TGCT
                                GG AGA   GGCAGAGACAGC
                                || |||   ||||||||||||
                                CC TCT   CCGTCTCTGTCG
                                 T  CC__
GAM1000 GAL3ST-4 5' GGCTGTCTCCAGCTGTCTCTGC 44940      T  T   A_
            C                    GGCAGA GC GGC  GAGACAGCC
                                ||||||| || |||  |||||||||
                                CCGTCT TG TCG  CTCTGTCGG
                                   C  _  AC
GAM1000 GFR     3' CTGTCTCCAGAGGTTTGCC   24471      G_   CAG
                                GGCAGAT  CTGG   AGACAG
                                |||||||  ||||   ||||||
                                CCGTTTG  GACC   TCTGTC
                                   GA   ___
GAM1000 HN1L    3' GGCTGCTAAATCCAGCATCCC  57999    CA      CAG_ A
                                GG  GATGCTGG    AG CAGCC
                                ||  ||||||||    || |||||
                                CC  CTACGACC    TC GTCGG
                                 __       TAAA  _
GAM1000 HT014   3' GGCTGCCACAGCCTCTGCC   39797      T   GCAGAGA
                                GGCAGA GCTG      CAGCC
                                |||||| ||||      |||||
                                CCGTCT CGAC      GTCGG
                                   C   ACC_____
GAM1000 KCNS1   3' TGGCTATCTCTGTCCCATC   9585      CT      C
                                GATG  GGCAGAGA AGCCA
                                ||||  |||||||| |||||
                                CTAC  CTGTCTCT TCGGT
                                  C_       A
GAM1000 KIAA0450 5' TGGCCATCTGAACGCATCTGCC 27652        TGG   GACA
                                GGCAGATGC   CAGA   GCCA
                                |||||||||   ||||   ||||
                                CCGTCTACG   GTCT   CGGT
                                     CAA   AC__
GAM1000 MGC15631 5' GCCGTCTCCCCACCATCTGTC  51267       C  CA   A
                                GGCAGATG TGG  GAGAC GC
                                |||||||| |||  ||||| ||
                                CTGTCTAC ACC  CTCTG CG
                                     C  C_   C
GAM1000 MGC15906 5' GCAATCTCCAGCATCCACC   51818   CA      C  GACA
                                GG  GATGCTGG AGA   GC
                                ||  |||||||| |||   ||
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                                CC  CTACGACC TCT    CG
                                 AC       _   AA__
GAM1000  MGC3731   3'  TGGCTGTCCCTGTAGCCCAGCC 44229     AGAT   G   A
                                GGC    GCTG CAG GACAGCCA
                                |||    |||| ||| ||||||||
                                CCG    CGAT GTC CTGTCGGT
                                  ACC_    _   C
GAM1000  MRF2      5'  GCTACCCCCAGTACTGCC     76522      A     CAGAGAC
                                GGCAG TGCTGG      AGC
                                ||||| ||||||      |||
                                CCGTC ATGACC      TCG
                                   _     CCCA___
GAM1000  PAK6      3'  GCTGCCTCCACAGACTGCT    39408      ATG   GCA   A
                                GGCAG   CTG   GAG CAGC
                                |||||   |||   ||| ||||
                                TCGTC   GAC   CTC GTCG
                                   A__   AC_   C
GAM1000  PDEF      3'  TGCTCCCCAACACCTGCC     24753      A  C   CA   A
                                GGCAG TG TGG  GAG CA
                                ||||| || |||  ||| ||
                                CCGTC AC ACC  CTC GT
                                   C  A   C_   _
GAM1000  PIB5PA    3'  GCTGTATCTGCACCTGCC     66054      ATGCTG    G
                                GGCAG     GCAGA ACAGC
                                |||||     ||||| |||||
                                CCGTC     CGTCT TGTCG
                                   CA_____     A
GAM1000  PLAC3     5'  GCTGCCTCTTTCTCGTCTGCC  69344       CT  C    A
                                GGCAGATG  GG AGAG CAGC
                                ||||||||  || |||| ||||
                                CCGTCTGC  CT TCTC GTCG
                                     T_  T    C
GAM1000  PRO1866   5'  TGGCCACCTCTGATCTCATCTG 37553       CTGG    ACA
            CT                   GGCAGATG   CAGAG   GCCA
                                ||||||||   |||||   ||||
                                TCGTCTAC   GTCTC   CGGT
                                     TCTA    CAC
GAM1000  RPIA      5'  GGGGACTCCAACAGCATCTGCC 57968         GCA   ACAG
                                GGCAGATGCTG   GAG    CC
                                ||||||||||   |||    ||
                                CCGTCTACGAC   CTC    GG
                                      AAC   AGG_
GAM1000  SCAND2    3'  TCACTGCAACATCTGCC     41890       CTG    A
                                GGCAGATG   GCAG GA
                                ||||||||   |||| ||
                                CCGTCTAC   CGTC CT
                                     AA_    A
GAM1000  SCYA25    3'  GCTGTCCCCACGCCTCTGTC   18839      T  _   CAGA
                                GGCAGA GC TGG    GACAGC
                                |||||| || |||    ||||||
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                                CTGTCT CG ACC   CTGTCG
                                   C  C   C___
GAM1000  SHAPY    3'  TGGCTGTCTCCTTGACCCGC   57113    T  _  __
                                GC GG CA  GAGACAGCCA
                                || || ||  ||||||||||
                                CG CC GT  CTCTGTCGGT
                                 C  A  TC
GAM1000  SIAT4A   3'  GCCGTTGACAGCATCTACT   11670    C      GCAGA   A
                                GG AGATGCTG    GAC GC
                                || ||||||||    ||| ||
                                TC TCTACGAC    TTG CG
                                 A       AG___   C
GAM1000  SULT1C2  5'  TGGCCGCCTCTGCTGTGACGCC 21679     AGA   T      ACA
                                GGC   TGC GGCAGAG   GCCA
                                |||   ||| |||||||   ||||
                                CCG   GTG TCGTCTC   CGGT
                                  CA_   _      CGC
GAM1000  TJP4     5'  GCTGTTAGCAGCATCTGCC   54611          G AGA
                                GGCAGATGCTG C   GACAGC
                                |||||||||||  |   ||||||
                                CCGTCTACGAC G   TTGTCG
                                       _ A__
GAM1000  VAV3     3'  GGCTGTTCAACATCCTCC    20364    CA   C  GCAGA
                                GG  GATG TG    GACAGCC
                                ||  |||| ||    |||||||
                                CC  CTAC AC    TTGTCGG
                                 TC    A  _____
GAM1000  VR22     5'  CTGCCCCACTGTCATCTGCC   25169         _ T____
                                GGCAGATG C     GGCAG
                                ||||||||  |    |||||
                                CCGTCTAC G     CCGTC
                                     T TCACC
GAM1000  ZNF185   3'  GGCTGTCCCCAGTTTTGCC    23116       T    CAGA
                                GGCAGA GCTGG    GACAGCC
                                ||||||  |||||   |||||||
                                CCGTTT TGACC    CTGTCGG
                                   _    C___
GAM1000  LOC126549 5'  GGCCCTTGCCGGCACCTGCC   75712       A      G  ACA
                                GGCAG TGCTGGCA AG   GCC
                                |||||  |||||||  ||   |||
                                CCGTC ACGGCCGT TC   CGG
                                   C       _  C__
GAM1000  LOC128989 3'  GGCTTGGCCAGCATCCCCC    74815    CA       AGAGAC
                                GG  GATGCTGGC     AGCC
                                ||  |||||||||     ||||
                                CC  CTACGACCG     TCGG
                                 CC        GT_____
GAM1000  LOC136345 5'  GGCTGTCCCCATTTCTCC    76207    C   TGC   CAGA
                                GG AGA   TGG    GACAGCC
                                || |||   |||    |||||||
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                                CC TCT   ACC    CTGTCGG
                                 _   TT_   C___
GAM1000  LOC138050 5'  GCTGCCTCTGTCAGCACCC    75297    CAGA         A
                                GG    TGCTGGCAGAG CAGC
                                ||    |||||||||||| ||||
                                CC    ACGACTGTCTC GTCG
                                 C___          C
GAM1000  LOC143101 5'  GGCTATCTAAAGTCCAGCATCT 82895    C       _ AG_   C
              TCC                  GG AGATGCTGG C   AGA AGCC
                                || |||||||||  |   ||| ||||
                                CC TCTACGACC G   TCT TCGG
                                 T        T AAA   A
GAM1000  LOC146237 3'  TGGCCACTAGGGTGCAGCATCT 83637           _  AG_  ACA
              GCC                    GGCAGATGCTG GC   AG   GCCA
                                |||||||||||  ||   ||   ||||
                                CCGTCTACGAC TG   TC   CGGT
                                       G  GGA  AC_
GAM1000  LOC146420 3'  TGACTGTCTCTACAGATAACC  83668    CAG  G   GC       C
                                GG   AT CTG  AGAGACAG CA
                                ||   || |||  |||||||| ||
                                CC   TA GAC  TCTCTGTC GT
                                 AA_  _   A_       A
GAM1000  LOC148887 5'  GGCTCACTGCAACATCTGCC   84244         CTG    A  CA
                                GGCAGATG   GCAG GA  GCC
                                ||||||||   |||| ||  |||
                                CCGTCTAC   CGTC CT  CGG
                                     AA_    A  __
GAM1000  LOC154084 3'  TGGCTGCCCCAGTAGCATCTGC 86166          G AGAGA
                                GCAGATGCTG C     CAGCCA
                                ||||||||||  |    ||||||
                                CGTCTACGAT G     GTCGGT
                                       _ ACCCC
GAM1000  LOC157349 5'  GGCTGTCTCCGGCAGCCCCTGC 81420       AT    G A_
              C                  GGCAG  GCTG C  GAGACAGCC
                                |||||  |||| |  |||||||||
                                CCGTC  CGAC G  CTCTGTCGG
                                   CC    _ GC
GAM1000  LOC157695 5'  CTGGCCAGCTCTGCC       86517       T     AG
                                GGCAGA GCTGGC  AG
                                ||||||  ||||||  ||
                                CCGTCT CGACCG  TC
                                    _     G_
GAM1000  LOC220573 5'  GGCTCTCTGCCAGCATCAACC  69603    CA          CA
                                GG  GATGCTGGCAGAGA  GCC
                                ||  ||||||||||||||  |||
                                CC  CTACGACCGTCTCT  CGG
                                 AA           __
GAM1000  LOC220980 3'  CTGCCTCTGCTGGACGCTGCC  93152       ATG TG     A
                                GGCAG   C  GCAGAG CAG
                                |||||   |  |||||| |||
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                                CCGTC   G  CGTCTC GTC
                                   GCA GT     C
GAM1000  LOC221477 3'  TGGCTAGGACTCTGCCAGCACC 92163    CAGA        AC__
              C                    GG    TGCTGGCAGAG    AGCCA
                                   ||    ||||||||||    |||||
                                   CC    ACGACCGTCTC    TCGGT
                                    C___         AGGA
GAM1000  LOC221683 5'  GGCTGGAGTGGCGCCAGCATCC 93716    CA       AGAGA__
              C                    GG  GATGCTGGC      CAGCC
                                   ||  |||||||||      |||||
                                   CC  CTACGACCG      GTCGG
                                    __       CGGTGAG
GAM1000  LOC221814 3'  TGAATCTGCAGCATCTACC   93947    C      G    GA
                                   GG AGATGCTG CAGA  CA
                                   || |||||||| ||||  ||
                                   CC TCTACGAC GTCT  GT
                                    A       _    AA
GAM1000  LOC222068 3'  GCTCACTGGCAACATCTGCC   92710        C  G   A  CA
                                   GGCAGATG TG CAG GA  GC
                                   |||||||| || ||| ||  ||
                                   CCGTCTAC AC GTC CT  CG
                                        A  G   A  __
GAM1000  LOC253975 5'  GCTGTCTCCAGTCTG      95996     AT    CAG
                                   CAG  GCTGG   AGACAGC
                                   |||  |||||   |||||||
                                   GTC  TGACC   TCTGTCG
                                     __    ____
GAM1000  LOC254722 5'  GCTGTCCCCGCACTCC      97567    C  A   T  CAGA
                                   GG AG TGC GG    GACAGC
                                   || || ||| ||    ||||||
                                   CC TC ACG CC    CTGTCG
                                    _ _   C  _____
GAM1000  LOC254956 3'  CATGGCTGCCTCCACCAGAGGT 96161  _______   CA   A     III
               TTCCATCTGCC                    CTGG  GAG CAGCCA   TG
                                     ||||  ||| ||||||   ||
                                     GACC  CTC GTCGGT   AC
                                   TTTGGA    AC   C     III
GAM1000  LOC51066  3'  TGGCTGTCCCCAGAGCCTGCC  31937      ATG    CAGA
                                   GGCAG   CTGG    GACAGCCA
                                   |||||   ||||    ||||||||
                                   CCGTC   GACC    CTGTCGGT
                                     CGA    C___
GAM1000  LOC90092  5'  GGCACCCAGCAGCATCTGCC   61413          G AGAGACA
                                   GGCAGATGCTG C      GCC
                                   |||||||||| |      |||
                                   CCGTCTACGAC G      CGG
                                         _ ACCCA__
GAM1000  LOC91056  3'  GTCTCTGCCCTCTTCTGCT   94761       TGCT
                                   GGCAGA    GGCAGAGAC
                                   ||||||    |||||||||
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                                TCGTCT   CCGTCTCTG
                                   TCTC
GAM1000 LOC91097 3' TGGCTGTCCCTGCAGGCGCCTC 64840   C A   G   A
            C                   GG AG TGCT GCAG GACAGCCA
                                || || |||| |||| ||||||||
                                CC TC GCGG CGTC CTGTCGGT
                                 _ C   A   C
GAM1000 LOC92231 3' TGACTATCTCTGCTGCTTTCTC 68555   C  T_ T      C C
            C                   GG AGA  GC GGCAGAGA AG CA
                                || |||  || |||||||| || ||
                                CC TCT  CG TCGTCTCT TC GT
                                 _  TT  _      A  A
GAM1000 LOC92691 5' GGCTGTCCGCAACCTCCGCC  56424    A  TGCTG  AGA
                                GGC GA    GC   GACAGCC
                                ||| ||    ||   |||||||
                                CCG CT    CG   CTGTCGG
                                  C  CCAA_  C__
GAM1000 LOC92710 3' GGCTGTCCCCAGCCTGC    70357     AT    CAGA
                                GCAG  GCTGG   GACAGCC
                                ||||  |||||   |||||||
                                CGTC  CGACC   CTGTCGG
                                  __    C___
GAM1001 E48     3' ATTTTGTACTCAAATCTCTACA 13504        C       T
                                TGTAGAGA TTGGGTATG GAT
                                |||||||| ||||||||| |||
                                ACATCTCT AACTCATGT TTA
                                     A       T
GAM1001 RBM8A   3' GTACCACATACCCAGT     17547     T       A
                                ACT GGGTATGTG TAC
                                ||| ||||||||| |||
                                TGA CCCATACAC ATG
                                  _       C
GAM1001 TSPY    3' ACCAGCAAGTCTCTGCA    82102          __
                                TGTAGAGACTTG  GGT
                                ||||||||||||  |||
                                ACGTCTCTGAAC  CCA
                                       GA
GAM1001 C1QTNF7  3' TATCCCTTCCAAGTCTCACA  49162    A       TATGT
                                TGT GAGACTTGGG    GATA
                                ||| ||||||||||    ||||
                                ACA CTCTGAACCT    CTAT
                                  _        TCC__
GAM1001 KIAA0449 3' CACCCCAAATCTCTA      34197       C    TAT
                                TAGAGA TTGGG   GTG
                                |||||| |||||   |||
                                ATCTCT AACCC   CAC
                                   A    ____
GAM1001 MSP     3' GCATCCCCCAAGTCACTACA  49418      A      T_
                                TGTAG GACTTGGG  ATGT
                                ||||| ||||||||  ||||
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                                ACATC CTGAACCC  TACG
                                   A       CC
GAM1001  LOC142779 3'  CACCCCAAGTCCTTACA     76392       A       TAT
                                TGTAG GACTTGGG   GTG
                                ||||| ||||||||   |||
                                ACATT CTGAACCC   CAC
                                   C       ___
GAM1001  LOC150113 5'  ATCAATACCCAACCCCCTACA  87209       AGAC       G
                                TGTAG    TTGGGTAT TGAT
                                |||||    |||||||| ||||
                                ACATC    AACCCATA ACTA
                                   CCCC       _
GAM1001  LOC197379 3'  GTACCACACTAAGTCTCCAC   89744    A       GTA    A
                                GT GAGACTTGG   TGTG TAC
                                || |||||||||   |||| |||
                                CA CTCTGAATC   ACAC ATG
                                 C         ___    C
GAM1002  ADD1     3'  ATGAACCTTCAGAAGCACTCGG 26377    A       A  AT
                                TC AGTGCTTC GA  AGGTTCAT
                                || |||||||| ||  ||||||||
                                GG TCACGAAG CT  TCCAAGTA
                                 C       A  __
GAM1002  MCM2     3'  AACCAGAGCACTTGA       67925          CAGAATA
                                TCAAGTGCTT      GGTT
                                ||||||||||      ||||
                                AGTTCACGAG      CCAA
                                      A_______
GAM1002  C17orf26  3'  GTTCTTCCGAAGCACTGA    57543     A      ___
                                TCA GTGCTTC   AGAAT
                                ||| |||||||   |||||
                                AGT CACGAAG   TCTTG
                                  _      CCT
GAM1002  FLJ13231  3'  ATGAACCCTATTTTAAAACAC  43547     C  C       _
                                GTG TT AGAATAGG TTCAT
                                ||| || |||||||| |||||
                                CAC AA TTTTATCC AAGTA
                                  A  A       C
GAM1002  HCA4     3'  ACTGTATTTTTGAAGCACTT   77579           TA__
                                AAGTGCTTCAGAA    GGT
                                ||||||||||||    |||
                                TTCACGAAGTTTT    TCA
                                       TATG
GAM1002  MEGF11    3'  ATGAGAGTTCTGAAACCCTTGA 50577       TGC       AGG
                                TCAAG   TTCAGAAT   TTCAT
                                |||||   ||||||||   |||||
                                AGTTC   AAGTCTTG   GAGTA
                                   CCA       A__
GAM1002  OR2C3     3'  TGTTCTGAAGTACCTGA     75450     A
                                TCA GTGCTTCAGAATA
                                ||| ||||||||||||
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                                AGT CATGAAGTCTTGT
                                  C
GAM1002  TRIM6    3'  ATGAACAATATAAAGCACTT   54132        CAGAATAG
                                AAGTGCTT       GTTCAT
                                ||||||||       ||||||
                                TTCACGAA       CAAGTA
                                    ATATAA__
GAM1002  LOC123036 3'  ATGAACCTACTCTGAAACAT   74189     C      A
                                GTG TTCAGA TAGGTTCAT
                                ||| |||||| |||||||||
                                TAC AAGTCT ATCCAAGTA
                                  A     C
GAM1002  LOC126964 3'  ATTTGATCTAAAGCACTTGA   74615          C   A
                                TCAAGTGCTT AGA TAGGT
                                |||||||||| ||| |||||
                                AGTTCACGAA TCT GTTTA
                                      A   A
GAM1002  LOC219654 3'  ACCCTCTGAGCACTT       91295        T    ATA
                                AAGTGCT CAGA   GGT
                                ||||||| ||||   |||
                                TTCACGA GTCT   CCA
                                   _    C__
GAM1002  LOC56920  3'  GAACCAGAAGCACTGA      39387     A      AGAATA
                                TCA GTGCTTC     GGTTC
                                ||| |||||||     |||||
                                AGT CACGAAG     CCAAG
                                  _      A_____
GAM1003  DMC1     3'  TGTTTATAGGACACACACA    22980     A  T     TT
                                TGT TGT TCCTAT  ATA
                                ||| ||| ||||||  |||
                                ACA ACA AGGATA  TGT
                                  C  C     TT
GAM1003  ITSN1    3'  AATCTATAAATAGACATGCA   11615        TTC
                                TGTATGT   CTATTTATAGATT
                                |||||||   ||||||||||||||
                                ACGTACA   GATAAATATCTAA
                                      ___
GAM1003  NOTCH2   3'  AAATAGGAAACATCA       44310    T
                                TG ATGTTTCCTATTT
                                || ||||||||||||
                                AC TACAAAGGATAAA
                                  _
GAM1003  KIAA0672 3'  GAATCTATAAAACAAAACAAAC 29410     A    CCTA
              A                  TGT TGTTT    TTTATAGATTC
                                ||| |||||    ||||||||||
                                ACA ACAAA    AAATATCTAAG
                                  A    ACA_
GAM1003  THEA     3'  AAATAGGAAAAATACA      66273       G
                                TGTAT TTTCCTATTT
                                ||||| ||||||||||
```

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                                ACATA AAAGGATAAA
                                  A
GAM1003  TRAP-1    3'  AATCCCCAAAACAGAAACATAC 14921          CTATTTATA
            A                    TGTATGTTTC        GATT
                                 ||||||||||        ||||
                                 ACATACAAAG        CTAA
                                      ACAAAACCC
GAM1003  LOC130074 3'  AAATGGAAACATACA       76123           T
                                 TGTATGTTTCC ATTT
                                 |||||||||||| ||||
                                 ACATACAAAGG TAAA
                                           _
GAM1003  LOC148418 3'  TTTGTAAACAGAATACATACA  78852        TTC  A
                                 TGTATGT   CT TTTATAGA
                                 |||||||   || ||||||||
                                 ACATACA   GA AAATGTTT
                                     TAA  C
GAM1003  LOC254700 5'  AAACAGGAAGCACACA      96220     A       A
                                 TGT TGTTTCCT TTT
                                 ||| |||||||| |||
                                 ACA ACGAAGGA AAA
                                   C       C
GAM1004  ARHGEF6   3'  CAAACTTGAAGCCAGGC     68198       ACCA
                                 GCCTGG    CAAGTTTG
                                 ||||||    ||||||||
                                 CGGACC    GTTCAAAC
                                    GAA_
GAM1004  BIG1      3'  TCAAACTTGCAACACTCCAG   21205      CCA___
                                 CTGGA     CAAGTTTGA
                                 |||||     |||||||||
                                 GACCT     GTTCAAACT
                                    CACAAC
GAM1004  CABC1     5'  TCAAGCTGACCCAGGCGG    39658        ACCACA
                                 TCGCCTGG     AGTTTGA
                                 ||||||||     |||||||
                                 GGCGGACC     TCGAACT
                                      CAG___
GAM1004  CORO2A    3'  TCAAACTGTGGTCCAGAGA    53403    GC        A
                                 TC  CTGGACCACA GTTTGA
                                 ||  |||||||||| ||||||
                                 AG  GACCTGGTGT CAAACT
                                  A_        _
GAM1004  CORO2A    3'  TCAAACTGTGGTCCAGAGA    12647    GC        A
                                 TC  CTGGACCACA GTTTGA
                                 ||  |||||||||| ||||||
                                 AG  GACCTGGTGT CAAACT
                                  A_        _
GAM1004  DISC1     3'  TCAAACTCCTGACCTCAGGCGA 37892        _ AC  CA
                                 TCGCCTG G  CA  AGTTTGA
                                 ||||||| |  ||  |||||||
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                                AGCGGAC C  GT  TCAAACT
                                    T CA  CC
GAM1004  EN2      5'  CGGGCGGCCCAGGCGG      7459         A  ACAA
                                TCGCCTGG CC    GTTTG
                                |||||||| ||    |||||
                                GGCGGACC GG    CGGGC
                                    C  ____
GAM1004  FOXD2    5'  CAGAGGGGGCCCAGGCGA    15562        A  ACAAG
                                TCGCCTGG CC    TTTG
                                |||||||| ||    ||||
                                AGCGGACC GG    AGAC
                                    C  GGG__
GAM1004  GPX3     5'  TCAGGCAGCGGCTCAGGCGA  9125         GA  ACAA
                                TCGCCTG  CC    GTTTGA
                                |||||||  ||    ||||||
                                AGCGGAC  GG    CGGACT
                                    TC  CGA_
GAM1004  HNF3G    3'  AACTCTGGTCCAGGAGA     72339    G       CA
                                TC CCTGGACCA  AGTT
                                || |||||||||  ||||
                                AG GGACCTGGT  TCAA
                                 A        C_
GAM1004  IL13RA1  3'  TCAAACTTGAGTCACAAAGA  7778     GCC  _   CA
                                TC   TG GAC  CAAGTTTGA
                                ||   || |||  |||||||||
                                AG   AC CTG  GTTCAAACT
                                 AA_  A  A_
GAM1004  KCNS2    3'  CAAACTTGTATTGAAGGGA   68300    G   GGACC
                                TC CCT     ACAAGTTTG
                                || |||     |||||||||
                                AG GGA     TGTTCAAAC
                                 _  AGTTA
GAM1004  LMO4     5'  CAAACTTGCAGCAGCGA     22251     __   GACCA
                                TCGC  CTG    CAAGTTTG
                                ||||  |||    ||||||||
                                AGCG  GAC    GTTCAAAC
                                  AC  _____
GAM1004  LZTS1    3'  TCAAACTTGTGGCCTCAAGC  40695    CT__  A
                                GC    GG CCACAAGTTTGA
                                ||    || ||||||||||||
                                CG    CC GGTGTTCAAACT
                                 AACT  _
GAM1004  MATK     3'  CAAGGAGGGTCCAGGCGG    57816          ACAAG
                                TCGCCTGGACC    TTTG
                                ||||||||||     ||||
                                GGCGGACCTGG    GAAC
                                      GAG__
GAM1004  MATK     3'  CAAGGAGGGTCCAGGCGG    57819          ACAAG
                                TCGCCTGGACC    TTTG
                                ||||||||||     ||||
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                                GGCGGACCTGG    GAAC
                                      GAG__
GAM1004  MATK     3'  CAAGGAGGGTCCAGGCGG    9915          ACAAG
                                TCGCCTGGACC    TTTG
                                ||||||||||    ||||
                                GGCGGACCTGG    GAAC
                                      GAG__
GAM1004  MIR16    3'  TCAAACTTGTGGCCA      33565     A
                                TGG CCACAAGTTTGA
                                ||| ||||||||||||
                                ACC GGTGTTCAAACT
                                  _
GAM1004  PIK3C2B  3'  AGCTCGGTCCAGGTGA      10559          ACA
                                TCGCCTGGACC   AGTT
                                ||||||||||   ||||
                                AGTGGACCTGG   TCGA
                                      C__
GAM1004  PLCG2    5'  CAAACCCGGGGCAGGCGG    72463       GA  ACAA
                                TCGCCTG  CC    GTTTG
                                |||||||  ||    |||||
                                GGCGGAC  GG    CAAAC
                                    GG  CC__
GAM1004  PLIN     3'  CAAACTTGTGGCCAAAAGA   10640    GCC   A
                                TC   TGG CCACAAGTTTG
                                ||   ||| ||||||||||
                                AG   ACC GGTGTTCAAAC
                                 AAA  _
GAM1004  POU2AF1  3'  CAGATTTACAGTCCAGGC    20648        CAC
                                GCCTGGAC   AAGTTTG
                                ||||||||   |||||||
                                CGGACCTG   TTTAGAC
                                     ACA
GAM1004  SLC6A12  3'  CGAATGTGCTCCAGGCGA    11734         C    AG
                                TCGCCTGGA CACA  TTTG
                                ||||||||| ||||  ||||
                                AGCGGACCT GTGT  AAGC
                                      C   __
GAM1004  STARD4   3'  TCAAACTTGTAGTACTACAGA  57516    GCC   _  C
                                TC   TGG AC ACAAGTTTGA
                                ||   ||| || ||||||||||
                                AG   ATC TG TGTTCAAACT
                                 AC_   A  A
GAM1004  TP53     3'  TCAAACTCCTGGGCTCAGGCGA 5043         A_   CA
                                TCGCCTGG  CCA  AGTTTGA
                                ||||||||  |||  |||||||
                                AGCGGACT  GGT  TCAAACT
                                     CG   CC
GAM1004  TR2      5'  CAAACTTTCCAGGC       72314        CCAC
                                GCCTGGA    AAGTTTG
                                |||||||    |||||||
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                                CGGACCT   TTCAAAC
                                      ____
GAM1004 C21orf42 5' TCAAACTTGTAGCTGTATGA  54207    CC  ACC
                                TCG TGG  ACAAGTTTGA
                                ||| |||  ||||||||||
                                AGT GTC  TGTTCAAACT
                                  AT  GA_
GAM1004 DAZAP1   3' CAAACTTGTGAACTCGTGA   38536    CT AC
                                TCGC GG CACAAGTTTG
                                |||| || ||||||||||
                                AGTG TC GTGTTCAAAC
                                  C_ AA
GAM1004 DBR1     3' AACTCCTGACCTCAGGCGA   32523      _ AC CA
                                TCGCCTG G CA AGTT
                                ||||||| |  ||  ||||
                                AGCGGAC C GT TCAA
                                    T CA CC
GAM1004 DC-TM4F2 3' CAAACTTGTGACTGC      48171    CT AC
                                GC GG CACAAGTTTG
                                ||  ||  ||||||||||
                                CG TC GTGTTCAAAC
                                 __ A_
GAM1004 DKFZp434N2030 5' TCAAACTTGTCCTCGC     65525    CT   CAC
                                GC GGAC  AAGTTTGA
                                ||  ||||  ||||||||
                                CG CCTG  TTCAAACT
                                 CT   ___
GAM1004 DKFZP564I1171 3' TCAGAAGCTGAGTCCAGGC   71592       _ CAAG
                                GCCTGGAC CA   TTTGA
                                |||||||| ||   |||||
                                CGGACCTG GT   AGACT
                                    A CGA_
GAM1004 DKFZP564O0423 3' TCAAACTCCTGGCCTCAGGCGA 91699       _ A  CA
                                TCGCCTG G CCA AGTTTGA
                                ||||||| | |||  |||||||
                                AGCGGAC C GGT TCAAACT
                                    T C  CC
GAM1004 EPN2     5' CAAACTTGTGGACAGG     30321     GA
                                CCTG CCACAAGTTTG
                                ||||  ||||||||||
                                GGAC GGTGTTCAAAC
                                  A_
GAM1004 EREG     3' TCAAACTTATGGGCAGGGA   7510     G   GA  C
                                TC CCTG  CCA AAGTTTGA
                                || ||||  ||| ||||||||
                                AG GGAC  GGT TTCAAACT
                                 _   G_  A
GAM1004 FLJ10718 3' TCAAACTCTTAGGCTCAGGCGA 36496       GA ACA_
                                TCGCCTG  CC   AGTTTGA
                                |||||||  ||   |||||||
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                                AGCGGAC  GG   TCAAACT
                                    TC  ATTC
GAM1004  FLJ10803  3'  TCAAACTTGTATGGATGA    36671    _  TGGACC
                                TCG CC     ACAAGTTTGA
                                ||| ||     ||||||||||
                                AGT GG     TGTTCAAACT
                                  A  TA____
GAM1004  FLJ20312  5'  TCAAACTTGTGTGCTGAGG   34928    _  AC
                                CCT GG  CACAAGTTTGA
                                ||| ||  ||||||||||
                                GGA TC  GTGTTCAAACT
                                  G  GT
GAM1004  FLJ23420  3'  CAAGTGGGTCCAGGC      46846        A  AG
                                GCCTGGACC CA  TTTG
                                ||||||||| ||  ||||
                                CGGACCTGG GT  GAAC
                                    _  __
GAM1004  FREQ     3'  TCAGCTGCTGGCCCGGGCGA  26585       A   CA   T
                                TCGCCTGG CCA  AGTT GA
                                |||||||| |||  |||| ||
                                AGCGGGCC GGT  TCGA CT
                                    C   CG   _
GAM1004  H2AV     3'  TCAAACTCCTGACCTCAGGCGA 56858      _ AC  CA
                                TCGCCTG G  CA  AGTTTGA
                                ||||||| |  ||  |||||||
                                AGCGGAC C  GT  TCAAACT
                                    T CA  CC
GAM1004  HSA249128 5'  GGCGCGGTCCAGGCGG     34153         ACAA
                                TCGCCTGGACC   GTT
                                ||||||||||    |||
                                GGCGGACCTGG   CGG
                                      CG__
GAM1004  KIAA0089  5'  AAGCACGGTCCAGGCGG     69960         ACAA
                                TCGCCTGGACC   GTTT
                                ||||||||||    ||||
                                GGCGGACCTGG   CGAA
                                      CA__
GAM1004  KIAA0256  3'  CAAACTTGTCCTGAGTGC    64417    _ __   CAC
                                GC CT  GGAC   AAGTTTG
                                || ||  ||||   |||||||
                                CG GA  CCTG   TTCAAAC
                                 T  GT   ___
GAM1004  KIAA1026  3'  TCAACTCCTGACCTCAGGCGA 71207       _ AC  CA   T
                                TCGCCTG G  CA  AGTT GA
                                ||||||| |  ||  |||| ||
                                AGCGGAC C  GT  TCAA CT
                                    T CA  CC   _
GAM1004  KIAA1981  3'  CAGAGGATGATTCAGGCGA   88341        C  CAAG
                                TCGCCTGGA CA   TTTG
                                ||||||||| ||   ||||
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                                AGCGGACTT GT    AGAC
                                     A  AGG_
GAM1004  MGC13090  5'  TCAAACTTGTCCGCCAAGT   51141    C   ACC
                                GC TGG   ACAAGTTTGA
                                || |||   ||||||||||
                                TG ACC   TGTTCAAACT
                                 A   GCC
GAM1004  MGC2452   5'  TCAAGGAGATGTGGTCCAGG   50990          AG__
                                CCTGGACCACA    TTTGA
                                ||||||||||    |||||
                                GGACCTGGTGT    GAACT
                                      AGAG
GAM1004  MYT1L     5'  TCAAACTTGTGGTGG      66825    TGG
                                CC   ACCACAAGTTTGA
                                ||   ||||||||||||
                                GG   TGGTGTTCAAACT
                                 ___
GAM1004  NUDT13    3'  TCAGTTTGTGACCCAGGGA   63215    G    AC   AGT
                                TC CCTGG  CACA   TTGA
                                || |||||  ||||   ||||
                                AG GGACC  GTGT   GACT
                                 _    CA    TT_
GAM1004  PCDH17    3'  CAAACTTGTATTAGG      27087      ACC
                                CCTGG   ACAAGTTTG
                                |||||   |||||||||
                                GGATT   TGTTCAAAC
                                   A__
GAM1004  PGRMC1    3'  TCAAACTTGTAATTGTGGT   21895     TG  CC
                                GCC  GA  ACAAGTTTGA
                                |||  ||  ||||||||||
                                TGG  TT  TGTTCAAACT
                                  TG  AA
GAM1004  PTDSS2    3'  CATGGTGTGGTCCAGGC     47884          AGTT
                                GCCTGGACCACA    TG
                                ||||||||||||    ||
                                CGGACCTGGTGT    AC
                                      GGT_
GAM1004  RPS6KB1   3'  TCAAACTTTTCCCAGGC     12038       ACCAC
                                GCCTGG    AAGTTTGA
                                ||||||    ||||||||
                                CGGACC    TTCAAACT
                                   CTT__
GAM1004  USP22     3'  TCAAACTCCTGACCTCAGGCGA 68023       _ AC  CA
                                TCGCCTG G  CA  AGTTTGA
                                ||||||| |  ||  |||||||
                                AGCGGAC C  GT  TCAAACT
                                    T CA  CC
GAM1004  LOC129011 5'  CAGACCTGCGGTCCAGGC    74865         A  A
                                GCCTGGACC CA GTTTG
                                ||||||||| || |||||
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                                CGGACCTGG GT CAGAC
                                     C  C
GAM1004  LOC130595 5'  CAGGCTCAGTCCAGGC      75748         CACA
                                GCCTGGAC    AGTTTG
                                ||||||||    ||||||
                                CGGACCTG    TCGGAC
                                     AC__
GAM1004  LOC131873 5'  CTGGTGGTCCAGGAGA      75879    G         A
                                TC CCTGGACCAC AG
                                || ||||||||||  ||
                                AG GGACCTGGTG TC
                                 A         G
GAM1004  LOC145978 3'  TCAAACTTTAACAGGTGA     77600         GACCAC
                                TCGCCTG     AAGTTTGA
                                |||||||     ||||||||
                                AGTGGAC     TTCAAACT
                                     AAT___
GAM1004  LOC146890 5'  TCAGAAGTAGTCAGGCGA     83854        G  C  AAG
                                TCGCCTG AC AC   TTTGA
                                ||||||| || ||   |||||
                                AGCGGAC TG TG   AGACT
                                     _  A  A__
GAM1004  LOC150622 5'  CTGGTGGTCCAGGGA       79957    G         A
                                TC CCTGGACCAC AG
                                || ||||||||||  ||
                                AG GGACCTGGTG TC
                                 _         G
GAM1004  LOC152002 3'  CAAACCAGCTCCAGGTGA     80431          CCACAA
                                TCGCCTGGA     GTTTG
                                |||||||||     |||||
                                AGTGGACCT     CAAAC
                                      CGAC__
GAM1004  LOC153474 3'  TCAGAAGCTGAGTCCAGGC    80847         _  CAAG
                                GCCTGGAC CA    TTTGA
                                |||||||| ||    |||||
                                CGGACCTG GT    AGACT
                                     A  CGA_
GAM1004  LOC154007 3'  TCAAACTCCTAGGCTCAGGCGA 81021         GA  ACA_
                                TCGCCTG  CC    AGTTTGA
                                |||||||  ||    |||||||
                                AGCGGAC  GG    TCAAACT
                                     TC  ATCC
GAM1004  LOC154789 5'  TCAAACTTGAGCAGGC       81141       GACCA
                                GCCTG     CAAGTTTGA
                                |||||     |||||||||
                                CGGAC     GTTCAAACT
                                   GA___
GAM1004  LOC158301 3'  CAAACCTGTGGTTCCA       81869       _    A
                                TGGA CCACA GTTTG
                                |||| ||||| |||||
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                                ACCT GGTGT CAAAC
                                  T    C
GAM1004  LOC199906 3'  TCAAACTCCTGACCTCAGGCGA 88487       _ AC  CA
                                TCGCCTG G  CA  AGTTTGA
                                ||||||| |  ||  |||||||
                                AGCGGAC C  GT  TCAAACT
                                    T CA  CC
GAM1004  LOC199991 5'  TCAGAGCGTTCCAGGCGA    89916        CC  AAG
                                TCGCCTGGA  AC   TTTGA
                                |||||||||  ||   |||||
                                AGCGGACCT  TG   AGACT
                                     __ CG_
GAM1004  LOC219529 5'  TCAAACTCCTGAGCCCAGGTGA 92974        AC_  CA
                                TCGCCTGG   CA  AGTTTGA
                                ||||||||   ||  |||||||
                                AGTGGACC   GT  TCAAACT
                                    CGA  CC
GAM1004  LOC220753 3'  CAAACTTGTAGAGGTGGGC   92941     GG  ___
                                GCCT  ACC   ACAAGTTTG
                                ||||  |||   |||||||||
                                CGGG  TGG   TGTTCAAAC
                                  __  AGA
GAM1004  LOC221718 3'  TCAAACTTATTGGTGAAG    93632    GG   C_
                                CT  ACCA  AAGTTTGA
                                ||  ||||  ||||||||
                                GA  TGGT  TTCAAACT
                                 AG   TA
GAM1004  LOC253927 3'  TCAAACTTAGACTTCAGGC   95025       CCAC
                                GCCTGGA    AAGTTTGA
                                |||||||    ||||||||
                                CGGACTT    TTCAAACT
                                   CAGA
GAM1004  LOC51028  3'  CAAATATGGTCCAGG      32179        CAA
                                CCTGGACCA  GTTTG
                                |||||||||  |||||
                                GGACCTGGT  TAAAC
                                    A__
GAM1005  CSPG2    5'  GATCTTCGGCCAGCCCC     15225   A     GTTG
                                G GGCTGGT   TGAAGATC
                                | |||||||   ||||||||
                                C CCGACCG   GCTTCTAG
                                 C     ____
GAM1005  EMP1     3'  CTGCCACAACACCAGCC     7444           A_
                                GGCTGGTGTTGTG  AG
                                ||||||||||||  ||
                                CCGACCACAACAC  TC
                                       CG
GAM1005  F2RL3    3'  CAGGAGTTCAACACCAGCCT   14173          TGAAGA
                                AGGCTGGTGTTG     TCCTG
                                ||||||||||||     |||||
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                                TCCGACCACAAC     AGGAC
                                      TTG___
GAM1005  GNAI2    3'  CTTTGCCCAACACCAGCC    67547          __ TG
                                GGCTGGTGTT  G  AAG
                                ||||||||||  |  |||
                                CCGACCACAA  C  TTC
                                     CC GT
GAM1005  NUCB1    3'  AGGACCTAGGCCCAGCC     20526       T   GTGA  A
                                GGCTGG GTT    AG TCCT
                                ||||||  |||    ||  ||||
                                CCGACC CGG    TC AGGA
                                   _   A___  C
GAM1005  PRCC     3'  AGGATCTCCTGCCAGCCC    19931    A      TTGT  A
                                G GGCTGGTG    GA GATCCT
                                |  ||||||||    ||  ||||||
                                C CCGACCGT    CT CTAGGA
                                 _       C___  _
GAM1005  SURF6    3'  CAGGATCTCCACAGACCTCGGC 22188         T  _    A
              CTC                   GAGGCTGG GT TGTG AGATCCTG
                                ||||||||  ||  ||||  ||||||||
                                CTCCGGCT CA ACAC TCTAGGAC
                                     C  G    C
GAM1005  TNXB     5'  AGGACACACCAGCC        50636          T TGAAGA
                                GGCTGGTGT G     TCCT
                                |||||||||  |     ||||
                                CCGACCACA C     AGGA
                                      _ _______
GAM1005  UCP2     3'  AGAATCTTCGTCCTGCC     12530     T  TGTTG      C
                                GGC GG     TGAAGAT CT
                                |||  ||     |||||||  ||
                                CCG CC     GCTTCTA GA
                                  T  T_____       A
GAM1005  A        5'  CAGAACCCCCCAGCCAGCCTC  27073          _______  G
                                GAGGCTGGT     GTT TG
                                |||||||||     |||  ||
                                CTCCGACCG     CAA AC
                                      ACCCCC   G
GAM1005  A        5'  CAGAACCCCCCAGCCAGCCTC  39093          _______  G
                                GAGGCTGGT     GTT TG
                                |||||||||     |||  ||
                                CTCCGACCG     CAA AC
                                      ACCCCC   G
GAM1005  CHPT1    5'  CAGGACCCGGCCGCCAGCCTC  39619          _   TGAAGA
                                GAGGCTGGTG TTG     TCCTG
                                ||||||||||  |||     |||||
                                CTCCGACCGC GGC     AGGAC
                                      C   CC_____
GAM1005  FLJ13993 3'  CAGGACCCTCCCCACCAGCT   60457         TTGT  AGA
                                GGCTGGTG    GA   TCCTG
                                ||||||||    ||   |||||
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                                TCGACCAC   CT  AGGAC
                                    CC__  CCC
GAM1005  FLJ20209  3'  AGGTACAACACCAGCC     85516          AAGAT
                                GGCTGGTGTTGTG    CCT
                                ||||||||||||    |||
                                CCGACCACAACAT    GGA
                                      _____
GAM1005  HPCAL4   3'  GATCTTTGAGGGACCACCTC  32737     C   G TG
                                GAGG TGGT T  TGAAGATC
                                |||| |||| |  ||||||||
                                CTCC ACCA G  GTTTCTAG
                                  _   G GA
GAM1005  KIAA1789  5'  ATCTTCAAGATGATCAGCCTC  67099        _  G
                                GAGGCTGGT GTT TGAAGAT
                                ||||||||| ||| |||||||
                                CTCCGACTA TAG ACTTCTA
                                     G   A
GAM1005  LYPLA2   3'  CAGGACCTCACTCACTAGCC  23428       TT   A A
                                GGCTGGTG  GTGA G TCCTG
                                ||||||||  |||| | |||||
                                CCGATCAC  CACT C AGGAC
                                    T_   _ C
GAM1005  PP591    5'  CAGGAATTCAACACCAGCCT  47367          TGAAGA
                                AGGCTGGTGTTG     TCCTG
                                ||||||||||||     |||||
                                TCCGACCACAAC     AGGAC
                                      TTA___
GAM1005  RENT2    3'  CAGGAGGCAGAAACACCAGCCT 54589          G_  AAGA
            C                    GAGGCTGGTGTT  TG   TCCTG
                                ||||||||||||  ||   |||||
                                CTCCGACCACAA  AC   AGGAC
                                      AG  GG__
GAM1005  RENT2    3'  CAGGAGGCAGAAACACCAGCCT 31418          G_  AAGA
            C                    GAGGCTGGTGTT  TG   TCCTG
                                ||||||||||||  ||   |||||
                                CTCCGACCACAA  AC   AGGAC
                                      AG  GG__
GAM1005  TRIM38   3'  CAGGAGTTCAACACCAGCCT   20985          TGAAGA
                                AGGCTGGTGTTG     TCCTG
                                ||||||||||||     |||||
                                TCCGACCACAAC     AGGAC
                                      TTG___
GAM1005  LOC149086 3'  AGGATCTTCCTCCAGCT     84335       TGTTGT
                                GGCTGG     GAAGATCCT
                                ||||||     |||||||||
                                TCGACC     CTTCTAGGA
                                   TC____
GAM1005  LOC149668 5'  GGATCCCACCAGCCC       84545   A      TTGTGAA
                                G GGCTGGTG      GATCC
                                | ||||||||      |||||
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                                C CCGACCAC      CTAGG
                                 _      C_______
GAM1005  LOC162137 5'  CAGAACCTTCTCCTACCAGCT  87112        TTGT    ATC
                                GGCTGGTG    GAAG   CTG
                                ||||||||    ||||   |||
                                TCGACCAT    CTTC   GAC
                                    CCT_    CAA
GAM1005  LOC197285 3'  AGGACCTCCTGCCAGCT     87788        TTGT  A A
                                GGCTGGTG    GA G TCCT
                                ||||||||    || | ||||
                                TCGACCGT    CT C AGGA
                                    C___   _ C
GAM1005  LOC197414 3'  AGAATCCGGCATCAGCC     88060          TGAA   C
                                GGCTGGTGTTG    GAT CT
                                ||||||||||    ||| ||
                                CCGACTACGGC    CTA GA
                                      ____   A
GAM1005  LOC219818 3'  CAGGACCTGGATGACACCCGCC 90885      T    TG GA  A
            TC                    GAGGC GGTGT  T  AG TCCTG
                                |||||  |||||  |  || |||||
                                CTCCG CCACA  A  TC AGGAC
                                   C    GT GG  C
GAM1005  LOC51236  3'  CAGGATCTCCTCTCACCTGCC  33200     T   TTGT  A
                                GGC GGTG    GA GATCCTG
                                |||  ||||    || |||||||
                                CCG CCAC    CT CTAGGAC
                                  T    TCTC  _
GAM1005  LOC92714  3'  GGACCTGCCCAGCCTC      70375        T  TGTGA  A
                                GAGGCTGG GT     AG TCC
                                ||||||||  ||     ||  |||
                                CTCCGACC CG     TC AGG
                                    _  ______  C
GAM1006  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                ||||  |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM1006  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   |||  ||  |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM1006  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                ||||||||||||  |||
                                GTAAAGTGAAAG GAT
                                              _
GAM1006  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
            TG                    CATTTCACTTTCACTGTCTGAGAT
                                ||||||||||||||||||||||||
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                                GTAAAGTGAAAGTGACAGACTCTA

GAM1006 KLF4     3' TCCCAGACAGTGGATATG    14891    CT        A
                                CA TTCACTGTCTG GA
                                || |||||||||| ||
                                GT AGGTGACAGAC CT
                                 AT         C
GAM1006 PHYH     3' ACAGTAAAAGTGAAAT      20608         C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM1006 PKD2     3' TCCAGGTTGAAAGTGAAA    60096          CTG   A
                                TTTCACTTTCA  TCTG GA
                                ||||||||||  |||| ||
                                AAAGTGAAAGT  GGAC CT
                                       T__   _
GAM1006 WRN      3' GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM1006 ZNF216   3' ATCTGCACAGCAAAGTGAAA  20017        CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||| ||||  ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_   CG_
GAM1006 CG012    5' CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM1006 EIF2C2   3' ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                |||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM1006 FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
             G                   CATTTC        GTCTGAGAT
                                 ||||||        |||||||||
                                 GTAAAG        CAGACTCTA
                                    AAACATTT_
GAM1006 FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                    C__
GAM1006 KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534      C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
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                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM1006  KLHL6    3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM1006  NIR3     3'  GCAGTGAAAGTGCAAT      66242      T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM1006  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM1006  PP35     3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM1006  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148         TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__   TT
GAM1006  SEP15    3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM1006  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                     AAAGG
GAM1006  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC       CTGTCTGAGAT
                                ||||       ||||||||||||
                                AAAG       GACAGACTCTA
                                  GTTTGCC
GAM1006  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM1006  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
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                                AAAG GAAAGTGA   ACT
                                  _      ATTT
GAM1006 LOC222134 5' ACAGTGAAGTGAAATG     94136         T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM1007 CTSB    3' CCAGTGGAACAGCGGGAGACCT 64725    A___   G_ TCAT
          G                      CAG   CCCG GT   TCCACTGG
                                |||   |||| ||   ||||||||
                                GTC   GGGC CA   AGGTGACC
                                  CAGA   GA ____
GAM1007 HIVEP3   5' CCAATAGAATAGCGTGGGCCCT 44432    A_   G  C   CAC
          GA                     TCAG CCCG GTT ATTC  TGG
                                |||| |||| ||| ||||  |||
                                AGTC GGGT CGA TAAG  ACC
                                  CC   G  _   ATA
GAM1007 SPAG8   3' CAGTGAAATGGACCTG     24898         C
                                CGGGTTCATT CACTG
                                |||||||||| |||||
                                GTCCAGGTAA GTGAC
                                      A
GAM1007 FLJ13614 3' CAGTGGAACTCAGAACTGA   57450     ACCC   TCAT
                                TCAG   GGGT   TCCACTG
                                ||||   ||||   |||||||
                                AGTC   CTCA   AGGTGAC
                                  AAGA   ____
GAM1007 FLJ32468 5' CAGTGGAGGTCAAGCCTG   59040      CA__
                                CGGGTT   TTCCACTG
                                ||||||   ||||||||
                                GTCCGA   GAGGTGAC
                                   ACTG
GAM1007 JM11    3' CAGTGGATCTGGACCC     53254       T_
                                GGGTTCA  TCCACTG
                                |||||||  |||||||
                                CCCAGGT  AGGTGAC
                                    CT
GAM1007 KIAA0800 3' AGTGGAATAGTCTGA      28145      CCGGGTTC
                                TCAGAC      ATTCCACT
                                ||||||      ||||||||
                                AGTCTG      TAAGGTGA
                                   A_______
GAM1007 KIAA1962 3' CCAGCAGAATGAAGGGATGGG 81916     GG__     CA
                                CCCG   TTCATTC  CTGG
                                ||||   |||||||  ||||
                                GGGT   AAGTAAG  GACC
                                  AGGG     AC
GAM1007 RASGRP4  3' AATGAGCAGCCCAGGCCTGG  53645     A  C   ___
                                TCAG CC GGGT   TCATT
                                |||| || ||||   |||||
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                                GGTC GG CCCG   AGTAA
                                  C A    ACG
GAM1007 SC4MOL    3' CCAGTAAAACCATAGGCCTGA 22153     A CG_   CATTCC
                                TCAG CC   GGTT     ACTGG
                                |||| ||   ||||     |||||
                                AGTC GG   CCAA     TGACC
                                  C ATA    AA____
GAM1007 ZNF31     5' CAGTGGATCCCTGGCCTGA   64982     A C   TTCAT
                                TCAG CC GGG    TCCACTG
                                |||| || |||    |||||||
                                AGTC GG CCC    AGGTGAC
                                  C T   T____
GAM1007 LOC118611 5' CAGTGGAACAGAAGCCC     75471      _ A_
                                GGGTT C  TTCCACTG
                                ||||| |  ||||||||
                                CCCGA G  AAGGTGAC
                                   A AC
GAM1007 LOC121133 3' CCAGTGGAAGCTCGTGCCTGA 75990     ACC    TCA
                                TCAG   CGGGT   TTCCACTGG
                                ||||   |||||   |||||||||
                                AGTC   GCTCG   AAGGTGACC
                                  CGT    ___
GAM1007 LOC127281 3' CCAGTGGGGCTCCCCGCATCTG 74644      CC    TTCA
             A                   TCAGA  CGGG    TTCCACTGG
                                |||||  ||||    |||||||||
                                AGTCT  GCCC    GGGGTGACC
                                   AC    CTC_
GAM1007 LOC127687 3' AATGAATACCCAGTCTGA    74687       CC    __
                                TCAGAC  GGGT  TCATT
                                ||||||  ||||  |||||
                                AGTCTG  CCCA  AGTAA
                                   A_    TA
GAM1007 LOC146987 3' CCAGTGGAATAAATCT      83898       C
                                GGGTT ATTCCACTGG
                                ||||| ||||||||||
                                TCTAA TAAGGTGACC
                                   A
GAM1007 LOC152457 3' CAGTGGAATAGGACCT      80607       _
                                GGGTTC ATTCCACTG
                                |||||| |||||||||
                                TCCAGG TAAGGTGAC
                                   A
GAM1007 LOC220980 5' CCAGCAGTGGGCCCAGG     93150    C       CCA
                                CC GGGTTCATT   CTGG
                                || |||||||||   ||||
                                GG CCCGGGTGA   GACC
                                 A        C__
GAM1007 LOC51016  3' CAGCGGGGCCCGGTTC      63736    C     TCAT   A
                                GA CCGGGT    TCC CTG
                                || ||||||    ||| |||
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                                CT GGCCCG   GGG GAC
                                 T    _____  C
GAM1007 LOC92095 3' CAGCAGAGCCCGAGCCCGG   68091       A__  CA
                                CCGGGTTC  TTC  CTG
                                ||||||||  |||  |||
                                GGCCCGAG  GAG  GAC
                                    CCC   AC
GAM1007 LOC92096 3' CAGCAGAGCCCGAGCCCGG   68097       A__  CA
                                CCGGGTTC  TTC  CTG
                                ||||||||  |||  |||
                                GGCCCGAG  GAG  GAC
                                    CCC   AC
GAM1007 LOC92710 3' CCAGTGGAATAGGATAGCTGA 70355     ACCCGG  _
                                TCAG     GTTC ATTCCACTGG
                                ||||     |||| ||||||||||
                                AGTC     TAGG TAAGGTGACC
                                  GA_____   A
GAM1008 ABCC3    3' GCGGTGGACTCTCATGTGGCC  39156     G      GAGA
                                GGCCA ATGAGAGT   CACCGC
                                ||||| ||||||||   ||||||
                                CCGGT TACTCTCA   GTGGCG
                                  G      G___
GAM1008 ADCY2    3' GCAGTGCACCTCTCATCAGCC  65018     CA      _ AGA  C
                                GGC  GATGAGAG TG   CAC GC
                                |||  |||||||| ||   ||| ||
                                CCG  CTACTCTC AC   GTG CG
                                  A_       C ___   A
GAM1008 ARHA     3' CGATGTCCAACCCGTCTGGCC  70695       AGAG  A   C
                                GGCCAGATG    TG GACA CG
                                |||||||||    || |||| ||
                                CCGGTCTGC    AC CTGT GC
                                     CCA_ _    A
GAM1008 BIG1     3' TTGATTCCCATCTGGC     21207       A   G
                                GCCAGATG GAGT AG
                                |||||||| |||| ||
                                CGGTCTAC CTTA TT
                                     C   G
GAM1008 BMPR2    5' GCTAGGTCCTCTCATCAGCC   6835     CA      TGA  ACC
                                GGC  GATGAGAG   GAC   GC
                                |||  ||||||||   |||   ||
                                CCG  CTACTCTC   CTG   CG
                                  A_       ___   GAT
GAM1008 CLECSF5  3' GGACACCGCGCAATCTCCATCT 25127      _ A_______  AGACAC
             GGCC                  CAGATG AG       GTG     C
                                ||||||  ||       |||     |
                                GTCTAC TC       CGC     G
                                   C  TAACGIII   CACAGA
GAM1008 COL4A5   3' GCAGTGTCTCATTGTC     52969    G       C
                                GA AGTGAGACAC GC
                                || ||||||||| ||
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                                CT TTACTCTGTG CG
                                 G         A
GAM1008  COL4A5    3'  GCAGTGTCTCATTGTC      52973     G         C
                                GA AGTGAGACAC GC
                                || |||||||||| ||
                                CT TTACTCTGTG CG
                                 G         A
GAM1008  COL4A5    3'  GCAGTGTCTCATTGTC      4939      G         C
                                GA AGTGAGACAC GC
                                || |||||||||| ||
                                CT TTACTCTGTG CG
                                 G         A
GAM1008  HLX1      5'  CTCGCTCTCATCCAGCC     41706     CA
                                GGC  GATGAGAGTGAG
                                |||  ||||||||||||
                                CCG  CTACTCTCGCTC
                                  AC
GAM1008  ITGA7     3'  GTTTCCCCTCTCATCTGACC   9381      C         T_
                                GG CAGATGAGAG  GAGAC
                                || ||||||||||  |||||
                                CC GTCTACTCTC  CTTTG
                                 A         CC
GAM1008  SEPN1     3'  GTCTCACTCCCCTCTGACC    66377     C    TGA
                                GG CAGA   GAGTGAGAC
                                || ||||   |||||||||
                                CC GTCT   CTCACTCTG
                                 A    CCC
GAM1008  SERPINB9  3'  GTGCCTCACTCTGTC       14760     G       A
                                GAT AGAGTGAG CAC
                                ||| |||||||| |||
                                CTG TCTCACTC GTG
                                  _       C
GAM1008  SIAH2     3'  GTGTCCCATCTGGCT        17374          AGAGTGA
                                GGCCAGATG      GACAC
                                |||||||||      |||||
                                TCGGTCTAC      CTGTG
                                     C_______
GAM1008  ADAMTSL1  3'  GCAGTGTCTCACTGGTTGTAGC 53502     CA_   GAG        C
            T                    GGC   GAT   AGTGAGACAC GC
                                 |||   |||   |||||||||| ||
                                 TCG   TTG   TCACTCTGTG CG
                                   ATG   G__         A
GAM1008  BTBD2     3'  GCAGTGTCCGTTCTCATCCACC 35106    CCA        A    C
                                GG   GATGAGAGTG GACAC GC
                                ||   |||||||||| ||||| ||
                                CC   CTACTCTTGC CTGTG CG
                                 AC_         _     A
GAM1008  C14orf4   5'  GCGGTGCTGGCGGCCCCGTCTG 67337          AGA__  G  A
            GCC                    GGCCAGATG    GT AG CACCGC
                                   |||||||||    || || ||||||
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                                CCGGTCTGC    CG TC GTGGCG
                                     CCCGG  G  _
GAM1008 CRSP3    3' GCAGGTTGACACTCTCACCTG 60635    A      AGAC  _
                                CAG TGAGAGTG   ACC GC
                                ||| ||||||||   ||| ||
                                GTC ACTCTCAC   TGG CG
                                  C       AGT_  A
GAM1008 FLJ10713 3' GTGTCTCACTGTTGCCCAGGC 36470    AGAT_ G
                                GCC    GA AGTGAGACAC
                                |||    || ||||||||||
                                CGG    TT TCACTCTGTG
                                  ACCCG  G
GAM1008 FLJ12806 3' CGTGTCAGTACCTGGCC    43086      ATGAGA  A_   C
                                GGCCAG    GTG  GACAC G
                                ||||||    |||  ||||| |
                                CCGGTC    CAT  CTGTG C
                                   _______  GA    A
GAM1008 FLJ14327 3' GCGGTACTTCTCTGCATCTGGC 46141        _   T  AC
             C                   GGCCAGATG AGAG GAG  ACCGC
                                ||||||||| |||| |||  |||||
                                CCGGTCTAC TCTC TTC  TGGCG
                                     G   _  A_
GAM1008 FLJ23499 3' CGGTGCCATTGCTCTCCAGCC  42820    CAGAT    TG GA_
                                GGC    GAGAG  A   CACCG
                                |||    |||||  |   |||||
                                CCG    CTCTC  T   GTGGC
                                  AC___    GT ACC
GAM1008 FLJ32894 3' GCAGTGTCTCACTCTGTTGTCC 58340    C   ATG        C
                                GG CAG   AGAGTGAGACAC GC
                                || |||   |||||||||||| ||
                                CC GTT   TCTCACTCTGTG CG
                                 T  G__         A
GAM1008 KCNT1    3' CGATGCTTCTCATCTACC    61831    CC      GTG  A  C
                                GG  AGATGAGA   AG CA CG
                                ||  ||||||||   || || ||
                                CC  TCTACTCT   TC GT GC
                                 A_       ___ _  A
GAM1008 KIAA1320 5' GTATCTCACTCTTTC      69307    T       C
                                GA GAGAGTGAGA AC
                                || ||||||||| ||
                                CT TTCTCACTCT TG
                                 _        A
GAM1008 MGC33345 3' CGGTGGCCCCTGCATCTGGCC  58275        AG  TGAGA
                                GGCCAGATG  AG    CACCG
                                |||||||||  ||    |||||
                                CCGGTCTAC  TC    GTGGC
                                     G_  CCCG_
GAM1008 NMU2R    5' CTCACTCTCTCCCAGCC     39400     CA_  T
                                GGC   GA GAGAGTGAG
                                |||   || |||||||||
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                                CCG   CT CTCTCACTC
                                  ACC  _
GAM1008  phospho1  3'  CGGTGTCTCCTTGCATCCCAGC 82370     CA_   AG  T
              C                    GGC   GATG  AG GAGACACCG
                                   |||   ||||  || |||||||||
                                   CCG   CTAC  TC CTCTGTGGC
                                     ACC    GT  _
GAM1008  SLC26A10  5'  GCGGTGTCTGCCTCCCTGGCC  56031       AT   A  G
                                   GGCCAG  GAG GT AGACACCGC
                                   ||||||  ||| || |||||||||
                                   CCGGTC  CTC CG TCTGTGGCG
                                      C_  _ _
GAM1008  LOC151031 5'  GTCTCATCCCATCCGGCC    87190      A    A  G
                                   GGCC GATG GA TGAGAC
                                   |||| |||| || ||||||
                                   CCGG CTAC CT ACTCTG
                                     C   C  _
GAM1008  LOC163231 3'  TGTTCACTCTCACCAGCC    82447     CAGA        A
                                   GGC    TGAGAGTGAG CA
                                   |||    |||||||||| ||
                                   CCG    ACTCTCACTT GT
                                     ACC_         _
GAM1008  LOC201616 3'  TCCACTCTCATCTGCC      90233     C          A
                                   GGC AGATGAGAGTG GA
                                   ||| |||||||||| ||
                                   CCG TCTACTCTCAC CT
                                     _          _
GAM1008  LOC204084 3'  CGGTGTCTCAAGAATTCGGCC  89445      AG  GAGAG
                                   GGCC  AT    TGAGACACCG
                                   ||||  ||    ||||||||||
                                   CCGG  TA    ACTCTGTGGC
                                     CT  AGA__
GAM1008  LOC222224 5'  GTCTCACTCTGTTACC      94201    CCA   G
                                   GG   GAT AGAGTGAGAC
                                   ||   ||| ||||||||||
                                   CC   TTG TCTCACTCTG
                                    A__   _
GAM1008  LOC253264 3'  TGTTTTACTCCTCTGACC    94692    C    TGA
                                   GG CAGA   GAGTGAGACA
                                   || ||||   ||||||||||
                                   CC GTCT   CTCATTTTGT
                                    A    C__
GAM1008  LOC255452 3'  CGGTGTCTCACTGCGGCC    97530      AGAT AG
                                   GGCC    G  AGTGAGACACCG
                                   ||||    |  ||||||||||||
                                   CCGG    C  TCACTCTGTGGC
                                     _____ G_
GAM1008  LOC90485  3'  CGGTGCCTGGCCAGCTGGCC   63013       A  AGA  G  A
                                   GGCCAG TG   GT AG CACCG
                                   |||||| ||   || || |||||
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                                CCGGTC AC   CG TC GTGGC
                                   G ___  G  C
GAM1009 AGL     5' CCAGCTGCCTCGGCGCT    5345    A    GA
                                AG TGCTG  GCAGCTGG
                                || |||||  ||||||||
                                TC GCGGC  CGTCGACC
                                 _    TC
GAM1009 ARCN1   3' CCAGCTGCTCCTTTATT    7976      CT
                                GATG  GGAGCAGCTGG
                                ||||  ||||||||||
                                TTAT  CCTCGTCGACC
                                  TT
GAM1009 ATRN    3' TCCGTGTTCCAGCATCT    57804          GC
                                AGATGCTGGAGCA  TGGA
                                ||||||||||||  ||||
                                TCTACGACCTTGT  GCCT
                                              __
GAM1009 BCL11A  3' CCTACATTCCAGCATCTT   43162          CAGCT
                                AAGATGCTGGAG    GG
                                ||||||||||||    ||
                                TTCTACGACCTT    CC
                                      ACAT_
GAM1009 CACNA2D3 3' GTCCAACCATCAGCATCTCATC 37255   CA       AGCAGC
                                GA  AGATGCTGG     TGGAC
                                ||  |||||||||     |||||
                                CT  TCTACGACT     ACCTG
                                 AC        ACCA__
GAM1009 CDC25A  3' TCGGGCTCCAGCATCT     8366          AG
                                AGATGCTGGAGC  CTGG
                                ||||||||||||  ||||
                                TCTACGACCTCG  GGCT
                                              __
GAM1009 CLDN5   3' GTCTCACTCCAGCATCT    12346          CAGCT
                                AGATGCTGGAG    GGAC
                                ||||||||||    ||||
                                TCTACGACCTC    TCTG
                                      AC___
GAM1009 CST3    5' TCTAGCTCCAGCCTCT     3645     T      AGC
                                AGA GCTGGAGC   TGGA
                                ||| ||||||||   ||||
                                TCT CGACCTCG   ATCT
                                  C       ___
GAM1009 CSTA    5' CTTTGGTTCCAGCATCCTGTC  17806     A        AGCT
                                GACA GATGCTGGAGC    GG
                                |||| ||||||||||    ||
                                CTGT CTACGACCTTG    TC
                                  C         GTT_
GAM1009 DDX11   3' TCCAGCTGTGCACTTTG    47663     A   TGGA
                                CAAG TGC    GCAGCTGGA
                                |||| |||    |||||||||
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                                GTTT ACG   TGTCGACCT
                                  C  ____
GAM1009 DLEC1    3' TCCAGCTGCCTCGTTGTC   23707     GATGC GA
                                GACAA   TG GCAGCTGGA
                                |||||   || |||||||||
                                CTGTT   GC CGTCGACCT
                                  _____ TC
GAM1009 FBN2     3' TCCAGCTGATACACACCTGATC 8848    CA A C GAG
                                GA AG TG TG  CAGCTGGA
                                || || || ||  ||||||||
                                CT TC AC AC  GTCGACCT
                                 AG C _ ATA
GAM1009 ISL1     5' CCACAGCTCCAGCATC     9363         AGC
                                GATGCTGGAGC  TGG
                                ||||||||||  |||
                                CTACGACCTCG  ACC
                                      AC_
GAM1009 MEN1     5' TCCCCTCCAGCACCTTTC   93380  C  A     CAGCT
                                A AAG TGCTGGAG   GGA
                                | ||| ||||||||   |||
                                C TTC ACGACCTC   CCT
                                 T  C      C____
GAM1009 MXI1     3' CCAGCTGCCACCTCTCCATC  55260    CT__ A_
                                GATG   GG GCAGCTGG
                                ||||   || ||||||||
                                CTAC   CC CGTCGACC
                                  CTCT AC
GAM1009 MXI1     3' CCAGCTGCCACCTCTCCATC  19899    CT__ A_
                                GATG   GG GCAGCTGG
                                ||||   || ||||||||
                                CTAC   CC CGTCGACC
                                  CTCT AC
GAM1009 PIK3R3   3' TTTAGGCTTCAGCATCT    61067        AG
                                AGATGCTGGAGC CTGGA
                                |||||||||||| |||||
                                TCTACGACTTCG GATTT
                                          __
GAM1009 ROM1     5' GCTGACTCAGCATCCTG    4383    A     AG
                                CA GATGCTGG CAGC
                                || |||||||| ||||
                                GT CTACGACT GTCG
                                 C      CA
GAM1009 SERPINI1 5' GCTCCAGCATCCCGTC     17232    AA
                                GAC GATGCTGGAGC
                                ||| ||||||||||
                                CTG CTACGACCTCG
                                  CC
GAM1009 SLC16A2  3' CCAGTCCAGCTCTTATC    21501   C   T   AGCA
                                GA AAGA GCTGG   GCTGG
                                || |||| |||||   |||||
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                                CT TTCT CGACC    TGACC
                                 A   _    ____
GAM1009 SMARCD3  3' GTCCCGGGCCCCAGCATTTTG 11831          A  AGCT
                                CAAGATGCTGG GC    GGAC
                                |||||||||| ||    ||||
                                GTTTTACGACC CG    CCTG
                                      C  GGC_
GAM1009 SORCS2   3' GCCACCCCAGCATCTGTC    40418      A       AGCA
                                GACA GATGCTGG    GC
                                |||| ||||||||    ||
                                CTGT CTACGACC    CG
                                  _       CCAC
GAM1009 SPN      3' CCAGCCTCCAGCACCTT     11919     A       CA
                                AAG TGCTGGAG  GCTGG
                                ||| ||||||||  |||||
                                TTC ACGACCTC  CGACC
                                  C       __
GAM1009 TAGLN    3' CCAGCCTGCCCCCTATC     59633      CT  A   _
                                GATG  GG GCAG CTGG
                                ||||  || |||| ||||
                                CTAT  CC CGTC GACC
                                   CC  _    C
GAM1009 TIMP2    3' GTCCAGCTCTGACATC      94436      CT    AGC
                                GATG  GGAGC   TGGAC
                                ||||  |||||   |||||
                                CTAC  TCTCG   ACCTG
                                  AG    ___
GAM1009 USP11    5' CCAGGACTCCAGCACCTT    16202     A       CAG
                                AAG TGCTGGAG   CTGG
                                ||| ||||||||   ||||
                                TTC ACGACCTC   GACC
                                  C       AG_
GAM1009 VAT1     5' TCCAGCTGTGCGCTCTCGTC  21049     A   T  TGGA
                                GAC AGA GC    GCAGCTGGA
                                ||| ||| ||    |||||||||
                                CTG TCT CG    TGTCGACCT
                                  C   _ CG__
GAM1009 XPC      3' TCTGGCTCCAGCCCTTGTC   16139       AT     GCA  TG
                                GACAAG  GCTGGA   GC  GA
                                ||||||  ||||||   ||  ||
                                CTGTTC  CGACCT   CG  CT
                                   C_     ___  GT
GAM1009 C20orf140 3' CAGAAGCTCCAGCATTT     58243           AG
                                AGATGCTGGAGC  CTG
                                ||||||||||||  |||
                                TTTACGACCTCG  GAC
                                      AA
GAM1009 C20orf55  5' GTCCAGCTGCCTACTTTCT   48661     TGC   A
                                AGA   TGG GCAGCTGGAC
                                |||   ||| ||||||||||
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                                TCT   ATC CGTCGACCTG
                                  TTC   _
GAM1009  CGB7     5'  GTCCAGCTCACTCCAGCATC   52472          C_
                                GATGCTGGAG  AGCTGGAC
                                ||||||||||  ||||||||
                                CTACGACCTC  TCGACCTG
                                      AC
GAM1009  CRA      3'  GTTAACTGCTCCAACTCTTGTC 21975        TGC       CTG
                                GACAAGA   TGGAGCAG   GAC
                                |||||||   ||||||||   |||
                                CTGTTCT   ACCTCGTC   TTG
                                    CA_       AA_
GAM1009  DDX12    3'  CCAGCTGTTTGCATCCTGC    59695    A  A     TG
                                G CA GATGC  GAGCAGCTGG
                                | || |||||  ||||||||||
                                C GT CTACG  TTTGTCGACC
                                _ C     __
GAM1009  DKFZp434I099 5'  TCCAGCTGCGCTACCACT    50084    A  C   A
                                AG TG TGG GCAGCTGGA
                                || || ||| |||||||||
                                TC AC ATC CGTCGACCT
                                  _ C   G
GAM1009  DKFZP434O047 5'  CCAGATGGCAGCATCT      31510         GAG  G
                                AGATGCTG   CA CTGG
                                ||||||||   || ||||
                                TCTACGAC   GT GACC
                                     G__  A
GAM1009  DKFZP761I2123 3'  CCAGCCTGCTTCTTGTC     48759        TGCTGG    _
                                GACAAGA     AGCAG CTGG
                                |||||||     ||||| ||||
                                CTGTTCT     TCGTC GACC
                                    _______    C
GAM1009  FLJ10079  3'  CCTCCTCCCCATCATCTTGTC  60201         C   AGC  CT
                                GACAAGATG TGG   AG  GG
                                ||||||||| |||   ||  ||
                                CTGTTCTAC ACC   TC  CC
                                      T   CC_  CT
GAM1009  FLJ10110  5'  CCCTCCAGCGTCCTGTC     35820      A        CAGCT
                                GACA GATGCTGGAG     GG
                                |||| ||||||||||     ||
                                CTGT CTGCGACCTC     CC
                                  C         _____
GAM1009  FLJ11783  5'  TCCCTTCCAGCACCTTG     46032      A       CAGCT
                                CAAG TGCTGGAG     GGA
                                |||| ||||||||     |||
                                GTTC ACGACCTT     CCT
                                  C       C____
GAM1009  FLJ12650  3'  TCTTCGCCCAGCATCCTG    44530    A       A  AGCT
                                CA GATGCTGG GC    GGA
                                || |||||||| ||    |||
```

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                                GT CTACGACC CG    TCT
                                 C       _ CT__
GAM1009  FLJ12788  3'  TTGGGCTCCAGCATCTGTC   42552      A         AG TG
                                GACA GATGCTGGAGC  C  G
                                |||| ||||||||||  |  |
                                CTGT CTACGACCTCG  G  T
                                  _         __ GT
GAM1009  FLJ14327  3'  GCCCTCCAGCATCTGTC     46139      A         CA
                                GACA GATGCTGGAG  GC
                                |||| ||||||||||  ||
                                CTGT CTACGACCTC  CG
                                  _         C_
GAM1009  FLJ20277  3'  TCCCCTGCTCCAACACCCCGTT 34836     AAGA  C       CT
                                GAC    TG TGGAGCAG  GGA
                                |||    || ||||||||  |||
                                TTG    AC ACCTCGTC  CCT
                                  CCCC  A       C_
GAM1009  FLJ22362  3'  CCAGCTGCCCCACATCTTG   43072        C   A
                                CAAGATG TGG GCAGCTGG
                                ||||||| ||| ||||||||
                                GTTCTAC ACC CGTCGACC
                                    _  C
GAM1009  FLJ22530  3'  CCAGCCTCAGATCCTGTC    60345      A   G   G  CA
                                GACA GAT CTG AG  GCTGG
                                |||| ||| ||| ||  |||||
                                CTGT CTA GAC TC  CGACC
                                  C  _  _ __
GAM1009  KIAA0445  5'  CCAGCCCAGCATCT        27952          AGCA
                                AGATGCTGG    GCTGG
                                |||||||||    |||||
                                TCTACGACC    CGACC

                                     _____
GAM1009  KIAA0773  3'  CCAGGCTTCAGCATCT      28049            AG
                                AGATGCTGGAGC  CTGG
                                ||||||||||||  ||||
                                TCTACGACTTCG  GACC
                                     __
GAM1009  KIAA1548  3'  CTCTCCAGCATTCCGTC     40502     AA        C
                                GAC  GATGCTGGAG AG
                                |||  |||||||||| ||
                                CTG  TTACGACCTC TC
                                  CC         _
GAM1009  KIAA1655  3'  TCCAGCTGCCTCAGCCTC    66630    T   GA
                                GA GCTG  GCAGCTGGA
                                || ||||  |||||||||
                                CT CGAC  CGTCGACCT
                                 C    TC
GAM1009  KIAA1872  3'  CCAGCTGCCACGATTTGTC    62925       A  C  GA
                                GACAAG TG TG  GCAGCTGG
                                ||||||  || ||  ||||||||
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                                CTGTTT GC AC  CGTCGACC
                                   A  _ ___
GAM1009  KIAA1909  5'  GTCCAGCTGCCCCTGCCGTCT  73840      _ T  A
                                AGATG C GG GCAGCTGGAC
                                ||||| | || ||||||||||
                                TCTGC G CC CGTCGACCTG
                                   C T  C
GAM1009  KPNA6    3'  CCAGCTGCCTGCATT       24603       T  A
                                GATGC GG GCAGCTGG
                                ||||| || ||||||||
                                TTACG TC CGTCGACC
                                   _  _
GAM1009  MGC4707  3'  CCAGCCTCCTCTCCAGCACCTT 44118      A       CA___
              G                  CAAG TGCTGGAG    GCTGG
                                |||| ||||||||    |||||
                                GTTC ACGACCTC    CGACC
                                   C       TCCTC
GAM1009  MGC5356  5'  TCTTCCTCCAGCATCTTCC   43931   C         CAGCT
                                A AAGATGCTGGAG    GGA
                                | ||||||||||||    |||
                                C TTCTACGACCTC    TCT
                                 C          CT___
GAM1009  MMP24    3'  CCAGCTGCCAGCCTTCTGTC   21941     AG T   GA
                                GACA  A GCTG  GCAGCTGG
                                ||||  | ||||  ||||||||
                                CTGT  T CGAC  CGTCGACC
                                   CT C   __
GAM1009  PP1665   3'  GTGGGCTCCAGCCCCTTGTC   47921       AT      A_
                                GACAAG  GCTGGAGC  GC
                                ||||||  ||||||||  ||
                                CTGTTC  CGACCTCG  TG
                                    CC       GG
GAM1009  SES2     3'  CCATCCCAGTATCTCATC    48807    CA       AGCAGC
                                GA  AGATGCTGG     TGG
                                ||  |||||||||     |||
                                CT  TCTATGACC     ACC
                                 AC        CT_____
GAM1009  SIAT4A   3'  TCCAGCCCCAGCATCTTG    11676          AGCA
                                CAAGATGCTGG    GCTGGA
                                ||||||||||    ||||||
                                GTTCTACGACC    CGACCT
                                       C___
GAM1009  SLC2A10  3'  CCATCTCCAGCATCCTG     47819    A       CAGC
                                CA GATGCTGGAG    TGG
                                || ||||||||||    |||
                                GT CTACGACCTC    ACC
                                 C         T___
GAM1009  ST7L     3'  GTCCAGCTGCTCCATCG     34859    C
                                TG TGGAGCAGCTGGAC
                                || ||||||||||||||
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                                GC ACCTCGTCGACCTG
                                 T
GAM1009  ST7L     3'  GTCCAGCTGCTCCATCG     57003    C
                                TG TGGAGCAGCTGGAC
                                || ||||||||||||||
                                GC ACCTCGTCGACCTG
                                 T
GAM1009  ST7L     3'  GTCCAGCTGCTCCATCG     57580    C
                                TG TGGAGCAGCTGGAC
                                || ||||||||||||||
                                GC ACCTCGTCGACCTG
                                 T
GAM1009  STRAIT11499 5'  GTCCAGCTGCTCCAATC     41147     GC
                                GAT  TGGAGCAGCTGGAC
                                |||  ||||||||||||||
                                CTA  ACCTCGTCGACCTG
                                  __
GAM1009  TPD52    3'  CCAAGCACATCTTGTC      17426         CTGGAGCA  _
                                GACAAGATG       GCT GG
                                |||||||||       ||| ||
                                CTGTTCTAC       CGA CC
                                     A________   A
GAM1009  UBCE7IP5  3'  GCCTCTCCAGAATCTTGTC   30156         G     CA
                                GACAAGAT CTGGAG  GC
                                |||||||| ||||||  ||
                                CTGTTCTA GACCTC  CG
                                     A     TC
GAM1009  UBF-fl   3'  CCAGCCACTGTTAGTGTC    51556         _  CA
                                GATGCTGG AG  GCTGG
                                |||||||| ||  |||||
                                CTGTGATT TC  CGACC
                                     G  AC
GAM1009  ZNF213   3'  CCAGCCACGGCACATCCTG   65093    A __    GAGCA
                                CA GA  TGCTG    GCTGG
                                || ||  |||||    |||||
                                GT CT  ACGGC    CGACC
                                 C  AC    AC___
GAM1009  LOC128954 5'  CCAGCTGCTCCCATC      75793      CT
                                GATG  GGAGCAGCTGG
                                ||||  ||||||||||
                                CTAC  CCTCGTCGACC
                                  __
GAM1009  LOC144165 5'  CCAGCTGCCAGCGCCGTC    76679     AAGA    GA
                                GAC   TGCTG  GCAGCTGG
                                |||   |||||  ||||||||
                                CTG   GCGAC  CGTCGACC
                                  CC__    __
GAM1009  LOC144373 3'  CCAGCTGTTTGCATCCTGC   76817   A  A    TG
                                G CA GATGC  GAGCAGCTGG
                                | || |||||  ||||||||||
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                                C GT CTACG  TTTGTCGACC
                                 _ C    __
GAM1009  LOC145501 3'  CCAGCTGCCCGTGTGCCT    77252    AT  _  A
                                AG  GC TGG GCAGCTGG
                                ||  || ||| ||||||||
                                TC  TG GCC CGTCGACC
                                 CG  T  _
GAM1009  LOC145676 5'  TTGCTCCAGCATCTTTC     77343    C
                                A AAGATGCTGGAGCAG
                                | ||||||||||||||
                                C TTCTACGACCTCGTT
                                 T
GAM1009  LOC146229 3'  TCCTACCCAGCATCTTTC    77777    C        AGCAGCT
                                A AAGATGCTGG      GGA
                                | ||||||||||      |||
                                C TTCTACGACC      CCT
                                 T        CAT____
GAM1009  LOC146712 5'  CCAGCTGCTCGGCTCCCTC    83715    CAA  T    G
                                GA   GA GCTG AGCAGCTGG
                                ||   || |||| |||||||||
                                CT   CT CGGC TCGTCGACC
                                 CC_ _   _
GAM1009  LOC147807 3'  GTCCAGCTGCCTTCAGC     84076        _
                                GCTGGAG CAGCTGGAC
                                ||||||| |||||||||
                                CGACTTC GTCGACCTG
                                     C
GAM1009  LOC148709 5'  CCAGCTACTGCTTCACCA    78937    C      ___
                                TG TGGAGCA   GCTGG
                                || |||||||   |||||
                                AC ACTTCGT   CGACC
                                 C      CAT
GAM1009  LOC149426 3'  CCAGCTGCCCCTGGCCTCT    84414     T  _  A
                                AGA GCT GG GCAGCTGG
                                ||| ||| || ||||||||
                                TCT CGG CC CGTCGACC
                                  C   T  C
GAM1009  LOC149461 3'  CCCCTTGCCCAGCATC      79399        A    CT
                                GATGCTGG GCAG  GG
                                |||||||| ||||  ||
                                CTACGACC CGTT  CC
                                     _   CC
GAM1009  LOC149579 5'  CCAGCCCAGCATCT       71132         AGCA
                                AGATGCTGG    GCTGG
                                |||||||||    |||||
                                TCTACGACC    CGACC
                                      ____
GAM1009  LOC149935 5'  CCAGCTGCTGTCTGGATC    60296     G TG  __
                                GAT C  GA  GCAGCTGG
                                ||| |  ||  ||||||||
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                                CTA G  CT  CGTCGACC
                                  _ GT  GT
GAM1009  LOC150245 3'  GTCCAGCTGCTCCGGCTC    84938    T
                                GA GCTGGAGCAGCTGGAC
                                || ||||||||||||||||
                                CT CGGCCTCGTCGACCTG
                                 _
GAM1009  LOC151512 5'  CCTGCCTCCAGCATCT      85428          CA  T
                                AGATGCTGGAG  GC GG
                                ||||||||||  || ||
                                TCTACGACCTC  CG CC
                                       __ T
GAM1009  LOC153346 5'  CCAGCTGCTGACCTTGTT    86021       ATGCTGG
                                GACAAG      AGCAGCTGG
                                ||||||      |||||||||
                                TTGTTC      TCGTCGACC
                                   CAG____
GAM1009  LOC154313 5'  CCAACTGCTCCGACCGTC    81062     C_      C
                                GATG  TGGAGCAG TGG
                                ||||  |||||||| |||
                                CTGC  GCCTCGTC ACC
                                  CA       A
GAM1009  LOC158434 5'  CCTCCTGCTCCAGCTC      86821    T        CT
                                GA GCTGGAGCAG  GG
                                || ||||||||||  ||
                                CT CGACCTCGTC  CC
                                 _         CT
GAM1009  LOC196985 5'  CCAGCTGCCTTTGTGATC    89661     _ T_  A
                                GAT GC  GG GCAGCTGG
                                ||| ||  || ||||||||
                                CTA TG  TC CGTCGACC
                                  G  TT  _
GAM1009  LOC196986 5'  CCAGCTGCCTTTGTGATC    89656     _ T_  A
                                GAT GC  GG GCAGCTGG
                                ||| ||  || ||||||||
                                CTA TG  TC CGTCGACC
                                  G  TT  _
GAM1009  LOC199986 5'  CCGAAGCTCCAGCACCT     89903    A       AGC
                                AG TGCTGGAGC   TGG
                                || |||||||||   |||
                                TC ACGACCTCG   GCC
                                 C        AA_
GAM1009  LOC220021 3'  CCACTCTCCAGCATCT      93392          C  C
                                AGATGCTGGAG AG TGG
                                |||||||||| || |||
                                TCTACGACCTC TC ACC
                                       _ _
GAM1009  LOC220739 3'  GCTTCACTCCAGCACCCTGTC  92933      AGA       C__
                                GACA   TGCTGGAG   AGC
                                ||||   ||||||||   |||
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                                CTGT   ACGACCTC   TCG
                                  CCC       ACT
GAM1009  LOC220824 5'  CCAGCTGCCAGATCTGCGTC   90805    A_   G   GA
                                GAC  AGAT CTG  GCAGCTGG
                                |||  |||| |||  ||||||||
                                CTG  TCTA GAC  CGTCGACC
                                  CG   _  __
GAM1009  LOC221927 5'  CCAGCTGCTCCCGGCTCT    92648    T    _
                                AGA GCTGG AGCAGCTGG
                                ||| ||||| |||||||||
                                TCT CGGCC TCGTCGACC
                                  _    C
GAM1009  LOC254439 3'  CCAACTGCCCTTCTTGTC    94744       TGCT  A   C
                                GACAAGA    GG GCAG TGG
                                |||||||    || |||| |||
                                CTGTTCT    CC CGTC ACC
                                    T___  _   A
GAM1009  LOC255170 3'  CCAGCTGCCACCCCTATCT   97517      CT  A_
                                AGATG  GG  GCAGCTGG
                                |||||  ||  ||||||||
                                TCTAT  CC  CGTCGACC
                                   CC  AC
GAM1009  LOC256158 5'  TCCAGCTGCTCCCAGGC     97682     __
                                GCT  GGAGCAGCTGGA
                                |||  ||||||||||||
                                CGG  CCTCGTCGACCT
                                  AC
GAM1009  LOC56961  5'  GTCCAGCTGCCGCGGCCTC   62910    T   GA
                                GA GCTG  GCAGCTGGAC
                                || ||||  ||||||||||
                                CT CGGC  CGTCGACCTG
                                 C   GC
GAM1009  LOC89919  3'  AGCCACCCCAGCATCCTGC   60715   A  A      AGCA
                                G CA GATGCTGG    GCT
                                | || ||||||||    |||
                                C GT CTACGACC    CGA
                                 _ C       CCAC
GAM1009  LOC91301  5'  GTCCAGCTGCCTGGTCTTTGTC 65546       AT  TG A
                                GACAAG  GC  G GCAGCTGGAC
                                ||||||  ||  | ||||||||||
                                CTGTTT  TG  C CGTCGACCTG
                                   C_  GT _
GAM1009  LOC91974  5'  GTCCAGCTGCTAAGATC     67758     G  GG
                                GAT CT  AGCAGCTGGAC
                                ||| ||  ||||||||||
                                CTA GA  TCGTCGACCTG
                                  _  A_
GAM1009  LOC92080  3'  CCGACTCAGCATCCTGTC    68044      A      GAGC  C
                                GACA GATGCTG    AG TGG
                                |||| |||||||    || |||
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                                CTGT CTACGAC    TC GCC
                                  C      _____  A
GAM1010 ACT      5'  CAGGAAGAAGCGGCTTTAA   40040         CAACGG  C
                                TTAAAGCTGC     CT CCTG
                                ||||||||||     || ||||
                                AATTTCGGCG     GA GGAC
                                     AA_____  A
GAM1010 ATP11A   3'  AGGCCACGCCGGCAGCTT    77017         AAC   TC__
                                AAGCTGCC   GGC    CCT
                                ||||||||   |||    |||
                                TTCGACGG   CCG    GGA
                                     ___   CACC
GAM1010 CLASP2   3'  CAGGAATGCTTAAAGCTTTAA  64592         GCCAAC   TC_
                                TTAAAGCT     GGC   CCTG
                                ||||||||     |||   ||||
                                AATTTCGA     TCG   GGAC
                                     AAT___   TAA
GAM1010 LTB4R    3'  GCTCCCACAGGCAGCTTTAA   5648          AAC___
                                TTAAAGCTGCC     GGC
                                ||||||||||      |||
                                AATTTCGACGG     TCG
                                      ACACCC
GAM1010 POU3F1   3'  GCAGGAAATAGCCAAAGCTTTA 59310         GCCAAC    C___
              A                  TTAAAGCT     GGCT    CCTGC
                                 ||||||||     ||||    |||||
                                 AATTTCGA     CCGA    GGACG
                                      AA_____    TAAA
GAM1010 RAP1B    3'  CAGGGAGCCACAGTATTTAA   31598       _   CCAAC
                                TTAAA GCTG     GGCTCCCTG
                                ||||| ||||     |||||||||
                                AATTT TGAC     CCGAGGGAC
                                   A    A_____
GAM1010 RBBP2    3'  GCAAGGAGCCGTTTTTTGGCTT 17323         CC_       C
              TGA                   TTAAAGCTG   AACGGCTCC TGC
                                    |||||||||   ||||||||| |||
                                    AGTTTCGGT   TTGCCGAGG ACG
                                         TTT        A
GAM1010 SLC21A9  3'  CAGGGAGCCACCAGCAGT    23418       CAAC
                                GCTGC    GGCTCCCTG
                                |||||    |||||||||
                                TGACG    CCGAGGGAC
                                   ACCA
GAM1010 UCP2     5'  AGCCACTGGCAGCTTTGA     12531           AC
                                TTAAAGCTGCCA  GGCT
                                ||||||||||||  ||||
                                AGTTTCGACGGT  CCGA
                                       CA
GAM1010 CDC42BPB 3'  CAGAAGACGGCAGTTTTAA   20099          AACGG  CC
                                TTAAAGCTGCC    CT  CTG
                                ||||||||||     ||  |||
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                                AATTTTGACGG    GA  GAC
                                      CA___  A_
GAM1010  CLDN4    3'  GCAGGGAGGAGGGGACAGCTT  7137       _  AACGG
                                AAGCTG CC    CTCCCTGC
                                |||||| ||    ||||||||
                                TTCGAC GG    GAGGGACG
                                   A  GGAG_
GAM1010  CXYorf1  3'  CAGGGAGCCACCGGTCGC    82038    T   AAC
                                GC GCC   GGCTCCCTG
                                || |||   |||||||||
                                CG TGG   CCGAGGGAC
                                 C   CCA
GAM1010  DKFZP434J193 3'  CAGAAGCCTGGCAGCT      71001        AC    CC
                                AGCTGCCA  GGCT  CTG
                                ||||||||  ||||  |||
                                TCGACGGT  CCGA  GAC
                                     __    A_
GAM1010  DKFZp586H0623 3'  CAGGGAGCAGAGACTGCTTTAA 34066        TGCCAACG
                                TTAAAGC       GCTCCCTG
                                |||||||       ||||||||
                                AATTTCG       CGAGGGAC
                                    TCAGAGA_
GAM1010  FLJ20034  3'  CAGGGAGCCCGGTCAGCT    34362      _  AAC
                                AGCTG CC   GGCTCCCTG
                                ||||| ||   |||||||||
                                TCGAC GG   CCGAGGGAC
                                   T  C__
GAM1010  FLJ22031  3'  CAGGGAGACAGCTTTAG     46886         CCAACGG
                                TTAAAGCTG      CTCCCTG
                                |||||||||      |||||||
                                GATTTCGAC      GAGGGAC
                                     A_______
GAM1010  GOLPH2   3'  GCAAAGTAGCAACAGCTTTAA  33322         CCAACG   CCC_
                                TTAAAGCTG     GCT    TGC
                                |||||||||     |||    |||
                                AATTTCGAC     CGA    ACG
                                     AA_____   TGAA
GAM1010  GPR      3'  GCAGGGAGCAGGAGC      23333     G  AACG
                                GCT CC    GCTCCCTGC
                                ||| ||    |||||||||
                                CGA GG    CGAGGGACG
                                  _  A___
GAM1010  KIAA0335 3'  GCAGTAGATGGGCAGCTT    28992        AACGG  CC
                                AAGCTGCC    CT  CTGC
                                ||||||||    ||  ||||
                                TTCGACGG    GA  GACG
                                     GTA__  T_
GAM1010  KIAA0355 3'  CAAGGGTGGTTGGCAGCT    28023          G  T  C
                                AGCTGCCAAC GC CC TG
                                |||||||||| || || ||
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                                TCGACGGTTG TG GG AC
                                      G _ A
GAM1010 KIAA1211 3' AGGGACTTGGCAGTTT     68890        AC  C
                                AAGCTGCCA  GG TCCCT
                                |||||||||  || |||||
                                TTTGACGGT  TC AGGGA
                                      __ _
GAM1010 MGC4251  3' CAGGGAGCCACTGAGGGT    50456    GC  AC
                                GCT  CA  GGCTCCCTG
                                |||  ||  |||||||||
                                TGG  GT  CCGAGGGAC
                                  GA  CA
GAM1010 SFRS10   5' GCAAGAGGTTGGCAGCTTCGA 15977   TA        GG   CC
                                T  AAGCTGCCAAC  CTC  TGC
                                |  ||||||||||  |||  |||
                                A  TTCGACGGTTG  GAG  ACG
                                 GC         __   A_
GAM1010 TFPT     5' AGAAAGACGTTGGCAACT    25318    C      G  CC
                                AG TGCCAACG CT  CT
                                || ||||||| ||  ||
                                TC ACGGTTGC GA  GA
                                 A       A  AA
GAM1010 LOC146669 5' CAGAGAGAGCAGCTTT      78054        CAACGG   C
                                AAAGCTGC     CTC CTG
                                ||||||||     ||| |||
                                TTTCGACG     GAG GAC
                                     A_____   A
GAM1010 LOC149076 3' GCAGAGGGGTGCGGCAGCTT  79153        AACG    _
                                AAGCTGCC    GCTCC CTGC
                                ||||||||    ||||| ||||
                                TTCGACGG    TGGGG GACG
                                     CG__     A
GAM1010 LOC151475 5' AGACATTGACAGCTTTAA    85388         C   CGG
                                TTAAAGCTG CAA   CT
                                ||||||||| |||   ||
                                AATTTCGAC GTT   GA
                                      A   ACA
GAM1010 LOC153416 3' CAGGGAGCCACAGTATTTAA  60539      _   CCAAC
                                TTAAA GCTG    GGCTCCCTG
                                ||||| ||||    |||||||||
                                AATTT TGAC    CCGAGGGAC
                                   A    A____
GAM1010 LOC153768 3' CCCCTGCACAGTGTTGGCAGCT 56714          G_______  TCCCT
             T                   AAGCTGCCAAC       GC    G
                                 ||||||||||       ||    |
                                 TTCGACGGTTG       CG    C
                                       TGACAIII  TCCCT
GAM1010 LOC51760  3' CAGGGAAGGCAGCTTT      33265         AACGGC
                                AAAGCTGCC     TCCCTG
                                |||||||||     ||||||
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                                TTTCGACGG     AGGGAC
                                     A_____
GAM1010 LOC91040 3' CAGGGAGCCACCGGTCGC    64709    T   AAC
                                GC GCC   GGCTCCCTG
                                || |||   |||||||||
                                CG TGG   CCGAGGGAC
                                 C   CCA
GAM1010 LOC92181 3' CAAAGAGCCAGGCTTTGA    68401        GCCAAC    CC
                                TTAAAGCT     GGCTC  TG
                                ||||||||     |||||  ||
                                AGTTTCGG     CCGAG  AC
                                     A_____     AA
GAM1011 ACT      5' CAGGAAGAAGCGGCTTTAA    40040         CAACGG  C
                                TTAAAGCTGC     CT CCTG
                                ||||||||||     || ||||
                                AATTTCGGCG     GA GGAC
                                      AA____  A
GAM1011 ATP11A   3' AGGCCACGCCGGCAGCTT    77017        AAC   TC__
                                AAGCTGCC   GGC    CCT
                                ||||||||   |||    |||
                                TTCGACGG   CCG    GGA
                                     ___   CACC
GAM1011 CLASP2   3' CAGGAATGCTTAAAGCTTTAA  64592        GCCAAC   TC_
                                TTAAAGCT     GGC   CCTG
                                ||||||||     |||   ||||
                                AATTTCGA     TCG   GGAC
                                     AAT___   TAA
GAM1011 LTB4R    3' GCTCCCACAGGCAGCTTTAA   5648          AAC___
                                TTAAAGCTGCC     GGC
                                ||||||||||     |||
                                AATTTCGACGG     TCG
                                      ACACCC
GAM1011 POU3F1   3' GCAGGAAATAGCCAAAGCTTTA 59310        GCCAAC    C___
            A                    TTAAAGCT     GGCT    CCTGC
                                ||||||||     ||||    |||||
                                AATTTCGA     CCGA    GGACG
                                     AA____    TAAA
GAM1011 RAP1B    3' CAGGGAGCCACAGTATTTAA   31598      _   CCAAC
                                TTAAA GCTG    GGCTCCCTG
                                ||||| ||||    |||||||||
                                AATTT TGAC    CCGAGGGAC
                                   A   A____
GAM1011 RBBP2    3' GCAAGGAGCCGTTTTTTGGCTT 17323        CC_       C
            TGA                   TTAAAGCTG   AACGGCTCC TGC
                                |||||||||   ||||||||| |||
                                AGTTTCGGT   TTGCCGAGG ACG
                                     TTT       A
GAM1011 SLC21A9  3' CAGGGAGCCACCAGCAGT    23418      CAAC
                                GCTGC    GGCTCCCTG
                                |||||    |||||||||
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                                TGACG   CCGAGGGAC
                                   ACCA
GAM1011 UCP2     5' AGCCACTGGCAGCTTTGA    12531          AC
                                TTAAAGCTGCCA GGCT
                                |||||||||||| ||||
                                AGTTTCGACGGT CCGA
                                       CA
GAM1011 CDC42BPB 3' CAGAAGACGGCAGTTTTAA   20099         AACGG CC
                                TTAAAGCTGCC    CT CTG
                                ||||||||||    || |||
                                AATTTTGACGG    GA GAC
                                      CA___ A_
GAM1011 CLDN4    3' GCAGGGAGGAGGGGACAGCTT 7137       _ AACGG
                                AAGCTG CC    CTCCCTGC
                                |||||| ||    ||||||||
                                TTCGAC GG    GAGGGACG
                                   A GGAG_
GAM1011 CXYorf1  3' CAGGGAGCCACCGGTCGC    82038    T  AAC
                                GC GCC   GGCTCCCTG
                                || |||   |||||||||
                                CG TGG   CCGAGGGAC
                                 C   CCA
GAM1011 DKFZP434J193 3' CAGAAGCCTGGCAGCT     71001        AC   CC
                                AGCTGCCA GGCT CTG
                                |||||||| |||| |||
                                TCGACGGT CCGA GAC
                                   __   A_
GAM1011 DKFZp586H0623 3' CAGGGAGCAGAGACTGCTTTAA 34066        TGCCAACG
                                TTAAAGC       GCTCCCTG
                                |||||||       ||||||||
                                AATTTCG       CGAGGGAC
                                    TCAGAGA_
GAM1011 FLJ20034 3' CAGGGAGCCCGGTCAGCT    34362      _ AAC
                                AGCTG CC   GGCTCCCTG
                                ||||| ||   |||||||||
                                TCGAC GG   CCGAGGGAC
                                   T  C__
GAM1011 FLJ22031 3' CAGGGAGACAGCTTTAG     46886         CCAACGG
                                TTAAAGCTG      CTCCCTG
                                |||||||||      |||||||
                                GATTTCGAC      GAGGGAC
                                     A_______
GAM1011 GOLPH2   3' GCAAAGTAGCAACAGCTTTAA 33322         CCAACG  CCC_
                                TTAAAGCTG     GCT   TGC
                                |||||||||     |||   |||
                                AATTTCGAC     CGA   ACG
                                     AA_____  TGAA
GAM1011 GPR      3' GCAGGGAGCAGGAGC      23333     G  AACG
                                GCT CC    GCTCCCTGC
                                ||| ||    |||||||||
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                                CGA GG   CGAGGGACG
                                  _ A___
GAM1011 KIAA0335 3' GCAGTAGATGGGCAGCTT   28992       AACGG CC
                                AAGCTGCC   CT CTGC
                                ||||||||   || ||||
                                TTCGACGG   GA GACG
                                    GTA__ T_
GAM1011 KIAA0355 3' CAAGGGTGGTTGGCAGCT   28023        G T C
                                AGCTGCCAAC GC CC TG
                                |||||||||| || || ||
                                TCGACGGTTG TG GG AC
                                     G _ A
GAM1011 KIAA1211 3' AGGGACTTGGCAGTTT     68890       AC C
                                AAGCTGCCA GG TCCCT
                                |||||||||  || |||||
                                TTTGACGGT TC AGGGA
                                    __ _
GAM1011 MGC4251  3' CAGGGAGCCACTGAGGGT   50456    GC AC
                                GCT CA GGCTCCCTG
                                |||  ||  |||||||||
                                TGG GT CCGAGGGAC
                                  GA CA
GAM1011 SFRS10   5' GCAAGAGGTTGGCAGCTTCGA 15977   TA       GG  CC
                                T AAGCTGCCAAC CTC TGC
                                | ||||||||||  |||  |||
                                A TTCGACGGTTG GAG ACG
                                 GC         __  A_
GAM1011 TFPT     5' AGAAAGACGTTGGCAACT   25318   C     G CC
                                AG TGCCAACG CT CT
                                || ||||||||  ||  ||
                                TC ACGGTTGC GA GA
                                 A      A AA
GAM1011 LOC146669 5' CAGAGAGAGCAGCTTT     78054       CAACGG  C
                                AAAGCTGC     CTC CTG
                                ||||||||     ||| |||
                                TTTCGACG     GAG GAC
                                    A_____  A
GAM1011 LOC149076 3' GCAGAGGGGTGCGGCAGCTT 79153       AACG   _
                                AAGCTGCC   GCTCC CTGC
                                ||||||||   ||||| ||||
                                TTCGACGG   TGGGG GACG
                                    CG__    A
GAM1011 LOC151475 5' AGACATTGACAGCTTTAA   85388       C  CGG
                                TTAAAGCTG CAA  CT
                                |||||||||  |||  ||
                                AATTTCGAC GTT  GA
                                     A  ACA
GAM1011 LOC153416 3' CAGGGAGCCACAGTATTTAA 60539     _  CCAAC
                                TTAAA GCTG   GGCTCCCTG
                                |||||  ||||   |||||||||
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                                AATTT TGAC    CCGAGGGAC
                                  A   A____
GAM1011 LOC153768 3' CCCCTGCACAGTGTTGGCAGCT 56714          G_______ TCCCT
             T                   AAGCTGCCAAC       GC    G
                                 ||||||||||        ||    |
                                 TTCGACGGTTG       CG    C
                                       TGACAIII  TCCCT
GAM1011 LOC51760 3' CAGGGAAGGCAGCTTT     33265        AACGGC
                                 AAAGCTGCC     TCCCTG
                                 |||||||||     ||||||
                                 TTTCGACGG     AGGGAC
                                       A_____
GAM1011 LOC91040 3' CAGGGAGCCACCGGTCGC    64709    T   AAC
                                 GC GCC   GGCTCCCTG
                                 || |||   |||||||||
                                 CG TGG   CCGAGGGAC
                                  C   CCA
GAM1011 LOC92181 3' CAAAGAGCCAGGCTTTGA    68401        GCCAAC    CC
                                 TTAAAGCT     GGCTC  TG
                                 ||||||||     |||||  ||
                                 AGTTTCGG     CCGAG  AC
                                      A_____    AA
GAM1012 ACT      5' CAGGAAGAAGCGGCTTTAA   40040        CAACGG  C
                                 TTAAAGCTGC     CT CCTG
                                 ||||||||||     || ||||
                                 AATTTCGGCG     GA GGAC
                                       AA____  A
GAM1012 ATP11A   3' AGGCCACGCCGGCAGCTT    77017        AAC   TC__
                                 AAGCTGCC   GGC    CCT
                                 ||||||||   |||    |||
                                 TTCGACGG   CCG    GGA
                                      ___   CACC
GAM1012 CLASP2   3' CAGGAATGCTTAAAGCTTTAA 64592        GCCAAC   TC_
                                 TTAAAGCT     GGC   CCTG
                                 ||||||||     |||   ||||
                                 AATTTCGA     TCG   GGAC
                                      AAT___   TAA
GAM1012 LTB4R    3' GCTCCCACAGGCAGCTTTAA   5648          AAC___
                                 TTAAAGCTGCC     GGC
                                 ||||||||||      |||
                                 AATTTCGACGG     TCG
                                       ACACCC
GAM1012 POU3F1   3' GCAGGAAATAGCCAAAGCTTTA 59310        GCCAAC    C___
             A                    TTAAAGCT     GGCT    CCTGC
                                  ||||||||     ||||    |||||
                                  AATTTCGA     CCGA    GGACG
                                       AA____    TAAA
GAM1012 RAP1B    3' CAGGGAGCCACAGTATTTAA   31598       _   CCAAC
                                 TTAAA GCTG    GGCTCCCTG
                                 ||||| ||||    |||||||||
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                                AATTT TGAC    CCGAGGGAC
                                  A   A____
GAM1012 RBBP2    3' GCAAGGAGCCGTTTTTTGGCTT 17323        CC_      C
           TGA                   TTAAAGCTG  AACGGCTCC TGC
                                 |||||||||  ||||||||| |||
                                 AGTTTCGGT  TTGCCGAGG ACG
                                     TTT       A
GAM1012 SLC21A9  3' CAGGGAGCCACCAGCAGT    23418      CAAC
                                 GCTGC   GGCTCCCTG
                                 ||||||  |||||||||
                                 TGACG   CCGAGGGAC
                                   ACCA
GAM1012 UCP2     5' AGCCACTGGCAGCTTTGA    12531          AC
                                 TTAAAGCTGCCA  GGCT
                                 ||||||||||||  ||||
                                 AGTTTCGACGGT  CCGA
                                       CA
GAM1012 CDC42BPB 3' CAGAAGACGGCAGTTTTAA   20099         AACGG  CC
                                 TTAAAGCTGCC    CT  CTG
                                 ||||||||||     ||  |||
                                 AATTTTGACGG    GA  GAC
                                       CA___  A_
GAM1012 CLDN4    3' GCAGGGAGGAGGGGACAGCTT  7137       _  AACGG
                                 AAGCTG CC    CTCCCTGC
                                 |||||| ||    ||||||||
                                 TTCGAC GG    GAGGGACG
                                    A  GGAG_
GAM1012 CXYorf1  3' CAGGGAGCCACCGGTCGC    82038    T   AAC
                                 GC GCC   GGCTCCCTG
                                 || |||   |||||||||
                                 CG TGG   CCGAGGGAC
                                  C   CCA
GAM1012 DKFZP434J193 3' CAGAAGCCTGGCAGCT      71001        AC    CC
                                 AGCTGCCA  GGCT  CTG
                                 ||||||||  ||||  |||
                                 TCGACGGT  CCGA  GAC
                                      __    A_
GAM1012 DKFZp586H0623 3' CAGGGAGCAGAGACTGCTTTAA 34066        TGCCAACG
                                 TTAAAGC       GCTCCCTG
                                 |||||||       ||||||||
                                 AATTTCG       CGAGGGAC
                                     TCAGAGA_
GAM1012 FLJ20034  3' CAGGGAGCCCGGTCAGCT    34362      _  AAC
                                 AGCTG CC   GGCTCCCTG
                                 ||||| ||   |||||||||
                                 TCGAC GG   CCGAGGGAC
                                   T  C__
GAM1012 FLJ22031  3' CAGGGAGACAGCTTTAG     46886         CCAACGG
                                 TTAAAGCTG      CTCCCTG
                                 |||||||||      |||||||
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                                GATTTCGAC      GAGGGAC
                                     A_______
GAM1012 GOLPH2   3' GCAAAGTAGCAACAGCTTTAA 33322        CCAACG  CCC_
                                TTAAAGCTG     GCT   TGC
                                |||||||||     |||   |||
                                AATTTCGAC     CGA   ACG
                                     AA____   TGAA
GAM1012 GPR      3' GCAGGGAGCAGGAGC      23333     G  AACG
                                GCT CC    GCTCCCTGC
                                ||| ||    |||||||||
                                CGA GG    CGAGGGACG
                                  _ A___
GAM1012 KIAA0335 3' GCAGTAGATGGGCAGCTT    28992        AACGG  CC
                                AAGCTGCC    CT  CTGC
                                ||||||||    ||  ||||
                                TTCGACGG    GA  GACG
                                     GTA__  T_
GAM1012 KIAA0355 3' CAAGGGTGGTTGGCAGCT    28023         G  T  C
                                AGCTGCCAAC GC CC TG
                                |||||||||| || || ||
                                TCGACGGTTG TG GG AC
                                      G  _  A
GAM1012 KIAA1211 3' AGGGACTTGGCAGTTT      68890         AC  C
                                AAGCTGCCA  GG TCCCT
                                |||||||||  || |||||
                                TTTGACGGT  TC AGGGA
                                           __  _
GAM1012 MGC4251  3' CAGGGAGCCACTGAGGGT    50456     GC  AC
                                GCT  CA  GGCTCCCTG
                                |||  ||  |||||||||
                                TGG  GT  CCGAGGGAC
                                  GA  CA
GAM1012 SFRS10   5' GCAAGAGGTTGGCAGCTTCGA 15977   TA        GG   CC
                                T  AAGCTGCCAAC  CTC  TGC
                                |  ||||||||||  |||  |||
                                A  TTCGACGGTTG  GAG  ACG
                                 GC          __   A_
GAM1012 TFPT     5' AGAAAGACGTTGGCAACT    25318    C      G  CC
                                AG TGCCAACG CT  CT
                                || ||||||| ||  ||
                                TC ACGGTTGC GA  GA
                                 A       A  AA
GAM1012 LOC146669 5' CAGAGAGAGCAGCTTT      78054         CAACGG   C
                                AAAGCTGC     CTC CTG
                                ||||||||     ||| |||
                                TTTCGACG     GAG GAC
                                     A_____   A
GAM1012 LOC149076 3' GCAGAGGGGTGCGGCAGCTT  79153         AACG    _
                                AAGCTGCC    GCTCC CTGC
                                ||||||||    ||||| ||||
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                                TTCGACGG    TGGGG GACG
                                     CG__     A
GAM1012  LOC151475 5'  AGACATTGACAGCTTTAA    85388         C   CGG
                                TTAAAGCTG CAA   CT
                                ||||||||| |||   ||
                                AATTTCGAC GTT   GA
                                     A   ACA
GAM1012  LOC153416 3'  CAGGGAGCCACAGTATTTAA   60539      _   CCAAC
                                TTAAA GCTG    GGCTCCCTG
                                ||||| ||||    |||||||||
                                AATTT TGAC    CCGAGGGAC
                                   A    A____
GAM1012  LOC153768 3'  CCCCTGCACAGTGTTGGCAGCT 56714          G________  TCCCT
              T                  AAGCTGCCAAC       GC     G
                                ||||||||||       ||    |
                                TTCGACGGTTG       CG    C
                                      TGACAIII  TCCCT
GAM1012  LOC51760  3'  CAGGGAAGGCAGCTTT      33265         AACGGC
                                AAAGCTGCC     TCCCTG
                                |||||||||     ||||||
                                TTTCGACGG     AGGGAC
                                     A_____
GAM1012  LOC91040  3'  CAGGGAGCCACCGGTCGC    64709    T   AAC
                                GC GCC   GGCTCCCTG
                                || |||   |||||||||
                                CG TGG   CCGAGGGAC
                                 C   CCA
GAM1012  LOC92181  3'  CAAAGAGCCAGGCTTTGA    68401        GCCAAC    CC
                                TTAAAGCT     GGCTC  TG
                                ||||||||     |||||  ||
                                AGTTTCGG     CCGAG  AC
                                     A_____     AA
GAM1013  ANXA5     5'  ATCCTTCAGCGTCTGCATCTCG 6714      A       TCATA  ___
              GC                   GCC AGATGCAG    GC   AGGAT
                                ||| ||||||||    ||   |||||
                                CGG TCTACGTC    CG   TCCTA
                                  C       TG___  ACT
GAM1013  FBXL11    3'  TCTTTTGACTGCACCTT     24575     A       TAGC
                                AAG TGCAGTCA    AGGA
                                ||| ||||||||    ||||
                                TTC ACGTCAGT    TTCT
                                  C       T___
GAM1013  IRAK1     3'  TTGTATGACTGCACTCCAGC   7813     CA_  A        G
                                GC   AG TGCAGTCATA CAG
                                ||   || |||||||||| |||
                                CG   TC ACGTCAGTAT GTT
                                 ACC  _        _
GAM1013  NRIP1     3'  ATCTTCCATCTGCATCTT     59950          TCATAGC
                                AAGATGCAG      AGGAT
                                |||||||||      |||||
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                                TTCTACGTC      TTCTA
                                     TACC___
GAM1013  RNPEPL1   3'  CCTGCCATGACTGCGTCTCGGC 36675     A          A
                                GCC AGATGCAGTCAT GCAGG
                                ||| |||||||||||| |||||
                                CGG TCTGCGTCAGTA CGTCC
                                  C          C
GAM1013  SYT1      3'  TCCCACACTGCATCTAGC     18903     CA       CATAGCA
                                GC  AGATGCAGT      GGA
                                ||  |||||||||      |||
                                CG  TCTACGTCA      CCT
                                 A_        CAC____
GAM1013  TCF3      3'  ATCCTGAAACTGCATCTTGGC  70729            CATAG
                                GCCAAGATGCAGT     CAGGAT
                                ||||||||||||     ||||||
                                CGGTTCTACGTCA     GTCCTA
                                       AA___
GAM1013  CSMD1     3'  ATCCTGAAGGACTGCATTTGGC 73119      A        ATAG
                                GCCA GATGCAGTC    CAGGAT
                                |||| |||||||||    ||||||
                                CGGT TTACGTCAG    GTCCTA
                                  _        GAA_
GAM1013  DKFZp434A1010 3'  CCTCACTGGATCTTGGC      71343         G    CATAGC
                                GCCAAGAT CAGT      AGG
                                |||||||| ||||      |||
                                CGGTTCTA GTCA      TCC
                                     G    C_____
GAM1013  KIAA0844  3'  ATGATTGCACCTTAGC      30197     C   A
                                GC AAG TGCAGTCAT
                                || ||| |||||||||
                                CG TTC ACGTTAGTA
                                 A   C
GAM1013  MGC5466   3'  ATCCTGCCTGCTGTTGCAGCCT 73054      AGA     T _  _
            GGC                    GCCA   TGCAG CA TAG CAGGAT
                                |||||   ||||| || ||| ||||||
                                CGGT   ACGTT GT GTC GTCCTA
                                  CCG     _ C   C
GAM1013  OPRL1     3'  TCCCTGACTGCAGCTTG      6200       A       TAGCA
                                CAAG TGCAGTCA     GGA
                                |||| ||||||||     |||
                                GTTC ACGTCAGT     CCT
                                  G       C____
GAM1013  RAB35     3'  CTTGATGACTGCTC        22478     T       AG
                                GA GCAGTCAT  CAGG
                                || ||||||||  ||||
                                CT CGTCAGTA  GTTC
                                 _       ___
GAM1013  SEMA4G    5'  ATCCTGCTATGACTGCATCTTG 94671
            GC                     GCCAAGATGCAGTCATAGCAGGAT
                                |||||||||||||||||||||||
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                                CGGTTCTACGTCAGTATCGTCCTA

GAM1013  LOC144114 5'  ATCCTGCTACGGGCACCGTGGC 82208      AGA   AG  A
                                GCCA   TGC  TC TAGCAGGAT
                                ||||   |||  || |||||||||
                                CGGT   ACG  GG ATCGTCCTA
                                  GCC   __  C
GAM1013  LOC154386 3'  CCTGCTATAAACTGTGGC    81082     AAGAT    C_
                                GCC    GCAGT  ATAGCAGG
                                |||    |||||  ||||||||
                                CGG    TGTCA  TATCGTCC
                                  _____    AA
GAM1013  LOC164159 5'  ATGACTGCACCTTAGG      82173    _   A
                                CC AAG TGCAGTCAT
                                || ||| |||||||||
                                GG TTC ACGTCAGTA
                                 A   C
GAM1013  LOC256126 3'  CTATAATGCATCTTGGC     95302          GTC
                                GCCAAGATGCA   ATAG
                                ||||||||||   ||||
                                CGGTTCTACGT   TATC
                                      AA_
GAM1013  LOC257078 5'  CCACAGTTGACTGCACCTGGGC 97129     A  A       TAGCA
                                GCC AG TGCAGTCA    GG
                                ||| || ||||||||    ||
                                CGG TC ACGTCAGT    CC
                                  G  C       TGACA
GAM1014  ADAM19    3'  CAGGAAGAAGACTGGCCATTAT 52703      C    CTGAG
             G                   CATGA GGCT    TTCTTCCTG
                                |||||  ||||    |||||||||
                                GTATT CCGG    AAGAAGGAC
                                   A   TCAG_
GAM1014  FACL5     5'  CAGGAAGAACTCAGAGCCG   64186
                                CGGCTCTGAGTTCTTCCTG
                                ||||||||||||||||||
                                GCCGAGACTCAAGAAGGAC

GAM1014  GNAL      5'  CAGGAAAGAGAGGAGCCGTCG  9058          GAG TC
                                TGACGGCTCT   T  TTCCTG
                                ||||||||||   |  ||||||
                                GCTGCCGAGG   A  AAGGAC
                                      AG_ GA
GAM1014  KAL1      3'  CAGGAAGAACTTCTGTCA    4013        CTCT
                                TGACGG   GAGTTCTTCCTG
                                ||||||   ||||||||||||
                                ACTGTC   TTCAAGAAGGAC
                                    ____
GAM1014  MYO1E     3'  CAGGAGGACAAAACCACCATG  17187      AC  CTC  AGT
                                CATG  GG   TG   TCTTCCTG
                                ||||  ||   ||   ||||||||
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                                GTAC  CC   AC   AGGAGGAC
                                  CA  AAA  ___
GAM1014  PRKAR2B  3'  CAGAAAGAACTCAGATGT    10804    _        C
                                GC TCTGAGTTCTT CTG
                                || |||||||||| |||
                                TG AGACTCAAGAA GAC
                                 T         A
GAM1014  PUM2     3'  AGGATCAAAGCTGTCATG    31014         C   GTTCT
                                CATGACGGCT TGA    TCCT
                                |||||||||| |||    ||||
                                GTACTGTCGA ACT    AGGA
                                      A  _____
GAM1014  SKI      3'  CAGGAAGTGCAGAGCCGCA   11701    A      AGTT
                                TG CGGCTCTG   CTTCCTG
                                || ||||||||   |||||||
                                AC GCCGAGAC   GAAGGAC
                                 _      GT__
GAM1014  TEM8     3'  AGGAAGATGCAACCCCATG   36326     AC  CTC  AGT
                                CATG  GG   TG   TCTTCCT
                                ||||  ||   ||   |||||||
                                GTAC  CC   AC   AGAAGGA
                                  C_  A__  GT_
GAM1014  ARHGEF4  5'  AGAAAAAACTCAGGGC     52207         C  C
                                GCTCTGAGTT TT CT
                                |||||||||| || ||
                                CGGGACTCAA AA GA
                                      A  A
GAM1014  FLJ31978 3'  CAGGAAGGAACAAGCGCC    58348     T  GAG
                                GGC CT   TTCTTCCTG
                                ||| ||   |||||||||
                                CCG GA   AGGAAGGAC
                                  C  ACA
GAM1014  HSU24186 5'  AGAACTCAAAGCCGTC      25324        C
                                GACGGCT TGAGTTCT
                                ||||||| ||||||||
                                CTGCCGA ACTCAAGA
                                    A
GAM1014  KCNT1    3'  AGCTCCCAGGGCCGCCA     61825    A     __
                                TG CGGCTCT  GAGTT
                                || |||||||  |||||
                                AC GCCGGGA  CTCGA
                                 C      CC
GAM1014  KIAA1867 3'  CAGGAAGAACCCAAGAGCTCAT 94822     CG    GA_
                                ATGA  GCTCT   GTTCTTCCTG
                                ||||  |||||   ||||||||||
                                TACT  CGAGA   CAAGAAGGAC
                                  __    ACC
GAM1014  KIAA1878 3'  AATTCAGAGAATCGTCATG   91707        __
                                CATGACGG  CTCTGAGTT
                                ||||||||  |||||||||
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                                GTACTGCT  GAGACTTAA
                                    AA
GAM1014  MFN1     3'  CAGGAAGAACTCATGA      35541    _
                                TC TGAGTTCTTCCTG
                                || ||||||||||||
                                AG ACTCAAGAAGGAC
                                 T
GAM1014  MIDORI   3'  CAGGGCCCTTCCAGAGCCTGTC 73784       _      AGTTCT
              ATG                  CATGAC GGCTCTG     TCCTG
                                |||||| |||||||      |||||
                                GTACTG CCGAGAC      GGGAC
                                   T      CTTCCC
GAM1014  MYH7B    3'  CAGGAAGAACCTGGCTCGCATG 70530      A _  CTGA
                                CATG CG GCT    GTTCTTCCTG
                                |||| || |||    ||||||||||
                                GTAC GC CGG    CAAGAAGGAC
                                  _ T   TC__
GAM1014  RNAHP    3'  AGAAAGCAGCAGCCGTCAT    23761         _  AG
                                ATGACGGCT CTG  TTCT
                                ||||||||| |||  ||||
                                TACTGCCGA GAC  AAGA
                                     C   GA
GAM1014  SLC37A1  3'  AGACGGAGCTCAGACCC      38561    C        TC
                                GG TCTGAGTTCT  CT
                                || ||||||||||  ||
                                CC AGACTCGAGG  GA
                                 C         CA
GAM1014  LOC116236 3'  CAGGAAAAGCACAAACCTCAT  73809      C  CTC  A   C
                                ATGA GG   TG GTT TTCCTG
                                |||| ||   || ||| ||||||
                                TACT CC   AC CGA AAGGAC
                                  _ AA_  A   A
GAM1014  LOC124801 3'  CAGGAAGAACTCTCTTGCATG  74336      A   CTCT
                                CATG CGG    GAGTTCTTCCTG
                                |||| |||    ||||||||||||
                                GTAC GTT    CTCAAGAAGGAC
                                  _   CT__
GAM1014  LOC222160 5'  AGGAAGAACTCACCCC      94117    CTC
                                GG   TGAGTTCTTCCT
                                ||   ||||||||||||
                                CC   ACTCAAGAAGGA
                                 CC_
GAM1014  LOC51094  3'  CAGGAAGAATAAAGCC      32045      CTGA
                                GGCT    GTTCTTCCTG
                                ||||    ||||||||||
                                CCGA    TAAGAAGGAC
                                  AA__
GAM1014  LOC92078  3'  CAGGAAGAAGAATCGACCGTC  67977       C  T  G__
                                GACGG TC GA   TTCTTCCTG
                                ||||| || ||   |||||||||
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                                CTGCC AG CT   AAGAAGGAC
                                  _ _ AAG
GAM1015 NRAP     3' CCAGCTGCAGAGTGAT      20508          __
                                ATCACTTTGCAG  GG
                                ||||||||||||  ||
                                TAGTGAGACGTC  CC
                                      GA
GAM1015 SLC16A7  3' TAATCCTACAAAGTGA      16405        CA
                                TCACTTTG  GGGATTA
                                ||||||||  |||||||
                                AGTGAAAC  TCCTAAT
                                    A_
GAM1015 XYLB     3' ATCAGCTGAAAAGTGAT     17558        G  G_
                                ATCACTTT CAG  GAT
                                |||||||| |||  |||
                                TAGTGAAA GTC  CTA
                                    A   GA
GAM1015 C8orf13  3' CATTAGTAAAGGAGCAAAGTGA 81569         AGGGA
                                TCACTTTGC    TTACTAATG
                                |||||||||    |||||||||
                                AGTGAAACG    AATGATTAC
                                    AGGA_
GAM1015 FLJ21477 3' CATCCGTGTCCCTGCAAAGGA  47146    A         T  TA
                                TC CTTTGCAGGGAT AC  ATG
                                || ||||||||||| ||  |||
                                AG GAAACGTCCCTG TG  TAC
                                 _         _ CC
GAM1015 HZFW1    3' CATCAGTATTGGTAAAGTGA   47458        AGGGAT   A
                                TCACTTTGC     TACT ATG
                                |||||||||     |||| |||
                                AGTGAAATG     ATGA TAC
                                    GTT___    C
GAM1015 LOC256021 3' ATTAAAACCCCAAAGTGAT   96514        CA  A  AC
                                ATCACTTTG  GGG TT  TAAT
                                |||||||||  ||| ||  ||||
                                TAGTGAAAC  CCC AA  ATTA
                                    __  A  __
GAM1015 LOC51291  5' GGTCCCTGCAGAGCGAT     33364     A
                                ATC CTTTGCAGGGATT
                                ||| ||||||||||||
                                TAG GAGACGTCCCTGG
                                  C
GAM1016 HAP1     3' AATATGCACATGAAAGATGACC 14163         AT_______  GATA
          TTG                     AGGTCATCTT       GCA   T
                                ||||||||||       |||   |
                                TCCAGTAGAA       CGT   A
                                    AGTACAIII   ATAG
GAM1016 PRKAR2B  3' CATACTGATAAAATGACTTTG  10805         C   G   A
                                CAAGGTCAT TTAT CAG TATG
                                ||||||||| |||| ||| ||||
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                                GTTTCAGTA AATA GTC ATAC
                                     A   _  _
GAM1016  TP53     3'  GCACATCTGCATTTTCACC   5040      CATCTT       A
                                GGT     ATGCAGAT TGC
                                |||     |||||||| |||
                                CCA     TACGTCTA ACG
                                  CTTT__       C
GAM1016  DKFZp434E169 3'  TGCATAAGATGACTTTG     50064
                                CAAGGTCATCTTATGCA
                                ||||||||||||||||
                                GTTTCAGTAGAATACGT

GAM1016  KIAA0329  3'  CAAATCTGCATAAAATACCTCA 29269    A    C  C        A
                                C AGGT AT TTATGCAGAT TG
                                | |||| || |||||||||| ||
                                A TCCA TA AATACGTCTA AC
                                 C   _ A         A
GAM1016  PRO2012   3'  CATATCTGTAGGAATAAACCT  37779      CATCTTA
                                AGGT      TGCAGATATG
                                ||||      ||||||||||
                                TCCA      ATGTCTATAC
                                  AATAAGG
GAM1016  RA-GEF-2  3'  CATACCCATTTGGATGACC    32953        T_   CAGA
                                GGTCATCT  ATG    TATG
                                ||||||||  |||    ||||
                                CCAGTAGG  TAC    ATAC
                                     TT   CC__
GAM1016  RENT2     3'  GCACATCTGTATGCGACAACTT 31420      CA  T       A
                                AGGT  TC TATGCAGAT TGC
                                ||||  || |||||||||| |||
                                TTCA  AG GTATGTCTA ACG
                                  AC  C        C
GAM1016  RENT2     3'  GCACATCTGTATGCGACAACTT 54591      CA  T       A
                                AGGT  TC TATGCAGAT TGC
                                ||||  || |||||||||| |||
                                TTCA  AG GTATGTCTA ACG
                                  AC  C        C
GAM1016  SARCOSIN  3'  TGCCATAAGATGACTTCA    20235    A          _
                                C AGGTCATCTTATG CA
                                | ||||||||||||| ||
                                A TTCAGTAGAATAC GT
                                 C           C
GAM1016  TIGA1     5'  CACATCCGCAGAGGTGACTCG  53800    A       A   A   A
                                A GGTCATCTT TGC GAT TG
                                | ||||||||| ||| ||| ||
                                G TCAGTGGAG ACG CTA AC
                                 C        _  C   C
GAM1016  VAV3      3'  CAGATATGCACACACAAAGATG 20363        AT_________  GATA
              ACCT                  GTCATCTT        GCA    TG
                                ||||||||        |||    ||
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                                CAGTAGAA        CGT    AC
                                    ACACACAIII   ATAG
GAM1016  LOC221755 3'  TATGTCTTCAAGATGACC    92397         TA  C
                                GGTCATCT  TG AGATATG
                                ||||||||  || |||||||
                                CCAGTAGA  AC TCTGTAT
                                    __  T
GAM1016  LOC255330 3'  GCATATCTTTAAGACAACC    95813     CA     TGC
                                GGT  TCTTA   AGATATGC
                                |||  |||||   ||||||||
                                CCA  AGAAT   TCTATACG
                                  AC    T__
GAM1016  LOC51071  3'  CACATCTGAAATGATCTT    31977         CTTATG     A
                                AAGGTCAT     CAGAT TG
                                ||||||||     ||||| ||
                                TTCTAGTA     GTCTA AC
                                    AA____    C
GAM1017  ADRA1D    3'  ACTGCCCCATCCTCCA     5444       A    A  _
                                TGGA GATGG GG AGT
                                |||| ||||| || |||
                                ACCT CTACC CC TCA
                                  C    _ G
GAM1017  CHST1     3'  AACCCCTCCCTCTCCCA     13332     A  T    A
                                TGG AGA GGAGG GTT
                                ||| ||| ||||| |||
                                ACC TCT CCTCC CAA
                                  C  C    C
GAM1017  GCN1L1    3'  TACAACTGAAAATTGCCTCCTC 69756         _______    C   III
            CATCTCTCA               TGGAGGAG     TTCAG TGT   A
                                ||||||||     ||||| |||   |
                                ACCTCCTC     AAGTC ACA   T
                                    CGTTAA    A   III
GAM1017  PCDHB4    3'  ACAGCTTCTCCCCATCTTTCA  38434          A    TTC
                                TGGAAGATGG GGAG   AGCTGT
                                |||||||||| ||||   ||||||
                                ACTTTCTACC CCTC   TCGACA
                                    _   T__
GAM1017  PCDHGA1   3'  ACAGCTGAACTCCTCCATCTTC 38279
            CA                  TGGAAGATGGAGGAGTTCAGCTGT
                                ||||||||||||||||||||||||
                                ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGA10  3'  ACAGCTGAACTCCTCCATCTTC 38286
            CA                  TGGAAGATGGAGGAGTTCAGCTGT
                                ||||||||||||||||||||||||
                                ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGA11  3'  ACAGCTGAACTCCTCCATCTTC 38293
            CA                  TGGAAGATGGAGGAGTTCAGCTGT
                                ||||||||||||||||||||||||
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                                ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGA11  3'  ACAGCTGAACTCCTCCATCTTC 49457
                CA                TGGAAGATGGAGGAGTTCAGCTGT
                                  ||||||||||||||||||||||
                                  ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGA12  3'  ACAGCTGAACTCCTCCATCTTC 13589
                CA                TGGAAGATGGAGGAGTTCAGCTGT
                                  ||||||||||||||||||||||
                                  ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGA2   3'  ACAGCTGAACTCCTCCATCTTC 38300
                CA                TGGAAGATGGAGGAGTTCAGCTGT
                                  ||||||||||||||||||||||
                                  ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGA3   3'  ACAGCTGAACTCCTCCATCTTC 38310
                CA                TGGAAGATGGAGGAGTTCAGCTGT
                                  ||||||||||||||||||||||
                                  ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGA4   3'  ACAGCTGAACTCCTCCATCTTC 38317
                CA                TGGAAGATGGAGGAGTTCAGCTGT
                                  ||||||||||||||||||||||
                                  ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGA5   3'  ACAGCTGAACTCCTCCATCTTC 38324
                CA                TGGAAGATGGAGGAGTTCAGCTGT
                                  ||||||||||||||||||||||
                                  ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGA6   3'  ACAGCTGAACTCCTCCATCTTC 38331
                CA                TGGAAGATGGAGGAGTTCAGCTGT
                                  ||||||||||||||||||||||
                                  ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGA7   3'  ACAGCTGAACTCCTCCATCTTC 38338
                CA                TGGAAGATGGAGGAGTTCAGCTGT
                                  ||||||||||||||||||||||
                                  ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGA8   3'  ACAGCTGAACTCCTCCATCTTC 49449
                CA                TGGAAGATGGAGGAGTTCAGCTGT
                                  ||||||||||||||||||||||
                                  ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGA9   3'  ACAGCTGAACTCCTCCATCTTC 38345
                CA                TGGAAGATGGAGGAGTTCAGCTGT
                                  ||||||||||||||||||||||
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                                ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGB1   3'  ACAGCTGAACTCCTCCATCTTC 38352
              CA                 TGGAAGATGGAGGAGTTCAGCTGT
                                 ||||||||||||||||||||||
                                 ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGB2   3'  ACAGCTGAACTCCTCCATCTTC 38359
              CA                 TGGAAGATGGAGGAGTTCAGCTGT
                                 ||||||||||||||||||||||
                                 ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGB3   3'  ACAGCTGAACTCCTCCATCTTC 38366
              CA                 TGGAAGATGGAGGAGTTCAGCTGT
                                 ||||||||||||||||||||||
                                 ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGB4   3'  ACAGCTGAACTCCTCCATCTTC 13596
              CA                 TGGAAGATGGAGGAGTTCAGCTGT
                                 ||||||||||||||||||||||
                                 ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGB5   3'  ACAGCTGAACTCCTCCATCTTC 38373
              CA                 TGGAAGATGGAGGAGTTCAGCTGT
                                 ||||||||||||||||||||||
                                 ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGB6   3'  ACAGCTGAACTCCTCCATCTTC 38380
              CA                 TGGAAGATGGAGGAGTTCAGCTGT
                                 ||||||||||||||||||||||
                                 ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGB7   3'  ACAGCTGAACTCCTCCATCTTC 38387
              CA                 TGGAAGATGGAGGAGTTCAGCTGT
                                 ||||||||||||||||||||||
                                 ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGC3   3'  ACAGCTGAACTCCTCCATCTTC 10450
              CA                 TGGAAGATGGAGGAGTTCAGCTGT
                                 ||||||||||||||||||||||
                                 ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGC3   3'  ACAGCTGAACTCCTCCATCTTC 50513
              CA                 TGGAAGATGGAGGAGTTCAGCTGT
                                 ||||||||||||||||||||||
                                 ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGC4   3'  ACAGCTGAACTCCTCCATCTTC 38394
              CA                 TGGAAGATGGAGGAGTTCAGCTGT
                                 ||||||||||||||||||||||
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                                ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PCDHGC5   3'  ACAGCTGAACTCCTCCATCTTC 38401
                CA                  TGGAAGATGGAGGAGTTCAGCTGT
                                    ||||||||||||||||||||||
                                    ACCTTCTACCTCCTCAAGTCGACA

GAM1017  PKM2      3'  ACACTCCACCCTCCACCTTCCA 10600       A     A  TC  C
                                    TGGAAG TGGAGG GT  AG TGT
                                    |||||| |||||| ||  || |||
                                    ACCTTC ACCTCC CA  TC ACA
                                       C      _  CC  _
GAM1017  TGM3      3'  AACCCTCTCCATCTCCCA     12278     A       _ A
                                    TGG AGATGGAG G GTT
                                    ||| |||||||| | |||
                                    ACC TCTACCTC C CAA
                                      C       T C
GAM1017  UBE2L3    3'  CAGCCACACCCCTCCTCCA    12498      AGAT     A  TCA
                                    TGGA    GGAGG GT   GCTG
                                    ||||    ||||| ||   ||||
                                    ACCT    CCTCC CA   CGAC
                                       _____     C  CAC
GAM1017  BAIAP1    3'  ACTTCTCCATCCCCCA      16447     AA
                                    TGG  GATGGAGGAGT
                                    |||  ||||||||||
                                    ACC  CTACCTCTTCA
                                      CC
GAM1017  C20orf110 3'  CAGCCTTGCTCCTCTCCCA    79544     AAGAT       TCA
                                    TGG    GGAGGAGT   GCTG
                                    |||    ||||||||   ||||
                                    ACC    TCTCCTCG   CGAC
                                      C_____       TTC
GAM1017  FLJ12816  3'  ACACCTTCCTCCTCCATCCCCC 41931     AA        TTC  C
                A                    TGG  GATGGAGGAG   AG TGT
                                    |||  ||||||||||   || |||
                                    ACC  CTACCTCCTC   TC ACA
                                      CC         CT_  C
GAM1017  FLJ20232  3'  ACAGCCAGCCCTTCATCCTCCA 38666      A       A   CA
                                    TGGA GATGGAGG GTT  GCTGT
                                    |||| |||||||| |||  |||||
                                    ACCT CTACTTCC CGA  CGACA
                                      C       _   C_
GAM1017  HSA250303 3'  AGGTGTCCTCCATCCCCCA    37409     AA       GTT  G
                                    TGG  GATGGAGGA   CA CT
                                    |||  |||||||||   || ||
                                    ACC  CTACCTCCT   GT GA
                                      CC         ___  G
GAM1017  KIAA0450  3'  ACAGCGTTTCCTCCTCCTCCA  27615      A  T      TTCA
                                    TGGA GA GGAGGAG    GCTGT
                                    |||| || |||||||    |||||
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                                ACCT CT CCTCCTT   CGACA
                                  C _     TG__
GAM1017 KIAA0819 3' ACAGCTTTCTGTCCCCTCCTCC 63572     A T A  GTTC_
            A                    TGGA GA GG GGA    AGCTGT
                                ||||  ||  ||  |||    ||||||
                                ACCT CT CC CCT    TCGACA
                                  C _ _  GTCTT
GAM1017 KLK11    3' ACAGCCCATCACCCTCCATTTC 58615     A      A TCA__
            CA                   TGGA GATGGAGG GT    GCTGT
                                ||||  ||||||||  ||    |||||
                                ACCT TTACCTCC CA    CGACA
                                  _      _ CTACC
GAM1017 PRRG1    3' ACTCCCCCACACTTCCA    6281       A_  A
                                TGGAAG  TGG GGAGT
                                ||||||  |||  |||||
                                ACCTTC  ACC CCTCA
                                   AC  C
GAM1017 ZNF384   5' ACAGACCCTCCTCCTCCTCCA 55983     A T     TTCAG
                                TGGA GA GGAGGAG    CTGT
                                ||||  ||  |||||||    ||||
                                ACCT CT CCTCCTC    GACA
                                  C _     CCA__
GAM1017 LOC145757 3' AGCTCCCCATCTTCC      77452        A
                                GGAAGATGG GGAGTT
                                |||||||||  ||||||
                                CCTTCTACC CCTCGA
                                       _
GAM1017 LOC149465 3' CAGCTGCCTCCTCCTCCA    79392     AGAT     TT
                                TGGA   GGAGGAG  CAGCTG
                                ||||   |||||||  ||||||
                                ACCT   CCTCCTC  GTCGAC
                                  _____     C_
GAM1017 LOC169943 5' AACTACCCAGTCTTCCA     87240       GGA  _
                                TGGAAGAT   GG AGTT
                                ||||||||   ||  ||||
                                ACCTTCTG   CC TCAA
                                     AC_  A
GAM1017 LOC200269 3' CAGCTGAACTCATCTCTC    88667    T  G
                                GA GGA GAGTTCAGCTG
                                ||  |||  ||||||||||
                                CT TCT CTCAAGTCGAC
                                 C  A
GAM1017 LOC219972 3' ACCCCTTCATCTTCCA      91637          A
                                TGGAAGATGGAGG GT
                                ||||||||||||  ||
                                ACCTTCTACTTCC CA
                                        C
GAM1017 LOC221540 3' AACTGCTCCATCTTCCA     93834          G
                                TGGAAGATGGAG AGTT
                                ||||||||||| ||||
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                                ACCTTCTACCTC TCAA
                                       G
GAM1017  LOC257464 3'  TGAACTCCTCCTCCTCC     89674     A  T
                                GGA GA GGAGGAGTTCA
                                ||| || ||||||||||
                                CCT CT CCTCCTCAAGT
                                  C  _
GAM1017  LOC257545 3'  AACTGCTCCATCTTCCA     97802           G
                                TGGAAGATGGAG AGTT
                                |||||||||||| ||||
                                ACCTTCTACCTC TCAA
                                       G
GAM1017  LOC257598 3'  AACTGCTCCATCTTCCA     97917           G
                                TGGAAGATGGAG AGTT
                                |||||||||||| ||||
                                ACCTTCTACCTC TCAA
                                       G
GAM1018  CALU     3'  GATCCCTTTGCTCTA       6887          TGTTTCA
                                TAGAGCAAA      GGATC
                                |||||||||      |||||
                                ATCTCGTTT      CCTAG
                                     C_______
GAM1018  CCND2    3'  GGAATCCTGGATTTTGCCCT   8296     A    TGT      _
                                AG GCAAA   TTCAGGAT CC
                                || |||||   |||||||| ||
                                TC CGTTT   AGGTCCTA GG
                                 C    T__       A
GAM1018  CTLA4    5'  GGATCCTGAAAGGTTTTGCTCT 17808          _ G
              AC                   GTAGAGCAAA T TTTCAGGATCC
                                |||||||||| | ||||||||||
                                CATCTCGTTT G AAAGTCCTAGG
                                      T G
GAM1018  CYP1A1   3'  GGATCCTGCCTGCCCCTAC   4945      A_  AATGTTT
                                GTAG  GCA      CAGGATCC
                                ||||  |||      ||||||||
                                CATC  CGT      GTCCTAGG
                                  CC   CC_____
GAM1018  ETF1     3'  CCTGAAGCTGATGCTTCAC   16394    AG   AAT
                                GT  AGCA   GTTTCAGG
                                ||  ||||   ||||||||
                                CA  TCGT   CGAAGTCC
                                 CT    AGT
GAM1018  HDAC4    3'  GGGATCCTGCCACCTGCCCT   20115    A   AA  TTT
                                AG GCA  TG   CAGGATCCC
                                || |||  ||   |||||||||
                                TC CGT  AC   GTCCTAGGG
                                 C   CC  C__
GAM1018  PIGA     3'  GAAACACATTGCTCTAC     40004         A_
                                GTAGAGCAA  TGTTTC
                                |||||||||  ||||||
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                                CATCTCGTT  ACAAAG
                                     AC
GAM1018  PIGA     3'  GAAACACATTGCTCTAC     40013         A_
                                GTAGAGCAA  TGTTTC
                                |||||||||  ||||||
                                CATCTCGTT  ACAAAG
                                     AC
GAM1018  PIGA     3'  GAAACACATTGCTCTAC     10552         A_
                                GTAGAGCAA  TGTTTC
                                |||||||||  ||||||
                                CATCTCGTT  ACAAAG
                                     AC
GAM1018  PLCB2    3'  GGGATCCTGGCCCCACTCTGC  15894       CAAA  TT_
                                GTAGAG   TG   TCAGGATCCC
                                ||||||   ||   ||||||||||
                                CGTCTC   AC   GGTCCTAGGG
                                   ____  CCC
GAM1018  STK6     3'  GGAACACGTGCTCTAC      13187         AA
                                GTAGAGCA  TGTTTC
                                ||||||||  ||||||
                                CATCTCGT  ACAAGG
                                     GC
GAM1018  TMOD2    5'  GGGATCCTGGCCCCGCTCCAC  27251    A    AAATGTT
                                GT GAGC      TCAGGATCCC
                                || ||||      ||||||||||
                                CA CTCG      GGTCCTAGGG
                                 C   CCCC___
GAM1018  DKFZP434K1421 3'  GGAAAATTTGCTCCAC      49553    A      G
                                GT GAGCAAAT TTTC
                                || ||||||||  ||||
                                CA CTCGTTTA AAGG
                                 C       A
GAM1018  DKFZP434N178 5'  GGGATCCTTGCCTCTCTGCCCT 71908      A   AATGTTTC
            GC                    GTAG GCA       AGGATCCC
                                ||||  |||       ||||||||
                                CGTC CGT       TCCTAGGG
                                  C   CTCTCCGT
GAM1018  EST-YD1  3'  GACCTCGACATTTGCTC     41080          TC   A
                                GAGCAAATGTT  AGG TC
                                ||||||||||  |||  ||
                                CTCGTTTACAG  TCC AG
                                      C_  _
GAM1018  FLJ11026 5'  GGATCACCAGTTTGCTCCAC   36993    A      GTTTCAG
                                GT GAGCAAAT      GATCC
                                || ||||||||      |||||
                                CA CTCGTTTG      CTAGG
                                 C       ACCA___
GAM1018  FLJ13769 3'  GACCCTGAAACACTCAGC    46609    A   CAAA       A
                                GT GAG    TGTTTCAGG TC
                                || |||    |||||||||  ||
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                                CG CTC    ACAAAGTCC AG
                                 A  _____        C
GAM1018  FLJ20294  3'  GGATCCTGCTGCACCCCTCCAC 34879    A   CAAA   TT
                                GT GAG    TGT  CAGGATCC
                                || |||    |||  ||||||||
                                CA CTC    ACG  GTCCTAGG
                                 C   CCC_   TC
GAM1018  FLJ21918  3'  GATCCCAATGTTCTAC      46289         AA  TTTCA
                                GTAGAGCA  TG    GGATC
                                ||||||||  ||    |||||
                                CATCTTGT  AC    CCTAG
                                     A_  _____
GAM1018  GAB1      3'  GAAACATTTGTTCCAC      8977     A
                                GT GAGCAAATGTTTC
                                || ||||||||||||
                                CA CTTGTTTACAAAG
                                 C
GAM1018  HSMPP8    3'  TCTAAAACATTTGCTT      93486           C
                                GAGCAAATGTTT AGG
                                |||||||||||| |||
                                TTCGTTTACAAA TCT
                                       A
GAM1018  KIAA0143  3'  GAAACACAAACTTTGCTCTAC  64785          _____
                                GTAGAGCAAA     TGTTTC
                                ||||||||||     ||||||
                                CATCTCGTTT     ACAAAG
                                      CAAAC
GAM1018  KIAA0759  3'  GATCCTGGGCCAGCCCCTCCAC 67323    A   CAAA  TT
                                GT GAG    TG  TCAGGATC
                                || |||    ||  ||||||||
                                CA CTC    AC  GGTCCTAG
                                 C   CCCG  CG
GAM1018  KIAA1211  3'  GTCCAAAACATTTACTCTAC   68896       C       CA
                                GTAGAG AAATGTTT  GGAT
                                |||||| ||||||||  ||||
                                CATCTC TTTACAAA  CCTG
                                    A       A_
GAM1018  KIAA1373  3'  GGGATCCTGATTAATGCTCTA  70948        AATGTT
                                TAGAGCA     TCAGGATCCC
                                |||||||     ||||||||||
                                ATCTCGT     AGTCCTAGGG
                                     AATT__
GAM1018  KIAA1511  3'  GGGCACTGAAACATTTGT    70169           GA
                                GCAAATGTTTCAG  TCC
                                ||||||||||||  |||
                                TGTTTACAAAGTC  GGG
                                       AC
GAM1018  KIAA1586  5'  GATCATGCCATTGTGCTCTAC  92330         _   TTT  G
                                GTAGAGCA AATG   CA GATC
                                |||||||| ||||   || ||||
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                                CATCTCGT TTAC   GT CTAG
                                     G   C__  A
GAM1018  MGC9753   5'  GGGATCCTGCCCCCGCCCTGC  53056     A  AAATGTTT
                                GTAG GC       CAGGATCCC
                                |||| ||       |||||||||
                                CGTC CG       GTCCTAGGG
                                  C  CCCCC___
GAM1018  NFKBIE    3'  GGACCCTGAAACACCGTTGTTT 15851       A__       A
                                GAGCAA   TGTTTCAGG TCC
                                ||||||   ||||||||| |||
                                TTTGTT   ACAAAGTCC AGG
                                   GCC       C
GAM1018  LOC123435 5'  GGGACCCTGGGATTTTGCTCT  74208        T  TT   A
                                AGAGCAAA GT  CAGG TCCC
                                |||||||| ||  |||| ||||
                                TCTCGTTT TA  GTCC AGGG
                                     _ GG   C
GAM1018  LOC136895 5'  GGACCCTATTTGCTCTGC    57170          GTTTC   A
                                GTAGAGCAAAT    AGG TCC
                                ||||||||||    ||| |||
                                CGTCTCGTTTA    TCC AGG
                                      _____  C
GAM1018  LOC144248 5'  GGAATCCACCCTTATTTGCTCT 76741          TTTCA   _
                                AGAGCAAATG    GGAT CC
                                |||||||||    |||| ||
                                TCTCGTTTAT    CCTA GG
                                     TCCCA   A
GAM1018  LOC148189 5'  GGATCCGCACCGCCCTAC    78716     A  AAA   TTCA
                                GTAG GC   TGT   GGATCC
                                |||| ||   |||   ||||||
                                CATC CG   ACG   CCTAGG
                                  C  CC_  ____
GAM1018  LOC149711 5'  ATCCACTATCTGCTCTAC    84670        A   TTTCA
                                GTAGAGCA ATG    GGAT
                                |||||||| |||    ||||
                                CATCTCGT TAT    CCTA
                                     C   CA___
GAM1018  LOC165693 3'  GACCCTGAAACAGCTC      82597      AAA       A
                                GAGC   TGTTTCAGG TC
                                ||||   ||||||||| ||
                                CTCG   ACAAAGTCC AG
                                  ___        C
GAM1018  LOC253985 5'  ATCCACCATGCTCTAC      96482        AAT  TTCA
                                GTAGAGCA   GT   GGAT
                                ||||||||   ||   ||||
                                CATCTCGT   CA   CCTA
                                     AC_  ____
GAM1018  LOC256568 3'  GATCAGACACATTGCTCTAC  94843         A   T  AG
                                GTAGAGCAA TGT TC  GATC
                                ||||||||| ||| ||  ||||
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                                CATCTCGTT ACA AG  CTAG
                                     _  C  A_
GAM1018 LOC91266 5'  CCTGAAACATGTTC       65412       AA
                                GAGCA  TGTTTCAGG
                                |||||  |||||||||
                                CTTGT  ACAAAGTCC
                                  __
GAM1019 TNFAIP1   3'  CATCAGCTGAGGACAGCAAACT 40917     AG     G
           CC                     GGA  TTGCTG CTTCAGCTGATG
                                |||  |||||| ||||||||||||
                                CCT  AACGAC GGAGTCGACTAC
                                  CA     A
GAM1019 C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 21681     AA      _ ___
           CCC                      GG  GTTGCTGG CT   TCAGCTG
                                ||  |||||||| ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM1019 C1orf2    3'  CAGCTGGTTGGGACCAGCAGCC 94622     AA      _ ___
           CCC                      GG  GTTGCTGG CT   TCAGCTG
                                ||  |||||||| ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM1019 C20orf59  3'  CATCCCTAGCCAGCAGCTCC   41992     A       TC  CT
                                GGA GTTGCTGGCT  AG  GATG
                                ||| ||||||||||  ||  ||||
                                CCT CGACGACCGA  TC  CTAC
                                  _        __  C_
GAM1019 FLJ20079  3'  CATTCTGGTAAACCAGCAGCCT 34490     A      CT__   CT
           CC                     GGA GTTGCTGG    TCAG  GATG
                                ||| ||||||||    ||||  ||||
                                CCT CGACGACC    GGTC  TTAC
                                  C       AAAT   __
GAM1019 SSAT2     3'  CATCAGCTGAAGCACTCTTC   56041      TTGCTG
                                GAAG     GCTTCAGCTGATG
                                ||||     ||||||||||||
                                CTTC     CGAAGTCGACTAC
                                   TCA___
GAM1019 SYNJ2     3'  ATCAGCTTAAGCAATTCC     61763      GTTGCTG   C
                                GGAA      GCTT AGCTGAT
                                ||||      |||| |||||||
                                CCTT      CGAA TCGACTA
                                  AA_____    T
GAM1019 LOC162333 5'  CTGAAGCCAGCAATTCC     87131      G
                                GGAA TTGCTGGCTTCAG
                                |||| ||||||||||||
                                CCTT AACGACCGAAGTC
                                  _
GAM1019 LOC222060 5'  CACCTCCCACCAGCAACCCCC  94104     AA       CTTC  C
                                GG  GTTGCTGG    AG TG
                                ||  ||||||||    || ||
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                                CC  CAACGACC    TC AC
                                 CC       ACCC  C
GAM1019  LOC255650 3'  CATCAGCCCCAGGCAACTTCC  96711         _   CTTCA
                                GGAAGTTGC TGG     GCTGATG
                                ||||||||| |||     |||||||
                                CCTTCAACG ACC     CGACTAC
                                     G   C____
GAM1020  PDYN     3'  CCAACCTGTTCACGTGACTC  44321    A         CAA  C
                                GA TCACGTGAATAG   GT GG
                                || ||||||||||||   || ||
                                CT AGTGCACTTGTC   CA CC
                                 C          ___  A
GAM1020  FLJ10724  3'  CTACTCAGTGATTCA       36500         G   A
                                TGAATCAC TGA TAG
                                |||||||| ||| |||
                                ACTTAGTG ACT ATC
                                     _  C
GAM1020  FLJ23120  3'  CCAACTTGCTATTCTAGCTTGA 85146     C  __         C
                                TCA GT  GAATAGCAAGT GG
                                ||| ||  |||||||||||| ||
                                AGT CG  CTTATCGTTCA CC
                                  T  AT          A
GAM1020  LOC163115 5'  CCGACTGCCCTATTCACATGCT 82412     AT  C       CA_
            CA                    TGA  CA GTGAATAG   AGTCGG
                                |||  || ||||||||   ||||||
                                ACT  GT CACTTATC   TCAGCC
                                  C_  A       CCG
GAM1020  LOC90550  3'  CTTTTCTTTCACGTGATTCA   73092           TAGC
                                TGAATCACGTGAA    AAG
                                ||||||||||||    |||
                                ACTTAGTGCACTT    TTC
                                       TCTT
GAM1021  ARNTL    5'  GAAGCTGACCGCCTG       6784        AAAA
                                CAGGTG    TCAGCTTC
                                ||||||    ||||||||
                                GTCCGC    AGTCGAAG
                                   C___
GAM1021  ARSB     3'  GAAGCTGATAAAATCTG     3498       GAAA
                                CAGGT    ATCAGCTTC
                                |||||    |||||||||
                                GTCTA    TAGTCGAAG
                                  AAA_
GAM1021  BAZ2A    3'  CTGCCATTTTCACCTGCTGA   25600     C         __
                                TCA CAGGTGAAAAT  CAG
                                ||| ||||||||||  |||
                                AGT GTCCACTTTTA  GTC
                                  C         CC
GAM1021  COL16A1   5'  GGAAGCTGGGGACCCGTGA   8501      CA   GAAAA
                                TCAC  GGT    TCAGCTTCC
                                ||||  |||    |||||||||
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                                AGTG  CCA    GGTCGAAGG
                                  C_  GG___
GAM1021  EYA1    3'  AGCAATTTCCGCCTGGTGA   4951          A   CA
                                TCACCAGGTG AAAT  GCT
                                |||||||||| ||||  |||
                                AGTGGTCCGC TTTA  CGA
                                      C   A_
GAM1021  FEN1    3'  AGATGGTGATGTTCACCTGG  14642         A   G  TC
                                CCAGGTGAA ATCA CT  CT
                                ||||||||| |||| ||  ||
                                GGTCCACTT TAGT GG  GA
                                      G   _ TA
GAM1021  GNAZ    3'  GAAGGTTCTTTCACCTGGGA  9065    A        ATCAG
                                TC CCAGGTGAAA    CTTC
                                || ||||||||||    ||||
                                AG GGTCCACTTT    GAAG
                                 _        CTTG_
GAM1021  GNGT2   5'  GATTTTCAGCTGATGA     48987    C  G
                                TCA CAG TGAAAATC
                                ||| ||| ||||||||
                                AGT GTC ACTTTTAG
                                  A  G
GAM1021  NHP2L1  3'  AGAAAGCTGATGGAGCCAGG  17199    A  GAAA      C
                                CC GGT   ATCAGCTT CT
                                || |||   |||||||| ||
                                GG CCG   TAGTCGAA GA
                                 A  AGG_      A
GAM1021  NUMB    5'  GGAAACTGAGGCTTGGTGA   13624        GAAAA   C
                                TCACCAGGT    TCAG TTCC
                                |||||||||    |||| ||||
                                AGTGGTTCG    AGTC AAGG
                                      G____   A
GAM1021  OLFM1   3'  GGAAGGGCTCACCTGGGGA  26556    A      AAATCAG
                                TC CCAGGTGA      CTTCC
                                || ||||||||      |||||
                                AG GGTCCACT      GAAGG
                                 G       CGG____
GAM1021  PTHLH   5'  GAAGCTGACTTCAGAGGGGGA  11013    A  AGG   AA
                                TC CC   TGAA  TCAGCTTC
                                || ||   ||||  ||||||||
                                AG GG   ACTT  AGTCGAAG
                                 G  GAG   C_
GAM1021  SIM1    3'  TGAGTTTTCACCTGGT     17380          _
                                ACCAGGTGAAAA TCA
                                |||||||||||| |||
                                TGGTCCACTTTT AGT
                                       G
GAM1021  SLC21A2 3'  GGAAGCTACAACACAGTGA   18863    CAG   AAAATC
                                TCAC   GTG    AGCTTCC
                                ||||   |||    |||||||
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                                AGTG  CAC     TCGAAGG
                                  A__  AACA__
GAM1021  TAP2     3'  AGGAAACTTAATTCCCTGGTGA 5024         T  AATC  C
                                TCACCAGG GAA   AG TTCCT
                                |||||||| |||   || |||||
                                AGTGGTCC CTT   TC AAGGA
                                     _  AAT_  A
GAM1021  ZNF136   5'  AGGAAGCTGGGACACCCGGGA  59885    A  A   AAAA
                                TC CC GGTG   TCAGCTTCCT
                                || || ||||   ||||||||||
                                AG GG CCAC   GGTCGAAGGA
                                 _ C   AG__
GAM1021  ZNF140   3'  GATTCTTCCATCTGGT      12870         _ _
                                ACCAGGTG AA AATC
                                |||||||| || ||||
                                TGGTCTAC TT TTAG
                                     C  C
GAM1021  AKAP11   3'  AGGAAATGGCTTTTCACCTG   57828          _  GC
                                CAGGTGAAAA TCA  TTCCT
                                |||||||||| |||  |||||
                                GTCCACTTTT GGT  AAGGA
                                      C   A_
GAM1021  BTBD1    3'  GAAGCTGACTTTATATTTGGTG 47476          _  A
            G                    TCACCAGGTG AAA TCAGCTTC
                                |||||||||| ||| ||||||||
                                GGTGGTTTAT TTT AGTCGAAG
                                      A   C
GAM1021  CDW92    3'  AGGAAGCTGGGGCACC      54504      AAAA
                                GGTG   TCAGCTTCCT
                                ||||   ||||||||||
                                CCAC   GGTCGAAGGA
                                  GG__
GAM1021  EPN2     3'  AAGTCATTCACCTGGGA     30319    A       AATCA
                                TC CCAGGTGAA    GCTT
                                || |||||||||    ||||
                                AG GGTCCACTT    TGAA
                                 _       AC___
GAM1021  FLJ10057 5'  GAAGTTAATTCACCTG      35780         AATC
                                CAGGTGAA   AGCTTC
                                ||||||||   ||||||
                                GTCCACTT   TTGAAG
                                     AA__
GAM1021  FLJ10718 3'  GGCTTTTCACCCTGGTGA    36495         _    ATC
                                TCACCAGG TGAAA  AGCT
                                |||||||| |||||  ||||
                                AGTGGTCC ACTTT  TCGG
                                     C   ___
GAM1021  FLJ12688 3'  GAAGGATGTCTACCTGGTGA  73178          AAA  AG
                                TCACCAGGTG  ATC  CTTC
                                ||||||||||  |||  ||||
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                                AGTGGTCCAT   TAG  GAAG
                                     CTG   __
GAM1021  FLJ22938  3'  AGGAAGCTGACCGACATCTGGG 45156    A      AAAA
             A                    TC CCAGGTG    TCAGCTTCCT
                                  || |||||||    ||||||||||
                                  AG GGTCTAC    AGTCGAAGGA
                                   _      AGCC
GAM1021  KIAA0801  3'  GAAACTGGTACTTGGT      29150        GAAA    C
                                  ACCAGGT    ATCAG TTC
                                  |||||||    ||||| |||
                                  TGGTTCA    TGGTC AAG
                                      _____     A
GAM1021  KIAA1200  3'  AGGAAGCTAATTTTCTTTCTGG 62369       T_     C
                                  CCAGG  GAAAAT AGCTTCCT
                                  |||||  |||||| ||||||||
                                  GGTCT  CTTTTA TCGAAGGA
                                     TT     A
GAM1021  LGALS8    5'  AGGAAGCTGAGAAAACCCTGG  21447       TGAAAA
                                  CCAGG     TCAGCTTCCT
                                  |||||     ||||||||||
                                  GGTCC     AGTCGAAGGA
                                     CAAAAG
GAM1021  NPTXR     3'  GGAAGCTGAAGCCCGGGGA    26647    A  A   GAAAA
                                  TC CC GGT     TCAGCTTCC
                                  || || |||     |||||||||
                                  AG GG CCG     AGTCGAAGG
                                   G  C   A_____
GAM1021  NPTXR     3'  GGAAGCTGAAGCCCGGGGA    54183    A  A   GAAAA
                                  TC CC GGT     TCAGCTTCC
                                  || || |||     |||||||||
                                  AG GG CCG     AGTCGAAGG
                                   G  C   A_____
GAM1021  NYD-SP15  3'  AGGAAGCTAATTTATTTCTAGG 48109     _   TGA    C
                                  CC AGG   AAAT AGCTTCCT
                                  || |||   |||| ||||||||
                                  GG TCT   TTTA TCGAAGGA
                                   A   TTA    A
GAM1021  PRO0943   5'  AAGTCTATTTTCACCCCGT    37699    CA        CA
                                  AC  GGTGAAAAT  GCTT
                                  ||  |||||||||  ||||
                                  TG  CCACTTTTA  TGAA
                                   CC         TC
GAM1021  SV2B      5'  AGTGTGACTTTCACCT      29293         A   _
                                  AGGTGAAA TCA GCT
                                  |||||||| ||| |||
                                  TCCACTTT AGT TGA
                                       C   G
GAM1021  ZMPSTE24  3'  TGATTTCACCTGGTGA      19598             A
                                  TCACCAGGTGAAA TCA
                                  |||||||||||| |||
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                                AGTGGTCCACTTT AGT
                                          _
GAM1021  LOC112687 3'  AAGCCCCACACTTCACCTGGT  72853          AATCA__
                                ACCAGGTGAA      GCTT
                                ||||||||||      ||||
                                TGGTCCACTT      CGAA
                                     CACACCC
GAM1021  LOC143920 3'  GGAGGCTCTCACTGGTGA    76626       G   AAATC
                                TCACCAG TGA    AGCTTCC
                                ||||||| |||    |||||||
                                AGTGGTC ACT    TCGGAGG
                                   _  C____
GAM1021  LOC144161 3'  CTATTTTCACCTGGT       83006           C
                                ACCAGGTGAAAAT AG
                                |||||||||||| ||
                                TGGTCCACTTTTA TC
                                          _
GAM1021  LOC145195 3'  AGGACTTCTCCCTCACCTGGTG 83271          AAATCAGCT
                                CACCAGGTGA       TCCT
                                ||||||||||       ||||
                                GTGGTCCACT       AGGA
                                     CCCTCTTC_
GAM1021  LOC158525 5'  AGAAAGCTGATCACCT      81943       AAA      C
                                AGGTGA   TCAGCTT CT
                                ||||||   ||||||| ||
                                TCCACT   AGTCGAA GA
                                   ___       A
GAM1021  LOC220936 3'  AGGAAGCTGACCAGCCTG    91407       GAAAA
                                CAGGT    TCAGCTTCCT
                                |||||    ||||||||||
                                GTCCG    AGTCGAAGGA
                                  ACC__
GAM1021  LOC221218 5'  GAAGCTGACTTCCTCTCGGCGG 91762    A  _   T   AA
                                TC CC AGG GAA  TCAGCTTC
                                || || ||| |||  ||||||||
                                GG GG TCT CTT  AGTCGAAG
                                 C  C   C   C_
GAM1021  LOC221504 3'  AGGAGTTGGTCTCCACCT    92419       AAA      T
                                AGGTG   ATCAGCT CCT
                                |||||   ||||||| |||
                                TCCAC   TGGTTGA GGA
                                  CTC      _
GAM1021  LOC221528 5'  AGGAAGCTCCCCATCCCCATCT 92091          AAAATC___
           GGTGA                  TCACCAGGTG       AGCTTCCT
                                  ||||||||||       ||||||||
                                  AGTGGTCTAC       TCGAAGGA
                                       CCCTACCCC
GAM1021  LOC257552 5'  AGGAAGCTCCCCATCCCCATCT 97759          AAAATC___
           GGTGA                  TCACCAGGTG       AGCTTCCT
                                  ||||||||||       ||||||||
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                                AGTGGTCTAC       TCGAAGGA
                                     CCCTACCCC
GAM1021  LOC257602 5'  AGGAAGCTCCCCATCCCCATCT 97851          AAAATC___
             GGTGA                  TCACCAGGTG       AGCTTCCT
                                |||||||||||       ||||||||
                                AGTGGTCTAC       TCGAAGGA
                                     CCCTACCCC
GAM1021  LOC51281  5'  AGGAAGCTGAGGGCCCGCT   33323     AAAA_
                                GGTG    TCAGCTTCCT
                                ||||    ||||||||||
                                TCGC    AGTCGAAGGA
                                  CCGGG
GAM1021  LOC92539  3'  AGGAAGCTAATAACCTTGA   69627    CC   GAAAATC
                                TCA  AGGT      AGCTTCCT
                                |||  ||||      ||||||||
                                AGT  TCCA      TCGAAGGA
                                  __   ATAA___
GAM1022  COL4A1    3'  ATGGCACTTTTGATGAA     8461      _
                                TTCA CAAAAGTGCCAT
                                |||| ||||||||||||
                                AAGT GTTTTCACGGTA
                                  A
GAM1022  GLRX      3'  GCACTTCTGGTGGATGA     9036        AA_
                                TCATTCAC   AAGTGC
                                ||||||||   ||||||
                                AGTAGGTG   TTCACG
                                     GTC
GAM1022  HIVEP2    3'  CACTTGGATCTAAATGATGTAA 22119         CACAA__
                                TTACATCATT      AAGTG
                                ||||||||||      |||||
                                AATGTAGTAA      TTCAC
                                     ATCTAGG
GAM1022  MASP1     3'  ATGGCACATGTAAATGATGT   57470        C   AAA
                                ACATCATT ACA   GTGCCAT
                                |||||||| |||   |||||||
                                TGTAGTAA TGT   CACGGTA
                                     A   A__
GAM1022  PSAP      3'  GGCTTTTTAAATGATGTAA    69356         CAC    T
                                TTACATCATT   AAAAG GCC
                                |||||||||   ||||| |||
                                AATGTAGTAA   TTTTT CGG
                                     A__    _
GAM1022  PTGFRN    3'  GGCACTTTCTGATGTAA     67191        TTCACA
                                TTACATCA     AAAGTGCC
                                ||||||||     ||||||||
                                AATGTAGT     TTTCACGG
                                     C_____
GAM1022  RNASE4    3'  GCACTTATAATGATGT      11354        CACAA
                                ACATCATT     AAGTGC
                                ||||||||     ||||||
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                                TGTAGTAA    TTCACG
                                    TA___
GAM1022  TRIM14   3'  ATGGCACTTTTGATATGA    28852     TCA
                                TCAT   CAAAAGTGCCAT
                                ||||   ||||||||||||
                                AGTA   GTTTTCACGGTA
                                  TA_
GAM1022  WHSC1    3'  GCACTTAGAATGATGTAA    23661         ACAA
                                TTACATCATTC    AAGTGC
                                ||||||||||    ||||||
                                AATGTAGTAAG    TTCACG
                                      A___
GAM1022  ALDH9    3'  ATGGCCACGCTGTGAATGATGT 5511            AAA  _
            GA                    TTACATCATTCACA   GTG CCAT
                                ||||||||||||||   ||| ||||
                                AGTGTAGTAAGTGT   CAC GGTA
                                        CG_   C
GAM1022  DKFZP566K1924 3'  GGCTTTGTGAAAATGTAA    73775       CA       AGT
                                TTACAT  TTCACAAA   GCC
                                ||||||  ||||||||   |||
                                AATGTA  AAGTGTTT   CGG
                                   A_      ___
GAM1022  HSU54999  3'  TATTTTTAGAATGATGTAA    25242          AC
                                TTACATCATTC  AAAAGTG
                                ||||||||||  |||||||
                                AATGTAGTAAG  TTTTTAT
                                      A_
GAM1022  KIAA0256  3'  TTTGTAAATGATGTAA      64426          C
                                TTACATCATT ACAAA
                                |||||||||| |||||
                                AATGTAGTAA TGTTT
                                      A
GAM1022  KIAA1468  3'  ATGGTACTTAAAATAATGTAA  91773       C   CACAA
                                TTACAT ATT    AAGTGCCAT
                                |||||| |||    |||||||||
                                AATGTA TAA    TTCATGGTA
                                   A   AA___
GAM1022  NTN4     3'  ATGGCACTTGTCTATG     62913     TC   AA
                                CAT  ACA  AGTGCCAT
                                |||  |||  ||||||||
                                GTA  TGT  TCACGGTA
                                  TC   __
GAM1022  TRIM36   3'  GCACTTTATGATGTAG      38013         TCACA
                                TTACATCAT    AAAGTGC
                                |||||||||    |||||||
                                GATGTAGTA    TTTCACG
                                      _____
GAM1022  USP8     3'  TACTCTAGAATGATGTAA    17667          ACAAA
                                TTACATCATTC    AGTG
                                ||||||||||    ||||
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                                AATGTAGTAAG     TCAT
                                      ATC__
GAM1022  LOC120526 3'  TTTGTGAATAATGTGA      74018        C
                                TTACAT ATTCACAAA
                                |||||| |||||||||
                                AGTGTA TAAGTGTTT
                                   A
GAM1022  LOC169026 5'  GTATCTTGTGAATGAT      82727           AA
                                ATCATTCACAA  GTGC
                                ||||||||||  ||||
                                TAGTAAGTGTT  TATG
                                      C_
GAM1022  LOC220766 5'  ACTTTTGTGAATGATGTAA    90792
                                TTACATCATTCACAAAAGT
                                ||||||||||||||||||
                                AATGTAGTAAGTGTTTTCA

GAM1022  LOC221810 3'  TTTGTTAATGATGTAA      93934           C
                                TTACATCATT ACAAA
                                |||||||||| |||||
                                AATGTAGTAA TGTTT
                                      T
GAM1022  LOC91149  3'  TGGGGCTGAATGATG       65086         CAAAA  G
                                CATCATTCA     GT CCA
                                |||||||||     || |||
                                GTAGTAAGT     CG GGT
                                      _____  G
GAM1023  ADH5     5'  ACCCCGGATGTCAGCCCC     5415     A       ATATT
                                GG GCTGACATT     GGT
                                || |||||||||     |||
                                CC CGACTGTAG     CCA
                                  C        GCC__
GAM1023  ALDOB    3'  CAATATCGGCTCCT        68086          CATTA
                                AGGAGCTGA     TATTG
                                |||||||||     |||||
                                TCCTCGGCT     ATAAC
                                      _____
GAM1023  AQP1     3'  TTACCAATTCACCCACTCC    4608       C  ACATTAT
                                GGAG TG       ATTGGTAA
                                |||| ||       ||||||||
                                CCTC AC       TAACCATT
                                   _  CCACT__
GAM1023  CAST     5'  ACCAAGGTGTCAGCTTCCT    8254       _       ATA
                                AGGA GCTGACATT   TTGGT
                                |||| |||||||||   |||||
                                TCCT CGACTGTGG   AACCA
                                   T        ___
GAM1023  CRAT     3'  ACCAGGGCTCAGCTCCTT     14349          CATTATA
                                AAGGAGCTGA      TTGGT
                                ||||||||||      |||||
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                                TTCCTCGACT      GACCA
                                     CGG____
GAM1023 CRAT    3' ACCAGGGCTCAGCTCCTT    5657          CATTATA
                                AAGGAGCTGA      TTGGT
                                ||||||||||      |||||
                                TTCCTCGACT      GACCA
                                     CGG____
GAM1023 EGLN2   5' TACCAATTTCAGGCCCTT    34103     A  GACATTAT
                                AAGG GCT       ATTGGTA
                                |||| |||       |||||||
                                TTCC CGG       TAACCAT
                                  _  ACTT____
GAM1023 GCA     3' AATGTAATGTCAACTCTTT   24165       C
                                AAGGAG TGACATTATATT
                                |||||| ||||||||||||
                                TTTCTC ACTGTAATGTAA
                                   A
GAM1023 HS2ST1  3' TGCCAATTCAGCTCCT      24337        CATTAT
                                AGGAGCTGA     ATTGGTA
                                |||||||||     |||||||
                                TCCTCGACT     TAACCGT
                                      _______
GAM1023 MYEOV   3' TCATGATAACCCAGCTCCTT  57055        ACA   AT
                                AAGGAGCTG   TTAT  TGG
                                |||||||||   ||||  |||
                                TTCCTCGAC   AATA  ACT
                                     CC_    GT
GAM1023 SYN2    3' ATGCAGTGTCAGCTCCT     12072           A
                                AGGAGCTGACATT TAT
                                |||||||||||| |||
                                TCCTCGACTGTGA GTA
                                       C
GAM1023 BRD4    3' ACCAACCAAAGTCAGTTCCTT 54271         ATTATA
                                AAGGAGCTGAC     TTGGT
                                ||||||||||      |||||
                                TTCCTTGACTG     AACCA
                                      AAACC_
GAM1023 GMPPA   5' TACCAACCTGATGAGCCCCT  72196    A  GA    TA
                                AGG GCT  CATTA  TTGGTA
                                ||| |||  |||||  ||||||
                                TCC CGA  GTAGT  AACCAT
                                  C  __     CC
GAM1023 KIAA0252 3' CCAGTATACCAGCCTCTT   62789    GA   ACAT
                                AAG  GCTG   TATATTGG
                                |||  ||||   ||||||||
                                TTC  CGAC   ATATGACC
                                  TC   C___
GAM1023 KIAA0552 3' GCCAATGTCAGCTGCTT    28315    G       TATAT
                                AAG AGCTGACAT    TGGT
                                ||| |||||||||    ||||
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                                TTC TCGACTGTA    ACCG
                                  G      _____
GAM1023  KIAA0662  3'  TCAACTTTAATACCAGCTCTTT 81860       AC   TA_
                                AAGGAGCTG  ATTA   TTGG
                                |||||||||  ||||   ||||
                                TTTCTCGAC  TAAT   AACT
                                     CA    TTC
GAM1023  KIAA0953  3'  ACCAGTATCAGTTCCTT     66776        CATTA
                                AAGGAGCTGA    TATTGGT
                                ||||||||||    |||||||
                                TTCCTTGACT    ATGACCA
                                      _____
GAM1023  KIAA1635  5'  ACTAAACTCCAGCTCCTT    67858        ACATTATA
                                AAGGAGCTG      TTGGT
                                |||||||||      |||||
                                TTCCTCGAC      AATCA
                                     CTCA____
GAM1023  KIAA1937  3'  ACCAACCAGGTGAGCTCCTT  73692       G  ATTATA
                                AAGGAGCT AC     TTGGT
                                ||||||||  ||    |||||
                                TTCCTCGA TG     AACCA
                                     G  GACC__
GAM1023  SDF1      3'  TACTAACAATCAGCTCCTT   90860        CATTATA
                                AAGGAGCTGA     TTGGTA
                                ||||||||||     ||||||
                                TTCCTCGACT     AATCAT
                                     AAC____
GAM1023  SERHL     3'  CCAGTATCATCAGCTCCTT   95604        CATT
                                AAGGAGCTGA    ATATTGG
                                ||||||||||    |||||||
                                TTCCTCGACT    TATGACC
                                     AC__
GAM1023  LOC121133 5'  CCGAAATGCCAGCTCCT     75991        A    ATA
                                AGGAGCTG CATT   TTGG
                                |||||||| ||||   ||||
                                TCCTCGAC GTAA   AGCC
                                     C    ___
GAM1023  LOC129676 5'  TTAATAAGTGCCAACTCCTT  75737       C  A    A
                                AAGGAG TG CATT TATTGG
                                |||||| || |||| ||||||
                                TTCCTC AC GTGA ATAATT
                                   A  C    _
GAM1023  LOC136337 3'  CCAACAATATCAGCTCC     76209        C   ATA
                                GGAGCTGA ATT   TTGG
                                |||||||| |||   ||||
                                CCTCGACT TAA   AACC
                                     A   C__
GAM1023  LOC145946 3'  TACCAGTGCCACAGCTCC    83570        ACATTA
                                GGAGCTG     TATTGGTA
                                |||||||     ||||||||
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                                CCTCGAC     GTGACCAT
                                   ACC___
GAM1023  LOC152687 5'  TTACCAGTGCTTGTCAACTACC 80642    _ C    TTA
                                GG AG TGACA   TATTGGTAA
                                || || |||||   |||||||||
                                CC TC ACTGT   GTGACCATT
                                 A  A    TC_
GAM1023  LOC158263 5'  ACCAATATGGTGAACTCTT   81841      CTGA
                                AGGAG   CATTATATTGGT
                                |||||   ||||||||||||
                                TTCTC   GTGGTATAACCA
                                  AA__
GAM1023  LOC197342 3'  ACCAGAACGTGAGCTCCTT   87986       G  A  ATA
                                AAGGAGCT AC TT   TTGGT
                                |||||||| || ||   |||||
                                TTCCTCGA TG AA   GACCA
                                   G  C  ___
GAM1023  LOC201911 5'  TACCAACTCCTCAGCTCC    90265       CATTATA
                                GGAGCTGA     TTGGTA
                                ||||||||     ||||||
                                CCTCGACT     AACCAT
                                   CCTC___
GAM1023  LOC254423 3'  CCAGCAGTGTCAGCTCCTT   97436           ATA
                                AAGGAGCTGACATT   TTGG
                                ||||||||||||||  ||||
                                TTCCTCGACTGTGA   GACC
                                      C__
GAM1023  LOC90155  3'  TACCAATAACAGCTC      61698      ACATTA
                                GAGCTG     TATTGGTA
                                ||||||     ||||||||
                                CTCGAC     ATAACCAT
                                  A_____
GAM1023  LOC92736  3'  TACCAAAATCAGCTTC     70431       CATTATA
                                GGAGCTGA     TTGGTA
                                ||||||||     ||||||
                                CTTCGACT     AACCAT
                                   AA_____
GAM1023  LOC93496  3'  TTACTAGAATGTGAGCTCCTT  72442       G    ATA
                                AAGGAGCT ACATT   TTGGTAA
                                ||||||| |||||   |||||||
                                TTCCTCGA TGTAA   GATCATT
                                   G    ___
GAM1024  ARF3      3'  CACTGCCCACTGGAGCCT    7998        CGA_   C
                                AGGCTCCA    GCAG TG
                                ||||||||    |||| ||
                                TCCGAGGT    CGTC AC
                                   CACC    _
GAM1024  ARVCF     3'  CTGCCGCATCTGCCTGGAGCCT 8027        CGA   C   AA
                                AGGCTCCA   GCAG TGC  CAG
                                |||||||   |||| |||  |||
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                                TCCGAGGT  CGTC ACG  GTC
                                    C__   T  CC
GAM1024 B4GALT5  3' CTGCCGTGGTCCTGCCGTGGAG 16498        A   __ TG AA
            CCT                   AGGCTCCACG GCAG  C  C  CAG
                                  |||||||||| ||||  |  |  |||
                                  TCCGAGGTGC CGTC  G  G  GTC
                                      _   CT GT CC
GAM1024 CALM3    5' CTGCTGCAGCTGCTGCCGCC  17742    TCCACG       A
                                  GGC     AGCAGCTGCA CAG
                                  |||     |||||||||| |||
                                  CCG     TCGTCGACGT GTC
                                    CCG___        C
GAM1024 CYP1A1   3' TAGATGCTGATGGAGCCT   4947        CG   G
                                  AGGCTCCA  AGCA CTG
                                  ||||||||  |||| |||
                                  TCCGAGGT  TCGT GAT
                                      AG   A
GAM1024 GFPT2    3' CTGTTCTCTGACATCCGTGGAG 17576        AG___  CTGC
            CC                    GGCTCCACG    CAG   AACAG
                                  |||||||||    |||   |||||
                                  CCGAGGTGC    GTC   TTGTC
                                       CTACA   TC__
GAM1024 GJA4     3' TTGCTGGCCATGGAGCCT    59370       CGA  AGCT
                                  AGGCTCCA   GC   GCAA
                                  ||||||||   ||   ||||
                                  TCCGAGGT   CG   CGTT
                                      AC_  GT__
GAM1024 GLI2     5' GTAGCTGCCCAAGGAGCC    47528      ACGA
                                  GGCTCC   GCAGCTGC
                                  ||||||   ||||||||
                                  CCGAGG   CGTCGATG
                                     AACC
GAM1024 HDAC7A   3' TGCCCACTCGGGGAGCCT    31213       A   CAGCT
                                  AGGCTCC CGAG    GCA
                                  ||||||| ||||    |||
                                  TCCGAGG GCTC    CGT
                                      G   ACC__
GAM1024 HDAC7A   3' TGCCCACTCGGGGAGCCT    33454       A   CAGCT
                                  AGGCTCC CGAG    GCA
                                  ||||||| ||||    |||
                                  TCCGAGG GCTC    CGT
                                      G   ACC__
GAM1024 HSD17B1  5' CACCTGCTTGTAAAGCCT    4682       CC      C
                                  AGGCT  ACGAGCAG TG
                                  |||||  |||||||| ||
                                  TCCGA  TGTTCGTC AC
                                     AA      C
GAM1024 LGALS3BP 5' GTTGCAGCTACCGCAGCC    69319     CCA  AGC
                                  GGCT   CG   AGCTGCAAC
                                  ||||   ||   |||||||||
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                                CCGA  GC  TCGACGTTG
                                  C__ CA_
GAM1024 NRL     5' GCCCTGCTCCATGGAGCCT  20515       C_    CT
                                AGGCTCCA GAGCAG GC
                                |||||||| |||||| ||
                                TCCGAGGT CTCGTC CG
                                    AC    C_
GAM1024 SLC2A3  3' CTGTTCCCTCTGCTCCTGGAGC 22661       C    CTGC
            CT                   AGGCTCCA GAGCAG   AACAG
                                |||||||| |||||| |||||
                                TCCGAGGT CTCGTC   TTGTC
                                    C    TCCC
GAM1024 SLC9A1  3' TGCCTGCTGTGGAGCC     70415       G    CT
                                GGCTCCAC AGCAG GCA
                                |||||||| ||||| |||
                                CCGAGGTG TCGTC CGT
                                    _   __
GAM1024 SRRM1   3' CTGCTGCAGCTGCTGTGACCC 19553    CTC  G       A
                                GG  CAC AGCAGCTGCA CAG
                                ||  ||| |||||||||| |||
                                CC  GTG TCGTCGACGT GTC
                                 CA_ _       C
GAM1024 USP14   5' GCAGCTGCTCCTGGTCCC    17659    CT  C
                                GG CCA GAGCAGCTGC
                                || ||| ||||||||||
                                CC GGT CTCGTCGACG
                                 CT  C
GAM1024 VWF     3' CTGCTGCAGCTGCATGGGTGCC 5093      T A A       A
            T                    AGGC CC CG GCAGCTGCA CAG
                                |||| || || ||||||||| |||
                                TCCG GG GT CGTCGACGT GTC
                                  T _ A       C
GAM1024 XPNPEP2 3' CTGCTACAGCTGCTCCCCTCCC 12682    CTCCAC       CAA
                                GG    GAGCAGCTG  CAG
                                ||    |||||||||  |||
                                CC    CTCGTCGAC  GTC
                                 CTCCC_       ATC
GAM1024 ZNFN2A1 3' GCTGCTCTTGGAGCCT     60739       C
                                AGGCTCCA GAGCAGC
                                |||||||| |||||||
                                TCCGAGGT CTCGTCG
                                    T
GAM1024 AIP     3' TGCTGCAGCTGCCAGCC    14280     CCACGA       A
                                GGCT    GCAGCTGCA CA
                                ||||    ||||||||| ||
                                CCGA    CGTCGACGT GT
                                  C_____       C
GAM1024 ARHGEF3 5' GCCGCCCGGCATCGTGGAGCT 38955         _ A__  T
                                GGCTCCACGA GC  GC GC
                                |||||||||| ||  || ||
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                                TCGAGGTGCT CG   CG CG
                                      A  GCC  C
GAM1024  C14orf4   5'  GCTGCCCGGGCGGTGGAGCC   67339        _____ A
                                GGCTCCAC     G GCAGC
                                ||||||||     | |||||
                                CCGAGGTG     C CGTCG
                                     GCGGG C
GAM1024  C8orf2    3'  CTGCTGCAGCTGCCCCACCCC  23160    CTCCACGA        A
                                GG       GCAGCTGCA CAG
                                ||       ||||||||| |||
                                CC       CGTCGACGT GTC
                                 CCACCC__        C
GAM1024  Dlc2      5'  CTGCTGCAGCTGCAGGAGGAGC 54759       ACGA        A
               C                 GGCTCC    GCAGCTGCA CAG
                                ||||||    ||||||||| |||
                                CCGAGG    CGTCGACGT GTC
                                    AGGA        C
GAM1024  FBXO27    3'  TGCAGCTGCTGCTT       74515      TCCACG
                                AGGC      AGCAGCTGCA
                                ||||      ||||||||||
                                TTCG      TCGTCGACGT
                                  _______
GAM1024  FLJ10898  5'  GCAGCTGCTGCAGCC       59435      C  CGA
                                GGCT CA   GCAGCTGC
                                |||| ||   ||||||||
                                CCGA GT   CGTCGACG
                                  C  ___
GAM1024  FLJ11710  3'  TGCAGACGTGGAGCT       45834          AGCAG
                                GGCTCCACG     CTGCA
                                |||||||||     |||||
                                TCGAGGTGC     GACGT
                                     A____
GAM1024  FLJ13456  5'  GCCGCTCGCCGGAGCCT     65942        A_     A
                                AGGCTCC  CGAGC GC
                                |||||||  ||||| ||
                                TCCGAGG  GCTCG CG
                                    CC     C
GAM1024  FLJ20034  3'  AGCTGCTCGTGCAGCC      34357      C
                                GGCT CACGAGCAGCT
                                |||| ||||||||||
                                CCGA GTGCTCGTCGA
                                  C
GAM1024  FLJ20275  3'  TGCAGCTGCCGATGTAGCCT   34827       C  _  A
                                AGGCT CA CG GCAGCTGCA
                                ||||| || || |||||||||
                                TCCGA GT GC CGTCGACGT
                                  T  A  _
GAM1024  FLJ20507  3'  CTGGGGCCTTCTCGTGGAACC  35284    C       C  CT  AA
                                GG TCCACGAG AG  GC  CAG
                                || ||||||| ||  ||  |||
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                                CC AGGTGCTC TC  CG  GTC
                                 A       T __  GG
GAM1024  FLJ20507  3'  CTGGGGCCTTCTCGTGGAACC  60219    C       C  CT  AA
                                GG TCCACGAG AG  GC  CAG
                                || |||||||| ||  ||  |||
                                CC AGGTGCTC TC  CG  GTC
                                 A       T __  GG
GAM1024  FLJ21865  3'  TGCAGCTGCACAGCCT      42812       CCACGA
                                AGGCT     GCAGCTGCA
                                |||||     |||||||||
                                TCCGA     CGTCGACGT
                                   CA____
GAM1024  HEMK      3'  TGCTGCAGCTGGGAGAGCT   32444       CACGAG       A
                                GGCTC     CAGCTGCA CA
                                |||||     |||||||| ||
                                TCGAG     GTCGACGT GT
                                   AGG___       C
GAM1024  JAM1      3'  CAGCTGCTCAGGAGCCT     33750        AC
                                AGGCTCC  GAGCAGCTG
                                |||||||  |||||||||
                                TCCGAGG  CTCGTCGAC
                                   A_
GAM1024  JAM1      3'  CAGCTGCTCAGGAGCCT     57888        AC
                                AGGCTCC  GAGCAGCTG
                                |||||||  |||||||||
                                TCCGAGG  CTCGTCGAC
                                   A_
GAM1024  JAM1      3'  CAGCTGCTCAGGAGCCT     57917        AC
                                AGGCTCC  GAGCAGCTG
                                |||||||  |||||||||
                                TCCGAGG  CTCGTCGAC
                                   A_
GAM1024  JAM1      3'  CAGCTGCTCAGGAGCCT     57943        AC
                                AGGCTCC  GAGCAGCTG
                                |||||||  |||||||||
                                TCCGAGG  CTCGTCGAC
                                   A_
GAM1024  KIAA0062  3'  TAGCCACTGTGGAGCC      70244         G  CA
                                GGCTCCAC AG  GCTG
                                |||||||| ||  ||||
                                CCGAGGTG TC  CGAT
                                   _  AC
GAM1024  KIAA0140  3'  TGCCGTCCACCCGTGGGGCC  27817         AGCA_  T
                                GGCTCCACG    GC GCA
                                |||||||||    || |||
                                CCGGGGTGC    TG CGT
                                     CCACC  C
GAM1024  KIAA0828  3'  TGCTGTTTCTCAGCAAAGCCT  81201       CCAC_  C   T
                                AGGCT    GAG AGC GCA
                                |||||    ||| ||| |||
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                                TCCGA    CTC TTG CGT
                                  AACGA  T  T
GAM1024 KIAA0982 3' CTGCCACAGCTGCTCACCTTGT 25848     TCCAC       CAA
             CT                   AGGC    GAGCAGCTG  CAG
                                |||| |||||||||  |||
                                TCTG    CTCGTCGAC  GTC
                                  TTCCA       ACC
GAM1024 KIAA1068 5' CTGCTGCAGCTGAGAAGGAGCC 31031      ACGAG      A
                                GGCTCC    CAGCTGCA CAG
                                |||||| ||||||| |||
                                CCGAGG    GTCGACGT GTC
                                   AAGA_      C
GAM1024 KIAA1157 5' TGCTGCAGCTGCAGCC     72252     CCACGA       A
                                GGCT    GCAGCTGCA CA
                                |||| |||||||| ||
                                CCGA    CGTCGACGT GT
                                  _______       C
GAM1024 KIAA1838 3' CTGTTGCAGCTGCAAGGAGACC 64731   _   ACGA
                                GG CTCC   GCAGCTGCAACAG
                                || ||||  ||||||||||||
                                CC GAGG   CGTCGACGTTGTC
                                 A   AA__
GAM1024 KIAA1922 5' CTGCTGCAGCTGGGAGGGGAGC 73627      ACGAG      A
             T                   GGCTCC    CAGCTGCA CAG
                                |||||| ||||||| |||
                                TCGAGG    GTCGACGT GTC
                                   GGAGG      C
GAM1024 MEF-2    3' TTGCAGCTTGAGGGACCT    64399    CT  A  AGC
                                AGG  CC CG   AGCTGCAA
                                |||  || ||   ||||||||
                                TCC  GG GT   TCGACGTT
                                 AG  A  ___
GAM1024 MGC4415  3' TGGCCGCCATGGAGCCT     48955       CGA  A
                                AGGCTCCA   GC GCTG
                                ||||||||   || ||||
                                TCCGAGGT   CG CGGT
                                    AC_  C
GAM1024 SAE1     3' GTTGCTCGGGAGCCT       18533       A
                                AGGCTCC CGAGCAGC
                                ||||||| ||||||||
                                TCCGAGG GCTCGTTG
                                  _
GAM1024 SHANK3   3' TGCAGCTGCCCAGTCT      65505      CCACGA
                                AGGCT     GCAGCTGCA
                                |||||     |||||||||
                                TCTGA     CGTCGACGT
                                  CC_____
GAM1024 TP53TG3  3' CTGGGAGCTGCTGTGGAGCCT  31104        G      GCAA
                                AGGCTCCAC AGCAGCT    CAG
                                ||||||||| |||||||    |||
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                                TCCGAGGTG TCGTCGA   GTC
                                      _     GG__
GAM1024 VAV3    3' TGTTGCATTTCATGGGCCT   20367     T  C  CAGC
                                AGGC CCA GAG   TGCAACA
                                |||| ||| |||   |||||||
                                TCCG GGT CTT   ACGTTGT
                                  _  A  T___
GAM1024 ZDHHC5  3' TGGCCCCTTGGAGCCT     91563       CG  CA
                                AGGCTCCA  AG  GCTG
                                ||||||||  ||  ||||
                                TCCGAGGT  TC  CGGT
                                     __ CC
GAM1024 ZIN     3' TGTTTGCCATGGAGCCT    25495       CGA   CT
                                AGGCTCCA   GCAG  GCA
                                ||||||||   ||||  |||
                                TCCGAGGT   CGTT  TGT
                                    AC_   __
GAM1024 ZNF304  5' GCGGCTCTCGTGGAACCT   40315    C      C
                                AGG TCCACGAG AGCTGC
                                ||| |||||||| ||||||
                                TCC AGGTGCTC TCGGCG
                                  A      _
GAM1024 LOC125268 3' TGCCCCTGCCCAGTGGAGCCT 76081        GA_   CT
                                AGGCTCCAC   GCAG  GCA
                                |||||||||   ||||  |||
                                TCCGAGGTG   CGTC  CGT
                                     ACC   CC
GAM1024 LOC148443 3' CTGTTGCAACTCAAAGAGC   78856     CAC   CAGC
                                GCTC   GAG   TGCAACAG
                                ||||   |||   ||||||||
                                CGAG   CTC   ACGTTGTC
                                  AAA   A___
GAM1024 LOC150157 5' CTGCACAGCTGCTCCCAGAGCC 84877       CAC       CAA
           T                     AGGCTC   GAGCAGCTG   CAG
                                ||||||   |||||||||   |||
                                TCCGAG   CTCGTCGAC   GTC
                                   ACC       AC_
GAM1024 LOC150984 5' TGCTGCAGCTGCAGCC     60371     CCACGA       A
                                GGCT     GCAGCTGCA CA
                                ||||     ||||||||| ||
                                CCGA     CGTCGACGT GT
                                  _______        C
GAM1024 LOC161247 5' GCAGCTGCCTGGCAGCC    82267     _  CGA
                                GGCT CCA   GCAGCTGC
                                |||| |||   ||||||||
                                CCGA GGT   CGTCGACG
                                  C   C__
GAM1024 LOC166034 5' TTGCAGCTGAAGAGCCT    87258       CACGAG
                                AGGCTC     CAGCTGCAA
                                ||||||     |||||||||
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                                TCCGAG     GTCGACGTT
                                   AA____
GAM1024  LOC166842 5'  TGCTGCAGCTGAGGGAGCT   82666       ACGAG       A
                                GGCTCC    CAGCTGCA CA
                                ||||||    |||||||| ||
                                TCGAGG    GTCGACGT GT
                                   GA___       C
GAM1024  LOC196890 5'  CTGCACAGCTGCTCCCAGAGCC 89647       CAC       CAA
              T                   AGGCTC   GAGCAGCTG   CAG
                                ||||||   |||||||||   |||
                                TCCGAG   CTCGTCGAC   GTC
                                   ACC       AC_
GAM1024  LOC200471 5'  GCAGCTGTGGAACCT      90054     C   ACGA
                                AGG TCC    GCAGCTGC
                                ||| |||    ||||||||
                                TCC AGG    TGTCGACG
                                  A  _____
GAM1024  LOC201115 5'  GCTGCTCGTGGGCCT      88106      T
                                AGGC CCACGAGCAGC
                                |||| ||||||||||
                                TCCG GGTGCTCGTCG
                                  _
GAM1024  LOC204970 3'  GTGCAGCTGCAGGCT      89415      CCACGA       A
                                GGCT      GCAGCTGCA C
                                ||||      ||||||||| |
                                TCGG      CGTCGACGT G
                                  A_____         C
GAM1024  LOC219513 3'  TGCGGCTGCTCACAGAGC    94335      CAC
                                GCTC   GAGCAGCTGCA
                                ||||   ||||||||||
                                CGAG   CTCGTCGGCGT
                                  ACA
GAM1024  LOC256848 5'  TGCTGCGGCTGCGGAACC    97515    C   ACGA       A
                                GG TCC    GCAGCTGCA CA
                                || |||    ||||||||| ||
                                CC AGG    CGTCGGCGT GT
                                 A  _____        C
GAM1024  LOC51083  5'  CTGTTGGAGCCCAGTGGAGCCT 31999         GAGCA   G
                                AGGCTCCAC     GCT CAACAG
                                |||||||||     ||| ||||||
                                TCCGAGGTG     CGA GTTGTC
                                     ACC__   G
GAM1024  LOC51246  3'  TTGCTCCCTGGAGCCT      33219        C_
                                AGGCTCCA  GAGCAG
                                ||||||||  ||||||
                                TCCGAGGT  CTCGTT
                                     CC
GAM1024  LOC91097  5'  GCTGCGTGTGGAGCCT      64838          A
                                AGGCTCCACG GCAGC
                                |||||||||| |||||
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                                TCCGAGGTGT CGTCG
                                      G
GAM1024 LOC93082 3' CTGTTGTGACTGGTGAAGCC  56443     C  GAG  CT
                                GGCT CAC  CAG  GCAACAG
                                |||| |||  |||  |||||||
                                CCGA GTG  GTC  TGTTGTC
                                  A  ___  AG
GAM1024 LOC93538 5' TGTTGCAGGTGATGGAACT   72564    C   CGAG  G
                                GG TCCA   CA CTGCAACA
                                || ||||   || ||||||||
                                TC AGGT   GT GACGTTGT
                                 A   A___  G
GAM1025 KIAA0256 3' CATCACAGAATCAACCA     64418        _ C
                                TGGTTGAT C GTGATG
                                |||||||| | ||||||
                                ACCAACTA G CACTAC
                                     A A
GAM1025 LOC196808 3' ACAAGGCCAAATCAATCA   87521        CCG  AT
                                TGGTTGAT  TG  GCCTTGT
                                ||||||||  ||  |||||||
                                ACTAACTA  AC  CGGAACA
                                     A__  __
GAM1026 ADCY6   3' CACACCCTGGATCCCCGTACCA 40614    ACCAGAA      _
           C                     GTG      GGTCCAGG TGTG
                                |||      |||||||| ||||
                                CAC      CTAGGTCC ACAC
                                  CATGCCC       C
GAM1026 ADCY6   3' CACACCCTGGATCCCCGTACCA 30923    ACCAGAA      _
           C                     GTG      GGTCCAGG TGTG
                                |||      |||||||| ||||
                                CAC      CTAGGTCC ACAC
                                  CATGCCC       C
GAM1026 CACNA2D2 3' CACACCATTCATTCTGGTCAT  20079         GGTCCA
                                GTGACCAGAA     GGTGTG
                                ||||||||||     ||||||
                                TACTGGTCTT     CCACAC
                                     ACTTA_
GAM1026 CXorf6  3' CACTCACCTTCTGGCCA     18513    A       CCA
                                TG CCAGAAGGT   GGTG
                                || |||||||||   ||||
                                AC GGTCTTCCA   TCAC
                                 C        C__
GAM1026 GNE     3' CACACCTGGCCCTAGTG     18477    GA   T
                                CA  AGG CCAGGTGTG
                                ||  ||| |||||||||
                                GT  TCC GGTCCACAC
                                 GA   C
GAM1026 GPR30   3' ACACCTGGGTGGACAC      7689      A   GAAGG
                                GTG CCA    TCCAGGTGT
                                ||| |||    |||||||||
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                                CAC GGT    GGGTCCACA
                                  A  _____
GAM1026 LPIN1    3' CACCACCTTCTGAACAC    67391    AC      CCA
                                GTG CAGAAGGT  GGTG
                                ||| ||||||||  ||||
                                CAC GTCTTCCA  CCAC
                                  AA     ____
GAM1026 LSS      3' CACAGCGCCTTCTGCCAC   9814     AC      CCAG
                                GTG CAGAAGGT  GTG
                                ||| ||||||||  |||
                                CAC GTCTTCCG  CAC
                                  C_      CGA_
GAM1026 MAFK     3' CACACCCCTCGTACCTGTCAC 9878      CAGA   CCA___
                                GTGAC   AGGT    GGTGTG
                                |||||   ||||    ||||||
                                CACTG   TCCA    CCACAC
                                   _____  TGCTCC
GAM1026 MOCS1    3' CACACCTGGCCCTGTTCAC   92031    C  AA  T
                                GTGA CAG  GG CCAGGTGTG
                                |||| |||  || |||||||||
                                CACT GTC  CC GGTCCACAC
                                  T  __ _
GAM1026 PKIA     3' CACTTTGACCCTCGACCAC   22381    ACCA A   C
                                GTG   GA GGTC AGGTG
                                |||   || |||| |||||
                                CAC   CT CCAG TTCAC
                                  CAG_ C   T
GAM1026 PRKAR2A  3' CACCAAAACCTTCTGGTCA   14775         CCA
                                TGACCAGAAGGT  GGTG
                                ||||||||||||  ||||
                                ACTGGTCTTCCA  CCAC
                                      AAA
GAM1026 RAMP3    3' ACACCCCACCTGGTCAT    19585       AA  TCCA
                                GTGACCAG  GG   GGTGT
                                ||||||||  ||   |||||
                                TACTGGTC  CC   CCACA
                                    CA  _____
GAM1026 SELP     3' CACCGTGGACCTTCCTGCCAC  11535    AC  _     _
                                GTG  CAG AAGGTCCA GGTG
                                |||  ||| |||||||| ||||
                                CAC  GTC TTCCAGGT CCAC
                                  C_  C      G
GAM1026 SORCS2   3' CACACCTGTCCCTGGCCA   40413   A   AA  TC
                                TG CCAG  GG  CAGGTGTG
                                || ||||  ||  ||||||||
                                AC GGTC  CC  GTCCACAC
                                 C   __  T_
GAM1026 TGFB1    5' CACCCACCTTCTGGT      5399         CCA
                                ACCAGAAGGT  GGTG
                                ||||||||||  ||||
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                                TGGTCTTCCA   CCAC
                                      C__
GAM1026 ALOX15B   3'  CACTGATTGGACCTTATGGTCA 6688        G       GT_
              C                    GTGACCA AAGGTCCAG   GTG
                                   ||||||| |||||||||   |||
                                   CACTGGT TTCCAGGTT   CAC
                                       A        AGT
GAM1026 ARHGDIG   3'  CACACCCTGGGCCTGG      6776      GAA      _
                                   CCA   GGTCCAGG TGTG
                                   |||   |||||||| ||||
                                   GGT   CCGGGTCC ACAC
                                     ____       C
GAM1026 BICD2     3'  CACACCCAGACCTGGGCAT    70388     A  AGA    CA
                                   GTG CC   AGGTC  GGTGTG
                                   ||| ||   |||||  ||||||
                                   TAC GG   TCCAG  CCACAC
                                     _ G__     AC
GAM1026 DKFZP434L0718 3'  CACACCTGACGGGATGGTTAC  49546        GAAG   C
                                   GTGACCA    GTC AGGTGTG
                                   |||||||    ||| |||||||
                                   CATTGGT    CAG TCCACAC
                                       AGGG   _
GAM1026 DRF1      3'  CATGTGAGCTTCTGGTCAC    47027          G  C G
                                   GTGACCAGAAG TC A GTG
                                   |||||||||||| || | |||
                                   CACTGGTCTTC AG T TAC
                                         G  _ G
GAM1026 FLJ10774  3'  CACACCTGGAAGCTGGCCGC   45082     A    AAGG
                                   GTG CCAG    TCCAGGTGTG
                                   ||| ||||    ||||||||||
                                   CGC GGTC    AGGTCCACAC
                                     C    GA__
GAM1026 FLJ12747  3'  CACTAACTCTTCTGGTCAC    49710          _  CCA
                                   GTGACCAGAAG GT   GGTG
                                   |||||||||||| ||   ||||
                                   CACTGGTCTTC CA   TCAC
                                         T  A__
GAM1026 FLJ14154  3'  CACACCTGCCCCTAATCAC    45811      CCAGA   TC
                                   GTGA    AGG  CAGGTGTG
                                   ||||    |||  ||||||||
                                   CACT    TCC  GTCCACAC
                                     AA___   CC
GAM1026 KIAA1013  3'  CAGTTGGACCTCCTGACCA    88887    AC   A      G
                                   TG  CAG AGGTCCAG TG
                                   ||  ||| |||||||| ||
                                   AC  GTC TCCAGGTT AC
                                    CA   C       G
GAM1026 KIAA1054  3'  CACAAACCTTCTTGGTCAC    68427        _     CCAG
                                   GTGACCA GAAGGT    GTG
                                   ||||||| ||||||    |||
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                                CACTGGT CTTCCA   CAC
                                   T     AA__
GAM1026 MGC2452  5' CACACCTGAGCCTGCCCAC  50979    ACCAGA  TC
                                GTG     AGG  CAGGTGTG
                                |||     |||  ||||||||
                                CAC     TCC  GTCCACAC
                                  CCG___   GA
GAM1026 MGC4189  3' CACACCTGAATTTTCAGTCAC 50229      CA     C
                                GTGAC  GAAGGT CAGGTGTG
                                |||||  |||||| ||||||||
                                CACTG  CTTTTA GTCCACAC
                                   A_     A
GAM1026 QPRT     3' GGACCCTCTGGGTCAC      59791       _  A
                                GTGACC AGA GGTCC
                                |||||| ||| |||||
                                CACTGG TCT CCAGG
                                   G   C
GAM1026 RCD-8    3' CACACCTGTACCCTCTGCCCAC 26749     AC   A   C
                                GTG  CAGA GGT CAGGTGTG
                                |||  |||| ||| ||||||||
                                CAC  GTCT CCA GTCCACAC
                                  CC    C   T
GAM1026 LOC115110 5' CATTGCCCTCCTGGTCAC    71714        A   TCCA
                                GTGACCAG AGG    GGTG
                                |||||||| |||    ||||
                                CACTGGTC TCC    TTAC
                                     C   CG__
GAM1026 LOC115129 3' CACCCAACCTTTAATCAC    73226     CCA     CCA
                                GTGA   GAAGGT   GGTG
                                ||||   ||||||   ||||
                                CACT   TTTCCA   CCAC
                                  AA_     AC_
GAM1026 LOC121219 3' CACAGCTCCTCCCTGGTCAC  74042        A_   TCC  G
                                GTGACCAG  AGG   AG TGTG
                                ||||||||  |||   || ||||
                                CACTGGTC  TCC   TC ACAC
                                     CC   ___  G
GAM1026 LOC121344 3' CACACCTGTTCTCTGG      74065      AG TC
                                CCAGA  G  CAGGTGTG
                                |||||  |  ||||||||
                                GGTCT  C  GTCCACAC
                                  __ TT
GAM1026 LOC138835 5' CACACCTGCCCCTGGATCAC  75953     _   AA  TC
                                GTGA CCAG  GG  CAGGTGTG
                                |||| ||||  ||  ||||||||
                                CACT GGTC  CC  GTCCACAC
                                  A   __  C_
GAM1026 LOC144395 5' CACACCTGGACGGACCGGTCA 76825      AGAAG
                                TGACC    GTCCAGGTGTG
                                |||||    ||||||||||
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                                ACTGG    CAGGTCCACAC
                                   CCAGG
GAM1026  LOC145453 3'  CACACCTGTAATCTGAGCAC  77136    AC   AGGTC
                                GTG  CAGA    CAGGTGTG
                                |||  ||||    ||||||||
                                CAC  GTCT    GTCCACAC
                                  GA   AAT__
GAM1026  LOC145725 5'  ACACCTTGCTGGTCAC     77395       AAGGTCC
                                GTGACCAG     AGGTGT
                                ||||||||     ||||||
                                CACTGGTC     TCCACA
                                     GT_____
GAM1026  LOC145732 5'  ACACCTTGCTGGTCAC     77417       AAGGTCC
                                GTGACCAG     AGGTGT
                                ||||||||     ||||||
                                CACTGGTC     TCCACA
                                     GT_____
GAM1026  LOC146562 5'  CACCCGGACCTTCCGGTCA   57531     A      A
                                TGACC GAAGGTCC GGTG
                                ||||| |||||||| ||||
                                ACTGG CTTCCAGG CCAC
                                   C       C
GAM1026  LOC146733 3'  CACAGGGACCTTCCGCTCAC  83755     CCA      AG
                                GTGA  GAAGGTCC  GTG
                                ||||  ||||||||  |||
                                CACT  CTTCCAGG  CAC
                                  CGC       GA
GAM1026  LOC155036 5'  CACACCTGAACCAGTCA     86337     CAGAA  C
                                TGAC    GGT CAGGTGTG
                                ||||    ||| ||||||||
                                ACTG    CCA GTCCACAC
                                  A____   A
GAM1026  LOC158055 3'  CACACCTGGAGGCTGGACAC  81665     A   AAGG
                                GTG CCAG    TCCAGGTGTG
                                ||| ||||    ||||||||||
                                CAC GGTC    AGGTCCACAC
                                  A   GG__
GAM1026  LOC168082 5'  CACACCTGGAAAAGGCTCAC  82689     _  AGAAGG
                                GTGA CC     TCCAGGTGTG
                                |||| ||     ||||||||||
                                CACT GG     AGGTCCACAC
                                  C  AAA___
GAM1026  LOC196957 5'  ACACCTTGCTGGTCAC     87811       AAGGTCC
                                GTGACCAG     AGGTGT
                                ||||||||     ||||||
                                CACTGGTC     TCCACA
                                     GT_____
GAM1026  LOC196961 5'  ACACCTTGCTGGTCAC     87832       AAGGTCC
                                GTGACCAG     AGGTGT
                                ||||||||     ||||||
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                                CACTGGTC      TCCACA
                                    GT_____
GAM1026  LOC197138 5'  ACACCTTGCTGGTCAC      87905        AAGGTCC
                                GTGACCAG      AGGTGT
                                ||||||||      ||||||
                                CACTGGTC      TCCACA
                                    GT_____
GAM1026  LOC219917 3'  CATTTCACCTTCTGGCCAC    91535     A       CC
                                GTG CCAGAAGGT  AGGTG
                                ||| |||||||||  |||||
                                CAC GGTCTTCCA  TTTAC
                                  C        C_
GAM1026  LOC221463 3'  CATCTGCAACCCTCCAGTC    92066     CA  A   C_
                                GAC  GA GGT  CAGGTG
                                |||  || |||  ||||||
                                CTG  CT CCA  GTCTAC
                                  AC  C   AC
GAM1026  LOC253985 5'  CACACCTGGATTTAGG       96484     AGA
                                CC   AGGTCCAGGTGTG
                                ||   |||||||||||||
                                GG   TTTAGGTCCACAC
                                 A__
GAM1026  LOC255988 5'  GGAACGCTCCTGGTCAC      97610         A  _  _
                                GTGACCAG AG GT CC
                                |||||||| || || ||
                                CACTGGTC TC CA GG
                                    C  G  A
GAM1026  LOC256536 3'  CACACCTGGACCGTGGATCAC  94711      _   GAA
                                GTGA CCA   GGTCCAGGTGTG
                                |||| |||   ||||||||||||
                                CACT GGT   CCAGGTCCACAC
                                  A   G__
GAM1026  LOC51161  3'  CTGGACTTCTGACCAC       32510     AC     G
                                GTG  CAGAAG TCCAG
                                |||  |||||| |||||
                                CAC  GTCTTC AGGTC
                                  CA     _
GAM1027  ABR       3'  GGTCTCCTGGCAGCCT       6577          CA
                                AGGCTGCCAG  AGATC
                                ||||||||||  |||||
                                TCCGACGGTC  TCTGG
                                     C_
GAM1027  ABR       3'  GGTCTCCTGGCAGCCT       41729         CA
                                AGGCTGCCAG  AGATC
                                ||||||||||  |||||
                                TCCGACGGTC  TCTGG
                                     C_
GAM1027  BCL7B     3'  GAGCTGCTGGCAGCTTCT     8133       G       AGA
                                AGAAG CTGCCAGCA   TC
                                ||||| |||||||||   ||
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                                TCTTC GACGGTCGT   AG
                                  _       CG_
GAM1027 CGTHBA   3' GTCTCTCTGACAGCCTTC    23864        C   CA
                                GAAGGCTG CAG  AGAT
                                |||||||| |||  ||||
                                CTTCCGAC GTC  TCTG
                                     A   TC
GAM1027 DNAJB1   3' CTGGGTCTGGCAGCCCTC    20444    A       _ A_
                                GA GGCTGCCAG C  AG
                                || |||||||||  |  ||
                                CT CCGACGGTC G  TC
                                 C        T GG
GAM1027 HK2      5' CTCGCCGGTAGCCTTCT     3951           A  A
                                AGAAGGCTGCC GC AG
                                |||||||||||  || ||
                                TCTTCCGATGG CG TC
                                       C  C
GAM1027 IL10RA   3' ATCTTGCTGACAACTTC     59639      GC  C
                                GAAG  TG CAGCAAGAT
                                ||||  ||  |||||||||
                                CTTC  AC GTCGTTCTA
                                  A_  A
GAM1027 INPPL1   3' GGTCTTGCAAGCAGCCTCCT   7804     A      CA
                                AG AGGCTGC  GCAAGATC
                                || |||||||  ||||||||
                                TC TCCGACG  CGTTCTGG
                                 C       AA
GAM1027 MPP3     3' TTGATCTTAACCTTTT      8641        CTGCCAGC
                                AGAAGG       AAGATCAA
                                ||||||       ||||||||
                                TTTTCC       TTCTAGTT
                                   AA_______
GAM1027 P53AIP1  3' TGACCTTGAGGAGCCTTTT   42084        G  AG    A
                                AGAAGGCT CC  CAAG TCA
                                |||||||| ||  |||| |||
                                TTTTCCGA GG  GTTC AGT
                                     _  A_    C
GAM1027 PACSIN1  3' TCTCCCTGCTGGCAGCCCTTC  92264      _       ____
                                GAAGG CTGCCAGCA   AGA
                                ||||| |||||||||   |||
                                CTTCC GACGGTCGT   TCT
                                   C        CCC
GAM1027 RAB36    3' CTTGCAGGCAGCCTTCT     16961          A
                                AGAAGGCTGCC GCAAG
                                |||||||||||| |||||
                                TCTTCCGACGG CGTTC
                                       A
GAM1027 SLC21A9  3' TTGATCCTCTCTCAGCCTTT   23425        CC  CAA
                                GAAGGCTG  AG   GATCAA
                                ||||||||  ||   ||||||
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                                TTTCCGAC  TC   CTAGTT
                                     TC  TC_
GAM1027  THBD     3'  TTGGTCGGCAGCCTTCT     4498          AGCAA
                                AGAAGGCTGCC    GATCAA
                                ||||||||||     ||||||
                                TCTTCCGACGG    CTGGTT
                                       _____
GAM1027  TMEM1    3'  GTCAGCCTGGGAGCCTTC    12337       G    CAA
                                GAAGGCT CCAG   GAT
                                |||||||  ||||   |||
                                CTTCCGA GGTC   CTG
                                    G    CGA
GAM1027  ATP6V1F  3'  GGCTTGCCATCAGCCTTCT   14875        CCA    A
                                AGAAGGCTG   GCAAG TC
                                |||||||||   ||||| ||
                                TCTTCCGAC   CGTTC GG
                                     TAC    _
GAM1027  BMF      3'  TGGGCCACTGGCAGCCTTCT   53166          CAAGA
                                AGAAGGCTGCCAG    TCA
                                ||||||||||||     |||
                                TCTTCCGACGGTC    GGT
                                       ACCG_
GAM1027  BOLL     5'  TCTCGCTGGCTAGCCTTCT    52282        _     A
                                AGAAGGCT GCCAGC AGA
                                ||||||||  ||||||  |||
                                TCTTCCGA CGGTCG TCT
                                     T     C
GAM1027  FLJ12891 3'  TGATCATGGCAGCCTGCT    46349    A       GCAA
                                AG AGGCTGCCA    GATCA
                                ||  |||||||||    |||||
                                TC TCCGACGGT    CTAGT
                                 G       A___
GAM1027  FLJ22940 5'  TTGGTCCTGGCAGCCTTC    44699          CAA
                                GAAGGCTGCCAG   GATCAA
                                ||||||||||||   ||||||
                                CTTCCGACGGTC   CTGGTT
                                       ____
GAM1027  HEMK     3'  TCTGCTGGCACCTTCT      32442       C       A
                                AGAAGG TGCCAGCA GA
                                ||||||  ||||||||  ||
                                TCTTCC ACGGTCGT CT
                                       _       _
GAM1027  HSD17B12 3'  TTGAGACTGGCAGCCATCT    32342     A       CAAGA
                                AGA GGCTGCCAG    TCAA
                                |||  |||||||||    ||||
                                TCT CCGACGGTC    AGTT
                                  A       AG___
GAM1027  KIAA0863 3'  GATCTCCTTCAGCTTTC     29876        CC  CA
                                GAAGGCTG  AG  AGATC
                                ||||||||  ||  |||||
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                                CTTTCGAC  TC  TCTAG
                                     T_  C_
GAM1027  KIAA0863  3'  GATCTCCTTCAGCTTTC     95245        CC  CA
                                GAAGGCTG  AG  AGATC
                                ||||||||  ||  |||||
                                CTTTCGAC  TC  TCTAG
                                     T_  C_
GAM1027  KIAA1538  3'  ATCAAAATGGCAGCCTTTT   71529           GCAA
                                AGAAGGCTGCCA   GAT
                                ||||||||||||   |||
                                TTTTCCGACGGT   CTA
                                       AAAA
GAM1027  KIAA1940  3'  CTTGCTGCAGCCTTCT      79983          C
                                AGAAGGCTGC AGCAAG
                                |||||||||| ||||||
                                TCTTCCGACG TCGTTC
                                       _
GAM1027  KPNA6     3'  TTGATCTTGAATTTGCCCTCT  24615     A   TGCCAG
                                AGA GGC     CAAGATCAA
                                ||| |||     |||||||||
                                TCT CCG     GTTCTAGTT
                                  C   TTTAA_
GAM1027  NIN283    3'  CTCGCTGCCAGCCTTCT     50070         C   A
                                AGAAGGCTG CAGC AG
                                |||||||| |||| ||
                                TCTTCCGAC GTCG TC
                                     C   C
GAM1027  PRO0767   5'  TCTCATGGCAGCCTTC      26025          GCA
                                GAAGGCTGCCA   AGA
                                ||||||||||   |||
                                CTTCCGACGGT   TCT
                                       AC_
GAM1027  SCAM-1    3'  CTTGCTGGCTGCCCTCT     19327     A   T
                                AGA GGC GCCAGCAAG
                                ||| ||| |||||||||
                                TCT CCG CGGTCGTTC
                                  C   T
GAM1027  TREX1     5'  TCCTGCTGGCACCCCCCT    53282    AA  C      A
                                AG  GG TGCCAGCA GA
                                ||  || |||||||| ||
                                TC  CC ACGGTCGT CT
                                 CC  C       C
GAM1027  TREX1     5'  TCCTGCTGGCACCCCCCT    53292    AA  C      A
                                AG  GG TGCCAGCA GA
                                ||  || |||||||| ||
                                TC  CC ACGGTCGT CT
                                 CC  C       C
GAM1027  UBCE7IP5  3'  TGACCTTGATGCAGCCTTC   30163         CAG   A
                                GAAGGCTGC   CAAG TCA
                                |||||||||   |||| |||
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                                CTTCCGACG   GTTC AGT
                                     TA_    C
GAM1027  LOC125268 3'  TGAGGTGCTGGCAGCT      76080          AGA
                                GGCTGCCAGCA   TCA
                                ||||||||||   |||
                                TCGACGGTCGT   AGT
                                     GG_
GAM1027  LOC142901 5'  CGTTGATCCCGCGGTCCCTTC  60498      CT   A  AA
                                GAAGG  GCC GC  GATCAACG
                                |||||  ||| ||  ||||||||
                                CTTCC  TGG CG  CTAGTTGC
                                   C_   _  CC
GAM1027  LOC155435 3'  TCACCTGGCAGCCCTCT     81355     A       CAA
                                AGA GGCTGCCAG   GA
                                ||| |||||||||   ||
                                TCT CCGACGGTC   CT
                                  C        CA_
GAM1027  LOC158656 5'  GATCCAGGCAGCCTTCT     73035          AGCAA
                                AGAAGGCTGCC     GATC
                                ||||||||||     ||||
                                TCTTCCGACGG     CTAG
                                     AC___
GAM1027  LOC159976 5'  TGATGCGGGCAGCTTTCT    87059          A   AGA
                                AGAAGGCTGCC GCA   TCA
                                |||||||||| |||   |||
                                TCTTTCGACGG CGT   AGT
                                     G   ___
GAM1027  LOC221479 3'  GTCAGTCCGGCAGCCTC     92224    A     AGCAA   CA
                                GA GGCTGCC     GAT  AC
                                || |||||||     |||  ||
                                CT CCGACGG     CTG  TG
                                 _      C____   AC
GAM1027  LOC255031 5'  GGGCTCCTGGCAGCCCCCT    97237    AA       CA  AT
                                AG  GGCTGCCAG  AG  C
                                ||  |||||||||  ||  |
                                TC  CCGACGGTC  TC  G
                                 CC        C_  GG
GAM1028  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A     T__
GAM1028  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM1028  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                ||||||||||| |||
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                                GTAAAGTGAAAG GAT
                                          _
GAM1028 JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                  CATTTCACTTTCACTGTCTGAGAT
                                  ||||||||||||||||||||||||
                                  GTAAAGTGAAAGTGACAGACTCTA

GAM1028 KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                  CA  TTCACTGTCTG GA
                                  ||  ||||||||||| ||
                                  GT  AGGTGACAGAC CT
                                   AT         C
GAM1028 PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                  ATTTCACTTT ACTGT
                                  |||||||||| |||||
                                  TAAAGTGAAA TGACA
                                        A
GAM1028 PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                  TTTCACTTTCA   TCTG GA
                                  ||||||||||   |||| ||
                                  AAAGTGAAAGT   GGAC CT
                                         T__   _
GAM1028 WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                  TTTCA TTTCACTGTCT
                                  ||||| ||||||||||
                                  AAAGT AAAGTGACGGG
                                     A
GAM1028 ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                  TTTCACTTT  CTGT   AGAT
                                  |||||||||  ||||   ||||
                                  AAAGTGAAA  GACA   TCTA
                                        C_   CG_
GAM1028 CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                  TTCACTTTCA  GT  GAG
                                  ||||||||||  ||  |||
                                  AAGTGAAAGT  CA  CTC
                                         CT  __
GAM1028 EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                  CTTTCACT TC  GAGAT
                                  |||||||| ||  |||||
                                  GAAAGTGA AG  TTCTA
                                       G  TC
GAM1028 FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
              G                    CATTTC        GTCTGAGAT
                                   ||||||        |||||||||
                                   GTAAAG        CAGACTCTA
                                      AAACATTT_
GAM1028 FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                  CATTTCA   TCACTGTCTGAGAT
                                  |||||||   ||||||||||||||
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                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM1028 KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM1028 KLHL6    3' ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM1028 NIR3     3' GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM1028 PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM1028 PP35     3' ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM1028 PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148       TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM1028 SEP15    3' TCCTACAGTAAGAGTGAAA   14934       C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM1028 SFXN2    3' CTCAGGGGAAAAAAGTGAAA  73941       CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM1028 LOC149703 3' ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM1028 LOC154007 3' ATCTCAAACCCTTTAGTGAAA  81015      TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
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                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM1028  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                   _       ATTT
GAM1028  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM1029  ARNT2    3'  AAACAACCCGTGCATCCCTGC  29450     A    TTTTA
                                GTA GGAT     GGGTTGTTT
                                ||| ||||     |||||||||
                                CGT CCTA     CCCAACAAA
                                  C    CGTG_
GAM1029  LCT      3'  AACCGTAAAAATCCTT      9697           G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
                                TTCCTAAAAAT CCAA
                                       G
GAM1029  RPL15    3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM1029  FBXO30   3'  AACTAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                 G        AA
GAM1029  KIAA0494  3'  AACAACCCTTACTTAC      28736      GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM1029  PRO0641   5'  AAACAACCCCAAAACTTG    26210      GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                   ___    C
GAM1029  SMT3H2    3'  AACAACATAAAAATCCTTGC   22670           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                       A_
GAM1029  LOC120103 3'  AACCTATGAAAAATCCTTGC   74002           A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
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                                CGTTCCTAAAAA  TCCAA
                                      GTA
GAM1029  LOC129831 3'  AAACAACCCCAATGTCC     74889     TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM1029  LOC133088 5'  AAACAAAATAGAAAAATCCCTG 75075     A      AGGG_
           C                     GTA GGATTTTT    TTGTTT
                                ||| ||||||||    ||||||
                                CGT CCTAAAAA    AACAAA
                                  C       GATAA
GAM1029  LOC148089 3'  GGCCCTAAAAATTCCTAC    78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM1029  LOC154547 3'  AACAACATAAAAATCCTTGC   76050           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM1029  LOC158104 3'  ACAGCCAAAAATCCTTA     60313          AG
                                TAAGGATTTTT  GGTTGT
                                ||||||||||  ||||||
                                ATTCCTAAAAA  CCGACA
                                      __
GAM1029  LOC205880 5'  AAACAACCATCATCCTGAC   90709    A    TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM1029  LOC221561 3'  AACAACATAAAAATCCTTGC   92130           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM1029  LOC257591 3'  AACAACATAAAAATCCTTGC   97840           GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM1029  LOC51145  3'  AGCTAAAATCCTTAC       32393          TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
                                CATTCCTAAAA   TCGA
                                      ___
GAM1030  C5        3'  CAAGGAACAGGAAACTGA    8196          CTCTCTC
                                TCAGTTTTCT      TCCTTG
                                ||||||||||      ||||||
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                                AGTCAAAGGA      AGGAAC
                                    CA_____
GAM1030  CHES1    3'  AAGGAGAGAGAGAGAAAACTGA 17769
                                TCAGTTTTCTCTCTCTCTCCTT
                                ||||||||||||||||||||||
                                AGTCAAAAGAGAGAGAGGAA

GAM1030  DDAH2    5'  AGGTGAAGAAACAAGAAAACT  25660        C___  C  T
                                AGTTTTCT   TCT TC CCT
                                ||||||||   ||| || |||
                                TCAAAAGA   AGA AG GGA
                                    ACAA  _  T
GAM1030  DIO3     3'  CCAGGGAGAGAGAAAAAGCTGA 7242         CTC
                                TCAGTTTT  TCTCTCTCCTTGG
                                ||||||||  ||||||||||||
                                AGTCGAAA  AGAGAGAGGGACC
                                    A__
GAM1030  EMX2     3'  GAGAGAGAGAGAAAGCTGA   87565
                                TCAGTTTTCTCTCTCTCTC
                                |||||||||||||||||||
                                AGTCGAAAGAGAGAGAGAG

GAM1030  IL1RAP   3'  CAAAGATAGAAAAAACTGG   56243        C  C  CTCC
                                TCAGTTTT TCT TCT   TTG
                                |||||||| ||| |||   |||
                                GGTCAAAA AGA AGA   AAC
                                    A  T  _____
GAM1030  PAX2     3'  CCAAGGAGATTAAGAAGAAAAC 14323       C  C__
                                GTTTTCT TCT  TCTCCTTGG
                                ||||||| |||  |||||||||
                                CAAAAGA AGA  AGAGGAACC
                                    _  ATT
GAM1030  PAX2     3'  CCAAGGAGATTAAGAAGAAAAC 14332       C  C__
                                GTTTTCT TCT  TCTCCTTGG
                                ||||||| |||  |||||||||
                                CAAAAGA AGA  AGAGGAACC
                                    _  ATT
GAM1030  POH1     5'  AGGAGAGAAAGAAAAAAT    19408      C  C
                                GTTTT TCT TCTCTCCT
                                ||||| ||| ||||||||
                                TAAAA AGA AGAGAGGA
                                   A  A
GAM1030  PVR      3'  CCAAGGAGCAGAGAAAACT   21475         CTCT
                                AGTTTTCTCT   CTCCTTGG
                                ||||||||||   ||||||||
                                TCAAAAGAGA   GAGGAACC
                                    C___
GAM1030  SDPR     3'  CCAAGATTGAAGAAGAAACTGA 16224       TC  C  TCTC
                                TCAGTTT  TCT TC   CTTGG
                                |||||||  ||| ||   |||||
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                                AGTCAAA  AGA AG   GAACC
                                   GA   _  TTA_
GAM1030  TCERG1   3'  GGGTAAAAGAGAAAACACTGA  21995      T  C    CTCT
                                TCAGT TT TCTCT   CCT
                                ||||| || |||||   |||
                                AGTCA AA AGAGA   GGG
                                   C  A    AAAT
GAM1030  TRPS1    3'  CCAAGGCACAAGAGAAAATTGA 26075          CTCTCT
                                TCAGTTTTCTCT    CCTTGG
                                ||||||||||||    ||||||
                                AGTTAAAAGAGA    GGAACC
                                      ACAC__
GAM1030  BY55     3'  AAGGAAAGAGAGAGAAAAC   59342           C
                                GTTTTCTCTCTCT TCCTT
                                |||||||||||| |||||
                                CAAAAGAGAGAGA AGGAA
                                      A
GAM1030  C20orf12  5'  GAGAGAGAGAGAAAAT     36323
                                GTTTTCTCTCTCTCTC
                                ||||||||||||||||
                                TAAAAGAGAGAGAGAG

GAM1030  C20orf4   3'  CCAAAAGTCCAAGAAAGAACTG 31332        C   CTCT  CC
            A                    TCAGTTTT TCT   CT  TTGG
                                ||||||||| |||   ||  ||||
                                AGTCAAGA AGA   GA  AACC
                                     A   ACCT  A_
GAM1030  CCNE2    5'  CAAGAAGAGGAAAACT     16290       TCTCT   C
                                AGTTTTC    CTCT CTTG
                                |||||||    |||| ||||
                                TCAAAAG    GAGA GAAC
                                    _____   A
GAM1030  DKFZP434C171 5'  AGTGAAAGAGAAAAATCTGA   31552     __      C  T
                                TCAG  TTTTCTCT TC CT
                                ||||  |||||||| || ||
                                AGTC  AAAAGAGA AG GA
                                   TA       A  T
GAM1030  DKFZP434D1335 3'  CCAATTTCAAGAAAGAAAACTG 65115        C   CTCTCC
                                CAGTTTTCT TCT     TTGG
                                |||||||||| |||     ||||
                                GTCAAAAGA AGA     AACC
                                     A   ACTTT_
GAM1030  DKFZP564D1378 3'  CAAAGAAAGGGAAAGCTGA   49528          C   CTCC
                                TCAGTTTTCTCT TCT   TTG
                                |||||||||||| |||   |||
                                AGTCGAAAGGGA AGA   AAC
                                      A  _____
GAM1030  FLJ10036  3'  CCAAAAAGAGAAAGAGAAAA  94948        C    CC
                                TTTTCTCT TCTCT  TTGG
                                |||||||| |||||  ||||
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                                AAAAGAGA AGAGA  AACC
                                    A     AA
GAM1030  FLJ23093  3'  CAAGGAAAATGAAAACGGA   44977    A     TCTCTCTC
                                TC GTTTTC       TCCTTG
                                || ||||||       ||||||
                                AG CAAAAG       AGGAAC
                                 G     TAAA____
GAM1030  GAB1     3'  CCATTTCTGAACAAAAGAAAAC 8976          CTCTC  TCCT_
             TGA                  TCAGTTTTCT     TC     TGG
                                ||||||||||     ||     |||
                                AGTCAAAAGA     AG     ACC
                                     AAACA  TCTTT
GAM1030  GDAP1L1   3'  GAGAGAGAGAAAAAAC      43831       C
                                GTTTT TCTCTCTCTC
                                ||||| ||||||||||
                                CAAAA AGAGAGAGAG
                                   A
GAM1030  KIAA0738  3'  CAAGAAAAGAAAGAGAAGACTG 28216           C   CTC
             A                    TCAGTTTTCTCT TCT   CTTG
                                ||||||||||||| |||   ||||
                                AGTCAGAAGAGA AGA   GAAC
                                      A   AAA
GAM1030  KIAA0894  3'  CAAGGAGGAAAAAAC       29702       C  TCTCT
                                GTTTT TC     CTCCTTG
                                ||||| ||     |||||||
                                CAAAA AG     GAGGAAC
                                   A  _____
GAM1030  KIAA1084  3'  CCAATTTGTAGATGAGAAAACT 29835           _   CTCTCC
             GA                   TCAGTTTTCTC TCT      TTGG
                                ||||||||||| |||      ||||
                                AGTCAAAAGAG AGA      AACC
                                      T   TGTTT_
GAM1030  KIAA1209  3'  AGAGAAAAAGCAAAACTGA    60748         _  CTC
                                TCAGTTTT CT   TCTCT
                                |||||||| ||   |||||
                                AGTCAAAA GA   AGAGA
                                     C  AAA
GAM1030  KIAA1393  3'  CCAAAGGGAAAAAGAGAAAAGC 72097         C     C__    C
             TGA                    TCAGTTTT TCTCT   TCTC TTGG
                                ||||||||| |||||   |||| ||||
                                AGTCGAAA AGAGA   AGGG AACC
                                     _    AAA    A
GAM1030  KIAA1922  5'  AGAGATGAGAAAACTGA     73614           _
                                TCAGTTTTCTC TCTCT
                                |||||||||||| |||||
                                AGTCAAAAGAG AGAGA
                                      T
GAM1030  LHX9     3'  AAGAGAGAGAGAGAGA      84175           _
                                TCTCTCTCTCTC CTT
                                |||||||||||| |||
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                                AGAGAGAGAGAG GAA
                                       A
GAM1030  NUDT13   3'  CCAGTGTGAGAAGAAAACTGA  63214          C    TCTCC
                                TCAGTTTTCT TCTC     TTGG
                                |||||||||| ||||     ||||
                                AGTCAAAAGA AGAG     GACC
                                      _    TGT__
GAM1030  TIGD4    5'  CCAAAGAGAAAAAGACTGAGAA 89068         TC   C__    C
           CTG                    CAGTTTTC  TCT   TCTC TTGG
                                |||||||| |||   |||| ||||
                                GTCAAGAG  AGA   AGAG AACC
                                     TC   AAA    A
GAM1030  TSPEAR   3'  CCAAGAAGAAAAAAGCTGAAAG 58717         T_  CTC_   C
           CTGA                    TCAGTTTTC  CT    TCT CTTGG
                                |||||||||  ||    ||| |||||
                                AGTCGAAAG  GA    AGA GAACC
                                      TC  AAAA   A
GAM1030  LOC120939 5'  GAGAGAGAGAAAAGCTGA     76254         C
                                TCAGTTTT TCTCTCTCTC
                                |||||||| ||||||||||
                                AGTCGAAA AGAGAGAGAG
                                      _
GAM1030  LOC133584 3'  CCAAGAAGAAAGTACACACTGA 75099       TTTCTCT  C   C
                                TCAGT       CT TCT CTTGG
                                |||||       || ||| |||||
                                AGTCA       GA AGA GAACC
                                   CACAT__  A   A
GAM1030  LOC144747 5'  CCACTTTTCAGAGGAGAAAACT 76951           T    CTCCT_
           GA                     TCAGTTTTCTC CTCT      TGG
                                |||||||||||| ||||      |||
                                AGTCAAAAGAG GAGA      ACC
                                      _    CTTTTC
GAM1030  LOC146212 5'  CCAAGGAGAGAGAAAGCCCTG  77707     TTTT  C
                                CAG    CT TCTCTCTCCTTGG
                                |||    || ||||||||||||
                                GTC    GA AGAGAGAGGAACC
                                  CC__  A
GAM1030  LOC149997 5'  CCAAGGAGAAAATGAAGCTGA  76340        CTCTCTC
                                TCAGTTTT      TCTCCTTGG
                                ||||||||      |||||||||
                                AGTCGAAG      AGAGGAACC
                                     TAAA___
GAM1030  LOC153196 5'  AAGGAGAGAGAAATAACTGA   85951       TTCTC
                                TCAGTT    TCTCTCTCCTT
                                ||||||    ||||||||||
                                AGTCAA    AGAGAGAGGAA
                                   TAA__
GAM1030  LOC200609 3'  CCAGAGAAAGAGGGAAAAC    90096          C    CT
                                GTTTTCTCTCT TCTC  TGG
                                |||||||||| ||||  |||
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                                CAAAAGGGAGA AGAG  ACC
                                      A   __
GAM1030  LOC221336 5'  CCAAGGAGCCAGGGGGAAAACC 92271    A        CT
              GA                  TC GTTTTCTCTCT  CTCCTTGG
                                  || |||||||||||  ||||||||
                                  AG CAAAAGGGGGA  GAGGAACC
                                   C          CC
GAM1030  LOC221344 5'  AGAGAAAAAGAGAAAAC     93652         C__
                                  GTTTTCTCT   TCTCT
                                  |||||||||   |||||
                                  CAAAAGAGA   AGAGA
                                        AAA
GAM1030  LOC256352 5'  CCAAGGAGAGAGAAAGCCCTG  96628     TTTT  C
                                  CAG    CT TCTCTCTCCTTGG
                                  |||    || ||||||||||||
                                  GTC    GA AGAGAGAGGAACC
                                    CC__  A
GAM1030  LOC91801  3'  CCAAGGAAAGAAAGAGGAGATG 57074     G       C   C
              A                    TCA TTTTCTCT TCT TCCTTGG
                                  ||| |||||||| ||| |||||||
                                  AGT AGAGGAGA AGA AGGAACC
                                    _       A   A
GAM1030  LOC93444  3'  CCAAGGTCGTTAGAGAAGAACT 72385         C     CTCT_
              GA                    TCAGTTTT TCTCT     CCTTGG
                                  |||||||| |||||     ||||||
                                  AGTCAAGA AGAGA     GGAACC
                                       _     TTGCT
GAM1031  CYYR1    3'  TGACCATGAAGATACACAA    53675       GAG       C
                                  TTGTG   TTTCATGG CA
                                  |||||   |||||||| ||
                                  AACAC   GAAGTACC GT
                                     ATA       A
GAM1031  DORFIN   3'  CCATGAAATCAAAGCAC     31258      A   TGGA
                                  GTGC TTG    GTTTCATGG
                                  |||| |||    |||||||||
                                  CACG AAC    TAAAGTACC
                                    A  _____
GAM1031  FLJ10704  3'  GCCATGAAACCAGAGGCGC    36455      A  G   AG
                                  GTGC TT TGG  TTTCATGGC
                                  |||| || |||  |||||||||
                                  CGCG GA ACC  AAAGTACCG
                                    _ G  __
GAM1031  MGC3248   3'  CATAAACTCCACAATTCAC    50653     C          C
                                  GTG ATTGTGGAGTTT ATG
                                  ||| ||||||||||| |||
                                  CAC TAACACCTCAAA TAC
                                    T          _
GAM1031  XYLT1     3'  TGACCATGAAACTCACAAGGCA 77852     A    G        C
                                  TGC TTGTG AGTTTCATGG CA
                                  ||| ||||| |||||||||| ||
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                                ACG AACAC TCAAAGTACC GT
                                  G    _        A
GAM1031  LOC142941 3'  GCCATTCCACAATGGAC     82884    G       GTTTC
                                GT CATTGTGGA    ATGGC
                                || |||||||||    |||||
                                CA GTAACACCT    TACCG
                                 G       _____
GAM1031  LOC167190 5'  GGCCACCTCCACAATGCA    87270          TTTCA
                                TGCATTGTGGAG    TGGCC
                                ||||||||||||    |||||
                                ACGTAACACCTC    ACCGG
                                       C____
GAM1031  LOC169436 5'  GGCCTTGCTCCACATGCAC   82742       T      TTCAT
                                GTGCAT GTGGAGT    GGCC
                                |||||| |||||||    ||||
                                CACGTA CACCTCG    CCGG
                                   _      TT___
GAM1032  ALDH8A1   3'  AATATGCAATCAGGCA     42606        G   C
                                TGCCTGAT GCA ATT
                                |||||||| ||| |||
                                ACGGACTA CGT TAA
                                     A   A
GAM1032  CNTNAP2   3'  AGGGTTACAATGTGGCCATCAG 26228    C       _    C_   T
            ACA                   TG CTGATGGC ACATT  AGC CCT
                                || |||||||| |||||  ||| |||
                                AC GACTACCG TGTAA  TTG GGA
                                 A       G    CA  _
GAM1032  TBL1X    3'  AATGGCCATCAGACA      18924    C       A
                                TG CTGATGGC CATT
                                || |||||||| ||||
                                AC GACTACCG GTAA
                                 A       _
GAM1032  VCAM1    5'  AGGAGCTGAATACCCTCCCAGG 6544        AT_  CAC
            CA                    TGCCTG   GG   ATTCAGCTCCT
                                ||||||   ||   ||||||||||
                                ACGGAC   CC   TAAGTCGAGGA
                                   CCT  CA_
GAM1032  VCAM1    5'  AGGAGCTGAATACCCTCCCAGG 54768       AT_  CAC
            CA                    TGCCTG   GG   ATTCAGCTCCT
                                ||||||   ||   ||||||||||
                                ACGGAC   CC   TAAGTCGAGGA
                                   CCT  CA_
GAM1032  C20orf140 3'  GAGCTGAACATGTGGAGGG    58245     GATGG    __
                                CCT    CACAT  TCAGCTC
                                |||    |||||  |||||||
                                GGG    GTGTA  AGTCGAG
                                  AG___     CA
GAM1032  DKFZP434C0826 5'  GAGTGTGCATCAGACA      84037    C     G
                                TG CTGATG CACATTC
                                || |||||| |||||||
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                                AC GACTAC GTGTGAG
                                 A     _
GAM1032 FLJ10898 5' GAACTAAATGTGCTGACA    59431    A       C  C
                                TG TGGCACATT AG TC
                                || ||||||||| || ||
                                AC GTCGTGTAA TC AG
                                 A       A  A
GAM1032 FLJ20666 3' AGAAGCTGAACATTTGCTTCAG 35508      T   CA__     C
             G                   CCTGA GGCA   TTCAGCT CT
                                 ||||| ||||   ||||||| ||
                                 GGACT TCGT   AAGTCGA GA
                                    _   TTAC     A
GAM1032 HOMER-2B 3' TTGAATGTCCACCAGACA    16722    C   A   C
                                TG CTG TGG ACATTCAG
                                || ||| ||| ||||||||
                                AC GAC ACC TGTAAGTT
                                 A   C   _
GAM1032 KIAA0435 5' GAGTGTGCCACCACGCA     28975     C  A
                                TGC TG TGGCACATTC
                                ||| || ||||||||||
                                ACG AC ACCGTGTGAG
                                  C  C
GAM1032 KIAA0459 3' AGGAACTGAATGTGTC      60982           C
                                GGCACATTCAG TCCT
                                |||||||||| ||||
                                CTGTGTAAGTC AGGA
                                       A
GAM1032 KIAA1210 3' AGCTGTACTTTCCATCAGGCA  96324          CACATT
                                TGCCTGATGG     CAGCT
                                ||||||||||     |||||
                                ACGGACTACC     GTCGA
                                      TTTCAT
GAM1032 KIAA1775 3' GGAGCTGCCCCACCAGCCA   52383    C   A   CACATT
                                TG CTG TGG     CAGCTCC
                                || ||| |||     |||||||
                                AC GAC ACC     GTCGAGG
                                 C   C   CC____
GAM1032 MGC15705 3' GGAGGTATGCCATCA       51282        C  TCAG
                                TGATGGCA AT    CTCC
                                |||||||| ||    ||||
                                ACTACCGT TG    GAGG
                                     A  ____
GAM1032 MGC2629  5' AGGGTTGAATGCACCCTCAGGC 50714        T  CA      T
             A                   TGCCTGA GG  CATTCAGC CCT
                                 ||||||| ||  |||||||| |||
                                 ACGGACT CC  GTAAGTTG GGA
                                    C  AC       _
GAM1032 ORCTL3   3' GAGCTGGACCATCAGCA     14919     C     CACA
                                TGC TGATGG    TTCAGCTC
                                ||| ||||||    ||||||||
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                                ACG ACTACC   AGGTCGAG
                                  _    ____
GAM1032 RALGPS1A 3' AGTTGATGCCATCA      27595       CAT
                                TGATGGCA  TCAGCT
                                ||||||||  ||||||
                                ACTACCGT  AGTTGA
                                   ___
GAM1032 SERP1    3' AGTCCAATGTGCCATAAGACA 27059   C G       CA
                                TG CT ATGGCACATT  GCT
                                || || ||||||||||  |||
                                AC GA TACCGTGTAA  TGA
                                 A A       CC
GAM1032 THTPA    5' GGAGCTGAGCACCAGGC    44260     ATG  ACAT
                                GCCTG  GC   TCAGCTCC
                                |||||  ||   ||||||||
                                CGGAC  CG   AGTCGAGG
                                   CA_ ____
GAM1032 TOM1L1   3' CTGAATGTATTATTCAGG   18505     _  C
                                CCTGA TGG ACATTCAG
                                ||||| ||| ||||||||
                                GGACT ATT TGTAAGTC
                                   T  A
GAM1032 LOC143524 3' AGGAGCTGAATGTGCTAGCA  76591    CTGA
                                TGC   TGGCACATTCAGCTCCT
                                |||   |||||||||||||||||
                                ACG   ATCGTGTAAGTCGAGGA
                                  ____
GAM1032 LOC144559 5' GGAGCTGAATCTGCCAGCA  76883    CTGA   C
                                TGC   TGGCA ATTCAGCTCC
                                |||   ||||| ||||||||||
                                ACG   ACCGT TAAGTCGAGG
                                  ____   C
GAM1032 LOC197285 3' AGGAGCTGAACATGTCCATCA 87789      _ CA
                                TGATGG CA  TTCAGCTCCT
                                |||||| ||  ||||||||||
                                ACTACC GT  AAGTCGAGGA
                                   T  AC
GAM1032 LOC219918 5' GGAGCTGAATCTGCCAGCA  91541    CTGA   C
                                TGC   TGGCA ATTCAGCTCC
                                |||   ||||| ||||||||||
                                ACG   ACCGT TAAGTCGAGG
                                  ____   C
GAM1032 LOC220071 5' GGAGCTGAATCTGCCAGCA  93437    CTGA   C
                                TGC   TGGCA ATTCAGCTCC
                                |||   ||||| ||||||||||
                                ACG   ACCGT TAAGTCGAGG
                                  ____   C
GAM1032 LOC255515 3' GGAGCTGAATCTGCCAACA  96097    A   C
                                TG TGGCA ATTCAGCTCC
                                || ||||| ||||||||||
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                                AC ACCGT TAAGTCGAGG
                                 A    C
GAM1032  LOC257486 3'  AGCTGTACTTTCCATCAGGCA  69241          CACATT
                                TGCCTGATGG     CAGCT
                                ||||||||||     |||||
                                ACGGACTACC     GTCGA
                                      TTTCAT
GAM1032  LOC90906  3'  GGAGCTGAATCTGCCAGCA   64304     CTGA    C
                                TGC   TGGCA ATTCAGCTCC
                                |||   ||||| ||||||||||
                                ACG   ACCGT TAAGTCGAGG
                                  _____    C
GAM1033  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM1033  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM1033  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM1033  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
             TG                   CATTTCACTTTCACTGTCTGAGAT
                                ||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM1033  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM1033  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM1033  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                       T__    _
GAM1033  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
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                                AAAGT AAAGTGACGGG
                                   A
GAM1033 ZNF216   3' ATCTGCACAGCAAAGTGAAA  20017        CA   CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM1033 CG012    5' CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM1033 EIF2C2   3' ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                |||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM1033 FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
             G                   CATTTC        GTCTGAGAT
                                 ||||||        |||||||||
                                 GTAAAG        CAGACTCTA
                                    AAACATTT_
GAM1033 FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                    C__
GAM1033 KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM1033 KLHL6    3' ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM1033 NIR3     3' GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM1033 PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM1033 PP35     3' ATCTCAGACTGAAA        22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
```

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                                AAAGT  CAGACTCTA
                                  __
GAM1033  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148         TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                    TA__   TT
GAM1033  SEP15     3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                    A    TC
GAM1033  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                    AAAGG
GAM1033  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM1033  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM1033  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM1033  LOC222134 5'  ACAGTGAAGTGAAATG       94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                    _
GAM1034  ABCC3     3'  TGGTGGGGCCTGTGGGCTGT   39163       GCA    T
                                GCAGCT   GCAG GTTCTACCG
                                ||||||   |||| |||||||||
                                TGTCGG   TGTC CGGGGTGGT
                                   G__   _
GAM1034  ACE2      3'  TGGGAACTGGTGTAGCTGCA   41440         G    G
                                TGCAGCTGCA CAGT TTCTA
                                |||||||||| |||| |||||
                                ACGTCGATGT GTCA AGGGT
                                    G   _
GAM1034  ALDH3B2   5'  CGAGGACACACTGCGGCGGCTG 5503         A      _  ACCG
              C                  GCAGCTGC GCAGTGT TCT
                                |||||||| ||||||| |||
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                                CGTCGGCG CGTCACA AGG
                                    G      C   AGC
GAM1034  APTX     3'  GAGCTGCTGCTGTGGTGT    34659     G TG      _
                                GCA C  CAGCAGT GTTC
                                ||| |  ||||||| ||||
                                TGT G  GTCGTCG CGAG
                                  _ GT      T
GAM1034  ARSD     3'  TGGCTCACGTTCTGCAGCTGCA 23798          CA_   TT
                                TGCAGCTGCAG   GTG  CTA
                                ||||||||||   |||  |||
                                ACGTCGACGTC   CAC  GGT
                                      TTG   TC
GAM1034  ASNA1    3'  TGGTGGGGAGCTGTAGTTGC   62980          AGTG
                                GCAGCTGCAGC    TTCTACCG
                                ||||||||||    ||||||||
                                CGTTGATGTCG    GGGGTGGT
                                      A___
GAM1034  ASNA1    3'  TGGTGGGGCTGGTGGGGAGCTG 62981        G__  G    GT
              TA                  TGCAGCT   CA CAGT  TCTACCG
                                  |||||||   || ||||  |||||||
                                  ATGTCGA   GT GTCG  GGGTGGT
                                     GGG  G    __
GAM1034  BRCA2    3'  TGGTATACTTTTGCTTCAGTTG 3552          C     T_  TC
              CA                  TGCAGCTG AGCAG  GT  TACCG
                                  |||||||| |||||  ||  |||||
                                  ACGTTGAC TCGTT  CA  ATGGT
                                      T    TT  T_
GAM1034  CCND2    3'  TGTACGTGCATGCTGTAGCTGC 8300            G   TC_   CG
              A                   TGCAGCTGCAGCA TGT   TAC
                                  |||||||||||||| |||   |||
                                  ACGTCGATGTCGT ACG   ATG
                                        _   TGC   T
GAM1034  CDC6     5'  TGGAGTTTGCTGCTGCCGCTGT 6987        T        TT  A
                                GCAGC GCAGCAGTG  CT CCG
                                ||||| |||||||||  || |||
                                TGTCG CGTCGTCGT  GA GGT
                                  C        TT  _
GAM1034  CDH11    5'  TGGTGGAAGGGGTGACAGCTGC 53367         CA  AGTG
              A                   TGCAGCTG  GC    TTCTACCG
                                  ||||||||  ||    ||||||||
                                  ACGTCGAC  TG    AAGGTGGT
                                      AG  GGG_
GAM1034  CDS1     5'  TGGTGGGGCCGCGTTAGTGGCT 7007        TG _   A   _
              GC                    GCAGC  C AGC GTG TTCTACCG
                                    |||||  | ||| ||| ||||||||
                                    CGTCG  G TTG CGC GGGGTGGT
                                      GT A   _   C
GAM1034  CENPE    3'  TGGTAATGATGTTGTAGTGCA  8417       G       GTGTTC
                                TGCA CTGCAGCA      TACCG
                                |||| ||||||||      |||||
```

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                                ACGT GATGTTGT     ATGGT
                                  _       AGTA__
GAM1034  COL16A1   5'  CGGCCACCGGTGCTGTGGCTGT 8499       TG    G  TTCTA
             A                    TGCAGC  CAGCA TG    CCG
                                  ||||||  ||||| ||    |||
                                  ATGTCG  GTCGT GC    GGC
                                     GT    G  CACC_
GAM1034  CRACC     3'  TGGTGGGGCACGGGGGGGCAGT  41012      AGCA_
                                  GCTGC    GTGTTCTACCG
                                  ||||||    ||||||||||
                                  TGACG    CACGGGGTGGT
                                    GGGGG
GAM1034  CRY1      3'  AGGAGGAATACTGTTGCAGCTG 14519              A  G
                                  CAGCTGCAGCAGTGTTCT CC
                                  |||||||||||||||||| ||
                                  GTCGACGTTGTCATAAGG GG
                                              A  AC
GAM1034  CX3CR1    3'  GGCACTGCTGTGCTGT      70646      T
                                  GCAGC GCAGCAGTGTT
                                  ||||| ||||||||||
                                  TGTCG TGTCGTCACGG
                                    _
GAM1034  DEDD      5'  CGGTGGGGATTGCAGCTGC    52223        GCAGTG
                                  GCAGCTGCA     TTCTACCG
                                  |||||||||     ||||||||
                                  CGTCGACGT     GGGGTGGC
                                        TA_____
GAM1034  DMD       5'  GACGTTGTAGCAGCTGCA    3664          A
                                  TGCAGCTGC GCAGTGTT
                                  ||||||||| ||||||||
                                  ACGTCGACG TGTTGCAG
                                        A
GAM1034  DPH2L2    3'  GGTAGGGTGCTCAGCAGC    7280       AGC  TG
                                  GCTGC   AG  TTCTACC
                                  |||||   ||  |||||||
                                  CGACG   TC  GGGATGG
                                     AC_  GT
GAM1034  DRPLA     3'  AAGAGGGTGCTGCTCAGTTGCA 8665        C    TG    ACCG
                                  TGCAGCTG AGCAG  TTCT
                                  |||||||| |||||  ||||
                                  ACGTTGAC TCGTC  GGGA
                                       _    GT    GAAC
GAM1034  DSCR2     5'  CGGTCCCGCGGCGCTGCAGTTG 13557          AG   TCT
             T                     GCAGCTGCAGC  TGT   ACCG
                                   ||||||||||  |||   ||||
                                   TGTTGACGTCG  GCG   TGGC
                                          CG   CCC
GAM1034  DXF68S1E  3'  GGTGGAGTGATTGTCTGT    60007      _   _
                                  GCAG CAGT GTTCTACC
                                  |||| |||| ||||||||
```

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                                TGTC GTTA TGAGGTGG
                                  T   G
GAM1034  EHF      3'  GAAATATGATGCTGTATGTGGT 24062       TG  _       CTACCG
                TGT                  GCAGC  CA GCAGTGTT
                                     |||||  || ||||||||
                                     TGTTG  GT TGTCGTAG
                                       GT  A       TATAAAGT
GAM1034  ENC1     3'  CGGTAGAGTTGGAAATCAGTTG 13280        CAGCAGTG
                T                    GCAGCTG       TTCTACCG
                                     |||||||       ||||||||
                                     TGTTGAC       GAGATGGC
                                        TAAAGGTT
GAM1034  FBXL5    3'  AATACTGTTGTGTTGT      24074       T
                                     GCAGC GCAGCAGTGTT
                                     ||||| ||||||||||
                                     TGTTG TGTTGTCATAA
                                       _
GAM1034  FBXL5    3'  AATACTGTTGTGTTGT      53199       T
                                     GCAGC GCAGCAGTGTT
                                     ||||| ||||||||||
                                     TGTTG TGTTGTCATAA
                                       _
GAM1034  FRZB     5'  TGGCGTCCACTGCGCGGCTGCA 7592          A     TTCTA
                                     TGCAGCTGC GCAGTG     CCG
                                     |||||||| ||||||     |||
                                     ACGTCGGCG CGTCAC     GGT
                                           _     CTGC_
GAM1034  FUT6     3'  CGGTCACCTGTTGCAGCTTCA  3810     C         T  TCT
                                     TG AGCTGCAGCAG GT   ACCG
                                     || ||||||||||| ||   ||||
                                     AC TCGACGTTGTC CA   TGGC
                                      T         _  C__
GAM1034  GFRA2    3'  GTGGGTCTGCAGCTG       7661          CAGTGT
                                     CAGCTGCAG     TCTAC
                                     |||||||||     |||||
                                     GTCGACGTC     GGGTG
                                           T_____
GAM1034  GJA5     3'  TGTCTTTATGCTGGCTGTGGCT 74676       TG   _    TCTACCG
                GCA                  TGCAGC  CAGC AGTGT
                                     ||||||  |||| |||||
                                     ACGTCG  GTCG TCGTA
                                        GT   G     TTTCTGT
GAM1034  GLI2     5'  GGTGGTGGCTGCAGCGGCA   47527     A       AGTGTT
                                     TGC GCTGCAGC     CTACC
                                     ||| ||||||||     |||||
                                     ACG CGACGTCG     GGTGG
                                       G       GT____
GAM1034  GNGT2    3'  TGGTGGGGTGTGAGAAGCCTGC 48988       _  GCAGCA TG
                A                    TGCAG CT     G  TTCTACCG
                                     ||||| ||     |  ||||||||
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                                ACGTC GA     T  GGGGTGGT
                                   C  AGAG__ GT
GAM1034  GUCY2D    3'  GTGACACTGCATTGCTGGGCTG 3936       __  __       CTACCG
               T                    CAGCT  GCA  GCAGTGTT
                                    ||||||  |||  ||||||||
                                    GTCGG  CGT  CGTCACAG
                                       GT   TA       T   GC
GAM1034  HDAC4     3'  TGGTGGATTTTTGTGGCTG   20122      TG   CAGTGT
                                    CAGC  CAG     TCTACCG
                                    ||||  |||     |||||||
                                    GTCG  GTT     AGGTGGT
                                      GT   TTT___
GAM1034  HLX1      3'  TGGTAGGGCAGGAGACGCAGC  41707       AGCAG_
                                    GCTGC     TGTTCTACCG
                                    ||||||     ||||||||||
                                    CGACG     ACGGGATGGT
                                       CAGAGG
GAM1034  HRH1      3'  GTGGGGCATGCCTGTA      5986       CA
                                    TGCAG  GTGTTCTAC
                                    ||||||  |||||||||
                                    ATGTC  TACGGGGTG
                                       CG
GAM1034  IRTA2     3'  TGGTGGGGCTACTGCAGTGT   48413     G     CAGT
                                    GCA CTGCAG    GTTCTACCG
                                    ||| ||||||    |||||||||
                                    TGT GACGTC    CGGGGTGGT
                                      _     AT__
GAM1034  ISLR      3'  TGGTGGAATTCCAGGCACTGT  18671      C   AGCAGT
                                    GCAG TGC     GTTCTACCG
                                    |||| |||     |||||||||
                                    TGTC ACG     TAAGGTGGT
                                      _   GACCT_
GAM1034  ITGA6     3'  AGGACGTTGTTTTGGTTGTA   3982         C
                                    TGCAGCTG AGCAGTGTTCT
                                    |||||||| ||||||||||
                                    ATGTTGGT TTGTTGCAGGA
                                         T
GAM1034  ITIH1     3'  GACCTGCTGCTGAGGCTGTA   9412         ___      T
                                    TGCAGCT   GCAGCAG GTT
                                    |||||||   ||||||| |||
                                    ATGTCGG   CGTCGTC CAG
                                       AGT      _
GAM1034  ITK       3'  CGGTGGAGAACCATGTGGTGCA 18680      G TG  GCA  G
                                    TGCA C  CA   GT TTCTACCG
                                    |||| |  ||   || ||||||||
                                    ACGT G  GT   CA GAGGTGGC
                                      _ GT  AC_  A
GAM1034  JAG2      3'  CGGTGGGACTCGTGGCTGT    9469       TG AGCAGT
                                    GCAGC  C     GTTCTACCG
                                    |||||  |     |||||||||
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                                TGTCG  G     CAGGGTGGC
                                  GT CT_____
GAM1034  JAG2     3'  TGGTGGGACCCGTGGCTG    9473       TG AGCAGT
                                CAGC  C     GTTCTACCG
                                ||||  |     |||||||||
                                GTCG  G     CAGGGTGGT
                                  GT CC_____
GAM1034  LMO4     5'  GGGGCTGTTGTGTCTGC     22255      C        G
                                GCAG TGCAGCAGT TT
                                |||| ||||||||| ||
                                CGTC GTGTTGTCG GG
                                  T        G
GAM1034  MAP1A    3'  GGTCATCTGCTGTGGCTTG   9901     C   TG     _  TTCT
                                G AGC  CAGCAG TG    ACC
                                | |||  |||||| ||    |||
                                G TCG  GTCGTC AC    TGG
                                 T   GT     T  _____
GAM1034  NOVA1    3'  GATACTCTGTAGCTGT      10247          C
                                GCAGCTGCAG AGTGTT
                                |||||||||| ||||||
                                TGTCGATGTC TCATAG
                                          _
GAM1034  NOVA1    3'  GATACTCTGTAGCTGT      21409          C
                                GCAGCTGCAG AGTGTT
                                |||||||||| ||||||
                                TGTCGATGTC TCATAG
                                          _
GAM1034  NPR2L    3'  GGTGGAGTAGCAGCAGCA    21562     A    A  AGTGT
                                TGC GCTGC GC     TCTACC
                                ||| ||||| ||     ||||||
                                ACG CGACG TG     AGGTGG
                                  A    A  _____
GAM1034  ODC1     5'  CGGCCGAGCGCTCCTGCGGCTG 10320          C       TA
              C                  GCAGCTGCAG AGTGTTC  CCG
                                 |||||||||| |||||||  |||
                                 CGTCGGCGTC TCGCGAG  GGC
                                       C      CC
GAM1034  OPA1     3'  TTAATGAATATTTTTGCAGTTG 55535          C      TACCG
              TA                   TGCAGCTGCAG AGTGTTC
                                   |||||||||| |||||||
                                   ATGTTGACGTT TTATAAG
                                         T      TAATTG
GAM1034  OPA1     3'  TTAATGAATATTTTTGCAGTTG 55544          C      TACCG
              TA                   TGCAGCTGCAG AGTGTTC
                                   |||||||||| |||||||
                                   ATGTTGACGTT TTATAAG
                                         T      TAATTG
GAM1034  OPA1     3'  TTAATGAATATTTTTGCAGTTG 55553          C      TACCG
              TA                   TGCAGCTGCAG AGTGTTC
                                   |||||||||| |||||||
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                                ATGTTGACGTT TTATAAG
                                      T      TAATTG
GAM1034  OPA1     3'  TTAATGAATATTTTTGCAGTTG 55562          C      TACCG
                TA                    TGCAGCTGCAG AGTGTTC
                                      |||||||||||| |||||||
                                ATGTTGACGTT TTATAAG
                                      T      TAATTG
GAM1034  OPA1     3'  TTAATGAATATTTTTGCAGTTG 55571          C      TACCG
                TA                    TGCAGCTGCAG AGTGTTC
                                      |||||||||||| |||||||
                                ATGTTGACGTT TTATAAG
                                      T      TAATTG
GAM1034  OTX1     3'  GATCCTGTTGCTGCTGC     27306       T      TG
                                GCAGC GCAGCAG  TT
                                ||||| |||||||  ||
                                CGTCG CGTTGTC  AG
                                   T      CT
GAM1034  PI3      3'  GGTCCTTGCTGCACCTGT     10546      C       TGTTCT
                                GCAG TGCAGCAG      ACC
                                |||| ||||||||      |||
                                TGTC ACGTCGTT      TGG
                                  C       CC____
GAM1034  PKIA     5'  AGCGATGCTGCAGCTGTA     22379           G
                                TGCAGCTGCAGCA TGTT
                                |||||||||||| ||||
                                ATGTCGACGTCGT GCGA
                                      A
GAM1034  PRKAR1A  3'  TGGTAGGGTATAATGTGTCTGT 10802      C    GCA   TT
                                GCAG TGCA   GTG  CTACCG
                                |||| ||||   |||  ||||||
                                TGTC GTGT   TAT  GATGGT
                                  T   AA_   GG
GAM1034  PTBP1    3'  TGTATTATATACTTTGCAGTTG 11010          C    TC__   CG
                CA                    TGCAGCTGCAG AGTGT    TAC
                                      |||||||||| |||||    |||
                                ACGTTGACGTT TCATA    ATG
                                      _    TATT   T
GAM1034  PTBP1    3'  TGTATTATATACTTTGCAGTTG 49255          C    TC__   CG
                CA                    TGCAGCTGCAG AGTGT    TAC
                                      |||||||||| |||||    |||
                                ACGTTGACGTT TCATA    ATG
                                      _    TATT   T
GAM1034  RAB1A    3'  TGAATTGTACTGTATGTAGCTG 70235        _    ___    TACCG
                CA                    CAGCTGCA GCAGT   GTTC
                                      |||||||| |||||   ||||
                                GTCGATGT TGTCA   TAAG
                                     A    TGT    T  G
GAM1034  RAB3A    3'  GGTGGGGGGGGTGTGCTGT     11184       T   G AGTG
                                GCAGC GCA C    TTCTACC
                                ||||| ||| |    |||||||
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                                TGTCG TGT G    GGGGTGG
                                  _   _ GG__
GAM1034  ROCK2    3'  ACTTGCTGCAGTTGCA      66006            T
                                TGCAGCTGCAGCAG GT
                                |||||||||||||| ||
                                ACGTTGACGTCGTT CA
                                                _
GAM1034  RPL17    5'  TGGTGGGGGAAAGTATGGCTGC 6389        GCA  AGTG
                                GCAGCT   GC    TTCTACCG
                                ||||||   ||    ||||||||
                                CGTCGG   TG    GGGGTGGT
                                   TA_  AAAG
GAM1034  RUNX3    3'  TGGTGGGAGCCTCTGGCTGCA  15120       TG   C  TG
                                TGCAGC  CAG AG  TTCTACCG
                                ||||||  ||| ||  ||||||||
                                ACGTCG  GTC TC  AGGGTGGT
                                   __   _  CG
GAM1034  SDC4     3'  TGGTGGGATATTTGTGTCTGT  11483      C    CA
                                GCAG TGCAG  GTGTTCTACCG
                                |||| |||||  ||||||||||
                                TGTC GTGTT  TATAGGGTGGT
                                  T    __
GAM1034  SGCG     5'  TGGTAGAGCTCGGGCCAGCTGT 4064         CA  AGT_
           A                     TGCAGCTG  GC    GTTCTACCG
                                 ||||||||  ||    |||||||||
                                 ATGTCGAC  CG    CGAGATGGT
                                    __  GGCT
GAM1034  SIRT7    3'  GCACTGCTGCGGTTGTA     33294
                                TGCAGCTGCAGCAGTGT
                                |||||||||||||||||
                                ATGTTGGCGTCGTCACG

GAM1034  SLC13A3  3'  GGTGGGAGATGCGTTGTA    60471       A_  G
                                TGCAGC  GT TTCTACC
                                ||||||  || |||||||
                                ATGTTG  TA AGGGTGG
                                   CG  G
GAM1034  SLC14A1  3'  TGGTGGGTGCCTGTAGTTCCA  31841    C      _  GTGT
                                TG AGCTGCAG CA    TCTACCG
                                || |||||||| ||    |||||||
                                AC TTGATGTC GT    GGGTGGT
                                 C       C  ____
GAM1034  SMARCD1  5'  GGTTCTTTGTGCGGCTGCA   11819         G   TGTTCT
                                TGCAGCTGCA CAG     ACC
                                |||||||||| |||     |||
                                ACGTCGGCGT GTT     TGG
                                      _   TCT___
GAM1034  SMARCD1  5'  GGTTCTTTGTGCGGCTGCA   57437         G   TGTTCT
                                TGCAGCTGCA CAG     ACC
                                |||||||||| |||     |||
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                                ACGTCGGCGT GTT     TGG
                                      _  TCT___
GAM1034  SNX13    3'  AATACTGTTGTGTCTGCA    30699      C
                                TGCAG TGCAGCAGTGTT
                                ||||| ||||||||||||
                                ACGTC GTGTTGTCATAA
                                   T
GAM1034  SORCS3   3'  TGGTGGGGGTGGATGTAGCTGC 30375          GCAGTG
              A                  TGCAGCTGCA     TTCTACCG
                                ||||||||||     ||||||||
                                ACGTCGATGT     GGGGTGGT
                                      AGGTG_
GAM1034  STXBP1   3'  TGGCTGGCACTGTTGCCGCTGC 12050       T         CTA
              A                  TGCAGC GCAGCAGTGTT   CCG
                                ||||||| ||||||||||   |||
                                ACGTCG CGTTGTCACGG   GGT
                                   C         TC_
GAM1034  SURF5    3'  GGCACTGCTGAGCTGCA     22184        G
                                TGCAGCT CAGCAGTGTT
                                ||||||| ||||||||||
                                ACGTCGA GTCGTCACGG
                                      _
GAM1034  TAP2     3'  GGTGGGAGGCTGTCTGT     5030       _   G      G
                                GCAG CAGT TTCTACC
                                |||| |||| |||||||
                                TGTC GTCG AGGGTGG
                                  T   G      G
GAM1034  TCEA1    3'  CAGAAGAACACTGTTGTAGTTT 80441    C             ACCG
              A                  G AGCTGCAGCAGTGTTCT
                                | ||||||||||||||||
                                A TTGATGTTGTCACAAGA
                                 T             AGACG
GAM1034  TFF1     3'  ACGCTTCTGCAGCTGT      59957          C
                                GCAGCTGCAG AGTGT
                                |||||||||| |||||
                                TGTCGACGTC TCGCA
                                      T
GAM1034  TNFRSF5  3'  TGGTGCTGCTGCTGCTGTGGC  6978     TG      _ TC
                                GC  CAGCAGT GT  TACCG
                                ||  ||||||| ||  |||||
                                CG  GTCGTCG CG  GTGGT
                                 GT      T  TC
GAM1034  TOP3B    5'  TGGTAATAGTGCTGTGCTGC   14131      T     G   TC
                                GCAGC GCAGCA TGT  TACCG
                                ||||| |||||| |||  |||||
                                CGTCG TGTCGT ATA  ATGGT
                                   _     G   __
GAM1034  TPST1    5'  GGTGGGACCAGCGGCTG     13180        AGCAGT
                                CAGCTGC     GTTCTACC
                                |||||||     ||||||||
```

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                                GTCGGCG     CAGGGTGG
                                   AC_____
GAM1034  TPST1    3'  TGGTGGAGCGTCTGCACCTTGG 13181      CA__   _
              CTGC                 AGCTG    GCAG TGTTCTACCG
                                |||||    |||| ||||||||||
                                TCGGT    CGTC GCGAGGTGGT
                                   TCCA    T
GAM1034  TRIM9    3'  TGGTGGGGTGCAGAGTTGGC   30771    TG    A__ TG
                                GC  CAGC   G  TTCTACCG
                                ||  ||||   |  ||||||||
                                CG  GTTG   C  GGGGTGGT
                                 __    AGA GT
GAM1034  TRIM9    3'  TGGTGGGGTGCTAGAGCTGT   53762       GC    GTG
                                GCAGCT  AGCA   TTCTACCG
                                ||||||  ||||   ||||||||
                                TGTCGA  TCGT   GGGGTGGT
                                   GA   ___
GAM1034  TTC3     5'  GTGTATTGCAGTAGTTGT    12420         A     TTC
                                GCAGCTGC GCAGTG   TAC
                                |||||||| ||||||   |||
                                TGTTGATG CGTTAT   GTG
                                   A     ___
GAM1034  UFD1L    3'  TGGCTGTCCCACTACTGTGGCT 73288       TG   C    TTCTA_
              GCA                  TGCAGC  CAG AGTG     CCG
                                ||||||  ||| ||||     |||
                                ACGTCG  GTC TCAC     GGT
                                   GT   A    CCTGTC
GAM1034  UQCRC1   5'  GGACACGCTGTGGCTGCA    12556       TG    A
                                TGCAGC  CAGC GTGTTC
                                ||||||  |||| ||||||
                                ACGTCG  GTCG CACAGG
                                   GT   _
GAM1034  ZNF26    3'  GGTGGAGTATAAAGTTGT    72981       GCAGCA
                                GCAGCT     GTGTTCTACC
                                ||||||     ||||||||||
                                TGTTGA     TATGAGGTGG
                                   AA_____
GAM1034  ZNF6     5'  GGCGGCAGCTGTAGCTGCA   41818          AG    CTA
                                TGCAGCTGCAGC  TGTT   CC
                                ||||||||||||  ||||   ||
                                ACGTCGATGTCG  ACGG   GG
                                      __    C__
GAM1034  ABIN-2   3'  TGCTGCTGTGACTGCA     44209      CT
                                TGCAG  GCAGCAGTG
                                |||||  |||||||||
                                ACGTC  TGTCGTCGT
                                   AG
GAM1034  ABLIM    3'  CGGCTCCGCGCTGCTGTGCCTG 9765       CT         TCTA
              T                   GCAG  GCAGCAGTGT    CCG
                                ||||  ||||||||||    |||
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                                TGTC  TGTCGTCGCG   GGC
                                  CG        CCTC
GAM1034  ABLIM    3'  CGGCTCCGCGCTGCTGTGCCTG 22026     CT        TCTA
             T                   GCAG  GCAGCAGTGT   CCG
                                 ||||  ||||||||||   |||
                                TGTC  TGTCGTCGCG   GGC
                                  CG        CCTC
GAM1034  AKAP11   3'  AATATTGCTGTGCTGTA     32698       T
                                TGCAGC GCAGCAGTGTT
                                ||||||| ||||||||||
                                ATGTCG TGTCGTTATAA
                                   _
GAM1034  APOL3    3'  CGGTGGAGGTGGTGGTTGTAGT 26812     G      AGTG__
             GT                   GCA CTGCAGC     TTCTACCG
                                 ||| |||||||     ||||||||
                                 TGT GATGTTG     GAGGTGGC
                                  _      GTGGTG
GAM1034  APOL4    3'  GGTGGTGGTTGTAGTGT     47628     G      AGTGTT
                                 GCA CTGCAGC     CTACC
                                 ||| |||||||     |||||
                                 TGT GATGTTG     GGTGG
                                  _      GT_____
GAM1034  ATP6V1B2  3'  TGGTATGCCTGTATTGCTGGGC 8087       G       TTC___
             TGT                   CAGCT CAGCAGTG     TACCG
                                 |||||| ||||||||     |||||
                                 GTCGG GTCGTTAT     ATGGT
                                   _       GTCCGT
GAM1034  C11orf11  5'  AGGAAGACAACTGCTGTGGCTG 93248       TG      GT   A  G
             TA                    TGCAGC  CAGCAGT  TCT CC
                                 ||||||  |||||||  ||| ||
                                 ATGTCG  GTCGTCA  AGA GG
                                    GT      AC   A  AG
GAM1034  C17orf1A  5'  GGTGGCGTTGCCGTTGCA    48801       T     AGTGTT
                                 TGCAGC GCAGC     CTACC
                                 |||||| |||||     |||||
                                 ACGTTG CGTTG     GGTGG
                                    C    C_____
GAM1034  C5orf5    3'  TGGTAGAATTAGGCAGTTG    33471        AGCAGT
                                 CAGCTGC     GTTCTACCG
                                 |||||||     |||||||||
                                 GTTGACG     TAAGATGGT
                                     GAT___
GAM1034  C6orf31   5'  GCGCTGCTGCCGGCTGC     47644        _
                                 GCAGCTG CAGCAGTGT
                                 ||||||| |||||||||
                                 CGTCGGC GTCGTCGCG
                                     C
GAM1034  C7orf11   5'  CGGTGGGAGAACGCGGCTGC   56938         AGCA  G_
                                 GCAGCTGC   GT  TTCTACCG
                                 ||||||||   ||  ||||||||
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                                CGTCGGCG   CA  AGGGTGGC
                                     _____  AG
GAM1034  C8orf13   3'  TGTACAGTGCTGTTTGCAGTTG 81579          _  TG  C   CG
              TA                    TGCAGCTGCAG CAG  TT TAC
                                    |||||||||| |||  || |||
                                    ATGTTGACGTT GTC  GA ATG
                                          T   GT  C   T
GAM1034  CAP      3'  TGGTACTAGCTGCTGTAGC   21026          GTTC
                                    GCTGCAGCAGT   TACCG
                                    ||||||||||   |||||
                                    CGATGTCGTCG   ATGGT
                                          ATC_
GAM1034  CAPN13   3'  GGAACTATGTTGTGGTTGCA  58014       TG    GT
                                    TGCAGC  CAGCA  GTTCT
                                    ||||||  |||||  |||||
                                    ACGTTG  GTTGT  CAAGG
                                       GT    AT
GAM1034  CLIC5    3'  GCGCTGCTGCTGCTGC     33718       T
                                    GCAGC GCAGCAGTGT
                                    ||||| ||||||||||
                                    CGTCG CGTCGTCGCG
                                       T
GAM1034  CRIPT    5'  GCTGCTGCTGCTGTTGC     73806       T      _
                                    GCAGC GCAGCAGT GT
                                    ||||| |||||||| ||
                                    CGTTG CGTCGTCG CG
                                       T       T
GAM1034  DKFZp434F1819 5'  GGTTTCTTGTTGCACTGT    50008      C       TGTTCT
                                    GCAG TGCAGCAG     ACC
                                    |||| ||||||||     |||
                                    TGTC ACGTTGTT     TGG
                                      _       CTT___
GAM1034  DKFZP434G156 3'  TGGTATTCTTGGCTATTGCAGC 69783          C   GTTC__
              TGT                     GCAGCTGCAG AGT     TACCG
                                    |||||||||| |||     |||||
                                    TGTCGACGTT TCG     ATGGT
                                          A   GTTCTT
GAM1034  DKFZP434J1813 5'  TGGTAGTCGCCGGTGTGGCTGC 61794       TG  GCA   TT
              A                     TGCAGC  CA   GTG  CTACCG
                                    ||||||  ||   |||  ||||||
                                    ACGTCG  GT   CGC  GATGGT
                                       GT  GGC   T_
GAM1034  DKFZp434N035 3'  CGCAGGAGCTGCTGCTGCAGTT 50048             _    ACCG
              GCA                     TGCAGCTGCAGCAGT GTTCT
                                    |||||||||||||| |||||
                                    ACGTTGACGTCGTCG CGAGG
                                             T    ACGC
GAM1034  DKFZP564B1162 3'  AGAAGAATACTTTGTGGCTGT  48527       TG   C       ACCG
                                    GCAGC  CAG AGTGTTCT
                                    |||||  ||| ||||||||
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                                TGTCG  GTT TCATAAGA
                                   GT  _      AGAC
GAM1034  DKFZP564L0864 5'  TGGTGGGACGGCACTAGCTGC  72557       CA  AG
                                GCAGCTG  GC  TGTTCTACCG
                                |||||||  ||  ||||||||||
                                CGTCGAT  CG  GCAGGGTGGT
                                    CA  __
GAM1034  DKFZp564O1278 5'  AGAACATTGCTGTAGCTTG   63721   C
                                G AGCTGCAGCAGTGTTCT
                                | ||||||||||||||||
                                G TCGATGTCGTTACAAGA
                                 T
GAM1034  DKFZP566G1424 5'  GCCTGTTGCAGCTGT      84786           T
                                GCAGCTGCAGCAG GT
                                |||||||||||| ||
                                TGTCGACGTTGTC CG
                                          _
GAM1034  DKFZP586M1120 3'  GGATGCTGCTGTGGCTG    48465     TG
                                CAGC  CAGCAGTGTTC
                                ||||  ||||||||||
                                GTCG  GTCGTCGTAGG
                                  GT
GAM1034  DKFZp761H079 5'  GGCCAGTTGCTGCGGCTG    58734          _  TT
                                CAGCTGCAGCAG TG  C
                                |||||||||||| ||  |
                                GTCGGCGTCGTT AC  G
                                       G  CG
GAM1034  Dlc2     5'  CGGCGGCGGCTGCTGCAGCTGC 54758            GTT TA
            A                    TGCAGCTGCAGCAGT   C  CCG
                                ||||||||||||||   |  |||
                                ACGTCGACGTCGTCG   G  GGC
                                         GC_ GC
GAM1034  DNAJA2   3'  ACATTAGCTGTGGTTGTA    59778       TG   _
                                TGCAGC  CAGC AGTGT
                                ||||||  |||| |||||
                                ATGTTG  GTCG TTACA
                                   GT   A
GAM1034  ELL2     3'  TGGTAGAATATTTAGAAATTTG 23874      CTGCAGC
            CA                   TGCAG      AGTGTTCTACCG
                                |||||      ||||||||||||
                                ACGTT      TTATAAGATGGT
                                  TAAAGAT
GAM1034  FBP17    3'  GCTAGAATACTGTTGTGTTGTA 72795       T          CCG
                                TGCAGC GCAGCAGTGTTCTA
                                |||||| ||||||||||||||
                                ATGTTG TGTTGTCATAAGAT
                                   _          CGT
GAM1034  FLJ00024  5'  TGGTAGAGCTCAGCGCGTCTGT 63773      C   A  AGT
                                GCAG TGC GC   GTTCTACCG
                                |||| ||| ||   |||||||||
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                                TGTC GCG CG   CGAGATGGT
                                  T   _  ACT
GAM1034  FLJ10159  3'  CGTGCACTTGTACAGTTGTAGC 35861        _______    TCTACCG
                TGC                  GCTGCAGC      AGTGT
                                |||||||||      |||||
                                CGATGTTG      TCACG
                                     ACATGT     T   GCC
GAM1034  FLJ10350  3'  TGGTGGGGTACAGTGGATGT   95513     G TG AGCA   TT
                                GCA C  C    GTG  CTACCG
                                ||| |  |    |||  ||||||
                                TGT G  G    CAT  GGTGGT
                                  A GT A___   GG
GAM1034  FLJ10415  3'  GACGCTGCTGGAGTTGT     36097       G
                                GCAGCT CAGCAGTGTT
                                |||||| ||||||||||
                                TGTTGA GTCGTCGCAG
                                   G
GAM1034  FLJ10415  5'  GGGGATTGTTGTGTTGCA     36099       T       G
                                TGCAGC GCAGCAGT TTC
                                |||||| |||||||| |||
                                ACGTTG TGTTGTTA GGG
                                   _       G
GAM1034  FLJ10597  3'  TGGTGTGATGCTGTGTCTGTA  36320      CT   G      C
                                TGCAG  GCA CAGTGTT TACCG
                                |||||  ||| ||||||| |||||
                                ATGTC  TGT GTCGTAG GTGGT
                                   __  _       T
GAM1034  FLJ12425  3'  TGGTAGGATATTAACGGGCTCA 85895    C    GCAGC
                                TG AGCT     AGTGTTCTACCG
                                || ||||     ||||||||||||
                                AC TCGG     TTATAGGATGGT
                                  _    GCAA_
GAM1034  FLJ12595  5'  GGTAGAATACTCTGATGT     46506     TG   C
                                GC  CAG AGTGTTCTACC
                                ||  ||| ||||||||||
                                TG  GTC TCATAAGATGG
                                  TA   _
GAM1034  FLJ12750  3'  TGGTCCTTCTGTTGCAGCT    45125          TGTTCT
                                AGCTGCAGCAG      ACCG
                                ||||||||||      ||||
                                TCGACGTTGTC      TGGT
                                      TTCC__
GAM1034  FLJ13154  3'  CCTCCTGCCTGCTGCAGCTGCA 44795            T  TCTACCG
                                TGCAGCTGCAGCAG GT
                                |||||||||||||| ||
                                ACGTCGACGTCGTC CG
                                         _  TCCTCCG
GAM1034  FLJ13204  5'  TGGAAAACACTGTTGGGCTGT  45420       G        CTA
                                GCAGCT CAGCAGTGTT   CCG
                                |||||| ||||||||||   |||
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                                TGTCGG GTTGTCACAA   GGT
                                   _        AA_
GAM1034  FLJ13456  3'  GACACTGCTTCAGTTGTA    65939        C
                                TGCAGCTG AGCAGTGTT
                                |||||||| |||||||||
                                ATGTTGAC TCGTCACAG
                                     T
GAM1034  FLJ14001  3'  GCATTGCTGGCAGCTGTA    45167         _
                                TGCAGCTGC AGCAGTGT
                                ||||||||| ||||||||
                                ATGTCGACG TCGTTACG
                                      G
GAM1034  FLJ14117  3'  GTGGGGCATGCCTGTA     42915      CA
                                TGCAG  GTGTTCTAC
                                |||||  |||||||||
                                ATGTC  TACGGGGTG
                                   CG
GAM1034  FLJ14251  3'  GGAATATTTTGTAGTTGT    45974         C
                                GCAGCTGCAG AGTGTTCT
                                |||||||||| ||||||||
                                TGTTGATGTT TTATAAGG
                                      _
GAM1034  FLJ14399  3'  TGGTGGGGCGTGGTGGCTTCA  51333    C   TG AG  G
                                TG AGC  C  CA TGTTCTACCG
                                || |||  |  || ||||||||||
                                AC TCG  G  GT GCGGGGTGGT
                                 T   GT __  _
GAM1034  FLJ14642  3'  TGGTGGCTGAGTGCTGTGGCTC 51510    C   TG    GTGTT
            A                    TG AGC  CAGCA     CTACCG
                                || |||  |||||     ||||||
                                AC TCG  GTCGT     GGTGGT
                                 _   GT     GAGTC
GAM1034  FLJ14957  3'  TGGTAGGGTGGCTGGTTTGTA  51766      CTG    AGT TT
                                TGCAG   CAGC   G  CTACCG
                                |||||   ||||   |  ||||||
                                ATGTT   GTCG   T  GATGGT
                                   TG_    G__ GG
GAM1034  FLJ20152  3'  TATTTCTGCAGTTGTA      38648          C
                                TGCAGCTGCAG AGTG
                                |||||||||| ||||
                                ATGTTGACGTC TTAT
                                      T
GAM1034  FLJ20308  3'  TGGAAAATTGTTGTGGTGT    66857     G TG      G
                                GCA C  CAGCAGT TTCTA
                                ||| |  ||||||| |||||
                                TGT G  GTTGTTA AAGGT
                                  _ GT      A
GAM1034  FLJ20315  5'  TGGTTGAAGTGCATTGCTGCAG 34937             ___  T
            CTG                    CAGCTGCAGCAGTGT   TC ACCG
                                |||||||||||||||   || ||||
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                                GTCGACGTCGTTACG   AG TGGT
                                        TGA  T
GAM1034  FLJ20701  3'  GCTGCTGCTGTGACTGT     35590      CT       _
                                GCAG  GCAGCAGT GT
                                ||||  |||||||| ||
                                TGTC  TGTCGTCG CG
                                  AG       T
GAM1034  FLJ22611  5'  TGGTGCTTCCTGTTCGCAGCTG 81893         _    TGTTC
              C                   GCAGCTGC AGCAG    TACCG
                                ||||||||| |||||    |||||
                                CGTCGACG TTGTC    GTGGT
                                     C    CTTC_
GAM1034  FLJ23416  3'  GGTGGAATAGTCTGTTGTA   49953         __
                                TGCAGCAG  TGTTCTACC
                                ||||||||  |||||||||
                                ATGTTGTC  ATAAGGTGG
                                     TG
GAM1034  FN5      3'  ATGTTGCTGAGCTGTA      39428        G     TG
                                TGCAGCT CAGCAG  T
                                ||||||| ||||||  |
                                ATGTCGA GTCGTT  A
                                     _     GT
GAM1034  FOXN4     5'  CGGTGGATGTGCCTCGGCTGCA 75573         CA   GTGT
                                TGCAGCTG  GCA    TCTACCG
                                ||||||||  |||   |||||||
                                ACGTCGGC  CGT    AGGTGGC
                                     TC   GT__
GAM1034  GIOT-3    5'  GGTGGGGCAGAGGCTGC     32753       AG_
                                GCAGC   TGTTCTACC
                                |||||   |||||||||
                                CGTCG   ACGGGGTGG
                                   GAG
GAM1034  HERPUD1   3'  TGGTGTTTGTGCTGTAGCTGT  28021           GTGTTC
                                GCAGCTGCAGCA     TACCG
                                ||||||||||||     |||||
                                TGTCGATGTCGT     GTGGT
                                       GTTT__
GAM1034  HPCAL4    3'  TGGTAGAGCACTGGCCCTGC   32742      CT  AG
                                GCAG  GC  CAGTGTTCTACCG
                                ||||  ||  ||||||||||||||
                                CGTC  CG  GTCACGAGATGGT
                                  C_  __
GAM1034  HSJ1      3'  GGTGGAGCCAGTCGCTGTA    22136       T  AGCAGT
                                TGCAGC GC     GTTCTACC
                                |||||| ||     ||||||||
                                ATGTCG TG     CGAGGTGG
                                   C  AC_____
GAM1034  HSPC129   5'  TGGTTCTGTTGCTGCTGC    33075       T      TGTT
                                GCAGC GCAGCAG    CTA
                                ||||| |||||||    |||
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                                CGTCG CGTTGTC   GGT
                                  T     TT__
GAM1034 HSPC150  5' TGGTCCGCGCGTTGCTGCGTTG 26349     T    __   TCT
            T                    GCAGC GCAGCA GTGT  ACCG
                                 ||||| ||||||  ||||  ||||
                                 TGTTG CGTCGT CGCG  TGGT
                                   _    TG   CC_
GAM1034 HSSEXGENE 5' TGGTGGCTGCGGCGGCGGCTGC 34000       A A GTT
                                 GCAGCTGC GC GT  CTACCG
                                 |||||||| || ||  ||||||
                                 CGTCGGCG CG CG  GGTGGT
                                     G G TC_
GAM1034 HTEX4    5' CGGTATTTCCCTTTTGCGGCTG 92096         C TGTTC
            CA                    TGCAGCTGCAG AG    TACCG
                                  |||||||||| ||    |||||
                                  ACGTCGGCGTT TC    ATGGC
                                        T CCTTT
GAM1034 HTEX4    5' CGGTATTTCCCTTTTGCGGCTG 97722         C TGTTC
            CA                    TGCAGCTGCAG AG    TACCG
                                  |||||||||| ||    |||||
                                  ACGTCGGCGTT TC    ATGGC
                                        T CCTTT
GAM1034 HTEX4    5' CGGTATTTCCCTTTTGCGGCTG 97897         C TGTTC
            CA                    TGCAGCTGCAG AG    TACCG
                                  |||||||||| ||    |||||
                                  ACGTCGGCGTT TC    ATGGC
                                        T CCTTT
GAM1034 IDI1     3' GGTGGGGTCTGTGCTGT    67044      TGCA   T TT
                                 GCAGC   GCAG G  CTACC
                                 |||||   |||| |  |||||
                                 TGTCG   TGTC T  GGTGG
                                   ____   _ GG
GAM1034 IRF7     3' TGGTGGGACACCCGAGCTGCA  14444       GCAGCA
                                 TGCAGCT    GTGTTCTACCG
                                 |||||||    ||||||||||
                                 ACGTCGA    CACAGGGTGGT
                                    GCC___
GAM1034 KCNK13   5' CGGTGGGGCGCCCGGGAGCTG  41908      GCAGCA
                                 CAGCT    GTGTTCTACCG
                                 |||||    ||||||||||
                                 GTCGA    CGCGGGGTGGC
                                   GGGCC_
GAM1034 KIAA0077 3' TGGAAGACTGCTGTGTTTGT  67022     CT      G
                                 GCAG  GCAGCAGT TTCTA
                                 ||||  |||||||| |||||
                                 TGTT  TGTCGTCA AAGGT
                                   TG      G
GAM1034 KIAA0164 5' GGCCGCTGTGTGGTTGCA    28450      TG  G    TT
                                 TGCAGC  CA CAGTG  C
                                 ||||||  || |||||  |
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                              ACGTTG  GT GTCGC  G
                                 GT _    CG
GAM1034  KIAA0173  3'  TGGTGTGGTTGCTGAGTTGTA  27672       G     TGT  _
                              TGCAGCT CAGCAG   TC TACCG
                              ||||||| ||||||   || |||||
                              ATGTTGA GTCGTT   GG GTGGT
                                 _    ___  T
GAM1034  KIAA0193  3'  GCCTGTTGTTCGGTTGT     28656       __      T
                              GCAGCT  GCAGCAG GT
                              ||||||  ||||||| ||
                              TGTTGG  TGTTGTC CG
                                 CT      _
GAM1034  KIAA0227  3'  GGGCTGGGATGCTGTTGTGGCT 60700     TG          _ G
                              AGC  CAGCAGTGTTCTA CC
                              |||  |||||||||||| ||
                              TCG  GTTGTCGTAGGGT GG
                                GT           C  GT
GAM1034  KIAA0438  3'  TGGTGGAAATTTGTGGCTAGT  29074    _  TG   CAGTG
                              GC AGC  CAG     TTCTACCG
                              || |||  |||     ||||||||
                              TG TCG  GTT     AAGGTGGT
                               A   GT   TA___
GAM1034  KIAA0446  3'  GAATATTCACTGTTGCACTGTA 68867       C         TTCTACCG
                              TGCAG TGCAGCAGTG
                              ||||| ||||||||||
                              ATGTC ACGTTGTCAC
                                 _         TTATAAGT
GAM1034  KIAA0459  3'  TGGTGGGGCAATCTCGGCTCA  61011    C     C  CAG
                              TG AGCTG AG   TGTTCTACCG
                              || ||||| ||   ||||||||||
                              AC TCGGC TC   ACGGGGTGGT
                               _    _  TA_
GAM1034  KIAA0513  3'  TGGGAGCGCGGCGCTGCCTGTA 28383        _     ___  A
            GCTGC                  GCTGCAG CAGTGTT   CT CCG
                              ||||||| |||||||   || |||
                              CGATGTC GTCGCGG   GA GGT
                                  C      CGC  G
GAM1034  KIAA0542  5'  CGATTCTCATTGCTGCTGCTGC 66084       T       TTCTACCG
            A                   TGCAGC GCAGCAGTG
                              ||||||| |||||||||
                              ACGTCG CGTCGTTAC
                                 T        TCTTAGC
GAM1034  KIAA0677  3'  TGGAATGCTGTGGCTGCA    27833       TG    GTG
                              TGCAGC  CAGCA   TTCTA
                              ||||||  |||||   |||||
                              ACGTCG  GTCGT   AAGGT
                                 GT    ____
GAM1034  KIAA0861  3'  GGTAGGATGTTTAGTAGC    88932       AGC  TG
                              GCTGC   AG  TTCTACC
                              |||||   ||  |||||||
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                                CGATG   TT  AGGATGG
                                   AT_  GT
GAM1034  KIAA1016  5'  CGGTGGAGCACTGCGGCACTCA 91733    C  C   A
                                TG AG TGC GCAGTGTTCTACCG
                                || || ||| ||||||||||||||
                                AC TC ACG CGTCACGAGGTGGC
                                 _ _  G
GAM1034  KIAA1068  3'  GGTGGCCGCTGTGGCTG     31036      TG    A TGTT
                                CAGC  CAGC G    CTACC
                                ||||  |||| |    |||||
                                GTCG  GTCG C    GGTGG
                                  GT    C ____
GAM1034  KIAA1089  5'  GGTGGCGGCGGCGGCTGC    68847         A  AGTGTT
                                GCAGCTGC GC     CTACC
                                |||||||| ||     |||||
                                CGTCGGCG CG     GGTGG
                                     G  GC____
GAM1034  KIAA1157  5'  GGGAAGGGACCTGCTGCAGCTG 72249            T    A_  G
            CA                    TGCAGCTGCAGCAG GTTCT  CC
                                ||||||||||||||| |||||  ||
                                ACGTCGACGTCGTC CAGGG  GG
                                       _    AA  GG
GAM1034  KIAA1194  5'  CGGTGGCGGCGCTGCAGCAGC  95938       A      _
                                GCTGC GCAGTGTT CTACCG
                                ||||| |||||||| ||||||
                                CGACG CGTCGCGG GGTGGC
                                   A       C
GAM1034  KIAA1198  3'  GGTAATGCTGTCAGTTGTA   63327         _    GTGTTC
                                TGCAGCTG CAGCA     TACC
                                |||||||| |||||     ||||
                                ATGTTGAC GTCGT     ATGG
                                     T    A_____
GAM1034  KIAA1228  3'  GGTGGAGCGCACGCCTGTA   65048       CT  AGCA
                                TGCAG  GC   GTGTTCTACC
                                |||||  ||   ||||||||||
                                ATGTC  CG   CGCGAGGTGG
                                   __  CA__
GAM1034  KIAA1244  3'  GTAGGATGCACCTGTA      71993       CA
                                TGCAG  GTGTTCTAC
                                |||||  |||||||||
                                ATGTC  CGTAGGATG
                                   CA
GAM1034  KIAA1280  5'  GTGGATAGCGGCTGTA      69729         AGCAGTGT
                                TGCAGCTGC       TCTAC
                                |||||||||       |||||
                                ATGTCGGCG       AGGTG
                                     AT_______
GAM1034  KIAA1322  3'  GAACCGTTTTGCAGCTGC    72735          CAGT
                                GCAGCTGCAG    GTTC
                                ||||||||||    ||||
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                                CGTCGACGTT   CAAG
                                     TTGC
GAM1034 KIAA1432 5' TGGACAGAATATTGCTGTGGTT 66752     TG         A_
            G                    CAGC  CAGCAGTGTTCT  CCG
                                 ||||  ||||||||||||  |||
                                 GTTG  GTCGTTATAAGA  GGT
                                   GT          CA
GAM1034 KIAA1462 3' GACACTGTTGTAGCTG     91385
                                 CAGCTGCAGCAGTGTT
                                 ||||||||||||||||
                                 GTCGATGTTGTCACAG

GAM1034 KIAA1494 5' GGTGGGGCCGCATCTGCA    68462      C   A  AGTGT
                                 TGCAG TGC GC    TCTACC
                                 ||||| ||| ||    ||||||
                                 ACGTC ACG CG    GGGTGG
                                    T   C  _____
GAM1034 KIAA1666 5' GGGAGTTGCGGCAGCTGCA   65250        A    TGTT  A
                                 TGCAGCTGC GCAG   CT CC
                                 |||||||||  ||||   || ||
                                 ACGTCGACG CGTT   GA GG
                                      G   _____  G
GAM1034 KIAA1808 5' CGGCACCCGCTGCTTCAGCTGC 85862       C      TTCTA
                                 GCAGCTG AGCAGTG    CCG
                                 |||||||  |||||||    |||
                                 CGTCGAC TCGTCGC    GGC
                                     T      CCAC_
GAM1034 KIAA1821 3' TGGTTTGATTGTTGTGGGTGTA 71800     G TG      GTTCT
                                 TGCA C  CAGCAGT    ACCG
                                 |||| |  |||||||    ||||
                                 ATGT G  GTTGTTA    TGGT
                                   G GT      GTT__
GAM1034 KIAA1871 3' GTGGGGCACGCCTGTA     61236      CA
                                 TGCAG  GTGTTCTAC
                                 |||||  |||||||||
                                 ATGTC  CACGGGGTG
                                    CG
GAM1034 KIAA1924 3' CGGTGGGACGTGGGTAGTGTGT 73669    _    AG  G
                                 GCA GCTGC  CA TGTTCTACCG
                                 ||| |||||  || ||||||||||
                                 TGT TGATG  GT GCAGGGTGGC
                                   G    G_ _
GAM1034 LCP      3' GCATTGTTGTAGTTTG     26706   C
                                 G AGCTGCAGCAGTGT
                                 | ||||||||||||||
                                 G TTGATGTTGTTACG
                                  T
GAM1034 LSFR2    3' GGCGGCTGCTGTCGTTGT    60568      T      _
                                 GCAGC GCAGCAGT GTT
                                 ||||| |||||||| |||
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                                TGTTG TGTCGTCG CGG
                                   C       G
GAM1034 LW-1     5' AGCCAGGGCTTTGCTGTAGTTG 60258          T    ACCG
              T                    GCAGCTGCAGCAG GTTCT
                                   |||||||||||| |||||
                                   TGTTGATGTCGTT CGGGA
                                          T    CCGAG
GAM1034 LW-1     5' AGCCAGGGCTTTGCTGTAGTTG 32367          T    ACCG
              T                    GCAGCTGCAGCAG GTTCT
                                   |||||||||||| |||||
                                   TGTTGATGTCGTT CGGGA
                                          T    CCGAG
GAM1034 MAST205  5' GGTGGTTGGCGCGGCTGC    30669       A  AGTGTT
                                   GCAGCTGC GC     CTACC
                                   |||||||| ||     |||||
                                   CGTCGGCG CG     GGTGG
                                        _ GTT___
GAM1034 MGC10854 5' GGCGTTGCTGTAGCGC      50204    A
                                   GC GCTGCAGCAGTGTT
                                   || ||||||||||||||
                                   CG CGATGTCGTTGCGG
                                    _
GAM1034 MGC12217 3' GGTAGAATACCGTGCTGT    51313      __
                                   GCAGCA  GTGTTCTACC
                                   ||||||  ||||||||||
                                   TGTCGT  CATAAGATGG
                                      GC
GAM1034 MGC14376 3' TGGTGGAACAAAGTCACTGTA  51850     C  CA  AG
                                   TGCAG TG  GC  TGTTCTACCG
                                   ||||| ||  ||  ||||||||||
                                   ATGTC AC  TG  ACAAGGTGGT
                                      _ __  AA
GAM1034 MGC20806 3' GGTGGTGTCGCGGCTGC     58754       A  GTGTT
                                   GCAGCTGC GCA    CTACC
                                   |||||||| |||    |||||
                                   CGTCGGCG TGT    GGTGG
                                        C  _____
GAM1034 MGC2217  3' TGGTATGTTGCTGTTGGCTGT  44181       _    TG TCT
                                   GCAGCTG CAGCAG  T   ACCG
                                   ||||||| ||||||  |   ||||
                                   TGTCGGT GTCGTT  A   TGGT
                                      T     GT ___
GAM1034 MGC27171 3' TGGGACTCTATATTGTTGTAGT 58087   C          TCTA__
              TCA                    G AGCTGCAGCAGTGT     CCG
                                   | ||||||||||||||     |||
                                   C TTGATGTTGTTATA     GGT
                                   _          TCTCAG
GAM1034 MGC2827  3' TGGTGGTCCGTTGCAGTTTCA  43746    C       AGT TT
                                   TG AGCTGCAGC   G  CTACCG
                                   || |||||||||   |  ||||||
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                                AC TTGACGTTG   C  GGTGGT
                                 T        ___ CT
GAM1034  MGC3248   3'  GGCCAGTTGTTGCAGTTGC    50655            _  TT
                                GCAGCTGCAGCAG TG  C
                                |||||||||||| ||  |
                                CGTTGACGTTGTT AC  G
                                      G  CG
GAM1034  MPN       3'  GCTGCTGTTGCACCTGT     49209      C        _
                                GCAG TGCAGCAGT GT
                                |||| ||||||||| ||
                                TGTC ACGTTGTCG CG
                                  C        T
GAM1034  MRPL48    5'  CGGTGGGATATTGCTGCTGC   32133    T
                                GC GCAGCAGTGTTCTACCG
                                || ||||||||||||||||
                                CG CGTCGTTATAGGGTGGC
                                 T
GAM1034  MSE55     5'  TGGTAGGCATGGACTAGCAGCT 22943         _  CA_    T
                GT                   GCAGCTGC AG   GTGT CTACCG
                                |||||||| ||   |||| ||||||
                                TGTCGACG TC   TACG GATGGT
                                     A  AGG   _
GAM1034  MSRA      3'  GGTGGGAGTGGAGCTGT     24683        G  G AGTG
                                GCAGCT CA C    TTCTACC
                                |||||| || |    |||||||
                                TGTCGA GT G    AGGGTGG
                                   G  _ _____
GAM1034  MTCH1     3'  GGTTACCTGTGCAGTTGT     26781          G   T  TCT
                                GCAGCTGCA CAG GT   ACC
                                ||||||||| ||| ||   |||
                                TGTTGACGT GTC CA   TGG
                                     _   _  T__
GAM1034  MYOM1     3'  CGGAATTGGGATTTGCTGCAGC 13736            T     ___
                TGT                   CAGCTGCAGCAG GTTCTA   CCG
                                |||||||||||| ||||||   |||
                                GTCGACGTCGTT TAGGGT   GGC
                                      _      TAA
GAM1034  MYT1      3'  CGGTGGAGTCCTGTTGCTGT   15773    T      TG
                                GC GCAGCAG  TTCTACCG
                                || |||||||  ||||||||
                                TG CGTTGTC  GAGGTGGC
                                 T      CT
GAM1034  NCK1      3'  ACTGCTGTGTAGCTGTA     20469        __
                                TGCAGCT  GCAGCAGT
                                |||||||  ||||||||
                                ATGTCGA  TGTCGTCA
                                     TG
GAM1034  NETO1     5'  CGGTGGGGATGCTGCTGGCTGC 57253       TG          _
                                GCAGC  CAGCAGTGTTCT ACCG
                                |||||  |||||||||||| ||||
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                                CGTCG  GTCGTCGTAGGG TGGC
                                  __         G
GAM1034  NUBP2    3'  TGGTCTGCGTGCTCTGCAGCTG 64233         C  TG TCT_
             T                   GCAGCTGCAG AG  T    ACCG
                                 |||||||||| ||  |   ||||
                                 TGTCGACGTC TC  G    TGGT
                                      _  GT CGTC
GAM1034  OS4      3'  TGGTGGGAGTGTCCCTGCTGCA 19186   C      TG____
             TCTGCA                G TGCAGCAG     TTCTACCG
                                 | ||||||||     ||||||||
                                 C ACGTCGTC     AGGGTGGT
                                  T       CCTGTG
GAM1034  PARG1    5'  GGCTGCGGCTGCGGCTGC    16682          A  _
                                 GCAGCTGCAGC GT GTT
                                 |||||||||| || |||
                                 CGTCGGCGTCG CG CGG
                                       G  T
GAM1034  PCDH19   3'  ACTGTTGCTCCAGCTGT     63694       ___
                                 GCAGCT   GCAGCAGT
                                 ||||||   ||||||||
                                 TGTCGA   CGTTGTCA
                                    CCT
GAM1034  PCDH19   3'  TGCAAAATATTGGTGTGGCTGC 63711       TG  G      CTACCG
             A                   TGCAGC  CA CAGTGTT
                                 ||||||  || |||||||
                                 ACGTCG  GT GTTATAA
                                    GT  G      AACGT
GAM1034  POP5     3'  TGGTGAAGTGTTGCAGGTTGT  31923      _     GTG   T
                                 GCAGC TGCAGCA   TTC ACCG
                                 ||||| |||||||   ||| ||||
                                 TGTTG ACGTTGT   AAG TGGT
                                    G      G__   _
GAM1034  PRDM13   3'  TGGTAGAATACAAATGTGGTGT 41241     _  TG  GCA
             GT                    GCA GC  CA   GTGTTCTACCG
                                 ||| ||  ||   ||||||||||
                                 TGT TG  GT   CATAAGATGGT
                                   G  GT  AAA
GAM1034  PRO2032  5'  GGTGGGGTATGAAGCTCA    37781    C   GCAGCA   TT
                                 TG AGCT     GTG  CTACC
                                 || ||||     |||  |||||
                                 AC TCGA     TAT  GGTGG
                                  _   AG_____   GG
GAM1034  RAB24    5'  GGTGGAGCGCTACGTGCA    55392      GC_
                                 TGCA   AGTGTTCTACC
                                 ||||   ||||||||||
                                 ACGT   TCGCGAGGTGG
                                   GCA
GAM1034  RABEX5   3'  GGTAGAATGTTCAGCAGC    27187       AGC  TG
                                 GCTGC   AG  TTCTACC
                                 |||||   ||  |||||||
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                                CGACG   TT  AAGATGG
                                  AC_  GT
GAM1034  RASD2    3'  GCTTTGTTGTGGTTGCA     26687       TG     T
                                TGCAGC  CAGCAG GT
                                ||||||  |||||| ||
                                ACGTTG  GTTGTT CG
                                   GT     T
GAM1034  RGS19    5'  GAGTCCCTGCTGCTGCAGTGCA 19651      G         TTCTACCG
                                TGCA CTGCAGCAGTG
                                |||| ||||||||||
                                ACGT GACGTCGTCGT
                                  _         CCCTGAGT
GAM1034  RIL      3'  TGGTGGGGTGCTGGCAGC    13491       AG   TG
                                GCTGC  CAG  TTCTACCG
                                |||||  |||  ||||||||
                                CGACG  GTC  GGGGTGGT
                                  __  GT
GAM1034  SBBI26   5'  GGGCGCTGCAGCTGCA      38135           AGT
                                TGCAGCTGCAGC   GTTC
                                ||||||||||||   ||||
                                ACGTCGACGTCG   CGGG
                                               ___
GAM1034  SCAMP5   3'  GGTAGAGGCTCTAGCTGT    57260        C   AGTG
                                GCAGCTG AGC    TTCTACC
                                ||||||| |||    |||||||
                                TGTCGAT TCG    GAGATGG
                                   C  _____
GAM1034  SCYA18   3'  TATTGTTGAGCTGCA       11461        G
                                TGCAGCT CAGCAGTG
                                ||||||| ||||||||
                                ACGTCGA GTTGTTAT
                                  _
GAM1034  SCYD1    3'  GGTCCTGCTGCAGTTGC     90933           TG
                                GCAGCTGCAGCAG  TT
                                ||||||||||||  ||
                                CGTTGACGTCGTC  GG
                                       CT
GAM1034  SEC23B   5'  CGGAGCCTGCTTGTTGCAGCTG 21018        _____   T    ACCG
           T                     CAGCTGCA    GCAG GTTCT
                                 ||||||||    |||| |||||
                                 GTCGACGT    CGTC CGAGG
                                      TGTT   _     C
GAM1034  SEC23B   5'  CGGAGCCTGCTTGTTGCAGCTG 52177        _____   T    ACCG
           T                     CAGCTGCA    GCAG GTTCT
                                 ||||||||    |||| |||||
                                 GTCGACGT    CGTC CGAGG
                                      TGTT   _     C
GAM1034  SEC61A1  3'  AGTGCTGTATGCGGCTGCA    25307          _    TG
                                TGCAGCTGCA GCAG  TT
                                |||||||||| ||||  ||
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                                ACGTCGGCGT TGTC  GA
                                     A    GT
GAM1034  SID6-306  5'  TGAGCGCGCTGCTGCGGCTGC  22600            T  ACCG
                                GCAGCTGCAGCAGTGT CT
                                |||||||||||||||| ||
                                CGTCGGCGTCGTCGCG GA
                                        C  GT
GAM1034  SLC26A10  5'  TCGGTGCTGCTGTGGCTG    56035     TG      GTTCT
                                CAGC  CAGCAGT    ACCG
                                ||||  |||||||    ||||
                                GTCG  GTCGTCG    TGGC
                                  GT      _____   TG
GAM1034  SMC2L1    3'  TGGTCCAATTATTGTGGTTGT  21239      TG   C   GTTCT
                                GCAGC  CAG AGT    ACCG
                                |||||  ||| |||    ||||
                                TGTTG  GTT TTA    TGGT
                                   GT   A   ACC__
GAM1034  SNX11     5'  GGTGGGGCGCGGGCGGT     25272      AGCA
                                GCTGC   GTGTTCTACC
                                |||||   ||||||||||
                                TGGCG   CGCGGGGTGG
                                   GG__
GAM1034  STIM2     3'  TTGTTGCTTAGTTGCA      40482        __
                                TGCAGCT  GCAGCAG
                                |||||||  |||||||
                                ACGTTGA  CGTTGTT
                                     TT
GAM1034  STK16     3'  TGGTGGGATATGGAACATGGCT 72120      GCAGCA_
                                AGCT      GTGTTCTACCG
                                ||||      ||||||||||
                                TCGG      TATAGGGTGGT
                                  TACAAGG
GAM1034  TCFL5     3'  AGTCACGTGCTGCTGTATTGCA 21720       C       TG TCTACCG
                                TGCAG TGCAGCAG  T
                                ||||| |||||||  |
                                ACGTT ATGTCGTC  G
                                   _       GT CACTGAG
GAM1034  TFB2M     5'  TGGGGTTCACTGTAGTAGCTGC 42309          A     TT  A
              A                  TGCAGCTGC GCAGTG  CT CCG
                                 |||||||| ||||||  || |||
                                 ACGTCGATG TGTCAC  GG GGT
                                      A     TT  _
GAM1034  TNKS2     5'  CGGTTGCTGGCGCTGTTGCTGG 47452      _         CT__
              CTGT                 AGCT GCAGCAGTGTT    ACCG
                                   ||||  ||||||||||    ||||
                                   TCGG CGTTGTCGCGG    TGGC
                                     T         TCGT
GAM1034  TOB2      3'  TGGTGGGGTGACACCGCTGTGG 95627   C   TG    A     ___
              CTTA                  AGC  CAGC GTGTT   CTACCG
                                    |||  |||| |||||   ||||||
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                                TCG  GTCG CACAG   GGTGGT
                                T   GT    C     TGG
GAM1034  TRAG3    5'  ATACTGCTCAGCTGT       16931        C
                                GCAGCTG AGCAGTGT
                                ||||||| ||||||||
                                TGTCGAC TCGTCATA
                                   _
GAM1034  TRAG3    5'  ATACTGCTCAGCTGT       67524        C
                                GCAGCTG AGCAGTGT
                                ||||||| ||||||||
                                TGTCGAC TCGTCATA
                                   _
GAM1034  TRIM26   5'  GCGCTGCTGTAGTTGC      12890
                                GCAGCTGCAGCAGTGT
                                ||||||||||||||||
                                CGTTGATGTCGTCGCG

GAM1034  TRIP10   5'  GGTGGTGGCTGCGGCGGC    14900    A      AGTGTT
                                GC GCTGCAGC     CTACC
                                || ||||||||     |||||
                                CG CGGCGTCG     GGTGG
                                 G       GT____
GAM1034  UBCE7IP5 3'  GGTGGAGTGCCTGTCTGT    30158     CT    CA TG
                                GCAG  GCAG  G  TTCTACC
                                ||||  ||||  |  |||||||
                                TGTC  TGTC  C  GAGGTGG
                                  __   __ GT
GAM1034  UK114    5'  GGCGCTGCTGTGGTTG      19547     TG
                                CAGC  CAGCAGTGTT
                                ||||  ||||||||||
                                GTTG  GTCGTCGCGG
                                  GT
GAM1034  WNT10A   3'  CGGTGGGGTGCGTGGGGGTGGC 47402    TG AG_  _ TG
                                GC  C   CA G  TTCTACCG
                                ||  |   || |  ||||||||
                                CG  G   GT C  GGGGTGGC
                                 GT GGG  G GT
GAM1034  YME1L1   5'  CGTTGCAGTAGCTGTA      57777         A
                                TGCAGCTGC GCAGTG
                                ||||||||| ||||||
                                ATGTCGATG CGTTGC
                                      A
GAM1034  YME1L1   5'  CGTTGCAGTAGCTGTA      57786         A
                                TGCAGCTGC GCAGTG
                                ||||||||| ||||||
                                ATGTCGATG CGTTGC
                                      A
GAM1034  YME1L1   5'  CGTTGCAGTAGCTGTA      26527         A
                                TGCAGCTGC GCAGTG
                                ||||||||| ||||||
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                                ATGTCGATG CGTTGC
                                      A
GAM1034  ZNF340    5'  GGTGTGTGCTGTGGTGCA    84562      G TG    GTGTTC
                                TGCA C  CAGCA     TACC
                                |||| |  |||||     ||||
                                ACGT G  GTCGT     GTGG
                                  _ GT    GT____
GAM1034  LOC122830 5'  GGAGGCTGCCGCGGCTGC    74166         A    G
                                GCAGCTGC GCAGT TTC
                                |||||||| ||||| |||
                                CGTCGGCG CGTCG AGG
                                      C    G
GAM1034  LOC125967 3'  TGGTGGATGAGGCTGCGGCGGC 74425    A       AGTGT
                                GC GCTGCAGC     TCTACCG
                                || ||||||||     |||||||
                                CG CGGCGTCG     AGGTGGT
                                 G       GAGT_
GAM1034  LOC126432 5'  GGAGCTGCGGCGGCTGC     74518         A    GT
                                GCAGCTGC GCAGT  TCT
                                |||||||| |||||  |||
                                CGTCGGCG CGTCG  AGG
                                      G    __
GAM1034  LOC126669 3'  TGGTGGATGCCTGTGGTTCCA  75424    C   TG  _  GTGT
                                TG AGC  CAG CA    TCTACCG
                                || |||  ||| ||    |||||||
                                AC TTG  GTC GT    AGGTGGT
                                 C   GT   C  ____
GAM1034  LOC127428 3'  GCATTTGCTGTTCCAGTTGCA  74669         ___     _
                                TGCAGCTG   CAGCAG TGT
                                ||||||||   |||||| |||
                                ACGTTGAC   GTCGTT ACG
                                      CTT     T
GAM1034  LOC129450 5'  ATGTTGCTGCAGTTGCA     74872             TG
                                TGCAGCTGCAGCAG  T
                                ||||||||||||||  |
                                ACGTTGACGTCGTT  A
                                         GT
GAM1034  LOC131368 3'  AGCTGCTGTTGCAGCTGT    75856             _
                                GCAGCTGCAGCAGT GTT
                                |||||||||||||| |||
                                TGTCGACGTTGTCG CGA
                                         T
GAM1034  LOC131583 3'  GTAAAATGTTGTTCAGTTGTA  75866         C    TG  C
                                TGCAGCTG AGCAG  TT TAC
                                |||||||| |||||  || |||
                                ATGTTGAC TTGTT  AA ATG
                                      _    GT  A
GAM1034  LOC135932 3'  TGGAATTGTGTGCTGCGGCTGT 76201           GT__     CCG
                                GCAGCTGCAGCA    GTTCTA
                                ||||||||||||   ||||||
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                                TGTCGGCGTCGT   TAAGGT
                                      GTGT
GAM1034  LOC138389 3'  CGGTGGGACGTGGGTGGTGCA  76223     G TG AG  G
                                TGCA C  C  CA TGTTCTACCG
                                |||| |  |  || ||||||||||
                                ACGT G  G  GT GCAGGGTGGC
                                  _ GT G_  _
GAM1034  LOC139046 5'  CGGTGGAGCGGCGCTGGCGC   75810    A  TG   AG
                                GC GC  CAGC  TGTTCTACCG
                                || ||  ||||  ||||||||||
                                CG CG  GTCG  GCGAGGTGGC
                                 _ __    CG
GAM1034  LOC143098 5'  GGTAGACAACGTGGCTGCA   76455      TG AGCAG   T
                                TGCAGC  C    TGT CTACC
                                ||||||  |    ||| |||||
                                ACGTCG  G    ACA GATGG
                                   GT CA___   _
GAM1034  LOC143451 3'  TGGATGGCTGCAGCTGT     76569          AGTGT
                                GCAGCTGCAGC    TCTA
                                ||||||||||     ||||
                                TGTCGACGTCG    AGGT
                                      GT___
GAM1034  LOC143903 5'  GCTGCTGCCGCGGTTGCA    76621         A    _
                                TGCAGCTGC GCAGT GT
                                ||||||||| ||||| ||
                                ACGTTGGCG CGTCG CG
                                      C    T
GAM1034  LOC143920 3'  TGGAGCCTCTGCTGTAGCTGT  76627           T_
                                GCAGCTGCAGCAG  GTTCTA
                                ||||||||||||  ||||||
                                TGTCGATGTCGTC  CGAGGT
                                        TC
GAM1034  LOC145125 3'  TGGATGGCTGCAGCTGT     77012          AGTGT
                                GCAGCTGCAGC    TCTA
                                ||||||||||     ||||
                                TGTCGACGTCG    AGGT
                                      GT___
GAM1034  LOC145225 3'  TGGTGGGGTGGGCCACAGTTGT 83310       CA  AG  TT
                                GCAGCTG  GC  TG  CTACCG
                                |||||||  ||  ||  ||||||
                                TGTTGAC  CG  GT  GGTGGT
                                    AC  G_  GG
GAM1034  LOC145226 3'  TGGTGGAAGAGCTGCAGCT   77048        AGTG
                                AGCTGCAGC    TTCTACCG
                                |||||||||    ||||||||
                                TCGACGTCG    AAGGTGGT
                                      AG__
GAM1034  LOC145371 3'  GCACTGCGTGGCTGCA      77154       TG A
                                TGCAGC  C GCAGTGT
                                ||||||  | |||||||
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                                ACGTCG  G CGTCACG
                                   GT _
GAM1034  LOC146443 5'  TGGTGGAGGACCCTGTGGTGCA 77888     G TG   CA  G
                                TGCA C  CAG  GT TTCTACCG
                                |||| |  |||  || ||||||||
                                ACGT G  GTC  CA GAGGTGGT
                                  _ GT   C_  G
GAM1034  LOC146657 3'  TACATAGAGTGTCTGCTGTAGC 60451           _ GT    CCG
            TGT                   GCAGCTGCAGCAG T  TCTA
                                |||||||||||| |  ||||
                                TGTCGATGTCGTC G  AGAT
                                       T TG    ACATG
GAM1034  LOC146988 5'  TGGTGGAGCCGGTGGCTGCG   83897       TG AGCAGT
                                TGCAGC  C     GTTCTACCG
                                ||||||  |     |||||||||
                                GCGTCG  G     CGAGGTGGT
                                   GT GC_____
GAM1034  LOC147077 5'  AGCCAGGGCACTGCTCAGCTGT 78246        C          ACCG
                                GCAGCTG AGCAGTGTTCT
                                ||||||| ||||||||||
                                TGTCGAC TCGTCACGGGA
                                   _         CCGAG
GAM1034  LOC147694 3'  TTGTTGTTGAGTTGTA      78459        __
                                TGCAGCT  GCAGCAG
                                |||||||  |||||||
                                ATGTTGA  TGTTGTT
                                    GT
GAM1034  LOC148223 3'  CGGTAGTGGCTGCTGTGGCTGC 78737      TG      GTT
                                GCAGC  CAGCAGT   CTACCG
                                |||||  |||||||   ||||||
                                CGTCG  GTCGTCG   GATGGC
                                  GT      GT_
GAM1034  LOC148231 3'  TGGTGGCACCAGCTGCGGCTGC 78754           A_   TT
            A                   TGCAGCTGCAGC  GTG  CTACCG
                                ||||||||||||  |||  ||||||
                                ACGTCGGCGTCG  CAC  GGTGGT
                                       AC   __
GAM1034  LOC148418 3'  TGAATTGGTGCTTTGTGGTTGC 78850      TG  __   GT_    TACCG
            A                    GCAGC  CA  GCA   GTTC
                                |||||  ||  |||   ||||
                                CGTTG  GT  CGT   TAAG
                                   GT  TT   GGT    T   G
GAM1034  LOC148981 5'  TGGTGGAGGTAATTTTGGCTGT 84318       GCAGCAGTG
                                GCAGCT        TTCTACCG
                                ||||||        ||||||||
                                TGTCGG        GAGGTGGT
                                   TTTTAATG_
GAM1034  LOC149386 5'  TGGTGGGGCACTGAGTGTGGC  84410    TG  G_
                                GC  CA  CAGTGTTCTACCG
                                ||  ||  ||||||||||||
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                                CG  GT  GTCACGGGGTGGT
                                 GT  GA
GAM1034  LOC149566 3'  GGCATTTTGTGGCTGCA     84492       TG   C
                                TGCAGC  CAG AGTGTT
                                ||||||  ||| ||||||
                                ACGTCG  GTT TTACGG
                                   GT   _
GAM1034  LOC149566 3'  TGGAAAGCTGTTGTAGCTTG   84497    C          G
                                G AGCTGCAGCAGT TTCTA
                                | ||||||||||| |||||
                                G TCGATGTTGTCG AAGGT
                                 T          A
GAM1034  LOC149767 3'  TGGTAGAGTATGGGGGTTGTA  79496        GCAGCA
                                TGCAGCT     GTGTTCTACCG
                                |||||||     ||||||||||
                                ATGTTGG     TATGAGATGGT
                                    GGG___
GAM1034  LOC150221 5'  GGGAGTTGCGGCAGCTGCA    65276         A    TGTT  A
                                TGCAGCTGC GCAG    CT CC
                                ||||||||| ||||    || ||
                                ACGTCGACG CGTT    GA GG
                                     G    _____  G
GAM1034  LOC150245 3'  GCTGTGCTGTAGCTGTA     84935            GT
                                TGCAGCTGCAGCA  GT
                                ||||||||||||  ||
                                ATGTCGATGTCGT  CG
                                       GT
GAM1034  LOC151610 3'  TGAGCACCATGGCTGCAGTTGT 80290           A___      TACCG
                                GCAGCTGCAGC    GTGTTC
                                ||||||||||    ||||||
                                TGTTGACGTCG    CACGAG
                                      GTAC     T   G
GAM1034  LOC151778 5'  CGGTGGGGCTGGAGTGGCTG   71450      TG AG    GT
                                CAGC  C  CAGT  TCTACCG
                                ||||  |  ||||  |||||||
                                GTCG  G  GTCG  GGGTGGC
                                  GT AG    __
GAM1034  LOC152059 3'  TGGTGCTAGCTGCTGTAGC    80452           GTTC
                                GCTGCAGCAGT    TACCG
                                ||||||||||    |||||
                                CGATGTCGTCG    GTGGT
                                      ATC_
GAM1034  LOC152992 3'  GGTCTCTGCTCTGGCTGT     80758        C     TGTTCT
                                GCAGCTG AGCAG      ACC
                                ||||||| |||||      |||
                                TGTCGGT TCGTC      TGG
                                    C     TC_____
GAM1034  LOC153338 3'  GGTGGGGTGTGGTGGCTCA    85999     C   TG A   GTG
                                TG AGC  C GCA   TTCTACC
                                || |||  | |||   |||||||
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                                AC TCG  G TGT   GGGGTGG
                                 _   GT G   ___
GAM1034  LOC154739 5'  AACATTTTGTGGCTGT      86221       TG   C
                                GCAGC  CAG AGTGTT
                                |||||  ||| ||||||
                                TGTCG  GTT TTACAA
                                   GT   _
GAM1034  LOC155340 5'  CGGTGGGGCTGGAGTGGCTG   73378      TG AG    GT
                                CAGC  C  CAGT  TCTACCG
                                ||||  |  ||||  |||||||
                                GTCG  G  GTCG  GGGTGGC
                                  GT AG    __
GAM1034  LOC157773 3'  TAGAAGGCACTGTTGTAGTTG  81609              __    CCG
                                CAGCTGCAGCAGTGT  TCTA
                                ||||||||||||||  ||||
                                GTTGATGTTGTCACG  AGAT
                                          GA
GAM1034  LOC162239 3'  TGGTAGGATGCTTCTGTAGTTC 82343    C       C
            A                    TG AGCTGCAG AGTGTTCTACCG
                                || ||||||||  ||||||||||||
                                AC TTGATGTC TCGTAGGATGGT
                                 _       T
GAM1034  LOC165552 3'  CGGTGGAATGAGACAGTTGT   82486        CAGCAG
                                GCAGCTG     TGTTCTACCG
                                |||||||     ||||||||||
                                TGTTGAC     GTAAGGTGGC
                                    AGA___
GAM1034  LOC165693 5'  GGACACTTCTGTGGCTGTA    82599       TG   C
                                TGCAGC  CAG AGTGTTC
                                ||||||  ||| |||||||
                                ATGTCG  GTC TCACAGG
                                    GT   T
GAM1034  LOC166219 5'  TGGTGGGGTGTCCACTTCTGGC 82626     TG   C   _____
            TGC                    AGC  CAG AGTG    TTCTACCG
                                |||  ||| ||||   ||||||||
                                TCG  GTC TCAC    GGGGTGGT
                                  __   T    CTGT
GAM1034  LOC195977 3'  CACTGCTGCTGTGTTGT     87535       T__
                                GCAGC   GCAGCAGTG
                                |||||   |||||||||
                                TGTTG   CGTCGTCAC
                                   TGT
GAM1034  LOC196761 3'  TGGTGGGGCGGGGCCAGTTG  89558       CA  AG
                                CAGCTG  GC  TGTTCTACCG
                                ||||||  ||  ||||||||||
                                GTTGAC  CG  GCGGGGTGGT
                                    __ GG
GAM1034  LOC200470 5'  GGCGCTGCCGCTGCGGTTGT   90065          ___
                                GCAGCTGCAGC   AGTGTT
                                ||||||||||   ||||||
```

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                                TGTTGGCGTCG   TCGCGG
                                      CCG
GAM1034  LOC200471 5'  ATGCTGTTGCAGCAGTA     90049     A
                                TGC GCTGCAGCAGTGT
                                ||| ||||||||||||
                                ATG CGACGTTGTCGTA
                                  A
GAM1034  LOC200734 3'  GGTGGGTTTTGTAGTTG     88865         CAGTGT
                                CAGCTGCAG     TCTACC
                                |||||||||     ||||||
                                GTTGATGTT     GGGTGG
                                      TT____
GAM1034  LOC201116 3'  CGGCACAGCTGTTCCAGCTGCA 88102         C     GTTCTA
                                TGCAGCTG AGCAGT     CCG
                                |||||||| ||||||     |||
                                ACGTCGAC TTGTCG     GGC
                                     C     ACAC__
GAM1034  LOC203084 3'  CAGAAGAACACTGTTGTAGTTT 87490    C             ACCG
            A                    G AGCTGCAGCAGTGTTCT
                                | ||||||||||||||||
                                A TTGATGTTGTCACAAGA
                                 T              AGACG
GAM1034  LOC203276 3'  AACATTTTGTGGCTGT      90469       TG   C
                                GCAGC  CAG AGTGTT
                                |||||  ||| ||||||
                                TGTCG  GTT TTACAA
                                   GT  _
GAM1034  LOC203305 3'  AACATTTTGTGGCTGT      90513       TG   C
                                GCAGC  CAG AGTGTT
                                |||||  ||| ||||||
                                TGTCG  GTT TTACAA
                                   GT  _
GAM1034  LOC203871 5'  AGCGCACTGTTTGGCTGCA    89440         C       T
                                TGCAGCTG AGCAGTGT CT
                                |||||||| |||||||| ||
                                ACGTCGGT TTGTCACG GA
                                     _       C
GAM1034  LOC204970 3'  AGGGGCTGCTGCAGCTGCA    89407              G
                                TGCAGCTGCAGCAGT TTCT
                                |||||||||||||| ||||
                                ACGTCGACGTCGTCG GGGA
                                                _
GAM1034  LOC205795 5'  TTTGGGACATCTGCTGTAGCTG 90708             _      CCG
            CA                    TGCAGCTGCAGCAG TGTTCTA
                                |||||||||||||| |||||||
                                ACGTCGATGTCGTC ACAGGGT
                                          T      TT
GAM1034  LOC220045 3'  TGGTGGGACTGAAAGAGCTGCA 93413         GCAG    GT
                                TGCAGCT    CAGT  TCTACCG
                                |||||||    ||||  |||||||
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                                ACGTCGA    GTCA  GGGTGGT
                                    GAAA    __
GAM1034  LOC220729 5'  ACACTGTTGCAGCGCA      71598     A
                                TGC GCTGCAGCAGTGT
                                ||| ||||||||||||
                                ACG CGACGTTGTCACA
                                  _
GAM1034  LOC220729 3'  TGGTGGAGACCCTGGAGCTGCA 71600        G   CA  G
                                TGCAGCT CAG  GT TTCTACCG
                                ||||||| |||  || ||||||||
                                ACGTCGA GTC  CA GAGGTGGT
                                    G   C_  _
GAM1034  LOC221025 3'  CAAAAAGCACTGCTGTACCTGT 93174      C          CTACCG
                                GCAG TGCAGCAGTGTT
                                |||| ||||||||||||
                                TGTC ATGTCGTCACGA
                                  C          AAAAC
GAM1034  LOC221271 5'  CGGTGGGACCGGGAGCAAGCTG 91853       _  AGCAGT
              C                  GCAGCT GC      GTTCTACCG
                                ||||||| ||      |||||||||
                                CGTCGA CG      CAGGGTGGC
                                    A  AGGGC_
GAM1034  LOC221683 5'  CGGTTTTTGTTGTCTGTAGTTG 93713          _  GT TTCT
              T                  GCAGCTGCAG CA  G    ACCG
                                |||||||||| ||  |    ||||
                                TGTTGATGTC GT  T    TGGC
                                      T  TG TTT_
GAM1034  LOC221929 5'  CACCCGAATGTTGCTGTGGCTC 92674    C   TG     TG   TACCG
              A                  TG AGC  CAGCAG  TTC
                                || |||  ||||||  |||
                                AC TCG  GTCGTT  AAG
                                 _  GT     GT   CCCACG
GAM1034  LOC222119 5'  CCTTTAACACTGTTGCAGTTTA 94074    C           CTACCG
                                G AGCTGCAGCAGTGTT
                                | ||||||||||||||||
                                A TTGACGTTGTCACAA
                                 T            TTTCCG
GAM1034  LOC222160 3'  GTGGGGCATGCCTGTA      94131       CA
                                TGCAG  GTGTTCTAC
                                |||||  |||||||||
                                ATGTC  TACGGGGTG
                                   CG
GAM1034  LOC253064 5'  TGGAGCCGACACTGCTGTGCTG 97483        T         __  A
              CA                   TGCAGC GCAGCAGTGTT  CT CCG
                                |||||| ||||||||||  || |||
                                ACGTCG TGTCGTCACAG  GA GGT
                                   _          CC  _
GAM1034  LOC253405 5'  GGGGCTGCTGCGCCTGC     97502      C        G
                                GCAG TGCAGCAGT TT
                                |||| ||||||||| ||
```

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                                CGTC GCGTCGTCG GG
                                  C       G
GAM1034  LOC254243 3'  AACATTTTGTGGCTGT     97398      TG   C
                                GCAGC  CAG AGTGTT
                                |||||  ||| ||||||
                                TGTCG  GTT TTACAA
                                   GT   _
GAM1034  LOC254440 3'  TGGATGGCTGCAGCTGT     97073          AGTGT
                                GCAGCTGCAGC    TCTA
                                ||||||||||    ||||
                                TGTCGACGTCG    AGGT
                                      GT___
GAM1034  LOC254670 5'  GAGGCTAGAACATCGCTGTGGC 97208      TG    A      _  G
           TGC                    GCAGC  CAGC GTGTTCTA CC
                                |||||  |||| |||||||| ||
                                CGTCG  GTCG TACAAGAT GG
                                   GT    C       C  AGG
GAM1034  LOC255031 5'  CGGTAGGACACCCAGCTGT   97234       CAGCA
                                GCAGCTG    GTGTTCTACCG
                                |||||||    ||||||||||
                                TGTCGAC    CACAGGATGGC
                                    C____
GAM1034  LOC255055 5'  GATTGCTCTGTGGCTGCA    94870       TG   C   GT
                                TGCAGC  CAG AGT  TC
                                ||||||  ||| |||  ||
                                ACGTCG  GTC TCG  AG
                                    GT   _   TT
GAM1034  LOC255328 3'  GGTAGAATATAAAAGCTCA   96562    C    GCAGCA
                                TG AGCT     GTGTTCTACC
                                || ||||     ||||||||||
                                AC TCGA     TATAAGATGG
                                 _    AAA___
GAM1034  LOC255475 5'  TGGTGGGAGGCAGCTGTGGTGC 97617      G TG    A  G
           A                     TGCA C  CAGC GT TTCTACCG
                                |||| |  |||| || ||||||||
                                ACGT G  GTCG CG AGGGTGGT
                                  _ GT    A  G
GAM1034  LOC255620 5'  CGGTGGGGCTGGAGCGGCTG   97085       AG    GT
                                CAGCTGC  CAGT  TCTACCG
                                |||||||  ||||  |||||||
                                GTCGGCG  GTCG  GGGTGGC
                                    AG   __
GAM1034  LOC255671 3'  GAGCTGTTGTTGGAGCTGCA   97256       G    GT_
                                TGCAGCT CAGCA   GTTC
                                ||||||| |||||   ||||
                                ACGTCGA GTTGT   CGAG
                                    G    TGT
GAM1034  LOC256310 5'  GACCCGTGCTGCGGCTGCA    96346          GT_
                                TGCAGCTGCAGCA   GTT
                                ||||||||||||   |||
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                                ACGTCGGCGTCGT  CAG
                                      GCC
GAM1034  LOC256586 3'  ACCTGCTGCAGTTGCA     94944          T
                                TGCAGCTGCAGCAG GT
                                |||||||||||||| ||
                                ACGTTGACGTCGTC CA
                                       _
GAM1034  LOC256598 5'  CGGTGGGGCTGGAGCGGCTG  96350      AG   GT
                                CAGCTGC  CAGT  TCTACCG
                                |||||||  ||||  |||||||
                                GTCGGCG  GTCG  GGGTGGC
                                   AG   __
GAM1034  LOC257159 5'  GCAGGTTGCTGCAGCTGT   97179          __
                                GCAGCTGCAGCAG  TGT
                                ||||||||||||  |||
                                TGTCGACGTCGTT  ACG
                                      GG
GAM1034  LOC257319 3'  TGGTGGGACACTGTTG     95780
                                CAGCAGTGTTCTACCG
                                ||||||||||||||||
                                GTTGTCACAGGGTGGT

GAM1034  LOC257494 5'  GCGCTGCTGTAGTTGC     97794
                                GCAGCTGCAGCAGTGT
                                ||||||||||||||||
                                CGTTGATGTCGTCGCG

GAM1034  LOC64116  3'  GACTTATGTTGTGGTTGCA   42200      TG    GT_
                                TGCAGC  CAGCA  GTT
                                ||||||  |||||  |||
                                ACGTTG  GTTGT  CAG
                                   GT    ATT
GAM1034  LOC81691  5'  CGGTTGTTGTTGGCAGCTGT  48191       _    TGTTCT
                                GCAGCTGC AGCAG    ACCG
                                |||||||| |||||    ||||
                                TGTCGACG TTGTT    TGGC
                                     G    GT____
GAM1034  LOC90038  3'  AACATTTTGTGGCTGT     61142      TG  C
                                GCAGC  CAG AGTGTT
                                |||||  ||| ||||||
                                TGTCG  GTT TTACAA
                                   GT  _
GAM1034  LOC90231  5'  GCTGCTGCGGCGGTTGC    61868    ___
                                GCA  GCTGCAGCAGT
                                |||  ||||||||||
                                CGT  CGGCGTCGTCG
                                  TGG
GAM1034  LOC90494  5'  GGTGTTCTGCTTGGCTGT   63056       C    TGTTC
                                GCAGCTG AGCAG    TACC
                                |||||||| |||||    ||||
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                                TGTCGGT TCGTC    GTGG
                                   _    TT___
GAM1034  LOC91355  5'  GAGTGTTGCTGTGGCTGC    65714      TG    TG
                                GCAGC  CAGCAG  TTC
                                |||||  ||||||  |||
                                CGTCG  GTCGTT  GAG
                                   GT     GT
GAM1034  LOC91355  5'  GGTGGGACTTGTGGTTG    65717     TG  CAGT
                                CAGC  CAG   GTTCTACC
                                ||||  |||   ||||||||
                                GTTG  GTT   CAGGGTGG
                                  GT  ____
GAM1034  LOC91421  3'  TGGTGGAATATTGGTGTTTGTG 65994     GCT  G
            CA                    TGCA   GCA CAGTGTTCTACCG
                                ||||   ||| ||||||||||||
                                ACGT   TGT GTTATAAGGTGGT
                                  GTT   G
GAM1034  LOC91442  5'  CGGTGGGGTTCCTGCCGGCTGT 66049       CA   T_ TT
            A                    TGCAGCTG  GCAG  G  CTACCG
                                ||||||||  ||||  |  ||||||
                                ATGTCGGC  CGTC  T  GGTGGC
                                    __    CT GG
GAM1034  LOC91585  5'  CGCTGCTCCTGCAGTTGC    66574        ___
                                GCAGCTGCA   GCAGTG
                                |||||||||   ||||||
                                CGTTGACGT   CGTCGC
                                     CCT
GAM1034  LOC91923  5'  TGGTTGTTTGTTGTTGTTGCA  67556      T     TGTTCT
                                TGCAGC GCAGCAG     ACCG
                                ||||||| |||||||     ||||
                                ACGTTG TGTTGTT     TGGT
                                   T      TGT___
GAM1034  LOC92293  3'  CATTGGCTGCGGCTGCA     68762          _
                                TGCAGCTGCAGC AGTG
                                |||||||||||| ||||
                                ACGTCGGCGTCG TTAC
                                       G
GAM1034  LOC92305  3'  AGAAGAGGGCACTGCTGTGGTG 56409     G TG         ACCG
            T                    GCA C  CAGCAGTGTTCT
                                ||| |  ||||||||||||
                                TGT G  GTCGTCACGGGA
                                  _ GT          GAAGAG
GAM1034  LOC92345  5'  AGTGTTGCTGCGGTTGC     56420           TG
                                GCAGCTGCAGCAG  TT
                                ||||||||||||  ||
                                CGTTGGCGTCGTT  GA
                                       GT
GAM1034  LOC92360  5'  CAAATGAGCATTGCTGCAGTGT 69069     G          TACCG
                                GCA CTGCAGCAGTGTTC
                                ||| ||||||||||||||
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                                TGT GACGTCGTTACGAG
                                  _           TAAACG
GAM1034  LOC92405  3'  GTGGAGCATGTCTGTA      69193       CA
                                TGCAG  GTGTTCTAC
                                |||||  |||||||||
                                ATGTC  TACGAGGTG
                                   TG
GAM1034  LOC92578  5'  TGGTGGGTTTTGTTGCAGTTTA 69834    C         TGT
                                G AGCTGCAGCAG   TCTACCG
                                | ||||||||||   |||||||
                                A TTGACGTTGTT   GGGTGGT
                                 T         TT_
GAM1034  LOC93081  3'  AGCACTGTTACAGTTGTA    57076         C
                                TGCAGCTG AGCAGTGTT
                                |||||||| |||||||||
                                ATGTTGAC TTGTCACGA
                                     A
GAM1035  AIM1      3'  ATATCAAGATTTCAAGACTGTG 91815         _  TT
                                CACAGTCT GG  TCTTGATAT
                                |||||||| ||  |||||||||
                                GTGTCAGA CT  AGAACTATA
                                     A  TT
GAM1035  BAAT      3'  CAAGCTAACCAAACTGGA    8113     A    C    T_
                                TC CAGT TGGTT  CTTG
                                || |||| |||||  ||||
                                AG GTCA ACCAA  GAAC
                                 _   A     TC
GAM1035  LIPA      3'  ATCAAACCTAACTGTGA     4078         CT    TCT
                                TCACAGT  GGTT   TGAT
                                |||||||  ||||   ||||
                                AGTGTCA  CCAA   ACTA
                                     AT   ____
GAM1035  NCALD     3'  AAACCAGCCTGTGATG      49367         T
                                CATCACAG CTGGTTT
                                |||||||| |||||||
                                GTAGTGTC GACCAAA
                                     C
GAM1035  SOS2      5'  TATCAGCAAACCAGGAC     68537     _     C
                                GTC TGGTTT TTGATA
                                ||| |||||| ||||||
                                CAG ACCAAA GACTAT
                                  G     C
GAM1035  EVI5      3'  ATCAAGAAATCTGAATG     18990    G  T
                                CA TC GGTTTCTTGAT
                                || || ||||||||||
                                GT AG CTAAAGAACTA
                                 A  T
GAM1035  FLJ23375  5'  ATATCAAAGGAAATCATGATG  46355       CAGTC       __
                                CATCA    TGGTTTCT  TGATAT
                                |||||    ||||||||  ||||||
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                                GTAGT    ACTAAAGG  ACTATA
                                  _____      AA
GAM1035  KIAA1958  3'  AGAAACCAAACATGAT     81899     CA  C
                                ATCA  GT TGGTTTCT
                                ||||  || ||||||||
                                TAGT  CA ACCAAAGA
                                  A_  A
GAM1035  MAPK6    5'  ATCAAGAAACCATCTTGCTGTG 10833      C___
                                CACAGT   TGGTTTCTTGAT
                                ||||||   ||||||||||||
                                GTGTCG   ACCAAAGAACTA
                                   TTCT
GAM1035  MGC13102  3'  CATCAAATGGGACTGTGGTG  50314         G   CT
                                CATCACAGTCT GTTT  TG
                                |||||||||| ||||  ||
                                GTGGTGTCAGG TAAA  AC
                                       G   CT
GAM1035  SCMH1    5'  TATCAAGAAGCTGCTG     24257     CT
                                CAGT  GGTTTCTTGATA
                                ||||  ||||||||||||
                                GTCG  TCGAAGAACTAT
                                  __
GAM1035  SLC6A14   3'  ATATCAAGGAAAACTGTGA   23346       CTGG
                                TCACAGT   TTTCTTGATAT
                                |||||||   ||||||||||
                                AGTGTCA   AAGGAACTATA
                                   A___
GAM1035  LOC151126 3'  TATCAACAAGACTGGAATG   80130    CA    G  TTCT
                                CAT  CAGTCT GT   TGATA
                                |||  |||||| ||   |||||
                                GTA  GTCAGA CA   ACTAT
                                  AG     A  ____
GAM1035  LOC155081 3'  ATATCAGTGCCACAGATTGT  81289       GTTTC
                                ACAGTCTG    TTGATAT
                                ||||||||    |||||||
                                TGTTAGAC    GACTATA
                                     ACCGT
GAM1035  LOC202802 3'  ATATCAGTGCCACAGATTGT  89203       GTTTC
                                ACAGTCTG    TTGATAT
                                ||||||||    |||||||
                                TGTTAGAC    GACTATA
                                     ACCGT
GAM1035  LOC219401 5'  ATCAAGAAACACATAT     92812    C  _
                                GT TG GTTTCTTGAT
                                || || ||||||||||
                                TA AC CAAAGAACTA
                                 T  A
GAM1035  LOC221399 5'  ATCAAGAAGGTTAACTGTG   93845       CTGG
                                CACAGT   TTTCTTGAT
                                ||||||   |||||||||
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                                GTGTCA   GAAGAACTA
                                   ATTG
GAM1035 LOC222228 3' ATATCAGTGCCACAGATTGT  94293       GTTTC
                                ACAGTCTG    TTGATAT
                                ||||||||    |||||||
                                TGTTAGAC    GACTATA
                                    ACCGT
GAM1035 LOC222233 3' ATATCAGTGCCACAGATTGT  94250       GTTTC
                                ACAGTCTG    TTGATAT
                                ||||||||    |||||||
                                TGTTAGAC    GACTATA
                                    ACCGT
GAM1035 LOC90643  3' ATCAAGACCCTGACTGGA    63688    A    T  TT
                                TC CAGTC GG  TCTTGAT
                                || ||||| ||  |||||||
                                AG GTCAG CC  AGAACTA
                                 _    T  C_
GAM1035 LOC91138  5' CAAGTAACTAGACTATGAT   65029     C       T
                                ATCA AGTCTGGTT CTTG
                                |||| ||||||||| ||||
                                TAGT TCAGATCAA GAAC
                                  A       T
GAM1035 LOC91818  5' ATCAAGACCCTGACTGGA    67269    A    T  TT
                                TC CAGTC GG  TCTTGAT
                                || ||||| ||  |||||||
                                AG GTCAG CC  AGAACTA
                                 _    T  C_
GAM1035 LOC93052  5' GAACCAAACTGTGATG      71261        C
                                CATCACAGT TGGTTT
                                ||||||||| ||||||
                                GTAGTGTCA ACCAAG
                                     A
GAM1036 AVPR1A    5' CAGGAAGCAGGACTCCAGA   5536       TCC    CA
                                TCTGGA   GTCTT  CTTCCTG
                                ||||||   |||||  |||||||
                                AGACCT   CAGGA  GAAGGAC
                                   ____    C_
GAM1036 SFTPA2    3' GGCAAAGACTGGATCCA     22649       _    CA
                                TGGATCC GTCTT  CT
                                ||||||| |||||  ||
                                ACCTAGG CAGAA  GG
                                    T    AC
GAM1036 SLC25A15  3' ACAGGAAGTAAACTGCTTCAGA 26506      TCC  CTTC
                                TCTGGA   GT   ACTTCCTGT
                                ||||||   ||   |||||||||
                                AGACTT   CA   TGAAGGACA
                                   CGT  AA__
GAM1036 CABYR     3' TGAAAACTGATCCAGA      24112        C  C
                                TCTGGATC GT TTCA
                                |||||||| || ||||
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                                AGACCTAG CA AAGT
                                     T  A
GAM1036  DKFZP566D193 3'  ACAAGAAATGAAGTGGACAGA  85566     GA   T    C  C
                                TCTG  TCCG CTTCA TTC TGT
                                |||| |||| ||||| ||| |||
                                AGAC  AGGT GAAGT AAG ACA
                                  __   _    A  A
GAM1036  FLJ11726  3'  ACAGGAAGTAAAAAGGCCCA  46405    ATCC    C__
                                TGG   GTCTT  ACTTCCTGT
                                |||   |||||  |||||||||
                                ACC   CGGAA  TGAAGGACA
                                  _____   AAA
GAM1036  KIAA0367  3'  ACAGGAAGTAATGAAAAATCCA 67290      CCG  TTC
              G                  CTGGAT   TC   ACTTCCTGT
                                ||||||  ||  |||||||||
                                GACCTA   AG   TGAAGGACA
                                   AAA  TAA
GAM1036  ROBO4    3'  ACAGGAAGTGGAGGAGCCAGA  38788     ATCCG
                                TCTGG    TCTTCACTTCCTGT
                                |||||    ||||||||||||||
                                AGACC    GGAGGTGAAGGACA
                                  GA___
GAM1036  LOC139673 5'  ACAGGAAGTGAGTCATCGCAGA 75975     _  CCGTC
                                TCTG GAT    TTCACTTCCTGT
                                |||| |||    ||||||||||||
                                AGAC CTA    GAGTGAAGGACA
                                  G  CT___
GAM1036  LOC152024 5'  CAGAGAAGACGGATCCA    80434          ACTTC
                                TGGATCCGTCTTC    CTG
                                ||||||||||||    |||
                                ACCTAGGCAGAAG    GAC
                                       A____
GAM1036  LOC159036 3'  CAGAAAGTTGGATTCAGA    86970         TCTTC   C
                                TCTGGATCCG    ACTT CTG
                                ||||||||||    |||| |||
                                AGACTTAGGT    TGAA GAC
                                     _____   A
GAM1036  LOC222112 5'  ACAGGAAGCACTTTGGTCCAGA 92802      T  TCTTCA
                                TCTGGA CCG    CTTCCTGT
                                |||||| |||    ||||||||
                                AGACCT GGT    GAAGGACA
                                   _  TTCAC_
GAM1037  HPGD    3'  ACATACAAGTTCATACTTT   5977       GCTTT
                                AAAGTG    CTTGTATGT
                                ||||||    |||||||||
                                TTTCAT    GAACATACA
                                   ACTT_
GAM1037  MBD1    3'  ACATTACAAAGCCAC      9945        TCT   _
                                GTGGCTT   TGTA TGT
                                |||||||   |||| |||
```

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                                CACCGAA   ACAT ACA
                                   ___    T
GAM1037  MBD1     3'  ACATTACAAAGCCAC       31771        TCT   _
                                GTGGCTT   TGTA TGT
                                |||||||   |||| |||
                                CACCGAA   ACAT ACA
                                   ___    T
GAM1037  MBD1     3'  ACATTACAAAGCCAC       31779        TCT   _
                                GTGGCTT   TGTA TGT
                                |||||||   |||| |||
                                CACCGAA   ACAT ACA
                                   ___    T
GAM1037  MBD1     3'  ACATTACAAAGCCAC       31786        TCT   _
                                GTGGCTT   TGTA TGT
                                |||||||   |||| |||
                                CACCGAA   ACAT ACA
                                   ___    T
GAM1037  OTX1     5'  AAGACAAGCCACTCCGA     27302     AA      _
                                TC  AGTGGCTT TCTT
                                ||  |||||||| ||||
                                AG  TCACCGAA AGAA
                                 CC       C
GAM1037  C1QTNF7  3'  ACATACAAGGTTTCCACTT    49155       CTT
                                AAGTGG   TCTTGTATGT
                                ||||||   ||||||||||
                                TTCACC   GGAACATACA
                                   TTT
GAM1037  HMG17L1  3'  ACACACATAGCCACTTT      40707         TTCT   A
                                AAAGTGGCT    TGT TGT
                                |||||||||    ||| |||
                                TTTCACCGA    ACA ACA
                                      T___   C
GAM1037  KIAA1393 3'  ACAAGGCAAAACAACTTTGATA 72094          _ GC  _
                                TATCAAAGT G  TT TCTTGT
                                ||||||||| |  || ||||||
                                ATAGTTTCA C  AA GGAACA
                                      A AA  C
GAM1037  KIAA1610 3'  ACAGTGTTAAAAGCCACTTTG  67156           CTTGTA
                                CAAAGTGGCTTT      TGT
                                ||||||||||||      |||
                                GTTTCACCGAAA      ACA
                                      ATTGTG
GAM1037  MRPS10   3'  ATGAGCAAACCACTTTGA     36290         C  _  TG
                                TCAAAGTGG TTT CT  T
                                ||||||||| ||| ||  |
                                AGTTTCACC AAA GA  A
                                      _  C  GT
GAM1037  PAK6     3'  AGGAAAGCCACCTTGA       39404      A
                                TCAA GTGGCTTTCTT
                                |||| ||||||||||
```

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                                AGTT CACCGAAAGGA
                                  C
GAM1037  PHCA     3'  ACAGAAAGCACACCTTGATA   37173       A  _     T
                                TATCAA GTG GCTTTCT GT
                                |||||| ||| ||||||| ||
                                ATAGTT CAC CGAAAGA CA
                                   C   A      _
GAM1037  RNF24    3'  ACAACCAAAGCACTTTGA    23312        G   C_
                                TCAAAGTG CTTT  TTGT
                                |||||||| ||||  ||||
                                AGTTTCAC GAAA  AACA
                                     _   CC
GAM1037  SDR1     3'  ACAGCCAGAAGCCACCTTGA   16461      A       CT  TA
                                TCAA GTGGCTTT  TG  TGT
                                |||| ||||||||  ||  |||
                                AGTT CACCGAAG  AC  ACA
                                  C       __  CG
GAM1037  ST7L     3'  ACACACAAGAAACCATCTCTGA 57005      A  _  C       A
                T                ATCA AG TGG TTTCTTGT TGT
                                |||| || ||| |||||||| |||
                                TAGT TC ACC AAAGAACA ACA
                                  C  T  _       C
GAM1037  ST7L     3'  ACACACAAGAAACCATCTCTGA 57567      A  _  C       A
                T                ATCA AG TGG TTTCTTGT TGT
                                |||| || ||| |||||||| |||
                                TAGT TC ACC AAAGAACA ACA
                                  C  T  _       C
GAM1037  LOC127262 3'  TGAGAAAGTCACCTTGA     76113      A
                                TCAA GTGGCTTTCTTG
                                |||| ||||||||||||
                                AGTT CACTGAAAGAGT
                                  C
GAM1037  LOC146728 5'  CATGTGAAGCCACTCTG     83747     A      TTC TG
                                CA AGTGGCT   T  TATG
                                || |||||||   |  ||||
                                GT TCACCGA   A  GTAC
                                 C       ___ GT
GAM1037  LOC158293 3'  ACAAGAAACCACCCTGATA    81862       AA    C
                                TATCA  GTGG TTTCTTGT
                                |||||  |||| ||||||||
                                ATAGT  CACC AAAGAACA
                                   CC   _
GAM1038  A1BG     3'  GCTGGGACTACAGGCAT     55424        AC     TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TCAGG  CG
                                    A_    GT
GAM1038  A1BG     3'  GTTGGGATTACAGGTGTGA   55429      GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG  TGGAC  TTAGG  TG
                                  __    A_    GT
GAM1038  ABCA1    3'  GCTGGGGCTGCAAGCTGCTGA  18547    T  _  C  A    TG
                                TCA GT GC TG CAGTCT  GC
                                ||| || || || ||||||  ||
                                AGT CG CG AC GTCGGG  CG
                                  _  T  A  _    GT
GAM1038  ABCA2    5'  GCTGAGGCGGCGGAGCGTGG  7835      GC   ACA   TG
                                TCATGT  CTG   GTCT  GC
                                ||||||  |||   ||||  ||
                                GGTGCG  GGC   CGGA  CG
                                   A_   GG_   GT
GAM1038  ABCB11   3'  GTTAGGGCTGTTGATTTATG  13617    TGCCT
                                CATG    GACAGTCTTGGC
                                ||||    ||||||||||||
                                GTAT    TTGTCGGGATTG
                                  TTAG_
GAM1038  ABCB4    5'  GCCAGACAGCTGGTACATGG  4793       TGACA   T
                                TCATGTGCC    GTCT GGC
                                |||||||||    |||| |||
                                GGTACATGG    CAGA CCG
                                     TCGA_   _
GAM1038  ABCB4    5'  GCCAGACAGCTGGTACATGG  38142      TGACA   T
                                TCATGTGCC    GTCT GGC
                                |||||||||    |||| |||
                                GGTACATGG    CAGA CCG
                                     TCGA_   _
GAM1038  ABCB6    5'  GCTGAGACGGCGTACGTG    19097      _ GACA   TG
                                CATGTGC CT   GTCT  GC
                                |||||||  ||   ||||  ||
                                GTGCATG GG   CAGA  CG
                                   C  ____   GT
GAM1038  ABL1     5'  GCCAGGGGCCCCTGGGTGCGGA 17677    A  TG   ACA   _
                                TC TG  CCTG   GTCT TGGC
                                || ||  ||||   |||| ||||
                                AG GC  GGGT   CGGG ACCG
                                 _  GT   CCC   G
GAM1038  ACADS    3'  GTCCTGGTGTTGGGCAGGTGG  3410     G   TG   G  TT
                                TCAT TGCC  ACA TC  GGC
                                |||| ||||  ||| ||  |||
                                GGTG ACGG  TGT GG  CTG
                                  G   GT   _  TC
GAM1038  ACADSB   3'  GCGCTGTTTAACTTAGGCACAG 7845   A     ______    CTTGGC
           GA                     TGTGCCT     GACAGT
                                  |||||||     ||||||
                                  ACACGGA     TTGTCG
                                  G      TTCAAT       CGG
GAM1038  ACN      3'  GCCAGGACTGGGTCACCTATGA 30368     __   _  TGA
                                TCAT  GTG CC   CAGTCTTGGC
                                ||||  ||| ||   ||||||||||
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                                AGTA  CAC GG   GTCAGGACCG
                                  TC   T ___
GAM1038  ACOX3    5'  GTTGAACTGTGGAGTGTGTGG  13025      TG _  G    C TG
                                TCATG  C CT ACAGT T  GC
                                |||||  | || ||||| |  ||
                                GGTGT  G GG TGTCA A  TG
                                   GT A  _    _ GT
GAM1038  ADAM11   3'  GCTGTCCCTGTCAGGACACATG 9968         _       TCT
           G                     TCATGTG CCTGACAG   TGGC
                                |||||||  ||||||||   ||||
                                GGTACAC GGACTGTC   GTCG
                                    A       CCT
GAM1038  ADAM11   3'  GCTGGGGCTGTCCTGGTTG   41215   T   T_      TG
                                G GCC  GACAGTCT  GC
                                | |||  ||||||||  ||
                                G TGG  CTGTCGGG  CG
                                 T   TC       GT
GAM1038  ADAM11   3'  GCTGTCCCTGTCAGGACACATG 41216        _       TCT
           G                     TCATGTG CCTGACAG   TGGC
                                |||||||  ||||||||   ||||
                                GGTACAC GGACTGTC   GTCG
                                    A       CCT
GAM1038  ADAM20   3'  GTCAGGATTGCAAGCATTA   13769   T   C  A
                                A GTGC TG CAGTCTTGGC
                                | |||| || ||||||||||
                                A TACG AC GTTAGGACTG
                                 T   A  _
GAM1038  ADAMTS4  3'  GCTAGGAAATCCAGGGTGGTGG 17509     GTG    ACAG
                                TCAT   CCTG    TCTTGGC
                                ||||   ||||    |||||||
                                GGTG   GGAC    AGGATCG
                                  GTG    CTAA
GAM1038  ADAMTS4  3'  GCTGGGATTACAGGCGTGA   17513     GT     AC     TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  ADAMTS4  3'  GCTGGGATTACAGGTGTGA   17514     GT     AC     TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  ADCY6    5'  GCTGGGATTACGGACGTGA   30933      G  TGAC    TG
                                TCATGT CC    AGTCT  GC
                                ||||||  ||   |||||  ||
                                AGTGCA GG    TTAGG  CG
                                   _ CA__    GT
GAM1038  ADCY6    3'  GCTGGGGTAGCATGG      30934      _    GA
                                TCATG TGCCT  CAGT
                                ||||| |||||  ||||
```

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                                GGTAC ATGGG  GTCG
                                  G    __
GAM1038  ADCY6    3'  GCTGGGGTAGCATGG      40619      _    GA
                                TCATG TGCCT  CAGT
                                ||||| |||||  ||||
                                GGTAC ATGGG  GTCG
                                  G    __
GAM1038  ADCY9    3'  GTCATCCGTTCAGCACGTGG  6659        C   CAGTCT
                                TCATGTGC TGA     TGGC
                                |||||||| |||     ||||
                                GGTGCACG ACT     ACTG
                                     _  TGCCT_
GAM1038  ADD2     5'  GCTAAGATGCCGCGCAGGA   33931    A    CTGACA
                                TC TGTGC     GTCTTGGC
                                || |||||     ||||||||
                                AG ACGCG     TAGAATCG
                                 G    CCG___
GAM1038  ADD2     5'  GCTAAGATGCCGCGCAGGA   33934    A    CTGACA
                                TC TGTGC     GTCTTGGC
                                || |||||     ||||||||
                                AG ACGCG     TAGAATCG
                                 G    CCG___
GAM1038  ADD2     5'  GCTAAGATGCCGCGCAGGA   33942    A    CTGACA
                                TC TGTGC     GTCTTGGC
                                || |||||     ||||||||
                                AG ACGCG     TAGAATCG
                                 G    CCG___
GAM1038  ADD2     5'  GCTAAGATGCCGCGCAGGA   33945    A    CTGACA
                                TC TGTGC     GTCTTGGC
                                || |||||     ||||||||
                                AG ACGCG     TAGAATCG
                                 G    CCG___
GAM1038  ADD2     5'  GCTAAGATGCCGCGCAGGA   33951    A    CTGACA
                                TC TGTGC     GTCTTGGC
                                || |||||     ||||||||
                                AG ACGCG     TAGAATCG
                                 G    CCG___
GAM1038  ADD2     5'  GCTAAGATGCCGCGCAGGA   33959    A    CTGACA
                                TC TGTGC     GTCTTGGC
                                || |||||     ||||||||
                                AG ACGCG     TAGAATCG
                                 G    CCG___
GAM1038  ADD2     5'  GCTAAGATGCCGCGCAGGA   33962    A    CTGACA
                                TC TGTGC     GTCTTGGC
                                || |||||     ||||||||
                                AG ACGCG     TAGAATCG
                                 G    CCG___
GAM1038  ADK      5'  GCCGGCCGCGCGGGGTGTGTGA 6661       TG   GACA  C_
                                TCATG  CCT   GT  TTGGC
                                |||||  |||   ||  |||||
```

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                                AGTGT  GGG   CG  GGCCG
                                   GT   GCG_  CC
GAM1038  ADK     5'  GCCGGCCGCGCGGGGTGTGTGA 22045      TG   GACA  C_
                                TCATG  CCT   GT  TTGGC
                                |||||  |||   ||  |||||
                                AGTGT  GGG   CG  GGCCG
                                   GT   GCG_  CC
GAM1038  ADORA1   5'  GTCGAGGTGTGGGGGCACTTGG 5428      T    _ G   G
                                TCA GTGCC T ACA TCTTGGC
                                ||| ||||| | ||| |||||||
                                GGT CACGG G TGT GGAGCTG
                                  T    G G  _
GAM1038  ADRA1A   3'  GCTGGGATTACAGGCGTGA   52788     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  ADRA2B   3'  GCTGGGATGGGGGGCTTATGG   5462      T   GACA   TG
                                TCATG GCCT   GTCT  GC
                                ||||| ||||   ||||  ||
                                GGTAT CGGG   TAGG  CG
                                   T   GG__   GT
GAM1038  AGRN     3'  GTCAAGGGGCAGGTGCAGA   78838    A  TG   ACAG
                                TC TG  CCTG   TCTTGGC
                                || ||  ||||   |||||||
                                AG AC  GGAC   GGAACTG
                                 _ GT   GG__
GAM1038  AHR      3'  GCTGGGATTGCGGGCATGGTGG 7881      _     A     TG
                                TCAT GTGCCTG CAGTCT  GC
                                |||| ||||||| ||||||  ||
                                GGTG TACGGGC GTTAGG  CG
                                  G     _     GT
GAM1038  AK3      5'  GTCGGGGCTGCGCGTTTGA   25498    TG   CT A
                                TCA  TGC  G CAGTCTTGGC
                                |||  |||  | ||||||||||
                                AGT  GCG  C GTCGGGGCTG
                                  TT  __ _
GAM1038  ALDH1B1  3'  GCTGGGATTATAGGTACATG   5495         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTACATGGAT  TTAGG  CG
                                     A_    GT
GAM1038  ALDH2    3'  GCTGAGGGTAAGAGTATATGA  59713       _ G  AG   TG
                                TCATGTGC CT AC  TCT  GC
                                |||||||| || ||  |||  ||
                                AGTATATG GA TG  GGA  CG
                                    A  A  __   GT
GAM1038  ALDH3B1  3'  GCCGAGGTGGGAGGCATGGGA  91527    AT     GA  G
                                TC  GTGCCT  CA TCTTGGC
                                ||  ||||||  || |||||||
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                                AG  TACGGA  GT GGAGCCG
                                 GG     GG  _
GAM1038  ALDH3B1   3'  GCTGAGATTGCGTCACTGA   91529     T   CC  A     TG
                                TCA GTG  TG CAGTCT  GC
                                ||| |||  || ||||||  ||
                                AGT CAC  GC GTTAGA  CG
                                  _  T_ _     GT
GAM1038  ALDH3B2   3'  GCCAGGGCTGCAAAGCA     5507      C_  A
                                TGC  TG CAGTCTTGGC
                                |||  || ||||||||||
                                ACG  AC GTCGGGACCG
                                  AA  _
GAM1038  ANK1      3'  GCCAAGAAGAGCAGGTGCAGGA 60390    A  TG    ACAG
                                TC TG  CCTG    TCTTGGC
                                || ||  ||||    |||||||
                                AG AC  GGAC    AGAACCG
                                 G  GT    GAGA
GAM1038  ANXA5     5'  CCGGGGTGGGGCGCTGG     6715      T     G  AGT
                                TCA GTGCCT AC   CTTGG
                                ||| ||||||  ||   |||||
                                GGT CGCGGG TG   GGGCC
                                  _     G  ___
GAM1038  APAF1     3'  GCTGAGACTGCAGGCACG    6732         A     TG
                                TGTGCCTG CAGTCT  GC
                                |||||||| ||||||  ||
                                GCACGGAC GTCAGA  CG
                                     _     GT
GAM1038  APAF1     3'  GCTGAGATTACAGGCGTGA   6733      GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGA  CG
                                  __     A_    GT
GAM1038  APAF1     3'  GTTGGGATTGCAGATATGA   6735       GC   A     TG
                                TCATGT  CTG CAGTCT  GC
                                ||||||  ||| ||||||  ||
                                AGTATA  GAC GTTAGG  TG
                                   __  _     GT
GAM1038  APAF1     3'  GCTGAGACTGCAGGCACG    25041        A     TG
                                TGTGCCTG CAGTCT  GC
                                |||||||| ||||||  ||
                                GCACGGAC GTCAGA  CG
                                     _     GT
GAM1038  APAF1     3'  GCTGAGATTACAGGCGTGA   25042     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGA  CG
                                  __     A_    GT
GAM1038  APAF1     3'  GTTGGGATTGCAGATATGA   25044       GC   A     TG
                                TCATGT  CTG CAGTCT  GC
                                ||||||  ||| ||||||  ||
```

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                                AGTATA  GAC GTTAGG  TG
                                  __  _     GT
GAM1038  APBA2    5'  GCCAGGACTGTCCTGT     18559    CT
                                GC  GACAGTCTTGGC
                                ||  ||||||||||||
                                TG  CTGTCAGGACCG
                                 TC
GAM1038  APM1     3'  GCTGGGATTACAGGCAT     16596       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  APM1     3'  GCTGGGATTACAGGCAT     16597       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  APOL1    3'  GCTGGGATTACAGGCGTGA   13350     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  APPL     3'  GCTGGGATTACAGGCGTGA   23928     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  APXL     5'  GCCGGGACTGCCCGGAGTGCAT 7929       TG _  A_
            GG                    TCATG  C CTG  CAGTCTTGGC
                                |||||  | |||  ||||||||||
                                GGTAC  G GGC  GTCAGGGCCG
                                  GT A   CC
GAM1038  AQP5     5'  CCAACCTGGGCGCAT      7934        TGA   TC
                                ATGTGCC   CAG  TTGG
                                |||||||   |||  ||||
                                TACGCGG   GTC  AACC
                                   ____   C_
GAM1038  AQP6     5'  GCTGGAGCAGGTATATGA    7956          A__
                                TCATGTGCCTG   CAGT
                                ||||||||||   ||||
                                AGTATATGGAC   GTCG
                                     GAG
GAM1038  AQP6     3'  GCTGGGATTACAGGCGTGA   7957     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  AQP6     5'  GCTGGAGCAGGCATATGA    53933         A__
                                TCATGTGCCTG   CAGT
                                ||||||||||   ||||
```

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                                AGTATACGGAC  GTCG
                                      GAG
GAM1038 AQP6    3' GCTGGGATTACAGGCGTGA  53934    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG CG
                                  __   A_   GT
GAM1038 AQP6    5' GCTGGGTTCGGGCACGTG   53935       CAGT TG
                                CATGTGCCTGA  CT GC
                                ||||||||||  || ||
                                GTGCACGGGCT  GG CG
                                      T___ GT
GAM1038 ARCN1   3' GTTGGGATTACAGGCAT    7983       AC   TG
                                GTGCCTG AGTCT GC
                                ||||||| ||||| ||
                                TACGGAC TTAGG TG
                                    A_   GT
GAM1038 ARHGAP6 5' GCCGAGATGTCCGCGCAGA  6764    A   CT   G
                                TC TGTGC GACA TCTTGGC
                                || ||||| |||| |||||||
                                AG ACGCG CTGT AGAGCCG
                                 _   C_  _
GAM1038 ARNT2   3' GCCAGGGTCTGTGGGGCACTGA 29462    T    G  _
                                TCA GTGCCT ACAG TCTTGGC
                                ||| |||||| |||| |||||||
                                AGT CACGGG TGTC GGGACCG
                                 _    G  T
GAM1038 ARNT2   3' GTTGAGGCTTTTCTTAGGTGCA 29464    TG   C___   TG
            T                    ATG CCTGA  AGTCT GC
                                ||| |||||  ||||| ||
                                TAC GGATT  TCGGA TG
                                 GT   CTTT   GT
GAM1038 ARSA    3' GCTGGCCTGGGCATGTGA   4913        GA__
                                TCATGTGCCT  CAGT
                                ||||||||||  ||||
                                AGTGTACGGG  GTCG
                                      TCCG
GAM1038 ARSD    3' GCTGAGGCTGCAATGACTGA  23795    T GCC A    TG
                                TCA GT  TG CAGTCT GC
                                ||| ||  || ||||||  ||
                                AGT CA  AC GTCGGA CG
                                 _ GTA _    GT
GAM1038 ARSF    5' GCTGGGATTACAGGCGTGA  64600    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG CG
                                  __   A_   GT
GAM1038 ASB2    5' GCTGGCAGGTGGGCGTGG   32357      __   A
                                TCATGT GCCTG CAGT
                                |||||| ||||| ||||
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                                GGTGCG  TGGAC GTCG
                                   GG    G
GAM1038 ASIC4    5' GCTGGGGCTGCGCGGCGTGG  37921     GT  _ A    TG
                                TCAT  GCC TG CAGTCT  GC
                                ||||  ||| || ||||||  ||
                                GGTG  CGG GC GTCGGG  CG
                                  __  C  _    GT
GAM1038 ATM      3' GCTGGGATTACAGGCAT    56308       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038 ATP1B2   3' GCTGGGACTACAGGCATGTG  8052         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTACGGAC  TCAGG  CG
                                     A_    GT
GAM1038 ATP1B2   3' GTTGGGATTACAGGCGTGA   8055      GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  TG
                                  __    A_    GT
GAM1038 ATP2B4   5' GCTAAGGTTGCTGCCATGG   70343      T  CTGA  GT
                                TCATG GC    CA  CTTGGC
                                |||||  ||    ||  ||||||
                                GGTAC CG    GT  GAATCG
                                  _  TC__  TG
GAM1038 ATP5B    5' GCTGAGGCTCCAGAGTTCATGG 59662      T  _  AC    TG
                                TCATG GC CTG  AGTCT  GC
                                |||||  ||  |||  |||||  ||
                                GGTAC TG GAC  TCGGA  CG
                                   T  A  C_    GT
GAM1038 ATP6V1A1 3' GCTGGGATTACAGGCGTGA   8080      GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 ATP7A    3' GCTGGGATTACAGGTGTGA   3526      GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 ATP8B2   5' CCAGTCTCAGGTGCTGA     65217     T TG    CA T  T
                                TCA G  CCTGA  G CT GG
                                |||  |  |||||  | || ||
                                AGT C  GGACT  C GA CC
                                  _ GT    __ T  _
GAM1038 ATP8B2   3' GCTGAGATTACAGGCGTGA   65230     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
```

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                                AGTG  CGGAC  TTAGA  CG
                                  __    A_    GT
GAM1038 ATSV    3' GCTAGCACACGGGTGTAT    15056    TG   ACA  C
                                ATG  CCTG   GT TTGGC
                                |||  ||||   || |||||
                                TAT  GGGC   CA GATCG
                                  GT   A__  C
GAM1038 AVPR1A  5' GCCAGGTTCAGGTGCAGGA   5539    A  TG   CAGT
                                TC TG  CCTGA   CTTGGC
                                || ||  |||||   ||||||
                                AG AC  GGACT   GGACCG
                                 G  GT   T___
GAM1038 AXIN1   3' GCCAAGATGCCAGTGGCACTGG 60856    T    TGACA_
                                TCA GTGCC    GTCTTGGC
                                |||  |||||    ||||||||
                                GGT CACGG    TAGAACCG
                                  _    TGACCG
GAM1038 AXL     3' GCTGGGATTACAGGTGTGTG  41599    TG   AC   TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGT  GGAC  TTAGG  CG
                                  GT   A_    GT
GAM1038 AXL     3' GCTGAGATTACAGGCAT    8101       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGA  CG
                                   A_    GT
GAM1038 AXL     3' GCTGGGATTACAGGTGTGTG  8102     TG   AC   TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGT  GGAC  TTAGG  CG
                                  GT   A_    GT
GAM1038 AXL     3' GCTGAGATTACAGGCAT    41598      AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGA  CG
                                   A_    GT
GAM1038 B4GALT5  5' GCCGAGGCCCAGGCGGTGG   16503     G    ACA
                                TCAT TGCCTG   GTCTTGGC
                                ||||  ||||||   ||||||||
                                GGTG GCGGAC   CGGAGCCG
                                  _     C__
GAM1038 B4GALT5  3' GCTGGGATTATGGGCGGGTG  16507    G    GAC    TG
                                CAT TGCCT   AGTCT  GC
                                |||  |||||   |||||  ||
                                GTG GCGGG   TTAGG  CG
                                  G    TA_    GT
GAM1038 B4GALT7  3' GCTGGGCCAGGACACGTGG   23414       _   ACA T  TG
                                TCATGTG CCTG   G CT  GC
                                |||||||  ||||   | ||  ||
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                                GGTGCAC GGAC   C GG  CG
                                   A    ___ _  GT
GAM1038  BACE2    3'  GCCAAGACCCAACAGGTGCTGA 23981     T TG    ACA_
                                TCA G  CCTG    GTCTTGGC
                                ||| |  ||||    ||||||||
                                AGT C  GGAC    CAGAACCG
                                  _ GT    AACC
GAM1038  BACE2    3'  GCCAAGACCCAACAGGTGCTGA 57295     T TG    ACA_
                                TCA G  CCTG    GTCTTGGC
                                ||| |  ||||    ||||||||
                                AGT C  GGAC    CAGAACCG
                                  _ GT    AACC
GAM1038  BACE2    3'  GCCAAGACCCAACAGGTGCTGA 57297     T TG    ACA_
                                TCA G  CCTG    GTCTTGGC
                                ||| |  ||||    ||||||||
                                AGT C  GGAC    CAGAACCG
                                  _ GT    AACC
GAM1038  BAK1     3'  GCCAGGACGTCTGGGGTGTGG  91992     TG G  T   A
                                TCA  T CC GAC GTCTTGGC
                                |||  | || ||| ||||||||
                                GGT  G GG CTG CAGGACCG
                                  GT G  T   _
GAM1038  BARX1    5'  GCCAAACCGCGGGCGCACGA   41203    A       ACA  C
                                TC TGTGCCTG   GT TTGGC
                                || ||||||||   || |||||
                                AG ACGCGGGC   CA AACCG
                                 C       GC_ _
GAM1038  BAZ2B    5'  GCTGGGATTACAGGCAT     25621        AC     TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  BBS4     3'  GCTGAGTCAGCAAGGTACATGA 52281          GACAGT  TG
                                TCATGTGCCT     CT  GC
                                ||||||||||     ||  ||
                                AGTACATGGA     GA  CG
                                     ACGACT  GT
GAM1038  BCL10    3'  GCTGAGACTACAAGTGTGTG   14060     TG C  AC    TG
                                CATG  C TG  AGTCT  GC
                                ||||  | ||  |||||  ||
                                GTGT  G AC  TCAGA  CG
                                  GT A  A_    GT
GAM1038  BCL11A   3'  GCCAAATAATTGGCATGTGA   35867         TGACAGTC
                                TCATGTGCC       TTGGC
                                |||||||||       |||||
                                AGTGTACGG       AACCG
                                     TTAATA__
GAM1038  BCL11A   3'  GCCAAATAATTGGCATGTGA   56724         TGACAGTC
                                TCATGTGCC       TTGGC
                                |||||||||       |||||
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                                AGTGTACGG       AACCG
                                     TTAATA__
GAM1038  BCL2L2   3'  GCCTATAGGTGTGGGCACATGA 14469          G   G   T__
                                TCATGTGCCT ACA TCT   GGC
                                |||||||||| ||| |||   |||
                                AGTACACGGG TGT GGA   CCG
                                     _  _   TAT
GAM1038  BCL7A    5'  CGGGCCAGGCGCGCGG      40640    A      ACA T  TG
                                TC TGTGCCTG   G CT  G
                                || ||||||||   | ||  |
                                GG GCGCGGAC   C GG  C
                                 C       ____ _  GT
GAM1038  BDP1     5'  GCCGGGGCTCGGGGCTGTGA   37364      T    GAC
                                TCATG GCCT   AGTCTTGGC
                                ||||| ||||   |||||||||
                                AGTGT CGGG   TCGGGGCCG
                                   _    GC_
GAM1038  BF       3'  GCTGGACAGGGGCGTGG     8139        G    A_
                                TCATGT CCTG  CAGT
                                |||||| ||||  ||||
                                GGTGCG GGAC  GTCG
                                   G    AG
GAM1038  BIN1     5'  GGCTCCGCTGTCGGGTGCGCGG 15039    A  TG       CTT
                                TC TG  CCTGACAGT   GGC
                                || ||  |||||||||   |||
                                GG GC  GGGCTGTCG   TCG
                                 C  GT       CC_   GT
GAM1038  BIN1     5'  GGCTCCGCTGTCGGGTGCGCGG 57812    A  TG       CTT
                                TC TG  CCTGACAGT   GGC
                                || ||  |||||||||   |||
                                GG GC  GGGCTGTCG   TCG
                                 C  GT       CC_   GT
GAM1038  BRCA1    3'  CCAGCCACAGGTACAGA     23517    A      ACA  CT
                                TC TGTGCCTG   GT  TGG
                                || ||||||||   ||  |||
                                AG ACATGGAC   CG  ACC
                                 _       AC_  __
GAM1038  BRCA1    3'  CCAGCCACAGGTACAGA     23525    A      ACA  CT
                                TC TGTGCCTG   GT  TGG
                                || ||||||||   ||  |||
                                AG ACATGGAC   CG  ACC
                                 _       AC_  __
GAM1038  BRCA1    3'  CCAGCCACAGGTACAGA     23542    A      ACA  CT
                                TC TGTGCCTG   GT  TGG
                                || ||||||||   ||  |||
                                AG ACATGGAC   CG  ACC
                                 _       AC_  __
GAM1038  BRCA1    3'  CCAGCCACAGGTACAGA     23550    A      ACA  CT
                                TC TGTGCCTG   GT  TGG
                                || ||||||||   ||  |||
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                                AG ACATGGAC  CG  ACC
                                 _      AC_  __
GAM1038  BRCA1   3'  CCAGCCACAGGTACAGA    23567   A     ACA  CT
                                TC TGTGCCTG  GT  TGG
                                || ||||||||  ||  |||
                                AG ACATGGAC  CG  ACC
                                 _      AC_  __
GAM1038  BRCA1   3'  CCAGCCACAGGTACAGA    23575   A     ACA  CT
                                TC TGTGCCTG  GT  TGG
                                || ||||||||  ||  |||
                                AG ACATGGAC  CG  ACC
                                 _      AC_  __
GAM1038  BRCA1   3'  CCAGCCACAGGTACAGA    23583   A     ACA  CT
                                TC TGTGCCTG  GT  TGG
                                || ||||||||  ||  |||
                                AG ACATGGAC  CG  ACC
                                 _      AC_  __
GAM1038  BRCA1   3'  CCAGCCACAGGTACAGA    23591   A     ACA  CT
                                TC TGTGCCTG  GT  TGG
                                || ||||||||  ||  |||
                                AG ACATGGAC  CG  ACC
                                 _      AC_  __
GAM1038  BRIP1   3'  GCTGGGATTACAGGTGTGA  49399    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  BTK     5'  GTCAGGACTGAGCACA     3554      CTGA
                                TGTGC   CAGTCTTGGC
                                |||||   ||||||||||
                                ACACG   GTCAGGACTG
                                  A___
GAM1038  C14orf1  3'  CTAAGACAAGAGCATGG    23177     GC  GACA
                                TCATGT  CT   GTCTTGG
                                ||||||  ||   |||||||
                                GGTACG  GA   CAGAATC
                                   A_  A___
GAM1038  C14orf1  3'  GCTGGGACTGCAAGTGTGT  23181    TG C  A    TG
                                ATG  C TG CAGTCT  GC
                                |||  | || ||||||  ||
                                TGT  G AC GTCAGG  CG
                                  GT A  _     GT
GAM1038  C21orf33 3'  TGGTGCCAGGCCGTGG     16198     T   ACA  C TG
                                TCATG GCCTG  GT T  G
                                ||||| |||||  || |  |
                                GGTGC CGGAC  CG G  T
                                  _    ____ T GT
GAM1038  C4orf1   3'  GCTAAATCTTGGTATGTGG  59506       TGAC  TC
                                TCATGTGCC   AG  TTGGC
                                |||||||||   ||  |||||
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                                GGTGTATGG   TC  AATCG
                                     T___  TA
GAM1038 C7     3' GCTGGGATTACAGACATGA   5165      GC  AC   TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTACA  GAC  TTAGG  CG
                                   __   A_   GT
GAM1038 CAMLG   3' GCTGGGATTACAGGCGTGA   8241     GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_   GT
GAM1038 CASP10  3' GTTGAGACTTCTGAACGTGG  52092     GCCT  C   TG
                                TCATGT   GA AGTCT  GC
                                ||||||   || |||||  ||
                                GGTGCA   CT TCAGA  TG
                                   AGT_  _   GT
GAM1038 CASP10  3' GCTGAGACTACAGGTGTGTG  52105    TG   AC   TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGT  GGAC  TCAGA  CG
                                  GT   A_   GT
GAM1038 CASP10  3' GCTGAGGCCTGGGGATGTGA  52106     G   ACA   TG
                                TCATGT CCTG   GTCT  GC
                                |||||| ||||   ||||  ||
                                AGTGTA GGGT   CGGA  CG
                                   G   C__   GT
GAM1038 CASP10  3' GCTGAGACTACAGGTGTGTG  52121    TG   AC   TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGT  GGAC  TCAGA  CG
                                  GT   A_   GT
GAM1038 CASP10  3' GCTGAGGCCTGGGGATGTGA  52122     G   ACA   TG
                                TCATGT CCTG   GTCT  GC
                                |||||| ||||   ||||  ||
                                AGTGTA GGGT   CGGA  CG
                                   G   C__   GT
GAM1038 CASP2   3' GTTGGGATTACAGGCGTGA   52145    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  TG
                                  __    A_   GT
GAM1038 CASP2   3' GTTGGGATTACAGGCGTGA   52159    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  TG
                                  __    A_   GT
GAM1038 CASP2   3' GTTGGGATTACAGGCGTGA   52174    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG CGGAC TTAGG TG
                                  __   A_   GT
GAM1038 CASP2   3' GTTGGGATTACAGGCGTGA  6903    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG TG
                                  __   A_   GT
GAM1038 CASP8   3' GCTGGGATTACAGGCGTGA  6917    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG CG
                                  __   A_   GT
GAM1038 CASP8   3' GCTGGGATTACAGGCGTGA  52923   GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG CG
                                  __   A_   GT
GAM1038 CASP8   3' GCTGGGATTACAGGCGTGA  52934   GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG CG
                                  __   A_   GT
GAM1038 CASP8   3' GCTGGGATTACAGGCGTGA  52948   GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG CG
                                  __   A_   GT
GAM1038 CBFA2T2  3' GCCAGGATTACAGGCAT   17467     AC
                                GTGCCTG AGTCTTGGC
                                ||||||| |||||||||
                                TACGGAC TTAGGACCG
                                   A_
GAM1038 CBFA2T2  3' GCTGGGATTGCAGGCAT   17472     A    TG
                                GTGCCTG CAGTCT GC
                                ||||||| ||||||  ||
                                TACGGAC GTTAGG CG
                                   _    GT
GAM1038 CBFA2T3  3' GTCGGGATATTTGGGTGCAGA 17762   A TG TG CA
                                TC TG CC A GTCTTGGC
                                || ||  ||  | ||||||||
                                AG AC GG T TAGGGCTG
                                 _ GT GT TA
GAM1038 CCKBR   3' GTTGAGGCAGGGCAAATGA  5588    G   GACA   TG
                                TCAT TGCCT   GTCT GC
                                |||| |||||   |||| ||
                                AGTA ACGGG   CGGA TG
                                  A   A___   GT
GAM1038 CCNF    3' GCTGGGATTACAGGCAT    8321      AC   TG
                                GTGCCTG AGTCT GC
                                ||||||| ||||| ||
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                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  CD68    3'  GCCAGGATTAAAAGCCATGA  59798      T  CTGAC
                                TCATG GC    AGTCTTGGC
                                |||||  ||    |||||||||
                                AGTAC CG    TTAGGACCG
                                  _ AAAA_
GAM1038  CDC6    3'  GCTGGGATTATAGGCGTGA   6984      GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAT  TTAGG  CG
                                  __    A_    GT
GAM1038  CDH1    3'  GCTGGGATTGTGGGCAT     15148      G      TG
                                GTGCCT ACAGTCT  GC
                                ||||||  |||||||  ||
                                TACGGG TGTTAGG  CG
                                  _      GT
GAM1038  CDH10   3'  GCCGCTTCTGTTAGGTACATG  22056           TCT
                                CATGTGCCTGACAG   TGGC
                                ||||||||||||||   ||||
                                GTACATGGATTGTC   GCCG
                                       TTC
GAM1038  CDH16   5'  CCAGTCTTGGGCGCTGG     14496     T    TG CA T  T
                                TCA GTGCC  A  G CT GG
                                |||  |||||  |  | || ||
                                GGT CGCGG  T  C GA CC
                                  _    GT __ T  _
GAM1038  CDKN1A  5'  CCGGAGCTGGGCGCGGA     54296    A     TGA   TC
                                TC TGTGCC   CAG  TTGG
                                ||  ||||||   |||  ||||
                                AG GCGCGG   GTC  GGCC
                                 _     ____   GA
GAM1038  CDR2    5'  GTTGGGGCCGTCGGTAGGCGCG 76023        ___   A    TG
                                TGTGCCT   GAC GTCT  GC
                                |||||||   ||| ||||  ||
                                GCGCGGA   CTG CGGG  TG
                                    TGG   C    GT
GAM1038  CDSN    3'  GCCAGTGCCCAGGCATA     7008         ACA  C
                                TGTGCCTG   GT TTGGC
                                ||||||||   || |||||
                                ATACGGAC   CG GACCG
                                    C__  T
GAM1038  CEACAM1 3'  GTCAGGGTTGTCTACCTG    8151     T   CCT    GT
                                CA GTG   GACA  CTTGGC
                                || |||   ||||  ||||||
                                GT CAT   CTGT  GGACTG
                                 C   ____   TG
GAM1038  CENTD2  5'  GCTGTATGTGGGTGGGCATGTG 30871          A_  GTCT
            G                    TCATGTGCCTG  CA    TGGC
                                ||||||||||  ||    ||||
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                                GGTGTACGGGT GT   GTCG
                                      GG GTAT
GAM1038 CENTD2   5' GTCGGGGCTGTGTGGACAGA 30875   A  G TG
                                TC TGT CC ACAGTCTTGGC
                                || ||| ||  ||||||||||
                                AG ACA GG TGTCGGGGCTG
                                 _  _ TG
GAM1038 CERD4    3' GCCAAGACTTCTCTGAATGG 23852    GTGCCT C
                                TCAT    GA AGTCTTGGC
                                ||||    || |||||||||
                                GGTA    CT TCAGAACCG
                                  AGTCT_ _
GAM1038 CETN1    3' GTCAACCTGGAGCACATGA 95260      CTGA TC
                                TCATGTGC  CAG TTGGC
                                ||||||||  ||| |||||
                                AGTACACG  GTC AACTG
                                     AG__ C_
GAM1038 CHRNA4   3' GCCAGGGCTCTGGCAGGTGG 5617     G  TGAC
                                TCAT TGCC  AGTCTTGGC
                                |||| ||||  |||||||||
                                GGTG ACGG  TCGGGACCG
                                  G  TC__
GAM1038 CHRNB4   3' GCCACATCAGTCAGGGCATGG 5631      G    AGTCT
                                TCATGT CCTGAC   TGGC
                                |||||| ||||||   ||||
                                GGTACG GGACTG   ACCG
                                   _    ACTAC
GAM1038 CHRNB4   3' GCTGGGATTACAGGTGTGA 5634     GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG TGGAC TTAGG CG
                                  __   A_   GT
GAM1038 CHST2    5' CCAGCCTTGGGCGCTGG   62693    T   TG CA CT
                                TCA GTGCC A GT TGG
                                ||| ||||| | || |||
                                GGT CGCGG T CG ACC
                                  _   GT C_ __
GAM1038 CHST5    3' GCTGGGGCGCATGG      24028       GA
                                TCATGTGCCT CAGT
                                |||||||||| ||||
                                GGTACGCGGG GTCG
                                       __
GAM1038 CIAS1    5' GCTGGGATTACAGGCGTGA 16902    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG CG
                                  __   A_   GT
GAM1038 CLASP1   3' GCTGGGTGCCAGAGCACGTGA 65304      _ A GT TG
                                TCATGTGC CTG CA CT GC
                                |||||||| ||| || || ||
```

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                                AGTGCACG GAC GT  GG  CG
                                    A   C  __ GT
GAM1038  CLASP2   3'  GCCAAGGCTGTCTTTGTATA  64593      CT_
                                TGTGC   GACAGTCTTGGC
                                |||||   ||||||||||||
                                ATATG   CTGTCGGAACCG
                                   TTT
GAM1038  CLCN6    3'  GCTGGGGCTGTTCCGGGGCATG 41386      G  T_      TG
                                CATGT CC  GACAGTCT  GC
                                ||||| ||  ||||||||  ||
                                GTACG GG  TTGTCGGG  CG
                                   G  CC       GT
GAM1038  CLCN6    3'  GCTGGGGCTGTTCCGGGGCATG 41401      G  T_      TG
                                CATGT CC  GACAGTCT  GC
                                ||||| ||  ||||||||  ||
                                GTACG GG  TTGTCGGG  CG
                                   G  CC       GT
GAM1038  CLCN6    3'  GCTGGGGCTGTTCCGGGGCATG 7079       G  T_      TG
                                CATGT CC  GACAGTCT  GC
                                ||||| ||  ||||||||  ||
                                GTACG GG  TTGTCGGG  CG
                                   G  CC       GT
GAM1038  CLDN14   5'  CCACTCTTGGGCACTGG     57839     T    TG C   CTT
                                TCA GTGCC  A AGT   GG
                                ||| |||||  | |||   ||
                                GGT CACGG  T TCA   CC
                                  _    GT C  ____
GAM1038  CLECSF12 3'  GCTGGGACTACAGGTGCATG   76694     TG    AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTAC  GGAC  TCAGG  CG
                                  GT    A_    GT
GAM1038  CLECSF12 3'  GCTGGGATTACAGATGTGA   76695      GC   AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTGTA  GAC  TTAGG  CG
                                   __   A_    GT
GAM1038  CLECSF12 3'  GCTGGGATTACAGGCGTGA   76696     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  CLN3     5'  GCTGGGACCGGCAATCGGGCGT 3598    TGT     CA____    TG
            TGA                   A   GCCTGA     GTCT  GC
                                |   ||||||     ||||  ||
                                T   CGGGCT     CAGG  CG
                                 TG_     AACGGC    GT
GAM1038  CLN3     5'  GCTGGGACCGGCAATCGGGCGT 72254   TGT     CA____    TG
            TGA                   A   GCCTGA     GTCT  GC
                                |   ||||||     ||||  ||
```

```
                              T  CGGGCT    CAGG  CG
                               TG_    AACGGC   GT
GAM1038 CLOCK   3' GTTGAGGTTGTTAAAACAGA  16911   A  GCC   GT  TG
                              TC TGT  TGACA  CT  GC
                              || |||  |||||  ||  ||
                              AG ACA  ATTGT  GA  TG
                                _  AA_   TG  GT
GAM1038 CLTB    3' GCTGGGCCTGGGCACAGGA   8449    A    TGA  T  TG
                              TC TGTGCC  CAG CT  GC
                              || ||||||  ||| ||  ||
                              AG ACACGG  GTC GG  CG
                               G    ___  C  GT
GAM1038 CLTB    3' GCTGGGCCTGGGCACAGGA   23017   A    TGA  T  TG
                              TC TGTGCC  CAG CT  GC
                              || ||||||  ||| ||  ||
                              AG ACACGG  GTC GG  CG
                               G    ___  C  GT
GAM1038 CMAR    5' GCCAAGGCTGGAGTGCA    17775   _  GA
                              TGC CT  CAGTCTTGGC
                              ||| ||  ||||||||||
                              ACG GA  GTCGGAACCG
                                T  G_
GAM1038 CNN2    3' GCTGAGATTACAGGTGTGA   15177    GT   AC   TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
                              AGTG  TGGAC  TTAGA  CG
                                __   A_   GT
GAM1038 CNTNAP2  3' GCTGAGAGCTGGGCACA    26231     TGA  _  TG
                              TGTGCC  CAG TCT  GC
                              ||||||  ||| |||  ||
                              ACACGG  GTC AGA  CG
                                 ___  G  GT
GAM1038 COCH    3' GCTGAGGCTTCATAATCATGG  14559    TGCC  C   TG
                              TCATG   TGA AGTCT  GC
                              |||||   ||| |||||  ||
                              GGTAC   ACT TCGGA  CG
                                 TAAT  _   GT
GAM1038 COL18A1  3' CGAGGCTGGCACAGGA    55289   A    TGAC   TG
                              TC TGTGCC   AGTCT  G
                              || ||||||   |||||  |
                              AG ACACGG   TCGGA  C
                               G    ____   GT
GAM1038 COL18A1  3' CGAGGCTGGCACAGGA    55293   A    TGAC   TG
                              TC TGTGCC   AGTCT  G
                              || ||||||   |||||  |
                              AG ACACGG   TCGGA  C
                               G    ____   GT
GAM1038 COL18A1  3' CGAGGCTGGCACAGGA    47577   A    TGAC   TG
                              TC TGTGCC   AGTCT  G
                              || ||||||   |||||  |
```

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                                AG ACACGG   TCGGA  C
                                 G     ____    GT
GAM1038  COL4A6   3'  GCTGGGTTGGGGGTGGTGG   8472     G    GA   T  TG
                                TCAT TGCCT  CAG CT  GC
                                |||| |||||  ||| ||  ||
                                GGTG GTGGG  GTT GG  CG
                                  _    G_  _  GT
GAM1038  COL4A6   3'  GCTGGGTTGGGGGTGGTGG   53318    G    GA   T  TG
                                TCAT TGCCT  CAG CT  GC
                                |||| |||||  ||| ||  ||
                                GGTG GTGGG  GTT GG  CG
                                  _    G_  _  GT
GAM1038  COX15    3'  GCTGAGATTACAGGCAT    54318      AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGA  CG
                                    A_    GT
GAM1038  COX7A2L  3'  GCCAAGGTCATGTGCATGA   16351     TG C    AGT
                                TCATG  C TGAC   CTTGGC
                                |||||  | ||||   ||||||
                                AGTAC  G ACTG   GAACCG
                                  GT T   ___
GAM1038  CPNE3    3'  GTTAGGACTGTTTTGTCCAGGA 14031    A  TG CT
                                TC TG  C  GACAGTCTTGGC
                                || ||  |  ||||||||||||
                                AG AC  G  TTGTCAGGATTG
                                 G  CT TT
GAM1038  CPSF4    3'  CAACCTGCTGGGCATGTGG   21952       GA   TC
                                TCATGTGCCT  CAG  TTG
                                ||||||||||  |||  |||
                                GGTGTACGGG  GTC  AAC
                                     TC   C_
GAM1038  CR1      3'  GTTGGGACTACCAGTAGATGG  5136     G   C  AC    TG
                                TCAT TGC TG  AGTCT  GC
                                |||| ||| ||  |||||  ||
                                GGTA ATG AC  TCAGG  TG
                                  G   _ CA    GT
GAM1038  CRLF1    3'  GCCAGGGCTGGGGGT      16453     GA
                                GCCT  CAGTCTTGGC
                                ||||  ||||||||||
                                TGGG  GTCGGGACCG
                                  G_
GAM1038  CRMP1    5'  GCCGGGGCAGCCGCGCGTGG  7153       CTGACA
                                TCATGTGC    GTCTTGGC
                                ||||||||    ||||||||
                                GGTGCGCG    CGGGGCCG
                                    CCGA__
GAM1038  CRTAP    3'  GCTGGGATTACAGGCGTGA   21038    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
```

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                                AGTG  CGGAC  TTAGG  CG
                                  __     A_     GT
GAM1038  CRYAA    3'  GCCGGGGCTTCTGTGCACCTGG 4618      T    CT_  C
                                TCA GTGC   GA AGTCTTGGC
                                ||| ||||   || |||||||||
                                GGT CACG   CT TCGGGGCCG
                                  C    TGT  _
GAM1038  CSNK1G2  3'  CCGCGTGGGGCGCGTGG     7168          G  A  CTT
                                TCATGTGCCT AC GT   GG
                                |||||||||| || ||   ||
                                GGTGCGCGGG TG CG   CC
                                      G  _  ___
GAM1038  CST      3'  GCCAAGACTGGGCCCATGA    16790       T   TGA
                                TCATG GCC   CAGTCTTGGC
                                ||||| |||   ||||||||||
                                AGTAC CGG   GTCAGAACCG
                                   C   ___
GAM1038  CTF1     3'  GCTGGGATTGCAGGCGTGA    7181       GT    A     TG
                                TCAT  GCCTG CAGTCT  GC
                                ||||  ||||| ||||||  ||
                                AGTG  CGGAC GTTAGG  CG
                                  __    _     GT
GAM1038  CTNNA2   3'  GCCAATACGCTTAAGTGTGTGG 15245       TG C   CA  C
                                TCATG  C TGA  GT TTGGC
                                |||||  | |||  || |||||
                                GGTGT  G ATT  CA AACCG
                                   GT A   CG  T
GAM1038  CTNS     3'  GCTAGGACTTTGGGGTTAGGCC 17044    T      _____
            ATGG                   TG GCCTGAC     AGTCTTGGC
                                || |||||||     |||||||||
                                AC CGGATTG     TCAGGATCG
                                 _      GGGTT
GAM1038  CTPS     5'  TCGGGGTTGTTCACTGG     88596     T   CCT    GT
                                TCA GTG   GACA  CTTGG
                                ||| |||   ||||  |||||
                                GGT CAC   TTGT  GGGCT
                                  _  ___    TG
GAM1038  CXCL16   3'  GCTGGGATTAAAGGTGTGA   41922      GT   GAC    TG
                                TCAT  GCCT   AGTCT  GC
                                ||||  ||||   |||||  ||
                                AGTG  TGGA   TTAGG  CG
                                  __    AA_    GT
GAM1038  CYLN2    3'  GCCGGGACTGTCACTTTGG   12634    ____
                                CC    TGACAGTCTTGGC
                                ||    ||||||||||||
                                GG    ACTGTCAGGGCCG
                                 TTTC
GAM1038  CYP11B1  3'  GCCAGGGCCCCTGCGCAGA   62163    A    CTGACA
                                TC TGTGC     GTCTTGGC
                                || |||||     ||||||||
```

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                                AG ACGCG     CGGGACCG
                                 _    TCCC__
GAM1038 CYP1A2   3' GCTGGGATTAACAGGTAT    69117       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TATGGAC  TTAGG  CG
                                    AA    GT
GAM1038 CYP1A2   3' GCTGGGATTAACAGGTAT    5697        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TATGGAC  TTAGG  CG
                                    AA    GT
GAM1038 CYP2A6   3' GCTAAGACTGGGGGCA      5712       GA
                                TGCCT  CAGTCTTGGC
                                |||||  ||||||||||
                                ACGGG  GTCAGAATCG
                                   G_
GAM1038 CYP2B6   3' GCTGGGATTACAGGCATGT   5735         AC    TG
                                ATGTGCCTG  AGTCT  GC
                                |||||||||  |||||  ||
                                TGTACGGAC  TTAGG  CG
                                     A_    GT
GAM1038 CYP2B6   3' GCTGGGATTACAGGCGTGA   5736      GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 CYP51    3' GCTGGGATTACAGGCAT     5785        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038 DAP3     3' GCCAAGATCACAGCATGTGA  53353        C  ACA
                                TCATGTGC TG   GTCTTGGC
                                ||||||||  ||   ||||||||
                                AGTGTACG AC   TAGAACCG
                                     _ AC_
GAM1038 DAP3     3' GCCAAGATCACAGCATGTGA  16151        C  ACA
                                TCATGTGC TG   GTCTTGGC
                                ||||||||  ||   ||||||||
                                AGTGTACG AC   TAGAACCG
                                     _ AC_
GAM1038 DCTN1    5' GTTGAGTGCTGAGGGTCTGTGG 14555     GT   GA   _  TG
                                TCAT  GCCT  CAGT CT  GC
                                ||||  ||||  |||| ||  ||
                                GGTG  TGGG  GTCG GA  TG
                                  TC    A_    T  GT
GAM1038 DCX      5' ACTGTTAGTCATGTGG      5100        C
                                TCATGTG CTGACAGT
                                |||||||  ||||||||
```

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                                GGTGTAC GATTGTCA
                                    T
GAM1038 DCX     5' GTTAGTCATGTGGGCATGTG  5101        G  GTC
                                CATGTGCCT ACA  TTGGC
                                ||||||||| |||  |||||
                                GTGTACGGG TGT  GATTG
                                    _  ACT
GAM1038 DDB2    3' GCTGGGACCTGGGGCACTGTGG 3660     _    GA  _  TG
                                TCAT GTGCCT  CAG TCT  GC
                                |||| ||||||  ||| |||  ||
                                GGTG CACGGG  GTC AGG  CG
                                  T    __  C  GT
GAM1038 DDX11   3' GCCAGGACCCAGGCACA    15300       ACA
                                TGTGCCTG  GTCTTGGC
                                ||||||||  ||||||||
                                ACACGGAC  CAGGACCG
                                    C__
GAM1038 DDX11   3' GCCAGGACCCAGGCACA    47656       ACA
                                TGTGCCTG  GTCTTGGC
                                ||||||||  ||||||||
                                ACACGGAC  CAGGACCG
                                    C__
GAM1038 DDX11   3' GCCGGGGTGGAAGCTGAGCGCG 47657      ____ GA  G
          TGG                   ATGTGC   CT  CA TCTTGGC
                                ||||||   ||  || |||||||
                                TGCGCG   GA  GT GGGGCCG
                                   AGTC  AG  _
GAM1038 DES     3' GCCAGGACTGAGCCCCGCAGA  72129   A   CCTGA
                                TC TGTG    CAGTCTTGGC
                                || ||||    ||||||||||
                                AG ACGC    GTCAGGACCG
                                 _   CCCGA
GAM1038 DFFB    3' GCTCATGTCAGCCGTGTGG   87387    TG  C    GTCTT
                                TCA  TG CTGACA    GGC
                                |||  || ||||||    |||
                                GGT  GC GACTGT    TCG
                                  GT  C    AC___
GAM1038 DFFB    3' GCTGGGATGACAGGTGTGA   87388     GT   ACA   TG
                                TCAT  GCCTG  GTCT  GC
                                ||||  |||||  ||||  ||
                                AGTG  TGGAC  TAGG  CG
                                  __   AG_   GT
GAM1038 DFFB    3' GCTGGGATTACAGGCAT    87389       AC   TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_   GT
GAM1038 DFFB    3' GCTGGGATTACAGGCATGTG  87390        AC   TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
```

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                                GTGTACGGAC  TTAGG  CG
                                     A_    GT
GAM1038  DHCR24   3'  GCCAGTCATGGTTGTGGCGTGT 28629    TG   _   AGTC_
             GA                    TCA  TGCC TGAC    TTGGC
                                   |||  |||| ||||    |||||
                                   AGT  GCGG GTTG    GACCG
                                     GT   T   GTACT
GAM1038  DHCR24   3'  GCCAGTGGGCAGTGCATGTGG  28630       _  A_  GTC
                                   TCATGTGC CTG  CA   TTGGC
                                   ||||||||  |||  ||   |||||
                                   GGTGTACG GAC  GT   GACCG
                                        T  GG  ___
GAM1038  DHCR7    5'  GCCAGGGGAAGGTGGGCGCA  7235       G  AG__
                                   TGTGCCT AC    TCTTGGC
                                   |||||||  ||    |||||||
                                   ACGCGGG TG    GGGACCG
                                      _  GAAG
GAM1038  DISC1    3'  GCTGAGATTACAGGTGTGA   37883     GT    AC    TG
                                   TCAT  GCCTG  AGTCT  GC
                                   ||||  |||||  |||||  ||
                                   AGTG  TGGAC  TTAGA  CG
                                     __    A_    GT
GAM1038  DISC1    3'  GTCAGGATTGGCCACAT     37889      CCTGA
                                   ATGTG    CAGTCTTGGC
                                   |||||    ||||||||||
                                   TACAC    GTTAGGACTG
                                     CG___
GAM1038  DLEC1    3'  GCCAGCTCCCAGCCACATGG   23687       C   AC   CT
                                   TCATGTG CTG  AGT  TGGC
                                   |||||||  |||  |||  ||||
                                   GGTACAC GAC  TCG  ACCG
                                      C   CC   __
GAM1038  DLEC1    3'  GCCAGGACCTGCTGTGTGA   23688     TG _  CTGACA
                                   TCA  T GC     GTCTTGGC
                                   |||  | ||     ||||||||
                                   AGT  G CG     CAGGACCG
                                     GT T  TC____
GAM1038  DLEC1    3'  GTCATCCTGCAGGCACATGA   23691         A   TCT
                                   TCATGTGCCTG CAG   TGGC
                                   ||||||||||| |||   ||||
                                   AGTACACGGAC GTC   ACTG
                                         _  CT_
GAM1038  DLEC1    3'  GCCAGCTCCCAGCCACATGG   23700       C   AC   CT
                                   TCATGTG CTG  AGT  TGGC
                                   |||||||  |||  |||  ||||
                                   GGTACAC GAC  TCG  ACCG
                                      C   CC   __
GAM1038  DLEC1    3'  GCCAGGACCTGCTGTGTGA   23701     TG _  CTGACA
                                   TCA  T GC     GTCTTGGC
                                   |||  | ||     ||||||||
```

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                                AGT  G CG     CAGGACCG
                                  GT T  TC____
GAM1038  DLEC1    3'  GTCATCCTGCAGGCACATGA   23705          A   TCT
                                TCATGTGCCTG CAG   TGGC
                                |||||||||| |||   ||||
                                AGTACACGGAC GTC   ACTG
                                      _  CT_
GAM1038  DLG1     5'  GCTAGGGCAAGGTGTGTG    14560     TG   GACA
                                CATG  CCT   GTCTTGGC
                                ||||  |||   ||||||||
                                GTGT  GGA   CGGGATCG
                                  GT   A___
GAM1038  DLST     3'  GCCAGGGGATCTGGGTGTGTGA 8644       TG   _  CAG
                                TCATG  CCT GA   TCTTGGC
                                |||||  ||| ||   |||||||
                                AGTGT  GGG CT   GGGACCG
                                   GT   T  AG_
GAM1038  DMC1     3'  GTTGGGAAAGGAGTACGTGA   22979        _  GACAG   TG
                                TCATGTGC CT    TCT  GC
                                |||||||| ||    |||  ||
                                AGTGCATG GG    AGG  TG
                                     A  AA___   GT
GAM1038  DMP1     3'  GCCAAGGCCAGTGAGGCTATGA 15319      T   G  A_
                                TCATG GCCT AC  GTCTTGGC
                                ||||| |||| ||  ||||||||
                                AGTAT CGGA TG  CGGAACCG
                                   _   G  AC
GAM1038  DMPK     5'  GTTAAGGCTGGGAGGCG     15325      GA
                                TGCCT  CAGTCTTGGC
                                |||||  ||||||||||
                                GCGGA  GTCGGAATTG
                                   GG
GAM1038  DNASE1L1 5'  GCTGGGATTACAGGCAT     22077       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                     A_    GT
GAM1038  DNCI1    3'  GCCAGATATGATTGGGTGCAGA 91064    A  TG  TG _  _   T
                                TC TG  CC  A CA GTCT GGC
                                || ||  ||  | || |||| |||
                                AG AC  GG  T GT TAGA CCG
                                 _  GT  GT A  A   _
GAM1038  DNLC2A   3'  GTCAGTGGACTAGCACATGG   26362        CTGAC   __
                                TCATGTGC    AGTCT  TGGC
                                ||||||||    |||||  ||||
                                GGTACACG    TCAGG  ACTG
                                     A____    TG
GAM1038  DNM2     3'  GCTGGGGTGCAGGGGTAT    17056      G   A  G   TG
                                ATGT CCTG CA TCT  GC
                                |||| |||| || |||  ||
```

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                                TATG GGAC GT GGG  CG
                                  G   _ _  GT
GAM1038 DPH2L2   3' TGTGGGGCTGTCTGGTGTATGG 7282       TG  T       GC
                                TCATG  CC GACAGTCTTG
                                |||||  || ||||||||||
                                GGTAT  GG CTGTCGGGGT
                                   GT  T       GTT
GAM1038 DRD5     5' TGGGACCGCGCACAGA     5850     A    C  ACA   TG
                                TC TGTGC TG   GTCT  G
                                || ||||| ||   ||||  |
                                AG ACACG GC   CAGG  T
                                 _    C ___    GT
GAM1038 DRG2     3' GCCAGGGCCTAAAGCAGATGG  7321      G   CTGACA
                                TCAT TGC     GTCTTGGC
                                |||| |||     ||||||||
                                GGTA ACG     CGGGACCG
                                  G  AAATC_
GAM1038 DSC3     3' GCTGGGATTACAGGCAT     44343       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038 DSC3     3' GCTGGGATTACAGGCAT     8678        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038 DSCR3    3' GCTGAGATTACAGGTGTGA   20188     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGA  CG
                                  __    A_    GT
GAM1038 DSCR3    3' GCTGGGATTACAGGTGTGA   20189     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 DUSP7    5' TCGGGGTCCGGCGCA      65435       T  AGT
                                TGTGCC GAC   CTTGG
                                ||||||  |||  |||||
                                ACGCGG CTG   GGGCT
                                   C  ___
GAM1038 DXF68S1E 3' GTCAAGCTGATGGAGTATGTGA 60008         _  A  T
                                TCATGTGC CTG CAG CTTGGC
                                |||||||| ||| ||| ||||||
                                AGTGTATG GGT GTC GAACTG
                                   A  A  _
GAM1038 E2F1     5' GCCGAGGCCTGCCGCCATGG  84799      T  CTGA  _
                                TCATG GC   CAG TCTTGGC
                                |||||  ||   |||  |||||||
```

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                                GGTAC CG   GTC GGAGCCG
                                  _ CC__   C
GAM1038 E2F3    3' GTCGGGTGGCAATTGTCAGGGT 8700   TG G      _____
             GTGG                   T CCTGACAGT    CTTGGC
                                  | |||||||||    ||||||
                                  G GGACTGTTA    GGGCTG
                                GT _       ACGGT
GAM1038 EBP     3' GTCACACTCAGGCTCATGG   21667     T    CA  CT
                                TCATG GCCTGA  GT  TGGC
                                ||||| ||||||  ||  ||||
                                GGTAC CGGACT  CA  ACTG
                                  T     __ C_
GAM1038 EFNB1   3' GCCAGGGCTGTTCACGCCCATG 15400     T  C  _
                                CATG GC TGA CAGTCTTGGC
                                |||| || ||| ||||||||||
                                GTAC CG ACT GTCGGGACCG
                                  C  C   T
GAM1038 EFNB2   3' TCAAGGTGAAGCACAT     14576      CTGA  G
                                ATGTGC   CA TCTTGG
                                ||||||   || ||||||
                                TACACG   GT GGAACT
                                   AA__  _
GAM1038 EGFL4   5' GCCAGTGCAACGGGCACG   61812       ACA  C
                                TGTGCCTG   GT TTGGC
                                ||||||||   || |||||
                                GCACGGGC   CG GACCG
                                     AA_  T
GAM1038 EGFL4   3' GCTGGGGGCAGTGGGCATGGGA 61814   AT     ACAG   TG
                                TC  GTGCCTG   TCT  GC
                                ||  |||||||   |||  ||
                                AG  TACGGGT   GGG  CG
                                 GG      GACG   GT
GAM1038 EGFL5   3' GTCAGGATTAAAGGTGGTGA   86627     G    GAC
                                TCAT TGCCT   AGTCTTGGC
                                |||| |||||   |||||||||
                                AGTG GTGGA   TTAGGACTG
                                  _    AA_
GAM1038 EGLN2   5' GTTGAGGCCCATTCAGGTGTTG 34102     T TG    CA__   TG
             G                   TCA G  CCTGA   GTCT  GC
                                ||| |  |||||   ||||  ||
                                GGT T  GGACT   CGGA  TG
                                 _ GT    TACC   GT
GAM1038 EGLN2   5' GCCAGGCCCCAGGTATGTG   34100        ACA   T
                                CATGTGCCTG   GTCT GGC
                                ||||||||||   |||| |||
                                GTGTATGGAC   CGGA CCG
                                     CC_   _
GAM1038 EGR3    3' GCTGGGGGTCCGCACGTGG   59558       CT   AG   TG
                                TCATGTGC  GAC  TCT  GC
                                ||||||||  |||  |||  ||
```

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                                GGTGCACG  CTG  GGG  CG
                                    C_   __   GT
GAM1038  EIF2S3   3'  GCTGGGATTACAGGCGTGA   7418      GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  EIF3S10  5'  GCTGGCGAGGCGCGTGG     71708         GA_
                                TCATGTGCCT   CAGT
                                ||||||||||   ||||
                                GGTGCGCGGA   GTCG
                                      GCG
GAM1038  EMR1     3'  CCCTTGTTGGTGCATGG     8773       TG  T    TCTT
                                TCATG  CC GACAG   GG
                                |||||  || |||||   ||
                                GGTAC  GG TTGTT   CC
                                   GT  _    C___
GAM1038  EMX2     3'  AGTTGTTGGGCGAATGG     87562     G   TG   T
                                TCAT TGCC  ACAG CT
                                |||| ||||  |||| ||
                                GGTA GCGG  TGTT GA
                                  A   GT   _
GAM1038  EN2      3'  GCTAAAGGCCTGGGGTGTGTGG 7466       TG   GA  _   _
                                TCATG  CCT  CAG TCTT GGC
                                |||||  |||  ||| |||| |||
                                GGTGT  GGG  GTC GGAA TCG
                                   GT  __   C   A
GAM1038  ENO2     3'  GGGAGTGTTGGGCATGTGA   8778         TG   G
                                TCATGTGCC  ACA TCTT
                                |||||||||  ||| ||||
                                AGTGTACGG  TGT AGGG
                                     GT   G
GAM1038  ENSA     3'  GTCAGGAGGTGGCTCGGGTGTG 15427     GT    __  G_
            G                    TCAT  GCCTGA  CA  TCTTGGC
                                ||||  ||||||  ||  |||||||
                                GGTG  TGGGCT  GT  AGGACTG
                                  __     CG  GG
GAM1038  EPHA2    3'  CCAGGGCTGGGGACAGA     15403    A   G  TGA
                                TC TGT CC   CAGTCTTGG
                                || ||| ||   |||||||||
                                AG ACA GG   GTCGGGACC
                                 _   G  ___
GAM1038  EPHA8    5'  GCCAAGCCCGAGGGTGCGTGG  40060      TG   GACA T
                                TCATG  CCT    G CTTGGC
                                |||||  |||    | ||||||
                                GGTGC  GGG    C GAACCG
                                   GT   AGCC _
GAM1038  EPHA8    3'  GTTAAGGCTGGAGGCACATG   40065         GA
                                CATGTGCCT  CAGTCTTGGC
                                |||||||||  ||||||||||
```

```
                                GTACACGGA  GTCGGAATTG
                                     G_
GAM1038  ERH     3'  GCCAAGATTGACTGTATTA   15477   T   CTGA
                                A GTGC   CAGTCTTGGC
                                | ||||   ||||||||||
                                A TATG   GTTAGAACCG
                                 T   TCA_
GAM1038  EXTL1   5'  GCCAGGGCTGCTCAGGCA    15493       _
                                TGCCTGA CAGTCTTGGC
                                ||||||| ||||||||||
                                ACGGACT GTCGGGACCG
                                    C
GAM1038  EXTL3   3'  GCCAAAGAGTGTGGTGTGTGG  7532      TG  TG   G   _
                                TCATG  CC  ACA TCTT GGC
                                |||||  ||  ||| |||| |||
                                GGTGT  GG  TGT AGAA CCG
                                   GT  __   G   A
GAM1038  EYA1    3'  GTCAAGACCAAAAGCATGG   4956       GCC  ACA
                                TCATGT   TG   GTCTTGGC
                                ||||||   ||   ||||||||
                                GGTACG   AC   CAGAACTG
                                   AAA  ____
GAM1038  F2RL3   3'  GCCGAGATTGCGCCACTGG   14184    T   CC  A
                                TCA GTG  TG CAGTCTTGGC
                                ||| |||  || ||||||||||
                                GGT CAC  GC GTTAGAGCCG
                                  _  C_  _
GAM1038  F2RL3   3'  GCCGGGGGTGCGGGCGCGCGG  14185    A      A  G
                                TC TGTGCCTG CA TCTTGGC
                                || |||||||| || |||||||
                                GG GCGCGGGC GT GGGGCCG
                                 C       _  G
GAM1038  FANCE   3'  GCTGGGACTACATGCACATGA  41613        C  AC    TG
                                TCATGTGC TG  AGTCT  GC
                                |||||||| ||  |||||  ||
                                AGTACACG AC  TCAGG  CG
                                     T  A_    GT
GAM1038  FANCE   3'  GTTGAGATTTACAGGTGTGA   41614     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGA  TG
                                  __    AT    GT
GAM1038  FANCF   3'  GCTGGGATTACAGGCGTGA   42676     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  FBLN2   3'  GCCAGGGCTCACACTGCGTGG  8843       GCC  AC
                                TCATGT   TG  AGTCTTGGC
                                ||||||   ||  |||||||||
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                                GGTGCG  AC  TCGGGACCG
                                   TC_  AC
GAM1038  FBXL5   5'  GCTGAGGCAGTGGCGATGG   53202     G   TG  A   TG
                                TCAT TGCC  AC GTCT  GC
                                |||| ||||  || ||||  ||
                                GGTA GCGG  TG CGGA  CG
                                  _   __  A   GT
GAM1038  FCAR    3'  GCTGAGATTATAGGCAT    55750      AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGA  CG
                                   A_    GT
GAM1038  FCAR    3'  GCTGAGATTATAGGCAT    55761      AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGA  CG
                                   A_    GT
GAM1038  FCAR    3'  GCTGAGATTATAGGCAT    55772      AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGA  CG
                                   A_    GT
GAM1038  FCAR    3'  GCTGAGATTATAGGCAT    55783      AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGA  CG
                                   A_    GT
GAM1038  FCAR    3'  GCCAAGGCTGGAGTGCAGTGG  55799     G  _  GA
                                TCAT TGC CT  CAGTCTTGGC
                                |||| ||| ||  ||||||||||
                                GGTG ACG GA  GTCGGAACCG
                                  _  T  G_
GAM1038  FCAR    3'  GCTGGGATTACAGGCGTGA   55801     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  FCAR    3'  GCCAAGGCTGGAGTGCAGTGG  55815     G  _  GA
                                TCAT TGC CT  CAGTCTTGGC
                                |||| ||| ||  ||||||||||
                                GGTG ACG GA  GTCGGAACCG
                                  _  T  G_
GAM1038  FCAR    3'  GCTGAGATTATAGGCAT    8855       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGA  CG
                                   A_    GT
GAM1038  FCGR2A  3'  GCTGGGATTAGAGGCATGTG  79263        GAC    TG
                                CATGTGCCT   AGTCT  GC
                                |||||||||   |||||  ||
```

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                                GTGTACGGA  TTAGG CG
                                    GA_    GT
GAM1038 FCRH1   3' GCTGGGACTACAGGCACATG  53627       AC   TG
                                CATGTGCCTG AGTCT GC
                                |||||||||| ||||| ||
                                GTACACGGAC TCAGG CG
                                    A_    GT
GAM1038 FCRH3   3' GCTGGGCTGCAGGGTATGTGA 53632       GA  T TG
                                TCATGTGCCT CAG CT GC
                                |||||||||| ||| ||  ||
                                AGTGTATGGG GTC GG CG
                                    AC  _ GT
GAM1038 FE65L2  5' GTCGGTCTTCAGGCGCCTGA  55677    T     C T T
                                TCA GTGCCTGA AG CT GGC
                                ||| |||||||| || || |||
                                AGT CGCGGACT TC GG CTG
                                  C      _ T _
GAM1038 FE65L2  5' GTCGGTCTTCAGGCGCCTGA  55680    T     C T T
                                TCA GTGCCTGA AG CT GGC
                                ||| |||||||| || || |||
                                AGT CGCGGACT TC GG CTG
                                  C      _ T _
GAM1038 FE65L2  5' GTCGGTCTTCAGGCGCCTGA  55685    T     C T T
                                TCA GTGCCTGA AG CT GGC
                                ||| |||||||| || || |||
                                AGT CGCGGACT TC GG CTG
                                  C      _ T _
GAM1038 FE65L2  5' GTCGGTCTTCAGGCGCCTGA  20168    T     C T T
                                TCA GTGCCTGA AG CT GGC
                                ||| |||||||| || || |||
                                AGT CGCGGACT TC GG CTG
                                  C      _ T _
GAM1038 FEZ1    5' CCAGGACCCGCACAGA     42569   A   CTGACA
                                TC TGTGC    GTCTTGG
                                || |||||    |||||||
                                AG ACACG    CAGGACC
                                 _    CC____
GAM1038 FEZ1    3' GCTGGGATTACAGGCGTGA  42575    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG CG
                                  __    A_    GT
GAM1038 FEZ1    5' CCAGGACCCGCACAGA     17528   A   CTGACA
                                TC TGTGC    GTCTTGG
                                || |||||    |||||||
                                AG ACACG    CAGGACC
                                 _    CC____
GAM1038 FGF2    3' GTTGAGACTTTCTTATATGA  8874       CCT C   TG
                                TCATGTG  GA AGTCT GC
                                |||||||  || ||||| ||
```

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                                AGTATAT   CT TCAGA  TG
                                   T__  T    GT
GAM1038  FGF5    3'  GCTGGGATTACAGGTACAATGA 52490     _     AC    TG
                                TCAT GTGCCTG  AGTCT  GC
                                |||| |||||||  |||||  ||
                                AGTA CATGGAC  TTAGG  CG
                                  A      A_    GT
GAM1038  FGF5    3'  GCTGGGATTACAGGTACAATGA 15544     _     AC    TG
                                TCAT GTGCCTG  AGTCT  GC
                                |||| |||||||  |||||  ||
                                AGTA CATGGAC  TTAGG  CG
                                  A      A_    GT
GAM1038  FHL1    3'  GCCAGGGCTGTCATCAACATGG 7559       GCC
                                TCATGT   TGACAGTCTTGGC
                                ||||||   ||||||||||||
                                GGTACA   ACTGTCGGGACCG
                                   ACT
GAM1038  FKRP    3'  GTCGAGAACCGGGTGCTGG   44188    T TG   ACAG
                                TCA G  CCTG   TCTTGGC
                                ||| |  ||||   |||||||
                                GGT C  GGGC   AGAGCTG
                                 _ GT   CA__
GAM1038  FLRT2   3'  GTCAAGGTTGCGAGTACA    25063      C  A  GT
                                TGTGC TG CA  CTTGGC
                                ||||| || ||  ||||||
                                ACATG GC GT  GAACTG
                                  A  _  TG
GAM1038  FMOD    3'  GTCAGGAGACCCCAAGGCATGT 8933         GACAG__
           GA                    TCATGTGCCT     TCTTGGC
                                ||||||||||     |||||||
                                AGTGTACGGA     AGGACTG
                                     ACCCCAG
GAM1038  FMR2    5'  GTCGGGTCGCTGGGTGCGCG  8944      CTGA   __
                                TGTGC   CAGT  CTTGGC
                                |||||   ||||  ||||||
                                GCGCG   GTCG  GGGCTG
                                  TGG_   CT
GAM1038  FOSB    3'  GCTGGGACAGATTGGCAATGG  22107     G   TGACA   TG
                                TCAT TGCC    GTCT  GC
                                |||| ||||    ||||  ||
                                GGTA ACGG    CAGG  CG
                                  _   TTAGA   GT
GAM1038  FOXD2   5'  GCTGGGGCGGCGTGG      15566      _   GA
                                TCATGT GCCT  CAGT
                                |||||| ||||  ||||
                                GGTGCG CGGG  GTCG
                                   G   __
GAM1038  FSTL1   3'  GTTAAGATCCAGTGTCCATGG  23013     TG _  ACA
                                TCATG  C CTG   GTCTTGGC
                                |||||  | |||   ||||||||
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                                GGTAC  G GAC   TAGAATTG
                                   CT T   C__
GAM1038  FSTL3    3'  GCCAAGACTCACGCATGTG   19609       C   CA
                                CATGTGC TGA  GTCTTGGC
                                ||||||| |||  ||||||||
                                GTGTACG ACT  CAGAACCG
                                    C   __
GAM1038  FUS1     5'  CGGGGCAGGTTATGG      23447      T   GACA   TG
                                TCATG GCCT   GTCT  G
                                ||||| ||||   ||||  |
                                GGTAT TGGA   CGGG  C
                                   _   ____   GT
GAM1038  FUT1     3'  GCTGGGATTACCGGCGTGA   3795      GT   T AC    TG
                                TCAT  GCC G  AGTCT  GC
                                ||||  ||| |  |||||  ||
                                AGTG  CGG C  TTAGG  CG
                                  __  _ CA    GT
GAM1038  FUT7     5'  CTAGGGCGTAGCTGTGA     15582      T  CTG  A
                                TCATG GC   AC GTCTTGG
                                ||||| ||   || |||||||
                                AGTGT CG   TG CGGGATC
                                   _ A__  _
GAM1038  FUT7     3'  GCCGGGGGGAGGTGGGTGTGG   15585     GT   G  AG_
                                TCAT  GCCT AC   TCTTGGC
                                ||||  |||| ||   |||||||
                                GGTG  TGGG TG   GGGGCCG
                                  __   _  GAG
GAM1038  FZD3     5'  GCTGAGACCTGCAGGTGTAT   33782    TG   A  _  TG
                                ATG  CCTG CAG TCT  GC
                                |||  |||| ||| |||  ||
                                TAT  GGAC GTC AGA  CG
                                  GT   _  C  GT
GAM1038  FZD4     3'  GCTGGGACTACAGGTGCGTG   24143     TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGC  GGAC  TCAGG  CG
                                   GT   A_    GT
GAM1038  FZD4     3'  GCTGGGGCGCAATGG      24144      _    GA
                                TCAT GTGCCT  CAGT
                                |||| ||||||  ||||
                                GGTA CGCGGG  GTCG
                                   A    __
GAM1038  G6PC     3'  GCTAGGATTACAGGCAT     3828        AC
                                GTGCCTG  AGTCTTGGC
                                |||||||  |||||||||
                                TACGGAC  TTAGGATCG
                                    A_
GAM1038  GAA      5'  GCCAGGGCGCGCGTGCGCG   3843       C  ACA
                                TGTGC TG   GTCTTGGC
                                ||||| ||   ||||||||
```

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                                GCGCG GC   CGGGACCG
                                   T  GCG
GAM1038  GAB2     3'  GCTGGGCGACCAAGCACATGG  54454        C  ACA T  TG
                                TCATGTGC TG   G CT  GC
                                |||||||| ||   | ||  ||
                                GGTACACG AC   C GG  CG
                                     A  CAG _  GT
GAM1038  GAB2     3'  GCTGGGCGACCAAGCACATGG  24497        C  ACA T  TG
                                TCATGTGC TG   G CT  GC
                                |||||||| ||   | ||  ||
                                GGTACACG AC   C GG  CG
                                     A  CAG _  GT
GAM1038  GATA2    3'  GCCAGGGCTGGGTCACAGGA  8999     A   _  TGA
                                TC TGTG CC   CAGTCTTGGC
                                || |||| ||   ||||||||||
                                AG ACAC GG   GTCGGGACCG
                                 G   T ___
GAM1038  GBF1     3'  GCCCACGGTCAGGCATTGA   14834     T       A  CTT
                                TCA GTGCCTGAC GT   GGC
                                ||| ||||||||| ||   |||
                                AGT TACGGACTG CA   CCG
                                  _       G  C__
GAM1038  GFAP     3'  GATCTGTTGTGTACGTGG    9015         C     _
                                TCATGTGC TGACAG TC
                                |||||||| |||||| ||
                                GGTGCATG GTTGTC AG
                                     T     T
GAM1038  GFI1     3'  CCATGTTAGGTATTGG      17933     T        GTCT
                                TCA GTGCCTGACA    TGG
                                ||| ||||||||||    |||
                                GGT TATGGATTGT    ACC
                                  _        _____
GAM1038  GFI1     3'  GCTAGCAGGCATGTGG      17934          AC
                                TCATGTGCCTG  AGT
                                ||||||||||  |||
                                GGTGTACGGAC  TCG
                                      GA
GAM1038  GIPR     3'  GTTGGGATTTCATTTCAGGTGC 3897      TG    C____    TG
              AT                  ATG  CCTGA    AGTCT  GC
                                ||| |||||    |||||  ||
                                TAC  GGACT    TTAGG  TG
                                  GT    TTACT    GT
GAM1038  GJB3     3'  GCTAGGGTGGGGGCTGTGG   43769      T   GA  G
                                TCATG GCCT  CA TCTTGGC
                                ||||| ||||  || |||||||
                                GGTGT CGGG  GT GGGATCG
                                   _   G_  _
GAM1038  GLO1     5'  GCCGAGGCGTAGTGTGGGTGA  22000      G   _   A A
                                TCAT TGC CTG C GTCTTGGC
                                |||| ||| ||| | ||||||||
```

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                                AGTG GTG GAT G CGGAGCCG
                                  G  T  _ _
GAM1038 GLTSCR1  5' GCTAAGACCACAGGCACATG  31673        ACA
                                CATGTGCCTG  GTCTTGGC
                                ||||||||||  ||||||||
                                GTACACGGAC  CAGAATCG
                                     AC_
GAM1038 GLTSCR1  3' GCTGGGGGGTGGGCGTGG   31674      __  GA
                                TCATGT  GCCT  CAGT
                                ||||||  ||||  ||||
                                GGTGCG  TGGG  GTCG
                                   GG   GG
GAM1038 GNA11    3' CCACGTGGGCATGTGG     76095        G  AGTCT
                                TCATGTGCCT AC    TGG
                                |||||||||| ||    |||
                                GGTGTACGGG TG    ACC
                                     _  C____
GAM1038 GNA14    5' GCCCCGTCGGGTACTGA    15030    T      AGTCTT
                                TCA GTGCCTGAC    GGC
                                ||| |||||||||    |||
                                AGT CATGGGCTG    CCG
                                  _       CC____
GAM1038 GNAL     3' GCTGGCCTCAGGCATTTGA  9059     T     CA  TT
                                TCA GTGCCTGA  GTC  GGC
                                ||| ||||||||  |||  |||
                                AGT TACGGACT  CGG  TCG
                                  T      C_  __
GAM1038 GNE      3' GCTGGGATTGCGGGCACATG  18481        A    TG
                                CATGTGCCTG CAGTCT  GC
                                |||||||||| ||||||  ||
                                GTACACGGGC GTTAGG  CG
                                     _    GT
GAM1038 GPC4     3' GCTAACAGTGTAGGTACAGA  7554    A     A  GTC
                                TC TGTGCCTG CA   TTGGC
                                || |||||||| ||   |||||
                                AG ACATGGAT GT   AATCG
                                 _       _  GAC
GAM1038 GPR30    5' GCCGGGGCTGGCGGTGCCTGA 7692    T TG  TGA
                                TCA G  CC   CAGTCTTGGC
                                ||| |  ||   ||||||||||
                                AGT C  GG   GTCGGGGCCG
                                  C GT  CG_
GAM1038 GPR56    5' GCTGGGATTACAGGTGGTGA  19071    G    AC    TG
                                TCAT TGCCTG  AGTCT  GC
                                |||| ||||||  |||||  ||
                                AGTG GTGGAC  TTAGG  CG
                                  _    A_    GT
GAM1038 GPR81    3' GCTAAGTAAATGGGTATATG  50761       GACAGT
                                CATGTGCCT     CTTGGC
                                |||||||||     ||||||
```

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                                GTATATGGG     GAATCG
                                     TAAAT_
GAM1038  GPX3     3'  TCTGTGTACTGCCAGGCATGTG 9126          A    CTTGGC
              G                   TCATGTGCCTG CAGT
                                  |||||||||| ||||
                                  GGTGTACGGAC GTCA
                                        C    TGTGTCTT
GAM1038  GRAF     3'  GCTGGGACTGCAGGCAT     30566       A     TG
                                  GTGCCTG CAGTCT  GC
                                  ||||||| ||||||  ||
                                  TACGGAC GTCAGG  CG
                                     _     GT
GAM1038  GRAF     3'  GCTGGGATTCCAGGTGTGA   30567     GT    AC    TG
                                  TCAT  GCCTG  AGTCT  GC
                                  ||||  |||||  |||||  ||
                                  AGTG  TGGAC  TTAGG  CG
                                    __    C_    GT
GAM1038  GRB14    5'  GCCGGGGCCCCGAGCGCA    15674      C  ACA
                                  TGTGC TG   GTCTTGGC
                                  ||||| ||   ||||||||
                                  ACGCG GC   CGGGGCCG
                                     A  CC_
GAM1038  GRF2     3'  GACCTTGGACCTGTTAGGCGCA 17994            _   T_  C
              TGG                   TCATGTGCCTGACAG TCT  GG
                                  |||||||||||||| |||  ||
                                  GGTACGCGGATTGTC AGG  CC
                                        C   TT  AG
GAM1038  GRIN2A   5'  GCTGGGGCCGCAGCATGCGG   5896     AT   C  ACA   TG
                                  TC  GTGC TG   GTCT  GC
                                  ||  |||| ||   ||||  ||
                                  GG  TACG AC   CGGG  CG
                                   CG    _  GC_   GT
GAM1038  GRM7     5'  GCTGGGATTACAGGCAT     5946        AC    TG
                                  GTGCCTG  AGTCT  GC
                                  |||||||  |||||  ||
                                  TACGGAC  TTAGG  CG
                                     A_    GT
GAM1038  GSPT1    5'  GCTGGGACCAGGCGGACATGG  9142        __    ACA   TG
                                  TCATGT  GCCTG   GTCT  GC
                                  ||||||  |||||   ||||  ||
                                  GGTACA  CGGAC   CAGG  CG
                                     GG     ___    GT
GAM1038  GSTM3    5'  GTCAGGGCGCCCGCGCGTGG   68070        CTGACA
                                  TCATGTGC     GTCTTGGC
                                  ||||||||     ||||||||
                                  GGTGCGCG     CGGGACTG
                                       CCCG__
GAM1038  GTF2E2   5'  GCCGAGGCGGAGGCGCAGGA   9147     A      GACA
                                  TC TGTGCCT    GTCTTGGC
                                  || |||||||    ||||||||
```

```
                                AG ACGCGGA   CGGAGCCG
                                 G     GG__
GAM1038 GTF2F1   5' GTTGGGGTCCTCGCTCAGGCAC 9154   A      C__ __  TG
            AGA                   TGTGCCTGA  AG  TCT  GC
                                 |||||||||  ||  |||  ||
                                 ACACGGACT  TC  GGG  TG
                                _      CGC  CT   GT
GAM1038 HAP1    3' GTCAGCCTGTGTGCGTGTGG  14170    TG  CTG   T  T
                                TCA  TGC   ACAG CT GGC
                                |||  |||   |||| || |||
                                GGT  GCG   TGTC GA CTG
                                  GT   TG_   C  _
GAM1038 HARS    3' GTTAAGACAAACTGCATATG  9177       CTGACA
                                CATGTGC    GTCTTGGC
                                |||||||    ||||||||
                                GTATACG    CAGAATTG
                                    TCAAA_
GAM1038 HCS     3' GCCAAGGCTGGAGTGCAGTGG 38471     G  _  GA
                                TCAT TGC CT  CAGTCTTGGC
                                |||| ||| ||  ||||||||||
                                GGTG ACG GA  GTCGGAACCG
                                  _  T  G_
GAM1038 HCS     3' GCTGGGATTACAGGCGTGA   38475    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 HCS     3' GCTGGGATTGCAGGCGTGA   38476    GT    A     TG
                                TCAT  GCCTG CAGTCT  GC
                                ||||  ||||| ||||||  ||
                                AGTG  CGGAC GTTAGG  CG
                                  __    _     GT
GAM1038 HD      5' GCTAGGGCTGTCAATCATG   9187     TGCC
                                CATG   TGACAGTCTTGGC
                                ||||   ||||||||||||
                                GTAC   ACTGTCGGGATCG
                                  TA__
GAM1038 HDAC4   5' GCCGGGGCGGGGGCGCG    20110      GACA
                                TGTGCCT   GTCTTGGC
                                |||||||   ||||||||
                                GCGCGGG   CGGGGCCG
                                    GG__
GAM1038 HFE     3' GCTGAGATTACAGGTGTGA   4653     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGA  CG
                                  __    A_    GT
GAM1038 HK1     3' GCCAGGGCCTGCCGGCGCG   53120      T A  _
                                TGTGCC G CAG TCTTGGC
                                |||||| | ||| |||||||
```

```
                                GCGCGG C GTC GGGACCG
                                   _ C   C
GAM1038  HK1     3'  GCCAGGGCCTGCCGGCGCG   53124      T A  _
                                TGTGCC G CAG TCTTGGC
                                |||||| | ||| |||||||
                                GCGCGG C GTC GGGACCG
                                   _ C   C
GAM1038  HK1     3'  GCCAGGGCCTGCCGGCGCG   53128      T A  _
                                TGTGCC G CAG TCTTGGC
                                |||||| | ||| |||||||
                                GCGCGG C GTC GGGACCG
                                   _ C   C
GAM1038  HK1     3'  GCCAGGGCCTGCCGGCGCG   53133      T A  _
                                TGTGCC G CAG TCTTGGC
                                |||||| | ||| |||||||
                                GCGCGG C GTC GGGACCG
                                   _ C   C
GAM1038  HK1     3'  GCCAGGGCCTGCCGGCGCG   3949       T A  _
                                TGTGCC G CAG TCTTGGC
                                |||||| | ||| |||||||
                                GCGCGG C GTC GGGACCG
                                   _ C   C
GAM1038  HLCS    5'  GCTGGGATTACAGGTGTGA   4669     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  HNF4G   3'  GCCAAGGCTTCTTCATTGG   14700    T   CCT  C
                                TCA GTG   GA AGTCTTGGC
                                ||| |||   || |||||||||
                                GGT TAC   CT TCGGAACCG
                                  _   TT_ _
GAM1038  HNRPM   5'  GCGTCGGGTCACGTGG      19916      _     A
                                TCATGTG CCTGAC GT
                                ||||||| |||||| ||
                                GGTGCAC GGGCTG CG
                                    T     _
GAM1038  HOXC10  3'  GCCGGGATGTGGGGTGT     61270   TG   G   G
                                G  CCT ACA TCTTGGC
                                |  ||| ||| |||||||
                                T  GGG TGT AGGGCCG
                                 GT   G  _
GAM1038  HPS1    5'  GCCGCGATCCGGTACGTGG   3967        T  CAG  T
                                TCATGTGCC GA   TC TGGC
                                ||||||||| ||   || ||||
                                GGTGCATGG CT   AG GCCG
                                    C ____ C
GAM1038  HRB     5'  CCAGGGCGGCCCGTGG      15706      T   TGACA
                                TCATG GCC    GTCTTGG
                                ||||| |||    |||||||
```

```
                                GGTGC CGG    CGGGACC
                                  C  _____
GAM1038  HS2ST1   3'  GTTAAGATTTTCACACAT    24335      CC   C
                                ATGTG  TGA AGTCTTGGC
                                |||||  ||| |||||||||
                                TACAC  ACT TTAGAATTG
                                  __  T
GAM1038  HSD17B3  3'  GCTGGGGTCACAGAGGCATAGA 3975    A     ____  AGT  TG
                                TC TGTGCCT   GAC   CT  GC
                                || |||||||   |||  ||  ||
                                AG ATACGGA   CTG   GG  CG
                                 _     GACA  ___ GT
GAM1038  HSPA1L   5'  GCTGGGGCTGCGTAATCTGG  92021    T  GCC  A    TG
                                TCA GT   TG CAGTCT  GC
                                ||| ||   || ||||||  ||
                                GGT TA   GC GTCGGG  CG
                                  C  AT_ _    GT
GAM1038  HSPA1L   5'  GCTGGGGCTGCGTAATCTGG  97768    T  GCC  A    TG
                                TCA GT   TG CAGTCT  GC
                                ||| ||   || ||||||  ||
                                GGT TA   GC GTCGGG  CG
                                  C  AT_ _    GT
GAM1038  HSPA6    3'  TCAGGGCTATGCTATGG    76335      T  CTGAC
                                TCATG GC    AGTCTTGG
                                |||||  ||   ||||||||
                                GGTAT CG    TCGGGACT
                                  _  TA___
GAM1038  HSPCB    5'  GTTGGGACTGTCTGGGTAT   23735      _      TG
                                GTGCCT GACAGTCT  GC
                                |||||| ||||||||  ||
                                TATGGG CTGTCAGG  TG
                                   T      GT
GAM1038  HTR1D    3'  GCTGGGATTACAGGCAT    6000       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  HUNK     3'  GCTGAGATTACAGGCGTGA   27456     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGA  CG
                                  __    A_    GT
GAM1038  ICMT     3'  GCTGGGATTGCAGCGTGA    24817     TGC   A    TG
                                TCATG   CTG CAGTCT  GC
                                |||||   ||| ||||||  ||
                                AGTGC   GAC GTTAGG  CG
                                  ___  _     GT
GAM1038  ID1      3'  GCTGAGGCTGAGGCACTGG   70032    T    GA    TG
                                TCA GTGCCT  CAGTCT  GC
                                ||| ||||||  ||||||  ||
```

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                                GGT CACGGA  GTCGGA  CG
                                  _     __      GT
GAM1038  IDH2     3'  GCCAGGGCTGAGCCGGCG    9296      TGA_
                                TGCC    CAGTCTTGGC
                                ||||    ||||||||||
                                GCGG    GTCGGGACCG
                                  CCGA
GAM1038  IDH3B    3'  AGACTGTTGGGTGGTGA     22576     G    TG
                                TCAT TGCC  ACAGTCT
                                |||| ||||  |||||||
                                AGTG GTGG  TGTCAGA
                                  _    GT
GAM1038  IER3     3'  GCTGGGGCTAGGCCCGGTGG   13996     _ T    GAC     TG
                                TCAT G GCCT   AGTCT  GC
                                |||| | ||||   |||||  ||
                                GGTG C CGGA   TCGGG  CG
                                  G C    ___     GT
GAM1038  IFI35    3'  GCCAAGGTTCTCACACTGG    63030     T   CC    C GT
                                TCA GTG  TGA A  CTTGGC
                                ||| |||  ||| |  ||||||
                                GGT CAC  ACT T  GAACCG
                                  _  __   C TG
GAM1038  IGF2R    3'  TGAGGCTGTCAGTGTATGG    6053       TG C
                                TCATG  C TGACAGTCTTG
                                |||||  | ||||||||||
                                GGTAT  G ACTGTCGGAGT
                                   GT _
GAM1038  IGFBP2   3'  GTCGGGGAGCTGGGGTACA    5183        GA   __
                                TGTGCCT  CAGT  CTTGGC
                                |||||||  ||||  ||||||
                                ACATGGG  GTCG  GGGCTG
                                    __    AG
GAM1038  IGHMBP2  3'  GTTAGGATGAGGGTGCTGA    9306     T TG   GACA
                                TCA G  CCT    GTCTTGGC
                                ||| |  |||    ||||||||
                                AGT C  GGG    TAGGATTG
                                  _ GT   AG__
GAM1038  IL11     3'  GCTGGGATTACAGGTGTGA    5328      GT    AC     TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __     A_     GT
GAM1038  IL20RA   5'  GCCGGGGGAGCGCGCGTGG    27048        _ GACAG
                                TCATGTGC CT     TCTTGGC
                                ||||||||  ||    |||||||
                                GGTGCGCG GA     GGGGCCG
                                    C  G____
GAM1038  INHBB    3'  GTCATTCTGTTGGGCTGTGG   9342       T   TG    TCT
                                TCATG GCC  ACAG   TGGC
                                ||||| |||  ||||   ||||
```

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                                GGTGT CGG  TGTC   ACTG
                                  _  GT    TT_
GAM1038  INMT     3'  GCTGGGATTACAGGCGTGA   22274     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  INSM1    5'  CCGGGGCCGAGCGCGGA     9350     A    C  ACA
                                TC TGTGC TG   GTCTTGG
                                || |||||  ||   |||||||
                                AG GCGCG GC   CGGGGCC
                                 _    A  ___
GAM1038  IRAK1    3'  GTCAAGACCAGCCAGGGCAACA 7812       _   GACA__
              TGA                  CATGT GCCT     GTCTTGGC
                                |||||  ||||     ||||||||
                                GTACA CGGG     CAGAACTG
                                   A    ACCGAC
GAM1038  IRF1     5'  GCCGGGACCCTCGCGCGCG   64346      C   CA
                                TGTGC TGA  GTCTTGGC
                                |||||  |||  ||||||||
                                GCGCG GCT  CAGGGCCG
                                   C   CC
GAM1038  IRTA1    3'  GTCAGGATTCAGTTGCAGA   48420    A   GC    CA
                                TC TGT  CTGA  GTCTTGGC
                                ||  |||  ||||  ||||||||
                                AG ACG  GACT  TAGGACTG
                                 _   TT    __
GAM1038  ITGA1    3'  GCTAAGGGTTCCAGTATGTGA  63533        CT  CAG
                                TCATGTGC  GA   TCTTGGC
                                ||||||||  ||   |||||||
                                AGTGTATG  CT   GGAATCG
                                     AC  TG_
GAM1038  ITGA11   3'  GTTGAGACCCAGGCCTGTGG   24206      T    ACA    TG
                                TCATG GCCTG   GTCT  GC
                                |||||  |||||   ||||  ||
                                GGTGT CGGAC   CAGA  TG
                                   C    C__    GT
GAM1038  ITGA2    3'  CGCCAGGGTTTGCTGTTTGCGT 9372    TG CT_     _____
              GCATGG                 G  C   GACAGT    CTTGGC   G
                                |  |   ||||||    ||||||   |
                                C  G   TTGTCG    GGACCG   C
                                 GT CGT      TTTG
GAM1038  ITGAM    3'  GCTGTGGCTCACGTGTGTGA   5288       TG C   CA   T
                                TCATG  C TGA  GTC TGGC
                                |||||  | |||  ||| ||||
                                AGTGT  G ACT  CGG GTCG
                                   GT C   __   T
GAM1038  ITGAM    3'  GTCAAGATTGTGTTTTGA    5290      TGT  CTG
                                TCA   GC   ACAGTCTTGGC
                                |||   ||   ||||||||||
```

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                                AGT  TG  TGTTAGAACTG
                                  TT_ ___
GAM1038 ITGB2   3' GTTGGTGAGGTTAGGTGCGTG 3991     TG    AG _ TG
                                CATG CCTGAC TC T GC
                                |||| |||||| || | ||
                                GTGC GGATTG AG G TG
                                  GT    G_ T GT
GAM1038 ITGB3   3' GTTGGGAGAATGTCAGTATGTG 3997       C   G__ TG
          G                      TCATGTGC TGACA  TCT GC
                                |||||||| |||||  ||| ||
                                GGTGTATG ACTGT  AGG TG
                                     _   AAG  GT
GAM1038 ITPR2   3' GTTGGGACCCAGAGCAATGA  9451     G  _  ACA  TG
                                TCAT TGC CTG  GTCT GC
                                |||| ||| |||  |||| ||
                                AGTA ACG GAC  CAGG TG
                                  _  A  C__   GT
GAM1038 JAG2    3' GCCGAGGCCATGTGCAT    9470     TG C ACA
                                ATG C TG  GTCTTGGC
                                |||  | ||  ||||||||
                                TAC  G AC  CGGAGCCG
                                  GT T ___
GAM1038 JPH2    5' GTCGGGGCTCCCGGGCAT   94451      AC
                                GTGCCTG AGTCTTGGC
                                |||||||  |||||||||
                                TACGGGC TCGGGGCTG
                                    CC
GAM1038 JPH3    3' GCCGGGGCTCTGGGTGTGTG  40307    TG  GAC
                                CATG CCT  AGTCTTGGC
                                |||| |||  |||||||||
                                GTGT GGG  TCGGGGCCG
                                  GT  TC_
GAM1038 JRK     5' GCCAAGGCCTAGGTGTGTGG  86528     TG  ACA
                                TCATG CCTG  GTCTTGGC
                                ||||| ||||  ||||||||
                                GGTGT GGAT  CGGAACCG
                                  GT  C__
GAM1038 JRK     3' GCTGGGACTTGGCACCTGG   86532    T   TGAC   TG
                                TCA GTGCC   AGTCT GC
                                ||| |||||   ||||| ||
                                GGT CACGG   TCAGG CG
                                  C   T___    GT
GAM1038 JRK     3' GCTGGGATTACAGGTGTGA   86533    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG TGGAC TTAGG CG
                                  __   A_   GT
GAM1038 JUP     3' GCTGACCCCTCTGGTGTGTGG 9488     TG T CA_  TT
                                TCATG CC GA  GTC GGC
                                ||||| || ||  ||| |||
```

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                                GGTGT  GG CT   CAG  TCG
                                  GT  T  CCC  __
GAM1038  KCNH1    5'  CCGGGACTGCGTGCG      9523      C  A
                                TGC TG CAGTCTTGG
                                ||| || |||||||||
                                GCG GC GTCAGGGCC
                                  T  _
GAM1038  KCNJ10   3'  GCCAGGGTTTGCCACTGTGA  9537      _  CCT   AGT
                                TCAT GTG   GAC   CTTGGC
                                |||| |||   |||   ||||||
                                AGTG CAC   TTG   GGACCG
                                  T  CGT  ___
GAM1038  KCNMB4   3'  GTCAAGATCTTAGCTGTATGG  27192     GT C    CA
                                TCAT  G CTGA  GTCTTGGC
                                ||||  | ||||  ||||||||
                                GGTA  T GATT  TAGAACTG
                                  TG C   C_
GAM1038  KCNS2    3'  GCCAAGGCTGATGGTATTGG   68308     T    TGA
                                TCA GTGCC   CAGTCTTGGC
                                ||| |||||   ||||||||||
                                GGT TATGG   GTCGGAACCG
                                  _    TA_
GAM1038  KIAA0857 5'  GTTGGGGCGGCGGGCGCG    66677        ACA    TG
                                TGTGCCTG   GTCT  GC
                                ||||||||   ||||  ||
                                GCGCGGGC   CGGG  TG
                                     GG_   GT
GAM1038  KIFC3    5'  GTTGAGAACTGGGCGTGG    18689     GT   TGA   _  TG
                                TCAT  GCC   CAGT CT  GC
                                ||||  |||   |||| ||  ||
                                GGTG  CGG   GTCA GA  TG
                                  __  ___    A  GT
GAM1038  KLHL1    5'  GCCAGGGACAGGGGCGCA    40488        GACAG
                                TGTGCCT    TCTTGGC
                                |||||||    |||||||
                                ACGCGGG    GGGACCG
                                     GACA_
GAM1038  KLHL3    3'  GTTGGGGGGTGAGCGTGTGTGA 87462      TG _  G  AG   TG
                                TCATG  C CT AC  TCT  GC
                                |||||  | || ||  |||  ||
                                AGTGT  G GA TG  GGG  TG
                                   GT C  G  G_   GT
GAM1038  KLRD1    3'  GTCATATACAATTGTCATGTAT 23681       C      CT____
            GTGA                  ATGTGC TGACAGT     TGGC
                                |||||| |||||||     ||||
                                TGTATG ACTGTTA     ACTG
                                   T      ACATAT
GAM1038  KLRD1    3'  GTCATATACAATTGTCATGTAT 9622        C      CT____
            GTGA                  ATGTGC TGACAGT     TGGC
                                |||||| |||||||     ||||
```

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                                TGTATG ACTGTTA     ACTG
                                   T      ACATAT
GAM1038 KNS2    5' GCCAAGGGGACAGCGCGTGG  18691        C  ACAG
                                TCATGTGC TG    TCTTGGC
                                ||||||| ||    |||||||
                                GGTGCGCG AC    GGAACCG
                                    _ AGG_
GAM1038 KRTHA8  5' GTCAAGGTCTAAGCATCTGA  22261    T   CT_  AGT
                                TCA GTGC   GAC   CTTGGC
                                ||| ||||   |||   ||||||
                                AGT TACG   CTG   GAACTG
                                  C   AAT  ___
GAM1038 L1CAM   3' CGGGACTGGGAACAGA     4716     A  G  TGA     TG
                                TC TGT CC   CAGTCT  G
                                || ||| ||   ||||||  |
                                AG ACA GG   GTCAGG  C
                                 _  A  ___     GT
GAM1038 L1CAM   3' CGGGACTGGGAACAGA     43754    A  G  TGA     TG
                                TC TGT CC   CAGTCT  G
                                || ||| ||   ||||||  |
                                AG ACA GG   GTCAGG  C
                                 _  A  ___     GT
GAM1038 LAMC2   3' GCCAAAGAACAGGTGTAT    38149     TG   ACAG   _
                                ATG  CCTG    TCTT GGC
                                |||  ||||    |||| |||
                                TAT  GGAC    AGAA CCG
                                  GT   A___    A
GAM1038 LAMP1   3' GCCAGGACGCGCGACACGTGG  18704        CC  ACA
                                TCATGTG  TG   GTCTTGGC
                                |||||||  ||   ||||||||
                                GGTGCAC  GC   CAGGACCG
                                    A_  GCG
GAM1038 LASS1   3' GCCAGGGCGCGGGCGCGGA   41197    A      ACA
                                TC TGTGCCTG   GTCTTGGC
                                || ||||||||   ||||||||
                                AG GCGCGGGC   CGGGACCG
                                 _      G__
GAM1038 LDB1    5' GCCGAGGCTGTGCGTGCG    13985     C  _
                                TGC TG ACAGTCTTGGC
                                ||| || ||||||||||
                                GCG GC TGTCGGAGCCG
                                  T  G
GAM1038 LDHB    5' GTCAAGGTTGCTGCTGTGTGTG 9716       TG CTGA_  GT
           G                     TCATG  C    CA  CTTGGC
                                 |||||  |    ||  ||||||
                                 GGTGT  G    GT  GAACTG
                                    GT TCGTC  TG
GAM1038 LDLR    5' GCTAGGACACAGCAGGTCGTGA 4991       T    ACA_
                                TCATG GCCTG    GTCTTGGC
                                ||||| |||||    ||||||||
```

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                                AGTGC TGGAC   CAGGATCG
                                  _    GACA
GAM1038 LENG4   5' GCTGGGGCTGTCGACATGA  44166      GCC      TG
                                TCATGT  TGACAGTCT  GC
                                ||||||  |||||||||  ||
                                AGTACA  GCTGTCGGG  CG
                                   ___       GT
GAM1038 LFG     3' GCCAAGAACTGGCGGGT    76720      A   _
                                GCCTG CAGT CTTGGC
                                ||||| |||| ||||||
                                TGGGC GTCA GAACCG
                                  G   A
GAM1038 LFNG    5' GCTCTTTGTGTGGGTGTGTGA 92642     TG   _   TCTT
                                TCATG  CCTG ACAG   GGC
                                |||||  |||| ||||   |||
                                AGTGT  GGGT TGTT   TCG
                                  GT   G   TC__
GAM1038 LFNG    3' GCTGGGTCTGGGGGTGCGTGA 92643     TG  GA  T  TG
                                TCATG  CCT  CAG CT  GC
                                |||||  |||  ||| ||  ||
                                AGTGC  GGG  GTC GG  CG
                                  GT   G_   T  GT
GAM1038 LHX5    5' GCCGGGGCGTGCGGCCCGTGG 42305     T   T ACA
                                TCATG GCC G   GTCTTGGC
                                ||||| ||| |   ||||||||
                                GGTGC CGG C   CGGGGCCG
                                  C  _ GTG
GAM1038 LIF     3' GCTGGGGCCAGGCGAGTGG   9737     G    ACA   TG
                                TCAT TGCCTG   GTCT  GC
                                |||| ||||||   ||||  ||
                                GGTG GCGGAC   CGGG  CG
                                  A     ___    GT
GAM1038 LIG1    3' GTCAGGGGAGGGGTGTGTG   4076     TG   GACAG
                                CATG  CCT    TCTTGGC
                                ||||  |||    |||||||
                                GTGT  GGG    GGGACTG
                                  GT   GAG__
GAM1038 LIG3    5' GCCAGGGTTGCATGTGG     9753       CTGAC GT
                                TCATGTGC    A  CTTGGC
                                ||||||||    |  ||||||
                                GGTGTACG    T  GGACCG
                                     _____ TG
GAM1038 LIG3    5' GCCAGGGTTGCATGTGG     25666      CTGAC GT
                                TCATGTGC    A  CTTGGC
                                ||||||||    |  ||||||
                                GGTGTACG    T  GGACCG
                                     _____ TG
GAM1038 LIMD1   3' GCTGGGGCTGGGGAAGTGA   26461     GTG  GA    TG
                                TCAT   CCT  CAGTCT  GC
                                ||||   |||  ||||||  ||
```

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                                AGTG  GGG  GTCGGG  CG
                                  AA_  __     GT
GAM1038  LIMD1    3'  GTCAAGATTTGAAATAGGT   26464      A__  _
                                GCCTG  CAG TCTTGGC
                                |||||  ||| |||||||
                                TGGAT  GTT AGAACTG
                                   AAA  T
GAM1038  LMO7     3'  GCCATATTTCAGTATGTGG   18090       C  C  CT
                                TCATGTGC TGA AGT  TGGC
                                |||||||| ||| |||  ||||
                                GGTGTATG ACT TTA  ACCG
                                     _  _  T_
GAM1038  LMO7     3'  GCCATATTTCAGTATGTGG   31766       C  C  CT
                                TCATGTGC TGA AGT  TGGC
                                |||||||| ||| |||  ||||
                                GGTGTATG ACT TTA  ACCG
                                     _  _  T_
GAM1038  LPIN2    3'  GCCCCTTGTCAGGCTGTGA   27709      T       TCTT
                                TCATG GCCTGACAG   GGC
                                ||||| |||||||||   |||
                                AGTGT CGGACTGTT   CCG
                                   _       CC__
GAM1038  LPO      3'  GTCAAGACTTAGCCCCGCTGA  67868    T  C__  AC
                                TCA GTG  CTG  AGTCTTGGC
                                ||| |||  |||  |||||||||
                                AGT CGC  GAT  TCAGAACTG
                                  _  CCC  __
GAM1038  LRP4     3'  GCTGGGACATGGGGGTGTGG  64442    TG G   ACA   TG
                                TCA  T CCTG  GTCT  GC
                                |||  | ||||  ||||  ||
                                GGT  G GGGT  CAGG  CG
                                  GT G   A__   GT
GAM1038  LRRC2    5'  GCCAGGACTGTCAGTGCCCG  44471    T  _
                                TG GC CTGACAGTCTTGGC
                                || || ||||||||||||||
                                GC CG GACTGTCAGGACCG
                                 C  T
GAM1038  LRRC2    5'  GTTAGCGCACAGGCACGGGA  44478    A      ACA  C
                                TC TGTGCCTG  GT TTGGC
                                || ||||||||  || |||||
                                AG GCACGGAC  CG GATTG
                                 G      A__  C
GAM1038  LTB4R    5'  GCTGAGACTACAGGCACATG  5649         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTACACGGAC  TCAGA  CG
                                      A_    GT
GAM1038  LUZP1    3'  CCGGGGCTTACACTGG     53298     T  CCTGAC
                                TCA GTG     AGTCTTGG
                                ||| |||     ||||||||
```

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                                GGT CAC     TCGGGGCC
                                  _  AT____
GAM1038 LYAAT1   5' GCCAAGACTGACAGCA     54349    C  A
                                TGC TG CAGTCTTGGC
                                ||| || ||||||||||
                                ACG AC GTCAGAACCG
                                  _  A
GAM1038 LYL1     5' GCCGGGGCCTGGAGCATTGA  18758    T   CTGA  _
                                TCA GTGC   CAG TCTTGGC
                                ||| ||||   ||| |||||||
                                AGT TACG   GTC GGGGCCG
                                  _   AG__  C
GAM1038 LYZ      3' GCTGGGATTACAGGCGTGA   4105     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 LZTS1    3' GCTGAGATTGCAGATGTGA   40692     GC   A    TG
                                TCATGT  CTG CAGTCT  GC
                                ||||||  ||| ||||||  ||
                                AGTGTA  GAC GTTAGA  CG
                                   __  _    GT
GAM1038 MADH3    3' GCTGAGGCCCAGTGCATATG  19738      _  ACA   TG
                                CATGTGC CTG  GTCT  GC
                                ||||||| |||  ||||  ||
                                GTATACG GAC  CGGA  CG
                                    T  C__   GT
GAM1038 MAK      3' GCTGGGATTAGAGGCGTGTG  19762   TG    GAC    TG
                                CA  TGCCT   AGTCT  GC
                                ||  |||||   |||||  ||
                                GT  GCGGA   TTAGG  CG
                                 GT    GA_    GT
GAM1038 MAN2A1   5' GCCGGAGACTAGGTGCGGA   9894    A  TG   GAC    _
                                TC TG  CCT   AGTCTT GGC
                                || ||  |||   |||||| |||
                                AG GC  GGA   TCAGAG CCG
                                 _ GT  ____    G
GAM1038 MAN2A2   5' GCCGGGCGCTGACGGTGTGTGT 20397     TG _  A   _
            GG                   TCATG  C CTG CAGT CTTGGC
                                |||||  | ||| |||| ||||||
                                GGTGT  G GGC GTCG GGGCCG
                                   GT T   A   C
GAM1038 MAP3K12  3' TAGGAGACTGATAGCATGTGA  20865       C  A     GGC
                                TCATGTGC TG CAGTCTT
                                |||||||| || |||||||
                                AGTGTACG AT GTCAGAG
                                    _ A      GATT
GAM1038 MAPK3    3' CCGGGGTGGAGCATGG      73383       GCCTGA  G
                                TCATGT     CA TCTTGG
                                ||||||     || ||||||
```

```
                                GGTACG     GT GGGGCC
                                   AG____  _
GAM1038  MAPK8IP1  5'  GCCAGGGCTGTGCCCGAGA   18403    A  T  CTG
                                TC TG GC   ACAGTCTTGGC
                                || || ||   ||||||||||
                                AG GC CG   TGTCGGGACCG
                                 A  C  ___
GAM1038  MAPK9     3'  GTTGAGATGTATGTGCATGTGA 10854        CTG_  G  TG
                                TCATGTGC    ACA TCT  GC
                                ||||||||    ||| |||  ||
                                AGTGTACG    TGT AGA  TG
                                     TGTA   _   GT
GAM1038  MAPK9     3'  GTTGAGATGTATGTGCATGTGA 57414        CTG_  G  TG
                                TCATGTGC    ACA TCT  GC
                                ||||||||    ||| |||  ||
                                AGTGTACG    TGT AGA  TG
                                     TGTA   _   GT
GAM1038  MAPK9     3'  GTTGAGATGTATGTGCATGTGA 57419        CTG_  G  TG
                                TCATGTGC    ACA TCT  GC
                                ||||||||    ||| |||  ||
                                AGTGTACG    TGT AGA  TG
                                     TGTA   _   GT
GAM1038  MAPK9     3'  GTTGAGATGTATGTGCATGTGA 57424        CTG_  G  TG
                                TCATGTGC    ACA TCT  GC
                                ||||||||    ||| |||  ||
                                AGTGTACG    TGT AGA  TG
                                     TGTA   _   GT
GAM1038  MATN1     5'  GCTGGGCGGGCAGTGG      9923       G     A_
                                TCAT TGCCTG  CAGT
                                |||| ||||||  ||||
                                GGTG ACGGGC  GTCG
                                   _     GG
GAM1038  MATN4     3'  GTCGGGGCGGAGGCGCTGG    13823     T     GACA
                                TCA GTGCCT    GTCTTGGC
                                ||| ||||||    ||||||||
                                GGT CGCGGA    CGGGGCTG
                                  _     GG__
GAM1038  MATN4     3'  GTCGGGGCGGAGGCGCTGG    47588     T     GACA
                                TCA GTGCCT    GTCTTGGC
                                ||| ||||||    ||||||||
                                GGT CGCGGA    CGGGGCTG
                                  _     GG__
GAM1038  MB        3'  GCTGGGGCTGGGGTGTTGA    18115     T TG  GA     TG
                                TCA G  CCT  CAGTCT  GC
                                ||| |  |||  ||||||  ||
                                AGT T  GGG  GTCGGG  CG
                                  _ GT   __     GT
GAM1038  MBTPS1    5'  GCTGAGGCTCCCAGCTGTGG   13705      T  C  AC    TG
                                TCATG GC TG  AGTCT  GC
                                ||||| || ||  |||||  ||
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                                GGTGT CG AC  TCGGA  CG
                                  _ _ CC    GT
GAM1038  MDM2    3'  GCTGGGATTACAGGCAT    9972        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  MDM2    3'  GCTGGGATTACAGGCAT    22510       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  MDM2    3'  GCTGGGATTACAGGCAT    22514       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  MDM2    3'  GCTGGGATTACAGGCAT    22518       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  MDM2    3'  GCTGGGATTACAGGCAT    22522       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  MEFV    3'  GCTGGGATTACAGGCAT    4146        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  MEFV    3'  GCTGGGATTACAGGTGCGTG  4147      TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGC  GGAC  TTAGG  CG
                                  GT   A_    GT
GAM1038  MFAP2   5'  GCCAGGGTGGGAGCAGTGA   33922     G  _  G  AGT
                                TCAT TGC CT AC   CTTGGC
                                |||| ||| || ||   ||||||
                                AGTG ACG GG TG   GGACCG
                                  _   A  G  ___
GAM1038  MFAP4   3'  GCCAAGGTAGGCATGCATATGA 69255        C  ACAG
                                TCATGTGC TG    TCTTGGC
                                ||||||||  ||    |||||||
                                AGTATACG AC    GGAACCG
                                    T  GGAT
GAM1038  MGA     3'  ACTGTCAGGATATGA      62803       G
                                TCATGT CCTGACAGT
                                ||||||  |||||||||
```

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                                AGTATA GGACTGTCA
                                  _
GAM1038 MGAT1    5' GTCGGGAGGACCTGGTGCATGG 10011      TG  TGACAG
                                TCATG  CC     TCTTGGC
                                |||||  ||     |||||||
                                GGTAC  GG     AGGGCTG
                                   GT  TCCAGG
GAM1038 MGAT3    5' GCTGAGACCCAGCGGGCGATGG 10016     G     ACA_   TG
                                TCAT TGCCTG   GTCT  GC
                                |||| ||||||   ||||  ||
                                GGTA GCGGGC   CAGA  CG
                                  _    GACC   GT
GAM1038 MHC2TA   3' GCTGGGACTACAGGTGTGA   4178      GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TCAGG  CG
                                  __    A_    GT
GAM1038 MHC2TA   3' GCTGGGATTACAGGTGTGA   4179      GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 MLC1     3' GTCAGAATTAGGCACTTGG   57595    T      CAG   T
                                TCA GTGCCTGA   TCT GGC
                                |||  ||||||||   ||| |||
                                GGT CACGGATT   AGA CTG
                                  T      A__   _
GAM1038 MLC1     3' GTCAGAATTAGGCACTTGG   30782    T      CAG   T
                                TCA GTGCCTGA   TCT GGC
                                |||  ||||||||   ||| |||
                                GGT CACGGATT   AGA CTG
                                  T      A__   _
GAM1038 MLLT7    3' GCCAAGGTCTGAGCACTGG   19861    T   CTGA  _
                                TCA GTGC   CAG TCTTGGC
                                |||  ||||   ||| |||||||
                                GGT CACG   GTC GGAACCG
                                  _   A___   T
GAM1038 MMP15    3' GCCCACAGTGTCAGGCACTGG  10074    T       GTCTT
                                TCA GTGCCTGACA    GGC
                                |||  ||||||||||    |||
                                GGT CACGGACTGT    CCG
                                  _       GACAC
GAM1038 MPL      3' GCTGGGATTACAGGTGTGA   18149     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 MPL      3' GTTAGGATTACAGGCAT     18150       AC
                                GTGCCTG  AGTCTTGGC
                                |||||||  |||||||||
```

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                                TACGGAC  TTAGGATTG
                                   A_
GAM1038  MPP2    3'  GCTGGGTTGGAACAGGTGTGTG 59824     TG   A__  T  TG
                                CATG  CCTG   CAG CT  GC
                                ||||  ||||   ||| ||  ||
                                GTGT  GGAC   GTT GG  CG
                                  GT    AAG   _  GT
GAM1038  MRPL49   3'  GTTGGGATTATAGGCAT    69573       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGG  TG
                                   A_    GT
GAM1038  MSF     3'  GCCAGGGCCCAGGCCATG    88085     T    ACA
                                CATG GCCTG   GTCTTGGC
                                |||| |||||   ||||||||
                                GTAC CGGAC   CGGGACCG
                                  _    C__
GAM1038  MSF     3'  GTTGGGGCACTGGGCGTCTGA  88087    TG    ACA   TG
                                TCA  TGCCTG   GTCT  GC
                                |||  ||||||   ||||  ||
                                AGT  GCGGGT   CGGG  TG
                                  CT     CA_   GT
GAM1038  MSL3L1   3'  GCTAAAACAGGTGCCATGA   54368     _ TG   ACAGTC
                                TCAT G  CCTG     TTGGC
                                |||| |  ||||     |||||
                                AGTA C  GGAC     AATCG
                                  C GT   AA____
GAM1038  MSLN    3'  CCAGGAGCAGGCACG      19502       ACAG
                                TGTGCCTG   TCTTGG
                                ||||||||   ||||||
                                GCACGGAC   AGGACC
                                   G___
GAM1038  MSLN    3'  CCAGGAGCAGGCACG      25496       ACAG
                                TGTGCCTG   TCTTGG
                                ||||||||   ||||||
                                GCACGGAC   AGGACC
                                   G___
GAM1038  MTCP1   5'  GTCGGGGCGGAGGGCGGTGG  26433     G   GACA
                                TCAT TGCCT   GTCTTGGC
                                |||| |||||   ||||||||
                                GGTG GCGGG   CGGGGCTG
                                  _    AGG_
GAM1038  MTR     3'  GCTGGGATTACAGGCGTGA   4213     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  MUCDHL  3'  GCCAGAGGGCGGGTACA    48371       ACAG  T
                                TGTGCCTG   TCT GGC
                                |||||||   ||| |||
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                                ACATGGGC   AGA CCG
                                    GGG_  _
GAM1038  MYBL1    3'  GTTATAGATAGGTGTATGA   64074      TG  GACA  _
                                TCATG  CCT   GTCT TGGC
                                |||||  |||   |||| ||||
                                AGTAT  GGA   TAGA ATTG
                                   GT  ____   T
GAM1038  MYBPC2   3'  GCCAAGACAATTGGTGGTGG  15771     G   TGACA
                                TCAT TGCC    GTCTTGGC
                                |||| ||||    ||||||||
                                GGTG GTGG    CAGAACCG
                                  _   TTAA_
GAM1038  MYO9A    3'  GCTAAGACTGTATGTGCTGA  22582     T TG CTG
                                TCA G  C   ACAGTCTTGGC
                                ||| |  |   ||||||||||
                                AGT C  G   TGTCAGAATCG
                                  _ GT TA_
GAM1038  MYOM2    3'  GTCGAGGCTTTGAAGCATGTG  14268       CTGAC
                                CATGTGC    AGTCTTGGC
                                |||||||    |||||||||
                                GTGTACG    TCGGAGCTG
                                    AAGTT
GAM1038  NAP1L4   3'  GCCGAGGTCTGGTGATGTGG  19921       _  T  AGT
                                TCATGT GCC GAC   CTTGGC
                                |||||| ||| |||   ||||||
                                GGTGTA TGG CTG   GAGCCG
                                   G   T  ___
GAM1038  NAP1L4   3'  GTCGGGACTCCAGGCCTGTGG  19923     T    AC
                                TCATG GCCTG  AGTCTTGGC
                                |||||  |||||  |||||||||
                                GGTGT CGGAC  TCAGGGCTG
                                   C    C_
GAM1038  NCOA6    5'  GCTGGGACTGCAGGCATGTG  25972        A     TG
                                CATGTGCCTG CAGTCT  GC
                                ||||||||||  ||||||  ||
                                GTGTACGGAC GTCAGG  CG
                                      _     GT
GAM1038  NCOA6    5'  GCTGGGATTACAGGTGTGA   25973     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  NCOA6    5'  GCTGGGATTACAGGTGTGA   25974     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  NDRG1    3'  GTCGAGGCTAGAGGCATTTGG  59571    T     GAC
                                TCA GTGCCT   AGTCTTGGC
                                ||| ||||||   |||||||||
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                                GGT TACGGA   TCGGAGCTG
                                  T     GA_
GAM1038  NDRG2    3'  GTTAAGGTGGAGAGGGCATATG 32719         GA__  G
                                CATGTGCCT    CA TCTTGGC
                                |||||||||    || |||||||
                                GTATACGGG    GT GGAATTG
                                     AGAG  _
GAM1038  NDRG3    3'  GCTGGGATTACAGGCAT     49300        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  NEK6     5'  GCCGAGCTGACGGGCG      26932        A   T
                                TGCCTG CAG CTTGGC
                                |||||| ||| ||||||
                                GCGGGC GTC GAGCCG
                                   A  _
GAM1038  NEU3     5'  GCTGAGATTGTAGGCATA    21851         A     TG
                                TGTGCCTG CAGTCT  GC
                                |||||||| ||||||  ||
                                ATACGGAT GTTAGA  CG
                                     _     GT
GAM1038  NFE2L1   5'  GCCAGGGTGGGGTACG      12173        G  AGT
                                TGTGCCT AC   CTTGGC
                                ||||||| ||   ||||||
                                GCATGGG TG   GGACCG
                                   G  ___
GAM1038  NFE2L1   3'  GCTGTTGAGCACATGA      12174         CT
                                TCATGTGC  GACAGT
                                ||||||||  ||||||
                                AGTACACG  TTGTCG
                                     AG
GAM1038  NHLH1    3'  GCTGAGGCCCAGCTGTGCAGA  18803    A  TG __   ACA    TG
                                TC TG  C  CTG   GTCT  GC
                                || ||  |  |||   ||||  ||
                                AG AC  G  GAC   CGGA  CG
                                 _  GT TC   C__    GT
GAM1038  NOLA1    5'  GCCAGGGCCAGAGGGGCACGTG 38606          GACA_
              G                  TCATGTGCCT    GTCTTGGC
                                 ||||||||||    ||||||||
                                 GGTGCACGGG    CGGGACCG
                                      GAGAC
GAM1038  NP       3'  GCTGGGATTACAGGTGTGA   4250       GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038  NPHS1    3'  GCCAGGAGTAGTGGCGCATG   16191         TG_  AG
                                CATGTGCC   AC  TCTTGGC
                                ||||||||   ||  |||||||
```

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                                GTACGCGG  TG  AGGACCG
                                    TGA  __
GAM1038  NPR2L    3'  GCTGGGATTACAGGCAT    21561       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  NQO1     3'  GCTGGGATTACAGGCGTGA   6162      GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  NRAS     5'  GCCGGGGCGGGGACTCAGGCGC 10274   T      CA____
             CTGG                  A GTGCCTGA     GTCTTGGC
                                | ||||||||     ||||||||
                                T CGCGGACT     CGGGGCCG
                                 C       CAGGGG
GAM1038  NRXN2    3'  CCAGGCAGGGCACGTG     57010        GACAGT
                                CATGTGCCT     CTTGG
                                |||||||||     |||||
                                GTGCACGGG     GGACC
                                    AC____
GAM1038  NRXN2    3'  CCAGGCAGGGCACGTG     57021        GACAGT
                                CATGTGCCT     CTTGG
                                |||||||||     |||||
                                GTGCACGGG     GGACC
                                    AC____
GAM1038  NRXN2    3'  CCAGGCAGGGCACGTG     30624        GACAGT
                                CATGTGCCT     CTTGG
                                |||||||||     |||||
                                GTGCACGGG     GGACC
                                    AC____
GAM1038  NT5C2    3'  GCTGAACTGCATGTATATGG   24239        C  A    C TG
                                TCATGTGC TG CAGT T  GC
                                |||||||| || |||| |  ||
                                GGTATATG AC GTCA A  CG
                                    T  _   _ GT
GAM1038  NYX      5'  TCAGGGCTGTAGCCTGA     42605     TGT  CTG
                                TCA   GC   ACAGTCTTGG
                                |||   ||   ||||||||||
                                AGT   CG   TGTCGGGACT
                                  C__  A__
GAM1038  OCRL     5'  GCCGAGGTGGGTGGGTGTGG   7827      GT    A_  G
                                TCAT  GCCTG  CA TCTTGGC
                                ||||  |||||  || |||||||
                                GGTG  TGGGT  GT GGAGCCG
                                  __    GG  _
GAM1038  OCRL     5'  GCCGAGGTGGGTGGGTGTGG   4261      GT    A_  G
                                TCAT  GCCTG  CA TCTTGGC
                                ||||  |||||  || |||||||
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                                GGTG  TGGGT  GT GGAGCCG
                                  __    GG  _
GAM1038  OPA3    3'  GCCAAGATTGTACCAC     47109     CCTG
                                GTG   ACAGTCTTGGC
                                |||   ||||||||||
                                CAC   TGTTAGAACCG
                                  CA__
GAM1038  OPHN1   3'  GCCAAGGTTGTAGCATGG    10358      GCCTG  GT
                                TCATGT    ACA  CTTGGC
                                ||||||    |||  ||||||
                                GGTACG    TGT  GAACCG
                                   A____  TG
GAM1038  OPRD1   5'  GCCGGGGCGCGGCACGCGG   6191     A     TGACA
                                TC TGTGCC    GTCTTGGC
                                || ||||||    ||||||||
                                GG GCACGG    CGGGGCCG
                                 C     CG___
GAM1038  ORC1L   3'  GCTGAAACTACAGGCACATG   14738         AC   C TG
                                CATGTGCCTG  AGT T  GC
                                ||||||||||  ||| |  ||
                                GTACACGGAC  TCA A  CG
                                      A_   A GT
GAM1038  OVOL1   3'  GCCGAGGCTGTTCTGAGCCTGG 15859     T  GCCT
                                TCA GT    GACAGTCTTGGC
                                ||| ||    ||||||||||||
                                GGT CG    TTGTCGGAGCCG
                                  C  AGTC
GAM1038  OXCT    3'  CCAAGAAGGGCTGTGG      4752       T   GACAG
                                TCATG GCCT    TCTTGG
                                ||||| ||||    ||||||
                                GGTGT CGGG    AGAACC
                                   _   A____
GAM1038  OXTR    3'  GCCAGGGCCTGGAGGCTGTGA  6210       T   GA  _
                                TCATG GCCT  CAG TCTTGGC
                                ||||| ||||  ||| |||||||
                                AGTGT CGGA  GTC GGGACCG
                                   _   G_  C
GAM1038  P3      3'  CGAGTTAGGTAGGTGG      39065      G      AGTC TG
                                TCAT TGCCTGAC    T  G
                                |||| ||||||||    |  |
                                GGTG ATGGATTG    A  C
                                  G       ____ GT
GAM1038  PA2G4   3'  GCTGAATTTGAGGTACATGA   71300         GA   TC TG
                                TCATGTGCCT  CAG  T  GC
                                ||||||||||  |||  |  ||
                                AGTACATGGA  GTT  A  CG
                                      __   TA GT
GAM1038  PAICS   3'  GCTAGGGTTACAGACATGA   21257       GC   AC GT
                                TCATGT  CTG  A  CTTGGC
                                ||||||  |||  |  ||||||
```

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                                AGTACA  GAC  T  GGATCG
                                   __   A_ TG
GAM1038  PBP      3'  CTGTTGTTGGGACATGG     10382       G  TG    TCT
                                TCATGT CC  ACAG   TGG
                                ||||||  ||  ||||   |||
                                GGTACA GG  TGTT   GTC
                                   _  GT   ___
GAM1038  PCDHA9   3'  GCTGGGATTACAGGCGTGA   25765     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038  PCDHA9   3'  GCTGGGATTATAGGCACATG   25766         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTACACGGAT  TTAGG  CG
                                      A_    GT
GAM1038  PCDHB9   3'  GCTGGGATTTACAGGCAT    38942       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    AT    GT
GAM1038  PCLO     3'  TATCAGATGTGTTGGGCATGTG 94228         TG  _   TGGC
            A                    TCATGTGCC  ACA GTCT
                                |||||||||  |||  ||||
                                AGTGTACGG  TGT TAGA
                                     GT   G    CTATG
GAM1038  PCMT1    3'  GTTAAGATTCTTGGTATTTGG  18225     T    TGAC
                                TCA GTGCC    AGTCTTGGC
                                |||  |||||    |||||||||
                                GGT TATGG    TTAGAATTG
                                  T    TTC_
GAM1038  PCOLN3   3'  GCTGGGGTTGGGGCTGCTGTGA 10911      _  _   GA  GT  TG
                                TCAT GT GCCT  CA  CT  GC
                                ||||  ||  ||||  ||  ||  ||
                                AGTG CG CGGG  GT  GG  CG
                                  T  T   __  TG  GT
GAM1038  PDE6B    3'  GCTGGGATTACAGGCAT     4286        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  PDE7A    3'  GCCAAGGTTTCCAAGTGAGTGA 65522      G   C  AC GT
                                TCAT TGC TG  A  CTTGGC
                                ||||  |||  ||  |  ||||||
                                AGTG GTG AC  T  GAACCG
                                  A   A  CT TG
GAM1038  PDGFRA   3'  CCAAGGAAAGGCATGT      20595        GACAG
                                ATGTGCCT    TCTTGG
                                ||||||||    ||||||
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                                TGTACGGA    GGAACC
                                    AA___
GAM1038 PDGFRB   3' GTCAGGGTTGTAGCCAAGA   65980   A T CTG  GT
                                TC TG GC   ACA  CTTGGC
                                || || ||   |||  ||||||
                                AG AC CG   TGT  GGACTG
                                 A  _ A__   TG
GAM1038 PER2     3' GCTGGGATTACAGGCGTGA   43037     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038 PGK1     3' GTCAAGATTCAGCTAGTGG   4303      GT  C   CA
                                TCAT  GC TGA  GTCTTGGC
                                ||||  || |||  ||||||||
                                GGTG  CG ACT  TAGAACTG
                                  AT  _  __
GAM1038 PGLS     3' GCTGGGACCAGGCACGCGG   23885    A      ACA   TG
                                TC TGTGCCTG   GTCT  GC
                                || ||||||||   ||||  ||
                                GG GCACGGAC   CAGG  CG
                                 C       ___    GT
GAM1038 PIGR     3' GCTGGGACTACAGATGTGG   72603      GC   AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                GGTGTA  GAC  TCAGG  CG
                                   __   A_    GT
GAM1038 PIGR     3' GCTGGGATTACAGGCGTGA   72604     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038 PIGR     3' GTTGAGAGAACCTCAGGTACGG 72605    A       CAG__   TG
            A                    TC TGTGCCTGA    TCT  GC
                                || |||||||||    |||  ||
                                AG GCATGGACT    AGA  TG
                                 _       CCAAG   GT
GAM1038 PIK3C2B  3' GCTGGGATTACAGGCATGTG   10571         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTACGGAC  TTAGG  CG
                                     A_    GT
GAM1038 PIK3C2B  3' GCTGGGATTACAGGCGTGA   10572     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038 PIK3CD   3' GCTGGGATTACAGGCAT     17247       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
```

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                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  PITX2    5'  GTCAGGGCTGCCGCGTGG    4380        CCTGA
                                TCATGTG    CAGTCTTGGC
                                |||||||    ||||||||||
                                GGTGCGC    GTCGGGACTG
                                   C_____
GAM1038  PKIG     5'  GCCGGCGGCCCAGGCACGGA   22961    A      ACA  _
                                TC TGTGCCTG   GTC TTGGC
                                || ||||||||   ||| |||||
                                AG GCACGGAC   CGG GGCCG
                                 _      C__  C
GAM1038  PLA2G10  5'  GCTGGGATTACAGGCGTGA   13089     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  PLDN     5'  GCCAACTCTCGAGCGCGTGA   24744       C   C   CT
                                TCATGTGC TGA AGT  TGGC
                                |||||||| ||| |||  ||||
                                AGTGCGCG GCT TCA  ACCG
                                    A  C  __
GAM1038  PLOD3    5'  GCTGGGATCCAGGCGCGT    6556         ACA   TG
                                ATGTGCCTG   GTCT  GC
                                |||||||||   ||||  ||
                                TGCGCGGAC   TAGG  CG
                                    C__    GT
GAM1038  PML      3'  GTCAGGGTTGTCCGCTCTGA   52658    TGT  CT   GT
                                TCA   GC  GACA  CTTGGC
                                |||   ||  ||||  ||||||
                                AGT   CG  CTGT  GGACTG
                                  CT_  C_   TG
GAM1038  PML      3'  GCCAGGATCTAAGCCCATGA   52662     T  C  ACA
                                TCATG GC TG   GTCTTGGC
                                ||||| || ||   ||||||||
                                AGTAC CG AT   TAGGACCG
                                   C  A  C__
GAM1038  PML      3'  GCCAGGATCTAAGCCCATGA   52668     T  C  ACA
                                TCATG GC TG   GTCTTGGC
                                ||||| || ||   ||||||||
                                AGTAC CG AT   TAGGACCG
                                   C  A  C__
GAM1038  PML      3'  GCCAGGATCTAAGCCCATGA   52674     T  C  ACA
                                TCATG GC TG   GTCTTGGC
                                ||||| || ||   ||||||||
                                AGTAC CG AT   TAGGACCG
                                   C  A  C__
GAM1038  PML      3'  GCCAGGATCTAAGCCCATGA   52677     T  C  ACA
                                TCATG GC TG   GTCTTGGC
                                ||||| || ||   ||||||||
```

```
                                AGTAC CG AT   TAGGACCG
                                  C  A  C__
GAM1038  POU2AF1  3'  GCTGGGATCACAGGCGTGA   20654     GT    ACA   TG
                                TCAT  GCCTG   GTCT  GC
                                ||||  |||||   ||||  ||
                                AGTG  CGGAC   TAGG  CG
                                  __    AC_   GT
GAM1038  POU2AF1  3'  GCTGGGATTACAGGTGCATG  20655     TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTAC  GGAC  TTAGG  CG
                                  GT   A_    GT
GAM1038  POU2AF1  5'  GCTGGGGCGCGCACAGTGG   20656    _    CTGACA   TG
                                TCA TGTGC     GTCT  GC
                                |||  |||||     ||||  ||
                                GGT ACACG     CGGG  CG
                                  G    CG____   GT
GAM1038  POU2F2   5'  GTTGGGCCTGGGGCAGATGA   10691     G    GA   T  TG
                                TCAT TGCCT  CAG CT  GC
                                ||||  |||||  |||  ||  ||
                                AGTA ACGGG  GTC GG  TG
                                  G     __   C  GT
GAM1038  PPEF2    3'  GCTGGGATTACAGGCAT    20672       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  PPEF2    3'  GTTGGGGTGTTGTGTATG    20673     TG CT   G   TG
                                CATG  C  GACA TCT  GC
                                ||||  |  ||||  |||  ||
                                GTAT  G  TTGT GGG  TG
                                  GT __    _   GT
GAM1038  PPID     3'  GCTGGGATTACAGGCACGTG  87434        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGCACGGAC  TTAGG  CG
                                     A_    GT
GAM1038  PPID     3'  GCTGGGATTACAGGTGTGA   87435     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  PPIF     3'  GCCAGGGTGCTGGCATGGTGG  19170     _    TGA  G
                                TCAT GTGCC   CA TCTTGGC
                                |||| |||||   || |||||||
                                GGTG TACGG   GT GGGACCG
                                  G    TC_  _
GAM1038  PPP1CB   3'  GTCAAGACTAAGTATGT     10713       CTGAC
                                ATGTGC    AGTCTTGGC
                                ||||||    |||||||||
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                                TGTATG    TCAGAACTG
                                  AA___
GAM1038 PPP1R2   5' GTCGGGGTCGTTGTGTCGTGA 20693      T C   AG
                                TCATG GC TGAC  TCTTGGC
                                ||||| || ||||  |||||||
                                AGTGC TG GTTG  GGGGCTG
                                  _ T   CT
GAM1038 PPP2R4   3' GCTGGGGTGGGGTGGGTGG   60560     G    G  AGT  TG
                                TCAT TGCCT AC   CT  GC
                                |||| ||||| ||   ||  ||
                                GGTG GTGGG TG   GG  CG
                                  G    G ___ GT
GAM1038 PPP3CA   3' GCTGAGGCAACTATGGCATAGA 6271     A     TGACA_   TG
                                TC TGTGCC     GTCT  GC
                                || ||||||     ||||  ||
                                AG ATACGG     CGGA  CG
                                 _     TATCAA    GT
GAM1038 PPP3CB   3' TCAAGACTGCATGTTGA     40900     TGT  C  A
                                TCA   GC TG CAGTCTTGG
                                |||   || || |||||||||
                                AGT   TG AC GTCAGAACT
                                  ___  T  _
GAM1038 PRKAR2A  5' CCGGGGCCGTGCGCG      14776      CTG  A
                                TGTGC   AC GTCTTGG
                                |||||   || |||||||
                                GCGCG   TG CGGGGCC
                                  ___  C
GAM1038 PRKCABP  5' CCGGGACCCGGCTGTGG     24830      T   TGACA
                                TCATG GCC    GTCTTGG
                                ||||| |||    |||||||
                                GGTGT CGG    CAGGGCC
                                  _  CC___
GAM1038 PRKCABP  3' GCCGGGGGCAGGGTGCGTGG  24831      TG   GACAG
                                TCATG  CCT    TCTTGGC
                                |||||  |||    |||||||
                                GGTGC  GGG    GGGGCCG
                                  GT   ACG__
GAM1038 PRKR     3' GCTGGATTACAGGCATGTG   10884         AC    T
                                CATGTGCCTG  AGTCT GGC
                                ||||||||||  ||||| |||
                                GTGTACGGAC  TTAGG TCG
                                    A_    _
GAM1038 PRX      3' GCCAGGCGAGGCGGGTGCTGA 40532     T TG    ACA_   T
                                TCA G  CCTG    GTCT GGC
                                ||| |  ||||    |||| |||
                                AGT C  GGGC    CGGA CCG
                                 _ GT    GGAG   _
GAM1038 PSMD9    3' GCTGGGATCACAGGCGTGA   10987     GT    ACA   TG
                                TCAT  GCCTG   GTCT  GC
                                ||||  |||||   ||||  ||
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                                AGTG  CGGAC   TAGG  CG
                                  __    AC_   GT
GAM1038  PTAFR    3'  TCAGGGCCAGGTGCAGA    6300    A  TG   ACA
                                TC TG  CCTG   GTCTTGG
                                || ||  ||||   |||||||
                                AG AC  GGAC   CGGGACT
                                 _  GT   ___
GAM1038  PTBP1    3'  GCCTGTGTCGGGCGTGG    11008    GT     GTCTT
                                TCAT  GCCTGACA    GGC
                                ||||  ||||||||    |||
                                GGTG  CGGGCTGT    CCG
                                  __      GT___
GAM1038  PTBP1    3'  GCCTGTGTCGGGCGTGG    49253    GT     GTCTT
                                TCAT  GCCTGACA    GGC
                                ||||  ||||||||    |||
                                GGTG  CGGGCTGT    CCG
                                  __      GT___
GAM1038  PTGES    3'  GCTGGGATTACAGGCGCGT   16862       AC    TG
                                ATGTGCCTG  AGTCT  GC
                                |||||||||  |||||  ||
                                TGCGCGGAC  TTAGG  CG
                                     A_    GT
GAM1038  PTGIS    3'  GCTAGGATTACAGGCAT    6335       AC
                                GTGCCTG  AGTCTTGGC
                                |||||||  |||||||||
                                TACGGAC  TTAGGATCG
                                   A_
GAM1038  PTGIS    3'  GCTGGGATTACAGGTGTGA   6337     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  PTK2B    3'  GCCTTGCTGTTGGTCATGTGG  14629      C TG    CTT
                                TCATGTG C  ACAGT   GGC
                                |||||||  |  |||||   |||
                                GGTGTAC G  TGTCG   CCG
                                    T GT    TT_
GAM1038  PTP4A2   3'  GCTAAGATAGATGGTGTTGA   12983    T TG  TGACA
                                TCA G  CC    GTCTTGGC
                                |||  |  ||    ||||||||
                                AGT T  GG    TAGAATCG
                                  _ GT  TAGA_
GAM1038  PTPN18   3'  GCTGAGATTACAGGTGTGA   26868     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGA  CG
                                  __    A_    GT
GAM1038  PTPRF    3'  GCCAAGGTGAATAGCACA    55268      CTGA  G
                                TGTGC    CA TCTTGGC
                                |||||    || |||||||
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                                ACACG   GT GGAACCG
                                  ATAA  _
GAM1038  PTPRF    3'  GCCAAGGTGAATAGCACA    11106      CTGA  G
                                TGTGC   CA TCTTGGC
                                ||||||   || |||||||
                                ACACG   GT GGAACCG
                                  ATAA  _
GAM1038  PTPRJ    3'  GCCAGGATTGTGTTGGGTTGA  11118    TGT   TG  __
                                TCA   GCC  ACA  GTCTTGGC
                                |||   |||  |||  ||||||||
                                AGT   TGG  TGT  TAGGACCG
                                  ___   GT   GT
GAM1038  PTTG1IP  3'  CTAGGGCTCGGTTGTGA     15090      T   TGAC
                                TCATG GCC    AGTCTTGG
                                ||||| |||    ||||||||
                                AGTGT TGG    TCGGGATC
                                  _   C___
GAM1038  PXR1     3'  GCTACAGAGTGTCTGGGTGTGT 4351       TG  _   G  _
            GG                    TCATG  CCT GACA TCT TGGC
                                ||||||  ||| |||| ||| ||||
                                GGTGT  GGG CTGT AGA ATCG
                                  GT   T    G   C
GAM1038  RAB36    3'  GCTGGGACTACAGGCACGTG   16967         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGCACGGAC  TCAGG  CG
                                     A_    GT
GAM1038  RABL2B   3'  GCTGGGATTACAGGCAT     23003       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  RABL2B   3'  GCTGGGGCTAGGGGTGGGTGG  23004     G    GAC    TG
                                TCAT TGCCT   AGTCT  GC
                                |||| |||||   |||||  ||
                                GGTG GTGGG   TCGGG  CG
                                  G    GA_    GT
GAM1038  RAD23A   5'  GCTAAGATGGCGGCGGCGTGA  17311       _   T ACA
                                TCATGT GCC G   GTCTTGGC
                                ||||||| ||| |   ||||||||
                                AGTGCG CGG C   TAGAATCG
                                   G   _ GG_
GAM1038  RAD23B   5'  GCTGGCGCTCGGCGCGTGA   11216         TGAC   C TG
                                TCATGTGCC    AGT T  GC
                                |||||||||    ||| |  ||
                                AGTGCGCGG    TCG G  CG
                                     C___   C GT
GAM1038  RAF1     3'  GCCCCAGCTGTTGGCTACATGA 80529       _   T     CTT
                                TCATGT GCC GACAGT   GGC
                                |||||| ||| ||||||   |||
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                                AGTACA CGG TTGTCG   CCG
                                   T  _     ACC
GAM1038  RAG1    3'  GCCAAGCCACTCAGGTGCAT  4814     TG    CAGT
                                ATG  CCTGA    CTTGGC
                                |||  |||||    ||||||
                                TAC  GGACT    GAACCG
                                  GT    CACC
GAM1038  RAI14   3'  GCTGAGGCCTCCTGCAGTGA  31480     G  CT  CA   TG
                                TCAT TGC  GA  GTCT  GC
                                |||| |||  ||  ||||  ||
                                AGTG ACG  CT  CGGA  CG
                                  _  TC  C_   GT
GAM1038  RAI3    3'  GCTGGGATGACAGGCGTGA   14286     GT    ACA   TG
                                TCAT  GCCTG   GTCT  GC
                                ||||  |||||   ||||  ||
                                AGTG  CGGAC   TAGG  CG
                                  __    AG_   GT
GAM1038  RARG    5'  GCCAGGCAGGGCGGGTACGGA  6380     A      ACAGT
                                TC TGTGCCTG    CTTGGC
                                || ||||||||    ||||||
                                AG GCATGGGC    GGACCG
                                 _      GGGAC
GAM1038  RARG    5'  GCTGGGGCAGTGGGCAT    6381       G  A   TG
                                GTGCCT AC GTCT  GC
                                |||||| || ||||  ||
                                TACGGG TG CGGG  CG
                                   _ A   GT
GAM1038  RB1     3'  GCCAGATCTTAGGTATAGA   90915    A      CA   T
                                TC TGTGCCTGA  GTCT GGC
                                || |||||||||  |||| |||
                                AG ATATGGATT  TAGA CCG
                                 _       C_   _
GAM1038  RBBP9   3'  GTTGGGATTACAGGCAT    70138       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  TG
                                   A_    GT
GAM1038  RBM8A   3'  GTTGGGATTACAGGCACATG  17548        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTACACGGAC  TTAGG  TG
                                     A_    GT
GAM1038  RDS     3'  GCCAAGATTGACAGGT     4360       A
                                GCCTG CAGTCTTGGC
                                ||||| ||||||||||
                                TGGAC GTTAGAACCG
                                  A
GAM1038  RECK    3'  GCCAAGGAAAGGCACATG    40870        GACAG
                                CATGTGCCT    TCTTGGC
                                |||||||||    |||||||
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                                GTACACGGA    GGAACCG
                                     AA___
GAM1038 RECQL5   3' GCTGGGACTTCTTAGTGCATCA 14931   T   _   C_    TG
                                A GTGC CTGA  AGTCT  GC
                                | |||| ||||  |||||  ||
                                A TACG GATT  TCAGG  CG
                                 C   T   CT    GT
GAM1038 RENT1    3' GCCAGGACTGGCCCTGTGG   11290     GT_  TGAC
                                TCAT   GCC   AGTCTTGGC
                                ||||   |||   |||||||||
                                GGTG   CGG   TCAGGACCG
                                  TCC  ____
GAM1038 REPS2    5' GCTGAGGCCGAGGAGGCGGTGG 16373     G    GACA_   TG
                                TCAT TGCCT    GTCT  GC
                                |||| |||||    ||||  ||
                                GGTG GCGGA    CGGA  CG
                                  _    GGAGC   GT
GAM1038 RET      3' GCCAAGGCTTGGATGCGTGTG  4369    TG   CTGAC
                                CA  TGC    AGTCTTGGC
                                ||  |||    |||||||||
                                GT  GCG    TCGGAACCG
                                 GT   TAGGT
GAM1038 RET      3' GCCAAGGCTTGGATGCGTGTG  40591    TG   CTGAC
                                CA  TGC    AGTCTTGGC
                                ||  |||    |||||||||
                                GT  GCG    TCGGAACCG
                                 GT   TAGGT
GAM1038 RET      3' GCCAAGGCTTGGATGCGTGTG  40167    TG   CTGAC
                                CA  TGC    AGTCTTGGC
                                ||  |||    |||||||||
                                GT  GCG    TCGGAACCG
                                 GT   TAGGT
GAM1038 RET      3' GCCAAGGCTTGGATGCGTGTG  40174    TG   CTGAC
                                CA  TGC    AGTCTTGGC
                                ||  |||    |||||||||
                                GT  GCG    TCGGAACCG
                                 GT   TAGGT
GAM1038 RFX2     3' CCAGGGCTCCCACTGG     5307     T   CCTGAC
                                TCA GTG     AGTCTTGG
                                ||| |||     ||||||||
                                GGT CAC     TCGGGACC
                                  _  CC_____
GAM1038 RGL      5' GCTGGGACTTGGCTGTGG    30735     T   TGAC    TG
                                TCATG GCC    AGTCT  GC
                                ||||| |||    |||||  ||
                                GGTGT CGG    TCAGG  CG
                                   _  T___     GT
GAM1038 RGN      3' GCCAGGGTGGGTGGGTACAT   16262        A_  G
                                ATGTGCCTG  CA TCTTGGC
                                |||||||||  || |||||||
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                                TACATGGGT  GT GGGACCG
                                     GG  _
GAM1038  RHCG     3'  GCTGGGACCTGGTGGGTGA   32866     G   TGACA   TG
                                TCAT TGCC    GTCT  GC
                                |||| ||||    ||||  ||
                                AGTG GTGG    CAGG  CG
                                  G   TC___   GT
GAM1038  RHD      3'  GCTGGGATTACAGGTGTGA   32620     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  RHD      3'  GCTGGGATTACAGGTGTGA   32311     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  RHEB2    5'  GCCGGTCACGTGGGCGTGT   18833   TG    G  A  C_
                                A  TGCCT AC GT  TTGGC
                                |  ||||| || ||  |||||
                                T  GCGGG TG CA  GGCCG
                                 GT    _ _  CT
GAM1038  RIMS1    5'  GCCGAGGCTGGGCTGCGGGA   72632    A   _   TGA
                                TC TGT GCC   CAGTCTTGGC
                                || ||| |||   ||||||||||
                                AG GCG CGG   GTCGGAGCCG
                                 G   T  ___
GAM1038  RNH      5'  GCCGGGCGCCCAGGCGTGTGG  11365     TG     ACA   T
                                TCA  TGCCTG   GTCT GGC
                                |||  ||||||   |||| |||
                                GGT  GCGGAC   CGGG CCG
                                  GT     CCG   _
GAM1038  RNH      5'  GCCGGGCGCCCAGGCGTGTGG  59620     TG     ACA   T
                                TCA  TGCCTG   GTCT GGC
                                |||  ||||||   |||| |||
                                GGT  GCGGAC   CGGG CCG
                                  GT     CCG   _
GAM1038  RP2      3'  GCTGGGATTACAGGTGTGA   22619     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  RP42     3'  GTTAAGGTTGTTCACTATGA   40204     _   CCT   GT
                                TCAT GTG   GACA  CTTGGC
                                |||| |||   ||||  ||||||
                                AGTA CAC   TTGT  GAATTG
                                  T   ___   TG
GAM1038  RPH3AL   3'  GCTGGGATTACAGGTGTGA   22750     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  RPLP1    5'  GCTAAGGCTGCGTTGGGGTGA  6400      GTG  TG  __
                                TCAT   CC  AC  AGTCTTGGC
                                ||||   ||  ||  |||||||||
                                AGTG   GG  TG  TCGGAATCG
                                  ___  GT  CG
GAM1038  SACM1L   5'  GCCGAGGTGGCGGCGCG    25825       TGA  G
                                TGTGCC   CA TCTTGGC
                                ||||||   || |||||||
                                GCGCGG   GT GGAGCCG
                                   CG_  _
GAM1038  SAS      3'  GCTGGGATTATAGGCGTGA   19956     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAT  TTAGG  CG
                                  __    A_    GT
GAM1038  SAT      5'  GCCGAGGTTCCTTGGGTCATGG 11435       T   TG C_ GT
                                TCATG GCC  A  A  CTTGGC
                                ||||| |||  |  |  ||||||
                                GGTAC TGG  T  T  GAGCCG
                                  _  GT CC TG
GAM1038  SCA7     5'  GTCGGGATTTCGTCGGT     4405      T  __
                                GCC GAC  AGTCTTGGC
                                ||| |||  |||||||||
                                TGG CTG  TTAGGGCTG
                                  _  CT
GAM1038  SCAMP1   5'  GCCTGGGTCGGGTGGGTGA   16816      G       AGTCTT
                                TCAT TGCCTGAC     GGC
                                |||| ||||||||     |||
                                AGTG GTGGGCTG     CCG
                                  G       GGT___
GAM1038  SCAMP1   5'  GCCTGGGTCGGGTGGGTGA   53406      G       AGTCTT
                                TCAT TGCCTGAC     GGC
                                |||| ||||||||     |||
                                AGTG GTGGGCTG     CCG
                                  G       GGT___
GAM1038  SCAMP3   3'  GCTGAACCTGACAGGCGTGTGG 53421     TG     A   TC TG
                                TCA  TGCCTG CAG  T  GC
                                |||  |||||| |||  |  ||
                                GGT  GCGGAC GTC  A  CG
                                  GT     A   CA GT
GAM1038  SCAMP3   3'  GCTGAACCTGACAGGCGTGTGG 19102     TG     A   TC TG
                                TCA  TGCCTG CAG  T  GC
                                |||  |||||| |||  |  ||
                                GGT  GCGGAC GTC  A  CG
                                  GT     A   CA GT
GAM1038  SCML2    3'  GCTGGGATTACAGGCAT     20320        AC     TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
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                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  SCN2B    3'  GCCAAGGCTGGGAAATGA    15939     GTG  TGA
                                TCAT   CC   CAGTCTTGGC
                                ||||   ||   ||||||||||
                                AGTA   GG   GTCGGAACCG
                                  AA_  ___
GAM1038  SCNN1B   3'  GCCAAGACTGTTGCCCGAGG   4418    A  T  CT
                                TC TG GC  GACAGTCTTGGC
                                || || ||  ||||||||||||
                                GG GC CG  TTGTCAGAACCG
                                 A  C  __
GAM1038  SCNN1G   3'  GCCGAGGCAGTGGTGCTGG   6433     T TG  TG  A
                                TCA G  CC  AC GTCTTGGC
                                ||| |  ||  || ||||||||
                                GGT C  GG  TG CGGAGCCG
                                  _ GT  __  A
GAM1038  SCNN1G   3'  GTCAGGACCACCAGCCATGG   6434      T  C  ACA
                                TCATG GC TG   GTCTTGGC
                                ||||| || ||   ||||||||
                                GGTAC CG AC   CAGGACTG
                                   _  _  CAC
GAM1038  SCNN1G   3'  GTTGGGGCCCAAGGATGTGA   6435      G   GACA   TG
                                TCATGT CCT    GTCT  GC
                                |||||| |||    ||||  ||
                                AGTGTA GGA    CGGG  TG
                                   _   ACC_   GT
GAM1038  SEDL     3'  GCTAGGATTACAGGCAT     27341       AC
                                GTGCCTG  AGTCTTGGC
                                |||||||  |||||||||
                                TACGGAC  TTAGGATCG
                                   A_
GAM1038  SEDL     3'  GCTGGGACTACAGGCGCGTG  27347        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGCGCGGAC  TCAGG  CG
                                     A_    GT
GAM1038  SEDL     3'  GCTGGGATTACAGGCGTGTGA 27348    TG    AC    TG
                                TCA  TGCCTG  AGTCT  GC
                                |||  ||||||  |||||  ||
                                AGT  GCGGAC  TTAGG  CG
                                  GT     A_    GT
GAM1038  SEDL     3'  GCTGGGATTACAGGTGTGA   27349     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038  SEL1L    3'  CCAATGTTGTGTGCATGA    17357      TG CTG   TC
                                TCATG  C   ACAG  TTGG
                                |||||  |   ||||  ||||
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                                AGTAC  G   TGTT  AACC
                                  GT ___   GT
GAM1038  SELENBP1  3'  GCTGAGACTGTGGCAATGTG   14153      _  TG     TG
                                CATGT GCC  ACAGTCT  GC
                                ||||| |||  |||||||  ||
                                GTGTA CGG  TGTCAGA  CG
                                  A  __      GT
GAM1038  SEPN1   3'  GCTGGGATTACAGGCGTGA   66374     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  SEPN1   3'  GCTGGGATTACAGGTGCATG   66375     TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTAC  GGAC  TTAGG  CG
                                  GT   A_    GT
GAM1038  SERPINI1  5'  GTCAGGGGTTGCAGGTGTGTGG 17234      TG   A  GT  _
                                TCATG  CCTG CA  CT TGGC
                                |||||  |||| ||  || ||||
                                GGTGT  GGAC GT  GG ACTG
                                  GT   _ TG  G
GAM1038  SFRP4   5'  GCCGGGGTCGCAGCGCGAGA   11579    A    C_   AGT
                                TC TGTGC  TGAC   CTTGGC
                                || |||||  ||||   ||||||
                                AG GCGCG  GCTG   GGGCCG
                                 A    AC   ___
GAM1038  SFRS2IP  5'  GTTGAGGCTTCTGTGCGCG   16357     CT_  C    TG
                                TGTGC   GA AGTCT  GC
                                |||||   || |||||  ||
                                GCGCG   CT TCGGA  TG
                                  TGT  _    GT
GAM1038  SFRS7   5'  GCCGGGACTCTTGGCGGGTGA  59447     G    TGAC
                                TCAT TGCC    AGTCTTGGC
                                |||| ||||    |||||||||
                                AGTG GCGG    TCAGGGCCG
                                  G    TTC_
GAM1038  SH3BP2   3'  GCCGAGGCTGGAGCACA     11604      CTGA
                                TGTGC    CAGTCTTGGC
                                |||||    ||||||||||
                                ACACG    GTCGGAGCCG
                                  AG__
GAM1038  SH3BP2   3'  GCTGGGATTACAGGCAT     11606       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  SH3GL3   5'  GCTGGGATTACAGGTGTGA   11634     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
```

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                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  SHB     5'  GCCGGGACGGGCACGGGCGCGC 11641    A      ACA__
              GG                   TC TGTGCCTG    GTCTTGGC
                                || ||||||||    ||||||||
                                GG GCGCGGGC    CAGGGCCG
                                 C       ACGGG
GAM1038  SHOX    3'  GCTGAGGCTGAGGACGTGA   4837       G   GA    TG
                                TCATGT CCT  CAGTCT  GC
                                |||||| |||  ||||||  ||
                                AGTGCA GGA  GTCGGA  CG
                                   _  __     GT
GAM1038  SHOX    3'  GCTGGGATGACAGGCGTGA   22540     GT    ACA   TG
                                TCAT  GCCTG   GTCT  GC
                                ||||  |||||   ||||  ||
                                AGTG  CGGAC   TAGG  CG
                                  __    AG_   GT
GAM1038  SIAT4C   3'  GTCAGGGTGGGGGCGCTGG   20788    T    GA  G
                                TCA GTGCCT  CA TCTTGGC
                                ||| ||||||  || |||||||
                                GGT CGCGGG  GT GGGACTG
                                  _     G_  _
GAM1038  SIGLEC11 3'  GCTGGGATTGCAGACGTGA   53544      GC   A    TG
                                TCATGT  CTG CAGTCT  GC
                                ||||||  ||| ||||||  ||
                                AGTGCA  GAC GTTAGG  CG
                                   __   _     GT
GAM1038  SIGLEC5  5'  GCTGGGGCCCTGGCGGATGG   13818     G   TGACA   TG
                                TCAT TGCC    GTCT  GC
                                |||| ||||    ||||  ||
                                GGTA GCGG    CGGG  CG
                                  G   TCC__   GT
GAM1038  SIL     3'  GCTGGGATTACAGGCATGTG   11692         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTACGGAC  TTAGG  CG
                                     A_    GT
GAM1038  SIL     3'  GCTGGGATTACAGGCGTGA   11693     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  SIP     3'  GTCAGGACCAGTGCCTGTGA   26975      T  _   ACA
                                TCATG GC CTG   GTCTTGGC
                                ||||| || |||   ||||||||
                                AGTGT CG GAC   CAGGACTG
                                  C  T   ___
GAM1038  SKI     5'  GCCGGGGGGGCCCGGGCGCGCG 11702    A      ACAG_
              G                    TC TGTGCCTG    TCTTGGC
                                || ||||||||    |||||||
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                                GG GCGCGGGC    GGGGCCG
                                 C      CCGGG
GAM1038 SLA2    3' GCTGGGATTACAGGTGTGA   49902     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 SLC12A7  3' GTGGATCATCTGTCGGGTGTGT 21707      TG      TC__  G
           GG                    TCATG  CCTGACAG   TT GC
                                |||||  ||||||||   || ||
                                GGTGT  GGGCTGTC   AG TG
                                  GT      TACT  G
GAM1038 SLC13A3  3' GCCAGGACTCTCCTACATG   60470      CCT  C
                                CATGTG   GA AGTCTTGGC
                                ||||||   || |||||||||
                                GTACAT   CT TCAGGACCG
                                   C__  C
GAM1038 SLC14A2  5' GCTAGGACTACAAGTGTGTG   23133     TG C  AC
                                CATG  C TG  AGTCTTGGC
                                ||||  | ||  |||||||||
                                GTGT  G AC  TCAGGATCG
                                  GT A  A_
GAM1038 SLC14A2  5' GCTGGGATTACAGGCGTGG   23136     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                GGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 SLC17A5  3' GTTGAGACTACAGGCAT     24894       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TCAGA  TG
                                   A_    GT
GAM1038 SLC20A2  3' GTCTGGTGTTGGCGTGTGG   22176    TG   T   G  TT
                                TCA  TGCC GACA TC  GGC
                                |||  |||| |||| ||  |||
                                GGT  GCGG TTGT GG  CTG
                                  GT   _   _  T_
GAM1038 SLC21A9  3' GCCAAGATTTCACACATGTGA  23420       CC   C
                                TCATGTG  TGA AGTCTTGGC
                                |||||||  ||| |||||||||
                                AGTGTAC  ACT TTAGAACCG
                                   AC  _
GAM1038 SLC22A2  5' GCCGGGACGGCTGGGTGTACGA 59533    A  TG   ACA
                                TC TG  CCTG   GTCTTGGC
                                || ||  ||||   ||||||||
                                AG AT  GGGT   CAGGGCCG
                                 C  GT   CGG
GAM1038 SLC24A1  5' GTCAAGGTCTGAAGGGTTGTGG 16378      T   GA  _
                                TCATG GCCT  CAG TCTTGGC
                                |||||  ||||  |||  |||||||
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                                GGTGT TGGG  GTC GGAACTG
                                  _   AA  T
GAM1038 SLC24A1  3' TGGGATAGGCGCACGA     16382    A     GACA   TG
                                TC TGTGCCT   GTCT  G
                                || |||||||   ||||  |
                                AG ACGCGGA   TAGG  T
                                 C     ____   GT
GAM1038 SLC25A15 3' TCAGGGCTTTTACGTA     26512    C   C
                                TGC TGA AGTCTTGG
                                ||| ||| ||||||||
                                ATG ATT TCGGGACT
                                  C   T
GAM1038 SLC35A2  3' GCTGGGATTGAAGACATTGG   18979    T   C  GA     TG
                                TCA GTG CT  CAGTCT  GC
                                ||| ||| ||  ||||||  ||
                                GGT TAC GA  GTTAGG  CG
                                  _  A  A_     GT
GAM1038 SLC4A1   3' GCTGAGGCCCCAGGGCTGTGG  4426      T   GACA   TG
                                TCATG GCCT   GTCT  GC
                                ||||| ||||   ||||  ||
                                GGTGT CGGG   CGGA  CG
                                  _   ACCC   GT
GAM1038 SLC6A8   5' GCCGGGGCGGGGGGCGCG    18850       GACA
                                TGTGCCT   GTCTTGGC
                                |||||||   ||||||||
                                GCGCGGG   CGGGGCCG
                                    GGG_
GAM1038 SLC6A8   3' TTCGAGCTGTTGCGTGTGTGA  18854      TG C     T    C
                                TCATG  C TGACAG CTTGG
                                |||||  | |||||| |||||
                                AGTGT  G GTTGTC GAGCT
                                  GT C     _    TC
GAM1038 SLC7A5   3' GCCGAGTAATGACGTGTGTGG  13010      TG CTGA  GT_
                                TCATG  C   CA   CTTGGC
                                |||||  |   ||   ||||||
                                GGTGT  G   GT   GAGCCG
                                  GT CA__  AAT
GAM1038 SLC8A1   5' ATTGTTAGGTTGTGA      40839      T
                                TCATG GCCTGACAGT
                                ||||| ||||||||||
                                AGTGT TGGATTGTTA
                                  _
GAM1038 SLC9A6   3' GCCAAAGTACAGGTGTAT    21007     TG   _ AGTC
                                ATG  CCTG AC   TTGGC
                                |||  |||| ||   |||||
                                TAT  GGAC TG   AACCG
                                  GT   A  A___
GAM1038 SLIT3    3' TGGGACAGCCATGTGG      11769       C  GACA   TG
                                TCATGTG CT   GTCT  G
                                ||||||| ||   ||||  |
```

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                                GGTGTAC GA    CAGG  T
                                    C _____    GT
GAM1038  SLN      3'  GCTAGGATTGATTATGTGT    11770    TG C  _
                                G  C TGA CAGTCTTGGC
                                |  | ||| ||||||||||
                                T  G ATT GTTAGGATCG
                                 GT T   A
GAM1038  SMAC     5'  GCTAGGATTACAGGCGTGA    57212      GT     AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  CGGAC  TTAGGATCG
                                  __     A_
GAM1038  SMARCC1  5'  GCCGGGGTGGGCCAGGCTGTGG 11800       T     A__  G
                                TCATG GCCTG   CA TCTTGGC
                                ||||| |||||   || |||||||
                                GGTGT CGGAC   GT GGGGCCG
                                  _     CGG  _
GAM1038  SMARCD2  3'  GCCAGGGTAAGGTGAATGG    11824      G     GACAG
                                TCAT TGCCT     TCTTGGC
                                |||| |||||     |||||||
                                GGTA GTGGA     GGGACCG
                                  A     AT___
GAM1038  SMOH     5'  GCCGAGGGGCCGGGGCGCGCGG 18867     A       GACAG
                                TC TGTGCCT     TCTTGGC
                                || |||||||     |||||||
                                GG GCGCGGG     GGAGCCG
                                 C       GCCGG
GAM1038  SMOH     5'  GCCGAGGTCGTGCGTGTGG    18868     TG   C    AGT
                                TCA  TGC TGAC   CTTGGC
                                |||  ||| ||||   ||||||
                                GGT  GCG GCTG   GAGCCG
                                 GT   T   ___
GAM1038  SMT3H1   3'  GTTGAATGGTGAGCACGTGA   59960         C G  AGTC TG
                                TCATGTGC T AC    T  GC
                                |||||||| | ||    |  ||
                                AGTGCACG A TG    A  TG
                                     _ G  GTA_ GT
GAM1038  SMURF1   3'  GGGACTGGGCGTGG       92457      GT   TGA
                                TCAT  GCC   CAGTCTT
                                ||||  |||   |||||||
                                GGTG  CGG   GTCAGGG
                                  __   ___
GAM1038  SNAP23   3'  GCTGGGATTACAGGCGTGTG   55465    TG     AC     TG
                                CA  TGCCTG  AGTCT  GC
                                ||  ||||||  |||||  ||
                                GT  GCGGAC  TTAGG  CG
                                 GT     A_    GT
GAM1038  SNAP23   3'  GCTGGGATTACAGGCGTGTG   13812    TG     AC     TG
                                CA  TGCCTG  AGTCT  GC
                                ||  ||||||  |||||  ||
```

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                                GT  GCGGAC  TTAGG  CG
                                 GT     A_    GT
GAM1038  SNX15    3'  GCTGAGATTGCAGGCACATG   73745          A     TG
                                CATGTGCCTG CAGTCT  GC
                                |||||||||| ||||||  ||
                                GTACACGGAC GTTAGA  CG
                                      _     GT
GAM1038  SNX15    3'  GCTGAGATTACAGGCAT     73744        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGA  CG
                                   A_    GT
GAM1038  SON      3'  GCTAAATATAGTGCACATGA   49829         _  ACAGTC
                                TCATGTGC CTG     TTGGC
                                |||||||| |||     |||||
                                AGTACACG GAT     AATCG
                                     T   ATA___
GAM1038  SORCS2   3'  ACATGTTGGGCATGTGG     40411         TG  _
                                TCATGTGCC  ACA GT
                                |||||||||  ||| ||
                                GGTGTACGG  TGT CA
                                     GT   A
GAM1038  SPN      3'  GCTGAGATTACAGACATGA    11923       GC   AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTACA  GAC  TTAGA  CG
                                   __  A_    GT
GAM1038  SPTBN4   3'  GCTGGGGCCCGGGGGTGTGG  47388     TG G    ACA    TG
                                TCA  T CCTG   GTCT  GC
                                |||  | ||||   ||||  ||
                                GGT  G GGGC   CGGG  CG
                                  GT G   C__    GT
GAM1038  SRRM2    3'  GTTGGGACTGGAGGTTGTATA  32916       __ GA     TG
                                TGTGC  CT  CAGTCT  GC
                                |||||  ||  ||||||  ||
                                ATATG  GG  GTCAGG  TG
                                   TT  AG     GT
GAM1038  STAT6    3'  GCTGAGATTCTTCGTGTATA   12022       C   C_    TG
                                TGTGC TGA  AGTCT  GC
                                ||||| |||  |||||  ||
                                ATATG GCT  TTAGA  CG
                                   T   TC    GT
GAM1038  STEAP    5'  GCTAAGGCGAAGAGTGGGTGG  24917      G  _  GACA
                                TCAT TGC CT    GTCTTGGC
                                |||| ||| ||    ||||||||
                                GGTG GTG GA    CGGAATCG
                                  G   A  AG__
GAM1038  STIM1    5'  GCCAGCCGCCTGGGCACGGGA  60150    A      GACAGTC
                                TC TGTGCCT      TTGGC
                                || |||||||      |||||
```

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                                AG GCACGGG      GACCG
                                 G      TCCGCC_
GAM1038 STK11    5' GCCGGGACTGACGTGTA    4848      C  A
                                TGC TG CAGTCTTGGC
                                ||| || ||||||||||
                                ATG GC GTCAGGGCCG
                                  T  A
GAM1038 STK6     3' CCAGGGCTGCCATAT      13185      CCTGA
                                ATGTG    CAGTCTTGG
                                |||||    |||||||||
                                TATAC    GTCGGGACC
                                   C____
GAM1038 STX1A    3' GCCCCGTGTCGTGTGCATGA  16013      TG C    GTCTT
                                TCATG  C TGACA    GGC
                                |||||  | |||||    |||
                                AGTAC  G GCTGT    CCG
                                   GT T    GCC__
GAM1038 SYNGR3   3' GCTGGCAGGCACAGA      14855    A      A
                                TC TGTGCCTG CAGT
                                || |||||||| ||||
                                AG ACACGGAC GTCG
                                 _      G
GAM1038 TAL1     3' GCCAACACTGTGGGTGTGTGA 12105      TG   G    C
                                TCATG  CCT ACAGT TTGGC
                                |||||  ||| ||||| |||||
                                AGTGT  GGG TGTCA AACCG
                                   GT  _    C
GAM1038 TAPBP    3' GCTGGGATTACAGGCACATG  12129        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTACACGGAC  TTAGG  CG
                                      A_    GT
GAM1038 TAPBP    3' GCTGGGATTACAGGCGTGA   12130     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 TAPBP    3' GCTGGGATTACAGGCGTGA   12131     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 TAT      3' GTTGGGACTACAGGCGTGA   4475      GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TCAGG  TG
                                  __    A_    GT
GAM1038 TBL1X    3' CCAGCTCGAGGCGTGTGG    18927    TG    GAC   CT   C
                                TCA  TGCCT   AGT  TGG
                                |||  |||||   |||  |||
```

```
                                GGT  GCGGA   TCG  ACC
                                  GT    GC_  __   A
GAM1038  TBL1X    3'  GCCAGCCTGTCGTTAGGGCATG 18933       G  ___    T  T
             G                   TCATGT CCT   GACAG CT GGC
                                 |||||| |||   ||||| || |||
                                 GGTACG GGA   CTGTC GA CCG
                                    _  TTG    C  _
GAM1038  TBX1     3'  CGAGGCCGGGCCATGG     54668      T    ACA   TG
                                 TCATG GCCTG   GTCT  G
                                 ||||| |||||   ||||  |
                                 GGTAC CGGGC   CGGA  C
                                    _    ___    GT
GAM1038  TBX1     3'  GCCGGGCCATGGGCACATGG   54669          ACA   T
                                 TCATGTGCCTG   GTCT GGC
                                 ||||||||||   |||| |||
                                 GGTACACGGGT   CGGG CCG
                                       AC_   _
GAM1038  TBX6     5'  GCCGGGGCTCCCCACCGTGG   54965      _  CCTGAC
                                 TCATG TG     AGTCTTGGC
                                 |||||  ||    |||||||||
                                 GGTGC AC     TCGGGGCCG
                                    C  CCC___
GAM1038  TBX6     5'  GCCGGGGCTCCCCACCGTGG   16038      _  CCTGAC
                                 TCATG TG     AGTCTTGGC
                                 |||||  ||    |||||||||
                                 GGTGC AC     TCGGGGCCG
                                    C  CCC___
GAM1038  TCTA     3'  GCTGGCCATTCAGGTATA    42239        CA_  TT
                                 TGTGCCTGA   GTC  GGC
                                 |||||||||   |||  |||
                                 ATATGGACT   CGG  TCG
                                       TAC   __
GAM1038  TDGF1    3'  GCTGAGATTACACACGTGA   12200       CC  AC    TG
                                 TCATGTG  TG  AGTCT  GC
                                 |||||||  ||  |||||  ||
                                 AGTGCAC  AC  TTAGA  CG
                                    __  A_    GT
GAM1038  TEC      3'  GTCAAGACTGTGTGTGTGG   12221      TG CTG
                                 TCATG  C   ACAGTCTTGGC
                                 |||||  |   ||||||||||
                                 GGTGT  G   TGTCAGAACTG
                                    GT ___
GAM1038  TEM5     3'  CTAGCCCAGCACATGA      51319        C  ACA  CT
                                 TCATGTGC TG   GT  TGG
                                 ||||||||  ||   ||  |||
                                 AGTACACG AC   CG  ATC
                                    _  C__   __
GAM1038  TERF1    3'  GCTGAGATTACAGACGTGA   33974       GC   AC    TG
                                 TCATGT  CTG  AGTCT  GC
                                 ||||||  |||  |||||  ||
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                                AGTGCA  GAC  TTAGA  CG
                                   __  A_    GT
GAM1038  TERF2    3'  GCTGGGATTACAGGCAT    18948       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  TES      3'  GCTGGGATTACAGGTGCATG  72007     TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTAC  GGAC  TTAGG  CG
                                  GT   A_    GT
GAM1038  TES      3'  GCTGGGATTACAGGTGTGGGA  72008   AT TG   AC    TG
                                TC  G  CCTG  AGTCT  GC
                                ||  |  ||||  |||||  ||
                                AG  T  GGAC  TTAGG  CG
                                 GG GT   A_    GT
GAM1038  TGFB2    5'  GTTTTTCTGTTGGGCATTGA  12257    T    TG   TCTT
                                TCA GTGCC  ACAG   GGC
                                |||  |||||  ||||   |||
                                AGT TACGG  TGTC   TTG
                                  _    GT   TTT_
GAM1038  THRA     5'  GCTGAGGCGGGTATCATGG   12286     _    GACA   TG
                                TCATG TGCCT   GTCT  GC
                                |||||  |||||   ||||  ||
                                GGTAC ATGGG   CGGA  CG
                                   T    _____   GT
GAM1038  THY1     3'  GCCAGGATTGGGGACCTGA   20811    T  G  TGA
                                TCA GT CC   CAGTCTTGGC
                                |||  ||  ||   ||||||||||
                                AGT CA GG   GTTAGGACCG
                                  C  G  ___
GAM1038  TIMP3    3'  GTCAAGGGCCTGGGCACAGGA  4514     A      GACAG
                                TC TGTGCCT    TCTTGGC
                                ||  |||||||    |||||||
                                AG ACACGGG    GGAACTG
                                 G      TCCG_
GAM1038  TIMP3    5'  GTCAAGGTCTCTAGGACATGG  4515       G   AC  _
                                TCATGT CCTG  AG TCTTGGC
                                ||||||  ||||  ||  |||||||
                                GGTACA GGAT  TC GGAACTG
                                   _   C_  T
GAM1038  TIRAP    3'  GCTGGGATTACAGGCGTGA   53570     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038  TMC1     5'  GCTGGGATTTCAGGCCATGA   56905      T     C    TG
                                TCATG GCCTGA AGTCT  GC
                                |||||  ||||||  |||||  ||
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                                AGTAC CGGACT TTAGG  CG
                                  _    _    GT
GAM1038  TMEM4    5'  GCCGGGACACCCCGTGTGTGG  26516      TG CTGACA
                                TCATG  C     GTCTTGGC
                                |||||  |     ||||||||
                                GGTGT  G     CAGGGCCG
                                   GT CCCCA_
GAM1038  TMEPAI   3'  CCAAGGTTTGTACACGA     39443    A    CT   AGT
                                TC TGTGC  GAC   CTTGG
                                || |||||  |||   |||||
                                AG ACATG  TTG   GAACC
                                 C    T_  ___
GAM1038  TMOD     3'  GCCAGGGCCTCAGCGCTATGG  12341      T  _    CA
                                TCATG GC CTGA  GTCTTGGC
                                ||||| || ||||  ||||||||
                                GGTAT CG GACT  CGGGACCG
                                   _ C   C_
GAM1038  TMP21    5'  GTTGAGGCCTTCGGTGGTGA  22403     G    T  CA    TG
                                TCAT TGCC GA  GTCT  GC
                                |||| |||| ||  ||||  ||
                                AGTG GTGG CT  CGGA  TG
                                  _    _ TC    GT
GAM1038  TMPRSS3  3'  GCTGGGATTACAGGCAT    43798       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  TMPRSS3  3'  GCTGGGATTACAGGCAT    50509       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  TMPRSS3  3'  GCTGGGATTACAGGCAT    50530       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  TMPRSS4  5'  CCAGGACCTGTGTGGG     39115     _   _
                                CCTG ACAG TCTTGG
                                |||| |||| ||||||
                                GGGT TGTC AGGACC
                                  G   C
GAM1038  TNFAIP2  3'  GCTGGGATTATAGGCAT    20831       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGG  CG
                                   A_    GT
GAM1038  TNFRSF10B 3'  GCTGGGACAGAGGCAGATGG  13872     G    GACA   TG
                                TCAT TGCCT   GTCT  GC
                                |||| |||||   ||||  ||
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                                GGTA ACGGA   CAGG  CG
                                  G    GA__   GT
GAM1038  TNFRSF10B 3'  GCTGGGATTACAGGCGTGA   13873     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  TNFRSF1B  3'  CCACTTTGGTACATGG     6518         TGAC   CTT
                                TCATGTGCC   AGT   GG
                                |||||||||   |||   ||
                                GGTACATGG   TCA   CC
                                     TT__   ___
GAM1038  TNFRSF6B  5'  GTCCCCACGTCAGGGTGTATGA 31605      TG  _   A  CTT
                                TCATG  CC TGAC GT   GGC
                                |||||  || |||| ||   |||
                                AGTAT  GG ACTG CA   CTG
                                   GT  G   _  CCC
GAM1038  TNFRSF8   5'  CCGGGACCGCACGTGG     6958         CTGACA
                                TCATGTGC     GTCTTGG
                                ||||||||     |||||||
                                GGTGCACG     CAGGGCC
                                     C_____
GAM1038  TNFRSF9   3'  GCTGGGATTACAGACATGA   7790       GC   AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTACA  GAC  TTAGG  CG
                                   __   A_    GT
GAM1038  TNFSF15   3'  GCCGGGCGTGGTAGCGCATGG  17595        CTGA  GT
                                TCATGTGC   CA  CTTGGC
                                ||||||||   ||  ||||||
                                GGTACGCG   GT  GGGCCG
                                     ATG_  GC
GAM1038  TNFSF9    3'  GCCAAGGTTGTTTACATG    13755      CCT   GT
                                CATGTG   GACA  CTTGGC
                                ||||||   ||||  ||||||
                                GTACAT   TTGT  GAACCG
                                   ___    TG
GAM1038  TPMT      3'  GCTAGGATTACAGGTAT     4541         AC
                                GTGCCTG  AGTCTTGGC
                                |||||||  |||||||||
                                TATGGAC  TTAGGATCG
                                   A_
GAM1038  TPMT      3'  GCTGGGATTACAGGCGTGA   4543      GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038  TRAF1     3'  GTTAGGATGGCAGGACGTGG   18976       G   ACA
                                TCATGT CCTG   GTCTTGGC
                                ||||||  ||||   ||||||||
```

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                                GGTGCA GGAC   TAGGATTG
                                   _   GG_
GAM1038  TRAF5    3'  GCTGAGATTACAGGCAT     16082        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGA  CG
                                   A_    GT
GAM1038  TRH      3'  GCCCTCTTCCTTTAGGCATGTG 23056          CAGTCTT_
            A                    TCATGTGCCTGA       GGC
                                ||||||||||||       |||
                                AGTGTACGGATT       CCG
                                      TCCTTCTC
GAM1038  TRPC1    3'  GTTAAGAGGATATTAGGTATAT 12394          CAG__
                                ATGTGCCTGA    TCTTGGC
                                ||||||||||    |||||||
                                TATATGGATT    AGAATTG
                                     ATAGG
GAM1038  TRPM6    3'  GCTGGGATTACAGGCGTGA   34542     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  TRPV1    3'  GCTGGGATTACAGGCACGTG   38088         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGCACGGAC  TTAGG  CG
                                     A_    GT
GAM1038  TRPV1    3'  GCTGGGATTACAGGTGTGA   38089     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  TRPV1    3'  GCTGGGATTACAGGTGTGA   38090     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  TRPV1    3'  GCTGGGATTACAGGCACGTG   54806         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGCACGGAC  TTAGG  CG
                                     A_    GT
GAM1038  TRPV1    3'  GCTGGGATTACAGGTGTGA   54807     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  TRPV1    3'  GCTGGGATTACAGGTGTGA   54808     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
```

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                                AGTG TGGAC TTAGG CG
                                  __   A_   GT
GAM1038 TRPV1   3' GCTGGGATTACAGGCACGTG 54839       AC   TG
                                CATGTGCCTG AGTCT GC
                                |||||||||| ||||| ||
                                GTGCACGGAC TTAGG CG
                                     A_   GT
GAM1038 TRPV1   3' GCTGGGATTACAGGTGTGA 54840   GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG TGGAC TTAGG CG
                                  __   A_   GT
GAM1038 TRPV1   3' GCTGGGATTACAGGTGTGA 54841   GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG TGGAC TTAGG CG
                                  __   A_   GT
GAM1038 TRPV1   3' GCTGGGATTACAGGCACGTG 54872       AC   TG
                                CATGTGCCTG AGTCT GC
                                |||||||||| ||||| ||
                                GTGCACGGAC TTAGG CG
                                     A_   GT
GAM1038 TRPV1   3' GCTGGGATTACAGGTGTGA 54873   GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG TGGAC TTAGG CG
                                  __   A_   GT
GAM1038 TRPV1   3' GCTGGGATTACAGGTGTGA 54874   GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG TGGAC TTAGG CG
                                  __   A_   GT
GAM1038 TRPV4   3' GCTGGGGCCCTCGGCGTGG 60685   GT  T CA   TG
                                TCAT GCC GA GTCT GC
                                |||| ||| ||  |||| ||
                                GGTG CGG CT CGGG CG
                                  __  _ CC   GT
GAM1038 TSG    3' GTTGAGATTTAGCTCATGG  40237    T C  CA   TG
                                TCATG GC TGA GTCT GC
                                ||||| || |||  |||| ||
                                GGTAC CG ATT TAGA TG
                                   T  _  __   GT
GAM1038 TXNRD1  3' GCCAAGACTGCAAACCACTGG 12460   T  CC_ A
                                TCA GTG  TG CAGTCTTGGC
                                ||| |||  || ||||||||||
                                GGT CAC  AC GTCAGAACCG
                                  _  CAA _
GAM1038 UBE2G2  3' GCTGTGGAGGTGGGCATGTGG 64862       G AG T
                                TCATGTGCCT AC  TC TGGC
                                |||||||||| ||  || ||||
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                                GGTGTACGGG TG  GG GTCG
                                      _ GA  T
GAM1038 UBE2L3   3' GCCTAACATTGTTCAGGCGCAT 12502          _   C _
             GG                   TCATGTGCCTGA CAGT TT GGC
                                  |||||||||||| |||| || |||
                                  GGTACGCGGACT GTTA AA CCG
                                        T   C  T
GAM1038 UGDH     3' GCTGGGATTACAGGTGTGA   12544     GT    AC    TG
                                  TCAT  GCCTG  AGTCT  GC
                                  ||||  |||||  |||||  ||
                                  AGTG  TGGAC  TTAGG  CG
                                    __    A_    GT
GAM1038 UMPS     3' GCTGGGATTACAGGTGTGA   4553      GT    AC    TG
                                  TCAT  GCCTG  AGTCT  GC
                                  ||||  |||||  |||||  ||
                                  AGTG  TGGAC  TTAGG  CG
                                    __    A_    GT
GAM1038 UNC119   3' GCTGAGATTGCAGCCCATGG  17645      T  C  A    TG
                                  TCATG GC TG CAGTCT  GC
                                  ||||| || || ||||||  ||
                                  GGTAC CG AC GTTAGA  CG
                                     C  _ _     GT
GAM1038 UNC119   3' GCTGAGATTGCAGCCCATGG  54014      T  C  A    TG
                                  TCATG GC TG CAGTCT  GC
                                  ||||| || || ||||||  ||
                                  GGTAC CG AC GTTAGA  CG
                                     C  _ _     GT
GAM1038 USP6     5' GCCGGGGCAGGATGGACATGG  91147       G  TGACA
                                  TCATGT CC    GTCTTGGC
                                  ||||||  ||    ||||||||
                                  GGTACA GG    CGGGGCCG
                                     _ TAGGA
GAM1038 VANGL2   3' GCTGGGGCCAGGGTTATGA   71650      TG   ACA   TG
                                  TCATG  CCTG   GTCT  GC
                                  |||||  ||||   ||||  ||
                                  AGTAT  GGAC   CGGG  CG
                                     TG   ___   GT
GAM1038 VANGL2   3' GTCAGGATGAATTGTCAGACAT 71653      C    ____
             ATGG                  ATGTG CTGACA   GTCTTGGC
                                   ||||| ||||||   ||||||||
                                   TATAC GACTGT   TAGGACTG
                                     A     TAAG
GAM1038 VENTX2   3' GCTGGGATTACGGGCAT    27115       AC    TG
                                  GTGCCTG  AGTCT  GC
                                  |||||||  |||||  ||
                                  TACGGGC  TTAGG  CG
                                     A_    GT
GAM1038 VIPR2    3' GCTGAGGAAGTGGGCGTGA   12614     GT   G  AG   TG
                                  TCAT  GCCT AC  TCT  GC
                                  ||||  |||| ||  |||  ||
```

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                                AGTG  CGGG TG  GGA  CG
                                  __   _ AA   GT
GAM1038  WASF3    3'  GCTACCTGTTGGGCTTGTGG  21826     T   TG    TCT
                                TCATG GCC  ACAG   TGGC
                                ||||| |||  ||||   ||||
                                GGTGT CGG  TGTC   ATCG
                                   T   GT    C__
GAM1038  WBSCR5   5'  GCTGGGATTATAGGCGTGA   41859     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAT  TTAGG  CG
                                  __    A_    GT
GAM1038  WBSCR5   5'  GCTGGGATTATAGGCGTGA   50612     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAT  TTAGG  CG
                                  __    A_    GT
GAM1038  WHSC1    3'  GCTGAATGCCTGTTAGCATATG 23664        C     TC__ TG
            A                    TCATGTGC TGACAG    T  GC
                                |||||||| ||||||    |  ||
                                AGTATACG ATTGTC    A  CG
                                   _     CGTA GT
GAM1038  WHSC1    5'  GCTGGGATTACAGGCAT    23665       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  WHSC1    3'  TCGAGGCCTGCCCATGA    23671      T  CTGACA
                                TCATG GC     GTCTTGG
                                ||||| ||     |||||||
                                AGTAC CG     CGGAGCT
                                  C  TC_____
GAM1038  WHSC1    5'  GCTGGGATTACAGGCAT    29911       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  WHSC1    5'  GCTGGGATTACAGGCAT    55830       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  WHSC1    5'  GCTGGGATTACAGGCAT    55847       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  WSX1     5'  GTATGGTTGTTGGGCGTAGGA  16739    A     TG   GT TTG
                                TC TGTGCC  ACA  C   GC
                                || ||||||  |||  |   ||
```

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                                AG ATGCGG  TGT  G   TG
                                 G     GT   TG TA_
GAM1038  WT1     3'  GCCAGGGCATGTGTATGTG   44353       CTG  _
                                CATGTGC   ACA GTCTTGGC
                                |||||||   ||| ||||||||
                                GTGTATG   TGT CGGGACCG
                                    ___   A
GAM1038  WT1     3'  GCCAGGGCATGTGTATGTG   44363       CTG  _
                                CATGTGC   ACA GTCTTGGC
                                |||||||   ||| ||||||||
                                GTGTATG   TGT CGGGACCG
                                    ___   A
GAM1038  WT1     3'  GCCAGGGCATGTGTATGTG   44373       CTG  _
                                CATGTGC   ACA GTCTTGGC
                                |||||||   ||| ||||||||
                                GTGTATG   TGT CGGGACCG
                                    ___   A
GAM1038  WT1     3'  GCCAGGGCATGTGTATGTG   4588        CTG  _
                                CATGTGC   ACA GTCTTGGC
                                |||||||   ||| ||||||||
                                GTGTATG   TGT CGGGACCG
                                    ___   A
GAM1038  YES1    3'  GCTGGGATTACAGGCGTGA   18355     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  YY1     5'  CGAGGCCAGCGCGGA      12689    A    C  ACA    TG
                                TC TGTGC TG   GTCT  G
                                || ||||| ||   ||||  |
                                AG GCGCG AC   CGGA  C
                                 _    _ ___    GT
GAM1038  YY1     5'  GCCGAGCGAGCGCGGGCGCG   12690        ACA__ T
                                TGTGCCTG    G CTTGGC
                                ||||||||    | ||||||
                                GCGCGGGC    C GAGCCG
                                     GCGAG _
GAM1038  YY1     5'  GCCGAGGCCGCCGCGGCCGTGG 12691      T  _  ACA
                                TCATG GCC TG   GTCTTGGC
                                ||||| ||| ||   ||||||||
                                GGTGC CGG GC   CGGAGCCG
                                  _  C  CGC
GAM1038  ZFP36L1  5'  GCCGGGAACTGGCGTGTGG   17007    TG   TGACAG
                                TCA  TGCC     TCTTGGC
                                |||  ||||     |||||||
                                GGT  GCGG     AGGGCCG
                                 GT   TCA___
GAM1038  ZNF133   5'  GCTGGGATTACAGGCAT     12838       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
```

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                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  ZNF137   3' GCTGGGATTACAGGTAT    12864       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TATGGAC  TTAGG  CG
                                   A_    GT
GAM1038  ZNF157   3' GTTGGGATTACAGGTGTGA   12881     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  TG
                                  __    A_    GT
GAM1038  ZNF175   5' GTTGGGGGTGGGGGTGCGTGA  23098      TG   GA  G   TG
                                TCATG  CCT  CA TCT  GC
                                |||||  |||  || |||  ||
                                AGTGC  GGG  GT GGG  TG
                                   GT   G_  G   GT
GAM1038  ZNF189   3' GCCATTTGTTTGGCATGTGA   12904        T    TCT
                                TCATGTGCC GACAG   TGGC
                                |||||||||  |||||   ||||
                                AGTGTACGG TTGTT   ACCG
                                     T    T__
GAM1038  ZNF205   3' GCTGGGGCGGTGAGGGCATGG  12914       G   G  A    TG
                                TCATGT CCT AC GTCT  GC
                                ||||||  ||| || ||||  ||
                                GGTACG GGA TG CGGG  CG
                                   _  G  G   GT
GAM1038  ZNF217   3' GCTGAGTTTATTAGTACATGG  21517        C   C  T  TG
                                TCATGTGC TGA AG CT  GC
                                ||||||||  ||| || ||  ||
                                GGTACATG ATT TT GA  CG
                                     _  A  T  GT
GAM1038  ZNF239   5' CGTTAAGGTTGTCAGGATAATG 19039     GTG      GT
            G                    TCAT   CCTGACA  CTTGGC   G
                                ||||   |||||||  ||||||   |
                                GGTA   GGACTGT  GAATTG   C
                                  ATA      TG
GAM1038  ZNF239   5' GCTGAGATCATTGGCACTGTGG 19040     _    TGACA   TG
                                TCAT GTGCC    GTCT  GC
                                |||| |||||    ||||  ||
                                GGTG CACGG    TAGA  CG
                                  T    TTAC_   GT
GAM1038  ZNF264   3' GCTGGGGTTACAGGTGTGA   12760     GT    AC GT  TG
                                TCAT  GCCTG  A  CT  GC
                                ||||  |||||  |  ||  ||
                                AGTG  TGGAC  T  GG  CG
                                  __    A_ TG  GT
GAM1038  ZNF268   3' GGGTTTCAGGTACATGG     62900          C GT
                                TCATGTGCCTGA A  CT
                                ||||||||||| |  ||
```

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                                GGTACATGGACT T  GG
                                      _ TG
GAM1038 ZNF74    5' CCGGGAGGAGCGTGTGG     12791     TG  _  GACAG
                                TCA  TGC CT    TCTTGG
                                |||  ||| ||    ||||||
                                GGT  GCG GG    AGGGCC
                                  GT   A  _____
GAM1038 ZNF74    5' GCTGGGATTACAGGCGTGA   12799     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038 20D7-FC4 5' GCTGGGACTACAGGTGGCATG 60904      _    AC    TG
                                CATGT GCCTG  AGTCT  GC
                                ||||| |||||  |||||  ||
                                GTACG TGGAC  TCAGG  CG
                                   G    A_    GT
GAM1038 54TM     5' GTCGGTACCCTGGGCGCGGA   94795    A      ACA  C
                                TC TGTGCCTG   GT TTGGC
                                || ||||||||   || |||||
                                AG GCGCGGGT   CA GGCTG
                                 _       CC_  T
GAM1038 AAK1     3' GCTGGGATTGCAGGGGTGA    29850     GTG   A     TG
                                TCAT   CCTG CAGTCT  GC
                                ||||   |||| ||||||  ||
                                AGTG   GGAC GTTAGG  CG
                                  G__    _     GT
GAM1038 ABCC13   5' GCCGGGGCGGAGTGCGTG    56993     TG _  GACA
                                CATG  C CT    GTCTTGGC
                                ||||  | ||    ||||||||
                                GTGC  G GG    CGGGGCCG
                                  GT A  ____
GAM1038 AD024    5' CTAGAGTGGGCGCGGA      40340    A     TGA  G   T
                                TC TGTGCC   CA TCT GG
                                || ||||||   || ||| ||
                                AG GCGCGG   GT AGA TC
                                 _     ___  G   _
GAM1038 AD7C-NTP 3' GCTGGGATTACAGGCGTGA   27165     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038 ADAR3    3' GTTAAGACCTGTGACGTGG    38019      GCCTG   _
                                TCATGT    ACAG TCTTGGC
                                ||||||    |||| |||||||
                                GGTGCA    TGTC AGAATTG
                                   G____    C
GAM1038 ADNP     5' GCCGAGTCAAGGTGTGA     31048     GT    GACAGT
                                TCAT  GCCT     CTTGGC
                                ||||  ||||     ||||||
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                                AGTG  TGGA     GAGCCG
                                  __    ACT___
GAM1038  ADNP     3'  GTTGGACTGTGGGGCATGTGG  31050          G      TGGC
                                TCATGTGCCT ACAGTCT
                                |||||||||| |||||||
                                GGTGTACGGG TGTCAGG
                                      G      TTG
GAM1038  AGS3     5'  CCGAGGACAGGCACTGG     73112     T      ACAG
                                TCA GTGCCTG    TCTTGG
                                ||| |||||||    ||||||
                                GGT CACGGAC    GGAGCC
                                  _      A___
GAM1038  AK5      3'  GCTAGTCAGTACATGA      23911         C    _
                                TCATGTGC TGAC AGT
                                |||||||| |||| |||
                                AGTACATG ACTG TCG
                                     _    A
GAM1038  AKAP6    3'  CCTCTGTTGGGATATGG     14990       G  TG    TCTT
                                TCATGT CC  ACAG    GG
                                |||||| ||  ||||    ||
                                GGTATA GG  TGTC    CC
                                   _ GT    T___
GAM1038  AKR1D1   3'  CCAAGACGGTGCAATGG     19975      _ TG  TGACA
                                TCAT G  CC    GTCTTGG
                                |||| |  ||    |||||||
                                GGTA C  GG    CAGAACC
                                  A GT  ______
GAM1038  ALTE     3'  GCCAGGACTGATGGCATGTG   16389         TGA
                                CATGTGCC   CAGTCTTGGC
                                ||||||||   ||||||||||
                                GTGTACGG   GTCAGGACCG
                                     TA_
GAM1038  ALTE     3'  GCCAGGACTGATGGCATGTG   60360         TGA
                                CATGTGCC   CAGTCTTGGC
                                ||||||||   ||||||||||
                                GTGTACGG   GTCAGGACCG
                                     TA_
GAM1038  ALY      3'  GCTGGGGCTGTGCGCCCAATGA 19351      ___    CTG      TG
                                TCAT   GTGC   ACAGTCT  GC
                                ||||   ||||   |||||||  ||
                                AGTA   CGCG   TGTCGGG  CG
                                  ACC    ___      GT
GAM1038  AP1S3    3'  GCTGGGGCTACAGGTGTGTG   74920      TG    AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGT  GGAC  TCGGG  CG
                                  GT    A_    GT
GAM1038  APBA3    5'  TCGGGGCCGTCCGTGG      16884       TGCCT   A
                                TCATG    GAC GTCTTGG
                                |||||    ||| |||||||
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                                GGTGC    CTG CGGGGCT
                                  _____  C
GAM1038 API5    3' GCCGAGGTTGGGGCACACGA  21689    A     GA  GT
                                TC TGTGCCT  CA  CTTGGC
                                || |||||||  ||  ||||||
                                AG ACACGGG  GT  GAGCCG
                                 C      __  TG
GAM1038 APOARGC 3' CCACATCAGCACATGG     44418       C   CAGTCT
                                TCATGTGC TGA     TGG
                                |||||||| |||     |||
                                GGTACACG ACT     ACC
                                     _  AC____
GAM1038 APOL2   3' GCTGGGATTACAGGCGTGA  48050     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 APOL2   3' GTTGGGGTGGTTGTCATGTGA 48053       CCT   AG   TG
                                TCATGTG   GAC  TCT  GC
                                |||||||   |||  |||  ||
                                AGTGTAC   TTG  GGG  TG
                                    TG_   GT   GT
GAM1038 APOL4   3' GTCGAGACTGTAGGGAT    47629    G    A
                                GT CCTG CAGTCTTGGC
                                || |||| ||||||||||
                                TA GGAT GTCAGAGCTG
                                 G   _
GAM1038 APPD    3' GTTAGGACTCAGTTGCAAGA  44217    A   GC    CA
                                TC TGT  CTGA  GTCTTGGC
                                || |||  ||||  ||||||||
                                AG ACG  GACT  CAGGATTG
                                 A  TT   __
GAM1038 APXL2   5' GCTGGGACTACAGGCGTGTG  75191    TG     AC     TG
                                CA  TGCCTG  AGTCT  GC
                                ||  ||||||  |||||  ||
                                GT  GCGGAC  TCAGG  CG
                                 GT     A_    GT
GAM1038 APXL2   5' GTTGGGGAGGAAAGGAACATGG 75194       G   GACAG   TG
                                TCATGT CCT    TCT  GC
                                |||||| |||    |||  ||
                                GGTACA GGA    GGG  TG
                                   A   AAGGA   GT
GAM1038 ARGBP2  5' CGGGACGGGCACTGG      13194     T     GACA    TG
                                TCA GTGCCT    GTCT  G
                                ||| ||||||    ||||  |
                                GGT CACGGG    CAGG  C
                                  _     ____    GT
GAM1038 ARHF    3' GCTGGGATTACAGGCGTGA   38746     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 ARHGAP11A 3' GCTGGGATTACAGGCAT    28796       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038 ARHGDIG  3' GCTGGGACTGGGCCTGTG    6779      T  TGA    TG
                                CATG GCC   CAGTCT  GC
                                ||||  |||   ||||||  ||
                                GTGT CGG   GTCAGG  CG
                                  C  ___     GT
GAM1038 ARHGEF15 3' GCTGAGGAGGGGGCACATG   30260        GACAG  TG
                                CATGTGCCT    TCT  GC
                                |||||||||    |||  ||
                                GTACACGGG    GGA  CG
                                     GGA__   GT
GAM1038 ARHGEF4  3' CCTGGGTCAGTATATGG     52210       C   AGTCTT
                                TCATGTGC TGAC     GG
                                ||||||||  ||||     ||
                                GGTATATG ACTG     CC
                                    _   GGT___
GAM1038 ARPC4    3' TGGGGTGGGCATTTGA      19143     T     ACAG  TG
                                TCA GTGCCTG   TCT  G
                                |||  |||||||   |||  |
                                AGT TACGGGT   GGG  T
                                  T     _____  GT
GAM1038 ASAHL    3' CGAGATCATGCCATGG      63563      T  C   CAG  TG
                                TCATG GC TGA   TCT  G
                                |||||  ||  |||   |||  |
                                GGTAC CG ACT   AGA  C
                                   _  T   ___   GT
GAM1038 ASB16    3' GCTGGGATTACAGGTGTGA   69940     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 ASB16    3' GCTGGGACTACAGGCAT     55109       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TCAGG  CG
                                   A_    GT
GAM1038 ASB16    3' GTTGGGATTGCAGGCAT     55110       A     TG
                                GTGCCTG CAGTCT  GC
                                |||||||  ||||||  ||
                                TACGGAC GTTAGG  TG
                                   _     GT
GAM1038 ATP1B4   3' GCTGGGATTACAGGCGTGA   23823     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                              AGTG  CGGAC  TTAGG  CG
                                __    A_    GT
GAM1038 ATP6V1G3 5' GCTAAGATTGGCAGAAATGA  55712    GTGC  A
                              TCAT   CTG CAGTCTTGGC
                              ||||   ||| ||||||||||
                              AGTA   GAC GTTAGAATCG
                                AA__  G
GAM1038 ATP6V1G3 5' GCTAAGATTGGCAGAAATGA  55819    GTGC  A
                              TCAT   CTG CAGTCTTGGC
                              ||||   ||| ||||||||||
                              AGTA   GAC GTTAGAATCG
                                AA__  G
GAM1038 B3GNT1   5' CCGGGACGTGGATGTGG    21661      G  TGACA
                              TCATGT CC    GTCTTGG
                              |||||| ||    |||||||
                              GGTGTA GG    CAGGGCC
                                 _ TG___
GAM1038 B3GNT6   3' CGGGCTGGGTATGTG      22506       TGA  T  TG
                              CATGTGCC   CAG CT  G
                              ||||||||   ||| ||  |
                              GTGTATGG   GTC GG  C
                                 ___   _  GT
GAM1038 BAG5     3' GCTGGGAGTACAGGCATGTGG 16848         _ AG   TG
                              TCATGTGCCTG AC  TCT  GC
                              |||||||||||| ||  |||  ||
                              GGTGTACGGAC TG  AGG  CG
                                    A __  GT
GAM1038 BAG5     3' GCTGGGATTAACGGGTGTGA  16849    GT    AC    TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
                              AGTG  TGGGC  TTAGG  CG
                                __    AA    GT
GAM1038 BAG5     3' GTTGAGATTTCACCATGA    16850     TGCC  C    TG
                              TCATG   TGA AGTCT  GC
                              |||||   ||| |||||  ||
                              AGTAC   ACT TTAGA  TG
                                C___  _    GT
GAM1038 BIRC5    3' GTTGAGGCTGTCACAGTCCTGA 6751     TGTGCC       TG
                              TCA     TGACAGTCT  GC
                              |||     |||||||||  ||
                              AGT     ACTGTCGGA  TG
                                CCTGAC       GT
GAM1038 BLu      3' CCAGGGCCGGATGTGG     31905       G  TGACA
                              TCATGT CC    GTCTTGG
                              |||||| ||    |||||||
                              GGTGTA GG    CGGGACC
                                 _ C____
GAM1038 BM045    5' GCAGGATTGGCGTGTGG    78015    TG   TGAC     GC
                              TCA  TGCC   AGTCTTG
                              |||  ||||   |||||||
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                                GGT  GCGG   TTAGGAC
                                  GT  _____    GA
GAM1038 BNIP-S   3' GCCGAGATTACAGGTGTGA  56260    GT   AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  TGGAC  TTAGAGCCG
                                  __    A_
GAM1038 BP75     3' GCCAAGATTACCCATATG    23989      CCTGAC
                                CATGTG    AGTCTTGGC
                                ||||||    |||||||||
                                GTATAC    TTAGAACCG
                                   CCA___
GAM1038 BPESC1   3' GATGTTAGGTAATGG      41474     G       G
                                TCAT TGCCTGACA TC
                                |||| ||||||||| ||
                                GGTA ATGGATTGT AG

                                  _       _
GAM1038 BPESC1   3' GTTAAGTGATCAGTACGTGG  41476       C   CAGT
                                TCATGTGC TGA   CTTGGC
                                |||||||| |||   ||||||
                                GGTGCATG ACT   GAATTG
                                    _  AGT_
GAM1038 BPNT1    3' GCCGGGATTACAGGTGTGA   64756    GT   AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  TGGAC  TTAGGGCCG
                                  __    A_
GAM1038 BRPF3    5' GCCGGGGCCCCAGCGCG    92318     C  ACA
                                TGTGC TG   GTCTTGGC
                                ||||| ||   ||||||||
                                GCGCG AC   CGGGGCCG
                                  _ CC_
GAM1038 BS69     3' GTCACACCAGTGGGTATATGA 21768         ACA  CT
                                TCATGTGCCTG   GT  TGGC
                                ||||||||||   ||  ||||
                                AGTATATGGGT   CA  ACTG
                                      GAC  C_
GAM1038 BTN2A2   3' AAGCTGTTGGGCAGTGA    22775    G   TG   T
                                TCAT TGCC  ACAG CTT
                                |||| ||||  |||| |||
                                AGTG ACGG  TGTC GAA
                                  _   GT   _
GAM1038 BTN3A3   3' GCTGAGGCAGGGCAACATGA  22772      _   GACA   TG
                                TCATGT GCCT   GTCT  GC
                                |||||| ||||   ||||  ||
                                AGTACA CGGG   CGGA  CG
                                   A   A___   GT
GAM1038 C11orf14 5' GCTGAGGCTGCCGGGGGGCTGT 40229     _ G  _ A    TG
            GG                   TCAT GT CCT G CAGTCT  GC
                                |||| || ||| | ||||||  ||
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                                GGTG CG GGG C GTCGGA  CG
                                  T  G   G C     GT
GAM1038  C11orf17  3'  GTTGGGATTACAGGCGTGA   40213     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  TG
                                  __    A_    GT
GAM1038  C11orf21  3'  GCTGAGGCTGGCATGGGGTGA  26240     GTG  _  A     TG
                                TCAT   CC TG CAGTCT  GC
                                ||||   || || ||||||  ||
                                AGTG   GG AC GTCGGA  CG
                                  G__  T  G     GT
GAM1038  C11orf23  3'  GCCAGGGTTTGGCTCCACTGG  37013     _  T_   T   AGT
                                TCA TG  GCC GAC   CTTGGC
                                ||| ||  ||| |||   ||||||
                                GGT AC  CGG TTG   GGACCG
                                  C  CT   T  ___
GAM1038  C14orf4   5'  GCTGAAGCGGGCGCACGG    67338    A      A__
                                TC TGTGCCTG   CAGT
                                || ||||||||   ||||
                                GG ACGCGGGC   GTCG
                                 C       GAA
GAM1038  C16orf5   5'  GAGGGGTGGTCGGGTGTGTGG  25448      TG     AG    GGC
                                TCATG  CCTGAC  TCTT
                                |||||  ||||||  ||||
                                GGTGT  GGGCTG  GGGG
                                   GT     GT    AG
GAM1038  C16orf5   3'  GCTGAGGCTGACAGGCA     25451       A     TG
                                TGCCTG CAGTCT  GC
                                |||||| ||||||  ||
                                ACGGAC GTCGGA  CG
                                   A     GT
GAM1038  C17orf26  3'  GTTGAGATTAACTGGTGTGGTG 57545     _ TG  TGAC    TG
            G                    TCAT G  CC    AGTCT  GC
                                ||||  |  ||    |||||  ||
                                GGTG T  GG    TTAGA  TG
                                  G GT  TCAA    GT
GAM1038  C1orf17   5'  GCCGAGGCCAGTGTGTGA    68214      TG C  ACA
                                TCATG  C TG   GTCTTGGC
                                |||||  | ||   ||||||||
                                AGTGT  G AC   CGGAGCCG
                                   GT _  ___
GAM1038  C1orf24   3'  CGGGATTACAGCGTGA     53712      TGC   AC    TG
                                TCATG   CTG  AGTCT  G
                                |||||   |||  |||||  |
                                AGTGC   GAC  TTAGG  C
                                   ___   A_    GT
GAM1038  C1orf24   5'  CTAGCAGCGGGCGCGGA     53713    A      ACA  CT
                                TC TGTGCCTG   GT  TGG
                                || ||||||||   ||  |||
```

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                                AG GCGCGGGC   CG  ATC
                                 _      GA_  __
GAM1038  C1orf24   3'  GCCAAGGCTGGAGTGCAGTGG  53719     G   _  GA
                                TCAT TGC CT  CAGTCTTGGC
                                |||| ||| ||  ||||||||||
                                GGTG ACG GA  GTCGGAACCG
                                  _   T  G_
GAM1038  C1orf34   3'  GCTGGGGCTAACCATATGG   60675       CCTGAC    TG
                                TCATGTG     AGTCT  GC
                                |||||||     |||||  ||
                                GGTATAC     TCGGG  CG
                                    CAA___     GT
GAM1038  C1QTNF6   3'  GCTGGAGAGCTCAGGTGCTGG  49148     T TG    CAG  _ TG
                                TCA G  CCTGA   TC T  GC
                                ||| |  |||||   || |  ||
                                GGT C  GGACT   AG G  CG
                                  _ GT    CG_  A GT
GAM1038  C1QTNF6   3'  GCTGGGATTACAGGTGTGA   49149     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  C20orf110 3'  GTTGAGACTGGCTGAAATGA   79548     GT__   TGAC    TG
                                TCAT    GCC    AGTCT  GC
                                ||||    |||    |||||  ||
                                AGTA    CGG    TCAGA  TG
                                  AAGT   _____     GT
GAM1038  C20orf114 3'  GCTGGGAGTATGGGTGTGA   52602     GT    _  AG   TG
                                TCAT  GCCTG AC  TCT  GC
                                ||||  ||||| ||  |||  ||
                                AGTG  TGGGT TG  AGG  CG
                                  __    A  __   GT
GAM1038  C20orf126 3'  GCCACCAGTGGGTGTGTGG   47997      TG   G  AGTCT
                                TCATG  CCT AC    TGGC
                                |||||  ||| ||    ||||
                                GGTGT  GGG TG    ACCG
                                  GT   _  ACC__
GAM1038  C20orf142 3'  GCTGGGATTACAGGCAT     74778       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  C20orf167 3'  GCTGGGACTGCTCCTAGATGG  53663     G  CCT  _     TG
                                TCAT TG   GA CAGTCT  GC
                                |||| ||   || ||||||  ||
                                GGTA AT   CT GTCAGG  CG
                                  G  C__  C     GT
GAM1038  C20orf183 3'  GCTGGGGGTGGGCGCATG    47806       TGA  G   TG
                                CATGTGCC   CA TCT  GC
                                ||||||||   || |||  ||
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                                GTACGCGG  GT GGG  CG
                                   ___  G  GT
GAM1038  C20orf21  3'  GCTGGATGGTGTTGGGGCATGA 35115      G  TG  __   T
                                TCATGT CC  ACA  GTCT GGC
                                |||||| ||  |||  |||| |||
                                AGTACG GG  TGT  TAGG TCG
                                   _  GT  GG   _
GAM1038  C20orf28  5'  GCTGGGGCGGCCAGGCCGTGA  31226     T    ACA   TG
                                TCATG GCCTG  GTCT  GC
                                ||||| |||||  ||||  ||
                                AGTGC CGGAC  CGGG  CG
                                   _   CGG   GT
GAM1038  C20orf40  5'  GTTGGGGCTGGCCAGGGGTGG  25917     GTG   A_    TG
                                TCAT  CCTG  CAGTCT  GC
                                ||||  ||||  ||||||  ||
                                GGTG  GGAC  GTCGGG  TG
                                  G__   CG    GT
GAM1038  C20orf59  5'  GCCGGGGCCTTGGCAGGTGA  41995     G   TGACA
                                TCAT TGCC    GTCTTGGC
                                |||| ||||    ||||||||
                                AGTG ACGG    CGGGGCCG
                                  G   TTC__
GAM1038  C20orf64  3'  GCACCCTGTTGGGTATTGG   53221    T   TG   TCTTG
                                TCA GTGCC  ACAG    GC
                                ||| |||||  ||||    ||
                                GGT TATGG  TGTC    CG
                                  _   GT   CCA__
GAM1038  C20orf64  3'  GCACCCTGTTGGGTATTGG   53222    T   TG   TCTTG
                                TCA GTGCC  ACAG    GC
                                ||| |||||  ||||    ||
                                GGT TATGG  TGTC    CG
                                  _   GT   CCA__
GAM1038  C20orf72  3'  GCTGAGATTGGAAGGCAGTGA  53496     G   GA    TG
                                TCAT TGCCT  CAGTCT  GC
                                |||| |||||  ||||||  ||
                                AGTG ACGGA  GTTAGA  CG
                                  _   AG    GT
GAM1038  C21orf25  3'  GCTGGGATTATAGGCAT    63550       AC   TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGG  CG
                                   A_   GT
GAM1038  C22orf19  3'  CGAGGTGGGCGGATGA     13420     G    ACAG  TG
                                TCAT TGCCTG   TCT  G
                                |||| ||||||   |||  |
                                AGTA GCGGGT   GGA  C
                                  G     ____  GT
GAM1038  C22orf19  3'  GCTAGGATTATAGGCAT    13424       AC
                                GTGCCTG  AGTCTTGGC
                                |||||||  |||||||||
```

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                                TACGGAT  TTAGGATCG
                                   A_
GAM1038  C22orf19  3'  GCTGGGACCGCAGGTGTGTG  13426     TG   ACA   TG
                                CATG  CCTG   GTCT  GC
                                ||||  ||||   ||||  ||
                                GTGT  GGAC   CAGG  CG
                                  GT    GC_    GT
GAM1038  C22orf2   3'  GTTGGTGTTTGGCGTGTGA   94457    TG   T   GTC TG
                                TCA  TGCC GACA   T  GC
                                |||  |||| ||||   |  ||
                                AGT  GCGG TTGT   G  TG
                                  GT   T   ___ GT
GAM1038  C22orf23  3'  CCACGTCAGGTGGTGG     50783     G      AGTCT
                                TCAT TGCCTGAC    TGG
                                |||| ||||||||    |||
                                GGTG GTGGACTG    ACC
                                  _      C____
GAM1038  C22orf4   3'  GCCAAGACTGAATGTGA     60643      GCCTGA
                                TCATGT     CAGTCTTGGC
                                ||||||     ||||||||||
                                AGTGTA     GTCAGAACCG
                                   A_____
GAM1038  C3F       3'  GCTGGGATTACAGGCGTGA   19296     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  C6orf37   5'  GCTGGGGTGGCAGCGGCGCA  67479      __  A  G   TG
                                TGTGCC  TG CA TCT  GC
                                ||||||  || || |||  ||
                                ACGCGG  AC GT GGG  CG
                                   CG  G  _   GT
GAM1038  C6orf5    3'  GCTGGGATTACAGGTGTGA   31356     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  C9orf9    3'  GCTGGGATTACAGGCGTGA   38519     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  C9orf9    3'  GCTGGGATTACAGGTGTGA   38520     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  CAMTA1    5'  CCAGGGCGGGTGCGCGG    67915    A  TG   GACA
                                TC TG  CCT    GTCTTGG
                                ||  ||  |||   |||||||
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                                GG GC  GGG    CGGGACC
                                 C  GT  ____
GAM1038  caspr5   3'  GCTCTTAGGCACATGA      55382           C
                                TCATGTGCCTGA AGT
                                |||||||||||| |||
                                AGTACACGGATT TCG
                                       C
GAM1038  CBX6     3'  GTCAAGGTTGCTGGTACTGG  26624     T    TGA  GT
                                TCA GTGCC   CA  CTTGGC
                                ||| |||||   ||  ||||||
                                GGT CATGG   GT  GAACTG
                                  _    TC_  TG
GAM1038  CCR5     3'  GTCAGAGTTGTGCACATGG   5151        CTG   TC
                                TCATGTGC   ACAG  TTGGC
                                ||||||||   ||||  |||||
                                GGTACACG   TGTT  GACTG
                                     ___   GA
GAM1038  CDV-1    3'  GTTAGGATTACAGGCGTGA   48906     GT    AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  CGGAC  TTAGGATTG
                                  __    A_
GAM1038  CEBPG    5'  GCTAGAGGAGCAGGTACATG  8407          ACAG  _
                                CATGTGCCTG    TCT TGGC
                                ||||||||||    ||| ||||
                                GTACATGGAC    GGA ATCG
                                      GA__   G
GAM1038  CENTA2   3'  GCCAGGACTGAAGCTGTGG   37265      T  CTGA
                                TCATG GC    CAGTCTTGGC
                                ||||| ||    ||||||||||
                                GGTGT CG    GTCAGGACCG
                                  _ AA__
GAM1038  CENTA2   3'  GTCAATGGCCGGGCGCAGTGA  37268     _       ACA  _
                                TCA TGTGCCTG   GTC TTGGC
                                ||| ||||||||   ||| |||||
                                AGT ACGCGGGC   CGG AACTG
                                  G       ___   T
GAM1038  CG005    3'  AGATAGTAGGTATAT       29683          A A
                                ATGTGCCTG C GTCT
                                ||||||||| | ||||
                                TATATGGAT G TAGA
                                     _ A
GAM1038  CGRP-RCP 3'  GCTGAGGTTGTCAGGGCAGA  27131    A   G      GT  TG
                                TC TGT CCTGACA  CT  GC
                                || ||| |||||||  ||  ||
                                AG ACG GGACTGT  GA  CG
                                 _  _      TG  GT
GAM1038  ChGn     3'  GCTGATTCTGTCAGGCACTGA  37195     T         TC TG
                                TCA GTGCCTGACAG  T  GC
                                ||| ||||||||||  |  ||
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                                AGT CACGGACTGTC  A  CG
                                  _        TT GT
GAM1038 CHRAC1   3' GCCGGGATTACAGGCGTGA   33871     GT    AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  CGGAC  TTAGGGCCG
                                  __    A_
GAM1038 CHRAC1   3' GCTGGGATTACAGGCGTGTG  33874    TG    AC    TG
                                CA  TGCCTG  AGTCT  GC
                                ||  ||||||  |||||  ||
                                GT  GCGGAC  TTAGG  CG
                                 GT     A_    GT
GAM1038 CHRFAM7A 3' GCCAAGGTTGCTCGGGT    95019       _ GT
                                GCCTGA CA  CTTGGC
                                ||||||  ||  ||||||
                                TGGGCT GT  GAACCG
                                   C  TG
GAM1038 CILP     3' GCTACTGATTGGCACGTGG   13222        TGA   CTT
                                TCATGTGCC   CAGT   GGC
                                |||||||||   ||||   |||
                                GGTGCACGG   GTCA   TCG
                                     TTA   ___
GAM1038 CIP29    3' GCTGGATTACAGGCATA     50405        AC    T
                                TGTGCCTG  AGTCT GGC
                                ||||||||  ||||| |||
                                ATACGGAC  TTAGG TCG
                                   A_    _
GAM1038 CLL-1    5' GTCAAGATTTCTTTACAT    56367      CCT  C
                                ATGTG   GA AGTCTTGGC
                                |||||   || |||||||||
                                TACAT   CT TTAGAACTG
                                  TT_  _
GAM1038 CLPTM1   3' GTCAGGGCCCAGCGTGTGA   7105     TG   C  ACA
                                TCA  TGC TG   GTCTTGGC
                                |||  ||| ||   ||||||||
                                AGT  GCG AC   CGGGACTG
                                 GT   _ C__
GAM1038 CMG2     3' TGAGGCGGCAGTATGA      54166      _   TGACA   TG
                                TCATG TGCC    GTCT  G
                                ||||| ||||    ||||  |
                                AGTAT ACGG    CGGA  T
                                  G   _____   GT
GAM1038 COQ7     3' GCTGGGATTACAGGTGTGA   32333     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 CPSF2    3' GCTGGGACTACGGGCACATG  61591         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
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                                GTACACGGGC  TCAGG  CG
                                     A_    GT
GAM1038  CPSF2    3'  GCTGGGATTACAGGCAT    61592       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  CPSF2    3'  GCTGGGATTACAGGCGTGA   61593     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  CRMP5    3'  GCTGGTGCCAGGCGCGTG    39293         ACA  C TG
                                CATGTGCCTG   GT T  GC
                                ||||||||||   || |  ||
                                GTGCGCGGAC   CG G  CG
                                     ____  T GT
GAM1038  CRR9     5'  GCCGGGGGCGCCGGGCGCG   47879        ACA    _
                                TGTGCCTG   GTCTT GGC
                                ||||||||   ||||| |||
                                GCGCGGGC   CGGGG CCG
                                    CG_    G
GAM1038  CRTAM    3'  CTAGGGCAGCAACATGA     38980       _ CTGACA
                                TCATGT GC     GTCTTGG
                                ||||||  ||     |||||||
                                AGTACA CG     CGGGATC
                                   A  A_____
GAM1038  CSNK1G1  3'  GCCGAGGTGGAGGTAGTGG   41871     G    GA  G
                                TCAT TGCCT  CA TCTTGGC
                                ||||  |||||  ||  |||||||
                                GGTG ATGGA  GT GGAGCCG
                                  _    G_  _
GAM1038  D2S448   3'  GCCGAGGGCCAAGGGTGTGTG  73525     TG   GACAG
                                CATG  CCT    TCTTGGC
                                ||||  |||    |||||||
                                GTGT  GGG    GGAGCCG
                                  GT   AACCG
GAM1038  DBR1     3'  GCTGGGATTACAGGCGTGA   32535     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  DCAMKL1  3'  GCTAGGATCTGCAGTATGT   16413       C  A  _
                                ATGTGC TG CAG TCTTGGC
                                ||||||  ||  |||  |||||||
                                TGTATG AC GTC AGGATCG
                                   _  _   T
GAM1038  DCOHM    3'  GCTGGGACTACAGGTGCATG  49607     TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
```

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                                GTAC  GGAC  TCAGG  CG
                                  GT    A_    GT
GAM1038  DCOHM    3'  GCTGGGATTACAGGCAT     49608       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  DD96     3'  TGGGGCTCGGCTGTGG      19271      T   TGAC    TG
                                TCATG GCC    AGTCT  G
                                ||||| |||    |||||  |
                                GGTGT CGG    TCGGG  T
                                   _  C___    GT
GAM1038  DDM36    3'  TTAAGCTAAGGCATTGA     40580     T     GAC  T
                                TCA GTGCCT   AG CTTGG
                                ||| ||||||   || |||||
                                AGT TACGGA   TC GAATT
                                  _     A__  _
GAM1038  DDX12    3'  GCCGGGACCCAGGCACA     59700        ACA
                                TGTGCCTG   GTCTTGGC
                                ||||||||   ||||||||
                                ACACGGAC   CAGGGCCG
                                    C__
GAM1038  DDX25    3'  GTTGAGGCTTTTTCGACGTGA  25168       GCCT  C    TG
                                TCATGT    GA AGTCT  GC
                                ||||||    || |||||  ||
                                AGTGCA    TT TCGGA  TG
                                   GCT_  T    GT
GAM1038  DDX30    3'  CGGGGCTGTGTACAGA      94627    A    CTG     TG
                                TC TGTGC   ACAGTCT  G
                                || |||||   |||||||  |
                                AG ACATG   TGTCGGG  C
                                  _    ___      GT
GAM1038  DDX34    3'  GCTGGGATTACAGGCGTGA   27986     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  DEPP     3'  GCTGGGAATTGCGCATGTGA   22822        CT A   _  TG
                                TCATGTGC  G CAGT CT  GC
                                ||||||||  | |||| ||  ||
                                AGTGTACG  C GTTA GG  CG
                                    __ _    A  GT
GAM1038  DEPP     3'  GCTGGGACTGATCAGAGGTGA  22823     GTGC   _     TG
                                TCAT    CTGA CAGTCT  GC
                                ||||    |||| ||||||  ||
                                AGTG    GACT GTCAGG  CG
                                  GA__    A     GT
GAM1038  DJ159A19.3 5'  GTCGAGGCCTTCGGCGTGGGA  31652    ATG    T  CA
                                TC   TGCC GA  GTCTTGGC
                                ||   |||| ||  ||||||||
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                                AG  GCGG CT  CGGAGCTG
                                 GGT   _ TC
GAM1038  DKFZp434A2417 3'  GCTGGGATTAGAGGCGTGA   66106     GT   GAC    TG
                                TCAT  GCCT   AGTCT  GC
                                ||||  ||||   |||||  ||
                                AGTG  CGGA   TTAGG  CG
                                  __   GA_    GT
GAM1038  DKFZP434B044 3'   GCTGGGATTACAGGCAT    48927       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  DKFZP434B044 3'   GTCAGCCTGTCAGGTCGTGA  48928      T       T  T
                                TCATG GCCTGACAG CT GGC
                                ||||| ||||||||| || |||
                                AGTGC TGGACTGTC GA CTG
                                  _       C  _
GAM1038  DKFZP434B103 5'   GCCAGGATAAGGGGCACA    31591       GACA
                                TGTGCCT   GTCTTGGC
                                |||||||   ||||||||
                                ACACGGG   TAGGACCG
                                   GAA_
GAM1038  DKFZP434B103 3'   GTCAGGGCTGGAGGGCACA   31592       GA
                                TGTGCCT  CAGTCTTGGC
                                |||||||  ||||||||||
                                ACACGGG  GTCGGGACTG
                                   AG
GAM1038  DKFZP434C212 3'   GCTAGGACTACAGGCGCATG  68912         AC
                                CATGTGCCTG  AGTCTTGGC
                                ||||||||||  |||||||||
                                GTACGCGGAC  TCAGGATCG
                                     A_
GAM1038  DKFZP434D146 3'   GCTGGGATTATAGGCAT    31526       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGG  CG
                                   A_    GT
GAM1038  DKFZP434D146 3'   GCTGGGATTGTAAGAGTAT   31527     _ G     TG
                                GTGC CT ACAGTCT  GC
                                |||| || |||||||  ||
                                TATG GA TGTTAGG  CG
                                  A  A      GT
GAM1038  DKFZp434D177 5'   GTTGAGACAGCGGCGGTACTGG 79442    T    __ ACA   TG
                                TCA GTGCC  TG   GTCT  GC
                                |||  |||||  ||   ||||  ||
                                GGT CATGG  GC   CAGA  TG
                                  _    CG  GA_    GT
GAM1038  DKFZp434E2220 5'  GTTGAGGCCGGGCGCTGTGG   34301     _     ACA   TG
                                TCAT GTGCCTG   GTCT  GC
                                ||||  |||||||   ||||  ||
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                                GGTG CGCGGGC  CGGA  TG
                                  T     ___   GT
GAM1038  DKFZP434F0318 3' GCTGGGATTACAGGCAT    48013       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  DKFZp434F1819 5' GCTGGGATTACAGGCAT    50007       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  DKFZp434G171 5' CGGGGCTGGGAGCTGA     79432     T  G  TGA     TG
                                TCA GT CC   CAGTCT  G
                                ||| || ||   ||||||  |
                                AGT CG GG   GTCGGG  C
                                  _ A ___     GT
GAM1038  DKFZp434G171 3' TGGGGCACAGCCATGG     79439      T  C  ACA    TG
                                TCATG GC TG   GTCT  G
                                ||||| || ||   ||||  |
                                GGTAC CG AC   CGGG  T
                                   _ _ A__    GT
GAM1038  DKFZP434J037 3' GCTGGGATTACAGGCGTGA   48216     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038  DKFZP434K1172 5' GTCAGGACTGAAAGGGCACAGA 48444    A      GA_
                                TC TGTGCCT   CAGTCTTGGC
                                || |||||||   ||||||||||
                                AG ACACGGG   GTCAGGACTG
                                  _      AAA
GAM1038  DKFZP434K2235 3' GCTACCTGTTAGGAACATGA   83498       G       TCT
                                TCATGT CCTGACAG   TGGC
                                |||||| ||||||||   ||||
                                AGTACA GGATTGTC   ATCG
                                   A       C__
GAM1038  DKFZP434N161 3' GCCAGGGCTGATGCTGGGGTGT 78520     TG G  TGA__
            GG                    TCA  T CC    CAGTCTTGGC
                                |||  | ||    ||||||||||
                                GGT  G GG    GTCGGGACCG
                                  GT G  TCGTA
GAM1038  DKFZP434O125 3' CCAGGACTGCAAAGTGA     64959      GTGCC  A
                                TCAT    TG CAGTCTTGG
                                ||||    || |||||||||
                                AGTG    AC GTCAGGACC
                                  AA___  _
GAM1038  DKFZP434P0111 3' GCCAAGATGGGCAGTACGT    67371       C  ACA
                                ATGTGC TG   GTCTTGGC
                                |||||| ||   ||||||||
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                                TGCATG AC   TAGAACCG
                                   _ GGG
GAM1038  DKFZp547C176 3'  GCCTAATTGTCAGTTATATGA  67226       C       CTT
                                TCATGTG CTGACAGT   GGC
                                ||||||| ||||||||   |||
                                AGTATAT GACTGTTA   CCG
                                    T       AT_
GAM1038  DKFZP547E1010 5'  GCCGAGGCCGAGGCCGTGG   66936      T   GACA
                                TCATG GCCT    GTCTTGGC
                                ||||| ||||    ||||||||
                                GGTGC CGGA    CGGAGCCG
                                   _    GC__
GAM1038  DKFZP547E1010 5'  GCCGAGGCCGAGGCCGTGG   31543      T   GACA
                                TCATG GCCT    GTCTTGGC
                                ||||| ||||    ||||||||
                                GGTGC CGGA    CGGAGCCG
                                   _    GC__
GAM1038  DKFZp547G183 3'  ACTGTCAGGCAGGTGA      38021      G
                                TCAT TGCCTGACAGT
                                |||| ||||||||||
                                AGTG ACGGACTGTCA
                                  G
GAM1038  DKFZp547H025 3'  GCTGGGATTAAAGGCACGTG   39362        GAC    TG
                                CATGTGCCT   AGTCT  GC
                                |||||||||   |||||  ||
                                GTGCACGGA   TTAGG  CG
                                     AA_    GT
GAM1038  DKFZp547H025 3'  GCTGGGATTACAGGTGTGA   39363     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038  DKFZp547H236 5'  GCCGGGGTCCATGCGCGGA   78545    A    CT_   AGT
                                TC TGTGC   GAC   CTTGGC
                                || |||||   |||   ||||||
                                AG GCGCG   CTG   GGGCCG
                                 _    TAC   ____
GAM1038  DKFZp547J036 5'  GCTGGGGCTACGTCCATGTGG  50128       CCT   __    TG
                                TCATGTG   GAC  AGTCT  GC
                                |||||||   |||  |||||  ||
                                GGTGTAC   CTG  TCGGG  CG
                                    ___   CA    GT
GAM1038  DKFZp547M072 3'  GCTGGGGCTGAGGTCCCCATGG 61081      T__    GA     TG
                                TCATG   GCCT  CAGTCT  GC
                                |||||   ||||  ||||||  ||
                                GGTAC   TGGA  GTCGGG  CG
                                   CCC    __     GT
GAM1038  DKFZP547N043 3'  AATCCTGTCAGGTGTTTGG   49316    T TG      TC
                                TCA G  CCTGACAG  TT
                                ||| |  ||||||||  ||
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                                GGT T  GGACTGTC  AA
                                  T GT       CT
GAM1038  DKFZP564B147 3'  GCCAGGGCTTAAGTGTGCCTGG 82083     T TG _  GAC
                                TCA G  C CT   AGTCTTGGC
                                ||| |  | ||   |||||||||
                                GGT C  G GA   TCGGGACCG
                                  C GT T  AT_
GAM1038  DKFZP564D166 3'  GCCAGGAGTATAGGTATGTG   47679          _  AG
                                CATGTGCCTG AC  TCTTGGC
                                |||||||||| ||  |||||||
                                GTGTATGGAT TG  AGGACCG
                                      A  __
GAM1038  DKFZP564G0222 5'  GCTGGGGTTGGGAAGAACATGG 25898       GC  GA_  GT  TG
                                TCATGT  CT   CA  CT  GC
                                ||||||  ||   ||  ||  ||
                                GGTACA  GA   GT  GG  CG
                                   A_  AGG  TG  GT
GAM1038  DKFZP564I052 3'  GCTAGGGTTGTTAGTGGGTGA  66711     G   C    GT
                                TCAT TGC TGACA  CTTGGC
                                |||| ||| |||||  ||||||
                                AGTG GTG ATTGT  GGATCG
                                  G   _    TG
GAM1038  DKFZP564K0322 3'  GCTGGGATTACAGATGTGA   49360       GC   AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTGTA  GAC  TTAGG  CG
                                   __   A_    GT
GAM1038  DKFZP564O0423 3'  GCTGAGCCTCAGGTGTCTGG   91693     T TG    CA T  TG
                                TCA G  CCTGA  G CT  GC
                                ||| |  |||||  | ||  ||
                                GGT T  GGACT  C GA  CG
                                  C GT    C_ _  GT
GAM1038  DKFZP564O0423 3'  GCTGGGGTTACAGGTGTGA   91694      GT    AC GT  TG
                                TCAT  GCCTG  A  CT  GC
                                ||||  |||||  |  ||  ||
                                AGTG  TGGAC  T  GG  CG
                                  __    A_ TG  GT
GAM1038  DKFZp566H0824 5'  GCTGGGATTACAGGTAT     34053        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TATGGAC  TTAGG  CG
                                   A_    GT
GAM1038  DKFZP566I1024 3'  GCTGGGATTACAGGTGTGA   70105     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  DKFZP566M1046 3'  GCTGGGGCTAGGGCACA     49537        GAC    TG
                                TGTGCCT   AGTCT  GC
                                |||||||   |||||  ||
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                                ACACGGG  TCGGG  CG
                                    A__    GT
GAM1038  DKFZP566N034 3'  GTTAAGTGGTAATGGGTACAT  80142        __  AGT
                                ATGTGCCTG  AC   CTTGGC
                                |||||||||  ||   ||||||
                                TACATGGGT  TG   GAATTG
                                     AA  GT_
GAM1038  DKFZP586A0522 3'  GTTGGGATTACAGGTGTGA   25872     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  TG
                                   __    A_    GT
GAM1038  DKFZP586C1619 3'  CGCCAGGGCCCACCATGTCGGG 61934   G     _______
            GTATGG                T CCTGACA     GTCTTGGC   G
                                | |||||||     ||||||||   |
                                G GGGCTGT     CGGGACCG   C
                                _     ACCACC
GAM1038  DKFZP586C1619 3'  GCCGAGGCCAGGGCCTGTGG   61935      T   GACA
                                TCATG GCCT    GTCTTGGC
                                ||||| ||||    ||||||||
                                GGTGT CGGG    CGGAGCCG
                                   C    AC__
GAM1038  DKFZP586I2223 3'  GCCAGGTGGAGTGTATGTGG   54911        _ GA  GT
                                TCATGTGC CT  CA  CTTGGC
                                |||||||| ||  ||  ||||||
                                GGTGTATG GA  GT  GGACCG
                                     T  G_  __
GAM1038  DKFZP586I2223 3'  GCCAGGTGGAGTGTATGTGG   54920        _ GA  GT
                                TCATGTGC CT  CA  CTTGGC
                                |||||||| ||  ||  ||||||
                                GGTGTATG GA  GT  GGACCG
                                     T  G_  __
GAM1038  DKFZP586I2223 3'  GCCAGGTGGAGTGTATGTGG   31269        _ GA  GT
                                TCATGTGC CT  CA  CTTGGC
                                |||||||| ||  ||  ||||||
                                GGTGTATG GA  GT  GGACCG
                                     T  G_  __
GAM1038  DKFZP586M1120 3'  TCAGGGCTGGAGGTA      48470      GA
                                TGCCT  CAGTCTTGG
                                |||||  |||||||||
                                ATGGA  GTCGGGACT
                                   G_
GAM1038  DKFZp761J139 5'  GCTGGGATTACAGGCGTGA   50113     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038  DKFZp761J139 5'  GTCAGTGAGTGGTATGTGA   50116        TGAC G  _
                                TCATGTGCC    A TC TTGGC
                                |||||||||    | || |||||
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                                AGTGTATGG   T AG GACTG
                                     ____ G  T
GAM1038  DKFZp761N1114 3'  GCTGGGATTACAGGCGTGA   79020     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  DKFZp761O0113 5'  GCTGAGATTTACAGGCGTGA   37280     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGA  CG
                                  __    AT    GT
GAM1038  DKFZp761O17121 3'  CGAGCTGGGCATGTG      50139       TGA   T  TG
                                CATGTGCC   CAG CT  G
                                ||||||||   ||| ||  |
                                GTGTACGG   GTC GA  C
                                     ___   _  GT
GAM1038  DKFZp761O17121 5'  GCCAAGGCTGTTCAGGT     50140      _
                                GCCTGA CAGTCTTGGC
                                |||||| ||||||||||
                                TGGACT GTCGGAACCG
                                   T
GAM1038  DKFZP762D096 5'  GCCAGGAGCTGGCCCGGCGCGT 65578        TGA_  _
           GG                    TCATGTGCC    CAG TCTTGGC
                                |||||||||    ||| |||||||
                                GGTGCGCGG    GTC AGGACCG
                                     CCCG   G
GAM1038  DKFZp762P2111 3'  GCTGGGATTACAGGCGTGA   86358     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  Dlc2     3'  GCTGGGACTGTTTTGCACTGG  54760     T    CT       TG
                                TCA GTGC  GACAGTCT  GC
                                |||  ||||  ||||||||  ||
                                GGT CACG  TTGTCAGG  CG
                                  _   TT       GT
GAM1038  DNAL4    3'  GCCAGGGGCTGGTGTGTGG    19217      TG  TGAC    _
                                TCATG  CC    AGTCT TGGC
                                |||||  ||    ||||| ||||
                                GGTGT  GG    TCGGG ACCG
                                   GT  _____     G
GAM1038  DNLC2B   3'  GCCAAGGCTGTTTAAGCG    55652     CT_
                                TGC   GACAGTCTTGGC
                                |||   ||||||||||||
                                GCG   TTGTCGGAACCG
                                  AAT
GAM1038  DOCK3    3'  GCTGGCTCAGGCATGTGA    66504           __
                                TCATGTGCCTGA  CAGT
                                ||||||||||||  ||||
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                                AGTGTACGGACT GTCG
                                      CG
GAM1038 DOK4    3' GTCAAGGCTGTTTTTGAGTAT 36180     CT___
                                GTGC   GACAGTCTTGGC
                                ||||   ||||||||||||
                                TATG   TTGTCGGAACTG
                                  AGTTT
GAM1038 DORFIN  3' ACTCTCAGTATATGA     31256       C  C
                                TCATGTGC TGA AGT
                                |||||||| ||| |||
                                AGTATATG ACT TCA
                                     _  C
GAM1038 DRCTNNB1A 5' GTCGAGGTCCTGCAGGT    50844      A  __
                                GCCTG CAG  TCTTGGC
                                ||||| |||  |||||||
                                TGGAC GTC  GGAGCTG
                                  _  CT
GAM1038 DRIM    3' GCTGGGATTATAGGTGTGA   27179     GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAT  TTAGG  CG
                                  __   A_   GT
GAM1038 DSCR6   3' GCTGGGATTACAGGCGTGA   38550     GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __   A_   GT
GAM1038 DSCR6   3' GCTGGGATTGCAGGCAT    38551       A    TG
                                GTGCCTG CAGTCT  GC
                                ||||||| ||||||  ||
                                TACGGAC GTTAGG  CG
                                     _    GT
GAM1038 DVL2    3' GCCGGGCGCTCCTGGTGTGTGA 15361      TG  TGAC  _
                                TCATG  CC   AGT CTTGGC
                                |||||  ||   ||| ||||||
                                AGTGT  GG   TCG GGGCCG
                                  GT  TCC_  C
GAM1038 E2IG5   3' CCAGTTGAGTATATGG     26852       CT  AGTCT
                                TCATGTGC  GAC   TGG
                                ||||||||  |||   |||
                                GGTATATG  TTG   ACC
                                    AG  _____
GAM1038 E46L    5' GTTAGGGCTGTGTAGGGCG   25084     G__
                                TGCCT   ACAGTCTTGGC
                                |||||   ||||||||||
                                GCGGG   TGTCGGGATTG
                                  ATG
GAM1038 EDG2    3' GCCAGGGCAAGGTGGGGTGTGA 54066    GT   G  A__
                                TCAT  GCCT AC   GTCTTGGC
                                ||||  |||| ||   ||||||||
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                                AGTG  TGGG TG   CGGGACCG
                                  __    G  GAA
GAM1038  EDG2     3'  GCCAGGGCAAGGTGGGGTGTGA 7382      GT    G  A__
                                TCAT  GCCT AC   GTCTTGGC
                                ||||  |||| ||   ||||||||
                                AGTG  TGGG TG   CGGGACCG
                                  __    G  GAA
GAM1038  EFS2     3'  GCTGGGGCTCAGACATGG    19623       GC    CA    TG
                                TCATGT  CTGA  GTCT  GC
                                ||||||  ||||  ||||  ||
                                GGTACA  GACT  CGGG  CG
                                  __    __    GT
GAM1038  EIF2S2   3'  GCCAAGATTTTTGGCGAGTGG  14023     G    T  C
                                TCAT TGCC GA AGTCTTGGC
                                |||| |||| || |||||||||
                                GGTG GCGG TT TTAGAACCG
                                  A    T  _
GAM1038  EIF2S2   5'  TTGAAGACATTGTCGGGTGGTG 14024     G       __    GGC
              G                  TCAT TGCCTGACA  GTCTT
                                ||||  |||||||||  |||||
                                GGTG GTGGGCTGT  CAGAA
                                  _       TA    GTTG
GAM1038  EIF3S8   5'  GTCAGGGCCTGCGGTGTGA   13631     GT   T A  _
                                TCAT  GCC G CAG TCTTGGC
                                ||||  ||| | ||| |||||||
                                AGTG  TGG C GTC GGGACTG
                                  __  _ _  C
GAM1038  ENDOGLYX1 5'  CCAAGGCTGAGTGTGA     45400     GT  CTGA
                                TCAT  GC   CAGTCTTGG
                                ||||  ||   |||||||||
                                AGTG  TG   GTCGGAACC
                                  __ A___
GAM1038  EPS8R1   5'  TCAAGATAGAACATGA     34804       GC  GACA
                                TCATGT  CT   GTCTTGG
                                ||||||  ||   |||||||
                                AGTACA  GA   TAGAACT
                                   A_ _____
GAM1038  EREG     3'  GCTGGGACTACAGGCGCATG  7505          AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTACGCGGAC  TCAGG  CG
                                     A_    GT
GAM1038  EREG     3'  GCTGGGATTACAGGCGTGA   7506      GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  ERp44    3'  GTTAAGGCTGTTTTGCTTGGA  81696    ATGT  CT
                                TC   GC  GACAGTCTTGGC
                                ||   ||  ||||||||||||
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                                AG   CG  TTGTCGGAATTG
                                 GTT_  TT
GAM1038  ERp44    3'  GTTCACAGCCTAGTCAGGCATA 81697          _  T  _  C
              TGG                  TCATGTGCCTGAC AG CT TGG
                                ||||||||||||| || || |||
                                GGTATACGGACTG TC GA ACT
                                       A  C  C   TG
GAM1038  EVI5     3'  GCTGGGATTACAGGTGTGA   19003     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  EVI5     3'  GTTAAGCCTTCAGGTACGT   19009         C  T
                                ATGTGCCTGA AG CTTGGC
                                |||||||||| || ||||||
                                TGCATGGACT TC GAATTG
                                      _  C
GAM1038  EZF-2    3'  GCCAGGAGGAGCTTGGGCGCA  37102       TG CAG__
                                TGTGCC  A    TCTTGGC
                                ||||||  |    |||||||
                                ACGCGG  T    AGGACCG
                                   GT CGAGG
GAM1038  FADS1    3'  GCCAAGTAGCTTTGGGCATA   25479       TG C  __
                                TGTGCC  A AGT  CTTGGC
                                ||||||  | |||  ||||||
                                ATACGG  T TCG  GAACCG
                                   GT _  AT
GAM1038  FBP17    3'  GCTGAGATTACAGGTGTGA   72797     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGA  CG
                                  __    A_    GT
GAM1038  FBP17    3'  GCTGAGGCCCAGGCAGGTGA   72798     G     ACA   TG
                                TCAT TGCCTG   GTCT  GC
                                |||| ||||||   ||||  ||
                                AGTG ACGGAC   CGGA  CG
                                  G     C__    GT
GAM1038  FBXO24   5'  GCCAGATACAGGCGAGTGA   24092     G     ACA   T
                                TCAT TGCCTG   GTCT GGC
                                |||| ||||||   |||| |||
                                AGTG GCGGAC   TAGA CCG
                                  A     A__    _
GAM1038  FBXO24   5'  GCCAGATACAGGCGAGTGA   53169     G     ACA   T
                                TCAT TGCCTG   GTCT GGC
                                |||| ||||||   |||| |||
                                AGTG GCGGAC   TAGA CCG
                                  A     A__    _
GAM1038  FER1L4   3'  GCTGGGATTACAGGCGTGG   47354     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                GGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  FER1L4   3'  GCTGGGATTACAGGCGTGG   47355     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                GGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  FER1L4   3'  GCTGGGATTACAGGTGTGA   47356     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  FGD3     3'  GCCACTGAGTGGCAGGCGCATG 72897          A  G  T_
            A                    TCATGTGCCTG CA TC  TGGC
                                ||||||||||| || ||  ||||
                                AGTACGCGGAC GT AG  ACCG
                                      G  G  TC
GAM1038  FGF19    5'  GCTGGGGCCGGAGGCGGGGTGT 17588     TG G    ACA___    TG
            GA                   TCA  T CCTG     GTCT  GC
                                |||  | ||||     ||||  ||
                                AGT  G GGGC     CGGG  CG
                                  GT _   GGAGGC    GT
GAM1038  FJX1     5'  GCCGGGACCCGGGTGCCTGG   26788     T TG    ACA
                                TCA G  CCTG   GTCTTGGC
                                ||| |  ||||   ||||||||
                                GGT C  GGGC   CAGGGCCG
                                  C GT    C__
GAM1038  FKBP9    3'  GTTGGGATTACAGGCAT     94068       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  TG
                                    A_    GT
GAM1038  FLB6421  3'  GCTGGGATTACAGGCAT     39226       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  FLJ00007 3'  GCTAGGACCTGGGGCTGTGG   71277      T   GA  _
                                TCATG GCCT  CAG TCTTGGC
                                |||||  ||||  |||  |||||||
                                GGTGT CGGG  GTC AGGATCG
                                  _    __   C
GAM1038  FLJ00060 5'  GCTGGGATTACAGGCGTGA   61100     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  FLJ10035 5'  CCGGGGCAGCAAGTGA     35747     G   CTGACA
                                TCAT TGC     GTCTTGG
                                ||||  |||     |||||||
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                                AGTG ACG     CGGGGCC
                                  A  A_____
GAM1038  FLJ10044  3'  GCCAGGGCCATGCAGATGG   35768     G   C  ACA
                                TCAT TGC TG   GTCTTGGC
                                |||| ||| ||   ||||||||
                                GGTA ACG AC   CGGGACCG
                                  G   T  ___
GAM1038  FLJ10058  3'  GCGTTGTTAGACACGTGA    35785       C    A_____
                                TCATGTG CTGAC     GT
                                |||||||  |||||     ||
                                AGTGCAC GATTG     CG
                                    A     TTG
GAM1038  FLJ10081  3'  GCCCTGGACAGGTGTGTGG   35800      TG   A_   TCTT
                                TCATG  CCTG  CAG   GGC
                                |||||  ||||  |||   |||
                                GGTGT  GGAC  GTC   CCG
                                   GT   AG  _____
GAM1038  FLJ10101  3'  GCTGGGATGCCAGGCGTGA   45266     GT    ACA   TG
                                TCAT  GCCTG   GTCT  GC
                                ||||  |||||   ||||  ||
                                AGTG  CGGAC   TAGG  CG
                                  __    CG_   GT
GAM1038  FLJ10298  5'  GCCGAGACCCCCGCGCGGA   35990    A    CTGACA
                                TC TGTGC     GTCTTGGC
                                || |||||     ||||||||
                                AG GCGCG     CAGAGCCG
                                 _    CCCC__
GAM1038  FLJ10298  3'  GCTGGGATTACAGGCAT     35991       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  FLJ10346  5'  GCTGGGATTACAGGCGTGA   36046     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  FLJ10350  5'  GCCGGGAGGCTGCGGGCGCG   95506        A     __
                                TGTGCCTG CAGTCTT  GGC
                                |||||||| |||||||  |||
                                GCGCGGGC GTCGGAG  CCG
                                    _      GG
GAM1038  FLJ10420  3'  CCAAGGCGGGTGCTGG     36106     T TG   GACA
                                TCA G  CCT    GTCTTGG
                                ||| |  |||   |||||||
                                GGT C  GGG    CGGAACC
                                  _ GT   _____
GAM1038  FLJ10468  3'  CGGGGCCATGCCATGG     36145      T  C  ACA    TG
                                TCATG GC TG   GTCT  G
                                |||||  || ||   ||||  |
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                                GGTAC CG AC   CGGG  C
                                  _ T ___   GT
GAM1038 FLJ10521 3' GCCAGACGGGCAGGCACACGA 36218   A      ACA   T
                                TC TGTGCCTG   GTCT GGC
                                || ||||||||   |||| |||
                                AG ACACGGAC   CAGA CCG
                                 C       GGG   _
GAM1038 FLJ10535 3' GCTGGGATTACAGACATGA   36243      GC  AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTACA  GAC  TTAGG  CG
                                   __  A_    GT
GAM1038 FLJ10535 3' GCTGGGATTACAGGCAT     36244       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038 FLJ10560 3' GCTGGGATTACAGGCGTGA   36281     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 FLJ10579 5' GCCAGGGCGCCGGGTTTGTGG 36301      T    ACA
                                TCATG GCCTG   GTCTTGGC
                                ||||| |||||   ||||||||
                                GGTGT TGGGC   CGGGACCG
                                   T    CG_
GAM1038 FLJ10607 3' GCTGGAACTACAGGTGTGTG  77119     TG   AC   C TG
                                CATG  CCTG  AGT T  GC
                                ||||  ||||  ||| |  ||
                                GTGT  GGAC  TCA G  CG
                                  GT   A_   A GT
GAM1038 FLJ10607 3' GCTGGGACTATAGGTGCATG  77120     TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTAC  GGAT  TCAGG  CG
                                  GT   A_    GT
GAM1038 FLJ10704 3' CCGAGACTCTCATGTCA     36452   T  C   C
                                G GC TGA AGTCTTGG
                                | || ||| ||||||||
                                A TG ACT TCAGAGCC
                                 C  T   C
GAM1038 FLJ10704 3' GCTGAGGTTAGTGTGCTTGG  36457    T TG _    AGT  TG
                                TCA G  C CTGAC   CT  GC
                                ||| |  | |||||  ||  ||
                                GGT C  G GATTG   GA  CG
                                  T GT T    ___  GT
GAM1038 FLJ10718 3' GCTGCCTCAGGTATCATGG   36492      _     __
                                TCATG TGCCTGA  CAGT
                                ||||| |||||||  ||||
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                                GGTAC ATGGACT  GTCG
                                   T      CC
GAM1038  FLJ10718  3'  GCTGGGACCACAGGCACGTG   36493         ACA    TG
                                CATGTGCCTG   GTCT  GC
                                ||||||||||   ||||  ||
                                GTGCACGGAC   CAGG  CG
                                     AC_    GT
GAM1038  FLJ10724  5'  GTTGGGAACTCGCGGCGCGCGT 36506        _   AC   _  TG
           GA                    TCATGTGC CTG  AGT CT  GC
                                ||||||||  |||  |||  ||  ||
                                AGTGCGCG GGC  TCA GG  TG
                                    C   GC   A  GT
GAM1038  FLJ10748  5'  GCTGAGACTCGGGGCACGGTGA 36559      _     GAC    TG
                                TCAT GTGCCT   AGTCT  GC
                                ||||  ||||||   |||||  ||
                                AGTG CACGGG   TCAGA  CG
                                  G     GC_    GT
GAM1038  FLJ10781  3'  CCAAGATTGTGCCACG      36630      CCTG
                                TGTG    ACAGTCTTGG
                                ||||    ||||||||||
                                GCAC    TGTTAGAACC
                                  CG__
GAM1038  FLJ10781  3'  GCCGTGACTGTTCAGGTGTATG 36633       TG    _    T
           G                     TCATG  CCTGA CAGTC TGGC
                                |||||  |||||  |||||  ||||
                                GGTAT  GGACT GTCAG GCCG
                                   GT    T    T
GAM1038  FLJ10829  3'  GCCAAGGCTGAGCGGCA     36709      TGA
                                TGCC   CAGTCTTGGC
                                ||||   ||||||||||
                                ACGG   GTCGGAACCG
                                  CGA
GAM1038  FLJ10829  5'  GCTGGGATTACAGGCACGTG   36711         AC     TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGCACGGAC  TTAGG  CG
                                     A_    GT
GAM1038  FLJ10847  3'  GCTGAGACCACAGGCGTGTG   36752    TG     ACA    TG
                                CA  TGCCTG   GTCT  GC
                                ||  ||||||   ||||  ||
                                GT  GCGGAC   CAGA  CG
                                 GT     AC_    GT
GAM1038  FLJ10847  3'  GTTGGGATTATAGGCAT     36755       AC     TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGG  TG
                                    A_    GT
GAM1038  FLJ10876  3'  GTCAAGGCTCTTAGTACAGGA  36792    A    C   C
                                TC TGTGC TGA AGTCTTGGC
                                || ||||| ||| |||||||||
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                                AG ACATG ATT TCGGAACTG
                                 G    _  C
GAM1038  FLJ10901  3'  GCTGGGATTACAGGCAT    36830       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  FLJ10916  3'  GCTGAGTGAGGGGCTGTGA   36858     T   GA  GT  TG
                                TCATG GCCT  CA  CT  GC
                                ||||| ||||  ||  ||  ||
                                AGTGT CGGG  GT  GA  CG
                                   _   GA  __  GT
GAM1038  FLJ10922  3'  GCTGGGACCGCGGGTGTGTG  36878     TG   ACA   TG
                                CATG  CCTG   GTCT  GC
                                ||||  ||||   ||||  ||
                                GTGT  GGGC   CAGG  CG
                                  GT   GC_    GT
GAM1038  FLJ10925  3'  GCTGAGATTAGAGGGTGGTGA  36886     G    GAC    TG
                                TCAT TGCCT   AGTCT  GC
                                |||| |||||   |||||  ||
                                AGTG GTGGG   TTAGA  CG
                                  _    AGA    GT
GAM1038  FLJ10936  5'  GCGCAGCTGTCGGGACGTGA   36909      G       CT  _
                                TCATGT CCTGACAGT  TG GC
                                |||||| |||||||||  || ||
                                AGTGCA GGGCTGTCG  AC CG
                                   _       __  G  T
GAM1038  FLJ10956  3'  GCTGGGATTACAGGTAT    36917       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TATGGAC  TTAGG  CG
                                   A_    GT
GAM1038  FLJ10983  3'  GCCACTTTTTAGGTATATG   36940         CAGTCT
                                CATGTGCCTGA     TGGC
                                ||||||||||     ||||
                                GTATATGGATT     ACCG
                                      TTTC__
GAM1038  FLJ11042  3'  GCTGGGCGTGGTGGCATGTGG  37006        TGA  GT  TG
                                TCATGTGCC   CA  CT  GC
                                |||||||||   ||  ||  ||
                                GGTGTACGG   GT  GG  CG
                                    TG_  GC  GT
GAM1038  FLJ11125  3'  GCCAAGATTGAGAAACCTGG   59580    T  GC  GA
                                TCA GT  CT  CAGTCTTGGC
                                ||| ||  ||  ||||||||||
                                GGT CA  GA  GTTAGAACCG
                                  C  AA  __
GAM1038  FLJ11149  3'  GCTATCTTTAGGTGTGTGA   37109      TG    C  TCT
                                TCATG  CCTGA AG   TGGC
                                |||||  ||||| ||   ||||
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                              AGTGT  GGATT TC   ATCG
                                GT    _  T__
GAM1038  FLJ11159  3'  GCCAAGGCTATCATATAT    37119      CC   C
                              ATGTG  TGA AGTCTTGGC
                              |||||  ||| |||||||||
                              TATAT  ACT TCGGAACCG
                                __   A
GAM1038  FLJ11186  3'  GTTGGGATTACAGGCAT     37145       AC    TG
                              GTGCCTG  AGTCT  GC
                              |||||||  |||||  ||
                              TACGGAC  TTAGG  TG
                                 A_    GT
GAM1038  FLJ11280  5'  GTTAGGGCCCGGAGCGCATG   37211       _   ACA
                              CATGTGC CTG   GTCTTGGC
                              ||||||| |||   ||||||||
                              GTACGCG GGC   CGGGATTG
                                 A   C__
GAM1038  FLJ11370  3'  GTCAAGGCAGGGCACAGTGG   46373     _      GACA
                              TCA TGTGCCT    GTCTTGGC
                              ||| |||||||    ||||||||
                              GGT ACACGGG    CGGAACTG
                                G      A___
GAM1038  FLJ11560  5'  GCCAGTGCAGCAGGCAT     47216       ACA  C
                              GTGCCTG   GT TTGGC
                              |||||||   || |||||
                              TACGGAC   CG GACCG
                                 GA_  T
GAM1038  FLJ11560  3'  TCAGGGCCAAGCACTGG     47220     T    C  ACA
                              TCA GTGC TG   GTCTTGG
                              ||| |||| ||   |||||||
                              GGT CACG AC   CGGGACT
                                _    A  ___
GAM1038  FLJ11722  3'  GTTGGGAGGTCGAGGCAGGTGG 46398      G    _   AG   TG
                              TCAT TGCCT GAC  TCT  GC
                              |||| ||||| |||  |||  ||
                              GGTG ACGGA CTG  AGG  TG
                                G    G  G_   GT
GAM1038  FLJ11939  5'  GCCAGGACTTCTCCGTGTA    45175    TG CT_  C
                              TG  C   GA AGTCTTGGC
                              ||  |   || |||||||||
                              AT  G   CT TCAGGACCG
                                GT CCT  _
GAM1038  FLJ12078  3'  ACTGTGCTAGGCACGTGG     46450          __
                              TCATGTGCCTG  ACAGT
                              ||||||||||  |||||
                              GGTGCACGGAT  TGTCA
                                     CG
GAM1038  FLJ12287  3'  GCCGGGGCTGCGGTGCA     42316    TG  T A
                              TG  CC G CAGTCTTGGC
                              ||  || | ||||||||||
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                                AC  GG C GTCGGGGCCG
                                 GT  _ _
GAM1038  FLJ12438  3'  GCTGTCCTAGGTTGGGCAGGTG 41645     G    TG  AGTCT_
             G                   TCAT TGCC  AC     TGGC
                                 |||| ||||  ||     ||||
                                 GGTG ACGG  TG     GTCG
                                   G   GT  GATCCT
GAM1038  FLJ12476  3'  GTTAAGATTGTAGTAGTGCTGA 42953     T TG CTG_
                                 TCA G  C    ACAGTCTTGGC
                                 ||| |  |   ||||||||||
                                 AGT C  G    TGTTAGAATTG
                                  _ GT ATGA
GAM1038  FLJ12484  3'  CGGGGCAGGGCATTGG     42856     T     GACA    TG
                                 TCA GTGCCT    GTCT  G
                                 ||| ||||||    ||||  |
                                 GGT TACGGG    CGGG  C
                                   _     A___    GT
GAM1038  FLJ12484  3'  CGGGGCAGGGCATTGG     69653     T     GACA    TG
                                 TCA GTGCCT    GTCT  G
                                 ||| ||||||    ||||  |
                                 GGT TACGGG    CGGG  C
                                   _     A___    GT
GAM1038  FLJ12547  3'  GCCGAGGCTCTGTGGCTGTGG  46492      T   TGAC
                                 TCATG GCC    AGTCTTGGC
                                 ||||| |||    |||||||||
                                 GGTGT CGG    TCGGAGCCG
                                    _  TGTC
GAM1038  FLJ12581  3'  GCTGGGATTACAGGCGTGA    45880     GT    AC    TG
                                 TCAT  GCCTG  AGTCT  GC
                                 ||||  |||||  |||||  ||
                                 AGTG  CGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038  FLJ12610  3'  GCTGGGATTACAGGCAT     45513       AC    TG
                                 GTGCCTG  AGTCT  GC
                                 |||||||  |||||  ||
                                 TACGGAC  TTAGG  CG
                                     A_    GT
GAM1038  FLJ12649  3'  GCTGGGATTACAGGCATGTG   44781         AC    TG
                                 CATGTGCCTG  AGTCT  GC
                                 ||||||||||  |||||  ||
                                 GTGTACGGAC  TTAGG  CG
                                       A_    GT
GAM1038  FLJ12649  3'  GTTGGGATTACAGGTGTGA    44784     GT    AC    TG
                                 TCAT  GCCTG  AGTCT  GC
                                 ||||  |||||  |||||  ||
                                 AGTG  TGGAC  TTAGG  TG
                                   __    A_    GT
GAM1038  FLJ12671  3'  GTTGGGGCCAGGCATGGTGG   48283     _     ACA    TG
                                 TCAT GTGCCTG   GTCT  GC
                                 |||| |||||||   ||||  ||
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                                GGTG TACGGAC   CGGG  TG
                                  G      ___    GT
GAM1038  FLJ12687  3'  GCTAGGATTGAAGGTGCGTG   46197     TG   GA
                                CATG  CCT  CAGTCTTGGC
                                ||||  |||  ||||||||||
                                GTGC  GGA  GTTAGGATCG
                                  GT   A_
GAM1038  FLJ12687  3'  GCTGGGATTATAGGCGTGA    46199     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAT  TTAGG  CG
                                  __     A_    GT
GAM1038  FLJ12707  5'  GTCAGGGCGACCCTTGGGCGCT 41950     T     TG CA___
            GG                    TCA GTGCC  A    GTCTTGGC
                                ||| |||||  |    ||||||||
                                GGT CGCGG  T    CGGGACTG
                                  _    GT CCCAG
GAM1038  FLJ12747  5'  GCTAGGAATAAGGTGTACATGA 49719         _ GACAG
                                TCATGTGC CT    TCTTGGC
                                |||||||| ||    |||||||
                                AGTACATG GG    AGGATCG
                                     T  AATA_
GAM1038  FLJ12747  3'  GCTGGGATTACAGGCGTGA    49721     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __     A_    GT
GAM1038  FLJ12783  3'  GCCAAGACTGAGAAATACA    48680     CCTGA
                                TGTG    CAGTCTTGGC
                                ||||    ||||||||||
                                ACAT    GTCAGAACCG
                                  AAAGA
GAM1038  FLJ12788  3'  GCTGGGACTGTCAGCTCAT    42549     T  C       TG
                                ATG GC TGACAGTCT  GC
                                ||| || |||||||||  ||
                                TAC CG ACTGTCAGG  CG
                                  T  _       GT
GAM1038  FLJ12888  3'  GCTGGGACTATAGGCATGT    46320         AC    TG
                                ATGTGCCTG  AGTCT  GC
                                |||||||||  |||||  ||
                                TGTACGGAT  TCAGG  CG
                                     A_    GT
GAM1038  FLJ12891  5'  GCCCCTGTGTTAGGCCGTGA   46341      T      GTCTT
                                TCATG GCCTGACA    GGC
                                ||||| ||||||||    |||
                                AGTGC CGGATTGT    CCG
                                  _       GTCC_
GAM1038  FLJ12891  3'  GCTGGGACCACAGGCACGTG   46344          ACA   TG
                                CATGTGCCTG   GTCT  GC
                                ||||||||||   ||||  ||
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                              GTGCACGGAC  CAGG  CG
                                   AC_   GT
GAM1038  FLJ12903  3'  GCTGGGATTACAGGCAT    42775      AC    TG
                              GTGCCTG  AGTCT  GC
                              |||||||  |||||  ||
                              TACGGAC  TTAGG  CG
                                 A_    GT
GAM1038  FLJ12910  3'  GCTTGATTTTGGGCACATGA  44704       TG C   TT
                              TCATGTGCC  A AGTC  GGC
                              |||||||||  | ||||  |||
                              AGTACACGG  T TTAG  TCG
                                   GT _   T_
GAM1038  FLJ12969  5'  GCTGAGACGGGTGGGGGTATAT 43112       _ G  A_   TG
                              ATGTGCC T AC  GTCT  GC
                              |||||||  | ||  ||||  ||
                              TATATGG G TG  CAGA  CG
                                 G G  GG   GT
GAM1038  FLJ12969  5'  GTCAAGGCTGAGACGGGT   43114     A__
                              GCCTG   CAGTCTTGGC
                              |||||   ||||||||||
                              TGGGC   GTCGGAACTG
                                AGA
GAM1038  FLJ12975  3'  GCTGAGATTACAGGCAT    69588      AC    TG
                              GTGCCTG  AGTCT  GC
                              |||||||  |||||  ||
                              TACGGAC  TTAGA  CG
                                 A_    GT
GAM1038  FLJ12975  3'  GCTGGGATCACAGACGTGA   69589      GC   ACA   TG
                              TCATGT  CTG   GTCT  GC
                              ||||||  |||   ||||  ||
                              AGTGCA  GAC   TAGG  CG
                                 __  AC_   GT
GAM1038  FLJ13055  5'  CCAGGAGCGGCTGTGA     42711      T   TGACAG
                              TCATG GCC     TCTTGG
                              ||||| |||     ||||||
                              AGTGT CGG     AGGACC
                                 _  CG____
GAM1038  FLJ13057  5'  GTTGGGGCTGCGCGTGA     95650       CTGAC    TG
                              TCATGTGC    AGTCT  GC
                              ||||||||    |||||  ||
                              AGTGCGCG    TCGGG  TG
                                   _____    GT
GAM1038  FLJ13072  5'  GCTAAGATACCAGCTTGTGA  89815      T  C  ACA
                              TCATG GC TG   GTCTTGGC
                              ||||| || ||   ||||||||
                              AGTGT CG AC   TAGAATCG
                                 T  _  CA_
GAM1038  FLJ13072  5'  GCTGGGATTACAGGCATGTG  89817        AC    TG
                              CATGTGCCTG  AGTCT  GC
                              ||||||||||  |||||  ||
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                              GTGTACGGAC TTAGG CG
                                   A_   GT
GAM1038 FLJ13072 5' GCTGGGATTACAGGTGTGA  89818    GT   AC   TG
                              TCAT GCCTG AGTCT GC
                              |||| ||||| ||||| ||
                              AGTG TGGAC TTAGG CG
                                __   A_   GT
GAM1038 FLJ13102 3' GCTGGGATTACAGGCAT    46013      AC   TG
                              GTGCCTG AGTCT GC
                              ||||||| ||||| ||
                              TACGGAC TTAGG CG
                                 A_   GT
GAM1038 FLJ13114 3' GCTGGGATTACAGGCGTGA  44601    GT   AC   TG
                              TCAT GCCTG AGTCT GC
                              |||| ||||| ||||| ||
                              AGTG CGGAC TTAGG CG
                                __   A_   GT
GAM1038 FLJ13197 3' GCTGGGATTATAGGCGTGA  44859    GT   AC   TG
                              TCAT GCCTG AGTCT GC
                              |||| ||||| ||||| ||
                              AGTG CGGAT TTAGG CG
                                __   A_   GT
GAM1038 FLJ13305 5' GCTGGGATTACAGGCAT    90130      AC   TG
                              GTGCCTG AGTCT GC
                              ||||||| ||||| ||
                              TACGGAC TTAGG CG
                                 A_   GT
GAM1038 FLJ13310 5' GTTAGGGCTTATAGCAGCACAT 47086       C AC___
           GG                   TCATGTGC TG   AGTCTTGGC
                              |||||||| ||   |||||||||
                              GGTACACG AC   TCGGGATTG
                                 _ GATAT
GAM1038 FLJ13330 3' GCTGGGATTCCAGGCGTGA  46975    GT   AC   TG
                              TCAT GCCTG AGTCT GC
                              |||| ||||| ||||| ||
                              AGTG CGGAC TTAGG CG
                                __   C_   GT
GAM1038 FLJ13340 3' GCTAACAAAGCAGGTGTGTGG 54106     TG   ACAGTC
                              TCATG CCTG    TTGGC
                              ||||| ||||    |||||
                              GGTGT GGAC    AATCG
                                 GT   GAAAC_
GAM1038 FLJ13340 3' GTTGGGGCTTTAGCATCTGA  54109    T   C  C   TG
                              TCA GTGC TGA AGTCT GC
                              ||| |||| ||| ||||| ||
                              AGT TACG ATT TCGGG TG
                                C   _  _   GT
GAM1038 FLJ13352 3' GCCAAGAGTGGTGGCACATG  44754       TGA G
                              CATGTGCC  CA TCTTGGC
                              ||||||||  || |||||||
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                              GTACACGG  GT AGAACCG
                                  TG_  G
GAM1038 FLJ13397 3' TCAAGACTGGCAATTGG    46328    TG   TGAC
                              TCA  TGCC   AGTCTTGG
                              |||  ||||   ||||||||
                              GGT  ACGG   TCAGAACT
                                TA   ____
GAM1038 FLJ13590 5' GCTGGGATTCCAGGTGTGA   45787    GT    AC    TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
                              AGTG  TGGAC  TTAGG  CG
                                __    C_    GT
GAM1038 FLJ13769 3' GCTATGGTGTCAGGCACTGG  46617    T       G  T
                              TCA GTGCCTGACA TC TGGC
                              ||| ||||||||||| || ||||
                              GGT CACGGACTGT GG ATCG
                                _       _ T
GAM1038 FLJ13769 5' GTTGGGATTACAGGCGTGA   46624    GT    AC    TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
                              AGTG  CGGAC  TTAGG  TG
                                __    A_    GT
GAM1038 FLJ13912 3' GTCAGGACTTGGGTGCTGA   42865    T TG  TG CA
                              TCA G  CC  A  GTCTTGGC
                              ||| |  ||  |  ||||||||
                              AGT C  GG  T  CAGGACTG
                                _ GT  GT __
GAM1038 FLJ13940 3' GCCAAGAGGGCGTTTGGGCACT 46661    T    TG CA   ___
           GA                   TCA GTGCC  A  GTCT   TGGC
                              |||  |||||  |  ||||   ||||
                              AGT CACGG  T  CGGG   ACCG
                                _    GT TG    AGA
GAM1038 FLJ13952 3' GCTGGGATTACGGGCGTGA   45618    GT    AC    TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
                              AGTG  CGGGC  TTAGG  CG
                                __    A_    GT
GAM1038 FLJ13964 5' GTTGAGGCTGCTCGGTTGTGG  49794     T  T  _    TG
                              TCATG GCC GA CAGTCT  GC
                              ||||| ||| || ||||||  ||
                              GGTGT TGG CT GTCGGA  TG
                                _  _ C     GT
GAM1038 FLJ13993 5' GCTGAAGTAGGCGCGGA    60462    A      A__
                              TC TGTGCCTG   CAGT
                              || ||||||||   ||||
                              AG GCGCGGAT   GTCG
                               _      GAA
GAM1038 FLJ14054 3' GCTGTCACGGTGCATGA    44661      TG  _
                              TCATG  CC TGACAGT
                              |||||  || |||||||
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                                AGTAC  GG ACTGTCG
                                   GT  C
GAM1038  FLJ14100  5'  GCCAAGGGAGGTCTGGGCGTGA 46682       G  T   AG_
                                TCATGT CC GAC   TCTTGGC
                                |||||| || |||   |||||||
                                AGTGCG GG CTG   GGAACCG
                                   _  T   GAG
GAM1038  FLJ14146  3'  GTCAGGTTCACGGGTACAGA   45245    A      ACAGT
                                TC TGTGCCTG    CTTGGC
                                || ||||||||    ||||||
                                AG ACATGGGC    GGACTG
                                 _      ACTT_
GAM1038  FLJ14154  3'  GTCAGTGCCGCAGGTGCAT    45820    TG   ACA  C
                                ATG  CCTG   GT TTGGC
                                |||  ||||   || |||||
                                TAC  GGAC   CG GACTG
                                  GT   GC_  T
GAM1038  FLJ14213  3'  GCTGAGAATTTCTAGCATGTGA 45795        CT  CAG   TG
                                TCATGTGC  GA   TCT  GC
                                ||||||||  ||   |||  ||
                                AGTGTACG  CT   AGA  CG
                                     AT  TTA   GT
GAM1038  FLJ14225  3'  GCTGAGATGGTAGCATAGA   45903    A    C  ACA    TG
                                TC TGTGC TG   GTCT  GC
                                || ||||| ||   ||||  ||
                                AG ATACG AT   TAGA  CG
                                 _    _ GG_   GT
GAM1038  FLJ14299  5'  GCCGGGGCCAGCGGCGGTGG   46865     G    T ACA
                                TCAT TGCC G   GTCTTGGC
                                |||| |||| |   ||||||||
                                GGTG GCGG C   CGGGGCCG
                                  _   _ GAC
GAM1038  FLJ14346  5'  GCTGGGACTGAGAGTGTCATGG 46713      T  _  GA     TG
                                TCATG GC CT  CAGTCT  GC
                                ||||| || ||  ||||||  ||
                                GGTAC TG GA  GTCAGG  CG
                                   _  T  GA     GT
GAM1038  FLJ14351  3'  GCTAGGATTACAGGCGTGA   45326     GT    AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  CGGAC  TTAGGATCG
                                  __    A_
GAM1038  FLJ14351  3'  GCTGAGGAAGTGGCAGGTGTGT 45327      TG   __  AG   TG
           GG                    TCATG  CCTG  AC  TCT  GC
                                |||||  ||||  ||  |||  ||
                                GGTGT  GGAC  TG  GGA  CG
                                   GT   GG  AA  GT
GAM1038  FLJ14431  3'  GCTGAGGCAGGAGTATTGTGA  51354      _  _  GACA   TG
                                TCATG TGC CT   GTCT  GC
                                ||||| ||| ||   ||||  ||
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                              AGTGT ATG GG   CGGA  CG
                                 T   A  A___   GT
GAM1038  FLJ14442  3'  GCCAAGACCAGAGTGGTGG   51368     G  _  ACA
                              TCAT TGC CTG   GTCTTGGC
                              |||| ||| |||   ||||||||
                              GGTG GTG GAC   CAGAACCG
                                 _   A  ___
GAM1038  FLJ14547  5'  GCCGGGCAGTTGCGGGCGCGTG 51434          A   T__
            G                   TCATGTGCCTG CAG   CTTGGC
                              ||||||||||| |||   ||||||
                              GGTGCGCGGGC GTT   GGGCCG
                                    _  GAC
GAM1038  FLJ14564  3'  GCTGAGGCAGGGCCTGTGA   76503      T   GACA   TG
                              TCATG GCCT   GTCT  GC
                              ||||| ||||   ||||  ||
                              AGTGT CGGG   CGGA  CG
                                 C   A___   GT
GAM1038  FLJ14621  5'  GCCAAGGCCACGGTGTTTGA   51473     T TG  _  ACA
                              TCA G  CC TG   GTCTTGGC
                              ||| |  || ||   ||||||||
                              AGT T  GG AC   CGGAACCG
                                T GT  C  ___
GAM1038  FLJ14641  3'  GTTAGGACCTTTGCATTTGA   51490     T   CTGACA
                              TCA GTGC     GTCTTGGC
                              ||| ||||     ||||||||
                              AGT TACG     CAGGATTG
                                T   TTTC__
GAM1038  FLJ14721  3'  GCCAAGGTGGGGTGCAGGA   51584    A  TG   G  AGT
                              TC TG  CCT AC   CTTGGC
                              || ||  ||| ||   ||||||
                              AG AC  GGG TG   GAACCG
                               G  GT   G  ___
GAM1038  FLJ14950  3'  CCAAGGCTGGGCCTGA     51715     TGT   TGA
                              TCA   GCC   CAGTCTTGG
                              |||   |||   |||||||||
                              AGT   CGG   GTCGGAACC
                                C__   ___
GAM1038  FLJ14950  3'  GCTGGGATTACAGGCATGTG   51723          AC    TG
                              CATGTGCCTG  AGTCT  GC
                              ||||||||||  |||||  ||
                              GTGTACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  FLJ14957  3'  CTAAGACTGAGCATA      51746      CTGA
                              TGTGC   CAGTCTTGG
                              |||||   |||||||||
                              ATACG   GTCAGAATC
                                 A___
GAM1038  FLJ14957  3'  GCCGAGGCTGGAGTGCAATGG  51750     G  _  GA
                              TCAT TGC CT  CAGTCTTGGC
                              |||| ||| ||  ||||||||||
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                                GGTA ACG GA  GTCGGAGCCG
                                  _  T  G_
GAM1038  FLJ14957  3'  GCTGAGATTACAGGCAT    51753       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGA  CG
                                   A_    GT
GAM1038  FLJ20004  3'  GCTGGGATAACAGGTGTGGTGG 95295     _ TG   ACA   TG
                                TCAT G  CCTG   GTCT  GC
                                ||||  |  ||||   ||||  ||
                                GGTG T  GGAC   TAGG  CG
                                  G GT   AA_   GT
GAM1038  FLJ20005  5'  GCCAGGGTTTTCCTACGT    34317      CCT  C GT
                                ATGTG   GA A  CTTGGC
                                |||||   ||  |  ||||||
                                TGCAT   CT T  GGACCG
                                   C__  T TG
GAM1038  FLJ20015  3'  GTCAAGGTGACAGGCGTTGTGG 38639     GT_    A  G
                                TCAT   GCCTG CA TCTTGGC
                                ||||   ||||| || |||||||
                                GGTG   CGGAC GT GGAACTG
                                  TTG    A  _
GAM1038  FLJ20045  3'  GCTGGGATTACAGGCACATG   34423        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTACACGGAC  TTAGG  CG
                                     A_    GT
GAM1038  FLJ20045  3'  GCTGGGATTACAGGCAT     34424       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  FLJ20079  3'  GCCGAGACCAGCTGGGTCGTGG 34495      T   GACA_
                                TCATG GCCT    GTCTTGGC
                                |||||  ||||    ||||||||
                                GGTGC TGGG    CAGAGCCG
                                  _   TCGAC
GAM1038  FLJ20094  3'  GTCAGGATATCTGGCAGTGG   34558     G   T  CA
                                TCAT TGCC GA  GTCTTGGC
                                ||||  |||| ||  ||||||||
                                GGTG ACGG CT  TAGGACTG
                                  _   T  A_
GAM1038  FLJ20097  3'  GCTGGGATTACAGGCAT     34563       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  FLJ20136  3'  GCTAGGATTACAGGTGTGTG   34613     TG   AC
                                CATG  CCTG  AGTCTTGGC
                                ||||  ||||  |||||||||
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                                GTGT  GGAC  TTAGGATCG
                                  GT   A_
GAM1038  FLJ20136  3'  GCTGGGATTACAGGCAT    34615       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  FLJ20139  3'  GCTAAGATAGTAGATATGA   34625      GC   A A
                                TCATGT  CTG C GTCTTGGC
                                ||||||  ||| | ||||||||
                                AGTATA  GAT G TAGAATCG
                                   __   _ A
GAM1038  FLJ20147  3'  ACTGTCAGGGCATGG      34634       G
                                TCATGT CCTGACAGT
                                |||||| |||||||||
                                GGTACG GGACTGTCA

                                  _
GAM1038  FLJ20147  3'  GCTAAGACCACAGGTGTGTG  34640     TG   ACA
                                CATG  CCTG   GTCTTGGC
                                ||||  ||||   ||||||||
                                GTGT  GGAC   CAGAATCG
                                  GT   AC_
GAM1038  FLJ20150  3'  GCCAACCTTAGGGCACGTGG  34647         GAC  TC
                                TCATGTGCCT   AG  TTGGC
                                ||||||||||   ||  |||||
                                GGTGCACGGG   TC  AACCG
                                     AT_  C_
GAM1038  FLJ20151  3'  GCCAGTACTGTGGTGTGTGA  34651     TG  TG    C
                                TCATG  CC  ACAGT TTGGC
                                |||||  ||  ||||| |||||
                                AGTGT  GG  TGTCA GACCG
                                   GT  __    T
GAM1038  FLJ20151  3'  GCCAGTACTGTGGTGTGTGA  77528     TG  TG    C
                                TCATG  CC  ACAGT TTGGC
                                |||||  ||  ||||| |||||
                                AGTGT  GG  TGTCA GACCG
                                   GT  __    T
GAM1038  FLJ20154  3'  GCTGGGACTGTGCCCTGACATG 72929      ____  CTG      TG
                                CATGT   GC   ACAGTCT  GC
                                |||||   ||   |||||||  ||
                                GTACA   CG   TGTCAGG  CG
                                   GTCC  ___      GT
GAM1038  FLJ20188  3'  GTTAAGACTCAGGGGCACCTGA 34699     T     GAC
                                TCA GTGCCT   AGTCTTGGC
                                |||  ||||||   |||||||||
                                AGT CACGGG   TCAGAATTG
                                  C     GAC
GAM1038  FLJ20195  3'  GCTGGGACTACCGTACCTGG  34711     T   CTGAC    TG
                                TCA GTGC    AGTCT  GC
                                |||  ||||    |||||  ||
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                              GGT CATG    TCAGG  CG
                                C    CCA__    GT
GAM1038  FLJ20208  3'  GCTGGGATTACAGGCAT    34745       AC    TG
                              GTGCCTG  AGTCT  GC
                              |||||||  |||||  ||
                              TACGGAC  TTAGG  CG
                                 A_    GT
GAM1038  FLJ20308  3'  GAAAATTGTTGTGGTGTGTGG  66854      TG  _     CTTGGC
                              TCATG  CC TGACAGT
                              |||||  || |||||||
                              GGTGT  GG GTTGTTA
                                 GT  T      AAAG
GAM1038  FLJ20320  5'  GCCGAGGCCTGGAGTGGGT   34943     GA__  _
                              GCCT    CAG TCTTGGC
                              ||||    ||| |||||||
                              TGGG    GTC GGAGCCG
                                TGAG   C
GAM1038  FLJ20330  5'  GCTAGAGGTGGGTGTGTG    38620     TG   G  AG   T
                              CATG  CCT AC  TCT GGC
                              ||||  ||| ||  ||| |||
                              GTGT  GGG TG  AGA TCG
                                GT   _  G_  _
GAM1038  FLJ20333  5'  GCCGGGAAAAGTGGCACTGA   34957     T    TGACAG
                              TCA GTGCC     TCTTGGC
                              ||| |||||     |||||||
                              AGT CACGG     AGGGCCG
                                _     TGAAA_
GAM1038  FLJ20340  3'  GCCGAGATTGTGCCAC     34975     CCTG
                              GTG    ACAGTCTTGGC
                              |||    ||||||||||
                              CAC    TGTTAGAGCCG
                                CG__
GAM1038  FLJ20342  3'  GCCAGGGGCTACAGGCATAT   34989        AC    _
                              ATGTGCCTG  AGTCT TGGC
                              |||||||||  ||||| ||||
                              TATACGGAC  TCGGG ACCG
                                   A_    G
GAM1038  FLJ20342  3'  GCTGGGATTACAGGCGTGA   34991     GT    AC    TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
                              AGTG  CGGAC  TTAGG  CG
                                __     A_    GT
GAM1038  FLJ20344  3'  GCTGGGATTACAGGCAT     35014       AC    TG
                              GTGCCTG  AGTCT  GC
                              |||||||  |||||  ||
                              TACGGAC  TTAGG  CG
                                 A_    GT
GAM1038  FLJ20344  3'  GTTGGGATTACAGGCACATG   35015        AC    TG
                              CATGTGCCTG  AGTCT  GC
                              ||||||||||  |||||  ||
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                                GTACACGGAC  TTAGG  TG
                                     A_    GT
GAM1038  FLJ20356  5'  GCCGCAGGGCCAGGCATGTGA  38617         ACA   __
                                TCATGTGCCTG   GTCT  TGGC
                                ||||||||||   ||||  ||||
                                AGTGTACGGAC   CGGG  GCCG
                                      ___    AC
GAM1038  FLJ20359  3'  CCAGAGACAGGCGCA      35036       GACA   _
                                TGTGCCT    GTCT TGG
                                |||||||    |||| |||
                                ACGCGGA    CAGA ACC
                                    _____   G
GAM1038  FLJ20378  3'  GTCAGGGCCGACAGGTGTGG  35096     GT    ACA
                                TCAT  GCCTG   GTCTTGGC
                                ||||  |||||   ||||||||
                                GGTG  TGGAC   CGGGACTG
                                  __    AGC
GAM1038  FLJ20413  3'  CCGGGCCTGGCACATGG     35132        TGAC  T
                                TCATGTGCC    AG CTTGG
                                |||||||||    || |||||
                                GGTACACGG    TC GGGCC
                                     _____ C
GAM1038  FLJ20452  3'  GCCAGGGTTGGCACATGG    35203        TGAC GT
                                TCATGTGCC    A  CTTGGC
                                |||||||||    |  ||||||
                                GGTACACGG    T  GGACCG
                                     _____ TG
GAM1038  FLJ20489  3'  CCAGGTTGGGCACCTGG     35249     T    TG  AGTC
                                TCA GTGCC  AC    TTGG
                                ||| |||||  ||    ||||
                                GGT CACGG  TG    GACC
                                  C    GT  _____
GAM1038  FLJ20499  5'  GTCGGGACGGGAGCGCG     35260      _  GACA
                                TGTGC CT    GTCTTGGC
                                |||||  ||    ||||||||
                                GCGCG GG    CAGGGCTG
                                   A  G___
GAM1038  FLJ20506  3'  GCCAACAGCCACGTACGTGA  35267        C  ACAGTC
                                TCATGTGC TG     TTGGC
                                |||||||| ||     |||||
                                AGTGCATG AC     AACCG
                                     C  CGAC__
GAM1038  FLJ20507  3'  GCTGGGATTATAGGCAT     35295       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGG  CG
                                    A_    GT
GAM1038  FLJ20507  3'  GCTGGGATTATAGGCAT     60230       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
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                                TACGGAT  TTAGG  CG
                                   A_    GT
GAM1038  FLJ20508  3'  GCTGAGGGTATGTGA      35308         GA
                                TCATGTGCCT  CAGT
                                ||||||||||  ||||
                                AGTGTATGGG  GTCG
                                     A_
GAM1038  FLJ20511  3'  GCTGGGATTATAGGCGTGA   35328     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAT  TTAGG  CG
                                  __    A_    GT
GAM1038  FLJ20552  3'  GCCAGGACGGGCCACGTGG   35391       _  GACA
                                TCATGTG CCT    GTCTTGGC
                                |||||||  |||    ||||||||
                                GGTGCAC GGG    CAGGACCG
                                   C  ____
GAM1038  FLJ20584  3'  GCCAAGGCTGCCCTGGCGCTGA 35429     T    TGA_
                                TCA GTGCC    CAGTCTTGGC
                                |||  |||||    ||||||||||
                                AGT CGCGG    GTCGGAACCG
                                  _    TCCC
GAM1038  FLJ20623  5'  GCCGGACGGGCGGGCGCGGA   35467    A      ACA    T
                                TC TGTGCCTG   GTCT GGC
                                ||  ||||||||   ||||  |||
                                AG GCGCGGGC   CAGG CCG
                                  _      GGG   _
GAM1038  FLJ20643  5'  CCAGAGCAGGCACTGG      35490     T      ACAG   T
                                TCA GTGCCTG    TCT GG
                                |||  |||||||    |||  ||
                                GGT CACGGAC    AGA CC
                                  _      G___   _
GAM1038  FLJ20671  3'  GCTGGGATTACAGGCAT     35528        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  FLJ20699  3'  GTTAGGGCTGTTAGAGGGTGA  35565      GTGC
                                TCAT    CTGACAGTCTTGGC
                                ||||    ||||||||||||||
                                AGTG    GATTGTCGGGATTG
                                  GGA_
GAM1038  FLJ20700  3'  GCTGGGATTACAGGCGTGA   35579     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  FLJ20859  3'  GCCAGGGCTGAAGCTGCCTGG  42700     T  GC  GA
                                TCA GT  CT  CAGTCTTGGC
                                |||  ||  ||  ||||||||||
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                                GGT CG  GA  GTCGGGACCG
                                  C  TC  A_
GAM1038  FLJ20897  5'  GTTGGGATTACAGGTGTGA   50469     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  TG
                                  __    A_    GT
GAM1038  FLJ20958  3'  GCTGGGATTACAGGCGTGA   42059     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  FLJ20958  3'  GTTAGGATTACAGGCGTGA   42060     GT    AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  CGGAC  TTAGGATTG
                                  __    A_
GAM1038  FLJ20967  5'  GCCAGGATTGTGAGCTGTTTGG 41961     TG GC  G
                                TCA  T  CT ACAGTCTTGGC
                                |||  |  || ||||||||||
                                GGT  G  GA TGTTAGGACCG
                                  TT TC  G
GAM1038  FLJ21034  3'  GCTGCTTTCAGGTATGTG    46294          C   CTT
                                CATGTGCCTGA AGT   GGC
                                |||||||||| |||   |||
                                GTGTATGGACT TCG   TCG
                                      T  ___
GAM1038  FLJ21302  3'  GCTGGGATTACAGGCAT     43217        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  FLJ21308  5'  GTTAAGACTGATGATGTGTGTG 44867      TG CTGA_
                                CATG  C    CAGTCTTGGC
                                ||||  |    ||||||||||
                                GTGT  G    GTCAGAATTG
                                  GT TAGTA
GAM1038  FLJ21313  5'  GCCGGGGCAGAGCCAGGCGCGC 43685    A       ACA__
           GG                   TC TGTGCCTG    GTCTTGGC
                                || ||||||||    ||||||||
                                GG GCGCGGAC    CGGGGCCG
                                 C       CGAGA
GAM1038  FLJ21313  3'  GTCAAGAATCTGTGAGGCATGT 43688          G   __
           GA                   TCATGTGCCT ACAG  TCTTGGC
                                |||||||||| ||||  |||||||
                                AGTGTACGGA TGTC  AGAACTG
                                      G   TA
GAM1038  FLJ21324  5'  GCTGGGATTACAGGCAT     91205        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
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                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  FLJ21438  5'  GCTGAGCGTGTGGGTGCACG  61523      _ G  GT  TG
                                TGTGC CT ACA  CT  GC
                                |||||| || |||  ||  ||
                                GCACG GG TGT  GA  CG
                                   T  G   GC  GT
GAM1038  FLJ21459  3'  GCTGGGATTACAGGTGTGA   44518     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  FLJ21477  3'  GCTGATGGGCACTGG      47147     T      A
                                TCA GTGCCTG CAGT
                                ||| ||||||| ||||
                                GGT CACGGGT GTCG
                                  _      A
GAM1038  FLJ21603  3'  GTTGGGATTGCAGGCGTGA   45426     GT    A     TG
                                TCAT  GCCTG CAGTCT  GC
                                ||||  ||||| ||||||  ||
                                AGTG  CGGAC GTTAGG  TG
                                  __    _     GT
GAM1038  FLJ21616  3'  GCTGAGGTCGTGGCACAGGA   44689    A    _   AGT  TG
                                TC TGTGCC TGAC   CT  GC
                                || |||||| ||||   ||  ||
                                AG ACACGG GCTG   GA  CG
                                 G     T   ____ GT
GAM1038  FLJ21820  3'  GCCAGGATGGAGAGGCACTGG  41625     T     GACA
                                TCA GTGCCT    GTCTTGGC
                                ||| ||||||    ||||||||
                                GGT CACGGA    TAGGACCG
                                  _     GAGG
GAM1038  FLJ21820  3'  GTTAAGAGTATAGTTAGATATG 41626       C    AG___
            TGA                    CATGTG CTGAC    TCTTGGC
                                ||||||| |||||    |||||||
                                GTGTAT GATTG     AGAATTG
                                   A     ATATG
GAM1038  FLJ21841  3'  GCTAAGGTGAAAAGGGGTGTGG 44834     TG G   GA_  G
                                TCA  T CCT   CA TCTTGGC
                                |||  | |||   || |||||||
                                GGT  G GGA   GT GGAATCG
                                  GT G   AAA  _
GAM1038  FLJ21865  3'  TCAGCACAGGTGCGTGG     42811      TG   ACA  CT
                                TCATG  CCTG   GT  TGG
                                |||||  ||||   ||  |||
                                GGTGC  GGAC   CG  ACT
                                   GT   A__  __
GAM1038  FLJ22002  3'  GCTAGGATTACAGGCGTGA   45773     GT    AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
```

```
                                AGTG  CGGAC  TTAGGATCG
                                  __    A_
GAM1038  FLJ22035  3'  GTTAGGACTGAGAAGTGCA   44539    _  GA_
                                TGC CT   CAGTCTTGGC
                                ||| ||   ||||||||||
                                ACG GA   GTCAGGATTG
                                  T  AGA
GAM1038  FLJ22037  5'  GCCGAGCTGACGGAGCATGTGG 93915       _  A   T
                                TCATGTGC CTG CAG CTTGGC
                                |||||||| ||| ||| ||||||
                                GGTGTACG GGC GTC GAGCCG
                                    A  A  _
GAM1038  FLJ22060  3'  GCTATATATCAGGTATGTGA  44839         CAGTCT
                                TCATGTGCCTGA     TGGC
                                ||||||||||||     ||||
                                AGTGTATGGACT     ATCG
                                       ATAT__
GAM1038  FLJ22087  3'  GTCAGGGTTGTTGGAACAT   41958     GC TG   GT
                                ATGT  C  ACA  CTTGGC
                                ||||  |  |||  ||||||
                                TACA  G  TGT  GGACTG
                                  A_ GT   TG
GAM1038  FLJ22127  3'  TCAGGAGGTGCACATGG    42888       CTG  AG
                                TCATGTGC   AC  TCTTGG
                                ||||||||   ||  ||||||
                                GGTACACG   TG  AGGACT
                                    ____  G_
GAM1038  FLJ22167  5'  GCTGGGATTACAGGCGTGA   44579     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  FLJ22167  3'  GCTGGGGCGCATGG      44580        GA
                                TCATGTGCCT  CAGT
                                ||||||||||  ||||
                                GGTACGCGGG  GTCG
                                      __
GAM1038  FLJ22316  5'  GCTGGGACTACAGGTGTGG   46921     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                GGTG  TGGAC  TCAGG  CG
                                  __    A_    GT
GAM1038  FLJ22316  5'  GCTGGGATTACAGGCAT    46922       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  FLJ22329  3'  GCCGAGTGCTGGGGCACAGA  45072    A     GA   _
                                TC TGTGCCT  CAGT CTTGGC
                                || |||||||  |||| ||||||
```

```
                                AG ACACGGG  GTCG GAGCCG
                                 _     __   T
GAM1038  FLJ22329  3'  GCTAGGGTTACAGGCAT    45073       AC GT
                                GTGCCTG  A  CTTGGC
                                |||||||  |  ||||||
                                TACGGAC  T  GGATCG
                                   A_ TG
GAM1038  FLJ22329  3'  GCTGGGACTATAGGTGCGTG  45074     TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGC  GGAT  TCAGG  CG
                                  GT   A_    GT
GAM1038  FLJ22362  5'  GCCACCGAGTCGGGCGATGG  43077     G      AGTCT
                                TCAT TGCCTGAC    TGGC
                                |||| ||||||||    ||||
                                GGTA GCGGGCTG    ACCG
                                  _      AGCC_
GAM1038  FLJ22378  3'  GCCGGGGCCGTGGCCATGG   46900     T  TG  A
                                TCATG GCC  AC GTCTTGGC
                                ||||| |||  || ||||||||
                                GGTAC CGG  TG CGGGGCCG
                                  _  __  C
GAM1038  FLJ22378  3'  GCTGAGGCTGTGCACATG    46901       CTG     TG
                                CATGTGC   ACAGTCT  GC
                                |||||||   |||||||  ||
                                GTACACG   TGTCGGA  CG
                                   ____     GT
GAM1038  FLJ22477  3'  GCCTGGAGGACTGTTGGGCATG 45346       TG      ___
          T                      ATGTGCC  ACAGTCTT   GGC
                                |||||||  ||||||||   |||
                                TGTACGG  TGTCAGGA   CCG
                                   GT      GGT
GAM1038  FLJ22479  3'  GCTGTAATTGGGGTGCATGA   46076     TG   GA   CT
                                TCATG  CCT  CAGT  TGGC
                                |||||  |||  ||||  ||||
                                AGTAC  GGG  GTTA  GTCG
                                  GT   __   AT
GAM1038  FLJ22529  3'  GCTGGGATTACAGGCGTGA   45575     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  FLJ22625  5'  GTTAAGATGGCGGCGCG     45260       T ACA
                                TGTGCC G   GTCTTGGC
                                ||||||  |   ||||||||
                                GCGCGG C   TAGAATTG
                                   _ GG_
GAM1038  FLJ22625  3'  GTTGGGATTGCAGGTGTGA   45261     GT    A     TG
                                TCAT  GCCTG CAGTCT  GC
                                ||||  ||||| ||||||  ||
```

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                                AGTG  TGGAC GTTAGG  TG
                                  __    _     GT
GAM1038  FLJ22679  3'  GCTGGGATTGCTATGCACTGG  49923    T   C  A    TG
                                TCA GTGC TG CAGTCT  GC
                                ||| |||| || ||||||  ||
                                GGT CACG AT GTTAGG  CG
                                  _   T  C     GT
GAM1038  FLJ22679  3'  GCTGGGATTGCTATGCACTGG  34680    T   C  A    TG
                                TCA GTGC TG CAGTCT  GC
                                ||| |||| || ||||||  ||
                                GGT CACG AT GTTAGG  CG
                                  _   T  C     GT
GAM1038  FLJ22684  3'  GCTGGGATTACAGGCAT    46797       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  FLJ22756  3'  GCTAGGATTGAAGCCATCTGG  45582    T   C  GA
                                TCA GTG CT  CAGTCTTGGC
                                ||| ||| ||  ||||||||||
                                GGT TAC GA  GTTAGGATCG
                                  C   C  A_
GAM1038  FLJ22800  3'  GCTGGGACTACAGGTGCGTG  45605     TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGC  GGAC  TCAGG  CG
                                  GT   A_    GT
GAM1038  FLJ22940  5'  GCCGGGGCTGGCGGCGATGG  44697     G   TGA
                                TCAT TGCC   CAGTCTTGGC
                                |||| ||||   ||||||||||
                                GGTA GCGG   GTCGGGGCCG
                                  _   CG_
GAM1038  FLJ22965  3'  GCTGGGATTACGGGCATGTG  42052        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTACGGGC  TTAGG  CG
                                     A_    GT
GAM1038  FLJ22969  3'  GCTGGGATTACAGATGTGA   68655      GC  AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTGTA  GAC  TTAGG  CG
                                   __   A_    GT
GAM1038  FLJ23024  3'  GCTGGGATTACAGGCAT    46271       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  FLJ23047  3'  GTTGAGGATCACATGGTACGTG 44625        _  ACAG   TG
            G                    TCATGTGCC TG   TCT  GC
                                ||||||||| ||   |||  ||
```

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                                GGTGCATGG AC   GGA  TG
                                     T  ACTA   GT
GAM1038  FLJ23074  3'  GTTAAGGAGTAGGGCTGTGG  46821     T   G  AG
                                TCATG GCCT AC  TCTTGGC
                                ||||| |||| ||  |||||||
                                GGTGT CGGG TG  GGAATTG
                                   _   A  A_
GAM1038  FLJ23209  3'  CTAGGATTACAGCGTGA    46053     TGC   AC
                                TCATG   CTG  AGTCTTGG
                                |||||   |||  ||||||||
                                AGTGC   GAC  TTAGGATC
                                   ___   A_
GAM1038  FLJ23231  5'  GCCGCCGCTGGCGCATGG    46912       TGAC   CT
                                TCATGTGCC    AGT  TGGC
                                |||||||||    |||  ||||
                                GGTACGCGG    TCG  GCCG
                                     ____   CC
GAM1038  FLJ23231  3'  GCTCTCGCTGGGCACGTGG   46913       TGA   CTT
                                TCATGTGCC   CAGT   GGC
                                |||||||||   ||||   |||
                                GGTGCACGG   GTCG   TCG
                                     ___    CTC
GAM1038  FLJ23323  3'  GCTGGGATTACAGGCGTGA   45054    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038  FLJ23356  3'  GCTGAGGCTGGAGTGCAGTGA  49941    G  _  GA    TG
                                TCAT TGC CT  CAGTCT  GC
                                |||| ||| ||  ||||||  ||
                                AGTG ACG GA  GTCGGA  CG
                                   _  T  G_     GT
GAM1038  FLJ23356  3'  GCTGGGATTACAGGCGTGA   49942    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038  FLJ23375  5'  GTTGGGATCCAGGCAGCATGA  46359     _    ACA   TG
                                TCATG TGCCTG   GTCT  GC
                                ||||| ||||||   ||||  ||
                                AGTAC ACGGAC   TAGG  TG
                                   G     C__    GT
GAM1038  FLJ23392  3'  GCTGGGATTAAAGGCGTGA   45541    GT   GAC    TG
                                TCAT  GCCT   AGTCT  GC
                                ||||  ||||   |||||  ||
                                AGTG  CGGA   TTAGG  CG
                                   __   AA_    GT
GAM1038  FLJ23392  3'  GCTGGGATTACAGGCAT     45542       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
```

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                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  FLJ23471  5' GCTGGGGCTGGGCGCCGTGG  45299     _   TGA    TG
                                TCATG TGCC   CAGTCT  GC
                                ||||| ||||   ||||||  ||
                                GGTGC GCGG   GTCGGG  CG
                                   C   ___     GT
GAM1038  FLJ23519  3' GCTGGGATTACAGGCGTGA   49969    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  FLJ23519  5' GCCGGGCGCCCAGGCGTGTGG 69203    TG    ACA   T
                                TCA  TGCCTG   GTCT GGC
                                |||  ||||||   |||| |||
                                GGT  GCGGAC   CGGG CCG
                                  GT     CCG   _
GAM1038  FLJ23556  3' GCTGGGACTGTGGATGCTGG   45952    T  GC  G     TG
                                TCA GT  CT ACAGTCT  GC
                                ||| ||  || |||||||  ||
                                GGT CG  GG TGTCAGG  CG
                                  _ TA  _      GT
GAM1038  FLJ23556  3' GCTGGGATTACAGGCGTGA   45953    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  FLJ23556  3' GCTGGGATTACAGGCGTGTG  45954   TG    AC    TG
                                CA  TGCCTG  AGTCT  GC
                                ||  ||||||  |||||  ||
                                GT  GCGGAC  TTAGG  CG
                                 GT     A_    GT
GAM1038  FLJ23598  3' ACTTACACTGTGGGCATGTGG 45520        G    CTTGGC
                                TCATGTGCCT ACAGT
                                |||||||||| |||||
                                GGTGTACGGG TGTCA
                                      _    CATTCAT
GAM1038  FLJ25193  3' GCTGGGTGGGCACAGTGG    58700    _      A_
                                TCA TGTGCCTG  CAGT
                                ||| |||||||  ||||
                                GGT ACACGGGT  GTCG
                                  G       GG
GAM1038  FLJ30294  3' GCTATCATTCAGCATGTGA   58250       C   CA  CT
                                TCATGTGC TGA  GT  TGGC
                                |||||||| |||  ||  ||||
                                AGTGTACG ACT  TA  ATCG
                                     _  __  CT
GAM1038  FLJ30532  3' CGGGATTCAGGTGTGA     58544     GT    CA   TG
                                TCAT  GCCTGA  GTCT  G
                                ||||  ||||||  ||||  |
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                                AGTG  TGGACT  TAGG  C
                                  __    __    GT
GAM1038  FLJ30532  3'  GTTGGGATTACAGGCGTGA   58551     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  TG
                                  __    A_    GT
GAM1038  FLJ30567  3'  GTTGGGACTGTCTGCTCTATG 58829     T_ CT      TG
                                CATG  GC  GACAGTCT  GC
                                ||||  ||  ||||||||  ||
                                GTAT  CG  CTGTCAGG  TG
                                  CT  T_      GT
GAM1038  FLJ31101  3'  CGGGATTAGGTGTGA      35709     GT    ACA   TG
                                TCAT  GCCTG   GTCT  G
                                ||||  |||||   ||||  |
                                AGTG  TGGAT   TAGG  C
                                  __    ___   GT
GAM1038  FLJ31153  3'  GCTGGGATTACAGGTGTGA   58126     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  FLJ31300  3'  GTCAGGGCCAGGGCTCATGA  58287      T   GACA
                                TCATG GCCT    GTCTTGGC
                                |||||  ||||   ||||||||
                                AGTAC CGGG    CGGGACTG
                                   T   AC__
GAM1038  FLJ31528  3'  GCTGAGGCTGGGTTTGGTGCAT 58375     TG  TGA__     TG
            G                    CATG  CC    CAGTCT  GC
                                ||||  ||    ||||||  ||
                                GTAC  GG    GTCGGA  CG
                                  GT  TTTGG     GT
GAM1038  FLJ31890  5'  GCCGAGACCCTGCAGGT     91340      A  __
                                GCCTG CA  GTCTTGGC
                                |||||  ||  ||||||||
                                TGGAC GT  CAGAGCCG
                                   _  CC
GAM1038  FLJ31978  3'  GACTCTGACAGGCACGTGG    58350          AC__
                                TCATGTGCCTG    AGTC
                                ||||||||||    ||||
                                GGTGCACGGAC    TCAG
                                      AGTC
GAM1038  FLJ32334  3'  GCTGGGATTACAGGCGTGA   57984     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  FLJ32865  3'  GCTGGGATTACAGGCGTGA   58178     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
```

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                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  FLJ32919  3'  GCTGGGGCTGTGCAGCCA   58077   C  _     TG
                                TG CTG ACAGTCT  GC
                                || ||| |||||||  ||
                                AC GAC TGTCGGG  CG
                                 C  G     GT
GAM1038  FOXD4   3'  GTCAGGGGAGCGGGTACA   82750       ACAG
                                TGTGCCTG   TCTTGGC
                                ||||||||   |||||||
                                ACATGGGC   GGGACTG
                                    GAG_
GAM1038  FOXP1   5'  CGGGGCTCAGCATGG     51063     TGC   CA   TG
                                TCATG  CTGA  GTCT  G
                                |||||  ||||  ||||  |
                                GGTAC  GACT  CGGG  C
                                  ____   __   GT
GAM1038  FUK     3'  CCAGCCTTGGCATATGG    58973       TGACA  CT
                                TCATGTGCC    GT  TGG
                                |||||||||    ||  |||
                                GGTATACGG    CG  ACC
                                    TTC__  __
GAM1038  GCAT    3'  CGGGCTGGGACGTGA      59966      G  TGA   T  TG
                                TCATGT CC   CAG CT  G
                                |||||| ||   ||| ||  |
                                AGTGCA GG   GTC GG  C
                                  _ ____   _  GT
GAM1038  GGA2    3'  GCTGGGACTACAGGCGTGA   56885    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TCAGG  CG
                                  __    A_    GT
GAM1038  GGA2    3'  GCTGGGATTACAGGCGTGA   56886    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  GGA2    3'  GCTGGGACTACAGGCGTGA   30471    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TCAGG  CG
                                  __    A_    GT
GAM1038  GGA2    3'  GCTGGGATTACAGGCGTGA   30472    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  GIT1    3'  GCCTGCGTGTTGAGTGTGTGG  25867     TG CT   _  CTT
                                TCATG  C  GACA GT   GGC
                                |||||  |  |||| ||   |||
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                              GGTGT  G  TTGT CG   CCG
                                GT AG   G  T__
GAM1038  GK001    3'  TGAGGCTGGGTATGT     39501       TGA    TG
                              ATGTGCC   CAGTCT  G
                              |||||||   ||||||  |
                              TGTATGG   GTCGGA  T
                                 ___     GT
GAM1038  GLYAT    3'  GTTGGGCAGGTCTGGGCGTAT  91631        _   AGT  TG
                              ATGTGCCT GAC   CT  GC
                              |||||||| |||   ||  ||
                              TATGCGGG CTG   GG  TG
                                  T   GAC  GT
GAM1038  GMPPB    3'  GCCAGGGCCAGGGCTGTATGG  25302     GT_   GACA
                              TCAT   GCCT   GTCTTGGC
                              ||||   ||||   ||||||||
                              GGTA   CGGG   CGGGACCG
                                TGT   AC__
GAM1038  GMPPB    5'  GCCAGGGCCAGGGCTGTATGG  95741     GT_   GACA
                              TCAT   GCCT   GTCTTGGC
                              ||||   ||||   ||||||||
                              GGTA   CGGG   CGGGACCG
                                TGT   AC__
GAM1038  GMPPB    5'  GCTGGGATTACAGGCGTGA   95745     GT    AC    TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
                              AGTG  CGGAC  TTAGG  CG
                                __    A_    GT
GAM1038  GMPPB    3'  GCCAGGGCCAGGGCTGTATGG  41746     GT_   GACA
                              TCAT   GCCT   GTCTTGGC
                              ||||   ||||   ||||||||
                              GGTA   CGGG   CGGGACCG
                                TGT   AC__
GAM1038  GNG4     3'  GCTGGGATTACAGGCGTGA   15620     GT    AC    TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
                              AGTG  CGGAC  TTAGG  CG
                                __    A_    GT
GAM1038  GP5      3'  GCTGGGATTAGAGGCGTGTG  15653    TG    GAC    TG
                              CA  TGCCT   AGTCT  GC
                              ||  |||||   |||||  ||
                              GT  GCGGA   TTAGG  CG
                               GT    GA_    GT
GAM1038  GPA33    5'  GCTGAGGCTGGGCAGAGGTGG  19455     G__   TGA    TG
                              TCAT   TGCC   CAGTCT  GC
                              ||||   ||||   ||||||  ||
                              GGTG   ACGG   GTCGGA  CG
                                GAG    ___     GT
GAM1038  GPR      5'  GCCGGGGTTGGCGATGTGG   23334       _   TGAC GT
                              TCATGT GCC    A  CTTGGC
                              |||||| |||    |  ||||||
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                                GGTGTA CGG   T  GGGCCG
                                   G  ____ TG
GAM1038  GPR88    3'  GCTAGAACTTATTGGGCATGTG 41880        TG C_  CT
              G                    TCATGTGCC  A  AGT  TGGC
                                   |||||||||  |  |||  ||||
                                   GGTGTACGG  T  TCA  ATCG
                                        GT AT   AG
GAM1038  GPS2     5'  GTCGGCCTGTGGGCGTACG   87162      _ G   T  T
                                   TGTGC CT ACAG CT GGC
                                   |||||  ||  ||||  ||  |||
                                   GCATG GG TGTC GG CTG
                                     C  G   C  _
GAM1038  GPT2     3'  GCCGGGAGCGCAGTAGCACGTG 55956        __  ACAG
              G                    TCATGTGC  CTG   TCTTGGC
                                   ||||||||  |||   |||||||
                                   GGTGCACG  GAC   AGGGCCG
                                       AT   GCG_
GAM1038  GREB1    3'  GCTGGGATTACAGGCAT    27880       AC    TG
                                   GTGCCTG  AGTCT  GC
                                   |||||||  |||||  ||
                                   TACGGAC  TTAGG  CG
                                       A_    GT
GAM1038  GREB1    3'  GCTGGGATTACAGGCGTGA   27881     GT    AC    TG
                                   TCAT  GCCTG  AGTCT  GC
                                   ||||  |||||  |||||  ||
                                   AGTG  CGGAC  TTAGG  CG
                                     __    A_    GT
GAM1038  GRP3     3'  GCTGGGACTGAGCCTGTGA   31120     T  CTGA     TG
                                   TCATG GC   CAGTCT  GC
                                   |||||  ||   ||||||  ||
                                   AGTGT CG   GTCAGG  CG
                                     C  A___     GT
GAM1038  GRWD     3'  GCCAGGATTTCTCCGTGTGG  48966    TG  CCT  C
                                   TCA  TG   GA AGTCTTGGC
                                   |||  ||   ||  |||||||||
                                   GGT  GC   CT TTAGGACCG
                                     GT  CT_  _
GAM1038  GRWD     3'  GCTGGGATTACAGGCATGTG  48969        AC    TG
                                   CATGTGCCTG  AGTCT  GC
                                   ||||||||||  |||||  ||
                                   GTGTACGGAC  TTAGG  CG
                                        A_    GT
GAM1038  GRWD     3'  GTTGGGATTACAGGCGTGA   48970     GT    AC    TG
                                   TCAT  GCCTG  AGTCT  GC
                                   ||||  |||||  |||||  ||
                                   AGTG  CGGAC  TTAGG  TG
                                     __    A_    GT
GAM1038  GSH-2    5'  GCCGGGGCGCCGGGCGGGTGG  55740     G     ACA
                                   TCAT TGCCTG   GTCTTGGC
                                   |||| ||||||   ||||||||
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                                GGTG GCGGGC  CGGGGCCG
                                  G    CG_
GAM1038 GTF2H3   3' GCTGGGATTACAGGCGTGA  7706     GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG CG
                                  __   A_   GT
GAM1038 GTPBG3   3' GCTGGGATCACAGGCGTGA  50903    GT   ACA  TG
                                TCAT GCCTG  GTCT GC
                                |||| |||||  |||| ||
                                AGTG CGGAC  TAGG CG
                                  __   AC_  GT
GAM1038 GTPBG3   3' GCTGGGATTACAGGCATGTG  50904       AC   TG
                                CATGTGCCTG AGTCT GC
                                |||||||||| ||||| ||
                                GTGTACGGAC TTAGG CG
                                     A_   GT
GAM1038 GTPBP1   3' GTTGGGCCTCAGGCACTGG  15016    T     CA T TG
                                TCA GTGCCTGA G CT GC
                                ||| |||||||| | ||  ||
                                GGT CACGGACT C GG TG
                                 _     C_ _ GT
GAM1038 H17      3' GCCGAGGCCAATAGCGAGTGA 34090    G  CTGACA
                                TCAT TGC    GTCTTGGC
                                |||| |||    ||||||||
                                AGTG GCG    CGGAGCCG
                                  A  ATAAC_
GAM1038 H326     3' GCTGGGGCTGCCAACCTGA  31708    T GCC A    TG
                                TCA GT  TG CAGTCT GC
                                ||| ||  || ||||||  ||
                                AGT CA  AC GTCGGG CG
                                  C ___ C    GT
GAM1038 HAIK1    5' GCCAGGGTTGTTTGGTTTTGA 31334    TGT  T   GT
                                TCA  GCC GACA CTTGGC
                                |||  ||| |||| ||||||
                                AGT  TGG TTGT GGACCG
                                  TT_  T   TG
GAM1038 HARS2    3' GCTGGGATTACAGGTGTGA  55036    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG TGGAC TTAGG CG
                                  __   A_   GT
GAM1038 HCA4     3' GCTAGGATTACAGGCAT    77587      AC
                                GTGCCTG AGTCTTGGC
                                ||||||| |||||||||
                                TACGGAC TTAGGATCG
                                   A_
GAM1038 HDAC10   5' GCCGGAAGCCAGGCGCG    49319       ACAG  T
                                TGTGCCTG   TCT GGC
                                ||||||||   ||| |||
```

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                                GCGCGGAC   AGG CCG
                                    CGA_  _
GAM1038 HEMK    3' GCTGAGATACTGGGCACA   32435       ACA   TG
                                TGTGCCTG  GTCT  GC
                                ||||||||  ||||  ||
                                ACACGGGT  TAGA  CG
                                    CA_   GT
GAM1038 HEMK    3' GCTGGGACTTCCCATGTGG  32436       CCT  C    TG
                                TCATGTG  GA AGTCT  GC
                                |||||||  || |||||  ||
                                GGTGTAC  CT TCAGG  CG
                                   C__ _    GT
GAM1038 HEY2    3' GCTGAAATCAAGCACGTGA  24319       C  ___
                                TCATGTGC TGA  CAGT
                                |||||||| |||  ||||
                                AGTGCACG ACT  GTCG
                                    A  AAA
GAM1038 HEYL    3' GCCAGGGTTGAGCAATGG   27396     G  CTGA  GT
                                TCAT TGC   CA  CTTGGC
                                |||| |||   ||  ||||||
                                GGTA ACG   GT  GGACCG
                                  _  A___  TG
GAM1038 HEYL    3' GCCATCCTCCAGGCGTGTGG 27397     TG    AC  TCT
                                TCA  TGCCTG  AG  TGGC
                                |||  ||||||  ||  ||||
                                GGT  GCGGAC  TC  ACCG
                                 GT    C_  CT_
GAM1038 HGC6.1.1 3' GCCAGGACTGTTTTCATG   26829     TGCCT
                                CATG   GACAGTCTTGGC
                                ||||   ||||||||||||
                                GTAC   TTGTCAGGACCG
                                  TT___
GAM1038 HIC     3' GCCGAGATTGTGCCACTGA   67449     T  CCTG
                                TCA GTG   ACAGTCTTGGC
                                ||| |||   ||||||||||
                                AGT CAC   TGTTAGAGCCG
                                  _  CG__
GAM1038 HOMER-3 3' GCCGGGGCTGGTTTTCTATGA 16714      TGCCTGA
                                TCATG     CAGTCTTGGC
                                |||||     ||||||||||
                                AGTAT     GTCGGGGCCG
                                   CTTTTG_
GAM1038 HRH4    3' GCTGGGATTATAGGCACAAGA 41253    A      AC    TG
                                TC TGTGCCTG  AGTCT  GC
                                || ||||||||  |||||  ||
                                AG ACACGGAT  TTAGG  CG
                                 A      A_    GT
GAM1038 HRH4    3' GCTGGGATTGCAGGTGCATG  41254     TG   A    TG
                                CATG  CCTG CAGTCT  GC
                                ||||  |||| ||||||  ||
```

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                                GTAC  GGAC GTTAGG  CG
                                  GT   _     GT
GAM1038  HSA249128 3'  GCCAGGAAGCTCCCAGGCATAT 34151         AC  __
                                ATGTGCCTG  AGT  CTTGGC
                                |||||||||  |||  ||||||
                                TATACGGAC  TCG  GGACCG
                                     CC   AA
GAM1038  HSA404617 5'  GCCGGGGCTGAGTCGGCA    72710     T  __
                                TGCC GAC  AGTCTTGGC
                                |||| |||  |||||||||
                                ACGG CTG  TCGGGGCCG
                                  _  AG
GAM1038  HSA9947   5'  CCGGGGCCGGCGATGA     42022     G   TGACA
                                TCAT TGCC    GTCTTGG
                                |||| ||||    |||||||
                                AGTA GCGG    CGGGGCC
                                  _   C____
GAM1038  HSGP25L2G 3'  ACTGATCAGGGATGTGA     62165      G   _
                                TCATGT CCTGA CAGT
                                |||||| ||||| ||||
                                AGTGTA GGACT GTCA
                                   G    A
GAM1038  HSJ1      3'  GCTGGGGCCGGTAGGGCTGTGA 22132      T   G  A_   TG
                                TCATG GCCT AC  GTCT  GC
                                ||||| |||| ||  ||||  ||
                                AGTGT CGGG TG  CGGG  CG
                                  _   A  GC   GT
GAM1038  HSMPP8    3'  GCCAAACCTGGCTGTCAGCTGT 93478   TG GC       ____
            GTGG                   A  T  CTGACAGTC   TTGGC
                                |  |  |||||||||   |||||
                                T  G  GACTGTCGG   AACCG
                                 GT TC       TCCA
GAM1038  HSNOV1    3'  GCTAGGATTACAGATGTGA   34010      GC   AC
                                TCATGT  CTG  AGTCTTGGC
                                ||||||  |||  |||||||||
                                AGTGTA  GAC  TTAGGATCG
                                   __  A_
GAM1038  HSNOV1    3'  GCTGGGATTACAAAAGCATGTG 34011        CTGAC_    TG
            G                   TCATGTGC     AGTCT  GC
                                ||||||||     |||||  ||
                                GGTGTACG     TTAGG  CG
                                     AAAACA    GT
GAM1038  HSPBAP1   5'  GCCGGGGCTTCTTCCTGTGG   44838     GTGCCT  C
                                TCAT     GA AGTCTTGGC
                                ||||     || |||||||||
                                GGTG     CT TCGGGGCCG
                                  TCCTT_  _
GAM1038  HSPC065   3'  GCCAAGGCCAGACATGTGA    26302       C   ACA
                                TCATGTG CTG   GTCTTGGC
                                |||||||  |||   ||||||||
```

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                                AGTGTAC GAC   CGGAACCG
                                   A  ___
GAM1038 HSPC065  3' GTTGGGATTACAGGCGTGA   26320     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  TG
                                  __    A_    GT
GAM1038 HSPC166  3' GCCAGGGCCACTGCCATGA   26367      T  CTGACA
                                TCATG GC     GTCTTGGC
                                |||||  ||     ||||||||
                                AGTAC CG     CGGGACCG
                                  _ TCAC__
GAM1038 HSPC232  3' GTTGAGATTACAGGCGTGA   33233     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGA  TG
                                  __    A_    GT
GAM1038 IGF2AS   3' GCTGGGGCTCAGGCTGTGG   33099     T     CA    TG
                                TCATG GCCTGA  GTCT  GC
                                |||||  ||||||  ||||  ||
                                GGTGT CGGACT  CGGG  CG
                                  _     __    GT
GAM1038 IL14     5' GTCAAGACCTGGGTGTAT    95434     TG   ACA
                                ATG  CCTG   GTCTTGGC
                                |||  ||||   ||||||||
                                TAT  GGGT   CAGAACTG
                                  GT   C__
GAM1038 IMP-2    3' GTTAAGATATGTGGCCTGTGG  21572      T   TG  _
                                TCATG GCC  ACA GTCTTGGC
                                |||||  |||  |||  ||||||||
                                GGTGT CGG  TGT TAGAATTG
                                  C   __   A
GAM1038 IMPACT   3' GCTGGGATTACAGACAGGCATG 37390         AC___    TG
            TG                    CATGTGCCTG    AGTCT  GC
                                ||||||||||    |||||  ||
                                GTGTACGGAC    TTAGG  CG
                                     AGACA    GT
GAM1038 INSM2    3' GCTGCTTTTGGGGTGCATGG   50867     TG   GA   TCT
                                TCATG  CCT  CAG   TGGC
                                |||||  |||  |||   ||||
                                GGTAC  GGG  GTT   GTCG
                                  GT   __   TTC
GAM1038 ITGA10   3' GCCAGGGCCTGGTGCCTGA   59380     T TG  TGACA
                                TCA G  CC    GTCTTGGC
                                |||  |  ||    ||||||||
                                AGT C  GG    CGGGACCG
                                  C GT  TC___
GAM1038 ITGB8    5' GCCAGGCGGCGGGCGCG     9409         ACA   T
                                TGTGCCTG   GTCT GGC
                                ||||||||   |||| |||
```

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                                GCGCGGGC  CGGA CCG
                                    GG_  _
GAM1038  ITM3    3'  GTTGGGGGAGCCGGGCATGTGA 48167          ACAG  TG
                                TCATGTGCCTG   TCT  GC
                                ||||||||||   |||  ||
                                AGTGTACGGGC   GGG  TG
                                     CGAG  GT
GAM1038  ITPK1   3'  CCCATGTCGGGCTGTGG    26409     T     GTCTT
                                TCATG GCCTGACA   GG
                                |||||  ||||||||   ||
                                GGTGT CGGGCTGT   CC
                                  _     AC___
GAM1038  ITPK1   3'  GCTGATCGGTGCATGTGA   26411       _  _
                                TCATGTGC CTGA CAGT
                                |||||||| |||| ||||
                                AGTGTACG GGCT GTCG
                                    T   A
GAM1038  JAM1    3'  GCTGGGATTACGGGTGCGTG  33764    TG  AC   TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGC  GGGC  TTAGG  CG
                                  GT   A_   GT
GAM1038  JAM1    3'  GCTGGGATTACGGGTGCGTG  57902    TG  AC   TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGC  GGGC  TTAGG  CG
                                  GT   A_   GT
GAM1038  JAM1    3'  GCTGGGATTACGGGTGCGTG  57931    TG  AC   TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGC  GGGC  TTAGG  CG
                                  GT   A_   GT
GAM1038  JAM1    3'  GCTGGGATTACGGGTGCGTG  57957    TG  AC   TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGC  GGGC  TTAGG  CG
                                  GT   A_   GT
GAM1038  JM11    3'  GCCAGGGCAGTTGGGGCAGTGG 53261    G  _ TG  A
                                TCAT TGC C  AC GTCTTGGC
                                |||| ||| |  || ||||||||
                                GGTG ACG G  TG CGGGACCG
                                  _  G GT  A
GAM1038  JM11    3'  GCTGGGATTACAGCCGTGA   53264     T  C  AC   TG
                                TCATG GC TG  AGTCT  GC
                                |||||  || ||  |||||  ||
                                AGTGC CG AC  TTAGG  CG
                                  _  _  A_   GT
GAM1038  KCNH8   3'  CGGGATTGGCAATGA     58254    G   TGAC   TG
                                TCAT TGCC   AGTCT  G
                                |||| ||||   |||||  |
```

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                                AGTA ACGG    TTAGG  C
                                  _   ____     GT
GAM1038 KCNJ9    3' ACCAAGATGGGCACATGA    17149         GACA      C
                                TCATGTGCCT    GTCTTGG
                                ||||||||||    |||||||
                                AGTACACGGG    TAGAACC
                                     ____       AG
GAM1038 KCNQ5    3' GCTAATGCTATGGGGTGTATGA 39049      TG   GAC   C
                                TCATG  CCT   AGT TTGGC
                                |||||  |||   ||| |||||
                                AGTAT  GGG   TCG AATCG
                                   GT   GTA   T
GAM1038 KDELR3   5' GCTGGGCGCGGGCGCACGA   33607    A       ACAGT  TG
                                TC TGTGCCTG    CT  GC
                                || ||||||||    ||  ||
                                AG ACGCGGGC    GG  CG
                                 C       GC___  GT
GAM1038 KDELR3   5' GCTGGGCGCGGGCGCACGA   22459    A       ACAGT  TG
                                TC TGTGCCTG    CT  GC
                                || ||||||||    ||  ||
                                AG ACGCGGGC    GG  CG
                                 C       GC___  GT
GAM1038 KHDRBS3  5' GCTGTGGCTCGGGTGCTGG   21620     T TG    CA   T
                                TCA G  CCTGA  GTC TGGC
                                ||| |  |||||  ||| ||||
                                GGT C  GGGCT  CGG GTCG
                                  _ GT    __   T
GAM1038 KIAA0014 3' GCCGAGGTTGGGGGCATGT   27846        GA  GT
                                ATGTGCCT  CA  CTTGGC
                                ||||||||  ||  ||||||
                                TGTACGGG  GT  GAGCCG
                                     G_  TG
GAM1038 KIAA0022 3' GCTGGGATTACATGCGTGA   29667        CC  AC    TG
                                TCATGTG  TG  AGTCT  GC
                                |||||||  ||  |||||  ||
                                AGTGCGT  AC  TTAGG  CG
                                    __ A_    GT
GAM1038 KIAA0033 5' CCGGGGCGGGGCACTGA     76585     T     GACA
                                TCA GTGCCT    GTCTTGG
                                ||| ||||||    |||||||
                                AGT CACGGG    CGGGGCC
                                  _     G___
GAM1038 KIAA0057 3' GCTGTTTCCTTGGGTACAGA   24434    A      _____
                                TC TGTGCCT    GACAGT
                                || |||||||    ||||||
                                AG ACATGGG    TTGTCG
                                 _      TTCCT
GAM1038 KIAA0063 3' GCTGGGATTACAGGCGTGA   29633     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
```

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                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  KIAA0082  3'  GTCAGTGCCTAGGGCACGTGG  92166        GACA  C
                                TCATGTGCCT   GT TTGGC
                                ||||||||||   || |||||
                                GGTGCACGGG   CG GACTG
                                     ATC_  T
GAM1038  KIAA0087  3'  GCTGGGATTACATGCATGA   28699      CC  AC    TG
                                TCATGTG  TG  AGTCT  GC
                                |||||||  ||  |||||  ||
                                AGTACGT  AC  TTAGG  CG
                                   __ A_    GT
GAM1038  KIAA0090  3'  GCCGGGATTACAGGCAT    88443      AC
                                GTGCCTG  AGTCTTGGC
                                |||||||  |||||||||
                                TACGGAC  TTAGGGCCG
                                   A_
GAM1038  KIAA0095  3'  GTCAGTACATCAGGCACATGG  90919         CA  C
                                TCATGTGCCTGA  GT TTGGC
                                ||||||||||||  || |||||
                                GGTACACGGACT  CA GACTG
                                      A_  T
GAM1038  KIAA0133  3'  GCTTTTTACTTTGGGTACATGG 28767        TG C   CTT_
                                TCATGTGCC  A AGT   GGC
                                |||||||||  | |||   |||
                                GGTACATGG  T TCA   TCG
                                     GT _   TTTT
GAM1038  KIAA0140  3'  GCTGAGGCTGAGGCAT    27811      GA    TG
                                GTGCCT  CAGTCT  GC
                                ||||||  ||||||  ||
                                TACGGA  GTCGGA  CG
                                   __    GT
GAM1038  KIAA0140  3'  GCTGGGGTGGGAGGCACATGG  27812        GA  G   TG
                                TCATGTGCCT  CA TCT  GC
                                ||||||||||  || |||  ||
                                GGTACACGGA  GT GGG  CG
                                     GG  _   GT
GAM1038  KIAA0143  3'  CCAGTTCAGGTACTGA     64784     T      CAGTC
                                TCA GTGCCTGA    TTGG
                                |||  ||||||||    ||||
                                AGT CATGGACT    GACC
                                  _       T_____
GAM1038  KIAA0144  3'  CGAGCTGAGGCCATGG     29284      T   GA   T  TG
                                TCATG GCCT  CAG CT  G
                                |||||  ||||  |||  ||  |
                                GGTAC CGGA  GTC GA  C
                                  _   __   _  GT
GAM1038  KIAA0161  3'  GCTGAGGCCCCAGGTGTGGTGG 28509     _ TG   ACA   TG
                                TCAT G  CCTG   GTCT  GC
                                ||||  |  ||||   ||||  ||
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                                GGTG T  GGAC   CGGA  CG
                                  G GT    CC_    GT
GAM1038 KIAA0182 3' GCCAGGGCTGCCAGTCACTGG 72033     T   C   A
                                TCA GTG CTG CAGTCTTGGC
                                ||| ||| ||| ||||||||||
                                GGT CAC GAC GTCGGGACCG
                                  _  T   C
GAM1038 KIAA0186 3' GCTGGGATTACAGGCACA    40756        AC    TG
                                TGTGCCTG  AGTCT  GC
                                ||||||||  |||||  ||
                                ACACGGAC  TTAGG  CG
                                    A_    GT
GAM1038 KIAA0186 3' GCTGGGATTACAGGCGTGA   40757     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 KIAA0186 3' GCTGGGGTGCAGTGGCGTGA  40758      GC   A  G   TG
                                TCATGT  CTG CA TCT  GC
                                ||||||  ||| || |||  ||
                                AGTGCG  GAC GT GGG  CG
                                   GT   _ _   GT
GAM1038 KIAA0186 3' GTTGAGATCACAGGCGTGA   40762     GT    ACA   TG
                                TCAT  GCCTG   GTCT  GC
                                ||||  |||||   ||||  ||
                                AGTG  CGGAC   TAGA  TG
                                  __    AC_   GT
GAM1038 KIAA0189 5' GCCGAGGCCAAAAGAGCATGTG 28276        _ GACA
            A                    TCATGTGC CT    GTCTTGGC
                                ||||||||  ||    ||||||||
                                AGTGTACG GA    CGGAGCCG
                                    A  AAAC
GAM1038 KIAA0205 5' GCCGGGGAACGGGCGCG     29584        ACAG
                                TGTGCCTG    TCTTGGC
                                ||||||||    |||||||
                                GCGCGGGC    GGGGCCG
                                    AA__
GAM1038 KIAA0205 3' GCTGGGATTGCAGGCGTGA   29588     GT    A    TG
                                TCAT  GCCTG CAGTCT  GC
                                ||||  ||||| ||||||  ||
                                AGTG  CGGAC GTTAGG  CG
                                  __    _     GT
GAM1038 KIAA0210 5' GCTGGGATTACAGACGTGA   28480      GC   AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTGCA  GAC  TTAGG  CG
                                   __   A_    GT
GAM1038 KIAA0217 3' GCCAGGGCATCAGTGC      67038    _   CA
                                GC CTGA  GTCTTGGC
                                || ||||  ||||||||
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                              CG GACT  CGGGACCG
                               T   A_
GAM1038 KIAA0226 3' GCTGAGGCTCCACCAGCGTGA 63518      GCC  AC    TG
                              TCATGT   TG  AGTCT  GC
                              ||||||   ||  |||||  ||
                              AGTGCG   AC  TCGGA  CG
                                 ACC  C_    GT
GAM1038 KIAA0227 3' TTAAGAAATGCATATGA     60704        CTGACAG
                              TCATGTGC      TCTTGG
                              ||||||||      ||||||
                              AGTATACG      AGAATT
                                   TAA____
GAM1038 KIAA0232 3' GCTGAGATTGTTTTTCCCGTGG 72750      TGCCT      TG
                              TCATG    GACAGTCT  GC
                              |||||    ||||||||  ||
                              GGTGC    TTGTTAGA  CG
                                 CCTTT       GT
GAM1038 KIAA0240 3' CCGGGATAGAGCCATGA     92435      T  _  GACA
                              TCATG GC CT    GTCTTGG
                              ||||| || ||    |||||||
                              AGTAC CG GA    TAGGGCC
                                 _  A  _____
GAM1038 KIAA0254 5' GTCGGGGCTGAGTGTGGGCGCG 28599    A      A___
           CGG                   C TGTGCCTG    CAGTCTTGGC
                              | ||||||||    ||||||||||
                              G GCGCGGGT    GTCGGGGCTG
                               C       GTGA
GAM1038 KIAA0254 3' GTTGGGATTGTTGCTGGTGA   28600     GT  CT      TG
                              TCAT  GC  GACAGTCT  GC
                              ||||  ||  ||||||||  ||
                              AGTG  CG  TTGTTAGG  TG
                                GT  __       GT
GAM1038 KIAA0265 5' CGGGTCAGGCGCTGA      69877     T       AGTC TG
                              TCA GTGCCTGAC    T  G
                              ||| |||||||||    |  |
                              AGT CGCGGACTG    G  C
                                _       _____ GT
GAM1038 KIAA0316 3' GTTAAAACTCCAGGTATATGA  69675          AC   C
                              TCATGTGCCTG  AGT TTGGC
                              ||||||||||  ||| |||||
                              AGTATATGGAC  TCA AATTG
                                    C_   A
GAM1038 KIAA0317 3' GCTGGGGGGCACGTGG      29085         GA
                              TCATGTGCCT  CAGT
                              ||||||||||  ||||
                              GGTGCACGGG  GTCG
                                    G_
GAM1038 KIAA0318 3' CCAACTCAGGCACATG      68949          CAGTC
                              CATGTGCCTGA    TTGG
                              ||||||||||     ||||
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                              GTACACGGACT    AACC
                                    C____
GAM1038 KIAA0342 3' GTTGGGACTCCTCACTGCATGG 70620      GCC  C_    TG
                              TCATGT  TGA  AGTCT  GC
                              ||||||  |||  |||||  ||
                              GGTACG  ACT  TCAGG  TG
                                 TC_  CC    GT
GAM1038 KIAA0350 3' GTCAGGGCTGGACAGCAT    61176     C  A_
                              GTGC TG  CAGTCTTGGC
                              |||| ||  ||||||||||
                              TACG AC  GTCGGGACTG
                                _ AG
GAM1038 KIAA0356 3' GCTGGGACAGGGTCTATGG   66193      T   GACA   TG
                              TCATG GCCT   GTCT  GC
                              ||||| ||||   ||||  ||
                              GGTAT TGGG   CAGG  CG
                                 C   A___   GT
GAM1038 KIAA0391 3' GCTGGGATTACAGGTGTGA   27916     GT    AC    TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
                              AGTG  TGGAC  TTAGG  CG
                                __    A_    GT
GAM1038 KIAA0420 3' GTTGGTGTTTGGGCACCTGG  63364    T    TG _  GTC TG
                              TCA GTGCC  A CA   T  GC
                              ||| |||||  | ||   |  ||
                              GGT CACGG  T GT   G  TG
                                C    GT T  ___ GT
GAM1038 KIAA0427 3' TTAGGACCAGAGTGTGA     28725    TG GC   ACA
                              TCA  T  CTG   GTCTTGG
                              |||  |  |||   |||||||
                              AGT  G  GAC   CAGGATT
                                GT A_  ___
GAM1038 KIAA0429 3' GCTGATGCATTGTGCATATGA 28559       CTG    C__ TG
                              TCATGTGC   ACAGT   T  GC
                              ||||||||   |||||   |  ||
                              AGTATACG   TGTTA   A  CG
                                   ___    CGT GT
GAM1038 KIAA0429 3' GTTGGGATTGGGGGGAGGGCCA 28561    T   GA____     TG
           TGG                  ATG GCCT     CAGTCT  GC
                              ||| ||||     ||||||  ||
                              TAC CGGG     GTTAGG  TG
                                _   AGGGGG     GT
GAM1038 KIAA0431 5' GTTGGGACTTGAACAGTACG  30896     C  AC__    TG
                              TGTGC TG   AGTCT  GC
                              ||||| ||   |||||  ||
                              GCATG AC   TCAGG  TG
                                 _ AAGT    GT
GAM1038 KIAA0435 5' GTTGGGATTACAGGCGTGA   28982     GT    AC    TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
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                                AGTG  CGGAC  TTAGG  TG
                                  __    A_    GT
GAM1038 KIAA0446 5' GCTGGGACCACAGGTGCATG  68873    TG   ACA   TG
                                CATG  CCTG   GTCT  GC
                                ||||  ||||   ||||  ||
                                GTAC  GGAC   CAGG  CG
                                  GT    AC_    GT
GAM1038 KIAA0446 5' GTTGGGATTATAGGCGTGA   68878    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAT  TTAGG  TG
                                  __    A_    GT
GAM1038 KIAA0447 3' GCTGGAACCACAGGCACGTG  71671        ACA  C TG
                                CATGTGCCTG   GT T  GC
                                ||||||||||   || |  ||
                                GTGCACGGAC   CA G  CG
                                     AC_  A GT
GAM1038 KIAA0447 3' GCTGGGGTGCAGGACATGG   71672      G   A  G   TG
                                TCATGT CCTG CA TCT  GC
                                ||||||| |||| || |||  ||
                                GGTACA GGAC GT GGG  CG
                                  _   _ _   GT
GAM1038 KIAA0447 3' GTCGAGAATATAGGCGTGG   71675    GT    ACAG
                                TCAT  GCCTG   TCTTGGC
                                ||||  |||||   |||||||
                                GGTG  CGGAT   AGAGCTG
                                  __    ATA_
GAM1038 KIAA0449 5' GCTAAGGAAACCAGGTGTGG  34201    GT    ACAG
                                TCAT  GCCTG   TCTTGGC
                                ||||  |||||   |||||||
                                GGTG  TGGAC   GGAATCG
                                  __    CAAA
GAM1038 KIAA0451 3' GCTGAGGCTGTTTCCAGGTGA 29110    G  CCT      TG
                                TCAT TG   GACAGTCT  GC
                                |||| ||   ||||||||  ||
                                AGTG AC   TTGTCGGA  CG
                                  G  CT_      GT
GAM1038 KIAA0453 3' GTTGAGGTGAGGGCTGTGG   69052     T   GA  G   TG
                                TCATG GCCT  CA TCT  GC
                                ||||| ||||  || |||  ||
                                GGTGT CGGG  GT GGA  TG
                                  _   A_ _   GT
GAM1038 KIAA0459 3' GCTAGGATTACGGGTGTGA   60998    GT    AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  TGGGC  TTAGGATCG
                                  __    A_
GAM1038 KIAA0459 3' GCTGGGATTACAGGTGTGTG  61001    TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
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                              GTGT  GGAC  TTAGG  CG
                                GT   A_    GT
GAM1038 KIAA0459 3' GTTAGGACTGTTTTGT     61003    CT
                              GC  GACAGTCTTGGC
                              ||  ||||||||||||
                              TG  TTGTCAGGATTG
                               TT
GAM1038 KIAA0469 3' GCTAGGATTATAGGCGTGA   29337     GT    AC
                              TCAT  GCCTG  AGTCTTGGC
                              ||||  |||||  |||||||||
                              AGTG  CGGAT  TTAGGATCG
                                __    A_
GAM1038 KIAA0469 3' GCTGAGACTACAGGCGTGTG  29340   TG    AC    TG
                              CA  TGCCTG  AGTCT  GC
                              ||  ||||||  |||||  ||
                              GT  GCGGAC  TCAGA  CG
                               GT    A_    GT
GAM1038 KIAA0469 3' GCTGGGATTACAGGCAT     29341       AC    TG
                              GTGCCTG  AGTCT  GC
                              |||||||  |||||  ||
                              TACGGAC  TTAGG  CG
                                 A_    GT
GAM1038 KIAA0471 3' GTCAGGATCATTTGGGCTGTGG 29398      T   TG CA_
                              TCATG GCC  A   GTCTTGGC
                              ||||| |||  |  ||||||||
                              GGTGT CGG  T   TAGGACTG
                                _  GT TAC
GAM1038 KIAA0475 3' GCTGGGATTACAGGCAT     29497       AC    TG
                              GTGCCTG  AGTCT  GC
                              |||||||  |||||  ||
                              TACGGAC  TTAGG  CG
                                 A_    GT
GAM1038 KIAA0478 3' GCTAGGATTACAGACATGA   29550      GC   AC
                              TCATGT  CTG  AGTCTTGGC
                              ||||||  |||  |||||||||
                              AGTACA  GAC  TTAGGATCG
                                 __   A_
GAM1038 KIAA0478 3' GCTGGGACCACAGGCGTGA   29552     GT    ACA   TG
                              TCAT  GCCTG   GTCT  GC
                              ||||  |||||   ||||  ||
                              AGTG  CGGAC   CAGG  CG
                                __    AC_   GT
GAM1038 KIAA0481 3' GCCGGGATGGGAGGCACGTGG 71848         GA  G
                              TCATGTGCCT  CA TCTTGGC
                              ||||||||||  || |||||||
                              GGTGCACGGA  GT AGGGCCG
                                    GG  _
GAM1038 KIAA0494 5' GTTGGGATTGTAGCTGCTGG  28746    T  GC   A     TG
                              TCA GT  CTG CAGTCT  GC
                              ||| ||  ||| ||||||  ||
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                                GGT CG  GAT GTTAGG  TG
                                  _ TC  _     GT
GAM1038 KIAA0495 3' GCTGGGATTACACGCGTGTG  62594   TG  C  AC    TG
                                CA  TGC TG  AGTCT  GC
                                ||  ||| ||  |||||  ||
                                GT  GCG AC  TTAGG  CG
                                 GT   C  A_    GT
GAM1038 KIAA0495 3' GCTGGGATTACAGGCGTGA   62595    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 KIAA0513 3' GCCAGGGCTGGAAGCTACA   28362    C  GA
                                TGTG CT  CAGTCTTGGC
                                ||||  ||  ||||||||||
                                ACAT GA  GTCGGGACCG
                                  C  AG
GAM1038 KIAA0513 3' GCTGGGATTACAGGCGTGA   28363    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 KIAA0513 5' GTTGGGATTACAGGCGTGA   28370    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  TG
                                  __    A_    GT
GAM1038 KIAA0515 3' GCCAGGAAATTGCATGTGA   63808       CTGACAG
                                TCATGTGC     TCTTGGC
                                ||||||||     |||||||
                                AGTGTACG     AGGACCG
                                    TTAA___
GAM1038 KIAA0515 3' GCTGGTGGTCTTCGGGCATGTG 63811          C  _  _ TG
          A                      TCATGTGCCTGA AG TC T  GC
                                ||||||||||| || || |  ||
                                AGTGTACGGGCT TC GG G  CG
                                      _  T  T GT
GAM1038 KIAA0527 3' GCTAGGATTCCAGGTGTGA   95801    GT    AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  TGGAC  TTAGGATCG
                                  __    C_
GAM1038 KIAA0532 3' GCTGGGATTACAGGTGTGA   70774    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 KIAA0544 3' GCTGAGATTACAGGCGTGA   70904    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG  CGGAC  TTAGA  CG
                                  __    A_    GT
GAM1038 KIAA0544 3' GCTGGGGCTGCCCACGTG    70905      CCTGA    TG
                                CATGTG    CAGTCT  GC
                                ||||||    ||||||  ||
                                GTGCAC    GTCGGG  CG
                                   CC___     GT
GAM1038 KIAA0545 3' CCAGGCCGGGGCGGTGG     63145     G    GACA   T
                                TCAT TGCCT    GTCT GG
                                |||| |||||    |||| ||
                                GGTG GCGGG    CGGA CC
                                  _    GC__   _
GAM1038 KIAA0546 3' GCCGAGACTGTTTAACTTGA  71310    T  GCCT
                                TCA GT    GACAGTCTTGGC
                                ||| ||    ||||||||||||
                                AGT CA    TTGTCAGAGCCG
                                  T  AT__
GAM1038 KIAA0556 3' GCTGAGATGTGGGTACA     69085      G   G   TG
                                TGTGCCT ACA TCT  GC
                                ||||||| ||| |||  ||
                                ACATGGG TGT AGA  CG
                                   _  _  GT
GAM1038 KIAA0557 3' GCTGGGATTACAGGCGTGA   77999     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 KIAA0557 3' GCTGGGCACTGGGTGCAGA   78000    A  TG  TGA   _  TG
                                TC TG  CC   CAGT CT  GC
                                || ||  ||   |||| ||  ||
                                AG AC  GG   GTCA GG  CG
                                 _ GT  ___    C  GT
GAM1038 KIAA0560 3' GCCAAGGCTGGTTAGGC     61504       _
                                GCCTGAC AGTCTTGGC
                                ||||||| |||||||||
                                CGGATTG TCGGAACCG
                                    G
GAM1038 KIAA0561 3' GCTGGGATTACAGGCGTGA   65893     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 KIAA0562 3' GCTGGGATTACAGGCGTGTG  28157    TG     AC    TG
                                CA  TGCCTG  AGTCT  GC
                                ||  ||||||  |||||  ||
                                GT  GCGGAC  TTAGG  CG
                                 GT    A_    GT
GAM1038 KIAA0594 3' GCTGGGATTATAGGCGTGA   64899     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                              AGTG  CGGAT  TTAGG  CG
                                __    A_    GT
GAM1038  KIAA0596  3'  GTCGAGGTGAGAGGTGATGTGG 62838      _   GA  G
                              TCATGT GCCT  CA TCTTGGC
                              ||||||| ||||  || |||||||
                              GGTGTA TGGA  GT GGAGCTG
                                 G   GA  _
GAM1038  KIAA0599  3'  GCTGGGACTACAGGCAT    77184       AC    TG
                              GTGCCTG  AGTCT  GC
                              |||||||  |||||  ||
                              TACGGAC  TCAGG  CG
                                 A_    GT
GAM1038  KIAA0601  3'  GTCAATTTGTTCGGGCATGT   62513        _  TC
                              ATGTGCCTGA CAG  TTGGC
                              |||||||||| |||  |||||
                              TGTACGGGCT GTT  AACTG
                                    T   T_
GAM1038  KIAA0616  3'  GCTGGGATCGGAGGCCGTGA   46663     T   GACA   TG
                              TCATG GCCT   GTCT  GC
                              ||||| ||||   ||||  ||
                              AGTGC CGGA   TAGG  CG
                                 _   GGC_   GT
GAM1038  KIAA0618  5'  GCCGGGACCCCCGAGCGTGA   29166      GCCTGACA
                              TCATGT      GTCTTGGC
                              ||||||      ||||||||
                              AGTGCG      CAGGGCCG
                                 AGCCCC__
GAM1038  KIAA0628  3'  GCTAGGACTGTTCGAAAGCA   28872    GCCT_
                              TGT    GACAGTCTTGGC
                              |||    ||||||||||||
                              ACG    TTGTCAGGATCG
                                AAAGC
GAM1038  KIAA0649  3'  GCCAGCGAGCGAGCACGTGG   29049       C  ACA  CT
                              TCATGTGC TG   GT  TGGC
                              |||||||| ||   ||  ||||
                              GGTGCACG GC   CG  ACCG
                                  A  GAG  __
GAM1038  KIAA0663  3'  CCTTGTTGGGAATATGG    29126      G  TG   TCTT
                              TCATGT CC  ACAG   GG
                              |||||| ||  ||||   ||
                              GGTATA GG  TGTT   CC
                                 A  GT   _____
GAM1038  KIAA0677  3'  GCCATTTCTGGGCACGTGG   27829       TGA   TCT
                              TCATGTGCC   CAG   TGGC
                              |||||||||   |||   ||||
                              GGTGCACGG   GTC   ACCG
                                   ___   TTT
GAM1038  KIAA0682  3'  GCCGAGATTGAAATATGA    29366      GCCTGA
                              TCATGT     CAGTCTTGGC
                              ||||||     ||||||||||
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                              AGTATA    GTTAGAGCCG
                                 AA____
GAM1038 KIAA0682 3' GCTGAGATTACAGGTGTGA  29368    GT   AC   TG
                              TCAT GCCTG AGTCT GC
                              |||| ||||| ||||| ||
                              AGTG TGGAC TTAGA CG
                                __   A_   GT
GAM1038 KIAA0711 3' GCCGAGTGACAGTGGGCATAGA 29521   A     ACAGT_
                              TC TGTGCCTG    CTTGGC
                              || ||||||||    ||||||
                              AG ATACGGGT    GAGCCG
                               _     GACAGT
GAM1038 KIAA0721 3' TCAAGGCTTAGTTATGA    95973    TGC  AC
                              TCATG  CTG AGTCTTGG
                              |||||  ||| ||||||||
                              AGTAT  GAT TCGGAACT
                                 T__  __
GAM1038 KIAA0721 3' TCAAGGCTTAGTTATGA    41345    TGC  AC
                              TCATG  CTG AGTCTTGG
                              |||||  ||| ||||||||
                              AGTAT  GAT TCGGAACT
                                 T__  __
GAM1038 KIAA0737 3' GCTGGGATTACAGGCAT    29142     AC   TG
                              GTGCCTG AGTCT GC
                              ||||||| ||||| ||
                              TACGGAC TTAGG CG
                                 A_   GT
GAM1038 KIAA0746 3' CGGGGCCAGGGCATGA     69453     G  ACA  TG
                              TCATGT CCTG  GTCT G
                              |||||| ||||  |||| |
                              AGTACG GGAC  CGGG C
                                 _  ___   GT
GAM1038 KIAA0759 3' GCTAGGGTAGTGGTAT     67325    TG AG
                              GTGCC AC TCTTGGC
                              ||||| || |||||||
                              TATGG TG GGGATCG
                                 __ AT
GAM1038 KIAA0766 5' GCTGAGGTGATCTGGCGCAGA 29007   A   T _ G  TG
                              TC TGTGCC GA CA TCT GC
                              || |||||| || || ||| ||
                              AG ACGCGG CT GT GGA CG
                               _    T A _  GT
GAM1038 KIAA0767 3' GCTGGGGCCGGGCGCAGTGA 60628   _    ACA  TG
                              TCA TGTGCCTG  GTCT GC
                              ||| ||||||||  |||| ||
                              AGT ACGCGGGC  CGGG CG
                                G      ___  GT
GAM1038 KIAA0767 3' GTTGAGATTGTTGTTTTTTGA 60631   TGT_ CT     TG
                              TCA   GC GACAGTCT GC
                              |||   || |||||||| ||
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                                AGT   TG  TTGTTAGA  TG
                                  TTTT  __      GT
GAM1038 KIAA0769 3' GCCCCCACGTCAGGTGCTGA  29096    T TG    A  CTT
                                TCA G  CCTGAC GT   GGC
                                ||| |  |||||| ||   |||
                                AGT C  GGACTG CA   CCG
                                  _ GT     _  CCC
GAM1038 KIAA0790 5' GCCGGGGCATGCAGCGCG   68695     C  A  _
                                TGTGC TG CA GTCTTGGC
                                ||||| || || ||||||||
                                GCGCG AC GT CGGGGCCG
                                  _ _ A
GAM1038 KIAA0798 3' GCTGGGATTACAGGCAT    27724       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038 KIAA0826 3' GTTGGGATGTATGGATATGTGA 82639       _  TG   G   TG
                                TCATGTG CC  ACA TCT  GC
                                |||||||  ||  |||  |||  ||
                                AGTGTAT GG  TGT AGG  TG
                                    A  TA   _   GT
GAM1038 KIAA0831 3' GCTGGGATTGCAGGCCTGA   29979    TGT    A     TG
                                TCA   GCCTG CAGTCT  GC
                                |||   |||||  ||||||  ||
                                AGT   CGGAC GTTAGG  CG
                                  C__     _     GT
GAM1038 KIAA0841 3' GCTGGGATTACAGGCAT    71391       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038 KIAA0841 3' GTCAAGAGCAGCGGCGGTGA  71394     G    T ACAG
                                TCAT TGCC G    TCTTGGC
                                ||||  ||||  |    |||||||
                                AGTG GCGG C    AGAACTG
                                  _    _ GACG
GAM1038 KIAA0843 5' GCCGGGGCCTCCGTATTGA   30114    T   CT  CA
                                TCA GTGC  GA  GTCTTGGC
                                |||  ||||  ||  ||||||||
                                AGT TATG  CT  CGGGGCCG
                                  _    C_  C_
GAM1038 KIAA0861 3' GCTGGGATTACAGGCGTGA   88929     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __     A_    GT
GAM1038 KIAA0864 5' GCTGACAGAGCGCGTGG     63251        _  A
                                TCATGTGC CTG CAGT
                                |||||||| ||| ||||
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                                GGTGCGCG GAC GTCG
                                    A   A
GAM1038 KIAA0889 3' GTTGGGATTACAGGCGTGA   31146     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  TG
                                  __    A_    GT
GAM1038 KIAA0907 3' GCTGGCACCTTCAGGCACAT   30177         CA  C TG
                                ATGTGCCTGA  GT T  GC
                                ||||||||||  || |  ||
                                TACACGGACT  CA G  CG
                                     TC  C GT
GAM1038 KIAA0923 5' GCTAGGACGCCGAGCGGTGA   25835     G   C  ACA
                                TCAT TGC TG   GTCTTGGC
                                |||| ||| ||   ||||||||
                                AGTG GCG GC   CAGGATCG
                                  _   A  CG_
GAM1038 KIAA0924 3' GCTGGGACTACAGGTGCATG   29718     TG    AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTAC  GGAC  TCAGG  CG
                                  GT    A_    GT
GAM1038 KIAA0924 3' GCTGGGATTACAGGCGTGA   29719     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 KIAA0930 3' CGGGTCAGGGCGTGG       70540       G     AGTC TG
                                TCATGT CCTGAC    T  G
                                ||||||| ||||||    |  |
                                GGTGCG GGACTG    G  C
                                  _     _____ GT
GAM1038 KIAA0930 3' GCCCTCAATTTGTAAGGCATGT 70544         G    TCTT__
            GA                    TCATGTGCCT ACAG     GGC
                                ||||||||||| ||||     |||
                                AGTGTACGGA TGTT     CCG
                                     A    TAACTC
GAM1038 KIAA0930 3' GTCAAACCCAGGCACGCGG    70551    A       ACA  C
                                TC TGTGCCTG   GT TTGGC
                                || ||||||||   || |||||
                                GG GCACGGAC   CA AACTG
                                 C       C__  _
GAM1038 KIAA0945 3' GCTGGGGAGGCCAGGGTATAAG 30211    A      GACAG_   TG
            A                    TC TGTGCCT     TCT  GC
                                || |||||||     |||  ||
                                AG ATATGGG     GGG  CG
                                 A      ACCGGA   GT
GAM1038 KIAA0961 3' GCTGGGATTGCAGGCGTGA   29736     GT    A     TG
                                TCAT  GCCTG CAGTCT  GC
                                ||||  ||||| ||||||  ||
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                                AGTG  CGGAC GTTAGG  CG
                                  __    _     GT
GAM1038  KIAA0963  3'  GCTGGGGGCCGGGGCGTGG   30318      G   ACAG   TG
                                TCATGT CCTG   TCT  GC
                                |||||| ||||   |||  ||
                                GGTGCG GGGC   GGG  CG
                                   _   CG__   GT
GAM1038  KIAA0964  5'  GCCGAGGCGCCCGGCGCA   29763      TGACA
                                TGTGCC   GTCTTGGC
                                ||||||   ||||||||
                                ACGCGG   CGGAGCCG
                                   CCCG_
GAM1038  KIAA0964  5'  GCCGGGGCCTAGGCGCGCGG  29764   A      ACA
                                TC TGTGCCTG  GTCTTGGC
                                || ||||||||  ||||||||
                                GG GCGCGGAT  CGGGGCCG
                                 C       C__
GAM1038  KIAA0970  3'  GCTGAGGTTGGCATTTTAGTGA 29963     ____    TGAC GT  TG
                                TCAT   GTGCC   A  CT  GC
                                ||||   |||||   |  ||  ||
                                AGTG   TACGG   T  GA  CG
                                  ATTT    ____ TG  GT
GAM1038  KIAA0993  3'  GCTAAGACTGGATTGATTGTGG 64143     TGCCTGA
                                TCATG     CAGTCTTGGC
                                |||||     ||||||||||
                                GGTGT     GTCAGAATCG
                                   TAGTTAG
GAM1038  KIAA1013  5'  GTCGGGGCTGCACGTACGAGA  88890   A    C  A
                                TC TGTGC TG CAGTCTTGGC
                                || ||||| || ||||||||||
                                AG GCATG AC GTCGGGGCTG
                                 A    C  _
GAM1038  KIAA1014  5'  GCTGGAGGCGGTGTCACGGTGT 65353    TG  _    __   _ TG
           ATGA                   ATG  CC TGACA  GTC T  GC
                                |||  || |||||  ||| |  ||
                                TAT  GG ACTGT  CGG G  CG
                                  GT  C    GG   A GT
GAM1038  KIAA1026  3'  GCTGGGATTATAGACATGA   71201      GC   AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTACA  GAT  TTAGG  CG
                                   __   A_    GT
GAM1038  KIAA1026  3'  TCGAGGCTCTAACATGA    71211      GCCTGAC
                                TCATGT     AGTCTTGG
                                ||||||     ||||||||
                                AGTACA     TCGGAGCT
                                   ATC____
GAM1038  KIAA1028  3'  GCTGGGATTATAGGTGTGA   91941    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG  TGGAT  TTAGG  CG
                                  __    A_    GT
GAM1038  KIAA1029  3'  GCCGATGAGCTTGGGTACGTGA 23476        TG CAG  _
                                TCATGTGCC  A   TC TTGGC
                                |||||||||  |   || |||||
                                AGTGCATGG  T   AG AGCCG
                                     GT CG_  T
GAM1038  KIAA1029  3'  GCTGAGGCAGTAGCATAGA   23477    A    CTG  A    TG
                                TC TGTGC   AC GTCT  GC
                                || |||||   || ||||  ||
                                AG ATACG   TG CGGA  CG
                                 _    A__  A    GT
GAM1038  KIAA1033  5'  GTTGGGGCTGTGTCTGTGG   64517     GT  CTG      TG
                                TCAT  GC   ACAGTCT  GC
                                ||||  ||   |||||||  ||
                                GGTG  TG   TGTCGGG  TG
                                  TC  ___      GT
GAM1038  KIAA1036  3'  GCTGAGACTTCGGGGCTGTGG  29823     _ G    C    TG
                                TCAT GT CCTGA AGTCT  GC
                                |||| || ||||| |||||  ||
                                GGTG CG GGGCT TCAGA  CG
                                  T  _    _    GT
GAM1038  KIAA1041  3'  GCTGGGATTACAGACATGA   30135      GC   AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTACA  GAC  TTAGG  CG
                                    __   A_    GT
GAM1038  KIAA1042  5'  GCCGGGGCTGAGCTCTCATGG  30341     T__  CTGA
                                TCATG   GC    CAGTCTTGGC
                                |||||   ||    ||||||||||
                                GGTAC   CG    GTCGGGGCCG
                                  TCT  A___
GAM1038  KIAA1054  3'  GCCCGCTGTCAGCTACATGA   68440       C       CTT
                                TCATGTG CTGACAGT   GGC
                                ||||||| ||||||||   |||
                                AGTACAT GACTGTCG   CCG
                                    C       C__
GAM1038  KIAA1054  3'  GCTGGGATTACAGGCGTGA   68442     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  KIAA1084  3'  GCTGACAGACAAGTACATGA   29838        ____  A
                                TCATGTGC    CTG CAGT
                                ||||||||    ||| ||||
                                AGTACATG    GAC GTCG
                                     AACA   A
GAM1038  KIAA1086  3'  GCCGAGATTGCGCTACTGA   70748    T  _  CT A
                                TCA GT GC  G CAGTCTTGGC
                                ||| || ||  | ||||||||||
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                              AGT CA CG  C GTTAGAGCCG
                                _  T __ _
GAM1038  KIAA1091  3'  GCTGGTGGAGTATGTGA     69684        _  GA
                              TCATGTGC CT  CAGT
                              ||||||| ||  ||||
                              AGTGTATG GG  GTCG
                                   A  TG
GAM1038  KIAA1126  3'  GCCACAGTCACTGTCAGGGTAT 71928       G       __ _
            GA                   TCATGT CCTGACAGT  CT TGGC
                              |||||| |||||||||  || ||||
                              AGTATG GGACTGTCA  GA ACCG
                                 _       CT  C
GAM1038  KIAA1128  3'  GCTGGGACTACAGGCATGTG   68481         AC    TG
                              CATGTGCCTG  AGTCT  GC
                              ||||||||||  |||||  ||
                              GTGTACGGAC  TCAGG  CG
                                    A_    GT
GAM1038  KIAA1143  3'  GCCACTTTTAGGCATA      68680        C   CTT
                              TGTGCCTGA AGT   GGC
                              ||||||||| |||   |||
                              ATACGGATT TCA   CCG
                                    T  ___
GAM1038  KIAA1155  5'  GCCGAGACTGTTGTGGCGACG  62235     _  _
                              TGT GCC TGACAGTCTTGGC
                              ||| ||| ||||||||||||
                              GCA CGG GTTGTCAGAGCCG
                                G  T
GAM1038  KIAA1161  5'  GTTGGGATTACAGGCAT     81759       AC    TG
                              GTGCCTG  AGTCT  GC
                              |||||||  |||||  ||
                              TACGGAC  TTAGG  TG
                                 A_    GT
GAM1038  KIAA1170  3'  GCTGGGACTAGCTTTCAGGTAT 69856   T      C____    TG
            TGA                  A GTGCCTGA    AGTCT  GC
                              | ||||||||    |||||  ||
                              T TATGGACT    TCAGG  CG
                              _      TTCGA    GT
GAM1038  KIAA1170  3'  GCTGGGATTACAGGTGTGA   69857     GT    AC    TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
                              AGTG  TGGAC  TTAGG  CG
                                __    A_    GT
GAM1038  KIAA1185  3'  GCTGGGACTACAGGTGTGTG  62606     TG   AC    TG
                              CATG  CCTG  AGTCT  GC
                              ||||  ||||  |||||  ||
                              GTGT  GGAC  TCAGG  CG
                                GT   A_    GT
GAM1038  KIAA1185  3'  GCTGGGATTACAGGCGTGA   62607     GT    AC    TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
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                                AGTG CGGAC TTAGG CG
                                  __   A_   GT
GAM1038 KIAA1193 3' GCTGGGATTACAGGCGTGA  67643    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG CG
                                  __   A_   GT
GAM1038 KIAA1196 3' GCCAGGGAGTGGGTGTGG   61468    GT   ACAG
                                TCAT GCCTG  TCTTGGC
                                |||| |||||  |||||||
                                GGTG TGGGT  GGGACCG
                                  __   GA__
GAM1038 KIAA1196 3' GCTGGGGCAGAGATGGGCGTGA 61471     G TGACA_  TG
                                TCATGT CC    GTCT GC
                                |||||| ||    |||| ||
                                AGTGCG GG    CGGG CG
                                   _ TAGAGA  GT
GAM1038 KIAA1196 3' GCTGGGGCCCATAGGCATGTGG 61472       ACA  TG
                                TCATGTGCCTG  GTCT GC
                                ||||||||||  |||| ||
                                GGTGTACGGAT  CGGG CG
                                     ACC  GT
GAM1038 KIAA1198 3' GCTGGGACTATAGGCGCGTG  63319       AC   TG
                                CATGTGCCTG AGTCT GC
                                |||||||||| ||||| ||
                                GTGCGCGGAT TCAGG CG
                                     A_   GT
GAM1038 KIAA1198 3' GCTGGGATTACAGGCGCGTG  63320       AC   TG
                                CATGTGCCTG AGTCT GC
                                |||||||||| ||||| ||
                                GTGCGCGGAC TTAGG CG
                                     A_   GT
GAM1038 KIAA1198 3' GCTGGGATTACAGGCGTGA   63321    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG CG
                                  __   A_   GT
GAM1038 KIAA1198 3' GCTGGGATTACAGGCGTGA   63322    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG CG
                                  __   A_   GT
GAM1038 KIAA1198 3' GCTGGGATTACAGGTGTGA   63323    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG TGGAC TTAGG CG
                                  __   A_   GT
GAM1038 KIAA1198 3' GCTGGGATTATAGGCGTGA   63324    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
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                                AGTG  CGGAT  TTAGG  CG
                                  __    A_    GT
GAM1038  KIAA1198  3'  GTCAGGGTTCACAAGCCATGG  63328     T  C  AC GT
                                TCATG GC TG  A  CTTGGC
                                ||||| || ||  |  ||||||
                                GGTAC CG AC  T  GGACTG
                                  _  A  AC TG
GAM1038  KIAA1200  3'  GACTATTTCAGGCATGTGG   62375         C__
                                TCATGTGCCTGA   AGTC
                                ||||||||||||   ||||
                                GGTGTACGGACT   TCAG
                                       TTA
GAM1038  KIAA1200  3'  GCTGGGATTACAGGCAT    62378       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  KIAA1200  3'  GTTAAGGCTTTCTGCACTGG  62380    T   CT  C
                                TCA GTGC  GA AGTCTTGGC
                                ||| ||||  || |||||||||
                                GGT CACG  CT TCGGAATTG
                                  _   T_  T
GAM1038  KIAA1205  3'  GCCGGGGAAAGGGGGTCATGG  70045     T   GACAG
                                TCATG GCCT    TCTTGGC
                                ||||| ||||    |||||||
                                GGTAC TGGG    GGGGCCG
                                  _   GGAAA
GAM1038  KIAA1209  3'  GCTGGGATTACAGGCAT    60759       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  KIAA1210  3'  GCTGGGATTACAGGCGTGA   96334     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  KIAA1223  3'  GCCAAGGTTGTGGATTTGA   71148    TGTG  TG   GT
                                TCA   CC  ACA  CTTGGC
                                |||   ||  |||  ||||||
                                AGT   GG  TGT  GAACCG
                                  TTA_  __   TG
GAM1038  KIAA1229  3'  GCCAAGATTGACAAATGG    62067    ___  A
                                CC   TG CAGTCTTGGC
                                ||   || ||||||||||
                                GG   AC GTTAGAACCG
                                 TAA  A
GAM1038  KIAA1240  3'  GCCAGGACTTGCCAAATGG   66733     GT_  CTGAC
                                TCAT   GC    AGTCTTGGC
                                ||||   ||    |||||||||
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                                GGTA  CG    TCAGGACCG
                                  AAC  T____
GAM1038 KIAA1254 3' GCTGGGACTATAGGCACGTG  70021        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGCACGGAT  TCAGG  CG
                                     A_    GT
GAM1038 KIAA1254 3' GCTGGGATTACAGTCGTGA   70022     TGC   AC    TG
                                TCATG   CTG  AGTCT  GC
                                |||||   |||  |||||  ||
                                AGTGC   GAC  TTAGG  CG
                                  T__   A_    GT
GAM1038 KIAA1255 3' CCATGTGAGGCATGTGG     67162        G   GTCT
                                TCATGTGCCT ACA    TGG
                                |||||||||| |||    |||
                                GGTGTACGGA TGT    ACC
                                     G  ____
GAM1038 KIAA1255 5' GTTGGGGACAGGCACAT     67164        ACAG   TG
                                ATGTGCCTG   TCT  GC
                                |||||||||   |||  ||
                                TACACGGAC   GGG  TG
                                     A___   GT
GAM1038 KIAA1257 3' GCTGGGATTACAGGCGCATG  62747        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                |||||||||  |||||  ||
                                GTACGCGGAC  TTAGG  CG
                                     A_    GT
GAM1038 KIAA1257 3' GCTGGGATTACAGGCGTGA   62748     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 KIAA1257 3' GCTGGGATTATAGGCGTGA   62749     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAT  TTAGG  CG
                                  __    A_    GT
GAM1038 KIAA1260 3' GTCAGGTTGCACAGGTGCATG 60030     TG   A_  T
                                CATG  CCTG  CAG CTTGGC
                                ||||  ||||  ||| ||||||
                                GTAC  GGAC  GTT GGACTG
                                  GT   AC  _
GAM1038 KIAA1271 3' TCAGGGCAGGTATGTGG     69553        GACA
                                TCATGTGCCT   GTCTTGG
                                ||||||||||   |||||||
                                GGTGTATGGA   CGGGACT
                                     ____
GAM1038 KIAA1276 5' GCTGAGGCCAGCATGG      66433       __   GA
                                TCATGT  GCCT  CAGT
                                ||||||  ||||  ||||
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                                GGTACG  CGGA  GTCG
                                   AC   __
GAM1038 KIAA1277 3' CGGGGCGGCGTCATGA     64452      _   TGACA   TG
                                TCATG TGCC    GTCT  G
                                ||||| ||||    ||||  |
                                AGTAC GCGG    CGGG  C
                                   T   _____   GT
GAM1038 KIAA1280 5' GCCAGGGCCTCTGGTGTACGG 69720    A  TG  T  CA
                                TC TG  CC GA  GTCTTGGC
                                || ||  || ||  ||||||||
                                GG AT  GG CT  CGGGACCG
                                 C  GT  T  C_
GAM1038 KIAA1287 3' GCTGGGATTACAGGTGTGA   78328     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038 KIAA1297 3' GCTGGGGCTGCGGCTGCTGA   72182     T  _  T A     TG
                                TCA GT GCC G CAGTCT  GC
                                ||| || ||| | ||||||  ||
                                AGT CG CGG C GTCGGG  CG
                                  _ T  _ _     GT
GAM1038 KIAA1303 3' GCTGGGGCTGGCCGGGACGTGA 66004       G   A_    TG
                                TCATGT CCTG  CAGTCT  GC
                                |||||| ||||  ||||||  ||
                                AGTGCA GGGC  GTCGGG  CG
                                   _   CG    GT
GAM1038 KIAA1320 5' GCTGGGATTACAGGCGTGA   69306     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038 KIAA1323 5' GTTAAGGCTGCTGCCAATGG  63045     GT  CTGA
                                TCAT  GC   CAGTCTTGGC
                                ||||  ||   ||||||||||
                                GGTA  CG   GTCGGAATTG
                                   AC  TC__
GAM1038 KIAA1328 5' GCTGGGATTACAGACGTGA   61652      GC   AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTGCA  GAC  TTAGG  CG
                                   __   A_    GT
GAM1038 KIAA1349 5' GCTGAGATTATAGGCAT    70757       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGA  CG
                                   A_    GT
GAM1038 KIAA1373 5' GCCGGGACCATCGCAGTGA   70938     G   CT  CA
                                TCAT TGC  GA  GTCTTGGC
                                |||| |||  ||  ||||||||
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                                AGTG ACG  CT  CAGGGCCG
                                  _  __  AC
GAM1038  KIAA1373  3'  GCTGAGATTATAGGCAT    70945       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGA  CG
                                   A_    GT
GAM1038  KIAA1373  3'  GCTGGGATTACAGACATGA   70946      GC   AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTACA  GAC  TTAGG  CG
                                   __  A_    GT
GAM1038  KIAA1393  3'  TCAGGGTTGGCTTGTGA     72100      T   TGAC GT
                                TCATG GCC    A  CTTGG
                                |||||  |||    |  |||||
                                AGTGT CGG    T  GGACT
                                   T  _____ TG
GAM1038  KIAA1423  3'  GGCTGGGCATGCTGG       61727     _     TGA
                                TCA TGTGCC   CAGTC
                                |||  ||||||   |||||
                                GGT GTACGG   GTCGG
                                  C     ___
GAM1038  KIAA1430  3'  GTTAAGGATCAGGCCTGTGA   80768      T     CAG
                                TCATG GCCTGA   TCTTGGC
                                |||||  ||||||   |||||||
                                AGTGT CGGACT   GGAATTG
                                   C     A__
GAM1038  KIAA1432  3'  GCTATAGTCTGTCAGGTACTTG 66748     T         T  _
            A                    TCA GTGCCTGACAG CT TGGC
                                |||  ||||||||||  ||  ||||
                                AGT CATGGACTGTC GA ATCG
                                  T         T  T
GAM1038  KIAA1434  3'  GTTGGGACTAGGATGTGG    69619       G   GAC    TG
                                TCATGT CCT   AGTCT  GC
                                ||||||  |||   |||||  ||
                                GGTGTA GGA   TCAGG  TG
                                   _  ___    GT
GAM1038  KIAA1443  3'  GCTGGGATTATAGGCAT     63834       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGG  CG
                                   A_    GT
GAM1038  KIAA1443  3'  GCTGGGATTGGATCAGCA    63835     C  __     TG
                                TGC TGA  CAGTCT  GC
                                |||  |||  ||||||  ||
                                ACG ACT  GTTAGG  CG
                                  _  AG     GT
GAM1038  KIAA1443  3'  GTTGGGATCAGCTATATGG    63839       C   CAG   TG
                                TCATGTG CTGA   TCT  GC
                                |||||||  ||||   |||  ||
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                                GGTATAT GACT  AGG  TG
                                   C   ___  GT
GAM1038 KIAA1456 3' GCTGGGATTACAGGCGTGA  67000    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_   GT
GAM1038 KIAA1463 3' CGAGATGGCTACATGA    72274      _  TGACA   TG
                                TCATGT GCC    GTCT  G
                                |||||| |||    ||||  |
                                AGTACA CGG    TAGA  C
                                   T  _____   GT
GAM1038 KIAA1465 5' GCTGGCGGGACAGGCGCGTGA 60832        ACA_  TT
                                TCATGTGCCTG   GTC  GGC
                                ||||||||||    |||  |||
                                AGTGCGCGGAC   CGG  TCG
                                      AGGG  __
GAM1038 KIAA1465 3' GCTGGGATTACAGGCGTGA  60833    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_   GT
GAM1038 KIAA1467 3' GCTGGGATTACAGGCGTGA  71611    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_   GT
GAM1038 KIAA1473 3' CCGAGATCATGCCATGG    70666     T  C  CAG
                                TCATG GC TGA  TCTTGG
                                ||||| || |||  ||||||
                                GGTAC CG ACT  AGAGCC
                                  _ T  ___
GAM1038 KIAA1497 5' GCTGGGATTACAGGCACGT  67512       AC   TG
                                ATGTGCCTG  AGTCT  GC
                                |||||||||  |||||  ||
                                TGCACGGAC  TTAGG  CG
                                     A_   GT
GAM1038 KIAA1497 5' GCTGGGATTACAGGCGTGA  67513    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_   GT
GAM1038 KIAA1508 3' GCTGGGATTACAGGCGTGA  61887    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_   GT
GAM1038 KIAA1530 3' GCTGGGATTACAGGTGTGA  67955    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                              AGTG  TGGAC  TTAGG  CG
                                __    A_    GT
GAM1038 KIAA1530 3' GTTGGGATTACAGGCAT    67959       AC    TG
                              GTGCCTG  AGTCT  GC
                              |||||||  |||||  ||
                              TACGGAC  TTAGG  TG
                                 A_    GT
GAM1038 KIAA1557 3' GTCAGGATTGTGACTATAT   61137      CCTG
                              ATGTG   ACAGTCTTGGC
                              |||||   ||||||||||
                              TATAT   TGTTAGGACTG
                                CAG_
GAM1038 KIAA1571 3' GCTGGGATTACAGTCATGA   60958      TGC  AC    TG
                              TCATG  CTG  AGTCT  GC
                              |||||  |||  |||||  ||
                              AGTAC  GAC  TTAGG  CG
                                 T__  A_    GT
GAM1038 KIAA1580 5' TCAGGACGTGGCATTGG     69450     T    TGACA
                              TCA GTGCC    GTCTTGG
                              ||| |||||    |||||||
                              GGT TACGG    CAGGACT
                                _    TG___
GAM1038 KIAA1615 3' GCTGGGATTACAGGCAT     68719       AC    TG
                              GTGCCTG  AGTCT  GC
                              |||||||  |||||  ||
                              TACGGAC  TTAGG  CG
                                 A_    GT
GAM1038 KIAA1615 3' GCTGGGATTACAGGCAT     68720       AC    TG
                              GTGCCTG  AGTCT  GC
                              |||||||  |||||  ||
                              TACGGAC  TTAGG  CG
                                 A_    GT
GAM1038 KIAA1617 3' GCTGGCAGCATATGA       91432        C  A
                              TCATGTGC TG CAGT
                              |||||||| || ||||
                              AGTATACG AC GTCG
                                 _ G
GAM1038 KIAA1617 3' GCTGGGATTACAGGTGTGA   91433     GT    AC    TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
                              AGTG  TGGAC  TTAGG  CG
                                __    A_    GT
GAM1038 KIAA1627 3' GCCTTTTGTTATGTGCGTGA  80753      TG C     TCTT
                              TCATG  C TGACAG   GGC
                              |||||  | ||||||   |||
                              AGTGC  G ATTGTT   CCG
                                 GT T     TT__
GAM1038 KIAA1643 3' CCAAGACCCGCGATGG      64549     G   CTGACA
                              TCAT TGC     GTCTTGG
                              |||| |||     |||||||
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                                GGTA GCG     CAGAACC
                                  _  CC____
GAM1038  KIAA1644  5'  GCTTCTCACCTGTCAAGTGTGT 85030      TG C     TCTT__
              GA                  TCATG  C TGACAG     GGC
                                  ||||||  | ||||||     |||
                                  AGTGT  G ACTGTC     TCG
                                    GT A     CACTCT
GAM1038  KIAA1649  3'  GCCAAGGCTGGAGTGCAGTGG  50265     G  _  GA
                                  TCAT TGC CT  CAGTCTTGGC
                                  |||| ||| ||  ||||||||||
                                  GGTG ACG GA  GTCGGAACCG
                                    _  T  G_
GAM1038  KIAA1649  3'  GCTGGGACTGCAGGCG      50272       A     TG
                                  TGCCTG CAGTCT  GC
                                  |||||| ||||||  ||
                                  GCGGAC GTCAGG  CG
                                     _     GT
GAM1038  KIAA1655  3'  GCCAGGACTGTATTGTGTGTG  66613     TG CTG
                                  CATG  C   ACAGTCTTGGC
                                  ||||  |   ||||||||||
                                  GTGT  G   TGTCAGGACCG
                                    GT TTA
GAM1038  KIAA1655  3'  GCTGGGATTACAGGCGTGA   66619     GT    AC    TG
                                  TCAT  GCCTG  AGTCT  GC
                                  ||||  |||||  |||||  ||
                                  AGTG  CGGAC  TTAGG  CG
                                    __    A_    GT
GAM1038  KIAA1655  5'  GTCAGGGCCTGGCACAT     66622       TGACA
                                  ATGTGCC    GTCTTGGC
                                  |||||||    ||||||||
                                  TACACGG    CGGGACTG
                                     TC___
GAM1038  KIAA1656  3'  GCTGAGGCTGACCCACCTGA   65798     T   CCTGA     TG
                                  TCA GTG    CAGTCT  GC
                                  ||| |||    ||||||  ||
                                  AGT CAC    GTCGGA  CG
                                    C   CCA__     GT
GAM1038  KIAA1668  3'  GCTGGGACTACAGGCGCATG   66477         AC    TG
                                  CATGTGCCTG  AGTCT  GC
                                  ||||||||||  |||||  ||
                                  GTACGCGGAC  TCAGG  CG
                                       A_    GT
GAM1038  KIAA1668  3'  GCTGGGATTACAGGCGTGA   66478     GT    AC    TG
                                  TCAT  GCCTG  AGTCT  GC
                                  ||||  |||||  |||||  ||
                                  AGTG  CGGAC  TTAGG  CG
                                    __    A_    GT
GAM1038  KIAA1671  3'  GCTGGGACTACAGGTGTATG   65682     TG   AC    TG
                                  CATG  CCTG  AGTCT  GC
                                  ||||  ||||  |||||  ||
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                                GTAT  GGAC  TCAGG  CG
                                  GT    A_    GT
GAM1038  KIAA1674  3'  GAGTTGTTGGGTACAT     68780       TG    T
                                ATGTGCC  ACAG CTT
                                |||||||  |||| |||
                                TACATGG  TGTT GAG
                                   GT    _
GAM1038  KIAA1679  3'  GCTGAGGTCCCTGCGCTGTGG  70153     _    CT_   AGT  TG
                                TCAT GTGC   GAC   CT  GC
                                |||| ||||   |||   ||  ||
                                GGTG CGCG   CTG   GA  CG
                                  T    TCC   ___  GT
GAM1038  KIAA1706  5'  GCCCGAGTTGGGCGCAGGA   92789    A     TG  AG  TT
                                TC TGTGCC  AC  TC  GGC
                                || ||||||  ||  ||  |||
                                AG ACGCGG  TG  AG  CCG
                                 G     GT  __  C_
GAM1038  KIAA1719  3'  CCAGAGGCAGGCAGTGG     68156     G     ACAG   T
                                TCAT TGCCTG    TCT GG
                                ||||  ||||||    |||  ||
                                GGTG ACGGAC    AGA CC
                                  _     GG__   _
GAM1038  KIAA1719  3'  GCCAGGGCTGGGGATGTG    68164      G  TGA
                                CATGT CC   CAGTCTTGGC
                                |||||  ||   ||||||||||
                                GTGTA GG   GTCGGGACCG
                                  G  ___
GAM1038  KIAA1727  3'  GCTGGGATTACAGGTGTGA   64059     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  KIAA1728  3'  GTTTTATATGTTGGGATGTGA  68419      G  TG   GTCTT
                                TCATGT CC  ACA    GGC
                                ||||||  ||  |||    |||
                                AGTGTA GG  TGT    TTG
                                   _  GT   ATATT
GAM1038  KIAA1751  3'  GCTTTTGTGTTGAGGTGTATGA 71702      TG   _   GTCTT
                                TCATG  CCT GACA    GGC
                                |||||  ||| ||||    |||
                                AGTAT  GGA TTGT    TCG
                                   GT   G   GTTT_
GAM1038  KIAA1766  3'  GTCATGTTGTCGGGGTGTGA   71355     TG G      TCT
                                TCA  T CCTGACAG   TGGC
                                |||  | ||||||||   ||||
                                AGT  G GGGCTGTT   ACTG
                                  GT _       GT_
GAM1038  KIAA1784  3'  GCTGGCCAGGGCATGG      65152       G    A_
                                TCATGT CCTG  CAGT
                                ||||||  ||||  ||||
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                                GGTACG GGAC  GTCG
                                   _   CG
GAM1038 KIAA1786 3' GTTAAGGCCACAGTGTGTGA  66037      TG C  ACA
                                TCATG  C TG   GTCTTGGC
                                |||||  | ||   ||||||||
                                AGTGT  G AC   CGGAATTG
                                   GT _  AC_
GAM1038 KIAA1789 5' GCCAAGGGCTAAGGTAATGG  67102      G    GACAG
                                TCAT TGCCT    TCTTGGC
                                |||| |||||    |||||||
                                GGTA ATGGA    GGAACCG
                                   _    ATCG_
GAM1038 KIAA1805 5' GTGAAATTGTTAGGCGTGG   79968     GT       C  G
                                TCAT  GCCTGACAGT TT GC
                                ||||  |||||||||| || ||
                                GGTG  CGGATTGTTA AA TG
                                   __       _ G
GAM1038 KIAA1805 3' GTTAAGGACATGGTATATG   79969       TGACAG
                                CATGTGCC     TCTTGGC
                                ||||||||     |||||||
                                GTATATGG     GGAATTG
                                     TACA__
GAM1038 KIAA1808 3' GCCAAGAGTGGGGTGTGTGA  85864      TG   G  AG
                                TCATG  CCT AC  TCTTGGC
                                |||||  ||| ||  |||||||
                                AGTGT  GGG TG  AGAACCG
                                   GT   G  __
GAM1038 KIAA1808 3' GCCCCGGTGCTGGGCACGTGG 85865        GA  G  TT
                                TCATGTGCCT  CA TC  GGC
                                ||||||||||  || ||  |||
                                GGTGCACGGG  GT GG  CCG
                                     TC  _  CC
GAM1038 KIAA1808 3' GCCGGGACGTGAGCTGTGA   85866      T  C G  A
                                TCATG GC T AC GTCTTGGC
                                ||||| || | || ||||||||
                                AGTGT CG A TG CAGGGCCG
                                   _ _ G  _
GAM1038 KIAA1813 5' GCTGGGGGCTGGGGTGTGTGG 70304      TG   GA    _ TG
                                TCATG  CCT  CAGTC T  GC
                                |||||  |||  ||||| |  ||
                                GGTGT  GGG  GTCGG G  CG
                                   GT   __    G GT
GAM1038 KIAA1814 3' GCCAAGGCGGAGGCTGTGG   70362      T   GACA
                                TCATG GCCT    GTCTTGGC
                                ||||| ||||   ||||||||
                                GGTGT CGGA    CGGAACCG
                                   _    GG__
GAM1038 KIAA1829 3' GCTGGGATTATGGGCGTGA   61952      G  TGAC    TG
                                TCATGT CC    AGTCT  GC
                                |||||| ||    |||||  ||
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                                AGTGCG GG   TTAGG  CG
                                   _ TA__    GT
GAM1038 KIAA1872 3' GCTGGGACATTTAGGGACATGG 62938      G    CA   TG
                                TCATGT CCTGA  GTCT  GC
                                |||||| |||||  ||||  ||
                                GGTACA GGATT  CAGG  CG
                                   G    TA   GT
GAM1038 KIAA1877 3' GTTAAGACTTGTTGCAATGA  66175     G  CT   _
                                TCAT TGC  GACA GTCTTGGC
                                |||| |||  |||| ||||||||
                                AGTA ACG  TTGT CAGAATTG
                                  _  __   T
GAM1038 KIAA1881 3' GCTCAGGTCGGGTGTGA     95342     GT     AGT  T
                                TCAT  GCCTGAC   CT GGC
                                ||||  |||||||   || |||
                                AGTG  TGGGCTG   GA TCG
                                  __      ___  C
GAM1038 KIAA1904 3' GCTGGGGCAGCAGCAGTGG   73490     G  C  ACA   TG
                                TCAT TGC TG   GTCT  GC
                                |||| ||| ||   ||||  ||
                                GGTG ACG AC   CGGG  CG
                                  _  _ GA_   GT
GAM1038 KIAA1904 3' GTTGGCTGTGGTTGGGCACCTG 73497    T    TG ___   TTGGC
           G                     TCA GTGCC  AC   AGTC
                                ||| |||||  ||   ||||
                                GGT CACGG  TG   TCGG
                                  C    GT  GTG   TTG
GAM1038 KIAA1906 3' GCTAGACGACCAGCGTATGA  73194       C  ACA   T
                                TCATGTGC TG   GTCT GGC
                                |||||||| ||   |||| |||
                                AGTATGCG AC   CAGA TCG
                                    _ CAG   _
GAM1038 KIAA1908 3' CGGGACTGTCCACAGA     73398    A   CCT     TG
                                TC TGTG   GACAGTCT  G
                                || ||||   ||||||||  |
                                AG ACAC   CTGTCAGG  C
                                 _   ___      GT
GAM1038 KIAA1913 5' CCGAGATTCCCGCTGA     73885    T  CCT  CA
                                TCA GTG   GA  GTCTTGG
                                ||| |||   ||  |||||||
                                AGT CGC   CT  TAGAGCC
                                  _  C__  __
GAM1038 KIAA1922 5' GCTGAGATTACAGGTGTGA  73631     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGA  CG
                                  __    A_    GT
GAM1038 KIAA1922 5' GCTGGGATTACAGGCATGTG  73632        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
```

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                                GTGTACGGAC  TTAGG  CG
                                     A_    GT
GAM1038  KIAA1924  3'  GACTGTCAGCGCATGG     73673       C
                                TCATGTGC TGACAGTC
                                |||||||| ||||||||
                                GGTACGCG ACTGTCAG
                                   _
GAM1038  KIAA1925  5'  GCCGAGGGAAGGGTGCATG   92079     TG   GACAG
                                CATG  CCT    TCTTGGC
                                ||||  |||    |||||||
                                GTAC  GGG    GGAGCCG
                                  GT   AAG__
GAM1038  KIAA1940  3'  GCTAGGGCTGAGGATGGGA   79985    ATGTG   GA
                                TC    CCT  CAGTCTTGGC
                                ||    |||  ||||||||||
                                AG    GGA  GTCGGGATCG
                                 GGTA_  __
GAM1038  KIAA1940  3'  GTTGGGGTGTATGGGTAGTGA  79989     G    _  G  TG
                                TCAT TGCCTG ACA TCT  GC
                                |||| |||||| ||| |||  ||
                                AGTG ATGGGT TGT GGG  TG
                                  _     A   _  GT
GAM1038  KIAA1949  5'  GCCGAGATTGTCAGTCTGTGC  92084   TG ___
                                G  C   CTGACAGTCTTGGC
                                |  |   ||||||||||||||
                                C  G   GACTGTTAGAGCCG
                                 GT TCT
GAM1038  KIAA1949  5'  GCCGAGATTGTCAGTCTGTGC  97752   TG ___
                                G  C   CTGACAGTCTTGGC
                                |  |   ||||||||||||||
                                C  G   GACTGTTAGAGCCG
                                 GT TCT
GAM1038  KIAA1949  5'  GCCGAGATTGTCAGTCTGTGC  97874   TG ___
                                G  C   CTGACAGTCTTGGC
                                |  |   ||||||||||||||
                                C  G   GACTGTTAGAGCCG
                                 GT TCT
GAM1038  KIAA1957  3'  CCAGGGCGGGGCCGTGG     75715      T   GACA
                                TCATG GCCT    GTCTTGG
                                ||||| ||||    |||||||
                                GGTGC CGGG    CGGGACC
                                   _   G___
GAM1038  KIAA1957  3'  GCTGGCTTTTTGGGTACA    75718      TG C_   TT
                                TGTGCC  A  AGTC  GGC
                                ||||||  |  ||||  |||
                                ACATGG  T  TCGG  TCG
                                   GT TT   __
GAM1038  KIAA1971  3'  GCTGGGATTACAGGTGTGA   74222     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 KIAA1971 3' GTTGGGATTATAGGCAT    74225       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGG  TG
                                   A_    GT
GAM1038 KIAA1975 5' GCTAGGATTACAGGTGTGA   73974     GT    AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  TGGAC  TTAGGATCG
                                  __    A_
GAM1038 KLHL6    3' GCTGGGATTACAGGTGTGA   55306     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 KLK7     3' GCTGGGATTACAGGCAT     57733       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038 KLK7     3' GCTGGGATTACAGGCAT     17293       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038 LALP1    3' GTTGATGATGTTAGTACATGA 39786        C    G  _ TG
                                TCATGTGC TGACA TC T  GC
                                |||||||| ||||| || |  ||
                                AGTACATG ATTGT AG A  TG
                                   _    _  T GT
GAM1038 LAMP3    3' GCTGGGATTACAGGCAT     59491       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038 LANCL2   3' GCTAAGGCTTGTGTCATGA   38000      T  CTG  _
                                TCATG GC   ACA GTCTTGGC
                                |||||  ||   |||  ||||||||
                                AGTAC TG   TGT CGGAATCG
                                  _  ___   T
GAM1038 LAP1B    3' GTCAAACATAGGTATATGA   64586         ACA  C
                                TCATGTGCCTG   GT TTGGC
                                ||||||||||   ||  |||||
                                AGTATATGGAT   CA AACTG
                                     A__  _
GAM1038 LAP1B    3' GTCAGGCCAAGGCAGGTGG   64587     G    GACA   T
                                TCAT TGCCT    GTCT GGC
                                ||||  |||||    ||||  |||
```

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                                GGTG ACGGA   CGGA CTG
                                  G    AC__   _
GAM1038 LATS1   3' GCTAAGGCTGAGCATAACATGA 60279      GCC  A_
                                TCATGT  TG  CAGTCTTGGC
                                ||||||  ||  ||||||||||
                                AGTACA  AC  GTCGGAATCG
                                   AT_  GA
GAM1038 LBP-9   3' GCCAGTCTTTTATCAGGTATAT 27278         C___  T  T
            GA                   TCATGTGCCTGA   AG CT GGC
                                ||||||||||||   || || |||
                                AGTATATGGACT   TC GA CCG
                                      ATTT  T  _
GAM1038 LGALS9  3' GCCGGGGGCTGGGGTGTGG  23791    GT   GA    _
                                TCAT  GCCT  CAGTCTT GGC
                                ||||  ||||  ||||||| |||
                                GGTG  TGGG  GTCGGGG CCG
                                  __   __     G
GAM1038 LGALS9  3' GCCGGGGGCTGGGGTGTGG  9723     GT   GA    _
                                TCAT  GCCT  CAGTCTT GGC
                                ||||  ||||  ||||||| |||
                                GGTG  TGGG  GTCGGGG CCG
                                  __   __     G
GAM1038 LHFPL2  3' TTAGGATTGTGCTTTGA    69957    TGT  CTG
                                TCA  GC  ACAGTCTTGG
                                |||  ||  ||||||||||
                                AGT  CG  TGTTAGGATT
                                 TT_  ___
GAM1038 LIECG3  3' GCTGGGATTGCAGGCAT    87411       A    TG
                                GTGCCTG CAGTCT  GC
                                ||||||| ||||||  ||
                                TACGGAC GTTAGG  CG
                                   _    GT
GAM1038 LIP8    5' GTTGGGACGTTTTGGGTGTGA  88151    GT   TG CA_   TG
                                TCAT  GCC  A   GTCT  GC
                                ||||  |||  |   ||||  ||
                                AGTG  TGG  T   CAGG  TG
                                  __  GT TTG   GT
GAM1038 LW-1    5' GCTGGGGTCTGTGGGCCCATGA 60260      T   G   _  TG
                                TCATG GCCT ACAG TCT  GC
                                ||||| |||| |||| |||  ||
                                AGTAC CGGG TGTC GGG  CG
                                  C   _   T  GT
GAM1038 LW-1    5' GCTGGGGTCTGTGGGCCCATGA 32369      T   G   _  TG
                                TCATG GCCT ACAG TCT  GC
                                ||||| |||| |||| |||  ||
                                AGTAC CGGG TGTC GGG  CG
                                  C   _   T  GT
GAM1038 LY75    3' GCTGGGATTACAGGCAT    9842        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
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                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038 LYPLA3   3' GTCAGGGCTGCCTTCATGG   24635      TGCCTGA
                                TCATG      CAGTCTTGGC
                                |||||      ||||||||||
                                GGTAC      GTCGGGACTG
                                   TTCC___
GAM1038 LZ16     3' GCTGAGACTCTCGGCACAT   25182       T  C    TG
                                ATGTGCC GA AGTCT  GC
                                ||||||| || |||||  ||
                                TACACGG CT TCAGA  CG
                                   _ C    GT
GAM1038 MAB21L2  5' GCTGAGACTGTGGGGCGTCA  21232    _    G     TG
                                TG TGCCT ACAGTCT  GC
                                || ||||| |||||||  ||
                                AC GCGGG TGTCAGA  CG
                                 T    G      GT
GAM1038 MAN1C1   3' TCAGGCCAGGGCCATGG     39821      T   GACA   T
                                TCATG GCCT   GTCT GG
                                ||||| ||||   |||| ||
                                GGTAC CGGG   CGGA CT
                                   _   AC__   _
GAM1038 MAP-1    3' GCTGGGACTACAGGCATGTG  42182         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTACGGAC  TCAGG  CG
                                      A_    GT
GAM1038 MAP-1    3' GCTGGGATTACAGGCGTGA   42183     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 MAP1LC3A 3' GCTGGGCAGGCATGTG     50708         A_
                                CATGTGCCTG  CAGT
                                ||||||||||  ||||
                                GTGTACGGAC  GTCG
                                      GG
GAM1038 MAPK8IP3 3' GCTGGGACGCGGTGGGTGTGG 52988     GT    ACA_   TG
                                TCAT  GCCTG   GTCT  GC
                                ||||  |||||   ||||  ||
                                GGTG  TGGGT   CAGG  CG
                                  __    GGCG   GT
GAM1038 MAPK8IP3 3' GTCAGGGTTGAGCTTAGTGA  52992     GT_ CTGA  GT
                                TCAT   GC   CA  CTTGGC
                                ||||   ||   ||  ||||||
                                AGTG   CG   GT  GGACTG
                                  ATT  A___  TG
GAM1038 MAST205  5' GCCGGGACAGTCGCGGCGCTGA 30668     T    _    A
                                TCA GTGCC TGAC GTCTTGGC
                                ||| ||||| |||| ||||||||
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                                AGT CGCGG GCTG CAGGGCCG
                                  _    C   A
GAM1038  MAT2B   5'  GCTGAGGCTGCGGCGTGA   25223    GT  T A    TG
                                TCAT  GCC G CAGTCT  GC
                                ||||  ||| | ||||||  ||
                                AGTG  CGG C GTCGGA  CG
                                  __  _ _    GT
GAM1038  MBIP    3'  GTCAAGGTTTATTTTCACATGA 33428       CCTGAC GT
                                TCATGTG    A  CTTGGC
                                |||||||    |  ||||||
                                AGTACAC    T  GAACTG
                                    TTTTAT TG
GAM1038  MCAM    3'  GCCGGGGCCAGGTGTGGTGG  21455    _ TG   ACA
                                TCAT G  CCTG  GTCTTGGC
                                |||| |  ||||  ||||||||
                                GGTG T  GGAC  CGGGGCCG
                                  G GT  ___
GAM1038  MCAM    3'  GCTAGAGCTTCGGGTGTGTG  21456    TG   C  TC
                                CATG  CCTGA AG  TTGGC
                                ||||  ||||| ||  |||||
                                GTGT  GGGCT TC  GATCG
                                  GT   _ GA
GAM1038  MCLC    3'  GCTGGGATTACAGGCAT    30688      AC   TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_   GT
GAM1038  MCM10   3'  GCTAGGACTACAGGCGTGCGTG 37575      __   AC
           A                     TCATGT  GCCTG  AGTCTTGGC
                                ||||||  |||||  |||||||||
                                AGTGCG  CGGAC  TCAGGATCG
                                   TG   A_
GAM1038  MCPR    5'  GCCGGGGCTCGCCGCGCCTGA  42647    T   CTGAC
                                TCA GTGC    AGTCTTGGC
                                ||| ||||    |||||||||
                                AGT CGCG    TCGGGGCCG
                                  C   CCGC_
GAM1038  MDA5    5'  ATTGTCAGGCACAGA      42223    A
                                TC TGTGCCTGACAGT
                                || ||||||||||||
                                AG ACACGGACTGTTA
                                 _
GAM1038  MEF-2   3'  GCTGGGATTACAGGCACATG  64390       AC   TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTACACGGAC  TTAGG  CG
                                    A_   GT
GAM1038  MESDC1  5'  GCCGGGGCGGCGGCAGTGG   42595    G   T ACA
                                TCAT TGCC G   GTCTTGGC
                                |||| |||| |   ||||||||
```

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                                GGTG ACGG C   CGGGGCCG
                                  _   _ GG_
GAM1038  MFN2     3'  GGAGGGCTGTTGGATGTATGG  29603       GC TG      GGC
                                TCATGT  C  ACAGTCTT
                                ||||||  |  ||||||||
                                GGTATG  G  TGTCGGGA
                                   TA GT       GG
GAM1038  MGC10731 3'  CGGGGCAGGAACATGG      48108       G   GACA    TG
                                TCATGT CCT    GTCT  G
                                |||||| |||    ||||  |
                                GGTACA GGA    CGGG  C
                                   A  ____    GT
GAM1038  MGC10812 3'  GCCAAGGCCTGTGGCATCTGA  48668     T    TG   _
                                TCA GTGCC  ACAG TCTTGGC
                                ||| |||||  |||| |||||||
                                AGT TACGG  TGTC GGAACCG
                                  C    __   C
GAM1038  MGC10911 5'  GCCGGGATGACAGGCAT     50210        ACA
                                GTGCCTG   GTCTTGGC
                                |||||||   ||||||||
                                TACGGAC   TAGGGCCG
                                   AG_
GAM1038  MGC10960 3'  GCCGGGGCCTGAGTGGACGTGA 51006       G  TGA   _
                                TCATGT CC   CAG TCTTGGC
                                |||||| ||   ||| |||||||
                                AGTGCA GG   GTC GGGGCCG
                                   _  TGA   C
GAM1038  MGC10986 3'  GCTGCAGCCTCAGGCACTGG   47564     T      CA  CT
                                TCA GTGCCTGA  GT  TGGC
                                ||| ||||||||  ||  ||||
                                GGT CACGGACT  CG  GTCG
                                  _      C_  AC
GAM1038  MGC11115 3'  ATTGTCAGGCACGGA       50236     A
                                TC TGTGCCTGACAGT
                                || ||||||||||||
                                AG GCACGGACTGTTA
                                 _
GAM1038  MGC11115 3'  GCTGGGATGTGGGGGGCATAT  50240         GA  _   TG
                                ATGTGCCT  CA GTCT  GC
                                ||||||||  || ||||  ||
                                TATACGGG  GT TAGG  CG
                                    GG  G    GT
GAM1038  MGC11303 5'  GCCGGGACTCGGCGCGGGA   50705    A     TGAC
                                TC TGTGCC    AGTCTTGGC
                                || ||||||    |||||||||
                                AG GCGCGG    TCAGGGCCG
                                 G     C___
GAM1038  MGC11352 5'  TCGAAGTGGGGACATGG     64807       G   G  AGTC
                                TCATGT CCT AC    TTGG
                                |||||| ||| ||    ||||
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                                GGTACA GGG TG    AGCT
                                   _  G  A___
GAM1038  MGC12518  3'  GCTGGGATTACAGGCAT    64081       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  MGC12679  3'  GCTGGGGCTGCGGCCGCGTGG  51205       C   A     TG
                                TCATGTG CTG CAGTCT  GC
                                ||||||| ||| ||||||  ||
                                GGTGCGC GGC GTCGGG  CG
                                   C  _     GT
GAM1038  MGC12966  5'  GCCGGGGCGACGCGGCGCGGA  51125    A     TGACA
                                TC TGTGCC    GTCTTGGC
                                || ||||||    ||||||||
                                AG GCGCGG    CGGGGCCG
                                 _     CGCAG
GAM1038  MGC13090  3'  GCCAGGGGAGGTTGTGTGTGTG 51140      TG C    AG_
            G                    TCATG  C TGAC   TCTTGGC
                                |||||  | ||||  |||||||
                                GGTGT  G GTTG   GGGACCG
                                  GT T    GAG
GAM1038  MGC13138  3'  GCTGGGATTACAGGCGTGA   53021     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  MGC13168  3'  GCCAGGGTTGAGGATGTG    51211      G   GA  GT
                                CATGT CCT  CA  CTTGGC
                                ||||| |||  ||  ||||||
                                GTGTA GGA  GT  GGACCG
                                  _  __  TG
GAM1038  MGC13186  3'  GTCGAGGCTGTATGCCTATGG  50317      T  CTG
                                TCATG GC   ACAGTCTTGGC
                                ||||| ||   ||||||||||
                                GGTAT CG   TGTCGGAGCTG
                                  C  TA_
GAM1038  MGC14289  3'  GCTAGGATTACAGGCAT     54704       AC
                                GTGCCTG  AGTCTTGGC
                                |||||||  |||||||||
                                TACGGAC  TTAGGATCG
                                   A_
GAM1038  MGC14859  3'  GCCAGGGTATGGGGCATGTG   61918        GACAG
                                CATGTGCCT    TCTTGGC
                                |||||||||    |||||||
                                GTGTACGGG    GGGACCG
                                     GTAT_
GAM1038  MGC15416  3'  GCCAAGGCCTGTGCAGTACGTG 50426        C  _   _
            G                    TCATGTGC TG ACAG TCTTGGC
                                |||||||| || |||| |||||||
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                                GGTGCATG AC TGTC GGAACCG
                                    _ G   C
GAM1038  MGC15416  3'  GCCAAGGCCTGTGCAGTACGTG 56541       C _   _
             G                   TCATGTGC TG ACAG TCTTGGC
                                 |||||||| || |||| |||||||
                                 GGTGCATG AC TGTC GGAACCG
                                    _ G   C
GAM1038  MGC15438  3'  GCCAAGATGGCGGCGCTGA   51791    T    T ACA
                                 TCA GTGCC G   GTCTTGGC
                                 ||| ||||| |   ||||||||
                                 AGT CGCGG C   TAGAACCG
                                   _   _ GG_
GAM1038  MGC15438  3'  GCCGGGGCCGCCGGGACATGG  51792      G   ACA
                                 TCATGT CCTG   GTCTTGGC
                                 |||||| ||||   ||||||||
                                 GGTACA GGGC   CGGGGCCG
                                    _   CGC
GAM1038  MGC15631  3'  GCTGGGACTGGCAAGCACG   51268     C A    TG
                                 TGTGC TG CAGTCT  GC
                                 ||||| || ||||||  ||
                                 GCACG AC GTCAGG  CG
                                    A  G     GT
GAM1038  MGC15705  5'  GCTGAGGCTGGCTGCCTGG   51281    T _  TGAC    TG
                                 TCA GT GCC    AGTCT  GC
                                 ||| || |||    |||||  ||
                                 GGT CG CGG    TCGGA  CG
                                   C  T  ____     GT
GAM1038  MGC15730  3'  GCCACTCCATCAGGCACTGA   51802    T      CAGTCT
                                 TCA GTGCCTGA     TGGC
                                 ||| ||||||||     ||||
                                 AGT CACGGACT     ACCG
                                   _       ACCTC_
GAM1038  MGC16279  5'  ACATTAGCTGTCTAGGCGTGTG 51883    TG   _    CTTGGC
             G                   TCA  TGCCT GACAGT
                                 |||  ||||| ||||||
                                 GGT  GCGGA CTGTCG
                                   GT    T     ATTACAG
GAM1038  MGC16279  3'  ACATTAGCTGTCTAGGCGTGTG 62873    TG   _    CTTGGC
             G                   TCA  TGCCT GACAGT
                                 |||  ||||| ||||||
                                 GGT  GCGGA CTGTCG
                                   GT    T     ATTACAG
GAM1038  MGC16385  5'  CGGGCTAGGCAGTGG      58886     G    GAC  T  TG
                                 TCAT TGCCT   AG CT  G
                                 |||| |||||   || ||  |
                                 GGTG ACGGA   TC GG  C
                                   _    ___ _  GT
GAM1038  MGC16703  3'  GCTGAGGCTGGGCACGGTGG   73101     _    TGA    TG
                                 TCAT GTGCC   CAGTCT  GC
                                 |||| |||||   ||||||  ||
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                                GGTG CACGG  GTCGGA  CG
                                  G   ___     GT
GAM1038 MGC17299 3' GCCAGGGTGTGAGTGCATGTGA 58237       _ G  G
                                TCATGTGC CT ACA TCTTGGC
                                |||||||| || ||| |||||||
                                AGTGTACG GA TGT GGGACCG
                                    T  G  _
GAM1038 MGC1842  3' GCTGGGACTACAGGCACATG  65652       AC   TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTACACGGAC  TCAGG  CG
                                     A_    GT
GAM1038 MGC1842  3' GTTAGGGCTGTCACTAGG   65656    ___
                                CCT   GACAGTCTTGGC
                                |||   ||||||||||||
                                GGA   CTGTCGGGATTG
                                  TCA
GAM1038 MGC1842  3' TCAGGACAGTATGTGA     65659       CTGACA
                                TCATGTGC     GTCTTGG
                                ||||||||     |||||||
                                AGTGTATG     CAGGACT
                                    A_____
GAM1038 MGC20460 5' CCGAGACCTGCCGTGG     53845     T  CTGACA
                                TCATG GC     GTCTTGG
                                ||||| ||     |||||||
                                GGTGC CG     CAGAGCC
                                   _ TC____
GAM1038 MGC21675 3' GCTGAGATTACAGGCAT    53485      AC   TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGA  CG
                                    A_    GT
GAM1038 MGC21688 3' GCTGGGCTGGGGGCGCATG   58268       GA  T  TG
                                CATGTGCCT  CAG CT  GC
                                |||||||||  ||| ||  ||
                                GTACGCGGG  GTC GG  CG
                                     G_   _  GT
GAM1038 MGC21738 3' GCTGGGATTACAGGTGTGA   58917    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 MGC22014 3' GCCAAGCCCCTCGGGCGCTGG 64495    T      CAGT
                                TCA GTGCCTGA   CTTGGC
                                ||| ||||||||   ||||||
                                GGT CGCGGGCT   GAACCG
                                  _      CCCC
GAM1038 MGC22776 3' CCATCCGGGCATGTGG     58619          ACAGTCT
                                TCATGTGCCTG     TGG
                                ||||||||||      |||
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                                GGTGTACGGGC      ACC
                                      CT_____
GAM1038 MGC2306  3' GCCAGGGCTGGGTCACAGGA  50962    A   _  TGA
                                TC TGTG CC   CAGTCTTGGC
                                || |||| ||   ||||||||||
                                AG ACAC GG   GTCGGGACCG
                                 G   T ___
GAM1038 MGC23280 3' GCCAGGATGCTTGCCATGG   58395     T  CTGACA
                                TCATG GC     GTCTTGGC
                                ||||| ||     ||||||||
                                GGTAC CG     TAGGACCG
                                   _  TTCG__
GAM1038 MGC2452  5' GCTGAGGCGCACAGCCTGTGG 50987     T  C  ACA   TG
                                TCATG GC TG   GTCT  GC
                                ||||| || ||   ||||  ||
                                GGTGT CG AC   CGGA  CG
                                   C  _  ACG   GT
GAM1038 MGC2474  3' GCTGGGATTACAGGCGTGA   43727     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038 MGC2477  5' GCTGGGATTACAGGTGTGA   44067     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038 MGC2488  3' GCTAGGACCACAGGTGCGTG  43872     TG   ACA
                                CATG  CCTG   GTCTTGGC
                                ||||  ||||   ||||||||
                                GTGC  GGAC   CAGGATCG
                                  GT   AC_
GAM1038 MGC2562  3' GCCAGCTTGTTGTCACGTACGT 50442       C     TC__
           GG                     TCATGTGC TGACAG    TTGGC
                                ||||||||  ||||||    |||||
                                GGTGCATG ACTGTT    GACCG
                                     C     GTTC
GAM1038 MGC2601  5' GCCGGGGCAGCGGTGGTGA   43879     G   T ACA
                                TCAT TGCC G   GTCTTGGC
                                |||| |||| |   ||||||||
                                AGTG GTGG C   CGGGGCCG
                                   _   _ GA_
GAM1038 MGC2605  3' GCCGAGACCTGGGTGTCTGG  50219    T TG   ACA
                                TCA G  CCTG   GTCTTGGC
                                ||| |  ||||   ||||||||
                                GGT T  GGGT   CAGAGCCG
                                  C GT   C__
GAM1038 MGC2865  5' GTCATGATTGAGCATATGA   50454       CTGA    T
                                TCATGTGC    CAGTC TGGC
                                ||||||||    ||||| ||||
```

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                                AGTATACG   GTTAG ACTG
                                    A___    T
GAM1038 MGC29891 3' GCTGGGAGGACAGGCATATG  58208       ACAG  TG
                                CATGTGCCTG   TCT  GC
                                ||||||||||   |||  ||
                                GTATACGGAC   AGG  CG
                                     AGG_   GT
GAM1038 MGC29898 3' GCTGGGACTATAGGCGTGTG  58929   TG    AC    TG
                                CA  TGCCTG  AGTCT  GC
                                ||  ||||||  |||||  ||
                                GT  GCGGAT  TCAGG  CG
                                 GT    A_    GT
GAM1038 MGC29898 3' GCTGGGATTACAGGTGTGA   58930    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 MGC32043 3' GCTGGCAGGTACAGA      58052    A      A
                                TC TGTGCCTG CAGT
                                || ||||||||  ||||
                                AG ACATGGAC GTCG
                                 _      G
GAM1038 MGC35521 3' GTCAGGATGGCTGGAGCATGG 59012      G  TGACA
                                TCATGT CC    GTCTTGGC
                                ||||||  ||    ||||||||
                                GGTACG GG    TAGGACTG
                                   A  TCGG_
GAM1038 MGC3771  3' GCTGGGATTACAGGCGTGA   48247    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 MGC4368  3' GCCAGGATCTCGGCGCATAGA  44461   _     T  CA
                                TC ATGTGCC GA  GTCTTGGC
                                || |||||||  ||  ||||||||
                                AG TACGCGG CT  TAGGACCG
                                 A      _  C_
GAM1038 MGC4400  5' GCCAGGTGGCAAGTGTATGG   51053     TG C  ACAGT
                                TCATG  C TG    CTTGGC
                                |||||  | ||    ||||||
                                GGTAT  G AC    GGACCG
                                   GT A  GGT__
GAM1038 MGC4415  3' GCTGAGACTAAGACGTGG    48952      GC  GAC    TG
                                TCATGT  CT   AGTCT  GC
                                ||||||  ||   |||||  ||
                                GGTGCA  GA   TCAGA  CG
                                   __ A__    GT
GAM1038 MGC4655  3' GCCAAGGCTGGGTGGTAGATGA 52801     G    TGA
                                TCAT TGCC   CAGTCTTGGC
                                |||| ||||   ||||||||||
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                                AGTA ATGG   GTCGGAACCG
                                  G    TGG
GAM1038  MGC4677   5' GCTAGGCCCAGGTGTAT     53510     TG    ACA    T
                                ATG  CCTG   GTCT GGC
                                |||  ||||   |||| |||
                                TAT  GGAC   CGGA TCG
                                  GT    C__    _
GAM1038  MGC4701   5' GTCGGGGCTGCCTCAGCGCTGG 64558     T    C   __
                                TCA GTGC TGA  CAGTCTTGGC
                                ||| |||| |||  ||||||||||
                                GGT CGCG ACT  GTCGGGGCTG
                                  _    _  CC
GAM1038  MGC4737   5' GCTTCCCATCGTCAGGCATGTG 48850            A  CTT_
             A                   TCATGTGCCTGAC GT    GGC
                                ||||||||||||| ||    |||
                                AGTGTACGGACTG TA    TCG
                                       C  CCCT
GAM1038  MGC4766   5' GCTGGGATTACAGGGCACTGA  48777     T     GAC     TG
                                TCA GTGCCT   AGTCT  GC
                                ||| ||||||   |||||  ||
                                AGT CACGGG   TTAGG  CG
                                  _     ACA     GT
GAM1038  MGC4767   3' GGCTGTAGGGTGTGTGG     50287      TG   G
                                TCATG  CCT ACAGTC
                                |||||  ||| ||||||
                                GGTGT  GGG TGTCGG
                                   GT   A
GAM1038  MGC4796   3' GCCAGGGTCTTGTGCTGTGG   61489     _ TG CT   AGT
                                TCAT G  C  GAC   CTTGGC
                                ||||  |  |  |||   ||||||
                                GGTG C  G  CTG   GGACCG
                                  T GT TT   ___
GAM1038  MGC4832   3' ACTCTGCTGTCAGGTTGTGA   58996      T        CTTGGC
                                TCATG GCCTGACAGT
                                ||||| ||||||||||
                                AGTGT TGGACTGTCG
                                   _         TCTCAA
GAM1038  MGC5139   5' GCCAGGGCTGTTAGCAC     74106     C
                                GTGC TGACAGTCTTGGC
                                |||| ||||||||||||
                                CACG ATTGTCGGGACCG
                                  _
GAM1038  MGC5149   3' GCTGGGACTACAGGCACGTG   72294          AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGCACGGAC  TCAGG  CG
                                      A_    GT
GAM1038  MGC5149   3' GCTGGGATTACAGGCGTGA   72295     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  MGC5242  3'  GTTGAGGCCACAGTGTATAGA  43826    A    _  ACA   TG
                                TC TGTGC CTG   GTCT  GC
                                || ||||| |||   ||||  ||
                                AG ATATG GAC   CGGA  TG
                                 _    T   AC_   GT
GAM1038  MGC5309  3'  GCTGGGACTGCGAGTGCTGA   80814    T TG C  A    TG
                                TCA G  C TG CAGTCT  GC
                                ||| |  | || ||||||  ||
                                AGT C  G GC GTCAGG  CG
                                  _ GT A  _     GT
GAM1038  MGC5384  3'  GTCGGGAGGCCAAGGCACAT   48273       GACAG
                                ATGTGCCT    TCTTGGC
                                ||||||||    |||||||
                                TACACGGA    AGGGCTG
                                     ACCGG
GAM1038  MGC5469  5'  GCCAGGACTGACTGCGCCGTGG 50397     _  CTGA
                                TCATG TGC    CAGTCTTGGC
                                ||||| |||    ||||||||||
                                GGTGC GCG    GTCAGGACCG
                                   C   TCA_
GAM1038  MGC9753  5'  GCTGGGGCAGCGGCGCTGG   53052    T    T ACA   TG
                                TCA GTGCC G   GTCT  GC
                                ||| ||||| |   ||||  ||
                                GGT CGCGG C   CGGG  CG
                                  _    _ GA_   GT
GAM1038  MGC9753  3'  GCTGGTGGGCATGTGA     53053         GA
                                TCATGTGCCT  CAGT
                                ||||||||||  ||||
                                AGTGTACGGG  GTCG
                                      TG
GAM1038  MGC9912  3'  GCTGGGACTACAGGCAT    54721       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TCAGG  CG
                                    A_    GT
GAM1038  MIL1     3'  GTTGGGGCTGTCCTGTGTGTGG 31096      TG CT      TG
                                TCATG  C  GACAGTCT  GC
                                |||||  |  ||||||||  ||
                                GGTGT  G  CTGTCGGG  TG
                                   GT TC       GT
GAM1038  MKRN1    3'  GAGTGTGTGGGTGTGTGA    25575      TG   _  G
                                TCATG  CCTG ACA TC
                                |||||  |||| ||| ||
                                AGTGT  GGGT TGT AG
                                   GT   G  G
GAM1038  MKRN4    3'  GCTGGGACTACAGGTGCATG  47751     TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
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                                GTAC  GGAC  TCAGG  CG
                                  GT   A_    GT
GAM1038  MLZE     5'  GCTGGAGTGCAGCGCATGG   48623        C  A  G   T
                                TCATGTGC TG CA TCT GGC
                                |||||||| || || ||| |||
                                GGTACGCG AC GT AGG TCG
                                    _ _ G  _
GAM1038  MLZE     5'  GCTGGGATTACAGACGTGA   48624       GC  AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTGCA  GAC  TTAGG  CG
                                   __   A_    GT
GAM1038  MMS19L   3'  GCTGAGGGGTGAGTGCATATGA 42301         _  G  AG   TG
                                TCATGTGC CT AC  TCT  GC
                                |||||||| || ||  |||  ||
                                AGTATACG GA TG  GGA  CG
                                    T  G  G_  GT
GAM1038  moblak   3'  GCTGGGATTACAGGCAT     55505        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  moblak   3'  GCTGGGATTACAGGCGTGA   55506      GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  MOCS3    3'  GCTGGGATTACAGGCGTGA   27154     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  mPA-PLA1 3'  GCTGGGACTAGATAGTGGATGA 57683      G   CTGAC    TG
                                TCAT TGC    AGTCT  GC
                                |||| |||    |||||  ||
                                AGTA GTG    TCAGG  CG
                                  G  ATAGA    GT
GAM1038  MRAS     5'  GCCGGGGCTGGAGCGCGCG   24227      _  GA
                                TGTGC CT  CAGTCTTGGC
                                |||||  ||  ||||||||||
                                GCGCG GA  GTCGGGGCCG
                                   C  G_
GAM1038  MRPL20   3'  GCTGGGATTACAGGCGTGA   35738     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  MRPL3    3'  GCTGAAATTGGTGTTGGGCATA 23285        TG  ___  C TG
            T                    ATGTGCC  ACA   GT T  GC
                                |||||||  |||   || |  ||
```

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                                TATACGG  TGT   TA A  CG
                                   GT   GGT  A GT
GAM1038  MRPL44   3'  GCTGGGATTACAGGTGTGA   43322     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  MRPS27   3'  GCTGGGATGATAGGCGTGA   30639     GT    ACA   TG
                                TCAT  GCCTG   GTCT  GC
                                ||||  |||||   ||||  ||
                                AGTG  CGGAT   TAGG  CG
                                  __    AG_   GT
GAM1038  MRPS27   3'  GTTGGGGCTTGAAGTGCATCA  30643   T   _  GAC    TG
                                A GTGC CT   AGTCT  GC
                                | |||| ||   |||||  ||
                                A TACG GA   TCGGG  TG
                                 C    T  AGT    GT
GAM1038  MSH5     5'  GCTGGGGTCCTGGCGCGTGG   10123        T_   AGT  TG
                                TCATGTGCC  GAC   CT  GC
                                |||||||||  |||   ||  ||
                                GGTGCGCGG  CTG   GG  CG
                                     TC   ___  GT
GAM1038  MSTP031  5'  GCTGGCAAGCATGTGG     49343        C  A
                                TCATGTGC TG CAGT
                                |||||||| || ||||
                                GGTGTACG AC GTCG
                                     A  G
GAM1038  MT-ACT48  3'  AGGAGGCTGAGGTGAGTGG   24685     G    GA     GGC
                                TCAT TGCCT  CAGTCTT
                                |||| |||||  |||||||
                                GGTG GTGGA  GTCGGAG
                                  A    __      GAT
GAM1038  MUC17    3'  GCCAGGATTGATTTGGTTGA   94274     TGT   T  _
                                TCA   GCC GA CAGTCTTGGC
                                |||   ||| || ||||||||||
                                AGT   TGG TT GTTAGGACCG
                                  ___   T  A
GAM1038  MYL6     5'  GCTGAGCAGTCAAGATGTGTGA 54383     TG GC  _   A T  TG
                                TCA  T  CT GAC G CT  GC
                                |||  |  || ||| | ||  ||
                                AGT  G  GA CTG C GA  CG
                                  GT TA  A   A _  GT
GAM1038  MYO5C    3'  GCTAGGATTACAGGCGTGTG   38108    TG     AC
                                CA  TGCCTG  AGTCTTGGC
                                ||  ||||||  |||||||||
                                GT  GCGGAC  TTAGGATCG
                                 GT     A_
GAM1038  MYT1     3'  GCTGAGGCTGTGCAGATGTGTA 15776     TG __   _      TG
            TGG                   CATG  C  CTG ACAGTCT  GC
                                ||||  |  ||| |||||||  ||
```

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                                GTAT  G  GAC TGTCGGA  CG
                                  GT TA   G     GT
GAM1038  MYT1L    5' GCCAAGGACGAGGTGTGTG   66824     TG   GACAG
                                CATG  CCT    TCTTGGC
                                ||||  |||    |||||||
                                GTGT  GGA    GGAACCG
                                  GT   GCA__
GAM1038  N-PAC    3' GCAGGATTGGCGTGTGG    70880    TG   TGAC     GC
                                TCA  TGCC   AGTCTTG
                                |||  ||||   |||||||
                                GGT  GCGG   TTAGGAC
                                 GT   ____     GA
GAM1038  N4BP3    3' GTCAGGGGACGGGTGTGA   66269     GT    ACAG
                                TCAT  GCCTG   TCTTGGC
                                ||||  |||||   |||||||
                                AGTG  TGGGC   GGGACTG
                                  __    AG__
GAM1038  N4BP3    3' GTCGGGATTGAGGCTGTTGA  66270    TGT   GA
                                TCA   GCCT  CAGTCTTGGC
                                |||   ||||  ||||||||||
                                AGT   CGGA  GTTAGGGCTG
                                 TGT   __
GAM1038  NAPG     5' GCTGGGATTGTAGACATA    96726     C   A     TG
                                TGTG CTG CAGTCT  GC
                                |||| ||| ||||||  ||
                                ATAC GAT GTTAGG  CG
                                  A  _     GT
GAM1038  NAV3     3' GCTGAGATTTCCTGTACAT   29772      CT  C    TG
                                ATGTGC  GA AGTCT  GC
                                ||||||  || |||||  ||
                                TACATG  CT TTAGA  CG
                                   TC  _    GT
GAM1038  NDP52    3' GCTGGGATTACAGGTGTGTG  19533     TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGT  GGAC  TTAGG  CG
                                  GT   A_    GT
GAM1038  NDUFC2   3' GCTGGGACTACAGGTGCATG  15838     TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTAC  GGAC  TCAGG  CG
                                  GT   A_    GT
GAM1038  NEIL2    3' GCTAGGGTGTGGTGGTGTGA  58908     GT   TG_  G
                                TCAT  GCC   ACA TCTTGGC
                                ||||  |||   ||| |||||||
                                AGTG  TGG   TGT GGGATCG
                                  __  TGG  _
GAM1038  NEIL2    3' GCTGGGACTACAGGCATGTGA  58909          AC    TG
                                TCATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
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                                AGTGTACGGAC TCAGG CG
                                      A_    GT
GAM1038 NEIL2    3' GTTGGGACCACGGGTGTGA  58911     GT   ACA   TG
                                TCAT GCCTG  GTCT GC
                                |||| |||||  |||| ||
                                AGTG TGGGC  CAGG TG
                                  __    AC_   GT
GAM1038 NEUGRIN  3' GTCGGGGCTTGGCTTATGG  33573     T  TGAC
                                TCATG GCC   AGTCTTGGC
                                ||||| |||   |||||||||
                                GGTAT CGG   TCGGGGCTG
                                   T  T___
GAM1038 NIBAN    5' CTAGCAGCGGGCGCGGA    42000    A      ACA CT
                                TC TGTGCCTG  GT TGG
                                || ||||||||  ||  |||
                                AG GCGCGGGC  CG ATC
                                 _      GA_ __
GAM1038 NICN1    3' GCTGGGATTACAGGCAT    50292       AC    TG
                                GTGCCTG AGTCT GC
                                ||||||| ||||| ||
                                TACGGAC TTAGG CG
                                    A_    GT
GAM1038 NIFU     5' GCTGGGGCTTTCCGTCTGA  67315    TG CCT C    TG
                                TCA TG  GA AGTCT GC
                                |||  ||  || ||||| ||
                                AGT GC  CT TCGGG CG
                                 CT ___ T    GT
GAM1038 NIP30    3' CCAGTATGGGCGCAT      46323       GACA C
                                ATGTGCCT   GT TTGG
                                ||||||||   || ||||
                                TACGCGGG   TA GACC
                                     ____ T
GAM1038 NIR3     3' GTCTGGTGTTGGGACGCATGG 66244       _ TG  G TT
                                TCATGTG CC  ACA TC  GGC
                                ||||||| ||  ||| ||  |||
                                GGTACGC GG  TGT GG  CTG
                                    A GT  _ T_
GAM1038 NOL4     5' GCCGGGGCTGCATTTTTCATGA 13696     TGCC_ A
                                TCATG    TG CAGTCTTGGC
                                |||||    || ||||||||||
                                AGTAC    AC GTCGGGGCCG
                                   TTTTT _
GAM1038 NR2F1    3' GTCGAGGCTGTTCTTCAAGA  95949   A TGCCT
                                TC TG    GACAGTCTTGGC
                                || ||    ||||||||||||
                                AG AC    TTGTCGGAGCTG
                                 A TTC__
GAM1038 NR5A1    3' GCCGGGACTGGGGGCG     17102     GA
                                TGCCT CAGTCTTGGC
                                ||||| ||||||||||
```

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                                GCGGG  GTCAGGGCCG
                                  G_
GAM1038  NTKL     5'  GCCGAACCCGCGGCGCGTGG  40347        T ACA  C
                                TCATGTGCC G   GT TTGGC
                                |||||||||  |   || |||||
                                GGTGCGCGG C   CA AGCCG
                                     _ GCC  _
GAM1038  NUDT9    5'  GCCGGGACTCGGAGCTGTGG  43890      T  _   CA
                                TCATG GC CTGA  GTCTTGGC
                                |||||  ||  ||||  ||||||||
                                GGTGT CG GGCT  CAGGGCCG
                                  _ A   __
GAM1038  Nup37    5'  GTCAGGGTTGATGGCATA    43923       TGA  GT
                                TGTGCC   CA  CTTGGC
                                ||||||   ||  ||||||
                                ATACGG   GT  GGACTG
                                   TA_  TG
GAM1038  NXN      3'  GCTGGGATTACAGGCGTGA   42420     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  NXP-2    3'  GCCAGGATTTTGTTGTGCTGA  71108     T TG CT   __
                                TCA G  C  GACA  GTCTTGGC
                                |||  |  |  ||||  ||||||||
                                AGT C  G  TTGT  TAGGACCG
                                  _ GT __    TT
GAM1038  OCT11    3'  GCTGGGATTACAGGTGTGA   26820     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  OR51E2   3'  GTTGGGATTACAGGTGTGA   47795     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  TG
                                  __    A_    GT
GAM1038  OSBPL2   3'  GCTGGGATTACAGGCGTGA   29216     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  OSBPL2   3'  GCTGGGATTACAGGCGTGA   57867     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  P2RXL1   3'  GCCAGGCAGGCCTCAGGTGCAT 18383     TG    CA   ___
            G                    CATG  CCTGA  GTCT   TGGC
                                ||||  |||||  ||||   ||||
```

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                                GTAC  GGACT  CGGA   ACCG
                                  GT    C_   CGG
GAM1038  P5-1    5'  GCCAAGGTTGCGGGTCATGG  21919      T    A  GT
                                TCATG GCCTG CA  CTTGGC
                                ||||| ||||| ||  ||||||
                                GGTAC TGGGC GT  GAACCG
                                  _    _ TG
GAM1038  P5326   3'  GCCAGGACCATGGACATGA   48773      G  TGACA
                                TCATGT CC    GTCTTGGC
                                |||||| ||    ||||||||
                                AGTACA GG    CAGGACCG
                                   _ TAC__
GAM1038  PADI1   3'  GTCAGGGTAGCAGAGTGTGTGA 61999      TG _   ACAG
                                TCATG  C CTG   TCTTGGC
                                |||||  | |||   |||||||
                                AGTGT  G GAC   GGGACTG
                                   GT A   GAT_
GAM1038  PASK    5'  GCTGAGGCTGGAGTGCAGTGG  30719     G   _  GA     TG
                                TCAT TGC CT  CAGTCT  GC
                                |||| ||| ||  ||||||  ||
                                GGTG ACG GA  GTCGGA  CG
                                  _  T  G_     GT
GAM1038  PASK    5'  GCTGGGATTACAGGTGTGA   30720     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  PCDH10  5'  GCCAAGACTGTCGGAATA    40426    GC
                                TGT  CTGACAGTCTTGGC
                                |||  ||||||||||||||
                                ATA  GGCTGTCAGAACCG
                                  A_
GAM1038  PCDH10  5'  GCCAAGACTGTCGGAATA    51992    GC
                                TGT  CTGACAGTCTTGGC
                                |||  ||||||||||||||
                                ATA  GGCTGTCAGAACCG
                                  A_
GAM1038  PCDH17  5'  GCCGCAGCTCGGGTGCAGA   27089    A  TG    CA  CT
                                TC TG  CCTGA  GT  TGGC
                                || ||  |||||  ||  ||||
                                AG AC  GGGCT  CG  GCCG
                                  _ GT    __  AC
GAM1038  PCDH19  3'  ACTTCAGCATATGA       63695        C   C
                                TCATGTGC TGA AGT
                                |||||||| ||| |||
                                AGTATACG ACT TCA
                                   _  _
GAM1038  PDZD2   5'  GCCAAGAGTTGGATTAGGCATT 80873     T      __   _
            GG                    TCA GTGCCTGA  CAG TCTTGGC
                                ||| ||||||||  ||| |||||||
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                                GGT TACGGATT  GTT AGAACCG
                                  _      AG   G
GAM1038  PDZD2    5'  GTCGAGACTGCATTCGTGG   80876      TGCC  A
                                TCATG    TG CAGTCTTGGC
                                |||||    || ||||||||||
                                GGTGC    AC GTCAGAGCTG
                                  TT__  _
GAM1038  PELI1    5'  GCTAGGACTACAGGCACGTG  40270         AC
                                CATGTGCCTG  AGTCTTGGC
                                ||||||||||  |||||||||
                                GTGCACGGAC  TCAGGATCG
                                      A_
GAM1038  PELI1    5'  GCTGGGATTACAGGCATGTG  40273         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTACGGAC  TTAGG  CG
                                      A_    GT
GAM1038  PELI1    5'  GCTGGGATTACAGGCGTGA   40274     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  PHRET1   3'  GCTGGGATCAGACCGTGG    41060      TGC   CAG   TG
                                TCATG   CTGA   TCT  GC
                                |||||   ||||   |||  ||
                                GGTGC   GACT   AGG  CG
                                  CA_   ____   GT
GAM1038  PIG7     3'  GCTGGGATTGCAGGCATA    16794        A     TG
                                TGTGCCTG CAGTCT  GC
                                |||||||| ||||||  ||
                                ATACGGAC GTTAGG  CG
                                      _     GT
GAM1038  PIP3-E   3'  GCTGGGATTACAGGTGTGA   66807     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  PMF1     3'  GTCAAGGTCAAGAGCCTGTGG  23328      T  _  _   AGT
                                TCATG GC CT GAC   CTTGGC
                                ||||| || || |||   ||||||
                                GGTGT CG GA CTG   GAACTG
                                  C  A  A  ____
GAM1038  PMX2B    3'  GCCAGGGCTCCGCCTGCTGA  14083     T   CC  AC
                                TCA GTG  TG  AGTCTTGGC
                                ||| |||  ||  |||||||||
                                AGT CGT  GC  TCGGGACCG
                                  _  CC  C_
GAM1038  PORIMIN  3'  GCTGGGGTGGGGGCATTGG   53606     T     GA  G   TG
                                TCA GTGCCT  CA TCT  GC
                                ||| ||||||  || |||  ||
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                                GGT TACGGG  GT GGG  CG
                                  _     G_ _   GT
GAM1038  PP1201   3'  GCTGGGGTTGTGAGGAATATGA 42194       G   G   GT  TG
                                TCATGT CCT ACA  CT  GC
                                |||||| ||| |||  ||  ||
                                AGTATA GGA TGT  GG  CG
                                   A   G   TG  GT
GAM1038  PP1628   5'  TCAGGGTTTGGCCATGA     47307      T   T   AGT
                                TCATG GCC GAC   CTTGG
                                ||||| ||| |||   |||||
                                AGTAC CGG TTG   GGACT
                                  _  T  ____
GAM1038  PP1665   5'  GCCAGGCGCCAGGGCCGTGG   47914      T   GACA   T
                                TCATG GCCT    GTCT GGC
                                ||||| ||||    |||| |||
                                GGTGC CGGG    CGGA CCG
                                  _   ACCG   _
GAM1038  PP3501   5'  GCTGGGATTACAGGTGTGG    41371     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                GGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  PPAP2C   3'  CCTGGTTAGGCACTGA      13544     T       AGTCTT
                                TCA GTGCCTGAC     GG
                                ||| |||||||||     ||
                                AGT CACGGATTG     CC
                                  _       GT_____
GAM1038  PPIL3    5'  GTTAGGATTATAGGCGTGA    55660     GT    AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  CGGAT  TTAGGATTG
                                  __    A_
GAM1038  PRDM14   3'  GCTGGGGGTGGTGGCACATG   44448       TGA  G   TG
                                CATGTGCC   CA TCT  GC
                                ||||||||   || |||  ||
                                GTACACGG   GT GGG  CG
                                     TG_  G   GT
GAM1038  PRO0245  5'  GCTGAGATTATAGGCGTGA    26133     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAT  TTAGA  CG
                                  __    A_    GT
GAM1038  PRO0365  5'  GCTGGGATTATAGGCGTGTG   26166    TG    AC    TG
                                CA  TGCCTG  AGTCT  GC
                                ||  ||||||  |||||  ||
                                GT  GCGGAT  TTAGG  CG
                                 GT    A_    GT
GAM1038  PRO0456  5'  GCTAGGACTACAGGCGTGTG   26177    TG    AC
                                CA  TGCCTG  AGTCTTGGC
                                ||  ||||||  |||||||||
```

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                                GT  GCGGAC  TCAGGATCG
                                 GT     A_
GAM1038  PRO0529   3' GTCAGTGGACTAGCACATGG   25998        CTGAC    __
                                TCATGTGC    AGTCT  TGGC
                                ||||||||    |||||  ||||
                                GGTACACG    TCAGG  ACTG
                                    A____     TG
GAM1038  PRO0800   3' GCTAATTTGTCAGCATATGG   37742        C     TC
                                TCATGTGC TGACAG  TTGGC
                                |||||||| ||||||  |||||
                                GGTATACG ACTGTT  AATCG
                                    _     T_
GAM1038  PRO1048   3' GCTGGGACCACAGGTGTGTG   37520     TG   ACA   TG
                                CATG  CCTG   GTCT  GC
                                ||||  ||||   ||||  ||
                                GTGT  GGAC   CAGG  CG
                                  GT    AC_    GT
GAM1038  PRO1048   3' GTTGGGACCACAGGCGTGA    37523     GT    ACA   TG
                                TCAT  GCCTG   GTCT  GC
                                ||||  |||||   ||||  ||
                                AGTG  CGGAC   CAGG  TG
                                  __     AC_    GT
GAM1038  PRO1855   3' GCTGCAGATTGGTACATGA    37547        TGAC    _
                                TCATGTGCC    AGTCT TGGC
                                |||||||||    ||||| ||||
                                AGTACATGG    TTAGA GTCG
                                     ____     C
GAM1038  PRO1992   3' GCTGGGATTACAGGCAT     26059       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  PRO2533   3' CCAAGACAGTAAGTGA      37800     G  CTGACA
                                TCAT TGC     GTCTTGG
                                |||| |||     |||||||
                                AGTG ATG     CAGAACC
                                  A  A_____
GAM1038  PRO2955   3' GCTGGGATTACAGGCGTGA    37641     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __     A_    GT
GAM1038  PSMD12    3' GCTGGGATTACAGGCAT     11001       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  PSR      5' GCCGGGACTGAGCGAAGGGCGT 65183   TG    GA____
            TTGG                  A  TGCCT     CAGTCTTGGC
                                |  |||||     ||||||||||
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                                T  GCGGG     GTCAGGGCCG
                                 TT    AAGCGA
GAM1038  PSTPIP2   3'  GCTGGGATTACAGGCGTGA   44393     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  PTDSS2    5'  GCCGGTGACCCGGTGTGCGTGG 47887      TG _   ACA  _
                                TCATG  C CTG   GTC TTGGC
                                |||||  | |||   ||| |||||
                                GGTGC  G GGC   CAG GGCCG
                                   GT T   C__   T
GAM1038  RAB21     3'  GCTGGGATTACAGGCGTGA   30389     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  RAB24     5'  GCTGGGCAAGGAGTACGTGG   55390        _  GACA T  TG
                                TCATGTGC CT    G CT  GC
                                ||||||||  ||    | ||  ||
                                GGTGCATG GG    C GG  CG
                                    A  AA__ _  GT
GAM1038  RAB33B    3'  GCTGGGATTACAGGTGTGA   48497     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  RAB3IL1   5'  GCTGACAGGCGGTGG      25464     G     A
                                TCAT TGCCTG CAGT
                                |||| |||||| ||||
                                GGTG GCGGAC GTCG
                                  _     A
GAM1038  RAB40A    5'  GCCAAGAGACTGGGTGTGGGA  82069    AT TG  TGA     __
                                TC  G  CC   CAGTCT  TGGC
                                ||  |  ||   ||||||  ||||
                                AG  T  GG   GTCAGA  ACCG
                                 GG GT  ___     GA
GAM1038  RAB40A    5'  GTCAACTGTATCAAGCACATGG 55148        C   __    CT
                                TCATGTGC TGA  CAGT  TGGC
                                |||||||| |||  ||||  ||||
                                GGTACACG ACT  GTCA  ACTG
                                    A   AT   __
GAM1038  RAD51     5'  GCCGTGCGGGTCGGGCGCGTG  56017          A_  CT
                                CATGTGCCTGAC  GT  TGGC
                                ||||||||||||  ||  ||||
                                GTGCGCGGGCTG  CG  GCCG
                                       GG  T_
GAM1038  RAD51     5'  GCCGTGCGGGTCGGGCGCGTG  11223          A_  CT
                                CATGTGCCTGAC  GT  TGGC
                                ||||||||||||  ||  ||||
```

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                                GTGCGCGGGCTG CG GCCG
                                      GG T_
GAM1038 RAD52B   5' GCCGAGGCTTTGCATGTGA  88226       CTGAC
                                TCATGTGC   AGTCTTGGC
                                ||||||||   |||||||||
                                AGTGTACG   TCGGAGCCG
                                    TT___
GAM1038 RAI     5' GCTGGGATTGCAGGCGTGTG  21884   TG    A    TG
                                CA TGCCTG CAGTCT GC
                                || |||||| |||||| ||
                                GT GCGGAC GTTAGG CG
                                 GT     _    GT
GAM1038 RAI16   3' GCCAGGGCCAAGCCTGTGA  42757     T C ACA
                                TCATG GC TG  GTCTTGGC
                                ||||| || ||  ||||||||
                                AGTGT CG AC  CGGGACCG
                                   C A ___
GAM1038 RAI17   3' GTTGGGGGGCGCGGGCATAT  91285       ACAG  TG
                                ATGTGCCTG   TCT GC
                                |||||||||   ||| ||
                                TATACGGGC   GGG TG
                                     GCGG  GT
GAM1038 RASGRP4  3' GTCACACTGGGTCGGCATGTGG 53659       TGA_  CT
                                TCATGTGCC   CAGT TGGC
                                |||||||||   |||| ||||
                                GGTGTACGG   GTCA ACTG
                                     CTGG   C_
GAM1038 RASSF2   3' GTTGGGATTACAGGCGTGA  28442    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG TG
                                  __   A_   GT
GAM1038 RBM12    5' GCTGGGGCTGTCGGCCGCG  20159    C       TG
                                TGTG CTGACAGTCT GC
                                |||| |||||||||| ||
                                GCGC GGCTGTCGGG CG
                                  C       GT
GAM1038 RINZF    5' GTCGGGACTCCTCGGCGCGCG 43698     _   C_
                                TGTGC CTGA AGTCTTGGC
                                ||||| |||| |||||||||
                                GCGCG GGCT TCAGGGCTG
                                   C   CC
GAM1038 RLUCL    5' GCCAGCGCGCGGGCGCGCGG  54219   A     ACA CT
                                TC TGTGCCTG  GT TGGC
                                || ||||||||  ||  ||||
                                GG GCGCGGGC  CG ACCG
                                 C      GCG __
GAM1038 RNF20    3' GTCAGGACTGAGCTGGTGA  38967    GT CTGA
                                TCAT GC   CAGTCTTGGC
                                ||||  ||  ||||||||||
```

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                                AGTG  CG   GTCAGGACTG
                                  GT  A___
GAM1038  RNF8     3'  GCTGAGATTACAGGCAT     14233       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGA  CG
                                   A_    GT
GAM1038  RNF8     3'  GCTGGGACTACAGGCATATG  14234         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTATACGGAC  TCAGG  CG
                                     A_    GT
GAM1038  RNF8     3'  GCTGGGATTACAGGCGTGA   14235     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  RNF8     3'  GTTGAGGCAGTAGGAGTGTGG  14237      TG   ACA   TG
                                TCATG  CCTG   GTCT  GC
                                |||||  ||||   ||||  ||
                                GGTGT  GGAT   CGGA  TG
                                   GA   GA_   GT
GAM1038  RNO2     5'  GCTGGGATTATAGGTGTGA   52773     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAT  TTAGG  CG
                                  __    A_    GT
GAM1038  RNP24    3'  GCCAAGTTTTTTGTGTGTGTGA 22357      TG C   C  T
                                TCATG  C TGA AG CTTGGC
                                |||||  | ||| || ||||||
                                AGTGT  G GTT TT GAACCG
                                   GT T   T  T
GAM1038  RODH-4   3'  GCTAAGGTTGGATGCATGG   13535      GC TG  AGT
                                TCATGT  C  AC   CTTGGC
                                ||||||  |  ||   ||||||
                                GGTACG  G  TG   GAATCG
                                   TA GT  ___
GAM1038  RoXaN    3'  GCTTGGGGTTGGGTATGTGA   46649        TG  AG   T
                                TCATGTGCC  AC  TCT GGC
                                |||||||||  ||  ||| |||
                                AGTGTATGG  TG  GGG TCG
                                     GT  __   T
GAM1038  RP4-622L5 3'  CGGGGTCTGGCATAGA     38929    A     T   AGT  TG
                                TC TGTGCC GAC   CT  G
                                || |||||| |||   ||  |
                                AG ATACGG CTG   GG  C
                                 _     T   ___  GT
GAM1038  Rpo1-2   3'  GCTAGGATTACAGGTGTGA   38702     GT    AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
```

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                                AGTG  TGGAC  TTAGGATCG
                                  __     A_
GAM1038  Rpo1-2   3'  GCTAGGATTACAGGTGTGA   49877     GT    AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  TGGAC  TTAGGATCG
                                  __     A_
GAM1038  RPS6KB1  3'  GCTGAACTCTTAGGCACAT   12037         C   C TG
                                ATGTGCCTGA AGT T  GC
                                |||||||||| ||| |  ||
                                TACACGGATT TCA A  CG
                                     C   _ GT
GAM1038  SARM     3'  CCAGAGCCAGGGCATGG     30599       G    ACA TC
                                TCATGT CCTG   G  TTGG
                                |||||| ||||   |  ||||
                                GGTACG GGAC   C  GACC
                                  _    ____ GA
GAM1038  SARM     3'  CCAGGGCATGGATATGA     30600       G  TGACA
                                TCATGT CC     GTCTTGG
                                |||||| ||     |||||||
                                AGTATA GG     CGGGACC
                                   _ TA____
GAM1038  SARM     3'  GCTGGGACTACCAGTGCATA  30609       _  AC    TG
                                TGTGC CTG  AGTCT  GC
                                ||||| |||  |||||  ||
                                ATACG GAC  TCAGG  CG
                                   T   CA    GT
GAM1038  SARM     3'  GTCAGGCTTGGGCACGGGA   30614    A     TG CA    T
                                TC TGTGCC  A  GTCT GGC
                                || ||||||  |  |||| |||
                                AG GCACGG  T  CGGA CTG
                                 G     GT __    _
GAM1038  SCYA16   3'  GCTGGGATTACAGGCGTGA   15962     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __     A_    GT
GAM1038  SCYA22   3'  GCTGAGATTACAGGCGTGA   90947     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGA  CG
                                  __     A_    GT
GAM1038  SCYA22   3'  GCTGGGATTACAGGCGTGA   90948     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __     A_    GT
GAM1038  SCYA22   3'  GCTGGGATTACAGGCGTGA   90949     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                              AGTG  CGGAC  TTAGG  CG
                                __    A_    GT
GAM1038 SCYA22   3' GCTGGGATTACAGGTGTGTG  90950     TG   AC    TG
                              CATG  CCTG  AGTCT  GC
                              ||||  ||||  |||||  ||
                              GTGT  GGAC  TTAGG  CG
                                GT    A_    GT
GAM1038 SCYA28   3' GCTGGGATTACAGGCAT    39059       AC    TG
                              GTGCCTG  AGTCT  GC
                              |||||||  |||||  ||
                              TACGGAC  TTAGG  CG
                                 A_    GT
GAM1038 SDC3     5' CGGGGTCTGGCACAGA     27749    A     T   AGT  TG
                              TC TGTGCC GAC   CT  G
                              || |||||| |||   ||  |
                              AG ACACGG CTG   GG  C
                               _     T   ___  GT
GAM1038 SDC3     5' GCTGAGACTGGGCCCAGTGA  27755     GT_  TGA     TG
                              TCAT   GCC   CAGTCT  GC
                              ||||   |||   ||||||  ||
                              AGTG   CGG   GTCAGA  CG
                                ACC   ___     GT
GAM1038 SDC3     3' GGGCAGGGCTTAGGGTGTGTGG 27759      TG   GAC      GC
                              TCATG  CCT   AGTCTTG
                              |||||  |||   |||||||
                              GGTGT  GGG   TCGGGAC
                                 GT   AT_     GGGT
GAM1038 SDCCAG43 3' GCTGGGGCAGGGCACACTGG  70372     _     GACA   TG
                              TCA TGTGCCT    GTCT  GC
                              ||| |||||||    ||||  ||
                              GGT ACACGGG    CGGG  CG
                                C      A___    GT
GAM1038 SEC24D   5' CCGGCACTAGGCGCAGA     29092    A      GAC   C
                              TC TGTGCCT   AGT TTGG
                              || |||||||   ||| ||||
                              AG ACGCGGA   TCA GGCC
                               _     ___   C
GAM1038 SEC61A1  3' GTCAGGTTCGGGGTGCATGG  25312      TG   GACAGT
                              TCATG  CCT     CTTGGC
                              |||||  |||     ||||||
                              GGTAC  GGG     GGACTG
                                 GT   GCTT__
GAM1038 SEMA3B   3' GTTGGGGCCGGGCACAT     16156        ACA   TG
                              ATGTGCCTG   GTCT  GC
                              |||||||||   ||||  ||
                              TACACGGGC   CGGG  TG
                                    ___    GT
GAM1038 SEMA3C   5' GCCGGGGCTGCGCGGTGGTGA 21062      G   _  A
                              TCAT TGCC TG CAGTCTTGGC
                              |||| |||| || ||||||||||
```

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                                AGTG GTGG GC GTCGGGGCCG
                                  _   C  _
GAM1038 SEMA6B   3' GCCGGGGAGGTGGGCGTGTG  49491   TG   G AG
                                CA  TGCCT AC  TCTTGGC
                                ||  ||||| ||  |||||||
                                GT  GCGGG TG  GGGGCCG
                                 GT    _ GA
GAM1038 SERF1B   3' GCTGGGATTACAGGCGTGA   43419    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 SFXN2    3' GCTGGGATTACAGGCAT    73950      AC   TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038 SGK2     3' GCTTATTTGCTGGGTACGTGA 32779       GA  TCTT
                                TCATGTGCCT  CAG   GGC
                                ||||||||||  |||   |||
                                AGTGCATGGG  GTT   TCG
                                      TC   TAT_
GAM1038 SHAPY    3' ACTTCAGGCATTGA      57107    T     C
                                TCA GTGCCTGA AGT
                                ||| |||||||| |||
                                AGT TACGGACT TCA
                                  _      _
GAM1038 SIMRP7   3' GCCAAGATCCTGTGTAT    92367    CTG   __
                                GTGC   ACAG  TCTTGGC
                                ||||   ||||  |||||||
                                TATG   TGTC  AGAACCG
                                  ___    CT
GAM1038 SIRPB1   3' GCTGGGATTACAGGCAT    20257      AC   TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038 SIRPB1   3' GCTGGGATTACAGGCATGT   20258       AC   TG
                                ATGTGCCTG  AGTCT  GC
                                |||||||||  |||||  ||
                                TGTACGGAC  TTAGG  CG
                                     A_    GT
GAM1038 SLC11A1  3' GCCAAGGCTGGAGTGCAGTGG 59458    G  _  GA
                                TCAT TGC CT  CAGTCTTGGC
                                |||| ||| ||  ||||||||||
                                GGTG ACG GA  GTCGGAACCG
                                  _  T  G_
GAM1038 SLC16A4  3' GCTGGGATTACAGGCAT    16282      AC   TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
```

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                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  SLC17A3   5' GTCGGGGCCAGAGCGCA    21810      _  ACA
                                TGTGC CTG   GTCTTGGC
                                ||||| |||   ||||||||
                                ACGCG GAC   CGGGGCTG
                                  A  ____
GAM1038  SLC19A3   3' GCTGAGATTACAGGCGTGA   47493     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGA  CG
                                  __    A_    GT
GAM1038  SLC26A1   3' GTCAGGGCCCAGGGTGCTGTGA 41867     _ TG   GACA
                                TCAT G  CCT   GTCTTGGC
                                |||| |  |||   ||||||||
                                AGTG C  GGG   CGGGACTG
                                  T GT   ACC_
GAM1038  SLC2A10   3' GCTGGGATTACAGGCGCGTG   47823        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGCGCGGAC  TTAGG  CG
                                     A_    GT
GAM1038  SLC39A3   3' GCCAGGACCTCACAGGGTAT   57975      GACA__
                                GTGCCT     GTCTTGGC
                                ||||||     ||||||||
                                TATGGG     CAGGACCG
                                   ACACTC
GAM1038  SLC39A3   3' GCTGGTCAGGCGGATGA     57976     G      _
                                TCAT TGCCTGAC AGT
                                |||| |||||||| |||
                                AGTA GCGGACTG TCG
                                  G       G
GAM1038  SLC6A14   3' GCTGAGATTACAGGTGTGA   23354     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGA  CG
                                  __    A_    GT
GAM1038  SNFT     5' GCCGGGACTGGCGCGCG     37898      CTGA
                                TGTGC   CAGTCTTGGC
                                |||||   ||||||||||
                                GCGCG   GTCAGGGCCG
                                  CG__
GAM1038  SNPH     3' GCTGGGGCTGCCCCCGCAGGA  28243    A   CCTGA     TG
                                TC TGTG    CAGTCT  GC
                                || ||||    ||||||  ||
                                AG ACGC    GTCGGG  CG
                                 G   CCCC_     GT
GAM1038  SNRK     3'  TAAACATTGACAGGTATGTGA  34768          A   CTTGGC
                                TCATGTGCCTG CAGT
                                |||||||||| ||||
```

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                                AGTGTATGGAC GTTA
                                      A    CAAATG
GAM1038 SP2     3' GTTGAGGGTTGGGGGCAATGA 11893     _ G TG AG  TG
                                TCAT GT CC  AC  TCT  GC
                                |||| || ||  ||  |||  ||
                                AGTA CG GG  TG  GGA  TG
                                  A  G  GT  __  GT
GAM1038 SPTLC2   3' GTCAGGAGGCTGAGGCACAGGA 16807    A     GA    __
                                TC TGTGCCT  CAGTCT  TGGC
                                || |||||||  ||||||  ||||
                                AG ACACGGA  GTCGGA  ACTG
                                 G      __     GG
GAM1038 SPTLC2   3' GTTAGGAGCTGGGTGCGGA   16808    A  TG  TGA  _
                                TC TG  CC   CAG TCTTGGC
                                || ||  ||   ||| |||||||
                                AG GC  GG   GTC AGGATTG
                                 _  GT  ___   G
GAM1038 SSBP2    5' GCTGTGATGGGTTGACAGGTGC 59527     TG   A  GT  ____
            GTGA                   ATG  CCTG CA  CT   TGGC
                                ||| |||| ||  ||   ||||
                                TGC  GGAC GT  GG   GTCG
                                  GT   A  TG  TAGT
GAM1038 SSBP4    3' GCTGAGGTCACACCTCGGGCAC 50935   T      CAG____  TG
            CTGG                   A GTGCCTGA      TCT  GC
                                | ||||||||      |||  ||
                                T CACGGGCT      GGA  CG
                                 C       CCACACT   GT
GAM1038 SSH2     3' CCAAGGCTGGGTCTGA     62202     TGT   TGA
                                TCA   GCC   CAGTCTTGG
                                |||   |||   |||||||||
                                AGT   TGG   GTCGGAACC
                                  C__   ___
GAM1038 SSH2     3' GTTGATGTTTTGGTGTATGG   62211      TG  T_   GTC TG
                                TCATG  CC  GACA   T  GC
                                |||||  ||  ||||   |  ||
                                GGTAT  GG  TTGT   A  TG
                                   GT  TT    ___ GT
GAM1038 ST7L     3' GTCAGGGACAGGGCATAT    57579        GACAG
                                ATGTGCCT    TCTTGGC
                                ||||||||    |||||||
                                TATACGGG    GGGACTG
                                     ACA__
GAM1038 ST7L     3' GTCAGGGACAGGGCATAT    57002        GACAG
                                ATGTGCCT    TCTTGGC
                                ||||||||    |||||||
                                TATACGGG    GGGACTG
                                     ACA__
GAM1038 ST7L     3' GTCAGGGACAGGGCATAT    34858        GACAG
                                ATGTGCCT    TCTTGGC
                                ||||||||    |||||||
```

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                                TATACGGG    GGGACTG
                                    ACA__
GAM1038  STAF65(gamma) 3'  GCTGGGATTACACGCACATG   29437       C  AC    TG
                                CATGTGC TG  AGTCT  GC
                                ||||||| ||  |||||  ||
                                GTACACG AC  TTAGG  CG
                                    C  A_    GT
GAM1038  STAF65(gamma) 3'  GCTGGGATTACAGGCGTGA   29438     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  STAG1    5'  GTTAGGATTGCAGCTCCGTTGA 19613     _  TGC   A
                                TCA TG   CTG CAGTCTTGGC
                                ||| ||   ||| ||||||||||
                                AGT GC   GAC GTTAGGATTG
                                  T  CTC  _
GAM1038  STAM2    5'  GTTGGGACAGGAGCGCGGGA   19566    A    _ GACA    TG
                                TC TGTGC CT    GTCT  GC
                                || ||||| ||    ||||  ||
                                AG GCGCG GG    CAGG  TG
                                 G    A  A___    GT
GAM1038  STAM2    5'  GCCGGGGTCCTAGCGCTGG    19565     T    CT_   AGT
                                TCA GTGC   GAC   CTTGGC
                                ||| ||||   |||   ||||||
                                GGT CGCG   CTG   GGGCCG
                                  _    ATC   ___
GAM1038  STIM2    3'  GCCGAGGTGGGGGGGATATGG   40475       G   GA  G
                                TCATGT CCT  CA TCTTGGC
                                |||||| |||  || |||||||
                                GGTATA GGG  GT GGAGCCG
                                   G   G_  _
GAM1038  STK22B   3'  GTCGGGGTTGGGGGGCAT    53813       GA  GT
                                GTGCCT  CA  CTTGGC
                                ||||||  ||  ||||||
                                TACGGG  GT  GGGCTG
                                    GG  TG
GAM1038  STK29    5'  GCTAGAACACGTGTCAGGTGGT 87577      G       ___  CT
              GA                  TCAT TGCCTGACA   GT  TGGC
                                ||||| |||||||||   ||  ||||
                                AGTG GTGGACTGT   CA  ATCG
                                  _       GCA  AG
GAM1038  STOML1   3'  GCGGGATTGGGCATGGGA    16672    AT    TGA      GC
                                TC  GTGCC   CAGTCTTG
                                ||  |||||   ||||||||
                                AG  TACGG   GTTAGGGC
                                 GG    ___       GG
GAM1038  STOML1   3'  GCTGGGGCCCAGGGCAGCATGA 16673       _    GACA    TG
                                TCATG TGCCT    GTCT  GC
                                ||||| |||||    ||||  ||
```

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                                AGTAC ACGGG   CGGG  CG
                                   G    ACC_   GT
GAM1038  STRAIT11499 5'  GCCAGGGCTCGACCCACAGA  41144    A   CCTGAC
                                TC TGTG     AGTCTTGGC
                                || ||||     |||||||||
                                AG ACAC     TCGGGACCG
                                 _   CCAGC_
GAM1038  SULT4A1   3'  GCCAGGCAGGTGGCACGTGG  68492        TG  AGT
                                TCATGTGCC  AC   CTTGGC
                                |||||||||  ||   ||||||
                                GGTGCACGG  TG   GGACCG
                                      __  GAC
GAM1038  SYNE-2    3'  GCCAAGGGTGCCCAGCACGTGG 30800        C  A_  G
                                TCATGTGC TG  CA TCTTGGC
                                |||||||| ||  || |||||||
                                GGTGCACG AC  GT GGAACCG
                                     _ CC  G
GAM1038  SYT12     5'  GCCAAGACCTGGGGTGATGG  94731     G    GA  _
                                TCAT TGCCT  CAG TCTTGGC
                                |||| |||||  ||| |||||||
                                GGTA GTGGG  GTC AGAACCG
                                  _    __  C
GAM1038  TA-LRRP   3'  GCCGAGATTGTGCCAC     31069     CCTG
                                GTG   ACAGTCTTGGC
                                |||   ||||||||||
                                CAC   TGTTAGAGCCG
                                  CG__
GAM1038  TADA3L    3'  GCCGGGATTACAGGCGTGA   55994     GT    AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  CGGAC  TTAGGGCCG
                                   __    A_
GAM1038  TBDN100   3'  GCTAACAAAGCAGGTGTGTGG  46955      TG   ACAGTC
                                TCATG  CCTG     TTGGC
                                |||||  ||||     |||||
                                GGTGT  GGAC     AATCG
                                   GT   GAAAC_
GAM1038  TBDN100   3'  GTTGGGGCTTTAGCATCTGA  46958     T   C  C    TG
                                TCA GTGC TGA AGTCT  GC
                                ||| |||| ||| |||||  ||
                                AGT TACG ATT TCGGG  TG
                                  C   _  _    GT
GAM1038  TBL1Y     5'  GCTAAGGCTGGTCCCCACAGA  56134    A   CCTGA
                                TC TGTG    CAGTCTTGGC
                                || ||||    ||||||||||
                                AG ACAC    GTCGGAATCG
                                 _   CCCTG
GAM1038  TCL6      3'  GCTGAGACTACAGGTGTGA   40107     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
```

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                                AGTG TGGAC TCAGA CG
                                  __   A_   GT
GAM1038 TCL6    3' GCTGAGACTACAGGTGTGA  40139    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG TGGAC TCAGA CG
                                  __   A_   GT
GAM1038 TCL6    5' GCTGGGATTACAGGCGTGA  40140    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG CG
                                  __   A_   GT
GAM1038 TCL6    5' GCTGGGATTACAGGCGTGA  40161    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG CG
                                  __   A_   GT
GAM1038 TCL6    3' GCTGGGATTACAGGCGTGA  27000    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG CG
                                  __   A_   GT
GAM1038 TCL6    3' GCTGGGATTACAGGCGTGA  24984    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG CGGAC TTAGG CG
                                  __   A_   GT
GAM1038 TEX27   3' GCTGAGATTGGCCACGTGG  41664      CCTGA    TG
                                TCATGTG   CAGTCT GC
                                |||||||   |||||| ||
                                GGTGCAC   GTTAGA CG
                                   CG___    GT
GAM1038 THEA    3' GCTGGGATTACAGGCAT    66290      AC   TG
                                GTGCCTG AGTCT GC
                                ||||||| ||||| ||
                                TACGGAC TTAGG CG
                                   A_   GT
GAM1038 THEA    3' GCTGGGATTACAGGTGTGA  66291    GT   AC   TG
                                TCAT GCCTG AGTCT GC
                                |||| ||||| ||||| ||
                                AGTG TGGAC TTAGG CG
                                  __   A_   GT
GAM1038 THEA    3' GCTGGGATTGCAGGCAT    66292      A    TG
                                GTGCCTG CAGTCT GC
                                ||||||| |||||| ||
                                TACGGAC GTTAGG CG
                                   _    GT
GAM1038 TIP120A 3' GTTAGGATTTTATGGAGTATGG 37427     TG _  C
                                TCATG CC TGA AGTCTTGGC
                                ||||| || ||| |||||||||
```

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                                GGTAT  GG ATT TTAGGATTG
                                  GA  T  _
GAM1038  TNK1     3'  GCCCAGAGTTGGGCACTGG   14319    T    TG  AG   T
                                TCA GTGCC  AC  TCT GGC
                                ||| |||||  ||  ||| |||
                                GGT CACGG  TG  AGA CCG
                                  _    GT  __  C
GAM1038  TOLLIP   3'  CCTGTGTCAGGTGTGG     38680     GT      GTCTT
                                TCAT  GCCTGACA    GG
                                ||||  ||||||||    ||
                                GGTG  TGGACTGT    CC
                                  __       GT___
GAM1038  TOLLIP   3'  GCCAGGGTGTTGGAGGTGGTGG 38683     G    __   G
                                TCAT TGCCT  GACA TCTTGGC
                                |||| |||||  |||| |||||||
                                GGTG GTGGA  TTGT GGGACCG
                                  _    GG   _
GAM1038  TOR1B    3'  GCTGGGATTACAGGCAT    27201       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  TP53INP1 5'  CCGGCCTGGGCGCACGA    52724    A    TGA   T  T
                                TC TGTGCC   CAG CT GG
                                || ||||||   ||| || ||
                                AG ACGCGG   GTC GG CC
                                 C     ____   C  _
GAM1038  TPSG1    5'  GCTGGGACTACAGGTGCATG   24973     TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTAC  GGAC  TCAGG  CG
                                  GT   A_    GT
GAM1038  TRAF2    3'  GCCGCGCTTGGGCGCTTGG   40928    T    TG CA  CTT
                                TCA GTGCC  A  GT   GGC
                                ||| |||||  |  ||   |||
                                GGT CGCGG  T  CG   CCG
                                  T    GT CG  ___
GAM1038  TRAF3    3'  GCCAGGGCTCCCACTGCACTGG 59741    T   C_  AC
                                TCA GTGC  TG  AGTCTTGGC
                                ||| ||||  ||  |||||||||
                                GGT CACG  AC  TCGGGACCG
                                  _   TC  CC
GAM1038  TReP-132 5'  GCCAAGGCCCTGGCTGTGG   37294      T   TGACA
                                TCATG GCC    GTCTTGGC
                                ||||| |||    ||||||||
                                GGTGT CGG    CGGAACCG
                                   _  TCC__
GAM1038  TReP-132 5'  GCCAAGGCCCTGGCTGTGG   53141      T   TGACA
                                TCATG GCC    GTCTTGGC
                                ||||| |||    ||||||||
```

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                                GGTGT CGG    CGGAACCG
                                  _  TCC__
GAM1038 TReP-132 5' GCCAAGGCCCTGGCTGTGG   53149      T  TGACA
                                TCATG GCC    GTCTTGGC
                                ||||| |||    ||||||||
                                GGTGT CGG    CGGAACCG
                                  _  TCC__
GAM1038 TRIM16   3' GCTGGGATTACATGCGTGA   21342      CC  AC    TG
                                TCATGTG  TG  AGTCT  GC
                                |||||||  ||  |||||  ||
                                AGTGCGT  AC  TTAGG  CG
                                   __ A_    GT
GAM1038 TRIM38   3' GTTAAGACTGGCTTACAATGA  20989     _  CCTGA
                                TCAT GTG    CAGTCTTGGC
                                |||| |||    ||||||||||
                                AGTA CAT    GTCAGAATTG
                                  A  TCG__
GAM1038 TRIM5    3' GCTGGGATTACAGGCGTGA   52299     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 TRIM5    3' GCTGGGATTACAGGCGTGA   52366     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 TRIM6    3' GCTGGGATTACAGATGTGA   54141      GC  AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTGTA  GAC  TTAGG  CG
                                   __  A_    GT
GAM1038 TRIP-Br2 3' GACATGTTTGGTGCATGG    28582      TG  T   _
                                TCATG  CC GACA GTC
                                |||||  || |||| |||
                                GGTAC  GG TTGT CAG
                                   GT  T    A
GAM1038 TRIP13   5' GCTGAGGCAGCGGCTGTGG   14897      T   T ACA   TG
                                TCATG GCC G   GTCT  GC
                                ||||| ||| |   ||||  ||
                                GGTGT CGG C   CGGA  CG
                                  _  _ GA_    GT
GAM1038 TRPV6    3' GCTGGCAGGGCGTGA      37839       G    A
                                TCATGT CCTG CAGT
                                |||||| |||| ||||
                                AGTGCG GGAC GTCG
                                   _   G
GAM1038 TU12B1-TY 3' GCTGGGACTACTGGTACATG   33391        TGAC    TG
                                CATGTGCC    AGTCT  GC
                                ||||||||    |||||  ||
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                                GTACATGG   TCAGG  CG
                                    TCA_    GT
GAM1038  TU12B1-TY 3'  GCTGGGATTACAGGCAT    33392       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  TU12B1-TY 3'  GCTGGGATTACAGGTGTGA   33393     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  TU12B1-TY 3'  GCTGGGATTCTGGGTGTGA   33394     GT   GAC    TG
                                TCAT  GCCT   AGTCT  GC
                                ||||  ||||   |||||  ||
                                AGTG  TGGG   TTAGG  CG
                                  __    TC_    GT
GAM1038  TUB     3'  GTCAGGATTGCAGGTGCCTGG  12429     T TG   A
                                TCA G  CCTG CAGTCTTGGC
                                ||| |  |||| ||||||||||
                                GGT C  GGAC GTTAGGACTG
                                 C GT   _
GAM1038  TUCAN    3'  GCTAGGACTACAGGTGCATG   30275     TG   AC
                                CATG  CCTG  AGTCTTGGC
                                ||||  ||||  |||||||||
                                GTAC  GGAC  TCAGGATCG
                                  GT   A_
GAM1038  TUCAN    3'  GCTGGGATTACAGGCAT     30278       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  TUSP     3'  GCTGGGATTACAGACGTGA   39637      GC   AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTGCA  GAC  TTAGG  CG
                                   __   A_    GT
GAM1038  UBAP     3'  AGAAGGTCAGGTGTGG      76350      GT      AG
                                TCAT  GCCTGAC  TCT
                                ||||  |||||||  |||
                                GGTG  TGGACTG  AGA
                                  __      GA
GAM1038  UBCE7IP5  3'  GCCAGGCCCCAGGCACAGA   30155    A       ACA   T
                                TC TGTGCCTG   GTCT GGC
                                || ||||||||   |||| |||
                                AG ACACGGAC   CGGA CCG
                                 _       CC_   _
GAM1038  UBE4B    3'  GCTGAGACCTGAAAGGACATGG 20165       G   GA   _   TG
                                TCATGT CCT  CAG TCT  GC
                                ||||||  |||  |||  |||  ||
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                                GGTACA GGA  GTC AGA  CG
                                   _  AA  C  GT
GAM1038  UBN1    3'  GCTAAGTGATCAGGCACGTTGA 33730    _      CAGT
                                TCA TGTGCCTGA   CTTGGC
                                ||| |||||||||   ||||||
                                AGT GCACGGACT   GAATCG
                                  T       AGT_
GAM1038  UNC5D   3'  GTCAGGATTGCACAGTATGT  55144      C_ A
                                ATGTGC  TG CAGTCTTGGC
                                ||||||  || ||||||||||
                                TGTATG  AC GTTAGGACTG
                                   AC  _
GAM1038  USP22   3'  GCTGGGATTATAGGCGTGA  68017    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAT  TTAGG  CG
                                  __    A_   GT
GAM1038  USP24   3'  GCTGTGGCATTGTGTGGGCATG 91153        _  __  T
            TGG                   CATGTGCCTG ACA  GTC TGGC
                                |||||||||| |||  ||| ||||
                                GTGTACGGGT TGT  CGG GTCG
                                     G   TA   T
GAM1038  USP25   5'  GCTGAGGCGGGCCGCGTGG   25442      _  GACA   TG
                                TCATGTG CCT   GTCT  GC
                                ||||||| |||   ||||  ||
                                GGTGCGC GGG   CGGA  CG
                                   C  _____   GT
GAM1038  VDU1    3'  GCTGGGATTACAGGTGTGA   30423    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_   GT
GAM1038  VPS33A  3'  GCTGAGACTGAGGAGGTGA   43340    GTG  GA   TG
                                TCAT   CCT  CAGTCT  GC
                                ||||   |||  ||||||  ||
                                AGTG   GGA  GTCAGA  CG
                                  GA_  __    GT
GAM1038  VPS39   3'  GCTAGTTGATTGTCAGGTATGT 62846          __
                                ATGTGCCTGACAGTC  TTGGC
                                ||||||||||||||  |||||
                                TGTATGGACTGTTAG  GATCG
                                      TT
GAM1038  WAC     3'  GCTGGACAGGCATGTG     33554        A_
                                CATGTGCCTG  CAGT
                                ||||||||||  ||||
                                GTGTACGGAC  GTCG
                                     AG
GAM1038  WAC     3'  GCTGGACAGGCATGTG     55188        A_
                                CATGTGCCTG  CAGT
                                ||||||||||  ||||
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                                GTGTACGGAC  GTCG
                                      AG
GAM1038  WAC      3'  GCTGGACAGGCATGTG      55194          A_
                                CATGTGCCTG  CAGT
                                ||||||||||  ||||
                                GTGTACGGAC  GTCG
                                      AG
GAM1038  WBSCR16  3'  GCCAAGGCCATGCGTGTG    94511    TG   C  ACA
                                CA  TGC TG   GTCTTGGC
                                ||  ||| ||   ||||||||
                                GT  GCG AC   CGGAACCG
                                 GT   T  ___
GAM1038  WBSCR20A 5'  GCCAAGGGTGCTAGTGTATGA 49652       TG C  A  G
                                TCATG  C TG CA TCTTGGC
                                |||||  | || || |||||||
                                AGTAT  G AT GT GGAACCG
                                   GT _  C  G
GAM1038  YKT6     3'  GCTAGGGCTGGGGTGGGTGG  21603      G    GA
                                TCAT TGCCT  CAGTCTTGGC
                                ||||  |||||  ||||||||||
                                GGTG GTGGG  GTCGGGATCG
                                  G    __
GAM1038  YME1L1   3'  GCCAGGTGTGGGGTGCATG   57779      TG   G   GT
                                CATG  CCT ACA  CTTGGC
                                ||||  |||  |||  ||||||
                                GTAC  GGG TGT  GGACCG
                                  GT   G  __
GAM1038  YME1L1   3'  GCCAGGTGTGGGGTGCATG   26529      TG   G   GT
                                CATG  CCT ACA  CTTGGC
                                ||||  |||  |||  ||||||
                                GTAC  GGG TGT  GGACCG
                                  GT   G  __
GAM1038  ZAK      3'  GCTGAGGCTGCAATATGG    33603       GCC  A     TG
                                TCATGT   TG CAGTCT  GC
                                ||||||   || ||||||  ||
                                GGTATA   AC GTCGGA  CG
                                   ___  _     GT
GAM1038  ZFP100   3'  GTCAAACCTGTGGTGTGTGG   70057      TG  TG    TC
                                TCATG  CC  ACAG  TTGGC
                                |||||  ||  ||||  |||||
                                GGTGT  GG  TGTC  AACTG
                                   GT  __   CA
GAM1038  ZFP100   3'  GTCGGGGAGATGGGCATGT   70058        GACAG
                                ATGTGCCT    TCTTGGC
                                ||||||||    |||||||
                                TGTACGGG    GGGGCTG
                                    TAGA_
GAM1038  ZNF17    3'  GCTGGGATTACAGGCAT     82392        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
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                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  ZNF185   3'  GCTGGGGCCCCAGGTACTTGG  23114    T     ACA    TG
                                TCA GTGCCTG   GTCT  GC
                                ||| |||||||   ||||  ||
                                GGT CATGGAC   CGGG  CG
                                  T     CC_   GT
GAM1038  ZNF263   3'  GCCAAGGTGCGATTTGGGCACC 19227    T    TG CA_  __
            TGA                   CA GTGCC  A   GT  CTTGGC
                                || |||||  |   ||  ||||||
                                GT CACGG  T   CG  GAACCG
                                 C    GT TAG  TG
GAM1038  ZNF302   3'  GCTAGTGGGCATGTGA     37926          AC
                                TCATGTGCCTG  AGT
                                ||||||||||  |||
                                AGTGTACGGGT  TCG
                                      GA
GAM1038  ZNF302   3'  GCTAGTGGGCATGTGA     37417          AC
                                TCATGTGCCTG  AGT
                                ||||||||||  |||
                                AGTGTACGGGT  TCG
                                      GA
GAM1038  ZNF31    5'  GTCGGGACTGGAATTGCATA  64987      CTGA_
                                TGTGC    CAGTCTTGGC
                                |||||    ||||||||||
                                ATACG    GTCAGGGCTG
                                   TTAAG
GAM1038  ZNF323   3'  GCCAGGGTTAAACATATG    48080      CC    AGT
                                CATGTG  TGAC   CTTGGC
                                ||||||  ||||   ||||||
                                GTATAC  ATTG   GGACCG
                                   AA   ___
GAM1038  ZNF338   3'  GCTGGGACCACAGGTGTACGA 42013    A  TG    ACA    TG
                                TC TG  CCTG   GTCT  GC
                                || ||  ||||   ||||  ||
                                AG AT  GGAC   CAGG  CG
                                 C  GT   AC_   GT
GAM1038  ZNF338   3'  GCTGGGATTACAGGTGTGA   42014     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  ZNF339   3'  GCTGGGACTATAGGTGTGTG  41122     TG    AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGT  GGAT  TCAGG  CG
                                  GT   A_    GT
GAM1038  ZNF387   3'  GCTGTACATTTGGTGTATGG  27997     TG  ___  _
                                TCATG  CC   TG ACAGT
                                |||||  ||   || |||||
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                                GGTAT  GG   AC TGTCG
                                   GT  TTT  A
GAM1038  ZNF84    5'  GCCGACGGTTTGGGCGCGTG   12816        TG CA_   TT
                                CATGTGCC  A   GTC  GGC
                                ||||||||  |   |||  |||
                                GTGCGCGG  T   CAG  CCG
                                    GT TGG   __
GAM1038  ZTL1     3'  GCTAGGATTACAGGCAT     43917        AC
                                GTGCCTG  AGTCTTGGC
                                |||||||  |||||||||
                                TACGGAC  TTAGGATCG
                                   A_
GAM1038  LOC112687 3'  GCTGGGATTACAGGCATGTG   72863         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTACGGAC  TTAGG  CG
                                     A_    GT
GAM1038  LOC112817 3'  GCTGGGATTACAGCTGTGA    56514      T  C  AC    TG
                                TCATG GC TG  AGTCT  GC
                                |||||  ||  ||  |||||  ||
                                AGTGT CG AC  TTAGG  CG
                                  _  _  A_    GT
GAM1038  LOC112885 3'  CCGGGACGCTGCAGTGA     56522      G   CTGACA
                                TCAT TGC     GTCTTGG
                                ||||  |||     |||||||
                                AGTG ACG     CAGGGCC
                                  _   TCG___
GAM1038  LOC113026 3'  GCTGGGACTACAGGCACA    55904        AC    TG
                                TGTGCCTG  AGTCT  GC
                                ||||||||  |||||  ||
                                ACACGGAC  TCAGG  CG
                                     A_    GT
GAM1038  LOC113026 3'  GCTGGGATTACAGGTGTGA    55905      GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC113523 5'  GCTGGGATTACAGATGTGA    73047      GC  AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTGTA  GAC  TTAGG  CG
                                   __   A_    GT
GAM1038  LOC114984 5'  GCTGGGGCCCTTGGCGCGGA   73169    A     TGACA   TG
                                TC TGTGCC    GTCT  GC
                                ||  ||||||    ||||  ||
                                AG GCGCGG    CGGG  CG
                                 _     TTCC_   GT
GAM1038  LOC115219 3'  GCTGGGATTACAGGCAT     73311        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
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                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC115273 3'  TCGAGGCTTTCTACAGA     73360    A   CCT  C
                                TC TGTG   GA AGTCTTGG
                                || ||||   || ||||||||
                                AG ACAT   CT TCGGAGCT
                                 _   ___  T
GAM1038  LOC115330 3'  GCCAAGGCTGTGGTCCCCGTGG 56609      T__   TG
                                TCATG   GCC  ACAGTCTTGGC
                                |||||   |||  ||||||||||
                                GGTGC   TGG  TGTCGGAACCG
                                   CCC  __
GAM1038  LOC115648 3'  GCTGGGATTACAGACGTGA   59301      GC   AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTGCA  GAC  TTAGG  CG
                                   __   A_    GT
GAM1038  LOC116113 3'  GCCAAGGACTGGGCGTAT    92217       TGA    _
                                ATGTGCC   CAGTC TTGGC
                                |||||||   ||||| |||||
                                TATGCGG   GTCAG AACCG
                                   ___    G
GAM1038  LOC116411 5'  CCGGGATTGCAGACG      73856    C   A
                                TG CTG CAGTCTTGG
                                || ||| |||||||||
                                GC GAC GTTAGGGCC
                                 A  _
GAM1038  LOC118709 5'  GCCGAGGCTGTGCTCCAAGA   73926    A  T_  CTG
                                TC TG  GC   ACAGTCTTGGC
                                || ||  ||   ||||||||||
                                AG AC  CG   TGTCGGAGCCG
                                 A  CT  ___
GAM1038  LOC118738 3'  GTTGGCATTCAGGTCACATGA  75494       _    CA   TTGGC
                                TCATGTG CCTGA  GTC
                                ||||||| |||||  |||
                                AGTACAC GGACT  CGG
                                   T    TA   TTG
GAM1038  LOC118851 3'  GCCGGGACAAGAAGTGCATTG  75503   T   _  GACA
                                A GTGC CT    GTCTTGGC
                                | |||| ||    ||||||||
                                G TACG GA    CAGGGCCG
                                 T   T  AGAA
GAM1038  LOC118851 5'  GTTGAGATTGTGTCAGGCCTGT 75504      T      __   TG
            GG                   TCATG GCCTGACA  GTCT  GC
                                |||||  ||||||||  ||||  ||
                                GGTGT CGGACTGT  TAGA  TG
                                   C       GT   GT
GAM1038  LOC118978 5'  GCTGGGGCTGCAGCCATGG   75984      T  C  A     TG
                                TCATG GC TG CAGTCT  GC
                                ||||| || || ||||||  ||
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                                GGTAC CG AC GTCGGG  CG
                                  _ _ _     GT
GAM1038  LOC118987 3'  GTCAACTGATGGGTATGCTGG  73958     _      A    CT
                                TCA TGTGCCTG CAGT  TGGC
                                ||| |||||||| ||||  ||||
                                GGT GTATGGGT GTCA  ACTG
                                  C       A   __
GAM1038  LOC120114 3'  GCTGGGATTACAGGCAT     75534        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC120224 3'  GCCGAGATGCGGAGGGCGCAGA 57100     A      GACA_
                                TC TGTGCCT    GTCTTGGC
                                || |||||||    ||||||||
                                AG ACGCGGG    TAGAGCCG
                                 _      AGGCG
GAM1038  LOC120224 5'  GCTGGGATTACAGGCGTGA   57102     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC120534 3'  GTCAAGATTGTTCTGGG     74020     __
                                CCT  GACAGTCTTGGC
                                |||  ||||||||||||
                                GGG  TTGTTAGAACTG
                                  TC
GAM1038  LOC120892 3'  GTCCTTTGTTGGTATGTGA   74036         T    TCTT
                                TCATGTGCC GACAG   GGC
                                ||||||||| |||||   |||
                                AGTGTATGG TTGTT   CTG
                                     _    TC__
GAM1038  LOC122553 3'  GCCATAGCTTAGGTGTAT    74133     TG   AC   CT
                                ATG  CCTG  AGT  TGGC
                                |||  ||||  |||  ||||
                                TAT  GGAT  TCG  ACCG
                                  GT   __   AT
GAM1038  LOC122614 3'  CGAGCTGAGGCAGTGA      75579      G    GA   T  TG
                                TCAT TGCCT  CAG CT  G
                                |||| |||||  ||| ||  |
                                AGTG ACGGA  GTC GA  C
                                  _    __   _ GT
GAM1038  LOC122726 5'  GCTGAGGCGCACTGA       75581     _      GA
                                TCA TGTGCCT  CAGT
                                ||| |||||||  ||||
                                AGT ACGCGGA  GTCG
                                  C      __
GAM1038  LOC122786 3'  GCCAAAGATACGTATGTGA   74157         CTGACA    _
                                TCATGTGC     GTCTT GGC
                                ||||||||     ||||| |||
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                                AGTGTATG     TAGAA CCG
                                    CA____     A
GAM1038  LOC122970 3'  GTCAAGATTGGTGCAGTGA   74186     G   CTGA
                                TCAT TGC    CAGTCTTGGC
                                |||| |||    ||||||||||
                                AGTG ACG    GTTAGAACTG
                                  _   TG__
GAM1038  LOC122970 3'  TCAAGGGGGGCATAT       74187        GACAG
                                ATGTGCCT    TCTTGG
                                ||||||||    ||||||
                                TATACGGG    GGAACT
                                    G____
GAM1038  LOC123096 3'  GCCAGGGCTTCATCCCTGTGA  74203     GTGCC   C
                                TCAT    TGA AGTCTTGGC
                                ||||    ||| |||||||||
                                AGTG    ACT TCGGGACCG
                                  TCCCT   _
GAM1038  LOC123591 5'  GAGGCCGGCACGTGG       75612         TGACA
                                TCATGTGCC    GTCTT
                                |||||||||    |||||
                                GGTGCACGG    CGGAG
                                    C____
GAM1038  LOC123643 5'  GCTGAGGCTGGGGCTCATGG   76019      T    GA     TG
                                TCATG GCCT  CAGTCT  GC
                                ||||| ||||  ||||||  ||
                                GGTAC CGGG  GTCGGA  CG
                                   T    __     GT
GAM1038  LOC123879 5'  GCTGATGGCATGTTGAGGTACA 75634          _   _   _ TG
           TGG                    CATGTGCCT GACA GTC T  GC
                                |||||||||| |||| ||| |  ||
                                GTACATGGA TTGT CGG A  CG
                                    G    A   T GT
GAM1038  LOC124216 3'  GCTGGGATTACAGATGTGA   74264      GC   AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTGTA  GAC  TTAGG  CG
                                   __   A_    GT
GAM1038  LOC124222 3'  GCTGGCCACAGGCACA      74273        ACA   TT
                                TGTGCCTG   GTC  GGC
                                ||||||||   |||  |||
                                ACACGGAC   CGG  TCG
                                    AC_   __
GAM1038  LOC124512 5'  GCCAGTTCTGCGCGTGTGA   74300     TG   CT A   TC
                                TCA  TGC  G CAG  TTGGC
                                |||  |||  | |||  |||||
                                AGT  GCG  C GTC  GACCG
                                  GT   __ _   TT
GAM1038  LOC124538 5'  TTCATTTTCTTCAGGTGTATGG 75649      TG    C  TCT_   C
                                TCATG  CCTGA AG    TGG
                                |||||  ||||| ||    |||
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                                GGTAT  GGACT TC    ACT
                                   GT    _ TTTT   TG
GAM1038  LOC124599 3'  GCTGGAATAACTCGGGCACAGA 75653    A       CA_  C TG
                                TC TGTGCCTGA   GT T  GC
                                || |||||||||   || |  ||
                                AG ACACGGGCT   TA G  CG
                                 _       CAA  A GT
GAM1038  LOC124739 5'  GCTGGATCGTGTACATGA    74329        C  __
                                TCATGTGC TGA  CAGT
                                |||||||| |||  ||||
                                AGTACATG GCT  GTCG
                                     T   AG
GAM1038  LOC124817 5'  GCTAAGGGGGTCGGTATGTGG  74344        T   AG
                                TCATGTGCC GAC  TCTTGGC
                                ||||||||| |||  |||||||
                                GGTGTATGG CTG  GGAATCG
                                     _   GG
GAM1038  LOC125194 5'  GCTGGGATTACAGGTGTGA    74397     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC125268 3'  GTTAGGAGACAGGTACAGA    76078    A      ACAG
                                TC TGTGCCTG    TCTTGGC
                                || ||||||||    |||||||
                                AG ACATGGAC    AGGATTG
                                 _       AG__
GAM1038  LOC125943 3'  CTAGGGCTGGGGACAGA     74420    A   G  TGA
                                TC TGT CC   CAGTCTTGG
                                || ||| ||   |||||||||
                                AG ACA GG   GTCGGGATC
                                 _  G  ___
GAM1038  LOC126257 5'  GCTGGGACGGCGGCATGA    74467       _  TGACA   TG
                                TCATGT GCC    GTCT  GC
                                |||||| |||    ||||  ||
                                AGTACG CGG    CAGG  CG
                                   G  _____   GT
GAM1038  LOC126364 3'  GCTGGCTCAGGGTGCGTGG    75693      TG   GAC   TT
                                TCATG  CCT   AGTC  GGC
                                |||||  |||   ||||  |||
                                GGTGC  GGG   TCGG  TCG
                                   GT   AC_   __
GAM1038  LOC126364 3'  GCTGGGATTACAGGCGTGG    75694     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                GGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC126374 3'  GCCGGGGTGGGTGTGGGTGTGG 74502     GT    _  AG_
                                TCAT  GCCTG AC   TCTTGGC
                                ||||  ||||| ||   |||||||
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                                GGTG  TGGGT TG   GGGGCCG
                                  __    G  GGT
GAM1038  LOC126526 3'  TGAGACTGTTAGCCGC     74538     C        TG
                                GTG CTGACAGTCT  G
                                ||| ||||||||||  |
                                CGC GATTGTCAGA  T
                                  C        GT
GAM1038  LOC126767 5'  GCTGGAAGCAGCATGTGG    75433         __  GA
                                TCATGTGC  CT  CAGT
                                ||||||||  ||  ||||
                                GGTGTACG  GA  GTCG
                                    AC  AG
GAM1038  LOC126917 3'  GCCGAGGTTGGTCATGA     74584      T   TGAC GT
                                TCATG GCC    A  CTTGGC
                                ||||| |||    |  ||||||
                                AGTAC TGG    T  GAGCCG
                                  _  ____ TG
GAM1038  LOC126964 3'  GTTAAGGAGGGGTGTGTGA   74621      TG   GACAG
                                TCATG  CCT    TCTTGGC
                                |||||  |||    |||||||
                                AGTGT  GGG    GGAATTG
                                   GT   GA___
GAM1038  LOC127702 3'  GCCAGGACTGCAGCCCCCATGG 75460      TGC_   A
                                TCATG    CTG CAGTCTTGGC
                                |||||    ||| ||||||||||
                                GGTAC    GAC GTCAGGACCG
                                   CCCC  _
GAM1038  LOC127702 3'  GTCAGGGCTGCACCCCATA   75461     CC_  A
                                TGTG   TG CAGTCTTGGC
                                ||||   || ||||||||||
                                ATAC   AC GTCGGGACTG
                                  CCC  _
GAM1038  LOC128077 3'  GCTGGGATTACAGGCGTGA   74715     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC128308 5'  CCAGGGCCTGTACTGA     74732     T   CTGACA
                                TCA GTGC     GTCTTGG
                                ||| ||||     |||||||
                                AGT CATG     CGGGACC
                                  _   TC_____
GAM1038  LOC128954 5'  GCCAAGACATCTGATGTGA   75799      GCCT  CA
                                TCATGT   GA  GTCTTGGC
                                ||||||   ||  ||||||||
                                AGTGTA   CT  CAGAACCG
                                   GT__  A_
GAM1038  LOC128954 5'  GCTGAGACCAGGGAGGACATGA 75800      G   GACA_   TG
                                TCATGT CCT    GTCT  GC
                                |||||| |||    ||||  ||
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                                AGTACA GGA    CAGA  CG
                                   _  GGGAC   GT
GAM1038  LOC128954 5' GTCAGGACTTGAGGTGGATGA 75803     G    GAC
                                TCAT TGCCT  AGTCTTGGC
                                |||| |||||  |||||||||
                                AGTA GTGGA  TCAGGACTG
                                  G   GT_
GAM1038  LOC129080 3' GCTGGGGCTCGGCACATG   55980       TGAC    TG
                                CATGTGCC   AGTCT  GC
                                ||||||||   |||||  ||
                                GTACACGG   TCGGG  CG
                                     C___    GT
GAM1038  LOC129642 5' CCGAGGCCCGGCCATGG    57126      T  TGACA
                                TCATG GCC    GTCTTGG
                                ||||| |||    |||||||
                                GGTAC CGG    CGGAGCC
                                   _  CC___
GAM1038  LOC129880 3' CCGGGATTGCAGACG      74902    C  A
                                TG CTG CAGTCTTGG
                                || ||| |||||||||
                                GC GAC GTTAGGGCC
                                 A  _
GAM1038  LOC130162 3' GCTGGGACTCTTGGCATGT   74912       TGAC    TG
                                ATGTGCC   AGTCT  GC
                                |||||||   |||||  ||
                                TGTACGG   TCAGG  CG
                                    TTC_   GT
GAM1038  LOC130589 3' GTTGAGGCCGGGCACGGTGG  57136     _     ACA   TG
                                TCAT GTGCCTG  GTCT  GC
                                |||| |||||||  ||||  ||
                                GGTG CACGGGC  CGGA  TG
                                  G     ____   GT
GAM1038  LOC130639 5' GCTGGGATTAAAGACGTGA   74975      GC  GAC    TG
                                TCATGT  CT  AGTCT  GC
                                ||||||  ||  |||||  ||
                                AGTGCA  GA  TTAGG  CG
                                   __ AA_    GT
GAM1038  LOC130813 3' GCTGGGATTACAGGTGTGA   75773     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC131308 3' GCTGGGACTACAGGCATGT   75005        AC    TG
                                ATGTGCCTG  AGTCT  GC
                                |||||||||  |||||  ||
                                TGTACGGAC  TCAGG  CG
                                     A_    GT
GAM1038  LOC131870 3' GCTGGGCACTCAGGTGTGTG  75021     TG    CA  _  TG
                                CATG  CCTGA  GT CT  GC
                                ||||  |||||  || ||  ||
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                                GTGT  GGACT  CA GG  CG
                                  GT    __  C  GT
GAM1038  LOC131870 3'  TCAAGATGGTGTGATGA     75024      _ TG  TGACA
                                TCAT G  CC    GTCTTGG
                                |||| |  ||    |||||||
                                AGTA T  GG    TAGAACT
                                  G GT  _____
GAM1038  LOC132625 3'  GCTGGGACTACAGGTGTGTG   75911      TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGT  GGAC  TCAGG  CG
                                  GT   A_    GT
GAM1038  LOC132625 3'  GCTGGGATTACAGGTGTGA   75912      GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC133539 3'  GTTAAGGCTGAGAAGCCGTGG  75097       T  CTGA
                                TCATG GC    CAGTCTTGGC
                                |||||  ||   ||||||||||
                                GGTGC CG    GTCGGAATTG
                                   _ AAGA
GAM1038  LOC133686 3'  GTTGAGACTGCTTGCCCGTGG  75125       T  CTGA     TG
                                TCATG GC    CAGTCT  GC
                                |||||  ||   ||||||  ||
                                GGTGC CG    GTCAGA  TG
                                   C  TTC_     GT
GAM1038  LOC133957 3'  GCCGCTGTTGGGGATATGG   59176       G  TG    CTT
                                TCATGT CC  ACAGT   GGC
                                ||||||  ||  |||||   |||
                                GGTATA GG  TGTCG   CCG
                                   G  GT    ___
GAM1038  LOC134121 5'  GCCAAGGCGGGGGCGCTGG   75152     T     GACA
                                TCA GTGCCT    GTCTTGGC
                                |||  ||||||    ||||||||
                                GGT CGCGGG    CGGAACCG
                                  _     GG__
GAM1038  LOC134359 5'  GCTGAGGCTGCACTTGCTGA   75183     T   CC  A     TG
                                TCA GTG  TG CAGTCT  GC
                                |||  |||  ||  ||||||  ||
                                AGT CGT  AC GTCGGA  CG
                                  _  TC  _     GT
GAM1038  LOC135154 3'  GCTGGGATTGCAGGTGTGA   75218     GT    A     TG
                                TCAT  GCCTG CAGTCT  GC
                                ||||  ||||| ||||||  ||
                                AGTG  TGGAC GTTAGG  CG
                                  __    _     GT
GAM1038  LOC135293 3'  GCTGGGATTACAGGCAT     76185       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
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                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC135293 3'  GCTGGGATTACAGGTGTGTGG  76186      TG   AC    TG
                                TCATG  CCTG  AGTCT  GC
                                |||||  ||||  |||||  ||
                                GGTGT  GGAC  TTAGG  CG
                                   GT   A_    GT
GAM1038  LOC135293 3'  GTTGGGATTTCAGGTATGAGA  76189    A       C    TG
                                TC TGTGCCTGA AGTCT  GC
                                || |||||||| |||||  ||
                                AG GTATGGACT TTAGG  TG
                                 A       _    GT
GAM1038  LOC135818 3'  GCTGGGATTACAGGCGTGA   75239     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC137362 3'  GCCAAGATTGCACCATTGA   75265     T   CC  A
                                TCA GTG  TG CAGTCTTGGC
                                ||| |||  || ||||||||||
                                AGT TAC  AC GTTAGAACCG
                                  _  C_  _
GAM1038  LOC138241 5'  GTCGAGGCTGCGCCGCGTGG   75312        CC  A
                                TCATGTG  TG CAGTCTTGGC
                                |||||||  || ||||||||||
                                GGTGCGC  GC GTCGGAGCTG
                                    C_  _
GAM1038  LOC138399 5'  GCTAGGGCTGCATGCTTTATGG 75328      T_  C  A
                                TCATG  GC TG CAGTCTTGGC
                                |||||  || || ||||||||||
                                GGTAT  CG AC GTCGGGATCG
                                   TT  T  _
GAM1038  LOC139231 3'  GCCAAGGTCTGTGATATGG   75375       GCCTG   _
                                TCATGT    ACAG TCTTGGC
                                ||||||    |||| |||||||
                                GGTATA    TGTC GGAACCG
                                   G____   T
GAM1038  LOC139231 3'  GTTAGGGCTGTGCTGATG    75377     GT  CTG
                                CAT  GC   ACAGTCTTGGC
                                |||  ||   ||||||||||
                                GTA  CG   TGTCGGGATTG
                                  GT  ___
GAM1038  LOC142927 5'  GCTGGGATTACAGGTGTGA   76427     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC142941 5'  GTTGAGACCCCCAGGTGTCTGA 82886     T TG   ACA   TG
                                TCA G  CCTG   GTCT  GC
                                ||| |  ||||   ||||  ||
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                                AGT T  GGAC   CAGA  TG
                                  C GT    CCC    GT
GAM1038  LOC143153 3'  GCTGGGACCTGTTGGACGTGA  76466      G  T    _  TG
                                TCATGT CC GACAG TCT  GC
                                |||||| || ||||| |||  ||
                                AGTGCA GG TTGTC AGG  CG
                                   _ _    C   GT
GAM1038  LOC143153 3'  GCTGGGATTAATGGCGTGA   76467     GT   TGAC    TG
                                TCAT  GCC    AGTCT  GC
                                ||||  |||    |||||  ||
                                AGTG  CGG    TTAGG  CG
                                  __  TAA_    GT
GAM1038  LOC143154 3'  GCTGGGACCTGTTGGACGTGA  76482      G  T    _  TG
                                TCATGT CC GACAG TCT  GC
                                |||||| || ||||| |||  ||
                                AGTGCA GG TTGTC AGG  CG
                                   _ _    C   GT
GAM1038  LOC143154 3'  GCTGGGATTAATGGCGTGA   76483     GT   TGAC    TG
                                TCAT  GCC    AGTCT  GC
                                ||||  |||    |||||  ||
                                AGTG  CGG    TTAGG  CG
                                  __  TAA_    GT
GAM1038  LOC143458 3'  GTCAAGACAACAGTGATGA   76573     GTGC   ACA
                                TCAT    CTG   GTCTTGGC
                                ||||    |||   ||||||||
                                AGTA    GAC   CAGAACTG
                                  GT__   AA_
GAM1038  LOC143914 5'  GTCAAGACTGTCAAAGTGGTTG 76614   T  ____
                                G GCC    TGACAGTCTTGGC
                                | |||    ||||||||||||
                                G TGG    ACTGTCAGAACTG
                                 T   TGAA
GAM1038  LOC143916 3'  GCTGGGATTACAGGCGTGA   76643     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC144305 3'  GCTGGGGTGTGGGTGATGG   83034     G    G  G  TG
                                TCAT TGCCT ACA TCT  GC
                                |||| ||||| ||| |||  ||
                                GGTA GTGGG TGT GGG  CG
                                  _    _  _  GT
GAM1038  LOC144305 3'  GTTGGGATTATGGGTGTGA   83036     GT   GAC    TG
                                TCAT  GCCT   AGTCT  GC
                                ||||  ||||   |||||  ||
                                AGTG  TGGG   TTAGG  TG
                                  __   TA_    GT
GAM1038  LOC144317 5'  GCTGGGATGACAGGTGCCTGA  76794    T TG   ACA   TG
                                TCA G  CCTG   GTCT  GC
                                ||| |  ||||   ||||  ||
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                                AGT C  GGAC   TAGG  CG
                                  C GT    AG_   GT
GAM1038  LOC144317 5'  GCTGGGATTACAGGTGTGA   76795     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC144347 3'  ACTGTTAGGTGGTGG      76809     G
                                TCAT TGCCTGACAGT
                                |||| ||||||||||
                                GGTG GTGGATTGTCA
                                  _
GAM1038  LOC144486 3'  GCTGGGAGGCCAAGGCAGGTGG 83085     G    GACAG   TG
                                TCAT TGCCT    TCT  GC
                                |||| |||||    |||  ||
                                GGTG ACGGA    AGG  CG
                                  G    ACCGG   GT
GAM1038  LOC144558 3'  GTTGAGGCTGGGTAGAGTGA   83149     G_   TGA     TG
                                TCAT  TGCC   CAGTCT  GC
                                ||||  ||||   ||||||  ||
                                AGTG  ATGG   GTCGGA  TG
                                  AG    ___     GT
GAM1038  LOC144667 3'  CCAGGGCAGGGATGTGG     83165       G   GACA
                                TCATGT CCT    GTCTTGG
                                ||||||  |||   |||||||
                                GGTGTA GGA    CGGGACC
                                   G  ____
GAM1038  LOC144742 5'  GCTGGGACTACAGGCACATG   76945         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTACACGGAC  TCAGG  CG
                                      A_    GT
GAM1038  LOC144742 3'  GTTGGAAATGTCAGGTATTTGA 76947     T        GTC TG
                                TCA GTGCCTGACA   T  GC
                                |||  ||||||||||   |  ||
                                AGT TATGGACTGT   G  TG
                                  T         AAA GT
GAM1038  LOC144817 3'  GAGGCCGGGCACGGGA      76968    A       ACA
                                TC TGTGCCTG   GTCTT
                                ||  ||||||||   |||||
                                AG GCACGGGC   CGGAG
                                 G       ___
GAM1038  LOC144871 3'  GTTGGGATTACAGGCGTGA    83202     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  TG
                                  __    A_    GT
GAM1038  LOC145009 3'  GCTGGGATTACAGGCAT     60350        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
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                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC145082 5'  GCTGGGATTACAGGCAT     83243       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC145134 5'  TCGAGATGAGGCTGTGG     83257      T   GACA
                                TCATG GCCT   GTCTTGG
                                ||||| ||||   |||||||
                                GGTGT CGGA   TAGAGCT
                                  _   G___
GAM1038  LOC145216 3'  GTTAGGATTTCAACACATGA   83269       CC   C
                                TCATGTG  TGA AGTCTTGGC
                                |||||||  ||| |||||||||
                                AGTACAC  ACT TTAGGATTG
                                   A_  _
GAM1038  LOC145231 3'  GCTGGGGCCGTTGCTCATGG   83291      T  CT   A   TG
                                TCATG GC  GAC GTCT  GC
                                ||||| ||  ||| ||||  ||
                                GGTAC CG  TTG CGGG  CG
                                  T  __   C   GT
GAM1038  LOC145376 3'  GCCGAGATGCAAAAGCATGTGG 77200        CTGACA
                                TCATGTGC     GTCTTGGC
                                ||||||||     ||||||||
                                GGTGTACG     TAGAGCCG
                                     AAAACG
GAM1038  LOC145387 3'  GCCAAGGCCAGGTGCAGTGG   83356    _ TG   ACA
                                TCA TG  CCTG   GTCTTGGC
                                ||| ||  ||||   ||||||||
                                GGT AC  GGAC   CGGAACCG
                                  G  GT   ___
GAM1038  LOC145453 5'  GCTGGGATTACAGGCAT     77143       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC145581 5'  GCCGGGATTGTACCTGCA    77280    CTG_
                                TGC   ACAGTCTTGGC
                                |||   ||||||||||
                                ACG   TGTTAGGGCCG
                                  TCCA
GAM1038  LOC145622 3'  GCTGGGATTACAGGCGTGA   77305     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC145725 3'  GCTAGGACTACAGGCACATG   77408         AC
                                CATGTGCCTG  AGTCTTGGC
                                ||||||||||  |||||||||
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                                GTACACGGAC  TCAGGATCG
                                     A_
GAM1038  LOC145732 3'  GCTAGGACTACAGGCACATG   77430         AC
                                CATGTGCCTG  AGTCTTGGC
                                ||||||||||  |||||||||
                                GTACACGGAC  TCAGGATCG
                                     A_
GAM1038  LOC145758 5'  ACTGTTAGGGACATGG      83481       G
                                TCATGT CCTGACAGT
                                ||||||  |||||||||
                                GGTACA GGATTGTCA
                                   G
GAM1038  LOC145801 3'  GCTGAGGTGGATGGTGTGG   77498     GT   TGA  G   TG
                                TCAT  GCC   CA TCT  GC
                                ||||  |||   || |||  ||
                                GGTG  TGG   GT GGA  CG
                                  __   TAG  _   GT
GAM1038  LOC145813 5'  GTTGGGATTATAGGCGTGA   83512     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAT  TTAGG  TG
                                  __    A_    GT
GAM1038  LOC145858 3'  CCAAGTCAGGTAGTGA      77543      G       AGTC    C
                                TCAT TGCCTGAC    TTGG
                                |||| ||||||||    ||||
                                AGTG ATGGACTG    AACC
                                  _       _____    T
GAM1038  LOC145864 3'  GCCGGGAGTCCGGGCATGGTGG 77558      _      _ AG
                                TCAT GTGCCTG AC  TCTTGGC
                                |||| |||||||  ||  |||||||
                                GGTG TACGGGC TG  AGGGCCG
                                  G      C  __
GAM1038  LOC145988 5'  GCTGGGATTTGGCTGACGTGG  77609       __   TGAC    TG
                                TCATGT  GCC    AGTCT  GC
                                ||||||  |||    |||||  ||
                                GGTGCA  CGG    TTAGG  CG
                                   GT   T___     GT
GAM1038  LOC145988 5'  GGATGGACTGTTGGGTACTGG  77610     T    TG      TGGC
                                TCA GTGCC  ACAGTCT
                                ||| |||||  |||||||
                                GGT CATGG  TGTCAGG
                                  _    GT      TAGGT
GAM1038  LOC146050 3'  GCTGGGATTACAGGCAT     77643        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC146050 3'  GCTGGGATTACAGGTGTGA   77644     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC146083 5'  GCTGAGGCGCGGTGG      83611     _     GA
                                TCAT GTGCCT  CAGT
                                |||| ||||||  ||||
                                GGTG CGCGGA  GTCG
                                  G     __
GAM1038  LOC146108 5'  GCCGGGATGCAGGGCGCGCGG  77667    A      GACA
                                TC TGTGCCT    GTCTTGGC
                                || |||||||    ||||||||
                                GG GCGCGGG    TAGGGCCG
                                 C      ACG_
GAM1038  LOC146108 3'  GCTGGGATTACAGGCAT     77669        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  LOC146136 5'  GCCAGTGCTGGGTGTAAGA   72944    A  TG  TGA   C
                                TC TG  CC   CAGT TTGGC
                                || ||  ||   |||| |||||
                                AG AT  GG   GTCG GACCG
                                 A  GT  ____   T
GAM1038  LOC146136 5'  GTCAGGACTGGCTAACGCGGA  72946    A   CCTGA
                                TC TGTG    CAGTCTTGGC
                                || ||||    ||||||||||
                                AG GCGC    GTCAGGACTG
                                 _   AATCG
GAM1038  LOC146229 3'  GCTGGGATTACAGGCGTGA   77758     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC146229 3'  GCTGGGATTACAGGCGTGA   77759     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC146229 3'  GCTGGGATTATAGGCGTGA   77760     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAT  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC146229 3'  GCTGGGATTATAGGTGTGA   77761     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAT  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC146268 3'  CGCTGGGGCTCTGTCTTGGTGC 77806     _ __   __    TG
            ACATGG                GTGC CT  GACA  GTCT  GC   G
                                |||| ||  ||||  ||||  ||   |
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                                CACG GG  CTGT  CGGG  CG   C
                                  T  TT    CT    GT
GAM1038  LOC146272 5'  GCTGAAGAACAGGCACAT    77789        ACAG   _
                                ATGTGCCTG    TCTT GGC
                                |||||||||    |||| |||
                                TACACGGAC    AGAA TCG
                                     A___    G
GAM1038  LOC146315 5'  GCCAGGACCCAGGCACA     60888        ACA
                                TGTGCCTG   GTCTTGGC
                                ||||||||   ||||||||
                                ACACGGAC   CAGGACCG
                                     C__
GAM1038  LOC146332 3'  GCTGAGGGCTCAGGCACAGGA 77826    A       CAG   TG
                                TC TGTGCCTGA   TCT  GC
                                || |||||||||   |||  ||
                                AG ACACGGACT   GGA  CG
                                 G       CG_   GT
GAM1038  LOC146332 5'  GCTGGGTGGGGGGCACGTGG   77827        GA  GT  TG
                                TCATGTGCCT  CA  CT  GC
                                ||||||||||  ||  ||  ||
                                GGTGCACGGG  GT  GG  CG
                                      GG  __  GT
GAM1038  LOC146429 3'  GTCAAGGCCTGGGGCATGG    83673       G  TGACA
                                TCATGT CC    GTCTTGGC
                                |||||| ||    ||||||||
                                GGTACG GG    CGGAACTG
                                   G  TC___
GAM1038  LOC146435 5'  GCCGAGGTTGCAGTCCATGA   77897      TG C  A  GT
                                TCATG  C TG CA  CTTGGC
                                |||||  | || ||  ||||||
                                AGTAC  G AC GT  GAGCCG
                                   CT _  _  TG
GAM1038  LOC146438 3'  GCTGGGATTACAGGCGTGA    77892     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC146443 5'  GCTGGGATTACAGGTGTGA    77883     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC146445 3'  GTTGGGGCAGGGCGGGCGCATG 83683          ACA_   TG
           G                     TCATGTGCCTG   GTCT  GC
                                ||||||||||    ||||  ||
                                GGTACGCGGGC   CGGG  TG
                                      GGGA   GT
GAM1038  LOC146603 5'  GTTGGGATTACAGGCGTGA    78019     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG  CGGAC  TTAGG  TG
                                  __    A_    GT
GAM1038  LOC146667 3'  CCGGGGTGAGCATCTGG    83703    T   CTGA  G
                                TCA GTGC   CA TCTTGG
                                ||| ||||   || ||||||
                                GGT TACG   GT GGGGCC
                                  C   A___  _
GAM1038  LOC146713 5'  GCTGAGGGCATGTGG      83729         GA
                                TCATGTGCCT  CAGT
                                ||||||||||  ||||
                                GGTGTACGGG  GTCG
                                     A_
GAM1038  LOC146784 5'  GCTGGGATTACAGGCAT    78121       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC146823 3'  GCCAGGACCCTGGCATATGA  83798        TGACA
                                TCATGTGCC    GTCTTGGC
                                |||||||||    ||||||||
                                AGTATACGG    CAGGACCG
                                     TCC__
GAM1038  LOC146839 3'  GCTGGGATTACAGGCGTGA   83813     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC146850 3'  GCCAGGACCTCCGGCATGT   83822       T  CA
                                ATGTGCC GA  GTCTTGGC
                                ||||||| ||  ||||||||
                                TGTACGG CT  CAGGACCG
                                   C  C_
GAM1038  LOC146894 3'  GCCGGGATTACAGGCAT     59191       AC
                                GTGCCTG  AGTCTTGGC
                                |||||||  |||||||||
                                TACGGAC  TTAGGGCCG
                                   A_
GAM1038  LOC146895 5'  GCTGAGGCTGTCTAAGGTTACA 83825       _  __      TG
           TGG                   CATGTG CCT  GACAGTCT  GC
                                ||||||| |||  ||||||||  ||
                                GTACAT GGA  CTGTCGGA  CG
                                   T  AT      GT
GAM1038  LOC146901 3'  GCTGGGATTACAGGCAT     83843       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC146909 3'  GCTGAGATTACAGGCAT     78178       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
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                                TACGGAC  TTAGA  CG
                                   A_    GT
GAM1038  LOC146909 3'  GCTGGGATTACAGGCGTGA   78179     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC146952 5'  GCTGGGATTACAGGTGTGTG   83871     TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGT  GGAC  TTAGG  CG
                                  GT   A_    GT
GAM1038  LOC147011 3'  GCCAGGGTGGTCAGGGTGCAGA 78226    A  TG  _   AG
                                TC TG  CC TGAC  TCTTGGC
                                || ||  || ||||  |||||||
                                AG AC  GG ACTG  GGGACCG
                                 _ GT  G   GT
GAM1038  LOC147040 3'  GTCGGGACTCTCCTGCACCTGA 78236     T   CT  C
                                TCA GTGC  GA AGTCTTGGC
                                ||| ||||  || |||||||||
                                AGT CACG  CT TCAGGGCTG
                                  C   TC  C
GAM1038  LOC147042 3'  GTTGAGATTGAGCAGCGCTTGG 83914     T   C  A_     TG
                                TCA GTGC TG  CAGTCT  GC
                                ||| |||| ||  ||||||  ||
                                GGT CGCG AC  GTTAGA  TG
                                  T   _ GA     GT
GAM1038  LOC147054 3'  GCTGGGACTACAGGCATGTG   83922         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTACGGAC  TCAGG  CG
                                     A_    GT
GAM1038  LOC147054 3'  GCTGGGATTACAGGCGTGA   83923     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC147071 5'  GCTGGGATTGCAGGTAT     73002        A     TG
                                GTGCCTG CAGTCT  GC
                                ||||||| ||||||  ||
                                TATGGAC GTTAGG  CG
                                   _     GT
GAM1038  LOC147080 5'  GCTGGGATTACAGGCGTGA   83936     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC147093 5'  GCTGGGACTACAGGCGTGG   83945     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                GGTG  CGGAC  TCAGG  CG
                                  __    A_    GT
GAM1038  LOC147123 5'  GCTGGGGCAGGATGGACATGG  78254      G  TGACA   TG
                                TCATGT CC    GTCT  GC
                                |||||| ||    ||||  ||
                                GGTACA GG    CGGG  CG
                                   _ TAGGA    GT
GAM1038  LOC147124 3'  GCCGGGGGCTGGGGTGTGG   76303     GT   GA    _
                                TCAT  GCCT  CAGTCTT GGC
                                ||||  ||||  ||||||| |||
                                GGTG  TGGG  GTCGGGG CCG
                                  __   __      G
GAM1038  LOC147160 5'  GCTGGGATTACAGGTGTGA   83967     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC147165 3'  GTCAGCCCTGCGGGTGTTGG   83981    T TG   A   TC
                                TCA G  CCTG CAG  TTGGC
                                ||| |  |||| |||  |||||
                                GGT T  GGGC GTC  GACTG
                                  _ GT   _   CC
GAM1038  LOC147166 3'  GCTGGGATTACAGGCGTGA   78289     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC147178 3'  GTCAAGTCCAAGGTACGT    61326       GACAGT
                                ATGTGCCT     CTTGGC
                                ||||||||     ||||||
                                TGCATGGA     GAACTG
                                    ACCT__
GAM1038  LOC147229 3'  GCCCTGGCTGGCGGGCATGTGG 78321          A    TT
                                TCATGTGCCTG CAGTC  GGC
                                |||||||||| |||||  |||
                                GGTGTACGGGC GTCGG  CCG
                                      G    TC
GAM1038  LOC147276 3'  GCTGGGATTACAGGCAT     78337       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC147276 3'  GCTGGGATTACAGGCATGTG   78338        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTACGGAC  TTAGG  CG
                                     A_    GT
GAM1038  LOC147343 5'  GCTAGGACCACAGGCACGTG   84001         ACA
                                CATGTGCCTG   GTCTTGGC
                                ||||||||||   ||||||||
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                                GTGCACGGAC  CAGGATCG
                                     AC_
GAM1038  LOC147429 3'  GCTGGGATTACAGGCGTGA   78363     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC147645 3'  CCAGGGCCTGCTATGA     78421      T  CTGACA
                                TCATG GC     GTCTTGG
                                |||||  ||     |||||||
                                AGTAT CG     CGGGACC
                                   _ TC____
GAM1038  LOC147694 3'  GCTGGGATTACGGGCGTGA   78453     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGGC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC147779 3'  GCTGGGGTTGGTGGTGGGTGG  78481     G   TGA  GT  TG
                                TCAT TGCC   CA  CT  GC
                                |||| ||||   ||  ||  ||
                                GGTG GTGG   GT  GG  CG
                                  G   TG_  TG  GT
GAM1038  LOC147817 3'  GTTGGGATTATAGGCAT     78503       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGG  TG
                                    A_    GT
GAM1038  LOC147841 3'  GCTAGGATTCCAGGCGTGA   78529     GT    AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  CGGAC  TTAGGATCG
                                  __    C_
GAM1038  LOC147858 5'  CCCAGTGGGCATGTGA      78569          ACAGT  T
                                TCATGTGCCTG    CT GG
                                ||||||||||    || ||
                                AGTGTACGGGT    GA CC
                                      _____ C
GAM1038  LOC147976 5'  GCCTCTGTCAAGTGTATGA   78589      TG C     TCTT
                                TCATG  C TGACAG    GGC
                                |||||  | ||||||    |||
                                AGTAT  G ACTGTC    CCG
                                   GT A     T___
GAM1038  LOC147990 3'  GCTGGGACTATAGGTGCGTG   84096     TG    AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGC  GGAT  TCAGG  CG
                                  GT    A_    GT
GAM1038  LOC147990 3'  GCTGGGATTACAGGCGTGA   84097     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC148014 3'  GCCAGGAAATTGGGGTGTGTG  78607     TG   GACAG
                                CATG  CCT    TCTTGGC
                                ||||  |||    |||||||
                                GTGT  GGG    AGGACCG
                                  GT   GTTAA
GAM1038  LOC148089 3'  CCAGGACAGTATCTGA     78629     T    CTGACA
                                TCA GTGC     GTCTTGG
                                |||  ||||     |||||||
                                AGT TATG     CAGGACC
                                  C   A_____
GAM1038  LOC148137 3'  GCTGGGATTGCAGGCGTGA   58436     GT    A     TG
                                TCAT  GCCTG CAGTCT  GC
                                ||||  ||||| ||||||  ||
                                AGTG  CGGAC GTTAGG  CG
                                  __    _     GT
GAM1038  LOC148147 3'  GCTGGGATTACAGGCGTGA   78685     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC148189 5'  GCTGGGATTACAGGCGTGA   78714     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC148195 5'  GCTGGGACTACAGGCGTGG   84132     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                GGTG  CGGAC  TCAGG  CG
                                  __    A_    GT
GAM1038  LOC148195 3'  GCTGGGATTACAGGCATAAGA  84133    A      AC    TG
                                TC TGTGCCTG  AGTCT  GC
                                || ||||||||  |||||  ||
                                AG ATACGGAC  TTAGG  CG
                                 A      A_    GT
GAM1038  LOC148198 3'  CCGAGATCATGCCATGG     70680      T  C   CAG
                                TCATG GC TGA   TCTTGG
                                |||||  || |||   ||||||
                                GGTAC CG ACT   AGAGCC
                                  _  T  ____
GAM1038  LOC148223 3'  GCCAGGGCTGTGCTCCCTGA   78741    TGT_  CTG
                                TCA   GC   ACAGTCTTGGC
                                |||   ||   ||||||||||
                                AGT   CG   TGTCGGGACCG
                                  CCCT  ____
GAM1038  LOC148398 5'  GCTAGGCTCTGGGCACAAGA   78826    A     GAC    T
                                TC TGTGCCT   AGTCT GGC
                                || |||||||   ||||| |||
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                                AG ACACGGG   TCGGA TCG
                                 A      TC_    _
GAM1038  LOC148443 3'  GCTGGGATTACAGGTGTGA   78858     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC148446 5'  GCTGAGATTGAAATTCGGGT   78864       ____     TG
                                GCCTGA   CAGTCT  GC
                                ||||||   ||||||  ||
                                TGGGCT   GTTAGA  CG
                                   TAAA     GT
GAM1038  LOC148529 5'  GTTGAGGCCGGGTGTGA     84171     GT    ACA   TG
                                TCAT  GCCTG   GTCT  GC
                                ||||  |||||   ||||  ||
                                AGTG  TGGGC   CGGA  TG
                                  __    ___    GT
GAM1038  LOC148645 5'  GCCAAGGCTGGAATGCAGTGG  84181     G   CTGA
                                TCAT TGC    CAGTCTTGGC
                                |||| |||    ||||||||||
                                GGTG ACG    GTCGGAACCG
                                  _   TAAG
GAM1038  LOC148709 5'  GCTGGGATTGCAGGTGTGA   78947     GT    A     TG
                                TCAT  GCCTG CAGTCT  GC
                                ||||  ||||| ||||||  ||
                                AGTG  TGGAC GTTAGG  CG
                                  __    _     GT
GAM1038  LOC148887 5'  GCTGGGATTACAGGCGTGA   84243     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC148932 3'  GCCGGGGTGTGTGTGTGTG   79109     TG CTG   G
                                CATG  C   ACA TCTTGGC
                                ||||  |   ||| |||||||
                                GTGT  G   TGT GGGGCCG
                                  GT TG_   _
GAM1038  LOC148936 5'  GTTGAGACTGCGAGTGCACAGA 84301    A    _  GA     TG
                                TC TGTGC CT  CAGTCT  GC
                                || ||||| ||  ||||||  ||
                                AG ACACG GA  GTCAGA  TG
                                 _    T  GC     GT
GAM1038  LOC148938 5'  GTTGAGACTGCGAGTGCACAGA 84282    A    _  GA     TG
                                TC TGTGC CT  CAGTCT  GC
                                || ||||| ||  ||||||  ||
                                AG ACACG GA  GTCAGA  TG
                                 _    T  GC     GT
GAM1038  LOC148946 3'  GCTGGGGCTGCAACAGTGA   84310     G  CC  A     TG
                                TCAT TG  TG CAGTCT  GC
                                |||| ||  || ||||||  ||
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                                AGTG AC  AC GTCGGG  CG
                                  _ A_ _     GT
GAM1038  LOC149073 3'  GTCAGGAGTGGTGGCATGTG   84330        TGA  G
                                CATGTGCC   CA TCTTGGC
                                ||||||||   || |||||||
                                GTGTACGG   GT AGGACTG
                                    TG_  G
GAM1038  LOC149113 5'  GTTGGGGCCAGGTGCGGTGG   79170     _ TG    ACA    TG
                                TCAT G  CCTG   GTCT  GC
                                |||| |  ||||   ||||  ||
                                GGTG C  GGAC   CGGG  TG
                                  G GT    ___    GT
GAM1038  LOC149175 3'  GCTAGTGCCTGGGCACA     79212        ACA  C
                                TGTGCCTG   GT TTGGC
                                ||||||||   || |||||
                                ACACGGGT   CG GATCG
                                    C__  T
GAM1038  LOC149271 3'  GCCAAGGTTGAGAGTCACTGA  79242     T   C  GA  GT
                                TCA GTG CT  CA  CTTGGC
                                ||| ||| ||  ||  ||||||
                                AGT CAC GA  GT  GAACCG
                                  _  T  GA  TG
GAM1038  LOC149301 3'  GTTAAGGCATGAGCATGTG    79251        CTGA  _
                                CATGTGC    CA GTCTTGGC
                                |||||||    || ||||||||
                                GTGTACG    GT CGGAATTG
                                    A___  A
GAM1038  LOC149319 5'  GCCAGGGCTTCCCCGTGG    79295      TGCCT  C
                                TCATG     GA AGTCTTGGC
                                |||||     || |||||||||
                                GGTGC     CT TCGGGACCG
                                  CC___  _
GAM1038  LOC149421 3'  GCTGGGATTACAGGCAT     79361        AC     TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  LOC149426 3'  GCCGGGACTCCCCTGGTGATGG 84417      G    TGAC_
                                TCAT TGCC     AGTCTTGGC
                                |||| ||||     |||||||||
                                GGTA GTGG     TCAGGGCCG
                                  _    TCCCC
GAM1038  LOC149460 5'  GCCAAGGGCCCCCTGGGTGTGT 84440     TG   GACA_  _
                                ATG  CCT     GTC TTGGC
                                |||  |||     ||| |||||
                                TGT  GGG     CGG AACCG
                                  GT   TCCCC   G
GAM1038  LOC149461 3'  GCCAAGGGCCCCCTGGGTGTGT 79403     TG   GACA_  _
                                ATG  CCT     GTC TTGGC
                                |||  |||     ||| |||||
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                                TGT  GGG    CGG AACCG
                                  GT   TCCCC   G
GAM1038  LOC149466 5'  GTTGAGGCTGAGACTCACTGG  79398    T   CCTGA    TG
                                TCA GTG    CAGTCT  GC
                                ||| |||    ||||||  ||
                                GGT CAC    GTCGGA  TG
                                  _  TCAGA     GT
GAM1038  LOC149478 3'  GTCGAGGCTGGAGTGTAGTGG  79381     G  _  GA
                                TCAT TGC CT  CAGTCTTGGC
                                |||| ||| ||  ||||||||||
                                GGTG ATG GA  GTCGGAGCTG
                                   _  T  G_
GAM1038  LOC149577 3'  GCTGGGATTACAGGCAT    84515       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  LOC149577 3'  GCTGGGATTACAGGCGTGA   84516    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC149577 3'  GCTGGGATTACAGGTGTGTG  84517    TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGT  GGAC  TTAGG  CG
                                  GT   A_    GT
GAM1038  LOC149603 5'  GCCAGGACCTTGCAGGT    70639     A  __
                                GCCTG CA  GTCTTGGC
                                |||||  ||  ||||||||
                                TGGAC GT  CAGGACCG
                                  _  TC
GAM1038  LOC149603 5'  GCCAGGACTTGCGCGGTGA   70640    _   CTGAC
                                TCAT GTGC    AGTCTTGGC
                                |||| ||||    |||||||||
                                AGTG CGCG    TCAGGACCG
                                  G   T____
GAM1038  LOC149650 3'  GTCAAGTGTGTGTGTGTGA   79470     TG CTG   GT
                                TCATG  C   ACA  CTTGGC
                                |||||  |   |||  ||||||
                                AGTGT  G   TGT  GAACTG
                                   GT ___   GT
GAM1038  LOC149653 3'  GCCAGGGCGTCCGTGCACG   84555     CT_  A
                                TGTGC   GAC GTCTTGGC
                                |||||   ||| ||||||||
                                GCACG   CTG CGGGACCG
                                   TGC   _
GAM1038  LOC149653 3'  GTTGAGGCTGTTGCAGTGG   84556    G  CT      TG
                                TCAT TGC  GACAGTCT  GC
                                |||| |||  ||||||||  ||
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                                GGTG ACG  TTGTCGGA  TG
                                  _  __       GT
GAM1038  LOC149657 3'  TCGGGGCTGACGTGGC     84578     _  A
                                GCC TG CAGTCTTGG
                                ||| || |||||||||
                                CGG GC GTCGGGGCT
                                  T  A
GAM1038  LOC149668 5'  GCTGGGGCGAGGGTCTGTGA  84544     GT   GACA   TG
                                TCAT  GCCT   GTCT  GC
                                ||||  ||||   ||||  ||
                                AGTG  TGGG   CGGG  CG
                                  TC   AG__   GT
GAM1038  LOC149692 3'  GCTAAGATTACAGGCGTGA   84588     GT    AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  CGGAC  TTAGAATCG
                                  __    A_
GAM1038  LOC149692 3'  GCTGGGATTACAGGTGTGTG  84590     TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGT  GGAC  TTAGG  CG
                                  GT   A_    GT
GAM1038  LOC149703 5'  GCTGGGATTACAGGCGTGA   84655     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC149722 5'  GCCAAAGGCAAGTCAGGCAT  84602        A_    _
                                GTGCCTGAC  GTCTT GGC
                                |||||||||  ||||| |||
                                TACGGACTG  CGGAA CCG
                                     AA    A
GAM1038  LOC149821 5'  GCTGGGATTACAGGCGTGA   84765     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC149832 5'  GCCGGGGAGGGGGTTGTGG   84702      T   GACAG
                                TCATG GCCT    TCTTGGC
                                ||||| ||||    |||||||
                                GGTGT TGGG    GGGGCCG
                                  _   GGA__
GAM1038  LOC149911 3'  GCCAGGGCTGAGTGCACCTGG  84709     T   _  GA
                                TCA GTGC CT  CAGTCTTGGC
                                ||| |||| ||  ||||||||||
                                GGT CACG GA  GTCGGGACCG
                                  C   T __
GAM1038  LOC149951 3'  GCTGGGGCGCGCGCCATGG   84805      T  C  ACA   TG
                                TCATG GC TG   GTCT  GC
                                ||||| || ||   ||||  ||
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                                GGTAC CG GC   CGGG  CG
                                  _ C  G__    GT
GAM1038  LOC149992 5'  TCAGGGCGGGTGCGGGA     79559    A  TG   GACA
                                TC TG  CCT    GTCTTGG
                                || ||  |||    |||||||
                                AG GC  GGG    CGGGACT
                                 G  GT  ____
GAM1038  LOC149997 5'  GCTGAGGCGTGAGCAATGG    76342     G   C G  A    TG
                                TCAT TGC T AC GTCT  GC
                                |||| ||| | || ||||  ||
                                GGTA ACG A TG CGGA  CG
                                  _  _ G  _    GT
GAM1038  LOC150035 5'  GTTAAGACAAGGTTGTACTTGA 84811     T    CT   A__
                                TCA GTGC  GAC   GTCTTGGC
                                ||| ||||  |||   ||||||||
                                AGT CATG  TTG   CAGAATTG
                                  T   __   GAA
GAM1038  LOC150054 5'  GCTGGGATTATAGGCAT     84836       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGG  CG
                                    A_    GT
GAM1038  LOC150094 3'  GCTGAGACAGCGGGTGCTGG   84863     T TG    ACA    TG
                                TCA G  CCTG   GTCT  GC
                                ||| |  ||||   ||||  ||
                                GGT C  GGGC   CAGA  CG
                                 _ GT   GA_   GT
GAM1038  LOC150225 3'  GCTGGGATTACAGGTGTGA   85000     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC150236 3'  GTTGGGGGTGGGGCGTGTG   79689    TG    G  AG   TG
                                CA  TGCCT AC  TCT  GC
                                ||  ||||| ||  |||  ||
                                GT  GCGGG TG  GGG  TG
                                 GT    G  __   GT
GAM1038  LOC150282 5'  GCTGGGATTACAGGCAT     79729       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  LOC150311 5'  GCTAGGGCTGCAAAGCGAGA   79756    A   GCC  A
                                TC TGT   TG CAGTCTTGGC
                                || |||   || ||||||||||
                                AG GCG   AC GTCGGGATCG
                                 A  AA_ _
GAM1038  LOC150372 3'  GTTGGGAGGCCGAGGCGGGTGG 79807      G    GACAG   TG
                                TCAT TGCCT    TCT  GC
                                |||| |||||    |||  ||
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                                GGTG GCGGA    AGG  TG
                                  G    GCCGG  GT
GAM1038  LOC150397 3'  GCTGGGATTACAGGCGTGA   79848     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC150407 3'  GCCAGGGCTGCTGGCG     79824     TGA
                                TGCC   CAGTCTTGGC
                                ||||   ||||||||||
                                GCGG   GTCGGGACCG
                                  TC_
GAM1038  LOC150407 3'  GCTGGGATTACAGGCGTGA   79828     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC150538 3'  GCCGGGACTCTCAGCACAGA   79937    A    C   C
                                TC TGTGC TGA AGTCTTGGC
                                || ||||| ||| |||||||||
                                AG ACACG ACT TCAGGGCCG
                                 _    _  C
GAM1038  LOC150577 3'  GCCATCCTGATAGGTGTGTGG  85076      TG   A   TCT
                                TCATG  CCTG CAG   TGGC
                                |||||  |||| |||   ||||
                                GGTGT  GGAT GTC   ACCG
                                   GT   A   CT_
GAM1038  LOC150577 3'  GCTGAGATAGTCGCGGATGA   85078     G   CT   A   TG
                                TCAT TGC  GAC GTCT  GC
                                |||| |||  ||| ||||  ||
                                AGTA GCG  CTG TAGA  CG
                                  G   __   A   GT
GAM1038  LOC150587 3'  GCTGGGAAGATAGGCACGTG   85064         ACAG   TG
                                CATGTGCCTG   TCT  GC
                                ||||||||||   |||  ||
                                GTGCACGGAT   AGG  CG
                                      AGA_   GT
GAM1038  LOC150606 3'  GACTGTTGTGTGTGTGG     85089      TG C
                                TCATG  C TGACAGTC
                                |||||  | ||||||||
                                GGTGT  G GTTGTCAG
                                   GT T
GAM1038  LOC150622 3'  GTCAAGGCTGGGCTGGTGA   79964     GT   TGA
                                TCAT  GCC   CAGTCTTGGC
                                ||||  |||   ||||||||||
                                AGTG  CGG   GTCGGAACTG
                                  GT   ____
GAM1038  LOC150630 5'  GCTGGGATTACAGGCGTGA   85108     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC150696 3'  GCTAGCATCCGGGCATGT    58482        ACA  C
                                ATGTGCCTG   GT TTGGC
                                |||||||||   || |||||
                                TGTACGGGC   TA GATCG
                                     C__  C
GAM1038  LOC150696 3'  GCTGGGACTGCAGGTGTGTG   58484     TG   A    TG
                                CATG  CCTG CAGTCT  GC
                                ||||  |||| ||||||  ||
                                GTGT  GGAC GTCAGG  CG
                                  GT   _     GT
GAM1038  LOC150886 5'  GCCGAGGCTGCATTATCTGTGA 85154     GTGCC_  A
                                TCAT     TG CAGTCTTGGC
                                ||||     || ||||||||||
                                AGTG     AC GTCGGAGCCG
                                  TCTATT  _
GAM1038  LOC150889 5'  GCCAGCAGAGGTCTGGGCACAT 80027         _  AG  __
            GG                    TCATGTGCCT GAC  TCT  TGGC
                                |||||||||| |||  |||  ||||
                                GGTACACGGG CTG  AGA  ACCG
                                     T   G_   CG
GAM1038  LOC150935 5'  CGGGGCTCAGCTGTGG     80032      T  C   CA   TG
                                TCATG GC TGA  GTCT  G
                                ||||| || |||  ||||  |
                                GGTGT CG ACT  CGGG  C
                                  _ _  __   GT
GAM1038  LOC150967 5'  GTCAGGATTAAATGAGCATGA  80083      GCCTGAC
                                TCATGT      AGTCTTGGC
                                ||||||      |||||||||
                                AGTACG      TTAGGACTG
                                   AGTAAA_
GAM1038  LOC151057 3'  GCCAGGGTCTCACAGCCATGG  85212      T  C  AC  _
                                TCATG GC TG  AG TCTTGGC
                                ||||| || ||  || |||||||
                                GGTAC CG AC  TC GGGACCG
                                  _ _  AC  T
GAM1038  LOC151057 3'  GCTGGGATTACAGGTGTGA   85214     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC151195 3'  TTTGGCGCGTTGTTAGGTACTG 80171    T       A_______  CTTG
            A                   CA GTGCCTGAC       GT    G
                                || |||||||||       ||   |
                                GT CATGGATTG       CG    T
                                 _       TTGCG    GTTC
GAM1038  LOC151201 3'  GCTGGGATTACAGGCGTGA   85286     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC151475 5'  GCTGGGATTACAGGCAT    85413      AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC151614 3'  GCTGGGATTACAGGTGTGA   80306    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC151623 3'  GTTGAGGCTGGGTAGAGTGA  85459    G_   TGA    TG
                                TCAT  TGCC   CAGTCT  GC
                                ||||  ||||   ||||||  ||
                                AGTG  ATGG   GTCGGA  TG
                                  AG    ___     GT
GAM1038  LOC151826 3'  GCTGGGATTACAGGCACATG  80360        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTACACGGAC  TTAGG  CG
                                     A_    GT
GAM1038  LOC151826 3'  GCTGGGATTACAGGCAT    80361      AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC151877 3'  GCTGGGATTACAGACGTGA   85507     GC   AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTGCA  GAC  TTAGG  CG
                                   __    A_    GT
GAM1038  LOC151979 5'  GCTGGGATTATAGGCGTGA   80424    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAT  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC152137 3'  GCCATTTTGTTAGGTAT    80480         TCT
                                GTGCCTGACAG   TGGC
                                ||||||||||   ||||
                                TATGGATTGTT   ACCG
                                      TT_
GAM1038  LOC152190 5'  GCCAAGATTATCCATATG    69659      CCT  C
                                CATGTG   GA AGTCTTGGC
                                ||||||   || |||||||||
                                GTATAC   CT TTAGAACCG
                                   ___  A
GAM1038  LOC152195 5'  GCCGAGGCCCTGGCGCTGG   85563    T    TGACA
                                TCA GTGCC    GTCTTGGC
                                |||  |||||    ||||||||
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                                GGT CGCGG    CGGAGCCG
                                  _    TCC__
GAM1038  LOC152286 3'  TCCAACGTTGCTGGGCACGTGG 85633         GA  TC   C
                                TCATGTGCCT  CAG  TTGG
                                ||||||||||  |||  ||||
                                GGTGCACGGG  GTT  AACC
                                      TC   GC   TC
GAM1038  LOC152317 5'  GTCGGGGCTTTTGCAT     85648     CT  C
                                GTGC  GA AGTCTTGGC
                                ||||  || |||||||||
                                TACG  TT TCGGGGCTG
                                  __ T
GAM1038  LOC152328 5'  GCCGGGACCGGTGCGGGCGCG  80525        _  A_
                                TGTGCCTG AC  GTCTTGGC
                                ||||||||  ||  ||||||||
                                GCGCGGGC TG  CAGGGCCG
                                     G  GC
GAM1038  LOC152343 3'  GCTGGGATTACAGGTGTGA   80567     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC152348 3'  GCTGGGATTACAGTCATGA   85694      TGC   AC    TG
                                TCATG   CTG  AGTCT  GC
                                |||||   |||  |||||  ||
                                AGTAC   GAC  TTAGG  CG
                                   T__   A_    GT
GAM1038  LOC152359 3'  GCCGAGGTGTGAGCACAGA   85703    A    C G   G
                                TC TGTGC T ACA TCTTGGC
                                || ||||| | ||| |||||||
                                AG ACACG A TGT GGAGCCG
                                 _    _ G   _
GAM1038  LOC152426 5'  GTTAGGATGCCGTGCATGTG   85719       C  ACA
                                CATGTGC TG   GTCTTGGC
                                |||||||  ||   ||||||||
                                GTGTACG GC   TAGGATTG
                                     T  CG_
GAM1038  LOC152445 3'  GCTAGGACCATAGGCACATG   85753         ACA
                                CATGTGCCTG   GTCTTGGC
                                ||||||||||   ||||||||
                                GTACACGGAT   CAGGATCG
                                      AC_
GAM1038  LOC152445 3'  GCTGGGATTACAGGCGTGA   85755     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC152445 3'  GTTGAGATTGCAGGCAT     85759       A     TG
                                GTGCCTG CAGTCT  GC
                                |||||||  ||||||  ||
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                                TACGGAC GTTAGA  TG
                                   _    GT
GAM1038  LOC152620 3'  GCTGAGATTACAGATGTGA   60084      GC  AC   TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTGTA  GAC  TTAGA  CG
                                   __   A_   GT
GAM1038  LOC152633 5'  GCCGGGCAGGGGGCTGTGTGG  85811    TG _   GACA   T
                                TCA  T GCCT   GTCT GGC
                                |||  | ||||   |||| |||
                                GGT  G CGGG   CGGG CCG
                                  GT T   GGA_   _
GAM1038  LOC152719 5'  GCTGGGATTACAGGCGTGA   85852    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_   GT
GAM1038  LOC152719 5'  GCTGGGATTACAGGTGCGTG   85853    TG   AC   TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGC  GGAC  TTAGG  CG
                                  GT   A_   GT
GAM1038  LOC152719 5'  GCTGGGATTTACAGGCAT    85854      AC   TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    AT    GT
GAM1038  LOC152794 5'  GCTGGGATTACAGGCAT    80680      AC   TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_   GT
GAM1038  LOC152845 5'  GCTGTATAGGCACATGG    60334        _
                                TCATGTGCCTG ACAGT
                                |||||||||||  |||||
                                GGTACACGGAT TGTCG
                                      A
GAM1038  LOC152851 3'  GCTGGGATTACAGGCGTGA   80714    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_   GT
GAM1038  LOC153077 3'  GCTGGGACTACAGGCGCATG  85912       AC   TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTACGCGGAC  TCAGG  CG
                                      A_   GT
GAM1038  LOC153196 5'  GCCGGGACTTGCAGGTAT    85963      AC
                                GTGCCTG  AGTCTTGGC
                                |||||||  |||||||||
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                                TATGGAC  TCAGGGCCG
                                    GT
GAM1038  LOC153232 3'  GCCCAGCTGTTGGGGTGTGA   85985    TG G  TG    T  T
                                TCA  T CC  ACAG CT GGC
                                |||  | ||  |||| || |||
                                AGT  G GG  TGTC GA CCG
                                  GT _  GT    _  C
GAM1038  LOC153338 3'  GCTAGGGCTGGTGTATATG   85996       CTGA
                                CATGTGC    CAGTCTTGGC
                                |||||||    ||||||||||
                                GTATATG    GTCGGGATCG
                                    TG__
GAM1038  LOC153339 5'  GCTAAGACAAATCGAATATGA  86009       GCCTGACA
                                TCATGT       GTCTTGGC
                                ||||||       ||||||||
                                AGTATA       CAGAATCG
                                   AGCTAAA_
GAM1038  LOC153443 3'  GCTGGGACTGCAGGTGCATG   80824     TG    A     TG
                                CATG  CCTG CAGTCT  GC
                                ||||  |||| ||||||  ||
                                GTAC  GGAC GTCAGG  CG
                                  GT    _     GT
GAM1038  LOC153454 3'  GTCAAGACTGGATAGGTGTTA  80836    T TG    A_
                                A G  CCTG  CAGTCTTGGC
                                | |  ||||  ||||||||||
                                A T  GGAT  GTCAGAACTG
                                 T GT    AG
GAM1038  LOC153454 3'  GTTAGATGGTTAGGTGTTTGA  80837     T TG     A    TGGC
                                TCA G  CCTGAC GTCT
                                ||| |  |||||| ||||
                                AGT T  GGATTG TAGA
                                  T GT     G    TTG
GAM1038  LOC153546 5'  GCTGGGCGCCACCAGGCGCGGA 80887     A       ACA  _  TG
                                TC TGTGCCTG   GT CT  GC
                                || ||||||||   || ||  ||
                                AG GCGCGGAC   CG GG  CG
                                 _       CAC  C  GT
GAM1038  LOC153603 5'  GCCGAGACCTGAGACGTGG    80901       GC  GA   _
                                TCATGT  CT  CAG TCTTGGC
                                ||||||  ||  ||| |||||||
                                GGTGCA  GA  GTC AGAGCCG
                                   __  __   C
GAM1038  LOC153606 5'  GCTGGGATTATAGGTGTGA    86073     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAT  TTAGG  CG
                                  __     A_    GT
GAM1038  LOC153606 5'  GCTGGTACTACAGGTGCGTG   86074     TG    AC   C TG
                                CATG  CCTG  AGT T  GC
                                ||||  ||||  ||| |  ||
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                                GTGC  GGAC  TCA G  CG
                                  GT   A_   T GT
GAM1038  LOC153688 3'  GCTAGGATTACAGGCAT    86112       AC
                                GTGCCTG  AGTCTTGGC
                                |||||||  |||||||||
                                TACGGAC  TTAGGATCG
                                   A_
GAM1038  LOC153811 3'  GCTGGGATTACAGGTAT    80953       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TATGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC153883 5'  GCTGAGATTACAGGCACATG  80983         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTACACGGAC  TTAGA  CG
                                     A_    GT
GAM1038  LOC154007 3'  AGGCTTCAGGTATGGGA    81011    AT      C
                                TC  GTGCCTGA AGTCT
                                ||  ||||||||  |||||
                                AG  TATGGACT TCGGA
                                 GG       _
GAM1038  LOC154141 5'  GCTGGGATTACAGGCGTGA   86171     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC154282 5'  GCTGGGACTACAGGCACATG  86204         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTACACGGAC  TCAGG  CG
                                     A_    GT
GAM1038  LOC154282 5'  GCTGGGATTACAGGCAT    86205       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC154321 5'  GCTGGGGTTTTGCAGACGTGA  81066      GC   AC_ GT  TG
                                TCATGT  CTG   A  CT  GC
                                ||||||  |||   |  ||  ||
                                AGTGCA  GAC   T  GG  CG
                                   __  GTT TG  GT
GAM1038  LOC154403 5'  GTTGGGGCCAGGTGCGGTGG  81075     _ TG   ACA   TG
                                TCAT G  CCTG   GTCT  GC
                                ||||  |  ||||   ||||  ||
                                GGTG C  GGAC   CGGG  TG
                                  G GT    ___    GT
GAM1038  LOC154726 5'  GCTGGGATTACAGGCAT    81107       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
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                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC154739 3'  GCTGGGACAGTGGTGCATG   86233     TG  TG  A   TG
                                CATG  CC  AC GTCT  GC
                                ||||  ||  || ||||  ||
                                GTAC  GG  TG CAGG  CG
                                  GT  __  A   GT
GAM1038  LOC154739 3'  GCTGGGATTACAGGCATGTG  86234        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTACGGAC  TTAGG  CG
                                     A_    GT
GAM1038  LOC154739 5'  GCTGGGTGTGGAGGCACATG  86235        GA  GT  TG
                                CATGTGCCT  CA  CT  GC
                                |||||||||  ||  ||  ||
                                GTACACGGA  GT  GG  CG
                                     G_  GT  GT
GAM1038  LOC154791 3'  CGAGATCGCGCCATGG     81155      T  C   CAG   TG
                                TCATG GC TGA   TCT  G
                                ||||| || |||   |||  |
                                GGTAC CG GCT   AGA  C
                                  _ C   ___   GT
GAM1038  LOC154877 3'  GCTGGGATTACAGGCGTGA   86301     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC154877 5'  GCTGGGGCTCCAGGCAT    86302       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TCGGG  CG
                                   C_    GT
GAM1038  LOC154930 3'  GCTGGGACTACAGGCATGT   81179        AC    TG
                                ATGTGCCTG  AGTCT  GC
                                |||||||||  |||||  ||
                                TGTACGGAC  TCAGG  CG
                                     A_    GT
GAM1038  LOC154992 5'  GTTGGGGCCAGGTGTGGTGG  81219     _ TG   ACA   TG
                                TCAT G  CCTG   GTCT  GC
                                |||| |  ||||   ||||  ||
                                GGTG T  GGAC   CGGG  TG
                                  G GT   ___    GT
GAM1038  LOC155004 3'  GCTGGGACTGAGGCAT     81224      GA     TG
                                GTGCCT  CAGTCT  GC
                                ||||||  ||||||  ||
                                TACGGA  GTCAGG  CG
                                   __     GT
GAM1038  LOC155046 3'  GCTAAGGCTTGCGGGCACCTGA 81287     T      AC
                                TCA GTGCCTG  AGTCTTGGC
                                ||| |||||||  |||||||||
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                                AGT CACGGGC  TCGGAATCG
                                  C      GT
GAM1038  LOC155060 5'  GCCAAGGCTCAGAGGTGGATGA 86331     G    GAC
                                TCAT TGCCT   AGTCTTGGC
                                |||| |||||   |||||||||
                                AGTA GTGGA   TCGGAACCG
                                  G    GAC
GAM1038  LOC155066 5'  GCCGAGCCGGCGCGGCGCGTGA 81280         _  ACA T
                                TCATGTGCC TG   G CTTGGC
                                ||||||||| ||   | ||||||
                                AGTGCGCGG GC   C GAGCCG
                                     C  GGC _
GAM1038  LOC155435 3'  GCTGGACAGGCACACGG     81351    A       A_
                                TC TGTGCCTG  CAGT
                                || ||||||||  ||||
                                GG ACACGGAC  GTCG
                                 C       AG
GAM1038  LOC155438 3'  GTTGGGGTTGTCATCCAGTGG  86397     G  CC    GT  TG
                                TCAT TG  TGACA  CT  GC
                                |||| ||  |||||  ||  ||
                                GGTG AC  ACTGT  GG  TG
                                  _ CT    TG  GT
GAM1038  LOC157247 5'  GCTGGGATTACAGGCAT     81372        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC157254 3'  GCCGGGGGGCACGGGCACA    81386        ACAG
                                TGTGCCTG    TCTTGGC
                                ||||||||    |||||||
                                ACACGGGC    GGGGCCG
                                     ACG_
GAM1038  LOC157292 3'  GCCAATACGTGGGCACAGA    86416    A      G  A  C
                                TC TGTGCCT AC GT TTGGC
                                || ||||||| || || |||||
                                AG ACACGGG TG CA AACCG
                                 _      _ _  T
GAM1038  LOC157381 3'  GCCAGGCACCGTGTTAGGTAAT 86439      G       __  _
            GA                    TCAT TGCCTGACA  GT CTTGGC
                                |||| |||||||||  || ||||||
                                AGTA ATGGATTGT  CA GGACCG
                                  _       GC  C
GAM1038  LOC157464 5'  GCTAGGACCTGGGGTGTGTGA  86449      TG   GA  _
                                TCATG  CCT  CAG TCTTGGC
                                |||||  |||  ||| |||||||
                                AGTGT  GGG  GTC AGGATCG
                                   GT   __   C
GAM1038  LOC157506 3'  GCTGGGATTACAGGCAT     81444        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
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                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC157507 5'  GCTGGGATTACAGGCAT     81459        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC157567 5'  GCCGGGACAAGCTGTTGGGGTG 81480    TG G  TG    ____
            TGA                   A  T CC  ACAGT    CTTGGC
                                |  | ||  |||||   ||||||
                                T  G GG  TGTCG    GGGCCG
                                 GT _  GT    AACA
GAM1038  LOC157638 3'  GCCATTCTTAAGCACGTGG    81513         C   CAGTCT
                                TCATGTGC TGA     TGGC
                                |||||||| |||     ||||
                                GGTGCACG ATT     ACCG
                                   A   CTT___
GAM1038  LOC157695 3'  GCTGTTTCATGCATGTGG     86518         CT__
                                TCATGTGC    GACAGT
                                ||||||||    ||||||
                                GGTGTACG    TTGTCG
                                    TACT
GAM1038  LOC157773 3'  GCCAGGATGTTGATGGTACAGA 81607     A     T__    G
                                TC TGTGCC   GACA TCTTGGC
                                || ||||||   |||| |||||||
                                AG ACATGG   TTGT AGGACCG
                                 _     TAG   _
GAM1038  LOC157798 5'  GCTGGGATTACAGGCAT     86550        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC157858 5'  GCTGGGATTACAGGCAT     86594        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC157858 5'  GCTGGGATTACAGGCATGTG   86595          AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  LOC157931 3'  CCAAGGCTTCTTACTGG     86657     T   CCT  C
                                TCA GTG   GA AGTCTTGG
                                ||| |||   || ||||||||
                                GGT CAT   CT TCGGAACC
                                  _   T__  _
GAM1038  LOC158055 3'  GCTGCCTCTCAGGCGTGG     81669      GT     C  TCT
                                TCAT  GCCTGA AG   TGGC
                                ||||  |||||| ||   ||||
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                                GGTG  CGGACT TC   GTCG
                                  __     C  C__
GAM1038  LOC158117 3'  GTCAGGGCTGGGGTCCGTGG   81711      TG   GA
                                TCATG  CCT  CAGTCTTGGC
                                |||||  |||  ||||||||||
                                GGTGC  GGG  GTCGGGACTG
                                   CT   __
GAM1038  LOC158236 5'  GCCAAGGCCCTGGTGCAGGA   86707    A  TG  TGACA
                                TC TG  CC    GTCTTGGC
                                || ||  ||    ||||||||
                                AG AC  GG    CGGAACCG
                                 G  GT  TCC__
GAM1038  LOC158288 5'  GCTGGGACGCCGGCACCGTGA  86718      _   TGACA   TG
                                TCATG TGCC    GTCT  GC
                                ||||| ||||    ||||  ||
                                AGTGC ACGG    CAGG  CG
                                   C    CCG__    GT
GAM1038  LOC158310 3'  GCCAGGGTTGCAGTTCACGTG  86754      C_   A  GT
                                CATGTG  CTG CA  CTTGGC
                                ||||||  ||| ||  ||||||
                                GTGCAC  GAC GT  GGACCG
                                    TT   _  TG
GAM1038  LOC158476 3'  GCTGGGATTACAGGCAT     86849       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  LOC158629 5'  GTTGGGATTATGGATGCATGG  86881       _  TGAC    TG
                                TCATGTG CC    AGTCT  GC
                                |||||||  ||    |||||  ||
                                GGTACGT GG    TTAGG  TG
                                    A  TA__     GT
GAM1038  LOC158668 5'  GCCGAGGCCGAGGCCGTGG   69369      T   GACA
                                TCATG GCCT    GTCTTGGC
                                ||||| ||||    ||||||||
                                GGTGC CGGA    CGGAGCCG
                                   _    GC__
GAM1038  LOC158668 3'  GCTGAGATTACAGATGTGA   69372      GC   AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTGTA  GAC  TTAGA  CG
                                   __    A_    GT
GAM1038  LOC158709 3'  GCTGGGATTACAGGCGTGA   81983     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                   __    A_    GT
GAM1038  LOC158865 5'  GCTGGGATTACAGGCGCATG  86938        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
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                                GTACGCGGAC  TTAGG  CG
                                     A_    GT
GAM1038  LOC158865 5'  GCTGGGATTACAGGCGTGA   86939     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC158972 3'  GCCGAGATTGCACCAGCCTGG  86951     T  GCC  A
                                TCA GT   TG CAGTCTTGGC
                                ||| ||   || ||||||||||
                                GGT CG   AC GTTAGAGCCG
                                 C  ACC  _
GAM1038  LOC158972 3'  GCTGGGATGGCCGGCTTGTGG  86953      T   TGACA   TG
                                TCATG GCC    GTCT  GC
                                ||||| |||    ||||  ||
                                GGTGT CGG    TAGG  CG
                                   T  CCGG_   GT
GAM1038  LOC158987 3'  GCTGGGTGTGGGGGCATGTG  86965        GA  GT  TG
                                CATGTGCCT  CA  CT  GC
                                |||||||||  ||  ||  ||
                                GTGTACGGG  GT  GG  CG
                                     G_  GT  GT
GAM1038  LOC159199 5'  GCCAGGACCTGGTGTTCATGG  82183      T  CTGA  _
                                TCATG GC    CAG TCTTGGC
                                ||||| ||    ||| |||||||
                                GGTAC TG    GTC AGGACCG
                                   T  TG__   C
GAM1038  LOC160646 3'  GCTGGGATTACAGGCGTGA   82229     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC160897 5'  GCCGAGGCGTCGGTGCAGA   82247    A  TG  T   A
                                TC TG  CC GAC GTCTTGGC
                                || ||  || ||| ||||||||
                                AG AC  GG CTG CGGAGCCG
                                 _  GT  _  _
GAM1038  LOC161734 3'  GCCAGACAGTGGGTGCAGGA  87101    A  TG   G  A   T
                                TC TG  CCT AC GTCT GGC
                                || ||  ||| || |||| |||
                                AG AC  GGG TG CAGA CCG
                                 G  GT   _  A   _
GAM1038  LOC161829 3'  GCTGGGATTACAGGTGCGTG  82317     TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGC  GGAC  TTAGG  CG
                                  GT   A_    GT
GAM1038  LOC161829 3'  GCTGGGATTACAGGTGTGA   82318     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC162952 5'  GCCAGGCCGGGGAGTATGA   82381     TG   GACA   T
                                TCATG  CCT   GTCT GGC
                                |||||  |||   |||| |||
                                AGTAT  GGG   CGGA CCG
                                   GA   GC__   _
GAM1038  LOC162952 5'  GCCGGGGAGTATGAGTGCGTGA 82382     TG CTG_  AG
                                TCATG  C   AC  TCTTGGC
                                |||||  |   ||  |||||||
                                AGTGC  G   TG  GGGGCCG
                                   GT AGTA  A_
GAM1038  LOC163071 5'  GCCAGGACTGGCCGTCACGT   82397     CCTGA
                                ATGTG    CAGTCTTGGC
                                |||||    ||||||||||
                                TGCAC    GTCAGGACCG
                                   TGCCG
GAM1038  LOC163412 5'  GCCGGGGCGTGCGGCGCATGG  82133       T ACA
                                TCATGTGCC G   GTCTTGGC
                                |||||||||  |  ||||||||
                                GGTACGCGG C   CGGGGCCG
                                     _ GTG
GAM1038  LOC163412 5'  GCTGGGACAACGGGCGGGTGA  82135     G     ACA   TG
                                TCAT TGCCTG   GTCT  GC
                                |||| ||||||   ||||  ||
                                AGTG GCGGGC   CAGG  CG
                                  G     AA_   GT
GAM1038  LOC163590 5'  GCTGGGATTACAGGCGTGA   58861     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC163682 3'  GCCAAGACGTCCTGGGCATAGG 87034    A     __   A
            A                    TC TGTGCCT  GAC GTCTTGGC
                                || |||||||  ||| ||||||||
                                AG ATACGGG  CTG CAGAACCG
                                 G      TC  _
GAM1038  LOC164582 5'  CCCACCTGTCAGGCCTGTGA   82540     T       TCT   C
                                TCATG GCCTGACAG   TGG
                                ||||| |||||||||   |||
                                AGTGT CGGACTGTC   ACC
                                   C        C__   CC
GAM1038  LOC164714 5'  GCCGAGACATAGTGTGCATGG  87234     TG _   ACA
                                TCATG  C CTG   GTCTTGGC
                                |||||  | |||   ||||||||
                                GGTAC  G GAT   CAGAGCCG
                                   GT T   A__
GAM1038  LOC168391 5'  TCTATGTTAGGTACAGA     82693    A        GTCTT
                                TC TGTGCCTGACA    GG
                                || ||||||||||     ||
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                                AG ACATGGATTGT    CT
                                 _        AT___
GAM1038  LOC169611 3'  GCTGGGACTGGGCATGAGGTGG 82770     ___    TGA    TG
                                TCAT   GTGCC   CAGTCT  GC
                                ||||   |||||   ||||||  ||
                                GGTG   TACGG   GTCAGG  CG
                                  GAG    ___     GT
GAM1038  LOC169611 3'  GTTGGGATTACAGGCAT    82773       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  TG
                                   A_    GT
GAM1038  LOC169611 3'  GTTGGGATTACAGGCAT    82774       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  TG
                                   A_    GT
GAM1038  LOC170394 5'  GCCAGGACCCCGAGGTGCTGG  82851    T TG   GACA
                                TCA G  CCT    GTCTTGGC
                                |||  |  |||   ||||||||
                                GGT C  GGA    CAGGACCG
                                 _ GT   GCCC
GAM1038  LOC170409 5'  GCTGGGATTACAGATGTGA   82864      GC   AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTGTA  GAC  TTAGG  CG
                                   __   A_    GT
GAM1038  LOC170409 3'  GTTAGGGCTTTTTGTGTGTG   82867     TG CT  C
                                CATG  C  GA AGTCTTGGC
                                ||||  |  || |||||||||
                                GTGT  G  TT TCGGGATTG
                                  GT T_  T
GAM1038  LOC196047 5'  GCCAGGGTTTCACCATG     89601     TGCC   C GT
                                CATG    TGA A  CTTGGC
                                ||||    |||  |  ||||||
                                GTAC    ACT T  GGACCG
                                  C___   _ TG
GAM1038  LOC196264 3'  GTTGGGATTACAGGCAT     87609       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  TG
                                   A_    GT
GAM1038  LOC196337 3'  ACATCACTGTTAGGGTATGG   87643       G       CT  GC
                                TCATGT CCTGACAGT  TG
                                |||||| |||||||||  ||
                                GGTATG GGATTGTCA  AC
                                   _       CT  AG
GAM1038  LOC196337 3'  GTTAGGGTATGGTGGAGTGTGT 87650      TG _  GA  GT_
            GA                   TCATG  C CT  CA   CTTGGC
                                |||||  | ||  ||   ||||||
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                                AGTGT  G GG  GT   GGATTG
                                   GT A  TG  ATG
GAM1038  LOC196527 3'  GTCTATTCTCAGGCGCATGA  87758          C   CTT
                                TCATGTGCCTGA AGT   GGC
                                |||||||||||| |||   |||
                                AGTACGCGGACT TTA   CTG
                                       C   T__
GAM1038  LOC196529 3'  GCTGGGATGACAGGCGTGA   87777     GT    ACA   TG
                                TCAT  GCCTG   GTCT  GC
                                ||||  |||||   ||||  ||
                                AGTG  CGGAC   TAGG  CG
                                   __    AG_   GT
GAM1038  LOC196529 3'  GTTGGGATTACAGGTGTGA   87779     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  TG
                                   __    A_    GT
GAM1038  LOC196549 5'  CCGGGGCGATGCTGTGG     59231      T  CTGACA
                                TCATG GC     GTCTTGG
                                ||||| ||     |||||||
                                GGTGT CG     CGGGGCC
                                   _ TAG___
GAM1038  LOC196549 3'  GCTGCAGATTCAGCGTGTGG   59232     TG   C   CA   _
                                TCA  TGC TGA  GTCT TGGC
                                |||  ||| |||  |||| ||||
                                GGT  GCG ACT  TAGA GTCG
                                  GT   _   __    C
GAM1038  LOC196707 3'  GCCGAGACTTGCTGGCACGGA  87529    A     TGAC
                                TC TGTGCC    AGTCTTGGC
                                || ||||||    |||||||||
                                AG GCACGG    TCAGAGCCG
                                  _     TCGT
GAM1038  LOC196759 5'  CTAGGGCTTCTAATGA      87516      GTGCCT  C
                                TCAT     GA AGTCTTGG
                                ||||     || ||||||||
                                AGTA     CT TCGGGATC
                                   AT_____  _
GAM1038  LOC196812 3'  GCTGAGGTTTGGGGTACAGA   89570    A     GAC GT  TG
                                TC TGTGCCT   A  CT  GC
                                || |||||||   |  ||  ||
                                AG ACATGGG   T  GA  CG
                                  _      GT_ TG  GT
GAM1038  LOC196951 5'  GTCAAGGCGTAGTTGCAGTGA  87810     G   CTG_  A
                                TCAT TGC    AC GTCTTGGC
                                |||| |||    || ||||||||
                                AGTG ACG    TG CGGAACTG
                                   _   TTGA  _
GAM1038  LOC196955 3'  GCCAGGACCAGAGCAGTGG    77380     G   _   ACA
                                TCAT TGC CTG   GTCTTGGC
                                |||| ||| |||   ||||||||
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                                GGTG ACG GAC   CAGGACCG
                                  _  A  ____
GAM1038  LOC196955 5'  GCTAGGGACCAGTGCATGTGA  77382        _  ACAG
                                TCATGTGC CTG    TCTTGGC
                                |||||||| |||    |||||||
                                AGTGTACG GAC    GGGATCG
                                    T  CA__
GAM1038  LOC196957 3'  GCTAGGACTACAGGCACATG  87824         AC
                                CATGTGCCTG  AGTCTTGGC
                                ||||||||||  |||||||||
                                GTACACGGAC  TCAGGATCG
                                    A_
GAM1038  LOC196961 3'  GCTAGGACTACAGGCACATG  87845         AC
                                CATGTGCCTG  AGTCTTGGC
                                ||||||||||  |||||||||
                                GTACACGGAC  TCAGGATCG
                                    A_
GAM1038  LOC196989 3'  GCCGGGGGGCGGTGGGCACAT  89666        G  A    _
                                ATGTGCCT AC GTCTT GGC
                                |||||||| || ||||| |||
                                TACACGGG TG CGGGG CCG
                                    _ G    G
GAM1038  LOC196996 3'  CTAAGACTGCCTATGA      87859       T  CTGAC
                                TCATG GC    AGTCTTGG
                                ||||| ||    ||||||||
                                AGTAT CG    TCAGAATC
                                  C  ______
GAM1038  LOC197114 5'  GCCAGAGGCCTGGGCACAT   89705         ACA   _
                                ATGTGCCTG   GTCT TGGC
                                |||||||||   |||| ||||
                                TACACGGGT   CGGA ACCG
                                    C__   G
GAM1038  LOC197117 5'  GCCAGAGGCCTGGGCACAT   89718         ACA   _
                                ATGTGCCTG   GTCT TGGC
                                |||||||||   |||| ||||
                                TACACGGGT   CGGA ACCG
                                    C__   G
GAM1038  LOC197117 3'  GTCAGTGCCCTTGGGCACTGG  89723     T    TG CA  C
                                TCA GTGCC  A  GT TTGGC
                                ||| |||||  |  || |||||
                                GGT CACGG  T  CG GACTG
                                  _    GT CC  T
GAM1038  LOC197125 3'  GCCAGGAGCCCAGGCACA    87900         ACAG
                                TGTGCCTG    TCTTGGC
                                ||||||||    |||||||
                                ACACGGAC    AGGACCG
                                    CCG_
GAM1038  LOC197125 3'  GCTGGGCAGAAGGGCTGTGG   87901       T   GACA T  TG
                                TCATG GCCT    G CT  GC
                                ||||| ||||    | ||  ||
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                                GGTGT CGGG   C GG  CG
                                   _   AAGA _  GT
GAM1038  LOC197138 3'  GCTAGGACTACAGGCACATG  87918        AC
                                CATGTGCCTG  AGTCTTGGC
                                ||||||||||  |||||||||
                                GTACACGGAC  TCAGGATCG
                                     A_
GAM1038  LOC197285 3'  TCGAGATTGCACGCG      87793     C  A
                                TGC TG CAGTCTTGG
                                ||| || |||||||||
                                GCG AC GTTAGAGCT
                                  C  _
GAM1038  LOC197342 3'  GCCAGGCAGAGGGCGCG    88002       GACA   T
                                TGTGCCT   GTCT GGC
                                |||||||   |||| |||
                                GCGCGGG   CGGA CCG
                                    AGA_   _
GAM1038  LOC197342 3'  GTCAGGAGCCCGGGCACAGA  88006   A      ACAG
                                TC TGTGCCTG   TCTTGGC
                                || |||||||   |||||||
                                AG ACACGGGC   AGGACTG
                                 _      CCG_
GAM1038  LOC197358 3'  GCTGGGATTACAGGTGTGA   88043    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_   GT
GAM1038  LOC199725 5'  GCTGGGATTACAGGCAT    89839      AC   TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_   GT
GAM1038  LOC199725 3'  GTTAGGCAGAGTTCAGGTAT  89840       CAGT__
                                GTGCCTGA    CTTGGC
                                ||||||||    ||||||
                                TATGGACT    GGATTG
                                     TGAGAC
GAM1038  LOC199775 5'  GCTGGGATTAAAGGCGTGA   88358    GT   GAC   TG
                                TCAT  GCCT   AGTCT  GC
                                ||||  ||||   |||||  ||
                                AGTG  CGGA   TTAGG  CG
                                  __   AA_   GT
GAM1038  LOC199786 3'  GCTGGGATTACAGGCAT    88388      AC   TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_   GT
GAM1038  LOC199786 3'  GCTGGGATTACAGGTGTGA   88389    GT   AC   TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC199796 5' GCTGAGACACTGGCAGTGG   74455     G   TGACA   TG
                                TCAT TGCC    GTCT  GC
                                |||| ||||    ||||  ||
                                GGTG ACGG    CAGA  CG
                                  _   TCA__   GT
GAM1038  LOC199864 5' CTAGGGCTTCTAATGA     89865     GTGCCT  C
                                TCAT     GA AGTCTTGG
                                ||||     || ||||||||
                                AGTA     CT TCGGGATC
                                  AT_____ _
GAM1038  LOC199886 3' GCTGAGACCTATGGTGGTGG  88454     G   TGACA   TG
                                TCAT TGCC    GTCT  GC
                                |||| ||||    ||||  ||
                                GGTG GTGG    CAGA  CG
                                  _   TATC_   GT
GAM1038  LOC199907 3' GCCAGGACTGCCCTTGGGCATA 88466       TG ___
             T                   ATGTGCC  A   CAGTCTTGGC
                                |||||||  |  ||||||||||
                                TATACGG  T   GTCAGGACCG
                                    GT CCC
GAM1038  LOC199986 5' GTTGGGGCCAGGCGTGA    89909     GT    ACA   TG
                                TCAT  GCCTG   GTCT  GC
                                ||||  |||||   ||||  ||
                                AGTG  CGGAC   CGGG  TG
                                  __    ___   GT
GAM1038  LOC200010 5' GTTAGGACTTCGACACAGA   89923    A   CC   C
                                TC TGTG  TGA AGTCTTGGC
                                || ||||  ||| |||||||||
                                AG ACAC  GCT TCAGGATTG
                                  _   A_  _
GAM1038  LOC200014 3' GCCAGGGTAGCAGTAACATGA  88529      GC   ACAG
                                TCATGT  CTG   TCTTGGC
                                ||||||  |||   |||||||
                                AGTACA  GAC   GGGACCG
                                   AT   GAT_
GAM1038  LOC200014 3' GCTGGGATTACAGGTGTGA   88535     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC200169 5' GCTGGGATTACAGGCAT     89953       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC200298 3' GCTGAGGTTGCCACACACCTGA 89974     T   CC  A  GT  TG
                                TCA GTG  TG CA  CT  GC
                                ||| |||  || ||  ||  ||
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                                AGT CAC  AC GT  GA  CG
                                  C   AC  C  TG  GT
GAM1038  LOC200301 5'  GCTGGGATTACAGGCGTGA   88747     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC200310 3'  GCTAGGATTACAGGCGTGA   65738     GT    AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  CGGAC  TTAGGATCG
                                  __    A_
GAM1038  LOC200312 3'  GTCAAGGCTGTCTGC      89996    CT
                                GC  GACAGTCTTGGC
                                ||  ||||||||||||
                                CG  CTGTCGGAACTG
                                 T_
GAM1038  LOC200314 3'  GCTGGGATTACAGGCACACGA  90013    A      AC    TG
                                TC TGTGCCTG  AGTCT  GC
                                || ||||||||  |||||  ||
                                AG ACACGGAC  TTAGG  CG
                                 C      A_    GT
GAM1038  LOC200314 3'  GCTGGGATTACAGGCAT     90014       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC200316 5'  GCTGGGATTACAGGCGTGA   88771     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC200316 3'  GCTGGGATTACGGGCGTGA   88772     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGGC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC200339 3'  GCTGGGATTACAGGTGTGA   90037     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC200339 3'  GTCGAGACTGGGGTGTAGTGG  90038    _  TG   GA
                                TCA TG  CCT  CAGTCTTGGC
                                ||| ||  |||  ||||||||||
                                GGT AT  GGG  GTCAGAGCTG
                                  G  GT  __
GAM1038  LOC200575 5'  GCGCTGCAACTCGGTGCGCGTG 88829       _   ____    CTTGGC
            G                    CATGTGC CTGA    CAGT
                                |||||||  ||||    ||||
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                                GTGCGCG GGCT   GTCG
                                   T   CAAC     CGG
GAM1038  LOC200576 5' GCCGGGGCAGGAGGCGCAGA  88826   A     GACA
                                TC TGTGCCT   GTCTTGGC
                                || |||||||   ||||||||
                                AG ACGCGGA   CGGGGCCG
                                 _     GGA_
GAM1038  LOC200597 5' GCTGAGGACAGGGCTGTGG   88841     T   GACAG   TG
                                TCATG GCCT    TCT  GC
                                ||||| ||||    |||  ||
                                GGTGT CGGG    GGA  CG
                                   _   ACA__   GT
GAM1038  LOC200781 3' GCTGGGGGTCTCTCAGGCACCT 90139    T      C __   TG
            GG                    TCA GTGCCTGA AG  TCT  GC
                                ||| |||||||| ||  |||  ||
                                GGT CACGGACT TC  GGG  CG
                                  C      C  TG   GT
GAM1038  LOC200845 5' GCTGGGATTATAGGCAT    88902       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAT  TTAGG  CG
                                   A_    GT
GAM1038  LOC200860 3' GCTGGGACCACAGGTGTATGG  90166     TG   ACA   TG
                                TCATG  CCTG   GTCT  GC
                                |||||  ||||   ||||  ||
                                GGTAT  GGAC   CAGG  CG
                                   GT   AC_   GT
GAM1038  LOC200860 3' GCTGGGATTACAGGCGTGA   90167    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC200860 3' GTCAGGGCTCAGCCAGGTGG  90169     G  C   CA
                                TCAT TG CTGA  GTCTTGGC
                                |||| || ||||  ||||||||
                                GGTG AC GACT  CGGGACTG
                                  G  C   __
GAM1038  LOC200860 3' GTTGAGGGTGCGTGGGCACAGA 90171   A      A_  G   TG
                                TC TGTGCCTG  CA TCT  GC
                                || ||||||||  || |||  ||
                                AG ACACGGGT  GT GGA  TG
                                 _      GC  G   GT
GAM1038  LOC201116 5' CGGGACTGCACAGTGA     88103    _   CTGAC    TG
                                TCA TGTGC    AGTCT  G
                                ||| |||||    |||||  |
                                AGT ACACG    TCAGG  C
                                  G    _____    GT
GAM1038  LOC201164 3' GCTGGGATTACAGGTGTGA   88119     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC201173 5'  GCTGGGATTGCAGGTAT    87332       A    TG
                                GTGCCTG CAGTCT  GC
                                ||||||| ||||||  ||
                                TATGGAC GTTAGG  CG
                                   _    GT
GAM1038  LOC201220 5'  GCTGGGATTGCAGGTAT    87353       A    TG
                                GTGCCTG CAGTCT  GC
                                ||||||| ||||||  ||
                                TATGGAC GTTAGG  CG
                                   _    GT
GAM1038  LOC201245 3'  GCCCAGAGTTGGGCACTGG   87363    T   TG  AG  T
                                TCA GTGCC  AC  TCT GGC
                                ||| |||||  ||  ||| |||
                                GGT CACGG  TG  AGA CCG
                                  _   GT  __  C
GAM1038  LOC201283 3'  GCTGGGACTGGCGGTAATGA  60415    G   TGA    TG
                                TCAT TGCC   CAGTCT  GC
                                |||| ||||   ||||||  ||
                                AGTA ATGG   GTCAGG  CG
                                  _   CG_    GT
GAM1038  LOC201292 5'  GCCAAGACGCAGGCGCTGG   88189    T     ACA
                                TCA GTGCCTG   GTCTTGGC
                                ||| |||||||   ||||||||
                                GGT CGCGGAC   CAGAACCG
                                  _     G__
GAM1038  LOC201292 3'  GCTGAGATTGCACCACTGG   88191    T  CC  A    TG
                                TCA GTG  TG CAGTCT  GC
                                ||| |||  || ||||||  ||
                                GGT CAC  AC GTTAGA  CG
                                  _  C_  _    GT
GAM1038  LOC201294 3'  GCCAGGCAACAGGCGGTGG   88209    G    ACA   T
                                TCAT TGCCTG   GTCT GGC
                                |||| ||||||   |||| |||
                                GGTG GCGGAC   CGGA CCG
                                  _    AA_   _
GAM1038  LOC201294 3'  GCTGGGACTACAGGCACGTG  88215       AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGCACGGAC  TCAGG  CG
                                     A_    GT
GAM1038  LOC201294 3'  GCTGGGATTACAGGCGTGA   88216    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC201411 3'  GCTGGGATTACAGGCGTGA   62959    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC201617 3'  CCAAGCTGAGTATATGA    90234       CTGA   T
                                TCATGTGC   CAG CTTGG
                                ||||||||   ||| |||||
                                AGTATATG   GTC GAACC
                                    A___  _
GAM1038  LOC201626 3'  GTTGGGATTACAGGCGTGA   88995    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  TG
                                  __    A_    GT
GAM1038  LOC201627 3'  GCTGGGATTACAGGTATGTG  89018        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTATGGAC  TTAGG  CG
                                     A_    GT
GAM1038  LOC201627 3'  GCTGGGATTACAGGTGTGA   89019    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC201696 3'  GCTGGGATTACAGGTGTGA   63135    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC201705 5'  GCTGGGATTACAGGCGTGA   90253    GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC201736 5'  GCTGGGCTGGTTGGGTATGTG  89051       TG  _  T  TG
                                CATGTGCC  AC AG CT  GC
                                ||||||||  || || ||  ||
                                GTGTATGG  TG TC GG  CG
                                     GT  G  _  GT
GAM1038  LOC201799 3'  CGAGGCTGCCAACAGA     89058    A  GCC  A     TG
                                TC TGT   TG CAGTCT  G
                                || |||   || ||||||  |
                                AG ACA   AC GTCGGA  C
                                  _  ___  C     GT
GAM1038  LOC201799 3'  GTTTATTCTGTCAGGGTATATG 89065        _     TCTT
            A                    TCATGTGCC TGACAG    GGC
                                ||||||||| ||||||   |||
                                AGTATATGG ACTGTC    TTG
                                     G     TTAT
GAM1038  LOC201868 5'  GTTGGGGCCAGGTGCAGTGG   89082     _  TG    ACA    TG
                                TCA TG  CCTG   GTCT  GC
                                ||| ||  ||||   ||||  ||
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                                GGT AC  GGAC   CGGG  TG
                                  G  GT    ___    GT
GAM1038  LOC201895 3'  GCCAGGGTTGGTGCATGTG   89088       CTGA  GT
                                CATGTGC    CA  CTTGGC
                                |||||||    ||  ||||||
                                GTGTACG    GT  GGACCG
                                    TG__  TG
GAM1038  LOC202460 5'  CCTGTTGTTAGGCAATGA    89180     G        TCTT  C
                                TCAT TGCCTGACAG    GG
                                |||| ||||||||||    ||
                                AGTA ACGGATTGTT    CC
                                  _        GT__  A
GAM1038  LOC202460 5'  GCTGGATTACAGGTGCATG   89183     TG    AC    T
                                CATG  CCTG  AGTCT GGC
                                ||||  ||||  ||||| |||
                                GTAC  GGAC  TTAGG TCG
                                  GT    A_    _
GAM1038  LOC202559 5'  CCGGGGCTCTGCGCG      89196      CT  CA
                                TGTGC  GA  GTCTTGG
                                |||||  ||  |||||||
                                GCGCG  CT  CGGGGCC
                                   T_  __
GAM1038  LOC202559 5'  GTCGCAGGTGCTGGGTGCATGG 89198      TG   GA  G   _
                                TCATG  CCT  CA TCT TGGC
                                |||||  |||  || ||| ||||
                                GGTAC  GGG  GT GGA GCTG
                                   GT   TC  _   C
GAM1038  LOC202908 5'  GCTGGGATTACAGTAAGTGA   89243     G   C  AC    TG
                                TCAT TGC TG  AGTCT  GC
                                |||| ||| ||  |||||  ||
                                AGTG ATG AC  TTAGG  CG
                                  A   _  A_    GT
GAM1038  LOC202908 5'  GCTGGGATTATAGGTAT     89244       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TATGGAT  TTAGG  CG
                                    A_    GT
GAM1038  LOC202915 3'  CCCTCGTGGGCACGTGG     90389         G  _  TCTT
                                TCATGTGCCT AC AG    GG
                                |||||||||| || ||    ||
                                GGTGCACGGG TG TC    CC
                                      _  C  ____
GAM1038  LOC202915 3'  GCCAGGGGGTCAGGGCACCTGA 90393     T    _    AG
                                TCA GTGCC TGAC  TCTTGGC
                                ||| ||||| ||||  |||||||
                                AGT CACGG ACTG  GGGACCG
                                  C    G   G_
GAM1038  LOC202915 5'  GTTGGGGCCACGTGGCCATGA  90396      T   TGACA   TG
                                TCATG GCC    GTCT  GC
                                ||||| |||    ||||  ||
```

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                                AGTAC CGG    CGGG  TG
                                  _  TGCAC   GT
GAM1038  LOC202934 3'  GCTGGGACTATAGGCATGTG  90419        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTACGGAT  TCAGG  CG
                                     A_    GT
GAM1038  LOC202934 3'  GCTGGGATTACAGGCGTGA   90420     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC203025 3'  GCCAAGATTGCACCATTGA   89251     T   CC  A
                                TCA GTG  TG CAGTCTTGGC
                                ||| |||  || ||||||||||
                                AGT TAC  AC GTTAGAACCG
                                  _  C_ _
GAM1038  LOC203042 3'  GCTGAGGGAGCTAGGTGTGG  90447     GT    ACAG   TG
                                TCAT  GCCTG   TCT  GC
                                ||||  |||||   |||  ||
                                GGTG  TGGAT   GGA  CG
                                  __    CGAG   GT
GAM1038  LOC203197 3'  GCTGGGATTACAGACGTGA   89292      GC   AC    TG
                                TCATGT  CTG  AGTCT  GC
                                ||||||  |||  |||||  ||
                                AGTGCA  GAC  TTAGG  CG
                                   __  A_    GT
GAM1038  LOC203273 3'  GCTGAGGTATCAGGCAGTGG  87498     G     CAG   TG
                                TCAT TGCCTGA   TCT  GC
                                |||| |||||||   |||  ||
                                GGTG ACGGACT   GGA  CG
                                  _     AT_   GT
GAM1038  LOC203275 3'  GTCAGGGCTGGGGTCCGTGG  89327      TG   GA
                                TCATG  CCT  CAGTCTTGGC
                                |||||  |||  ||||||||||
                                GGTGC  GGG  GTCGGGACTG
                                   CT   __
GAM1038  LOC203276 3'  GCCAGGACAGTGGTGCATG   90484     TG  TG  A
                                CATG  CC  AC GTCTTGGC
                                ||||  ||  || ||||||||
                                GTAC  GG  TG CAGGACCG
                                  GT  __  A
GAM1038  LOC203276 3'  GCTGGGATTACAGGCATGTG  90485        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTACGGAC  TTAGG  CG
                                     A_    GT
GAM1038  LOC203286 3'  GCCATGGTTGGGTGGGTGA   90499     G   TG  AGTCT
                                TCAT TGCC  AC    TGGC
                                |||| ||||  ||    ||||
```

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                                AGTG GTGG  TG    ACCG
                                  G   GT  GT___
GAM1038  LOC203305 3'  GCCAGGACAGTGGTGCATG   90528     TG  TG  A
                                CATG  CC  AC GTCTTGGC
                                |||| ||  || ||||||||
                                GTAC  GG  TG CAGGACCG
                                  GT  __  A
GAM1038  LOC203305 3'  GCTGGGATTACAGGCATGTG  90529         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTACGGAC  TTAGG  CG
                                      A_    GT
GAM1038  LOC203338 3'  GCTGAGGTATCAGGCAGTGG  87499     G     CAG   TG
                                TCAT TGCCTGA   TCT  GC
                                |||| |||||||   |||  ||
                                GGTG ACGGACT   GGA  CG
                                  _     AT_  GT
GAM1038  LOC203339 3'  GCTGGGACTAGAGGCGTGTG  90546   TG    GAC    TG
                                CA  TGCCT   AGTCT  GC
                                ||  |||||   |||||  ||
                                GT  GCGGA   TCAGG  CG
                                 GT    GA_    GT
GAM1038  LOC203339 3'  GCTGGGATTGCAGGTGCG    90547    TG   A     TG
                                TG  CCTG CAGTCT  GC
                                ||  |||| ||||||  ||
                                GC  GGAC GTTAGG  CG
                                 GT   _     GT
GAM1038  LOC203350 3'  GCTGGGATTCCAGGCAT     90570       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    C_    GT
GAM1038  LOC203369 3'  GCTGGGATTACAGGCGTGA   89344     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC203378 3'  GCTGGGATTACAGGCAT     90609       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  LOC203427 3'  GCTAGGATTAGAGGTGTGA   89359     GT   GAC
                                TCAT  GCCT   AGTCTTGGC
                                ||||  ||||   |||||||||
                                AGTG  TGGA   TTAGGATCG
                                  __    GA_
GAM1038  LOC203429 3'  GCCAGGGCTAGAGCCATGG   89366      T  _  GAC
                                TCATG GC CT   AGTCTTGGC
                                |||||  || ||   |||||||||
```

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                                GGTAC CG GA   TCGGGACCG
                                  _ A ___
GAM1038  LOC203503 3'  GCCAGGGCTTAAGTGTGCCTGG 89369     T TG _  GAC
                                TCA G  C CT   AGTCTTGGC
                                ||| |  | ||  |||||||||
                                GGT C  G GA   TCGGGACCG
                                  C GT T  AT_
GAM1038  LOC204804 3'  GCTGGGATTACAGGCGTGG   89479     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                GGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC204804 3'  GCTGGGGTTACAGGTGTGA   89480     GT    AC GT  TG
                                TCAT  GCCTG  A  CT  GC
                                ||||  |||||  |  ||  ||
                                AGTG  TGGAC  T  GG  CG
                                  __    A_ TG  GT
GAM1038  LOC204970 3'  GCCGGGGCTGGGGGCAT    89411       GA
                                GTGCCT  CAGTCTTGGC
                                ||||||  ||||||||||
                                TACGGG  GTCGGGGCCG
                                   G_
GAM1038  LOC204970 3'  GCTGCTTCGGCATGTGG     89413        T  _
                                TCATGTGCC GA CAGT
                                ||||||||| || ||||
                                GGTGTACGG TT GTCG
                                     C  C
GAM1038  LOC205251 5'  GCTGGGATTACAGGCAT     90671       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC205418 3'  GCCAAGGTGACGGCGTGG    90686     GT   T A  G
                                TCAT  GCC G CA TCTTGGC
                                ||||  ||| | || |||||||
                                GGTG  CGG C GT GGAACCG
                                  __  _ A  _
GAM1038  LOC205418 3'  GCCAAGGTGACGGCGTGG    90687     GT   T A  G
                                TCAT  GCC G CA TCTTGGC
                                ||||  ||| | || |||||||
                                GGTG  CGG C GT GGAACCG
                                  __  _ A  _
GAM1038  LOC205418 5'  GCCAGGACAATGGATGTGA   90688       G  TGACA
                                TCATGT CC    GTCTTGGC
                                |||||| ||    ||||||||
                                AGTGTA GG    CAGGACCG
                                   _  TAA__
GAM1038  LOC206292 5'  GATTGGACTGTTGGGCACCTGA 90714     T    TG      TGGC
                                TCA GTGCC  ACAGTCT
                                ||| |||||  |||||||
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                                AGT CACGG  TGTCAGG
                                  C    GT     TTAGT
GAM1038  LOC219294 3'  GCTGGGACCTGTTGGACGTGA  93008      G  T   _  TG
                                TCATGT CC GACAG TCT  GC
                                |||||| || ||||| |||  ||
                                AGTGCA GG TTGTC AGG  CG
                                   _ _    C   GT
GAM1038  LOC219294 3'  GCTGGGATTAATGGCGTGA   93009     GT   TGAC    TG
                                TCAT  GCC   AGTCT  GC
                                ||||  |||   |||||  ||
                                AGTG  CGG   TTAGG  CG
                                  __  TAA_    GT
GAM1038  LOC219295 3'  GCTGGGACCTGTTGGACGTGA  92992      G  T   _  TG
                                TCATGT CC GACAG TCT  GC
                                |||||| || ||||| |||  ||
                                AGTGCA GG TTGTC AGG  CG
                                   _ _    C   GT
GAM1038  LOC219295 3'  GCTGGGATTAATGGCGTGA   92993     GT   TGAC    TG
                                TCAT  GCC   AGTCT  GC
                                ||||  |||   |||||  ||
                                AGTG  CGG   TTAGG  CG
                                  __  TAA_    GT
GAM1038  LOC219347 5'  GCCAGGATTTAATCACTGG   92984    T   CC   CA
                                TCA GTG  TGA  GTCTTGGC
                                ||| |||  |||  ||||||||
                                GGT CAC  ATT  TAGGACCG
                                  _  TA  __
GAM1038  LOC219347 5'  GTCGGGATTGTGCTTGCACG   92985     CTG_
                                TGTGC   ACAGTCTTGGC
                                |||||   ||||||||||
                                GCACG   TGTTAGGGCTG
                                   TTCG
GAM1038  LOC219401 5'  GCTGAGTGTAATGTACGTGG   92816       CTG   GT  TG
                                TCATGTGC   ACA  CT  GC
                                ||||||||   |||  ||  ||
                                GGTGCATG   TGT  GA  CG
                                     TAA   __  GT
GAM1038  LOC219513 5'  GCTGGGAGCCCGCGGGCGCGTG 94331         ACA _   TG
                                CATGTGCCTG   G TCT  GC
                                ||||||||||   | |||  ||
                                GTGCGCGGGC   C AGG  CG
                                      GCC G   GT
GAM1038  LOC219654 3'  GCCAGGGCTTCCCTGCACG   91306     CT_  C
                                TGTGC   GA AGTCTTGGC
                                |||||   || |||||||||
                                GCACG   CT TCGGGACCG
                                   TCC  _
GAM1038  LOC219673 5'  GCTAGGATTACAGGCAT    93032       AC
                                GTGCCTG  AGTCTTGGC
                                |||||||  |||||||||
```

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                                TACGGAC  TTAGGATCG
                                   A_
GAM1038  LOC219731 5' GCCACACTCGGGTATACGG   93095    A       CA  CT
                                TC TGTGCCTGA  GT  TGGC
                                || |||||||||  ||  ||||
                                GG ATATGGGCT  CA  ACCG
                                 C       __  C_
GAM1038  LOC219731 5' GCTGGGATGACAGGTGTGA   93096     GT    ACA    TG
                                TCAT  GCCTG   GTCT  GC
                                ||||  |||||   ||||  ||
                                AGTG  TGGAC   TAGG  CG
                                   __    AG_   GT
GAM1038  LOC219735 3' GTTGGGATTACAGGCAT     93113       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  TG
                                   A_    GT
GAM1038  LOC219894 3' GCTGGGATTATAGGTGTGA   93283     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAT  TTAGG  CG
                                   __    A_    GT
GAM1038  LOC219940 5' GTTGGGGCGACAGGTGGATGA  93357     G     ACA    TG
                                TCAT TGCCTG   GTCT  GC
                                |||| ||||||   ||||  ||
                                AGTA GTGGAC   CGGG  TG
                                   G     AG_   GT
GAM1038  LOC219942 3' GCCGGGACACGGGTGCACTGA  93346     _ TG    ACA
                                TCA TG  CCTG   GTCTTGGC
                                ||| ||  ||||   ||||||||
                                AGT AC  GGGC   CAGGGCCG
                                  C  GT   A__
GAM1038  LOC220021 5' GCTGGGGCTAGGACAGTGA   93397     GTG   GAC    TG
                                TCAT   CCT   AGTCT  GC
                                ||||   |||   |||||  ||
                                AGTG   GGA   TCGGG  CG
                                   ACA   ___    GT
GAM1038  LOC220058 3' GTCATGACACTGTGTGGGCATA 91728          _    CT__
            TGG                   CATGTGCCTG ACAGT    TGGC
                                |||||||||| |||||   ||||
                                GTATACGGGT TGTCA    ACTG
                                     G    CAGT
GAM1038  LOC220107 5' GCCGGGGCCCGGGCGCG     93468        ACA
                                TGTGCCTG   GTCTTGGC
                                ||||||||   ||||||||
                                GCGCGGGC   CGGGGCCG
                                     C__
GAM1038  LOC220110 5' GCCGAGGCGGGCCACGTGA   93464        _  GACA
                                TCATGTG CCT    GTCTTGGC
                                ||||||| |||    ||||||||
```

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                                AGTGCAC GGG    CGGAGCCG
                                    C  ____
GAM1038  LOC220164 3'  GTTAAGATTGTTATGTTGA   91798     TGT  C
                                TCA   GC TGACAGTCTTGGC
                                |||   || ||||||||||||||
                                AGT   TG ATTGTTAGAATTG
                                  ___  T
GAM1038  LOC220283 5'  GCCAAGAGCTTGGGCACTGG   94319     T    TG CAG
                                TCA GTGCC  A   TCTTGGC
                                ||| |||||  |   |||||||
                                GGT CACGG  T   AGAACCG
                                  _    GT CG_
GAM1038  LOC220565 3'  GTCAGGACTGGCTAACGCGGA  90752    A    CCTGA
                                TC TGTG    CAGTCTTGGC
                                || ||||    ||||||||||
                                AG GCGC    GTCAGGACTG
                                 _   AATCG
GAM1038  LOC220587 3'  GCCGGGCGCTCCTGGTGTGTGA 90764      TG  TGAC  _
                                TCATG  CC    AGT CTTGGC
                                |||||  ||    ||| ||||||
                                AGTGT  GG    TCG GGGCCG
                                   GT  TCC_   C
GAM1038  LOC220662 3'  GTTGGGATTACAGGCAT     91177       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  TG
                                    A_    GT
GAM1038  LOC220739 3'  GCTGGGACTGGATGTGCCGTGG 92932      T  CTGA_    TG
                                TCATG GC    CAGTCT  GC
                                ||||| ||    ||||||  ||
                                GGTGC CG    GTCAGG  CG
                                   _ TGTAG     GT
GAM1038  LOC220766 5'  CGAGATTTGGATATGA      90796       G  TGAC    TG
                                TCATGT CC    AGTCT  G
                                |||||| ||    |||||  |
                                AGTATA GG    TTAGA  C
                                    _ T___     GT
GAM1038  LOC220929 5'  GTCAAATCACTTCAGGTATGT  91404         C   C__
                                ATGTGCCTGA AGT   TTGGC
                                |||||||||| |||   |||||
                                TGTATGGACT TCA   AACTG
                                      _   CTA
GAM1038  LOC220992 5'  GCCGGGATTGACTTACGCAGGA 91469    A    CCTGA
                                TC TGTG    CAGTCTTGGC
                                || ||||    ||||||||||
                                AG ACGC    GTTAGGGCCG
                                 G   ATTCA
GAM1038  LOC221042 3'  GCCAAGGCTGGGCTCAT     93186     T   TGA
                                ATG GCC   CAGTCTTGGC
                                ||| |||   ||||||||||
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                                TAC CGG   GTCGGAACCG
                                  T  ___
GAM1038  LOC221042 3'  GCCGAGAACACCAGGCACACGG 93187    A       ACAG
                                TC TGTGCCTG    TCTTGGC
                                || ||||||||    |||||||
                                GG ACACGGAC    AGAGCCG
                                 C       CACA
GAM1038  LOC221060 3'  GCTGGGATTACAGGCAT     93212        AC     TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  LOC221078 5'  GCCGAGAAATAGGGGGCGCGTG 93203         GACAG_
                                CATGTGCCT     TCTTGGC
                                |||||||||     |||||||
                                GTGCGCGGG     AGAGCCG
                                     GGATAA
GAM1038  LOC221140 3'  GCCGGAGGGCATGCATGTGG   93489        C  ACAG   T
                                TCATGTGC TG    TCT GGC
                                |||||||| ||    ||| |||
                                GGTGTACG AC    AGG CCG
                                     T  GGG_  _
GAM1038  LOC221271 3'  GTTGAGATTACAGGCAT     91870        AC     TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGA  TG
                                    A_    GT
GAM1038  LOC221271 3'  GTTGAGGCCGGGTGCGGTGG   91871     _ TG    ACA    TG
                                TCAT G  CCTG   GTCT  GC
                                |||| |  ||||   ||||  ||
                                GGTG C  GGGC   CGGA  TG
                                  G GT    ___    GT
GAM1038  LOC221337 3'  GCCAAGCAGAATAGTATATGG  92110        CTGACA T
                                TCATGTGC     G CTTGGC
                                ||||||||     | ||||||
                                GGTATATG     C GAACCG
                                     ATAAGA _
GAM1038  LOC221466 5'  CGGGGTAGGCATTGG       93686     T     ACAG   TG
                                TCA GTGCCTG    TCT  G
                                ||| |||||||    |||  |
                                GGT TACGGAT    GGG  C
                                  _      _____   GT
GAM1038  LOC221491 5'  GTCGGGGTGGTGGTGGCTGTGG 92012       T   TG_  AG
                                TCATG GCC   AC  TCTTGGC
                                ||||| |||   ||  |||||||
                                GGTGT CGG   TG  GGGGCTG
                                   _  TGG  GT
GAM1038  LOC221495 3'  GTTAAGACTGTCAAATACTGG  93862     T   CC
                                TCA GTG  TGACAGTCTTGGC
                                ||| |||  |||||||||||||
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                                GGT CAT  ACTGTCAGAATTG
                                  _  AA
GAM1038  LOC221540 3'  GCTGAGATTACAGGTGTGA   93839     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGA  CG
                                  __    A_    GT
GAM1038  LOC221656 3'  GTTGAGACTCATTGGTACTGA  92230    T    TGAC    TG
                                TCA GTGCC    AGTCT  GC
                                ||| |||||    |||||  ||
                                AGT CATGG    TCAGA  TG
                                  _    TTAC    GT
GAM1038  LOC221663 5'  GCCAAGGCTGGAGTGCAGTGG  93816     G  _  GA
                                TCAT TGC CT  CAGTCTTGGC
                                |||| ||| ||  ||||||||||
                                GGTG ACG GA  GTCGGAACCG
                                  _  T  G_
GAM1038  LOC221663 5'  GCCGGGATTACAGGCAT     93817       AC
                                GTGCCTG  AGTCTTGGC
                                |||||||  |||||||||
                                TACGGAC  TTAGGGCCG
                                   A_
GAM1038  LOC221692 3'  GCTCGGTGTTGGGTGGTGG   92241     G   TG  GT  T
                                TCAT TGCC  ACA  CT GGC
                                |||| ||||  |||  || |||
                                GGTG GTGG  TGT  GG TCG
                                  _   GT  __  C
GAM1038  LOC221747 3'  GCCAAATGAGGACAGGCGCATG 92355          ACAGTC_
            A                   TCATGTGCCTG      TTGGC
                                ||||||||||       |||||
                                AGTACGCGGAC      AACCG
                                      AGGAGTA
GAM1038  LOC221760 5'  GCCAGCCTTATGCATGTGG   93787       C  CA  CT
                                TCATGTGC TGA  GT  TGGC
                                |||||||| |||  ||  ||||
                                GGTGTACG ATT  CG  ACCG
                                   T  C_  __   A
GAM1038  LOC221773 3'  GCTGGGATTACAGGTGTGA   91049     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC221814 5'  GCTGTGTTTGGGTATATG    93944         ___
                                CATGTGCCTG   ACAGT
                                ||||||||||   |||||
                                GTATATGGGT   TGTCG
                                      TTG
GAM1038  LOC221935 3'  GCCAGGATGTGAGCACTGG   92622     T   C G   G
                                TCA GTGC T ACA TCTTGGC
                                ||| |||| | ||| |||||||
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                                GGT CACG A TGT AGGACCG
                                  _   _ G  _
GAM1038  LOC222057 3'  CCAAGATCATGCCGTGA     92768      T  C   CAG
                                TCATG GC TGA   TCTTGG
                                ||||| || |||   ||||||
                                AGTGC CG ACT   AGAACC
                                  _ T  ____
GAM1038  LOC222060 5'  GCCAAGGCTGTCCCCGCAATGG 94108      G   CT_
                                TCAT TGC   GACAGTCTTGGC
                                |||| |||   ||||||||||||
                                GGTA ACG   CTGTCGGAACCG
                                  _  CCC
GAM1038  LOC222070 5'  AAGGCTGTTAGCATATGG    94143        C
                                TCATGTGC TGACAGTCTT
                                |||||||| ||||||||||
                                GGTATACG ATTGTCGGAA
                                  _
GAM1038  LOC222070 5'  GCTGGGATTACAGGCGTGA   94157     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC222134 3'  GTCACATGGTCAGGCACAT   94142          AGTCT
                                ATGTGCCTGAC    TGGC
                                ||||||||||    ||||
                                TACACGGACTG    ACTG
                                     GTAC_
GAM1038  LOC222178 3'  TCGAGATGCCGACGTGA     94174       GCC  ACA
                                TCATGT   TG   GTCTTGG
                                ||||||   ||   |||||||
                                AGTGCA   GC   TAGAGCT
                                   ____  CG_
GAM1038  LOC222224 5'  GCTGGGATTATAGGTGTGTG   94200     TG    AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGT  GGAT  TTAGG  CG
                                  GT   A_    GT
GAM1038  LOC222225 3'  GCCACCTGCGGGTGCGTGG    94306      TG   A   TCT
                                TCATG  CCTG CAG   TGGC
                                |||||  |||| |||   ||||
                                GGTGC  GGGC GTC   ACCG
                                  GT   _  C__
GAM1038  LOC222510 5'  GCCGGGATAATAAGGTCTGTGG 94350     GT    GACA
                                TCAT  GCCT    GTCTTGGC
                                ||||  ||||    ||||||||
                                GGTG  TGGA    TAGGGCCG
                                  TC    ATAA
GAM1038  LOC222962 5'  GCTGGGGGAGCGGGGCGGCGTG 92873       _   GACAG   TG
            G                   TCATGT GCCT    TCT  GC
                                ||||||  ||||    |||  ||
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                                GGTGCG CGGG    GGG  CG
                                   G   GCGAG   GT
GAM1038  LOC245771 5' GCTGGGATTACAGGCAT    92895       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC253019 3' CCTTGTTGGGAATATGG    95366      G  TG   TCTT
                                TCATGT CC  ACAG   GG
                                ||||||  ||  ||||   ||
                                GGTATA GG  TGTT   CC
                                   A  GT   ____
GAM1038  LOC253196 3' CCAGGACAGCAAGTGG     96882     G   CTGACA
                                TCAT TGC     GTCTTGG
                                ||||  |||     |||||||
                                GGTG ACG     CAGGACC
                                  A  A_____
GAM1038  LOC253219 3' GCCGGGACTGCAGCCAGGTGG  97485     G  C   A
                                TCAT TG CTG CAGTCTTGGC
                                ||||  ||  |||  ||||||||||
                                GGTG AC GAC GTCAGGGCCG
                                  G  C  _
GAM1038  LOC253219 5' GCCGGGACTGCAGCCAGGTGG  97486     G  C   A
                                TCAT TG CTG CAGTCTTGGC
                                ||||  ||  |||  ||||||||||
                                GGTG AC GAC GTCAGGGCCG
                                  G  C  _
GAM1038  LOC253292 5' GTCAGGGCTGTTGGAGACAGA  96992    A   GC TG
                                TC TGT  C  ACAGTCTTGGC
                                ||  |||  |  ||||||||||
                                AG ACA  G  TGTCGGGACTG
                                 _  GA GT
GAM1038  LOC253405 5' GTCAAGGGAACGGGTGTGG   97503     GT    ACAG
                                TCAT  GCCTG   TCTTGGC
                                ||||  |||||   |||||||
                                GGTG  TGGGC   GGAACTG
                                  __    AAG_
GAM1038  LOC253634 5' GCCAAGGTTGAGGACGCGCGCG 96617       C  A___  GT
            TGA                   CATGTGC TG   CA  CTTGGC
                                |||||||  ||   ||  ||||||
                                GTGCGCG GC   GT  GAACCG
                                   C  AGGA  TG
GAM1038  LOC253666 5' GCTGGGATTACAGGTAT    95066       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TATGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC253681 3' GTCGGGACTCTCCTGCACCTGA 95133     T   CT  C
                                TCA GTGC  GA AGTCTTGGC
                                |||  ||||  ||  |||||||||
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                                AGT CACG  CT TCAGGGCTG
                                  C   TC  C
GAM1038  LOC253737 5'  GCTGGTCAAGCACGTGA     96240        C   _
                                TCATGTGC TGAC AGT
                                |||||||| |||| |||
                                AGTGCACG ACTG TCG
                                     A   G
GAM1038  LOC253778 3'  GCTGGGATTACAGGCGTGA   94873     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC253778 5'  GCTGGGCATGGTGGCATGTGG 94874        TGA  GT  TG
                                TCATGTGCC   CA  CT  GC
                                |||||||||   ||  ||  ||
                                GGTGTACGG   GT  GG  CG
                                     TG_  AC  GT
GAM1038  LOC253782 3'  GCCAAGATTTCTTCAATGG   95696     G  CCT  C
                                TCAT TG   GA AGTCTTGGC
                                |||| ||   || |||||||||
                                GGTA AC   CT TTAGAACCG
                                  _ TT_ _
GAM1038  LOC253805 5'  GCCAGGGTGGGGTGAGTGG   96431     G    G  AGT
                                TCAT TGCCT AC   CTTGGC
                                |||| ||||| ||   ||||||
                                GGTG GTGGG TG   GGACCG
                                  A    G ___
GAM1038  LOC253832 3'  AGGATTATCAGGCATGTGA   94920          C
                                TCATGTGCCTGA AGTCTT
                                |||||||||||| ||||||
                                AGTGTACGGACT TTAGGA
                                       A
GAM1038  LOC253836 5'  CCTGGTCAGGCACGGA     97630    A        AGTCTT
                                TC TGTGCCTGAC     GG
                                || ||||||||||     ||
                                AG GCACGGACTG     CC
                                 _        GT____
GAM1038  LOC253842 5'  GCTGGGATTACAGGCGTGA   97390     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC253975 3'  CCTTGTTGGGAATATGG     95995      G  TG   TCTT
                                TCATGT CC  ACAG   GG
                                |||||| ||  ||||   ||
                                GGTATA GG  TGTT   CC
                                   A  GT   _____
GAM1038  LOC254018 5'  GTTGGGATTACAGGCGTGA   96969     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
```

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                                AGTG  CGGAC  TTAGG  TG
                                  __    A_    GT
GAM1038  LOC254065 5'  CCAGGACTTTCAATGA     97426     GTGCC   C
                                TCAT    TGA AGTCTTGG
                                ||||    ||| ||||||||
                                AGTA    ACT TCAGGACC
                                  _____  T
GAM1038  LOC254173 3'  GCCAAGACCCGGAGCATGG   96843      GC   ACA
                                TCATGT  CTG   GTCTTGGC
                                ||||||  |||   ||||||||
                                GGTACG  GGC   CAGAACCG
                                   A_   C__
GAM1038  LOC254182 5'  GCCACCTGATTGGAGCACATGG 96036       _ TG _   TCT
                                TCATGTGC C  A CAG   TGGC
                                ||||||||  |  | |||   ||||
                                GGTACACG G  T GTC   ACCG
                                    A GT A   C__
GAM1038  LOC254228 3'  GTTAAGATTTCAACATATGA   95956      CC   C
                                TCATGTG  TGA AGTCTTGGC
                                |||||||  ||| |||||||||
                                AGTATAC  ACT TTAGAATTG
                                   A_   _
GAM1038  LOC254243 3'  GCCAGGACAGTGGTGCATG   97413     TG  TG  A
                                CATG  CC  AC GTCTTGGC
                                ||||  ||  || ||||||||
                                GTAC  GG  TG CAGGACCG
                                  GT  __  A
GAM1038  LOC254243 3'  GCTGGGATTACAGGCATGTG   97414        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTACGGAC  TTAGG  CG
                                     A_    GT
GAM1038  LOC254268 3'  GCTGAGATTACAGGTGCATG   95411     TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTAC  GGAC  TTAGA  CG
                                  GT   A_    GT
GAM1038  LOC254268 3'  GTTGGGATTACAGGCAT     95413       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  TG
                                   A_    GT
GAM1038  LOC254351 3'  GCTGGGATTGCAGGCGTGA   94996     GT    A     TG
                                TCAT  GCCTG CAGTCT  GC
                                ||||  ||||| ||||||  ||
                                AGTG  CGGAC GTTAGG  CG
                                  __    _     GT
GAM1038  LOC254351 5'  GCTGGGATTGCAGGCGTGA   94997     GT    A     TG
                                TCAT  GCCTG CAGTCT  GC
                                ||||  ||||| ||||||  ||
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                                AGTG  CGGAC GTTAGG  CG
                                  __    _     GT
GAM1038  LOC254381 5'  GCCCCCGGCTCGGGCACGTGG  97461          CA   TT_
                                TCATGTGCCTGA  GTC   GGC
                                ||||||||||||  |||   |||
                                GGTGCACGGGCT  CGG   CCG
                                      __  CCC
GAM1038  LOC254532 5'  GCTGGGATTACAGGCGTGA   96638     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC254552 5'  GCCGAATTTGGGTATCTGA   94775     T    TG CAGTC
                                TCA GTGCC  A    TTGGC
                                ||| |||||  |    |||||
                                AGT TATGG  T    AGCCG
                                  C    GT TA___
GAM1038  LOC254655 3'  GCTGGGATTACAGGCGTGA   95473     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC254778 3'  GCTGGGATGACAGGCACATG   96129         ACA   TG
                                CATGTGCCTG   GTCT  GC
                                ||||||||||   ||||  ||
                                GTACACGGAC   TAGG  CG
                                     AG_   GT
GAM1038  LOC254806 5'  GTTAAGACGAAAGGTACTGA   95785     T     GACA
                                TCA GTGCCT    GTCTTGGC
                                ||| ||||||    ||||||||
                                AGT CATGGA    CAGAATTG
                                  _     AAG_
GAM1038  LOC254942 5'  GCTGGGGCCGGGGCGCTGA   97454     T     GACA    TG
                                TCA GTGCCT    GTCT  GC
                                ||| ||||||    ||||  ||
                                AGT CGCGGG    CGGG  CG
                                  _     GC__    GT
GAM1038  LOC255017 3'  GCTGAACCTGACAGGCGTGTGG 94625     TG     A   TC TG
                                TCA  TGCCTG CAG  T  GC
                                |||  |||||| |||  |  ||
                                GGT  GCGGAC GTC  A  CG
                                  GT     A   CA GT
GAM1038  LOC255196 5'  GCTGAGATTACAGGTGTGA   97171     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGA  CG
                                  __    A_    GT
GAM1038  LOC255196 5'  GCTGGGACTACCTGTAGGTGCG 97172      TG    AC___    TG
            TG                  CATG  CCTG    AGTCT  GC
                                ||||  ||||    |||||  ||
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                                GTGC  GGAT    TCAGG  CG
                                  GT    GTCCA    GT
GAM1038  LOC255308 3'  GCCGGGATTACAGGCGTGA   94537     GT    AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  CGGAC  TTAGGGCCG
                                  __    A_
GAM1038  LOC255308 3'  GCTGAGATTACAGGTGTGTG   94538     TG    AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGT  GGAC  TTAGA  CG
                                  GT    A_    GT
GAM1038  LOC255328 3'  GCCAGGGCTGTGGGCCTGA   96560    TGT    G
                                TCA   GCCT ACAGTCTTGGC
                                |||   |||| ||||||||||
                                AGT   CGGG TGTCGGGACCG
                                  C__    _
GAM1038  LOC255452 3'  ACTCAACTGTGGGCACATGA   97522         G     CTTGGC
                                TCATGTGCCT ACAGT
                                |||||||||| |||||
                                AGTACACGGG TGTCA
                                      _    ACTCAG
GAM1038  LOC255463 3'  TAAGTTGTCAGTCATATGA   94884       C      T
                                TCATGTG CTGACAG CTTG
                                ||||||| ||||||| ||||
                                AGTATAC GACTGTT GAAT
                                    T     _
GAM1038  LOC255465 3'  GCTGGGACTATAGGCACGTG   97294         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGCACGGAT  TCAGG  CG
                                      A_    GT
GAM1038  LOC255465 3'  GCTGGGATTACAGGCGTGA   97295     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC255527 5'  GCCAGGGTCCCGCACACTGG   96853     _    CT   AGT
                                TCA TGTGC  GAC   CTTGGC
                                ||| |||||  |||   ||||||
                                GGT ACACG  CTG   GGACCG
                                  C    CC  ___
GAM1038  LOC255696 5'  CCAGGACTGAAGCACG      97499      CTGA
                                TGTGC    CAGTCTTGG
                                |||||    |||||||||
                                GCACG    GTCAGGACC
                                   AA__
GAM1038  LOC255707 3'  GCTGGGACTACAGGTGCATG   96960     TG    AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
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                                GTAC  GGAC  TCAGG  CG
                                  GT   A_    GT
GAM1038  LOC255707 3'  GCTGGGATTACAGGCGTGA   96961     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC255919 3'  GCTGGGACTACAGGCGCATG   95037         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTACGCGGAC  TCAGG  CG
                                      A_    GT
GAM1038  LOC255926 3'  GTCGGGACTGAGCAGGCAATGG 96123      G     A_
                                TCAT TGCCTG  CAGTCTTGGC
                                |||| ||||||  ||||||||||
                                GGTA ACGGAC  GTCAGGGCTG
                                  _     GA
GAM1038  LOC255981 3'  GCTGGGATTACAGGCAT     97133       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  LOC256158 5'  CGGGCCAGGACATGG       97661       G    ACA T  TG
                                TCATGT CCTG   G CT  G
                                |||||| ||||   | ||  |
                                GGTACA GGAC   C GG  C
                                  _   ____ _  GT
GAM1038  LOC256158 5'  GCTAGACTGTGTGGTGCGTGG  97670      TG  TG     T
                                TCATG  CC  ACAGTCT GGC
                                |||||  ||  ||||||| |||
                                GGTGC  GG  TGTCAGA TCG
                                   GT  TG     _
GAM1038  LOC256158 5'  GCTAGGATTGGCCGGTGCAGA  97671    A  TG  TGA
                                TC TG  CC   CAGTCTTGGC
                                || ||  ||   ||||||||||
                                AG AC  GG   GTTAGGATCG
                                 _ GT  CCG
GAM1038  LOC256158 5'  GTCAGGACCACCTGCAGTGA   97678     G   CTGACA
                                TCAT TGC     GTCTTGGC
                                |||| |||     ||||||||
                                AGTG ACG     CAGGACTG
                                  _   TCCAC_
GAM1038  LOC256221 3'  GCTGGGATTACAGGCGTGA   95211     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC256222 5'  GCTGAGATGACAGGCCTGTGG  97223      T    ACA   TG
                                TCATG GCCTG   GTCT  GC
                                ||||| |||||   ||||  ||
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                                GGTGT CGGAC   TAGA  CG
                                   C    AG_   GT
GAM1038  LOC256306 3'  GTTGGGATTACAGGCGTGA   96696     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                |||| ||||| ||||| ||
                                AGTG  CGGAC  TTAGG  TG
                                  __    A_    GT
GAM1038  LOC256337 3'  GCCAGGAGGCCAAGGCTGTGA  94695      T   GACAG
                                TCATG GCCT    TCTTGGC
                                ||||| ||||    |||||||
                                AGTGT CGGA    AGGACCG
                                   _   ACCGG
GAM1038  LOC256364 5'  GCTGGGATTACAGGCAT    94801       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038  LOC256447 5'  GCCGTCAGGCACTGA      95269     T       A
                                TCA GTGCCTGAC GT
                                ||| |||||||| ||
                                AGT CACGGACTG CG
                                  _       C
GAM1038  LOC256471 5'  GCTGAGGCCCCCGTAGGCGCA  95837        ACA__   TG
                                TGTGCCTG    GTCT  GC
                                ||||||||    ||||  ||
                                ACGCGGAT    CGGA  CG
                                     GCCCC   GT
GAM1038  LOC256471 5'  GTCGCGAGAGTTGGGCGCAAGA 95838    A     TG  AG  T
                                TC TGTGCC  AC  TC TGGC
                                || ||||||  ||  || ||||
                                AG ACGCGG  TG  AG GCTG
                                 A     GT  AG  C
GAM1038  LOC256530 5'  GCTGGAATAGGACATGA     96814       G   A__
                                TCATGT CCTG   CAGT
                                |||||| ||||   ||||
                                AGTACA GGAT   GTCG
                                   _   AAG
GAM1038  LOC256741 3'  GTTAAACCGCAGGGCGCATGG  96778         GACA  C
                                TCATGTGCCT    GT TTGGC
                                ||||||||||    || |||||
                                GGTACGCGGG    CA AATTG
                                      ACGC  _
GAM1038  LOC256790 5'  GCCAGGGCTGGAGCTGTGTG   94834    TG GC  GA
                                CA  T  CT  CAGTCTTGGC
                                ||  |  ||  ||||||||||
                                GT  G  GA  GTCGGGACCG
                                 GT TC  G_
GAM1038  LOC257000 3'  CCGAGGCTACGCATG       96782       CCTGAC
                                CATGTG     AGTCTTGG
                                ||||||     ||||||||
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                                GTACGC     TCGGAGCC
                                   A_____
GAM1038  LOC257017 5'  GCTGGGATTACAGGCAT     97375        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC257115 3'  GTCACACCTCATGCACATGA   96525         C   CA  CT
                                TCATGTGC TGA  GT  TGGC
                                |||||||| |||  ||  ||||
                                AGTACACG ACT  CA  ACTG
                                     T  C_  C_
GAM1038  LOC257127 5'  GCTGGGATTACAGGTGTGA    96672     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC257282 5'  GCCAAGACTGTCATTGCCTGTG 96400      T  C_
                                CATG GC  TGACAGTCTTGGC
                                |||| ||  ||||||||||||
                                GTGT CG  ACTGTCAGAACCG
                                  C  TT
GAM1038  LOC257354 3'  GTTGGTGTTTGGGCACCTGG   95097     T    TG _  GTC TG
                                TCA GTGCC  A CA   T  GC
                                ||| |||||  | ||   |  ||
                                GGT CACGG  T GT   G  TG
                                  C    GT T  ___ GT
GAM1038  LOC257364 3'  GCTGGGCACCCAGGGCTGTGA  94967      T   GACA  _  TG
                                TCATG GCCT    GT CT  GC
                                ||||| ||||    || ||  ||
                                AGTGT CGGG    CA GG  CG
                                   _    ACC_  C  GT
GAM1038  LOC257441 5'  GTTGAGACAGCGGCGGTACTGG 95565     T    __  ACA    TG
                                TCA GTGCC  TG   GTCT  GC
                                ||| |||||  ||   ||||  ||
                                GGT CATGG  GC   CAGA  TG
                                  _    CG  GA_    GT
GAM1038  LOC257465 3'  GCTGGGATTACAGGCAT     81596        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038  LOC257465 3'  GCTGGGATTACAGGCGCGTG   81597         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGCGCGGAC  TTAGG  CG
                                     A_    GT
GAM1038  LOC257486 3'  GCTGGGATTACAGGCGTGA    69249     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC257545 3'  GCTGAGATTACAGGTGTGA   97807     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGA  CG
                                  __    A_    GT
GAM1038  LOC257598 3'  GCTGAGATTACAGGTGTGA   97922     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAC  TTAGA  CG
                                  __    A_    GT
GAM1038  LOC257618 5'  GCTGGGGCTGCGTAATCTGG  97855     T  GCC  A     TG
                                TCA GT   TG CAGTCT  GC
                                |||  ||   ||  ||||||  ||
                                GGT TA   GC GTCGGG  CG
                                  C  AT_  _     GT
GAM1038  LOC51008  3'  GCTGAGATGGTGGTGGGCATA  31966       GA  __   TG
                                TGTGCCT  CA  GTCT  GC
                                |||||||  ||  ||||  ||
                                ATACGGG  GT  TAGA  CG
                                    TG  GG   GT
GAM1038  LOC51008  5'  GCTGGGATTACAGGCGTGA   31967     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038  LOC51014  5'  GCTGAGGCCTGCCGCGCGCG  65850      C  A  _  TG
                                TGTGC TG CAG TCT  GC
                                |||||  ||  |||  |||  ||
                                GCGCG GC GTC GGA  CG
                                   C  C   C   GT
GAM1038  LOC51027  5'  GCCGAGGCTGAGCGGCA     59365     TGA
                                TGCC   CAGTCTTGGC
                                ||||   ||||||||||
                                ACGG   GTCGGAGCCG
                                  CGA
GAM1038  LOC51030  3'  GTTGGGGCTAGAAAGTATGTG  32185       CTGAC    TG
                                CATGTGC    AGTCT  GC
                                |||||||    |||||  ||
                                GTGTATG    TCGGG  TG
                                    AAAGA    GT
GAM1038  LOC51087  5'  GCCGGGGCGGTGGCGGCTGTGG 32012      T   TG_  A
                                TCATG GCC   AC GTCTTGGC
                                |||||  |||   ||  ||||||||
                                GGTGT CGG   TG CGGGGCCG
                                  _  CGG  G
GAM1038  LOC51193  3'  GCTAGGACTACAGGCATGTGG  32909         AC
                                TCATGTGCCTG  AGTCTTGGC
                                ||||||||||  |||||||||
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                                GGTGTACGGAC  TCAGGATCG
                                      A_
GAM1038 LOC51193 5' GCTGGGATTACAGGCGTGA   32910     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 LOC51195 3' GCCAGATCCTTGGGCACCTGG 32944    T    TG CA    T
                                TCA GTGCC  A  GTCT GGC
                                ||| |||||  |  |||| |||
                                GGT CACGG  T  TAGA CCG
                                  C    GT CC   _
GAM1038 LOC51219 5' GCTGGGATTACAGGCAT     33123       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038 LOC51337 3' GCCGGGGCTAGAGGCAGATGG 33587     G    GAC
                                TCAT TGCCT   AGTCTTGGC
                                |||| |||||   |||||||||
                                GGTA ACGGA   TCGGGGCCG
                                  G    GA_
GAM1038 LOC51647 5' GCTAGGATCAGCGGTGGTGG  32158     G    T ACA
                                TCAT TGCC G   GTCTTGGC
                                |||| |||| |   ||||||||
                                GGTG GTGG C   TAGGATCG
                                  _   _ GAC
GAM1038 LOC51652 3' GCTATGGCCAGGCATATGG   32193         ACA   T
                                TCATGTGCCTG   GTC TGGC
                                ||||||||||   ||| ||||
                                GGTATACGGAC   CGG ATCG
                                      ___   T
GAM1038 LOC51667 3' CCAGGGTGCCACATGG      32271       CCTGA  G
                                TCATGTG    CA TCTTGG
                                |||||||    || ||||||
                                GGTACAC    GT GGGACC
                                    C____  _
GAM1038 LOC51696 5' GCCAGGATGGCGCGGCACG   32548      _  ACA
                                TGTGCC TG   GTCTTGGC
                                |||||| ||   ||||||||
                                GCACGG GC   TAGGACCG
                                   C  GG_
GAM1038 LOC51696 3' GCTGGGACTATAGGCACGTG  32552         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGCACGGAT  TCAGG  CG
                                      A_    GT
GAM1038 LOC51696 3' GCTGGGATTACAGGCGTGA   32553     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
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                              AGTG  CGGAC  TTAGG  CG
                                __    A_    GT
GAM1038 LOC51716 3' CCATGTTGGGCAGTGA     32788     G   TG  GTCT
                              TCAT TGCC  ACA   TGG
                              |||| ||||  |||   |||
                              AGTG ACGG  TGT   ACC
                                _   GT  ____
GAM1038 LOC51716 3' GCTGGGACTCCAGCTCATGG  32793      T  C  AC    TG
                              TCATG GC TG  AGTCT  GC
                              ||||| || ||  |||||  ||
                              GGTAC CG AC  TCAGG  CG
                                 T  _  C_    GT
GAM1038 LOC54103 5' GCCAGACACGGGCATGTG    94213         ACA   T
                              CATGTGCCTG   GTCT GGC
                              ||||||||||   |||| |||
                              GTGTACGGGC   CAGA CCG
                                    A__    _
GAM1038 LOC54518 5' TCGAGGCTGCAAAATGG     38773     GTGCC  A
                              TCAT    TG CAGTCTTGG
                              ||||    || |||||||||
                              GGTA    AC GTCGGAGCT
                                AA___  _
GAM1038 LOC55893 5' GCCAGGCTACCAGGCGCG    37861        AC    T
                              TGTGCCTG  AGTCT GGC
                              ||||||||  ||||| |||
                              GCGCGGAC  TCGGA CCG
                                   CA    _
GAM1038 LOC56181 5' GCTGGGATTACAGATGTGA   95539      GC  AC    TG
                              TCATGT  CTG  AGTCT  GC
                              ||||||  |||  |||||  ||
                              AGTGTA  GAC  TTAGG  CG
                                 __   A_    GT
GAM1038 LOC56270 3' GTCACACCTCAGGCGTGTG   39022    TG     CA  CT
                              CA  TGCCTGA  GT  TGGC
                              ||  |||||||  ||  ||||
                              GT  GCGGACT  CA  ACTG
                               GT      C_  C_
GAM1038 LOC56963 3' GCCAAGGGCTCAGGCACGGA  71456    A       CAG
                              TC TGTGCCTGA   TCTTGGC
                              || |||||||||   |||||||
                              AG GCACGGACT   GGAACCG
                               _       CG_
GAM1038 LOC57107 3' GCCAGGGCGGTGGCCTGTGG  39836      T  TG  A
                              TCATG GCC  AC GTCTTGGC
                              ||||| |||  || ||||||||
                              GGTGT CGG  TG CGGGACCG
                                 C  __  G
GAM1038 LOC57146 3' GCTGGGATTACAGGCGTGA   39925     GT    AC    TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
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                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 LOC57805 3' GCTGGGGGCTGTGCTATGTGG 40988      _ CTG    _ TG
                                TCATGT GC   ACAGTC T  GC
                                |||||| ||   |||||| |  ||
                                GGTGTA CG   TGTCGG G  CG
                                   T ____     G GT
GAM1038 LOC81034 3' GCTGGGATTACAGGCGTGA   47856     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 LOC85414 5' GCCAGGATCTGAGTGATGA   52397     G   CTGA  _
                                TCAT TGC    CAG TCTTGGC
                                |||| |||    ||| |||||||
                                AGTA GTG    GTC AGGACCG
                                  _   A___   T
GAM1038 LOC89894 5' GCTGGGACTGAAGTCCCTATGA 60604      TGC_  GA     TG
                                TCATG    CT  CAGTCT  GC
                                |||||    ||  ||||||  ||
                                AGTAT    GA  GTCAGG  CG
                                   CCCT  A_     GT
GAM1038 LOC89919 5' GTTAGGACTTCAACAAATGA  60728     G  CC   C
                                TCAT TG  TGA AGTCTTGGC
                                |||| ||  ||| |||||||||
                                AGTA AC  ACT TCAGGATTG
                                  A  A_  _
GAM1038 LOC89932 3' GCTGGGATTACAGGCAT     60808       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038 LOC89932 3' GCTGGGATTACAGGTATGTG  60809         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTATGGAC  TTAGG  CG
                                     A_    GT
GAM1038 LOC89932 3' GCTGGGATTAGAGGTGTGA   60810     GT   GAC    TG
                                TCAT  GCCT   AGTCT  GC
                                ||||  ||||   |||||  ||
                                AGTG  TGGA   TTAGG  CG
                                  __    GA_    GT
GAM1038 LOC89941 3' GCCGGGGAGCACAGGTGTGGGA 57060    AT TG    ACAG
                                TC  G  CCTG    TCTTGGC
                                ||  |  ||||    |||||||
                                AG  T  GGAC    GGGGCCG
                                 GG GT    ACGA
GAM1038 LOC89944 3' CGCCGAGGCTGTCGGGC     91545
                                GCCTGACAGTCTTGGC   G
                                ||||||||||||||||  |
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                              CGGGCTGTCGGAGCCG  C

GAM1038 LOC90019 5' GCTGAGTCAGTGTGTGTGG  56764     TG _   AGTC TG
                              TCATG  C CTGAC   T  GC
                              |||||  | |||||   |  ||
                              GGTGT  G GACTG   A  CG
                                 GT T    ____ GT
GAM1038 LOC90038 3' GCCAGGACAGTGGTGCATG  61156     TG  TG  A
                              CATG  CC  AC GTCTTGGC
                              ||||  ||  || ||||||||
                              GTAC  GG  TG CAGGACCG
                                GT  __  A
GAM1038 LOC90038 3' GCTGGGATTACAGGCATGTG  61157        AC    TG
                              CATGTGCCTG  AGTCT  GC
                              ||||||||||  |||||  ||
                              GTGTACGGAC  TTAGG  CG
                                    A_    GT
GAM1038 LOC90072 3' GTTAGGATTACAGGCGTGA  61303     GT    AC
                              TCAT  GCCTG  AGTCTTGGC
                              ||||  |||||  |||||||||
                              AGTG  CGGAC  TTAGGATTG
                                __    A_
GAM1038 LOC90092 3' GCCAGGGCGACGGTGCAAGA  61407    A  TG  TGACA
                              TC TG  CC    GTCTTGGC
                              || ||  ||    ||||||||
                              AG AC  GG    CGGGACCG
                               A  GT  CAG__
GAM1038 LOC90119 5' GTCGAGGTTGGGTCAGGTA  61531       AG__
                              TGCCTGAC   TCTTGGC
                              ||||||||   |||||||
                              ATGGACTG   GGAGCTG
                                   GGTT
GAM1038 LOC90120 5' GCTGAGACTTCTGTGATGG  61538     G  CT  C    TG
                              TCAT TGC  GA AGTCT  GC
                              |||| |||  || |||||  ||
                              GGTA GTG  CT TCAGA  CG
                                _  T_  _    GT
GAM1038 LOC90120 5' GCTGGGCCGCCGGCGCGTGG  61539        TGACA T  TG
                              TCATGTGCC    G CT  GC
                              |||||||||    | ||  ||
                              GGTGCGCGG    C GG  CG
                                   CCGC_ _  GT
GAM1038 LOC90133 3' GCTGAGGCTGAGAGCACGT  61605      _  GA    TG
                              ATGTGC CT  CAGTCT  GC
                              ||||||  ||  ||||||  ||
                              TGCACG GA  GTCGGA  CG
                                 A  __     GT
GAM1038 LOC90268 5' GCCGAGACGCCGGCGCGGGA  61964    A     TGACA
                              TC TGTGCC    GTCTTGGC
                              || ||||||    ||||||||
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                                AG GCGCGG    CAGAGCCG
                                 G     CCG__
GAM1038 LOC90288 3' GCTGGGACTACAGGCACGTG  62098        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGCACGGAC  TCAGG  CG
                                      A_    GT
GAM1038 LOC90288 3' GCTGGGATTACTGGCGTGA   62099     GT   TGAC    TG
                                TCAT  GCC    AGTCT  GC
                                ||||  |||    |||||  ||
                                AGTG  CGG    TTAGG  CG
                                  __   TCA_    GT
GAM1038 LOC90333 5' AAGACTGTTGGTACGTGA    62274        T
                                TCATGTGCC GACAGTCTT
                                ||||||||| |||||||||
                                AGTGCATGG TTGTCAGAA

                                      _
GAM1038 LOC90342 5' GCCGAGATGGTGAGTGTATGA 62358      TG C G  A
                                TCATG  C T AC GTCTTGGC
                                |||||  | | || ||||||||
                                AGTAT  G A TG TAGAGCCG
                                   GT _ G  G
GAM1038 LOC90342 5' GCCGGCGCTGGGCGCGTG    62359        TGA   C
                                CATGTGCC   CAGT TTGGC
                                ||||||||   |||| |||||
                                GTGCGCGG   GTCG GGCCG
                                     ____    C
GAM1038 LOC90371 5' GCCAAGGTTTTTGCACTGG    62499    T   CT  C GT
                                TCA GTGC  GA A  CTTGGC
                                ||| ||||  || |  ||||||
                                GGT CACG  TT T  GAACCG
                                  _    __  T TG
GAM1038 LOC90459 3' GCCAGGATGGAGTGCAGTGG   62888     G  _  GACA
                                TCAT TGC CT    GTCTTGGC
                                |||| ||| ||    ||||||||
                                GGTG ACG GA    TAGGACCG
                                  _   T  GG__
GAM1038 LOC90485 3' GCCAAGGCCTTCGCGCAGA    63019    A    CT  CA
                                TC TGTGC  GA  GTCTTGGC
                                || |||||  ||  ||||||||
                                AG ACGCG  CT  CGGAACCG
                                 _    __  TC
GAM1038 LOC90485 3' GCTGGGATTACAGGCAT     63021        AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                    A_    GT
GAM1038 LOC90509 3' GCTAAGACTTTCACTATGTGA 63105       CC   C
                                TCATGTG  TGA AGTCTTGGC
                                |||||||  ||| |||||||||
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                                AGTGTAT  ACT TCAGAATCG
                                   C_  T
GAM1038 LOC90529 5' GAATGTTAGGCCTGTGG    63162     T      G
                                TCATG GCCTGACA TC
                                ||||| |||||||| ||
                                GGTGT CGGATTGT AG
                                   C       A
GAM1038 LOC90538 3' TCAGGACTGAAACATG     63194     GCCTGA
                                CATGT    CAGTCTTGG
                                |||||    |||||||||
                                GTACA    GTCAGGACT
                                   AA____
GAM1038 LOC90591 3' GCTGAGGCTGAGAACAGTGG  63435    _  GC  GA    TG
                                TCA TGT  CT  CAGTCT  GC
                                ||| |||  ||  ||||||  ||
                                GGT ACA  GA  GTCGGA  CG
                                  G  A_  __    GT
GAM1038 LOC90591 3' GCTGGGATTACAGGTAT    63436      AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TATGGAC  TTAGG  CG
                                   A_    GT
GAM1038 LOC90625 3' CCAATTGTTGGGTATGCGG  63609   AT    TG    CT  C
                                TC  GTGCC  ACAGT  TGG
                                ||  |||||  |||||  |||
                                GG  TATGG  TGTTA  ACC
                                 CG    GT    __  T
GAM1038 LOC90750 3' TTAAGATTGCTGCATA     63926     CTGA
                                TGTGC    CAGTCTTGG
                                |||||    |||||||||
                                ATACG    GTTAGAATT
                                   TC__
GAM1038 LOC90826 5' CCGGGGGTGGCGCTGG     64090     T    TGAC G
                                TCA GTGCC    A TCTTGG
                                ||| |||||    | ||||||
                                GGT CGCGG    T GGGGCC
                                  _    ____ G
GAM1038 LOC90841 5' GCTAAGATGGCAGTCTGTGG  64199     GT  C  ACA
                                TCAT  GC TG   GTCTTGGC
                                ||||  || ||   ||||||||
                                GGTG  TG AC   TAGAATCG
                                   TC  _  GG_
GAM1038 LOC90841 5' GCTGGGCGTGGAGGCGCGTG  64200        GA  GT  TG
                                CATGTGCCT  CA  CT  GC
                                |||||||||  ||  ||  ||
                                GTGCGCGGA  GT  GG  CG
                                     G_  GC  GT
GAM1038 LOC90841 3' GTTGGGGCAGGGGCCTGTGG  64202     T   GACA   TG
                                TCATG GCCT    GTCT  GC
                                ||||| ||||    ||||  ||
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                              GGTGT CGGG   CGGG  TG
                                 C   GA__   GT
GAM1038  LOC90917  3'  GCCGAGGTTGTCAGAGC    64339   _    GT
                              GC CTGACA  CTTGGC
                              || ||||||  ||||||
                              CG GACTGT  GAGCCG
                               A     TG
GAM1038  LOC90936  5'  CGAGCTGAGGCAGTGA     64433    G   GA  T  TG
                              TCAT TGCCT  CAG CT  G
                              |||| |||||  ||| ||  |
                              AGTG ACGGA  GTC GA  C
                                _    __  _ GT
GAM1038  LOC91050  3'  GTTGAGGCCTGTGTGCTGA   64750    T TG CTG   _  TG
                              TCA G  C   ACAG TCT  GC
                              ||| |  |   |||| |||  ||
                              AGT C  G   TGTC GGA  TG
                                _ GT ___   C   GT
GAM1038  LOC91056  3'  GCTGGGACTACAGGTGTGA   94758    GT   AC   TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
                              AGTG  TGGAC  TCAGG  CG
                                __    A_   GT
GAM1038  LOC91115  3'  GCTGGGATTACAGGCGTGA   64945    GT   AC   TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
                              AGTG  CGGAC  TTAGG  CG
                                __    A_   GT
GAM1038  LOC91301  5'  GCCGGGGCACTGATGCGTGG  65544     GCCTGACA
                              TCATGT      GTCTTGGC
                              ||||||      ||||||||
                              GGTGCG      CGGGGCCG
                                 TAGTCA__
GAM1038  LOC91301  5'  GCTGGGGCTGTCCTGGGGT   65545    ___      TG
                              GCCT   GACAGTCT  GC
                              ||||   ||||||||  ||
                              TGGG   CTGTCGGG  CG
                                GTC      GT
GAM1038  LOC91308  3'  GCTGAGACCACAGGTGCGTG  65560    TG   ACA   TG
                              CATG  CCTG   GTCT  GC
                              ||||  ||||   ||||  ||
                              GTGC  GGAC   CAGA  CG
                                GT   AC_   GT
GAM1038  LOC91308  3'  GCTGGGATTACAGGCGTGA   65561    GT   AC   TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
                              AGTG  CGGAC  TTAGG  CG
                                __    A_   GT
GAM1038  LOC91308  3'  GTTAAGTTGTAGCACGTGA   65563      CTG   T
                              TCATGTGC   ACAG CTTGGC
                              ||||||||   |||| ||||||
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                                AGTGCACG   TGTT GAATTG
                                    A__   _
GAM1038 LOC91355 5' GCCAGAGCCTGGGCGCA     65715        ACA TC
                                TGTGCCTG   G  TTGGC
                                ||||||||   |  |||||
                                ACGCGGGT   C  GACCG
                                    C__ GA
GAM1038 LOC91355 5' GTTGGGGCTGGTGTGTGG    65721      TG  TGAC    TG
                                TCATG  CC   AGTCT  GC
                                |||||  ||   |||||  ||
                                GGTGT  GG   TCGGG  TG
                                   GT _____    GT
GAM1038 LOC91373 3' GCTGGGATTATAGGTGTGA   65842     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  TGGAT  TTAGG  CG
                                   __    A_    GT
GAM1038 LOC91421 3' CCCGGGAAGTGTCGGGCGTGTG 65990     TG       G_     C
             G                   TCA  TGCCTGACA  TCTTGG
                                 |||  |||||||||  ||||||
                                 GGT  GCGGGCTGT  AGGGCC
                                   GT       GA     CG
GAM1038 LOC91464 5' GCTGAGCCGTGGGCACAGGA  66141    A      G  A T  TG
                                 TC TGTGCCT AC G CT  GC
                                 || ||||||| || | ||  ||
                                 AG ACACGGG TG C GA  CG
                                  G      _ C _  GT
GAM1038 LOC91547 3' GCCAGGATTACAGATGTGA   66403      GC   AC
                                 TCATGT  CTG  AGTCTTGGC
                                 ||||||  |||  |||||||||
                                 AGTGTA  GAC  TTAGGACCG
                                    __   A_
GAM1038 LOC91561 5' GCTGGGACTACAGGCGCTGG  66453     T      AC    TG
                                 TCA GTGCCTG  AGTCT  GC
                                 ||| |||||||  |||||  ||
                                 GGT CGCGGAC  TCAGG  CG
                                   _      A_    GT
GAM1038 LOC91661 3' CTAAGGAAGCACGTGG      56399        CTGACAG
                                 TCATGTGC      TCTTGG
                                 ||||||||      ||||||
                                 GGTGCACG      GGAATC
                                     AA_____
GAM1038 LOC91752 3' TCATCTATGTGGGTACATGG  67075         G  GTCT  C
                                 TCATGTGCCT ACA    TGG
                                 |||||||||| |||    |||
                                 GGTACATGGG TGT    ACT
                                       _  ATCT   T
GAM1038 LOC91948 3' GTCAGGGCCTTTGCACATG   67619       CTGACA
                                 CATGTGC     GTCTTGGC
                                 |||||||     ||||||||
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                              GTACACG    CGGGACTG
                                 TTTC__
GAM1038 LOC91960 5' GTTAGGACCCGGAGGCGCG  67665      GACA
                              TGTGCCT   GTCTTGGC
                              |||||||   ||||||||
                              GCGCGGA   CAGGATTG
                                 GGCC
GAM1038 LOC91963 5' GCCGTATCTTCAGGTATGT  67695       C  TCT
                              ATGTGCCTGA AG   TGGC
                              |||||||||| ||   ||||
                              TGTATGGACT TC   GCCG
                                    _ TAT
GAM1038 LOC91974 5' GCTGAGTGAGAGGCGTAT   67755      GA  GT  TG
                              ATGTGCCT  CA  CT  GC
                              ||||||||  ||  ||  ||
                              TATGCGGA  GT  GA  CG
                                 GA  __  GT
GAM1038 LOC92078 5' GCACTAGTGGCAGGCATGTGA 67982        ACAGT  TG_
                              TCATGTGCCTG    CT   GC
                              ||||||||||    ||   ||
                              AGTGTACGGAC    GA   CG
                                    GGT__  TCA
GAM1038 LOC92148 5' GCTGGGATTACAGGTGTGA  68334     GT    AC    TG
                              TCAT  GCCTG  AGTCT  GC
                              ||||  |||||  |||||  ||
                              AGTG  TGGAC  TTAGG  CG
                                __    A_    GT
GAM1038 LOC92218 3' GCTGAGATTTACATATGA   68507      CCTGAC    TG
                              TCATGTG     AGTCT  GC
                              |||||||     |||||  ||
                              AGTATAC     TTAGA  CG
                                 AT____     GT
GAM1038 LOC92267 3' GCTGGGATTGCAGGCACCTGA 68620    T     A     TG
                              TCA GTGCCTG CAGTCT  GC
                              ||| ||||||| ||||||  ||
                              AGT CACGGAC GTTAGG  CG
                                C      _     GT
GAM1038 LOC92285 5' GTCACAACTTCAGGTACAT   68752       C   CT
                              ATGTGCCTGA AGT  TGGC
                              |||||||||| |||  ||||
                              TACATGGACT TCA  ACTG
                                    _  AC
GAM1038 LOC92391 5' GCTGGGGCCTGCGCACTGG   69156    T   CT A  _  TG
                              TCA GTGC  G CAG TCT  GC
                              ||| ||||  | ||| |||  ||
                              GGT CACG  C GTC GGG  CG
                                _   ___ _  C  GT
GAM1038 LOC92465 5' GCCAAGGCTAGAGCACAGA   69407    A    _ GAC
                              TC TGTGC CT   AGTCTTGGC
                              || |||||  ||   |||||||||
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                                AG ACACG GA   TCGGAACCG
                                 _    A ____
GAM1038 LOC92465 5' GCTGGGACTAAAGGCATGTG  69408        GAC    TG
                                CATGTGCCT   AGTCT  GC
                                |||||||||   |||||  ||
                                GTGTACGGA   TCAGG  CG
                                     AA_    GT
GAM1038 LOC92568 3' GCTAGGGATGGTGGTGCGTG  69773     TG  TGA  GT
                                CATG  CC   CA  CTTGGC
                                ||||  ||   ||  ||||||
                                GTGC  GG   GT  GGATCG
                                  GT  TG_  AG
GAM1038 LOC92573 5' GCTAGGACCCATGCAGATGA  69808     G   C  ACA
                                TCAT TGC TG   GTCTTGGC
                                |||| ||| ||   ||||||||
                                AGTA ACG AC   CAGGATCG
                                  G   T  C__
GAM1038 LOC92606 3' GTTGATGCCTTTAGGTATGT  69989        CA  C TG
                                ATGTGCCTGA  GT T  GC
                                ||||||||||  || |  ||
                                TGTATGGATT  CG A  TG
                                     TC  T GT
GAM1038 LOC92609 3' GCTAGGATTCCAGGTGTGA   72847     GT    AC
                                TCAT  GCCTG  AGTCTTGGC
                                ||||  |||||  |||||||||
                                AGTG  TGGAC  TTAGGATCG
                                  __    C_
GAM1038 LOC92661 5' GCTGGGATTACAGGCAT     70083      AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038 LOC92661 5' GCTGGGATTGTGAGACAGGA  70084    A   GC  G     TG
                                TC TGT  CT ACAGTCT  GC
                                || |||  || |||||||  ||
                                AG ACA  GA TGTTAGG  CG
                                 G   __ G      GT
GAM1038 LOC92689 3' GCTGGGACTACAGGTGTGTG  70225     TG   AC    TG
                                CATG  CCTG  AGTCT  GC
                                ||||  ||||  |||||  ||
                                GTGT  GGAC  TCAGG  CG
                                  GT   A_    GT
GAM1038 LOC92697 5' GCTGGGATTACAGGCATGTG  70276        AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTGTACGGAC  TTAGG  CG
                                     A_    GT
GAM1038 LOC92840 5' GCCAACCCCGGGCGCGT     56433        ACAGTC
                                ATGTGCCTG     TTGGC
                                |||||||||     |||||
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                                TGCGCGGGC     AACCG
                                     CCC___
GAM1038 LOC92841 3' GCTGAGATTACAGGCATATG  70713         AC    TG
                                CATGTGCCTG  AGTCT  GC
                                ||||||||||  |||||  ||
                                GTATACGGAC  TTAGA  CG
                                     A_    GT
GAM1038 LOC92841 3' GCTGGGATTACAGGCAT    70714       AC    TG
                                GTGCCTG  AGTCT  GC
                                |||||||  |||||  ||
                                TACGGAC  TTAGG  CG
                                   A_    GT
GAM1038 LOC93052 5' GCCAGGGCGTGCGTACGTGCGT 71262      TG C__  ACA
           GA                    TCATG  C   TG   GTCTTGGC
                                 |||||  |   ||   ||||||||
                                 AGTGC  G   GC   CGGGACCG
                                    GT CAT  GTG
GAM1038 LOC93070 5' GCGCAGCTGTCGGGACGTGA  71294      G       CT  _
                                TCATGT CCTGACAGT  TG GC
                                |||||| |||||||||  || ||
                                AGTGCA GGGCTGTCG  AC CG
                                   _       __ G  T
GAM1038 LOC93129 3' GCTGGTACTACAGGTGTGTG  71467     TG   AC   C TG
                                CATG  CCTG  AGT T  GC
                                ||||  ||||  ||| |  ||
                                GTGT  GGAC  TCA G  CG
                                  GT   A_   T GT
GAM1038 LOC93132 5' GCTGGGACTACAAGCACATG  71492       C  AC    TG
                                CATGTGC TG  AGTCT  GC
                                |||||||  ||  |||||  ||
                                GTACACG AC  TCAGG  CG
                                    A  A_    GT
GAM1038 LOC93268 5' GCCGGGACTGCTGGGGTGA   71881     GTG   GA
                                TCAT   CCT  CAGTCTTGGC
                                ||||   |||  ||||||||||
                                AGTG   GGG  GTCAGGGCCG
                                  ___   TC
GAM1038 LOC93356 3' GCTGGGATTACAGGCGTGA   72078     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 LOC93496 3' GCTGGGATTACAGGCGTGA   72436     GT    AC    TG
                                TCAT  GCCTG  AGTCT  GC
                                ||||  |||||  |||||  ||
                                AGTG  CGGAC  TTAGG  CG
                                  __    A_    GT
GAM1038 LOC93512 3' GTCAGCCCTGCGGGTGTTGG  72462    T TG   A   TC
                                TCA G  CCTG CAG  TTGGC
                                ||| |  |||| |||  |||||
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                                GGT T  GGGC GTC  GACTG
                                  _ GT   _  CC
GAM1038 LOC93626 3' CCACGTGGGCATGTGG     72767         G  AGTCT
                                TCATGTGCCT AC    TGG
                                |||||||||| ||    |||
                                GGTGTACGGG TG    ACC
                                      _  C____
GAM1038 LOC94431 5' GTCAAGACGCTGGGCGCGTCGA 68594    _       ACA
                                TC ATGTGCCTG   GTCTTGGC
                                || |||||||||   ||||||||
                                AG TGCGCGGGT   CAGAACTG
                                 C       CG_
GAM1038 LOC96652 3' GTCAGGGTTGAGCAGGTA    65473       A_  GT
                                TGCCTG  CA  CTTGGC
                                ||||||  ||  ||||||
                                ATGGAC  GT  GGACTG
                                    GA  TG
GAM1039 TNFAIP1  3' CATCAGCTGAGGACAGCAAACT 40917     AG     G
             CC                   GGA  TTGCTG CTTCAGCTGATG
                                |||  |||||| ||||||||||||
                                CCT  AACGAC GGAGTCGACTAC
                                  CA     A
GAM1039 C1orf2   3' CAGCTGGTTGGGACCAGCAGCC 21681    AA      _ ___
             CCC                   GG  GTTGCTGG CT   TCAGCTG
                                ||  |||||||| ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM1039 C1orf2   3' CAGCTGGTTGGGACCAGCAGCC 94622    AA      _ ___
             CCC                   GG  GTTGCTGG CT   TCAGCTG
                                ||  |||||||| ||   |||||||
                                CC  CGACGACC GG   GGTCGAC
                                 CC       A  GTT
GAM1039 C20orf59 3' CATCCCTAGCCAGCAGCTCC   41992     A       TC  CT
                                GGA GTTGCTGGCT  AG  GATG
                                ||| ||||||||||  ||  ||||
                                CCT CGACGACCGA  TC  CTAC
                                  _        __  C_
GAM1039 FLJ20079 3' CATTCTGGTAAACCAGCAGCCT 34490     A      CT__   CT
             CC                   GGA GTTGCTGG    TCAG  GATG
                                ||| ||||||||    ||||  ||||
                                CCT CGACGACC    GGTC  TTAC
                                  C       AAAT   __
GAM1039 SSAT2    3' CATCAGCTGAAGCACTCTTC   56041      TTGCTG
                                GAAG     GCTTCAGCTGATG
                                ||||     ||||||||||||||
                                CTTC     CGAAGTCGACTAC
                                  TCA___
GAM1039 SYNJ2    3' ATCAGCTTAAGCAATTCC    61763      GTTGCTG   C
                                GGAA      GCTT AGCTGAT
                                ||||      |||| |||||||
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                                CCTT      CGAA TCGACTA
                                  AA_____   T
GAM1039  LOC162333 5'  CTGAAGCCAGCAATTCC     87131      G
                                GGAA TTGCTGGCTTCAG
                                |||| ||||||||||||
                                CCTT AACGACCGAAGTC
                                  _
GAM1039  LOC222060 5'  CACCTCCCACCAGCAACCCCC  94104    AA       CTTC  C
                                GG  GTTGCTGG    AG TG
                                ||  ||||||||    || ||
                                CC  CAACGACC    TC AC
                                 CC       ACCC  C
GAM1039  LOC255650 3'  CATCAGCCCCAGGCAACTTCC  96711          _   CTTCA
                                GGAAGTTGC TGG     GCTGATG
                                |||||||| |||     |||||||
                                CCTTCAACG ACC     CGACTAC
                                     G   C____
GAM1040  ACADS     3'  ACCACTGTGCCTCAAGTTCC   3406       AAGACA
                                GGAG      GGGCACAGTGGT
                                ||||      ||||||||||||
                                CCTT      TCCGTGTCACCA
                                  GAAC__
GAM1040  AIPL1     3'  ACCCCTCCCTGTCTCCCCA    59849     A  A      CAC  T
                                TGG GA GACAGGG   AG GGT
                                ||| || |||||||   || |||
                                ACC CT CTGTCCC   TC CCA
                                 C  _      ___  C
GAM1040  B3GAT1    5'  TGCTCTGTCCTCTCCA      53979       A
                                TGGAGA GACAGGGCA
                                |||||| |||||||||
                                ACCTCT CTGTCTCGT
                                   C
GAM1040  COG5      3'  TGTACCCTGCTTCCCC      20954     A   A    C
                                GG GAAG CAGGG ACA
                                || |||| ||||| |||
                                CC CTTC GTCCC TGT
                                 C   _    A
GAM1040  CRTAP     3'  ACCTTCATCCCTGTCTTCCTCA 21028     GA        CACAGT
                                TG  GAAGACAGGG     GGT
                                ||  ||||||||||     |||
                                AC  CTTCTGTCCC     CCA
                                 TC        TACTT_
GAM1040  EPB72     3'  ACCACAACCAGCTTCTCCA    14594         ACA  GCACA
                                TGGAGAAG   GG    GTGGT
                                ||||||||   ||    |||||
                                ACCTCTTC   CC    CACCA
                                     GA_  AA___
GAM1040  GAB2      3'  TACCACTGTCCTCTGCCCCCA  24502     AGAAGA    C
                                TGG     CAGGG ACAGTGGTA
                                |||     ||||| |||||||||
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                                ACC     GTCTC TGTCACCAT
                                  CCC___    C
GAM1040  GAB2    3'  TACCACTGTCCTCTGCCCCCA  54459    AGAAGA    C
                                TGG     CAGGG ACAGTGGTA
                                |||     ||||| |||||||||
                                ACC     GTCTC TGTCACCAT
                                  CCC___    C
GAM1040  GPD1    3'  TGCCCTGTCCCTCTCCA    59672      A_
                                TGGAGA  GACAGGGCA
                                ||||||  |||||||||
                                ACCTCT  CTGTCCCGT
                                   CC
GAM1040  GSTT1   3'  ACCATCCCCACCCTGTCTTCCA 73457    GA       CACA_
            CA                    TG  GAAGACAGGG    GTGGT
                                ||  ||||||||||    |||||
                                AC  CTTCTGTCCC    TACCA
                                 AC        ACCCC
GAM1040  MATN1   3'  ACCACTGTGGCCTCTCCA    9916       AGACA  G
                                TGGAGA    GG CACAGTGGT
                                ||||||    || |||||||||
                                ACCTCT    CC GTGTCACCA
                                   _____  G
GAM1040  MAZ     3'  TGCCCTGTCTTCCCA      73390    A
                                TGG GAAGACAGGGCA
                                ||| ||||||||||||
                                ACC CTTCTGTCCCGT
                                  _
GAM1040  NR1D1   3'  ACCACTCTGTCTCCCCCA   41361    AGA    GGCAC
                                TGG   AGACAG    AGTGGT
                                |||   ||||||    ||||||
                                ACC   TCTGTC    TCACCA
                                  CCC     _____
GAM1040  OTOF    3'  CACACCCTGTCTTCCCA    16639    A       CACA
                                TGG GAAGACAGGG    GTG
                                ||| ||||||||||    |||
                                ACC CTTCTGTCCC    CAC
                                  _        A___
GAM1040  PCTP    3'  ACCACTGTTCAGCCTTCCCC  41094    A   ACAG  C
                                GG GAAG    GG ACAGTGGT
                                || ||||    || ||||||||
                                CC CTTC    CT TGTCACCA
                                 C    CGA_  _
GAM1040  PPP2R1A 3'  CACCTCCCGTCCTCCCCA    26442    A  A   A   CACA
                                TGG GA GAC GGG    GTG
                                ||| || ||| |||    |||
                                ACC CT CTG CCC    CAC
                                  C  C   _   TC__
GAM1040  PPP2R4  3'  TGTGCCTGCCTTCCCCA    60563    A    ACA
                                TGG GAAG   GGGCACA
                                ||| ||||   |||||||
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                                ACC CTTC   TCCGTGT
                                  C    CG_
GAM1040  SH3BP2   3'  CACGCCCTGTTCCCTCCA    11595      AA      ACA
                                TGGAG  GACAGGGC   GTG
                                |||||  ||||||||   |||
                                ACCTC  TTGTCCCG   CAC
                                   CC       ____
GAM1040  SMAC     3'  CACTGCCCTGTCTCCCCA    39111     A  A       CA
                                TGG GA GACAGGGCA  GTG
                                ||| || |||||||||  |||
                                ACC CT CTGTCCCGT  CAC
                                  C  _       __
GAM1040  SMAC     3'  CACTGCCCTGTCTCCCCA    57195     A  A       CA
                                TGG GA GACAGGGCA  GTG
                                ||| || |||||||||  |||
                                ACC CT CTGTCCCGT  CAC
                                  C  _       __
GAM1040  SMAC     3'  CACTGCCCTGTCTCCCCA    57205     A  A       CA
                                TGG GA GACAGGGCA  GTG
                                ||| || |||||||||  |||
                                ACC CT CTGTCCCGT  CAC
                                  C  _       __
GAM1040  UVRAG    3'  TACTGTCGCCCCATCTTCTCC  12562         CA   _
                                GGAGAAGA  GGGC ACAGTG
                                ||||||||  |||| ||||||
                                CCTCTTCT  CCCG TGTCAT
                                     AC    C
GAM1040  XPA      3'  ACCACTGTACCCCAGGTTCT   4596       GACA   C
                                AGAA    GGG ACAGTGGT
                                ||||    ||| ||||||||
                                TCTT    CCC TGTCACCA
                                  GGAC   A
GAM1040  ZNF261   3'  CCATTCCCTGCCTTCTCTA    17493        A    CAC
                                TGGAGAAG CAGGG   AGTGG
                                |||||||| |||||   |||||
                                ATCTCTTC GTCCC   TTACC
                                     C    ____
GAM1040  B3GNT7   3'  ACCGCACCCTGCTTCTCCA    71123        A    CACA
                                TGGAGAAG CAGGG    GTGGT
                                |||||||| |||||    |||||
                                ACCTCTTC GTCCC    CGCCA
                                     _    A____
GAM1040  CBCIP2   3'  CACCTTTCCCCTCTTCTCCA   51589         CA   CACA
                                TGGAGAAGA  GGG    GTG
                                |||||||||  |||    |||
                                ACCTCTTCT  CCC    CAC
                                     C_   TTTC
GAM1040  DKFZP434P1750 3'  GCCCTCCCTGTCTCCCCCA   31377     AGA      CAC  T
                                TGG   AGACAGGG   AG GGT
                                |||   ||||||||   || |||
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                                ACC   TCTGTCCC   TC CCG
                                  CCC       ___ _
GAM1040  DKFZp547I094 5'  ACCCCTGTTGCCCTGCCTTCTT 49629        A      _  T
             CA                    TGGAGAAG CAGGGCA CAG GGT
                                |||||||| ||||||| ||| |||
                                ACTTCTTC GTCCCGT GTC CCA
                                    C      T   C
GAM1040  DKFZp564I1922 3'  ACCACTGTTATATTACCTTCTC 31232        AC  GGC_
             CA                    TGGAGAAG  AG   ACAGTGGT
                                |||||||| ||   ||||||||
                                ACCTCTTC  TT   TGTCACCA
                                    CA  ATAT
GAM1040  DUSP9    3'  CACCTCCCTGTTTCTCCA    7341        A      CACA
                                TGGAGA GACAGGG   GTG
                                |||||| |||||||   |||
                                ACCTCT TTGTCCC   CAC
                                   _      TC__
GAM1040  FLJ14708  3'  ACCACTGTGGGCCCTCCTTC   51538     AC    __
                                GAAG  AGGGC  ACAGTGGT
                                ||||  |||||  ||||||||
                                CTTC  TCCCG  TGTCACCA
                                  C_    GG
GAM1040  FLJ23120  3'  ACCACTGCACCACTGTACTCCA 85143      AAG   _ CA
                                TGGAG   ACAG GG  CAGTGGT
                                |||||   |||| ||  |||||||
                                ACCTC   TGTC CC  GTCACCA
                                   A__   A  AC
GAM1040  IMAGE:4907098 3'  ACCACTGTGGTCCCCTCCA   91656      AA   AGGG
                                TGGAG  GAC   CACAGTGGT
                                |||||  |||   |||||||||
                                ACCTC  CTG   GTGTCACCA
                                   CC  _____
GAM1040  KIAA0416  3'  ACCACTACCCACTCCA     31462      AAGACA   CAC
                                TGGAG     GGG   AGTGGT
                                |||||     |||   ||||||
                                ACCTC     CCC   TCACCA
                                   A_____   A__
GAM1040  KIAA0545  3'  CCACGCTGTTCCTCCA     63144      AAGACA    CA
                                TGGAG     GGGCA  GTGG
                                |||||     |||||  ||||
                                ACCTC     CTTGT  CACC
                                   _______    CG
GAM1040  KIAA0924  3'  TGCCCTGTCCTCTGCA     29724    G   A
                                TG AGA GACAGGGCA
                                || ||| |||||||||
                                AC TCT CTGTCCCGT
                                 G   C
GAM1040  KIAA1111  3'  CATCCTGCCTGCCTTCTCCA   96206        ACA    CA
                                TGGAGAAG   GGGCA  GTG
                                ||||||||   |||||  |||
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                                ACCTCTTC  TCCGT  TAC
                                    CG_   CC
GAM1040 KIAA1184 3' TGTGCCCCTCCCCTCCA    42620     AA  CA
                                TGGAG  GA  GGGCACA
                                |||||  ||  |||||||
                                ACCTC  CT  CCCGTGT
                                   CC  C_
GAM1040 MGC13138 3' TACCACCATGCCTGGCTTC   53022    ACA   CA
                                GAAG  GGGCA  GTGGTA
                                ||||  |||||  ||||||
                                CTTC  TCCGT  CACCAT
                                  GG_   AC
GAM1040 MGC5590  5' TACCACTGTCAGCACTCTCCA 43927     AGACAGG __
                                TGGAGA    GC  ACAGTGGTA
                                ||||||    ||  |||||||||
                                ACCTCT    CG  TGTCACCAT
                                   CA_____  AC
GAM1040 moblak   3' CCACACCTCTGTCTCCCCCA  55490    AGA     CACA
                                TGG  AGACAGGG  GTGG
                                |||  ||||||||  ||||
                                ACC  TCTGTCTC  CACC
                                 CCC     CA__
GAM1040 NR6A1    3' ACCACTGCGAACTTTCCA    52866     AAGAC  GGCA
                                TGGAG   AG   CAGTGGT
                                |||||   ||   |||||||
                                ACCTT   TC   GTCACCA
                                  _____  AAGC
GAM1040 NR6A1    3' ACCACTGCGAACTTTCCA    52878     AAGAC  GGCA
                                TGGAG   AG   CAGTGGT
                                |||||   ||   |||||||
                                ACCTT   TC   GTCACCA
                                  _____  AAGC
GAM1040 NR6A1    3' ACCACTGCGAACTTTCCA    7641      AAGAC  GGCA
                                TGGAG   AG   CAGTGGT
                                |||||   ||   |||||||
                                ACCTT   TC   GTCACCA
                                  _____  AAGC
GAM1040 PEG10    3' TACCACTGCCGGATGTATTCTC 30530      G  G__   CA
           CA                    TGGAGAA ACA  GGCA  GTGGTA
                                |||||||  |||  ||||  ||||||
                                ACCTCTT TGT  CCGT  CACCAT
                                   A  AGG   __
GAM1040 STMN3    3' TACCACTGCAGCATCCCCCACT 31902      ACA  CA____
           TCTCCA                 GGAGAAG  GGG    CAGTGGTA
                                |||||||  |||    ||||||||
                                CCTCTTC  CCC    GTCACCAT
                                   ACC  TACGAC
GAM1040 LOC126964 3' ACCACTGTGTGCGCCTCCA  74610     AAGACAGG
                                TGGAG     GCACAGTGGT
                                |||||     ||||||||||
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                                ACCTC       TGTGTCACCA
                                   CGCG____
GAM1040  LOC145837 5'  CATCTGCCCTGTCTCTCCA   83543       A       CA
                                TGGAGA GACAGGGCA  GTG
                                |||||| |||||||||  |||
                                ACCTCT CTGTCCCGT  TAC
                                   _       C_
GAM1040  LOC148930 3'  GCTTTGCCCTGTGTTCTCCA   79097       G       C
                                TGGAGAA ACAGGGCA AGT
                                ||||||| |||||||| |||
                                ACCTCTT TGTCCCGT TCG
                                    G       T
GAM1040  LOC150372 3'  TACCACTGTGCCCTGGCCCA   79808     AGAAGA
                                TGG     CAGGGCACAGTGGTA
                                |||     ||||||||||||||
                                ACC     GTCCCGTGTCACCAT
                                  CG____
GAM1040  LOC151162 5'  GCCACCCCATTTCTCCA     85244       ACA   CACA
                                TGGAGAAG   GGG   GTGGT
                                ||||||||   |||   |||||
                                ACCTCTTT   CCC   CACCG
                                    A__   _____
GAM1040  LOC154761 3'  ACCACACCCACTTCTCCA    81120       ACA   CACA
                                TGGAGAAG   GGG   GTGGT
                                ||||||||   |||   |||||
                                ACCTCTTC   CCC   CACCA
                                    A__   A___
GAM1040  LOC199964 3'  TGCCGTGCCTTCTCCA      89891       A  G
                                TGGAGAAG CA GGCA
                                |||||||| || ||||
                                ACCTCTTC GT CCGT
                                    C  G
GAM1040  LOC203377 5'  GCCACCCCATTTCTCCA     90582       ACA   CACA
                                TGGAGAAG   GGG   GTGGT
                                ||||||||   |||   |||||
                                ACCTCTTT   CCC   CACCG
                                    A__   _____
GAM1040  LOC203504 5'  ACCCCTCCCCAGTCTTCTCCA 90635         A   CAC  T
                                TGGAGAAGAC GGG   AG GGT
                                |||||||||| |||   || |||
                                ACCTCTTCTG CCC   TC CCA
                                    A   C__  C
GAM1040  LOC219654 3'  CGTTGTTCCCCGTCTTCTCCA 91302         A   C
                                TGGAGAAGAC GGG ACAGTG
                                |||||||||| ||| ||||||
                                ACCTCTTCTG CCC TGTTGC
                                    C   T
GAM1040  LOC221416 3'  TGGCACCCTATCTTCTCCA    93772         C    CA_
                                TGGAGAAGA AGGG   CA
                                ||||||||| ||||   ||
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                                ACCTCTTCT TCCC   GT
                                     A    ACG
GAM1040  LOC221491 5'  ACCACTGTGCCCAATGCCCCCC 92010     AGAAGACA
              A                   TGG       GGGCACAGTGGT
                                  |||       ||||||||||||
                                  ACC       CCCGTGTCACCA
                                    CCCCGTAA
GAM1040  LOC222001 3'  ACCACTAATTAAGTTTTCTCCA 92903          AGGGCAC
                                  TGGAGAAGAC      AGTGGT
                                  ||||||||||      ||||||
                                  ACCTCTTTTG      TCACCA
                                       AATTAA_
GAM1040  LOC255975 5'  TACCACCCGGCAGCCTCTCCA  95897       AGACAGG  ACA
                                  TGGAGA      GC   GTGGTA
                                  ||||||      ||   ||||||
                                  ACCTCT      CG   CACCAT
                                     CCGA___  GCC
GAM1040  LOC256901 3'  ACCACTTCCCCCTTCTCCA    96619        ACA   CAC
                                  TGGAGAAG   GGG   AGTGGT
                                  ||||||||   |||   ||||||
                                  ACCTCTTC   CCC   TCACCA
                                       C__   T__
GAM1040  LOC54550  3'  ACCACTGTGCCCAGGCGCCA   77688     AGAAGACA
                                  TGG       GGGCACAGTGGT
                                  |||       ||||||||||||
                                  ACC       CCCGTGTCACCA
                                    GCGGA___
GAM1040  LOC93097  3'  ACCACCAGCATTTCCTCCA    71357      AA  CAGG  ACA
                                  TGGAG  GA    GC   GTGGT
                                  |||||  ||    ||   |||||
                                  ACCTC  CT    CG   CACCA
                                     __  TTA_  AC_
GAM1040  LOC96652  3'  ACCACCTGCACCAGCTTCTCCA 65462         ACA  _   CA
                                  TGGAGAAG   GG GCA  GTGGT
                                  ||||||||   || |||  |||||
                                  ACCTCTTC   CC CGT  CACCA
                                       GA_  A   C_
GAM1041  BRCA1     3'  CCACAGGTACAAGCCACAGGA  23558     A       CA  TCA
                                  TC CTGTGGCT  GT   TGTGG
                                  || ||||||||  ||   |||||
                                  AG GACACCGA  CA   ACACC
                                   _       A_  TGG
GAM1041  MXI1      3'  CCAAGGTCTGAGCCACAG     55259          TTCATG
                                  CTGTGGCTCAG     TGG
                                  ||||||||||      |||
                                  GACACCGAGTC     ACC
                                         TGGA__
GAM1041  MXI1      3'  CCAAGGTCTGAGCCACAG     19898          TTCATG
                                  CTGTGGCTCAG     TGG
                                  ||||||||||      |||
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                                GACACCGAGTC     ACC
                                      TGGA__
GAM1041  MYO1C    3'  CAGGCCGGGCCACAG      61202         A   CATG
                                CTGTGGCTC GTT    TG
                                ||||||||| |||    ||
                                GACACCGGG CGG    AC
                                     C  ____
GAM1041  RBBP2    3'  ACTGAGCCACAGTGAT     17318
                                ATCACTGTGGCTCAGT
                                ||||||||||||||||
                                TAGTGACACCGAGTCA

GAM1041  TCF3     3'  CCACACGAACTAGGGCAGTGGT 70731        GG TC     A
                                ATCACTGT  C  AGTTC TGTGG
                                ||||||||  |  ||||| |||||
                                TGGTGACG  G  TCAAG ACACC
                                     __ GA     C
GAM1041  C20orf20 3'  CCACCCCCCAGGCCACAGTGAT 36852          CAGTTCAT
                                ATCACTGTGGCT       GTGG
                                ||||||||||||       ||||
                                TAGTGACACCGG       CACC
                                      ACCCCC__
GAM1041  FLJ12132 3'  CACCCCAAGCCACAGTGA    46466          CAGTTCAT
                                TCACTGTGGCT       GTG
                                ||||||||||        |||
                                AGTGACACCGA       CAC
                                      ACCC_____
GAM1041  MGC2408  3'  CACATGAACCAATACAG     50324       GCTCA
                                CTGTG     GTTCATGTG
                                |||||     |||||||||
                                GACAT     CAAGTACAC
                                   AAC__
GAM1041  LOC163231 5'  CACACATTCACCACAGTG    82436        CTC   TCA
                                CACTGTGG   AGT   TGTG
                                ||||||||   |||   ||||
                                GTGACACC   TTA   ACAC
                                     AC_   C__
GAM1041  LOC201229 3'  CCACATGAACCAAGGAGAGAC  88142    GG   A___
                                GT  CTC    GTTCATGTGG
                                ||  |||    ||||||||||
                                CA  GAG    CAAGTACACC
                                 GA   GAAC
GAM1042  ACK1     5'  GAGGAGGTGGTGACTGG     19343       T  TG     C
                                TCAGTC GT  TCTCC TC
                                ||||||  ||  |||||  ||
                                GGTCAG TG  GGAGG AG
                                    _ GT     _
GAM1042  ACVRL1   3'  GGTGGGGGGGCAGTGGAT     3421      TG        T
                                GTC  TTGTCTCCC CT
                                |||  |||||||||  ||
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                              TAG  GACGGGGGG GG
                                GT       T
GAM1042  ADCY7    3'  GATTATACAGGGTTGCAGATTG 6641         TGTCT   C__
            G                  TCAGTCTGT    CCCT   TAATC
                               |||||||||    ||||  |||||
                               GGTTAGACG    GGGA   ATTAG
                                    TT___    CAT
GAM1042  ADD2     5'  TAGGGGGTGCAGACTGA     33932        TGTCT
                               TCAGTCTGT    CCCTCTA
                               |||||||||    |||||||
                               AGTCAGACG    GGGGGAT
                                    T____
GAM1042  ADD2     5'  TAGGGGGTGCAGACTGA     33936        TGTCT
                               TCAGTCTGT    CCCTCTA
                               |||||||||    |||||||
                               AGTCAGACG    GGGGGAT
                                    T____
GAM1042  ADD2     5'  TAGGGGGTGCAGACTGA     33943        TGTCT
                               TCAGTCTGT    CCCTCTA
                               |||||||||    |||||||
                               AGTCAGACG    GGGGGAT
                                    T____
GAM1042  ADD2     5'  TAGGGGGTGCAGACTGA     33947        TGTCT
                               TCAGTCTGT    CCCTCTA
                               |||||||||    |||||||
                               AGTCAGACG    GGGGGAT
                                    T____
GAM1042  ADD2     5'  TAGGGGGTGCAGACTGA     33953        TGTCT
                               TCAGTCTGT    CCCTCTA
                               |||||||||    |||||||
                               AGTCAGACG    GGGGGAT
                                    T____
GAM1042  ADD2     5'  TAGGGGGTGCAGACTGA     33960        TGTCT
                               TCAGTCTGT    CCCTCTA
                               |||||||||    |||||||
                               AGTCAGACG    GGGGGAT
                                    T____
GAM1042  ADD2     5'  TAGGGGGTGCAGACTGA     33964        TGTCT
                               TCAGTCTGT    CCCTCTA
                               |||||||||    |||||||
                               AGTCAGACG    GGGGGAT
                                    T____
GAM1042  ADD3     3'  GATTGGGGGATGTAGCAAACTG 33672      C    TC   T
            G                  TCAGT TGTTG  TCCC CTAATC
                               |||||  |||||  ||||  ||||||
                               GGTCA ACGAT  AGGG GGTTAG
                                  A    GT   _
GAM1042  ADH1B    3'  GATTATTTAGATGATGACTGA  72646       T  TG   CCCTC
                               TCAGTC GT  TCT    TAATC
                               ||||||  ||  |||    |||||
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                                AGTCAG TA  AGA    ATTAG
                                   _ GT   TTT__
GAM1042 ADRB3    3' GTGCCGTGGAGCAGCAGGCTGG 3438          T   CTCTAATC
                                TCAGTCTGTTG CTCC
                                |||||||||| ||||
                                GGTCGGACGAC GAGG
                                      _   TGCCGTGG
GAM1042 AHR      5' GGCGGGAGGCAGTGGCTGG   7882      T TG       T
                                TCAG C  TTGTCTCCC CT
                                |||| |  ||||||||| ||
                                GGTC G  GACGGAGGG GG
                                  _ GT        C
GAM1042 ARHGEF7  5' GGTTGGCATCTGGGGCAGCGGG 14010           CCT__
             CT                   AGTCTGTTGTCTC    CTAATC
                                ||||||||||||    ||||||
                                TCGGGCGACGGGG    GGTTGG
                                      TCTAC
GAM1042 ATP2C1   5' GAGCGGGGGTGACAGCCTGG   26887     T   TG    _
                                TCAG CTGT  TCTCC CTC
                                |||| ||||  ||||| |||
                                GGTC GACA  GGGGG GAG
                                  C   GT    C
GAM1042 B3GNT4   3' GGTTGGGCAACAGCCTGA    66446     T       C_
                                TCAG CTGTTGTCT  CC
                                |||| |||||||||  ||
                                AGTC GACAACGGG  GG
                                  C        TT
GAM1042 BAK1     3' TAACTTGGGGAGGCAAGAGACT 91993       G        CTAATC
             GG                   TCAGTCT TTGTCTCCCT
                                ||||||| ||||||||||
                                GGTCAGA AACGGAGGGG
                                    G        TTCAATA
GAM1042 BAP1     3' GTTGGGGTGAGCAGGCTG    16218       TTGT   C
                                CAGTCTG    CTC CTCTAAT
                                |||||||    ||| |||||||
                                GTCGGAC    GAG GGGGTTG
                                    ____  T
GAM1042 BCL11B   3' GATTAGGCTACATAAAATGGGC 43190         GTCTCCC_
             TGA                  TCAGTCTGTT       TCTAATC
                                ||||||||||       |||||||
                                AGTCGGGTAA       GGATTAG
                                     AATACATC
GAM1042 BCL2L2   3' GGGGAGGTGGTAGGCTG     14471        TG
                                CAGTCTGT  TCTCCCT
                                ||||||||  |||||||
                                GTCGGATG  GGAGGGG
                                    GT
GAM1042 BCL7C    5' GGGGGGACGGCAGGCCGA    16481    A
                                TC GTCTGTTGTCTCCCT
                                || ||||||||||||||
```

```
                                AG CGGACGGCAGGGGGG
                                 C
GAM1042  CBFA2T2   3'  GGCTGGAGGCGGCAGGC     17476            CT
                                GTCTGTTGTCTCC  CT
                                ||||||||||||  ||
                                CGGACGGCGGAGG  GG
                                       TC
GAM1042  CCND2     3'  GGTGGGACAATGGGTGG     8297      G        _
                                TCA TCTGTTGTCTC CC
                                ||| ||||||||||| ||
                                GGT GGGTAACAGGG GG
                                  _         T
GAM1042  CD79B     3'  GGGGGAGGCAGAGACTGG     5273         G
                                TCAGTCT TTGTCTCCCTC
                                ||||||| ||||||||||
                                GGTCAGA GACGGAGGGGG
                                   _
GAM1042  CD79B     3'  GGGGGAGGCAGAGACTGG     41209        G
                                TCAGTCT TTGTCTCCCTC
                                ||||||| ||||||||||
                                GGTCAGA GACGGAGGGGG
                                   _
GAM1042  CD8A      3'  GGTTGGAGCAGTAGCTGG     8334       T     T    CT
                                TCAG CTGTTG CTCC  CT
                                |||| |||||| ||||  ||
                                GGTC GATGAC GAGG  GG
                                  _     _    TT
GAM1042  CD97      3'  GGTGGGGACAGGGGCTGG     8360         G    T   T
                                TCAGTCT TTGTC CCC CT
                                ||||||| ||||| ||| ||
                                GGTCGGG GACAG GGG GG
                                   _     _   T
GAM1042  CD97      3'  GGTGGGGACAGGGGCTGG     54348        G    T   T
                                TCAGTCT TTGTC CCC CT
                                ||||||| ||||| ||| ||
                                GGTCGGG GACAG GGG GG
                                   _     _   T
GAM1042  CDC25C    3'  GATTAGGTTTCAGCAGAGCTGA 43019      _      TCTCCC
                                TCAG TCTGTTG      TCTAATC
                                |||| |||||||      |||||||
                                AGTC AGACGAC      GGATTAG
                                  G       TTT___
GAM1042  CDC25C    3'  GATTAGGTTTCAGCAGAGCTGA 8367       _      TCTCCC
                                TCAG TCTGTTG      TCTAATC
                                |||| |||||||      |||||||
                                AGTC AGACGAC      GGATTAG
                                  G       TTT___
GAM1042  CETP      3'  GGTTAGGAGTACGGAGATGGAG 3580      G TG    ___   _
              ATTGG                  TCT T  TCTCC   CTC TAATC
                                ||| |  |||||   ||| |||||
```

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                                AGA G  AGAGG   GAG ATTGG
                                  _ GT    CAT   G
GAM1042  CHN1     5'  GGGTGCGGCGGGCTGA      8432            CT
                                TCAGTCTGTTGT  CCC
                                ||||||||||||  |||
                                AGTCGGGCGGCG  GGG
                                       T_
GAM1042  CNN1     3'  GGTTAGAGTTTGGAGAGAGCAG 7117         G    ___
              ACTGG                  GTCTGTT TCTCC   CTCTAATC
                                ||||||| |||||   ||||||||
                                CAGACGA AGAGG   GAGATTGG
                                    G    TTT
GAM1042  COG3     3'  GGGAGGAGCAGGCTGA      48699          G
                                TCAGTCTGTT TCTCCC
                                |||||||||| ||||||
                                AGTCGGACGA GGAGGG

                                  _
GAM1042  COG8     3'  GATTGCCAAGGCATGGCAGACT 50482         TG CTC   C__
              GA                   TCAGTCTGT  T   CCT   TAATC
                                |||||||||  |   |||   |||||
                                AGTCAGACG  A   GGA   GTTAG
                                     GT C__   ACC
GAM1042  CPO      3'  GGTGAGATGGCAGATTG     3638          TG   _
                                CAGTCTGT  TCTC CC
                                ||||||||  |||| ||
                                GTTAGACG  AGAG GG
                                     GT    T
GAM1042  CTSD     3'  GGTTGGGATTGGGGGCTGG   8585         GTT    __
                                TCAGTCT   GTCTC  CC
                                |||||||   |||||  ||
                                GGTCGGG   TAGGG  GG
                                    GGT    TT
GAM1042  CYP1A1   3'  GGTTGGGCAGCCAGACCAGCAG 4946          _  CC  __
              GCTGG                GTCTGTTG TCT  CT  CTAATC
                                |||||||| |||  ||  ||||||
                                CGGACGAC AGA  GA  GGTTGG
                                     C   CC  CG
GAM1042  DAAM2    3'  GGGAGACAGGGACTGG      92290         G
                                TCAGTCT TTGTCTCCC
                                ||||||| |||||||||
                                GGTCAGG GACAGAGGG

                                  _
GAM1042  DLEU1    3'  GATAAAAGGAGACAGAAGATTG 19696        G       CTCTAATC
              A                   TCAGTCT TTGTCTCC
                                ||||||| ||||||||
                                AGTTAGA GACAGAGG
                                    A       AAAATAG
GAM1042  DLG5     3'  GGTACTGAGCTGACAGACTGG  82920          T  _____
                                TCAGTCTGTTG CTC    CC
                                |||||||||| |||    ||
```

```
                                GGTCAGACAGT GAG   GG
                                      C   TCAT
GAM1042  DLST    3'  GGTTAGCCTGGTGACAGGC   8647       TG  TCCCT
                                GTCTGT  TC    CTAATC
                                ||||||  ||    ||||||
                                CGGACA  GG    GATTGG
                                   GT  TCC__
GAM1042  DVL1    3'  GGTGGGGGGCAGGCTGG     59338        TGT    T
                                TCAGTCTGT   CTCCC CT
                                |||||||||   ||||| ||
                                GGTCGGACG   GGGGG GG
                                      ___     T
GAM1042  EDG8    3'  GATTTTAGAGGCAGCAGAC   78477          CCTCT
                                GTCTGTTGTCTC    AATC
                                ||||||||||||    ||||
                                CAGACGACGGAG    TTAG
                                      ATT__
GAM1042  EDNRA   5'  GACGGGGAGGACAGACTGG   64109         G    C
                                TCAGTCTGTT TCTCC TC
                                |||||||||| ||||| ||
                                GGTCAGACAG AGGGG AG
                                      G    C
GAM1042  EIF5A   5'  GGAGGCAGCGGTTGG      8767      T
                                TCAG CTGTTGTCTCC
                                |||| ||||||||||
                                GGTT GGCGACGGAGG
                                  _
GAM1042  EMD     3'  AGGGAGGCAGCAGACT      3678
                                AGTCTGTTGTCTCCCT
                                ||||||||||||||||
                                TCAGACGACGGAGGGA

GAM1042  ENC1    5'  GGGGACGACAGACGGA      13282    A
                                TC GTCTGTTGTCTCC
                                || ||||||||||||
                                AG CAGACAGCAGGGG
                                 G
GAM1042  EPHA2   3'  TGACCAGGGATGCTGGGCTGG  15409       GTT  C    CTAATC
                                TCAGTCT   GT TCCCT
                                |||||||   || |||||
                                GGTCGGG   CG AGGGA
                                   T__  T    CCAGTA
GAM1042  EXT1    5'  GGCGGGAAGATGGCGGACTGG  3714         TG  _  T
                                TCAGTCTGT  TCT CCC CT
                                |||||||||  ||| ||| ||
                                GGTCAGGCG  AGA GGG GG
                                      GT   A   C
GAM1042  FBXL11  3'  AGGGAGTAGCAGATTGA     24566          T
                                TCAGTCTGTTG CTCCCT
                                |||||||||| ||||||
```

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                                AGTTAGACGAT GAGGGA
                                        _
GAM1042  FBXW7    3'  GGCTTGGGGCAACAGATTGA   37026              ___
                                TCAGTCTGTTGTCTC   CC
                                ||||||||||||||   ||
                                AGTTAGACAACGGGG   GG
                                    TTC
GAM1042  FBXW7    3'  GGCTTGGGGCAACAGATTGA   53304              ___
                                TCAGTCTGTTGTCTC   CC
                                ||||||||||||||   ||
                                AGTTAGACAACGGGG   GG
                                    TTC
GAM1042  FETUB    3'  GATGGGGACGATGGAC      26881          C
                                GTCTGTTGTCTCC TC
                                |||||||||||| ||
                                CAGGTAGCAGGGG AG
                                    T
GAM1042  FGF23    3'  GGTTAGGTTTTCTGTGGACTGA 40195       TG TGTCTCCC
                                TCAGTC  T       TCTAATC
                                ||||||  |       |||||||
                                AGTCAG  G       GGATTGG
                                   GT TCTTTT__
GAM1042  FGFR1    5'  GAGCCCGGGGGCGGCGGGCCGG 43615    A         ___
                                TC GTCTGTTGTCTCC   CTC
                                || ||||||||||||   |||
                                GG CGGGCGGCGGGGG   GAG
                                 C           CCC
GAM1042  FGFR1    5'  GAGCCCGGGGGCGGCGGGCCGG 43622    A         ___
                                TC GTCTGTTGTCTCC   CTC
                                || ||||||||||||   |||
                                GG CGGGCGGCGGGGG   GAG
                                 C           CCC
GAM1042  FGFR1    5'  GAGCCCGGGGGCGGCGGGCCGG 43632    A         ___
                                TC GTCTGTTGTCTCC   CTC
                                || ||||||||||||   |||
                                GG CGGGCGGCGGGGG   GAG
                                 C           CCC
GAM1042  FGFR1    5'  GAGCCCGGGGGCGGCGGGCCGG 43639    A         ___
                                TC GTCTGTTGTCTCC   CTC
                                || ||||||||||||   |||
                                GG CGGGCGGCGGGGG   GAG
                                 C           CCC
GAM1042  FGFR1    5'  GAGCCCGGGGGCGGCGGGCCGG 5205     A         ___
                                TC GTCTGTTGTCTCC   CTC
                                || ||||||||||||   |||
                                GG CGGGCGGCGGGGG   GAG
                                 C           CCC
GAM1042  FGFR1    5'  GAGCCCGGGGGCGGCGGGCCGG 31798    A         ___
                                TC GTCTGTTGTCTCC   CTC
                                || ||||||||||||   |||
```

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                                GG CGGGCGGCGGGGG  GAG
                                 C          CCC
GAM1042  G2A     3'  GGCAGGGGGATGGCAGGTTGG  25321    GT   TG    _
                                TCA  CTGT  TCTCCCT CT
                                |||  ||||  ||||||| ||
                                GGT  GACG  AGGGGGA GG
                                  TG   GT     C
GAM1042  G2A     3'  GTGGCAGGGGGATGGCAGGTTG 25322    GT   TG    _  ATC
              G                  TCA  CTGT  TCTCCCT CTA
                                |||  ||||  ||||||| |||
                                GGT  GACG  AGGGGGA GGT
                                  TG   GT     C  G
GAM1042  GCDH    3'  AGGGAGGTGGCGGATGGA    3853    A    TG
                                TC GTCTGT  TCTCCCT
                                || ||||||  |||||||
                                AG TAGGCG  GGAGGGA
                                 G     GT
GAM1042  GDI1    3'  GATGGCTTGGGAGATGGGGGGT 59977    GT  G TG    TCTA_
              TGG                  TCA  CT T  TCTCCC    ATC
                                |||  || |  ||||||    |||
                                GGT  GG G  AGAGGG    TAG
                                  TG  G GT     TTCGG
GAM1042  GLI     3'  GATGGGAGGTATGGGCTGG   17948        T GT   _
                                TCAGTCTG T  CTCCC TC
                                ||||||||  |  ||||| ||
                                GGTCGGGT A  GAGGG AG
                                     _ TG    T
GAM1042  GPR2    3'  GAGGAGGGGGCAGGCTGA    33462         G    C
                                TCAGTCTGTT TCTCC TC
                                ||||||||||  ||||| ||
                                AGTCGGACGG GGAGG AG
                                      G   _
GAM1042  GRAF    3'  GATGGGATAGTAGCTGG    30560     T      T  C
                                TCAG CTGTTGTC CC TC
                                ||||  |||||||  || ||
                                GGTC GATGATAG GG AG
                                  _      _ T
GAM1042  HARS    5'  GGTCGAGACAGCAGGC      9176           __
                                GTCTGTTGTCTC  CC
                                ||||||||||||  ||
                                CGGACGACAGAG  GG
                                       CT
GAM1042  HCCS    5'  GTTTGGTCTGGGGACCACGGGC 18047        T    CT_   TC
              TGG                  TCAGTCTGT GTCTCC   CTAA
                                |||||||||  ||||||   ||||
                                GGTCGGGCA CAGGGG   GGTT
                                     C     TCT    TGG
GAM1042  HOXB3   5'  GAAGGAGGCAAAGGCTGG    9260        G      C
                                TCAGTCT TTGTCTCC TC
                                |||||||  |||||||| ||
```

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                                GGTCGGA AACGGAGG AG
                                   _       A
GAM1042  HRH1     5'  GATGGCAGATAACAGACTGA   5984              _  C
                                TCAGTCTGTTGTCT CC TC
                                |||||||||||||| || ||
                                AGTCAGACAATAGA GG AG
                                       C  T
GAM1042  IKBKG    5'  GGTTACTTGGGCGGCGAGCTGG 13313      CTG    T   TC_
                                TCAGT   TTGTC CCC   TAATC
                                |||||   ||||| |||   |||||
                                GGTCG   AGCGG GGG   ATTGG
                                   ____    C   TTC
GAM1042  IL21R    3'  GAGGGGGCTGCAGGTTGG    41428     GT    T   T
                                TCA  CTGT GTC CCCTC
                                |||  |||| ||| |||||
                                GGT  GACG CGG GGGAG
                                  TG    T   _
GAM1042  IRTA2    3'  GCCTTCAGGAGATGCCGGGCTG 48407         TT     CTCTAATC
              G                   TCAGTCTG  GTCTCC
                                |||||||||  ||||||
                                GGTCGGGC  TAGAGG
                                     CG     ACTTCCGG
GAM1042  KCNMB4   5'  GGGGGGCGGAGGCTGG      27191         G
                                TCAGTCT TTGTCTCCC
                                ||||||| |||||||||
                                GGTCGGA GGCGGGGGG
                                   _
GAM1042  KIT      3'  AAAGAGAGGGAGGTATGGACTG 4037         T GT       AATC
              G                   TCAGTCTG T  CTCCCTCT
                                |||||||| |  ||||||||
                                GGTCAGGT A  GAGGGAGA
                                     _ TG       GAAAA
GAM1042  KRT4     5'  GAGCTAGGAGGTGGCAGGCTG  9636         TG    ___
                                CAGTCTGT  TCTCC   CTC
                                |||||||||  |||||   |||
                                GTCGGACG  GGAGG   GAG
                                     GT     ATC
GAM1042  LAMB3    3'  GGTTGGGGGCAGATTGGGTTGG 4042      GT   TT    C
                                TCA  CTG  GTCT CCTCTAATC
                                |||  |||  |||| |||||||||
                                GGT  GGT  TAGA GGGGGTTGG
                                  TG   __    C
GAM1042  LAMC2    3'  GGTTAGAGAGAAGGCAGGTTGA 38150     GT    TG    CC
                                TCA  CTGT  TCTC  TCTAATC
                                |||  ||||  ||||  |||||||
                                AGT  GACG  AGAG  AGATTGG
                                  TG   GA   __
GAM1042  LIF      3'  GAAGGAGGCAGCAGAGTTGG   9736      _          C
                                TCAG TCTGTTGTCTCC TC
                                |||| |||||||||||| ||
```

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                                GGTT AGACGACGGAGG AG
                                  G          A
GAM1042  LTF      5'  GGTGAGGTGCAGGCTGG     9825          T GT   _
                                TCAGTCTG T  CTC CC
                                |||||||| |  ||| ||
                                GGTCGGAC G  GAG GG
                                    _ TG   T
GAM1042  MADD     5'  GGGGGACGTCGGGCTGG     55351         T
                                TCAGTCTG TGTCTCCC
                                |||||||| ||||||||
                                GGTCGGGC GCAGGGGG
                                     T
GAM1042  MADD     5'  GGGGGACGTCGGGCTGG     55357         T
                                TCAGTCTG TGTCTCCC
                                |||||||| ||||||||
                                GGTCGGGC GCAGGGGG
                                     T
GAM1042  MAFF     3'  GGTTTTCAGGGGGACAGTGGAC 24653     TG        CT_
                                GTC  TTGTCTCCCT   AATC
                                |||  ||||||||||   ||||
                                CAG  GACAGGGGGA   TTGG
                                  GT         CTT
GAM1042  MAFK     3'  GGCGGGGGGGTGGCGGGC     9879        TG     T
                                GTCTGT  TCTCCC CT
                                ||||||  |||||| ||
                                CGGGCG  GGGGGG GG
                                    GT     C
GAM1042  MAGEA3   5'  GGTTCTGAGGGGACAGGCTGA  18102          GTCT    T_
                                TCAGTCTGTT    CCCTC  AATC
                                ||||||||||    |||||  ||||
                                AGTCGGACAG    GGGAG  TTGG
                                      ____     TC
GAM1042  MAP3K8   5'  AAAGTCGGGGAGGCGGTGGCTG 17788      T TG        CTAATC
              G                   TCAG C  TTGTCTCCCT
                                ||||  |  ||||||||||
                                GGTC G  GGCGGAGGGG
                                  _ GT         CTGAAAA
GAM1042  MATN4    3'  GCGTCAGGGGGATAGCGGGTGG 13822     G           CTAATC
                                TCA TCTGTTGTCTCCCT
                                ||| ||||||||||||||
                                GGT GGGCGATAGGGGGA
                                  _            CTGCGG
GAM1042  MATN4    3'  GCGTCAGGGGGATAGCGGGTGG 47587     G           CTAATC
                                TCA TCTGTTGTCTCCCT
                                ||| ||||||||||||||
                                GGT GGGCGATAGGGGGA
                                  _            CTGCGG
GAM1042  MBD3     3'  ACCCGCATGGAGGCAGTGGGCT 14091       TG       CTCTAATC
              GG                    TCAGTC  TTGTCTCC
                                ||||||  ||||||||
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                                GGTCGG  GACGGAGG
                                   GT       TACGCCCAG
GAM1042  MEN1     5'  GGGGAGATAAGGGCTGA     93376        G
                                TCAGTCT TTGTCTCCCT
                                ||||||| ||||||||||
                                AGTCGGG AATAGAGGGG
                                  _
GAM1042  MMP25    3'  GATTGTGGGGGGCAGTAGCTGG 42443      T          TC
                                TCAG CTGTTGTCTCCC  TAATC
                                |||| ||||||||||||  |||||
                                GGTC GATGACGGGGGG  GTTAG
                                  _          T_
GAM1042  MRPS12   3'  GGGGGCACAGTGGGCTGG    40867       TG   _
                                TCAGTC  TTGT CTCCC
                                ||||||  |||| |||||
                                GGTCGG  GACA GGGGG
                                   GT    C
GAM1042  MRPS12   3'  GGGGGCACAGTGGGCTGG    52961       TG   _
                                TCAGTC  TTGT CTCCC
                                ||||||  |||| |||||
                                GGTCGG  GACA GGGGG
                                   GT    C
GAM1042  MRPS12   3'  GGGGGCACAGTGGGCTGG    52964       TG   _
                                TCAGTC  TTGT CTCCC
                                ||||||  |||| |||||
                                GGTCGG  GACA GGGGG
                                   GT    C
GAM1042  MTCP1    5'  GCCTGGGGGGGAGGGAGTGGGTT 26432     GT TG  G        ATC
            GA                    TCA  C  TT TCTCCCTCTA
                                ||| |  || ||||||||||
                                AGT  G  GA GGAGGGGGGT
                                  TG GT  G         CCGG
GAM1042  MYOC     3'  CCTGGGGGGGAGCAGGCTGA   4230         TTGT       ATC
                                TCAGTCTG    CTCCCTCTA
                                ||||||||    |||||||||
                                AGTCGGAC    GAGGGGGGT
                                     ____         CCT
GAM1042  MYOD1    5'  GGTGGGGGGACAGTGGGTGG   64997     G  TG       T
                                TCA TC  TTGTCTCCC CT
                                ||| ||  ||||||||| ||
                                GGT GG  GACAGGGGG GG
                                  _ GT       T
GAM1042  NAGLU    5'  GGAGGCGGCAGCTGA       4241       T
                                TCAG CTGTTGTCTCC
                                |||| ||||||||||
                                AGTC GACGGCGGAGG
                                  _
GAM1042  NDST1    3'  GGGGGAGACAGACTGG      7747         GTT
                                TCAGTCT   GTCTCCCTC
                                |||||||   |||||||||
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                                GGTCAGA   CAGAGGGGG
                                    ___
GAM1042  NELL2    5'  AGAGGGAGACGATGGACTGA   20477
                                TCAGTCTGTTGTCTCCCTCT
                                ||||||||||||||||||||
                                AGTCAGGTAGCAGAGGGAGA

GAM1042  NEUROD2  3'  GAGGGGAAGTGGATTGA     20481       TG  G  T
                                TCAGTC  TT TC CCCTC
                                ||||||  || || |||||
                                AGTTAG  GA AG GGGAG
                                   GT  _  _
GAM1042  NFATC1   3'  AGGGAGGTGGCCGGGCTGA   20483        _ TG
                                TCAGTCTG T  TCTCCCT
                                ||||||||  |  |||||||
                                AGTCGGGC G  GGAGGGA
                                     C GT
GAM1042  NHLH1    3'  GCCCTGGGGAGGCAGGGGTTGG 18801      T  G        CTAATC
                                TCAG CT TTGTCTCCCT
                                ||||  ||  ||||||||||
                                GGTT GG GACGGAGGGG
                                  _  G         TCCCGG
GAM1042  NPR3     3'  ATTCTTTAAGGAGATAGACGGG 6174     GT   _      CTCTAATC
            TTGA                   CA  CTGT TGTCTCC
                                ||  ||||  |||||||
                                GT  GGCA ATAGAGG
                                 TG    G      AATTTCTTAG
GAM1042  NPY1R    3'  GATTAGATTGTCAACAGATTGG 6180           TCTCCC
                                TCAGTCTGTTG     TCTAATC
                                ||||||||||      |||||||
                                GGTTAGACAAC     AGATTAG
                                      TGTT__
GAM1042  NR3C1    3'  AGAGGGAGATGGAGACTGG    3921         G TG
                                TCAGTCT T  TCTCCCTCT
                                |||||||  |  |||||||||
                                GGTCAGA G  AGAGGGAGA
                                   _ GT
GAM1042  NYX      5'  GACTTGGGAGATGGATGGGCTG 42601          _      TCTAATC
            A                   TCAGTCTGTT GTCTCCC
                                ||||||||| |||||||
                                AGTCGGGTAG TAGAGGG
                                      G       TTCAG
GAM1042  OCLN     5'  GGACGCAGCAGATTGG      10317           C
                                TCAGTCTGTTGT TCC
                                ||||||||||| |||
                                GGTTAGACGACG AGG
                                       C
GAM1042  OPCML    3'  GGTTGGGGGCGGGGTGGGCAG  10347     _ TG   _
                                CTG T  TCTC CCTCTAATC
                                ||| |  |||| |||||||||
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                                GAC G  GGGG GGGGGTTGG
                                  G GT    C
GAM1042  PABPN1   5'  ATTGGAGGGGTGACATTGG   16175    GT   _
                                CT  TGTC TCCCTCTAAT
                                ||  |||| ||||||||||
                                GG  ACAG GGGGAGGTTA
                                 TT    T
GAM1042  PACE     3'  TCCCAGTGGGAGGGGCAGGCTG 10399          G     T  AATC
             A                   TCAGTCTGTT TCTCCC CT
                                 |||||||||| |||||| ||
                                 AGTCGGACGG GGAGGG GA
                                       _     T  CCCTG
GAM1042  PIM1     3'  TAGGGGGGAAACAGGTTGG   91031     GT    G     T
                                TCA  CTGTT TCTCCC CTA
                                |||  ||||| |||||| |||
                                GGT  GACAA AGGGGG GAT
                                  TG    _     _
GAM1042  POP4     3'  GGGGAGGAACAGACTGG     21780          G
                                TCAGTCTGTT TCTCCCT
                                |||||||||| |||||||
                                GGTCAGACAA GGAGGGG
                                       _
GAM1042  PPP2R5E  5'  GGTCCGGGGCAACGAGCTGA  20727      TC       ___
                                TCAG  TGTTGTCTC   CC
                                ||||  |||||||||   ||
                                AGTC  GCAACGGGG   GG
                                   GA        CCT
GAM1042  PRDM2    3'  GGTTTCAGGGATGACAGATT   31850         TC    CT
                                AGTCTGTTG  TCCCT  AATC
                                |||||||||  |||||  ||||
                                TTAGACAGT  AGGGA  TTGG
                                      __    CT
GAM1042  PTGS1    5'  GGGGAGGGGATGGGCTGG    54573          G
                                TCAGTCTGTT TCTCCCT
                                |||||||||| |||||||
                                GGTCGGGTAG GGAGGGG
                                      G
GAM1042  PTGS1    5'  GGGGAGGGGATGGGCTGG    6354           G
                                TCAGTCTGTT TCTCCCT
                                |||||||||| |||||||
                                GGTCGGGTAG GGAGGGG
                                      G
GAM1042  RAB27A   3'  GATTGGGGTGGGGCAGGCTGG  15925         TTGT   _
                                TCAGTCTG    CTCC CTCTAATC
                                ||||||||    |||| ||||||||
                                GGTCGGAC    GGGG GGGGTTAG
                                      ____   T
GAM1042  RAD23B   5'  GGTCCGGGGCACGGGCTGG    11217         T    ___
                                TCAGTCTGT GTCTC   CC
                                ||||||||| |||||   ||
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                                GGTCGGGCA CGGGG   GG
                                    _    CCT
GAM1042  RARG     3'  GGTTGGGGCTTCAGGCAGCAGA 6382            CC__
              CTGA                   CAGTCTGTTGTCT    CTCTAATC
                                |||||||||||||    ||||||||
                                GTCAGACGACGGA    GGGGTTGG
                                     CTTC
GAM1042  RAX      5'  GGCGGCAGCGGGCTGA      25538            T
                                TCAGTCTGTTGTC CC
                                |||||||||||| ||
                                AGTCGGGCGACGG GG
                                     C
GAM1042  RBM3     5'  CCGCCTGGGAGGCGACGACTGG 70486       T        TCTAATC
                                TCAGTC GTTGTCTCCC
                                |||||| ||||||||||
                                GGTCAG CAGCGGAGGG
                                   _        TCCGCCG
GAM1042  RELA     3'  AGTGGGGGAGAGCAGGCTGG   41752         G     T
                                TCAGTCTGTT TCTCCC CT
                                |||||||||| ||||||| ||
                                GGTCGGACGA AGGGGG GA
                                     G     T
GAM1042  RET      5'  GGGGCGGCCAGACTGA      40596        TT   T
                                TCAGTCTG  GTC CCCT
                                ||||||||  ||| ||||
                                AGTCAGAC  CGG GGGG
                                   __  C
GAM1042  RET      5'  GGGGCGGCCAGACTGA      4372         TT   T
                                TCAGTCTG  GTC CCCT
                                ||||||||  ||| ||||
                                AGTCAGAC  CGG GGGG
                                   __  C
GAM1042  RET      5'  GGGGCGGCCAGACTGA      40169        TT   T
                                TCAGTCTG  GTC CCCT
                                ||||||||  ||| ||||
                                AGTCAGAC  CGG GGGG
                                   __  C
GAM1042  RET      5'  GGGGCGGCCAGACTGA      40180        TT   T
                                TCAGTCTG  GTC CCCT
                                ||||||||  ||| ||||
                                AGTCAGAC  CGG GGGG
                                   __  C
GAM1042  RGS3     5'  GGTTGGCAGAGGCAGGCTGA   40863         ___   TC
                                TCAGTCTGT   TGTC  CC
                                |||||||||   ||||  ||
                                AGTCGGACG   ACGG  GG
                                     GAG    TT
GAM1042  ROM1     3'  GGTTGGGGGGGATCGTAGGATTA 4385     _    GTTGTC
              GA                   TC AGTCT     TCCCTCTAATC
                                || |||||     ||||||||||
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                                AG TTAGG     AGGGGGGTTGG
                                 A    ATGCT_
GAM1042  RXRA     3'  GGTTGGACCGGGAGGCAGTGGC 11415     T TG       __
              TTGG                  CAG C  TTGTCTCCC  TCTAATC
                                |||  |  |||||||||  |||||||
                                GTT G  GACGGAGGG  AGGTTGG
                                  C GT        CC
GAM1042  S100A4   3'  GGTTGGGGGGGTCTGCCAGCTGG 11423      T   TTGTCT
                                TCAG CTG     CCCTCTAATC
                                ||||  |||     ||||||||||
                                GGTC GAC     GGGGGGGTTGG
                                  _   CGTCT_
GAM1042  S100A4   3'  GGTTGGGGGGGTCTGCCAGCTGG 38953      T   TTGTCT
                                TCAG CTG     CCCTCTAATC
                                ||||  |||     ||||||||||
                                GGTC GAC     GGGGGGGTTGG
                                  _   CGTCT_
GAM1042  SEL1L    3'  GGTTTGAGAAACAGGCTGA    17362          G    ____
                                TCAGTCTGTT TCTC   CC
                                ||||||||||  ||||   ||
                                AGTCGGACAA AGAG   GG
                                      _    TTT
GAM1042  SET      3'  GGTGGGATAATGGACT      11556            _
                                AGTCTGTTGTCTC CC
                                ||||||||||||  ||
                                TCAGGTAATAGGG GG
                                       T
GAM1042  SH3BP2   3'  AGGGAGGTAGGGGCTGG     11590        G  GT
                                TCAGTCT TT  CTCCCT
                                |||||||  ||  ||||||
                                GGTCGGG GA  GAGGGA
                                    _  TG
GAM1042  SLC25A17  3'  GGTTGGATTTTGGGGTGGCAGT 20998     T   TG    CC__
              TGG                   CAG CTGT  TCTC    TCTAATC
                                |||  ||||  ||||   |||||||
                                GTT GACG  GGGG    AGGTTGG
                                  _   GT    TTTT
GAM1042  STAM     3'  GATAGAGGCAATGGATAGA    12961    A         CC
                                TC GTCTGTTGTCTC  TC
                                ||  ||||||||||||  ||
                                AG TAGGTAACGGAG  AG
                                 A          AT
GAM1042  STARD5   5'  GGCGGGACACAGCAGGCTGG   47558           C    T
                                TCAGTCTGTTGT TCCC CT
                                ||||||||||||  ||||  ||
                                GGTCGGACGACA AGGG GG
                                       C    C
GAM1042  STCH     3'  GATTAGACGTGACCAGATTGA  22709         TT   TCCC
                                TCAGTCTG  GTC    TCTAATC
                                ||||||||  |||    |||||||
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                                AGTTAGAC  CAG   AGATTAG
                                    __  TGC_
GAM1042  TAGLN    3'  GGGGAGAAGCGGGCTGG     59638         G
                                TCAGTCTGTT TCTCCCT
                                |||||||||| |||||||
                                GGTCGGGCGA AGAGGGG
                                    _
GAM1042  TCF2     3'  GACTCAGGCAGACAGCAGGCTG 21377           C  CTAATC
           G                     TCAGTCTGTTGTCT CCT
                                |||||||||||||| |||
                                GGTCGGACGACAGA GGA
                                      C  CTCAG
GAM1042  TEAD2    3'  GGTTGGAGAGCTGAACAGGCTG 13183        G___   CT  AATC
           G                     CAGTCTGTT   TCTCC  CT
                                |||||||||   |||||  ||
                                GTCGGACAA   AGAGG  GG
                                     GTCG    TT    C
GAM1042  TFAP4    3'  GGTTGGGGGGTAAGACTAGGCTG 12240       TT   C_
           G                     TCAGTCTG  GTCT  CCTCTAATC
                                |||||||||  ||||  |||||||||
                                GGTCGGAT  CAGA  GGGGGTTGG
                                    __   AT
GAM1042  TGFB3    3'  TTAGAGGAAGGCTGA      12262       GTTGTCTC
                                TCAGTCT      CCTCTAA
                                |||||||      |||||||
                                AGTCGGA      GGAGATT
                                   A_______
GAM1042  THBD     3'  ATTAGAGGGAGGAGAATGA   4493     G  GTTG
                                TCA TCT   TCTCCCTCTAAT
                                ||| |||   ||||||||||||
                                AGT AGA   GGAGGGAGATTA
                                  A  ____
GAM1042  THBS1    3'  AGGGAGACAAAGACTGG     12281       G
                                TCAGTCT TTGTCTCCCT
                                ||||||| ||||||||||
                                GGTCAGA AACAGAGGGA
                                    _
GAM1042  TIF1     5'  GGTCGTCGGGGGCGGCGGGCGG 60379    A         CTCTAATC
           A                     TC GTCTGTTGTCTCC
                                || ||||||||||||
                                AG CGGGCGGCGGGGG
                                  G          CTGCTGG
GAM1042  TNFRSF1B 3'  GATTCTGGGAGGAAGCAGGTTG 6523     GT   GT   TCT
           A                     TCA  CTGTT  CTCCC   AATC
                                |||  |||||  |||||  ||||
                                AGT  GACGA  GAGGG   TTAG
                                  TG    AG    TC_
GAM1042  TNFSF11  3'  GATTGGAGCAATTACGGGTTGA 52240    GT   TGTCTCC
                                TCA  CTGT     CTCTAATC
                                |||  ||||     ||||||||
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                                AGT  GGCA      GAGGTTAG
                                  TG   TTAAC__
GAM1042  TNFSF11   3'  GATTGGAGCAATTACGGGTTGA 13513     GT    TGTCTCC
                                TCA  CTGT      CTCTAATC
                                |||  ||||      ||||||||
                                AGT  GGCA      GAGGTTAG
                                  TG   TTAAC__
GAM1042  TRAF1     3'  GGTTAGGATGGCAGGACGTGGG 18975      TG T    __  C_
            CTGG                    AGTC  T GTCT  CC  TCTAATC
                                |||| | ||||  ||  |||||||
                                TCGG  G CAGG  GG  GGATTGG
                                  GT _    AC  TA
GAM1042  TRIM9     5'  GAGGGGATGACAGGCT      30759        TG  T
                                AGTCTGT  TC CCCTC
                                |||||||  || |||||
                                TCGGACA  AG GGGAG
                                    GT  _
GAM1042  TYRP1     3'  GGTTGAATATAATAGATTGA   72317           ___  TC
                                TCAGTCTGTTG   TC  CC
                                ||||||||||   ||  ||
                                AGTTAGATAAT   AG  GG
                                      ATA  TT
GAM1042  UBE3A     5'  GGCGGAGGCGGCGGGC      55592            C
                                GTCTGTTGTCTCC TC
                                |||||||||||| ||
                                CGGGCGGCGGAGG GG
                                       C
GAM1042  UBTF      3'  GGTGGGGGTAGGGGGCTGG    26450        G   T    T
                                TCAGTCT TTG CTCCC CT
                                ||||||| ||| ||||| ||
                                GGTCGGG GAT GGGGG GG
                                    G   _    T
GAM1042  VANGL2    3'  GTCTGAGGAGCAGGTTGG     71654     GT    GTCTC    TA
                                TCA  CTGTT    CCTC  AT
                                |||  |||||    ||||  ||
                                GGT  GACGA    GGAG  TG
                                  TG    _____    TC
GAM1042  WFS1      3'  GGCTGGGGGAGGCGGCACATTG 20012       C           TAATC
            G                    TCAGT TGTTGTCTCCCTC
                                ||||| ||||||||||||
                                GGTTA ACGGCGGAGGGGG
                                   C           TCGG
GAM1042  WHSC1     3'  GAGGAGATGATAACTGG      23660       C  TG    C
                                TCAGT TGT  TCTCC TC
                                ||||| |||  ||||| ||
                                GGTCA ATA  AGAGG AG
                                   _  GT    _
GAM1042  ZNF142    3'  GGTCTGAGATGTGCAGACTGG  17433          _     ___
                                TCAGTCTGT TGTCTC   CC
                                |||||||| ||||||   ||
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                                GGTCAGACG GTAGAG   GG
                                     T     TCT
GAM1042  ZNF76    3'  GATTGGGGCTGCTATGGGGACT 12811        GTTGTCTCC
              GG                   TCAGTCT        CTCTAATC
                                   |||||||        ||||||||
                                   GGTCAGG        GGGGTTAG
                                      GGTATCGTC
GAM1042  ABLIM    3'  GGGGACATTAGACTGA      22034         T
                                   TCAGTCTG TGTCTCC
                                   |||||||| |||||||
                                   AGTCAGAT ACAGGGG
                                        T
GAM1042  ABLIM    3'  GGGGACATTAGACTGA      9773          T
                                   TCAGTCTG TGTCTCC
                                   |||||||| |||||||
                                   AGTCAGAT ACAGGGG
                                        T
GAM1042  AFAP     3'  CGAGCCTCTGGGGGCAGGGGCT 41301      G      _____   TAATC
              GG                   GTCT TTGTCTCC     CTC
                                   |||| ||||||||     |||
                                   CGGG GACGGGGG     GAG
                                     _       TCTCC     CT
GAM1042  ALY      3'  GGGGGGCGGTGGCTGG      19352      T TG
                                   TCAG C  TTGTCTCCC
                                   |||| |  |||||||||
                                   GGTC G  GGCGGGGGG
                                     _ GT
GAM1042  AP1G2    5'  GGTTAGGGGGAGGAAACGGTAG 54502    AGT    GT
              A                     TC   CTGTT  CTCCCTCTAATC
                                   ||   |||||  ||||||||||||
                                   AG   GGCAA  GAGGGGGATTGG
                                    AT_     AG
GAM1042  APCL     5'  GAGCCTGGGGGTGCTGGGCTGG 19674        GT GT   ___
                                   TCAGTCT  T  CTCC   CTC
                                   |||||||  |  ||||   |||
                                   GGTCGGG  G  GGGG   GAG
                                        TC TG    TCC
GAM1042  ARHGAP9  5'  GAGGAGGTGGTGGTATTGG    50679      _ TG TG    C
                                   TCAGT C  T  TCTCC TC
                                   ||||| |  |  ||||| ||
                                   GGTTA G  G  GGAGG AG
                                      T GT GT    _
GAM1042  C19orf7  3'  GGGGAGGCAGGCTGG       61130          TGT
                                   TCAGTCTGT   CTCCCT
                                   |||||||||   ||||||
                                   GGTCGGACG   GAGGGG
                                               ___
GAM1042  C20orf151 3'  TGGAGGGAGACAGTGGGC    88704     TG
                                   GTC  TTGTCTCCCTCTA
                                   |||  ||||||||||||
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                                CGG  GACAGAGGGAGGT
                                  GT
GAM1042  C20orf28  3'  GGTTGGGGGGGCACGGTACGCTG 31230      C  TT  CT
              A                    TCAGT TG  GT  CCCTCTAATC
                                   ||||| ||  ||  ||||||||||
                                   AGTCG AT  CA  GGGGGGTTGG
                                     C  GG  C_
GAM1042  C22orf20  3'  GATGGGGGGTAGGCTGG     47431         TTG     _
                                   TCAGTCTG   TCTCCC TC
                                   ||||||||   ||||||  ||
                                   GGTCGGAT   GGGGGG AG
                                        ___      T
GAM1042  C5orf6    3'  GGTTGGGGCTCACTGAGGGATT 33486        G  GTCTCC
              GG                     TCAGTCT TT     CTCTAATC
                                   |||||||  ||     ||||||||
                                   GGTTAGG AG     GGGGTTGG
                                       G  TCACTC
GAM1042  C5orf7    5'  GGTGGGAGGCGGCGGGC     63869             T
                                   GTCTGTTGTCTCCC CT
                                   ||||||||||||||  ||
                                   CGGGCGGCGGAGGG GG
                                            T
GAM1042  C6.1A     3'  GGTTGCCAGGGATAGGGACTGG 44286        G      CCTC
                                   TCAGTCT TTGTCTC    TAATC
                                   |||||||  |||||||    |||||
                                   GGTCAGG GATAGGG    GTTGG
                                      _       ACC_
GAM1042  C8orf14   5'  GAGCTGGAGGTGTGCAGACTGG 53999          _ GT    __
                                   TCAGTCTGT T  CTCC  CTC
                                   |||||||||  |  ||||  |||
                                   GGTCAGACG G  GAGG  GAG
                                         T TG    TC
GAM1042  C8orf14   5'  GATGGAGGCAGGGGGCTGA    54000        G       C
                                   TCAGTCT TTGTCTCC TC
                                   |||||||  ||||||||  ||
                                   AGTCGGG GACGGAGG AG
                                      G       T
GAM1042  C9orf12   5'  GAGCGGGGGCGGCAGCTGA    42791      T         _
                                   TCAG CTGTTGTCTCC CTC
                                   ||||  ||||||||||  |||
                                   AGTC GACGGCGGGGG GAG
                                     _         C
GAM1042  C9orf7    3'  GGAGTGGCAGGCTGG       34177           T
                                   TCAGTCTGTTG CTCC
                                   ||||||||||  ||||
                                   GGTCGGACGGT GAGG
                                              _
GAM1042  CHSY1     5'  GGGCGGGGGCAGCGGGCTGA   29902              _
                                   TCAGTCTGTTGTCTCC CTC
                                   ||||||||||||||  |||
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                                AGTCGGGCGACGGGGG GGG
                                          C
GAM1042  CXYorf1   5'  GATGGGGTGGCAGCTGA     82049      T    TG  T  C
                                TCAG CTGT  TC CC TC
                                |||| ||||  || || ||
                                AGTC GACG  GG GG AG
                                  _   GT  _  T
GAM1042  CYLD      3'  GATTAGGGTATTTAGCAGTTGA 30885      T     TCTCC
                                TCAG CTGTTG    CTCTAATC
                                |||| ||||||    ||||||||
                                AGTT GACGAT    GGGATTAG
                                  _     TTAT_
GAM1042  DDX31     3'  AAGCCCCGGGTGGCAGTGGATT 42924       TG    T   TCTAATC
              GA                  TCAGTC  TTGTC CCC
                                |||||| ||||| |||
                                AGTTAG  GACGG GGG
                                   GT    T   CCCCGAAG
GAM1042  DKFZP434K028 3'  GAGGAGGTGGTAGACCGA    93232    A     TG    C
                                TC GTCTGT  TCTCC TC
                                || ||||||  ||||| ||
                                AG CAGATG  GGAGG AG
                                 C     GT    _
GAM1042  DKFZp434N127 3'  CCTAGGGGGAGGACAGGTTGG  50057     GT    GT       ATC
                                TCA  CTGTT  CTCCCTCTA
                                |||  |||||  |||||||||
                                GGT  GACAG  GAGGGGGAT
                                  TG    __        CCG
GAM1042  DKFZP586B2420 3'  GACGGGGGCAGGGGCTGA    74996        G      C
                                TCAGTCT TTGTCTCC TC
                                ||||||| |||||||| ||
                                AGTCGGG GACGGGGG AG
                                    _       C
GAM1042  DKFZP586F1524 3'  GGCGGGGGGTGCTGGACTGG    31491        GTTGT    T
                                TCAGTCT    CTCCC CT
                                |||||||    ||||| ||
                                GGTCAGG    GGGGG GG
                                    TCGT_    C
GAM1042  DKFZP586K0717 5'  GTTGGAGGGGGCTGTTGA    48136    TGTT   T
                                TC    GTC CCCTCTAAT
                                ||    ||| |||||||||
                                AG    CGG GGGAGGTTG
                                 TTGT   _
GAM1042  DKFZP586N0721 3'  GGGGAGATGATGGGCT      31204        TG
                                AGTCTGT  TCTCCCT
                                |||||||  |||||||
                                TCGGGTA  AGAGGGG
                                    GT
GAM1042  DKFZp761K1824 3'  AGCAGGAGGTGGTAGACT    34206        TG    CT
                                AGTCTGT  TCTCC  CT
                                |||||||  |||||  ||
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                                TCAGATG  GGAGG  GA
                                   GT    AC
GAM1042  DKFZp761O17121 3'  GGTGGGGTGGCAGTTGG    50142     T   TG   _
                                TCAG CTGT  TCTC CC
                                |||| ||||  |||| ||
                                GGTT GACG  GGGG GG
                                  _   GT   T
GAM1042  E       3'  GATTAGAGGGTCACATATAACT 40389      CTGT   CT
            GG                    TCAGT   TGT  CCCTCTAATC
                                |||||   |||  ||||||||||
                                GGTCA   ACA  GGGAGATTAG
                                  ATAT   CT
GAM1042  ELF4     5'  GGGGAGAGGACGGGCTGG    7435          G
                                TCAGTCTGTT TCTCCCT
                                |||||||||| |||||||
                                GGTCGGGCAG AGAGGGG
                                     G
GAM1042  ESDN     3'  GGTTGGGGAAAATGTGGTGACT 55178       TGTTGTCTCC
            GA                    TCAGTC        CTCTAATC
                                ||||||        ||||||||
                                AGTCAG        GGGGTTGG
                                   TGGTGTAAAA
GAM1042  EZF-2    3'  GGGGTTGGGGGAGGCAGCGGGT 37103     G          T
            GA                    TCA TCTGTTGTCTCCC CTAATC
                                ||| ||||||||||||| ||||||
                                AGT GGGCGACGGAGGG GGTTGG
                                _          _     GGG
GAM1042  FADS2    3'  GAGGAGGTGGGGGCTGG     14953       G TG    C
                                TCAGTCT T  TCTCC TC
                                ||||||| |  ||||| ||
                                GGTCGGG G  GGAGG AG
                                   _ GT    _
GAM1042  FADS2    3'  GAGGGGGCGGCAGGGCTGG   14954       _      T
                                TCAGTC TGTTGTC CCCTC
                                |||||| ||||||| |||||
                                GGTCGG ACGGCGG GGGAG
                                   G     _
GAM1042  FLJ10120 3'  GGTGAGAGACAGATTGA     35835          G   _
                                TCAGTCTGTT TCTC CC
                                |||||||||| |||| ||
                                AGTTAGACAG AGAG GG
                                      _   T
GAM1042  FLJ10439 5'  GGGAGGCGGAGGTTGA      36118     GT  G
                                TCA  CT TTGTCTCCC
                                |||  || |||||||||
                                AGT  GA GGCGGAGGG
                                  TG  _
GAM1042  FLJ10597 3'  GTGGGGCAGGGAGGTGGGGGTT 36318      T  G TG      _  AATC
            GG                    TCAG CT T  TCTCCCT CT
                                |||| || |  ||||||| ||
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                                GGTT GG G  GGAGGGA GG
                                  _ G GT      C  GGTGG
GAM1042  FLJ10871  3'  GGCGGAGGTGACTGGCTGG   36779       T  TG    C
                                TCAGTC GT  TCTCC TC
                                ||||||  ||  |||||  ||
                                GGTCGG CA  GGAGG GG
                                   T  GT    C
GAM1042  FLJ11181  3'  GAGGAATGACAGGCTGG     37138         TG CTC
                                TCAGTCTGT  T   CCTC
                                |||||||||  |   ||||
                                GGTCGGACA  A   GGAG
                                     GT A__
GAM1042  FLJ11715  3'  GATTAGGGGTGGAGGCAGCAGG 44672    GT        __
                   ATGA                CA  CTGTTGTCTCC  CTCTAATC
                                ||  ||||||||||  ||||||||
                                GT  GACGACGGAGG  GGGATTAG
                                 AG         TG
GAM1042  FLJ12089  3'  ATTTCTGGGGTGGCTAGACTGG 44641        TT   T    CTAATC
                                TCAGTCTG  GTC CCCT
                                ||||||||  ||| ||||
                                GGTCAGAT  CGG GGGG
                                     __   T    TCTTTAT
GAM1042  FLJ12190  3'  GATGGGGATAATGAGCTGG    46874      CT       C
                                TCAGT  GTTGTCTCC TC
                                |||||  |||||||||  ||
                                GGTCG  TAATAGGGG AG
                                   AG        T
GAM1042  FLJ12529  3'  GATTGGGAGGGGTGGCAGAC   45660       TG  T  CT
                                GTCTGT  TC CC  CTAATC
                                ||||||  ||  ||  ||||||
                                CAGACG  GG GG  GGTTAG
                                   GT  _  AG
GAM1042  FLJ12547  3'  GGTCATGGGAGGCAAAAGGCTG 46494        G        TCTAATC
                   G                 TCAGTCT TTGTCTCCC
                                |||||||  |||||||||
                                GGTCGGA AACGGAGGG
                                     A        TACTGG
GAM1042  FLJ13659  3'  GGGAGGCAGAGGTTGA      47249     GT  G
                                TCA  CT TTGTCTCCC
                                |||  ||  |||||||||
                                AGT  GA GACGGAGGG
                                  TG  _
GAM1042  FLJ13693  3'  GGTTAGAGGAGGGGTGAAGATT 45649        G TG   _
                   GG                  TCAGTCT T  TCTC CCTCTAATC
                                |||||||  |  ||||  |||||||||
                                GGTTAGA A  GGGG GGAGATTGG
                                     _ GT    A
GAM1042  FLJ13769  3'  GGTTTAGTAAGGGGGACAGAGG 46622       G        __    TC
                   GCTGA                AGTCT TTGTCTCCCT  CTAA
                                |||||  ||||||||||  ||||
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                                TCGGG GACAGGGGGA  GATT
                                   A         AT    TGG
GAM1042  FLJ13881  3'  GGCAGGGAGGCAAGGACTGG   45311        G        _
                                TCAGTCT TTGTCTCCCT CT
                                ||||||| |||||||||| ||
                                GGTCAGG AACGGAGGGA GG
                                    _         C
GAM1042  FLJ14642  3'  GATGGAGACAGTGATTGG    51501       TGT      C
                                TCAGTC   TGTCTCC TC
                                ||||||   ||||||| ||
                                GGTTAG   ACAGAGG AG
                                   TG_      T
GAM1042  FLJ20255  3'  GATGGCAGGTGATAGACTGG   34798         TG   _  C
                                TCAGTCTGT  TCT CC TC
                                |||||||||  ||| || ||
                                GGTCAGATA  GGA GG AG
                                     GT   C  T
GAM1042  FLJ20294  3'  AGTGGGGGGGTGTAGGCTGG    34870        TTG      T
                                TCAGTCTG   TCTCCC CT
                                ||||||||   |||||| ||
                                GGTCGGAT   GGGGGG GA
                                     GT_      T
GAM1042  FLJ20359  3'  GCTGCAGGGAGACAACGGGTGG 35043     G           CTAATC
                                TCA TCTGTTGTCTCCCT
                                ||| ||||||||||||||
                                GGT GGGCAACAGAGGGA
                                  _           CGTCGG
GAM1042  FLJ20378  5'  GAGGGGGTGGTAACTGA     35093       C  TT T
                                TCAGT TG  G CTCCCTC
                                ||||| ||  | |||||||
                                AGTCA AT  T GGGGGAG
                                   _  GG _
GAM1042  FLJ20378  3'  GGTGGGGGTGGGGGGCTGG     35095        G TG   _
                                TCAGTCT T  TCTC CC
                                ||||||| |  |||| ||
                                GGTCGGG G  GGGG GG
                                     G GT    T
GAM1042  FLJ20729  3'  GATTGGGGTATTGTCAATGGGT 35648     G      TCTCC_
            GA                    TCA TCTGTTG      CTCTAATC
                                ||| |||||||      ||||||||
                                AGT GGGTAAC      GGGGTTAG
                                  _      TGTTAT
GAM1042  FLJ20772  3'  GGGAGGTAGATTGA        35658         TTG
                                TCAGTCTG   TCTCCC
                                ||||||||   ||||||
                                AGTTAGAT   GGAGGG
                                     ___
GAM1042  FLJ20847  5'  ATTGGAGGGAGAGAACAGA   94828        G
                                TCTGTT TCTCCCTCTAAT
                                |||||| ||||||||||||
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                                AGACAA AGAGGGAGGTTA
                                   G
GAM1042  FLJ22055  3'  GATTGGGTCTCTGTCATAGATT 45497        TGTCTCCC
             GA                   TCAGTCTGT       TCTAATC
                                  |||||||||       |||||||
                                  AGTTAGATA       GGGTTAG
                                     CTGTCTCT
GAM1042  FLJ22393  3'  GGTGGGGGGTGGCAGGTGG    47062    G    TG  T   T
                                  TCA TCTGT  TC CCC CT
                                  ||| |||||  || ||| ||
                                  GGT GGACG  GG GGG GG
                                    _    GT  _   T
GAM1042  FLJ22477  3'  GATAGAGTGATAGACTGG    45345          T   CC
                                  TCAGTCTGTTG CTC  TC
                                  |||||||||||| |||  ||
                                  GGTCAGATAGT GAG  AG
                                        _   AT
GAM1042  FLJ22494  3'  GAGGGAGGCAAGAGGCTGG    45676       G
                                  TCAGTCT TTGTCTCCCTC
                                  ||||||| ||||||||||
                                  GGTCGGA AACGGAGGGAG
                                     G
GAM1042  FLJ22662  3'  GGAGGGAGATGACGGACT    45723       TG
                                  AGTCTGT  TCTCCCTCT
                                  |||||||  |||||||||
                                  TCAGGCA  AGAGGGAGG
                                     GT
GAM1042  FLJ23071  3'  TTGTTTGGGAAATGGACTGA   47269         GTC    TCTAATC
                                  TCAGTCTGTT   TCCC
                                  ||||||||||   ||||
                                  AGTCAGGTAA   AGGG
                                        ____   TTTGTTT
GAM1042  FLJ23306  5'  GATGGGGCAGCAGGTGG     44558     G       T  C
                                  TCA TCTGTTGTC CC TC
                                  ||| |||||||| || ||
                                  GGT GGACGACGG GG AG
                                    _        _  T
GAM1042  FLJ23436  3'  GGTTGGAGGGAGGCCAGGCCGG 45143    A    TT
                                  TC GTCTG  GTCTCCCTCTAATC
                                  || |||||  ||||||||||||||
                                  GG CGGAC  CGGAGGGAGGTTGG
                                   C    __
GAM1042  FLJ32449  3'  GGTTACATTAGGTACCGGGCTG 58724        T GT  CCCTC
             A                    TCAGTCTG T  CT     TAATC
                                  ||||||||  |  ||    |||||
                                  AGTCGGGC A  GA    ATTGG
                                       C TG  TTAC_
GAM1042  G10      5'  GAGGGGACGGTAGATT      91066       TT   T
                                  AGTCTG  GTC CCCTC
                                  ||||||  ||| |||||
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                                TTAGAT  CAG GGGAG
                                   GG  _
GAM1042  G4       3'  ATTAGGGGGTCTGGATAG    90992       GTCT
                                CTGTT    CCCTCTAAT
                                |||||    |||||||||
                                GATAG    GGGGGATTA
                                   GTCT
GAM1042  GBL      3'  GATTGGGGACGGGCCAGGCTGG 42335         TT    CC
                                TCAGTCTG  GTCT  CTCTAATC
                                ||||||||  ||||  ||||||||
                                GGTCGGAC  CGGG  GGGGTTAG
                                     __   CA
GAM1042  GENX-3414 3'  GGTTGGGCATAGGCTGA     14148          T    C_
                                TCAGTCTGT GTCT  CC
                                |||||||| ||||  ||
                                AGTCGGATA CGGG  GG
                                     _   TT
GAM1042  GOLGB1    3'  GGTTGGAGCTGCAGGGACTGG  15635        G    CTCC
                                TCAGTCT TTGT    CTCTAATC
                                ||||||| ||||    ||||||||
                                GGTCAGG GACG    GAGGTTGG
                                     _   TC__
GAM1042  GPR107    3'  GAACAGGAGGGATAATGGATTG 40562              _  CTAATC
            G                    TCAGTCTGTTGTCTC CCT
                                |||||||||||||| |||
                                GGTTAGGTAATAGGG GGA
                                        A   CAAG
GAM1042  GPS2      5'  ATTGGGGTGACAGCGCTGG    87151       CT     T    CT
                                TCAGT  GTTGTC CCCT  AAT
                                |||||  |||||| ||||  |||
                                GGTCG  CGACAG GGGG  TTA
                                   __      T   __
GAM1042  GTPBP5    3'  GGTTGGGGTGCCCATAACGGGG 65361     G       CTCC_
            TGG                    TCA TCTGTTGT    CTCTAATC
                                ||| ||||||||    ||||||||
                                GGT GGGCAATA    GGGGTTGG
                                  G       CCCGT
GAM1042  H11       3'  GGGGGTGAGGACTGA       26850        GTTG  T
                                TCAGTCT    TC CCCTC
                                |||||||    || |||||
                                AGTCAGG    AG GGGGG
                                     _____  T
GAM1042  H326      3'  GGTGGGGTGATAGGGTGG    31709     G     TG   _
                                TCA TCTGT  TCTC CC
                                ||| |||||  |||| ||
                                GGT GGATA  GGGG GG
                                  G    GT    T
GAM1042  HCA127    3'  GATGGGGATGGGGGCTGA    37950        G TG    C
                                TCAGTCT T  TCTCC TC
                                |||||||  |  ||||| ||
```

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                                AGTCGGG G  AGGGG AG
                                   _ GT    T
GAM1042  HEAB     5'  GGTGGGAGATGACAGCTTGG   22414     T   TG     T
                                TCAG CTGT  TCTCCC CT
                                |||| ||||  |||||| ||
                                GGTT GACA  AGAGGG GG
                                  C   GT     T
GAM1042  HEMK     3'  GATGGAGCCAGCAGGCTGG   32431          T   C
                                TCAGTCTGTTG CTCC TC
                                |||||||||||| |||| ||
                                GGTCGGACGAC GAGG AG
                                      C   T
GAM1042  HIC2     3'  GGTGGGAGACAGAGGACTGG   65267        G       T
                                TCAGTCT TTGTCTCCC CT
                                ||||||| ||||||||| ||
                                GGTCAGG GACAGAGGG GG
                                   A       T
GAM1042  IL-17RE   3'  GGTTGGGGGTGGGGTGGGTGG  58296    TG TG   _
                                TC  T  TCTC CCTCTAATC
                                ||  |  |||| |||||||||
                                GG  G  GGGG GGGGGTTGG
                                 TG GT    T
GAM1042  IMAGE:4215339 5'  GGCCGGCGGCGGGCCGG     72976    A        TC
                                TC GTCTGTTGTC  CC
                                || ||||||||||  ||
                                GG CGGGCGGCGG  GG
                                 C         CC
GAM1042  IMPACT    3'  GATAGAGGTGGCAGAATGA   37389     G    TG   CC
                                TCA TCTGT  TCTC  TC
                                ||| |||||  ||||  ||
                                AGT AGACG  GGAG  AG
                                  A    GT    AT
GAM1042  KCNE4     3'  GATTAGAGGGGGATTTTTGAT  54754     TGTT
                                GTC    GTCTCCCTCTAATC
                                |||    ||||||||||||||
                                TAG    TAGGGGGAGATTAG
                                  TTTT
GAM1042  KCNT1     3'  GGCGGGGGGCAGCAAGCTGG   61837      TC        C
                                TCAG  TGTTGTCTCC TC
                                ||||  |||||||||| ||
                                GGTC  ACGACGGGGG GG
                                   GA         C
GAM1042  KIAA0140  3'  GGCAGGGATGCAGCAGGCTGG  27813           C    _
                                TCAGTCTGTTGT TCCCT CT
                                |||||||||||| ||||| ||
                                GGTCGGACGACG AGGGA GG
                                      T    C
GAM1042  KIAA0171  3'  GATTGTAAAAGAAGCAGATTGA 27854          G   CCCTC
                                TCAGTCTGTT TCT     TAATC
                                |||||||||| |||     |||||
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                                AGTTAGACGA AGA    GTTAG
                                      _  AAAT_
GAM1042  KIAA0194  3' GAAGGGGAAGCAGACTGG   65986        G    C
                                TCAGTCTGTT TCTCC TC
                                |||||||||| ||||| ||
                                GGTCAGACGA AGGGG AG
                                      _    A
GAM1042  KIAA0229  3' GGTGTGGCAATGGACTGA   92432          TC_
                                TCAGTCTGTTGTC  CC
                                ||||||||||||  ||
                                AGTCAGGTAACGG  GG
                                       TGT
GAM1042  KIAA0258  3' GAGGGGGCACTGGACTGG   28817       GT   T
                                TCAGTCT  TGTC CCCTC
                                |||||||  |||| |||||
                                GGTCAGG  ACGG GGGAG
                                    TC   _
GAM1042  KIAA0337  3' GGTGGGGGACATGTGGGCTGA 28835      TG _     T
                                TCAGTC  T TGTCTCCC CT
                                ||||||  | |||||||| ||
                                AGTCGG  G ACAGGGGG GG
                                   GT T       T
GAM1042  KIAA0342  3' ATTGGAGCAAGTGGACAGA   70617      GT  CC
                                TCTGTT  CT  CTCTAAT
                                ||||||  ||  |||||||
                                AGACAG  GA  GAGGTTA
                                   GT  AC
GAM1042  KIAA0429  3' GATTGGGGGGAGGGCCATGG   28558     T  _
                                CTGT GTC TCCCTCTAATC
                                |||| ||| ||||||||||
                                GGTA CGG AGGGGGGTTAG
                                  C   G
GAM1042  KIAA0444  3' AGGGAGGGTGGGCTGG      62335      TG TG
                                TCAGTC  T  TCTCCCT
                                ||||||  |  |||||||
                                GGTCGG  G  GGAGGGA
                                   GT ___
GAM1042  KIAA0447  3' CACTTTGGGAGGCAGCAGCTGG 71667     T         TCTAATC
                                TCAG CTGTTGTCTCCC
                                |||| ||||||||||||
                                GGTC GACGACGGAGGG
                                  _         TTTCACG
GAM1042  KIAA0513  3' AGGGGAGAGACGATGGGCTGG  28339             _
                                TCAGTCTGTTGTCTC CCTCT
                                |||||||||||||| |||||
                                GGTCGGGTAGCAGAG GGGGA
                                       A
GAM1042  KIAA0632  5' GATTGGGGGCTGCGGGCGGGTT 31426    GT    _  CT   T
            GG                    TCA  CTGTT GT  CCC CTAATC
                                |||  ||||| ||  ||| ||||||
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                                GGT  GGCGG CG  GGG GGTTAG
                                  TG    G  TC  _
GAM1042  KIAA0674  5'  GAAGGGGTAATAGGCTGG    60612          T    C
                                TCAGTCTGTTG CTCC TC
                                |||||||||||  ||||  ||
                                GGTCGGATAAT GGGG AG
                                      _    A
GAM1042  KIAA0789  3'  AGGGGGAGGGTAGACTGG    63680        TTG
                                TCAGTCTG   TCTCCCTCT
                                ||||||||   |||||||||
                                GGTCAGAT   GGAGGGGGA
                                     G__
GAM1042  KIAA0819  3'  ATGCTGGGATGCAGGCTGG    63574         TGTC    TCTA
                                TCAGTCTGT    TCCC    AT
                                |||||||||    ||||    ||
                                GGTCGGACG    AGGG    TA
                                     T___    TCG_
GAM1042  KIAA0821  3'  GATGGAGGCAGTGGCTGG    29946      T TG       C
                                TCAG C  TTGTCTCC TC
                                ||||  |  ||||||||  ||
                                GGTC G  GACGGAGG AG
                                  _ GT       T
GAM1042  KIAA0843  3'  GATTGGGGGGAGATTCTAAATT 30113       C  TT
            GA                    TCAGT TG  GTCTCCCTCTAATC
                                ||||| ||  ||||||||||||||
                                AGTTA AT  TAGAGGGGGGTTAG
                                   A  CT
GAM1042  KIAA0844  3'  GATTAGCACCCAGCATGGGCTG 30202         T  CTCCCT
            G                    TCAGTCTGT GT      CTAATC
                                |||||||||  ||      ||||||
                                GGTCGGGTA CG      GATTAG
                                     _  ACCCAC
GAM1042  KIAA0844  3'  GGTTGGAATGACAGTGGACTG  30203      TG    TCCC
                                CAGTC  TTGTC    TCTAATC
                                |||||  |||||   |||||||
                                GTCAG  GACAG    AGGTTGG
                                   GT    TA__
GAM1042  KIAA0861  3'  GGCGGGGGCCGCAGACTGG    88930         T     C
                                TCAGTCTGT GTCTCC TC
                                |||||||||  ||||||  ||
                                GGTCAGACG CGGGGG GG
                                     C     C
GAM1042  KIAA0980  3'  GATGGAGGTGGGGGCTGG    47204        G TG    C
                                TCAGTCT T  TCTCC TC
                                |||||||  |  |||||  ||
                                GGTCGGG G  GGAGG AG
                                    _ GT    T
GAM1042  KIAA1016  3'  GGGGAGATGATGGACT      91734         TG
                                AGTCTGT  TCTCCCT
                                |||||||  |||||||
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                              TCAGGTA  AGAGGGG
                                  GT
GAM1042  KIAA1089  5'  GGAGACGGCAGTGTTGG    68844    GT_
                              TCA   CTGTTGTCTCC
                              |||   ||||||||||
                              GGT   GACGGCAGAGG
                                TGT
GAM1042  KIAA1130  3'  GATGGGACAGTGGGTGA    62421    G  TG    T  C
                              TCA TC  TTGTC CC TC
                              ||| ||  ||||| || ||
                              AGT GG  GACAG GG AG
                                _ GT    _ T
GAM1042  KIAA1171  3'  GGTGGGGCGGTGGGCCGA   87984    A   TG     _
                              TC GTC  TTGTCTC CC
                              || |||  ||||||| ||
                              AG CGG  GGCGGGG GG
                               C   GT      T
GAM1042  KIAA1189  3'  GATTGGTGGGCAGCAGACT   72043        TCT   T
                              AGTCTGTTG   CCC CTAATC
                              |||||||||   ||| ||||||
                              TCAGACGAC   GGG GGTTAG
                                   ___   T
GAM1042  KIAA1228  3'  ATTGGAGTGAGTAGACAG    65036      GT   C
                              CTGTT  CTC CTCTAAT
                              |||||  ||| |||||||
                              GACAG  GAG GAGGTTA
                                 AT   T
GAM1042  KIAA1300  3'  GATTGGGGCAGACAGCACTGG  62864      CT     C  T
                              TCAGT  GTTGTCT CC CTAATC
                              |||||  ||||||| || ||||||
                              GGTCA  CGACAGA GG GGTTAG
                                 __      C  _
GAM1042  KIAA1317  3'  GGTTGGGGGGGAATGGCAGATT  86031        TG C
                              AGTCTGT  T TCCCTCTAATC
                              |||||||  | ||||||||||
                              TTAGACG  A AGGGGGGTTGG
                                  GT _
GAM1042  KIAA1495  3'  GATTATTTTTCAGAAAGCAGAC 73186         G   CCCTC_
          TGA                   TCAGTCTGTT TCT     TAATC
                              |||||||||| |||     |||||
                              AGTCAGACGA AGA     ATTAG
                                    A   CTTTTT
GAM1042  KIAA1538  3'  GGGGGGCAGTGGGCTG     71551      TG
                              CAGTC  TTGTCTCCC
                              |||||  |||||||||
                              GTCGG  GACGGGGGG
                                 GT
GAM1042  KIAA1548  5'  ATTAGAGCCGGTGGGCT     40499     TG   TCTCC
                              AGTC  TTG    CTCTAAT
                              ||||  |||    |||||||
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                                TCGG  GGC    GAGATTA
                                  GT   C____
GAM1042  KIAA1602  3'  GAGCTGGGGACCACAGACTGG  64631         T     __
                                TCAGTCTGT GTCTCC  CTC
                                |||||||||| ||||||  |||
                                GGTCAGACA CAGGGG  GAG
                                     C      TC
GAM1042  KIAA1649  5'  GAGCCTAGGAGATGGAGGCTGA 50262        G TG    ____
                                TCAGTCT T  TCTCC    CTC
                                |||||||  |  |||||    |||
                                AGTCGGA G  AGAGG    GAG
                                    _ GT     ATCC
GAM1042  KIAA1656  3'  GGGGAGATAGAGGCTGA     65804        G
                                TCAGTCT TTGTCTCCCT
                                ||||||| ||||||||||
                                AGTCGGA GATAGAGGGG
                                   _
GAM1042  KIAA1681  5'  GGCGGAGGCAGCGGCTGG     61072      T         C
                                TCAG CTGTTGTCTCC TC
                                |||| |||||||||| ||
                                GGTC GGCGACGGAGG GG
                                  _          C
GAM1042  KIAA1776  3'  GGCGGGGGGCAGGGGGTTGG   50592     GT  G        T
                                TCA  CT TTGTCTCCC CT
                                |||  || |||||||| ||
                                GGT  GG GACGGGGGG GG
                                  TG  G        C
GAM1042  KIAA1853  3'  TCCCTTAGGGAGGCACCAGATT 69398         T        CTAATC
              GG                  TCAGTCTG TGTCTCCCT
                                |||||||| |||||||||
                                GGTTAGAC ACGGAGGGA
                                     C        TTCCCTG
GAM1042  KIAA1944  3'  GGTCGGGGGGCAGCGGGTGG    75566     G          CT
                                TCA TCTGTTGTCTCC  CT
                                ||| ||||||||||||  ||
                                GGT GGGCGACGGGGG  GG
                                  _          CT
GAM1042  KLHL6     3'  GATGTTCTGGCACAGCAGACTG 55305           CT  CTCTA
              G                   TCAGTCTGTTGT  CC     ATC
                                ||||||||||||  ||    |||
                                GGTCAGACGACA  GG     TAG
                                       C_  TCTTG
GAM1042  KRTHB2    3'  TGGAGGAGGTGTGGGCTGA    52289       TG TGT    C
                                TCAGTC  T   CTCC TCTA
                                ||||||  |   |||| ||||
                                AGTCGG  G   GAGG AGGT
                                   GT TG_    _
GAM1042  LANO      5'  AGAGGGCAGCGGACTGA     47186          TCT
                                TCAGTCTGTTG   CCCTCT
                                ||||||||||   ||||||
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                                AGTCAGGCGAC   GGGAGA
                                      ___
GAM1042  LGI4     3'  CAACCTGGGGGGTGCAGGCTGG 57763        T GT    TCTAATC
                                TCAGTCTG T  CTCCC
                                |||||||| |  |||||
                                GGTCGGAC G  GGGGG
                                     _ TG    TCCAACG
GAM1042  LIMK2    3'  GGTTTAGGCAGCAGCTTGG   18728      T       C__
                                TCAG CTGTTGTCT   CC
                                |||| |||||||||   ||
                                GGTT GACGACGGA   GG
                                  C        TTT
GAM1042  LIMK2    3'  GGTTTAGGCAGCAGCTTGG   33628      T       C__
                                TCAG CTGTTGTCT   CC
                                |||| |||||||||   ||
                                GGTT GACGACGGA   GG
                                  C        TTT
GAM1042  MAP2K6   5'  GAGTCTGGAGACAGGAGGCTGG 49243        G       ___
                                TCAGTCT TTGTCTCC   CTC
                                |||||||| ||||||||   |||
                                GGTCGGA GACAGAGG   GAG
                                    G        TCT
GAM1042  MAPKAPK3 3'  GGTTGGGGAAGGCGACTGA   16153       T  TG    CT
                                TCAGTC GT  TCTCC  CT
                                |||||| ||  |||||  ||
                                AGTCAG CG  AGGGG  GG
                                   _ GA    TT
GAM1042  MGC10963 5'  GGGGCGACAACGGGCCGG    47555    A        T
                                TC GTCTGTTGTC CCCT
                                || |||||||||| ||||
                                GG CGGGCAACAG GGGG
                                 C         C
GAM1042  MGC13102 3'  AGTAGGGGGTAGCGGCTTGG   50312      T     T     _
                                TCAG CTGTTG CTCCCT CT
                                |||| |||||| |||||| ||
                                GGTT GGCGAT GGGGGA GA
                                  C     _      T
GAM1042  MGC14839 3'  GGTTGGAGTTAATAGTTGG    54699      T     T    CT
                                TCAG CTGTTG CTCC  CT
                                |||| |||||| ||||  ||
                                GGTT GATAAT GAGG  GG
                                  _     T    TT
GAM1042  MGC15619 5'  GGTTGGGGGCTGCAGACTGG   50422         T     CT
                                TCAGTCTGT GTCTCC  CT
                                |||||||||| ||||||  ||
                                GGTCAGACG CGGGGG  GG
                                      T     TT
GAM1042  MGC16703 5'  GTTGTGGGAGGTGGGCTGG    73105       TG TGT    TC
                                TCAGTC  T   CTCCC  TAAT
                                ||||||  |   |||||  ||||
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                                GGTCGG  G   GAGGG  GTTG
                                   GT ___    T_
GAM1042  MGC2508   3'  GAGTGGGGGTAGCAATTGG   44254      C   GT   _
                                TCAGT TGTT  CTCC CTC
                                ||||| ||||  |||| |||
                                GGTTA ACGA  GGGG GAG
                                  _   TG   T
GAM1042  MGC2731   3'  GGGAGGCGGAGGTTGA     43953     GT  G
                                TCA  CT TTGTCTCCC
                                |||  || |||||||||
                                AGT  GA GGCGGAGGG
                                  TG  _
GAM1042  MGC2865   3'  GGTTGGGGGATCGGCAGTTGG  50453     T     TC    T
                                TCAG CTGTTG  TCCC CTAATC
                                |||| ||||||  |||| ||||||
                                GGTT GACGGC  AGGG GGTTGG
                                  _     T_   _
GAM1042  MGC3295   5'  GGTCGGCGGCGGCGGACTGG   47502           T  CT
                                TCAGTCTGTTGTC CC  CT
                                |||||||||||| ||  ||
                                GGTCAGGCGGCGG GG  GG
                                       C  CT
GAM1042  MGC35521  3'  GGTGGGTGGGTGGCAGGCTGG  59011         TG  _  T
                                TCAGTCTGT  TCT CCC CT
                                |||||||||  ||| ||| ||
                                GGTCGGACG  GGG GGG GG
                                     GT   T   T
GAM1042  MGC4309   3'  GAGCTGGAGGTGTAGATTGA   44129        TTG    __
                                TCAGTCTG   TCTCC  CTC
                                ||||||||   |||||  |||
                                AGTTAGAT   GGAGG  GAG
                                     GT_    TC
GAM1042  MGC4309   3'  GGGGAGGTGAAAGATTGA    44132        G TG
                                TCAGTCT T  TCTCCCT
                                ||||||| |  |||||||
                                AGTTAGA A  GGAGGGG
                                     A GT
GAM1042  MGC5306   5'  GTTGGAGGAGGTCGGCTGG   44138       TGTT T TC
                                TCAGTC    G C  CCTCTAAT
                                ||||||    | |  ||||||||
                                GGTCGG    C G  GGAGGTTG
                                   ____ T GA
GAM1042  MGC5590   3'  GGTTGTGAGGTAATAGGCT   43926         TCTC   _
                                AGTCTGTTG    CCTC TAATC
                                |||||||||    |||| |||||
                                TCGGATAAT    GGAG GTTGG
                                     ____    T
GAM1042  MIDORI    3'  GCAGTGAGGGGGTTGATGGGCT 73786          T      TAATC
            GG                    TCAGTCTGTTG CTCCCTC
                                |||||||||| |||||||
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                                GGTCGGGTAGT GGGGGAG
                                      T      TGACGG
GAM1042  MKRN4    3'  GGTGGGGACGACAAACTGA   47754      C      T   T
                                TCAGT TGTTGTC CCC CT
                                ||||| ||||||| ||| ||
                                AGTCA ACAGCAG GGG GG
                                   A      _   T
GAM1042  moblak   3'  GGGGAGGCAAGAGGCTGA    55509       G
                                TCAGTCT TTGTCTCCCT
                                ||||||| ||||||||||
                                AGTCGGA AACGGAGGGG
                                    G
GAM1042  MOT8     5'  GGCGGGAGGCGGCGGACCGA  38119    A           T
                                TC GTCTGTTGTCTCCC CT
                                || ||||||||||||| ||
                                AG CAGGCGGCGGAGGG GG
                                 C           C
GAM1042  MVD      3'  GAGCGGATGTGGTGGGCTGG  10143      TG TG C  _
                                TCAGTC  T  T TCC CTC
                                ||||||  |  | ||| |||
                                GGTCGG  G  G AGG GAG
                                   GT GT T   C
GAM1042  MY050    5'  GGTTTGGGGGTGAATAGGCTGG 50925        TG  T    T
                                TCAGTCTGT  TC CCCTC AATC
                                |||||||||  || ||||| ||||
                                GGTCGGATA  AG GGGGG TTGG
                                     __ T    T
GAM1042  MYH10    3'  AGTAGGAGGGGTGGGCTGG   69139      TG  G    CT
                                TCAGTC  TT TCTCC  CT
                                ||||||  || |||||  ||
                                GGTCGG  GG GGAGG  GA
                                   GT  _    AT
GAM1042  NEUROG3  3'  GCCTCCACGGGGGCGGTAGGCT 40656        TT     CTCTAATC
            GG                    TCAGTCTG  GTCTCC
                                ||||||||  ||||||
                                GGTCGGAT  CGGGGG
                                     GG     CACCTCCGG
GAM1042  NR6A1    3'  GGTAGGAGGTGAGGATTGA   7648       G TG    CT
                                TCAGTCT T  TCTCC  CT
                                ||||||| |  |||||  ||
                                AGTTAGG A  GGAGG  GG
                                   _ GT    AT
GAM1042  NR6A1    3'  GGTAGGAGGTGAGGATTGA   52873      G TG    CT
                                TCAGTCT T  TCTCC  CT
                                ||||||| |  |||||  ||
                                AGTTAGG A  GGAGG  GG
                                   _ GT    AT
GAM1042  NR6A1    3'  GGTAGGAGGTGAGGATTGA   52885      G TG    CT
                                TCAGTCT T  TCTCC  CT
                                ||||||| |  |||||  ||
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                                AGTTAGG A  GGAGG  GG
                                   _ GT    AT
GAM1042  OGFR     3'  AGTGGGGGGCGGCGGGC     61334            T
                                GTCTGTTGTCTCCC CT
                                |||||||||||||| ||
                                CGGGCGGCGGGGGG GA
                                       T
GAM1042  PABPC5   3'  GGTGAGGCAATTGATTGA    55072       T      _
                                TCAGTC GTTGTCTC CC
                                |||||| |||||||| ||
                                AGTTAG TAACGGAG GG
                                   T       T
GAM1042  PCDH10   5'  GGTTAGAGGGAAAGAGGCT   51994       G  GTC
                                AGTCT TT   TCCCTCTAATC
                                ||||| ||   ||||||||||
                                TCGGA AA   AGGGAGATTGG
                                   G  ___
GAM1042  PCDH10   5'  GGTTAGAGGGAAAGAGGCT   40428       G  GTC
                                AGTCT TT   TCCCTCTAATC
                                ||||| ||   ||||||||||
                                TCGGA AA   AGGGAGATTGG
                                   G  ___
GAM1042  PELI1    5'  GGTTGGAGTGCAGTGGCACTGA 40276      _ TG   _   CT
                                TCAGT C  TTGT CTCC  CT
                                ||||| |  |||| ||||  ||
                                AGTCA G  GACG GAGG  GG
                                   C GT   T   TT
GAM1042  PEPP3    3'  AGGGGATATCAGATTGG     30035        T   T
                                TCAGTCTG TGTC CCCT
                                |||||||| |||| ||||
                                GGTTAGAC ATAG GGGA
                                     T   _
GAM1042  PHRET1   3'  GGTTGGGGAACAGGTGA     41062     G    TG    CT
                                TCA TCTGT  TCTCC  CT
                                ||| |||||  |||||  ||
                                AGT GGACA  AGGGG  GG
                                  _    __     TT
GAM1042  PORIMIN  3'  GAAGGAGAGGTGGGCTGA    53605       TG  G    C
                                TCAGTC  TT TCTCC TC
                                ||||||  || ||||| ||
                                AGTCGG  GG AGAGG AG
                                   GT  _    A
GAM1042  PP1628   5'  GATTGGAGGGCTTAGGTCTGG  47298      T  GTTGTCT
                                TCAG CT      CCCTCTAATC
                                ||||  ||      ||||||||||
                                GGTC GG      GGGAGGTTAG
                                  T  ATTC___
GAM1042  PPP1R10  3'  GGTTAGAGCCAAAATGGATTTG 10736      _     GTCTCC
            A                    TCAG TCTGTT     CTCTAATC
                                ||||  ||||||     ||||||||
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                                AGTT AGGTAA     GAGATTGG
                                  T     AACC__
GAM1042  PPP1R13B  3'  GGTTGGGGCTGGGGGTGGACTG 31009       TG  G  TC  T
             G                     TCAGTC  TT TC  CC CTAATC
                                   ||||||  || ||  || |||||||
                                   GGTCAG  GG GG  GG GGTTGG
                                     GT  G  TC  _
GAM1042  PRO0650  5'  GGTAGGGACAGCAGGC      26215          __
                                   GTCTGTTGTCTC  CC
                                   ||||||||||||  ||
                                   CGGACGACAGGG  GG
                                         AT
GAM1042  PRO2266  3'  GATTGGAGGGGTGAAGAATGA  37580     G   GTTG  _
                                   TCA TCT    TC TCCCTCTAATC
                                   ||| |||    || ||||||||||
                                   AGT AGA    AG GGGGAGGTTAG
                                     A  _____  T
GAM1042  PRO2605  3'  GGTGAGGTGGCAGCTGG     94859      T    TG    _
                                   TCAG CTGT  TCTC CC
                                   |||| ||||  |||| ||
                                   GGTC GACG  GGAG GG
                                     _   GT    T
GAM1042  PRO2730  5'  GATTGGATCATTTGACTGGGCT 47416       GTT   TCCC__
             GG                      TCAGTCT   GTC     TCTAATC
                                     |||||||   |||     |||||||
                                     GGTCGGG   CAG     AGGTTAG
                                        T__   TTTACT
GAM1042  PSR      3'  GGGGGGGTGATACATTGG    65187      C   TG
                                   TCAGT TGT  TCTCCCT
                                   ||||| |||  |||||||
                                   GGTTA ATA  GGGGGGG
                                     C   GT
GAM1042  PTK6     3'  GGCTGAGGCAGCAGACTGG    19940           __
                                   TCAGTCTGTTGTCTC  CC
                                   ||||||||||||||  ||
                                   GGTCAGACGACGGAG  GG
                                            TC
GAM1042  RBM9     5'  GATTGGGGGGGGAGGGGGGTGG 26682    AGT  G  G
             A                       TC   CT TT TCTCCCTCTAATC
                                     ||   || || ||||||||||||
                                     AG   GG GG AGGGGGGGGTTAG
                                      GT_  G  G
GAM1042  RELB     3'  GGTGGGGGGGTAGGTTGG     21489     GT   TTG     T
                                   TCA  CTG   TCTCCC CT
                                   |||  |||   |||||| ||
                                   GGT  GAT   GGGGGG GG
                                     TG   ___      T
GAM1042  SC65     3'  GGTTGGCAAGTGGGCTGA     21294         _    TC
                                   TCAGTCTG TTGTC  CC
                                   |||||||| |||||  ||
```

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                                AGTCGGGT AACGG  GG
                                     G    TT
GAM1042  SCYD1    3'  ATTGGAGGGGGGAGGTGG    90925   TG TG
                                C  T  TCTCCCTCTAAT
                                |  |  ||||||||||||
                                G  G  GGGGGGAGGTTA
                                 GT GA
GAM1042  SDC3     3'  TCTGGAGGGGGCGGGTTGG   27767    GT   TTGT      ATC
                                TCA  CTG   CTCCCTCTA
                                |||  |||   |||||||||
                                GGT  GGC   GGGGGAGGT
                                  TG  ____       CTA
GAM1042  SEMA3B   3'  GGTTGGGGCCGGGCACATTGG  16155     CTGT    CC
                                TCAGT   TGTCT  CTCTAATC
                                |||||   |||||  ||||||||
                                GGTTA   ACGGG  GGGGTTGG
                                   C___    CC
GAM1042  SETBP1   3'  GCCCCCAGGAGGAGCAGGCTGG 31457         G    CTCTAATC
                                TCAGTCTGTT TCTCC
                                |||||||||| |||||
                                GGTCGGACGA GGAGG
                                      _    ACCCCCGG
GAM1042  SLC11A1  5'  GAGGGGGTGCAGGCTGA     59456        TGT
                                TCAGTCTGT   CTCCCTC
                                |||||||||   |||||||
                                AGTCGGACG   GGGGGAG
                                     T__
GAM1042  SLC19A3  3'  GGTGGGAGGATGGGTTGA    47496    GT    G   _
                                TCA  CTGTT TCTC CC
                                |||  ||||| |||| ||
                                AGT  GGTAG AGGG GG
                                  TG    G   T
GAM1042  SLC37A1  5'  GGGGGGAGGTGGGGGCTGG   38567       G TG
                                TCAGTCT T  TCTCCCTCT
                                |||||||  |  |||||||||
                                GGTCGGG G  GGAGGGGGG
                                    _ GT
GAM1042  SNRK     5'  GAGGGGCTGGCGGGCTGG    34766         T T
                                TCAGTCTGTTG C CCCTC
                                ||||||||||| | |||||
                                GGTCGGGCGGT G GGGAG
                                      C _
GAM1042  SPEC1    3'  GGTGAGATAAATAGGTTGA   39613    GT    _    _
                                TCA  CTGTT GTCTC CC
                                |||  ||||| ||||| ||
                                AGT  GATAA TAGAG GG
                                  TG    A    T
GAM1042  SRp25    3'  GGCAGGGGGGTGGAGGTTGG   37980    GT  G TG  T   _
                                TCA  CT T  TC CCCT CT
                                |||  || |  || |||| ||
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                                GGT  GA G  GG GGGA GG
                                  TG  _ GT  _    C
GAM1042  SRp25    3'  GGCAGGGGGTGGAGGTTGG   33559     GT  G TG  T   _
                                TCA  CT T  TC CCCT CT
                                |||  || |  || |||| ||
                                GGT  GA G  GG GGGA GG
                                  TG  _ GT  _    C
GAM1042  STK22D   3'  GGTTGGGGGTTGGGTGGGGCTG 49324       TG TG   C_
             G                   TCAGTC  T  TCT  CCTCTAATC
                                 ||||||  |  |||  |||||||||
                                 GGTCGG  G  GGG  GGGGGTTGG
                                    __ GT   TT
GAM1042  SYNE-2   3'  GGTGGGGGCGGGGGGTTGG   30802     GT  G    T   T
                                TCA  CT TTGTC CCC CT
                                |||  || ||||| ||| ||
                                GGT  GG GGCGG GGG GG
                                  TG  G    _  T
GAM1042  TIP47    3'  GATGGGGTGGTACACTGA    19481      C  TT T    C
                                TCAGT TG  G CTCC TC
                                |||||  ||  | |||| ||
                                AGTCA AT  T GGGG AG
                                   C  GG _   T
GAM1042  TLN2     5'  GGAGAGAATGAGACTGA     61689        _  G
                                TCAGTCT GTT TCTCC
                                |||||||  ||| |||||
                                AGTCAGA TAA AGAGG
                                    G  G
GAM1042  TOMM70A  3'  AGGGGGAAAGCAGACTGA    29077          G
                                TCAGTCTGTT TCTCCCT
                                ||||||||||  |||||||
                                AGTCAGACGA AGGGGGA
                                      A
GAM1042  TReP-132  3'  GGTTGGGGGGAATAAATAATTG 37295      C   GTC
             G                   TCAGT TGTT   TCCCTCTAATC
                                 |||||  ||||   ||||||||||
                                 GGTTA ATAA   AGGGGGGTTGG
                                    _   ATA
GAM1042  TReP-132  3'  GGTTGGGGGAATAAATAATTGG 53142      C   GTC   T
                                TCAGT TGTT   TCCC CTAATC
                                |||||  ||||   |||| ||||||
                                GGTTA ATAA   AGGG GGTTGG
                                   _   ATA   _
GAM1042  TReP-132  3'  GGTTGGGGGAATAAATAATTGG 53150      C   GTC   T
                                TCAGT TGTT   TCCC CTAATC
                                |||||  ||||   |||| ||||||
                                GGTTA ATAA   AGGG GGTTGG
                                   _   ATA   _
GAM1042  TRPV6    5'  AGGGAGACGGTGGGCCGG    37838    A  TG
                                TC GTC  TTGTCTCCCT
                                ||  |||  ||||||||||
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                                GG CGG  GGCAGAGGGA
                                 C   GT
GAM1042  TTYH2    3'  GGGGGATCACAGGCTGG     50996         T
                                TCAGTCTGT GTCTCCC
                                ||||||||| |||||||
                                GGTCGGACA TAGGGGG
                                      C
GAM1042  UBE4B    3'  GGGGAGATGAGGGTTGG     20166      T  G TG
                                TCAG CT T  TCTCCCT
                                |||| || |  |||||||
                                GGTT GG A  AGAGGGG
                                  _  G GT
GAM1042  VIT1     5'  GATTGGAAACTATGCAGCAGAT 37975          CTCCC_
                                GTCTGTTGT     TCTAATC
                                |||||||||     |||||||
                                TAGACGACG     AGGTTAG
                                      TATCAA
GAM1042  VTS58635  5'  GGTTGGTCCTGACGGTGGCTGA 52811      T TG     TCCCT
                                TCAG C  TTGTC     CTAATC
                                |||| |  |||||     ||||||
                                AGTC G  GGCAG     GGTTGG
                                  _ GT     TCCT_
GAM1042  ZIC4     5'  GAGGGGGTGGCGGTTGG     49621      T    TG  T
                                TCAG CTGT  TC CCCTC
                                |||| ||||  || |||||
                                GGTT GGCG  GG GGGAG
                                  _    GT  _
GAM1042  ZNF185   3'  ATTTTGGGGGTGGACTGA    23108         TTGT    TCT
                                TCAGTCTG    CTCCC   AAT
                                ||||||||    |||||  |||
                                AGTCAGGT    GGGGG   TTA
                                     _____     TT_
GAM1042  ZNF31    5'  GGGAGGTGACAGCTGA      64984      T    TG
                                TCAG CTGT  TCTCCC
                                |||| ||||  ||||||
                                AGTC GACA  GGAGGG
                                  _    GT
GAM1042  ZNF339   3'  GGGAGGCAGGGGTTGG      41125      T  G
                                TCAG CT TTGTCTCCC
                                |||| || |||||||||
                                GGTT GG GACGGAGGG
                                  _  G
GAM1042  ZNF364   5'  GGGAGGTAGCGGCCTGG     66773      T    GT
                                TCAG CTGTT  CTCCC
                                |||| |||||  |||||
                                GGTC GGCGA  GAGGG
                                  C    TG
GAM1042  ZNF384   3'  GAAGGGGGCAAGGGCTGA    55984         G       C
                                TCAGTCT TTGTCTCC TC
                                ||||||| |||||||| ||
```

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                                AGTCGGG AACGGGGG AG
                                   _      A
GAM1042  LOC112885 3'  GGGGGGACTCTGGCTGA     56529       TGTT
                                TCAGTC   GTCTCCCT
                                ||||||   ||||||||
                                AGTCGG   CAGGGGGG
                                   TCT_
GAM1042  LOC112885 3'  GGTGGGGTACGACAGGCTGG   56530          CT   T
                                TCAGTCTGTTGT  CCC CT
                                ||||||||||||  ||| ||
                                GGTCGGACAGCA  GGG GG
                                      TG   T
GAM1042  LOC116123 5'  GATTGGAGCTGGAATTAGCGGA 57086         TC  __
            CTGG                   CAGTCTGTTG  TCC  CTCTAATC
                                ||||||||||  |||  ||||||||
                                GTCAGGCGAT  AGG  GAGGTTAG
                                      TA   TC
GAM1042  LOC120425 3'  GGTTTGGGGTGAATGGGTTGG  74009     GT   TG  T   CT
                                TCA  CTGT  TC CCCT  AATC
                                |||  ||||  || ||||  ||||
                                GGT  GGTA  AG GGGG  TTGG
                                  TG   __  T   T_
GAM1042  LOC121219 5'  GGTTGGGGGGGAGCTGGTGGGTG 74048     G  TG   T
            A                   TCA TC  TTG CTCCCTCTAATC
                                ||| ||  ||| ||||||||||||
                                AGT GG  GGT GAGGGGGGTTGG
                                  _ GT   C
GAM1042  LOC122210 5'  GATGGAGATGGAGGATTGA   74118       G TG    C
                                TCAGTCT T  TCTCC TC
                                |||||||  |  ||||| ||
                                AGTTAGG G  AGAGG AG
                                    A GT    T
GAM1042  LOC122210 5'  GATTGAATAACAGATTGA    74119          C  CC
                                TCAGTCTGTTGT TC  TC
                                ||||||||||| ||  ||
                                AGTTAGACAATA AG  AG
                                      _  TT
GAM1042  LOC123803 5'  GGCGGGGGCGGCGGGC      74233           C
                                GTCTGTTGTCTCC TC
                                ||||||||||||| ||
                                CGGGCGGCGGGGG GG
                                      C
GAM1042  LOC123879 5'  GAGCGGGGATGGTAGGTGG   75632     G   TT    _
                                TCA TCTG  GTCTCC CTC
                                ||| ||||  |||||| |||
                                GGT GGAT  TAGGGG GAG
                                  _   GG    C
GAM1042  LOC124739 3'  GGTGAGTGGCGGGCTGA     74331          T  _
                                TCAGTCTGTTG CTC CC
                                |||||||||| ||| ||
```

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                                AGTCGGGCGGT GAG GG
                                      _  T
GAM1042  LOC124930 3'  GATGCCAGGGGCACCAGACTGA 74358        T  CT   CTA
                                TCAGTCTG TGT  CCCT   ATC
                                |||||||| |||  ||||   |||
                                AGTCAGAC ACG  GGGA   TAG
                                    C  __   CCG
GAM1042  LOC126528 3'  GGTGGGGTACGGGCTGG     74529         TGTC   T
                                TCAGTCTGT    TCCC CT
                                |||||||||    |||| ||
                                GGTCGGGCA    GGGG GG
                                     T___    T
GAM1042  LOC127703 5'  GGTTGGATAGCAGTTGG     74680      T       C_
                                TCAG CTGTTGTCT  CC
                                |||| |||||||||  ||
                                GGTT GACGATAGG  GG
                                  _       TT
GAM1042  LOC130574 5'  GATGGGGCAGCGGGCTG     74957          T  C
                                CAGTCTGTTGTC CC TC
                                |||||||||||| || ||
                                GTCGGGCGACGG GG AG
                                      _ T
GAM1042  LOC133452 5'  GGGGGACGGCGGCTGG      75925      T
                                TCAG CTGTTGTCTCCC
                                |||| ||||||||||||
                                GGTC GGCGGCAGGGGG
                                  _
GAM1042  LOC138128 5'  GGCGGGGGGTGGCGGCTGG    75942      T   TG     T
                                TCAG CTGT  TCTCCC CT
                                |||| ||||  |||||| ||
                                GGTC GGCG  GGGGGG GG
                                  _   GT     C
GAM1042  LOC138649 5'  GGTTGTGGGGGGGGATGGCGGAT 75359        TG      _
           T                     AGTCTGT  TCTCCCTC TAATC
                                |||||||  |||||||| |||||
                                TTAGGCG  AGGGGGGG GTTGG
                                    GT       T
GAM1042  LOC143098 5'  GGTGTCCGGAGAGCGGTGGGCT 76456       TG  _    CTCTAATC
           GA                     TCAGTC  TTG TCTCC
                                |||||| |||  |||||
                                AGTCGG  GGC AGAGG
                                   GT   G    CCTGTGG
GAM1042  LOC143243 5'  GGAGGCAGCGGTTGG       60306      T
                                TCAG CTGTTGTCTCC
                                |||| ||||||||||
                                GGTT GGCGACGGAGG
                                  _
GAM1042  LOC143286 5'  GAAAGAGATGATGGACTGA    82947         TG   CC
                                TCAGTCTGT  TCTC  TC
                                |||||||||  ||||  ||
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                                AGTCAGGTA  AGAG  AG
                                     GT    AA
GAM1042  LOC144317 5'  GATGGGACGGCGGGCT      76792          T  C
                                AGTCTGTTGTC CC TC
                                |||||||||||  ||  ||
                                TCGGGCGGCAG GG AG
                                      _  T
GAM1042  LOC145098 5'  GAGGAGGTACATGGGCTGG    76991         T  _ TC
                                TCAGTCTGT GT C  CCTC
                                |||||||||  ||  |  ||||
                                GGTCGGGTA CA G  GGAG
                                     _  T GA
GAM1042  LOC145098 5'  GATTGGTGTCCAGGCTAGTGGA 76993       TG  _    CCCT_
           CTGA                    CAGTC  TT GTCT     CTAATC
                                |||||  ||  ||||     ||||||
                                GTCAG  GA CGGA     GGTTAG
                                   GT  T    CCTGT
GAM1042  LOC145317 3'  GAAGGAGGCACACAGATTGG   83323          _      C
                                TCAGTCTGT TGTCTCC TC
                                |||||||||  |||||||  ||
                                GGTTAGACA ACGGAGG AG
                                     C       A
GAM1042  LOC145547 3'  AGGGGGAAATGGGTTGG     77263     GT     G
                                TCA  CTGTT TCTCCCT
                                |||  |||||  |||||||
                                GGT  GGTAA AGGGGGA
                                  TG    _
GAM1042  LOC145623 5'  AGGGAGATGATAGATAGA     83391     A     TG
                                TC GTCTGT  TCTCCCT
                                ||  ||||||  |||||||
                                AG TAGATA  AGAGGGA
                                  A     GT
GAM1042  LOC146272 5'  GGTGGAGGCGCCAGGCTGA    77794         T      C
                                TCAGTCTG TGTCTCC TC
                                ||||||||  |||||||  ||
                                AGTCGGAC GCGGAGG GG
                                     C      T
GAM1042  LOC146272 5'  GTTGGAGGGGGCTGGTGGA    77795     TG   T
                                TC  TTG CTCCCTCTAAT
                                ||  |||  ||||||||||||
                                AG  GGT GGGGGAGGTTG
                                  GT   C
GAM1042  LOC146435 3'  AATCATGGGGGAAACGGGTTGG 77894      GT     G     TCTAATC
                                TCA  CTGTT TCTCCC
                                |||  |||||  ||||||
                                GGT  GGCAA AGGGGG
                                  TG    _      TACTAAG
GAM1042  LOC146517 3'  GGTTGGACATGGATTGA      77947          T    C_
                                TCAGTCTGT GTCT  CC
                                |||||||||  ||||  ||
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                                AGTTAGGTA CAGG  GG
                                      _   TT
GAM1042  LOC146909 3'  GGTGGGAGGTGGGCTGG     78180       TG TGT    T
                                TCAGTC  T   CTCCC CT
                                ||||||  |   ||||| ||
                                GGTCGG  G   GAGGG GG
                                   GT ___     T
GAM1042  LOC148397 3'  GGTTGGCAGGGGATGGGTTGA  78822     GT  GTT   T   _
                                TCA  CT   GTC CCCT CTAATC
                                |||  ||   ||| |||| ||||||
                                AGT  GG   TAG GGGA GGTTGG
                                  TG  ___  _   C
GAM1042  LOC148738 3'  GGAGATACAGATTGG       59202          T
                                TCAGTCTGT GTCTCC
                                ||||||||| ||||||
                                GGTTAGACA TAGAGG

                                      _
GAM1042  LOC149072 5'  AGGGAGGAGATGGGCTGA    79156          GT
                                TCAGTCTGTT  CTCCCT
                                ||||||||||  ||||||
                                AGTCGGGTAG  GAGGGA
                                      AG
GAM1042  LOC149127 3'  GGTCAGAGGAGATGGAGGCTGG 84350        G TG    C   A
                                TCAGTCT T  TCTCC TCT ATC
                                |||||||  |  ||||| ||| |||
                                GGTCGGA G  AGAGG AGA TGG
                                    _ GT    _   C
GAM1042  LOC149668 3'  GGGAAGCAGGCTGG        84548          GTC
                                TCAGTCTGTT   TCCC
                                ||||||||||   ||||
                                GGTCGGACGA   AGGG

                                      ___
GAM1042  LOC149910 5'  GGAGACAAGTGGGCTGA     79534          _
                                TCAGTCTG TTGTCTCC
                                |||||||| ||||||||
                                AGTCGGGT AACAGAGG
                                      G
GAM1042  LOC150170 5'  GATGGAGGCAGTGGCTGG    79590      T TG       C
                                TCAG C  TTGTCTCC TC
                                |||| |  |||||||| ||
                                GGTC G  GACGGAGG AG
                                  _ GT       T
GAM1042  LOC150175 5'  GATGGAGGCAGTGGCTGG    79631      T TG       C
                                TCAG C  TTGTCTCC TC
                                |||| |  |||||||| ||
                                GGTC G  GACGGAGG AG
                                  _ GT       T
GAM1042  LOC150215 5'  GATGGAGGCAGTGGCTGG    79639      T TG       C
                                TCAG C  TTGTCTCC TC
                                |||| |  |||||||| ||
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                                GGTC G  GACGGAGG AG
                                  _ GT       T
GAM1042  LOC150218 5'  GATGGAGGCAGTGGCTGG    79720      T TG       C
                                TCAG C  TTGTCTCC TC
                                |||| |  |||||||| ||
                                GGTC G  GACGGAGG AG
                                  _ GT       T
GAM1042  LOC150225 3'  GAGGGGATGGTGGCATTGG   84996      _ TG TG  T
                                TCAGT C  T  TC CCCTC
                                ||||| |  |  || |||||
                                GGTTA G  G  AG GGGAG
                                   C GT GT  _
GAM1042  LOC150290 5'  GGCAGGGCGGGTAACAGGTTGA 79776     GT    GT _   _
                                TCA  CTGTT  CT CCCT CT
                                |||  |||||  || |||| ||
                                AGT  GACAA  GG GGGA GG
                                  TG    TG  C    C
GAM1042  LOC150397 3'  GGTTAGAGTGCAATGGCTTGA  79849      T      CTCC
                                TCAG CTGTTGT    CTCTAATC
                                |||| |||||||    ||||||||
                                AGTT GGTAACG    GAGATTGG
                                  C      T___
GAM1042  LOC150519 3'  GATTTGTGGGAAATGGGTTGG  79920     GT    GTC    TCT
                                TCA  CTGTT   TCCC   AATC
                                |||  |||||   ||||   ||||
                                GGT  GGTAA   AGGG   TTAG
                                  TG    ___    TGT
GAM1042  LOC150577 3'  AGAGGGAGGCAGAGATTGG    85070       G
                                TCAGTCT TTGTCTCCCTCT
                                ||||||| ||||||||||||
                                GGTTAGA GACGGAGGGAGA
                                   _
GAM1042  LOC150886 5'  GATGGGGGCGGAGACTGA     85153       G       C
                                TCAGTCT TTGTCTCC TC
                                ||||||| |||||||| ||
                                AGTCAGA GGCGGGGG AG
                                   _       T
GAM1042  LOC150889 3'  GATTGACTGTAGATACAGATTG 80025         T    CCCTC
            G                    TCAGTCTGT GTCT     TAATC
                                |||||||| ||||     |||||
                                GGTTAGACA TAGA     GTTAG
                                   _    TGTCA
GAM1042  LOC151361 5'  GGGGGAGGATAGGCTGA     85327          G
                                TCAGTCTGTT TCTCCC
                                |||||||||| ||||||
                                AGTCGGATAG AGGGGG
                                      G
GAM1042  LOC151516 3'  GAGGGAGAGCAGGCTGG     80270          TG
                                TCAGTCTGT  TCTCCCTC
                                |||||||||  ||||||||
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                                GGTCGGACG  AGAGGGAG
                                          __
GAM1042  LOC151647 5'  GATTGGTTCTAGCAACAGAT   80332         CTCCCT
                                GTCTGTTGT     CTAATC
                                |||||||||     ||||||
                                TAGACAACG     GGTTAG
                                     ATCTT_
GAM1042  LOC151987 5'  GGTTGGTGGTAGCGGCTTGG   67467     T    GT T  CT
                                TCAG CTGTT  C CC  CT
                                |||| |||||  | ||  ||
                                GGTT GGCGA  G GG  GG
                                  C    TG T  TT
GAM1042  LOC152018 3'  GATGGAGATGATGACTGG    85546       T  TG    C
                                TCAGTC GT  TCTCC TC
                                ||||||  ||  ||||| ||
                                GGTCAG TA  AGAGG AG
                                   _  GT    T
GAM1042  LOC152633 5'  CCCTAGAGGGGACGACGGGCTG 85807           T      ATC
            G                    TCAGTCTGTTGTC CCCTCTA
                                |||||||||||| |||||||
                                GGTCGGGCAGCAG GGGAGAT
                                       _      CCCG
GAM1042  LOC152633 5'  GAGGGGACGACGGGCTGG    85810           T
                                TCAGTCTGTTGTC CCCTC
                                |||||||||||| |||||
                                GGTCGGGCAGCAG GGGAG
                                          _
GAM1042  LOC152762 3'  TCCAGAGGAGACGGTGACTGG  80656       T TT     C   AATC
                                TCAGTC G  GTCTCC TCT
                                ||||||  |  |||||| |||
                                GGTCAG T  CAGAGG AGA
                                   _ GG     _   CCTG
GAM1042  LOC153196 5'  GGCAGGAGAGGTGGGCTGG    85965       TG  G    CT
                                TCAGTC  TT TCTCC  CT
                                ||||||  || |||||  ||
                                GGTCGG  GG AGAGG  GG
                                   GT  _    AC
GAM1042  LOC153196 5'  GGGGGAGACAGACTGG      85968        GTT
                                TCAGTCT   GTCTCCCTC
                                |||||||   |||||||||
                                GGTCAGA   CAGAGGGGG
                                          ___
GAM1042  LOC153688 3'  GAAGGAGGCAGGGGTTGG    86106      T  G       C
                                TCAG CT TTGTCTCC TC
                                |||| || |||||||| ||
                                GGTT GG GACGGAGG AG
                                  _ G       A
GAM1042  LOC153733 5'  GATTGGAGGGGGACTCTGTGCT 80922     CTGTT
                                AGT    GTCTCCCTCTAATC
                                |||    ||||||||||||||
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                                TCG     CAGGGGGAGGTTAG
                                  TGTCT
GAM1042  LOC155063 3'  GGTAGCTTGGGAGATAACGGGT 86368     G          T__   ATC
                GG                  CA TCTGTTGTCTCCC   CTA
                                || ||||||||||||   |||
                                GT GGGCAATAGAGGG   GAT
                                  _          TTC   GG
GAM1042  LOC155435 3'  GGACACAGCAGGCTGG      81352           C
                                TCAGTCTGTTGT TCC
                                |||||||||||| |||
                                GGTCGGACGACA AGG
                                       C
GAM1042  LOC157313 5'  AGAAGGGGGAGGTGGCGGAGTG 81397     G     TG        AATC
                A                   TCA TCTGT  TCTCCCTCT
                                ||| |||||  |||||||||
                                AGT AGGCG  GGAGGGGGA
                                  G     GT        AGAG
GAM1042  LOC157740 5'  GCCGCGGGGAGACAGGGGCTGG 81563        G        CTAATC
                                TCAGTCT TTGTCTCCCT
                                ||||||| ||||||||||
                                GGTCGGG GACAGAGGGG
                                    _         CGCCGG
GAM1042  LOC157848 3'  GGAGGGAGGCAGCTGGCTGG   81620       T
                                TCAGTC GTTGTCTCCCTCT
                                |||||| ||||||||||||
                                GGTCGG CGACGGAGGGAGG
                                    T
GAM1042  LOC158314 3'  GGTAGGGGGGCAAAGGTTGG   86771     GT  G        _
                                TCA  CT TTGTCTCCCT CT
                                |||  || |||||||||| ||
                                GGT  GA AACGGGGGGA GG
                                  TG  _         T
GAM1042  LOC158510 5'  GGTTCTGAGGGGACAGGCTGA  81942          GTCT     T_
                                TCAGTCTGTT    CCCTC  AATC
                                ||||||||||    |||||  ||||
                                AGTCGGACAG    GGGAG  TTGG
                                      _____     TC
GAM1042  LOC158535 5'  GAGGAGATGGAAGATTGA     87241        G TG     C
                                TCAGTCT T  TCTCC TC
                                ||||||| |  ||||| ||
                                AGTTAGA G  AGAGG AG
                                    A GT     _
GAM1042  LOC158572 3'  GGAGGGGGGCAGCAGGTGGA   81956     AG
                                TC  TCTGTTGTCTCCCTCT
                                ||  ||||||||||||||||
                                AG  GGACGACGGGGGGAGG
                                  GT
GAM1042  LOC158629 5'  GGTGAACGATAGATTGA      86880           C  _
                                TCAGTCTGTTGT TC CC
                                |||||||||||| || ||
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                                AGTTAGATAGCA AG GG
                                      _  T
GAM1042  LOC158969 3'  GATGCCCATGAGGTGTTGGGCT 82061       GT GT   CCTCTA
              GG                  TCAGTCT  T  CTC     ATC
                                  |||||||  |  |||     |||
                                  GGTCGGG  G  GAG     TAG
                                     TT TG   TACCCG
GAM1042  LOC159091 5'  GATTGTCAAAGGCGGCAGATTG 57186           CCCTC
                                  CAGTCTGTTGTCT    TAATC
                                  ||||||||||||    |||||
                                  GTTAGACGGCGGA    GTTAG
                                        AACT_
GAM1042  LOC164714 3'  GCAGCAGGGGGGGCAGCAGACT 87231              CTAATC
              G                   CAGTCTGTTGTCTCCCT
                                  |||||||||||||||||
                                  GTCAGACGACGGGGGGG
                                        ACGACGG
GAM1042  LOC170395 3'  GATTAACATTTGAGTCAGTGGA 76370      TG   T   CCTC__
              CTGG                  CAGTC  TTG CTC     TAATC
                                  |||||  ||| |||     |||||
                                  GTCAG  GAC GAG     ATTAG
                                     GT   T   TTTACA
GAM1042  LOC196214 3'  GGCAGGAGGCGGCGGGCTG   89620           CT
                                  CAGTCTGTTGTCTCC  CT
                                  ||||||||||||||  ||
                                  GTCGGGCGGCGGAGG  GG
                                        AC
GAM1042  LOC199858 3'  GATTAATATTTGAGTCAGTGGG 88419      TG   T   CCTC__
              CTGG                  CAGTC  TTG CTC     TAATC
                                  |||||  ||| |||     |||||
                                  GTCGG  GAC GAG     ATTAG
                                     GT   T   TTTATA
GAM1042  LOC199986 5'  GGAGGCAGCAGCCTGG     89906     T
                                  TCAG CTGTTGTCTCC
                                  |||| ||||||||||
                                  GGTC GACGACGGAGG
                                     C
GAM1042  LOC200093 5'  GAGCCAGGGGGTGACGGGTGG  63096     G    TG    ___
                                  TCA TCTGT  TCTCC   CTC
                                  ||| |||||  |||||   |||
                                  GGT GGGCA  GGGGG   GAG
                                    _    GT    ACC
GAM1042  LOC200093 5'  GATGGGATGGCAGCTGA     63097     T   TG  T  C
                                  TCAG CTGT  TC CC TC
                                  |||| ||||  || || ||
                                  AGTC GACG  AG GG AG
                                     _   GT  _  T
GAM1042  LOC200316 3'  GGGGAGGTGGAGGCTGG     88773       G TG
                                  TCAGTCT T  TCTCCCT
                                  |||||||  |  |||||||
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                                GGTCGGA G  GGAGGGG
                                    _ GT
GAM1042  LOC200470 5'  GGGGGACGCCAGGCTGG     90067         T
                                TCAGTCTG TGTCTCCC
                                |||||||| ||||||||
                                GGTCGGAC GCAGGGGG
                                     C
GAM1042  LOC200862 5'  GGGGGGCGGCGGGCCGG     90182     A
                                TC GTCTGTTGTCTCCC
                                || ||||||||||||||
                                GG CGGGCGGCGGGGGG
                                 C
GAM1042  LOC200918 5'  GAGGGGGTGACAGGCT      88941         TG  T
                                AGTCTGT  TC CCCTC
                                |||||||  || |||||
                                TCGGACA  GG GGGAG
                                    GT  _
GAM1042  LOC200933 3'  GATTAGGGACACCCAGCAGCTG 90198      T     TCTCC
            G                    TCAG CTGTTG     CTCTAATC
                                |||| ||||||     ||||||||
                                GGTC GACGAC     GGGATTAG
                                  _     CCACA
GAM1042  LOC201115 5'  GGTTGGGGACCAGGCAGCTGA  88107      T    __     CT
                                TCAG CTGTT  GTCTCC  CT
                                |||| |||||  ||||||  ||
                                AGTC GACGG  CAGGGG  GG
                                  _    AC      TT
GAM1042  LOC202266 5'  GGTTGGGGGCCGGAACAGCCTG 90332      T    G  TC
            A                    TCAG CTGTT TC  CCTCTAATC
                                |||| ||||| ||  |||||||||
                                AGTC GACAA GG  GGGGGTTGG
                                  C    _  CC
GAM1042  LOC202865 5'  GGTGGGGATAATGAGCTGG    59256      CT     T  T
                                TCAGT  GTTGTC CCC CT
                                |||||  |||||| ||| ||
                                GGTCG  TAATAG GGG GG
                                   AG     _  T
GAM1042  LOC203668 5'  GACGCCCGGGGACGCGTAGATT 89435         TT_     CTCTAATC
            GG                    TCAGTCTG   GTCTCC
                                |||||||   ||||||
                                GGTTAGAT   CAGGGG
                                     GCG     CCCGCAG
GAM1042  LOC219848 3'  GGGAGAAGCAGGCTGG      91495          G
                                TCAGTCTGTT TCTCCC
                                |||||||||| ||||||
                                GGTCGGACGA AGAGGG
                                          _
GAM1042  LOC219914 5'  GATTGAGGGGAGACAGCATGCT 93326       C          TC
            GG                    TCAGT TGTTGTCTCCC  TAATC
                                ||||| ||||||||||  |||||
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                                GGTCG ACGACAGAGGG  GTTAG
                                   T          GA
GAM1042  LOC219920 5'  GAAGGAGATGGAGGCTGA    93311        G TG     C
                                TCAGTCT T  TCTCC TC
                                ||||||| |  ||||| ||
                                AGTCGGA G  AGAGG AG
                                    _ GT     A
GAM1042  LOC220846 3'  GTGCCGTGGAGCAGCAGGCTGG 90820           T    CTCTAATC
                                TCAGTCTGTTG CTCC
                                |||||||||||| ||||
                                GGTCGGACGAC GAGG
                                       _   TGCCGTGG
GAM1042  LOC221463 3'  GAAGTATGGGGACGATGGGGTG 92070     G          CT_  AATC
            G                    TCA TCTGTTGTCTCC   CT
                                ||| ||||||||||||   ||
                                GGT GGGTAGCAGGGG   GA
                                  G          TAT  AG
GAM1042  LOC221915 3'  GGTCGGAGAAGCGGATTGG    93952          G     CT
                                TCAGTCTGTT TCTCC  CT
                                |||||||||| |||||  ||
                                GGTTAGGCGA AGAGG  GG
                                      _    CT
GAM1042  LOC221922 5'  CCGTGGGAGGGGGGTTGTGGGC 92691        TG TG        AATC
            TGG                   TCAGTC  T  TCTCCCTCT
                                ||||||  |  |||||||||
                                GGTCGG  G  GGGGGGAGG
                                   GT TT        GTGCCG
GAM1042  LOC221922 5'  GATGGAGGTGGAAGGCTGG   92696        G TG     C
                                TCAGTCT T  TCTCC TC
                                ||||||| |  ||||| ||
                                GGTCGGA G  GGAGG AG
                                    A GT     T
GAM1042  LOC222183 3'  GGTCTGGGACGTGGGCTGG   94168        TG T     ___
                                TCAGTC  T GTCTC   CC
                                ||||||  | |||||   ||
                                GGTCGG  G CAGGG   GG
                                   GT _     TCT
GAM1042  LOC253044 5'  GGTTCAGATAGCAGCTGG    96577      T        C__
                                TCAG CTGTTGTCT   CC
                                |||| |||||||||   ||
                                GGTC GACGATAGA   GG
                                  _        CTT
GAM1042  LOC253239 3'  GATTATGAAAGAAGCAGTAGAC 96490           TC  CC  _
            TGG                   TCAGTCTGTTG  TC  TC TAATC
                                ||||||||||  ||  || |||||
                                GGTCAGATGAC  AG  AG ATTAG
                                      GA  AA  T
GAM1042  LOC253489 5'  GAGGTGGCGGCGGGCTGG    95494           TC
                                TCAGTCTGTTGTC  CCTC
                                ||||||||||||  ||||
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                                GGTCGGGCGGCGG  GGAG
                                       T_
GAM1042  LOC253517 5'  GAGGGGGCGGTGGGCT      95105      TG     T
                                AGTC  TTGTC CCCTC
                                ||||  ||||| |||||
                                TCGG  GGCGG GGGAG
                                  GT    _
GAM1042  LOC253596 5'  GGGGGCCATGGGCTGG      95479          T
                                TCAGTCTGT GTCTCC
                                ||||||||| ||||||
                                GGTCGGGTA CGGGGG
                                      C
GAM1042  LOC253893 3'  GGAGGGAGGCAGCTGGCTGG   96114        T
                                TCAGTC GTTGTCTCCCTCT
                                |||||| ||||||||||||
                                GGTCGG CGACGGAGGGAGG
                                    T
GAM1042  LOC255272 3'  GGTTGGGGGGTCTGCCAGCTGG 94601      T   TTGTCT
                                TCAG CTG      CCCTCTAATC
                                |||| |||     ||||||||||
                                GGTC GAC      GGGGGGTTGG
                                  _   CGTCT_
GAM1042  LOC256597 5'  GATGCCCACGAGAAACAGGCTG 96288          G    CCTCTA
           G                     TCAGTCTGTT TCTC      ATC
                                |||||||||| ||||      |||
                                GGTCGGACAA AGAG      TAG
                                      _    CACCCG
GAM1042  LOC256790 5'  GGTTGTCATGGCAACAGGATGG 94836     GT       TCCCTC
                                TCA  CTGTTGTC      TAATC
                                |||  ||||||||      |||||
                                GGT  GACAACGG      GTTGG
                                  AG       TACT__
GAM1042  LOC257078 5'  GGGGCAGCAGGGCTGG      97130        _
                                TCAGTC TGTTGTCTC
                                |||||| |||||||||
                                GGTCGG ACGACGGGG
                                    G
GAM1042  LOC257554 3'  ATTAGGGGGTCTGGATAG     97692       GTCT
                                CTGTT    CCCTCTAAT
                                |||||    |||||||||
                                GATAG    GGGGGATTA
                                   GTCT
GAM1042  LOC51068  5'  GGCGGAGACAGCCAGGTTGG   31947     GT  _      C
                                TCA  CTG TTGTCTCC TC
                                |||  ||| |||||||| ||
                                GGT  GAC GACAGAGG GG
                                  TG   C       C
GAM1042  LOC51134  5'  GGTGGAGACAGTGGATTGA    32287       TG       C
                                TCAGTC  TTGTCTCC TC
                                ||||||  |||||||| ||
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                                AGTTAG  GACAGAGG GG
                                   GT       T
GAM1042  LOC51236  3'  GGTGGAGGTGGCAGGCGGA   33203    A     TG    C
                                TC GTCTGT  TCTCC TC
                                || ||||||  ||||| ||
                                AG CGGACG  GGAGG GG
                                 G     GT    T
GAM1042  LOC51295  3'  GCCCGAGGAGGCGGTGGACTGA 33425       TG      C  TAATC
                                TCAGTC  TTGTCTCC TC
                                ||||||  |||||||| ||
                                AGTCAG  GGCGGAGG AG
                                   GT       _ CCCGG
GAM1042  LOC57115  3'  AGGTGAGACAATGGGCTGG   39860             _
                                TCAGTCTGTTGTCTC CCT
                                |||||||||||||| |||
                                GGTCGGGTAACAGAG GGA
                                         T
GAM1042  LOC58525  5'  GGTTGGATAACAGGATGA    78651     GT       C_
                                TCA  CTGTTGTCT  CC
                                |||  |||||||||  ||
                                AGT  GACAATAGG  GG
                                  AG        TT
GAM1042  LOC64146  3'  GATTGCCAAGGCATGGCAGACT 42276         TG CTC   C__
           GA                     TCAGTCTGT  T   CCT   TAATC
                                |||||||||  |   |||   |||||
                                AGTCAGACG  A   GGA   GTTAG
                                      GT C__   ACC
GAM1042  LOC90019  5'  GATGGGGTAGCGGGC      56763        T    C
                                GTCTGTTG CTCC TC
                                |||||||| |||| ||
                                CGGGCGAT GGGG AG
                                      _    T
GAM1042  LOC90719  3'  GGGATGTTACAGGCTGG     63885         T TC
                                TCAGTCTGT G  TCCC
                                |||||||||  |  ||||
                                GGTCGGACA T  AGGG
                                      T GT
GAM1042  LOC90906  3'  GATTGGCTCAGATAATGGGCTG 64301             CCCT
           G                     TCAGTCTGTTGTCT    CTAATC
                                ||||||||||||||    ||||||
                                GGTCGGGTAATAGA    GGTTAG
                                         CTC_
GAM1042  LOC91012  3'  GGTTGGGGCACAATTGTGGACT 64641       ___    _   CT  AATC
           GG                     AGTCT   GTTGT CTCC  CT
                                |||||   ||||| ||||  ||
                                TCAGG   TAACA GGGG  GG
                                   TGT    C    TT    C
GAM1042  LOC91040  5'  GATGGGGTGGCAGCTGA     64720      T    TG  T  C
                                TCAG CTGT  TC CC TC
                                |||| ||||  || || ||
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                                AGTC GACG  GG GG AG
                                  _   GT  _  T
GAM1042  LOC91149  3'  GATTGGAGGATACTGGGCAGCT 65077     T    GTCTC_
              GA                  TCAG CTGTT     CCTCTAATC
                                  |||| |||||     |||||||||
                                  AGTC GACGG     GGAGGTTAG
                                    _    GTCATA
GAM1042  LOC91149  3'  GGAGGCAGAGATTGG       65080        G
                                  TCAGTCT TTGTCTCC
                                  ||||||| ||||||||
                                  GGTTAGA GACGGAGG
                                     _
GAM1042  LOC91263  3'  ATTGGAGGGTAGGGCTGA    65377        GTTGTCT
                                  TCAGTCT      CCCTCTAAT
                                  |||||||      |||||||||
                                  AGTCGGG      GGGAGGTTA
                                      AT_____
GAM1042  LOC91464  3'  GGTTCAGAAGACAGGCTGG   66143         G   C__
                                  TCAGTCTGTT TCT   CC
                                  |||||||||| |||   ||
                                  GGTCGGACAG AGA   GG
                                       A   CTT
GAM1042  LOC91517  5'  TCTTGCGGGAGGCGTGGGCTGG 66311       TG T      TCTAATC
                                  TCAGTC  T GTCTCCC
                                  ||||||  | |||||||
                                  GGTCGG  G CGGAGGG
                                     GT _      CGTTCTG
GAM1042  LOC91759  3'  GTTAGTAAGCACAGGCTGA   67089         T T  CCCT
                                  TCAGTCTGT G CT    CTAAT
                                  ||||||||| | ||    |||||
                                  AGTCGGACA C GA    GATTG
                                       _ _  AT__
GAM1042  LOC92305  3'  CAAAGAGGGGCAGTGGGTTGG  56412     GT TG    CT     AATC
                                  TCA  C  TTGT  CCCTCT
                                  |||  |  ||||  ||||||
                                  GGT  G  GACG  GGGAGA
                                    TG GT    __      AACC
GAM1042  LOC92465  5'  GGTTATAACTGATACAGACTGA 69412         T   TCCCTC
                                  TCAGTCTGT GTC     TAATC
                                  ||||||||| |||     |||||
                                  AGTCAGACA TAG     ATTGG
                                       _   TCAAT_
GAM1042  LOC93624  5'  AGAGGACAACAGGCTGG     72723           CTC
                                  TCAGTCTGTTGT   CCTCT
                                  ||||||||||||   |||||
                                  GGTCGGACAACA   GGAGA
                                                 ___
GAM1043  CDKN1A    3'  CTAGACTGTAAACCTCT     54297     GA   C
                                  AG  GTT ACAGTCTAG
                                  ||  ||| |||||||||
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                                TC  CAA TGTCAGATC
                                 TC   A
GAM1043  LHCGR    3'  CTGTAGACTGTAAACTCCT   4072        C      G
                                AGGAGTT ACAGTCTA AG
                                ||||||| |||||||| ||
                                TCCTCAA TGTCAGAT TC
                                    A       G
GAM1043  MEF2A    3'  CTTACCTGCAAACTCCTTG   18782        CA   TCT
                                CAAGGAGTT  CAG   AG
                                |||||||||  |||   ||
                                GTTCCTCAA  GTC   TC
                                     AC   CAT
GAM1043  TBX3     3'  CAGCTCCACTTCAAATTCCTT  33353       CAC   CTA
                                AAGGAGTT   AGT   GAGCTG
                                ||||||||   |||   ||||||
                                TTCCTTAA   TCA   CTCGAC
                                    ACT   C__
GAM1043  C4.4A    3'  CTAGACTGTGAGCTCCT     26943
                                AGGAGTTCACAGTCTAG
                                |||||||||||||||||
                                TCCTCGAGTGTCAGATC

GAM1043  C5orf4   3'  AGCCCCAGATAACTCCTT    50486        CACA    AGA
                                AAGGAGTT   GTCT   GCT
                                ||||||||   ||||   |||
                                TTCCTCAA   TAGA   CGA
                                    _____   CCC
GAM1043  C5orf4   3'  AGCCCCAGATAACTCCTT    32976        CACA    AGA
                                AAGGAGTT   GTCT   GCT
                                ||||||||   ||||   |||
                                TTCCTCAA   TAGA   CGA
                                    _____   CCC
GAM1043  C7orf13  3'  CTAAACCATGAGCTCCTT    50929         CA  C
                                AAGGAGTTCA  GT TAG
                                ||||||||||  || |||
                                TTCCTCGAGT  CA ATC
                                     AC  A
GAM1043  E2F6     3'  TTAGACTGTGAGCTCCTTG   8718
                                CAAGGAGTTCACAGTCTAG
                                |||||||||||||||||||
                                GTTCCTCGAGTGTCAGATT

GAM1043  FER1L4   3'  CTGGTTTGTGAACCC      47347    A      T
                                GG GTTCACAG CTAG
                                || |||||||| ||||
                                CC CAAGTGTT GGTC
                                 _       T
GAM1043  FLJ13848 3'  CAGTGGGACTGGGAACTCCTT  45463         A     AGA
                                AAGGAGTTC CAGTCT   GCTG
                                ||||||||| ||||||   ||||
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                                TTCCTCAAG GTCAGG   TGAC
                                     G     G__
GAM1043  FLJ20113  3'  CAGCCCCCAGGCTGTGAGCTCC 34573              AGA_
              TTG                   CAAGGAGTTCACAGTCT    GCTG
                                    |||||||||||||||||    ||||
                                    GTTCCTCGAGTGTCGGA    CGAC
                                          CCCC
GAM1043  FLJ20618  3'  AGGCACAGTGAACTCCTCA    35455    A        A__
                                    C AGGAGTTCAC   GTCT
                                    | ||||||||||   ||||
                                    A TCCTCAAGTG   CGGA
                                     C         ACA
GAM1043  KIAA0321  5'  CAGCTGCTGCTGTGAGCCCCTT 62390       A        CT  _
              G                     CAAGG GTTCACAGT  AG AGCTG
                                    ||||| |||||||||  || |||||
                                    GTTCC CGAGTGTCG  TC TCGAC
                                       C        __ G
GAM1043  KIAA0984  3'  CAGCTCTAGACTGCAGAC     65526     CA
                                    GTT  CAGTCTAGAGCTG
                                    |||  ||||||||||||
                                    CAG  GTCAGATCTCGAC
                                      AC
GAM1043  KIAA1184  3'  CTAGACTGTGAATCCTT      42614       G
                                    AAGGA TTCACAGTCTAG
                                    ||||| ||||||||||||
                                    TTCCT AAGTGTCAGATC
                                      _
GAM1043  KIAA1239  3'  CAGCTCTGCCATAAACTCATTG 71328     G     CACAGTC
                                    CAA GAGTT      TAGAGCTG
                                    ||| |||||      ||||||||
                                    GTT CTCAA      GTCTCGAC
                                      A     ATACC__
GAM1043  KIAA1328  3'  CAGCATGTCCTTTGAACTCC   61642         C  TC  GA
                                    GGAGTTCA AG  TA  GCTG
                                    |||||||| ||  ||  ||||
                                    CCTCAAGT TC  GT  CGAC
                                         T  CT  A_
GAM1043  KIAA1416  3'  AGCTCTAAACTAGCCTTG     86455       AGTTCAC   C
                                    CAAGG      AGT TAGAGCT
                                    |||||      ||| |||||||
                                    GTTCC      TCA ATCTCGA
                                       GA_____   A
GAM1043  NDUFB5    3'  CTCTAAAATGTTAACTCCTT   10194         C   GTC
                                    AAGGAGTT ACA   TAGAG
                                    |||||||| |||   |||||
                                    TTCCTCAA TGT   ATCTC
                                         T   AAA
GAM1043  PCDH16    3'  CAGCTCTCCACCCTGAACTCC  13604         CA  CT
                                    GGAGTTCA  GT  AGAGCTG
                                    ||||||||  ||  |||||||
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                                CCTCAAGT  CA  TCTCGAC
                                    CC  CC
GAM1043  PIP3-E   3'  CAGCCTTTCAACTGTAAACTCC 66802        C    CT   _
              TT                  AAGGAGTT ACAGT  AGAG CTG
                                  |||||||| |||||  |||| |||
                                  TTCCTCAA TGTCA  TTTC GAC
                                     A    AC   C
GAM1043  URG4     3'  AGACTGTGAGCTCCTTG     35501
                                  CAAGGAGTTCACAGTCT
                                  |||||||||||||||||
                                  GTTCCTCGAGTGTCAGA

GAM1043  LOC115129 3'  CAGCTCTAAACTCTCTGCCTCC 73227      TTCAC_   C
                                  GGAG     AGT TAGAGCTG
                                  ||||     ||| ||||||||
                                  CCTC     TCA ATCTCGAC
                                    CGTCTC   A
GAM1043  LOC124460 5'  CAGGGTGGACTGTGACCCCTTG 76042      A  T       GAG
                                  CAAGG GT CACAGTCTA   CTG
                                  ||||| || |||||||||   |||
                                  GTTCC CA GTGTCAGGT   GAC
                                     C  _       GG_
GAM1043  LOC137964 3'  CAGGCTAACCCTGAACTCC    75278        CA  C   AG
                                  GGAGTTCA  GT TAG  CTG
                                  ||||||||  || |||  |||
                                  CCTCAAGT  CA ATC  GAC
                                       CC  _   G_
GAM1043  LOC144519 3'  AGCCCTTCTGAACTCCT     76864         CAGTCT  A
                                  AGGAGTTCA     AG GCT
                                  |||||||||     || |||
                                  TCCTCAAGT     TC CGA
                                        CT_____  C
GAM1043  LOC146268 3'  CTAGACTGTGAGCTCCT     77808
                                  AGGAGTTCACAGTCTAG
                                  |||||||||||||||||
                                  TCCTCGAGTGTCAGATC

GAM1043  LOC146774 3'  CAGCCACCGTGTGAACTCTTTG 78095            GTCTAGA
                                  CAAGGAGTTCACA      GCTG
                                  ||||||||||||      ||||
                                  GTTTCTCAAGTGT      CGAC
                                          GCCAC__
GAM1043  LOC147837 5'  CAGCTCTAGACTCAGTCGCTC  78514     TCAC_
                                  GAGT    AGTCTAGAGCTG
                                  ||||    ||||||||||||
                                  CTCG    TCAGATCTCGAC
                                    CTGAC
GAM1043  LOC158267 3'  GCTCCTGAATTCCTCA      81833   A       CAGTCTA
                                  C AGGAGTTCA      GAGC
                                  | |||||||||      ||||
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                                A TCCTTAAGT      CTCG
                                 C       C_______
GAM1043  LOC163404 3'  CTAGACTGTGAGCTCCT     82127
                                AGGAGTTCACAGTCTAG
                                ||||||||||||||||
                                TCCTCGAGTGTCAGATC

GAM1043  LOC203197 3'  CTAGACTGTAAACTCCTT     89286         C
                                AAGGAGTT ACAGTCTAG
                                |||||||| |||||||||
                                TTCCTCAA TGTCAGATC
                                     A
GAM1043  LOC253897 3'  CAGGCTAACCCTGAACTCC    96103         CA  C   AG
                                GGAGTTCA  GT TAG  CTG
                                ||||||||  || |||  |||
                                CCTCAAGT  CA ATC  GAC
                                     CC  _   G_
GAM1043  LOC254100 3'  CAGCCCTACCCTGAATTCCTCA 96412    A       CA TC   A
                                C AGGAGTTCA  G  TAG GCTG
                                | |||||||||  |  ||| ||||
                                A TCCTTAAGT  C  ATC CGAC
                                 C       __ CC   C
GAM1043  LOC254552 5'  AGCGGCCGGGAACTCCT     94773         ACA   TAGA
                                AGGAGTTC   GTC    GCT
                                ||||||||   |||    |||
                                TCCTCAAG   CGG    CGA
                                     GGC   ____
GAM1043  LOC90786  5'  CAGCCTTTCCTGTGACTCCTTG 64028         T    TCT  A
                                CAAGGAGT CACAG   AG GCTG
                                |||||||| |||||   || ||||
                                GTTCCTCA GTGTC   TC CGAC
                                     _    CTT  _
GAM1043  LOC91750  3'  CAGCCTGACCTGTGAACTCT   67058          TC   A
                                GGAGTTCACAG  TAG GCTG
                                ||||||||||  ||| ||||
                                TCTCAAGTGTC  GTC CGAC
                                       CA   _
GAM1044  FUT9     3'  TACTACTTTTGTGTCACA     67846       CGTT TG
                                TGTGAT    G  AAAGTAGTA
                                ||||||    |  |||||||||
                                ACACTG    T  TTTCATCAT
                                    ____ GT
GAM1044  TMEFF1   3'  ACTTCTTCCACAATGACCACA  13497      A      A   T
                                TGTG TCGTTGTG AAG AGT
                                |||| |||||||| ||| |||
                                ACAC AGTAACAC TTC TCA
                                  C       C   T
GAM1044  FLJ21195  3'  TACTACTTTCACTGCCATGACA 42452     G  C  T
                                TGT AT GT GTGAAAGTAGTA
                                ||| || || ||||||||||||
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                                ACA TA CG CACTTTCATCAT
                                  G  C  T
GAM1044  GABBR1   3'  GTACTACCCTCAGTCTACA   7610     _  CGTTG   AA
                                TGT GAT    TGA  GTAGTAC
                                ||| |||    |||  |||||||
                                ACA CTG    ACT  CATCATG
                                  T  _____  CC
GAM1044  GABBR1   3'  GTACTACCCTCAGTCTACA   41575    _  CGTTG   AA
                                TGT GAT    TGA  GTAGTAC
                                ||| |||    |||  |||||||
                                ACA CTG    ACT  CATCATG
                                  T  _____  CC
GAM1044  HERPUD1  3'  TGTACTACTTTATATAATCA  28022     CG TGTG
                                TGAT  T    AAAGTAGTACA
                                ||||  |    ||||||||||
                                ACTA  A    TTTCATCATGT
                                  AT TA__
GAM1044  PEX12    5'  TACTACTTCCACCCACG     4298     T_  A
                                CGT  GTG AAGTAGTA
                                |||  ||| ||||||||
                                GCA  CAC TTCATCAT
                                  CC   C
GAM1044  RAB40A   5'  TGGTTCCATAACGATCACA   82073          A  G
                                TGTGATCGTTGTG AA TA
                                |||||||||||| || ||
                                ACACTAGCAATAC TT GT
                                       C  G
GAM1044  LOC162239 3'  TGTACTACTCAGTATGCACCAC 82344     AT_  TG   AA
             A                   TGTG   CGT  TGA  GTAGTACA
                                ||||   |||  |||  ||||||||
                                ACAC   GTA  ACT  CATCATGT
                                  CAC   TG  __
GAM1044  LOC92249  3'  ATTTTCACAACAATCCCA    68564    T   C
                                TG GAT GTTGTGAAAGT
                                || ||| ||||||||||
                                AC CTA CAACACTTTTA
                                 C   A
GAM1045  ACADS    3'  CCACTGTGCCTCAAGTTCC    3408      AAGACA
                                GGAG     GGGCACAGTGG
                                ||||     ||||||||||
                                CCTT     TCCGTGTCACC
                                  GAAC__
GAM1045  ADCY2    3'  CCACTACGCTCCTGTCTCCA   65015     GAA    _  AC
                                TGGA   GACAGG GC  AGTGG
                                ||||   |||||| ||  |||||
                                ACCT   CTGTCC CG  TCACC
                                  ___     T  CA
GAM1045  AKAP13   3'  CCACTGGCTGTGTCCCCTGCCA 89682    _  AA   G   A
                                TGG AG  GACA GGC CAGTGG
                                ||| ||  |||| ||| ||||||
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                                ACC TC  CTGT TCG GTCACC
                                  G  CC    G  _
GAM1045  APOB48R  3'  CCACTGTGGACACATCCTCTCC 37958      A  CAGGG_
                                GGAGA GA     CACAGTGG
                                |||||  ||     ||||||||
                                CCTCT CT     GTGTCACC
                                   C  ACACAG
GAM1045  APOL1    3'  TGCCCTGTCTTTCCA       13355       A
                                TGGAGA GACAGGGCA
                                |||||| |||||||||
                                ACCTTT CTGTCCCGT
                                     _
GAM1045  AR       5'  CCACCGTGTGTCTTCTTC    3488          AGG    A
                                GGAGAAGAC   GCAC GTGG
                                |||||||||   ||||  ||||
                                CTTCTTCTG   TGTG CACC
                                      ___    C
GAM1045  ATBF1    5'  CCACCATGAGCTCCCCTCC    22549     AAGACA    A  __
                                GGAG     GGGC CA  GTGG
                                ||||     ||||  ||  ||||
                                CCTC     CTCG GT  CACC
                                  CC_____    A  AC
GAM1045  B3GAT1   5'  TGCTCTGTCCTCTCCA      53980       A
                                TGGAGA GACAGGGCA
                                |||||| |||||||||
                                ACCTCT CTGTCTCGT
                                   C
GAM1045  BID      3'  CACTGTGCAGGTTCCCA     6822      A  AG  AGG
                                TGG GA  AC   GCACAGTG
                                |||  ||  ||   ||||||||
                                ACC CT  TG   CGTGTCAC
                                  _  __  GA_
GAM1045  BMP1     3'  CCACAGGCTCCCCATCTTCTCC 20418        CA__    ACA
                                GGAGAAGA    GGGC   GTGG
                                ||||||||    ||||   ||||
                                CCTCTTCT    CTCG   CACC
                                     ACCC    GA_
GAM1045  C14orf1  3'  CCACTGTGTCTCCTTCCCC    23175    A    ACA
                                GG GAAG   GGGCACAGTGG
                                || ||||   ||||||||||
                                CC CTTC   TCTGTGTCACC
                                 C    C__
GAM1045  C5R1     3'  CCATGTTGCCTGTCTTTCCCA  8201      AG       G  CA
                                TGG  AAGACAGG CA  GTGG
                                |||  |||||||| ||  ||||
                                ACC  TTCTGTCC GT  TACC
                                  CT       _  TG
GAM1045  CACNA1G  3'  CACTCACCTTTCTCCA      38157        GAC   GCAC
                                TGGAGAA   AGG    AGTG
                                |||||||   |||    ||||
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                                ACCTCTT  TCC   TCAC
                                   ___  AC__
GAM1045 CARKL   3' GTCCCTGTGTTCCCCA    25190    A  G    C
                                TGG GAA ACAGGG AC
                                ||| ||| |||||| ||
                                ACC CTT TGTCCC TG
                                  C  G    _
GAM1045 CDKN1A  3' CCAGCTACCCTTCTTCTCCA  54295       C   CAC  _
                                TGGAGAAGA AGGG  AG TGG
                                ||||||||| ||||  || |||
                                ACCTCTTCT TCCC  TC ACC
                                     _  A__  G
GAM1045 COG5    3' TGTACCCTGCTTCCCC    20954    A   A    C
                                GG GAAG CAGGG ACA
                                || |||| ||||| |||
                                CC CTTC GTCCC TGT
                                 C  _    A
GAM1045 CRTAP   3' CCTTCATCCCTGTCTTCCTCA 21033    GA       CACAGT
                                TG  GAAGACAGGG    GG
                                ||  ||||||||||    ||
                                AC  CTTCTGTCCC    CC
                                 TC       TACTT_
GAM1045 CRY1    5' CCAGCGCCCCCGCCTTCTCC  14520      ACA_   ACAG
                                GGAGAAG   GGGC   TGG
                                |||||||   ||||   |||
                                CCTCTTC   CCCG   ACC
                                    CGCC   CG__
GAM1045 CRY2    3' CCACCTCCGCCTACTTCTCCA 72205       ACA   ACA_
                                TGGAGAAG  GGGC   GTGG
                                ||||||||  ||||   ||||
                                ACCTCTTC  TCCG   CACC
                                    A__   CCTC
GAM1045 CSRP1   3' CACTCCACCCTTCTCCA    14527      AGAC   CAC
                                TGGAGA   AGGG  AGTG
                                ||||||   ||||  ||||
                                ACCTCT   TCCC  TCAC
                                   ____   ACC
GAM1045 CSRP1   3' CCAAGACCCTGCCTCTTCCA  14529    GA  A   CACAG
                                TGGA  AG CAGGG    TGG
                                ||||  || |||||    |||
                                ACCT  TC GTCCC    ACC
                                  TC  C    AGA__
GAM1045 DES     3' CGGTGGCCCTGTCCCTCC    72125    AA      A  G
                                GGAG  GACAGGGC CA TG
                                ||||  |||||||| || ||
                                CCTC  CTGTCCCG GT GC
                                  C_       _  G
GAM1045 DHCR7   3' CCTCTCCACACCTTCTCCA   7233        ACAG  CAC  T
                                TGGAGAAG   GG  AG GG
                                ||||||||   ||  || ||
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                                ACCTCTTC   CC  TC CC
                                    CACA ___ T
GAM1045 DYRK1A   3' CCATGACATCCCTGTCTTCCTC 55202   GA       CACA_
          A                  TG  GAAGACAGGG   GTGG
                             ||  ||||||||||    ||||
                             AC  CTTCTGTCCC    TACC
                              TC        TACAG
GAM1045 EDG8     3' CACGACTGTCTTCCCA     78476    A     GGCACA
                             TGG GAAGACAG     GTG
                             ||| ||||||||     |||
                             ACC CTTCTGTC     CAC
                               _      AG____
GAM1045 FBXL11   3' CTGTGCCCCTCCTCC      24571     A  ACA
                             GGAG AG   GGGCACAG
                             |||| ||   ||||||||
                             CCTC TC   CCCGTGTC
                               C ___
GAM1045 FCN2     3' CTGTCCCCTGGCTTCTCCA   31732       A    C
                             TGGAGAAG CAGGG ACAG
                             |||||||| ||||| ||||
                             ACCTCTTC GTCCC TGTC
                                  G    C
GAM1045 FCN2     3' CTGTCCCCTGGCTTCTCCA   31739       A    C
                             TGGAGAAG CAGGG ACAG
                             |||||||| ||||| ||||
                             ACCTCTTC GTCCC TGTC
                                  G    C
GAM1045 FXR2     3' CTGCACCCCTCCCTTCTCCA  16787       AC   CA_
                             TGGAGAAG  AGGG   CAG
                             ||||||||  ||||  |||
                             ACCTCTTC  TCCC   GTC
                                  CC   CAC
GAM1045 GALNT2   3' CCACTCCTGGCCGCCTTCTCCA 15595       ACA  G  C_
                             TGGAGAAG   GG CA  AGTGG
                             ||||||||   || ||  |||||
                             ACCTCTTC   CC GT  TCACC
                                  CG_  G  CC
GAM1045 GALNT2   3' CCACTGTGTGTCTTCCTCC   15596    _   AGG
                             GGAG AAGAC   GCACAGTGG
                             |||| |||||   |||||||||
                             CCTC TTCTG   TGTGTCACC
                               C    ___
GAM1045 GGT1     3' CCACTGTGCCAGGTGCCTCC  17938     AAG  AG
                             GGAG   AC  GGCACAGTGG
                             ||||   ||  ||||||||||
                             CCTC   TG  CCGTGTCACC
                               CG_  GA
GAM1045 GGT2     3' CACTGTGCCAGGCTCCA     73709      AAGACAG
                             TGGAG      GGCACAGTG
                             |||||      |||||||||
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                                ACCTC      CCGTGTCAC
                                   GGA_____
GAM1045  GPD1     3'  TGCCCTGTCCCTCTCCA     59673        A_
                                TGGAGA  GACAGGGCA
                                ||||||  |||||||||
                                ACCTCT  CTGTCCCGT
                                    CC
GAM1045  GPR81    3'  TGCCCTGGCTTCTCCA      50768         A
                                TGGAGAAG CAGGGCA
                                |||||||| |||||||
                                ACCTCTTC GTCCCGT
                                     G
GAM1045  HAO2     3'  CCAAACCCCTGTGTTCCCCA   33266     A   G     CACAG
                                TGG GAA ACAGGG     TGG
                                ||| ||| ||||||     |||
                                ACC CTT TGTCCC     ACC
                                  C   G     CAA__
GAM1045  HSPB1    3'  CCACTGGCTGTGCCTCC      7739       AAGA  G   A
                                GGAG    CA GGC CAGTGG
                                ||||    || ||| ||||||
                                CCTC    GT TCG GTCACC
                                  C___  G   _
GAM1045  IL8      3'  CCACTGTGCCTTGGTTTCTCC  94478         A
                                GGAGAAG CAGGGCACAGTGG
                                ||||||| ||||||||||||
                                CCTCTTT GTTCCGTGTCACC
                                     G
GAM1045  IRTA2    3'  CCACTATCTTTGTTTCCCCA   48403     A  A      CAC
                                TGG GA GACAGGG   AGTGG
                                ||| || |||||||   |||||
                                ACC CT TTGTTTC   TCACC
                                  C  _      TA_
GAM1045  LTBP2    3'  CCGCATGAGGCCCTGTC      4722          A_  _
                                GACAGGGC  CA GTGG
                                ||||||||  || ||||
                                CTGTCCCG  GT CGCC
                                     GA  A
GAM1045  LY95     5'  CCTCTCCCCAGTCTTCTCCA   16704          A   CAC  T
                                TGGAGAAGAC GGG   AG GG
                                |||||||||| |||   || ||
                                ACCTCTTCTG CCC   TC CC
                                      A   C__  T
GAM1045  MAPRE2   3'  CCACTGCGCTTGGTTCCCA    26540     A  AG  AG   A
                                TGG GA  AC  GGC CAGTGG
                                ||| ||  ||  ||| ||||||
                                ACC CT  TG  TCG GTCACC
                                  _  __  GT   C
GAM1045  MATN1    3'  CACTGTGGCCTCTCCA      9917        AGACA  G
                                TGGAGA    GG CACAGTG
                                ||||||    || |||||||
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                                ACCTCT    CC GTGTCAC
                                   _____  G
GAM1045  MLLT2    3'  CCACTGTGCCCCACTTTCT   19842      ACA
                                AGAAG  GGGCACAGTGG
                                |||||  ||||||||||
                                TCTTT  CCCGTGTCACC
                                  CAC
GAM1045  MMP19    5'  CCACTGTGCCCCCAGTGCCCA  42969     AGAAGACA
                                TGG      GGGCACAGTGG
                                |||      ||||||||||
                                ACC      CCCGTGTCACC
                                 CGTGACC_
GAM1045  MMP19    5'  CCACTGTGCCCCCAGTGCCCA  42983     AGAAGACA
                                TGG      GGGCACAGTGG
                                |||      ||||||||||
                                ACC      CCCGTGTCACC
                                 CGTGACC_
GAM1045  OTX1     3'  CTTTGCCTCGTCTTCTCCA   27305        AG   C
                                TGGAGAAGAC  GGCA AG
                                ||||||||||  |||| ||
                                ACCTCTTCTG  CCGT TC
                                     CT   T
GAM1045  OVOL1    5'  CTGGACCCTCTCTTCTCCA   15857        C   CA
                                TGGAGAAGA AGGG  CAG
                                |||||||| ||||  |||
                                ACCTCTTCT TCCC  GTC
                                     C   AG
GAM1045  PITX3    3'  CATCCCGCCTTCTCCA     17265       ACA  CACA
                                TGGAGAAG  GGG   GTG
                                ||||||||  |||   |||
                                ACCTCTTC  CCC   TAC
                                    CG_  ____
GAM1045  PKD2     3'  CCACCATGACTGAGTCTTCTC  60091       AG  _  CA
                                GAGAAGAC  GG CA  GTGG
                                ||||||||  || ||  ||||
                                CTCTTCTG  TC GT  CACC
                                    AG  A  AC
GAM1045  PPP2R1A  3'  CCACCTCCCGTCCTCCCCA   26443    A  A   A   CACA
                                TGG GA GAC GGG   GTGG
                                ||| || ||| |||   ||||
                                ACC CT CTG CCC   CACC
                                  C  C   _   TC__
GAM1045  PPP2R4   3'  CTGTGCCTGCCTTCCCCA    60558    A   ACA
                                TGG GAAG  GGGCACAG
                                ||| ||||  ||||||||
                                ACC CTTC  TCCGTGTC
                                  C   CG_
GAM1045  RAD50    3'  CACCACCTTCTTCTCC      56006       C  GCACA
                                GGAGAAGA AGG    GTG
                                |||||||| |||    |||
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                                CCTCTTCT TCC    CAC
                                     _  AC___
GAM1045  RAD50   3'  CACCACCTTCTTCTCC     19192        C  GCACA
                                GGAGAAGA AGG    GTG
                                |||||||| |||    |||
                                CCTCTTCT TCC    CAC
                                     _  AC___
GAM1045  RGS9    5'  CCACCGCACCTGGCCTTCCCCA 13832    A   A_   _  ACA
                                TGG GAAG  CAGG GC   GTGG
                                ||| ||||  |||| ||   ||||
                                ACC CTTC  GTCC CG   CACC
                                  C   CG   A  C__
GAM1045  RRAS    3'  CCACTGTGTGCCTTCTGCCA  20775    _    A AGG
                                TGG AGAAG C   GCACAGTGG
                                ||| ||||| |   |||||||||
                                ACC TCTTC G   TGTGTCACC
                                  G    C ___
GAM1045  SCAP1   3'  CACATCTGCCTTTTCCA    13573        A   GCACA
                                TGGAGAAG CAGG    GTG
                                |||||||| ||||    |||
                                ACCTTTTC GTCT    CAC
                                     C   A____
GAM1045  SCNN1A  3'  CCACATCTTGTCTTCCCCA  6422     A        CACA
                                TGG GAAGACAGGG   GTGG
                                ||| ||||||||||   ||||
                                ACC CTTCTGTTCT   CACC
                                  C        A___
GAM1045  SEPN1   3'  CACTGAGCCTTCCCCA     66361    A  AGACA   A
                                TGG GA    GGGC CAGTG
                                ||| ||    |||| |||||
                                ACC CT    TCCG GTCAC
                                  C _____   A
GAM1045  SIGLECL1 3'  CACCATTCTCTTCTCTA    52830        C  GGCACA
                                TGGAGAAGA AG    GTG
                                ||||||||| ||    |||
                                ATCTCTTCT TT    CAC
                                     C  AC____
GAM1045  SIGLECL1 3'  CACCATTCTCTTCTCTA    53810        C  GGCACA
                                TGGAGAAGA AG    GTG
                                ||||||||| ||    |||
                                ATCTCTTCT TT    CAC
                                     C  AC____
GAM1045  SIRT3   3'  CCACTGGAATGTCTTCTC    24268        GGGCA
                                GAGAAGACA    CAGTGG
                                |||||||||    ||||||
                                CTCTTCTGT    GTCACC
                                     AAG__
GAM1045  SMAC    3'  TGCCCTGTCTCCCCA      39114    A  A
                                TGG GA GACAGGGCA
                                ||| || |||||||||
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                                ACC CT CTGTCCCGT
                                  C  _
GAM1045  SMAC     3'  TGCCCTGTCTCCCCA       57198     A  A
                                TGG GA GACAGGGCA
                                ||| || |||||||||
                                ACC CT CTGTCCCGT
                                  C  _
GAM1045  SMAC     3'  TGCCCTGTCTCCCCA       57220     A  A
                                TGG GA GACAGGGCA
                                ||| || |||||||||
                                ACC CT CTGTCCCGT
                                  C  _
GAM1045  STX1A    3'  TGCCCTGTCCTCTCCA      16014       A
                                TGGAGA GACAGGGCA
                                |||||| |||||||||
                                ACCTCT CTGTCCCGT
                                    C
GAM1045  TCTA     3'  CACTAGCATCTTCTCTA     42235         CAGG  AC
                                TGGAGAAGA   GC  AGTG
                                |||||||||   ||  ||||
                                ATCTCTTCT   CG  TCAC
                                     A___  A_
GAM1045  TRPV1    5'  GTCCCTGTGTTCCCCA      54812     A  G     C
                                TGG GAA ACAGGG AC
                                ||| ||| |||||| ||
                                ACC CTT TGTCCC TG
                                  C  G     _
GAM1045  VDR      3'  CAGTGAGCCGCATCTTCTCCA 4566          CAG   A  G
                                TGGAGAAGA   GGC CA TG
                                |||||||||   ||| || ||
                                ACCTCTTCT   CCG GT AC
                                     ACG   A  G
GAM1045  VEGF     3'  CCACTAGTTCTGTCCCCCCA  12586     AGAA       AC
                                TGG    GACAGGGC  AGTGG
                                |||    ||||||||  |||||
                                ACC    CTGTCTTG  TCACC
                                  CCC_       A_
GAM1045  XPA      3'  CCACTGTACCCCAGGTTCT   4597      GACA   C
                                AGAA    GGG ACAGTGG
                                ||||    ||| |||||||
                                TCTT    CCC TGTCACC
                                  GGAC   A
GAM1045  ZNF236   3'  CGGTGGCCCTGTCCACCCCA  23713     AGAA      A  G
                                TGG    GACAGGGC CA TG
                                |||    |||||||| || ||
                                ACC    CTGTCCCG GT GC
                                  CCAC       _  G
GAM1045  ZNF261   3'  CCATTCCCTGCCTTCTCTA   17494         A    CAC
                                TGGAGAAG CAGGG   AGTGG
                                |||||||| |||||   |||||
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                                ATCTCTTC GTCCC  TTACC
                                    C   ___
GAM1045 ZNF278  3' CCACTCCAACTCCTTCTCCA  26726      ACAG_ CAC
                                TGGAGAAG  GG  AGTGG
                                ||||||||  ||  |||||
                                ACCTCTTC  CC  TCACC
                                    CTCAA ___
GAM1045 ZNF278  3' CCACTCCAACTCCTTCTCCA  49433      ACAG_ CAC
                                TGGAGAAG  GG  AGTGG
                                ||||||||  ||  |||||
                                ACCTCTTC  CC  TCACC
                                    CTCAA ___
GAM1045 ZNF278  3' CCACTCCAACTCCTTCTCCA  49441      ACAG_ CAC
                                TGGAGAAG  GG  AGTGG
                                ||||||||  ||  |||||
                                ACCTCTTC  CC  TCACC
                                    CTCAA ___
GAM1045 ZNF42   5' GCTTCCGCCTTCTCCA    12785      ACA  CAC
                                TGGAGAAG  GGG  AGT
                                ||||||||  |||  |||
                                ACCTCTTC  CCT  TCG
                                    CG_  ___
GAM1045 APBA3   3' CCACTGTGCCTTCGCCTCCA  16881    AA  CA
                                TGGAG  GA  GGGCACAGTGG
                                |||||  ||  ||||||||||
                                ACCTC  CT  TCCGTGTCACC
                                   CG  __
GAM1045 APOL3   3' TGCCCTGTCTTTCCA     26817     A
                                TGGAGA GACAGGGCA
                                |||||| |||||||||
                                ACCTTT CTGTCCCGT
                                   _
GAM1045 B3GNT7  3' CCACCGCACCCTGCTTCTCCA 71126      A   CACA
                                TGGAGAAG CAGGG  GTGG
                                |||||||| |||||  ||||
                                ACCTCTTC GTCCC  CACC
                                    _   ACGC
GAM1045 C16orf7 3' CCACTGTGGTGTGCTCTCCA  16936     AG  GGG
                                TGGAGA  ACA  CACAGTGG
                                ||||||  |||  ||||||||
                                ACCTCT  TGT  GTGTCACC
                                   CG  G__
GAM1045 C20orf130 3' CACTGTGCTGCTCTTC    61754     CAG
                                GAAGA  GGCACAGTG
                                |||||  |||||||||
                                CTTCT  TCGTGTCAC
                                   CG_
GAM1045 C3F     3' CAAGGCCCTGCCTGCTCCA   19285     A A    ACAG
                                TGGAG AG CAGGGC  TG
                                ||||| || ||||||  ||
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                                ACCTC TC GTCCCG   AC
                                  G  C    GA__
GAM1045  C8orf17  3'  CCACCGCGGCCGCTTCTCCA  39595       ACAG  ACA_
                                TGGAGAAG  GGC  GTGG
                                ||||||||  |||  ||||
                                ACCTCTTC  CCG  CACC
                                    G___  GCGC
GAM1045  CCNE1    3'  CACCCCATCCTTCTCCA    54116       ACA  CACA
                                TGGAGAAG  GGG  GTG
                                ||||||||  |||  |||
                                ACCTCTTC  CCC  CAC
                                    CTA  ____
GAM1045  CCNE1    3'  CACCCCATCCTTCTCCA    6948        ACA  CACA
                                TGGAGAAG  GGG  GTG
                                ||||||||  |||  |||
                                ACCTCTTC  CCC  CAC
                                    CTA  ____
GAM1045  CGI-94   5'  CCACTGATCTTTTCCA     32096        _  _
                                TGGAGAAGA CAG GG
                                ||||||||| ||| ||
                                ACCTTTTCT GTC CC
                                     A  A
GAM1045  DDX33    3'  CCACTCTGTGTCTGTCTCCA  39371      _   G  CAC
                                TGGAGA AGACA GG  AGTGG
                                |||||| ||||| ||  |||||
                                ACCTCT TCTGT TC  TCACC
                                   G   G ___
GAM1045  DKFZp434J0226 3'  GTCCCTGTCTCCTCCA     72335      A      C
                                TGGAG AGACAGGG AC
                                ||||| |||||||| ||
                                ACCTC TCTGTCCC TG
                                  C      _
GAM1045  DKFZp547I094 5'  CTGTTGCCCTGCCTTCTTCA  49641       A    _
                                TGGAGAAG CAGGGCA CAG
                                |||||||| ||||||| |||
                                ACTTCTTC GTCCCGT GTC
                                    C      T
GAM1045  DKFZP564D166 3'  CACTGTGGCCTCCCA      47671    A  AGACA  G
                                TGG GA    GG CACAGTG
                                ||| ||    || |||||||
                                ACC CT    CC GTGTCAC
                                  _ _____  G
GAM1045  DKFZp564I1922 3'  CCACTGTTATATTACCTTCTCC 31233       AC  GGC_
           A                    TGGAGAAG  AG   ACAGTGG
                                ||||||||  ||   |||||||
                                ACCTCTTC  TT   TGTCACC
                                    CA  ATAT
GAM1045  FADS1    3'  CACTGTGGCCTTCTC      25474     AGAC  G
                                GAGA   AGG CACAGTG
                                ||||   ||| |||||||
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                                CTCT    TCC GTGTCAC
                                  ____  G
GAM1045  FAM3D    5' CACCTCGCCTTCTCCA     57151       ACA   CACA
                                TGGAGAAG  GGG   GTG
                                ||||||||  |||   |||
                                ACCTCTTC  CTC   CAC
                                    CG_   ____
GAM1045  FLJ10613 3' CCACTGTGTGTCTTCTCC   38821       AGG
                                GGAGAAGAC  GCACAGTGG
                                |||||||||  ||||||||
                                CCTCTTCTG  TGTGTCACC
                                    ___
GAM1045  FLJ10774 5' CCACGTGCTTCCCCTTCTCCA 45083       ACA     A
                                TGGAGAAG  GGGCAC GTGG
                                ||||||||  |||||| ||||
                                ACCTCTTC  TTCGTG CACC
                                    CCC     _
GAM1045  FLJ10936 3' CCACTGTGCTAGTTGCCCA  36906    AGAA   AG
                                TGG   GAC  GGCACAGTGG
                                |||   |||  ||||||||||
                                ACC   TTG  TCGTGTCACC
                                  CG__   A_
GAM1045  FLJ11294 3' CTGGCCCTGTCCTGTCCA   37222     GAA      A
                                TGGA  GACAGGGC CAG
                                ||||  |||||||| |||
                                ACCT  CTGTCCCG GTC
                                  GTC      _
GAM1045  FLJ14451 3' CCACTCACCTAGCCTTCCCCA 51379    A   AC_  GCAC
                                TGG GAAG  AGG   AGTGG
                                ||| ||||  |||   |||||
                                ACC CTTC  TCC   TCACC
                                  C   CGA  AC__
GAM1045  FLJ14466 3' CCACCTGGGTGCCTCCTCC   51392    AAGACA    A___
                                GGAG    GGGCAC   GTGG
                                ||||    ||||||   ||||
                                CCTC    TCCGTG   CACC
                                  C_____    GGTC
GAM1045  FLJ14708 3' CCACTGTGGGCCCTCCTTC   51541    AC    __
                                GAAG  AGGGC  ACAGTGG
                                ||||  |||||  |||||||
                                CTTC  TCCCG  TGTCACC
                                  C_    GG
GAM1045  FLJ20174 5' CCACATCTCCACTTCTCCA   34686       ACA   CACA
                                TGGAGAAG  GGG   GTGG
                                ||||||||  |||   ||||
                                ACCTCTTC  CCT   CACC
                                    A__   CTA_
GAM1045  FLJ20300 3' CCACTGTCAGCTTTTCTCCA  34907       ACAG   __
                                TGGAGAAG   GGC  ACAGTGG
                                ||||||||   |||  |||||||
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                                ACCTCTTT   TCG  TGTCACC
                                     ____  AC
GAM1045  FLJ20371  3'  CCACTGTGCTGTCTTGCTCCA  35059     _    GG
                                TGGAG AAGACA  GCACAGTGG
                                ||||| ||||||  |||||||||
                                ACCTC TTCTGT  CGTGTCACC
                                   G    __
GAM1045  FLJ20619  3'  CCATCCCCTCATCTTCTCCA  35462       C_   CACA
                                TGGAGAAGA  AGGG   GTGG
                                |||||||||  ||||   ||||
                                ACCTCTTCT  TCCC   TACC
                                     AC   C___
GAM1045  FLJ22746  3'  CCACCTGCACCTGTCTTCTC  45552        _  CA
                                GAGAAGACAGG GCA  GTGG
                                |||||||||| |||  ||||
                                CTCTTCTGTCC CGT  CACC
                                      A  C_
GAM1045  GAL3ST2   3'  CCACAACCTGTCTTTTCCA   52311          GCACA
                                TGGAGAAGACAGG   GTGG
                                ||||||||||||    ||||
                                ACCTTTTCTGTCC   CACC
                                      AA___
GAM1045  GGTLA4    3'  CACTGTGCCAGGCTCCA    55161      AAGACAG
                                TGGAG     GGCACAGTG
                                |||||     |||||||||
                                ACCTC     CCGTGTCAC
                                   GGA____
GAM1045  GT650     3'  CTGGGCCCCATCTCTCCA   53456      A  CA   A
                                TGGAGA GA  GGGC CAG
                                |||||| ||  |||| |||
                                ACCTCT CT  CCCG GTC
                                   _ AC   G
GAM1045  HIF1AN    3'  CCACTGCTTACCTTTTCCA   61970       AC   GCA
                                TGGAGAAG  AGG   CAGTGG
                                ||||||||  |||   ||||||
                                ACCTTTTC  TTC   GTCACC
                                     CA  ___
GAM1045  HRIHFB2072 3'  CCATCTTGTGCCTCTTCTCCA  50725        CAG    __
                                TGGAGAAGA   GGCACA  GTGG
                                |||||||||   ||||||  ||||
                                ACCTCTTCT   CCGTGT  TACC
                                     ___     TC
GAM1045  JAM1      3'  CCACTCTCTTCTGTCTTCCCA  57879    A       CAC
                                TGG GAAGACAGGG   AGTGG
                                ||| ||||||||||   |||||
                                ACC CTTCTGTCTT   TCACC
                                  _        CTC
GAM1045  JAM1      3'  CCACTCTCTTCTGTCTTCCCA  33752    A       CAC
                                TGG GAAGACAGGG   AGTGG
                                ||| ||||||||||   |||||
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                                ACC CTTCTGTCTT   TCACC
                                  _        CTC
GAM1045  JAM1     3'  CCACTCTCTTCTGTCTTCCCA  57890     A        CAC
                                TGG GAAGACAGGG   AGTGG
                                ||| ||||||||||   |||||
                                ACC CTTCTGTCTT   TCACC
                                  _        CTC
GAM1045  JAM1     3'  CCACTCTCTTCTGTCTTCCCA  57918     A        CAC
                                TGG GAAGACAGGG   AGTGG
                                ||| ||||||||||   |||||
                                ACC CTTCTGTCTT   TCACC
                                  _        CTC
GAM1045  JAM1     3'  CCACTCTCTTCTGTCTTCCCA  57945     A        CAC
                                TGG GAAGACAGGG   AGTGG
                                ||| ||||||||||   |||||
                                ACC CTTCTGTCTT   TCACC
                                  _        CTC
GAM1045  KIAA0144 3'  CTGACCCTGTCTTACCCA    29285     AG       CA
                                TGG  AAGACAGGG  CAG
                                |||  |||||||||  |||
                                ACC  TTCTGTCCC  GTC
                                  CA       A_
GAM1045  KIAA0222 3'  CACTGAGTCCTCCCG       27678     A  AGACA    A
                                TGG GA    GGGC CAGTG
                                ||| ||    |||| |||||
                                GCC CT    CCTG GTCAC
                                  _ _____    A
GAM1045  KIAA0435 3'  CCACTGTGCTGGCCCTCTA   28971      AAGACAG
                                TGGAG     GGCACAGTGG
                                |||||     ||||||||||
                                ATCTC     TCGTGTCACC
                                   CCGG___
GAM1045  KIAA0555 3'  CCACTGTGCCCGGCCTCC    28880     AAGACA
                                GGAG     GGGCACAGTGG
                                ||||     ||||||||||
                                CCTC     CCCGTGTCACC
                                  CGG___
GAM1045  KIAA0677 3'  CCACCTCTTTGTCTTCCCC   27825    A        CACA
                                GG GAAGACAGGG    GTGG
                                || ||||||||||    ||||
                                CC CTTCTGTTTC    CACC
                                 C         TC__
GAM1045  KIAA0763 3'  CACCTGTGTCCTCCCA      29531     A  AGACA      _
                                TGG GA    GGGCACAG TG
                                ||| ||    |||||||| ||
                                ACC CT    CCTGTGTC AC
                                  _ _____       C
GAM1045  KIAA0773 3'  CTGGTTCCTCACCTTCTCCA  28055        AC_   CA
                                TGGAGAAG   AGGG  CAG
                                ||||||||   ||||  |||
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                              ACCTCTTC  TCCT  GTC
                                  CAC   TG
GAM1045 KIAA0870 3' CCACTGTGGGCTCTCTCC   81467     AGACA   __
                              GGAGA   GGGC  ACAGTGG
                              |||||   ||||  |||||||
                              CCTCT   CTCG  TGTCACC
                                _____   GG
GAM1045 KIAA0924 3' TGCCCTGTCCTCTGCA     29725    G   A
                              TG AGA GACAGGGCA
                              || ||| |||||||||
                              AC TCT CTGTCCCGT
                               G   C
GAM1045 KIAA1045 3' CCTAATGGGCCCCGCTTTCTCC 71048        ACA   A  GT_
          A                    TGGAGAAG   GGGC CA   GG
                              ||||||||   |||| ||   ||
                              ACCTCTTT   CCCG GT   CC
                                  CGC   G  AAT
GAM1045 KIAA1055 3' TGCTCTGTCCCCTCCA     66070      AA
                              TGGAG  GACAGGGCA
                              |||||  |||||||||
                              ACCTC  CTGTCTCGT
                                 CC
GAM1045 KIAA1170 3' CCACCATGCCCAGCCTCTTC  69847      CA__    CA
                              GAAGA   GGGCA  GTGG
                              |||||   |||||  ||||
                              CTTCT   CCCGT  CACC
                                 CCGA    AC
GAM1045 KIAA1181 3' CACTGTGCTCCTCCA      68372      AAGACA
                              TGGAG    GGGCACAGTG
                              |||||    ||||||||||
                              ACCTC    CTCGTGTCAC
                                 _______
GAM1045 KIAA1184 3' CTGTGCCCCTCCCCTCCA   42615      AA  CA
                              TGGAG  GA  GGGCACAG
                              |||||  ||  ||||||||
                              ACCTC  CT  CCCGTGTC
                                 CC  C_
GAM1045 KIAA1373 3' CCACTGTGCCCTGCCTCT   70933     AAGA
                              GGAG   CAGGGCACAGTGG
                              ||||   ||||||||||||
                              TCTC   GTCCCGTGTCACC
                                C___
GAM1045 KIAA1755 3' CCACTGTGCCCCACCCTC   61340    AAGACA
                              GAG    GGGCACAGTGG
                              |||    ||||||||||
                              CTC    CCCGTGTCACC
                                CCAC__
GAM1045 KIAA1854 3' CCACCTCGCACTGTCTTTCCCA 71741    AG     G  ACA
                              TGG  AAGACAG GC   GTGG
                              |||  ||||||| ||   ||||
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                                ACC  TTCTGTC CG   CACC
                                  CT      A  CTC
GAM1045 KIAA1856 3' CCACGGGCATGATCTTCTCCA 92661        _ GG  ACA
                                TGGAGAAGA CA  GC   GTGG
                                |||||||||  ||  ||   ||||
                                ACCTCTTCT GT  CG   CACC
                                     A  A_  GG_
GAM1045 LRG      3' CTGACTCTGTCTTCCCCA    53749     A        CA
                                TGG GAAGACAGGG  CAG
                                |||  ||||||||||  |||
                                ACC CTTCTGTCTC  GTC
                                  C        A_
GAM1045 MGC10818 3' CCTTCATCCTTGTCTTCTCCA 47539            CACAGT
                                TGGAGAAGACAGGG     GG
                                ||||||||||||||     ||
                                ACCTCTTCTGTTCC     CC
                                         TACTT_
GAM1045 MGC13016 3' CCACTGTGCCCTGCCGTTTCC 50349      AGA
                                GGAGA   CAGGGCACAGTGG
                                |||||   ||||||||||||||
                                CCTTT   GTCCCGTGTCACC
                                   GCC
GAM1045 MGC15854 5' CCACTTCCCCATCTTCTCC   58846        CA   CAC
                                GGAGAAGA  GGG   AGTGG
                                ||||||||  |||   |||||
                                CCTCTTCT  CCC   TCACC
                                     AC   T__
GAM1045 MGC16025 3' CCACTGTGGGCCCTTCCCC   51916    A  AGAC    __
                                GG GA    AGGGC  ACAGTGG
                                || ||    |||||  |||||||
                                CC CT    TCCCG  TGTCACC
                                 C _____     GG
GAM1045 MGC22014 3' CACACCTGTCTTCTC       64491          GCACA
                                GAGAAGACAGG    GTG
                                ||||||||||     |||
                                CTCTTCTGTCC    CAC
                                       A_____
GAM1045 MGC35558 3' CCAATAGCCCTGTGCTCCCCA 58778     A  AG      ACAG
                                TGG GA  ACAGGGC    TGG
                                |||  ||  |||||||    |||
                                ACC CT  TGTCCCG    ACC
                                  C  CG      ATA_
GAM1045 MKRN1    3' CCAGGGCCTGTCTTCTC     25573          G ACAG
                                GAGAAGACAGG C    TGG
                                ||||||||||| |    |||
                                CTCTTCTGTCC G    ACC
                                       _ GG__
GAM1045 moblak   3' CCACACCTCTGTCTCCCCCA  55491     AGA       CACA
                                TGG   AGACAGGG   GTGG
                                |||   ||||||||   ||||
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                                ACC   TCTGTCTC    CACC
                                  CCC       CA__
GAM1045  moblak    5'  TGCCTTGTCTTCTCCA      55517
                                TGGAGAAGACAGGGCA
                                ||||||||||||||||
                                ACCTCTTCTGTTCCGT

GAM1045  NTT5      3'  CCACCATCATTGTTTTCCCCA  25881     A       GGCACA
                                TGG GAAGACAG      GTGG
                                ||| ||||||||      ||||
                                ACC CTTTTGTT      CACC
                                  C       ACTAC_
GAM1045  NXPH3     3'  CCGGGGGCCTTGTCTCCTCCA  65757       A       ACAG
                                TGGAG AGACAGGGC    TGG
                                ||||| |||||||||    |||
                                ACCTC TCTGTTCCG    GCC
                                   C        GGG_
GAM1045  PASK      5'  CCACTGTGCGTGGCCTCC    30714      AAGA  GG
                                GGAG    CA  GCACAGTGG
                                ||||    ||  |||||||||
                                CCTC    GT  CGTGTCACC
                                  CG__  G_
GAM1045  PLAGL2    3'  CCACTCCTGTGTCCTCCCA    70443     A  A    G  CAC
                                TGG GA GACA GG   AGTGG
                                ||| || |||| ||   |||||
                                ACC CT CTGT TC   TCACC
                                  _ C    G  C__
GAM1045  PMX2B     5'  CCACTCCAGCCACCTTCTCCA  14079         ACAG   AC_
                                TGGAGAAG    GGC   AGTGG
                                ||||||||    |||   |||||
                                ACCTCTTC    CCG   TCACC
                                     CA__   ACC
GAM1045  PRO2605   3'  CCACTGTGGGCCCTCTCC    94856      AGACA    __
                                GGAGA    GGGC  ACAGTGG
                                |||||    ||||  |||||||
                                CCTCT    CCCG  TGTCACC
                                  ______   GG
GAM1045  RASD2     3'  CCACTGTGCGCATCTCC     26686      AGACAGG
                                GGAGA      GCACAGTGG
                                |||||      |||||||||
                                CCTCT      CGTGTCACC
                                   ACG____
GAM1045  RPH3A     3'  GCCACCGCACCCTGATCTCTCT 30245      ______    CACA    III
            TCTCTA                 GAAGA    CAGGG    GTGG   C
                                |||||    |||||    ||||  |
                                CTTCT    GTCCC    CACC   G
                                   CTCTA    ACGC    III
GAM1045  Rpo1-2    3'  CCACTGTGCCTGGCCTCC    38698      AAGACA
                                GGAG     GGGCACAGTGG
                                ||||     ||||||||||
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                                CCTC     TCCGTGTCACC
                                  CGG___
GAM1045 Rpo1-2   3' CCACTGTGCCTGGCCTCC    49875     AAGACA
                                GGAG     GGGCACAGTGG
                                ||||     ||||||||||
                                CCTC     TCCGTGTCACC
                                  CGG___
GAM1045 SDC3     3' CCACAGCCTGTCTTTTCCA   27743           G ACA
                                TGGAGAAGACAGG C   GTGG
                                |||||||||||| |   ||||
                                ACCTTTTCTGTCC G   CACC
                                       _ A__
GAM1045 SDCCAG43 3' CCACTTCCCTCCCTTCTCCA  70371        AC   CAC
                                TGGAGAAG  AGGG   AGTGG
                                ||||||||  ||||   |||||
                                ACCTCTTC  TCCC   TCACC
                                     CC   T__
GAM1045 SLC26A10 5' CCACCATGCCTTTGTCTCTCC 56026      A   _   CA
                                GGAGA GACAG GGCA  GTGG
                                ||||| ||||| ||||  ||||
                                CCTCT CTGTT CCGT  CACC
                                  _    T   AC
GAM1045 ST7L     3' CCACCACTTGGTCTTTTCCA   56997         AG  CACA
                                TGGAGAAGAC  GG   GTGG
                                ||||||||||  ||   ||||
                                ACCTTTTCTG  TC   CACC
                                     GT  AC__
GAM1045 ST7L     3' CCACCACTTGGTCTTTTCCA   57573         AG  CACA
                                TGGAGAAGAC  GG   GTGG
                                ||||||||||  ||   ||||
                                ACCTTTTCTG  TC   CACC
                                     GT  AC__
GAM1045 ST7L     3' CCACCACTTGGTCTTTTCCA   34853         AG  CACA
                                TGGAGAAGAC  GG   GTGG
                                ||||||||||  ||   ||||
                                ACCTTTTCTG  TC   CACC
                                     GT  AC__
GAM1045 STMN3    3' CCACTGCAGCATCCCCCACTTC 31898        ACA  CA____
           TCCA                    TGGAGAAG   GGG     CAGTGG
                                ||||||||   |||     ||||||
                                ACCTCTTC   CCC     GTCACC
                                    ACC   TACGAC
GAM1045 STRBP    5' CCACTGTGCCTGGCCTC     37230     AAGACA
                                GAG     GGGCACAGTGG
                                |||     ||||||||||
                                CTC     TCCGTGTCACC
                                  CGG___
GAM1045 TMG3     3' CCAACATCCTGTCTTTCCA    43992       A      CACAG
                                TGGAGA GACAGGG    TGG
                                |||||| |||||||     |||
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                                ACCTTT CTGTCCT    ACC
                                   _     ACA__
GAM1045  VELI1    5'  CCACCCAAGCTTTCTTCTCCA  16235        CA   ACA_
                                TGGAGAAGA  GGGC   GTGG
                                |||||||||  ||||   ||||
                                ACCTCTTCT  TTCG   CACC
                                     __   AACC
GAM1045  LOC113828 3'  CCTTTGTGCCCCACCCCCTCC  56583     AAGACA      T
                                GGAG     GGGCACAG GG
                                ||||     |||||||| ||
                                CCTC     CCCGTGTT CC
                                  CCCCAC       T
GAM1045  LOC120224 5'  CCACCGCACCTGGCCTCTC   57095     AGA   _  ACA
                                GAGA   CAGG GC   GTGG
                                ||||   |||| ||   ||||
                                CTCT   GTCC CG   CACC
                                  CCG    A  C__
GAM1045  LOC123242 5'  CCACTCTGTACCTTCTCCA   75593       ACAGG   C
                                TGGAGAAG    GCA AGTGG
                                ||||||||    ||| |||||
                                ACCTCTTC    TGT TCACC
                                     CA___   C
GAM1045  LOC124045 3'  CACCGCCCCCTTCTCCA     76031       ACA   ACA
                                TGGAGAAG   GGGC   GTG
                                ||||||||   ||||   |||
                                ACCTCTTC   CCCG   CAC
                                     C__    C__
GAM1045  LOC124460 3'  CCACTGTGCCTTCGCTCTC   76043     A AC
                                GAGA G  AGGGCACAGTGG
                                |||| |  ||||||||||||
                                CTCT C  TTCCGTGTCACC
                                  _ GC
GAM1045  LOC132625 3'  CCACTGTGCCTGGCCCCCCA   75902     AGAAGACA
                                TGG       GGGCACAGTGG
                                |||       ||||||||||
                                ACC       TCCGTGTCACC
                                  CCCCGG__
GAM1045  LOC137964 3'  CCACTGCTGTGTCCTTTCCA   75279       A   G   CA
                                TGGAGA GACA GGCA  GTGG
                                |||||| |||| ||||  ||||
                                ACCTTT CTGT TCGT  CACC
                                   C   G   __
GAM1045  LOC145622 3'  CCACTGTGCCAGCACTCTA    77296      AAGACAG
                                TGGAG      GGCACAGTGG
                                |||||      ||||||||||
                                ATCTC      CCGTGTCACC
                                  ACGA___
GAM1045  LOC145837 5'  CCATCTGCCCTGTCTCTCCA   83544       A       CA
                                TGGAGA GACAGGGCA  GTGG
                                |||||| |||||||||  ||||
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                                ACCTCT CTGTCCCGT  TACC
                                  _       C_
GAM1045  LOC147895 5'  CCACTGCGCCCGCGCTCTCTTC 84078        CA____   A
                TCC                  GGAGAAGA     GGGC CAGTGG
                                |||||||||     |||| ||||||
                                CCTCTTCT     CCCG GTCACC
                                    CTCGCG   C
GAM1045  LOC148930 3'  CTTTGCCCTGTGTTCTCCA   79096       G      C
                                TGGAGAA ACAGGGCA AG
                                ||||||| |||||||| ||
                                ACCTCTT TGTCCCGT TC
                                    G       T
GAM1045  LOC149175 3'  CCACATCATCTGTCTTCTCTA  79209           GCACA
                                TGGAGAAGACAGG    GTGG
                                ||||||||||||    ||||
                                ATCTCTTCTGTCT    CACC
                                       ACTA_
GAM1045  LOC149706 5'  CCACTGCCCATACCTCCTCC   84638     A  ACA_    CA
                                GGAG AG   GGGCA  GTGG
                                |||| ||   |||||  ||||
                                CCTC TC   CCCGT  CACC
                                  C  CATA    __
GAM1045  LOC150372 3'  CCACTGTGCCCTGGCCCA    79793     AGAAGA
                                TGG     CAGGGCACAGTGG
                                |||     ||||||||||||
                                ACC     GTCCCGTGTCACC
                                  CG____
GAM1045  LOC150967 5'  CACCACTCCTTTTCCA      80078        ACA   CACA
                                TGGAGAAG   GGG   GTG
                                ||||||||   |||   |||
                                ACCTTTTC   CTC   CAC
                                    ___   AC__
GAM1045  LOC151568 5'  CCAGGTGGCCTGTGCTCCCCA  56690     A  AG    G   AG
                                TGG GA  ACAGG CAC  TGG
                                ||| ||  ||||| |||  |||
                                ACC CT  TGTCC GTG  ACC
                                  C  CG    G   G_
GAM1045  LOC152274 3'  CCAGGTCCCTGCCTCCTACCA  80504     _  A  A    C  AG
                                TGG AG AG CAGGG AC  TGG
                                ||| || || ||||| ||  |||
                                ACC TC TC GTCCC TG  ACC
                                  A  C  C    _  G_
GAM1045  LOC154761 3'  CACACCCACTTCTCCA      81122        ACA   CACA
                                TGGAGAAG   GGG   GTG
                                ||||||||   |||   |||
                                ACCTCTTC   CCC   CAC
                                    A__   A___
GAM1045  LOC155006 3'  CCACCTCAGGTCCTTCTCCA   81232       AGAC    ACA__
                                TGGAGA   AGGGC    GTGG
                                ||||||   |||||    ||||
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                                ACCTCT   TCCTG    CACC
                                   ____    GACTC
GAM1045  LOC157623 3'  CCACTGTGCCTGACCCTC    81495     AAGACA
                                GAG     GGGCACAGTGG
                                |||     ||||||||||
                                CTC     TCCGTGTCACC
                                  CCAG__
GAM1045  LOC158219 3'  CCACTGTGCCCTGTGTGTCACC 81791     A  AG_
            A                    TGG GA   ACAGGGCACAGTGG
                                ||| ||   ||||||||||||||
                                ACC CT   TGTCCCGTGTCACC
                                  A  GTG
GAM1045  LOC159121 5'  CCACTTGCTGTGCCTCC     86992     AAGA  G   C
                                GGAG    CA GGCA AGTGG
                                ||||    || |||| |||||
                                CCTC    GT TCGT TCACC
                                  C___  G   _
GAM1045  LOC163782 3'  CACTCCAACTTCTCCA      82154       ACAG  CAC
                                TGGAGAAG    GG   AGTG
                                ||||||||    ||   ||||
                                ACCTCTTC    CC   TCAC
                                     AA__  ___
GAM1045  LOC196812 3'  CACTCCTCCTTCTCCA      89565       AC   GCAC
                                TGGAGAAG  AGG    AGTG
                                ||||||||  |||    ||||
                                ACCTCTTC  TCC    TCAC
                                     C_  _____
GAM1045  LOC197003 3'  CCACTCCCTACCTGTCTTCTAC 87872     G        GCAC_
            A                    TG AGAAGACAGG     AGTGG
                                || ||||||||||     |||||
                                AC TCTTCTGTCC     TCACC
                                 A         ATCCC
GAM1045  LOC199964 3'  TGCCGTGCCTTCTCCA      89892       A  G
                                TGGAGAAG CA GGCA
                                |||||||| || ||||
                                ACCTCTTC GT CCGT
                                     C  G
GAM1045  LOC200268 3'  CCACTGTGCCTGGCCCCCTC   88680     AAGACA
                                GAG     GGGCACAGTGG
                                |||     ||||||||||||
                                CTC     TCCGTGTCACC
                                  CCCCGG
GAM1045  LOC202934 3'  CCACTGTGCCAGGCTCCTTCA  90409      A  ACAG
                                TGGAG AG    GGCACAGTGG
                                ||||| ||    ||||||||||
                                ACTTC TC    CCGTGTCACC
                                   C  GGA_
GAM1045  LOC219654 3'  CGTTGTTCCCCGTCTTCTCCA  91303         A   C
                                TGGAGAAGAC GGG ACAGTG
                                |||||||||| ||| ||||||
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                                ACCTCTTCTG CCC TGTTGC
                                      C   T
GAM1045  LOC220045 3'  CCACTGTGTTCCCCTTATCCA  93407     G   ACA
                                TGGA AAG   GGGCACAGTGG
                                |||| |||   ||||||||||
                                ACCT TTC   CTTGTGTCACC
                                  A  CC_
GAM1045  LOC220469 3'  CCAAAGCCCAACCTTCTCCA   76384        ACA    ACAG
                                TGGAGAAG   GGGC    TGG
                                ||||||||   ||||    |||
                                ACCTCTTC   CCCG    ACC
                                     CAA    AA__
GAM1045  LOC220567 3'  CCACTGTGGACACATCCTCTCC 90736      A  CAGGG_
                                GGAGA GA     CACAGTGG
                                ||||| ||     ||||||||
                                CCTCT CT     GTGTCACC
                                   C  ACACAG
GAM1045  LOC220739 3'  CCACTGTGCCCCCCGTCCCTCC 92927     AA   A__
                                GGAG  GAC   GGGCACAGTGG
                                ||||  |||   ||||||||||
                                CCTC  CTG   CCCGTGTCACC
                                  C_   CCC
GAM1045  LOC221491 5'  CCACTGTGCCCAATGCCCCCCA 92011     AGAAGACA
                                TGG       GGGCACAGTGG
                                |||       ||||||||||
                                ACC       CCCGTGTCACC
                                  CCCCGTAA
GAM1045  LOC222001 3'  CCACTAATTAAGTTTTCTCCA  92904         AGGGCAC
                                TGGAGAAGAC      AGTGG
                                ||||||||||      |||||
                                ACCTCTTTTG      TCACC
                                      AATTAA_
GAM1045  LOC222031 3'  CCACATACCTGCCTTGTCCA   94019     G   A    GCACA
                                TGGA AAG CAGG    GTGG
                                |||| ||| ||||    ||||
                                ACCT TTC GTCC    CACC
                                  G   C    ATA__
GAM1045  LOC253001 5'  CCACTCTGTACCTTCTCCA    96251        ACAGG   C
                                TGGAGAAG    GCA AGTGG
                                ||||||||    ||| |||||
                                ACCTCTTC    TGT TCACC
                                     CA___   C
GAM1045  LOC253216 3'  CACTGTGGCCCTTCCA      94955      GAAGAC    _
                                TGGA     AGGGC ACAGTG
                                ||||     ||||| ||||||
                                ACCT     TCCCG TGTCAC
                                  _______    G
GAM1045  LOC253897 3'  CCACTGCTGTGTCCTTTCCA   96104       A   G    CA
                                TGGAGA GACA GGCA  GTGG
                                |||||| |||| ||||  ||||
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                                ACCTTT CTGT TCGT  CACC
                                   C   G   __
GAM1045  LOC254018 5'  CCACTGTGCCCAGCCTCCA   96966      AAGACA
                                TGGAG     GGGCACAGTGG
                                |||||     ||||||||||
                                ACCTC     CCCGTGTCACC
                                  CGA___
GAM1045  LOC255465 3'  CCACTGTGCCAGGCTCCTTCA  97286      A  ACAG
                                TGGAG AG    GGCACAGTGG
                                ||||| ||    ||||||||||
                                ACTTC TC    CCGTGTCACC
                                  C  GGA_
GAM1045  LOC256542 5'  CCATTTACTGCCTTCTCCA   95547        A   GGCAC
                                TGGAGAAG CAG     AGTGG
                                |||||||| |||     |||||
                                ACCTCTTC GTC     TTACC
                                     C   AT___
GAM1045  LOC256901 3'  CACTTCCCCCTTCTCCA     96620        ACA   CAC
                                TGGAGAAG   GGG   AGTG
                                ||||||||   |||   ||||
                                ACCTCTTC   CCC   TCAC
                                     C__   T__
GAM1045  LOC256937 5'  CCACTGAATCTGTTTCTCCA   97127       A     GCA
                                TGGAGA GACAGG   CAGTGG
                                |||||| ||||||   ||||||
                                ACCTCT TTGTCT   GTCACC
                                   _     AA_
GAM1045  LOC257481 3'  CCACTGTGGGCCCTCTCC    61108      AGACA   __
                                GGAGA    GGGC  ACAGTGG
                                |||||    ||||  |||||||
                                CCTCT    CCCG  TGTCACC
                                   ______   GG
GAM1045  LOC51200  3'  CCACTGTGCCGGTCCCGTCCCC 32992      AA   A  ____
            TCC                    GGAG  GAC GG    GCACAGTGG
                                ||||  ||| ||   |||||||||
                                CCTC  CTG CC    CGTGTCACC
                                  CC   C  TGGC
GAM1045  LOC54550  3'  CCACTGTGCCCAGGCGCCA   77689     AGAAGACA
                                TGG       GGGCACAGTGG
                                |||       ||||||||||
                                ACC       CCCGTGTCACC
                                  GCGGA___
GAM1045  LOC56920  3'  CACCGCCTCTTCTCCA      39382        CAG   ACA
                                TGGAGAAGA   GGC   GTG
                                |||||||||   |||   |||
                                ACCTCTTCT   CCG   CAC
                                     ___   C__
GAM1045  LOC57105  3'  CCACAACTTCCCCAGCTTCTCC 39818        ACA   CACA_
            A                   TGGAGAAG   GGG    GTGG
                                ||||||||   |||    ||||
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                                ACCTCTTC  CCC    CACC
                                    GAC  TTCAA
GAM1045 LOC91565 3' CCACTTGTGTGTCTTCTTCA  66459        AGG   _
                                TGGAGAAGAC  GCACA GTGG
                                ||||||||||  ||||| ||||
                                ACTTCTTCTG  TGTGT CACC
                                      ___   T
GAM1045 LOC92080 5' CCACTGCTGAAGTTCCTCCA  68042     AA  AGGG _
                                TGGAG  GAC   CA CAGTGG
                                |||||  |||   || ||||||
                                ACCTC  TTG   GT GTCACC
                                   C_  AA__  C
GAM1045 LOC92181 3' CCACTGTGCCCCTGAGAATCCA 68405     GAAGA   _
                                TGGA    CAGGG CACAGTGG
                                ||||    ||||| ||||||||
                                ACCT    GTCCC GTGTCACC
                                  AAGA_    C
GAM1045 LOC92482 3' CCACCGCACCAGTCCCCCA  69486    AGAA  A _ ACA
                                TGG   GAC GG GC  GTGG
                                |||   ||| || ||  ||||
                                ACC   CTG CC CG  CACC
                                  CC__  A  A  C__
GAM1045 LOC92578 3' CTGGCCCTCCCTCTCCA    69827      A AC    A
                                TGGAGA G  AGGGC CAG
                                |||||| |  ||||| |||
                                ACCTCT C  TCCCG GTC
                                   _ CC    _
GAM1045 LOC93070 3' CCACTGTGCTAGTTGCCCA  71291    AGAA  AG
                                TGG   GAC  GGCACAGTGG
                                |||   |||  ||||||||||
                                ACC   TTG  TCGTGTCACC
                                  CG__  A_
GAM1045 LOC96652 3' CCACCTGCACCAGCTTCTCCA 65464       ACA _  CA
                                TGGAGAAG  GG GCA  GTGG
                                ||||||||  || |||  ||||
                                ACCTCTTC  CC CGT  CACC
                                     GA_  A  C_
GAM1046 ADAMTS9  3' ACAACTCCAGTTCTCTGCC  39670   G  AA
                                GG GGA  AACTGGAGTTGT
                                || |||  ||||||||||||
                                CC TCT  TTGACCTCAACA
                                 G  C_
GAM1046 ALDOA    3' CAACTCCAGGCCCTG      3467      GAAAAA
                                CGGGG    CTGGAGTTG
                                |||||    |||||||||
                                GTCCC    GACCTCAAC
                                   G_____
GAM1046 AOC3     3' CAACTCCAGCCACCC      13583    _ AAAAA
                                GGG GG   CTGGAGTTG
                                ||| ||   |||||||||
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                                CCC CC    GACCTCAAC
                                  A _____
GAM1046 ARPC2    5' AGCTCTCCCTCCGTC      19189      _   AAAACTG
                                GACGG GGGA     GAGTT
                                ||||| ||||     |||||
                                CTGCC CCCT     CTCGA
                                  T  _______
GAM1046 CHRNA7   3' ACAACTCCAGTGTTCCCTTCT 5619     CG     AA
                                AGA  GGGGAA  ACTGGAGTTGT
                                |||  ||||||  ||||||||||
                                TCT  TCCCTT  TGACCTCAACA
                                  __     G_
GAM1046 CHRNE    3' ACTTCAATTTCCCACCCATCT 3581     C_ _     AAC
                                AGA  GG GGGAAA   TGGAGT
                                |||  || ||||||   ||||||
                                TCT  CC CCCTTT   ACTTCA
                                  AC  A     A__
GAM1046 COL6A2   3' TTCCAGTCTCTCCTCCGTCT   54170         AAA
                                AGACGGGGGGA   ACTGGAG
                                ||||||||||   |||||||
                                TCTGCCTCCT   TGACCTT
                                     CTC
GAM1046 CXorf6   3' CAACCCCAGCTTCAGCCTG   18511     G_   AAA    A
                                CGGG  GAA   CTGG GTTG
                                ||||  |||   |||| ||||
                                GTCC  CTT   GACC CAAC
                                  GA   C__    C
GAM1046 EXTL3    3' CACCTTCCCCCCGCCT     7527     A     AAAAACT    T
                                AG CGGGGGG      GGAG TG
                                || ||||||       |||| ||
                                TC GCCCCC       CTTC AC
                                 C     ________    C
GAM1046 GRB7     5' GGCTCCCCCCCCGCCT      17967    A     AAAAACT
                                AG CGGGGGG      GGAGTT
                                || ||||||       ||||||
                                TC GCCCCC       CCTCGG
                                 C     ________
GAM1046 HBZ      3' ACAGGCTGCGGCCCCTCCCCCG 18046          AAAA   G   _
             TC                   GACGGGGGA    CTG AGT TGT
                                |||||||||    ||| ||| |||
                                CTGCCCCCT    GGC TCG ACA
                                     CCCC   G   G
GAM1046 POLA     3' CAACTCCAGAGCCCCT      33736       AAAAA
                                GGGGG    CTGGAGTTG
                                |||||    |||||||||
                                TCCCC    GACCTCAAC
                                  GA___
GAM1046 POLR2E   3' CAGCTCCGCCCCCATC      59914    C    AAAAAC
                                GA GGGGG     TGGAGTTG
                                || |||||     ||||||||
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                                CT CCCCC     GCCTCGAC
                                 A   _______
GAM1046 RAD23A   3' AGCTGTCCCCCCGTC      17310        AAAA  TGG
                                GACGGGGG   AC   AGTT
                                ||||||||   ||   ||||
                                CTGCCCCC   TG   TCGA
                                    C___  ___
GAM1046 RELA     3' ACTCAAACTTTTCCCCTGTC  41750          ACTG
                                GACGGGGGAAAA   GAGT
                                ||||||||||||   ||||
                                CTGTCCCCTTTT   CTCA
                                       CAAA
GAM1046 SLC7A8   3' ACAAATCGGGATTCTCTCCCCC 24272       AAAA__  G  G
                                GGGGGA     CT GA TTGT
                                ||||||     || || ||||
                                CCCCCT     GG CT AACA
                                   CTCTTA  G  A
GAM1046 SMARCD1  3' ACAGCAGAATTTTCTCCCCGTC 57427        _    ACTGGA
             T                   AGACGGGG GAAAA     GTTGT
                                 ||||||||| |||||     |||||
                                 TCTGCCCC CTTTT     CGACA
                                    T    AAGA__
GAM1046 SMARCD1  3' ACAGCAGAATTTTCTCCCCGTC 11809        _    ACTGGA
             T                   AGACGGGG GAAAA     GTTGT
                                 ||||||||| |||||     |||||
                                 TCTGCCCC CTTTT     CGACA
                                    T    AAGA__
GAM1046 FADS1    3' ACAACTCCAACTTCTATGTTT  25469      GG   AAAC
                                AGACG  GGAA   TGGAGTTGT
                                |||||  ||||   |||||||||
                                TTTGT  TCTT   ACCTCAACA
                                  A_   CA__
GAM1046 FJX1     3' ACTTCAGCTTTTCACCC     26786     G    A
                                GGG GAAAA CTGGAGT
                                ||| ||||| |||||||
                                CCC CTTTT GACTTCA
                                  A    C
GAM1046 FLJ13955 3' ATTTCAGTCCTTTCCCCC    45406        A_
                                GGGGGAAA  ACTGGAGT
                                ||||||||  ||||||||
                                CCCCCTTT  TGACTTTA
                                    CC
GAM1046 FLJ20208 3' ACAAAAGTGTTTTCCCCCC   34738      A    TGGAG
                                GGGGG AAAAC    TTGT
                                ||||| |||||    ||||
                                CCCCC TTTTG    AACA
                                  C    TGAA_
GAM1046 FLJ22938 5' ACAACTTTGTACTCCCACC   45155    _   AAA  T
                                GG GGGA   AC GGAGTTGT
                                || ||||   || ||||||||
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                                CC CCCT   TG TTTCAACA
                                 A   CA_ _
GAM1046 FLJ31528 3' ACAAGCCACTGCTCCCCCGTC 58374        AAAAC  AG
                                GACGGGGGA    TGG  TTGT
                                |||||||||    |||  ||||
                                CTGCCCCCT    ACC  AACA
                                     CGTC_   G_
GAM1046 KIAA1238 3' CAGTTTTTCCCCCGTTT     71077
                                AGACGGGGGAAAAACTG
                                ||||||||||||||||
                                TTTGCCCCCTTTTTGAC

GAM1046 KIAA1240 3' TCATATTTTTCCCCCATCT   66739     C       CTG
                                AGA GGGGGAAAAA   GA
                                ||| ||||||||||   ||
                                TCT CCCCCTTTTT   CT
                                  A         ATA
GAM1046 KIAA1918 3' CAAACCCTTCTCCCATCT    73160     C     AAACT  AG
                                AGA GGGGGAA    GG  TTG
                                ||| |||||||    ||  |||
                                TCT CCCTCTT    CC  AAC
                                  A      _____  CA
GAM1046 MESDC1   5' ACAACTCCCAGCTTCCCCGTC  42591        AAAA   _
                                GACGGGGGGA   CTGG AGTTGT
                                |||||||||   |||| ||||||
                                CTGCCCCTT   GACC TCAACA
                                     C___   C
GAM1046 MGC20255 3' ACAATTTTCCCTTCCTCCGCCT 53436    A       AAACT
                                AG CGGGGGAA    GGAGTTGT
                                || ||||||||    ||||||||
                                TC GCCTCCTT    TTTTAACA
                                 C       CCC__
GAM1046 MGC21621 3' ACAACCTCCCTTCCCCCCGTC  58792        AAAAACT   _
                                GACGGGGG      GGAG TTGT
                                ||||||||      |||| ||||
                                CTGCCCCC      CCTC AACA
                                     CTTC___   C
GAM1046 LOC124753 5' CAGGCCTTCCCCCTGTCT    74318     _     AAA
                                AGAC GGGGGAA   CTG
                                |||| |||||||   |||
                                TCTG CCCCCTT   GAC
                                  T      CCG
GAM1046 LOC145719 5' TCCAGCTTCTCCCTCCATCT  83455     C  _   A  A
                                AGA GG GGGA AA CTGGA
                                ||| || |||| || |||||
                                TCT CC CCCT TT GACCT
                                  A  T   C  C
GAM1046 LOC145720 5' TCCAGCTTCTCCCTCCATCT  83437     C  _   A  A
                                AGA GG GGGA AA CTGGA
                                ||| || |||| || |||||
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                                TCT CC CCCT TT GACCT
                                  A T   C C
GAM1046  LOC145926 3'  ACAACTCCAGTGTTCCCTTCT  77573     CG     AA
                                AGA  GGGGAA  ACTGGAGTTGT
                                |||  ||||||  ||||||||||
                                TCT  TCCCTT  TGACCTCAACA
                                 __     G_
GAM1046  LOC152926 5'  AGCTCCTCCCCCGTC       80743         AAAACT
                                GACGGGGGA     GGAGTT
                                |||||||||     ||||||
                                CTGCCCCCT     CCTCGA
                                          _______
GAM1046  LOC165721 5'  GCCACTTCTCCCCCGTC     82602         AAAACT    T
                                GACGGGGGA     GGAGT GT
                                |||||||||     ||||| ||
                                CTGCCCCCT     CTTCA CG
                                    _______    C
GAM1046  LOC221060 5'  CAACCCCAGCCCCTGTC     93207         AAAAA   A
                                GACGGGGGG     CTGG GTTG
                                |||||||||     |||| ||||
                                CTGTCCCC     GACC CAAC
                                    ______   C
GAM1046  LOC221662 3'  ATTCTAATCCCTCTCCCCATC  92401    C   _  AAAAC
                                GA GGGG GA     TGGAGT
                                || |||| ||     ||||||
                                CT CCCC CT     ATCTTA
                                 A    T  CCCTA
GAM1046  LOC257065 5'  ACTGTCCCAGTTCCACCCCC   97635      AAA     AG T
                                GGGGG   AACTGG  T GT
                                |||||   ||||||  | ||
                                CCCCC   TTGACC  G CA
                                   ACC     CT T
GAM1046  LOC92181  3'  CAATTTTCCTCCCTCATCT   68403     C     AAAACT  __
                                AGA GGGGGA     GGA  GTTG
                                |||  ||||||     |||  ||||
                                TCT CTCCCT     CCT  TAAC
                                  A     _______   TT
GAM1047  AQP6      3'  CTCAAACTCCTGACCT      7949         A
                                AGGTCAG AGTTTGAG
                                |||||||  ||||||||
                                TCCAGTC TCAAACTC
                                    C
GAM1047  AQP6      3'  CTCAAACTCCTGACCT      53924        A
                                AGGTCAG AGTTTGAG
                                |||||||  ||||||||
                                TCCAGTC TCAAACTC
                                    C
GAM1047  ARSF      5'  CTCGAACTCCCGACCTCA    64599        AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
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                                ACTCCAG   TCAAGCTC
                                    CCC
GAM1047 ATP1B2   3' CTCGAACTCCCGACCTCA    8048        AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
                                ACTCCAG   TCAAGCTC
                                    CCC
GAM1047 ATP7A    3' CTTAAACTCCTAACCTCA    3524        C  A
                                TGAGGT AG AGTTTGAG
                                |||||| || ||||||||
                                ACTCCA TC TCAAATTC
                                   A  C
GAM1047 AXL      3' CTAAAACTCCTGACCTCA    8097         A    G
                                TGAGGTCAG AGTTT AG
                                ||||||||| ||||| ||
                                ACTCCAGTC TCAAA TC
                                      C    A
GAM1047 AXL      3' CTAAAACTCCTGACCTCA    41594        A    G
                                TGAGGTCAG AGTTT AG
                                ||||||||| ||||| ||
                                ACTCCAGTC TCAAA TC
                                      C    A
GAM1047 C7       3' CTCCAACTCCTGACCTCA    5159         A   T
                                TGAGGTCAG AGTT GAG
                                ||||||||| |||| |||
                                ACTCCAGTC TCAA CTC
                                      C   C
GAM1047 CAMLG    3' CTCGAACTTCTGACCTCA    8238
                                TGAGGTCAGAAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCTTCAAGCTC

GAM1047 CBFA2T2  3' CTCAAACCCCGGACCTCA    17464       AGAA
                                TGAGGTC   GTTTGAG
                                |||||||   |||||||
                                ACTCCAG   CAAACTC
                                    GCCC
GAM1047 CHRNA2   5' CAAAGCCCTGACCTGACCTC  5601        AA  TGAGA
                                GAGGTCAG GTT   CTTTG
                                |||||||| |||   |||||
                                CTCCAGTC CAG   GAAAC
                                    __  TCCC_
GAM1047 CLECSF12 3' CGAACTCCTGACCTCA      76687       A
                                TGAGGTCAG AGTTTG
                                ||||||||| ||||||
                                ACTCCAGTC TCAAGC
                                      C
GAM1047 CYP1A2   3' AGTCTCAAACTCCTGACCTCA 69095        A
                                TGAGGTCAG AGTTTGAGACT
                                ||||||||| ||||||||||
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                                ACTCCAGTC TCAAACTCTGA
                                      C
GAM1047  CYP1A2   3'  CTCGAACTCCTGACCCCA    69110    A     A
                                TG GGTCAG AGTTTGAG
                                || |||||| ||||||||
                                AC CCAGTC TCAAGCTC
                                 C     C
GAM1047  CYP1A2   3'  AGTCTCAAACTCCTGACCTCA  5676          A
                                TGAGGTCAG AGTTTGAGACT
                                ||||||||| ||||||||||
                                ACTCCAGTC TCAAACTCTGA
                                      C
GAM1047  CYP1A2   3'  CTCGAACTCCTGACCCCA    5690     A     A
                                TG GGTCAG AGTTTGAG
                                || |||||| ||||||||
                                AC CCAGTC TCAAGCTC
                                 C     C
GAM1047  DFFB     3'  CTCAAACTCCTGACCTCA    87381          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  DFFB     3'  CTCGAACTCCTGACCTCA    87382          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  DISC1    3'  CTCAAACTCCTGACCTCA    37877          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  EVC      3'  CTCGAACTCCTGACCTCA    27295          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  FCAR     3'  CTCGAACTCCTGACCTCA    55748          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  FCAR     3'  CTCGAACTCCTGACCTCA    55759          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  FCAR     3'  CTCGAACTCCTGACCTCA    55770          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
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                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  FCAR     3'  CTCGAACTCCTGACCTCA    55781         A
                                TGAGGTCAG AGTTTGAG
                                |||||||||  ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  FCAR     3'  CTCGAACTCCCGACCTCA    55796        AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
                                ACTCCAG   TCAAGCTC
                                    CCC
GAM1047  FCAR     3'  CTCGAACTCCTGACCTCA    8853          A
                                TGAGGTCAG AGTTTGAG
                                |||||||||  ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  FZD4     3'  CTCGAACTCCTGACCTCA    24137         A
                                TGAGGTCAG AGTTTGAG
                                |||||||||  ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  G6PC     3'  CTCGAACTCCTGACCTCA    3825          A
                                TGAGGTCAG AGTTTGAG
                                |||||||||  ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  GRAF     3'  CTCGAACTCCTGACCTCA    30558         A
                                TGAGGTCAG AGTTTGAG
                                |||||||||  ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  HCS      3'  CTCAAACTCCTGAGCTCA    38466       G   A
                                TGAG TCAG AGTTTGAG
                                ||||  ||||  ||||||||
                                ACTC AGTC TCAAACTC
                                  G   C
GAM1047  IFNAR2   3'  CTCGAACTCCTGACCTCA    6040          A
                                TGAGGTCAG AGTTTGAG
                                |||||||||  ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  IL11     3'  GGTTTCGAACTCCTGACCTCA 5333          A
                                TGAGGTCAG AGTTTGAGACT
                                |||||||||  ||||||||||
                                ACTCCAGTC TCAAGCTTTGG
                                      C
GAM1047  JAK3     3'  CTCGAACTCCTAACCTCA    4004        C  A
                                TGAGGT AG AGTTTGAG
                                ||||||  ||  ||||||||
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                                ACTCCA TC TCAAGCTC
                                   A  C
GAM1047  KMO      3'  AGTCTCAAACTCCTGGCCTCA  13444          A
                                TGAGGTCAG AGTTTGAGACT
                                ||||||||| ||||||||||
                                ACTCCGGTC TCAAACTCTGA
                                     C
GAM1047  MAK      3'  CTCAAACTCCTGACCTCA    19757          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                     C
GAM1047  MEFV     3'  CTCAAACTCCTGACCTCA    4133           A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                     C
GAM1047  MEFV     3'  CTCGAACTCCTGACCTCA    4135           A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                     C
GAM1047  MICB     3'  AGTTTCAAACTCCTGACCTCA  19820          A
                                TGAGGTCAG AGTTTGAGACT
                                ||||||||| ||||||||||
                                ACTCCAGTC TCAAACTTTGA
                                     C
GAM1047  MLANA    3'  CTCAAACTCCTGACCTCA    18585          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                     C
GAM1047  NCOA6    5'  CTCAAACTCCTGACCTCA    25961          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                     C
GAM1047  NDRG3    3'  CTCAAACTCCTGACCTCA    49298          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                     C
GAM1047  NQO1     3'  CTCAAACTCCTGACCTCA    6158           A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                     C
GAM1047  PDE6B    3'  CTCGAACTCCTGACCTCA    4277           A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
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                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  PER2     3'  CTCGAACTCCTGACCTCA    43032          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  PIK3CD   3'  CTCGAACTCCTGACCTCA    17244          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  PRKR     3'  CTCAAACTCCTGACCTCA    10880          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  RHD      3'  CTCAAACTCCTGACCTCA    32305          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  RHD      3'  CTCAAACTCCTGACCTCA    32614          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  RP2      3'  CTCGAACTCCTGACCTCA    22617          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  RPP30    3'  CTCAATCTCCTGACCTCA    21165          A  T
                                TGAGGTCAG AG TTGAG
                                ||||||||| || |||||
                                ACTCCAGTC TC AACTC
                                      C  T
GAM1047  SAS      3'  CTCGAACTCCTGACCTCA    19953          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  SCML2    3'  CTCAAACTCCTGACCTCA    20317          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  SEDL     3'  GGTTTCAAACTCCTGACCTCA 27353          A
                                TGAGGTCAG AGTTTGAGACT
                                ||||||||| ||||||||||
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                                ACTCCAGTC TCAAACTTTGG
                                      C
GAM1047  SH3BP2   3'  CTCGAACTCCTGACCTCA    11601         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  SHOX     3'  CTCGAACTCCTGACCTCA    22536         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  SIL      3'  CTCAAACTCCCGACCTCA    11689        AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
                                ACTCCAG   TCAAACTC
                                    CCC
GAM1047  SLA2     3'  GGTGTCGAACTCCTGACCTCA 49904         A     G
                                TGAGGTCAG AGTTTGA ACT
                                ||||||||| ||||||| |||
                                ACTCCAGTC TCAAGCT TGG
                                      C     G
GAM1047  SNX15    3'  CTCGAACTCCTGACCTCA    73739         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  SPN      3'  CTCAAACTCCTGACCTCA    11922         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  SULT2B1  5'  CTCAAACTCCTGACCTCA    16026         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  TAT      3'  CTCAAACTCCTGACCTCA    4466          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  TES      3'  CTCAAACTCCTGACCTCA    72005         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  TIM3     3'  CTCAAACTCCTGACCTCA    51342         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
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                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  TMPRSS3   3'  CTCAAACCCCTGACCTCA    50505        AA
                                TGAGGTCAG  GTTTGAG
                                |||||||||  |||||||
                                ACTCCAGTC  CAAACTC
                                      CC
GAM1047  TMPRSS3   3'  CTCAAACCCCTGACCTCA    50526        AA
                                TGAGGTCAG  GTTTGAG
                                |||||||||  |||||||
                                ACTCCAGTC  CAAACTC
                                      CC
GAM1047  TMPRSS3   3'  CTCAAACCCCTGACCTCA    43793        AA
                                TGAGGTCAG  GTTTGAG
                                |||||||||  |||||||
                                ACTCCAGTC  CAAACTC
                                      CC
GAM1047  TNFRSF10B 3'  CTCGAACTCCTGACCTCA    13869        A
                                TGAGGTCAG AGTTTGAG
                                |||||||||  ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  TRAF5     3'  CTCAAACTCCTGACCTCA    16079        A
                                TGAGGTCAG AGTTTGAG
                                |||||||||  ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  TRPM6     3'  CTCAAACTCCTGACCTCA    34539        A
                                TGAGGTCAG AGTTTGAG
                                |||||||||  ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  TRPV1     3'  CTCGAACTCCTGACCTCA    38077        A
                                TGAGGTCAG AGTTTGAG
                                |||||||||  ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  TRPV1     3'  CTCGAACTCCTGACCTCA    54798        A
                                TGAGGTCAG AGTTTGAG
                                |||||||||  ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  TRPV1     3'  CTCGAACTCCTGACCTCA    54831        A
                                TGAGGTCAG AGTTTGAG
                                |||||||||  ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  TRPV1     3'  CTCGAACTCCTGACCTCA    54863        A
                                TGAGGTCAG AGTTTGAG
                                |||||||||  ||||||||
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                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047 VHL      3' GGTTTCAAACTCCTGACCTCA 5079         A
                                TGAGGTCAG AGTTTGAGACT
                                ||||||||| ||||||||||
                                ACTCCAGTC TCAAACTTTGG
                                      C
GAM1047 XRCC2    3' CTCGAACTCCTGACCTCA    18321        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047 ZNF157   3' CTCTAACTCCTGACCTCA    12878        A   T
                                TGAGGTCAG AGTT GAG
                                ||||||||| |||| |||
                                ACTCCAGTC TCAA CTC
                                      C   T
GAM1047 AAK1     3' CTCGAACTCCTGACCTCA    29845        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047 ATP1B4   3' CTCGAACTCCTGACCTCA    23818        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047 AUTL1    3' CAAAGTCTTCCACCTGAGCCCA 51660    A _   AA  TT
                                TG GG TCAG  GT  GAGACTTTG
                                || || ||||  ||  |||||||||
                                AC CC AGTC  CA  TTCTGAAAC
                                 _  G   __  CC
GAM1047 BA108L7.2 3' AGTCTCGAACTCCTGACCTCA 48254        A
                                TGAGGTCAG AGTTTGAGACT
                                ||||||||| ||||||||||
                                ACTCCAGTC TCAAGCTCTGA
                                      C
GAM1047 C13orf1  3' CTCAAACTCCTGACCTCA    39968        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047 C20orf142 3' CTCAAACTCCTGACCGCA   74772    A    A
                                TG GGTCAG AGTTTGAG
                                || |||||| ||||||||
                                AC CCAGTC TCAAACTC
                                 G     C
GAM1047 C21orf25 3' CTCGAACTCCTGACCTCA    63545        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
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                                ACTCCAGTC TCAAGCTC
                                     C
GAM1047 C9orf9   3' CTCAATCTCCTGACCTCA    38511        A  T
                                TGAGGTCAG AG TTGAG
                                ||||||||| || |||||
                                ACTCCAGTC TC AACTC
                                     C  T
GAM1047 CDC14B   3' CTCGAACTCCTGACCTCA    52851         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                     C
GAM1047 CHRAC1   3' CTCAAACTCCTAACCTCA    33870       C  A
                                TGAGGT AG AGTTTGAG
                                |||||| || ||||||||
                                ACTCCA TC TCAAACTC
                                   A  C
GAM1047 CPSF2    3' CTCAAACTCCCGACCTCA    61582       AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
                                ACTCCAG   TCAAACTC
                                    CCC
GAM1047 CPSF2    3' CTCAAACTCCTGACCTCA    61584        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                     C
GAM1047 CSL4     3' CTCAAACTCCTGGCCTCA    32111        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCGGTC TCAAACTC
                                     C
GAM1047 DBR1     3' CTCCAACTCCTGACCTCA    32532        A   T
                                TGAGGTCAG AGTT GAG
                                ||||||||| |||| |||
                                ACTCCAGTC TCAA CTC
                                     C   C
GAM1047 DCOHM    3' CTCAAACTCCTGGCCTCA    49599        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCGGTC TCAAACTC
                                     C
GAM1047 DKFZp434A2417 3' CTCAAACTCCCAACCTCA    66101       CAGA
                                TGAGGT    AGTTTGAG
                                ||||||    ||||||||
                                ACTCCA    TCAAACTC
                                   ACCC
GAM1047 DKFZP434J037 3' CTCAAACTCCCGACCTCA    48211       AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
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                                ACTCCAG   TCAAACTC
                                    CCC
GAM1047  DKFZP564K0322 3'  AGCCTCAAACTTCTGGCCTCA  49357              A
                                TGAGGTCAGAAGTTTGAG CT
                                |||||||||||||||||| ||
                                ACTCCGGTCTTCAAACTC GA
                                          C
GAM1047  DKFZP564O0423 3'  CTCAAACTCCTGGCCTCA    91685         A
                                TGAGGTCAG AGTTTGAG
                                |||||||| ||||||||
                                ACTCCGGTC TCAAACTC
                                     C
GAM1047  EVI5     3'  CTCAAACTTCTGACCTCA    18996
                                TGAGGTCAGAAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCTTCAAACTC

GAM1047  EVI5     3'  CTCGAACTCCTAACCTCA    18999       C  A
                                TGAGGT AG AGTTTGAG
                                |||||| || ||||||||
                                ACTCCA TC TCAAGCTC
                                   A  C
GAM1047  FBP17    3'  CTCAAACTCCTGACCTCA    72789         A
                                TGAGGTCAG AGTTTGAG
                                |||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                     C
GAM1047  FER1L4   3'  AAAGTCTTCCTGACACCA    47324    AG    AAGTTT
                                TG  GTCAG     GAGACTTT
                                ||  |||||     ||||||||
                                AC  CAGTC     TTCTGAAA
                                 CA    C_____
GAM1047  FLJ10232 3'  CGAACTCCTGACCTCA      35924         A
                                TGAGGTCAG AGTTTG
                                |||||||| ||||||
                                ACTCCAGTC TCAAGC
                                     C
GAM1047  FLJ10298 3'  CTCAAACTCCTGACCT      35988        A
                                AGGTCAG AGTTTGAG
                                ||||||| ||||||||
                                TCCAGTC TCAAACTC
                                   C
GAM1047  FLJ10607 3'  CTCAAACTCCTGAGCTCA    77110      G   A
                                TGAG TCAG AGTTTGAG
                                |||| |||| ||||||||
                                ACTC AGTC TCAAACTC
                                  G   C
GAM1047  FLJ10901 3'  CTCGAACTCCTGACCTCA    36822         A
                                TGAGGTCAG AGTTTGAG
                                |||||||| ||||||||
```

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                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  FLJ11151  3'  CAAAGTCTGCCTATCGACCTCA 67870       A  _  TTTG
                                TGAGGTC GA AG    AGACTTTG
                                ||||||| || ||    ||||||||
                                ACTCCAG CT TC    TCTGAAAC
                                    _  A  CG__
GAM1047  FLJ12363  3'  CTCAAACTCCTGACCTCA    49677        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  FLJ12668  3'  CTCAAACTCCTGACCTCA    46516        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  FLJ12687  3'  CTCAAACTCCTGACCTCA    46191        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  FLJ12787  3'  CTAAAACTCCTGACCTCA    49747        A    G
                                TGAGGTCAG AGTTT AG
                                ||||||||| ||||| ||
                                ACTCCAGTC TCAAA TC
                                      C    A
GAM1047  FLJ12975  3'  CTCGAACTCCTGACCTCA    69583        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  FLJ13072  5'  CTCGAACTCCTGACCTCA    89812        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  FLJ13102  3'  CTCGAACTCCTGACCTCA    46008        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  FLJ14442  3'  CTCAAACTTCTGACCTC     51366
                                GAGGTCAGAAGTTTGAG
                                ||||||||||||||||
                                CTCCAGTCTTCAAACTC

GAM1047  FLJ20034  3'  CTCAAACTCCCGACCTCA    34370        AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
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                                ACTCCAG   TCAAACTC
                                    CCC
GAM1047  FLJ20452  3'  CTCGAACTCCTGACCTCA    35200        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                    C
GAM1047  FLJ20700  3'  CTCGAACTCCTGACCTCA    35575        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                    C
GAM1047  FLJ20813  3'  CTCAAACTCCTGACCTCA    35683        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                    C
GAM1047  FLJ21324  5'  CTCAAACTCCTGACCTCA    91199        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                    C
GAM1047  FLJ21459  3'  CTCGAACTCCTGACCTCA    44516        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                    C
GAM1047  FLJ22329  3'  CTCGAACTCCTGACCTCA    45065        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                    C
GAM1047  FLJ22529  3'  CTCAAACCCCTGACCTTA    45567        AA
                                TGAGGTCAG  GTTTGAG
                                |||||||||  |||||||
                                ATTCCAGTC  CAAACTC
                                    CC
GAM1047  FLJ22529  3'  CTCGAACTCCTGACCTCA    45569        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                    C
GAM1047  FLJ22684  3'  CTCAAACTCCTGACCTCA    46792        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                    C
GAM1047  FLJ23392  3'  CTCAAATTCCTGACCCCA    45533    A   A
                                TG GGTCAG AGTTTGAG
                                || |||||| ||||||||
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                                AC CCAGTC TTAAACTC
                                 C     C
GAM1047  FLJ23556  3'  CTCGAACTCCTGACCTCA    45948        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                     C
GAM1047  FLJ25416  5'  CTCAAACTCCCTACCTCA    58809      C  A_
                                TGAGGT AG  AGTTTGAG
                                |||||| ||  ||||||||
                                ACTCCA TC  TCAAACTC
                                   _  CC
GAM1047  FLJ30532  3'  CTCAAGCTCCTGACCTCA    58546        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCGAACTC
                                     C
GAM1047  FLJ32865  3'  CTCAAACCCCTGACCTCA    58173        AA
                                TGAGGTCAG  GTTTGAG
                                |||||||||  |||||||
                                ACTCCAGTC  CAAACTC
                                     CC
GAM1047  GGA2      3'  CTCGAACTCCTGACCTCA    56879        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                     C
GAM1047  GGA2      3'  CTCGAACTCCTGACCTCA    30465        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                     C
GAM1047  GNG4      3'  CTCAAACTCCTGACCTC     15615        A
                                GAGGTCAG AGTTTGAG
                                |||||||| ||||||||
                                CTCCAGTC TCAAACTC
                                     C
GAM1047  GTF2H3    3'  CTCAAACTCCTGAGCTCA    7703       G   A
                                TGAG TCAG AGTTTGAG
                                |||| |||| ||||||||
                                ACTC AGTC TCAAACTC
                                  G   C
GAM1047  H2AV      3'  CTCAAACTCCTGACCTCA    56850        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                     C
GAM1047  HSPC065   3'  CTCGAACTCCTGACCTCA    26296        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
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                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  JAM1      3'  CTCAAACTCCTGACCTC     57896        A
                                GAGGTCAG AGTTTGAG
                                |||||||| ||||||||
                                CTCCAGTC TCAAACTC
                                      C
GAM1047  JAM1      3'  CTCAAACTCCTGACCTC     57925        A
                                GAGGTCAG AGTTTGAG
                                |||||||| ||||||||
                                CTCCAGTC TCAAACTC
                                      C
GAM1047  JAM1      3'  CTCAAACTCCTGACCTC     57951        A
                                GAGGTCAG AGTTTGAG
                                |||||||| ||||||||
                                CTCCAGTC TCAAACTC
                                      C
GAM1047  JAM1      3'  CTCAAACTCCTGACCTC     33758        A
                                GAGGTCAG AGTTTGAG
                                |||||||| ||||||||
                                CTCCAGTC TCAAACTC
                                      C
GAM1047  KIAA0022  3'  CTCAAACTCCTGACCTCA    29664         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  KIAA0063  3'  CTCAAACTCCCGACCTCA    29624        AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
                                ACTCCAG   TCAAACTC
                                     CCC
GAM1047  KIAA0161  3'  CTCAAACTCCTGACCTCA    28503         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  KIAA0186  3'  CTCAAACTCCTGGCCTCA    40748         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCGGTC TCAAACTC
                                      C
GAM1047  KIAA0186  3'  GGTTTCAAACTCCTGACCTCA 40761          A
                                TGAGGTCAG AGTTTGAGACT
                                ||||||||| ||||||||||
                                ACTCCAGTC TCAAACTTTGG
                                      C
GAM1047  KIAA0205  3'  CTCGAACTCCTGACCTCA    29583         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
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                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  KIAA0391  3'  CTCAAACTCCTGACCTCA    27912        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  KIAA0513  3'  CTCGAACTCCTGACCTCA    28354        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  KIAA0555  3'  CTCGAACTCCTGACCTCA    28883        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  KIAA0561  3'  CTCGAACTCCTGACCTCA    65882        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  KIAA0563  5'  CTCGAACTTCTGACCTCA    29186
                                TGAGGTCAGAAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCTTCAAGCTC

GAM1047  KIAA0599  3'  CTCGAACTTCTGACCTCA    77175
                                TGAGGTCAGAAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCTTCAAGCTC

GAM1047  KIAA0720  3'  CTCGAACTCCTGACCCCA    62321    A     A
                                TG GGTCAG AGTTTGAG
                                || |||||| ||||||||
                                AC CCAGTC TCAAGCTC
                                  C     C
GAM1047  KIAA0737  3'  CTCGAACTCCTGACCTCA    29135        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  KIAA0841  3'  CTCGAACTCCTGACCTCA    71383        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  KIAA0889  3'  CTCGAACTCCCGACCTCA    31138       AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
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                                ACTCCAG   TCAAGCTC
                                    CCC
GAM1047  KIAA0961  3' CTCAACTCCTGACCTCA     29732        A   T
                                TGAGGTCAG AGTT GAG
                                ||||||||| |||| |||
                                ACTCCAGTC TCAA CTC
                                    C   _
GAM1047  KIAA1026  3' CTTCAACTCCTGACCTCA     71195        A   T
                                TGAGGTCAG AGTT GAG
                                ||||||||| |||| |||
                                ACTCCAGTC TCAA TTC
                                    C   C
GAM1047  KIAA1054  3' CTCGAACTCCTGACCTCA     68434        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                    C
GAM1047  KIAA1128  3' CTCGAACTCCTGACCTCA     68477        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                    C
GAM1047  KIAA1143  3' CTCAATCTCCTGACCTCA     68677        A  T
                                TGAGGTCAG AG TTGAG
                                ||||||||| || |||||
                                ACTCCAGTC TC AACTC
                                    C  T
GAM1047  KIAA1161  5' CTCAAACTCCTGACCT       81746        A
                                AGGTCAG AGTTTGAG
                                ||||||| ||||||||
                                TCCAGTC TCAAACTC
                                   C
GAM1047  KIAA1170  3' CTCAAACTCCTGACCTCA     69851        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                    C
GAM1047  KIAA1198  3' CTCAAACTCCTGACCTCA     63305        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                    C
GAM1047  KIAA1200  3' CTCGAACTCCTGACCTCA     62374        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                    C
GAM1047  KIAA1257  3' CTCAAACTCCCGACTTCA     62737        AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
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                                ACTTCAG   TCAAACTC
                                    CCC
GAM1047  KIAA1467  3'  CGAACTCCTGACCTCA      71605          A
                                TGAGGTCAG AGTTTG
                                ||||||||| ||||||
                                ACTCCAGTC TCAAGC
                                    C
GAM1047  KIAA1493  3'  CTCAAACTCCTGACCTCA     64160          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                    C
GAM1047  KIAA1497  5'  CTCGAACTCCTGACCTCA     67509          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                    C
GAM1047  KIAA1615  3'  CTCAAACTCCCGACCTCA     68706          AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
                                ACTCCAG   TCAAACTC
                                    CCC
GAM1047  KIAA1655  3'  CTCAAACTCCTGACCTC      66606          A
                                GAGGTCAG AGTTTGAG
                                |||||||| ||||||||
                                CTCCAGTC TCAAACTC
                                    C
GAM1047  KIAA1712  3'  CTCAAACTCCTGACCTCA     67537          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                    C
GAM1047  KIAA1737  3'  CTCGAACTCCTGACCTCA     67356          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                    C
GAM1047  KIAA1922  5'  CTCGAACTCCTGACCTCA     73626          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                    C
GAM1047  KIAA1987  5'  CTCGAACTTCTGACCTCA     88014
                                TGAGGTCAGAAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCTTCAAGCTC

GAM1047  MCLC      3'  CTCGAACTCCTGACCTCA     30683          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
```

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                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  MEF-2    3'  CTCAAACTCCTGACCTC     64383        A
                                GAGGTCAG AGTTTGAG
                                |||||||| ||||||||
                                CTCCAGTC TCAAACTC
                                      C
GAM1047  MGC13204 3'  CTCAAAATCCTGACCTCA    48838        AAG
                                TGAGGTCAG   TTTGAG
                                |||||||||   ||||||
                                ACTCCAGTC   AAACTC
                                      CTA
GAM1047  MKRN4    3'  CTCGAACTCCTGACCTCA    47744        A
                                TGAGGTCAG AGTTTGAG
                                |||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  moblak   3'  CTCAAACTCCTGACTTCA    55499        A
                                TGAGGTCAG AGTTTGAG
                                |||||||||| ||||||||
                                ACTTCAGTC TCAAACTC
                                      C
GAM1047  MRPS27   3'  CTCAACCTCCTGACCTCA    30636        A  T
                                TGAGGTCAG AG TTGAG
                                |||||||||| || |||||
                                ACTCCAGTC TC AACTC
                                      C  C
GAM1047  NAPG     5'  CTCAAACTCCTAAGCTCA    96724     GTC  A
                                TGAG   AG AGTTTGAG
                                ||||   || ||||||||
                                ACTC   TC TCAAACTC
                                  GAA  C
GAM1047  NXN      3'  CTCGAACTCCTGACCTCA    42419        A
                                TGAGGTCAG AGTTTGAG
                                |||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  OSBPL2   3'  CTCAAACTCCCGACCTCA    57863        AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
                                ACTCCAG   TCAAACTC
                                    CCC
GAM1047  OSBPL2   3'  CTCAAACTCCCGACCTCA    29212        AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
                                ACTCCAG   TCAAACTC
                                    CCC
GAM1047  PELI1    5'  CTCAAACTCCCAACCTCA    40264        CAGA
                                TGAGGT    AGTTTGAG
                                ||||||    ||||||||
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                                ACTCCA    TCAAACTC
                                   ACCC
GAM1047  PIP3-E    3'  GGTTTCAAACTCCTGACCTCA  66811          A
                                TGAGGTCAG AGTTTGAGACT
                                ||||||||| ||||||||||
                                ACTCCAGTC TCAAACTTTGG
                                     C
GAM1047  PRO0245   5'  AGTCTCAAACTCCCGAGCCCA  26123     A   CAGA_
                                TG GGT    AGTTTGAGACT
                                || |||    ||||||||||
                                AC CCG    TCAAACTCTGA
                                 _  AGCCC
GAM1047  PRO0529   5'  CTCAAACTCCTGACCTCA    25991          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                     C
GAM1047  PRO2955   3'  CTCAAACTCCTGACCTCA    37636          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                     C
GAM1047  PSTPIP2   3'  CTCAAACTCCTGACCTCA    44388          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                     C
GAM1047  RAI       5'  CTCAAACTCCTGATCTCA    21879          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCTAGTC TCAAACTC
                                     C
GAM1047  SC4MOL    3'  CTCAAACTTCTGACCTCA    22156
                                TGAGGTCAGAAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCTTCAAACTC

GAM1047  SCAMP-4   3'  CTCGAACTCCTGACCTCA    54394          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                     C
GAM1047  SFXN2     3'  CTCGAACTCCTGACCTCA    73943          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                     C
GAM1047  SLC19A3   3'  CTCAAACTCCTGACTTCA    47486          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
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                                    ACTTCAGTC TCAAACTC
                                          C
GAM1047  STAF65(gamma) 3'  CTCAAAACTCCTGACCTCA   29431          A    _
                                    TGAGGTCAG AGTTT GAG
                                    ||||||||| ||||| |||
                                    ACTCCAGTC TCAAA CTC
                                          C    A
GAM1047  TBCC     3'  CTCGAACTCCTGACCTCA    12141          A
                                    TGAGGTCAG AGTTTGAG
                                    ||||||||| ||||||||
                                    ACTCCAGTC TCAAGCTC
                                          C
GAM1047  TCL6     3'  CTCAAACTCCTGAGCTCA    40101      G   A
                                    TGAG TCAG AGTTTGAG
                                    |||| |||| ||||||||
                                    ACTC AGTC TCAAACTC
                                      G   C
GAM1047  TCL6     3'  CTCAAACTCCTGAGCTCA    40131      G   A
                                    TGAG TCAG AGTTTGAG
                                    |||| |||| ||||||||
                                    ACTC AGTC TCAAACTC
                                      G   C
GAM1047  THEA     3'  CTCAAACTCCTGACTTCA    66280          A
                                    TGAGGTCAG AGTTTGAG
                                    ||||||||| ||||||||
                                    ACTTCAGTC TCAAACTC
                                          C
GAM1047  TRIM16   3'  CAGATCTCAAACTCCTGACCTC 21335        A       C
                                    GAGGTCAG AGTTTGAGA TTTG
                                    |||||||| ||||||||| ||||
                                    CTCCAGTC TCAAACTCT AGAC
                                          C       _
GAM1047  TU12B1-TY 3'  CTCAAACTCCTAGCCTCA    33378       TC  A
                                    TGAGG  AG AGTTTGAG
                                    |||||  ||  ||||||||
                                    ACTCC  TC TCAAACTC
                                       GA  C
GAM1047  TU12B1-TY 3'  CTCGAACTCCTGACCTCA    33380          A
                                    TGAGGTCAG AGTTTGAG
                                    ||||||||| ||||||||
                                    ACTCCAGTC TCAAGCTC
                                          C
GAM1047  UBF-fl   3'  CTCAAACTCCTGACCTCA    51562          A
                                    TGAGGTCAG AGTTTGAG
                                    ||||||||| ||||||||
                                    ACTCCAGTC TCAAACTC
                                          C
GAM1047  USP22    3'  GTCTCAAACTCCTGACCTCA   68021          A
                                    TGAGGTCAG AGTTTGAGAC
                                    ||||||||| ||||||||||
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                                ACTCCAGTC TCAAACTCTG
                                      C
GAM1047  VDU1     3'  AGTCTCAAACTCCTGACCTCA  30410          A
                                TGAGGTCAG AGTTTGAGACT
                                ||||||||| ||||||||||
                                ACTCCAGTC TCAAACTCTGA
                                      C
GAM1047  VPS33A   3'  CTCAAACTCCTGACCTCA     43337          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  WBSCR23  3'  CTCAAACTCCTGACCTCA     46757          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  ZNF17    3'  CTCAAACTCCCGACCTCA     82390        AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
                                ACTCCAG   TCAAACTC
                                     CCC
GAM1047  LOC112687 3'  CAAACTCCTGACCTCA      72855          A
                                TGAGGTCAG AGTTTG
                                ||||||||| ||||||
                                ACTCCAGTC TCAAAC
                                      C
GAM1047  LOC115648 3'  CTCGAACTCCTGACCTCA     59299          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  LOC119392 3'  CTCGAACTCCTGACCTCA     59135          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  LOC120114 3'  CTCAAACTCCTGACCTC      75525          A
                                GAGGTCAG AGTTTGAG
                                |||||||| ||||||||
                                CTCCAGTC TCAAACTC
                                      C
GAM1047  LOC120224 5'  CTCGAACTCCTGACCTCA     57098          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  LOC124216 3'  AGTCTCAAACTCCTGACCTC   74259          A
                                GAGGTCAG AGTTTGAGACT
                                |||||||| ||||||||||
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                                CTCCAGTC TCAAACTCTGA
                                     C
GAM1047  LOC126364 3'  CTCGAACTCCTGACCTCA    75688        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                     C
GAM1047  LOC126669 3'  CTCAAACTCCTGACCTCA    75404        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                     C
GAM1047  LOC130639 5'  CTCGAACTCCTGACCTCA    74972        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                     C
GAM1047  LOC132625 3'  AGTCTCAAACTCCTGACCTC  75896        A
                                GAGGTCAG AGTTTGAGACT
                                |||||||| ||||||||||
                                CTCCAGTC TCAAACTCTGA
                                     C
GAM1047  LOC135154 3'  CTCGAACTCCTGACCTCA    75217        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                     C
GAM1047  LOC135293 3'  CTCGAACTCCTGACCTCA    76179        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                     C
GAM1047  LOC142927 5'  GGTGTCAAACTCCTGGCCTCA 76432        A      G
                                TGAGGTCAG AGTTTGA ACT
                                ||||||||| ||||||| |||
                                ACTCCGGTC TCAAACT TGG
                                     C      G
GAM1047  LOC143916 3'  CTCAAACTTCTGACCTCA    76641
                                TGAGGTCAGAAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCTTCAAACTC

GAM1047  LOC144317 5'  CTCGAACTCCTGACCTCA    76790        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                     C
GAM1047  LOC144524 5'  CTCAAACTCCTGAACTCA    83126      G   A
                                TGAG TCAG AGTTTGAG
                                |||| |||| ||||||||
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                                ACTC AGTC TCAAACTC
                                  A    C
GAM1047  LOC145453 5'  CTCAAACTCCTGACCTCA    77138          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                     C
GAM1047  LOC146050 3'  CTCAAACTCCCGACCTCA    77636         AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
                                ACTCCAG   TCAAACTC
                                    CCC
GAM1047  LOC146229 3'  CTCAAACTCCTGACCTCA    77743          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                     C
GAM1047  LOC146229 3'  CTCAAACTCCTGACCTCA    77745          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                     C
GAM1047  LOC146229 3'  CTCAAACTCCTGACTTCA    77747          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTTCAGTC TCAAACTC
                                     C
GAM1047  LOC146901 3'  CTCGAACTCCTGACCTCA    83838          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                     C
GAM1047  LOC146952 5'  CTCAAACTCCTGACCTCA    83865          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                     C
GAM1047  LOC147071 5'  CTCGAACTTCTGACCTCA    72997
                                TGAGGTCAGAAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCTTCAAGCTC

GAM1047  LOC147166 3'  CAGATCTCAAACTTCTGACCTC 78284                C
                                GAGGTCAGAAGTTTGAGA TTTG
                                |||||||||||||||||| ||||
                                CTCCAGTCTTCAAACTCT AGAC
                                                  _
GAM1047  LOC147817 3'  CTCAAACTCCTGACCTTA    78497          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
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                                ATTCCAGTC TCAAACTC
                                      C
GAM1047  LOC148709 3'  CTCAAACTCCCGACCTTA    78941        AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
                                ATTCCAG   TCAAACTC
                                   CCC
GAM1047  LOC148918 5'  CTCGAACTCCTGACCTCA    79069         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  LOC149171 5'  CTCGAACTTCTGACCTCA    79218
                                TGAGGTCAGAAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCTTCAAGCTC

GAM1047  LOC149577 3'  CTCGAACTCCTGACCTCA    84511         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  LOC149692 3'  CTCAAAGTCCTGACCTCA    84583         AAG
                                TGAGGTCAG   TTTGAG
                                |||||||||   ||||||
                                ACTCCAGTC   AAACTC
                                      CTG
GAM1047  LOC149692 3'  CTCGAACTCCTGACCTCA    84585         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  LOC149711 3'  CAAACTCCTGACCTCA      84675         A
                                TGAGGTCAG AGTTTG
                                ||||||||| ||||||
                                ACTCCAGTC TCAAAC
                                      C
GAM1047  LOC150225 3'  CTCAAACTCCTGACCTCA    84991         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  LOC150290 3'  CTCAAACTCCTGGCCTCA    79773         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCGGTC TCAAACTC
                                      C
GAM1047  LOC150960 3'  CTCAAATTCCTGACCTCA    80061         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
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                                ACTCCAGTC TTAAACTC
                                      C
GAM1047  LOC151701 3'  CTCGAACTCCTGACCTCA    85484         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  LOC152137 3'  CTCGAACCCCTGACCTCA    80479         AA
                                TGAGGTCAG  GTTTGAG
                                |||||||||  |||||||
                                ACTCCAGTC  CAAGCTC
                                      CC
GAM1047  LOC153688 3'  CTCGAACTCCCAACCTCA    86104       CAGA
                                TGAGGT    AGTTTGAG
                                ||||||    ||||||||
                                ACTCCA    TCAAGCTC
                                   ACCC
GAM1047  LOC153811 3'  CTCAAACTCCTGACCTCA    80948         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  LOC154877 3'  GGTTTCGAACTCCCGACCTCA  86305        AGA
                                TGAGGTC   AGTTTGAGACT
                                |||||||   ||||||||||
                                ACTCCAG   TCAAGCTTTGG
                                     CCC
GAM1047  LOC157247 5'  CTCGAACTCCTGACCTCA    81365         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  LOC157858 5'  CTCAAACTCCTGACCTC     86587         A
                                GAGGTCAG AGTTTGAG
                                |||||||| ||||||||
                                CTCCAGTC TCAAACTC
                                      C
GAM1047  LOC158014 5'  CTCGAACTCCTGACCTCA    81649         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  LOC162427 3'  CTCAAACTCCTGACCTCA    82351         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  LOC169611 3'  AGTCTCAAACTCCTGACCTCA  82754         A
                                TGAGGTCAG AGTTTGAGACT
                                ||||||||| ||||||||||
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                                ACTCCAGTC TCAAACTCTGA
                                      C
GAM1047  LOC196047 5'  AGTCTCAAACTCCTGACCTCA  89590          A
                                TGAGGTCAG AGTTTGAGACT
                                ||||||||| ||||||||||
                                ACTCCAGTC TCAAACTCTGA
                                      C
GAM1047  LOC197358 3'  CTCGAACTCCTGACCTCA     88031          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  LOC199699 3'  CTCAAACTCCTGGCCTCA     88303          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCGGTC TCAAACTC
                                      C
GAM1047  LOC199906 3'  CTCAAACTCCTGACCTCA     88481          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  LOC200014 3'  CTCGAACTCCTGACCTCA     88525          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  LOC200314 3'  CTCGAACTCCTGACCTCA     90008          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  LOC200407 3'  CTCAAACTCCTGACCTCA     90044          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  LOC201164 3'  CTCAAACTCCTGACCTCA     88117          A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  LOC201173 5'  CTCGAACTTCTGACCTCA     87327
                                TGAGGTCAGAAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCTTCAAGCTC

GAM1047  LOC201220 5'  CTCGAACTTCTGACCTCA     87348
                                TGAGGTCAGAAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCAGTCTTCAAGCTC

GAM1047  LOC201627 3'  CTCAAACTCCCGACCTCA    89010        AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
                                ACTCCAG   TCAAACTC
                                    CCC
GAM1047  LOC219529 5'  AGCCTCAAACTCCTGAGCCCA  92966    A _   A       A
                                TG GG TCAG AGTTTGAG CT
                                || || |||| |||||||| ||
                                AC CC AGTC TCAAACTC GA
                                 _ G   C       C
GAM1047  LOC219673 5'  CTCAAACGCCTGACCTCA    93026         AA
                                TGAGGTCAG  GTTTGAG
                                |||||||||  |||||||
                                ACTCCAGTC  CAAACTC
                                    CG
GAM1047  LOC220074 3'  CTCAAACTCCTGACCTCA    59272         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                    C
GAM1047  LOC221060 3'  CTCGAACTCCTGACCTCA    93210         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                    C
GAM1047  LOC221271 3'  CTCAAACTCCTGATCTCA    91855         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCTAGTC TCAAACTC
                                    C
GAM1047  LOC221418 3'  CAAACCCTGACCTCA       93636         AA
                                TGAGGTCAG  GTTTG
                                |||||||||  |||||
                                ACTCCAGTC  CAAAC
                                    C_
GAM1047  LOC245771 5'  CTCGAACTCCTGACCTCA    92888         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                    C
GAM1047  LOC253805 3'  CTCGAACTCCTGACCTCA    96430         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                    C
GAM1047  LOC254268 3'  CTCAAACTCCTGACCTCA    95406         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
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                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  LOC254532 5'  CTCAAACTCCTGACCTCA    96635        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  LOC254655 3'  CTCGAACTCCTGACCTCA    95471        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  LOC255065 5'  CTCAAACTCCTGACCTCA    96584        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047  LOC255497 3'  CTCGAACTCCTGACCTCA    97191        A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  LOC256364 5'  CAAACTCCTGGCCTCA      94796        A
                                TGAGGTCAG AGTTTG
                                ||||||||| ||||||
                                ACTCCGGTC TCAAAC
                                      C
GAM1047  LOC51200  3'  CTCAAACTCCCAACCTCA    32996       CAGA
                                TGAGGT    AGTTTGAG
                                ||||||    ||||||||
                                ACTCCA    TCAAACTC
                                   ACCC
GAM1047  LOC51219  5'  CTCGAACTCCCGACCTCA    33119        AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
                                ACTCCAG   TCAAGCTC
                                     CCC
GAM1047  LOC57107  3'  AGTCTCGAACTCCTGACCTCA  39827         A
                                TGAGGTCAG AGTTTGAGACT
                                ||||||||| ||||||||||
                                ACTCCAGTC TCAAGCTCTGA
                                      C
GAM1047  LOC57146  3'  AGTCTCAAACTCCTGACCTCA  39912         A
                                TGAGGTCAG AGTTTGAGACT
                                ||||||||| ||||||||||
                                ACTCCAGTC TCAAACTCTGA
                                      C
GAM1047  LOC89932  3'  CTCGAACTTCTGACCTCA    60796
                                TGAGGTCAGAAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCAGTCTTCAAGCTC

GAM1047 LOC90072 3' CTCGAACTCCCGACCTCA    61296       AGA
                                TGAGGTC   AGTTTGAG
                                |||||||   ||||||||
                                ACTCCAG   TCAAGCTC
                                    CCC
GAM1047 LOC90110 5' CTCGAACTTCTGACCTCA    61510
                                TGAGGTCAGAAGTTTGAG
                                |||||||||||||||||
                                ACTCCAGTCTTCAAGCTC

GAM1047 LOC90591 3' CTCGAACTCCTGACCTCA    63422         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047 LOC90918 3' CTCAAACTCCTGACCTTA    64356         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ATTCCAGTC TCAAACTC
                                      C
GAM1047 LOC91115 3' CTCCAACTCCTGACCTCA    64934         A   T
                                TGAGGTCAG AGTT GAG
                                ||||||||| |||| |||
                                ACTCCAGTC TCAA CTC
                                      C   C
GAM1047 LOC91561 5' CTCGAACTCCTGACCTCA    66449         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047 LOC91963 3' CTCAAACTCCTGAGCTCA    67692      G  A
                                TGAG TCAG AGTTTGAG
                                |||| |||| ||||||||
                                ACTC AGTC TCAAACTC
                                   G   C
GAM1047 LOC92267 3' CTCAAACTCCTGACCTCA    68610         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAACTC
                                      C
GAM1047 LOC92697 5' CTCGAACTCCCAACCTCA    70269       CAGA
                                TGAGGT    AGTTTGAG
                                ||||||    ||||||||
                                ACTCCA    TCAAGCTC
                                    ACCC
GAM1047 LOC92841 3' CGAACTCCTGACCTCA      70708         A
                                TGAGGTCAG AGTTTG
                                ||||||||| ||||||
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                                ACTCCAGTC TCAAGC
                                      C
GAM1047  LOC93349  3'  CTCGAACTCCTGACCTCA    56456         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCAGTC TCAAGCTC
                                      C
GAM1047  LOC93408  5'  CTCAAACTCCTGGCCTCA    56479         A
                                TGAGGTCAG AGTTTGAG
                                ||||||||| ||||||||
                                ACTCCGGTC TCAAACTC
                                      C
GAM1048  FBXL11    3'  TTCAACAGGAAACCGATCTTCC 24578        _  GG  ATAC
                C                GGGAAGAT GGT  CT    TGAA
                                ||||||||| |||  ||    ||||
                                CCCTTCTA CCA  GG    ACTT
                                     G   AA  ACA_
GAM1048  GRINL1A   3'  GTTCAGTATGTGAAACCACCAT 69517     A       C____
                TTCCC                GGA GATGGTGG     TATACTGAAC
                                ||| ||||||||     ||||||||||
                                CCT TTACCACC     GTATGACTTG
                                  _       AAAGT
GAM1048  HD        3'  TCAACATAGAGTTTGTCTTCCT 9191         TG TGG    AC
                                GGGAAGA  G   CTAT  TGA
                                |||||||  |   ||||  |||
                                TCCTTCT  T   GATA  ACT
                                     GT TGA    CA
GAM1048  IL8       3'  TAGCCACCATCTTACC      94480    G
                                GG AAGATGGTGGCTA
                                || ||||||||||||
                                CC TTCTACCACCGAT
                                 A
GAM1048  LASS1     3'  TCCCTGCGGCCACCACCTCCT  41200      A A      TA  CT
                                GGGA G TGGTGGC  TA  GA
                                |||| | |||||||  ||  ||
                                TCCT C ACCACCG  GT  CT
                                  _ C      GC  CC
GAM1048  PNUTL1    3'  TCAGCACCACCCCCTCCC    10675      A AT    CTATA
                                GGGA G  GGTGG    CTGA
                                |||| |  |||||    ||||
                                CCCT C  CCACC    GACT
                                  _ CC    AC___
GAM1048  SUFU      3'  GTTCAGCACATCACACACCATC 32413     AA      GCTATA___
                CCC                  GGG  GATGGTG       CTGAAC
                                |||  |||||||       ||||||
                                CCC  CTACCAC       GACTTG
                                  __      ACACTACAC
GAM1048  UBE4A     3'  TTCAATATTTATCATCCTCCT  16567      A       C   AC
                                GGGA GATGGTGG TAT  TGAA
                                |||| |||||||| |||  ||||
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                                TCCT CTACTATT ATA  ACTT
                                  C       T  __
GAM1048  VARS2    5'  AGTCTGACCATCTCCC      20848      A     __
                                GGGA GATGGT  GGCT
                                |||| ||||||  ||||
                                CCCT CTACCA  CTGA
                                  _     GT
GAM1048  XK       3'  GGAGTAGCCACCAGCCTCCC   40801      AGA        A
                                GGGA   TGGTGGCTAT CT
                                ||||   |||||||||| ||
                                CCCT   ACCACCGATG GG
                                  CCG         A
GAM1048  APM2     3'  CGGGCAGCCACCACCTCCT    22406      A A       ATA
                                GGGA G TGGTGGCT   CTG
                                |||| | ||||||||   |||
                                TCCT C ACCACCGA   GGC
                                  _ C       CG_
GAM1048  ARPP-19  3'  TCAGCACACACTGCCAGTCTTC 21803        _   TG CTATA_
              CC                  GGGAAGA TGG  G     CTGA
                                ||||||| |||  |     ||||
                                CCCTTCT ACC  C     GACT
                                   G   GT ACACAC
GAM1048  DEPP     3'  TCAGTGCTACCATCCCC     22824     AA       TAT
                                GGG  GATGGTGGC   ACTGA
                                |||  |||||||||   |||||
                                CCC  CTACCATCG   TGACT
                                  __       ____
GAM1048  FLJ00058 5'  CAGACCCCACCATCTCCC    78763      A       CTATA
                                GGGA GATGGTGG    CTG
                                |||| ||||||||    |||
                                CCCT CTACCACC    GAC
                                  _       CCA__
GAM1048  FLJ14810 3'  AGCACGCTGTCATCCC      51620      A      _
                                GGGA GATGGTG GCT
                                |||| ||||||| |||
                                CCCT CTGTCGC CGA
                                  A      A
GAM1048  GPS1     3'  CAGTGGCACCATTTCCC      14678      A      G  AT
                                GGGA GATGGTG CT  ACTG
                                |||| ||||||| ||  ||||
                                CCCT TTACCAC GG  TGAC
                                  _      _ __
GAM1048  GTPBP1   3'  TAGAACCCCATCTTCCC      15017          T  __
                                GGGAAGATGG GG  CTA
                                ||||||||||  ||  |||
                                CCCTTCTACC CC  GAT
                                      _  AA
GAM1048  GTPBP1   3'  TAGAACCCCATCTTCCC      15018          T  __
                                GGGAAGATGG GG  CTA
                                ||||||||||  ||  |||
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                                CCCTTCTACC CC  GAT
                                      _  AA
GAM1048  KIAA0552  3'  AGCACATCATCTTCCT      28306           _
                                GGGAAGATGGTG GCT
                                |||||||||||| |||
                                TCCTTCTACTAC CGA
                                       A
GAM1048  KIAA1344  3'  TTCAGCATTCTGCCATCTCCT  72453      A     TG CT  A
                                GGGA GATGG  G  AT CTGAA
                                |||| |||||  |  || |||||
                                TCCT CTACC  C  TA GACTT
                                  _    GT T_  C
GAM1048  KIAA1464  3'  TTCAGTGAACATCTCCC     68277      A    GTGGCTA
                                GGGA GATG      TACTGAA
                                |||| ||||      |||||||
                                CCCT CTAC      GTGACTT
                                  _    AA_____
GAM1048  MGC2452   5'  TAGCCACCACTTCCC       50989       A
                                GGGAAG TGGTGGCTA
                                |||||| |||||||||
                                CCCTTC ACCACCGAT
                                  _
GAM1048  NCBP2     3'  CAGTATAATTTTCCC       23746         GGTGGC
                                GGGAAGAT     TATACTG
                                ||||||||     |||||||
                                CCCTTTTA     ATATGAC
                                      _______
GAM1048  PLSCR3    3'  TATAGCCACCGCCCCCC     39794     AAGA
                                GGG    TGGTGGCTATA
                                |||    ||||||||||
                                CCC    GCCACCGATAT
                                  CCC_
GAM1048  PLSCR3    3'  TATAGCCACCGCCCCCC     90761     AAGA
                                GGG    TGGTGGCTATA
                                |||    ||||||||||
                                CCC    GCCACCGATAT
                                  CCC_
GAM1048  POLR2D    3'  ATAACACCACCTTCCC      16654       A    GC
                                GGGAAG TGGTG  TAT
                                |||||| |||||  |||
                                CCCTTC ACCAC  ATA
                                   C    A_
GAM1048  RPH3A     3'  TTCAGTAACACACCCTCCC   30247     AGAT    GCTA
                                GGGA   GGTG   TACTGAA
                                ||||   ||||   |||||||
                                CCCT   CCAC   ATGACTT
                                  C___    ACA_
GAM1048  SLC5A6    3'  TTCAACATAGCCATAGTCCT  40835     AGATG       AC
                                GGGA    GTGGCTAT  TGAA
                                ||||    ||||||||  ||||
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                                TCCT    TACCGATA  ACTT
                                  GA___      CA
GAM1048  LOC132946 5'  CAGTGTGGCACCCACCC    75073    AAGA  TG
                                GGG   TGG  GCTATACTG
                                |||   |||  |||||||||
                                CCC   ACC  CGGTGTGAC
                                 _____  CA
GAM1048  LOC139422 5'  TCAGTATAGCCTAGAACTCCT  75847     AGATGGT
                                GGGA     GGCTATACTGA
                                ||||     ||||||||||
                                TCCT     CCGATATGACT
                                  CAAGAT_
GAM1048  LOC146822 3'  TCTCCATGCCACCACCTGCCC  78154    A  A     TATACT
                                GGG AG TGGTGGC     GA
                                ||| || |||||||     ||
                                CCC TC ACCACCG     CT
                                  G  C      TACCT_
GAM1048  LOC151816 5'  GTCCAGCCACCATCTTCCT   85499            AT
                                GGGAAGATGGTGGCT  AC
                                ||||||||||||||  ||
                                TCCTTCTACCACCGA  TG
                                         CC
GAM1048  LOC221712 5'  GTTCAGGGGCCACCATCCCCC  93626    AA        ATA
                                GGG  GATGGTGGCT   CTGAAC
                                |||  ||||||||||   ||||||
                                CCC  CTACCACCGG   GACTTG
                                  C_        G__
GAM1048  LOC253430 5'  CAGAGCCACCATCCCCCC    96236    AA        ATA
                                GGG  GATGGTGGCT   CTG
                                |||  ||||||||||   |||
                                CCC  CTACCACCGA   GAC
                                  CC        ___
GAM1048  LOC253715 3'  TTCAGTATCCAACCATCCTCTC 96928     A     _  CT
                                GGGA GATGGT GG  ATACTGAA
                                |||| |||||| ||  ||||||||
                                CTCT CTACCA CC  TATGACTT
                                  C     A  __
GAM1048  LOC90190  3'  CAGTCCATCCCACCATCACCCC 61775    AA      CTAT_
                                GGG  GATGGTGG    ACTG
                                |||  ||||||||    ||||
                                CCC  CTACCACC    TGAC
                                  CA       CTACC
GAM1049  AMT      3'  CAAACCATGGCAGACTCACCAC 4904     CAA_  T  GG    A
             CT                   AGG    GA TT  GCCAT GTTTG
                                |||    || ||  ||||| |||||
                                TCC    CT AG  CGGTA CAAAC
                                  ACCA  C  A_    C
GAM1049  CSPG3    3'  TGACCCAAATCCTGCT      15240      A      C
                                GGCA GATTTGGG CA
                                |||| |||||||| ||
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                                TCGT CTAAACCC GT
                                  C       A
GAM1049  FMOD     3'  GGCAGCCAAATCTTGCCT    8930            __
                                AGGCAAGATTTGG  GCC
                                ||||||||||||  |||
                                TCCGTTCTAAACC  CGG
                                      GA
GAM1049  GASC1    5'  AAATTTCCCAAATCTCCCT    64241     CA       CCAT
                                AGG  AGATTTGGG    AGTTT
                                |||  |||||||||    |||||
                                TCC  TCTAAACCC    TTAAA
                                  C_       T___
GAM1049  TUBG1    3'  TGGCCCAAGCCCTGCCT     63399      AGA
                                AGGCA   TTTGGGCCA
                                |||||   |||||||||
                                TCCGT   GAACCCGGT
                                   CCC
GAM1049  CCR6     5'  CAAACGTTCCCAAATCTTCC   48581    C       CCATA
                                GG AAGATTTGGG    GTTTG
                                || ||||||||||    |||||
                                CC TTCTAAACCC    CAAAC
                                 _       TTG__
GAM1049  CCR6     5'  CAAACGTTCCCAAATCTTCC   15166    C       CCATA
                                GG AAGATTTGGG    GTTTG
                                || ||||||||||    |||||
                                CC TTCTAAACCC    CAAAC
                                 _       TTG__
GAM1049  CGI-01   3'  GCAAACTATATCTAAACCCAAA 31943        CC_____      III
            TCTCACTT                GATTTGGG     ATAGTTTG   C
                                ||||||||     ||||||||   |
                                CTAAACCC     TATCAAAC   G
                                     AAATCTA      III
GAM1049  FLJ23058 3'  TGAGCCCAAATCCTGGCC    45204     AA_       _
                                GGC   GATTTGGGC CA
                                |||   ||||||||| ||
                                CCG   CTAAACCCG GT
                                  GTC       A
GAM1049  HTMP10   3'  CAAACTATAACCAGGTTGCCT  52607      AG     GCC
                                AGGCA  ATTTGG   ATAGTTTG
                                |||||  ||||||   ||||||||
                                TCCGT  TGGACC   TATCAAAC
                                   __      AA_
GAM1049  KIAA0367 3'  CAAACCACAGCTAAGTCTCGCT 67294     A       G CATA
                                GGC AGATTTGG C    GTTTG
                                ||| ||||||| |    |||||
                                TCG TCTGAATC G    CAAAC
                                  C       _ ACAC
GAM1049  KIAA1068 3'  TTATGGCCCAATCTTACCT    31043     C     T
                                AGG AAGATT GGGCCATAG
                                ||| |||||| |||||||||
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                                TCC TTCTAA CCCGGTATT
                                  A     _
GAM1049  ORCTL3    3'  CAAAGATGGCCCAACCCCCGCC 14918     AAGAT       AG
                                GGC    TTGGGCCAT  TTTG
                                |||    |||||||||  ||||
                                CCG    AACCCGGTA  AAAC
                                  CCCCC        G_
GAM1049  P5-1      3'  AGCTCCACCCCAAATCTTACC  21913    C        CCAT
                                GG AAGATTTGGG    AGTT
                                || ||||||||||    ||||
                                CC TTCTAAACCC    TCGA
                                 A         CACC
GAM1049  LOC200819 3'  TGGCCCAAACCTGCC       90145      A A
                                GGCA G TTTGGGCCA
                                |||| | |||||||||
                                CCGT C AAACCCGGT
                                  _ C
GAM1049  LOC81501  3'  CCACATGATCTTGCCT      47904          _ _
                                AGGCAAGATT TG GG
                                |||||||||| || ||
                                TCCGTTCTAG AC CC
                                      T  A
GAM1050  ABR       3'  CGGTCTCCTGGCAGCCTCC    6572      A       CAAAAT
                                GGA GCTGCCAG     CTG
                                ||| ||||||||     |||
                                CCT CGACGGTC     GGC
                                  C       CTCT__
GAM1050  ABR       3'  CGGTCTCCTGGCAGCCTCC    41724     A       CAAAAT
                                GGA GCTGCCAG     CTG
                                ||| ||||||||     |||
                                CCT CGACGGTC     GGC
                                  C       CTCT__
GAM1050  ANK1      3'  CAGATTTTACTGTGACTTCT   40025      CT  C  C
                                GGAAG  GC AG AAAATCTG
                                |||||  || || ||||||||
                                TCTTC  TG TC TTTTAGAC
                                   AG  _  A
GAM1050  ANK1      3'  CAGATTTTACTGTGACTTCT   60388      CT  C  C
                                GGAAG  GC AG AAAATCTG
                                |||||  || || ||||||||
                                TCTTC  TG TC TTTTAGAC
                                   AG  _  A
GAM1050  ANK1      3'  CAGATTTTACTGTGACTTCT   3471       CT  C  C
                                GGAAG  GC AG AAAATCTG
                                |||||  || || ||||||||
                                TCTTC  TG TC TTTTAGAC
                                   AG  _  A
GAM1050  ATP11A    3'  AGGCCACGCCGGCAGCTTCC   77018          A  AAAA
                                GGAAGCTGCC GC    TCT
                                |||||||||| ||    |||
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                                CCTTCGACGG CG    GGA
                                      C  CACC
GAM1050  BAP1     3'  GCGAGGTACTGCAGCTTCC    16216          C  CAAA   _
                                GGAAGCTGC AG    ATCT GC
                                ||||||||| ||    |||| ||
                                CCTTCGACG TC    TGGA CG
                                      _ A___    G
GAM1050  BCL7B    3'  CGGAGCTGCTGGCAGCTTCT   8131              AAA
                                GGAAGCTGCCAGCA   TCTG
                                ||||||||||||||   ||||
                                TCTTCGACGGTCGT   AGGC
                                      CG_
GAM1050  BMP4     5'  GCACTGCTGCAGCTTCC     55639          C    AAATC
                                GGAAGCTGC AGCA     TGC
                                ||||||||| ||||     |||
                                CCTTCGACG TCGT     ACG
                                      _    C_____
GAM1050  BMP4     5'  GCACTGCTGCAGCTTCC     6831           C    AAATC
                                GGAAGCTGC AGCA     TGC
                                ||||||||| ||||     |||
                                CCTTCGACG TCGT     ACG
                                      _    C_____
GAM1050  BMP4     5'  GCACTGCTGCAGCTTCC     55635          C    AAATC
                                GGAAGCTGC AGCA     TGC
                                ||||||||| ||||     |||
                                CCTTCGACG TCGT     ACG
                                      _    C_____
GAM1050  CD28     3'  CAGCCGGCTGGCAGCCCCC   20436    AA        AAAAT
                                GG  GCTGCCAGC     CTG
                                ||  |||||||||     |||
                                CC  CGACGGTCG     GAC
                                 CC        GCC__
GAM1050  CENPB    3'  GCAAGGCTGGCAGCCCCC    69536    AA        AAAATC
                                GG  GCTGCCAGC     TGC
                                ||  |||||||||     |||
                                CC  CGACGGTCG     ACG
                                 CC        GA_____
GAM1050  EIF1A    3'  TTTACTGGTAACTTCC      88609      C     C
                                GGAAG TGCCAG AAA
                                ||||| |||||| |||
                                CCTTC ATGGTC TTT
                                   A      A
GAM1050  FRAP1    3'  CAGATCGCTGGCAGCCTC    17098    A        AAA
                                GA GCTGCCAGC   ATCTG
                                || |||||||||   |||||
                                CT CGACGGTCG   TAGAC
                                 C        C__
GAM1050  GCN1L1   3'  CAGCTCTGGCAGTTCC      69754      G      CAAAAT
                                GGAA CTGCCAG     CTG
                                |||| |||||||     |||
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                                CCTT GACGGTC     GAC
                                  _      TC_____
GAM1050 LIF     3'  TGGGGGCTGCTGGCAGACCC  9741    AAG       AAA  G
                                GG  CTGCCAGCA  TCT CA
                                ||  |||||||||  ||| ||
                                CC  GACGGTCGT  GGG GT
                                 CA_       C__  G
GAM1050 MDFI    3'  TGCAGATTCCAGCAGGGTCC  18773    AG   CAGCAA
                                GGA  CTGC     AATCTGCA
                                |||  ||||     ||||||||
                                CCT  GACG     TTAGACGT
                                  GG   ACC___
GAM1050 MYLK    3'  TGCAGATGTCTAGCAGCTTC  97022       C  CAAA
                                GAAGCTGC AG    ATCTGCA
                                |||||||| ||    |||||||
                                CTTCGACG TC    TAGACGT
                                     A  TG__
GAM1050 NUP62   3'  CAGAAATAGCCACAGCTTCC  33327       CCA  AAAA
                                GGAAGCTG   GC    TCTG
                                ||||||||   ||    ||||
                                CCTTCGAC   CG    AGAC
                                     AC_  ATAA
GAM1050 PIM2    3'  TGCAGATTCTTGCAACCTCC  59992    AGC   C  CAA
                                GGA   TGC AG   AATCTGCA
                                |||   ||| ||   ||||||||
                                CCT   ACG TC   TTAGACGT
                                  CCA   T  ___
GAM1050 S100B   3'  GCTCAGCGCTGGCAGCGTCC  20778    A       AAAATCT
                                GGA GCTGCCAGC      GC
                                ||| |||||||||      ||
                                CCT CGACGGTCG      CG
                                  G       CGACT__
GAM1050 SHMT2   3'  TGCAGATTCCTGAGCCTCC   18272    A   GC   CAA
                                GGA GCT  CAG   AATCTGCA
                                ||| |||  |||   ||||||||
                                CCT CGA  GTC   TTAGACGT
                                  C   __   C__
GAM1050 SPAG8   3'  TGCAGAGGGCTACAACTTCC  24904     C  CC   AAAA
                                GGAAG TG  AGC    TCTGCA
                                |||||  ||  |||    ||||||
                                CCTTC AC  TCG    AGACGT
                                   A  A_   GG__
GAM1050 TEM8    3'  TGCAAATTCTTCCAGTTTCC  49859       CC  CAA   C
                                GGAAGCTG  AG   AAT TGCA
                                ||||||||  ||   ||| ||||
                                CCTTTGAC  TC   TTA ACGT
                                     CT   ___   A
GAM1050 XKRY    5'  CAGCAAAATCTGGCAGCTCC  16254    A      CAAAAT
                                GGA GCTGCCAG     CTG
                                ||| ||||||||     |||
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                                CCT CGACGGTC     GAC
                                  _      TAAAAC
GAM1050 XKRY     5' CAGCAAAATCTGGCAGCTCC  60015    A      CAAAAT
                                GGA GCTGCCAG     CTG
                                ||| ||||||||     |||
                                CCT CGACGGTC     GAC
                                  _      TAAAAC
GAM1050 A2BP1    5' TGCAAGTGGAACTTACAGCTTC 38063        CC  CAAA TC
              C                  GGAAGCTG  AG   A  TGCA
                                ||||||||  ||   |  ||||
                                CCTTCGAC  TC   T  ACGT
                                    AT  AAGG GA
GAM1050 C15orf5  3' TGCATTCACTTACAGCTTCC  48199        CC  CA  ATC
                                GGAAGCTG  AG  AA   TGCA
                                ||||||||  ||  ||   ||||
                                CCTTCGAC  TC  TT   ACGT
                                    AT  AC  ___
GAM1050 C6orf37  3' TGCTGTAGCAGCTTCC     67480         __
                                GGAAGCTGC  CAGCA
                                |||||||||  |||||
                                CCTTCGACG  GTCGT
                                     AT
GAM1050 CPR2     3' CAGGACCCTGGCAGCCTCC   48092    A      CAAAA
                                GGA GCTGCCAG    TCTG
                                ||| ||||||||    ||||
                                CCT CGACGGTC    GGAC
                                  C       CCA__
GAM1050 DKFZP434J193 3' CAGAAGCCTGGCAGCTCC    71002    A      CAAAA
                                GGA GCTGCCAG    TCTG
                                ||| ||||||||    ||||
                                CCT CGACGGTC    AGAC
                                  _      CGA__
GAM1050 DKFZp547H236 5' GCAGCCCTGGCTAGCTTCC   78544        _    CAAAAT
                                GGAAGCT GCCAG     CTGC
                                ||||||| |||||     ||||
                                CCTTCGA CGGTC     GACG
                                    T    CC_____
GAM1050 EZFIT    3' GCACGCTGGCAGCCACC     41108    AA       AAAATC
                                GG  GCTGCCAGC     TGC
                                ||  |||||||||     |||
                                CC  CGACGGTCG     ACG
                                 AC       C______
GAM1050 FLJ10276 3' CAGATTCTGGTGGCTCC     35964    A  TG   CAA
                                GGA GC  CCAG   AATCTG
                                ||| ||  ||||   ||||||
                                CCT CG  GGTC   TTAGAC
                                  _ GT   ____
GAM1050 FLJ10704 3' TGCAGACCCCGCCTGGCCCCC  36460    AAGCT    _ AAAA
                                GG    GCCAG C    TCTGCA
                                ||    ||||| |    ||||||
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                                CC    CGGTC G   AGACGT
                                 CC___    C CCCC
GAM1050  FLJ10898  5'  TTTGCCAGCAGCTTCT     59442        CA
                                GGAAGCTGC  GCAAA
                                |||||||||  |||||
                                TCTTCGACG  CGTTT
                                     AC
GAM1050  FLJ12057  3'  TGCAGCACCTGGCAGCCACC  45441   AA      CAAAAT
                                GG  GCTGCCAG    CTGCA
                                ||  ||||||||    |||||
                                CC  CGACGGTC    GACGT
                                 AC      CAC___
GAM1050  FLJ12788  3'  AGATCCTGGCAGCTTCC    42540          CAAA
                                GGAAGCTGCCAG   ATCT
                                ||||||||||||   ||||
                                CCTTCGACGGTC   TAGA
                                       C___
GAM1050  FLJ13693  3'  CAGAGGGGTTGGCAGCTTCT  45648          AAAA
                                GGAAGCTGCCAGC   TCTG
                                ||||||||||||   ||||
                                TCTTCGACGGTTG   AGAC
                                       GGG_
GAM1050  FLJ14966  3'  GCACGCATGGCAGCTTCC    51770         _ AAAATC
                                GGAAGCTGCCA GC    TGC
                                |||||||||| ||    |||
                                CCTTCGACGGT CG    ACG
                                       A  C_____
GAM1050  FLJ23189  3'  CAGATGCTGCTGGCAGTCC   46839   AA       AA
                                GG  GCTGCCAGCA  ATCTG
                                ||  ||||||||||  |||||
                                CC  TGACGGTCGT  TAGAC
                                 __       CG
GAM1050  GEMIN4    3'  TGCAGAAGATCAGCAGCTTCT  31699        CAGCAAAA
                                GGAAGCTGC      TCTGCA
                                |||||||||      ||||||
                                TCTTCGACG      AGACGT
                                     ACTAGA__
GAM1050  GPR9      3'  CGGGACTCACTGGCAGCCCC   7686    AA      CAAAA
                                GG  GCTGCCAG    TCTG
                                ||  ||||||||    ||||
                                CC  CGACGGTC    GGGC
                                 C_      ACTCA
GAM1050  HTR3A     5'  TGCAGGAAAACTTGGCAGCTCC 6027     A      CAAAA
                                GGA GCTGCCAG    TCTGCA
                                ||| ||||||||    ||||||
                                CCT CGACGGTT    GGACGT
                                  _      CAAAA
GAM1050  KIAA0296  3'  CAGACCTCAGCTTCT      28109        CC  CAAAA
                                GGAAGCTG  AG    TCTG
                                ||||||||  ||    ||||
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                                TCTTCGAC  TC    AGAC
                                   __  C____
GAM1050  KIAA0450  5'  CAGTGGCCAGCAGCTTCC    27623        CA  AAAAT
                                GGAAGCTGC  GC    CTG
                                |||||||||  ||    |||
                                CCTTCGACG  CG    GAC
                                     AC  GT___
GAM1050  KIAA0478  3'  GCAATCCTCCTGCCACAGCTTC 29547        CCA   AAATC__
              C                  GGAAGCTG   GCA      TGC
                                 ||||||||   |||      |||
                                 CCTTCGAC   CGT      ACG
                                     AC_   CCTCCTA
GAM1050  KIAA0543  3'  GCAGATTCTAGGCTGC      68937    T  _  CAA
                                GC GCC AG   AATCTGC
                                || ||| ||   |||||||
                                CG CGG TC   TTAGACG
                                 T   A  ___
GAM1050  KIAA0660  3'  CAGATTTTCATAGTTTCC    24513        CCAGC
                                GGAAGCTG    AAAATCTG
                                ||||||||    ||||||||
                                CCTTTGAT    TTTTAGAC
                                     AC___
GAM1050  KIAA1190  3'  CAGTGCCAGCAGCTTCC     71097        CA   AAAT
                                GGAAGCTGC  GCA   CTG
                                |||||||||  |||   |||
                                CCTTCGACG  CGT   GAC
                                     AC  _____
GAM1050  KIAA1508  3'  GTTCTGCTGGCAGCTTCC    61890           A
                                GGAAGCTGCCAGCA AAT
                                |||||||||||||| |||
                                CCTTCGACGGTCGT TTG
                                        C
GAM1050  LAP1B     3'  TGCAGATTATATGCAGTTCC   64590      G   CAGCAA
                                GGAA CTGC     AATCTGCA
                                |||| ||||     ||||||||
                                CCTT GACG     TTAGACGT
                                  _   TATA__
GAM1050  MGC10960  3'  CAGAAGTGCTGGCAGCCACC   51004    AA       AAA
                                GG  GCTGCCAGCA   TCTG
                                ||  ||||||||||   ||||
                                CC  CGACGGTCGT   AGAC
                                 AC        GA_
GAM1050  MGC3101   3'  CAGAGCCCAGCAGCTTTC    43881        CA_  AAAA
                                GGAAGCTGC   GC   TCTG
                                |||||||||   ||   ||||
                                CTTTCGACG   CG   AGAC
                                     ACC  _____
GAM1050  MGC4342   3'  CGGGTTCTGCCACAGCTTCC   44266        CCA   A
                                GGAAGCTG   GCA AATCTG
                                ||||||||   ||| ||||||
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                                CCTTCGAC  CGT TTGGGC
                                    AC_  C
GAM1050 MIL1    3' TGCAGATTCTAGTTTGGCTTTC 31098       CC  AA_
                                GGAAGCTG AGC  AATCTGCA
                                |||||||| |||  ||||||||
                                CTTTCGGT TTG  TTAGACGT
                                    __  ATC
GAM1050 NR4A3   5' TGCAGATTTCGGGACAGCTCTC 22736   GA   _ AGCA
                                G AGCTG CC   AAATCTGCA
                                | ||||| ||   |||||||||
                                C TCGAC GG   TTTAGACGT
                                 TC   A GC__
GAM1050 OSBPL7  3' TGCAAAATGCCTGCAGCTTCC 34810       CA  AAATC
                                GGAAGCTGC GCA   TGCA
                                ||||||||| |||   ||||
                                CCTTCGACG CGT   ACGT
                                     TC  AAA__
GAM1050 P2RX5   3' GCAAGTGCCACAGCTTCC   10370       CCA  AAATC
                                GGAAGCTG  GCA   TGC
                                ||||||||  |||   |||
                                CCTTCGAC  CGT   ACG
                                    AC_  GA___
GAM1050 PASK    3' GATTTCTAATGACAGCTTCC  30718       C GCA_
                                GGAAGCTG CA   AAATC
                                |||||||| ||   |||||
                                CCTTCGAC GT   TTTAG
                                    A AATC
GAM1050 RANBP6  5' CAGATTTTGCACCCAATTTCC 61635      C CCA
                                GGAAG TG  GCAAAATCTG
                                ||||| ||  ||||||||||
                                CCTTT AC  CGTTTTAGAC
                                   A CCA
GAM1050 SEC14L1 3' GCGATTTTGCTGACAGCTGCC 11502   A   C       T
                                GG AGCTG CAGCAAAATC GC
                                || ||||| |||||||||| ||
                                CC TCGAC GTCGTTTTAG CG
                                 G   A       _
GAM1050 SH3BGRL 3' CAGATTTTCTGAGCTTCT   61941      GC  C
                                GGAAGCT  CAG AAAATCTG
                                |||||||  ||| ||||||||
                                TCTTCGA  GTC TTTTAGAC
                                    __  _
GAM1050 SIAT8C  5' GCAGCCTGGCAGCCTC     31881   A      CAAAAT
                                GA GCTGCCAG     CTGC
                                || ||||||||     ||||
                                CT CGACGGTC     GACG
                                 C      C_____
GAM1050 STX6    3' CAGACTCCACTGGTGTTTT   19486      T   CAAAA
                                GAAGC GCCAG    TCTG
                                ||||| |||||    ||||
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                                TTTTG TGGTC     AGAC
                                  _     ACCTC
GAM1050  TRAF3     3'  GCAGATTCGCAGCCTCT     59740     A     CAGCAA
                                GGA GCTGC      AATCTGC
                                ||| |||||      |||||||
                                TCT CGACG      TTAGACG
                                  C     C_____
GAM1050  TRIM31    5'  CAGACTTGGCACAGCTTCC    90999         CCA  A  A
                                GGAAGCTG   GC AA TCTG
                                ||||||||   || || ||||
                                CCTTCGAC   CG TT AGAC
                                     A__  G  C
GAM1050  TTYH2     3'  TGCAGATTTTGCTGGCACT    50998     C
                                AG TGCCAGCAAAATCTGCA
                                || ||||||||||||||||
                                TC ACGGTCGTTTTAGACGT
                                 _
GAM1050  LOC146562 3'  GCAGCCTGGCGGCCTCC      57534     A       CAAAAT
                                GGA GCTGCCAG      CTGC
                                ||| ||||||||      ||||
                                CCT CGGCGGTC      GACG
                                  C       C_____
GAM1050  LOC146774 5'  TTTGCTGGAAGCCTCC       78101     A   G
                                GGA GCT CCAGCAAA
                                ||| ||| ||||||||
                                CCT CGA GGTCGTTT
                                  C   A
GAM1050  LOC148147 3'  TAGATCCACTGGCAGCTTGC   78687    G        CAAA
                                G AAGCTGCCAG    ATCTG
                                | ||||||||||    |||||
                                C TTCGACGGTC    TAGAT
                                 G         ACC_
GAM1050  LOC148343 5'  CAGCCTTGCTGGCTACTTCC   78792       CT       AAT
                                GGAAG  GCCAGCAA   CTG
                                |||||  ||||||||   |||
                                CCTTC  CGGTCGTT   GAC
                                   AT       CC_
GAM1050  LOC149670 3'  GCAGATTAGCAGCCCC       79490     AA     CAGCAA
                                GG  GCTGC      AATCTGC
                                ||  |||||      |||||||
                                CC  CGACG      TTAGACG
                                 C_     A_____
GAM1050  LOC161190 5'  GCAGCTCTGGCGGCTCC      82263     A       CAAAAT
                                GGA GCTGCCAG      CTGC
                                ||| ||||||||      ||||
                                CCT CGGCGGTC      GACG
                                  _       TC____
GAM1050  LOC196410 5'  TGCTGGGCTGCTGGCAGCCCC  87660     AA         AAA  T
                                GG  GCTGCCAGCA   TC GCA
                                ||  ||||||||||   || |||
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                                CC  CGACGGTCGT   GG CGT
                                 C_        CG_  T
GAM1050  LOC200268 3'  CAGTGAGCCGGTAGCTTCC   88679         A  AAAAT
                                GGAAGCTGCC GC     CTG
                                |||||||||| ||     |||
                                CCTTCGATGG CG     GAC
                                      C  AGT__
GAM1050  LOC202908 5'  CAGAGCTCACTGCAGCTTCC   89226         C  CAAAA
                                GGAAGCTGC AG     TCTG
                                ||||||||| ||     ||||
                                CCTTCGACG TC     AGAC
                                      _ ACTCG
GAM1050  LOC203378 5'  GCTGTTGCGGCAGCTTCC    90610         A   AATCT
                                GGAAGCTGCC GCAA     GC
                                |||||||||| ||||     ||
                                CCTTCGACGG CGTT     CG
                                      _   GT___
GAM1050  LOC205313 5'  GCCTGTGCTGGCAGCGCCC   90676    AA        AAATCT
                                GG  GCTGCCAGCA     GC
                                ||  ||||||||||     ||
                                CC  CGACGGTCGT     CG
                                 CG        GTC___
GAM1050  LOC221975 5'  GCAGCGCTGGCAGTCC      92607    AA       AAAAT  _
                                GG  GCTGCCAGC     CTG C
                                ||  |||||||||     ||| |
                                CC  TGACGGTCG     GAC G
                                 __        C_____  C
GAM1050  LOC253921 3'  TTTTGCTGCCAGCCCCC     94854    AA   C
                                GG  GCTG CAGCAAAA
                                ||  |||| ||||||||
                                CC  CGAC GTCGTTTT
                                 CC    C
GAM1050  LOC254191 5'  CAGAGGGAGTGATAGCTTCC   94766         CCA  AAAA
                                GGAAGCTG   GC    TCTG
                                ||||||||   ||    ||||
                                CCTTCGAT   TG    AGAC
                                     AG_  AGGG
GAM1050  LOC254973 5'  TGTAACCCTCTGGCAGCCCCC  96294    AA       CAAAATC
                                GG  GCTGCCAG      TGCA
                                ||  ||||||||      ||||
                                CC  CGACGGTC      ATGT
                                 CC       TCCCA__
GAM1050  LOC255031 5'  CAGGGCTCCTGGCAGCCCCC   97232    AA       CAAAA
                                GG  GCTGCCAG     TCTG
                                ||  ||||||||     ||||
                                CC  CGACGGTC     GGAC
                                 CC       CTCG_
GAM1050  LOC255975 5'  TGCTGAGCTGCTGGCAGCCTCT 95900     A        AAA  T
                                GGA GCTGCCAGCA   TC GCA
                                ||| ||||||||||   || |||
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                                TCT CGACGGTCGT   AG CGT
                                  C        CG_  T
GAM1050  LOC256306 5'  TGCAGGGAGGCCTGGCAGC   96700        _ AAAA
                                GCTGCCAG C    TCTGCA
                                |||||||| |    ||||||
                                CGACGGTC G    GGACGT
                                    C GAG_
GAM1050  LOC257608 5'  CAGACTTGGCACAGCTTCC   97827        CCA  A  A
                                GGAAGCTG   GC AA TCTG
                                ||||||||   || || ||||
                                CCTTCGAC   CG TT AGAC
                                    A__  G  C
GAM1050  LOC90246  5'  TGCAGATTCTCATTAGCTTC   61910       CCAGCAA
                                GAAGCTG      AATCTGCA
                                |||||||      ||||||||
                                CTTCGAT      TTAGACGT
                                    TACTC__
GAM1050  LOC90268  3'  GGATTCTACTGGCAGCCCC   61965    AA      CAA
                                GG  GCTGCCAG   AATCT
                                ||  ||||||||   |||||
                                CC  CGACGGTC   TTAGG
                                 C_       ATC
GAM1050  LOC91151  5'  CAACTGGCAGCTTTC       52616          CAAAATC
                                GGAAGCTGCCAG      TG
                                ||||||||||||      ||
                                CTTTCGACGGTC      AC
                                      A_______
GAM1051  ACP2      3'  AGAAAGTTCTAGACTG      7851      GC  TC
                                CAGT  CT  AGAACTTTCT
                                ||||  ||  ||||||||||
                                GTCA  GA  TCTTGAAAGA
                                  __  __
GAM1051  APTX      5'  AAGAGAAAGAGATCAGGCA   34655      TCAGAA
                                TGCCT     CTTTCTCTT
                                |||||     |||||||||
                                ACGGA     GAAAGAGAA
                                   CTAGA_
GAM1051  BCL7A     3'  AGGCTGTCTCCTTAAGGCACTG 40637         C  A__  TT
                                CAGTGCCTT AG   AC  TCT
                                |||||||| ||   ||  |||
                                GTCACGGAA TC   TG  GGA
                                     T  CTC  TC
GAM1051  CLC       3'  AAGAGAAAATACTGAAAGCACA 25105    A   C    AAC
           GG                     CC GTGC TTCAG   TTTCTCTT
                                || |||| |||||   ||||||||
                                GG CACG AAGTC   AAAGAGAA
                                 A   A    ATA
GAM1051  CNK       3'  AAGCCCTGAAGGCCTG      14517     T      AA
                                CAG GCCTTCAG  CTT
                                ||| ||||||||  |||
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                                GTC CGGAAGTC  GAA
                                  _       CC
GAM1051  COL4A3   3'  AAGTGCAGGTTCTGAGGGCACC 48549    A           TCT
                GG                  CC GTGCCTTCAGAACTT   CTT
                                    || ||||||||||||||   |||
                                    GG CACGGGAGTCTTGGA   GAA
                                     C            CGT
GAM1051  CSPG4    3'  AAGAGAGACCTGGAGACAC    8570     C     AAC
                                    GTG CTTCAG   TTTCTCTT
                                    ||| ||||||   ||||||||
                                    CAC GAGGTC   AGAGAGAA
                                      A     C__
GAM1051  CYP1B1   3'  AAGAGAAAAGAGAGAAACACTG 3651       CC   AGAAC
                                    CAGTG  TTC    TTTCTCTT
                                    |||||  |||    ||||||||
                                    GTCAC  AAG    AAAGAGAA
                                       A_   AGAGA
GAM1051  DLG3     3'  AAGAGAAAAGAGGAGGACTG   40880     G    AGAAC
                                    CAGT CCTTC    TTTCTCTT
                                    |||| |||||    ||||||||
                                    GTCA GGAGG    AAAGAGAA
                                      _     AGA__
GAM1051  DLG5     5'  AGGCAGACTCTGAAGGC     82909         A_  T
                                    GCCTTCAGA  CT TCT
                                    |||||||||  || |||
                                    CGGAAGTCT  GA GGA
                                          CA  C
GAM1051  FLT1     3'  AAGAGAAACCGGGAGAAGGCAT 8910         AGAAC_
                                    GTGCCTTC     TTTCTCTT
                                    ||||||||     ||||||||
                                    TACGGAAG     AAAGAGAA
                                         AGGGCC
GAM1051  GRB10    3'  AGAGAAAATGGCACCTGG    17971     _   TTCAGAAC
                                    CCAG TGCC       TTTCTCT
                                    |||| ||||       |||||||
                                    GGTC ACGG       AAAGAGA
                                      C   TA_______
GAM1051  LFG      3'  AAGAGAAAAGGAGCCAAGAACT 76711      GC   CAGAA   _
                GG                  CCAGT  CTT    CTTT CTCTT
                                    |||||  |||    |||| |||||
                                    GGTCA  GAA    GAAA GAGAA
                                      A_   CCGAG    A
GAM1051  MAN2A2   3'  AAGAGAAAGTTCATTCAC    20391     CCTTCA
                                    GTG     GAACTTTCTCTT
                                    |||     ||||||||||||
                                    CAC     CTTGAAAGAGAA
                                     TTA___
GAM1051  NLGN3    3'  AAGAAAAGTTCTTAAAACACT  38596     CC  C       C
                                    AGTG  TT AGAACTTT TCTT
                                    ||||  || |||||||| ||||
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                                TCAC  AA TCTTGAAA AGAA
                                  AA  T       _
GAM1051  NPAS1    5'  AAGGTCTCCCGAGGGCACT    59879         A_  _
                                AGTGCCTTC  GA ACTTT
                                |||||||||  || |||||
                                TCACGGGAG  CT TGGAA
                                     CC  C
GAM1051  PLAG1    3'  AGTGTGTTCCAAAGGCATT    10605        CA    TTT
                                AGTGCCTT  GAAC   CT
                                ||||||||  ||||   ||
                                TTACGGAA  CTTG   GA
                                     AC    TGT
GAM1051  PLXNA1   3'  AGAAAATGAAGGCAGTGG    72309     G       GAAC
                                CCA TGCCTTCA    TTTCT
                                ||| ||||||||    |||||
                                GGT ACGGAAGT    AAAGA
                                  G       A___
GAM1051  PPP4R1   3'  AAGAGAAAGTACAGTAAACACT 17620      CCTTCAGA
                                AGTG       ACTTTCTCTT
                                ||||       ||||||||||
                                TCAC       TGAAAGAGAA
                                  AAATGACA
GAM1051  ACYP2    3'  AAGAGAAAAATTGTAACACACT 56612       CC  _   AAC
           G                     CAGTG  TT CAG   TTTCTCTT
                                |||||  || |||   ||||||||
                                GTCAC  AA GTT   AAAGAGAA
                                   AC  T   AA_
GAM1051  B3GNT6   3'  AGAAATCAGATGAAGGCAT    22503         GAAC_
                                GTGCCTTCA     TTTCT
                                |||||||||     |||||
                                TACGGAAGT     AAAGA
                                     AGACT
GAM1051  BAG5     3'  AAGAGAAGGGATAAAGGAC    16835     G   CAGAA
                                GT CCTT     CTTTCTCTT
                                || ||||     |||||||||
                                CA GGAA     GGAAGAGAA
                                 _    ATAG_
GAM1051  BIVM     3'  AAGAGAAAAGACTCAAGAAACT 34665      GC   C  AAC
           G                     CAGT  CTT AG   TTTCTCTT
                                ||||  ||| ||   ||||||||
                                GTCA  GAA TC   AAAGAGAA
                                   AA   C  AGA
GAM1051  C15orf5  3'  AGAGAAAAGAAAGCAC      48195      C   AGAAC
                                GTGC TTC     TTTCTCT
                                |||| |||     |||||||
                                CACG AAG     AAAGAGA
                                   A   A_____
GAM1051  C20orf80 5'  AAGAGAAGAAGATGAAGAAAC  65282     GC     GAAC
                                GT  CTTCA    TTTCTCTT
                                ||  |||||    ||||||||
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                                CA  GAAGT    GAAGAGAA
                                 AA     AGAA
GAM1051  CLSTN1    3'  AGTTCTGAGGACACTGG     30103        C
                                CCAGTG CTTCAGAACT
                                |||||| ||||||||||
                                GGTCAC GGAGTCTTGA
                                   A
GAM1051  DKFZP434P0111 3'  AAGAGAAAGTTTCTGCAC    67368      CTTCA
                                GTGC     GAACTTTCTCTT
                                ||||     ||||||||||||
                                CACG     TTTGAAAGAGAA
                                  TC___
GAM1051  DORFIN    5'  AGAATTCTCTGAAGGAAC    31257    G       ACT
                                GT CCTTCAGA   TTCT
                                || ||||||||   ||||
                                CA GGAAGTCT   AAGA
                                 A       CTT
GAM1051  FLJ10300  5'  AAGAGAAAGATGAAGACTCTG  35997     TGC    GAA
                                CAG   CTTCA   CTTTCTCTT
                                |||   |||||   |||||||||
                                GTC   GAAGT   GAAAGAGAA
                                  TCA    A__
GAM1051  FLJ20373  3'  AAGAGAAGAAGGAAAGGCACAG 35070    A      _ AGAAC
            G                    CC GTGCCTT C     TTTCTCTT
                                || ||||||| |     ||||||||
                                GG CACGGAA G     GAAGAGAA
                                 A      A GAA__
GAM1051  FLJ23511  5'  AGAGAAAAACAAGGCAT     49956        CAGAAC
                                GTGCCTT     TTTCTCT
                                |||||||     |||||||
                                TACGGAA     AAAGAGA
                                   CAA___
GAM1051  FLJ30681  3'  AGAGAAGAAAGACCACTGG    91782       CCT  AGAAC
                                CCAGTG   TC     TTTCTCT
                                ||||||   ||     |||||||
                                GGTCAC   AG     GAAGAGA
                                   C__   AAA__
GAM1051  HDAC11    3'  GAGCTATAGGCACTGG      45717         TC  AACTTT
                                CCAGTGCCT  AG     CTC
                                |||||||||  ||     |||
                                GGTCACGGA  TC     GAG
                                    TA  _______
GAM1051  IKKE      5'  AGTGAGCCCTGAAAGCTCTGG  25745      T  C     AA   T
                                CCAG GC TTCAG  CTT CT
                                |||| || |||||  ||| ||
                                GGTC CG AAGTC  GAG GA
                                  T  A    CC   T
GAM1051  KIAA0680  3'  AGAGAAAATTGAAGCAT     28232      C     AAC
                                GTGC TTCAG   TTTCTCT
                                |||| |||||   |||||||
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                                TACG AAGTT   AAAGAGA
                                  _    A__
GAM1051  KIAA1228  3'  AGGGGGTGATTCTGAGGCACTG 65035        T   ___   TT
                                CAGTGCCT CAGA   ACT  CT
                                |||||||| ||||   |||  ||
                                GTCACGGA GTCT   TGG  GA
                                    _   TAG   GG
GAM1051  KIAA1300  5'  AGGAACCCTGAAGGCA      62860         AAC
                                TGCCTTCAG   TTTCT
                                |||||||||   |||||
                                ACGGAAGTC   AAGGA
                                     CC_
GAM1051  KIAA1805  3'  AAGAGAAAGTAGAAGCAGCA   79966     __    AGA
                                TGC  CTTC   ACTTTCTCTT
                                |||  ||||   ||||||||||
                                ACG  GAAG   TGAAAGAGAA
                                  AC    A__
GAM1051  LENG1     5'  AAGAGAAAGCTCTGGGCATCCT 84074     __    TT    A
             G                   CAG  TGCC  CAGA CTTTCTCTT
                                |||  ||||  |||| |||||||||
                                GTC  ACGG  GTCT GAAAGAGAA
                                  CT    __    C
GAM1051  LHX6      3'  AAGAGAAAACTCTGGGGTCA   26854    C      AC
                                TG CTTCAGA  TTTCTCTT
                                || |||||||  ||||||||
                                AC GGGGTCT  AAAGAGAA
                                  T      CA
GAM1051  N4BP3     3'  AGCTCCAGAAGGCACTGG     66250          A_  A
                                CCAGTGCCTTC  GA CT
                                ||||||||||  || ||
                                GGTCACGGAAG  CT GA
                                       AC  C
GAM1051  NASP      3'  AGAGGGTGAAGAAACTG     67966      GC    AGA
                                CAGT  CTTC   ACTTTCT
                                ||||  ||||   |||||||
                                GTCA  GAAG   TGGGAGA
                                  AA   ___
GAM1051  SMARCF1   3'  AAAATTCTGAAGGAC       57480    G       C
                                GT CCTTCAGAA TTT
                                || |||||||| |||
                                CA GGAAGTCTT AAA
                                  _       A
GAM1051  SMARCF1   3'  AAAATTCTGAAGGAC       37430    G       C
                                GT CCTTCAGAA TTT
                                || |||||||| |||
                                CA GGAAGTCTT AAA
                                  _       A
GAM1051  SMARCF1   3'  AAAATTCTGAAGGAC       20034    G       C
                                GT CCTTCAGAA TTT
                                || |||||||| |||
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                                CA GGAAGTCTT AAA
                                 _       A
GAM1051  TED      3'  AAGAGAAAGTCCAGGGACTGG  31630      G   TCA  A
                                CCAGT CCT   GA CTTTCTCTT
                                ||||| |||   || |||||||||
                                GGTCA GGA   CT GAAAGAGAA
                                   G   C__  _
GAM1051  TGIF2    3'  AGAAGGGTGCTGAAGGC     41447        AA_
                                GCCTTCAG   CTTTCT
                                ||||||||   ||||||
                                CGGAAGTC   GGAAGA
                                     GTG
GAM1051  WBSCR20A  3'  AAGAGAAAGAAGAGACAGCA   35958     CT  AGAA
                                TGC  TC    CTTTCTCTT
                                |||  ||    |||||||||
                                ACG  AG    GAAAGAGAA
                                  AC  AGAA
GAM1051  LOC115273 3'  AGAAAGTTCTGATGGCCAGG   73356    AGT   T
                                CC   GCC TCAGAACTTTCT
                                ||   ||| ||||||||||||
                                GG   CGG AGTCTTGAAAGA
                                 AC_   T
GAM1051  LOC145761 5'  AAGAGAAAGTGGAAGGCATGG  83472     G      AGA
                                CCA TGCCTTC   ACTTTCTCTT
                                ||| |||||||   ||||||||||
                                GGT ACGGAAG   TGAAAGAGAA
                                  _      G__
GAM1051  LOC146179 5'  AGAAAGTTTTGGGCCT      77700    T   TT
                                AG GCC  CAGAACTTTCT
                                || |||  ||||||||||||
                                TC CGG  GTTTTGAAAGA
                                 _  __
GAM1051  LOC147072 3'  AAGAGAAAGTGAGAAGAAACTG 60407      GC    AGA
                                CAGT  CTTC   ACTTTCTCTT
                                ||||  ||||   ||||||||||
                                GTCA  GAAG   TGAAAGAGAA
                                  AA    AG_
GAM1051  LOC148758 5'  AGAAAGTTCTGAGAAAC     78962    GCC
                                GT   TTCAGAACTTTCT
                                ||   ||||||||||||
                                CA   GAGTCTTGAAAGA
                                 AA_
GAM1051  LOC148932 3'  AGGAATCTGAAGGCACTGG    79103            AC
                                CCAGTGCCTTCAGA  TTTCT
                                ||||||||||||||  |||||
                                GGTCACGGAAGTCT  AAGGA
                                                __
GAM1051  LOC149386 5'  AAGTTTTGAAAGCACT      84400       C
                                AGTGC TTCAGAACTT
                                ||||| ||||||||||
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                                TCACG AAGTTTTGAA
                                   A
GAM1051  LOC150139 3'  AGAAAATAGAAAAAGGCGCTGG 79583          CAGAAC_
                                CCAGTGCCTT      TTTCT
                                ||||||||||      |||||
                                GGTCGCGGAA      AAAGA
                                     AAAGATA
GAM1051  LOC152756 3'  AAGATGCAGTTCTGAAAACCTG 85871     TGCC       TTC
                                CAG   TTCAGAACT   TCTT
                                |||   |||||||||   ||||
                                GTC   AAGTCTTGA   AGAA
                                  CAA_       CGT
GAM1051  LOC162333 5'  AAGAGAAAGCGATGACACTG   87114      CCT   GAA
                                CAGTG   TCA   CTTTCTCTT
                                |||||   |||   |||||||||
                                GTCAC   AGT   GAAAGAGAA
                                   ___   AGC
GAM1051  LOC199221 3'  AAGAGAAGCTCGAAAGCATGG  80347     G   C   A A   T
                                CCA TGC TTC GA CTT CTCTT
                                ||| ||| ||| || ||| |||||
                                GGT ACG AAG CT GAA GAGAA
                                  _   A   _  C   _
GAM1051  LOC203339 3'  AGAGAAAATTGGGCCTG     90542     T   TCAGAAC
                                CAG GCCT      TTTCTCT
                                ||| ||||      |||||||
                                GTC CGGG      AAAGAGA
                                  _    TTA____
GAM1051  LOC255017 3'  AGAAAGAGGAACTGG       94624       G   TCAGAA
                                CCAGT CCT     CTTTCT
                                ||||| |||     ||||||
                                GGTCA GGA     GAAAGA
                                   A  _______
GAM1051  LOC256021 3'  AAGAGAAACAAAGACAACACTG 96512       CCT  AGAAC
            G                    CCAGTG   TC    TTTCTCTT
                                ||||||  ||    ||||||||
                                GGTCAC   AG    AAAGAGAA
                                    AAC  AAAC_
GAM1051  LOC90139  3'  AGAATCCCGAAGGCAT      55396        A_  ACT
                                GTGCCTTC  GA   TTCT
                                ||||||||  ||   ||||
                                TACGGAAG  CT   AAGA
                                     CC  ___
GAM1052  A1BG     3'  TCAAGCGATCCTCCTGCCTCA  55430
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAGCGAACT

GAM1052  A1BG     3'  TCAAGTGATCCTCCCGCCTCA  55431       TA      TG
                                TGAGG  GGAGGAT  TTTGA
                                |||||  |||||||  |||||
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                                ACTCC  CCTCCTA  GAACT
                                  GC      GT
GAM1052  A1BG     3'  TGATCCTCCCACCTCA      55437       A
                                TGAGGT GGAGGATTG
                                |||||| |||||||||
                                ACTCCA CCTCCTAGT
                                   C
GAM1052  AIM1     3'  TCAGGTGATCCTCCCACCTCA  91828       A      TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
                                ACTCCA CCTCCTA  GGACT
                                   C      GT
GAM1052  ALOX15   3'  TCAAATGATCCTCCCACCTCA  6687        A      TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
                                ACTCCA CCTCCTA  AAACT
                                   C      GT
GAM1052  APAF1    3'  TCAAGCAATCCTCCTGCCTCA  6736
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAACGAACT

GAM1052  APAF1    3'  TCAAGTAATCCTCCTGCCTCA  6737
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAATGAACT

GAM1052  APAF1    3'  TCAAGCAATCCTCCTGCCTCA  25045
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAACGAACT

GAM1052  APAF1    3'  TCAAGTAATCCTCCTGCCTCA  25046
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAATGAACT

GAM1052  APOC3    3'  CAGTGCTCTCCTACCCCA    3485     A      _ _
                                TG GGTAGGAG G ATTG
                                || |||||||| | ||||
                                AC CCATCCTC C TGAC
                                  C       T G
GAM1052  ARCN1    3'  TCAGGCAATCCGCCCACCTCA  7989        A  A
                                TGAGGT GG GGATTGTTTGA
                                |||||| || ||||||||||
                                ACTCCA CC CCTAACGGACT
                                   C  G
GAM1052  ARL2     3'  CAGATGCCCCCCACCT      8023       A  A  AT
                                AGGT GG GG  TGTTTG
                                |||| || ||  ||||||
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                                TCCA CC CC  GTAGAC
                                  _ _  CC
GAM1052 AXL     3'  TCAAGTGATCTGCCCACCTCA  8106       A  A   TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC TCTA  GAACT
                                   C  G   GT
GAM1052 AXL     3'  TCAAGTGATCTGCCCACCTCA  41603      A  A   TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC TCTA  GAACT
                                   C  G   GT
GAM1052 BCL10   3'  TGATCCTCTCACCTCA      14064       AG
                                TGAGGT  GAGGATTG
                                ||||||  ||||||||
                                ACTCCA  CTCCTAGT
                                   CT
GAM1052 BDKRB1  5'  CGATTCTCCCACCTCA      5542        A
                                TGAGGT GGAGGATTG
                                |||||| |||||||||
                                ACTCCA CCTCTTAGC
                                   C
GAM1052 BIN2    3'  CAAGACTCCTCCTGCCCCA   32823    A        TTG
                                TG GGTAGGAGGA   TTTG
                                || ||||||||||   ||||
                                AC CCGTCCTCCT   GAAC
                                 C         CA_
GAM1052 BRF2    3'  TCATGAGATCCTCTACCTCA  37010        G     GTT
                                TGAGGTAG AGGATT   TGA
                                |||||||| ||||||   |||
                                ACTCCATC TCCTAG   ACT
                                     _     AGT
GAM1052 BSN     3'  TCATTTTCCCTTCCTACCCCA  12928    A       ATTGTT
                                TG GGTAGGAGG     TGA
                                || |||||||||     |||
                                AC CCATCCTTC     ACT
                                 C        CCTTTT
GAM1052 BTG2    3'  CAAACACTCTCCCTACCCA   22209    A     AG  T
                                TG GGTAGG  GA TGTTTG
                                || ||||||  || ||||||
                                AC CCATCC  CT ACAAAC
                                 _     CT  C
GAM1052 CAPN5   3'  CAAATAGTCCTCCCC      90912    TA
                                GG  GGAGGATTGTTTG
                                ||  ||||||||||||
                                CC  CCTCCTGATAAAC
                                    __
GAM1052 CASP10  3'  TCAAGCGATCCTCCCACCTCA  52107       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
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                                ACTCCA CCTCCTAGCGAACT
                                   C
GAM1052 CASP10   3' TCAAGCGATCCTCCCACCTCA 52123      A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCCTAGCGAACT
                                   C
GAM1052 CD4     3' CAGTACCTCCTGCCCCA    5222    A      _
                                TG GGTAGGAGG ATTG
                                || ||||||||| ||||
                                AC CCGTCCTCC TGAC
                                 C       A
GAM1052 CDK3    3' AGCTGCCTCCTACCCA     6999    A      ATT
                                TG GGTAGGAGG  GTT
                                || |||||||||  |||
                                AC CCATCCTCC  CGA
                                 _      GT_
GAM1052 CIAS1   5' CAATTCTCCTACCTCA     16898
                                TGAGGTAGGAGGATTG
                                ||||||||||||||||
                                ACTCCATCCTCTTAAC

GAM1052 CLECSF11 5' CAATCCGCCCACCTCA     55273      A  A
                                TGAGGT GG GGATTG
                                |||||| || ||||||
                                ACTCCA CC CCTAAC
                                   C  G
GAM1052 CNGA1   5' TCAAGTGATCTGCCCACCTCA 59511      A  A   TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC TCTA  GAACT
                                   C  G   GT
GAM1052 COL1A1   3' CAAGTGGCCCCCACCCTCA  3602      TA  A  A TG
                                TGAGG  GG GG T  TTTG
                                |||||  || || |  ||||
                                ACTCC  CC CC G  GAAC
                                  CA  _  C GT
GAM1052 CPLX2   3' CAGGCCTCCTGCCCCA     21832   A      A
                                TG GGTAGGAGG TTG
                                || |||||||| |||
                                AC CCGTCCTCC GAC
                                 C       G
GAM1052 CRTAP   3' ACACCTGCCACCTCA      21027      A  _  AT
                                TGAGGT GG AGG  TGT
                                |||||| || |||  |||
                                ACTCCA CC TCC  ACA
                                   _ G  __
GAM1052 CST     5' TCAAGCAATCCTCCCGCCTCA 16792      TA
                                TGAGG  GGAGGATTGTTTGA
                                |||||  ||||||||||||||
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                                ACTCC  CCTCCTAACGAACT
                                  GC
GAM1052  CYP1A2   3'  CAAACTCCTGACCTCA      69096       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  CYP1A2   3'  TCAAGCAATCCTCCCACTTCA  69123       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTTCA CCTCCTAACGAACT
                                   C
GAM1052  CYP1A2   3'  CAAACTCCTGACCTCA      5677        _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  CYP1A2   3'  TCAAGCAATCCTCCCACTTCA  5703        A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTTCA CCTCCTAACGAACT
                                   C
GAM1052  CYP2B6   3'  TCAGGTGATCCACCCACCTCA  5740        A  A   TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC CCTA  GGACT
                                   C  A   GT
GAM1052  DDX11    3'  AGACACCTTCTACCCCA     47646    A       AT
                                TG GGTAGGAGG  TGTTT
                                || |||||||||  |||||
                                AC CCATCTTCC  ACAGA
                                 C       __
GAM1052  DDX11    3'  AGACACCTTCTACCCCA     15297    A       AT
                                TG GGTAGGAGG  TGTTT
                                || |||||||||  |||||
                                AC CCATCTTCC  ACAGA
                                 C       __
GAM1052  DFFB     3'  CAAACTCCTGACCTCA      87375       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  DFFB     3'  TCAGGTGATCCGCCCACCTCA  87395       A  A   TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC CCTA  GGACT
                                   C  G   GT
GAM1052  DISC1    3'  CAAACTCCTGACCTCA      37871       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
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                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  DLG4     5'  CAAACAATTTCTACC       7250         GG
                                GGTAGGA  ATTGTTTG
                                |||||||  ||||||||
                                CCATCTT  TAACAAAC
                                   __
GAM1052  ELMO1    3'  TCAAATCTCCTCCCACCTC    55284       A     TT
                                GAGGT GGAGGA  GTTTGA
                                ||||| ||||||  ||||||
                                CTCCA CCTCCT  TAAACT
                                   C     C_
GAM1052  F2RL3    3'  TCAAATGATTCTCCTGCCTCA  14192             TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
                                ACTCCGTCCTCTTA  AAACT
                                        GT
GAM1052  FABP2    3'  TCAAGCAATCCTCCTGCCTCA  3746
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAACGAACT

GAM1052  G6PC     3'  TCAAGCAGTCCTCCCACC     3833      A
                                GGT GGAGGATTGTTTGA
                                |||  ||||||||||||||
                                CCA CCTCCTGACGAACT
                                  C
GAM1052  GALE     3'  AGGCCTCCCCTACCTCA      63157         A   TT
                                TGAGGTAGG GGA  GTTT
                                |||||||||  |||  ||||
                                ACTCCATCC CCT  CGGA
                                      _  C_
GAM1052  GCN5L1   3'  CAAACCCTATCCCTCCTACCTC 7636            _  T__
              A                  TGAGGTAGGAGG AT   GTTTG
                                ||||||||||||  ||   |||||
                                ACTCCATCCTCC TA   CAAAC
                                       C  TCC
GAM1052  GLTSCR1  5'  AGTGATCCTCTCACCTCA     31668       AG     TG
                                TGAGGT  GAGGAT  TT
                                ||||||  ||||||  ||
                                ACTCCA  CTCCTA  GA
                                   CT     GT
GAM1052  GLUL     3'  TCAACTGTCTCCTACCTC     9046           ATT   T
                                GAGGTAGGAGG   GTT GA
                                ||||||||||||  |||  ||
                                CTCCATCCTCT   CAA CT
                                      GT_   _
GAM1052  HSPA5    3'  CAAGTGATCCTTCCACCTCA   18079       A      TG
                                TGAGGT GGAGGAT  TTTG
                                ||||||  |||||||  ||||
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                                ACTCCA CTTCCTA  GAAC
                                   C      GT
GAM1052  HUNK     3'  TCAAGTGATCCTCCCATCTCA  27461       A      TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
                                ACTCTA CCTCCTA  GAACT
                                   C      GT
GAM1052  ICAM1    3'  TCAAGTGATCCTCCCACCTCA  71578       A      TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
                                ACTCCA CCTCCTA  GAACT
                                   C      GT
GAM1052  ICMT     3'  CAATACCACCTACCTCA     24809         A  _
                                TGAGGTAGG GG ATTG
                                ||||||||| || ||||
                                ACTCCATCC CC TAAC
                                      A  A
GAM1052  IL2RB    3'  TCAAACAACATTCCACCCCA   6076     A   A    GA
                                TG GGT GGAG  TTGTTTGA
                                || ||| ||||  ||||||||
                                AC CCA CCTT  AACAAACT
                                 C   _    AC
GAM1052  JRK      3'  TCAAGCGATCCTCCTTCCTCA  86538       T
                                TGAGG AGGAGGATTGTTTGA
                                ||||| ||||||||||||||
                                ACTCC TCCTCCTAGCGAACT
                                   T
GAM1052  KCNAB2   3'  TCAAACGGTCCCACCCA     13309    A   AGGA
                                TG GGT    GGATTGTTTGA
                                || |||    ||||||||||
                                AC CCA    CCTGGCAAACT
                                 _   C___
GAM1052  KMO      3'  TCAAGCAATCCTCCCACTTCA  13454       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| |||||||||||||
                                ACTTCA CCTCCTAACGAACT
                                   C
GAM1052  LZTS1    3'  TCAAGCAATCCTCCTGCCTCA  40696
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAACGAACT

GAM1052  MAK      3'  CAAACTCCTGACCTCA      19755       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  MCCC2    3'  TCAAACAACAGCGCTCCCC   42140    TA   GA___
                                GG  GGAG    TTGTTTGA
                                ||  ||||    ||||||||
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                                CC  CCTC    AACAAACT
                                 __   GCGAC
GAM1052  MEFV    3'  CAAACTCCTGACCTCA     4126       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  MFI2    3'  CAAACCCCCAGCCTCA     52812      A  A  ATT
                                TGAGGT GG GG   GTTTG
                                |||||| || ||   |||||
                                ACTCCG CC CC   CAAAC
                                   A  _ ____
GAM1052  MHC2TA  3'  TCGGGTGATCCACCCACCTCA  4194       A  A   TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC CCTA  GGGCT
                                   C  A   GT
GAM1052  MHC2TA  3'  TGATCCTCCCACCTCA     4195       A
                                TGAGGT GGAGGATTG
                                |||||| |||||||||
                                ACTCCA CCTCCTAGT
                                   C
GAM1052  MICB    3'  CAAACTCCTGACCTCA     19821      _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  MLANA   3'  CAAACTCCTGACCTCA     18582      _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  NCOA6   5'  CAAACTCCTGACCTCA     25957      _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  NCOA6   5'  TCAAGCAACCCTCCCACCTC  25976      A    A
                                GAGGT GGAGG TTGTTTGA
                                ||||| ||||| ||||||||
                                CTCCA CCTCC AACGAACT
                                  C    C
GAM1052  NDRG3   3'  CAAACTCCTGACCTCA     49292      _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  NGFB    3'  TGGGCCCCTCCCTACCTCA   10221        _  ATT  TT
                                TGAGGTAGG AGG   GT  G
                                |||||||| |||   ||  |
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                                ACTCCATCC TCC   CG  T
                                     C   C__  GG
GAM1052  NQO1     3'  CAAACTCCTGACCTCA      6152        _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  NQO1     3'  TCAGGTGATCCGCCTACCTCA  6168         A    TG
                                TGAGGTAGG GGAT  TTTGA
                                ||||||||| ||||  |||||
                                ACTCCATCC CCTA  GGACT
                                     G   GT
GAM1052  NR1I2    5'  CATGCTGTCCTCCTACCCCA   13965    A        T  T
                                TG GGTAGGAGGAT GT TG
                                || ||||||||||| || ||
                                AC CCATCCTCCTG CG AC
                                 C         T  T
GAM1052  OGG1     5'  TCATTGGCGCCTCCTACCTC   10332          ATTGTT
                                GAGGTAGGAGG     TGA
                                ||||||||||      |||
                                CTCCATCCTCC     ACT
                                      GCGGTT
GAM1052  OGG1     5'  TCATTGGCGCCTCCTACCTC   33662          ATTGTT
                                GAGGTAGGAGG     TGA
                                ||||||||||      |||
                                CTCCATCCTCC     ACT
                                      GCGGTT
GAM1052  OGG1     5'  TCATTGGCGCCTCCTACCTC   33668          ATTGTT
                                GAGGTAGGAGG     TGA
                                ||||||||||      |||
                                CTCCATCCTCC     ACT
                                      GCGGTT
GAM1052  OXTR     3'  GATCCTCCTGACCTCA      6208        _
                                TGAGGT AGGAGGATT
                                |||||| |||||||||
                                ACTCCA TCCTCCTAG
                                   G
GAM1052  PAICS    3'  TCAAGCAGTTCTCCCACCTCA  21261       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCTTGACGAACT
                                   C
GAM1052  PCDHB16  3'  TCAACGGATCCTTCCACCTCA  40553       A       GT
                                TGAGGT GGAGGATT  TTGA
                                |||||| ||||||||  ||||
                                ACTCCA CTTCCTAG  AACT
                                   C       GC
GAM1052  PIK3C2B  3'  TCAAGCGATTCTCCTACCTCA  10576
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
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                                ACTCCATCCTCTTAGCGAACT

GAM1052  PLCB2    3'  CGAACCCTCCTGCCCCA     15891    A       ATT
                                TG GGTAGGAGG   GTTTG
                                || |||||||||   |||||
                                AC CCGTCCTCC   CAAGC
                                 C       ___
GAM1052  POLL     3'  CACCCCTTCTACCTCA      25177           AT
                                TGAGGTAGGAGG  TG
                                ||||||||||||  ||
                                ACTCCATCTTCC  AC
                                       CC
GAM1052  PPAT     3'  TCAAACAATCCCTTTATC    10701      GA
                                GGTAG  GGATTGTTTGA
                                |||||  ||||||||||
                                CTATT  CCTAACAAACT
                                   TC
GAM1052  PPT2     3'  CAGGCCTCCCCTACCTCA    17669        A   TT
                                TGAGGTAGG GGA  GTTTG
                                |||||||| |||  |||||
                                ACTCCATCC CCT  CGGAC
                                      _  C_
GAM1052  PPT2     3'  CAGGCCTCCCCTACCTCA    56965        A   TT
                                TGAGGTAGG GGA  GTTTG
                                |||||||| |||  |||||
                                ACTCCATCC CCT  CGGAC
                                      _  C_
GAM1052  PRIM2A   3'  TCAAGCGATCCTCACACCTCA  6274       AG
                                TGAGGT  GAGGATTGTTTGA
                                ||||||  |||||||||||||
                                ACTCCA  CTCCTAGCGAACT
                                   CA
GAM1052  PRIM2A   3'  TCAAGTGATCCTCCTACCTCA  6275            TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
                                ACTCCATCCTCCTA  GAACT
                                       GT
GAM1052  PRKR     3'  CAAACTCCTGACCTCA      10877       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  PTPN18   3'  TCAAGCAATCCTCCTGCCTCA  26869
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAACGAACT

GAM1052  RABL2A   3'  TCAAACGATTCTCCTGCCTCA  25504
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
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                                ACTCCGTCCTCTTAGCAAACT

GAM1052  RABL2B   3'  TCAAACGATTCTCCTGCCTCA  23005
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCTTAGCAAACT

GAM1052  RBBP9    3'  TCAAGTGATCCACCCACCTCA  70141       A  A    TG
                                TGAGGT GG GGAT  TTTGA
                                ||||||  ||  ||||  |||||
                                ACTCCA CC CCTA  GAACT
                                    C  A    GT
GAM1052  RGS9     5'  TCAGGCAACCCTCTCACCTCA  13837       AG    A
                                TGAGGT  GAGG TTGTTTGA
                                ||||||  ||||  ||||||||
                                ACTCCA  CTCC AACGGACT
                                    CT    C
GAM1052  RHD      3'  CAAACTCCTGACCTCA      32296        _    GA
                                TGAGGT AGGAG  TTG
                                ||||||  |||||  |||
                                ACTCCA TCCTC  AAC
                                    G     A_
GAM1052  RHD      3'  CAAACTCCTGACCTCA      32605        _    GA
                                TGAGGT AGGAG  TTG
                                ||||||  |||||  |||
                                ACTCCA TCCTC  AAC
                                    G     A_
GAM1052  SALL2    3'  CAAGACCCCTACCCA       63857    A     A  ATTG
                                TG GGTAGG GG    TTTG
                                ||  ||||||  ||    ||||
                                AC CCATCC CC    GAAC
                                 _     _  A___
GAM1052  SAS      3'  TCAAGCGATCCTCCTGCCTCA  19958
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAGCGAACT

GAM1052  SCML2    3'  CAAACTCCTGACCTCA      20311        _    GA
                                TGAGGT AGGAG  TTG
                                ||||||  |||||  |||
                                ACTCCA TCCTC  AAC
                                    G     A_
GAM1052  SERPINB9 3'  TCAAGCAATCCGCCTACCTCA  14762         A
                                TGAGGTAGG GGATTGTTTGA
                                |||||||||  ||||||||||
                                ACTCCATCC CCTAACGAACT
                                      G
GAM1052  SHOX     3'  TCAAGCAATCCTCCCACCTCA  22544       A
                                TGAGGT GGAGGATTGTTTGA
                                ||||||  ||||||||||||||
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                                ACTCCA CCTCCTAACGAACT
                                   C
GAM1052  SIL     3'  CAAACTCCCGACCTCA      11684       AGGA   TT
                                TGAGGT   GGA  GTTTG
                                ||||||   |||  |||||
                                ACTCCA   CCT  CAAAC
                                   GC__  __
GAM1052  SLA2    3'  TCAAACAATTCTCCTGCCTCA  49905
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCTTAACAAACT

GAM1052  SPN     3'  CAAACTCCTGACCTCA      11915       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  STAU    3'  TCAAATGCTTCCTACTCA    16009      G     ATT
                                TGAG TAGGAGG   GTTTGA
                                |||| |||||||   ||||||
                                ACTC ATCCTTC   TAAACT
                                  _      G__
GAM1052  STAU    3'  TCAAATGCTTCCTACTCA    33897      G     ATT
                                TGAG TAGGAGG   GTTTGA
                                |||| |||||||   ||||||
                                ACTC ATCCTTC   TAAACT
                                  _      G__
GAM1052  STAU    3'  TCAAATGCTTCCTACTCA    33903      G     ATT
                                TGAG TAGGAGG   GTTTGA
                                |||| |||||||   ||||||
                                ACTC ATCCTTC   TAAACT
                                  _      G__
GAM1052  STAU    3'  TCAAATGCTTCCTACTCA    33910      G     ATT
                                TGAG TAGGAGG   GTTTGA
                                |||| |||||||   ||||||
                                ACTC ATCCTTC   TAAACT
                                  _      G__
GAM1052  SULT2B1  5'  CAAACTCCTGACCTCA      16021       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  TAF11    3'  TCAAGCAGTCCTCCTGCCTCA  18917
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTGACGAACT

GAM1052  TAL1    3'  TCAAGCAATCCTCTCACCTCA  12113       AG
                                TGAGGT  GAGGATTGTTTGA
                                ||||||  ||||||||||||
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                                ACTCCA  CTCCTAACGAACT
                                   CT
GAM1052  TAT     3'  CAAACTCCTGACCTCA      4461        _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  TES     3'  CAAACTCCTGACCTCA      72000       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  TIM3    3'  CAAACTCCTGACCTCA      51338       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  TMPRSS3  3'  CAAACCCCTGACCTCA      43789       A  A  ATT
                                TGAGGT GG GG   GTTTG
                                |||||| || ||   |||||
                                ACTCCA TC CC   CAAAC
                                   G  _  ___
GAM1052  TMPRSS3  3'  CAAACCCCTGACCTCA      50502       A  A  ATT
                                TGAGGT GG GG   GTTTG
                                |||||| || ||   |||||
                                ACTCCA TC CC   CAAAC
                                   G  _  ___
GAM1052  TMPRSS3  3'  CAAACCCCTGACCTCA      50523       A  A  ATT
                                TGAGGT GG GG   GTTTG
                                |||||| || ||   |||||
                                ACTCCA TC CC   CAAAC
                                   G  _  ___
GAM1052  TNFRSF10B 3'  TCAAGCGATTCTCCCACCTCA  13877       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCTTAGCGAACT
                                   C
GAM1052  TNFRSF11A 3'  CAAGTGATCCTCCCACCTCA   13851       A      TG
                                TGAGGT GGAGGAT  TTTG
                                |||||| |||||||  ||||
                                ACTCCA CCTCCTA  GAAC
                                   C      GT
GAM1052  TNFRSF9  3'  TCAAGTGATCCTCCTGCCTCA  7793            TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
                                ACTCCGTCCTCCTA  GAACT
                                         GT
GAM1052  TNFSF9   3'  CGATCCTCCTGCCTCA      13754
                                TGAGGTAGGAGGATTG
                                |||||||||||||||
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                                ACTCCGTCCTCCTAGC

GAM1052 TNFSF9   3' TCAGGTGATCCTCCCATCTCA 13757      A     TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
                                ACTCTA CCTCCTA  GGACT
                                   C      GT
GAM1052 TRAF5    3' CAAACTCCTGACCTCA     16073      _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052 TRPC1    3' CAAACGGATCCTTCCCC    12384    TA      _
                                GG  GGAGGATT GTTTG
                                ||  |||||||| |||||
                                CC  CTTCCTAG CAAAC
                                 C_      G
GAM1052 TRPM6    3' CAAACTCCTGACCTCA     34530      _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052 UBE2G2   3' TCAAACCTTTCCTACTTCA   64864          ATT
                                TGAGGTAGGAGG   GTTTGA
                                ||||||||||||   ||||||
                                ACTTCATCCTTT   CAAACT
                                      C__
GAM1052 UMPS     3' CAGGTGATCCTCCCACCTCA  4550      A     TG
                                TGAGGT GGAGGAT  TTTG
                                |||||| |||||||  ||||
                                ACTCCA CCTCCTA  GGAC
                                   C      GT
GAM1052 UMPS     3' TCAAGCGATCCTCCTGCCTCA 4557
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAGCGAACT

GAM1052 VHL      3' CAAACTCCTGACCTCA     5062       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052 VHL      3' TCAGGTGATCCGCCCACCTCA 5088      A A   TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC CCTA  GGACT
                                   C G   GT
GAM1052 XYLB     3' ACAACCTCCCACCCA      17554    A  A    A
                                TG GGT GGAGG TTGT
                                || ||| ||||| ||||
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                                AC CCA CCTCC AACA
                                 _  C   _
GAM1052 ZNF142   5' ACCTGTCTCCTACCTCA    17431          ATT
                                TGAGGTAGGAGG  GT
                                ||||||||||||  ||
                                ACTCCATCCTCT  CA
                                      GTC
GAM1052 ANKRD6   3' GTGATCCTCCTGCCTCA    30087           TG
                                TGAGGTAGGAGGAT  T
                                ||||||||||||||  |
                                ACTCCGTCCTCCTA  G
                                      GT
GAM1052 ARHGAP8  3' ACGCTCCTCCTGCCCCA    34696   A       T
                                TG GGTAGGAGGA TGT
                                || ||||||||| |||
                                AC CCGTCCTCCT GCA
                                 C        C
GAM1052 BTN3A1   3' TCAAACAATTCTCCTGCCTCA 22924
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCTTAACAAACT

GAM1052 C(27)-3BETA-HSD 3' TCAAGCAATCCTCCTGCCTCA 47275
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAACGAACT

GAM1052 C20orf98 3' CAAAACTTCCTACCCA     71510   A       ATTG
                                TG GGTAGGAGG   TTTG
                                || |||||||||   ||||
                                AC CCATCCTTC   AAAC
                                 _       A___
GAM1052 C21orf67 5' CGATCCTCCCGCCTCA     54210       TA
                                TGAGG  GGAGGATTG
                                |||||  |||||||||
                                ACTCC  CCTCCTAGC
                                   GC
GAM1052 C22orf19 3' TCAGGTGATCCTCCTGCCTCA 13434          TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
                                ACTCCGTCCTCCTA  GGACT
                                      GT
GAM1052 C22orf19 3' TCGGGTGATCCTCCCACCTC  13437     A    TG
                                GAGGT GGAGGAT  TTTGA
                                ||||| |||||||  |||||
                                CTCCA CCTCCTA  GGGCT
                                   C      GT
GAM1052 C4orf6   5' CAGCCTCCTACCTCA      19239          A
                                TGAGGTAGGAGG TTG
                                |||||||||||| |||
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                                ACTCCATCCTCC GAC
                                           _
GAM1052  C6orf33   3'  TCAAGCAATCCTCCCACCTCA  55886       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCCTAACGAACT
                                    C
GAM1052  C6orf33   3'  TCAAGTGATCCGCCCACCTCA  55887       A  A    TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC CCTA  GAACT
                                    C  G    GT
GAM1052  CASP9     3'  AAGCTTTCCTGCCCCA      6924     A       ATT
                                TG GGTAGGAGG   GTTT
                                || |||||||||   ||||
                                AC CCGTCCTTT   CGAA
                                 C       ____
GAM1052  CHL1      3'  TCAAGATTGCTCCTACTCA   21751      G     GATTG
                                TGAG TAGGAG    TTTGA
                                |||| ||||||    |||||
                                ACTC ATCCTC    GAACT
                                   _     GTTA_
GAM1052  CHRAC1    3'  CAAACTCCTAACCTCA      33866       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                    A    A_
GAM1052  CLDN1     3'  TGATCTTCCCACCTCA      40851       A
                                TGAGGT GGAGGATTG
                                |||||| |||||||||
                                ACTCCA CCTTCTAGT
                                    C
GAM1052  CNOT3     5'  CAGTCCCACCTACCTCA     27217         A_
                                TGAGGTAGG  GGATTG
                                |||||||||  ||||||
                                ACTCCATCC  CCTGAC
                                      AC
GAM1052  COLEC12   3'  TCAAGCAACCCTCCTGCCTCA  47872           A
                                TGAGGTAGGAGG TTGTTTGA
                                |||||||||||| ||||||||
                                ACTCCGTCCTCC AACGAACT
                                      C
GAM1052  COQ7      3'  TCAAGCAATCCACCCACCTCA  32334       A  A
                                TGAGGT GG GGATTGTTTGA
                                |||||| || ||||||||||
                                ACTCCA CC CCTAACGAACT
                                    C  A
GAM1052  CPSF2     3'  CAAACTCCCGACCTCA      61571       AGGA   TT
                                TGAGGT    GGA  GTTTG
                                ||||||    |||  |||||
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                                ACTCCA   CCT  CAAAC
                                   GC__  __
GAM1052  CPSF2    3'  CAAACTCCTGACCTCA     61572       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  CPSF2    3'  TCAAGTGATTCTCCCACCTCA  61597       A     TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
                                ACTCCA CCTCTTA  GAACT
                                   C      GT
GAM1052  DAPK2    3'  CATGCTCCCTCTACCTCA    26737        GA   TT  T
                                TGAGGTAG  GGA  GT TG
                                ||||||||  |||  || ||
                                ACTCCATC  CCT  CG AC
                                     TC  __  T
GAM1052  DCOHM    3'  TCAAGTGATCCTCCCACCTTA  49610       A     TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
                                ATTCCA CCTCCTA  GAACT
                                   C      GT
GAM1052  DKFZp434A2417 3'  CAAACTCCCAACCTCA      66096       A  A  ATT
                                TGAGGT GG GG   GTTTG
                                |||||| || ||   |||||
                                ACTCCA CC CT   CAAAC
                                   A  _  ____
GAM1052  DKFZp434C0923 3'  TCAAGCAATTCTCCCACCTCA  34220       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCTTAACGAACT
                                   C
GAM1052  DKFZp434C0923 3'  TCAAGCGATCCTCCCACCTCA  34221       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| |||||||||||||
                                ACTCCA CCTCCTAGCGAACT
                                   C
GAM1052  DKFZp434F142 3'  CAGCCTCTACCTCA       50018        G   A
                                TGAGGTAG AGG TTG
                                |||||||| ||| |||
                                ACTCCATC TCC GAC
                                     _  _
GAM1052  DKFZP434J037 3'  CAAACTCCCGACCTCA      48205       AGGA   TT
                                TGAGGT    GGA  GTTTG
                                ||||||    |||  |||||
                                ACTCCA    CCT  CAAAC
                                   GC__   __
GAM1052  DKFZP566I1024 3'  CAAGCAATTCTCCCACCTCA   70098       A
                                TGAGGT GGAGGATTGTTTG
                                |||||| |||||||||||||
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                                ACTCCA CCTCTTAACGAAC
                                   C
GAM1052  DKFZP566I1024 3'  TCAAGCGATCCTCCCACCTC   70106      A
                                GAGGT GGAGGATTGTTTGA
                                ||||| |||||||||||||
                                CTCCA CCTCCTAGCGAACT
                                   C
GAM1052  DORFIN    5'  TCAAGCAACCCTGCCACCTCA  31262      A _  A
                                TGAGGT GG AGG TTGTTTGA
                                |||||| || ||| ||||||||
                                ACTCCA CC TCC AACGAACT
                                   _ G  C
GAM1052  DRG1      3'  CAAGCACCCTACCCCA      14732    A    AGGAT
                                TG GGTAGG    TGTTTG
                                || ||||||    ||||||
                                AC CCATCC    ACGAAC
                                 C    C____
GAM1052  DRIM      3'  TCAAGTGATCCTCTCACCTCA  27181      AG    TG
                                TGAGGT  GAGGAT  TTTGA
                                ||||||  ||||||  |||||
                                ACTCCA  CTCCTA  GAACT
                                   CT     GT
GAM1052  EREG      3'  TCAAGAGATCCTCCTGCCTCA  7511           G
                                TGAGGTAGGAGGATT TTTGA
                                |||||||||||||| |||||
                                ACTCCGTCCTCCTAG GAACT
                                      A
GAM1052  ERO1L     3'  TGATCTTCCCACCTCA      27433      A
                                TGAGGT GGAGGATTG
                                |||||| |||||||||
                                ACTCCA CCTTCTAGT
                                   C
GAM1052  EVI5      3'  TCAAGTGGTCCTCCTGCCTCA  19010          TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
                                ACTCCGTCCTCCTG  GAACT
                                      GT
GAM1052  FBP17     3'  CAAACTCCTGACCTCA      72781      _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  FLB6421   3'  TCAAGTGATCCTCCTACCTCA  39232          TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
                                ACTCCATCCTCCTA  GAACT
                                      GT
GAM1052  FLJ10297  3'  TCAAGTGATCCTCCTGCCTCA  35984          TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
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                                ACTCCGTCCTCCTA  GAACT
                                      GT
GAM1052  FLJ10307  3'  CAGTGTACCTCCTACCTCA   36005          ___
                                TGAGGTAGGAGG  ATTG
                                ||||||||||||  ||||
                                ACTCCATCCTCC  TGAC
                                      ATG
GAM1052  FLJ10520  3'  TCAAGCAATCCTCCCACCTCA  36215      A
                                TGAGGT GGAGGATTGTTTGA
                                ||||||| ||||||||||||||
                                ACTCCA CCTCCTAACGAACT
                                   C
GAM1052  FLJ10581  3'  GCAGCTCCTCCTACACCA    36304    AG      _
                                TG  GTAGGAGGA TTGT
                                ||  ||||||||| ||||
                                AC  CATCCTCCT GACG
                                 CA       C
GAM1052  FLJ10607  3'  CATCCCTCCTGCCTCA      77107          AT
                                TGAGGTAGGAGG  TG
                                ||||||||||||  ||
                                ACTCCGTCCTCC  AC
                                      CT
GAM1052  FLJ10607  3'  TCAAATGATCCTTCCACCTCA  77126      A     TG
                                TGAGGT GGAGGAT  TTTGA
                                ||||||| |||||||  |||||
                                ACTCCA CTTCCTA  AAACT
                                   C      GT
GAM1052  FLJ10607  3'  TCAAGTGATCCTCCCACCTCA  77127      A     TG
                                TGAGGT GGAGGAT  TTTGA
                                ||||||| |||||||  |||||
                                ACTCCA CCTCCTA  GAACT
                                   C      GT
GAM1052  FLJ10687  3'  TCAAGGATCCTCCTGCCTCA   36411          G
                                TGAGGTAGGAGGATT TTTGA
                                ||||||||||||||| |||||
                                ACTCCGTCCTCCTAG GAACT
                                                _
GAM1052  FLJ10713  3'  TCAAATGATTCTCCTGCCTCA  36472          TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
                                ACTCCGTCCTCTTA  AAACT
                                      GT
GAM1052  FLJ10847  3'  TCAAGTGATCCTCCCACCTCA  36757      A     TG
                                TGAGGT GGAGGAT  TTTGA
                                ||||||| |||||||  |||||
                                ACTCCA CCTCCTA  GAACT
                                   C      GT
GAM1052  FLJ10925  5'  CGGGCCCTGCTACCTCA     36884       G   ATT
                                TGAGGTAG AGG   GTTTG
                                |||||||| |||   |||||
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                                ACTCCATC TCC   CGGGC
                                    G  ___
GAM1052  FLJ10956  3'  TCAAGCAATTCTCCTACCTCA  36918
                                TGAGGTAGGAGGATTGTTTGA
                                ||||||||||||||||||||
                                ACTCCATCCTCTTAACGAACT

GAM1052  FLJ11560  3'  TCTGACCCACCTACCTCA    47222        A  ATT   T
                                TGAGGTAGG GG   GTT GA
                                |||||||| ||   ||| ||
                                ACTCCATCC CC   CAG CT
                                    A  ___   T
GAM1052  FLJ11715  3'  CGGTCCTCATACCCCA     44670    A   G
                                TG GGTA GAGGATTG
                                || |||| ||||||||
                                AC CCAT CTCCTGGC
                                 C   A
GAM1052  FLJ11800  3'  TCAAGCGATCCTCCCACTTCA  46431       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTTCA CCTCCTAGCGAACT
                                    C
GAM1052  FLJ12363  3'  CAAACTCCTGACCTCA     49672       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                    G    A_
GAM1052  FLJ12610  3'  CAATCCTCCCGCCTCA     45510      TA
                                TGAGG  GGAGGATTG
                                |||||  |||||||||
                                ACTCC  CCTCCTAAC
                                   GC
GAM1052  FLJ12687  3'  CAAACTCCTGACCTCA     46186       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                    G    A_
GAM1052  FLJ12975  3'  CAAGCAATCCTCCCACCTCA   69576       A
                                TGAGGT GGAGGATTGTTTG
                                |||||| |||||||||||||
                                ACTCCA CCTCCTAACGAAC
                                    C
GAM1052  FLJ13072  5'  TCAGGTAATCCTCCCACCTCA  89828       A       TT
                                TGAGGT GGAGGATTG  TGA
                                |||||| |||||||||  |||
                                ACTCCA CCTCCTAAT  ACT
                                    C        GG
GAM1052  FLJ13162  3'  CAGGCAGTCCCTCCTGCCTCA  46552           _
                                TGAGGTAGGAGG ATTGTTTG
                                |||||||||||| ||||||||
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                                ACTCCGTCCTCC TGACGGAC
                                      C
GAM1052  FLJ14345  5'  GCACCCTCCACCTCA      45336       A    AT
                                TGAGGT GGAGG  TGT
                                |||||| |||||  |||
                                ACTCCA CCTCC  ACG
                                   _    C_
GAM1052  FLJ14351  3'  TCAAGCAATCCTCCCACCTCA  45329       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCCTAACGAACT
                                   C
GAM1052  FLJ14351  3'  TCAAGCAATCCTCCTGCCTCA  45330
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAACGAACT

GAM1052  FLJ20034  3'  CAAACTCCCGACCTCA      34358       AGGA   TT
                                TGAGGT    GGA  GTTTG
                                ||||||    |||  |||||
                                ACTCCA    CCT  CAAAC
                                   GC__   __
GAM1052  FLJ20045  3'  TCAGGCAATTCTCCCACCTCA  34430       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCTTAACGGACT
                                   C
GAM1052  FLJ20200  5'  CAGTCCTCCCACCCG       34728    A  A
                                TG GGT GGAGGATTG
                                || ||| |||||||||
                                GC CCA CCTCCTGAC
                                 _  C
GAM1052  FLJ20254  3'  CAGCCTCCTACCCA        34787    A       A
                                TG GGTAGGAGG TTG
                                || ||||||||| |||
                                AC CCATCCTCC GAC
                                 _       _
GAM1052  FLJ20254  3'  CAGTTGCCTCCACCTCA     34788       A    ATTGT
                                TGAGGT GGAGG    TTG
                                |||||| |||||    |||
                                ACTCCA CCTCC    GAC
                                   _    GTT__
GAM1052  FLJ20342  3'  TCAAACGATTCTCCTACCTCA  34992
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCATCCTCTTAGCAAACT

GAM1052  FLJ20729  3'  TCAAGCAATCCTTCCACCTCA  35651       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
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                                ACTCCA CTTCCTAACGAACT
                                   C
GAM1052  FLJ21324  5' CAAACTCCTGACCTCA     91190       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  FLJ21438  3' AAGCACCCTGCCTCA      61516        AGGAT
                                TGAGGTAGG    TGTTT
                                |||||||||    |||||
                                ACTCCGTCC    ACGAA
                                     C____
GAM1052  FLJ22684  3' CAAACTCCTGACCTCA     46787       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  FLJ22969  3' TCAAGCAATTCTCCCACCTCA  68660       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCTTAACGAACT
                                   C
GAM1052  FLJ23047  3' TCAAGTGATCTCCCACTTCA   44628       A  AG   TG
                                TGAGGT GG  GAT  TTTGA
                                |||||| ||  |||  |||||
                                ACTTCA CC  CTA  GAACT
                                   _ CT   GT
GAM1052  FLJ23185  3' CAAGTGATCCTCCCACCTC    46826      A      TG
                                GAGGT GGAGGAT  TTTG
                                ||||| |||||||  ||||
                                CTCCA CCTCCTA  GAAC
                                   C      GT
GAM1052  FLJ23356  3' TCAAGCAATTCTCCCACCTCA  49943       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCTTAACGAACT
                                   C
GAM1052  FLJ23563  3' TCAGGTGATCCTCCCACCTC   67601      A      TG
                                GAGGT GGAGGAT  TTTGA
                                ||||| |||||||  |||||
                                CTCCA CCTCCTA  GGACT
                                   C      GT
GAM1052  FLJ30532  3' CAAGCTCCTGACCTCA     58542       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    G_
GAM1052  FLJ31101  3' TCAAATGATTCTCCTGCCTCA  35716           TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
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                                ACTCCGTCCTCTTA  AAACT
                                      GT
GAM1052  FLJ32865  3'  CAAACCCCTGACCTCA      58167       A  A  ATT
                                TGAGGT GG GG   GTTTG
                                |||||| || ||   |||||
                                ACTCCA TC CC   CAAAC
                                   G  _  ___
GAM1052  GAB3      3'  CATTCCTCTACCTCA       54626        G    T
                                TGAGGTAG AGGA TG
                                |||||||| |||| ||
                                ACTCCATC TCCT AC
                                     _    T
GAM1052  GCHFR     3'  CAAGCTCCTGCCTCA       17921          GA
                                TGAGGTAGGAG  TTG
                                ||||||||||  |||
                                ACTCCGTCCTC  AAC
                                      G_
GAM1052  H2AV      3'  CAAACTCCTGACCTCA      56844        _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  HIC2      3'  AACTTTCCCCACCTCA      65254       A  A   TT
                                TGAGGT GG GGA  GTT
                                |||||| || |||  |||
                                ACTCCA CC CCT  CAA
                                   _  _   TT
GAM1052  HSPC065   3'  TCAAGCAATTCTCCCACCTCA  26321       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCTTAACGAACT
                                   C
GAM1052  HSPC065   3'  TCAAGCGATTCTCCTACCTCA  26322
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCATCCTCTTAGCGAACT

GAM1052  HTMP10    3'  ACCTTCCTCCTACCTC      52603          TT
                                GAGGTAGGAGGA  GT
                                ||||||||||||  ||
                                CTCCATCCTCCT  CA
                                      TC
GAM1052  KIAA0022  3'  CAAACTCCTGACCTCA      29660       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  KIAA0063  3'  CAAACTCCCGACCTCA      29617       AGGA   TT
                                TGAGGT   GGA  GTTTG
                                ||||||   |||  |||||
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                                ACTCCA   CCT  CAAAC
                                   GC__  __
GAM1052  KIAA0063  3'  TCAACCCGCCCCTACCTC    29640        A  ATT   T
                                GAGGTAGG GG   GTT GA
                                |||||||| ||   ||| ||
                                CTCCATCC CC   CAA CT
                                     _  GCC  _
GAM1052  KIAA0161  3'  CAAACTCCTGACCTCA      28498       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  KIAA0186  3'  CAAACTCCTGACCTCA      40744       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  KIAA0186  3'  TCAAGCAGTCCTCCCACCTTA  40764       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ATTCCA CCTCCTGACGAACT
                                   C
GAM1052  KIAA0210  5'  TCAAACACTTCTCCTGCCTCA  28484           T
                                TGAGGTAGGAGGA TGTTTGA
                                |||||||||||| |||||||
                                ACTCCGTCCTCTT ACAAACT
                                      C
GAM1052  KIAA0370  3'  TCAAGCCTCCCCCGCCCCA    73210    A  TA  A   TT
                                TG GG  GG GGA  GTTTGA
                                || ||  || |||  ||||||
                                AC CC  CC CCT  CGAACT
                                 C  GC  _   C_
GAM1052  KIAA0379  3'  CAAGTGACTCTACCTCA      68146        G  GA TG
                                TGAGGTAG AG  T  TTTG
                                |||||||| ||  |  ||||
                                ACTCCATC TC  A  GAAC
                                     _  ___ GT
GAM1052  KIAA0391  3'  CAAACTCCTGACCTCA      27905       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  KIAA0418  5'  TCAAGCAATCCTCCCACTTCA  27564       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTTCA CCTCCTAACGAACT
                                   C
GAM1052  KIAA0426  3'  TCAAACCTAAGATCCTACCTTA 28263          GGATT_
                                TGAGGTAGGA     GTTTGA
                                ||||||||||     ||||||
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                                ATTCCATCCT     CAAACT
                                      AGAATC
GAM1052 KIAA0441 3' TCAAGCAACCCTCCCACCTTA 28961       A    A
                                TGAGGT GGAGG TTGTTTGA
                                |||||| ||||| ||||||||
                                ATTCCA CCTCC AACGAACT
                                   C    C
GAM1052 KIAA0445 5' CAAACTCCTGCCTCA       27949          GA
                                TGAGGTAGGAG  TTG
                                ||||||||||  |||
                                ACTCCGTCCTC  AAC
                                      A_
GAM1052 KIAA0446 5' TCAGGTGATCCTCCCACCTCA 68879       A      TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
                                ACTCCA CCTCCTA  GGACT
                                   C      GT
GAM1052 KIAA0447 3' TCAAATGATCCTCCCACCTCA 71677       A      TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
                                ACTCCA CCTCCTA  AAACT
                                   C      GT
GAM1052 KIAA0469 3' GCAGTCCTCCCACCGCA     29333    A  A
                                TG GGT GGAGGATTGT
                                || ||| ||||||||||
                                AC CCA CCTCCTGACG
                                 G  C
GAM1052 KIAA0472 5' TCAAACGATCTGCCCACCCCA 71870    A  A A
                                TG GGT GG GGATTGTTTGA
                                || ||| || ||||||||||
                                AC CCA CC TCTAGCAAACT
                                 C  C  G
GAM1052 KIAA0493 5' TCAAGCAATCTTCCCACCTCA 64282       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTTCTAACGAACT
                                   C
GAM1052 KIAA0513 3' TCAGGTGATCCCCCCCACCTC 28375      A A_   TG
                                GAGGT GG  GGAT  TTTGA
                                ||||| ||  ||||  |||||
                                CTCCA CC  CCTA  GGACT
                                  C  CC    GT
GAM1052 KIAA0527 3' TCAAGAACTCCTGACCTCA   95807       _    GATTG
                                TGAGGT AGGAG    TTTGA
                                |||||| |||||    |||||
                                ACTCCA TCCTC    GAACT
                                   G    AA___
GAM1052 KIAA0532 3' TCAAGCAATCCTCCCACCTCA 70778       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
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                                ACTCCA CCTCCTAACGAACT
                                    C
GAM1052  KIAA0557  3'  TCAAGTGTTCCTCCTGCCTCA  78007          T GT
                                TGAGGTAGGAGGA T  TTGA
                                |||||||||||| |  ||||
                                ACTCCGTCCTCCT G  AACT
                                     T TG
GAM1052  KIAA0638  3'  CAAAGATCCCCTCCTGCCTCA  72394          ATTG_
                                TGAGGTAGGAGG    TTTG
                                ||||||||||||    ||||
                                ACTCCGTCCTCC    AAAC
                                      CCTAG
GAM1052  KIAA0705  5'  CAAGCTCTCCTACCTC     24533          ATT
                                GAGGTAGGAGG   GTTTG
                                ||||||||||   |||||
                                CTCCATCCTCT   CGAAC

                                    ___
GAM1052  KIAA0720  3'  TCAAACGATTCTCCTGCCCCA  62328    A
                                TG GGTAGGAGGATTGTTTGA
                                || ||||||||||||||||||
                                AC CCGTCCTCTTAGCAAACT
                                 C
GAM1052  KIAA0828  3'  TCAAGCAATCCTCCTGCCTCA  81198
                                TGAGGTAGGAGGATTGTTTGA
                                ||||||||||||||||||||
                                ACTCCGTCCTCCTAACGAACT

GAM1052  KIAA1026  3'  TCAAACAATTCTCCTGCCTCA  71206
                                TGAGGTAGGAGGATTGTTTGA
                                ||||||||||||||||||||
                                ACTCCGTCCTCTTAACAAACT

GAM1052  KIAA1054  3'  TCAAGTGATTCTCCCACCTCA  68448      A      TG
                                TGAGGT GGAGGAT  TTTGA
                                ||||||| |||||||  |||||
                                ACTCCA CCTCTTA  GAACT
                                    C      GT
GAM1052  KIAA1143  3'  CAATCTCCTGACCTCA      68671      _    G
                                TGAGGT AGGAG ATTG
                                |||||| ||||| ||||
                                ACTCCA TCCTC TAAC
                                    G    _
GAM1052  KIAA1145  3'  TCAAGGGATCCTCCCACCTCA  65627      A      G
                                TGAGGT GGAGGATT TTTGA
                                |||||| |||||||| |||||
                                ACTCCA CCTCCTAG GAACT
                                    C       G
GAM1052  KIAA1170  3'  CAAACTCCTGACCTCA      69844      _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
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                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  KIAA1198  3'  AAGCAATCCTGCCTCA     63278       AGG
                                TGAGGT   AGGATTGTTT
                                ||||||   ||||||||||
                                ACTCCG   TCCTAACGAA
                                  ___
GAM1052  KIAA1198  3'  CAAACTCCTGACCTCA     63289       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  KIAA1280  5'  TCAAGTGACCCTCCTGCCTCA  69730          A TG
                                TGAGGTAGGAGG T  TTTGA
                                |||||||||||| |  |||||
                                ACTCCGTCCTCC A  GAACT
                                      C GT
GAM1052  KIAA1297  3'  TGACTCTCCTACCTCA     72189          GA
                                TGAGGTAGGAG  TTG
                                ||||||||||  |||
                                ACTCCATCCTC  AGT
                                      TC
GAM1052  KIAA1396  3'  TCAAGTGACCCTCCCACCTCA  62993       A    A TG
                                TGAGGT GGAGG T  TTTGA
                                |||||| ||||| |  |||||
                                ACTCCA CCTCC A  GAACT
                                   C    C GT
GAM1052  KIAA1493  3'  CAAACTCCTGACCTCA     64155       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  KIAA1615  3'  CAAACTCCCGACCTCA     68699       AGGA   TT
                                TGAGGT    GGA  GTTTG
                                ||||||    |||  |||||
                                ACTCCA    CCT  CAAAC
                                   GC__   __
GAM1052  KIAA1649  3'  TCAAGTGATCCTCCCACCTCA  50279       A      TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
                                ACTCCA CCTCCTA  GAACT
                                   C      GT
GAM1052  KIAA1656  5'  CAGGCCTCCTAGCTCA     65783     G      A
                                TGAG TAGGAGG TTG
                                |||| ||||||| |||
                                ACTC ATCCTCC GAC
                                  G      G
GAM1052  KIAA1671  3'  TCAAGTGATTCTCCCACCTCA  65691       A      TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
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                                ACTCCA CCTCTTA  GAACT
                                   C      GT
GAM1052  KIAA1712  3'  CAAACTCCTGACCTCA      67531       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  KIAA1727  3'  CAAGTGATCCTCCCACCTCA   64054       A      TG
                                TGAGGT GGAGGAT  TTTG
                                |||||| |||||||  ||||
                                ACTCCA CCTCCTA  GAAC
                                   C      GT
GAM1052  KIAA1727  3'  TCAAGTGATCCTCCCACCTCA  64065       A      TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
                                ACTCCA CCTCCTA  GAACT
                                   C      GT
GAM1052  KIAA1751  3'  TCAAGCAATCCTCCTGCCTCA  71705
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAACGAACT

GAM1052  KIAA1755  3'  TCAACCAATCCTCCCACCTCA  61354       A       T
                                TGAGGT GGAGGATTG TTGA
                                |||||| ||||||||| ||||
                                ACTCCA CCTCCTAAC AACT
                                   C        C
GAM1052  KIAA1762  3'  TGATCCTCCTCCTCA       63794       T
                                TGAGG AGGAGGATTG
                                ||||| ||||||||||
                                ACTCC TCCTCCTAGT
                                  _
GAM1052  KIAA1821  3'  TCAAGTGATCCTCCCACCTCA  71796       A      TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
                                ACTCCA CCTCCTA  GAACT
                                   C      GT
GAM1052  KIAA1829  3'  TCAAGCAATCCTCCTGCCTCA  61954
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAACGAACT

GAM1052  KIAA1829  3'  TCAAGCGACCCTCCCACCTCA  61955       A    A
                                TGAGGT GGAGG TTGTTTGA
                                |||||| ||||| ||||||||
                                ACTCCA CCTCC AGCGAACT
                                   C    C
GAM1052  KIAA1924  3'  TCAAGCAGTCCTCCCACCTCA  73687       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
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                                ACTCCA CCTCCTGACGAACT
                                   C
GAM1052 KRTHA3B  3' TGATCCTCCTCACCCCA    9646    A  _
                                TG GGT AGGAGGATTG
                                || ||| ||||||||||
                                AC CCA TCCTCCTAGT
                                 C  C
GAM1052 LAMP3    3' TCAAACAATGTAAACCACC   59494    A AGG__
                                GGT GG    ATTGTTTGA
                                ||| ||    |||||||||
                                CCA CC    TAACAAACT
                                  _ AAATG
GAM1052 LAMP3    3' TCAGGTGATCCACCCACCTCA 59496      A A   TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC CCTA  GGACT
                                   C  A   GT
GAM1052 LIECG3   3' TCAAGTGACCCTCCCACCTCA 87412      A    A TG
                                TGAGGT GGAGG T  TTTGA
                                |||||| ||||| |  |||||
                                ACTCCA CCTCC A  GAACT
                                   C    C GT
GAM1052 LNIR     3' TCAAGCAATCCTCCTGCCTCA 48135
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAACGAACT

GAM1052 MAIL     3' TCAAGTGATCCTCCTACCT   48652          TG
                                AGGTAGGAGGAT  TTTGA
                                ||||||||||||  |||||
                                TCCATCCTCCTA  GAACT
                                       GT
GAM1052 MCM10    3' TCAAGCAGTCCTCCCACCTCA 37576      A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCCTGACGAACT
                                   C
GAM1052 MEF-2    3' TCAAACAATTCTCCTGCCTCA 64394
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCTTAACAAACT

GAM1052 MGC10200 3' TCAAACAATCCACCCTCCTCA 58992     TA  A
                                TGAGG  GG GGATTGTTTGA
                                |||||  || ||||||||||
                                ACTCC  CC CCTAACAAACT
                                   TC  A
GAM1052 MGC10200 3' TCAAGTGATCCTCCCACCTCA 58993      A     TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
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                                ACTCCA CCTCCTA  GAACT
                                   C      GT
GAM1052  MGC12466 3'  TCAAGCTATCCTCCTGCCTCA  79034          T
                                TGAGGTAGGAGGAT GTTTGA
                                ||||||||||||| ||||||
                                ACTCCGTCCTCCTA CGAACT
                                      T
GAM1052  MGC13061 3'  TCAAGCAGTCCTCCCACCTCA  50310       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCCTGACGAACT
                                   C
GAM1052  MGC13159 3'  TCAAGTGATCCTCCTGCCTCA  51931          TG
                                TGAGGTAGGAGGAT  TTTGA
                                |||||||||||||  |||||
                                ACTCCGTCCTCCTA  GAACT
                                      GT
GAM1052  MGC14289 3'  TCAAGTGATCATCCCACCTCA  54706       A  G  TG
                                TGAGGT GGA GAT  TTTGA
                                |||||| ||| |||  |||||
                                ACTCCA CCT CTA  GAACT
                                   C  A  GT
GAM1052  MGC15606 5'  TCAAGCAATTCTCCTACCTCA  58878
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCATCCTCTTAACGAACT

GAM1052  MGC1842  3'  TCAAGCGATCCTCCTGCCTCA  65658
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAGCGAACT

GAM1052  MGC2474  3'  TCAAGGAATCCTCCTGCCCCA  43729    A         G
                                TG GGTAGGAGGATT TTTGA
                                || |||||||||||| |||||
                                AC CCGTCCTCCTAA GAACT
                                  C          G
GAM1052  MGC2477  5'  CAAGCGATCCTCCTGCCTCA  44059
                                TGAGGTAGGAGGATTGTTTG
                                |||||||||||||||||||
                                ACTCCGTCCTCCTAGCGAAC

GAM1052  MGC2477  3'  CAGATTTCCTCCTACCT     44060          TT
                                AGGTAGGAGGA  GTTTG
                                ||||||||||  |||||
                                TCCATCCTCCT  TAGAC
                                      T_
GAM1052  MGC2488  3'  TCAAGTGATCCTCCTGCCTCA  43876          TG
                                TGAGGTAGGAGGAT  TTTGA
                                |||||||||||||  |||||
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                                ACTCCGTCCTCCTA  GAACT
                                       GT
GAM1052  MGC3113   3'  TCATGTGATCCTCCCACCTCA  43852       A      TG T
                                TGAGGT GGAGGAT  T TGA
                                |||||| |||||||  | |||
                                ACTCCA CCTCCTA  G ACT
                                   C      GT T
GAM1052  MISS      3'  CAAACAAATGATGCCTCA    58028       GGAGGA
                                TGAGGTA     TTGTTTG
                                |||||||     |||||||
                                ACTCCGT     AACAAAC
                                   AGTA__
GAM1052  MOST2     5'  CAGCTCCCCACCTCA       39677       A  A  _
                                TGAGGT GG GGA TTG
                                |||||| || ||| |||
                                ACTCCA CC CCT GAC
                                   _ _  C
GAM1052  MRPL35    3'  TCAAGTGGTCCTCCTGCCTCA  33544           TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
                                ACTCCGTCCTCCTG  GAACT
                                       GT
GAM1052  MRPS27    3'  CAACCTCCTGACCTCA      30634       _     A
                                TGAGGT AGGAGG TTG
                                |||||| |||||| |||
                                ACTCCA TCCTCC AAC
                                   G    _
GAM1052  MYO5C     3'  TCAAACAATTCTCCTGCCTCA  38110
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCTTAACAAACT

GAM1052  OS4       3'  AAAGGAGCCCCACCTCA     19173       A  A  A  G
                                TGAGGT GG GG TT TTT
                                |||||| || || || |||
                                ACTCCA CC CC AG AAA
                                   _ _  G  G
GAM1052  OSBPL2    3'  CAAACTCCCGACCTCA      57853       AGGA   TT
                                TGAGGT   GGA  GTTTG
                                ||||||   |||  |||||
                                ACTCCA   CCT  CAAAC
                                   GC__  __
GAM1052  OSBPL2    3'  CAAACTCCCGACCTCA      29202       AGGA   TT
                                TGAGGT   GGA  GTTTG
                                ||||||   |||  |||||
                                ACTCCA   CCT  CAAAC
                                   GC__  __
GAM1052  PELI1     5'  CAAACTCCCAACCTCA      40254       A  A  ATT
                                TGAGGT GG GG   GTTTG
                                |||||| || ||   |||||
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                                ACTCCA CC CT   CAAAC
                                   A  _ ____
GAM1052  PELI1    5'  TCAAGTGATCCTCCTGCCTCA  40282            TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
                                ACTCCGTCCTCCTA  GAACT
                                      GT
GAM1052  PIP3-E   3'  CAAACTCCTGACCTCA      66798       _    GA
                                TGAGGT AGGAG  TTG
                                ||||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  PPIL2    3'  TCAAGCAATCCTCCTGCCTCA  26768
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAACGAACT

GAM1052  PRO0611  3'  TGATCCTCCCACCCA       26014    A  A
                                TG GGT GGAGGATTG
                                || ||| |||||||||
                                AC CCA CCTCCTAGT
                                  _  C
GAM1052  PRO0899  5'  CAAGAGATCCTCCCACCTC   37693      A      G
                                GAGGT GGAGGATT TTTG
                                ||||| |||||||| ||||
                                CTCCA CCTCCTAG GAAC
                                   C       A
GAM1052  PRO1048  3'  TCAAGCGATCCTCCTGCCTCA  37524
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAGCGAACT

GAM1052  PRO2955  3'  CAAACTCCTGACCTCA      37631       _    GA
                                TGAGGT AGGAG  TTG
                                ||||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  PSTPIP2  3'  CAAACTCCTGACCTCA      44382       _    GA
                                TGAGGT AGGAG  TTG
                                ||||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  PTD002   3'  ACGCTCCTGCCACCTCA     32345       A  _   T
                                TGAGGT GG AGGA TGT
                                ||||||| || |||| |||
                                ACTCCA CC TCCT GCA
                                   _ G   C
GAM1052  RAB33B   3'  TCAAGCAATCCTCCCACCTCA  48505       A
                                TGAGGT GGAGGATTGTTTGA
                                ||||||| ||||||||||||||
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                                ACTCCA CCTCCTAACGAACT
                                   C
GAM1052 RAB40A   5' CAAAGCCACCACCTCA     82068       A  A  ATTG
                                TGAGGT GG GG    TTTG
                                |||||| || ||    ||||
                                ACTCCA CC CC    AAAC
                                   _  A  G___
GAM1052 RPS6KB1  3' TCAATTTGCCTCCCTACCTCA  60977         _  ATTGT
                                TGAGGTAGG AGG    TTGA
                                ||||||||| |||    ||||
                                ACTCCATCC TCC    AACT
                                     C   GTTT_
GAM1052 SAMHD1   3' TCAAGCGACCCTCCTGCCTCA  61320          A
                                TGAGGTAGGAGG TTGTTTGA
                                |||||||||||| ||||||||
                                ACTCCGTCCTCC AGCGAACT
                                      C
GAM1052 SARM     3' TCAAGTGATCCTCCTGCCTCA  30617           TG
                                TGAGGTAGGAGGAT  TTTGA
                                |||||||||||||  |||||
                                ACTCCGTCCTCCTA  GAACT
                                       GT
GAM1052 SARM     3' TCAAGTGGTCCTCCTGCCTCA  30618           TG
                                TGAGGTAGGAGGAT  TTTGA
                                |||||||||||||  |||||
                                ACTCCGTCCTCCTG  GAACT
                                       GT
GAM1052 SCAM-1   3' ACATCCTCCTTCCCCA      19323    A  T      T
                                TG GG AGGAGGAT GT
                                || || |||||||| ||
                                AC CC TCCTCCTA CA
                                 C  T      _
GAM1052 SCYA16   3' TCAAGTGATCCTCCCACCCCA  15966    A   A     TG
                                TG GGT GGAGGAT  TTTGA
                                || ||| |||||||  |||||
                                AC CCA CCTCCTA  GAACT
                                 C   C      GT
GAM1052 SCYA22   3' TCAAGCGATTCTCCCACCCCA  90955    A   A
                                TG GGT GGAGGATTGTTTGA
                                || ||| ||||||||||||||
                                AC CCA CCTCTTAGCGAACT
                                 C   C
GAM1052 SCYA22   3' TCAGGTAATCCGCCCACCTCA  90958       A  A     TT
                                TGAGGT GG GGATTG  TGA
                                |||||| || ||||||  |||
                                ACTCCA CC CCTAAT  ACT
                                   C  G     GG
GAM1052 SERF2    5' TCAAGCAATCCTCCCATCTCA  19309       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
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                                ACTCTA CCTCCTAACGAACT
                                   C
GAM1052 SLC16A6  5' TCAAGCAATCCTCCCACCTCA 16275      A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCCTAACGAACT
                                   C
GAM1052 SLC2A10  3' TCAAGTGATCCACCCACCTCA 47825      A A   TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC CCTA  GAACT
                                   C A   GT
GAM1052 SMC1L1   3' AACCTTCCCCCTACCTC     71956       A  TT
                                GAGGTAGG GGA  GTT
                                |||||||| |||  |||
                                CTCCATCC CCT  CAA
                                     C  TC
GAM1052 SNAPC1   3' TCAAGCTATCCTCCTGCCTCA 11844           T
                                TGAGGTAGGAGGAT GTTTGA
                                |||||||||||||| ||||||
                                ACTCCGTCCTCCTA CGAACT
                                         T
GAM1052 STAF65(gamma) 3' CAAAACTCCTGACCTCA     29426       _   GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    AA
GAM1052 STX12    3' TCAAAGGGCTGCCCCCTACCTT 66354        A  AT__ G
            A                    TGAGGTAGG GG   T TTTGA
                                |||||||||  ||   | |||||
                                ATTCCATCC CC   G AAACT
                                     C  GTCG G
GAM1052 SYTL4    5' TCAAGAGATCCTCCTGCCTCA  54944           G
                                TGAGGTAGGAGGATT TTTGA
                                |||||||||||||| |||||
                                ACTCCGTCCTCCTAG GAACT
                                         A
GAM1052 TCL6     5' TCAAGAGATCCTCCCACTTCA  40146      A      G
                                TGAGGT GGAGGATT TTTGA
                                |||||| |||||||| |||||
                                ACTTCA CCTCCTAG GAACT
                                   C       A
GAM1052 TCL6     5' TCAAGAGATCCTCCCACTTCA  40162      A      G
                                TGAGGT GGAGGATT TTTGA
                                |||||| |||||||| |||||
                                ACTTCA CCTCCTAG GAACT
                                   C       A
GAM1052 TRIM6    3' TCAAGCGAACCTCCTGCCTCA  54143          A
                                TGAGGTAGGAGG TTGTTTGA
                                ||||||||||| ||||||||
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                                ACTCCGTCCTCC AGCGAACT
                                      A
GAM1052  TUCAN    3'  TCAAGTGATCCACCCACCTCA  30280       A  A    TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC CCTA  GAACT
                                   C  A    GT
GAM1052  TXNL2    3'  CAAGCGATCCTCCTGCCTCA  21549
                                TGAGGTAGGAGGATTGTTTG
                                ||||||||||||||||||||
                                ACTCCGTCCTCCTAGCGAAC

GAM1052  UBF-fl   3'  CAAACTCCTGACCTCA      51552       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  USP22    3'  CAAACTCCTGACCTCA      68005       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  USP22    3'  TCAGGCGATCCACCCACCTCA  68025       A  A
                                TGAGGT GG GGATTGTTTGA
                                |||||| || ||||||||||
                                ACTCCA CC CCTAGCGGACT
                                   C  A
GAM1052  VDU1     3'  CAAACTCCTGACCTCA      30413       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  VMP      3'  TCAAGCGATCCTCCCACCTCA  54902       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCCTAGCGAACT
                                   C
GAM1052  VPS33A   3'  CAAACTCCTGACCTCA      43333       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  WBSCR23  3'  CAAACTCCTGACCTCA      46754       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  ZNF17    3'  CAAACTCCCGACCTCA      82387       AGGA  TT
                                TGAGGT   GGA  GTTTG
                                ||||||   |||  |||||
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                                ACTCCA   CCT  CAAAC
                                   GC__  __
GAM1052  ZNF177   5'  TCAAGTGATCCTCCTGCCTCA  12902          TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
                                ACTCCGTCCTCCTA  GAACT
                                      GT
GAM1052  ZNF323   3'  TCAAATCTTTCCTCCCC    48082    TA    TT_
                                GG  GGAGGA   GTTTGA
                                ||  ||||||   ||||||
                                CC  CCTCCT   TAAACT
                                 __     TTC
GAM1052  ZNF338   3'  TCAAGTGATCTGCCCACCTCA  42015      A  A   TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC TCTA  GAACT
                                   C  G   GT
GAM1052  LOC113026 3'  TCAAGTGATCCTCCTGCCCCA  55907    A        TG
                                TG GGTAGGAGGAT  TTTGA
                                || ||||||||||  |||||
                                AC CCGTCCTCCTA  GAACT
                                 C         GT
GAM1052  LOC115098 5'  TCAAGCAATCCTCCTGCCTCA  56594
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAACGAACT

GAM1052  LOC115196 3'  TCAAGTAATCCTCCCACCCCA  73266    A  A
                                TG GGT GGAGGATTGTTTGA
                                || ||| ||||||||||||||
                                AC CCA CCTCCTAATGAACT
                                 C  C
GAM1052  LOC115219 5'  TCAAACAATTCTCCTGCCTCA  73318
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCTTAACAAACT

GAM1052  LOC125144 3'  TCAGATGGTCCTCCTGCCTCA  74394          TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
                                ACTCCGTCCTCCTG  AGACT
                                      GT
GAM1052  LOC126661 3'  CAATCCTCCCACCTTA      74544       A
                                TGAGGT GGAGGATTG
                                |||||| |||||||||
                                ATTCCA CCTCCTAAC
                                   C
GAM1052  LOC126669 3'  CAAACTCCTGACCTCA      75398       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
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                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  LOC126669 3'  TCAAATGATCCACCCACCTCA  75418      A  A   TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC CCTA  AAACT
                                   C  A   GT
GAM1052  LOC130639 5'  TCAAGTGATCCTCCCACCTCA  74977      A     TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
                                ACTCCA CCTCCTA  GAACT
                                   C      GT
GAM1052  LOC130813 3'  TCAAGCAATCCTCCCACCTCA  75775      A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCCTAACGAACT
                                   C
GAM1052  LOC132946 3'  CAAAGGTTTCCACCTCA     75072      A    ATTG
                                TGAGGT GGAGG   TTTG
                                |||||| |||||   ||||
                                ACTCCA CCTTT   AAAC
                                   _   GG__
GAM1052  LOC134266 3'  TCAAGTGATCCTCCCACCTCA  75169      A     TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
                                ACTCCA CCTCCTA  GAACT
                                   C      GT
GAM1052  LOC135293 3'  TCAAGCAGTCCTCCCACCTCA  76190      A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| |||||||||||||
                                ACTCCA CCTCCTGACGAACT
                                   C
GAM1052  LOC135398 3'  TGATCCTCCCACCTCA      75938      A
                                TGAGGT GGAGGATTG
                                |||||| |||||||||
                                ACTCCA CCTCCTAGT
                                   C
GAM1052  LOC139422 5'  TCAAGCAATCCTCCCACCTCA  75846      A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| |||||||||||||
                                ACTCCA CCTCCTAACGAACT
                                   C
GAM1052  LOC144305 3'  TGATCCTCCCACCTCA      83040      A
                                TGAGGT GGAGGATTG
                                |||||| |||||||||
                                ACTCCA CCTCCTAGT
                                   C
GAM1052  LOC144519 5'  TCAGGTGATCCTCCTGCCTCA  76874          TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
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                                ACTCCGTCCTCCTA  GGACT
                                       GT
GAM1052  LOC144667 3'  TCAAGCGATCCTCCCAGCTCA  83173     GTA
                                TGAG   GGAGGATTGTTTGA
                                ||||   ||||||||||||||
                                ACTC   CCTCCTAGCGAACT
                                  GAC
GAM1052  LOC145082 5'  TCAAATCATCCTCCTGCCTCA  83248           T
                                TGAGGTAGGAGGAT GTTTGA
                                |||||||||||||| ||||||
                                ACTCCGTCCTCCTA TAAACT
                                       C
GAM1052  LOC145268 5'  TCGGGTGATCCACCCACCTCA  77063      A  A    TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC CCTA  GGGCT
                                    C  A    GT
GAM1052  LOC145453 5'  CAAACTCCTGACCTCA      77135       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                    G    A_
GAM1052  LOC145622 3'  TCAAACGATTCTCCTACCTCA  77312
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||
                                ACTCCATCCTCTTAGCAAACT

GAM1052  LOC146050 3'  CAAACTCCCGACCTCA      77629       AGGA   TT
                                TGAGGT    GGA  GTTTG
                                ||||||    |||  |||||
                                ACTCCA    CCT  CAAAC
                                    GC__   __
GAM1052  LOC146050 3'  TCAAACAATTTTCCTGCCTCA  77646
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||
                                ACTCCGTCCTTTTAACAAACT

GAM1052  LOC146229 3'  CAAACTCCTGACCTCA      77730       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                    G    A_
GAM1052  LOC146229 3'  CAAACTCCTGACCTCA      77731       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                    G    A_
GAM1052  LOC146229 3'  TCAGGTGATCCACCCACCTCA  77773      A  A    TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
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                                ACTCCA CC CCTA  GGACT
                                   C  A    GT
GAM1052  LOC146336 3'  TCAAGCGATCCTCCCACCTCA  77835       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCCTAGCGAACT
                                   C
GAM1052  LOC146599 5'  TCAAGTGATCCTCCTGCCTCA  78027            TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
                                ACTCCGTCCTCCTA  GAACT
                                         GT
GAM1052  LOC146952 5'  CAAACTCCTGACCTCA      83860       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  LOC147071 5'  TCAGTGATCCCCCCACCTC    73007      A  A    TG  T
                                GAGGT GG GGAT  TT GA
                                ||||| || ||||  || ||
                                CTCCA CC CCTA  GA CT
                                  C  C    GT  _
GAM1052  LOC147136 3'  CAAACCCAGACCCACCTC     78258      A  A__  ATT
                                GAGGT GG   GG   GTTTG
                                ||||| ||   ||   |||||
                                CTCCA CC   CC   CAAAC
                                  C  AGA  ____
GAM1052  LOC147343 5'  TCAAGTGATCCTCCCACCTCA  84004       A      TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
                                ACTCCA CCTCCTA  GAACT
                                   C      GT
GAM1052  LOC147935 3'  TCAAGTGATCCTCCTGCCTCA  84083            TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
                                ACTCCGTCCTCCTA  GAACT
                                         GT
GAM1052  LOC148195 5'  TCAAGAGATCCTCTCACCTCA  84137       AG      G
                                TGAGGT  GAGGATT TTTGA
                                ||||||  ||||||| |||||
                                ACTCCA  CTCCTAG GAACT
                                   CT      A
GAM1052  LOC148223 3'  TCATGGGTGCCTCCTGCCCCA  78743    A       ATTGTT
                                TG GGTAGGAGG     TGA
                                || |||||||||     |||
                                AC CCGTCCTCC     ACT
                                 C        GTGGGT
GAM1052  LOC148443 3'  TCAAGCAATCCTCCCACCTTA  78859       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
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                                ATTCCA CCTCCTAACGAACT
                                   C
GAM1052  LOC148443 3'  TCAAGTGACCCTCCCACCTCA  78860       A    A TG
                                TGAGGT GGAGG T  TTTGA
                                |||||| ||||| |  |||||
                                ACTCCA CCTCC A  GAACT
                                   C    C GT
GAM1052  LOC148918 5'  TCAAGCGATCCTCCCACCTCA  79081       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCCTAGCGAACT
                                   C
GAM1052  LOC148918 5'  TCAGGTGATCCACCCACCTCA  79085       A A   TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC CCTA  GGACT
                                   C A   GT
GAM1052  LOC148930 3'  TCAAAAAATCTCCTACCCA   79100    A      G  G
                                TG GGTAGGAG ATT TTTGA
                                || |||||||| ||| |||||
                                AC CCATCCTC TAA AAACT
                                 _      _  A
GAM1052  LOC149113 3'  CAATCCTCCCACCTTA      79161       A
                                TGAGGT GGAGGATTG
                                |||||| |||||||||
                                ATTCCA CCTCCTAAC
                                   C
GAM1052  LOC149132 5'  CGATCCTCCCACGTCA      79175     G  A
                                TGA GT GGAGGATTG
                                ||| || |||||||||
                                ACT CA CCTCCTAGC
                                  G  C
GAM1052  LOC149276 3'  ATAACCTCCTACTCA       84381      G      A
                                TGAG TAGGAGG TTGT
                                |||| ||||||| ||||
                                ACTC ATCCTCC AATA
                                  _      _
GAM1052  LOC149579 5'  CAAACTCCTGCCTCA       71129           GA
                                TGAGGTAGGAG  TTG
                                ||||||||||  |||
                                ACTCCGTCCTC  AAC
                                      A_
GAM1052  LOC149711 3'  TCAGGTGATCCACCCACCTCA  84690       A A   TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC CCTA  GGACT
                                   C A   GT
GAM1052  LOC149734 3'  ATGATCCTCCTGCCTCA     84630            TG
                                TGAGGTAGGAGGAT  T
                                |||||||||||||  |
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                                ACTCCGTCCTCCTA  A
                                        GT
GAM1052  LOC149911 3'  GACATCCTCCTCCTCA      84707       T       T
                                TGAGG AGGAGGAT GTT
                                ||||| |||||||| |||
                                ACTCC TCCTCCTA CAG
                                  _       _
GAM1052  LOC150225 3'  CAAACTCCTGACCTCA       84982        _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G     A_
GAM1052  LOC150407 3'  TCAAGCAGTCCTCCCACCTCA  79830        A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCCTGACGAACT
                                   C
GAM1052  LOC150538 3'  TCAAACAACCCTATTACTTCA  79940        G   A
                                TGAGGTAG AGG TTGTTTGA
                                |||||||| ||| ||||||||
                                ACTTCATT TCC AACAAACT
                                     A   C
GAM1052  LOC150587 3'  TCAAGCAATCCTCCTGCCTCA  85066
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAACGAACT

GAM1052  LOC151201 3'  TCAAGCGATCCTCCCACCTC   85290       A
                                GAGGT GGAGGATTGTTTGA
                                ||||| |||||||||||||
                                CTCCA CCTCCTAGCGAACT
                                   C
GAM1052  LOC151201 3'  TCATGTGATCCTCCCATCTCA  85293        A      TG T
                                TGAGGT GGAGGAT  T TGA
                                |||||| |||||||  | |||
                                ACTCTA CCTCCTA  G ACT
                                   C       GT T
GAM1052  LOC151473 3'  TCAAACAATGCCACCCC      80259     TA  A  _
                                GG  GG GG ATTGTTTGA
                                ||  || || |||||||||
                                CC  CC CC TAACAAACT
                                 __  A  G
GAM1052  LOC151701 3'  TCAAGCAATCCTCCTGCCTCA  85489
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAACGAACT

GAM1052  LOC151826 3'  TCAAGTGATCCTCCTGCCTCA  80364             TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
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                                ACTCCGTCCTCCTA  GAACT
                                      GT
GAM1052  LOC151877 3'  CAAATGATCTTCCCACCCCA   85502    A  A      TG
                                TG GGT GGAGGAT  TTTG
                                || ||| |||||||  ||||
                                AC CCA CCTTCTA  AAAC
                                 C  C       GT
GAM1052  LOC152282 5'  TCAAACAATCCTTCTTCCTC   80554      T
                                GAGG AGGAGGATTGTTTGA
                                |||| ||||||||||||||||
                                CTCC TCTTCCTAACAAACT
                                  T
GAM1052  LOC152804 3'  TCAAGCGAGCCTCCCACCTC   85890      A    A
                                GAGGT GGAGG TTGTTTGA
                                ||||| ||||| ||||||||
                                CTCCA CCTCC AGCGAACT
                                   C    G
GAM1052  LOC153443 3'  TCAAGTGATCCTCCCACCTC   80826      A      TG
                                GAGGT GGAGGAT  TTTGA
                                ||||| |||||||  |||||
                                CTCCA CCTCCTA  GAACT
                                   C       GT
GAM1052  LOC153688 3'  TCAAACCATTCTCCTGCCTCA  86120            T
                                TGAGGTAGGAGGAT GTTTGA
                                |||||||||||||| ||||||
                                ACTCCGTCCTCTTA CAAACT
                                      C
GAM1052  LOC153811 3'  CAAACTCCTGACCTCA      80943       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  LOC153894 3'  CAAACAAGTGATGCCTCA    80973       GGAGGA
                                TGAGGTA     TTGTTTG
                                |||||||     |||||||
                                ACTCCGT     AACAAAC
                                     AGTG__
GAM1052  LOC153910 5'  TCAAGCGGTCCTTCTACCTCA  81000
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCATCTTCCTGGCGAACT

GAM1052  LOC154403 3'  CAATCCTCCCACCTTA      81069       A
                                TGAGGT GGAGGATTG
                                |||||| |||||||||
                                ATTCCA CCTCCTAAC
                                   C
GAM1052  LOC154739 3'  TCAAATGATACTCCTGCCTCA  86239          G  TG
                                TGAGGTAGGAG AT  TTTGA
                                |||||||||| ||  |||||
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                                ACTCCGTCCTC TA  AAACT
                                      A  GT
GAM1052  LOC154877 3'  TCAAGCAATCCTCCCTCCTCA  86308      TA
                                TGAGG  GGAGGATTGTTTGA
                                |||||  ||||||||||||||
                                ACTCC  CCTCCTAACGAACT
                                   TC
GAM1052  LOC154992 3'  CGATCCTCCCACCTTA      81214       A
                                TGAGGT GGAGGATTG
                                |||||| |||||||||
                                ATTCCA CCTCCTAGC
                                   C
GAM1052  LOC155434 3'  TGATCCTCCACCCCA       86408    A  A
                                TG GGT GGAGGATTG
                                || ||| |||||||||
                                AC CCA CCTCCTAGT
                                 C  _
GAM1052  LOC158267 3'  CAAACAATATCACACCTC    81824      AG  GG
                                GAGGT  GA  ATTGTTTG
                                |||||  ||  ||||||||
                                CTCCA  CT  TAACAAAC
                                   CA  A_
GAM1052  LOC162427 3'  CAAACTCCTGACCTCA      82348       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  LOC162461 5'  TCAAGTGATCCTCCTACCTCA  82365            TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
                                ACTCCATCCTCCTA  GAACT
                                      GT
GAM1052  LOC163590 5'  TCAAGCGATTCTCCCACCTCA  58863       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| |||||||||||||||
                                ACTCCA CCTCTTAGCGAACT
                                   C
GAM1052  LOC164832 3'  CAAACATTGAGTCCTCCTCA   82454      T   GGAT_
                                TGAGG AGGA    TGTTTG
                                ||||| ||||    ||||||
                                ACTCC TCCT    ACAAAC
                                   _   GAGTT
GAM1052  LOC169611 3'  CAAACTCCTGACCTCA      82757       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  LOC196047 5'  CAAACTCCTGACCTCA      89592       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
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                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  LOC196337 3'  CAGTTCCTCCCACCTC      87646       A    _
                                GAGGT GGAGGA TTG
                                ||||| |||||| |||
                                CTCCA CCTCCT GAC
                                   C     T
GAM1052  LOC196529 3'  TCAGGCAATCCACCCACCTCA  87782       A  A
                                TGAGGT GG GGATTGTTTGA
                                |||||| || ||||||||||
                                ACTCCA CC CCTAACGGACT
                                   C  A
GAM1052  LOC197358 3'  TCAAGTGATCCACCCACCTCA  88048       A  A   TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC CCTA  GAACT
                                   C  A   GT
GAM1052  LOC199906 3'  CAAACTCCTGACCTCA      88475       _   GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  LOC200268 3'  TCAAGTGATCCTCCCACCTCA  88689       A     TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
                                ACTCCA CCTCCTA  GAACT
                                   C      GT
GAM1052  LOC200268 3'  TCAAGTGATCCTCCCACCTCA  88690       A     TG
                                TGAGGT GGAGGAT  TTTGA
                                |||||| |||||||  |||||
                                ACTCCA CCTCCTA  GAACT
                                   C      GT
GAM1052  LOC200316 3'  ATAGTGCCCCCCTGCCTCA    88764        A_  _
                                TGAGGTAGG  GG ATTGT
                                |||||||||  || |||||
                                ACTCCGTCC  CC TGATA
                                     CC  G
GAM1052  LOC200407 3'  CAAACTCCTGACCTCA      90042       _   GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  LOC200845 5'  GGTGATCCTCCTGCCTCA    88904           TG
                                TGAGGTAGGAGGAT  TT
                                ||||||||||||||  ||
                                ACTCCGTCCTCCTA  GG
                                        GT
GAM1052  LOC200860 3'  TCAAGCAATCCTCCCGCCTCA  90173      TA
                                TGAGG  GGAGGATTGTTTGA
                                |||||  ||||||||||||||
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                                ACTCC  CCTCCTAACGAACT
                                   GC
GAM1052  LOC201164 3'  CAAACTCCTGACCTCA      88112        _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  LOC201164 3'  TCAAACGATTGTCCTGCCTCA  88124          G
                                TGAGGTAGGA GATTGTTTGA
                                |||||||||| ||||||||||
                                ACTCCGTCCT TTAGCAAACT
                                      G
GAM1052  LOC201173 5'  TCAGTGATCCCCCCACCTC    87336      A  A    TG  T
                                GAGGT GG GGAT  TT GA
                                ||||| || ||||  || ||
                                CTCCA CC CCTA  GA CT
                                   C  C    GT  _
GAM1052  LOC201220 5'  TCAGTGATCCCCCCACCTC    87357      A  A    TG  T
                                GAGGT GG GGAT  TT GA
                                ||||| || ||||  || ||
                                CTCCA CC CCTA  GA CT
                                   C  C    GT  _
GAM1052  LOC201292 3'  TCAAAGGATCCTCCCACCTCA  88193        A       G
                                TGAGGT GGAGGATT TTTGA
                                |||||| |||||||| |||||
                                ACTCCA CCTCCTAG AAACT
                                   C       G
GAM1052  LOC201292 3'  TCATGGGATTCTCCTACCTCA  88194             GTT
                                TGAGGTAGGAGGATT   TGA
                                ||||||||||||||   |||
                                ACTCCATCCTCTTAG   ACT
                                         GGT
GAM1052  LOC201627 3'  CAAACTCCCGACCTCA      89006       AGGA   TT
                                TGAGGT    GGA  GTTTG
                                ||||||    |||  |||||
                                ACTCCA    CCT  CAAAC
                                   GC__   __
GAM1052  LOC201868 3'  CAATCCTCCCACCTTA      89074       A
                                TGAGGT GGAGGATTG
                                |||||| |||||||||
                                ATTCCA CCTCCTAAC
                                   C
GAM1052  LOC202908 5'  CGATCCTCCCATCTCA      89231       A
                                TGAGGT GGAGGATTG
                                |||||| |||||||||
                                ACTCTA CCTCCTAGC
                                   C
GAM1052  LOC202934 3'  TCAAATGGTCCTCCTGCCTCA  90427             TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
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                                ACTCCGTCCTCCTG  AAACT
                                       GT
GAM1052  LOC204804 3'  TCAAGTGATCCTCCCAGCTCA  89484     GTA      TG
                                TGAG   GGAGGAT  TTTGA
                                ||||   |||||||  |||||
                                ACTC   CCTCCTA  GAACT
                                  GAC      GT
GAM1052  LOC219529 5'  CAGGTGATCCTCCTGCCTCA   92969           TG
                                TGAGGTAGGAGGAT  TTTG
                                ||||||||||||||  ||||
                                ACTCCGTCCTCCTA  GGAC
                                       GT
GAM1052  LOC219673 3'  CAATCCTCCCACCTTA      93020       A
                                TGAGGT GGAGGATTG
                                ||||||| |||||||||
                                ATTCCA CCTCCTAAC
                                    C
GAM1052  LOC219673 5'  TCAAGTGATCCTCCCGCCTCA  93041      TA      TG
                                TGAGG  GGAGGAT  TTTGA
                                |||||  |||||||  |||||
                                ACTCC  CCTCCTA  GAACT
                                  GC      GT
GAM1052  LOC219731 5'  TCAAGCAGTCCTCCCACCTCA  93099       A
                                TGAGGT GGAGGATTGTTTGA
                                ||||||| ||||||||||||||
                                ACTCCA CCTCCTGACGAACT
                                    C
GAM1052  LOC220018 5'  TCAAAGGGGGTCCTATCTCA   93404         GGA  G
                                TGAGGTAGGA   TT TTTGA
                                ||||||||||   || |||||
                                ACTCTATCCT   GG AAACT
                                      GG_  G
GAM1052  LOC220074 3'  CAAACTCCTGACCTCA      59265       _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                    G    A_
GAM1052  LOC220575 3'  TCAAGCGATCCTCCCACTTCA  76317       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTTCA CCTCCTAGCGAACT
                                    C
GAM1052  LOC221271 3'  TCAAGTGATCTGCCCACCTCA  91872       A  A    TG
                                TGAGGT GG GGAT  TTTGA
                                |||||| || ||||  |||||
                                ACTCCA CC TCTA  GAACT
                                    C  G    GT
GAM1052  LOC221540 3'  TCAGGCAATCCTCCTGCCTCA  93840
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
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                                ACTCCGTCCTCCTAACGGACT

GAM1052  LOC221760 5'  TCAAGGGATCCTCCTGCCTCA  93790            G
                                TGAGGTAGGAGGATT TTTGA
                                |||||||||||||| |||||
                                ACTCCGTCCTCCTAG GAACT
                                     G
GAM1052  LOC221814 5'  TCAAGTGATCCTCCTGCCTCA  93946           TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||  |||||
                                ACTCCGTCCTCCTA  GAACT
                                     GT
GAM1052  LOC221815 5'  TCAAGTGATCCTCCTGCCTCA  93939           TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||  |||||
                                ACTCCGTCCTCCTA  GAACT
                                     GT
GAM1052  LOC221960 3'  TCAAGCAATCCTCCCACCTCA  91085      A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCCTAACGAACT
                                    C
GAM1052  LOC222057 5'  CGATCCTCCCACCTCA      92772      A
                                TGAGGT GGAGGATTG
                                |||||| |||||||||
                                ACTCCA CCTCCTAGC
                                    C
GAM1052  LOC222068 3'  TCAAATGATTCTCCTGCCTCA  92712           TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||  |||||
                                ACTCCGTCCTCTTA  AAACT
                                     GT
GAM1052  LOC253805 3'  TCAAACCATTCTCCTGCCTCA  96437           T
                                TGAGGTAGGAGGAT GTTTGA
                                |||||||||||||| ||||||
                                ACTCCGTCCTCTTA CAAACT
                                     C
GAM1052  LOC254100 3'  TCAAGTGATCCTCACACCTCA  96416      AG    TG
                                TGAGGT  GAGGAT  TTTGA
                                ||||||  ||||||  |||||
                                ACTCCA  CTCCTA  GAACT
                                    CA     GT
GAM1052  LOC254268 3'  CAAACTCCTGACCTCA      95402      _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
                                ACTCCA TCCTC  AAC
                                    G    A_
GAM1052  LOC254532 5'  CAAACTCCTGACCTCA      96631      _    GA
                                TGAGGT AGGAG  TTG
                                |||||| |||||  |||
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                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  LOC254685 3'  TCAGGTGATCCTCCCGCCTCA  96489      TA      TG
                                TGAGG  GGAGGAT  TTTGA
                                |||||  |||||||  |||||
                                ACTCC  CCTCCTA  GGACT
                                   GC       GT
GAM1052  LOC255065 5'  CAAACTCCTGACCTCA      96580       _    GA
                                TGAGGT AGGAG  TTG
                                ||||||  |||||  |||
                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052  LOC255196 5'  TCAAGCAATCCTCCCACCTCA  97176       A
                                TGAGGT GGAGGATTGTTTGA
                                ||||||  ||||||||||||||
                                ACTCCA CCTCCTAACGAACT
                                   C
GAM1052  LOC255458 5'  TCAAGCGATCCTCCCACCTCA  97150       A
                                TGAGGT GGAGGATTGTTTGA
                                ||||||  ||||||||||||||
                                ACTCCA CCTCCTAGCGAACT
                                   C
GAM1052  LOC255465 3'  CAATTCTCCTGCCTCA      97281
                                TGAGGTAGGAGGATTG
                                ||||||||||||||||
                                ACTCCGTCCTCTTAAC

GAM1052  LOC255465 3'  TCAAATGGTCCTCCTGCCTCA  97301            TG
                                TGAGGTAGGAGGAT  TTTGA
                                ||||||||||||||  |||||
                                ACTCCGTCCTCCTG  AAACT
                                         GT
GAM1052  LOC255707 3'  TCAAGAAATCCTCCCACCTCA  96963       A       G
                                TGAGGT GGAGGATT TTTGA
                                ||||||  ||||||||  |||||
                                ACTCCA CCTCCTAA GAACT
                                   C       A
GAM1052  LOC256878 5'  CGATCCTCCCATCTCA      96902       A
                                TGAGGT GGAGGATTG
                                ||||||  |||||||||
                                ACTCTA CCTCCTAGC
                                   C
GAM1052  LOC256923 5'  TCAAGCAGTCCTCCCACCCCA  95140    A   A
                                TG GGT GGAGGATTGTTTGA
                                ||  |||  ||||||||||||||
                                AC CCA CCTCCTGACGAACT
                                 C   C
GAM1052  LOC257054 5'  TCAAGCAATCCTCCCGCCTCA  95669      TA
                                TGAGG  GGAGGATTGTTTGA
                                |||||  ||||||||||||||
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                                ACTCC  CCTCCTAACGAACT
                                   GC
GAM1052  LOC257438 3'  CAGTGTACCTCCTACCTCA   93970          ___
                                TGAGGTAGGAGG  ATTG
                                ||||||||||||  ||||
                                ACTCCATCCTCC  TGAC
                                      ATG
GAM1052  LOC257465 3'  TCAAACAATTCTCCTGCCTCA  81601
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCTTAACAAACT

GAM1052  LOC257545 3'  TCAGGCAATCCTCCTGCCTCA  97808
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAACGGACT

GAM1052  LOC257598 3'  TCAGGCAATCCTCCTGCCTCA  97923
                                TGAGGTAGGAGGATTGTTTGA
                                |||||||||||||||||||||
                                ACTCCGTCCTCCTAACGGACT

GAM1052  LOC51193  3'  CAATCCTCCCACTTCA      32903       A
                                TGAGGT GGAGGATTG
                                |||||| |||||||||
                                ACTTCA CCTCCTAAC
                                   C
GAM1052  LOC51200  3'  CAAACTCCCAACCTCA      32989       A  A  ATT
                                TGAGGT GG GG   GTTTG
                                |||||| || ||   |||||
                                ACTCCA CC CT   CAAAC
                                   A  _  ___
GAM1052  LOC51336  3'  TCAAGTGATCCTCTCACCTCA  33582       AG     TG
                                TGAGGT  GAGGAT  TTTGA
                                ||||||  ||||||  |||||
                                ACTCCA  CTCCTA  GAACT
                                   CT     GT
GAM1052  LOC51336  3'  TCATGAAGTTCCCCCTACCTC  33583        A   TTGTT_
                                GAGGTAGG GGA     TGA
                                |||||||| |||     |||
                                CTCCATCC CCT     ACT
                                     C   TGAAGT
GAM1052  LOC51622  3'  TCAAGCAATCCTCCCACCTCA  31570       A
                                TGAGGT GGAGGATTGTTTGA
                                |||||| ||||||||||||||
                                ACTCCA CCTCCTAACGAACT
                                   C
GAM1052  LOC57106  3'  CAACCCCTACCTCA        64135         A  A
                                TGAGGTAGG GG TTG
                                ||||||||| || |||
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                              ACTCCATCC CC AAC
                                    _ _
GAM1052 LOC57146 3' CAAACTCCTGACCTCA     39914      _    GA
                              TGAGGT AGGAG  TTG
                              |||||| |||||  |||
                              ACTCCA TCCTC  AAC
                                 G    A_
GAM1052 LOC89231 3' TCAAGCAATCCTCTCACCTCA 92735      AG
                              TGAGGT  GAGGATTGTTTGA
                              ||||||  |||||||||||||
                              ACTCCA  CTCCTAACGAACT
                                 CT
GAM1052 LOC90288 3' CAATCCTCCCACTTCA     62082      A
                              TGAGGT GGAGGATTG
                              |||||| |||||||||
                              ACTTCA CCTCCTAAC
                                 C
GAM1052 LOC90485 3' TCAAGTGATTCCCCTACCTCA 63024       A   TG
                              TGAGGTAGG GGAT  TTTGA
                              ||||||||| ||||  |||||
                              ACTCCATCC CTTA  GAACT
                                   C   GT
GAM1052 LOC91056 3' TCAGGTGATCCTCCCATCTCA 94763      A     TG
                              TGAGGT GGAGGAT  TTTGA
                              |||||| |||||||  |||||
                              ACTCTA CCTCCTA  GGACT
                                 C     GT
GAM1052 LOC91301 5' TCACCGCACCTCCTGCCTCA  65548         AT  T_
                              TGAGGTAGGAGG  TGT  TGA
                              ||||||||||||  |||  |||
                              ACTCCGTCCTCC  ACG  ACT
                                     __  CC
GAM1052 LOC91650 5' TCAAACAATCCCACTTC     66862      AGGA
                              GAGGT   GGATTGTTTGA
                              |||||   ||||||||||
                              CTTCA   CCTAACAAACT
                                 C___
GAM1052 LOC91661 3' AACAATCCTCCCATCTCA    56395       A
                              TGAGGT GGAGGATTGTT
                              |||||| ||||||||||
                              ACTCTA CCTCCTAACAA
                                 C
GAM1052 LOC91963 3' TGATCCTCCCACCTCA      67702       A
                              TGAGGT GGAGGATTG
                              |||||| |||||||||
                              ACTCCA CCTCCTAGT
                                 C
GAM1052 LOC92267 3' CAAACTCCTGACCTCA      68604       _    GA
                              TGAGGT AGGAG  TTG
                              |||||| |||||  |||
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                                ACTCCA TCCTC  AAC
                                   G    A_
GAM1052 LOC92578 3' CAAATTCTTCCCCACCTC    69823      A  A   TT_
                                GAGGT GG GGA   GTTTG
                                ||||| || |||   |||||
                                CTCCA CC CCT   TAAAC
                                  _ _   TCT
GAM1052 LOC92609 3' CAAGTGACCCTCCTGCCTCA   72845          A TG
                                TGAGGTAGGAGG T  TTTG
                                |||||||||||| |  ||||
                                ACTCCGTCCTCC A  GAAC
                                       C GT
GAM1052 LOC92841 3' TCAAGTGATCCCCCACCTC    70720      A  A    TG
                                GAGGT GG GGAT  TTTGA
                                ||||| || ||||  |||||
                                CTCCA CC CCTA  GAACT
                                  C  _   GT
GAM1052 LOC96810 3' TCTGGCCCCTCCTGCCTCA    70565          ATT  TT
                                TGAGGTAGGAGG   GT  GA
                                ||||||||||||   ||  ||
                                ACTCCGTCCTCC   CG  CT
                                       C__  GT
GAM1053 DDEF1    3' GAGCTTTAGCAGCCTC      59564    A   AGATAC       A
                                GA GCT     CTAAAGCT C
                                || |||     |||||||| |
                                CT CGA     GATTTCGA G
                                 C   C_____       C
GAM1053 DDX3     3' GAGCCTTAGGTATTTG      43759          A   A
                                TAGATACCTAA GCT C
                                |||||||||||| ||| |
                                GTTTATGGATT CGA G
                                       C   C
GAM1053 GRAF     3' GGTAACTCCCTCCCTAGCTTC  30573        ATACCTAA  C
                                GAAGCTAG       AG TACC
                                ||||||||       || ||||
                                CTTCGATC       TC ATGG
                                     CCTCCC__  A
GAM1053 MAT1A    3' AGCTTTAGAATCCCAGC     90825     A_   AC
                                GCT  GAT  CTAAAGCT
                                |||  |||  ||||||||
                                CGA  CTA  GATTTCGA
                                  CC   A_
GAM1053 MYLK     3' AGCTTCAGACATTTGGTT    97018        AC  A
                                AGCTAGAT  CT AAGCT
                                ||||||||  || |||||
                                TTGGTTTA  GA TTCGA
                                     CA  C
GAM1053 RGL      3' GTAGCTAAAACTTAGCTTCA  30736         ATACCTAA
                                TGAAGCTAG       AGCTAC
                                |||||||||       ||||||
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                                ACTTCGATT       TCGATG
                                     CAAAA___
GAM1053  ZFP93    3'  GTAGCCTTAATAACGTTAGTTT 14887         ATACC_   A
              CA                    TGAAGCTAG     TAA GCTAC
                                    |||||||||      ||| |||||
                                    ACTTTGATT     ATT CGATG
                                         GCAATA   C
GAM1053  C3orf4   3'  AGCATTGACACATAGCTTCA   39118        GATACC   A
                                    TGAAGCTA     TAA GCT
                                    ||||||||     ||| |||
                                    ACTTCGAT     GTT CGA
                                         ACACA_   A
GAM1053  D2S448   3'  GGCAGGAGTCCTAGCTTCA   73527         _ A   AAA
                                    TGAAGCTAG AT CCT   GCT
                                    ||||||||| || |||   |||
                                    ACTTCGATC TG GGA   CGG
                                         C  A   ___
GAM1053  FLJ12604 3'  AGCTTTAGTATTGACTTCA   64436      CTA    C
                                    TGAAG   GATAC TAAAGCT
                                    |||||   ||||| |||||||
                                    ACTTC   TTATG ATTTCGA
                                       AG_    _
GAM1053  FLJ14280 5'  GGTAGCTCCTGGCCAGCTCA   45999     A   AGATA  TAA
                                    TGA GCT     CC   AGCTACC
                                    ||| |||     ||   |||||||
                                    ACT CGA     GG   TCGATGG
                                      _   CC___  TCC
GAM1053  H2AFJ    3'  GTTGTCAAGTTTCTAGCTTCA  36842         T  CTAA_
                                    TGAAGCTAGA AC     AGC
                                    |||||||||| ||     |||
                                    ACTTCGATCT TG     TTG
                                          T  AACTG
GAM1053  KIAA0441 3'  TAGCTTTGTTAATCTAGCCTC  28960    A      ACC
                                    GA GCTAGAT   TAAAGCTA
                                    || |||||||   ||||||||
                                    CT CGATCTA   GTTTCGAT
                                     C       ATT
GAM1053  KIAA1128 3'  TAGCTTTATGTGCAGCTTGCA  68483    _    AGA   C
                                    TG AAGCT   TAC TAAAGCTA
                                    || |||||   ||| ||||||||
                                    AC TTCGA   GTG ATTTCGAT
                                     G    C__   T
GAM1053  KIAA1750 3'  TAGCCCCAGGAGTGGGCTTTA  68254       AG  A   AAA
                                    TGAAGCT  AT CCT   GCTA
                                    |||||||  || |||   ||||
                                    ATTTCGG  TG GGA   CGAT
                                         G_  A   CCC
GAM1053  KPNA5    3'  GGTAGCTTCAGGTAACT     9629     A    A
                                    AG TACCT AAGCTACC
                                    || ||||| ||||||||
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                                TC ATGGA TTCGATGG
                                 A    C
GAM1053  MAGEH1    5'  GGTAGCTTCAGCGGCAGCAGCT 25924       AGATAC_  A
              TC                   GAAGCT      CT AAGCTACC
                                   ||||||      || ||||||||
                                   CTTCGA      GA TTCGATGG
                                      CGACGGC  C
GAM1053  MGC12921  3'  AGCCCTATTTAGCTTC      63774          CCTAAA
                                   GAAGCTAGATA     GCT
                                   ||||||||||      |||
                                   CTTCGATTTAT     CGA
                                         CC____
GAM1053  MGC30052  3'  AGCTTTAGAATAGCTTC     58532        GATAC
                                   GAAGCTA    CTAAAGCT
                                   |||||||    ||||||||
                                   CTTCGAT    GATTTCGA
                                       AA___
GAM1053  RNF34     3'  AGCAAGGGCTGCATCTAGCTTC 47094          A___   AAA
                                   GAAGCTAGAT   CCT   GCT
                                   ||||||||||   |||   |||
                                   CTTCGATCTA   GGG   CGA
                                         CGTC   AA_
GAM1053  TNFRSF19L 3'  GTAGCTTTTATCCCAGC     51779     A_   CCT
                                   GCT  GATA   AAAGCTAC
                                   |||  ||||   ||||||||
                                   CGA  CTAT   TTTCGATG
                                     CC    ___
GAM1053  LOC121536 3'  AGCAAATCACATTTAGCTTCA  74082          ACCTAAA
                                   TGAAGCTAGAT      GCT
                                   ||||||||||       |||
                                   ACTTCGATTTA      CGA
                                         CACTAAA
GAM1053  LOC255452 3'  TAGGTACCTACCTTCA      97544       C   A
                                   TGAAG TAG TACCTA
                                   ||||| ||| ||||||
                                   ACTTC ATC ATGGAT
                                      C   C
GAM1053  LOC257396 3'  GGCAGCTTTAGGCTTAACTT   97139     C   ATA       A
                                   AAG TAG   CCTAAAGCT CC
                                   ||| |||   ||||||||| ||
                                   TTC ATT   GGATTTCGA GG
                                     A   C__       C
GAM1053  LOC92710  3'  GTACAAGGCATCTAGCTT    70359         A   AAAGC
                                   AAGCTAGAT CCT     TAC
                                   |||||||| |||     |||
                                   TTCGATCTA GGA     ATG
                                         C   AC___
GAM1054  ADAM19    3'  CAGGAAGAAGACTGGCCATTAT 52703       C    CTGAG
              G                     CATGA GGCT     TTCTTCCTG
                                   ||||| ||||     |||||||||
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                              GTATT CCGG    AAGAAGGAC
                                 A   TCAG_
GAM1054  FACL5    5'  CAGGAAGAACTCAGAGCCG   64186
                              CGGCTCTGAGTTCTTCCTG
                              ||||||||||||||||||
                              GCCGAGACTCAAGAAGGAC

GAM1054  GNAL     5'  CAGGAAAGAGAGGAGCCGTCG  9058         GAG TC
                              TGACGGCTCT   T  TTCCTG
                              ||||||||||   |  ||||||
                              GCTGCCGAGG   A  AAGGAC
                                    AG_ GA
GAM1054  KAL1     3'  CAGGAAGAACTTCTGTCA    4013       CTCT
                              TGACGG   GAGTTCTTCCTG
                              ||||||   ||||||||||||
                              ACTGTC   TTCAAGAAGGAC
                                   ____
GAM1054  MYO1E    3'  CAGGAGGACAAAACCACCATG  17187     AC  CTC  AGT
                              CATG  GG   TG   TCTTCCTG
                              ||||  ||   ||   ||||||||
                              GTAC  CC   AC   AGGAGGAC
                                CA  AAA  ___
GAM1054  PRKAR2B  3'  CAGAAAGAACTCAGATGT    10804    _        C
                              GC TCTGAGTTCTT CTG
                              || ||||||||||| |||
                              TG AGACTCAAGAA GAC
                               T         A
GAM1054  PUM2     3'  AGGATCAAAGCTGTCATG    31014         C   GTTCT
                              CATGACGGCT TGA    TCCT
                              |||||||||| |||    ||||
                              GTACTGTCGA ACT    AGGA
                                    A  _____
GAM1054  SKI      3'  CAGGAAGTGCAGAGCCGCA   11701    A      AGTT
                              TG CGGCTCTG   CTTCCTG
                              || ||||||||   |||||||
                              AC GCCGAGAC   GAAGGAC
                               _      GT__
GAM1054  TEM8     3'  AGGAAGATGCAACCCCATG   36326     AC  CTC  AGT
                              CATG  GG   TG   TCTTCCT
                              ||||  ||   ||   |||||||
                              GTAC  CC   AC   AGAAGGA
                                C_  A__  GT_
GAM1054  ARHGEF4  5'  AGAAAAAACTCAGGGC     52207         C  C
                              GCTCTGAGTT TT CT
                              |||||||||| || ||
                              CGGGACTCAA AA GA
                                    A  A
GAM1054  FLJ31978 3'  CAGGAAGGAACAAGCGCC    58348     T  GAG
                              GGC CT   TTCTTCCTG
                              ||| ||   |||||||||
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                                CCG GA   AGGAAGGAC
                                  C  ACA
GAM1054  HSU24186  5'  AGAACTCAAAGCCGTC      25324        C
                                GACGGCT TGAGTTCT
                                ||||||| ||||||||
                                CTGCCGA ACTCAAGA
                                    A
GAM1054  KCNT1     3'  AGCTCCCAGGGCCGCCA     61825    A     __
                                TG CGGCTCT  GAGTT
                                || |||||||  |||||
                                AC GCCGGGA  CTCGA
                                 C      CC
GAM1054  KIAA1867  3'  CAGGAAGAACCCAAGAGCTCAT 94822     CG    GA_
                                ATGA  GCTCT   GTTCTTCCTG
                                ||||  |||||   ||||||||||
                                TACT  CGAGA   CAAGAAGGAC
                                  __    ACC
GAM1054  KIAA1878  3'  AATTCAGAGAATCGTCATG   91707        __
                                CATGACGG  CTCTGAGTT
                                ||||||||  |||||||||
                                GTACTGCT  GAGACTTAA
                                    AA
GAM1054  MFN1      3'  CAGGAAGAACTCATGA      35541    _
                                TC TGAGTTCTTCCTG
                                || ||||||||||||
                                AG ACTCAAGAAGGAC
                                 T
GAM1054  MIDORI    3'  CAGGGCCCTTCCAGAGCCTGTC 73784       _      AGTTCT
            ATG                    CATGAC GGCTCTG     TCCTG
                                ||||||| |||||||      |||||
                                GTACTG CCGAGAC     GGGAC
                                   T      CTTCCC
GAM1054  MYH7B     3'  CAGGAAGAACCTGGCTCGCATG 70530      A _  CTGA
                                CATG CG GCT    GTTCTTCCTG
                                |||| || |||    ||||||||||
                                GTAC GC CGG    CAAGAAGGAC
                                  _ T   TC__
GAM1054  RNAHP     3'  AGAAAGCAGCAGCCGTCAT    23761         _  AG
                                ATGACGGCT CTG  TTCT
                                ||||||||| |||  ||||
                                TACTGCCGA GAC  AAGA
                                    C   GA
GAM1054  SLC37A1   3'  AGACGGAGCTCAGACCC     38561    C        TC
                                GG TCTGAGTTCT  CT
                                || ||||||||||  ||
                                CC AGACTCGAGG  GA
                                 C         CA
GAM1054  LOC116236 3'  CAGGAAAAGCACAAACCTCAT  73809      C  CTC  A   C
                                ATGA GG   TG GTT TTCCTG
                                |||| ||   || ||| ||||||
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                                TACT CC   AC CGA AAGGAC
                                  _ AA_ A   A
GAM1054 LOC124801 3' CAGGAAGAACTCTCTTGCATG 74336     A  CTCT
                                CATG CGG   GAGTTCTTCCTG
                                |||| |||   ||||||||||||
                                GTAC GTT   CTCAAGAAGGAC
                                  _  CT__
GAM1054 LOC222160 5' AGGAAGAACTCACCCC     94117    CTC
                                GG  TGAGTTCTTCCT
                                ||  ||||||||||||
                                CC  ACTCAAGAAGGA
                                 CC_
GAM1054 LOC51094 3' CAGGAAGAATAAAGCC     32045     CTGA
                                GGCT   GTTCTTCCTG
                                ||||   ||||||||||
                                CCGA   TAAGAAGGAC
                                  AA__
GAM1054 LOC92078 3' CAGGAAGAAGAATCGACCGTC 67977     C  T  G__
                                GACGG TC GA  TTCTTCCTG
                                ||||| || ||  |||||||||
                                CTGCC AG CT  AAGAAGGAC
                                  _ _ AAG
GAM1055 ACADL    3' TTGCTGACATCTGAGA     7842    C       A
                                TC CAGATGTTAG CAA
                                || |||||||||| |||
                                AG GTCTACAGTC GTT
                                 A       _
GAM1055 ADCY7    3' GTTGCCTTTTTTACACA    6644     _   C
                                TGT TAGA AAGGCAAC
                                ||| |||| ||||||||
                                ACA ATTT TTCCGTTG
                                  C   T
GAM1055 ANXA9    5' GGTCCTCTCCCACATCTGGGA 13104        TA  CA  CA
                                TCCCAGATGT  GA  AGG  ACC
                                ||||||||||  ||  |||  |||
                                AGGGTCTACA  CT  TCC  TGG
                                      CC  C_  __
GAM1055 AVP      5' GGCTGCCTTGTCCACGAGGCAG 4922     AGA   A____      A
            GG                  CCC   TGTT    GACAAGGCA CC
                                |||   ||||    ||||||||| ||
                                GGG   ACGG    CTGTTCCGT GG
                                  ___   AGCAC       C
GAM1055 C1orf1   3' GTTGCCTTACAGAGCCAGGA  6866     CAGAT  AGAC
                                TCC    GTT   AAGGCAAC
                                |||    |||   ||||||||
                                AGG    CGA   TTCCGTTG
                                  AC___  GACA
GAM1055 CACNB1   3' GTTGCCTTGGGACCTCGG    5573     A  T  AGA
                                CC GA GTT   CAAGGCAAC
                                || || |||   |||||||||
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                                GG CT CAG   GTTCCGTTG
                                 _ C   G__
GAM1055  HLA-A    3'  TGCCTTGTGTGGGACTGAGA   9204     C   ATG   G
                                TC CAG   TTA ACAAGGCA
                                || |||   ||| ||||||||
                                AG GTC   GGT TGTTCCGT
                                 A   AG_   G
GAM1055  HLA-A    3'  TGCCTTGTGTGGGACTGAGA   89194    C   ATG   G
                                TC CAG   TTA ACAAGGCA
                                || |||   ||| ||||||||
                                AG GTC   GGT TGTTCCGT
                                 A   AG_   G
GAM1055  HLA-E    3'  TGCCTTGTGTGCGACTGAGA   91026    C   A   T G
                                TC CAG TGT A ACAAGGCA
                                || ||| ||| | ||||||||
                                AG GTC GCG T TGTTCCGT
                                 A   A   _ G
GAM1055  HLA-E    3'  TGCCTTGTGTGCGACTGAGA   91027    C   A   T G
                                TC CAG TGT A ACAAGGCA
                                || ||| ||| | ||||||||
                                AG GTC GCG T TGTTCCGT
                                 A   A   _ G
GAM1055  IFRD1    3'  GGTTGCTAACCTTAACATCTGA 60123    C        ACAA
              GA                  TC CAGATGTTAG    GGCAACC
                                || ||||||||||    |||||||
                                AG GTCTACAATT    TCGTTGG
                                 A         CCAA
GAM1055  NAGA     5'  GGTGTGAGGTCTGACATC     4236          AAG   A
                                GATGTTAGAC   GCA CC
                                ||||||||||   ||| ||
                                CTACAGTCTG   TGT GG
                                      GAG   _
GAM1055  PLOD     3'  GTGCCCTGAGTCTGGGA     4321         G    ACAA    A
                                TCCCAGAT TTAG    GGCA C
                                |||||||| ||||    |||| |
                                AGGGTCTG AGTC    CCGT G
                                   _   _____    C
GAM1055  PTGER3   3'  TGCCTAACCCTGGGA      6311        AT   AGACA
                                TCCCAG  GTT    AGGCA
                                ||||||  |||    |||||
                                AGGGTC  CAA    TCCGT
                                   C_   ______
GAM1055  ACAA2    5'  GGCTGCCTTGTCTGCTGG    91768     ATGT         A
                                CCAG    TAGACAAGGCA CC
                                ||||    |||||||||||| ||
                                GGTC    GTCTGTTCCGT GG
                                  _____          C
GAM1055  BA108L7.2 3'  GCCCCCAGTGATAACATCTGTG 48263    C        G_  AA__
              A                   TC CAGATGTTA  AC    GGC
                                || |||||||||  ||    |||
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                                AG GTCTACAAT  TG   CCG
                                 T       AG  ACCC
GAM1055  CDC14B   3'  TGTCTCTAGCATCCAGGA   52840    CA      CAA
                                TCC  GATGTTAGA   GGCA
                                |||  |||||||||   ||||
                                AGG  CTACGATCT   CTGT
                                  AC       ___
GAM1055  cerk     3'  GCCACCTGCTGACATTCAGA   42847    CCA      A  A__
                                TC   GATGTTAG CA   GGC
                                ||   |||||||| ||   |||
                                AG   TTACAGTC GT   CCG
                                 AC_       _ CCA
GAM1055  CPEB1    5'  GTCATGTACAACATCTGG    47599        AG   A
                                CCAGATGTT  ACA GGC
                                |||||||||  ||| |||
                                GGTCTACAA  TGT CTG
                                      CA   A
GAM1055  DKFZP434B044 3'  GTTACCACCAAACATCTGGGA  48929          AGACAA  C
                                TCCCAGATGTT     GG AAC
                                ||||||||||      || |||
                                AGGGTCTACAA     CC TTG
                                      ACCA__  A
GAM1055  FKBP9    5'  GTTGCCCTCAGACCATCCAGG  94067    CA   _  A  CAA
                                CC  GATG TT GA   GGCAAC
                                ||  |||| || ||   ||||||
                                GG  CTAC AG CT   CCGTTG
                                 AC    C  A  C__
GAM1055  FLJ10101 3'  GGCTGCCCCGCCTGGGTCTGGG 45268        G   ACAA   A
            G                    TCCCAGAT TTAG    GGCA CC
                                |||||||| ||||    |||| ||
                                GGGGTCTG GGTC    CCGT GG
                                     _   CGCC    C
GAM1055  FLJ10101 3'  GGCTGCCCCGCCTGGGTCTGGG 45269        G   ACAA   A
            G                    TCCCAGAT TTAG    GGCA CC
                                |||||||| ||||    |||| ||
                                GGGGTCTG GGTC    CCGT GG
                                     _   CGCC    C
GAM1055  FLJ10101 3'  GGCTGCCCCGCCTGGGTCTGGG 45270        G   ACAA   A
            G                    TCCCAGAT TTAG    GGCA CC
                                |||||||| ||||    |||| ||
                                GGGGTCTG GGTC    CCGT GG
                                     _   CGCC    C
GAM1055  FLJ10101 3'  GGCTGCCCCGCCTGGGTCTGGG 45271        G   ACAA   A
            G                    TCCCAGAT TTAG    GGCA CC
                                |||||||| ||||    |||| ||
                                GGGGTCTG GGTC    CCGT GG
                                     _   CGCC    C
GAM1055  FLJ10101 3'  GGCTGCCCCGCCTGGGTCTGGG 45272        G   ACAA   A
            G                    TCCCAGAT TTAG    GGCA CC
                                |||||||| ||||    |||| ||
```

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                                GGGGTCTG GGTC   CCGT GG
                                    _   CGCC   C
GAM1055  FLJ10101  3'  GGCTGCCCCGCCTGGGTCTGGG 45273       G   ACAA   A
              G                  TCCCAGAT TTAG   GGCA CC
                                 |||||||| ||||   |||| ||
                                 GGGGTCTG GGTC   CCGT GG
                                    _   CGCC   C
GAM1055  FLJ20277  3'  GGCTACCTTGTTTTTAACAT   34834       __     CAA
                                 ATGTTA  GACAAGG   CC
                                 ||||||  |||||||   ||
                                 TACAAT  TTGTTCC   GG
                                    TT      ATC
GAM1055  FLJ20507  3'  GGTCACCTTGTTTGCTCTGGG  35297      T  T      CA
                                 CCCAGA GT AGACAAGG  ACC
                                 ||||||  || ||||||||  |||
                                 GGGTCT CG TTTGTTCC  TGG
                                    _ _      AC
GAM1055  FLJ20507  3'  GGTCACCTTGTTTGCTCTGGG  60232      T  T      CA
                                 CCCAGA GT AGACAAGG  ACC
                                 ||||||  || ||||||||  |||
                                 GGGTCT CG TTTGTTCC  TGG
                                    _ _      AC
GAM1055  FLJ20509  3'  GGTTGCCTTGTTTTGACTTGAG 35313    C   AT     _
              A                  TC CAG  GTTAGA CAAGGCAACC
                                 ||  |||  ||||||  ||||||||||
                                 AG GTT  CAGTTT GTTCCGTTGG
                                  A   __     T
GAM1055  FLJ21007  5'  TTGCTCTCAATATCTGAGA   47927    C      A  CAA
                                 TC CAGATGTT GA   GGCAA
                                 ||  ||||||||  ||   |||||
                                 AG GTCTATAA CT   TCGTT
                                  A       _ C__
GAM1055  FLJ22938  3'  GCTGACCGACATCTGGGA    45161          AGACAA
                                 TCCCAGATGTT     GGC
                                 ||||||||||      |||
                                 AGGGTCTACAG     TCG
                                       CCAG__
GAM1055  FLJ23129  3'  CCTCAAAAACATTTGGGA    45428          AGACA
                                 TCCCAGATGTT     AGG
                                 ||||||||||     |||
                                 AGGGTTTACAA     TCC
                                       AAAC_
GAM1055  FLJ23209  3'  GCTGGGTCTAAACATCTG    46054        _   AA
                                 CAGATGTT AGAC  GGC
                                 ||||||||  ||||  |||
                                 GTCTACAA TCTG  TCG
                                    A   GG
GAM1055  FLJ23550  3'  GTAGTTAACATCTGGGA     46855          ACAAG
                                 TCCCAGATGTTAG    GC
                                 ||||||||||||     ||
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                              AGGGTCTACAATT    TG
                                     GA___
GAM1055 KIAA0009 3' TGCCTTTTTCATCTGGGG   27614       TTAGAC
                              TCCCAGATG    AAGGCA
                              |||||||||    ||||||
                              GGGGTCTAC    TTCCGT
                                   TTT___
GAM1055 KIAA0349 3' TGCCCAACACTGGGA     92309     A   AGACAA  A
                              TCCCAG TGTT    GGC A
                              |||||| ||||    ||| |
                              AGGGTC ACAA    CCG T
                                 _   C_____  G
GAM1055 KIAA0430 3' GTTGCCTTATTCTAAGAT   38842   G   C_
                              AT TTAGA  AAGGCAAC
                              || |||||  ||||||||
                              TA AATCT  TTCCGTTG
                               G    TA
GAM1055 KIAA0513 3' GGTTACCTTATCACCCTGG   28368    AT  TA  C   C
                              CCAG  GT  GA AAGG AACC
                              ||||  ||  || |||| ||||
                              GGTC  CA  CT TTCC TTGG
                                C_  __  A   A
GAM1055 KIAA0793 3' GCCTCATGTAACATCTGGGA  29026        GACA
                              TCCCAGATGTTA   AGGC
                              ||||||||||||   ||||
                              AGGGTCTACAAT   TCCG
                                     GTAC
GAM1055 KIAA0865 3' CCTTGTCTTGCTACTTGGA   61247    C  AT  T
                              TCC AG  GT AGACAAGG
                              ||| ||  || ||||||||
                              AGG TC  CG TCTGTTCC
                                T  AT  T
GAM1055 KIAA0923 3' TGCCCCTGGTGGAACATTTG  25839       AG  AA__
                              CAGATGTT  AC   GGCA
                              ||||||||  ||   ||||
                              GTTTACAA  TG   CCGT
                                   GG  GTCC
GAM1055 KIAA0960 3' TGCCTCTTTTCATGTGGGA   92656     G  TT_  CAA
                              TCCCA ATG   AGA   GGCA
                              ||||| |||   |||   ||||
                              AGGGT TAC   TCT   CCGT
                                 G   TTT   ___
GAM1055 KIAA1277 3' TGCCTTGTTCTCTTAGA    64461    CC   TGTTA
                              TC  AGA    GACAAGGCA
                              ||  |||    |||||||||
                              AG  TCT    TTGTTCCGT
                               AT   C____
GAM1055 KIAA1691 3' GTGTGATTTAACATCCAGGA  92564    CA       _ AG
                              TCC  GATGTTAGA CA  GC
                              |||  |||||||| ||  ||
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                                AGG  CTACAATTT GT  TG
                                  AC        A  G_
GAM1055  KIAA1729  5'  TTGCCTTGAAGCTGGGA     89134       ATGTTAGA
                                TCCCAG       CAAGGCAA
                                ||||||       ||||||||
                                AGGGTC       GTTCCGTT
                                   GAA_____
GAM1055  KIAA1855  3'  TGCCTACATCTGGGG       92348          TAGACA
                                TCCCAGATGT     AGGCA
                                ||||||||||     |||||
                                GGGGTCTACA     TCCGT
                                       _______
GAM1055  MGC25056  3'  GTTTGACACAACATCTGAGA   79118    C       AGACA
                                TC CAGATGTT    AGGC
                                || ||||||||    ||||
                                AG GTCTACAA    TTTG
                                 A       CACAG
GAM1055  MGC3079   3'  GCCGCTGACATCTAGGA     50952     C       ACAA
                                TCC AGATGTTAG   GGC
                                ||| |||||||||   |||
                                AGG TCTACAGTC   CCG
                                  A        G___
GAM1055  RNF9      3'  TGTAGTGACATCTGAGA     53416    C       G_
                                TC CAGATGTTA  ACA
                                || |||||||||  |||
                                AG GTCTACAGT  TGT
                                 A        GA
GAM1055  SFRS12    3'  GTTGCCTTACCTCATGGGA   57528      _  T  TAGAC
                                TCCCA GA GT    AAGGCAAC
                                ||||| || ||    ||||||||
                                AGGGT CT CA    TTCCGTTG
                                   A  C  _____
GAM1055  SPTLC2    3'  GTCACTGTCAGCATCTGAGA   16806    C       A    A_
                                TC CAGATGTT GACA  GGC
                                || |||||||| ||||  |||
                                AG GTCTACGA CTGT  CTG
                                 A       _    CA
GAM1055  WBSCR17   3'  GGCTGCTCCCCCCAACATCTGG 81301          AGACAA    A
                                CCAGATGTT     GGCA CC
                                |||||||||     |||| ||
                                GGTCTACAA     TCGT GG
                                      CCCCCC    C
GAM1055  LOC124044 3'  GTTGCCTTGTCCCTGGGG    76027       ATGTTA
                                TCCCAG     GACAAGGCAAC
                                ||||||     ||||||||||
                                GGGGTC     CTGTTCCGTTG
                                   C_____
GAM1055  LOC126669 3'  TGCCTTGTACTATACA      75423     _   _
                                TGT TAG ACAAGGCA
                                ||| ||| ||||||||
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                                ACA ATC TGTTCCGT
                                  T   A
GAM1055  LOC130026 3'  GTTGCCTTGCTGGCTGTGAGA  56651    C  GAT    A
                                TC CA   GTTAG CAAGGCAAC
                                || ||   ||||| |||||||||
                                AG GT   CGGTC GTTCCGTTG
                                 A  GT_    _
GAM1055  LOC153516 3'  GGTACCCTACACCTGGGA    56710       A   TAGACA   CA
                                TCCCAG TGT     AGG  ACC
                                |||||| |||     |||  |||
                                AGGGTC ACA     TCC  TGG
                                   C   _______   CA
GAM1055  LOC154452 3'  TGCCTTGTGTGGGACTGAGA   81098    C   ATG   G
                                TC CAG   TTA ACAAGGCA
                                || |||   ||| ||||||||
                                AG GTC   GGT TGTTCCGT
                                 A   AG_   G
GAM1055  LOC158777 3'  TGTCAACATCTGGGA       82002          A
                                TCCCAGATGTT GACA
                                |||||||||||| ||||
                                AGGGTCTACAA CTGT
                                          _
GAM1055  LOC196955 5'  TTGCCTCGCCTCTAGCATTGGG 77394       A      CA__
            A                    TCCCAG TGTTAGA    AGGCAA
                                |||||| |||||||    ||||||
                                AGGGTT ACGATCT    TCCGTT
                                   _      CCGC
GAM1055  LOC199695 3'  GGCCACCTTGCTGGACATCTGG 88319          _ A    CAA
            G                    CCCAGATGTT AG CAAGG   CC
                                |||||||||| || |||||   ||
                                GGGTCTACAG TC GTTCC   GG
                                      G _    ACC
GAM1055  LOC205418 5'  TGCCCTGCCCTGGCATC     90690         A_ A
                                GATGTTAG  CA GGCA
                                ||||||||  || ||||
                                CTACGGTC  GT CCGT
                                     CC  C
GAM1055  LOC220058 5'  GCCAGGACCCAGACATCTGGGA 91727           AGACAA__
                                TCCCAGATGTT       GGC
                                ||||||||||       |||
                                AGGGTCTACAG       CCG
                                      ACCCAGGA
GAM1055  LOC253613 3'  GTTGCCTTGAAGTATTGGGA   96193       _ GTTAGA
                                TCCCAG AT     CAAGGCAAC
                                |||||| ||     |||||||||
                                AGGGTT TG     GTTCCGTTG
                                   A  AA____
GAM1055  LOC253776 3'  TGCCTTGTCTTTGTCATGG    97433     _   TT
                                CCA GATG  AGACAAGGCA
                                ||| ||||  ||||||||||
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                                GGT CTGT  TCTGTTCCGT
                                  A   T_
GAM1055  LOC257490 3'  TGCCTTGTGTGGGACTGAGA  97714   C  ATG  G
                                TC CAG   TTA ACAAGGCA
                                || |||   ||| ||||||||
                                AG GTC   GGT TGTTCCGT
                                 A  AG_   G
GAM1055  LOC257492 3'  TGCCTTGTGTGGGACTGAGA  97717   C  ATG  G
                                TC CAG   TTA ACAAGGCA
                                || |||   ||| ||||||||
                                AG GTC   GGT TGTTCCGT
                                 A  AG_   G
GAM1055  LOC257539 3'  TGCCTTGTGTGCGACTGAGA  97704   C  A  T G
                                TC CAG TGT A ACAAGGCA
                                || ||| ||| | ||||||||
                                AG GTC GCG T TGTTCCGT
                                 A  A  _ G
GAM1055  LOC257539 3'  TGCCTTGTGTGCGACTGAGA  97705   C  A  T G
                                TC CAG TGT A ACAAGGCA
                                || ||| ||| | ||||||||
                                AG GTC GCG T TGTTCCGT
                                 A  A  _ G
GAM1055  LOC257578 3'  TGCCTTGTGTGCGACTGAGA  97824   C  A  T G
                                TC CAG TGT A ACAAGGCA
                                || ||| ||| | ||||||||
                                AG GTC GCG T TGTTCCGT
                                 A  A  _ G
GAM1055  LOC257578 3'  TGCCTTGTGTGCGACTGAGA  97825   C  A  T G
                                TC CAG TGT A ACAAGGCA
                                || ||| ||| | ||||||||
                                AG GTC GCG T TGTTCCGT
                                 A  A  _ G
GAM1055  LOC257606 3'  TGCCTTGTGTGGGACTGAGA  97893   C  ATG  G
                                TC CAG   TTA ACAAGGCA
                                || |||   ||| ||||||||
                                AG GTC   GGT TGTTCCGT
                                 A  AG_   G
GAM1056  ADH1B   3'  CTTAGACATAAAGTAAAAT   72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM1056  AHR     3'  ATCTCAGATGTTAAAATAAATG 7875       CAC  C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM1056  FDFT1   3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
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                                GTAAAGTGAAAG GAT
                                           _
GAM1056 JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                   CATTTCACTTTCACTGTCTGAGAT
                                   ||||||||||||||||||||||||
                                   GTAAAGTGAAAGTGACAGACTCTA

GAM1056 KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                   CA  TTCACTGTCTG GA
                                   ||  ||||||||||| ||
                                   GT  AGGTGACAGAC CT
                                    AT         C
GAM1056 PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                   ATTTCACTTT ACTGT
                                   |||||||||| |||||
                                   TAAAGTGAAA TGACA
                                         A
GAM1056 PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                   TTTCACTTTCA   TCTG GA
                                   ||||||||||   ||||| ||
                                   AAAGTGAAAGT   GGAC CT
                                         T__   _
GAM1056 WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                   TTTCA TTTCACTGTCT
                                   ||||| ||||||||||
                                   AAAGT AAAGTGACGGG
                                      A
GAM1056 ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                   TTTCACTTT  CTGT   AGAT
                                   |||||||||  ||||   ||||
                                   AAAGTGAAA  GACA   TCTA
                                         C_   CG_
GAM1056 CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                   TTCACTTTCA  GT  GAG
                                   ||||||||||  ||  |||
                                   AAGTGAAAGT  CA  CTC
                                         CT  __
GAM1056 EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                   CTTTCACT TC  GAGAT
                                   |||||||| ||  |||||
                                   GAAAGTGA AG  TTCTA
                                        G  TC
GAM1056 FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
              G                     CATTTC        GTCTGAGAT
                                    ||||||        |||||||||
                                    GTAAAG        CAGACTCTA
                                       AAACATTT_
GAM1056 FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                   CATTTCA   TCACTGTCTGAGAT
                                   |||||||   ||||||||||||||
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                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM1056 KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM1056 KLHL6    3' ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM1056 NIR3     3' GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM1056 PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM1056 PP35     3' ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM1056 PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148       TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM1056 SEP15    3' TCCTACAGTAAGAGTGAAA   14934       C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM1056 SFXN2    3' CTCAGGGGAAAAAAGTGAAA  73941       CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM1056 LOC149703 3' ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM1056 LOC154007 3' ATCTCAAACCCTTTAGTGAAA  81015      TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
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                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM1056  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM1056  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                      _
GAM1057  AHR      3'  AATAAATGGTTTGGT       7872      TTAG
                                ACC    AAACCATTTATT
                                |||    ||||||||||||
                                TGG    TTTGGTAAATAA
                                  _____
GAM1057  BDKRB2    3'  AATAAATGGATGAGGTTT     5260         GAAA
                                AAACCTTA    CCATTTATT
                                ||||||||    |||||||||
                                TTTGGAGT    GGTAAATAA
                                     A___
GAM1057  DKFZp761D112 3'  AATAAATGGTGCTAAAGTGTAT 50186     A  C    AA
                                ATA AC TTAG  ACCATTTATT
                                ||| || ||||  ||||||||||
                                TAT TG AATC  TGGTAAATAA
                                  G  A   G_
GAM1057  DNM1L    3'  AATAAATGGCTGTTTCTAAAGT 23801    T    C      ___
            TTCC                    A AAAC TTAGAAA   CCATTTATT
                                | |||| |||||||   |||||||||
                                C TTTG AATCTTT   GGTAAATAA
                                 C    A      GTC
GAM1057  EAT2     3'  TGGTTTTTAAGGTTTA      79283
                                TAAACCTTAGAAACCA
                                ||||||||||||||||
                                ATTTGGAATTTTTGGT

GAM1057  ENDOFIN   3'  TGGTTTCTAAAGTCTGT     28388     A  C
                                ATA AC TTAGAAACCA
                                ||| || ||||||||||
                                TGT TG AATCTTTGGT
                                  C  A
GAM1057  FLJ14640  3'  AATAAATGGTCTCATAGTTTA  51478       CTTA  A
                                TAAAC    GA ACCATTTATT
                                |||||    || ||||||||||
                                ATTTG    CT TGGTAAATAA
                                   ATA_  C
GAM1057  KIAA0284  3'  AGGTGGGCTTCCAAGGT     63114       A   A_
                                ACCTT GAA  CCATTT
                                ||||| |||  ||||||
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                                TGGAA CTT  GGTGGA
                                   C   CG
GAM1057  KIAA0825  3'  GTGGGTGTTTCTAAGG      61028          C
                                CCTTAGAAAC ATTTAT
                                |||||||||| ||||||
                                GGAATCTTTG TGGGTG
                                          _
GAM1057  KIAA1374  3'  AATAAATGGTTAAAAGGTTTTA 61238    T      AGA
                                A AAACCTT   AACCATTTATT
                                | |||||||   ||||||||||
                                A TTTGGAA   TTGGTAAATAA
                                 T      AA_
GAM1057  OSBPL8    3'  GGTTTCTAGGATTTAT      40459       C
                                ATAAA CTTAGAAACC
                                ||||| ||||||||||
                                TATTT GGATCTTTGG
                                   A
GAM1057  LOC130814 3'  AATAAATGACTAGGGTT     74983         AAAC
                                AACCTTAG    CATTTATT
                                ||||||||    ||||||||
                                TTGGGATC    GTAAATAA
                                     A___
GAM1057  LOC160897 3'  AATAAATGATTTCTCTAAGGT  82242         __  C
                                ACCTTAGA  AA CATTTATT
                                ||||||||  || ||||||||
                                TGGAATCT  TT GTAAATAA
                                     CT  A
GAM1057  LOC202347 3'  AATAAATGGTTCTATGTTTTC  90342    T    CT     A
                                A AAAC  TAGAA CCATTTATT
                                | ||||  ||||| |||||||||
                                C TTTG  ATCTT GGTAAATAA
                                 T   T_    _
GAM1057  LOC253609 3'  GGTTTCTAGGGTTTAT      96762
                                ATAAACCTTAGAAACC
                                ||||||||||||||||
                                TATTTGGGATCTTTGG

GAM1057  LOC57151  3'  AATAAATGGTTTTCTTGG    39938    TTA
                                CC   GAAACCATTTATT
                                ||   ||||||||||||
                                GG   TTTTGGTAAATAA
                                  TTC
GAM1058  CDH6      3'  ACACTTGAACCTAATACC     17026          TG   T_
                                GGTATTAGGT  TCA  TGT
                                ||||||||||  |||  |||
                                CCATAATCCA  AGT  ACA
                                      __   TC
GAM1058  SH3BP2    3'  CATAAATGCACAACCTAACAC  11597    A       _    G
                                GT TTAGGTTGT CATT TATG
                                || |||||||| |||| ||||
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                                CA AATCCAACA GTAA ATAC
                                 C        C   _
GAM1058  DKFZP434I116 5'  CATACAATGATCCAACAACCT  31322      ATTA  TT
                                AGGT    GG  GTCATTGTATG
                                ||||    ||  ||||||||||
                                TCCA    CC  TAGTAACATAC
                                  ACAA  __
GAM1058  LOC145844 3'  ATAGGTACAACCTAACAC    77537    A       CA
                                GT TTAGGTTGT  TTGT
                                || |||||||||  ||||
                                CA AATCCAACA  GATA
                                 C        TG
GAM1058  LOC146952 5'  CATATGCCTCAACCTAACACTT 83863      A       TCATT
                                AGGT TTAGGTTG    GTATG
                                |||| ||||||||    |||||
                                TTCA AATCCAAC    TATAC
                                  C       TCCG_
GAM1059  CORO1C    3'  ACTTTTTAAAAAGTGCTA    26732       C       TT
                                TAGCAC TTTTTAAA  GGT
                                |||||| ||||||||  |||
                                ATCGTG AAAAATTT  TCA
                                   _       T_
GAM1059  MSL3L1    3'  ACTGTTTTTAAAAAGGTGCTA  54361            T_
                                TAGCACCTTTTTAAA  TGGT
                                ||||||||||||||  ||||
                                ATCGTGGAAAAATTT  GTCA
                                        TT
GAM1059  PKP2      3'  GATACCAATTTTTAAA      15887     TT
                                TTT  AAATTGGTATC
                                |||  ||||||||||
                                AAA  TTTAACCATAG
                                  TT
GAM1059  PVR       3'  CAAGTTAAAAAGGTCTA     21473     C        A
                                TAG ACCTTTTTAA TTG
                                ||| |||||||||| |||
                                ATC TGGAAAAATT AAC
                                  _        G
GAM1059  ZFHX1B    3'  ATACATTTTAAAAAGGTGC    28921           TTG
                                GCACCTTTTTAAA   GTAT
                                ||||||||||||   ||||
                                CGTGGAAAAATTT   CATA
                                       TA_
GAM1059  AKAP11    3'  AATTTAAAAAGGTGCT      32699
                                AGCACCTTTTTAAATT
                                ||||||||||||||||
                                TCGTGGAAAAATTTAA

GAM1059  ARGBP2    5'  ACCTTTTAAAAAGGGCTA    13193      A        TT
                                TAGC CCTTTTTAAA  GGT
                                |||| ||||||||||  |||
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                                ATCG GGAAAAATTT  CCA
                                  _        T_
GAM1059  ARGBP2   5'  ACCTTTTAAAAAGGGCTA    40771      A        TT
                                TAGC CCTTTTTAAA  GGT
                                |||| ||||||||||  |||
                                ATCG GGAAAAATTT  CCA
                                  _        T_
GAM1059  BHC80    3'  GATTTCTATTAAAAAGGTGT   33534           ATT  T
                                GCACCTTTTTAA   GG ATC
                                ||||||||||||   || |||
                                TGTGGAAAAATT   CT TAG
                                       AT_  T
GAM1059  CLDN1    3'  AATTTAAAAAGTGCTA      40846       C
                                TAGCAC TTTTTAAATT
                                |||||| ||||||||||
                                ATCGTG AAAAATTTAA

                                  _
GAM1059  CXorf1   3'  AATTTAAAAAGGTACT      16302     C
                                AG ACCTTTTTAAATT
                                || ||||||||||||
                                TC TGGAAAAATTTAA
                                 A
GAM1059  DDX31    3'  GTACCGTTAAAAAGG       42925         AT
                                CCTTTTTAA  TGGTAT
                                |||||||||  ||||||
                                GGAAAAATT  GCCATG

                                    __
GAM1059  EBF2     3'  GATACCAATTTAGTTTATGC   42645     CCTTT
                                GCA    TTAAATTGGTATC
                                |||    ||||||||||||||
                                CGT    GATTTAACCATAG
                                  ATTT_
GAM1059  KIAA0648 3'  GATACCAATGATAGAAA     82654       A_
                                TTTTTA  ATTGGTATC
                                ||||||  |||||||||
                                AAAGAT  TAACCATAG
                                    AG
GAM1059  MGC22014 3'  ATACTGAAAAAGGGCTA     64488      A     TAAA TG
                                TAGC CCTTTT    T  GTAT
                                |||| ||||||    |  ||||
                                ATCG GGAAAA    A  CATA
                                  _     _____ GT
GAM1059  MGC2452  5'  GATACGTGCAAAAGGTGCTA  50984          TAA  TG
                                TAGCACCTTTT   AT  GTATC
                                ||||||||||   ||  |||||
                                ATCGTGGAAAA   TG  CATAG
                                       CG_  __
GAM1059  MGC29937 3'  AATTTAAAAAGTGCTA      58108       C
                                TAGCAC TTTTTAAATT
                                |||||| ||||||||||
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                                ATCGTG AAAAATTTAA
                                      _
GAM1059  PDGFC    3'  ACCTGGTTTTTAAAAAGGAACT 32494     CA        TT___
              A                  TAG  CCTTTTTAAA    GGT
                                 |||  ||||||||||    |||
                                 ATC  GGAAAAATTT    CCA
                                   AA         TTGGT
GAM1059  PSP1     3'  GCCATTTAAAAACATGCTA   36914      CC        T
                                 TAGCA  TTTTTAAAT GGT
                                 |||||  ||||||||| |||
                                 ATCGT  AAAAATTTA CCG
                                    AC        _
GAM1059  THEA     3'  ATCACCAAAAAGGTGGC     66275    _      TAAAT    _
                                 GC ACCTTTT    TGGT AT
                                 || |||||||    |||| ||
                                 CG TGGAAAA    ACCA TA
                                  G      _____   C
GAM1059  LOC149506 3'  GATACCAACTGGGGGACGGC   84463    A__    TTAAA
                                 GC   CCTTT    TTGGTATC
                                 ||   |||||    ||||||||
                                 CG   GGGGG    AACCATAG
                                  GCA    TC___
GAM1059  LOC196047 3'  ACCAATTCCGTAAGGTGCT    89585        TTTA
                                 AGCACCTT    AATTGGT
                                 ||||||||    |||||||
                                 TCGTGGAA    TTAACCA
                                      TGCC
GAM1059  LOC255231 3'  ATACCAATCTAGAGAG      95370        A
                                 CTTTTTA ATTGGTAT
                                 ||||||| ||||||||
                                 GAGAGAT TAACCATA
                                     C
GAM1059  LOC57228  3'  GATACCACAGTAAAAGG     39999        AAT
                                 CTTTTTA   TGGTATC
                                 |||||||   |||||||
                                 GGAAAAT   ACCATAG
                                     GAC
GAM1059  LOC91960  3'  GATACCAATTATGTGGCTGC   67663     _  TTTTTA
                                 GCA CC     AATTGGTATC
                                 ||| ||     ||||||||||
                                 CGT GG     TTAACCATAG
                                   C  TGTA__
GAM1060  SLC17A4   3'  CAACAGTTCTTCATGTAGC    18525      CAGT
                                 GCTGC    TGAAGAACTGTTG
                                 |||||    |||||||||||||
                                 CGATG    ACTTCTTGACAAC
                                    T___
GAM1060  CITED1    5'  CAACAGCTCCAGCTGGCAGC   14729          AA  A
                                 GCTGCCAGTTG  GA CTGTTG
                                 ||||||||||  || ||||||
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                                CGACGGTCGAC  CT GACAAC
                                      __ C
GAM1060  FLJ10900  5'  CAACAGTTCTTGCTGAAGCAGT 65590       __    TG
              T                    AGCTGC  CAGT  AAGAACTGTTG
                                   ||||||  ||||  ||||||||||
                                   TTGACG  GTCG  TTCTTGACAAC
                                     AA   __
GAM1060  HS6ST     3'  CAACAGTTCCTTTGCCAGCAGC 62025      CA  T  A
                                   GCTGC  GT GA GAACTGTTG
                                   |||||  || || |||||||||
                                   CGACG  CG TT CTTGACAAC
                                     AC  T  C
GAM1060  MGC4638   3'  CAACAGTTCTTCAAGTG     48939    G
                                   CA TTGAAGAACTGTTG
                                   || ||||||||||||||
                                   GT AACTTCTTGACAAC
                                    G
GAM1060  ZNF262    3'  TTCCCCAATGGCAGCTT     17492         G   AA
                                   AAGCTGCCA TTG  GAA
                                   |||||||||  |||  |||
                                   TTCGACGGT AAC  CTT
                                        _  CC
GAM1060  LOC115051 3'  CAACAGTTCCTTTGCCAGCAGC 60036      CA  T  A
                                   GCTGC  GT GA GAACTGTTG
                                   |||||  || || |||||||||
                                   CGACG  CG TT CTTGACAAC
                                     AC  T  C
GAM1060  LOC143153 3'  CAGCCTCAAGCTGGCAGC    76463         GA  AA
                                   GCTGCCAGTT  AG  CTG
                                   ||||||||||  ||  |||
                                   CGACGGTCGA  TC  GAC
                                        AC  C_
GAM1060  LOC168512 5'  CAACAGCCTCTCTGGCAGCTT  82714          TTGA   A_
                                   AAGCTGCCAG   AGA  CTGTTG
                                   ||||||||||   |||  ||||||
                                   TTCGACGGTC   TCT  GACAAC
                                        _____  CC
GAM1060  LOC199923 3'  AACAGTTCCAGACCAGC     88494     CCA   GAA
                                   GCTG   GTT   GAACTGTT
                                   ||||   |||   ||||||||
                                   CGAC   CAG   CTTGACAA
                                     ___   AC_
GAM1060  LOC199926 3'  TAGTCCTTCAACTCACAGCTT  89880       CC       A
                                   AAGCTG  AGTTGAAG ACTG
                                   ||||||  |||||||| ||||
                                   TTCGAC  TCAACTTC TGAT
                                     AC       C
GAM1060  LOC202316 3'  TAGTCCTTCAACTCACAGCTT  90340       CC       A
                                   AAGCTG  AGTTGAAG ACTG
                                   ||||||  |||||||| ||||
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                                TTCGAC  TCAACTTC TGAT
                                   AC       C
GAM1060  LOC221479 3'  CAACAACTACAGCAGCAGC   92222      CA    A  AAC
                                GCTGC  GTTG AG   TGTTG
                                |||||  |||| ||   |||||
                                CGACG  CGAC TC   ACAAC
                                   A_    A  A__
GAM1061  ADCY6     3'  AGCTGAAGGGACCAA      30922        C    ACCA
                                TTGGTCCC TTCA    GCT
                                |||||||| ||||    |||
                                AACCAGGG AAGT    CGA
                                   _    _____
GAM1061  ADCY6     3'  AGCTGAAGGGACCAA      40613        C    ACCA
                                TTGGTCCC TTCA    GCT
                                |||||||| ||||    |||
                                AACCAGGG AAGT    CGA
                                   _    _____
GAM1061  COL6A1    3'  TAGCTGGTTTTTCCCACCAA   8479       CCCCTTC
                                TTGGT      AACCAGCTA
                                |||||      |||||||||
                                AACCA      TTGGTCGAT
                                   CCCTTT_
GAM1061  DDX9      3'  TTGTAGTTTAAGGAAACCAA   88551      CC    CAACC
                                TTGGT  CCTT    AGCTACAG
                                |||||  ||||    ||||||||
                                AACCA  GGAA    TTGATGTT
                                   AA   T_____
GAM1061  GNS       3'  CTGTAGCTAGTCTTCAAGACCA 9084       CCCTTCA  C
                                TGGTC      AC AGCTACAG
                                |||||      || ||||||||
                                ACCAG      TG TCGATGTC
                                   AACTTC_  A
GAM1061  MYO1F     3'  CTGTGTGTGTCAAAGGGGACTA 82424          CA  _  GC
            A                    TTGGTCCCCTT  AC CA  TACAG
                                ||||||||||  ||  ||  |||||
                                AATCAGGGGAA  TG GT  GTGTC
                                      AC  T  __
GAM1061  PDE6D     3'  CTGCAGCCACCAGGGGACCAG  10491         TCAACCA   A
                                TTGGTCCCCT      GCT CAG
                                ||||||||||      ||| |||
                                GACCAGGGGA      CGA GTC
                                      CCAC___   C
GAM1061  RFX2      5'  CTGTTACTTACCAACGGGGACC 5310         TTCAACC  CT
            AA                    TTGGTCCCC      AG  ACAG
                                |||||||||      ||  ||||
                                AACCAGGGG      TC  TGTC
                                      CAACCAT  AT
GAM1061  SLC1A4    3'  CTGTGAAGCCAAAAGGGACCAG 11715         _______    AC
                                TTGGTCCC     CTTCA  CAG
                                ||||||||     |||||  |||
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                                GACCAGGG     GAAGT  GTC
                                     AAAACC    __
GAM1061  TBL1X    3'  CTGCCCCAAGGGGGACCAA   18932          CAAC_
                                TTGGTCCCCTT     CAG
                                ||||||||||     |||
                                AACCAGGGGGA     GTC
                                      ACCCC
GAM1061  TCF2     3'  AGTGTTGAGGGGACCAA     21373          T   CA
                                TTGGTCCCCT CAAC  GCT
                                |||||||||| ||||  |||
                                AACCAGGGGA GTTG  TGA
                                      _   __
GAM1061  TRIM14   3'  AGCTGCAGGGGCCAA       28849      T    TCAAC
                                TTGG CCCCT     CAGCT
                                |||| |||||     |||||
                                AACC GGGGA     GTCGA
                                  _    C____
GAM1061  C11orf14 3'  AGTGACTGAAGGGACCAA    40225        C   ACCA
                                TTGGTCCC TTCA    GCT
                                |||||||| ||||    |||
                                AACCAGGG AAGT    TGA
                                     _   CAG_
GAM1061  KIAA1305 5'  AGCGGTCGAAGGGGACCAA   46927          A   A
                                TTGGTCCCCTTC ACC GCT
                                |||||||||||| ||| |||
                                AACCAGGGGAAG TGG CGA
                                      C  _
GAM1061  LEAP-2   5'  TAGACAAGGCTGAAAGGGGCCA 53744        C    A  AG__
           A                     TTGGTCCC TTCA CC    CTA
                                |||||||| |||| ||    |||
                                AACCGGGG AAGT GG    GAT
                                     A    C  AACA
GAM1061  MGC13090 3'  CTGTGGTTTGGTGAAAGGAACC 51138      C  C    A   _
           AA                     TTGGT CC TTCA CCAG CTACAG
                                ||||| || |||| |||| ||||||
                                AACCA GG AAGT GGTT GGTGTC
                                   A  A    _    T
GAM1061  LOC148089 3'  CTGGGGTCACAGGGGACCAA   78632          TCAA__
                                TTGGTCCCCT     CCAG
                                ||||||||||     ||||
                                AACCAGGGGA     GGTC
                                      CACTGG
GAM1061  LOC255536 3'  GGTTGAGGGGACCAA       94474          T
                                TTGGTCCCCT CAACC
                                |||||||||| |||||
                                AACCAGGGGA GTTGG
                                      _
GAM1061  LOC257106 3'  AGCCCTGGGCAAAGGGGACCAG 95383          CAA  __
                                TTGGTCCCCTT   CCA  GCT
                                ||||||||||   |||  |||
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                                GACCAGGGGAA   GGT  CGA
                                      ACG   CC
GAM1062  AKAP13   3'  TCCTCAGAGACAAAGAAGA   89688        T    CTCCAT
                                TCTTCTTT TCTCT     GGA
                                |||||||| |||||     |||
                                AGAAGAAA AGAGA     CCT
                                     C    CT____
GAM1062  ASCL1    3'  CATGGATAAAAAAAGAAGAAGA 72776         CTC_______  CATG
            AGA                   TTCTTTTTCT        TC   G
                                |||||||||         ||   |
                                AAGAAGAAGA        AG   C
                                      AAAAAAIIIT  GTAC
GAM1062  ATP10C   3'  TCCATGGATATTGAAAAGAAAA 44413        CTC_________  CATG
            AGAAGA                CTTTTTCT         TC   GA
                                ||||||||         ||   ||
                                GAAAAAGA         AG   CT
                                     AAAGTTAIIIT  GTAC
GAM1062  BTC      5'  AGAAAGAAGAAAGAAGA     96341          _  C
                                TCTTCTTTTT CT TCT
                                |||||||||| || |||
                                AGAAGAAAGA GA AGA
                                      A  A
GAM1062  CBFA2T1  3'  ATGGAAAAAAAAAAAAGAGGA  15105         CTCTC_
                                TCTTCTTTTT     TCCAT
                                ||||||||||     |||||
                                AGGAGAAAAA     AGGTA
                                      AAAAAA
GAM1062  CD83     3'  ATCCATAAAGAAGCAATAAAGA 14882        TT__  C   CC
            AGA                   TCTTCTTT    CT TCT  ATGGAT
                                ||||||||    || |||  ||||||
                                AGAAGAAA    GA AGA  TACCTA
                                     TAAC  _   AA
GAM1062  CDH19    3'  TCCATGGAAAATAGACGA    40953    T   T   CTCTC
                                TC TCT TTT     TCCATGGA
                                || ||| |||     ||||||||
                                AG AGA AAA     AGGTACCT
                                 C   T   _____
GAM1062  CELL     3'  CCATCCCAGGAGAATAAGAAGA 8409         T     CTCC
                                TCTTCTT TTCTCT    ATGG
                                ||||||| ||||||    ||||
                                AGAAGAA AAGAGG    TACC
                                     T     ACCC
GAM1062  CHD3     3'  CATGGATATCAAAAGAAAAAGA 7040          CTC_______  CATG
            GGA                   TTCTTTTTCT        TC   G
                                ||||||||||        ||   |
                                GAGAAAAAGA        AG   C
                                      AAACTAIIIT  GTAC
GAM1062  CPNE3    3'  GGAAAGAAAAAAGAAGA     14029          C   C
                                TCTTCTTTTT TCT TCC
                                |||||||||| ||| |||
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                                AGAAGAAAAA AGA AGG
                                      _  A
GAM1062  CYP4F3   3'  GGAAAGAAAGAAAGAA     6119        C  C
                                TTCTTTTT TCT TCC
                                |||||||| ||| |||
                                AAGAAAGA AGA AGG
                                     A  A
GAM1062  DTR      3'  CATGGATAAAAAAAGAAGAAGA 8689          CTC_______  CATG
             AGA                   TTCTTTTTCT        TC   G
                                |||||||||          ||   |
                                AAGAAGAAGA        AG   C
                                     AAAAAAIIIT  GTAC
GAM1062  EFNB2    3'  TGGAAAGGAAAAAAGAA     14578        CT  C
                                TTCTTTTT  CT TCCA
                                ||||||||  || ||||
                                AAGAAAAA  GA AGGT
                                     AG  A
GAM1062  ENC1     3'  ATGAAGAGAAAAAAAGGA     13279        C    C
                                TTCTTTTT TCTCT CAT
                                |||||||| ||||| |||
                                AGGAAAAA AGAGA GTA
                                     A    A
GAM1062  HMGCS2   3'  CATGGATAGAGAAAGAGAA    18626          TC___  CATG
                                TTCTTTTTCTC    TC   G
                                ||||||||||    ||   |
                                AAGAGAAAGAG    AG   C
                                      AIIIT  GTAC
GAM1062  HOXB9    3'  TGGAAGAAAAAAAGAA      43780        C  C
                                TTCTTTTT TCT TCCA
                                |||||||| ||| ||||
                                AAGAAAAA AGA AGGT
                                     A  _
GAM1062  HOXC9    3'  GGAGAGACGAAAAAGAA     61264         _
                                TTCTTTTTC TCTCTCC
                                ||||||||| |||||||
                                AAGAAAAAG AGAGAGG
                                     C
GAM1062  IRS2     3'  ATGGAAAAAGAAAAAGAAGA   59715          CTC
                                TCTTCTTTTTCT   TCCAT
                                ||||||||||||   |||||
                                AGAAGAAAAAGA   AGGTA
                                      AAA
GAM1062  IRS2     3'  ATTGATGGAAAAAGAAAAAGAA 59716          CTC    G
             GA                   TCTTCTTTTTCT   TCCAT GAT
                                ||||||||||||   ||||| |||
                                AGAAGAAAAAGA   AGGTA TTA
                                      AAA    G
GAM1062  KCNK6    3'  GAGAAAGAAAAAGAAAGA     16694      _      C
                                TCTT CTTTTTCT TCTC
                                |||| |||||||| ||||
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                                AGAA GAAAAAGA AGAG
                                  A       A
GAM1062  KIF1B    3'  TCCATGGATACCTGAGAGGAAA 30592   C        _________  CATG
                AAAAGA                  TTTTTCTCTC       TC    GA
                                 ||||||||||       ||    ||
                                 AAAAGGAGAG       AG    CT
                                A         TCCAIIIT  GTAC
GAM1062  KLRC1    3'  CCATGGAGACAGAAAGTAGA   9614      _     C
                                TCT TTTTCT TCTCCATGG
                                ||| |||||| |||||||||
                                AGA GAAAGA AGAGGTACC
                                  T     C
GAM1062  KLRC1    3'  CCATGGAGACAGAAAGTAGA   23647     _     C
                                TCT TTTTCT TCTCCATGG
                                ||| |||||| |||||||||
                                AGA GAAAGA AGAGGTACC
                                  T     C
GAM1062  KLRC2    3'  CCATGGAGACAGAAAGTAGA   94528     _     C
                                TCT TTTTCT TCTCCATGG
                                ||| |||||| |||||||||
                                AGA GAAAGA AGAGGTACC
                                  T     C
GAM1062  LDHB     5'  AGAAGAAAAAGAAGA       9700            C
                                TCTTCTTTTTCT TCT
                                |||||||||||| |||
                                AGAAGAAAAAGA AGA
                                           _
GAM1062  LDHB     5'  CATGGATAGAAAAAGAAGAAGA 9706          CTC________  CATG
                AGA                   TTCTTTTTCT        TC    G
                                 ||||||||||        ||    |
                                 AAGAAGAAGA        AG    C
                                       AAAAGAIIIT  GTAC
GAM1062  LPIN2    5'  CCAGCCAGAGAAGAAAAAGA   27705         _    CCA
                                TCTTTTTCT CTCT   TGG
                                ||||||||| ||||   |||
                                AGAAAAAGA GAGA   ACC
                                      A    CCG
GAM1062  MAP1B    3'  CCAGAGAGAAAAAGAGAGA   19774     _          CCAT
                                TCT TCTTTTTCTCTCT    GG
                                ||| ||||||||||||    ||
                                AGA AGAAAAAGAGAGA    CC
                                  G          _____
GAM1062  MAP1B    3'  CCAGAGAGAAAAAGAGAGA   49270     _          CCAT
                                TCT TCTTTTTCTCTCT    GG
                                ||| ||||||||||||    ||
                                AGA AGAAAAAGAGAGA    CC
                                  G          _____
GAM1062  MMP16    3'  GAGGAGAAAAAGAAGA      19877           T
                                TCTTCTTTTTCTC CTC
                                |||||||||||| |||
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                                AGAAGAAAAAGAG GAG
                                              _
GAM1062  NAV2     3'  AGAGAGAAAAAAAAAAAGA   60153      C___
                                TCTT   TTTTTCTCTCT
                                ||||   ||||||||||
                                AGAA   AAAAAGAGAGA
                                  AAAA
GAM1062  NRXN1    5'  TGGAAGAAGAAAAAGAA     16636          _ C
                                TTCTTTTTCT CT TCCA
                                |||||||||| || ||||
                                AAGAAAAAGA GA AGGT
                                      A _
GAM1062  OGG1     3'  ATCCTGGGTCAAAAAAAAGAA  33670        CTCTC   T
                                TTCTTTTT    TCCA GGAT
                                ||||||||    |||| ||||
                                AAGAAAAA    GGGT CCTA
                                     AAACT   _
GAM1062  OGG1     3'  ATCCTGGGTCAAAAAAAAGAA  33673        CTCTC   T
                                TTCTTTTT    TCCA GGAT
                                ||||||||    |||| ||||
                                AAGAAAAA    GGGT CCTA
                                     AAACT   _
GAM1062  OGG1     3'  ATCCTGGGTCAAAAAAAAGAA  33674        CTCTC   T
                                TTCTTTTT    TCCA GGAT
                                ||||||||    |||| ||||
                                AAGAAAAA    GGGT CCTA
                                     AAACT   _
GAM1062  OGG1     3'  ATCCTGGGTCAAAAAAAAGAA  33675        CTCTC   T
                                TTCTTTTT    TCCA GGAT
                                ||||||||    |||| ||||
                                AAGAAAAA    GGGT CCTA
                                     AAACT   _
GAM1062  PABPN1   3'  GAGAGAGGAAAAAAAGA     16181      C
                                TCTT TTTTTCTCTCTC
                                |||| ||||||||||||
                                AGAA AAAAGGAGAGAG
                                  A
GAM1062  RORB     5'  TGGAGAGAAAGAAAAAGAA   22610          __
                                TTCTTTTTC  TCTCTCCA
                                |||||||||  ||||||||
                                AAGAAAAAG  AGAGAGGT
                                     AA
GAM1062  RP42     3'  TCCATGGATAGAAAAAGGAAAA 40206        CTC_________  CATG
            AGAAGA                  CTTTTTCT         TC   GA
                                ||||||||         ||   ||
                                GAAAAAGG         AG   CT
                                     AAAAAGAIIIT  GTAC
GAM1062  RXRA     3'  ATCCATAAAGAGAGTAAAGA  11402      TT     CC
                                TCTTT  CTCTCT  ATGGAT
                                |||||  ||||||  ||||||
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                                AGAAA  GAGAGA  TACCTA
                                  T_     AA
GAM1062  SCN3A    5'  ATCCACAGAGAAAGAAAGAA  22630        C    CCA
                                TTCTTTTT TCTCT   TGGAT
                                |||||||| |||||   |||||
                                AAGAAAGA AGAGA   ACCTA
                                    A    C__
GAM1062  SLC1A3   3'  GGAAGAATAAAAAAGAAGA   14798         C__  C
                                TCTTCTTTTT   TCT TCC
                                ||||||||||   ||| |||
                                AGAAGAAAAA   AGA AGG
                                      ATA  _
GAM1062  SNAI2    3'  CCACAGAGAGAGAGCTGCAAGA 11774     CTTT       CA
                                TCTT   TTCTCTCTC  TGG
                                ||||   |||||||||  |||
                                AGAA   GAGAGAGAG  ACC
                                  CGTC       AC
GAM1062  STAU2    5'  AGACAGAAAAAGAAGA      26901          C
                                TCTTCTTTTTCT TCT
                                |||||||||||| |||
                                AGAAGAAAAAGA AGA
                                       C
GAM1062  STS      3'  CATGGATAAAAAAAGAAAGAGA 4450         CTC________  CATG
            AGA                   TTCTTTTTCT        TC   G
                                  |||||||||         ||   |
                                  AAGAGAAAGA        AG   C
                                       AAAAAAIIIT  GTAC
GAM1062  TMOD3    3'  GGTAAGAGAAAAAAGAA     27245        _   CT
                                TTCTTTTT CTCT  CC
                                |||||||| ||||  ||
                                AAGAAAAA GAGA  GG
                                     A   AT
GAM1062  TRHDE    5'  CATGGATAGAAAAAGAAGA   25386          CTC_  CATG
                                TCTTCTTTTTCT   TC   G
                                ||||||||||||   ||   |
                                AGAAGAAAAAGA   AG   C
                                       IIIT  GTAC
GAM1062  TRIM9    5'  CATGGATAAAAAAAGAAGAAGA 30756         CTC________  CATG
            AGA                   TTCTTTTTCT        TC   G
                                  |||||||||         ||   |
                                  AAGAAGAAGA        AG   C
                                       AAAAAAIIIT  GTAC
GAM1062  VIP      3'  AGAGAGAAAATAAAGA      12603      CT
                                TCTT  TTTTCTCTCT
                                ||||  ||||||||||
                                AGAA  AAAAGAGAGA
                                  AT
GAM1062  VPS26    3'  CAGGAGAAAAAAAGAA      16907        CTC     A
                                TTCTTTTT   TCTCC TG
                                ||||||||   ||||| ||
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                                AAGAAAAA   AGAGG AC
                                   A__     _
GAM1062  XPC      3'  TCAGGAAAGAAAAGGAA     16138          CTC   A
                                TTCTTTTTCT   TCC TGG
                                ||||||||||   ||| |||
                                AAGGAAAAGA   AGG ACT
                                   A__   _
GAM1062  ABLIM    3'  ATCCAACTTGAGAAGAAAAA  9757         _  TCCA
                                TTTTTCT CTC    TGGAT
                                |||||||  |||    |||||
                                AAAAAGA GAG    ACCTA
                                   A   TTCA
GAM1062  ABLIM    3'  ATCCAACTTGAGAAGAAAAA  22018        _  TCCA
                                TTTTTCT CTC    TGGAT
                                |||||||  |||    |||||
                                AAAAAGA GAG    ACCTA
                                   A   TTCA
GAM1062  BRUNOL6  3'  AGAAAGAAACAGAAGA      53427        T    C
                                TCTTCT TTTCT TCT
                                ||||||  |||||  |||
                                AGAAGA AAAGA AGA
                                   C    A
GAM1062  C1orf22  3'  ATCCTTAAAAAAAGAAAAGGAA 47254           CTCTCCAT
                                TTCTTTTTCT       GGAT
                                ||||||||||       ||||
                                AAGGAAAAGA       CCTA
                                    AAAAAATT
GAM1062  C20orf50 5'  TCCTGGAGAAAAAGAAGA    70074          TCTC     T
                                TCTTCTTTT    TCTCCA GGA
                                |||||||||    ||||||  |||
                                AGAAGAAAA    AGAGGT CCT
                                    ____     _
GAM1062  C20orf80 5'  AGAGAAAAAGAGAAGA      65284          C
                                TCTTCTTTTT TCTCT
                                |||||||||| |||||
                                AGAAGAGAAA AGAGA
                                    A
GAM1062  C6.1A    3'  CCATGGCGAGGAGAAAAAAGA  44281      C     T   T
                                TCTT TTTTTC CTC CCATGG
                                ||||  ||||||  |||  ||||||
                                AGAA AAAGAG GAG GGTACC
                                  A     _  C
GAM1062  C6orf37  3'  CAGGAGAGAAAAAAA       67476       C      A
                                TTTTT TCTCTCC TG
                                |||||  |||||||  ||
                                AAAAA AGAGAGG AC
                                  A      _
GAM1062  CENTA2   3'  AGAAAGAAAAAGAGGA       37263           C
                                TCTTCTTTTTCT TCT
                                ||||||||||||  |||
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                                AGGAGAAAAAGA AGA
                                      A
GAM1062  CHRFAM7A  3'  CATGGATAAAAAAAGAAGAAGA 95018          CTC_______  CATG
            AGA                   TTCTTTTTCT         TC    G
                                  ||||||||||         ||    |
                                  AAGAAGAAGA         AG    C
                                       AAAAAAIIIT  GTAC
GAM1062  CLONE24945 3'  TGTGGAGAAAGAAAAA      31625        C
                                  TTTTTCT TCTCCATG
                                  ||||||| ||||||||
                                  AAAAAGA AGAGGTGT
                                      A
GAM1062  DKFZp434L0850 5'  CCAAGGTGAGAAAAAAA     34108       C    T  A
                                  TTTTT TCTC CC TGG
                                  ||||| |||| || |||
                                  AAAAA AGAG GG ACC
                                     A    T  A
GAM1062  E2IG3    3'  TGGAATAAAAAAAGAAGA    26851          CTCTC
                                  TCTTCTTTTT     TCCA
                                  ||||||||||     ||||
                                  AGAAGAAAAA     AGGT
                                       AATA_
GAM1062  EPB41L1   3'  TCCATGGATTGAAATGAGAAAA 70597         TC_________  CATG
            AGAA                    CTTTTTCTC         TC    GA
                                    |||||||||         ||    ||
                                    GAAAAAGAG         AG    CT
                                         TAAAGTIIIT  GTAC
GAM1062  FLJ10300  5'  CAGGGAAAAAGAAAAAGACAGA 36000     _       CTC   A
                                  TCT TCTTTTTCT   TCC TG
                                  ||| |||||||||   ||| ||
                                  AGA AGAAAAAGA   AGG AC
                                    C        AAA   G
GAM1062  FLJ11710  5'  AGAGAGAAAAAGAAAGA     45824      _
                                  TCTT CTTTTTCTCTCT
                                  |||| ||||||||||||
                                  AGAA GAAAAAGAGAGA
                                     A
GAM1062  FLJ11710  5'  CATGGATAGAGAAAAAGAAAGA 45826      _       TC___  CATG
                                  TCTT CTTTTTCTC     TC    G
                                  |||| |||||||||     ||    |
                                  AGAA GAAAAAGAG     AG    C
                                     A        AIIIT  GTAC
GAM1062  FLJ12838  3'  ATCTATTGAAGAAAAAAAGAA  44967        C   C  C
                                  TTCTTTTT TCT TC ATGGAT
                                  |||||||| ||| || ||||||
                                  AAGAAAAA AGA AG TATCTA
                                       A   _  T
GAM1062  FLJ20464  3'  ATCCACAAAGAAAGAGAAAG   35227        C   CCA
                                  CTTTTTCT TCT   TGGAT
                                  |||||||| |||   |||||
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                                GAAAGAGA AGA   ACCTA
                                    A   AAC
GAM1062  FLJ20574  3'  CCAGGAAGAAAAAAAAAAGA   35419     C    C  C  A
                                TCTT TTTTT TCT TCC TGG
                                |||| ||||| ||| ||| |||
                                AGAA AAAAA AGA AGG ACC
                                  A    A  _  _
GAM1062  FLJ22774  3'  ATGGGGAAAAAAAAAAGAAGA   63725         CTC
                                TCTTCTTTTT   TCTCCAT
                                ||||||||||   |||||||
                                AGAAGAAAAA   AGGGGTA
                                      AAA
GAM1062  FLJ22774  3'  CTATGGGGAAAAAAAAAGAAGA 63726         CTC
                                TCTTCTTTTT   TCTCCATGG
                                ||||||||||   |||||||||
                                AGAAGAAAAA   AGGGGTATC
                                      AAA
GAM1062  GBA2      5'  CCATGTGGAAAAGAAGA     71023          TCTCTC
                                TCTTCTTTTTC     CATGG
                                ||||||||||      |||||
                                AGAAGAAAAGG     GTACC
                                      T_____
GAM1062  GBP2      5'  CCGTGAGAGAAAAAAAGAGGA  14656         C     C
                                TCTTCTTTTT TCTCTC ATGG
                                |||||||||| |||||| ||||
                                AGGAGAAAAA AGAGAG TGCC
                                      A     _
GAM1062  HDCMA18P  5'  GGAAGAGAAGAAAAAGAA    33592         _   _
                                TTCTTTTTCT CTCT CC
                                |||||||||| |||| ||
                                AAGAAAAAGA GAGA GG
                                      A   A
GAM1062  HDCMA18P  5'  TCCATGGATAAAAAGAAAAAGA 33594         CTC_____  CATG
            AGA                   CTTCTTTTTCT       TC   GA
                                ||||||||||       ||   ||
                                GAAGAAAAAGA       AG   CT
                                      AAAAIIIT  GTAC
GAM1062  HDCMA18P  5'  TCCATGGATAGAAAAAGAAAAA 33595        CTC_______  CATG
              GAAGA                 TCTTTTTCT        TC   GA
                                |||||||||        ||   ||
                                AGAAAAAGA        AG   CT
                                      AAAAGAIIIT  GTAC
GAM1062  KHDRBS3   3'  CCTGGGCAGAAAAAAAGAA   21618       C  C   T
                                TTCTTTTT TCT TCCA GG
                                |||||||| ||| |||| ||
                                AAGAAAAA AGA GGGT CC
                                      A  C   _
GAM1062  KIAA0042  3'  CCATGAAAGAAAAAGAA     29608         CTCTC
                                TTCTTTTTCT    CATGG
                                ||||||||||    |||||
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                                AAGAAAAAGA    GTACC
                                      AA___
GAM1062 KIAA0316 3' GAGAGAGAAAAGAAAAGA    69673     C_
                                TCTT  TTTTTCTCTCTC
                                ||||  ||||||||||||
                                AGAA  GAAAAGAGAGAG
                                  AA
GAM1062 KIAA0527 3' CACGGGAGAAAAAAAAAAGA  95793     C    C   T  A
                                TCTT TTTTT TCTC CC TG
                                |||| ||||| |||| || ||
                                AGAA AAAAA AGAG GG AC
                                  A    A   _ C
GAM1062 KIAA0527 3' GGGAGAAAAAAAAAAAGA    95804     C    C
                                TCTT TTTTT TCTCTC
                                |||| ||||| ||||||
                                AGAA AAAAA AGAGGG
                                  A    A
GAM1062 KIAA0595 3' ATCAACTAGAGAGAGAAAAA  30498          CATG_
                                TTTTTCTCTCTC    GAT
                                ||||||||||||    |||
                                AAAAAGAGAGAG    CTA
                                      ATCAA
GAM1062 KIAA0912 3' GAATGAGAAAAAGAAGA     64410          TC
                                TCTTCTTTTTCTC  TC
                                ||||||||||||  ||
                                AGAAGAAAAAGAG  AG
                                       TA
GAM1062 KIAA1209 3' CTGTTGAAAGAGAAAAAG    60754         C  C
                                CTTTTTCTCT TC ATGG
                                |||||||||| || ||||
                                GAAAAAGAGA AG TGTC
                                      A  T
GAM1062 KIAA1301 3' TGGAAGAGAAAAAAAGAA    66344        C    _
                                TTCTTTTT TCTCT CCA
                                |||||||| ||||| |||
                                AAGAAAAA AGAGA GGT
                                     A    A
GAM1062 KIAA1853 5' CATGGATAGAAAAAGAAGA   69390          CTC_ CATG
                                TCTTCTTTTTCT   TC   G
                                ||||||||||||   ||   |
                                AGAAGAAAAAGA   AG   C
                                       IIIT  GTAC
GAM1062 KIAA1853 5' GGAAAGAAGAAAAAGAAGA   69396          _ C
                                TCTTCTTTTTCT CT TCC
                                |||||||||||| || |||
                                AGAAGAAAAAGA GA AGG
                                       A  A
GAM1062 KIAA1906 3' GGCAAGAGAAAAAAAGA     73195     C       CT
                                TCTT TTTTTCTCT  CC
                                |||| |||||||||  ||
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                                AGAA AAAAAGAGA  GG
                                  _       AC
GAM1062  KR18     3'  ATCTAAAGAAGAAAAAGAA   52739        C   CCA
                                TTCTTTTTCT TCT   TGGAT
                                |||||||||| |||   |||||
                                AAGAAAAAGA AGA   ATCTA
                                     _   A__
GAM1062  METAP2   3'  ATCCATGTTTAAAAAAGAAGG  60168        CTCTCTC
                                TCTTCTTTTT      CATGGAT
                                ||||||||||      |||||||
                                GGAAGAAAAA      GTACCTA
                                     ATTT___
GAM1062  MGC20647 5'  GGAAAGAAAGAAAGAA      95606        C   C
                                TTCTTTTT TCT TCC
                                |||||||| ||| |||
                                AAGAAAGA AGA AGG
                                    A   A
GAM1062  MGC33177 3'  TCCACAGAAAGAGAAGA     58010          CTCTCCA
                                TCTTCTTTTTCT      TGGA
                                ||||||||||||      ||||
                                AGAAGAGAAAGA      ACCT
                                     C_______
GAM1062  NR1H4    5'  GAAAGAAGAAAAGAAGA     17606        TC   C
                                TCTTCTTTT  TCT TC
                                |||||||||  ||| ||
                                AGAAGAAAA  AGA AG
                                     GA   A
GAM1062  NUP54    3'  CATGGAGGGAAAAAGAA     60098        T T
                                TTCTTTTTC C CTCCATG
                                ||||||||| | |||||||
                                AAGAAAAAG G GAGGTAC
                                     _ _
GAM1062  PAK2     5'  CATGGATACAAACAGAAAAAGA 66535        CTC________  CATG
           AGA                    TTCTTTTTCT        TC    G
                                |||||||||         ||    |
                                AAGAAAAAGA        AG    C
                                     CAAACAIIIT  GTAC
GAM1062  PMAIP1   3'  CATGGATATAAAAAGAAAAAGA 40889         CTC________  CATG
           AG                     TTCTTTTTCT        TC    G
                                |||||||||         ||    |
                                AAGAAAAAGA        AG    C
                                     AAAATAIIIT  GTAC
GAM1062  PRO0245  5'  GGAAAGTAGAAAAAGAAGA   26134          _  C
                                TCTTCTTTTTCT CT TCC
                                |||||||||||| || |||
                                AGAAGAAAAAGA GA AGG
                                     T  A
GAM1062  PRO2133  3'  ATCCTGTTTCAGAGAAAAAAAA 37786      C        CTCCAT
           GA                     TCTT TTTTTCTCT     GGAT
                                |||| |||||||||     ||||
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                                AGAA AAAAAGAGA     CCTA
                                  A        CTTTGT
GAM1062  PRO2949   5'  GAGAAAGAAAAGGAAGA     37620           C
                                TCTTCTTTTTCT TCTC
                                |||||||||||| ||||
                                AGAAGGAAAAGA AGAG
                                       A
GAM1062  PS-PLA1   3'  TTCATGGAGTAAAAAAAA    31909      CTCT
                                TTTTT   CTCCATGGA
                                |||||   |||||||||
                                AAAAA   GAGGTACTT
                                   AAAT
GAM1062  PSCD1     5'  TCCACAGAGGAAAGGAA     78252           CTCCA
                                TTCTTTTTCTCT    TGGA
                                ||||||||||||    ||||
                                AAGGAAAGGAGA    ACCT
                                       C____
GAM1062  SAMHD1    3'  AGAGAGAAAGAAAAGA      61307      C
                                TCTT TTTTTCTCTCT
                                |||| ||||||||||
                                AGAA AGAAAGAGAGA
                                  A
GAM1062  SAMHD1    3'  GAGAAAGAAAAGAAAGA     61312      CT     C
                                TCTT  TTTTCT TCTC
                                ||||  |||||| ||||
                                AGAA  AAAAGA AGAG
                                  AG     A
GAM1062  SAMHD1    3'  GGAAAGAGAGAAAGAA      61315           C
                                TTCTTTTTCTCT TCC
                                |||||||||||| |||
                                AAGAAAGAGAGA AGG
                                       A
GAM1062  SCYA16    3'  GAGAGAGAAGAAGAAGA     15959
                                TCTTCTTTTTCTCTCTC
                                |||||||||||||||||
                                AGAAGAAGAAGAGAGAG

GAM1062  Sfmbt     5'  GGAAAGAAAGAAAGAA      32897         C   C
                                TTCTTTTT TCT TCC
                                |||||||| ||| |||
                                AAGAAAGA AGA AGG
                                     A   A
GAM1062  SLC12A8   5'  GGAAGAGAAAAGAAGAAGA   44902          C    _
                                TCTTCTTTTT TCTCT CC
                                |||||||||| ||||| ||
                                AGAAGAAGAA AGAGA GG
                                       A     A
GAM1062  SMARCF1   3'  CGTTGAGGAGAAAAA       37433         T   C
                                TTTTTCTC CTC ATG
                                |||||||| ||| |||
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                                AAAAAGAG GAG TGC
                                    _  T
GAM1062  SMARCF1   3'  CGTTGAGGAGAAAAA      57483        T  C
                                TTTTTCTC CTC ATG
                                |||||||| ||| |||
                                AAAAAGAG GAG TGC
                                    _  T
GAM1062  SMARCF1   3'  CGTTGAGGAGAAAAA      20037        T  C
                                TTTTTCTC CTC ATG
                                |||||||| ||| |||
                                AAAAAGAG GAG TGC
                                    _  T
GAM1062  TCF-3     3'  CATGGATAGAAAAAGAAAAAGG 48423         CTC_______  CATG
            AGA                   TTCTTTTTCT        TC   G
                                |||||||||         ||   |
                                AGGAAAAAGA        AG   C
                                     AAAAGAIIIT  GTAC
GAM1062  URB       5'  CATGGATAGAAAAAGAAGA   80378          CTC_  CATG
                                TCTTCTTTTTCT   TC   G
                                ||||||||||||   ||   |
                                AGAAGAAAAAGA   AG   C
                                      IIIT  GTAC
GAM1062  URB       5'  GAAAGAAGAAAAAGAAGA    80379          _  C
                                TCTTCTTTTTCT CT TC
                                |||||||||||| || ||
                                AGAAGAAAAAGA GA AG
                                      A  A
GAM1062  LOC113523 5'  ATGGAGAGAAAAAAGAAGA   73042          C
                                TCTTCTTTTT TCTCTCCAT
                                |||||||||| |||||||||
                                AGAAGAAAAA AGAGAGGTA
                                    _
GAM1062  LOC115757 3'  CATGGATAAAAAAAGAAGAAGA 73576         CTC_______  CATG
            AGA                   TTCTTTTTCT        TC   G
                                |||||||||         ||   |
                                AAGAAGAAGA        AG   C
                                     AAAAAAIIIT  GTAC
GAM1062  LOC123876 3'  GAGAAAGAGAAAGAAGA     74247          C
                                TCTTCTTTTTCT TCTC
                                |||||||||||| ||||
                                AGAAGAAAGAGA AGAG
                                      A
GAM1062  LOC129852 3'  ATGGAAAAAGAGAAAAAAGA   74898      CT      C__
                                TCTT  TTTTCTCT   TCCAT
                                ||||  ||||||||  |||||
                                AGAA  AAAAGAGA   AGGTA
                                   __       AAA
GAM1062  LOC131870 3'  TATCCATGGAGAGAGAAAAAGA 75023                  III
            AGA                   CTTCTTTTTCTCTCTCCATGGAT   A
                                |||||||||||||||||||||||  |
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                                  GAAGAAAAAGAGAGAGGTACCTA   T
                                                        III
GAM1062  LOC145098 5'  ATCCAAAACAGAGAGAAAAAAC 76989     TC         CCA_
             AGA                    TCT  TTTTTCTCTCT    TGGAT
                                  |||  ||||||||||    |||||
                                  AGA  AAAAAGAGAGA    ACCTA
                                    CA          CAAA
GAM1062  LOC146723 3'  GAAAGAGAAAGAAAAAGA     78084      C        C
                                  TCTT TTTTTCTCT TC
                                  |||| ||||||||| ||
                                  AGAA AGAAAGAGA AG
                                    A        A
GAM1062  LOC146894 3'  ATGGAGGAGAAAAAGAA      59185           T
                                  TTCTTTTTCTC CTCCAT
                                  |||||||||| ||||||
                                  AAGAAAAAGAG GAGGTA

                                                  _
GAM1062  LOC146894 3'  CATGGATAGAAAAAGAAAAGGA 59187          CTC_______  CATG
             AGA                    TTCTTTTTCT         TC    G
                                  ||||||||||         ||    |
                                  AAGGAAAAGA         AG    C
                                        AAAAGAIIIT  GTAC
GAM1062  LOC146950 5'  TCCATGGATATCTGAAAGGAAA 83879         C  _________  CATG
             AGAAGA                 CTTTTTCT TC       TC    GA
                                  ||||||| ||       ||    ||
                                  GAAAAGGA AG       AG    CT
                                       A  TCTAIIIT  GTAC
GAM1062  LOC148145 3'  CCAGTTGGAGACAAAAAAGA   84115        CTC      __
                                  TCTTTTT   TCTCCA  TGG
                                  |||||||   ||||||  |||
                                  AGAAAAA   AGAGGT  ACC
                                      AC_     TG
GAM1062  LOC151126 3'  TGGTCAGAAAGAAAAAGAAAGA 80133      _       C   __
                                  TCTT CTTTTTCT TCT  CCA
                                  |||| |||||||| |||  |||
                                  AGAA GAAAAAGA AGA  GGT
                                    A       A   CT
GAM1062  LOC151429 5'  CCATGAAGGAAAAGAAG     85349           CTCTC
                                  CTTCTTTTTCT     CATGG
                                  ||||||||||     |||||
                                  GAAGAAAAGGA     GTACC
                                         A____
GAM1062  LOC152179 5'  CCATAAAATGAAAAGAGAAGA  85560          C  TCTCC
                                  TCTTCTTTTT TC     ATGG
                                  |||||||||| ||     ||||
                                  AGAAGAGAAA AG     TACC
                                         _ TAAAA
GAM1062  LOC152453 3'  CCTGTCTCAAGAAAAAAAGGAG 80594          C   CTCCAT_
             A                     TCTTCTTTTT TCT       GG
                                  |||||||||| |||       ||
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                                AGAGGAAAAA AGA      CC
                                     A   ACTCTGT
GAM1062  LOC157489 3'  CATGGATAAAAAAAGAGAAAGA 81433          CTC_______  CATG
              AGA                  TTCTTTTTCT        TC    G
                                   ||||||||||        ||    |
                                   AAGAAAGAGA        AG    C
                                        AAAAAAIIIT  GTAC
GAM1062  LOC157489 3'  GGGGAAGAAAGAAAAAAGA   81434      C__      C
                                   TCTT   TTTTTCT TCTCC
                                   ||||   ||||||| |||||
                                   AGAA   AGAAAGA AGGGG
                                     AAA      _
GAM1062  LOC157909 5'  TCCATGGATAAAAAAAGAAAAA 81629          CTC_______  CATG
              GAAGA                  TCTTTTTCT        TC    GA
                                   |||||||||        ||    ||
                                   AGAAAAAGA        AG    CT
                                        AAAAAAIIIT  GTAC
GAM1062  LOC158927 3'  AGACAGAAAAAGAAGA      86945           C
                                   TCTTCTTTTTCT TCT
                                   |||||||||||| |||
                                   AGAAGAAAAAGA AGA
                                         C
GAM1062  LOC163782 5'  TCCATAATGAAAAAGAA     82159          TCTCTCC
                                   TTCTTTTTC      ATGGA
                                   |||||||||      |||||
                                   AAGAAAAAG      TACCT
                                        TAA____
GAM1062  LOC169611 3'  ATCCACAGAGAAGCCCCAAGAA 82755         TTTCTC    CA
              GG                   TCTTCTT     TCTC  TGGAT
                                   |||||||     ||||  |||||
                                   GGAAGAA     AGAG  ACCTA
                                      CCCCGA    AC
GAM1062  LOC221395 3'  GAAAGGGAAAAAGAAGA     92029           C
                                   TCTTCTTTTTCTCT TC
                                   |||||||||||||| ||
                                   AGAAGAAAAAGGGA AG
                                         A
GAM1062  LOC253024 5'  AGACAGAAAAAGAAGA      97615           C
                                   TCTTCTTTTTCT TCT
                                   |||||||||||| |||
                                   AGAAGAAAAAGA AGA
                                         C
GAM1062  LOC253039 3'  AGAGAGACAAAAAAAAGA     96152      C   _
                                   TCTT TTTT TCTCTCT
                                   |||| |||| |||||||
                                   AGAA AAAA AGAGAGA
                                     A    C
GAM1062  LOC253263 3'  GGAAAGAAAAAAAGGA      97034         C   C
                                   TTCTTTTT TCT TCC
                                   |||||||| ||| |||
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                                AGGAAAAA AGA AGG
                                    A   A
GAM1062  LOC253296 3'  GGGAAGAGAAAAAGAA      94493          CT
                                TTCTTTTTCTCT  CC
                                ||||||||||||  ||
                                AAGAAAAAGAGA  GG
                                    AG
GAM1062  LOC253298 5'  GGGAAGAGAAAAAGAA      97217          CT
                                TTCTTTTTCTCT  CC
                                ||||||||||||  ||
                                AAGAAAAAGAGA  GG
                                    AG
GAM1062  LOC253612 5'  CATGGATAAAAAAAGAAGAAGA 96743         CTC________  CATG
           AGA                    TTCTTTTTCT        TC    G
                                ||||||||||        ||    |
                                AAGAAGAAGA        AG    C
                                    AAAAAAIIIT  GTAC
GAM1062  LOC253918 5'  ATCCAAGGTTGAAAAGAAAAAG 96232          C_  T_  A
           AAGG                   TCTTCTTTTTCT  TC  CC TGGAT
                                ||||||||||||  ||  || |||||
                                GGAAGAAAAAGA  AG  GG ACCTA
                                    AA  TT  A
GAM1062  LOC256283 5'  AGAGAATAAAAAGAAGA     97036          C_
                                TCTTCTTTTT  TCTCT
                                ||||||||||  |||||
                                AGAAGAAAAA  AGAGA
                                    TA
GAM1062  LOC257415 3'  GGAGAAAGAAAAAGAAGA    96077           C
                                TCTTCTTTTTCT TCTCC
                                |||||||||||| |||||
                                AGAAGAAAAAGA AGAGG
                                    A
GAM1062  LOC257415 3'  TCCATGGATACAAAAAAGAAAA 96079         CTC_________  CATG
           AGAAG                  CTTTTTCT          TC    GA
                                |||||||||         ||    ||
                                GAAAAAGA          AG    CT
                                    AAAAACAIIIT  GTAC
GAM1062  LOC257570 3'  GGGAAGAGAAAAAGAA      97836          CT
                                TTCTTTTTCTCT  CC
                                ||||||||||||  ||
                                AAGAAAAAGAGA  GG
                                    AG
GAM1062  LOC257571 5'  GGGAAGAGAAAAAGAA      97947          CT
                                TTCTTTTTCTCT  CC
                                ||||||||||||  ||
                                AAGAAAAAGAGA  GG
                                    AG
GAM1062  LOC56270  5'  ATCCACTAAAAGAAAAAGAGA  39017     T       CTCTCCA
                                TCT CTTTTTCT      TGGAT
                                ||| ||||||||      |||||
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                                AGA GAAAAAGA      ACCTA
                                  _       AAATC__
GAM1062 LOC90573 5' CATGGATAAAAAAAGAAGAAGA 63272          CTC________ CATG
              AGA                  TTCTTTTTCT        TC    G
                                   ||||||||||        ||    |
                                   AAGAAGAAGA        AG    C
                                        AAAAAAIIIT  GTAC
GAM1062 LOC92539 3' TCCATGAAGATGAGGAAAA    69642        _  C
                                   TTTTTCTC TCT CATGGA
                                   |||||||| ||| ||||||
                                   AAAAGGAG AGA GTACCT
                                        T   A
GAM1063 HAX1     3' CCAAACTGACCAAT       20383          GCA
                                   ATTGGTCAGT   TTGG
                                   ||||||||||   ||||
                                   TAACCAGTCA   AACC
                                        ___
GAM1063 ZNF135   5' CCACATCAACCAATGAC     12851         CA   CAT
                                   GTCATTGGT  GTG   TGG
                                   |||||||||  |||   |||
                                   CAGTAACCA  TAC   ACC
                                        AC   ___
GAM1063 CSNK1G1  3' TCCAATGCACCAATCACA    41872     C     CAGT
                                   TGT ATTGGT    GCATTGGA
                                   ||| ||||||    ||||||||
                                   ACA TAACCA    CGTAACCT
                                     C     _____
GAM1063 FLJ13840 5' TCCCTGCTGACCAATGAC    45366            CATT
                                   GTCATTGGTCAGTG    GGA
                                   ||||||||||||||    |||
                                   CAGTAACCAGTCGT    CCT
                                             C___
GAM1063 HSPC152  3' CCAACCCTTGACCCAATGACAC 94518          _   TGCA
                                   GTGTCATTGG TCAG    TTGG
                                   |||||||||| ||||    ||||
                                   CACAGTAACC AGTT    AACC
                                         C    CCC_
GAM1063 HSPC152  3' CCAACCCTTGACCCAATGACAC 33084          _   TGCA
                                   GTGTCATTGG TCAG    TTGG
                                   |||||||||| ||||    ||||
                                   CACAGTAACC AGTT    AACC
                                         C    CCC_
GAM1063 KIAA0523 3' TCCTGGACTAAGCCAATGACAC 67744          C_  G  TT
                                   GTGTCATTGGT  AGT CA  GGA
                                   ||||||||||  ||| ||  |||
                                   CACAGTAACCG  TCA GT  CCT
                                         AA   G  __
GAM1063 UBE2D3   3' TTCCAATACACTGTTTAATATA 12481      C__    T    C
              GCAC                    GTGT   ATTGG CAGTG ATTGGAA
                                   ||||   ||||| ||||| |||||||
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                                CACG   TAATT GTCAC TAACCTT
                                  ATA    T    A
GAM1063  LOC134121 3'  GCCTGACCAACAACAC      75153      CA       T
                                GTGT  TTGGTCAG GC
                                ||||  |||||||| ||
                                CACA  AACCAGTC CG
                                  AC       _
GAM1063  LOC221179 5'  TCCATTTTTGACCAAAGACAC  93548       A       TGCAT
                                GTGTC TTGGTCAG    TGGA
                                ||||| ||||||||    ||||
                                CACAG AACCAGTT    ACCT
                                  A       TTT__
GAM1064  ABCB1    5'  CCAGAACATTCCTCCTGGAA   6247       CTGT  CT
                                TTCC   GG  ATGTTCTGG
                                ||||   ||  |||||||||
                                AAGG   CC  TACAAGACC
                                  TCCT  T_
GAM1064  AGT      3'  CCAGAACACAGTGCCTGGCA   3454      __   TA__
                                TGT  GGC   TGTTCTGG
                                |||  |||   ||||||||
                                ACG  CCG   ACAAGACC
                                 GT   TGAC
GAM1064  ALDOB    3'  CCAGAATACCCACCCAAGAA   68087     CCT_   CTA
                                TTC   GTGG   TGTTCTGG
                                |||   ||||  ||||||||
                                AAG   CACC   ATAAGACC
                                  AACC   C__
GAM1064  ARL4     3'  CCAGAACACAGTTGTGGGAA   19198      T TG   A
                                TTCCC G  GCT TGTTCTGG
                                ||||| |  ||| ||||||||
                                AAGGG T  TGA ACAAGACC
                                  _ GT   C
GAM1064  B3GAT1   3'  CCAGAACAAAGGACAGAGAA   37827     C    GG  A
                                TTC CTGT  CT TGTTCTGG
                                ||| ||||  || ||||||||
                                AAG GACA  GA ACAAGACC
                                  A   G_  A
GAM1064  B3GAT1   3'  CCAGAACAAAGGACAGAGAA   53972     C    GG  A
                                TTC CTGT  CT TGTTCTGG
                                ||| ||||  || ||||||||
                                AAG GACA  GA ACAAGACC
                                  A   G_  A
GAM1064  CD79B    3'  CCAGAAGAGCCACAGG      41207         ATG
                                CCTGTGGCT   TTCTGG
                                |||||||||   ||||||
                                GGACACCGA   AAGACC
                                     G__
GAM1064  CD79B    3'  CCAGAAGAGCCACAGG      5271          ATG
                                CCTGTGGCT   TTCTGG
                                |||||||||   ||||||
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                                GGACACCGA   AAGACC
                                     G__
GAM1064  CDH3     3'  CCAAACGTCAGGCCACAG    8380          __    C
                                CTGTGGCT  ATGTT TGG
                                ||||||||  ||||| |||
                                GACACCGG  TGCAA ACC
                                     AC    _
GAM1064  COL5A1   5'  GCCAGAACAGCCGCCGCCACAA 3634    CC     TA____       III
              AGAA                   C  TGTGGC     TGTTCTGG   C
                                |  ||||||     ||||||||  |
                                G  ACACCG     ACAAGACC   G
                                 AA     CCGCCG       III
GAM1064  CRIM1    3'  CCAGAACAAAGGCAG       33173      GG  A
                                CTGT  CT TGTTCTGG
                                ||||  || ||||||||
                                GACG  GA ACAAGACC
                                  __ A
GAM1064  DIAPH2   3'  CCAAAACAAGTCTAGCAGGGAA 22063         __    A    C
                                TTCCCTGT  GGCT TGTT TGG
                                ||||||||  |||| |||| |||
                                AAGGGACG  CTGA ACAA ACC
                                     AT    _   A
GAM1064  DMD      3'  AGAAAATATAGTCACAGG    14414            __
                                CCTGTGGCTATGT  TCT
                                ||||||||||||  |||
                                GGACACTGATATA  AGA
                                      AA
GAM1064  ED1      3'  TTGGAACAATCACAGGGAA    7376          CTA    TG
                                TTCCCTGTGG   TGTTC  G
                                ||||||||||   |||||  |
                                AAGGGACACT   ACAAG  T
                                     A__     GT
GAM1064  EXTL3    3'  CCAAAACATGCCGCAGGGAG   7528           T    C
                                TTCCCTGTGGC ATGTT TGG
                                |||||||||||  ||||| |||
                                GAGGGACGCCG TACAA ACC
                                     _     A
GAM1064  FCRH3    3'  CCAGAGTGGCCCACAGG     53630        _   GT
                                CCTGTGG CTAT  TCTGG
                                |||||||  ||||  |||||
                                GGACACC GGTG  AGACC
                                     C   __
GAM1064  FECH     3'  CGTGGTGCCACAGGGAA     3753           __
                                TTCCCTGTGGC  TATG
                                ||||||||||  ||||
                                AAGGGACACCG  GTGC
                                      TG
GAM1064  FGFRL1   3'  CCAGAACATACAAGGA      41619     C   GGCT
                                TCC TGT    ATGTTCTGG
                                |||  |||    |||||||||
```

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                                AGG ACA    TACAAGACC
                                  A  ____
GAM1064  GATA4    3'  CCAGAACAACAACTGGGAA   9004       T  GGCTA
                                TTCCC GT    TGTTCTGG
                                ||||| ||    ||||||||
                                AAGGG CA    ACAAGACC
                                   T  ACA__
GAM1064  GNRH1    5'  CCATCACCAGCCACAGAGA   5883     C      AT  TC
                                TC CTGTGGCT  GT  TGG
                                || ||||||||  ||  |||
                                AG GACACCGA  CA  ACC
                                 A       C_  CT
GAM1064  HAMP     3'  CCAGAACATAGGTCTTGGAA  40991     CTGT  _
                                TTCC    GGC TATGTTCTGG
                                ||||    ||| ||||||||||
                                AAGG    CTG ATACAAGACC
                                  TT__   G
GAM1064  IPP      3'  TAGTTTGAGCCACAGAGAA   19729     C      ATGTT
                                TTC CTGTGGCT    CTG
                                ||| ||||||||    |||
                                AAG GACACCGA    GAT
                                  A       GTTT_
GAM1064  ITGB1    3'  CCAGTGTGGCCCAGGGAA    53369       T     GTT
                                TTCCCTG GGCTAT   CTGG
                                ||||||| ||||||   ||||
                                AAGGGAC CCGGTG   GACC
                                    _     T__
GAM1064  KCNQ1    3'  CCAGCTGCTGAGCCGCAGAGAA 4021     C      AT  T_
                                TTC CTGTGGCT  GT  CTGG
                                ||| ||||||||  ||  ||||
                                AAG GACGCCGA  CG  GACC
                                  A       GT  TC
GAM1064  KDR      3'  CAGAATACCACAAAGAA     9591     CC    CTA
                                TTC  TGTGG   TGTTCTG
                                |||  |||||   |||||||
                                AAG  ACACC   ATAAGAC
                                  AA    ___
GAM1064  LEP      3'  CCAGGGGCCCACAGGGAA    4047          _  ATGT
                                TTCCCTGTGG CT    TCTGG
                                |||||||||| ||    |||||
                                AAGGGACACC GG    GGACC
                                      C  ____
GAM1064  MKI67    3'  CCAGTGACCAGCCACAGGAGA  10041    _       AT  _
                                TC CCTGTGGCT  GTT CTGG
                                || |||||||||  ||| ||||
                                AG GGACACCGA  CAG GACC
                                 A        C_  T
GAM1064  NEFH     3'  CCGGAACAGCCAAAG       40780    G    AT
                                CT TGGCT  GTTCTGG
                                || |||||  |||||||
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                                GA ACCGA  CAAGGCC
                                 A    __
GAM1064 NXF2    5' CCAGAACATCACCAAG     35136    G   CT
                                CT TGG  ATGTTCTGG
                                || |||  |||||||||
                                GA ACC  TACAAGACC
                                 _  AC
GAM1064 PDE6D   3' CCAGCATACACACAGGGAA   10489        GC    TT
                                TTCCCTGTG  TATG  CTGG
                                |||||||||  ||||  ||||
                                AAGGGACAC  ATAC  GACC
                                     AC   __
GAM1064 PHEMX   5' CCAGCTGGAAACCACAGGGAG 57359         CTATGTT
                                TTCCCTGTGG     CTGG
                                ||||||||||     ||||
                                GAGGGACACC     GACC
                                      AAAGGTC
GAM1064 PHEMX   5' CCAGCTGGAAACCACAGGGAG 57364         CTATGTT
                                TTCCCTGTGG     CTGG
                                ||||||||||     ||||
                                GAGGGACACC     GACC
                                      AAAGGTC
GAM1064 PODXL   3' CCAGAATGACACAAAGGA    18230    C_   GCTAT
                                TCC  TGTG    GTTCTGG
                                |||  ||||    |||||||
                                AGG  ACAC    TAAGACC
                                  AA   AG___
GAM1064 PRODH   3' CTGGGACAGCCACTGGAA    32925     CT    AT   TG
                                TTCC  GTGGCT  GTTC  G
                                ||||  ||||||  ||||  |
                                AAGG  CACCGA  CAGG  C
                                  T_     __   GT
GAM1064 RANBP2L1 3' CCAGAATAAAACCACCAGGAA 17313     CT   CTA
                                TTCC  GTGG   TGTTCTGG
                                ||||  ||||   ||||||||
                                AAGG  CACC   ATAAGACC
                                  AC   AAA
GAM1064 REGL    3' CCAGAACATGAATTCAGG    21486     TGGC
                                CCTG    TATGTTCTGG
                                ||||    ||||||||||
                                GGAC    GTACAAGACC
                                  TTAA
GAM1064 SLC19A1  5' CCAGAATGCATCCAGAGGGAA 11755       G   CTA
                                TTCCCT TGG   TGTTCTGG
                                |||||| |||   ||||||||
                                AAGGGA ACC   GTAAGACC
                                   G   TAC
GAM1064 ST14    3' CCAGAACATACACTGTGAA   41765    CCT   GC
                                TTC   GTG  TATGTTCTGG
                                |||   |||  ||||||||||
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                                AAG   CAC  ATACAAGACC
                                  TGT   __
GAM1064  TBL2     3'  CCAGAACAACCTAGAGAA    52182     C   T  CTA
                                TTC CTG GG   TGTTCTGG
                                ||| ||| ||   ||||||||
                                AAG GAT CC   ACAAGACC
                                  A   _  A__
GAM1064  TBL2     3'  CCAGAACAACCTAGAGAA    24926     C   T  CTA
                                TTC CTG GG   TGTTCTGG
                                ||| ||| ||   ||||||||
                                AAG GAT CC   ACAAGACC
                                  A   _  A__
GAM1064  TCFL4    3'  CCAGGATAAGACCACAGGGAA 63461          _  A
                                TTCCCTGTGG CT TGTTCTGG
                                |||||||||| || ||||||||
                                AAGGGACACC GA ATAGGACC
                                      A  _
GAM1064  TFAP4    3'  CCGGGGCAGCCACAGGGAG   12237           AT
                                TTCCCTGTGGCT  GTTCTGG
                                ||||||||||||  |||||||
                                GAGGGACACCGA  CGGGGCC
                                              __
GAM1064  UBE2L6   3'  CCAGGGGGAGCCACGG     14873         ATG
                                CTGTGGCT   TTCTGG
                                ||||||||   ||||||
                                GGCACCGA   GGGACC
                                     GG_
GAM1064  UBQLN3   3'  CAAAACATAGTGGAG      33926      CTGTG      C
                                TTCC    GCTATGTT TG
                                ||||    |||||||| ||
                                GAGG    TGATACAA AC
                                  _____       A
GAM1064  UMOD     3'  CCAGTGCTCCAGCCACAG    12548         AT_  T
                                CTGTGGCT   GT CTGG
                                ||||||||   || ||||
                                GACACCGA   CG GACC
                                     CCT  T
GAM1064  WBSCR5   3'  CCAGAACAGGGCAGAG      26256    G  G  A
                                CT TG CT TGTTCTGG
                                || || || ||||||||
                                GA AC GG ACAAGACC
                                 G  G  _
GAM1064  WBSCR5   3'  CCAGAACAGGGCAGAG      41856    G  G  A
                                CT TG CT TGTTCTGG
                                || || || ||||||||
                                GA AC GG ACAAGACC
                                 G  G  _
GAM1064  WBSCR5   3'  CCAGAACAGGGCAGAG      50610    G  G  A
                                CT TG CT TGTTCTGG
                                || || || ||||||||
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                                GA AC GG ACAAGACC
                                 G  G  _
GAM1064  ZNF134   3'  CAGTTTAAGCCACAGGGAA   12846          A  TT
                                TTCCCTGTGGCT TG  CTG
                                |||||||||||| ||  |||
                                AAGGGACACCGA AT  GAC
                                       _  TT
GAM1064  ZNF36    3'  CCTTCGTAGCCACAAGG    93960    C       TTCT
                                CC TGTGGCTATG    GG
                                || ||||||||||    ||
                                GG ACACCGATGC    CC
                                 A        TT__
GAM1064  ABCA9    5'  CAGAACATGCAGAGA      54410    C   GGCT
                                TC CTGT    ATGTTCTG
                                || ||||    ||||||||
                                AG GACG    TACAAGAC
                                 A   _____
GAM1064  ADAMTSL1 3'  CCTCAAATAGCACAGGGAA   57686        G   GTTCT
                                TTCCCTGTG CTAT     GG
                                ||||||||| ||||     ||
                                AAGGGACAC GATA     CC
                                      _    AACT_
GAM1064  BAIAP1   3'  CCAGAACGGCAGCAGG     16449      G   AT
                                CCTGT GCT  GTTCTGG
                                ||||| |||  |||||||
                                GGACG CGG  CAAGACC
                                   A  __
GAM1064  BCKDK    3'  CCAGAACTTGGAGCAGGGAA  59793       GG   T
                                TTCCCTGT  CTA GTTCTGG
                                ||||||||  ||| |||||||
                                AAGGGACG  GGT CAAGACC
                                     A_   T
GAM1064  C11orf25 3'  CCAAATTAGGGCCACAG     48639        AT_   C
                                CTGTGGCT   GTT TGG
                                ||||||||   ||| |||
                                GACACCGG   TAA ACC
                                     GAT   _
GAM1064  C20orf112 3' CCAGTGCTGCCACAGGGA    54640         TAT  T
                                TCCCTGTGGC   GT CTGG
                                ||||||||||   || ||||
                                AGGGACACCG   CG GACC
                                      T__  T
GAM1064  C6orf26  3'  CCAAAACACAGAGCAGG     47509      GG  A    C
                                CCTGT  CT TGTT TGG
                                |||||  || |||| |||
                                GGACG  GA ACAA ACC
                                   A_  C    A
GAM1064  CGGBP1   5'  CTGGCACCACAGGGAA      13362         CTA    CT
                                TTCCCTGTGG   TGTT  G
                                ||||||||||   ||||  |
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                                AAGGGACACC   ACGG  C
                                      ____    T_
GAM1064  DKFZP566G1424 5'  CCAGTGCTGCCACAGGGA    84779          TAT  T
                                TCCCTGTGGC   GT CTGG
                                ||||||||||   || ||||
                                AGGGACACCG   CG GACC
                                     T__  T
GAM1064  DKFZp586I021 5'  CCAGACGTCACCACAGGGA    50088         CT    T
                                TCCCTGTGG  ATGT CTGG
                                |||||||||  |||| ||||
                                AGGGACACC  TGCA GACC
                                     AC   _
GAM1064  DKFZP727M111 5'  CCAATCTGGTCACAGGGAA    31407           T  TC
                                TTCCCTGTGGCTA GT  TGG
                                ||||||||||||| ||  |||
                                AAGGGACACTGGT TA  ACC
                                       C  __
GAM1064  ELF4     3'  CCGTGGATCAGCCACAGGGA   7431           AT   _
                                TCCCTGTGGCT  GTTC TGG
                                ||||||||||  |||| |||
                                AGGGACACCGA  TAGG GCC
                                      C_   T
GAM1064  ERG-1    3'  CCAGGATGCCAAAGG      41842     G    TAT
                                CCT TGGC   GTTCTGG
                                ||| ||||   |||||||
                                GGA ACCG   TAGGACC
                                  A   ____
GAM1064  FLJ00058  5'  CCAGAAATGCCAGCAGGGAA   78765       _   TATG
                                TTCCCTG TGGC    TTCTGG
                                ||||||| ||||    ||||||
                                AAGGGAC ACCG    AAGACC
                                    G   TA__
GAM1064  FLJ12816  3'  CCAGAACAGGACGACAGTGAA  41932     C    GGCTA
                                TTC CTGT    TGTTCTGG
                                ||| ||||    ||||||||
                                AAG GACA    ACAAGACC
                                  T   GCAGG
GAM1064  FLJ13315  3'  CCAGAACATAATACA      46568     GC
                                TGTG  TATGTTCTGG
                                ||||  ||||||||||
                                ACAT  ATACAAGACC
                                  A_
GAM1064  FLJ20010  3'  CCAGAACGATTGGAACAGG   38716      GG  __
                                CCTGT  CTA  TGTTCTGG
                                |||||  |||  ||||||||
                                GGACA  GGT  GCAAGACC
                                   A_   TA
GAM1064  FLJ22369  5'  ATGGCGCGACAGGGAA      49918        _ _
                                TTCCCTGT G GCTAT
                                |||||||| | |||||
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                                AAGGGACA C CGGTA
                                     G G
GAM1064  FLJ23563  3'  CCAGAATGCTACAAAAGAA   67593    CC_    TAT
                                TTC   TGTGGC   GTTCTGG
                                |||   ||||||   |||||||
                                AAG   ACATCG   TAAGACC
                                  AAA     ___
GAM1064  FLJ32332  3'  CACAGCACACAGGGAA      58299        _  A
                                TTCCCTGTG GCT TG
                                ||||||||| ||| ||
                                AAGGGACAC CGA AC
                                     A  C
GAM1064  GRIN3A    3'  CCAAGTGAAGCAGCCACAGGGA 55968         ATG  ___
                                TCCCTGTGGCT   TTC   TGG
                                ||||||||||   |||   |||
                                AGGGACACCGA   AAG   ACC
                                      CG_   TGA
GAM1064  HSPC166   3'  CCAGAACACATGGAGGGAA   26366      G  GCTA
                                TTCCCT TG    TGTTCTGG
                                ||||||  ||    ||||||||
                                AAGGGA GT    ACAAGACC
                                   G  AC__
GAM1064  HSPC251   3'  CCAGGCTAGAGCCACAGAGA   33249    C      A  TT
                                TC CTGTGGCT TG  CTGG
                                || ||||||| ||  ||||
                                AG GACACCGA AT  GACC
                                 A       G  CG
GAM1064  IGF2AS    3'  CCAGGGTGCAACAGAGAA    33095    C    G  TAT TT
                                TTC CTGT GC   G  CTGG
                                ||| |||| ||   |  ||||
                                AAG GACA CG   T  GACC
                                  A    A  ___ GG
GAM1064  ILF3      3'  CCAAAACACGCTGGGAA     15722      T   GCTA    C
                                TTCCC GTG    TGTT TGG
                                ||||| |||    |||| |||
                                AAGGG CGC    ACAA ACC
                                   T  _____    A
GAM1064  KIAA0040  3'  CCAAAGTTTCCAGCAGGGAA   27780       _  CT  GTTC
                                TTCCCTG TGG  AT    TGG
                                ||||||| |||  ||    |||
                                AAGGGAC ACC  TG    ACC
                                    G   TT  AA__
GAM1064  KIAA0254  3'  CAGACAGTCACAGGGAA     28596          ATGT
                                TTCCCTGTGGCT    TCTG
                                ||||||||||||   ||||
                                AAGGGACACTGA    AGAC
                                      C___
GAM1064  KIAA0336  3'  CCAGAATAAAACCACCAGGAA  27589     CT    CTA
                                TTCC  GTGG   TGTTCTGG
                                ||||  ||||   ||||||||
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                                AAGG  CACC   ATAAGACC
                                  AC    AAA
GAM1064  KIAA0494  3'  CCAGAACACATTTGGG     28740     T_  GCTA
                                CCC  GTG    TGTTCTGG
                                |||  |||    ||||||||
                                GGG  TAC    ACAAGACC
                                  TT  _____
GAM1064  KIAA0537  3'  CCAGAACAGCCTACAGGGGA  29244        _   AT
                                TTCCCTGT GGCT  GTTCTGG
                                |||||||| ||||  |||||||
                                AGGGGACA CCGA  CAAGACC
                                     T   __
GAM1064  KIAA0774  5'  CGGGATGCCACAAGGAA     91752     C     TAT    TG
                                TTCC TGTGGC   GTTC  G
                                |||| ||||||   ||||  |
                                AAGG ACACCG   TAGG  C
                                  A     ___    GT
GAM1064  KIAA0828  3'  CCATGAAAGCCACAGAGGA    81194     _      ATG  _
                                TCC CTGTGGCT   TTC TGG
                                |||  ||||||||   ||| |||
                                AGG GACACCGA   AAG ACC
                                  A       ___   T
GAM1064  KIAA1118  3'  CCAGAGGCCCACAGGGA     69606         _ ATGT
                                TCCCTGTGG CT    TCTGG
                                |||||||||  ||    |||||
                                AGGGACACC GG    AGACC
                                     C  _____
GAM1064  KIAA1742  3'  CAGATCCACAGGGAG       77657          CTATGT
                                TTCCCTGTGG     TCTG
                                ||||||||||     ||||
                                GAGGGACACC     AGAC
                                     T_______
GAM1064  KIAA1944  5'  CCAACCTAGCCACAGGGA    75558           T  TC
                                TCCCTGTGGCTA GT  TGG
                                ||||||||||||  ||  |||
                                AGGGACACCGAT CA  ACC
                                      C  __
GAM1064  KIAA1981  3'  CGGAACAGCACAAGGAA     88342     C   G  AT   TG
                                TTCC TGTG CT  GTTC  G
                                |||| |||| ||  ||||  |
                                AAGG ACAC GA  CAAG  C
                                  A   _ __    GT
GAM1064  NXPH3     3'  ACGGAGCCACAGAGAG      65747     C       A
                                TTC CTGTGGCT TGT
                                |||  |||||||  |||
                                GAG GACACCGA GCA
                                  A       G
GAM1064  PP5395    3'  TCAGGATAGCACAGGGAA    72110         G  AT
                                TTCCCTGTG CT  GTTCTGG
                                |||||||||  ||  |||||||
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                                AAGGGACAC GA  TAGGACT
                                      _ __
GAM1064  PRDM7    3'  CCAGAAGGGCCACAGAGAA   53788    C      ATG
                                TTC CTGTGGCT   TTCTGG
                                ||| ||||||||   ||||||
                                AAG GACACCGG   AAGACC
                                  A       G__
GAM1064  PRDM9    3'  CCAGAAGGGCCACAGAGAA   39575    C      ATG
                                TTC CTGTGGCT   TTCTGG
                                ||| ||||||||   ||||||
                                AAG GACACCGG   AAGACC
                                  A       G__
GAM1064  PXR2b    3'  ATATAGCCCAAGGAA      33337     C  T
                                TTCC TG GGCTATGT
                                |||| || ||||||||
                                AAGG AC CCGATATA
                                  A  _
GAM1064  RAB33B   3'  CCAGCTTAGCCACAAAGAA   48490    CC      TGTT
                                TTC  TGTGGCTA   CTGG
                                |||  ||||||||   ||||
                                AAG  ACACCGAT   GACC
                                  AA       TC__
GAM1064  SH120    3'  CCAGAACATGAGAGGGAG    94606      GTGGC
                                TTCCCT    TATGTTCTGG
                                ||||||    ||||||||||
                                GAGGGA    GTACAAGACC
                                   GA___
GAM1064  SH120    3'  CCAGAACATGAGAGGGAG    32920      GTGGC
                                TTCCCT    TATGTTCTGG
                                ||||||    ||||||||||
                                GAGGGA    GTACAAGACC
                                   GA___
GAM1064  SLC2A12  3'  CCAGAACACACAGTGTGGA   59078    ___    GCTA
                                TCC   CTGTG   TGTTCTGG
                                |||   |||||   ||||||||
                                AGG   GACAC   ACAAGACC
                                  TGT   _____
GAM1064  SP329    3'  CCAGAGTGCTCCACAGGGA   47924       CTA GT
                                TCCCTGTGG   T  TCTGG
                                |||||||||   |  |||||
                                AGGGACACC   G  AGACC
                                     TC_ TG
GAM1064  SSH2     3'  TCAGTAAGCCCACAGGGAA   62213       _  ATGTT
                                TTCCCTGTGG CT    CTGG
                                |||||||||| ||    ||||
                                AAGGGACACC GA    GACT
                                      C  AT___
GAM1064  SYTL4    5'  CCAGTCAGCCACAGGGAA    54939         ATGTT
                                TTCCCTGTGGCT    CTGG
                                ||||||||||||    ||||
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                                AAGGGACACCGA    GACC
                                      CT___
GAM1064  TNRC4    3'  CCAGTCAGCCACAGAGA     23221    C      ATGTT
                                TC CTGTGGCT    CTGG
                                || ||||||||    ||||
                                AG GACACCGA    GACC
                                 A      CT___
GAM1064  UBE3B    3'  CCAGACTGTCAGCACAGGGAA  76919        G  _  GT
                                TTCCCTGTG CT AT  TCTGG
                                ||||||||| || ||  |||||
                                AAGGGACAC GA TG  AGACC
                                      _  C  TC
GAM1064  VPS4A    3'  CCTTGCAGCCACAGAGA     25102    C      AT  TCT
                                TC CTGTGGCT  GT   GG
                                || ||||||||  ||   ||
                                AG GACACCGA  CG   CC
                                 A       __  TT_
GAM1064  XYLT1    5'  CCAACAGCAGCCACGGGAA   77847      T     A_   TC
                                TTCCC GTGGCT  TGT  TGG
                                ||||| ||||||  |||  |||
                                AAGGG CACCGA  ACA  ACC
                                   _     CG  __
GAM1064  ZFP100   3'  CCAGAAAGCCAAAAAGAA    70050     CCTG    ATG
                                TTC    TGGCT   TTCTGG
                                |||    |||||   ||||||
                                AAG    ACCGA   AAGACC
                                  AAAA    ____
GAM1064  ZNF213   5'  CAGCTACCACAGGGGA      65091         C  TGTT
                                TTCCCTGTGG TA    CTG
                                |||||||||| ||    |||
                                AGGGGACACC AT    GAC
                                      _  C___
GAM1064  LOC112609 3'  CCAGTGTGGCACAGGGAA    72837        G    GTT
                                TTCCCTGTG CTAT   CTGG
                                ||||||||| ||||   ||||
                                AAGGGACAC GGTG   GACC
                                      _   T__
GAM1064  LOC115073 5'  CCAGGCGTCAAACCACAGGGA  73204        CT__    T
                                TCCCTGTGG    ATGT CTGG
                                |||||||||    |||| ||||
                                AGGGACACC    TGCG GACC
                                     AAAC   _
GAM1064  LOC122962 5'  CCAGACAGTGGCCACTGAGAA  75587     CCT      GT
                                TTC   GTGGCTAT  TCTGG
                                |||   ||||||||  |||||
                                AAG   CACCGGTG  AGACC
                                  AGT       AC
GAM1064  LOC124044 3'  CCAGAACACTCAGAGGGA    76025      G   CTA
                                TCCCT TGG   TGTTCTGG
                                ||||| |||   ||||||||
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                                AGGGA ACT   ACAAGACC
                                  G   C__
GAM1064  LOC143308 5'  CCAAATTTGGCCACAG      82936         T   C
                                CTGTGGCTA GTT TGG
                                ||||||||| ||| |||
                                GACACCGGT TAA ACC
                                     T   _
GAM1064  LOC145314 3'  CCAGAACACATCACCTGAG    77086     CCT    CTA
                                TTC   GTGG   TGTTCTGG
                                |||   ||||   ||||||||
                                GAG   CACT   ACAAGACC
                                  TC_    AC_
GAM1064  LOC146420 3'  CCAGAACCAGTTACAG      83667         AT
                                CTGTGGCT  GTTCTGG
                                ||||||||  |||||||
                                GACATTGA  CAAGACC
                                     C_
GAM1064  LOC146445 3'  CCAGAGCCACCACAGGGA     83678         CTAT
                                TCCCTGTGG    GTTCTGG
                                |||||||||    |||||||
                                AGGGACACC    CGAGACC
                                     AC__
GAM1064  LOC147178 3'  CCAGCCAGCCACGGAGAA     61323     C       ATGTT
                                TTC CTGTGGCT     CTGG
                                ||| ||||||||     ||||
                                AAG GGCACCGA     GACC
                                  A       CC___
GAM1064  LOC148529 5'  CACAGCCACAGGAGAA       84166     _       A
                                TTC CCTGTGGCT TG
                                ||| ||||||||| ||
                                AAG GGACACCGA AC
                                  A        C
GAM1064  LOC148930 5'  CCAGGGGCAGACCACGGGGAA  79093          CTA    _
                                TTCCCTGTGG   TGTTC TGG
                                ||||||||||   ||||| |||
                                AAGGGGCACC   ACGGG ACC
                                     AG_     G
GAM1064  LOC149950 5'  CCAGAACATGATCTCAGG     79551      T GC
                                CCTG G  TATGTTCTGG
                                |||| |  ||||||||||
                                GGAC C  GTACAAGACC
                                  T TA
GAM1064  LOC150378 5'  CCAGAAACAAGCCACGGGAA   79742       T     ATG
                                TTCCC GTGGCT   TTCTGG
                                ||||| ||||||   ||||||
                                AAGGG CACCGA   AAGACC
                                   _     ACA
GAM1064  LOC150951 5'  CCAGGGCCACACAGGGAA     85167         GCTAT
                                TTCCCTGTG     GTTCTGG
                                |||||||||     |||||||
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                                AAGGGACAC    CGGGACC
                                     AC___
GAM1064  LOC151429 3'  CCAGGAGACCACAGGGA    85347        _  ATGT
                                TCCCTGTGG CT   TCTGG
                                ||||||||| ||   |||||
                                AGGGACACC GA   GGACC
                                     A  ____
GAM1064  LOC158434 3'  CCAGAATAAACCACTGGGAA  86819     T   CTA
                                TTCCC GTGG  TGTTCTGG
                                ||||| ||||  ||||||||
                                AAGGG CACC  ATAAGACC
                                   T   AA_
GAM1064  LOC170106 5'  CCAAGGCAGTCAGCCACAGG  82571       A__  TC
                                CCTGTGGCT  TGT  TGG
                                |||||||||  |||  |||
                                GGACACCGA  ACG  ACC
                                     CTG  GA
GAM1064  LOC196446 3'  CGGAAAGCCACAGAGAA    87708    C      ATG  TG
                                TTC CTGTGGCT  TTC  G
                                ||| ||||||||  |||  |
                                AAG GACACCGA  AAG  C
                                  A       ___  GT
GAM1064  LOC197136 3'  CCAGAACACTCAGAGGGA    89728      G  CTA
                                TCCCT TGG  TGTTCTGG
                                ||||| |||  ||||||||
                                AGGGA ACT  ACAAGACC
                                   G  C__
GAM1064  LOC197342 3'  CCAGGAGAAGCCACAGGGGA  87993          ATG
                                TTCCCTGTGGCT  TTCTGG
                                ||||||||||||  ||||||
                                AGGGGACACCGA  AGGACC
                                      AG_
GAM1064  LOC200734 3'  CCATCCGCAGCCACAGGGGA  88860          A  TTC
                                TTCCCTGTGGCT TG  TGG
                                |||||||||||| ||  |||
                                AGGGGACACCGA GC  ACC
                                      C  CT_
GAM1064  LOC201102 3'  CCTGACCAGCCACAGGAGA   88090   _      AT  CT
                                TC CCTGTGGCT  GTT  GG
                                || |||||||||  |||  ||
                                AG GGACACCGA  CAG  CC
                                  A       C_  T_
GAM1064  LOC201283 3'  CCAGAACACAGTCGTGAGGA  60413    CT    A
                                TCC  GTGGCT TGTTCTGG
                                |||  |||||| ||||||||
                                AGG  TGCTGA ACAAGACC
                                  AG    C
GAM1064  LOC202915 3'  CCACACGCCAGCCACAGGGGA 90388          A_  TC
                                TTCCCTGTGGCT  TGT  TGG
                                ||||||||||||  |||  |||
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                                AGGGGACACCGA  GCA  ACC
                                      CC   C_
GAM1064  LOC204965 5'  CAGAGTGCACAGAGAA      90647     C     G TATG
                                TTC CTGTG C    TTCTG
                                ||| ||||| |    |||||
                                AAG GACAC G    GAGAC
                                  A    _ T___
GAM1064  LOC205418 3'  CACAGCCAGCAGGGAA      90681         _     A
                                TTCCCTG TGGCT TG
                                ||||||| ||||| ||
                                AAGGGAC ACCGA AC
                                    G    C
GAM1064  LOC220692 3'  CCAGAATAAAACCACCAGGAA  91220      CT    CTA
                                TTCC  GTGG   TGTTCTGG
                                ||||  ||||   ||||||||
                                AAGG  CACC   ATAAGACC
                                  AC    AAA
GAM1064  LOC222631 5'  CCAGAACACAGCTGGAA     92838      CTGT    A
                                TTCC    GGCT TGTTCTGG
                                ||||    |||| ||||||||
                                AAGG    TCGA ACAAGACC
                                  _____   C
GAM1064  LOC253039 3'  CCAAATACATCTACAGGGAA   96153          CT    TC_
                                TTCCCTGTGG  ATGT   TGG
                                ||||||||||  ||||   |||
                                AAGGGACATC  TACA   ACC
                                     __    TAA
GAM1064  LOC253841 5'  CCAGAATGTAGCCACAG     96342
                                CTGTGGCTATGTTCTGG
                                ||||||||||||||||
                                GACACCGATGTAAGACC

GAM1064  LOC254028 3'  CCAGAACAGAAGCACCAAGAA  96539     CC  TG   A_
                                TTC  TG  GCT  TGTTCTGG
                                |||  ||  |||  ||||||||
                                AAG  AC  CGA  ACAAGACC
                                  A_  CA   AG
GAM1064  LOC257449 3'  CAGATCCACAGGGAG       62718          CTATGT
                                TTCCCTGTGG     TCTG
                                ||||||||||     ||||
                                GAGGGACACC     AGAC
                                     T_____
GAM1064  LOC89231  3'  GGACAGCACAGGGAA       92733         G  AT
                                TTCCCTGTG CT  GTTC
                                ||||||||| ||  ||||
                                AAGGGACAC GA  CAGG
                                     _  __
GAM1064  LOC90550  3'  CCAGAACACAAATCAGAGGGA  73090       G   CTA_
                                TCCCT TGG    TGTTCTGG
                                ||||| |||    ||||||||
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                                AGGGA ACT    ACAAGACC
                                   G   AAAC
GAM1064  LOC91373  3'  CCAGCAAGGCCACAG       65834         A  TT
                                CTGTGGCT TG  CTGG
                                |||||||| ||  ||||
                                GACACCGG AC  GACC
                                     A  __
GAM1064  LOC91445  3'  CCAGAACCTGCCACAGG     60547         TAT
                                CCTGTGGC   GTTCTGG
                                ||||||||   |||||||
                                GGACACCG   CAAGACC
                                     TC_
GAM1065  ALDH1B1   3'  CTTGAACTCCTGACCTCA    5494            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                        GT
GAM1065  AQP6      3'  CTCAAACTCCTGACCT      7948
                                AGGTCAGGAGTTTGAG
                                ||||||||||||||||
                                TCCAGTCCTCAAACTC

GAM1065  AQP6      3'  CTCAAACTCCTGACCT      53923
                                AGGTCAGGAGTTTGAG
                                ||||||||||||||||
                                TCCAGTCCTCAAACTC

GAM1065  ARSF      5'  CTCGAACTCCCGACCTCA    64598         A
                                TGAGGTC GGAGTTTGAG
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAGCTC
                                     C
GAM1065  ATP1B2    3'  CTCGAACTCCCGACCTCA    8047          A
                                TGAGGTC GGAGTTTGAG
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAGCTC
                                     C
GAM1065  ATP7A     3'  CTTAAACTCCTAACCTCA    3523          C
                                TGAGGT AGGAGTTTGAG
                                |||||| ||||||||||
                                ACTCCA TCCTCAAATTC
                                    A
GAM1065  AXL       3'  TCTAAAACTCCTGACCTCA   41606             GAGCCT
                                TGAGGTCAGGAGTTT     GA
                                ||||||||||||||     ||
                                ACTCCAGTCCTCAAA     CT
                                        AT_____
GAM1065  AXL       3'  TCTAAAACTCCTGACCTCA   8109              GAGCCT
                                TGAGGTCAGGAGTTT     GA
                                ||||||||||||||     ||
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                                ACTCCAGTCCTCAAA     CT
                                       AT____
GAM1065 C7      3' CTCCAACTCCTGACCTCA    5158           T
                                TGAGGTCAGGAGTT GAG
                                |||||||||||||| |||
                                ACTCCAGTCCTCAA CTC
                                       C
GAM1065 CDH1    3' CTTAAACTCCTGGCCTCA    15143
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCGGTCCTCAAATTC

GAM1065 CLECSF12 3' CGAACTCCTGACCTCA     76686
                                TGAGGTCAGGAGTTTG
                                ||||||||||||||||
                                ACTCCAGTCCTCAAGC

GAM1065 CORO2B   3' CTCTAACCTCCTGACCTCA   64572          _ T
                                TGAGGTCAGGAG TT GAG
                                |||||||||||| || |||
                                ACTCCAGTCCTC AA CTC
                                       C  T
GAM1065 COX15    3' CTTGAACTCCTGACCTCA    54312          TG
                                TGAGGTCAGGAGTT  AG
                                |||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                       GT
GAM1065 CYP1A2   3' CTCAAACTCCTGACCTCA    5688
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 CYP1A2   3' CTCGAACTCCTGACCCCA    5689    A
                                TG GGTCAGGAGTTTGAG
                                || ||||||||||||||
                                AC CCAGTCCTCAAGCTC
                                  C
GAM1065 CYP1A2   3' CTCAAACTCCTGACCTCA    69108
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 CYP1A2   3' CTCGAACTCCTGACCCCA    69109   A
                                TG GGTCAGGAGTTTGAG
                                || ||||||||||||||
                                AC CCAGTCCTCAAGCTC
                                  C
GAM1065 DFFB     3' CTCAAACTCCTGACCTCA    87380
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAACTC

GAM1065  DISC1    3'  CTCAAACTCCTGACCTCA    37876
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  F2RL2    3'  CTTGAACTCCTGACCTCA    14622            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                        GT
GAM1065  FCAR     3'  CTCGAACTCCTGACCTCA    8852
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  FCAR     3'  CTCGAACTCCTGACCTCA    55747
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  FCAR     3'  CTCGAACTCCTGACCTCA    55758
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  FCAR     3'  CTCGAACTCCTGACCTCA    55769
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  FCAR     3'  CTCGAACTCCTGACCTCA    55780
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  FCAR     3'  CTCGAACTCCCGACCTCA    55795        A
                                TGAGGTC GGAGTTTGAG
                                ||||||| |||||||||
                                ACTCCAG CCTCAAGCTC
                                    C
GAM1065  FEN1     3'  GTCAGGCTCAAACCACTTCTCA 14645      TC  GA
                                TGAGG  AG  GTTTGAGCCTGAC
                                |||||  ||  ||||||||||||
                                ACTCT  TC  CAAACTCGGACTG
                                   __  AC
GAM1065  FZD4     3'  CTCGAACTCCTGACCTCA    24136
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTC

GAM1065  G6PC     3'  CTCGAACTCCTGACCTCA    3824
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  GAGEC1   5'  CAGGCTCTCTGCTGACTCA   22798     G   G  TTT
                                TGAG TCAG AG   GAGCCTG
                                |||| |||| ||   |||||||
                                ACTC AGTC TC   CTCGGAC
                                  _   G  T__
GAM1065  GBF1     3'  CAGGCTTTCCTTGACCCCA   14829    A    _  GTTT
                                TG GGTCA GGA    GAGCCTG
                                || ||||| |||    |||||||
                                AC CCAGT CCT    TTCGGAC
                                 C    T  _____
GAM1065  GNE      3'  CTTGAACTCCTGACCTCA    18479            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                        GT
GAM1065  GRAF     3'  CTCGAACTCCTGACCTCA    30557
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  HCS      3'  CTCAAACTCCTGAGCTCA    38465     G
                                TGAG TCAGGAGTTTGAG
                                |||| ||||||||||||
                                ACTC AGTCCTCAAACTC
                                  G
GAM1065  HSD3B1   3'  TCAAGCTCCACCCTCCTGGCCT 5989           TT  _  C
            CA                    TGAGGTCAGGAG  TG AGC TGA
                                ||||||||||||  || ||| |||
                                ACTCCGGTCCTC  AC TCG ACT
                                       CC  C   A
GAM1065  IFNAR2   3'  CTCGAACTCCTGACCTCA    6039
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  JAK3     3'  CTCGAACTCCTAACCTCA    4003       C
                                TGAGGT AGGAGTTTGAG
                                ||||||  ||||||||||
                                ACTCCA TCCTCAAGCTC
                                   A
GAM1065  KMO      3'  CAGTCTCAAACTCCTGGCCTCA 13448              C
                                TGAGGTCAGGAGTTTGAG CTG
                                |||||||||||||||||  |||
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                                ACTCCGGTCCTCAAACTC GAC
                                                  T
GAM1065 MAFG    5' TCAGACCTTCCTGACCTC   70097          __
                                GAGGTCAGGA GTTTGA
                                |||||||||| ||||||
                                CTCCAGTCCT CAGACT
                                      TC
GAM1065 MAK     3' CTCAAACTCCTGACCTCA   19756
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 MEFV    3' CTCAAACTCCTGACCTCA   4132
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 MEFV    3' CTCGAACTCCTGACCTCA   4134
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065 MICB    3' TTCAAACTCCTGACCTCA   19837
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTT

GAM1065 MLANA   3' CTCAAACTCCTGACCTCA   18584
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 NCOA6   5' CTCAAACTCCTGACCTCA   25960
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 NDRG3   3' CTCAAACTCCTGACCTCA   49297
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 NQO1    3' CTCAAACTCCTGACCTCA   6157
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 NXF3    5' TCTTCTCCAAACTCCCGTCCCC 41902   A TCA     _ CCT
          A                      TG GG  GGAGTTTG AG  GA
                                || ||  |||||||| ||  ||
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                                AC CC   CCTCAAAC TC   CT
                                 C  TGC       C  TT_
GAM1065  PDE6B    3'  CTCGAACTCCTGACCTCA    4276
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  PDE6D    3'  CAGACTAAACTCCCAACCCCA  10488    A   CA      G  C
                                TG GGT  GGAGTTT AG CTG
                                || |||  ||||||| || |||
                                AC CCA  CCTCAAA TC GAC
                                 C   AC      _ A
GAM1065  PER2     3'  CTCGAACTCCTGACCTCA    43031
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  PIK3CD   3'  CTCGAACTCCTGACCTCA    17243
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  PPEF2    3'  CTTGAACTCCCAACCTCA    20670       CA     TG
                                TGAGGT  GGAGTT  AG
                                ||||||  ||||||  ||
                                ACTCCA  CCTCAA  TC
                                    AC     GT
GAM1065  PRKR     3'  CTCAAACTCCTGACCTCA    10879
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  PTPN18   3'  CTTGAACTCCCAACCTCA    26865       CA     TG
                                TGAGGT  GGAGTT  AG
                                ||||||  ||||||  ||
                                ACTCCA  CCTCAA  TC
                                    AC     GT
GAM1065  RAB3A    3'  CAGACCTGTTCTGACCTCA   11182          ___
                                TGAGGTCAGGA  GTTTG
                                ||||||||||   |||||
                                ACTCCAGTCTT  CAGAC
                                      GTC
GAM1065  RHD      3'  CTCAAACTCCTGACCTCA    32304
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  RHD      3'  CTCAAACTCCTGACCTCA    32613
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAACTC

GAM1065 RP2      3' CTCGAACTCCTGACCTCA    22616
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065 RPP30    3' CTCAATCTCCTGACCTCA    21164          T
                                TGAGGTCAGGAG TTGAG
                                |||||||||||| |||||
                                ACTCCAGTCCTC AACTC
                                       T
GAM1065 SAS      3' CTCGAACTCCTGACCTCA    19952
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065 SCML2    3' CTCAAACTCCTGACCTCA    20316
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 SEDL     3' TTCAAACTCCTGACCTCA    27370
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTT

GAM1065 SH3BP2   3' CTCGAACTCCTGACCTCA    11600
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065 SH3BP2   3' CTTGAACTCCTGACCTCA    11603          TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                       GT
GAM1065 SHOX     3' CTCGGAACTCCTGACCTCA    4834           _
                                TGAGGTCAGGAGTTT GAG
                                |||||||||||||| |||
                                ACTCCAGTCCTCAAG CTC
                                       G
GAM1065 SHOX     3' CTCGAACTCCTGACCTCA    22535
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065 SIL      3' CTCAAACTCCCGACCTCA    11688        A
                                TGAGGTC GGAGTTTGAG
                                ||||||| |||||||||
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                                ACTCCAG CCTCAAACTC
                                    C
GAM1065  SLA2     3'  TCGAACTCCTGACCTCA     49909
                                TGAGGTCAGGAGTTTGA
                                |||||||||||||||||
                                ACTCCAGTCCTCAAGCT

GAM1065  SLC6A12  3'  CAAACCCCTGACTTCA      11731          A
                                TGAGGTCAGG GTTTG
                                |||||||||| |||||
                                ACTTCAGTCC CAAAC
                                      C
GAM1065  SNX15    3'  CTCGAACTCCTGACCTCA    73738
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  SPN      3'  CTCAAACTCCTGACCTCA    11921
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  STK11    3'  CAGGCTCCTGACCCCG      4846     A
                                TG GGTCAGGAGTTTG
                                || ||||||||||||
                                GC CCAGTCCTCGGAC
                                  C
GAM1065  SULT2B1  5'  CTCAAACTCCTGACCTCA    16025
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  TAT      3'  CTCAAACTCCTGACCTCA    4465
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  TBXA2R   3'  CTTGAACTCCTGACCTCA    6490             TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                      GT
GAM1065  TCIRG1   3'  GCCAGACCTCCTTCCTGACCTC 20059          _____    A
                                GAGGTCAGGA    GTTTG GC
                                ||||||||||    ||||| ||
                                CTCCAGTCCT    CAGAC CG
                                      TCCTC    _
GAM1065  TCIRG1   3'  GCCAGACCTCCTTCCTGACCTC 20201          _____    A
                                GAGGTCAGGA    GTTTG GC
                                ||||||||||    ||||| ||
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                                CTCCAGTCCT    CAGAC CG
                                      TCCTC   _
GAM1065  TES      3'  CTCAAACTCCTGACCTCA    72004
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  TIM3     3'  CTCAAACTCCTGACCTCA    51341
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  TMPRSS3  3'  CAGGCTGCTCTCAAACCCCTGA 50503          A     _____
           CCTCA                    TGAGGTCAGG GTTTGA    GCCTG
                                ||||||||||| ||||||    |||||
                                ACTCCAGTCC CAAACT    CGGAC
                                      C     CTCGT
GAM1065  TMPRSS3  3'  CAGGCTGCTCTCAAACCCCTGA 50524          A     _____
           CCTCA                    TGAGGTCAGG GTTTGA    GCCTG
                                ||||||||||| ||||||    |||||
                                ACTCCAGTCC CAAACT    CGGAC
                                      C     CTCGT
GAM1065  TMPRSS3  3'  CAGGCTGCTCTCAAACCCCTGA 43790          A     _____
           CCTCA                    TGAGGTCAGG GTTTGA    GCCTG
                                ||||||||||| ||||||    |||||
                                ACTCCAGTCC CAAACT    CGGAC
                                      C     CTCGT
GAM1065  TNFRSF10B 3'  CTCGAACTCCTGACCTCA    13868
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  TRAF5    3'  CTCAAACTCCTGACCTCA    16078
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  TRPM6    3'  CTCAAACTCCTGACCTCA    34538
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  TRPV1    3'  CTCGAACTCCTGACCTCA    38076
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  TRPV1    3'  CTCGAACTCCTGACCTCA    54797
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTC

GAM1065 TRPV1    3' CTCGAACTCCTGACCTCA    54830
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065 TRPV1    3' CTCGAACTCCTGACCTCA    54862
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065 UROS     3' TCAGACTCCTGCCTCA      4563       T
                                TGAGG CAGGAGTTTGA
                                ||||| ||||||||||
                                ACTCC GTCCTCAGACT

                                  _
GAM1065 VHL      3' CAGGCTGGTTTCAAACTCCTGA 5065              _____
              CCTCA                  TGAGGTCAGGAGTTTGA    GCCTG
                                ||||||||||||||||    |||||
                                ACTCCAGTCCTCAAACT    CGGAC
                                        TTGGT
GAM1065 WBSCR5   3' CAAGCCCTCTCCCGACCCA   50609    A   A   TTTGA  C
                                TG GGTC GGAG    GC TG
                                || |||| ||||    || ||
                                AC CCAG CCTC    CG AC
                                 _   C   TCC__  A
GAM1065 WBSCR5   3' CAAGCCCTCTCCCGACCCA   41855    A   A   TTTGA  C
                                TG GGTC GGAG    GC TG
                                || |||| ||||    || ||
                                AC CCAG CCTC    CG AC
                                 _   C   TCC__  A
GAM1065 WBSCR5   3' CAAGCCCTCTCCCGACCCA   26255    A   A   TTTGA  C
                                TG GGTC GGAG    GC TG
                                || |||| ||||    || ||
                                AC CCAG CCTC    CG AC
                                 _   C   TCC__  A
GAM1065 XRCC2    3' CTCGAACTCCTGACCTCA    18320
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065 ZNF157   3' CTCTAACTCCTGACCTCA    12877           T
                                TGAGGTCAGGAGTT GAG
                                |||||||||||||| |||
                                ACTCCAGTCCTCAA CTC
                                        T
GAM1065 AAK1     3' CTCGAACTCCTGACCTCA    29844
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTC

GAM1065 ACY-3    3' CAGGCCTCCCCAACCCCTGGCC 54695          A  T__  _
             TCA                  TGAGGTCAGG GTT  GAG CCTG
                                  |||||||||| |||  ||| ||||
                                  ACTCCGGTCC CAA  CTC GGAC
                                       C  CCC  C
GAM1065 AGS3     5' CAGGCCCACCCTGCCCCCA   73110    A  T   A  TT A
                                  TG GG CAGG GT  G GCCTG
                                  || || |||| ||  | |||||
                                  AC CC GTCC CA  C CGGAC
                                   C  C   _  __ C
GAM1065 ARHGAP5  5' TCGAACTCCCAACCTCA    77080       CA
                                  TGAGGT  GGAGTTTGA
                                  ||||||  |||||||||
                                  ACTCCA  CCTCAAGCT
                                      AC
GAM1065 ARPP-19  3' CTTGAACTCCTGACCTCA    21795           TG
                                  TGAGGTCAGGAGTT  AG
                                  ||||||||||||||  ||
                                  ACTCCAGTCCTCAA  TC
                                         GT
GAM1065 ATP1B4   3' CTCGAACTCCTGACCTCA    23817
                                  TGAGGTCAGGAGTTTGAG
                                  ||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTC

GAM1065 BA108L7.2 3' CTCGAACTCCTGACCTCA    48261
                                  TGAGGTCAGGAGTTTGAG
                                  ||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTC

GAM1065 C13orf1  3' CTCAAACTCCTGACCTCA    39967
                                  TGAGGTCAGGAGTTTGAG
                                  ||||||||||||||||||
                                  ACTCCAGTCCTCAAACTC

GAM1065 C20orf142 3' CTCAAACTCCTGACCGCA    74771    A
                                  TG GGTCAGGAGTTTGAG
                                  || ||||||||||||||
                                  AC CCAGTCCTCAAACTC
                                   G
GAM1065 C20orf18  3' TCAAGGCGCTCCTGACC     48344         TTGA  _
                                  GGTCAGGAGT   GCCT GA
                                  ||||||||||   |||| ||
                                  CCAGTCCTCG   CGGA CT
                                        ____   A
GAM1065 C21orf25  3' CTCGAACTCCTGACCTCA    63544
                                  TGAGGTCAGGAGTTTGAG
                                  ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTC

GAM1065  C9orf9   3'  CTCAATCTCCTGACCTCA    38510          T
                                TGAGGTCAGGAG TTGAG
                                |||||||||||| |||||
                                ACTCCAGTCCTC AACTC
                                       T
GAM1065  C9orf9   3'  CTTGAACTCCTGACCTCA    38514           TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                       GT
GAM1065  CARD6    3'  CTTGAACTCCCGACCTCA    50856       A     TG
                                TGAGGTC GGAGTT  AG
                                ||||||| ||||||  ||
                                ACTCCAG CCTCAA  TC
                                     C     GT
GAM1065  CDC14B   3'  CTCGAACTCCTGACCTCA    52850
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  CDV-1    3'  CTTAAACTCCCGGCCTCA    48904       A
                                TGAGGTC GGAGTTTGAG
                                ||||||| |||||||||
                                ACTCCGG CCTCAAATTC
                                     C
GAM1065  CEACAM7  3'  GTCAAACCCAAATATTTGACCT 22561        A    AGCC
                                AGGTCAGG GTTTG   TGAC
                                |||||||| |||||   ||||
                                TCCAGTTT TAAAC   ACTG
                                      A    CCAA
GAM1065  CHRAC1   3'  CTCAAACTCCTAACCTCA    33869       C
                                TGAGGT AGGAGTTTGAG
                                |||||| ||||||||||
                                ACTCCA TCCTCAAACTC
                                     A
GAM1065  CPSF2    3'  CTCAAACTCCCGACCTCA    61580       A
                                TGAGGTC GGAGTTTGAG
                                ||||||| |||||||||
                                ACTCCAG CCTCAAACTC
                                     C
GAM1065  CPSF2    3'  CTCAAACTCCTGACCTCA    61583
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  CSL4     3'  CTCAAACTCCTGGCCTCA    32110
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCGGTCCTCAAACTC

GAM1065  DBR1     3'  CTCCAACTCCTGACCTCA    32531            T
                                TGAGGTCAGGAGTT GAG
                                |||||||||||||| |||
                                ACTCCAGTCCTCAA CTC
                                       C
GAM1065  DCOHM    3'  CTCAAACTCCTGGCCTCA    49598
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTCCGGTCCTCAAACTC

GAM1065  DCOHM    3'  CTTAGACTCCTGACCTCA    49601
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTCCAGTCCTCAGATTC

GAM1065  DGS-A    3'  CAAACTCCTTCCTTTA      84893      TC
                                TGAGG  AGGAGTTTG
                                |||||  |||||||||
                                ATTTC  TCCTCAAAC
                                   CT
GAM1065  DKFZp434A2417 3'  CTCAAACTCCCAACCTCA    66100       CA
                                TGAGGT  GGAGTTTGAG
                                ||||||  ||||||||||
                                ACTCCA  CCTCAAACTC
                                    AC
GAM1065  DKFZp434F054 5'  CAGGCCAGCCCACCTCA     50042       CA  A   T A
                                TGAGGT  GG GTT G GCCTG
                                ||||||  || ||| | |||||
                                ACTCCA  CC CGA C CGGAC
                                   __ _  _ _
GAM1065  DKFZP434J037 3'  CTCAAACTCCCGACCTCA    48210       A
                                TGAGGTC GGAGTTTGAG
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAACTC
                                    C
GAM1065  DKFZP564G092 5'  CTTGAACTCCTGACCTCA    31536            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                       GT
GAM1065  DKFZP564O0423 3'  CTCAAACTCCTGGCCTCA    91684
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTCCGGTCCTCAAACTC

GAM1065  DKFZP761I2123 3'  GTCAGGTTCCTCTCCCCACCCC 48768    A   CA    TTT
            A                    TG GGT  GGAG   GAGCCTGAC
                                || |||  ||||   |||||||||
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                                AC CCA  CCTC   CTTGGACTG
                                 C   CC    TC_
GAM1065  EVI5     3'  CTCAAACTTCTGACCTCA    18995
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCTTCAAACTC

GAM1065  EVI5     3'  CTCGAACTCCTAACCTCA    18998       C
                                TGAGGT AGGAGTTTGAG
                                ||||||| ||||||||||
                                ACTCCA TCCTCAAGCTC
                                   A
GAM1065  FBP17    3'  CTCAAACTCCTGACCTCA    72788
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  FER1L4   3'  CTTGAACCCCTGACCTCA    47349          A   TG
                                TGAGGTCAGG GTT  AG
                                |||||||||| |||  ||
                                ACTCCAGTCC CAA  TC
                                      C   GT
GAM1065  FLJ10232 3'  CGAACTCCTGACCTCA     35923
                                TGAGGTCAGGAGTTTG
                                ||||||||||||||||
                                ACTCCAGTCCTCAAGC

GAM1065  FLJ10298 3'  CTCAAACTCCTGACCT     35987
                                AGGTCAGGAGTTTGAG
                                ||||||||||||||||
                                TCCAGTCCTCAAACTC

GAM1065  FLJ10607 3'  CTCAAACTCCTGAGCTCA    77109      G
                                TGAG TCAGGAGTTTGAG
                                |||| ||||||||||||
                                ACTC AGTCCTCAAACTC
                                  G
GAM1065  FLJ10901 3'  CTCGAACTCCTGACCTCA    36821
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  FLJ12363 3'  CTCAAACTCCTGACCTCA    49676
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  FLJ12668 3'  CTCAAACTCCTGACCTCA    46515
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAACTC

GAM1065  FLJ12687  3'  CTCAAACTCCTGACCTCA    46190
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  FLJ12787  3'  TCTAAAACTCCTGACCTCA   49753            GAGCCT
                                TGAGGTCAGGAGTTT     GA
                                |||||||||||||||     ||
                                ACTCCAGTCCTCAAA     CT
                                          AT_____
GAM1065  FLJ12903  3'  CTTGAACTCCTGACCTCA    42773            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                          GT
GAM1065  FLJ12975  3'  CTCGAACTCCTGACCTCA    69583
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  FLJ13072  5'  CTCGAACTCCTGACCTCA    89811
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  FLJ13102  3'  CTCGAACTCCTGACCTCA    46007
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  FLJ13197  3'  CTTGAACTCCTGACCTCA    44852            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                          GT
GAM1065  FLJ13590  5'  CTTGAACTCCTGACCTCA    45785            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                          GT
GAM1065  FLJ14351  3'  CAGTCTTGAACTCCTGAGCTCA 45320      G       TG  C
                                TGAG TCAGGAGTT  AG CTG
                                ||||  |||||||||  ||  |||
                                ACTC AGTCCTCAA  TC GAC
                                  G       GT  T
GAM1065  FLJ14957  3'  CTTGAACTCCTGACCTCA    51748            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
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                                ACTCCAGTCCTCAA  TC
                                      GT
GAM1065  FLJ20034  3' CTCAAACTCCCGACCTCA    34369       A
                                TGAGGTC GGAGTTTGAG
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAACTC
                                   C
GAM1065  FLJ20344  3' CTTGAACTCCTGACCTCA    35011           TG
                                TGAGGTCAGGAGTT  AG
                                |||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                      GT
GAM1065  FLJ20419  3' CAAACTCCCGCCTCA      35138       CA
                                TGAGGT  GGAGTTTG
                                ||||||  ||||||||
                                ACTCCG  CCTCAAAC
                                   C_
GAM1065  FLJ20452  3' CTCGAACTCCTGACCTCA    35199
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  FLJ20507  3' CTGGAACTCCTAACCTCA    35283       C       G
                                TGAGGT AGGAGTTT AG
                                |||||| |||||||| ||
                                ACTCCA TCCTCAAG TC
                                   A       G
GAM1065  FLJ20507  3' CTGGAACTCCTAACCTCA    60218       C       G
                                TGAGGT AGGAGTTT AG
                                |||||| |||||||| ||
                                ACTCCA TCCTCAAG TC
                                   A       G
GAM1065  FLJ20700  3' CTCGAACTCCTGACCTCA    35574
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  FLJ20813  3' CTCAAACTCCTGACCTCA    35682
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  FLJ21324  5' CTCAAACTCCTGACCTCA    91198
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  FLJ21459  3' CTCGAACTCCTGACCTCA    44515
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTC

GAM1065  FLJ22169  3'  GTCAGGCTGTGGCCCTTACCTC 44006       C  A  TG
              A                  TGAGGT AGG GTT  AGCCTGAC
                                 |||||| ||| |||  ||||||||
                                 ACTCCA TCC CGG  TCGGACTG
                                    T  _  TG
GAM1065  FLJ22329  3'  CTCGAACTCCTGACCTCA    45064
                                 TGAGGTCAGGAGTTTGAG
                                 ||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTC

GAM1065  FLJ22529  3'  CTCAAACCCCTGACCTTA    45566          A
                                 TGAGGTCAGG GTTTGAG
                                 |||||||||| |||||||
                                 ATTCCAGTCC CAAACTC
                                       C
GAM1065  FLJ22529  3'  CTCGAACTCCTGACCTCA    45568
                                 TGAGGTCAGGAGTTTGAG
                                 ||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTC

GAM1065  FLJ22684  3'  CTCAAACTCCTGACCTCA    46791
                                 TGAGGTCAGGAGTTTGAG
                                 ||||||||||||||||||
                                 ACTCCAGTCCTCAAACTC

GAM1065  FLJ23392  3'  CTCAAATTCCTGACCCCA    45532    A
                                 TG GGTCAGGAGTTTGAG
                                 || ||||||||||||||
                                 AC CCAGTCCTTAAACTC
                                   C
GAM1065  FLJ23556  3'  CTCGAACTCCTGACCTCA    45947
                                 TGAGGTCAGGAGTTTGAG
                                 ||||||||||||||||||
                                 ACTCCAGTCCTCAAGCTC

GAM1065  FLJ25416  5'  CTCAAACTCCCTACCTCA    58808       CA
                                 TGAGGT  GGAGTTTGAG
                                 ||||||  ||||||||||
                                 ACTCCA  CCTCAAACTC
                                    TC
GAM1065  FLJ30532  3'  CTCAAGCTCCTGACCTCA    58545
                                 TGAGGTCAGGAGTTTGAG
                                 ||||||||||||||||||
                                 ACTCCAGTCCTCGAACTC

GAM1065  FLJ31101  3'  CTTGAACTCCTGACCTCA    35710            TG
                                 TGAGGTCAGGAGTT  AG
                                 ||||||||||||||  ||
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                                ACTCCAGTCCTCAA  TC
                                        GT
GAM1065  FLJ31153  3'  CTTGAACTCCTGACCTCA    58123            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                        GT
GAM1065  FLJ32865  3'  CTCAAACCCCTGACCTCA    58172          A
                                TGAGGTCAGG GTTTGAG
                                |||||||||| |||||||
                                ACTCCAGTCC CAAACTC
                                      C
GAM1065  FLNC      3'  GCCAGATACCCTCCTGACCCCG 7583     A       ____    A
                                TG GGTCAGGAG    TTTG GC
                                || |||||||||    |||| ||
                                GC CCAGTCCTC    AGAC CG
                                 C        CCAT   _
GAM1065  GGA2      3'  CTCGAACTCCTGACCTCA    56878
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  GGA2      3'  CTCGAACTCCTGACCTCA    30464
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  GNG4      3'  CTCAAACTCCTGACCTC     15614
                                GAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                CTCCAGTCCTCAAACTC

GAM1065  GTF2H3    3'  CTCAAACTCCTGAGCTCA    7702       G
                                TGAG TCAGGAGTTTGAG
                                |||| ||||||||||||
                                ACTC AGTCCTCAAACTC
                                   G
GAM1065  H2AV      3'  CTCAAACTCCTGACCTCA    56849
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  HCA127    3'  TCAGGCTCCCCAAGCCCCA   37951    A   CA  AGTTT
                                TG GGT  GG    GAGCCTGA
                                || |||  ||    ||||||||
                                AC CCG  CC    CTCGGACT
                                 C   AA  C____
GAM1065  HN1L      3'  TCAGGCTCATGCTGCCTCA   58003       CAGG   T
                                TGAGGT    AGT TGAGCCTGA
                                ||||||    ||| |||||||||
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                                ACTCCG   TCG ACTCGGACT
                                   ____  T
GAM1065  HSMPP8   3'  CTTGAACTCCTGACCTCA   93475          TG
                                TGAGGTCAGGAGTT  AG
                                |||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                      GT
GAM1065  HSPC065  3'  CTCGAACTCCTGACCTCA   26295
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  JAM1     3'  CTCAAACTCCTGACCTC    57895
                                GAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                CTCCAGTCCTCAAACTC

GAM1065  JAM1     3'  CTCAAACTCCTGACCTC    57924
                                GAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                CTCCAGTCCTCAAACTC

GAM1065  JAM1     3'  CTCAAACTCCTGACCTC    57950
                                GAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                CTCCAGTCCTCAAACTC

GAM1065  JAM1     3'  CTCAAACTCCTGACCTC    33757
                                GAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                CTCCAGTCCTCAAACTC

GAM1065  KIAA0022 3'  CTCAAACTCCTGACCTCA   29663
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  KIAA0063 3'  CTCAAACTCCCGACCTCA   29623       A
                                TGAGGTC GGAGTTTGAG
                                ||||||| |||||||||
                                ACTCCAG CCTCAAACTC
                                     C
GAM1065  KIAA0161 3'  CAGGCTACTCTCAAACTCCTGA 28501            _____
            CCTCA                  TGAGGTCAGGAGTTTGA   GCCTG
                                ||||||||||||||||||   |||||
                                ACTCCAGTCCTCAAACT    CGGAC
                                      CTCAT
GAM1065  KIAA0186 3'  CAGGCTGGTTTCAAACTCCTGA 40745            _____
            CCTCA                  TGAGGTCAGGAGTTTGA   GCCTG
                                ||||||||||||||||||   |||||
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                                ACTCCAGTCCTCAAACT    CGGAC
                                      TTGGT
GAM1065  KIAA0186  3'  CTCAAACTCCTGGCCTCA    40747
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCGGTCCTCAAACTC

GAM1065  KIAA0186  3'  TTCAAACTCCTGACCTCA    40766
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTT

GAM1065  KIAA0205  3'  CTCGAACTCCTGACCTCA    29581
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  KIAA0391  3'  CTCAAACTCCTGACCTCA    27911
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  KIAA0445  5'  GTTTCTCTCCAAACTCCTGCCT 27956      T       _  CCT
          CA                      TGAGG CAGGAGTTTG AG   GAC
                                |||||  |||||||||| ||   |||
                                ACTCC GTCCTCAAAC TC   TTG
                                  _        C  TCT
GAM1065  KIAA0472  5'  CTTGAACTCCTGACCTCA    71863           TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                      GT
GAM1065  KIAA0513  3'  CTCGAACTCCTGACCTCA    28353
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  KIAA0513  5'  CTTGAACTCCTGACCTCA    28356           TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                      GT
GAM1065  KIAA0527  3'  TCAAGAACTCCTGACCTCA   95806            GAGCC
                                TGAGGTCAGGAGTTT    TGA
                                ||||||||||||||    |||
                                ACTCCAGTCCTCAAG    ACT
                                      A_____
GAM1065  KIAA0555  3'  CTCGAACTCCTGACCTCA    28882
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTC

GAM1065  KIAA0561  3' CTCGAACTCCTGACCTCA    65881
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  KIAA0682  3' CTTGAACTCCCAACCTCA    29364       CA     TG
                                TGAGGT  GGAGTT  AG
                                ||||||  ||||||  ||
                                ACTCCA  CCTCAA  TC
                                    AC     GT
GAM1065  KIAA0720  3' CTCGAACTCCTGACCCCA    62320    A
                                TG GGTCAGGAGTTTGAG
                                || ||||||||||||||
                                AC CCAGTCCTCAAGCTC
                                 C
GAM1065  KIAA0737  3' CTCGAACTCCTGACCTCA    29134
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  KIAA0841  3' CTCGAACTCCTGACCTCA    71382
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  KIAA0889  3' CTCGAACTCCCGACCTCA    31137       A
                                TGAGGTC GGAGTTTGAG
                                ||||||| |||||||||
                                ACTCCAG CCTCAAGCTC
                                    C
GAM1065  KIAA0961  3' CAGGCTGGTCTCAACTCCTGAC 29730            TG____
             CTCA                   TGAGGTCAGGAGTT     AGCCTG
                                ||||||||||||||     ||||||
                                ACTCCAGTCCTCAA     TCGGAC
                                       CTCTGG
GAM1065  KIAA1040  3' CTTGAACTCCTGACCTCA    72225           TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                       GT
GAM1065  KIAA1054  3' CTCGAACTCCTGACCTCA    68433
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  KIAA1128  3' CTCGAACTCCTGACCTCA    68476
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTC

GAM1065 KIAA1143 3' CTCAATCTCCTGACCTCA    68676          T
                                TGAGGTCAGGAG TTGAG
                                |||||||||||| |||||
                                ACTCCAGTCCTC AACTC
                                       T
GAM1065 KIAA1161 5' CTCAAACTCCTGACCT      81745
                                AGGTCAGGAGTTTGAG
                                ||||||||||||||||
                                TCCAGTCCTCAAACTC

GAM1065 KIAA1170 3' CTCAAACTCCTGACCTCA    69850
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 KIAA1198 3' CTCAAACTCCTGACCTCA    63304
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 KIAA1198 3' CTTAAACTCTTGACCTCA    63308
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTTCTCAAATTC

GAM1065 KIAA1198 3' CTTGAACTCCTGACCTCA    63309          TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                       GT
GAM1065 KIAA1200 3' CTCGAACTCCTGACCTCA    62373
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065 KIAA1257 3' CTCAAACTCCCGACTTCA    62736        A
                                TGAGGTC GGAGTTTGAG
                                ||||||| |||||||||
                                ACTTCAG CCTCAAACTC
                                    C
GAM1065 KIAA1493 3' CTCAAACTCCTGACCTCA    64159
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 KIAA1497 5' CTCGAACTCCTGACCTCA    67508
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTC

GAM1065 KIAA1615 3' CTCAAACTCCCGACCTCA    68705       A
                                TGAGGTC GGAGTTTGAG
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAACTC
                                     C
GAM1065 KIAA1617 3' CTTGAACTCCCAACCTCA    91426       CA     TG
                                TGAGGT  GGAGTT  AG
                                ||||||  ||||||  ||
                                ACTCCA  CCTCAA  TC
                                    AC     GT
GAM1065 KIAA1655 3' CTCAAACTCCTGACCTC     66605
                                GAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                CTCCAGTCCTCAAACTC

GAM1065 KIAA1712 3' CTCAAACTCCTGACCTCA    67536
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 KIAA1737 3' CTCGAACTCCTGACCTCA    67355
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065 KIAA1922 5' CTCGAACTCCTGACCTCA    73625
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065 MCLC     3' CTCGAACTCCTGACCTCA    30682
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065 MEF-2    3' CTCAAACTCCTGACCTC     64382
                                GAGGTCAGGAGTTTGAG
                                ||||||||||||||||
                                CTCCAGTCCTCAAACTC

GAM1065 MGC12837 5' CAGGCTGGGCTTCCTGATCCCA 51182    A       T  G
                                TG GGTCAGGAG TT AGCCTG
                                || ||||||||| || ||||||
                                AC CTAGTCCTT GG TCGGAC
                                 C       C  G
GAM1065 MGC13204 3' CTCAAAATCCTGACCTCA    48837         G
                                TGAGGTCAGGA TTTGAG
                                |||||||||| ||||||
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                                ACTCCAGTCCT AAACTC
                                      A
GAM1065  MGC15737  3'  CAGGCCCAATGCTTTAACCTTA 51928       CA    _  A
                                TGAGGT  GGAGT TTG GCCTG
                                ||||||  ||||| ||| |||||
                                ATTCCA  TTTCG AAC CGGAC
                                   A_    T  C
GAM1065  MGC21675  3'  CTTGAACTCCTGACCTCA    53482            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                        GT
GAM1065  MGC21738  3'  TCGAACTCCTGACCTCA     58921
                                TGAGGTCAGGAGTTTGA
                                |||||||||||||||||
                                ACTCCAGTCCTCAAGCT

GAM1065  MKRN4    3'  CTCGAACTCCTGACCTCA    47743
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  moblak   3'  CTCAAACTCCTGACTTCA    55498
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTTCAGTCCTCAAACTC

GAM1065  MRPL44   3'  CTTGAACTCCTGACCTCA    43319            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                        GT
GAM1065  MRPS27   3'  CGTCAGGCTGGTCTCAACCTCC 30635       T  _____     III
            TGACCTCA                CAGGAG TTGA    GCCTGAC   G
                                |||||| ||||    |||||||  |
                                GTCCTC AACT    CGGACTG   C
                                   C   CTGGT     III
GAM1065  NAPG     5'  CTCAAACTCCTAAGCTCA    96723     GTC
                                TGAG   AGGAGTTTGAG
                                ||||   ||||||||||
                                ACTC   TCCTCAAACTC
                                  GAA
GAM1065  NINJ2    3'  CTTGAACTCCTGACCTCA    33284            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                        GT
GAM1065  NXN      3'  CTCGAACTCCTGACCTCA    42418
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
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                                ACTCCAGTCCTCAAGCTC

GAM1065 OPN4     3' CTCAAAACTCCTGCCCCA    52718    A T       _
                                TG GG CAGGAGTTT GAG
                                || || ||||||||| |||
                                AC CC GTCCTCAAA CTC
                                 C _       A
GAM1065 OSBPL2   3' CTCAAACTCCCGACCTCA    57862       A
                                TGAGGTC GGAGTTTGAG
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAACTC
                                    C
GAM1065 OSBPL2   3' CTCAAACTCCCGACCTCA    29211       A
                                TGAGGTC GGAGTTTGAG
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAACTC
                                    C
GAM1065 PELI1    5' CTCAAACTCCCAACCTCA    40263       CA
                                TGAGGT  GGAGTTTGAG
                                ||||||  ||||||||||
                                ACTCCA  CCTCAAACTC
                                   AC
GAM1065 PELI1    5' CTTGAACTCCTGACCTCA    40267           TG
                                TGAGGTCAGGAGTT  AG
                                |||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                      GT
GAM1065 PIP3-E   3' TTCAAACTCCTGACCTCA    66821
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTT

GAM1065 POFUT1   3' GCCAAGGCTCTGACCTCA    70470        G    GA
                                TGAGGTCAG AGTTT  GC
                                ||||||||| |||||  ||
                                ACTCCAGTC TCGGA  CG
                                      _    AC
GAM1065 PRO0245  5' CTCAAACTCCCGAGCCCA    26128    A _ A
                                TG GG TC GGAGTTTGAG
                                || || || ||||||||||
                                AC CC AG CCTCAAACTC
                                 _ G  C
GAM1065 PRO0529  5' CTCAAACTCCTGACCTCA    25990
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 PRO2955  3' CTCAAACTCCTGACCTCA    37635
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAACTC

GAM1065 PSTPIP2  3' CTCAAACTCCTGACCTCA    44387
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 RAI      5' CTCAAACTCCTGATCTCA    21878
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCTAGTCCTCAAACTC

GAM1065 RTCD1    5' TCAGGCTCCTGCAACCCCA   13577    A  __
                                TG GGT  CAGGAGTTTGA
                                || |||  ||||||||||
                                AC CCA  GTCCTCGGACT
                                 C   AC
GAM1065 SC4MOL   3' CTCAAACTTCTGACCTCA    22155
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCTTCAAACTC

GAM1065 SCAMP-4  3' CTCGAACTCCTGACCTCA    54393
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065 SCYA22   3' CTTGAACTCCTGACCTCA    90945           TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                        GT
GAM1065 SFXN2    3' CTCGAACTCCTGACCTCA    73942
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065 SIRPB1   3' CTTGAACTCCCGACCTCA    20251       A     TG
                                TGAGGTC GGAGTT  AG
                                |||||||  ||||||  ||
                                ACTCCAG CCTCAA  TC
                                     C     GT
GAM1065 SLC19A3  3' CTCAAACTCCTGACTTCA    47485
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTTCAGTCCTCAAACTC

GAM1065 SLC6A14  3' CTTGAACTCCCGACCTCA    23351       A     TG
                                TGAGGTC GGAGTT  AG
                                |||||||  ||||||  ||
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                                  ACTCCAG CCTCAA  TC
                                      C     GT
GAM1065  STAF65(gamma) 3'  CTCAAAACTCCTGACCTCA    29430
                                  TGAGGTCAGGAGTTT GAG
                                  |||||||||||||| |||
                                  ACTCCAGTCCTCAAA CTC
                                           A
GAM1065  TBCC     3'  CTCGAACTCCTGACCTCA     12140
                                  TGAGGTCAGGAGTTTGAG
                                  ||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTC

GAM1065  TCL6     3'  CTCAAACTCCTGAGCTCA     40100      G
                                  TGAG TCAGGAGTTTGAG
                                  |||| ||||||||||||
                                  ACTC AGTCCTCAAACTC
                                     G
GAM1065  TCL6     3'  CTCAAACTCCTGAGCTCA     40130      G
                                  TGAG TCAGGAGTTTGAG
                                  |||| ||||||||||||
                                  ACTC AGTCCTCAAACTC
                                     G
GAM1065  THEA     3'  CTCAAACTCCTGACTTCA     66279
                                  TGAGGTCAGGAGTTTGAG
                                  ||||||||||||||||||
                                  ACTTCAGTCCTCAAACTC

GAM1065  TRIM16   3'  CTCAAACTCCTGACCTC      21337
                                  GAGGTCAGGAGTTTGAG
                                  |||||||||||||||||
                                  CTCCAGTCCTCAAACTC

GAM1065  TU12B1-TY 3'  CTCAAACTCCTAGCCTCA     33377       TC
                                  TGAGG  AGGAGTTTGAG
                                  |||||  ||||||||||
                                  ACTCC  TCCTCAAACTC
                                     GA
GAM1065  TU12B1-TY 3'  CTCGAACTCCTGACCTCA     33379
                                  TGAGGTCAGGAGTTTGAG
                                  ||||||||||||||||||
                                  ACTCCAGTCCTCAAGCTC

GAM1065  TUSP     3'  CTTGAACTCCTGACCTCA     39633            TG
                                  TGAGGTCAGGAGTT  AG
                                  ||||||||||||||  ||
                                  ACTCCAGTCCTCAA  TC
                                           GT
GAM1065  UBF-fl   3'  CTCAAACTCCTGACCTCA     51561
                                  TGAGGTCAGGAGTTTGAG
                                  |||||||||||||||||
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                                ACTCCAGTCCTCAAACTC

GAM1065 USP22    3' CTCAAACTCCTGACCTCA    68010
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 VDU1     3' CTCAAACTCCTGACCTCA    30417
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 VPS33A   3' CTCAAACTCCTGACCTCA    43336
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 WBSCR23  3' CTCAAACTCCTGACCTCA    46756
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 ZNF17    3' CTCAAACTCCCGACCTCA    82389       A
                                TGAGGTC GGAGTTTGAG
                                ||||||| |||||||||
                                ACTCCAG CCTCAAACTC
                                    C
GAM1065 ZNF338   3' TCATGTTGAACTCCTGACCTCA 42017           G   C
                                TGAGGTCAGGAGTTT AGC TGA
                                ||||||||||||||| ||| |||
                                ACTCCAGTCCTCAAG TTG ACT
                                        _  T
GAM1065 ZTL1     3' CTTGAACTCCTGACCTCA    43915          TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                      GT
GAM1065 LOC112687 3' CAAACTCCTGACCTCA     72854
                                TGAGGTCAGGAGTTTG
                                |||||||||||||||
                                ACTCCAGTCCTCAAAC

GAM1065 LOC112817 3' CTTGAACTCCTGACCTCA    56511          TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                      GT
GAM1065 LOC113523 3' CTTGAACTCCTGACCTCA    73046          TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
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                                ACTCCAGTCCTCAA  TC
                                       GT
GAM1065  LOC115648 3'  CTCGAACTCCTGACCTCA    59298
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC119392 3'  CTCGAACTCCTGACCTCA    59134
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC120114 3'  CTCAAACTCCTGACCTC     75524
                                GAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                CTCCAGTCCTCAAACTC

GAM1065  LOC120224 5'  CTCGAACTCCTGACCTCA    57097
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC124216 3'  CTCAAACTCCTGACCTC     74262
                                GAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                CTCCAGTCCTCAAACTC

GAM1065  LOC124871 3'  CAGGCCCAAACCTAGCTTC   74345     TC  AG   A
                                GAGG  AGG  TTTG GCCTG
                                ||||  |||  |||| |||||
                                CTTC  TCC  AAAC CGGAC
                                  GA  __   C
GAM1065  LOC126364 3'  CTCGAACTCCTGACCTCA    75687
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC126669 3'  CTCAAACTCCTGACCTCA    75403
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  LOC130639 5'  CTCGAACTCCTGACCTCA    74970
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC132241 3'  CTTAAACTCCTGGCCTCA    75047
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
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                                ACTCCGGTCCTCAAATTC

GAM1065  LOC132625 3'  CTCAAACTCCTGACCTC     75904
                                GAGGTCAGGAGTTTGAG
                                ||||||||||||||||
                                CTCCAGTCCTCAAACTC

GAM1065  LOC135154 3'  CTCGAACTCCTGACCTCA     75216
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC135293 3'  CTCGAACTCCTGACCTCA     76178
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC135818 3'  CTTGAACTCCTGACCTCA     75235            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                        GT
GAM1065  LOC142927 5'  TCAAACTCCTGGCCTCA     76433
                                TGAGGTCAGGAGTTTGA
                                |||||||||||||||||
                                ACTCCGGTCCTCAAACT

GAM1065  LOC143916 3'  CTCAAACTTCTGACCTCA     76640
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCTTCAAACTC

GAM1065  LOC144317 5'  CTCGAACTCCTGACCTCA     76789
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC144524 5'  CTCAAACTCCTGAACTCA     83125      G
                                TGAG TCAGGAGTTTGAG
                                |||| ||||||||||||
                                ACTC AGTCCTCAAACTC
                                   A
GAM1065  LOC145453 5'  CTCAAACTCCTGACCTCA     77137
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  LOC146050 3'  CTCAAACTCCCGACCTCA     77635        A
                                TGAGGTC GGAGTTTGAG
                                ||||||| |||||||||
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                                ACTCCAG CCTCAAACTC
                                    C
GAM1065  LOC146229 3'  CTCAAACTCCTGACCTCA    77742
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  LOC146229 3'  CTCAAACTCCTGACCTCA    77744
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  LOC146229 3'  CTCAAACTCCTGACTTCA    77746
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTTCAGTCCTCAAACTC

GAM1065  LOC146784 5'  CTTGAACCCCTGACCTCA    78113          A   TG
                                TGAGGTCAGG GTT  AG
                                |||||||||| |||  ||
                                ACTCCAGTCC CAA  TC
                                      C   GT
GAM1065  LOC146894 3'  CTTGAACTCCTGACCTCA    59190            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                       GT
GAM1065  LOC146901 3'  CTCGAACTCCTGACCTCA    83837
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC146909 3'  CTTGAACTCCTGACCTCA    78172            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                       GT
GAM1065  LOC146952 5'  CTCAAACTCCTGACCTCA    83864
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  LOC147276 3'  CTGGAACTCCTGACCTCA    78333             G
                                TGAGGTCAGGAGTTT AG
                                ||||||||||||||| ||
                                ACTCCAGTCCTCAAG TC
                                       G
GAM1065  LOC147817 3'  CTCAAACTCCTGACCTTA    78496
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
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                                ATTCCAGTCCTCAAACTC

GAM1065  LOC147841 3'  CTTGAACTCCTGACCTCA    78526            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                      GT
GAM1065  LOC148223 3'  CAGGGGGAGACTCCTGGCCTCA 78734             GAG
                                TGAGGTCAGGAGTTT  CCTG
                                ||||||||||||||||  ||||
                                ACTCCGGTCCTCAGA  GGAC
                                      GGG
GAM1065  LOC148709 3'  CTCAAACTCCCGACCTTA    78940       A
                                TGAGGTC GGAGTTTGAG
                                ||||||| ||||||||||
                                ATTCCAG CCTCAAACTC
                                     C
GAM1065  LOC148918 5'  CTCGAACTCCTGACCTCA    79068
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC149577 3'  CTCGAACTCCTGACCTCA    84510
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC149579 5'  GTTTCTCTCCAAACTCCTGCCT 71138      T       _  CCT
                CA                TGAGG CAGGAGTTTG AG   GAC
                                |||||  |||||||||| ||   |||
                                ACTCC GTCCTCAAAC TC   TTG
                                   _        C  TCT
GAM1065  LOC149692 3'  CTCAAAGTCCTGACCTCA    84582          G
                                TGAGGTCAGGA TTTGAG
                                |||||||||| ||||||
                                ACTCCAGTCCT AAACTC
                                      G
GAM1065  LOC149692 3'  CTCGAACTCCTGACCTCA    84584
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC150225 3'  CTCAAACTCCTGACCTCA    84990
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  LOC150290 3'  CTCAAACTCCTGGCCTCA    79772
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCGGTCCTCAAACTC

GAM1065  LOC150397 3'  CTTGAACCCCTGACCTCA    79845          A   TG
                                TGAGGTCAGG GTT  AG
                                |||||||||| |||  ||
                                ACTCCAGTCC CAA  TC
                                     C   GT
GAM1065  LOC150960 3'  CTCAAATTCCTGACCTCA    80060
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTCCAGTCCTTAAACTC

GAM1065  LOC151475 5'  CAGGCTAGTTTCAAACTCCTGA 85396                 _____
                CCTTA                TGAGGTCAGGAGTTTGA    GCCTG
                                |||||||||||||||||    |||||
                                ATTCCAGTCCTCAAACT    CGGAC
                                      TTGAT
GAM1065  LOC151701 3'  CTCGAACTCCTGACCTCA    85483
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC152137 3'  CTCGAACCCCTGACCTCA    80478          A
                                TGAGGTCAGG GTTTGAG
                                |||||||||| |||||||
                                ACTCCAGTCC CAAGCTC
                                     C
GAM1065  LOC152794 5'  CTTGAACTCCTGACCTCA    80677            TG
                                TGAGGTCAGGAGTT  AG
                                |||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                      GT
GAM1065  LOC153077 3'  CTTGAACTCCTGACCTCA    85910            TG
                                TGAGGTCAGGAGTT  AG
                                |||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                      GT
GAM1065  LOC153688 3'  CTCGAACTCCCAACCTCA    86103       CA
                                TGAGGT  GGAGTTTGAG
                                ||||||  ||||||||||
                                ACTCCA  CCTCAAGCTC
                                   AC
GAM1065  LOC153811 3'  CTCAAACTCCTGACCTCA    80947
                                TGAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  LOC153883 5'  CTTGAACTCCTGACCTCA    80980            TG
                                TGAGGTCAGGAGTT  AG
                                |||||||||||||  ||
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                                ACTCCAGTCCTCAA  TC
                                        GT
GAM1065  LOC154877 3'  TTCGAACTCCCGACCTCA    86317        A
                                TGAGGTC GGAGTTTGAG
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAGCTT
                                    C
GAM1065  LOC157247 5'  CTCGAACTCCTGACCTCA    81364
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC157858 5'  CTCAAACTCCTGACCTC     86586
                                GAGGTCAGGAGTTTGAG
                                |||||||||||||||||
                                CTCCAGTCCTCAAACTC

GAM1065  LOC158014 5'  CTCGAACTCCTGACCTCA    81648
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC158263 3'  GCCAGATCTCCTGACTCCA   81849    AG      _   A
                                TG  GTCAGGAG TTTG GC
                                ||  |||||||| |||| ||
                                AC  CAGTCCTC AGAC CG
                                 CT       T   _
GAM1065  LOC158476 3'  CTTGAACTCCTGACCCCA    86844    A        TG
                                TG GGTCAGGAGTT  AG
                                || ||||||||||  ||
                                AC CCAGTCCTCAA  TC
                                 C         GT
GAM1065  LOC158865 5'  CTTGAACTCCTGACCTCA    86935            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                        GT
GAM1065  LOC158931 3'  CAGGCCCAATGCTTTAACCTTA 61901       CA    _  A
                                TGAGGT  GGAGT TTG GCCTG
                                ||||||  ||||| ||| |||||
                                ATTCCA  TTTCG AAC CGGAC
                                   A_    T  C
GAM1065  LOC162427 3'  CTCAAACTCCTGACCTCA    82350
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  LOC169611 3'  CAGTCTCAAACTCCTGACCTCA 82759               C
                                TGAGGTCAGGAGTTTGAG CTG
                                |||||||||||||||||| |||
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                                ACTCCAGTCCTCAAACTC GAC
                                           T
GAM1065  LOC196047 5'  CTCAAACTCCTGACCTCA    89598
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  LOC197358 3'  CTCGAACTCCTGACCTCA    88030
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC197358 3'  CTTTAACTCCTGACCTCA    88035           T
                                TGAGGTCAGGAGTT GAG
                                |||||||||||||| |||
                                ACTCCAGTCCTCAA TTC
                                           T
GAM1065  LOC199699 3'  CTCAAACTCCTGGCCTCA    88302
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCGGTCCTCAAACTC

GAM1065  LOC199786 3'  CTTGAACTCCTGACCTCA    88381          TG
                                TGAGGTCAGGAGTT  AG
                                |||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                           GT
GAM1065  LOC199906 3'  CTCAAACTCCTGACCTCA    88480
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  LOC200014 3'  CTCGAACTCCTGACCTCA    88524
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC200314 3'  CTCGAACTCCTGACCTCA    90007
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC200316 3'  CTTGAACTCCTGACCTCA    88768          TG
                                TGAGGTCAGGAGTT  AG
                                |||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                           GT
GAM1065  LOC200407 3'  CTCAAACTCCTGACCTCA    90043
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAACTC

GAM1065  LOC201164 3'  CTCAAACTCCTGACCTCA    88116
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  LOC201626 3'  CTTGAACTCCTGACCTCA    88990           TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                          GT
GAM1065  LOC201627 3'  CTCAAACTCCCGACCTCA    89009       A
                                TGAGGTC GGAGTTTGAG
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAACTC
                                     C
GAM1065  LOC203197 3'  CTTGAACTCCTGACCTCA    89289           TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                          GT
GAM1065  LOC219529 5'  CTCAAACTCCTGAGCCCA    92970    A  _
                                TG GG TCAGGAGTTTGAG
                                || || ||||||||||||
                                AC CC AGTCCTCAAACTC
                                 _  G
GAM1065  LOC219673 5'  CTCAAACGCCTGACCTCA    93025        A
                                TGAGGTCAGG GTTTGAG
                                |||||||||| |||||||
                                ACTCCAGTCC CAAACTC
                                      G
GAM1065  LOC220074 3'  CTCAAACTCCTGACCTCA    59271
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  LOC220074 3'  CTTGAACTCCTGACCTCA    59273           TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                          GT
GAM1065  LOC221060 3'  CTCGAACTCCTGACCTCA    93209
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC221271 3'  CTCAAACTCCTGATCTCA    91854
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCTAGTCCTCAAACTC

GAM1065  LOC221418 3'  CAAACCCTGACCTCA       93635          A
                                TGAGGTCAGG GTTTG
                                |||||||||| |||||
                                ACTCCAGTCC CAAAC
                                  _
GAM1065  LOC221964 3'  CTTGAACTCCTGACCTCA     93979            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                        GT
GAM1065  LOC222031 3'  CTTGAACTCCTGACCTCA     94021            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                        GT
GAM1065  LOC222068 3'  CAGGCTGGTCTTAGACTCCTGA 92709                 _____
           CCTCA                    TGAGGTCAGGAGTTTG    AGCCTG
                                ||||||||||||||||    ||||||
                                ACTCCAGTCCTCAGAT    TCGGAC
                                        TCTGG
GAM1065  LOC245771 5'  CTCGAACTCCTGACCTCA     92887
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC253805 3'  CTCGAACTCCTGACCTCA     96429
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC253981 3'  CTTGAACTCCTGACCTCA     95829            TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                        GT
GAM1065  LOC254268 3'  CTCAAACTCCTGACCTCA     95405
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  LOC254532 5'  CTCAAACTCCTGACCTCA     96634
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  LOC254655 3'  CTCGAACTCCTGACCTCA     95470
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC255065 5'  CTCAAACTCCTGACCTCA    96582
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  LOC255065 5'  CTCAAACTCCTGACCTCA    96583
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065  LOC255308 3'  CAGGCCAGTCTCTCCTGACCTC 94531          T__  A
              A                  TGAGGTCAGGAG  TTG GCCTG
                                ||||||||||||  ||| |||||
                                ACTCCAGTCCTC  GAC CGGAC
                                       TCT  _
GAM1065  LOC255497 3'  CTCGAACTCCTGACCTCA    97190
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065  LOC257127 5'  CTTGAACTCCTGACCTCA    96671           TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                       GT
GAM1065  LOC51008  5'  CTTGAACTCCCGACCTCA    31963       A    TG
                                TGAGGTC GGAGTT  AG
                                |||||||  ||||||  ||
                                ACTCCAG CCTCAA  TC
                                    C     GT
GAM1065  LOC51200  3'  CTCAAACTCCCAACCTCA    32995       CA
                                TGAGGT  GGAGTTTGAG
                                ||||||  ||||||||||
                                ACTCCA  CCTCAAACTC
                                   AC
GAM1065  LOC51219  5'  CTCGAACTCCCGACCTCA    33118       A
                                TGAGGTC GGAGTTTGAG
                                |||||||  ||||||||||
                                ACTCCAG CCTCAAGCTC
                                    C
GAM1065  LOC56181  5'  GCCAGAGCTCTGACCTCA    95537         G    GA
                                TGAGGTCAG AGTTT  GC
                                |||||||||  |||||  ||
                                ACTCCAGTC TCGAG  CG
                                      _    AC
GAM1065  LOC57107  3'  CTCGAACTCCTGACCTCA    39834
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTC

GAM1065 LOC57146 3' CTCAAACTCCTGACCTCA    39919
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 LOC89932 3' CTTGAACTCCCGACCTCA    60800       A     TG
                                TGAGGTC GGAGTT  AG
                                ||||||| ||||||  ||
                                ACTCCAG CCTCAA  TC
                                    C     GT
GAM1065 LOC90072 3' CTCGAACTCCCGACCTCA    61295       A
                                TGAGGTC GGAGTTTGAG
                                ||||||| ||||||||||
                                ACTCCAG CCTCAAGCTC
                                    C
GAM1065 LOC90459 3' CTTGAACTCCTGACCTCA    62887           TG
                                TGAGGTCAGGAGTT  AG
                                ||||||||||||||  ||
                                ACTCCAGTCCTCAA  TC
                                        GT
GAM1065 LOC90485 3' CAGGCTGTCTCGAACTCCTAAC 63009     G  C       ____
          ATCA                    TGA GT AGGAGTTTGA    GCCTG
                                ||| || ||||||||||    |||||
                                ACT CA TCCTCAAGCT    CGGAC
                                  A  A        CTGT
GAM1065 LOC90591 3' CTCGAACTCCTGACCTCA    63421
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065 LOC90918 3' CTCAAACTCCTGACCTTA    64355
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ATTCCAGTCCTCAAACTC

GAM1065 LOC91115 3' AGGCTTCTCCTGGCCTCA    64923          TTT
                                TGAGGTCAGGAG   GAGCCT
                                ||||||||||||   ||||||
                                ACTCCGGTCCTC   TTCGGA
                                               ___
GAM1065 LOC91115 3' CTCCAACTCCTGACCTCA    64933           T
                                TGAGGTCAGGAGTT GAG
                                |||||||||||||| |||
                                ACTCCAGTCCTCAA CTC
                                        C
GAM1065 LOC91561 5' CTCGAACTCCTGACCTCA    66448
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
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                                ACTCCAGTCCTCAAGCTC

GAM1065 LOC91963 3' CTCAAACTCCTGAGCTCA    67691      G
                                TGAG TCAGGAGTTTGAG
                                |||| ||||||||||||
                                ACTC AGTCCTCAAACTC
                                  G
GAM1065 LOC92267 3' CTCAAACTCCTGACCTCA    68609
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAACTC

GAM1065 LOC92697 5' CTCGAACTCCCAACCTCA    70268       CA
                                TGAGGT  GGAGTTTGAG
                                ||||||  ||||||||||
                                ACTCCA  CCTCAAGCTC
                                    AC
GAM1065 LOC93349 3' CTCGAACTCCTGACCTCA    56455
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCAGTCCTCAAGCTC

GAM1065 LOC93408 5' CTCAAACTCCTGGCCTCA    56478
                                TGAGGTCAGGAGTTTGAG
                                ||||||||||||||||||
                                ACTCCGGTCCTCAAACTC

GAM1066 ACADSB   3' CAGCTCACTGCAGCCTTGACCT 7843      CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||
                                TCC   TTCCGACGTCACTCGAC
                                  AG_
GAM1066 ADAMTS4   3' CAGCTCACTGCAACCTTCGCC  17503     AA
                                GGC  GAGGTTGCAGTGAGCTG
                                |||  ||||||||||||||||
                                CCG  TTCCAACGTCACTCGAC
                                  C_
GAM1066 ADRB3     3' CAGCCTTTCCACAACCTCTACC 3431      CA       CAGT  _
             T                   AGG  AGAGGTTG    GAG CTG
                                |||  ||||||||    ||| |||
                                TCC  TCTCCAAC    TTC GAC
                                  A_       ACCT   C
GAM1066 AHR      3' CACTGCAACCTCTACCT     7876      CA
                                AGG  AGAGGTTGCAGTG
                                |||  |||||||||||||
                                TCC  TCTCCAACGTCAC
                                  A_
GAM1066 AK2      3' CTGCAACCTCTTGACC      25500     _
                                GG CAAGAGGTTGCAG
                                || |||||||||||||
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                                CC GTTCTCCAACGTC
                                 A
GAM1066 ALDH1B1  3' CACTGCAACCTCCGCCT    5490      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066 AP3B2    5' CGCCGCAACCTCCTCCT    16186    CAA      A
                                AGG   GAGGTTGC GTG
                                |||   |||||||| |||
                                TCC   CTCCAACG CGC
                                  TC_      C
GAM1066 APM1     3' CTTACTGCAACCTTTGCCT   16591      A
                                AGGCA GAGGTTGCAGTGAG
                                ||||| ||||||||||||||
                                TCCGT TTCCAACGTCATTC
                                  _
GAM1066 APOL1    3' CAGCTCACTGCAAGCTCTGCCT 13343      A   G
                                AGGCA GAG TTGCAGTGAGCTG
                                ||||| ||| ||||||||||||
                                TCCGT CTC AACGTCACTCGAC
                                   _  G
GAM1066 APPBP2   3' CACTGCAACCTCCGCCT    21073     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066 AQP6     3' CACTGCAACCTCTACCT    7940     CA
                                AGG  AGAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  TCTCCAACGTCAC
                                  A_
GAM1066 AQP6     3' CACTGCAACCTCTACCT    53911    CA
                                AGG  AGAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  TCTCCAACGTCAC
                                  A_
GAM1066 ARCN1    3' CAGCTCACTGCAACCTCCGCCT 7973      AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066 ATP1B2   3' CAGCTCACTGCAACTTCCGC  8045     AA
                                GC  GAGGTTGCAGTGAGCTG
                                ||  |||||||||||||||||
                                CG  CTTCAACGTCACTCGAC
                                 C_
GAM1066 ATP7A    3' CACTGCAACCTCTGCCT    3520      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
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                                TCCGT CTCCAACGTCAC
                                  _
GAM1066 ATP8B2   3' CAGCTCACTGCAACCTCCACCT 65214    CAA
                                AGG  GAGGTTGCAGTGAGCTG
                                |||  ||||||||||||||||
                                TCC  CTCCAACGTCACTCGAC
                                  AC_
GAM1066 AXL     3' CACTGCAACCTTCACCT    8094     CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  TTCCAACGTCAC
                                  AC_
GAM1066 AXL     3' CACTGCAACCTTCACCT    41591    CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  TTCCAACGTCAC
                                  AC_
GAM1066 BMP1    3' CAGCTCACTAGGCCGATCCTGC 20417    A __   GC
              T                  GGCA GA  GGTT  AGTGAGCTG
                                |||| ||  ||||  |||||||||
                                TCGT CT  CCGG  TCACTCGAC
                                  C  AG   A_
GAM1066 BRIP1   3' CACTGCAACCTTCACCT    49396    CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  TTCCAACGTCAC
                                  AC_
GAM1066 C7      3' CTGCAACCTCCGCCT      5160     AA
                                AGGC  GAGGTTGCAG
                                ||||  ||||||||||
                                TCCG  CTCCAACGTC
                                  C_
GAM1066 CAMLG   3' CACCGCAACCTCCACCT    8232     CAA      A
                                AGG  GAGGTTGC GTG
                                |||  |||||||| |||
                                TCC  CTCCAACG CAC
                                  AC_      C
GAM1066 CASP2   3' CAGCTCACTGCAAGCTC    6895     G
                                GAG TTGCAGTGAGCTG
                                ||| ||||||||||||
                                CTC AACGTCACTCGAC
                                  G
GAM1066 CASP2   3' CAGCTCACTGCAAGCTC    52137    G
                                GAG TTGCAGTGAGCTG
                                ||| ||||||||||||
                                CTC AACGTCACTCGAC
                                  G
GAM1066 CASP2   3' CAGCTCACTGCAAGCTC    52150    G
                                GAG TTGCAGTGAGCTG
                                ||| ||||||||||||
```

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                                CTC AACGTCACTCGAC
                                  G
GAM1066 CASP2    3' CAGCTCACTGCAAGCTC     52165     G
                                GAG TTGCAGTGAGCTG
                                ||| |||||||||||||
                                CTC AACGTCACTCGAC
                                  G
GAM1066 CBFA2T3  3' ACTCCAACCTCTCGGCC     17755     A_      C
                                GGC  AGAGGTTG AGT
                                |||  |||||||| |||
                                CCG  TCTCCAAC TCA
                                  GC       C
GAM1066 CCNF     3' CTCACTGTAACCTCCGCCT    8317      AA
                                AGGC  GAGGTTGCAGTGAG
                                ||||  ||||||||||||||
                                TCCG  CTCCAATGTCACTC
                                  C_
GAM1066 CD5L     5' AGCTCATCACCTTCACCT     19708     CAA    TGCA
                                AGG   GAGGT    GTGAGCT
                                |||   |||||    |||||||
                                TCC   TTCCA    TACTCGA
                                  AC_    C___
GAM1066 CD81     3' CAGCTCACCTTGTTCCCTC    15132     TT   __
                                GAGG  GCA  GTGAGCTG
                                ||||  |||  ||||||||
                                CTCC  TGT  CACTCGAC
                                  CT   TC
GAM1066 CDH1     3' CAGCTCACTGCAGCCTTGTCCT 15142     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   |||||||||||||||||
                                TCC   TTCCGACGTCACTCGAC
                                  TG_
GAM1066 CDH17    3' CAGCTCACTGCAACCTCCGCCT 14502     AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066 CDK10    3' AGCTCATCCCCTTGGCT     13399     G    A  TTGCA
                                AG CAAG GG     GTGAGCT
                                || |||| ||     |||||||
                                TC GTTC CC     TACTCGA
                                 G    C  _____
GAM1066 CDK10    3' AGCTCATCCCCTTGGCT     53766     G    A  TTGCA
                                AG CAAG GG     GTGAGCT
                                || |||| ||     |||||||
                                TC GTTC CC     TACTCGA
                                 G    C  _____
GAM1066 CDK10    3' AGCTCATCCCCTTGGCT     53774     G    A  TTGCA
                                AG CAAG GG     GTGAGCT
                                || |||| ||     |||||||
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                                TC GTTC CC    TACTCGA
                                 G   C _____
GAM1066 CHST1    3' CAGCTCACCCCACTCCCTTCTG 13333     AG  T__ CA
             CC                   GGCA AGG  TG GTGAGCTG
                                  |||| |||  || ||||||||
                                  CCGT TCC  AC CACTCGAC
                                    CT  CTC CC
GAM1066 CLECSF12 3' CACCGCAACCTCCGCC     76684     AA      A
                                  GGC GAGGTTGC GTG
                                  ||| |||||||| |||
                                  CCG CTCCAACG CAC
                                    C_      C
GAM1066 CRTAP    3' CAGCTCACTGCAACCTCCGCCT 21031     AA
                                  AGGC GAGGTTGCAGTGAGCTG
                                  |||| ||||||||||||||||
                                  TCCG CTCCAACGTCACTCGAC
                                    C_
GAM1066 CSNK2A2  5' CAGCTCACTGCAACCTCCACCT 8560     CAA
                                  AGG  GAGGTTGCAGTGAGCTG
                                  |||  ||||||||||||||||
                                  TCC  CTCCAACGTCACTCGAC
                                    AC_
GAM1066 CYP1A2   3' CAGCTCACTACAACCTCCGCCT 69100     AA      C
                                  AGGC GAGGTTG AGTGAGCTG
                                  |||| ||||||| |||||||||
                                  TCCG CTCCAAC TCACTCGAC
                                    C_      A
GAM1066 CYP1A2   3' CAGCTCACTGCAACCTCCACCT 69101    CAA
                                  AGG  GAGGTTGCAGTGAGCTG
                                  |||  ||||||||||||||||
                                  TCC  CTCCAACGTCACTCGAC
                                    AC_
GAM1066 CYP1A2   3' CAGCTCACTGCAACCTCTGCCT 69103     A
                                  AGGCA GAGGTTGCAGTGAGCTG
                                  ||||| ||||||||||||||||
                                  TCCGT CTCCAACGTCACTCGAC
                                     _
GAM1066 CYP1A2   3' CAGCTCACTACAACCTCCGCCT 5681      AA      C
                                  AGGC GAGGTTG AGTGAGCTG
                                  |||| ||||||| |||||||||
                                  TCCG CTCCAAC TCACTCGAC
                                    C_      A
GAM1066 CYP1A2   3' CAGCTCACTGCAACCTCCACCT 5682     CAA
                                  AGG  GAGGTTGCAGTGAGCTG
                                  |||  ||||||||||||||||
                                  TCC  CTCCAACGTCACTCGAC
                                    AC_
GAM1066 CYP1A2   3' CAGCTCACTGCAACCTCTGCCT 5684      A
                                  AGGCA GAGGTTGCAGTGAGCTG
                                  ||||| ||||||||||||||||
```

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                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  CYP2B6   3'  CACTGCAACCTCCACC     5724     CAA
                                GG  GAGGTTGCAGTG
                                ||  ||||||||||||
                                CC  CTCCAACGTCAC
                                 AC_
GAM1066  CYP2B6   3'  CACTGCAACCTCTGCCT     5725       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  CYP4F3   3'  CATTGCAACCTCCGCCT     6111       AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTTAC
                                  C_
GAM1066  CYP51    3'  CAGCTCACTGCATCCTCTGCCT 5781       A   T
                                AGGCA GAGG TGCAGTGAGCTG
                                ||||| |||| ||||||||||||
                                TCCGT CTCC ACGTCACTCGAC
                                  _   T
GAM1066  CYP8B1   3'  CACTACAACCTCTGCCT     15257      A     C
                                AGGCA GAGGTTG AGTG
                                ||||| ||||||| ||||
                                TCCGT CTCCAAC TCAC
                                  _     A
GAM1066  CYP8B1   3'  CACTGCAACCTCTGCCT     15259      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  DFFB     3'  CACTGCAACCTCCGCCT     87377      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  DHFR     3'  CTTACTGCAACCTCCGCCT    5804       AA
                                AGGC  GAGGTTGCAGTGAG
                                ||||  ||||||||||||||
                                TCCG  CTCCAACGTCATTC
                                  C_
GAM1066  DISC1    3'  CACTGCAACCTCTACCT     37872     CA
                                AGG  AGAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  TCTCCAACGTCAC
                                  A_
GAM1066  DSCR3    3'  CAGCTCACTGCAACCTCCACCT 20173     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   |||||||||||||||||
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                                TCC   CTCCAACGTCACTCGAC
                                  AC_
GAM1066  EFNB2    3'  CAGCTCACTGCTGCTGCCT    14570       AGAG  T
                                AGGCA    GT GCAGTGAGCTG
                                |||||    || ||||||||||
                                TCCGT    CG CGTCACTCGAC
                                  _____  T
GAM1066  EHD2     3'  CAGCTCACTGCAACCTCCACCT 27489     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGAC
                                  AC_
GAM1066  EIF2S3   3'  GTGATCTGCAACCTCTGCC    7419       A         TGA
                                GGCA GAGGTTGCAG   GC
                                |||| ||||||||||   ||
                                CCGT CTCCAACGTC   TG
                                  _         TAG
GAM1066  EPB72    3'  CACTGCAACCTCCGCCT     14599      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  F2RL2    3'  CATTGCAACCTCTGCCT     14619      A
                                AGGCA GAGGTTGCAGTG
                                |||||  ||||||||||||
                                TCCGT CTCCAACGTTAC
                                  _
GAM1066  FANCF    3'  CAGTGCAACCTCTGCCT     42670      A       G
                                AGGCA GAGGTTGCA TG
                                |||||  ||||||||| ||
                                TCCGT CTCCAACGT AC
                                  _       G
GAM1066  FCAR     3'  CACTGCAACCTTCGCCT     55791      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  TTCCAACGTCAC
                                  C_
GAM1066  FCAR     3'  CACTGCAACCTTCGCCT     55810      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  TTCCAACGTCAC
                                  C_
GAM1066  FEZ1     3'  CACTGCAACCTCCACCT     42566     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  FGFR1    3'  CAGCTCACCTCTCCCTCCACCT 43628     CAA    TTGCA
                                AGG   GAGG    GTGAGCTG
                                |||   ||||    ||||||||
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                                TCC  CTCC    CACTCGAC
                                  AC_   CTCTC
GAM1066  FGFR1    3'  CAGCTCACCTCTCCCTCCACCT 31795     CAA   TTGCA
                                AGG  GAGG    GTGAGCTG
                                |||  ||||    ||||||||
                                TCC  CTCC    CACTCGAC
                                  AC_   CTCTC
GAM1066  FGFR1    3'  CAGCTCACCTCTCCCTCCACCT 5202      CAA   TTGCA
                                AGG  GAGG    GTGAGCTG
                                |||  ||||    ||||||||
                                TCC  CTCC    CACTCGAC
                                  AC_   CTCTC
GAM1066  FHL2     5'  CAGCTCACTGCAAGCTCTACCT 7561      CA   G
                                AGG  AGAG TTGCAGTGAGCTG
                                |||  |||| ||||||||||||
                                TCC  TCTC AACGTCACTCGAC
                                  A_   G
GAM1066  FUT1     3'  CAGCTCACTGCAAGCTCTGCCT 3786       A   G
                                AGGCA GAG TTGCAGTGAGCTG
                                ||||| ||| ||||||||||||
                                TCCGT CTC AACGTCACTCGAC
                                   _   G
GAM1066  FZD4     3'  CACTGCAACCTCTGCCT     24128       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||
                                TCCGT CTCCAACGTCAC
                                   _
GAM1066  G6PC     3'  GGCTCACTGCAACCTCTTCCT  3831      C
                                AGG AAGAGGTTGCAGTGAGCT
                                ||| ||||||||||||||||
                                TCC TTCTCCAACGTCACTCGG
                                   _
GAM1066  GM2A     3'  CACTGCAACCTCCGCCT     67773      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  GNE      3'  CAATGCAACCTCTGCC      18476      A       G
                                GGCA GAGGTTGCA TG
                                |||| ||||||||| ||
                                CCGT CTCCAACGT AC
                                   _       A
GAM1066  GPR81    3'  CACTGCAACCTCTGCCT     50753       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||
                                TCCGT CTCCAACGTCAC
                                   _
GAM1066  GRAF     3'  CACTGCAACCTCCGCCT     30550      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||
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                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  HCS      3'  CACCGCAACCTCCGCCT     38459      AA       A
                                AGGC  GAGGTTGC GTG
                                ||||  |||||||| |||
                                TCCG  CTCCAACG CAC
                                  C_       C
GAM1066  HCS      3'  CACTGCAACCTCCGCCT     38460      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  HLCS     5'  CACCACAACCTCTGCCT     4661       A      CA
                                AGGCA GAGGTTG  GTG
                                |||||  |||||||  |||
                                TCCGT CTCCAAC  CAC
                                   _      AC
GAM1066  HOXC5    3'  AGTGAGCTGCTCCACAACCTCT 38492   C      G_________   TGAG
              TCCC                    AAGAGGTT       CAG    CT
                                 ||||||||       |||    ||
                                 TTCTCCAA       GTC    GA
                                C       CACCTCIII   GAGT
GAM1066  HTR1D    3'  CAGCTCACTGCAACCTCCGC   5993     AA
                                GC  GAGGTTGCAGTGAGCTG
                                ||  ||||||||||||||||
                                CG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  HTR1E    5'  CATTGCAACCTCCGCCT     6011       AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTTAC
                                  C_
GAM1066  ITGAM    3'  CACTGCAACCTCCGCCT     71835      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  JRK      3'  CAGCTCACTGCAGCCTCGACCT 86523     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||
                                TCC   CTCCGACGTCACTCGAC
                                  AG_
GAM1066  KMO      3'  CACTGCAACCTCTGCCT     13446      A
                                AGGCA GAGGTTGCAGTG
                                |||||  ||||||||||||
                                TCCGT CTCCAACGTCAC
                                   _
GAM1066  LANCL1   3'  CTCACTGCATGACCCT      20212     A  __
                                AG GGT  TGCAGTGAG
                                || |||  |||||||||
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                                TC CCA  ACGTCACTC
                                 _  GT
GAM1066 LILRA3   3'  CACTGCAACCTCCGCCT    95307     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066 LNK      3'  CACTGCAACCTCCACCT    18458     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066 LYZ      3'  CACTGCAACCTCCACCT    4096      CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066 MAK      3'  CTTACTGCAACCTCCACCT   19759     CAA
                                AGG   GAGGTTGCAGTGAG
                                |||   ||||||||||||||
                                TCC   CTCCAACGTCATTC
                                  AC_
GAM1066 MEF2A    5'  CACTGCAACCTCCGCCT    18780     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066 MEFV     3'  CACTGCAACCTCCGCCT    4127      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066 MEFV     3'  CAGCTCACTGCAACCTCCACCT 4129     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   |||||||||||||||||
                                TCC   CTCCAACGTCACTCGAC
                                  AC_
GAM1066 MGST2    5'  CAGCCCCAGACCTGCCTGCCT  10032     AG_    GCAGTGA
                                AGGCA  AGGTT     GCTG
                                |||||  |||||     ||||
                                TCCGT  TCCAG     CGAC
                                   CCG    ACCC___
GAM1066 MHC2TA   3'  CACTGCAACCTCCGCCT    4165      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066 MICB     3'  CAGCTCACTGCAACCTCTGCCT 19823      A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| |||||||||||||||||
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                                TCCGT CTCCAACGTCACTCGAC
                                     _
GAM1066 MPL      3' CACTGCAACCTCTGCCT     18132       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                     _
GAM1066 MPL      3' CAGCTCACTGCAACCTCCACCT 18134     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||||
                                TCC   CTCCAACGTCACTCGAC
                                  AC_
GAM1066 MYCL2    3' CACTGCAACCTCTGCCT     18176       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                     _
GAM1066 MYO1C    3' CACCTGCAATCTCCCACCT    61201     CAA        _
                                AGG   GAGGTTGCAG TG
                                |||   |||||||||| ||
                                TCC   CTCTAACGTC AC
                                  ACC         C
GAM1066 NCOA6IP  3' CAGCTCACTGCAGGTTCAGCCT 45735      AA   G
                                AGGC  GAG TTGCAGTGAGCTG
                                ||||  ||| ||||||||||||||
                                TCCG  CTT GACGTCACTCGAC
                                  A_  G
GAM1066 NDRG3    3' CACTGCAACCTCTGCC      49293      A
                                GGCA GAGGTTGCAGTG
                                |||| ||||||||||||
                                CCGT CTCCAACGTCAC
                                     _
GAM1066 NQO1     3' CACTGCAACCTCTGCCT     6153       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                     _
GAM1066 OAS3     3' CAGCTCACACACTCCCCTGCCT 20538      A A  TTGCA
                                AGGCA G GG    GTGAGCTG
                                ||||| | ||    ||||||||
                                TCCGT C CC    CACTCGAC
                                  _ C  TCACA
GAM1066 OVOL1    3' GCAGCCCACCCTCCTGCAACCT 15858         _____  A   III
            CTCACC                 AGAGGTTGCA    GTG GCTG   C
                                ||||||||||    ||| ||||   |
                                TCTCCAACGT    CAC CGAC   G
                                      CCTCC   C    III
GAM1066 PCDHB11  3' CAGCTCACTGCAACCTCTGCCT 38412      A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||||
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                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  PCDHB11   3'  CAGCTCACTGCACCCTCCGCCT 38413      AA    T
                                AGGC  GAGG TGCAGTGAGCTG
                                ||||  |||| ||||||||||||
                                TCCG  CTCC ACGTCACTCGAC
                                  C_   C
GAM1066  PCDHB16   3'  CACTGCAACCTCTGCCT     40550       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  PCDHB9    3'  CAGCTCACTGCAACCTCCGCCT 38937      AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  PDCL      3'  CACTGCAACCTCCACCT     18210     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  PDE6B     3'  CAGCTCACTGCAACCTCCACCT 4274      CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGAC
                                  AC_
GAM1066  PER2      3'  CACTGCAACCTCTGCCT     43028       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  PIGR      3'  CACTGCAACCTCCGCCT     72591      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  PIM2      3'  CAGATTCTTGCAACCTCCTCCT 59989     CAA        T  _
                                AGG   GAGGTTGCAG GAG CTG
                                |||   |||||||||| ||| |||
                                TCC   CTCCAACGTT CTT GAC
                                  TC_         _   A
GAM1066  PLA2G4C   5'  AGCCCGCGACCTCCTCC     73412    CAA       AGT A
                                GG   GAGGTTGC   G GCT
                                ||   ||||||||   | |||
                                CC   CTCCAGCG   C CGA
                                  TC_       ___ C
GAM1066  PRKCM     3'  CAGCTGCTCAGCAACCTTTCAC 10812     CA        __   G
                CT                AGG  AGAGGTTGC  AGT AGCTG
                                |||  |||||||||  ||| |||||
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                                TCC  TTTCCAACG  TCG TCGAC
                                  AC        AC  _
GAM1066  PRKWNK3   3'  TGCTGCAACCTCCCCCT     61557     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCGT
                                  CC_
GAM1066  PSMB2     3'  CACTGCAACCTCCGCCT     10949      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  PSMD9     3'  CAGCCCACTGCTAGTTTGACT  10981    G    AGGTT     A
                                AG CAAG     GCAGTG GCTG
                                || ||||     |||||| ||||
                                TC GTTT     CGTCAC CGAC
                                 A   GAT__     C
GAM1066  PTGIS     3'  CAGCTCACCACAACCTCCACCT 6325      CAA      CA
                                AGG   GAGGTTG  GTGAGCTG
                                |||   |||||||  ||||||||
                                TCC   CTCCAAC  CACTCGAC
                                  AC_      AC
GAM1066  RAB36     3'  CAGTGCAACCTCTGCCT     16950       A        G
                                AGGCA GAGGTTGCA TG
                                ||||| |||||||||  ||
                                TCCGT CTCCAACGT AC
                                   _        G
GAM1066  RALBP1    3'  CAGCTCACTTTGTACCCCTC   22293      T_    __
                                GAGG  TGCA  GTGAGCTG
                                ||||  ||||  ||||||||
                                CTCC  ATGT  CACTCGAC
                                  CC    TT
GAM1066  RBBP9     3'  CAGCTCACTCTAACCTGCACCT 70130     CAAG     C
                                AGG    AGGTTG AGTGAGCTG
                                |||    ||||||  |||||||||
                                TCC    TCCAAT TCACTCGAC
                                  ACG_     C
GAM1066  RHD       3'  CACTGCAACCTCCGCCT     32297      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  RHD       3'  CACTGCAACCTCTACCT     32299     CA
                                AGG  AGAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  TCTCCAACGTCAC
                                  A_
GAM1066  RHD       3'  CACTGCAACCTCCGCCT     32606      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  RHD      3'  CACTGCAACCTCTACCT     32608     CA
                                AGG  AGAGGTTGCAGTG
                                |||  |||||||||||||
                                TCC  TCTCCAACGTCAC
                                  A_
GAM1066  RPH3AL   3'  CACTGCAACCTCCACCT     22741     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  RPP30    3'  CAGCTCACTGCAACCTCAATCC 21162     CAA
                T                AGG   GAGGTTGCAGTGAGCTG
                                |||   |||||||||||||||||
                                TCC   CTCCAACGTCACTCGAC
                                  TAA
GAM1066  SAS      3'  CACCGCAACCTCTGCCT     19949       A       A
                                AGGCA GAGGTTGC GTG
                                ||||| |||||||| |||
                                TCCGT CTCCAACG CAC
                                  _       C
GAM1066  SDPR     5'  CACCGCAACTTCTCACC     16223     CA        A
                                GG  AGAGGTTGC GTG
                                ||  ||||||||| |||
                                CC  TCTTCAACG CAC
                                  AC        C
GAM1066  SEDL     3'  CACTGCAACCTCCACCT     27323     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  SEDL     3'  CACTGCAACCTCCACCT     27324     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  SEDL     3'  CACTGCAACCTCCGCCT     27327      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  SEPN1    3'  CACTGCAACCTCCACCT     66362     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  SERPINB9 3'  GGCTCACTGCAACCTCCTCCT 14759     CAA
                                AGG   GAGGTTGCAGTGAGCT
                                |||   ||||||||||||||||
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                                TCC   CTCCAACGTCACTCGG
                                  TC_
GAM1066  SFRP4    3'  CTCACTGCAGTGCTCT      11576      _
                                AGAG GTTGCAGTGAG
                                |||| ||||||||||
                                TCTC TGACGTCACTC
                                  G
GAM1066  SHOX     3'  CACTGCAACCTCCGCCT     22530      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  SHOX     3'  CAGCTCACCGCCACCTCCGCC  4832      AA    T  A
                                GGC  GAGGT GC GTGAGCTG
                                |||  ||||| || ||||||||
                                CCG  CTCCA CG CACTCGAC
                                  C_    C  C
GAM1066  SIL      3'  CACTGCAACCTCTGCCT     11685      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  SLA2     3'  CAGCTCACTGCAACCTC     49893
                                GAGGTTGCAGTGAGCTG
                                |||||||||||||||||
                                CTCCAACGTCACTCGAC

GAM1066  SLC14A2  5'  CACTGCAACCTCCACCT     23129     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  SLC15A1  3'  CAGCTCACTGCAACCTCCGCCT 17399      AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  SMAC     5'  CACTGCAACCTCTGCCT     57203      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  SMAC     5'  CAGCTCACTGCAACCTGTGCCT 57206      AG
                                AGGCA  AGGTTGCAGTGAGCTG
                                |||||  |||||||||||||||||
                                TCCGT  TCCAACGTCACTCGAC
                                  G_
GAM1066  SMP1     3'  ACTGAGCACAACCTCTTTCC   26695    C      ____
                                GG AAGAGGTTG    CAGT
                                || |||||||||    ||||
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                                CC TTCTCCAAC    GTCA
                                 T       ACGA
GAM1066  SNAP23   3'  CACTGCAACCTCCGCCT     55458      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  SNAP23   3'  CACTGCAACCTCCGCCT     13805      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  SNX15    3'  CACTGCAACCTCCACCT     73734     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  SOST     3'  GGAGCTGCAGACAACCTCTTAC 47470    C       G________   TGAG
             TT                   GG AAGAGGTT       CAG    C
                                || ||||||||       |||    |
                                TC TTCTCCAA       GTC    G
                                 A       CAGACIII   GAGT
GAM1066  SPG3A    5'  AGCTCACCGCCACCAGCT    31914     AAGA   T  A
                                GGC    GGT GC GTGAGCT
                                |||    ||| || |||||||
                                TCG    CCA CG CACTCGA
                                  A___   C  C
GAM1066  SPN      3'  CACTGCAACCTCTGCCT     11916      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                   _
GAM1066  SS18     3'  CAGCTCACTGCAACCTCCGCCT 18884      AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  STAU     5'  CACTGCAACCTCCACCT     15996     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  SULT2B1  5'  CACTGCAACCTCCGCCT     16022      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  TAGLN    3'  AGCCCAACTTCTTACC      59632    C       CAGTGA
                                GG AAGAGGTTG     GCT
                                || |||||||||     |||
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                                CC TTCTTCAAC     CGA
                                 A       C_____
GAM1066 TAPBP    3'  CTTACTGCAACCTCCGCCT   12124     AA
                                AGGC  GAGGTTGCAGTGAG
                                ||||  ||||||||||||||
                                TCCG  CTCCAACGTCATTC
                                  C_
GAM1066 TAT      3'  CACTGCAACCTCCACCT     4462      CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066 TBXA2R   3'  CACTGCAACCTCCGCCT     6482      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066 TBXA2R   3'  CAGCTCACTGCAACCTCCACCT 6484     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   |||||||||||||||||
                                TCC   CTCCAACGTCACTCGAC
                                  AC_
GAM1066 TCF2     3'  AGTGTAGCAGCCTCCTGCCT   21372      A       AGTGA
                                AGGCA GAGGTTGC     GCT
                                |||||| ||||||||     |||
                                TCCGT CTCCGACG     TGA
                                   C       ATG__
GAM1066 TJP1     5'  CAGCTCACTGCAGCCTTGACCT 12297     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   |||||||||||||||||
                                TCC   TTCCGACGTCACTCGAC
                                  AG_
GAM1066 TMC1     5'  CTGCAACCTCCGCCT       56901      AA
                                AGGC  GAGGTTGCAG
                                ||||  |||||||||
                                TCCG  CTCCAACGTC
                                  C_
GAM1066 TNFRSF10B 3'  CAGTGCAACCTCCGCCT     13866      AA       G
                                AGGC  GAGGTTGCA TG
                                ||||  ||||||||| ||
                                TCCG  CTCCAACGT AC
                                  C_       G
GAM1066 TPMT     3'  CACTGCAACCTCTGCCT     4533       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                   _
GAM1066 TRAF5    3'  CAGCTCACTGCAAACTCTGCCT 16075      A   G
                                AGGCA GAG TTGCAGTGAGCTG
                                ||||| ||| ||||||||||||
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                                TCCGT CTC AACGTCACTCGAC
                                  _  A
GAM1066  TRIM9    5'  CACTGCAACCTCCGCCT    30754     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  TRPM6    3'  CACTGCAACCTCTGCCT    34534      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  TRPV1    3'  CACTGCAACCTCTGCCT    38072      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  TRPV1    3'  CTGCAACCTCCGCCT      38079     AA
                                AGGC  GAGGTTGCAG
                                ||||  |||||||||||
                                TCCG  CTCCAACGTC
                                  C_
GAM1066  TRPV1    3'  CACTGCAACCTCTGCCT    54791      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  TRPV1    3'  CTGCAACCTCCGCCT      54800     AA
                                AGGC  GAGGTTGCAG
                                ||||  |||||||||||
                                TCCG  CTCCAACGTC
                                  C_
GAM1066  TRPV1    3'  CACTGCAACCTCTGCCT    54826      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  TRPV1    3'  CTGCAACCTCCGCCT      54833     AA
                                AGGC  GAGGTTGCAG
                                ||||  |||||||||||
                                TCCG  CTCCAACGTC
                                  C_
GAM1066  TRPV1    3'  CACTGCAACCTCTGCCT    54858      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  TRPV1    3'  CTGCAACCTCCGCCT      54865     AA
                                AGGC  GAGGTTGCAG
                                ||||  |||||||||||
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                                TCCG  CTCCAACGTC
                                  C_
GAM1066  TUFT1    3'  CAGCTCACTGCAACCTCTGCCT 39254       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  VENTX2   3'  CACTGCAACCTCCGCCT     27107      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  VHL      3'  CACTGCAACCTCTGCCT     5063       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  ZNF133   5'  CTCACTGCAACCTCCACCC   12836    CAA
                                GG   GAGGTTGCAGTGAG
                                ||   ||||||||||||||
                                CC   CTCCAACGTCACTC
                                 CAC
GAM1066  ZNF157   3'  CAGCTCATTTCAACCTTCGCCT 12876      AA      C
                                AGGC  GAGGTTG AGTGAGCTG
                                ||||  ||||||| |||||||||
                                TCCG  TTCCAAC TTACTCGAC
                                  C_      T
GAM1066  ZNF264   3'  CACTGCAACCTCCGCCT     12745      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  ZNF264   3'  CTGCAACCTCTGCCT       12752       A
                                AGGCA GAGGTTGCAG
                                ||||| |||||||||
                                TCCGT CTCCAACGTC
                                  _
GAM1066  20D7-FC4 5'  CAGCTCACTGCAGCCTCCACCT 60897     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||
                                TCC   CTCCGACGTCACTCGAC
                                  AC_
GAM1066  APCL     5'  CAGCCCGACTCCATCCTCCCAC 19665     CAA   T  C   _ A
            CT                    AGG   GAGG TG AGT G GCTG
                                |||   |||| || ||| | ||||
                                TCC   CTCC AC TCA C CGAC
                                  ACC    T  C   G C
GAM1066  ARPP-19  3'  CACTGCAACCTCTGCCT     21790       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
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                                TCCGT CTCCAACGTCAC
                                  _
GAM1066 ARPP-19   3' CAGCTCACTGCAACCTTACTCC 21792     CAA
             T                   AGG   GAGGTTGCAGTGAGCTG
                                 |||   |||||||||||||||||
                                 TCC   TTCCAACGTCACTCGAC
                                   TCA
GAM1066 ASB16     5' CACTGCAACCTCCGCCT     69931      AA
                                 AGGC  GAGGTTGCAGTG
                                 ||||  ||||||||||||
                                 TCCG  CTCCAACGTCAC
                                   C_
GAM1066 ASE-1     3' CACTGCAACCTCCGCCT     23945      AA
                                 AGGC  GAGGTTGCAGTG
                                 ||||  ||||||||||||
                                 TCCG  CTCCAACGTCAC
                                   C_
GAM1066 ATP1B4    3' CACTGCAACCTCCACCT     23813     CAA
                                 AGG   GAGGTTGCAGTG
                                 |||   ||||||||||||
                                 TCC   CTCCAACGTCAC
                                   AC_
GAM1066 BA108L7.2 3' CACTGCAACCTCTGCCT     48258      A
                                 AGGCA GAGGTTGCAGTG
                                 |||||| ||||||||||||
                                 TCCGT CTCCAACGTCAC
                                   _
GAM1066 BAG5      3' CAGCTCACTGCAACCTCCACCT 16839     CAA
                                 AGG   GAGGTTGCAGTGAGCTG
                                 |||   |||||||||||||||||
                                 TCC   CTCCAACGTCACTCGAC
                                   AC_
GAM1066 BNIP-S    3' CACTGCAACCTCCGCCT     56256      AA
                                 AGGC  GAGGTTGCAGTG
                                 ||||  ||||||||||||
                                 TCCG  CTCCAACGTCAC
                                   C_
GAM1066 BTN3A1    3' CAGCTCCCTGCAACCTCCACCT 22915     CAA        T
                                 AGG   GAGGTTGCAG GAGCTG
                                 |||   |||||||||| ||||||
                                 TCC   CTCCAACGTC CTCGAC
                                   AC_        C
GAM1066 C14orf4   5' CAGCTCACCGTGCCCCCCAACC 67333     CAAGA  TT  A
             T                   AGG     GG  GC GTGAGCTG
                                 |||     ||  || ||||||||
                                 TCC     CC  TG CACTCGAC
                                   AACCC  CG  C
GAM1066 C1orf24   3' CACTGCAACCTCCGCCT     53709      AA
                                 AGGC  GAGGTTGCAGTG
                                 ||||  ||||||||||||
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                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066 C1QTNF6  3'  CACTGCAACCTCTGCCT     49138       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066 C21orf25 3'  CAGCTTACTGCAACCTCCACCT 63543     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   |||||||||||||||||
                                TCC   CTCCAACGTCATTCGAC
                                  AC_
GAM1066 C3F      3'  CAGCTCACCGCAACCTCCACCT 19286     CAA       A
                                AGG   GAGGTTGC GTGAGCTG
                                |||   |||||||| ||||||||
                                TCC   CTCCAACG CACTCGAC
                                  AC_       C
GAM1066 C6orf5   3'  CAGCTCACTGCAGCTTTGACCT 31343     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   |||||||||||||||||
                                TCC   TTTCGACGTCACTCGAC
                                  AG_
GAM1066 C9orf9   3'  CACTGCAACCTCCACCT     38503     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066 C9orf9   3'  CACTGCAACCTCCGCCT     38505      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066 CEACAM8  3'  CTCACTGCAAGCTCCGCCT   8422       AA   G
                                AGGC  GAG TTGCAGTGAG
                                ||||  ||| ||||||||||
                                TCCG  CTC AACGTCACTC
                                  C_  G
GAM1066 CENPH    3'  CACTGCAACCTCTGCCT     43270       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066 CHRAC1   3'  CAGCTCACTGCAACCTCCGCCT 33868      AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066 CL24751  5'  CAGCTCACCTGACCCCCTC   64685      TTG_  _
                                GAGG   CAG TGAGCTG
                                ||||   ||| |||||||
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                                CTCC    GTC ACTCGAC
                                  CCCA   C
GAM1066  CPSF2     3'  CACCGCAACCTCTGCCT     61573       A       A
                                AGGCA GAGGTTGC GTG
                                ||||| |||||||| |||
                                TCCGT CTCCAACG CAC
                                  _       C
GAM1066  DBR1      3'  CACCGCAACCTCCGCCT     32527       AA      A
                                AGGC  GAGGTTGC GTG
                                ||||  |||||||| |||
                                TCCG  CTCCAACG CAC
                                  C_      C
GAM1066  DKFZP434C212 3'  CACTGCAACCTCCACCT     68905     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  DKFZp434E2220 5'  CACTGCAACCTCCGCCT     34293      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  DKFZp434F1719 3'  CAGCTCACTGCAGGCTCTGCCT 49997       A   G
                                AGGCA GAG TTGCAGTGAGCTG
                                ||||| ||| ||||||||||||
                                TCCGT CTC GACGTCACTCGAC
                                  _   G
GAM1066  DKFZP434J037 3'  CAGCTCACCTCAACCTCCGCCT 48207      AA      CA
                                AGGC  GAGGTTG  GTGAGCTG
                                ||||  |||||||  ||||||||
                                TCCG  CTCCAAC  CACTCGAC
                                  C_      TC
GAM1066  DKFZp547H025 3'  CAGCTCACTGCAACCTCCACCT 39352     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGAC
                                  AC_
GAM1066  DKFZP564G092 5'  CAGCTCACTGGAGCCTCTGCCT 31534       A     G
                                AGGCA GAGGTT CAGTGAGCTG
                                ||||| |||||| ||||||||||
                                TCCGT CTCCGA GTCACTCGAC
                                  _     G
GAM1066  DKFZP564O0523 3'  CACTGCAACCTCCACCT     49511     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  DKFZp761J139 5'  CAGCTCACTGCAACGTCCACCT 50105     CAA  G
                                AGG   GA GTTGCAGTGAGCTG
                                |||   || ||||||||||||||
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                                TCC   CT CAACGTCACTCGAC
                                  AC_  G
GAM1066  DKFZp761N1114 3'  CACTGCAACCTCCGCCT     79014      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  DKFZp762L0311 3'  CACTGCAACCTTTGCCT     38054      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT TTCCAACGTCAC
                                   _
GAM1066  DKFZp762P2111 3'  CACTGCAACCTCCGCCT     86352      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  DRIM     3'  CAGCTCACTGCAGCCTCAACCT 27176     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   |||||||||||||||||
                                TCC   CTCCGACGTCACTCGAC
                                  AA_
GAM1066  FBP17    3'  CACTACAACCTCCACCT     72782     CAA      C
                                AGG   GAGGTTG AGTG
                                |||   ||||||| ||||
                                TCC   CTCCAAC TCAC
                                  AC_      A
GAM1066  FBXO4    3'  CAGCCCACCTTGTCCTGCCT   24097      AGA  TTGCA   A
                                AGGCA   GG    GTG GCTG
                                |||||   ||    ||| ||||
                                TCCGT   CC    CAC CGAC
                                   ____ TGTTC   C
GAM1066  FER1L4   3'  CTGACTGCAACCTCCACCT    47341     CAA         G
                                AGG   GAGGTTGCAGT AG
                                |||   |||||||||| ||
                                TCC   CTCCAACGTCA TC
                                  AC_         G
GAM1066  FER1L4   3'  CTGACTGCAACCTCCACCT    47342     CAA         G
                                AGG   GAGGTTGCAGT AG
                                |||   |||||||||| ||
                                TCC   CTCCAACGTCA TC
                                  AC_         G
GAM1066  FKBP9    3'  CAGCTCATCACACCCCGCC    94062     AAGA  T  CA
                                GGC    GG TG  GTGAGCTG
                                |||    || ||  ||||||||
                                CCG    CC AC  TACTCGAC
                                  C____  C  AC
GAM1066  FLJ00024 5'  CACTGCAACCTCTGCCT     63752      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
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                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  FLJ10232  3'  CACTGCAACCTCCGCCT    35921     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  FLJ10297  3'  CAGCTCACTGTGACCTTGACCT 35978    CAA    TG
                                AGG   GAGGT  CAGTGAGCTG
                                |||   |||||  ||||||||||
                                TCC   TTCCA  GTCACTCGAC
                                  AG_    GT
GAM1066  FLJ10535  3'  CACTGCAACCTCTGCCT    36234      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  FLJ10916  3'  AGCTCACCACCTTCACGC    36857    AA_    TGCA
                                GC   GAGGT   GTGAGCT
                                ||   |||||   |||||||
                                CG   TTCCA   CACTCGA
                                 CAC    C___
GAM1066  FLJ10922  3'  CACTGCAACCTCCGCCT    36870     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  FLJ11004  5'  CACTGCAACCTCTACCT    36966    CA
                                AGG  AGAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  TCTCCAACGTCAC
                                  A_
GAM1066  FLJ11151  3'  CAGCTGCACACAACCTCTTGCT 67872          CA  _
                                GGCAAGAGGTTG  GTG AGCTG
                                ||||||||||||  ||| |||||
                                TCGTTCTCCAAC  CAC TCGAC
                                       A_   G
GAM1066  FLJ11467  3'  CAGCTCACTGCAGCCTTGACCT 46375    CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   |||||||||||||||||
                                TCC   TTCCGACGTCACTCGAC
                                  AG_
GAM1066  FLJ12190  3'  AGCTCATCTCCTTGCCT    46870       AG TTGCA
                                AGGCAAG  G    GTGAGCT
                                |||||||  |    |||||||
                                TCCGTTC  C    TACTCGA
                                    CT _____
GAM1066  FLJ12363  3'  CAGCTCACTGCAACCTCCACCT 49674    CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   |||||||||||||||||
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                                TCC   CTCCAACGTCACTCGAC
                                  AC_
GAM1066  FLJ12409  3'  CACTGCAACCTCCGCCT     47043      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  FLJ12572  5'  CACTGCAACCTCTGCCT     43246      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                   _
GAM1066  FLJ12649  3'  CACTGCAACCTCCGCCT     44776      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  FLJ12687  3'  CACTGCAACCTCCGCCT     46187      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  FLJ12747  3'  CACTGCAACCTCTGCCT     49711      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                   _
GAM1066  FLJ12787  3'  CACTGCAACCTCTGCC      49746      A
                                GGCA GAGGTTGCAGTG
                                |||| ||||||||||||
                                CCGT CTCCAACGTCAC
                                   _
GAM1066  FLJ12973  3'  CACCGCAACCTCCGCCT     46102      AA       A
                                AGGC  GAGGTTGC GTG
                                ||||  |||||||| |||
                                TCCG  CTCCAACG CAC
                                  C_       C
GAM1066  FLJ12975  3'  CGGCTCACCACAACCTCCTCCT 69580      CAA      CA
                                AGG   GAGGTTG  GTGAGCTG
                                |||   |||||||  ||||||||
                                TCC   CTCCAAC  CACTCGGC
                                  TC_      AC
GAM1066  FLJ13072  5'  CACTGCAACCTCTGCCT     89803      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                   _
GAM1066  FLJ13089  5'  CTCACTGCAGGCACTGACT   70861    GCA  AG  _
                                AG   AG  GT TGCAGTGAG
                                ||   ||  || |||||||||
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                              TC   TC  CG ACGTCACTC
                               AG_  A_  G
GAM1066  FLJ13105  3'  ACTAAAAATCTCCTGCCT    46542      A     GC_
                              AGGCA GAGGTT   AGT
                              ||||| ||||||   |||
                              TCCGT CTCTAA   TCA
                                 C     AAA
GAM1066  FLJ13162  3'  GCTGCGACCCCCTGCCT     46558      AGA
                              AGGCA   GGTTGCAGT
                              |||||   |||||||||
                              TCCGT   CCAGCGTCG
                                 CCC
GAM1066  FLJ13197  3'  CACTGCAACCTCTACCT     44848     CA
                              AGG  AGAGGTTGCAGTG
                              |||  |||||||||||||
                              TCC  TCTCCAACGTCAC
                                A_
GAM1066  FLJ14442  3'  CAGCTCACTGCAACTTCTGCCT 51362       A
                              AGGCA GAGGTTGCAGTGAGCTG
                              ||||| |||||||||||||||||
                              TCCGT CTTCAACGTCACTCGAC
                                 _
GAM1066  FLJ14810  3'  CAGCTCACTGATCTCTTGCCT  51624           TG
                              AGGCAAGAGGT  CAGTGAGCTG
                              ||||||||||  |||||||||
                              TCCGTTCTCTA  GTCACTCGAC
                                    __
GAM1066  FLJ14871  3'  CAGCTCACTGGATTCCATC    51665    _  TTG_
                              GA GG    CAGTGAGCTG
                              || ||    ||||||||||
                              CT CC    GTCACTCGAC
                               A  TTAG
GAM1066  FLJ14950  3'  CACTGCAACCTCCACCT     51713     CAA
                              AGG   GAGGTTGCAGTG
                              |||   ||||||||||||
                              TCC   CTCCAACGTCAC
                                AC_
GAM1066  FLJ14957  3'  CACTGCAACCTCTGCCT     51741      A
                              AGGCA GAGGTTGCAGTG
                              ||||| ||||||||||||
                              TCCGT CTCCAACGTCAC
                                 _
GAM1066  FLJ20004  3'  CATTGCAACCTCCGCCT     95290     AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTTAC
                                C_
GAM1066  FLJ20034  5'  CAGCTCACCTGACCTGC     34360     AGA   GCA
                              GCA   GGTT   GTGAGCTG
                              |||   ||||   ||||||||
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                                CGT   CCAG   CACTCGAC
                                  ____   TC_
GAM1066  FLJ20034  3'  CAGCTCACTGCAACCTCTGCCT 34361      A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC

                                  _
GAM1066  FLJ20045  3'  CACTGCAACCTCTGCCT     34415      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC

                                  _
GAM1066  FLJ20079  3'  CACCGCAACCTCCACCT     34487     CAA      A
                                AGG   GAGGTTGC GTG
                                |||   |||||||| |||
                                TCC   CTCCAACG CAC
                                  AC_       C
GAM1066  FLJ20342  3'  CACTGCAACCTCTGCCT     34986      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC

                                  _
GAM1066  FLJ20344  3'  CACTGCAACCTCCGCCT     35005      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  FLJ20507  3'  CAGCTCACTGCAACCTCTGCCT 35277      A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC

                                  _
GAM1066  FLJ20507  3'  CAGCTCACTGCAACCTCTGCCT 60212      A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC

                                  _
GAM1066  FLJ21302  3'  CACTGCAACCTCCGCCT     43211      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  FLJ21432  3'  CAGCTCACTACCAACAGCCT  44631     AAGA  TGC
                                AGGC   GGT   AGTGAGCTG
                                ||||   |||   |||||||||
                                TCCG   CCA   TCACTCGAC
                                  ACAA  ___
GAM1066  FLJ22002  3'  CAGCTCACTGCAACCTCCGCCT 45769     AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  ||||||||||||||||||
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                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  FLJ22167  5'  CAGCTCACTGCCACCTCTGCCT 44566      A    T
                                AGGCA GAGGT GCAGTGAGCTG
                                ||||| ||||| ||||||||||
                                TCCGT CTCCA CGTCACTCGAC
                                  _    C
GAM1066  FLJ22531  5'  CACTGCAACCTCCACCT     45027     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  FLJ22684  3'  CTGCAACCTCTGCCT       46793      A
                                AGGCA GAGGTTGCAG
                                ||||| |||||||||
                                TCCGT CTCCAACGTC

                                  _
GAM1066  FLJ22794  3'  CAGCTCACTGCAACTTCCACCT 91604     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||
                                TCC   CTTCAACGTCACTCGAC
                                  AC_
GAM1066  FLJ22965  3'  CACTGCAACCTCCGCCT     42048     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  FLJ22969  3'  CACTGCAACCTCTGCCT     68645      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC

                                  _
GAM1066  FLJ23024  3'  CAGCTCACTGCAACCTCTGCCT 46267      A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC

                                  _
GAM1066  FLJ23042  3'  AGTGAGCTGCAACCCACCTCTT 47169        TG_______  TGAG
            GCCT                  GCAAGAGGT       CAG   CT
                                |||||||||       |||   ||
                                CGTTCTCCA       GTC   GA
                                     CCCAACIII  GAGT
GAM1066  FLJ23392  3'  CAGCTCACTGCAACCTCTGCCT 45528      A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC

                                  _
GAM1066  FLJ23563  3'  CACTGCAACCTCTGCCT     67591      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
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                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  FLJ31101  3'  CAGCTCACTGCAACCTCTGCCT 35707       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  FLJ32332  3'  CAGCCCACCAGGTCCTGCCT   58300       A A GT GCA   A
                                AGGCA G G  T   GTG GCTG
                                ||||| | |  |   ||| ||||
                                TCCGT C C  G   CAC CGAC
                                   _ _ TG AC_   C
GAM1066  FLJ32356  5'  CACCCCGCAACCTCGCGCCT   58359      AA       A__
                                AGGC  GAGGTTGC   GTG
                                ||||  ||||||||   |||
                                TCCG  CTCCAACG   CAC
                                  CG       CCC
GAM1066  FLJ32865  3'  CAGCTCACTGCAACCTCTGCCT 58170       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  FOXD4     5'  CAGCATCCGCCACAACCTCTCG 82744     A       CA   A__
           CT                     GGC AGAGGTTG  GTG   GCTG
                                ||| ||||||||  |||   ||||
                                TCG TCTCCAAC  CGC   CGAC
                                  C       AC   CTA
GAM1066  FXYD5     3'  CAGCTCACCGTGCCCAGCCT   26341     AAGA  TT  A
                                AGGC    GG  GC GTGAGCTG
                                ||||    ||  || ||||||||
                                TCCG    CC  TG CACTCGAC
                                  A___  CG  C
GAM1066  GAL3ST-4  3'  CACTGCAACCTCTGCCT     44933       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  GBA2      3'  AGCCCAGCCTCCAGCCT     71022      AA      CAGTGA
                                AGGC  GAGGTTG     GCT
                                ||||  |||||||     |||
                                TCCG  CTCCGAC     CGA
                                  AC      C_____
GAM1066  GMPPB     5'  CACTGCAACCTCCACCT     95724     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  GNG4      3'  CAGCTCACTGCGACCTCCACCT 15610     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||||
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                                TCC   CTCCAGCGTCACTCGAC
                                  AC_
GAM1066  GREB1    3'  CACTGCAACCTCTGCCT     27864       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  GRWD     3'  CACTGCAACCTCCGCCT     48962       AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  GTF2E1   3'  CACTGCAACCTCTGCCT     18610       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  GTPBG3   3'  CTTACTGCAACCTCCACCT   50899      CAA
                                AGG   GAGGTTGCAGTGAG
                                |||   ||||||||||||||
                                TCC   CTCCAACGTCATTC
                                  AC_
GAM1066  H-plk    5'  CACTGCAACCTCCACCT     31804      CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  HPRP3P   3'  TACTGCAAGCCCTTGCCT    16284        A   _
                                AGGCAAG GGTT GCAGTG
                                ||||||| |||| ||||||
                                TCCGTTC CCGA CGTCAT
                                    _   A
GAM1066  HRH4     3'  CACTGCAACCTCTGCCT     41247       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  HRH4     3'  CAGCTCACTGCAGCCCTGACT  41249    GCA  A
                                AG   AG GGTTGCAGTGAGCTG
                                ||   || ||||||||||||||||
                                TC   TC CCGACGTCACTCGAC
                                  AG_  _
GAM1066  HRIHFB2436 5'  CAGCTCACCGCCGCCTTCCGCC 26791      AA    T  A
                                GGC  GAGGT GC GTGAGCTG
                                |||  ||||| || ||||||||
                                CCG  TTCCG CG CACTCGAC
                                  CC    C  C
GAM1066  HSPC065  3'  CACTGCAACCTCCACCT     26289      CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
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                              TCC   CTCCAACGTCAC
                                AC_
GAM1066 HSPC065  3' CGCTGCAACCTCCTCCT     26292     CAA
                              AGG   GAGGTTGCAGTG
                              |||   ||||||||||||
                              TCC   CTCCAACGTCGC
                                TC_
GAM1066 ICK      3' CTGCAACCTCTGCCT       29926       A
                              AGGCA GAGGTTGCAG
                              ||||| ||||||||||
                              TCCGT CTCCAACGTC
                                 _
GAM1066 JAM1     5' CGGCTCACTGCAACCTCCTCCT 57922     CAA
                              AGG   GAGGTTGCAGTGAGCTG
                              |||   |||||||||||||||||
                              TCC   CTCCAACGTCACTCGGC
                                TC_
GAM1066 JM11     3' CAGCTCACTGCAACCTCTGCCT 53253       A
                              AGGCA GAGGTTGCAGTGAGCTG
                              ||||| |||||||||||||||||
                              TCCGT CTCCAACGTCACTCGAC
                                 _
GAM1066 KIAA0063 3' CACTGCAACCTCCACCT     29619     CAA
                              AGG   GAGGTTGCAGTG
                              |||   ||||||||||||
                              TCC   CTCCAACGTCAC
                                AC_
GAM1066 KIAA0205 3' CAGCTCACTGCAGTCTCTGCCT 29577       A   GT
                              AGGCA GAG  TGCAGTGAGCTG
                              ||||| |||  ||||||||||||
                              TCCGT CTC  ACGTCACTCGAC
                                 _  TG
GAM1066 KIAA0210 5' CAGCTCACCGCAATCTCCGCCT 28471      AA       A
                              AGGC  GAGGTTGC GTGAGCTG
                              ||||  |||||||| ||||||||
                              TCCG  CTCTAACG CACTCGAC
                                C_       C
GAM1066 KIAA0247 3' CAGCCTTTTACCCTCTTGCCT  28391          TTGCA   ___
                              AGGCAAGAGG    GTGA   GCTG
                              ||||||||||    ||||   ||||
                              TCCGTTCTCC    CATT   CGAC
                                    _____   TTC
GAM1066 KIAA0391 3' CACTGCAACCTCTGCCT     27908       A
                              AGGCA GAGGTTGCAGTG
                              ||||| ||||||||||||
                              TCCGT CTCCAACGTCAC
                                 _
GAM1066 KIAA0426 3' CACTGCAACCTCCGCCT     28254       AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
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                              TCCG  CTCCAACGTCAC
                                C_
GAM1066 KIAA0459 3' CACTGCAACCTCCACCT    60985    CAA
                              AGG   GAGGTTGCAGTG
                              |||   ||||||||||||
                              TCC   CTCCAACGTCAC
                                AC_
GAM1066 KIAA0472 5' CAGCTCACTGCAACCTCCTCCT 71860    CAA
                              AGG   GAGGTTGCAGTGAGCTG
                              |||   |||||||||||||||||
                              TCC   CTCCAACGTCACTCGAC
                                TC_
GAM1066 KIAA0513 3' CACTGCAACCTCCACCT    28342    CAA
                              AGG   GAGGTTGCAGTG
                              |||   ||||||||||||
                              TCC   CTCCAACGTCAC
                                AC_
GAM1066 KIAA0527 3' CACTGCAACCTCTGCCT    95794     A
                              AGGCA GAGGTTGCAGTG
                              ||||| ||||||||||||
                              TCCGT CTCCAACGTCAC
                                _
GAM1066 KIAA0537 5' CAGCTCACGGCGGCCCCGGCC 29243    AAGA    A
                              GGC    GGTTGC GTGAGCTG
                              |||    |||||| ||||||||
                              CCG    CCGGCG CACTCGAC
                                GCC_     G
GAM1066 KIAA0544 3' CACTGCAACCTCCGCCT    70895    AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1066 KIAA0561 3' CAGCTCACTGCAACCTCCGCCT 65876    AA
                              AGGC  GAGGTTGCAGTGAGCTG
                              ||||  |||||||||||||||||
                              TCCG  CTCCAACGTCACTCGAC
                                C_
GAM1066 KIAA0562 3' CTGCAACCTCCGCCT      28151    AA
                              AGGC  GAGGTTGCAG
                              ||||  |||||||||
                              TCCG  CTCCAACGTC
                                C_
GAM1066 KIAA0563 5' CACTGCAACCTCTGCCT    29183     A
                              AGGCA GAGGTTGCAGTG
                              ||||| ||||||||||||
                              TCCGT CTCCAACGTCAC
                                _
GAM1066 KIAA0594 3' CTTACTGCAACCTCCGCCT  64896    AA
                              AGGC  GAGGTTGCAGTGAG
                              ||||  ||||||||||||||
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                              TCCG  CTCCAACGTCATTC
                                C_
GAM1066  KIAA0599  3'  CACTGCAACCTCCGCCT     77168      AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1066  KIAA0599  3'  CTTACTGCAACCTCCGCCT    77176      AA
                              AGGC  GAGGTTGCAGTGAG
                              ||||  ||||||||||||||
                              TCCG  CTCCAACGTCATTC
                                C_
GAM1066  KIAA0682  3'  CAGCCTGAGACGCAGCCTCCCG 32473      AA       AG__ GA
              CCT                 AGGC  GAGGTTGC    T  GCTG
                              ||||  ||||||||    |  ||||
                              TCCG  CTCCGACG    G  CGAC
                                CC       CAGA TC
GAM1066  KIAA0720  3'  CACTGCAACCTCTGCCT     62317      A
                              AGGCA GAGGTTGCAGTG
                              |||||| ||||||||||||
                              TCCGT CTCCAACGTCAC
                                _
GAM1066  KIAA0737  3'  CAGCTCACTGAAACCTCTGCCT 29132       A     G
                              AGGCA GAGGTT CAGTGAGCTG
                              |||||| |||||| ||||||||||
                              TCCGT CTCCAA GTCACTCGAC
                                _     A
GAM1066  KIAA0828  3'  GGAGCTGCCTCCAACCTCTTAC 81197     C       G________   TGAG
              CT                   GG AAGAGGTT       CAG    C
                              || ||||||||       |||    |
                              CC TTCTCCAA       GTC    G
                               A       CCTCCIII   GAGT
GAM1066  KIAA0841  3'  CAGCTCACTGCAACCTCCGCCT 71378      AA
                              AGGC  GAGGTTGCAGTGAGCTG
                              ||||  ||||||||||||||||
                              TCCG  CTCCAACGTCACTCGAC
                                C_
GAM1066  KIAA0841  3'  CAGCTCACTGCAACCTCTGCCT 71379       A
                              AGGCA GAGGTTGCAGTGAGCTG
                              |||||| ||||||||||||||||
                              TCCGT CTCCAACGTCACTCGAC
                                _
GAM1066  KIAA1026  3'  CAGCTCACTGCAACCAACACCT 71188     CAAGA
                              AGG     GGTTGCAGTGAGCTG
                              |||     ||||||||||||||
                              TCC     CCAACGTCACTCGAC
                                ACAA_
GAM1066  KIAA1041  3'  CACTGCAACCTCCGCCT     30127      AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
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                              TCCG  CTCCAACGTCAC
                                C_
GAM1066 KIAA1054 3' CACTGCAACCTCCGCCT     68428      AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1066 KIAA1143 3' CAGCTCACTGCAAGCTCCGCCT 68673      AA   G
                              AGGC  GAG TTGCAGTGAGCTG
                              ||||  ||| ||||||||||||||
                              TCCG  CTC AACGTCACTCGAC
                                C_  G
GAM1066 KIAA1161 5' CAGCTCACTGCAACCCCTCCT  81738     CA  A
                              AGG  AG GGTTGCAGTGAGCTG
                              |||  || ||||||||||||||||
                              TCC  TC CCAACGTCACTCGAC
                               __ C
GAM1066 KIAA1170 3' CACTGCAACCTCCGCCT     69845      AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1066 KIAA1193 3' CACTGCAACCTCCGCCT     67631      AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1066 KIAA1198 3' CACCGCAACCTCCGCCT     63290      AA       A
                              AGGC  GAGGTTGC GTG
                              ||||  |||||||| |||
                              TCCG  CTCCAACG CAC
                                C_       C
GAM1066 KIAA1198 3' CAGCTCACTGCAAGCTCCGCCT 63295      AA   G
                              AGGC  GAG TTGCAGTGAGCTG
                              ||||  ||| ||||||||||||||
                              TCCG  CTC AACGTCACTCGAC
                                C_  G
GAM1066 KIAA1254 3' CAGCTCACTGCAACCTCTGTCT 70016      A
                              AGGCA GAGGTTGCAGTGAGCTG
                              ||||| ||||||||||||||||||
                              TCTGT CTCCAACGTCACTCGAC
                                _
GAM1066 KIAA1257 3' CAGCTCACCGCAACCTCCGCCT 62732      AA       A
                              AGGC  GAGGTTGC GTGAGCTG
                              ||||  |||||||| ||||||||
                              TCCG  CTCCAACG CACTCGAC
                                C_       C
GAM1066 KIAA1320 5' CACTGCAACCTCTGCCT     69296       A
                              AGGCA GAGGTTGCAGTG
                              ||||| ||||||||||||
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                                TCCGT CTCCAACGTCAC
                                  _
GAM1066 KIAA1320 5' CAGCTCACTGTAGCCTTGACT  69298    GCAA
                                AG   GAGGTTGCAGTGAGCTG
                                ||   ||||||||||||||||
                                TC   TTCCGATGTCACTCGAC
                                 AG__
GAM1066 KIAA1373 3' CAGCTCACTGCAACCTCCACCT 70931     CAA
                                AGG  GAGGTTGCAGTGAGCTG
                                |||  ||||||||||||||||
                                TCC  CTCCAACGTCACTCGAC
                                 AC_
GAM1066 KIAA1443 3' CAGCTCACTGCAAGCTCCGCCT 63826     AA  G
                                AGGC GAG TTGCAGTGAGCTG
                                ||||  ||| ||||||||||||
                                TCCG CTC AACGTCACTCGAC
                                  C_  G
GAM1066 KIAA1467 3' CACTGCAACCTTCGCCT     71603     AA
                                AGGC GAGGTTGCAGTG
                                |||| ||||||||||||
                                TCCG TTCCAACGTCAC
                                  C_
GAM1066 KIAA1473 3' CAGCTCACTGCAACCTCCGTCT 70664     AA
                                AGGC GAGGTTGCAGTGAGCTG
                                |||| ||||||||||||||||
                                TCTG CTCCAACGTCACTCGAC
                                  C_
GAM1066 KIAA1493 3' CAGCTCACTACAAGCTCCCCT 64156    CAA  G  C
                                AGG  GAG TTG AGTGAGCTG
                                |||  ||| ||| |||||||||
                                TCC  CTC AAC TCACTCGAC
                                 C__  G  A
GAM1066 KIAA1497 5' CACTGCAACCTCTGCCT     67504      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066 KIAA1508 3' CAGCTCACTGCAACCTCCGCCT 61880     AA
                                AGGC GAGGTTGCAGTGAGCTG
                                |||| ||||||||||||||||
                                TCCG CTCCAACGTCACTCGAC
                                  C_
GAM1066 KIAA1571 3' CACCGCAACCTCCACCT     60951     CAA      A
                                AGG  GAGGTTGC GTG
                                |||  |||||||| |||
                                TCC  CTCCAACG CAC
                                 AC_      C
GAM1066 KIAA1615 3' CACTGCAACCTCCACCT     68701     CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
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                              TCC   CTCCAACGTCAC
                                AC_
GAM1066 KIAA1617 3' CAGCTCACTGCAACCTCTCTCT 91424    CA
                              GG  AGAGGTTGCAGTGAGCTG
                              ||  ||||||||||||||||||
                              TC  TCTCCAACGTCACTCGAC
                               TC
GAM1066 KIAA1649 3' CAGCTCACTGCAACCTCCGC   50246    AA
                              GC  GAGGTTGCAGTGAGCTG
                              ||  ||||||||||||||||
                              CG  CTCCAACGTCACTCGAC
                               C_
GAM1066 KIAA1655 3' CAGCTCACTGTAACCTCCACCT 66599     CAA
                              AGG   GAGGTTGCAGTGAGCTG
                              |||   ||||||||||||||||
                              TCC   CTCCAATGTCACTCGAC
                                AC_
GAM1066 KIAA1655 3' CATTGCAACCTCCGCCT     66600      AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTTAC
                                C_
GAM1066 KIAA1668 3' CAGCTCACTGCAAGCTCCGCCT 66469      AA   G
                              AGGC  GAG TTGCAGTGAGCTG
                              ||||  ||| ||||||||||||
                              TCCG  CTC AACGTCACTCGAC
                                C_  G
GAM1066 KIAA1712 3' CACCGCAACCTCTGCCT     67533       A       A
                              AGGCA GAGGTTGC GTG
                              ||||| |||||||| |||
                              TCCGT CTCCAACG CAC
                                 _      C
GAM1066 KIAA1737 3' CACTGCAACCTCCGCCT     67350      AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1066 KIAA1751 3' CAGCTCACTGCAGCCTCGACCT 71690     CAA
                              AGG   GAGGTTGCAGTGAGCTG
                              |||   ||||||||||||||||
                              TCC   CTCCGACGTCACTCGAC
                                AG_
GAM1066 KIAA1784 3' CACTGCAACCTCCGCCT     65144      AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1066 KIAA1855 3' GGAGCTGCAGAAACCTCTTGCC 92344           GC_______  TGAG
             T                 AGGCAAGAGGTT       AG    C
                              ||||||||||||       ||    |
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                                TCCGTTCTCCAA      TC   G
                                      AGACIIIG  GAGT
GAM1066 KIAA1922 5' CAGCTCACTGCAACCTCCGCCT 73618     AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066 KIAA1956 3' CAGCTCACTGCAGCCTCCACCT 78432    CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||
                                TCC   CTCCGACGTCACTCGAC
                                  AC_
GAM1066 KIAA1971 3' CTTACTGCAACCTCCACCT   74217    CAA
                                AGG   GAGGTTGCAGTGAG
                                |||   ||||||||||||||
                                TCC   CTCCAACGTCATTC
                                  AC_
GAM1066 KLK7     3' CACTGCAACCTCCGCCT     57728     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066 KLK7     3' CACTGCAACCTCCGCCT     17288     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066 LMOD1    5' CAGCTCACCCCGCGCCCTTTCC 24041    C   A   T  A__
             T                   AGG AAG GGT GC   GTGAGCTG
                                ||| ||| ||| ||   ||||||||
                                TCC TTC CCG CG   CACTCGAC
                                  T   _   _  CCC
GAM1066 LRRN3    5' GCTGCAGCCTCCTGCCT     69438      A
                                AGGCA GAGGTTGCAGT
                                ||||| ||||||||||
                                TCCGT CTCCGACGTCG
                                   C
GAM1066 MCLC     3' CACTGCAACCTCCACCT     30678     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066 MEF-2    3' CACTGCAACCTCCGCCT     64378      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066 MGC12518 3' TACTGCAACCTCTGCC      64083      A
                                GGCA GAGGTTGCAGTG
                                |||| ||||||||||||
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                                CCGT CTCCAACGTCAT
                                  _
GAM1066  MGC13138  3'  CAGCTCACTGCAACCTCTGCCT 53015      A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  MGC13198  5'  CAGCTCACTGCAACCTCCGTCT 51094      AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  ||||||||||||||||||
                                TCTG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  MGC14836  3'  CACTGCAACCTCCGCCT     53036      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  MGC15873  5'  CAGCTCACTGCAGCCTTGACCT 51901     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||||
                                TCC   TTCCGACGTCACTCGAC
                                 AG_
GAM1066  MGC16025  3'  CAGCCCACTGTGGGCCCTTCCC 51915    C   A  _ TG    A
                                GG AAG GG T  CAGTG GCTG
                                || ||| || |  ||||| ||||
                                CC TTC CC G  GTCAC CGAC
                                 C   _  G GT    C
GAM1066  MGC1842   3'  CTTACTACAACCTCCGCCT    65647      AA      C
                                AGGC  GAGGTTG AGTGAG
                                ||||  ||||||| ||||||
                                TCCG  CTCCAAC TCATTC
                                  C_      A
GAM1066  MGC21675  3'  CAGCTCACTGCAATCTCTGCC  53480      A
                                GGCA GAGGTTGCAGTGAGCTG
                                |||| ||||||||||||||||||
                                CCGT CTCTAACGTCACTCGAC
                                  _
GAM1066  MGC27171  3'  GCTGCAGCCTCTTGCCT     58086
                                AGGCAAGAGGTTGCAGT
                                |||||||||||||||||
                                TCCGTTCTCCGACGTCG

GAM1066  MGC29891  3'  CACTGCAACCTCCGCCT     58201      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  MGC3113   3'  CAGCTCACTGCAGCCTCCACCT 43841     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||||
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                                TCC   CTCCGACGTCACTCGAC
                                  AC_
GAM1066  MGC3329   3'  CACTGCAACCCCCGCCT     44014      AAGA
                                AGGC    GGTTGCAGTG
                                ||||    ||||||||||
                                TCCG    CCAACGTCAC
                                  CCC_
GAM1066  MGC5149   3'  CAGCTCACTGCAACCTCTGCCT 72287       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  MGC5508   3'  CAGCCCTCCTGCCAGCCCCCTG 44033      AGA    _   T  __
             CC                   GGCA   GGTTG CAG GA  GCTG
                                ||||   ||||| ||| ||  ||||
                                CCGT   CCGAC GTC CT  CGAC
                                  CCC    C   _  CC
GAM1066  MGC9912   3'  CACTGCAACCTCCACCT     54714     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  MLZE      5'  CAGCTCACTGCAACCTCTGCCT 48616       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  MOCS3     3'  CAGCTCACTGCAACCTCCGCCT 27150      AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  MRPL44    3'  CACTGCAACCTCCACCT     43314     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  MtFMT     3'  CAGCTCACTGCAACCTCCGCCT 57650      AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  ||||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  N4BP3     3'  CAGCTCACCAGTCTCTTCCCT  66254     C    GT  CA
                                AGG AAGAG  TG  GTGAGCTG
                                ||| |||||  ||  ||||||||
                                TCC TTCTC  AC  CACTCGAC
                                  C    TG  __
GAM1066  NDUFB1    5'  CAGCTCACTGCAACCTCTGCCT 15816       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||||
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                                TCCGT CTCCAACGTCACTCGAC
                                     _
GAM1066 NDUFC2   3' CACTGCAACCTCCACCT     15827     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066 Nup43    3' CACTGCAACCTCCACCT     44995     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066 OSBPL2   3' CACCGCAACCTCCGCCT     57855      AA       A
                                AGGC  GAGGTTGC GTG
                                ||||  |||||||| |||
                                TCCG  CTCCAACG CAC
                                  C_       C
GAM1066 OSBPL2   3' CACCGCAACCTCCGCCT     29204      AA       A
                                AGGC  GAGGTTGC GTG
                                ||||  |||||||| |||
                                TCCG  CTCCAACG CAC
                                  C_       C
GAM1066 PASK     5' CACTGCAACCTCTGCCT     30712       A
                                AGGCA GAGGTTGCAGTG
                                |||||  ||||||||||||
                                TCCGT CTCCAACGTCAC
                                     _
GAM1066 PELI1    5' CACTGCAACCTCTGCCT     40256       A
                                AGGCA GAGGTTGCAGTG
                                |||||  ||||||||||||
                                TCCGT CTCCAACGTCAC
                                     _
GAM1066 PELI1    5' CGGCTCACTGCAACCTCCTCCT 40260     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   |||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  TC_
GAM1066 PIP3-E   3' CACTGCAACCTCTGCCT     66800       A
                                AGGCA GAGGTTGCAGTG
                                |||||  ||||||||||||
                                TCCGT CTCCAACGTCAC
                                     _
GAM1066 PPP1R10  3' CAGCTCACTCCCTGCTCCCACC 10729     CAA   GTTGC
             T                   AGG   GAG    AGTGAGCTG
                                 |||   |||    |||||||||
                                 TCC   CTC    TCACTCGAC
                                   ACC   GTCCC
GAM1066 PRO0365  5' CAGCTCACTGCAACCTCCACCT 26152     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   |||||||||||||||||
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                                TCC  CTCCAACGTCACTCGAC
                                  AC_
GAM1066 PRO1048  3' CAGCTCACTGAAGTCTCGACCT 37513    CAA  GT G
                                AGG  GAG  T CAGTGAGCTG
                                |||  |||  | ||||||||||
                                TCC  CTC  A GTCACTCGAC
                                  AG_  TG A
GAM1066 PRO1992  5' CACTGCAACCTCTGCCT    26053      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066 PRO2955  3' CAGCTCACTGCAACCTCTGCCT 37633      A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066 PSTPIP2  3' CAGCTCACTGCAACCTCTGCCT 44385      A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066 RAB33B   3' CACTGCAACCTCCGCCT    48488     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066 RAI     5' CACTGCAACCTCCGCCT    21873     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066 RASSF2   3' CAGCTCACTGCAACATCCGCCT 28430     AA  G
                                AGGC  GA GTTGCAGTGAGCTG
                                ||||  || ||||||||||||||
                                TCCG  CT CAACGTCACTCGAC
                                  C_ A
GAM1066 RNF8    3' CAGCTCACTGCAACCTCCACCT 14217    CAA
                                AGG  GAGGTTGCAGTGAGCTG
                                |||  ||||||||||||||||
                                TCC  CTCCAACGTCACTCGAC
                                  AC_
GAM1066 RNO2    5' CAGCTCACTGCAACCTCCACCT 52765    CAA
                                AGG  GAGGTTGCAGTGAGCTG
                                |||  ||||||||||||||||
                                TCC  CTCCAACGTCACTCGAC
                                  AC_
GAM1066 SARM    3' AGCTCAGGGCTCCTGCC    30594     AGA  TT  AG
                                GGCA  GG  GC  TGAGCT
                                ||||  ||  ||  ||||||
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                                CCGT   CC  CG  ACTCGA
                                  ___  T_  GG
GAM1066  SC4MOL    3'  CAGCTCACTGCAACCTCTGCCT 22152       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  SCAMP-4   3'  CACTGCAACCTCTGCCT     54390       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  SDC3      3'  CACTGCAACCTCTTGCT     27741
                                GGCAAGAGGTTGCAGTG
                                |||||||||||||||||
                                TCGTTCTCCAACGTCAC

GAM1066  SERF1B    3'  CACTGCAACCTCCGCCT     43409      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  SERF1B    3'  CAGCTCCATGCAACCTCTGCCT 43411       A        GT
                                AGGCA GAGGTTGCA  GAGCTG
                                ||||| |||||||||  ||||||
                                TCCGT CTCCAACGT  CTCGAC
                                  _        AC
GAM1066  SHANK3    5'  CAGCTCACCCCTGGCCCTTGCC 65490       A    CA_
                                GGCAAG GGTTG   GTGAGCTG
                                |||||| |||||   ||||||||
                                CCGTTC CCGGT   CACTCGAC
                                  _    CCC
GAM1066  SIRPB1    3'  CACTGCAACCCCCCGCCT     20243      AAGA
                                AGGC    GGTTGCAGTG
                                ||||    ||||||||||
                                TCCG    CCAACGTCAC
                                  CCC_
GAM1066  SLC11A1   3'  CATTGCAACCTCCACCT     59452     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTTAC
                                  AC_
GAM1066  SLC6A14   3'  CAGCTCACTGCAACCTCTGCCT 23348       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  SQV7L     5'  CAGCTCACTGCAACCACTGCCT 70569       A A
                                AGGCA G GGTTGCAGTGAGCTG
                                ||||| | |||||||||||||||
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                                TCCGT C CCAACGTCACTCGAC
                                  _ A
GAM1066  STAF65(gamma) 3'  CACTGCAACCTCTGCCT     29427       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  SULT1C2   5'  GCTCACTTTCTCCCT       21677     CAA    TTGC
                                AGG   GAGG    AGTGAGC
                                |||   ||||    |||||||
                                TCC   CTCT    TCACTCG
                                  ____   T___
GAM1066  SYT13     3'  CACTGCAACCTCCGCCT     93450      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  TGIF2     3'  CAGCTCACTGTACTCCAGCC   41448     AA   GT
                                GGC  GAG  TGCAGTGAGCTG
                                |||  |||  ||||||||||||
                                CCG  CTC  ATGTCACTCGAC
                                  AC   __
GAM1066  THEA      3'  CAGCTCACTGCAACCTCGGCCT 66277      AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  G_
GAM1066  TLN1      3'  CAGCCCACTCCACCCTGCC    20816      A A   T C    A
                                GGCA G GGT G AGTG GCTG
                                |||| | ||| | |||| ||||
                                CCGT C CCA C TCAC CGAC
                                  _ _  _ C    C
GAM1066  TM4SF11   3'  GGAGCTGCAACCAACCTCTCCC 32037     CA      G________   TGAG
              T                  GG  AGAGGTT       CAG    C
                                ||  |||||||       |||    |
                                CC  TCTCCAA       GTC    G
                                 C_     CCAACIII   GAGT
GAM1066  TNRC4     3'  CAGCTCACCCTCACCCCAGCCT 23220      AAGA   TGCA
                                AGGC    GGT    GTGAGCTG
                                ||||    |||    ||||||||
                                TCCG    CCA    CACTCGAC
                                  ACC_   CTCC
GAM1066  TOR1B     3'  CTCACTGCAACCTCCGCT     27198     AA
                                GGC  GAGGTTGCAGTGAG
                                |||  ||||||||||||||
                                TCG  CTCCAACGTCACTC
                                  C_
GAM1066  TPRA40    5'  CAGCTCACTGGGCGGCTCTC   33038     _    __
                                GAG GTTGC  AGTGAGCTG
                                ||| |||||  |||||||||
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                                CTC CGGCG  TCACTCGAC
                                  T    GG
GAM1066  TRAF3    3'  AGCTCACTGCAAGGGC      59732    AAGAGG
                                GC     TTGCAGTGAGCT
                                ||     ||||||||||||
                                CG     AACGTCACTCGA
                                 GG____
GAM1066  TRIM5    3'  CACTGCAACCTCCACCT     52294     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  TRIM6    3'  CACTGCAACCTCTGCCT     54134       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC

                                  _
GAM1066  TU12B1-TY 3'  AGCCCACCCCTCCAGCCT    33368      AA    TTGCA   A
                                AGGC  GAGG    GTG GCT
                                ||||  ||||    ||| |||
                                TCCG  CTCC    CAC CGA
                                  AC    C____   C
GAM1066  TU12B1-TY 3'  CAGCTCACTGCAACCTCTGCCT 33372       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC

                                  _
GAM1066  TU12B1-TY 3'  CGGCTCACTGCAACCTCTTGCC 33376
            T                    AGGCAAGAGGTTGCAGTGAGCTG
                                ||||||||||||||||||||||||
                                TCCGTTCTCCAACGTCACTCGGC

GAM1066  TUCAN    3'  CAGCTCACTGCAACCTCTGCCT 30272       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC

                                  _
GAM1066  UBF-fl   3'  CACTGCAACCTCTGCCT     51554       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC

                                  _
GAM1066  USP22    3'  CACTGCAACCTCCACCT     68006     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  VDU1     3'  CAGCTCACTGCAGCCTCCACCT 30415     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   |||||||||||||||||
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                                TCC   CTCCGACGTCACTCGAC
                                  AC_
GAM1066  VPS33A    3'  CACTGCAACCTCCACCT     43335     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  WBSCR20A  5'  CACCGCAACCTCTGCCT     49649       A       A
                                AGGCA GAGGTTGC GTG
                                ||||| |||||||| |||
                                TCCGT CTCCAACG CAC
                                   _       C
GAM1066  YWHAQ     3'  CACTTACACCTCCTGCCT     22394       A     TGC
                                AGGCA GAGGT   AGTG
                                ||||| |||||   ||||
                                TCCGT CTCCA   TCAC
                                   C     CAT
GAM1066  ZIC4      5'  CAGCTCACCGCCGCCTCCAGCC 49616     AA     T  A
                                GGC  GAGGT GC GTGAGCTG
                                |||  ||||| || ||||||||
                                CCG  CTCCG CG CACTCGAC
                                  AC     C  C
GAM1066  ZTL1      3'  CACTGCAACCTCTGCCT     43910       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                   _
GAM1066  LOC112724 5'  CACTGCAACCTCCACCT     56492     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  LOC113675 5'  CACTGCAACCTCCGCCT     56569      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC115219 5'  CACTGCAACCTCCGCCT     73297      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC115648 3'  CAGCTCATCAAAACCTTTGCCT 59295       A     GCA
                                AGGCA GAGGTT   GTGAGCTG
                                ||||| ||||||   ||||||||
                                TCCGT TTCCAA   TACTCGAC
                                   _     AAC
GAM1066  LOC116349 5'  CTCAGGCCCTCTCGCT      73829     A    TT  AG
                                GGC AGAGG  GC  TGAG
                                ||| |||||  ||  ||||
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                                TCG TCTCC  CG  ACTC
                                  C    __ G_
GAM1066  LOC116411 5' CGCTACAACCTCCACCT     73859     CAA      C
                                AGG   GAGGTTG AGTG
                                |||   ||||||| ||||
                                TCC   CTCCAAC TCGC
                                  AC_      A
GAM1066  LOC116411 5' CGGCTCACTGCAACCTCCCTGC 73861       A_
              CT                  AGGCA  GAGGTTGCAGTGAGCTG
                                |||||  ||||||||||||||||
                                TCCGT  CTCCAACGTCACTCGGC
                                   CC
GAM1066  LOC119392 3' CACTGCAACCTCTGCCT     59131       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||
                                TCCGT CTCCAACGTCAC
                                   _
GAM1066  LOC120114 3' CAGCTCACTGCAATCTCCACCT 75520     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||
                                TCC   CTCTAACGTCACTCGAC
                                  AC_
GAM1066  LOC120939 3' CAGCTCACTGTAACCTCCACCT 76249     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||
                                TCC   CTCCAATGTCACTCGAC
                                  AC_
GAM1066  LOC126364 3' CAGCTCACTGCAACCTCCGCCT 75685      AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  LOC126661 3' CAGCTCACTGCAACCTCCGCCT 74546      AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  LOC127534 3' CAGCTCACCCAGACCTGCC    75437     AGA    GCA
                                GGCA   GGTT   GTGAGCTG
                                ||||   ||||   ||||||||
                                CCGT   CCAG   CACTCGAC
                                   ___    ACC
GAM1066  LOC128077 3' CACTGCAACCTCCGCCT     74706      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC128077 3' CACTGCAACCTCTGCCT     74708       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
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                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  LOC128989 3'  CACTGCAACCTCCGCCT     74805      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC130813 3'  CACCGCAACCTCCGCCT     75763      AA       A
                                AGGC  GAGGTTGC GTG
                                ||||  |||||||| |||
                                TCCG  CTCCAACG CAC
                                  C_       C
GAM1066  LOC132625 3'  CACTGCAACCTCCACCT     75899     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  LOC135154 3'  CTCACTGCAACTTCCGCC    75214     AA
                                GGC  GAGGTTGCAGTGAG
                                |||  ||||||||||||||
                                CCG  CTTCAACGTCACTC
                                  C_
GAM1066  LOC135293 3'  CACTGCAACCTCTGCCT     76174      A
                                AGGCA GAGGTTGCAGTG
                                |||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  LOC135763 3'  CACTGCAACCTCCGCCT     56786      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC135818 3'  CAGCTCACCACAACCTCCGCCT 75232      AA       CA
                                AGGC  GAGGTTG  GTGAGCTG
                                ||||  |||||||  ||||||||
                                TCCG  CTCCAAC  CACTCGAC
                                  C_      AC
GAM1066  LOC143187 3'  CACTGCAACCTCCACCT     59095     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  LOC143241 5'  CAGCTCACTGCAACCTCTGCCT 57175       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                |||||| |||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  LOC144248 5'  CACTGCAACCTCCACCT     76735     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
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                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  LOC144317 5'  CTCACTGCAACCTCTTCCT    76787     C
                                AGG AAGAGGTTGCAGTGAG
                                ||| ||||||||||||||||
                                TCC TTCTCCAACGTCACTC
                                  _
GAM1066  LOC144524 5'  CAGCTCACTGCAACCTCCACCT 83122     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||||
                                TCC   CTCCAACGTCACTCGAC
                                  AC_
GAM1066  LOC144742 5'  CTGCAACCTTCGCCT       76943      AA
                                AGGC  GAGGTTGCAG
                                ||||  ||||||||||
                                TCCG  TTCCAACGTC
                                  C_
GAM1066  LOC145009 3'  CAGCTCACTGCATCCTCCGCCT 60346      AA    T
                                AGGC  GAGG TGCAGTGAGCTG
                                ||||  |||| ||||||||||||
                                TCCG  CTCC ACGTCACTCGAC
                                  C_    T
GAM1066  LOC145268 5'  CACTGCAACCTCCACC      77054     CAA
                                GG   GAGGTTGCAGTG
                                ||   ||||||||||||
                                CC   CTCCAACGTCAC
                                  AC_
GAM1066  LOC145757 5'  CACTACAACCTCTGCCT     77456      A      C
                                AGGCA GAGGTTG AGTG
                                ||||| ||||||| ||||
                                TCCGT CTCCAAC TCAC
                                  _      A
GAM1066  LOC146050 3'  CAGCTCACTGCAACCTCTGCCT 77632       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  LOC146050 3'  CAGCTCACTGCAACCTCTGCTT 77633       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||||
                                TTCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  LOC146229 3'  CACTGCAACCTCCACCT     77733     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  LOC146733 3'  CAGCTCACTCCTCCCTCTGGCC 83756     A     TTGC
                                GGC AGAGG    AGTGAGCTG
                                ||| |||||    |||||||||
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                                CCG TCTCC   TCACTCGAC
                                  G    CTCC
GAM1066  LOC146784 5'  CACTGCAACCTCCACCT    78104    CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  CTCCAACGTCAC
                                  AC_
GAM1066  LOC146839 3'  CACCACAACCTCCGCCT    83807     AA     CA
                                AGGC  GAGGTTG  GTG
                                ||||  |||||||  |||
                                TCCG  CTCCAAC  CAC
                                  C_     AC
GAM1066  LOC146901 3'  CATTGCAACCTCCACCT    83834    CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  CTCCAACGTTAC
                                  AC_
GAM1066  LOC146909 3'  CACTGCAACCTCCGCCT    78167     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC146952 5'  CAGCTCACTGCAACCTCCACCT 83861    CAA
                                AGG  GAGGTTGCAGTGAGCTG
                                |||  |||||||||||||||||
                                TCC  CTCCAACGTCACTCGAC
                                  AC_
GAM1066  LOC147071 5'  CACTGCAACCTCTGCCT    72994     A
                                AGGCA GAGGTTGCAGTG
                                |||||  ||||||||||||
                                TCCGT CTCCAACGTCAC
                                   _
GAM1066  LOC147276 3'  CAGCTCACTGCAACGTCTGCCT 78331     A  G
                                AGGCA GA GTTGCAGTGAGCTG
                                |||||  ||  |||||||||||||||
                                TCCGT CT CAACGTCACTCGAC
                                   _  G
GAM1066  LOC147407 3'  CACTGCAACCTCCGCCT    76323     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC147463 3'  CAGCTCAGGGACCCTCTTGCC  78369        TTGCAG
                                GGCAAGAGG    TGAGCTG
                                |||||||||    |||||||
                                CCGTTCTCC    ACTCGAC
                                     CAGGG_
GAM1066  LOC147817 3'  CACTGCAACCTCCACCT    78490    CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
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                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  LOC147841 3'  CAGCTCACAGCAACCTCTGCCT 78525       A       A
                                AGGCA GAGGTTGC GTGAGCTG
                                ||||| |||||||| ||||||||
                                TCCGT CTCCAACG CACTCGAC
                                   _       A
GAM1066  LOC147895 5'  CAGCTCACTGCAGCCTC     84077
                                GAGGTTGCAGTGAGCTG
                                ||||||||||||||||
                                CTCCGACGTCACTCGAC

GAM1066  LOC147990 3'  CACTACAACCTCTGCCT     84089       A       C
                                AGGCA GAGGTTG AGTG
                                ||||| ||||||| ||||
                                TCCGT CTCCAAC TCAC
                                   _       A
GAM1066  LOC148147 3'  CAGCTCACTGCAATCTCTGCCT 78672       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||
                                TCCGT CTCTAACGTCACTCGAC
                                   _
GAM1066  LOC148189 5'  CACTGCAACCTCCACCT     78705     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  LOC148198 3'  CAGCTCACTGCAACCTC     70677
                                GAGGTTGCAGTGAGCTG
                                ||||||||||||||||
                                CTCCAACGTCACTCGAC

GAM1066  LOC148293 3'  CAGCTCACTGGACCCCAGCCT  78778      AAGA    G
                                AGGC    GGTT CAGTGAGCTG
                                ||||    |||| ||||||||||
                                TCCG    CCAG GTCACTCGAC
                                   ACC_   _
GAM1066  LOC148438 3'  CAGCACCTAAAAACCTCTTGCC 84156            GCAGTGA
            T                    AGGCAAGAGGTT       GCTG
                                ||||||||||||       ||||
                                TCCGTTCTCCAA       CGAC
                                      AAATCCA
GAM1066  LOC148709 3'  CACTACAACCTCCGCCT     78934      AA      C
                                AGGC  GAGGTTG AGTG
                                ||||  ||||||| ||||
                                TCCG  CTCCAAC TCAC
                                   C_       A
GAM1066  LOC148887 5'  CAGCCCACCCTGCAGCCCTGCT 84230      A A      __   A
                                GGCA G GGTTGCA  GTG GCTG
                                |||| | |||||||  ||| ||||
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                                TCGT C CCGACGT  CAC CGAC
                                  _ _      CC   C
GAM1066  LOC149506 3'  CAGCTCACTGCAACCTCTGCCT 84455       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  LOC149703 5'  CAGCTTAATGCAACCTCTACCT 84649     CA        G
                                AGG  AGAGGTTGCA TGAGCTG
                                |||  |||||||||| |||||||
                                TCC  TCTCCAACGT ATTCGAC
                                  A_         A
GAM1066  LOC149832 5'  AGCTCACCTCCTCTGCC     84695      A    TTGCA
                                GGCA GAGG     GTGAGCT
                                |||| ||||     |||||||
                                CCGT CTCC     CACTCGA
                                  _    TC___
GAM1066  LOC150054 5'  CACTGCAACCTTCGCCT     84826      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  TTCCAACGTCAC
                                  C_
GAM1066  LOC150095 5'  CATCTGCAACCTGCTGCC     84856      AG        _
                                GGCA  AGGTTGCAG TG
                                ||||  ||||||||| ||
                                CCGT  TCCAACGTC AC
                                  CG         T
GAM1066  LOC150397 3'  CATTGCAACCTCCGCCT     79842      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTTAC
                                  C_
GAM1066  LOC150407 3'  CAGCTCACTGCAACCTC     79817
                                GAGGTTGCAGTGAGCTG
                                |||||||||||||||||
                                CTCCAACGTCACTCGAC

GAM1066  LOC150960 3'  CGCTGCAACCTCCGCCT     80057      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCGC
                                  C_
GAM1066  LOC151005 3'  AGCTCATACCCCTGCC      80095      A A   TGCA
                                GGCA G GGT    GTGAGCT
                                |||| | |||    |||||||
                                CCGT C CCA    TACTCGA
                                  _ C  _____
GAM1066  LOC151057 3'  CACTGCAACCTCTGCCT     85207       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
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                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  LOC151103 3'  CAGCTCACTACAAATTGT    85223     GAG  TGC
                                GCAA  GT   AGTGAGCTG
                                ||||  ||  |||||||||
                                TGTT  CA   TCACTCGAC
                                  AAA  ___
GAM1066  LOC151201 3'  CAGCTCACTGCAACCTCCACCT 85273     CAA
                                AGG  GAGGTTGCAGTGAGCTG
                                |||  ||||||||||||||||
                                TCC  CTCCAACGTCACTCGAC
                                 AC_
GAM1066  LOC151475 5'  CACTGCAACCTCCACCT     85392     CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  CTCCAACGTCAC
                                 AC_
GAM1066  LOC151475 5'  CAGCTCACTGCAACCTCTGCCT 85395      A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  LOC151826 3'  CAGCTCACTGCAACCTCCGCCT 80355     AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  LOC152220 3'  CAGCTCACTGCAACCTCCGCTT 85579     AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  ||||||||||||||||
                                TTCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  LOC152245 3'  CACTGCAACCTCCGCCT     85597     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC152300 3'  CAGCTCACTGCAAGCTCTGCCT 80542      A   G
                                AGGCA GAG TTGCAGTGAGCTG
                                ||||| ||| ||||||||||||
                                TCCGT CTC AACGTCACTCGAC
                                  _  G
GAM1066  LOC152343 3'  CAGTGCAACCTCCGCCT     80557     AA       G
                                AGGC  GAGGTTGCA TG
                                ||||  ||||||||| ||
                                TCCG  CTCCAACGT AC
                                  C_       G
GAM1066  LOC152445 3'  CACTGCAACCTCTGCCT     85748      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
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                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  LOC152582 5'  CACCGCAACCTCTGCCT    85788      A      A
                                AGGCA GAGGTTGC GTG
                                ||||| |||||||| |||
                                TCCGT CTCCAACG CAC
                                  _      C
GAM1066  LOC152620 3'  CAGCTCACTACAACCTCTGCCT 60079      A      C
                                AGGCA GAGGTTG AGTGAGCTG
                                ||||| ||||||| |||||||||
                                TCCGT CTCCAAC TCACTCGAC
                                  _     A
GAM1066  LOC152719 5'  CACTGCAACCTCTGCCT    85847      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  LOC152794 5'  CACTGCAACCTCTACCT    80672     CA
                                AGG  AGAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  TCTCCAACGTCAC
                                  A_
GAM1066  LOC152851 3'  CGCTGCAACCTCCACC     80707    CAA
                                GG   GAGGTTGCAGTG
                                ||   ||||||||||||
                                CC   CTCCAACGTCGC
                                  AC_
GAM1066  LOC153077 3'  CACTGCAACCTCCGCCT    85906     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC153688 3'  CACTGCAACCTCCACCT    86096    CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  LOC153883 5'  CACTGCAACCTCCACC     80979    CAA
                                GG   GAGGTTGCAGTG
                                ||   ||||||||||||
                                CC   CTCCAACGTCAC
                                  AC_
GAM1066  LOC154075 3'  CAGCTCACTGCAACCTCCGCCT 81045     AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  LOC154282 5'  CACTGCAACCTCCACCT    86193    CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
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                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  LOC154726 5'  CAGCTCACCACAACCTCCGCCT 81103      AA      CA
                                AGGC  GAGGTTG  GTGAGCTG
                                ||||  |||||||  ||||||||
                                TCCG  CTCCAAC  CACTCGAC
                                  C_      AC
GAM1066  LOC154877 3'  CAGCTCACTGCAACCTCTACCT 86283     CA
                                AGG  AGAGGTTGCAGTGAGCTG
                                |||  ||||||||||||||||||
                                TCC  TCTCCAACGTCACTCGAC
                                  A_
GAM1066  LOC154877 3'  CATTGCAACCTCCGCCT     86285      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTTAC
                                  C_
GAM1066  LOC157247 5'  CAGCTCACTGCAACCTCCACCC 81360    CAA
                                GG   GAGGTTGCAGTGAGCTG
                                ||   ||||||||||||||||||
                                CC   CTCCAACGTCACTCGAC
                                 CAC
GAM1066  LOC157798 5'  CACTGCAACCTCCGCCT     86547      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC157858 5'  CACTGCAACCTCTGCCT     86583       A
                                AGGCA GAGGTTGCAGTG
                                |||||  ||||||||||||
                                TCCGT CTCCAACGTCAC

                                  _
GAM1066  LOC158310 5'  CAGCTCACTGCAACCTTGGCCT 86750      AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  ||||||||||||||||||
                                TCCG  TTCCAACGTCACTCGAC
                                  G_
GAM1066  LOC158402 5'  CAGCTCACTGTAACCTCTGCCT 86801       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                |||||  ||||||||||||||||||
                                TCCGT CTCCAATGTCACTCGAC

                                  _
GAM1066  LOC158476 3'  CAGCTCACTGCAACCTCCGCC  86839     AA
                                GGC  GAGGTTGCAGTGAGCTG
                                |||  ||||||||||||||||||
                                CCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  LOC158668 3'  CAGCTCACTGCAACCTCTGCCT 69366       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                |||||  ||||||||||||||||||
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                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  LOC158828 3'  CTGCAACCTCTGACCT      82028     CA
                                AGG  AGAGGTTGCAG
                                |||  |||||||||||
                                TCC  TCTCCAACGTC
                                  AG
GAM1066  LOC158865 5'  CACTGCAACCTCTGCCT     86932       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  LOC161829 3'  CACTGCAACCTCCGCCT     82311      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC169611 3'  CAGCTCACTGCAATCTCCGCCT 82758      AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  |||||||||||||||||
                                TCCG  CTCTAACGTCACTCGAC
                                  C_
GAM1066  LOC196047 5'  CACTGCAACCTCCGCCT     89593      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC196264 3'  CACTGCAACCTCTGCCT     87602       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  LOC196411 3'  CACTGCAACCTCCGCCT     87667      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC196529 3'  CACTGCAACCTCCACCT     87769     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  LOC196529 3'  CAGCTTACCACAACCTCCACCT 87770     CAA      CA
                                AGG   GAGGTTG  GTGAGCTG
                                |||   |||||||  ||||||||
                                TCC   CTCCAAC  CATTCGAC
                                  AC_      AC
GAM1066  LOC197358 3'  CAGCTCACTGTAGGCTCTACCT 88025     CA    G
                                AGG  AGAG TTGCAGTGAGCTG
                                |||  |||| ||||||||||||||
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                                TCC  TCTC GATGTCACTCGAC
                                  A_    G
GAM1066  LOC197358 3'  CAGCTCCCTGCAACCTCCGCCT 88026      AA         T
                                AGGC  GAGGTTGCAG GAGCTG
                                ||||  |||||||||| ||||||
                                TCCG  CTCCAACGTC CTCGAC
                                  C_         C
GAM1066  LOC199699 3'  CAGCTCACTGCAAGCTCCACCT 88299     CAA   G
                                AGG   GAG TTGCAGTGAGCTG
                                |||   ||| ||||||||||||
                                TCC   CTC AACGTCACTCGAC
                                  AC_   G
GAM1066  LOC199725 5'  CTTACTGCAACCTTCGCCT    89837      AA
                                AGGC  GAGGTTGCAGTGAG
                                ||||  ||||||||||||||
                                TCCG  TTCCAACGTCATTC
                                  C_
GAM1066  LOC199786 3'  CACTGCAACCTCCGCCT     88369      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC199906 3'  CTTACTGCAACCTCCGCCT    88483      AA
                                AGGC  GAGGTTGCAGTGAG
                                ||||  ||||||||||||||
                                TCCG  CTCCAACGTCATTC
                                  C_
GAM1066  LOC200014 3'  CAGCTCGCTGCAACCCCCACCT 88519     CAAGA
                                AGG    GGTTGCAGTGAGCTG
                                |||    ||||||||||||||||
                                TCC    CCAACGTCGCTCGAC
                                  ACCC_
GAM1066  LOC200169 5'  CACTGCAACCTCTGCCT     89944       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                    _
GAM1066  LOC200268 3'  CACTGCAACCTCTGCCT     88677       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                    _
GAM1066  LOC200310 3'  CACTACAACCTCTGCCT     65728       A      C
                                AGGCA GAGGTTG AGTG
                                ||||| ||||||| ||||
                                TCCGT CTCCAAC TCAC
                                    _      A
GAM1066  LOC200314 3'  CACTGCAACCTCCACCT     90002      CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
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                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  LOC200316 3'  CAGCTCACTGCAAACTCTGCTT 88765      A   G
                                AGGCA GAG TTGCAGTGAGCTG
                                ||||| ||| ||||||||||||
                                TTCGT CTC AACGTCACTCGAC
                                  _   A
GAM1066  LOC200339 3'  CACTGCAACCTCTGCCT     90032      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  LOC200471 5'  CAGCTCACCAGCCCCACGCT   90051     AAGA    CA
                                GGC    GGTTG  GTGAGCTG
                                |||    |||||  ||||||||
                                TCG    CCGAC  CACTCGAC
                                  CACC    __
GAM1066  LOC200845 5'  CACTGCAACCTCCGCCT     88895      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC200860 3'  CACTGCAACCTCCACCT     90159     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  LOC201173 5'  CACTGCAACCTCTGCCT     87324      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  LOC201220 5'  CACTGCAACCTCTGCCT     87344      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  LOC201294 3'  CACTGCAACCTCCGCCT     88202      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC201294 3'  CAGCTCACTGCAACCTCCGCCT 88205      AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  LOC201411 3'  CAGCTCACTGCAACCTCTGCCT 62953      A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| |||||||||||||||||
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                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  LOC201626 3'  CACTGCAACCTCCGCC      88988     AA
                                GGC  GAGGTTGCAGTG
                                |||  ||||||||||||
                                CCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC201627 3'  CTGACTGCAACCTCCACCT    89011     CAA         G
                                AGG   GAGGTTGCAGT AG
                                |||   |||||||||||  ||
                                TCC   CTCCAACGTCA TC
                                  AC_         G
GAM1066  LOC201696 3'  CAGCTCACTGCAGCCACTGCCT 63130       A A
                                AGGCA G GGTTGCAGTGAGCTG
                                ||||| | ||||||||||||||||
                                TCCGT C CCGACGTCACTCGAC
                                  _ A
GAM1066  LOC201702 5'  CAGCTCACTGCAACCTCTGACT 89030     CA
                                GG  AGAGGTTGCAGTGAGCTG
                                ||  ||||||||||||||||||
                                TC  TCTCCAACGTCACTCGAC
                                 AG
GAM1066  LOC202025 3'  CACTGCAACCTCCGCCT     90283      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC202934 3'  CAGCTCACTACAACCTCTGCCT 90406       A      C
                                AGGCA GAGGTTG AGTGAGCTG
                                ||||| ||||||| |||||||||
                                TCCGT CTCCAAC TCACTCGAC
                                  _      A
GAM1066  LOC203297 5'  CACTGCAACCTCTGCCT     75348       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  LOC203350 3'  CTGACTGCAACCTCCGCCT    90566      AA          G
                                AGGC  GAGGTTGCAGT AG
                                ||||  |||||||||||  ||
                                TCCG  CTCCAACGTCA TC
                                  C_          G
GAM1066  LOC219690 3'  CAGCTATAAGCCTCTTGCCT   93070            GCAGTG
                                AGGCAAGAGGTT      AGCTG
                                ||||||||||||      |||||
                                TCCGTTCTCCGA      TCGAC
                                       ATA___
GAM1066  LOC219920 3'  CAGCTGAATAAACCTCTTCCT  93304     C       GCAGTG
                                AGG AAGAGGTT      AGCTG
                                ||| ||||||||      |||||
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                                TCC TTCTCCAA     TCGAC
                                  _      ATAAG_
GAM1066  LOC220074 3'  CAGCTCACTGCAACCTCCGCCT 59266     AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  LOC220662 3'  CACTGCAACCTCCACCT     91165     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  LOC220846 3'  CAGCCTTTCCACAACCTCTACC 90812     CA       CAGT   _
                  T              AGG  AGAGGTTG    GAG CTG
                                |||  ||||||||    ||| |||
                                TCC  TCTCCAAC    TTC GAC
                                  A_       ACCT   C
GAM1066  LOC221035 3'  CACTACAACCTCTGCCT     93161       A      C
                                AGGCA GAGGTTG AGTG
                                ||||| ||||||| ||||
                                TCCGT CTCCAAC TCAC
                                  _      A
GAM1066  LOC221174 5'  CAGCTCACTGCGACCTCCACCT 93500     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||
                                TCC   CTCCAGCGTCACTCGAC
                                  AC_
GAM1066  LOC221271 3'  CAGCTCACTGCAACCTCTGCCT 91851       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  LOC221296 3'  CACTGCAACCTCCACCT     91958     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  LOC221362 5'  CAGCCCTCCCAAACTCTTGCCT 93758         G   CAGTGA
                                AGGCAAGAG TTG     GCTG
                                ||||||||| |||     ||||
                                TCCGTTCTC AAC     CGAC
                                     A   CCTCC_
GAM1066  LOC221663 5'  CACTGCAACCTCCACCT     93810     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1066  LOC221773 3'  CAGCTCACTGTGACCTCCGCCT 91039      AA    TG
                                AGGC  GAGGT  CAGTGAGCTG
                                ||||  |||||  ||||||||||
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                                TCCG  CTCCA  GTCACTCGAC
                                  C_    GT
GAM1066  LOC222070 5'  CACTGCAACCTCTGCCT     94151       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  LOC253612 5'  CACTGCAACCTCCGCCT     96741       AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC253664 3'  CATTGCAACCTCTGCCT     94808       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTTAC
                                  _
GAM1066  LOC253666 5'  CAGCTCACTGCAACCTCCGCCT 95061      AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  LOC253779 3'  CACTGCAACCTCCGCCT     97143       AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC254268 3'  CAGCTCACTGCAACCTTTGTCT 95403      A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| |||||||||||||||||
                                TCTGT TTCCAACGTCACTCGAC
                                  _
GAM1066  LOC254655 3'  CACTGCAACCTCTGCCT     95469       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1066  LOC255177 3'  CAGCTCACCGCATCCTCCACCT 96603     CAA   T   A
                                AGG   GAGG TGC GTGAGCTG
                                |||   |||| ||| ||||||||
                                TCC   CTCC ACG CACTCGAC
                                  AC_   T   C
GAM1066  LOC255465 3'  CAGCTCACTGTATCCTCTGCCT 97283      A   T
                                AGGCA GAGG TGCAGTGAGCTG
                                ||||| |||| ||||||||||||
                                TCCGT CTCC ATGTCACTCGAC
                                  _   T
GAM1066  LOC255497 3'  CACTGCAACCTCCGCCT     97187       AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC255919 3'  CTTTCTGCAACCTCTGCCT    95034       A        T
                                AGGCA GAGGTTGCAG GAG
                                ||||| |||||||||| |||
                                TCCGT CTCCAACGTC TTC
                                  _        T
GAM1066  LOC256267 3'  CAGCTCACTGCAACCTCCGCCT 96799      AA
                                AGGC  GAGGTTGCAGTGAGCTG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGAC
                                  C_
GAM1066  LOC256273 5'  CAGTGAAACAACCTCCTCCCT  96404     CAA      CAGTGA
                                AGG   GAGGTTG     GCTG
                                |||   |||||||     ||||
                                TCC   CTCCAAC     TGAC
                                  CTC      AAAG__
GAM1066  LOC256306 3'  CAGCTCACTGCAACCTCCACCT 96682     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGAC
                                  AC_
GAM1066  LOC257054 5'  CAGCTCACTGCAGCCTCGACCT 95656     CAA
                                AGG   GAGGTTGCAGTGAGCTG
                                |||   ||||||||||||||||
                                TCC   CTCCGACGTCACTCGAC
                                  AG_
GAM1066  LOC257334 3'  CACTGCAACCTCCGCCT     97275      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1066  LOC51200  3'  CACCACAACCTCTGCCT     32990       A      CA
                                AGGCA GAGGTTG  GTG
                                ||||| |||||||  |||
                                TCCGT CTCCAAC  CAC
                                  _      AC
GAM1066  LOC51219  5'  CACCGCAACCTCCGCCT     33111      AA       A
                                AGGC  GAGGTTGC GTG
                                ||||  |||||||| |||
                                TCCG  CTCCAACG CAC
                                  C_       C
GAM1066  LOC51696  3'  CAGCTCACTGCAACCTCTGCCT 32544       A
                                AGGCA GAGGTTGCAGTGAGCTG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGAC
                                  _
GAM1066  LOC57107  3'  CACTGCAACCTCCGCCT     39830      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                              TCCG  CTCCAACGTCAC
                                C_
GAM1066 LOC81034 3' CAGCTCACTGCAACCTCCACCT 47845    CAA
                              AGG   GAGGTTGCAGTGAGCTG
                              |||   ||||||||||||||||
                              TCC   CTCCAACGTCACTCGAC
                                AC_
GAM1066 LOC89932 3' CACTGCAACCTCCACCT    60790    CAA
                              AGG   GAGGTTGCAGTG
                              |||   ||||||||||||
                              TCC   CTCCAACGTCAC
                                AC_
GAM1066 LOC89932 3' CAGCTCACTGCAACCTCCGTCT 60792     AA
                              AGGC  GAGGTTGCAGTGAGCTG
                              ||||  ||||||||||||||||
                              TCTG  CTCCAACGTCACTCGAC
                                C_
GAM1066 LOC90139 3' CAAGGCAGCCTCCTGCCT    55400      A      AG
                              AGGCA GAGGTTGC  TG
                              ||||| ||||||||  ||
                              TCCGT CTCCGACG  AC
                                 C      GA
GAM1066 LOC90288 3' CACTGCAACCTCCACCT    62084    CAA
                              AGG   GAGGTTGCAGTG
                              |||   ||||||||||||
                              TCC   CTCCAACGTCAC
                                AC_
GAM1066 LOC90333 3' CAGCTCACTGCAACCTCCTCCT 62286    CAA
                              AGG   GAGGTTGCAGTGAGCTG
                              |||   ||||||||||||||||
                              TCC   CTCCAACGTCACTCGAC
                                TC_
GAM1066 LOC90371 5' CACTGCAACCTCCACCT    62493    CAA
                              AGG   GAGGTTGCAGTG
                              |||   ||||||||||||
                              TCC   CTCCAACGTCAC
                                AC_
GAM1066 LOC90408 5' CACTGCAACCTCTACCT    62657    CA
                              AGG  AGAGGTTGCAGTG
                              |||  ||||||||||||
                              TCC  TCTCCAACGTCAC
                                A_
GAM1066 LOC90459 3' CACTGCAACCTCCGCCT    62882     AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1066 LOC90485 3' CACTGCAACCTCCGCCT    63007     AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
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                              TCCG  CTCCAACGTCAC
                                C_
GAM1066 LOC90591 3' CAGCTCACTGCAAGCTCCACCT 63417    CAA  G
                              AGG  GAG TTGCAGTGAGCTG
                              |||  ||| ||||||||||||
                              TCC  CTC AACGTCACTCGAC
                                AC_  G
GAM1066 LOC91115 3' CACTGCAACCTCCACCT    64925    CAA
                              AGG  GAGGTTGCAGTG
                              |||  ||||||||||||
                              TCC  CTCCAACGTCAC
                                AC_
GAM1066 LOC91115 3' CACTGCAACCTCCGCCT    64926     AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1066 LOC91115 3' CAGCTCACTGCAACTTCTGCCT 64928      A
                              AGGCA GAGGTTGCAGTGAGCTG
                              ||||| ||||||||||||||||||
                              TCCGT CTTCAACGTCACTCGAC
                                _
GAM1066 LOC91291 5' CAGCTCACTGCAACCTCGACCT 65477    CAA
                              AGG  GAGGTTGCAGTGAGCTG
                              |||  ||||||||||||||||||
                              TCC  CTCCAACGTCACTCGAC
                                AG_
GAM1066 LOC91547 3' CAGCTCACTGCAGCCTC    66400
                              GAGGTTGCAGTGAGCTG
                              |||||||||||||||||
                              CTCCGACGTCACTCGAC

GAM1066 LOC91561 5' CAGCTCACTGCAAGCTCCGCCT 66447     AA  G
                              AGGC  GAG TTGCAGTGAGCTG
                              ||||  ||| ||||||||||||
                              TCCG  CTC AACGTCACTCGAC
                                C_  G
GAM1066 LOC91813 5' CAGCTCACTGAGCTCTCTGCC  67245     A  _  G
                              GGCA GAG GTT CAGTGAGCTG
                              |||| ||| ||| ||||||||||
                              CCGT CTC CGA GTCACTCGAC
                                _  T  _
GAM1066 LOC91893 3' CAGCTCACTATAAGCTCCACCT 67459    CAA  G  C
                              AGG  GAG TTG AGTGAGCTG
                              |||  ||| ||| |||||||||
                              TCC  CTC AAT TCACTCGAC
                                AC_  G  A
GAM1066 LOC92267 3' CAGCTCACTGCAACCTCCACCT 68606    CAA
                              AGG  GAGGTTGCAGTGAGCTG
                              |||  |||||||||||||||||
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                              TCC   CTCCAACGTCACTCGAC
                                AC_
GAM1066  LOC92303  3'  CTCACTGCAACCTCTGCC    68823      A
                              GGCA GAGGTTGCAGTGAG
                              |||| ||||||||||||||
                              CCGT CTCCAACGTCACTC
                                _
GAM1066  LOC92466  3'  CAGCTCACTGCAACCTCCGCCT 69424      AA
                              AGGC  GAGGTTGCAGTGAGCTG
                              ||||  |||||||||||||||||
                              TCCG  CTCCAACGTCACTCGAC
                                C_
GAM1066  LOC92689  3'  CACTGCAACCTCCGCCT     70218      AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1066  LOC92697  5'  CACCGCAACCTCCGCCT     70261      AA       A
                              AGGC  GAGGTTGC GTG
                              ||||  |||||||| |||
                              TCCG  CTCCAACG CAC
                                C_       C
GAM1066  LOC92697  5'  CGCTACAACCTCCACCT     70263     CAA      C
                              AGG   GAGGTTG AGTG
                              |||   ||||||| ||||
                              TCC   CTCCAAC TCGC
                                AC_      A
GAM1066  LOC92841  3'  GGCTCACCGCAACCTCCTCCT  70716     CAA       A
                              AGG   GAGGTTGC GTGAGCT
                              |||   |||||||| |||||||
                              TCC   CTCCAACG CACTCGG
                                TC_       C
GAM1066  LOC93129  3'  CAGCTCACTGTAGCCTCGACCT 71462     CAA
                              AGG   GAGGTTGCAGTGAGCTG
                              |||   |||||||||||||||||
                              TCC   CTCCGATGTCACTCGAC
                                AG_
GAM1066  LOC93132  5'  CAGCTCACTGCAACCTCCGCCT 71486      AA
                              AGGC  GAGGTTGCAGTGAGCTG
                              ||||  |||||||||||||||||
                              TCCG  CTCCAACGTCACTCGAC
                                C_
GAM1066  LOC93349  3'  CAGCTCACTGCAACCTCTGCCT 56454       A
                              AGGCA GAGGTTGCAGTGAGCTG
                              ||||| |||||||||||||||||
                              TCCGT CTCCAACGTCACTCGAC
                                _
GAM1066  LOC93408  5'  CACTGCAACCTCTGCCT     56474       A
                              AGGCA GAGGTTGCAGTG
                              ||||| ||||||||||||
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                                TCCGT CTCCAACGTCAC
                                  _
GAM1067 CHRNA3   3' TCACCACTGACAGATGATTCA 5609        A_   CA A
                                TGAATCATT TCAG TG TGA
                                ||||||||| |||| || |||
                                ACTTAGTAG AGTC AC ACT
                                    AC   __ C
GAM1067 TCF2     3' CATCATGCTTGATTGA     21375     TT  _
                                TCA ATCA GCATGATG
                                ||| |||| ||||||||
                                AGT TAGT CGTACTAC
                                  __   T
GAM1067 CLIC4    3' TTTCATCATTTAATGATTCA  25637        TCAGC
                                TGAATCATTA    ATGATGAAA
                                ||||||||||    |||||||||
                                ACTTAGTAAT    TACTACTTT
                                    T____
GAM1067 LOC222008 3' TTATGTATCGATAATGACCCA 94015    AA      A__
                                TG TCATTATC  GCATGA
                                || ||||||||  ||||||
                                AC AGTAATAG  TGTATT
                                 CC      CTA
GAM1067 LOC256360 3' TTTCACATGAGATAATGA   96554       AG   A
                                TCATTATC CATG TGAAA
                                |||||||| |||| |||||
                                AGTAATAG GTAC ACTTT
                                    A_  _
GAM1067 LOC51218  3' TGCACTGTAATGATTCA    33106         CA_
                                TGAATCATTAT  GCA
                                |||||||||||  |||
                                ACTTAGTAATG  CGT
                                     TCA
GAM1068 A1BG     3' TCACAGCAACCTCTACCTCC  55433           A_
                                GGAGGTAGAGGTTGC TGA
                                |||||||||||||| |||
                                CCTCCATCTCCAACG ACT
                                      AC
GAM1068 ACVR1    5' CACTGCAGCCTCCACCTCC   6605       A      _
                                GGAGGT GAGGTTGCA TG
                                |||||| ||||||||| ||
                                CCTCCA CTCCGACGT AC
                                   C       C
GAM1068 AHR      3' TCACTGCAACCTCTACCTCC  7884            _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||| |||
                                CCTCCATCTCCAACGT ACT
                                      C
GAM1068 AIM1     3' TCACTGCAGCCTCTACCTCC  91827           _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||| |||
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                                CCTCCATCTCCGACGT ACT
                                        C
GAM1068 ALDH1B1  3' TCACTGCAACCTCCGCCTCC  5497      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068 APPBP2   3' TCACTGCAACCTCCGCCTCC  21083     TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068 AQP6     3' TCACTGCAACCTCTACCTCC  7961            _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCATCTCCAACGT ACT
                                        C
GAM1068 AQP6     3' TCACTGCAACCTCTACCTCC  53941           _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCATCTCCAACGT ACT
                                        C
GAM1068 ARCN1    3' TCACTGCAACCTCCGCCTCC  7986      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068 ATP8B2   3' TCACTGCAACCTCCACCTCC  65236      A      _
                                GGAGGT GAGGTTGCA TGA
                                ||||||  |||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068 BRIP1    3' TCACTGCAACCTTCACCTCC  49401      AG      _
                                GGAGGT  AGGTTGCA TGA
                                ||||||  |||||||| |||
                                CCTCCA  TCCAACGT ACT
                                   CT       C
GAM1068 C7       3' TGCAACCTCCGCCTCC     5170       TA
                                GGAGG  GAGGTTGCA
                                |||||  |||||||||
                                CCTCC  CTCCAACGT
                                   GC
GAM1068 CAMLG    3' TCACCGCAACCTCCACCTTC  8244       A      A_
                                GGAGGT GAGGTTGC  TGA
                                ||||||  ||||||||  |||
                                CTTCCA CTCCAACG  ACT
                                   C       CC
GAM1068 CASQ1    5' CAACCCAGATCCCACTACCTCC 6927        A  TTGCA  A
                                GGAGGTAG GG     TG GTTG
                                ||||||||  ||     ||  ||||
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                                CCTCCATC CC    AC CAAC
                                    A  CTAG_  C
GAM1068  CCNF    3'  TCAACTCACTGTAACCTCCGCC 8326       TA      _
             TCC                   GGAGG  GAGGTTGCA TGAGTTGA
                                |||||  ||||||||| ||||||||
                                CCTCC  CTCCAATGT ACTCAACT
                                   GC        C
GAM1068  CDH17   3'  TCACTGCAACCTCCGCCTCC   14508      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  CIAS1   5'  TCACTGCAGCCTCCACCTCC   16904      A       _
                                GGAGGT GAGGTTGCA TGA
                                ||||||  ||||||||| |||
                                CCTCCA CTCCGACGT ACT
                                    C        C
GAM1068  CLECSF12  3'  TCACCGCAACCTCCGCCCC   76701    A  TA      A_
                                GG GG  GAGGTTGC  TGA
                                || ||  ||||||||  |||
                                CC CC  CTCCAACG  ACT
                                 _  GC       CC
GAM1068  CSNK2A2   5'  TCACTGCAACCTCCACCTCC   8567       A       _
                                GGAGGT GAGGTTGCA TGA
                                ||||||  ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                    C        C
GAM1068  CYP1A2   3'  TCACTGCAACCTCCACCTC    5704       A       _
                                GAGGT GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CTCCA CTCCAACGT ACT
                                   C        C
GAM1068  CYP1A2   3'  TCACTGCAACCTCTGCCTCC   5706                 _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||  |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1068  CYP1A2   3'  TCACTGCAACCTCCACCTC    69124      A       _
                                GAGGT GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CTCCA CTCCAACGT ACT
                                   C        C
GAM1068  CYP1A2   3'  TCACTGCAACCTCTGCCTCC   69126                 _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||  |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1068  CYP2B6   3'  CACTGCAACCTCCACATCC    5723     G  A       _
                                GGA GT GAGGTTGCA TG
                                |||  ||  |||||||| ||
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                                CCT CA CTCCAACGT AC
                                  A C        C
GAM1068  CYP2B6   3'  TCACTGCAACCTCCACCCC   5739     A  A       _
                                GG GGT GAGGTTGCA TGA
                                || ||| ||||||||| |||
                                CC CCA CTCCAACGT ACT
                                 _  C        C
GAM1068  CYP4F3   3'  TCATTGCAACCTCCGCCTCC   6125       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        T
GAM1068  CYP8B1   3'  TCACTACAACCTCTGCCTCC   15271            CA_
                                GGAGGTAGAGGTTG   TGA
                                ||||||||||||||   |||
                                CCTCCGTCTCCAAC   ACT
                                        ATC
GAM1068  CYP8B1   3'  TCACTGCAACCTCTGCCTCC   15273             _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  DISC1    3'  TCACTGCAACCTCTACCTCC   37893              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCATCTCCAACGT ACT
                                        C
GAM1068  DSCR3    3'  TCACTGCAACCTCCACCTCC   20192       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  EHD2     3'  TCACTGCAACCTCCACCTCC   27499       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  EIF2S3   3'  TCTGCAACCTCTGCCCC     7420     A          T
                                GG GGTAGAGGTTGCA GA
                                || |||||||||||| ||
                                CC CCGTCTCCAACGT CT
                                  _          _
GAM1068  EPB72    3'  TCACTGCAACCTCCGCCTCC   14611      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  F2RL2    3'  TCATTGCAACCTCTGCCTCC   14627              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
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                                CCTCCGTCTCCAACGT ACT
                                       T
GAM1068  FANCF    3'  TCAGTGCAACCTCTGCCTCC   42680                  _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                       G
GAM1068  FEZ1     3'  TCACTGCAACCTCCACCTCC   42580       A          _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  FGF5     3'  TCACTGCAACCTCCAACTCC   52494      GTA         _
                                GGAG   GAGGTTGCA TGA
                                ||||   ||||||||| |||
                                CCTC   CTCCAACGT ACT
                                  AAC        C
GAM1068  FGF5     3'  TCACTGCAACCTCCAACTCC   15549      GTA         _
                                GGAG   GAGGTTGCA TGA
                                ||||   ||||||||| |||
                                CCTC   CTCCAACGT ACT
                                  AAC        C
GAM1068  FZD4     3'  TCACTGCAACCTCTGCCTCC   24150                  _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                       C
GAM1068  G6PC     3'  TCACTGCAACCTCTTCCTCC   3835        T          _
                                GGAGG AGAGGTTGCA TGA
                                ||||| |||||||||| |||
                                CCTCC TCTCCAACGT ACT
                                   T        C
GAM1068  GHR      3'  TCACTGCAATCTCCACCTCC   3887        A          _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCTAACGT ACT
                                   C        C
GAM1068  GM2A     3'  TCACTGCAACCTCCGCCTCC   67785       TA         _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068  GNE      3'  ATGCAACCTCTGCCCC      18475    A
                                GG GGTAGAGGTTGCAT
                                || ||||||||||||||
                                CC CCGTCTCCAACGTA
                                 _
GAM1068  GPR4     3'  TCACTGCAGCCTCCACCTCC   59908        A          _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
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                                CCTCCA CTCCGACGT ACT
                                   C       C
GAM1068  GPR56    5'  TCATCGTAACCTCCACCTCC   19074       A      _
                                GGAGGT GAGGTTGC ATGA
                                |||||| |||||||| ||||
                                CCTCCA CTCCAATG TACT
                                   C       C
GAM1068  GPR81    3'  TCACTGCAACCTCTGCCTCC   50766              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  GRAF     3'  TCACTGCAACCTCCGCCTCC   30577      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068  HTR1E    5'  TCATTGCAACCTCCGCCTCC   6016       TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       T
GAM1068  ITGAM    3'  TCACTGCAACCTCCGCCTCC   71843      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068  KMO      3'  TCACTGCAACCTCTGCCTCC   13456              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  LNK      3'  TCACTGCAACCTCCACCTTC   18471       A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CTTCCA CTCCAACGT ACT
                                   C       C
GAM1068  LYZ      3'  TCACTGCAACCTCCACCTCC   4108        A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C       C
GAM1068  MAK      3'  TGCAACCTCCACCTCC      19770       A
                                GGAGGT GAGGTTGCA
                                |||||| |||||||||
                                CCTCCA CTCCAACGT
                                   C
GAM1068  MEF2A    5'  TCACTGCAACCTCCGCCTCC   18785      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
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                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  MEFV     3'  TCACTGCAACCTCCACCTCC  4149       A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C       C
GAM1068  MEFV     3'  TCACTGCAACCTCCGCCTCC  4151       TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  MICB     3'  TCACTGCAACCTCTGCCTCC  19833             _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  MPL      3'  TCACTGCAACCTCCACCTCC  18153      A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C       C
GAM1068  MPL      3'  TCACTGCAACCTCTGCCTCC  18155             _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  MSN      3'  TCAACCCAGGAGCATCCACCTC 60254      A G  GCA A
            C                    GGAGGT GA GTT   TG GTTGA
                                |||||| || |||   || |||||
                                CCTCCA CT CGA   AC CAACT
                                   C A  GG_ C
GAM1068  MYCL2    3'  TCACTGCAACCTCTGCCTCC  18189             _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  NDRG3    3'  TCACTGCAACCTCTGCCCC  49304    A        _
                                GG GGTAGAGGTTGCA TGA
                                || |||||||||||| |||
                                CC CCGTCTCCAACGT ACT
                                 _        C
GAM1068  NQO1     3'  TCACTGCAACCTCTGCCTCC  6166              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  PCDHB11  3'  TCACTGCAACCTCTGCCTCC  38421             _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
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                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068  PCDHB16   3'  TCACTGCAACCTCTGCCTCC   40555                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068  PCDHB9    3'  TCACTGCAACCTCCGCCTCC   38948      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  |||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  PDCL      3'  TCACTGCAACCTCCACCTCC   18218       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| |||||||| |||
                                CCTCCA CTCCAACGT ACT
                                    C        C
GAM1068  PDE6B     3'  TCACTGCAACCTCCACCTCC   4289        A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| |||||||| |||
                                CCTCCA CTCCAACGT ACT
                                    C        C
GAM1068  PER2      3'  TCACTGCAACCTCTGCCTCC   43044               _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068  PIGR      3'  TCACTGCAACCTCCGCCTCC   72607       TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  |||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  PON1      3'  TCACTGCAACTTCTACCTCC   4805                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCATCTTCAACGT ACT
                                      C
GAM1068  PRKWNK3   3'  TCACTGCTGCAACCTCCCCCTC 61556      TA       TG   T
              C                  GGAGG  GAGGTTGCA  AGT GA
                                |||||  ||||||||  ||| ||
                                CCTCC  CTCCAACGT  TCA CT
                                   CC        CG  _
GAM1068  PSMB2     3'  TCACTGCAACCTCCGCCTCC   10954      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  |||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  PTGIS     3'  TCACCACAACCTCCACCTC    6343       A      CA_
                                GAGGT GAGGTTG   TGA
                                |||||  |||||||   |||
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                                CTCCA CTCCAAC   ACT
                                   C      ACC
GAM1068  RAB36    3'  TCAGTGCAACCTCTGCCTCC   16974          _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      G
GAM1068  RHD      3'  TCACTGCAACCTCCGCCTCC   32315      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  |||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068  RHD      3'  TCACTGCAACCTCTACCTCC   32317          _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCATCTCCAACGT ACT
                                      C
GAM1068  RHD      3'  TCACTGCAACCTCCGCCTCC   32624      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  |||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068  RHD      3'  TCACTGCAACCTCTACCTCC   32626          _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCATCTCCAACGT ACT
                                      C
GAM1068  RPH3AL   3'  TCACTGCAACCTCCACCTCC   22756       A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| |||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C       C
GAM1068  RTKN     3'  CAACTCTGCCCTACCTCC     52325       A  TGCAT
                                GGAGGTAG GGT    GAGTTG
                                |||||||| |||    ||||||
                                CCTCCATC CCG    CTCAAC
                                   _  T____
GAM1068  SAS      3'  TCACCGCAACCTCTGCCTCC   19960          A_
                                GGAGGTAGAGGTTGC  TGA
                                ||||||||||||||  |||
                                CCTCCGTCTCCAACG  ACT
                                      CC
GAM1068  SEDL     3'  TCACTGCAACCTCCACCTCC   27357       A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| |||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C       C
GAM1068  SEDL     3'  TCACTGCAACCTCCACCTCC   27358       A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| |||||||| |||
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                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068 SEDL     3' TCACTGCAACCTCCGCCTCC  27360      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068 SEPN1    3' TCACTGCAACCTCCACCTCC  66379       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068 SERPINB9 3' TCACTGCAACCTCCTCCTCC  14764      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   TC       C
GAM1068 SHOX     3' TCACTGCAACCTCCGCCTCC  22545      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068 SIL      3' TCACTGCAACCTCTGCCTCC  11696               _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068 SLA2     3' TCACTGCAACCTCCATCTCC  49906       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCTA CTCCAACGT ACT
                                   C        C
GAM1068 SLC14A2  5' TCACTGCAACCTCCACCTCC  23140       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068 SLC15A1  3' TCACTGCAACCTCCGCCTCC  17407      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068 SMAC     5' TCACTGCAACCTCTGCCTCC  57217               _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068 SNAP23   3' TCACTGCAACCTCCGCCTCC  55468      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
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                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  SNAP23   3'  TCACTGCAACCTCCGCCTCC   13815      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  SNX15    3'  TCACTGCAACCTCCACCTCC   73749      A        _
                                GGAGGT GAGGTTGCA TGA
                                ||||||  ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C       C
GAM1068  SPN      3'  TCACTGCAACCTCTGCCTCC   11926               _
                                GGAGGTAGAGGTTGCA TGA
                                ||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  SS18     3'  TCACTGCAACCTCCGCCTCC   18889      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  STAU     5'  TCACTGCAACCTCCACCTCC   16010      A        _
                                GGAGGT GAGGTTGCA TGA
                                ||||||  ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C       C
GAM1068  SULT2B1  5'  TCACTGCAACCTCCGCCTCC   16031      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  TAT      3'  TCACTGCAACCTCCACCTCC   4476       A        _
                                GGAGGT GAGGTTGCA TGA
                                ||||||  ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C       C
GAM1068  TBXA2R   3'  TCACTGCAACCTCCACCTCC   6501       A        _
                                GGAGGT GAGGTTGCA TGA
                                ||||||  ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C       C
GAM1068  TBXA2R   3'  TCACTGCAACCTCCGCCTCC   6503       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  TMC1     5'  TCTGCAACCTCCGCCTCC    56908      TA       T
                                GGAGG  GAGGTTGCA GA
                                |||||  ||||||||| ||
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                                CCTCC  CTCCAACGT CT
                                  GC       _
GAM1068  TNFRSF10B 3'  TCAGTGCAACCTCCGCCTCC   13879      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       G
GAM1068  TPMT      3'  TCACTGCAACCTCTGCCTCC   4545              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  TRIM9     5'  TCACTGCAACCTCCGCCTCC   30766      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  TRPM6     3'  TCACTGCAACCTCTGCCTCC   34546              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  TRPV1     3'  TCACTGCAACCTCTGCCTCC   38096              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  TRPV1     3'  TGCAACCTCCGCCTCC      38101      TA
                                GGAGG  GAGGTTGCA
                                |||||  |||||||||
                                CCTCC  CTCCAACGT
                                  GC
GAM1068  TRPV1     3'  TCACTGCAACCTCTGCCTCC   54814              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  TRPV1     3'  TGCAACCTCCGCCTCC      54819      TA
                                GGAGG  GAGGTTGCA
                                |||||  |||||||||
                                CCTCC  CTCCAACGT
                                  GC
GAM1068  TRPV1     3'  TCACTGCAACCTCTGCCTCC   54846              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  TRPV1     3'  TGCAACCTCCGCCTCC      54851      TA
                                GGAGG  GAGGTTGCA
                                |||||  |||||||||
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                                CCTCC  CTCCAACGT
                                   GC
GAM1068  TRPV1    3'  TCACTGCAACCTCTGCCTCC   54879                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  TRPV1    3'  TGCAACCTCCGCCTCC      54885       TA
                                GGAGG  GAGGTTGCA
                                |||||  |||||||||
                                CCTCC  CTCCAACGT
                                   GC
GAM1068  TUFT1    3'  TCACTGCAACCTCTGCCTCC   39264                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  VENTX2   3'  TCACTGCAACCTCCGCCTCC   27118       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  VHL      3'  TCACTGCAACCTCTGCCTCC   5085                 _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  ZNF133   5'  TCAACTCACTGCAACCTCCACC 12840    A   A       _
              CC                    GG GGT GAGGTTGCA TGAGTTGA
                                || ||| ||||||||| ||||||||
                                CC CCA CTCCAACGT ACTCAACT
                                 _  C        C
GAM1068  ZNF264   3'  TCACTGCAACCTCCGCCTCC   12765       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  ZNF264   3'  TCTGCAACCTCTGCCTCC     12768              T
                                GGAGGTAGAGGTTGCA GA
                                |||||||||||||||| ||
                                CCTCCGTCTCCAACGT CT
                                        _
GAM1068  20D7-FC4 5'  TCACTGCAGCCTCCACCTCC   60909       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCGACGT ACT
                                   C        C
GAM1068  ARPP-19  3'  TCACTGCAACCTCTGCCTCC   21802                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
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                                  CCTCCGTCTCCAACGT ACT
                                        C
GAM1068 ASB16    5' TCACTGCAACCTCCGCCTCC  69944      TA      _
                                  GGAGG  GAGGTTGCA TGA
                                  |||||  ||||||||| |||
                                  CCTCC  CTCCAACGT ACT
                                     GC        C
GAM1068 ASE-1    3' TCACTGCAACCTCCGCCTCC  23954      TA      _
                                  GGAGG  GAGGTTGCA TGA
                                  |||||  ||||||||| |||
                                  CCTCC  CTCCAACGT ACT
                                     GC        C
GAM1068 ATP1B4   3' TCACTGCAACCTCCACCTCC  23827       A      _
                                  GGAGGT GAGGTTGCA TGA
                                  ||||||  |||||||| |||
                                  CCTCCA CTCCAACGT ACT
                                     C         C
GAM1068 BA108L7.2 3' TCACTGCAACCTCTGCCTCC  48267             _
                                  GGAGGTAGAGGTTGCA TGA
                                  |||||||||||||||| |||
                                  CCTCCGTCTCCAACGT ACT
                                        C
GAM1068 BAG5     3' TCACTGCAACCTCCACCTCC  16852       A      _
                                  GGAGGT GAGGTTGCA TGA
                                  ||||||  |||||||| |||
                                  CCTCCA CTCCAACGT ACT
                                     C         C
GAM1068 BNIP-S   3' TCACTGCAACCTCCGCCTCC  56267      TA      _
                                  GGAGG  GAGGTTGCA TGA
                                  |||||  ||||||||| |||
                                  CCTCC  CTCCAACGT ACT
                                     GC        C
GAM1068 BTN3A1   3' TGCAACCTCCACCTCC      22929       A
                                  GGAGGT GAGGTTGCA
                                  ||||||  ||||||||
                                  CCTCCA CTCCAACGT
                                     C
GAM1068 C1orf24  3' TCACTGCAACCTCCGCCTCC  53726      TA      _
                                  GGAGG  GAGGTTGCA TGA
                                  |||||  ||||||||| |||
                                  CCTCC  CTCCAACGT ACT
                                     GC        C
GAM1068 C1QTNF6  3' TCACTGCAACCTCTGCCTCC  49151             _
                                  GGAGGTAGAGGTTGCA TGA
                                  |||||||||||||||| |||
                                  CCTCCGTCTCCAACGT ACT
                                        C
GAM1068 C21orf25 3' TGCAACCTCCACCTCC      63558       A
                                  GGAGGT GAGGTTGCA
                                  ||||||  ||||||||
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                                  CCTCCA CTCCAACGT
                                     C
GAM1068  C3F      3'  TCACCGCAACCTCCACCTCC   19297       A      A_
                                  GGAGGT GAGGTTGC  TGA
                                  |||||| ||||||||  |||
                                  CCTCCA CTCCAACG  ACT
                                     C       CC
GAM1068  C9orf9   3'  TCACTGCAACCTCCACCTCC   38524       A      _
                                  GGAGGT GAGGTTGCA TGA
                                  |||||| ||||||||| |||
                                  CCTCCA CTCCAACGT ACT
                                     C       C
GAM1068  C9orf9   3'  TCACTGCAACCTCCGCCTCC   38526       TA     _
                                  GGAGG  GAGGTTGCA TGA
                                  |||||  ||||||||| |||
                                  CCTCC  CTCCAACGT ACT
                                    GC       C
GAM1068  CENPH    3'  TCACTGCAACCTCTGCCTCC   43277              _
                                  GGAGGTAGAGGTTGCA TGA
                                  |||||||||||||||| |||
                                  CCTCCGTCTCCAACGT ACT
                                           C
GAM1068  CHRAC1   3'  TCACTGCAACCTCCGCCTCC   33877       TA     _
                                  GGAGG  GAGGTTGCA TGA
                                  |||||  ||||||||| |||
                                  CCTCC  CTCCAACGT ACT
                                    GC       C
GAM1068  CPSF2    3'  TCACCGCAACCTCTGCCTCC   61599            A_
                                  GGAGGTAGAGGTTGC  TGA
                                  ||||||||||||||  |||
                                  CCTCCGTCTCCAACG  ACT
                                           CC
GAM1068  DBR1     3'  TCACCGCAACCTCCGCCTCC   32538       TA     A_
                                  GGAGG  GAGGTTGC  TGA
                                  |||||  ||||||||  |||
                                  CCTCC  CTCCAACG  ACT
                                    GC       CC
GAM1068  DKFZp434A2417 3'  TCACTGCAACTTCCACCTCC   66108       A      _
                                  GGAGGT GAGGTTGCA TGA
                                  |||||| ||||||||| |||
                                  CCTCCA CTTCAACGT ACT
                                     C       C
GAM1068  DKFZP434C212 3'  TCACTGCAACCTCCACCTCC   68919       A      _
                                  GGAGGT GAGGTTGCA TGA
                                  |||||| ||||||||| |||
                                  CCTCCA CTCCAACGT ACT
                                     C       C
GAM1068  DKFZp434E2220 5'  TCACTGCAACCTCCGCCTCC   34303       TA     _
                                  GGAGG  GAGGTTGCA TGA
                                  |||||  ||||||||| |||
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                                  CCTCC  CTCCAACGT ACT
                                     GC        C
GAM1068  DKFZp547H025 3'  TCACTGCAACCTCCACCTCC   39364       A       _
                                  GGAGGT GAGGTTGCA TGA
                                  |||||| ||||||||| |||
                                  CCTCCA CTCCAACGT ACT
                                      C        C
GAM1068  DKFZP564O0523 3'  TCACTGCAACCTCCACCTCC   49519       A       _
                                  GGAGGT GAGGTTGCA TGA
                                  |||||| ||||||||| |||
                                  CCTCCA CTCCAACGT ACT
                                      C        C
GAM1068  DKFZp761N1114 3'  TCACTGCAACCTCCGCCTCC   79025       TA      _
                                  GGAGG  GAGGTTGCA TGA
                                  |||||  ||||||||| |||
                                  CCTCC  CTCCAACGT ACT
                                     GC        C
GAM1068  EREG     3'  TCACTGCAACCTCACCTCC    7512        A       _
                                  GGAGGT GAGGTTGCA TGA
                                  |||||| ||||||||| |||
                                  CCTCCA CTCCAACGT ACT
                                      _        C
GAM1068  FBP17    3'  TCACTACAACCTCCACCTC    72804       A      CA_
                                  GAGGT GAGGTTG   TGA
                                  ||||| |||||||   |||
                                  CTCCA CTCCAAC   ACT
                                     C       ATC
GAM1068  FER1L4   3'  TGCAACCTCCACCTCC      47364       A
                                  GGAGGT GAGGTTGCA
                                  |||||| |||||||||
                                  CCTCCA CTCCAACGT
                                      C
GAM1068  FER1L4   3'  TGCAACCTCCACCTCC      47365       A
                                  GGAGGT GAGGTTGCA
                                  |||||| |||||||||
                                  CCTCCA CTCCAACGT
                                      C
GAM1068  FLJ00024  5'  TCACTGCAACCTCTGCCTCC   63767             _
                                  GGAGGTAGAGGTTGCA TGA
                                  |||||||||||||||| |||
                                  CCTCCGTCTCCAACGT ACT
                                            C
GAM1068  FLJ00060  5'  CAACCCCTCCCCTACCTCC    61092        A  TTGCATGA
                                  GGAGGTAG GG       GTTG
                                  |||||||| ||       ||||
                                  CCTCCATC CC       CAAC
                                       C  TCCC____
GAM1068  FLJ10232  3'  TCACTGCAACCTCCGCCTCC   35930       TA      _
                                  GGAGG  GAGGTTGCA TGA
                                  |||||  ||||||||| |||
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                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  FLJ10535  3'  TCAACCCATTTCCCTCCCTACC 36247    A    A  TTGC__   A
             CC                   GG GGTAG GG     ATG GTTGA
                                || ||||| ||     ||| |||||
                                CC CCATC CC     TAC CAACT
                                 _    _ TCCCTT   C
GAM1068  FLJ10535  3'  TCACTGCAACCTCTGCCTCC   36249            _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1068  FLJ10761  3'  TCAACAGCCTCCACCTCC    36584       A      CA
                                GGAGGT GAGGTTG  TGA
                                |||||| |||||||  |||
                                CCTCCA CTCCGAC  ACT
                                   C      A_
GAM1068  FLJ10922  3'  TCACTGCAACCTCCGCCTCC   36880       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  FLJ11004  5'  TCACTGCAACCTCTACCTCC   36972            _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCATCTCCAACGT ACT
                                          C
GAM1068  FLJ12363  3'  TCACTGCAACCTCCACCTCC   49691       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| |||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C       C
GAM1068  FLJ12572  5'  TCACTGCAACCTCTGCCTCC   43256            _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1068  FLJ12586  3'  TCACAGCAACCTCTGCCTCC   44880            A_
                                GGAGGTAGAGGTTGC  TGA
                                |||||||||||||||  |||
                                CCTCCGTCTCCAACG  ACT
                                         AC
GAM1068  FLJ12649  3'  TCACTGCAACCTCCGCCTCC   44786       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  FLJ12668  3'  TCACTGCAACCTCCATCTCC   46525       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| |||||||| |||
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                                CCTCTA CTCCAACGT ACT
                                   C        C
GAM1068  FLJ12687  3'  TCACTGCAACCTCCGCCTCC   46203       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  FLJ12747  3'  TCACTGCAACCTCTGCCTCC   49725              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1068  FLJ12960  3'  TATGCAACCTCCACCTCC    44953       A
                                GGAGGT GAGGTTGCATG
                                ||||||| ||||||||||
                                CCTCCA CTCCAACGTAT
                                   C
GAM1068  FLJ12973  3'  TCACCGCAACCTCCGCCTCC   46108       TA       A_
                                GGAGG  GAGGTTGC  TGA
                                |||||  ||||||||  |||
                                CCTCC  CTCCAACG  ACT
                                   GC       CC
GAM1068  FLJ13197  3'  TCACTGCAACCTCTACCTCC   44862              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCATCTCCAACGT ACT
                                          C
GAM1068  FLJ13769  3'  CAACCCCACACCCCTCCACTTC 46601       A    TTGCATGA
            C                    GGAGGT GAGG       GTTG
                                |||||| ||||       ||||
                                CCTTCA CTCC       CAAC
                                   C   CCACACCC
GAM1068  FLJ14950  3'  TCACTGCAACCTCCACCTCC   51728       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  FLJ14957  3'  TCACTGCAACCTCTGCCTCC   51759              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1068  FLJ20004  3'  TCATTGCAACCTCCGCCTCC   95300       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        T
GAM1068  FLJ20034  3'  TCACTGCAACCTCTGCCTCC   34385              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
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                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068  FLJ20045  3'  TCACTGCAACCTCTGCCTCC   34429          _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068  FLJ20079  3'  TCACCGCAACCTCCACCTCC   34501      A     A_
                                GGAGGT GAGGTTGC  TGA
                                ||||||  ||||||||  |||
                                CCTCCA CTCCAACG  ACT
                                   C       CC
GAM1068  FLJ20342  3'  TCACTGCAACCTCTGCCTCC   34994          _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068  FLJ20507  3'  TCACTGCAACCTCTGCCTCC   35299          _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068  FLJ20507  3'  TCACTGCAACCTCTGCCTCC   60234          _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068  FLJ20813  3'  TCACTGCAACTCCACCTCC    35690     A  G   _
                                GGAGGT GAG TTGCA TGA
                                ||||||  |||  |||||  |||
                                CCTCCA CTC AACGT ACT
                                   C  _    C
GAM1068  FLJ21302  3'  TCACTGCAACCTCCGCCTCC   43220     TA     _
                                GGAGG  GAGGTTGCA TGA
                                |||||  |||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068  FLJ22002  3'  TCACTGCAACCTCCGCCTCC   45777     TA     _
                                GGAGG  GAGGTTGCA TGA
                                |||||  |||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068  FLJ22531  5'  TCACTGCAACCTCCACCTCC   45034      A     _
                                GGAGGT GAGGTTGCA TGA
                                ||||||  |||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C       C
GAM1068  FLJ22794  3'  TCACTGCAACTTCCACCTCC   91612      A     _
                                GGAGGT GAGGTTGCA TGA
                                ||||||  |||||||| |||
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                                CCTCCA CTTCAACGT ACT
                                   C        C
GAM1068  FLJ22965  3'  TCACTGCAACCTCCGCCTCC   42054       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  FLJ22969  3'  TCACTGCAACCTCTGCCTCC   68662              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1068  FLJ23024  3'  TCACTGCAACCTCTGCCTCC   46274              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1068  FLJ23392  3'  TCACTGCAACCTCTGCCTCC   45545              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1068  FLJ23563  3'  TCACTGCAACCTCTGCCTCC   67600              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1068  FLJ30213  3'  CAACCCCTCCCCTGCCTCC    58767        A  TTGCATGA
                                GGAGGTAG GG       GTTG
                                |||||||| ||       ||||
                                CCTCCGTC CC       CAAC
                                     C  TCCC_____
GAM1068  FLJ31101  3'  TCACTGCAACCTCTGCCTCC   35718              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1068  FLJ32865  3'  TCACTGCAACCTCTGCCTCC   58182              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1068  GAL3ST-4  3'  TCACTGCAACCTCTGCCTCC   44942               _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1068  GMPPB     5'  TCACTGCAACCTCCACCTCC   95753       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
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                                  CCTCCA CTCCAACGT ACT
                                     C        C
GAM1068  GNG4     3'  TCACTGCGACCTCCACCTCC   15623       A       _
                                  GGAGGT GAGGTTGCA TGA
                                  |||||| ||||||||| |||
                                  CCTCCA CTCCAGCGT ACT
                                     C        C
GAM1068  GREB1    3'  TCACTGCAACCTCTGCCTCC   27886             _
                                  GGAGGTAGAGGTTGCA TGA
                                  |||||||||||||||| |||
                                  CCTCCGTCTCCAACGT ACT
                                           C
GAM1068  GRWD     3'  TCACTGCAACCTCCGCCTCC   48973       TA      _
                                  GGAGG  GAGGTTGCA TGA
                                  |||||  ||||||||| |||
                                  CCTCC  CTCCAACGT ACT
                                    GC        C
GAM1068  GTF2E1   3'  TCACTGCAACCTCTGCCTCC   18619             _
                                  GGAGGTAGAGGTTGCA TGA
                                  |||||||||||||||| |||
                                  CCTCCGTCTCCAACGT ACT
                                           C
GAM1068  GTPBG3   3'  TGCAACCTCCACCTCC      50913       A
                                  GGAGGT GAGGTTGCA
                                  |||||| |||||||||
                                  CCTCCA CTCCAACGT
                                     C
GAM1068  GTPBG3   3'  TCACTGCAACCTCCATCTCC   50910       A       _
                                  GGAGGT GAGGTTGCA TGA
                                  |||||| ||||||||| |||
                                  CCTCTA CTCCAACGT ACT
                                     C        C
GAM1068  H-plk    5'  TCACTGCAACCTCCACCTCC   31812       A       _
                                  GGAGGT GAGGTTGCA TGA
                                  |||||| ||||||||| |||
                                  CCTCCA CTCCAACGT ACT
                                     C        C
GAM1068  HRH4     3'  TCACTGCAACCTCTGCCTCC   41257             _
                                  GGAGGTAGAGGTTGCA TGA
                                  |||||||||||||||| |||
                                  CCTCCGTCTCCAACGT ACT
                                           C
GAM1068  HSA404617 5'  CAACCCACCTCTGCCCC     72708    A       TGCAT A
                                  GG GGTAGAGGT     G GTTG
                                  || |||||||||     | ||||
                                  CC CCGTCTCCA     C CAAC
                                   _        _____ C
GAM1068  HSPC023  3'  CAACATCCCACCCCCTACCTCC 25909        A  T  CAT  _
                                  GGAGGTAG GG TG   GA GTTG
                                  |||||||| || ||   || ||||
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                                CCTCCATC CC AC   CT CAAC
                                     C  C  C__  A
GAM1068  HSPC065   3'  TCACTGCAACCTCCACCTCT   26324       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                TCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  HSPC065   3'  TCGCTGCAACCTCCTCCTCC   26327      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT GCT
                                  TC        C
GAM1068  ICK       3'  TCTGCAACCTCTGCCTCC    29936            T
                                GGAGGTAGAGGTTGCA GA
                                |||||||||||||||| ||
                                CCTCCGTCTCCAACGT CT
                                                _
GAM1068  JAM1      5'  TCACTGCAACCTCCTCCTCC   57934      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  TC        C
GAM1068  JM11      3'  TCACTGCAACCTCTGCCTCC   53269                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  KIAA0063  3'  CAACCCGCCCCTACCTCT    29618        A   TGCAT A
                                GGAGGTAG GGT    G GTTG
                                |||||||| |||    | ||||
                                TCTCCATC CCG    C CAAC
                                     C  _____ C
GAM1068  KIAA0063  3'  TCACTGCAACCTCCACCTCC   29641       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  KIAA0391  3'  TCACTGCAACCTCTGCCTCC   27921                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  KIAA0426  3'  TCACTGCAACCTCCGCCTCC   28265      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC        C
GAM1068  KIAA0459  3'  TCACTGCAACCTCCACCTCC   61005       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
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                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  KIAA0469  3'  TCACTGCAGCCTCCACCTCC   29351       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCGACGT ACT
                                   C        C
GAM1068  KIAA0513  3'  TCACTGCAACCTCCACCTCC   28371       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  KIAA0513  5'  TCACTGCAGCCTCCACCTCC   28373       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCGACGT ACT
                                   C        C
GAM1068  KIAA0527  3'  TCACTGCAACCTCTGCCTCC   95809               _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  KIAA0544  3'  TCACTGCAACCTCCGCCTCC   70909       TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068  KIAA0557  3'  TCACCACAACCTCCACCTC    78008       A     CA_
                                GAGGT GAGGTTG   TGA
                                ||||| |||||||   |||
                                CTCCA CTCCAAC   ACT
                                   C      ACC
GAM1068  KIAA0561  3'  TCACTGCAACCTCCGCCTC   65896       TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068  KIAA0562  3'  TGCAACCTCCGCCTCC      28160       TA
                                GGAGG  GAGGTTGCA
                                |||||  |||||||||
                                CCTCC  CTCCAACGT
                                   GC
GAM1068  KIAA0563  5'  TCACTGCAACCTCTGCCTCC   29193               _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  KIAA0599  3'  TCACTGCAACCTCCGCCTCC   77191       TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
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                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  KIAA0720  3'  TCACTGCAACCTCTGCCTCC   62330          _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                       C
GAM1068  KIAA0841  3'  TCACTGCAACCTCCGCCTCC   71397      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  |||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  KIAA0841  3'  TCACTGCAACCTCTGCCTCC   71399          _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                       C
GAM1068  KIAA1041  3'  TCACTGCAACCTCCGCCTCC   30140      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  |||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  KIAA1054  3'  TCACTGCAACCTCCGCCTCC   68450      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  |||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  KIAA1161  5'  TCACTGCAACCCCTCCTCC    81761     T A     _
                                GGAGG AG GGTTGCA TGA
                                ||||| || ||||||| |||
                                CCTCC TC CCAACGT ACT
                                  _ C      C
GAM1068  KIAA1170  3'  TCACTGCAACCTCCGCCTCC   69861      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  |||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  KIAA1193  3'  TCACTGCAACCTCCGCCTCC   67649      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  |||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  KIAA1198  3'  TCACCGCAACCTCCGCCTCC   63333      TA      A_
                                GGAGG  GAGGTTGC  TGA
                                |||||  ||||||||  |||
                                CCTCC  CTCCAACG  ACT
                                  GC       CC
GAM1068  KIAA1209  3'  TCACTGCAGCCTCCACCTCC   60762       A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| |||||||| |||
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                                CCTCCA CTCCGACGT ACT
                                   C        C
GAM1068  KIAA1257  3'  TCACCGCAACCTCCGCCTCC  62758      TA       A_
                                GGAGG  GAGGTTGC  TGA
                                |||||  ||||||||  |||
                                CCTCC  CTCCAACG  ACT
                                  GC       CC
GAM1068  KIAA1320  5'  TCACTGCAACCTCTGCCTCC  69310             _
                                GGAGGTAGAGGTTGCA TGA
                                ||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  KIAA1373  3'  TCACTGCAACCTCCACCTCC  70951       A       _
                                GGAGGT GAGGTTGCA TGA
                                ||||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  KIAA1497  5'  TCACTGCAACCTCTGCCTCC  67521             _
                                GGAGGTAGAGGTTGCA TGA
                                ||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  KIAA1500  3'  TCAACTCACAACTGAGCTACCT 64123        A__    CA
          C                      GAGGTAG   GGTTG  TGAGTTGA
                                 |||||||   |||||  ||||||||
                                 CTCCATC   TCAAC  ACTCAACT
                                    GAG    __
GAM1068  KIAA1508  3'  TCACTGCAACCTCCGCCTCC  61892      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  KIAA1571  3'  TCACCGCAACCTCCACCTCC  60961       A       A_
                                GGAGGT GAGGTTGC  TGA
                                |||||| ||||||||  |||
                                CCTCCA CTCCAACG  ACT
                                   C       CC
GAM1068  KIAA1615  3'  TCACTGCAACCTCCACCTCC  68729       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  KIAA1655  3'  TCACTGTAACCTCCACCTCC  66625       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAATGT ACT
                                   C        C
GAM1068  KIAA1655  3'  TCATTGCAACCTCCGCCTCC  66629       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
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                                CCTCC  CTCCAACGT ACT
                                  GC       T
GAM1068  KIAA1737  3'  TCACTGCAACCTCCGCCTCC  67363     TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  KIAA1784  3'  TCACTGCAACCTCCGCCTCC  65155     TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  KIAA1922  5'  TCACTGCAACCTCCGCCTCC  73642     TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  KIAA1956  3'  TCACTGCAGCCTCCACCTCC  78441      A      _
                                GGAGGT GAGGTTGCA TGA
                                ||||||| ||||||||| |||
                                CCTCCA CTCCGACGT ACT
                                   C       C
GAM1068  KIAA1971  3'  TGCAACCTCCACCTCC     74229      A
                                GGAGGT GAGGTTGCA
                                ||||||| |||||||||
                                CCTCCA CTCCAACGT
                                   C
GAM1068  KLK7      3'  TCACTGCAACCTCCGCCTCC  57737     TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  KLK7      3'  TCACTGCAACCTCCGCCTCC  17297     TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  MAP4K1    3'  CAGCAACCTCTACATCC    23206    G        A
                                GGA GTAGAGGTTGC TG
                                |||  |||||||||| ||
                                CCT CATCTCCAACG AC
                                  A        _
GAM1068  MCLC      3'  TCACTGCAACCTCCACCTCC  30692      A      _
                                GGAGGT GAGGTTGCA TGA
                                ||||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C       C
GAM1068  MEF-2     3'  TCACTGCAACCTCCGCCTCC  64396     TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
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                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  MGC13138  3'  TCACTGCAACCTCTGCCTCC   53024                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                       C
GAM1068  MGC14836  3'  TCACTGCAACCTCCGCCTCC   53040      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  |||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  MGC2474   3'  TCACTGCAACTTCCACCTCC   43730      A        _
                                GGAGGT GAGGTTGCA TGA
                                |||||| |||||||| |||
                                CCTCCA CTTCAACGT ACT
                                   C       C
GAM1068  MGC29891  3'  TCACTGCAACCTCCGCCTCC   58217      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  |||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  MGC3113   3'  TCACTGCAGCCTCCACCTCC   43851      A        _
                                GGAGGT GAGGTTGCA TGA
                                |||||| |||||||| |||
                                CCTCCA CTCCGACGT ACT
                                   C       C
GAM1068  MGC5149   3'  TCACTGCAACCTCTGCCTCC   72298                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                       C
GAM1068  MGC9912   3'  TCACTGCAACCTCCACCTCC   54723      A        _
                                GGAGGT GAGGTTGCA TGA
                                |||||| |||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C       C
GAM1068  MLZE      5'  TCACTGCAACCTCTGCCTCC   48626                  _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                       C
GAM1068  MMPL1     3'  TCACTGCAGCCTCCACCTCC   14725      A        _
                                GGAGGT GAGGTTGCA TGA
                                |||||| |||||||| |||
                                CCTCCA CTCCGACGT ACT
                                   C       C
GAM1068  MOCS3     3'  TCACTGCAACCTCCGCCTCC   27159      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  |||||||| |||
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                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  MRPL44   3'  TCACTGCAACCTCCACCTC   43326      A      _
                                GAGGT GAGGTTGCA TGA
                                ||||| ||||||||| |||
                                CTCCA CTCCAACGT ACT
                                  C       C
GAM1068  MtFMT    3'  TCACTGCAACCTCCGCCTCC   57658      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  NDUFB1   5'  TCACTGCAACCTCTGCCTCC   15820           _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                       C
GAM1068  NDUFC2   3'  TCACTGCAACCTCCACCTCC   15843      A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                  C       C
GAM1068  NSBP1    3'  CAACTTATCCCCCACCTCC   47771      AGA  TTGC
                                GGAGGT   GG   ATGAGTTG
                                ||||||   ||   ||||||||
                                CCTCCA   CC   TATTCAAC
                                  CCC  ____
GAM1068  Nup43    3'  TCACTGCAACCTCCACCTCC   45007      A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                  C       C
GAM1068  OR51E2   3'  TCACTGCAACCTCCACATCC   47798    G  A      _
                                GGA GT GAGGTTGCA TGA
                                ||| || ||||||||| |||
                                CCT CA CTCCAACGT ACT
                                 A  C       C
GAM1068  OSBPL2   3'  TCACCGCAACCTCCGCCTCC   29220     TA      A_
                                GGAGG  GAGGTTGC  TGA
                                |||||  |||||||  |||
                                CCTCC  CTCCAACG  ACT
                                  GC       CC
GAM1068  OSBPL2   3'  TCACCGCAACCTCCGCCTCC   57871     TA      A_
                                GGAGG  GAGGTTGC  TGA
                                |||||  |||||||  |||
                                CCTCC  CTCCAACG  ACT
                                  GC       CC
GAM1068  PASK     5'  TCACTGCAACCTCTGCCTCC   30725           _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
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                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068 PELI1    5' TCACTGCAACCTCCTCCTCC  40284      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   TC        C
GAM1068 PELI1    5' TCACTGCAACCTCTGCCTCC  40286              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068 PIP3-E   3' TCACTGCAACCTCTGCCTCC  66813              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068 PRO0365  5' TCACTGCAACCTCCACCTCC  26169       A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068 PRO1992  5' TCACTGCAACCTCTGCCTCC  26062              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068 PRO2955  3' TCACTGCAACCTCTGCCTCC  37646              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068 PSTPIP2  3' TCACTGCAACCTCTGCCTCC  44397              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068 RAB33B   3' TCACTGCAACCTCCGCCTCC  48507      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068 RAI      5' TCACTGCAACCTCCGCCTCC  21887      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068 RASGRP4  3' AGCTGAACAACCTCTACCTGC 53648   G         CATG
                                G AGGTAGAGGTTG   AGTT
                                | ||||||||||||   ||||
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                                C TCCATCTCCAAC    TCGA
                                 G          AAG_
GAM1068  RNF8     3'  TCACTGCAACCTCCACCTCC  14240       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  SC4MOL   3'  TCACTGCAACCTCTGCCTCC  22162              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  SCAMP-4  3'  TCACTGCAACCTCTGCCTCC  54400              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  SCYA16   3'  TCACTGTAACCTCCACCTCC  15968       A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAATGT ACT
                                   C        C
GAM1068  SERF1B   3'  CATGCAACCTCTGCCTCC    43413
                                GGAGGTAGAGGTTGCATG
                                ||||||||||||||||||
                                CCTCCGTCTCCAACGTAC

GAM1068  SERF1B   3'  TCACTGCAACCTCCGCCTCC  43423       TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC        C
GAM1068  SLC11A1  3'  TCATTGCAACCTCCACCTTC  59461       A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CTTCCA CTCCAACGT ACT
                                   C        T
GAM1068  SLC2A10  3'  TCACTGCAACCTCCACTTCC  47828       A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTTCA CTCCAACGT ACT
                                   C        C
GAM1068  SP2      3'  GCCACAACCTCTCCTCC     11891       T      CA  A
                                GGAGG AGAGGTTG  TG GT
                                ||||| ||||||||  || ||
                                CCTCC TCTCCAAC  AC CG
                                  _       __  _
GAM1068  STAF65(gamma) 3'  TCACTGCAACCTCTGCCTCC  29444              _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
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                                  CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  SUN1     3'  TCACTGCAGCCTCCACCTCC  47162       A       _
                                  GGAGGT GAGGTTGCA TGA
                                  |||||| ||||||||| |||
                                  CCTCCA CTCCGACGT ACT
                                     C        C
GAM1068  SYT13    3'  TCACTGCAACCTCCGCCTCC  93459       TA      _
                                  GGAGG  GAGGTTGCA TGA
                                  |||||  ||||||||| |||
                                  CCTCC  CTCCAACGT ACT
                                    GC        C
GAM1068  TRIM5    3'  TCACTGCAACCTCCACCTCT  52303       A       _
                                  GGAGGT GAGGTTGCA TGA
                                  |||||| ||||||||| |||
                                  TCTCCA CTCCAACGT ACT
                                     C        C
GAM1068  TRIM6    3'  TCACTGCAACCTCTGCCTCC  54145               _
                                  GGAGGTAGAGGTTGCA TGA
                                  |||||||||||||||| |||
                                  CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  TU12B1-TY 3'  TCACTGCAACCTCTGCCTCC  33405             _
                                  GGAGGTAGAGGTTGCA TGA
                                  |||||||||||||||| |||
                                  CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  TUCAN    3'  TCACTGCAACCTCTGCCTCC  30282             _
                                  GGAGGTAGAGGTTGCA TGA
                                  |||||||||||||||| |||
                                  CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  UBF-fl   3'  TCACTGCAACCTCTGCCTCC  51572             _
                                  GGAGGTAGAGGTTGCA TGA
                                  |||||||||||||||| |||
                                  CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  USP22    3'  TCACTGCAACCTCCACCTCC  68024       A       _
                                  GGAGGT GAGGTTGCA TGA
                                  |||||| ||||||||| |||
                                  CCTCCA CTCCAACGT ACT
                                     C        C
GAM1068  VDU1     3'  TCACTGCAGCCTCCACCTCC  30427       A       _
                                  GGAGGT GAGGTTGCA TGA
                                  |||||| ||||||||| |||
                                  CCTCCA CTCCGACGT ACT
                                     C        C
GAM1068  VPS33A   3'  TCACTGCAACCTCCACCTCC  43344       A       _
                                  GGAGGT GAGGTTGCA TGA
                                  |||||| ||||||||| |||
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                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  WBSCR20A  5'  TCACCGCAACCTCTGCCTCC  49657            A_
                                GGAGGTAGAGGTTGC  TGA
                                |||||||||||||||  |||
                                CCTCCGTCTCCAACG  ACT
                                      CC
GAM1068  ZTL1      3'  TCACTGCAACCTCTGCCTCC  43920             _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068  LOC112724 5'  TCACTGCAACCTCCACCTCC  56502       A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC113675 5'  TCACTGCAACCTCCGCCTCC  56573       TA     _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068  LOC115219 5'  TCACTGCAACCTCCGCCTCC  73321       TA     _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068  LOC116411 5'  GCTACAACCTCCACCTC     73866       A      CATG
                                GAGGT GAGGTTG    AGT
                                ||||| |||||||    |||
                                CTCCA CTCCAAC    TCG
                                   C      A___
GAM1068  LOC120114 3'  TCACTGCAATCTCCACCTCC  75538       A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCTAACGT ACT
                                   C        C
GAM1068  LOC120939 3'  TCACTGTAACCTCCACCTCC  76261       A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAATGT ACT
                                   C        C
GAM1068  LOC126364 3'  TCACTGCAACCTCCGCCTCC  75699       TA     _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068  LOC126661 3'  TCACTGCAACCTCCGCCTCC  74558       TA     _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
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                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  LOC128077 3'  TCACTGCAACCTCCGCCTCC   74719      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  LOC128077 3'  TCACTGCAACCTCTGCCTCC   74721            _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1068  LOC128387 3'  TCACTGCAACCTCCACTTCC   74753       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTTCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC128989 3'  TCACTGCAACCTCCGCCTCC   74817      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  LOC130813 3'  TCACCGCAACCTCCGCCTCC   75777      TA       A_
                                GGAGG  GAGGTTGC  TGA
                                |||||  |||||||  |||
                                CCTCC  CTCCAACG  ACT
                                   GC       CC
GAM1068  LOC132625 3'  TCACTGCAACCTCCACCTCC   75914       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC133686 3'  TCTGCAACCTCCATCTCC     75126       A       T
                                GGAGGT GAGGTTGCA GA
                                |||||| ||||||||| ||
                                CCTCTA CTCCAACGT CT
                                   C        _
GAM1068  LOC135293 3'  TCACTGCAACCTCTGCCTCC   76192            _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1068  LOC135763 3'  TCACTGCAACCTCCGCCTCC   56793      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  LOC142913 5'  CACTGCAGCCTCCACCTCC    76416       A       _
                                GGAGGT GAGGTTGCA TG
                                |||||| ||||||||| ||
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                                CCTCCA CTCCGACGT AC
                                   C        C
GAM1068  LOC143187 3'  TCACTGCAACCTCCACCTCC   59102       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC143241 5'  TCACTGCAACCTCTGCCTCC   57180               _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  LOC144248 5'  TCACTGCAACCTCCACCTCC   76746       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC144317 5'  TCAACTCACTGCAACCTCTTCC 76799       T       _
                 TCC                GGAGG AGAGGTTGCA TGAGTTGA
                                |||||| |||||||||| ||||||||
                                CCTCC TCTCCAACGT ACTCAACT
                                   T        C
GAM1068  LOC144524 5'  TCACTGCAACCTCCACCTCC   83136       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC145268 5'  TCACTGCAACCTCCACC     77060     A       _
                                GGT GAGGTTGCA TGA
                                ||| ||||||||| |||
                                CCA CTCCAACGT ACT
                                  C        C
GAM1068  LOC145725 3'  TCACTGCAGCCTCCACCTCC   77415       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCGACGT ACT
                                   C        C
GAM1068  LOC145732 3'  TCACTGCAGCCTCCACCTCC   77437       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCGACGT ACT
                                   C        C
GAM1068  LOC145757 5'  TCACTACAACCTCTGCCTCC   77474             CA_
                                GGAGGTAGAGGTTG   TGA
                                ||||||||||||||   |||
                                CCTCCGTCTCCAAC   ACT
                                         ATC
GAM1068  LOC146229 3'  TCACTGCAACCTCCACCTCC   77772       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
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                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC146229 3'  TGCAACCTCCACCTCC      77783        A
                                GGAGGT GAGGTTGCA
                                |||||| |||||||||
                                CCTCCA CTCCAACGT
                                   C
GAM1068  LOC146784 5'  TCACTGCAACCTCCACCTCC   78125        A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC146901 3'  TCATTGCAACCTCCACCTTC   83849        A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CTTCCA CTCCAACGT ACT
                                   C        T
GAM1068  LOC146909 3'  TCACTGCAACCTCCGCCTCC   78184        TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC        C
GAM1068  LOC146952 5'  TCACTGCAACCTCCACCTCT   83873        A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                TCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC147071 5'  TCACTGCAACCTCTGCCTCC   73006                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  LOC147407 3'  TCACTGCAACCTCCGCCTCC   76327        TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC        C
GAM1068  LOC147660 3'  TCACAGCAACCTCCGCCTCC   78397        TA       A_
                                GGAGG  GAGGTTGC  TGA
                                |||||  ||||||||  |||
                                CCTCC  CTCCAACG  ACT
                                  GC        AC
GAM1068  LOC147817 3'  TCACTGCAACCTCCACCTCC   78505        A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC147841 3'  TCACAGCAACCTCTGCCTCC   78533                A_
                                GGAGGTAGAGGTTGC  TGA
                                |||||||||||||||  |||
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                                CCTCCGTCTCCAACG  ACT
                                      AC
GAM1068  LOC148137 3'  TCACGGCAACCTCCACCTCC   58440       A       A_
                                GGAGGT GAGGTTGC  TGA
                                |||||| ||||||||  |||
                                CCTCCA CTCCAACG  ACT
                                   C       GC
GAM1068  LOC148189 5'  TCACTGCAACCTCCACCTCC   78722       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C       C
GAM1068  LOC148198 3'  TCACTGCAACCTCCATCTCC   70689       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCTA CTCCAACGT ACT
                                   C       C
GAM1068  LOC148918 5'  CAACTCAGCTTCTTCTACCTCC 79062           TT  A
                                GGAGGTAGAGG  GC TGAGTTG
                                |||||||||||  || |||||||
                                CCTCCATCTTC  CG ACTCAAC
                                      TT  _
GAM1068  LOC148918 5'  TCACTGCAGCCTCCACCTCC   79083       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCGACGT ACT
                                   C       C
GAM1068  LOC149506 3'  TCACTGCAACCTCTGCCTCC   84478               _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068  LOC149506 3'  TCACTGCAACTTCCACCTCC   84480       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTTCAACGT ACT
                                   C       C
GAM1068  LOC149577 3'  TCACCACAACCTCCACCTC    84520       A      CA_
                                GAGGT GAGGTTG   TGA
                                ||||| |||||||   |||
                                CTCCA CTCCAAC   ACT
                                   C       ACC
GAM1068  LOC149703 5'  ATGCAACCTCTACCTCC      84648
                                GGAGGTAGAGGTTGCAT
                                |||||||||||||||||
                                CCTCCATCTCCAACGTA

GAM1068  LOC150397 3'  TCATTGCAACCTCCGCCTCC   79851       TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
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                                CCTCC  CTCCAACGT ACT
                                  GC       T
GAM1068  LOC150519 3'  TCTGCAACCTGCCACCTCC   79924      AG_      T
                                GGAGGT   AGGTTGCA GA
                                ||||||   |||||||| ||
                                CCTCCA   TCCAACGT CT
                                   CCG      _
GAM1068  LOC150696 3'  TCACTGCAGCCTCCACCTCC   58488      A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCGACGT ACT
                                   C        C
GAM1068  LOC150960 3'  TCGCTGCAACCTCCGCCTCC   80073      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT GCT
                                  GC        C
GAM1068  LOC151057 3'  TCACTGCAACCTCTGCCTCC   85216               _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1068  LOC151201 3'  TCACTGCAACCTCCACCTCC   85291      A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC151475 5'  TCACTGCAACCTCCACCTCC   85417      A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC151475 5'  TCACTGCAACCTCTGCCTCC   85419               _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1068  LOC151826 3'  TCACTGCAACCTCCGCCTCC   80366      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC        C
GAM1068  LOC152343 3'  TCAGTGCAACCTCCGCCTCC   80570      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC        G
GAM1068  LOC152445 3'  TCACTGCAACCTCTGCCTCC   85761               _
                                GGAGGTAGAGGTTGCA TGA
                                ||||||||||||||| |||
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                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068  LOC152582 5'  TCACCGCAACCTCTGCCTCC   85794           A_
                                GGAGGTAGAGGTTGC  TGA
                                |||||||||||||||  |||
                                CCTCCGTCTCCAACG  ACT
                                      CC
GAM1068  LOC152620 3'  TCACTACAACCTCTGCCTCC   60087          CA_
                                GGAGGTAGAGGTTG   TGA
                                ||||||||||||||   |||
                                CCTCCGTCTCCAAC   ACT
                                      ATC
GAM1068  LOC152719 5'  TCACTGCAACCTCTGCCTCC   85856           _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068  LOC152794 5'  TCACTGCAACCTCTACCTCC   80683           _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCATCTCCAACGT ACT
                                      C
GAM1068  LOC153077 3'  TCACTGCAACCTCCGCCTCC   85917      TA     _
                                GGAGG  GAGGTTGCA TGA
                                |||||  |||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  LOC153688 3'  TCACTGCAACCTCCACCTCC   86121       A     _
                                GGAGGT GAGGTTGCA TGA
                                |||||| |||||||| |||
                                CCTCCA CTCCAACGT ACT
                                    C        C
GAM1068  LOC154075 3'  TCACTGCAACCTCCGCCTCC   81049      TA     _
                                GGAGG  GAGGTTGCA TGA
                                |||||  |||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  LOC154282 5'  TCACTGCAACCTCCACCTCC   86208       A     _
                                GGAGGT GAGGTTGCA TGA
                                |||||| |||||||| |||
                                CCTCCA CTCCAACGT ACT
                                    C        C
GAM1068  LOC154877 3'  TCACTGCAACCTCTACCTCC   86309           _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCATCTCCAACGT ACT
                                      C
GAM1068  LOC157247 5'  TCACTGCAACCTCCACCCC    81376    A  A     _
                                GG GGT GAGGTTGCA TGA
                                || ||| |||||||| |||
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                                CC CCA CTCCAACGT ACT
                                 _  C       C
GAM1068  LOC157798 5'  TCACTGCAACCTCCGCCTCC   86552      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068  LOC157858 5'  TCACTGCAACCTCTGCCTCC   86603             _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  LOC158476 3'  TCACTGCAACCTCCGCCCC    86852    A  TA      _
                                GG GG  GAGGTTGCA TGA
                                || ||  ||||||||| |||
                                CC CC  CTCCAACGT ACT
                                 _ GC       C
GAM1068  LOC158668 3'  TCACTGCAACCTCTGCCTCC   69375             _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  LOC158865 5'  TCACTGCAACCTCTGCCTCC   86941             _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  LOC161829 3'  TCACTGCAACCTCCGCCTCC   82322      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068  LOC196047 5'  TCACTGCAACCTCCGCCTCC   89611      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068  LOC196264 3'  TCACTGCAACCTCTGCCTCC   87614             _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  LOC196411 3'  TCACTGCAACCTCCGCCTCC   87686      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC       C
GAM1068  LOC196529 3'  TCACTGCAACCTCCACCTC    87780      A       _
                                GAGGT GAGGTTGCA TGA
                                |||||  ||||||||| |||
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                                CTCCA CTCCAACGT ACT
                                  C       C
GAM1068  LOC196957 3'  TCACTGCAGCCTCCACCTCC  87830      A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCGACGT ACT
                                  C       C
GAM1068  LOC196961 3'  TCACTGCAGCCTCCACCTCC  87851      A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCGACGT ACT
                                  C       C
GAM1068  LOC197138 3'  TCACTGCAGCCTCCACCTCC  87924      A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCGACGT ACT
                                  C       C
GAM1068  LOC197358 3'  TGCAACCTCCGCCTCC     88053      TA
                                GGAGG  GAGGTTGCA
                                |||||  |||||||||
                                CCTCC  CTCCAACGT
                                  GC
GAM1068  LOC199786 3'  TCACTGCAACCTCCGCCTCC  88392      TA     _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  LOC200014 3'  TCGCTGCAACCCCCACCTC   88542      AGA    _
                                GAGGT   GGTTGCA TGA
                                |||||   ||||||| |||
                                CTCCA   CCAACGT GCT
                                  CCC     C
GAM1068  LOC200169 5'  TCACTGCAACCTCTGCCTCC  89958          _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  LOC200268 3'  TCACTGCAACCTCTGCCTCC  88692          _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  LOC200310 3'  TCACTACAACCTCTGCCTCC  65742          CA_
                                GGAGGTAGAGGTTG   TGA
                                ||||||||||||   |||
                                CCTCCGTCTCCAAC   ACT
                                       ATC
GAM1068  LOC200314 3'  TCACTGCAACCTCCACCTCC  90017      A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
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                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC200339 3'  TCACTGCAACCTCTGCCTCC   90040                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  LOC200860 3'  TCACTGCAACCTCCACCTCC   90176       A        _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC201173 5'  TCACTGCAACCTCTGCCTCC   87335                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  LOC201220 5'  TCACTGCAACCTCTGCCTCC   87356                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  LOC201294 3'  TCACTGCAACCTCCGCCTCC   88221       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  LOC201294 3'  TCACTGCAACCTCCGCCTCC   88222       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  LOC201411 3'  TCACTGCAACCTCTGCCTCC   62961                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  LOC201626 3'  TCACTGCAACCTCCGCCCC    88997    A  TA       _
                                GG GG  GAGGTTGCA TGA
                                || ||  ||||||||| |||
                                CC CC  CTCCAACGT ACT
                                 _ GC        C
GAM1068  LOC201627 3'  TGCAACCTCCACCTCC       89029       A
                                GGAGGT GAGGTTGCA
                                |||||| |||||||||
                                CCTCCA CTCCAACGT
                                   C
GAM1068  LOC202025 3'  TCACTGCAACCTCCGCCTCC   90298       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
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                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  LOC202934 3'  TCACTACAACCTCTGCCTCC   90429           CA_
                                GGAGGTAGAGGTTG   TGA
                                |||||||||||||   |||
                                CCTCCGTCTCCAAC   ACT
                                      ATC
GAM1068  LOC203297 5'  TCACTGCAACCTCTGCCTCC   75354            _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068  LOC203350 3'  TCAACTGACTGCAACCTCCGCC 90572      TA       TG_
            TCC                   GGAGG  GAGGTTGCA   AGTTGA
                                |||||  |||||||||   ||||||
                                CCTCC  CTCCAACGT   TCAACT
                                   GC        CAG
GAM1068  LOC203378 3'  TCACGGCAACCTCTGCCTCC   90616            A_
                                GGAGGTAGAGGTTGC  TGA
                                ||||||||||||||  |||
                                CCTCCGTCTCCAACG  ACT
                                      GC
GAM1068  LOC204804 3'  TCACTGCAACCTCGACCTCC   89486       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   G        C
GAM1068  LOC219735 3'  TCACTGCAACCTCTGCCTCC   93116            _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                      C
GAM1068  LOC220662 3'  TCACTGCAACCTCCACCTCC   91180       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC220662 3'  TCACTGCAACCTCCACTTCC   91182       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTTCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC221035 3'  TCACTACAACCTCTGCCTCC   93170           CA_
                                GGAGGTAGAGGTTG   TGA
                                |||||||||||||   |||
                                CCTCCGTCTCCAAC   ACT
                                      ATC
GAM1068  LOC221174 5'  TCACTGCGACCTCCACCTCC   93505       A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
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                                CCTCCA CTCCAGCGT ACT
                                   C        C
GAM1068  LOC221271 3'  TCACTGCAACCTCTGCCTCC   91875                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  LOC221296 3'  TCACTGCAACCTCCACCTCC   91971        A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC221663 5'  TCACTGCAACCTCCACCTCC   93823        A       _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068  LOC222070 5'  TCACTGCAACCTCTGCCTCC   94161                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         C
GAM1068  LOC253612 5'  TCACTGCAACCTCCGCCTCC   96757       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  LOC253664 3'  TCATTGCAACCTCTGCCTCC   94816                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                         T
GAM1068  LOC253666 5'  TCACTGCAACCTCCGCCTCC   95068       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  LOC255497 3'  TCACTGCAACCTCCGCCTCC   97195       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  LOC255919 3'  TCTGCAACCTCTGCCTCC     95042                T
                                GGAGGTAGAGGTTGCA GA
                                |||||||||||||||| ||
                                CCTCCGTCTCCAACGT CT
                                         _
GAM1068  LOC256267 3'  TCACTGCAACCTCCGCCTCC   96808       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
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                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  LOC256306 3'  TCACTGCAACCTCCACCTCC  96697      A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C       C
GAM1068  LOC51008  5'  TCACAGCAACCTCTGCCTCC  31970          A_
                                GGAGGTAGAGGTTGC  TGA
                                |||||||||||||||  |||
                                CCTCCGTCTCCAACG  ACT
                                        AC
GAM1068  LOC51200  3'  TCACCACAACCTCTGCCTCC  33003          CA_
                                GGAGGTAGAGGTTG   TGA
                                ||||||||||||||  |||
                                CCTCCGTCTCCAAC   ACT
                                        ACC
GAM1068  LOC51219  5'  TCACCGCAACCTCCGCCTCC  33127      TA      A_
                                GGAGG  GAGGTTGC  TGA
                                |||||  ||||||||  |||
                                CCTCC  CTCCAACG  ACT
                                  GC       CC
GAM1068  LOC51696  3'  TCACTGCAACCTCTGCCTCC  32557          _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                        C
GAM1068  LOC57107  3'  TCACTGCAACCTCCGCCTCC  39843      TA      _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC       C
GAM1068  LOC57146  3'  TCACTGCAACCTCCAACTCC  39928     GTA      _
                                GGAG   GAGGTTGCA TGA
                                ||||   ||||||||| |||
                                CCTC   CTCCAACGT ACT
                                  AAC       C
GAM1068  LOC81034  3'  TCACTGCAACCTCCACCTCC  47857      A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C       C
GAM1068  LOC89932  3'  TCACTGCAACCTCCACCTCC  60816      A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C       C
GAM1068  LOC90288  3'  TCACTGCAACCTCCACCTCC  62104      A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
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                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068 LOC90333 5' TCACTGCAACCTCCACTTCC  62298      A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTTCA CTCCAACGT ACT
                                   C        C
GAM1068 LOC90333 3' TCACTGCAACCTCCTCCTCC  62300      TA     _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  TC        C
GAM1068 LOC90371 5' TCACTGCAACCTCCACCTCC  62503      A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068 LOC90408 5' TCACTGCAACCTCTACCTCC  62668             _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCATCTCCAACGT ACT
                                         C
GAM1068 LOC90459 3' TCACTGCAACCTCCGCCTCC  62893      TA     _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC        C
GAM1068 LOC90485 3' TCACTGCAACCTCCGCCTCC  63026      TA     _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC        C
GAM1068 LOC91115 3' TCACTGCAACCTCCACCTCC  64949      A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068 LOC91115 3' TCACTGCAACCTCCGCCTCC  64951      TA     _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                  GC        C
GAM1068 LOC92267 3' TCACTGCAACCTCCACCTCC  68624      A      _
                                GGAGGT GAGGTTGCA TGA
                                |||||| ||||||||| |||
                                CCTCCA CTCCAACGT ACT
                                   C        C
GAM1068 LOC92466 3' TCACTGCAACCTCCGCCTCC  69433      TA     _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
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                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  LOC92689  3'  TCACTGCAACCTCCGCCTCC   70229       TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  LOC92697  5'  GCTACAACCTCCACCTC     70273      A      CATG
                                GAGGT GAGGTTG    AGT
                                |||||  |||||||    |||
                                CTCCA CTCCAAC    TCG
                                   C      A___
GAM1068  LOC92697  5'  TCACCGCAACCTCCGCCTCC   70279      TA       A_
                                GGAGG  GAGGTTGC  TGA
                                |||||  ||||||||  |||
                                CCTCC  CTCCAACG  ACT
                                   GC       CC
GAM1068  LOC92841  3'  TCACCGCAACCTCCTCCTCC   70722      TA       A_
                                GGAGG  GAGGTTGC  TGA
                                |||||  ||||||||  |||
                                CCTCC  CTCCAACG  ACT
                                   TC       CC
GAM1068  LOC93132  5'  TCACTGCAACCTCCGCCTCC   71501      TA       _
                                GGAGG  GAGGTTGCA TGA
                                |||||  ||||||||| |||
                                CCTCC  CTCCAACGT ACT
                                   GC        C
GAM1068  LOC93349  3'  TCACTGCAACCTCTGCCTCC   56465                _
                                GGAGGTAGAGGTTGCA TGA
                                |||||||||||||||| |||
                                CCTCCGTCTCCAACGT ACT
                                          C
GAM1069  ACADM     3'  ATTTCATATGTTTGCATTTTGG 3403           T    GCAGGAT
              C                  GCCAAGATGCAG CATA
                                 |||||||||||| ||||
                                 CGGTTTTACGTT GTAT
                                       T    ACTTTA
GAM1069  ADAM12    3'  CCAGGCTGTGTTTGGC      12969      A       ATAGCA
                                 GCCA GATGCAGTC     GG
                                 ||||  |||||||||    ||
                                 CGGT TTGTGTCGG     CC
                                   _       A_____
GAM1069  AGA       3'  GTATGTGGCTGTATTTTG    3444              _
                                 CAAGATGCAGTCATA GC
                                 |||||||||||||| ||
                                 GTTTTATGTCGGTGT TG
                                          A
GAM1069  AK1       3'  TCTTGCTCTGTGCCTTGGC   4888        AT    TCAT
                                 GCCAAG  GCAG   AGCAGGA
                                 ||||||  ||||   |||||||
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                                CGGTTC  TGTC    TCGTTCT
                                   CG   ____
GAM1069  AMD1     3'  GTTTTGTTTTTGTTTTGTTTTG 7900          C  T  T_
                GT                   GCCAAGATG AG CA  AGCAGGAT
                                     |||||||||  || ||  ||||||||
                                     TGGTTTTGT TT GT  TTGTTTTG
                                        T  _  TT
GAM1069  BAZ1B    3'  GTCTTTTGAGTTGATCTTGGC  50540         G  _  TAGC
                                     GCCAAGAT CAG TCA    AGGAT
                                     ||||||||  ||| |||    |||||
                                     CGGTTCTA GTT AGT    TTCTG
                                        _  G  T___
GAM1069  CALCR    3'  GTCTTAATGTTGAATGTATTTT 8221           G  _  GC
                GGT                    GCCAAGATGCA TCA TA  AGGAT
                                     ||||||||||  ||| ||  |||||
                                     TGGTTTTATGT AGT GT  TTCTG
                                           A  T  AA
GAM1069  CIS4     3'  TCTTGGGTTTATTTTGGT    14879          C GT ATAG
                                     GCCAAGATG A  C    CAGGA
                                     |||||||||  |  |    |||||
                                     TGGTTTTAT T  G    GTTCT
                                        _ TG _____
GAM1069  CR1L     3'  GTCTGCTAGTCATTGTGTCTTG 89404            CA_      AT
                GC                     GCCAAGATGCAGT   TAGCAGG
                                     ||||||||||||   |||||||
                                     CGGTTCTGTGTTA   ATCGTCT
                                           CTG      G
GAM1069  CRI1     3'  ATTTTGTTTGTACATGTATCTT 26761          _  _  T
                G                      CAAGATGCA GT CA AGCAGGAT
                                     |||||||||  || || ||||||||
                                     GTTCTATGT CA GT TTGTTTTA
                                        A  T  _
GAM1069  CUL3     3'  TCTTGCAGCTGTGTTTTGG    13167           CATA
                                     CCAAGATGCAGT    GCAGGA
                                     ||||||||||||    ||||||
                                     GGTTTTGTGTCG    CGTTCT
                                           A___
GAM1069  CUL5     3'  TCCTAATTGTATTTTGG     12977           CATAGC
                                     CCAAGATGCAGT     AGGA
                                     ||||||||||||     ||||
                                     GGTTTTATGTTA     TCCT
                                           A_____
GAM1069  DPYS     3'  GTCTTTCTCACTGTGTTTTTGT 7286     C        CAT  C
                                     GC AAGATGCAGT   AG AGGAT
                                     || ||||||||||   || |||||
                                     TG TTTTGTGTCA   TC TTCTG
                                      T        C__  T
GAM1069  DR1      3'  TTTTGTATGCATCTTGGT    59373           GTCATA
                                     GCCAAGATGCA     GCAGGA
                                     ||||||||||      ||||||
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                                TGGTTCTACGT     TGTTTT
                                      A_____
GAM1069  EGLN2    5'  TCCTGTTGTGGCAGTGGC    34105      AGATGCA
                                GCCA      GTCATAGCAGGA
                                ||||      ||||||||||||
                                CGGT      CGGTGTTGTCCT
                                  GA_____
GAM1069  EIF1A    3'  ATTTTGATTGGGTTGCATTTTT 88601    C       GT ATAG
              GT                  GC AAGATGCA  C    CAGGAT
                                || ||||||||  |    ||||||
                                TG TTTTACGT  G    GTTTTA
                                 T       TG GTTA
GAM1069  ETV5     3'  GTTTTGTTTGTGTTTTTGGT   15489        _    T  T
                                GCCAAGA TGCAG CA AGC
                                ||||||| ||||| || |||
                                TGGTTTT GTGTT GT TTG
                                    T    T  T
GAM1069  FGF5     3'  CTATGATTTATTTTGGT     15540         C
                                GCCAAGATG AGTCATAG
                                |||||||||  ||||||||
                                TGGTTTTAT TTAGTATC
                                      _
GAM1069  FGF5     3'  CTATGATTTATTTTGGT     52486         C
                                GCCAAGATG AGTCATAG
                                |||||||||  ||||||||
                                TGGTTTTAT TTAGTATC
                                      _
GAM1069  FGF7     3'  TGTGACTATGTCTTGGC     8888          GC
                                GCCAAGAT  AGTCATA
                                ||||||||  |||||||
                                CGGTTCTG  TCAGTGT
                                    TA
GAM1069  FIGF     3'  GTTTTGTTTTTGTTTTTTGGT  15557        T    TCAT
                                GCCAAGA GCAG    AGCAGGAT
                                ||||||| ||||    ||||||||
                                TGGTTTT TGTT    TTGTTTTG
                                    T   T___
GAM1069  FMR1     3'  GTCCTGTGTCAGTTTATGTTTT 8938          GC  TCATA_
              GGT                   GCCAAGAT  AG     GCAGGAT
                                ||||||||  ||     |||||||
                                TGGTTTTG  TT     TGTCCTG
                                    TA  TGACTG
GAM1069  GRIN2A   3'  ATTTTGTTGTTGTTGTTGTTGG 5894       GAT    TC
              C                   GCCAA   GCAG  ATAGCAGGAT
                                |||||   ||||  ||||||||||
                                CGGTT   TGTT  TGTTGTTTTA
                                  GT_   GT
GAM1069  HADHB    3'  GTGGGTGGTTGTTTTTGGT   3941         T  GT   A_
                                GCCAAGA GCA  CAT  GC
                                ||||||| |||  |||  ||
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                                TGGTTTT TGT  GTG  TG
                                    _  TG   GG
GAM1069  HMGB3    3'  TTCTGCTGCCATCTTAGC    18073    C     CAGTCA
                                GC AAGATG     TAGCAGGA
                                || ||||||     ||||||||
                                CG TTCTAC     GTCGTCTT
                                 A     C_____
GAM1069  HNRPK    3'  TTTTGTGTAGTATCTTGGC    9251          AGTCATA
                                GCCAAGATGC      GCAGGA
                                ||||||||||      ||||||
                                CGGTTCTATG      TGTTTT
                                      ATG____
GAM1069  HNRPK    3'  TTTTGTGTAGTATCTTGGC    48361         AGTCATA
                                GCCAAGATGC      GCAGGA
                                ||||||||||      ||||||
                                CGGTTCTATG      TGTTTT
                                      ATG____
GAM1069  HSPB3    5'  GTGATTGCGTCTGGGC      20871     A
                                GCC AGATGCAGTCAT
                                ||| ||||||||||||
                                CGG TCTGCGTTAGTG
                                  G
GAM1069  HTR4     3'  TTCTGACTTTGATCTTGGC    6031        TGCAG   T  _
                                GCCAAGA    TCA AG CAGGA
                                |||||||    ||| || |||||
                                CGGTTCT    AGT TC GTCTT
                                    _____  T  A
GAM1069  JMJ      3'  TCTGTTATTTTTTGGT      17134        TGCAGTC
                                GCCAAGA      ATAGCAGG
                                |||||||      ||||||||
                                TGGTTTT      TATTGTCT
                                   T_______
GAM1069  MAP1A    3'  GTCTTGTTGTGGGGACTTGG  9902       ATGCAG
                                CCAAG     TCATAGCAGGAT
                                |||||     ||||||||||||
                                GGTTC     GGTGTTGTTCTG
                                  AGG___
GAM1069  MAP3K9   3'  CTGTGATTGATTTTGGT     60705        G
                                GCCAAGAT CAGTCATAG
                                |||||||| |||||||||
                                TGGTTTTA GTTAGTGTC
                                    _
GAM1069  MCCC2    3'  GTTTTGCTGGTTATGCTTGGT 42138      GAT   GTCA
                                GCCAA   GCA   TAGCAGGAT
                                |||||   |||   |||||||||
                                TGGTT   CGT   GTCGTTTTG
                                  ___   ATTG
GAM1069  MTCP1    5'  TTCTGTTCAGTATTTGGC    26436     A    AGTCAT
                                GCCA GATGC     AGCAGGA
                                |||| |||||     |||||||
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                              CGGT TTATG     TTGTCTT
                                _    AC____
GAM1069  NIPSNAP1  3'  GTCCTGCTGTCTTGGTTTTGTC 13292       C GT  ___
             TTGGC                  AAGATG A  CA   TAGCAGGAT
                              ||||||| |  ||   |||||||||
                              TTCTGT T  GT   GTCGTCCTG
                                 T TG  TCT
GAM1069  NOS1     3'  ATCTTGTTGTTCAGTTTGG   5242       A  CAGTC
                              CCAAG TG    ATAGCAGGAT
                              ||||| ||    ||||||||||
                              GGTTT AC    TGTTGTTCTA
                                 G  T____
GAM1069  ORC4L    3'  GTCTTGGCTGTGTCTTG     62057           TA
                              CAAGATGCAGTCA  GC
                              ||||||||||||  ||
                              GTTCTGTGTCGGT  TG
                                      TC
GAM1069  PARK2    3'  TTTTGCTAATACATTTGGC    15864      A   CAGTCA
                              GCCA GATG     TAGCAGGA
                              |||| ||||     ||||||||
                              CGGT TTAC     ATCGTTTT
                                _   ATA___
GAM1069  PARK2    3'  TTTTGCTAATACATTTGGC    25670      A   CAGTCA
                              GCCA GATG     TAGCAGGA
                              |||| ||||     ||||||||
                              CGGT TTAC     ATCGTTTT
                                _   ATA___
GAM1069  PARK2    3'  TTTTGCTAATACATTTGGC    25673      A   CAGTCA
                              GCCA GATG     TAGCAGGA
                              |||| ||||     ||||||||
                              CGGT TTAC     ATCGTTTT
                                _   ATA___
GAM1069  PCBP1    3'  GTTTTGTTTTGGGTTTTTTGGC 20568        T  AG   T
                              GCCAAGA GC  TCA AGCAGGAT
                              ||||||| ||  ||| ||||||||
                              CGGTTTT TG  GGT TTGTTTTG
                                  T __  T
GAM1069  PCDHA1   3'  CTGTGACTTGTCTTGGT     48592         C
                              GCCAAGATG AGTCATAG
                              ||||||||| ||||||||
                              TGGTTCTGT TCAGTGTC
                                        _
GAM1069  PCDHA1   3'  CTGTGACTTGTCTTGGT     38181         C
                              GCCAAGATG AGTCATAG
                              ||||||||| ||||||||
                              TGGTTCTGT TCAGTGTC
                                        _
GAM1069  PCDHA10  3'  CTGTGACTTGTCTTGGT     38189         C
                              GCCAAGATG AGTCATAG
                              ||||||||| ||||||||
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                                TGGTTCTGT TCAGTGTC
                                          _
GAM1069  PCDHA10  3'  CTGTGACTTGTCTTGGT    49025       C
                                GCCAAGATG AGTCATAG
                                ||||||||| ||||||||
                                TGGTTCTGT TCAGTGTC
                                          _
GAM1069  PCDHA11  3'  CTGTGACTTGTCTTGGT    38199       C
                                GCCAAGATG AGTCATAG
                                ||||||||| ||||||||
                                TGGTTCTGT TCAGTGTC
                                          _
GAM1069  PCDHA12  3'  CTGTGACTTGTCTTGGT    38208       C
                                GCCAAGATG AGTCATAG
                                ||||||||| ||||||||
                                TGGTTCTGT TCAGTGTC
                                          _
GAM1069  PCDHA13  3'  CTGTGACTTGTCTTGGT    38217       C
                                GCCAAGATG AGTCATAG
                                ||||||||| ||||||||
                                TGGTTCTGT TCAGTGTC
                                          _
GAM1069  PCDHA2   3'  CTGTGACTTGTCTTGGT    38225       C
                                GCCAAGATG AGTCATAG
                                ||||||||| ||||||||
                                TGGTTCTGT TCAGTGTC
                                          _
GAM1069  PCDHA2   3'  TTTTGTTGTTGTTTTGGT   48985       CAGTC
                                GCCAAGATG   ATAGCAGGA
                                |||||||||   |||||||||
                                TGGTTTTGT   TGTTGTTTT
                                          _____
GAM1069  PCDHA3   3'  CTGTGACTTGTCTTGGT    38233       C
                                GCCAAGATG AGTCATAG
                                ||||||||| ||||||||
                                TGGTTCTGT TCAGTGTC
                                          _
GAM1069  PCDHA4   3'  CTGTGACTTGTCTTGGT    38241       C
                                GCCAAGATG AGTCATAG
                                ||||||||| ||||||||
                                TGGTTCTGT TCAGTGTC
                                          _
GAM1069  PCDHA5   3'  CTGTGACTTGTCTTGGT    38249       C
                                GCCAAGATG AGTCATAG
                                ||||||||| ||||||||
                                TGGTTCTGT TCAGTGTC
                                          _
GAM1069  PCDHA6   3'  CTGTGACTTGTCTTGGT    38257       C
                                GCCAAGATG AGTCATAG
                                ||||||||| ||||||||
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                              TGGTTCTGT TCAGTGTC
                                        _
GAM1069  PCDHA6   3'  CTGTGACTTGTCTTGGT     48998         C
                              GCCAAGATG AGTCATAG
                              ||||||||| ||||||||
                              TGGTTCTGT TCAGTGTC
                                        _
GAM1069  PCDHA7   3'  CTGTGACTTGTCTTGGT     38265         C
                              GCCAAGATG AGTCATAG
                              ||||||||| ||||||||
                              TGGTTCTGT TCAGTGTC
                                        _
GAM1069  PCDHA8   3'  CTGTGACTTGTCTTGGT     38273         C
                              GCCAAGATG AGTCATAG
                              ||||||||| ||||||||
                              TGGTTCTGT TCAGTGTC
                                        _
GAM1069  PCDHA9   3'  CTGTGACTTGTCTTGGT     49014         C
                              GCCAAGATG AGTCATAG
                              ||||||||| ||||||||
                              TGGTTCTGT TCAGTGTC
                                        _
GAM1069  PCDHAC1  3'  CTGTGACTTGTCTTGGT     38163         C
                              GCCAAGATG AGTCATAG
                              ||||||||| ||||||||
                              TGGTTCTGT TCAGTGTC
                                        _
GAM1069  PCDHAC2  3'  CTGTGACTTGTCTTGGT     38173         C
                              GCCAAGATG AGTCATAG
                              ||||||||| ||||||||
                              TGGTTCTGT TCAGTGTC
                                        _
GAM1069  PDGFRA   3'  ATTTTGTTGGTGCTTTGCATTT 20592          T_  _
                TG                CAAGATGCAG  CAT AGCAGGAT
                              ||||||||||  ||| ||||||||
                              GTTTTACGTT  GTG TTGTTTTA
                                    TC   G
GAM1069  PIG8     3'  ATTCTAGCTGTTGTATTTTG   16868         GTC    _
                              CAAGATGCA   ATAGC AGGAT
                              |||||||||   ||||| |||||
                              GTTTTATGT   TGTCG TCTTA
                                    ____    A
GAM1069  PIM2     3'  ATTTTGCTAAGGAAGTTTATTT 59988        __  AG  A
                TGGT                  CCAAGAT  GC  TC TAGCAGGAT
                              |||||||  ||  || |||||||||
                              GGTTTTA  TG  GG ATCGTTTTA
                                  TT  AA  A
GAM1069  PLS1     3'  TTCTGCTGTGAAATGTGGT   10666      AGATGCAG
                              GCCA       TCATAGCAGGA
                              ||||       ||||||||||
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                                TGGT      AGTGTCGTCTT
                                  GTAA____
GAM1069  POLS     3'  GTCCTGGGAGTTGGTTGCATCT 22793        GT  TAG__
              TG                  CAAGATGCA  CA    CAGGAT
                                  |||||||||  ||    ||||||
                                  GTTCTACGT  GT    GTCCTG
                                       TG  TGAGG
GAM1069  PTHR2     3'  ATTTTGTTTGTAATGTATTTTG 17305        GT_  T
                                  CAAGATGCA   CA AGCAGGAT
                                  |||||||||   || ||||||||
                                  GTTTTATGT   GT TTGTTTTA
                                       AAT  _
GAM1069  PTPRJ     3'  ACCTACTGTGTCTTGG      11116          CATAGC   AT
                                  CCAAGATGCAGT     AGG
                                  ||||||||||||     |||
                                  GGTTCTGTGTCA     TCC
                                        _______  AT
GAM1069  RAB6A     3'  GTCTTTCAGGCTGGTTTTGGT  11198        G    ATAGC
                                  GCCAAGAT CAGTC    AGGAT
                                  |||||||| |||||    |||||
                                  TGGTTTTG GTCGG    TTCTG
                                       _    ACT__
GAM1069  RAP1      3'  ATTTTGCTAACTTAGTATTTGG 38583     A     __   CA
              GT                  GCC AGATGC  AGT  TAGCAGGAT
                                  ||| ||||||  |||  |||||||||
                                  TGG TTTATG  TCA  ATCGTTTTA
                                    G     AT  __
GAM1069  RAP1GA1   3'  GTTCTGCTGTGTGACTCTGGGC 11254     A   TG  GT
                                  GCC AGA  CA  CATAGCAGGAT
                                  ||| |||  ||  ||||||||||
                                  CGG TCT  GT  GTGTCGTCTTG
                                    G  CA  __
GAM1069  RASA1     3'  TGCTATGACTGTATCTTG    42639
                                  CAAGATGCAGTCATAGCA
                                  ||||||||||||||||||
                                  GTTCTATGTCAGTATCGT

GAM1069  RGS9      5'  TCCTTAATTGATCTTGGC     13839         G    CATAGC
                                  GCCAAGAT CAGT     AGGA
                                  |||||||| ||||     ||||
                                  CGGTTCTA GTTA     TCCT
                                       _    AT____
GAM1069  RTN4      3'  CTTGCCGCATCTTGGC      66863          AGTCATA
                                  GCCAAGATGC      GCAGG
                                  ||||||||||      |||||
                                  CGGTTCTACG      CGTTC
                                        C_______
GAM1069  SLC17A5   3'  GTTTTGTTCGTTTGTATTTTG  24895          TCAT
                                  CAAGATGCAG   AGCAGGAT
                                  ||||||||||   ||||||||
```

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                                GTTTTATGTT   TTGTTTTG
                                     TGC_
GAM1069  SLC2A3   3'  GTGACAGTATTTTGGT     22665         A
                                GCCAAGATGC GTCAT
                                |||||||||| |||||
                                TGGTTTTATG CAGTG
                                     A
GAM1069  SMARCA1  3'  TTTTGTGTACTGTATTTTG   57391         CATA
                                CAAGATGCAGT   GCAGGA
                                ||||||||||   ||||||
                                GTTTTATGTCA   TGTTTT
                                     TG__
GAM1069  SMARCA1  3'  TTTTGTGTACTGTATTTTG   11781         CATA
                                CAAGATGCAGT   GCAGGA
                                ||||||||||   ||||||
                                GTTTTATGTCA   TGTTTT
                                     TG__
GAM1069  SOX4     3'  GTTTTGTTTTATTTTGCTTCTT 11877       T   TCAT_
           GGT                    GCCAAGA GCAG    AGCAGGAT
                                ||||||| ||||    ||||||||
                                TGGTTCT CGTT    TTGTTTTG
                                   T   TTATT
GAM1069  STAT1    3'  TCTATGTGGCTGTATCTTG   23618           GC
                                CAAGATGCAGTCATA  AGG
                                |||||||||||||| |||
                                GTTCTATGTCGGTGT  TCT
                                     A_
GAM1069  STAT1    3'  TTCTGCTTTCATCTTGGT    23619        CAGTCAT
                                GCCAAGATG     AGCAGGA
                                |||||||||     |||||||
                                TGGTTCTAC     TCGTCTT
                                     TT_____
GAM1069  TACC1    3'  TTTTGCTGCTGTGTTTTGGT  20804          CAT     T
                                GCCAAGATGCAGT  AGCAGGA
                                ||||||||||||  |||||||
                                TGGTTTTGTGTCG  TCGTTTT
                                     ___     T
GAM1069  TCF3     3'  ATCCTGAAACTGCATCTTGGC  70729          CATAG
                                GCCAAGATGCAGT   CAGGAT
                                ||||||||||||   ||||||
                                CGGTTCTACGTCA   GTCCTA
                                     AA___
GAM1069  TERF1    3'  ATTTTGATCACTGCATTTTG  33969         CATAG
                                CAAGATGCAGT   CAGGAT
                                ||||||||||   ||||||
                                GTTTTACGTCA   GTTTTA
                                     CTA__
GAM1069  TEX15    3'  ATTCTGTTGACATTGTCTTTGT 48387   C    CA   TA
                                GC AAGATG  GTCA  GCAGGAT
                                || ||||||  ||||  |||||||
```

```
                                TG TTCTGT  CAGT  TGTCTTA
                                 T     TA   __
GAM1069  TRAF5    3'  GTTCGAATGTATTTTGGT    16085          G  AT
                                GCCAAGATGCA TC  AGC
                                |||||||||||  ||  |||
                                TGGTTTTATGT AG  TTG
                                      A  C_
GAM1069  TRIM39   3'  GTCCTGCTGGAACGTCTTCGT  41175    C     CAG  A
                                GC AAGATG   TC TAGCAGGAT
                                || ||||||   || |||||||||
                                TG TTCTGC   AG GTCGTCCTG
                                 C     A__ _
GAM1069  TRIM8    3'  TTTTGTTTTGGTTTTGGC    48116        GCAGT  T
                                GCCAAGAT    CA AGCAGGA
                                ||||||||    || |||||||
                                CGGTTTTG    GT TTGTTTT
                                     _____  T
GAM1069  TRIM9    3'  ATCCTGTTTATGTGTGTCTTGG 30751          GT    _
              T                  GCCAAGATGCA  CATAG CAGGAT
                                 ||||||||||  |||||| ||||||
                                 TGGTTCTGTGT  GTATT GTCCTA
                                      __    T
GAM1069  TSG      3'  TCTGTTGGTTGTATCTTG    40241        GT  TA
                                 CAAGATGCA  CA  GCAGG
                                 |||||||||  ||  |||||
                                 GTTCTATGT  GT  TGTCT
                                      TG  __
GAM1069  VPS41    3'  ATTTTGTTATTTATTTGTTTGG 54656      GAT   TC__
              C                  GCCAA   GCAG    ATAGCAGGAT
                                 |||||   ||||   ||||||||||
                                 CGGTT   TGTT    TATTGTTTTA
                                    ___    TATT
GAM1069  VPS41    3'  ATTTTGTTATTTATTTGTTTGG 26922      GAT   TC__
              C                  GCCAA   GCAG    ATAGCAGGAT
                                 |||||   ||||   ||||||||||
                                 CGGTT   TGTT    TATTGTTTTA
                                    ___    TATT
GAM1069  XT3      3'  CTCCGTGGTGTGTGTCTTGGT  39522          GT   A  A   T
                                 GCCAAGATGCA  CAT GC GGA
                                 ||||||||||  ||| || |||
                                 TGGTTCTGTGT  GTG TG CCT
                                      __  G  _   CC
GAM1069  ZNF236   5'  TCTTGTCGTGATTGCACTTGGT 23717       A      TA     T
                                 GCCAAG TGCAGTCA  GCAGGA
                                 ||||||  ||||||||  ||||||
                                 TGGTTC ACGTTAGT  TGTTCT
                                    _      GC     T
GAM1069  ACTR1A   3'  GTTTTGTTGCCATTTTGGT   62968         _  T  T
                                 GCCAAGATG CAG CA AGC
                                 |||||||||  ||| || |||
```

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                                TGGTTTTAC GTT GT TTG
                                     C  _ T
GAM1069  AF093680  3'  GTTCTGTTATTTATACTTGGT  25090       _  CAGTC
                                GCCAAG ATG    ATAGCAGGAT
                                |||||| |||    ||||||||||
                                TGGTTC TAT    TATTGTCTTG
                                   A  T____
GAM1069  AF9Q34   3'  TTTTGTAAATGTTCTTGGT   50743       T  GTCATA
                                GCCAAGA GCA    GCAGGA
                                ||||||| |||    ||||||
                                TGGTTCT TGT    TGTTTT
                                   _  AAA___
GAM1069  ARHGEF4  3'  GTTTTGTTTGGATTTTGGC   52217       G  T  T
                                GCCAAGAT CAG CA AGC
                                |||||||| ||| || |||
                                CGGTTTTA GTT GT TTG
                                     G  T  T
GAM1069  B3GNT1   3'  ATCTTGTTGTGATGTTATGGT  52683     A  GCA
                                GCCA GAT  GTCATAGCAGGAT
                                |||| |||  ||||||||||||
                                TGGT TTG  TAGTGTTGTTCTA
                                  A  ___
GAM1069  B3GNT1   3'  ATCTTGTTGTGATGTTATGGT  21658     A  GCA
                                GCCA GAT  GTCATAGCAGGAT
                                |||| |||  ||||||||||||
                                TGGT TTG  TAGTGTTGTTCTA
                                  A  ___
GAM1069  C1orf25  3'  ATTCTGCTGTGTAATTCTTG  72533      TGCAGT
                                CAAGA    CATAGCAGGAT
                                |||||    ||||||||||
                                GTTCT    GTGTCGTCTTA
                                   TAAT__
GAM1069  C20orf121 3'  TTTTGTTTTGCTTTTTGGT   44280       T   TCAT
                                GCCAAGA GCAG   AGCAGGA
                                ||||||| ||||   |||||||
                                TGGTTTT CGTT   TTGTTTT
                                   T  _____
GAM1069  C20orf98  3'  GTCTTCTACCTGCATTTTGGC  71515         TCA  C
                                GCCAAGATGCAG  TAG AGGAT
                                ||||||||||||  ||| |||||
                                CGGTTTTACGTC  ATC TTCTG
                                     C__  _
GAM1069  CAMK2G   5'  GTCAAGCTGGCTGATTTTGGC  68966       G    TA  AG
                                GCCAAGAT CAGTCA  GC  GAT
                                |||||||| ||||||  ||  |||
                                CGGTTTTA GTCGGT  CG  CTG
                                     _    __ AA
GAM1069  CBX6     3'  ATTTTGTTGTTTTGGTTTGTGG 26610     AGAT  AGTC
           T                    GCCA   GC   ATAGCAGGAT
                                ||||   ||   ||||||||||
```

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                                TGGT   TG   TGTTGTTTTA
                                  GTT_ GTTT
GAM1069 CGGBP1   3' ATCCTGTTGTGGGGATTTGGT 13360      ATGCAG
                                GCCAAG     TCATAGCAGGAT
                                ||||||     ||||||||||||
                                TGGTTT     GGTGTTGTCCTA
                                   AGG___
GAM1069 CHST3    3' GTTTCATGGCTGTGTTTTTGC 14979    C        __
                                GC AAGATGCAGTCAT  AGC
                                || ||||||||||||  |||
                                CG TTTTGTGTCGGTA  TTG
                                 T          CT
GAM1069 CNNM4    3' TTGTGATTTATTTTGGC     39485        C
                                GCCAAGATG AGTCATAG
                                ||||||||| ||||||||
                                CGGTTTTAT TTAGTGTT
                                          _
GAM1069 CSMD1    3' ATCCTGAAGGACTGCATTTGGC 73119     A       ATAG
                                GCCA GATGCAGTC    CAGGAT
                                |||| |||||||||    ||||||
                                CGGT TTACGTCAG    GTCCTA
                                  _       GAA_
GAM1069 CTPS2    3' GTTTCGACTGCATTTTG     39089          AT
                                CAAGATGCAGTC  AGC
                                ||||||||||||  |||
                                GTTTTACGTCAG  TTG
                                       CT
GAM1069 CYYR1    3' TTCTGCTCGTATTTTAGGT    53677    _     AGTCAT
                                GCC AAGATGC     AGCAGGA
                                ||| |||||||     |||||||
                                TGG TTTTATG     TCGTCTT
                                  A      C_____
GAM1069 DKFZp547E052 3' ATTCTGCTATAACACATCTTG  50095       CA  C
                                CAAGATG  GT ATAGCAGGAT
                                |||||||  || ||||||||||
                                GTTCTAC  CA TATCGTCTTA
                                    A_  A
GAM1069 DKFZP727G051 3' GTCTTGCTAAACCTGTTTCTGG 69475     A  T   TCA
           T                     GCCA GA GCAG   TAGCAGGAT
                                ||||  ||  ||||   |||||||||
                                TGGT CT TGTC   ATCGTTCTG
                                  _  T   CAA
GAM1069 DNAJA2   3' GTCCTGAAGCTTTGTGTTTGGC 59783     A     TCATAG
                                GCCA GATGCAG     CAGGAT
                                |||| |||||||     ||||||
                                CGGT TTGTGTT     GTCCTG
                                  _      TCGAA_
GAM1069 FADS1    3' ATCCTGGAACCACTGATTTTGG 25472       G   CATAG
           T                     GCCAAGAT CAGT    CAGGAT
                                |||||||| ||||    ||||||
```

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                                TGGTTTTA GTCA    GTCCTA
                                    _   CCAAG
GAM1069  FBXO30   3' GTTTTGCTGAAGAATGTGTCTG 49579    _     G  A_
             TGGT                  CCA AGATGCA TC  TAGCAGGAT
                                |||  |||||||  ||  |||||||||
                                GGT TCTGTGT AG  GTCGTTTTG
                                  G      A  AA
GAM1069  FLJ10587 3' TTGTGGCTGTGTTTTTGGT   36312       _
                                GCCAAGA TGCAGTCATAG
                                |||||||  ||||||||||
                                TGGTTTT GTGTCGGTGTT
                                    T
GAM1069  FLJ10700 3' GTCTTTGTATTGGCATCTTGGT 36428         AGTC   GC
                                GCCAAGATGC    ATA  AGGAT
                                ||||||||||    |||  |||||
                                TGGTTCTACG    TAT  TTCTG
                                      GT__   GT
GAM1069  FLJ10726 3' TCTTGTCTTCTATTTTGGC   36509        C_  TCATA
                                GCCAAGATG  AG    GCAGGA
                                |||||||||  ||    ||||||
                                CGGTTTTAT  TC    TGTTCT
                                     CT  _____
GAM1069  FLJ10921 3' TTCTGCTTTTGCATTTGGT   36862     A      TCAT
                                GCCA GATGCAG    AGCAGGA
                                ||||  |||||||   |||||||
                                TGGT TTACGTT    TCGTCTT
                                  _      T___
GAM1069  FLJ11116 3' GTTTTGTTATGTTTGTGTTTTC 82590    C       T
             GT                   GC AAGATGCAG CATAGCAGGAT
                                ||  |||||||||  ||||||||||
                                TG TTTTGTGTT GTATTGTTTTG
                                 C        T
GAM1069  FLJ11703 3' ATCTTCCAGACTGTATTTTG   46382          ATAGC
                                CAAGATGCAGTC    AGGAT
                                ||||||||||||    |||||
                                GTTTTATGTCAG    TTCTA
                                      ACC__
GAM1069  FLJ12688 3' GTTTTGGCCGCTGCATTTTG   73180          CATAG
                                CAAGATGCAGT    CAGGAT
                                ||||||||||    ||||||
                                GTTTTACGTCG    GTTTTG
                                      CCG__
GAM1069  FLJ13072 5' GTCCTGTGCACTCTGTGTCTTG 89820         TCATA
                                CAAGATGCAG    GCAGGAT
                                |||||||||    |||||||
                                GTTCTGTGTC    TGTCCTG
                                      TCACG
GAM1069  FLJ14437 5' GTCCTGCTATGGAATCCCTTTG 50829    C   ATGCAG
             C                   GC AAG     TCATAGCAGGAT
                                || |||     ||||||||||||
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                                CG TTC     GGTATCGTCCTG
                                 T  CCTAA_
GAM1069  FLJ14743  3'  TATGGTTGGTTTTGGC      68067        G  GT
                                GCCAAGAT CA  CATA
                                |||||||| ||  ||||
                                CGGTTTTG GT  GTAT
                                     _  TG
GAM1069  FLJ20298  5'  ATCTTGTTATTGGTGTTTGGGT 34900     A     AGTC
                                GCC AGATGC    ATAGCAGGAT
                                ||| ||||||    ||||||||||
                                TGG TTTGTG    TATTGTTCTA
                                  G     GT__
GAM1069  FLJ20729  3'  GTTTTATACTGTGTTTTG    35650          CAT_
                                CAAGATGCAGT    AGC
                                ||||||||||    |||
                                GTTTTGTGTCA    TTG
                                       TATT
GAM1069  FLJ21616  3'  ATCTTGCTGCTCCGTCTTAGC  44688    C     C   CAT
                                GC AAGATG AGT   AGCAGGAT
                                || |||||| |||   ||||||||
                                CG TTCTGC TCG   TCGTTCTA
                                 A     C  ___
GAM1069  FLJ21820  3'  TATGGTTTATTTTGGT      41627         C GT
                                GCCAAGATG A  CATA
                                ||||||||| |  ||||
                                TGGTTTTAT T  GTAT
                                     _ TG
GAM1069  FLJ21934  3'  ATTCTGTTATTTTATCTTAGC  45360    C     CAGTC
                                GC AAGATG    ATAGCAGGAT
                                || ||||||    ||||||||||
                                CG TTCTAT    TATTGTCTTA
                                 A     TT___
GAM1069  FLJ22378  3'  TCCTGCTTAGCTTTTTGGC    46908       T  AGTCAT
                                GCCAAGA GC     AGCAGGA
                                ||||||| ||     |||||||
                                CGGTTTT CG     TCGTCCT
                                    T  AT____
GAM1069  FLJ22494  5'  GTCCTGTTATGGCTGGCA    45678     _
                                TGC AGTCATAGCAGGAT
                                ||| ||||||||||||||
                                ACG TCGGTATTGTCCTG
                                  G
GAM1069  FLJ23071  3'  TTCTGCTGACATTTTGG     47268         CAGTCA
                                CCAAGATG     TAGCAGGA
                                ||||||||     ||||||||
                                GGTTTTAC     GTCGTCTT
                                    A_____
GAM1069  FLJ23462  3'  ATCTTAAAATTGTGTCTTGGT  45803           CATAGC
                                GCCAAGATGCAGT     AGGAT
                                ||||||||||||      |||||
```

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                                TGGTTCTGTGTTA     TTCTA
                                      AAA___
GAM1069  FLJ31952  5'  GTCTTTCAGGACTGATTTTGGT 58386        G    ATAGC
                                GCCAAGAT CAGTC    AGGAT
                                |||||||| |||||    |||||
                                TGGTTTTA GTCAG    TTCTG
                                   _    GACT_
GAM1069  FUSIP1    3'  ATCTTGCCTTTGTTTATTTTGG 21771        CAGT  TA_
              T                  GCCAAGATG   CA   GCAGGAT
                                |||||||||   ||   |||||||
                                TGGTTTTAT   GT   CGTTCTA
                                     TT__  TTC
GAM1069  GRIN3A    3'  GTTTTGTAAGTCTGCATTTTTG 55972    C       TCATA
              T                  GC AAGATGCAG    GCAGGAT
                                || |||||||||    |||||||
                                TG TTTTACGTC    TGTTTTG
                                 T       TGAA_
GAM1069  GTPBP1    3'  TCTTGCTGCTCCTCTTGGC    15019       TGC   CAT
                                GCCAAGA   AGT   AGCAGGA
                                |||||||   |||   |||||||
                                CGGTTCT   TCG   TCGTTCT
                                   CC_   ___
GAM1069  HRIHFB2436 3'  GTGTGCTTTGATTGTATTTTGG 26797             T    GGAT
              C                  GCCAAGATGCAGTCA AGCA
                                |||||||||||||| ||||
                                CGGTTTTATGTTAGT TCGT
                                      T   GTG
GAM1069  HSPC177   5'  GTTTTGCTCTAGTGTTTGGGT  33090     A     _  TCAT
                                GCC AGATGC AG    AGCAGGAT
                                ||| |||||| ||    ||||||||
                                TGG TTTGTG TC    TCGTTTTG
                                  G     A  _____
GAM1069  HSPC177   3'  GTTTTGTTGTGTCTTG      33091          T  T
                                CAAGATGCAG CA AGC
                                |||||||||| || |||
                                GTTCTGTGTT GT TTG
                                      _  T
GAM1069  HU-K4     5'  GTCCTGCTGGTCCTCATTCTGG 24370      AG   C  TCA
              C                  GCCA  ATG AG   TAGCAGGAT
                                ||||  ||| ||   |||||||||
                                CGGT  TAC TC   GTCGTCCTG
                                  CT   _  CTG
GAM1069  IMP-2     3'  ATTTTGTCTTTTTGCATTTTGG 21567           TCATA
              T                  GCCAAGATGCAG    GCAGGAT
                                ||||||||||||    |||||||
                                TGGTTTTACGTT    TGTTTTA
                                      TTTC_
GAM1069  ITGB8     5'  GTTTGGGTTTGATTGTGTTTGG 9410       A        T   A_
              C                  GCCA GATGCAGTCA AGC  GGAT
                                |||| |||||||||| |||  ||||
```

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                                CGGT TTGTGTTAGT TTG  TTTG
                                  _        _  GG
GAM1069  KIAA0087  3'  GTTTTGTTTTAAATGTGTCTGG 28703      A     GTCAT
                T                  GCCA GATGCA     AGCAGGAT
                                   |||| ||||||     ||||||||
                                   TGGT CTGTGT     TTGTTTTG
                                     _     AAATT
GAM1069  KIAA0095  3'  GTTTTGTTTCTGTTGTGTTTTG 90920          T  T_
                                   CAAGATGCAG CA  AGCAGGAT
                                   |||||||||| ||  ||||||||
                                   GTTTTGTGTT GT  TTGTTTTG
                                         _ CT
GAM1069  KIAA0161  3'  GTCCTGTTGCTAACCGTTTTGC 28512    C     CAGTCA
                                   GC AAGATG      TAGCAGGAT
                                   || ||||||      |||||||||
                                   CG TTTTGC      GTTGTCCTG
                                    _     CAATC_
GAM1069  KIAA0222  3'  GTCCTGTTTCTCTGTGTTTTAG 27684    C        TCAT
                T                  GC AAGATGCAG    AGCAGGAT
                                   || |||||||||    ||||||||
                                   TG TTTTGTGTC    TTGTCCTG
                                    A        TCT_
GAM1069  KIAA0337  3'  GTTTTGTTCTGTTTGGTTTTGG 28836         G   T  T
                T                  GCCAAGAT CAG CA AGCAGGAT
                                   |||||||| ||| || ||||||||
                                   TGGTTTTG GTT GT TTGTTTTG
                                        _  T  C
GAM1069  KIAA0367  3'  TCTGTTAGACTTCGTTTTGGT  67302          C    A
                                   GCCAAGATG AGTC TAGCAGG
                                   ||||||||| |||| |||||||
                                   TGGTTTTGC TCAG ATTGTCT
                                         T   _
GAM1069  KIAA0420  3'  GTTTAATTATGACTGTTTTTGG 63365         T         CA
                T                  GCCAAGA GCAGTCATAG  GGAT
                                   ||||||| ||||||||||  ||||
                                   TGGTTTT TGTCAGTATT  TTTG
                                      _        AA
GAM1069  KIAA0513  3'  ATCTTCTCTGTTGCATTTTTGC 28340    C       T  T  C
                                   GC AAGATGCAG CA AG AGGAT
                                   || |||||||| || || |||||
                                   CG TTTTACGTT GT TC TTCTA
                                    T       _ C  _
GAM1069  KIAA0596  3'  GTCTTGGGTCTTTGTCATCTTG 62839          _  TC  AG
                GT                   GCCAAGATG CAG  AT  CAGGAT
                                   ||||||||| |||  ||  ||||||
                                   TGGTTCTAC GTT  TG  GTTCTG
                                         T  TC  G_
GAM1069  KIAA0618  3'  GTTCTGCTGCAGCGCATCTTG  29175         A  CA
                                   CAAGATGC GT  TAGCAGGAT
                                   |||||||| ||  |||||||||
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                                GTTCTACG CG  GTCGTCTTG
                                     _ AC
GAM1069  KIAA0668  3'  GTTCCGGCTGTGTCTGGT    66526      A        AT
                                GCCA GATGCAGTC  AGC
                                |||| |||||||||  |||
                                TGGT CTGTGTCGG  TTG
                                   _       CC
GAM1069  KIAA0775  5'  TTCTGGGTTGCATCTTAGC    28284    C       GT ATAG
                                GC AAGATGCA  C    CAGGA
                                || ||||||||  |    |||||
                                CG TTCTACGT  G    GTCTT
                                 A       TG ____
GAM1069  KIAA0940  3'  GTCCTGCTGTGGCCTTTCCTTG 29873        ATGCA
                   GT                  GCCAAG    GTCATAGCAGGAT
                                |||||||    ||||||||||||||
                                TGGTTC    CGGTGTCGTCCTG
                                   CTTTC
GAM1069  KIAA1045  3'  GTCCGTGTGTTATGGCTCATCT 71057        C        ___
                   TGGC                 CAAGATG AGTCATAGCA   GGAT
                                ||||||| ||||||||||   ||||
                                GTTCTAC TCGGTATTGT   CCTG
                                   _        GTG
GAM1069  KIAA1076  3'  GTTTTGTTGTGTGTTTTTTG   65518      T   GT
                                CAAGA GCA  CATAGCAGGAT
                                ||||| |||  ||||||||||
                                GTTTT TGT  GTGTTGTTTTG
                                   T  __
GAM1069  KIAA1096  3'  ATTTGAAATGGTGCTGTGTTTT 68526           __  AG   AT
                   GGT                  CCAAGATGCAGT  CAT  CAGG
                                ||||||||||||  |||  ||||
                                GGTTTTGTGTCG  GTA  GTTT
                                      TG   AA   A
GAM1069  KIAA1332  3'  TTATGGTTGGTCTTGGT     71170        G  GT
                                GCCAAGAT CA  CATAG
                                |||||||| ||  |||||
                                TGGTTCTG GT  GTATT
                                   _ TG
GAM1069  KIAA1363  3'  TTTTGTTGTGTTTTTGGT    69269        TGCAGT
                                GCCAAGA     CATAGCAGGA
                                |||||||     ||||||||||
                                TGGTTTT     GTGTTGTTTT
                                   T_____
GAM1069  KIAA1414  3'  GTTCTGTTTTATTTGTATATTG 67992      G     TCAT
                   GT                  GCCAA ATGCAG    AGCAGGAT
                                ||||| ||||||    ||||||||
                                TGGTT TATGTT    TTGTCTTG
                                   A     TATT
GAM1069  KIAA1423  3'  ATCTTGTGATGCTGTTTATCTT 61723        __   T   A
                   GGT                  CCAAGAT  GCAG CAT GCAGGAT
                                |||||||  |||| ||| |||||||
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```
                                GGTTCTA  TGTC GTA TGTTCTA
                                   TT    _  G
GAM1069  KIAA1587  3'  TCTCTGTTGTATTTTGGT    40511          GTCATA   _
                                GCCAAGATGCA     GCAG GA
                                ||||||||||      |||| ||
                                TGGTTTTATGT     TGTC CT
                                       _____    T
GAM1069  KIAA1634  3'  ATCTTGTTGTGAAGCACATTAG 63385     _  GA   AG
           GT                    GCC AA  TGC  TCATAGCAGGAT
                                |||  ||  |||  ||||||||||||
                                TGG TT  ACG  AGTGTTGTTCTA
                                 A  AC   A_
GAM1069  KIAA1644  5'  ATCCTGCTGTGGTTGTGGCTGG 85024     A AT   GT
                                CCA G  GCA  CATAGCAGGAT
                                |||  |  |||  ||||||||||
                                GGT C  TGT  GTGTCGTCCTA
                                 _ GG   TG
GAM1069  KIAA1644  3'  TGTGGCTGTGCTTGGC      85033       A
                                GCCAAG TGCAGTCATA
                                ||||||  ||||||||||
                                CGGTTC GTGTCGGTGT
                                   _
GAM1069  KIAA1889  5'  GTCCTGCTCCTTCTGCATCTGG 73503      A      TCAT
           C                     GCCA GATGCAG    AGCAGGAT
                                ||||  |||||||    ||||||||
                                CGGT CTACGTC    TCGTCCTG
                                  _      TTCC
GAM1069  LEAP-2    3'  TTGATTAACTGCATTTTGGC   53746           CATAG
                                GCCAAGATGCAGT    CAG
                                ||||||||||||     |||
                                CGGTTTTACGTCA    GTT
                                       ATTA_
GAM1069  LEC3      5'  GTTCTGCTGAGCATGGTCTTGG 30862         G  GTCA
           C                     GCCAAGAT CA    TAGCAGGAT
                                ||||||||  ||    |||||||||
                                CGGTTCTG GT    GTCGTCTTG
                                    _  ACGA
GAM1069  LHFPL2    3'  GTTTTGTTGTTTTGTTTTGG   69953       AT    TC
                                CCAAG  GCAG  ATAGCAGGAT
                                |||||  ||||  ||||||||||
                                GGTTT  TGTT  TGTTGTTTTG
                                  ___    T_
GAM1069  MAN1      3'  GTGGTGGTTGTATTTTTGC   26713    C       GT   A
                                GC AAGATGCA  CAT GC
                                ||  ||||||||  |||  ||
                                CG TTTTATGT  GTG TG
                                 T       TG   G
GAM1069  MDS029    3'  GTCTTGTTGAAACATCGTGGT  37467      A   CAG   TA
                                GCCA GATG   TCA  GCAGGAT
                                ||||  ||||   |||  |||||||
```

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                                TGGT CTAC   AGT  TGTTCTG
                                  G   AA_  __
GAM1069  MGC10067  3'  GTCTTGACACAGCTGTGTCTTA 58938    C        CATAG
              GT                   GC AAGATGCAGT     CAGGAT
                                || ||||||||||     ||||||
                                TG TTCTGTGTCG     GTTCTG
                                 A         ACACA
GAM1069  MGC10924  3'  AACTTTTGTTATGACTGTGTTT 47548    C              T
              TTGC                   GC AAGATGCAGTCATAGCAGGA
                                || ||||||||||||||||||
                                CG TTTTGTGTCAGTATTGTTTT
                                 T               CAAA
GAM1069  MGC12466  3'  TTCTGTCATGAGTTTTGGC    79037        GCAG    AG
                                GCCAAGAT    TCAT  CAGGA
                                ||||||||    ||||  |||||
                                CGGTTTTG    AGTA  GTCTT
                                     ____    CT
GAM1069  MGC12966  3'  ATTTTGTAGAATGATTTTGGT  51123         G  G  ATA
                                GCCAAGAT CA TC   GCAGGAT
                                |||||||| || ||   |||||||
                                TGGTTTTA GT AG   TGTTTTA
                                     _  A  A__
GAM1069  MGC15705  3'  ATGGTAGTGTTTTGGT      51279          AG
                                GCCAAGATGC  TCAT
                                ||||||||||  ||||
                                TGGTTTTGTG  GGTA
                                      AT
GAM1069  MGC2217   3'  GTTGCTGTTGGCTGTGTTGTGG 44178      A        _     GAT
              C                    GCCA GATGCAGTCA TAGCAG
                                |||| |||||||||| ||||||
                                CGGT TTGTGTCGGT GTCGTT
                                  G         T     G
GAM1069  MGC2721   3'  CCTATGTATTTTGGC       51217          GTCATAGC
                                GCCAAGATGCA       AGG
                                ||||||||||       |||
                                CGGTTTTATGT       TCC
                                     A________
GAM1069  MGC3035   5'  TCCTGCTGTGGCCCCTGGT    44152      AGATGCA
                                GCCA      GTCATAGCAGGA
                                ||||      ||||||||||||
                                TGGT      CGGTGTCGTCCT
                                  CCC_____
GAM1069  MGC3062   3'  TTCTGTTAAATATTTTGG     43947        CAGTCA
                                CCAAGATG     TAGCAGGA
                                ||||||||     ||||||||
                                GGTTTTAT     ATTGTCTT
                                     AA_____
GAM1069  MGC4677   5'  ATTTTGTGTGCTACTGTATCTT 53508           __    G
              G                    CAAGATGCAGT  CATA CAGGAT
                                ||||||||||  |||| ||||||
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                                GTTCTATGTCA  GTGT GTTTTA
                                      TC   _
GAM1069  MGC5309   3'  GTTCTATTGTATTATGGT    80817     A      CAT
                                GCCA GATGCAGT   AGC
                                |||| ||||||||   |||
                                TGGT TTATGTTA   TTG
                                  A       TC_
GAM1069  MGC5528   3'  TCCTGATTTGTTTTGGT     44045       AT    TCATAG
                                GCCAAG  GCAG     CAGGA
                                ||||||  ||||     |||||
                                TGGTTT  TGTT     GTCCT
                                   __    TA____
GAM1069  NUDT12    5'  ATCTTTGGACTGCATCCTGGT  48721      A       ATAGC
                                GCCA GATGCAGTC     AGGAT
                                |||| |||||||||     |||||
                                TGGT CTACGTCAG     TTCTA
                                  C       GT___
GAM1069  OR2C3     3'  GTTTTGTTCAATTGCGTTGTTG 75448       _      CAT
              GT                  GCCAA GATGCAGT   AGCAGGAT
                                |||||  ||||||||   ||||||||
                                TGGTT TTGCGTTA   TTGTTTTG
                                  G       AC_
GAM1069  P66       3'  GTCCTGCCTTTCTGTATCTTGG 40368          TCATA
                                CCAAGATGCAG     GCAGGAT
                                ||||||||||     |||||||
                                GGTTCTATGTC     CGTCCTG
                                      TTTC_
GAM1069  PAFAH2    3'  GTTTTGCTAAGTGTATCTTG   4767         GTCA
                                CAAGATGCA    TAGCAGGAT
                                |||||||||    |||||||||
                                GTTCTATGT    ATCGTTTTG
                                     GA__
GAM1069  PEGASUS   3'  GTTTTGCTGTTTTTGTGGTTTG 42431       AT    TC
              GT                  GCCAAG  GCAG  ATAGCAGGAT
                                ||||||  ||||  ||||||||||
                                TGGTTT  TGTT  TGTCGTTTTG
                                   GG    TT
GAM1069  PER3      3'  GTTTTGGGGGTTGAGTTTTGGC 33682        G  GT ATAG
                                GCCAAGAT CA  C    CAGGAT
                                |||||||| ||  |    ||||||
                                CGGTTTTG GT  G    GTTTTG
                                     A  TG GG__
GAM1069  PRO1575   5'  ATTCTGTTACCAGAGTTTTTGG 26027        T  AGTCA
              T                   GCCAAGA GC     TAGCAGGAT
                                |||||||  ||     |||||||||
                                TGGTTTT TG     ATTGTCTTA
                                   _  AGACC
GAM1069  PRO1855   3'  ATCAGAAATGACTGTGTCATGG 37544      A         AGCAGGAT
              T                   GCCA GATGCAGTCAT
                                ||||  ||||||||||
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                                TGGT CTGTGTCAGTA
                                  A         AAGACTA
GAM1069  PRO1880   5'  ATTTTGTCTCCATGATTTTGGT 26042        G  GTCATA
                                GCCAAGAT CA     GCAGGAT
                                |||||||| ||     |||||||
                                TGGTTTTA GT     TGTTTTA
                                    _  ACCTC_
GAM1069  PROL2     3'  GTTTTGTTATGAAAGTATGTAT 22347        G____
           TTTG                   AGATGCA    TCATAGCAGGAT
                                |||||||     ||||||||||||
                                TTTATGT    AGTATTGTTTTG
                                    ATGAA
GAM1069  RA-GEF-2  3'  TTACAGAAATGATTGTCTCTTG 32959        T       AGCAGGAT
           GT                     GCCAAGA GCAGTCAT
                                ||||||| ||||||||
                                TGGTTCT TGTTAGTA
                                    C       AAGACATTG
GAM1069  RAB10     3'  ATTTGAGTAGTCTGCATTTTGG 85174           TCATAG    AT
           C                     GCCAAGATGCAG     CAGG
                                ||||||||||||     ||||
                                CGGTTTTACGTC     GTTT
                                       TGATGA    A
GAM1069  RAB3GAP   3'  ATTTTGCTTTTGTATTTTAGT  66947    C       TCAT
                                GC AAGATGCAG    AGCAGGAT
                                || |||||||||    ||||||||
                                TG TTTTATGTT    TCGTTTTA
                                 A        T___
GAM1069  RAB6C     3'  GTCTTTCAGGCTGGTTTTGGT  49570        G    ATAGC
                                GCCAAGAT CAGTC     AGGAT
                                |||||||| |||||     |||||
                                TGGTTTTG GTCGG     TTCTG
                                    _     ACT__
GAM1069  RDHL      3'  TCCTGCCCTGTATTTAGGC    60065     A       TCATA
                                GCC AGATGCAG     GCAGGA
                                ||| ||||||||     ||||||
                                CGG TTTATGTC     CGTCCT
                                  A       C____
GAM1069  Rpo1-2    3'  GTCCTGCTGGACGGCGTCATGG 38707      A    A   A
           T                     GCCA GATGC GTC TAGCAGGAT
                                |||| ||||| ||| |||||||||
                                TGGT CTGCG CAG GTCGTCCTG
                                  A    G  _
GAM1069  SARM      3'  TCCTGCTGTGGGCTGGGC     30619     AAGATG    _
                                GCC      CAGTC ATAGCAGGA
                                |||      ||||| |||||||||
                                CGG      GTCGG TGTCGTCCT
                                  _______    G
GAM1069  SBBI26    3'  GTTTTGGTTTGGTGTTTTGGT  38136          AG__   T
                                GCCAAGATGC    TCA AGC
                                ||||||||||    ||| |||
```

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                                TGGTTTTGTG   GGT TTG
                                     GTTT  T
GAM1069 SCYA16   3' ATCTTGGCTCACTTGATCTTGG 15954       GC  CAT  _
            C                    GCCAAGAT AGT  AGC AGGAT
                                 |||||||| |||  ||| |||||
                                 CGGTTCTA TCA  TCG TTCTA
                                     GT  C__  G
GAM1069 SEMA4G   5' GATCCTGCTATGACTGCATCTT 94681
            GGC                    GCCAAGATGCAGTCATAGCAGGAT
                                 ||||||||||||||||||||||||
                                 CGGTTCTACGTCAGTATCGTCCTA
                                                GC
GAM1069 SLC6A14  3' CTACCACTACATTTTGGT    23350        C  CA
                                 GCCAAGATG AGT  TAG
                                 ||||||||| |||  |||
                                 TGGTTTTAC TCA  ATC
                                     A  CC
GAM1069 SPRY2    3' GTTTTTAGATTGTATTTTG   19558         AT__
                                 CAAGATGCAGTC   AGC
                                 ||||||||||||   |||
                                 GTTTTATGTTAG   TTG
                                      ATTT
GAM1069 SRPK1    3' TTTTGTTTTGTTTTTTGGT   11969       T   TCAT
                                 GCCAAGA GCAG   AGCAGGA
                                 ||||||| ||||   |||||||
                                 TGGTTTT TGTT   TTGTTTT
                                     T  _____
GAM1069 SSH2     3' TCTGTTGGATTTTGGT      62215       G  GTCATA
                                 GCCAAGAT CA     GCAGG
                                 |||||||| ||     |||||
                                 TGGTTTTA GT     TGTCT
                                     G  _______
GAM1069 TGIF2    3' GTCCTGGGTTTCCGTTTTGGT  41457        C_ GT ATAG
                                 GCCAAGATG  A  C   CAGGAT
                                 |||||||||  |  |   ||||||
                                 TGGTTTTGC  T  G   GTCCTG
                                     CT TG _____
GAM1069 TIEG     3' TTTAACAAATGACTGTATCTAG 18961     A        AGCAGGAT
            GC                     GCC AGATGCAGTCAT
                                 ||| ||||||||||||
                                 CGG TCTATGTCAGTA
                                   A          AACAATTTG
GAM1069 TIMM22   3' GTCCTGCTGTGGTCATCTTGGT 78314        CAG
                                 GCCAAGATG   TCATAGCAGGAT
                                 |||||||||   ||||||||||||
                                 TGGTTCTAC   GGTGTCGTCCTG
                                     T__
GAM1069 TRIM6    3' ATTCTTTTGTTGTTTTTTGGT  54133       T   T  TAGC
                                 GCCAAGA GCAG CA   AGGAT
                                 ||||||| |||| ||   |||||
```

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                                TGGTTTT TGTT GT    TCTTA
                                    T   _  TT__
GAM1069  TUSP     3'  ATTTTGTTGTTACGTTTTGGT  39625         CAGTC
                                GCCAAGATG     ATAGCAGGAT
                                |||||||||     ||||||||||
                                TGGTTTTGC     TGTTGTTTTA
                                    AT___
GAM1069  UST      3'  ATGATTTTATTTTGGT      19134          C
                                GCCAAGATG AGTCAT
                                ||||||||| ||||||
                                TGGTTTTAT TTAGTA
                                    T
GAM1069  VDU1     3'  ATTCATGATGGCTTTGTTTTGG 30412         C     AGCA
              T                  GCCAAGATG AGTCAT    GGAT
                                ||||||||| ||||||    ||||
                                TGGTTTTGT TCGGTA    CTTA
                                    T     GTA_
GAM1069  VMP      3'  GTTTTTAGACTGTATCTTG    54900           AT__
                                CAAGATGCAGTC    AGC
                                ||||||||||||    |||
                                GTTCTATGTCAG    TTG
                                     ATTT
GAM1069  WSB1     3'  TCTTGTACTGCATTTTG     56142           CATA
                                CAAGATGCAGT    GCAGGA
                                ||||||||||    ||||||
                                GTTTTACGTCA    TGTTCT
                                     ____
GAM1069  WSB1     3'  TCTTGTACTGCATTTTG     56148           CATA
                                CAAGATGCAGT    GCAGGA
                                ||||||||||    ||||||
                                GTTTTACGTCA    TGTTCT
                                     ____
GAM1069  YKT6     3'  GTTCTGTTGTAAATCATTTGGC 21607      A    CAGTC
                                GCCA GATG     ATAGCAGGAT
                                |||| ||||     ||||||||||
                                CGGT TTAC     TGTTGTCTTG
                                  _    TAAA_
GAM1069  YWHAQ    3'  GTTCTGCAAGTGACTGTGTTTT 22396            A_
              G                  CAAGATGCAGTCAT  GCAGGAT
                                ||||||||||||||  |||||||
                                GTTTTGTGTCAGTG  CGTCTTG
                                     AA
GAM1069  ZNF340   3'  GTTTGTGTCTGTTTGTATTTTG 84564           T  TA_    AT
              GT                   GCCAAGATGCAG CA   GCAGG
                                ||||||||||||| ||   |||||
                                TGGTTTTATGTT GT   TGTTT
                                     T  CTG    G
GAM1069  LOC112476 3'  GTCCTGCTCCTGCATCTTG   59115          TCAT
                                CAAGATGCAG    AGCAGGAT
                                |||||||||    ||||||||
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                                GTTCTACGTC    TCGTCCTG
                                      C___
GAM1069  LOC115219 5'  TTCGGGGCTTATTTTGGT    73323         C    ATAGCA
                                GCCAAGATG AGTC     GGA
                                ||||||||| ||||     |||
                                TGGTTTTAT TCGG     CTT
                                      _   GG____
GAM1069  LOC116150 3'  GTTCTGGTTGTGTTTGGC    56635      A     GT  T
                                GCCA GATGCA  CA AGC
                                |||| ||||||  || |||
                                CGGT TTGTGT  GT TTG
                                  _     TG  C
GAM1069  LOC121219 5'  GTTTGATTTGACTGTATTTTCG 74049    C          TAG    AT
              C                  GC AAGATGCAGTCA   CAGG
                                || ||||||||||||   ||||
                                CG TTTTATGTCAGT   GTTT
                                 C          TTA    G
GAM1069  LOC122786 3'  GTTTTGCTGACATTGTTGGT   74158      _   _   T  T
                                GCCAA GATG CAG CA AGC
                                ||||| |||| ||| || |||
                                TGGTT TTAC GTC GT TTG
                                   G    A   _ T
GAM1069  LOC127253 3'  GTTCTGATGTGTCTTGGC    74640          G   T
                                GCCAAGATGCA TCA AGC
                                |||||||||| ||| |||
                                CGGTTCTGTGT AGT TTG
                                      _  C
GAM1069  LOC127703 3'  TGGCTGCAATTTTGGC      74682         _
                                GCCAAGAT GCAGTCA
                                |||||||| |||||||
                                CGGTTTTA CGTCGGT
                                     A
GAM1069  LOC129831 3'  TGTTTTGGGGTTGTTTTGTTTT 74897      ___   GT AT__   AGGAT
              GGC                  AAGAT   GCA  C    AGC
                                |||||   |||  |    |||
                                TTTTG   TGT  G    TTG
                                   TTT   TG GGTT     TA
GAM1069  LOC135398 3'  ATCTCTGAGAATGACTGGATCT 75935        G      AG_  _
              TGGC                  CCAAGAT CAGTCAT   CAG GAT
                                ||||||| |||||||   ||| |||
                                GGTTCTA GTCAGTA   GTC CTA
                                   G      AGA   T
GAM1069  LOC144501 3'  GTTCAAAACTGACTGTGTTTTG 83111            TAGCA
                                CAAGATGCAGTCA     GGAT
                                ||||||||||||     ||||
                                GTTTTGTGTCAGT     CTTG
                                      CAAAA
GAM1069  LOC144871 3'  GTTTTGTTGCACTTGTCTGTGG 83203      _    C   CA
              C                  GCCA AGATG AGT  TAGCAGGAT
                                |||| ||||| |||  |||||||||
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                                CGGT TCTGT TCA  GTTGTTTTG
                                  G    _   C_
GAM1069  LOC145815 5'  GTTCTGTATCTTCAGTATCTTG 83523         AGTCATA
                 GT                 GCCAAGATGC      GCAGGAT
                                    ||||||||||      |||||||
                                    TGGTTCTATG      TGTCTTG
                                         ACTTCTA
GAM1069  LOC145842 3'  ATTTTGCTTAGTGCATTTTG   77531        GTCAT
                                    CAAGATGCA    AGCAGGAT
                                    |||||||||    ||||||||
                                    GTTTTACGT    TCGTTTTA
                                         GAT__
GAM1069  LOC145842 5'  ATTTTGTTACCTCTATCCTGGC 77532     A   C  TCA
                                    GCCA GATG AG   TAGCAGGAT
                                    |||| |||| ||   |||||||||
                                    CGGT CTAT TC   ATTGTTTTA
                                      C   C  C__
GAM1069  LOC146050 3'  ATTCTGCTGTTGAATCTTAGT  77626    C    G  GTC
                                    GC AAGAT CA   ATAGCAGGAT
                                    || ||||| ||   ||||||||||
                                    TG TTCTA GT   TGTCGTCTTA
                                     A    A  ____
GAM1069  LOC146050 3'  ATTCTGTCATTCAGCTGCATTT 77627         C__  AG
                 TG                 CAAGATGCAGT   AT  CAGGAT
                                    ||||||||||   ||  ||||||
                                    GTTTTACGTCG   TA  GTCTTA
                                         ACT  CT
GAM1069  LOC146227 3'  GTGAGTGGCTGTGTTCTGGC   77712     AG       A_
                                    GCCA  ATGCAGTCAT  GC
                                    ||||  ||||||||||  ||
                                    CGGT  TGTGTCGGTG  TG
                                      CT        AG
GAM1069  LOC146489 5'  TTTTGAAATTGTATCTGGT    70802     A      CATAG
                                    GCCA GATGCAGT    CAGGA
                                    |||| ||||||||    |||||
                                    TGGT CTATGTTA    GTTTT
                                      _       AA____
GAM1069  LOC146515 3'  TTTTGTTTGGTTGGTTTTGGC  77968       G  GT  T     T
                                    GCCAAGAT CA  CA AGCAGGA
                                    |||||||| ||  || |||||||
                                    CGGTTTTG GT  GT TTGTTTT
                                         _  TG  _      T
GAM1069  LOC146839 3'  CTTCCACTGTGATTGTGTTTTG 83810            CA   T
                                    CAAGATGCAGTCATAG  GGA
                                    ||||||||||||||||  |||
                                    GTTTTGTGTTAGTGTC  CCT
                                              A_   TCT
GAM1069  LOC148479 3'  TTTCCTTGATTGCATTTTTGT  78881    C         TAGC    T
                                    GC AAGATGCAGTCA    AGGA
                                    || ||||||||||||    ||||
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                                TG TTTTACGTTAGT    TCCT
                                 T          ____    TTG
GAM1069  LOC149267 3'  TTCTGCATTTGTATCTTG    56680         TCATA
                                CAAGATGCAG    GCAGGA
                                ||||||||||    ||||||
                                GTTCTATGTT    CGTCTT
                                     TA___
GAM1069  LOC149711 3'  ATTTTGGTCTTTTGTATTTTGG 84674          TCATAG
                  T              GCCAAGATGCAG    CAGGAT
                                ||||||||||||    ||||||
                                TGGTTTTATGTT    GTTTTA
                                      TTCTG_
GAM1069  LOC150311 5'  GTTTTGGCAGCTCATTTTGGC  79758        CA__   T
                                GCCAAGATG   GTCA AGC
                                |||||||||   |||| |||
                                CGGTTTTAC   CGGT TTG
                                     TCGA   T
GAM1069  LOC150368 3'  TCCAAGGTTGCGTTTTGG    79703         GT ATAGCA
                                CCAAGATGCA  C     GGA
                                ||||||||||  |     |||
                                GGTTTTGCGT  G     CCT
                                     TG AA____
GAM1069  LOC150407 3'  GTTTTGTTGTTGTCATTGTTGG 79829      _   _ GTC
                  T              GCCAA GATG CA   ATAGCAGGAT
                                ||||| |||| ||   ||||||||||
                                TGGTT TTAC GT   TGTTGTTTTG
                                   G   T ___
GAM1069  LOC150837 3'  GTTTTGCTATGACAAGAACTTG 80017      ATGCA
                  G              CCAAG    GTCATAGCAGGAT
                                |||||    ||||||||||||||
                                GGTTC    CAGTATCGTTTTG
                                   AAGAA
GAM1069  LOC151254 3'  ATCTTGTTAGAACCATTTTG   80194       CAG  A
                                CAAGATG   TC TAGCAGGAT
                                |||||||   || |||||||||
                                GTTTTAC   AG ATTGTTCTA
                                    CA_  _
GAM1069  LOC151568 5'  TCTGGGGGCTTGTTTTGGT    56703        C    ATAG
                                GCCAAGATG AGTC    CAGG
                                ||||||||| ||||    ||||
                                TGGTTTTGT TCGG    GTCT
                                     _    GG__
GAM1069  LOC152215 3'  GTTTTAGCATCTGTATTTTGGT 80490          TCATA  _
                                GCCAAGATGCAG    GC AGGAT
                                ||||||||||||    || |||||
                                TGGTTTTATGTC    CG TTTTG
                                     TA___  A
GAM1069  LOC153688 5'  GTCTTAAAGGTGGCATCTTGGT 86119         AGT   AGC_
                                GCCAAGATGC   CAT    AGGAT
                                |||||||||   |||    |||||
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                                TGGTTCTACG  GTG   TTCTG
                                    ___  GAAA
GAM1069  LOC153811 3'  GTTTTGTCTTGTATTTTGGC  80956         _ T  T
                                GCCAAGATGCA G CA AGC
                                |||||||||||  | || |||
                                CGGTTTTATGT C GT TTG
                                     T T  T
GAM1069  LOC155434 3'  ATTCTGTTGTTTTGCAGTTTGG 86400      A    TC
           C                    GCCAAG TGCAG  ATAGCAGGAT
                                ||||||  |||||  ||||||||||
                                CGGTTT ACGTT  TGTTGTCTTA
                                   G    T_
GAM1069  LOC158116 3'  TGTGACTATGTCTTGGC    60324        GC
                                GCCAAGAT  AGTCATA
                                ||||||||  |||||||
                                CGGTTCTG  TCAGTGT
                                     TA
GAM1069  LOC158402 5'  ATTTTGTTATTCTGAACTCTTG 86800      TG_  TC
           GC                    GCCAAGA   CAG  ATAGCAGGAT
                                |||||||   |||  ||||||||||
                                CGGTTCT   GTC  TATTGTTTTA
                                   CAA   T_
GAM1069  LOC158668 3'  ATTTTGATCACTGCATTTTG   69364         CATAG
                                CAAGATGCAGT    CAGGAT
                                ||||||||||    ||||||
                                GTTTTACGTCA    GTTTTA
                                     CTA__
GAM1069  LOC159090 3'  GTTTTGCTGATCTCATTTTGG  82090       C  TCA
                                CCAAGATG AG   TAGCAGGAT
                                ||||||||  ||   |||||||||
                                GGTTTTAC TC   GTCGTTTTG
                                   _  TA_
GAM1069  LOC159250 5'  ATTTTGTTGTTCTGTTTTGTTT 87056      ___   TC
           TGGT                    CAAGAT   GCAG  ATAGCAGGAT
                                ||||||   ||||  ||||||||||
                                GTTTTG   TGTC  TGTTGTTTTA
                                   TTT   T_
GAM1069  LOC159250 5'  TTTTGTTTTGGTTTTGGT    87057       GCAGT  T
                                GCCAAGAT    CA AGCAGGA
                                ||||||||    || |||||||
                                TGGTTTTG    GT TTGTTTT
                                     _____  T
GAM1069  LOC202347 5'  GCTTTGTGGTTTTATTTTGGT  90347       C GT  __
                                GCCAAGATG A  CAT  AGC
                                |||||||||  |  |||  |||
                                TGGTTTTAT T  GTG  TCG
                                     T TG   TT
GAM1069  LOC219790 3'  ATTTTGCTATTGTTTGTTTTG  91357      __  GTC
                                CAAGAT  GCA   ATAGCAGGAT
                                ||||||  |||   ||||||||||
```

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                                GTTTTG  TGT   TATCGTTTTA
                                   TT  ___
GAM1069  LOC221296 3'  GTTTTTATTTCATTTTGGC   91970        C   CAT
                                GCCAAGATG AGT   AGC
                                ||||||||| |||   |||
                                CGGTTTTAC TTA   TTG
                                     T   TTT
GAM1069  LOC221301 3'  ATTTTGCTACCAAATGCTTTTG 91887       T   GTCA_
            GC                   GCCAAGA GCA    TAGCAGGAT
                                ||||||| |||    |||||||||
                                CGGTTTT CGT    ATCGTTTTA
                                   _  AAACC
GAM1069  LOC221303 3'  ATCTGCCATGGTTTTATTTTGG 91898        C GT   A    AT
            T                    GCCAAGATG A  CAT GCAGG
                                ||||||||| |  ||| |||||
                                TGGTTTTAT T  GTA CGTCT
                                     T TG   C    A
GAM1069  LOC221393 5'  TGATTGTGGTTTTGGT     92297        _
                                GCCAAGAT GCAGTCA
                                |||||||| |||||||
                                TGGTTTTG TGTTAGT
                                     G
GAM1069  LOC221405 5'  GTGATTGCGTTTGGC      93886     A
                                GCCA GATGCAGTCAT
                                |||| ||||||||||
                                CGGT TTGCGTTAGTG
                                  _
GAM1069  LOC221641 5'  AATCTTTGTGACTGTGGTTTGG 93722      AT       CA
            T                    GCCAAG  GCAGTCATAG  GGAT
                                ||||||  ||||||||||  ||||
                                TGGTTT  TGTCAGTGTT  TCTA
                                   GG        __   AA
GAM1069  LOC221718 5'  TCAGGTCGGTTGTATTTTG   93633        GT ATA  AG
                                CAAGATGCA  C   GC  GA
                                |||||||||  |   ||  ||
                                GTTTTATGT  G   TG  CT
                                     TG C__  GA
GAM1069  LOC221929 5'  ATCCTGCCTAGTGTGTTTTGG  92673        GTCATA
                                CCAAGATGCA     GCAGGAT
                                ||||||||||     |||||||
                                GGTTTTGTGT     CGTCCTA
                                     GATC__
GAM1069  LOC245806 3'  TCACTGGTTGTGATTTGGT   91893      GATGCA      _ _
                                GCCAA     GTCATAGC AG GA
                                |||||     |||||||| || ||
                                TGGTT     TAGTGTTG TC CT
                                  _______       G  A
GAM1069  LOC253955 3'  ATTTTGTTTTGTTTTGTTTTGG 94422        C  T  T
            T                    GCCAAGATG AG CA AGCAGGAT
                                ||||||||| || || ||||||||
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                                TGGTTTTGT TT GT TTGTTTTA
                                      T _ T
GAM1069  LOC254085 5'  TCCTGGTTTGTGTTTTG     96121          TCATAG
                                CAAGATGCAG     CAGGA
                                ||||||||||     |||||
                                GTTTTGTGTT     GTCCT
                                     TG____
GAM1069  LOC254428 3'  GTTTTGTTTTATTTTTGGTTTT 95462        G   TCAT__
                  GGT                CCAAGAT CAG     AGCAGGAT
                                ||||||| |||     ||||||||
                                GGTTTTG GTT     TTGTTTTG
                                   _  TTTATT
GAM1069  LOC254531 3'  ATTTTGTTATTGTTGTTTGGT  94981      GAT    TC
                                GCCAA   GCAG  ATAGCAGGAT
                                |||||   ||||  ||||||||||
                                TGGTT   TGTT  TATTGTTTTA
                                   ___    GT
GAM1069  LOC255299 5'  GTCCTGCTATGACCTCCTGGC  97468     A  TGCA
                                GCCA GA    GTCATAGCAGGAT
                                |||| ||    ||||||||||||
                                CGGT CT    CAGTATCGTCCTG
                                  C  C___
GAM1069  LOC255465 3'  ATTATTTATGGTTGCAGTTTGG 97279       A    GT    CAGGAT
                  T                 GCCAAG TGCA  CATAG
                                |||||| ||||  |||||
                                TGGTTT ACGT  GTATT
                                   G    TG     TATTA
GAM1069  LOC256126 3'  CTATAATGCATCTTGGC     95303          GTC
                                GCCAAGATGCA   ATAG
                                ||||||||||   ||||
                                CGGTTCTACGT   TATC
                                      AA_
GAM1069  LOC256476 5'  TGTTGTGGCTGATGTGCATTTT 96822        _____       AGGAT
                  GGT                AAGATGCA    GTCATAGC
                                ||||||||    ||||||||
                                TTTTACGT    CGGTGTTG
                                     GTAGT         TA
GAM1069  LOC256946 3'  ATCTTGCCTTTGTTTATTTTGG 94544        CAGT  TA_
                  T                 GCCAAGATG    CA   GCAGGAT
                                |||||||||    ||   |||||||
                                TGGTTTTAT    GT   CGTTCTA
                                     TT__  TTC
GAM1069  LOC257354 3'  GTTTAATTATGACTGTTTTTGG 95098       T        CA
                  T                 GCCAAGA GCAGTCATAG  GGAT
                                ||||||| ||||||||||  ||||
                                TGGTTTT TGTCAGTATT  TTTG
                                   _        AA
GAM1069  LOC51003  5'  GTCAGGCTGGTGGCGTTTTGGT 32151          AGTCA    AG
                                GCCAAGATGC    TAGC  GAT
                                ||||||||||    ||||  |||
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                                TGGTTTTGCG    GTCG  CTG
                                     GTG__    GA
GAM1069  LOC51725  3'  TCCAGGGCTCATTTTGGT    69868        C   ATAGCA
                                GCCAAGATG AGTC     GGA
                                ||||||||| ||||     |||
                                TGGTTTTAC TCGG     CCT
                                     _   GA____
GAM1069  LOC90333  3'  TCCAGTTGCATTTTGGC     62303         GTCATA  A
                                GCCAAGATGCA     GC GGA
                                ||||||||||     || |||
                                CGGTTTTACGT     TG CCT
                                     ______ A
GAM1069  LOC90841  5'  ATCTTTGTCACTGTGTTTTG   64192         C   CA
                                CAAGATGCAGT ATAG  GGAT
                                |||||||||| ||||  ||||
                                GTTTTGTGTCA TGTT  TCTA
                                     C   __
GAM1069  LOC90906  5'  TCCTGCTACATTTCTTGGT    64313       TGCAGTCA
                                GCCAAGA       TAGCAGGA
                                |||||||       ||||||||
                                TGGTTCT       ATCGTCCT
                                    TTAC____
GAM1069  LOC91496  5'  TTCTGTTAACACTTTGGC     66228      GATGC   CA
                                GCCAA    AGT  TAGCAGGA
                                |||||    |||  ||||||||
                                CGGTT    TCA  ATTGTCTT
                                   _____   CA
GAM1069  LOC92181  3'  GTTTTGTTTTGTTTTGTTTTGG 68406        C  T  T
            T                    GCCAAGATG AG CA AGCAGGAT
                                ||||||||| || || ||||||||
                                TGGTTTTGT TT GT TTGTTTTG
                                     T  _  T
GAM1069  LOC92573  5'  ATTCGATAGATGTGGTTGTGTT 69801        GT   GCA___
            TTG                    AAGATGCA  CATA     GGAT
                                ||||||||  ||||     ||||
                                TTTTGTGT  GTGT     CTTA
                                     TG   AGATAG
GAM1069  LOC92912  3'  TTCTTTTGATTCCATTTTGGT  70847        C    TAGC   T
                                GCCAAGATG AGTCA    AGGA
                                ||||||||| |||||    ||||
                                TGGTTTTAC TTAGT    TCTT
                                     C    TT__    T
GAM1069  LOC93166  3'  ATTCTGCTGTGTCAGTTTGGC  71622       A  CAGT
                                GCCAAG TG    CATAGCAGGAT
                                ||||||  ||   ||||||||||
                                CGGTTT AC    GTGTCGTCTTA
                                   G  T___
GAM1070  PRO2900   3'  TGTGCGCATCTCAATCA     37808        CC
                                TGATTGAG  GCGCACG
                                ||||||||  |||||||
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                                ACTAACTC  CGCGTGT
                                    TA
GAM1071  ABCA1    3'  CAATGCAATTCAATGCA     18546           C
                                TGCATTGAATTGCA TTG
                                |||||||||||||| |||
                                ACGTAACTTAACGT AAC
                                                _
GAM1071  AMFR     3'  CAACTCCCAGCTCAATGCA    57242        A   CACTT
                                TGCATTGA TTG    GTTG
                                |||||||| |||    ||||
                                ACGTAACT GAC    CAAC
                                    C   CCT__
GAM1071  ATP8B2   5'  AACAAGTGCTCCATCAAT    65209      ATT_
                                ATTGA   GCACTTGTT
                                |||||   |||||||||
                                TAACT   CGTGAACAA
                                   ACCT
GAM1071  MEF2D    3'  CAACAGCACACTCAGTGCAG   96909        AT_   ACT
                                CTGCATTGA   TGC   TGTTG
                                |||||||||   |||   |||||
                                GACGTGACT   ACG   ACAAC
                                    CAC   ____
GAM1071  PREP     3'  CAACAAGTTAGTTTTCAAGCAG 10771      A    TT  __
           T                     ACTGC TTGAA  GC  ACTTGTTG
                                |||||  |||||  ||  ||||||||
                                TGACG AACTT  TG  TGAACAAC
                                  _    T_  AT
GAM1071  PTP4A2   3'  GTGCAACCCAATGAGT     12986    G    AA
                                ACT CATTG  TTGCAC
                                |||  |||||  ||||||
                                TGA GTAAC  AACGTG
                                  _    CC
GAM1071  BC022889 3'  CAACAGTCTATTTCAATGCAG  83645         T  C   T
                                CTGCATTGAA TG ACT GTTG
                                |||||||||| ||  ||| ||||
                                GACGTAACTT AT TGA CAAC
                                    T  C  _
GAM1071  KIAA0426 3'  TGCAACATCAATGCAGT     28266         A_
                                ACTGCATTGA  TTGCA
                                |||||||||  |||||
                                TGACGTAACT  AACGT
                                    AC
GAM1071  KIAA1434 3'  CAACATACAAATTCAATTCAGT 69609     C       GCACT
                                ACTG ATTGAATT    TGTTG
                                |||| ||||||||    |||||
                                TGAC TAACTTAA    ACAAC
                                  T      ACAT_
GAM1071  KIAA1713 3'  CAACAAATAGAATAATGCAGT  72347         AA   CAC
                                ACTGCATTG  TTG   TTGTTG
                                |||||||||  |||   ||||||
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                                TGACGTAAT  GAT   AACAAC
                                     AA  A__
GAM1071  MGC2752   5'  CAACAAGTGCTGAGATCAG   78445    C   GAATT
                                CTG ATT    GCACTTGTTG
                                ||| |||    ||||||||||
                                GAC TAG    CGTGAACAAC
                                  _  AGT__
GAM1071  MLLT10    3'  CAACAAGAAACTCAATGCA   16167       A  GCA
                                TGCATTGA TT   CTTGTTG
                                |||||||| ||   |||||||
                                ACGTAACT AA   GAACAAC
                                     C  A__
GAM1071  MSTP033   3'  CAAGTGCCAATTCAATGGAG  50781    G       _
                                CT CATTGAATTG CACTTG
                                || ||||||||||| ||||||
                                GA GTAACTTAAC GTGAAC
                                  G         C
GAM1071  SLC5A7    3'  CAACAAGTTGTTTCAAACAG  41505    CA    TT  _
                                CTG  TTGAA  GCA CTTGTTG
                                |||  |||||  ||| |||||||
                                GAC  AACTT  TGT GAACAAC
                                  A_    __   T
GAM1071  STAT5A    3'  AGGCACTCAATGCAG       12009        AT   A
                                CTGCATTGA  TGC CT
                                |||||||||  ||| ||
                                GACGTAACT  ACG GA
                                     C_  _
GAM1071  LOC115265 3'  AACAATGTTCAATTCAG     73352        C  _
                                TTGAATTG AC TTGTT
                                |||||||| || |||||
                                GACTTAAC TG AACAA
                                     T  T
GAM1071  LOC165639 5'  AAGGCAATTCAGTACAG     87252     C       A
                                CTG ATTGAATTGC CTT
                                ||| |||||||||| |||
                                GAC TGACTTAACG GAA
                                  A        _
GAM1072  ADH1B     3'  CTTAGACATAAAGTAAAAT    72644     C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM1072  AHR       3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM1072  FDFT1     3'  TAGGAAAGTGAAATG       15518          A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
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                                GTAAAGTGAAAG GAT
                                             _
GAM1072 JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                   CATTTCACTTTCACTGTCTGAGAT
                                   ||||||||||||||||||||||||
                                   GTAAAGTGAAAGTGACAGACTCTA

GAM1072 KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                   CA  TTCACTGTCTG GA
                                   ||  ||||||||||| ||
                                   GT  AGGTGACAGAC CT
                                    AT         C
GAM1072 PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                   ATTTCACTTT ACTGT
                                   |||||||||| |||||
                                   TAAAGTGAAA TGACA
                                         A
GAM1072 PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                   TTTCACTTTCA   TCTG GA
                                   ||||||||||   |||| ||
                                   AAAGTGAAAGT   GGAC CT
                                         T__   _
GAM1072 WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                   TTTCA TTTCACTGTCT
                                   ||||| ||||||||||
                                   AAAGT AAAGTGACGGG
                                      A
GAM1072 ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                   TTTCACTTT  CTGT   AGAT
                                   |||||||||  ||||   ||||
                                   AAAGTGAAA  GACA   TCTA
                                        C_    CG_
GAM1072 CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                   TTCACTTTCA  GT  GAG
                                   ||||||||||  ||  |||
                                   AAGTGAAAGT  CA  CTC
                                         CT  __
GAM1072 EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                   CTTTCACT TC  GAGAT
                                   ||||||||  ||  |||||
                                   GAAAGTGA AG  TTCTA
                                        G  TC
GAM1072 FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
              G                     CATTTC        GTCTGAGAT
                                    ||||||        |||||||||
                                    GTAAAG        CAGACTCTA
                                       AAACATTT_
GAM1072 FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                   CATTTCA   TCACTGTCTGAGAT
                                   |||||||   ||||||||||||||
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                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM1072 KIAA0984 3' TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM1072 KLHL6    3' ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM1072 NIR3     3' GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM1072 PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM1072 PP35     3' ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM1072 PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148       TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM1072 SEP15    3' TCCTACAGTAAGAGTGAAA   14934       C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM1072 SFXN2    3' CTCAGGGGAAAAAAGTGAAA  73941       CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM1072 LOC149703 3' ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM1072 LOC154007 3' ATCTCAAACCCTTTAGTGAAA  81015      TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
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                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM1072  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM1072  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                      _
GAM1073  ABCC5     3'  CAAGCCCTGGAGCCA       19095       GA
                                TGGCT  CAGGGCTTG
                                |||||  |||||||||
                                ACCGA  GTCCCGAAC
                                   G_
GAM1073  ALPI      3'  CCAAGTCACAGCCACT      7896         ACAG
                                AGTGGCTG   GGCTTGG
                                ||||||||   |||||||
                                TCACCGAC   CTGAACC
                                    A___
GAM1073  ALPPL2    3'  CCAAGTCACAGCCACT      68837        ACAG
                                AGTGGCTG   GGCTTGG
                                ||||||||   |||||||
                                TCACCGAC   CTGAACC
                                    A___
GAM1073  CD4       3'  CCAGTGACCAGTCACTGA    5223          ACAGG   T
                                TCAGTGGCTG    GCT GG
                                ||||||||||    ||| ||
                                AGTCACTGAC    TGA CC
                                     CAG__  _
GAM1073  CEP2      3'  CAGGGCTCAGCCACTGA     22282          CAG G
                                TCAGTGGCTGA   G CTTG
                                ||||||||||   | ||||
                                AGTCACCGACT   C GGAC
                                      ___ G
GAM1073  CKAP1     3'  CAGCTCAGCCACTGA       73536          CAGG   T
                                TCAGTGGCTGA   GCT G
                                ||||||||||    ||| |
                                AGTCACCGACT   CGA C
                                      ____  T
GAM1073  CNK       3'  CCAAGCCCTGAAGGCC      14518      GA
                                GGCT  CAGGGCTTGG
                                ||||  ||||||||||
                                CCGG  GTCCCGAACC
                                  AA
GAM1073  COL4A3    3'  CAAGCCCACCACATGA      3618       _   CTGACA
                                TCA GTGG     GGGCTTG
                                ||| ||||     |||||||
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                                AGT CACC     CCCGAAC
                                  A   A_____
GAM1073  COL4A3   3'  CAAGCCCACCACATGA     48563    _   CTGACA
                                TCA GTGG     GGGCTTG
                                ||| ||||     |||||||
                                AGT CACC     CCCGAAC
                                  A   A_____
GAM1073  COL4A3   3'  CAAGCCCACCACATGA     48551    _   CTGACA
                                TCA GTGG     GGGCTTG
                                ||| ||||     |||||||
                                AGT CACC     CCCGAAC
                                  A   A_____
GAM1073  DNASE2   3'  AGTCCCAGCCACTGA      7261          ACA
                                TCAGTGGCTG   GGGCT
                                ||||||||||   |||||
                                AGTCACCGAC   CCTGA
                                     ___
GAM1073  DUSP2    3'  CCAAGCCCTGTGTTCCTGG   15346     TG  TG
                                TCAG  GC  ACAGGGCTTGG
                                ||||  ||  ||||||||||||
                                GGTC  TG  TGTCCCGAACC
                                  CT  __
GAM1073  EIF4G1   5'  CCAGGGTGTGCAGCCACTGA  17069         _  GGG
                                TCAGTGGCTG ACA   CTTGG
                                |||||||||| |||   |||||
                                AGTCACCGAC TGT   GGACC
                                     G   G__
GAM1073  F7       3'  CCAAGCCCCACCTGCACGTGA  3718     _   G TGACA
                                TCA GTG C    GGGCTTGG
                                ||| ||| |    ||||||||
                                AGT CAC G    CCCGAACC
                                  G   _ TCCAC
GAM1073  F7       3'  CCAAGCCCCACCTGCACGTGA  39028    _   G TGACA
                                TCA GTG C    GGGCTTGG
                                ||| ||| |    ||||||||
                                AGT CAC G    CCCGAACC
                                  G   _ TCCAC
GAM1073  FKBP2    5'  CCAAGCCCCCTTCTCACTGG   54042       CTGACA
                                TCAGTGG     GGGCTTGG
                                |||||||     ||||||||
                                GGTCACT     CCCGAACC
                                    CTTCC_
GAM1073  FN14     3'  CCAAGCTCCTCCAACCAC    33561     C  AC  _
                                GTGG TG  AGG GCTTGG
                                |||| ||  ||| ||||||
                                CACC AC  TCC CGAACC
                                  A  C_   T
GAM1073  GJA5     3'  CCAGATCATCAGCCACTGA    17940          CAG GC
                                TCAGTGGCTGA   G  TTGG
                                ||||||||||   |  ||||
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                                AGTCACCGACT  C  GACC
                                     A__ TA
GAM1073  HAP1    3'  CCAAGCCCCACACCCGC    14165     C  ACA
                                GTGG TG  GGGCTTGG
                                |||| ||  ||||||||
                                CGCC AC  CCCGAACC
                                  C  AC_
GAM1073  HCS     3'  CCAGTGTGGTAGCCACT    38462       A  GG  T
                                AGTGGCTG CA  GCT GG
                                |||||||| ||  ||| ||
                                TCACCGAT GT  TGA CC
                                    G  G_  _
GAM1073  HMGA1   3'  CCAAGCCCCATCTCATCCTGG  76934     T  C  CA__
                                TCAG GG TGA   GGGCTTGG
                                |||| || |||   ||||||||
                                GGTC CT ACT   CCCGAACC
                                  _ _  CTAC
GAM1073  HSPA5   3'  CCAAGCCCAATACAGCCATT  18080       ACA_
                                AGTGGCTG   GGGCTTGG
                                ||||||||   ||||||||
                                TTACCGAC   CCCGAACC
                                    ATAA
GAM1073  ITPKA   3'  CCAGGTGCCAGCCACT     9416        A AGG
                                AGTGGCTG C  GCTTGG
                                |||||||| |  ||||||
                                TCACCGAC G  TGGACC
                                    C ___
GAM1073  LAD1    3'  CCTGCTCCCAGCCACTGA   18699        ACA  TT
                                TCAGTGGCTG  GGGC  GG
                                ||||||||||  ||||  ||
                                AGTCACCGAC  CTCG  CC
                                     C__   T_
GAM1073  LEP     3'  CCAAGGTCTTCAGCCAT    4046        C  G
                                GTGGCTGA AGG CTTGG
                                |||||||| ||| |||||
                                TACCGACT TCT GAACC
                                    _  G
GAM1073  MAPT    3'  CCAAGCCTGGGCCACTGG   33706       GACA
                                TCAGTGGCT   GGGCTTGG
                                |||||||||   ||||||||
                                GGTCACCGG   TCCGAACC
                                    G___
GAM1073  MAPT    3'  CCAAGCCTGGGCCACTGG   33687       GACA
                                TCAGTGGCT   GGGCTTGG
                                |||||||||   ||||||||
                                GGTCACCGG   TCCGAACC
                                    G___
GAM1073  MAPT    3'  CCAAGCCTGGGCCACTGG   19776       GACA
                                TCAGTGGCT   GGGCTTGG
                                |||||||||   ||||||||
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                                GGTCACCGG   TCCGAACC
                                    G___
GAM1073 MAPT    3' CCAAGCCTGGGCCACTGG   33696       GACA
                                TCAGTGGCT   GGGCTTGG
                                |||||||||   ||||||||
                                GGTCACCGG   TCCGAACC
                                    G___
GAM1073 MATN1   5' CCAAGCCCCGCCCTTTGG   9918     T_  TGACA
                                TCAG GGC    GGGCTTGG
                                ||||  |||   ||||||||
                                GGTT CCG    CCCGAACC
                                  TC  C____
GAM1073 MNT     3' CAAACCCAGCCACTG      39703       GACA  C
                                CAGTGGCT    GGG TTG
                                ||||||||    ||| |||
                                GTCACCGA    CCC AAC
                                    ____  A
GAM1073 MPHOSPH1 3' CCTTACCAGCCACTGG    32470        AC
                                TCAGTGGCTG  AGGG
                                ||||||||||  ||||
                                GGTCACCGAC  TTCC
                                     CA
GAM1073 MUCDHL  3' CCAAGCCCGCGGAGGCACCGA 48364   A  G  GACA
                                TC GTG CT   GGGCTTGG
                                || ||| ||   ||||||||
                                AG CAC GA   CCCGAACC
                                 C  G  GGCG
GAM1073 MYCL2   3' CCAAGCCCTGGCTCATGA   18178    GT   TGA
                                TCA  GGC   CAGGGCTTGG
                                |||  |||   ||||||||||
                                AGT  TCG   GTCCCGAACC
                                  AC  ___
GAM1073 NAV2    3' CAGGTCCATCAGCCTCTGA  60156    T    CA
                                TCAG GGCTGA  GGGCTTG
                                ||||  ||||||  |||||||
                                AGTC CCGACT  CCTGGAC
                                  T     A_
GAM1073 NHLH1   3' CCAAATTTTCAGCCAC     18797       C  GC
                                GTGGCTGA AGG  TTGG
                                |||||||| |||  ||||
                                CACCGACT TTT  AACC
                                    _  A_
GAM1073 NOS1    3' CCCTCAGCCACTGA       5247         CA
                                TCAGTGGCTGA  GGG
                                ||||||||||  |||
                                AGTCACCGACT  CCC
                                     __
GAM1073 OAS2    3' CCAAGCCCTCCTACCTAC   10303    C  AC
                                GTGG TG  AGGGCTTGG
                                ||||  ||  |||||||||
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                                CATC AT  TCCCGAACC
                                  C  CC
GAM1073  OPRM1    3'  CCAAGCTTAGAAGCCAC     6201        GACA
                                GTGGCT   GGGCTTGG
                                ||||||   ||||||||
                                CACCGA   TTCGAACC
                                   AGA_
GAM1073  OSM      3'  CCTCTGCTACTAGCCACTGA  40075         ACAG   TT_
                                TCAGTGGCTG   GGC  GG
                                ||||||||||   |||  ||
                                AGTCACCGAT   TCG  CC
                                     CA__   TCT
GAM1073  PAWR     5'  CCAAGCCCCGCCGGCTGCTG  10428     TG   ACA
                                CAG  GCTG   GGGCTTGG
                                |||  ||||   ||||||||
                                GTC  CGGC   CCCGAACC
                                  GT   CGC
GAM1073  PRPH     3'  CCAAGCCCTACCCGGCCA    20758       AC_
                                TGGCTG   AGGGCTTGG
                                ||||||   |||||||||
                                ACCGGC   TCCCGAACC
                                   CCA
GAM1073  PTGER4   5'  CCAAAAATCGACAGCCACTGA  6315          ACA  GC_
                                TCAGTGGCTG   GG   TTGG
                                ||||||||||   ||   ||||
                                AGTCACCGAC   CT   AACC
                                     AG_  AAA
GAM1073  PYGB     3'  CCAAACACTTTGCCAGCCACTG 11173         A    C__
           G                     TCAGTGGCTG CAGGG   TTGG
                                ||||||||||  |||||   ||||
                                GGTCACCGAC GTTTC   AACC
                                     C    ACA
GAM1073  PYGM     5'  CCTGGTTCAGCCACTGA     18822          __
                                TCAGTGGCTGA  CAGG
                                ||||||||||   ||||
                                AGTCACCGACT  GTCC
                                      TG
GAM1073  RAB3A    3'  CCAAGCCCTGCCCCTCCTG   11183     TG CTGA
                                CAG  G   CAGGGCTTGG
                                |||  |   ||||||||||
                                GTC  C   GTCCCGAACC
                                  CT CCC_
GAM1073  RBM3     5'  CCAAGCCCCGCAGTGCCCAC  70485     ___  ACA
                                GTGG   CTG   GGGCTTGG
                                ||||   |||   ||||||||
                                CACC   GAC   CCCGAACC
                                  CGT   GC_
GAM1073  RS1      3'  CCAAGCCCTCTGCAACCAC   4389      C  AC_
                                GTGG TG   AGGGCTTGG
                                ||||  ||   |||||||||
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                                CACC AC   TCCCGAACC
                                  A  GTC
GAM1073  SFRP1    3'  CCAACAGCAACACAGCCACT   11565        ACAGG  __
                                AGTGGCTG    GCT  TGG
                                ||||||||    |||  |||
                                TCACCGAC    CGA  ACC
                                    ACAA_   CA
GAM1073  SLC2A3   3'  CCAAACCCTTGTCAGT      22659        _  C
                                GCTGACA GGG TTGG
                                ||||||| ||| ||||
                                TGACTGT CCC AACC
                                    T   A
GAM1073  SNAP25   5'  CAAACCCGTCACTGA       11833        TGACA  C
                                TCAGTGGC    GGG TTG
                                ||||||||    ||| |||
                                AGTCACTG    CCC AAC
                                    _____   A
GAM1073  SNAP25   5'  CAAACCCGTCACTGA       55526        TGACA  C
                                TCAGTGGC    GGG TTG
                                ||||||||    ||| |||
                                AGTCACTG    CCC AAC
                                    _____   A
GAM1073  SPOCK    5'  CCAAGCCCTGGACCCAT     62815     CTGA
                                GTGG   CAGGGCTTGG
                                ||||   ||||||||||
                                TACC   GTCCCGAACC
                                  CAG_
GAM1073  SSX4     3'  CCGTTGTATCAGTCACTGA   94662          __  _
                                TCAGTGGCTGA  CAG GG
                                ||||||||||  ||| ||
                                AGTCACTGACT  GTT CC
                                      AT   G
GAM1073  SSX4     3'  CCGTTGTATCAGTCACTGA   18878          __  _
                                TCAGTGGCTGA  CAG GG
                                ||||||||||  ||| ||
                                AGTCACTGACT  GTT CC
                                      AT   G
GAM1073  TCF15    3'  CCAGGAGCCAGCCACTGG    16040        ACAGGG
                                TCAGTGGCTG     CTTGG
                                ||||||||||     |||||
                                GGTCACCGAC     GGACC
                                     CGA___
GAM1073  TMC1     5'  CCAAACTAGCCAGCCACTGA  56898         ACAG  C
                                TCAGTGGCTG   GG TTGG
                                ||||||||||   || ||||
                                AGTCACCGAC   TC AACC
                                     CGA_  A
GAM1073  TMC2     3'  CCTTGTCAGCTACCGA      54962    A
                                TC GTGGCTGACAGGG
                                || ||||||||||||
```

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                                AG CATCGACTGTTCC
                                 C
GAM1073 TNFSF13B 5' CCAAGCCCTGCCAT      21652      TGAC
                                GTGGC   AGGGCTTGG
                                |||||   |||||||||
                                TACCG   TCCCGAACC
                                  ____
GAM1073 TSPY     3' CAGATGTCAGCCCTGA     82104     T      GGGCT
                                TCAG GGCTGACA    TG
                                |||| ||||||||    ||
                                AGTC CCGACTGT    AC
                                  _      AG___
GAM1073 TUBG1    3' CCAAGCCCTGCCTGACTGA   63397     __   TGAC
                                TCAGT  GGC   AGGGCTTGG
                                |||||  |||   |||||||||
                                AGTCA  CCG   TCCCGAACC
                                   GT  ____
GAM1073 TUFT1    3' CCAAGCCCCTGGCCACT    39257       ACA
                                AGTGGCTG   GGGCTTGG
                                ||||||||   ||||||||
                                TCACCGGT   CCCGAACC
                                    C__
GAM1073 XRCC3    5' CCAAGCCCCAGAGAGTGA   18337    GTGG   ACA
                                TCA   CTG   GGGCTTGG
                                |||   |||   ||||||||
                                AGT   GAC   CCCGAACC
                                  GAGA  ___
GAM1073 AHCYL1   3' CCAAGCCCTGTTTCCTGC   21762   TG CT
                                G  G  GACAGGGCTTGG
                                |  |  ||||||||||||
                                C  C  TTGTCCCGAACC
                                 GT CT
GAM1073 ALOXE3   3' CCAAGCCTAGAGCCAC     41261      GACA
                                GTGGCT   GGGCTTGG
                                ||||||   ||||||||
                                CACCGA   TCCGAACC
                                   GA__
GAM1073 APCL     5' CGAGCTCAGCCACCGA     19670    A      CAGG   TG
                                TC GTGGCTGA   GCT  G
                                || ||||||||   |||  |
                                AG CACCGACT   CGA  C
                                 C      ____   GT
GAM1073 APPD     3' CCAAGCCCTGCCGATCA    44212    GC  A
                                TG  TG CAGGGCTTGG
                                ||  || ||||||||||
                                AC  GC GTCCCGAACC
                                 TA  C
GAM1073 BMF      3' CCAGCTGGGTGTCAGCCACGGA 53153    A       G__    T
                                TC GTGGCTGACA   GGCT GG
                                || ||||||||||   |||| ||
```

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                                AG CACCGACTGT   TCGA CC
                                 G        GGG   _
GAM1073  BPESC1    3'  CAAGCCCTCCTCTGA      41470      T  CTGAC
                                TCAG GG    AGGGCTTG
                                |||| ||    ||||||||
                                AGTC CC    TCCCGAAC
                                  T ______
GAM1073  BRD4      3'  CCAAGCCCTGCATCCCCAC   54274      C__  A
                                GTGG   TG CAGGGCTTGG
                                ||||   || ||||||||||
                                CACC   AC GTCCCGAACC
                                  CCT  _
GAM1073  C20orf150 3'  CCACTGCCTCAGCCAC      65392        CAG   T_
                                GTGGCTGA   GGC  TGG
                                ||||||||   |||  |||
                                CACCGACT   CCG  ACC
                                     ___   TC
GAM1073  C20orf29  3'  CCAAGCCCGTTCCCAC      37125      CT   A
                                GTGG  GAC GGGCTTGG
                                ||||  ||| ||||||||
                                CACC  TTG CCCGAACC
                                  C_   _
GAM1073  C8orf13   5'  CCAACTGTGCCACCCAC     81570      C  A  G  C
                                GTGG TG CA GG TTGG
                                |||| || || || ||||
                                CACC AC GT TC AACC
                                  C  C  G  _
GAM1073  CALN1     3'  CCTAGATGTCAGCCACT     48862           ___
                                AGTGGCTGACA   GGG
                                ||||||||||   |||
                                TCACCGACTGT   TCC
                                      AGA
GAM1073  CXYorf1   3'  CCAAGGCAATGGTCAGCCACTG 82041           AGG_ _
                                CAGTGGCTGAC    GC TTGG
                                ||||||||||    || ||||
                                GTCACCGACTG    CG AACC
                                      GTAA  G
GAM1073  CYYR1     5'  CCAAGCCTCAGGCCACCGG    53672    A     GACA
                                TC GTGGCT    GGGCTTGG
                                || ||||||    ||||||||
                                GG CACCGG    TCCGAACC
                                 C     AC__
GAM1073  DJ37E16.5 3'  CCAAGCCCCACCCTTTCCTGG  39728      T___  C  ACA
                                TCAG    GG TG   GGGCTTGG
                                ||||    || ||   ||||||||
                                GGTC    CC AC   CCCGAACC
                                  CTTT  C  ___
GAM1073  DKFZP434O047 5'  CCAAGCCCTGGGCCAGACTGG  31507       __    GA
                                TCAGT  GGCT  CAGGGCTTGG
                                |||||  ||||  ||||||||||
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                                GGTCA  CCGG  GTCCCGAACC
                                   GA   __
GAM1073  DKFZP564O0423 3'  CCTTGTCAGCCTCTGA      91682      T
                                TCAG GGCTGACAGGG
                                |||| ||||||||||
                                AGTC CCGACTGTTCC
                                  T
GAM1073  DKFZp761O17121 3'  CCATGCTGCAGCCACTGA    50138          A   GGCT
                                TCAGTGGCTG CAG    TGG
                                |||||||||| |||    |||
                                AGTCACCGAC GTC    ACC
                                      _   GT__
GAM1073  DOCK3    3'  CCAAGGCTCAGTCAC       66499         CAG G
                                GTGGCTGA   G CTTGG
                                ||||||||   | |||||
                                CACTGACT   C GAACC
                                     ___ G
GAM1073  DOCK3    3'  CCAAGCCCTACCACCCCCGC   66498      C__  AC
                                GTGG   TG  AGGGCTTGG
                                ||||   ||  |||||||||
                                CGCC   AC  TCCCGAACC
                                  CCC  CA
GAM1073  DUSP10   3'  CCAAGCCCTGTTGTGCTCA   58560   T  _
                                G GGC TGACAGGGCTTGG
                                | ||| ||||||||||||
                                A TCG GTTGTCCCGAACC
                                 C   T
GAM1073  DUSP10   3'  CCAAGCCCTGTTGTGCTCA   23280   T  _
                                G GGC TGACAGGGCTTGG
                                | ||| ||||||||||||
                                A TCG GTTGTCCCGAACC
                                 C   T
GAM1073  FKSG83   3'  CCAAGATCACGCCACTGA    49326        _  CAGGG
                                TCAGTGGC TGA    CTTGG
                                |||||||| |||    |||||
                                AGTCACCG ACT    GAACC
                                     C   A____
GAM1073  FLJ00058 5'  CCAAGCCCGGCCCCACTGG   78764       CTGACA
                                TCAGTGG     GGGCTTGG
                                |||||||     ||||||||
                                GGTCACC     CCCGAACC
                                    CCGG__
GAM1073  FLJ10157 3'  CCAAGCCCTGTGAGACTGA   35859      GG  G
                                TCAGT  CT ACAGGGCTTGG
                                |||||  || ||||||||||
                                AGTCA  GA TGTCCCGAACC
                                   __  G
GAM1073  FLJ10307 3'  CCTTGCACAGCCACTGA     36006         A_
                                TCAGTGGCTG  CAGGG
                                ||||||||||  |||||
```

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                                AGTCACCGAC  GTTCC
                                      AC
GAM1073  FLJ12816  3'  CCTTATCAGCCACTGG      41933           C
                                TCAGTGGCTGA AGGG
                                |||||||||||  ||||
                                GGTCACCGACT TTCC
                                      A
GAM1073  FLJ13441  3'  CCAAGCCCCACGAACCCTGA   43659      T  CTGACA
                                TCAG GG     GGGCTTGG
                                ||||  ||     ||||||||
                                AGTC CC     CCCGAACC
                                  _  AAGCAC
GAM1073  FLJ14084  3'  CCAAGCCCCACCTATT      41297       C  ACA
                                AGTGG TG   GGGCTTGG
                                |||||  ||   ||||||||
                                TTATC AC   CCCGAACC
                                   C  ___
GAM1073  FLJ14103  5'  CCAAGCCCTGCCTCTG      96203     T   TGAC
                                CAG GGC    AGGGCTTGG
                                |||  |||    |||||||||
                                GTC CCG    TCCCGAACC
                                  T  _____
GAM1073  FLJ20320  3'  CCAAGTGTGCCCCAGCCACTGA 34938          ACA   ____
                                TCAGTGGCTG   GGGC    TTGG
                                ||||||||||   ||||    ||||
                                AGTCACCGAC   CCCG    AACC
                                      ___    TGTG
GAM1073  FLJ20539  3'  CCACCTGGTCAGCCAC      35362         A   CT
                                GTGGCTGAC GGG  TGG
                                |||||||||  |||  |||
                                CACCGACTG TCC  ACC
                                      G  __
GAM1073  FLJ21916  3'  CCAAGCCCTACAGCT       43642       AC
                                GGCTG  AGGGCTTGG
                                |||||  |||||||||
                                TCGAC  TCCCGAACC
                                   A_
GAM1073  FREQ     3'  CCAGCGGTGCCTGCCACTGA   26571         TGA  GG   T
                                TCAGTGGC   CA  GCT GG
                                ||||||||   ||  ||| ||
                                AGTCACCG   GT  CGA CC
                                     TCC  GG   _
GAM1073  FYCO1    3'  CCTTCTTCATCATGCCACTGA  44494         _   CA   CTT
                                TCAGTGGC TGA  GGG   GG
                                ||||||||  |||  |||   ||
                                AGTCACCG ACT  TTC   CC
                                     T   AC   TT_
GAM1073  GPR9     3'  CCAAGCCCCATCCTGCCGC    7684        T_  CA
                                GTGGC  GA  GGGCTTGG
                                |||||  ||  ||||||||
```

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                                CGCCG  CT  CCCGAACC
                                   TC  AC
GAM1073  GPS2     3'  CCAATAAAATCTACCTGCCACT 15663        TGAC   GC___
              GA                    TCAGTGGC    AGG    TTGG
                                ||||||||    |||    ||||
                                AGTCACCG    TCT    AACC
                                     TCCA   AAAAT
GAM1073  HIC2     3'  CCAAGCCCAGCTGGCACCA   65257     C  A  ___
                                TGG TG CA   GGGCTTGG
                                ||| || ||   ||||||||
                                ACC AC GT   CCCGAACC
                                  _  G  CGA
GAM1073  HIP-55   3'  CCAAGCCCTGCCTGTGGCCA   25928       A___
                                TGGCTG    CAGGGCTTGG
                                ||||||    ||||||||||
                                ACCGGT    GTCCCGAACC
                                   GTCC
GAM1073  HIP-55   3'  CCAAGCCCTGAGTGGCCACTG  25927         A_
                                CAGTGGCTG  CAGGGCTTGG
                                |||||||||  ||||||||||
                                GTCACCGGT  GTCCCGAACC
                                     GA
GAM1073  HSPB7    3'  CCAAGCCCCACGCCAGCGA   27025    AG    _  ACA
                                TC  TGGC TG   GGGCTTGG
                                ||  |||| ||   ||||||||
                                AG  ACCG AC   CCCGAACC
                                 CG    C  ___
GAM1073  HT008    3'  CCAAGCCTTTCACCAATGA   59802     G   C   C
                                TCA TGG TGA AGGGCTTGG
                                ||| ||| ||| |||||||||
                                AGT ACC ACT TTCCGAACC
                                  A  _  _
GAM1073  KIAA0798 3'  CCATGGTAGCCACTGA      27720          A  _
                                TCAGTGGCTG CA GG
                                |||||||||| || ||
                                AGTCACCGAT GT CC
                                      G  A
GAM1073  KIAA1045 3'  CCAAGCCCTGTCTCCCTG    71047     T  CT
                                CAG GG  GACAGGGCTTGG
                                |||  ||  ||||||||||||
                                GTC CC  CTGTCCCGAACC
                                  _  T_
GAM1073  KIAA1068 3'  CAAGCCTATGCCCTGA      31027      T   TGACA
                                TCAG GGC    GGGCTTG
                                ||||  |||    |||||||
                                AGTC CCG    TCCGAAC
                                  _   TA___
GAM1073  KIAA1297 3'  CCAAGCCCCACGCTGCTG    72171     TG  _  ACA
                                CAG  GC TG   GGGCTTGG
                                |||  ||  ||   ||||||||
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                                GTC  CG AC   CCCGAACC
                                  GT  C  ___
GAM1073  KIAA1322  3'  CACAGCCAGCCACTG       72732        GACAG   _
                                CAGTGGCT    GGCT TG
                                ||||||||    |||| ||
                                GTCACCGA    CCGA AC
                                     _____   C
GAM1073  KIAA1503  3'  CCAAACCCTGTCCCTTTCCTGA 68346      TG CT_      C
                                TCAG  G   GACAGGG TTGG
                                ||||  |   ||||||| ||||
                                AGTC  T   CTGTCCC AACC
                                  CT TCC      A
GAM1073  KIAA1550  3'  CAGAGCCAGCCACTGA      66553        GACAG   _
                                TCAGTGGCT    GGCT TG
                                |||||||||    |||| ||
                                AGTCACCGA    CCGA AC
                                     _____   G
GAM1073  KIAA1607  3'  CCAAGCCCAAGAGGCCAC    63797       GACA
                                GTGGCT    GGGCTTGG
                                ||||||    ||||||||
                                CACCGG    CCCGAACC
                                   AGAA
GAM1073  KIAA1872  5'  CTCTGCCAGCCCTGA       62930      T    A
                                TCAG GGCTG CAGGG
                                |||| ||||| |||||
                                AGTC CCGAC GTCTC
                                  _    C
GAM1073  KIAA1887  5'  CCAAGCTGTGCAACCACCGG   76771    A   C  A  G
                                TC GTGG TG CA GGCTTGG
                                || |||| || || |||||||
                                GG CACC AC GT TCGAACC
                                 C   A  _  G
GAM1073  KRTHA3B   3'  CAACCATCAGCCACCGG     9645     A      CAG  C
                                TC GTGGCTGA   GG TTG
                                || ||||||||   || |||
                                GG CACCGACT   CC AAC
                                 C       A__  _
GAM1073  LXN       5'  CCAAGCCCTGAAGTCACTG    39412        GA
                                CAGTGGCT  CAGGGCTTGG
                                ||||||||  ||||||||||
                                GTCACTGA  GTCCCGAACC
                                    A_
GAM1073  MGC19556  5'  TTCTTCAGCCACTGA       53235          C
                                TCAGTGGCTGA AGGG
                                |||||||||||| ||||
                                AGTCACCGACT TCTT
                                          _
GAM1073  MGC21636  5'  AGATCTGTCAGCCACTG     58855           GG
                                CAGTGGCTGACAG  CT
                                ||||||||||||  ||
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                                GTCACCGACTGTC  GA
                                      TA
GAM1073  MGC2721   3'  CCAAGCCCTGCGTCCAGC    51216     A___
                                GCTG   CAGGGCTTGG
                                ||||   ||||||||||
                                CGAC   GTCCCGAACC
                                  CTGC
GAM1073  MRPL10    3'  CCAAGCCCTCTGCTCTGA    59151     T   TGAC
                                TCAG GGC   AGGGCTTGG
                                |||| |||   |||||||||
                                AGTC TCG   TCCCGAACC
                                  _  TC__
GAM1073  PRPF8     3'  CCAGGACATAGCCACTGA    61188        ACAGGG
                                TCAGTGGCTG     CTTGG
                                ||||||||||     |||||
                                AGTCACCGAT     GGACC
                                      ACA___
GAM1073  RNF34     3'  TGGGCATCAGCCACTG      47095        CAGG
                                CAGTGGCTGA   GCTTG
                                ||||||||||   |||||
                                GTCACCGACT   CGGGT
                                      A___
GAM1073  SCYA18    5'  CCAAGCCCCAGCTCACT     11459     _   ACA
                                AGTG GCTG   GGGCTTGG
                                |||| ||||   ||||||||
                                TCAC CGAC   CCCGAACC
                                  T   ___
GAM1073  SIMRP7    3'  CAGGGCCAGCCACTG       92359       GACA  G
                                CAGTGGCT    GG CTTG
                                ||||||||    || ||||
                                GTCACCGA    CC GGAC
                                     _____  G
GAM1073  SLC37A1   3'  CCAGGCTTGCCAGCCAC     38563       ACA
                                GTGGCTG   GGGCTTGG
                                |||||||   ||||||||
                                CACCGAC   TTCGGACC
                                    CG_
GAM1073  SNT-2     3'  CCAGAGATATCAGCCACCGA   21840    A      CAGGG  _
                                TC GTGGCTGA    CT TGG
                                || ||||||||    || |||
                                AG CACCGACT    GA ACC
                                 C       ATA__  G
GAM1073  SSB-4     3'  CCTTCCCAGCCACTGA      55099        AC
                                TCAGTGGCTG  AGGG
                                ||||||||||  ||||
                                AGTCACCGAC  TTCC
                                      CC
GAM1073  SUI1      3'  CCAAGCCCAGAGCCCT      19401    T   GACA
                                AG GGCT    GGGCTTGG
                                || ||||    ||||||||
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                                TC CCGA   CCCGAACC
                                 _   GA__
GAM1073  WBSCR17   3' CCAAGCCCTGCCCAGAGCTGA 81299     GG  A_
                                TCAGT  CTG  CAGGGCTTGG
                                |||||  |||  ||||||||||
                                AGTCG  GAC  GTCCCGAACC
                                   A_   CC
GAM1073  LOC115399 5' CCAAGCCCTGCCCCTGA    73427     T   TGAC
                                TCAG GGC    AGGGCTTGG
                                |||| |||    |||||||||
                                AGTC CCG    TCCCGAACC
                                  C  ____
GAM1073  LOC118738 5' CCAAGCCCTCCAGAACCCCA  75488    ____  AC
                                TGG    CTG  AGGGCTTGG
                                |||    |||  |||||||||
                                ACC    GAC  TCCCGAACC
                                  CCAA   C_
GAM1073  LOC124977 5' CCTCACTGCAGCCACTGA    76058        A   GGCTT
                                TCAGTGGCTG CAG    GG
                                |||||||||| |||    ||
                                AGTCACCGAC GTC    CC
                                      _   ACT__
GAM1073  LOC126302 5' CCAAGCCCTGCAGTGCTAC   74493     __  A
                                GTGGC  TG CAGGGCTTGG
                                |||||  || ||||||||||
                                CATCG  AC GTCCCGAACC
                                   TG  _
GAM1073  LOC128439 3' CCAAGAGGTGCAGGCACTGA  57350      G   A  GGG
                                TCAGTG CTG CA   CTTGG
                                ||||||| ||| ||   |||||
                                AGTCAC GAC GT   GAACC
                                   G   _  GGA
GAM1073  LOC130813 3' CCAAGCCTGGAGCCCTGA    75766     T    GA    G
                                TCAG GGCT  CAGG CTTGG
                                |||| ||||  |||| |||||
                                AGTC CCGA  GTCC GAACC
                                  _    G_   _
GAM1073  LOC142927 3' CCAGCGCATCATGCCACTGA  76421        _  CAGG  _
                                TCAGTGGC TGA    GC TTGG
                                |||||||| |||    || ||||
                                AGTCACCG ACT    CG GACC
                                     T   A___  C
GAM1073  LOC145497 5' CCAAGCCCTGTCGACCA     77214     C
                                TGG TGACAGGGCTTGG
                                ||| ||||||||||||
                                ACC GCTGTCCCGAACC
                                  A
GAM1073  LOC145758 5' CCAAACTAAGCCACTGA     83483         GACA  GC
                                TCAGTGGCT    GG  TTGG
                                |||||||||    ||  ||||
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                                AGTCACCGA   TC  AACC
                                     A___  A_
GAM1073  LOC145845 3'  CCTGGCTGCCAGCCACT    83553       A  GG   T
                                AGTGGCTG CA  GCT GG
                                |||||||| ||  ||| ||
                                TCACCGAC GT  CGG CC
                                    C  __   T
GAM1073  LOC146562 3'  CCTGGCTGCCAGGCCACTGA  57532       GACAG   T
                                TCAGTGGCT    GGCT GG
                                |||||||||    |||| ||
                                AGTCACCGG    TCGG CC
                                     ACCG_   T
GAM1073  LOC147040 3'  CCAAACCTGAGCCCAC     78231     _  GA   GC
                                GTGG CT  CAGG  TTGG
                                |||| ||  ||||  ||||
                                CACC GA  GTCC  AACC
                                  C  __   A_
GAM1073  LOC148697 3'  CCACTGTCTGCCAGCCACTG  78921       ACA   T_
                                CAGTGGCTG   GGGC  TGG
                                |||||||||   ||||  |||
                                GTCACCGAC   TCTG  ACC
                                     CG_   TC
GAM1073  LOC148981 3'  CCAAAAAGTGCAGCTACTGA  84314       A  GGGC
                                TCAGTGGCTG CA   TTGG
                                |||||||||| ||   ||||
                                AGTCATCGAC GT   AACC
                                     _  GAAA
GAM1073  LOC150568 5'  CCAAGCCTGGGCCACTGA    85042       GACA
                                TCAGTGGCT   GGGCTTGG
                                |||||||||   ||||||||
                                AGTCACCGG   TCCGAACC
                                     G___
GAM1073  LOC150696 3'  CTGTGTCAGCCCTGA      58481     T     G
                                TCAG GGCTGACA GG
                                |||| |||||||| ||
                                AGTC CCGACTGT TC
                                  _      G
GAM1073  LOC150933 3'  CCAAACCCACCCAGCCACT   85158       ACA  C
                                AGTGGCTG   GGG TTGG
                                ||||||||   ||| ||||
                                TCACCGAC   CCC AACC
                                     CCA   A
GAM1073  LOC150933 5'  CTGAGCTCCCAGCCACTGA   85160       ACA   TG
                                TCAGTGGCTG   GGGCT  G
                                ||||||||||   |||||  |
                                AGTCACCGAC   CTCGA  C
                                     C__    GT
GAM1073  LOC150967 3'  CCATGACAGCCACTGA     80080       A  _
                                TCAGTGGCTG CA GG
                                |||||||||| || ||
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                                AGTCACCGAC GT CC
                                      A  A
GAM1073  LOC155060 3'  CCAACGTGTGCCAGCCACTGG  86328          A  GG  _
                                TCAGTGGCTG CA  GC TTGG
                                |||||||||| ||  || ||||
                                GGTCACCGAC GT  TG AACC
                                      C  G_  C
GAM1073  LOC155061 3'  CCAAGCCCCTGGGCAGTGA   81266     G  G   ACA
                                TCA TG CTG   GGGCTTGG
                                ||| || |||   ||||||||
                                AGT AC GGT   CCCGAACC
                                  G  G   C__
GAM1073  LOC157285 3'  CCAAGCCCCAGCCTGC      86435    _    ACA
                                GT GGCTG   GGGCTTGG
                                || |||||   ||||||||
                                CG CCGAC   CCCGAACC
                                 T    ____
GAM1073  LOC157556 5'  CCAAGCCCTGCACTCCA     86482     C_  A
                                TGG  TG CAGGGCTTGG
                                |||  || ||||||||||
                                ACC  AC GTCCCGAACC
                                  TC  _
GAM1073  LOC158476 5'  CCAAACCCTGTCAGTT      86841          C
                                GGCTGACAGGG TTGG
                                |||||||||| ||||
                                TTGACTGTCCC AACC
                                       A
GAM1073  LOC163682 5'  CCAGTGACCGTCAGCCAC    87027         A  GC_
                                GTGGCTGAC GG   TTGG
                                ||||||||| ||   ||||
                                CACCGACTG CC   GACC
                                      _  AGT
GAM1073  LOC164266 5'  CCAAGCCCCATAGACTGA    87202       GG   ACA
                                TCAGT  CTG   GGGCTTGG
                                |||||  |||   ||||||||
                                AGTCA  GAT   CCCGAACC
                                   ___  AC_
GAM1073  LOC199745 5'  CCAAAGTGCAGCCGCTGA    88351         A  GGGC
                                TCAGTGGCTG CA    TTGG
                                |||||||||| ||    ||||
                                AGTCGCCGAC GT    AACC
                                      _  GA__
GAM1073  LOC200010 3'  CCAAGCCTGTCAGCCAC     89921          G
                                GTGGCTGACAGG CTTGG
                                |||||||||||| |||||
                                CACCGACTGTCC GAACC
                                        _
GAM1073  LOC200032 5'  CCAGATCATCAGCCACTGA    84321          CAG GC
                                TCAGTGGCTGA   G  TTGG
                                ||||||||||   |  ||||
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                                AGTCACCGACT   C  GACC
                                      A__ TA
GAM1073  LOC200093 3'  CCAAGGCAATGGTCAGCCACTG 63090          AGG_ _
                                CAGTGGCTGAC    GC TTGG
                                ||||||||||    || ||||
                                GTCACCGACTG    CG AACC
                                      GTAA  G
GAM1073  LOC203197 3'  CCTGTGATGTCAGCCACTGG   89284           GG  TT
                                TCAGTGGCTGACA  GC  GG
                                ||||||||||||  ||  ||
                                GGTCACCGACTGT  TG  CC
                                       AG  T_
GAM1073  LOC221250 5'  CCGTGACAGCCACTGA      91834          A  G
                                TCAGTGGCTG CA GG
                                |||||||||| || ||
                                AGTCACCGAC GT CC
                                      A  G
GAM1073  LOC253681 3'  CCAAACCTGAGCCCAC      95128      _  GA    GC
                                GTGG CT  CAGG  TTGG
                                |||| ||  ||||  ||||
                                CACC GA  GTCC  AACC
                                  C  __    A_
GAM1073  LOC253868 3'  CCAAGCCCTGTCACTGCTG    95578     TG C
                                CAG  G TGACAGGGCTTGG
                                |||  | ||||||||||||
                                GTC  C ACTGTCCCGAACC
                                 GT _
GAM1073  LOC256789 3'  CAAGCCTGCCCACTGA      97443        CTGACA
                                TCAGTGG     GGGCTTG
                                |||||||     |||||||
                                AGTCACC     TCCGAAC
                                    CG____
GAM1073  LOC257438 3'  CCTTGCACAGCCACTGA     93972          A_
                                TCAGTGGCTG  CAGGG
                                ||||||||||  |||||
                                AGTCACCGAC  GTTCC
                                      AC
GAM1073  LOC51014  3'  CCAAGCCCTATTCTGCACTG   65849       G T  C_
                                CAGTG C GA  AGGGCTTGG
                                ||||| | ||  |||||||||
                                GTCAC G CT  TCCCGAACC
                                  _ T  TA
GAM1073  LOC55893  3'  CCTGCCGGCAGCCACTGA    37860          ACAG   TT
                                TCAGTGGCTG   GGC  GG
                                ||||||||||   |||  ||
                                AGTCACCGAC   CCG  CC
                                      GG__   T_
GAM1073  LOC56906  3'  CCAAGCCTGACACTACT     39315       C  ACA
                                AGTGG TG   GGGCTTGG
                                ||||| ||   ||||||||
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                                TCATC AC   TCCGAACC
                                  _ AG_
GAM1073 LOC89941 3' CCAAGCCCCCTCCCCTGA    57058     T CT  CA
                                TCAG GG  GA  GGGCTTGG
                                |||| ||  ||  ||||||||
                                AGTC CC  CT  CCCGAACC
                                  _ __  CC
GAM1073 LOC90249 5' CCAAGTTCCAGCTCAC      61923     _   ACA
                                GTG GCTG   GGGCTTGG
                                ||| ||||   ||||||||
                                CAC CGAC   CTTGAACC
                                 T   ____
GAM1073 LOC90379 5' CCAAGCCCCGACCAC       62536     C  ACA
                                GTGG TG   GGGCTTGG
                                |||| ||   ||||||||
                                CACC GC   CCCGAACC
                                  A ____
GAM1073 LOC91040 3' CCAAGGCAATGGTCAGCCACTG 64710          AGG_ _
                                CAGTGGCTGAC    GC TTGG
                                ||||||||||    || ||||
                                GTCACCGACTG    CG AACC
                                      GTAA  G
GAM1073 LOC91149 3' CCAAGCCTGTGCGCCGACTGA  65072      _  TG    G
                                TCAGT GGC  ACAGG CTTGG
                                ||||| |||  ||||| |||||
                                AGTCA CCG  TGTCC GAACC
                                  G  CG    _
GAM1074 NCALD    3' TGCTTTTCTGAGCAGATCAATA 49380          CC   CCTGT
                                TATTGATCTGT  CAG    GCA
                                ||||||||||  |||    |||
                                ATAACTAGACG  GTC    CGT
                                      A_  TTTT_
GAM1074 FLJ10242 5' TACTTCCTGAAGCAGATCAA   35934         CC   CCT
                                TTGATCTGT  CAG   GTG
                                |||||||||  |||   |||
                                AACTAGACG  GTC   CAT
                                     AA   CTT
GAM1074 FLJ13842 3' TGCACAGAACTGGAACAGATCA 44990         C    C_
                                TGATCTGT CCAG  CTGTGCA
                                |||||||| ||||  |||||||
                                ACTAGACA GGTC  GACACGT
                                    A   AA
GAM1074 GPR88    3' CACAGTCAAGACGGATCAATA  41878          CCAGC
                                TATTGATCTGTC    CTGTG
                                ||||||||||||    |||||
                                ATAACTAGGCAG    GACAC
                                      AACT_
GAM1074 KIAA0415 3' TGCACCGTGGAGCAGATCAA   92582         TC   GCCT
                                TTGATCTG  CCA    GTGCA
                                ||||||||  |||   |||||
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                                AACTAGAC  GGT   CACGT
                                    GA  GC__
GAM1074 KIAA0513 3' GCACAGGCTAAGACCACAGA  28359     CCC___
                                TCTGT    AGCCTGTGC
                                |||||    |||||||||
                                AGACA    TCGGACACG
                                   CCAGAA
GAM1074 TCL6    3' GCACAGGCTGGTCTCAA    40103     TCTGTC
                                TTGA    CCAGCCTGTGC
                                ||||    ||||||||||
                                AACT    GGTCGGACACG
                                  CT____
GAM1074 TCL6    3' GCACAGGCTGGTCTCAA    40135     TCTGTC
                                TTGA    CCAGCCTGTGC
                                ||||    ||||||||||
                                AACT    GGTCGGACACG
                                  CT____
GAM1074 LOC219529 5' TGCAACAGAAGACAGATTAA  92975         CCAGC  _
                                TTGATCTGTC    CTGT GCA
                                ||||||||||    |||| |||
                                AATTAGACAG    GACA CGT
                                      AA___   A
GAM1074 LOC253281 5' CACAGGCTGGAGGTGCTCA   97343     TC GT _
                                TGA  T  C CCAGCCTGTG
                                |||  |  | ||||||||||
                                ACT  G  G GGTCGGACAC
                                  C_ TG A
GAM1075 COL4A3   3' TTCACAGCCAAACCACTGACAT 48561     C   GCTCA__
            T                    AATG TCAG      GCTGTGAA
                                |||| ||||      ||||||||
                                TTAC AGTC      CGACACTT
                                  _   ACCAAAC
GAM1075 COL4A3   3' TTCACAGCCAAACCACTGACAT 48572     C   GCTCA__
            T                    AATG TCAG      GCTGTGAA
                                |||| ||||      ||||||||
                                TTAC AGTC      CGACACTT
                                  _   ACCAAAC
GAM1075 ESR1    3' TTCACAGCTGAACTCAGT    3712     C  GC
                                GCT AG  TCAGCTGTGAA
                                ||| ||  ||||||||||
                                TGA TC  AGTCGACACTT
                                  C  A_
GAM1075 FN1     3' TCACAGCTTCTCCAAGCATCA 8949    A    CA  CTC
                                A ATGCT  GG   AGCTGTGA
                                | |||||  ||   ||||||||
                                A TACGA  CC   TCGACACT
                                 C    A_  TCT
GAM1075 IL2RB   3' TCACAGCTGATTGGGCA     6077        GC
                                TGCTCAG  TCAGCTGTGA
                                |||||||  ||||||||||
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                                ACGGGTT  AGTCGACACT
                                   __
GAM1075 OGDH     3'  TTCATCTTGAGCCTGAGC    91110          CT
                                GCTCAGGCTCAG  GTGAA
                                ||||||||||| |||||
                                CGAGTCCGAGTT  TACTT
                                      C_
GAM1075 PCTP     3'  TTCACAGCCAGGTAAAATTTA 41103      GCTCAG   CA
                                TAAAT     GCT  GCTGTGAA
                                |||||     |||  ||||||||
                                ATTTA     TGG  CGACACTT
                                   AAA___   AC
GAM1075 SCN4A    3'  CACATGGCCTGAGCAT      4410          T  GC
                                ATGCTCAGGC CA  TGTG
                                |||||||||| ||  ||||
                                TACGAGTCCG GT  ACAC
                                   _  __
GAM1075 SH3BP5   3'  TTCACAGCCTTTGTGGAACATT 16745     C  AG  TCA_
                                AATG TC  GC   GCTGTGAA
                                |||| ||  ||   ||||||||
                                TTAC AG  TG   CGACACTT
                                  A  G_  TTTC
GAM1075 BPESC1   3'  CAGAGGAGCTAAGCATTTA   41471        CA    AG
                                TAAATGCT  GGCTC  CTG
                                ||||||||  |||||  |||
                                ATTTACGA  TCGAG  GAC
                                     A_    GA
GAM1075 C1QTNF6  3'  CACAGCTGATACGGCAT     49137      CAGGC
                                ATGCT    TCAGCTGTG
                                |||||    |||||||||
                                TACGG    AGTCGACAC
                                   CAT__
GAM1075 DKFZP434P0111 3'  TCACCTCACCTGAGCA     67373        CTC  CT
                                TGCTCAGG   AG  GTGA
                                ||||||||   ||  ||||
                                ACGAGTCC   TC  CACT
                                     AC_  __
GAM1075 FLJ10751 3'  TCACAGCTGCTGTGCA     36571     T  GCT
                                TGC CAG   CAGCTGTGA
                                ||| |||   |||||||||
                                ACG GTC   GTCGACACT
                                  T  ____
GAM1075 FLJ10751 3'  TCACAGCTGCTGTGCA     36732     T  GCT
                                TGC CAG   CAGCTGTGA
                                ||| |||   |||||||||
                                ACG GTC   GTCGACACT
                                  T  ____
GAM1075 FLJ23519 3'  CACCATGAGCCTGGACAT    49961     CT      GCT
                                ATG  CAGGCTCA   GTG
                                |||  ||||||||   |||
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                                TAC  GTCCGAGT   CAC
                                  AG       AC_
GAM1075  KIAA0237  3'  TCCAGGGGCAACTGAGCAT   28538        __   AG   T
                                ATGCTCAG  GCTC  CTG GA
                                ||||||||  ||||  ||| ||
                                TACGAGTC  CGGG  GAC CT
                                    AA   __  _
GAM1075  KIAA0316  3'  TTCACAGTGGTTCTAGCATTTA 69676        CA   CA
                                TAAATGCT  GGCT  GCTGTGAA
                                ||||||||  ||||  ||||||||
                                ATTTACGA  TTGG  TGACACTT
                                    TC   __
GAM1075  KIAA0431  5'  TTCACAGCCTAGGAACAT    30898     C  AGG  CA
                                ATG TC   CT  GCTGTGAA
                                ||| ||   ||  ||||||||
                                TAC AG   GA  CGACACTT
                                  A  ___  TC
GAM1075  KIAA1554  3'  CACAGTCCCTGGCATTTA    95146       T   CTCA
                                TAAATGC CAGG    GCTGTG
                                |||||||  ||||    ||||||
                                ATTTACG GTCC    TGACAC
                                    _   C___
GAM1075  KIAA1615  5'  TCCAGGAATGAGACTAAGCATT 68733        C  G   G__   T
            TA                    TAAATGCT AG CTCA   CTG GA
                                ||||||||  ||  ||||   ||| ||
                                ATTTACGA  TC  GAGT   GAC CT
                                    A  A    AAG   _
GAM1075  PDE3A    3'  TTCAAGCCAGCACAAGCATTTA 6228         CAG   CA   G
                                TAAATGCT   GCT  GCT TGAA
                                ||||||||   |||  ||| ||||
                                ATTTACGA   CGA  CGA ACTT
                                    ACA   C_  _
GAM1075  SLC38A4   3'  TCACAGTCAAAGCATTTA    35876        CA GCTCA
                                TAAATGCT  G    GCTGTGA
                                ||||||||  |    |||||||
                                ATTTACGA  C    TGACACT
                                    AA _____
GAM1075  TJP4     5'  CACAGCTGTTAGCAGCAT    54608       CAG   __
                                ATGCT   GCT  CAGCTGTG
                                |||||   |||  ||||||||
                                TACGA   CGA  GTCGACAC
                                   ___   TT
GAM1075  LOC143915 3'  CAGCTCAGCCTGAGCATCA   82993   A         C
                                A ATGCTCAGGCT AGCTG
                                | ||||||||||| |||||
                                A TACGAGTCCGA TCGAC
                                 C          C
GAM1075  LOC144266 5'  TTCACAGCTGCCGGAG      76765     A   TC
                                CTC GGC  AGCTGTGAA
                                ||| |||  |||||||||
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                                GAG CCG  TCGACACTT
                                  G  __
GAM1075  LOC145098 5'  GTGAAGGCCAAGCATTTA    76994        CA   CA_
                                TAAATGCT  GGCT   GC
                                ||||||||  ||||   ||
                                ATTTACGA  CCGG   TG
                                    A_    AAG
GAM1075  LOC145719 5'  CACAGCTGCTGCAGCG      83450      _  GCT
                                TGCT CAG   CAGCTGTG
                                |||| |||   ||||||||
                                GCGA GTC   GTCGACAC
                                  C  ___
GAM1075  LOC145720 5'  CACAGCTGCTGCAGCG      83432      _  GCT
                                TGCT CAG   CAGCTGTG
                                |||| |||   ||||||||
                                GCGA GTC   GTCGACAC
                                  C  ___
GAM1075  LOC169225 5'  TTCACAGCAAGCACTCAGCATT 87280       C  _  CA
                                AATGCT AG GCT  GCTGTGAA
                                |||||| || |||  ||||||||
                                TTACGA TC CGA  CGACACTT
                                   C  A   A_
GAM1075  LOC197114 5'  CACAGCTGCTGCAGCG      89702      _  GCT
                                TGCT CAG   CAGCTGTG
                                |||| |||   ||||||||
                                GCGA GTC   GTCGACAC
                                  C  ___
GAM1075  LOC221773 3'  TTCACAGCTTTGAGGAACATGC 91053     TCAGG_   __
            A                    TGC     CTCA  GCTGTGAA
                                |||     ||||  ||||||||
                                ACG     GAGT  CGACACTT
                                  TACAAG    TT
GAM1076  ABCA2    3'  CAGCTGCCATCGCTCTCCC   7834     AA      __
                                GG  GAGAGCGA  GCAGCTG
                                ||  ||||||||  |||||||
                                CC  CTCTCGCT  CGTCGAC
                                 __       AC
GAM1076  ABCA2    3'  CAGCTGCCATCGCTCTCCC   96169    AA      __
                                GG  GAGAGCGA  GCAGCTG
                                ||  ||||||||  |||||||
                                CC  CTCTCGCT  CGTCGAC
                                 __       AC
GAM1076  ADCY6    3'  TGCTCTCTTGCTGTCT      30937       G
                                AGACAG AAGAGAGCG
                                ||||||  |||||||||
                                TCTGTC TTCTCTCGT
                                   G
GAM1076  ADCY6    3'  TGCTCTCTTGCTGTCT      40621       G
                                AGACAG AAGAGAGCG
                                ||||||  |||||||||
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                                TCTGTC TTCTCTCGT
                                   G
GAM1076 ARHG     3' AGATGCTCTCTCCCTTCT    8014       A  C    G
                                GGAAG GAG GAGCA CT
                                ||||| ||| ||||| ||
                                TCTTC CTC CTCGT GA
                                   C  T    A
GAM1076 B4GALT5  3' GCTGCTCTCTCCCCATCT    16506     CA A     G
                                AGA  GG AGAGAGC AGC
                                |||  || ||||||| |||
                                TCT  CC TCTCTCG TCG
                                  AC  C      _
GAM1076 CALCRL   3' CTTGTCAACCTCTTCCTGTCT  19389          A___
                                AGACAGGAAGAG   GCGAG
                                ||||||||||||   |||||
                                TCTGTCCTTCTC   TGTTC
                                       CAAC
GAM1076 CD4      3' CAGGATCCCCTCTCTTCCT   5221          C_ GCAG
                                AGGAAGAGAG  GA   CTG
                                ||||||||||  ||   |||
                                TCCTTCTCTC  CT   GAC
                                     CC  AG__
GAM1076 CELSR2   3' CAGCCGCACTCATGCCCTGCTC 7406        AG  A  A____  A
             CTGTCT                GACAGGA  AG GCG    GC GCTG
                                |||||||  || |||    || ||||
                                CTGTCCT  TC CGT    CG CGAC
                                    CG  C   ACTCA  C
GAM1076 CELSR3   3' CAGCGGCCCTCTTTCCTGTCT  7396        A    CGA  A
                                AGACAGGA GAGAG   GC GCTG
                                |||||||| |||||   || ||||
                                TCTGTCCT TTCTC   CG CGAC
                                     _    C__  G
GAM1076 CNP      3' CTGACCCTCCCTTCCTGTC   52443        A  CGAG
                                GACAGGAAG GAG    CAG
                                ||||||||| |||    |||
                                CTGTCCTTC CTC    GTC
                                     C   CCA_
GAM1076 CREBBP   5' GCGCTCGCTCCTCTCC      15208     A  _     A
                                GGA GAG AGCGAGC GC
                                ||| ||| ||||||| ||
                                CCT CTC TCGCTCG CG
                                  _  C      _
GAM1076 DGKG     5' CAGCTTCGGTCCCCCTTCTGTC 7204        AGA_  G  GC
             T                   AGACAGGA    GA CGA  AGCTG
                                ||||||||    || |||  |||||
                                TCTGTCTT    CT GCT  TCGAC
                                     CCCC  G  __
GAM1076 DYRK1A   3' CAGCTGTGTCCCTTCCTGCT   7351     A      A  GCGA
                                AG CAGGAAG GA    GCAGCTG
                                || ||||||| ||    |||||||
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                                TC GTCCTTC CT    TGTCGAC
                                 _      C  G___
GAM1076  DYRK1A   3'  CAGCTGTGTCCCTTCCTGCT   55201    A      A  GCGA
                                AG CAGGAAG GA    GCAGCTG
                                || ||||||| ||    |||||||
                                TC GTCCTTC CT    TGTCGAC
                                 _      C  G___
GAM1076  DYRK1A   3'  CAGCTGTGTCCCTTCCTGCT   55242    A      A  GCGA
                                AG CAGGAAG GA    GCAGCTG
                                || ||||||| ||    |||||||
                                TC GTCCTTC CT    TGTCGAC
                                 _      C  G___
GAM1076  ELMO2    3'  CAGCCACTCACCTTTTCCT   55673        AGC   CA
                                AGGAAGAG   GAG  GCTG
                                ||||||||   |||  ||||
                                TCCTTTTC   CTC  CGAC
                                     CA_   AC
GAM1076  EPB49    3'  CAGCTGCTTTCCTCACCTG   8782      AA   AGC
                                CAGG  GAG   GAGCAGCTG
                                ||||  |||   |||||||||
                                GTCC  CTC   TTCGTCGAC
                                  A_   CT_
GAM1076  GAB2     3'  TTCAGCCTCTTCCTGTC     54464          A  _
                                GACAGGAAGAG GC GAG
                                |||||||||||  || |||
                                CTGTCCTTCTC CG CTT
                                       _ A
GAM1076  GAB2     3'  TTCAGCCTCTTCCTGTC     24507          A  _
                                GACAGGAAGAG GC GAG
                                |||||||||||  || |||
                                CTGTCCTTCTC CG CTT
                                       _ A
GAM1076  GFAP     3'  AGCTGCTCCCCTCCCTCCT   9011      A A   C_
                                AGGA G GAG  GAGCAGCT
                                ||||  |  |||  ||||||||
                                TCCT C CTC  CTCGTCGA
                                  _ C   CC
GAM1076  GPC3     3'  CTCACTCCCTCCCTTTCT    15605     C   A  A   C
                                AGA AGG AG GAG GAG
                                ||| ||| || ||| |||
                                TCT TCC TC CTC CTC
                                  T   C  C   A
GAM1076  GSBS     3'  CTGTTTAATCCCTTCTGTCT   91094       G   A  GC
                                AGACAG AAG GA  GAGCAG
                                ||||||  ||| ||  ||||||
                                TCTGTC TTC CT  TTTGTC
                                   _  C  AA
GAM1076  ICMT     3'  CTGCACTTTCTTCCTGCCT   24811    A         CGA
                                AG CAGGAAGAGAG   GCAG
                                || ||||||||||   ||||
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                                TC GTCCTTCTTTC   CGTC
                                 C         A__
GAM1076  IFRD2    3'  CAGCCCTGTGGCCCCTTCCTGT 22221         AGA  GA  __
                C                 GACAGGAAG   GC  GCA  GCTG
                                  |||||||||   ||  |||  ||||
                                  CTGTCCTTC   CG  TGT  CGAC
                                       CC_  G_   CC
GAM1076  IGF2R    3'  CAGCCACCGTTTCTTCCTG   6051          G  AGCA
                                  CAGGAAGAGA CG    GCTG
                                  ||||||||||  ||    ||||
                                  GTCCTTCTTT GC    CGAC
                                        _  CAC_
GAM1076  INPP5D   3'  AGCCTTTTCTTCCTATCT    82807     C        CGAGCA
                                  AGA AGGAAGAGAG     GCT
                                  |||  ||||||||||      |||
                                  TCT TCCTTCTTTT     CGA
                                    A         C_____
GAM1076  KRT14    5'  CTGCTCGCTCGCTCACCTCCCT 4980     AC   A_  A
                                  AG  AGG  AG GAGCGAGCAG
                                  ||  |||  ||  ||||||||||
                                  TC  TCC  TC CTCGCTCGTC
                                   CC   AC  G
GAM1076  KRT16    5'  CTGCTCGCTCGCTCACCTCCCT 95197    AC   A_  A
                                  AG  AGG  AG GAGCGAGCAG
                                  ||  |||  ||  ||||||||||
                                  TC  TCC  TC CTCGCTCGTC
                                   CC   AC  G
GAM1076  MLC1     3'  GCTCCTCTTCCTGCCT      57594     A        AGC
                                  AG CAGGAAGAG   GAGC
                                  ||  |||||||||   ||||
                                  TC GTCCTTCTC   CTCG
                                   C        ___
GAM1076  MLC1     3'  GCTCCTCTTCCTGCCT      30781     A        AGC
                                  AG CAGGAAGAG   GAGC
                                  ||  |||||||||   ||||
                                  TC GTCCTTCTC   CTCG
                                   C        ___
GAM1076  MUC3B    3'  CAGCTGCTGTTCCTCCCCATC  94267    CA  A  A   G
                                  GA  GG AG GAGC AGCAGCTG
                                  ||  ||  ||  ||||  ||||||||
                                  CT  CC TC CTTG TCGTCGAC
                                   AC  C  _   _
GAM1076  MYD88    3'  AGCTGTTCTCTCCCTCTCT    10162    GA  A   C
                                  AG  AG GAG GAGCAGCT
                                  ||  ||  |||  ||||||||
                                  TC  TC CTC CTTGTCGA
                                   TC  C   T
GAM1076  NHP2L1   3'  AGCCACTAGCTTCCTGTT     17201          AGAGCG  CA
                                  GACAGGAAG     AG  GCT
                                  |||||||||      ||  |||
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                                TTGTCCTTC     TC  CGA
                                     GA_____  AC
GAM1076  NXF1     3'  CTGTCATCTCCTCCTGTCT   21016        A   GC  G
                                AGACAGGA GAGA  GA CAG
                                |||||||| ||||  || |||
                                TCTGTCCT CTCT  CT GTC
                                    C   A_  _
GAM1076  PRG2     5'  CAGCCGTGCTGCTCTTCCTG   10779         _   AGCA
                                CAGGAAGAG AGCG   GCTG
                                ||||||||| ||||   ||||
                                GTCCTTCTC TCGT   CGAC
                                     G   GC__
GAM1076  PRKACA   3'  AGCTGCTCCCCCTCATCC    10786    A  AGC
                                GGA GAG   GAGCAGCT
                                ||| |||   ||||||||
                                CCT CTC   CTCGTCGA
                                  A   CCC
GAM1076  PRKACG   3'  CAGCTGCTCCCTCACCCCCC   10797   AAGA_  C
                                GG    GAG GAGCAGCTG
                                ||    ||| |||||||||
                                CC    CTC CTCGTCGAC
                                 CCCCA   C
GAM1076  PROML1   3'  CTCCCTCCCTTCCTGTCT    20054        A  C
                                AGACAGGAAG GAG GAG
                                |||||||||| ||| |||
                                TCTGTCCTTC CTC CTC
                                     C   C
GAM1076  PTGER2   5'  CAGCTCTCAGACCCTCTTCCT  6304        AGC__  C
                                AGGAAGAG    GAG AGCTG
                                ||||||||    ||| |||||
                                TCCTTCTC    CTC TCGAC
                                    CCAGA  _
GAM1076  RAD23B   3'  CAGCATTCACTCTCCCTGTCT  11214       AA   C  CA
                                AGACAGG  GAGAG GAG  GCTG
                                |||||||  ||||| |||  ||||
                                TCTGTCC  CTCTC CTT  CGAC
                                   __    A  A_
GAM1076  RNASE1   3'  CAGCTGCCTCTTCCCTCTTCCT 11347    C      AGC_  _
            TC                   GA AGGAAGAG   GAG CAGCTG
                                || ||||||||   ||| ||||||
                                CT TCCTTCTC   CTC GTCGAC
                                 _      CCTT  C
GAM1076  RNASE1   3'  CAGCTGCCTCTTCCCTCTTCCT 63876    C      AGC_  _
            TC                   GA AGGAAGAG   GAG CAGCTG
                                || ||||||||   ||| ||||||
                                CT TCCTTCTC   CTC GTCGAC
                                 _      CCTT  C
GAM1076  SOX10    3'  CAGCTGCTCAGGCCCTAACC  22682    AAG  A  __
                                GG   AG GC  GAGCAGCTG
                                ||   || ||  |||||||||
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                                CC   TC CG  CTCGTCGAC
                                 AA_  C  GA
GAM1076  STAC     3'  CAGGATCCCACTCCTTTCCTGT 11990          A   C__  GCAG
                CT                  AGACAGGAAG GAG   GA    CTG
                                    |||||||||| |||   ||    |||
                                    TCTGTCCTTT CTC   CT    GAC
                                         C   ACC  AG__
GAM1076  TAGLN2   3'  CTGGCCTCTTCCTTTC      13095    C       A  G
                                    GA AGGAAGAG GC AG
                                    || |||||||| || ||
                                    CT TCCTTCTC CG TC
                                     T       _  G
GAM1076  TMEPAI   3'  CAGCTGCTACCCCCTCCCTTCC 39442       A   CG___
                                    GGAAG GAG     AGCAGCTG
                                    ||||| |||     ||||||||
                                    CCTTC CTC     TCGTCGAC
                                       C   CCCCA
GAM1076  TNXB     5'  CAGCTGCTCGGTTGCCCAGCCT 38880     AAGA__  G
                                    AGG      GA CGAGCAGCTG
                                    |||      || ||||||||||
                                    TCC      TT GCTCGTCGAC
                                      GACCCG  G
GAM1076  USP14    5'  CAGCTGCTCCTGGTCCCCGTC  17657     A_   AGAG  C
                                    GAC  GGA    AG GAGCAGCTG
                                    |||  |||    || |||||||||
                                    CTG  CCT    TC CTCGTCGAC
                                      CC   GG__  _
GAM1076  YWHAG    5'  CAGCTGCTCGCTCTGTGGGTC  25017     AGGAAG
                                    GAC      AGAGCGAGCAGCTG
                                    |||      ||||||||||||||
                                    CTG      TCTCGCTCGTCGAC
                                      GGTG__
GAM1076  YWHAH    3'  CAGCTACTCAGATCTGCACTCC 12694         AG__   GC_   C
                TGTCT                   AGACAGGA    AGA   GAG AGCTG
                                    ||||||||    |||   ||| |||||
                                    TCTGTCCT    TCT   CTC TCGAC
                                         CACG   AGA   A
GAM1076  ADPRTL3  5'  CAGCCAGGACCTCTCCCATGTC 18501      _  AA     CGAGCA
                                    GACA GG  GAGAG      GCTG
                                    |||| ||  |||||      ||||
                                    CTGT CC  CTCTC      CGAC
                                      A  __     CAGGAC
GAM1076  ASTN2    5'  CAGCTGCCTCCTCTTCCT     73182         _  CGA
                                    AGGAAGAG AG   GCAGCTG
                                    |||||||| ||   |||||||
                                    TCCTTCTC TC   CGTCGAC
                                         C  ____
GAM1076  BAT8     3'  CAGCTGCTCGCAGCCCATGCCT 22003     AAGAGA__
                                    AGG       GCGAGCAGCTG
                                    |||       ||||||||||
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                                TCC       CGCTCGTCGAC
                                  GTACCCGA
GAM1076 C5orf4    3' CAGCTGGCTCCTCATCCTGTCT 50490         AGA   C    _
                                AGACAGGA   GAG GAGC AGCTG
                                ||||||||   ||| |||| |||||
                                TCTGTCCT   CTC CTCG TCGAC
                                    A__   _    G
GAM1076 CD109     3' CAGCCATTGCCCTCCCTCTCT  56047     C   AA   A    GCA
                                AGA AGG  GAG GCGA   GCTG
                                ||| |||  ||| ||||   ||||
                                TCT TCC  CTC CGTT   CGAC
                                  C   __   C    AC_
GAM1076 CECR6     3' CAGCTGCTCGCTGTTCCCATGT 49081      _  AA  G
              C                  GACA GG  GA AGCGAGCAGCTG
                                ||||  ||  ||  ||||||||||||
                                CTGT CC  TT TCGCTCGTCGAC
                                  A  C_  G
GAM1076 CRYL1     5' CAGCTGCTCATTTCCCCC    32000    AA    GC
                                GG  GAGA  GAGCAGCTG
                                ||  ||||  |||||||||
                                CC  CTTT  CTCGTCGAC
                                 CC    A_
GAM1076 DKFZp434H2215 3' CAGCTGCTAGACTCCCTCCT   34109      A A   CG_
                                AGGA G GAG   AGCAGCTG
                                |||| | |||   ||||||||
                                TCCT C CTC   TCGTCGAC
                                  _ C   AGA
GAM1076 DXS9928E  3' CAGCTGCTCGTGTCCTG     16285      AGAGA
                                CAGGA    GCGAGCAGCTG
                                |||||    ||||||||||||
                                GTCCT    TGCTCGTCGAC
                                   G____
GAM1076 EDR2      3' CGCTCTCTTCCCCTCT      60492     CA
                                AGA  GGAAGAGAGCG
                                |||  ||||||||||||
                                TCT  CCTTCTCTCGC
                                  CC
GAM1076 FLJ10199  3' CGCTCCCTCCTGTCT       71232         A A
                                AGACAGGA G GAGCG
                                |||||||| | |||||
                                TCTGTCCT C CTCGC
                                    _ C
GAM1076 FLJ10468  3' AGCCCTCCTCTTCCT       36143         AGC   CA
                                AGGAAGAG   GAG  GCT
                                ||||||||   |||  |||
                                TCCTTCTC   CTC  CGA
                                    ___   C_
GAM1076 FLJ11539  3' AGCCGCTCGCTTTCTCCT    45373      A         A
                                AGGA GAGAGCGAGC GCT
                                |||| |||||||||| |||
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                                TCCT CTTTCGCTCG CGA
                                  _       C
GAM1076 FLJ11715 3' AGCCGTCTCTTTCTACCT    44667    A    C  G A
                                AGG AGAGAG GA C GCT
                                ||| |||||| || | |||
                                TCC TCTTTC CT G CGA
                                  A     T _ C
GAM1076 FLJ11783 3' CAGCGTCCCCTTTCCCTGCCT 46030    A   AA    CGA  A
                                AG CAGG  GAGAG   GC GCTG
                                || ||||  |||||   || ||||
                                TC GTCC  CTTTC   TG CGAC
                                 C   __    CCC  _
GAM1076 FLJ12190 3' AGCGGCTCCCTCCCTCCT    46869     A A   C    A
                                AGGA G GAG GAGC GCT
                                |||| | ||| |||| |||
                                TCCT C CTC CTCG CGA
                                  _ C   C    G
GAM1076 FLJ13111 3' AGCTGCTCATCCCCTGT     46934      AAGA  GC
                                ACAGG    GA  GAGCAGCT
                                |||||    ||  ||||||||
                                TGTCC    CT  CTCGTCGA
                                   C___  A_
GAM1076 FLJ13154 3' CTCTCTCTCTTCCTGTC     44797           C
                                GACAGGAAGAGAG GAG
                                |||||||||||| |||
                                CTGTCCTTCTCTC CTC
                                         T
GAM1076 FLJ13855 3' CAGCTGCTCTTGTCACTGTCT 43581       GAA  G  C
                                AGACAG   GA AG GAGCAGCTG
                                ||||||   || || |||||||||
                                TCTGTC   CT TT CTCGTCGAC
                                   A__  G  _
GAM1076 FLJ14154 3' GCAGCCGCCCGCAGAGCCCGCC 45818     AGA_______  A  A   III
            TTCCTGTC                AAG        GCG GC GCTG   C
                                |||        ||| || ||||   |
                                TTC        CGC CG CGAC   G
                                  CGCCCGAGA   C  C    III
GAM1076 FLJ20123 3' CAGCTGCTGTGTCCTCCTCCT 34585     A   AG  _
                                AGGA GAG  CG AGCAGCTG
                                |||| |||  || ||||||||
                                TCCT CTC  GT TCGTCGAC
                                  C   CT  G
GAM1076 FLJ23322 3' CAGCTGGCTCTTCTCTCCC   88786    A     C   _
                                GG AGAGAG GAGC AGCTG
                                || |||||| |||| |||||
                                CC TCTCTT CTCG TCGAC
                                 C     _    G
GAM1076 FLJ32421 5' CTCTTCTCTTCCTGTCT     58448            C
                                AGACAGGAAGAGAG GAG
                                |||||||||||||| |||
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                                TCTGTCCTTCTCTT CTC
                                                _
GAM1076 GC20     5' TTCGCCTCTTCCTGCCT     68900    A       A
                                AG CAGGAAGAG GCGAG
                                || ||||||||| |||||
                                TC GTCCTTCTC CGCTT
                                 C       _
GAM1076 GDAP1L1  3' CAGCCATCATCCTCTTCCT   43828        AGC  GCA
                                AGGAAGAG   GA   GCTG
                                ||||||||   ||   ||||
                                TCCTTCTC   CT   CGAC
                                    CTA  AC_
GAM1076 HRH3     3' CAGCTGCTTCTGCCCACCCCGC 23366     AAGAGA__ __
             CT                   AGG       GC  GAGCAGCTG
                                |||       ||  |||||||||
                                TCC       CG  TTCGTCGAC
                                  GCCCCACC  TC
GAM1076 HRI      3' CAGCTGCCAGTCTTCCTG    26979       AGA  GA
                                CAGGAAG   GC  GCAGCTG
                                |||||||   ||  |||||||
                                GTCCTTC   TG  CGTCGAC
                                   ___  AC
GAM1076 HSA011916 3' AGCTGCTCCCCCTCCACCT   31058     AA   AGC
                                AGG  GAG   GAGCAGCT
                                |||  |||   ||||||||
                                TCC  CTC   CTCGTCGA
                                  AC   CCC
GAM1076 HSA011916 3' AGCTGCTCCCCCTCCACCT   60270     AA   AGC
                                AGG  GAG   GAGCAGCT
                                |||  |||   ||||||||
                                TCC  CTC   CTCGTCGA
                                  AC   CCC
GAM1076 HSPB7    3' CAGCTGCTCTCAACTCCCC   27024    AA   AGC_
                                GG  GAG    GAGCAGCTG
                                ||  |||    |||||||||
                                CC  CTC    CTCGTCGAC
                                 C_  AACT
GAM1076 HSU52521 5' CAGCTGCAGTTGCTCCCCGCC 27067    AAGA     __
                                GG   GAGCGA  GCAGCTG
                                ||   ||||||  |||||||
                                CC   CTCGTT  CGTCGAC
                                 GCCC     GA
GAM1076 KIAA0040 3' AGCTGCCCTTCCTGTCT     27775         AGAGCGA
                                AGACAGGAAG      GCAGCT
                                ||||||||||      ||||||
                                TCTGTCCTTC      CGTCGA
                                      C_______
GAM1076 KIAA0222 5' CAGCTGCTGCGCCCCCCATGT 27679     _  AAGAGA  _
                                ACA GG     GCG AGCAGCTG
                                ||| ||     ||| ||||||||
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                              TGT CC     CGC TCGTCGAC
                                A  CCC___   G
GAM1076  KIAA0450  3' CGCCTCTCTCCCTGCCT    27635    A   A    _
                              AG CAGG AGAGAG CG
                              || |||| |||||| ||
                              TC GTCC TCTCTC GC
                               C   C     C
GAM1076  KIAA0648  3' CTCTGTTCTCCCCCTTC    82653    C   AA    _
                              GA AGG  GAGAGC GAG
                              || |||  |||||| |||
                              CT TCC  CTCTTG CTC
                               _  CC     T
GAM1076  KIAA0652  3' CAGCTGCTCCCACCCCTCATCC 28459    A   AGC___
                              GGA GAG     GAGCAGCTG
                              ||| |||     |||||||||
                              CCT CTC     CTCGTCGAC
                                A   CCCACC
GAM1076  KIAA0889  3' AGCAGCTTCTCCCTGTCT    31128       AA   GCG   A
                              AGACAGG  GAGA   AGC GCT
                              |||||||  ||||   ||| |||
                              TCTGTCC  CTCT   TCG CGA
                                 __   ___  A
GAM1076  KIAA1161  5' CAGCCATTTTCTCTTCC     81737        C  GCA
                              GGAAGAGAG GA   GCTG
                              ||||||||| ||   ||||
                              CCTTCTCTT TT   CGAC
                                    _ AC_
GAM1076  KIAA1199  3' CAGCTAGCAGATCTCTTCC    72510        GCGA  _
                              GGAAGAGA    GC AGCTG
                              ||||||||    || |||||
                              CCTTCTCT    CG TCGAC
                                   AGA_  A
GAM1076  KIAA1202  3' TAGTGTGACCCTCTTCCTGTC  72022          AGCGA   G
                              GACAGGAAGAG     GCA CTG
                              ||||||||||     ||| |||
                              CTGTCCTTCTC     TGT GAT
                                     CCAG_  _
GAM1076  KIAA1505  5' CAGCTTGCTCCCCTCCTCCCT  94186     A  A   C_    _
                              AGG AG GAG  GAGCA GCTG
                              ||| || |||  ||||| ||||
                              TCC TC CTC  CTCGT CGAC
                                C  _   CC     T
GAM1076  KIAA1580  5' CAGCTGTTCCCCTCCCCC    69443    AA   AGC
                              GG  GAG   GAGCAGCTG
                              ||  |||   |||||||||
                              CC  CTC   CTTGTCGAC
                               CC   CC_
GAM1076  KIAA1668  3' CAGCCTTGTTTGCCTTCC    66468       A_      CA
                              GGAAG  GAGCGAG  GCTG
                              |||||  |||||||  ||||
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                                CCTTC  TTTGTTC  CGAC
                                  CG     __
GAM1076 KIAA1719 3' GGTTTGCTCCCCCTCTACC   68171    A   AGC    _
                                GG AGAG   GAGCAG CT
                                || ||||   |||||| ||
                                CC TCTC   CTCGTT GG
                                 A   CCC     T
GAM1076 KIAA1828 5' AGCTTTCCCTCCCTCCCT    73777    A A  C  C
                                AGG AG GAG GAG AGCT
                                ||| || ||| ||| ||||
                                TCC TC CTC CTT TCGA
                                 C C  C  _
GAM1076 KRTHB4   3' CAGCTAAGCTGGCTTCTCCCTG 52322    A   A  G  G  __
            CCT                   AG CAGG AGA AGC AGC  AGCTG
                                || |||| ||| ||| |||  |||||
                                TC GTCC TCT TCG TCG  TCGAC
                                 C   C  _  G  AA
GAM1076 LGALS9   3' CAGCTGCTGGAATCCTACC   23788    A  A  GCG_
                                GG AG GA   AGCAGCTG
                                || || ||   ||||||||
                                CC TC CT   TCGTCGAC
                                 A  _  AAGG
GAM1076 LGALS9   3' CAGCTGCTGGAATCCTACC   9720     A  A  GCG_
                                GG AG GA   AGCAGCTG
                                || || ||   ||||||||
                                CC TC CT   TCGTCGAC
                                 A  _  AAGG
GAM1076 LIN-7B   3' TGCACTCTCTTCCTGT     42218          CGA
                                ACAGGAAGAGAG   GCA
                                ||||||||||||   |||
                                TGTCCTTCTCTC   CGT
                                       A__
GAM1076 MAGE-E1  5' CAGCTGCTTCACCCTCCCT   47943    AA   AGC_
                                AGG  GAG   GAGCAGCTG
                                |||  |||   |||||||||
                                TCC  CTC   TTCGTCGAC
                                  __  CCAC
GAM1076 MAPK11   3' CAGCCTTGGGCTCTCTTCTGTC 10844      G      GAGCA
                                GACAG AAGAGAGC    GCTG
                                ||||| ||||||||    ||||
                                CTGTC TTCTCTCG    CGAC
                                   _      GGTTC
GAM1076 MAPK6    5' GCCGCCAGGCTTCCTGTT    10836        AGA_  A
                                GACAGGAAG   GCG GC
                                |||||||||   ||| ||
                                TTGTCCTTC   CGC CG
                                     GGAC  _
GAM1076 MGC16386 3' CAGCCACTCACTGGTGTCCTGT 54731        AGAG  C   CA
            CT                   AGACAGGA   AG GAG  GCTG
                                ||||||||   || |||  ||||
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                                TCTGTCCT   TC CTC  CGAC
                                    GTGG  A   AC
GAM1076 MGC1842  5' AGCCGCCGCCTCCCGTTCT   65640    CA  AA   A   A  A
                                AGA  GG  GAG GCG GC GCT
                                |||  ||  ||| ||| || |||
                                TCT  CC  CTC CGC CG CGA
                                  TG  __  _  _  C
GAM1076 MGC2452  5' CAGCTGCTCGCTCTGATGT   50981    GGAAG
                                ACA    AGAGCGAGCAGCTG
                                |||    ||||||||||||||
                                TGT    TCTCGCTCGTCGAC
                                  AG___
GAM1076 MGC27044 3' CTCATATCTTCCTGTCT     58671          GAGC
                                AGACAGGAAGA   GAG
                                ||||||||||    |||
                                TCTGTCCTTCT   CTC
                                      ATA_
GAM1076 MGC3047  3' AGCTGCACCTCTCCTGTCT   50359        A   AGCGA
                                AGACAGGA GAG    GCAGCT
                                |||||||| |||    ||||||
                                TCTGTCCT CTC    CGTCGA
                                    _  CA___
GAM1076 MGC5566  3' CAGCTTCTTCCCCTTTCCTGTC 43897        A   AGC   C
          T                      AGACAGGA GAG   GAG AGCTG
                                |||||||| |||   ||| |||||
                                TCTGTCCT TTC   TTC TCGAC
                                    _  CCC   T
GAM1076 PPP1R1B  3' AGCTGCTCTGCCCCTTTCC   49825      AGA  _
                                GGAAG   GC GAGCAGCT
                                |||||   || ||||||||
                                CCTTT   CG CTCGTCGA
                                   CCC  T
GAM1076 R32184_3 3' AGACGCCTCCTTCCTGTC    53060        A   CGA  AG
                                GACAGGAAG GAG   GC  CT
                                |||||||||| |||   ||  ||
                                CTGTCCTTC CTC   CG  GA
                                    _  ____  CA
GAM1076 RALY     5' GCCGCCCTTTTCCTCCCT    33618    AC      A   A
                                AG  AGGAAGAG GCG GC
                                ||  |||||||| ||| ||
                                TC  TCCTTTTC CGC CG
                                 CC       C  _
GAM1076 RDH-E2   3' CAGCCTTTGTCTCTTCCCTCT  57269    CA      G    CA
                                AGA  GGAAGAGA CGAG  GCTG
                                |||  |||||||| ||||  ||||
                                TCT  CCTTCTCT GTTT  CGAC
                                  C_       _   C_
GAM1076 RFX3     5' CTACTCCTCTCCTCCT     56225     A    C   C
                                AGGA GAGAG GAG AG
                                |||| ||||| ||| ||
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                                TCCT CTCTC CTC TC
                                  C    _  A
GAM1076  RFX3     5'  CTACTCCTCTCCTCCT      11314      A    C   C
                                AGGA GAGAG GAG AG
                                |||| ||||| ||| ||
                                TCCT CTCTC CTC TC
                                  C    _  A
GAM1076  SEPT3    3'  CAGCTGCTGGTCTCCACACC   38886    AA__    G G
                                GG   GAGA C AGCAGCTG
                                ||   |||| | ||||||||
                                CC   CTCT G TCGTCGAC
                                 ACAC   _ G
GAM1076  SRF      3'  CAGCCTCCCCTTCTTCC     11942        AGC   CA
                                GGAAGAG   GAG  GCTG
                                |||||||   |||  ||||
                                CCTTCTT   CTC  CGAC
                                    CCC   __
GAM1076  STRAIT11499 5'  CAGCTGCTCCAATCCCTCCTCC 41139      A   AGC___
              T                  AGGA GAG     GAGCAGCTG
                                 |||| |||     |||||||||
                                 TCCT CTC     CTCGTCGAC
                                   C   CCTAAC
GAM1076  STX12    5'  CAGCCTTAGCTCCTTCC     66350      A   _  CA
                                GGAAG GAGC GAG  GCTG
                                ||||| |||| |||  ||||
                                CCTTC CTCG TTC  CGAC
                                   _    A  __
GAM1076  THG-1    3'  CAGCCGCCTGCCCCCTCTTCCT 48182        A__   A  A
                                AGGAAGAG   GCG GC GCTG
                                ||||||||   ||| || ||||
                                TCCTTCTC   CGT CG CGAC
                                    CCC   C  C
GAM1076  TOMM34   3'  CAGCTGCTGTCCCTGCCCTGTC 22334       A_  A  G G
                                GACAGG  AG GA C AGCAGCTG
                                ||||||  || || | ||||||||
                                CTGTCC  TC CT G TCGTCGAC
                                   CG  C  _ _
GAM1076  TTY7     3'  AGCCACTCTTTTCCTCCT    49176      A    C   CA
                                AGGA GAGAG GAG  GCT
                                |||| ||||| |||  |||
                                TCCT CTTTT CTC  CGA
                                  C    _  AC
GAM1076  WIT-1    3'  CAGCTGTTCCTCCCCTCC    31820     AGA   C
                                GGA   GAG GAGCAGCTG
                                |||   ||| |||||||||
                                CCT   CTC CTTGTCGAC
                                  CCC   _
GAM1076  XT2      3'  CAGCTCTTCCTCACCTTCCTGT 42220          A_   C   C
              CT                  AGACAGGAAG  GAG GAG AGCTG
                                  ||||||||||  ||| ||| |||||
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                                TCTGTCCTTC  CTC TTC TCGAC
                                     CA   C  _
GAM1076  ZNF297    5'  GCCGCCCTCCTCCTTTCT    18391     C    A   A   A
                                AGA AGGA GAG GCG GC
                                ||| |||| ||| ||| ||
                                TCT TCCT CTC CGC CG
                                  T   C   C  _
GAM1076  LOC115399 3'  CAGCTGCTCGCCTGAGGCC    73426    AAG_  A
                                GG    AG GCGAGCAGCTG
                                ||    || ||||||||||
                                CC    TC CGCTCGTCGAC
                                 GGAG  _
GAM1076  LOC120448 5'  CAGCCGCTCGCTCCCCGGCCTG 75550    A    AAGA_      A
              CT                  AG CAGG     GAGCGAGC GCTG
                                || ||||     |||||||| ||||
                                TC GTCC     CTCGCTCG CGAC
                                 _    GGCCC       C
GAM1076  LOC126299 5'  CAGCTGCTGCTCTGCTCCTGTC 74483         AG     G
              T                   AGACAGGA  AGAGC AGCAGCTG
                                |||||||  ||||| ||||||||
                                TCTGTCCT  TCTCG TCGTCGAC
                                     CG    _
GAM1076  LOC126964 3'  CAGTGCTACTCCCTCCCTGCT  74617    A    A  A   CG    G
                                AG CAGG AG GAG  AGCA CTG
                                || |||| || |||  |||| |||
                                TC GTCC TC CTC  TCGT GAC
                                 _    C  C   A_   _
GAM1076  LOC133688 3'  CAGCCCTGCCTCCTCCTTTCT  75114     C    A   A  G  CA
                                AGA AGGA GAG GC AG  GCTG
                                ||| |||| ||| || ||  ||||
                                TCT TCCT CTC CG TC  CGAC
                                  T   C   _  _  C_
GAM1076  LOC138617 5'  CAGCCCAGTGCTCCTTCCTGTC 75946         A     AGCA
                                GACAGGAAG GAGCG    GCTG
                                |||||||| |||||    ||||
                                CTGTCCTTC CTCGT    CGAC
                                      _    GACC
GAM1076  LOC144563 5'  CTCATTTCCTTCCTGTCT    76889          AG  C
                                AGACAGGAAG  AG GAG
                                ||||||||||  || |||
                                TCTGTCCTTC  TT CTC
                                     CT  A
GAM1076  LOC145601 5'  CAGGGCTGCTCCCTTCTTGTC  83364         A   G   AG
                                GACAGGAAG GAGC AGC  CTG
                                ||||||||| |||| |||  |||
                                CTGTTCTTC CTCG TCG  GAC
                                     C    _   G_
GAM1076  LOC146506 3'  AGCTAATCCTTTCCTGCCT   77931    A    AGA   C  GC
                                AG CAGGA   GAG GA  AGCT
                                || |||||   ||| ||  ||||
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                                TC GTCCT   TTC CT  TCGA
                                 C    ___  _  AA
GAM1076  LOC146545 5'  CAGCTGCTCACAGTTCCTG   77982       GAGAGC
                                CAGGAA     GAGCAGCTG
                                ||||||     |||||||||
                                GTCCTT     CTCGTCGAC
                                   GACA__
GAM1076  LOC146756 3'  GCTCAGCCCTCTTCCTG     83782         A  _
                                CAGGAAGAG GC GAGC
                                ||||||||| || ||||
                                GTCCTTCTC CG CTCG
                                     C  A
GAM1076  LOC148930 3'  CAGCTGCTGCCTATTCCCTG   79092      _  G  A  G
                                CAGG AA AG GC AGCAGCTG
                                |||| || || || ||||||||
                                GTCC TT TC CG TCGTCGAC
                                  C  A  _  _
GAM1076  LOC149830 5'  TTGTCGCTCTCCTCC       84727     A       G
                                GGA GAGAGCGA CAG
                                ||| ||||||||| |||
                                CCT CTCTCGCT GTT
                                  C       _
GAM1076  LOC151632 5'  CTCATCTCCTTCCTGTC     85470         A   C_
                                GACAGGAAG GAG  GAG
                                ||||||||| |||  |||
                                CTGTCCTTC CTC  CTC
                                     _   TA
GAM1076  LOC157638 3'  AGCCGCTGCTCCCTTTCT    81509       A    G   A
                                AGGAAG GAGC AGC GCT
                                |||||| |||| ||| |||
                                TCTTTC CTCG TCG CGA
                                   C    _   C
GAM1076  LOC158056 5'  CAGCTGCTGCTGGGCACTTCCT 81682          AG___   G
           GTCT                   AGACAGGAAG    AGC AGCAGCTG
                                ||||||||||    ||| |||||||||
                                TCTGTCCTTC    TCG TCGTCGAC
                                     ACGGG  _
GAM1076  LOC158226 3'  AGCTGCTCGCTTCCTCC     81794     A AG
                                GGA G  AGCGAGCAGCT
                                ||| |  ||||||||||||
                                CCT C  TCGCTCGTCGA
                                  _ CT
GAM1076  LOC158434 5'  CAGCTGCTCCTGATTCCTG   86818       GAG  C
                                CAGGAA   AG GAGCAGCTG
                                ||||||   || |||||||||
                                GTCCTT   TC CTCGTCGAC
                                   AG_  _
GAM1076  LOC169693 3'  CAGCCACATGCCTTCCTGTT  87291         AGA   AGCA
                                GACAGGAAG   GCG   GCTG
                                |||||||||   |||   ||||
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                                TTGTCCTTC  CGT   CGAC
                                     ___  ACAC
GAM1076  LOC170221 3'  GCTGCTGCCCCCTGCT     82579    A   AAGAGA  G
                                AG CAGG     GC AGCAGC
                                || ||||     || |||||||
                                TC GTCC     CG TCGTCG
                                 _   CC_____  _
GAM1076  LOC196996 3'  GCTCTTCTCTTCCCTCT     87860     CA       C
                                AGA  GGAAGAGAG GAGC
                                |||  ||||||||| ||||
                                TCT  CCTTCTCTT CTCG
                                  C_       _
GAM1076  LOC199986 5'  AGCTTCTGCCTCCTGTCT    89896        AGA A  G  C
                                AGACAGGA   G GC AG AGCT
                                ||||||||   | || || ||||
                                TCTGTCCT   C CG TC TCGA
                                     ___ _  _ T
GAM1076  LOC200310 3'  CAGCCACTCTTCTGTTCC    65730     G   C   CA
                                GGAA AGAG GAG  GCTG
                                |||| |||| |||  ||||
                                CCTT TCTT CTC  CGAC
                                  G   _  AC
GAM1076  LOC200488 5'  AGCCGCCAGCCTCCTGTCT   90081        AGA A  GA  A
                                AGACAGGA   G GC  GC GCT
                                ||||||||   | ||  || |||
                                TCTGTCCT   C CG  CG CGA
                                     ___ _  AC  C
GAM1076  LOC200583 5'  CTCGCTCTCCTCCTGTC     88834        A
                                GACAGGA GAGAGCGAG
                                ||||||| |||||||||
                                CTGTCCT CTCTCGCTC
                                    C
GAM1076  LOC200940 5'  CAGCTGCTCCGCCTGTCCTG   88951      AG  A  _
                                CAGGA  AG GCG AGCAGCTG
                                |||||  || ||| ||||||||
                                GTCCT  TC CGC TCGTCGAC
                                  G_  _  C
GAM1076  LOC201139 5'  CTGCTCGCTCGCTCACCTCCCT 88130    AC  A_  A
                                AG  AGG  AG GAGCGAGCAG
                                ||  |||  || ||||||||||
                                TC  TCC  TC CTCGCTCGTC
                                 CC  AC  G
GAM1076  LOC203083 5'  CTCATCTCCTTCCTGTC     90463         A  C_
                                GACAGGAAG GAG  GAG
                                ||||||||| |||  |||
                                CTGTCCTTC CTC  CTC
                                     _  TA
GAM1076  LOC219731 5'  CAGCTGCTCTGGTGGCCTCCTG 93090    A    AGAGA  __
            CT                    AG CAGGA    GC  GAGCAGCTG
                                || |||||    ||  |||||||||
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                                TC GTCCT    TG  CTCGTCGAC
                                 _    CCGG_  GT
GAM1076  LOC219894 3'  CAGCTGTTCAGCCCTTCTGTCT 93278      GAA   A  _
                                AGACAG   GAG GC GAGCAGCTG
                                ||||||   ||| || |||||||||
                                TCTGTC   TTC CG CTTGTCGAC
                                   ___   C  A
GAM1076  LOC219919 5'  CTCATCTCCTTCCTGTC     93293         A   C_
                                GACAGGAAG GAG  GAG
                                |||||||||| |||  |||
                                CTGTCCTTC CTC  CTC
                                      _  TA
GAM1076  LOC221749 5'  GCCGGACCTCTTCCTTTC    92005    C       AG_  A
                                GA AGGAAGAG   CG GC
                                || ||||||||   || ||
                                CT TCCTTCTC   GC CG
                                 T       CAG  _
GAM1076  LOC221795 5'  CTCATCTCCTTCCTGTC     92478         A   C_
                                GACAGGAAG GAG  GAG
                                |||||||||| |||  |||
                                CTGTCCTTC CTC  CTC
                                      _  TA
GAM1076  LOC254015 3'  GCTCAGCCCTCTTCCTG     96704          A  _
                                CAGGAAGAG GC GAGC
                                ||||||||| || ||||
                                GTCCTTCTC CG CTCG
                                      C  A
GAM1076  LOC254176 5'  CTCATCTCCTTCCTGTC     97340         A   C_
                                GACAGGAAG GAG  GAG
                                |||||||||| |||  |||
                                CTGTCCTTC CTC  CTC
                                      _  TA
GAM1076  LOC254213 5'  CTGCTCGCTCACTCACCT    95160     A_  A
                                AGG  AG GAGCGAGCAG
                                |||  || ||||||||||
                                TCC  TC CTCGCTCGTC
                                  AC  A
GAM1076  LOC256515 5'  CTCATCTCCTTCCTGTC     96463         A   C_
                                GACAGGAAG GAG  GAG
                                |||||||||| |||  |||
                                CTGTCCTTC CTC  CTC
                                      _  TA
GAM1076  LOC256594 5'  CTCATCTCCTTCCTGTC     97078         A   C_
                                GACAGGAAG GAG  GAG
                                |||||||||| |||  |||
                                CTGTCCTTC CTC  CTC
                                      _  TA
GAM1076  LOC90010  5'  CAGCTGCTCACCCCCTTTCCC  61084    A   AGC__
                                GG AGAG    GAGCAGCTG
                                || ||||    |||||||||
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                                CC TTTC    CTCGTCGAC
                                 C   CCCCA
GAM1076 LOC90072 3' AGCAGCTTCTCCCTGTCT   61289       AA   GCG  A
                                AGACAGG  GAGA  AGC GCT
                                ||||||| ||||  ||| |||
                                TCTGTCC  CTCT  TCG CGA
                                   __   ____  A
GAM1076 LOC91301 5' CTGCCGCCCCCTCCCCTCC   65543   C   AA  A__  A
                                A AGG  GAG   GCG GCAG
                                | |||  |||   ||| ||||
                                C TCC  CTC   CGC CGTC
                                 C  C_  CCC  _
GAM1077 PMX1     3' GCATCAACATGGCCAACAGCA 22593     TATCA  ATTGA
                                TGCT    GC    GTTGATGC
                                ||||    ||    ||||||||
                                ACGA    CG    CAACTACG
                                  CAAC_ GTA__
GAM1077 KIAA1715 3' GCATTAATAATGATGATAAACA 68121    C     G   GA
                                TG TTATCA CATT  GTTGATGC
                                || |||||| ||||  ||||||||
                                AC AATAGT GTAA  TAATTACG
                                 A     A   __
GAM1077 PHCA     3' CATGGCAATGCTGTTAAACA  37174    C  T      AGT
                                TG TTA CAGCATTG   TG
                                || ||| ||||||||   ||
                                AC AAT GTCGTAAC   AC
                                 A  T       GGT
GAM1077 UBE2G1   3' GCCAGTTATCAATGCTGACAAG 12483     A        GTTGAT
                                CTT TCAGCATTGA     GC
                                ||| ||||||||||     ||
                                GAA AGTCGTAACT     CG
                                  C        ATTGAC
GAM1077 LOC124512 3' TCAATACTGATGAGCA     74301         C
                                TGCTTATCAG ATTGA
                                |||||||||| |||||
                                ACGAGTAGTC TAACT
                                      A
GAM1077 LOC124602 3' CATCAACTATCGCGACAGCA  74305     TATCA  ATTG
                                TGCT    GC    AGTTGATG
                                ||||    ||    ||||||||
                                ACGA    CG    TCAACTAC
                                  CAG__  CTA_
GAM1077 LOC145842 5' GCTTCTATCAATGCTGTAAACA 77534    C  T       GTT  T
                                TG TTA CAGCATTGA   GA GC
                                || ||| |||||||||   || ||
                                AC AAT GTCGTAACT   CT CG
                                 A  _        AT_  T
GAM1077 LOC203397 3' CATCAACTATCGCGACAGCA  89349     TATCA  ATTG
                                TGCT    GC    AGTTGATG
                                ||||    ||    ||||||||
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                                ACGA    CG   TCAACTAC
                                  CAG__  CTA_
GAM1077  LOC220143 3'  GCATCAACCCACCACCGACAAG 93588      A  AGCAT  A
             C                    GCTT TC    TG GTTGATGC
                                  |||| ||    || ||||||||
                                  CGAA AG    AC CAACTACG
                                    C  CCACC  C
GAM1078  FBXL11   3'  GCTCCCATGACCCTCT      24573     AA       T
                                  AGA  GTCATGGG AGC
                                  |||  |||||||| |||
                                  TCT  CAGTACCC TCG
                                    CC       _
GAM1078  GNB3     3'  CCATCTCCTCCCATGGCCTTC  9075      A       T  CTT
                                  GAA GTCATGGG AG   GATGG
                                  ||| |||||||| ||   |||||
                                  CTT CGGTACCC TC   CTACC
                                    C       _  CT_
GAM1078  KLK13    3'  CCATCCTGTCACCATGACTTCC 31531    A       GTA  TT
             T                    AG AAGTCATGG   GC  GATGG
                                  || |||||||||   ||  |||||
                                  TC TTCAGTACC   TG  CTACC
                                   C        AC_  TC
GAM1078  MUCDHL   3'  AGCCCCATGACCTTC       48363     A       TA
                                  GAA GTCATGGG  GCT
                                  ||| ||||||||  |||
                                  CTT CAGTACCC  CGA
                                    C       __
GAM1078  MUCDHL   3'  AGCCCCATGACCTTC       87298     A       TA
                                  GAA GTCATGGG  GCT
                                  ||| ||||||||  |||
                                  CTT CAGTACCC  CGA
                                    C       __
GAM1078  PROK1    3'  AGCTCCCATGACTCTC      50554     A       T
                                  GA AGTCATGGG AGCT
                                  || |||||||| ||||
                                  CT TCAGTACCC TCGA
                                   C        _
GAM1078  SEMG1    3'  CTGCCCATGCTTCCT       11539     A   T
                                  AG AAG CATGGGTAG
                                  || ||| |||||||||
                                  TC TTC GTACCCGTC
                                   C  _
GAM1078  SLC1A4   3'  CCATCAAGCCACACCCCCTTCT 11714     TCAT    A__
             T                    AAG    GGGT   GCTTGATGG
                                  |||    ||||   |||||||||
                                  TTC    CCCA   CGAACTACC
                                    TTCC    CAC
GAM1078  STS      3'  CTACCCATGTCTTTCT      4452        T
                                  AGAAAG CATGGGTAG
                                  |||||| |||||||||
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                                TCTTTC GTACCCATC
                                   T
GAM1078 ARHGEF4  3' TGGGCACCCATGACCCTCT   52219    AA       A
                                AGA  GTCATGGGT GCTTG
                                |||  ||||||||| |||||
                                TCT  CAGTACCCA CGGGT
                                  CC       _
GAM1078 DOC-1R   3' CCATGAGTCCCACCCATGAC  19578        A__   G
                                GTCATGGGT   GCTT ATGG
                                |||||||||   |||| ||||
                                CAGTACCCA   TGAG TACC
                                     CCC   _
GAM1078 FLJ14351 5' CCATCTGCCCCCATGACCTTCT 45321     A      TA  TT
                                AGAA GTCATGGG  GC  GATGG
                                |||| ||||||||  ||  |||||
                                TCTT CAGTACCC  CG  CTACC
                                  C       C_  T_
GAM1078 FLJ25416 3' CCATCAAGCTGGTTGTCTTCCT 58804    A   TC TG G
                                AG AAG  A  G TAGCTTGATGG
                                || |||  |  | ||||||||||
                                TC TTC  T  T GTCGAACTACC
                                 C   __ GT G
GAM1078 KIAA1229 3' CCATCAAGCTACCATTGACTTT 62065         TG
             CT                   AGAAAGTCA  GGTAGCTTGATGG
                                |||||||||  ||||||||||||
                                TCTTTCAGT  CCATCGAACTACC
                                     TA
GAM1078 KIAA1233 3' AGCAACCCATGACTTCCT    63078    A        A
                                AG AAGTCATGGGT GCT
                                || ||||||||||| |||
                                TC TTCAGTACCCA CGA
                                 C         A
GAM1078 KIAA1497 5' CCATCATTGGCCAAACTTTCT  67506       CATG   AGCT
                                AGAAAGT    GGT    TGATGG
                                |||||||    |||    ||||||
                                TCTTTCA    CCG    ACTACC
                                    AA__   GTT_
GAM1078 MGC4796  3' CCACGACGCACAGCCCATGAC  61482        A__  _   A
                                GTCATGGGT   GC TTG TGG
                                |||||||||   || ||| |||
                                CAGTACCCG   CG AGC ACC
                                     ACA  C   _
GAM1078 PAFAH2   3' CCAAGGGCACCCATGA      4761         A    GA
                                TCATGGGT GCTT  TGG
                                |||||||| ||||  |||
                                AGTACCCA CGGG  ACC
                                    _    A_
GAM1078 PYY2     3' CCATCAAGTCACATAAC     40824    C   GGTA
                                GT ATG    GCTTGATGG
                                || |||    |||||||||
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                                CA TAC    TGAACTACC
                                 A   AC__
GAM1078  SCYD1     3'  CCATCAAGCCACCAACATACT  90927     C   __   A
                                AGT ATG  GGT GCTTGATGG
                                ||| |||  ||| |||||||||
                                TCA TAC  CCA CGAACTACC
                                  _   AA   C
GAM1078  LOC160897 3'  CAACTACCCATGAATTC     82244     AG        C
                                GAA  TCATGGGTAG TTG
                                |||  |||||||||| |||
                                CTT  AGTACCCATC AAC
                                  A_         _
GAM1078  LOC166206 5'  CCATCGGTCATTACCCAGAACC 82624      A  CA      C__
              TTCT                  AGAA GT  TGGGTAG   TTGATGG
                                |||| ||  |||||||   |||||||
                                TCTT CA  ACCCATT   GGCTACC
                                  C  AG      ACT
GAM1078  LOC199720 3'  CCATCAAGCTGTCCGGCTCTCT 88337     A    AT  GT
                                AGA AGTC  GG  AGCTTGATGG
                                ||| ||||  ||  ||||||||||
                                TCT TCGG  CC  TCGAACTACC
                                  C    __  TG
GAM1078  LOC220549 5'  CCATGGTCACCCATGACTTCCT 92917     A         AG  TG
                                AG AAGTCATGGGT  CT  ATGG
                                || ||||||||||  ||  ||||
                                TC TTCAGTACCCA  GG  TACC
                                 C          CT  __
GAM1078  LOC256222 3'  CCATCAAGTCTCACAGCTTTCT 97221        CA    TA
                                AGAAAGT  TGGG  GCTTGATGG
                                |||||||  ||||  |||||||||
                                TCTTTCG  ACTC  TGAACTACC
                                    AC    __
GAM1078  LOC92228  3'  CCATCAAGTAGTTCTGACTTCC 68540     A     T GG A
              T                  AG AAGTCA G  T GCTTGATGG
                                || ||||||  |  | |||||||||
                                TC TTCAGT C  G TGAACTACC
                                 C     _ TT A
GAM1079  MMP20     3'  TCCAAATCAACACAATGCAC   16484            CAGGA
                                GTGCATTGTGTTG    TTGGG
                                ||||||||||||     |||||
                                CACGTAACACAAC    AACCT
                                        TA___
GAM1079  PIM2      3'  TCCCAATCCTACAAAGGAGC   59991    A  GTG   C
                                GC TT   TTG AGGATTGGGA
                                || ||   ||| ||||||||||
                                CG AG   AAC TCCTAACCCT
                                 _  GA_   A
GAM1079  RXRA      3'  CCCAATCCTTAGCAATGC    11405        GTTGC
                                GCATTGT    AGGATTGGG
                                |||||||    |||||||||
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                                CGTAACG    TCCTAACCC
                                   AT___
GAM1079  BRAG     3'  TCCCAATTCCAAAACACAATGC 29477          GCA
              AC                  GTGCATTGTGTT  GGATTGGGA
                                  ||||||||||||  |||||||||
                                  CACGTAACACAA  CTTAACCCT
                                        AAC
GAM1079  DKFZp547O146 5'  CCCAATCCCCCAACAC     39564       CA
                                  GTGTTG  GGATTGGG
                                  ||||||  ||||||||
                                  CACAAC  CCTAACCC
                                     CC
GAM1079  KIAA1762  3'  TCCCAATCCCCACAGACACACA 63792     CAT     GCA__
              C                    GTG   TGTGTT    GGATTGGGA
                                  |||   ||||||    |||||||||
                                  CAC   ACACAG    CCTAACCCT
                                   ___     ACACC
GAM1079  LOC145820 3'  CCCAATCCTTAAGCAATCAC   77512     C    GTTGC
                                  GTG ATTGT    AGGATTGGG
                                  ||| |||||    |||||||||
                                  CAC TAACG    TCCTAACCC
                                    _    AAT__
GAM1079  LOC253980 3'  TCCCAACCCCATTGCTAACAA  95076     GTT  ___  A
                                  TTGT   GCA   GG TTGGGA
                                  ||||   |||   || ||||||
                                  AACA   CGT   CC AACCCT
                                    AT_   TAC  C
GAM1080  APM1     3'  TACCCTAAACTCTCTGGG    16600        ACTCA   T
                                  TCCAGAGA    AGG GTG
                                  ||||||||    ||| |||
                                  GGGTCTCT    TCC CAT
                                       CAAA_  _
GAM1080  APPBP2   3'  TTGCATTTAAGTTCCCTAGGA  21086     _ A    CA    TG
                                  TCC AG GAACT  AGGTG  A
                                  ||| || |||||  |||||  |
                                  AGG TC CTTGA  TTTAC  T
                                    A  C    A_    GT
GAM1080  AQP6     5'  CATGCTTGAGTCCCCTGGG   53915      AGA      G
                                  TCCAG   ACTCAAG TGTG
                                  |||||   ||||||| ||||
                                  GGGTC   TGAGTTC GTAC
                                     CCC      _
GAM1080  ARAF1    3'  CACTCAGAACCTCTCTGGA   63937        AC_  AA
                                  TCCAGAGA   TC  GGTG
                                  ||||||||   ||  ||||
                                  AGGTCTCT   AG  TCAC
                                       CCA  AC
GAM1080  C8orf1   3'  TACTGGCTTGAATTTTCTGGA  15087         C    G _
                                  TCCAGAGAA TCAAG T GTG
                                  ||||||||| ||||| | |||
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                                AGGTCTTTT AGTTC G CAT
                                     A    G T
GAM1080  CA12    3'  CACTTCGGCTCTCTGGA    6875        A  CA
                                TCCAGAGA CT  AGGTG
                                |||||||| ||  |||||
                                AGGTCTCT GG  TTCAC
                                     C  C_
GAM1080  CANX    3'  ATTCACACCTCTGTCCCTC   87480    A_  TCA
                                GAG  AC   AGGTGTGAAT
                                |||  ||   ||||||||||
                                CTC  TG   TCCACACTTA
                                  CC  TC_
GAM1080  CEP1    5'  TAGACCCCGAACTCTTTGGA   22817        AC  AA   G
                                TCCAGAGA  TC  GGT TG
                                ||||||||  ||  ||| ||
                                AGGTTTCT  AG  CCA AT
                                     CA  CC   G
GAM1080  FCAR    3'  TTCCTCGCTAGAGTTCTCCAGA 55807    CA      AA    T_
                                TC  GAGAACTC  GGTG  GAA
                                ||  ||||||||  ||||  |||
                                AG  CTCTTGAG  TCGC  CTT
                                 AC       A_   TC
GAM1080  FCAR    3'  TTCCTCGCTAGAGTTCTCCAGA 55817    CA      AA    T_
                                TC  GAGAACTC  GGTG  GAA
                                ||  ||||||||  ||||  |||
                                AG  CTCTTGAG  TCGC  CTT
                                 AC       A_   TC
GAM1080  HMGCR   3'  ATTCACACAGGGCTCTTGGA   5972      _  AA  CAAG
                                TCCA GAG  CT   GTGTGAAT
                                ||||  |||  ||   ||||||||
                                AGGT CTC  GA   CACACTTA
                                  T  GG  ____
GAM1080  MME     3'  TACTCTTGTTGAGTTCTATAGA 6143     CAG       __  T
                                TC   AGAACTCAA  GG GTG
                                ||   |||||||||  || |||
                                AG   TCTTGAGTT  TC CAT
                                 ATA        GT  T
GAM1080  MME     3'  TACTCTTGTTGAGTTCTATAGA 23490    CAG       __  T
                                TC   AGAACTCAA  GG GTG
                                ||   |||||||||  || |||
                                AG   TCTTGAGTT  TC CAT
                                 ATA        GT  T
GAM1080  MME     3'  TACTCTTGTTGAGTTCTATAGA 23500    CAG       __  T
                                TC   AGAACTCAA  GG GTG
                                ||   |||||||||  || |||
                                AG   TCTTGAGTT  TC CAT
                                 ATA        GT  T
GAM1080  MME     3'  TACTCTTGTTGAGTTCTATAGA 23512    CAG       __  T
                                TC   AGAACTCAA  GG GTG
                                ||   |||||||||  || |||
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                                AG   TCTTGAGTT  TC CAT
                                 ATA        GT  T
GAM1080  NEU3     3'  CACCTGAACTCTCTGGA     21846         AC   A
                                TCCAGAGA  TCA GGTG
                                ||||||||  ||| ||||
                                AGGTCTCT  AGT CCAC
                                     CA  _
GAM1080  P53AIP1  3'  CACCCACTGAACTTTCTGGA  42080         AC   A_  T
                                TCCAGAGA  TCA  GG GTG
                                ||||||||  |||  || |||
                                AGGTCTTT  AGT  CC CAC
                                     CA  CA  _
GAM1080  PAICS    3'  TACCTTTAGTTCTCTG      21260          C
                                CAGAGAACT AAGGTG
                                ||||||||| ||||||
                                GTCTCTTGA TTCCAT
                                      T
GAM1080  PIR51    3'  CACTTTTTGTTAAGTTCTTTAG 21364     C       ___     T
              A                  TC AGAGAACT   CAAGG GTG
                                 || |||||||   ||||| |||
                                 AG TTTCTTGA   GTTTT CAC
                                  A       ATT     T
GAM1080  PLSCR1   5'  CATCGCCTGGCCCCGGCTCTCT 40856         A  CA____    _
              GGA                  TCCAGAGA CT      AGGTG TG
                                   |||||||| ||      ||||| ||
                                   AGGTCTCT GG      TCCGC AC
                                        C  CCCCGG     T
GAM1080  PTPN1    3'  TATTCACACCTCACGCTCTGGA 11050        AACTCA
                                   TCCAGAG     AGGTGTGAATA
                                   |||||||     ||||||||||||
                                   AGGTCTC     TCCACACTTAT
                                       GCAC__
GAM1080  RAP1A    3'  GTTTGCACAAGTTCCCTGGA   11248      A    CAAG   TG
                                   TCCAG GAACT    GTG  AAT
                                   ||||| |||||    |||  |||
                                   AGGTC CTTGA    CAC  TTG
                                      C     A___   GT
GAM1080  SYT4     3'  CACTATATTTGAGTTCTT     62435          GT__
                                   GAGAACTCAAG    GTG
                                   ||||||||||    |||
                                   TTCTTGAGTTT    CAC
                                         ATAT
GAM1080  TCTA     3'  TAGGCCCTGAGTTTTCTG     42241          A   G
                                   CAGAGAACTCA GGT TG
                                   |||||||||| ||| ||
                                   GTCTTTTGAGT CCG AT
                                         C   G
GAM1080  VAT1     3'  CACCCTTCACTGAGTTCTCTGG 21044           ____   T
              A                    TCCAGAGAACTCA    AGG GTG
                                   ||||||||||||    ||| |||
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                                AGGTCTCTTGAGT    TCC CAC
                                      CACT  _
GAM1080  ZFH4     5'  CACCTCAGCTCCCTGGA     45294       A  A  CA
                                TCCAG GA CT  AGGTG
                                ||||| || ||  |||||
                                AGGTC CT GA  TCCAC
                                   C  C  C_
GAM1080  ZFP103   5'  TATTCCGAGCTCTCTGGA     19026         A   AA  T
                                TCCAGAGA CTC  GG GTG
                                |||||||| |||  || |||
                                AGGTCTCT GAG  CC TAT
                                     C   __  T
GAM1080  ZNF202   3'  TTGCAGCCAAGTTCCCTGG    12913      A    CAA  _  TG
                                CCAG GAACT   GG TG  A
                                |||| |||||   || ||  |
                                GGTC CTTGA   CC AC  T
                                  C    A__  G  GT
GAM1080  C1orf25  5'  ATTCACGTCAGTTCTCTG     72532          CAA GT
                                CAGAGAACT   G  GTGAAT
                                |||||||||   |  ||||||
                                GTCTCTTGA   C  CACTTA
                                     ___ TG
GAM1080  C20orf177 3'  TACTTTTGAGTTCTC       62154            T
                                GAGAACTCAAGG GTG
                                |||||||||||| |||
                                CTCTTGAGTTTT CAT
                                          _
GAM1080  CG012    3'  GCAGTCTGAGTTCTTCAGA   83221    CA       A  _
                                TC  GAGAACTCA GG TGT
                                ||  ||||||||| || |||
                                AG  TTCTTGAGT CT ACG
                                 AC        _  G
GAM1080  CRK7     3'  TTCCATCCAGTTCTCTG     33256         CAA    T
                                CAGAGAACT   GGTG GAA
                                |||||||||   |||| |||
                                GTCTCTTGA   CTAC CTT
                                     C__    _
GAM1080  DIO2     3'  ATTCACACTGTTGTCCTT    5826      A  TCAA
                                GAG AC    GGTGTGAAT
                                ||| ||    |||||||||
                                TTC TG    TCACACTTA
                                  C  TTG_
GAM1080  DIO2     3'  ATTCACACTGTTGTCCTT    25678     A  TCAA
                                GAG AC    GGTGTGAAT
                                ||| ||    |||||||||
                                TTC TG    TCACACTTA
                                  C  TTG_
GAM1080  DKFZP434A043 3'  CACACTTAAACTCTGTGGA   31187      G   ACTCA
                                TCCA AGA    AGGTGTG
                                |||| |||    |||||||
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                                AGGT TCT    TTCACAC
                                  G  CAAA_
GAM1080  DKFZp434F1819 3'  TCACACCTCCTTTTTG     50009      ACTCA
                                CAGAGA    AGGTGTGA
                                ||||||    ||||||||
                                GTTTTT    TCCACACT
                                   CC___
GAM1080  DPCR1    3'  CATCTCTGAGTTCTCAGGA   55120    A      _
                                TCC GAGAACTCA AGGTG
                                ||| ||||||||| |||||
                                AGG CTCTTGAGT TCTAC
                                  A       C
GAM1080  FLJ10898 3'  ATTCACACTGATTTTGTCTGGA 59421      G  CTCAA
                                TCCAGA AA    GGTGTGAAT
                                |||||| ||    |||||||||
                                AGGTCT TT    TCACACTTA
                                   G  TTAG_
GAM1080  FLJ11193 3'  TATTTTGAATCTCTG      37154      AC
                                CAGAGA  TCAAGGTG
                                ||||||  ||||||||
                                GTCTCT  AGTTTTAT
                                   A_
GAM1080  FLJ13769 3'  CACTCAAGCTCTCTGGA    46603       A  CAA
                                TCCAGAGA CT   GGTG
                                |||||||| ||   ||||
                                AGGTCTCT GA   TCAC
                                     C  AC_
GAM1080  FLJ13782 3'  GCCTGAGCTTTCTGGA     46169       A   A
                                TCCAGAGA CTCA GGT
                                |||||||| |||| |||
                                AGGTCTTT GAGT CCG
                                     C   _
GAM1080  FLJ20555 3'  CAGACCTCAGCTCTCTGGA   35393       A  CA   G
                                TCCAGAGA CT  AGGT TG
                                |||||||| ||  |||| ||
                                AGGTCTCT GA  TCCA AC
                                     C  C_   G
GAM1080  FLJ23142 3'  TTTTGAGTTCCTAGA      44727    C  A
                                TC AG GAACTCAAGG
                                || || ||||||||||
                                AG TC CTTGAGTTTT
                                 A  _
GAM1080  FLJ30092 5'  TATTCACACCTCACTTCCTG  58691    A   CTCA
                                CAG GAA    AGGTGTGAATA
                                ||| |||    ||||||||||||
                                GTC CTT    TCCACACTTAT
                                  _  CAC_
GAM1080  GRID1    3'  TATTCAAGCAAGTTCTCTAGG  68501    _      CAAG  G
                                CC AGAGAACT    GT TGAATA
                                || ||||||||    || ||||||
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                              GG TCTCTTGA   CG ACTTAT
                               A      A___  A
GAM1080  HPCAL4   3' CATCTTGTGCCCTCTGGA    32732       AACT
                              TCCAGAG   CAAGGTG
                              |||||||   |||||||
                              AGGTCTC   GTTCTAC
                                  CCGT
GAM1080  KIAA0229 3' CATTTTGATTCTCTG      92423       C
                              CAGAGAA TCAAGGTG
                              ||||||| ||||||||
                              GTCTCTT AGTTTTAC
                                    _
GAM1080  KIAA0295 3' GCCTTGGGTTCTCCAGA    68105    CA
                              TC  GAGAACTCAAGGT
                              ||  ||||||||||||
                              AG  CTCTTGGGTTCCG
                               AC
GAM1080  KIAA0420 3' TACCCTGCACTCTCTGGA    63366       ACTCA   T
                              TCCAGAGA    AGG GTG
                              ||||||||    ||| |||
                              AGGTCTCT    TCC CAT
                                   CACG_  _
GAM1080  KIAA0565 3' TATTTTTAAGTCTCTGGA    66897       ACTC
                              TCCAGAGA   AAGGTG
                              ||||||||   ||||||
                              AGGTCTCT   TTTTAT
                                   GAAT
GAM1080  KIAA1036 3' CATCTTGGTCCTCCGGA     29816     A  A  T
                              TCC GAG AC CAAGGTG
                              ||| ||| || |||||||
                              AGG CTC TG GTTCTAC
                                C   C  _
GAM1080  KIAA1240 3' TATTCATGTTTGAGTTC     66737       G TG
                              GAACTCAA G  TGAATA
                              |||||||| |  ||||||
                              CTTGAGTT T  ACTTAT
                                   _ GT
GAM1080  KIAA1297 5' CACTGCAGCCCGAGTTCTCTGG 72170          AA  ____
                              CCAGAGAACTC  GGT   GTG
                              ||||||||||  |||   |||
                              GGTCTCTTGAG  CCG   CAC
                                    C_   ACGT
GAM1080  KIAA1579 3' CACTTTGATTTCCCTGGA    36605      A  C
                              TCCAG GAA TCAAGGTG
                              ||||| ||| ||||||||
                              AGGTC CTT AGTTTCAC
                                 C   T
GAM1080  MAB21L2  5' TTCGCAGCTCTCTGGA      21233       ACTCAA G
                              TCCAGAGA     G TGTGAA
                              ||||||||     | ||||||
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                                AGGTCTCT     C ACGCTT
                                      _______ G
GAM1080  MAP2K6   5'  CATCTTGATTCCCTG       10868     A   C
                                CAG GAA TCAAGGTG
                                ||| ||| ||||||||
                                GTC CTT AGTTCTAC
                                  C   _
GAM1080  MGC21688 3'  ATTCACGCAGAGCTCTCTG   58265       A   AAG
                                CAGAGA CTC   GTGTGAAT
                                |||||| |||   ||||||||
                                GTCTCT GAG   CGCACTTA
                                   C   A__
GAM1080  MMPL1    3'  TATTCCTCTGTGTGTTCTCTGG 14722         T  A  TGT
             A                   TCCAGAGAAC CA GG   GAATA
                                ||||||||||  || ||   |||||
                                AGGTCTCTTG GT TC   CTTAT
                                      T  G  TC_
GAM1080  NDUFB6   3'  ATTTACTGAATTTTCTGGA    10197         C   AGGT
                                TCCAGAGAA TCA    GTGAAT
                                ||||||||| |||    ||||||
                                AGGTCTTTT AGT    CATTTA
                                     A  _____
GAM1080  SSB-4    3'  CACTGACTCACAGTTCTCTGGA 55097          CA_  GT_
                                TCCAGAGAACT   AG   GTG
                                ||||||||||   ||   |||
                                AGGTCTCTTGA   TC   CAC
                                      CAC  AGT
GAM1080  STAM2    3'  TTCAAGCTAGTTCTCTG     19570         CAA   G
                                CAGAGAACT   GGT TGAA
                                |||||||||   ||| ||||
                                GTCTCTTGA   TCG ACTT
                                     ___   A
GAM1080  SYT12    3'  TAGCTTGAGTTCCCTAGA    94740    C  A       G
                                TC AG GAACTCAAG TG
                                || || ||||||||| ||
                                AG TC CTTGAGTTC AT
                                 A  C        G
GAM1080  TED      3'  TATTCACACCTTTCCATCCCTG 31643     A  ACTC
                                CAG GA    AAGGTGTGAATA
                                ||| ||    ||||||||||||
                                GTC CT    TTCCACACTTAT
                                  C  ACCT
GAM1080  TRAD     3'  CACTCCGTGCAGTTCTCTG    22951         _  A  T
                                CAGAGAACT CA GG GTG
                                ||||||||| || || |||
                                GTCTCTTGA GT CC CAC
                                      C  G  T
GAM1080  TRIM22   3'  CATCTACAAGTTCTCTGGA    20286          CA_
                                TCCAGAGAACT   AGGTG
                                ||||||||||   |||||
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                                AGGTCTCTTGA   TCTAC
                                      ACA
GAM1080  TUB      3'  ATTCAGAACTTCAAGTTCTCTT 12425    C      CA   G_
              GA                    TC AGAGAACT  AGGT  TGAAT
                                    || ||||||||  ||||  |||||
                                    AG TCTCTTGA  TTCA  ACTTA
                                     T       AC    AG
GAM1080  LOC120939 3'  CATCTCTCGAGTTCTTGGA   76250     G      A  GT
                                    TCCA AGAACTC AG  GTG
                                    |||| ||||||| ||  |||
                                    AGGT TCTTGAG TC  TAC
                                      _      C  TC
GAM1080  LOC122258 3'  CACGCCCACGTTCTCTG     59141         TCAA
                                    CAGAGAAC    GGTGTG
                                    ||||||||    ||||||
                                    GTCTCTTG    CCGCAC
                                         CAC_
GAM1080  LOC124842 3'  CACCTTCCTGAGTTCTCAGGA  75658     A       ___
                                    TCC GAGAACTCA   AGGTG
                                    ||| |||||||||   |||||
                                    AGG CTCTTGAGT   TCCAC
                                      A        CCT
GAM1080  LOC138050 5'  TCCATAATGAACTTCTCTGGA  75299         C_   AG   T
                                    TCCAGAGAA  TCA  GTG GA
                                    |||||||||  |||  ||| ||
                                    AGGTCTCTT  AGT  TAC CT
                                          CA   AA   _
GAM1080  LOC146839 5'  ATTCTCTTGAGTTTTCTAGA   83806    C          TGT
                                    TC AGAGAACTCAAGG   GAAT
                                    || ||||||||||||   ||||
                                    AG TCTTTTGAGTTCT   CTTA
                                     A          ___
GAM1080  LOC150095 5'  CACACCTTCCCTCTCTG     84855       ACTC
                                    CAGAGA    AAGGTGTG
                                    ||||||    ||||||||
                                    GTCTCT    TTCCACAC
                                        CCC_
GAM1080  LOC151094 3'  CACGCTTGGTTCCCT       65293    A    CA
                                    AG GAACT  AGGTGTG
                                    || |||||  |||||||
                                    TC CTTGG  TTCGCAC
                                     C    __
GAM1080  LOC153603 3'  CATCTTCGAGCTCTCTGGA    80900        A   _
                                    TCCAGAGA CTC AAGGTG
                                    |||||||| ||| ||||||
                                    AGGTCTCT GAG TTCTAC
                                          C   C
GAM1080  LOC153811 3'  ATTCACACAGCTCCCTGGG    80942      A  A  CAAG
                                    TCCAG GA CT    GTGTGAAT
                                    ||||| || ||    ||||||||
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                                GGGTC CT GA    CACACTTA
                                  C  C  ____
GAM1080  LOC163341 3'  CATCTTGAGCCCCTTGGA    82119      AGAA
                                TCCAG    CTCAAGGTG
                                |||||    |||||||||
                                AGGTT    GAGTTCTAC
                                   CCCC
GAM1080  LOC199800 5'  CACCCAGTGAGGTCTCTGGA   89856        A    A_  T
                                TCCAGAGA CTCA  GG GTG
                                |||||||| ||||  || |||
                                AGGTCTCT GAGT  CC CAC
                                     G    GA  _
GAM1080  LOC254439 3'  TTCACAGCTCTCTGGA      94749        ACTCAA G
                                TCCAGAGA     G TGTGAA
                                ||||||||     | ||||||
                                AGGTCTCT     C ACACTT
                                     _______ G
GAM1080  LOC255465 3'  GCCTTGAGTCTCTGGA      97289        A
                                TCCAGAGA CTCAAGGT
                                |||||||| ||||||||
                                AGGTCTCT GAGTTCCG
                                     _
GAM1080  LOC256207 3'  TATTTTCAAGTCTCTGGA    95176        ACTC
                                TCCAGAGA    AAGGTG
                                ||||||||    ||||||
                                AGGTCTCT    TTTTAT
                                     GAAC
GAM1080  LOC257354 3'  TACCCTGCACTCTCTGGA    95099        ACTCA   T
                                TCCAGAGA     AGG GTG
                                ||||||||     ||| |||
                                AGGTCTCT     TCC CAT
                                     CACG_  _
GAM1080  LOC91308  3'  TGTGCCTTAAGTTCTCT     65568        C    TG
                                AGAGAACT AAGG  TG
                                |||||||| ||||  ||
                                TCTCTTGA TTCC  GT
                                     A    GT
GAM1080  LOC91695  5'  TATTCCAATCAAGTTCTCTG   66971        CAAGG  T
                                CAGAGAACT     TG GAATA
                                |||||||||     || |||||
                                GTCTCTTGA     AC CTTAT
                                      ACTA_  _
GAM1080  LOC93259  5'  TACAGCCTTGAGTTCCTTGGA  71826      A        _
                                TCCAG GAACTCAAGG TGTG
                                ||||| |||||||||| ||||
                                AGGTT CTTGAGTTCC ACAT
                                   C         G
GAM1081  ABCG1     3'  ACACCATCTCCACTGAG      16981    G    AAGAC
                                CT CAGTG     AGATGGTGT
                                || |||||     |||||||||
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                                GA GTCAC    TCTACCACA
                                 _    C____
GAM1081  ADAM17   3'  GACACCATCCAGGAAGACCCCA 41556    CA  GAAGACA
             G                   CTG  GT     GATGGTGTC
                                 |||  ||     |||||||||
                                 GAC  CA     CTACCACAG
                                   CC  GAAGGAC
GAM1081  ADAM19   3'  GCTCCTGTCTTCCCTGCAG   52708      T      AT
                                 CTGCAG GAAGACAG  GGT
                                 ||||||| ||||||||  |||
                                 GACGTC CTTCTGTC  TCG
                                    C       C_
GAM1081  ATP11A   3'  CCATCACCACTGCAGT      77025        AAGACA
                                 ACTGCAGTG     GATGG
                                 |||||||||     |||||
                                 TGACGTCAC     CTACC
                                     CA____
GAM1081  CASR     5'  CATGTGTCCCCACTGCAG    4612        AA   G
                                 CTGCAGTG  GACA ATG
                                 ||||||||  |||| |||
                                 GACGTCAC  CTGT TAC
                                     CC    G
GAM1081  CPNE3    3'  CTGTCTTCACTAAGT      14027     GC
                                 ACT  AGTGAAGACAG
                                 |||  ||||||||||
                                 TGA  TCACTTCTGTC
                                   A_
GAM1081  FLNA     3'  GCCCGCCTGTCACTGCAG    7581        GAA    A   T
                                 CTGCAGT   GACAG TGG GT
                                 |||||||   ||||| ||| ||
                                 GACGTCA   CTGTC GCC CG
                                     ___     C   _
GAM1081  FXYD6    3'  ACACTTGCCTCCCCACTGCAG  41834        AA  CAGAT
                                 CTGCAGTG  GA    GGTGT
                                 ||||||||  ||    |||||
                                 GACGTCAC  CT    TCACA
                                     CC  CCGT_
GAM1081  IGFBP5   5'  ACGCCATCTCCACTGCA     5189        AAGAC
                                 TGCAGTG    AGATGGTGT
                                 |||||||    |||||||||
                                 ACGTCAC    TCTACCGCA
                                     C____
GAM1081  LILRB1   3'  GACACCATTGGACCCCACCCAG 21901     CA   AAGACA
                                 CTG  GTG     GATGGTGTC
                                 |||  |||     |||||||||
                                 GAC  CAC     TTACCACAG
                                   C_   CCCAGG
GAM1081  MCM5     3'  ACCTCTGCCTCCCCACTGCAG  59964        A__  A    T
                                 CTGCAGTG   AG CAGA GGT
                                 ||||||||   || |||| |||
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                                GACGTCAC   TC GTCT CCA
                                    CCC  C   _
GAM1081  NDUFV3   3'  CACCGTCTTCACTGCA      40778          AGAT
                                TGCAGTGAAGAC   GGTG
                                ||||||||||||   ||||
                                ACGTCACTTCTG   CCAC
                                     ____
GAM1081  NQO1     3'  GCCTTCATCTTCACTGCA    6160          CA  T
                                TGCAGTGAAGA  GA GGT
                                ||||||||||  || |||
                                ACGTCACTTCT  CT CCG
                                      A_  T
GAM1081  OGT      5'  ACATGAATTGCACTTCACTGCA 13198         ACA  G_
           G                     CTGCAGTGAAG  GAT  GTGT
                                ||||||||||   |||  ||||
                                GACGTCACTTC   TTA  TACA
                                      ACG   AG
GAM1081  PKIA     3'  GACAACTTATCTTCACTAAG  22383    GC      CAGAT  _
                                CT  AGTGAAGA    GGT GTC
                                ||  ||||||||    ||| |||
                                GA  TCACTTCT    TCA CAG
                                 A_      AT___   A
GAM1081  RHD      3'  ACACCATTTAGTCACTG     32288       AGAC
                                CAGTGA   AGATGGTGT
                                ||||||   |||||||||
                                GTCACT   TTTACCACA
                                   GA__
GAM1081  RHD      3'  ACACCATTTAGTCACTG     32597       AGAC
                                CAGTGA   AGATGGTGT
                                ||||||   |||||||||
                                GTCACT   TTTACCACA
                                   GA__
GAM1081  STAU2    3'  CATATCTTCACTGTAGT     26902          CAG
                                ACTGCAGTGAAGA  ATG
                                ||||||||||||   |||
                                TGATGTCACTTCT  TAC
                                      A__
GAM1081  STS      3'  CACCATCTTCACTACA      4449     C    AGAC
                                TG AGTGA   AGATGGTG
                                || |||||   ||||||||
                                AC TCACT   TCTACCAC
                                 A   ____
GAM1081  UBL3     3'  ACTATTTTCACTGCA       23029         GACA
                                TGCAGTGAA   GATGGT
                                |||||||||   ||||||
                                ACGTCACTT   TTATCA
                                     ____
GAM1081  BM045    3'  CGAGTGTCTTCACTCCAG    37457     C       GA
                                CTG AGTGAAGACA  TG
                                ||| ||||||||||  ||
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                                GAC TCACTTCTGT  GC
                                  C         GA
GAM1081  BM045    3'  CGAGTGTCTTCACTCCAG    78014     C         GA
                                CTG AGTGAAGACA  TG
                                ||| ||||||||||  ||
                                GAC TCACTTCTGT  GC
                                  C         GA
GAM1081  C1QTNF2  3'  TATCTGTCCTCATGCAG     49131      G   A
                                CTGCA TGA GACAGATG
                                ||||| ||| ||||||||
                                GACGT ACT CTGTCTAT
                                   _  C
GAM1081  FACTP140 3'  CTGTCCCACTGCAGT       23235          AA
                                ACTGCAGTG  GACAG
                                |||||||||  |||||
                                TGACGTCAC  CTGTC
                                     C_
GAM1081  FLJ10422 3'  ACACCATAACTCATGCA     36112      G   AGACAG
                                TGCA TGA     ATGGTGT
                                |||| |||     |||||||
                                ACGT ACT     TACCACA
                                   _  CAA___
GAM1081  FLJ11110 3'  ACTTCTGCCCCCACTGCA    37059        AAGA    T
                                TGCAGTG    CAGA GGT
                                |||||||    |||| |||
                                ACGTCAC    GTCT TCA
                                    CCCC   _
GAM1081  FLJ13902 3'  GTCTGCTCCCACTGCAG     45045        A_  A
                                CTGCAGTG  AG CAGAT
                                ||||||||  || |||||
                                GACGTCAC  TC GTCTG
                                     CC  _
GAM1081  FLJ14621 3'  ACAGCTGTCTTCCTGCAGT    51469        T       ATG
                                ACTGCAG GAAGACAG   GT
                                ||||||| ||||||||   ||
                                TGACGTC CTTCTGTC   CA
                                   _       GA_
GAM1081  FLJ14751 3'  GACAGCAATCTTCACTCCAGT  51596      C       CAGA  G
                                ACTG AGTGAAGA    TG TGTC
                                |||| ||||||||    || ||||
                                TGAC TCACTTCT    AC ACAG
                                  C       A___  G
GAM1081  FLJ20126 3'  ATTTTCTATCCTCACTGCAGT  34591          A  C   TG
                                ACTGCAGTGA GA AGA  GT
                                |||||||||| || |||  ||
                                TGACGTCACT CT TCT  TA
                                     C  A   TT
GAM1081  KIAA0377 3'  ACACCATCTGGCGACAG     27792     CA  GAAGA
                                CTG  GT    CAGATGGTGT
                                |||  ||    ||||||||||
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                                GAC  CG    GTCTACCACA
                                  AG  _____
GAM1081  KIAA0427  3'  GTCCTCCTCACTGCAG     28723        A  CA
                                CTGCAGTGA GA  GAT
                                ||||||||| ||  |||
                                GACGTCACT CT  CTG
                                     C  C_
GAM1081  KIAA0471  3'  ACTCTCCTTCACTGCA      29381         ACA  T
                                TGCAGTGAAG   GA GGT
                                ||||||||||   || |||
                                ACGTCACTTC   CT TCA
                                     ___  C
GAM1081  KIAA0757  3'  GCCACTGTCTTCCCTGCAGT   20134       T      A
                                ACTGCAG GAAGACAG TGGT
                                ||||||| |||||||| ||||
                                TGACGTC CTTCTGTC ACCG
                                    C      _
GAM1081  KIAA1170  3'  GACAGTAGTCCTTACTGCA   69852        A   AGA  G
                                TGCAGTGA GAC   TG TGTC
                                |||||||| |||   || ||||
                                ACGTCATT CTG   AT ACAG
                                     C   ___  G
GAM1081  KIAA1981  3'  GTGCCGTCTCCTACTGCAG   88347        AAGAC     TG
                                CTGCAGTG    AGATGG  T
                                ||||||||    ||||||  |
                                GACGTCAT    TCTGCC  G
                                     CC___     GT
GAM1081  LCE       3'  ACTTCATCTTCACTGCA     44026          CA  T
                                TGCAGTGAAGA  GA GGT
                                ||||||||||  ||  |||
                                ACGTCACTTCT  CT TCA
                                      A_  _
GAM1081  LGI3      3'  GCATCATCACTGCA       57745         AGACAGA
                                TGCAGTGA      TGGTGT
                                ||||||||      ||||||
                                ACGTCACT      ACTACG
                                      _______
GAM1081  MGC10818  3'  GACACATACCTTCACTGCA   47541          ACAGATG
                                TGCAGTGAAG      GTGTC
                                ||||||||||      |||||
                                ACGTCACTTC      CACAG
                                     CATA___
GAM1081  MOST2     5'  ACCTCCCTCTCCACTGCAG   39672        A   CA  T
                                CTGCAGTG AGA  GA GGT
                                |||||||| |||  || |||
                                GACGTCAC TCT  CT CCA
                                     C   CC  _
GAM1081  SCGB1D2   3'  GACACCCTGATCTTCACTGCAG 21592           _   AT
                                CTGCAGTGAAGA CAG  GGTGTC
                                |||||||||||| |||  ||||||
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                                GACGTCACTTCT GTC  CCACAG
                                      A  __
GAM1081  SGP28    3'  GACAAATGACGTCTTCACCAAG 20229     GCA       AGATGG
             T                   ACT   GTGAAGAC     TGTC
                                 |||   ||||||||     ||||
                                 TGA   CACTTCTG     ACAG
                                   AC_       CAGTAA
GAM1081  SRCRB4D  3'  ATGCCGTCTCCACCACAG    54954     CA   AAGAC
                                 CTG  GTG    AGATGGTGT
                                 |||  |||    |||||||||
                                 GAC  CAC    TCTGCCGTA
                                   AC   C____
GAM1081  ZTL1     3'  GACACGATCTTGTCTCACTGCA 43916         A   _   G
                                 TGCAGTGA GACA GAT GTGTC
                                 |||||||| |||| ||| |||||
                                 ACGTCACT CTGT CTA CACAG
                                      _   T   G
GAM1081  LOC121274 3'  ATCTGTTTCCACTACAG     74059     C    A
                                 CTG AGTG AGACAGAT
                                 ||| |||| ||||||||
                                 GAC TCAC TTTGTCTA
                                   A   C
GAM1081  LOC124977 5'  GCTTCCCTTCCTCACTGCAG   76060         A  C  AT_
                                 CTGCAGTGA GA AG   GGT
                                 |||||||| || ||   |||
                                 GACGTCACT CT TC   TCG
                                       C  _  CCT
GAM1081  LOC144266 5'  ACCATCTTCACTGAGT      76759     G     AGAC
                                 ACT CAGTGA    AGATGGT
                                 ||| ||||||    |||||||
                                 TGA GTCACT    TCTACCA
                                   _     _____
GAM1081  LOC158863 3'  ACCCTGTCTTCACT        86921           AT
                                 AGTGAAGACAG  GGT
                                 ||||||||||  |||
                                 TCACTTCTGTC  CCA
                                       __
GAM1081  LOC205418 3'  GACACCATCCTGAGTCCCACAG 90685    A   AA   A___
             C                    GC GTG  GAC    GATGGTGTC
                                  || |||  |||    |||||||||
                                  CG CAC  CTG    CTACCACAG
                                   A   C_   AGTC
GAM1081  LOC221466 3'  GTCTGTCTCCACCCCAG     93694     CA   A
                                 CTG  GTG AGACAGAT
                                 |||  ||| ||||||||
                                 GAC  CAC TCTGTCTG
                                   CC   C
GAM1081  LOC221683 5'  CACCCTGTCTTCACCCAG    93712     CA        AT
                                 CTG  GTGAAGACAG  GGTG
                                 |||  ||||||||||  ||||
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                                GAC  CACTTCTGTC  CCAC
                                  C_        __
GAM1081  LOC256412 3'  ACACCATCTACGCGTACGGC   95102    A   AAGAC
                                GC GTG     AGATGGTGT
                                || |||     |||||||||
                                CG CAT     TCTACCACA
                                 G   GCGCA
GAM1081  LOC257106 3'  ACTAGCTGTCTCCTCTGCAG   95382       TGA     A
                                CTGCAG   AGACAG TGGT
                                ||||||   |||||| ||||
                                GACGTC   TCTGTC ATCA
                                    TCC     G
GAM1081  LOC55885  3'  ACCATATTTTCACTACAG    37813     C       CAG
                                CTG AGTGAAGA   ATGGT
                                ||| ||||||||   |||||
                                GAC TCACTTTT   TACCA
                                  A       A__
GAM1081  LOC57149  3'  ACCTTACATCCTCACTGCAGT  39934         A  CAGAT
                                ACTGCAGTGA GA     GGT
                                ||||||||||  ||     |||
                                TGACGTCACT CT     CCA
                                      C  ACATT
GAM1082  CGTHBA    3'  CCTGGACCCTGGCCAGAAGA   23862    A       TAGCT
                                TC TTCTGGCCA     TCCAGG
                                || |||||||||     ||||||
                                AG AAGACCGGT     AGGTCC
                                 _        CCC__
GAM1082  FCN2      3'  GCCATTGCCAGAATGA      31741          C  A
                                TCATTCTGGC AT GC
                                |||||||||| || ||
                                AGTAAGACCG TA CG
                                      T  C
GAM1082  GCH1      3'  CCTGAACGAGCACAGAATGA   3859         GCCATA   C__
                                TCATTCTG     GCTT   CAGG
                                ||||||||     ||||   ||||
                                AGTAAGAC     CGAG   GTCC
                                     A_____    CAA
GAM1082  HOXB6     3'  CCTGGAAGCAGAGCAAAATG   59852     CTG  CATA
                                CATT   GC    GCTTCCAGG
                                ||||   ||    |||||||||
                                GTAA   CG    CGAAGGTCC
                                  AA_  AGA_
GAM1082  IL12B     3'  CTAGGTGACAGAATGA      9322          __   A
                                TCATTCTG  GCC TAG
                                ||||||||  ||| |||
                                AGTAAGAC  TGG ATC
                                     AG   _
GAM1082  PRNP      3'  TGGAAACCAGAATGA       4337          CCATAGC
                                TCATTCTGG      TTCCA
                                |||||||||      |||||
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                                AGTAAGACC      AAGGT
                                     A_______
GAM1082  RBBP5    3'  CTAGGTGACAGAATGA      17333         __   A
                                TCATTCTG  GCC TAG
                                ||||||||  ||| |||
                                AGTAAGAC  TGG ATC
                                     AG  _
GAM1082  SNX9     3'  GAACTATGCCAGAAT       32593         C    C
                                ATTCTGGC ATAG TTC
                                |||||||| |||| |||
                                TAAGACCG TATC AAG
                                     _    _
GAM1082  TNFRSF8  3'  CCTGGACATTGGCCAGAAGA  6959     A        TAGCT
                                TC TTCTGGCCA    TCCAGG
                                || |||||||||    ||||||
                                AG AAGACCGGT    AGGTCC
                                 _       TAC__
GAM1082  UBE2L3   3'  AAGCTACAGCCAGAATG     12496         CA
                                CATTCTGGC  TAGCTT
                                |||||||||  ||||||
                                GTAAGACCG  ATCGAA
                                     AC
GAM1082  APBA3    3'  CCTGGAAGCCACTAGAA     16882        CCATA
                                TTCTGG    GCTTCCAGG
                                ||||||    |||||||||
                                AAGATC    CGAAGGTCC
                                    AC___
GAM1082  CECR1    3'  GGCCTGGCCTAGAATGA     33817         _    TA
                                TCATTCT GGCCA  GCT
                                ||||||| |||||  |||
                                AGTAAGA CCGGT  CGG
                                     T    C_
GAM1082  FBX30    3'  CCGAAAGGTCTTGACCTGAATG 52586       T  C  TA   CCA
              A                  TCATTC GG CA  GCTT   GG
                                ||||||  ||  ||  ||||   ||
                                AGTAAG CC GT  TGGA   CC
                                    T  A  TC    AAG
GAM1082  FLJ10604 3'  CCTAGTCCTGGCCAGAAGGA  36337    A        TA   TCC
                                TC TTCTGGCCA  GCT   AGG
                                || |||||||||  |||   |||
                                AG AAGACCGGT  TGA   TCC
                                 G        CC   ___
GAM1082  FLJ10846 5'  CTGGAAGCCATGGTACAG    36738    _    A
                                CTG GCCAT GCTTCCAG
                                |||  |||||  ||||||||
                                GAC TGGTA CGAAGGTC
                                  A    C
GAM1082  FLJ14621 5'  GAAGAAGAGCCAGAATGA    51471          CATAG
                                TCATTCTGGC    CTTC
                                ||||||||||    ||||
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                                AGTAAGACCG    GAAG
                                     AGAA_
GAM1082  FLJ23027  3'  CCTGTCATCTTGATGACCAGAA 49930        C  AGCTTC__
             TGA                   TCATTCTGG CAT       CAGG
                                |||||||||  |||       ||||
                                AGTAAGACC GTA       GTCC
                                     A   GTTCTACT
GAM1082  HGC6.1.1  5'  CCGACCGAGCAGCCAGAGTGA  26827         CATA   CCA_
                                TCATTCTGGC   GCTT   GG
                                ||||||||||   ||||   ||
                                AGTGAGACCG   CGAG   CC
                                     A___    CCAG
GAM1082  HSZFP36   5'  CTGGAAGCTGGGAAATGA    63482      CTGG  A
                                TCATT    CC TAGCTTCCAG
                                |||||    || ||||||||||
                                AGTAA    GG GTCGAAGGTC
                                   A___  _
GAM1082  IL22R     3'  CCTGGAAAAGAACCAGAAGGA  41191     A     CCATAGC
                                TC TTCTGG      TTCCAGG
                                || ||||||      |||||||
                                AG AAGACC      AAGGTCC
                                 G     AAGAA__
GAM1082  ILF3      3'  CCCGGGGTCCGGCCAGAA     15723        ATA   T  A
                                TTCTGGCC   GCT CC GG
                                ||||||||   ||| || ||
                                AAGACCGG   TGG GG CC
                                     CC_   _  C
GAM1082  KIAA1344  3'  CCTAGAAGAGGACTCAGAATGA 72447        _ _  ATAG    C
                                TCATTCTG G CC    CTTC AGG
                                |||||||| | ||    |||| |||
                                AGTAAGAC C GG    GAAG TCC
                                     T A  A___    A
GAM1082  KIAA1855  3'  CCTGGAAGCCACTGTCAATGA  92339      TC    CATA
                                TCAT  TGGC    GCTTCCAGG
                                ||||  ||||    |||||||||
                                AGTA  ACTG    CGAAGGTCC
                                   __    TCAC
GAM1082  LIMK2     3'  CCTGAAAGCTGTGAAGAAGA   33623    A   GGC      C
                                TC TTCT   CATAGCTT CAGG
                                || ||||   |||||||| ||||
                                AG AAGA   GTGTCGAA GTCC
                                 _   A__       A
GAM1082  LIMK2     3'  CCTGAAAGCTGTGAAGAAGA   18725    A   GGC      C
                                TC TTCT   CATAGCTT CAGG
                                || ||||   |||||||| ||||
                                AG AAGA   GTGTCGAA GTCC
                                 _   A__       A
GAM1082  P450RAI-2 3'  CCTGAAAAACAGGCCAGAATGG 39101          ATAGCTTC
                                TCATTCTGGCC       CAGG
                                ||||||||||       ||||
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                                GGTAAGACCGG       GTCC
                                      ACAAAAA_
GAM1082  WIRE     3'  CCTGGAAGGTGCTCCAGGAT   78301        CCA  G
                                ATTCTGG   TA CTTCCAGG
                                |||||||   || ||||||||
                                TAGGACC   GT GAAGGTCC
                                    TC_  G
GAM1082  LOC131544 3'  CCTGGATCACTGAGCAGAATGA 75009         GC  TAGCT
                                TCATTCTG  CA    TCCAGG
                                ||||||||  ||    ||||||
                                AGTAAGAC  GT    AGGTCC
                                     GA  CACT_
GAM1082  LOC146346 5'  CTGAAAGGCCAGAATG      77841          ATAGC  C
                                CATTCTGGCC    TT CAG
                                ||||||||||    || |||
                                GTAAGACCGG    AA GTC
                                      _____  A
GAM1082  LOC149127 3'  CCTCTGCACACAGCCAGAATG  84345         CATA_  TTCC
                                CATTCTGGC    GC   AGG
                                |||||||||    ||   |||
                                GTAAGACCG    CG   TCC
                                      ACACA  TC__
GAM1082  LOC149276 5'  CCTGCTGTGAGAGCCAGAATGA 84385          ___     TTCC
                                TCATTCTGGC   CATAGC   AGG
                                ||||||||||   ||||||   |||
                                AGTAAGACCG   GTGTCG   TCC
                                      AGA    _____
GAM1082  LOC149992 5'  CCTGGAAGCTGGAGAGGATGA  79557       GG   TA
                                TCATTCT  CCA  GCTTCCAGG
                                |||||||  |||  |||||||||
                                AGTAGGA  GGT  CGAAGGTCC
                                    GA   __
GAM1082  LOC150225 3'  CCTGGAATTTTGTGGCCAGAAG 84988    A          C_
            GA                    TC TTCTGGCCATAG  TTCCAGG
                                || ||||||||||||  |||||||
                                AG AAGACCGGTGTT  AAGGTCC
                                 G          TT
GAM1082  LOC150372 3'  CCTGACCTGTGGTCAGAATGA  79796            CTTC
                                TCATTCTGGCCATAG    CAGG
                                ||||||||||||||    ||||
                                AGTAAGACTGGTGTC    GTCC
                                      CA__
GAM1082  LOC150426 3'  CCTGGAAGCTGGAGAGGATGA  79868       GG   TA
                                TCATTCT  CCA  GCTTCCAGG
                                |||||||  |||  |||||||||
                                AGTAGGA  GGT  CGAAGGTCC
                                    GA   __
GAM1082  LOC151318 3'  CCCAGAAGCTATCCTTGTATGA 80227      TCT_  CC       CA
                                TCAT    GG  ATAGCTTC  GG
                                ||||    ||  ||||||||  ||
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                                AGTA   CC  TATCGAAG  CC
                                  TGTT  __       AC
GAM1082  LOC151438 3'  CTGGAAGCTGGAAGA      85364     GG   TA
                                TCT  CCA  GCTTCCAG
                                |||  |||  ||||||||
                                AGA  GGT  CGAAGGTC
                                 A_  __
GAM1082  LOC153577 5'  CCTGGAGAGGGGCAGAATGA   86056        G  ATAG  T
                                TCATTCTG CC    CT CCAGG
                                |||||||| ||    || |||||
                                AGTAAGAC GG    GA GGTCC
                                     G  GA__  _
GAM1082  LOC157918 5'  AGGTGTGGCCAGAAGA      86640    A         G
                                TC TTCTGGCCATA CT
                                || ||||||||||| ||
                                AG AAGACCGGTGT GA
                                 _         G
GAM1082  LOC203429 3'  CCCGGAGTTTGTGGCCAAAGTG 89364      C        C    A
            A                    TCATT TGGCCATAG TTCC GG
                                |||||| ||||||||| |||| ||
                                AGTGA ACCGGTGTT GAGG CC
                                   A        T    C
GAM1082  LOC221474 5'  CCCGGAAACCGGCAGGATGA   92376        G  ATAGC   A
                                TCATTCTG CC     TTCC GG
                                |||||||| ||     |||| ||
                                AGTAGGAC GG     AAGG CC
                                     _  CCA__    C
GAM1082  LOC254722 5'  CCTGGGGAGCTAGCCAAAAAGA 97565    A  C    CA       _
                                TC TT TGGC  TAGCTTCC AGG
                                || || ||||  |||||||| |||
                                AG AA ACCG  ATCGAGGG TCC
                                 A  A   __       G
GAM1082  LOC255106 3'  AGGGTATAACCAGAATGA    95079         CC   G
                                TCATTCTGG  ATA CTT
                                |||||||||  ||| |||
                                AGTAAGACC  TAT GGA
                                      AA   G
GAM1083  COL10A1   3'  GGTGCATATATACTTGTT    4931          T   CGA
                                AACAAGTAT TAT   GCC
                                |||||||| |||   |||
                                TTGTTCATA ATA   TGG
                                      T   CG_
GAM1083  EGLN3     3'  GGGCTCAGTAAATACTTGTTGA 41971             C
            A                    TTCAACAAGTATTTAT GAGCCC
                                |||||||||||||| ||||||
                                AAGTTGTTCATAAATG CTCGGG
                                           A
GAM1083  FGA       3'  CTCAATAAATACATGTT     41560      A       C
                                AACA GTATTTAT GAG
                                |||| |||||||| |||
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                                TTGT CATAAATA CTC
                                  A       A
GAM1083  GUCY1B3   3'  GGCACCCAATAAATATTTGTTG 5967              CGA__
             AA                   TTCAACAAGTATTTAT    GCC
                                  ||||||||||||||||    |||
                                  AAGTTGTTTATAAATA    CGG
                                        ACCCA
GAM1083  KIF3B    3'  GGGCTCCCTTCTTGTTGAA   16610         TATTTATC
                                  TTCAACAAG       GAGCCC
                                  |||||||||       ||||||
                                  AAGTTGTTC       CTCGGG
                                      TTCC____
GAM1083  MDH1     5'  GGCTCATTTTGCAGTTGTTGAA 19793         __  TTT  C
                                  TTCAACAA  GTA   AT GAGCC
                                  ||||||||  |||   || |||||
                                  AAGTTGTT  CGT   TA CTCGG
                                       GA   TT_  _
GAM1083  MKI67    3'  TCATAAATACTTGCTGAA    10050      A         C
                                  TTCA CAAGTATTTAT GA
                                  |||| ||||||||||| ||
                                  AAGT GTTCATAAATA CT
                                    C         _
GAM1083  NCOA3    5'  GGATCAAAATACTTGCTGGA   21532      A        ATC  G
                                  TTCA CAAGTATTT   GA CC
                                  |||| |||||||||   || ||
                                  AGGT GTTCATAAA   CT GG
                                    C        A__  A
GAM1083  PCDHB6   3'  GCTTAATAAATATTTGCTGAA  38438      A         CG
                                  TTCA CAAGTATTTAT  AGC
                                  |||| ||||||||||  |||
                                  AAGT GTTTATAAATA  TCG
                                    C          AT
GAM1083  PML      3'  GGCTGCTCAATAAACACTTGTT 52663          A    C   __
             GAA                    TTCAACAAGT TTTAT GAGC  CC
                                    ||||||||||  |||||  ||||  ||
                                    AAGTTGTTCA AAATA CTCG  GG
                                          C    A   TC
GAM1083  PML      3'  GGCTGCTCAATAAACACTTGTT 52669          A    C   __
             GAA                    TTCAACAAGT TTTAT GAGC  CC
                                    ||||||||||  |||||  ||||  ||
                                    AAGTTGTTCA AAATA CTCG  GG
                                          C    A   TC
GAM1083  PML      3'  GGCTGCTCAATAAACACTTGTT 52675          A    C   __
             GAA                    TTCAACAAGT TTTAT GAGC  CC
                                    ||||||||||  |||||  ||||  ||
                                    AAGTTGTTCA AAATA CTCG  GG
                                          C    A   TC
GAM1083  PML      3'  GGCTGCTCAATAAACACTTGTT 52678          A    C   __
             GAA                    TTCAACAAGT TTTAT GAGC  CC
                                    ||||||||||  |||||  ||||  ||
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                                AAGTTGTTCA AAATA CTCG  GG
                                      C     A    TC
GAM1083  PX19     3'  CTCAATAAATACTTGTTGAA   25086             C
                                TTCAACAAGTATTTAT GAG
                                |||||||||||||||| |||
                                AAGTTGTTCATAAATA CTC
                                      A
GAM1083  SCNN1A   3'  GGAGCTCAATAAATGTTTGTTG 6425              C   _
                                CAACAAGTATTTAT GAGC CC
                                |||||||||||||| |||| ||
                                GTTGTTTGTAAATA CTCG GG
                                      A    A
GAM1083  SPAG11   3'  GTTCAATAAATATTTGTTGAA  33260             C
                                TTCAACAAGTATTTAT GAGC
                                |||||||||||||||| ||||
                                AAGTTGTTTATAAATA CTTG
                                      A
GAM1083  SPAG11   3'  GTTCAATAAATATTTGTTGAA  54245             C
                                TTCAACAAGTATTTAT GAGC
                                |||||||||||||||| ||||
                                AAGTTGTTTATAAATA CTTG
                                      A
GAM1083  SPAG11   3'  GTTCAATAAATATTTGTTGAA  54251             C
                                TTCAACAAGTATTTAT GAGC
                                |||||||||||||||| ||||
                                AAGTTGTTTATAAATA CTTG
                                      A
GAM1083  SPAG11   3'  GTTCAATAAATATTTGTTGAA  54253             C
                                TTCAACAAGTATTTAT GAGC
                                |||||||||||||||| ||||
                                AAGTTGTTTATAAATA CTTG
                                      A
GAM1083  SYBL1    3'  GGTTTAAATATTGTTGAA    18896        G     TCG
                                TTCAACAA TATTTA   AGCC
                                |||||||| ||||||   ||||
                                AAGTTGTT ATAAAT   TTGG
                                      _    ____
GAM1083  C20orf126 3'  GGGCTCAATAAATGTTAGCTGA 47998      ACAAG      C
           A                     TTCA     TATTTAT GAGCCC
                                ||||     ||||||| ||||||
                                AAGT     GTAAATA CTCGGG
                                  CGATT      A
GAM1083  FLJ10283 3'  GCTCAAGATACTTATTGAA    35969      C       ATC
                                TTCAA AAGTATTT   GAGC
                                ||||| ||||||||   ||||
                                AAGTT TTCATAGA   CTCG
                                  A       A__
GAM1083  FLJ20739 3'  GAGGAAACACTTGTTGAA     67857          A   A_
                                TTCAACAAGT TTT  TC
                                |||||||||| |||  ||
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                                AAGTTGTTCA AAA  AG
                                      C   GG
GAM1083  FLJ23024  3'  TCACTTAAATGCTTGTTGAA   46275            TC_
                                TTCAACAAGTATTTA   GA
                                ||||||||||||||   ||
                                AAGTTGTTCGTAAAT   CT
                                      TCA
GAM1083  GOA      3'  GCTCAATAAACACTTGTTGAA  78076          A    C
                                TTCAACAAGT TTTAT GAGC
                                |||||||||| ||||| ||||
                                AAGTTGTTCA AAATA CTCG
                                      C    A
GAM1083  KIAA0227  3'  GTTCAACAAATGCTTGTTGAA  60702           ATC
                                TTCAACAAGTATTT   GAGC
                                ||||||||||||||   ||||
                                AAGTTGTTCGTAAA   CTTG
                                      CAA
GAM1083  KIAA1219  3'  GCCCAGTAAATACTTGTTGAA  61368             CGA
                                TTCAACAAGTATTTAT   GC
                                ||||||||||||||||   ||
                                AAGTTGTTCATAAATG   CG
                                      ACC
GAM1083  KIAA1332  3'  GCTTAGAAATACTTGTGGAA   71169     A        ATC
                                TTC ACAAGTATTT   GAGC
                                ||| ||||||||||   ||||
                                AAG TGTTCATAAA   TTCG
                                  G        GA_
GAM1083  MGC18079  3'  GGGGCTCAATAAATGCTTGTTG 58373              C
            AA                    TTCAACAAGTATTTAT GAGCCCC
                                ||||||||||||||| |||||||
                                AAGTTGTTCGTAAATA CTCGGGG
                                      A
GAM1083  NICN1    3'  TCAATAAATACTTGTGGAA   50294     A         C
                                TTC ACAAGTATTTAT GA
                                ||| |||||||||||| ||
                                AAG TGTTCATAAATA CT
                                  G          A
GAM1083  PEG10    3'  GGACTGGCCAATACTTGTGGAA 30528     A       TA   AG
                                TTC ACAAGTATT  TCG  CC
                                ||| |||||||||  |||  ||
                                AAG TGTTCATAA  GGT  GG
                                  G        CC   CA
GAM1083  PXMP4    3'  GGGTTGTAAATACTT       23378          CG
                                AAGTATTTAT  AGCCC
                                ||||||||||  |||||
                                TTCATAAATG  TTGGG
                                          __
GAM1083  TCL6     3'  GGAGCCCGATAAATATTTATTG 24985       C          A  _
            AA                    TTCAA AAGTATTTATCG GC CC
                                ||||| |||||||||||| || ||
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                                AAGTT TTTATAAATAGC CG GG
                                  A          C  A
GAM1083  TCL6     3'  GGAGCCCGATAAATATTTATTG 27001       C          A  _
                AA                  TTCAA AAGTATTTATCG GC CC
                                    ||||| |||||||||||| || ||
                                    AAGTT TTTATAAATAGC CG GG
                                      A          C  A
GAM1083  TCL6     3'  GGAGCCCGATAAATATTTATTG 40085       C          A  _
                AA                  TTCAA AAGTATTTATCG GC CC
                                    ||||| |||||||||||| || ||
                                    AAGTT TTTATAAATAGC CG GG
                                      A          C  A
GAM1083  TP53INP1 3'  GGCCCATAAATACTGGTT    52726     A       CGA
                                    AAC AGTATTTAT   GCC
                                    ||| |||||||||   |||
                                    TTG TCATAAATA   CGG
                                      G        CC_
GAM1083  TP53INP1 3'  GGCCCATAAATACTGGTT    72953     A       CGA
                                    AAC AGTATTTAT   GCC
                                    ||| |||||||||   |||
                                    TTG TCATAAATA   CGG
                                      G        CC_
GAM1083  TRIM26   3'  GGTGCTCAATAAAGACTTGTTG 12891          A    C   _
                AA                  TTCAACAAGT TTTAT GAGC CC
                                    |||||||||| ||||| |||| ||
                                    AAGTTGTTCA AAATA CTCG GG
                                          G    A   T
GAM1083  TU12B1-TY 3'  GGCTCAGACACTTGTTGAA   33399          A   ATC
                                    TTCAACAAGT TTT   GAGCC
                                    |||||||||| |||   |||||
                                    AAGTTGTTCA AGA   CTCGG
                                          C  ____
GAM1083  ZER6     3'  GCAGATAAATTCTTGTTGAA   63378          T      GA
                                    TTCAACAAG ATTTATC  GC
                                    ||||||||| |||||||  ||
                                    AAGTTGTTC TAAATAG  CG
                                          T      A_
GAM1083  LOC120939 3'  TCAATAAATACTTGTTGA    76259             C
                                    TCAACAAGTATTTAT GA
                                    |||||||||||||| ||
                                    AGTTGTTCATAAATA CT
                                               A
GAM1083  LOC139221 3'  GGAGCTCTCATAGATACTAGTT 75825       A       C_   _
                GAA                   TTCAAC AGTATTTAT  GAGC CC
                                      |||||| |||||||||  |||| ||
                                      AAGTTG TCATAGATA  CTCG GG
                                        A        CT    A
GAM1083  LOC157660 3'  GGCACTCAACAAATATTTGTTG 86508             ATC   CC
                AA                    TTCAACAAGTATTT   GAG  CC
                                      ||||||||||||||   |||  ||
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                                AAGTTGTTTATAAA  CTC  GG
                                      CAA  AC
GAM1083  LOC197125 3'  GGCACTCAGTAAATACTTGTTG 87903            C  CC
              AA                  TTCAACAAGTATTTAT GAG  CC
                                  ||||||||||||||| |||  ||
                                  AAGTTGTTCATAAATG CTC  GG
                                        A  AC
GAM1083  LOC197407 3'  GGCATTCAATACTTGTTGAA  88059          TATCGA
                                  TTCAACAAGTATT     GCC
                                  ||||||||||||      |||
                                  AAGTTGTTCATAA     CGG
                                        CTTA__
GAM1083  LOC197408 5'  GGCATTCAATACTTGTTGAA  89750          TATCGA
                                  TTCAACAAGTATT     GCC
                                  ||||||||||||      |||
                                  AAGTTGTTCATAA     CGG
                                        CTTA__
GAM1083  LOC203335 3'  GGGCTTGAACCTGTTGAA    89335       A  ATTTA
                                  TTCAACA GT    TCGAGCCC
                                  ||||||| ||    ||||||||
                                  AAGTTGT CA    AGTTCGGG
                                     C  _____
GAM1083  LOC205251 5'  GAGGAAATACTTGTTGGA    90669           A_
                                  TTCAACAAGTATTT  TC
                                  ||||||||||||||  ||
                                  AGGTTGTTCATAAA  AG
                                        GG
GAM1083  LOC219894 3'  GTTCAATAAATACTTTGTTGAA 93285        _      C
                                  TTCAACAA GTATTTAT GAGC
                                  |||||||| |||||||| ||||
                                  AAGTTGTT CATAAATA CTTG
                                     T       A
GAM1083  LOC254794 3'  TCAATAAACACTTGTTGA    96209        A    C
                                  TCAACAAGT TTTAT GA
                                  ||||||||| ||||| ||
                                  AGTTGTTCA AAATA CT
                                     C    A
GAM1083  LOC256338 3'  CTCAATAAATAATTGTTGAA  94609        G     C
                                  TTCAACAA TATTTAT GAG
                                  |||||||| ||||||| |||
                                  AAGTTGTT ATAAATA CTC
                                     A      A
GAM1083  LOC257494 3'  GGTGCTCAATAAAGACTTGTTG 97795         A    C  _
              AA                  TTCAACAAGT TTTAT GAGC CC
                                  |||||||||| ||||| |||| ||
                                  AAGTTGTTCA AAATA CTCG GG
                                     G    A   T
GAM1083  LOC91355  5'  GGAGAAAACTTGTTGAA     65716         A  A
                                  TTCAACAAGT TTT TC
                                  |||||||||| ||| ||
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                                AAGTTGTTCA AAG GG
                                     A   A
GAM1084  BACH1    3'  ACAAGTAACTACACTACCTCA  6796          A_    GTA
                                TGAGGTAGT  AGTT   TTGT
                                |||||||||  ||||   ||||
                                ACTCCATCA  TCAA   AACA
                                     CA    TG_
GAM1085  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C     CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A     T__
GAM1085  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875        CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T  _
GAM1085  FDFT1    3'  TAGGAAAGTGAAATG       15518            A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM1085  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                  CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM1085  KLF4     3'  TCCCAGACAGTGGATATG     14891     CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||||  ||
                                GT  AGGTGACAGAC CT
                                 AT          C
GAM1085  PHYH     3'  ACAGTAAAAGTGAAAT      20608           C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                     A
GAM1085  PKD2     3'  TCCAGGTTGAAAGTGAAA     60096           CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM1085  WRN      3'  GGGCAGTGAAAATGAAA      5098        C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM1085  ZNF216   3'  ATCTGCACAGCAAAGTGAAA   20017          CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
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                                AAAGTGAAA  GACA   TCTA
                                     C_   CG_
GAM1085  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                ||||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                     CT  __
GAM1085  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||| ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM1085  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
           G                     CATTTC        GTCTGAGAT
                                ||||||        |||||||||
                                GTAAAG        CAGACTCTA
                                   AAACATTT_
GAM1085  FLJ23510 3'  ATCTCAGACAGTGACTGAAATG 45281        CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM1085  KIAA0984 3'  TTTGTCCAGTGAAAATGAA   65534     C       TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM1085  KLHL6    3'  ATCTCAGAGCAGGAAA      55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM1085  NIR3     3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM1085  PORIMIN  3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM1085  PP35     3'  ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM1085  PRTD-NY3 3'  CTCATTGCAATAAGTGAAATG  48148         TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
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                                GTAAAGTGAA   ACG  ACTC
                                     TA__   TT
GAM1085  SEP15    3'  TCCTACAGTAAGAGTGAAA   14934        C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM1085  SFXN2    3'  CTCAGGGGAAAAAAGTGAAA  73941        CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM1085  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM1085  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015       TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM1085  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226     A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM1085  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA
                                          _
GAM1086  ADAM19   3'  CAGGAAGAAGACTGGCCATTAT 52703      C    CTGAG
            G                    CATGA GGCT     TTCTTCCTG
                                ||||| ||||    |||||||||
                                GTATT CCGG     AAGAAGGAC
                                  A    TCAG_
GAM1086  FACL5    5'  CAGGAAGAACTCAGAGCCG   64186
                                CGGCTCTGAGTTCTTCCTG
                                ||||||||||||||||||
                                GCCGAGACTCAAGAAGGAC

GAM1086  GNAL     5'  CAGGAAAGAGAGGAGCCGTCG  9058          GAG TC
                                TGACGGCTCT   T  TTCCTG
                                ||||||||||   |  ||||||
                                GCTGCCGAGG   A  AAGGAC
                                     AG_ GA
GAM1086  KAL1     3'  CAGGAAGAACTTCTGTCA    4013        CTCT
                                TGACGG   GAGTTCTTCCTG
                                ||||||   ||||||||||||
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                                ACTGTC   TTCAAGAAGGAC
                                      ____
GAM1086 MYO1E   3' CAGGAGGACAAAACCACCATG 17187    AC  CTC  AGT
                                CATG  GG   TG   TCTTCCTG
                                ||||  ||   ||   ||||||||
                                GTAC  CC   AC   AGGAGGAC
                                  CA  AAA  ___
GAM1086 PRKAR2B 3' CAGAAAGAACTCAGATGT    10804   _        C
                                GC TCTGAGTTCTT CTG
                                || ||||||||||| |||
                                TG AGACTCAAGAA GAC
                                 T         A
GAM1086 PUM2    3' AGGATCAAAGCTGTCATG    31014         C   GTTCT
                                CATGACGGCT TGA    TCCT
                                |||||||||| |||    ||||
                                GTACTGTCGA ACT    AGGA
                                      A  _____
GAM1086 SKI     3' CAGGAAGTGCAGAGCCGCA   11701    A      AGTT
                                TG CGGCTCTG   CTTCCTG
                                || ||||||||   |||||||
                                AC GCCGAGAC   GAAGGAC
                                 _      GT__
GAM1086 TEM8    3' AGGAAGATGCAACCCCATG   36326     AC  CTC  AGT
                                CATG  GG   TG   TCTTCCT
                                ||||  ||   ||   |||||||
                                GTAC  CC   AC   AGAAGGA
                                  C_  A__  GT_
GAM1086 ARHGEF4 5' AGAAAAAACTCAGGGC      52207         C  C
                                GCTCTGAGTT TT CT
                                |||||||||| || ||
                                CGGGACTCAA AA GA
                                      A  A
GAM1086 FLJ31978 3' CAGGAAGGAACAAGCGCC   58348     T  GAG
                                GGC CT   TTCTTCCTG
                                ||| ||   |||||||||
                                CCG GA   AGGAAGGAC
                                  C  ACA
GAM1086 HSU24186 5' AGAACTCAAAGCCGTC     25324        C
                                GACGGCT TGAGTTCT
                                ||||||| ||||||||
                                CTGCCGA ACTCAAGA
                                    A
GAM1086 KCNT1   3' AGCTCCCAGGGCCGCCA     61825    A     __
                                TG CGGCTCT  GAGTT
                                || |||||||  |||||
                                AC GCCGGGA  CTCGA
                                 C      CC
GAM1086 KIAA1867 3' CAGGAAGAACCCAAGAGCTCAT 94822      CG    GA_
                                ATGA  GCTCT   GTTCTTCCTG
                                ||||  |||||   ||||||||||
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                                TACT  CGAGA   CAAGAAGGAC
                                  __    ACC
GAM1086  KIAA1878  3'  AATTCAGAGAATCGTCATG   91707        __
                                CATGACGG  CTCTGAGTT
                                ||||||||  |||||||||
                                GTACTGCT  GAGACTTAA
                                    AA
GAM1086  MFN1      3'  CAGGAAGAACTCATGA      35541    _
                                TC TGAGTTCTTCCTG
                                || ||||||||||||
                                AG ACTCAAGAAGGAC
                                 T
GAM1086  MIDORI    3'  CAGGGCCCTTCCAGAGCCTGTC 73784       _      AGTTCT
             ATG                   CATGAC GGCTCTG     TCCTG
                                |||||| |||||||     |||||
                                GTACTG CCGAGAC     GGGAC
                                   T      CTTCCC
GAM1086  MYH7B     3'  CAGGAAGAACCTGGCTCGCATG 70530      A _  CTGA
                                CATG CG GCT    GTTCTTCCTG
                                |||| || |||    ||||||||||
                                GTAC GC CGG    CAAGAAGGAC
                                  _ T   TC__
GAM1086  RNAHP     3'  AGAAAGCAGCAGCCGTCAT    23761         _  AG
                                ATGACGGCT CTG  TTCT
                                |||||||| |||  ||||
                                TACTGCCGA GAC  AAGA
                                     C   GA
GAM1086  SLC37A1   3'  AGACGGAGCTCAGACCC     38561    C        TC
                                GG TCTGAGTTCT  CT
                                || ||||||||||  ||
                                CC AGACTCGAGG  GA
                                 C         CA
GAM1086  LOC116236 3'  CAGGAAAAGCACAAACCTCAT  73809      C  CTC  A   C
                                ATGA GG   TG GTT TTCCTG
                                |||| ||   || ||| ||||||
                                TACT CC   AC CGA AAGGAC
                                  _ AA_  A   A
GAM1086  LOC124801 3'  CAGGAAGAACTCTCTTGCATG  74336      A  CTCT
                                CATG CGG    GAGTTCTTCCTG
                                |||| |||    ||||||||||||
                                GTAC GTT    CTCAAGAAGGAC
                                  _   CT__
GAM1086  LOC222160 5'  AGGAAGAACTCACCCC      94117     CTC
                                GG   TGAGTTCTTCCT
                                ||   ||||||||||||
                                CC   ACTCAAGAAGGA
                                 CC_
GAM1086  LOC51094  3'  CAGGAAGAATAAAGCC      32045      CTGA
                                GGCT    GTTCTTCCTG
                                ||||    ||||||||||
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                                CCGA   TAAGAAGGAC
                                  AA__
GAM1086 LOC92078 3' CAGGAAGAAGAATCGACCGTC 67977      C T G__
                                GACGG TC GA  TTCTTCCTG
                                |||||| || ||  |||||||||
                                CTGCC AG CT  AAGAAGGAC
                                  _ _ AAG
GAM1087 AQP6    3' GGACCAATTTTCAAACTTGGAT 53936    A       TT  AC
                                ATC CAAGTTTGAG  TTG  CC
                                ||| ||||||||||  |||  ||
                                TAG GTTCAAACTT  AAC  GG
                                  _       TT   CA
GAM1087 BIG1    3' GTCTTACTCAAACTTG     21204          TTT
                                CAAGTTTGAGT   GAC
                                ||||||||||   |||
                                GTTCAAACTCA   CTG
                                      TT_
GAM1087 CDH12   5' GGTCAAAACAATTTGAGAT   14493    A    TGA
                                ATC CAAGTT   GTTTTGACC
                                ||| ||||||   |||||||||
                                TAG GTTTAA   CAAAACTGG
                                  A    ___
GAM1087 FACL4   3' GTCAAACACTTGTGA      15512        TTGA   T
                                TCACAAGT   GTTT GAC
                                ||||||||   |||| |||
                                AGTGTTCA   CAAA CTG
                                     ____   _
GAM1087 FACL4   3' GTCAAACACTTGTGA      43402        TTGA   T
                                TCACAAGT   GTTT GAC
                                ||||||||   |||| |||
                                AGTGTTCA   CAAA CTG
                                     ____   _
GAM1087 GLUL    3' GTCAAAACACTTGT       9043       TTGA
                                ACAAGT   GTTTTGAC
                                ||||||   ||||||||
                                TGTTCA   CAAAACTG
                                    ____
GAM1087 HLA-DMB 3' AGATTCAAACTCAATGATG   9206      CA_
                                CATCA  AGTTTGAGTTT
                                |||||  ||||||||||
                                GTAGT  TCAAACTTAGA
                                   AAC
GAM1087 RAD54B  3' AGCTCAACTTGTGAT      56233         T
                                ATCACAAGTT GAGTT
                                |||||||||| |||||
                                TAGTGTTCAA CTCGA
                                      _
GAM1087 C1orf19 3' TCAAAACTCAAAATATGT   68193    AG_
                                ACA  TTTGAGTTTTGA
                                |||  ||||||||||||
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                                TGT   AAACTCAAAACT
                                  ATA
GAM1087  C20orf126 3'  GTCAAAACTCTTATGTG     48000      AGTTT
                                CACA    GAGTTTTGAC
                                ||||    ||||||||||
                                GTGT    CTCAAAACTG
                                  ATT__
GAM1087  DAZAP1    3'  GGATTCCAAACTTGTGA     38537          _
                                TCACAAGTTTG AGTTT
                                |||||||||||| |||||
                                AGTGTTCAAAC TTAGG
                                       C
GAM1087  FLJ14054  3'  AAGTTCAAGCCTGTGATG    44657        A     GT
                                CATCACA GTTTGA  TT
                                ||||||| ||||||  ||
                                GTAGTGT CGAACT  AA
                                    C     TG
GAM1087  FLJ14166  3'  GAACCCAACTTGTGATG     44684          T A
                                CATCACAAGTT G GTTT
                                |||||||||||  | ||||
                                GTAGTGTTCAA C CAAG
                                       _ C
GAM1087  FLJ20312  5'  GGACTTCTCTCAAACTTGTG   34927           TTTTGA
                                CACAAGTTTGAG     CC
                                ||||||||||||     ||
                                GTGTTCAAACTC     GG
                                       TCTTCA
GAM1087  HNRPU     3'  AGGCTCAAACTTGTGA      15693
                                TCACAAGTTTGAGTTT
                                ||||||||||||||||
                                AGTGTTCAAACTCGGA

GAM1087  HNRPU     3'  AGGCTCAAACTTGTGA      48989
                                TCACAAGTTTGAGTTT
                                ||||||||||||||||
                                AGTGTTCAAACTCGGA

GAM1087  KIAA0650  3'  TCAATGAGTGAACTTGTGA   88240          AGTT
                                TCACAAGTTTG    TTGA
                                ||||||||||    ||||
                                AGTGTTCAAGT    AACT
                                       GAGT
GAM1087  MGEA6     3'  AAACTCAAACTTATGTG     19814      __
                                CACA  AGTTTGAGTTT
                                ||||  ||||||||||
                                GTGT  TCAAACTCAAA
                                  AT
GAM1087  SCYA16    3'  GGCTGGTCTCAAACTCGTG   15963     A       TT  GA
                                CAC AGTTTGAG  TT  CC
                                ||| |||||||  ||  ||
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                                GTG TCAAACTC  GG  GG
                                  C       T_  TC
GAM1087  SNRK     3'  CAAAGCAATAACGTTGTGATG  34764         _   TGA
                                CATCACAA GTT   GTTTTG
                                |||||||| |||   ||||||
                                GTAGTGTT CAA   CGAAAC
                                    G   TAA
GAM1087  LOC115219 5'  GGCTAGTCTCAAACTCCTGA   73313     CA       TT   A
                                TCA  AGTTTGAG  TTG CC
                                |||  ||||||||  ||| ||
                                AGT  TCAAACTC  GAT GG
                                  CC       T_   C
GAM1087  LOC123624 3'  GTCAAAGCCAAACTCATG    75615    CA     A
                                CA  AGTTTG GTTTTGAC
                                ||  |||||| ||||||||
                                GT  TCAAAC CGAAACTG
                                 AC     _
GAM1087  LOC124977 5'  GGGTCAGGAGGAACCTGCGAT  76062     A  A    GAG
                                ATC CA GTTT   TTTTGACCC
                                ||| || ||||   |||||||||
                                TAG GT CAAG   AGGACTGGG
                                  C  C    G__
GAM1087  LOC145978 3'  GGGTTTATGACTCAAACTT    77599           TT_
                                AAGTTTGAGTT   GACCC
                                ||||||||||   |||||
                                TTCAAACTCAG   TTGGG
                                      TAT
GAM1087  LOC157621 3'  GGCCTTCAAACTGTGATG    86495        A      TTTTGA
                                CATCACA GTTTGAG     CC
                                ||||||| |||||||     ||
                                GTAGTGT CAAACTT     GG
                                    _      CC_____
GAM1087  LOC219401 3'  GTCAAAACTTATTGTG      92817       GTT
                                CACAA   TGAGTTTTGAC
                                |||||   ||||||||||
                                GTGTT   ATTCAAAACTG
                                   ___
GAM1087  LOC221092 5'  GTCAAAACCAGCAGGCTCAGAT 93241      ACA     A__
           G                     CATC   AGTTTG   GTTTTGAC
                                ||||   ||||||   ||||||||
                                GTAG   TCGGAC   CAAAACTG
                                  AC_     GAC
GAM1087  LOC221752 3'  GGCCAAAAGGCTCATACT    93780     T    __   A
                                AGT TGAGT  TTTG CC
                                ||| |||||  |||| ||
                                TCA ACTCG  AAAC GG
                                  T    GA   C
GAM1087  LOC254101 5'  AAACCAAAGATTGTGATG    96272         G_   A
                                CATCACAA  TTTG GTTT
                                ||||||||  |||| ||||
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                                GTAGTGTT  AAAC CAAA
                                    AG   _
GAM1087 LOC91291 5' GGCTGGTCTCAAACTCCTGA  65484    CA      TT  GA
                                TCA  AGTTTGAG  TT  CC
                                |||  ||||||||  ||  ||
                                AGT  TCAAACTC  GG  GG
                                  CC       T_  TC
GAM1088 LTBP2    3' ATCATCCTGACGATCCCA    4720    AT   C
                                TG  ATCG CAGGATGAT
                                ||  |||| |||||||||
                                AC  TAGC GTCCTACTA
                                 CC   A
GAM1088 C20orf40  5' AGACCACCCTGATGGCATC   25915    AT  C   A  A
                                GAT  CG CAGG TG TCT
                                |||  || |||| || |||
                                CTA  GT GTCC AC AGA
                                  CG  A   C  C
GAM1088 FLJ12891  3' ATCATCCTGCAACATCA    46337    ATC  C
                                TGAT   GC AGGATGAT
                                ||||   || ||||||||
                                ACTA   CG TCCTACTA
                                  CAA  _
GAM1088 LOC145842 5' CTAGACCTTTATCGATATCA  77533       CC__  ATGA
                                TGATATCG   AGG   TCTAG
                                ||||||||   |||   |||||
                                ACTATAGC   TCC   AGATC
                                     TATT  _____
GAM1088 LOC153443 3' AGATCACCCTTGTTAAAAATCA 80821     ATC__  C   A
                                TGAT    GC AGG TGATCT
                                ||||    || ||| ||||||
                                ACTA    TG TCC ACTAGA
                                  AAAAT  T   C
GAM1089 AQP6    5' AGCATCATCCCCACTG     53909       AC
                                CAGTGG  GTGATGCT
                                ||||||  ||||||||
                                GTCACC  TACTACGA
                                   CC
GAM1089 AXL     3' AGCATCACCATCTGTA     41590      _  ACG
                                TACAG TGG   TGATGCT
                                ||||| |||   |||||||
                                ATGTC ACC   ACTACGA
                                   T  ___
GAM1089 AXL     3' AGCATCACCATCTGTA     8093       _  ACG
                                TACAG TGG   TGATGCT
                                ||||| |||   |||||||
                                ATGTC ACC   ACTACGA
                                   T  ___
GAM1089 GYS1    3' GCTCTGCCCACTGTGAA    88401    T     A  T  T
                                TTC ACAGTGG CG GA GC
                                ||| ||||||| || || ||
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                                AAG TGTCACC GT CT CG
                                  _      C  _ _
GAM1089  HMGCS2   3'  AGCATCAGCCCTGTAGAG    18625        T  ACG
                                TTCTACAG GG   TGATGCT
                                |||||||| ||   |||||||
                                GAGATGTC CC   ACTACGA
                                     _ G__
GAM1089  MTM1     3'  GCATCATCCTTAGAA      4206       CAGT   CG
                                TTCTA   GGA  TGATGC
                                |||||   |||  ||||||
                                AAGAT   CCT  ACTACG
                                   T___  __
GAM1089  NPAT     3'  CATTTCTCAGTGTAGAA     67234        G  _  C
                                TTCTACA TG GA GTG
                                ||||||| || || |||
                                AAGATGT AC CT TAC
                                    G  T  T
GAM1089  PRKAR2B  3'  AGTGGTTAGTCCACTGAGAA   10803      A      GTGA
                                TTCT CAGTGGAC    TGCT
                                |||| ||||||||    ||||
                                AAGA GTCACCTG    GTGA
                                  _       ATTG
GAM1089  SH2D1A   3'  AGCATCACATGAACTTGTA    9847       _  GGAC
                                TACA GT    GTGATGCT
                                |||| ||    ||||||||
                                ATGT CA    CACTACGA
                                  T  AGTA
GAM1089  STAU     5'  AGCATAACCCCTACTGTAGAA  15995          AC  G
                                TTCTACAGTGG  GT ATGCT
                                ||||||||||  || |||||
                                AAGATGTCATC  CA TACGA
                                      CC  A
GAM1089  STAU     5'  AGCATAACCCCTACTGTAGAA  33892          AC  G
                                TTCTACAGTGG  GT ATGCT
                                ||||||||||  || |||||
                                AAGATGTCATC  CA TACGA
                                      CC  A
GAM1089  STAU     5'  AGCATAACCCCTACTGTAGAA  33905          AC  G
                                TTCTACAGTGG  GT ATGCT
                                ||||||||||  || |||||
                                AAGATGTCATC  CA TACGA
                                      CC  A
GAM1089  TCF19    3'  AGCATCATTTCTATAGAA    97732      ACA    C
                                TTCT   GTGGA GTGATGCT
                                ||||   ||||| ||||||||
                                AAGA   TATCT TACTACGA
                                   ___     T
GAM1089  TCF19    3'  AGCATCATTTCTATAGAA    97862      ACA    C
                                TTCT   GTGGA GTGATGCT
                                ||||   ||||| ||||||||
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                                AAGA   TATCT TACTACGA
                                  ___    T
GAM1089  UBE4A    3'  AGCATCACCAAGTTTAGAA   16554      CAG_   ACG
                                TTCTA    TGG   TGATGCT
                                |||||    |||   |||||||
                                AAGAT    ACC   ACTACGA
                                   TTGA  ___
GAM1089  C20orf150 3'  AGCATCGTGTCACTGTGAA   65388     T     G
                                TTC ACAGTG ACGTGATGCT
                                ||| |||||| ||||||||||
                                AAG TGTCAC TGTGCTACGA

                                  _     _
GAM1089  CNOT7    3'  CATGTTCATCATAGAA      53984       CA
                                TTCTA  GTGGACGTG
                                |||||  |||||||||
                                AAGAT  TACTTGTAC
                                   AC
GAM1089  CYLD     3'  AGCATTTTGCACTCTAGAA   30881      C    GA  T
                                TTCTA AGTG  CG GATGCT
                                ||||| ||||  || ||||||
                                AAGAT TCAC  GT TTACGA
                                   C    __  T
GAM1089  DKFZP434A043 3'  AGCATATATCACTGTGAA    31182     T      ACGTG
                                TTC ACAGTGG    ATGCT
                                ||| |||||||    |||||
                                AAG TGTCACT    TACGA
                                  _      ATA__
GAM1089  DKFZP586P0123 5'  AGCATCACGCCATGAAGAG   94837      ACA    A
                                TTCT   GTGG CGTGATGCT
                                ||||   |||| |||||||||
                                GAGA   TACC GCACTACGA
                                  AG_   _
GAM1089  DSCR1L1   3'  CACCACTCCCCTGTAGAA    19495        T   C   A
                                TTCTACAG GGA GTG TG
                                |||||||| ||| ||| ||
                                AAGATGTC CCT CAC AC
                                     C   _   C
GAM1089  FLJ10706  5'  AGCATATTCACTGTGAA     36461     T      CGTG
                                TTC ACAGTGGA    ATGCT
                                ||| ||||||||    |||||
                                AAG TGTCACTT    TACGA
                                  _       A___
GAM1089  FLJ20527  3'  AGCATCACCAAGCACTTAGAA  35350      C    GAC_
                                TTCTA AGTG    GTGATGCT
                                ||||| ||||    ||||||||
                                AAGAT TCAC    CACTACGA
                                   _    GAAC
GAM1089  FLJ20573  3'  ACTTCTCAACTGTAGAA     63909         __   C
                                TTCTACAGT  GGA GT
                                |||||||||  ||| ||
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                                AAGATGTCA  TCT CA
                                     AC   T
GAM1089  FLJ23416  3'  AGCAATGCCTGTCCATTGTAGA 49945          __  A
              A                   TTCTACAGTGGAC  GTG TGCT
                                  ||||||||||||  ||| ||||
                                  AAGATGTTACCTG  CGT ACGA
                                       TC   A
GAM1089  GOLGIN-67 3'  AGCATGGATGTCCATTACAGAA 94976     AC       G_
                                  TTCT  AGTGGACGT  ATGCT
                                  ||||  |||||||||  |||||
                                  AAGA  TTACCTGTA  TACGA
                                    CA       GG
GAM1089  HNK-1ST   3'  AGCATCACACAGCGTTAGGA   16767      CA  GGAC
                                  TTCTA  GT   GTGATGCT
                                  |||||  ||   ||||||||
                                  AGGAT  CG   CACTACGA
                                     TG  ACA_
GAM1089  HPCAL4    3'  AGCATCACAGACACATAGA    32730     CA   GAC
                                  TCTA  GTG   GTGATGCT
                                  ||||  |||   ||||||||
                                  AGAT  CAC   CACTACGA
                                    A_   AGA
GAM1089  KIAA0205  3'  AGCAATATGCCACTGTA     29576        A    A
                                  TACAGTGG CGTG TGCT
                                  ||||||||  |||| ||||
                                  ATGTCACC GTAT ACGA
                                       _    A
GAM1089  KIAA0285  5'  AGCATCACACCTACCAAGAA   29011     ACA    AC
                                  TTCT   GTGG  GTGATGCT
                                  ||||   ||||  ||||||||
                                  AAGA   CATC  CACTACGA
                                    AC_    CA
GAM1089  KIAA0855  3'  AGCATGGATGTCCATTACAGAA 30401      AC       G_
                                  TTCT  AGTGGACGT  ATGCT
                                  ||||  |||||||||  |||||
                                  AAGA  TTACCTGTA  TACGA
                                    CA       GG
GAM1089  KIAA1681  3'  GCATTGCTCTATAGAA      61071      ACA     C TG
                                  TTCT   GTGGA G  ATGC
                                  ||||   ||||| |  ||||
                                  AAGA   TATCT C  TACG
                                     ___     _ GT
GAM1089  LHFP      3'  TCTGTCCACTATAGGA      19339       C       T
                                  TTCTA AGTGGACG GA
                                  ||||| |||||||| ||
                                  AGGAT TCACCTGT CT
                                     A       _
GAM1089  MGC11061  3'  AGCATCACAGATCCTGCAGA   50284     A   T  AC_
                                  TCT CAG GG   GTGATGCT
                                  ||| ||| ||   ||||||||
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                                AGA GTC CT   CACTACGA
                                  C  _ AGA
GAM1089  MGC16291  3'  ACGCCCACTGCTAGAA      51304       _     A
                                TTCTA CAGTGG CGT
                                ||||| |||||| |||
                                AAGAT GTCACC GCA
                                   C     C
GAM1089  NY-BR-1   3'  AGCATCACCTTATGTTGAA   53793     T   GTGGAC
                                TTC ACA     GTGATGCT
                                ||| |||     ||||||||
                                AAG TGT     CACTACGA
                                  T  ATTC__
GAM1089  OAZIN     5'  AGTACAATCAACTGTAGAA   31873         G  CG  A
                                TTCTACAGT GA  TG TGCT
                                ||||||||| ||  || ||||
                                AAGATGTCA CT  AC ATGA
                                      A  A_  _
GAM1089  POPX1     3'  CACACTCCACTGTTGAA     29796     T      C   A
                                TTC ACAGTGGA GTG TG
                                ||| |||||||| ||| ||
                                AAG TGTCACCT CAC AC
                                  T       _  _
GAM1089  PTR4      3'  AGCCATATCTCACTGTA      74054        _ CG  AT
                                TACAGTG GA  TG  GCT
                                ||||||| ||  ||  |||
                                ATGTCAC CT  AC  CGA
                                    T  AT  __
GAM1089  RAB3D     3'  AGCCTTTTCCCATTGTAGAA   15005          ACGT  T
                                TTCTACAGTGG    GA GCT
                                ||||||||||    || |||
                                AAGATGTTACC    TT CGA
                                      CTT_  C
GAM1089  SCYA18    3'  AGCATTCTCACTGTGAA      11458     T      ACGT
                                TTC ACAGTGG    GATGCT
                                ||| |||||||    ||||||
                                AAG TGTCACT    TTACGA
                                  _      C___
GAM1089  LOC113523 5'  AGCATCACAAACACATCAGAA  73041      ACA   GAC
                                TTCT   GTG   GTGATGCT
                                ||||   |||   ||||||||
                                AAGA   CAC   CACTACGA
                                   CTA   AAA
GAM1089  LOC120856 3'  ACATCCAGCTGTAGAA      74024         _   C
                                TTCTACAG TGGA GT
                                |||||||| |||| ||
                                AAGATGTC ACCT CA
                                    G   A
GAM1089  LOC125228 3'  CATCTGTCACTGTGAA      74402     T     G   T
                                TTC ACAGTG ACG GATG
                                ||| |||||| ||| ||||
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                                AAG TGTCAC TGT CTAC
                                  _    _  _
GAM1089  LOC128977 3'  GTTGTGCCACTGTGAA     74828    T     A  TG
                                TTC ACAGTGG CG  AT
                                ||| ||||||| ||  ||
                                AAG TGTCACC GT  TG
                                  _     _ GT
GAM1089  LOC144871 3'  AGCATTATCCACTGTA     83195        CG
                                TACAGTGGA  TGATGCT
                                |||||||||  |||||||
                                ATGTCACCT  ATTACGA
                                     __
GAM1089  LOC150035 5'  CATGCCCACTGTGAA      84808    T     A
                                TTC ACAGTGG CGTG
                                ||| ||||||| ||||
                                AAG TGTCACC GTAC
                                  _     C
GAM1089  LOC150157 3'  CATCCCACTGTGAA       84873    T     ACGT
                                TTC ACAGTGG   GATG
                                ||| |||||||   ||||
                                AAG TGTCACC   CTAC
                                  _     _____
GAM1089  LOC151188 3'  AGCATCACTGTCTACTCAGAA  80156     AC     _
                                TTCT  AGTGGAC GTGATGCT
                                ||||  ||||||| ||||||||
                                AAGA  TCATCTG CACTACGA
                                  C_     T
GAM1089  LOC151657 3'  AGCATCATGATTCTATCAGAA  85474     ACA    __
                                TTCT   GTGGA  CGTGATGCT
                                ||||   |||||  |||||||||
                                AAGA   TATCT  GTACTACGA
                                  C__    TA
GAM1089  LOC153525 5'  AGCACCTTTTACTGTAGA    86044         CGTGA
                                TCTACAGTGGA    TGCT
                                ||||||||||    ||||
                                AGATGTCATTT    ACGA
                                      TCC__
GAM1089  LOC154007 3'  ATCTATCCATTGTAGAA     81014         CGT
                                TTCTACAGTGGA   GAT
                                ||||||||||||   |||
                                AAGATGTTACCT   CTA
                                      AT_
GAM1089  LOC154562 3'  ACATCCCTGACTGTGGAA    81089        ___  C
                                TTCTACAGT   GGA GT
                                |||||||||   ||| ||
                                AAGGTGTCA   CCT CA
                                     GTC   A
GAM1089  LOC163126 3'  AGCATCACAGAAGTAGAA    82415      AGTGGAC
                                TTCTAC      GTGATGCT
                                ||||||      ||||||||
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                                AAGATG      CACTACGA
                                   AAGA___
GAM1089  LOC163479 5'  ACAGTATCACTGTAGAA     82140          _ _
                                TTCTACAGTGG AC GT
                                |||||||||| || ||
                                AAGATGTCACT TG CA
                                      A  A
GAM1089  LOC196890 3'  CATCCCACTGTGAA       89645     T      ACGT
                                TTC ACAGTGG    GATG
                                ||| |||||||    ||||
                                AAG TGTCACC    CTAC
                                  _     _____
GAM1089  LOC220776 3'  AGCATCACTGGAGGCTCAGAA  68381      AC   GGA _
                                TTCT  AGT   C GTGATGCT
                                ||||  |||   | ||||||||
                                AAGA  TCG   G CACTACGA
                                  C_   GAG T
GAM1089  LOC222028 3'  AGCATCAGTATTACTGCAGGA  94056      A     _  G
                                TTCT CAGTGG AC TGATGCT
                                |||| |||||| || |||||||
                                AGGA GTCATT TG ACTACGA
                                  C      A  _
GAM1089  LOC253649 5'  AGCATCACGTTGCTAGAA    96166      AC  TG A
                                TTCT  AG  G CGTGATGCT
                                ||||  ||  | |||||||||
                                AAGA  TC  T GCACTACGA
                                  __  GT _
GAM1089  LOC253650 5'  AGCATCACGTTGCTAGAA    96163      AC  TG A
                                TTCT  AG  G CGTGATGCT
                                ||||  ||  | |||||||||
                                AAGA  TC  T GCACTACGA
                                  __  GT _
GAM1089  LOC255654 3'  CATCCACACTGTAGAA      96886          GACGT
                                TTCTACAGTG     GATG
                                ||||||||||     ||||
                                AAGATGTCAC     CTAC
                                      AC___
GAM1089  LOC256536 3'  TATCAATCCACTGCAGGA    94713      A      CG
                                TTCT CAGTGGA  TGATG
                                |||| |||||||  |||||
                                AGGA GTCACCT  ACTAT
                                  C      A_
GAM1089  LOC91796  3'  AGCATCACACTACCAGA     67209     ACA    AC
                                TCT   GTGG  GTGATGCT
                                |||   ||||  ||||||||
                                AGA   CATC  CACTACGA
                                  C__    A_
GAM1090  KCNN4     3'  ATGCTGCTATGGACGACCTC   9565      ATCA     ACA
                                GAG    TCGTT   AGCAGCAT
                                |||    |||||   ||||||||
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                                CTC   AGCAG  TCGTCGTA
                                  C___    GTA
GAM1090 TMEM1    3' GCCGCCTGTGATCTCA     12336       ATCGTT  A A
                                TGAGATC     ACA GC GC
                                |||||||     ||| || ||
                                ACTCTAG     TGT CG CG
                                   _______  C  C
GAM1090 DCOHM    3' ATGCTGCTCAGGCTGATCTCA 49592       TC  ACA
                                TGAGATCA  GTT  AGCAGCAT
                                ||||||||  |||  ||||||||
                                ACTCTAGT  CGG  TCGTCGTA
                                     __  AC_
GAM1090 KIAA0397 3' ATGCTGCTTGCTCGGCCATC  61672    CA  TTA
                                GAT  TCG  CAAGCAGCAT
                                |||  |||  ||||||||||
                                CTA  GGC  GTTCGTCGTA
                                  CC  TC_
GAM1090 MGC16386 3' CTGCCTGGATGCATCTCA    54732      _   GTTA  A
                                TGAGAT CATC   CA GCAG
                                |||||| ||||   || ||||
                                ACTCTA GTAG   GT CGTC
                                   C   _____ C
GAM1090 LOC149182 5' ATGCTGCTTGGACAACCCTCA  84373     ATCATC  A
                                TGAG     GTT CAAGCAGCAT
                                ||||     ||| ||||||||||
                                ACTC     CAG GTTCGTCGTA
                                  CCAA__  _
GAM1090 LOC152845 5' ATGCTGCCAGCAGCGGTGACCT 60329     A      ACAA
           CA                    TGAG TCATCGTT   GCAGCAT
                                |||| ||||||||   |||||||
                                ACTC AGTGGCGA   CGTCGTA
                                  C      CGAC
GAM1090 LOC199786 3' ATGCTGCCCAGGCTGATCTCA  88366       TC  ACAA
                                TGAGATCA  GTT   GCAGCAT
                                ||||||||  |||   |||||||
                                ACTCTAGT  CGG   CGTCGTA
                                     __  ACC_
GAM1090 LOC64116  3' GCCCAACAATGATCTCA     42201       C  ACAA
                                TGAGATCAT GTT   GC
                                |||||||| |||   ||
                                ACTCTAGTA CAA   CG
                                     A  CC__
GAM1091 ATP2A3   3' ATCCTCAGGTTCCTGACCGTG  17718    A  CTT  TA
                                TAC GTC   GA  ACCTGAGGAT
                                ||| |||   ||  ||||||||||
                                GTG CAG   CT  TGGACTCCTA
                                  C  TC_  __
GAM1091 COPS3    3' ATCCTCAGATTATTGTTACTG  13330     CCT     C
                                CAGT   TGATAA CTGAGGAT
                                ||||   |||||| ||||||||
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                                GTCA   GTTATT GACTCCTA
                                  TT_     A
GAM1091  CRI1     3'  CAGTTATCAAAGGCT      26762      C       C
                                AGTC TTGATAAC TG
                                |||| |||||||| ||
                                TCGG AACTATTG AC
                                  A       _
GAM1091  EHD2     3'  ATCCTCAGGTCTCGGGAC    27487       T  TA
                                GTCCT GA  ACCTGAGGAT
                                ||||| ||  ||||||||||
                                CAGGG CT  TGGACTCCTA
                                  _  C_
GAM1091  EIF5A2   3'  TCATGTTATCAAAAACTGT   39856       CC       C
                                ACAGT  TTGATAAC TGA
                                |||||  |||||||| |||
                                TGTCA  AACTATTG ACT
                                  AA       T
GAM1091  MGA      3'  ATCCTCAGGAAAAGAAGGAC  62805       GATAA
                                GTCCTT    CCTGAGGAT
                                ||||||    |||||||||
                                CAGGAA    GGACTCCTA
                                   GAAAA
GAM1091  FLJ21140 3'  TTTTGGTTACCAGGGACT    45484         A    T
                                AGTCCTTG TAACC GAG
                                |||||||| ||||| |||
                                TCAGGGAC ATTGG TTT
                                    C    T
GAM1091  KIAA0676 3'  TCCTCAGGCCTGGGCTGTA   30453         TTGATAA
                                TACAGTCC      CCTGAGGA
                                ||||||||      ||||||||
                                ATGTCGGG      GGACTCCT
                                    TCC____
GAM1091  OSBPL2   3'  TCCCTGATCAAGGATGTA    57873      G       AACCTGA
                                TACA TCCTTGAT      GGA
                                |||| ||||||||      |||
                                ATGT AGGAACTA      CCT
                                  _       GTC____
GAM1091  OSBPL2   3'  TCCCTGATCAAGGATGTA    29222      G       AACCTGA
                                TACA TCCTTGAT      GGA
                                |||| ||||||||      |||
                                ATGT AGGAACTA      CCT
                                  _       GTC____
GAM1091  PRO2176  3'  ATTCTTAGCTATCAAGGGCTG 37564           AC
                                CAGTCCTTGATA  CTGAGGAT
                                ||||||||||||  ||||||||
                                GTCGGGAACTAT  GATTCTTA
                                    C_
GAM1091  SNX16    3'  TTCTGTTATCAAGGC       42141    T       CT
                                G CCTTGATAAC  GAG
                                | ||||||||||  |||
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                                C GGAACTATTG  CTT
                                _       T_
GAM1091  LOC146268 3'  ATCCTCAGGCTCCCCAGACCTG 77800    TC  TGATAA
                                CAG  CT     CCTGAGGAT
                                |||  ||     |||||||||
                                GTC  GA     GGACTCCTA
                                  CA  CCCCTC
GAM1091  LOC147040 3'  CCTGAGCCCACCAAGGACTCA  78232   C      ATAAC  G
                                A AGTCCTTG    CT AGG
                                | ||||||||    || |||
                                A TCAGGAAC    GA TCC
                                 C       CACCC  G
GAM1091  LOC157623 5'  ATCCCCATGTGTCAAGGAC   81490         ACC  A
                                GTCCTTGATA   TG GGAT
                                ||||||||||   || ||||
                                CAGGAACTGT   AC CCTA
                                      GT_  C
GAM1091  LOC221755 3'  CCTTCCTCAAGGACTTA    92394   C      TAACCT
                                A AGTCCTTGA     GAGG
                                | |||||||||     ||||
                                A TCAGGAACT     TTCC
                                 T       CC____
GAM1091  LOC253681 3'  CCTGAGCCCACCAAGGACTCA  95129   C      ATAAC  G
                                A AGTCCTTG    CT AGG
                                | ||||||||    || |||
                                A TCAGGAAC    GA TCC
                                 C       CACCC  G
GAM1091  LOC91759  5'  ATCCTCAGACTGTGGAGCAC   67084   C  G   AC
                                GT CTT ATA  CTGAGGAT
                                || ||| |||  ||||||||
                                CA GAG TGT  GACTCCTA
                                 C  G   CA
GAM1092  ACP1      3'  TCGAGTCTACCTCTTCA     15034       C  GCACG
                                TGGAGAGG AGA    TTCGA
                                |||||||| |||    |||||
                                ACTTCTCC TCT    GAGCT
                                     A  _____
GAM1092  ACP1      3'  TCGAGTCTACCTCTTCA     23022       C  GCACG
                                TGGAGAGG AGA    TTCGA
                                |||||||| |||    |||||
                                ACTTCTCC TCT    GAGCT
                                     A  _____
GAM1092  B3GAT1    5'  AGCTGCTCTGTCCTCTCCA   53968       _     C
                                TGGAGAGG CAGAGCA GTT
                                |||||||| ||||||| |||
                                ACCTCTCC GTCTCGT CGA
                                     T     _
GAM1092  CYP26A1   3'  TGTCACTCTAACCTCTCCA   54050       C_   C_
                                TGGAGAGG  AGAG  ACG
                                ||||||||  ||||  |||
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                                ACCTCTCC  TCTC  TGT
                                    AA   AC
GAM1092 CYP26A1  3' TGTCACTCTAACCTCTCCA   5771        C_   C_
                                TGGAGAGG  AGAG  ACG
                                ||||||||  ||||  |||
                                ACCTCTCC  TCTC  TGT
                                    AA   AC
GAM1092 DBP     5' AGCCCTTCGCCTCTCCA    7215         AG  CAC
                                TGGAGAGGC  AG   GTT
                                |||||||||  ||   |||
                                ACCTCTCCG  TC   CGA
                                    CT  C__
GAM1092 EDAR    5' AACGTGCCCGCTCCAGCCTCTC 42263         A_   ____
           CA                    TGGAGAGGC  GAGC   ACGTT
                                |||||||||  ||||   |||||
                                ACCTCTCCG  CTCG   TGCAA
                                    AC   CCCG
GAM1092 EGR3    3'  GGCCGCGCCCTGGCCTCTCCA  59559         _  A  A  TT
                                TGGAGAGGC AG GC CG  C
                                |||||||||  || || ||  |
                                ACCTCTCCG TC CG GC  G
                                    G  C  C  CG
GAM1092 FN14    3'  GTCTCTGCCTCCCA       33562     A       C
                                TGG GAGGCAGAG AC
                                |||  |||||||||  ||
                                ACC CTCCGTCTC TG
                                  _       _
GAM1092 HOXD4   5'  GTCCCAGCTCTGCCCTCCA   27529      A      ACGTTC
                                TGGAG GGCAGAGC     GAC
                                |||||  ||||||||     |||
                                ACCTC CCGTCTCG     CTG
                                  _       ACC___
GAM1092 IHH     3'  AGTTTTCATACTCTGCCTCCCC 72111    A       CACGTTC
                                GG GAGGCAGAG      GACT
                                ||  |||||||||      ||||
                                CC CTCCGTCTC      TTGA
                                 C        ATACTT_
GAM1092 ITGA3   3'  TGGCTCTGCCCCTCC       18541     A      A
                                GGAG GGCAGAGC CG
                                ||||  ||||||||  ||
                                CCTC CCGTCTCG GT
                                  C       _
GAM1092 ITGA3   3'  TGGCTCTGCCCCTCC       9379      A      A
                                GGAG GGCAGAGC CG
                                ||||  ||||||||  ||
                                CCTC CCGTCTCG GT
                                  C       _
GAM1092 PPP1R3A  3'  GCCTGCACTCTGTCTCTCCA  10718          __  C
                                TGGAGAGGCAGA  GCA GT
                                ||||||||||||  |||  ||
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                                ACCTCTCTGTCT  CGT CG
                                      CA   C
GAM1092  PPP2R2B  3'  AGTCAGTATCTCCTGCCCCTCC 15904      A    _  CACGTTC
             A                   TGGAG GGCAG AG      GACT
                                 ||||| ||||| ||      ||||
                                 ACCTC CCGTC TC      CTGA
                                    C    C  TATGA__
GAM1092  TBP      3'  GACACATTCCACCTCTCCA   64738        CA   CAC
                                 TGGAGAGG  GAG   GTT
                                 ||||||||  |||   |||
                                 ACCTCTCC  CTT   CAG
                                      AC   ACA
GAM1092  TMPRSS2  3'  GTCCCCAGCCTACCTCTCCA   18966        C  A  ACGTTC
                                 TGGAGAGG AG GC     GAC
                                 |||||||| || ||     |||
                                 ACCTCTCC TC CG     CTG
                                      A  _  ACCC__
GAM1092  ZNFN2A1  3'  TCGAAGCATCTGCCTCCCA   60742     A       _  ACG
                                 TGG GAGGCAGA GC   TTCGA
                                 ||| |||||||| ||   |||||
                                 ACC CTCCGTCT CG   AAGCT
                                   _       A  ___
GAM1092  CALN1    3'  AGCTGCGCCCCACCTTTCCA   48854        CAGA__   C
                                 TGGAGAGG     GCA GTT
                                 ||||||||     ||| |||
                                 ACCTTTCC     CGT CGA
                                      ACCCCG  _
GAM1092  FLJ10415 3'  AGTTGGGAGCCCCTACCTCTCC 36094        C  A_  ACG
             A                   TGGAGAGG AG  GC   TTCGACT
                                 |||||||| ||  ||   |||||||
                                 ACCTCTCC TC  CG   GGGTTGA
                                      A  CC  A__
GAM1092  FLJ13195 3'  AATGTACACTTACCTCTCCA   43257        CA   C__
                                 TGGAGAGG  GAG   ACGTT
                                 ||||||||  |||   |||||
                                 ACCTCTCC  TTC   TGTAA
                                      A_   ACA
GAM1092  FLJ14249 3'  GTCAGGCCCTGCCTCTCCA   42407          A  ACGTTC
                                 TGGAGAGGCAG GC     GAC
                                 ||||||||||| ||     |||
                                 ACCTCTCCGTC CG     CTG
                                       C  GA____
GAM1092  FLJ14249 3'  GTCAGGCCCTGCCTCTCCA   55214          A  ACGTTC
                                 TGGAGAGGCAG GC     GAC
                                 ||||||||||| ||     |||
                                 ACCTCTCCGTC CG     CTG
                                       C  GA____
GAM1092  FLJ23112 3'  AACGCCTCTGCTCTGCCTTCCC 46246     AG        ____
             A                   TGG  AGGCAGAGCA   CGTT
                                 |||  ||||||||||   ||||
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                                ACC  TCCGTCTCGT    GCAA
                                  CT         CTCC
GAM1092  FLJ23584  3'  TGATTCTACTCTGCCTCCCA  44743     A        CACGT
                                TGG GAGGCAGAG    TCG
                                ||| |||||||||    |||
                                ACC CTCCGTCTC    AGT
                                  _        ATCTT
GAM1092  KIAA0084  3'  GTGCTCCGCCTCCCA       68144     A    A
                                TGG GAGGC GAGCAC
                                ||| ||||| ||||||
                                ACC CTCCG CTCGTG
                                  _    C
GAM1092  KIAA0872  3'  TCGAACATGGCCTCCCC     30074     A    AGAG  C
                                GG GAGGC    CA GTTCGA
                                || |||||    || ||||||
                                CC CTCCG    GT CAAGCT
                                 C     _____  A
GAM1092  KIAA0953  3'  TGTGCTCCACCTCTTCA     66792         CA
                                TGGAGAGG  GAGCACG
                                ||||||||  |||||||
                                ACTTCTCC  CTCGTGT
                                     AC
GAM1092  MGC10812  3'  GTGCCTGCCTCTCCA       48669           A
                                TGGAGAGGCAG GCAC
                                |||||||||||  ||||
                                ACCTCTCCGTC CGTG
                                                _
GAM1092  NIR3      3'  AGGTGGGCAGCCTGCCCCCCCA 66237     AGA    A  AC    A
                                TGG   GGCAG GC  GTTCG CT
                                |||   ||||| ||  ||||| ||
                                ACC   CCGTC CG  CGGGT GA
                                  CCC     _ A_    G
GAM1092  SCYD1     3'  CGGGCTCTGCCTCCCA      90929     A         A
                                TGG GAGGCAGAGC CG
                                ||| ||||||||||  ||
                                ACC CTCCGTCTCG GC
                                  _         G
GAM1092  SLC38A5   5'  ACTCTCTCTGCCCCTTCA    53190       A      CAC
                                TGGAG GGCAGAG   GT
                                ||||| |||||||   ||
                                ACTTC CCGTCTC   CA
                                   C       TCT
GAM1092  LOC146823 3'  TGCAGTCCGCCTCTCCA     83803          A __
                                TGGAGAGGC GA  GCA
                                |||||||||  ||  |||
                                ACCTCTCCG CT  CGT
                                      C  GA
GAM1092  LOC148930 3'  AACTGCCCTCCTCTCCA     79088         C  A   C
                                TGGAGAGG AG GCA GTT
                                ||||||||  || ||| |||
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                                ACCTCTCC TC CGT CAA
                                     _ C  _
GAM1092  LOC166983 5'  AGTCGAGCTAGCCCCACCTCTC 87262       CAGA  AC
                                GAGAGG   GC  GTTCGACT
                                ||||||   ||  ||||||||
                                CTCTCC   CG  CGAGCTGA
                                   ACCC  AT
GAM1092  LOC253842 3'  CGGTGGCCCTGCCTCTCC    97385         A  ACGT
                                GGAGAGGCAG GC   TCG
                                |||||||||| ||   |||
                                CCTCTCCGTC CG   GGC
                                      C  GT__
GAM1092  LOC255452 3'  TCGCACACACCCTGCCTTCCA  97546     G     AGCAC  T
                                TGGA AGGCAG    GT CGA
                                |||| ||||||    || |||
                                ACCT TCCGTC    CA GCT
                                  _    CCACA  C
GAM1092  LOC256639 5'  CGCTGCTCTCCGCCTCTCC   96218        __    _
                                GGAGAGGC  AGAGCA CG
                                ||||||||  |||||| ||
                                CCTCTCCG  TCTCGT GC
                                     CC     C
GAM1092  LOC51161  3'  GTCCCGTGCCCAGCCTCTCCA  32516         AGA    TTC
                                TGGAGAGGC   GCACG   GAC
                                |||||||||   |||||   |||
                                ACCTCTCCG   CGTGC   CTG
                                      ACC    C__
GAM1093  C1orf1    3'  GCCTAGGCGACAGAGTGAGAC  6862      TG      A
                                GTCT  TTCTGTC CCTAGGC
                                ||||  ||||||| |||||||
                                CAGA  GAGACAG GGATCCG
                                  GT      C
GAM1093  DMC1      3'  GCCTAGGTGACAGAGTGAGACT 22974      TG
                                AGTCT  TTCTGTCACCTAGGC
                                |||||  |||||||||||||||
                                TCAGA  GAGACAGTGGATCCG
                                   GT
GAM1093  ENPP3     3'  GCCTGGGTGACAGAGCAAGACT 17225
                                AGTCTTGTTCTGTCACCTAGGC
                                |||||||||||||||||||||
                                TCAGAACGAGACAGTGGGTCCG

GAM1093  FPR1      5'  CCTAGAACTACCCAGAGCAAGA 8958          TCAC___
            C                   GTCTTGTTCTG      CTAGG
                                ||||||||||       |||||
                                CAGAACGAGAC      GATCC
                                      CCATCAA
GAM1093  IL12B     3'  GCCTAGGTGACAGAATGAGAC  9324      TG
                                GTCT  TTCTGTCACCTAGGC
                                ||||  ||||||||||||||
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                                CAGA  AAGACAGTGGATCCG
                                  GT
GAM1093  KCNK3    3'  GCCTAGGTGACATAGTGAGAC  9550      TG  C
                                GTCT  TT TGTCACCTAGGC
                                ||||  || ||||||||||||
                                CAGA  GA ACAGTGGATCCG
                                  GT  T
GAM1093  MHC2TA   3'  GCCTAGGTGACAGAGTGAGACT 4174       TG
                                AGTCT  TTCTGTCACCTAGGC
                                |||||  ||||||||||||||||
                                TCAGA  GAGACAGTGGATCCG
                                  GT
GAM1093  NCOA6    5'  GCCCAGGCAACAGAGCGTGACT 25967      T      CA  A
                                AGTC TGTTCTGT  CCT GGC
                                ||||  ||||||||  |||  |||
                                TCAG GCGAGACA  GGA CCG
                                  T       AC  C
GAM1093  NKX3A    3'  CCCAAATAGAACAAGATGC    20501     G        CACCTA
                                GCA TCTTGTTCTGT     GG
                                |||  ||||||||||      ||
                                CGT AGAACAAGATA     CC
                                 _         AAC___
GAM1093  OGG1     5'  GCCTAGGCGACAGAGTGAGACT 33660      TG      A
                                AGTCT  TTCTGTC CCTAGGC
                                |||||  |||||||  |||||||
                                TCAGA  GAGACAG GGATCCG
                                  GT      C
GAM1093  OGG1     5'  GCCTAGGCGACAGAGTGAGACT 33666      TG      A
                                AGTCT  TTCTGTC CCTAGGC
                                |||||  |||||||  |||||||
                                TCAGA  GAGACAG GGATCCG
                                  GT      C
GAM1093  OGG1     5'  GCCTAGGCGACAGAGTGAGACT 10330      TG      A
                                AGTCT  TTCTGTC CCTAGGC
                                |||||  |||||||  |||||||
                                TCAGA  GAGACAG GGATCCG
                                  GT      C
GAM1093  RBBP5    3'  GCCTAGGTGACAGAATGAGACT 17336      TG
                                AGTCT  TTCTGTCACCTAGGC
                                |||||  |||||||||||||||
                                TCAGA  AAGACAGTGGATCCG
                                  GT
GAM1093  ZNF137   3'  GCCTAGGCAACATAGTAAGAC  12863       C   CA
                                GTCTTGTT TGT  CCTAGGC
                                ||||||||  |||  |||||||
                                CAGAATGA ACA  GGATCCG
                                     T  AC
GAM1093  C13orf1  3'  GCCTAGGCAACAGAGTGAGACT 39970      TG     CA
                                AGTCT  TTCTGT  CCTAGGC
                                |||||  ||||||  |||||||
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                                TCAGA  GAGACA  GGATCCG
                                   GT     AC
GAM1093  C20orf106 3'  GCCCAGGTGACAGAGTGAGACT 55056      TG         A
                                AGTCT  TTCTGTCACCT GGC
                                |||||  |||||||||| |||
                                TCAGA  GAGACAGTGGA CCG
                                   GT          C
GAM1093  C21orf108 3'  GCCTAGGTGACAGAGCAAGACT 88722
                                AGTCTTGTTCTGTCACCTAGGC
                                |||||||||||||||||||||
                                TCAGAACGAGACAGTGGATCCG

GAM1093  CAMKK1   5'  GCCCAGGTTCCCAACAAGGCT  50172         CTGTC    A
                                AGTCTTGTT     ACCT GGC
                                |||||||||     |||| |||
                                TCGGAACAA     TGGA CCG
                                      CCCT_    C
GAM1093  CG012    5'  GCCCAGGTGACAGAGGGAGACT 83223       G          A
                                AGTCTT TTCTGTCACCT GGC
                                |||||| |||||||||| |||
                                TCAGAG GAGACAGTGGA CCG
                                   G          C
GAM1093  DIS3     3'  GCCTGGGTGACAGAACAAGACT 30230
            GT                    GCAGTCTTGTTCTGTCACCTAGGC
                                |||||||||||||||||||||||
                                TGTCAGAACAAGACAGTGGGTCCG

GAM1093  ELOVL1   3'  CCTAAGTGCCTCAGGACTGC   43058         TTCT T   C
                                GCAGTCTTG    G CAC TAGG
                                |||||||||    | ||| ||||
                                CGTCAGGAC    C GTG ATCC
                                      TC__ _   A
GAM1093  FLJ10803  3'  GCCTGGGCAACAGAGCAAGACT 36665             CA
            GC                    GCAGTCTTGTTCTGT  CCTAGGC
                                |||||||||||||||  |||||||
                                CGTCAGAACGAGACA  GGGTCCG
                                         AC
GAM1093  FLJ10830  3'  GCCTAGGCAACAAAACAAGACT 36720         C   CA
                                AGTCTTGTT TGT  CCTAGGC
                                |||||||||| |||  |||||||
                                TCAGAACAA ACA  GGATCCG
                                      A   AC
GAM1093  FLJ12448  3'  GCCTAAGCAATGGAGCAAGAC  43178           CACC
                                GTCTTGTTCTGT    TAGGC
                                ||||||||||||    |||||
                                CAGAACGAGGTA    ATCCG
                                       ACGA
GAM1093  FLJ13769  3'  GCCTAGGCAACATAGCGAGAC  46615         C   CA
                                GTCTTGTT TGT  CCTAGGC
                                |||||||| |||  |||||||
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                                CAGAGCGA ACA  GGATCCG
                                     T   AC
GAM1093  FLJ13848  3'  GCCTAGGCGACAGAGTGAGACT 45467      TG      A
                                AGTCT  TTCTGTC CCTAGGC
                                |||||  ||||||| |||||||
                                TCAGA  GAGACAG GGATCCG
                                   GT      C
GAM1093  FLJ20886  3'  GACAAAAACAAGACTGC     95108          C_
                                GCAGTCTTGTT  TGTC
                                ||||||||||  ||||
                                CGTCAGAACAA  ACAG
                                       AA
GAM1093  FLJ22009  3'  GCCTAGGCAACATAGTGAGAC  60284     TG  C   CA
                                GTCT  TT TGT  CCTAGGC
                                ||||  || |||  |||||||
                                CAGA  GA ACA  GGATCCG
                                   GT  T   AC
GAM1093  GNB4      3'  GCCTAGGCGACAGAGTGAGACT 41269      TG      A
                                AGTCT  TTCTGTC CCTAGGC
                                |||||  ||||||| |||||||
                                TCAGA  GAGACAG GGATCCG
                                   GT      C
GAM1093  IMAGE:4907098 3'  GCCTGGGCGACAGAGCAAGACT 91659              A
            GC                     GCAGTCTTGTTCTGTC CCTAGGC
                                |||||||||||||||| |||||||
                                CGTCAGAACGAGACAG GGGTCCG
                                          C
GAM1093  KIAA0247  5'  GCCTAGACCCGAGAAGACTGC  28401        G  CT   ACC
                                GCAGTCTT TT  GTC   TAGGC
                                |||||||| ||  |||   |||||
                                CGTCAGAA AG  CAG   ATCCG
                                     G  CC  ___
GAM1093  KIAA0391  3'  GCCTAGGTGACAGAGTGAGAC  27914      TG
                                GTCT  TTCTGTCACCTAGGC
                                ||||  ||||||||||||||
                                CAGA  GAGACAGTGGATCCG
                                   GT
GAM1093  KIAA0596  3'  CCTAGGTGACAAAGCTACACGC 62828    A  CTT   C
                                GC GT   GTT TGTCACCTAGG
                                || ||   ||| ||||||||||
                                CG CA   CGA ACAGTGGATCC
                                 _  CAT   A
GAM1093  KIAA0793  3'  GCCCAGGTTTGGACACAACT   29025     CT    TGTC    A
                                AGT  TGTTC    ACCT GGC
                                |||  |||||    |||| |||
                                TCA  ACAGG    TGGA CCG
                                  AC    TT__    C
GAM1093  KIAA0853  3'  CCTAGGTGACAGAGCAAGAC   30539
                                GTCTTGTTCTGTCACCTAGG
                                ||||||||||||||||||||
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                                CAGAACGAGACAGTGGATCC

GAM1093 KIAA0953 3' GCCTAGGTGACAGAGTGAGAC 66785     TG
                                GTCT  TTCTGTCACCTAGGC
                                ||||  ||||||||||||||
                                CAGA  GAGACAGTGGATCCG
                                  GT
GAM1093 KIAA1086 3' GCCCAGACAACAGAGTGAGAC 70747     TG    CAC  A
                                GTCT  TTCTGT   CT GGC
                                ||||  ||||||   || |||
                                CAGA  GAGACA   GA CCG
                                  GT     ACA  C
GAM1093 KIAA1630 3' GCCTGGGTGACAGAGCAAGACT 38031
                GC                GCAGTCTTGTTCTGTCACCTAGGC
                                ||||||||||||||||||||||||
                                CGTCAGAACGAGACAGTGGGTCCG

GAM1093 KIAA1826 5' GCCCAGGCCACGGAAACAAGAC 67217          _   CA   A
                TGC                GCAGTCTTGTT CTGT  CCT GGC
                                |||||||||||| ||||  ||| |||
                                CGTCAGAACAA GGCA  GGA CCG
                                      A   CC   C
GAM1093 MGC10765 3' GCCTAGGCGACAGAGCGAGACT 44302           A
                                AGTCTTGTTCTGTC CCTAGGC
                                |||||||||||||| |||||||
                                TCAGAGCGAGACAG GGATCCG
                                      C
GAM1093 NY-BR-1   3' GCCTAGGTGACAGAGTGAGACT 53794      TG
                                AGTCT  TTCTGTCACCTAGGC
                                |||||  ||||||||||||||||
                                TCAGA  GAGACAGTGGATCCG
                                  GT
GAM1093 SLC2A11   3' GCCTAGGTAACATAGTGAGAC  47965     TG  C   C
                                GTCT  TT TGT ACCTAGGC
                                ||||  || ||| ||||||||
                                CAGA  GA ACA TGGATCCG
                                  GT  T   A
GAM1093 TCEA3     3' GCCCAGGCAACACAGCAAGAC  88508       C   CA   A
                                GTCTTGTT TGT  CCT GGC
                                |||||||| |||  ||| |||
                                CAGAACGA ACA  GGA CCG
                                     C   AC   C
GAM1093 WBSCR21   3' GCCTAGGCAACAGAGCAAGACT 48477           CA
                                AGTCTTGTTCTGT  CCTAGGC
                                ||||||||||||  |||||||
                                TCAGAACGAGACA  GGATCCG
                                      AC
GAM1093 LOC116228 3' GCCTAGGTGACAGAGTGAGACT 73800      TG
                                AGTCT  TTCTGTCACCTAGGC
                                |||||  ||||||||||||||
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                                TCAGA  GAGACAGTGGATCCG
                                   GT
GAM1093  LOC122970 3'  GCCCAGGTAACACAGCGAGAC  74180        C   C    A
                                GTCTTGTT TGT ACCT GGC
                                |||||||| ||| |||| |||
                                CAGAGCGA ACA TGGA CCG
                                     C   A   C
GAM1093  LOC130026 3'  GCCTAGGCAACAGAGCAAGACT 56646            CA
                                AGTCTTGTTCTGT  CCTAGGC
                                |||||||||||||  |||||||
                                TCAGAACGAGACA  GGATCCG
                                         AC
GAM1093  LOC134265 3'  GCCTAAGCAAATAGCAAGAC   75174        C__   CACC
                                GTCTTGTT   TGT    TAGGC
                                ||||||||   |||    |||||
                                CAGAACGA   ACG    ATCCG
                                     TAA   A___
GAM1093  LOC145082 5'  GCCTAGGTGACAGACAGAGACT 83242       GT
                                AGTCTT  TCTGTCACCTAGGC
                                ||||||  ||||||||||||||
                                TCAGAG  AGACAGTGGATCCG
                                   AC
GAM1093  LOC145757 3'  GCCTAGGTGACAGAGCGAGACT 77463
                                AGTCTTGTTCTGTCACCTAGGC
                                ||||||||||||||||||||||
                                TCAGAGCGAGACAGTGGATCCG

GAM1093  LOC146901 3'  GCCTAGACAACAGAGCAAGAC  83841           CAC
                                GTCTTGTTCTGT   CTAGGC
                                ||||||||||||   ||||||
                                CAGAACGAGACA   GATCCG
                                       ACA
GAM1093  LOC147669 3'  GCCTAGGCAACATAGCAAGAC  84062        C   CA
                                GTCTTGTT TGT  CCTAGGC
                                |||||||| |||  |||||||
                                CAGAACGA ACA  GGATCCG
                                     T   AC
GAM1093  LOC148166 3'  GCCTAGGCGACGGGGCAAGACT 78694             A
                                AGTCTTGTTCTGTC CCTAGGC
                                |||||||||||||| |||||||
                                TCAGAACGGGGCAG GGATCCG
                                         C
GAM1093  LOC148293 3'  GCCTAGATGACAGAATGAGAC  78780      TG       C
                                GTCT  TTCTGTCA CTAGGC
                                ||||  |||||||| ||||||
                                CAGA  AAGACAGT GATCCG
                                   GT       A
GAM1093  LOC150135 3'  GCCCAGCATGCAGAACAAAAGC 79571    AGTC        CAC  A
                                GC    TTGTTCTGT   CT GGC
                                ||    |||||||||   || |||
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                                CG   AACAAGACG  GA CCG
                                 AA__       TAC  C
GAM1093  LOC151248 3'  GCCCAGGTAACAGAGTGAGACT 80187       TG    C   A
                GT                GCAGTCT  TTCTGT ACCT GGC
                                  |||||||  |||||| |||| |||
                                  TGTCAGA  GAGACA TGGA CCG
                                     GT     A   C
GAM1093  LOC152263 3'  TGACAGAGCAAGACTGC     85677
                                  GCAGTCTTGTTCTGTCA
                                  ||||||||||||||||
                                  CGTCAGAACGAGACAGT

GAM1093  LOC152316 3'  GCCTAGGCAACAGAGCGAGAC  85612          CA
                                  GTCTTGTTCTGT  CCTAGGC
                                  ||||||||||||  |||||||
                                  CAGAGCGAGACA  GGATCCG
                                        AC
GAM1093  LOC155054 3'  GCCTAGGCAACATTGCAAGACT 81274        TC   CA
                                  AGTCTTGT  TGT  CCTAGGC
                                  ||||||||  |||  |||||||
                                  TCAGAACG  ACA  GGATCCG
                                       TT   AC
GAM1093  LOC203378 3'  GCCTGGGCGACAGAACAAGACT 90607           A
                                  AGTCTTGTTCTGTC CCTAGGC
                                  |||||||||||||| |||||||
                                  TCAGAACAAGACAG GGGTCCG
                                        C
GAM1093  LOC219722 5'  GCCTGGGCAACAGAACAAGACT 93083          CA
                                  AGTCTTGTTCTGT  CCTAGGC
                                  ||||||||||||  |||||||
                                  TCAGAACAAGACA  GGGTCCG
                                        AC
GAM1093  LOC221490 3'  GCCTAGGCGACAGAGCAAGACT 93662           A
                                  AGTCTTGTTCTGTC CCTAGGC
                                  |||||||||||||| |||||||
                                  TCAGAACGAGACAG GGATCCG
                                        C
GAM1093  LOC253612 3'  CCCAGGCGACAGAACAA     96745         A   A
                                  TTGTTCTGTC CCT GG
                                  |||||||||| ||| ||
                                  AACAAGACAG GGA CC
                                       C   C
GAM1093  LOC253612 5'  GCCTAGGCAACAGAGTGAGACT 96749       TG     CA
                                  AGTCT  TTCTGT  CCTAGGC
                                  |||||  ||||||  |||||||
                                  TCAGA  GAGACA  GGATCCG
                                     GT     AC
GAM1093  LOC255177 3'  GCCTAGGCAACAGAGTGAGACT 96606       TG     CA
                                  AGTCT  TTCTGT  CCTAGGC
                                  |||||  ||||||  |||||||
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                                TCAGA  GAGACA  GGATCCG
                                   GT     AC
GAM1093  LOC257282 5'  GCCTGGGCAACAGAGCAAGACT 96401            CA
              GC                   GCAGTCTTGTTCTGT  CCTAGGC
                                |||||||||||||||  |||||||
                                CGTCAGAACGAGACA  GGGTCCG
                                         AC
GAM1093  LOC90072  5'  GCCTGGGTGACAGAACAAGACT 61297
                                AGTCTTGTTCTGTCACCTAGGC
                                |||||||||||||||||||||
                                TCAGAACAAGACAGTGGGTCCG

GAM1093  LOC90233  3'  GCCCAGGCAACAGAGTGAGACT 56384      TG     CA   A
                                AGTCT  TTCTGT  CCT GGC
                                |||||  ||||||  ||| |||
                                TCAGA  GAGACA  GGA CCG
                                   GT     AC   C
GAM1093  LOC91862  3'  GCCCAGGTGACAGAGCGAGACT 53467              A
                                AGTCTTGTTCTGTCACCT GGC
                                |||||||||||||||||| |||
                                TCAGAGCGAGACAGTGGA CCG
                                         C
GAM1093  LOC92299  3'  GCCTAGGTGACAGAGCGAGAC  68812
                                GTCTTGTTCTGTCACCTAGGC
                                |||||||||||||||||||||
                                CAGAGCGAGACAGTGGATCCG

GAM1094  ADH4     3'  TAAAAAGATTTTTACTGGA   5408         CGT
                                TCCAGTGG   TCTTTTTA
                                ||||||||   ||||||||
                                AGGTCATT   AGAAAAAT
                                     TTT
GAM1094  B4GALT2   3'  AGTAAAAAAACGTGAATGGA   47580     GTG    CT
                                TCCA   GCGTT  TTTTACT
                                ||||   |||||  |||||||
                                AGGT   TGCAA  AAAATGA
                                   AAG    __
GAM1094  CTBP1     3'  AAAAAGAAAACCTGAAGGAG   67941     AGT_  CG
                                CTCC    GG  TTCTTTTT
                                ||||    ||  ||||||||
                                GAGG    CC  AAGAAAAA
                                   AAGT  AA
GAM1094  ENPP3     3'  TAAAAAGAACAGCAGAGAG   17226     CAGTG  _
                                CTC     GC GTTCTTTTTA
                                |||     || ||||||||||
                                GAG     CG CAAGAAAAAT
                                  AGA__  A
GAM1094  F8       3'  TAAAAAAATAAGTCAGGAGGA  3732        AG   GTTC_
                                TCCTCC  TGGC    TTTTTA
                                ||||||  ||||    ||||||
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                                AGGAGG  ACTG    AAAAAT
                                   __   AATAA
GAM1094  GK      3'  AGCAAAAAGAATGCTAT    3911            A
                                GTGGCGTTCTTTTT CT
                                |||||||||||||| ||
                                TATCGTAAGAAAAA GA
                                      C
GAM1094  ID4     3'  GAAAAAAAGCCACCGGAGGA  7755       A    GTTC
                                TCCTCC GTGGC   TTTTT
                                |||||| |||||   |||||
                                AGGAGG CACCG   AAAAG
                                   C    AAA_
GAM1094  PITX1   3'  GAAAAAGACGTCGGAG     10599     AGT    T    A
                                CTCC   GGCGT CTTTTT C
                                ||||   ||||| |||||| |
                                GAGG   CTGCA GAAAAA G
                                  ___    _     C
GAM1094  TDG     3'  GAAAAAGATGCTGGAG     12191       GCGT     A
                                CTCCAGTG   TCTTTTT C
                                ||||||||   ||||||| |
                                GAGGTCGT   AGAAAAA G
                                     ____      C
GAM1094  XRCC2   3'  AGCAAAAAGAACAAAGCTGGAG 18318       GGC       A
            G                    CCTCCAGT   GTTCTTTTT CT
                                ||||||||   ||||||||| ||
                                GGAGGTCG   CAAGAAAAA GA
                                     AAA       C
GAM1094  DKFZP727M111 5'  AAAAGGAAAAGCCCTGAAG   31401    C   T   G_
                                CT CAG GGC  TTCTTTTT
                                || ||| |||  ||||||||
                                GA GTC CCG  AAGGAAAA
                                 A   _   AA
GAM1094  ELKS    3'  AGTGGTCAACGCCCTGGAAGA  30501    C    T    CTTT
                                TC TCCAG GGCGTT   TTACT
                                || ||||| ||||||   |||||
                                AG AGGTC CCGCAA   GGTGA
                                 A    _     CT__
GAM1094  FLJ10648 3'  AGCAAAAAGAACAAAGTCCTGG 36378       T  ___      A
            AGGA                   TCCTCCAG GGC   GTTCTTTTT CT
                                ||||||| |||   ||||||||| ||
                                AGGAGGTC CTG   CAAGAAAAA GA
                                     _   AAA       C
GAM1094  FLJ20151 3'  AAAGACCCTGGAGGA      34648       T  CGT
                                TCCTCCAG GG   TCTTT
                                |||||||| ||   |||||
                                AGGAGGTC CC   AGAAA
                                     _ ___
GAM1094  FLJ20435 3'  TAAAAAGAGCCATCTGGAGGA  35162        _   GT
                                TCCTCCAG TGGC  TCTTTTTA
                                |||||||| ||||  ||||||||
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                                AGGAGGTC ACCG  AGAAAAAT
                                    T   __
GAM1094  MDS024    3'  AAAAAGAATTGCCAAGGA    41522     AG    _
                                TCC  TGGCG TTCTTTTT
                                |||  ||||| ||||||||
                                AGG  ACCGT AAGAAAAA
                                  A_    T
GAM1094  ShrmL     5'  AGAGCGCCACTGAAGGA     40463     C
                                TCCT CAGTGGCGTTCT
                                |||| ||||||||||||
                                AGGA GTCACCGCGAGA
                                  A
GAM1094  SIAT8C    5'  TAAAAAAGCCCCACAGAGGA   31883      CA   C   C
                                TCCTC  GTGG GTT TTTTTA
                                |||||  |||| ||| ||||||
                                AGGAG  CACC CGA AAAAAT
                                   A_   C   _
GAM1094  VEST1     5'  AAAAAGATGCACTGGGGA    53678     T     G   T
                                TCC CCAGTG CGT CTTTTT
                                ||| |||||| ||| ||||||
                                AGG GGTCAC GTA GAAAAA
                                  _     _   _
GAM1094  ZFD25     5'  AAAAAGAGCCCTGGA       32573       T   GT
                                TCCAG GGC  TCTTTTT
                                ||||| |||  |||||||
                                AGGTC CCG  AGAAAAA
                                  _   __
GAM1094  LOC124626 3'  AGTAAGACCAAACCACTGGA   74313         CGTTCT
                                TCCAGTGG     TTTTACT
                                ||||||||     |||||||
                                AGGTCACC     AGAATGA
                                     AAACC_
GAM1094  LOC144577 3'  TAAAAAGAAGCCACAAAGAG   76902     CA_    G
                                CTC   GTGGC TTCTTTTTA
                                |||   ||||| |||||||||
                                GAG   CACCG AAGAAAAAT
                                  AAA    _
GAM1094  LOC145837 5'  AGCAAAAAGAACCAAAGAGGA  83542       CAG   CG       A
                                TCCTC   TGG  TTCTTTTT CT
                                |||||   |||  |||||||| ||
                                AGGAG   ACC  AAGAAAAA GA
                                   AA_   __       C
GAM1094  LOC151194 3'  TAAAAAAACTGGGGA       59215     T    GGCGTTC
                                TCC CCAGT      TTTTTA
                                ||| |||||      ||||||
                                AGG GGTCA      AAAAAT
                                  _    A_______
GAM1094  LOC154789 5'  AGTAAAATCTCAGGCCACTAGA 81131     C     GTTCT_
             G                   CTC AGTGGC     TTTTACT
                                ||| ||||||     |||||||
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                                GAG TCACCG     AAAATGA
                                  A     GACTCT
GAM1094  LOC197322 3'  AAAGACTCCACTGGAGGA    89736          C  T
                                TCCTCCAGTGG GT CTTT
                                |||||||||||  || ||||
                                AGGAGGTCACC CA GAAA
                                       T  _
GAM1094  LOC221596 3'  TAAAAACCTCACACTGGAGAGA 91980    _      GCGTTC
                                TC CTCCAGTG     TTTTTA
                                ||  ||||||||     ||||||
                                AG GAGGTCAC     AAAAAT
                                 A       ACTCC_
GAM1094  LOC91796  3'  AGCAAAAAGAACAAGGCTGGA  67208       GGC       A
                                TCCAGT   GTTCTTTTT CT
                                ||||||   |||||||||  ||
                                AGGTCG   CAAGAAAAA GA
                                    GAA       C
GAM1094  LOC92539  5'  TAAAAAGTGTCACTG      69638        TT
                                CAGTGGCG  CTTTTTA
                                ||||||||  |||||||
                                GTCACTGT  GAAAAAT
                                          __
GAM1095  CASP3     3'  ACATACTCCTTCCATCA     15095    C     A
                                TG ATGGAA GAGTATGT
                                ||  ||||||  ||||||||
                                AC TACCTT CTCATACA
                                 _     C
GAM1095  CASP3     3'  ACATACTCCTTCCATCA     52191    C     A
                                TG ATGGAA GAGTATGT
                                ||  ||||||  ||||||||
                                AC TACCTT CTCATACA
                                 _     C
GAM1095  MSL3L1    3'  AAGAATACTCAGATTTCCAT   54359        GAGTAT
                                ATGGAAA     GTATTCTT
                                |||||||     ||||||||
                                TACCTTT     CATAAGAA
                                    AGACT_
GAM1095  SACM1L    3'  GCATACTTTTCCACACA     25824    CA    A
                                TG  TGGAA GAGTATGT
                                ||  |||||  ||||||||
                                AC  ACCTT TTCATACG
                                 AC    _
GAM1095  SURF6     3'  TAAGAATACATACTCTTTCCAT 22192                  III
            GCA                    GCATGGAAAGAGTATGTATTCTT   A
                                ||||||||||||||||||||||  |
                                CGTACCTTTCTCATACATAAGAA   T
                                                 III
GAM1095  UCHL1     3'  AATATATACCCCCCCATGCA   14814        AAAGA
                                TGCATGG    GTATGTATT
                                |||||||    |||||||||
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                                ACGTACC    CATATATAA
                                    CCCC_
GAM1095  DYRK4    5'  AAGAATACGGTAAGCTTCCCA  64225     A   AG   _
                                TGG AAG  TAT GTATTCTT
                                ||| |||  ||| ||||||||
                                ACC TTC  ATG CATAAGAA
                                  C   GA   G
GAM1095  FLJ10276 3'  ACATACTCTGTCCATACA    35961    C    A
                                TG ATGGA AGAGTATGT
                                || ||||| |||||||||
                                AC TACCT TCTCATACA
                                 A    G
GAM1095  KIAA0678  3'  AAGAATATTTCCCTCTCCTGCA 66851      T   AA   TAT_
                                TGCA GGA  GAG    GTATTCTT
                                |||| |||  |||    ||||||||
                                ACGT CCT  CTC    TATAAGAA
                                  _  __   CCTT
GAM1095  SGKL     3'  AAGAACAAGCATCCCTTCCATG 25138         A_  _  A   AT
             TA                   TGCATGGAA  GA GT TGT  TCTT
                                |||||||||  || || |||  ||||
                                ATGTACCTT  CT CG ACA  AGAA
                                     CC  A  A   __
GAM1095  LOC148638 3'  CACTCTCTTTCCACGCA     78919     A        TA
                                TGC TGGAAAGAG  TG
                                ||| |||||||||  ||
                                ACG ACCTTTCTC  AC
                                  C         TC
GAM1095  LOC196385 3'  ATCTCTTTCCATACA       87654    C        T
                                TG ATGGAAAGAG AT
                                || ||||||||||  ||
                                AC TACCTTTCTC TA
                                 A         _
GAM1095  LOC221178 3'  ATACTCCTTCATGCA       93526         AA
                                TGCATGGA  GAGTAT
                                ||||||||  ||||||
                                ACGTACTT  CTCATA
                                     C_
GAM1095  LOC221405 3'  AGAATTGCTTTCCATGCA    93880           AGTATGT
                                TGCATGGAAAG      ATTCT
                                ||||||||||       |||||
                                ACGTACCTTTC      TAAGA
                                      GT_____
GAM1096  ADH1B    3'  CTTAGACATAAAGTAAAAT    72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM1096  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
```

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                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T _
GAM1096  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM1096  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                  CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM1096  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT         A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM1096  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM1096  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM1096  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM1096  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_    CG_
GAM1096  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM1096  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM1096  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
              G                   CATTTC        GTCTGAGAT
                                ||||||        |||||||||
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                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM1096  FLJ23510  3'  ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA   TCACTGTCTGAGAT
                                |||||||   ||||||||||||||
                                GTAAAGT   AGTGACAGACTCTA
                                   C__
GAM1096  KIAA0984  3'  TTTGTCCAGTGAAAATGAA   65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM1096  KLHL6     3'  ATCTCAGAGCAGGAAA      55299      A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _   G
GAM1096  NIR3      3'  GCAGTGAAAGTGCAAT      66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM1096  PORIMIN   3'  ATCTCAGAGGGCCAAAGTGAA  53598        CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM1096  PP35      3'  ATCTCAGACTGAAA       22814       CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM1096  PRTD-NY3  3'  CTCATTGCAATAAGTGAAATG  48148         TCAC   C_
                                CATTTCACTT    TGT  TGAG
                                ||||||||||    |||  ||||
                                GTAAAGTGAA    ACG  ACTC
                                      TA__   TT
GAM1096  SEP15     3'  TCCTACAGTAAGAGTGAAA    14934         C     CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A     TC
GAM1096  SFXN2     3'  CTCAGGGGAAAAAAGTGAAA   73941         CACTG
                                TTTCACTTT     TCTGAG
                                |||||||||     ||||||
                                AAAGTGAAA     GGACTC
                                     AAAGG
GAM1096  LOC149703 3'  ATCTCAGACAGCCGTTTGGAAA 84647      ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
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                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM1096  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM1096  LOC155004 3'  TCATTTAAGTGAAAGGAAA    81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM1096  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA

                                          _
GAM1097  IL12B     3'  GAAACCTGACAATGCAA     9323          _
                                TTGCATTGT AGGTTTC
                                ||||||||| |||||||
                                AACGTAACA TCCAAAG
                                     G
GAM1097  KCNA4     3'  ATGCAAATGATCCAATGCA    9508         TAGGTT
                                TGCATTG     TCATTTGCAT
                                |||||||     ||||||||||
                                ACGTAAC     AGTAAACGTA
                                    CT_____
GAM1097  MAP3K8    3'  TGCAAATAAAACCCAAT     17792      TA     C
                                ATTG  GGTTT ATTTGCA
                                ||||  ||||| |||||||
                                TAAC  CCAAA TAAACGT
                                  __     A
GAM1097  NSF       3'  ATGCAAATGAAGGAATGCAAT  63069       GG_
                                ATTGTA   TTTCATTTGCAT
                                ||||||   ||||||||||||
                                TAACGT   GAAGTAAACGTA
                                   AAG
GAM1097  FLJ22332  5'  TGAAACCTACATTGCAA     45304      T
                                TTGCA TGTAGGTTTCA
                                ||||| ||||||||||
                                AACGT ACATCCAAAGT
                                  T
GAM1097  HTMP10    3'  CAAATGAAACTTATGCAG     52608      TTG
                                TTGCA   TAGGTTTCATTTG
                                |||||   |||||||||||||
                                GACGT   ATTCAAAGTAAAC
                                    ____
GAM1097  LOC118611 3'  CAAATGGAAATAAATGCAA    75468        GTAGG
                                TTGCATT     TTTCATTTG
                                |||||||     |||||||||
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                                AACGTAA    AAGGTAAAC
                                   ATA__
GAM1097  LOC133418 3'  AAACCTCACTATGCAA      75088       T  _
                                TTGCAT GT AGGTTT
                                |||||| || ||||||
                                AACGTA CA TCCAAA
                                   T  C
GAM1097  LOC151414 3'  TGAAACCTACAATCAA      80242     C
                                TTG ATTGTAGGTTTCA
                                ||| ||||||||||||
                                AAC TAACATCCAAAGT
                                  _
GAM1098  ARNT2    3'  AAACAACCCGTGCATCCCTGC  29450     A    TTTTA
                                GTA GGAT    GGGTTGTTT
                                ||| ||||    |||||||||
                                CGT CCTA    CCCAACAAA
                                  C   CGTG_
GAM1098  LCT      3'  AACCGTAAAAATCCTT      9697          G
                                AAGGATTTTTA GGTT
                                |||||||||| ||||
                                TTCCTAAAAAT CCAA
                                      G
GAM1098  RPL15    3'  AAACAACCCTAAAAATCCTTAC 11382
                                GTAAGGATTTTTAGGGTTGTTT
                                |||||||||||||||||||||
                                CATTCCTAAAAATCCCAACAAA

GAM1098  FBXO30   3'  AACTAAAAAAATCCTGAC    49573    A       AG
                                GT AGGATTTTT  GGTT
                                || |||||||||  ||||
                                CA TCCTAAAAA  TCAA
                                 G        AA
GAM1098  KIAA0494  3'  AACAACCCTTACTTAC      28736      GATTTTT
                                GTAAG      AGGGTTGTT
                                |||||      |||||||||
                                CATTC      TCCCAACAA
                                   AT_____
GAM1098  PRO0641   5'  AAACAACCCCAAAACTTG    26210     GAT    A
                                TAAG   TTTT GGGTTGTTT
                                ||||   |||| |||||||||
                                GTTC   AAAA CCCAACAAA
                                  ___    C
GAM1098  SMT3H2    3'  AACAACATAAAAATCCTTGC   22670          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM1098  LOC120103 3'  AACCTATGAAAAATCCTTGC   74002          A__
                                GTAAGGATTTTT   GGGTT
                                ||||||||||||   |||||
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                                CGTTCCTAAAAA  TCCAA
                                      GTA
GAM1098  LOC129831 3'  AAACAACCCCAATGTCC     74889     TT  A
                                GGAT  TT GGGTTGTTT
                                ||||  || |||||||||
                                CCTG  AA CCCAACAAA
                                  T_  C
GAM1098  LOC133088 5'  AAACAAAATAGAAAAATCCCTG 75075     A      AGGG_
            C                    GTA GGATTTTT    TTGTTT
                                ||| ||||||||    ||||||
                                CGT CCTAAAAA    AACAAA
                                  C       GATAA
GAM1098  LOC148089 3'  GGCCCTAAAAATTCCTAC    78637     A
                                GTA GGATTTTTAGGGTT
                                ||| ||||||||||||||
                                CAT CTTAAAAATCCCGG
                                  C
GAM1098  LOC154547 3'  AACAACATAAAAATCCTTGC   76050          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM1098  LOC158104 3'  ACAGCCAAAAATCCTTA     60313          AG
                                TAAGGATTTTT  GGTTGT
                                ||||||||||  ||||||
                                ATTCCTAAAAA  CCGACA
                                      __
GAM1098  LOC205880 5'  AAACAACCATCATCCTGAC   90709    A    TTTTAG
                                GT AGGAT     GGTTGTTT
                                || |||||     ||||||||
                                CA TCCTA     CCAACAAA
                                 G    CTA___
GAM1098  LOC221561 3'  AACAACATAAAAATCCTTGC  92130          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM1098  LOC257591 3'  AACAACATAAAAATCCTTGC  97840          GG
                                GTAAGGATTTTTA  GTTGTT
                                ||||||||||||  ||||||
                                CGTTCCTAAAAAT  CAACAA
                                      A_
GAM1098  LOC51145  3'  AGCTAAAATCCTTAC       32393          TAG
                                GTAAGGATTTT   GGTT
                                ||||||||||   ||||
                                CATTCCTAAAA   TCGA
                                      ___
GAM1099  ABR      3'  CTGGGAAGCAAAGGCACAGGC  6573       _   CCC   G
                                GCCTG GCCT   TGT TCCCAG
                                ||||| ||||   ||| ||||||
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                                CGGAC CGGA   ACG AGGGTC
                                  A    A__   A
GAM1099 ABR     3' CTGGGAAGCAAAGGCACAGGC  41725      _   CCC   G
                                GCCTG GCCT   TGT TCCCAG
                                ||||| ||||   ||| ||||||
                                CGGAC CGGA   ACG AGGGTC
                                  A    A__   A
GAM1099 APOL1   3' GCACTTTGGGAGGCCAAGG   13345    _      T__
                                CCT GGCCTCCC   GTGT
                                ||| ||||||||   ||||
                                GGA CCGGAGGG   CACG
                                 A       TTT
GAM1099 ARHGAP6 3' GGACCAGGGAGGCCAAGC    6766    C        T
                                GC TGGCCTCCCTG GTCC
                                || |||||||||| ||||
                                CG ACCGGAGGGAC CAGG
                                 A         _
GAM1099 CENTD2  5' GGGGCCAGGGGCCAGGC     57557        TC    T
                                GCCTGGCC  CCTG GTCCC
                                ||||||||  |||| |||||
                                CGGACCGG  GGAC CGGGG
                                            __   _
GAM1099 CLCN4   5' ATCTGAAAGCGGAAGGCCAGGC 8442         CC    GTCC
                                GCCTGGCCT  CTGT    CAGAT
                                |||||||||  ||||    |||||
                                CGGACCGGA  GGCG    GTCTA
                                     A_    AAA_
GAM1099 CSF3R   5' GACCAAGGAGGCCAAGC     5669     C      C  T
                                GC TGGCCTCC TG GTC
                                || |||||||| || |||
                                CG ACCGGAGG AC CAG
                                 A       A  _
GAM1099 GAS11   3' CTGAGATGGAGAGGCCAGG   7624         _ TGT   C
                                CCTGGCCTC CC   GTC CAG
                                ||||||||| ||   ||| |||
                                GGACCGGAG GG   TAG GTC
                                     A  ___   A
GAM1099 GCK     3' CTGGGCCAAAAGGGCAGGC   3869       G   CCCTG  T
                                GCCTG CCT    TG CCCAG
                                ||||| |||    || |||||
                                CGGAC GGA    AC GGGTC
                                  G   AA___  C
GAM1099 HOXB9   3' CTGTAGACAGGAAAGCCAGGC 43777       CTC    GTCC
                                GCCTGGC   CCTGT   CAG
                                |||||||   |||||   |||
                                CGGACCG   GGACA   GTC
                                    AAA    GAT_
GAM1099 ITPR2   3' ATCTGGGGGAATAAAAAGCCA 9448      CTCCC   G_
                                TGGC    TGT  TCCCAGAT
                                ||||    |||  ||||||||
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                                ACCG    ATA  GGGGTCTA
                                  AAAA_  AG
GAM1099  LDHB    5'  ATCTGGGACACCATCTTGACCA 9701     CCTCCCT_
                                TGG      GTGTCCCAGAT
                                |||      ||||||||||
                                ACC      CACAGGGTCTA
                                  AGTTCTAC
GAM1099  MAP1A   3'  ATCTGGGAGGTGGAAGCCAGGC 9896       C  _ GTG
                                GCCTGGC TCC CT   TCCCAGAT
                                ||||||| ||| ||   ||||||||
                                CGGACCG AGG GG   AGGGTCTA
                                    A  T ___
GAM1099  MTMR7   3'  CTGAAACACAACCCCATCCAGG 69152      CCTCCC_   CC
            T                    GCCTGG     TGTGT  CAG
                                ||||||     |||||  |||
                                TGGACC     ACACA  GTC
                                   TACCCCA    AA
GAM1099  PTPRE   5'  GACACACAGAGGCCAGGC    55237        CC
                                GCCTGGCCTC  TGTGTC
                                ||||||||||  ||||||
                                CGGACCGGAG  ACACAG
                                     AC
GAM1099  RAMP1   3'  GGCTGCAGGGTGAGGCCAGGC  19584        __     T
                                GCCTGGCCT  CCCTGTG CC
                                |||||||||  ||||||| ||
                                CGGACCGGA  GGGACGT GG
                                     GT      C
GAM1099  SLC6A12  5'  CTGGAGGCCAGAGGCTAGGC   11735        CC  T  _
                                GCCTGGCCTC  TG GTC CCAG
                                ||||||||||  || ||| ||||
                                CGGATCGGAG  AC CGG GGTC
                                     __  _  A
GAM1099  SUFU    3'  GATCCTGCAGGGGCCAGGC   32412       TC   ___
                                GCCTGGCC  CCTGT   GTC
                                ||||||||  |||||   |||
                                CGGACCGG  GGACG   TAG
                                    __    TCC
GAM1099  TDG     5'  ACATTGGGAGGCCAAGG     12185    _      T
                                CCT GGCCTCCC GTGT
                                ||| |||||||| ||||
                                GGA CCGGAGGG TACA
                                  A       T
GAM1099  TEP1    3'  ACCCAGAGGAGGCCGGGC    23043         _  T
                                GCCTGGCCTCC CTG GT
                                |||||||||||| ||| ||
                                CGGGCCGGAGG GAC CA
                                     A  C
GAM1099  TM7SF2  5'  CTGGGGCAAAGGCTAAGC    12331    C     CCCTG
                                GC TGGCCT    TGTCCCAG
                                || ||||||    ||||||||
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                                CG ATCGGA    ACGGGGTC
                                 A     A____
GAM1099  VCY      5'  ACACAGGGAGGCCAGGC     16258
                                GCCTGGCCTCCCTGTGT
                                |||||||||||||||||
                                CGGACCGGAGGGACACA

GAM1099  C20orf39  3'  ATCTAGGATGGGGAGGCAGGC  46042      G     GT   C
                                GCCTG CCTCCCT  GTCC AGAT
                                ||||| |||||||  |||| ||||
                                CGGAC GGAGGGG  TAGG TCTA
                                  _     __   A
GAM1099  CMG1     5'  CTGGGACAGCAAGACCAGGT   47020       C  CCC  _
                                GCCTGG CT   TG TGTCCCAG
                                |||||| ||   || ||||||||
                                TGGACC GA   AC ACAGGGTC
                                   A  ___  G
GAM1099  CRA      3'  ATCTGGGACCCCAGATCAGGC  21969      GC  CCCTGT
                                GCCTG  CT    GTCCCAGAT
                                |||||  ||    |||||||||
                                CGGAC  GA    CAGGGTCTA
                                  TA  CCC___
GAM1099  FBXL6    3'  CTGGGACACCTCAGCCAG    24078      CTCCCT
                                CTGGC    GTGTCCCAG
                                |||||    |||||||||
                                GACCG    CACAGGGTC
                                  ACTC__
GAM1099  FBXL6    3'  CTGGGACACCTCAGCCAG    44646      CTCCCT
                                CTGGC    GTGTCCCAG
                                |||||    |||||||||
                                GACCG    CACAGGGTC
                                  ACTC__
GAM1099  FLJ11106  3'  ATCTGGGGACAAAGGTCAAGC  37053    C    CCC   G
                                GC TGGCCT   TGT TCCCAGAT
                                || ||||||   ||| ||||||||
                                CG ACTGGA   ACA GGGGTCTA
                                 A     A__   _
GAM1099  FLJ13063  3'  GGGAGCGAGAAGCCAAGGC   71830     _  C  CC   G
                                GCCT GGC TC  TGT TCCC
                                |||| ||| ||  ||| ||||
                                CGGA CCG AG  GCG AGGG
                                  A  A  A_   _
GAM1099  FLJ13114  3'  CTGAAACAGGCCAGGT     44597       CCCTGT  CC
                                GCCTGGCCT    GT  CAG
                                |||||||||    ||  |||
                                TGGACCGGA    CA  GTC
                                     _______  AA
GAM1099  FLJ14721  3'  CACAGGGGAGCCAGGC     51576       CT
                                GCCTGGC  CCCTGTG
                                |||||||  |||||||
```

```
                                CGGACCG  GGGACAC
                                    AG
GAM1099  FLJ20203  3'  ATCTGGAGAGCAGGAGGCCAGG 34732          C   G  _
                                CCTGGCCTCC TGT TC CCAGAT
                                |||||||||| ||| || ||||||
                                GGACCGGAGG ACG AG GGTCTA
                                     _  _  A
GAM1099  FLJ20234  5'  CTGGAAGGAGAGGCCAGGC   34777          _  GTGTC
                                GCCTGGCCTC CCT    CCAG
                                |||||||||| |||    ||||
                                CGGACCGGAG GGA    GGTC
                                     A  A____
GAM1099  FLJ20257  5'  ATCCGGCCTTCAAGAGGCGCAG 38993       _    CC  TGTC  A
           GC                    GCCTG GCCTC  TG   CC GAT
                                ||||| |||||  ||   || |||
                                CGGAC CGGAG  AC   GG CTA
                                   G    A_  TTCC  C
GAM1099  HOMER-3   5'  CTGGCAGGGGGCCA       16713       T    TGTC
                                TGGCC CCCTG   CCAG
                                ||||| |||||   ||||
                                ACCGG GGGAC   GGTC
                                  _   _____
GAM1099  IMP-1     3'  ATCCGGGACACCTGGGCCGGGC 21565         CCCT      A
                                GCCTGGCCT   GTGTCCC GAT
                                |||||||||   ||||||| |||
                                CGGGCCGGG   CACAGGG CTA
                                     TC__      C
GAM1099  KIAA0040  5'  ATCTGGGACACCATCTTGACCA 27777     CCTCCCT_
                                TGG       GTGTCCCAGAT
                                |||       ||||||||||
                                ACC       CACAGGGTCTA
                                  AGTTCTAC
GAM1099  KIAA0557  3'  ACCCAGGAAGACCAGGC     77985       C  C    T
                                GCCTGG CT CCTG GT
                                |||||| || |||| ||
                                CGGACC GA GGAC CA
                                   A  A   C
GAM1099  KIAA1719  3'  CAGAGGCCAGGGCCAGGC     68155         C__   G
                                GCCTGGCCT   CCT TG
                                |||||||||   ||| ||
                                CGGACCGGG   GGA AC
                                     ACC   G
GAM1099  MGC26847  3'  ACACTGGGAGGCCAGGC     58762           T
                                GCCTGGCCTCCC GTGT
                                |||||||||||| ||||
                                CGGACCGGAGGG CACA
                                       T
GAM1099  MGC3178   3'  CTGGGGTGACAAGACCAG    47985      C  CCC  _ GT
                                CTGG CT   TG T  CCCAG
                                |||| ||   || |  |||||
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                                GACC GA   AC G  GGGTC
                                  A ___  A TG
GAM1099  MGC5139   5'  CTGGCCCCAGGAAGCCAAGGC  74105     _  CTC   TGTC
                                GCCT GGC   CCTG   CCAG
                                |||| |||   ||||   ||||
                                CGGA CCG   GGAC   GGTC
                                  A  AA_   CCC_
GAM1099  MRF-1     3'  GGACACCCGGGCCATGC     71326    C     CCCT
                                GC TGGCCT   GTGTCC
                                || ||||||   ||||||
                                CG ACCGGG   CACAGG
                                 T    CC__
GAM1099  MRPS10    3'  GCACAAAGCAGGCCAGGC    36293        CCC_
                                GCCTGGCCT   TGTGT
                                |||||||||   |||||
                                CGGACCGGA   ACACG
                                     CGAA
GAM1099  PRO0899   3'  ACCCAGGAACGAGGCCAGGC  37690         ___   T
                                GCCTGGCCTC  CCTG GT
                                ||||||||||  |||| ||
                                CGGACCGGAG  GGAC CA
                                     CAA   C
GAM1099  RAB40C    3'  CTGGGGGCCTCGGGAGGCTAGG 40978          TGT   _
           C                     GCCTGGCCTCCC  GTCCC AG
                                ||||||||||||  ||||| ||
                                CGGATCGGAGGG  CGGGG TC
                                      CTC    G
GAM1099  RNPS1     3'  CTGGGATGGTGGCCAGGC    54579       T  CTGT
                                GCCTGGCC CC   GTCCCAG
                                |||||||| ||   |||||||
                                CGGACCGG GG   TAGGGTC
                                     T _____
GAM1099  RNPS1     3'  CTGGGATGGTGGCCAGGC    22007       T  CTGT
                                GCCTGGCC CC   GTCCCAG
                                |||||||| ||   |||||||
                                CGGACCGG GG   TAGGGTC
                                     T _____
GAM1099  SLC19A3   3'  GCAATTTGGGAGGCCAAGG   47488    _      TG__
                                CCT GGCCTCCC   TGT
                                ||| ||||||||   |||
                                GGA CCGGAGGG   ACG
                                  A       TTTA
GAM1099  TNKS2     5'  ATCCGGTGACAGCAGGGAGCCA 47450    C   C    _   _ A
           AGC                    GC TGGC TCCCTG TGTC CC GAT
                                || |||| |||||| |||| || |||
                                CG ACCG AGGGAC ACAG GG CTA
                                 A   _     G   T  C
GAM1099  LOC112970 3'  ATCTGAGGCGTGGGAGAGCAG  56534     GC  _  TG   C
                                CTG  CTC CC  TGTC CAGAT
                                |||  ||| ||  |||| |||||
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                                GAC  GAG GG  GCGG GTCTA
                                  __  A  GT   A
GAM1099  LOC126823 5'  ACCCAGCTAGGGGCCAGGC   74572         C__  T
                                GCCTGGCCTC  CTG GT
                                ||||||||||  ||| ||
                                CGGACCGGGG  GAC CA
                                      ATC  C
GAM1099  LOC138307 5'  GCCACGGAGGCCAGGC     75314          C  T
                                GCCTGGCCTCC TG GT
                                |||||||||||| || ||
                                CGGACCGGAGG AC CG
                                      C  _
GAM1099  LOC143286 5'  ATCTGGGATCTGAGGTCAGGC  82944          CCTGT
                                GCCTGGCCTC   GTCCCAGAT
                                ||||||||||   |||||||||
                                CGGACTGGAG   TAGGGTCTA
                                      TC___
GAM1099  LOC143916 5'  CTGGCATGGGAGCCAGGC    76642       C   T  TC
                                GCCTGGC TCCC GTG  CCAG
                                ||||||| |||| |||  ||||
                                CGGACCG AGGG TAC  GGTC
                                   _   _  __
GAM1099  LOC144017 5'  CGCCGGGAGGCCAGGC     83003          T
                                GCCTGGCCTCCC GTG
                                |||||||||||| |||
                                CGGACCGGAGGG CGC
                                      C
GAM1099  LOC145453 3'  ATCTGAGCACATTGGGAGGCCA 77134    _     __   CC
            AGG                   CCT GGCCTCCC  TGTGT  CAGAT
                                ||| ||||||||  |||||  |||||
                                GGA CCGGAGGG  ACACG  GTCTA
                                  A       TT    A_
GAM1099  LOC146669 5'  ATCTGAGGACATGGACACCA   78051    CC   CT    _
                                TGG  TCC  GTGTCC CAGAT
                                |||  |||  |||||| |||||
                                ACC  AGG  TACAGG GTCTA
                                  AC   __     A
GAM1099  LOC146669 5'  ATCTGAGGACATGGACACCA   78052    CC   CT    _
                                TGG  TCC  GTGTCC CAGAT
                                |||  |||  |||||| |||||
                                ACC  AGG  TACAGG GTCTA
                                  AC   __     A
GAM1099  LOC146669 5'  ATCTGAGGATATGGACACCA   78053    CC   CT    _
                                TGG  TCC  GTGTCC CAGAT
                                |||  |||  |||||| |||||
                                ACC  AGG  TATAGG GTCTA
                                  AC   __     A
GAM1099  LOC146754 3'  CTAGGACTGAGGCCGG      78092        CCTGT   C
                                CTGGCCTC    GTCC AG
                                ||||||||    |||| ||
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                                GGCCGGAG    CAGG TC
                                    T____   A
GAM1099  LOC148089 3'  ATCTGGGGTCACAGGGGACCAA 78625    C   C T     _
              GC                   GC TGG C CCCTGTG TCCCAGAT
                                   || ||| | ||||||| ||||||||
                                   CG ACC G GGGACAC GGGGTCTA
                                    A  A _     T
GAM1099  LOC149171 3'  ACACAGGAAGGACAGGC     79214      G   C
                                   GCCTG CCT CCTGTGT
                                   ||||| ||| |||||||
                                   CGGAC GGA GGACACA
                                      A  A
GAM1099  LOC149319 5'  GGACACAGGAGAAACCAGGC   79298       CC  _
                                   GCCTGG  TC CCTGTGTCC
                                   ||||||  || |||||||||
                                   CGGACC  AG GGACACAGG
                                       AA  A
GAM1099  LOC150197 3'  TGCAGAGAGGTCAGGC      79600          C
                                   GCCTGGCCTC CTGTG
                                   |||||||||| |||||
                                   CGGACTGGAG GACGT
                                         A
GAM1099  LOC150358 3'  TCTGATGAGGGGCCAGGC    84929        T  CT  GTCC
                                   GCCTGGCC CC  GT   CAGA
                                   |||||||| ||  ||   ||||
                                   CGGACCGG GG  TA   GTCT
                                        _  AG  _____
GAM1099  LOC151031 5'  ATCTGGGACACAGGGAGCCGCC 87187      __
              GG                   CTGGC  CTCCCTGTGTCCCAGAT
                                   |||||  ||||||||||||||||
                                   GGCCG  GAGGGACACAGGGTCTA
                                      CC
GAM1099  LOC152829 3'  ATCTGGGACACAGCCTCAGGC  80692       CCTCC
                                   GCCTGG    CTGTGTCCCAGAT
                                   ||||||    ||||||||||||
                                   CGGACT    GACACAGGGTCTA
                                       CC___
GAM1099  LOC153027 3'  CTGGGATGGTGGCCAGGC    67433        T  CTGT
                                   GCCTGGCC CC    GTCCCAG
                                   |||||||| ||    |||||||
                                   CGGACCGG GG    TAGGGTC
                                        T  _____
GAM1099  LOC162333 5'  TCTGGGGACAGAAGCAG     87140     GC  CC   G
                                   CTG  CT  CTGT TCCCAGA
                                   |||  ||  |||| |||||||
                                   GAC  GA  GACA GGGGTCT
                                     __  A_   _
GAM1099  LOC196812 3'  ATCTATCAAACAAAGAGGCTAG 89563        CC   GTCCC
                                   CTGGCCTC  TGT    AGAT
                                   ||||||||  |||    ||||
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                                GATCGGAG  ACA    TCTA
                                    AA   AACTA
GAM1099  LOC197342 3'  ATCTAGGAACAGGGGCCAGGC  87989        TC    G   C
                                GCCTGGCC  CCTGT TCC AGAT
                                ||||||||  ||||| ||| ||||
                                CGGACCGG  GGACA AGG TCTA
                                    __    _   A
GAM1099  LOC197342 3'  ATCTGCAAGAGAGGCCCAGGC  87990       _   C  GTGTCC
                                GCCTGG CCTC CT     CAGAT
                                |||||| |||| ||     |||||
                                CGGACC GGAG GA     GTCTA
                                   C   A  AC____
GAM1099  LOC199800 3'  GCACACGGGACCAGGC      89858       CC   _
                                GCCTGG  TCCC TGTGT
                                ||||||  |||| |||||
                                CGGACC  AGGG ACACG
                                   __   C
GAM1099  LOC255215 5'  ATCCTCTCACAAAGGCCAGGC  96881        CCC   TCCCA
                                GCCTGGCCT   TGTG    GAT
                                |||||||||   ||||    |||
                                CGGACCGGA   ACAC    CTA
                                     A__   TCTC_
GAM1099  LOC255798 3'  GCACCTTAGGAGGCCAAGG    97004     _     CT__
                                CCT GGCCTCC    GTGT
                                ||| |||||||    ||||
                                GGA CCGGAGG    CACG
                                  A      ATTC
GAM1099  LOC256306 5'  CTGCATGTGCAGGGAGGCCTGG 96686     T        TG CC_
            C                    GCC GGCCTCCCTG  T   CAG
                                ||| ||||||||||  |   |||
                                CGG CCGGAGGGAC  G   GTC
                                  T        GT TAC
GAM1099  LOC90917  3'  ATCTGAACACAGAGGCCAGG   64335        CC    CC
                                CCTGGCCTC  TGTGT  CAGAT
                                |||||||||  |||||  |||||
                                GGACCGGAG  ACACA  GTCTA
                                     __    A_
GAM1099  LOC92822  3'  CACAGAGGGCCAGGC       70648         CC
                                GCCTGGCCT  CTGTG
                                |||||||||  |||||
                                CGGACCGGG  GACAC
                                     A_
GAM1100  ADH1B    3'  CTTAGACATAAAGTAAAAT   72644      C    CAC
                                ATTT ACTTT   TGTCTGAG
                                |||| |||||   ||||||||
                                TAAA TGAAA   ACAGATTC
                                  A    T__
GAM1100  AHR      3'  ATCTCAGATGTTAAAATAAATG 7875       CAC   C  T
                                CATTT   TTT AC GTCTGAGAT
                                |||||   ||| || |||||||||
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                                GTAAA   AAA TG TAGACTCTA
                                   TA_   T _
GAM1100  FDFT1    3'  TAGGAAAGTGAAATG       15518           A
                                CATTTCACTTTC CTG
                                |||||||||||| |||
                                GTAAAGTGAAAG GAT
                                          _
GAM1100  JTB      3'  ATCTCAGACAGTGAAAGTGAAA 21959
              TG                  CATTTCACTTTCACTGTCTGAGAT
                                |||||||||||||||||||||||
                                GTAAAGTGAAAGTGACAGACTCTA

GAM1100  KLF4     3'  TCCCAGACAGTGGATATG    14891    CT        A
                                CA  TTCACTGTCTG GA
                                ||  |||||||||| ||
                                GT  AGGTGACAGAC CT
                                 AT         C
GAM1100  PHYH     3'  ACAGTAAAAGTGAAAT      20608          C
                                ATTTCACTTT ACTGT
                                |||||||||| |||||
                                TAAAGTGAAA TGACA
                                      A
GAM1100  PKD2     3'  TCCAGGTTGAAAGTGAAA    60096          CTG    A
                                TTTCACTTTCA   TCTG GA
                                ||||||||||   |||| ||
                                AAAGTGAAAGT   GGAC CT
                                      T__    _
GAM1100  WRN      3'  GGGCAGTGAAAATGAAA     5098       C
                                TTTCA TTTCACTGTCT
                                ||||| ||||||||||
                                AAAGT AAAGTGACGGG
                                   A
GAM1100  ZNF216   3'  ATCTGCACAGCAAAGTGAAA  20017        CA    CTG
                                TTTCACTTT  CTGT   AGAT
                                |||||||||  ||||   ||||
                                AAAGTGAAA  GACA   TCTA
                                      C_    CG_
GAM1100  CG012    5'  CTCACTCTGAAAGTGAA     83218         CT  CT
                                TTCACTTTCA  GT  GAG
                                |||||||||  ||  |||
                                AAGTGAAAGT  CA  CTC
                                      CT  __
GAM1100  EIF2C2   3'  ATCTTCTGAGAGTGAAAG    71946        G  T_
                                CTTTCACT TC  GAGAT
                                ||||||||  ||  |||||
                                GAAAGTGA AG  TTCTA
                                     G  TC
GAM1100  FLJ23462 3'  ATCTCAGACTTTACAAAGAAAT 45802       ACTTTCACT
              G                  CATTTC        GTCTGAGAT
                                ||||||        |||||||||
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                                GTAAAG       CAGACTCTA
                                   AAACATTT_
GAM1100 FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281       CTT
                                CATTTCA  TCACTGTCTGAGAT
                                |||||||  ||||||||||||||
                                GTAAAGT  AGTGACAGACTCTA
                                   C__
GAM1100 KIAA0984 3' TTTGTCCAGTGAAAATGAA  65534     C      TC
                                TTCA TTTCACTG  TGAG
                                |||| ||||||||  ||||
                                AAGT AAAGTGAC  GTTT
                                  A       CT
GAM1100 KLHL6    3' ATCTCAGAGCAGGAAA     55299     A  _
                                TTTC CTG TCTGAGAT
                                |||| ||| ||||||||
                                AAAG GAC AGACTCTA
                                  _  G
GAM1100 NIR3     3' GCAGTGAAAGTGCAAT     66242     T
                                ATT CACTTTCACTGT
                                ||| ||||||||||||
                                TAA GTGAAAGTGACG
                                  C
GAM1100 PORIMIN  3' ATCTCAGAGGGCCAAAGTGAA 53598       CA  G
                                TTCACTTT  CT TCTGAGAT
                                ||||||||  || ||||||||
                                AAGTGAAA  GG AGACTCTA
                                     CC  G
GAM1100 PP35     3' ATCTCAGACTGAAA       22814      CT
                                TTTCA  GTCTGAGAT
                                |||||  |||||||||
                                AAAGT  CAGACTCTA
                                   __
GAM1100 PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148        TCAC  C_
                                CATTTCACTT   TGT  TGAG
                                ||||||||||   |||  ||||
                                GTAAAGTGAA   ACG  ACTC
                                      TA__   TT
GAM1100 SEP15    3' TCCTACAGTAAGAGTGAAA   14934       C    CT
                                TTTCACTTT ACTGT  GA
                                ||||||||| |||||  ||
                                AAAGTGAGA TGACA  CT
                                     A    TC
GAM1100 SFXN2    3' CTCAGGGGAAAAAAGTGAAA  73941       CACTG
                                TTTCACTTT    TCTGAG
                                |||||||||    ||||||
                                AAAGTGAAA    GGACTC
                                     AAAGG
GAM1100 LOC149703 3' ATCTCAGACAGCCGTTTGGAAA 84647     ACTTTCA
                                TTTC      CTGTCTGAGAT
                                ||||      ||||||||||
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                                AAAG      GACAGACTCTA
                                  GTTTGCC
GAM1100  LOC154007 3'  ATCTCAAACCCTTTAGTGAAA  81015        TTCACT  C
                                TTTCACT     GT TGAGAT
                                |||||||     || ||||||
                                AAAGTGA     CA ACTCTA
                                    TTTCC_  A
GAM1100  LOC155004 3'  TCATTTAAGTGAAAGGAAA   81226      A       GTC_
                                TTTC CTTTCACT    TGA
                                |||| ||||||||    |||
                                AAAG GAAAGTGA    ACT
                                  _       ATTT
GAM1100  LOC222134 5'  ACAGTGAAGTGAAATG      94136          T
                                CATTTCACTT CACTGT
                                |||||||||| ||||||
                                GTAAAGTGAA GTGACA

                                      _
GAM1101  ABCB1    5'  CCAGAACATTCCTCCTGGAA   6247      CTGT  CT
                                TTCC    GG  ATGTTCTGG
                                ||||    ||  |||||||||
                                AAGG    CC  TACAAGACC
                                  TCCT  T_
GAM1101  AGT      3'  CCAGAACACAGTGCCTGGCA   3454      __   TA__
                                TGT  GGC    TGTTCTGG
                                |||  |||    ||||||||
                                ACG  CCG    ACAAGACC
                                  GT   TGAC
GAM1101  ALDOB    3'  CCAGAATACCCACCCAAGAA   68087     CCT_    CTA
                                TTC    GTGG   TGTTCTGG
                                |||    ||||   ||||||||
                                AAG    CACC   ATAAGACC
                                  AACC    C__
GAM1101  ARL4     3'  CCAGAACACAGTTGTGGGAA   19198      T TG   A
                                TTCCC G  GCT TGTTCTGG
                                ||||| |  ||| ||||||||
                                AAGGG T  TGA ACAAGACC
                                   _ GT   C
GAM1101  B3GAT1   3'  CCAGAACAAAGGACAGAGAA   37827     C    GG  A
                                TTC CTGT  CT TGTTCTGG
                                ||| ||||  || ||||||||
                                AAG GACA  GA ACAAGACC
                                  A   G_  A
GAM1101  B3GAT1   3'  CCAGAACAAAGGACAGAGAA   53972     C    GG  A
                                TTC CTGT  CT TGTTCTGG
                                ||| ||||  || ||||||||
                                AAG GACA  GA ACAAGACC
                                  A   G_  A
GAM1101  CD79B    3'  CCAGAAGAGCCACAGG      41207         ATG
                                CCTGTGGCT   TTCTGG
                                |||||||||   ||||||
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                                GGACACCGA  AAGACC
                                    G__
GAM1101  CD79B    3'  CCAGAAGAGCCACAGG     5271         ATG
                                CCTGTGGCT  TTCTGG
                                |||||||||  ||||||
                                GGACACCGA  AAGACC
                                    G__
GAM1101  CDH3     3'  CCAAACGTCAGGCCACAG    8380        __    C
                                CTGTGGCT  ATGTT TGG
                                ||||||||  ||||| |||
                                GACACCGG  TGCAA ACC
                                   AC   _
GAM1101  COL5A1   5'  GCCAGAACAGCCGCCGCCACAA 3634    CC     TA____      III
           AGAA                   C  TGTGGC     TGTTCTGG  C
                                |  ||||||     ||||||||  |
                                G  ACACCG     ACAAGACC  G
                                 AA     CCGCCG       III
GAM1101  CRIM1    3'  CCAGAACAAAGGCAG      33173      GG  A
                                CTGT  CT TGTTCTGG
                                ||||  || ||||||||
                                GACG  GA ACAAGACC
                                  __ A
GAM1101  DIAPH2   3'  CCAAAACAAGTCTAGCAGGGAA 22063        __    A   C
                                TTCCCTGT  GGCT TGTT TGG
                                ||||||||  |||| |||| |||
                                AAGGGACG  CTGA ACAA ACC
                                   AT   _   A
GAM1101  DMD      3'  AGAAAATATAGTCACAGG    14414           __
                                CCTGTGGCTATGT  TCT
                                ||||||||||||  |||
                                GGACACTGATATA  AGA
                                      AA
GAM1101  ED1      3'  TTGGAACAATCACAGGGAA   7376         CTA    TG
                                TTCCCTGTGG  TGTTC  G
                                ||||||||||  |||||  |
                                AAGGGACACT  ACAAG  T
                                   A__    GT
GAM1101  EXTL3    3'  CCAAAACATGCCGCAGGGAG  7528          T    C
                                TTCCCTGTGGC ATGTT TGG
                                |||||||||| ||||| |||
                                GAGGGACGCCG TACAA ACC
                                     _    A
GAM1101  FCRH3    3'  CCAGAGTGGCCCACAGG     53630       _   GT
                                CCTGTGG CTAT  TCTGG
                                ||||||| ||||  |||||
                                GGACACC GGTG  AGACC
                                   C   __
GAM1101  FECH     3'  CGTGGTGCCACAGGGAA     3753          __
                                TTCCCTGTGGC  TATG
                                ||||||||||  ||||
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                                AAGGGACACCG  GTGC
                                      TG
GAM1101  FGFRL1   3'  CCAGAACATACAAGGA     41619     C   GGCT
                                TCC TGT    ATGTTCTGG
                                ||| |||    |||||||||
                                AGG ACA    TACAAGACC
                                  A  ____
GAM1101  GATA4    3'  CCAGAACAACAACTGGGAA   9004       T  GGCTA
                                TTCCC GT    TGTTCTGG
                                ||||| ||    ||||||||
                                AAGGG CA    ACAAGACC
                                   T  ACA__
GAM1101  GNRH1    5'  CCATCACCAGCCACAGAGA   5883     C       AT  TC
                                TC CTGTGGCT  GT  TGG
                                || ||||||||  ||  |||
                                AG GACACCGA  CA  ACC
                                 A       C_  CT
GAM1101  HAMP     3'  CCAGAACATAGGTCTTGGAA  40991     CTGT  _
                                TTCC    GGC TATGTTCTGG
                                ||||    ||| ||||||||||
                                AAGG    CTG ATACAAGACC
                                   TT__   G
GAM1101  IPP      3'  TAGTTTGAGCCACAGAGAA   19729     C       ATGTT
                                TTC CTGTGGCT    CTG
                                ||| ||||||||    |||
                                AAG GACACCGA    GAT
                                  A       GTTT_
GAM1101  ITGB1    3'  CCAGTGTGGCCCAGGGAA    53369       T     GTT
                                TTCCCTG GGCTAT   CTGG
                                ||||||| ||||||   ||||
                                AAGGGAC CCGGTG   GACC
                                     _     T__
GAM1101  KCNQ1    3'  CCAGCTGCTGAGCCGCAGAGAA 4021      C       AT  T_
                                TTC CTGTGGCT  GT  CTGG
                                ||| ||||||||  ||  ||||
                                AAG GACGCCGA  CG  GACC
                                  A       GT  TC
GAM1101  KDR      3'  CAGAATACCACAAAGAA     9591      CC    CTA
                                TTC  TGTGG   TGTTCTG
                                |||  |||||   |||||||
                                AAG  ACACC   ATAAGAC
                                  AA    ___
GAM1101  LEP      3'  CCAGGGGCCCACAGGGAA    4047          _  ATGT
                                TTCCCTGTGG CT    TCTGG
                                |||||||||| ||    |||||
                                AAGGGACACC GG    GGACC
                                      C  ____
GAM1101  MKI67    3'  CCAGTGACCAGCCACAGGAGA  10041    _       AT  _
                                TC CCTGTGGCT  GTT CTGG
                                || |||||||||  ||| ||||
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                                AG GGACACCGA  CAG GACC
                                 A       C_   T
GAM1101  NEFH    3'  CCGGAACAGCCAAAG      40780    G    AT
                                CT TGGCT  GTTCTGG
                                || |||||  |||||||
                                GA ACCGA  CAAGGCC
                                 A    __
GAM1101  NXF2    5'  CCAGAACATCACCAAG      35136    G   CT
                                CT TGG  ATGTTCTGG
                                || |||  |||||||||
                                GA ACC  TACAAGACC
                                 _  AC
GAM1101  PDE6D   3'  CCAGCATACACACAGGGAA   10489        GC    TT
                                TTCCCTGTG  TATG  CTGG
                                |||||||||  ||||  ||||
                                AAGGGACAC  ATAC  GACC
                                      AC   __
GAM1101  PHEMX   5'  CCAGCTGGAAACCACAGGGAG  57359         CTATGTT
                                TTCCCTGTGG      CTGG
                                ||||||||||      ||||
                                GAGGGACACC      GACC
                                      AAAGGTC
GAM1101  PHEMX   5'  CCAGCTGGAAACCACAGGGAG  57364         CTATGTT
                                TTCCCTGTGG      CTGG
                                ||||||||||      ||||
                                GAGGGACACC      GACC
                                      AAAGGTC
GAM1101  PODXL   3'  CCAGAATGACACAAAGGA    18230     C_    GCTAT
                                TCC  TGTG    GTTCTGG
                                |||  ||||    |||||||
                                AGG  ACAC    TAAGACC
                                  AA   AG___
GAM1101  PRODH   3'  CTGGGACAGCCACTGGAA    32925      CT     AT    TG
                                TTCC  GTGGCT  GTTC  G
                                ||||  ||||||  ||||  |
                                AAGG  CACCGA  CAGG  C
                                  T_     __    GT
GAM1101  RANBP2L1 3'  CCAGAATAAAACCACCAGGAA  17313      CT    CTA
                                TTCC  GTGG   TGTTCTGG
                                ||||  ||||   ||||||||
                                AAGG  CACC   ATAAGACC
                                  AC   AAA
GAM1101  REGL    3'  CCAGAACATGAATTCAGG    21486      TGGC
                                CCTG    TATGTTCTGG
                                ||||    ||||||||||
                                GGAC    GTACAAGACC
                                  TTAA
GAM1101  SLC19A1  5'  CCAGAATGCATCCAGAGGGAA  11755       G   CTA
                                TTCCCT TGG   TGTTCTGG
                                |||||| |||   ||||||||
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                                AAGGGA ACC  GTAAGACC
                                   G  TAC
GAM1101 ST14    3' CCAGAACATACACTGTGAA  41765    CCT  GC
                                TTC  GTG  TATGTTCTGG
                                |||  |||  ||||||||||
                                AAG  CAC  ATACAAGACC
                                  TGT  __
GAM1101 TBL2    3' CCAGAACAACCTAGAGAA   24926    C  T  CTA
                                TTC CTG GG  TGTTCTGG
                                ||| ||| ||  ||||||||
                                AAG GAT CC  ACAAGACC
                                  A  _ A__
GAM1101 TBL2    3' CCAGAACAACCTAGAGAA   52182    C  T  CTA
                                TTC CTG GG  TGTTCTGG
                                ||| ||| ||  ||||||||
                                AAG GAT CC  ACAAGACC
                                  A  _ A__
GAM1101 TCFL4   3' CCAGGATAAGACCACAGGGAA  63461        _ A
                                TTCCCTGTGG CT TGTTCTGG
                                |||||||||| || ||||||||
                                AAGGGACACC GA ATAGGACC
                                     A  _
GAM1101 TFAP4   3' CCGGGGCAGCCACAGGGAG   12237         AT
                                TTCCCTGTGGCT  GTTCTGG
                                ||||||||||||  |||||||
                                GAGGGACACCGA  CGGGGCC
                                           __
GAM1101 UBE2L6  3' CCAGGGGGAGCCACGG     14873       ATG
                                CTGTGGCT  TTCTGG
                                ||||||||  ||||||
                                GGCACCGA  GGGACC
                                    GG_
GAM1101 UBQLN3  3' CAAAACATAGTGGAG      33926     CTGTG      C
                                TTCC    GCTATGTT TG
                                ||||    |||||||| ||
                                GAGG    TGATACAA AC
                                  _____       A
GAM1101 UMOD    3' CCAGTGCTCCAGCCACAG   12548       AT_  T
                                CTGTGGCT  GT CTGG
                                ||||||||  || ||||
                                GACACCGA  CG GACC
                                    CCT  T
GAM1101 WBSCR5  3' CCAGAACAGGGCAGAG     41856   G  G  A
                                CT TG CT TGTTCTGG
                                || || || ||||||||
                                GA AC GG ACAAGACC
                                 G  G  _
GAM1101 WBSCR5  3' CCAGAACAGGGCAGAG     50610   G  G  A
                                CT TG CT TGTTCTGG
                                || || || ||||||||
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                                GA AC GG ACAAGACC
                                 G  G  _
GAM1101  WBSCR5   3'  CCAGAACAGGGCAGAG      26256    G  G  A
                                CT TG CT TGTTCTGG
                                || || || ||||||||
                                GA AC GG ACAAGACC
                                 G  G  _
GAM1101  ZNF134   3'  CAGTTTAAGCCACAGGGAA    12846          A  TT
                                TTCCCTGTGGCT TG  CTG
                                |||||||||||| ||  |||
                                AAGGGACACCGA AT  GAC
                                       _  TT
GAM1101  ZNF36    3'  CCTTCGTAGCCACAAGG     93960    C        TTCT
                                CC TGTGGCTATG    GG
                                || ||||||||||    ||
                                GG ACACCGATGC    CC
                                 A        TT__
GAM1101  ABCA9    5'  CAGAACATGCAGAGA       54410    C    GGCT
                                TC CTGT    ATGTTCTG
                                || ||||    ||||||||
                                AG GACG    TACAAGAC
                                 A   _____
GAM1101  ADAMTSL1 3'  CCTCAAATAGCACAGGGAA    57686         G    GTTCT
                                TTCCCTGTG CTAT     GG
                                ||||||||| ||||     ||
                                AAGGGACAC GATA     CC
                                      _    AACT_
GAM1101  BAIAP1   3'  CCAGAACGGCAGCAGG      16449      G   AT
                                CCTGT GCT  GTTCTGG
                                ||||| |||  |||||||
                                GGACG CGG  CAAGACC
                                   A  __
GAM1101  BCKDK    3'  CCAGAACTTGGAGCAGGGAA   59793        GG   T
                                TTCCCTGT  CTA GTTCTGG
                                ||||||||  ||| |||||||
                                AAGGGACG  GGT CAAGACC
                                     A_   T
GAM1101  C11orf25 3'  CCAAATTAGGGCCACAG     48639         AT_   C
                                CTGTGGCT   GTT TGG
                                ||||||||   ||| |||
                                GACACCGG   TAA ACC
                                     GAT   _
GAM1101  C20orf112 3' CCAGTGCTGCCACAGGGA    54640          TAT  T
                                TCCCTGTGGC   GT CTGG
                                ||||||||||   || ||||
                                AGGGACACCG   CG GACC
                                      T__  T
GAM1101  C6orf26  3'  CCAAAACACAGAGCAGG     47509       GG  A    C
                                CCTGT  CT TGTT TGG
                                |||||  || |||| |||
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                                GGACG  GA ACAA ACC
                                  A_  C   A
GAM1101  CGGBP1    5'  CTGGCACCACAGGGAA     13362         CTA   CT
                                TTCCCTGTGG  TGTT  G
                                ||||||||||  ||||  |
                                AAGGGACACC  ACGG  C
                                     ____   T_
GAM1101  DKFZP566G1424 5'  CCAGTGCTGCCACAGGGA    84779         TAT  T
                                TCCCTGTGGC  GT CTGG
                                ||||||||||  || ||||
                                AGGGACACCG  CG GACC
                                     T__  T
GAM1101  DKFZp586I021 5'  CCAGACGTCACCACAGGGA   50088        CT   T
                                TCCCTGTGG  ATGT CTGG
                                |||||||||  |||| ||||
                                AGGGACACC  TGCA GACC
                                     AC   _
GAM1101  DKFZP727M111 5'  CCAATCTGGTCACAGGGAA   31407          T  TC
                                TTCCCTGTGGCTA GT  TGG
                                ||||||||||||| ||  |||
                                AAGGGACACTGGT TA  ACC
                                      C  __
GAM1101  ELF4     3'  CCGTGGATCAGCCACAGGGA   7431          AT   _
                                TCCCTGTGGCT  GTTC TGG
                                ||||||||||  |||| |||
                                AGGGACACCGA  TAGG GCC
                                     C_   T
GAM1101  ERG-1    3'  CCAGGATGCCAAAGG      41842     G    TAT
                                CCT TGGC   GTTCTGG
                                ||| ||||   |||||||
                                GGA ACCG   TAGGACC
                                  A   ____
GAM1101  FLJ00058  5'  CCAGAAATGCCAGCAGGGAA   78765       _   TATG
                                TTCCCTG TGGC   TTCTGG
                                ||||||| ||||   ||||||
                                AAGGGAC ACCG   AAGACC
                                    G   TA__
GAM1101  FLJ12816  3'  CCAGAACAGGACGACAGTGAA  41932     C   GGCTA
                                TTC CTGT    TGTTCTGG
                                ||| ||||    ||||||||
                                AAG GACA    ACAAGACC
                                  T   GCAGG
GAM1101  FLJ13315  3'  CCAGAACATAATACA      46568     GC
                                TGTG  TATGTTCTGG
                                ||||  ||||||||||
                                ACAT  ATACAAGACC
                                  A_
GAM1101  FLJ20010  3'  CCAGAACGATTGGAACAGG   38716      GG  __
                                CCTGT  CTA  TGTTCTGG
                                |||||  |||  ||||||||
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                                GGACA  GGT  GCAAGACC
                                  A_   TA
GAM1101  FLJ22369  5'  ATGGCGCGACAGGGAA      49918         _ _
                                TTCCCTGT G GCTAT
                                |||||||| | |||||
                                AAGGGACA C CGGTA
                                     G G
GAM1101  FLJ23563  3'  CCAGAATGCTACAAAAGAA   67593     CC_     TAT
                                TTC   TGTGGC   GTTCTGG
                                |||   ||||||   |||||||
                                AAG   ACATCG   TAAGACC
                                  AAA     ___
GAM1101  FLJ32332  3'  CACAGCACACAGGGAA      58299         _   A
                                TTCCCTGTG GCT TG
                                ||||||||| ||| ||
                                AAGGGACAC CGA AC
                                     A   C
GAM1101  GRIN3A    3'  CCAAGTGAAGCAGCCACAGGGA 55968          ATG  ___
                                TCCCTGTGGCT   TTC   TGG
                                ||||||||||   |||   |||
                                AGGGACACCGA   AAG   ACC
                                      CG_   TGA
GAM1101  HSPC166   3'  CCAGAACACATGGAGGGAA   26366       G  GCTA
                                TTCCCT TG    TGTTCTGG
                                |||||| ||    ||||||||
                                AAGGGA GT    ACAAGACC
                                   G  AC__
GAM1101  HSPC251   3'  CCAGGCTAGAGCCACAGAGA   33249    C      A  TT
                                TC CTGTGGCT TG  CTGG
                                || |||||||| ||  ||||
                                AG GACACCGA AT  GACC
                                  A       G  CG
GAM1101  IGF2AS    3'  CCAGGGTGCAACAGAGAA    33095     C    G  TAT TT
                                TTC CTGT GC   G  CTGG
                                ||| |||| ||   |  ||||
                                AAG GACA CG   T  GACC
                                  A   A  ___ GG
GAM1101  ILF3      3'  CCAAAACACGCTGGGAA     15722      T   GCTA   C
                                TTCCC GTG    TGTT TGG
                                ||||| |||    |||| |||
                                AAGGG CGC    ACAA ACC
                                   T  _____    A
GAM1101  KIAA0040  3'  CCAAAGTTTCCAGCAGGGAA   27780        _   CT  GTTC
                                TTCCCTG TGG  AT    TGG
                                ||||||| |||  ||    |||
                                AAGGGAC ACC  TG    ACC
                                   G   TT  AA__
GAM1101  KIAA0254  3'  CAGACAGTCACAGGGAA     28596           ATGT
                                TTCCCTGTGGCT    TCTG
                                ||||||||||||   ||||
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                                AAGGGACACTGA   AGAC
                                      C___
GAM1101 KIAA0336 3' CCAGAATAAAACCACCAGGAA 27589     CT   CTA
                                TTCC  GTGG   TGTTCTGG
                                ||||  ||||   ||||||||
                                AAGG  CACC   ATAAGACC
                                  AC   AAA
GAM1101 KIAA0494 3' CCAGAACACATTTGGG     28740    T_  GCTA
                                CCC  GTG   TGTTCTGG
                                |||  |||   ||||||||
                                GGG  TAC   ACAAGACC
                                 TT  _____
GAM1101 KIAA0537 3' CCAGAACAGCCTACAGGGGA  29244       _   AT
                                TTCCCTGT GGCT  GTTCTGG
                                |||||||| ||||  |||||||
                                AGGGGACA CCGA  CAAGACC
                                     T   __
GAM1101 KIAA0774 5' CGGGATGCCACAAGGAA    91752     C    TAT   TG
                                TTCC TGTGGC   GTTC  G
                                |||| ||||||   ||||  |
                                AAGG ACACCG   TAGG  C
                                  A     ___    GT
GAM1101 KIAA0828 3' CCATGAAAGCCACAGAGGA   81194    _     ATG  _
                                TCC CTGTGGCT   TTC TGG
                                ||| ||||||||   ||| |||
                                AGG GACACCGA   AAG ACC
                                 A       ___   T
GAM1101 KIAA1118 3' CCAGAGGCCCACAGGGA     69606       _ ATGT
                                TCCCTGTGG CT    TCTGG
                                |||||||||  ||    |||||
                                AGGGACACC GG    AGACC
                                     C  _____
GAM1101 KIAA1742 3' CAGATCCACAGGGAG       77657        CTATGT
                                TTCCCTGTGG     TCTG
                                ||||||||||     ||||
                                GAGGGACACC     AGAC
                                     T_______
GAM1101 KIAA1944 5' CCAACCTAGCCACAGGGA    75558         T  TC
                                TCCCTGTGGCTA GT  TGG
                                ||||||||||||  ||  |||
                                AGGGACACCGAT CA  ACC
                                      C  __
GAM1101 KIAA1981 3' CGGAACAGCACAAGGAA     88342     C   G  AT   TG
                                TTCC TGTG CT  GTTC  G
                                |||| |||| ||  ||||  |
                                AAGG ACAC GA  CAAG  C
                                  A   _ ___   GT
GAM1101 NXPH3    3' ACGGAGCCACAGAGAG      65747     C      A
                                TTC CTGTGGCT TGT
                                ||| |||||||| |||
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                                GAG GACACCGA GCA
                                  A       G
GAM1101  PP5395   3'  TCAGGATAGCACAGGGAA    72110         G  AT
                                TTCCCTGTG CT  GTTCTGG
                                ||||||||| ||  |||||||
                                AAGGGACAC GA  TAGGACT
                                      _  __
GAM1101  PRDM7    3'  CCAGAAGGGCCACAGAGAA   53788     C       ATG
                                TTC CTGTGGCT   TTCTGG
                                ||| ||||||||   ||||||
                                AAG GACACCGG   AAGACC
                                  A       G__
GAM1101  PRDM9    3'  CCAGAAGGGCCACAGAGAA   39575     C       ATG
                                TTC CTGTGGCT   TTCTGG
                                ||| ||||||||   ||||||
                                AAG GACACCGG   AAGACC
                                  A       G__
GAM1101  PXR2b    3'  ATATAGCCCAAGGAA       33337      C  T
                                TTCC TG GGCTATGT
                                |||| || ||||||||
                                AAGG AC CCGATATA
                                  A  _
GAM1101  RAB33B   3'  CCAGCTTAGCCACAAAGAA   48490     CC       TGTT
                                TTC  TGTGGCTA   CTGG
                                |||  ||||||||   ||||
                                AAG  ACACCGAT   GACC
                                  AA       TC__
GAM1101  SH120    3'  CCAGAACATGAGAGGGAG    32920       GTGGC
                                TTCCCT    TATGTTCTGG
                                ||||||    ||||||||||
                                GAGGGA    GTACAAGACC
                                   GA___
GAM1101  SH120    3'  CCAGAACATGAGAGGGAG    94606       GTGGC
                                TTCCCT    TATGTTCTGG
                                ||||||    ||||||||||
                                GAGGGA    GTACAAGACC
                                   GA___
GAM1101  SLC2A12  3'  CCAGAACACACAGTGTGGA   59078     ___    GCTA
                                TCC   CTGTG   TGTTCTGG
                                |||   |||||   ||||||||
                                AGG   GACAC   ACAAGACC
                                  TGT   _____
GAM1101  SP329    3'  CCAGAGTGCTCCACAGGGA   47924         CTA GT
                                TCCCTGTGG   T  TCTGG
                                |||||||||   |  |||||
                                AGGGACACC   G  AGACC
                                      TC_ TG
GAM1101  SSH2     3'  TCAGTAAGCCCACAGGGAA   62213         _  ATGTT
                                TTCCCTGTGG CT    CTGG
                                |||||||||| ||    ||||
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                                AAGGGACACC GA    GACT
                                      C  AT___
GAM1101  SYTL4    5'  CCAGTCAGCCACAGGGAA    54939          ATGTT
                                TTCCCTGTGGCT    CTGG
                                ||||||||||||    ||||
                                AAGGGACACCGA    GACC
                                       CT___
GAM1101  TNRC4    3'  CCAGTCAGCCACAGAGA    23221    C      ATGTT
                                TC CTGTGGCT    CTGG
                                || ||||||||    ||||
                                AG GACACCGA    GACC
                                 A       CT___
GAM1101  UBE3B    3'  CCAGACTGTCAGCACAGGGAA  76919        G  _  GT
                                TTCCCTGTG CT AT  TCTGG
                                ||||||||| || ||  |||||
                                AAGGGACAC GA TG  AGACC
                                      _  C  TC
GAM1101  VPS4A    3'  CCTTGCAGCCACAGAGA    25102    C      AT  TCT
                                TC CTGTGGCT  GT   GG
                                || ||||||||  ||   ||
                                AG GACACCGA  CG   CC
                                 A       __  TT_
GAM1101  XYLT1    5'  CCAACAGCAGCCACGGGAA   77847      T     A_   TC
                                TTCCC GTGGCT  TGT  TGG
                                ||||| ||||||  |||  |||
                                AAGGG CACCGA  ACA  ACC
                                   _     CG  __
GAM1101  ZFP100   3'  CCAGAAAGCCAAAAAGAA    70050    CCTG    ATG
                                TTC    TGGCT   TTCTGG
                                |||    |||||   ||||||
                                AAG    ACCGA   AAGACC
                                  AAAA    ____
GAM1101  ZNF213   5'  CAGCTACCACAGGGGA     65091          C  TGTT
                                TTCCCTGTGG TA    CTG
                                |||||||||| ||    |||
                                AGGGGACACC AT    GAC
                                      _  C___
GAM1101  LOC112609 3'  CCAGTGTGGCACAGGGAA    72837         G    GTT
                                TTCCCTGTG CTAT   CTGG
                                ||||||||| ||||   ||||
                                AAGGGACAC GGTG   GACC
                                      _    T__
GAM1101  LOC115073 5'  CCAGGCGTCAAACCACAGGGA  73204         CT__    T
                                TCCCTGTGG    ATGT CTGG
                                |||||||||    |||| ||||
                                AGGGACACC    TGCG GACC
                                      AAAC    _
GAM1101  LOC122962 5'  CCAGACAGTGGCCACTGAGAA  75587     CCT       GT
                                TTC   GTGGCTAT  TCTGG
                                |||   ||||||||  |||||
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                                AAG   CACCGGTG  AGACC
                                  AGT       AC
GAM1101  LOC124044 3'  CCAGAACACTCAGAGGGA    76025      G   CTA
                                TCCCT TGG   TGTTCTGG
                                ||||| |||   ||||||||
                                AGGGA ACT   ACAAGACC
                                   G   C__
GAM1101  LOC143308 5'  CCAAATTTGGCCACAG      82936        T   C
                                CTGTGGCTA GTT TGG
                                ||||||||| ||| |||
                                GACACCGGT TAA ACC
                                      T   _
GAM1101  LOC145314 3'  CCAGAACACATCACCTGAG   77086    CCT    CTA
                                TTC   GTGG   TGTTCTGG
                                |||   ||||   ||||||||
                                GAG   CACT   ACAAGACC
                                  TC_    AC_
GAM1101  LOC146420 3'  CCAGAACCAGTTACAG      83667        AT
                                CTGTGGCT  GTTCTGG
                                ||||||||  |||||||
                                GACATTGA  CAAGACC
                                     C_
GAM1101  LOC146445 3'  CCAGAGCCACCACAGGGA    83678         CTAT
                                TCCCTGTGG    GTTCTGG
                                |||||||||    |||||||
                                AGGGACACC    CGAGACC
                                      AC__
GAM1101  LOC147178 3'  CCAGCCAGCCACGGAGAA    61323     C       ATGTT
                                TTC CTGTGGCT     CTGG
                                ||| ||||||||     ||||
                                AAG GGCACCGA     GACC
                                  A       CC___
GAM1101  LOC148529 5'  CACAGCCACAGGAGAA      84166     _       A
                                TTC CCTGTGGCT TG
                                ||| ||||||||| ||
                                AAG GGACACCGA AC
                                  A        C
GAM1101  LOC148930 5'  CCAGGGGCAGACCACGGGGAA  79093          CTA    _
                                TTCCCTGTGG   TGTTC TGG
                                |||||||||   ||||| |||
                                AAGGGGCACC   ACGGG ACC
                                      AG_    G
GAM1101  LOC149950 5'  CCAGAACATGATCTCAGG     79551      T GC
                                CCTG G  TATGTTCTGG
                                |||| |  ||||||||||
                                GGAC C  GTACAAGACC
                                   T TA
GAM1101  LOC150378 5'  CCAGAAACAAGCCACGGGAA   79742       T     ATG
                                TTCCC GTGGCT   TTCTGG
                                ||||| ||||||   ||||||
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                                AAGGG CACCGA   AAGACC
                                  _     ACA
GAM1101  LOC150951 5'  CCAGGGCCACACAGGGAA    85167        GCTAT
                                TTCCCTGTG    GTTCTGG
                                |||||||||    |||||||
                                AAGGGACAC    CGGGACC
                                     AC___
GAM1101  LOC151429 3'  CCAGGAGACCACAGGGA     85347        _ ATGT
                                TCCCTGTGG CT    TCTGG
                                ||||||||| ||    |||||
                                AGGGACACC GA    GGACC
                                     A ____
GAM1101  LOC158434 3'  CCAGAATAAACCACTGGGAA   86819      T   CTA
                                TTCCC GTGG   TGTTCTGG
                                ||||| ||||   ||||||||
                                AAGGG CACC   ATAAGACC
                                   T   AA_
GAM1101  LOC170106 5'  CCAAGGCAGTCAGCCACAGG   82571        A__   TC
                                CCTGTGGCT   TGT  TGG
                                |||||||||   |||  |||
                                GGACACCGA   ACG  ACC
                                     CTG   GA
GAM1101  LOC196446 3'  CGGAAAGCCACAGAGAA     87708     C      ATG   TG
                                TTC CTGTGGCT   TTC  G
                                ||| ||||||||   |||  |
                                AAG GACACCGA   AAG  C
                                  A       ___   GT
GAM1101  LOC197136 3'  CCAGAACACTCAGAGGGA    89728      G   CTA
                                TCCCT TGG   TGTTCTGG
                                ||||| |||   ||||||||
                                AGGGA ACT   ACAAGACC
                                   G   C__
GAM1101  LOC197342 3'  CCAGGAGAAGCCACAGGGGA   87993          ATG
                                TTCCCTGTGGCT   TTCTGG
                                ||||||||||||   ||||||
                                AGGGGACACCGA   AGGACC
                                      AG_
GAM1101  LOC200734 3'  CCATCCGCAGCCACAGGGGA   88860          A  TTC
                                TTCCCTGTGGCT TG   TGG
                                |||||||||||| ||   |||
                                AGGGGACACCGA GC   ACC
                                      C  CT_
GAM1101  LOC201102 3'  CCTGACCAGCCACAGGAGA    88090    _      AT   CT
                                TC CCTGTGGCT  GTT  GG
                                || |||||||||  |||  ||
                                AG GGACACCGA  CAG  CC
                                  A       C_   T_
GAM1101  LOC201283 3'  CCAGAACACAGTCGTGAGGA   60413     CT     A
                                TCC  GTGGCT TGTTCTGG
                                |||  |||||| ||||||||
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                                AGG  TGCTGA ACAAGACC
                                  AG     C
GAM1101  LOC202915 3'  CCACACGCCAGCCACAGGGGA  90388          A_   TC
                                TTCCCTGTGGCT  TGT  TGG
                                ||||||||||||  |||  |||
                                AGGGGACACCGA  GCA  ACC
                                       CC   C_
GAM1101  LOC204965 5'  CAGAGTGCACAGAGAA      90647     C     G TATG
                                TTC CTGTG C    TTCTG
                                ||| ||||| |    |||||
                                AAG GACAC G    GAGAC
                                  A     _ T___
GAM1101  LOC205418 3'  CACAGCCAGCAGGGAA      90681        _     A
                                TTCCCTG TGGCT TG
                                ||||||| ||||| ||
                                AAGGGAC ACCGA AC
                                    G    C
GAM1101  LOC220692 3'  CCAGAATAAAACCACCAGGAA  91220      CT    CTA
                                TTCC  GTGG   TGTTCTGG
                                ||||  ||||   ||||||||
                                AAGG  CACC   ATAAGACC
                                  AC    AAA
GAM1101  LOC222631 5'  CCAGAACACAGCTGGAA     92838      CTGT    A
                                TTCC    GGCT TGTTCTGG
                                ||||    |||| ||||||||
                                AAGG    TCGA ACAAGACC
                                  _____    C
GAM1101  LOC253039 3'  CCAAATACATCTACAGGGAA   96153         CT    TC_
                                TTCCCTGTGG  ATGT   TGG
                                ||||||||||  ||||   |||
                                AAGGGACATC  TACA   ACC
                                      __    TAA
GAM1101  LOC253841 5'  CCAGAATGTAGCCACAG     96342
                                CTGTGGCTATGTTCTGG
                                |||||||||||||||||
                                GACACCGATGTAAGACC

GAM1101  LOC254028 3'  CCAGAACAGAAGCACCAAGAA  96539     CC  TG   A_
                                TTC  TG  GCT  TGTTCTGG
                                |||  ||  |||  ||||||||
                                AAG  AC  CGA  ACAAGACC
                                  A_  CA   AG
GAM1101  LOC257449 3'  CAGATCCACAGGGAG       62718          CTATGT
                                TTCCCTGTGG     TCTG
                                ||||||||||     ||||
                                GAGGGACACC     AGAC
                                      T_____
GAM1101  LOC89231  3'  GGACAGCACAGGGAA       92733          G  AT
                                TTCCCTGTG CT  GTTC
                                ||||||||| ||  ||||
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                                AAGGGACAC GA  CAGG
                                    _ __
GAM1101 LOC90550 3' CCAGAACACAAATCAGAGGGA 73090      G  CTA_
                                TCCCT TGG   TGTTCTGG
                                ||||| |||   ||||||||
                                AGGGA ACT   ACAAGACC
                                   G  AAAC
GAM1101 LOC91373 3' CCAGCAAGGCCACAG      65834        A  TT
                                CTGTGGCT TG  CTGG
                                |||||||| ||  ||||
                                GACACCGG AC  GACC
                                     A  __
GAM1101 LOC91445 3' CCAGAACCTGCCACAGG    60547        TAT
                                CCTGTGGC  GTTCTGG
                                ||||||||  |||||||
                                GGACACCG  CAAGACC
                                     TC_
GAM1102 CD5L    3' TGCCAACATGGTTGACA     19711       __
                                TGTCGG  ATGTTGGCA
                                ||||||  |||||||||
                                ACAGTT  TACAACCGT
                                   GG
GAM1102 GUCY1B2  3' CAGCCTTCAGCTCCGACAAAG  14685         T    CAA
                                CTTTGTCGGA GTTGG  GCTG
                                |||||||||| |||||  ||||
                                GAAACAGCCT CGACT  CGAC
                                     _    TC_
GAM1102 ESDN    3' GCAGCTCACCATATGATAAA  55175       GATGT  CA
                                TTTGTCG   TGG  AGCTGC
                                |||||||   |||  ||||||
                                AAATAGT   ACC  TCGACG
                                    AT___  AC
GAM1102 GTF2E1   3' GCAGCTTGCCAACAGTC    18614   GA
                                G  TGTTGGCAAGCTGC
                                |  ||||||||||||||
                                C  ACAACCGTTCGACG
                                 TG
GAM1102 KIAA1904 3' CCAACATCAAACAAAG     73480       CG
                                CTTTGT  GATGTTGG
                                ||||||  ||||||||
                                GAAACA  CTACAACC
                                   AA
GAM1102 LOC154282 3' GCACATCAACATCAACAAA   86200      CG     _______
                                TTTGT  GATGTTG     GC
                                |||||  |||||||     ||
                                AAACA  CTACAAC     CG
                                   A_     TACAIII
GAM1102 LOC92539 3' GCGCATCAACATCAACAAA   69637      CG     _______
                                TTTGT  GATGTTG     GC
                                |||||  |||||||     ||
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                                AAACA  CTACAAC      CG
                                  A_       TACGIII
GAM1103  ANK2     3'  CCCAGTTCTCACACCA      6709       A   CA
                                TGGT TGA  GAACTGGG
                                |||| |||  ||||||||
                                ACCA ACT  CTTGACCC
                                  C   __
GAM1103  ANK2     3'  CCCAGTTCTCACACCA      40603      A   CA
                                TGGT TGA  GAACTGGG
                                |||| |||  ||||||||
                                ACCA ACT  CTTGACCC
                                  C   __
GAM1103  ATP11A   3'  CCAGTCCCTGCCACAGA     77022         TGACA  A
                                TCTGTGGTA    GA CTGG
                                |||||||||    || ||||
                                AGACACCGT    CT GACC
                                     CC___  _
GAM1103  ATP11A   3'  CCAGTCCCTGCCACAGA     77023         TGACA  A
                                TCTGTGGTA    GA CTGG
                                |||||||||    || ||||
                                AGACACCGT    CT GACC
                                     CC___  _
GAM1103  ATP11A   3'  CCAGTCCCTGCCACAGA     77024         TGACA  A
                                TCTGTGGTA    GA CTGG
                                |||||||||    || ||||
                                AGACACCGT    CT GACC
                                     CC___  _
GAM1103  DNCI1    5'  CCCAGTTCCGCCGCTGCCG   91062       _  ACA
                                TGGTA TG   GAACTGGG
                                ||||| ||   ||||||||
                                GCCGT GC   CTTGACCC
                                   C  CGC
GAM1103  GSTA4    3'  CCCAGCTCTGTCATGGTGC   7698      G        A
                                GTG TATGACAGA CTGGG
                                ||| ||||||||| |||||
                                CGT GTACTGTCT GACCC
                                  G        C
GAM1103  ITPKB    3'  CCCAGCCCTCGTCACCACAGG  9424          AT   _  AA
                                TCTGTGGT  GAC AG  CTGGG
                                ||||||||  ||| ||  |||||
                                GGACACCA  CTG TC  GACCC
                                     __   C  CC
GAM1103  LARS2    3'  CCCAGCTCTGTCATGC      31053          A
                                GTATGACAGA CTGGG
                                |||||||||| |||||
                                CGTACTGTCT GACCC
                                      C
GAM1103  LFNG     3'  CCCAGTTCCAGTGGCCCCACG  92638       TATG  A_
                                TGTGG    AC  GAACTGGG
                                |||||    ||  ||||||||
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                                GCACC   TG  CTTGACCC
                                   CCGG  AC
GAM1103  LZTS1    3'  CCCAGCCCCGGCAAGCCACAGG 40686        A  ACAGAA
                                TCTGTGGT TG     CTGGG
                                |||||||| ||     |||||
                                GGACACCG AC     GACCC
                                     A  GGCCCC
GAM1103  MAT1A    3'  CCCAGCTCCCAGGACCACAGG  90828        A_  ACA  A
                                TCTGTGGT  TG   GA CTGGG
                                |||||||| ||   || |||||
                                GGACACCA  AC   CT GACCC
                                     GG  C__  C
GAM1103  NORE1    3'  CCCAGGCTGTGCCCCACCACAG 48716        ATG__    AA
              A                  TCTGTGGT    ACAG  CTGGG
                                |||||||     ||||  |||||
                                AGACACCA    TGTC  GACCC
                                     CCCCG    G_
GAM1103  SCA7     5'  CCAATTCCACCACAGA      4403         ATGACA   C
                                TCTGTGGT     GAA TGG
                                ||||||||     ||| |||
                                AGACACCA     CTT ACC
                                     C_____   A
GAM1103  SP3      5'  CCAGAATCTCATACCACAGA   82496          CAGAA
                                TCTGTGGTATGA    CTGG
                                ||||||||||||    ||||
                                AGACACCATACT    GACC
                                      CTAA_
GAM1103  SRR      3'  CCCAACCTTTATACCACA    41687          C  AAC
                                TGTGGTATGA AG   TGGG
                                |||||||||| ||   ||||
                                ACACCATATT TC   ACCC
                                      _  CA_
GAM1103  VSNL1    3'  CTGGTCCACACACCACAGA   12624        A  ACA  A TG
                                TCTGTGGT TG   GA C  G
                                |||||||| ||   || |  |
                                AGACACCA AC   CT G  C
                                     C  AC_  _ GT
GAM1103  ABLIM    3'  CCCAATTCTGTCATCTCCA   9761      T_       C
                                TGG  ATGACAGAA TGGG
                                |||  ||||||||| ||||
                                ACC  TACTGTCTT ACCC
                                  TC       A
GAM1103  ABLIM    3'  CCCAATTCTGTCATCTCCA   22022     T_       C
                                TGG  ATGACAGAA TGGG
                                |||  ||||||||| ||||
                                ACC  TACTGTCTT ACCC
                                  TC       A
GAM1103  C14orf4  5'  CCCAACCTGCTACCGCAGA   67334         TGA   AAC
                                TCTGTGGTA   CAG   TGGG
                                |||||||||   |||   ||||
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                                AGACGCCAT  GTC  ACCC
                                    C__  CA_
GAM1103 CALN1    3' CCCAGCCCTGTTCACACA   48861    GTAT   AA
                                TGTG   GACAG  CTGGG
                                ||||   |||||  |||||
                                ACAC   TTGTC  GACCC
                                  AC__    CC
GAM1103 DKFZp547I094 3' CCAGGGCACATCACAGA    49634       A  ACAGAA
                                TCTGTGGT TG     CTGG
                                |||||||| ||     ||||
                                AGACACTA AC     GACC
                                    C  GG____
GAM1103 DKFZp761F2014 3' CCCAGTTCTGTCAGCTCTAGA  39536     T   A
                                TCTG GGT TGACAGAACTGGG
                                |||| ||| ||||||||||||
                                AGAT TCG ACTGTCTTGACCC
                                  C  _
GAM1103 FLJ11320  3' CCCAGTTCTACCTCCCCAGA   37243     T  TATGAC
                                TCTG GG     AGAACTGGG
                                |||| ||     |||||||||
                                AGAC CC     TCTTGACCC
                                  C  TCCA__
GAM1103 FLJ14871  3' CCCAGTTCTGCAGACACA    51667     GTA  A
                                TGTG   TG CAGAACTGGG
                                ||||   || ||||||||||
                                ACAC   AC GTCTTGACCC
                                  AG_  _
GAM1103 FLJ20452  3' CCCAGTCAGGTTACACA     35197     GTA   AGA
                                TGTG   TGAC   ACTGGG
                                ||||   ||||   ||||||
                                ACAC   ATTG   TGACCC
                                  ___    GAC
GAM1103 FLJ23168  3' CCCGCTTTGCACACCACAGA   46822       A  A   AC
                                TCTGTGGT TG CAGA  TGGG
                                |||||||| || ||||  ||||
                                AGACACCA AC GTTT  GCCC
                                    C  _   C_
GAM1103 KIAA0527  3' CCCAGTTCTGTTTTTAACA    95796    GGTAT
                                TGT    GACAGAACTGGG
                                |||    ||||||||||||
                                ACA    TTGTCTTGACCC
                                 ATTT_
GAM1103 KIAA0781  3' CCTGGTTCTGCCCCACCACA   67456      ATGA    TG
                                TGTGGT   CAGAAC  GG
                                ||||||   ||||||  ||
                                ACACCA   GTCTTG  CC
                                   CCCC    GT
GAM1103 KIAA1751  3' CCCAGCTCTGCCTGGTCACAGA 71691       ATGA   A
                                TCTGTGGT   CAGA CTGGG
                                ||||||||   |||| |||||
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                                AGACACTG   GTCT GACCC
                                    GTCC   C
GAM1103 KRTHB4   3' CCCAGCCCTGTCCACTGCAGG 52323    TG  AT    AA
                                TCTG  GT  GACAG  CTGGG
                                ||||  ||  |||||  |||||
                                GGAC  CA  CTGTC  GACCC
                                  GT  C_    CC
GAM1103 MGC10812 3' CCCAAATTTGACACCACAGA  48665      ATGA   AC
                                TCTGTGGT   CAGA  TGGG
                                ||||||||   ||||  ||||
                                AGACACCA   GTTT  ACCC
                                    CA__   AA
GAM1103 NTSR2    5' CCCAGTTCTAGAGGTTCCCAGA 24716    T  TATGAC_
                                TCTG GG     AGAACTGGG
                                |||| ||     |||||||||
                                AGAC CC     TCTTGACCC
                                  _ TTGGAGA
GAM1103 PDZD2    5' CCCAGTTCCCCCCAGCAGA   80865    _  TATGACA
                                TCTG TGG     GAACTGGG
                                |||| |||     ||||||||
                                AGAC ACC     CTTGACCC
                                  G  CCC_____
GAM1103 PGLYRP   3' CCCAGCCACATACCACA    53575       ACAGAA
                                TGTGGTATG    CTGGG
                                |||||||||    |||||
                                ACACCATAC    GACCC
                                    ACC___
GAM1103 PLCE1    3' CCCAATTCTGCCATTGTAG   32963    TG TA  A    C
                                CTG  G  TG CAGAA TGGG
                                |||  |  || ||||| ||||
                                GAT  T  AC GTCTT ACCC
                                  GT __  C    A
GAM1103 SV2B     5' CCCAAACCTCTACCACAGA   29296       T  CAGAAC
                                TCTGTGGTA GA     TGGG
                                ||||||||| ||     ||||
                                AGACACCAT CT     ACCC
                                    _ CCAA__
GAM1103 ZAP3     5' CCCAGTTCCACCAGCCTCCAG  77222    T_  A  ACA
                                CTG  GGT TG   GAACTGGG
                                |||  ||| ||   ||||||||
                                GAC  CCG AC   CTTGACCC
                                  CT   _  CAC
GAM1103 LOC112970 3' CCCTTTTTTCATACCACA   56535       C   CT
                                TGTGGTATGA AGAA  GGG
                                |||||||||| ||||  |||
                                ACACCATACT TTTT  CCC
                                    _   T_
GAM1103 LOC130574 3' CCCAAGTTCCATACCATA   74955       ACA   _
                                TGTGGTATG   GAACT GGG
                                |||||||||   ||||| |||
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                                ATACCATAC   CTTGA CCC
                                    ___     A
GAM1103  LOC131583 5'  CCCAACTCCCTACCACAGG   75864         TGACA  AC
                                TCTGTGGTA    GA  TGGG
                                |||||||||    ||  ||||
                                GGACACCAT    CT  ACCC
                                     CC___  CA
GAM1103  LOC138428 3'  CCAGCCACTGCCACAGA     75333         _  ACAGAA
                                TCTGTGGTA TG     CTGG
                                ||||||||| ||     ||||
                                AGACACCGT AC     GACC
                                     C  C_____
GAM1103  LOC142955 3'  CCCAACTCTGTCATCTGTA   76445    TG T       AC
                                TG  G ATGACAGA  TGGG
                                ||  | ||||||||  ||||
                                AT  C TACTGTCT  ACCC
                                 GT _       CA
GAM1103  LOC143308 5'  CCCAGTTCCATCCTGGCCA   82937      AT_  CA
                                TGGT   GA  GAACTGGG
                                ||||   ||  ||||||||
                                ACCG   CT  CTTGACCC
                                  GTC  AC
GAM1103  LOC145241 3'  CCCTTACGTCAGTACCACA   62867        _   AGAACT
                                TGTGGTA TGAC     GGG
                                ||||||| ||||     |||
                                ACACCAT ACTG     CCC
                                    G    CATT__
GAM1103  LOC148760 3'  CCCAACCCCTGCACCACAGG  84203        AT A   AAC_
                                TCTGTGGT  G CAG    TGGG
                                ||||||||  | |||    ||||
                                GGACACCA  C GTC    ACCC
                                     __ _   CCCA
GAM1103  LOC149271 3'  CCCACCTCCCACCCACCACAGA 79239         ATGACA  AC
                                TCTGTGGT     GA  TGGG
                                ||||||||     ||  ||||
                                AGACACCA     CT  ACCC
                                     CCCACC  CC
GAM1103  LOC196707 3'  CCCAGTTCCGCAGCAGA     87526      GGTA  ACA
                                TCTGT    TG   GAACTGGG
                                |||||    ||   ||||||||
                                AGACG    AC   CTTGACCC
                                   _____  GC_
GAM1103  LOC197287 5'  CCAGTCCCTGCCACAGA     60861         TGACA  A
                                TCTGTGGTA    GA CTGG
                                |||||||||    || ||||
                                AGACACCGT    CT GACC
                                     CC___  _
GAM1103  LOC197287 5'  CCAGTCCCTGCCACAGA     60862         TGACA  A
                                TCTGTGGTA    GA CTGG
                                |||||||||    || ||||
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                                AGACACCGT    CT GACC
                                     CC___  _
GAM1103  LOC197287 5'  CCAGTCCCTGCCACAGA     60863        TGACA  A
                                TCTGTGGTA    GA CTGG
                                |||||||||    || ||||
                                AGACACCGT    CT GACC
                                     CC___  _
GAM1103  LOC197358 3'  CCCAGTCTGATGCACCACGGA  88027       AT A   A
                                TCTGTGGT  G CAGA CTGGG
                                ||||||||  | |||| |||||
                                AGGCACCA  T GTCT GACCC
                                     CG A   _
GAM1103  LOC219857 5'  CTCGGCATCAGCACCACAGA   91510       A_  CAGAA
                                TCTGTGGT  TGA    CTGGG
                                ||||||||  |||    |||||
                                AGACACCA  ACT    GGCTC
                                     CG   AC___
GAM1103  LOC221472 3'  CCAGCTCCTGCCACAGA     92298        T  CAGAA
                                TCTGTGGTA GA    CTGG
                                |||||||||  ||    ||||
                                AGACACCGT CT    GACC
                                     C  C____
GAM1103  LOC253573 3'  CCCAGTTCTGACATTCACAG   97047      T   A
                                CTGTGG ATG CAGAACTGGG
                                |||||| ||| ||||||||||
                                GACACT TAC GTCTTGACCC
                                   _   A
GAM1103  LOC254263 3'  CCCAGCCCTGCCCCTTGGCCGC 94715       ATGA___   AA
            AGA                   TCTGTGGT      CAG  CTGGG
                                |||||||      |||  |||||
                                AGACGCCG      GTC  GACCC
                                     GTTCCCC   CC
GAM1103  LOC257065 5'  CCCAGTTCCACCCCCACCCAGA 97637     T   ATGACA_
                                TCTG GGT      GAACTGGG
                                |||| |||      ||||||||
                                AGAC CCA      CTTGACCC
                                  _   CCCCCAC
GAM1103  LOC257471 5'  CCAGAATCTCATACCACAGA   95687          CAGAA
                                TCTGTGGTATGA    CTGG
                                ||||||||||||    ||||
                                AGACACCATACT    GACC
                                      CTAA_
GAM1103  LOC92340  3'  CCAACTCCATCCACGGA     68988       T   ACA  AC
                                TCTGTGG ATG   GA  TGG
                                ||||||| |||   ||  |||
                                AGGCACC TAC   CT  ACC
                                   _   ___  CA
GAM1104  CRIM1     3'  CTACTGGAATATTGTCCA    33174       CT  CAC
                                TGGAC  TG   TCCAGTAG
                                |||||  ||   ||||||||
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                                ACCTG AT  AGGTCATC
                                  TT A__
GAM1104 LEAP-2  5' CTACTGGGAAGAAAGCCCAT 53742    AC  GCAC
                                ATGG CTT  TCCAGTAG
                                |||| |||  ||||||||
                                TACC GAA  GGGTCATC
                                  C_ AGAA
GAM1105 ABCB1   5' CCAGAACATTCCTCCTGGAA 6247     CTGT CT
                                TTCC  GG ATGTTCTGG
                                ||||  ||  |||||||||
                                AAGG  CC  TACAAGACC
                                  TCCT T_
GAM1105 AGT     3' CCAGAACACAGTGCCTGGCA 3454     __  TA__
                                TGT GGC  TGTTCTGG
                                ||| |||  ||||||||
                                ACG CCG  ACAAGACC
                                  GT  TGAC
GAM1105 ALDOB   3' CCAGAATACCCACCCAAGAA 68087    CCT_  CTA
                                TTC  GTGG  TGTTCTGG
                                |||  ||||  ||||||||
                                AAG  CACC  ATAAGACC
                                  AACC  C__
GAM1105 ARL4    3' CCAGAACACAGTTGTGGGAA 19198     T TG  A
                                TTCCC G  GCT TGTTCTGG
                                ||||| |  ||| ||||||||
                                AAGGG T  TGA ACAAGACC
                                  _ GT  C
GAM1105 B3GAT1  3' CCAGAACAAAGGACAGAGAA 37827    C   GG A
                                TTC CTGT  CT TGTTCTGG
                                ||| ||||  || ||||||||
                                AAG GACA  GA ACAAGACC
                                  A  G_ A
GAM1105 B3GAT1  3' CCAGAACAAAGGACAGAGAA 53972    C   GG A
                                TTC CTGT  CT TGTTCTGG
                                ||| ||||  || ||||||||
                                AAG GACA  GA ACAAGACC
                                  A  G_ A
GAM1105 CD79B   3' CCAGAAGAGCCACAGG     41207       ATG
                                CCTGTGGCT  TTCTGG
                                |||||||||  ||||||
                                GGACACCGA  AAGACC
                                     G__
GAM1105 CD79B   3' CCAGAAGAGCCACAGG     5271        ATG
                                CCTGTGGCT  TTCTGG
                                |||||||||  ||||||
                                GGACACCGA  AAGACC
                                     G__
GAM1105 CDH3    3' CCAAACGTCAGGCCACAG   8380        __   C
                                CTGTGGCT ATGTT TGG
                                |||||||| ||||| |||
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                                GACACCGG  TGCAA ACC
                                    AC    _
GAM1105  COL5A1   5'  GCCAGAACAGCCGCCGCCACAA 3634    CC     TA____      III
             AGAA                  C  TGTGGC     TGTTCTGG   C
                                |  ||||||     ||||||||  |
                                G  ACACCG     ACAAGACC   G
                                 AA     CCGCCG       III
GAM1105  CRIM1    3'  CCAGAACAAAGGCAG       33173      GG  A
                                CTGT  CT TGTTCTGG
                                ||||  || ||||||||
                                GACG  GA ACAAGACC
                                  __  A
GAM1105  DIAPH2   3'  CCAAAACAAGTCTAGCAGGGAA 22063         __    A    C
                                TTCCCTGT  GGCT TGTT TGG
                                ||||||||  |||| |||| |||
                                AAGGGACG  CTGA ACAA ACC
                                    AT    _   A
GAM1105  DMD      3'  AGAAAATATAGTCACAGG    14414            __
                                CCTGTGGCTATGT  TCT
                                ||||||||||||  |||
                                GGACACTGATATA  AGA
                                      AA
GAM1105  ED1      3'  TTGGAACAATCACAGGGAA    7376           CTA    TG
                                TTCCCTGTGG   TGTTC  G
                                ||||||||||   |||||  |
                                AAGGGACACT   ACAAG  T
                                     A__     GT
GAM1105  EXTL3    3'  CCAAAACATGCCGCAGGGAG   7528           T    C
                                TTCCCTGTGGC ATGTT TGG
                                |||||||||||  ||||| |||
                                GAGGGACGCCG TACAA ACC
                                      _     A
GAM1105  FCRH3    3'  CCAGAGTGGCCCACAGG     53630        _    GT
                                CCTGTGG CTAT  TCTGG
                                |||||||  ||||  |||||
                                GGACACC GGTG  AGACC
                                    C    __
GAM1105  FECH     3'  CGTGGTGCCACAGGGAA     3753           __
                                TTCCCTGTGGC  TATG
                                ||||||||||  ||||
                                AAGGGACACCG  GTGC
                                      TG
GAM1105  FGFRL1   3'  CCAGAACATACAAGGA      41619     C   GGCT
                                TCC TGT    ATGTTCTGG
                                |||  |||    |||||||||
                                AGG ACA    TACAAGACC
                                  A  _____
GAM1105  GATA4    3'  CCAGAACAACAACTGGGAA    9004        T  GGCTA
                                TTCCC GT     TGTTCTGG
                                |||||  ||    ||||||||
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                                AAGGG CA    ACAAGACC
                                  T  ACA__
GAM1105  GNRH1    5'  CCATCACCAGCCACAGAGA   5883    C      AT  TC
                                TC CTGTGGCT  GT  TGG
                                || ||||||||  ||  |||
                                AG GACACCGA  CA  ACC
                                 A       C_  CT
GAM1105  HAMP     3'  CCAGAACATAGGTCTTGGAA  40991     CTGT  _
                                TTCC    GGC TATGTTCTGG
                                ||||    ||| ||||||||||
                                AAGG    CTG ATACAAGACC
                                  TT__   G
GAM1105  IPP      3'  TAGTTTGAGCCACAGAGAA   19729    C      ATGTT
                                TTC CTGTGGCT    CTG
                                ||| ||||||||    |||
                                AAG GACACCGA    GAT
                                  A       GTTT_
GAM1105  ITGB1    3'  CCAGTGTGGCCCAGGGAA    53369       T     GTT
                                TTCCCTG GGCTAT   CTGG
                                ||||||| ||||||   ||||
                                AAGGGAC CCGGTG   GACC
                                    _     T__
GAM1105  KCNQ1    3'  CCAGCTGCTGAGCCGCAGAGAA 4021     C      AT  T_
                                TTC CTGTGGCT  GT  CTGG
                                ||| ||||||||  ||  ||||
                                AAG GACGCCGA  CG  GACC
                                  A       GT  TC
GAM1105  KDR      3'  CAGAATACCACAAAGAA     9591     CC    CTA
                                TTC  TGTGG   TGTTCTG
                                |||  |||||   |||||||
                                AAG  ACACC   ATAAGAC
                                  AA    ___
GAM1105  LEP      3'  CCAGGGGCCCACAGGGAA    4047          _  ATGT
                                TTCCCTGTGG CT    TCTGG
                                |||||||||| ||    |||||
                                AAGGGACACC GG    GGACC
                                      C  ____
GAM1105  MKI67    3'  CCAGTGACCAGCCACAGGAGA  10041    _       AT  _
                                TC CCTGTGGCT  GTT CTGG
                                || |||||||||  ||| ||||
                                AG GGACACCGA  CAG GACC
                                 A       C_   T
GAM1105  NEFH     3'  CCGGAACAGCCAAAG      40780    G    AT
                                CT TGGCT  GTTCTGG
                                || |||||  |||||||
                                GA ACCGA  CAAGGCC
                                 A    __
GAM1105  NXF2     5'  CCAGAACATCACCAAG      35136    G   CT
                                CT TGG  ATGTTCTGG
                                || |||  |||||||||
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                                GA ACC  TACAAGACC
                                 _  AC
GAM1105 PDE6D    3' CCAGCATACACACAGGGAA   10489        GC   TT
                                TTCCCTGTG  TATG  CTGG
                                |||||||||  ||||  ||||
                                AAGGGACAC  ATAC  GACC
                                     AC   __
GAM1105 PHEMX    5' CCAGCTGGAAACCACAGGGAG 57359        CTATGTT
                                TTCCCTGTGG     CTGG
                                ||||||||||     ||||
                                GAGGGACACC     GACC
                                     AAAGGTC
GAM1105 PHEMX    5' CCAGCTGGAAACCACAGGGAG 57364        CTATGTT
                                TTCCCTGTGG     CTGG
                                ||||||||||     ||||
                                GAGGGACACC     GACC
                                     AAAGGTC
GAM1105 PODXL    3' CCAGAATGACACAAAGGA    18230    C_   GCTAT
                                TCC  TGTG    GTTCTGG
                                |||  ||||    |||||||
                                AGG  ACAC    TAAGACC
                                  AA   AG___
GAM1105 PRODH    3' CTGGGACAGCCACTGGAA    32925     CT    AT   TG
                                TTCC  GTGGCT  GTTC  G
                                ||||  ||||||  ||||  |
                                AAGG  CACCGA  CAGG  C
                                  T_     __   GT
GAM1105 RANBP2L1 3' CCAGAATAAAACCACCAGGAA 17313     CT   CTA
                                TTCC  GTGG   TGTTCTGG
                                ||||  ||||   ||||||||
                                AAGG  CACC   ATAAGACC
                                  AC   AAA
GAM1105 REGL     3' CCAGAACATGAATTCAGG    21486     TGGC
                                CCTG   TATGTTCTGG
                                ||||   ||||||||||
                                GGAC   GTACAAGACC
                                  TTAA
GAM1105 SLC19A1  5' CCAGAATGCATCCAGAGGGAA 11755      G  CTA
                                TTCCCT TGG   TGTTCTGG
                                ||||||  |||  ||||||||
                                AAGGGA ACC   GTAAGACC
                                   G   TAC
GAM1105 ST14     3' CCAGAACATACACTGTGAA   41765    CCT   GC
                                TTC   GTG  TATGTTCTGG
                                |||   |||  ||||||||||
                                AAG   CAC  ATACAAGACC
                                  TGT   __
GAM1105 TBL2     3' CCAGAACAACCTAGAGAA    52182    C   T  CTA
                                TTC CTG GG   TGTTCTGG
                                ||| ||| ||   ||||||||
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                                AAG GAT CC   ACAAGACC
                                  A   _ A__
GAM1105  TBL2     3'  CCAGAACAACCTAGAGAA    24926     C   T  CTA
                                TTC CTG GG   TGTTCTGG
                                ||| ||| ||   ||||||||
                                AAG GAT CC   ACAAGACC
                                  A   _ A__
GAM1105  TCFL4    3'  CCAGGATAAGACCACAGGGAA  63461          _  A
                                TTCCCTGTGG CT TGTTCTGG
                                |||||||||| || ||||||||
                                AAGGGACACC GA ATAGGACC
                                      A  _
GAM1105  TFAP4    3'  CCGGGGCAGCCACAGGGAG   12237           AT
                                TTCCCTGTGGCT  GTTCTGG
                                ||||||||||||  |||||||
                                GAGGGACACCGA  CGGGGCC
                                              __
GAM1105  UBE2L6   3'  CCAGGGGGAGCCACGG      14873        ATG
                                CTGTGGCT   TTCTGG
                                ||||||||   ||||||
                                GGCACCGA   GGGACC
                                     GG_
GAM1105  UBQLN3   3'  CAAAACATAGTGGAG       33926      CTGTG       C
                                TTCC    GCTATGTT TG
                                ||||    |||||||| ||
                                GAGG    TGATACAA AC
                                  _____       A
GAM1105  UMOD     3'  CCAGTGCTCCAGCCACAG    12548         AT_  T
                                CTGTGGCT   GT CTGG
                                ||||||||   || ||||
                                GACACCGA   CG GACC
                                     CCT  T
GAM1105  WBSCR5   3'  CCAGAACAGGGCAGAG      26256    G  G  A
                                CT TG CT TGTTCTGG
                                || || || ||||||||
                                GA AC GG ACAAGACC
                                 G  G  _
GAM1105  WBSCR5   3'  CCAGAACAGGGCAGAG      41856    G  G  A
                                CT TG CT TGTTCTGG
                                || || || ||||||||
                                GA AC GG ACAAGACC
                                 G  G  _
GAM1105  WBSCR5   3'  CCAGAACAGGGCAGAG      50610    G  G  A
                                CT TG CT TGTTCTGG
                                || || || ||||||||
                                GA AC GG ACAAGACC
                                 G  G  _
GAM1105  ZNF134   3'  CAGTTTAAGCCACAGGGAA   12846           A  TT
                                TTCCCTGTGGCT TG  CTG
                                |||||||||||| ||  |||
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                                AAGGGACACCGA AT  GAC
                                      _  TT
GAM1105  ZNF36    3'  CCTTCGTAGCCACAAGG     93960    C        TTCT
                                CC TGTGGCTATG    GG
                                || ||||||||||    ||
                                GG ACACCGATGC    CC
                                 A         TT__
GAM1105  ABCA9    5'  CAGAACATGCAGAGA       54410    C    GGCT
                                TC CTGT    ATGTTCTG
                                || ||||    ||||||||
                                AG GACG    TACAAGAC
                                 A   _____
GAM1105  ADAMTSL1  3'  CCTCAAATAGCACAGGGAA   57686         G    GTTCT
                                TTCCCTGTG CTAT     GG
                                ||||||||| ||||     ||
                                AAGGGACAC GATA     CC
                                      _    AACT_
GAM1105  BAIAP1   3'  CCAGAACGGCAGCAGG      16449      G   AT
                                CCTGT GCT  GTTCTGG
                                ||||| |||  |||||||
                                GGACG CGG  CAAGACC
                                   A   __
GAM1105  BCKDK    3'  CCAGAACTTGGAGCAGGGAA   59793        GG   T
                                TTCCCTGT  CTA GTTCTGG
                                ||||||||  ||| |||||||
                                AAGGGACG  GGT CAAGACC
                                     A_   T
GAM1105  C11orf25  3'  CCAAATTAGGGCCACAG     48639        AT_   C
                                CTGTGGCT   GTT TGG
                                ||||||||   ||| |||
                                GACACCGG   TAA ACC
                                     GAT   _
GAM1105  C20orf112 3'  CCAGTGCTGCCACAGGGA    54640          TAT  T
                                TCCCTGTGGC   GT CTGG
                                ||||||||||   || ||||
                                AGGGACACCG   CG GACC
                                      T__  T
GAM1105  C6orf26   3'  CCAAAACACAGAGCAGG     47509      GG  A    C
                                CCTGT  CT TGTT TGG
                                |||||  || |||| |||
                                GGACG  GA ACAA ACC
                                   A_  C    A
GAM1105  CGGBP1    5'  CTGGCACCACAGGGAA      13362         CTA    CT
                                TTCCCTGTGG   TGTT  G
                                ||||||||||   ||||  |
                                AAGGGACACC   ACGG  C
                                      ____   T_
GAM1105  DKFZP566G1424 5'  CCAGTGCTGCCACAGGGA    84779          TAT  T
                                TCCCTGTGGC   GT CTGG
                                ||||||||||   || ||||
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                                AGGGACACCG   CG GACC
                                      T__  T
GAM1105  DKFZp586I021 5'  CCAGACGTCACCACAGGGA    50088         CT    T
                                TCCCTGTGG  ATGT CTGG
                                |||||||||  |||| ||||
                                AGGGACACC  TGCA GACC
                                     AC    _
GAM1105  DKFZP727M111 5'  CCAATCTGGTCACAGGGAA    31407           T  TC
                                TTCCCTGTGGCTA GT  TGG
                                |||||||||||||  ||  |||
                                AAGGGACACTGGT TA  ACC
                                       C  __
GAM1105  ELF4     3'  CCGTGGATCAGCCACAGGGA   7431           AT    _
                                TCCCTGTGGCT  GTTC TGG
                                ||||||||||  |||| |||
                                AGGGACACCGA  TAGG GCC
                                      C_    T
GAM1105  ERG-1    3'  CCAGGATGCCAAAGG      41842     G    TAT
                                CCT TGGC   GTTCTGG
                                |||  ||||   |||||||
                                GGA ACCG   TAGGACC
                                  A   ____
GAM1105  FLJ00058  5'  CCAGAAATGCCAGCAGGGAA   78765        _    TATG
                                TTCCCTG TGGC    TTCTGG
                                |||||||  ||||    ||||||
                                AAGGGAC ACCG    AAGACC
                                    G    TA__
GAM1105  FLJ12816  3'  CCAGAACAGGACGACAGTGAA  41932     C    GGCTA
                                TTC CTGT    TGTTCTGG
                                |||  ||||    ||||||||
                                AAG GACA    ACAAGACC
                                  T    GCAGG
GAM1105  FLJ13315  3'  CCAGAACATAATACA       46568      GC
                                TGTG  TATGTTCTGG
                                ||||  ||||||||||
                                ACAT  ATACAAGACC
                                  A_
GAM1105  FLJ20010  3'  CCAGAACGATTGGAACAGG    38716       GG   __
                                CCTGT  CTA  TGTTCTGG
                                |||||  |||  ||||||||
                                GGACA  GGT  GCAAGACC
                                   A_   TA
GAM1105  FLJ22369  5'  ATGGCGCGACAGGGAA      49918         _ _
                                TTCCCTGT G GCTAT
                                ||||||||  | |||||
                                AAGGGACA C CGGTA
                                     G G
GAM1105  FLJ23563  3'  CCAGAATGCTACAAAAGAA   67593     CC_     TAT
                                TTC   TGTGGC   GTTCTGG
                                |||   ||||||   |||||||
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                                AAG   ACATCG   TAAGACC
                                  AAA     ___
GAM1105  FLJ32332  3'  CACAGCACACAGGGAA      58299          _  A
                                TTCCCTGTG GCT TG
                                ||||||||| ||| ||
                                AAGGGACAC CGA AC
                                     A   C
GAM1105  GRIN3A    3'  CCAAGTGAAGCAGCCACAGGGA 55968          ATG  ___
                                TCCCTGTGGCT   TTC   TGG
                                ||||||||||   |||   |||
                                AGGGACACCGA   AAG   ACC
                                      CG_   TGA
GAM1105  HSPC166   3'  CCAGAACACATGGAGGGAA   26366       G  GCTA
                                TTCCCT TG    TGTTCTGG
                                ||||||  ||    ||||||||
                                AAGGGA GT    ACAAGACC
                                   G  AC__
GAM1105  HSPC251   3'  CCAGGCTAGAGCCACAGAGA   33249    C      A  TT
                                TC CTGTGGCT TG  CTGG
                                || ||||||||  ||  ||||
                                AG GACACCGA AT  GACC
                                 A       G  CG
GAM1105  IGF2AS    3'  CCAGGGTGCAACAGAGAA    33095     C    G  TAT TT
                                TTC CTGT GC   G  CTGG
                                ||| |||| ||   |  ||||
                                AAG GACA CG   T  GACC
                                  A   A  ___ GG
GAM1105  ILF3      3'  CCAAAACACGCTGGGAA     15722      T   GCTA    C
                                TTCCC GTG    TGTT TGG
                                ||||| |||    |||| |||
                                AAGGG CGC    ACAA ACC
                                   T  _____    A
GAM1105  KIAA0040  3'  CCAAAGTTTCCAGCAGGGAA   27780        _   CT  GTTC
                                TTCCCTG TGG  AT    TGG
                                ||||||| |||  ||    |||
                                AAGGGAC ACC  TG    ACC
                                    G   TT  AA__
GAM1105  KIAA0254  3'  CAGACAGTCACAGGGAA     28596           ATGT
                                TTCCCTGTGGCT    TCTG
                                ||||||||||||   ||||
                                AAGGGACACTGA    AGAC
                                      C___
GAM1105  KIAA0336  3'  CCAGAATAAAACCACCAGGAA  27589      CT    CTA
                                TTCC  GTGG   TGTTCTGG
                                ||||  ||||   ||||||||
                                AAGG  CACC   ATAAGACC
                                  AC    AAA
GAM1105  KIAA0494  3'  CCAGAACACATTTGGG      28740     T_  GCTA
                                CCC  GTG    TGTTCTGG
                                |||  |||    ||||||||
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                                GGG  TAC    ACAAGACC
                                  TT  _____
GAM1105  KIAA0537  3'  CCAGAACAGCCTACAGGGGA   29244         _   AT
                                TTCCCTGT GGCT  GTTCTGG
                                |||||||| ||||  |||||||
                                AGGGGACA CCGA  CAAGACC
                                    T   __
GAM1105  KIAA0774  5'  CGGGATGCCACAAGGAA     91752      C     TAT    TG
                                TTCC TGTGGC   GTTC  G
                                |||| ||||||   ||||  |
                                AAGG ACACCG   TAGG  C
                                  A     ___    GT
GAM1105  KIAA0828  3'  CCATGAAAGCCACAGAGGA    81194     _      ATG   _
                                TCC CTGTGGCT   TTC TGG
                                ||| ||||||||   ||| |||
                                AGG GACACCGA   AAG ACC
                                  A       ___  T
GAM1105  KIAA1118  3'  CCAGAGGCCCACAGGGA     69606         _ ATGT
                                TCCCTGTGG CT    TCTGG
                                |||||||||  ||    |||||
                                AGGGACACC GG    AGACC
                                    C  _____
GAM1105  KIAA1742  3'  CAGATCCACAGGGAG       77657          CTATGT
                                TTCCCTGTGG      TCTG
                                ||||||||||      ||||
                                GAGGGACACC      AGAC
                                    T_______
GAM1105  KIAA1944  5'  CCAACCTAGCCACAGGGA    75558           T  TC
                                TCCCTGTGGCTA GT  TGG
                                ||||||||||||  ||  |||
                                AGGGACACCGAT CA  ACC
                                    C  __
GAM1105  KIAA1981  3'  CGGAACAGCACAAGGAA     88342      C    G  AT    TG
                                TTCC TGTG CT  GTTC  G
                                |||| |||| ||  ||||  |
                                AAGG ACAC GA  CAAG  C
                                  A   _ __    GT
GAM1105  NXPH3     3'  ACGGAGCCACAGAGAG      65747     C       A
                                TTC CTGTGGCT TGT
                                ||| ||||||| |||
                                GAG GACACCGA GCA
                                  A       G
GAM1105  PP5395    3'  TCAGGATAGCACAGGGAA     72110         G  AT
                                TTCCCTGTG CT  GTTCTGG
                                |||||||| ||  |||||||
                                AAGGGACAC GA  TAGGACT
                                      _  __
GAM1105  PRDM7     3'  CCAGAAGGGCCACAGAGAA   53788     C       ATG
                                TTC CTGTGGCT   TTCTGG
                                ||| ||||||||   ||||||
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                                AAG GACACCGG   AAGACC
                                  A       G__
GAM1105  PRDM9    3'  CCAGAAGGGCCACAGAGAA   39575     C       ATG
                                TTC CTGTGGCT   TTCTGG
                                ||| ||||||||   ||||||
                                AAG GACACCGG   AAGACC
                                  A       G__
GAM1105  PXR2b    3'  ATATAGCCCAAGGAA      33337     C  T
                                TTCC TG GGCTATGT
                                |||| || ||||||||
                                AAGG AC CCGATATA
                                  A  _
GAM1105  RAB33B   3'  CCAGCTTAGCCACAAAGAA   48490     CC      TGTT
                                TTC  TGTGGCTA   CTGG
                                |||  ||||||||   ||||
                                AAG  ACACCGAT   GACC
                                  AA       TC__
GAM1105  SH120    3'  CCAGAACATGAGAGGGAG    32920      GTGGC
                                TTCCCT    TATGTTCTGG
                                ||||||    ||||||||||
                                GAGGGA    GTACAAGACC
                                   GA___
GAM1105  SH120    3'  CCAGAACATGAGAGGGAG    94606      GTGGC
                                TTCCCT    TATGTTCTGG
                                ||||||    ||||||||||
                                GAGGGA    GTACAAGACC
                                   GA___
GAM1105  SLC2A12  3'  CCAGAACACACAGTGTGGA   59078     ___    GCTA
                                TCC   CTGTG   TGTTCTGG
                                |||   |||||   ||||||||
                                AGG   GACAC   ACAAGACC
                                  TGT   _____
GAM1105  SP329    3'  CCAGAGTGCTCCACAGGGA   47924        CTA GT
                                TCCCTGTGG   T  TCTGG
                                |||||||||   |  |||||
                                AGGGACACC   G  AGACC
                                     TC_ TG
GAM1105  SSH2     3'  TCAGTAAGCCCACAGGGAA   62213        _  ATGTT
                                TTCCCTGTGG CT    CTGG
                                |||||||||| ||    ||||
                                AAGGGACACC GA    GACT
                                     C  AT___
GAM1105  SYTL4    5'  CCAGTCAGCCACAGGGAA    54939         ATGTT
                                TTCCCTGTGGCT    CTGG
                                ||||||||||||    ||||
                                AAGGGACACCGA    GACC
                                      CT___
GAM1105  TNRC4    3'  CCAGTCAGCCACAGAGA     23221     C      ATGTT
                                TC CTGTGGCT    CTGG
                                || ||||||||    ||||
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                                AG GACACCGA     GACC
                                 A       CT___
GAM1105  UBE3B    3'  CCAGACTGTCAGCACAGGGAA  76919         G  _  GT
                                TTCCCTGTG CT AT  TCTGG
                                ||||||||| || ||  |||||
                                AAGGGACAC GA TG  AGACC
                                      _  C  TC
GAM1105  VPS4A    3'  CCTTGCAGCCACAGAGA     25102    C      AT  TCT
                                TC CTGTGGCT  GT   GG
                                || ||||||||  ||   ||
                                AG GACACCGA  CG   CC
                                 A       __  TT_
GAM1105  XYLT1    5'  CCAACAGCAGCCACGGGAA   77847      T     A_   TC
                                TTCCC GTGGCT  TGT  TGG
                                ||||| ||||||  |||  |||
                                AAGGG CACCGA  ACA  ACC
                                   _     CG  __
GAM1105  ZFP100   3'  CCAGAAAGCCAAAAAGAA    70050     CCTG    ATG
                                TTC    TGGCT   TTCTGG
                                |||    |||||   ||||||
                                AAG    ACCGA   AAGACC
                                  AAAA    ____
GAM1105  ZNF213   5'  CAGCTACCACAGGGGA      65091          C  TGTT
                                TTCCCTGTGG TA    CTG
                                |||||||||| ||    |||
                                AGGGGACACC AT    GAC
                                      _  C___
GAM1105  LOC112609 3'  CCAGTGTGGCACAGGGAA    72837         G    GTT
                                TTCCCTGTG CTAT   CTGG
                                ||||||||| ||||   ||||
                                AAGGGACAC GGTG   GACC
                                      _   T__
GAM1105  LOC115073 5'  CCAGGCGTCAAACCACAGGGA  73204         CT__    T
                                TCCCTGTGG    ATGT CTGG
                                |||||||||    |||| ||||
                                AGGGACACC    TGCG GACC
                                     AAAC    _
GAM1105  LOC122962 5'  CCAGACAGTGGCCACTGAGAA  75587     CCT       GT
                                TTC   GTGGCTAT  TCTGG
                                |||   ||||||||  |||||
                                AAG   CACCGGTG  AGACC
                                  AGT       AC
GAM1105  LOC124044 3'  CCAGAACACTCAGAGGGA    76025      G   CTA
                                TCCCT TGG   TGTTCTGG
                                ||||| |||   ||||||||
                                AGGGA ACT   ACAAGACC
                                   G   C__
GAM1105  LOC143308 5'  CCAAATTTGGCCACAG      82936         T   C
                                CTGTGGCTA GTT TGG
                                ||||||||| ||| |||
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                                GACACCGGT TAA ACC
                                      T  _
GAM1105  LOC145314 3'  CCAGAACACATCACCTGAG   77086    CCT   CTA
                                TTC  GTGG  TGTTCTGG
                                |||  ||||  ||||||||
                                GAG  CACT  ACAAGACC
                                  TC_   AC_
GAM1105  LOC146420 3'  CCAGAACCAGTTACAG     83667       AT
                                CTGTGGCT  GTTCTGG
                                ||||||||  |||||||
                                GACATTGA  CAAGACC
                                     C_
GAM1105  LOC146445 3'  CCAGAGCCACCACAGGGA   83678        CTAT
                                TCCCTGTGG   GTTCTGG
                                |||||||||   |||||||
                                AGGGACACC   CGAGACC
                                      AC__
GAM1105  LOC147178 3'  CCAGCCAGCCACGGAGAA   61323    C      ATGTT
                                TTC CTGTGGCT    CTGG
                                ||| ||||||||    ||||
                                AAG GGCACCGA    GACC
                                  A       CC___
GAM1105  LOC148529 5'  CACAGCCACAGGAGAA     84166    _      A
                                TTC CCTGTGGCT TG
                                ||| ||||||||| ||
                                AAG GGACACCGA AC
                                  A       C
GAM1105  LOC148930 5'  CCAGGGGCAGACCACGGGGAA  79093         CTA   _
                                TTCCCTGTGG  TGTTC TGG
                                ||||||||||  ||||| |||
                                AAGGGGCACC  ACGGG ACC
                                      AG_   G
GAM1105  LOC149950 5'  CCAGAACATGATCTCAGG   79551     T GC
                                CCTG G  TATGTTCTGG
                                |||| |  ||||||||||
                                GGAC C  GTACAAGACC
                                  T TA
GAM1105  LOC150378 5'  CCAGAAACAAGCCACGGGAA  79742     T    ATG
                                TTCCC GTGGCT  TTCTGG
                                ||||| ||||||  ||||||
                                AAGGG CACCGA  AAGACC
                                   _    ACA
GAM1105  LOC150951 5'  CCAGGGCCACACAGGGAA   85167        GCTAT
                                TTCCCTGTG   GTTCTGG
                                |||||||||   |||||||
                                AAGGGACAC   CGGGACC
                                      AC___
GAM1105  LOC151429 3'  CCAGGAGACCACAGGGA    85347        _  ATGT
                                TCCCTGTGG CT   TCTGG
                                ||||||||| ||   |||||
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                                AGGGACACC GA    GGACC
                                     A _____
GAM1105  LOC158434 3'  CCAGAATAAACCACTGGGAA   86819      T    CTA
                                TTCCC GTGG   TGTTCTGG
                                ||||| ||||   ||||||||
                                AAGGG CACC   ATAAGACC
                                   T    AA_
GAM1105  LOC170106 5'  CCAAGGCAGTCAGCCACAGG   82571         A__   TC
                                CCTGTGGCT   TGT  TGG
                                |||||||||   |||  |||
                                GGACACCGA   ACG  ACC
                                     CTG   GA
GAM1105  LOC196446 3'  CGGAAAGCCACAGAGAA     87708     C       ATG   TG
                                TTC CTGTGGCT   TTC  G
                                ||| ||||||||   |||  |
                                AAG GACACCGA   AAG  C
                                  A       ___   GT
GAM1105  LOC197136 3'  CCAGAACACTCAGAGGGA    89728      G   CTA
                                TCCCT TGG   TGTTCTGG
                                ||||| |||   ||||||||
                                AGGGA ACT   ACAAGACC
                                   G   C__
GAM1105  LOC197342 3'  CCAGGAGAAGCCACAGGGGA   87993           ATG
                                TTCCCTGTGGCT   TTCTGG
                                ||||||||||||   ||||||
                                AGGGGACACCGA   AGGACC
                                     AG_
GAM1105  LOC200734 3'  CCATCCGCAGCCACAGGGGA   88860           A  TTC
                                TTCCCTGTGGCT TG   TGG
                                |||||||||||| ||   |||
                                AGGGGACACCGA GC   ACC
                                     C  CT_
GAM1105  LOC201102 3'  CCTGACCAGCCACAGGAGA    88090    _       AT   CT
                                TC CCTGTGGCT  GTT  GG
                                || |||||||||  |||  ||
                                AG GGACACCGA  CAG  CC
                                  A        C_   T_
GAM1105  LOC201283 3'  CCAGAACACAGTCGTGAGGA   60413     CT     A
                                TCC  GTGGCT TGTTCTGG
                                |||  |||||| ||||||||
                                AGG  TGCTGA ACAAGACC
                                  AG     C
GAM1105  LOC202915 3'  CCACACGCCAGCCACAGGGGA  90388           A_   TC
                                TTCCCTGTGGCT  TGT  TGG
                                ||||||||||||  |||  |||
                                AGGGGACACCGA  GCA  ACC
                                     CC   C_
GAM1105  LOC204965 5'  CAGAGTGCACAGAGAA      90647     C     G TATG
                                TTC CTGTG C    TTCTG
                                ||| ||||| |    |||||
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                                AAG GACAC G    GAGAC
                                  A    _ T___
GAM1105  LOC205418 3'  CACAGCCAGCAGGGAA      90681        _    A
                                TTCCCTG TGGCT TG
                                ||||||| ||||| ||
                                AAGGGAC ACCGA AC
                                    G    C
GAM1105  LOC220692 3'  CCAGAATAAAACCACCAGGAA  91220      CT   CTA
                                TTCC  GTGG   TGTTCTGG
                                ||||  ||||   ||||||||
                                AAGG  CACC   ATAAGACC
                                  AC   AAA
GAM1105  LOC222631 5'  CCAGAACACAGCTGGAA     92838     CTGT   A
                                TTCC    GGCT TGTTCTGG
                                ||||    |||| ||||||||
                                AAGG    TCGA ACAAGACC
                                  _____   C
GAM1105  LOC253039 3'  CCAAATACATCTACAGGGAA   96153         CT   TC_
                                TTCCCTGTGG  ATGT   TGG
                                ||||||||||  ||||   |||
                                AAGGGACATC  TACA   ACC
                                      __    TAA
GAM1105  LOC253841 5'  CCAGAATGTAGCCACAG     96342
                                CTGTGGCTATGTTCTGG
                                ||||||||||||||||
                                GACACCGATGTAAGACC

GAM1105  LOC254028 3'  CCAGAACAGAAGCACCAAGAA  96539     CC  TG   A_
                                TTC  TG  GCT  TGTTCTGG
                                |||  ||  |||  ||||||||
                                AAG  AC  CGA  ACAAGACC
                                  A_  CA   AG
GAM1105  LOC257449 3'  CAGATCCACAGGGAG       62718          CTATGT
                                TTCCCTGTGG     TCTG
                                ||||||||||     ||||
                                GAGGGACACC     AGAC
                                      T_____
GAM1105  LOC89231  3'  GGACAGCACAGGGAA       92733         G  AT
                                TTCCCTGTG CT  GTTC
                                |||||||| ||  ||||
                                AAGGGACAC GA  CAGG
                                      _ __
GAM1105  LOC90550  3'  CCAGAACACAAATCAGAGGGA  73090       G   CTA_
                                TCCCT TGG    TGTTCTGG
                                ||||| |||    ||||||||
                                AGGGA ACT    ACAAGACC
                                   G   AAAC
GAM1105  LOC91373  3'  CCAGCAAGGCCACAG       65834         A  TT
                                CTGTGGCT TG  CTGG
                                |||||||| ||  ||||
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                                GACACCGG AC  GACC
                                    A  __
GAM1105 LOC91445 3' CCAGAACCTGCCACAGG     60547        TAT
                                CCTGTGGC   GTTCTGG
                                ||||||||   |||||||
                                GGACACCG   CAAGACC
                                    TC_
GAM1106 JAM2     5' CCAAAACAGAACAGACCCCCA  41116     A  C   GCTTA   GTC
                                TGG GG CTG    TGT   TGG
                                ||| || |||    |||   |||
                                ACC CC GAC    ACA   ACC
                                  C  A   AAG__   AA_
GAM1106 MTMR3    3' CCAGACACACCTGGGTCCCCA  40811     A    TG CTTA
                                TGG GGCC  G    TGTGTCTGG
                                ||| ||||  |    |||||||||
                                ACC CTGG  C    ACACAGACC
                                  C    GT C___
GAM1106 STK10    3' CAGAGGAGCCAGGCCTGCA    19982    G         ATGTG
                                TG AGGCCTGGCTT    TCTG
                                || ||||||||||     ||||
                                AC TCCGGACCGAG    AGAC
                                 G         G____
GAM1106 TUFT1    3' CATAAGCCAGGCCTTCA     39256
                                TGGAGGCCTGGCTTATG
                                |||||||||||||||||
                                ACTTCCGGACCGAATAC

GAM1106 ZNFN2A1  3' CAGACACACAACCCCTCTA    60736       CCT  C  A
                                TGGAGG   GG TT TGTGTCTG
                                ||||||   || || ||||||||
                                ATCTCC   CC AA ACACAGAC
                                    ___  _  C
GAM1106 DKFZP566G1424 5' CCAGACCTCAGCAGGCCCCCA  84777     A     G  TATGT
                                TGG GGCCTG CT    GTCTGG
                                ||| |||||| ||    ||||||
                                ACC CCGGAC GA    CAGACC
                                  C     _  CTC__
GAM1106 FLJ13102 3' CACCTGTGAGCCAAGCCCCCA  46003     A   C      __
                                TGG GGC TGGCTTAT  GTG
                                ||| ||| ||||||||  |||
                                ACC CCG ACCGAGTG  CAC
                                  C   A       TC
GAM1106 FLJ13154 3' CCAGTGGCTGAAAGCCAGGCCT 44792           AT_  GT
           CCA                   TGGAGGCCTGGCTT   GT  CTGG
                                ||||||||||||||   ||  ||||
                                ACCTCCGGACCGAA   CG  GACC
                                        AGT  GT
GAM1106 FLJ30294 3' CCAGACACCAGCAAGCCTCTA 58249       CTG   TAT
                                TGGAGGC   GCT   GTGTCTGG
                                |||||||   |||   ||||||||
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                                ATCTCCG  CGA  CACAGACC
                                   AA_  C__
GAM1106 FLNC    3' CACCCAAGCCAGGCTCCCA  7582     AG      AT
                                TGG  GCCTGGCTT  GTG
                                |||  |||||||||  |||
                                ACC  CGGACCGAA  CAC
                                  CT       CC
GAM1106 KIAA1297 3' TATGAGCCAGACCCCCA   72185    A  C
                                TGG GG CTGGCTTATG
                                ||| || ||||||||||
                                ACC CC GACCGAGTAT
                                  C  A
GAM1106 MD-1    3' CAGACATCCCCAGACTCCA  14962     GC   CTTAT
                                TGGAG  CTGG    GTGTCTG
                                |||||  ||||    |||||||
                                ACCTC  GACC    TACAGAC
                                   A_   CC___
GAM1106 LOC146445 3' CAGACCTGCCAGGCCACCA  83676    A      TTATGT
                                TGG GGCCTGGC     GTCTG
                                ||| ||||||||     |||||
                                ACC CCGGACCG     CAGAC
                                  A       TC____
GAM1106 LOC150368 3' CCAAACACATAAAACTTGCCCC 79699    A  CT  C_      C
                                GG GGC  GG  TTATGTGT TGG
                                || |||  ||  ||||||||| |||
                                CC CCG  TC  AATACACA ACC
                                 _  T_  AA       A
GAM1106 LOC197083 3' CCAGGAGCCCAAGCCAGGCCCC 87880    A       AT  GT
            CA                    TGG GGCCTGGCTT  GT  CTGG
                                |||  ||||||||||  ||  ||||
                                ACC CCGGACCGAA  CG  GACC
                                  C        CC  AG
GAM1106 LOC205095 3' CACTCAACCAGGCCTCCA    90697          C  AT
                                TGGAGGCCTGG TT  GTG
                                ||||||||||| ||  |||
                                ACCTCCGGACC AA  CAC
                                       _ CT
GAM1106 LOC219672 5' CCAGACAAAATGCCAGGCTCCA 91330      G     TTATG
                                TGGAG CCTGGC    TGTCTGG
                                ||||| ||||||    |||||||
                                ACCTC GGACCG    ACAGACC
                                   _     TAAA_
GAM1107 C1orf1   3' TACCTCAGAGCTCCAGGGA   6867          C  C  T
                                TTCCTGGAGC CT AG GTG
                                |||||||||| || || |||
                                AGGGACCTCG GA TC CAT
                                       A  C  _
GAM1107 EIF4E   3' ACATTGGTGAAGGATCCAGGAA 8757         GC  ____
                                TTCCTGGA  CCT   CAGTGT
                                ||||||||  |||   ||||||
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                                AAGGACCT  GGA   GTTACA
                                    A_   AGTG
GAM1107  HRB      3'  ATGTGCAAAACCGAGGGCTCCA 15705          A  G_  _
              G                  CTGGAGCCCTC GT  TG ACAT
                                 |||||||||| ||  || ||||
                                 GACCTCGGGAG CA  AC TGTA
                                       C  AA  G
GAM1107  LDB3     3'  ATTGCCAGGGCTCCAGGAA   76405          __
                                 TTCCTGGAGCCCT  CAGT
                                 ||||||||||||  ||||
                                 AAGGACCTCGGGA  GTTA
                                       CC
GAM1107  MEN1     5'  GCACTGAGAACCGCAGGAA   93373       GAGCC
                                 TTCCTG    CTCAGTGT
                                 ||||||    ||||||||
                                 AAGGAC    GAGTCACG
                                    GCCAA
GAM1107  SIL      3'  ATGTCACACTGGCTATCA    11683     _   CTC
                                 TGG AGCC   AGTGTGACAT
                                 ||| ||||   ||||||||||
                                 ACT TCGG   TCACACTGTA
                                   A   ___
GAM1107  SMARCC2  3'  TCACGGTTCCAGGAA      11807          CTCAGT
                                 TTCCTGGAGCC     GTGA
                                 ||||||||||      ||||
                                 AAGGACCTTGG     CACT
                                                 _______
GAM1107  SMARCC2  3'  TCACGGTTCCAGGAA      57410          CTCAGT
                                 TTCCTGGAGCC     GTGA
                                 ||||||||||      ||||
                                 AAGGACCTTGG     CACT
                                                 _______
GAM1107  SOX10    3'  GCAGGGGCTCCAGGAA      22687           CAG
                                 TTCCTGGAGCCCT   TGT
                                 ||||||||||||   |||
                                 AAGGACCTCGGGG   ACG
                                                 ___
GAM1107  C20orf173 3'  TCAGACCAAGGGCTCCAAGGA  55061      _      CA  G
                                 TCCT GGAGCCCT  GT TGA
                                 |||| ||||||||  || |||
                                 AGGA CCTCGGGA  CA ACT
                                   A       AC  G
GAM1107  DKFZp434F2322 3'  ATGTCACACTAAGCAGCCAG   69737      AGCC  C
                                 CTGG    CT AGTGTGACAT
                                 ||||    || ||||||||||
                                 GACC    GA TCACACTGTA
                                   GAC_  A
GAM1107  DKFZp434K1815 5'  CGCCAGTGCCGGGCTCCAGGAG 94265           T_  G  _
                                 TTCCTGGAGCCC  CA TG TG
                                 ||||||||||||  || || ||
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                                GAGGACCTCGGG  GT AC GC
                                      CC  G  C
GAM1107  FBXO21    3'  TCATGGGGCTCCAGGAA     53240          CAGT
                                TTCCTGGAGCCCT   GTGA
                                ||||||||||||   ||||
                                AAGGACCTCGGGG   TACT
                                                ____
GAM1107  FLJ11026  3'  CATAAAAGAAGTCCAGGAA   36990        GCC  CAG
                                TTCCTGGA  CT  TGTG
                                ||||||||  ||  ||||
                                AAGGACCT  GA  ATAC
                                    GAA  AA_
GAM1107  FLJ11088  5'  ATACAAAGAACTTCAGGAA   37038        CC  CA
                                TTCCTGGAG  CT  GTGT
                                |||||||||  ||  ||||
                                AAGGACTTC  GA  CATA
                                     AA  AA
GAM1107  KIAA0781  3'  CACAGTGAAAATCCAGGAA   67454        GCCC  G
                                TTCCTGGA   TCA TGTG
                                ||||||||   ||| ||||
                                AAGGACCT   AGT ACAC
                                    AAA_  G
GAM1107  KIAA1143  3'  ATGTCACTCTTGAACTTCAGGA 68670         CCC  _ T
           A                     TTCCTGGAG  TCA G GTGACAT
                                |||||||||  ||| | |||||||
                                AAGGACTTC  AGT C CACTGTA
                                     A__  T T
GAM1107  MGC15435  3'  ACACCCGAGAGCTCCAGGAG  50418          C  A_
                                TTCCTGGAGC CTC  GTGT
                                |||||||||| |||  ||||
                                GAGGACCTCG GAG  CACA
                                      A  CC
GAM1107  PDGFC     5'  CACAGAAGAGGGCTCTAGGAA 32495           AG_
                                TTCCTGGAGCCCTC  TGTG
                                ||||||||||||||  ||||
                                AAGGATCTCGGGAG  ACAC
                                       AAG
GAM1107  PIP3-E    3'  TTACAAAGACTCCAGGAA    66817         CCC  AG
                                TTCCTGGAG  TC  TGTGA
                                |||||||||  ||  |||||
                                AAGGACCTC  AG  ACATT
                                     ___  AA
GAM1107  REPS1     5'  ACATTGAGAGCACCAAGAA   49171     C  A  C
                                TTC TGG GC CTCAGTGT
                                ||| ||| || ||||||||
                                AAG ACC CG GAGTTACA
                                  A  A  A
GAM1107  SCYD1     3'  TGTCCAAGAAGCCCAGGAA   90934       A  CC  AG  T
                                TTCCTGG GC  TC  TG GACA
                                |||||||  ||  ||  || ||||
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                                AAGGACC CG  AG  AC CTGT
                                   _ A_  A_  _
GAM1107  TCL6     3'  GTCAAAGAGGCTCCAG     40087        C  AGTG
                                CTGGAGCC TC    TGAC
                                |||||||| ||    ||||
                                GACCTCGG AG    ACTG
                                   _  AA__
GAM1107  TCL6     3'  GTCAAAGAGGCTCCAG     24988        C  AGTG
                                CTGGAGCC TC    TGAC
                                |||||||| ||    ||||
                                GACCTCGG AG    ACTG
                                   _  AA__
GAM1107  TCL6     3'  GTCAAAGAGGCTCCAG     27004        C  AGTG
                                CTGGAGCC TC    TGAC
                                |||||||| ||    ||||
                                GACCTCGG AG    ACTG
                                   _  AA__
GAM1107  TRIM16   3'  ATGTCACACTGTGCCCAG    21334      A  CCT
                                CTGG GC   CAGTGTGACAT
                                |||| ||   ||||||||||
                                GACC CG   GTCACACTGTA
                                  _  T__
GAM1107  LOC122509 3'  CACACTGAGGCAGGGA     59142       GAGC
                                TTCCTG    CCTCAGTGTG
                                ||||||    ||||||||||
                                AGGGAC    GGAGTCACAC
                                   ____
GAM1107  LOC147166 3'  ATGTCACACTGTGCCCAG    78283      A  CCT
                                CTGG GC   CAGTGTGACAT
                                |||| ||   ||||||||||
                                GACC CG   GTCACACTGTA
                                  _  T__
GAM1107  LOC150481 3'  GCCTCCAAGGGCTCCAGGGA  79888           C__  T
                                TTCCTGGAGCCCT   AG GT
                                ||||||||||||   || ||
                                AGGGACCTCGGGA   TC CG
                                      ACC  _
GAM1107  LOC153146 5'  TAGGCAAGGGCTCCCAGAA   85934     CT      CA  G
                                TTC  GGAGCCCT  GT TG
                                |||  ||||||||  || ||
                                AAG  CCTCGGGA  CG AT
                                  AC       A_  G
GAM1107  LOC158191 3'  GCTCCAAGGGCTCCAGGGA   81777           C__
                                TTCCTGGAGCCCT   AGT
                                ||||||||||||   |||
                                AGGGACCTCGGGA   TCG
                                      ACC
GAM1107  LOC164397 5'  ATACAAGACCTCCAGGAA    82518         CC  CA
                                TTCCTGGAG  CT  GTGT
                                |||||||||  ||  ||||
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                                AAGGACCTC  GA  CATA
                                     CA  A_
GAM1107  LOC219899 3'  ATGTAGAATGAAAACTCCAGGA 91499        CCC   GTGTG
              A                   TTCCTGGAG   TCA    ACAT
                                  |||||||||  |||    ||||
                                  AAGGACCTC   AGT    TGTA
                                       AAA   AAGA_
GAM1107  LOC221495 3'  ACAGTGGGATTAGGGCTCCA   93854        _____  G
                                  TGGAGCCCT    CA TGT
                                  |||||||||    || |||
                                  ACCTCGGGA    GT ACA
                                       TTAGG  G
GAM1107  LOC57228  3'  CATCACTGACTCCAGGGA    39996        CCC    _
                                  TTCCTGGAG   TCAGTG TG
                                  |||||||||   |||||| ||
                                  AGGGACCTC   AGTCAC AC
                                       ___     T
GAM1107  LOC91050  3'  ACATTGAAAGCCCCAGAGA   64741    _   A  CC
                                  TC CTGG GC  TCAGTGT
                                  || |||| ||  |||||||
                                  AG GACC CG  AGTTACA
                                   A   C  AA
GAM1108  DYRK2     3'  TAACATCAGTGGCAGGC     13128     AT  AAC
                                  GCTT  CA   CTGATGTTA
                                  ||||  ||   |||||||||
                                  CGGA  GT   GACTACAAT
                                    CG  ___
GAM1108  DYRK2     3'  TAACATCAGTGGCAGGC     21392     AT  AAC
                                  GCTT  CA   CTGATGTTA
                                  ||||  ||   |||||||||
                                  CGGA  GT   GACTACAAT
                                    CG  ___
GAM1108  EDNRA     3'  TAACATCAGGTTCCAGTTGCT  64111     TTATCA
                                  AGC     AACCTGATGTTA
                                  |||     ||||||||||||
                                  TCG     TTGGACTACAAT
                                    TTGACC
GAM1108  OGT       5'  AACAAATATTTGATAAGCT    13197          CCTGA
                                  AGCTTATCAAA    TGTT
                                  ||||||||||    ||||
                                  TCGAATAGTTT    ACAA
                                       ATAA_
GAM1108  CCR7      3'  CAGGGCTGATAAGCTA      8452          AA
                                  TAGCTTATCA  CCTG
                                  |||||||||  ||||
                                  ATCGAATAGT  GGAC
                                       CG
GAM1108  CNK2      3'  GACTCACAGATTGATAAGCTA  75962          AC  AT_
                                  TAGCTTATCAA  CTG   GTT
                                  ||||||||||  |||   |||
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                                ATCGAATAGTT  GAC   CAG
                                      A_   ACT
GAM1108  DKFZp434C0328 5'  TCAGGCTGATAAGCTA      34135          AA
                                TAGCTTATCA  CCTGA
                                ||||||||||  |||||
                                ATCGAATAGT  GGACT
                                      C_
GAM1108  DOCK3     3'  CAGGTTTGGATAAGCTA     66497          _
                                TAGCTTATC AAACCTG
                                ||||||||| |||||||
                                ATCGAATAG TTTGGAC
                                      G
GAM1108  FLJ10260  5'  GGTAACATATTTTGGCAAGC   35951      AT    CCTG
                                GCTT  CAAA    ATGTTACC
                                ||||  ||||    ||||||||
                                CGAA  GTTT    TACAATGG
                                  CG    TA__
GAM1108  FLJ20281  3'  GTGAGAGTTTTGATAAGC    90984          _ _  G
                                GCTTATCAAA C CT AT
                                |||||||||| | || ||
                                CGAATAGTTT G GA TG
                                      T A  G
GAM1108  FLJ20297  3'  GTAACATCAAGTGCTCAAAG   34897     ATCAA  C
                                CTT     AC TGATGTTAC
                                |||     || |||||||||
                                GAA     TG ACTACAATG
                                  ACTCG  A
GAM1108  FLJ20297  3'  GTAACATCAAGTGCTCAAAG   35637     ATCAA  C
                                CTT     AC TGATGTTAC
                                |||     || |||||||||
                                GAA     TG ACTACAATG
                                  ACTCG  A
GAM1108  FLJ23071  3'  AACAAATATTTGATAAGCT    47262          CCTGA
                                AGCTTATCAAA     TGTT
                                ||||||||||     ||||
                                TCGAATAGTTT     ACAA
                                      ATAA_
GAM1108  FREQ      3'  TAACATCAAGGCAAGC      26583      ATCAAA  _
                                GCTT      CCT GATGTTA
                                ||||      ||| |||||||
                                CGAA      GGA CTACAAT
                                  C_____   A
GAM1108  MRPL9     3'  GGCTGTAGATTTGATAAGCTA  48656          C   AT
                                TAGCTTATCAAA CTG  GTT
                                |||||||||||| |||  |||
                                ATCGAATAGTTT GAT  CGG
                                      A   GT
GAM1108  PDE10A    3'  GGTAACATCAAATAAATAAGT  21866       CAAACC
                                GCTTAT     TGATGTTACC
                                ||||||     ||||||||||
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                                TGAATA     ACTACAATGG
                                   AATAA_
GAM1108  ZNF238    5'  GACATAATTTGATAAGT     20961          CCTG
                                GCTTATCAAA    ATGTT
                                ||||||||||    |||||
                                TGAATAGTTT    TACAG
                                     AA__
GAM1108  LOC149386 5'  GTAACCCAGAAGTTTAATAAGC 84407        C    __   AT
              TG                   TAGCTTAT AAAC  CTG  GTTAC
                                ||||||||| ||||  |||  |||||
                                GTCGAATA TTTG  GAC  CAATG
                                     A   AA  C_
GAM1108  LOC150776 3'  GTAACATCAAGTGCTCAAAG   63225     ATCAA  C
                                CTT    AC TGATGTTAC
                                |||    || |||||||||
                                GAA    TG ACTACAATG
                                  ACTCG  A
GAM1108  LOC254428 3'  GGTACTGTGCCAGGCACTGATA 95461        AA_   __  GT
              AGC                   GCTTATCA   CCTG  AT  TACC
                                |||||||   ||||  ||  ||||
                                CGAATAGT   GGAC  TG  ATGG
                                     CAC    CG  TC
GAM1108  LOC255696 5'  GGCATCGGCCTGATCAGC    97500     T    AAC
                                GCT ATCA   CTGATGTT
                                ||| ||||   ||||||||
                                CGA TAGT   GGCTACGG
                                  C    CC_
GAM1108  LOC91308  3'  TAGGTTTGACTAGCTA     65564      TA
                                TAGCT  TCAAACCTG
                                |||||  |||||||||
                                ATCGA  AGTTTGGAT
                                   TC
GAM1109  ACP5      3'  CCCAGCCACAGTGTTATGCTCT 7855      A   TA    CA__
              GT                   ATA AGC  GTGAC    TGGCTGGG
                                ||| |||  |||||   ||||||||
                                TGT TCG  TATTG    ACCGACCC
                                  C   __     TGAC
GAM1109  CYP11B1   3'  CCCAGCCTGGCCACCAGC    62162     A   A   T
                                GCT GTG CCA GGCTGGG
                                ||| ||| ||| |||||||
                                CGA CAC GGT CCGACCC
                                  C   C   _
GAM1109  GLP1R     3'  CCCAGCCATGGTGAGGAAGC   9030      AGTG_
                                GCT    ACCATGGCTGGG
                                |||    ||||||||||||
                                CGA    TGGTACCGACCC
                                  AGGAG
GAM1109  HEM1      5'  CCCAGCCATGATTAACCCTGC  18050    TAG__   C
                                GC    TGA CATGGCTGGG
                                ||    ||| ||||||||||
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                              CG    ATT GTACCGACCC
                               TCCCA  A
GAM1109 LIF     3' CCAGCCAGTCCAGCT      9733      AGT  CA
                              AGCT  GAC  TGGCTGG
                              ||||  |||  |||||||
                              TCGA  CTG  ACCGACC
                                C__  __
GAM1109 LTK     3' CCAGCCACTTCCAGCTTT    9826       AGT  CCA
                              AAAGCT  GA  TGGCTGG
                              ||||||  ||  |||||||
                              TTTCGA  CT  ACCGACC
                                 C__  TC_
GAM1109 NHP2L1  3' CCAGCTTTCAGCCACTAGCTT  17202        ACCAT_
                              AAGCTAGTG    GGCTGG
                              |||||||||    ||||||
                              TTCGATCAC    TCGACC
                                   CGACTT
GAM1109 OGG1    3' CCCAACACTGTCACTAGT    33657        CA  GC
                              GCTAGTGAC  TG  TGGG
                              |||||||||  ||  ||||
                              TGATCACTG  AC  ACCC
                                   TC  A_
GAM1109 PLAB    5' CCCAGAAATGTGCCCTAGCTTT 65852        TGAC  GG
          A                    TAAAGCTAG   CAT  CTGGG
                              |||||||||   |||  |||||
                              ATTTCGATC   GTA  GACCC
                                   CCGT   AA
GAM1109 POLR2J  3' CCCAGCCATGGCCCGC     20645     A_
                              GTG  CCATGGCTGGG
                              |||  ||||||||||
                              CGC  GGTACCGACCC
                                CC
GAM1109 RFNG    3' CAGCCACGGCCATTGC     88172    T   A  A
                              GC AGTG CC TGGCTG
                              || |||| || ||||||
                              CG TTAC GG ACCGAC
                               _   C  C
GAM1109 SLC18A3 3' CCCAGCCACTCCTCAACCTT  11753    CTAG  CCA_
                              AAG   TGA   TGGCTGGG
                              |||   |||   ||||||||
                              TTC   ACT   ACCGACCC
                                CA__  CCTC
GAM1109 SSPN    3' CCCACCTCCAGTCATCAGC   17441    A    CAT_ C
                              GCT GTGAC   GG TGGG
                              ||| |||||   || ||||
                              CGA TACTG   CC ACCC
                                C    ACCT  _
GAM1109 VEGF    3' CGGTGACAGTCACTAGCTT   12588         CATG
                              AAGCTAGTGAC   GCTG
                              ||||||||||   ||||
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                                TTCGATCACTG   TGGC
                                      ACAG
GAM1109 ANKRD2   3' CCCAGCCAGCTACCCAGC   72116    A_  ACCA
                                GCT  GTG   TGGCTGGG
                                |||  |||   ||||||||
                                CGA  CAT   ACCGACCC
                                  CC   CG__
GAM1109 FLJ13241 3' CCCAGCTGGGCCCACCAGC   46966    A  A_ A
                                GCT GTG  CC TGGCTGGG
                                ||| |||  || ||||||||
                                CGA CAC  GG GTCGACCC
                                  C   CC  _
GAM1109 FLJ13441 3' CCACGTGGTCACTG       43660         GC
                                TAGTGACCATG  TGG
                                ||||||||||  |||
                                GTCACTGGTGC  ACC
                                      __
GAM1109 FLJ32784 3' CCCAGCTGTGCACCAGCT   58226    A  AC
                                AGCT GTG  CATGGCTGGG
                                |||| |||  ||||||||||
                                TCGA CAC  GTGTCGACCC
                                  C   __
GAM1109 FOXJ1    3' CCACATGGCCACCAGC     7571     A  A   GC
                                GCT GTG CCATG  TGG
                                ||| ||| |||||  |||
                                CGA CAC GGTAC  ACC
                                  C   C    __
GAM1109 HIC2     3' CCCACCCATCACTAGCTT   65258        CCA  C
                                AAGCTAGTGA   TGG TGGG
                                ||||||||||   ||| ||||
                                TTCGATCACT   ACC ACCC
                                      ____  C
GAM1109 IL18BP   3' CCCAGCCATCAAAACCAGC   19105    A  GACC
                                GCT GT    ATGGCTGGG
                                ||| ||    |||||||||
                                CGA CA    TACCGACCC
                                  C  AAAC
GAM1109 KIAA1924 3' CCCAGCCACGAGCTGCTTT   73667     T  GACCA
                                AAAGC AGT    TGGCTGGG
                                ||||| |||    ||||||||
                                TTTCG TCG    ACCGACCC
                                   _  AGC__
GAM1109 MGC2541  3' CCCAGCCATGGTGCATGACTCT 54747    CTA_  _
             T                   AAG   GTG ACCATGGCTGGG
                                 |||   ||| ||||||||||||
                                 TTC   TAC TGGTACCGACCC
                                   TCAG  G
GAM1109 NIN283   3' CCCAGCCATAACCCACTCAGT  50067    _   ACC_
                                GCT AGTG   ATGGCTGGG
                                ||| ||||   |||||||||
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                                TGA TCAC    TACCGACCC
                                  C    CCAA
GAM1109  SCYA18    3'  CCCAGCCACATTAACTAACTTT 11460       C    GACCA
               A                   TAAAG TAGT     TGGCTGGG
                                   ||||| ||||     ||||||||
                                   ATTTC ATCA     ACCGACCC
                                     A    ATTAC
GAM1109  TIX1      3'  CCCAGCCATGGGCACTAGCT   61740         A
                                   AGCTAGTG CCATGGCTGGG
                                   |||||||| ||||||||||
                                   TCGATCAC GGTACCGACCC
                                        G
GAM1109  LOC143903 3'  CCCAGCCAGTCATCCAGCT    76616      A_    CA
                                   AGCT  GTGAC  TGGCTGGG
                                   ||||  |||||  ||||||||
                                   TCGA  TACTG  ACCGACCC
                                     CC    __
GAM1109  LOC144455 3'  CCCAGCCACAGTAGAGCT     76850      AGTG  CA
                                   AGCT    AC  TGGCTGGG
                                   ||||    ||  ||||||||
                                   TCGA    TG  ACCGACCC
                                     GA__  AC
GAM1109  LOC146184 3'  CCCAGCCAGCAGCTAGC      83619       GACCA
                                   GCTAGT     TGGCTGGG
                                   ||||||     ||||||||
                                   CGATCG     ACCGACCC
                                      ACG__
GAM1109  LOC150819 5'  CAGTCCACTAGCTT         85118          ACCAT
                                   AAGCTAGTG     GGCTG
                                   |||||||||     |||||
                                   TTCGATCAC     CTGAC
                                                 _____
GAM1109  LOC155372 3'  CCCAGCCATGGCATCTGTTTTA 81341         TA   A
                                   TAAAGC  GTG CCATGGCTGGG
                                   ||||||  ||| ||||||||||
                                   ATTTTG  TAC GGTACCGACCC
                                      TC  _
GAM1109  LOC255473 5'  CCTTCGTGGTCACTTGCTT    96268      T         CT
                                   AAGC AGTGACCATGG  GG
                                   |||| ||||||||||  ||
                                   TTCG TCACTGGTGCT  CC
                                     T         T_
GAM1110  A1BG      3'  CGGCTCACTGCAGTTTTGACCT 55416     _    GG
                                   AGG CAAGA  TTGCAGTGAGCCG
                                   ||| |||||  ||||||||||||
                                   TCC GTTTT  GACGTCACTCGGC
                                     A    __
GAM1110  ACADSB    3'  GCTCACTGCAGCCTTGACCT   7846      CAA
                                   AGG   GAGGTTGCAGTGAGC
                                   |||   ||||||||||||||
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                                TCC   TTCCGACGTCACTCG
                                  AG_
GAM1110 ADAMTS4  3' CGGCTCACTGCATCCTCCGCCT 17505      AA    T
                                AGGC  GAGG TGCAGTGAGCCG
                                ||||  |||| ||||||||||||
                                TCCG  CTCC ACGTCACTCGGC
                                  C_    T
GAM1110 ADAMTS4  3' GCTCACTGCAACCTTCGCC   17510     AA
                                GGC  GAGGTTGCAGTGAGC
                                |||  ||||||||||||||
                                CCG  TTCCAACGTCACTCG
                                  C_
GAM1110 ADRB3    3' CTTTCCACAACCTCTACCT   3433      CA      CAGT
                                AGG  AGAGGTTG    GAG
                                |||  ||||||||    |||
                                TCC  TCTCCAAC    TTC
                                  A_       ACCT
GAM1110 AHR      3' CACTGCAACCTCTACCT     7876      CA
                                AGG  AGAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  TCTCCAACGTCAC
                                  A_
GAM1110 AIM1     3' CGGCTCACTGCAGCCTCTACCT 91821     CA
                                AGG  AGAGGTTGCAGTGAGCCG
                                |||  ||||||||||||||||
                                TCC  TCTCCGACGTCACTCGGC
                                  A_
GAM1110 AK2      3' CTGCAACCTCTTGACC      25500    _
                                GG CAAGAGGTTGCAG
                                || ||||||||||||
                                CC GTTCTCCAACGTC
                                 A
GAM1110 ALDH1B1  3' CACTGCAACCTCCGCCT     5490      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110 AP3B2    5' CGCCGCAACCTCCTCCT     16186     CAA      A
                                AGG   GAGGTTGC GTG
                                |||   |||||||| |||
                                TCC   CTCCAACG CGC
                                  TC_       C
GAM1110 APAF1    3' CGGCTCACCACAATCGCTGCCT 25037      A A    CA
                                AGGCA G GGTTG  GTGAGCCG
                                ||||| | |||||  ||||||||
                                TCCGT C CTAAC  CACTCGGC
                                   _ G     AC
GAM1110 APAF1    3' CGGCTCACCACAATCGCTGCCT 6728       A A    CA
                                AGGCA G GGTTG  GTGAGCCG
                                ||||| | |||||  ||||||||
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                                TCCGT C CTAAC  CACTCGGC
                                  _ G    AC
GAM1110  APM1    3'  CGGCTTACTGCAACCTTTGCCT 16588      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT TTCCAACGTCATTCGGC
                                  _
GAM1110  APM1    3'  GGCTCACTGCAGCCTC      16598
                                GAGGTTGCAGTGAGCC
                                ||||||||||||||||
                                CTCCGACGTCACTCGG

GAM1110  APOL1   3'  GCTCACTGCAAGCTCTGCCT   13348      A   G
                                AGGCA GAG TTGCAGTGAGC
                                ||||| ||| ||||||||||
                                TCCGT CTC AACGTCACTCG
                                  _  G
GAM1110  APPBP2  3'  CACTGCAACCTCCGCCT     21073     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  AQP6    3'  CGGCTCACTGCAACCTCTACCT 7946      CA
                                AGG  AGAGGTTGCAGTGAGCCG
                                |||  ||||||||||||||||||
                                TCC  TCTCCAACGTCACTCGGC
                                  A_
GAM1110  AQP6    3'  CGGCTCACTGCAACCTCTACCT 53921     CA
                                AGG  AGAGGTTGCAGTGAGCCG
                                |||  ||||||||||||||||||
                                TCC  TCTCCAACGTCACTCGGC
                                  A_
GAM1110  ARCN1   3'  GCTCACTGCAACCTCCGCCT   7980      AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  |||||||||||||||
                                TCCG  CTCCAACGTCACTCG
                                  C_
GAM1110  ATM     3'  CGGCTCACTGCATCCTCAACCT 56301     CAA   T
                                AGG   GAGG TGCAGTGAGCCG
                                |||   |||| ||||||||||||
                                TCC   CTCC ACGTCACTCGGC
                                  AA_   T
GAM1110  ATP1B2  3'  GCTCACTGCAACTTCCGC    8051     AA
                                GC  GAGGTTGCAGTGAGC
                                ||  |||||||||||||||
                                CG  CTTCAACGTCACTCG
                                 C_
GAM1110  ATP7A   3'  CACTGCAACCTCTGCCT     3520       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
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                                TCCGT CTCCAACGTCAC
                                  _
GAM1110 ATP8B2   3' GCTCACTGCAACCTCCACCT  65226    CAA
                                AGG  GAGGTTGCAGTGAGC
                                |||  ||||||||||||||
                                TCC  CTCCAACGTCACTCG
                                  AC_
GAM1110 AXL     3' CACTGCAACCTTCACCT    8094     CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  TTCCAACGTCAC
                                  AC_
GAM1110 AXL     3' CACTGCAACCTTCACCT    41591    CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  TTCCAACGTCAC
                                  AC_
GAM1110 BAZ2A    5' GCTTACTCAACCTCTGCCT  25605     A     C
                                AGGCA GAGGTTG AGTGAGC
                                ||||| ||||||| |||||||
                                TCCGT CTCCAAC TCATTCG
                                  _     _
GAM1110 BRIP1    3' CACTGCAACCTTCACCT    49396    CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  TTCCAACGTCAC
                                  AC_
GAM1110 BSG     3' ACTCTGACCTCTTGGCC    8181     _      C
                                GGC AAGAGGTTG AGT
                                ||| ||||||||| |||
                                CCG TTCTCCAGT TCA
                                  G       C
GAM1110 BSG     3' ACTCTGACCTCTTGGCC    67796    _      C
                                GGC AAGAGGTTG AGT
                                ||| ||||||||| |||
                                CCG TTCTCCAGT TCA
                                  G       C
GAM1110 C7      3' CTGCAACCTCCGCCT      5160     AA
                                AGGC  GAGGTTGCAG
                                ||||  ||||||||||
                                TCCG  CTCCAACGTC
                                  C_
GAM1110 CACNA1C  3' CGGCTCACTCCGTCCCTGCC  5561     A A  T  C
                                GGCA G GG TG AGTGAGCCG
                                |||| | || || |||||||||
                                CCGT C CC GC TCACTCGGC
                                  _ _  T  C
GAM1110 CAMLG    3' CGGCTCACCGCAACCTCCACCT 8237     CAA      A
                                AGG  GAGGTTGC GTGAGCCG
                                |||  |||||||| ||||||||
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                                TCC  CTCCAACG CACTCGGC
                                  AC_      C
GAM1110 CASP10   3' CGGCTCACTGTAGTCTCGACCT 52100    CAA  GT
                                AGG  GAG  TGCAGTGAGCCG
                                |||  |||  ||||||||||||
                                TCC  CTC  ATGTCACTCGGC
                                  AG_  TG
GAM1110 CASP10   3' CGGCTCACTGTAGTCTCGACCT 52117    CAA  GT
                                AGG  GAG  TGCAGTGAGCCG
                                |||  |||  ||||||||||||
                                TCC  CTC  ATGTCACTCGGC
                                  AG_  TG
GAM1110 CASP8    3' CGGCTCACCGCAAGCTCCGCCT 52921     AA  G   A
                                AGGC  GAG TTGC GTGAGCCG
                                ||||  ||| |||| ||||||||
                                TCCG  CTC AACG CACTCGGC
                                  C_  G   C
GAM1110 CASP8    3' CGGCTCACCGCAAGCTCCGCCT 52932     AA  G   A
                                AGGC  GAG TTGC GTGAGCCG
                                ||||  ||| |||| ||||||||
                                TCCG  CTC AACG CACTCGGC
                                  C_  G   C
GAM1110 CASP8    3' CGGCTCACCGCAAGCTCCGCCT 52945     AA  G   A
                                AGGC  GAG TTGC GTGAGCCG
                                ||||  ||| |||| ||||||||
                                TCCG  CTC AACG CACTCGGC
                                  C_  G   C
GAM1110 CASP8    3' CGGCTCACCGCAAGCTCCGCCT 6915      AA  G   A
                                AGGC  GAG TTGC GTGAGCCG
                                ||||  ||| |||| ||||||||
                                TCCG  CTC AACG CACTCGGC
                                  C_  G   C
GAM1110 CBFA2T2  3' CGGCTCACGGTAACCTCTGCCT 17462      A      A
                                AGGCA GAGGTTGC GTGAGCCG
                                ||||| |||||||| ||||||||
                                TCCGT CTCCAATG CACTCGGC
                                   _      G
GAM1110 CBFA2T3  3' ACTCCAACCTCTCGGCC     17755     A_      C
                                GGC  AGAGGTTG AGT
                                |||  |||||||| |||
                                CCG  TCTCCAAC TCA
                                  GC      C
GAM1110 CCNF     3' CTCACTGTAACCTCCGCCT    8317      AA
                                AGGC  GAGGTTGCAGTGAG
                                ||||  ||||||||||||||
                                TCCG  CTCCAATGTCACTC
                                  C_
GAM1110 CDH1     3' GCTCACTGCAGCCTTGTCCT   15147     CAA
                                AGG  GAGGTTGCAGTGAGC
                                |||  |||||||||||||||
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                              TCC  TTCCGACGTCACTCG
                                TG_
GAM1110 CDH17   3' GCTCACTGCAACCTCCGCCT  14505    AA
                              AGGC  GAGGTTGCAGTGAGC
                              ||||  ||||||||||||||
                              TCCG  CTCCAACGTCACTCG
                                C_
GAM1110 CHST1   3' GCTCACCCCACTCCCTTCTGCC 13334    AG  T__  CA
                              GGCA  AGG  TG  GTGAGC
                              ||||  |||  ||  ||||||
                              CCGT  TCC  AC  CACTCG
                                CT  CTC  CC
GAM1110 CLECSF12 3' CGGCTCACCGCAACCTCCGCC  76688    AA     A
                              GGC  GAGGTTGC GTGAGCCG
                              |||  |||||||| ||||||||
                              CCG  CTCCAACG CACTCGGC
                                C_     C
GAM1110 CLECSF12 3' GCTCACTGCAGCTATCT    76693    _       C
                              AGA GGTTGCAGTGAG C
                              ||| |||||||||||| |
                              TCT TCGACGTCACTC G
                                A         A
GAM1110 CNGA1   5' CGGCTCACTGCAGTCTTCACCT 59509    CAA  GT
                              AGG  GAG  TGCAGTGAGCCG
                              |||  |||  ||||||||||||
                              TCC  TTC  ACGTCACTCGGC
                                AC_  TG
GAM1110 CORO2B  5' CGGCTCACTGCAACCTCTGCC  64570    A
                              GGCA GAGGTTGCAGTGAGCCG
                              |||| ||||||||||||||||
                              CCGT CTCCAACGTCACTCGGC
                                _
GAM1110 CPS1    3' CGGCTCACTGCAATTTGCGTCT 8528     AAG
                              AGGC  AGGTTGCAGTGAGCCG
                              ||||  ||||||||||||||||
                              TCTG  TTTAACGTCACTCGGC
                                CG_
GAM1110 CR1     3' CGGCTCACTGCAACGTCCGCCT 5133     AA  G
                              AGGC  GA GTTGCAGTGAGCCG
                              ||||  || ||||||||||||||
                              TCCG  CT CAACGTCACTCGGC
                                C_  G
GAM1110 CRTAP   3' GCTCACTGCAACCTCCGCCT  21036    AA
                              AGGC  GAGGTTGCAGTGAGC
                              ||||  ||||||||||||||
                              TCCG  CTCCAACGTCACTCG
                                C_
GAM1110 CSNK2A2 5' GCTCACTGCAACCTCCACCT  8563     CAA
                              AGG  GAGGTTGCAGTGAGC
                              |||  ||||||||||||||
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                                TCC  CTCCAACGTCACTCG
                                  AC_
GAM1110 CXCL16   3' CGGCTCACTGCAACCCCC   41918   CAAGA
                                GG   GGTTGCAGTGAGCCG
                                ||   ||||||||||||||
                                CC   CCAACGTCACTCGGC
                                 C____
GAM1110 CYP1A2   3' GCTCACTGCAACCTCCACCT  5692    CAA
                                AGG  GAGGTTGCAGTGAGC
                                |||  ||||||||||||||
                                TCC  CTCCAACGTCACTCG
                                  AC_
GAM1110 CYP1A2   3' GCTCACTGCAACCTCTGCCT  5695     A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                TCCGT CTCCAACGTCACTCG

                                  _
GAM1110 CYP1A2   3' GCTCACTGCAACCTCCACCT  69112   CAA
                                AGG  GAGGTTGCAGTGAGC
                                |||  ||||||||||||||
                                TCC  CTCCAACGTCACTCG
                                  AC_
GAM1110 CYP1A2   3' GCTCACTGCAACCTCTGCCT  69115    A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                TCCGT CTCCAACGTCACTCG

                                  _
GAM1110 CYP2B6   3' CACTGCAACCTCTGCCT    5725     A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC

                                  _
GAM1110 CYP2B6   3' CGGCTCACTGCAACCTCCACCC 5729   CAA
                                GG  GAGGTTGCAGTGAGCCG
                                ||  ||||||||||||||||
                                CC  CTCCAACGTCACTCGGC
                                 CAC
GAM1110 CYP4F3   3' CATTGCAACCTCCGCCT    6111     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTTAC
                                  C_
GAM1110 CYP51    3' GCTCACTGCATCCTCTGCCT  5783     A  T
                                AGGCA GAGG TGCAGTGAGC
                                ||||| |||| ||||||||||
                                TCCGT CTCC ACGTCACTCG
                                  _  T
GAM1110 CYP8B1   3' CACTACAACCTCTGCCT    15257    A    C
                                AGGCA GAGGTTG AGTG
                                ||||| ||||||| ||||
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                                TCCGT CTCCAAC TCAC
                                  _      A
GAM1110  CYP8B1   3'  CACTGCAACCTCTGCCT     15259       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  DFFB     3'  CACTGCAACCTCCGCCT     87377       AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  DHFR     3'  CGGCTTACTGCAACCTCCGCCT 5802        AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCATTCGGC
                                  C_
GAM1110  DISC1    3'  CGGCTCACTGCAACCTCTACCT 37874     CA
                                AGG  AGAGGTTGCAGTGAGCCG
                                |||  |||||||||||||||||
                                TCC  TCTCCAACGTCACTCGGC
                                  A_
GAM1110  DLC1     5'  CGGCTCACGGACTTCTCGCC   20336     A      GCA
                                GGC AGAGGTT   GTGAGCCG
                                ||| |||||||   ||||||||
                                CCG TCTTCAG   CACTCGGC
                                  C      G__
GAM1110  DSCR3    3'  GCTCACTGCAACCTCCACCT   20184     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   |||||||||||||||
                                TCC   CTCCAACGTCACTCG
                                  AC_
GAM1110  EFNB2    3'  GCTCACTGCTGCTGCCT     14573       AGAG  T
                                AGGCA    GT GCAGTGAGC
                                |||||    || |||||||||
                                TCCGT    CG CGTCACTCG
                                  _____  T
GAM1110  EHD2     3'  CGGCTCACACACGCCCTGCCT  27491       A A   TGCA
                                AGGCA G GGT    GTGAGCCG
                                ||||| | |||    ||||||||
                                TCCGT C CCG    CACTCGGC
                                  _ _   CACA
GAM1110  EHD2     3'  GCTCACTGCAACCTCCACCT   27495     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   |||||||||||||||
                                TCC   CTCCAACGTCACTCG
                                  AC_
GAM1110  EIF2S3   3'  GTGATCTGCAACCTCTGCC    7419       A         TGA
                                GGCA GAGGTTGCAG   GC
                                |||| ||||||||||   ||
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                                CCGT CTCCAACGTC   TG
                                  _        TAG
GAM1110  EPB72    3'  CGGCTCACTGCAACCTCCGCCT 14602      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  ETV5     5'  GGCCCAGCCTTTCGCC      15487     A       CAGTGA
                                GGC AGAGGTTG     GCC
                                ||| ||||||||     |||
                                CCG TTTCCGAC     CGG
                                  C       C_____
GAM1110  F2RL2    3'  CATTGCAACCTCTGCCT     14619       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTTAC

                                  _
GAM1110  F2RL3    3'  CGGCTCACTGCAAGCTCGGCCT 14176      AA   G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||
                                TCCG  CTC AACGTCACTCGGC
                                  G_  G
GAM1110  FANCF    3'  CAGTGCAACCTCTGCCT     42670       A       G
                                AGGCA GAGGTTGCA TG
                                ||||| ||||||||| ||
                                TCCGT CTCCAACGT AC
                                  _       G
GAM1110  FCAR     3'  CGACTCACTGCAACCTTCGCCT 55793      AA           C
                                AGGC  GAGGTTGCAGTGAG CG
                                ||||  |||||||||||||| ||
                                TCCG  TTCCAACGTCACTC GC
                                  C_           A
GAM1110  FCAR     3'  CGACTCACTGCAACCTTCGCCT 55811      AA           C
                                AGGC  GAGGTTGCAGTGAG CG
                                ||||  |||||||||||||| ||
                                TCCG  TTCCAACGTCACTC GC
                                  C_           A
GAM1110  FEZ1     3'  CACTGCAACCTCCACCT     42566     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1110  FGF5     3'  CGGCTCACTGCAACCTC     52483
                                GAGGTTGCAGTGAGCCG
                                |||||||||||||||||
                                CTCCAACGTCACTCGGC

GAM1110  FGF5     3'  CGGCTCACTGCAACCTC     15537
                                GAGGTTGCAGTGAGCCG
                                |||||||||||||||||
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                                CTCCAACGTCACTCGGC

GAM1110 FHL2    5' GCTCACTGCAAGCTCTACCT  7564     CA   G
                                AGG  AGAG TTGCAGTGAGC
                                |||  |||| ||||||||||
                                TCC  TCTC AACGTCACTCG
                                  A_   G
GAM1110 FUT1    3' GCTCACTGCAAGCTCTGCCT  3793      A  G
                                AGGCA GAG TTGCAGTGAGC
                                ||||| ||| ||||||||||
                                TCCGT CTC AACGTCACTCG
                                   _  G
GAM1110 FZD4    3' CACTGCAACCTCTGCCT     24128     A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110 G6PC    3' GGCTCACTGCAACCTCTTCCT 3831     C
                                AGG AAGAGGTTGCAGTGAGCC
                                ||| ||||||||||||||||
                                TCC TTCTCCAACGTCACTCGG
                                  _
GAM1110 GM2A    3' CACTGCAACCTCCGCCT     67773     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110 GNE     3' CAATGCAACCTCTGCC      18476     A      G
                                GGCA GAGGTTGCA TG
                                |||| ||||||||| ||
                                CCGT CTCCAACGT AC
                                   _       A
GAM1110 GPR81   3' CGGCTCACTGCAACCTCTGCCT 50756      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                  _
GAM1110 GRAF    3' CACTGCAACCTCCGCCT     30550     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110 GUCY2D  5' CGGCCCTGTGACCCCTCACC  3934    CA A  TG  TGA
                                GG  AG GGT  CAG  GCCG
                                ||  || |||  |||  ||||
                                CC  TC CCA  GTC  CGGC
                                 AC  C  GT  C__
GAM1110 HCS     3' CACCGCAACCTCCGCCT     38459     AA     A
                                AGGC  GAGGTTGC GTG
                                ||||  |||||||| |||
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                                TCCG  CTCCAACG CAC
                                  C_       C
GAM1110  HCS      3'  CACTGCAACCTCCGCCT     38460      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  HLCS     5'  CGGCTCACCACAACCTCTGCCT 4664        A      CA
                                AGGCA GAGGTTG  GTGAGCCG
                                ||||| |||||||  ||||||||
                                TCCGT CTCCAAC  CACTCGGC
                                   _      AC
GAM1110  HOXC5    3'  CTCCACAACCTCTTCCC     38493    C       CAGT
                                GG AAGAGGTTG    GAG
                                || |||||||||    |||
                                CC TTCTCCAAC    CTC
                                 C        AC__
GAM1110  HTR1D    3'  GCTCACTGCAACCTCCGC     5998     AA
                                GC  GAGGTTGCAGTGAGC
                                ||  |||||||||||||||
                                CG  CTCCAACGTCACTCG
                                 C_
GAM1110  HTR1E    5'  CATTGCAACCTCCGCCT      6011       AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTTAC
                                  C_
GAM1110  INMT     3'  CGACTCACTGCAAGCTCCGCCT 22268      AA   G        C
                                AGGC  GAG TTGCAGTGAG CG
                                ||||  ||| ||||||||||| ||
                                TCCG  CTC AACGTCACTC GC
                                  C_  G        A
GAM1110  INMT     3'  CGGCTCACTGCAAGCTCTGC   22269     A   G
                                GCA GAG TTGCAGTGAGCCG
                                ||| ||| ||||||||||||||
                                CGT CTC AACGTCACTCGGC
                                  _  G
GAM1110  ITGAM    3'  CGGCTCACTGCAACCTCCGCCT 71838      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  JRK      3'  GCTCACTGCAGCCTCGACCT   86530     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   |||||||||||||||
                                TCC   CTCCGACGTCACTCG
                                  AG_
GAM1110  KMO      3'  CACTGCAACCTCTGCCT      13446       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
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                                TCCGT CTCCAACGTCAC
                                  _
GAM1110 KNSL1    3' GCTCACTTTCTCCCT      15748    CAA   TTGC
                                AGG  GAGG  AGTGAGC
                                |||  ||||  |||||||
                                TCC  CTCT  TCACTCG
                                 ____  T___
GAM1110 LANCL1   3' CTCACTGCATGACCCT     20212    A  __
                                AG GGT  TGCAGTGAG
                                || |||  |||||||||
                                TC CCA  ACGTCACTC
                                 _  GT
GAM1110 LILRA3   3' CACTGCAACCTCCGCCT    95307     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110 LNK      3' CACTGCAACCTCCACCT    18458    CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  CTCCAACGTCAC
                                  AC_
GAM1110 LYZ      3' CGGCTCACTGCAACCTCCACCT 4098     CAA
                                AGG  GAGGTTGCAGTGAGCCG
                                |||  |||||||||||||||||
                                TCC  CTCCAACGTCACTCGGC
                                  AC_
GAM1110 MAK      3' CTTACTGCAACCTCCACCT   19759    CAA
                                AGG  GAGGTTGCAGTGAG
                                |||  ||||||||||||||
                                TCC  CTCCAACGTCATTC
                                  AC_
GAM1110 MEF2A    5' CACTGCAACCTCCGCCT    18780     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110 MEFV     3' CACTGCAACCTCCGCCT    4127      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110 MEFV     3' GCTCACTGCAACCTCCACCT  4141     CAA
                                AGG  GAGGTTGCAGTGAGC
                                |||  |||||||||||||||
                                TCC  CTCCAACGTCACTCG
                                  AC_
GAM1110 MHC2TA   3' CACTGCAACCTCCGCCT    4165      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  MHC2TA   3'  CGGCTCACTGCAGCCTCAACCT 4172      CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCGACGTCACTCGGC
                                  AA_
GAM1110  MICB     3'  GCTCACTGCAACCTCTGCCT   19828       A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
                                TCCGT CTCCAACGTCACTCG

                                  _
GAM1110  MPL      3'  CGGCTCACTGCAACCTCTGCCT 18138       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC

                                  _
GAM1110  MPL      3'  GCTCACTGCAACCTCCACCT   18144     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                TCC   CTCCAACGTCACTCG
                                  AC_
GAM1110  MYCL2    3'  CGGCTCACTGCAACCTCTGCCT 18180       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC

                                  _
GAM1110  MYO1C    3'  CACCTGCAATCTCCCACCT    61201     CAA        _
                                AGG   GAGGTTGCAG TG
                                |||   |||||||||| ||
                                TCC   CTCTAACGTC AC
                                  ACC         C
GAM1110  NCOA6    5'  CGGCTCACTGCAGCCTCAACCT 25959     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCGACGTCACTCGGC
                                  AA_
GAM1110  NCOA6IP  3'  GCTCACTGCAGGTTCAGCCT   45739      AA   G
                                AGGC  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                TCCG  CTT GACGTCACTCG
                                  A_   G
GAM1110  NDRG3    3'  CACTGCAACCTCTGCC      49293      A
                                GGCA GAGGTTGCAGTG
                                |||| ||||||||||
                                CCGT CTCCAACGTCAC

                                  _
GAM1110  NONO     3'  CGGCTCACTGCAATCTCTGCCT 82017       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
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                                TCCGT CTCTAACGTCACTCGGC
                                     _
GAM1110 NQO1     3' CGGCTCACTGCAACCTCTGCCT 6156       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                     _
GAM1110 OVOL1    3' CTCCTGCAACCTCTCACC    15856    CA        T
                                GG  AGAGGTTGCAG GAG
                                ||  |||||||||| |||
                                CC  TCTCCAACGTC CTC
                                 AC        _
GAM1110 PCDHB11  3' GCTCACTGCAACCTCTGCCT   38416      A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                     _
GAM1110 PCDHB11  3' GCTCACTGCACCCTCCGCCT   38418     AA   T
                                AGGC  GAGG TGCAGTGAGC
                                ||||  |||| ||||||||||
                                TCCG  CTCC ACGTCACTCG
                                  C_   C
GAM1110 PCDHB16  3' CACTGCAACCTCTGCCT     40550      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                     _
GAM1110 PCDHB9   3' GCTCACTGCAACCTCCGCCT   38940     AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                TCCG  CTCCAACGTCACTCG
                                  C_
GAM1110 PDCL     3' CGGCTCACTGCAACCTCCACCT 18211     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  AC_
GAM1110 PDE6B    3' GCTCACTGCAACCTCCACCT   4282      CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   |||||||||||||
                                TCC   CTCCAACGTCACTCG
                                  AC_
GAM1110 PER2     3' CACTGCAACCTCTGCCT     43028      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                     _
GAM1110 PIGR     3' CGGCTCACTGAAACCTCTGCCT 72596      A     G
                                AGGCA GAGGTT CAGTGAGCCG
                                ||||| |||||| ||||||||||
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                                TCCGT CTCCAA GTCACTCGGC
                                  _     A
GAM1110 PIGR     3' CGGCTCACTGCAACCTCCGCCT 72597      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110 PIK3C2B  3' CGACTCACTGCAAAATCTGCCT 10564       A  GG        C
                                AGGCA GA  TTGCAGTGAG CG
                                ||||| ||  |||||||||| ||
                                TCCGT CT  AACGTCACTC GC
                                  _ AA        A
GAM1110 PIM2     3' TTCTTGCAACCTCCTCCT    59993     CAA        T
                                AGG   GAGGTTGCAG GAG
                                |||   |||||||||| |||
                                TCC   CTCCAACGTT CTT
                                  TC_       _
GAM1110 PMCHL1   3' CGGCTCACTGAAACCTCTGCCT 49070       A     G
                                AGGCA GAGGTT CAGTGAGCCG
                                ||||| |||||| ||||||||||
                                TCCGT CTCCAA GTCACTCGGC
                                  _     A
GAM1110 PPEF2    3' CGGCTCACCGCAAAGTCCGCCT 20668      AA  GG    A
                                AGGC  GA  TTGC GTGAGCCG
                                ||||  ||  |||| ||||||||
                                TCCG  CT  AACG CACTCGGC
                                  C_ GA   C
GAM1110 PPID     3' CGGCTCACTGCATCCTCTGCCT 87430       A   T
                                AGGCA GAGG TGCAGTGAGCCG
                                ||||| |||| ||||||||||||
                                TCCGT CTCC ACGTCACTCGGC
                                  _   T
GAM1110 PRKCM    3' GCTCAGCAACCTTTCACCT   10813     CA       AG
                                AGG  AGAGGTTGC  TGAGC
                                |||  |||||||||  |||||
                                TCC  TTTCCAACG  ACTCG
                                  AC       __
GAM1110 PRKWNK3  3' TGCTGCAACCTCCCCCT     61557     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCGT
                                  CC_
GAM1110 PSMB2    3' CACTGCAACCTCCGCCT      10949      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110 PSMD9    3' GCCCACTGCTAGTTTGACT    10985    G   AGGTT     A
                                AG CAAG    GCAGTG GC
                                || ||||    |||||| ||
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                                TC GTTT    CGTCAC CG
                                 A   GAT__     C
GAM1110  PTGIS    3'  CGGCTCACTGCAAGCTCTGCCT 6332       A   G
                                AGGCA GAG TTGCAGTGAGCCG
                                ||||| ||| ||||||||||||||
                                TCCGT CTC AACGTCACTCGGC
                                  _  G
GAM1110  RAB36    3'  CGGCTCAGTGCAACCTCTGCCT 16957      A       G
                                AGGCA GAGGTTGCA TGAGCCG
                                ||||| ||||||||| |||||||
                                TCCGT CTCCAACGT ACTCGGC
                                  _       G
GAM1110  RHD      3'  CACTGCAACCTCTACCT     32299     CA
                                AGG  AGAGGTTGCAGTG
                                |||  |||||||||||||
                                TCC  TCTCCAACGTCAC
                                  A_
GAM1110  RHD      3'  CGGCTCACTGCAACCTCCGCCT 32303      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  RHD      3'  CACTGCAACCTCTACCT     32608     CA
                                AGG  AGAGGTTGCAGTG
                                |||  |||||||||||||
                                TCC  TCTCCAACGTCAC
                                  A_
GAM1110  RHD      3'  CGGCTCACTGCAACCTCCGCCT 32612      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  RP2      3'  CGGCTCACCACAACATCCGCCT 22615      AA  G   CA
                                AGGC  GA GTTG  GTGAGCCG
                                ||||  || ||||  ||||||||
                                TCCG  CT CAAC  CACTCGGC
                                  C_ A   AC
GAM1110  RPH3AL   3'  CGGCTCACTGCAACCTCCACCT 22744     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  AC_
GAM1110  RPP30    3'  GCTCACTGCAACCTCAATCCT  21167     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   |||||||||||||
                                TCC   CTCCAACGTCACTCG
                                  TAA
GAM1110  SAS      3'  CGGCTCACCGCAACCTCTGCCT 19951      A       A
                                AGGCA GAGGTTGC GTGAGCCG
                                ||||| |||||||| ||||||||
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                                TCCGT CTCCAACG CACTCGGC
                                  _      C
GAM1110 SCML2    3' CGGCTCACTGCAACCTCGCCT 20315     AA
                                AGGC GAGGTTGCAGTGAGCCG
                                |||| ||||||||||||||||
                                TCCG CTCCAACGTCACTCGGC
                                  __
GAM1110 SDPR     5' CACCGCAACTTCTCACC    16223    CA       A
                                GG AGAGGTTGC GTG
                                || ||||||||| |||
                                CC TCTTCAACG CAC
                                 AC       C
GAM1110 SEDL     3' CACTGCAACCTCCACCT    27323    CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  CTCCAACGTCAC
                                  AC_
GAM1110 SEDL     3' CACTGCAACCTCCACCT    27324    CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  CTCCAACGTCAC
                                  AC_
GAM1110 SEDL     3' CACTGCAACCTCCGCCT    27327     AA
                                AGGC GAGGTTGCAGTG
                                |||| ||||||||||||
                                TCCG CTCCAACGTCAC
                                  C_
GAM1110 SEPN1    3' CACTGCAACCTCCACCT    66362    CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  CTCCAACGTCAC
                                  AC_
GAM1110 SERPINB9 3' GGCTCACTGCAACCTCCTCCT 14759    CAA
                                AGG  GAGGTTGCAGTGAGCC
                                |||  ||||||||||||||||
                                TCC  CTCCAACGTCACTCGG
                                  TC_
GAM1110 SFRP4    3' CTCACTGCAGTGCTCT     11576     _
                                AGAG GTTGCAGTGAG
                                |||| ||||||||||
                                TCTC TGACGTCACTC
                                  G
GAM1110 SHOX     3' CGACTCACTGCAACCTCCGCCT 22532     AA          C
                                AGGC GAGGTTGCAGTGAG CG
                                |||| |||||||||||||| ||
                                TCCG CTCCAACGTCACTC GC
                                  C_          A
GAM1110 SIGLEC11 3' CGGCTCACTGTAGCCTCAACCT 53542    CAA
                                AGG  GAGGTTGCAGTGAGCCG
                                |||  |||||||||||||||||
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                                TCC   CTCCGATGTCACTCGGC
                                  AA_
GAM1110 SIL      3' CACTGCAACCTCTGCCT     11685       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110 SLC13A1  3' CGGCTCACTGCAAGCTCCGCCT 42378      AA  G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||
                                TCCG  CTC AACGTCACTCGGC
                                  C_  G
GAM1110 SLC14A2  5' CACTGCAACCTCCACCT     23129     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1110 SLC15A1  3' GCTCACTGCAACCTCCGCCT   17404      AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  |||||||||||||||
                                TCCG  CTCCAACGTCACTCG
                                  C_
GAM1110 SLC7A5   3' ACGTCAGCCTCTTACCT     13007     C       CA
                                AGG AAGAGGTTG  GT
                                ||| |||||||||  ||
                                TCC TTCTCCGAC  CA
                                  A       TG
GAM1110 SMAC     5' CGGCTCACTGCAACCTCTGCCT 57208       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                  _
GAM1110 SMAC     5' GCTCACTGCAACCTGTGCCT   57214      AG
                                AGGCA  AGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                TCCGT  TCCAACGTCACTCG
                                   G_
GAM1110 SMP1     3' ACTGAGCACAACCTCTTTCC   26695    C       ____
                                GG AAGAGGTTG    CAGT
                                || |||||||||    ||||
                                CC TTCTCCAAC    GTCA
                                  T       ACGA
GAM1110 SNAP23   3' CACTGCAACCTCCGCCT     55458      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110 SNAP23   3' CACTGCAACCTCCGCCT     13805      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  SNX15    3'  CGGCTCACTGCAACCTCCACCT 73736     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  AC_
GAM1110  SPN      3'  CACTGCAACCTCTGCCT     11916      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  SS18     3'  GCTCACTGCAACCTCCGCCT   18886      AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                TCCG  CTCCAACGTCACTCG
                                  C_
GAM1110  STAU     5'  CGGCTCACTGCAACCTCCACCT 15999     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  AC_
GAM1110  SULT2B1  5'  CGGCTCACTGCAACCTCCGCCT 16024      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  TAPBP    3'  CGGCTCACTGCAAGCTCCGCCT 12123     AA  G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||
                                TCCG  CTC AACGTCACTCGGC
                                  C_  G
GAM1110  TAPBP    3'  CTTACTGCAACCTCCGCCT    12124     AA
                                AGGC  GAGGTTGCAGTGAG
                                ||||  ||||||||||||||
                                TCCG  CTCCAACGTCATTC
                                  C_
GAM1110  TAT      3'  CGGCTCACTGCAACCTCCACCT 4463      CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  AC_
GAM1110  TBXA2R   3'  CGGCTCACTGCAACCTCCGCCT 6487      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  TBXA2R   3'  GCTCACTGCAACCTCCACCT   6495      CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   |||||||||||||||
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                                TCC   CTCCAACGTCACTCG
                                  AC_
GAM1110  TERF1    3'  GCTCACTGAACCTCTGCCT   33972      A     G
                                AGGCA GAGGTT CAGTGAGC
                                ||||| |||||| ||||||||
                                TCCGT CTCCAA GTCACTCG
                                  _     _
GAM1110  TIM3     3'  CGGCTCACTGCAAGCTCCGCCT 51340      AA   G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||
                                TCCG  CTC AACGTCACTCGGC
                                  C_  G
GAM1110  TJP1     5'  GCTCACTGCAGCCTTGACCT   12299     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                TCC   TTCCGACGTCACTCG
                                  AG_
GAM1110  TMC1     5'  CGGCTCTCTGCAACCTCCGCCT 56899      AA        T
                                AGGC  GAGGTTGCAG GAGCCG
                                ||||  |||||||||| ||||||
                                TCCG  CTCCAACGTC CTCGGC
                                  C_        T
GAM1110  TNFRSF10B 3'  CAGTGCAACCTCCGCCT     13866      AA       G
                                AGGC  GAGGTTGCA TG
                                ||||  ||||||||| ||
                                TCCG  CTCCAACGT AC
                                  C_       G
GAM1110  TPMT     3'  CGGCTCACTGCAACCTCTGCCT 4538       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                  _
GAM1110  TRAF5    3'  GCTCACTGCAAACTCTGCCT   16080      A   G
                                AGGCA GAG TTGCAGTGAGC
                                ||||| ||| ||||||||||
                                TCCGT CTC AACGTCACTCG
                                  _  A
GAM1110  TRIM9    5'  CGGCTCACTGCAACCTCCGCCT 30758      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  TRPM6    3'  CACTGCAACCTCTGCCT     34534       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  TRPV1    3'  CACTGCAACCTCTGCCT     38072       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||
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                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  TRPV1    3' CTGCAACCTCCGCCT      38079      AA
                                AGGC  GAGGTTGCAG
                                ||||  ||||||||||
                                TCCG  CTCCAACGTC
                                  C_
GAM1110  TRPV1    3' CACTGCAACCTCTGCCT     54791       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  TRPV1    3' CTGCAACCTCCGCCT      54800      AA
                                AGGC  GAGGTTGCAG
                                ||||  ||||||||||
                                TCCG  CTCCAACGTC
                                  C_
GAM1110  TRPV1    3' CACTGCAACCTCTGCCT     54826       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  TRPV1    3' CTGCAACCTCCGCCT      54833      AA
                                AGGC  GAGGTTGCAG
                                ||||  ||||||||||
                                TCCG  CTCCAACGTC
                                  C_
GAM1110  TRPV1    3' CACTGCAACCTCTGCCT     54858       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  TRPV1    3' CTGCAACCTCCGCCT      54865      AA
                                AGGC  GAGGTTGCAG
                                ||||  ||||||||||
                                TCCG  CTCCAACGTC
                                  C_
GAM1110  TUFT1    3' GCTCACTGCAACCTCTGCCT  39261       A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110  UGDH     3' CGGCTCACTGCAAGCTCTGCTT 12543      A   G
                                AGGCA GAG TTGCAGTGAGCCG
                                ||||| ||| ||||||||||||
                                TTCGT CTC AACGTCACTCGGC
                                  _  G
GAM1110  UQCRC1   5' GCTGTGGCTGCAACTCCCCGCC 12555     AAGA       G__
                                GGC   GGTTGCAGT   AGC
                                |||   |||||||||   |||
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                                CCG   TCAACGTCG  TCG
                                  CCCC       GTG
GAM1110 VENTX2   3' CGGCTCACTGCAACCTCCGCCT 27110     AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110 VHL      3' CGGCTCACTGCAACCTCTGCCT 5068      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                   _
GAM1110 YES1     3' CGGCTCACTGCAAGCTCTGCCT 18352     A  G
                                AGGCA GAG TTGCAGTGAGCCG
                                ||||| ||| ||||||||||||
                                TCCGT CTC AACGTCACTCGGC
                                   _  G
GAM1110 ZNF133   5' CTCACTGCAACCTCCACCC   12836    CAA
                                GG   GAGGTTGCAGTGAG
                                ||   ||||||||||||||
                                CC   CTCCAACGTCACTC
                                 CAC
GAM1110 ZNF264   3' CACTGCAACCTCCGCCT     12745     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110 ZNF264   3' CGGCTCTCTGCAACCTCTGCCT 12749      A       T
                                AGGCA GAGGTTGCAG GAGCCG
                                ||||| |||||||||| ||||||
                                TCCGT CTCCAACGTC CTCGGC
                                   _       T
GAM1110 20D7-FC4 5' GCTCACTGCAGCCTCCACCT   60902    CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   |||||||||||||||
                                TCC   CTCCGACGTCACTCG
                                  AC_
GAM1110 AP3S2    3' CGGCTCACTGCAACCTCTGCTT 19519      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TTCGT CTCCAACGTCACTCGGC
                                   _
GAM1110 APOL2    3' CGGCTCACTGCAAACTCCGCCT 48046     AA  G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||
                                TCCG  CTC AACGTCACTCGGC
                                  C_  A
GAM1110 APXL2    5' CGGCTCACTACAACTTCCGCCT 75187     AA     C
                                AGGC  GAGGTTG AGTGAGCCG
                                ||||  ||||||| |||||||||
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                              TCCG  CTTCAAC TCACTCGGC
                                C_      A
GAM1110 ARHGAP5  5' CGGCTCACCACAACCCCCACCT 77072     CAAGA    CA
                              AGG    GGTTG  GTGAGCCG
                              |||    |||||  ||||||||
                              TCC    CCAAC  CACTCGGC
                                ACCC_    AC
GAM1110 ARPP-19  3' CACTGCAACCTCTGCCT     21790      A
                              AGGCA GAGGTTGCAGTG
                              ||||| ||||||||||||
                              TCCGT CTCCAACGTCAC
                                 _
GAM1110 ARPP-19  3' GCTCACTGCAACCTTACTCCT  21799     CAA
                              AGG   GAGGTTGCAGTGAGC
                              |||   ||||||||||||||
                              TCC   TTCCAACGTCACTCG
                                TCA
GAM1110 ASB16    5' CACTGCAACCTCCGCCT     69931      AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1110 ASB16    3' CGGCTCACTGCAACTTCTACC  55106    CA
                              GG  AGAGGTTGCAGTGAGCCG
                              ||  ||||||||||||||||||
                              CC  TCTTCAACGTCACTCGGC
                               A_
GAM1110 ASE-1    3' CACTGCAACCTCCGCCT     23945      AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1110 ASE-1    3' CGGCTCACTGCAAGCTCCGCCT 23949      AA  G
                              AGGC  GAG TTGCAGTGAGCCG
                              ||||  ||| ||||||||||||
                              TCCG  CTC AACGTCACTCGGC
                                C_  G
GAM1110 ATP1B4   3' CGGCTCACTGCAACCTCCACCT 23815     CAA
                              AGG   GAGGTTGCAGTGAGCCG
                              |||   ||||||||||||||||
                              TCC   CTCCAACGTCACTCGGC
                                AC_
GAM1110 BA108L7.2 3' CACTGCAACCTCTGCCT     48258      A
                              AGGCA GAGGTTGCAGTG
                              ||||| ||||||||||||
                              TCCGT CTCCAACGTCAC
                                 _
GAM1110 BAG5     3' GCTCACTGCAACCTCCACCT   16844     CAA
                              AGG   GAGGTTGCAGTGAGC
                              |||   |||||||||||||||
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                                TCC  CTCCAACGTCACTCG
                                  AC_
GAM1110 BNIP-S   3' CGGCTCACTGCAACCTCCGCCT 56259     AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110 BTN3A1   3' GCTCCCTGCAACCTCCACCT  22920    CAA       T
                                AGG  GAGGTTGCAG GAGC
                                |||  |||||||||| ||||
                                TCC  CTCCAACGTC CTCG
                                  AC_       C
GAM1110 C11orf17 3' CGGCTCACTGCAAGTTCCGCCT 40210     AA  G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||
                                TCCG  CTT AACGTCACTCGGC
                                  C_  G
GAM1110 C1orf24  3' CGGCTCACTGCAACCTCCGCCT 53711     AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110 C1QTNF6  3' CACTGCAACCTCTGCCT    49138      A
                                AGGCA GAGGTTGCAGTG
                                |||||  ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110 C21orf25 3' GCTTACTGCAACCTCCACCT  63552    CAA
                                AGG  GAGGTTGCAGTGAGC
                                |||  ||||||||||||||
                                TCC  CTCCAACGTCATTCG
                                  AC_
GAM1110 C22orf19 3' CGGCTCACTGCCGCCTCAACCT 13422    CAA   T
                                AGG  GAGGT GCAGTGAGCCG
                                |||  |||||  ||||||||||
                                TCC  CTCCG CGTCACTCGGC
                                  AA_   C
GAM1110 C3F      3' GCTCACCGCAACCTCCACCT  19292    CAA      A
                                AGG  GAGGTTGC GTGAGC
                                |||  ||||||||  ||||||
                                TCC  CTCCAACG CACTCG
                                  AC_       C
GAM1110 C6orf33  3' CGGCTCACTGCAGCCTCGACCT 55878    CAA
                                AGG  GAGGTTGCAGTGAGCCG
                                |||  ||||||||||||||||
                                TCC  CTCCGACGTCACTCGGC
                                  AG_
GAM1110 C6orf5   3' GCTCACTGCAGCTTTGACCT  31355    CAA
                                AGG  GAGGTTGCAGTGAGC
                                |||  |||||||||||||
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                              TCC  TTTCGACGTCACTCG
                                AG_
GAM1110 C8orf13  5' CGGCTCACTGCGCGGTCCCT  81571    CAA  GGT
                              AGG  GA  TGCAGTGAGCCG
                              |||  ||  ||||||||||||
                              TCC  CT  GCGTCACTCGGC
                                ___ GGC
GAM1110 C9orf9   3' CACTGCAACCTCCACCT    38503    CAA
                              AGG  GAGGTTGCAGTG
                              |||  ||||||||||||
                              TCC  CTCCAACGTCAC
                                AC_
GAM1110 C9orf9   3' CGGCTCACTGCAACCTCCGCCT 38509     AA
                              AGGC  GAGGTTGCAGTGAGCCG
                              ||||  ||||||||||||||||
                              TCCG  CTCCAACGTCACTCGGC
                                C_
GAM1110 CARD6    3' CGGCTCACCGCAACCTCTGCTT 50855     A     A
                              AGGCA GAGGTTGC GTGAGCCG
                              ||||| |||||||| ||||||||
                              TTCGT CTCCAACG CACTCGGC
                                _      C
GAM1110 CCRN4L   3' CGGCTCACTGCAAGATCCGCCT 24007     AA  GG
                              AGGC  GA  TTGCAGTGAGCCG
                              ||||  ||  ||||||||||||
                              TCCG  CT  AACGTCACTCGGC
                                C_  AG
GAM1110 CEACAM8  3' CTCACTGCAAGCTCCGCCT   8422     AA  G
                              AGGC  GAG TTGCAGTGAG
                              ||||  ||| ||||||||||
                              TCCG  CTC AACGTCACTC
                                C_  G
GAM1110 CECR1    3' CGGCTCACTGCAACTTC    33811
                              GAGGTTGCAGTGAGCCG
                              |||||||||||||||||
                              CTTCAACGTCACTCGGC

GAM1110 CENPH    3' CGGCTCACTGCAACCTCTGCCT 43273     A
                              AGGCA GAGGTTGCAGTGAGCCG
                              ||||| |||||||||||||||||
                              TCCGT CTCCAACGTCACTCGGC
                                _
GAM1110 CENTB5   3' CGGCCCCCCAACTCTCTTGCCT 95485       _   CAGTGA
                              AGGCAAGAG GTTG     GCCG
                              ||||||||| ||||     ||||
                              TCCGTTCTC CAAC     CGGC
                                   T   CCCC__
GAM1110 CHRAC1   3' GCTCACTGCAACCTCCGCCT  33872     AA
                              AGGC  GAGGTTGCAGTGAGC
                              ||||  ||||||||||||||
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                                TCCG  CTCCAACGTCACTCG
                                  C_
GAM1110  COLEC12   3'  CGGCTCACTGCAACCCCC    47863    CAAGA
                                GG    GGTTGCAGTGAGCCG
                                ||    ||||||||||||||
                                CC    CCAACGTCACTCGGC
                                 C____
GAM1110  CPSF2     3'  CGGCTCACCGCAACCTCTGCCT 61578       A       A
                                AGGCA GAGGTTGC GTGAGCCG
                                ||||| |||||||| ||||||||
                                TCCGT CTCCAACG CACTCGGC
                                   _       C
GAM1110  DBR1      3'  CGGCTCACCGCAACCTCCGCCT 32530      AA       A
                                AGGC  GAGGTTGC GTGAGCCG
                                ||||  |||||||| ||||||||
                                TCCG  CTCCAACG CACTCGGC
                                  C_       C
GAM1110  DKFZP434C212 3'  CACTGCAACCTCCACCT     68905     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1110  DKFZp434E2220 5'  CGGCTCACTGCAACCTCCGCCT 34295      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  DKFZP434F0318 3'  CGGCTCACTGCAACCTC     48007
                                GAGGTTGCAGTGAGCCG
                                |||||||||||||||||
                                CTCCAACGTCACTCGGC

GAM1110  DKFZp434F1719 3'  GCTCACTGCAGGCTCTGCCT   50000       A   G
                                AGGCA GAG TTGCAGTGAGC
                                ||||| ||| ||||||||||
                                TCCGT CTC GACGTCACTCG
                                   _   G
GAM1110  DKFZp547H025 3'  GCTCACTGCAACCTCCACCT   39358     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   |||||||||||||||
                                TCC   CTCCAACGTCACTCG
                                  AC_
GAM1110  DKFZp547M072 3'  CGGCTCGCCACCCTCTGCC    61078      A    T  CA
                                GGCA GAGG TG  GTGAGCCG
                                |||| |||| ||  ||||||||
                                CCGT CTCC AC  CGCTCGGC
                                   _    C  __
GAM1110  DKFZP564G092 5'  GCTCACTGGAGCCTCTGCCT   31538       A     G
                                AGGCA GAGGTT CAGTGAGC
                                ||||| |||||| ||||||||
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                                TCCGT CTCCGA GTCACTCG
                                  _     G
GAM1110  DKFZP564O0523 3'  CGGCTCACTGCAACCTCCACCT 49513     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  AC_
GAM1110  DKFZp761J139 5'  GCTCACTGCAACGTCCACCT   50111     CAA  G
                                AGG   GA GTTGCAGTGAGC
                                |||   || ||||||||||||
                                TCC   CT CAACGTCACTCG
                                  AC_  G
GAM1110  DKFZp761N1114 3'  CGGCTCACTGCAACCTCCGCCT 79017      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  DKFZp762L0311 3'  CGGCTCACTGCAACCTTTGCCT 38055      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT TTCCAACGTCACTCGGC
                                  _
GAM1110  DKFZp762P2111 3'  CACTGCAACCTCCGCCT     86352      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  DPYSL4   5'  CGGCTCACGCGTCCGCCCGCC  21215     AAGA  T   A
                                GGC    GG TGC GTGAGCCG
                                |||    || ||| ||||||||
                                CCG    CC GCG CACTCGGC
                                  CCCG  T   _
GAM1110  DRIM     3'  GCTCACTGCAGCCTCAACCT   27178     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                TCC   CTCCGACGTCACTCG
                                  AA_
GAM1110  DSCR6    3'  CGGCTCACTGCAACCTC     38545
                                GAGGTTGCAGTGAGCCG
                                |||||||||||||||||
                                CTCCAACGTCACTCGGC

GAM1110  EREG     3'  CGGCTCACTGCAACCTCACCT  7496      CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  A__
GAM1110  FBP17    3'  CGGCTCACTACAACCTCCACCT 72786     CAA      C
                                AGG   GAGGTTG AGTGAGCCG
                                |||   ||||||| |||||||||
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                              TCC   CTCCAAC TCACTCGGC
                                AC_      A
GAM1110  FER1L4   3'  CGGCTGACTGCAACCTCCACCT 47339     CAA         G
                              AGG   GAGGTTGCAGT AGCCG
                              |||   |||||||||||| |||||
                              TCC   CTCCAACGTCA TCGGC
                                AC_         G
GAM1110  FER1L4   3'  CGGCTGACTGCAACCTCCACCT 47340     CAA         G
                              AGG   GAGGTTGCAGT AGCCG
                              |||   |||||||||||| |||||
                              TCC   CTCCAACGTCA TCGGC
                                AC_         G
GAM1110  FKBP9    3'  CGGCTCACTGCAGCACTGTCT  94063      AGAG
                              AGGCA    GTTGCAGTGAGCCG
                              |||||    ||||||||||||||
                              TCTGT    CGACGTCACTCGGC
                                 CA__
GAM1110  FKBP9    3'  CGGCTCACTGCAGCCTCCGCCT 94064      AA
                              AGGC  GAGGTTGCAGTGAGCCG
                              ||||  ||||||||||||||||
                              TCCG  CTCCGACGTCACTCGGC
                                C_
GAM1110  FLJ00024 5'  CGGCTCACTGCAACCTCTGCCT 63758       A
                              AGGCA GAGGTTGCAGTGAGCCG
                              ||||| ||||||||||||||||
                              TCCGT CTCCAACGTCACTCGGC
                                    _
GAM1110  FLJ00060 5'  CGGCTCACTGCAAGCTCTGCCT 61096       A   G
                              AGGCA GAG TTGCAGTGAGCCG
                              ||||| ||| ||||||||||||
                              TCCGT CTC AACGTCACTCGGC
                                 _  G
GAM1110  FLJ10232 3'  CACTGCAACCTCCGCCT     35921      AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1110  FLJ10297 3'  GCTCACTGTGACCTTGACCT   35982     CAA    TG
                              AGG   GAGGT  CAGTGAGC
                              |||   |||||  ||||||||
                              TCC   TTCCA  GTCACTCG
                                AG_    GT
GAM1110  FLJ10346 5'  CGGCTCACTGCAAGCTCCACCT 36041     CAA   G
                              AGG   GAG TTGCAGTGAGCCG
                              |||   ||| ||||||||||||
                              TCC   CTC AACGTCACTCGGC
                                AC_   G
GAM1110  FLJ10535 3'  CACTGCAACCTCTGCCT     36234       A
                              AGGCA GAGGTTGCAGTG
                              ||||| ||||||||||||
                              TCCGT CTCCAACGTCACT
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                              TCCGT CTCCAACGTCAC
                                _
GAM1110  FLJ10560  3' CGGCTCACTGCAAGCTCTGCCT 36277      A   G
                              AGGCA GAG TTGCAGTGAGCCG
                              ||||| ||| ||||||||||||||
                              TCCGT CTC AACGTCACTCGGC
                                _  G
GAM1110  FLJ10716  5' CGGCTCACTGCAGCCTCAACCT 36483     CAA
                              AGG  GAGGTTGCAGTGAGCCG
                              |||  ||||||||||||||||
                              TCC  CTCCGACGTCACTCGGC
                               AA_
GAM1110  FLJ10901  3' CGGCTCACTGCAACCCCCGTCT 36819     AAGA
                              AGGC   GGTTGCAGTGAGCCG
                              ||||   ||||||||||||||
                              TCTG   CCAACGTCACTCGGC
                                CCC_
GAM1110  FLJ10922  3' CACTGCAACCTCCGCCT    36870     AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1110  FLJ11004  5' CGGCTCACTGCAACCTCTACCT 36967     CA
                              AGG  AGAGGTTGCAGTGAGCCG
                              |||  ||||||||||||||||||
                              TCC  TCTCCAACGTCACTCGGC
                               A_
GAM1110  FLJ11151  3' GCTGCACACAACCTCTTGCT  67879          CA  _
                              GGCAAGAGGTTG  GTG AGC
                              ||||||||||||  ||| |||
                              TCGTTCTCCAAC  CAC TCG
                                    A_  G
GAM1110  FLJ11467  3' GCTCACTGCAGCCTTGACCT  46376     CAA
                              AGG  GAGGTTGCAGTGAGC
                              |||  |||||||||||||||
                              TCC  TTCCGACGTCACTCG
                               AG_
GAM1110  FLJ12363  3' GCTCACTGCAACCTCCACCT  49683     CAA
                              AGG  GAGGTTGCAGTGAGC
                              |||  |||||||||||||||
                              TCC  CTCCAACGTCACTCG
                               AC_
GAM1110  FLJ12409  3' CACTGCAACCTCCGCCT    47043     AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1110  FLJ12572  5' CACTGCAACCTCTGCCT    43246      A
                              AGGCA GAGGTTGCAGTG
                              ||||| ||||||||||||
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                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  FLJ12649  3'  CGGCTCACTGCAACCTCCGCCT 44778     AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  FLJ12687  3'  CGGCTCACTGCAACCTCCGCCT 46189     AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  FLJ12747  3'  CACTGCAACCTCTGCCT     49711       A
                                AGGCA GAGGTTGCAGTG
                                |||||  ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  FLJ12787  3'  CACTGCAACCTCTGCC      49746      A
                                GGCA GAGGTTGCAGTG
                                ||||  ||||||||||||
                                CCGT CTCCAACGTCAC
                                  _
GAM1110  FLJ12876  3'  CGGCTCACTGCAAGCTCCGCCT 42785     AA   G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  |||  ||||||||||||
                                TCCG  CTC AACGTCACTCGGC
                                  C_   G
GAM1110  FLJ12891  3'  GCCTCAACTCTTGCCT      46343          G   C  TGA
                                AGGCAAGAG TTG AG   GC
                                |||||||||  |||  ||   ||
                                TCCGTTCTC AAC TC   CG
                                     _   _  ____
GAM1110  FLJ12960  3'  CGGCTCTATGCAACCTCCACCT 44948     CAA        GT
                                AGG   GAGGTTGCA  GAGCCG
                                |||   |||||||||  ||||||
                                TCC   CTCCAACGT  CTCGGC
                                  AC_        AT
GAM1110  FLJ12973  3'  CACCGCAACCTCCGCCT     46102      AA       A
                                AGGC  GAGGTTGC GTG
                                ||||  ||||||||  |||
                                TCCG  CTCCAACG CAC
                                  C_       C
GAM1110  FLJ12975  3'  CGGCTCACCACAACCTCCTCCT 69580     CAA      CA
                                AGG   GAGGTTG  GTGAGCCG
                                |||   |||||||  ||||||||
                                TCC   CTCCAAC  CACTCGGC
                                  TC_      AC
GAM1110  FLJ12975  3'  CGGCTCACTGCAATCTCTGCCT 69581       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                |||||  ||||||||||||||||
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                                TCCGT CTCTAACGTCACTCGGC
                                  _
GAM1110 FLJ13072 5' CACTGCAACCTCTGCCT    89803     A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110 FLJ13089 5' CTCACTGCAGGCACTGACT   70861   GCA  AG  _
                                AG  AG  GT TGCAGTGAG
                                ||  ||  || |||||||||
                                TC  TC  CG ACGTCACTC
                                 AG_ A_  G
GAM1110 FLJ13105 3' ACTAAAAATCTCCTGCCT    46542     A    GC_
                                AGGCA GAGGTT  AGT
                                ||||| ||||||  |||
                                TCCGT CTCTAA  TCA
                                   C     AAA
GAM1110 FLJ13162 3' GCTGCGACCCCCTGCCT     46558     AGA
                                AGGCA  GGTTGCAGT
                                |||||  |||||||||
                                TCCGT  CCAGCGTCG
                                   CCC
GAM1110 FLJ13197 3' CGGCTCACTGCAACCTCTACCT 44850    CA
                                AGG  AGAGGTTGCAGTGAGCCG
                                |||  |||||||||||||||||
                                TCC  TCTCCAACGTCACTCGGC
                                 A_
GAM1110 FLJ14442 3' GCTCACTGCAACTTCTGCCT  51369     A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
                                TCCGT CTTCAACGTCACTCG
                                  _
GAM1110 FLJ14810 3' GCTCACTGATCTCTTGCCT   51626       TG
                                AGGCAAGAGGT  CAGTGAGC
                                ||||||||||  ||||||||
                                TCCGTTCTCTA  GTCACTCG
                                    __
GAM1110 FLJ14950 3' CACTGCAACCTCCACCT     51713    CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  CTCCAACGTCAC
                                 AC_
GAM1110 FLJ14957 3' CACTGCAACCTCTGCCT     51741     A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110 FLJ20004 3' CATTGCAACCTCCGCCT     95290     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                TCCG  CTCCAACGTTAC
                                  C_
GAM1110  FLJ20034  3'  GCTCACTGCAACCTCTGCCT   34374      A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110  FLJ20045  3'  CGGCTCACTGCAACCTCTGCCT 34418      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| |||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                  _
GAM1110  FLJ20079  3'  CACCGCAACCTCCACCT     34487     CAA      A
                                AGG   GAGGTTGC GTG
                                |||   |||||||| |||
                                TCC   CTCCAACG CAC
                                  AC_       C
GAM1110  FLJ20342  3'  CACTGCAACCTCTGCCT     34986      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  FLJ20344  3'  CACTGCAACCTCCGCCT     35005      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  FLJ20507  3'  GCTCACTGCAACCTCTGCCT   35293      A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110  FLJ20507  3'  GCTCACTGCAACCTCTGCCT   60228      A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110  FLJ20511  3'  CGGCTCACTGCAAGCTCCACCT 35322     CAA   G
                                AGG   GAG TTGCAGTGAGCCG
                                |||   ||| ||||||||||||
                                TCC   CTC AACGTCACTCGGC
                                  AC_   G
GAM1110  FLJ20700  3'  CGGCTCACTGCAACCTCTGTCT 35573      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| |||||||||||||||||
                                TCTGT CTCCAACGTCACTCGGC
                                  _
GAM1110  FLJ20813  3'  CGGCTCACTGCAACTCCACCT  35681     CAA   G
                                AGG   GAG TTGCAGTGAGCCG
                                |||   ||| ||||||||||||
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                              TCC   CTC AACGTCACTCGGC
                                AC_  _
GAM1110 FLJ21135 5' CGGCTCACCGCCCCCTCCCCT 45884    CAA   TT  A
                              AGG   GAGG  GC GTGAGCCG
                              |||   ||||  || ||||||||
                              TCC   CTCC  CG CACTCGGC
                                C__    CC  C
GAM1110 FLJ21302 3' CACTGCAACCTCCGCCT     43211      AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1110 FLJ21324 5' CGGCTCACTGCAAACTCCGCTT 91197      AA   G
                              AGGC  GAG TTGCAGTGAGCCG
                              ||||  ||| ||||||||||||||
                              TTCG  CTC AACGTCACTCGGC
                                C_   A
GAM1110 FLJ21459 3' CGGCTCACTGCAAACTCCGCCT 44514      AA   G
                              AGGC  GAG TTGCAGTGAGCCG
                              ||||  ||| ||||||||||||||
                              TCCG  CTC AACGTCACTCGGC
                                C_   A
GAM1110 FLJ21603 3' CGGCTCACTGCAAGCCCTGCCT 45422       A A   _
                              AGGCA G GGTT GCAGTGAGCCG
                              ||||| | |||| ||||||||||
                              TCCGT C CCGA CGTCACTCGGC
                                 _ _    A
GAM1110 FLJ22002 3' GCTCACTGCAACCTCCGCCT   45774      AA
                              AGGC  GAGGTTGCAGTGAGC
                              ||||  ||||||||||||||
                              TCCG  CTCCAACGTCACTCG
                                C_
GAM1110 FLJ22167 5' GCTCACTGCCACCTCTGCCT   44576      A    T
                              AGGCA GAGGT GCAGTGAGC
                              ||||| ||||| |||||||||
                              TCCGT CTCCA CGTCACTCG
                                 _    C
GAM1110 FLJ22329 3' CGGCTCACTGCAGCCTGCGCCT 45063      AAG
                              AGGC   AGGTTGCAGTGAGCCG
                              ||||   ||||||||||||||||
                              TCCG   TCCGACGTCACTCGGC
                                CG_
GAM1110 FLJ22531 5' CGGCTCACTGCAACCTCCACCT 45028     CAA
                              AGG   GAGGTTGCAGTGAGCCG
                              |||   ||||||||||||||||
                              TCC   CTCCAACGTCACTCGGC
                                AC_
GAM1110 FLJ22684 3' CTGCAACCTCTGCCT       46793       A
                              AGGCA GAGGTTGCAG
                              ||||| ||||||||||
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                                TCCGT CTCCAACGTC
                                  _
GAM1110  FLJ22794  3' GCTCACTGCAACTTCCACCT  91608    CAA
                                AGG  GAGGTTGCAGTGAGC
                                |||  ||||||||||||||
                                TCC  CTTCAACGTCACTCG
                                  AC_
GAM1110  FLJ22965  3' CGGCTCACTGCAACCTCCGCCT 42050     AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  FLJ22969  3' CGGCTCACTGCAACCTCTGCCT 68650      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                  _
GAM1110  FLJ23024  3' GCTCACTGCAACCTCTGCCT  46269      A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110  FLJ23263  5' CGGCTCACTGCAAACTCCGCCT 47081     AA  G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||
                                TCCG  CTC AACGTCACTCGGC
                                  C_  A
GAM1110  FLJ23392  3' CGGCTCACTGCAAGCTCAGCCT 45531     AA  G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||
                                TCCG  CTC AACGTCACTCGGC
                                  A_  G
GAM1110  FLJ23392  3' GCTCACTGCAACCTCTGCCT  45538      A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110  FLJ23556  3' CGGCTCACTGCACCTCTGCCT  45946     A   T
                                AGGCA GAGGT GCAGTGAGCCG
                                ||||| ||||| ||||||||||
                                TCCGT CTCCA CGTCACTCGGC
                                  _   _
GAM1110  FLJ23563  3' CACTGCAACCTCTGCCT    67591      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  FLJ25416  5' CGGCTCACTGCAACCTCCGC  58807    AA
                                GC  GAGGTTGCAGTGAGCCG
                                ||  ||||||||||||||||
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                                CG  CTCCAACGTCACTCGGC
                                 C_
GAM1110  FLJ31101  3'  GCTCACTGCAACCTCTGCCT   35712      A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110  FLJ31153  3'  CGGCTCACTGCAATCTCTGCCT 58121      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| |||||||||||||||||
                                TCCGT CTCTAACGTCACTCGGC
                                  _
GAM1110  FLJ32356  5'  CACCCCGCAACCTCGCGCCT   58359      AA      A__
                                AGGC  GAGGTTGC   GTG
                                ||||  ||||||||   |||
                                TCCG  CTCCAACG   CAC
                                   CG       CCC
GAM1110  FLJ32865  3'  GCTCACTGCAACCTCTGCCT   58176      A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110  FOXD4     5'  CGCCACAACCTCTCGCT     82747     A       CA
                                GGC AGAGGTTG  GTG
                                ||| ||||||||  |||
                                TCG TCTCCAAC  CGC
                                  C       AC
GAM1110  GAL3ST-4  3'  CGGCTCACTGCAACCTCTGCCT 44936      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| |||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                  _
GAM1110  GMPPB     5'  CGGCTCACTGCAACCTCCACCT 95731     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  AC_
GAM1110  GNG4      3'  GCTCACTGCGACCTCCACCT   15617     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   |||||||||||||
                                TCC   CTCCAGCGTCACTCG
                                  AC_
GAM1110  GREB1     3'  CGGCTCACTGCAACCTCTGCCT 27868      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| |||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                  _
GAM1110  GREB1     3'  CGGCTCACTGCAAGCTCCGCCT 27869      AA  G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||
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                                TCCG  CTC AACGTCACTCGGC
                                  C_  G
GAM1110  GRWD     3'  CACTGCAACCTCCGCCT     48962      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  GTF2E1   3'  CGGCTCACTGCAACCTCTGCCT 18612       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                   _
GAM1110  GTPBG3   3'  CGGCTTACTGCAACCTCCACCT 50897     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCATTCGGC
                                  AC_
GAM1110  H-plk    5'  CGACTCACTGCAACCTCCACCT 31805     CAA          C
                                AGG   GAGGTTGCAGTGAG CG
                                |||   |||||||||||||| ||
                                TCC   CTCCAACGTCACTC GC
                                  AC_           A
GAM1110  HPRP3P   3'  TACTGCAAGCCCTTGCCT    16284        A   _
                                AGGCAAG GGTT GCAGTG
                                ||||||| |||| ||||||
                                TCCGTTC CCGA CGTCAT
                                    _   A
GAM1110  HRH4     3'  CACTGCAACCTCTGCCT     41247       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                   _
GAM1110  HRH4     3'  GCTCACTGCAGCCCTGACT   41252    GCA  A
                                AG   AG GGTTGCAGTGAGC
                                ||   || ||||||||||||
                                TC   TC CCGACGTCACTCG
                                 AG_  _
GAM1110  HSMPP8   3'  CGGCTCACTGCAAGCTCTGCCT 93473       A   G
                                AGGCA GAG TTGCAGTGAGCCG
                                ||||| ||| ||||||||||||
                                TCCGT CTC AACGTCACTCGGC
                                   _  G
GAM1110  HSPC065  3'  CACTGCAACCTCCACCT     26289     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1110  HSPC065  3'  CGGCTCGCTGCAACCTCCTCCT 26294     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
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                                TCC   CTCCAACGTCGCTCGGC
                                  TC_
GAM1110  ICK      3'  CTGCAACCTCTGCCT      29926       A
                                AGGCA GAGGTTGCAG
                                ||||| ||||||||||
                                TCCGT CTCCAACGTC
                                  _
GAM1110  IGSF2    3'  CGACTCACTGCGGCTGCGCC   14923     AAGA          C
                                GGC    GGTTGCAGTGAG CG
                                |||    |||||||||||| ||
                                CCG    TCGGCGTCACTC GC
                                  CG__          A
GAM1110  JAM1     3'  CGGCTCACCGCCTATCATCT   33755     _   T_  A
                                AGA GGT  GC GTGAGCCG
                                ||| |||  || ||||||||
                                TCT CTA  CG CACTCGGC
                                  A   TC  C
GAM1110  JAM1     3'  CGGCTCACCGCCTATCATCT   57881     _   T_  A
                                AGA GGT  GC GTGAGCCG
                                ||| |||  || ||||||||
                                TCT CTA  CG CACTCGGC
                                  A   TC  C
GAM1110  JAM1     3'  CGGCTCACCGCCTATCATCT   57893     _   T_  A
                                AGA GGT  GC GTGAGCCG
                                ||| |||  || ||||||||
                                TCT CTA  CG CACTCGGC
                                  A   TC  C
GAM1110  JAM1     3'  CGGCTCACCGCCTATCATCT   57921     _   T_  A
                                AGA GGT  GC GTGAGCCG
                                ||| |||  || ||||||||
                                TCT CTA  CG CACTCGGC
                                  A   TC  C
GAM1110  JAM1     5'  CGGCTCACTGCAACCTCCTCCT 57922     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  TC_
GAM1110  JAM1     3'  CGGCTCACCGCCTATCATCT   57948     _   T_  A
                                AGA GGT  GC GTGAGCCG
                                ||| |||  || ||||||||
                                TCT CTA  CG CACTCGGC
                                  A   TC  C
GAM1110  JM11     3'  GCTCACTGCAACCTCTGCCT   53262       A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110  KCNT1    3'  GCTCAGCCCTGCTGCC      61835      AG   TT  AG
                                GGCA  AGG  GC  TGAGC
                                ||||  |||  ||  |||||
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                              CCGT  TCC  CG  ACTCG
                                CG  __ __
GAM1110 KIAA0063 3' CGGCTCACTGCAACCTCCACCT 29621    CAA
                              AGG  GAGGTTGCAGTGAGCCG
                              |||  ||||||||||||||||
                              TCC  CTCCAACGTCACTCGGC
                                AC_
GAM1110 KIAA0161 3' CGGCTCACTGCAAGCTCTGCCT 28502     A  G
                              AGGCA GAG TTGCAGTGAGCCG
                              ||||| ||| ||||||||||||
                              TCCGT CTC AACGTCACTCGGC
                                 _  G
GAM1110 KIAA0205 3' GCTCACTGCAGTCTCTGCCT  29586     A  GT
                              AGGCA GAG  TGCAGTGAGC
                              ||||| |||  ||||||||||
                              TCCGT CTC  ACGTCACTCG
                                 _  TG
GAM1110 KIAA0210 5' CGGCTCACTGCCACCTCTCCCT 28476    CA    T
                              AGG  AGAGGT GCAGTGAGCCG
                              |||  |||||| ||||||||||
                              TCC  TCTCCA CGTCACTCGGC
                                C_    C
GAM1110 KIAA0210 5' GCTCACCGCAATCTCCGCCT  28478     AA     A
                              AGGC  GAGGTTGC GTGAGC
                              ||||  |||||||| ||||||
                              TCCG  CTCTAACG CACTCG
                                C_     C
GAM1110 KIAA0247 3' TTTACCCTCTTGCCT     28414         TTGCA
                              AGGCAAGAGG    GTGAG
                              ||||||||||    |||||
                              TCCGTTCTCC    CATTT
                                    _____
GAM1110 KIAA0391 3' CACTGCAACCTCTGCCT    27908     A
                              AGGCA GAGGTTGCAGTG
                              ||||| ||||||||||||
                              TCCGT CTCCAACGTCAC
                                 _
GAM1110 KIAA0426 3' CGGCTCACTGCAACCTCCGCCT 28256    AA
                              AGGC  GAGGTTGCAGTGAGCCG
                              ||||  ||||||||||||||||
                              TCCG  CTCCAACGTCACTCGGC
                                C_
GAM1110 KIAA0435 5' CGGCTCACTGCGACCTCGGCCT 28974    AA
                              AGGC  GAGGTTGCAGTGAGCCG
                              ||||  ||||||||||||||||
                              TCCG  CTCCAGCGTCACTCGGC
                                G_
GAM1110 KIAA0459 3' CGGCTCACTGCAACCTCCACCT 60988    CAA
                              AGG  GAGGTTGCAGTGAGCCG
                              |||  ||||||||||||||||
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                              TCC  CTCCAACGTCACTCGGC
                                AC_
GAM1110 KIAA0469 3' CGGCTCACTGCAAGCTC    29327    G
                              GAG TTGCAGTGAGCCG
                              ||| ||||||||||||
                              CTC AACGTCACTCGGC
                                G
GAM1110 KIAA0472 5' GCTCACTGCAACCTCCTCCT  71866    CAA
                              AGG  GAGGTTGCAGTGAGC
                              |||  ||||||||||||||
                              TCC  CTCCAACGTCACTCG
                                TC_
GAM1110 KIAA0495 3' CGGCTCACTGCAACCTCCGTCT 62579     AA
                              AGGC  GAGGTTGCAGTGAGCCG
                              ||||  ||||||||||||||||
                              TCTG  CTCCAACGTCACTCGGC
                                C_
GAM1110 KIAA0513 3' CACTGCAACCTCCACCT    28342    CAA
                              AGG  GAGGTTGCAGTG
                              |||  ||||||||||||
                              TCC  CTCCAACGTCAC
                                AC_
GAM1110 KIAA0527 3' CACTGCAACCTCTGCCT    95794     A
                              AGGCA GAGGTTGCAGTG
                              ||||| ||||||||||||
                              TCCGT CTCCAACGTCAC
                                 _
GAM1110 KIAA0544 3' CACTGCAACCTCCGCCT    70895    AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1110 KIAA0561 3' GCTCACTGCAACCTCCGCCT  65891    AA
                              AGGC  GAGGTTGCAGTGAGC
                              ||||  |||||||||||||||
                              TCCG  CTCCAACGTCACTCG
                                C_
GAM1110 KIAA0562 3' CTGCAACCTCCGCCT      28151    AA
                              AGGC  GAGGTTGCAG
                              ||||  |||||||||
                              TCCG  CTCCAACGTC
                                C_
GAM1110 KIAA0563 5' CGGCTCACTGCAACCTCTGCCT 29185     A
                              AGGCA GAGGTTGCAGTGAGCCG
                              ||||| |||||||||||||||||
                              TCCGT CTCCAACGTCACTCGGC
                                 _
GAM1110 KIAA0594 3' CGGCTTACTGCAACCTCCGCCT 64894    AA
                              AGGC  GAGGTTGCAGTGAGCCG
                              ||||  ||||||||||||||||
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                                TCCG  CTCCAACGTCATTCGGC
                                  C_
GAM1110  KIAA0599  3'  CACTGCAACCTCCGCCT     77168      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  KIAA0599  3'  CTTACTGCAACCTCCGCCT    77176      AA
                                AGGC  GAGGTTGCAGTGAG
                                ||||  ||||||||||||||
                                TCCG  CTCCAACGTCATTC
                                  C_
GAM1110  KIAA0682  3'  ACGCAGCCTCCCGCCT      32472      AA       A
                                AGGC  GAGGTTGC GT
                                ||||  |||||||| ||
                                TCCG  CTCCGACG CA
                                  CC       _
GAM1110  KIAA0720  3'  CGGCTCACTGCAACCTCTGCCT 62319       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                |||||  ||||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                   _
GAM1110  KIAA0737  3'  GCTCACTGAAACCTCTGCCT   29140       A     G
                                AGGCA GAGGTT CAGTGAGC
                                |||||  ||||||  ||||||||
                                TCCGT CTCCAA GTCACTCG
                                   _     A
GAM1110  KIAA0828  3'  CTCCAACCTCTTACCT      81196     C       C
                                AGG AAGAGGTTG AG
                                |||  |||||||||  ||
                                TCC TTCTCCAAC TC
                                  A        C
GAM1110  KIAA0841  3'  GCTCACTGCAACCTCCGCCT   71387      AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCG
                                  C_
GAM1110  KIAA0841  3'  GCTCACTGCAACCTCTGCCT   71389       A
                                AGGCA GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                   _
GAM1110  KIAA0861  3'  CGGCTCACTGCAAACCGCCT   88923      AAGA   _
                                AGGC    GGTT GCAGTGAGCCG
                                ||||    |||| ||||||||||
                                TCCG    CCAA CGTCACTCGGC
                                  ____    A
GAM1110  KIAA0889  3'  CGGCTCACTGTAACCTCCGCCT 31133      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
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                              TCCG  CTCCAATGTCACTCGGC
                                C_
GAM1110 KIAA0961 3' CGGCTCACTGCAAGCTCTGCCT 29731      A   G
                              AGGCA GAG TTGCAGTGAGCCG
                              ||||| ||| ||||||||||||||
                              TCCGT CTC AACGTCACTCGGC
                                _  G
GAM1110 KIAA1026 3' GCTCACTGCAACCAACACCT  71199     CAAGA
                              AGG    GGTTGCAGTGAGC
                              |||    ||||||||||||||
                              TCC    CCAACGTCACTCG
                               ACAA_
GAM1110 KIAA1041 3' CGGCTCACTGCAACCTCCGCCT 30131     AA
                              AGGC  GAGGTTGCAGTGAGCCG
                              ||||  ||||||||||||||||
                              TCCG  CTCCAACGTCACTCGGC
                                C_
GAM1110 KIAA1054 3' CACTGCAACCTCCGCCT     68428     AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1110 KIAA1128 3' CGGCTCACTGCAACTTCTGCCT 68475      A
                              AGGCA GAGGTTGCAGTGAGCCG
                              ||||| ||||||||||||||||
                              TCCGT CTTCAACGTCACTCGGC
                                _
GAM1110 KIAA1143 3' GCTCACTGCAAGCTCCGCCT  68682     AA  G
                              AGGC  GAG TTGCAGTGAGC
                              ||||  ||| ||||||||||
                              TCCG  CTC AACGTCACTCG
                                C_  G
GAM1110 KIAA1161 5' GCTCACTGCAACCCCTCCT   81755     CA  A
                              AGG  AG GGTTGCAGTGAGC
                              |||  || ||||||||||||
                              TCC  TC CCAACGTCACTCG
                                __  C
GAM1110 KIAA1170 3' CGGCTCACTGCAACCTCCGCCT 69849     AA
                              AGGC  GAGGTTGCAGTGAGCCG
                              ||||  ||||||||||||||||
                              TCCG  CTCCAACGTCACTCGGC
                                C_
GAM1110 KIAA1193 3' CGGCTCACTGCAACCTCCGCCT 67637     AA
                              AGGC  GAGGTTGCAGTGAGCCG
                              ||||  ||||||||||||||||
                              TCCG  CTCCAACGTCACTCGGC
                                C_
GAM1110 KIAA1198 3' CGGCTCACCGCAACCTCCGCCT 63302      AA      A
                              AGGC  GAGGTTGC GTGAGCCG
                              ||||  |||||||| ||||||||
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                                TCCG  CTCCAACG CACTCGGC
                                  C_       C
GAM1110  KIAA1198  3'  CGGCTCACTGCAATCTCTGCCT 63303       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCTAACGTCACTCGGC

                                  _
GAM1110  KIAA1198  3'  GCTCACTGCAAGCTCCGCCT   63316     AA   G
                                AGGC  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                TCCG  CTC AACGTCACTCG
                                  C_   G
GAM1110  KIAA1254  3'  GCTCACTGCAACCTCTGTCT   70019       A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                TCTGT CTCCAACGTCACTCG

                                  _
GAM1110  KIAA1257  3'  CGGCTCACTACAGCCTCTGCC  62735      A      C
                                GGCA GAGGTTG AGTGAGCCG
                                |||| ||||||| |||||||||
                                CCGT CTCCGAC TCACTCGGC
                                  _      A
GAM1110  KIAA1257  3'  GCTCACCGCAACCTCCGCCT   62744      AA       A
                                AGGC  GAGGTTGC GTGAGC
                                ||||  |||||||| ||||||
                                TCCG  CTCCAACG CACTCG
                                  C_       C
GAM1110  KIAA1320  5'  CACTGCAACCTCTGCCT     69296       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC

                                  _
GAM1110  KIAA1320  5'  GCTCACTGTAGCCTTGACT    69305    GCAA
                                AG    GAGGTTGCAGTGAGC
                                ||    ||||||||||||||||
                                TC    TTCCGATGTCACTCG
                                 AG__
GAM1110  KIAA1373  3'  GCTCACTGCAACCTCCACCT   70941     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCG
                                  AC_
GAM1110  KIAA1443  3'  GCTCACTGCAAGCTCCGCCT   63832      AA   G
                                AGGC  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                TCCG  CTC AACGTCACTCG
                                  C_   G
GAM1110  KIAA1456  3'  CGGCTCACTGTAAGCTCCGCCT 66993      AA   G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||
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                              TCCG  CTC AATGTCACTCGGC
                                C_  G
GAM1110 KIAA1465 3' CGGCTCACTGCATCTTCCGCCT 60827     AA   T
                              AGGC  GAGG TGCAGTGAGCCG
                              ||||  |||| ||||||||||||
                              TCCG  CTTC ACGTCACTCGGC
                                C_  T
GAM1110 KIAA1467 3' CGGCTCACTGCAACCTTCGCCT 71606     AA
                              AGGC  GAGGTTGCAGTGAGCCG
                              ||||  ||||||||||||||||
                              TCCG  TTCCAACGTCACTCGGC
                                C_
GAM1110 KIAA1473 3' GCTCACTGCAACCTCCGTCT  70669     AA
                              AGGC  GAGGTTGCAGTGAGC
                              ||||  |||||||||||||||
                              TCTG  CTCCAACGTCACTCG
                                C_
GAM1110 KIAA1497 5' CACTGCAACCTCTGCCT     67504      A
                              AGGCA GAGGTTGCAGTG
                              ||||| ||||||||||||
                              TCCGT CTCCAACGTCAC
                                 _
GAM1110 KIAA1508 3' GCTCACTGCAACCTCCGCCT  61884     AA
                              AGGC  GAGGTTGCAGTGAGC
                              ||||  |||||||||||||||
                              TCCG  CTCCAACGTCACTCG
                                C_
GAM1110 KIAA1530 3' CGGCTCACTGCAACTACCACCT 67950     CAAGA
                              AGG    GGTTGCAGTGAGCCG
                              |||    ||||||||||||||||
                              TCC    TCAACGTCACTCGGC
                                ACCA_
GAM1110 KIAA1571 3' CACCGCAACCTCCACCT     60951     CAA      A
                              AGG   GAGGTTGC GTG
                              |||   |||||||| |||
                              TCC   CTCCAACG CAC
                                AC_      C
GAM1110 KIAA1573 5' CGGCTCACCTAACCTCTCCCCT 62686     CA      CA
                              AGG  AGAGGTTG  GTGAGCCG
                              |||  ||||||||  ||||||||
                              TCC  TCTCCAAT  CACTCGGC
                                CC       C_
GAM1110 KIAA1615 3' CACTGCAACCTCCACCT     68701     CAA
                              AGG   GAGGTTGCAGTG
                              |||   ||||||||||||
                              TCC   CTCCAACGTCAC
                                AC_
GAM1110 KIAA1617 3' GCTCACTGCAACCTCTCTCT  91429    CA
                              GG  AGAGGTTGCAGTGAGC
                              ||  ||||||||||||||||
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                                TC  TCTCCAACGTCACTCG
                                 TC
GAM1110 KIAA1649 3' GCTCACTGCAACCTCCGC    50270    AA
                                GC  GAGGTTGCAGTGAGC
                                ||  ||||||||||||||
                                CG  CTCCAACGTCACTCG
                                 C_
GAM1110 KIAA1655 3' CATTGCAACCTCCGCCT     66600     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTTAC
                                  C_
GAM1110 KIAA1655 3' GCTCACTGTAACCTCCACCT   66615    CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||||
                                TCC   CTCCAATGTCACTCG
                                  AC_
GAM1110 KIAA1668 3' GCTCACTGCAAGCTCCGCCT   66475     AA   G
                                AGGC  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                TCCG  CTC AACGTCACTCG
                                  C_   G
GAM1110 KIAA1712 3' CACCGCAACCTCTGCCT     67533      A      A
                                AGGCA GAGGTTGC GTG
                                |||||| |||||||| |||
                                TCCGT CTCCAACG CAC
                                   _       C
GAM1110 KIAA1712 3' CGGCTCACTGCACCTTCTGCCT 67535      AG    T
                                AGGCA  AGGT GCAGTGAGCCG
                                ||||||  |||| ||||||||||
                                TCCGT  TCCA CGTCACTCGGC
                                   CT    _
GAM1110 KIAA1737 3' CGGCTCACTGCAACCTCCGCCT 67353      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110 KIAA1751 3' GCTCACTGCAGCCTCGACCT   71698    CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                TCC   CTCCGACGTCACTCG
                                  AG_
GAM1110 KIAA1784 3' CGGCTCACTGCAACCTCCGCCT 65148      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110 KIAA1894 3' CGAGGCAACCTTTGCCT     73843      A      AG
                                AGGCA GAGGTTGC  TG
                                ||||| ||||||||  ||
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                                TCCGT TTCCAACG  GC
                                  _      GA
GAM1110 KIAA1922 5' GCTCACTGCAACCTCCGCCT  73629     AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                TCCG  CTCCAACGTCACTCG
                                  C_
GAM1110 KIAA1956 3' GCTCACTGCAGCCTCCACCT  78436    CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                TCC   CTCCGACGTCACTCG
                                  AC_
GAM1110 KIAA1971 3' CGGCTCACCGCAAGCTCCGCTT 74214     AA  G   A
                                AGGC  GAG TTGC GTGAGCCG
                                ||||  ||| |||| ||||||||
                                TTCG  CTC AACG CACTCGGC
                                  C_  G   C
GAM1110 KIAA1971 3' CTTACTGCAACCTCCACCT   74217    CAA
                                AGG   GAGGTTGCAGTGAG
                                |||   ||||||||||||||
                                TCC   CTCCAACGTCATTC
                                  AC_
GAM1110 KIAA1975 5' CGGCTCACTGCAAGCTCCGCCT 73971     AA  G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||
                                TCCG  CTC AACGTCACTCGGC
                                  C_  G
GAM1110 KIAA1987 5' CGGCTCACTGCAATCTCCGCCT 88013     AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCTAACGTCACTCGGC
                                  C_
GAM1110 KLK7    3' CACTGCAACCTCCGCCT    57728     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110 KLK7    3' CACTGCAACCTCCGCCT    17288     AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110 LAMP3   3' CGGCTTATGGCAACCTCCGCCT 59489     AA      A
                                AGGC  GAGGTTGC GTGAGCCG
                                ||||  |||||||| ||||||||
                                TCCG  CTCCAACG TATTCGGC
                                  C_      G
GAM1110 LRRN3   5' GCTGCAGCCTCCTGCCT    69438     A
                                AGGCA GAGGTTGCAGT
                                ||||| ||||||||||
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                                TCCGT CTCCGACGTCG
                                  C
GAM1110 LY75     3' CGGCTCACTGCAAATCTCCGCC 9837       AA     _
              T                   AGGC  GAGGTT GCAGTGAGCCG
                                  ||||  |||||| ||||||||||
                                  TCCG  CTCTAA CGTCACTCGGC
                                    C_     A
GAM1110 MCLC     3' CGGCTCACTGCAACCTCCACCT 30680     CAA
                                  AGG   GAGGTTGCAGTGAGCCG
                                  |||   ||||||||||||||||
                                  TCC   CTCCAACGTCACTCGGC
                                   AC_
GAM1110 MEF-2    3' CGGCTCACTGCAACCTCCGCCT 64381      AA
                                  AGGC  GAGGTTGCAGTGAGCCG
                                  ||||  ||||||||||||||||
                                  TCCG  CTCCAACGTCACTCGGC
                                    C_
GAM1110 MESDC2   3' CGGCTCACTGAAGTCTCTACCT 72490     CA    GT G
                                  AGG  AGAG  T CAGTGAGCCG
                                  |||  ||||  | ||||||||||
                                  TCC  TCTC  A GTCACTCGGC
                                   A_    TG A
GAM1110 MGC12518 3' TACTGCAACCTCTGCC      64083      A
                                  GGCA GAGGTTGCAGTG
                                  |||| ||||||||||||
                                  CCGT CTCCAACGTCAT
                                    _
GAM1110 MGC13138 3' GCTCACTGCAACCTCTGCCT   53019       A
                                  AGGCA GAGGTTGCAGTGAGC
                                  ||||| |||||||||||||||
                                  TCCGT CTCCAACGTCACTCG
                                    _
GAM1110 MGC13198 5' GCTCACTGCAACCTCCGTCT   51095      AA
                                  AGGC  GAGGTTGCAGTGAGC
                                  ||||  ||||||||||||||||
                                  TCTG  CTCCAACGTCACTCG
                                    C_
GAM1110 MGC14289 3' CGGCTCACTGCAGCCTTGACT  54701    GCAA
                                  AG    GAGGTTGCAGTGAGCCG
                                  ||    ||||||||||||||||
                                  TC    TTCCGACGTCACTCGGC
                                   AG__
GAM1110 MGC14836 3' CACTGCAACCTCCGCCT     53036      AA
                                  AGGC  GAGGTTGCAGTG
                                  ||||  ||||||||||||
                                  TCCG  CTCCAACGTCAC
                                    C_
GAM1110 MGC15873 5' GCTCACTGCAGCCTTGACCT   51904     CAA
                                  AGG   GAGGTTGCAGTGAGC
                                  |||   |||||||||||||||
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                                TCC   TTCCGACGTCACTCG
                                  AG_
GAM1110 MGC16025 3' GCCCACTGTGGGCCCTTCCC   51920    C   A  _ TG    A
                                GG AAG GG T  CAGTG GC
                                || ||| || |  ||||| ||
                                CC TTC CC G  GTCAC CG
                                 C   _  G GT    C
GAM1110 MGC1842  3' CTTACTACAACCTCCGCCT    65647      AA      C
                                AGGC  GAGGTTG AGTGAG
                                ||||  ||||||| ||||||
                                TCCG  CTCCAAC TCATTC
                                  C_      A
GAM1110 MGC21675 3' GCTCACTGCAATCTCTGCC    53484      A
                                GGCA GAGGTTGCAGTGAGC
                                |||| ||||||||||||||
                                CCGT CTCTAACGTCACTCG
                                  _
GAM1110 MGC21854 3' CGGCTCACTCCCTTCTCCC    53490    CA    TTGC
                                GG  AGAGG    AGTGAGCCG
                                ||  |||||    |||||||||
                                CC  TCTTC    TCACTCGGC
                                 C_    CC__
GAM1110 MGC23284 5' CGGCTCACCTCATTCCTGCC   58702      A   GT  CA
                                GGCA GAG  TG  GTGAGCCG
                                |||| |||  ||  ||||||||
                                CCGT CTT  AC  CACTCGGC
                                  C   __  TC
GAM1110 MGC2474  3' CGACTCACTGCAACTTCCACCT 43721     CAA          C
                                AGG   GAGGTTGCAGTGAG CG
                                |||   |||||||||||||| ||
                                TCC   CTTCAACGTCACTC GC
                                 AC_           A
GAM1110 MGC2477  5' CGGCTCACTGCAAGCTCTGCCT 44062       A   G
                                AGGCA GAG TTGCAGTGAGCCG
                                ||||| ||| ||||||||||||
                                TCCGT CTC AACGTCACTCGGC
                                   _  G
GAM1110 MGC27171 3' GCTGCAGCCTCTTGCCT     58086
                                AGGCAAGAGGTTGCAGT
                                |||||||||||||||||
                                TCCGTTCTCCGACGTCG

GAM1110 MGC29891 3' CACTGCAACCTCCGCCT     58201      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110 MGC3113  3' GCTCACTGCAGCCTCCACCT   43847     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
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                              TCC  CTCCGACGTCACTCG
                                AC_
GAM1110 MGC3329  3' CACTGCAACCCCCGCCT    44014     AAGA
                              AGGC   GGTTGCAGTG
                              ||||   ||||||||||
                              TCCG   CCAACGTCAC
                                CCC_
GAM1110 MGC3771  5' CGGCTCACCCCAACCTCCGCCT 48244     AA     CA
                              AGGC  GAGGTTG  GTGAGCCG
                              ||||  |||||||  ||||||||
                              TCCG  CTCCAAC  CACTCGGC
                                C_     CC
GAM1110 MGC5149  3' GCTCACTGCAACCTCTGCCT   72292      A
                              AGGCA GAGGTTGCAGTGAGC
                              ||||| ||||||||||||||
                              TCCGT CTCCAACGTCACTCG
                                _
GAM1110 MGC5508  3' CTCCTGCCAGCCCCCTGCC   44036     AGA   _  T
                              GGCA  GGTTG CAG GAG
                              ||||  ||||| ||| |||
                              CCGT  CCGAC GTC CTC
                                CCC    C  _
GAM1110 MGC9912  3' CGGCTCACTGCAACCTCCACCT 54715     CAA
                              AGG  GAGGTTGCAGTGAGCCG
                              |||  ||||||||||||||||
                              TCC  CTCCAACGTCACTCGGC
                                AC_
GAM1110 MLZE     5' GCTCACTGCAACCTCTGCCT   48621      A
                              AGGCA GAGGTTGCAGTGAGC
                              ||||| ||||||||||||||
                              TCCGT CTCCAACGTCACTCG
                                _
GAM1110 moblak   3' CGGCTCACTGCAAGCTCCGCCT 55496     AA  G
                              AGGC  GAG TTGCAGTGAGCCG
                              ||||  ||| ||||||||||||
                              TCCG  CTC AACGTCACTCGGC
                                C_  G
GAM1110 moblak   3' CGGCTCACTGCATCCTCCACCT 55497     CAA   T
                              AGG  GAGG TGCAGTGAGCCG
                              |||  |||| ||||||||||||
                              TCC  CTCC ACGTCACTCGGC
                                AC_   T
GAM1110 MOCS3    3' GCTCACTGCAACCTCCGCCT   27152     AA
                              AGGC  GAGGTTGCAGTGAGC
                              ||||  ||||||||||||||
                              TCCG  CTCCAACGTCACTCG
                                C_
GAM1110 MRF2     5' CGGCTCACCGTGTGGCTTGC   76519      AGGT  A
                              GCAAG   TGC GTGAGCCG
                              |||||   ||| ||||||||
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                                CGTTC   GTG CACTCGGC
                                   GGT_  C
GAM1110 MRPL44   3' CGGCTCACTGCAACCTCCACCT 43316    CAA
                                AGG  GAGGTTGCAGTGAGCCG
                                |||  ||||||||||||||||
                                TCC  CTCCAACGTCACTCGGC
                                  AC_
GAM1110 MtFMT    3' GCTCACTGCAACCTCCGCCT  57654     AA
                                AGGC GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                TCCG CTCCAACGTCACTCG
                                  C_
GAM1110 N4BP3    3' GCTCACCAGTCTCTTCCCT   66265    C   GT  CA
                                AGG AAGAG  TG  GTGAGC
                                ||| |||||  ||  ||||||
                                TCC TTCTC  AC  CACTCG
                                  C    TG  __
GAM1110 NDUFB1   5' GCTCACTGCAACCTCTGCCT  15817     A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                   _
GAM1110 NDUFC2   3' CGGCTCACTGCAACCTCCACCT 15829    CAA
                                AGG  GAGGTTGCAGTGAGCCG
                                |||  ||||||||||||||||
                                TCC  CTCCAACGTCACTCGGC
                                  AC_
GAM1110 NINJ2    3' CGGCTCACTGCACCTCCGCCT  33282     AA   T
                                AGGC  GAGGT GCAGTGAGCCG
                                ||||  ||||| ||||||||||
                                TCCG  CTCCA CGTCACTCGGC
                                  C_    _
GAM1110 Nup43    3' CGGCTCACTGCAACCTCCACCT 44998    CAA
                                AGG  GAGGTTGCAGTGAGCCG
                                |||  ||||||||||||||||
                                TCC  CTCCAACGTCACTCGGC
                                  AC_
GAM1110 OR51E2   3' CGGCTCACTGCAACCTC    47792
                                GAGGTTGCAGTGAGCCG
                                |||||||||||||||
                                CTCCAACGTCACTCGGC

GAM1110 OSBPL2   3' CGGCTCACCGCAACCTCCGCCT 57861     AA      A
                                AGGC  GAGGTTGC GTGAGCCG
                                ||||  |||||||| ||||||||
                                TCCG  CTCCAACG CACTCGGC
                                  C_      C
GAM1110 OSBPL2   3' CGGCTCACCGCAACCTCCGCCT 29210     AA      A
                                AGGC  GAGGTTGC GTGAGCCG
                                ||||  |||||||| ||||||||
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                                TCCG  CTCCAACG CACTCGGC
                                  C_      C
GAM1110  PASK     5'  CACTGCAACCTCTGCCT     30712       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  PELI1    5'  CACTGCAACCTCTGCCT     40256       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  PELI1    5'  CGGCTCACTGCAACCTCCTCCT 40260     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  TC_
GAM1110  PIP3-E   3'  CACTGCAACCTCTGCCT     66800       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  PRO0365  5'  GCTCACTGCAACCTCCACCT   26161     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   |||||||||||||||
                                TCC   CTCCAACGTCACTCG
                                  AC_
GAM1110  PRO1048  3'  GCTCACTGAAGTCTCGACCT   37518     CAA   GT G
                                AGG   GAG  T CAGTGAGC
                                |||   |||  | ||||||||
                                TCC   CTC  A GTCACTCG
                                  AG_   TG A
GAM1110  PRO1992  5'  CGGCTCACTGCAACCTCTGCCT 26056       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                  _
GAM1110  PRO2955  3'  GCTCACTGCAACCTCTGCCT   37639       A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110  PSMF1    5'  CGGCTCACTGCACTACCCCCGC 22352     AAGA  __
            C                    GGC   GGT  TGCAGTGAGCCG
                                |||   |||  ||||||||||||
                                CCG   CCA  ACGTCACTCGGC
                                  CCC_   TC
GAM1110  PSPH     3'  CGGCTCACTGCAAGCTCTGCCT 15914       A   G
                                AGGCA GAG TTGCAGTGAGCCG
                                ||||| ||| ||||||||||||
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                                TCCGT CTC AACGTCACTCGGC
                                  _  G
GAM1110 PSTPIP2  3' GCTCACTGCAACCTCTGCCT  44391      A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110 RAB21    3' CGGCTCACTGCAAGCTCCACCT 30385     CAA  G
                                AGG  GAG TTGCAGTGAGCCG
                                |||  ||| ||||||||||||
                                TCC  CTC AACGTCACTCGGC
                                 AC_  G
GAM1110 RAB33B   3' CGGCTCACTGCAACCTCCGCCT 48491     AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110 RAI      5' CGGCTCACTGCAACCTCCGCCT 21877     AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110 RASSF2   3' GCTCACTGCAACATCCGCCT  28438     AA  G
                                AGGC  GA GTTGCAGTGAGC
                                ||||  ||  ||||||||||||
                                TCCG  CT CAACGTCACTCG
                                  C_  A
GAM1110 RNF8     3' GCTCACTGCAACCTCCACCT  14229     CAA
                                AGG  GAGGTTGCAGTGAGC
                                |||  ||||||||||||||
                                TCC  CTCCAACGTCACTCG
                                 AC_
GAM1110 RNO2     5' GCTCACTGCAACCTCCACCT  52771     CAA
                                AGG  GAGGTTGCAGTGAGC
                                |||  ||||||||||||||
                                TCC  CTCCAACGTCACTCG
                                 AC_
GAM1110 SC4MOL   3' GCTCACTGCAACCTCTGCCT  22157      A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110 SCAMP-4  3' CGGCTCACTGCAACCTCTGCCT 54392      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| |||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                  _
GAM1110 SCYA22   3' CGGCTCACTACAACCTCGACCT 90942     CAA      C
                                AGG  GAGGTTG AGTGAGCCG
                                |||  ||||||| |||||||||
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                                TCC   CTCCAAC TCACTCGGC
                                  AG_      A
GAM1110 SDC3     3'  CACTGCAACCTCTTGCT     27741
                                GGCAAGAGGTTGCAGTG
                                ||||||||||||||||
                                TCGTTCTCCAACGTCAC

GAM1110 SERF1B   3'  CACTGCAACCTCCGCCT     43409      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110 SERF1B   3'  GCTCCATGCAACCTCTGCCT   43417       A        GT
                                AGGCA GAGGTTGCA  GAGC
                                |||||  |||||||||  ||||
                                TCCGT CTCCAACGT  CTCG
                                   _        AC
GAM1110 SFXN2    3'  CGGCTCACTGCAAACTCTGCCT 73940       A   G
                                AGGCA GAG TTGCAGTGAGCCG
                                |||||  |||  ||||||||||||
                                TCCGT CTC AACGTCACTCGGC
                                   _  A
GAM1110 SIRPB1   3'  CACTGCAACCCCCCGCCT     20243      AAGA
                                AGGC    GGTTGCAGTG
                                ||||    ||||||||||
                                TCCG    CCAACGTCAC
                                  CCC_
GAM1110 SLC11A1  3'  CATTGCAACCTCCACCT     59452     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTTAC
                                  AC_
GAM1110 SLC16A4  3'  CGGCTCACTGTAATCTCCGCCT 16279      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCTAATGTCACTCGGC
                                  C_
GAM1110 SLC6A14  3'  GCTCACTGCAACCTCTGCCT   23352       A
                                AGGCA GAGGTTGCAGTGAGC
                                |||||  |||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                   _
GAM1110 SQV7L    5'  GCTCACTGCAACCACTGCCT   70575       A A
                                AGGCA G GGTTGCAGTGAGC
                                |||||  |  ||||||||||||
                                TCCGT C CCAACGTCACTCG
                                   _ A
GAM1110 SREC     3'  CGGCTCACTGCAAGCTCTGCCT 13500       A   G
                                AGGCA GAG TTGCAGTGAGCCG
                                |||||  |||  ||||||||||||
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                                TCCGT CTC AACGTCACTCGGC
                                  _  G
GAM1110 SS-56    3' CGGCTCACTGCAGGCTCTGCCT 59602      A  G
                                AGGCA GAG TTGCAGTGAGCCG
                                ||||| ||| ||||||||||||||
                                TCCGT CTC GACGTCACTCGGC
                                  _  G
GAM1110 STAF65(gamma) 3' CGACTCACTGCAACCTCTGCCT 29429      A           C
                                AGGCA GAGGTTGCAGTGAG CG
                                ||||| |||||||||||||| ||
                                TCCGT CTCCAACGTCACTC GC
                                  _          A
GAM1110 SULT1C2  3' CGGCTCACTGCAAGCTCTGCTT 21676      A  G
                                AGGCA GAG TTGCAGTGAGCCG
                                ||||| ||| ||||||||||||||
                                TTCGT CTC AACGTCACTCGGC
                                  _  G
GAM1110 SULT1C2  5' GCTCACTTTCTCCCT      21677    CAA   TTGC
                                AGG  GAGG   AGTGAGC
                                |||  ||||   |||||||
                                TCC  CTCT   TCACTCG
                                  ____   T___
GAM1110 SYT13    3' CGGCTCACTGCAACCTCCGCCT 93455     AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110 TADA3L   3' CGGCTCACTGCAAGCTCCGCCT 55991     AA  G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||
                                TCCG  CTC AACGTCACTCGGC
                                  C_  G
GAM1110 TCL6     5' CGGCTCACTGCAGCCTTCACCT 26995    CAA
                                AGG  GAGGTTGCAGTGAGCCG
                                |||  ||||||||||||||||
                                TCC  TTCCGACGTCACTCGGC
                                  AC_
GAM1110 TCL6     5' CGGCTCACTGCAGCCTTCACCT 24979    CAA
                                AGG  GAGGTTGCAGTGAGCCG
                                |||  ||||||||||||||||
                                TCC  TTCCGACGTCACTCGGC
                                  AC_
GAM1110 TCL6     5' CGGCTCACTGCAGCCTTCACCT 40082    CAA
                                AGG  GAGGTTGCAGTGAGCCG
                                |||  ||||||||||||||||
                                TCC  TTCCGACGTCACTCGGC
                                  AC_
GAM1110 TCL6     5' CGGCTCACTGCAGCCTTCACCT 40099    CAA
                                AGG  GAGGTTGCAGTGAGCCG
                                |||  ||||||||||||||||
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                                TCC  TTCCGACGTCACTCGGC
                                  AC_
GAM1110 TCL6    5' CGGCTCACTGTAGTCTCAACCT 40129    CAA  GT
                                AGG  GAG TGCAGTGAGCCG
                                |||  ||| ||||||||||||
                                TCC  CTC ATGTCACTCGGC
                                  AA_  TG
GAM1110 TCL6    5' CGGCTCACTGTAGTCTCAACCT 40156    CAA  GT
                                AGG  GAG TGCAGTGAGCCG
                                |||  ||| ||||||||||||
                                TCC  CTC ATGTCACTCGGC
                                  AA_  TG
GAM1110 TGIF2   3' GCTCACTGTACTCCAGCC   41455    AA  GT
                                GGC  GAG TGCAGTGAGC
                                |||  ||| ||||||||||
                                CCG  CTC ATGTCACTCG
                                  AC  __
GAM1110 THEA    3' GCTCACTGCAACCTCGGCCT  66287     AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCG
                                  G_
GAM1110 TLN1    3' GCCCACTCCACCCTGCC    20820     A A  T C   A
                                GGCA G GGT G AGTG GC
                                |||| | ||| | |||| ||
                                CCGT C CCA C TCAC CG
                                  _ _  _ C   C
GAM1110 TOR1B   3' CTCACTGCAACCTCCGCT   27198    AA
                                GGC  GAGGTTGCAGTGAG
                                |||  ||||||||||||||
                                TCG  CTCCAACGTCACTC
                                  C_
GAM1110 TPRA40  5' GCTCACTGGGCGGCTCTC   33041    _   __
                                GAG GTTGC  AGTGAGC
                                ||| |||||  |||||||
                                CTC CGGCG  TCACTCG
                                  T    GG
GAM1110 TRIM5   3' CACTGCAACCTCCACCT    52294    CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  CTCCAACGTCAC
                                  AC_
GAM1110 TRIM6   3' CGGCTCACTGCAACCTCTGCCT 54137     A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                  _
GAM1110 TU12B1-TY 3' CGGCTCACTGCAACCTCTTGCC 33376
             T                   AGGCAAGAGGTTGCAGTGAGCCG
                                 |||||||||||||||||||||||
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                                TCCGTTCTCCAACGTCACTCGGC

GAM1110  TU12B1-TY 3'  GCTCACTGCAACCTCTGCCT   33388      A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110  TUBB5    3'  GCTCCTACCTCTGACC      20304    CA     TGC  T
                                GG  AGAGGT   AG GAGC
                                ||  ||||||   || ||||
                                CC  TCTCCA   TC CTCG
                                 AG     ___  _
GAM1110  TUBB5    3'  GCTCCTACCTCTGACC      20305    CA     TGC  T
                                GG  AGAGGT   AG GAGC
                                ||  ||||||   || ||||
                                CC  TCTCCA   TC CTCG
                                 AG     ___  _
GAM1110  TUCAN    3'  GCTCACTGCAACCTCTGCCT   30276      A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110  UBF-fl   3'  CGGCTCACTGCAACCTCTGCCT 51560      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                  _
GAM1110  USP22    3'  CGGCTCACTGCAACCTCCACCT 68008     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                 AC_
GAM1110  VDU1     3'  GCTCACTGCAGCCTCCACCT   30421     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                TCC   CTCCGACGTCACTCG
                                 AC_
GAM1110  VPS33A   3'  CACTGCAACCTCCACCT     43335     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                 AC_
GAM1110  WBSCR20A 5'  CGGCTCACCGCAACCTCTGCCT 49651      A      A
                                AGGCA GAGGTTGC GTGAGCCG
                                ||||| |||||||| ||||||||
                                TCCGT CTCCAACG CACTCGGC
                                  _      C
GAM1110  YWHAQ    3'  CACTTACACCTCCTGCCT    22394      A    TGC
                                AGGCA GAGGT   AGTG
                                ||||| |||||   ||||
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                                TCCGT CTCCA   TCAC
                                  C    CAT
GAM1110  ZTL1     3'  CACTGCAACCTCTGCCT     43910       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  LOC112687 3'  CGGCTCACTGCAACCTCTGCC  72858      A
                                GGCA GAGGTTGCAGTGAGCCG
                                |||| ||||||||||||||||||
                                CCGT CTCCAACGTCACTCGGC
                                  _
GAM1110  LOC112724 5'  CGGCTCACTGCAACCTCCACCT 56495     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  AC_
GAM1110  LOC112817 3'  GGCCCCTGACCTCTCCCT    56515     CA     TG   TGA
                                AGG  AGAGGT  CAG   GCC
                                |||  ||||||  |||   |||
                                TCC  TCTCCA  GTC   CGG
                                  C_     __   CC_
GAM1110  LOC113675 5'  CACTGCAACCTCCGCCT     56569      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  LOC115219 5'  CGGCTCACTGCAACCTCCGCCT 73302      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  LOC116349 5'  CTCAGGCCCTCTCGCT      73829     A    TT  AG
                                GGC AGAGG  GC  TGAG
                                ||| |||||  ||  ||||
                                TCG TCTCC  CG  ACTC
                                  C    __  G_
GAM1110  LOC116411 5'  CGGCTCACTGCAACCTCCCTGC 73861       A_
              CT                  AGGCA  GAGGTTGCAGTGAGCCG
                                |||||  ||||||||||||||||||
                                TCCGT  CTCCAACGTCACTCGGC
                                   CC
GAM1110  LOC116411 5'  CGGCTCGCTACAACCTCCACCT 73862     CAA      C
                                AGG   GAGGTTG AGTGAGCCG
                                |||   ||||||| |||||||||
                                TCC   CTCCAAC TCGCTCGGC
                                  AC_      A
GAM1110  LOC119392 3'  CACTGCAACCTCTGCCT     59131       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
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                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  LOC120114 3'  GCTCACTGCAATCTCCACCT   75530     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                TCC   CTCTAACGTCACTCG
                                  AC_
GAM1110  LOC120224 5'  CGGCTCACTGCAACCTCCCT   57096     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   |||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  ____
GAM1110  LOC120939 3'  GCTCACTGTAACCTCCACCT   76257     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                TCC   CTCCAATGTCACTCG
                                  AC_
GAM1110  LOC126133 3'  CGGCCCACTGCAGCCTCGACCT 74440     CAA          A
                                AGG   GAGGTTGCAGTG GCCG
                                |||   |||||||||||| ||||
                                TCC   CTCCGACGTCAC CGGC
                                  AG_          C
GAM1110  LOC126364 3'  GCTCACTGCAACCTCCGCCT   75690      AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  |||||||||||||||
                                TCCG  CTCCAACGTCACTCG
                                  C_
GAM1110  LOC126661 3'  GCTCACTGCAACCTCCGCCT   74554      AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  |||||||||||||||
                                TCCG  CTCCAACGTCACTCG
                                  C_
GAM1110  LOC128077 3'  CGGCTCACTGCAACCTCCGCCT 74711      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  LOC128077 3'  CGGCTCACTGCAACCTCTGCCT 74712      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                |||||  |||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                  _
GAM1110  LOC128989 3'  CGGCTCACTGCAACCTCCGCCT 74809      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  LOC130813 3'  CACCGCAACCTCCGCCT     75763      AA       A
                                AGGC  GAGGTTGC GTG
                                ||||  |||||||| |||
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                                TCCG  CTCCAACG CAC
                                  C_      C
GAM1110  LOC132625 3'  CACTGCAACCTCCACCT     75899     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1110  LOC135154 3'  CTCACTGCAACTTCCGCC     75214     AA
                                GGC  GAGGTTGCAGTGAG
                                |||  ||||||||||||||
                                CCG  CTTCAACGTCACTC
                                  C_
GAM1110  LOC135293 3'  CGGCTCACTGCAACCTCTGCCT 76177       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                |||||| |||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC

                                  _
GAM1110  LOC135763 3'  CACTGCAACCTCCGCCT     56786      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  LOC142927 5'  CGGCTCACCGCAGCCTCTTCCT 76425     C         A
                                AGG AAGAGGTTGC GTGAGCCG
                                ||| |||||||||| ||||||||
                                TCC TTCTCCGACG CACTCGGC
                                  _         C
GAM1110  LOC143187 3'  CACTGCAACCTCCACCT     59095     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1110  LOC143241 5'  GCTCACTGCAACCTCTGCCT   57177       A
                                AGGCA GAGGTTGCAGTGAGC
                                |||||| |||||||||||||||
                                TCCGT CTCCAACGTCACTCG

                                  _
GAM1110  LOC144248 5'  CACTGCAACCTCCACCT     76735     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1110  LOC144317 5'  CTCACTGCAACCTCTTCCT    76787     C
                                AGG AAGAGGTTGCAGTGAG
                                ||| |||||||||||||||
                                TCC TTCTCCAACGTCACTC

                                  _
GAM1110  LOC144524 5'  GCTCACTGCAACCTCCACCT   83129     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   |||||||||||||||
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                                TCC   CTCCAACGTCACTCG
                                  AC_
GAM1110  LOC144742 5'  CGGCTCCCTGCAACCTTCGCCT 76941      AA         T
                                AGGC  GAGGTTGCAG GAGCCG
                                ||||  |||||||||| ||||||
                                TCCG  TTCCAACGTC CTCGGC
                                  C_         C
GAM1110  LOC145009 3'  GCTCACTGCATCCTCCGCCT   60348      AA    T
                                AGGC  GAGG TGCAGTGAGC
                                ||||  |||| ||||||||||
                                TCCG  CTCC ACGTCACTCG
                                  C_    T
GAM1110  LOC145268 5'  CACTGCAACCTCCACC      77054     CAA
                                GG   GAGGTTGCAGTG
                                ||   ||||||||||||
                                CC   CTCCAACGTCAC
                                  AC_
GAM1110  LOC145622 3'  CGGCTCACTGCAACTTCTGCCT 77299       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||||
                                TCCGT CTTCAACGTCACTCGGC
                                   _
GAM1110  LOC145757 5'  CGGCTCACTACAACCTCTGCCT 77458       A      C
                                AGGCA GAGGTTG AGTGAGCCG
                                ||||| ||||||| |||||||||
                                TCCGT CTCCAAC TCACTCGGC
                                   _      A
GAM1110  LOC145757 5'  CGGCTCACTGCAAGCTCCGCCT 77459      AA   G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||
                                TCCG  CTC AACGTCACTCGGC
                                  C_   G
GAM1110  LOC146050 3'  GCTCACTGCAACCTCTGCCT   77639       A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                   _
GAM1110  LOC146050 3'  GCTCACTGCAACCTCTGCTT   77641       A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
                                TTCGT CTCCAACGTCACTCG
                                   _
GAM1110  LOC146229 3'  CGGCTCACTGCAACCTCCACCT 77738     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  AC_
GAM1110  LOC146229 3'  CGGCTCACTGCAAGCTCCGGCT 77740     AA   G
                                GGC  GAG TTGCAGTGAGCCG
                                |||  ||| ||||||||||||
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                                TCG  CTC AACGTCACTCGGC
                                  GC   G
GAM1110  LOC146229 3'  CGGCTCCCTGCAACCTCCACCT 77741     CAA        T
                                AGG   GAGGTTGCAG GAGCCG
                                |||   |||||||||| ||||||
                                TCC   CTCCAACGTC CTCGGC
                                  AC_        C
GAM1110  LOC146346 5'  CGGCTCACTGCAACTTCTGCCT 77840      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTTCAACGTCACTCGGC
                                  _
GAM1110  LOC146455 3'  CGGCTCACTGCAATCTCTGCCT 77904      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCTAACGTCACTCGGC
                                  _
GAM1110  LOC146603 5'  CGGCTCACTGCAAGCTCCGCCT 78016     AA   G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||
                                TCCG  CTC AACGTCACTCGGC
                                  C_   G
GAM1110  LOC146784 5'  CGGCTCACTGCAACCTCCACCT 78108     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  AC_
GAM1110  LOC146820 5'  CGGCTCACTGCAACCTCCGC   78148    AA
                                GC  GAGGTTGCAGTGAGCCG
                                ||  ||||||||||||||||
                                CG  CTCCAACGTCACTCGGC
                                 C_
GAM1110  LOC146839 3'  CGGCTCACCACAACCTCCGCCT 83809      AA      CA
                                AGGC  GAGGTTG  GTGAGCCG
                                ||||  |||||||  ||||||||
                                TCCG  CTCCAAC  CACTCGGC
                                  C_      AC
GAM1110  LOC146880 3'  GTTGATGAACCTCTTACCT    78159     C       G  G G
                                AGG AAGAGGTT CA T AGC
                                ||| |||||||| || | |||
                                TCC TTCTCCAA GT A TTG
                                  A       _  _ G
GAM1110  LOC146901 3'  CGGCTCATTGCAACCTCCACCT 83836     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTTACTCGGC
                                  AC_
GAM1110  LOC146909 3'  CACTGCAACCTCCGCCT     78167      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  LOC146952 5'  GCTCACTGCAACCTCCACCT   83868     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                TCC   CTCCAACGTCACTCG
                                  AC_
GAM1110  LOC147071 5'  CGGCTCACTGCAACCTCTGCCT 72996       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                      _
GAM1110  LOC147160 5'  CGGCTCACCCACCGGCCCCACC 83964    CAAGA    CA__
                                GG    GGTTG   GTGAGCCG
                                ||    |||||   ||||||||
                                CC    CCGGC   CACTCGGC
                                  ACC__    CACC
GAM1110  LOC147276 3'  GCTCACTGCAACGTCTGCCT   78335      A  G
                                AGGCA GA GTTGCAGTGAGC
                                ||||| || ||||||||||||
                                TCCGT CT CAACGTCACTCG
                                   _  G
GAM1110  LOC147407 3'  CACTGCAACCTCCGCCT     76323      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  LOC147463 3'  GCTCAGGGACCCTCTTGCC    78372         TTGCAG
                                GGCAAGAGG     TGAGC
                                |||||||||     |||||
                                CCGTTCTCC     ACTCG
                                     CAGGG_
GAM1110  LOC147817 3'  CACTGCAACCTCCACCT     78490     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1110  LOC147841 3'  GCTCACAGCAACCTCTGCCT   78530      A      A
                                AGGCA GAGGTTGC GTGAGC
                                ||||| |||||||| ||||||
                                TCCGT CTCCAACG CACTCG
                                   _       A
GAM1110  LOC147990 3'  CACTACAACCTCTGCCT     84089      A      C
                                AGGCA GAGGTTG AGTG
                                ||||| ||||||| ||||
                                TCCGT CTCCAAC TCAC
                                   _      A
GAM1110  LOC148137 3'  CGGCTCACGGCAACCTCCACCT 58424     CAA       A
                                AGG   GAGGTTGC GTGAGCCG
                                |||   |||||||| ||||||||
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                                TCC   CTCCAACG CACTCGGC
                                  AC_       G
GAM1110  LOC148137 3'  CGGCTCACTGCAAGCTTCGCCT 58425      AA   G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||||
                                TCCG  TTC AACGTCACTCGGC
                                  C_   G
GAM1110  LOC148147 3'  GCTCACTGCAATCTCTGCCT   78683       A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                TCCGT CTCTAACGTCACTCG
                                   _
GAM1110  LOC148189 5'  CGGCTCACTGCAACCTCCACCT 78706     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  AC_
GAM1110  LOC148293 3'  GCTCACTGGACCCCAGCCT    78781      AAGA    G
                                AGGC    GGTT CAGTGAGC
                                ||||    |||| ||||||||
                                TCCG    CCAG GTCACTCG
                                  ACC_   _
GAM1110  LOC148438 3'  CACCTAAAAACCTCTTGCCT   84155           GCA__
                                AGGCAAGAGGTT     GTG
                                ||||||||||||     |||
                                TCCGTTCTCCAA     CAC
                                       AAATC
GAM1110  LOC148709 3'  CACTACAACCTCCGCCT     78934      AA      C
                                AGGC  GAGGTTG AGTG
                                ||||  ||||||| ||||
                                TCCG  CTCCAAC TCAC
                                  C_      A
GAM1110  LOC148887 5'  CGGCTCACTGCAACATCTGCCT 84235       A  G
                                AGGCA GA GTTGCAGTGAGCCG
                                ||||| || ||||||||||||||
                                TCCGT CT CAACGTCACTCGGC
                                   _  A
GAM1110  LOC148887 5'  GCCCACCCTGCAGCCCTGCT   84239      A A      __   A
                                GGCA G GGTTGCA  GTG GC
                                |||| | |||||||  ||| ||
                                TCGT C CCGACGT  CAC CG
                                  _ _      CC   C
GAM1110  LOC149421 3'  CGGCTCACTGCAAGCCCCACCT 79358     CAAGA   _
                                AGG     GGTT GCAGTGAGCCG
                                |||     |||| ||||||||||
                                TCC     CCGA CGTCACTCGGC
                                  ACC__    A
GAM1110  LOC149506 3'  CGGCTCACTGCAACTTCCACCT 84461     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
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                                TCC   CTTCAACGTCACTCGGC
                                  AC_
GAM1110  LOC149506 3'  GCTCACTGCAACCTCTGCCT   84471      A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110  LOC149577 3'  CGGCTCACCACAACCTCCACCT 84508     CAA      CA
                                AGG   GAGGTTG  GTGAGCCG
                                |||   |||||||  ||||||||
                                TCC   CTCCAAC  CACTCGGC
                                  AC_      AC
GAM1110  LOC149703 5'  GCTTAATGCAACCTCTACCT   84656     CA        G
                                AGG  AGAGGTTGCA TGAGC
                                |||  |||||||||| |||||
                                TCC  TCTCCAACGT ATTCG
                                  A_         A
GAM1110  LOC149711 3'  CGGCTCACTGCAACCTCTGCTT 84679       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TTCGT CTCCAACGTCACTCGGC
                                  _
GAM1110  LOC150054 5'  CGGCTCACTGCAACCTTCGCCT 84829      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  TTCCAACGTCACTCGGC
                                  C_
GAM1110  LOC150095 5'  CATCTGCAACCTGCTGCC    84856      AG       _
                                GGCA  AGGTTGCAG TG
                                ||||  ||||||||| ||
                                CCGT  TCCAACGTC AC
                                  CG        T
GAM1110  LOC150397 3'  CGGCTCATTGCAACCTCCGCCT 79844      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTTACTCGGC
                                  C_
GAM1110  LOC150960 3'  CGCTGCAACCTCCGCCT     80057      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCGC
                                  C_
GAM1110  LOC151057 3'  CGGCTCACTGCAACCTCTGCCT 85210       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                  _
GAM1110  LOC151188 5'  CGGCTTCCTTTGCAACCCGCCG 80158     AAGA       T__
            CC                    GGC    GGTTGCAG   GAGCCG
                                |||    ||||||||   ||||||
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                                CCG   CCAACGTT  TTCGGC
                                  CCGC      TCC
GAM1110  LOC151201 3'  GCTCACTGCAACCTCCACCT  85282    CAA
                                AGG  GAGGTTGCAGTGAGC
                                |||  ||||||||||||||
                                TCC  CTCCAACGTCACTCG
                                  AC_
GAM1110  LOC151475 5'  CACTGCAACCTCCACCT    85392    CAA
                                AGG  GAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  CTCCAACGTCAC
                                  AC_
GAM1110  LOC151475 5'  GCTCACTGCAACCTCTGCCT  85411     A
                                AGGCA GAGGTTGCAGTGAGC
                                |||||  ||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                   _
GAM1110  LOC151602 3'  CGGCTCACTGCAACCT     80293
                                AGGTTGCAGTGAGCCG
                                ||||||||||||||||
                                TCCAACGTCACTCGGC

GAM1110  LOC151826 3'  GCTCACTGCAACCTCCGCCT  80358    AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                TCCG  CTCCAACGTCACTCG
                                  C_
GAM1110  LOC151877 3'  CGGCTCACTACAACCACCACCT 85503    CAAGA   C
                                AGG    GGTTG AGTGAGCCG
                                |||    |||||  |||||||||
                                TCC    CCAAC TCACTCGGC
                                  ACCA_    A
GAM1110  LOC152220 3'  GCTCACTGCAACCTCCGCTT  85583    AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                TTCG  CTCCAACGTCACTCG
                                  C_
GAM1110  LOC152245 3'  CGGCTCACTGCAACCTCCGCCT 85601     AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  LOC152300 3'  GCTCACTGCAAGCTCTGCCT  80545     A  G
                                AGGCA GAG TTGCAGTGAGC
                                |||||  |||  ||||||||||
                                TCCGT CTC AACGTCACTCG
                                   _  G
GAM1110  LOC152343 3'  CGACTCAGTGCAACCTCCGCCT 80562     AA      G   C
                                AGGC  GAGGTTGCA TGAG CG
                                ||||  |||||||||  ||||  ||
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                                TCCG  CTCCAACGT ACTC GC
                                  C_       G   A
GAM1110  LOC152445 3'  CACTGCAACCTCTGCCT     85748       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  LOC152582 5'  CGGCTCACCGCAACCTCTGCCT 85790       A       A
                                AGGCA GAGGTTGC GTGAGCCG
                                ||||| |||||||| ||||||||
                                TCCGT CTCCAACG CACTCGGC
                                  _      C
GAM1110  LOC152620 3'  GCTCACTACAACCTCTGCCT   60081       A      C
                                AGGCA GAGGTTG AGTGAGC
                                ||||| ||||||| |||||||
                                TCCGT CTCCAAC TCACTCG
                                  _      A
GAM1110  LOC152719 5'  CACTGCAACCTCTGCCT     85847       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  LOC152794 5'  CACTGCAACCTCTACCT     80672     CA
                                AGG  AGAGGTTGCAGTG
                                |||  ||||||||||||
                                TCC  TCTCCAACGTCAC
                                  A_
GAM1110  LOC152851 3'  CGGCTCGCTGCAACCTCCACC  80709    CAA
                                GG   GAGGTTGCAGTGAGCCG
                                ||   |||||||||||||||||
                                CC   CTCCAACGTCGCTCGGC
                                 AC_
GAM1110  LOC152925 3'  CGGCTTACTCCAACCTCTGCCT 80735       A      C
                                AGGCA GAGGTTG AGTGAGCCG
                                ||||| ||||||| |||||||||
                                TCCGT CTCCAAC TCATTCGGC
                                  _      C
GAM1110  LOC153077 3'  CGGCTCACTGCAACCTCCGCCT 85908      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  LOC153205 5'  GCCCAGCCTCTTCCT       85945     C       CAGTGA
                                AGG AAGAGGTTG      GC
                                ||| |||||||||      ||
                                TCC TTCTCCGAC      CG
                                  _       C_____
GAM1110  LOC153688 3'  CGGCTCACTGCAACCTCCACCT 86101     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
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                                TCC   CTCCAACGTCACTCGGC
                                  AC_
GAM1110  LOC153811 3'  CGGCTCACTGCAAGCTCCGCCT 80946      AA   G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||||
                                TCCG  CTC AACGTCACTCGGC
                                  C_   G
GAM1110  LOC153883 5'  CACTGCAACCTCCACC      80979    CAA
                                GG   GAGGTTGCAGTG
                                ||   ||||||||||||
                                CC   CTCCAACGTCAC
                                 AC_
GAM1110  LOC154075 3'  GCTCACTGCAACCTCCGCCT   81046      AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  |||||||||||||||
                                TCCG  CTCCAACGTCACTCG
                                  C_
GAM1110  LOC154282 5'  CGGCTCACTGCAACCTCCACCT 86195     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   ||||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  AC_
GAM1110  LOC154877 3'  CGGCTCATTGCAACCTCCGCCT 86291      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTTACTCGGC
                                  C_
GAM1110  LOC154877 3'  GCTCACTGCAACCTCTACCT   86297     CA
                                AGG  AGAGGTTGCAGTGAGC
                                |||  ||||||||||||||||
                                TCC  TCTCCAACGTCACTCG
                                  A_
GAM1110  LOC157247 5'  GCTCACTGCAACCTCCACCC   81370    CAA
                                GG   GAGGTTGCAGTGAGC
                                ||   ||||||||||||||
                                CC   CTCCAACGTCACTCG
                                 CAC
GAM1110  LOC157506 3'  CGGCTCACTGCAATCTCTGCCT 81440       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCTAACGTCACTCGGC
                                    _
GAM1110  LOC157507 5'  CGGCTCACTGCAACGTCCGCCT 81456      AA  G
                                AGGC  GA GTTGCAGTGAGCCG
                                ||||  || ||||||||||||||
                                TCCG  CT CAACGTCACTCGGC
                                  C_  G
GAM1110  LOC157798 5'  CACTGCAACCTCCGCCT     86547      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
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                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  LOC157858 5'  CACTGCAACCTCTGCCT     86583       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  LOC158310 5'  GCTCACTGCAACCTTGGCCT   86756      AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                TCCG  TTCCAACGTCACTCG
                                  G_
GAM1110  LOC158402 5'  GCTCACTGTAACCTCTGCCT   86808       A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                TCCGT CTCCAATGTCACTCG
                                  _
GAM1110  LOC158476 3'  GCTCACTGCAACCTCCGCC    86847     AA
                                GGC  GAGGTTGCAGTGAGC
                                |||  ||||||||||||||||
                                CCG  CTCCAACGTCACTCG
                                  C_
GAM1110  LOC158549 5'  CGGCTCACTGTGACCTCCGCCT 86865      AA    TG
                                AGGC  GAGGT  CAGTGAGCCG
                                ||||  |||||  ||||||||||
                                TCCG  CTCCA  GTCACTCGGC
                                  C_    GT
GAM1110  LOC158668 3'  GCTCACTGCAACCTCTGCCT   69370       A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110  LOC158828 3'  CTGCAACCTCTGACCT       82028     CA
                                AGG  AGAGGTTGCAG
                                |||  ||||||||||
                                TCC  TCTCCAACGTC
                                  AG
GAM1110  LOC158865 5'  CGGCTCACTGCAACCTCTGCCT 86934       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| |||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                  _
GAM1110  LOC161829 3'  CACTGCAACCTCCGCCT      82311      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  LOC163748 5'  GGCTCACACTCTTGCC       87043         GTTGCA
                                GGCAAGAG     GTGAGCC
                                ||||||||     |||||||
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                                CCGTTCTC     CACTCGG
                                   A_____
GAM1110  LOC169611 3'  GCTCACTGCAATCTCCGCCT   82768      AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                TCCG  CTCTAACGTCACTCG
                                  C_
GAM1110  LOC196047 5'  CGGCTCACTGCAACCTCCGCCT 89597      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  |||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  LOC196264 3'  CACTGCAACCTCTGCCT     87602       A
                                AGGCA GAGGTTGCAGTG
                                |||||  ||||||||||||
                                TCCGT CTCCAACGTCAC

                                  _
GAM1110  LOC196411 3'  CGGCTCACTGCAACCTCCGCCT 87670      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  LOC196529 3'  CACTGCAACCTCCACCT     87769     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1110  LOC197358 3'  GCTCACTGTAGGCTCTACCT   88039     CA    G
                                AGG  AGAG TTGCAGTGAGC
                                |||  ||||  ||||||||||
                                TCC  TCTC GATGTCACTCG
                                  A_    G
GAM1110  LOC197358 3'  GCTCCCTGCAACCTCCGCCT   88041      AA         T
                                AGGC  GAGGTTGCAG GAGC
                                ||||  |||||||||| ||||
                                TCCG  CTCCAACGTC CTCG
                                  C_         C
GAM1110  LOC199699 3'  GCTCACTGCAAGCTCCACCT   88308     CAA   G
                                AGG   GAG TTGCAGTGAGC
                                |||   ||| ||||||||||
                                TCC   CTC AACGTCACTCG
                                  AC_   G
GAM1110  LOC199725 5'  CTTACTGCAACCTTCGCCT    89837      AA
                                AGGC  GAGGTTGCAGTGAG
                                ||||  ||||||||||||||
                                TCCG  TTCCAACGTCATTC
                                  C_
GAM1110  LOC199786 3'  CGGCTCACTGCAACCTCCGCCT 88377      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  |||||||||||||||||
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                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  LOC199906 3'  CGGCTTACTGCAACCTCCGCCT 88479      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCATTCGGC
                                  C_
GAM1110  LOC200014 3'  GCTCGCTGCAACCCCCACCT   88531     CAAGA
                                AGG    GGTTGCAGTGAGC
                                |||    ||||||||||||
                                TCC    CCAACGTCGCTCG
                                 ACCC_
GAM1110  LOC200107 3'  CGGCTCACCGCAACCTC     88574         A
                                GAGGTTGC GTGAGCCG
                                |||||||| ||||||||
                                CTCCAACG CACTCGGC
                                     C
GAM1110  LOC200169 5'  CACTGCAACCTCTGCCT     89944       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                   _
GAM1110  LOC200268 3'  CGGCTCACTGCAACCTCTGCCT 88682       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                   _
GAM1110  LOC200310 3'  CGGCTCACTACAACCTCTGCCT 65733       A      C
                                AGGCA GAGGTTG AGTGAGCCG
                                ||||| ||||||| |||||||||
                                TCCGT CTCCAAC TCACTCGGC
                                   _      A
GAM1110  LOC200314 3'  CACTGCAACCTCCACCT     90002     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1110  LOC200316 3'  GCTCACTGCAAACTCTGCTT   88770       A   G
                                AGGCA GAG TTGCAGTGAGC
                                ||||| ||| ||||||||||
                                TTCGT CTC AACGTCACTCG
                                   _  A
GAM1110  LOC200339 3'  CACTGCAACCTCTGCCT     90032       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                   _
GAM1110  LOC200845 5'  CGGCTCACTGCAACCTCCGCCT 88898      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||
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                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  LOC200860 3'  CACTGCAACCTCCACCT     90159     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1110  LOC201164 3'  CGGCTCACTGCATCCTCTGCCT 88115       A    T
                                AGGCA GAGG TGCAGTGAGCCG
                                ||||| |||| ||||||||||||
                                TCCGT CTCC ACGTCACTCGGC
                                   _    T
GAM1110  LOC201173 5'  CGGCTCACTGCAACCTCTGCCT 87326       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                   _
GAM1110  LOC201220 5'  CGGCTCACTGCAACCTCTGCCT 87347       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                   _
GAM1110  LOC201294 3'  CACTGCAACCTCCGCCT     88202      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  LOC201294 3'  GCTCACTGCAACCTCCGCCT   88212      AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  |||||||||||||||
                                TCCG  CTCCAACGTCACTCG
                                  C_
GAM1110  LOC201411 3'  GCTCACTGCAACCTCTGCCT   62957       A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| |||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                   _
GAM1110  LOC201626 3'  CGGCTCACTGCAACCTCCGCC  88989     AA
                                GGC  GAGGTTGCAGTGAGCCG
                                |||  |||||||||||||||||
                                CCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  LOC201627 3'  CGGCTGACTGCAACCTCCACCT 89008     CAA          G
                                AGG   GAGGTTGCAGT AGCCG
                                |||   |||||||||| |||||
                                TCC   CTCCAACGTCA TCGGC
                                  AC_          G
GAM1110  LOC201696 3'  GCTCACTGCAGCCACTGCCT   63133       A A
                                AGGCA G GGTTGCAGTGAGC
                                ||||| | ||||||||||||
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                                TCCGT C CCGACGTCACTCG
                                  _ A
GAM1110  LOC201702 5'  GCTCACTGCAACCTCTGACT   89031    CA
                                GG  AGAGGTTGCAGTGAGC
                                ||  ||||||||||||||||
                                TC  TCTCCAACGTCACTCG
                                 AG
GAM1110  LOC202025 3'  CGGCTCACTGCAACCTCCGCCT 90285      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  LOC202934 3'  GCTCACTACAACCTCTGCCT   90415      A      C
                                AGGCA GAGGTTG AGTGAGC
                                |||||| ||||||| |||||||
                                TCCGT CTCCAAC TCACTCG
                                   _      A
GAM1110  LOC203297 5'  CGGCTCACTGCAACCTCTGCCT 75350      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                |||||| ||||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                   _
GAM1110  LOC203350 3'  CTGACTGCAACCTCCGCCT    90566      AA         G
                                AGGC  GAGGTTGCAGT AG
                                ||||  |||||||||| ||
                                TCCG  CTCCAACGTCA TC
                                  C_         G
GAM1110  LOC203369 3'  CGGCTCACTGCAAGCTCCGCCT 89338      AA   G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||
                                TCCG  CTC AACGTCACTCGGC
                                  C_  G
GAM1110  LOC203378 3'  CGGCTCACGGCAACCTCTGCCT 90599      A       A
                                AGGCA GAGGTTGC GTGAGCCG
                                |||||| |||||||| ||||||||
                                TCCGT CTCCAACG CACTCGGC
                                   _       G
GAM1110  LOC204804 3'  CGGCTCACTGCCACCTCCACCT 89470     CAA    T
                                AGG   GAGGT GCAGTGAGCCG
                                |||   ||||| ||||||||||
                                TCC   CTCCA CGTCACTCGGC
                                  AC_    C
GAM1110  LOC219445 5'  CGGCTCACTGCAGCCTCCGCCT 91573      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||||
                                TCCG  CTCCGACGTCACTCGGC
                                  C_
GAM1110  LOC219673 5'  CGGCTCACTGTAGCCTCTGCCT 93024      A
                                AGGCA GAGGTTGCAGTGAGCCG
                                |||||| ||||||||||||||||||
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                                TCCGT CTCCGATGTCACTCGGC
                                  _
GAM1110  LOC219673 3'  GCTTAACCTCTCTCCT      93035     CA       C
                                AGG  AGAGGTTG AGT
                                |||  |||||||| |||
                                TCC  TCTCCAAT TCG
                                  TC       _
GAM1110  LOC219690 3'  GCTATAAGCCTCTTGCCT     93074           GCAGTG
                                AGGCAAGAGGTT      AGC
                                ||||||||||||      |||
                                TCCGTTCTCCGA      TCG
                                      ATA___
GAM1110  LOC219735 3'  CGGCTCACTGCAACCTCTGCCT 93108       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                ||||| ||||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                  _
GAM1110  LOC219920 3'  GCTGAATAAACCTCTTCCT    93315     C       G___
                                AGG AAGAGGTT    CAGT
                                ||| ||||||||    ||||
                                TCC TTCTCCAA    GTCG
                                  _       ATAA
GAM1110  LOC220064 3'  CGGCTCACTGTAACCTCCGCCT 93424      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  ||||||||||||||||||
                                TCCG  CTCCAATGTCACTCGGC
                                  C_
GAM1110  LOC220074 3'  CGGCTCACTGCAAACTCCGCCT 59270      AA   G
                                AGGC  GAG TTGCAGTGAGCCG
                                ||||  ||| ||||||||||||||
                                TCCG  CTC AACGTCACTCGGC
                                  C_   A
GAM1110  LOC220074 3'  GCTCACTGCAACCTCCGCCT   59277      AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCG
                                  C_
GAM1110  LOC220662 3'  CACTGCAACCTCCACCT     91165     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1110  LOC220846 3'  CTTTCCACAACCTCTACCT    90814     CA       CAGT
                                AGG  AGAGGTTG    GAG
                                |||  ||||||||    |||
                                TCC  TCTCCAAC    TTC
                                  A_       ACCT
GAM1110  LOC221035 3'  CGGCTCACTACAACCTCTGCCT 93163       A      C
                                AGGCA GAGGTTG AGTGAGCCG
                                ||||| ||||||| |||||||||
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                                TCCGT CTCCAAC TCACTCGGC
                                  _      A
GAM1110  LOC221174 5'  GCTCACTGCGACCTCCACCT   93502     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                TCC   CTCCAGCGTCACTCG
                                  AC_
GAM1110  LOC221271 3'  GCTCACTGCAACCTCTGCCT   91863      A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110  LOC221296 3'  CGGCTCACTGCAACCTCCACCT 91959     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   |||||||||||||||
                                TCC   CTCCAACGTCACTCGGC
                                  AC_
GAM1110  LOC221362 5'  CTCCCAAACTCTTGCCT     93759         G   CAGT
                                AGGCAAGAG TTG    GAG
                                ||||||||| |||    |||
                                TCCGTTCTC AAC    CTC
                                     A   C___
GAM1110  LOC221663 5'  CACTGCAACCTCCACCT     93810     CAA
                                AGG   GAGGTTGCAGTG
                                |||   ||||||||||||
                                TCC   CTCCAACGTCAC
                                  AC_
GAM1110  LOC221773 3'  GCTCACTGTGACCTCCGCCT   91046     AA    TG
                                AGGC  GAGGT  CAGTGAGC
                                ||||  |||||  ||||||||
                                TCCG  CTCCA  GTCACTCG
                                  C_    GT
GAM1110  LOC222070 5'  CACTGCAACCTCTGCCT     94151       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  LOC245771 5'  CGGCTCACTGCAACCCCCGTCT 92885      AAGA
                                AGGC    GGTTGCAGTGAGCCG
                                ||||    |||||||||||||||
                                TCTG    CCAACGTCACTCGGC
                                  CCC_
GAM1110  LOC253612 5'  CGGCTCACTGCAACCTCCGCCT 96747      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  LOC253664 3'  CATTGCAACCTCTGCCT     94808       A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
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                                TCCGT CTCCAACGTTAC
                                  _
GAM1110  LOC253666 5'  GCTCACTGCAACCTCCGCCT   95063      AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  |||||||||||||||
                                TCCG  CTCCAACGTCACTCG
                                  C_
GAM1110  LOC253779 3'  CACTGCAACCTCCGCCT     97143      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  LOC254013 3'  CGGCTCACTGTAGCCTCCACCT 94877     CAA
                                AGG   GAGGTTGCAGTGAGCCG
                                |||   |||||||||||||||||
                                TCC   CTCCGATGTCACTCGGC
                                  AC_
GAM1110  LOC254268 3'  GCTCACTGCAACCTTTGTCT   95409      A
                                AGGCA GAGGTTGCAGTGAGC
                                |||||| ||||||||||||||||
                                TCTGT TTCCAACGTCACTCG
                                  _
GAM1110  LOC254655 3'  CACTGCAACCTCTGCCT     95469      A
                                AGGCA GAGGTTGCAGTG
                                ||||| ||||||||||||
                                TCCGT CTCCAACGTCAC
                                  _
GAM1110  LOC254672 3'  CGGCTCACTGAAACCTCTGCCT 94643      A     G
                                AGGCA GAGGTT CAGTGAGCCG
                                ||||| |||||| ||||||||||
                                TCCGT CTCCAA GTCACTCGGC
                                  _     A
GAM1110  LOC255196 5'  CGGCTCACTGCAGTCTCGACCT 97166     CAA   GT
                                AGG   GAG  TGCAGTGAGCCG
                                |||   |||  ||||||||||||
                                TCC   CTC  ACGTCACTCGGC
                                  AG_   TG
GAM1110  LOC255465 3'  GCTCACTGTATCCTCTGCCT   97292      A    T
                                AGGCA GAGG TGCAGTGAGC
                                ||||| |||| ||||||||||
                                TCCGT CTCC ATGTCACTCG
                                  _    T
GAM1110  LOC255497 3'  CGGCTCACTGCAACCTCCGCCT 97189      AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110  LOC255919 3'  CTTTCTGCAACCTCTGCCT    95034      A        T
                                AGGCA GAGGTTGCAG GAG
                                ||||| |||||||||| |||
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                                TCCGT CTCCAACGTC TTC
                                  _       T
GAM1110  LOC256267 3'  GCTCACTGCAACCTCCGCCT  96804     AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                TCCG  CTCCAACGTCACTCG
                                  C_
GAM1110  LOC256273 5'  CAGTGAAACAACCTCCTCCCT  96404     CAA     ___  G
                                AGG   GAGGTTG   CA TG
                                |||   |||||||   || ||
                                TCC   CTCCAAC   GT AC
                                  CTC      AAA  G
GAM1110  LOC256306 3'  GCTCACTGCAACCTCCACCT  96691     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                TCC   CTCCAACGTCACTCG
                                  AC_
GAM1110  LOC257054 5'  GCTCACTGCAGCCTCGACCT  95664     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                TCC   CTCCGACGTCACTCG
                                  AG_
GAM1110  LOC257334 3'  CACTGCAACCTCCGCCT     97275      AA
                                AGGC  GAGGTTGCAGTG
                                ||||  ||||||||||||
                                TCCG  CTCCAACGTCAC
                                  C_
GAM1110  LOC51008  5'  CGGCTCACAGCAACCTCTGCCT 31962       A       A
                                AGGCA GAGGTTGC GTGAGCCG
                                ||||| |||||||| ||||||||
                                TCCGT CTCCAACG CACTCGGC
                                  _       A
GAM1110  LOC51200  3'  CACCACAACCTCTGCCT     32990      A      CA
                                AGGCA GAGGTTG  GTG
                                ||||| |||||||  |||
                                TCCGT CTCCAAC  CAC
                                  _       AC
GAM1110  LOC51219  5'  CGGCTCACCGCAACCTCCGCCT 33117      AA       A
                                AGGC  GAGGTTGC GTGAGCCG
                                ||||  |||||||| ||||||||
                                TCCG  CTCCAACG CACTCGGC
                                  C_       C
GAM1110  LOC51696  3'  GCTCACTGCAACCTCTGCCT   32550      A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                  _
GAM1110  LOC56181  5'  CGGCTCACTGCAAGCTCTGCCT 95534       A   G
                                AGGCA GAG TTGCAGTGAGCCG
                                ||||| ||| ||||||||||||
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                              TCCGT CTC AACGTCACTCGGC
                                _  G
GAM1110 LOC57107 3' CACTGCAACCTCCGCCT    39830     AA
                              AGGC  GAGGTTGCAGTG
                              ||||  ||||||||||||
                              TCCG  CTCCAACGTCAC
                                C_
GAM1110 LOC57146 3' CGGCTCACTGCAACCTC    39917
                              GAGGTTGCAGTGAGCCG
                              |||||||||||||||||
                              CTCCAACGTCACTCGGC

GAM1110 LOC64102 5' CGACTCACTTGCAACTCCACCT 42170    CAA  G   _   C
                              AGG   GAG TTGCA GTGAG CG
                              |||   ||| ||||| ||||| ||
                              TCC   CTC AACGT CACTC GC
                                AC_  _   T   A
GAM1110 LOC81034 3' GCTCACTGCAACCTCCACCT  47852    CAA
                              AGG   GAGGTTGCAGTGAGC
                              |||   |||||||||||||||
                              TCC   CTCCAACGTCACTCG
                                AC_
GAM1110 LOC89932 3' CACTGCAACCTCCACCT    60790    CAA
                              AGG   GAGGTTGCAGTG
                              |||   ||||||||||||
                              TCC   CTCCAACGTCAC
                                AC_
GAM1110 LOC89932 3' GCTCACTGCAACCTCCGTCT  60806     AA
                              AGGC  GAGGTTGCAGTGAGC
                              ||||  |||||||||||||||
                              TCTG  CTCCAACGTCACTCG
                                C_
GAM1110 LOC90120 5' CGGCCCGCACACCACCTGCCT 61533     AGA  TGCA  A
                              AGGCA  GGT   GTG GCCG
                              |||||  |||   ||| ||||
                              TCCGT  CCA   CGC CGGC
                                 CCA  CA__  C
GAM1110 LOC90139 3' CAAGGCAGCCTCCTGCCT    55400     A     AG
                              AGGCA GAGGTTGC  TG
                              ||||| ||||||||  ||
                              TCCGT CTCCGACG  AC
                                 C      GA
GAM1110 LOC90141 3' CGGCTCACTGCAACTTCCGCCT 61627     AA
                              AGGC  GAGGTTGCAGTGAGCCG
                              ||||  |||||||||||||||||
                              TCCG  CTTCAACGTCACTCGGC
                                C_
GAM1110 LOC90288 3' CACTGCAACCTCCACCT    62084    CAA
                              AGG   GAGGTTGCAGTG
                              |||   ||||||||||||
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                              TCC  CTCCAACGTCAC
                                AC_
GAM1110 LOC90288 3' CGGCTCACTGCAACCTCCAGGT 62087    AA_
            C                  GGC  GAGGTTGCAGTGAGCCG
                               |||  ||||||||||||||||
                               CTG  CTCCAACGTCACTCGGC
                                GAC
GAM1110 LOC90333 3' GCTCACTGCAACCTCCTCCT  62291    CAA
                               AGG  GAGGTTGCAGTGAGC
                               |||  |||||||||||||
                               TCC  CTCCAACGTCACTCG
                                TC_
GAM1110 LOC90371 5' CACTGCAACCTCCACCT    62493    CAA
                               AGG  GAGGTTGCAGTG
                               |||  ||||||||||
                               TCC  CTCCAACGTCAC
                                AC_
GAM1110 LOC90408 5' CACTGCAACCTCTACCT    62657    CA
                               AGG AGAGGTTGCAGTG
                               |||  ||||||||||||
                               TCC TCTCCAACGTCAC
                                A_
GAM1110 LOC90459 3' CACTGCAACCTCCGCCT    62882     AA
                               AGGC GAGGTTGCAGTG
                               ||||  ||||||||||
                               TCCG CTCCAACGTCAC
                                 C_
GAM1110 LOC90485 3' CGGCTCACTGAAACTTCTGCCT 63011      A    G
                               AGGCA GAGGTT CAGTGAGCCG
                               ||||| |||||| ||||||||||
                               TCCGT CTTCAA GTCACTCGGC
                                  _    A
GAM1110 LOC90485 3' CGGCTCACTGCAACCTCCGCCT 63012     AA
                               AGGC GAGGTTGCAGTGAGCCG
                               ||||  ||||||||||||||||
                               TCCG CTCCAACGTCACTCGGC
                                 C_
GAM1110 LOC90591 3' GCTCACTGCAAGCTCCACCT  63432    CAA  G
                               AGG  GAG TTGCAGTGAGC
                               |||  ||| ||||||||||
                               TCC  CTC AACGTCACTCG
                                AC_  G
GAM1110 LOC91115 3' CGGCTCACTGCAACCTCCACCT 64930    CAA
                               AGG  GAGGTTGCAGTGAGCCG
                               |||  ||||||||||||||||
                               TCC  CTCCAACGTCACTCGGC
                                AC_
GAM1110 LOC91115 3' CGGCTCACTGCAACCTCCGCCT 64932     AA
                               AGGC GAGGTTGCAGTGAGCCG
                               ||||  ||||||||||||||||
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                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110 LOC91115 3' GCTCACTGCAACTTCTGCCT  64943      A
                                AGGCA GAGGTTGCAGTGAGC
                                ||||| ||||||||||||||||
                                TCCGT CTTCAACGTCACTCG
                                  _
GAM1110 LOC91291 5' GCTCACTGCAACCTCGACCT  65480    CAA
                                AGG  GAGGTTGCAGTGAGC
                                |||  ||||||||||||||||
                                TCC  CTCCAACGTCACTCG
                                 AG_
GAM1110 LOC91561 5' GCTCACTGCAAGCTCCGCCT  66451     AA  G
                                AGGC  GAG TTGCAGTGAGC
                                ||||  ||| ||||||||||
                                TCCG  CTC AACGTCACTCG
                                  C_  G
GAM1110 LOC91813 5' GCTCACTGAGCTCTCTGCC   67255    A  _  G
                                GGCA GAG GTT CAGTGAGC
                                |||| ||| ||| ||||||||
                                CCGT CTC CGA GTCACTCG
                                  _  T  _
GAM1110 LOC92267 3' GCTCACTGCAACCTCCACCT  68616    CAA
                                AGG  GAGGTTGCAGTGAGC
                                |||  ||||||||||||||||
                                TCC  CTCCAACGTCACTCG
                                 AC_
GAM1110 LOC92303 3' CTCACTGCAACCTCTGCC    68823    A
                                GGCA GAGGTTGCAGTGAG
                                |||| ||||||||||||||
                                CCGT CTCCAACGTCACTC
                                  _
GAM1110 LOC92466 3' GCTCACTGCAACCTCCGCCT  69429     AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||||
                                TCCG  CTCCAACGTCACTCG
                                  C_
GAM1110 LOC92689 3' CGGCTCACTGCAACCTCCGCCT 70223     AA
                                AGGC  GAGGTTGCAGTGAGCCG
                                ||||  |||||||||||||||||
                                TCCG  CTCCAACGTCACTCGGC
                                  C_
GAM1110 LOC92697 5' CGGCTCACCGCAACCTCCGCCT 70265     AA      A
                                AGGC  GAGGTTGC GTGAGCCG
                                ||||  |||||||| ||||||||
                                TCCG  CTCCAACG CACTCGGC
                                  C_      C
GAM1110 LOC92697 5' CGGCTCACTGCAGCCTCCCTGC 70266     A_
            C                    GGCA  GAGGTTGCAGTGAGCCG
                                ||||  |||||||||||||||||
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                                CCGT  CTCCGACGTCACTCGGC
                                  CC
GAM1110  LOC92697  5'  CGGCTCGCTACAACCTCCACCT 70267     CAA      C
                                AGG   GAGGTTG AGTGAGCCG
                                |||   ||||||| |||||||||
                                TCC   CTCCAAC TCGCTCGGC
                                  AC_      A
GAM1110  LOC92841  3'  GGCTCACCGCAACCTCCTCCT  70716     CAA      A
                                AGG   GAGGTTGC GTGAGCC
                                |||   |||||||| |||||||
                                TCC   CTCCAACG CACTCGG
                                  TC_      C
GAM1110  LOC93129  3'  GCTCACTGTAGCCTCGACCT   71466     CAA
                                AGG   GAGGTTGCAGTGAGC
                                |||   ||||||||||||||
                                TCC   CTCCGATGTCACTCG
                                  AG_
GAM1110  LOC93132  5'  GCTCACTGCAACCTCCGCCT   71490      AA
                                AGGC  GAGGTTGCAGTGAGC
                                ||||  ||||||||||||||
                                TCCG  CTCCAACGTCACTCG
                                  C_
GAM1110  LOC93349  3'  GCTCACTGCAACCTCTGCCT   56460       A
                                AGGCA GAGGTTGCAGTGAGC
                                |||||| |||||||||||||
                                TCCGT CTCCAACGTCACTCG
                                   _
GAM1110  LOC93408  5'  CGGCTCACTGCAACCTCTGCCT 56477       A
                                AGGCA GAGGTTGCAGTGAGCCG
                                |||||| |||||||||||||||||
                                TCCGT CTCCAACGTCACTCGGC
                                   _
GAM1111  LOC133308 5'  AAGAATCCTATCTTCCCACCGC 75084         T_    TGTA
            A                    TGCGGTGG  AGGT    GATTCTT
                                |||||||| ||||    |||||||
                                ACGCCACC  TCTA    CTAAGAA
                                     CT    TC__
GAM1112  CLN5     3'  CTTCTAGATGTGGCAAATCCA  21426     AAG    A   TAA
                                TG   TTGC GCA   TCTAGAAG
                                ||   |||| |||   ||||||||
                                AC   AACG TGT   AGATCTTC
                                  CTA    G   ____
GAM1112  EHHADH   3'  TTCCAGATTATGCCTCAC     8753      T CA        A
                                GT G  GCATAATCT GAA
                                || |  ||||||||| |||
                                CA C  CGTATTAGA CTT
                                 _ TC        C
GAM1112  EPHB2    3'  AGGTCTGCAGCTCCA       15440     A       CATA
                                TG AGTTGCAG    ATCT
                                || ||||||||    ||||
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                                AC TCGACGTC    TGGA
                                 C      ____
GAM1112  EPHB2    3'  AGGTCTGCAGCTCCA      33884    A      CATA
                                TG AGTTGCAG    ATCT
                                || ||||||||    ||||
                                AC TCGACGTC    TGGA
                                 C      ____
GAM1112  LDOC1    3'  AGAACTATGCTGCCACTTCA   24617      T      A_
                                TGAAGT GCAGCATA  TCT
                                |||||| ||||||||  |||
                                ACTTCA CGTCGTAT  AGA
                                   C       CA
GAM1112  MTMR8    3'  CTAGTCTATGCCTGCAACTCCA 31291    A      _    AT
                                TG AGTTGCAG CATA  CTAG
                                || |||||||| ||||  ||||
                                AC TCAACGTC GTAT  GATC
                                 C       C    CT
GAM1112  PATE     3'  TCTAGACAGGGAACAGCTTCA  56315       CAGCATAA
                                TGAAGTTG       TCTAGA
                                ||||||||       ||||||
                                ACTTCGAC       AGATCT
                                     AAGGGAC_
GAM1112  PSCD4    3'  AGAATGCTGCAACTTC      25399          AA
                                GAAGTTGCAGCAT  TCT
                                ||||||||||||  |||
                                CTTCAACGTCGTA  AGA
                                              __
GAM1112  AFAP     3'  CTTCCAGAAAATCTCAACTTCA 41303       C  C  AA   A
                                TGAAGTTG AG AT  TCT GAAG
                                |||||||| || ||  ||| ||||
                                ACTTCAAC TC TA  AGA CTTC
                                     _ _  AA   C
GAM1112  C11orf9  3'  AGATGGTATTGCAGCTTCA    25204          C  A
                                TGAAGTTGCAG AT ATCT
                                |||||||||| || ||||
                                ACTTCGACGTT TG TAGA
                                       A  G
GAM1112  C1orf24  3'  CTTCTAAAGTCTGCAACTTCA  53716          C  AATC
                                TGAAGTTGCAG AT    TAGAAG
                                |||||||||| ||    ||||||
                                ACTTCAACGTC TG    ATCTTC
                                       _  AA__
GAM1112  DKFZP586D2223 5'  TCTAGTTTATCCTGCAACTCCA 37686    A      C    T
                                TG AGTTGCAG ATAA CTAGA
                                || |||||||| |||| |||||
                                AC TCAACGTC TATT GATCT
                                 C       C    T
GAM1112  FLJ00060  5'  CTGGATCACGCTGCAGCCTCA  61097     A       ATA
                                TGA GTTGCAGC   ATCTAG
                                ||| ||||||||   ||||||
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                                ACT CGACGTCG   TAGGTC
                                  C       CAC
GAM1112 KPNA6    3'  CTTCCAAATGGTGCGACCCAAC 24605        CA__    AATCTA
             TTCA                  TGAAGTTG    GCAT     GAAG
                                ||||||||   ||||     ||||
                                ACTTCAAC    CGTG     CTTC
                                    CCAG    GTAAAC
GAM1112 MMEL2    3'  CTTCCAGTATCTACAGCTTCA  53095        C  C   AT  A
                                TGAAGTTG AG ATA  CT GAAG
                                |||||||| || |||  || ||||
                                ACTTCGAC TC TAT  GA CTTC
                                    A  _   __  C
GAM1112 LOC144577 3'  TTCTAGATTATTGATTCA    76905      GTTGCAGC
                                TGAA       ATAATCTAGAA
                                ||||       ||||||||||||
                                ACTT       TATTAGATCTT
                                  AGT_____
GAM1113 ASK      5'  ATCTTCAACCGCCGCAGCC    22015       TCA_
                                GGCTGC    GTTGAAGAT
                                ||||||    |||||||||
                                CCGACG    CAACTTCTA
                                   CCGC
GAM1113 BACH2    3'  AGACCTGTTTGGCAGCCAT    41483        T   TTGA  A
                                ATGGCTGC CAG    AG TCT
                                |||||||| |||    || |||
                                TACCGACG GTT    TC AGA
                                    _   TG__  C
GAM1113 EVPL     3'  AGACCAGGACAGCAGCCA     8802         CA   GAAGA
                                TGGCTGCT  GTT    TCT
                                ||||||||  |||    |||
                                ACCGACGA  CAG    AGA
                                    __   GACC_
GAM1113 MAN1A1   3'  AGATCTTCTGTGACAGCC    91901       C   GTT
                                GGCTG TCA   GAAGATCT
                                ||||| |||   ||||||||
                                CCGAC AGT   CTTCTAGA
                                   _   GT_
GAM1113 MAZ      3'  AGAGGACACGAGCAGCCA     73386         A  TGAAGA
                                TGGCTGCTC GT     TCT
                                |||||||| ||     |||
                                ACCGACGAG CA     AGA
                                    _  CAGG__
GAM1113 MYLK2    3'  AGATCCCCAGGGCAGCC      52417        AGT  AA
                                GGCTGCTC   TG  GATCT
                                ||||||||   ||  |||||
                                CCGACGGG   AC  CTAGA
                                    ___  CC
GAM1113 CBX1     3'  AGATCTTCAAAGAGCA       22326       AG
                                TGCTC  TTGAAGATCT
                                |||||  ||||||||||
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                                ACGAG  AACTTCTAGA
                                  A_
GAM1113 FLJ22087 3' TAGAATGACTTAGCAGCCAT  41959       C    AAGA
                                ATGGCTGCT AGTTG   TCTA
                                ||||||||| |||||   ||||
                                TACCGACGA TCAGT   AGAT
                                    T    A___
GAM1113 HT007    5' AGATGTCAATAAGCAGCCA   37486      CA    AG
                                TGGCTGCT  GTTGA  ATCT
                                ||||||||  |||||  ||||
                                ACCGACGA  TAACT  TAGA
                                    A_    G_
GAM1113 KIAA0237 3' AGGGGCAACTGAGCATCCA   28521    C       AAGA
                                TGG TGCTCAGTTG   TCT
                                ||| ||||||||||   |||
                                ACC ACGAGTCAAC   GGA
                                  T       GG__
GAM1113 KIAA1046 3' ATCTTCAACTCTTGCCCCAT  29991    CT  TC_
                                ATGG  GC   AGTTGAAGAT
                                ||||  ||   ||||||||||
                                TACC  CG   TCAACTTCTA
                                  C_  TTC
GAM1113 KIF13B   3' AGACCCTCACAGCAGCCA    30903      CAGT   AGA
                                TGGCTGCT   TGA   TCT
                                ||||||||   |||   |||
                                ACCGACGA   ACT   AGA
                                    C___   CCC
GAM1113 KIF13B   3' AGACCCTCACAGCAGCCA    82819      CAGT   AGA
                                TGGCTGCT   TGA   TCT
                                ||||||||   |||   |||
                                ACCGACGA   ACT   AGA
                                    C___   CCC
GAM1113 PRO0097  3' AGACATTCCCAAAGCAGCCAT 26097       CAGTT   GA
                                ATGGCTGCT    GAA  TCT
                                |||||||||    |||  |||
                                TACCGACGA    CTT  AGA
                                    AACC_   AC
GAM1113 PRO2730  3' ATCTGCAACCAGAGCAGCCA  47410       A_   A
                                TGGCTGCTC  GTTG AGAT
                                |||||||||  |||| ||||
                                ACCGACGAG  CAAC TCTA
                                    AC    G
GAM1113 SEMA4G   5' AGACCCACATGTGAGCAGCC  94670       GT  AAGA
                                GGCTGCTCA  TG    TCT
                                |||||||||  ||    |||
                                CCGACGAGT  AC    AGA
                                    GT  ACCC
GAM1113 WIRE     3' TAGATCTTCCTTGGCAGCCA  78307       C  TT
                                TGGCTGCT AG  GAAGATCTA
                                |||||||| ||  |||||||||
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                                ACCGACGG TC  CTTCTAGAT
                                    T  __
GAM1113  ZFP106   3'  AGACCGATGGCAGCCAT    42461        CA   AAGA
                                ATGGCTGCT  GTTG   TCT
                                |||||||||  ||||   |||
                                TACCGACGG  TAGC   AGA
                                    __   C___
GAM1113  LOC142941 3'  AGAATACTATGCAGCCAT    82881        TC   TGAAGA
                                ATGGCTGC  AGT    TCT
                                ||||||||  |||    |||
                                TACCGACG  TCA    AGA
                                    TA  TA____
GAM1113  LOC143173 5'  ATCTTCAACCGCTGCAGCC   60374       TCA_
                                GGCTGC   GTTGAAGAT
                                ||||||   |||||||||
                                CCGACG   CAACTTCTA
                                   TCGC
GAM1113  LOC153338 3'  AGATCTTCTCTCAGCACCA   85992    C   C  TT
                                TGG TGCT AG  GAAGATCT
                                ||| |||| ||  ||||||||
                                ACC ACGA TC  CTTCTAGA
                                  _   C  T_
GAM1113  LOC196027 3'  AGATCTGGAAGCAGCCAT    87546        CAGTTGA
                                ATGGCTGCT     AGATCT
                                |||||||||     ||||||
                                TACCGACGA     TCTAGA
                                    AGG____
GAM1113  LOC221510 3'  AGACCTTCAACTTCCA     91054    CTGCTC      A
                                TGG     AGTTGAAG TCT
                                |||     |||||||| |||
                                ACC     TCAACTTC AGA
                                  T_____       C
GAM1113  LOC257428 5'  AGATCTTCAACCATGTTAACAT 94276    GCT  TCA
                                ATG   GC   GTTGAAGATCT
                                |||   ||   ||||||||||
                                TAC   TG   CAACTTCTAGA
                                  AAT  TAC
GAM1114  CDS2     3'  ATCCCTGCTTGGAGCTGCA   13775        C   A_
                                TGCAGCTCC AGCA  GAT
                                ||||||||| ||||  |||
                                ACGTCGAGG TCGT  CTA
                                    T   CC
GAM1114  FBXL11   3'  GATTGATCTGAGGGGAAAGCA  24572    AGC   AG  A
                                TGC   TCCC  CA GATCAATC
                                |||   ||||  || ||||||||
                                ACG   AGGG  GT CTAGTTAG
                                  AA_   GA  _
GAM1114  FETUB    3'  GACTGACCCTCGGCTTGGGCTG 26880      T  C   A_  A_   A
            CA                    TGCAGC CC AGC  AG  TCA TC
                                ||||||| || |||  ||  ||| ||
```

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                                ACGTCG GG TCG  TC  AGT AG
                                   _ T   GC  CC   C
GAM1114 FLOT2    3'  TCCTGCTAGGGCTGCA     15577       T  C    A
                                TGCAGC CC AGCA GA
                                |||||| || |||| ||
                                ACGTCG GG TCGT CT
                                   _ A   C
GAM1114 LDB3     3'  GATTTGTCAGGAGCTGCA    76407        CA   A
                                TGCAGCTCC  GCA GATC
                                |||||||||  ||| ||||
                                ACGTCGAGG  TGT TTAG
                                     AC  _
GAM1114 SLC14A1  3'  ATTGATTTTGTAAATGCCACA  31836    CA  TCCCA
                                TG  GC    GCAAGATCAAT
                                ||  ||    ||||||||||
                                AC  CG    TGTTTTAGTTA
                                 AC  TAAA_
GAM1114 SMARCD2  3'  GGTCCTTGCTGGGGCCGCA   11826     A  T      _
                                TGC GC CCCAGCAAG ATC
                                ||| || ||||||||| |||
                                ACG CG GGGTCGTTC TGG
                                  C _       C
GAM1114 TIC      3'  GGTCTGCCTGGCAGGAGCCACA 24938    CA    ___   CA
                                TG  GCTCC   CAG  AGATC
                                ||  |||||   |||  |||||
                                AC  CGAGG   GTC  TCTGG
                                 AC    ACG   CG
GAM1114 TSGA10   5'  GATTGATCTCATTTGCCAGC   47499    CC   CA_
                                GCT  CAG   AGATCAATC
                                |||  |||   |||||||||
                                CGA  GTT   TCTAGTTAG
                                  CC   TAC
GAM1114 VCL      3'  GAGTTGCTGGGAGCTG      25736          GA
                                CAGCTCCCAGCAA  TC
                                ||||||||||||  ||
                                GTCGAGGGTCGTT  AG
                                       G_
GAM1114 VCL      3'  GAGTTGCTGGGAGCTG      12577          GA
                                CAGCTCCCAGCAA  TC
                                ||||||||||||  ||
                                GTCGAGGGTCGTT  AG
                                       G_
GAM1114 BC008967 5'  GGACTTGAAGCAGGAGCTGCA  60766        CA  AAGA   _
                                TGCAGCTCC  GC   TCAA TCC
                                |||||||||  ||   |||| |||
                                ACGTCGAGG  CG   AGTT AGG
                                     A_  A___    C
GAM1114 CHST3    3'  GAGCTTACAAGGAGCTGCA   14976        CAGC   A
                                TGCAGCTCC    AAG TC
                                |||||||||    ||| ||
```

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                                ACGTCGAGG   TTC AG
                                     AACA  G
GAM1114  FLJ10211  5'  TCTGCAGGAGCTGCA      35904        CA  A
                                TGCAGCTCC  GCA GA
                                |||||||||  ||| ||
                                ACGTCGAGG  CGT CT
                                     A_  _
GAM1114  FLJ12750  3'  GGATTGAGGGACGGGGCTGCA  45123        CAGCAAGA
                                TGCAGCTCC      TCAATCC
                                |||||||||      |||||||
                                ACGTCGGGG      AGTTAGG
                                     CAGGG___
GAM1114  FLJ14927  5'  TCCTGCCGGGAGCTGC     51705        A  A
                                GCAGCTCCC GCA GA
                                ||||||||| ||| ||
                                CGTCGAGGG CGT CT
                                     C  C
GAM1114  FLJ14957  3'  TCCTGCAGGAGCTGCA     51762        CA  A
                                TGCAGCTCC  GCA GA
                                |||||||||  ||| ||
                                ACGTCGAGG  CGT CT
                                     A_  C
GAM1114  FLJ20051  3'  ATTGTGCTGGGGCTGCA    38850      T     A
                                TGCAGC CCCAGCA GAT
                                ||||||  ||||||| |||
                                ACGTCG GGGTCGT TTA
                                   _     G
GAM1114  GTF2A1    5'  GGACCGGACGGCTGGAGCTGCA 31831        C  AAGA  AA_
                                TGCAGCTCC AGC   TC  TCC
                                ||||||||| |||   ||  |||
                                ACGTCGAGG TCG   AG  AGG
                                     _  GC__  GCC
GAM1114  KIAA0014  3'  GACTGGCCAGGGGCTGCA    27843        CA  A  A
                                TGCAGCTCC  GC AG TC
                                |||||||||  || || ||
                                ACGTCGGGG  CG TC AG
                                     AC  G  _
GAM1114  KIAA1069  3'  GACTGGGAAACACTGAAGAGCT 67936       C_  CAAGA_  A
            GCA                    TGCAGCTC  CAG     TCA TC
                                |||||||  |||     ||| ||
                                ACGTCGAG  GTC     GGT AG
                                     AA  ACAAAG  C
GAM1114  KIAA1136  3'  GGATTGATCCTGCTAGAGATGT 91320    G  CC   A
                                GCA CTC  AGCA GATCAATCC
                                ||| |||  |||| |||||||||
                                TGT GAG  TCGT CTAGTTAGG
                                  A  A_   C
GAM1114  KIAA1573  3'  TGAGATCTGGGAGCTACA   62690   C      CAAGA
                                TG AGCTCCCAG    TCA
                                || |||||||||    |||
```

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                                AC TCGAGGGTC    AGT
                                 A       TAG__
GAM1114 KIAA1775 3' GATTGATCTTGCCAAGAGT   52381     CCA
                                GCTC   GCAAGATCAATC
                                ||||   ||||||||||||
                                TGAG   CGTTCTAGTTAG
                                  AAC
GAM1114 KIAA1863 3' GAGCGGCTCCGGGAGCTGCA  64870        __  AAGA
                                TGCAGCTCCC  AGC   TC
                                ||||||||||  |||   ||
                                ACGTCGAGGG  TCG   AG
                                      CC   GCG_
GAM1114 KIAA1979 3' ATTAATCTTGTTCATGCTGCA 88274      TCCC      C
                                TGCAGC   AGCAAGAT AAT
                                ||||||   |||||||| |||
                                ACGTCG   TTGTTCTA TTA
                                    TAC_      A
GAM1114 MGC16175 5' GGACCGAGCAGCTGGGGGCTGC 51300          AAGA  AA
             A                   TGCAGCTCCCAGC   TC  TCC
                                 ||||||||||||   ||  |||
                                 ACGTCGGGGGTCG   AG  AGG
                                       ACG_  CC
GAM1114 MGC23284 3' GATTGATGGGGAGAGC     58704    AG    AGCAAG
                                GC  CTCCC     ATCAATC
                                ||  |||||     |||||||
                                CG  GAGGG     TAGTTAG
                                 A_    G_____
GAM1114 MGC24447 5' GACTGACGTGTGAGCTGCA   56286       CCA   AGA   A
                                TGCAGCTC   GCA   TCA TC
                                ||||||||   |||   ||| ||
                                ACGTCGAG   TGT   AGT AG
                                     ___   GC_   C
GAM1114 MGC2550  3' CGGATTAATCCTGCTTGTGCTG 43959       A_______  C    III
             GGAAATGCA               CCCAGCA      GAT AATCC   G
                                ||||||||      ||| |||||   |
                                GGGTCGT      CTA TTAGG   C
                                    GTTCGTC   A    III
GAM1114 NPTXR    3' TGATGCAAGAGCTGCA     26652       CCA   AGA
                                TGCAGCTC   GCA   TCA
                                ||||||||   |||   |||
                                ACGTCGAG   CGT   AGT
                                     AA_   ___
GAM1114 NPTXR    3' TGATGCAAGAGCTGCA     54188       CCA   AGA
                                TGCAGCTC   GCA   TCA
                                ||||||||   |||   |||
                                ACGTCGAG   CGT   AGT
                                     AA_   ___
GAM1114 RODH-4   5' GTCACACTGGGAGCTGCA    13538          CAA
                                TGCAGCTCCCAG   GAT
                                ||||||||||||   |||
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                                ACGTCGAGGGTC  CTG
                                      ACA
GAM1114  TSPAN-5  3'  TGATCTTCGAGCTGCA     19159        CCAGC
                                TGCAGCTC    AAGATCA
                                ||||||||    |||||||
                                ACGTCGAG    TTCTAGT
                                    C____
GAM1114  LOC112473 5'  GATCGCTAGGGCTGCA     73201       T  C   AA
                                TGCAGC CC AGC  GATC
                                |||||| || |||  ||||
                                ACGTCG GG TCG  CTAG
                                   _ A  __
GAM1114  LOC116236 3'  GGATTACTCCAGAGAGCTGCA  73815        CCAGCAA  TC
                                TGCAGCTC      GA  AATCC
                                ||||||||      ||  |||||
                                ACGTCGAG      CT  TTAGG
                                    AGAC___  CA
GAM1114  LOC126823 5'  ATCTCTGACCGAGAGCTGCA   74573        CCAG_ _
                                TGCAGCTC    CA AGAT
                                ||||||||    || ||||
                                ACGTCGAG    GT TCTA
                                    AGCCA  C
GAM1114  LOC139728 5'  GGATTGACATAGAGAGCTGCA  75386        CCAGCAAGA
                                TGCAGCTC       TCAATCC
                                ||||||||       |||||||
                                ACGTCGAG       AGTTAGG
                                    AGATAC___
GAM1114  LOC146958 3'  GATCAAGAGGTTGAAGCTGCA  83881       CC    AA___
                                TGCAGCT  CAGC    GATC
                                |||||||  ||||    ||||
                                ACGTCGA  GTTG    CTAG
                                   A_   GAGAA
GAM1114  LOC148710 3'  GGACCTTTGTGCTGGGAACTG  84197     C       AGATCAA
                                CAG TCCCAGCA      TCC
                                ||| ||||||||      |||
                                GTC AGGGTCGT      AGG
                                  A       GTTTCC_
GAM1114  LOC149501 3'  GATCAAGAATGAGGAGCTGCA  75275         _  GCAA_
                                TGCAGCTCC CA    GATC
                                |||||||||  ||    ||||
                                ACGTCGAGG GT    CTAG
                                    A  AAGAA
GAM1114  LOC149722 5'  GATGGCCCGGGAGCTGCA    84600         A_  AAG
                                TGCAGCTCCC  GC   ATC
                                ||||||||||  ||   |||
                                ACGTCGAGGG  CG   TAG
                                    CC  G__
GAM1114  LOC150384 5'  GACTCATTGCCGGAGCTGCA   85035         CA   _ _
                                TGCAGCTCC  GCAA GA TC
                                |||||||||  |||| || ||
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                                ACGTCGAGG  CGTT CT AG
                                     C_    A  C
GAM1114  LOC197202 5'  GATCGCTAGGGCTGCA      87958       T  C   AA
                                TGCAGC CC AGC  GATC
                                |||||| || |||  ||||
                                ACGTCG GG TCG  CTAG
                                   _  A   __
GAM1114  LOC201685 3'  GATCACCTGGGGGCCGCA    90243     A       CAA
                                TGC GCTCCCAG   GATC
                                ||| ||||||||   ||||
                                ACG CGGGGGTC   CTAG
                                  C       CA_
GAM1114  LOC221174 5'  ATTGATTTTTCAGAAGCTG   93499       CCCAGC
                                CAGCT     AAGATCAAT
                                |||||     |||||||||
                                GTCGA     TTTTAGTTA
                                   AGACT_
GAM1114  LOC221496 5'  GAACTGCGGCGGGAGCTGCA  92001          A__   A A
                                TGCAGCTCCC   GCA G TC
                                ||||||||||   ||| | ||
                                ACGTCGAGGG   CGT C AG
                                      CGG   _ A
GAM1114  LOC222031 5'  GTCCTACTGGGAGCTCA     94028    C       CAA
                                TG AGCTCCCAG   GAT
                                || |||||||||   |||
                                AC TCGAGGGTC   CTG
                                 _       ATC
GAM1114  LOC254013 5'  GATCAAGTTGGGAGACACA   94878    CAG      AA
                                TG   CTCCCAGC  GATC
                                ||   ||||||||  ||||
                                AC   GAGGGTTG  CTAG
                                  ACA       AA
GAM1114  LOC255452 3'  GGCCTTCCTCTGAGAGCTGCA 97541        C   C__   AT
                                TGCAGCTC CAG   AAG  C
                                |||||||| |||   |||  |
                                ACGTCGAG GTC   TTC  G
                                     A   TCC   CG
GAM1114  LOC90133  3'  GATCAAGTATGTGGAGCTGCA 61604         _  _  AA
                                TGCAGCTCC CA GC  GATC
                                ||||||||| || ||  ||||
                                ACGTCGAGG GT TG  CTAG
                                      T  A  AA
GAM1114  LOC90148  3'  TCTTGCTGAGAATGCA      61667      GC  C
                                TGCA  TC CAGCAAGA
                                ||||  || ||||||||
                                ACGT  AG GTCGTTCT
                                  A_  A
GAM1115  ABCD1     3'  GCCCCTGGCACTGCAGGTG   3464     G       GAA
                                CA CTGCAGTGT   AGGGGC
                                || |||||||||   ||||||
```

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                                GT GACGTCACG   TCCCCG
                                 G       G__
GAM1115 ABR     3' GCCCTAACGCTGCAGC     6574         GAAA
                                GCTGCAGTGT   GGGGC
                                ||||||||||   |||||
                                CGACGTCGCA   TCCCG
                                     A___
GAM1115 ABR     3' GCCCTAACGCTGCAGC     41726        GAAA
                                GCTGCAGTGT   GGGGC
                                ||||||||||   |||||
                                CGACGTCGCA   TCCCG
                                     A___
GAM1115 ACTR1B  3' GCCCCTTTCACACTCTG    70821    CTGC
                                CAG   AGTGTGAAAGGGGC
                                |||   ||||||||||||||
                                GTC   TCACACTTTCCCCG

                                 _____
GAM1115 AR      5' GCTTCAGCACTGCAGC     3494         GAAA
                                GCTGCAGTGT   GGGGC
                                ||||||||||   |||||
                                CGACGTCACG   CTTCG
                                     A___
GAM1115 ARHA    3' GCCCAAGTTCATGCAGCTG   70696       GTG   AG_
                                CAGCTGCA  TGAA  GGGC
                                ||||||||  ||||  ||||
                                GTCGACGT  ACTT  CCCG
                                    ___   GAA
GAM1115 ARHGAP6 5' CCCCACACTGCAGC       6760         AAA
                                GCTGCAGTGTG  GGG
                                ||||||||||   |||
                                CGACGTCACAC  CCC

                                    ___
GAM1115 ARHGAP6 5' CCCCACACTGCAGC       20404        AAA
                                GCTGCAGTGTG  GGG
                                ||||||||||   |||
                                CGACGTCACAC  CCC

                                    ___
GAM1115 CACNA2D2 3' GCCCCTTTCAGGCCTACAGC  20087    CA_ G
                                GCTG  GT TGAAAGGGGC
                                ||||  || ||||||||||
                                CGAC  CG ACTTTCCCCG
                                  ATC  G
GAM1115 CASQ2   3' CCCCTTCTCTGTAGCTG    6935        TGTGA
                                CAGCTGCAG    AAGGGG
                                |||||||||    ||||||
                                GTCGATGTC    TTCCCC
                                     TC___
GAM1115 CLASP1  3' CCCTGACAGCTGCAGCTG   65299        GTGAA
                                CAGCTGCAGT    AGGG
                                ||||||||||    ||||
```

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                                GTCGACGTCG    TCCC
                                     ACAG_
GAM1115 CLASP1   3' GCCCCCTAGACCCTGACAGCTG 65303      _  T GAAA
                                CAGCTG CAG GT   GGGGC
                                |||||| ||| ||   |||||
                                GTCGAC GTC CA   CCCCG
                                   A  C GATC
GAM1115 COL1A1   3' CCCTCCTCCACAGCTG     3604      GCA  T AA
                                CAGCT  GTG GA GGGG
                                |||||  ||| ||  ||||
                                GTCGA  CAC CT TCCC
                                   ___  _ CC
GAM1115 COX10    3' GCCCCTTTCCCTCCGCTGC   7121       T___
                                GCAGTG   GAAAGGGGC
                                ||||||   |||||||||
                                CGTCGC   CTTTCCCCG
                                   CTCC
GAM1115 CPE     5' GCCCCCTGCCTCGCAGT    8526      _ T  AAA
                                GCTGC AG GTG  GGGGC
                                ||||| || |||  |||||
                                TGACG TC CGT  CCCCG
                                  C _  C__
GAM1115 DLK1     5' CCCCTTTCGCGTCCGCA    13841    AG_
                                TGC  TGTGAAAGGGG
                                |||  ||||||||||
                                ACG  GCGCTTTCCCC
                                 CCT
GAM1115 DMPK     3' GCCCCCCTCCTCACTTGCGCTG 15324    T  _  T_ AA
                                CAGC GCA GTG  GA  GGGGC
                                |||| ||| |||  ||  |||||
                                GTCG CGT CAC  CT  CCCCG
                                  _  T  TC  CC
GAM1115 ED1      5' CCCCTCGGAGTAGAGCTG    7365      __ AG  TGAA
                                CAGCT  GC  TG   AGGGG
                                |||||  ||  ||   |||||
                                GTCGA  TG  GC   TCCCC
                                  GA  AG  ____
GAM1115 ENSA     3' GCCCCTTCCTGCTTTTGCAGC  15426      T_  A_
                                GCTGCAG  GTG  AAGGGGC
                                |||||||  |||  |||||||
                                CGACGTT  CGT  TTCCCCG
                                   TT   CC
GAM1115 EPHB2    3' CCCCCAGGTCTGCAGCT     15443       _ G  AAA
                                AGCTGCAG T TG   GGGG
                                |||||||| | ||   ||||
                                TCGACGTC G AC   CCCC
                                   T G  ___
GAM1115 EPHB2    3' CCCCCAGGTCTGCAGCT     33886       _ G  AAA
                                AGCTGCAG T TG   GGGG
                                |||||||| | ||   ||||
```

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                                TCGACGTC G AC   CCCC
                                   T G  ___
GAM1115  FGFR1    3'  CCCCACACTGCGCTG      43638     T      AAA
                                CAGC GCAGTGTG   GGG
                                |||| ||||||||   |||
                                GTCG CGTCACAC   CCC
                                  _      ___
GAM1115  G6PT1    5'  CCCCTTTCTATCGCGC      7597     T  A   T
                                GC GC GTG GAAAGGGG
                                || || ||| ||||||||
                                CG CG TAT CTTTCCCC
                                 _ C  _
GAM1115  GABRE    3'  CCCCTTTCTCTGCAG       17109       TGT
                                CTGCAG   GAAAGGGG
                                ||||||   ||||||||
                                GACGTC   CTTTCCCC
                                   T__
GAM1115  GABRE    3'  CCCCTTTCTCTGCAG       41773       TGT
                                CTGCAG   GAAAGGGG
                                ||||||   ||||||||
                                GACGTC   CTTTCCCC
                                   T__
GAM1115  GABRE    3'  CCCCTTTCTCTGCAG       41782       TGT
                                CTGCAG   GAAAGGGG
                                ||||||   ||||||||
                                GACGTC   CTTTCCCC
                                   T__
GAM1115  GABRE    3'  CCCCTTTCTCTGCAG       41803       TGT
                                CTGCAG   GAAAGGGG
                                ||||||   ||||||||
                                GACGTC   CTTTCCCC
                                   T__
GAM1115  GNA11    5'  GCCCCCACACCGCAGC      76102      A     AAA
                                GCTGC GTGTG   GGGGC
                                ||||| |||||   |||||
                                CGACG CACAC   CCCCG
                                   C    ___
GAM1115  GNAI1    5'  GCCCCTTTGCGGACAGC      9054      CAG   G
                                GCTG   TGT AAAGGGGC
                                ||||   ||| ||||||||
                                CGAC   GCG TTTCCCCG
                                  AG_  _
GAM1115  GRB10    3'  CCCCTGCTGCTGCAGT      17975         TGAA
                                GCTGCAGTG    AGGGG
                                |||||||||    |||||
                                TGACGTCGT    TCCCC
                                     CG__
GAM1115  HDAC4    3'  TTTTTCCACTGCAGC       20125         T
                                GCTGCAGTG GAAAGG
                                ||||||||| ||||||
```

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                                CGACGTCAC CTTTTT
                                        _
GAM1115 HIRA    3' GCCCCTGCTGCTGCAGGC   12437   _     TGAA
                                GC TGCAGTG   AGGGGC
                                || |||||||   ||||||
                                CG ACGTCGT   TCCCCG
                                 G      CG__
GAM1115 HIS1    5' CCCCTTGGACCCGCTAGCTG  21314      _ AGT  GA
                                CAGCT GC   GT  AAGGGG
                                ||||| ||   ||  ||||||
                                GTCGA CG   CA  TTCCCC
                                   T  CC_  GG
GAM1115 HLA-E   3' CCCCTTCCTCACACTG     91022        __
                                CAGTGTGA  AAGGGG
                                ||||||||  ||||||
                                GTCACACT  TTCCCC
                                     CC
GAM1115 HMG20A  3' GCCCCACACCACTGCAGGC  36542   _     _ AAA
                                GC TGCAGTG TG   GGGGC
                                || ||||||| ||   |||||
                                CG ACGTCAC AC   CCCCG
                                 G      C  A__
GAM1115 HRC     3' CCCCTTTCCACGAGCT     9280      GCA   T
                                AGCT   GTG GAAAGGGG
                                ||||   ||| ||||||||
                                TCGA   CAC CTTTCCCC
                                  G__   _
GAM1115 IHPK1   3' CCCCTTCCTCTCCACTGCAGGC 95757   _     T _____
                                GC TGCAGTG GA    AAGGGG
                                || ||||||| ||    ||||||
                                CG ACGTCAC CT    TTCCCC
                                 G      _ CTCC
GAM1115 IVD     3' CCCCTTTTCCTGCACCT    9461    C    TGT
                                AG TGCAG   GAAAGGGG
                                || |||||   ||||||||
                                TC ACGTC   TTTTCCCC
                                 C    C__
GAM1115 JUND    3' GCCCCTTTGTACACCGCGC   18085   T  A   _
                                GC GC GTGTG AAAGGGGC
                                || || ||||| ||||||||
                                CG CG CACAT TTTCCCCG
                                 _ C    G
GAM1115 KCND2   5' CTGTCACACTGCACCTG    24397    C       A
                                CAG TGCAGTGTGA AG
                                ||| |||||||||| ||
                                GTC ACGTCACACT TC
                                  C        G
GAM1115 KLHL3   3' GCCCCTCATGTTCAGCTG   87458      C  TG   AA
                                CAGCTG AG  TGA  GGGGC
                                |||||| ||  |||  |||||
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                                GTCGAC TT  ACT  CCCCG
                                   _ GT  __
GAM1115 LARS2    3' CCCCACCCACACTGCAG     31054         AAA
                                CTGCAGTGTG  GGGG
                                ||||||||||  ||||
                                GACGTCACAC  CCCC
                                     CCA
GAM1115 LIMK1    3' GCCCCTTTCCACACGCCGCTG 33648     T  A    _
                                CAGC GC GTGTG AAAGGGGC
                                |||| || ||||| ||||||||
                                GTCG CG CACAC TTTCCCCG
                                  C _    C
GAM1115 LIMK1    3' GCCCCTTTCCACACGCCGCTG  9786      T  A    _
                                CAGC GC GTGTG AAAGGGGC
                                |||| || ||||| ||||||||
                                GTCG CG CACAC TTTCCCCG
                                  C _    C
GAM1115 MAP3K8   5' GCCCCTGACACTGCACTG    17790     C      GAA
                                CAG TGCAGTGT  AGGGGC
                                ||| ||||||||  ||||||
                                GTC ACGTCACA  TCCCCG
                                  _      G__
GAM1115 MAT1A    3' CCCCTTTCACAGGCA      90830     AG
                                TGC  TGTGAAAGGGG
                                |||  ||||||||||
                                ACG  ACACTTTCCCC
                                  G_
GAM1115 MSF      3' CCCCTTCGACATGCTGC     88080        A__
                                GCAGTGTG  AAGGGG
                                ||||||||  ||||||
                                CGTCGTAC  TTCCCC
                                     AGC
GAM1115 MVK      3' GCCCACGACACTGCAGC     60651         GAAAG
                                GCTGCAGTGT   GGGC
                                ||||||||||   ||||
                                CGACGTCACA   CCCG
                                     GCA__
GAM1115 NAP1L4   3' CCCCTCCTGCAGTTG      19920         TGTGAA
                                CAGCTGCAG    AGGGG
                                |||||||||    |||||
                                GTTGACGTC    TCCCC
                                     C_____
GAM1115 NGFR     3' CCCCTTCTCCCACACTGC    10223        A___
                                GCAGTGTG   AAGGGG
                                ||||||||   ||||||
                                CGTCACAC   TTCCCC
                                     CCTC
GAM1115 NKX3A    3' CTCCACACTGCTGCT      20502     T      AAA
                                AGC GCAGTGTG  GGG
                                ||| ||||||||  |||
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```
                                TCG CGTCACAC   CTC
                                  T      ___
GAM1115  OSCAR    3'  GCCCCAGGAGCACTGCAGC   55373         GAAA
                                GCTGCAGTGT   GGGGC
                                ||||||||||   |||||
                                CGACGTCACG   CCCCG
                                     AGGA
GAM1115  OSCAR    3'  GCCCCAGGAGCACTGCAGC   55666         GAAA
                                GCTGCAGTGT   GGGGC
                                ||||||||||   |||||
                                CGACGTCACG   CCCCG
                                     AGGA
GAM1115  OSCAR    3'  GCCCCAGGAGCACTGCAGC   55670         GAAA
                                GCTGCAGTGT   GGGGC
                                ||||||||||   |||||
                                CGACGTCACG   CCCCG
                                     AGGA
GAM1115  PGAM1    3'  GCCCCTCCCACCTGCA     76275      T  AA
                                TGCAG GTG  AGGGGC
                                ||||| |||  ||||||
                                ACGTC CAC  TCCCCG
                                   _  CC
GAM1115  PLD1     5'  GCCCCTTCGCCCTGCAGC    10625       T   A
                                GCTGCAG GTGAA GGGGC
                                ||||||| ||||| |||||
                                CGACGTC CGCTT CCCCG
                                    C   _
GAM1115  POLL     5'  GCCCCATCTCCCCGCAGCTG  25178       AGTGT  AA
                                CAGCTGC    GA  GGGGC
                                |||||||    ||  |||||
                                GTCGACG    CT  CCCCG
                                    CCCCT  A_
GAM1115  PPP1R2   3'  CTGTCACATGCAGCTG     20691       G   A
                                CAGCTGCA TGTGA AG
                                |||||||| ||||| ||
                                GTCGACGT ACACT TC
                                   _   G
GAM1115  RAB36    3'  CCTGGCACACTGCAGCTG    16955          AA
                                CAGCTGCAGTGTG  AGG
                                |||||||||||||  |||
                                GTCGACGTCACAC  TCC
                                      GG
GAM1115  RAD52    3'  GCCCTGGGACACCCACAGCTG 56197      CA_   GAAA
                                CAGCTG   GTGT   GGGGC
                                ||||||   ||||   |||||
                                GTCGAC   CACA   TCCCG
                                   ACC   GGG_
GAM1115  RAD52    3'  GCCCTGGGACACCCACAGCTG 56204      CA_   GAAA
                                CAGCTG   GTGT   GGGGC
                                ||||||   ||||   |||||
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                                GTCGAC  CACA   TCCCG
                                   ACC   GGG_
GAM1115 RAD52   3' GCCCTGGGACACCCACAGCTG 56213      CA_   GAAA
                                CAGCTG  GTGT   GGGGC
                                ||||||  ||||   |||||
                                GTCGAC  CACA   TCCCG
                                   ACC   GGG_
GAM1115 RAI3    3' CCCCTCTCTTCTTGCACTG   14283    C    TGT  A
                                CAG TGCAG  GA AGGGG
                                ||| |||||  || |||||
                                GTC ACGTT  CT TCCCC
                                  _    CTT  C
GAM1115 RHBG    3' GCCCCTTTCCACAGGCAGC   39901      A_   T
                                GCTGC  GTG GAAAGGGGC
                                |||||  ||| |||||||||
                                CGACG  CAC CTTTCCCCG
                                   GA  _
GAM1115 SLC2A4  3' TTCCTTTCCTCTGCAGC     6444        TGT
                                GCTGCAG  GAAAGGGG
                                |||||||  ||||||||
                                CGACGTC  CTTTCCTT
                                    TC_
GAM1115 SMURF1  3' GCCCCTTTCCCAGTGGCAGCT 92452       _ G  T
                                AGCTGC A TG GAAAGGGGC
                                |||||| | || |||||||||
                                TCGACG T AC CTTTCCCCG
                                   G G  C
GAM1115 SPOCK   3' GCCCCTTGGCTGCAGC     62818        GTGA
                                GCTGCAGT   AAGGGGC
                                ||||||||   |||||||
                                CGACGTCG   TTCCCCG
                                    G___
GAM1115 SRRM1   3' CCCCTGCAGCCATTGCAGCTG 19551          _ GAA
                                CAGCTGCAGTG T  AGGGG
                                |||||||||||| |  |||||
                                GTCGACGTTAC G  TCCCC
                                      C ACG
GAM1115 TARBP2  3' GCCCCCCCCATGGAACTGCAGC 56166        ___  AAA
                                GCTGCAGT  GTG  GGGGC
                                |||||||  |||  |||||
                                CGACGTCA  TAC  CCCCG
                                    AGG  CC_
GAM1115 TKTL1   3' GCCATCCCACCTGCAGCTG   24298        T  AAAGG
                                CAGCTGCAG GTG   GGC
                                ||||||||| |||   |||
                                GTCGACGTC CAC   CCG
                                    _  CCTA_
GAM1115 TNFRSF1A 5' GCCCCAGCACTGCCGCTG   6514      T     GAAA
                                CAGC GCAGTGT   GGGGC
                                |||| |||||||   |||||
```

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                                GTCG CGTCACG   CCCCG
                                  C      A___
GAM1115 UNRIP   5' GCCCGAGGCACTGCAGC    23201        GAAAG
                                GCTGCAGTGT    GGGC
                                ||||||||||    ||||
                                CGACGTCACG    CCCG
                                     GAG__
GAM1115 WNT3A   3' GCCCCCTTCTTTGCAGCTG   52433       TGT   A
                                CAGCTGCAG   GAA GGGGC
                                |||||||||   ||| |||||
                                GTCGACGTT   CTT CCCCG
                                     T__   C
GAM1115 WNT3A   3' GCCCCTTCCACGGGGGCTG   52434     GCA   T   A
                                CAGCT   GTG GAA GGGGC
                                |||||   ||| ||| |||||
                                GTCGG   CAC CTT CCCCG
                                   GGG   _   _
GAM1115 ZNF9    3' CCCCTTTCCGTGCCACTG    12772     CT   G  T
                                CAG  GCA TG GAAAGGGG
                                |||  ||| || ||||||||
                                GTC  CGT GC CTTTCCCC
                                 AC   _  _
GAM1115 AF9Q34  3' CCCCTCTGCCCCTGCAGCTG   50734        T_  GAA
                                CAGCTGCAG  GT   AGGGG
                                |||||||||  ||   |||||
                                GTCGACGTC  CG   TCCCC
                                     CC  TC_
GAM1115 APCL    3' CCCCTTTCAGGACACAGCGG   19668     A   ____
                                CTGC GTGT   GAAAGGGG
                                ||||| ||||   ||||||||
                                GGCG CACA   CTTTCCCC
                                  A    GGA
GAM1115 APELIN  3' GCCCCTTTACCTATGCTGCTG  33784     T   GTGTG
                                CAGC GCA    AAAGGGGC
                                |||| |||    ||||||||
                                GTCG CGT    TTTCCCCG
                                  T   ATCCA
GAM1115 ARHGAP4 3' GCCCCTTTTGGAGGCAGCTG   8020        AGTGT
                                CAGCTGC    GAAAGGGGC
                                |||||||    |||||||||
                                GTCGACG    TTTTCCCCG
                                    GAGG_
GAM1115 ARHGEF4 3' CCCCTCTTCAGGCTGC      52209      G   _
                                GCAGT TGAA AGGGG
                                ||||| |||| |||||
                                CGTCG ACTT TCCCC
                                  G   C
GAM1115 ASAH    3' CCGAACACTGCAGCTG      15049          GAAA
                                CAGCTGCAGTGT    GG
                                ||||||||||||   ||
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                                GTCGACGTCACA   CC
                                      AG__
GAM1115 BCL2L12  5' CCCCTTTCCCGTCAGCTG   56864      CAG  T
                                CAGCTG  TG GAAAGGGG
                                ||||||  || ||||||||
                                GTCGAC  GC CTTTCCCC
                                   T__  C
GAM1115 BICD2    3' CCGCACGCTGCAGCT      70390          AAAGG
                                AGCTGCAGTGTG    GG
                                ||||||||||||    ||
                                TCGACGTCGCAC    CC
                                      G____
GAM1115 BICD2    3' GCCCTGTCACACTGCAGC   70396          AA
                                GCTGCAGTGTGA  GGGGC
                                ||||||||||||  |||||
                                CGACGTCACACT  TCCCG
                                      G_
GAM1115 C11orf11 3' CCCCCAAGGCTGCAGC     93253        G_  AAA
                                GCTGCAGT  TG  GGGG
                                ||||||||  ||  ||||
                                CGACGTCG  AC  CCCC
                                    GA  ___
GAM1115 C16orf7  3' CCCATCGCTGCAGCTG     16938          TGAAAG
                                CAGCTGCAGTG    GGG
                                ||||||||||     |||
                                GTCGACGTCGC    CCC
                                      TA____
GAM1115 C1QTNF6  3' GCCTGCACCACTGCAGC    49147         _ AAAG
                                GCTGCAGTG TG   GGGC
                                ||||||||| ||   ||||
                                CGACGTCAC AC   TCCG
                                    C  G___
GAM1115 C20orf151 3' CCCCTGCTGTGCACTGCAGC  88699          AA__
                                GCTGCAGTGTG   AGGGG
                                ||||||||||   |||||
                                CGACGTCACGT   TCCCC
                                      GTCG
GAM1115 C20orf162 5' GCCCCCTGCCAGCTGCAGCTG 54602          GTGAAA
                                CAGCTGCAGT    GGGGC
                                |||||||||     |||||
                                GTCGACGTCG    CCCCG
                                      ACCGTC
GAM1115 CHIT1    3' GCCCCTTTCACTTGCA     12949      T
                                TGCAG GTGAAAGGGGC
                                ||||| ||||||||||
                                ACGTT CACTTTCCCCG
                                   _
GAM1115 CHST3    3' CCCCTTCACAGCATACACTG  14970    C___  AG    A
                                CAG   TGC  TGTGAA GGGG
                                |||   |||  |||||| ||||
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                                GTC    ACG  ACACTT CCCC
                                  ACAT  __    _
GAM1115  CHST8    5'  GCCCAGAAGCAGCTGCAGC   42438       _  GAAAG
                                GCTGCAG TGT    GGGC
                                ||||||| |||    ||||
                                CGACGTC ACG    CCCG
                                    G   AAGA_
GAM1115  DKFZP434C128 3'  CCCCAGTCTCCCTGCAGCTG   64845        TGT  AA
                                CAGCTGCAG   GA  GGGG
                                |||||||||   ||  ||||
                                GTCGACGTC   CT  CCCC
                                      CCT  GA
GAM1115  DKFZP434K1772 5'  CCCAGCACCGCCAGCTG    67710       _ A   GAAA
                                CAGCTG C GTGT   GGG
                                |||||| | ||||   |||
                                GTCGAC G CACG   CCC
                                   C C   A___
GAM1115  DKFZP586J0619 3'  GCCCCAGCATTGCAGC     81392         GAAA
                                GCTGCAGTGT   GGGGC
                                ||||||||||   |||||
                                CGACGTTACG   CCCCG
                                      A___
GAM1115  DKFZP586M1120 3'  CCCCTCCGCATTGCAGC    48454          AA
                                GCTGCAGTGTG  AGGGG
                                ||||||||||  |||||
                                CGACGTTACGC  TCCCC
                                       C_
GAM1115  DKFZP586M1120 3'  GCCCCCTGTGTTGCAGGC   48459   _    TG  AAA
                                GC TGCAG  TG   GGGGC
                                || |||||  ||   |||||
                                CG ACGTT  GT   CCCCG
                                 G    GT  C__
GAM1115  DKFZP727M111 5'  GCCCCAGCAGTGCAGCTG    31410        G   GAAA
                                CAGCTGCA TGT    GGGGC
                                |||||||| |||    |||||
                                GTCGACGT ACG    CCCCG
                                     G   A___
GAM1115  DKFZp762E1312 5'  GCCCCCGGATACTGCAGT    37285         GAAA
                                GCTGCAGTGT   GGGGC
                                ||||||||||   |||||
                                TGACGTCATA   CCCCG
                                      GGC_
GAM1115  DNAJC5   3'  CCCTTTCACGGCAGCTG     61450        AG
                                CAGCTGC  TGTGAAAGGG
                                |||||||  ||||||||||
                                GTCGACG  GCACTTTCCC
                                       __
GAM1115  EFA6R    3'  CCCCTCTCTAGGGTTGCAGTTG 30982         TGT__  A
                                CAGCTGCAG    GA AGGGG
                                |||||||||    || |||||
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                                GTTGACGTT    CT TCCCC
                                     GGGAT  C
GAM1115 ELF4    5' CCCCTATTTTACTGCAGCT   7430         T  A
                                AGCTGCAGTG GA AGGGG
                                |||||||||| || |||||
                                TCGACGTCAT TT TCCCC
                                     T  A
GAM1115 EPSIN   5' GCCCCTTGCTGCTGCAGC    25298        TGA
                                GCTGCAGTG   AAGGGGC
                                |||||||||   |||||||
                                CGACGTCGT   TTCCCCG
                                     CG_
GAM1115 FAM10A7  3' CCCCTCTCCCCCAAATGCAGCT 81244        GTGT___  A
           G                     CAGCTGCA      GA AGGGG
                                |||||||      || |||||
                                GTCGACGT      CT TCCCC
                                     AAACCCC  C
GAM1115 FATE    3' GCCCCTTTCATCTCCCAGC   52359     CAGT
                                GCTG   GTGAAAGGGGC
                                ||||   ||||||||||
                                CGAC   TACTTTCCCCG
                                  CCTC
GAM1115 FLJ10737 3' CCCCCTCCACGGCCTG     36521     CT  A   T  AA
                                CAG  GC GTG GA  GGGG
                                |||  || ||| ||  ||||
                                GTC  CG CAC CT  CCCC
                                  __  G   _  C_
GAM1115 FLJ10936 5' GCCCCTTTGCAGCCGCTG   36908     T  AG   G
                                CAGC GC  TGT AAAGGGGC
                                |||| ||  ||| ||||||||
                                GTCG CG  ACG TTTCCCCG
                                  C  __  _
GAM1115 FLJ11783 3' GCCCCTCCTTTCAAGGAGCTG  46031      GCAGTG   ___
                                CAGCT     TGAA   AGGGGC
                                |||||     ||||   ||||||
                                GTCGA     ACTT   TCCCCG
                                   GGA___    TCC
GAM1115 FLJ12650 3' GCCCCTTTCTACTCA      44527    C   T
                                TG AGTG GAAAGGGGC
                                || |||| |||||||||
                                AC TCAT CTTTCCCCG
                                  _   _
GAM1115 FLJ12921 3' CCCCTGTTTGCACTAAGC    45908    GC   TG  _
                                GCT  AGTG  AA AGGGG
                                |||  ||||  || |||||
                                CGA  TCAC  TT TCCCC
                                  A_   GT  G
GAM1115 FLJ13197 5' GCCCCCCCCCAACACCAGCGCTG 44854     T  A_   GAAA_
                                CAGC GC  GTGT    GGGGC
                                |||| ||  ||||    |||||
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                              GTCG CG  CACA    CCCCG
                                _ AC    ACCCC
GAM1115  FLJ14154  3' GCCCCTAATCACTGCAGT    45819        TGAA
                              GCTGCAGTG    AGGGGC
                              |||||||||    ||||||
                              TGACGTCAC    TCCCCG
                                   TAA_
GAM1115  FLJ14936  3' GCTCTCCCACACTGCGCT    50134    T      AAA
                              AGC GCAGTGTG   GGGGC
                              ||| ||||||||   |||||
                              TCG CGTCACAC   TCTCG
                                _      CC_
GAM1115  FLJ14957  3' GCCCCTGTTCCACAGC     51749    A  T  _
                              GC GTG GAA AGGGGC
                              || ||| ||| ||||||
                              CG CAC CTT TCCCCG
                               A  _  G
GAM1115  FLJ20040  3' GCCCCTCCCACTGCGGGCT   38631     _    T  AA
                              AGCT GCAGTG GA  GGGGC
                              |||| |||||| ||  |||||
                              TCGG CGTCAC CT  CCCCG
                                G     C __
GAM1115  FLJ20507  3' GCCCCCTTCACATTCA      35291    C      A
                              TG AGTGTGAA GGGGC
                              || ||||||||  |||||
                              AC TTACACTT CCCCG
                               _      C
GAM1115  FLJ20507  3' GCCCCTCCCTCAACTCTGCAGC 35292       TG_  A__
           T                   AGCTGCAG   TGA   AGGGGC
                              ||||||||   |||   ||||||
                              TCGACGTC   ACT   TCCCCG
                                   TCA   CCC
GAM1115  FLJ20507  3' GCCCCCTTCACATTCA      60226    C      A
                              TG AGTGTGAA GGGGC
                              || ||||||||  |||||
                              AC TTACACTT CCCCG
                               _      C
GAM1115  FLJ20507  3' GCCCCTCCCTCAACTCTGCAGC 60227       TG_  A__
           T                   AGCTGCAG   TGA   AGGGGC
                              |||||||   |||   ||||||
                              TCGACGTC   ACT   TCCCCG
                                   TCA   CCC
GAM1115  FLJ21865  3' GCCCAGGCCGCTGCAGCTG   42808        TGAAAG
                              CAGCTGCAGTG     GGGC
                              ||||||||||     ||||
                              GTCGACGTCGC     CCCG
                                    CGGA__
GAM1115  FLJ22169  3' CCCCTCACCCAGCTG      44001       CA   TGAA
                              CAGCTG  GTG    AGGGG
                              ||||||  |||    |||||
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                              GTCGAC  CAC   TCCCC
                                 C_  ____
GAM1115  FLJ23058  3'  CCCCTTTTCCACCAGC     45201     CA  TG
                              GCTG  GTG  AAAGGGG
                              ||||  |||  |||||||
                              CGAC  CAC  TTTCCCC
                                __  CT
GAM1115  GOLGA3   3'  CCCCCGGCTGCAGTTG     19713        GTGAAA
                              CAGCTGCAGT    GGGG
                              ||||||||||    ||||
                              GTTGACGTCG    CCCC
                                   GC____
GAM1115  H326     3'  GCCCCTTTCCCAGCAGCT   31706      AG  T
                              AGCTGC  TG GAAAGGGGC
                              ||||||  || |||||||||
                              TCGACG  AC CTTTCCCCG
                                 __  C
GAM1115  HGC6.1.1  5'  GCCCCCGTGACACTGCAGC   26830        GAAA
                              GCTGCAGTGT   GGGGC
                              ||||||||||   |||||
                              CGACGTCACA   CCCCG
                                   GTGC
GAM1115  HIF1AN   3'  CCCCTCTCAGGGCTGCAGCT   61971        G_  A
                              AGCTGCAGT  TGA AGGGG
                              |||||||||  ||| |||||
                              TCGACGTCG  ACT TCCCC
                                   GG  C
GAM1115  HRD1     3'  GCCCCTTTCCTCTGCAGCT   69558       TGT
                              AGCTGCAG   GAAAGGGGC
                              ||||||||   |||||||||
                              TCGACGTC   CTTTCCCCG
                                 TC_
GAM1115  HRD1     3'  GCGGAGTCACACTGCAGT    69559         AAGGG
                              GCTGCAGTGTGA    GC
                              ||||||||||||    ||
                              TGACGTCACACT    CG
                                    GAGG_
GAM1115  HRI      3'  GCCCCTTTCACACTGCAGCTG  26986
                              CAGCTGCAGTGTGAAAGGGGC
                              |||||||||||||||||||||
                              GTCGACGTCACACTTTCCCCG

GAM1115  HSPC166  3'  GCCCTTGCAGCTGCAGCTG   26368        GTGAA
                              CAGCTGCAGT    AGGGGC
                              ||||||||||    ||||||
                              GTCGACGTCG    TTCCCG
                                   ACG__
GAM1115  HSPC171  3'  GCCCCTGGTTCACTGCAG    26371        TGAA
                              CTGCAGTG   AGGGGC
                              ||||||||   ||||||
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                                GACGTCAC    TCCCCG
                                    TTGG
GAM1115  KCNH8    5'  TTTCACACCACGCTG       58262      _  CA
                                CAGC TG  GTGTGAAA
                                |||| ||  ||||||||
                                GTCG AC  CACACTTT
                                  C  __
GAM1115  KCNT1    3'  GCCCCCTTCTGCTGCCTGCGGC 61833          T  ____  A
              TG                  CAGCTGCAG GT    GAA GGGGC
                                |||||||||  ||    |||  |||||
                                GTCGGCGTC CG    CTT CCCCG
                                     _  TCGT   C
GAM1115  KIAA0064 3'  GCCCCTTCTCTTTTCAGAGCTG 28542       GCAGTGT  _
                                CAGCT       GA AAGGGGC
                                |||||       ||  |||||||
                                GTCGA       CT TTCCCCG
                                   GACTTTT  C
GAM1115  KIAA0169 3'  CCCCTCTCCACCAGC       72817      CA   T  A
                                GCTG  GTG GA AGGGG
                                ||||  |||  ||  |||||
                                CGAC  CAC CT TCCCC
                                  __   _  C
GAM1115  KIAA0296 3'  GCCCCTTTTCCCTCTGCTGC   28114    T    TGT_
                                GC GCAG    GAAAGGGGC
                                ||  ||||    |||||||||
                                CG CGTC    TTTTCCCCG
                                 T    TCCC
GAM1115  KIAA0329 3'  CCCCACACCGCACTG       29272     C   A    AAA
                                CAG TGC GTGTG   GGG
                                |||  |||  |||||   |||
                                GTC ACG CACAC   CCC
                                  _   C    ___
GAM1115  KIAA0367 3'  GCTACTTTCACACTACAGC    67300      C        GG
                                GCTG AGTGTGAAAG  GC
                                ||||  ||||||||||  ||
                                CGAC TCACACTTTC  CG
                                  A         AT
GAM1115  KIAA0542 3'  GCCCAGCAGAGACTGCAGCTG  66086          GTGAAAG
                                CAGCTGCAGT      GGGC
                                ||||||||||      ||||
                                GTCGACGTCA      CCCG
                                     GAGACGA
GAM1115  KIAA0562 3'  GCCCCTTCCACATCCATGTTG  28156      TGCA    A
                                CAGC    GTGTG AAGGGGC
                                ||||    |||||  |||||||
                                GTTG    TACAC TTCCCCG
                                  TACC    C
GAM1115  KIAA0657 5'  GCCCCCCCCACCGTTCGCCGCTG 72198      T  AGT__   AAA
                                CAGC GC    GTG   GGGGC
                                ||||  ||    |||   |||||
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                              GTCG CG    CAC   CCCCG
                                C  CTTGC   CC_
GAM1115 KIAA0779 3' CCCCAACCTCAGCTG      85724       C  T  GAAA
                              CAGCTG AG GT    GGGG
                              |||||| || ||    ||||
                              GTCGAC TC CA    CCCC
                                 _ _  A___
GAM1115 KIAA0789 3' GCCCCTTTCTATCCATGCTG  63684     TGCA   T
                              CAGC    GTG GAAAGGGGC
                              ||||    ||| |||||||||
                              GTCG    TAT CTTTCCCCG
                                TACC   _
GAM1115 KIAA0852 3' GCCCCTCAACCCTGTAGCTG  30079         T  GAA
                              CAGCTGCAG GT   AGGGGC
                              ||||||||| ||   ||||||
                              GTCGATGTC CA   TCCCCG
                                   C  AC_
GAM1115 KIAA0863 5' GCCCCTTTGTGACAACTG    95246     _  G__
                              CAGT GT   AAAGGGGC
                              |||| ||   ||||||||
                              GTCA CA   TTTCCCCG
                                A  GTG
GAM1115 KIAA0960 3' TTCCTCATCACTGCAGC     92658         _   AA
                              GCTGCAGTG TGA  GGGG
                              ||||||||| |||  ||||
                              CGACGTCAC ACT  CCTT
                                   T  __
GAM1115 KIAA1023 3' GCCCCTTTTTACACAGCTG   34262      GCA      _
                              CAGCT   GTGTGAAA GGGGC
                              |||||   |||||||| |||||
                              GTCGA   CACATTTT CCCCG
                                 ____       T
GAM1115 KIAA1054 3' GCCCCTCTCACAGACAG     68439     CAG    A
                              CTG   TGTGA AGGGGC
                              |||   ||||| ||||||
                              GAC   ACACT TCCCCG
                                AG_    C
GAM1115 KIAA1077 3' GCCCCGTCTCACTGCAG     72907        T  AA
                              CTGCAGTG GA  GGGGC
                              |||||||| ||  |||||
                              GACGTCAC CT  CCCCG
                                   T  G_
GAM1115 KIAA1130 3' CCCTATCCCTGCAGCTG     62414        TGT  A
                              CAGCTGCAG   GA AGGG
                              |||||||||   || ||||
                              GTCGACGTC   CT TCCC
                                   C__  A
GAM1115 KIAA1183 3' CCCCTCCCATAGGCTG      62528      GCAG   AA
                              CAGCT    TGTG  AGGGG
                              |||||    ||||  |||||
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                              GTCGG   ATAC  TCCCC
                                 ____   CC
GAM1115 KIAA1283 5' GCCCCTCTTTCACAACCAG   72059    CAG    __
                              CTG  TGTGAA  AGGGGC
                              |||  ||||||  ||||||
                              GAC  ACACTT  TCCCCG
                                CA_    TC
GAM1115 KIAA1297 5' GCCCCGCCCACTGCAGC    72180       TGAAA
                              GCTGCAGTG   GGGGC
                              |||||||||   |||||
                              CGACGTCAC   CCCCG
                                   CCG__
GAM1115 KIAA1441 3' GCCCCCTACCCCTGCAGT   88411      T_  AAA
                              GCTGCAG GTG  GGGGC
                              |||||||  |||  |||||
                              TGACGTC CAT  CCCCG
                                  CC  C__
GAM1115 KIAA1484 3' GCCCCCTGACACTGCAGC   69976       GAAA
                              GCTGCAGTGT   GGGGC
                              ||||||||||   |||||
                              CGACGTCACA   CCCCG
                                   GTC_
GAM1115 KIAA1614 3' GCCCTAGGCAACTGCAGCTG  70119       G  AAA
                              CAGCTGCAGT TG  GGGGC
                              |||||||||| ||  |||||
                              GTCGACGTCA AC  TCCCG
                                    _ GGA
GAM1115 KIAA1656 3' GCCCCTTTCACTAGGCA    65797    AGT
                              TGC  GTGAAAGGGGC
                              |||  ||||||||||
                              ACG  CACTTTCCCCG
                                GAT
GAM1115 KIAA1908 5' CCCCTTTTGCCAGCTG     73396      CAGT TG
                              CAGCTG   G  AAAGGGG
                              ||||||   |  |||||||
                              GTCGAC   C  TTTCCCC
                                 ____ GT
GAM1115 KIAA1949 3' GCCCCTTTGTTTACAGCT   92083     C  TGTG
                              AGCTG AG   AAAGGGGC
                              ||||| ||   ||||||||
                              TCGAC TT   TTTCCCCG
                                 A  TG__
GAM1115 KIAA1949 3' GCCCCTTTGTTTACAGCT   97751     C  TGTG
                              AGCTG AG   AAAGGGGC
                              ||||| ||   ||||||||
                              TCGAC TT   TTTCCCCG
                                 A  TG__
GAM1115 KIAA1949 3' GCCCCTTTGTTTACAGCT   97873     C  TGTG
                              AGCTG AG   AAAGGGGC
                              ||||| ||   ||||||||
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